



# Full wwPDB EM Validation Report ⓘ

Oct 26, 2024 – 09:58 PM EDT

PDB ID : 7JI3  
EMDB ID : EMD-22343  
Title : Cryo-EM structure of a proton-activated chloride channel  
Authors : Deng, Z.; Zhang, J.; Yuan, P.  
Deposited on : 2020-07-22  
Resolution : 3.46 Å(reported)

This is a Full wwPDB EM Validation 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

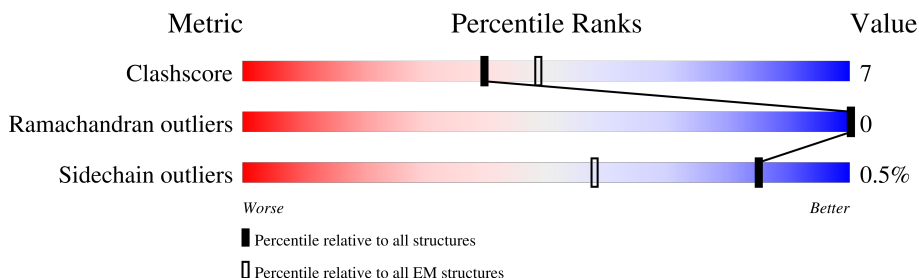
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.46 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	A	463	
1	B	463	
1	C	463	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6000 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 Proton-activated chloride channel.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	259	Total	C	N	O	S	0	0
			2000	1279	335	374	12		
1	B	259	Total	C	N	O	S	0	0
			2000	1279	335	374	12		
1	C	259	Total	C	N	O	S	0	0
			2000	1279	335	374	12		





MET	ARG	ARG	ASN	SER	TYR	ARG	GLU	PHE	ILE	ASP	GLU	ASP	ASP	GLU	ASP	ASP	GLY	ASN	LYS	ASP	VAL	PRO	ASN	CYS	PHE	ASP	ASP	VAL	ILE	ASP	SER	PRO	GLU	GLU	VAL	GLU	PRO	ASN	ASP	ASN	ASP	SER	ALA	ALA	SER	PRO	PRO	ASP	ASP	ASN	ARG	GLN	GLU	SER	SER	ARG	PHE	ARG	SER	LYS
LEU	CYS	VAL	LYS	M85		T88		L71	L72	L73	I74		L77	L78	Q88		V93	L94	E95		Q107	E108		R114		L119		Q125		C129	S130	H131		R145		D150		V159	GLY	PRO	PHE	SER	SER	GLN	GLY	GLU	K168	R169		S177		R180		E183	M184		F189			
E193		S235	G236		G251	LYS	ASN	D255		F268	N269	D270		A275	Y282		Q295		I299		A302		W305	S306	S307		I310		F315	M316		A322	N323		R334	MET	ARG	LYS	ARG	HIS	LEU	ARG	ASN	LYS	GLU	ARG	GLU	LEU	LYS	LYS	PHE	ARG	HIS	ALA	ASP	LEU	GLU	ASP	ASN	TRP
THR	LEU	ASN	ASP	ASN	LEU	LYS	VAL	VAL	ILE	GLU	LYS	ALA	ASP	ASN	ALA	GLN	VAL	LYS	ASP	ALA	LEU	THR	LYS	MET	ARG	ALA	ALA	ALA	LEU	ASP	ALA	GLN	LYS	ALA	THR	PRO	PRO	LYS	LEU	GLU	ASP	LYS	LYS	SER	PRO	PRO	ASP	ASN	GLU	MET	LYS	ASP	PHE	ARG	HIS	GLY	PHE	ASP	ILE	
LEU	VAL	GLY	GLN	ILE	ASP	ASP	ALA	LEU	LYS	LEU	ALA	ASN	GLU	LYS	VAL	GLU	ALA	GLN	LYS	GLN	ALA	ALA	GLN	LEU	ALA	TYR	ILE	GLN	LYS	LYS	THR	THR	ARG	ASN	ASN	ALA	ALA	ASN	SER	ASN	LEU	LEU	GLU	VAL	LEU	PHE														

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	505115	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 ( $e^-/\text{\AA}^2$ )	62, 62	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.069	Depositor
Minimum map value	-0.034	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.015	Depositor
Map size ( $\text{\AA}$ )	242.0, 242.0, 242.0	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	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	0.33	0/2045	0.49	0/2777
1	B	0.33	0/2045	0.50	0/2777
1	C	0.33	0/2045	0.50	0/2777
All	All	0.33	0/6135	0.50	0/8331

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	2000	0	1891	39	0
1	B	2000	0	1891	37	0
1	C	2000	0	1891	36	0
All	All	6000	0	5673	81	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 7.

All (81) 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:316:MET:HE1	1:C:316:MET:HG3	1.37	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ILE:O	1:B:78:LEU:HD13	1.63	0.98
1:A:316:MET:HG3	1:B:316:MET:HE1	1.51	0.90
1:A:310:ILE:HD13	1:C:306:SER:OG	1.73	0.89
1:A:316:MET:HG3	1:B:316:MET:CE	2.09	0.82
1:B:129:CYS:SG	1:B:150:ASP:HB2	2.22	0.79
1:A:306:SER:OG	1:B:310:ILE:HD13	1.83	0.78
1:A:316:MET:CE	1:C:316:MET:HG3	2.13	0.78
1:A:129:CYS:SG	1:A:150:ASP:HB2	2.23	0.78
1:B:306:SER:OG	1:C:310:ILE:HD13	1.84	0.77
1:A:73:LEU:O	1:A:77:LEU:HD13	1.85	0.76
1:A:316:MET:HE1	1:C:316:MET:CG	2.14	0.76
1:B:316:MET:HG3	1:C:316:MET:CE	2.16	0.75
1:C:129:CYS:SG	1:C:150:ASP:HB2	2.27	0.73
1:A:88:GLN:HG2	1:C:305:TRP:CD1	2.30	0.67
1:A:316:MET:HE2	1:B:316:MET:HE1	1.76	0.66
1:A:310:ILE:CD1	1:C:306:SER:OG	2.45	0.64
1:A:316:MET:CG	1:B:316:MET:HE1	2.29	0.61
1:B:74:ILE:O	1:B:78:LEU:CD1	2.44	0.59
1:A:306:SER:OG	1:B:310:ILE:CD1	2.51	0.59
1:B:316:MET:CE	1:C:316:MET:HE2	2.33	0.59
1:B:305:TRP:CD1	1:C:88:GLN:HG2	2.37	0.59
1:C:268:PHE:CE2	1:C:270:ASP:OD1	2.56	0.58
1:A:268:PHE:CE2	1:A:270:ASP:OD1	2.56	0.57
1:A:189:PHE:HB2	1:A:282:TYR:HB2	1.86	0.57
1:B:268:PHE:CE2	1:B:270:ASP:OD1	2.56	0.57
1:B:189:PHE:HB2	1:B:282:TYR:HB2	1.86	0.57
1:C:189:PHE:HB2	1:C:282:TYR:HB2	1.86	0.56
1:B:316:MET:HG3	1:C:316:MET:HE1	1.87	0.56
1:A:305:TRP:CD1	1:B:88:GLN:HG2	2.43	0.53
1:C:74:ILE:O	1:C:78:LEU:HG	2.08	0.53
1:A:93:VAL:HG21	1:A:307:SER:HB2	1.90	0.53
1:A:74:ILE:O	1:A:78:LEU:HG	2.08	0.53
1:C:93:VAL:HG21	1:C:307:SER:HB2	1.90	0.53
1:B:306:SER:OG	1:C:310:ILE:CD1	2.53	0.53
1:B:93:VAL:HG21	1:B:307:SER:HB2	1.90	0.52
1:A:193:GLU:OE1	1:C:269:ASN:ND2	2.43	0.52
1:C:107:GLN:NE2	1:C:295:GLN:OE1	2.44	0.51
1:B:107:GLN:NE2	1:B:295:GLN:OE1	2.44	0.51
1:A:107:GLN:NE2	1:A:295:GLN:OE1	2.44	0.51
1:B:235:SER:OG	1:B:236:GLY:N	2.46	0.49
1:A:235:SER:OG	1:A:236:GLY:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ASN:HD22	1:C:299:ILE:HD11	1.78	0.48
1:A:316:MET:SD	1:C:316:MET:HG3	2.54	0.48
1:B:119:LEU:HD13	1:B:189:PHE:HZ	1.79	0.48
1:B:262:GLU:OE2	1:B:289:ARG:HD3	2.14	0.48
1:A:88:GLN:CG	1:C:305:TRP:CD1	2.96	0.47
1:A:119:LEU:HD13	1:A:189:PHE:HZ	1.79	0.47
1:C:119:LEU:HD13	1:C:189:PHE:HZ	1.79	0.47
1:A:269:ASN:OD1	1:A:269:ASN:N	2.46	0.47
1:B:131:HIS:ND1	1:B:183:GLU:OE2	2.48	0.47
1:B:131:HIS:NE2	1:B:150:ASP:OD2	2.48	0.47
1:C:125:GLN:OE1	1:C:145:ARG:NH1	2.48	0.47
1:C:235:SER:OG	1:C:236:GLY:N	2.46	0.47
1:C:316:MET:SD	1:C:316:MET:C	2.94	0.46
1:A:125:GLN:OE1	1:A:145:ARG:NH1	2.48	0.46
1:A:131:HIS:ND1	1:A:183:GLU:OE2	2.48	0.46
1:C:131:HIS:NE2	1:C:150:ASP:OD2	2.48	0.46
1:B:125:GLN:OE1	1:B:145:ARG:NH1	2.48	0.46
1:B:316:MET:C	1:B:316:MET:SD	2.94	0.46
1:C:131:HIS:ND1	1:C:183:GLU:OE2	2.48	0.46
1:A:131:HIS:NE2	1:A:150:ASP:OD2	2.48	0.46
1:A:316:MET:SD	1:A:316:MET:C	2.94	0.45
1:B:262:GLU:OE2	1:B:289:ARG:CD	2.65	0.45
1:B:114:ARG:HG2	1:B:177:SER:HB2	1.99	0.45
1:A:114:ARG:HG2	1:A:177:SER:HB2	1.99	0.44
1:C:114:ARG:HG2	1:C:177:SER:HB2	1.99	0.43
1:C:108:GLU:OE1	1:C:180:ARG:NH2	2.47	0.43
1:A:316:MET:HG3	1:B:316:MET:SD	2.58	0.43
1:B:305:TRP:CD1	1:C:88:GLN:CG	3.02	0.43
1:C:184:MET:HE2	1:C:184:MET:HB3	1.91	0.43
1:A:184:MET:HE2	1:A:184:MET:HB3	1.86	0.42
1:A:108:GLU:OE1	1:A:180:ARG:NH2	2.47	0.42
1:A:299:ILE:HD11	1:B:99:ASN:HD22	1.85	0.42
1:A:99:ASN:HB2	1:C:299:ILE:CD1	2.51	0.41
1:B:269:ASN:ND2	1:C:193:GLU:OE1	2.53	0.41
1:B:184:MET:HE2	1:B:184:MET:HB3	1.87	0.41
1:A:305:TRP:CD1	1:B:88:GLN:CG	3.03	0.41
1:B:316:MET:HG3	1:C:316:MET:HE2	2.01	0.41
1:B:108:GLU:OE1	1:B:180:ARG:NH2	2.47	0.41
1:A:88:GLN:HG2	1:C:305:TRP:NE1	2.37	0.40

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	253/463 (55%)	244 (96%)	9 (4%)	0	100	100
1	B	253/463 (55%)	244 (96%)	9 (4%)	0	100	100
1	C	253/463 (55%)	244 (96%)	9 (4%)	0	100	100
All	All	759/1389 (55%)	732 (96%)	27 (4%)	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	208/410 (51%)	207 (100%)	1 (0%)	86	92
1	B	208/410 (51%)	207 (100%)	1 (0%)	86	92
1	C	208/410 (51%)	207 (100%)	1 (0%)	86	92
All	All	624/1230 (51%)	621 (100%)	3 (0%)	85	92

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

Mol	Chain	Res	Type
1	A	169	ARG
1	B	169	ARG
1	C	169	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	A	99	ASN
1	A	107	GLN
1	A	188	GLN
1	A	261	GLN
1	A	280	GLN
1	B	88	GLN
1	B	99	ASN
1	B	107	GLN
1	B	188	GLN
1	B	280	GLN
1	C	88	GLN
1	C	99	ASN
1	C	107	GLN
1	C	188	GLN
1	C	280	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 ⓘ

There are no chain breaks in this entry.

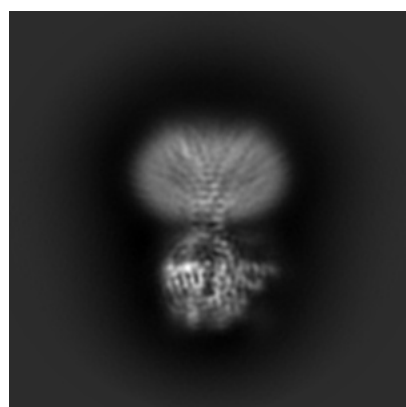
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22343. These allow visual inspection of the internal detail of the map and identification of artifacts.

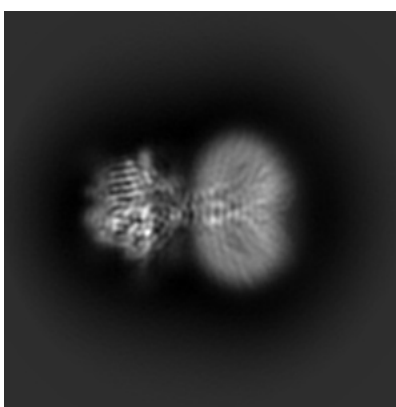
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

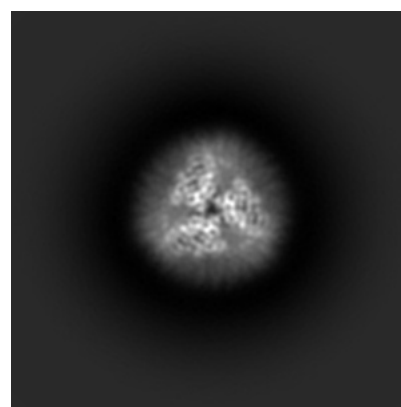
#### 6.1.1 Primary map



X



Y

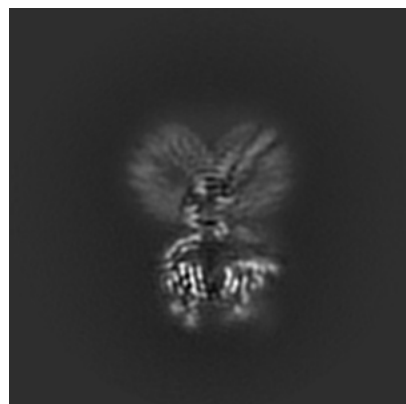


Z

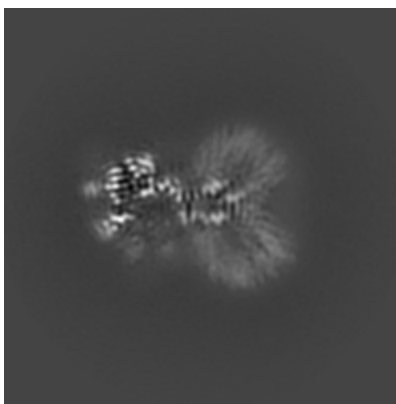
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

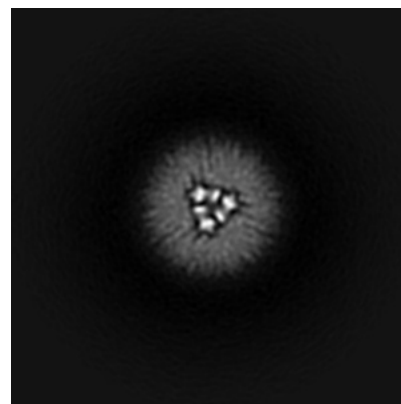
#### 6.2.1 Primary map



X Index: 110



Y Index: 110

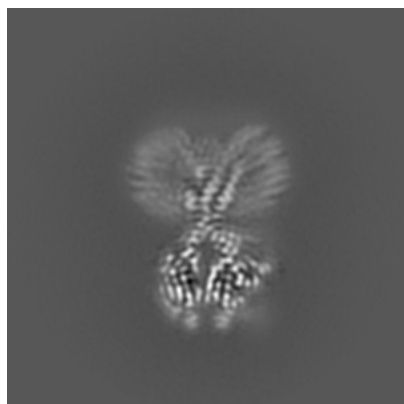


Z Index: 110

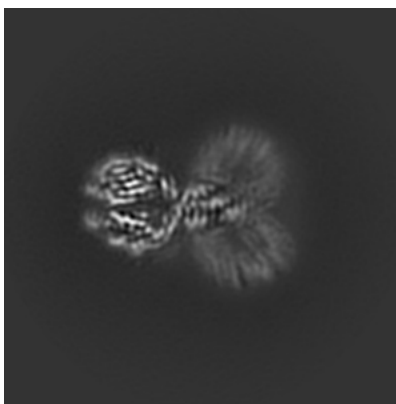
The images above show central slices of the map in three orthogonal directions.

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

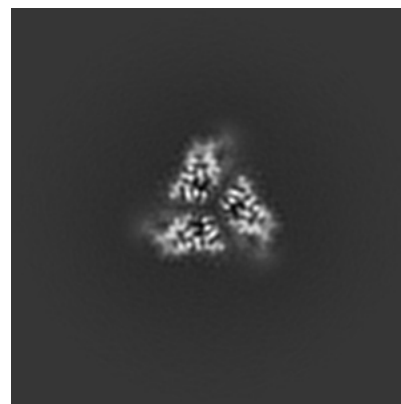
### 6.3.1 Primary map



X Index: 105



Y Index: 115



Z Index: 78

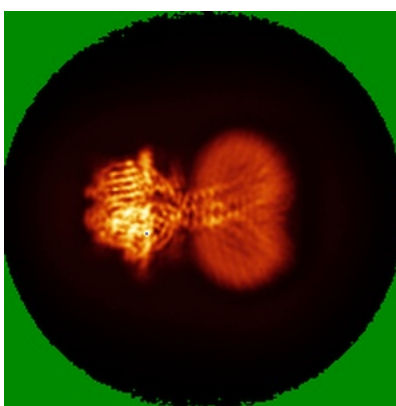
The images above show the largest variance slices of the map in three orthogonal directions.

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

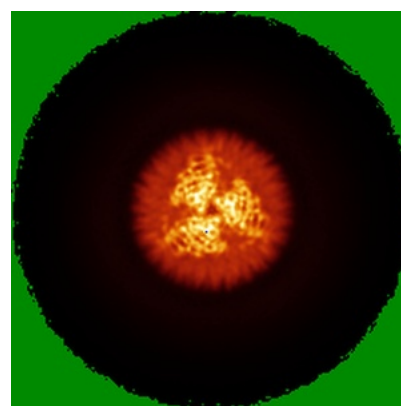
### 6.4.1 Primary map



X



Y

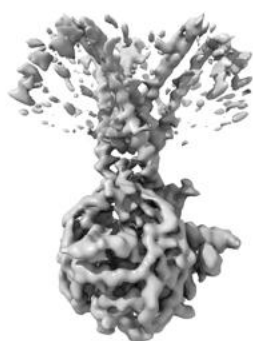


Z

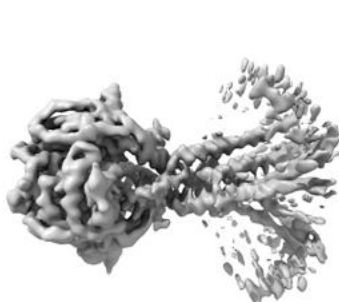
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

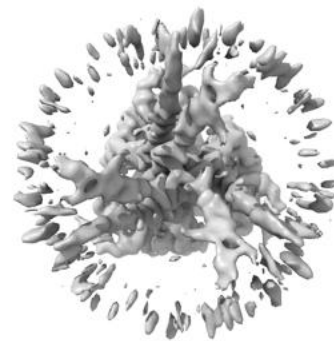
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

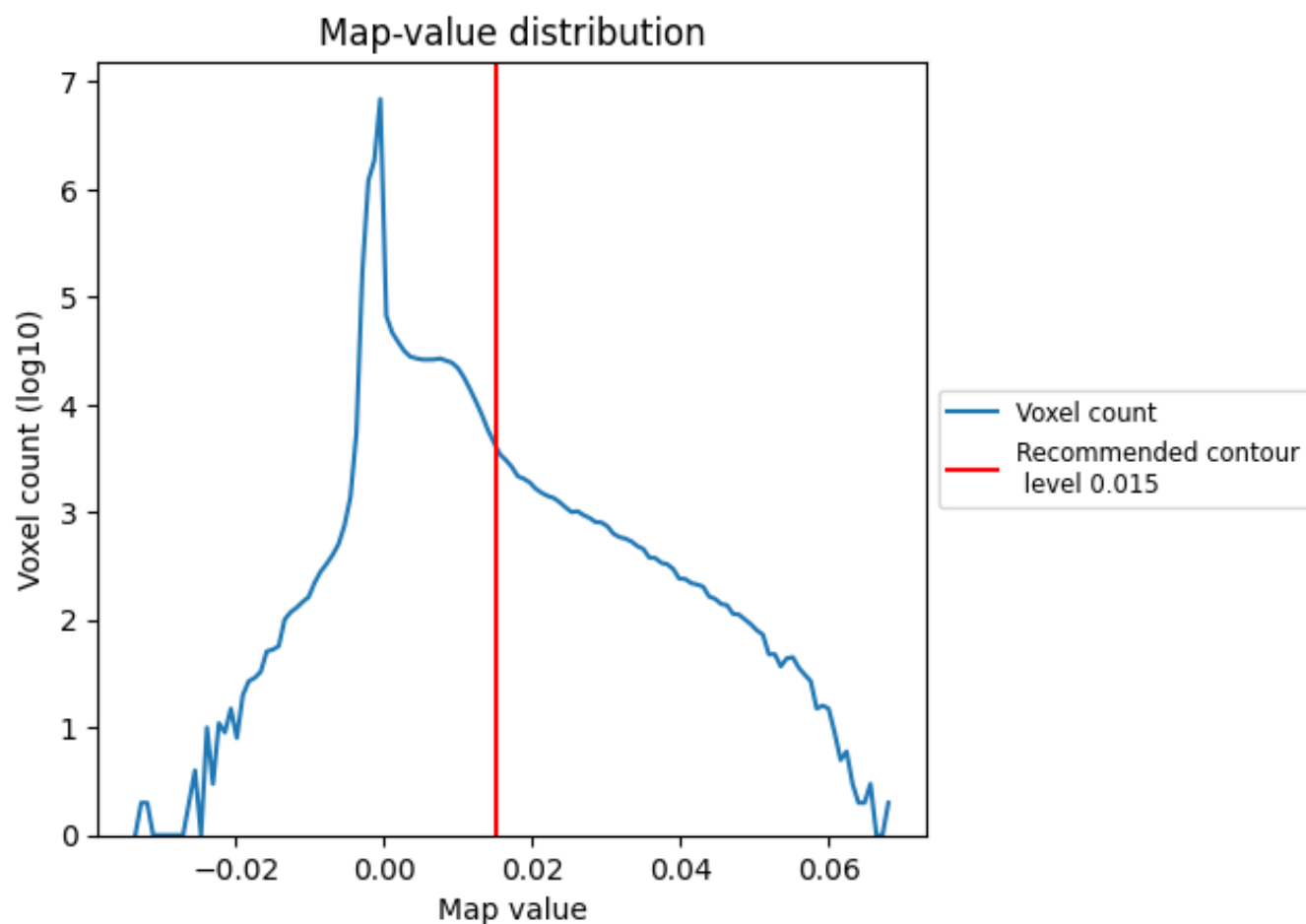
## 6.6 Mask visualisation [i](#)

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.

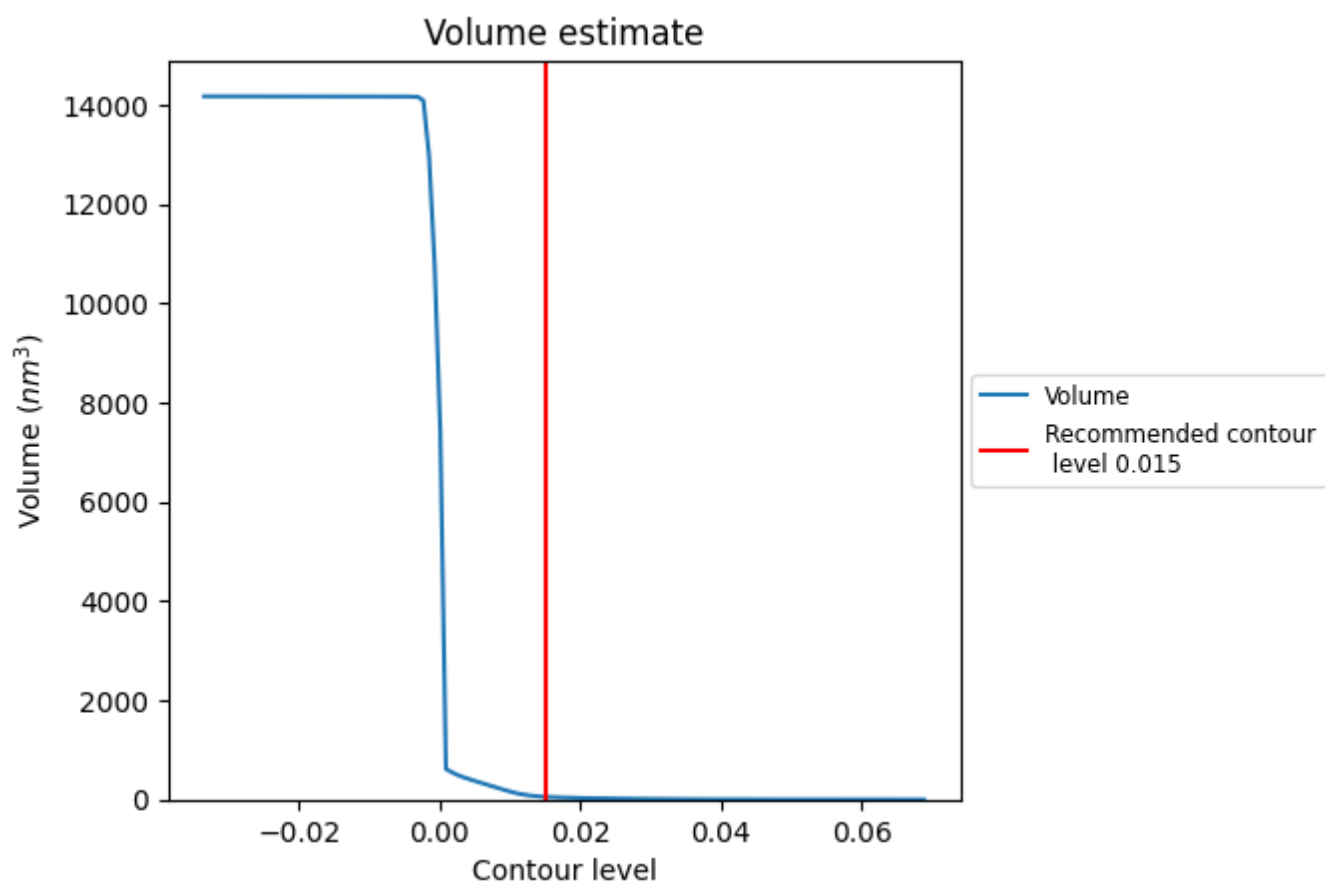
### 7.1 Map-value distribution [i](#)



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.



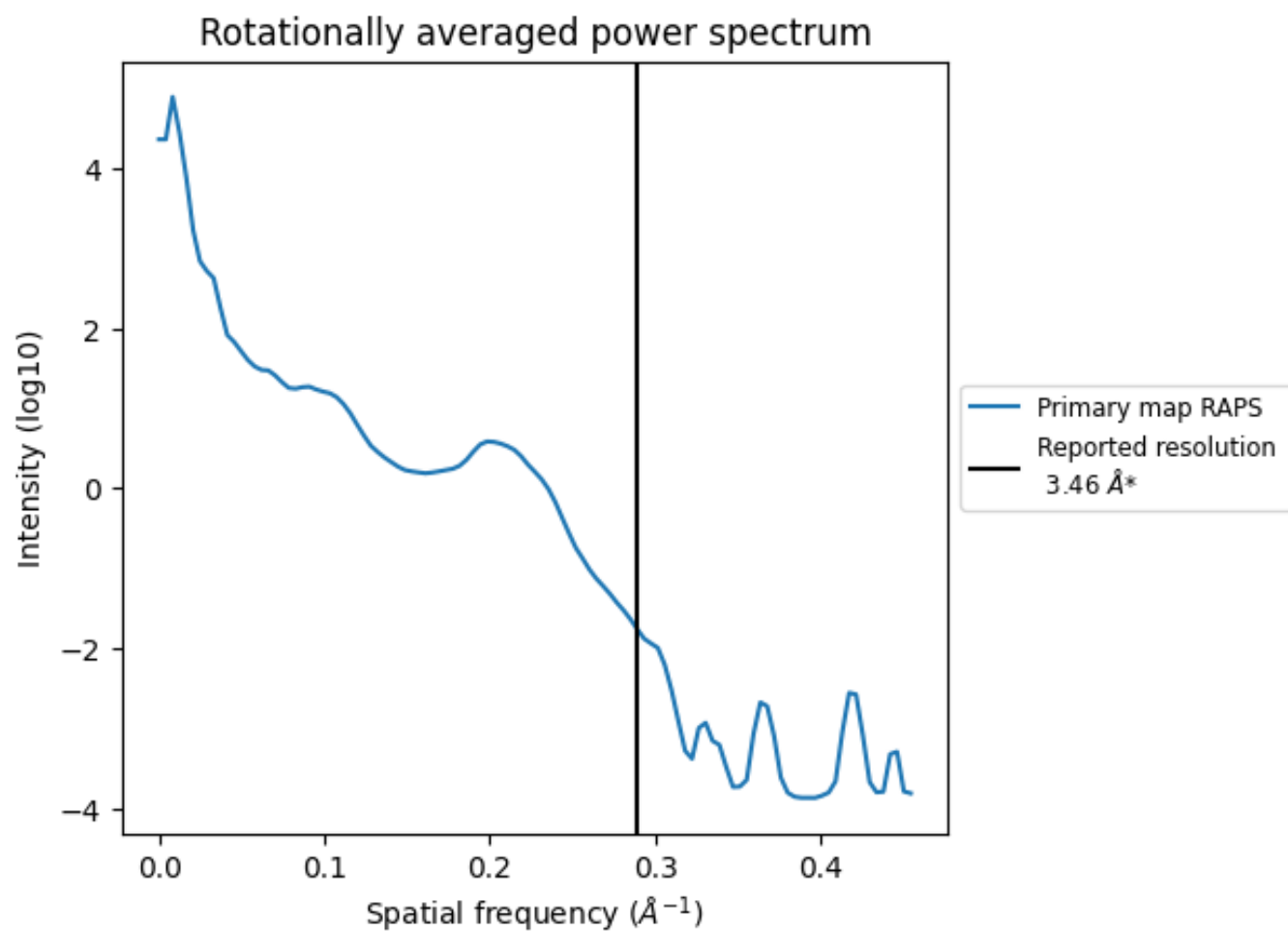
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 55 nm<sup>3</sup>; this corresponds to an approximate mass of 49 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 0.289 Å<sup>-1</sup>

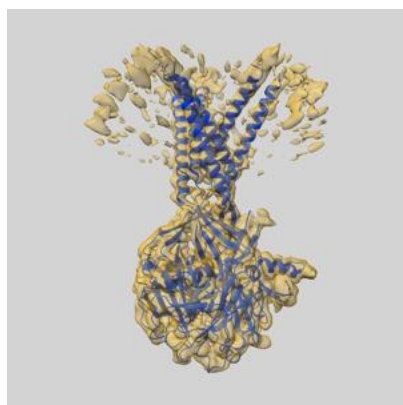
## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

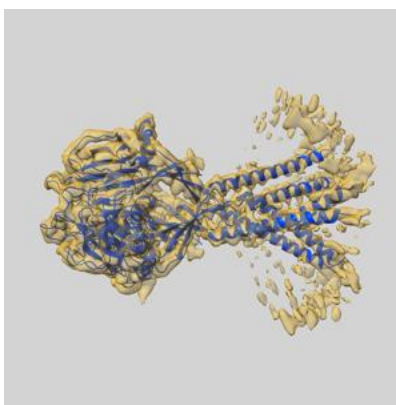
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22343 and PDB model 7JI3. Per-residue inclusion information can be found in section [3](#) on page [4](#).

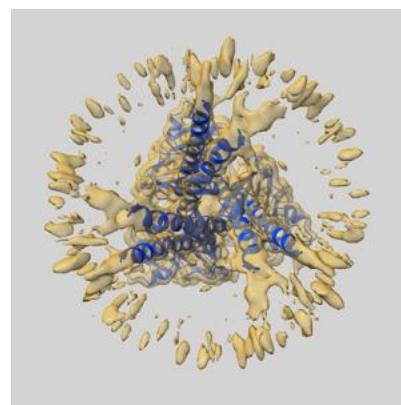
### 9.1 Map-model overlay [i](#)



X



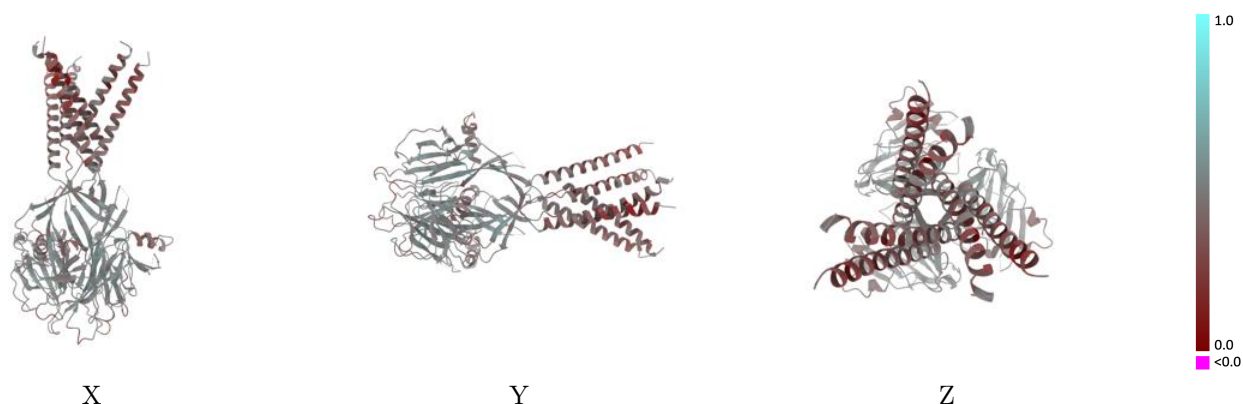
Y



Z

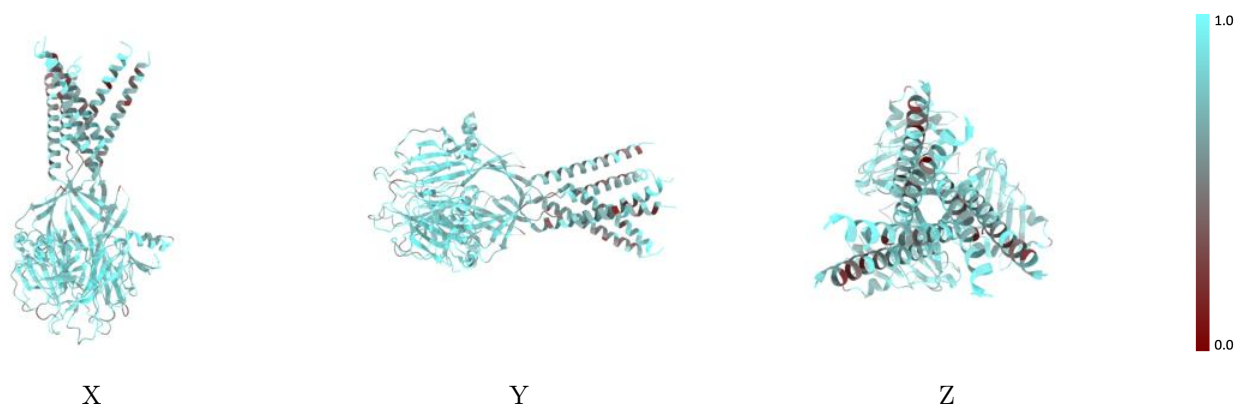
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



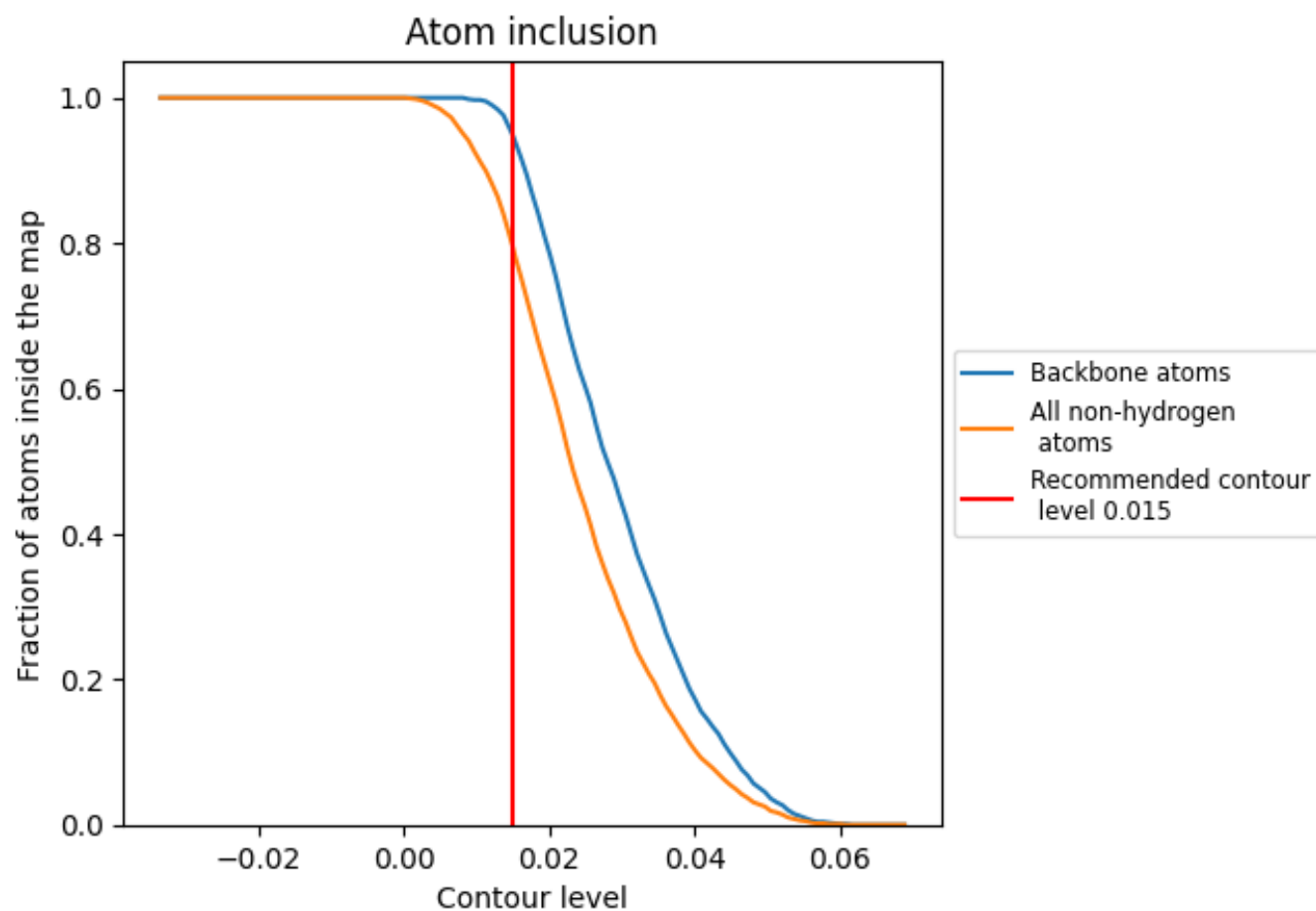
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 79% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7930	<div></div> 0.4430
A	<div></div> 0.7930	<div></div> 0.4440
B	<div></div> 0.7940	<div></div> 0.4440
C	<div></div> 0.7920	<div></div> 0.4430

