



## Full wwPDB EM Validation Report ⓘ

Nov 17, 2025 – 01:22 PM JST

PDB ID : 9V45 / pdb\_00009v45  
EMDB ID : EMD-64767  
Title : Soy storage protein fibril (glycinin A) PM1  
Authors : Li, S.; Cao, Q.; Cao, Y.  
Deposited on : 2025-05-22  
Resolution : 3.41 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.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46



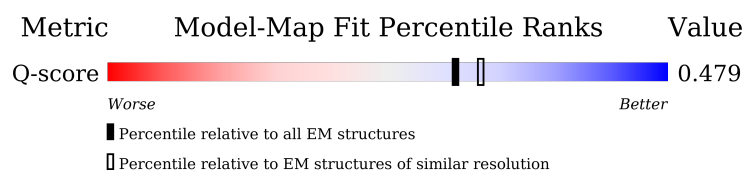
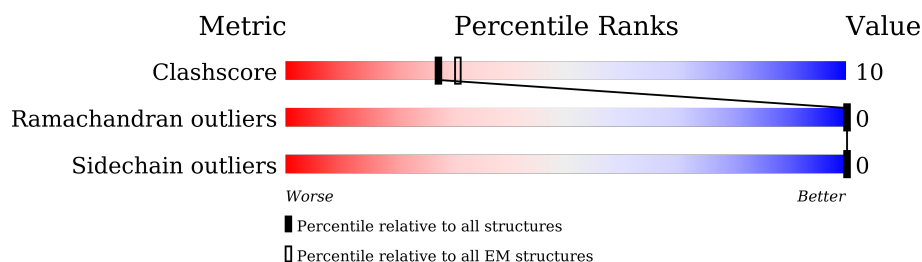
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

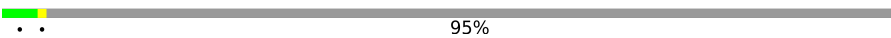
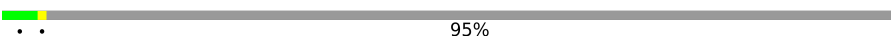
The reported resolution of this entry is 3.41 Å.

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.





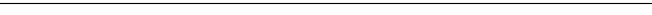


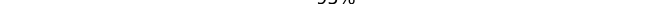
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	13997 ( 2.91 - 3.91 )

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	563	 95%
1	B	563	 95%
1	C	563	 95%
1	D	563	 95%

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Mol	Chain	Length	Quality of chain
1	E	563	 95%
1	F	563	 95%
1	G	563	 95%
1	H	563	 95%
1	I	563	 95%
1	J	563	 95%



## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2140 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 Glycinin G4.

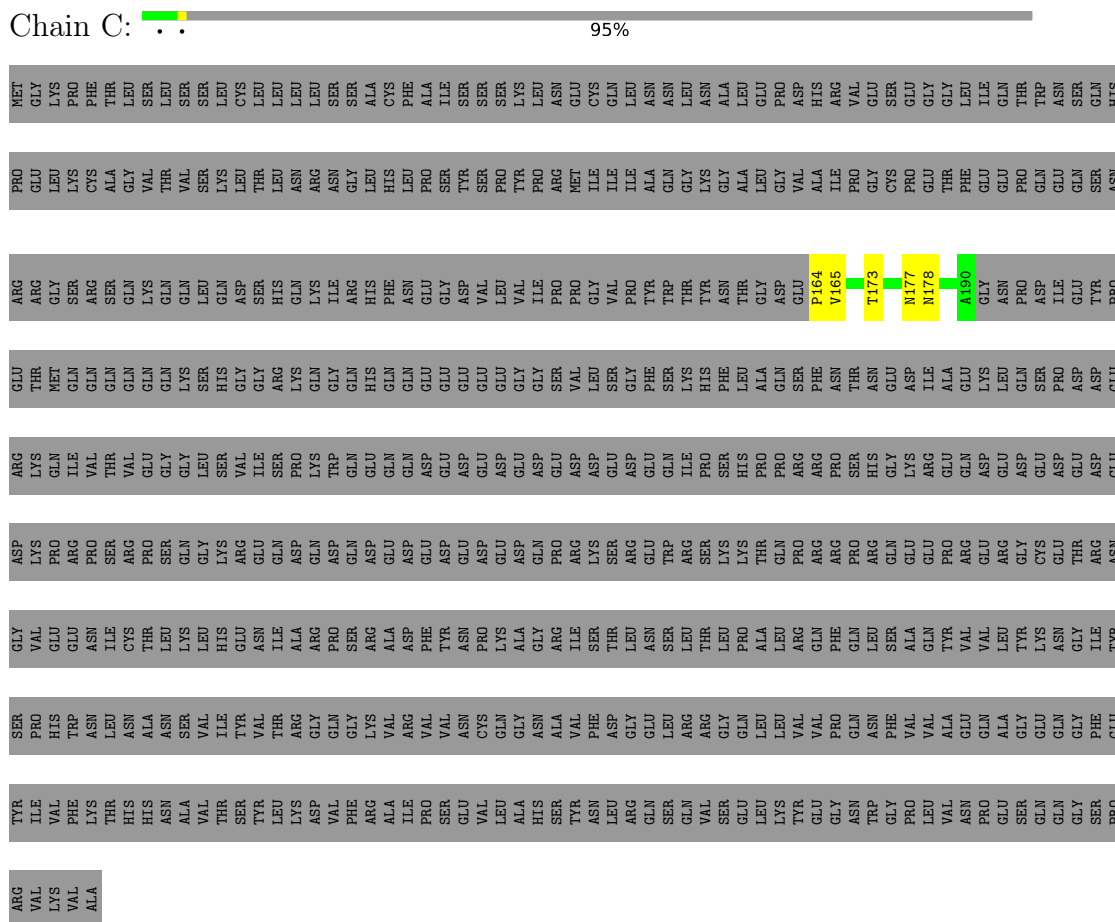
Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	27	Total	C	N	O	0	0
			214	138	35	41		
1	B	27	Total	C	N	O	0	0
			214	138	35	41		
1	C	27	Total	C	N	O	0	0
			214	138	35	41		
1	D	27	Total	C	N	O	0	0
			214	138	35	41		
1	E	27	Total	C	N	O	0	0
			214	138	35	41		
1	F	27	Total	C	N	O	0	0
			214	138	35	41		
1	G	27	Total	C	N	O	0	0
			214	138	35	41		
1	H	27	Total	C	N	O	0	0
			214	138	35	41		
1	I	27	Total	C	N	O	0	0
			214	138	35	41		
1	J	27	Total	C	N	O	0	0
			214	138	35	41		







- Molecule 1: Glycinin G4



- Molecule 1: Glycinin G4



95%

- Molecule 1: Glycinin G4

95%

VAL	LYS	LYS	LYS	THR	ARG	PRO	MET
GLU	PRO	ARG	GLN	MET	ARG	GLU	GLY
GLY	ARG	ILE	GLY	GLN	GLY	LEU	GLY
GLN	PRO	VAL	ASN	GLN	SER	LYS	PRO
ILE	ARG	THR	THR	GLN	ARG	CYS	PHE
CYS	ARG	VAL	VAL	GLN	SER	ALA	THR
THR	PRO	GLU	GLU	GLN	GLN	GLY	LEU
LEU	SER	GLY	GLY	GLN	LYS	VAL	SER
LYS	GLN	GLY	LYS	GLN	GLN	THR	LEU
GLY	GLY	LEU	LEU	SER	GLM	VAL	SER
HIS	LYS	SER	SER	HIS	LEU	SER	SER
GLU	ARG	VAL	VAL	GLY	GLM	LYS	LEU
ASN	GLU	ILE	ILE	GLY	ASP	LEU	CYS
ILE	GLN	PRO	PRO	ARG	SER	THR	LEU
ALA	ASP	ILE	GLN	ARG	HIS	LEU	LEU
ARG	GLU	GLN	GLN	HIS	ARG	ASN	SER
ASP	ASP	GLN	GLN	GLN	HIS	GLY	ALA
PHE	ASP	GLN	ASP	PHE	PHE	HIS	CYS
THR	ASP	GLU	ASP	GLU	ASN	LEU	PHE
ASN	ASP	GLU	GLU	GLU	GLY	PRO	ALA
PRO	GLU	ASP	GLU	GLU	GLY	SER	ILE
ILE	ARG	ASP	ASP	VAL	PRO	ARG	ASN
SER	LYS	LYS	GLY	LEU	PRO	MET	GLY
THR	SER	ARG	GLU	SER	GLY	ILE	CYS
LEU	ARG	ASP	GLY	GLY	VAL	ILE	GLN
ASN	GLU	GLU	GLU	PHE	PRO	ILE	LEU
SER	TRP	GLN	GLN	SER	THR	ALA	ASN
LEU	ARG	ILE	LYS	LYS	TRP	GLN	ASN
THR	SER	PRO	HIS	THR	THR	GLY	LEU
LYS	LYS	SER	PHE	PHE	TYR	LYS	ASN
PRO	LYS	HIS	LEU	LEU	ASN	GLY	ALA
THR	ALA	PRO	ALA	THR	THR	ALA	LEU
LEU	GLN	PRO	PRO	GLN	GLY	LEU	GLY
ARG	PRO	ARG	ARG	SER	ASP	GLY	PRO
GLM	ARG	ARG	ARG	PHE	GLU	VAL	ASP
PHE	ARG	PRO	PRO	ASN	P164	ALA	HIS
GLN	PRO	SER	SER	THR	T173	ILE	ARG
SER	GLN	HIS	ASN	ASN	N177	GLY	VAL
ALA	GLY	GLY	LYS	GLU	N178	CYS	SER
SER	GLU	ARG	LYS	ASP	A190	PRO	GLY
GLM	GLU	GLY	GLN	ALA	GLY	THR	GLY
VAL	ARG	GLU	GLN	GLU	ASN	PHE	LEU
VAL	GLU	ASP	ASP	LYS	ASN	LEU	ILE
THR	GLY	ASP	ASP	GLN	PRO	GLU	GLN
LYS	CYS	GLU	GLU	SER	ASP	PRO	THR
ASN	GLY	ASP	ASP	PRO	ILE	GLN	TRP
THR	GLU	GLU	GLU	GLU	THR	GLY	ASN
ILE	ARG	ASP	ASP	ASP	TYR	GLN	SER
GLY	THR	THR	THR	GLU	GLU	ASN	GLY
THR	GLY	ASP	ASP	GLU	PRO	ASN	HIS







- Molecule 1: Glycinin G4

Chain H:  95%

GLN	GLY	GLN	ASN	GLU	ASP	PRO	ILE	ARG	PRO	GLY	MET
GLY	PHE	GLY	GLY	THR	GLU	ASP	GLU	ARG	GLU	GLY	MET
GLY	ILE	GLY	ILE	THR	GLU	ASP	TYR	ARG	LEU	LEU	GLY
GLY	THR	GLY	ASN	ASN	GLU	GLU	PRO	SER	LYS	LYS	GLY
GLY	THR	GLY	PRO	VAL	LYS	ARG	THR	SER	ALA	ALA	THR
VAL	ILE	ILE	PRO	GLU	PRO	GLN	MET	GLN	GLY	GLY	LEU
VAL	THR	THR	HIS	GLU	ILE	ILE	GLN	LYS	VAL	VAL	SER
VAL	THR	THR	ASN	ASN	PRO	THR	GLN	GLN	THR	THR	SER
HIS	THR	THR	ASN	CYS	ARG	THR	GLN	LEU	SER	SER	SER
ASN	ASN	ASN	ASN	THR	GLU	GLY	GLN	GLN	LYS	LYS	LEU
ALA	ALA	ALA	ASN	LEU	SER	GLY	GLN	ASP	LEU	LEU	CYS
VAL	VAL	VAL	SER	LYS	GLY	GLY	LYS	SER	THR	THR	LEU
THR	THR	THR	ILE	HIS	ILE	SER	HIS	GLN	ASN	ASN	LEU
SER	SER	SER	TYR	GLU	ARG	VAL	GLY	LYS	ARG	ARG	SER
TYR	TYR	TYR	VAL	ASN	GLU	ILE	GLY	ILE	ASN	ASN	SER
LEU	LEU	LEU	THR	ILE	GLN	SER	ARG	ARG	GLY	GLY	SER
THR	THR	THR	ILE	THR	GLN	SER	GLN	ARG	THR	THR	ALA
VAL	VAL	VAL	ARG	ALA	GLU	PRO	GLN	THR	LEU	LEU	ALA
ARG	ARG	ARG	ASN	ARG	GLU	ASP	GLN	THR	GLY	GLY	TYR
ALA	ALA	ALA	VAL	ALA	GLU	GLY	GLN	THR	ASN	ASN	TYR
ILE	ILE	ILE	ARG	ASP	ASP	ASP	GLN	VAL	VAL	VAL	SER
PRO	PRO	PRO	VAL	PHE	GLU	ASP	GLU	PHE	GLY	GLY	SER
SER	SER	SER	ASN	ASN	GLU	GLU	GLY	ASN	GLY	GLY	LEU
GLY	GLY	GLY	VAL	ILE	ASN	ASP	VAL	TYR	ALA	ALA	GLN
ASN	ASN	ASN	PHE	SER	LYS	ASP	LEU	TRP	GLN	GLN	ASN
LEU	LEU	LEU	ASP	THR	SER	GLU	SER	THR	LEU	LEU	GLY
ARG	ARG	ARG	GLY	THR	SER	PRO	HIS	ASP	GLY	GLY	PRO
GLN	GLN	GLN	ARG	LEU	LYS	SER	PHE	GLU	VAL	VAL	ASP
GLY	GLY	GLY	GLN	PRO	SER	HIS	LEU	P164	ALA	HIS	ASP
LEU	LEU	LEU	LEU	ALA	THR	PRO	ALA	T173	ILE	ARG	GLY
TYR	TYR	TYR	VAL	ARG	PRO	ARG	GLN	T173	GLY	VAL	SER
VAL	VAL	VAL	VAL	GLN	ARG	ARG	SER	N177	CYS	GLY	GLY
GLY	GLY	GLY	PRO	PHE	ARG	PRO	PHE	N178	PRO	PRO	GLY
ASN	ASN	ASN	GLN	GLN	ARG	HIS	ASN	T163	THR	THR	GLY
THR	THR	THR	ASN	LEU	THR	SER	GLY	P164	PHE	PHE	LEU
PHE	PHE	PHE	VAL	ALA	GLU	GLY	ASP	R165	GLY	GLY	ILE
LEU	LEU	LEU	VAL	GLN	GLU	ARG	ILE	L189	GLY	GLY	GLN
VAL	VAL	VAL	ALA	TYR	PRO	GLU	ALA	A190	PRO	PRO	THR
ASN	ASN	ASN	VAL	VAL	ARG	GLU	GLY	GLY	GLN	GLN	THR
PRO	PRO	PRO	GLN	VAL	GLU	ASP	LYS	ASN	GLY	GLY	ASN
GLY	GLY	GLY	ALA	LEU	GLU	GLU	LEU	GLY	GLN	GLN	SER
SER	SER	SER	GLY	TYR	GLY	ASP	SER	PRO	ASN	ASN	GLN
GLN	GLN	GLN	CTR	CTR	CYS	CTR	CTR	CTR	CTR	CTR	ASN

- Molecule 1: Glycinin G4

Chain I:  95%

MET	GLY	LYS	PRO	PHE	THR	LEU	SER	LEU	SER	LEU	CYS	LEU	LEU	LEU	SER	SER	ALA	CYS	PHE	ALA	ILE	SER	SER	LYS	LEU	ASN	GLU	CYS	GLN	LEU	LEU	ASN	ASN	ASN	LEU	ALA	ALA	LEU	GLU	PRO	ASP	HIS	ARG	VAL	GLU	SER	GLU	GLU	GLY	GLY	LEU	ILE	GLN	THR	TRP	ASN	SER	SER	GLN	THR	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----







GLN  
GLY  
SER  
PRO  
ARG  
VAL  
LYS  
VAL  
ALA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=179.466°, rise=2.4 Å, axial sym=C1	Depositor
Number of segments used	71617	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{Å}^2$ )	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	27.392	Depositor
Minimum map value	-18.625	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	335.52, 335.52, 335.52	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	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	0.14	0/218	0.36	0/298
1	B	0.14	0/218	0.32	0/298
1	C	0.15	0/218	0.36	0/298
1	D	0.14	0/218	0.32	0/298
1	E	0.15	0/218	0.36	0/298
1	F	0.14	0/218	0.32	0/298
1	G	0.15	0/218	0.36	0/298
1	H	0.13	0/218	0.32	0/298
1	I	0.15	0/218	0.36	0/298
1	J	0.14	0/218	0.32	0/298
All	All	0.14	0/2180	0.34	0/2980

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	214	0	212	3	0
1	B	214	0	212	7	0
1	C	214	0	212	7	0
1	D	214	0	212	14	0
1	E	214	0	212	6	0
1	F	214	0	212	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	214	0	212	6	0
1	H	214	0	212	14	0
1	I	214	0	212	3	0
1	J	214	0	212	7	0
All	All	2140	0	2120	41	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.

All (41) 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:D:185:ARG:NH1	1:F:185:ARG:HH21	1.96	0.64
1:F:185:ARG:NH1	1:H:185:ARG:HH21	1.96	0.64
1:H:185:ARG:NH1	1:J:185:ARG:HH21	1.96	0.64
1:B:185:ARG:NH1	1:D:185:ARG:HH21	1.96	0.64
1:A:178:ASN:HB2	1:C:178:ASN:O	2.05	0.57
1:C:178:ASN:HB2	1:E:178:ASN:O	2.05	0.56
1:E:178:ASN:HB2	1:G:178:ASN:O	2.05	0.56
1:G:178:ASN:HB2	1:I:178:ASN:O	2.05	0.56
1:B:178:ASN:HB2	1:D:178:ASN:O	2.07	0.54
1:D:178:ASN:HB2	1:F:178:ASN:O	2.07	0.54
1:H:178:ASN:HB2	1:J:178:ASN:O	2.07	0.54
1:F:178:ASN:HB2	1:H:178:ASN:O	2.07	0.53
1:H:177:ASN:O	1:J:177:ASN:HA	2.12	0.50
1:D:177:ASN:O	1:F:177:ASN:HA	2.12	0.50
1:F:177:ASN:O	1:H:177:ASN:HA	2.12	0.50
1:B:177:ASN:O	1:D:177:ASN:HA	2.12	0.50
1:H:183:THR:OG1	1:J:183:THR:HG22	2.12	0.49
1:F:183:THR:OG1	1:H:183:THR:HG22	2.12	0.49
1:D:183:THR:OG1	1:F:183:THR:HG22	2.13	0.49
1:B:183:THR:OG1	1:D:183:THR:HG22	2.13	0.49
1:D:173:THR:O	1:F:173:THR:HA	2.17	0.45
1:B:173:THR:O	1:D:173:THR:HA	2.17	0.45
1:F:173:THR:O	1:H:173:THR:HA	2.17	0.45
1:H:173:THR:O	1:J:173:THR:HA	2.17	0.45
1:B:185:ARG:HH11	1:D:185:ARG:HH21	1.65	0.44
1:A:173:THR:O	1:C:173:THR:HA	2.17	0.43
1:C:173:THR:O	1:E:173:THR:HA	2.17	0.43
1:E:173:THR:O	1:G:173:THR:HA	2.17	0.43
1:G:173:THR:O	1:I:173:THR:HA	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:185:ARG:HH11	1:J:185:ARG:HH21	1.65	0.43
1:F:185:ARG:HH11	1:H:185:ARG:HH21	1.65	0.42
1:A:177:ASN:O	1:C:177:ASN:HA	2.19	0.42
1:C:177:ASN:O	1:E:177:ASN:HA	2.19	0.42
1:E:177:ASN:O	1:G:177:ASN:HA	2.19	0.42
1:D:185:ARG:HH11	1:F:185:ARG:HH21	1.65	0.42
1:G:177:ASN:O	1:I:177:ASN:HA	2.19	0.42
1:F:189:LEU:HD12	1:H:189:LEU:HD22	2.02	0.42
1:H:189:LEU:HD12	1:J:189:LEU:HD22	2.02	0.42
1:D:189:LEU:HD12	1:F:189:LEU:HD22	2.02	0.42
1:B:189:LEU:HD12	1:D:189:LEU:HD22	2.02	0.41
1:C:164:PRO:HB2	1:C:165:VAL:H	1.76	0.40

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	A	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	B	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	C	25/563 (4%)	23 (92%)	2 (8%)	0	100	100
1	D	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	E	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	F	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	G	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	H	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	I	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
1	J	25/563 (4%)	24 (96%)	1 (4%)	0	100	100
All	All	250/5630 (4%)	239 (96%)	11 (4%)	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	A	25/501 (5%)	25 (100%)	0	100	100
1	B	25/501 (5%)	25 (100%)	0	100	100
1	C	25/501 (5%)	25 (100%)	0	100	100
1	D	25/501 (5%)	25 (100%)	0	100	100
1	E	25/501 (5%)	25 (100%)	0	100	100
1	F	25/501 (5%)	25 (100%)	0	100	100
1	G	25/501 (5%)	25 (100%)	0	100	100
1	H	25/501 (5%)	25 (100%)	0	100	100
1	I	25/501 (5%)	25 (100%)	0	100	100
1	J	25/501 (5%)	25 (100%)	0	100	100
All	All	250/5010 (5%)	250 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.



## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



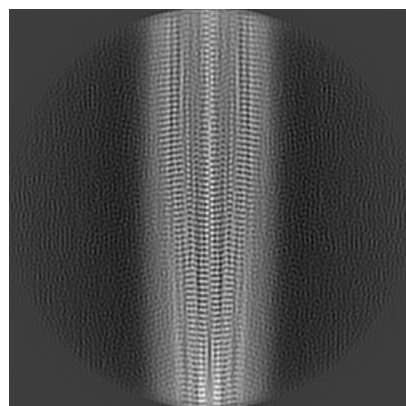
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64767. These allow visual inspection of the internal detail of the map and identification of artifacts.

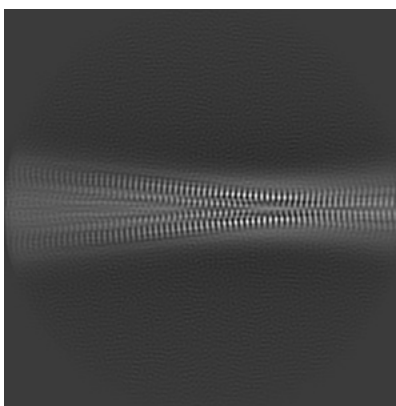
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

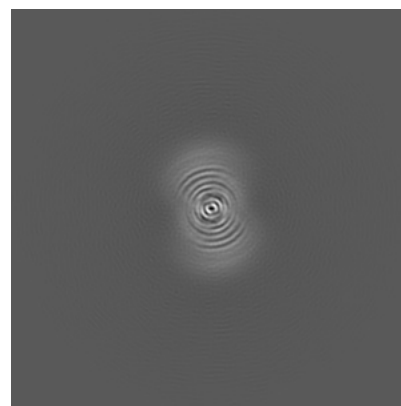
#### 6.1.1 Primary map



X

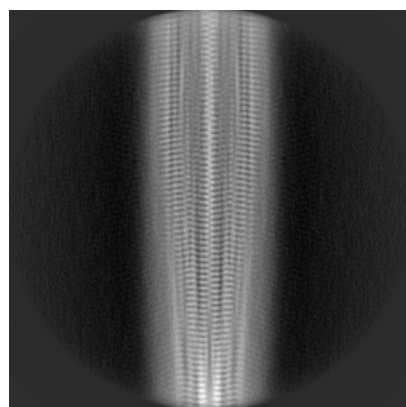


Y

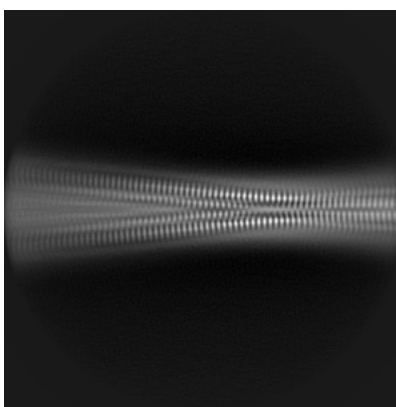


Z

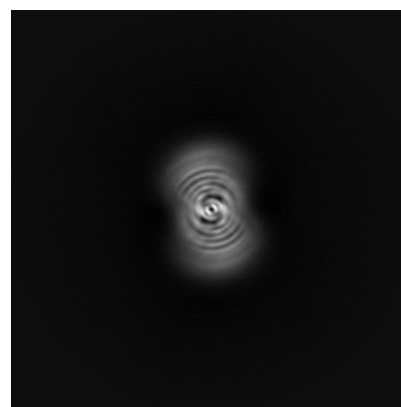
#### 6.1.2 Raw map



X



Y



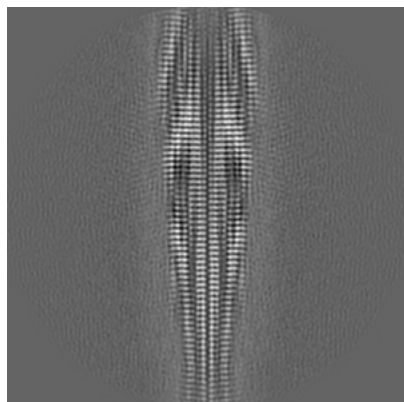
Z

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

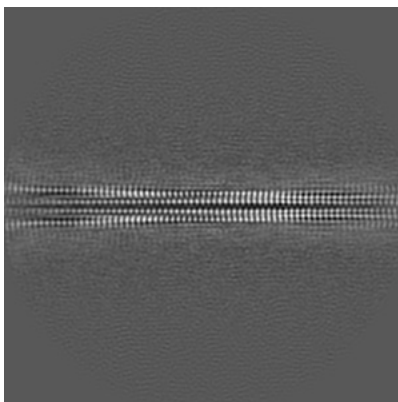


## 6.2 Central slices [i](#)

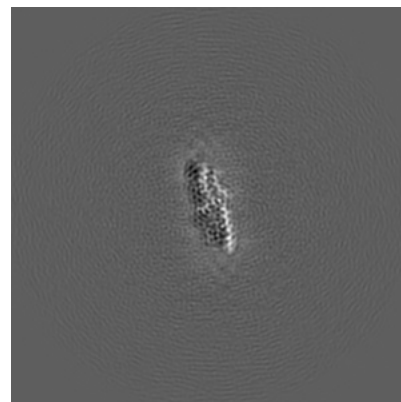
### 6.2.1 Primary map



X Index: 180

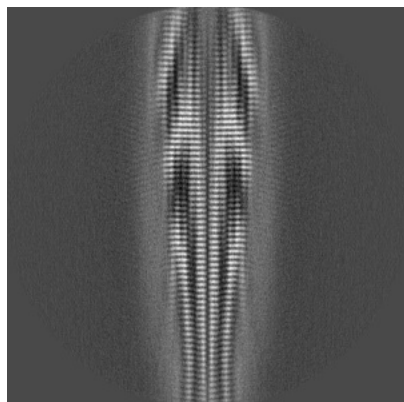


Y Index: 180

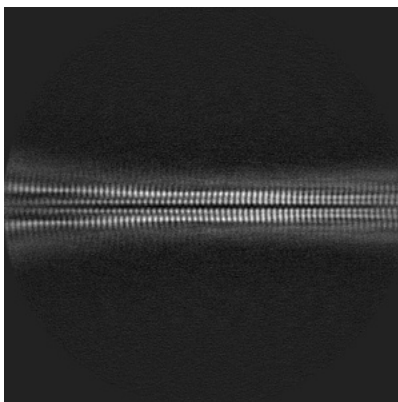


Z Index: 180

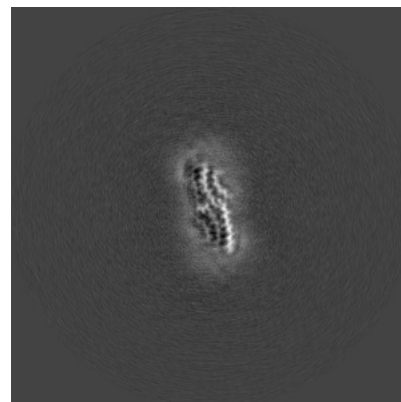
### 6.2.2 Raw map



X Index: 180



Y Index: 180



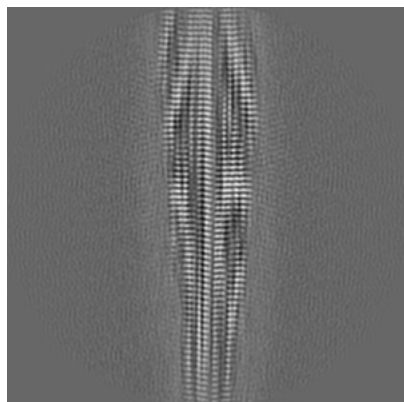
Z Index: 180

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

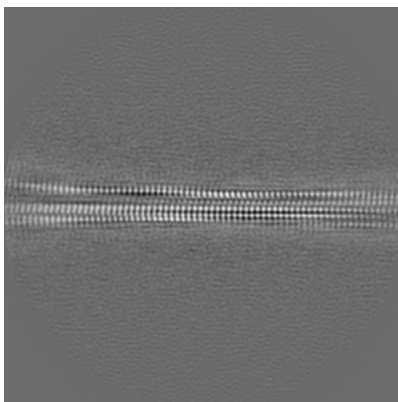


## 6.3 Largest variance slices [i](#)

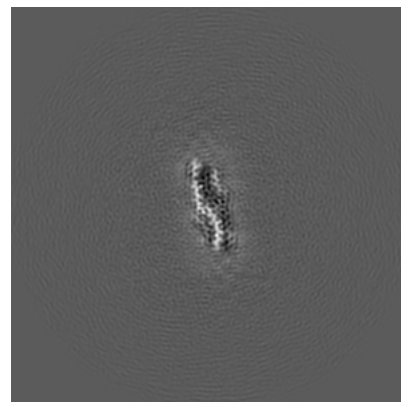
### 6.3.1 Primary map



X Index: 176

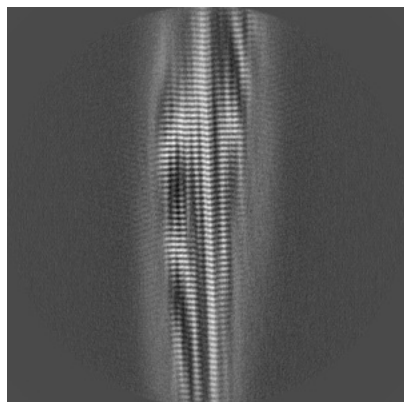


Y Index: 177

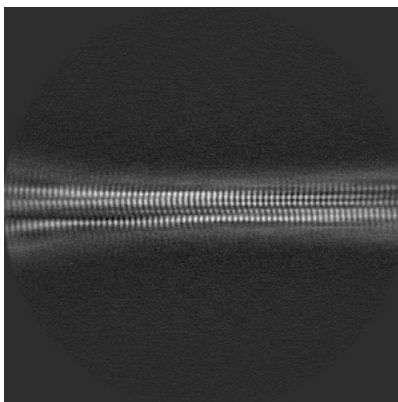


Z Index: 187

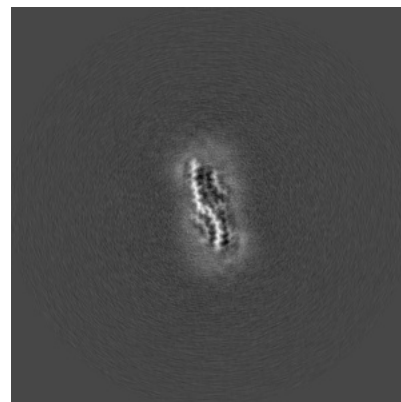
### 6.3.2 Raw map



X Index: 190



Y Index: 182



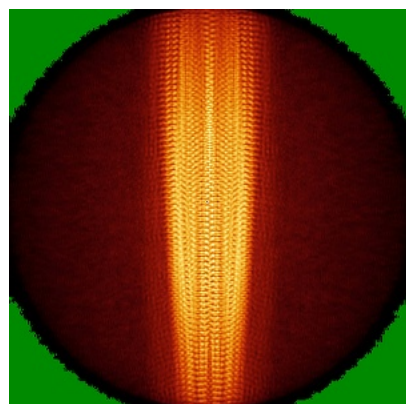
Z Index: 182

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

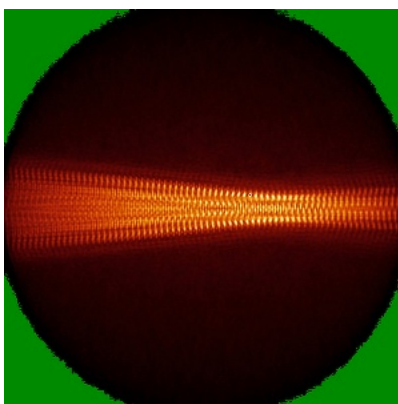


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

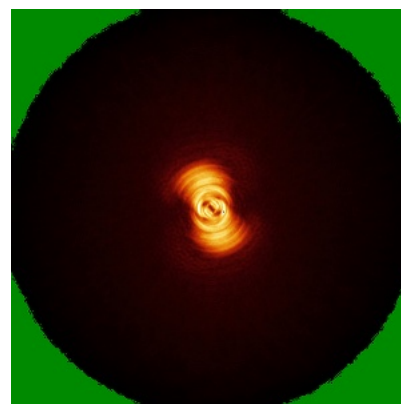
### 6.4.1 Primary map



X

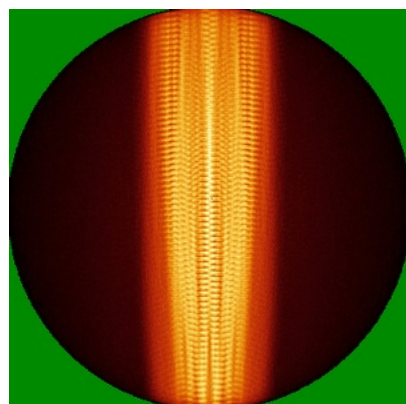


Y

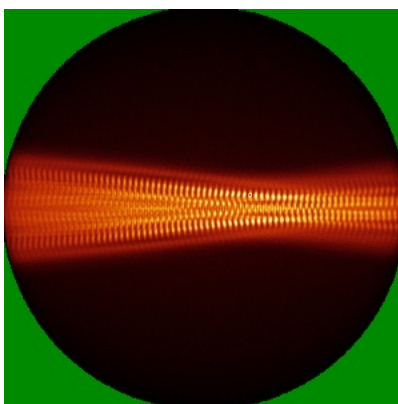


Z

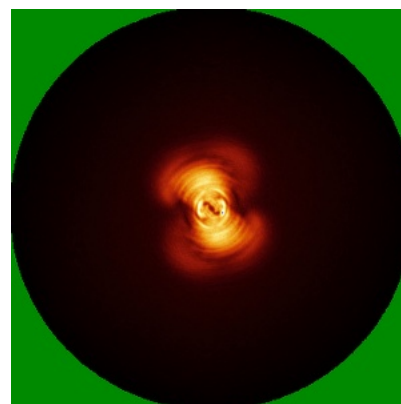
### 6.4.2 Raw map



X



Y



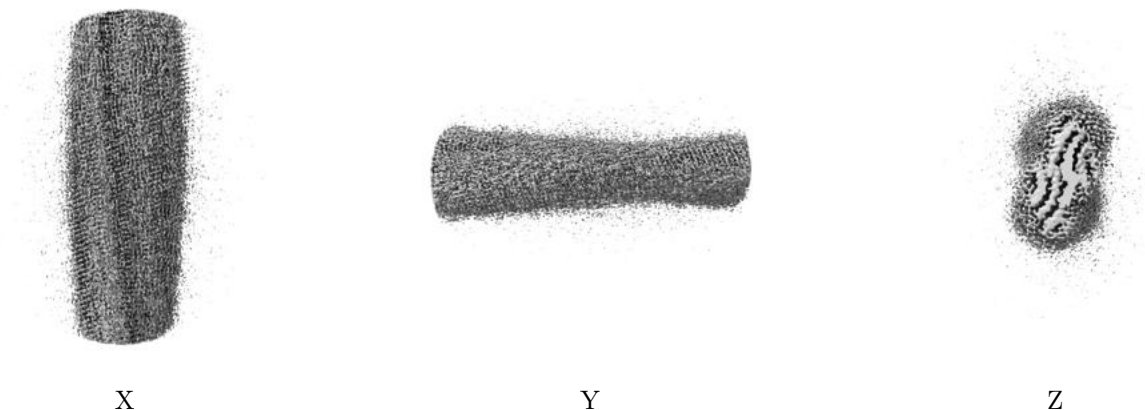
Z

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.



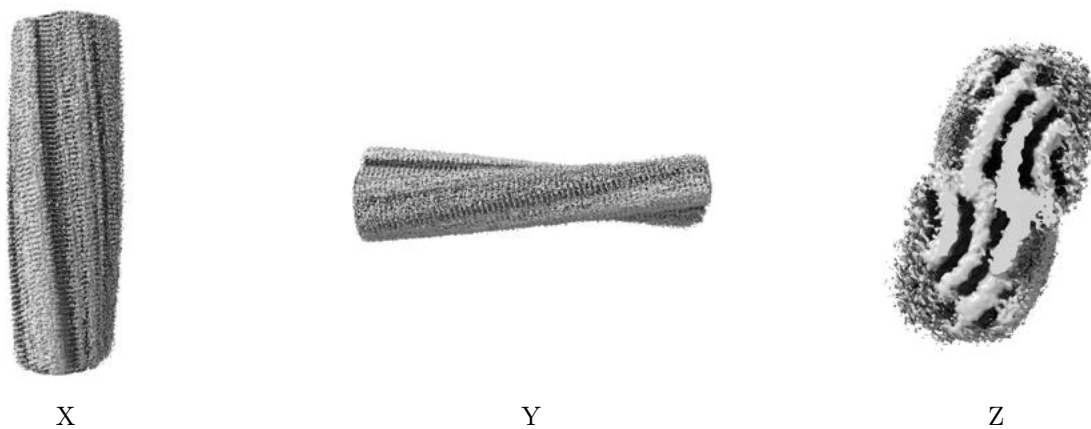
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. 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.



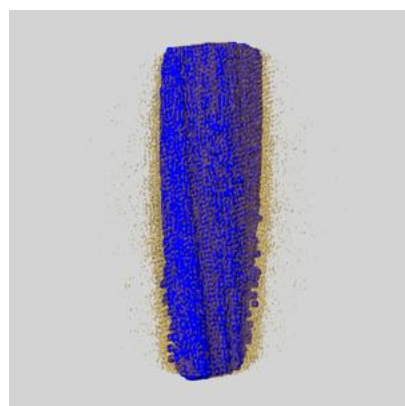
## 6.6 Mask visualisation [i](#)

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

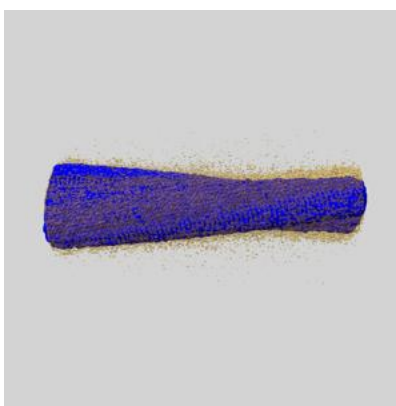
A mask typically either:

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

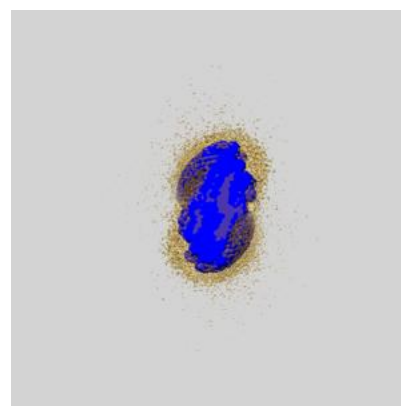
### 6.6.1 emd\_64767\_msk\_1.map [i](#)



X



Y



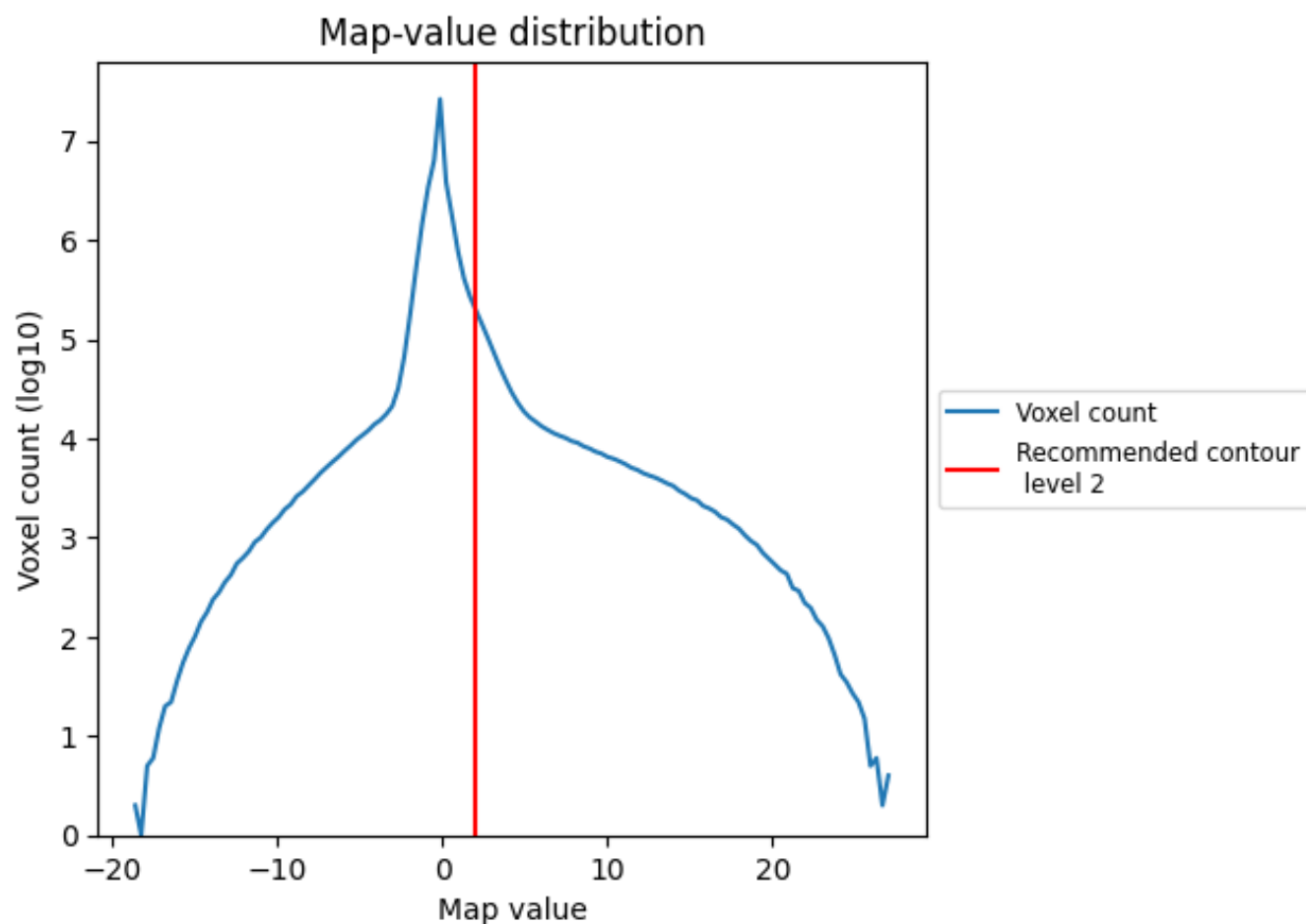
Z



## 7 Map analysis [i](#)

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

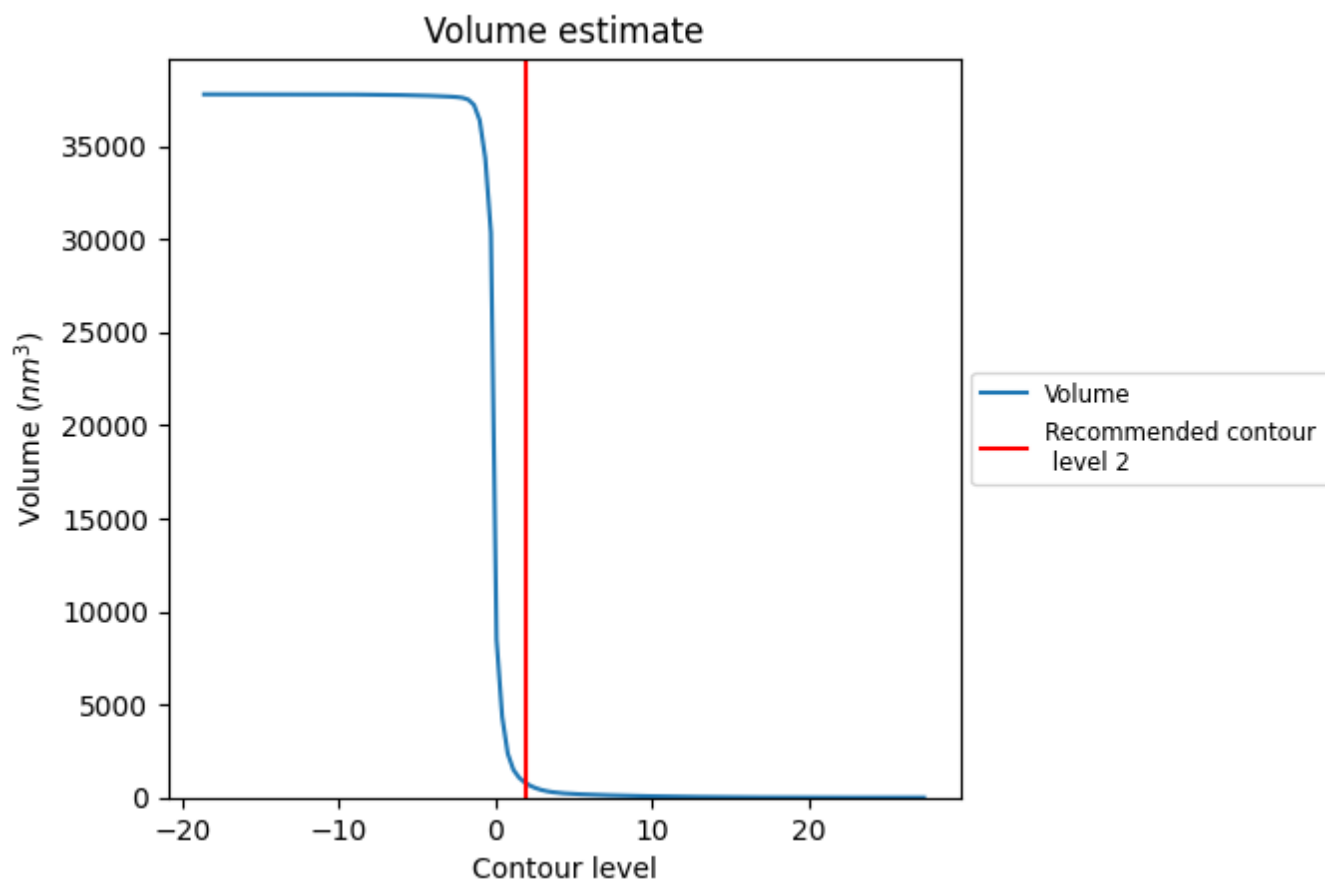
### 7.1 Map-value distribution [i](#)



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](#)

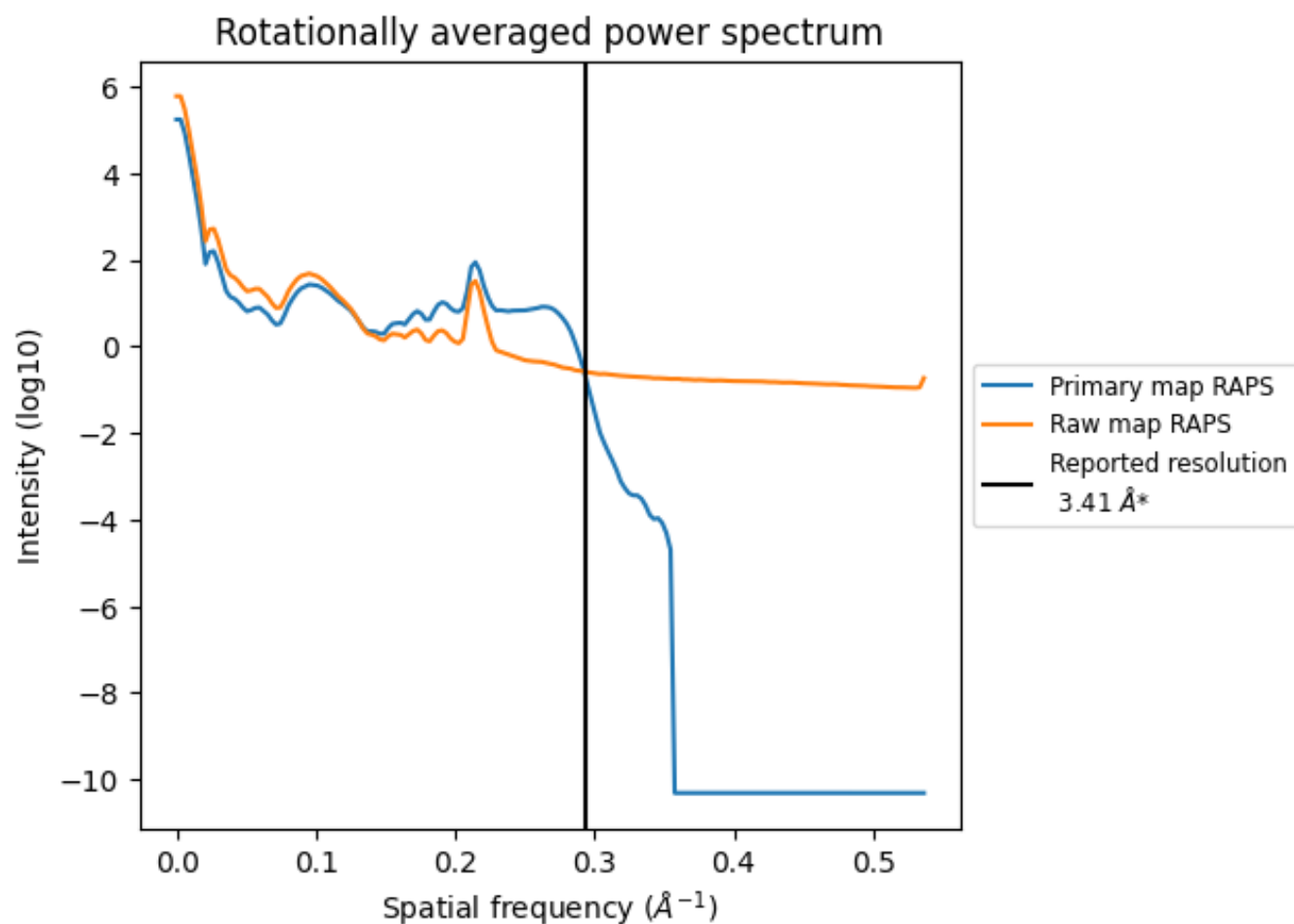


The volume at the recommended contour level is 750  $\text{nm}^3$ ; this corresponds to an approximate mass of 677 kDa.

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 ⓘ



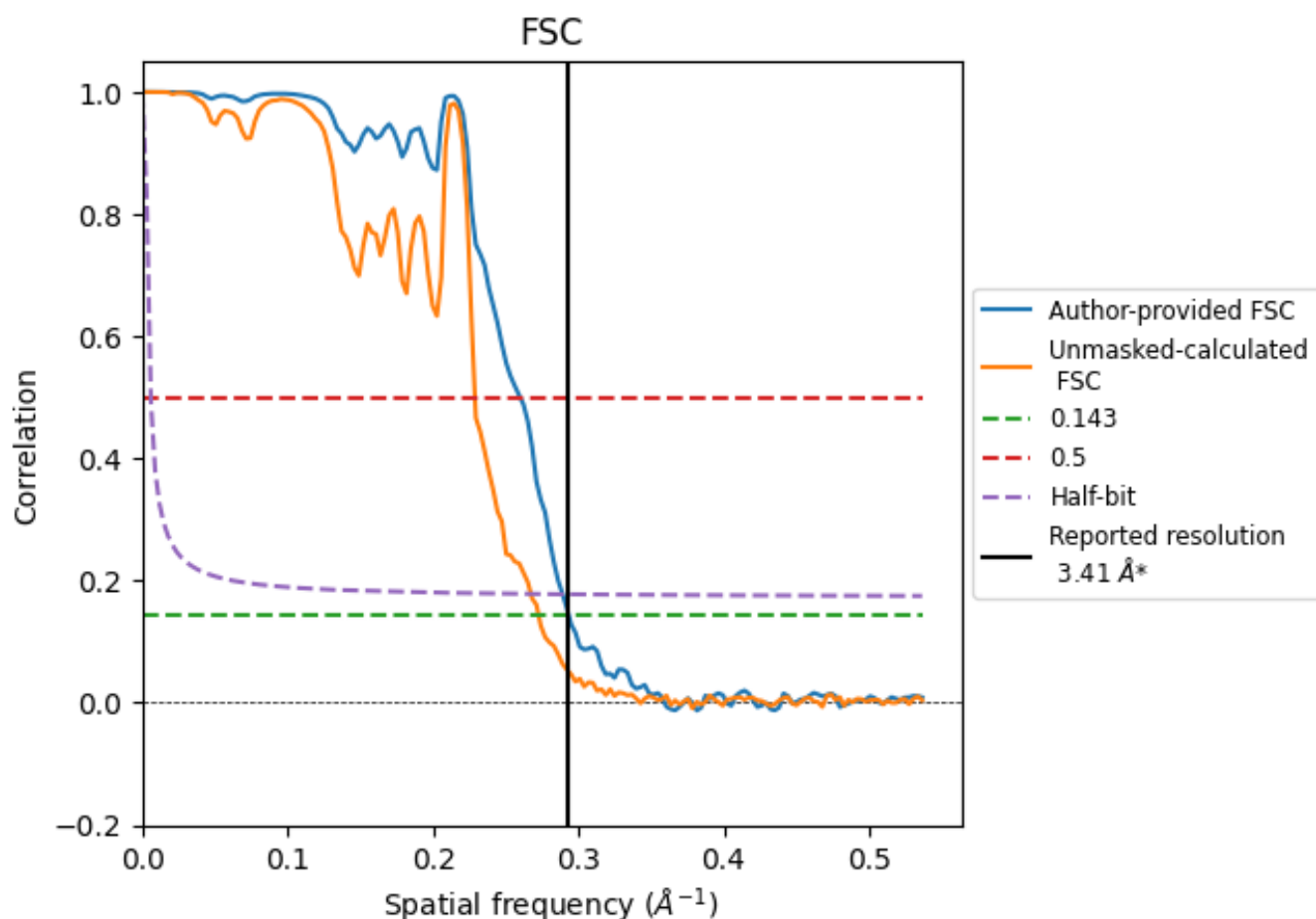
\*Reported resolution corresponds to spatial frequency of 0.293 Å<sup>-1</sup>



## 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 0.293  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.41	-	-
Author-provided FSC curve	3.41	3.85	3.46
Unmasked-calculated*	3.67	4.37	3.74

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



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

This section contains information regarding the fit between EMDB map EMD-64767 and PDB model 9V45. Per-residue inclusion information can be found in section [3](#) on page [5](#).

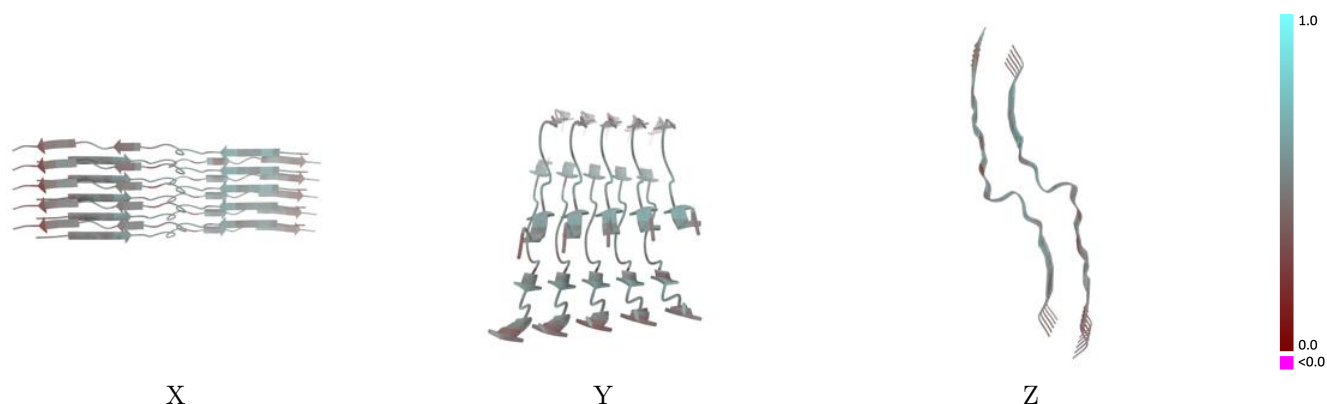
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 2.0 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.

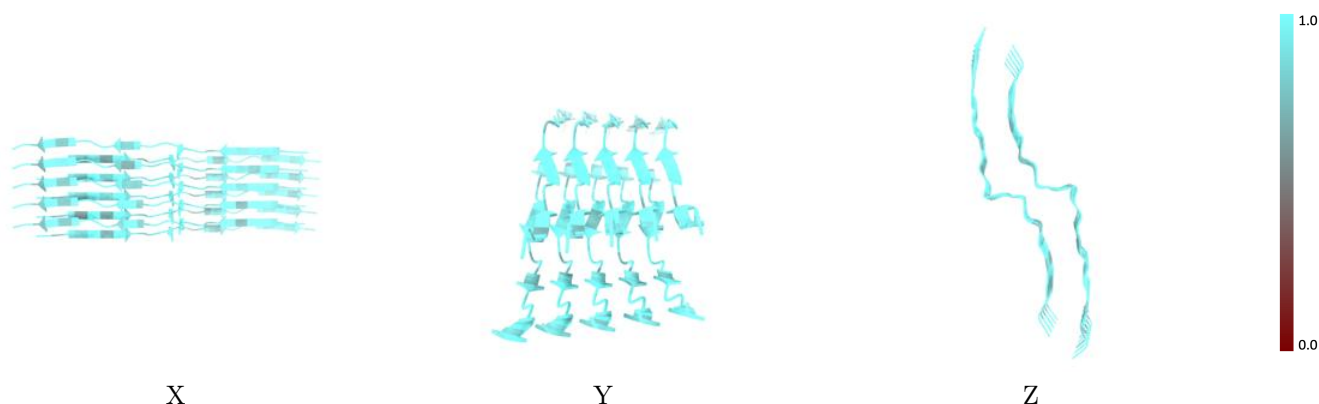


## 9.2 Q-score mapped to coordinate model [i](#)



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.

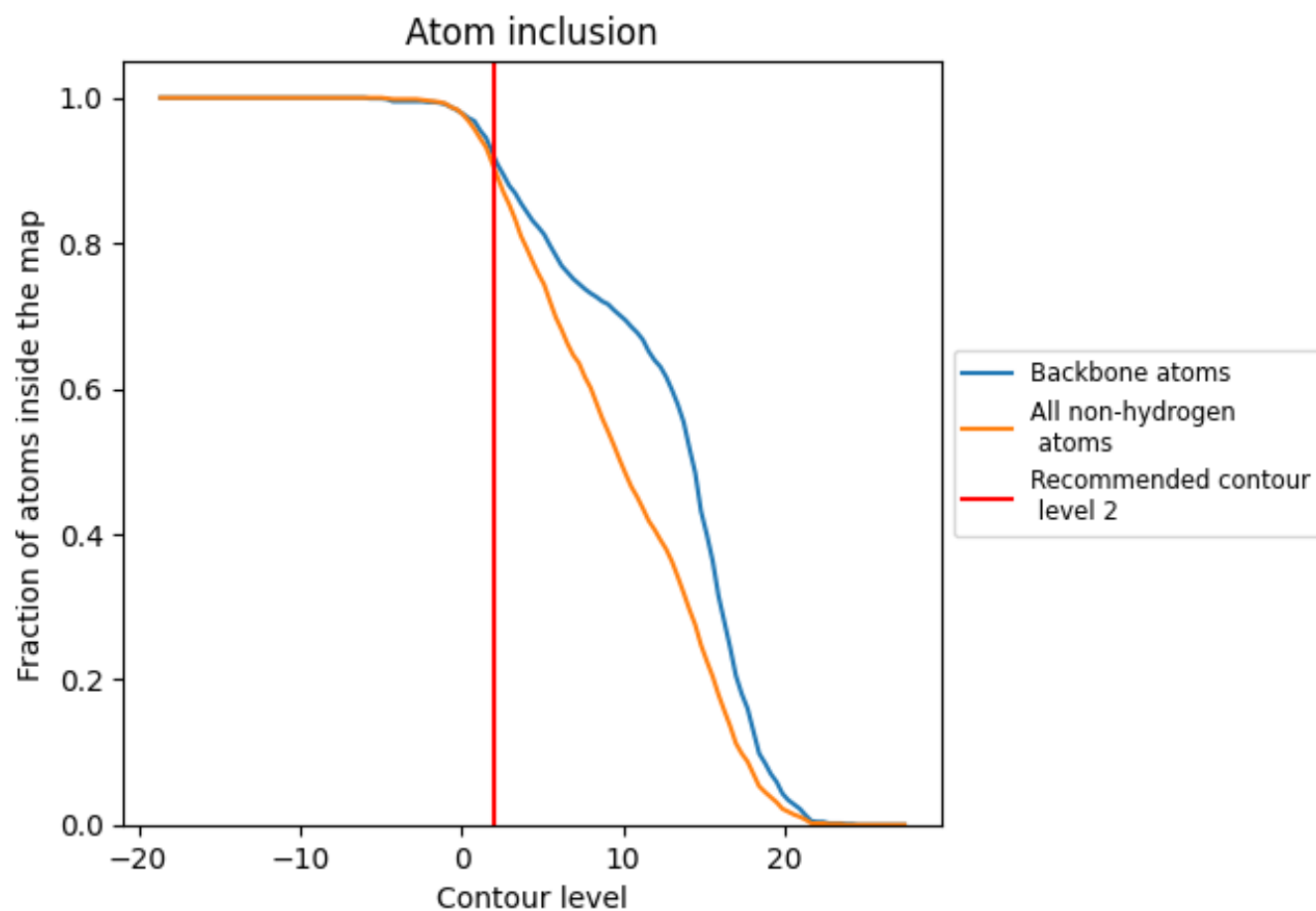
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (2).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9040	<div><div></div></div> 0.4790
A	<div><div></div></div> 0.8960	<div><div></div></div> 0.4790
B	<div><div></div></div> 0.8960	<div><div></div></div> 0.4680
C	<div><div></div></div> 0.8960	<div><div></div></div> 0.4800
D	<div><div></div></div> 0.9150	<div><div></div></div> 0.4750
E	<div><div></div></div> 0.9150	<div><div></div></div> 0.4820
F	<div><div></div></div> 0.9000	<div><div></div></div> 0.4790
G	<div><div></div></div> 0.9050	<div><div></div></div> 0.4850
H	<div><div></div></div> 0.8810	<div><div></div></div> 0.4800
I	<div><div></div></div> 0.9240	<div><div></div></div> 0.4820
J	<div><div></div></div> 0.9150	<div><div></div></div> 0.4790

1.0

0.0

<0.0