



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:42 PM UTC

PDB ID : 9V4F / pdb_00009v4f
EMDB ID : EMD-64778
Title : Soy storage protein fibril (glycinin A) PM2
Authors : Li, S.; Cao, Q.; Cao, Y.
Deposited on : 2025-05-23
Resolution : 3.52 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

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>.

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

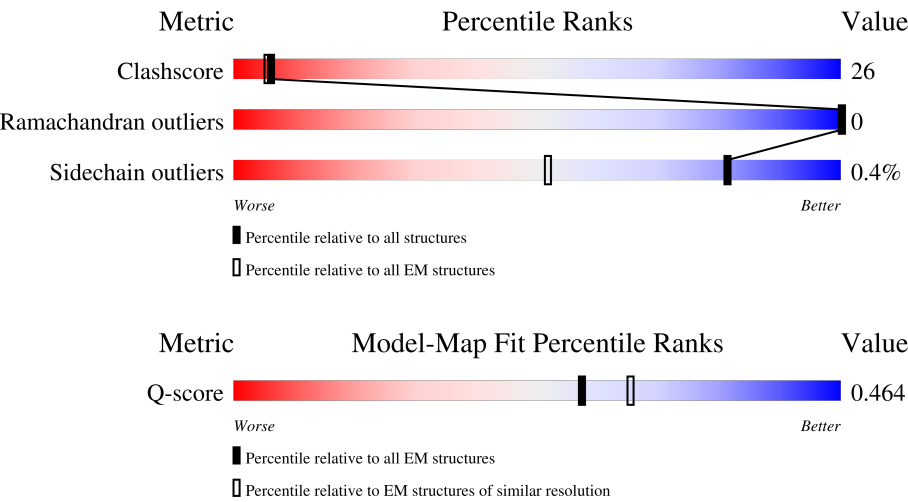
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.52 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.



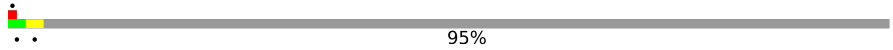
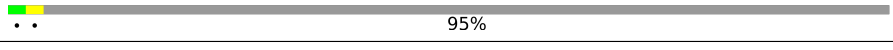
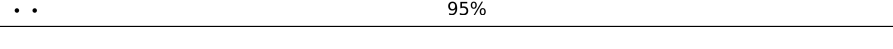
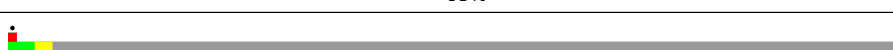
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13017 (3.02 - 4.02)

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 ≥ 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 1990 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	26	Total	C	N	O	0	0
			199	135	28	36		
1	B	26	Total	C	N	O	0	0
			199	135	28	36		
1	C	26	Total	C	N	O	0	0
			199	135	28	36		
1	D	26	Total	C	N	O	0	0
			199	135	28	36		
1	E	26	Total	C	N	O	0	0
			199	135	28	36		
1	F	26	Total	C	N	O	0	0
			199	135	28	36		
1	G	26	Total	C	N	O	0	0
			199	135	28	36		
1	H	26	Total	C	N	O	0	0
			199	135	28	36		
1	I	26	Total	C	N	O	0	0
			199	135	28	36		
1	J	26	Total	C	N	O	0	0
			199	135	28	36		

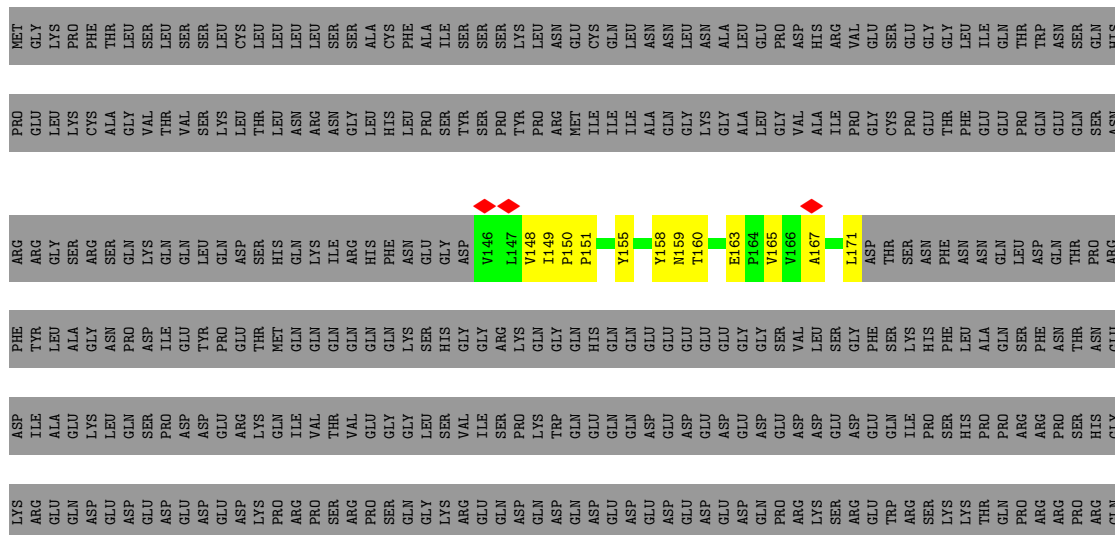
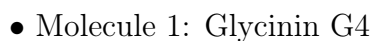
TRP	GLY	PHE	ASN	LEU	ARG	GLN	HIS	ASN	GLY	ASP	GLN	GLY	ASP	GLN	ARG	ARG
PRO	LEU	VAL	VAL	ALA	GLU	GLU	LYS	GLY	ASP	ILE	GLY	GLY	ASP	GLY	THR	GLY
VAL	VAL	ASN	GLU	GLN	ARG	PRO	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
PRO	PRO	GLN	GLY	VAL	GLY	GLY	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	SER	ALA	GLY	LEU	ARG	GLY	GLY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

● Molecule 1: Glycinin G4

Chain C: . . 95%

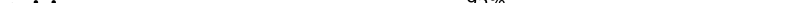
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GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY	GLY GLY
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Chain D: 95%



[illegible]

- Molecule 1: Glycinin G4

Chain F:  95%

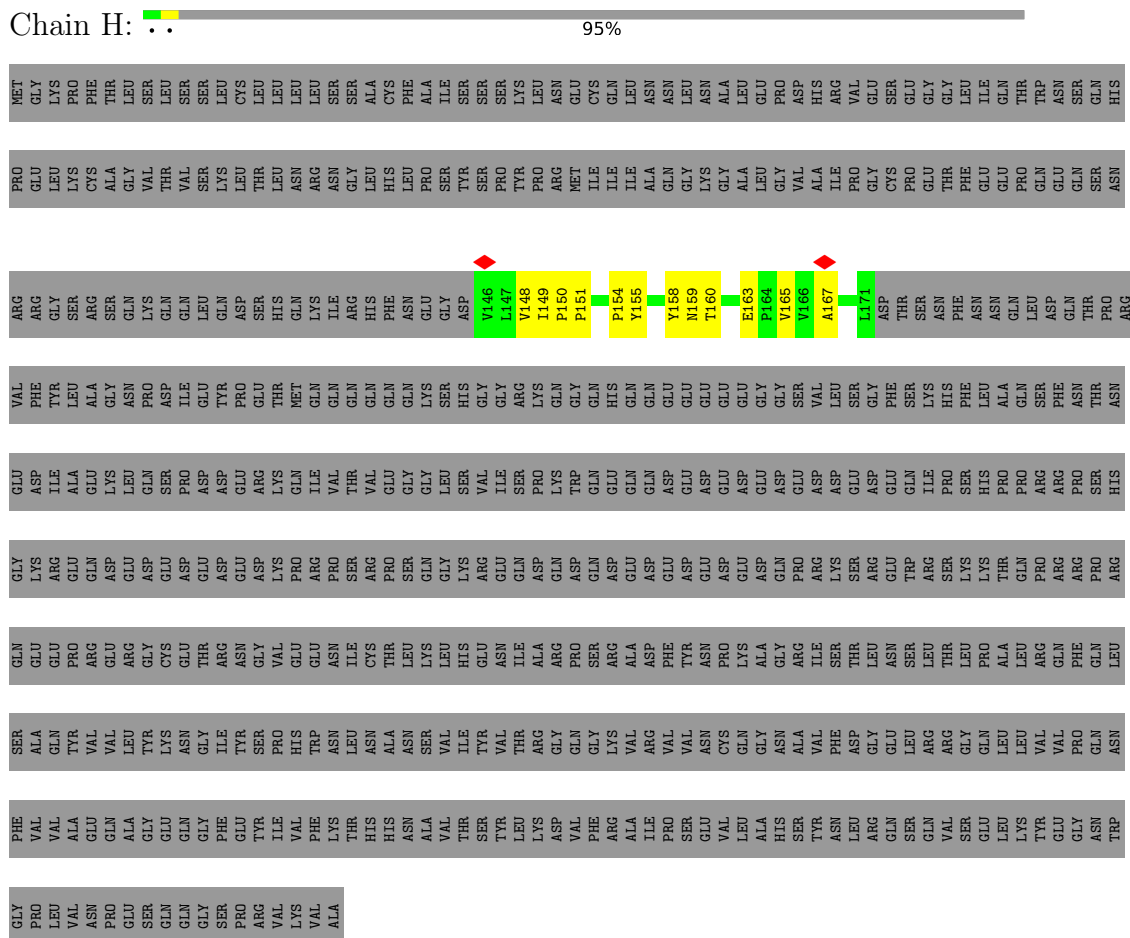
GLY	PRO	VAL	PHE	SER	GLN	GLY	GLU	VAL	ARG	PRO	MET
PRO	VAL	VAL	VAL	ALA	GLN	GLY	ASP	PHE	ARG	GLU	GLY
VAL	ALA	ALA	TTR	VAL	PRO	ARG	ALA	LEU	SER	LYS	LYS
ASN	GLU	GLU	VAL	VAL	ARG	GLN	ASP	GLY	ARG	CYS	PHE
PRO	GLN	GLN	VAL	VAL	GLU	ASP	LYS	ASN	SER	ALA	THR
GLU	ALA	ALA	LEU	LEU	ARG	GLU	LEU	ASN	GLN	GLY	LEU
SER	GLY	GLY	TTR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

- Molecule 1: Glycinin G4

Chain G: 95%

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

- Molecule 1: Glycinin G4



Chain I: 95%



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

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-1.6°, rise=4.8 Å, axial sym=C2	Depositor
Number of segments used	14488	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	7.326	Depositor
Minimum map value	-5.431	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	102.52, 102.52, 102.52	wwPDB
Map dimensions	110, 110, 110	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	0.19	0/206	0.50	0/288
1	B	0.34	0/206	0.57	0/288
1	C	0.19	0/206	0.50	0/288
1	D	0.34	0/206	0.57	0/288
1	E	0.19	0/206	0.50	0/288
1	F	0.34	0/206	0.57	0/288
1	G	0.19	0/206	0.50	0/288
1	H	0.34	0/206	0.57	0/288
1	I	0.19	0/206	0.50	0/288
1	J	0.34	0/206	0.57	0/288
All	All	0.27	0/2060	0.54	0/2880

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	199	0	201	13	0
1	B	199	0	201	11	0
1	C	199	0	201	23	0
1	D	199	0	201	16	0
1	E	199	0	201	23	0
1	F	199	0	201	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	199	0	201	23	0
1	H	199	0	201	16	0
1	I	199	0	201	13	0
1	J	199	0	201	10	0
All	All	1990	0	2010	104	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 26.

The worst 5 of 104 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:158:TYR:HB2	1:C:158:TYR:CD2	2.16	0.81
1:C:158:TYR:HB2	1:E:158:TYR:CD2	2.16	0.81
1:E:158:TYR:HB2	1:G:158:TYR:CD2	2.16	0.80
1:G:158:TYR:HB2	1:I:158:TYR:CD2	2.16	0.80
1:D:158:TYR:HB2	1:F:158:TYR:CD2	2.26	0.71

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	24/563 (4%)	21 (88%)	3 (12%)	0	100	100
1	B	24/563 (4%)	20 (83%)	4 (17%)	0	100	100
1	C	24/563 (4%)	21 (88%)	3 (12%)	0	100	100
1	D	24/563 (4%)	20 (83%)	4 (17%)	0	100	100
1	E	24/563 (4%)	21 (88%)	3 (12%)	0	100	100
1	F	24/563 (4%)	20 (83%)	4 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	24/563 (4%)	21 (88%)	3 (12%)	0	100	100
1	H	24/563 (4%)	20 (83%)	4 (17%)	0	100	100
1	I	24/563 (4%)	21 (88%)	3 (12%)	0	100	100
1	J	24/563 (4%)	20 (83%)	4 (17%)	0	100	100
All	All	240/5630 (4%)	205 (85%)	35 (15%)	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	23/501 (5%)	23 (100%)	0	100	100
1	B	23/501 (5%)	23 (100%)	0	100	100
1	C	23/501 (5%)	23 (100%)	0	100	100
1	D	23/501 (5%)	23 (100%)	0	100	100
1	E	23/501 (5%)	23 (100%)	0	100	100
1	F	23/501 (5%)	23 (100%)	0	100	100
1	G	23/501 (5%)	23 (100%)	0	100	100
1	H	23/501 (5%)	23 (100%)	0	100	100
1	I	23/501 (5%)	23 (100%)	0	100	100
1	J	23/501 (5%)	22 (96%)	1 (4%)	26	51
All	All	230/5010 (5%)	229 (100%)	1 (0%)	81	82

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	168	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	159	ASN
1	I	159	ASN
1	G	159	ASN
1	F	159	ASN
1	H	159	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

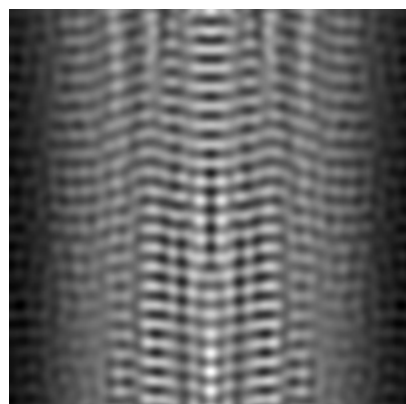
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64778. These allow visual inspection of the internal detail of the map and identification of artifacts.

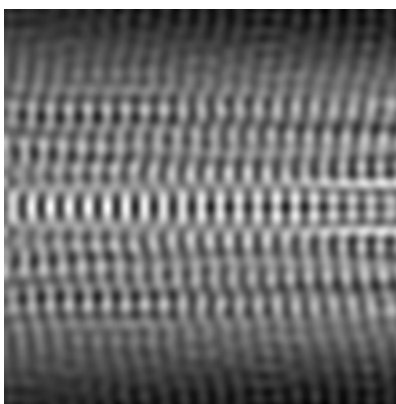
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

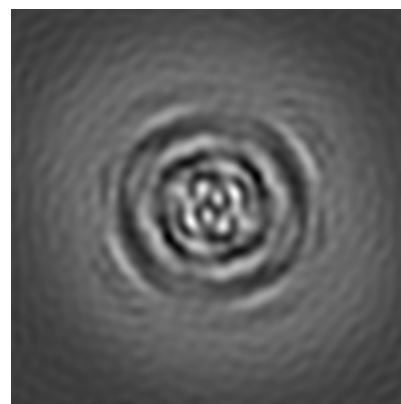
6.1.1 Primary map



X

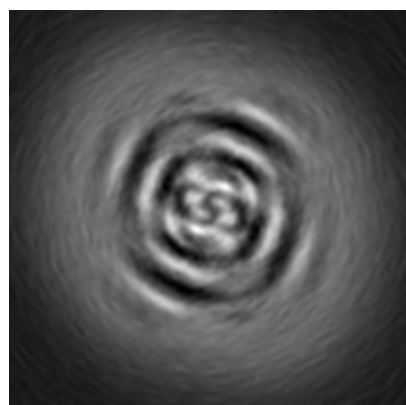


Y

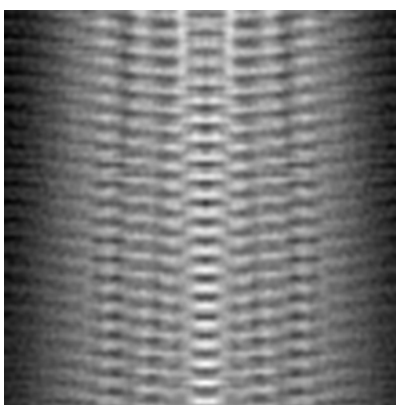


Z

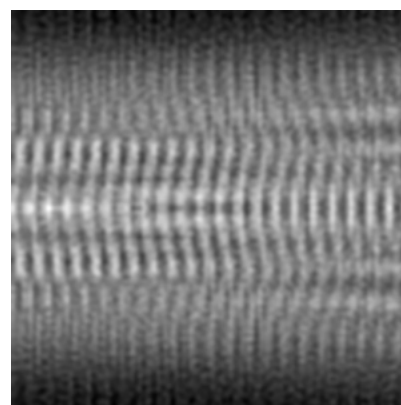
6.1.2 Raw map



X



Y

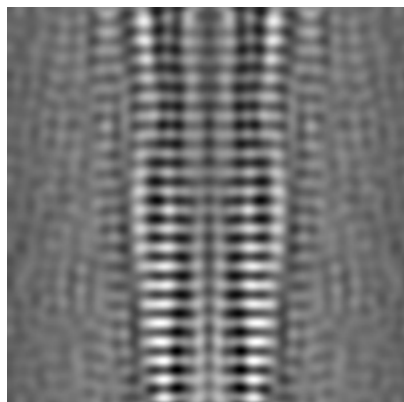


Z

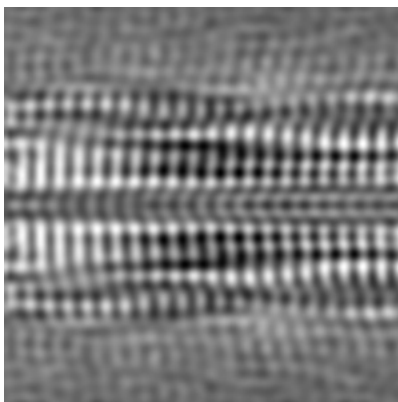
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

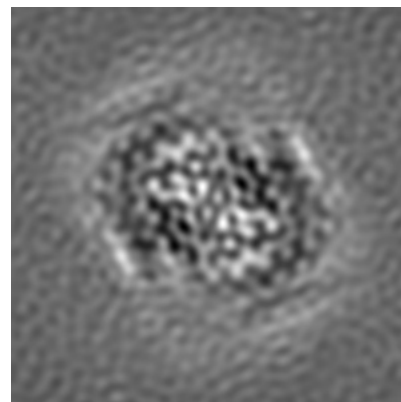
6.2.1 Primary map



X Index: 55

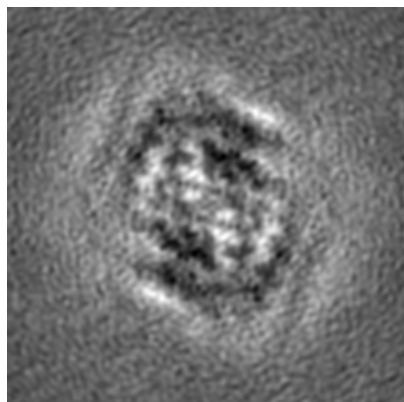


Y Index: 55

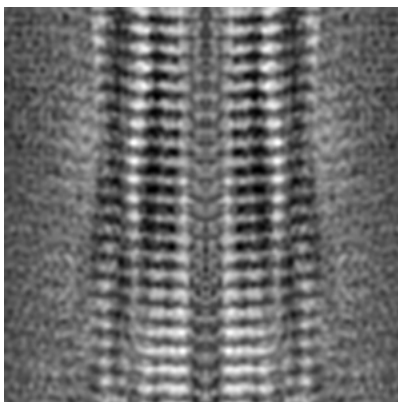


Z Index: 55

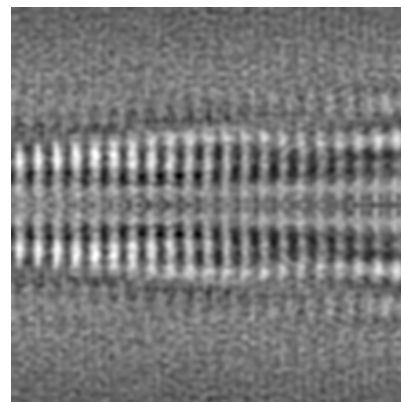
6.2.2 Raw map



X Index: 55



Y Index: 55

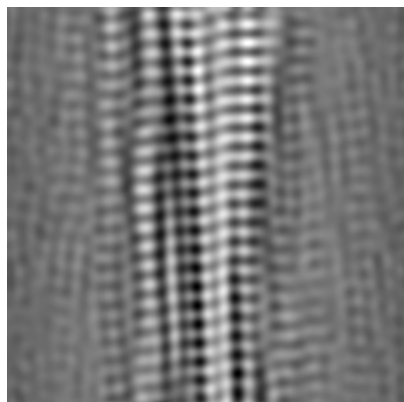


Z Index: 55

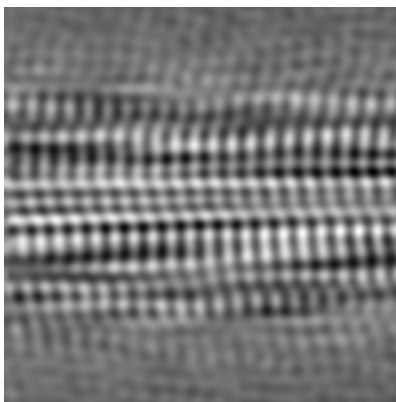
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

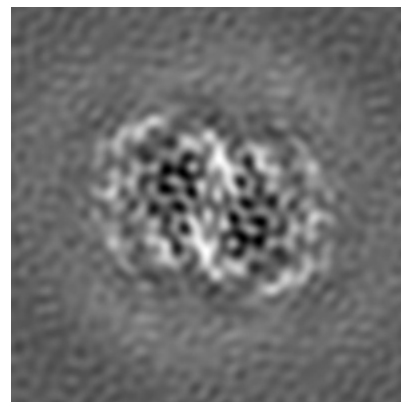
6.3.1 Primary map



X Index: 61

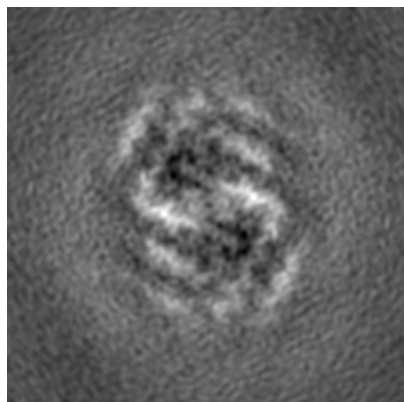


Y Index: 59

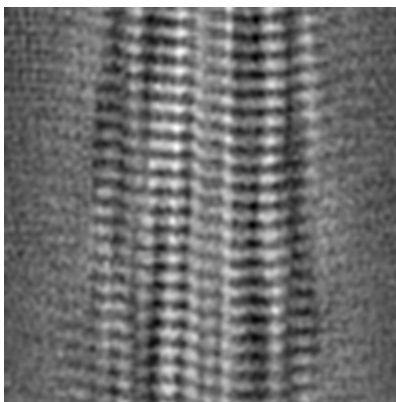


Z Index: 43

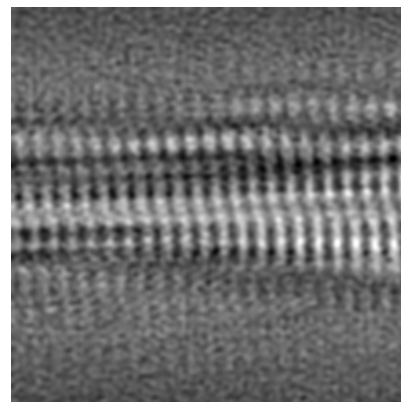
6.3.2 Raw map



X Index: 43



Y Index: 59

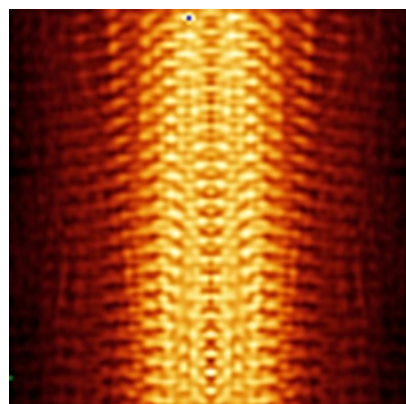


Z Index: 49

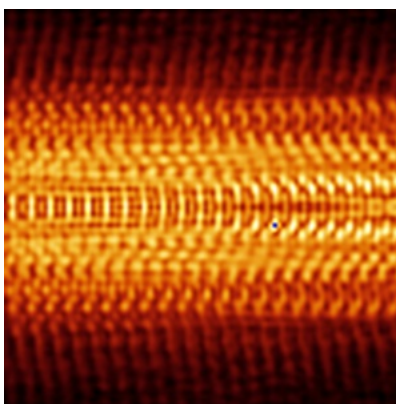
The images above show the largest variance slices of the map in three orthogonal directions.

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

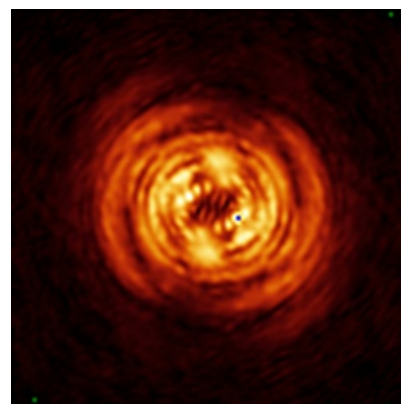
6.4.1 Primary map



X

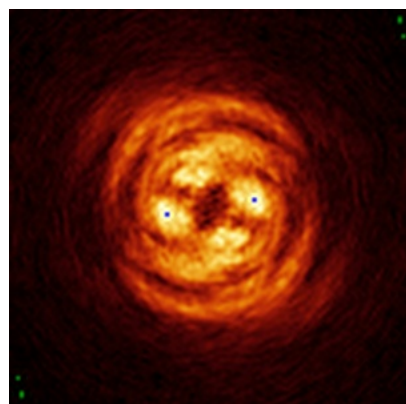


Y

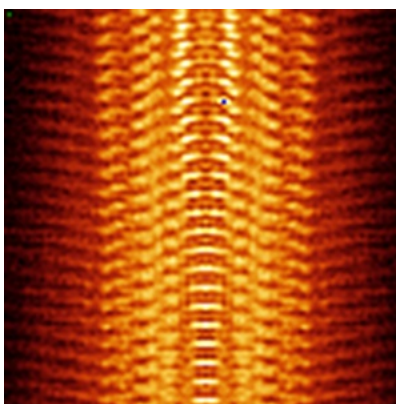


Z

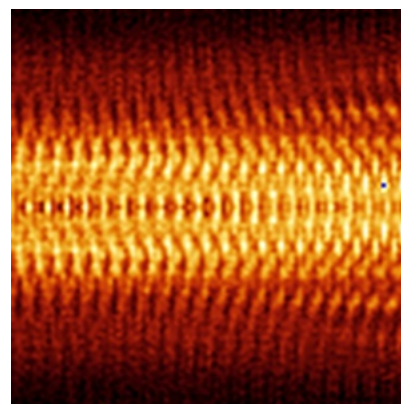
6.4.2 Raw map



X



Y

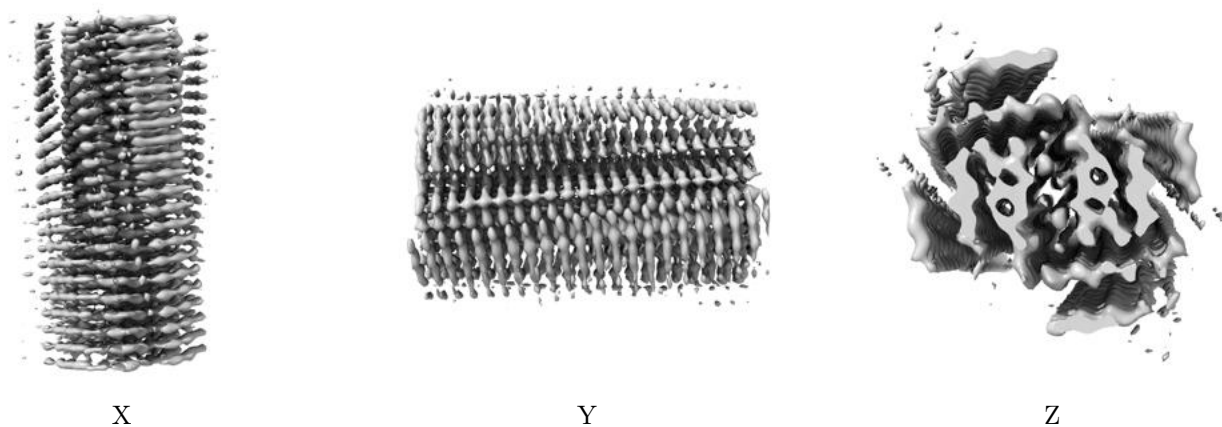


Z

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.

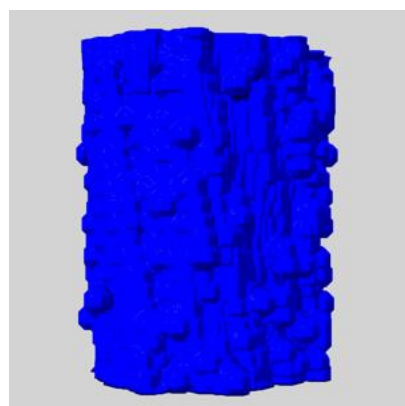
6.6 Mask visualisation [i](#)

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

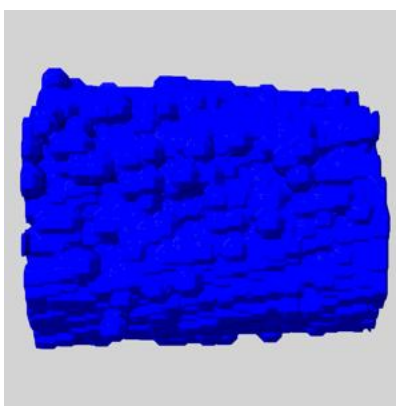
A mask typically either:

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

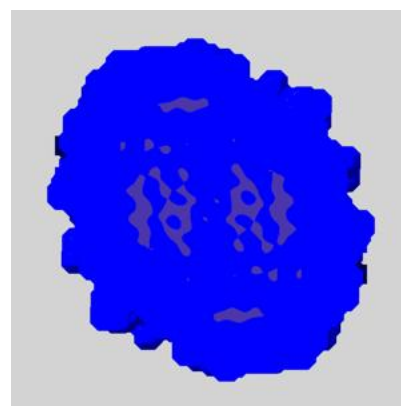
6.6.1 emd_64778_msk_1.map [i](#)



X



Y

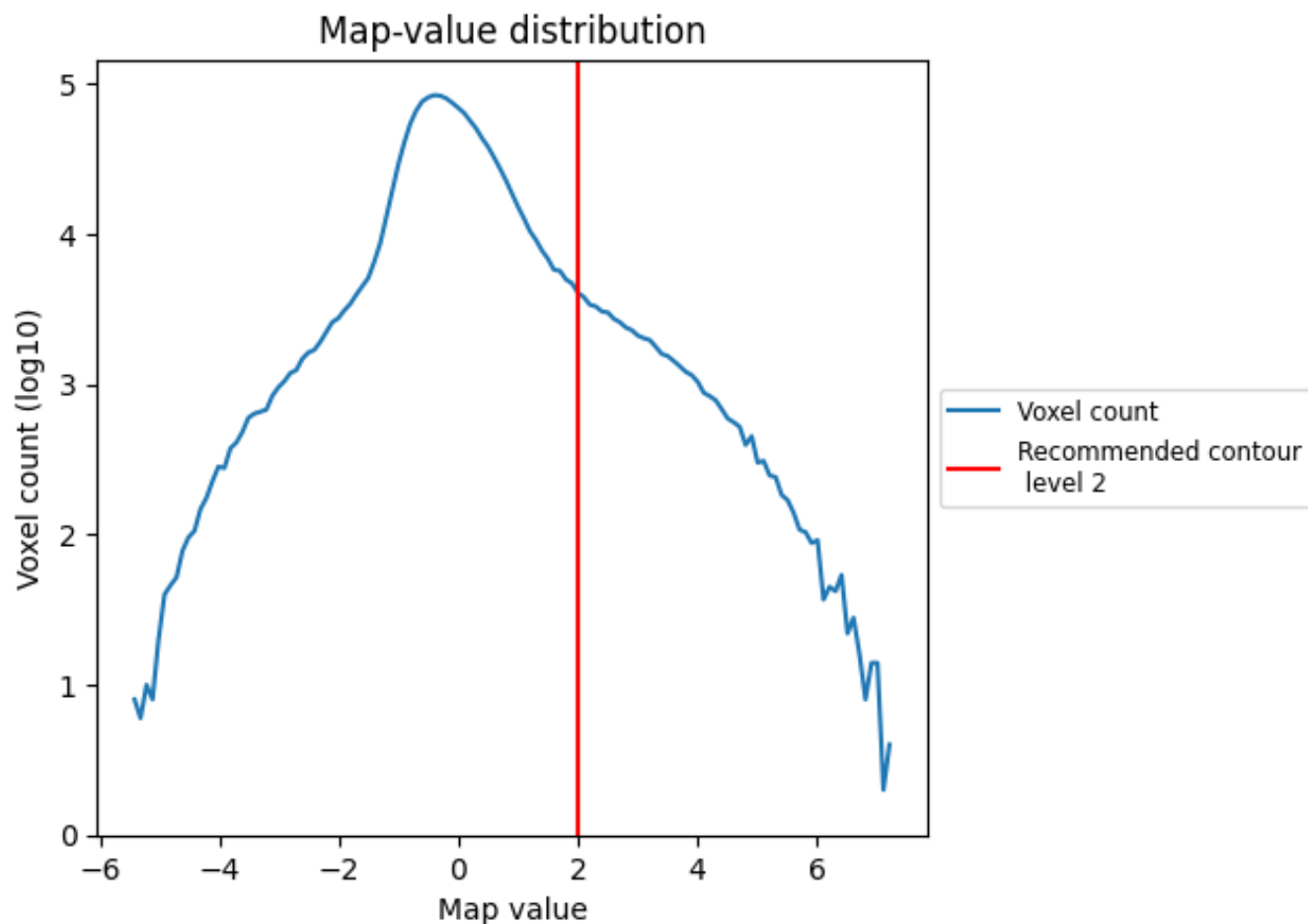


Z

7 Map analysis [i](#)

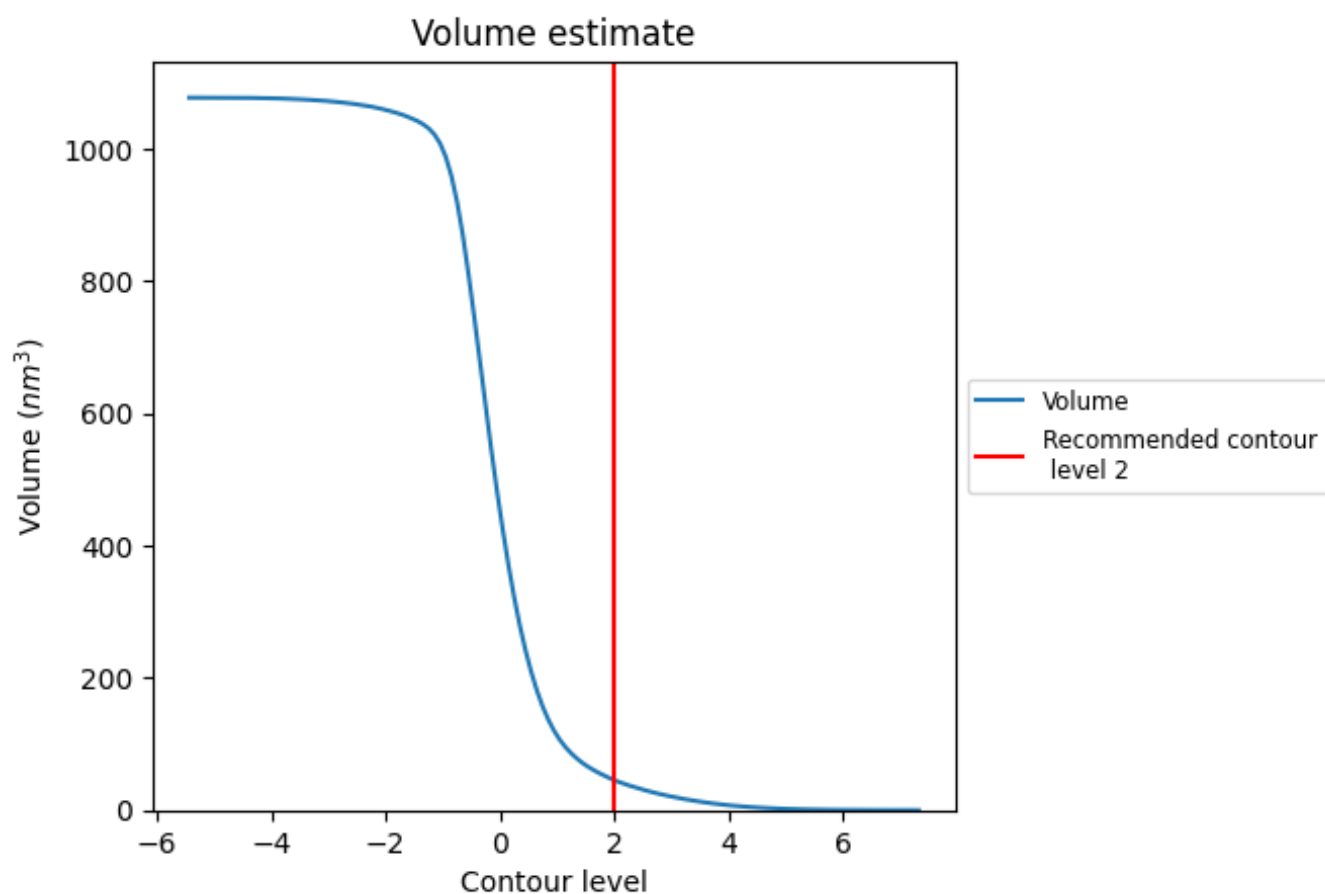
This section contains the results of statistical analysis of the map.

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.

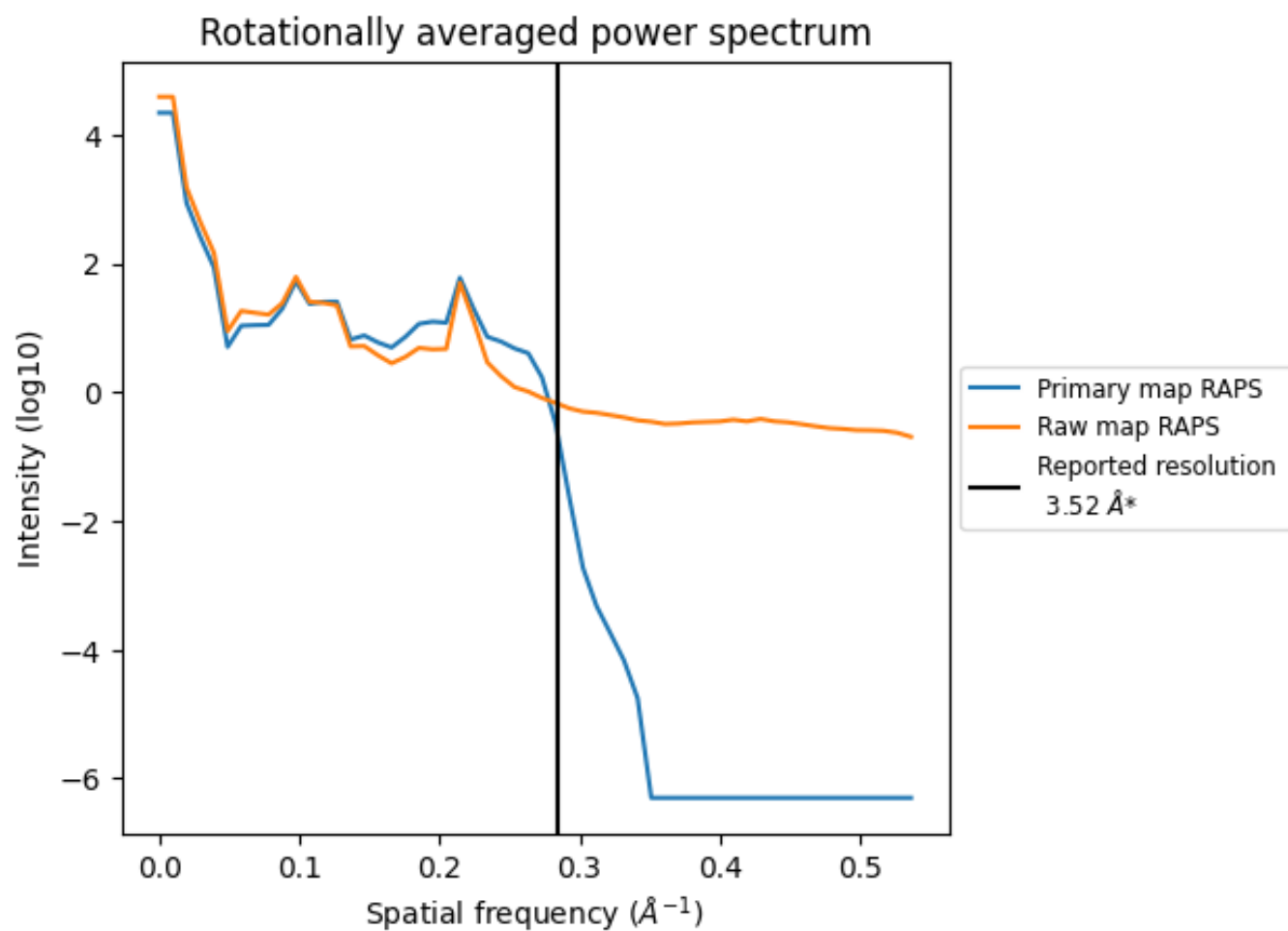
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 45 nm³; this corresponds to an approximate mass of 41 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 ⓘ

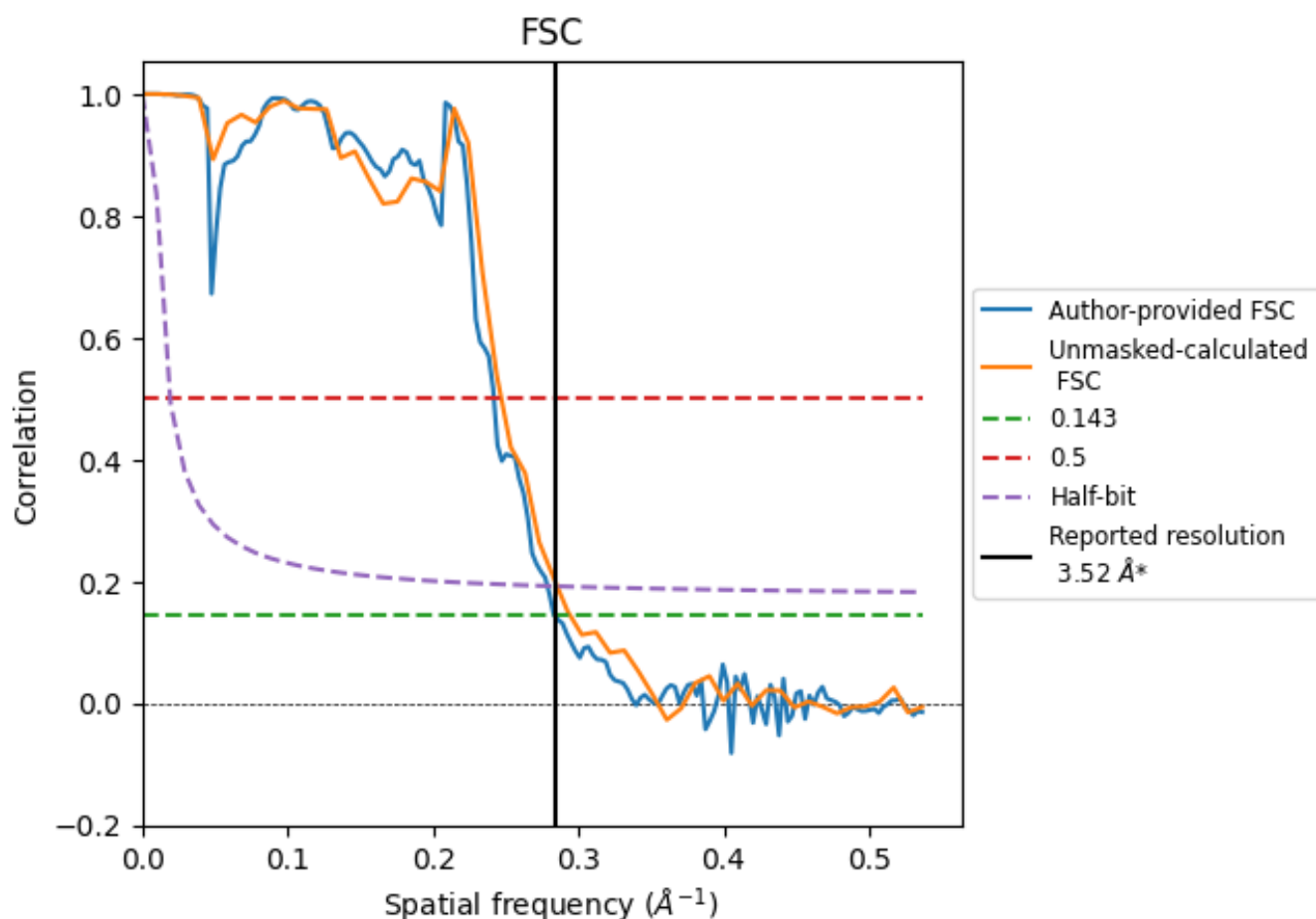


*Reported resolution corresponds to spatial frequency of 0.284 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.284 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

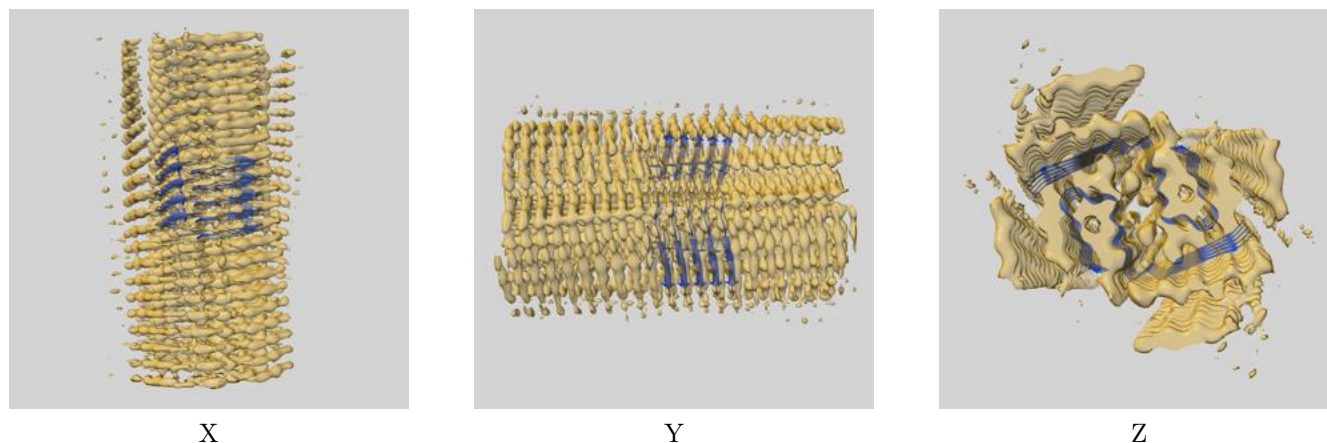
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.52	-	-
Author-provided FSC curve	3.52	4.13	3.57
Unmasked-calculated*	3.39	4.05	3.50

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

9 Map-model fit [i](#)

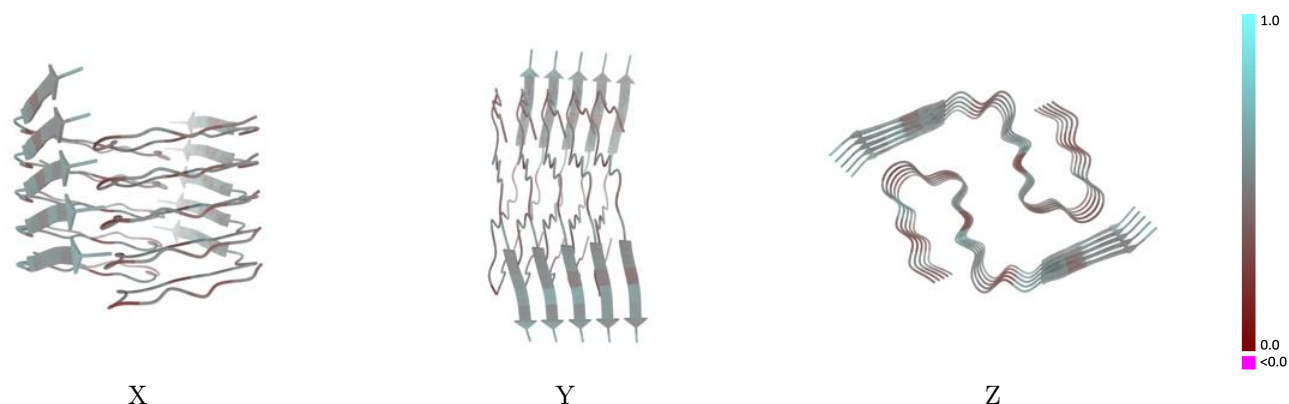
This section contains information regarding the fit between EMDB map EMD-64778 and PDB model 9V4F. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



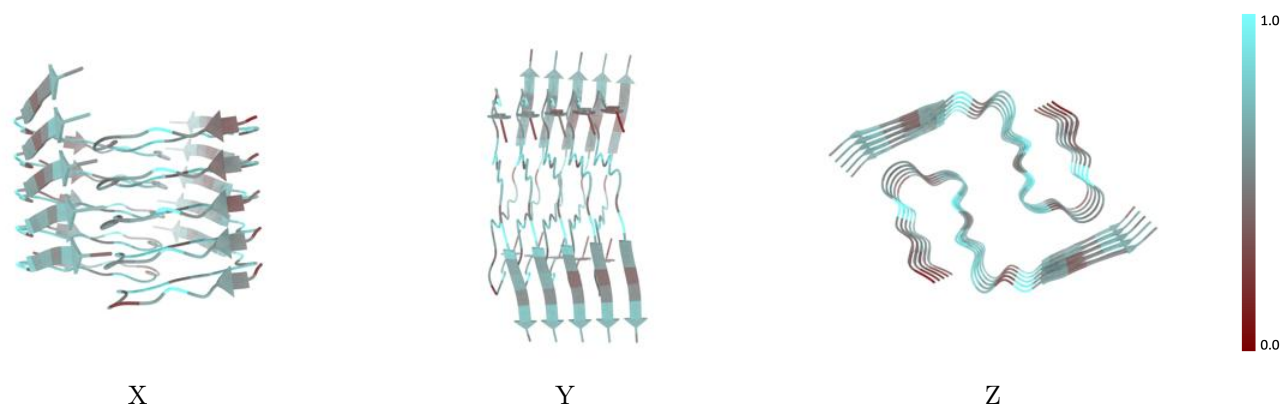
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



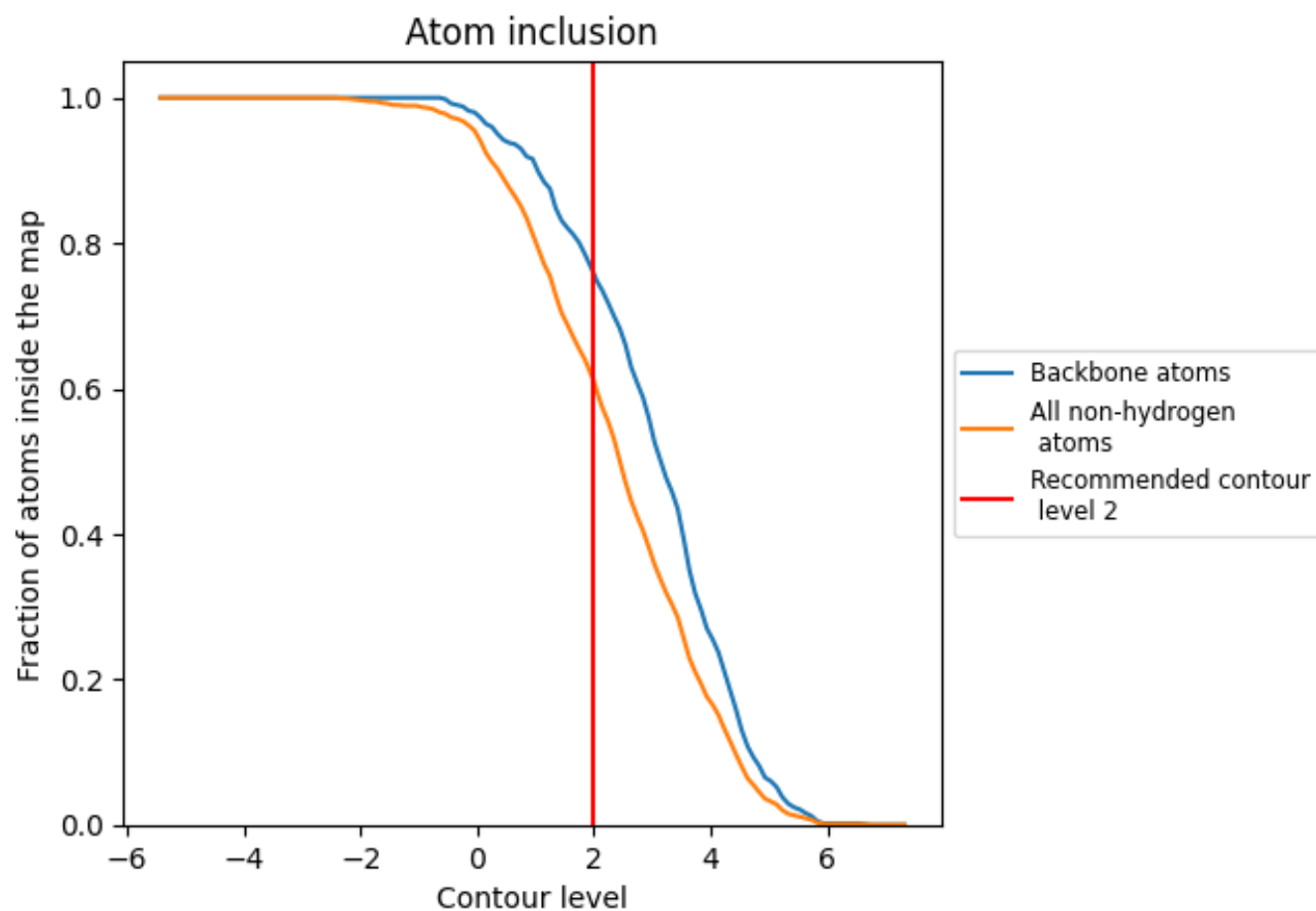
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 76% of all backbone atoms, 61% 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	0.6100	0.4640
A	0.5970	0.4620
B	0.6280	0.4640
C	0.6280	0.4670
D	0.6380	0.4700
E	0.5920	0.4670
F	0.6170	0.4690
G	0.6020	0.4630
H	0.6070	0.4640
I	0.5820	0.4570
J	0.6070	0.4580

1.0

0.0

<0.0