



wwPDB EM Validation Summary Report ⓘ

Jul 7, 2024 – 03:33 pm BST

PDB ID : 7QJY
EMDB ID : EMD-14026
Title : In vitro assembled 266/297 - 391 tau filaments with LiCl (9a)
Authors : Lovestam, S.; Scheres, S.H.W.
Deposited on : 2021-12-17
Resolution : 3.14 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

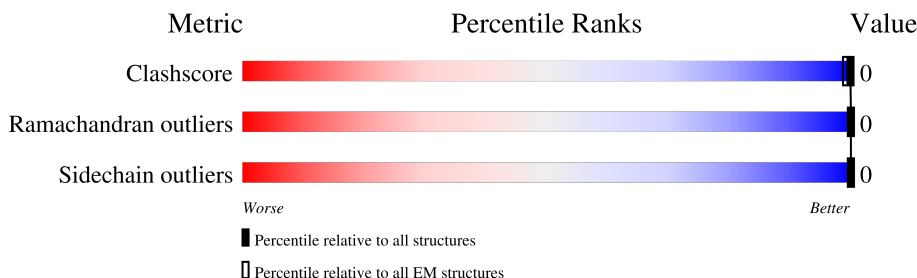
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.14 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 ≥ 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	441	
1	B	441	
1	C	441	
1	D	441	
1	E	441	
1	F	441	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3444 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 Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	75	Total 574	C 360	N 106	O 107	S 1	0	0
1	B	75	Total 574	C 360	N 106	O 107	S 1	0	0
1	C	75	Total 574	C 360	N 106	O 107	S 1	0	0
1	D	75	Total 574	C 360	N 106	O 107	S 1	0	0
1	E	75	Total 574	C 360	N 106	O 107	S 1	0	0
1	F	75	Total 574	C 360	N 106	O 107	S 1	0	0

PRO	GLY	GLY	S305	R379	GLU	ASN	ALA	LYS	LYS	THR	HIS	GLY	ALA	GLU	ILE	VAL	TYR	LYS	SER	PRO	VAL	VAL	SER	GLY	ASP	THR	SER	PRO	ARG	HIS	LEU	SER	ASN	VAL	SER	SER	THR	GLY	SER	ILE	ASP	MET	VAL	THR	PRO	GLN	LEU	ALA	THR	LEU	ALA	ASP	VAL
SER	ALA	SER	LEU	ALA	LYS	GLN	GLY	LEU																																													

● Molecule 1: Microtubule-associated protein tau

Chain C: 17% 83%

SER	ALA	LEU	ALA	LYS	GLN	GLY	LEU	ASN	ALA	LYS	ALA	HIS	GLY	ALA	THR	VAL	ILE	GLU	GLY	TYR	LYS	SER	GLY	VAL	THR	ASN	LEU	VAL	VAL	SER	GLY	THR	SER	GLY	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	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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● Molecule 1: Microtubule-associated protein tau

Chain D: 17% 83%

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

● Molecule 1: Microtubule-associated protein tau

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

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-1.26°, rise=4.74 Å, axial sym=C2	Depositor
Number of segments used	24754	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 ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0119	Depositor
Map size (Å)	279.04, 279.04, 279.04	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

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	0.54	0/583	0.94	1/780 (0.1%)
1	B	0.54	0/583	0.92	1/780 (0.1%)
1	C	0.55	0/583	0.92	0/780
1	D	0.55	0/583	0.96	1/780 (0.1%)
1	E	0.55	0/583	0.93	0/780
1	F	0.54	0/583	0.90	0/780
All	All	0.54	0/3498	0.93	3/4680 (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
1	F	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	379	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	B	379	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	A	379	ARG	NE-CZ-NH1	5.26	122.93	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	310	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	574	0	597	0	0
1	B	574	0	597	0	0
1	C	574	0	597	0	0
1	D	574	0	597	0	0
1	E	574	0	597	0	0
1	F	574	0	597	0	0
All	All	3444	0	3582	0	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.

There are no clashes within the asymmetric unit.

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	73/441 (17%)	68 (93%)	5 (7%)	0	100	100
1	B	73/441 (17%)	70 (96%)	3 (4%)	0	100	100
1	C	73/441 (17%)	68 (93%)	5 (7%)	0	100	100
1	D	73/441 (17%)	72 (99%)	1 (1%)	0	100	100
1	E	73/441 (17%)	67 (92%)	6 (8%)	0	100	100
1	F	73/441 (17%)	68 (93%)	5 (7%)	0	100	100
All	All	438/2646 (17%)	413 (94%)	25 (6%)	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	66/358 (18%)	66 (100%)	0	100	100
1	B	66/358 (18%)	66 (100%)	0	100	100
1	C	66/358 (18%)	66 (100%)	0	100	100
1	D	66/358 (18%)	66 (100%)	0	100	100
1	E	66/358 (18%)	66 (100%)	0	100	100
1	F	66/358 (18%)	66 (100%)	0	100	100
All	All	396/2148 (18%)	396 (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 [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.

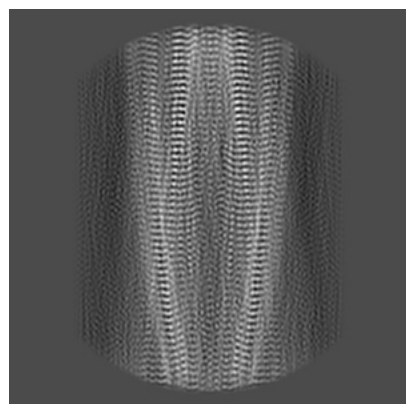
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14026. These allow visual inspection of the internal detail of the map and identification of artifacts.

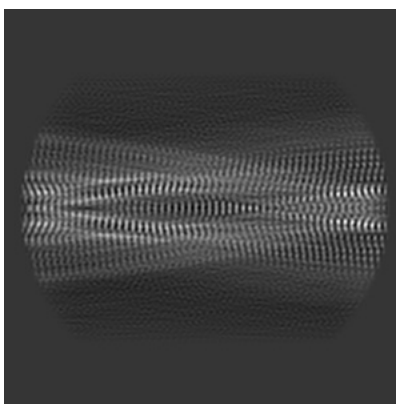
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

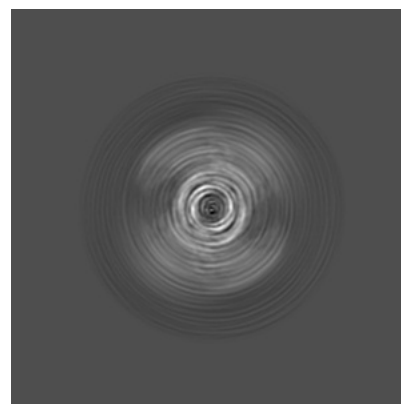
6.1.1 Primary map



X

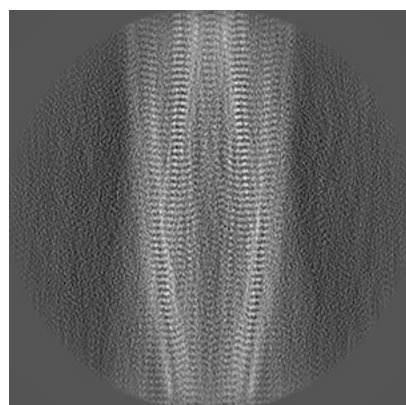


Y

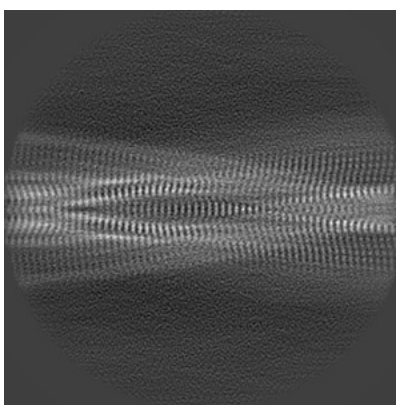


Z

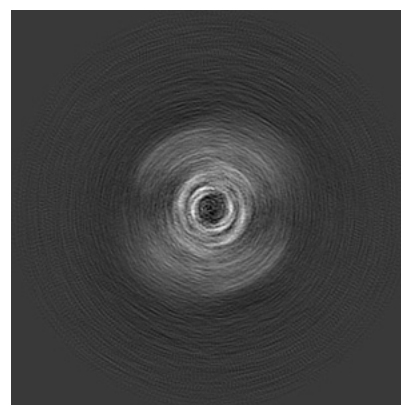
6.1.2 Raw map



X



Y

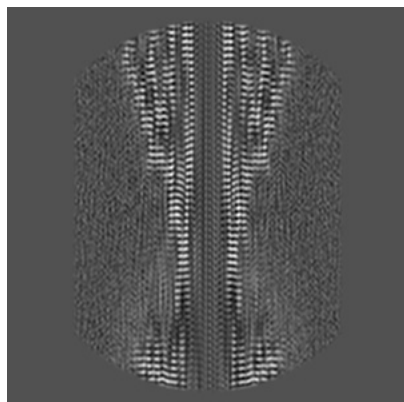


Z

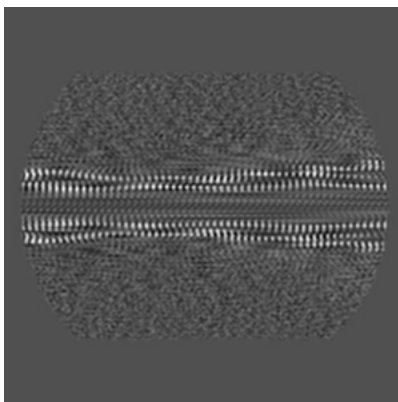
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

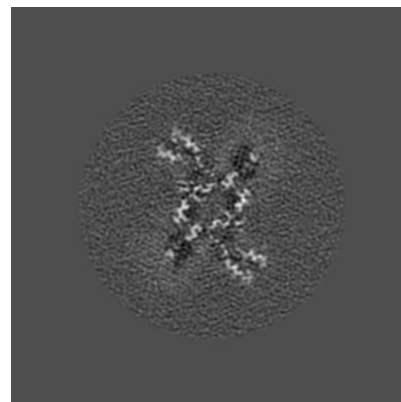
6.2.1 Primary map



X Index: 128

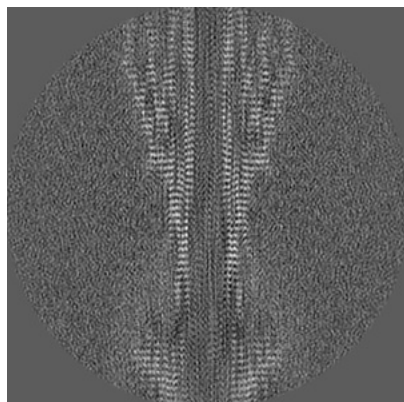


Y Index: 128

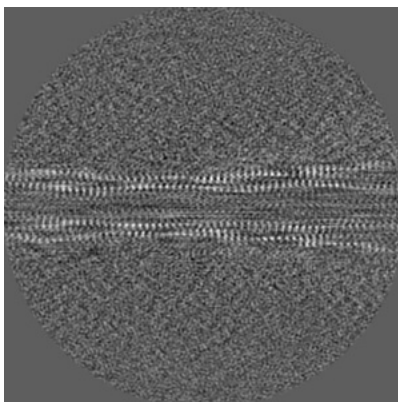


Z Index: 128

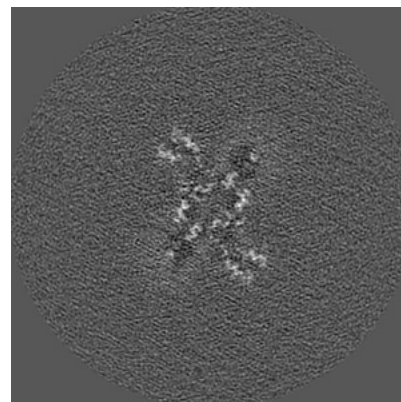
6.2.2 Raw map



X Index: 128



Y Index: 128

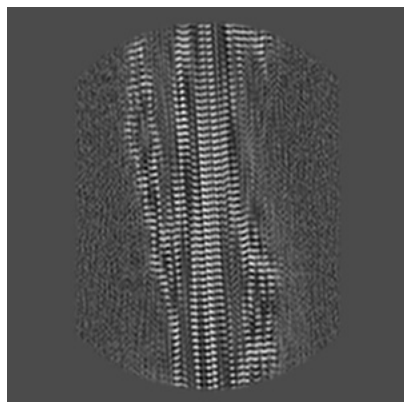


Z Index: 128

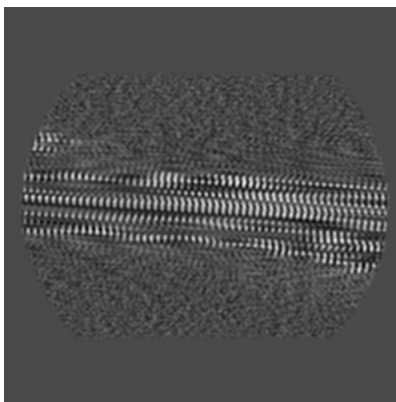
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

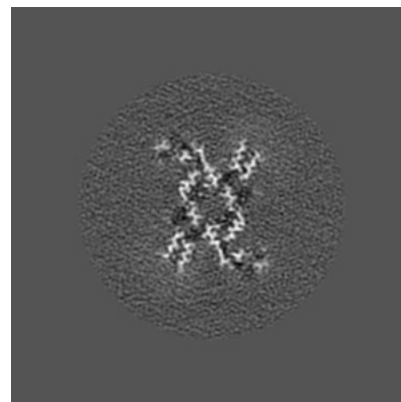
6.3.1 Primary map



X Index: 140

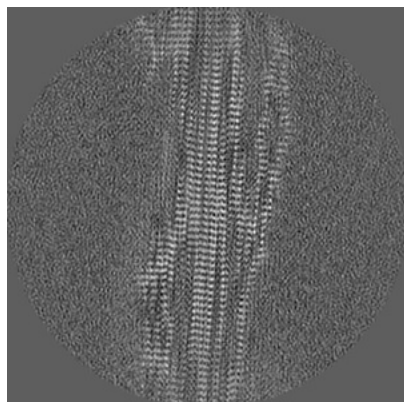


Y Index: 115

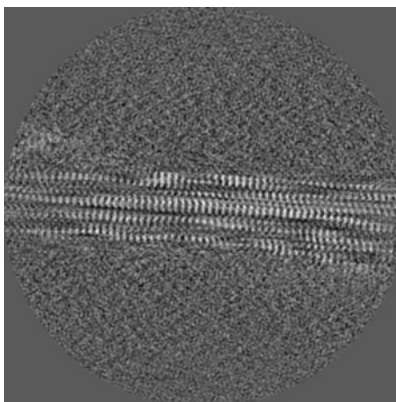


Z Index: 122

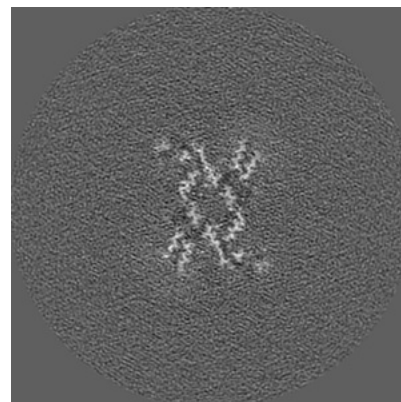
6.3.2 Raw map



X Index: 117



Y Index: 115

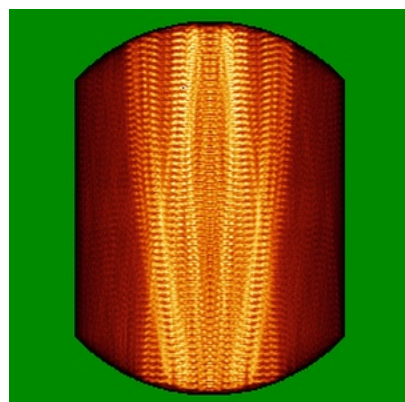


Z Index: 122

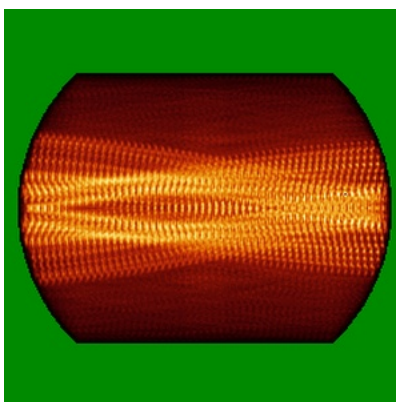
The images above show the largest variance slices of the map in three orthogonal directions.

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

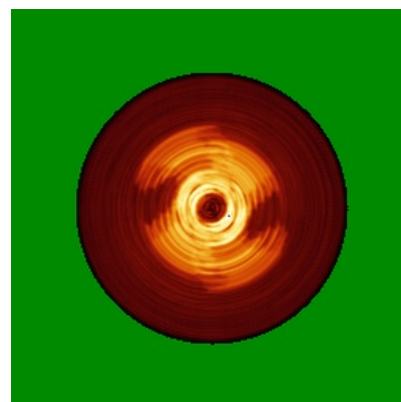
6.4.1 Primary map



X

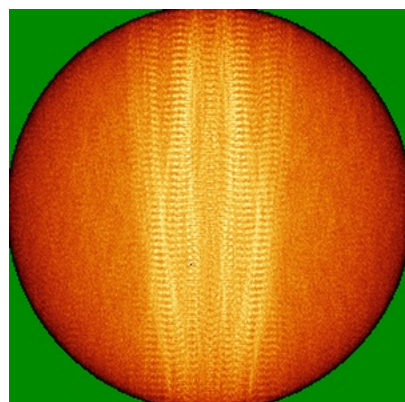


Y

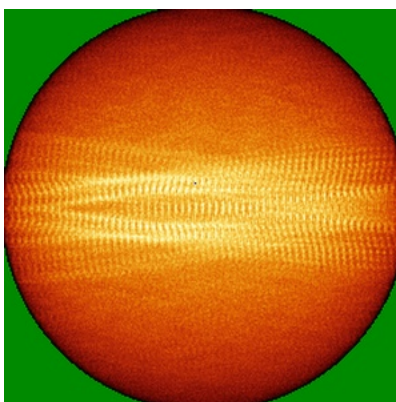


Z

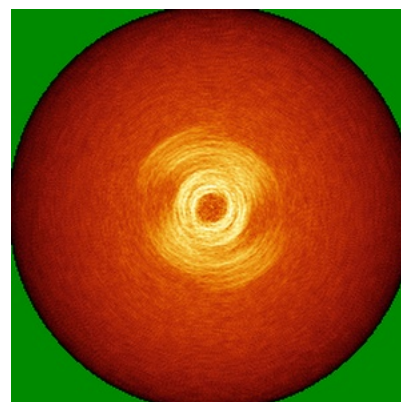
6.4.2 Raw map



X



Y

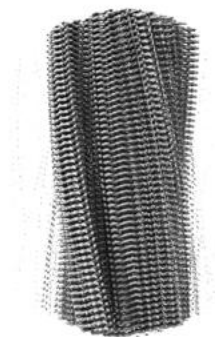


Z

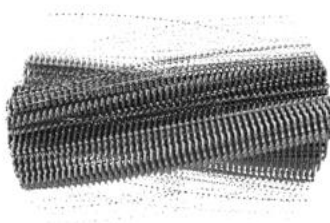
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

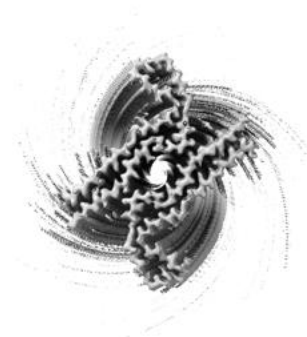
6.5.1 Primary map



X



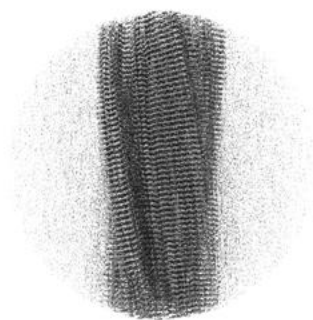
Y



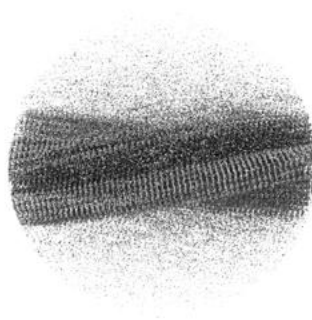
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0119. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

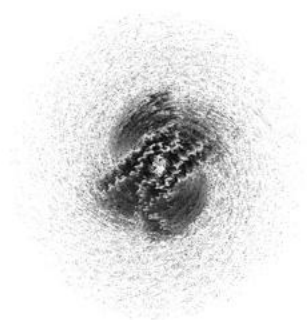
6.5.2 Raw map



X



Y



Z

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.

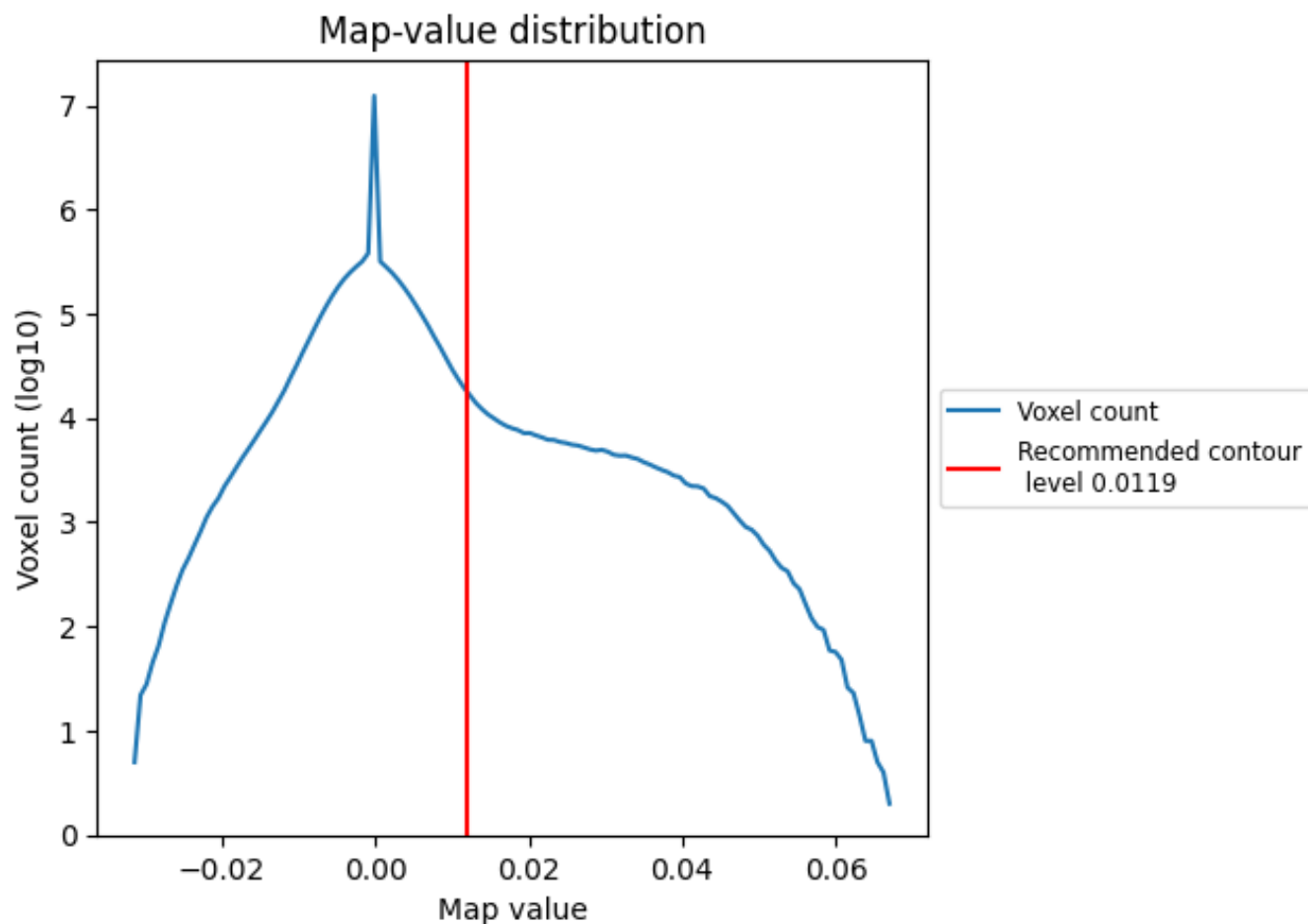
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

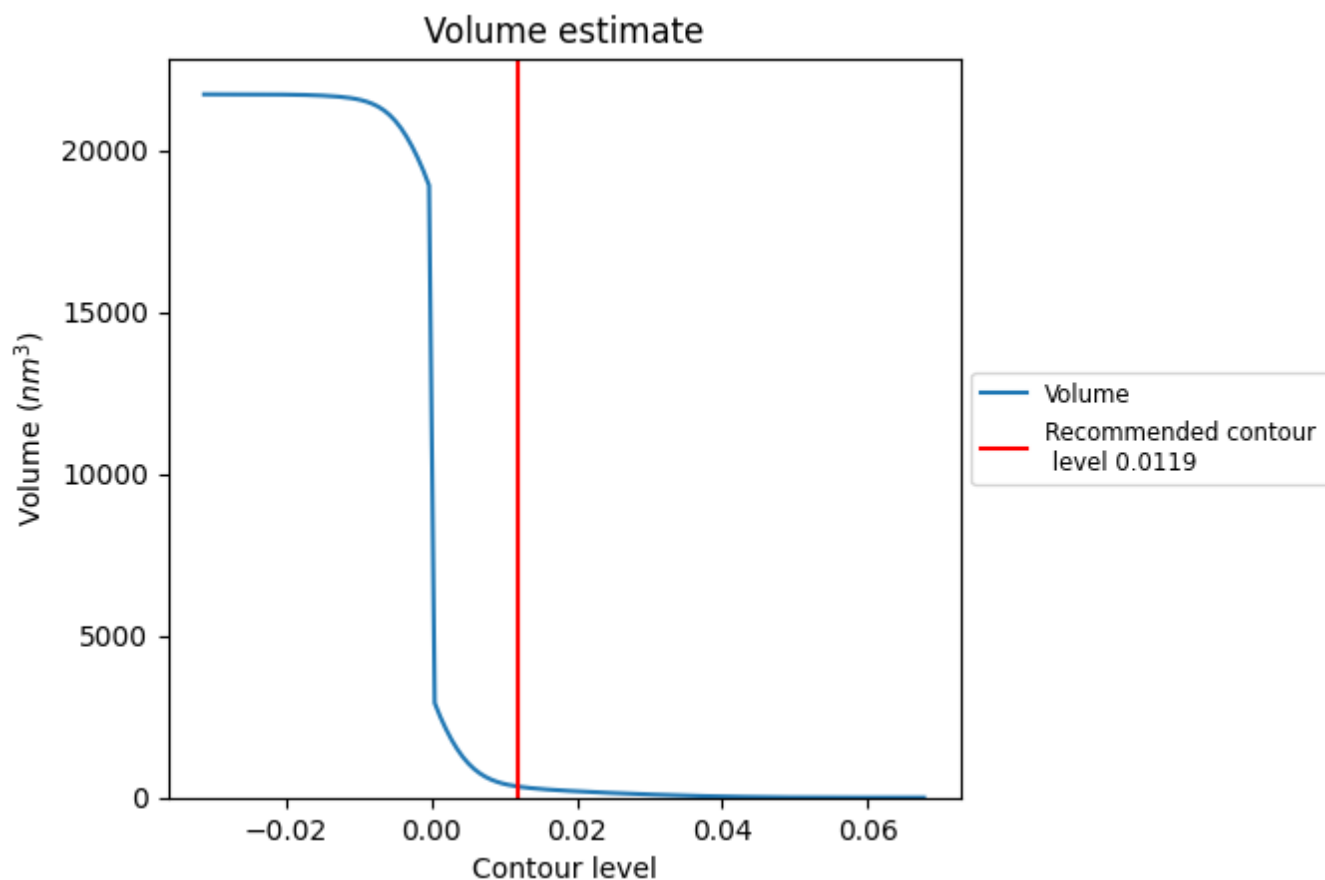
This section contains the results of statistical analysis of the map.

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.

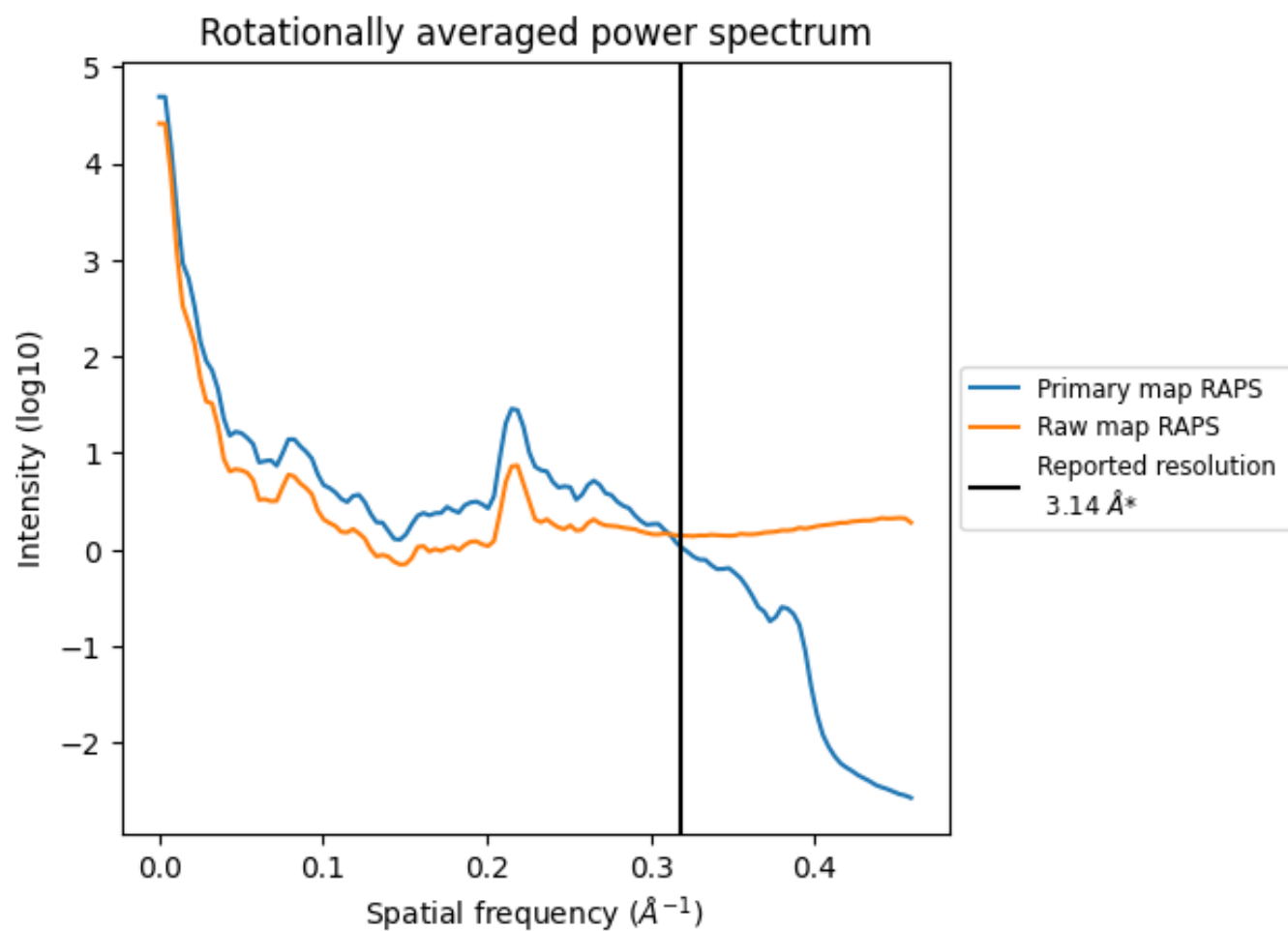
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 340 nm³; this corresponds to an approximate mass of 307 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 ⓘ

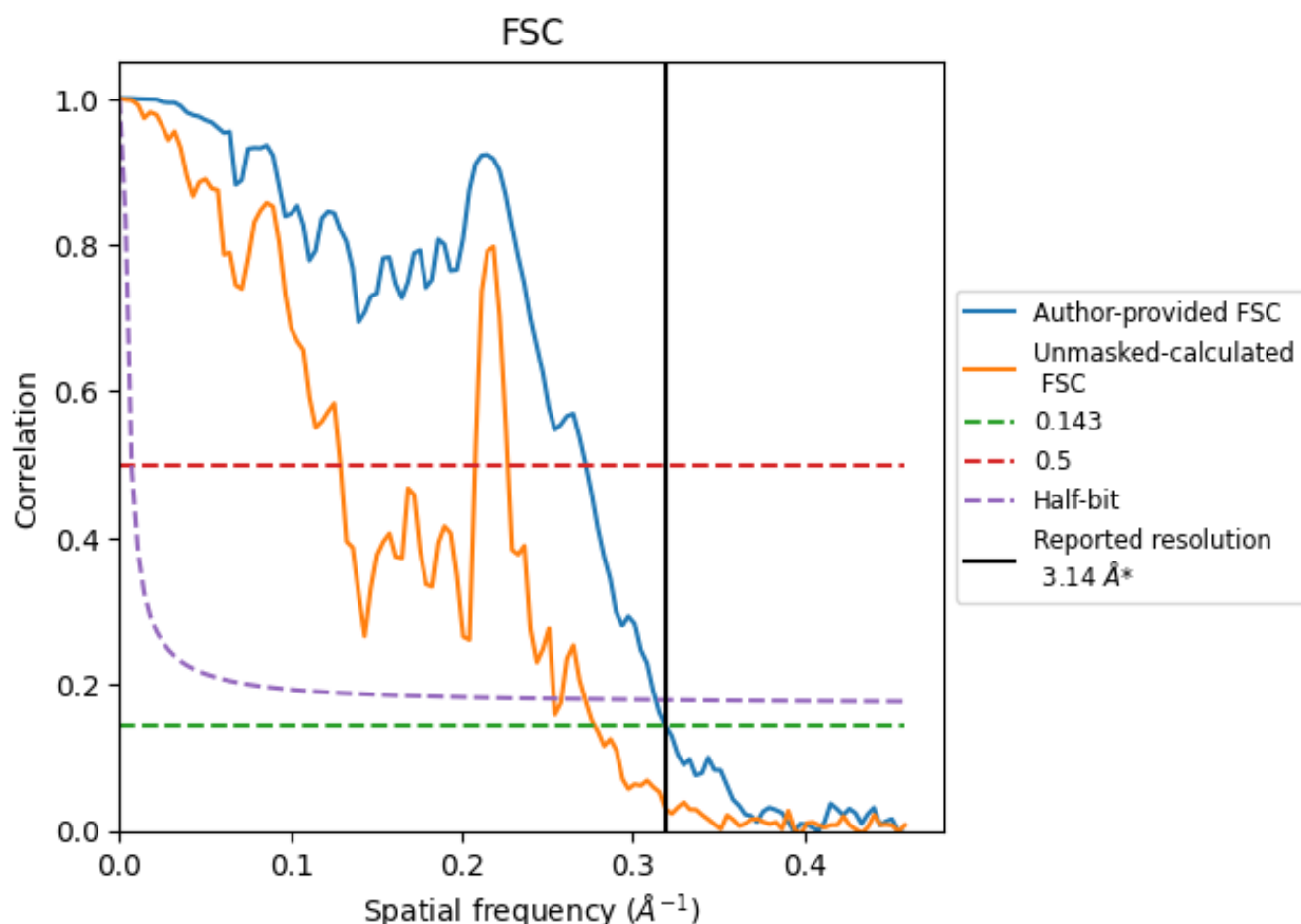


*Reported resolution corresponds to spatial frequency of 0.318 Å⁻¹

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 0.318 \AA^{-1}

8.2 Resolution estimates [i](#)

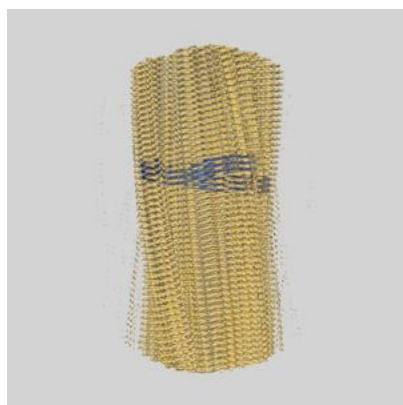
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.14	3.67	3.19
Unmasked-calculated*	3.60	7.75	3.94

*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 3.60 differs from the reported value 3.14 by more than 10 %

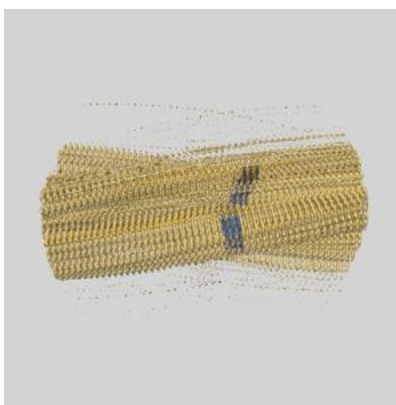
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14026 and PDB model 7QJY. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

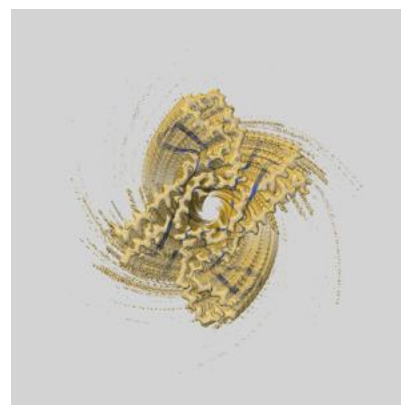
9.1 Map-model overlay [i](#)



X



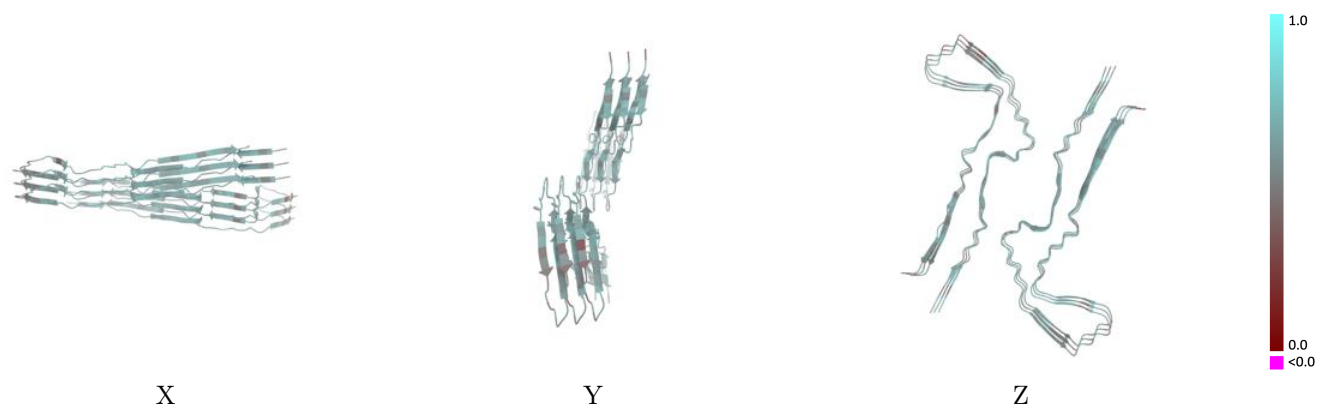
Y



Z

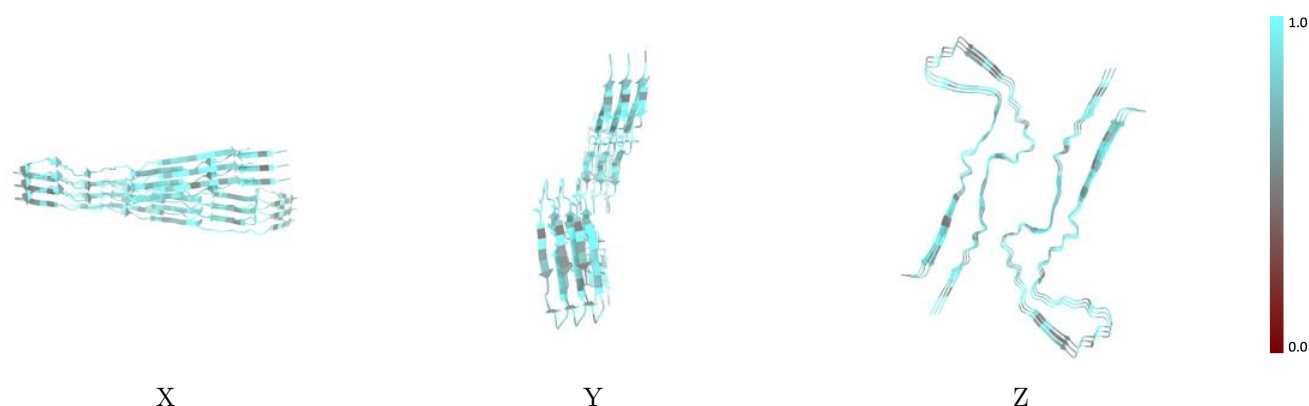
The images above show the 3D surface view of the map at the recommended contour level 0.0119 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



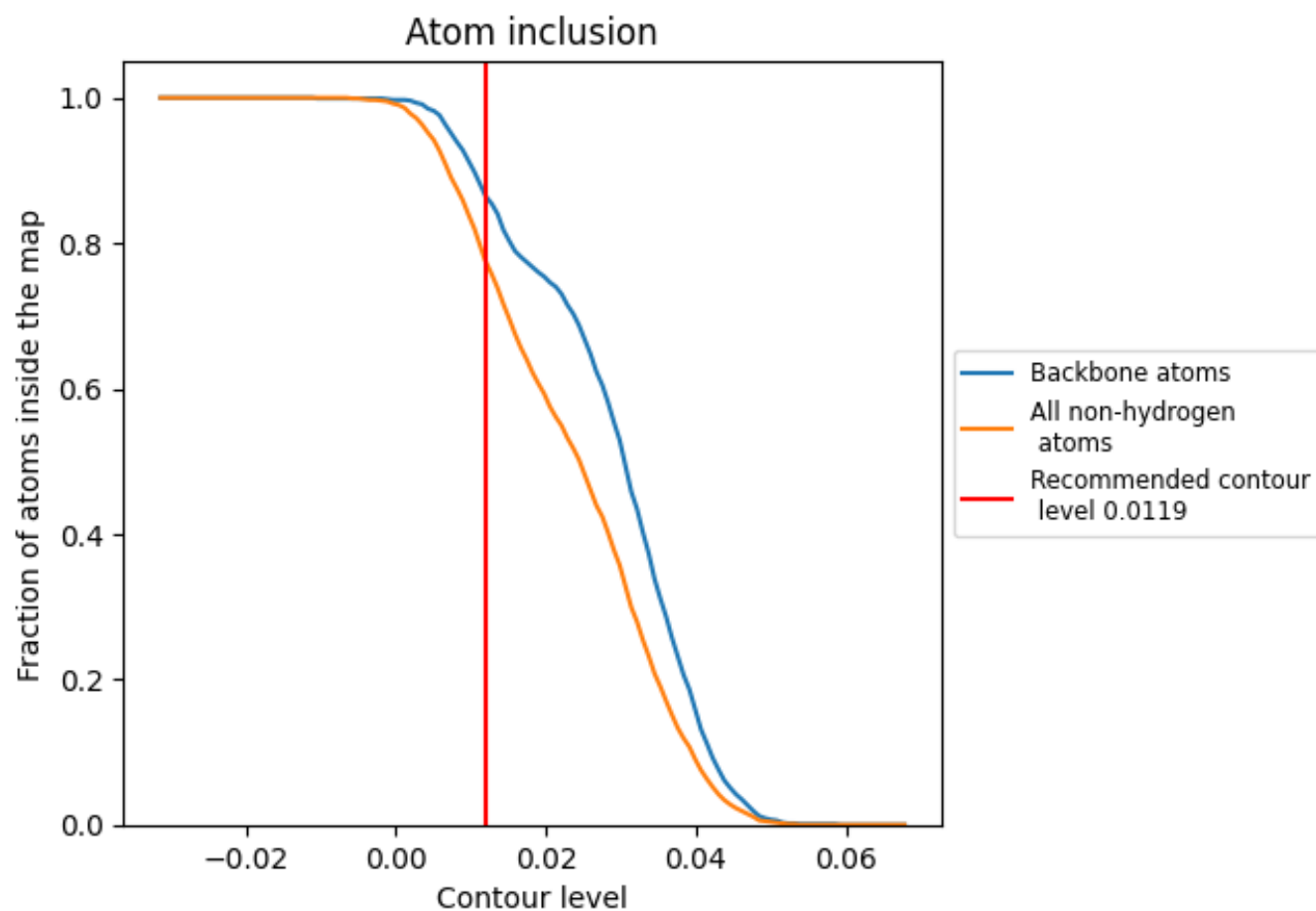
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0119).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 78% 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 (0.0119) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.7760	<div><div></div></div> 0.5620
A	<div><div></div></div> 0.7790	<div><div></div></div> 0.5660
B	<div><div></div></div> 0.7750	<div><div></div></div> 0.5520
C	<div><div></div></div> 0.7840	<div><div></div></div> 0.5690
D	<div><div></div></div> 0.7750	<div><div></div></div> 0.5580
E	<div><div></div></div> 0.7710	<div><div></div></div> 0.5640
F	<div><div></div></div> 0.7730	<div><div></div></div> 0.5620

1.0

0.0

<0.0