



# wwPDB EM Validation Summary Report ⓘ

May 21, 2024 – 03:42 PM EDT

PDB ID : 8VCI  
EMDB ID : EMD-43137  
Title : SARS-CoV-2 Frameshift Stimulatory Element with Upstream Multibranch Loop  
Authors : Peterson, J.M.; Becker, S.T.; O'Leary, C.A.; Juneja, P.; Yang, Y.; Moss, W.N.  
Deposited on : 2023-12-14  
Resolution : 6.10 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:

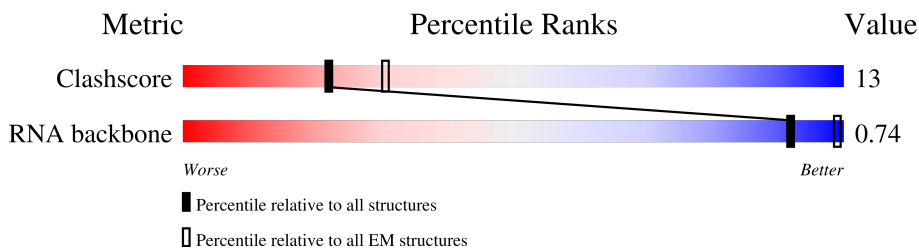
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 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 6.10 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)
Clashescore	158937	4297
RNA backbone	4643	859

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	1-A	118	
1	2-A	118	
1	3-A	118	
1	4-A	118	
1	5-A	118	
1	6-A	118	
1	7-A	118	
1	8-A	118	
1	9-A	118	

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 33930 atoms, of which 11394 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 RNA chain called Frameshift Stimulatory Element with Upstream Multi-branch Loop.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
1	1-A	118	3770	1120	1266	440	827	117	0	0
1	2-A	118	3770	1120	1266	440	827	117	0	0
1	3-A	118	3770	1120	1266	440	827	117	0	0
1	4-A	118	3770	1120	1266	440	827	117	0	0
1	5-A	118	3770	1120	1266	440	827	117	0	0
1	6-A	118	3770	1120	1266	440	827	117	0	0
1	7-A	118	3770	1120	1266	440	827	117	0	0
1	8-A	118	3770	1120	1266	440	827	117	0	0
1	9-A	118	3770	1120	1266	440	827	117	0	0

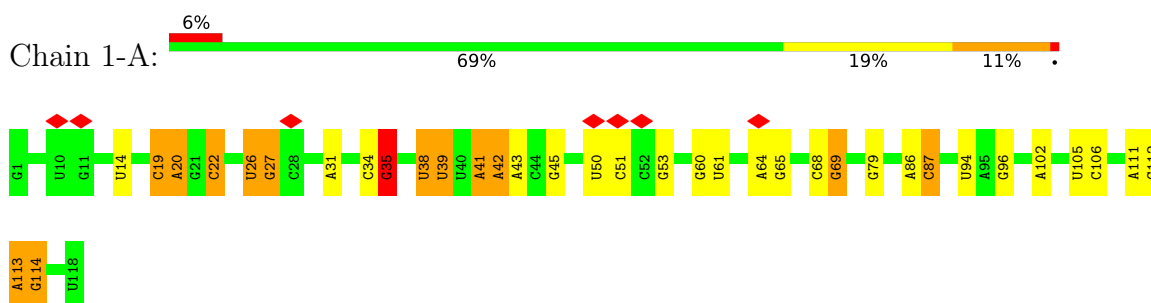
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	G	C	engineered mutation	GB NC_045512.2
A	51	C	G	engineered mutation	GB NC_045512.2

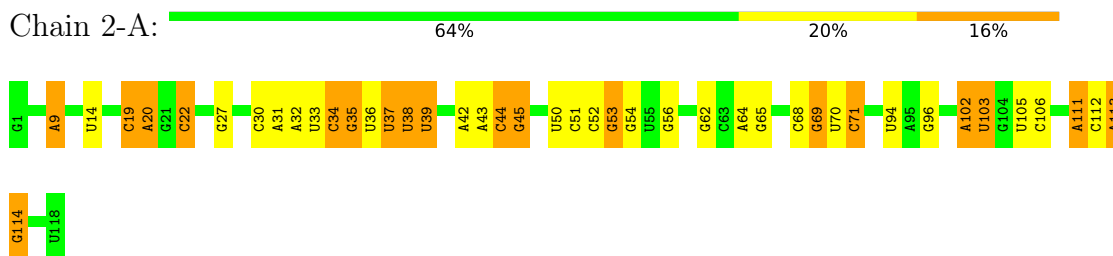
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

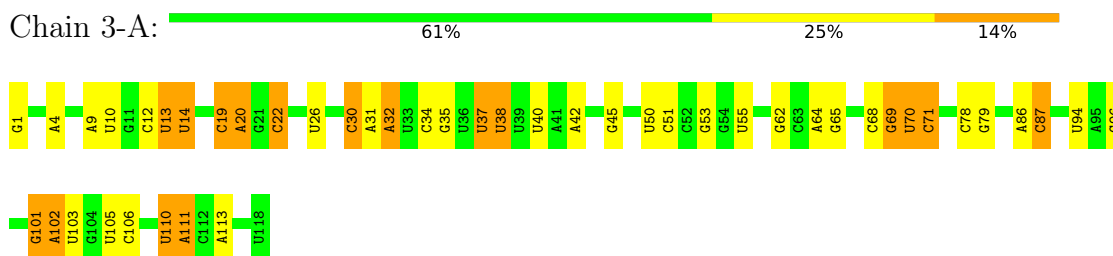
- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



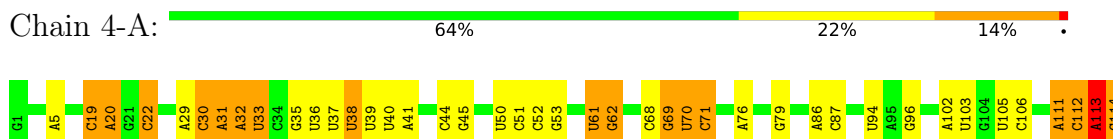
- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop

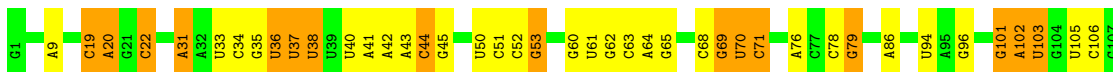


- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop

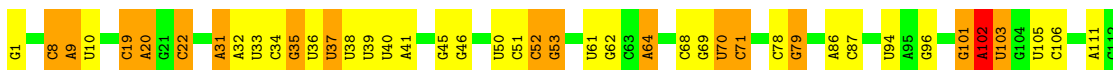




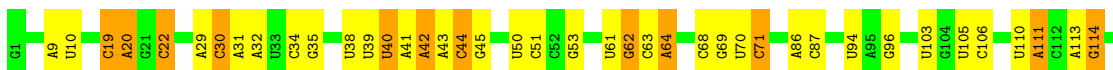
- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



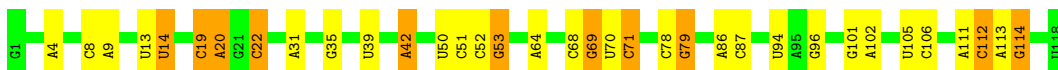
- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



- Molecule 1: Frameshift Stimulatory Element with Upstream Multi-branch Loop



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	627438	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.185	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size ( $\text{\AA}$ )	226.6, 226.6, 226.6	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.133, 1.133, 1.133	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	1-A	0.40	1/2796 (0.0%)	0.86	0/4353
1	2-A	0.38	0/2796	0.87	0/4353
1	3-A	0.38	0/2796	0.86	0/4353
1	4-A	0.39	0/2796	0.87	1/4353 (0.0%)
1	5-A	0.42	0/2796	0.90	1/4353 (0.0%)
1	6-A	0.40	0/2796	0.89	1/4353 (0.0%)
1	7-A	0.40	0/2796	0.87	0/4353
1	8-A	0.40	1/2796 (0.0%)	0.88	1/4353 (0.0%)
1	9-A	0.37	0/2796	0.86	0/4353
All	All	0.39	2/25164 (0.0%)	0.87	4/39177 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	8-A	37	U	O4'-C1'	5.87	1.49	1.41
1	1-A	35	G	C2'-C1'	-5.55	1.47	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5-A	113	A	P-O3'-C3'	13.11	135.43	119.70
1	6-A	102	A	O4'-C1'-N9	9.42	115.74	108.20
1	8-A	113	A	C4'-C3'-C2'	-5.70	96.90	102.60
1	4-A	113	A	C5'-C4'-O4'	-5.14	102.93	109.10

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	1-A	2504	1266	1268	32	0
1	2-A	2504	1266	1268	70	0
1	3-A	2504	1266	1268	46	0
1	4-A	2504	1266	1268	53	0
1	5-A	2504	1266	1268	63	0
1	6-A	2504	1266	1268	37	0
1	7-A	2504	1266	1268	38	0
1	8-A	2504	1266	1268	53	0
1	9-A	2504	1266	1268	27	0
All	All	22536	11394	11412	419	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 13.

The worst 5 of 419 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:64:A:OP1	1:A:64:A:H3'	1.22	1.29
1:A:64:A:OP2	1:A:64:A:C3'	1.81	1.27
1:A:64:A:H3'	1:A:64:A:P	1.78	1.22
1:A:103:U:C6	1:A:103:U:OP1	1.93	1.22
1:A:64:A:OP2	1:A:64:A:C3'	1.87	1.21

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

### 5.3.3 RNA [i](#)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1-A	116/118 (98%)	23 (19%)	2 (1%)
1	2-A	116/118 (98%)	26 (22%)	3 (2%)
1	3-A	116/118 (98%)	27 (23%)	4 (3%)
1	4-A	116/118 (98%)	26 (22%)	3 (2%)
1	5-A	116/118 (98%)	25 (21%)	5 (4%)
1	6-A	116/118 (98%)	27 (23%)	4 (3%)
1	7-A	116/118 (98%)	23 (19%)	0
1	8-A	116/118 (98%)	25 (21%)	5 (4%)
1	9-A	116/118 (98%)	20 (17%)	0
All	All	1044/1062 (98%)	222 (21%)	26 (2%)

5 of 222 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1-A	14	U
1	1-A	19	C
1	1-A	20	A
1	1-A	22	C
1	1-A	27	G

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5-A	101	G
1	6-A	8	C
1	8-A	70	U
1	5-A	113	A
1	6-A	52	C

## 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 monosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	6-A	1
1	9-A	1
1	4-A	1
1	5-A	1
1	2-A	1
1	3-A	1
1	8-A	1
1	1-A	1
1	7-A	1

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
6	A	68:C	O3'	69:G	P	4.79
9	A	63:C	O3'	64:A	P	3.98
4	A	63:C	O3'	64:A	P	3.95
5	A	63:C	O3'	64:A	P	3.84
2	A	63:C	O3'	64:A	P	3.62

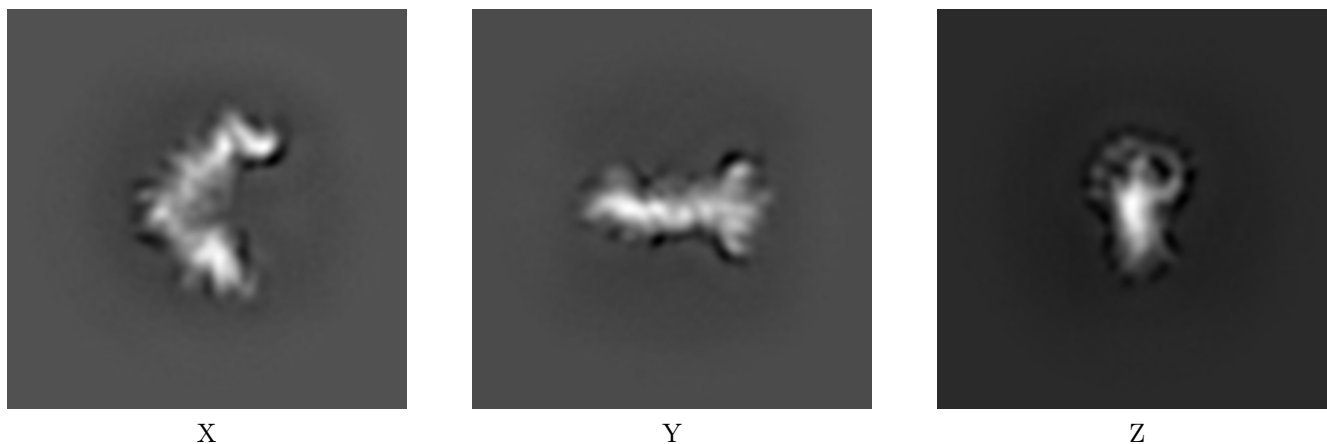
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43137. These allow visual inspection of the internal detail of the map and identification of artifacts.

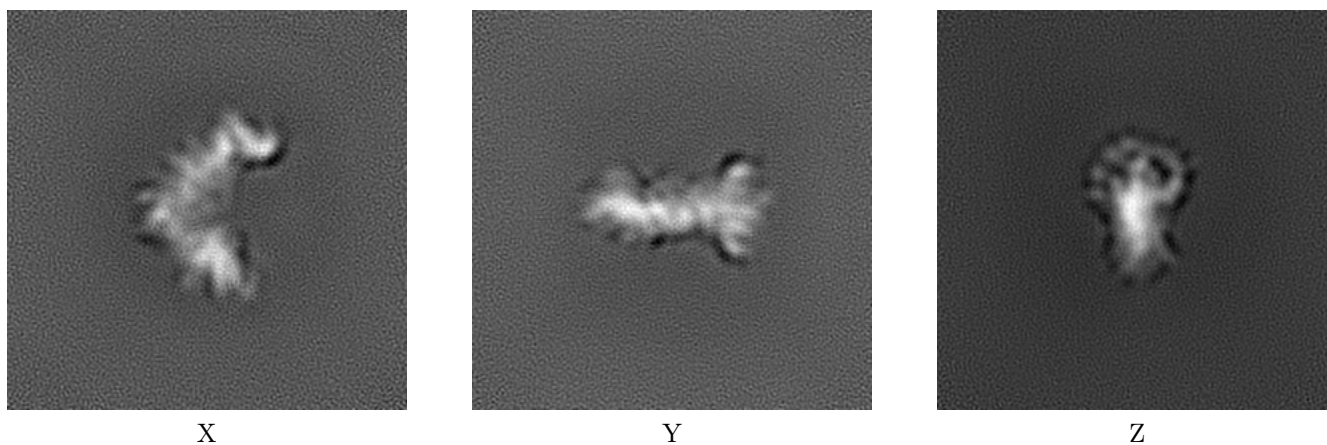
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

#### 6.1.1 Primary map



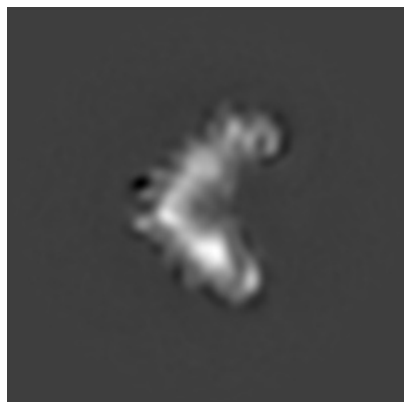
#### 6.1.2 Raw map



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

## 6.2 Central slices [i](#)

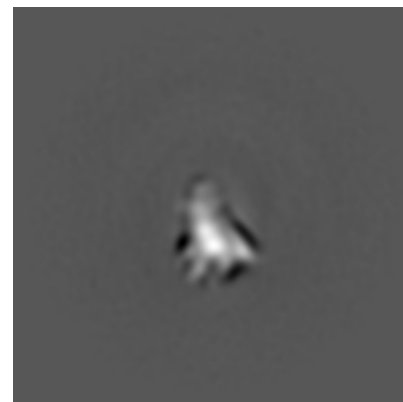
### 6.2.1 Primary map



X Index: 100



Y Index: 100

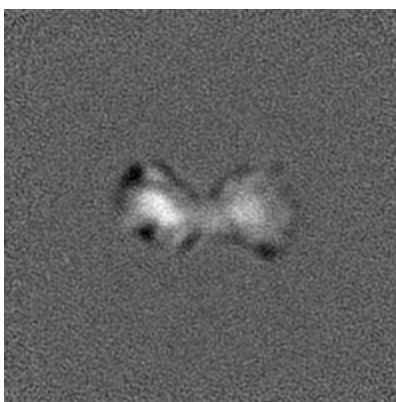


Z Index: 100

### 6.2.2 Raw map



X Index: 100



Y Index: 100



Z Index: 100

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: 99

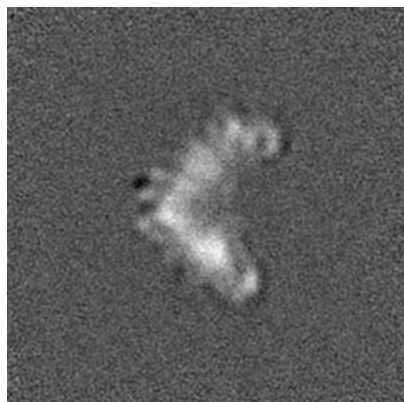


Y Index: 105

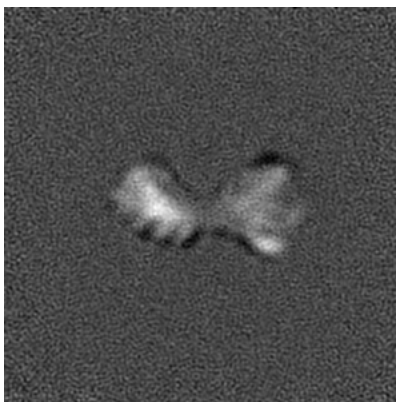


Z Index: 130

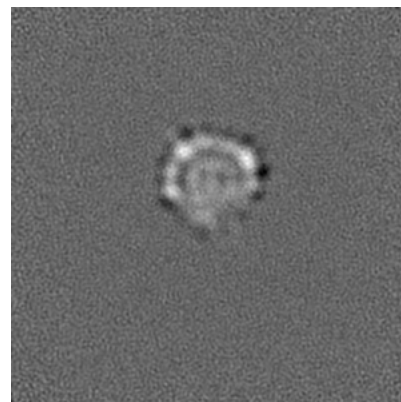
### 6.3.2 Raw map



X Index: 99



Y Index: 106

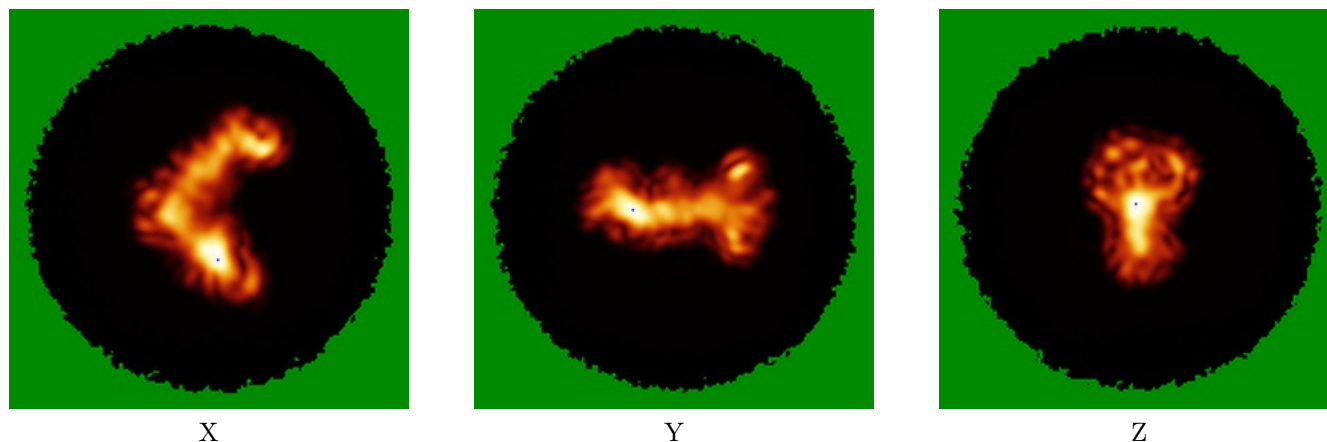


Z Index: 130

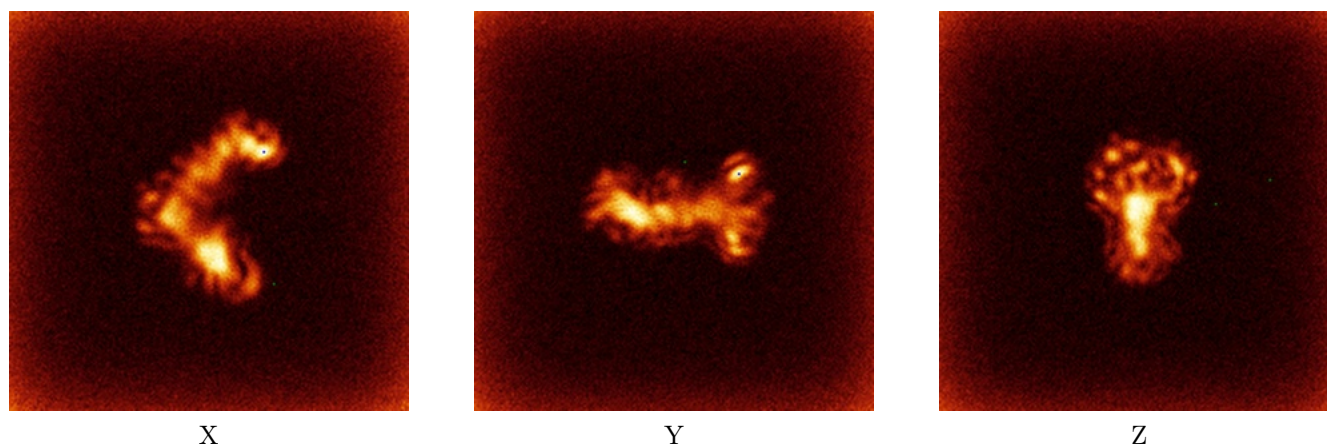
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



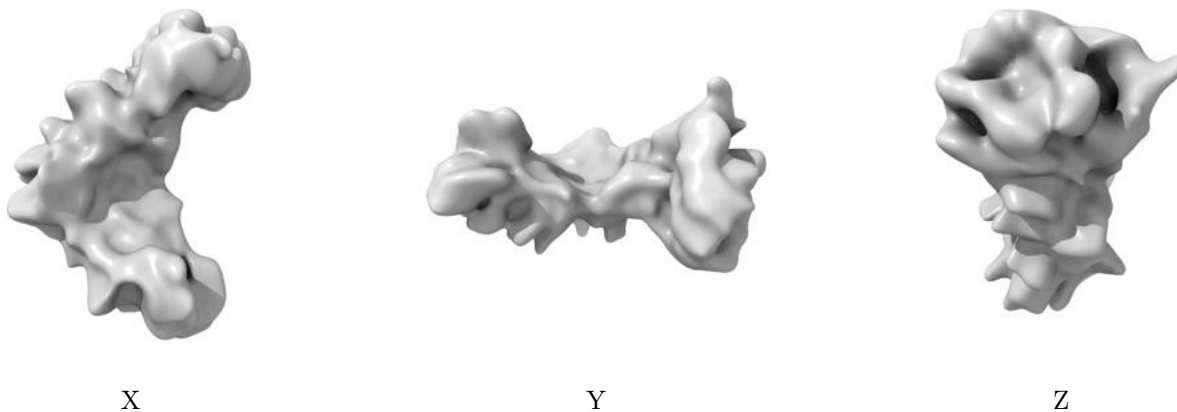
### 6.4.2 Raw map



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.

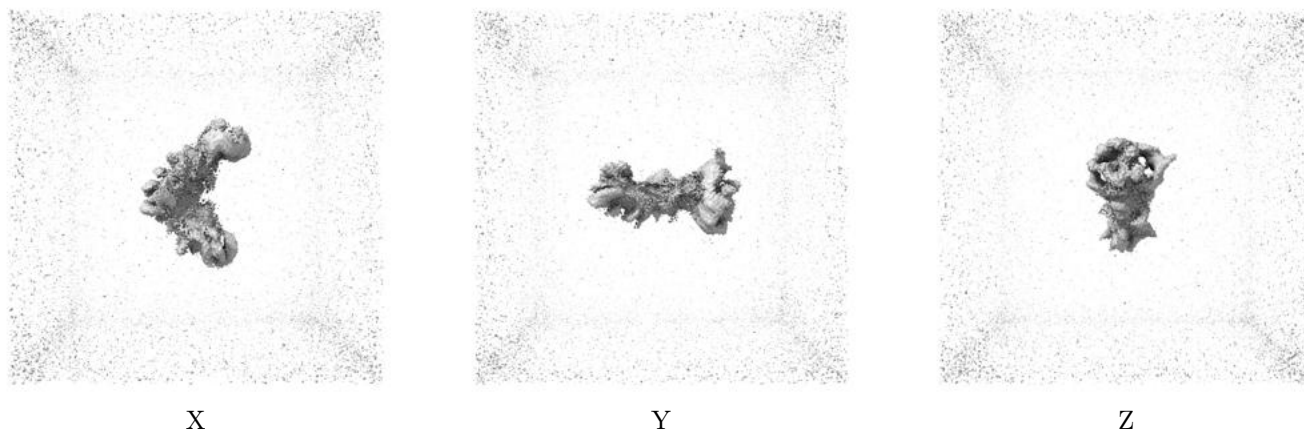
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

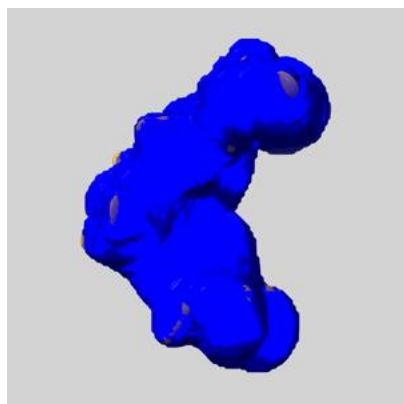
## 6.6 Mask visualisation [i](#)

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

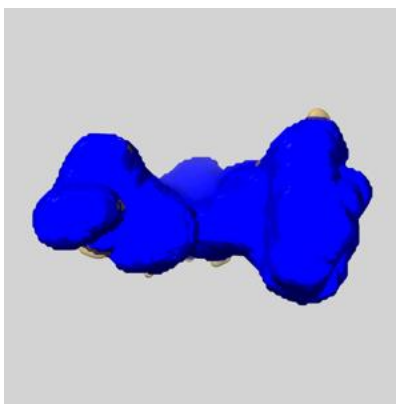
A mask typically either:

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

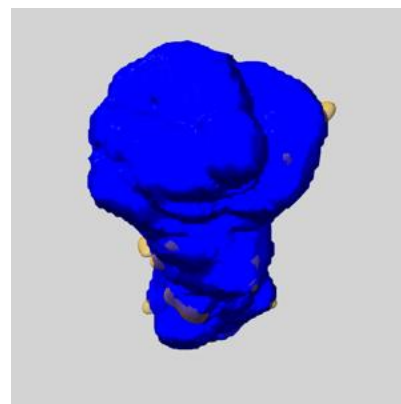
### 6.6.1 emd\_43137\_msk\_1.map [i](#)



X



Y



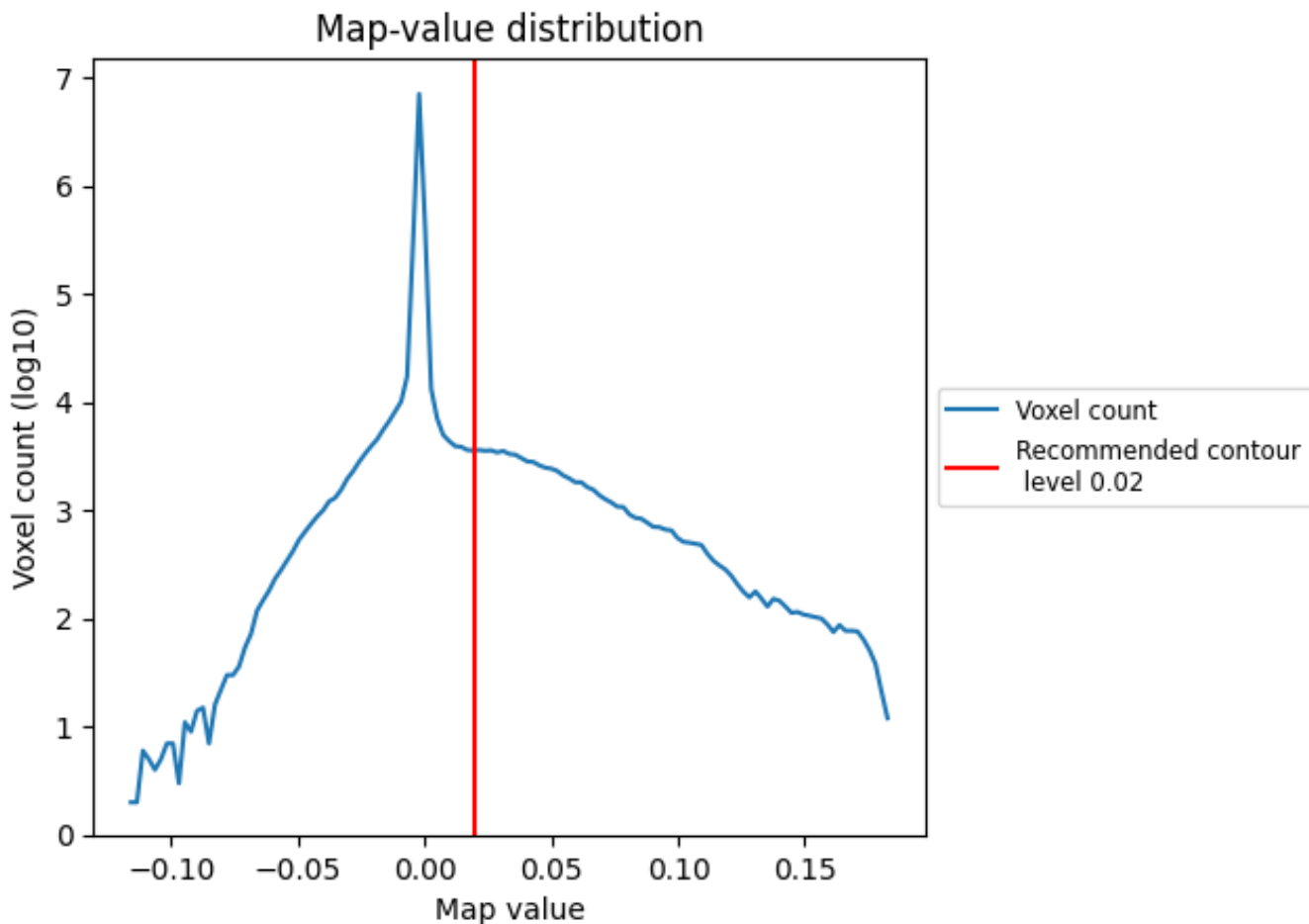
Z



## 7 Map analysis [i](#)

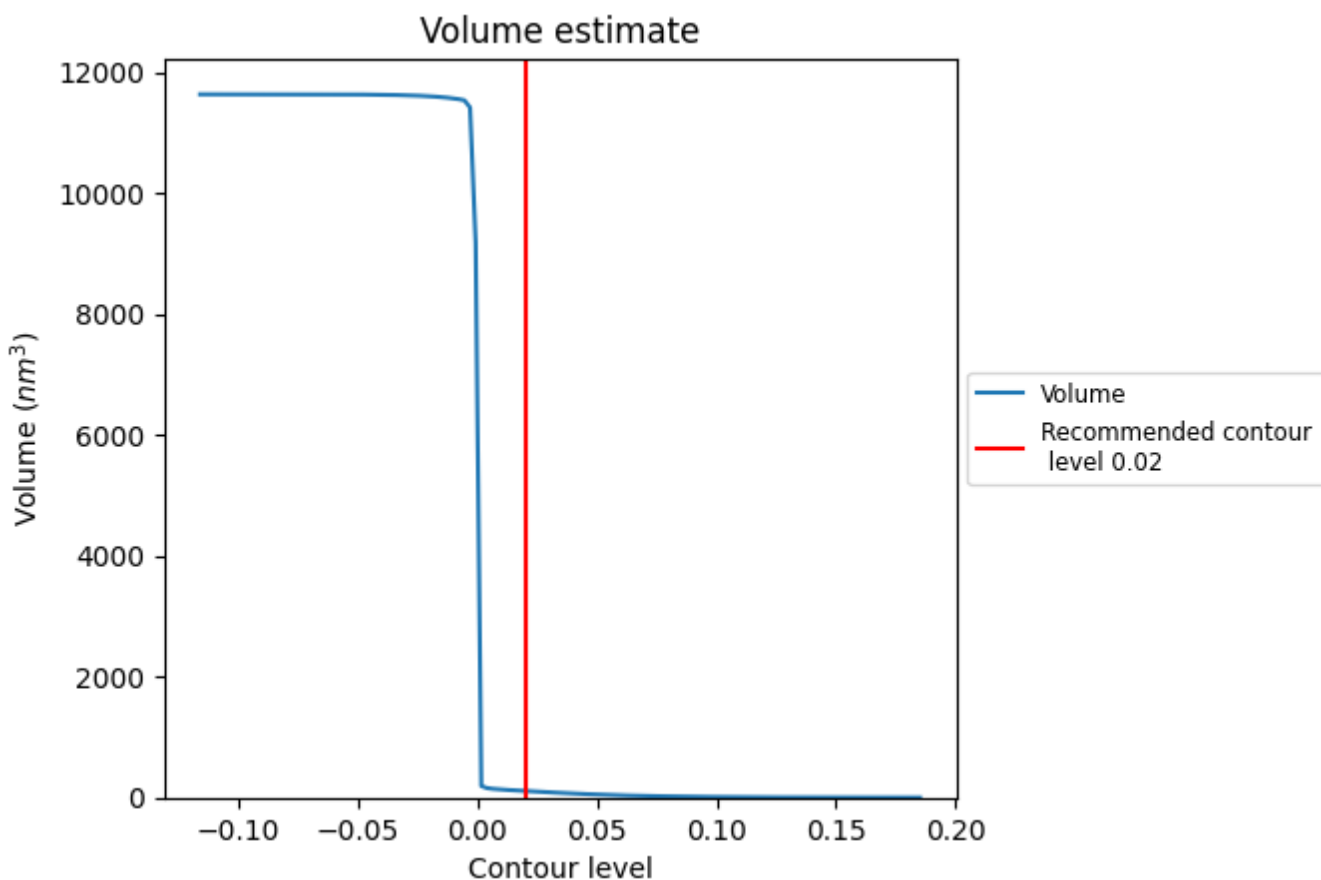
This section contains the results of statistical analysis of the map.

### 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.

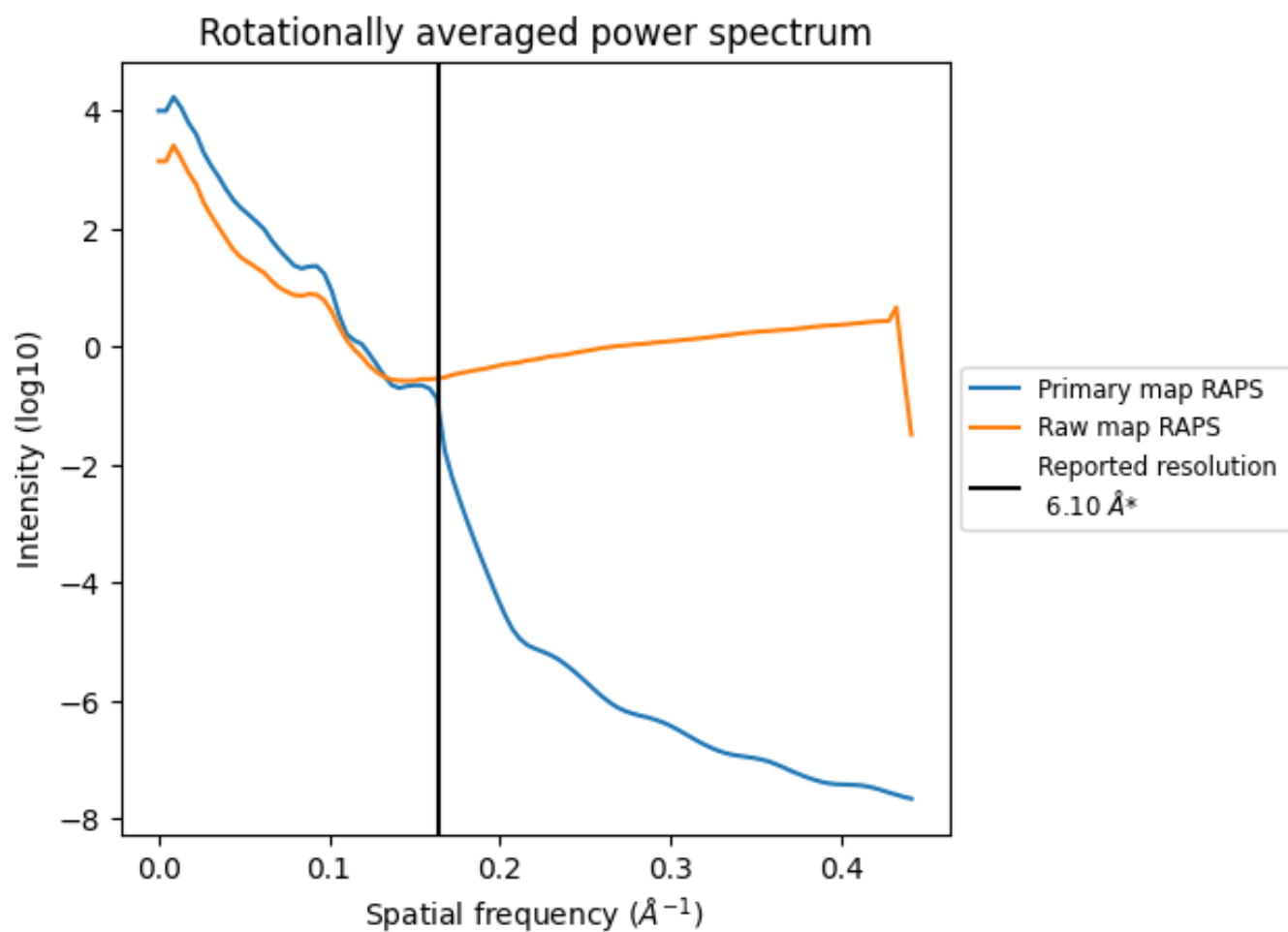
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 109 nm<sup>3</sup>; this corresponds to an approximate mass of 99 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 [i](#)

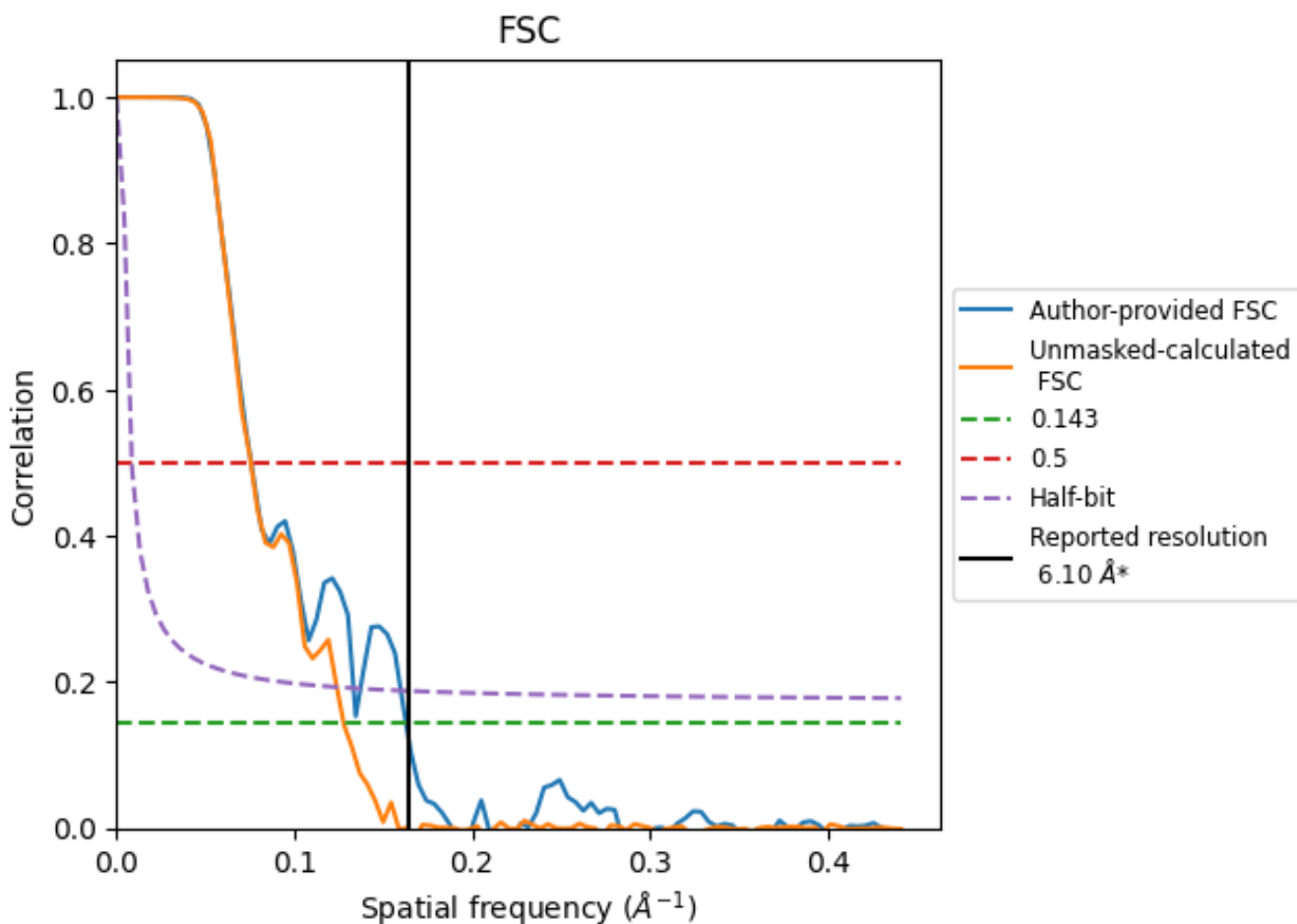


\*Reported resolution corresponds to spatial frequency of 0.164 Å<sup>-1</sup>

## 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 0.164 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

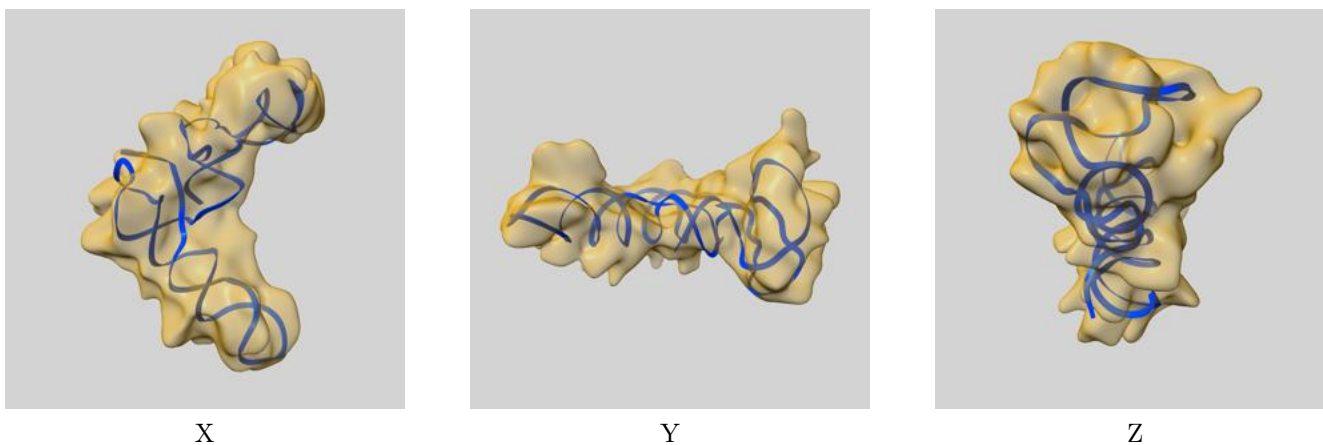
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.10	-	-
Author-provided FSC curve	6.14	13.19	7.50
Unmasked-calculated*	7.82	13.23	8.07

\*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 7.82 differs from the reported value 6.1 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43137 and PDB model 8VCI. Per-residue inclusion information can be found in section 3 on page 4.

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

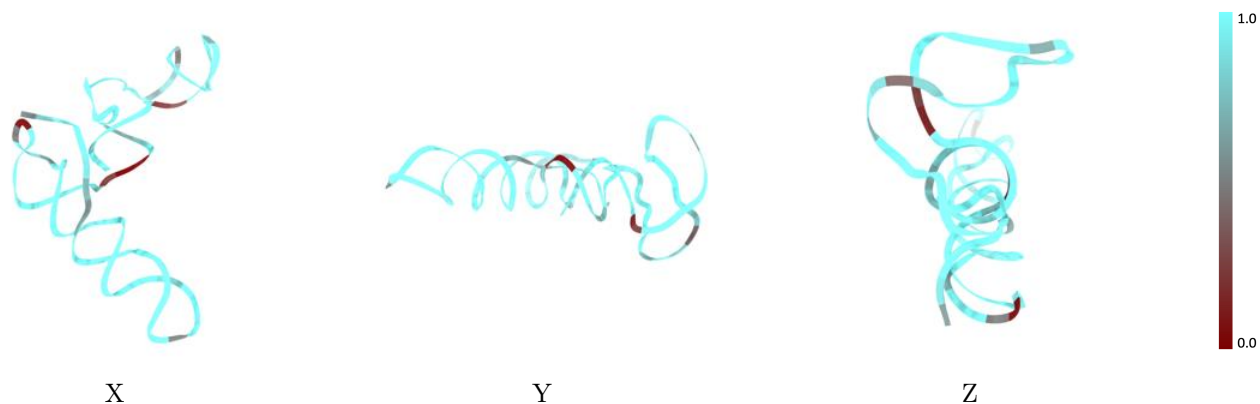


The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

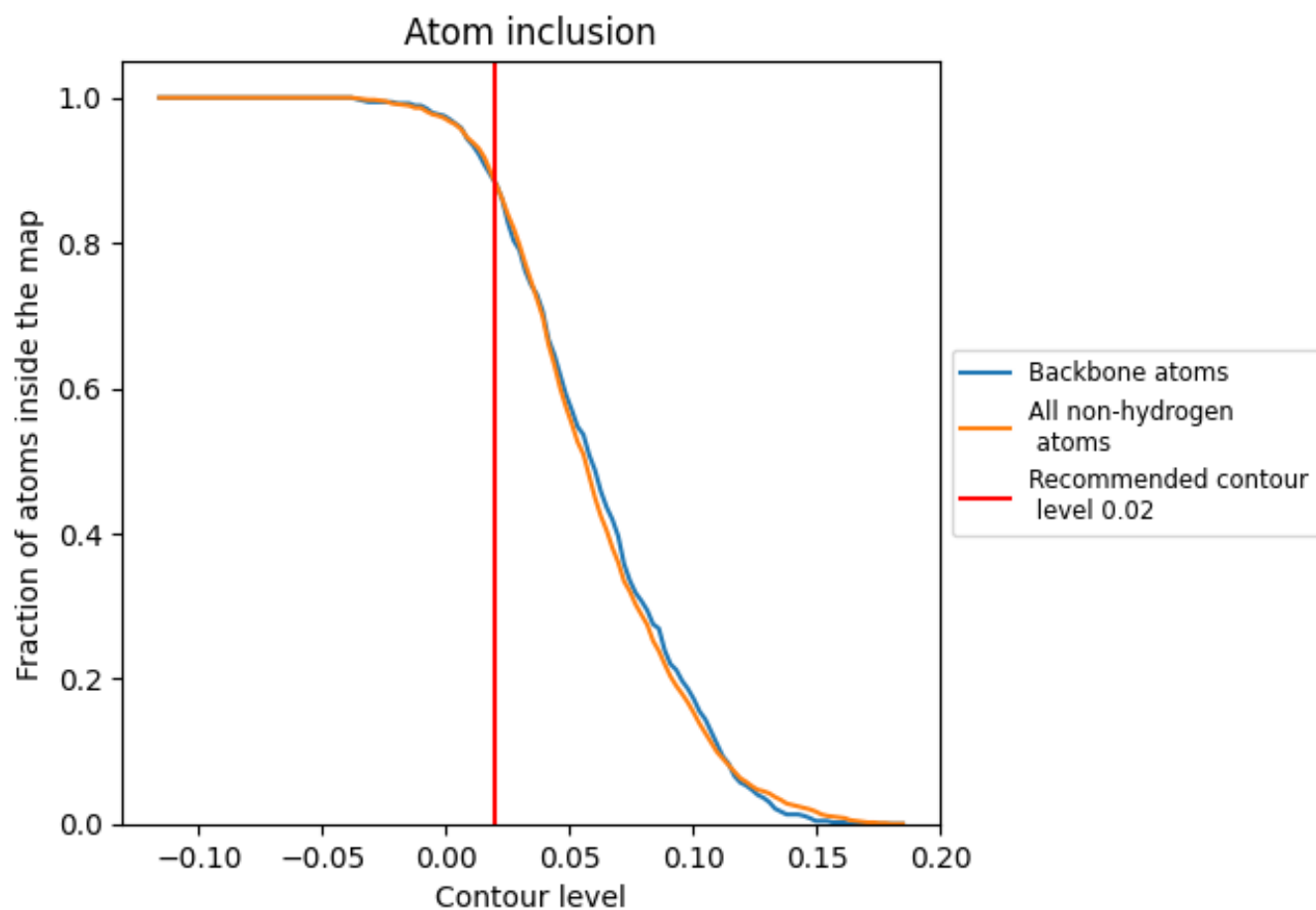
This section was not generated.

## 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 (0.02).

## 9.4 Atom inclusion [i](#)





At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	 0.8830
A	 0.8870

