



## wwPDB EM Validation Summary Report ⓘ

Nov 18, 2024 – 10:12 AM JST

PDB ID : 8X5X  
EMDB ID : EMD-38074  
Title : CryoEM structure of the histamine H1 receptor in apo-form  
Authors : Wang, D.D.; Guo, Q.; Tao, Y.Y.  
Deposited on : 2023-11-20  
Resolution : 3.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
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) : 2.39

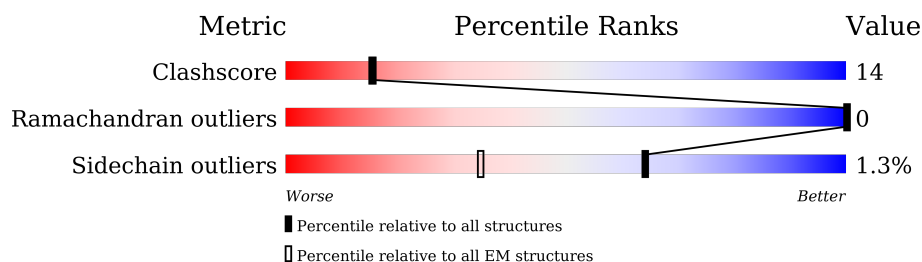
# 1 Overall quality at a glance

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)
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  $\geq 3$ , 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	B	438	<div> <div>15%</div> <div>38%</div> <div>20%</div> <div>42%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2105 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 Histamine H1 receptor,Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	256	Total	C	N	O	S	0	0
			2105	1410	339	337	19		

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	12	ASP	-	expression tag	UNP P35367
B	13	TYR	-	expression tag	UNP P35367
B	14	LYS	-	expression tag	UNP P35367
B	15	ASP	-	expression tag	UNP P35367
B	16	ASP	-	expression tag	UNP P35367
B	17	ASP	-	expression tag	UNP P35367
B	18	ASP	-	expression tag	UNP P35367
B	218	LYS	-	linker	UNP P35367
B	219	ARG	-	linker	UNP P35367
B	220	GLN	-	linker	UNP P35367
B	221	LEU	-	linker	UNP P35367
B	312	TRP	MET	conflict	UNP P0ABE7
B	?	-	THR	deletion	UNP P0ABE7
B	?	-	PRO	deletion	UNP P0ABE7
B	?	-	PRO	deletion	UNP P0ABE7
B	?	-	LYS	deletion	UNP P0ABE7
B	?	-	LEU	deletion	UNP P0ABE7
B	?	-	GLU	deletion	UNP P0ABE7
B	?	-	ASP	deletion	UNP P0ABE7
B	?	-	LYS	deletion	UNP P0ABE7
B	350	GLY	-	insertion	UNP P0ABE7
B	351	SER	PRO	conflict	UNP P0ABE7
B	352	GLY	ASP	conflict	UNP P0ABE7
B	400	ILE	HIS	conflict	UNP P0ABE7
B	404	LEU	-	linker	UNP P0ABE7
B	405	LYS	-	linker	UNP P0ABE7
B	406	PHE	-	linker	UNP P0ABE7
B	407	CYS	-	linker	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	484	LYS	-	expression tag	UNP P35367
B	485	ILE	-	expression tag	UNP P35367
B	486	ALA	-	expression tag	UNP P35367
B	487	ALA	-	expression tag	UNP P35367
B	488	LEU	-	expression tag	UNP P35367
B	489	LYS	-	expression tag	UNP P35367
B	490	GLU	-	expression tag	UNP P35367
B	491	LYS	-	expression tag	UNP P35367
B	492	ILE	-	expression tag	UNP P35367
B	493	ALA	-	expression tag	UNP P35367
B	494	ALA	-	expression tag	UNP P35367
B	495	LEU	-	expression tag	UNP P35367
B	496	LYS	-	expression tag	UNP P35367
B	497	GLU	-	expression tag	UNP P35367
B	498	LYS	-	expression tag	UNP P35367
B	499	ILE	-	expression tag	UNP P35367
B	500	ALA	-	expression tag	UNP P35367
B	501	ALA	-	expression tag	UNP P35367
B	502	LEU	-	expression tag	UNP P35367
B	503	LYS	-	expression tag	UNP P35367
B	504	GLU	-	expression tag	UNP P35367
B	505	ALA	-	expression tag	UNP P35367
B	506	GLU	-	expression tag	UNP P35367
B	507	GLU	-	expression tag	UNP P35367
B	508	LYS	-	expression tag	UNP P35367
B	509	ARG	-	expression tag	UNP P35367
B	510	ALA	-	expression tag	UNP P35367
B	511	SER	-	expression tag	UNP P35367
B	512	ARG	-	expression tag	UNP P35367
B	513	LEU	-	expression tag	UNP P35367
B	514	GLU	-	expression tag	UNP P35367
B	515	GLU	-	expression tag	UNP P35367
B	516	GLU	-	expression tag	UNP P35367
B	517	LEU	-	expression tag	UNP P35367
B	518	ARG	-	expression tag	UNP P35367
B	519	ARG	-	expression tag	UNP P35367
B	520	ARG	-	expression tag	UNP P35367
B	521	LEU	-	expression tag	UNP P35367
B	522	THR	-	expression tag	UNP P35367
B	523	GLU	-	expression tag	UNP P35367
B	524	GLY	-	expression tag	UNP P35367
B	525	SER	-	expression tag	UNP P35367

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Chain	Residue	Modelled	Actual	Comment	Reference
B	526	HIS	-	expression tag	UNP P35367
B	527	HIS	-	expression tag	UNP P35367
B	528	HIS	-	expression tag	UNP P35367
B	529	HIS	-	expression tag	UNP P35367
B	530	HIS	-	expression tag	UNP P35367
B	531	HIS	-	expression tag	UNP P35367
B	532	HIS	-	expression tag	UNP P35367
B	533	HIS	-	expression tag	UNP P35367



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	327890	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.111	Depositor
Minimum map value	-2.118	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.42	Depositor
Map size (Å)	299.6, 299.6, 299.6	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	B	0.26	0/2162	0.52	0/2933

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	B	2105	0	2172	62	0
All	All	2105	0	2172	62	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 62 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:431:TYR:HB2	1:B:453:THR:HB	1.68	0.75
1:B:88:LEU:HD13	1:B:451:MET:HG2	1.70	0.73
1:B:63:ASN:OD1	1:B:468:TYR:OH	2.09	0.70
1:B:196:ILE:HD13	1:B:200:TYR:HD2	1.58	0.67
1:B:476:LYS:HA	1:B:479:PHE:CE2	2.32	0.64



There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	B	246/438 (56%)	233 (95%)	13 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	232/382 (61%)	229 (99%)	3 (1%)	65	81

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	167	HIS
1	B	409	ARG
1	B	411	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	460	ASN

### 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.

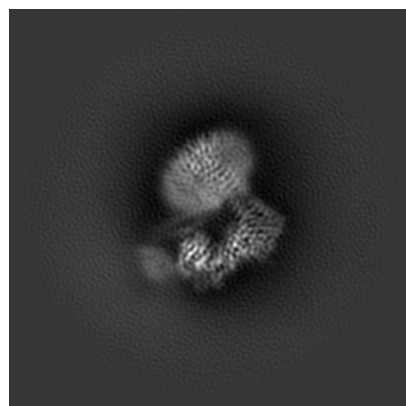
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38074. These allow visual inspection of the internal detail of the map and identification of artifacts.

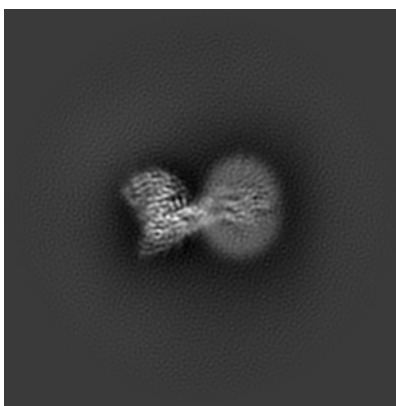
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

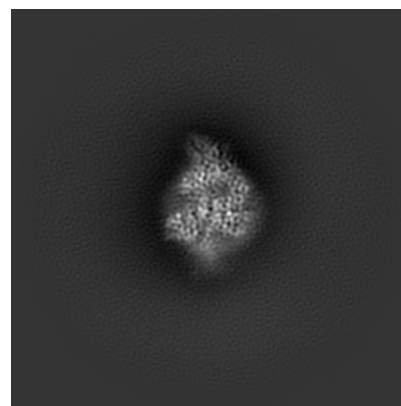
#### 6.1.1 Primary map



X

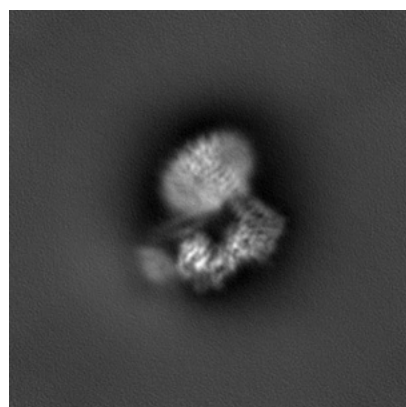


Y

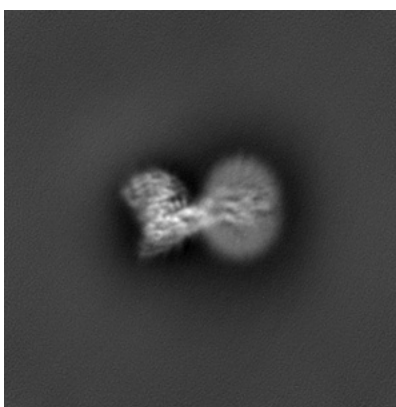


Z

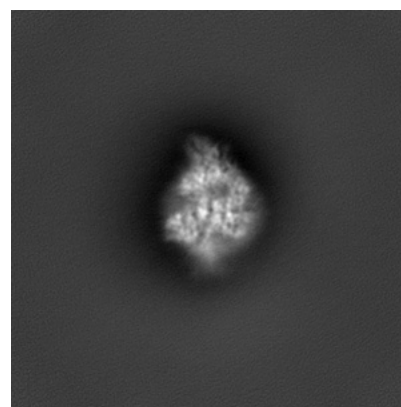
#### 6.1.2 Raw map



X



Y

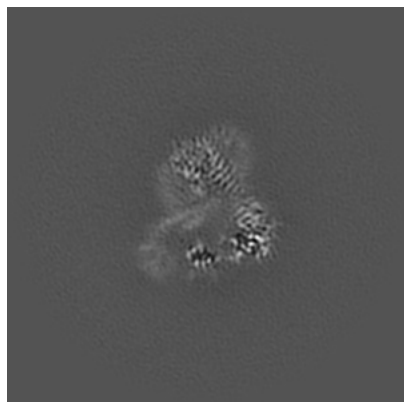


Z

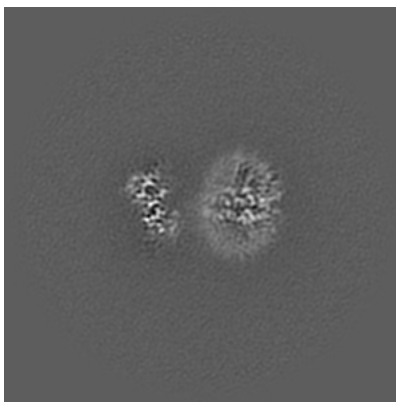
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

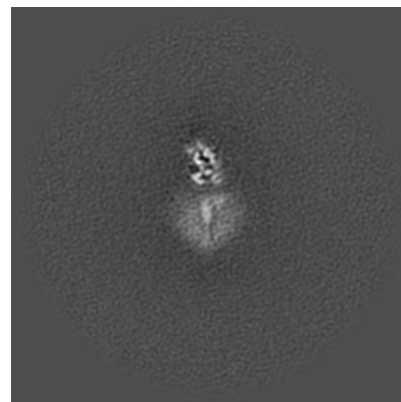
### 6.2.1 Primary map



X Index: 140

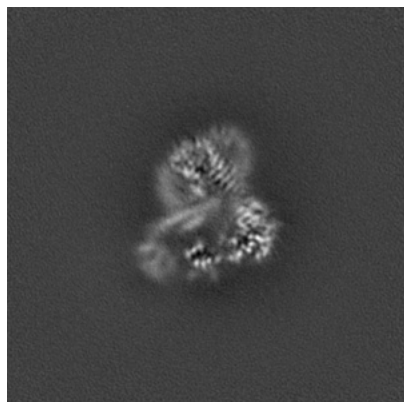


Y Index: 140

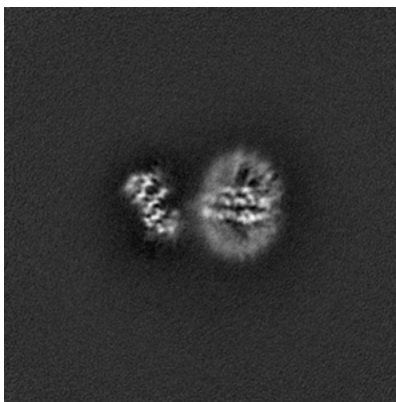


Z Index: 140

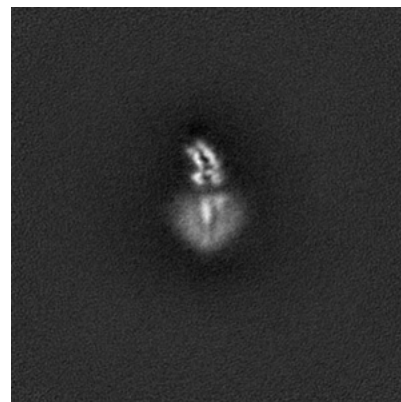
### 6.2.2 Raw map



X Index: 140



Y Index: 140

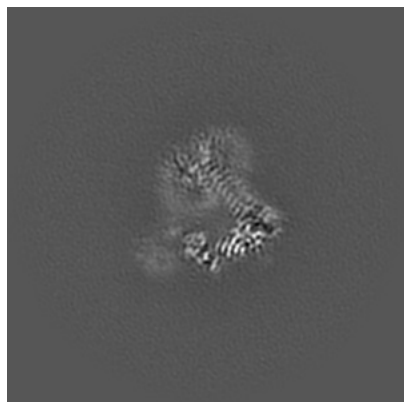


Z Index: 140

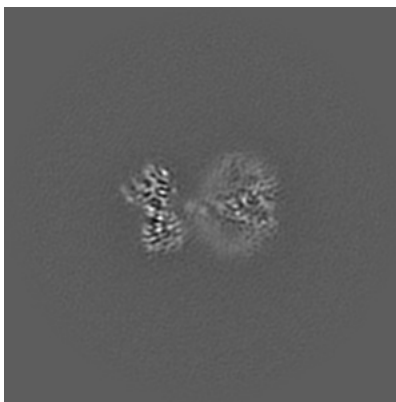
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

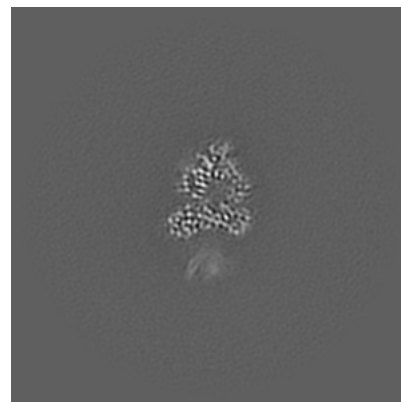
### 6.3.1 Primary map



X Index: 133

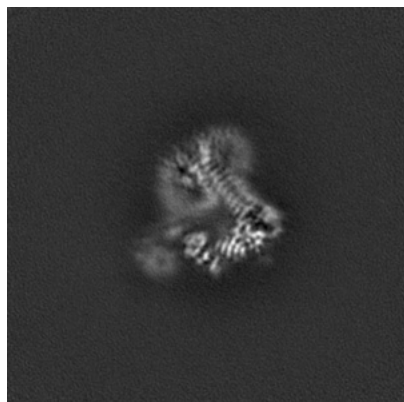


Y Index: 133

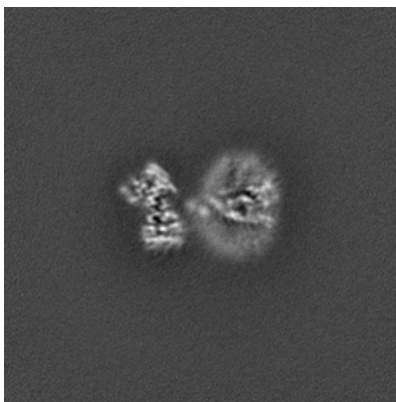


Z Index: 110

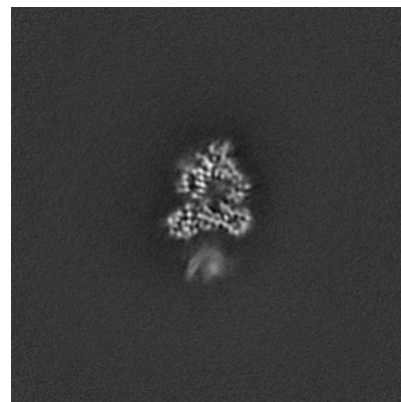
### 6.3.2 Raw map



X Index: 133



Y Index: 135

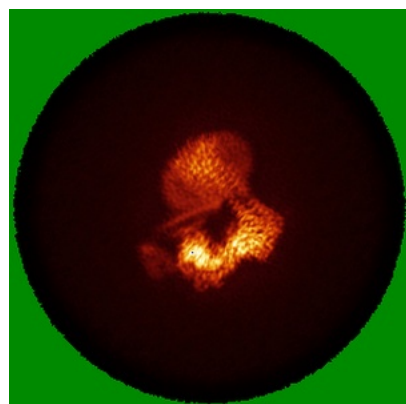


Z Index: 110

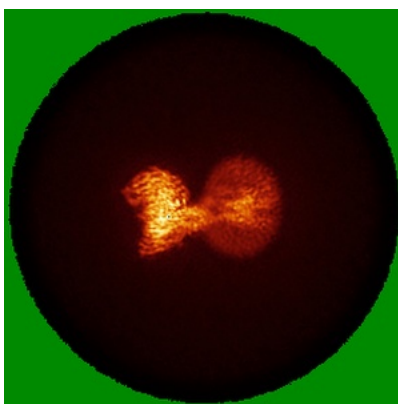
The images above show the largest variance slices of the map in three orthogonal directions.

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

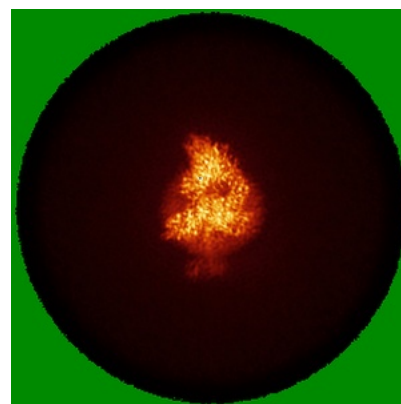
### 6.4.1 Primary map



X

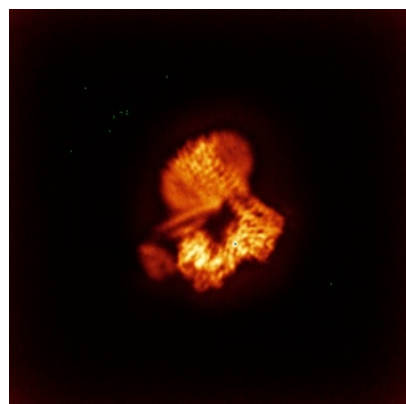


Y

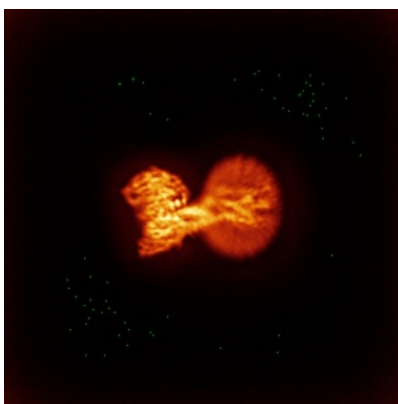


Z

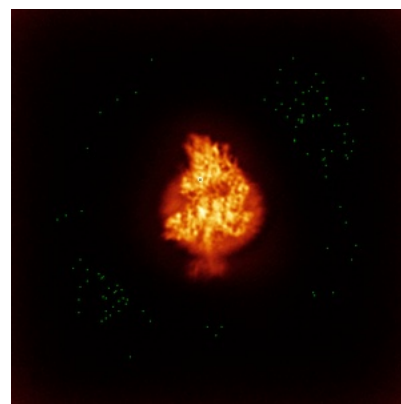
### 6.4.2 Raw map



X



Y

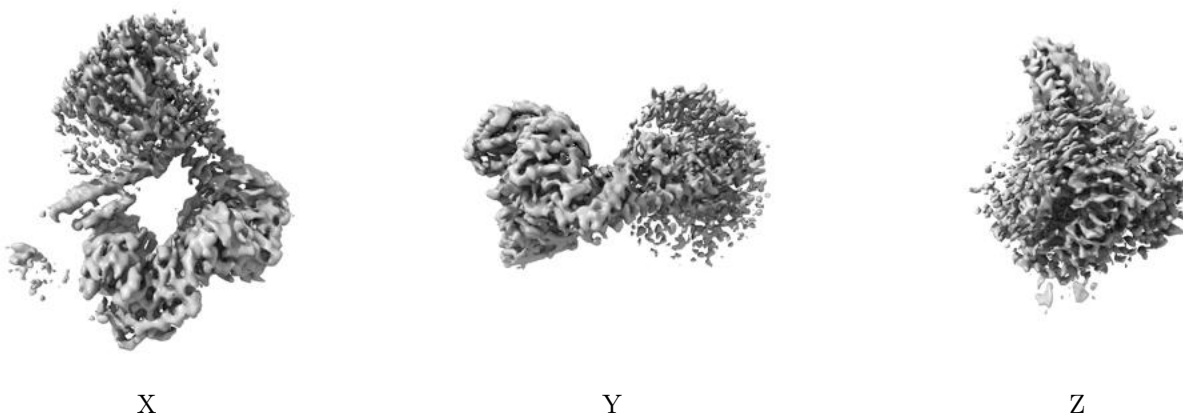


Z

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.

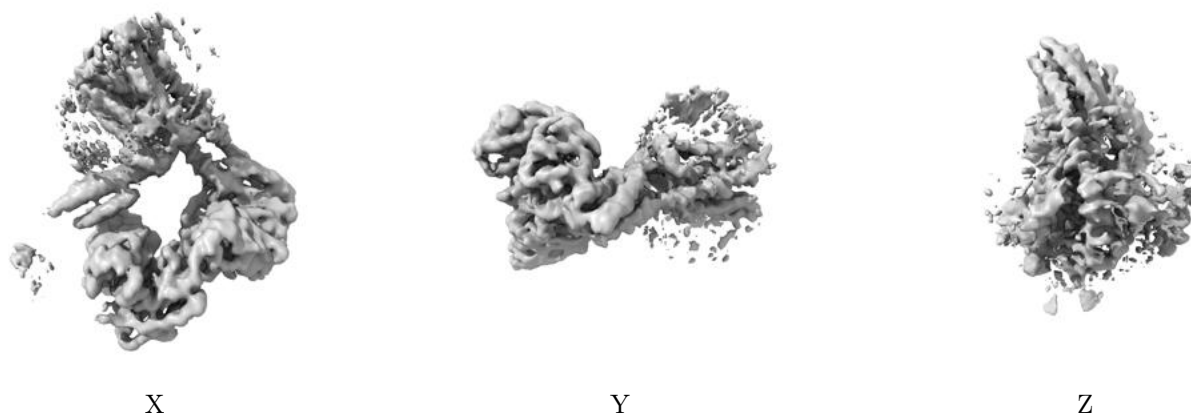
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.42. 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](#)

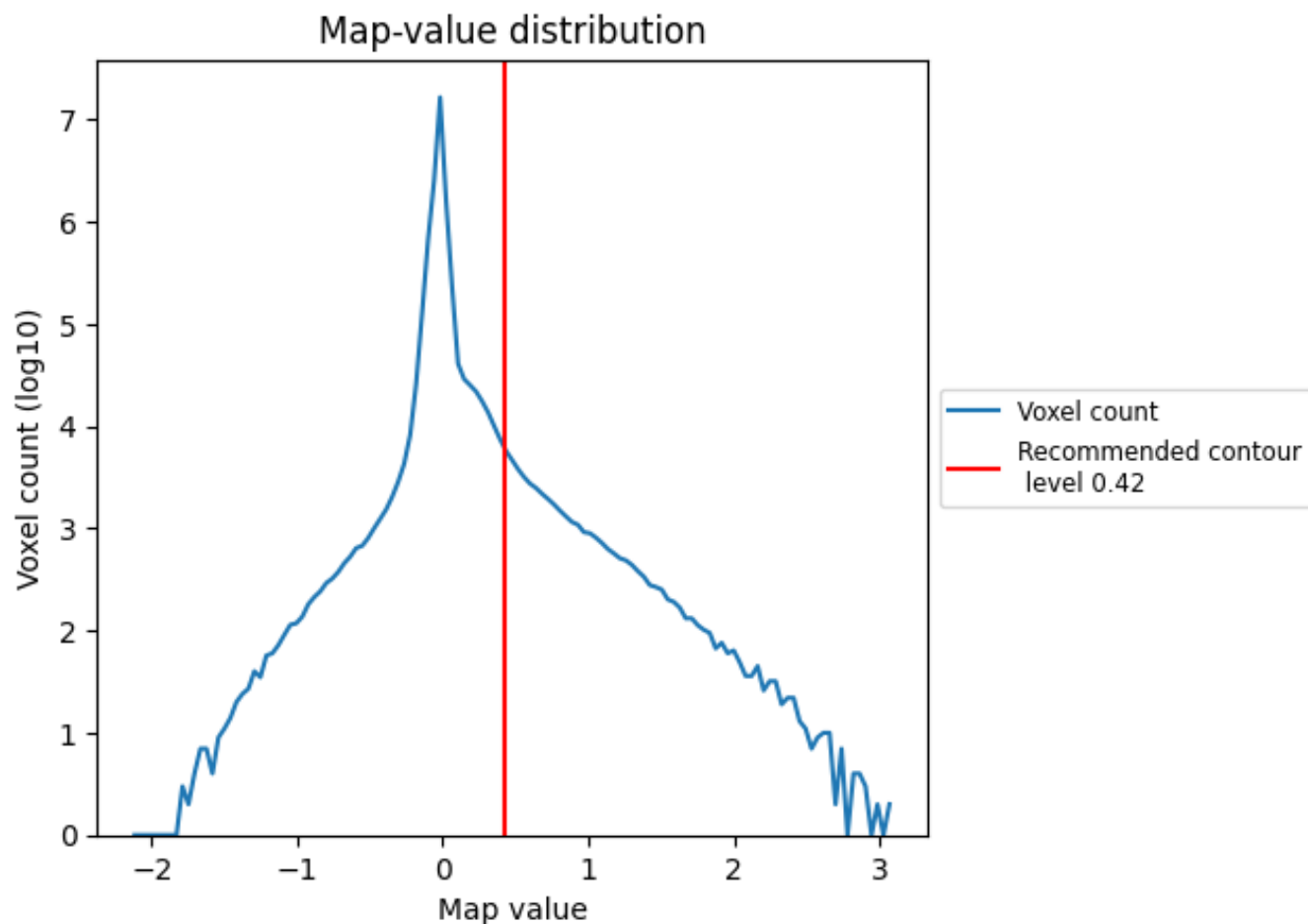
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

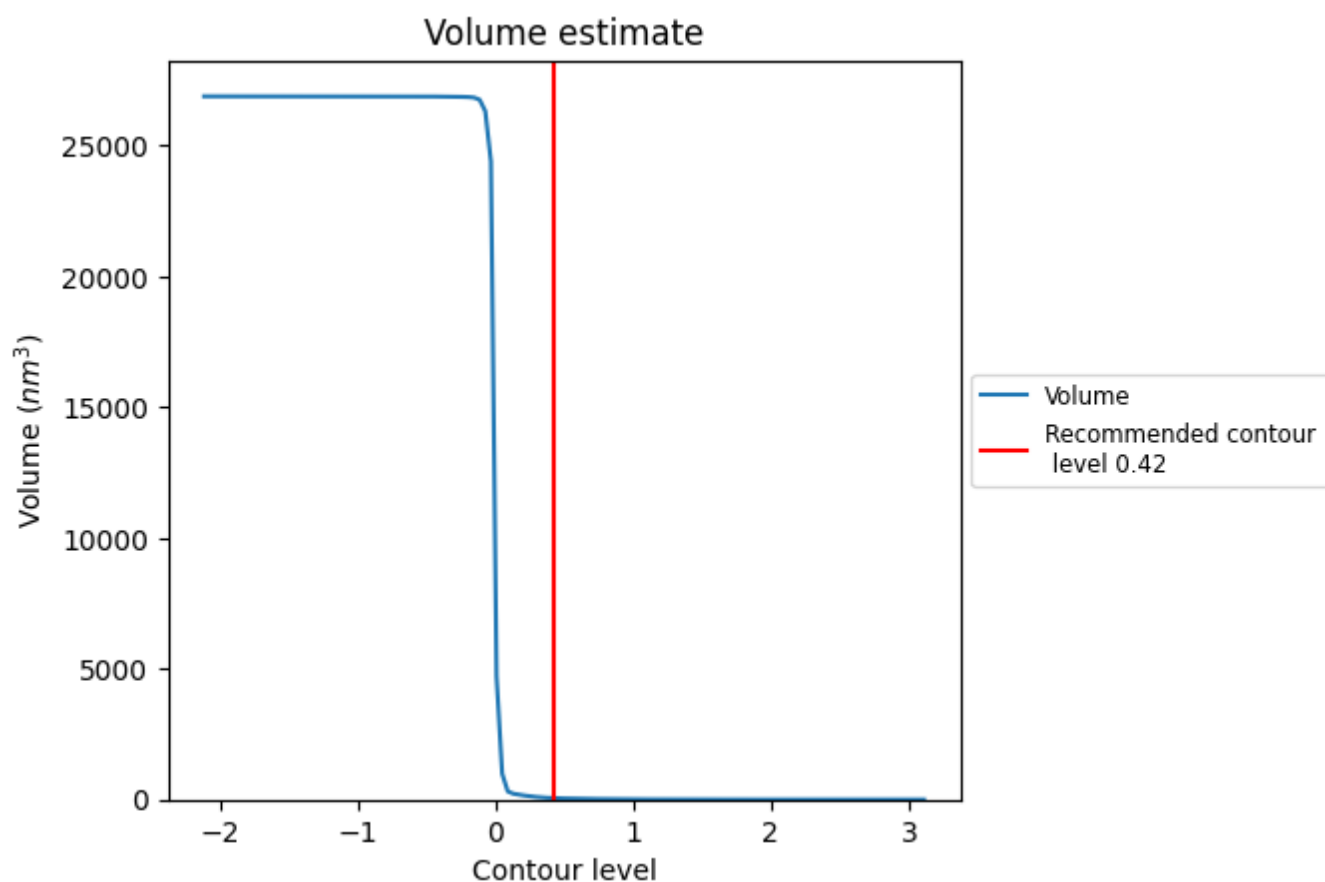
### 7.1 Map-value distribution [i](#)



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.



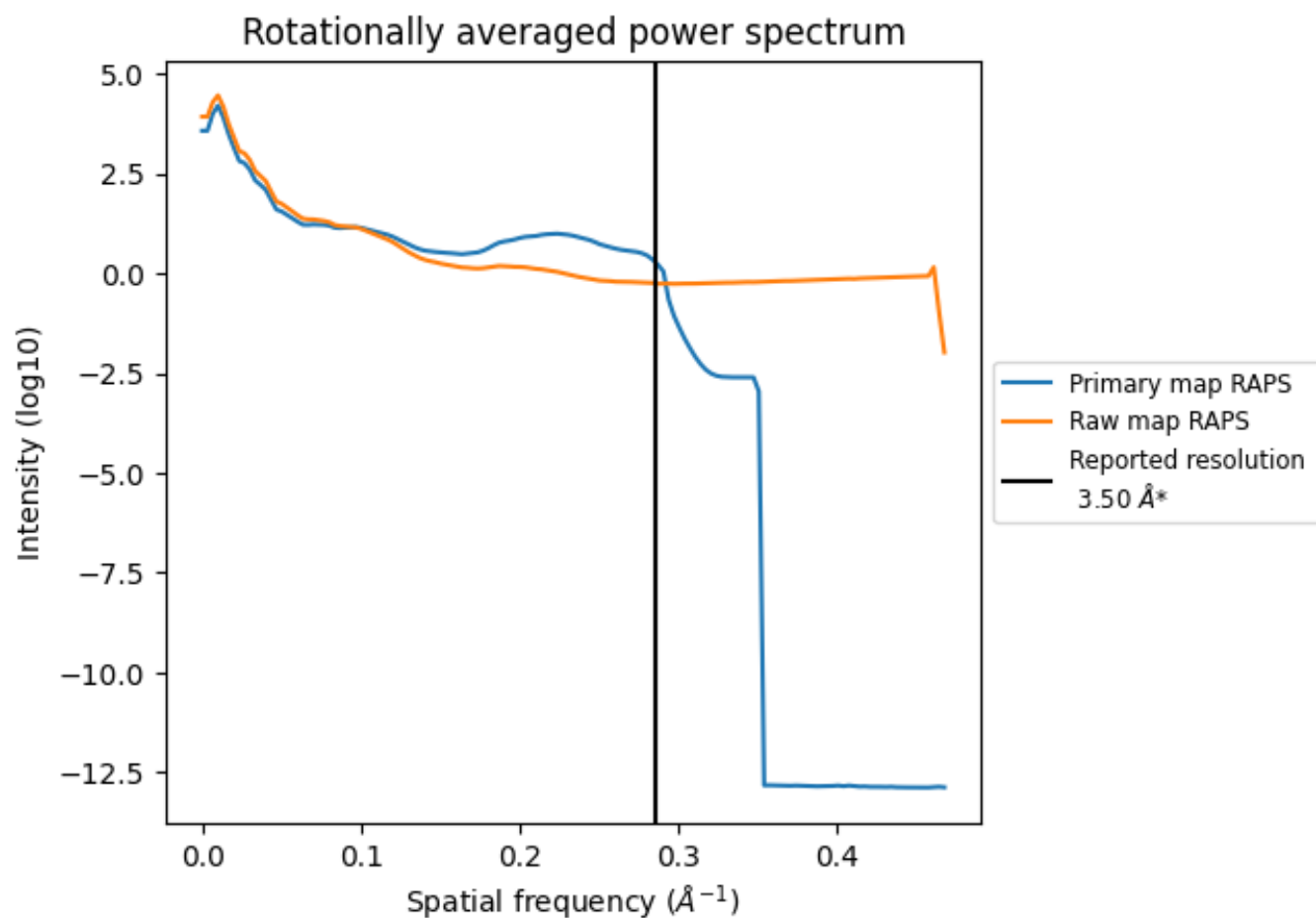
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 56 nm<sup>3</sup>; this corresponds to an approximate mass of 50 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 ⓘ

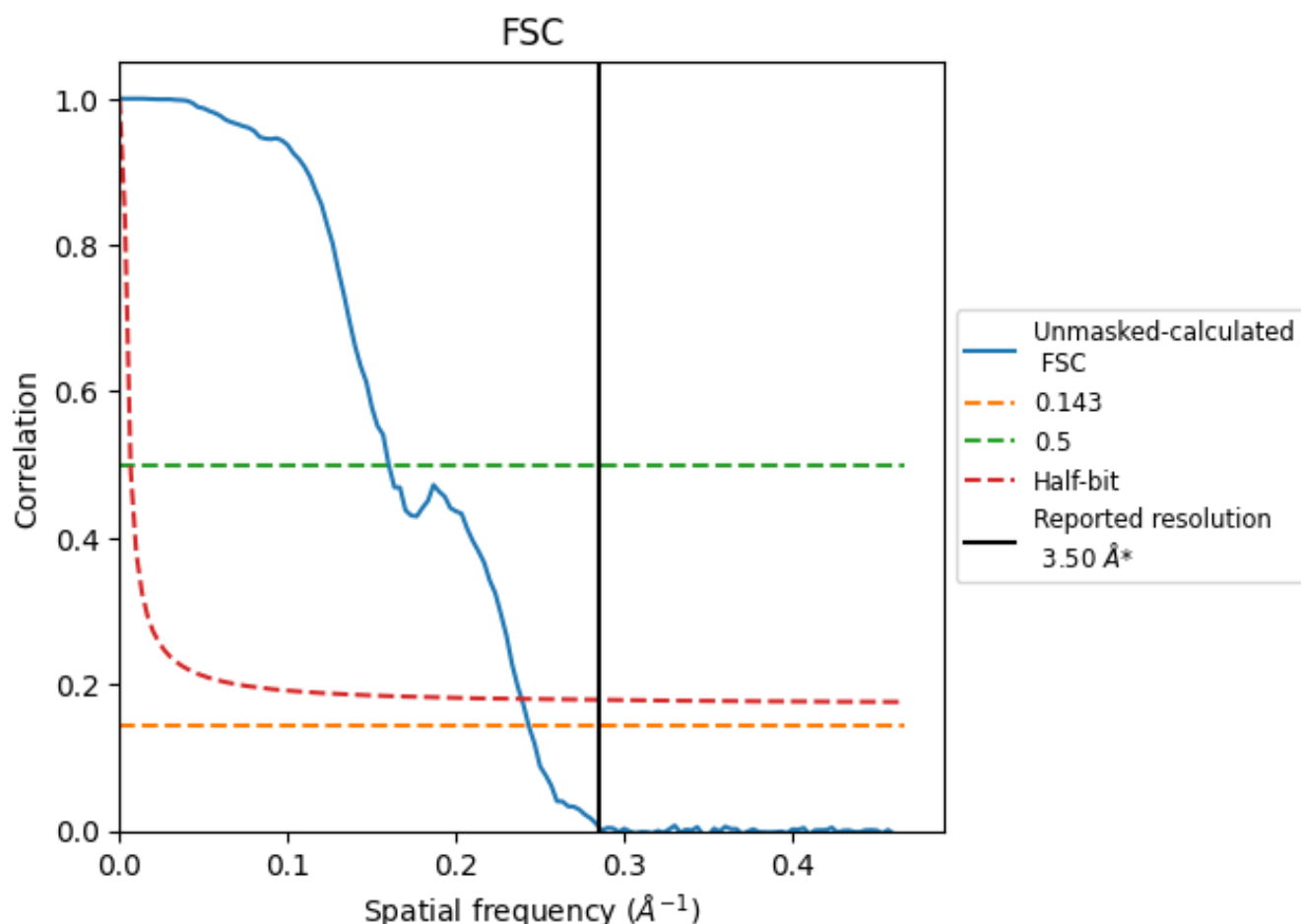


\*Reported resolution corresponds to spatial frequency of 0.286  $\text{\AA}^{-1}$

## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

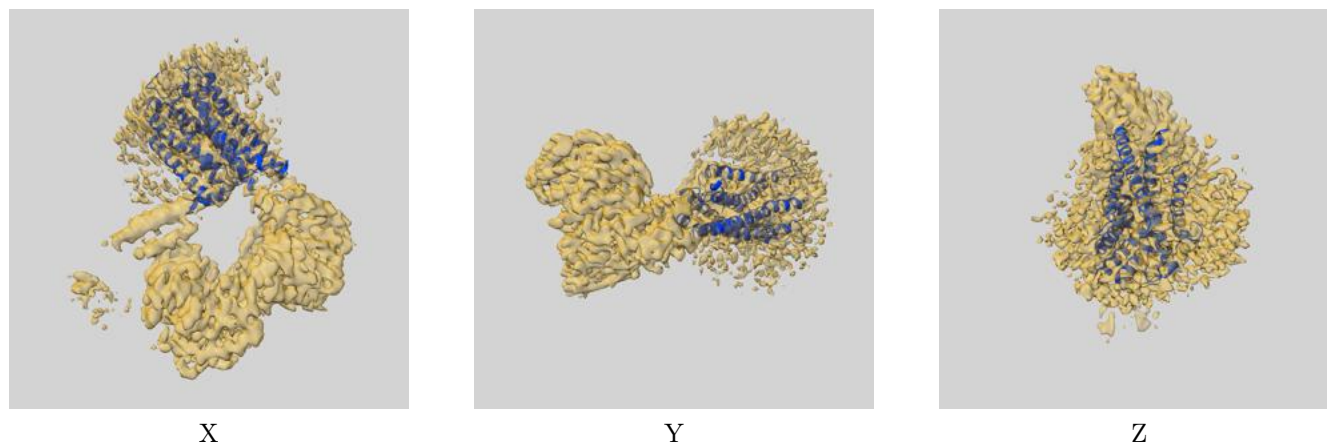
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.11	6.24	4.18

\*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 4.11 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-38074 and PDB model 8X5X. Per-residue inclusion information can be found in section [3](#) on page [6](#).

### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.42 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](#)



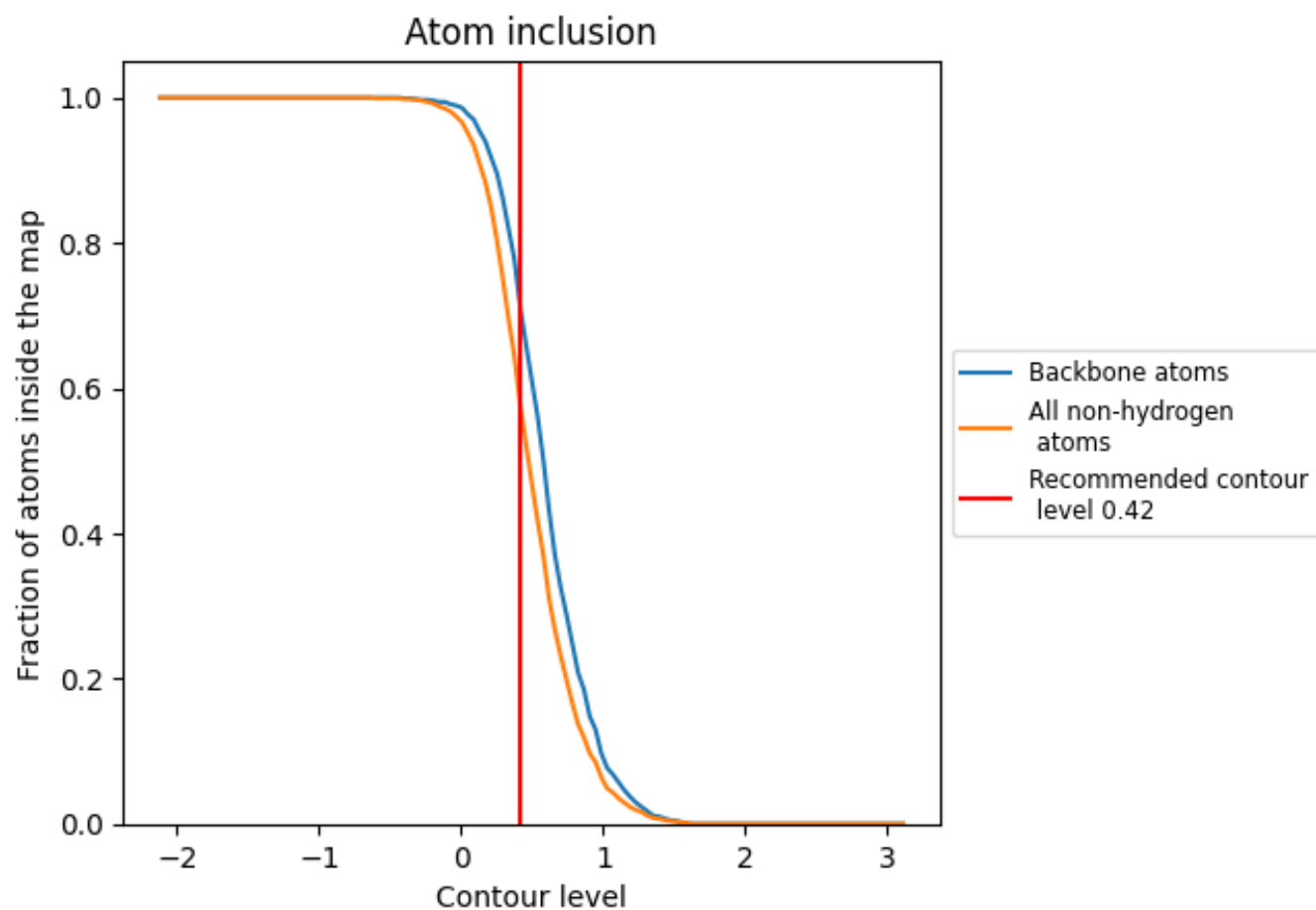
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.42).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 57% 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 (0.42) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5710	<div></div> 0.2730
B	<div></div> 0.5710	<div></div> 0.2730

