



Full wwPDB EM Validation Report ⓘ

Apr 29, 2026 – 04:41 am BST

PDB ID : 9H7U / pdb_00009h7u
EMDB ID : EMD-51914
Title : Hexagonally Ordered Nanofibrils Easily Yield by dual Amphiphilic Self-Assembling Peptide
Authors : Mazzotta, F.; Baptista, L.A.; Schmidt, M.; Gacanin, J.; Lieberwirth, I.; Weil, T.; Landfester, K.
Deposited on : 2024-10-28
Resolution : 2.96 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:

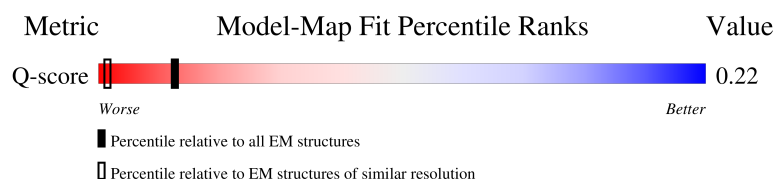
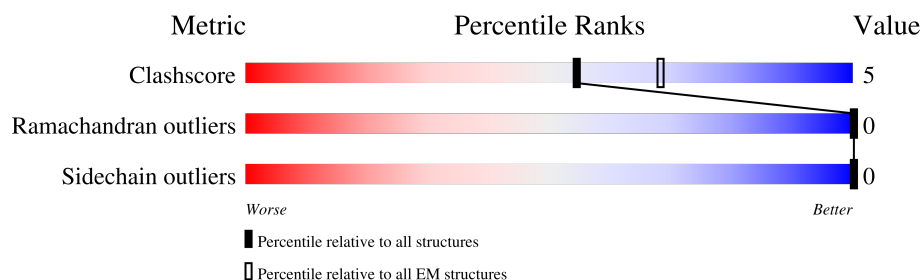
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	Aa	9	 89% 11%
1	Ab	9	 11% 89% 11%
1	Ac	9	 11% 89% 11%
1	Ad	9	 89% 11%

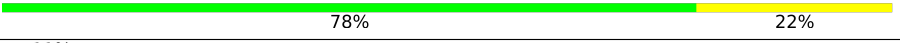



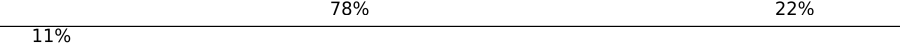
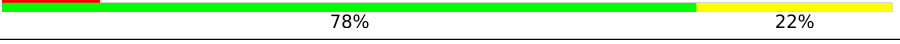



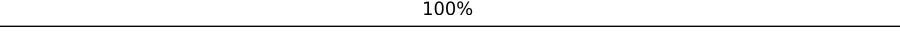
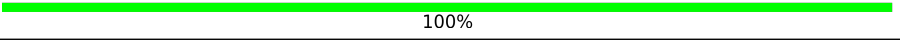
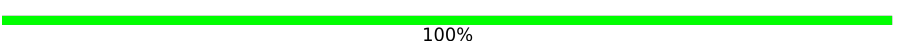



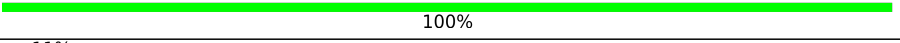



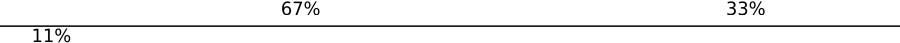





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Mol	Chain	Length	Quality of chain
1	Ae	9	<div> <div>11%</div> <div>89%</div> <div>11%</div> </div>
1	Af	9	<div> <div>89%</div> <div>11%</div> </div>
1	Ag	9	<div> <div>67%</div> <div>33%</div> </div>
1	Ah	9	<div> <div>67%</div> <div>33%</div> </div>
1	Ai	9	<div> <div>11%</div> <div>67%</div> <div>33%</div> </div>
1	Aj	9	<div> <div>11%</div> <div>67%</div> <div>33%</div> </div>
1	Ak	9	<div> <div>11%</div> <div>67%</div> <div>33%</div> </div>
1	Al	9	<div> <div>67%</div> <div>33%</div> </div>
1	Am	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	An	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Ao	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Ap	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Aq	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Ar	9	<div> <div>78%</div> <div>22%</div> </div>
1	Ci	9	<div> <div>89%</div> <div>11%</div> </div>
1	Cj	9	<div> <div>89%</div> <div>11%</div> </div>
1	Ck	9	<div> <div>11%</div> <div>89%</div> <div>11%</div> </div>
1	Cl	9	<div> <div>89%</div> <div>11%</div> </div>
1	Cm	9	<div> <div>11%</div> <div>89%</div> <div>11%</div> </div>
1	Cn	9	<div> <div>89%</div> <div>11%</div> </div>
1	Co	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Cp	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Cq	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Cr	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>
1	Cs	9	<div> <div>11%</div> <div>78%</div> <div>22%</div> </div>

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Mol	Chain	Length	Quality of chain
1	Ct	9	
1	Cu	9	
1	Cv	9	
1	Cw	9	
1	Cx	9	
1	Cy	9	
1	Cz	9	
1	Eq	9	
1	Er	9	
1	Es	9	
1	Et	9	
1	Eu	9	
1	Ev	9	
1	Ew	9	
1	Ex	9	
1	Ey	9	
1	Ez	9	
1	Fa	9	
1	Fb	9	
1	Fc	9	
1	Fd	9	
1	Fe	9	
1	Ff	9	
1	Fg	9	
1	Fh	9	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3888 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 Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ab	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ac	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ad	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ae	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Af	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ag	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ah	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ai	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Aj	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ak	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Al	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Am	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	An	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ao	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ap	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Aq	9	Total	C	N	O	S	0	0
			72	45	13	13	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ar	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ci	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cj	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ck	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cl	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cm	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cn	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Co	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cp	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cq	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cr	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cs	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ct	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cu	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cv	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cw	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cx	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cy	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Cz	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Eq	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Er	9	Total	C	N	O	S	0	0
			72	45	13	13	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Es	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Et	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Eu	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ev	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ew	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ex	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ey	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ez	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fa	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fb	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fc	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fd	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fe	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Ff	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fg	9	Total	C	N	O	S	0	0
			72	45	13	13	1		
1	Fh	9	Total	C	N	O	S	0	0
			72	45	13	13	1		

3 Residue-property plots [i](#)

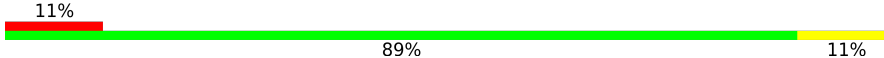
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Aa: 




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ab: 



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ac: 




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ad: 




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ae: 



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Af:  89% 11%



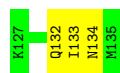
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ag:  67% 33%



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ah:  67% 33%



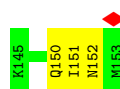
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ai:  11% 67% 33%



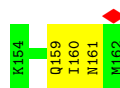
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Chain Aj:  11% 67% 33%



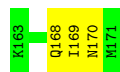
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Chain Ak:  11% 67% 33%

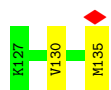
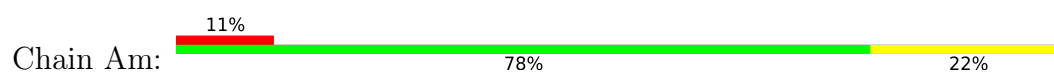


- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

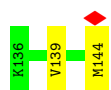
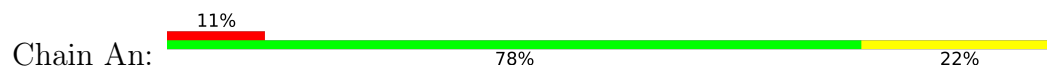
Chain Al:  67% 33%



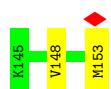
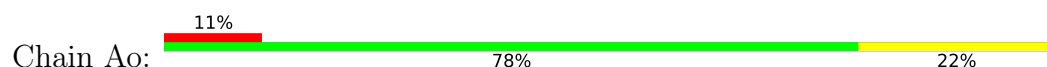
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



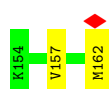
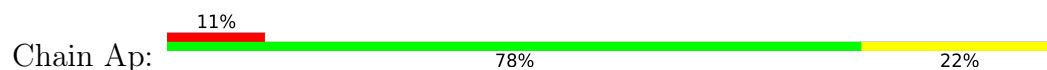
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



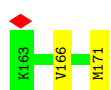
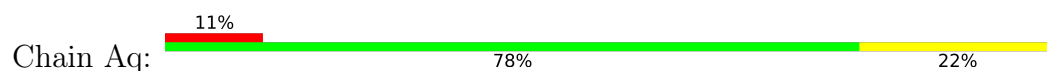
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



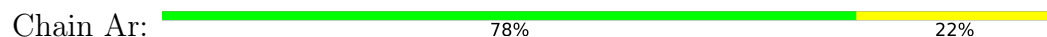
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



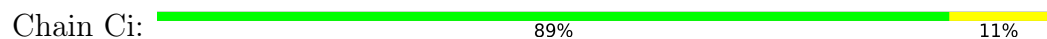
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Cj:  89% 11%




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ck:  11% 89% 11%




- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Cl:  89% 11%



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Cm:  11% 89% 11%




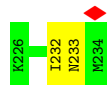
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Cn:  89% 11%




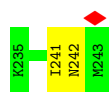
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Co:  11% 78% 22%

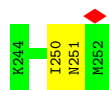
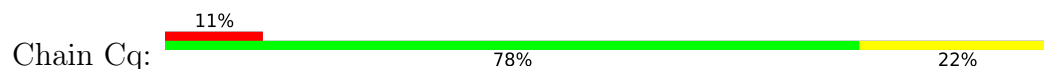


- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

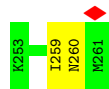
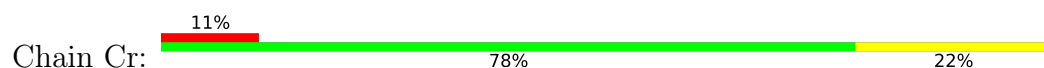
Chain Cp:  11% 78% 22%



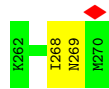
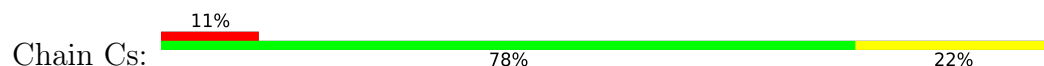
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



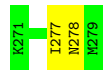
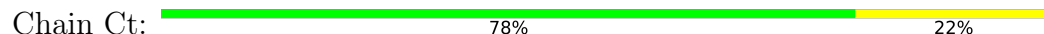
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



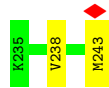
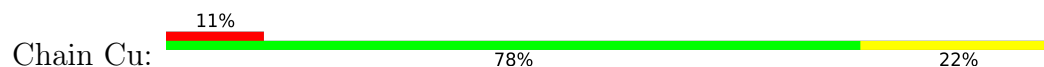
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



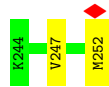
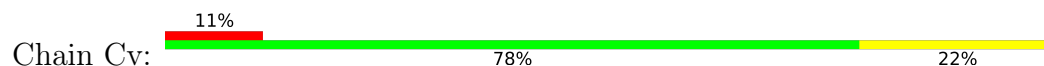
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



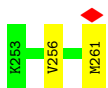
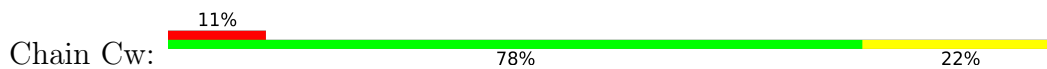
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



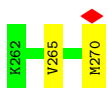
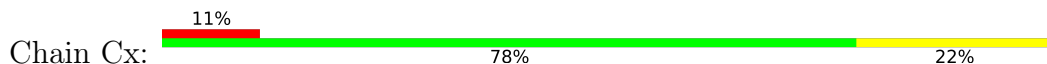
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



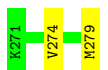
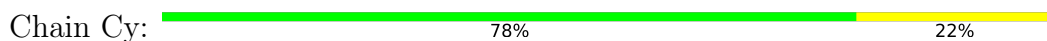
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



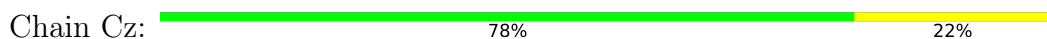
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



There are no outlier residues recorded for this chain.

- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



There are no outlier residues recorded for this chain.

- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



There are no outlier residues recorded for this chain.

- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



There are no outlier residues recorded for this chain.

- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

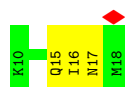


- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

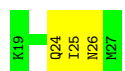


There are no outlier residues recorded for this chain.

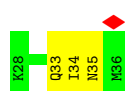
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



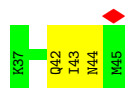
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



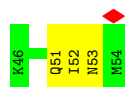
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

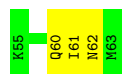


- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET




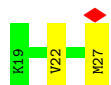
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Fb:  67% 33%




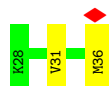
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Fc:  11% 78% 22%




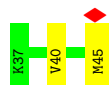
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Fd:  11% 78% 22%




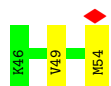
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Fe:  11% 78% 22%




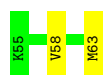
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Ff:  11% 78% 22%




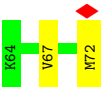
- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Fg:  78% 22%



- Molecule 1: Peptide LYS-VAL-LYS-VAL-SER-GLN-ILE-ASN-MET

Chain Fh:  11% 78% 22%



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-0.64°, rise=4.77 Å, axial sym=C6	Depositor
Number of segments used	108623	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	39.28839	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.018	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0022	Depositor
Map size (Å)	310.625, 310.625, 310.625	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8875, 0.8875, 0.8875	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	Aa	0.96	0/71	1.50	0/91
1	Ab	0.96	0/71	1.50	0/91
1	Ac	0.96	0/71	1.50	0/91
1	Ad	0.96	0/71	1.50	0/91
1	Ae	0.96	0/71	1.50	0/91
1	Af	0.96	0/71	1.50	0/91
1	Ag	0.90	0/71	1.34	0/91
1	Ah	0.90	0/71	1.34	0/91
1	Ai	0.90	0/71	1.35	0/91
1	Aj	0.90	0/71	1.34	0/91
1	Ak	0.90	0/71	1.34	0/91
1	Al	0.90	0/71	1.34	0/91
1	Am	1.14	0/71	1.64	1/91 (1.1%)
1	An	1.14	0/71	1.64	1/91 (1.1%)
1	Ao	1.14	0/71	1.64	1/91 (1.1%)
1	Ap	1.14	0/71	1.64	1/91 (1.1%)
1	Aq	1.14	0/71	1.64	1/91 (1.1%)
1	Ar	1.14	0/71	1.64	1/91 (1.1%)
1	Ci	0.96	0/71	1.50	0/91
1	Cj	0.96	0/71	1.51	0/91
1	Ck	0.96	0/71	1.50	0/91
1	Cl	0.96	0/71	1.50	0/91
1	Cm	0.96	0/71	1.50	0/91
1	Cn	0.96	0/71	1.50	0/91
1	Co	0.90	0/71	1.34	0/91
1	Cp	0.90	0/71	1.35	0/91
1	Cq	0.90	0/71	1.34	0/91
1	Cr	0.90	0/71	1.34	0/91
1	Cs	0.90	0/71	1.34	0/91
1	Ct	0.90	0/71	1.34	0/91
1	Cu	1.14	0/71	1.64	1/91 (1.1%)
1	Cv	1.14	0/71	1.63	1/91 (1.1%)
1	Cw	1.14	0/71	1.63	1/91 (1.1%)
1	Cx	1.14	0/71	1.64	1/91 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Cy	1.14	0/71	1.64	1/91 (1.1%)
1	Cz	1.14	0/71	1.64	1/91 (1.1%)
1	Eq	0.96	0/71	1.50	0/91
1	Er	0.96	0/71	1.50	0/91
1	Es	0.96	0/71	1.50	0/91
1	Et	0.96	0/71	1.50	0/91
1	Eu	0.96	0/71	1.50	0/91
1	Ev	0.96	0/71	1.50	0/91
1	Ew	0.90	0/71	1.34	0/91
1	Ex	0.90	0/71	1.34	0/91
1	Ey	0.90	0/71	1.34	0/91
1	Ez	0.90	0/71	1.34	0/91
1	Fa	0.90	0/71	1.34	0/91
1	Fb	0.90	0/71	1.34	0/91
1	Fc	1.14	0/71	1.64	1/91 (1.1%)
1	Fd	1.14	0/71	1.64	1/91 (1.1%)
1	Fe	1.13	0/71	1.64	1/91 (1.1%)
1	Ff	1.14	0/71	1.64	1/91 (1.1%)
1	Fg	1.14	0/71	1.64	1/91 (1.1%)
1	Fh	1.13	0/71	1.64	1/91 (1.1%)
All	All	1.00	0/3834	1.50	18/4914 (0.4%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ar	175	VAL	CB-CA-C	5.62	118.00	110.42
1	Aq	166	VAL	CB-CA-C	5.59	117.97	110.42
1	Fh	67	VAL	CB-CA-C	5.59	117.96	110.42
1	Cz	283	VAL	CB-CA-C	5.58	117.96	110.42
1	Am	130	VAL	CB-CA-C	5.58	117.96	110.42
1	Ap	157	VAL	CB-CA-C	5.58	117.96	110.42
1	Cy	274	VAL	CB-CA-C	5.57	117.94	110.42
1	Fd	31	VAL	CB-CA-C	5.57	117.94	110.42
1	Fc	22	VAL	CB-CA-C	5.57	117.94	110.42
1	Ff	49	VAL	CB-CA-C	5.57	117.94	110.42
1	An	139	VAL	CB-CA-C	5.57	117.93	110.42
1	Fg	58	VAL	CB-CA-C	5.56	117.93	110.42
1	Ao	148	VAL	CB-CA-C	5.56	117.92	110.42
1	Cu	238	VAL	CB-CA-C	5.55	117.92	110.42
1	Cx	265	VAL	CB-CA-C	5.55	117.92	110.42
1	Fe	40	VAL	CB-CA-C	5.55	117.92	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Cv	247	VAL	CB-CA-C	5.54	117.91	110.42
1	Cw	256	VAL	CB-CA-C	5.53	117.89	110.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	Aa	72	0	82	1	0
1	Ab	72	0	82	1	0
1	Ac	72	0	82	1	0
1	Ad	72	0	82	1	0
1	Ae	72	0	82	1	0
1	Af	72	0	82	1	0
1	Ag	72	0	82	4	0
1	Ah	72	0	82	4	0
1	Ai	72	0	82	4	0
1	Aj	72	0	82	4	0
1	Ak	72	0	82	4	0
1	Al	72	0	82	4	0
1	Am	72	0	82	1	0
1	An	72	0	82	1	0
1	Ao	72	0	82	1	0
1	Ap	72	0	82	1	0
1	Aq	72	0	82	1	0
1	Ar	72	0	82	1	0
1	Ci	72	0	82	1	0
1	Cj	72	0	82	1	0
1	Ck	72	0	82	1	0
1	Cl	72	0	82	1	0
1	Cm	72	0	82	1	0
1	Cn	72	0	82	1	0
1	Co	72	0	82	2	0
1	Cp	72	0	82	2	0
1	Cq	72	0	82	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Cr	72	0	82	2	0
1	Cs	72	0	82	2	0
1	Ct	72	0	82	2	0
1	Cu	72	0	82	1	0
1	Cv	72	0	82	1	0
1	Cw	72	0	82	1	0
1	Cx	72	0	82	1	0
1	Cy	72	0	82	1	0
1	Cz	72	0	82	1	0
1	Eq	72	0	85	0	0
1	Er	72	0	82	0	0
1	Es	72	0	82	0	0
1	Et	72	0	82	0	0
1	Eu	72	0	82	0	0
1	Ev	72	0	82	0	0
1	Ew	72	0	82	3	0
1	Ex	72	0	82	3	0
1	Ey	72	0	82	3	0
1	Ez	72	0	82	3	0
1	Fa	72	0	82	3	0
1	Fb	72	0	82	3	0
1	Fc	72	0	82	1	0
1	Fd	72	0	82	1	0
1	Fe	72	0	82	1	0
1	Ff	72	0	82	1	0
1	Fg	72	0	82	1	0
1	Fh	72	0	82	1	0
All	All	3888	0	4431	42	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 5.

All (42) 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:Ai:141:GLN:OE1	1:Cj:226:LYS:N	2.30	0.65
1:Ab:118:LYS:N	1:Ey:33:GLN:OE1	2.30	0.65
1:Ak:159:GLN:OE1	1:Cl:244:LYS:N	2.30	0.65
1:Al:168:GLN:OE1	1:Cm:253:LYS:N	2.30	0.65
1:Aa:109:LYS:N	1:Ex:24:GLN:OE1	2.30	0.65
1:Ae:145:LYS:N	1:Fb:60:GLN:OE1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:136:LYS:N	1:Fa:51:GLN:OE1	2.30	0.64
1:Ah:132:GLN:OE1	1:Ci:217:LYS:N	2.30	0.64
1:Af:154:LYS:N	1:Ew:15:GLN:OE1	2.30	0.64
1:Ag:123:GLN:OE1	1:Cn:262:LYS:N	2.29	0.64
1:Aj:150:GLN:OE1	1:Ck:235:LYS:N	2.29	0.64
1:Ac:127:LYS:N	1:Ez:42:GLN:OE1	2.30	0.63
1:Cp:241:ILE:HG12	1:Cv:252:MET:HE2	1.97	0.46
1:Ag:124:ILE:HG12	1:Am:135:MET:HE2	1.97	0.46
1:Ah:133:ILE:HG12	1:An:144:MET:HE2	1.97	0.46
1:Cs:268:ILE:HG12	1:Cy:279:MET:HE2	1.97	0.46
1:Co:232:ILE:HG12	1:Cu:243:MET:HE2	1.97	0.46
1:Ew:16:ILE:HG12	1:Fc:27:MET:HE2	1.97	0.46
1:Ak:160:ILE:HG12	1:Aq:171:MET:HE2	1.97	0.46
1:Ex:25:ILE:HG12	1:Fd:36:MET:HE2	1.97	0.46
1:Aj:151:ILE:HG12	1:Ap:162:MET:HE2	1.97	0.46
1:Ey:34:ILE:HG12	1:Fe:45:MET:HE2	1.97	0.46
1:Ai:142:ILE:HG12	1:Ao:153:MET:HE2	1.97	0.46
1:Cr:259:ILE:HG12	1:Cx:270:MET:HE2	1.97	0.46
1:Ez:43:ILE:HG12	1:Ff:54:MET:HE2	1.97	0.46
1:Fa:52:ILE:HG12	1:Fg:63:MET:HE2	1.97	0.46
1:Cq:250:ILE:HG12	1:Cw:261:MET:HE2	1.97	0.45
1:Fb:61:ILE:HG12	1:Fh:72:MET:HE2	1.97	0.45
1:Al:169:ILE:HG12	1:Ar:180:MET:HE2	1.97	0.45
1:Ct:277:ILE:HG12	1:Cz:288:MET:HE2	1.97	0.45
1:Al:170:ASN:HB3	1:Fb:62:ASN:HD22	1.84	0.43
1:Al:170:ASN:HD22	1:Ct:278:ASN:HB3	1.84	0.42
1:Aj:152:ASN:HD22	1:Cr:260:ASN:HB3	1.84	0.42
1:Ak:161:ASN:HD22	1:Cs:269:ASN:HB3	1.84	0.42
1:Ak:161:ASN:HB3	1:Fa:53:ASN:HD22	1.84	0.42
1:Aj:152:ASN:HB3	1:Ez:44:ASN:HD22	1.84	0.42
1:Ai:143:ASN:HB3	1:Ey:35:ASN:HD22	1.84	0.42
1:Ag:125:ASN:HB3	1:Ew:17:ASN:HD22	1.84	0.42
1:Ag:125:ASN:HD22	1:Co:233:ASN:HB3	1.84	0.42
1:Ai:143:ASN:HD22	1:Cq:251:ASN:HB3	1.84	0.42
1:Ah:134:ASN:HB3	1:Ex:26:ASN:HD22	1.84	0.41
1:Ah:134:ASN:HD22	1:Cp:242:ASN:HB3	1.84	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	7/9 (78%)	7 (100%)	0	0	100	100
1	Ab	7/9 (78%)	7 (100%)	0	0	100	100
1	Ac	7/9 (78%)	7 (100%)	0	0	100	100
1	Ad	7/9 (78%)	7 (100%)	0	0	100	100
1	Ae	7/9 (78%)	7 (100%)	0	0	100	100
1	Af	7/9 (78%)	7 (100%)	0	0	100	100
1	Ag	7/9 (78%)	7 (100%)	0	0	100	100
1	Ah	7/9 (78%)	7 (100%)	0	0	100	100
1	Ai	7/9 (78%)	7 (100%)	0	0	100	100
1	Aj	7/9 (78%)	7 (100%)	0	0	100	100
1	Ak	7/9 (78%)	7 (100%)	0	0	100	100
1	Al	7/9 (78%)	7 (100%)	0	0	100	100
1	Am	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	An	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Ao	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Ap	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Aq	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Ar	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Ci	7/9 (78%)	7 (100%)	0	0	100	100
1	Cj	7/9 (78%)	7 (100%)	0	0	100	100
1	Ck	7/9 (78%)	7 (100%)	0	0	100	100
1	Cl	7/9 (78%)	7 (100%)	0	0	100	100
1	Cm	7/9 (78%)	7 (100%)	0	0	100	100
1	Cn	7/9 (78%)	7 (100%)	0	0	100	100
1	Co	7/9 (78%)	7 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Cp	7/9 (78%)	7 (100%)	0	0	100	100
1	Cq	7/9 (78%)	7 (100%)	0	0	100	100
1	Cr	7/9 (78%)	7 (100%)	0	0	100	100
1	Cs	7/9 (78%)	7 (100%)	0	0	100	100
1	Ct	7/9 (78%)	7 (100%)	0	0	100	100
1	Cu	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Cv	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Cw	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Cx	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Cy	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Cz	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Eq	7/9 (78%)	7 (100%)	0	0	100	100
1	Er	7/9 (78%)	7 (100%)	0	0	100	100
1	Es	7/9 (78%)	7 (100%)	0	0	100	100
1	Et	7/9 (78%)	7 (100%)	0	0	100	100
1	Eu	7/9 (78%)	7 (100%)	0	0	100	100
1	Ev	7/9 (78%)	7 (100%)	0	0	100	100
1	Ew	7/9 (78%)	7 (100%)	0	0	100	100
1	Ex	7/9 (78%)	7 (100%)	0	0	100	100
1	Ey	7/9 (78%)	7 (100%)	0	0	100	100
1	Ez	7/9 (78%)	7 (100%)	0	0	100	100
1	Fa	7/9 (78%)	7 (100%)	0	0	100	100
1	Fb	7/9 (78%)	7 (100%)	0	0	100	100
1	Fc	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Fd	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Fe	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Ff	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Fg	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
1	Fh	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	378/486 (78%)	360 (95%)	18 (5%)	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	Aa	9/9 (100%)	9 (100%)	0	100	100
1	Ab	9/9 (100%)	9 (100%)	0	100	100
1	Ac	9/9 (100%)	9 (100%)	0	100	100
1	Ad	9/9 (100%)	9 (100%)	0	100	100
1	Ae	9/9 (100%)	9 (100%)	0	100	100
1	Af	9/9 (100%)	9 (100%)	0	100	100
1	Ag	9/9 (100%)	9 (100%)	0	100	100
1	Ah	9/9 (100%)	9 (100%)	0	100	100
1	Ai	9/9 (100%)	9 (100%)	0	100	100
1	Aj	9/9 (100%)	9 (100%)	0	100	100
1	Ak	9/9 (100%)	9 (100%)	0	100	100
1	Al	9/9 (100%)	9 (100%)	0	100	100
1	Am	9/9 (100%)	9 (100%)	0	100	100
1	An	9/9 (100%)	9 (100%)	0	100	100
1	Ao	9/9 (100%)	9 (100%)	0	100	100
1	Ap	9/9 (100%)	9 (100%)	0	100	100
1	Aq	9/9 (100%)	9 (100%)	0	100	100
1	Ar	9/9 (100%)	9 (100%)	0	100	100
1	Ci	9/9 (100%)	9 (100%)	0	100	100
1	Cj	9/9 (100%)	9 (100%)	0	100	100
1	Ck	9/9 (100%)	9 (100%)	0	100	100
1	Cl	9/9 (100%)	9 (100%)	0	100	100
1	Cm	9/9 (100%)	9 (100%)	0	100	100
1	Cn	9/9 (100%)	9 (100%)	0	100	100
1	Co	9/9 (100%)	9 (100%)	0	100	100
1	Cp	9/9 (100%)	9 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Cq	9/9 (100%)	9 (100%)	0	100	100
1	Cr	9/9 (100%)	9 (100%)	0	100	100
1	Cs	9/9 (100%)	9 (100%)	0	100	100
1	Ct	9/9 (100%)	9 (100%)	0	100	100
1	Cu	9/9 (100%)	9 (100%)	0	100	100
1	Cv	9/9 (100%)	9 (100%)	0	100	100
1	Cw	9/9 (100%)	9 (100%)	0	100	100
1	Cx	9/9 (100%)	9 (100%)	0	100	100
1	Cy	9/9 (100%)	9 (100%)	0	100	100
1	Cz	9/9 (100%)	9 (100%)	0	100	100
1	Eq	9/9 (100%)	9 (100%)	0	100	100
1	Er	9/9 (100%)	9 (100%)	0	100	100
1	Es	9/9 (100%)	9 (100%)	0	100	100
1	Et	9/9 (100%)	9 (100%)	0	100	100
1	Eu	9/9 (100%)	9 (100%)	0	100	100
1	Ev	9/9 (100%)	9 (100%)	0	100	100
1	Ew	9/9 (100%)	9 (100%)	0	100	100
1	Ex	9/9 (100%)	9 (100%)	0	100	100
1	Ey	9/9 (100%)	9 (100%)	0	100	100
1	Ez	9/9 (100%)	9 (100%)	0	100	100
1	Fa	9/9 (100%)	9 (100%)	0	100	100
1	Fb	9/9 (100%)	9 (100%)	0	100	100
1	Fc	9/9 (100%)	9 (100%)	0	100	100
1	Fd	9/9 (100%)	9 (100%)	0	100	100
1	Fe	9/9 (100%)	9 (100%)	0	100	100
1	Ff	9/9 (100%)	9 (100%)	0	100	100
1	Fg	9/9 (100%)	9 (100%)	0	100	100
1	Fh	9/9 (100%)	9 (100%)	0	100	100
All	All	486/486 (100%)	486 (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. All (39)

such sidechains are listed below:

Mol	Chain	Res	Type
1	Ag	125	ASN
1	Ah	134	ASN
1	Ai	143	ASN
1	Aj	152	ASN
1	Ak	161	ASN
1	Al	170	ASN
1	Am	134	ASN
1	An	141	GLN
1	An	143	ASN
1	Ao	152	ASN
1	Ap	161	ASN
1	Aq	170	ASN
1	Ar	179	ASN
1	Co	231	GLN
1	Cp	240	GLN
1	Cq	249	GLN
1	Cr	258	GLN
1	Cs	267	GLN
1	Ct	276	GLN
1	Cu	242	ASN
1	Cv	249	GLN
1	Cv	251	ASN
1	Cw	260	ASN
1	Cx	269	ASN
1	Cy	278	ASN
1	Cz	287	ASN
1	Ew	17	ASN
1	Ex	26	ASN
1	Ey	35	ASN
1	Ez	44	ASN
1	Fa	53	ASN
1	Fb	62	ASN
1	Fc	26	ASN
1	Fd	33	GLN
1	Fd	35	ASN
1	Fe	44	ASN
1	Ff	53	ASN
1	Fg	62	ASN
1	Fh	71	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.

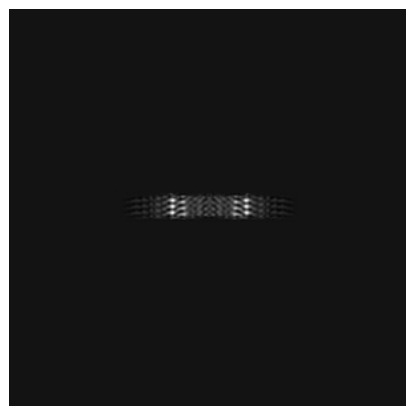
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51914. These allow visual inspection of the internal detail of the map and identification of artifacts.

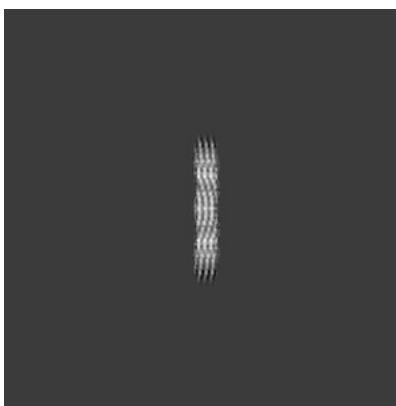
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

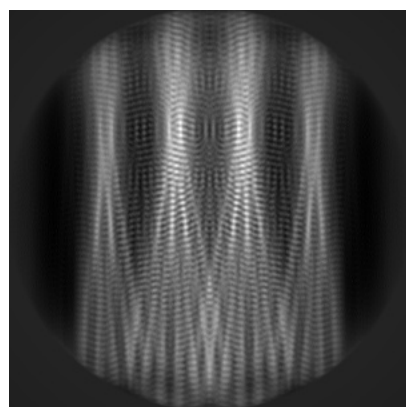


Y

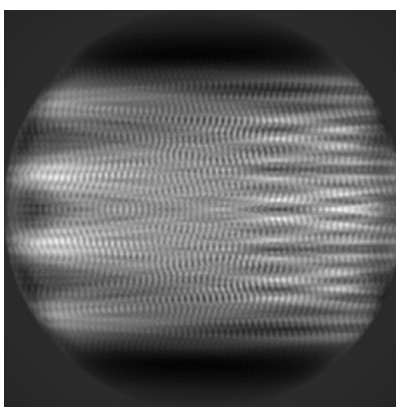


Z

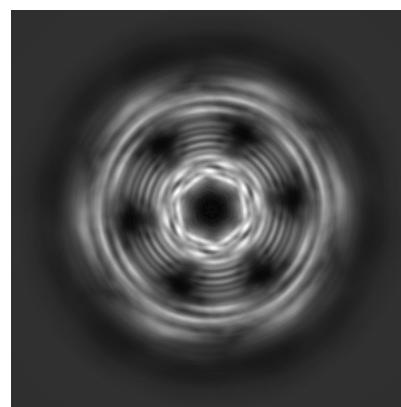
6.1.2 Raw map



X



Y

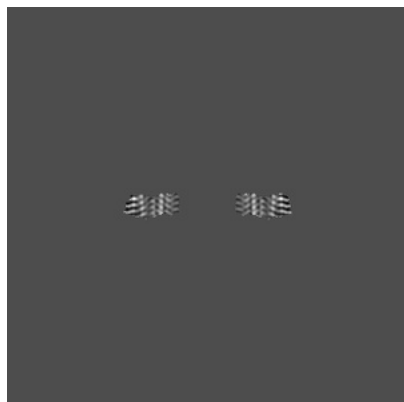


Z

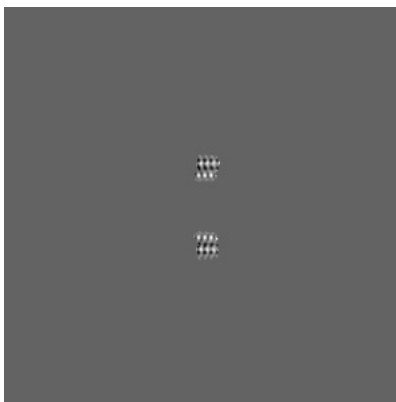
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

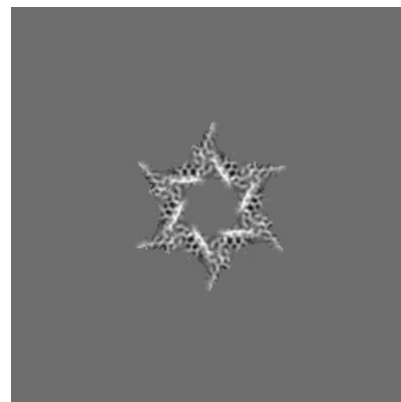
6.2.1 Primary map



X Index: 175

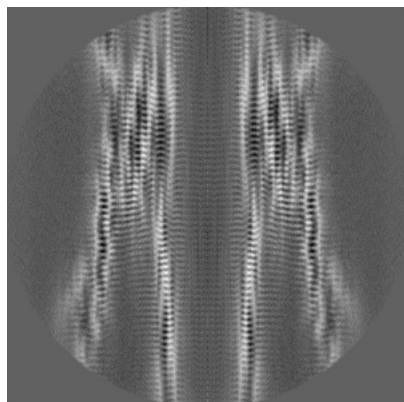


Y Index: 175

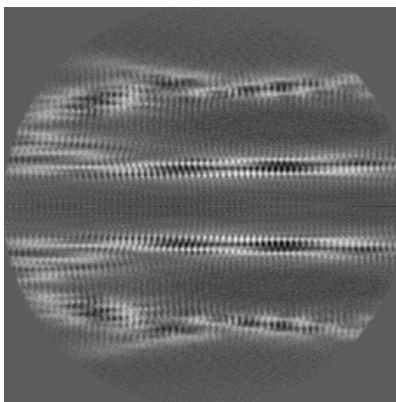


Z Index: 175

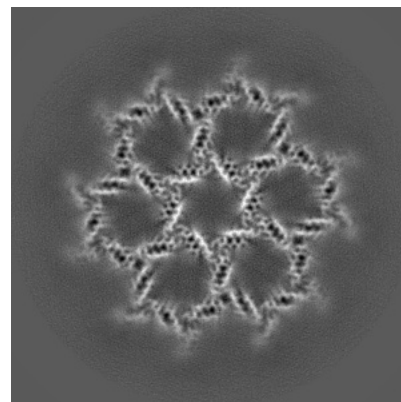
6.2.2 Raw map



X Index: 175



Y Index: 175

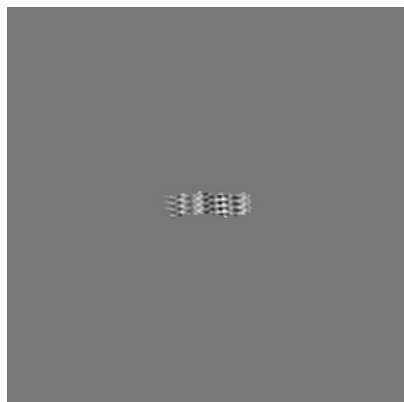


Z Index: 175

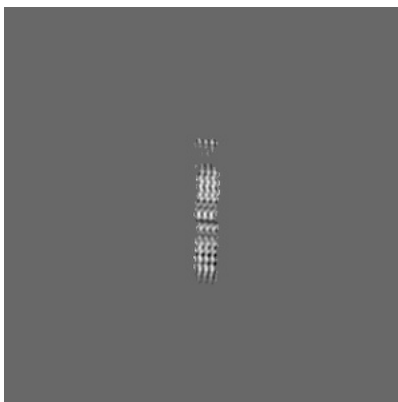
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 209

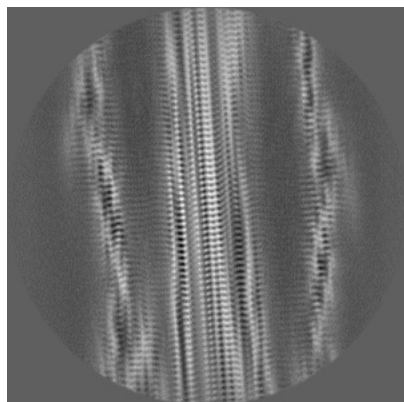


Y Index: 142

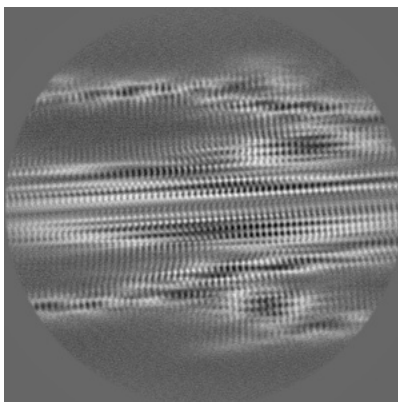


Z Index: 176

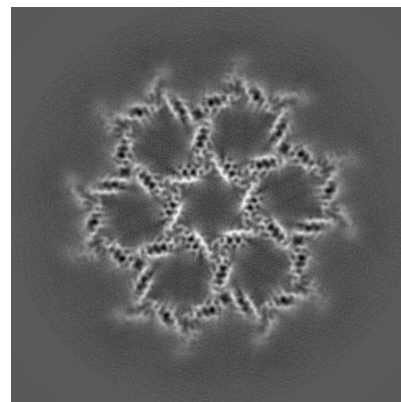
6.3.2 Raw map



X Index: 204



Y Index: 203

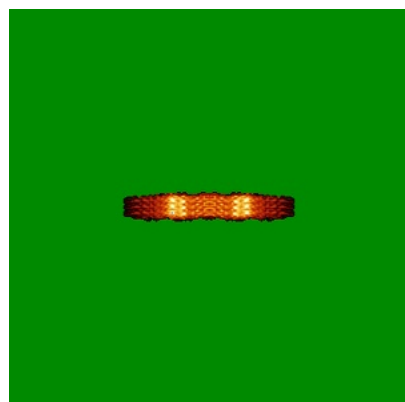


Z Index: 175

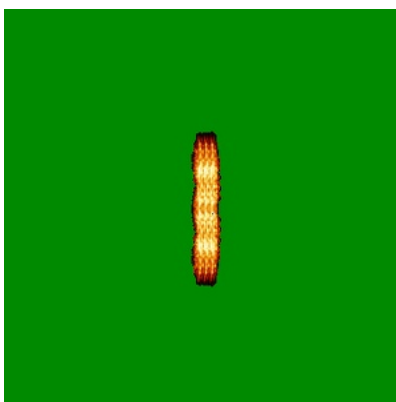
The images above show the largest variance slices of the map in three orthogonal directions.

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

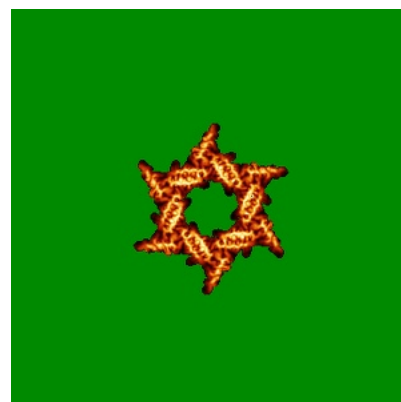
6.4.1 Primary map



X

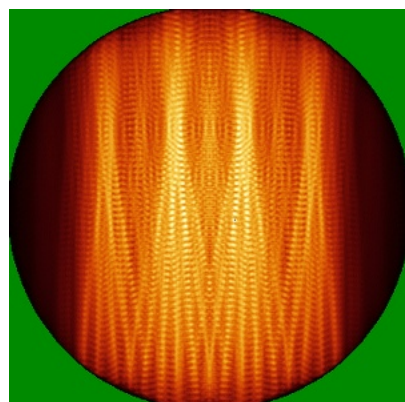


Y

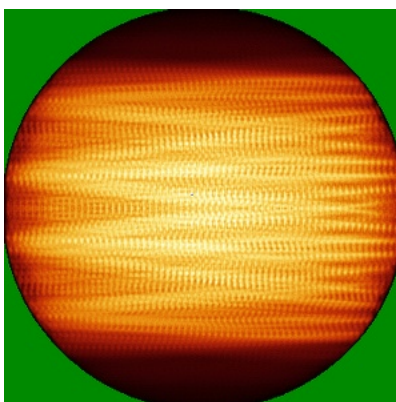


Z

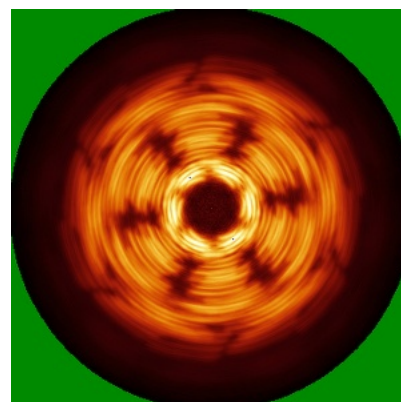
6.4.2 Raw map



X



Y

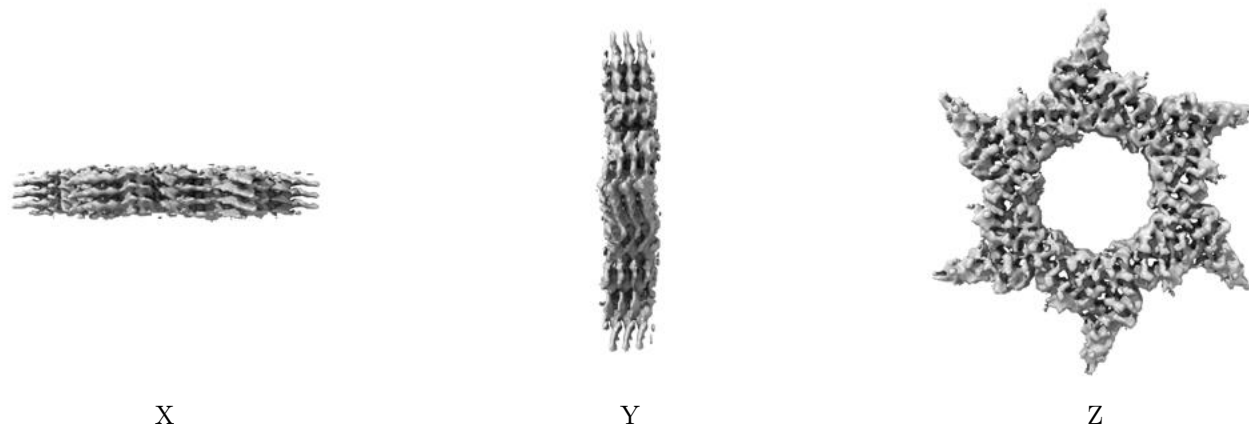


Z

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.

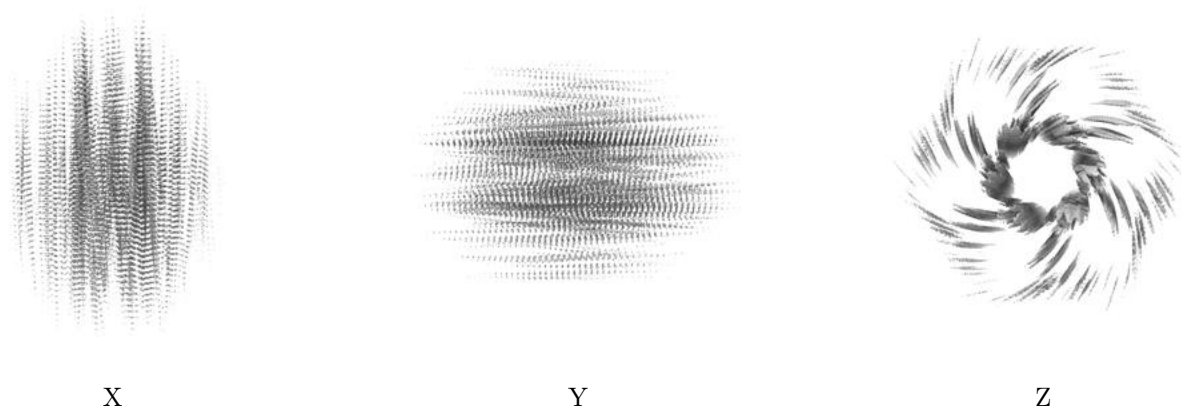
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

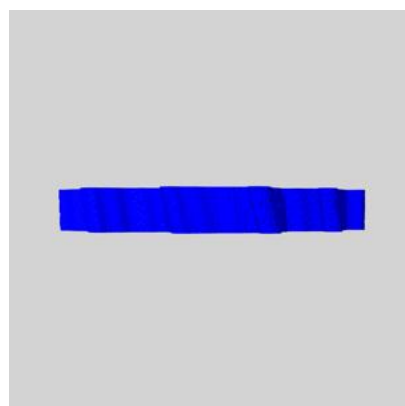
6.6 Mask visualisation [i](#)

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

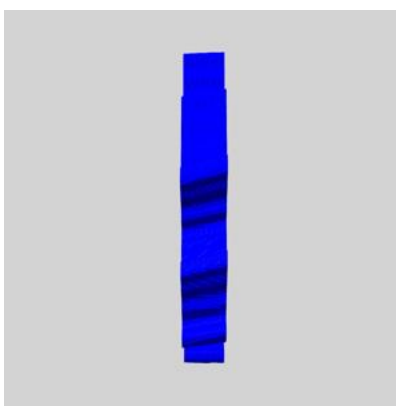
A mask typically either:

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

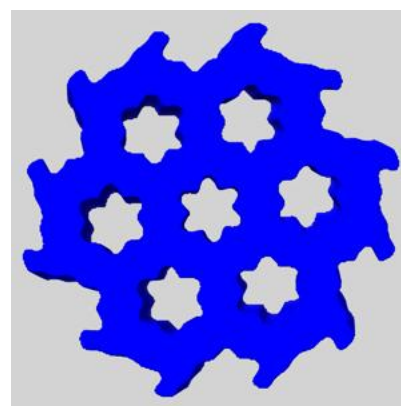
6.6.1 emd_51914_msk_1.map [i](#)



X



Y

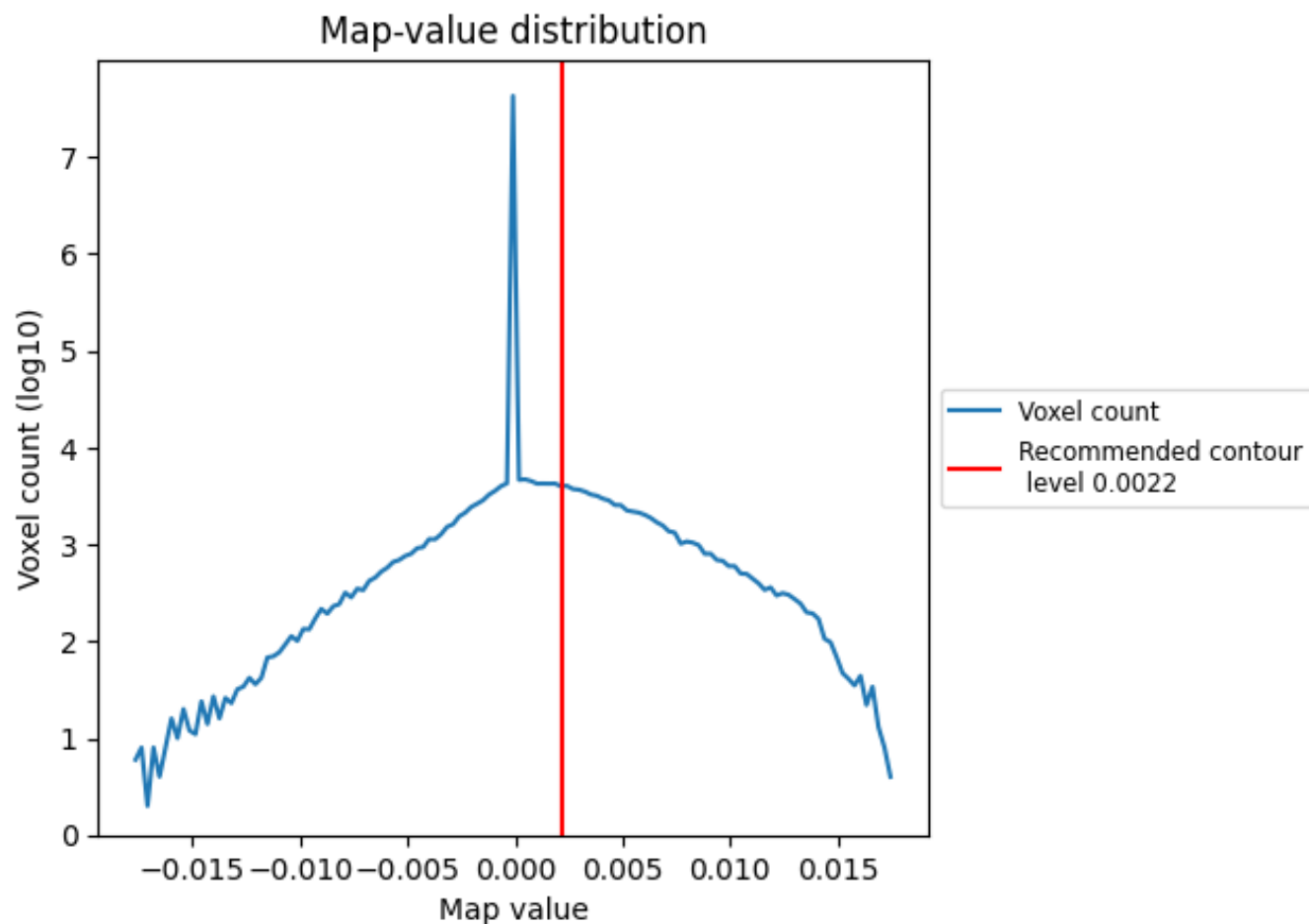


Z

7 Map analysis [i](#)

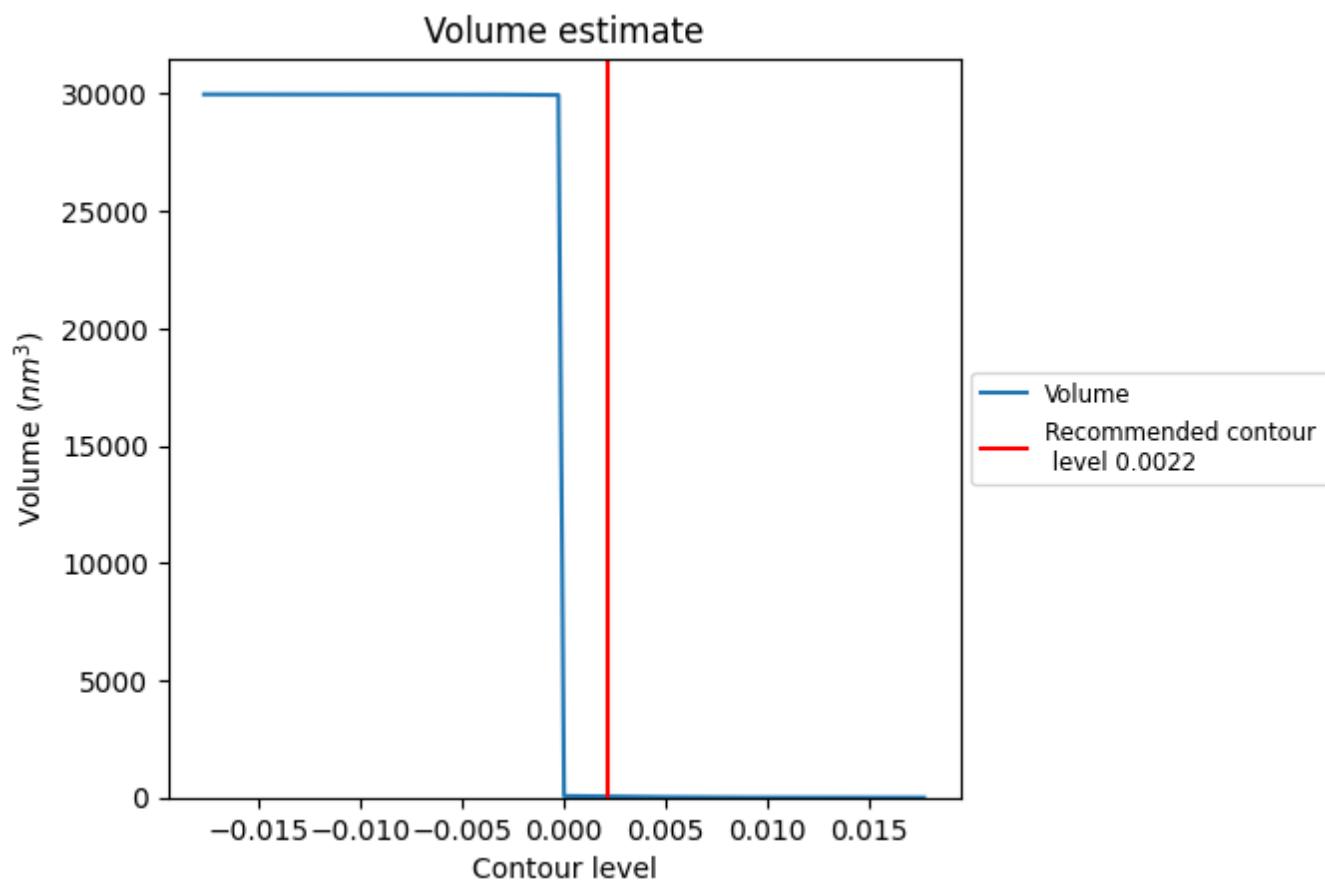
This section contains the results of statistical analysis of the map.

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.

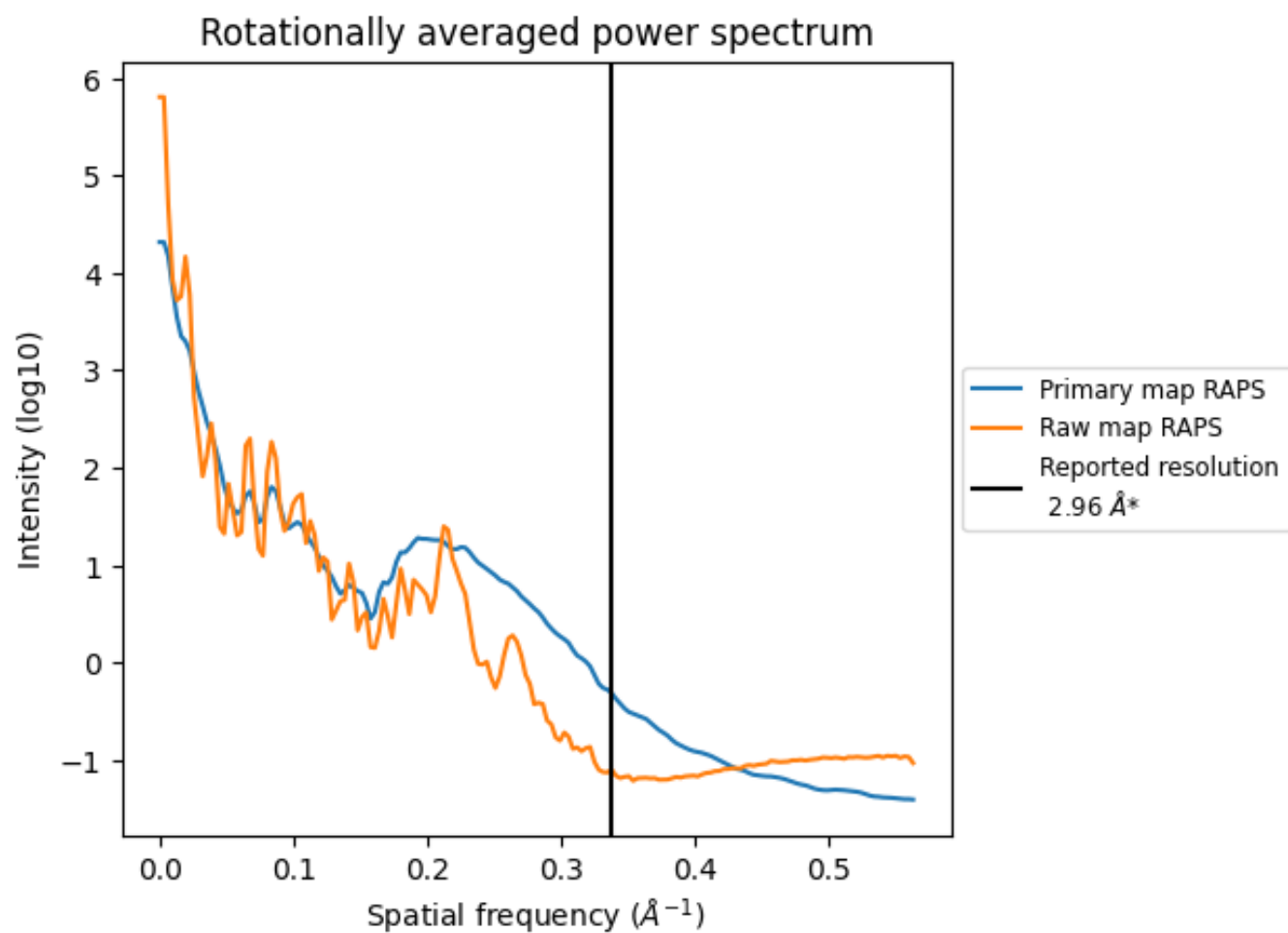
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 46 nm^3 ; 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 ⓘ

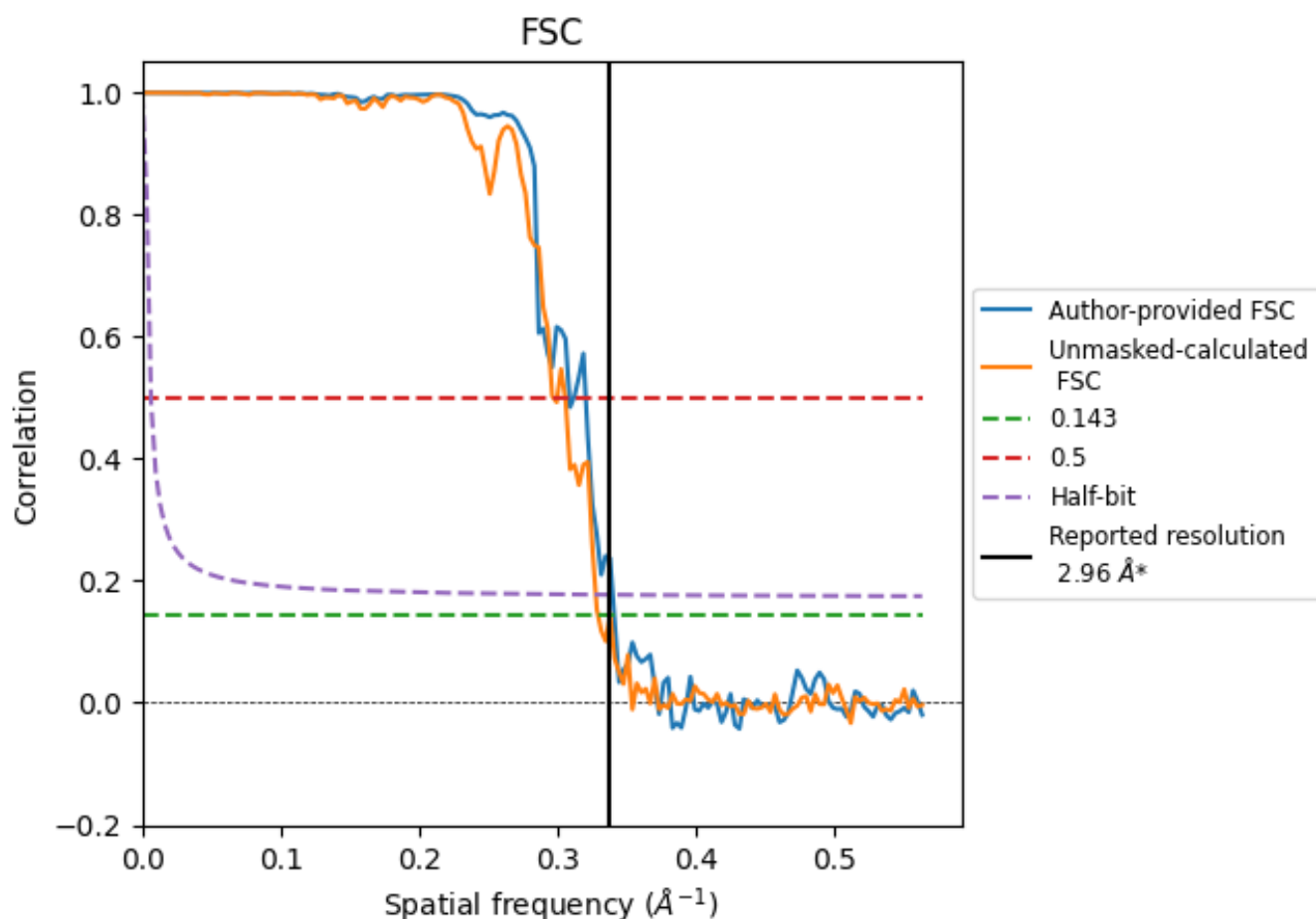


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 \AA^{-1}

8.2 Resolution estimates [i](#)

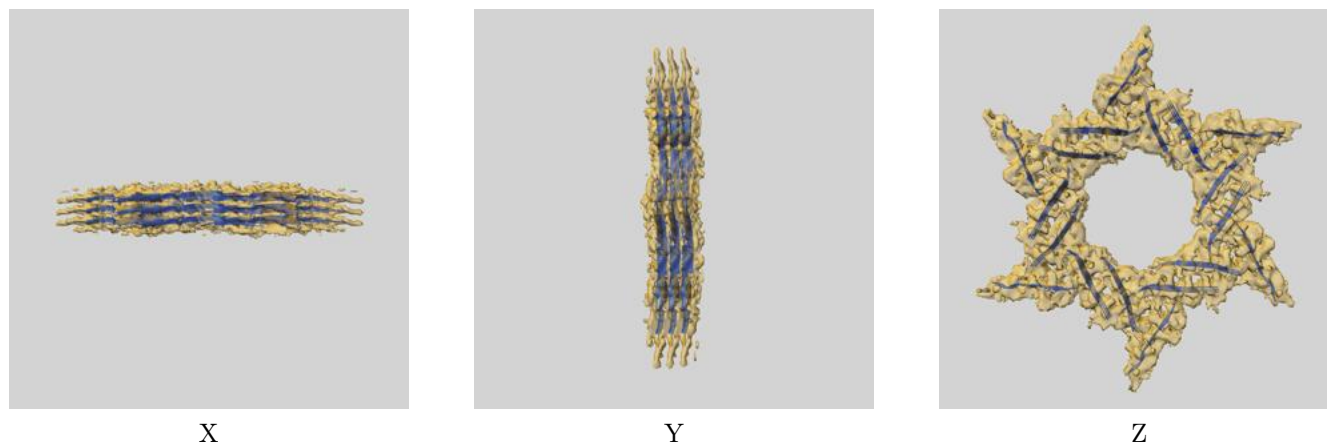
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.93	3.24	2.94
Unmasked-calculated*	3.04	3.37	3.05

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

9 Map-model fit [i](#)

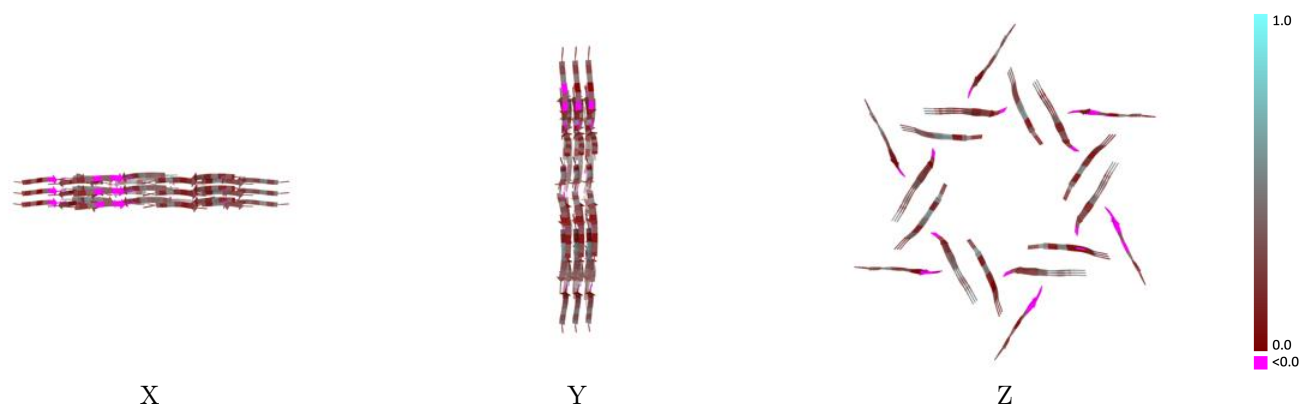
This section contains information regarding the fit between EMDB map EMD-51914 and PDB model 9H7U. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



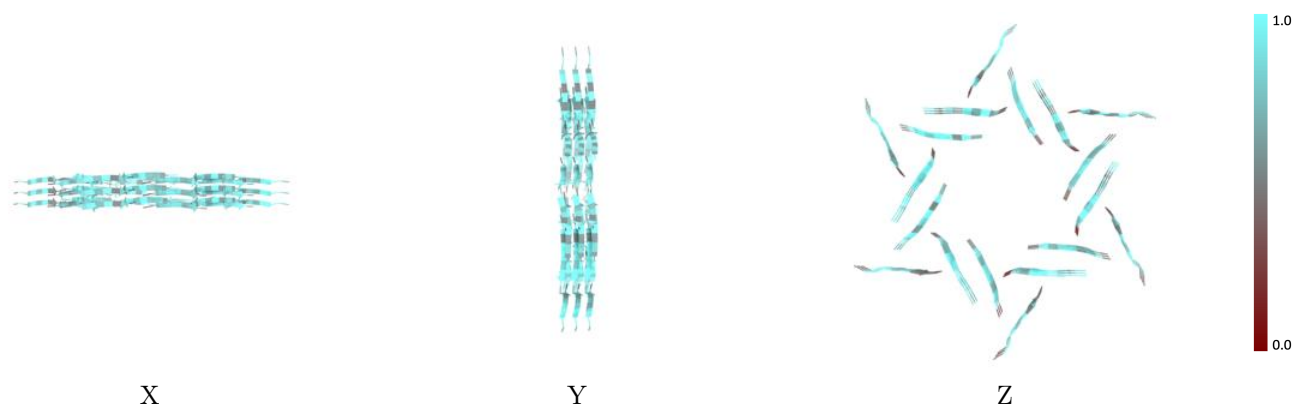
The images above show the 3D surface view of the map at the recommended contour level 0.0022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



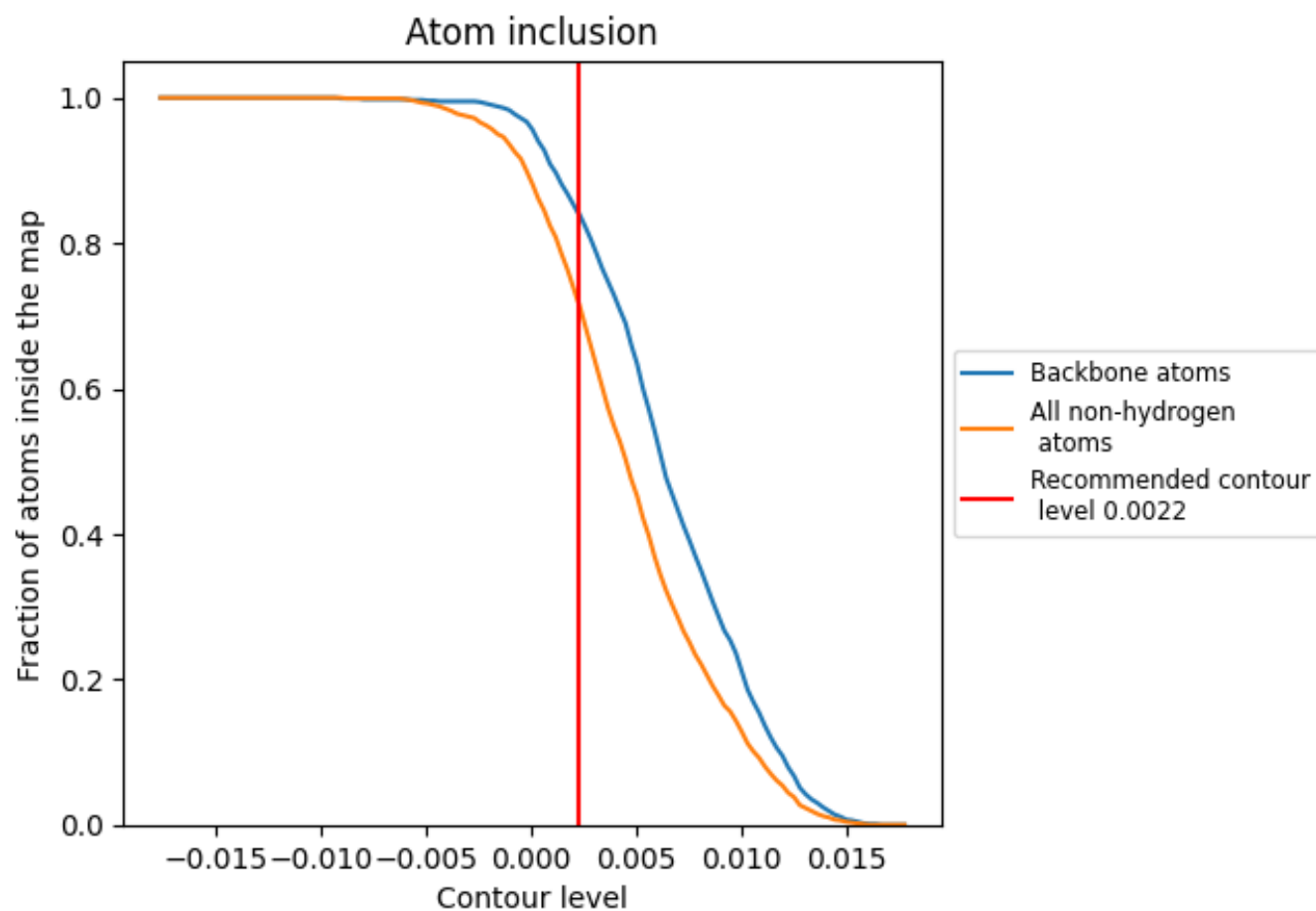
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0022).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 72% 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 (0.0022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7200	 0.2200
Aa	 0.7920	 0.2910
Ab	 0.7220	 0.2740
Ac	 0.6670	 0.2160
Ad	 0.6810	 0.1870
Ae	 0.6940	 0.2220
Af	 0.7920	 0.2860
Ag	 0.8470	 0.2500
Ah	 0.7360	 0.1960
Ai	 0.6940	 0.2070
Aj	 0.7080	 0.2600
Ak	 0.7500	 0.2840
Al	 0.7640	 0.2940
Am	 0.7220	 0.2360
An	 0.7360	 0.2190
Ao	 0.6670	 0.1450
Ap	 0.6530	 0.0770
Aq	 0.6250	 0.1040
Ar	 0.6530	 0.1810
Ci	 0.8190	 0.3010
Cj	 0.7360	 0.2780
Ck	 0.6940	 0.2210
Cl	 0.6940	 0.1920
Cm	 0.7080	 0.2280
Cn	 0.7780	 0.2890
Co	 0.8330	 0.2570
Cp	 0.7080	 0.2000
Cq	 0.7080	 0.2110
Cr	 0.7220	 0.2590
Cs	 0.7640	 0.2860
Ct	 0.7500	 0.2910
Cu	 0.7080	 0.2340
Cv	 0.7360	 0.2220
Cw	 0.6670	 0.1480
Cx	 0.6530	 0.0870



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Chain	Atom inclusion	Q-score
Cy	 0.6670	 0.1120
Cz	 0.6530	 0.1820
Eq	 0.8060	 0.2990
Er	 0.7360	 0.2790
Es	 0.6940	 0.2230
Et	 0.6810	 0.1930
Eu	 0.7080	 0.2300
Ev	 0.7780	 0.2920
Ew	 0.8330	 0.2470
Ex	 0.7220	 0.1920
Ey	 0.6940	 0.2050
Ez	 0.7360	 0.2640
Fa	 0.7500	 0.2870
Fb	 0.7920	 0.2900
Fc	 0.7220	 0.2250
Fd	 0.7360	 0.2190
Fe	 0.6810	 0.1520
Ff	 0.6530	 0.0840
Fg	 0.6390	 0.1070
Fh	 0.6390	 0.1810