



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 05:46 PM UTC

PDB ID : 9MOH / pdb_00009moh
EMDB ID : EMD-48460
Title : Structure of the middle part of the bacteriophage T4 tail
Authors : Fokine, A.; Zhu, J.; Klose, T.; Vago, F.; Arnaud, C.; Wang, Z.; Khare, B.;
Rossmann, M.G.; Chen, Z.; Sun, L.; Fang, Q.; Kuhn, R.; Rao, V.B.
Deposited on : 2024-12-26
Resolution : 3.40 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

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>.

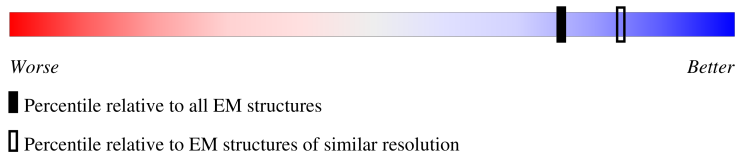
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : **FAILED**
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

i

ELECTRON MICROSCOPY

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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	14717 (2.90 - 3.90)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 521712 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 gp18, tail sheath protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	K0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K1	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K2	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	K9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L1	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L2	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	L7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	L9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LQ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LR	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LS	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LU	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LV	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LW	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LX	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LY	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	LZ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	La	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Lb	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Lc	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Ld	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Le	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Lv	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Lw	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Lx	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Lz	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	M0	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M1	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M2	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M3	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M4	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M5	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M6	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M7	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M8	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	M9	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MQ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MR	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MS	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MU	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MV	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MW	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MX	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MY	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	MZ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Ma	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Mb	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Mc	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Md	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Me	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Mv	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Mw	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Mx	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Mz	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	NV	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	NW	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	NX	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	NZ	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Na	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nb	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nc	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nd	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Ne	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nf	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Ng	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nh	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Ni	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nj	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Nv	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nw	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nx	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		
1	Nz	655	Total	C	N	O	S	0	0
			5000	3152	841	996	11		

There are 252 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K0	109	ASN	SER	conflict	UNP A0A7S9SVW9
K0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K1	109	ASN	SER	conflict	UNP A0A7S9SVW9
K1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K2	109	ASN	SER	conflict	UNP A0A7S9SVW9
K2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K3	109	ASN	SER	conflict	UNP A0A7S9SVW9
K3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K4	109	ASN	SER	conflict	UNP A0A7S9SVW9
K4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K5	109	ASN	SER	conflict	UNP A0A7S9SVW9
K5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K6	109	ASN	SER	conflict	UNP A0A7S9SVW9
K6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K7	109	ASN	SER	conflict	UNP A0A7S9SVW9
K7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K8	109	ASN	SER	conflict	UNP A0A7S9SVW9
K8	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
K9	109	ASN	SER	conflict	UNP A0A7S9SVW9
K9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
K9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L0	109	ASN	SER	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
L0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L1	109	ASN	SER	conflict	UNP A0A7S9SVW9
L1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L2	109	ASN	SER	conflict	UNP A0A7S9SVW9
L2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L3	109	ASN	SER	conflict	UNP A0A7S9SVW9
L3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L4	109	ASN	SER	conflict	UNP A0A7S9SVW9
L4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L5	109	ASN	SER	conflict	UNP A0A7S9SVW9
L5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L6	109	ASN	SER	conflict	UNP A0A7S9SVW9
L6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L7	109	ASN	SER	conflict	UNP A0A7S9SVW9
L7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L8	109	ASN	SER	conflict	UNP A0A7S9SVW9
L8	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
L9	109	ASN	SER	conflict	UNP A0A7S9SVW9
L9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
L9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LQ	109	ASN	SER	conflict	UNP A0A7S9SVW9
LQ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LQ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LR	109	ASN	SER	conflict	UNP A0A7S9SVW9
LR	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LR	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LS	109	ASN	SER	conflict	UNP A0A7S9SVW9
LS	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LS	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LU	109	ASN	SER	conflict	UNP A0A7S9SVW9
LU	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LU	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LV	109	ASN	SER	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
LV	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LW	109	ASN	SER	conflict	UNP A0A7S9SVW9
LW	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LX	109	ASN	SER	conflict	UNP A0A7S9SVW9
LX	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LX	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LY	109	ASN	SER	conflict	UNP A0A7S9SVW9
LY	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LY	399	VAL	ALA	conflict	UNP A0A7S9SVW9
LZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
LZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
LZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
La	109	ASN	SER	conflict	UNP A0A7S9SVW9
La	301	GLY	GLU	conflict	UNP A0A7S9SVW9
La	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lb	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lb	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lb	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lc	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lc	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lc	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ld	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ld	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ld	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Le	109	ASN	SER	conflict	UNP A0A7S9SVW9
Le	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Le	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lv	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lv	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lv	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lw	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lw	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lw	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Lz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Lz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Lz	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M0	109	ASN	SER	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
M0	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M0	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M1	109	ASN	SER	conflict	UNP A0A7S9SVW9
M1	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M1	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M2	109	ASN	SER	conflict	UNP A0A7S9SVW9
M2	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M2	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M3	109	ASN	SER	conflict	UNP A0A7S9SVW9
M3	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M3	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M4	109	ASN	SER	conflict	UNP A0A7S9SVW9
M4	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M4	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M5	109	ASN	SER	conflict	UNP A0A7S9SVW9
M5	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M5	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M6	109	ASN	SER	conflict	UNP A0A7S9SVW9
M6	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M6	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M7	109	ASN	SER	conflict	UNP A0A7S9SVW9
M7	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M7	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M8	109	ASN	SER	conflict	UNP A0A7S9SVW9
M8	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M8	399	VAL	ALA	conflict	UNP A0A7S9SVW9
M9	109	ASN	SER	conflict	UNP A0A7S9SVW9
M9	301	GLY	GLU	conflict	UNP A0A7S9SVW9
M9	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MQ	109	ASN	SER	conflict	UNP A0A7S9SVW9
MQ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MQ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MR	109	ASN	SER	conflict	UNP A0A7S9SVW9
MR	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MR	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MS	109	ASN	SER	conflict	UNP A0A7S9SVW9
MS	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MS	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MU	109	ASN	SER	conflict	UNP A0A7S9SVW9
MU	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MU	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MV	109	ASN	SER	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
MV	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MW	109	ASN	SER	conflict	UNP A0A7S9SVW9
MW	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MX	109	ASN	SER	conflict	UNP A0A7S9SVW9
MX	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MX	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MY	109	ASN	SER	conflict	UNP A0A7S9SVW9
MY	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MY	399	VAL	ALA	conflict	UNP A0A7S9SVW9
MZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
MZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
MZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ma	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ma	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ma	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mb	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mb	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mb	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mc	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mc	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mc	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Md	109	ASN	SER	conflict	UNP A0A7S9SVW9
Md	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Md	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Me	109	ASN	SER	conflict	UNP A0A7S9SVW9
Me	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Me	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mv	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mv	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mv	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mw	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mw	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mw	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Mz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Mz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Mz	399	VAL	ALA	conflict	UNP A0A7S9SVW9
NV	109	ASN	SER	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
NV	301	GLY	GLU	conflict	UNP A0A7S9SVW9
NV	399	VAL	ALA	conflict	UNP A0A7S9SVW9
NW	109	ASN	SER	conflict	UNP A0A7S9SVW9
NW	301	GLY	GLU	conflict	UNP A0A7S9SVW9
NW	399	VAL	ALA	conflict	UNP A0A7S9SVW9
NX	109	ASN	SER	conflict	UNP A0A7S9SVW9
NX	301	GLY	GLU	conflict	UNP A0A7S9SVW9
NX	399	VAL	ALA	conflict	UNP A0A7S9SVW9
NZ	109	ASN	SER	conflict	UNP A0A7S9SVW9
NZ	301	GLY	GLU	conflict	UNP A0A7S9SVW9
NZ	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Na	109	ASN	SER	conflict	UNP A0A7S9SVW9
Na	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Na	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nb	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nb	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nb	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nc	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nc	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nc	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nd	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nd	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nd	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ne	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ne	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ne	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nf	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nf	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nf	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ng	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ng	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ng	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nh	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nh	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nh	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Ni	109	ASN	SER	conflict	UNP A0A7S9SVW9
Ni	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Ni	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nj	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nj	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nj	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nv	109	ASN	SER	conflict	UNP A0A7S9SVW9

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Chain	Residue	Modelled	Actual	Comment	Reference
Nv	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nv	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nw	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nw	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nw	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nx	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nx	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nx	399	VAL	ALA	conflict	UNP A0A7S9SVW9
Nz	109	ASN	SER	conflict	UNP A0A7S9SVW9
Nz	301	GLY	GLU	conflict	UNP A0A7S9SVW9
Nz	399	VAL	ALA	conflict	UNP A0A7S9SVW9

- Molecule 2 is a protein called gp19, tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	OC	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OD	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	ON	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	OO	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Oh	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Oi	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Oj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Ok	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Ol	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Om	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	On	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Oo	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Op	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Oq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Or	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Os	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Ot	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PC	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PD	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	PL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PN	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	PO	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Ph	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pi	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pj	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Po	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pp	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pr	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Ps	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Pt	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RC	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RD	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RE	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RF	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	RG	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RH	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RI	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RJ	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RK	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RL	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RM	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RN	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RO	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RR	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RS	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	RT	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rk	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rl	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rm	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rn	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Ro	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rp	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rq	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rr	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		
2	Rs	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Rt	163	Total	C	N	O	S	0	0
			1304	828	219	253	4		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	113800	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	646.4, 646.4, 646.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.616, 1.616, 1.616	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

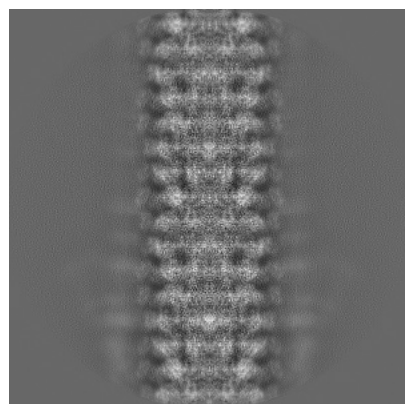
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48460. These allow visual inspection of the internal detail of the map and identification of artifacts.

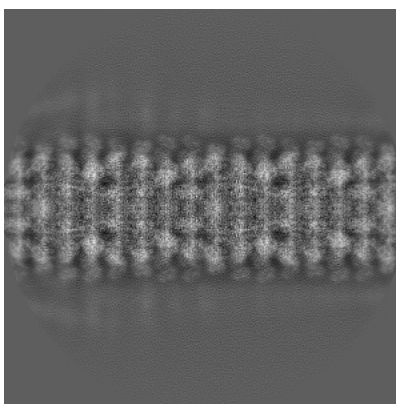
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

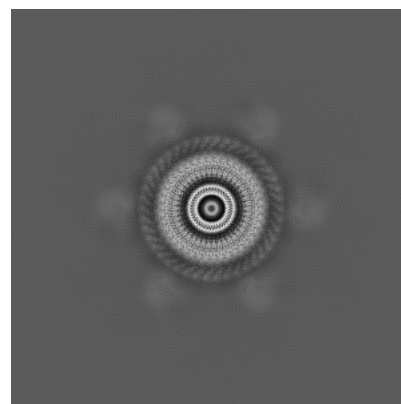
5.1.1 Primary map



X

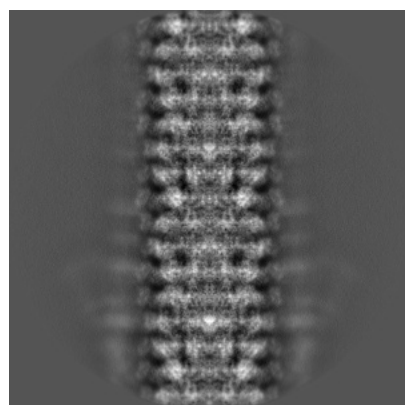


Y

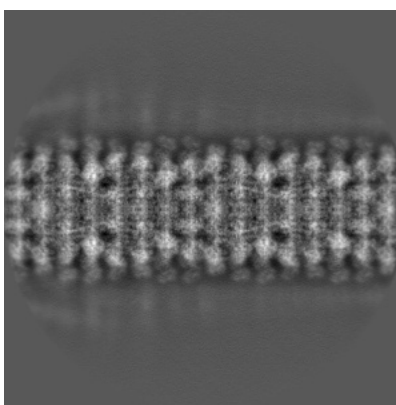


Z

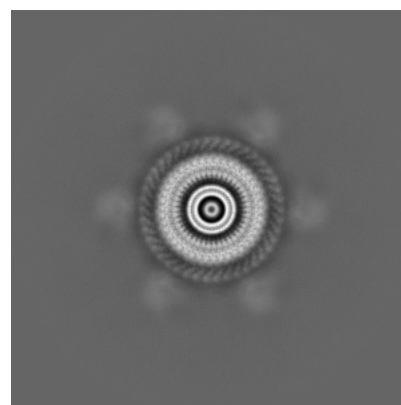
5.1.2 Raw map



X



Y

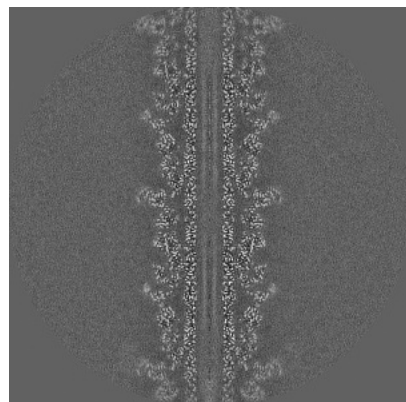


Z

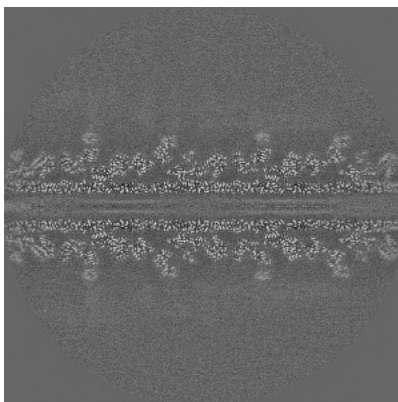
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

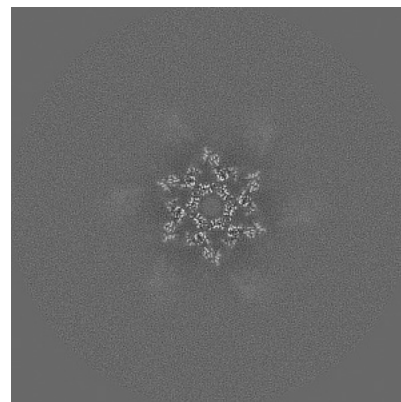
5.2.1 Primary map



X Index: 200

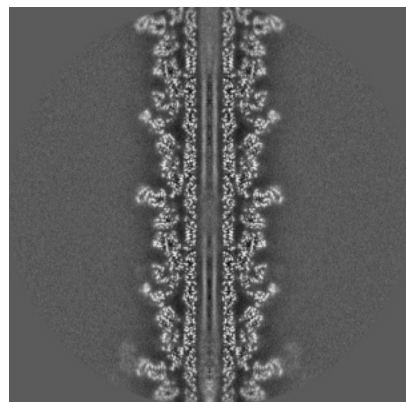


Y Index: 200

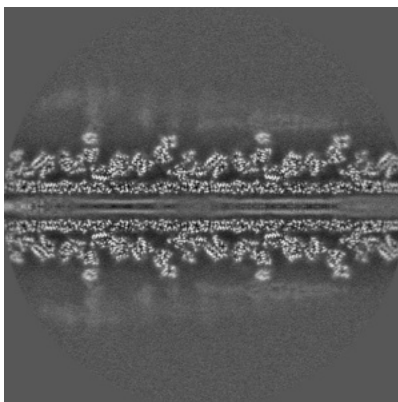


Z Index: 200

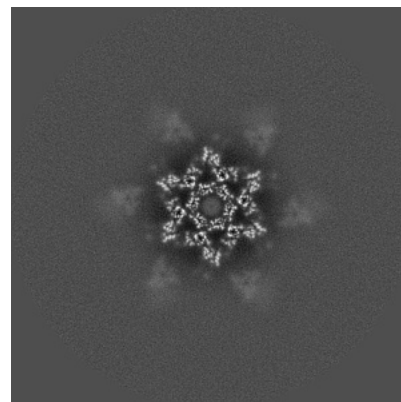
5.2.2 Raw map



X Index: 200



Y Index: 200

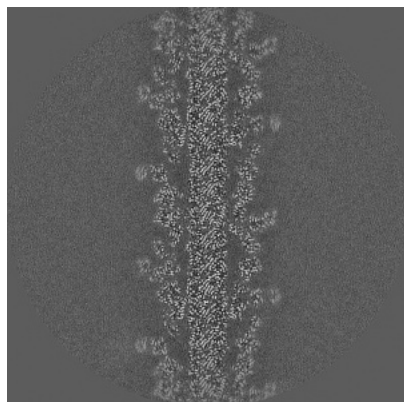


Z Index: 200

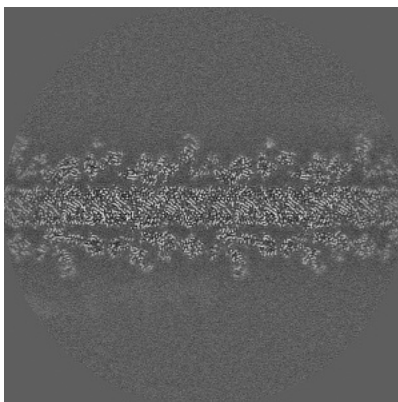
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

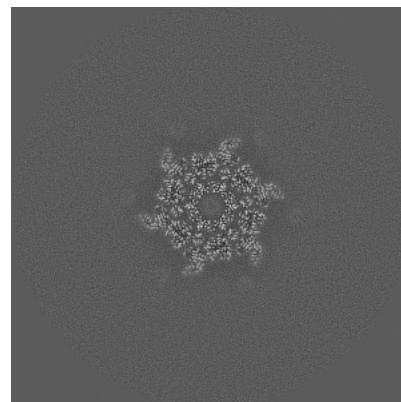
5.3.1 Primary map



X Index: 215

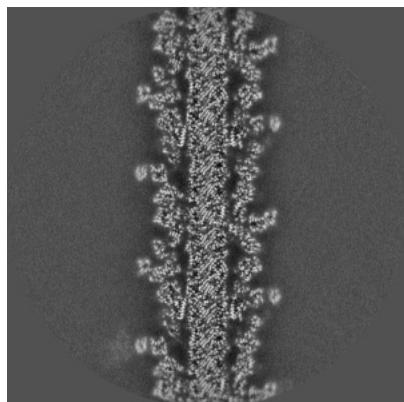


Y Index: 215

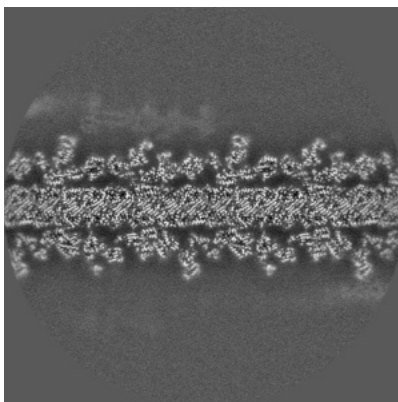


Z Index: 187

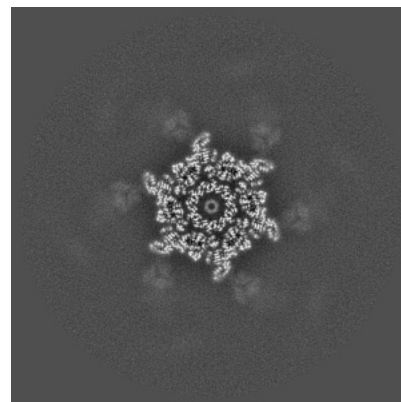
5.3.2 Raw map



X Index: 215



Y Index: 185

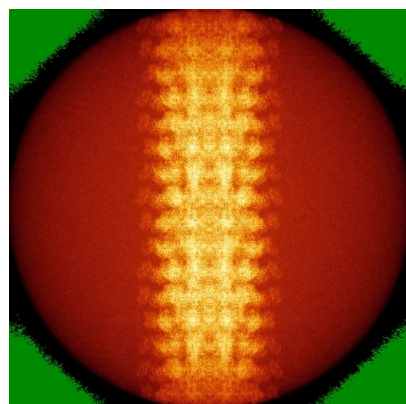


Z Index: 137

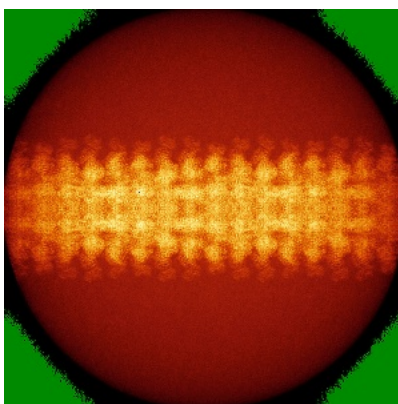
The images above show the largest variance slices of the map in three orthogonal directions.

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

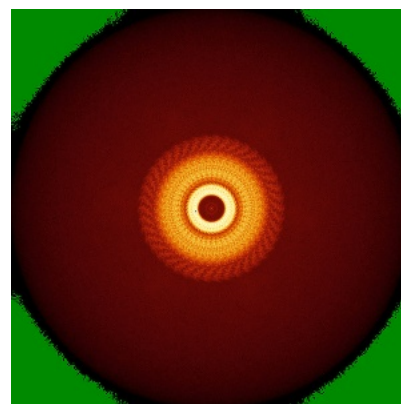
5.4.1 Primary map



X

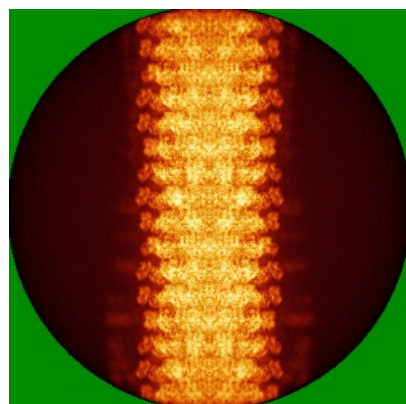


Y

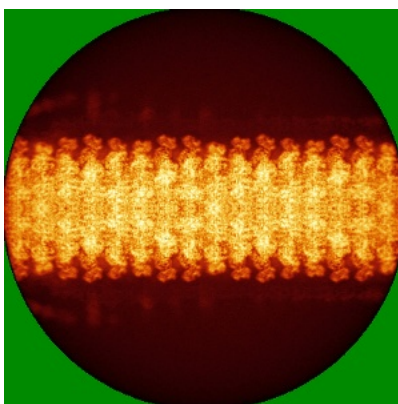


Z

5.4.2 Raw map



X



Y

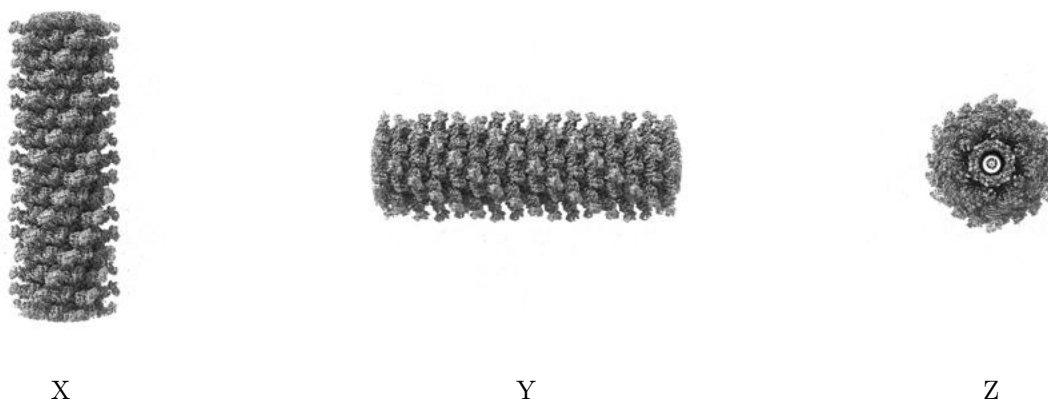


Z

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.

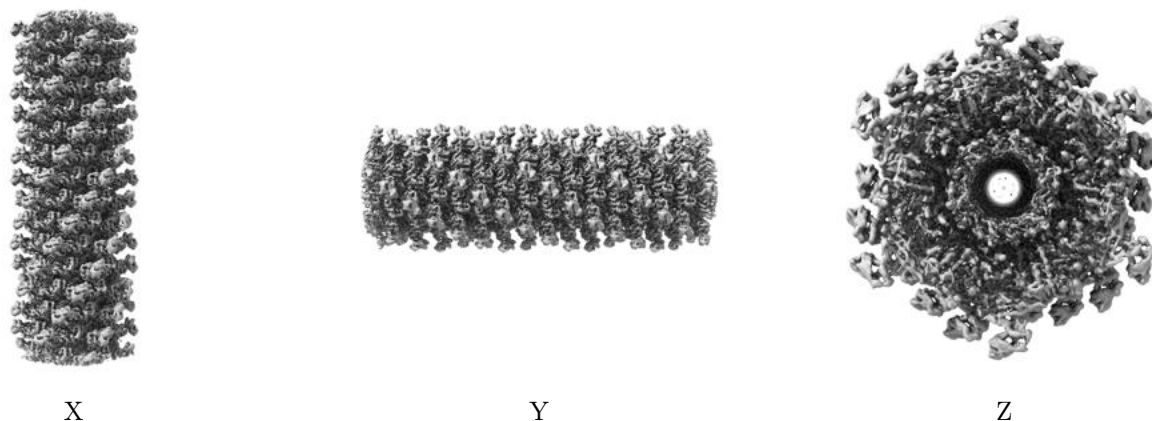
5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 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.

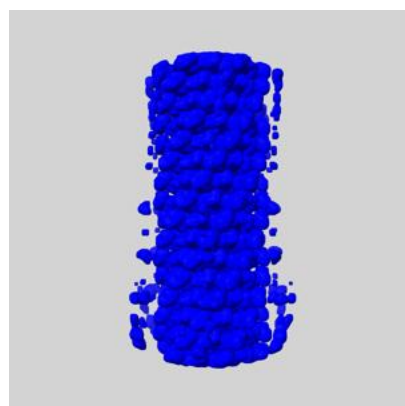
5.6 Mask visualisation [i](#)

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

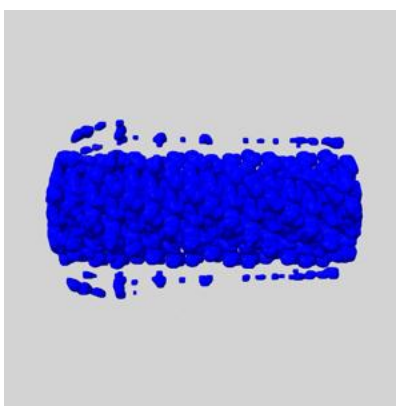
A mask typically either:

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

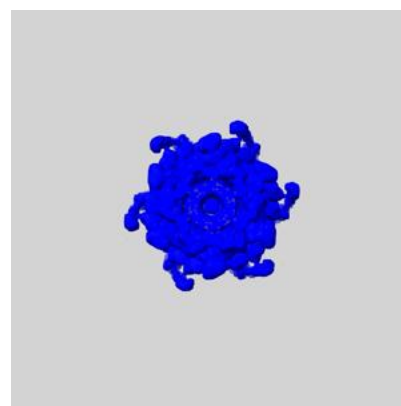
5.6.1 emd_48460_msk_1.map [i](#)



X



Y

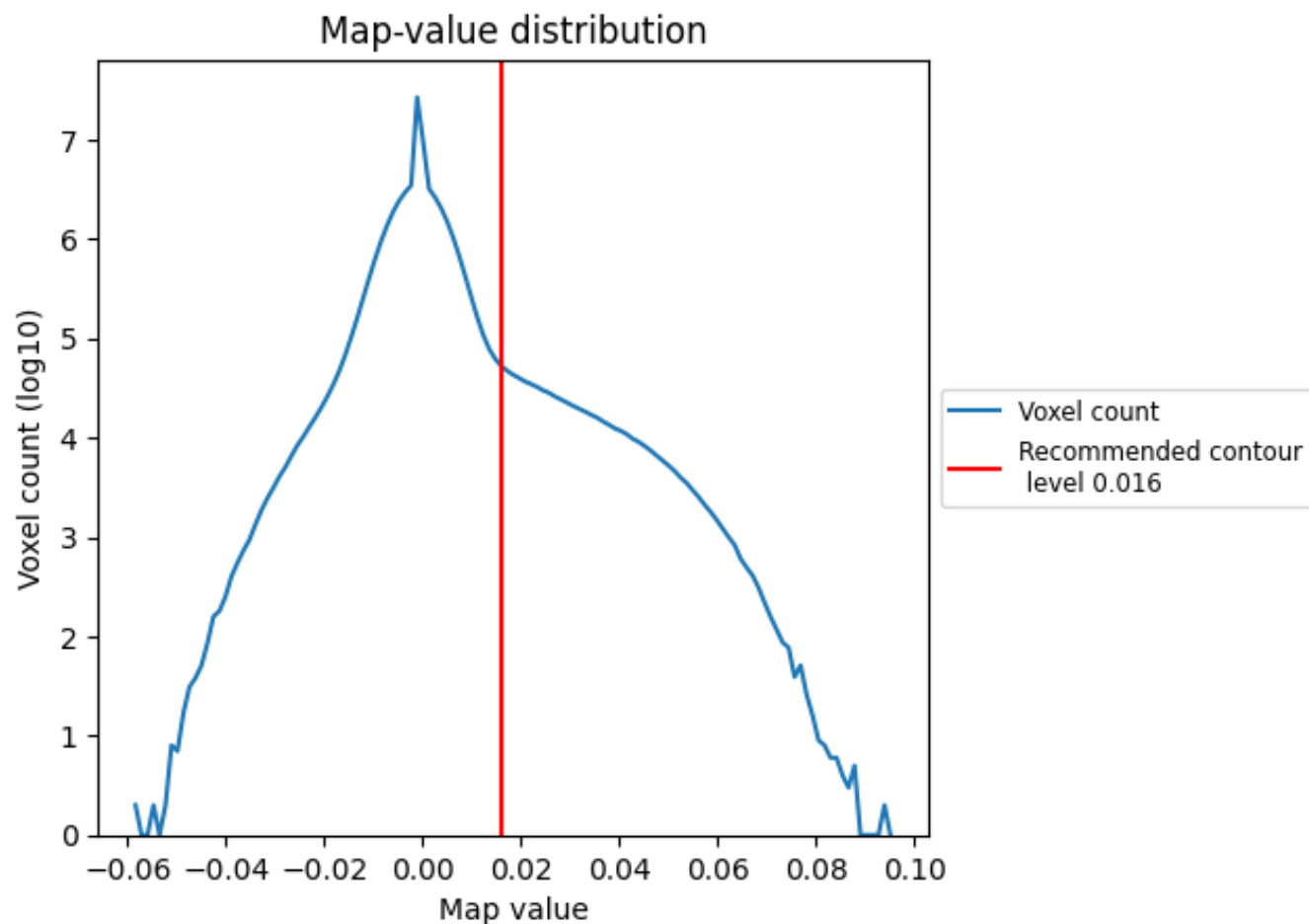


Z

6 Map analysis [i](#)

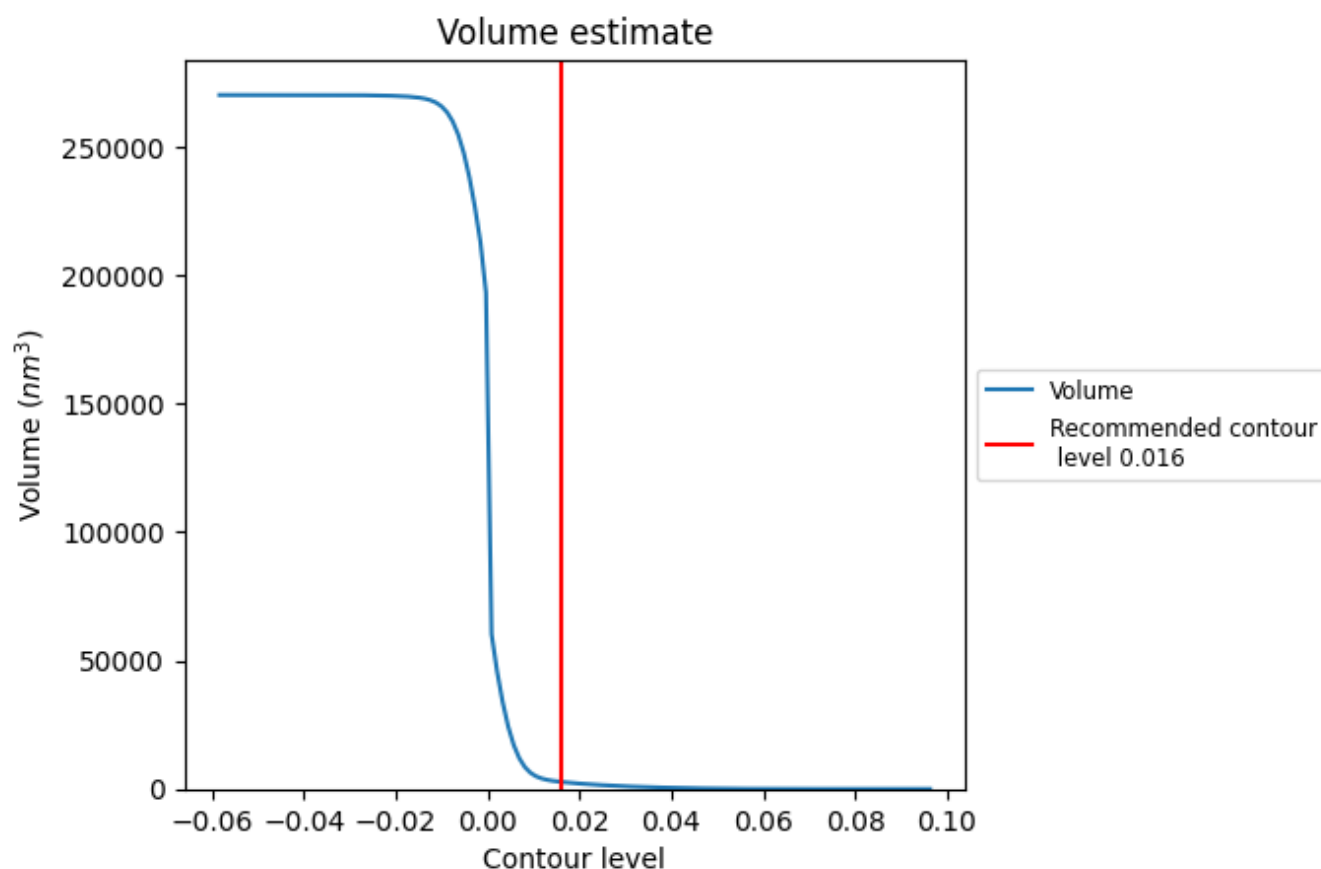
This section contains the results of statistical analysis of the map.

6.1 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.

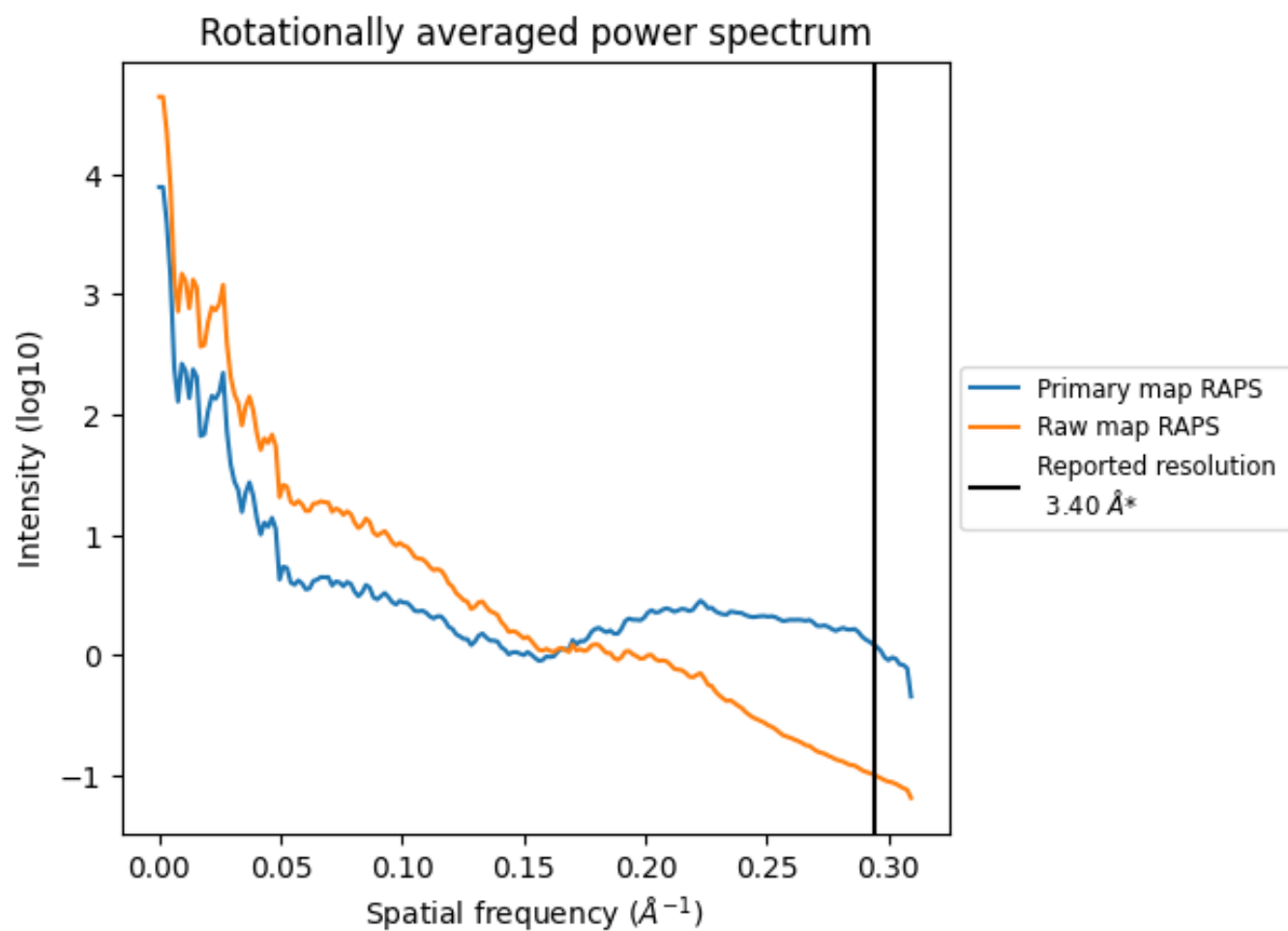
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 2747 nm³; this corresponds to an approximate mass of 2481 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.

6.3 Rotationally averaged power spectrum [i](#)

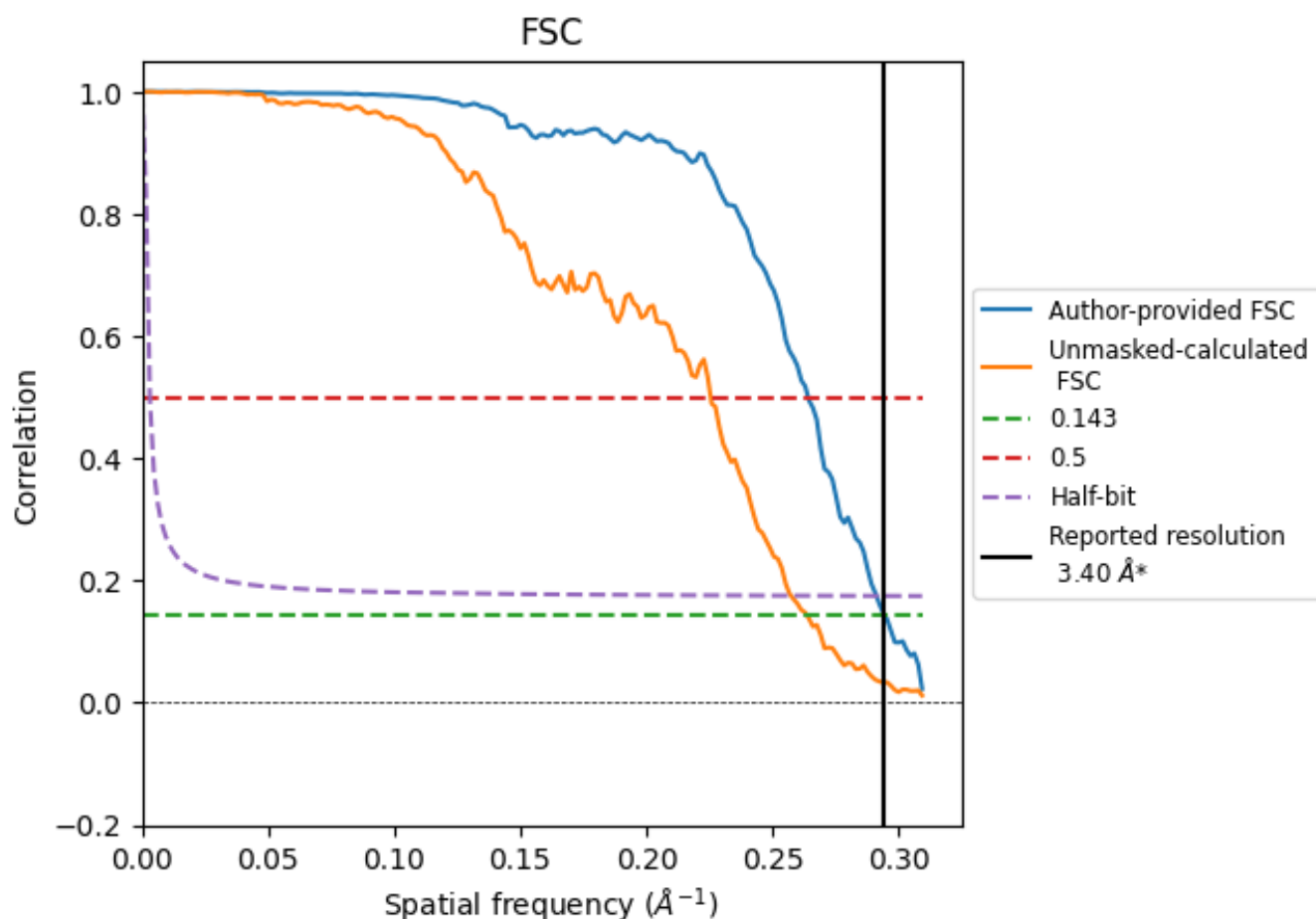


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

7.2 Resolution estimates [i](#)

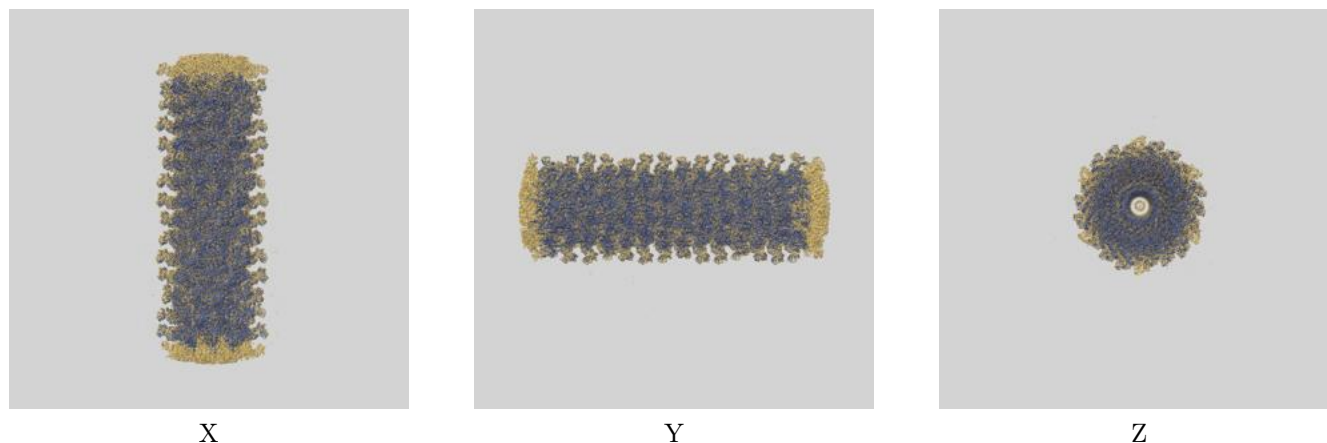
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.39	3.79	3.43
Unmasked-calculated*	3.79	4.43	3.89

*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 3.79 differs from the reported value 3.4 by more than 10 %

8 Map-model fit [i](#)

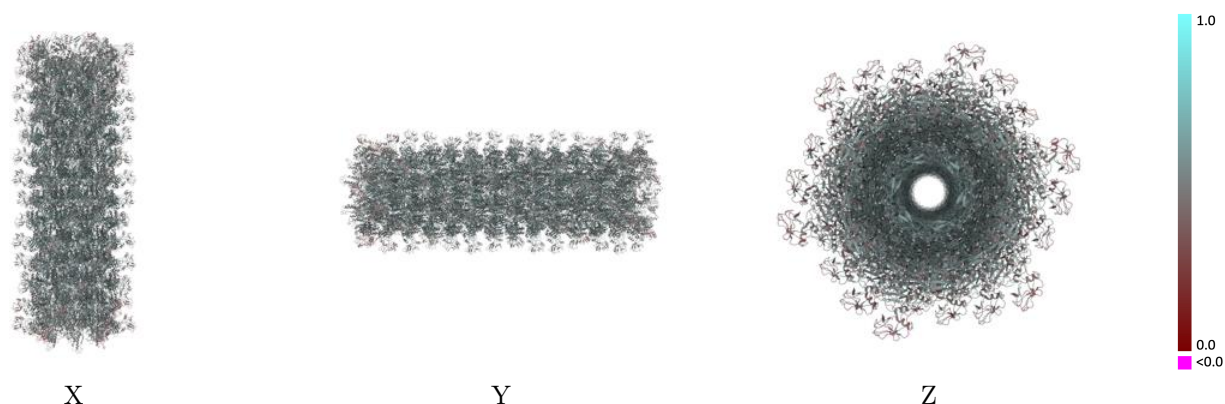
This section contains information regarding the fit between EMDB map EMD-48460 and PDB model 9MOH. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



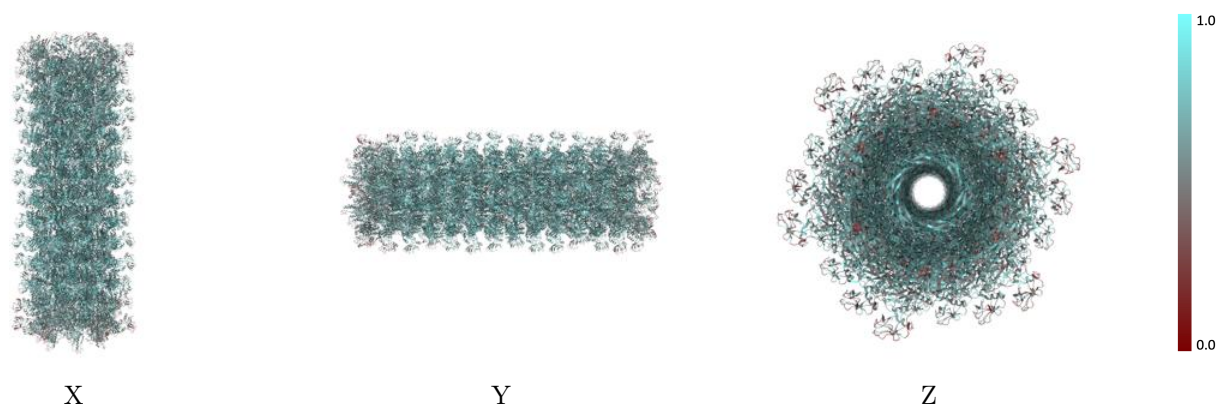
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



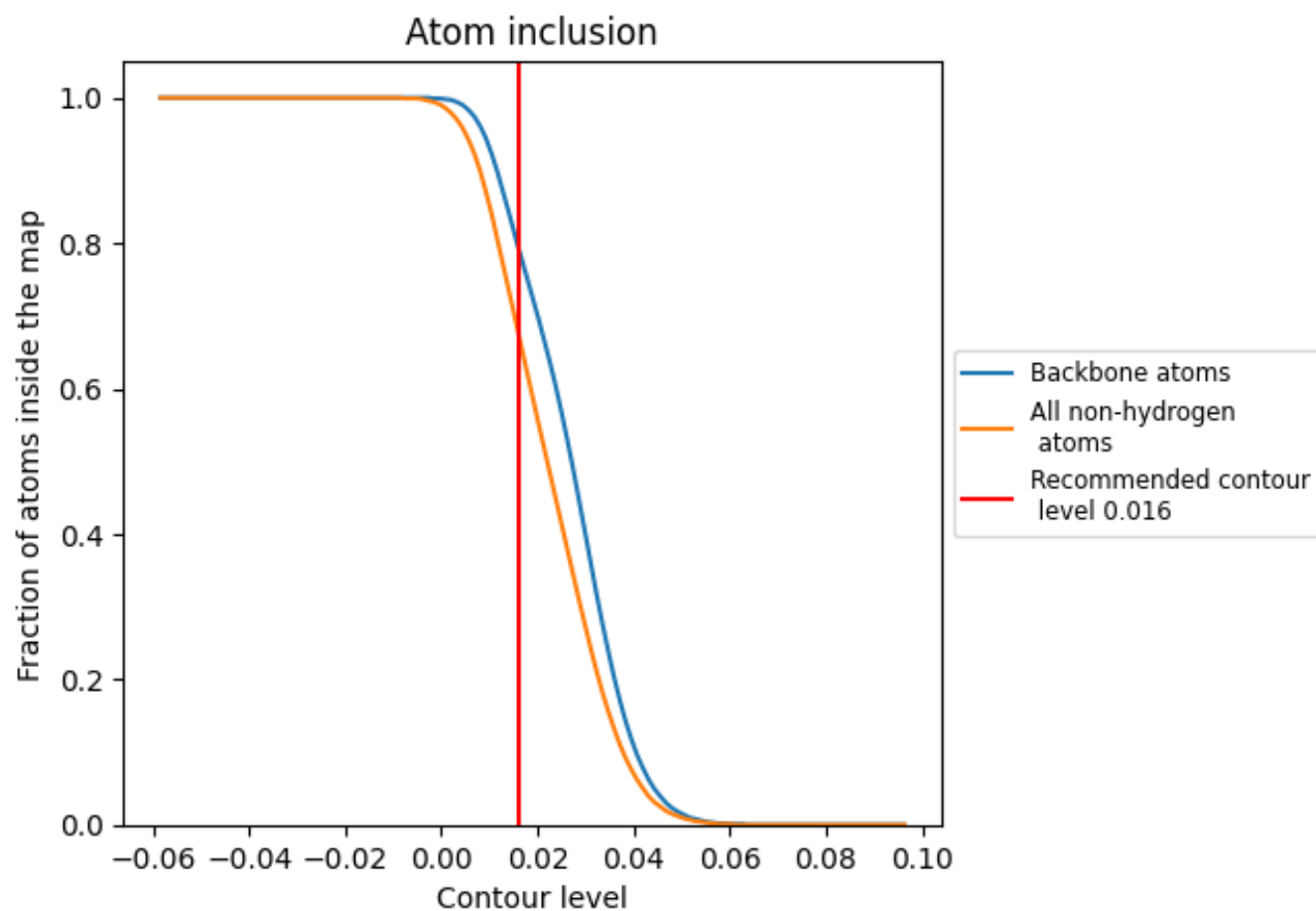
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (0.016).

8.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6750	 0.5240
K0	 0.5450	 0.4840
K1	 0.7110	 0.5290
K2	 0.7060	 0.5320
K3	 0.7010	 0.5300
K4	 0.6970	 0.5280
K5	 0.7020	 0.5310
K6	 0.7000	 0.5270
K7	 0.6910	 0.5260
K8	 0.6710	 0.5200
K9	 0.6220	 0.5070
L0	 0.5470	 0.4840
L1	 0.7110	 0.5290
L2	 0.7070	 0.5280
L3	 0.7060	 0.5320
L4	 0.6980	 0.5260
L5	 0.7020	 0.5300
L6	 0.7010	 0.5280
L7	 0.6940	 0.5270
L8	 0.6720	 0.5170
L9	 0.6210	 0.5060
LQ	 0.5310	 0.4740
LR	 0.6200	 0.5000
LS	 0.6910	 0.5230
LU	 0.7000	 0.5260
LV	 0.7130	 0.5330
LW	 0.7120	 0.5330
LX	 0.7030	 0.5290
LY	 0.7000	 0.5270
LZ	 0.6960	 0.5300
La	 0.6970	 0.5280
Lb	 0.6920	 0.5270
Lc	 0.6700	 0.5220
Ld	 0.6240	 0.5050
Le	 0.5430	 0.4800



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Chain	Atom inclusion	Q-score
Lv	0.5270	0.4720
Lw	0.6220	0.5010
Lx	0.6850	0.5220
Lz	0.6990	0.5260
M0	0.5450	0.4850
M1	0.7110	0.5310
M2	0.7070	0.5330
M3	0.6990	0.5310
M4	0.7040	0.5260
M5	0.7010	0.5310
M6	0.7030	0.5280
M7	0.6920	0.5250
M8	0.6720	0.5180
M9	0.6160	0.5050
MQ	0.5290	0.4740
MR	0.6240	0.5030
MS	0.6830	0.5230
MU	0.7000	0.5260
MV	0.7070	0.5300
MW	0.7100	0.5320
MX	0.7060	0.5300
MY	0.7000	0.5260
MZ	0.7000	0.5310
Ma	0.6950	0.5260
Mb	0.6900	0.5250
Mc	0.6730	0.5210
Md	0.6310	0.5070
Me	0.5480	0.4810
Mv	0.5300	0.4730
Mw	0.6250	0.5020
Mx	0.6880	0.5230
Mz	0.7010	0.5260
NV	0.5280	0.4740
NW	0.6230	0.5020
NX	0.6860	0.5220
NZ	0.7080	0.5250
Na	0.7150	0.5330
Nb	0.7090	0.5320
Nc	0.7070	0.5310
Nd	0.6990	0.5260
Ne	0.7040	0.5310
Nf	0.7020	0.5270

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Chain	Atom inclusion	Q-score
Ng	 0.6940	 0.5270
Nh	 0.6710	 0.5200
Ni	 0.6270	 0.5060
Nj	 0.5500	 0.4820
Nv	 0.5290	 0.4710
Nw	 0.6180	 0.5000
Nx	 0.6850	 0.5220
Nz	 0.7020	 0.5270
OC	 0.6510	 0.5320
OD	 0.7240	 0.5580
OE	 0.7420	 0.5630
OF	 0.7420	 0.5600
OG	 0.7560	 0.5580
OH	 0.7390	 0.5580
OI	 0.7270	 0.5550
OJ	 0.7190	 0.5530
OK	 0.7280	 0.5590
OL	 0.7460	 0.5550
OM	 0.7360	 0.5530
ON	 0.7140	 0.5550
OO	 0.6630	 0.5400
Oh	 0.6500	 0.5420
Oi	 0.7160	 0.5560
Oj	 0.7410	 0.5580
Ok	 0.7510	 0.5610
Ol	 0.7390	 0.5590
Om	 0.7240	 0.5550
On	 0.7370	 0.5590
Oo	 0.7230	 0.5540
Op	 0.7320	 0.5580
Oq	 0.7280	 0.5590
Or	 0.7190	 0.5540
Os	 0.7180	 0.5580
Ot	 0.6600	 0.5390
PC	 0.6530	 0.5320
PD	 0.7160	 0.5550
PE	 0.7420	 0.5610
PF	 0.7420	 0.5610
PG	 0.7490	 0.5630
PH	 0.7520	 0.5620
PI	 0.7300	 0.5570
PJ	 0.7260	 0.5490

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Chain	Atom inclusion	Q-score
PK	 0.7280	 0.5540
PL	 0.7390	 0.5580
PM	 0.7210	 0.5540
PN	 0.7000	 0.5530
PO	 0.6590	 0.5360
Ph	 0.6460	 0.5390
Pi	 0.7210	 0.5570
Pj	 0.7410	 0.5600
Pk	 0.7570	 0.5590
Pl	 0.7450	 0.5600
Pm	 0.7260	 0.5580
Pn	 0.7460	 0.5580
Po	 0.7320	 0.5570
Pp	 0.7350	 0.5600
Pq	 0.7300	 0.5550
Pr	 0.7160	 0.5550
Ps	 0.7070	 0.5560
Pt	 0.6740	 0.5400
RC	 0.6400	 0.5310
RD	 0.7210	 0.5590
RE	 0.7400	 0.5640
RF	 0.7440	 0.5630
RG	 0.7480	 0.5600
RH	 0.7470	 0.5620
RI	 0.7430	 0.5550
RJ	 0.7200	 0.5510
RK	 0.7250	 0.5580
RL	 0.7450	 0.5560
RM	 0.7270	 0.5570
RN	 0.7090	 0.5530
RO	 0.6630	 0.5330
RR	 0.6520	 0.5370
RS	 0.7180	 0.5570
RT	 0.7490	 0.5560
Rk	 0.7460	 0.5640
Rl	 0.7350	 0.5610
Rm	 0.7320	 0.5570
Rn	 0.7410	 0.5580
Ro	 0.7230	 0.5520
Rp	 0.7320	 0.5590
Rq	 0.7440	 0.5580
Rr	 0.7260	 0.5540

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Chain	Atom inclusion	Q-score
Rs	0.7130	0.5540
Rt	0.6520	0.5380