



Full wwPDB EM Validation Report ⓘ

May 23, 2026 – 03:08 PM EDT

PDB ID : 11DV / pdb_000011dv
EMDB ID : EMD-75642
Title : RNA Vault waist region, focused refinement (MVP/TEP1 sample)
Authors : Osinski, A.; Tagliabracci, V.S.
Deposited on : 2026-02-18
Resolution : 2.33 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

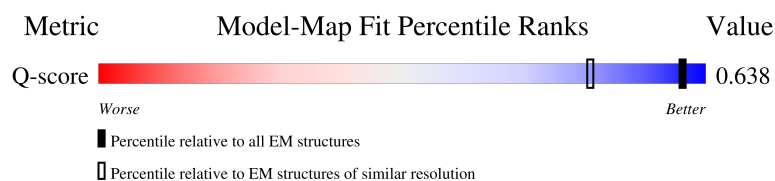
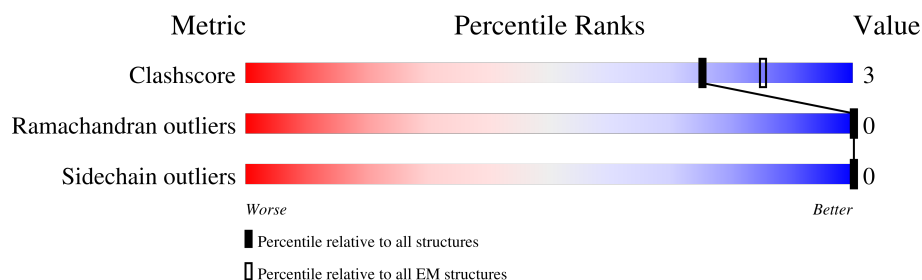
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.33 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	4434 (1.83 - 2.83)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	893	
1	B	893	
1	C	893	
1	D	893	

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Mol	Chain	Length	Quality of chain
1	E	893	11% . 88%
1	F	893	11% . 88%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18618 atoms, of which 9141 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 Major vault protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	267	Total	C	H	N	O	S	0	0
			4324	1374	2164	385	397	4		
1	B	267	Total	C	H	N	O	S	0	0
			4324	1374	2164	385	397	4		
1	C	267	Total	C	H	N	O	S	0	0
			4324	1374	2164	385	397	4		
1	D	108	Total	C	H	N	O	S	0	0
			1762	563	883	157	156	3		
1	E	108	Total	C	H	N	O	S	0	0
			1762	563	883	157	156	3		
1	F	108	Total	C	H	N	O	S	0	0
			1762	563	883	157	156	3		

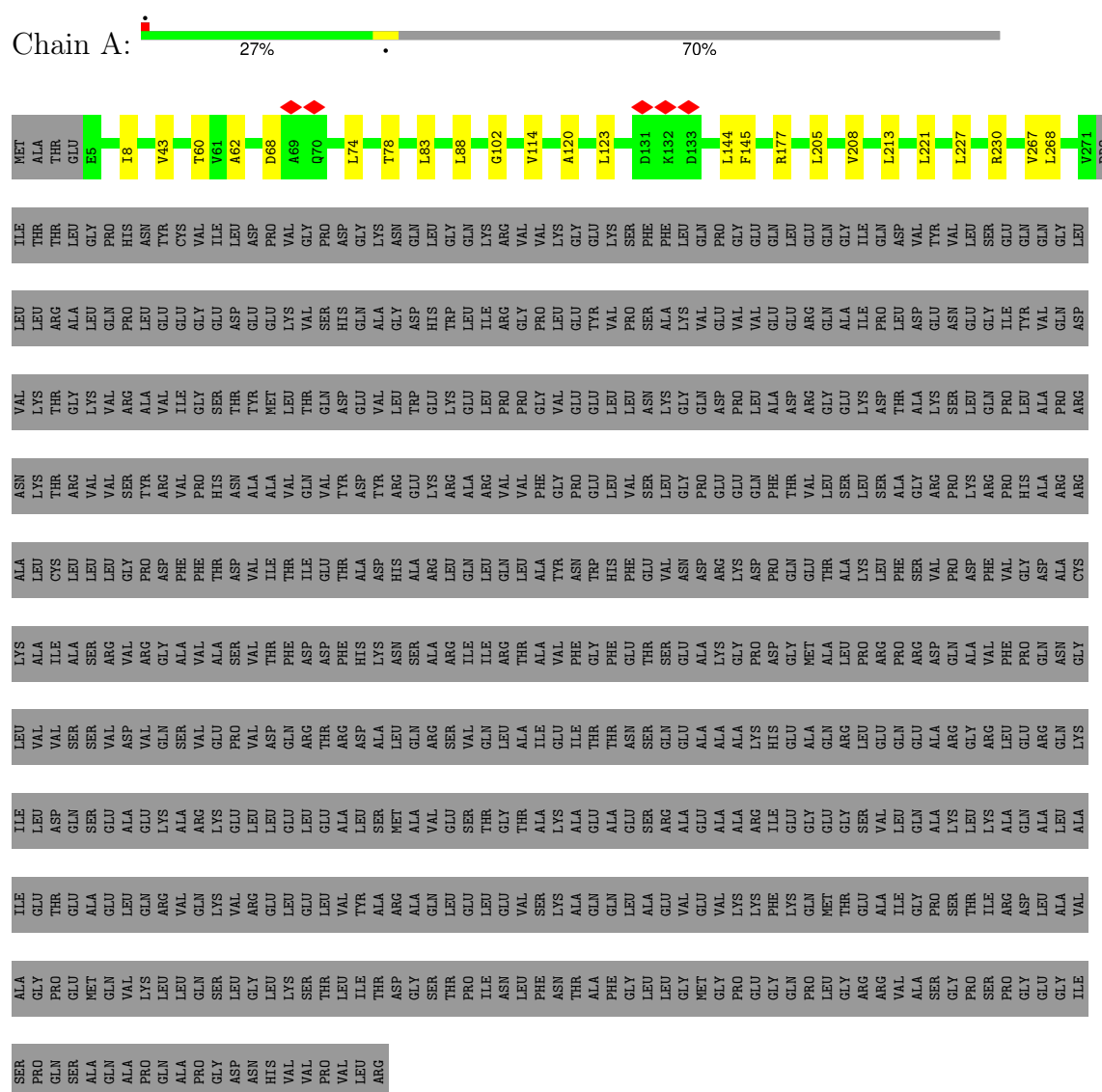
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		AltConf
2	A	89	Total	O	0
			89	89	
2	B	141	Total	O	0
			141	141	
2	C	101	Total	O	0
			101	101	
2	D	11	Total	O	0
			11	11	
2	E	12	Total	O	0
			12	12	
2	F	6	Total	O	0
			6	6	

3 Residue-property plots

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: Major vault protein



• Molecule 1: Major vault protein



GLN	SER	ALA	GLN	PRO	GLN	ALA	PRO	GLN	PRO	PRO	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
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● Molecule 1: Major vault protein

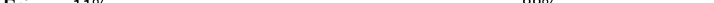


MET	ALA	THR	THR	GLU	E5	I8	V43	T60	V61	A62	V65	A69	Q70	V73	V77	T78	G79	Q80	V81	L88	E106	V115	A120	D131	K132	D133	G134	D135	F145	L174	R175	L176	R177	L206	V212	L213	L227	V267	V271	PRO	ILE	
THR	THR	LEU	GLY	PRO	HIS	ASN	TYR	CYS	VAL	ASP	VAL	GLY	GLY	ASN	GLN	GLY	GLN	LYS	ARG	VAL	VAL	LYS	SER	PHE	LEU	GLN	GLY	GLY	GLN	GLY	ILE	GLN	ASP	VAL	VAL	VAL	VAL	LEU	LEU	LEU		
LEU	ARG	LEU	GLN	PRO	HIS	LEU	GLY	GLY	GLY	ASP	VAL	SER	HIS	GLY	ASP	TRP	ILE	ILE	ARG	GLY	PRO	LEU	SER	ALA	LYS	VAL	GLY	GLU	ARG	GLN	ILE	PRO	LEU	ASP	GLY	ASN	GLY	GLY	VAL	VAL	VAL	
LYS	THR	THR	VAL	VAL	ARG	ALA	ILE	GLY	THR	TYR	LEU	GLN	ASP	VAL	TRP	GLY	GLU	GLU	PRO	PRO	GLY	VAL	LEU	ASN	LYS	GLY	GLN	PRO	GLY	GLY	LYS	THR	ALA	LYS	SER	LYS	LEU	GLN	ILE	VAL	VAL	
LYS	THR	VAL	VAL	SER	ARG	TYR	VAL	PRO	ASN	ALA	VAL	GLN	THR	TYR	GLY	ARG	ARG	LEU	VAL	PHE	GLY	VAL	SER	LEU	PRO	PRO	GLY	THR	VAL	LEU	LEU	ALA	GLY	ARG	PRO	VAL	VAL	VAL	VAL	VAL	VAL	
LEU	CYS	LEU	LEU	LEU	PRO	ASP	PHE	PHE	THR	ILE	THR	ILE	THR	ASP	ALA	ARG	GLN	LEU	VAL	ALA	ALA	ASN	GLY	VAL	ASN	ASP	GLY	GLN	PHE	THR	VAL	LEU	SER	LEU	LYS	ARG	PRO	VAL	GLY	ASP	ALA	LYS



[illegible]

- Molecule 1: Major vault protein

Chain E:  11% 88%

[illegible]

- Molecule 1: Major vault protein

Chain F: 11% 88%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1016071	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.453	Depositor
Minimum map value	-0.280	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.0476	Depositor
Map size (Å)	214.8, 214.8, 214.8	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.716, 0.716, 0.716	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.23	0/2207	0.28	0/3007
1	B	0.26	0/2207	0.29	0/3007
1	C	0.24	0/2207	0.28	0/3007
1	D	0.20	0/902	0.28	0/1232
1	E	0.19	0/902	0.27	0/1232
1	F	0.13	0/902	0.23	0/1232
All	All	0.23	0/9327	0.28	0/12717

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2160	2164	2164	15	0
1	B	2160	2164	2164	14	0
1	C	2160	2164	2164	13	0
1	D	879	883	883	5	0
1	E	879	883	883	6	0
1	F	879	883	883	5	0
2	A	89	0	0	0	0
2	B	141	0	0	0	0
2	C	101	0	0	0	0
2	D	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	12	0	0	0	0
2	F	6	0	0	0	0
All	All	9477	9141	9141	57	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 3.

All (57) 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:B:120:ALA:HB2	1:B:205:LEU:HD21	1.57	0.86
1:A:60:THR:HG22	1:A:88:LEU:HD22	1.72	0.70
1:A:60:THR:CG2	1:A:88:LEU:HD22	2.22	0.70
1:D:60:THR:HG22	1:D:88:LEU:HD22	1.76	0.66
1:D:8:ILE:HG13	1:D:43:VAL:HG21	1.78	0.66
1:B:8:ILE:HG13	1:B:43:VAL:HG21	1.77	0.66
1:E:8:ILE:HG13	1:E:43:VAL:HG21	1.78	0.66
1:B:174:LEU:HD11	1:B:212:VAL:HG13	1.78	0.65
1:C:174:LEU:HD11	1:C:212:VAL:HG13	1.79	0.65
1:C:120:ALA:HB2	1:C:205:LEU:HD21	1.80	0.64
1:D:60:THR:CG2	1:D:88:LEU:HD22	2.29	0.63
1:C:8:ILE:HG13	1:C:43:VAL:HG21	1.80	0.62
1:C:62:ALA:HB2	1:C:106:GLU:HG3	1.83	0.61
1:C:175:ARG:HG2	1:C:213:LEU:HD12	1.81	0.60
1:F:8:ILE:HG13	1:F:43:VAL:HG21	1.83	0.60
1:B:83:LEU:HD11	1:B:102:GLY:HA3	1.84	0.59
1:F:99:LEU:HD11	1:F:105:LEU:HG	1.85	0.59
1:E:60:THR:HG22	1:E:88:LEU:HD22	1.85	0.58
1:A:8:ILE:HG13	1:A:43:VAL:HG21	1.86	0.56
1:C:227:LEU:HD11	1:C:267:VAL:HG13	1.88	0.55
1:A:68:ASP:HB3	1:A:74:LEU:HD21	1.89	0.55
1:B:227:LEU:HD11	1:B:267:VAL:HG13	1.88	0.55
1:F:37:ARG:HD3	1:F:43:VAL:HG23	1.87	0.55
1:B:99:LEU:HD11	1:B:105:LEU:HG	1.90	0.54
1:A:83:LEU:HD11	1:A:102:GLY:HA3	1.91	0.52
1:A:177:ARG:HB2	1:A:213:LEU:HD11	1.92	0.52
1:C:177:ARG:HB2	1:C:213:LEU:HD11	1.92	0.51
1:B:87:ASP:C	1:B:88:LEU:HD12	2.35	0.51
1:C:65:VAL:CG2	1:C:73:VAL:HG13	2.41	0.50
1:B:60:THR:HG21	1:B:88:LEU:HD23	1.93	0.50
1:A:120:ALA:HB2	1:A:205:LEU:HD21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:ARG:HB2	1:B:213:LEU:HD11	1.95	0.48
1:A:123:LEU:HD11	1:A:145:PHE:HB2	1.96	0.48
1:E:62:ALA:HA	1:E:88:LEU:HD23	1.96	0.47
1:C:65:VAL:HG23	1:C:81:VAL:HG22	1.95	0.47
1:E:65:VAL:HG11	1:E:73:VAL:HG22	1.97	0.47
1:A:144:LEU:HG	1:A:208:VAL:HG13	1.97	0.46
1:A:221:LEU:HD21	1:A:227:LEU:HB2	1.97	0.46
1:C:60:THR:HG21	1:C:88:LEU:HD21	1.97	0.46
1:E:65:VAL:CG1	1:E:73:VAL:HG13	2.46	0.45
1:B:144:LEU:HG	1:B:208:VAL:HG13	1.98	0.45
1:E:60:THR:CG2	1:E:88:LEU:HD22	2.45	0.44
1:D:62:ALA:HA	1:D:88:LEU:HD23	1.98	0.44
1:A:230:ARG:HB2	1:A:268:LEU:HD11	2.00	0.44
1:C:115:VAL:HG21	1:C:145:PHE:CD2	2.53	0.44
1:D:65:VAL:HG23	1:D:81:VAL:HG22	1.99	0.43
1:A:62:ALA:HA	1:A:88:LEU:HD23	2.00	0.43
1:B:175:ARG:NH1	1:B:263:VAL:HG12	2.34	0.43
1:B:175:ARG:HG2	1:B:213:LEU:HD12	2.01	0.42
1:A:227:LEU:HD11	1:A:267:VAL:HG13	2.01	0.42
1:F:65:VAL:CG2	1:F:73:VAL:HG13	2.50	0.42
1:F:65:VAL:HG23	1:F:81:VAL:HG22	2.02	0.41
1:B:46:ALA:O	1:B:47:PRO:C	2.63	0.41
1:A:78:THR:HG21	1:B:32:PRO:CG	2.51	0.41
1:C:60:THR:CG2	1:C:88:LEU:HG	2.51	0.41
1:A:114:VAL:O	1:A:114:VAL:HG13	2.21	0.40
1:C:78:THR:HG23	1:C:80:GLN:H	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	265/893 (30%)	254 (96%)	11 (4%)	0	100	100
1	B	265/893 (30%)	257 (97%)	8 (3%)	0	100	100
1	C	265/893 (30%)	258 (97%)	7 (3%)	0	100	100
1	D	106/893 (12%)	100 (94%)	6 (6%)	0	100	100
1	E	106/893 (12%)	104 (98%)	2 (2%)	0	100	100
1	F	106/893 (12%)	103 (97%)	3 (3%)	0	100	100
All	All	1113/5358 (21%)	1076 (97%)	37 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	236/755 (31%)	236 (100%)	0	100	100
1	B	236/755 (31%)	236 (100%)	0	100	100
1	C	236/755 (31%)	236 (100%)	0	100	100
1	D	99/755 (13%)	99 (100%)	0	100	100
1	E	99/755 (13%)	99 (100%)	0	100	100
1	F	99/755 (13%)	99 (100%)	0	100	100
All	All	1005/4530 (22%)	1005 (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 (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	B	113	GLN
1	B	164	GLN
1	C	113	GLN
1	E	57	HIS

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Mol	Chain	Res	Type
1	F	63	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.

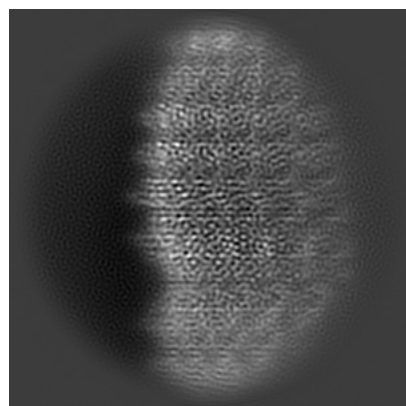
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75642. These allow visual inspection of the internal detail of the map and identification of artifacts.

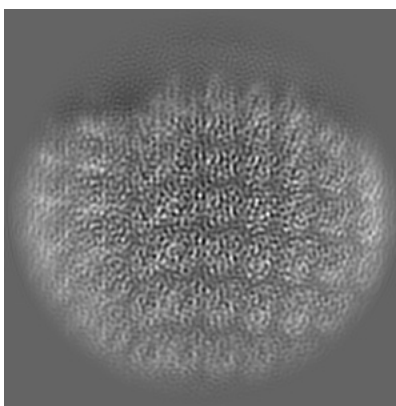
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

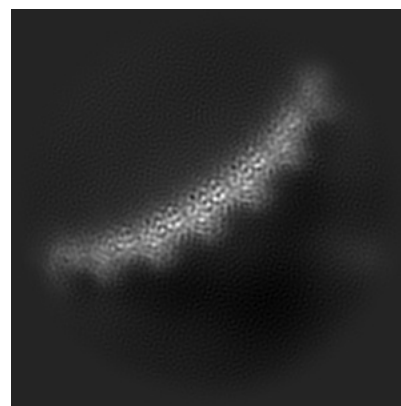
6.1.1 Primary map



X

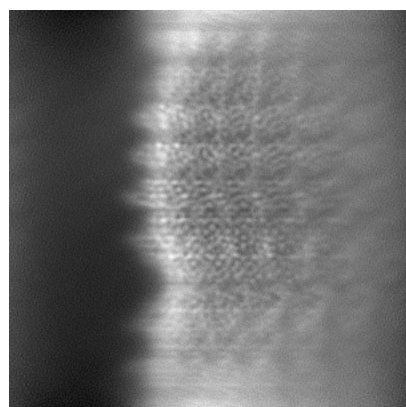


Y

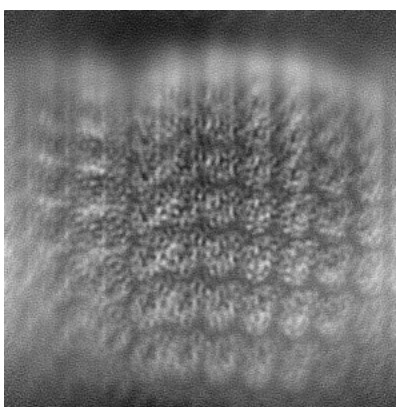


Z

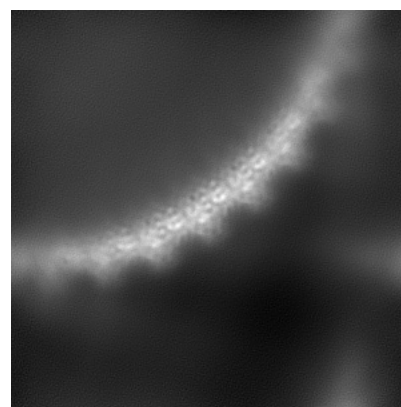
6.1.2 Raw map



X



Y

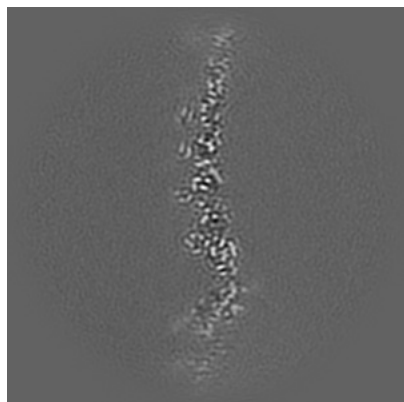


Z

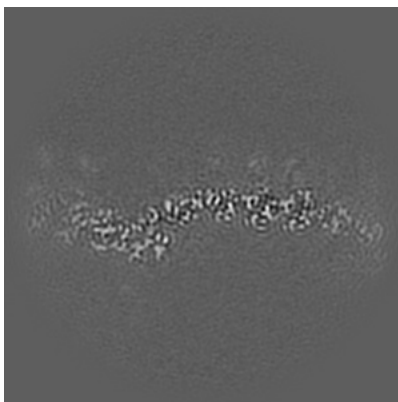
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

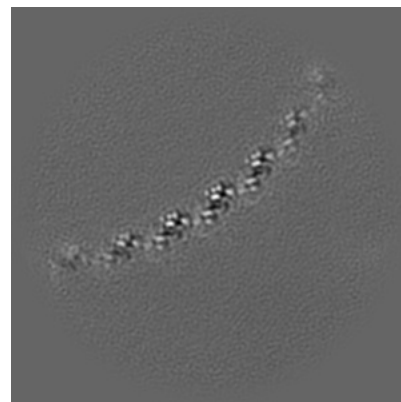
6.2.1 Primary map



X Index: 150

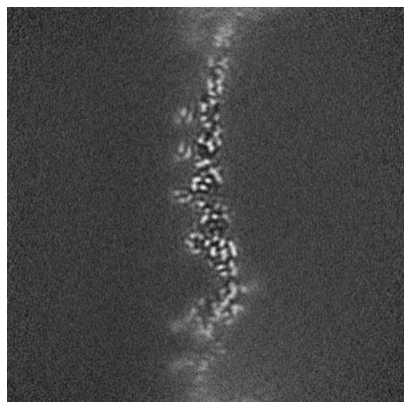


Y Index: 150

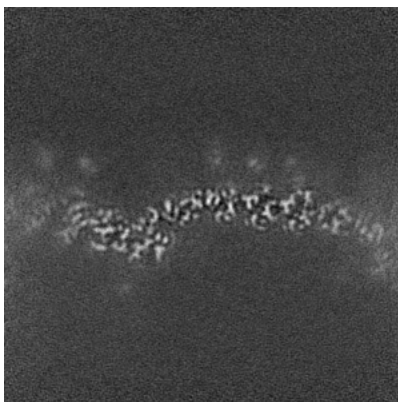


Z Index: 150

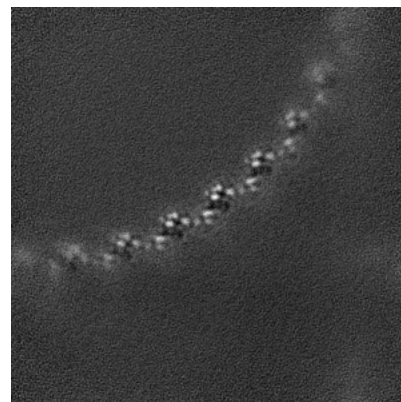
6.2.2 Raw map



X Index: 150



Y Index: 150

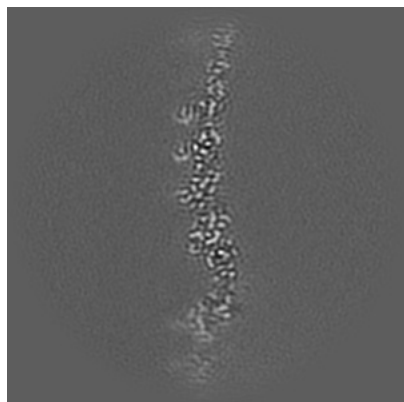


Z Index: 150

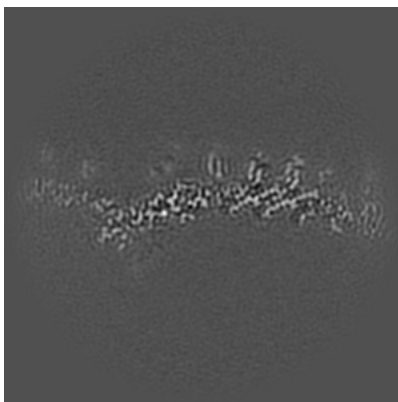
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

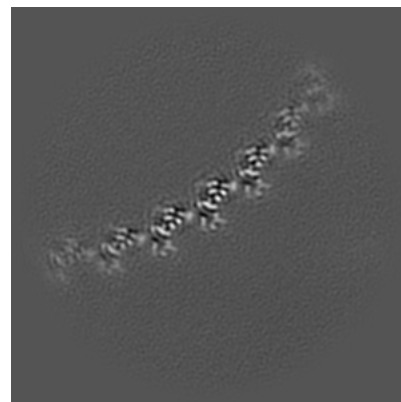
6.3.1 Primary map



X Index: 148

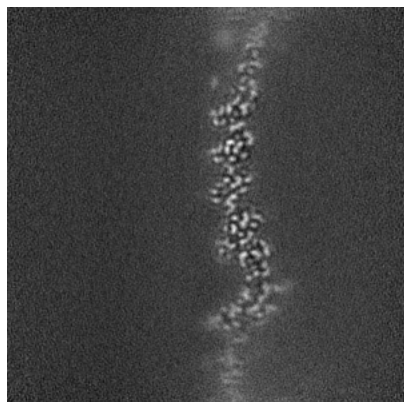


Y Index: 157

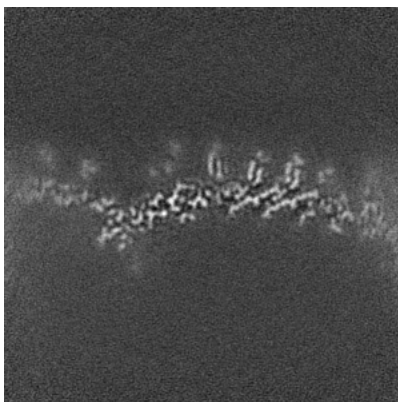


Z Index: 123

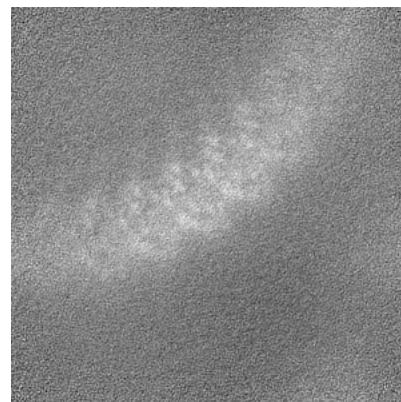
6.3.2 Raw map



X Index: 178



Y Index: 157

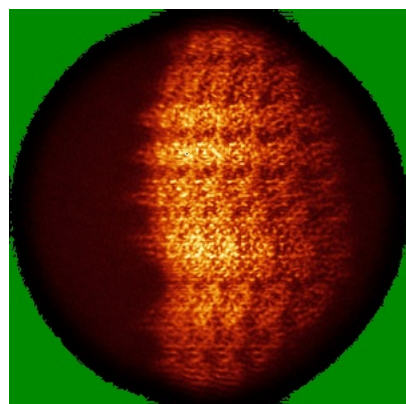


Z Index: 0

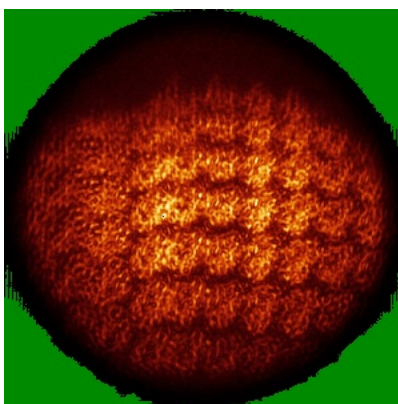
The images above show the largest variance slices of the map in three orthogonal directions.

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

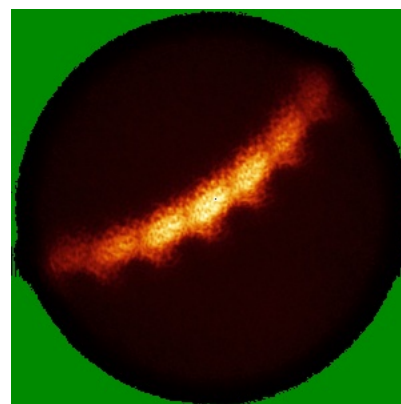
6.4.1 Primary map



X

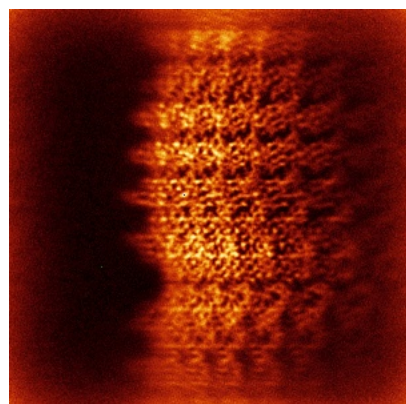


Y

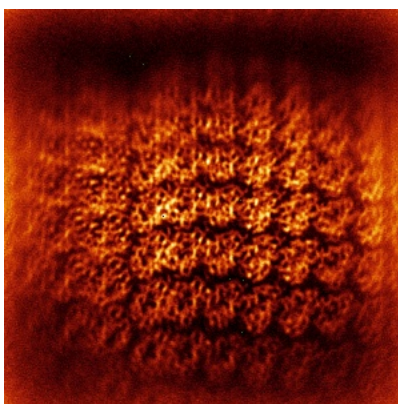


Z

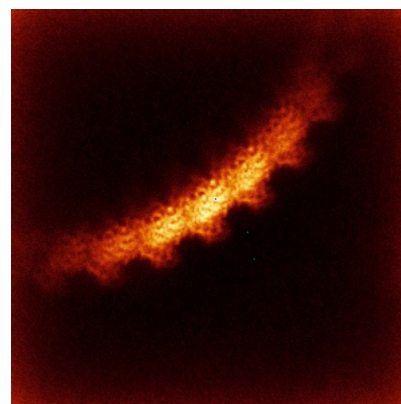
6.4.2 Raw map



X



Y

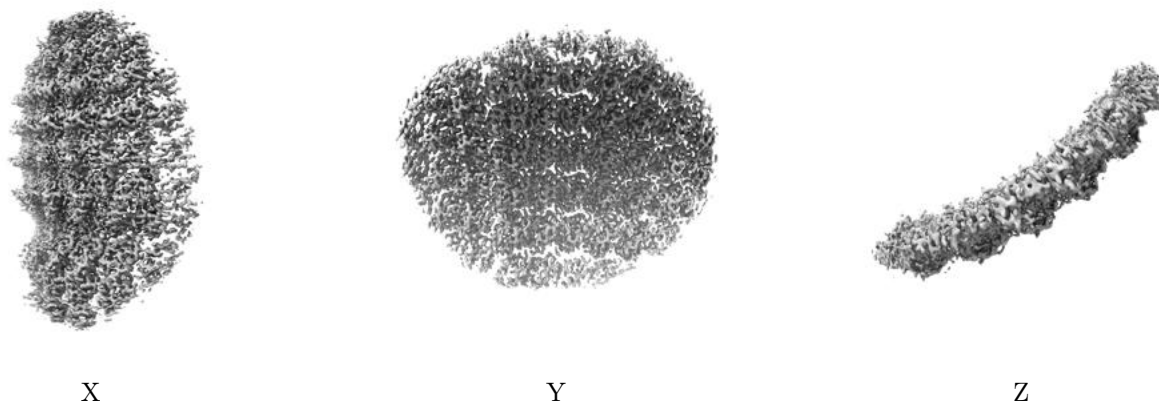


Z

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.

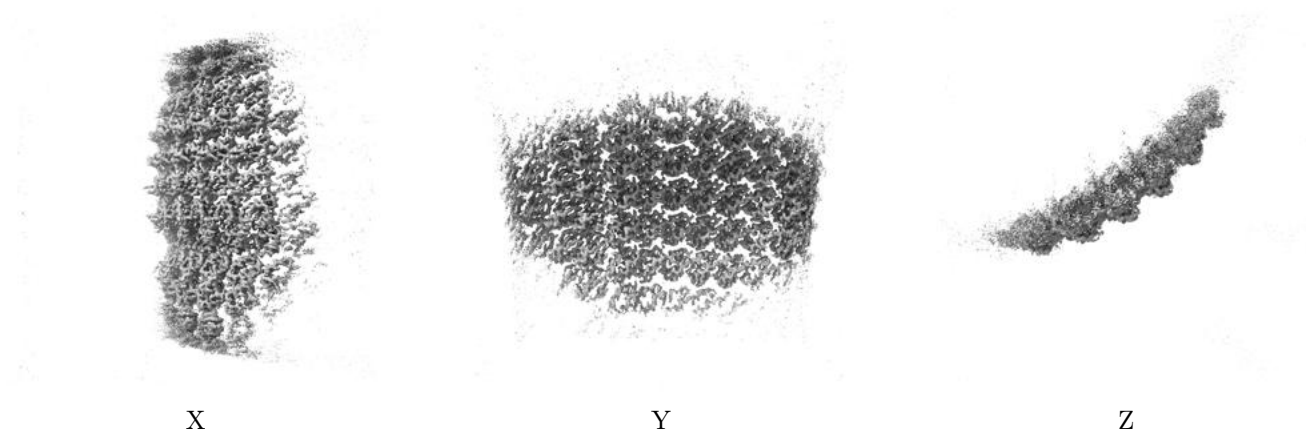
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0476. 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.

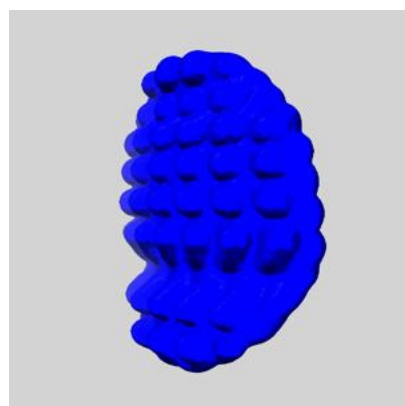
6.6 Mask visualisation [i](#)

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

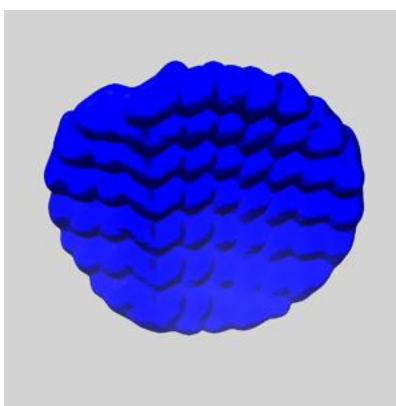
A mask typically either:

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

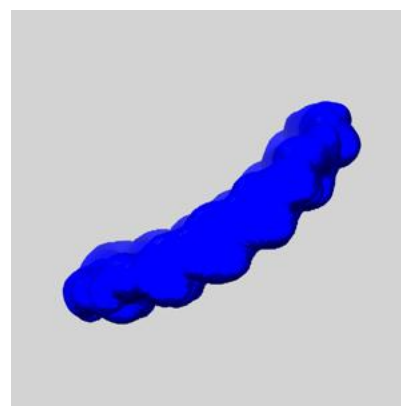
6.6.1 emd_75642_msk_1.map [i](#)



X



Y

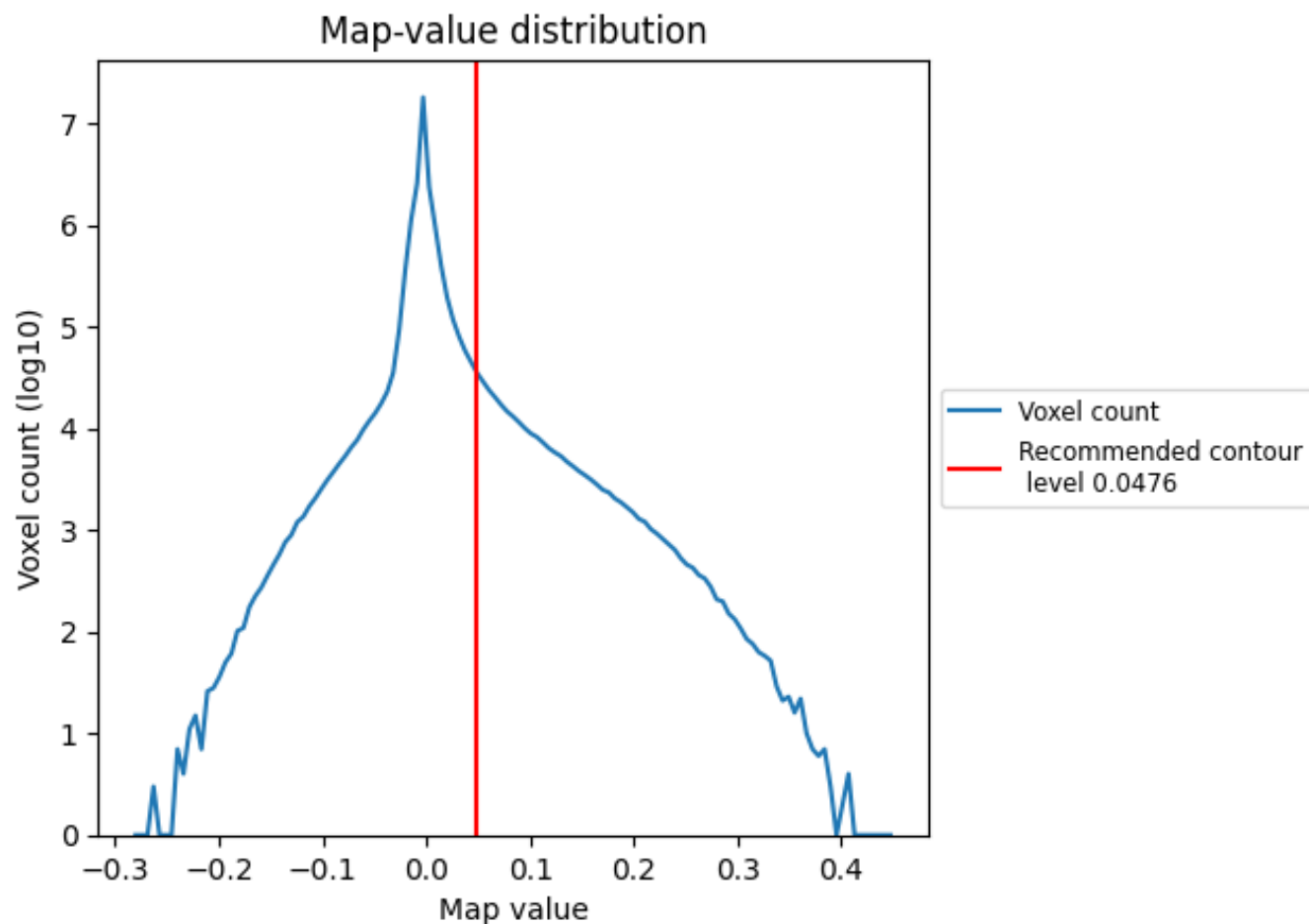


Z

7 Map analysis [i](#)

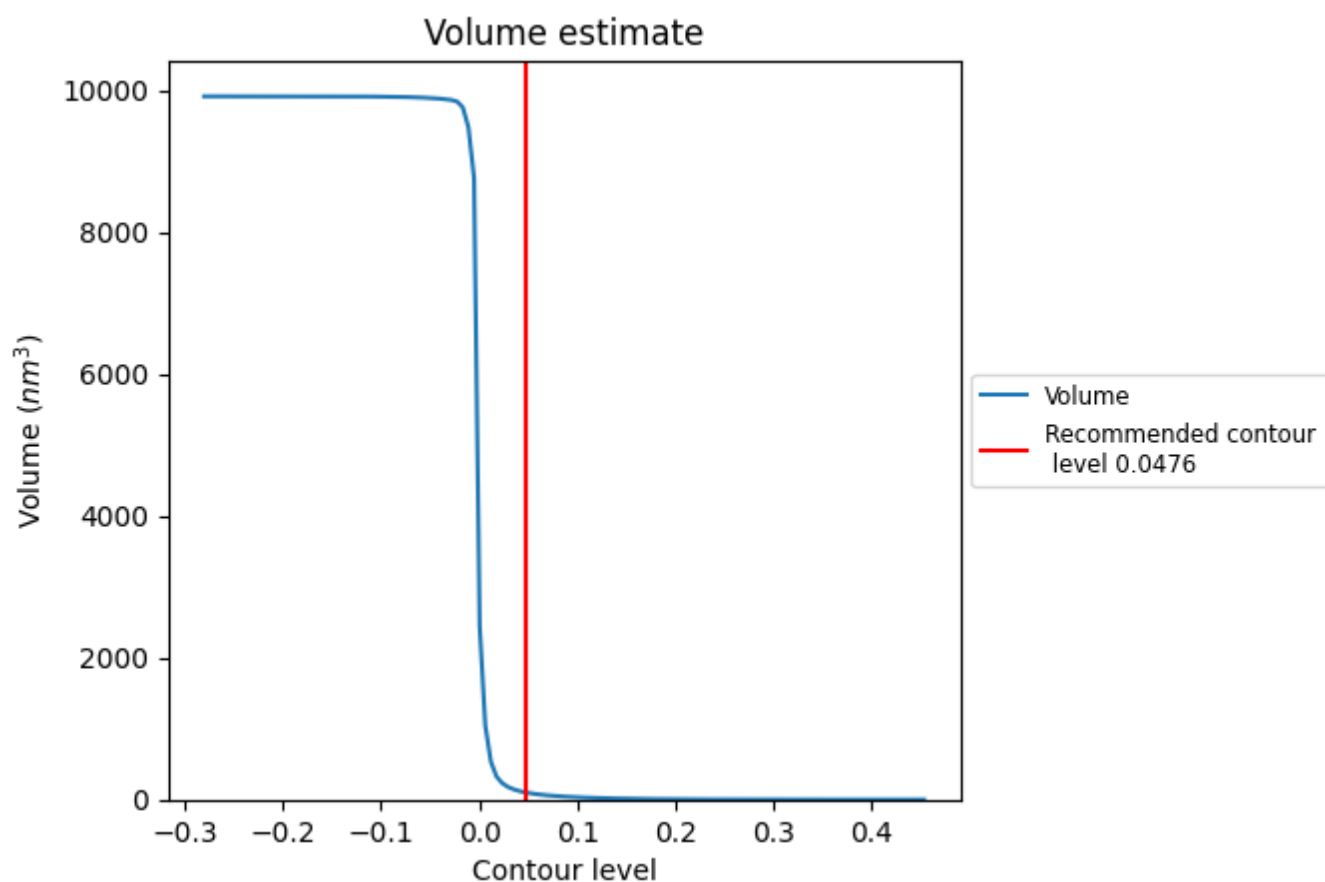
This section contains the results of statistical analysis of the map.

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.

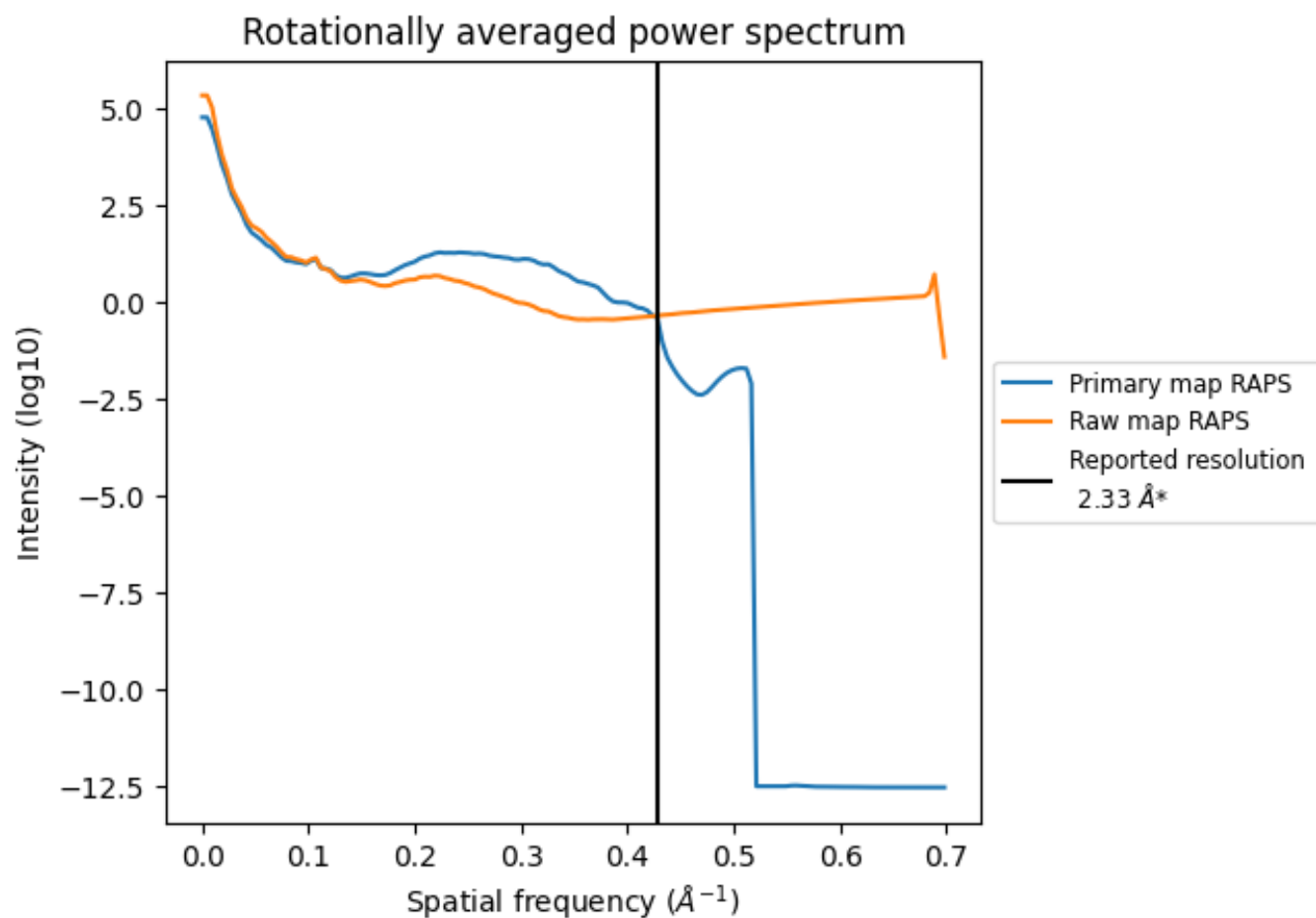
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 99 nm³; this corresponds to an approximate mass of 90 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 ⓘ

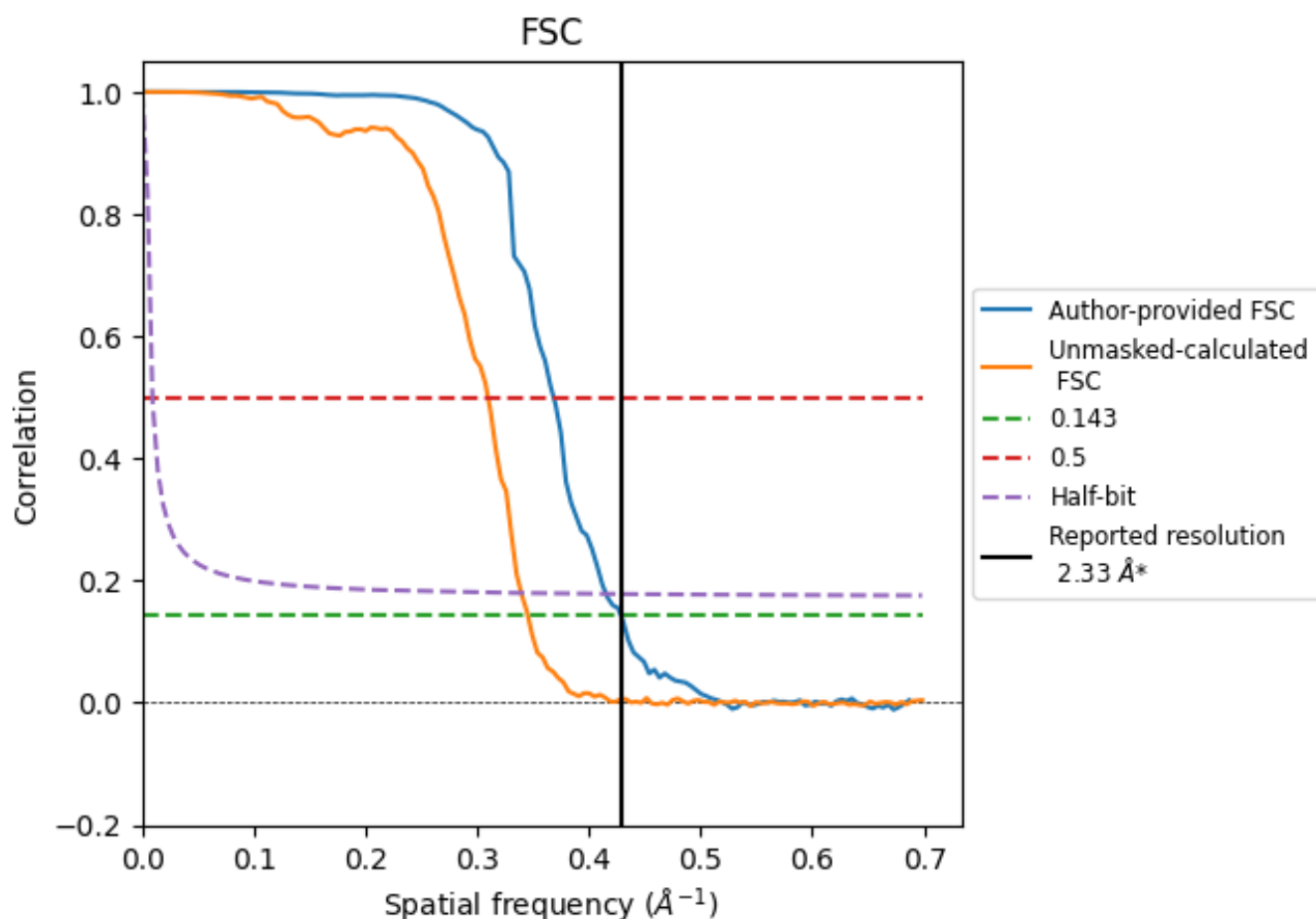


*Reported resolution corresponds to spatial frequency of 0.429 Å⁻¹

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 $0.429 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

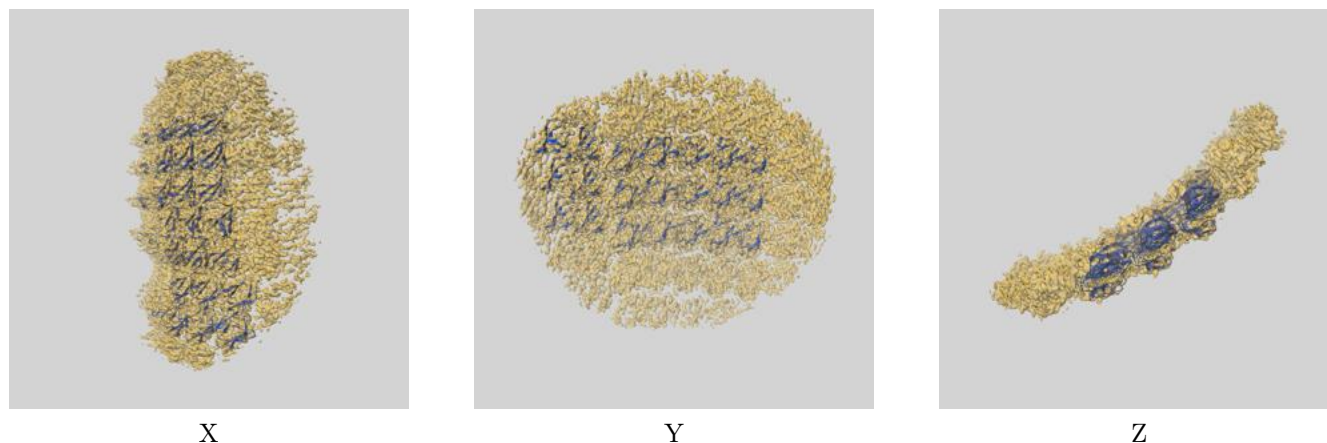
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.33	-	-
Author-provided FSC curve	2.33	2.72	2.41
Unmasked-calculated*	2.90	3.23	2.95

*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 2.90 differs from the reported value 2.33 by more than 10 %

9 Map-model fit [i](#)

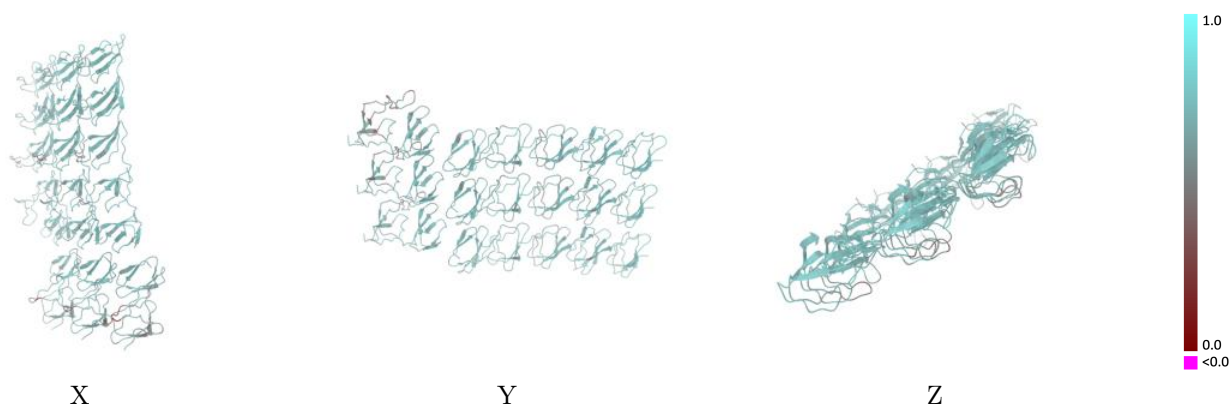
This section contains information regarding the fit between EMDB map EMD-75642 and PDB model 11DV. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



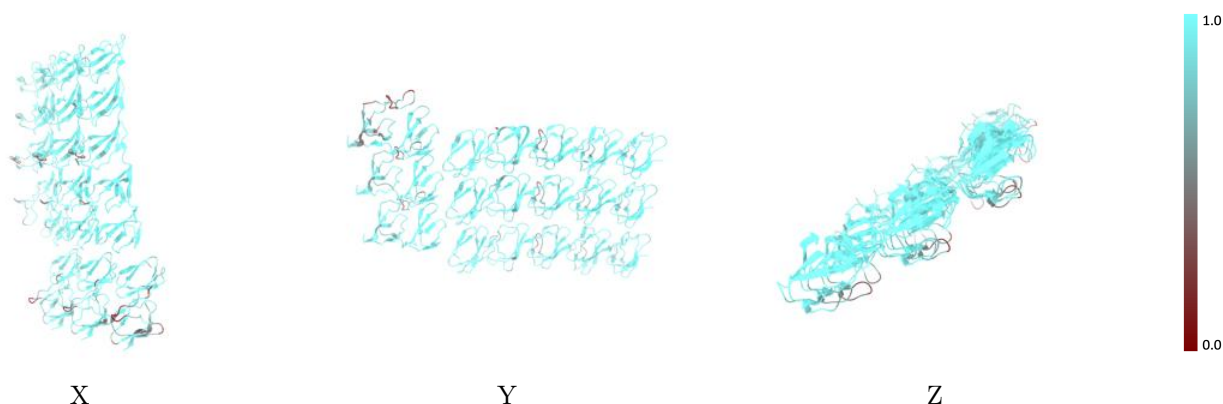
The images above show the 3D surface view of the map at the recommended contour level 0.0476 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



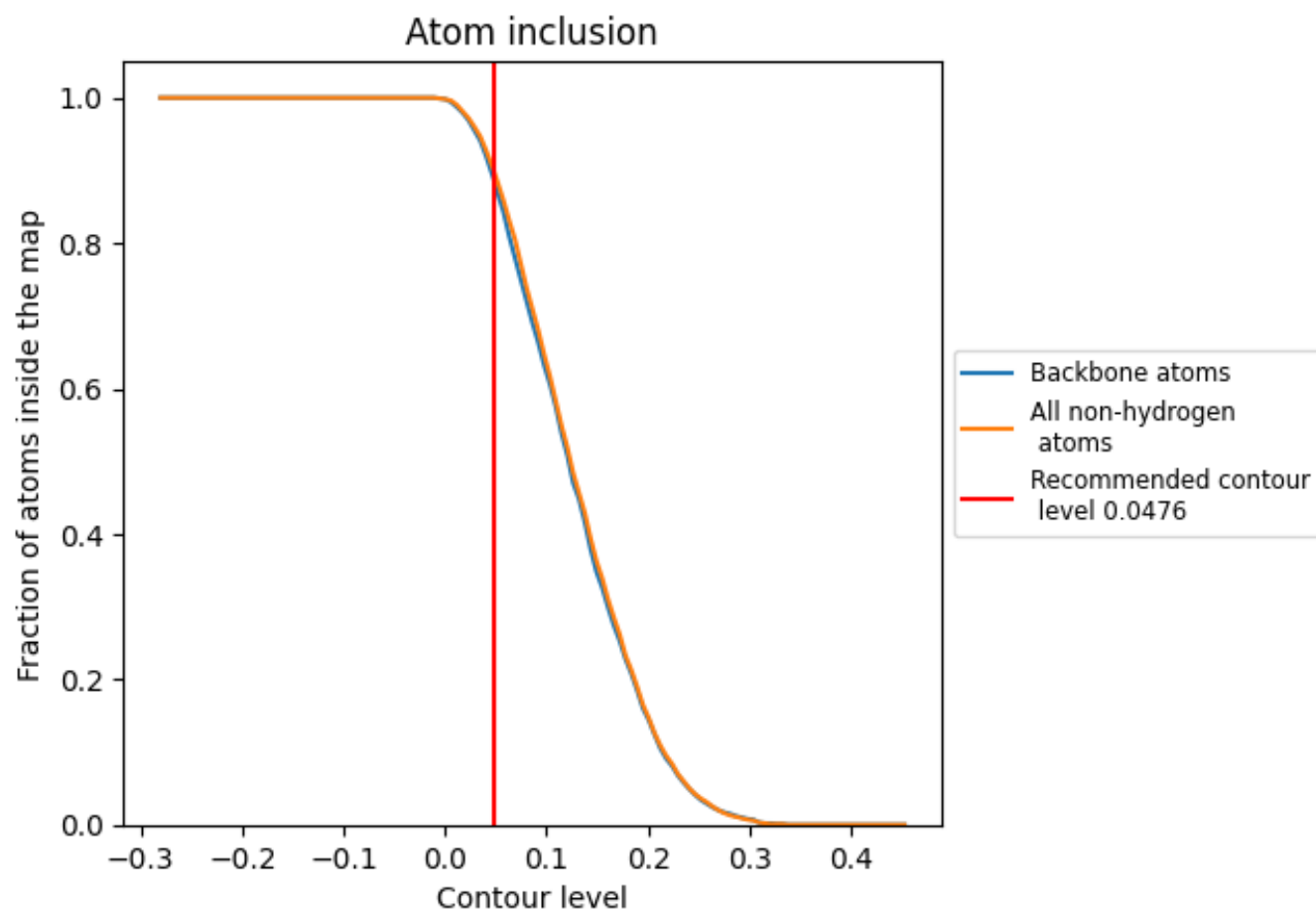
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0476).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0476) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9020	0.6380
A	0.9290	0.6460
B	0.9410	0.6520
C	0.9290	0.6460
D	0.8980	0.6310
E	0.8990	0.6250
F	0.7750	0.5900

1.0

0.0

<0.0