



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:24 AM UTC

PDB ID : 8IZP / pdb_00008izp
EMDB ID : EMD-35867
Title : Multidrug resistance-associated protein 3
Authors : Yun, C.H.; Gao, H.M.
Deposited on : 2023-04-07
Resolution : 3.31 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

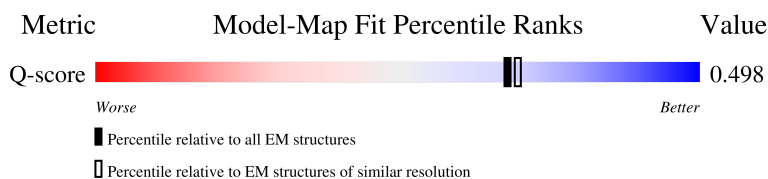
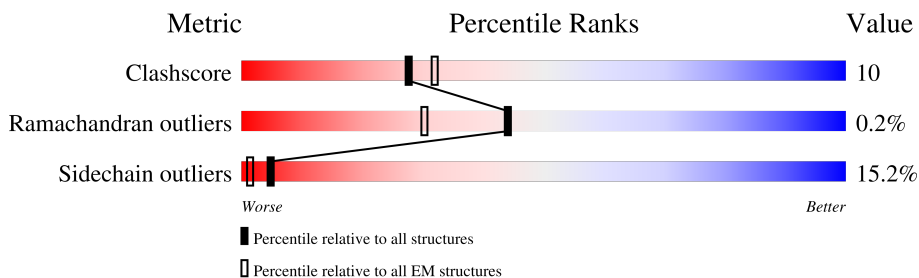
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.31 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	14550 (2.81 - 3.81)

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	1571	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9425 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 ATP-binding cassette sub-family C member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1210	Total	C	N	O	S	0	0
			9425	6084	1598	1695	48		

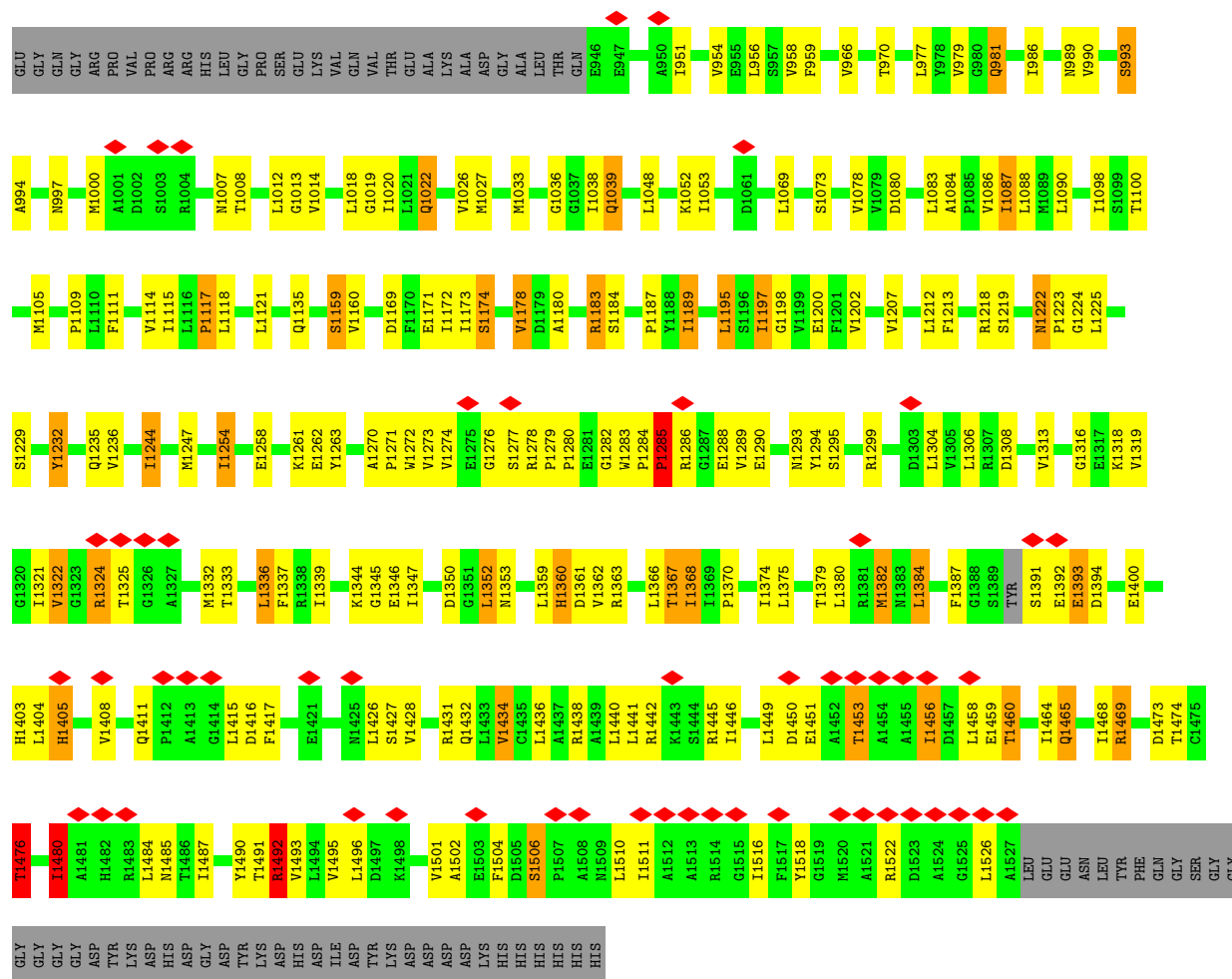
There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	344	GLY	ALA	conflict	UNP O15438
A	1362	VAL	LEU	conflict	UNP O15438
A	1528	LEU	-	expression tag	UNP O15438
A	1529	GLU	-	expression tag	UNP O15438
A	1530	GLU	-	expression tag	UNP O15438
A	1531	ASN	-	expression tag	UNP O15438
A	1532	LEU	-	expression tag	UNP O15438
A	1533	TYR	-	expression tag	UNP O15438
A	1534	PHE	-	expression tag	UNP O15438
A	1535	GLN	-	expression tag	UNP O15438
A	1536	GLY	-	expression tag	UNP O15438
A	1537	SER	-	expression tag	UNP O15438
A	1538	GLY	-	expression tag	UNP O15438
A	1539	GLY	-	expression tag	UNP O15438
A	1540	GLY	-	expression tag	UNP O15438
A	1541	GLY	-	expression tag	UNP O15438
A	1542	GLY	-	expression tag	UNP O15438
A	1543	GLY	-	expression tag	UNP O15438
A	1544	ASP	-	expression tag	UNP O15438
A	1545	TYR	-	expression tag	UNP O15438
A	1546	LYS	-	expression tag	UNP O15438
A	1547	ASP	-	expression tag	UNP O15438
A	1548	HIS	-	expression tag	UNP O15438
A	1549	ASP	-	expression tag	UNP O15438
A	1550	GLY	-	expression tag	UNP O15438
A	1551	ASP	-	expression tag	UNP O15438
A	1552	TYR	-	expression tag	UNP O15438
A	1553	LYS	-	expression tag	UNP O15438

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1554	ASP	-	expression tag	UNP O15438
A	1555	HIS	-	expression tag	UNP O15438
A	1556	ASP	-	expression tag	UNP O15438
A	1557	ILE	-	expression tag	UNP O15438
A	1558	ASP	-	expression tag	UNP O15438
A	1559	TYR	-	expression tag	UNP O15438
A	1560	LYS	-	expression tag	UNP O15438
A	1561	ASP	-	expression tag	UNP O15438
A	1562	ASP	-	expression tag	UNP O15438
A	1563	ASP	-	expression tag	UNP O15438
A	1564	ASP	-	expression tag	UNP O15438
A	1565	LYS	-	expression tag	UNP O15438
A	1566	HIS	-	expression tag	UNP O15438
A	1567	HIS	-	expression tag	UNP O15438
A	1568	HIS	-	expression tag	UNP O15438
A	1569	HIS	-	expression tag	UNP O15438
A	1570	HIS	-	expression tag	UNP O15438
A	1571	HIS	-	expression tag	UNP O15438



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	124494	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.269	Depositor
Minimum map value	-0.709	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.128	Depositor
Map size ($\text{\AA}$)	273.92, 273.92, 273.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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	A	1.11	14/9626 (0.1%)	1.53	97/13077 (0.7%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1187	PRO	C-O	-6.73	1.15	1.24
1	A	1223	PRO	C-O	-6.73	1.15	1.24
1	A	1012	LEU	C-O	6.52	1.31	1.24
1	A	329	PRO	C-O	-6.22	1.16	1.24
1	A	382	ARG	C-O	-5.66	1.17	1.24

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	664	GLY	N-CA-C	-10.05	101.10	115.27
1	A	1039	GLN	N-CA-C	-9.20	102.56	113.88
1	A	412	LEU	N-CA-C	-8.81	102.09	112.92
1	A	218	LEU	N-CA-C	-8.71	103.16	113.88
1	A	370	TYR	N-CA-C	-8.58	100.53	112.45

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	9425	0	9602	185	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9425	0	9602	185	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 10.

The worst 5 of 185 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:264:GLU:HA	1:A:267:THR:HB	1.67	0.77
1:A:632:GLY:HA2	1:A:683:GLY:HA3	1.68	0.76
1:A:444:LEU:HB3	1:A:452:VAL:HG11	1.70	0.74
1:A:243:LEU:HG	1:A:1183:ARG:HG3	1.73	0.69
1:A:1272:TRP:CG	1:A:1360:HIS:HD2	2.10	0.69

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	1200/1571 (76%)	1154 (96%)	44 (4%)	2 (0%)	43 72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	557	VAL
1	A	210	THR

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	1024/1335 (77%)	868 (85%)	156 (15%)	3 13

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1353	ASN
1	A	1480	ILE
1	A	1368	ILE
1	A	1434	VAL
1	A	1496	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1045	HIS
1	A	1165	ASN
1	A	1462	ASN
1	A	1135	GLN
1	A	1235	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.

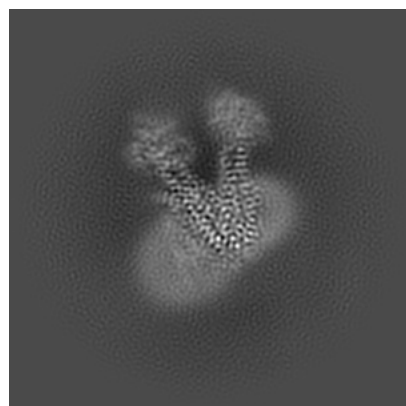
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35867. These allow visual inspection of the internal detail of the map and identification of artifacts.

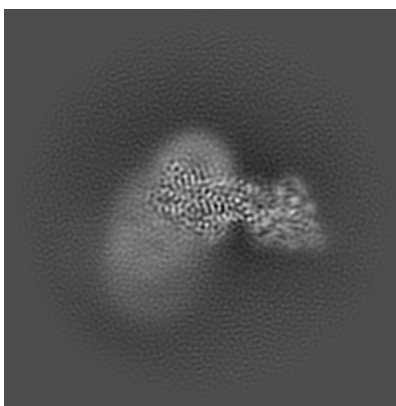
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

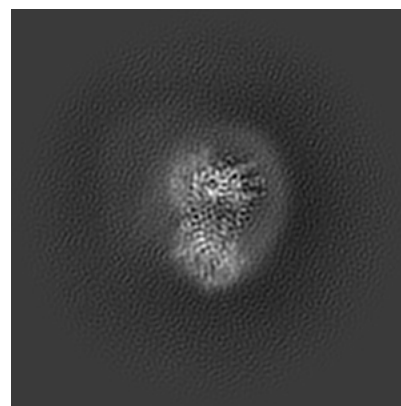
6.1.1 Primary map



X

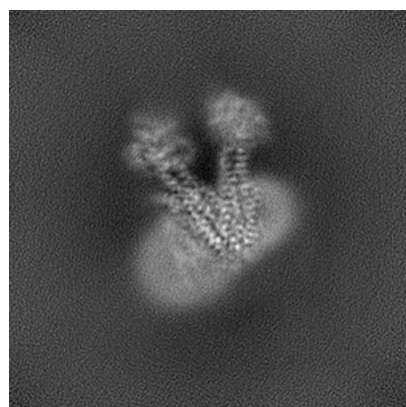


Y

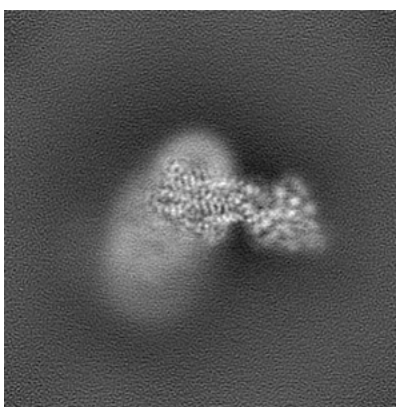


Z

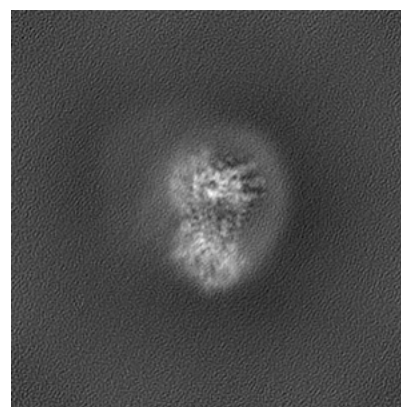
6.1.2 Raw map



X



Y

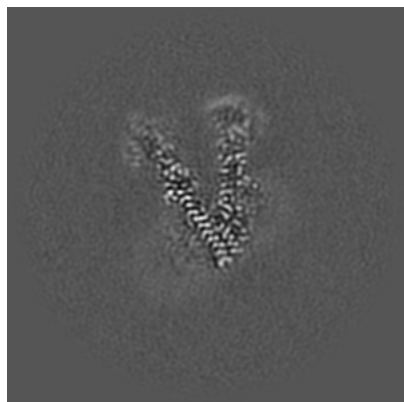


Z

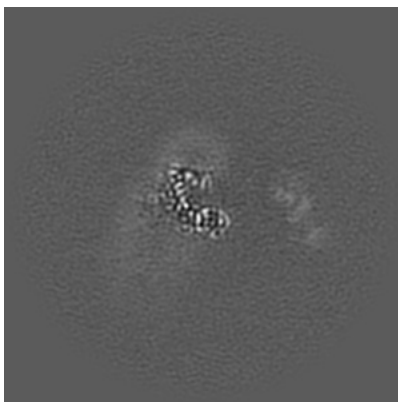
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

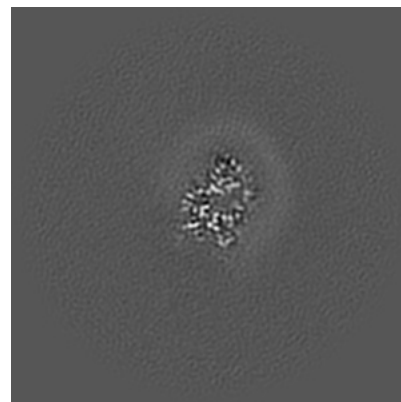
6.2.1 Primary map



X Index: 128

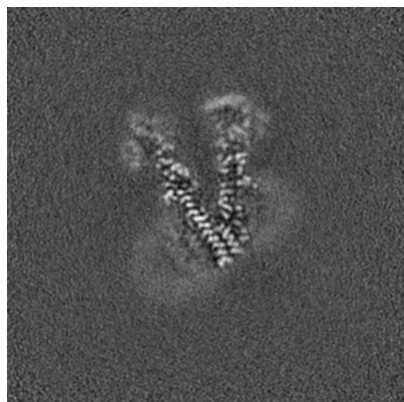


Y Index: 128

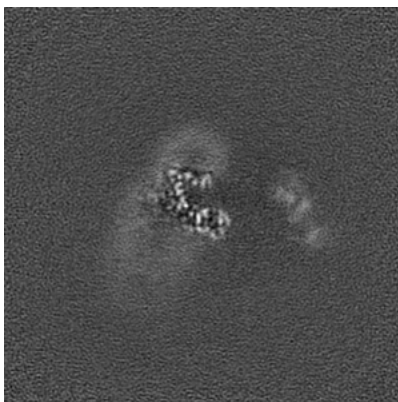


Z Index: 128

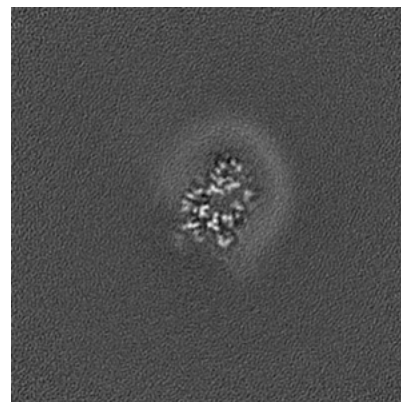
6.2.2 Raw map



X Index: 128



Y Index: 128

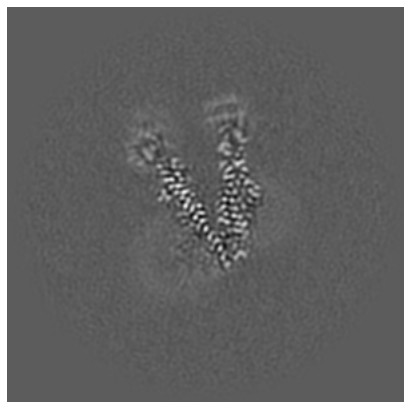


Z Index: 128

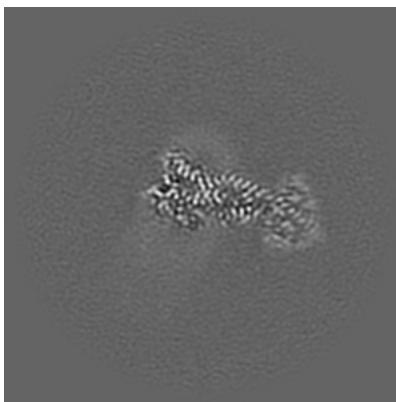
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

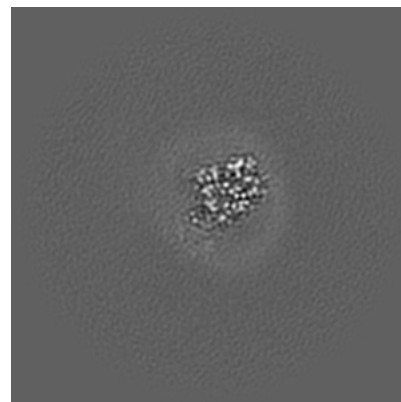
6.3.1 Primary map



X Index: 131

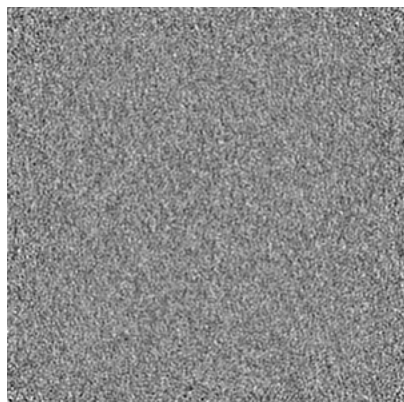


Y Index: 145

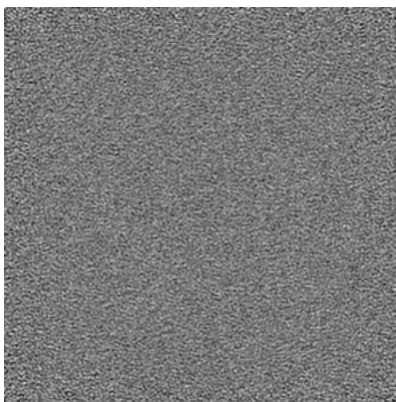


Z Index: 112

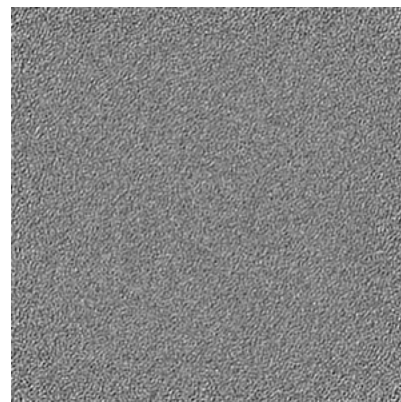
6.3.2 Raw map



X Index: 0



Y Index: 0

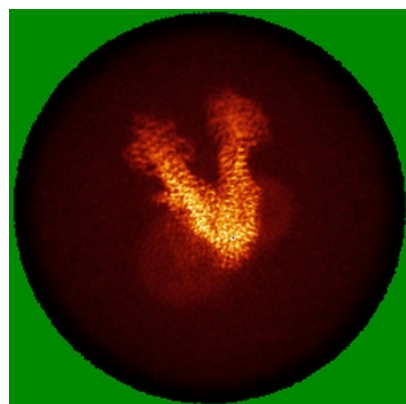


Z Index: 0

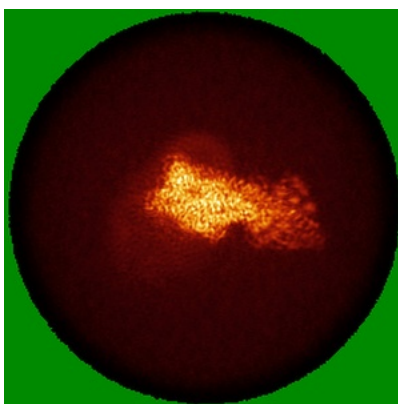
The images above show the largest variance slices of the map in three orthogonal directions.

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

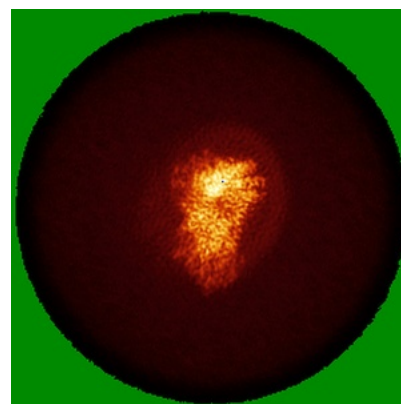
6.4.1 Primary map



X

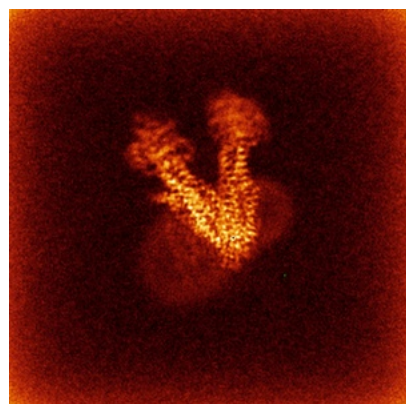


Y

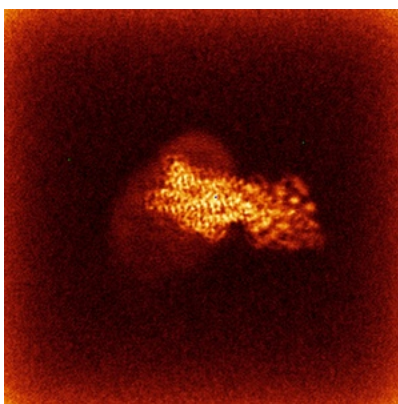


Z

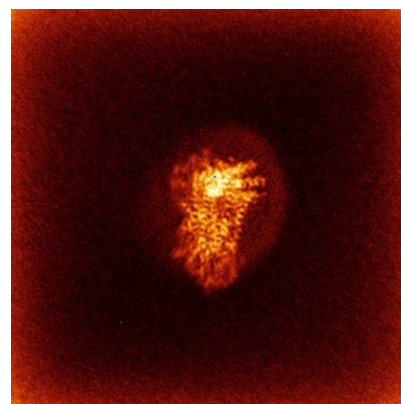
6.4.2 Raw map



X



Y

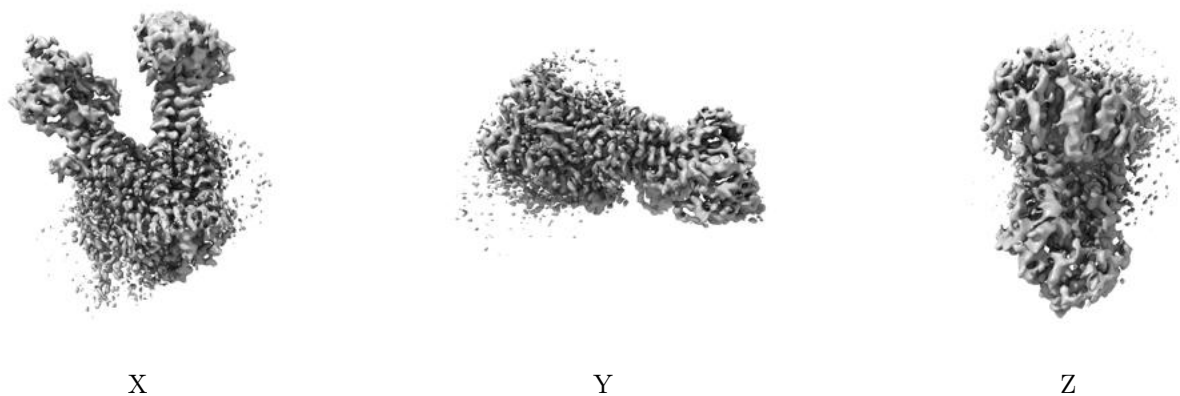


Z

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.

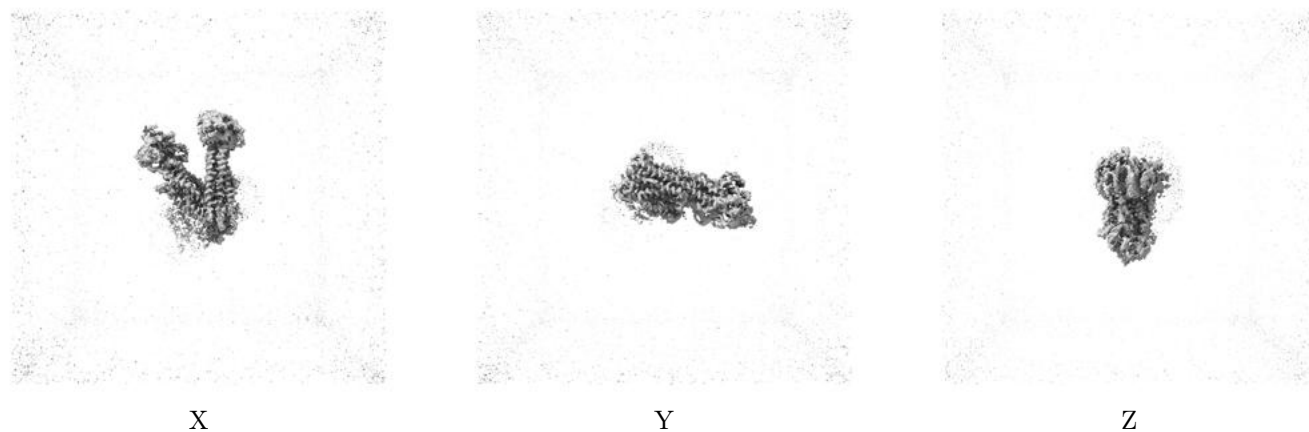
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.128. 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.

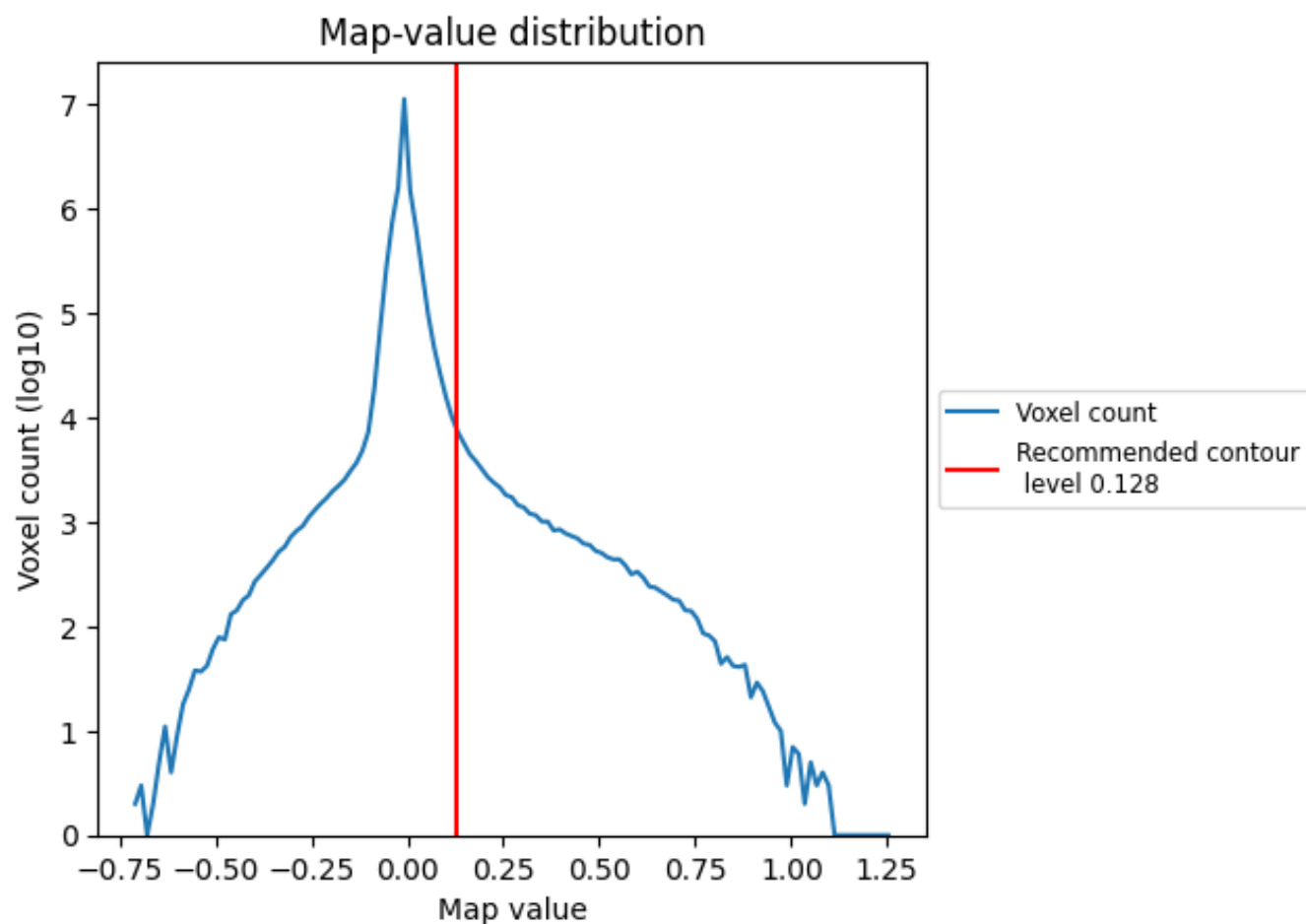
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

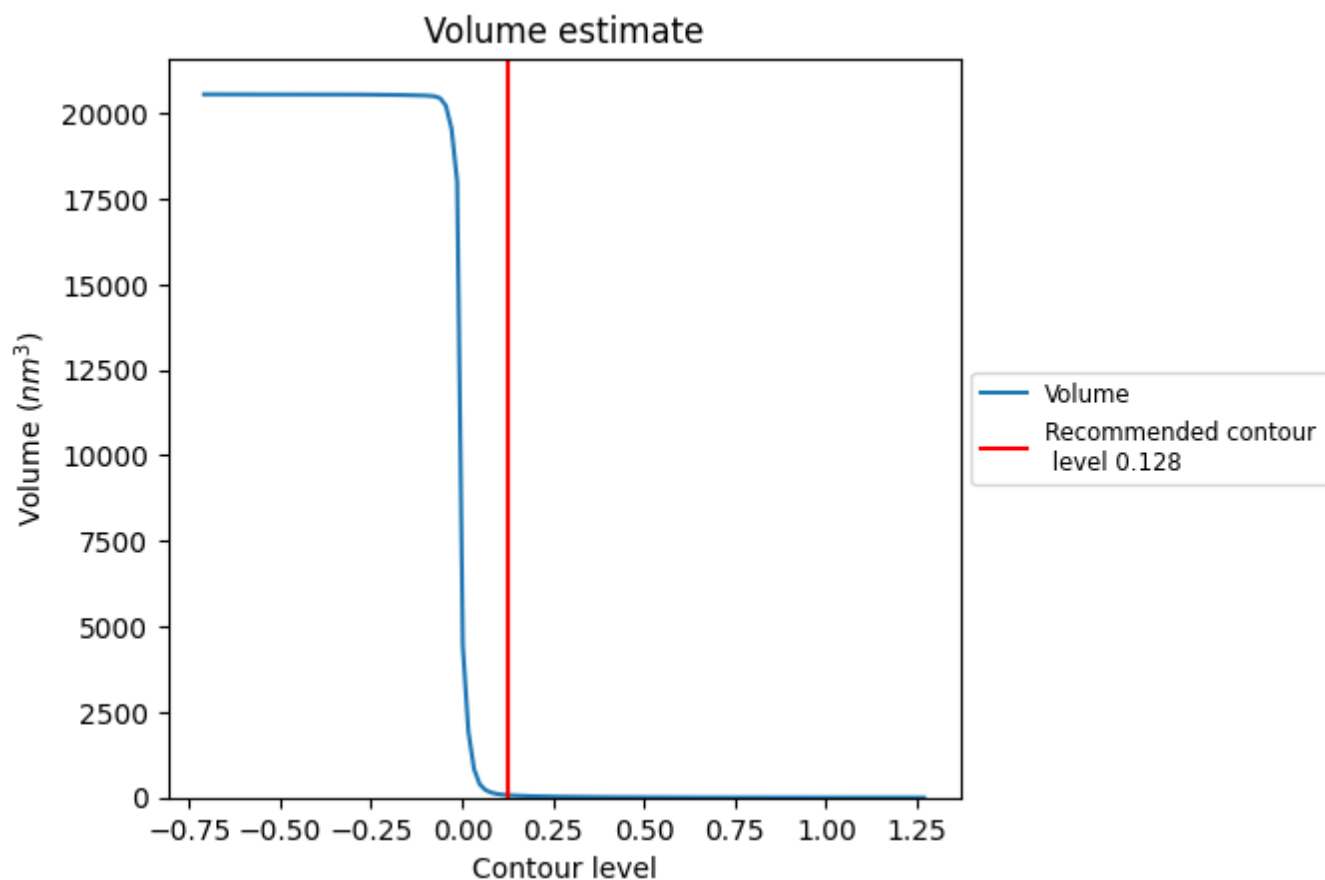
This section contains the results of statistical analysis of the map.

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.

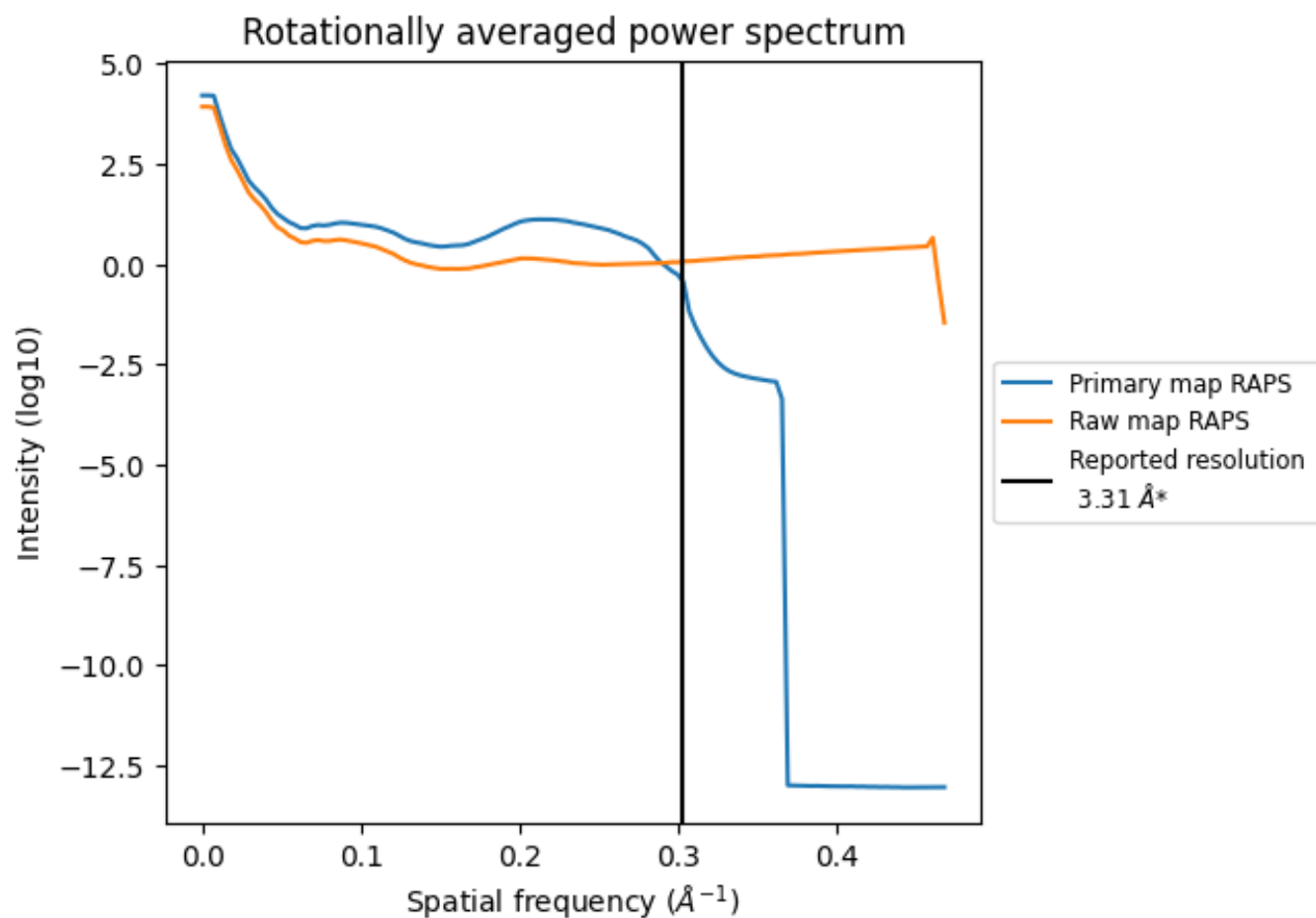
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 69 nm^3 ; this corresponds to an approximate mass of 62 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 ⓘ

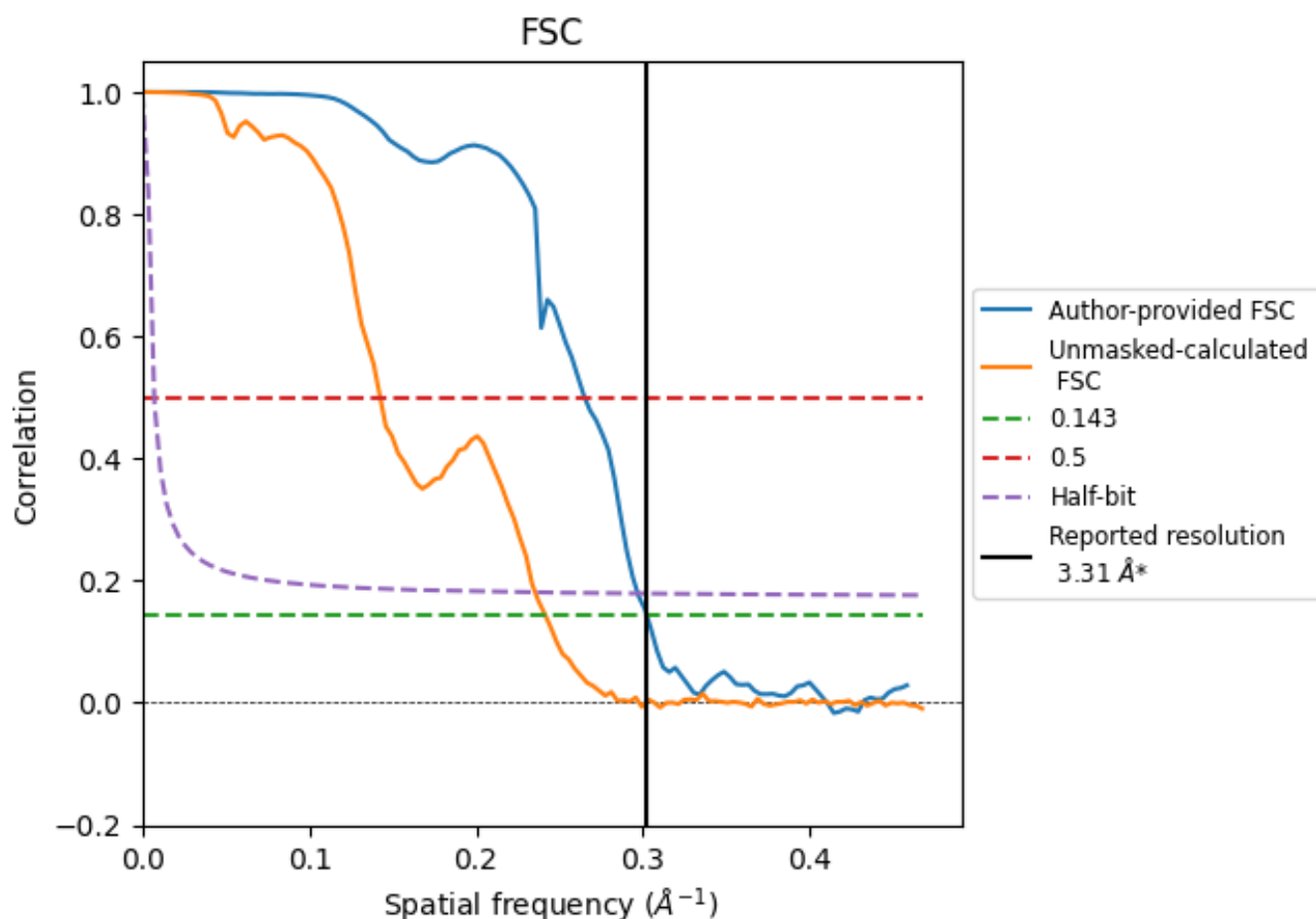


*Reported resolution corresponds to spatial frequency of 0.302 $\text{\AA}^{-1}$

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 0.302 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

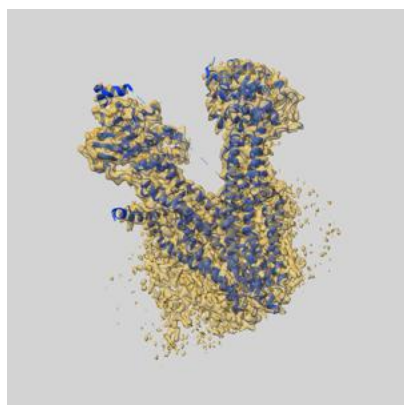
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.31	-	-
Author-provided FSC curve	3.31	3.77	3.37
Unmasked-calculated*	4.14	7.01	4.25

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

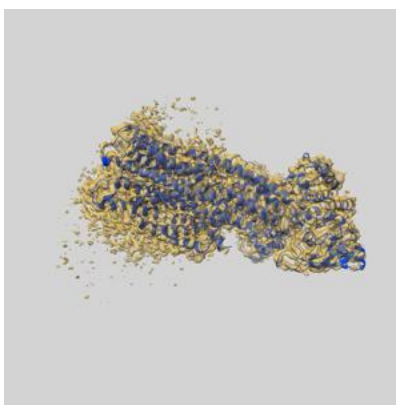
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35867 and PDB model 8IZP. Per-residue inclusion information can be found in section 3 on page 5.

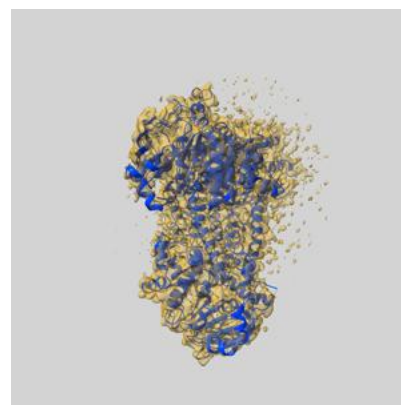
9.1 Map-model overlay [i](#)



X



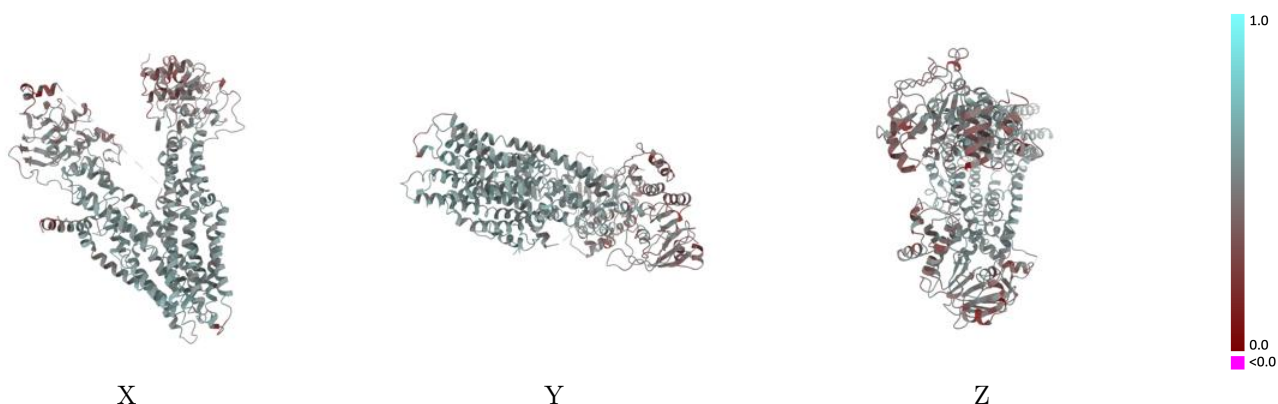
Y



Z

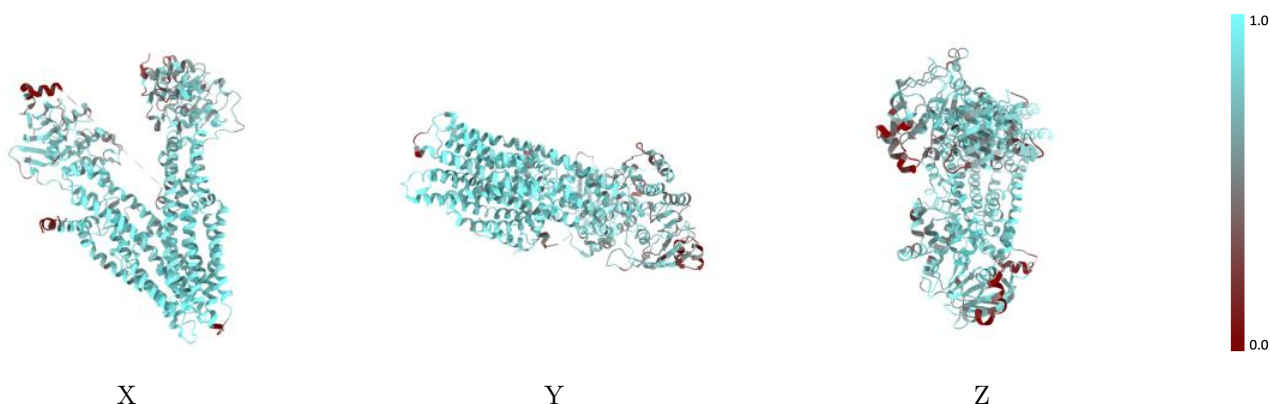
The images above show the 3D surface view of the map at the recommended contour level 0.128 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



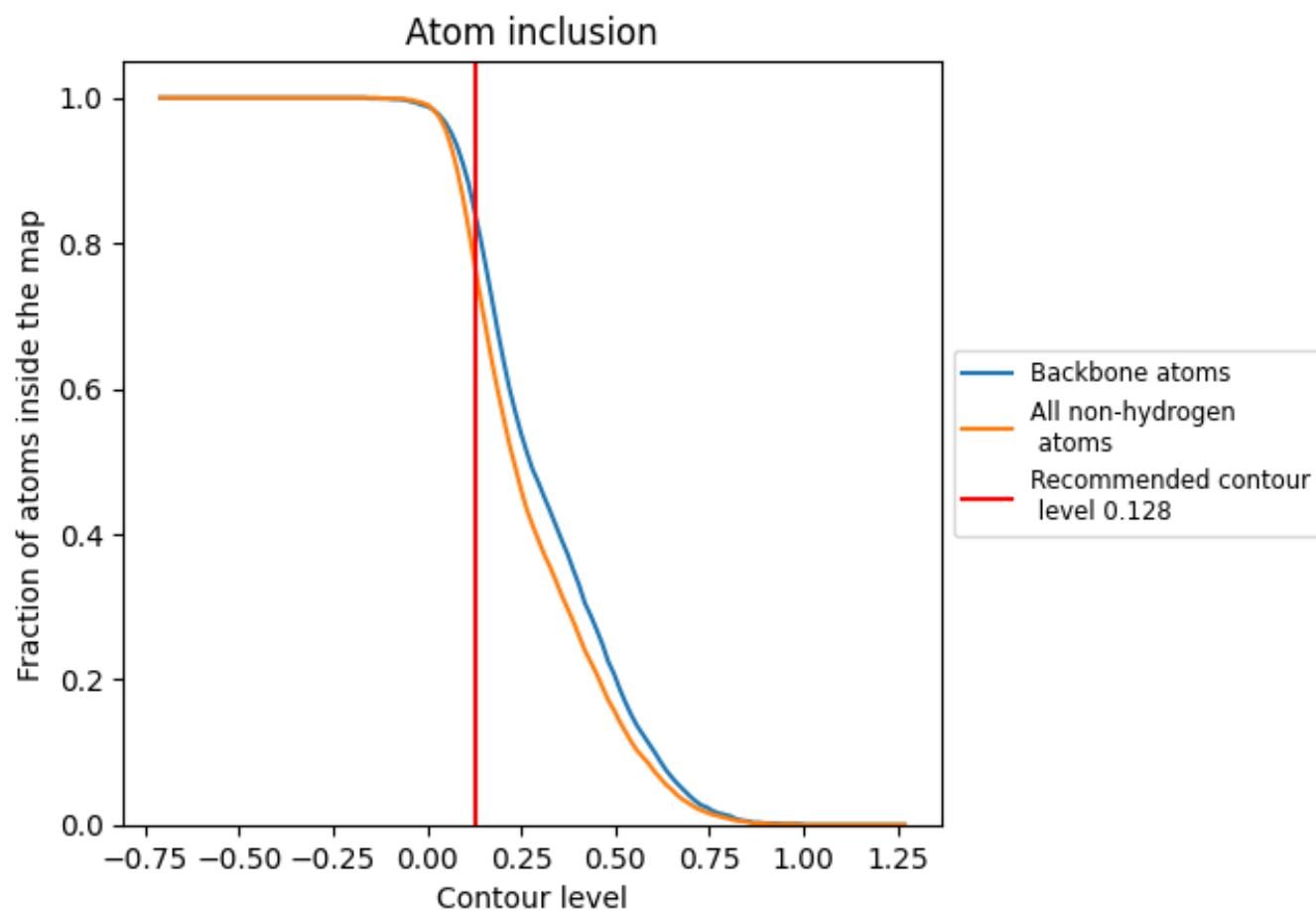
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.128).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 76% 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 (0.128) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7650	0.4980
A	0.7650	0.4980

