



## wwPDB EM Validation Summary Report ⓘ

Nov 14, 2023 – 06:19 pm GMT

PDB ID : 8CRB  
EMDB ID : EMD-16807  
Title : Cryo-EM structure of PcrV/Fab(11-E5)  
Authors : Yuan, B.; Simonis, A.; Marlovits, T.C.  
Deposited on : 2023-03-08  
Resolution : 4.60 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.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

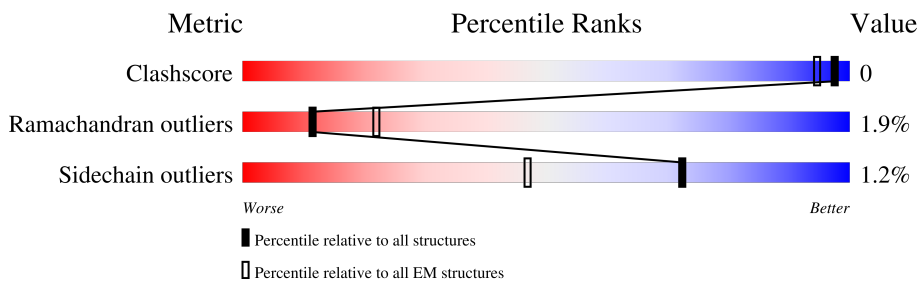
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.60 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	A	227	
2	B	216	
3	C	692	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 8665 atoms, of which 4286 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 Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	227	3320	1056	1631	284	341	8	0	0

- Molecule 2 is a protein called Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	B	216	3187	1010	1571	273	328	5	0	0

- Molecule 3 is a protein called Maltose/maltodextrin-binding periplasmic protein, Type III secretion protein PcrV.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
3	C	139	2158	677	1084	181	216	0	0

There are 53 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-397	MET	-	initiating methionine	UNP P0AEX9
C	-396	GLY	-	expression tag	UNP P0AEX9
C	-395	SER	-	expression tag	UNP P0AEX9
C	-394	TRP	-	expression tag	UNP P0AEX9
C	-393	SER	-	expression tag	UNP P0AEX9
C	-392	HIS	-	expression tag	UNP P0AEX9
C	-391	PRO	-	expression tag	UNP P0AEX9
C	-390	GLN	-	expression tag	UNP P0AEX9
C	-389	PHE	-	expression tag	UNP P0AEX9
C	-388	GLU	-	expression tag	UNP P0AEX9
C	-387	LYS	-	expression tag	UNP P0AEX9
C	-386	GLY	-	expression tag	UNP P0AEX9
C	-385	GLY	-	expression tag	UNP P0AEX9
C	-384	GLY	-	expression tag	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-383	SER	-	expression tag	UNP P0AEX9
C	-382	GLY	-	expression tag	UNP P0AEX9
C	-381	GLY	-	expression tag	UNP P0AEX9
C	-380	GLY	-	expression tag	UNP P0AEX9
C	-379	SER	-	expression tag	UNP P0AEX9
C	-378	GLY	-	expression tag	UNP P0AEX9
C	-377	GLY	-	expression tag	UNP P0AEX9
C	-376	GLY	-	expression tag	UNP P0AEX9
C	-375	SER	-	expression tag	UNP P0AEX9
C	-374	TRP	-	expression tag	UNP P0AEX9
C	-373	SER	-	expression tag	UNP P0AEX9
C	-372	HIS	-	expression tag	UNP P0AEX9
C	-371	PRO	-	expression tag	UNP P0AEX9
C	-370	GLN	-	expression tag	UNP P0AEX9
C	-369	PHE	-	expression tag	UNP P0AEX9
C	-368	GLU	-	expression tag	UNP P0AEX9
C	-367	LYS	-	expression tag	UNP P0AEX9
C	-366	SER	-	expression tag	UNP P0AEX9
C	-365	GLY	-	expression tag	UNP P0AEX9
C	-364	LEU	-	expression tag	UNP P0AEX9
C	-363	VAL	-	expression tag	UNP P0AEX9
C	-362	PRO	-	expression tag	UNP P0AEX9
C	-361	ARG	-	expression tag	UNP P0AEX9
C	-360	GLY	-	expression tag	UNP P0AEX9
C	-359	SER	-	expression tag	UNP P0AEX9
C	-358	ALA	-	expression tag	UNP P0AEX9
C	-357	SER	-	expression tag	UNP P0AEX9
C	-356	LYS	-	expression tag	UNP P0AEX9
C	-355	THR	-	expression tag	UNP P0AEX9
C	-275	ALA	ASP	conflict	UNP P0AEX9
C	-274	ALA	LYS	conflict	UNP P0AEX9
C	-185	ALA	GLU	conflict	UNP P0AEX9
C	-184	ALA	ASN	conflict	UNP P0AEX9
C	-142	HIS	ALA	conflict	UNP P0AEX9
C	-138	HIS	LYS	conflict	UNP P0AEX9
C	-45	VAL	ALA	conflict	UNP P0AEX9
C	-40	VAL	ILE	conflict	UNP P0AEX9
C	21	PRO	SER	conflict	UNP G3XD49
C	225	LYS	SER	conflict	UNP G3XD49



ALA  
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VAL  
LEU  
GLN  
THR  
GLN  
ASP  
GLY  
K127  
R128  
R163  
Y179  
D226  
D233  
N234  
T265  
SER  
SER  
ARG

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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	99625	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 ( $e^-/\text{\AA}^2$ )	1.24	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.026	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00418	Depositor
Map size ( $\text{\AA}$ )	142.8, 142.8, 142.8	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.85, 0.85, 0.85	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	0.71	0/1729	1.06	4/2350 (0.2%)
2	B	0.67	0/1657	1.04	2/2263 (0.1%)
3	C	0.62	0/1091	0.92	3/1475 (0.2%)
All	All	0.67	0/4477	1.02	9/6088 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	62	ARG	NE-CZ-NH2	7.13	123.86	120.30
1	A	87	ARG	NE-CZ-NH2	6.42	123.51	120.30
1	A	19	ARG	NE-CZ-NH2	6.21	123.40	120.30
1	A	38	ARG	NE-CZ-NH2	6.01	123.31	120.30
3	C	128	ARG	NE-CZ-NH2	5.90	123.25	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	195	TYR	Sidechain
2	B	37	TYR	Sidechain
2	B	99	TYR	Sidechain



## 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	1689	1631	1631	4	0
2	B	1616	1571	1571	2	0
3	C	1074	1084	1083	0	0
All	All	4379	4286	4285	4	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 0.

All (4) 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:78:THR:HG23	1:A:80:TYR:OH	2.13	0.48
1:A:97:ALA:HB2	1:A:117:TRP:CE3	2.52	0.44
1:A:45:LEU:HD12	2:B:101:PHE:CZ	2.55	0.42
1:A:117:TRP:CZ2	2:B:92:TRP:CZ3	3.08	0.41

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	225/227 (99%)	190 (84%)	30 (13%)	5 (2%)	6	37
2	B	214/216 (99%)	193 (90%)	17 (8%)	4 (2%)	8	40
3	C	137/692 (20%)	124 (90%)	11 (8%)	2 (2%)	10	46
All	All	576/1135 (51%)	507 (88%)	58 (10%)	11 (2%)	11	40

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	SER
1	A	60	TYR
3	C	233	ASP
2	B	95	SER
2	B	155	ASP

### 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	188/188 (100%)	186 (99%)	2 (1%)	73	85
2	B	181/181 (100%)	179 (99%)	2 (1%)	73	85
3	C	119/556 (21%)	117 (98%)	2 (2%)	60	78
All	All	488/925 (53%)	482 (99%)	6 (1%)	72	84

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	74	LEU
3	C	226	ASP
3	C	234	ASN
1	A	98	GLN
1	A	80	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 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](#)

There are no chain breaks in this entry.

## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16807. 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](#)

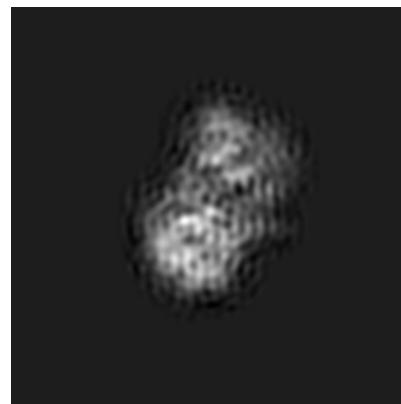
#### 6.1.1 Primary map



X

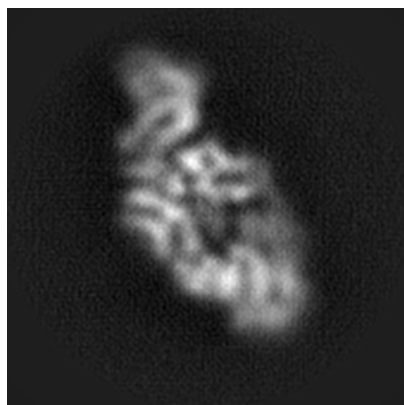


Y

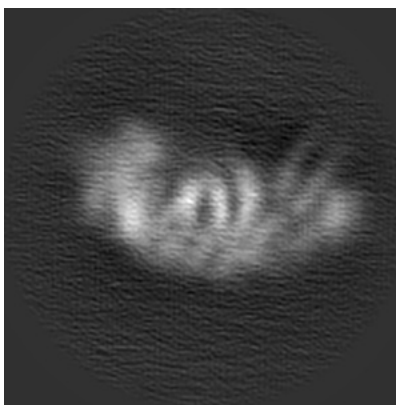


Z

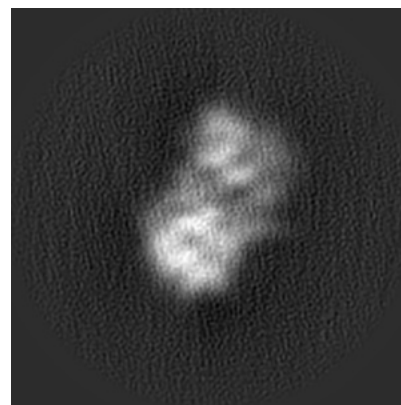
#### 6.1.2 Raw map



X



Y

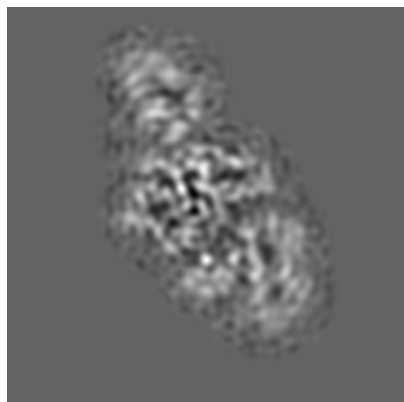


Z

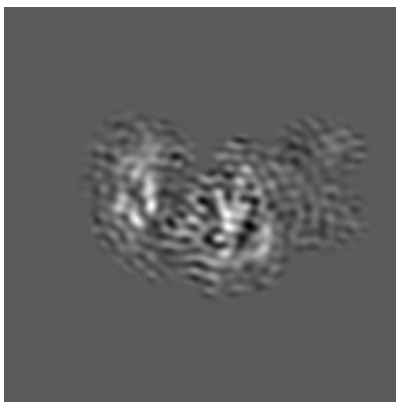
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 84

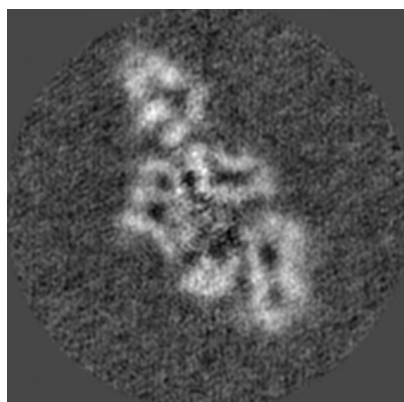


Y Index: 84

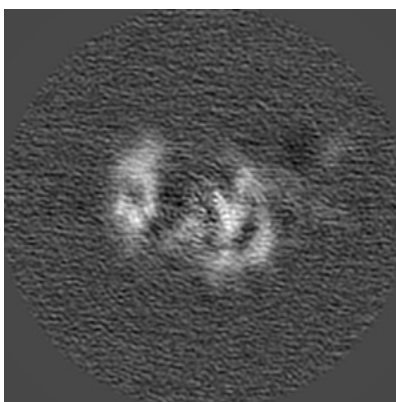


Z Index: 84

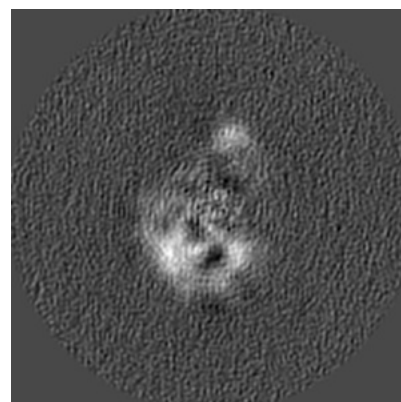
### 6.2.2 Raw map



X Index: 84



Y Index: 84

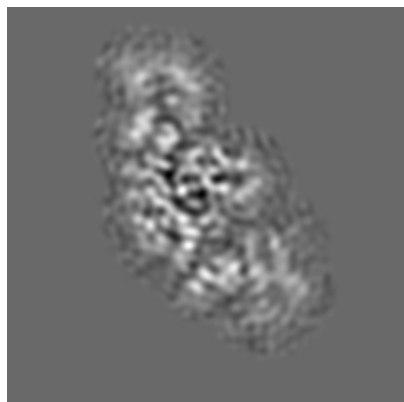


Z Index: 84

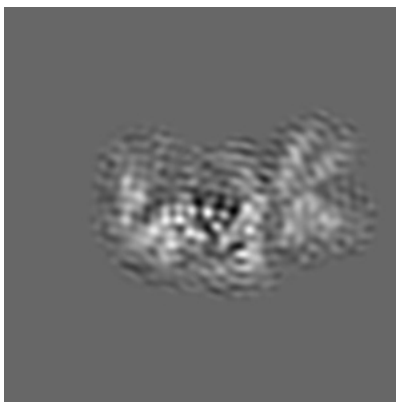
The images above show central slices of the map in three orthogonal directions.

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

### 6.3.1 Primary map



X Index: 79

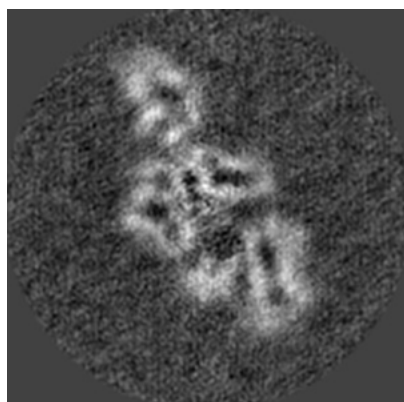


Y Index: 77

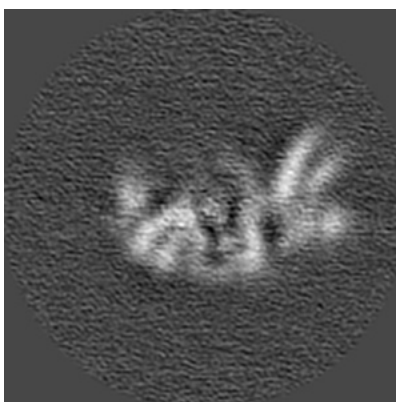


Z Index: 91

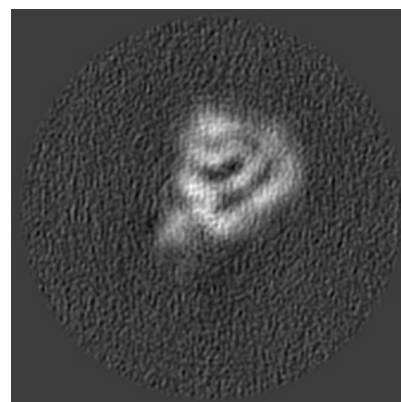
### 6.3.2 Raw map



X Index: 83



Y Index: 75



Z Index: 54

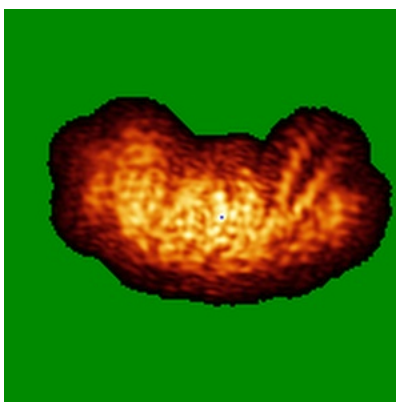
The images above show the largest variance slices of the map in three orthogonal directions.

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

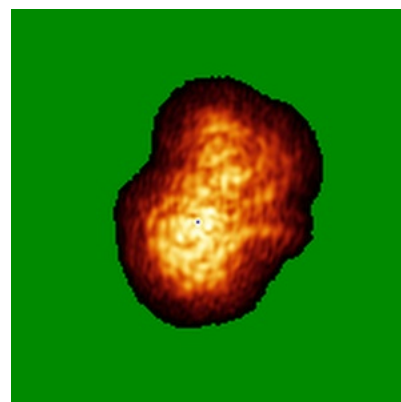
### 6.4.1 Primary map



X

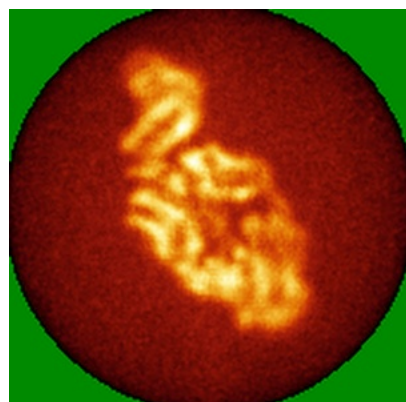


Y

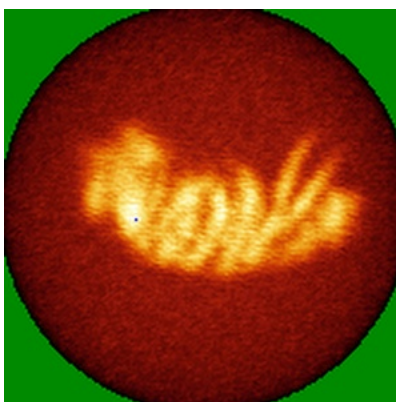


Z

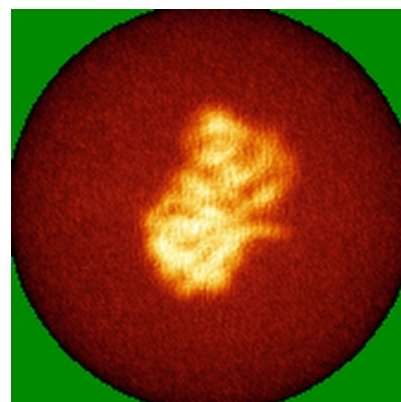
### 6.4.2 Raw map



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.



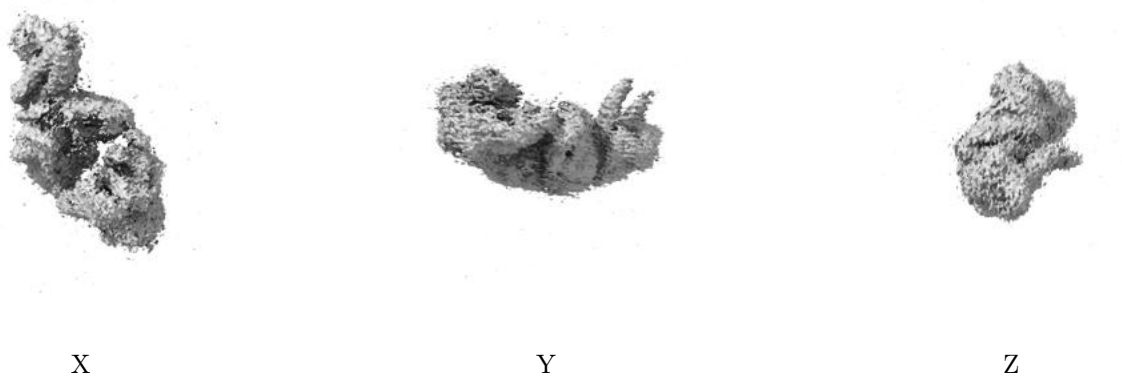
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00418. 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](#)

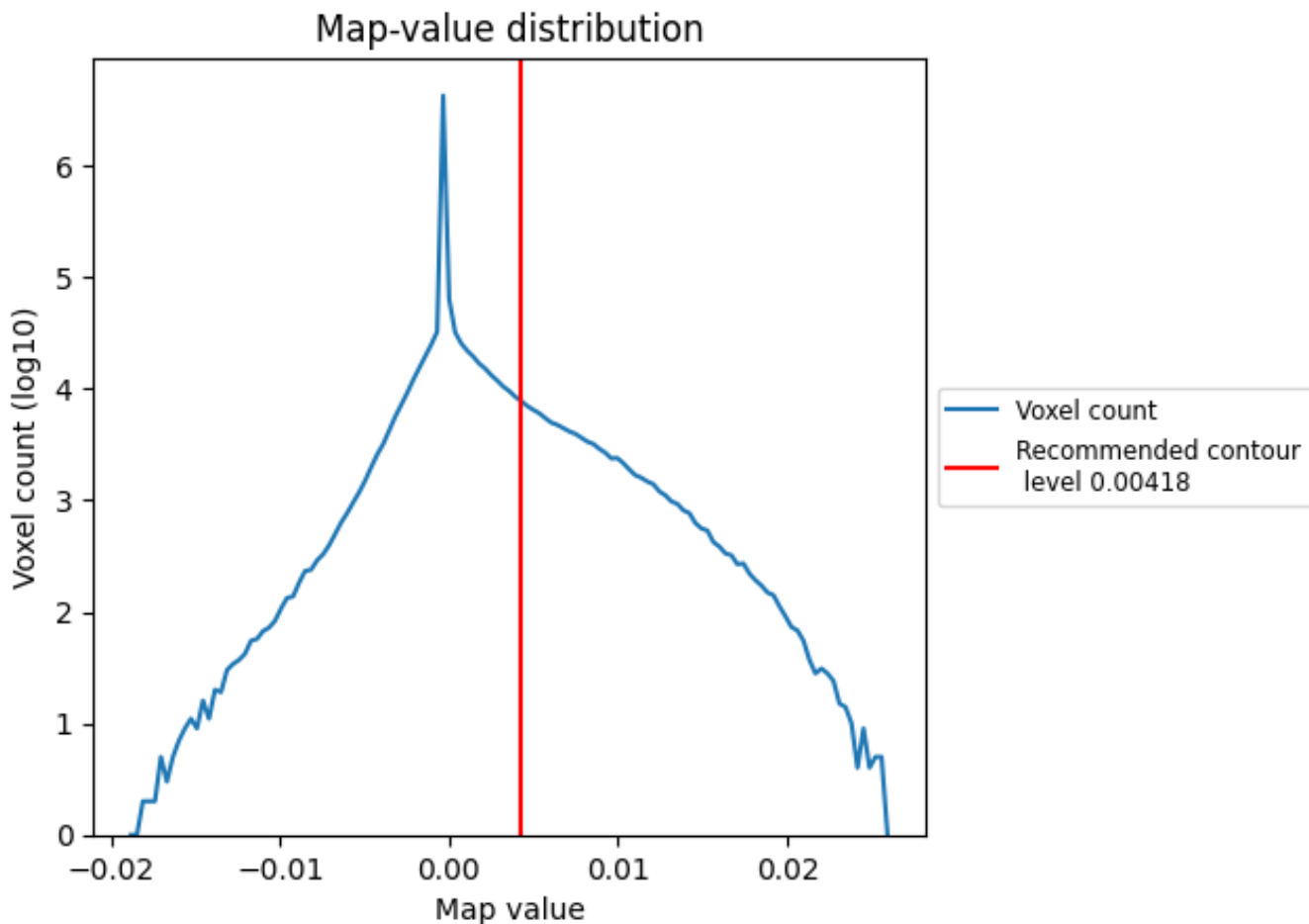
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

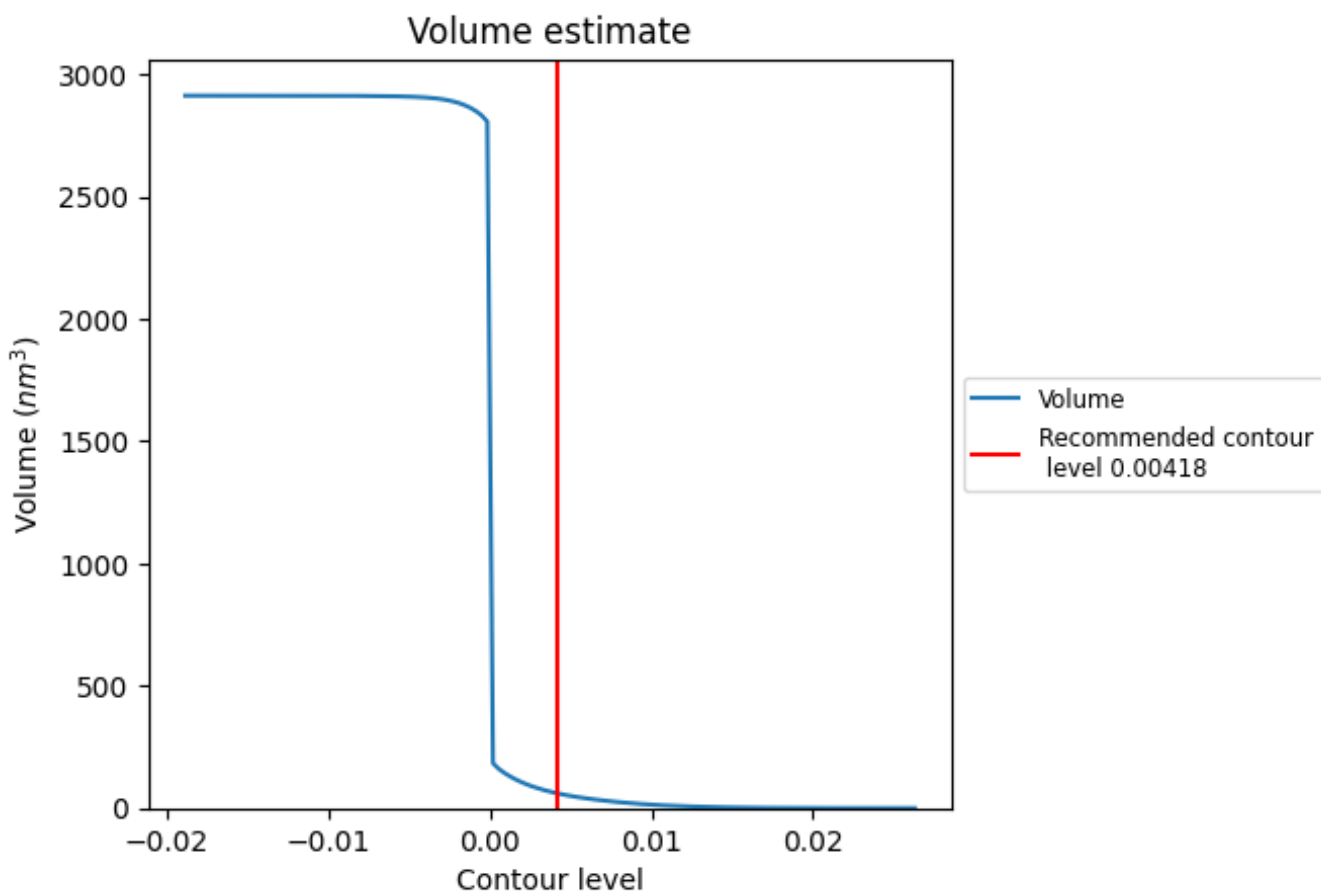
This section contains the results of statistical analysis of the map.

### 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.

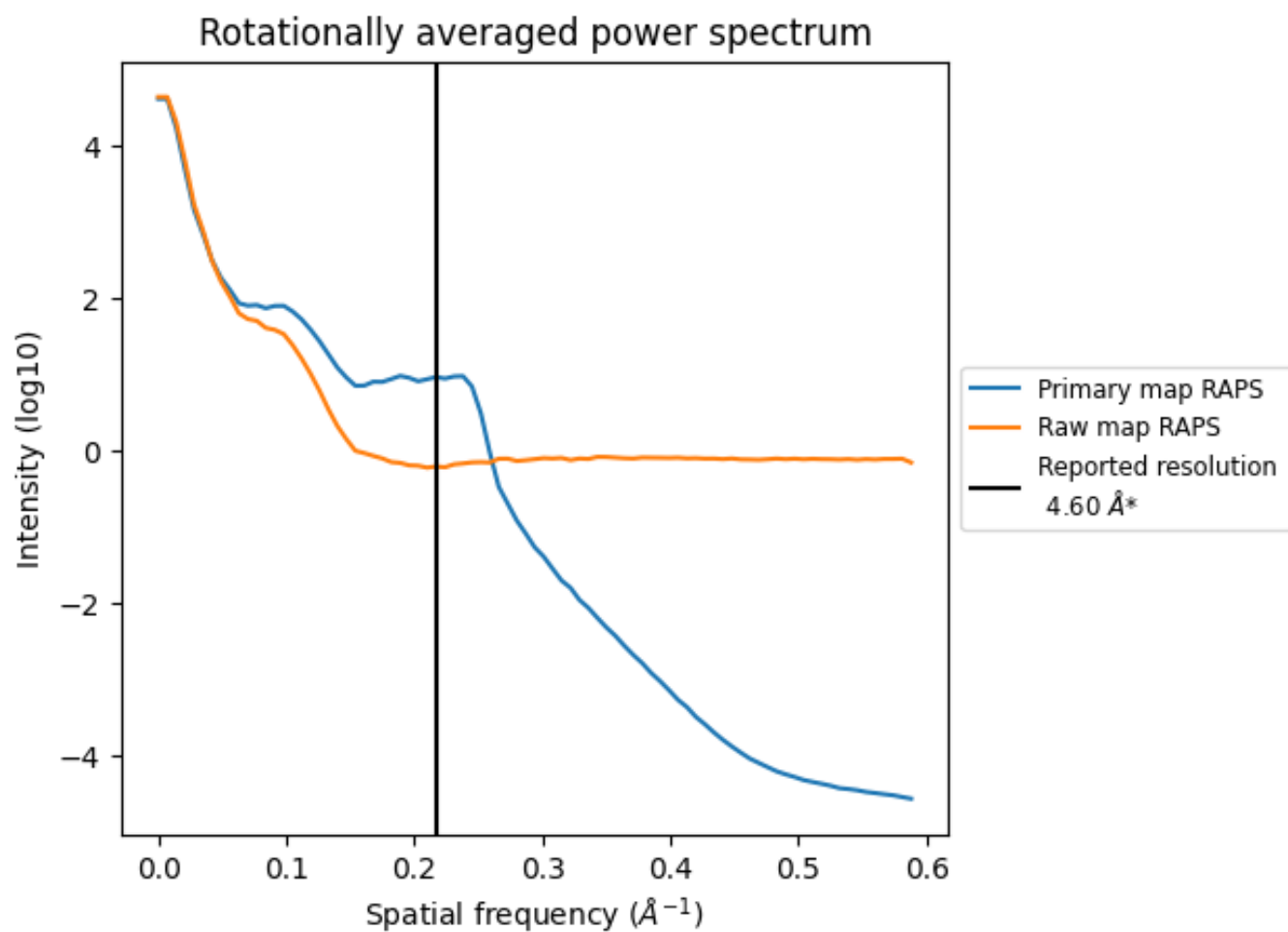
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 61  $\text{nm}^3$ ; this corresponds to an approximate mass of 55 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](#)

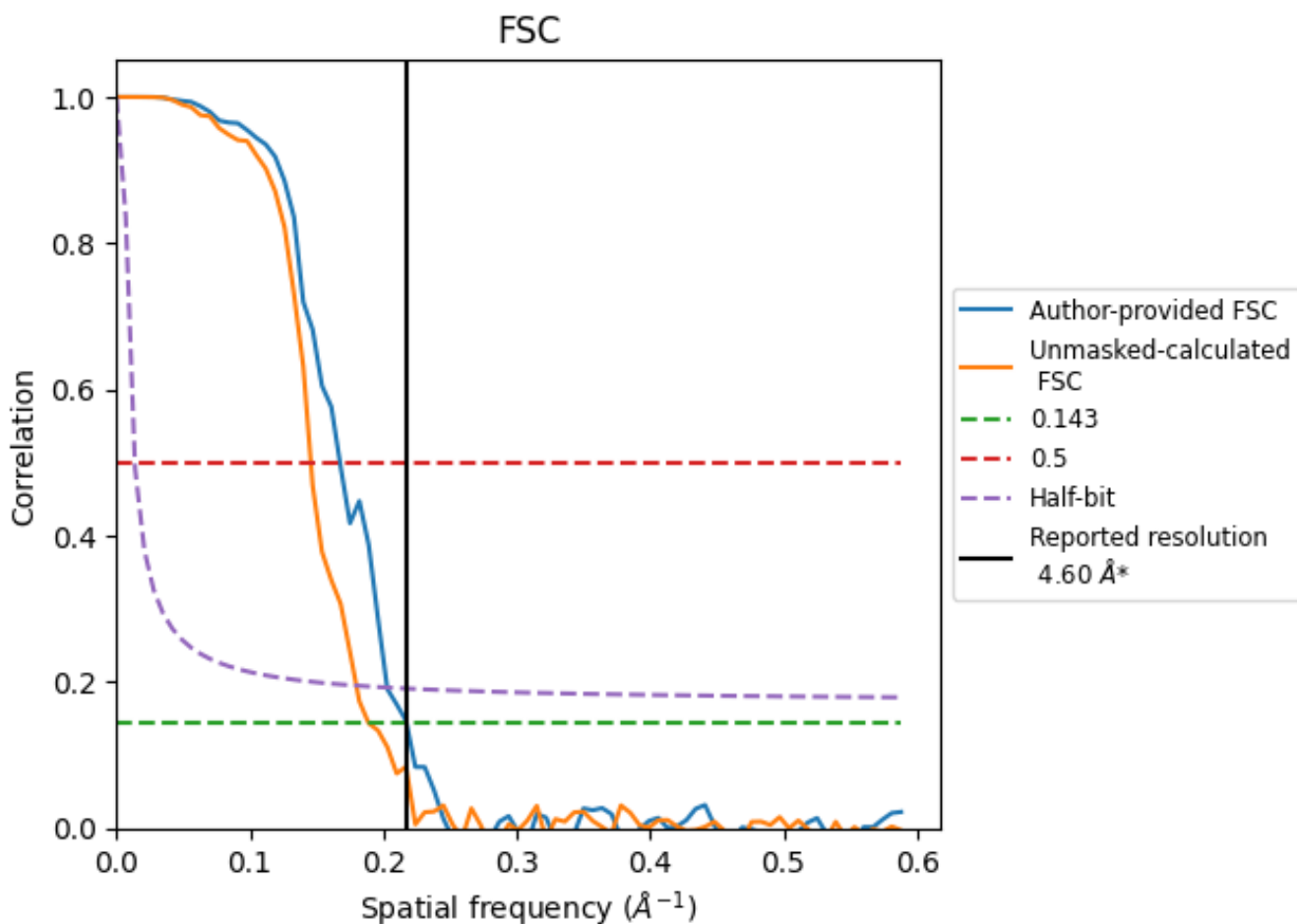


\*Reported resolution corresponds to spatial frequency of 0.217 Å<sup>-1</sup>

## 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 0.217 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

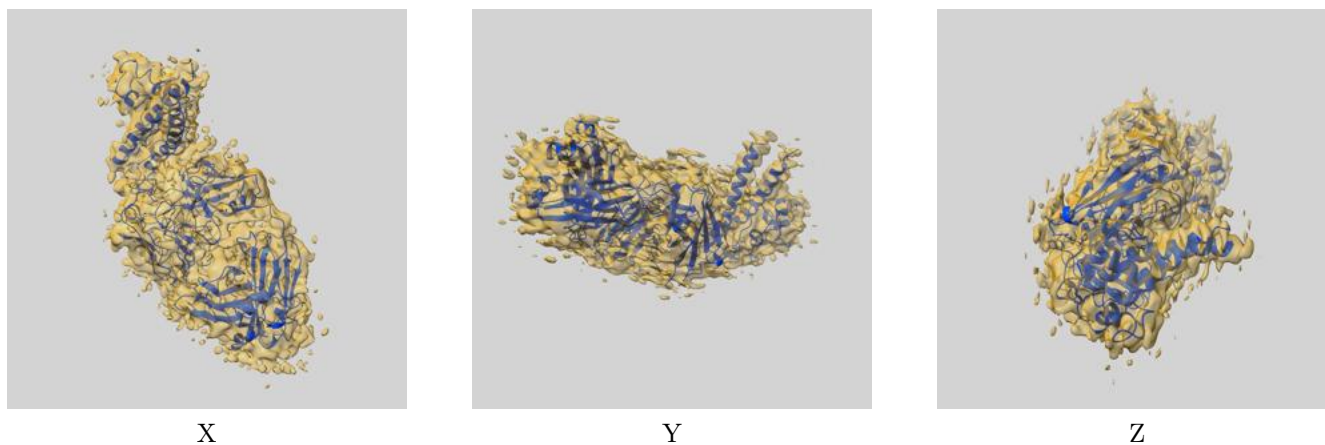
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.60	5.97	4.93
Unmasked-calculated*	5.29	6.86	5.56

\*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 5.29 differs from the reported value 4.6 by more than 10 %

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

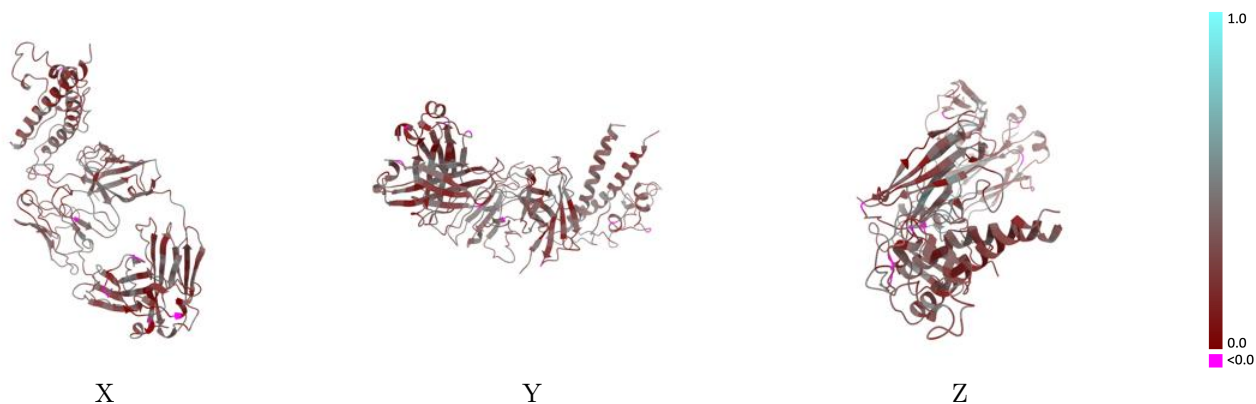
This section contains information regarding the fit between EMDB map EMD-16807 and PDB model 8CRB. Per-residue inclusion information can be found in section 3 on page 5.

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



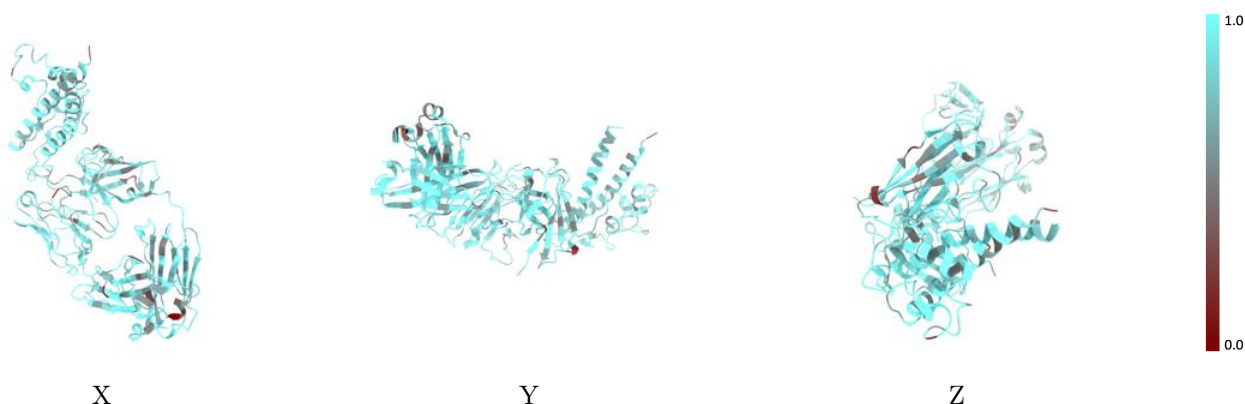
The images above show the 3D surface view of the map at the recommended contour level 0.00418 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



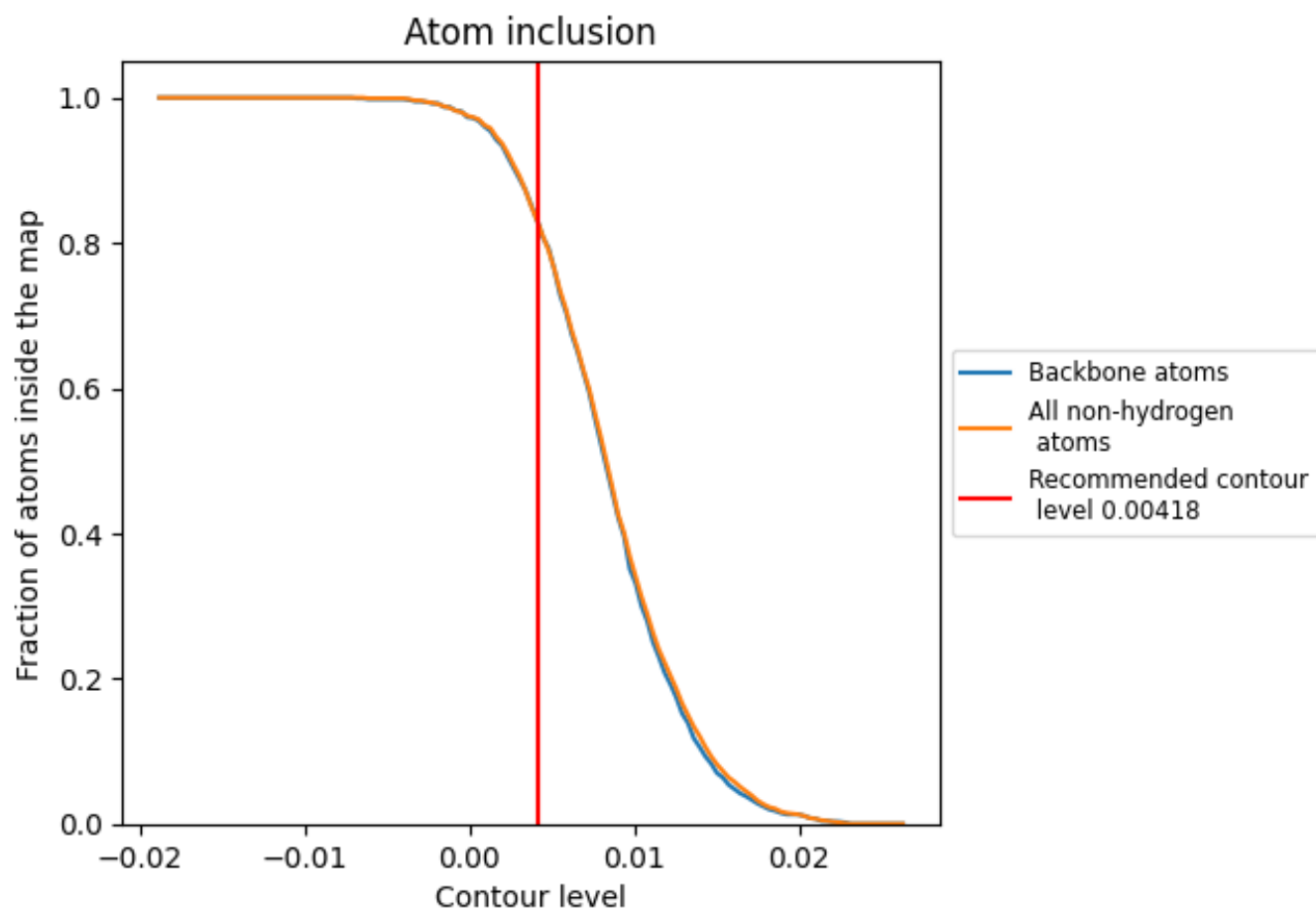
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00418).

## 9.4 Atom inclusion [i](#)











At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.00418) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8260	 0.3080
A	 0.8330	 0.3170
B	 0.8310	 0.3070
C	 0.8370	 0.2940

