



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 12:41 AM UTC

PDB ID : 9PM6 / pdb_00009pm6
EMDB ID : EMD-71728
Title : Cryo-EM structure of modified Zika virus E protein dimer complexed with a neutralizing antibody OZ-D4 Fab
Authors : Galkin, A.; Pozharski, E.; Li, Y.
Deposited on : 2025-07-16
Resolution : 3.45 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

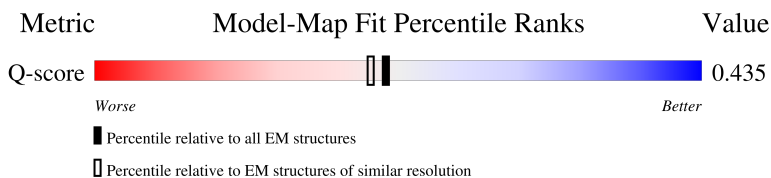
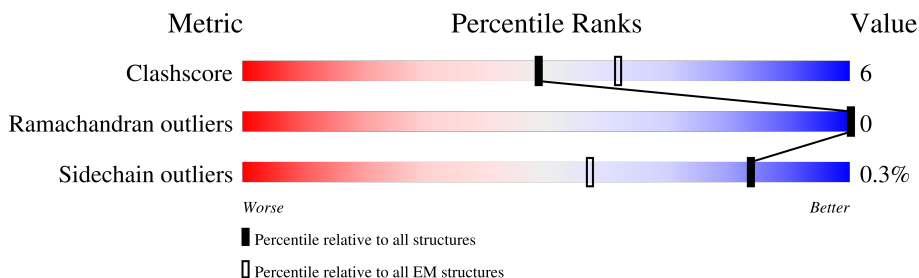
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.45 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	13836 (2.95 - 3.95)

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	434	
1	B	434	
2	C	227	
2	H	227	

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Mol	Chain	Length	Quality of chain
3	D	216	42%8%50%
3	L	216	40%10%50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9162 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 Envelope protein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	378	Total	C	N	O	S	0	0
			2906	1819	508	554	25		
1	B	378	Total	C	N	O	S	0	0
			2906	1819	508	554	25		

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	ARG	-	expression tag	UNP A0A1D6XWI9
A	-18	SER	-	expression tag	UNP A0A1D6XWI9
A	-17	GLY	-	expression tag	UNP A0A1D6XWI9
A	-16	SER	-	expression tag	UNP A0A1D6XWI9
A	-15	GLY	-	expression tag	UNP A0A1D6XWI9
A	-14	GLU	-	expression tag	UNP A0A1D6XWI9
A	-13	GLN	-	expression tag	UNP A0A1D6XWI9
A	-12	LYS	-	expression tag	UNP A0A1D6XWI9
A	-11	LEU	-	expression tag	UNP A0A1D6XWI9
A	-10	ILE	-	expression tag	UNP A0A1D6XWI9
A	-9	SER	-	expression tag	UNP A0A1D6XWI9
A	-8	GLU	-	expression tag	UNP A0A1D6XWI9
A	-7	GLU	-	expression tag	UNP A0A1D6XWI9
A	-6	ASP	-	expression tag	UNP A0A1D6XWI9
A	-5	LEU	-	expression tag	UNP A0A1D6XWI9
A	-4	GLY	-	expression tag	UNP A0A1D6XWI9
A	-3	GLY	-	expression tag	UNP A0A1D6XWI9
A	-2	GLY	-	expression tag	UNP A0A1D6XWI9
A	-1	GLY	-	expression tag	UNP A0A1D6XWI9
A	264	CYS	ALA	conflict	UNP A0A1D6XWI9
A	406	GLY	-	expression tag	UNP A0A1D6XWI9
A	407	THR	-	expression tag	UNP A0A1D6XWI9
A	408	GLY	-	expression tag	UNP A0A1D6XWI9
A	409	HIS	-	expression tag	UNP A0A1D6XWI9
A	410	HIS	-	expression tag	UNP A0A1D6XWI9
A	411	HIS	-	expression tag	UNP A0A1D6XWI9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	412	HIS	-	expression tag	UNP A0A1D6XWI9
A	413	HIS	-	expression tag	UNP A0A1D6XWI9
A	414	HIS	-	expression tag	UNP A0A1D6XWI9
B	-19	ARG	-	expression tag	UNP A0A1D6XWI9
B	-18	SER	-	expression tag	UNP A0A1D6XWI9
B	-17	GLY	-	expression tag	UNP A0A1D6XWI9
B	-16	SER	-	expression tag	UNP A0A1D6XWI9
B	-15	GLY	-	expression tag	UNP A0A1D6XWI9
B	-14	GLU	-	expression tag	UNP A0A1D6XWI9
B	-13	GLN	-	expression tag	UNP A0A1D6XWI9
B	-12	LYS	-	expression tag	UNP A0A1D6XWI9
B	-11	LEU	-	expression tag	UNP A0A1D6XWI9
B	-10	ILE	-	expression tag	UNP A0A1D6XWI9
B	-9	SER	-	expression tag	UNP A0A1D6XWI9
B	-8	GLU	-	expression tag	UNP A0A1D6XWI9
B	-7	GLU	-	expression tag	UNP A0A1D6XWI9
B	-6	ASP	-	expression tag	UNP A0A1D6XWI9
B	-5	LEU	-	expression tag	UNP A0A1D6XWI9
B	-4	GLY	-	expression tag	UNP A0A1D6XWI9
B	-3	GLY	-	expression tag	UNP A0A1D6XWI9
B	-2	GLY	-	expression tag	UNP A0A1D6XWI9
B	-1	GLY	-	expression tag	UNP A0A1D6XWI9
B	264	CYS	ALA	conflict	UNP A0A1D6XWI9
B	406	GLY	-	expression tag	UNP A0A1D6XWI9
B	407	THR	-	expression tag	UNP A0A1D6XWI9
B	408	GLY	-	expression tag	UNP A0A1D6XWI9
B	409	HIS	-	expression tag	UNP A0A1D6XWI9
B	410	HIS	-	expression tag	UNP A0A1D6XWI9
B	411	HIS	-	expression tag	UNP A0A1D6XWI9
B	412	HIS	-	expression tag	UNP A0A1D6XWI9
B	413	HIS	-	expression tag	UNP A0A1D6XWI9
B	414	HIS	-	expression tag	UNP A0A1D6XWI9

- Molecule 2 is a protein called OZ-D4 Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	116	Total	C	N	O	S	0	0
			904	578	147	177	2		
2	C	116	Total	C	N	O	S	0	0
			904	578	147	177	2		

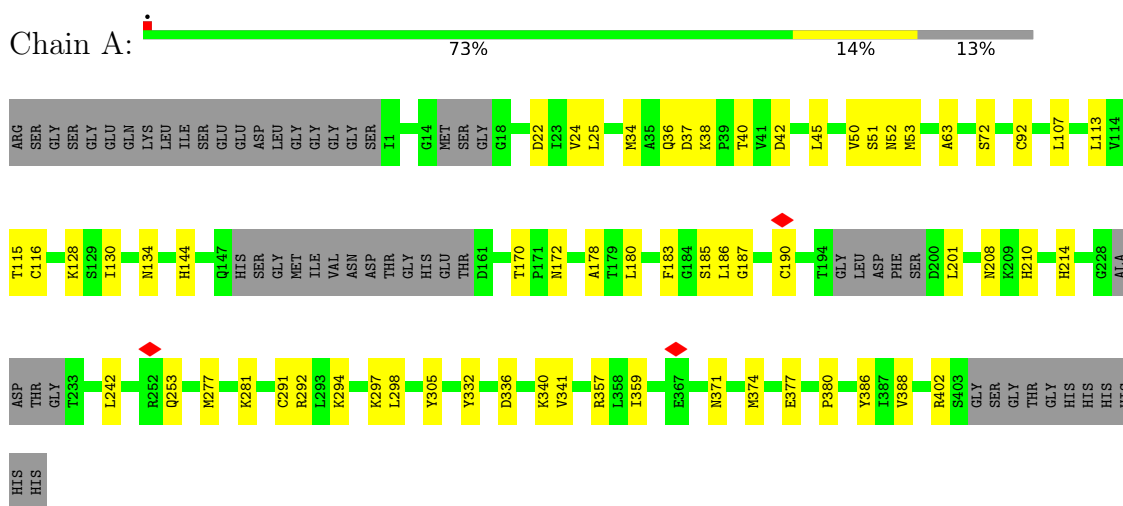
- Molecule 3 is a protein called OZ-D4 Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	108	Total 771	C 473	N 133	O 162	S 3	0	0
3	D	108	Total 771	C 473	N 133	O 162	S 3	0	0

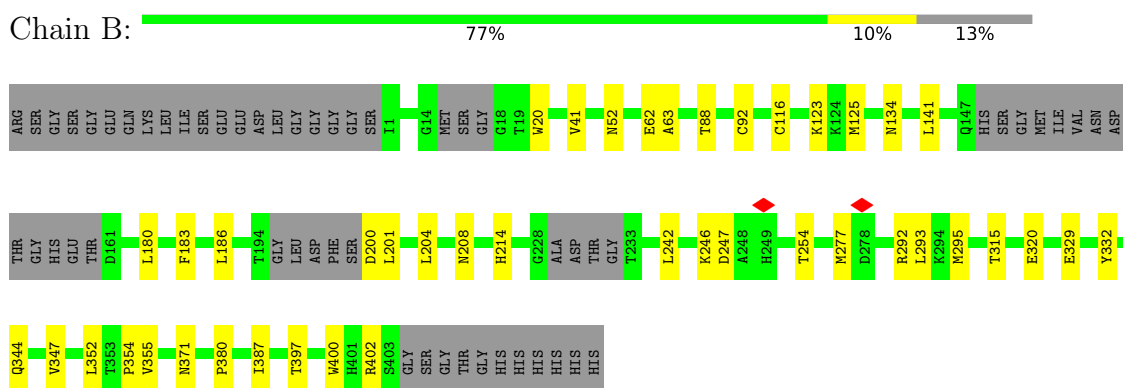
3 Residue-property plots

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.

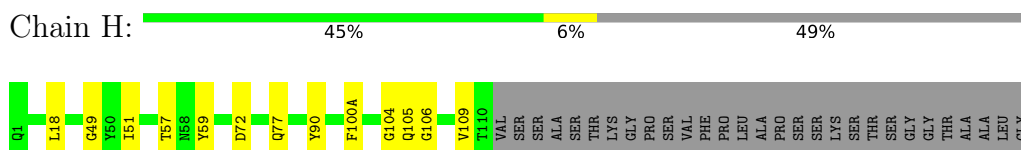
• Molecule 1: Envelope protein E



• Molecule 1: Envelope protein E

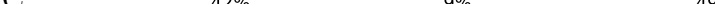


• Molecule 2: OZ-D4 Heavy chain



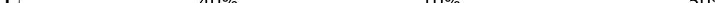
THR	LYS	VAL	ASP	LYS	ARG	VAL	GLU	PRO	TRP	LYS	HIS	HIS	HIS	HIS	HIS	PRO	THR	PHE	GLY	VAL	HIS	THR	TYR	PHE	PRO	ALA	VAL	LEU	GLN	SER	SER	GLY	LEU	TYR	SER	SER	LEU	SER	SER	VAL	VAL	THR	THR	VAL	PRO	SER	SER	SER	GLY	THR	GLN	THR	LEU	CYS	ILE	TYR	THR	THR	THR	THR	THR	ASN	VAL	ASN	HIS	LYS	PRO	PRO	SER	SER	ASN
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- Molecule 2: OZ-D4 Heavy chain

Chain C:  42% 9% 49%

THR	GLN	THR	THR	TYR	ILE	CYS	ASN	VAL	ASN	HIS	LYS	PRO	SER	ASN	THR	LYS	ASP	LYS	HIS	HIS	HIS	HIS	HIS	PRO
THR	GLY	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	GLY	THR
Q1	E6	T17	L18	C22	G44	E46	W47	I48	G49	Y59	D72	K75	F78	L82	V82C	T83	A84	Y90	R94	I102	G106	V109	T110	VAL
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	LYS	ASP	THR	THR	PRO	GLU	PRO	VAL	THR	THR	THR	THR	THR	THR
THR	SER	GLY	THR	ALA	ALA	LEU	GLY	CYS	LEU															

- Molecule 3: OZ-D4 Light chain

Chain L: 

THR	THR	SER	GLN
PRO	S2	SER	S2
GLU	A3	GLU	A3
GLN	L4	GLU	L4
TRP		LEU	
LYS	S18	GLN	S18
SER		ALA	
HIS	121	ASN	121
ARG		LYS	
SER	Y30	ALA	Y30
THR		THR	
SER	S34	LEU	S34
CYS		VAL	
GLN	Q38	CYS	Q38
VAL		LEU	
THR	P44	ILE	P44
HIS	K45	SER	K45
GLU	L46	ASP	L46
GLY		PHE	
SER	P55	THR	P55
THR		PRO	
VAL	N60	GLY	N60
GLU		ALA	
LYS	K66	VAL	K66
THR		THR	
VAL	L73	VAL	L73
ALA	T74	ALA	T74
PRO	I75	TRP	I75
THR		LYS	
GLU	E83	ALA	E83
CYS	A84	ASP	A84
SER	D85	SER	D85
	Y86	SER	Y86
		PRO	
	S89	VAL	S89
		LYS	
	L96	ALA	L96
	Y97	GLY	Y97
		VAL	
	G101	GLU	G101
	T102	THR	T102
	N103	THR	N103
	L104	THR	L104
	T105	PRO	T105
	V106	SER	V106
		LYS	
		GLN	
		GLY	
		GLN	
		SER	
		ASN	
		LYS	
		LYS	
		TVR	
		ALA	
		ALA	
		SER	
		VAL	
		THR	
		THR	
		LEU	
		PHE	
		PRO	
		SER	
		LEU	

- Molecule 3: OZ-D4 Light chain

Chain D: 42% 8% 50%

SER	TYR	SER	CYS	GLN	VAL	THR	ILE	SER	ASP	PHE	TYR	PRO	GLY	ALA	VAL	THR	VAL	ALA	TRP	LYS	ALA	ASP	SER	PRO	VAL	LYS	ALA	GLY	VAL	GLU	THR	THR	THR	PRO	SER	LYS	LEU	GLN	SER	ASN	LYS	ALA	TYR	ALA	SER	VAL	THR	THR	LEU	SER	PRO	THR	PRO	GLU	GLU	LEU	GLN	ALA	ASN	ASP
S2	T24	V27C	S34	W35	Q38	P44	M47	I48	K53	R61	K66	S70	S76	G77	D82	Y86	F87	C88	S89	V105	LEU	GLY	GLN	PRO	LYS	ALA	ALA	PRO	SER	THR	LEU	PHE	PRO	PRO	SER	SER	GLU <td>GLU<td>LEU<td>GLN<td>ASN<td>ASP</td> </td></td></td></td>	GLU <td>LEU<td>GLN<td>ASN<td>ASP</td> </td></td></td>	LEU <td>GLN<td>ASN<td>ASP</td> </td></td>	GLN <td>ASN<td>ASP</td> </td>	ASN <td>ASP</td>	ASP																		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	710140	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.79	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.964	Depositor
Minimum map value	-0.574	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	320.04, 320.04, 320.04	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.889, 0.889, 0.889	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	0.16	0/2964	0.44	0/4010
1	B	0.17	0/2964	0.41	0/4010
2	C	0.17	0/930	0.50	0/1268
2	H	0.23	0/930	0.53	0/1268
3	D	0.16	0/786	0.46	0/1066
3	L	0.15	0/786	0.39	0/1066
All	All	0.17	0/9360	0.45	0/12688

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	2906	0	2853	37	0
1	B	2906	0	2853	28	0
2	C	904	0	870	11	0
2	H	904	0	870	8	0
3	D	771	0	734	10	0
3	L	771	0	734	12	0
All	All	9162	0	8914	104	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 104 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:90:TYR:O	2:C:106:GLY:HA2	1.93	0.67
1:A:52:ASN:O	1:A:134:ASN:ND2	2.29	0.66
1:B:186:LEU:HD23	1:B:295:MET:HE2	1.78	0.64
3:L:83:GLU:HA	3:L:104:LEU:O	1.97	0.64
2:C:22:CYS:HB3	2:C:78:PHE:HB2	1.81	0.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	368/434 (85%)	358 (97%)	10 (3%)	0	100	100
1	B	368/434 (85%)	355 (96%)	13 (4%)	0	100	100
2	C	114/227 (50%)	104 (91%)	10 (9%)	0	100	100
2	H	114/227 (50%)	104 (91%)	10 (9%)	0	100	100
3	D	106/216 (49%)	101 (95%)	5 (5%)	0	100	100
3	L	106/216 (49%)	101 (95%)	5 (5%)	0	100	100
All	All	1176/1754 (67%)	1123 (96%)	53 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	319/360 (89%)	318 (100%)	1 (0%)	86	83
1	B	319/360 (89%)	318 (100%)	1 (0%)	86	83
2	C	101/198 (51%)	101 (100%)	0	100	100
2	H	101/198 (51%)	101 (100%)	0	100	100
3	D	85/178 (48%)	84 (99%)	1 (1%)	63	74
3	L	85/178 (48%)	85 (100%)	0	100	100
All	All	1010/1472 (69%)	1007 (100%)	3 (0%)	84	83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	VAL
1	B	88	THR
3	D	47	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	238	ASN
1	A	253	GLN
1	A	266	HIS
1	B	401	HIS
3	D	39	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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.

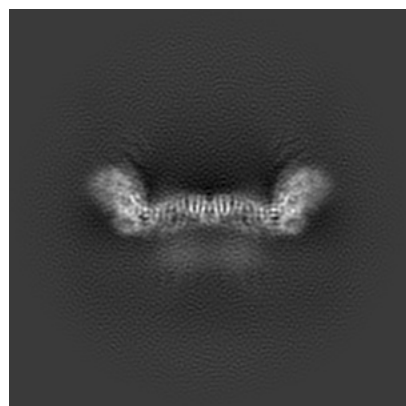
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71728. These allow visual inspection of the internal detail of the map and identification of artifacts.

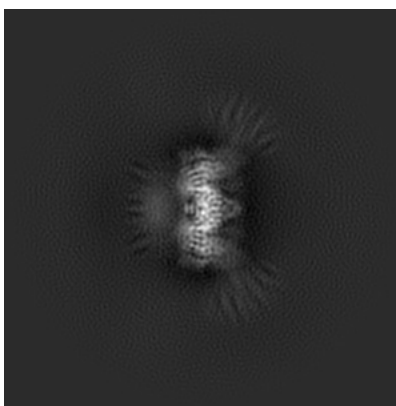
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

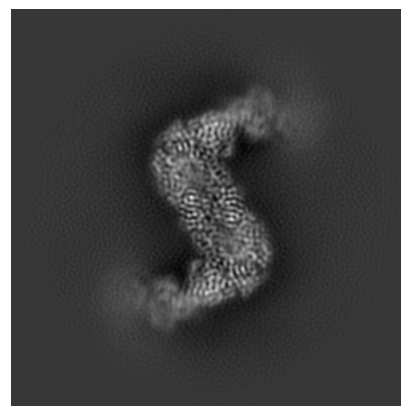
6.1.1 Primary map



X

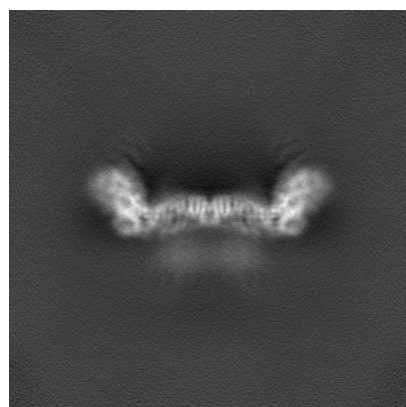


Y

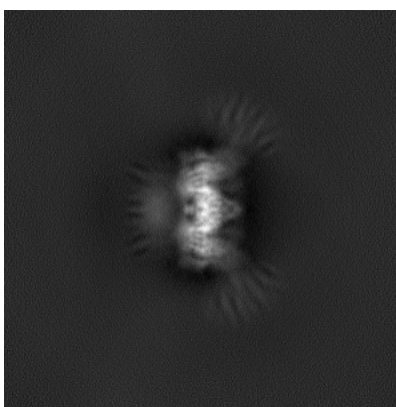


Z

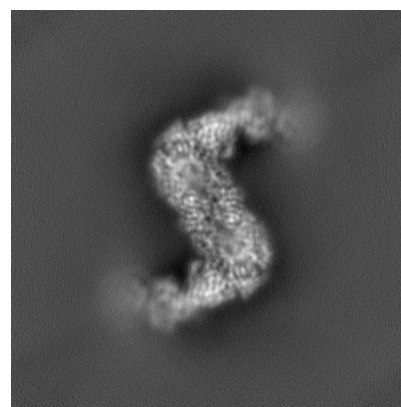
6.1.2 Raw map



X



Y

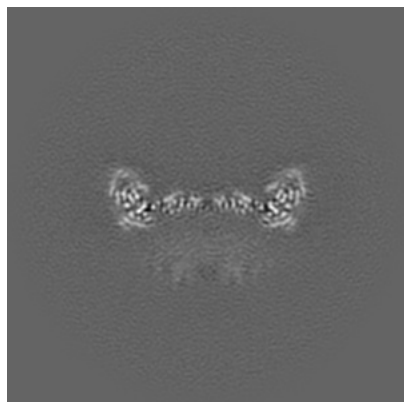


Z

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

6.2 Central slices [i](#)

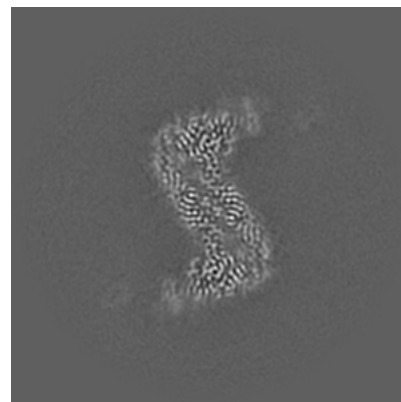
6.2.1 Primary map



X Index: 180

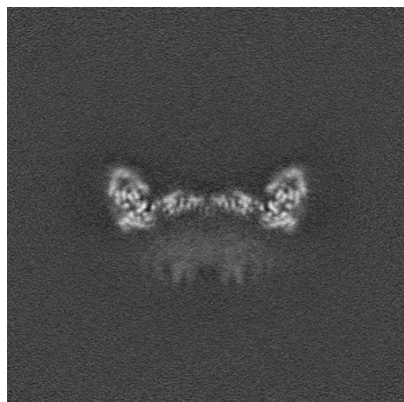


Y Index: 180



Z Index: 180

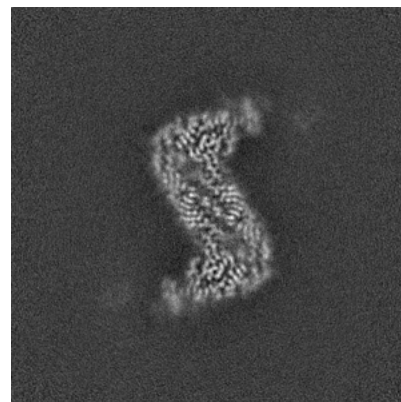
6.2.2 Raw map



X Index: 180



Y Index: 180

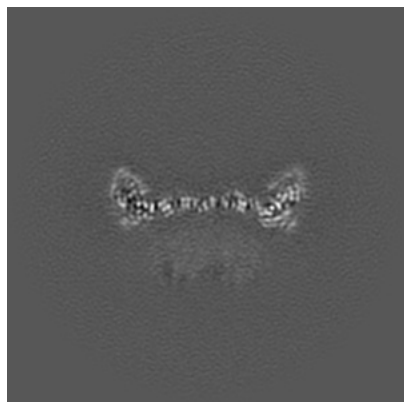


Z Index: 180

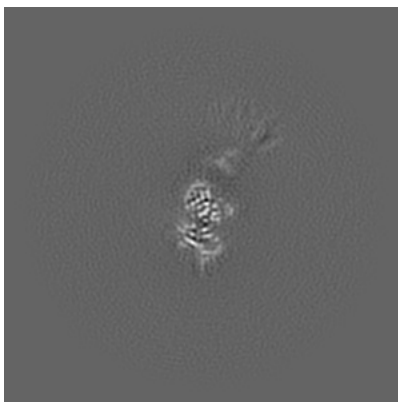
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

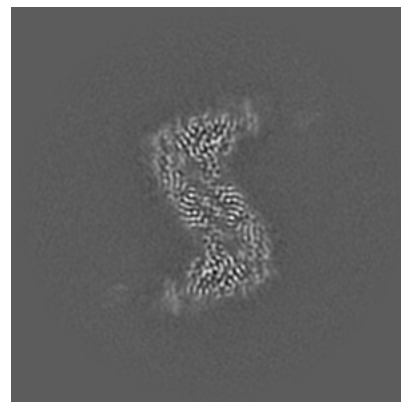
6.3.1 Primary map



X Index: 182

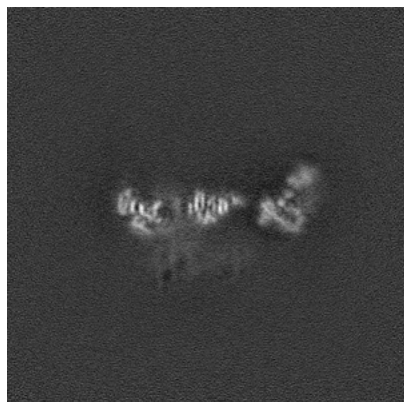


Y Index: 243

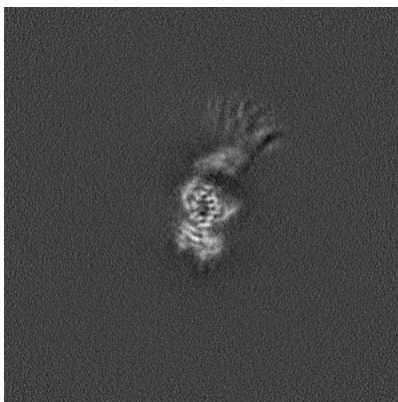


Z Index: 179

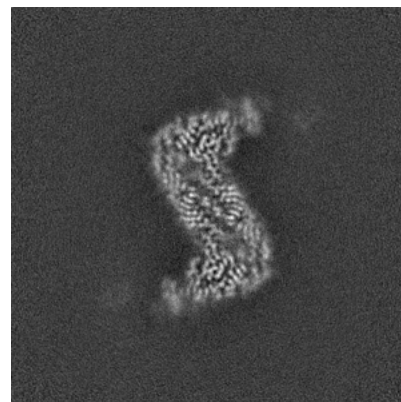
6.3.2 Raw map



X Index: 197



Y Index: 247

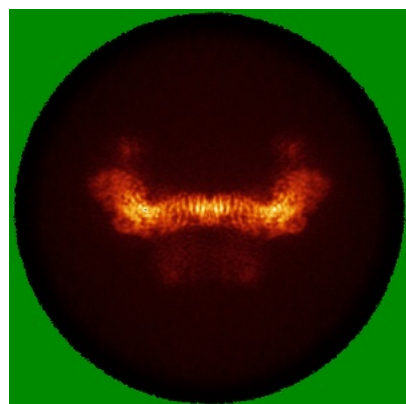


Z Index: 180

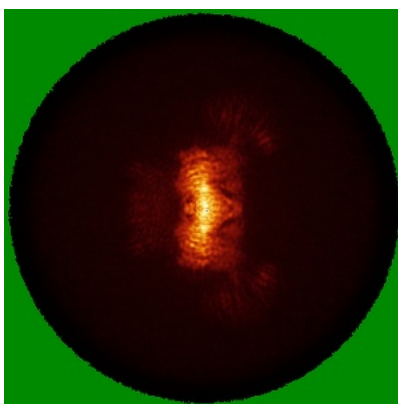
The images above show the largest variance slices of the map in three orthogonal directions.

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

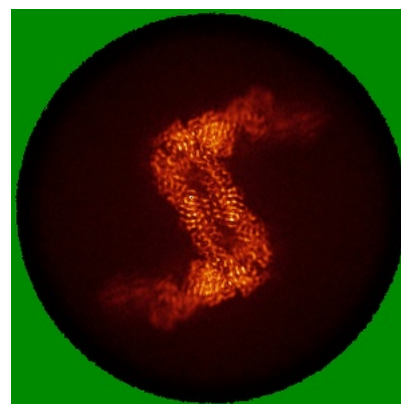
6.4.1 Primary map



X

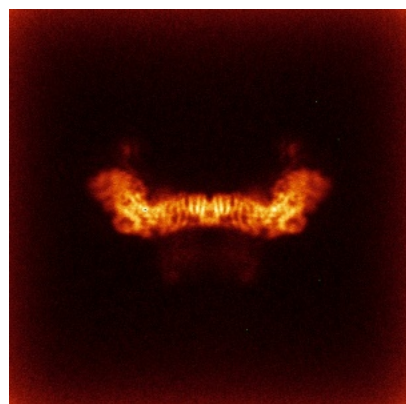


Y

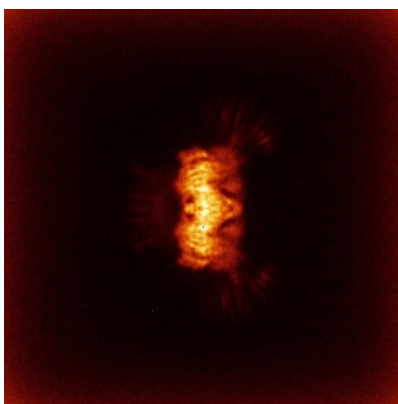


Z

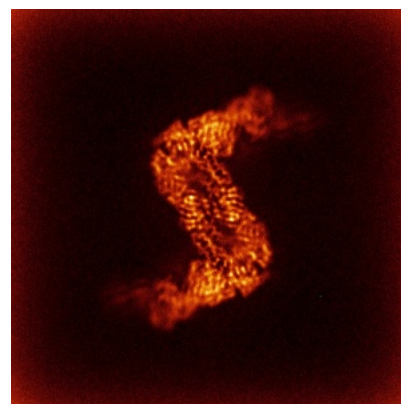
6.4.2 Raw map



X



Y

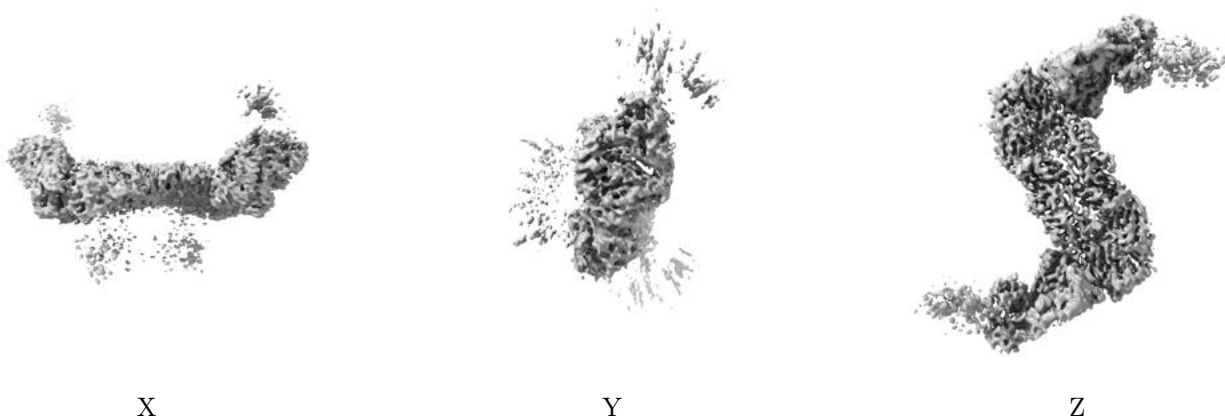


Z

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.

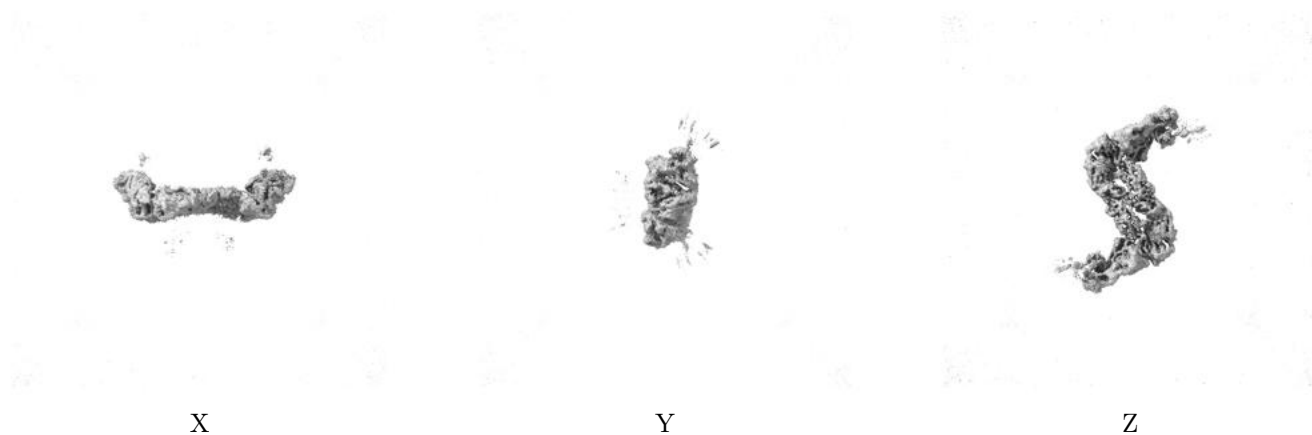
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

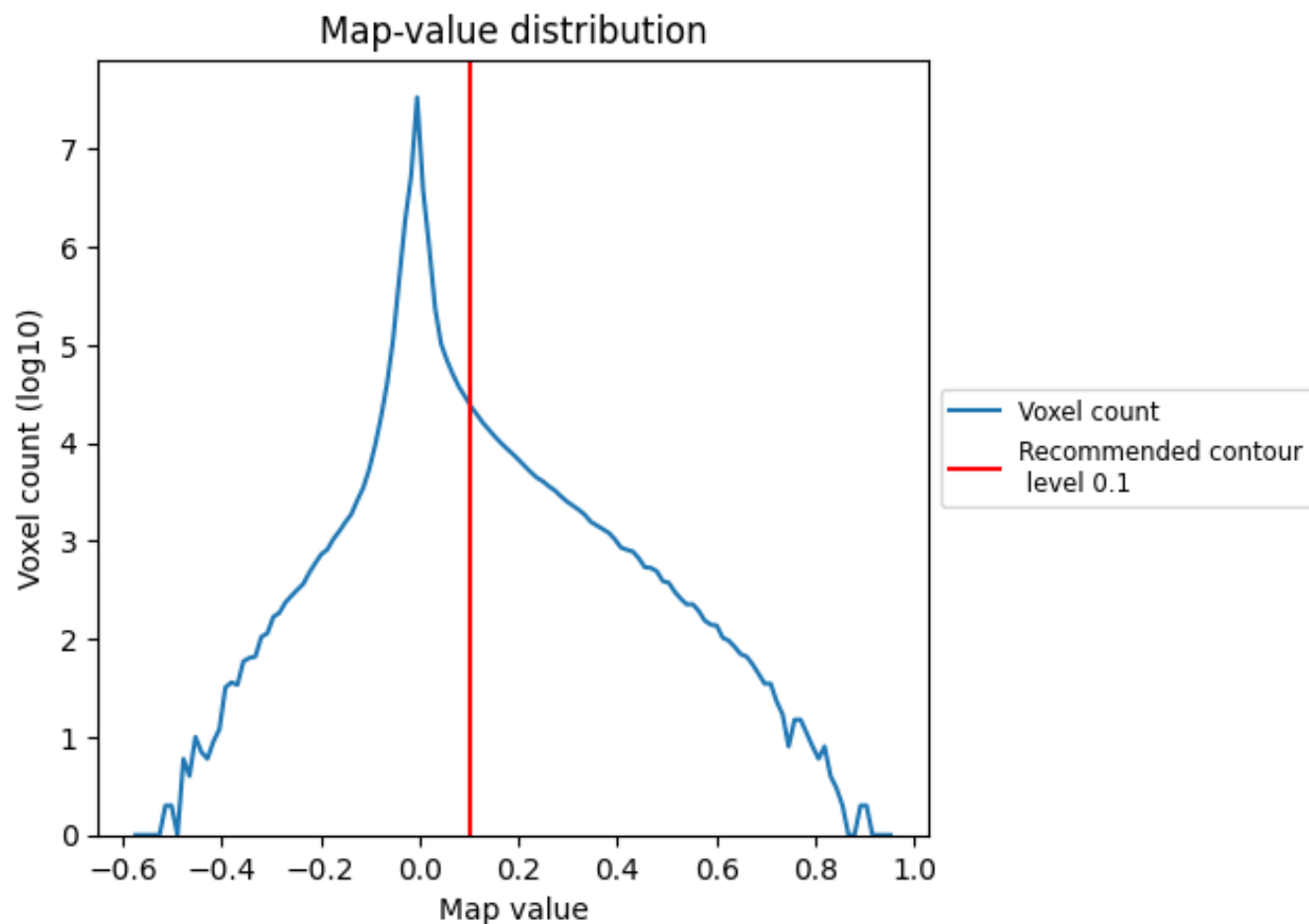
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

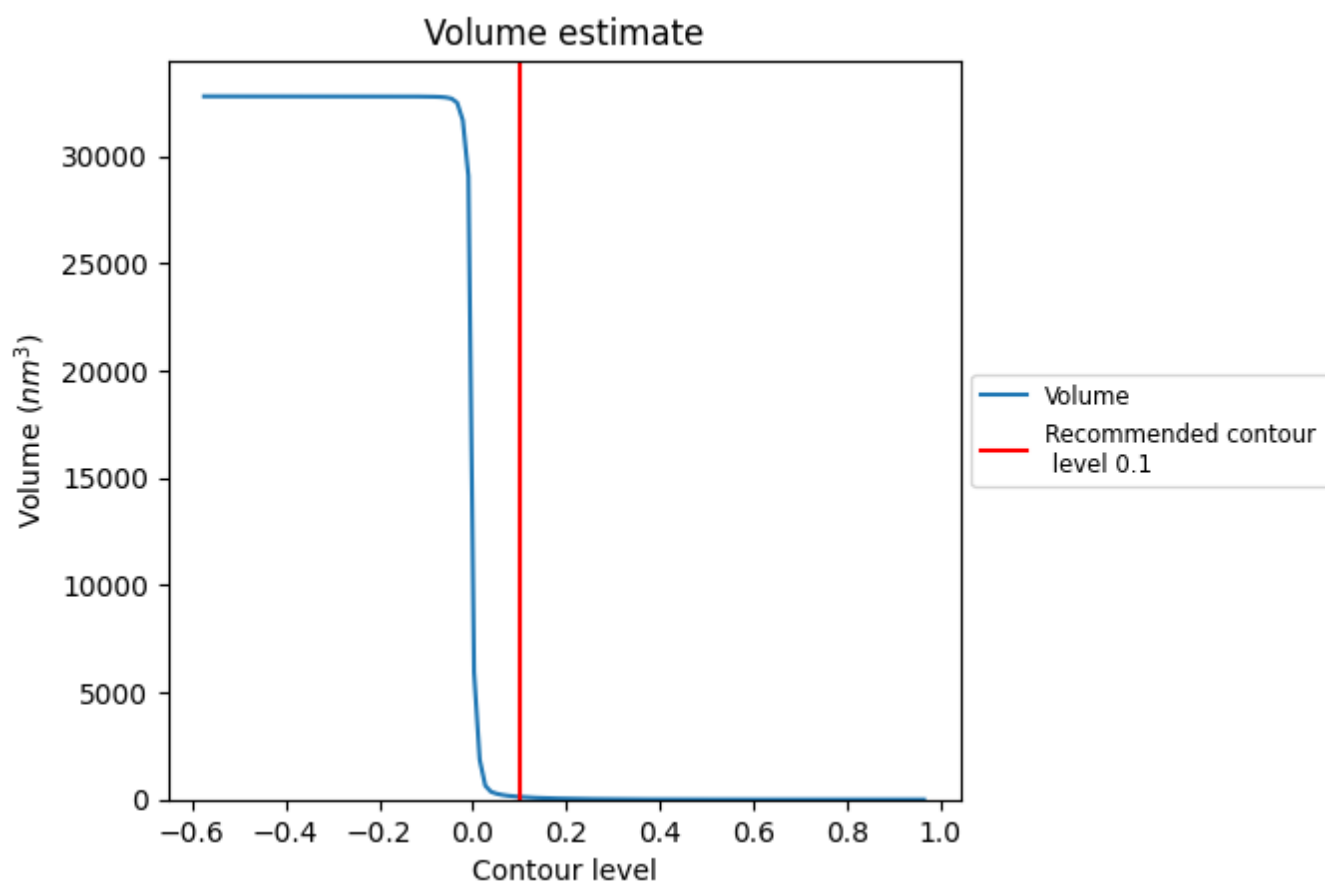
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

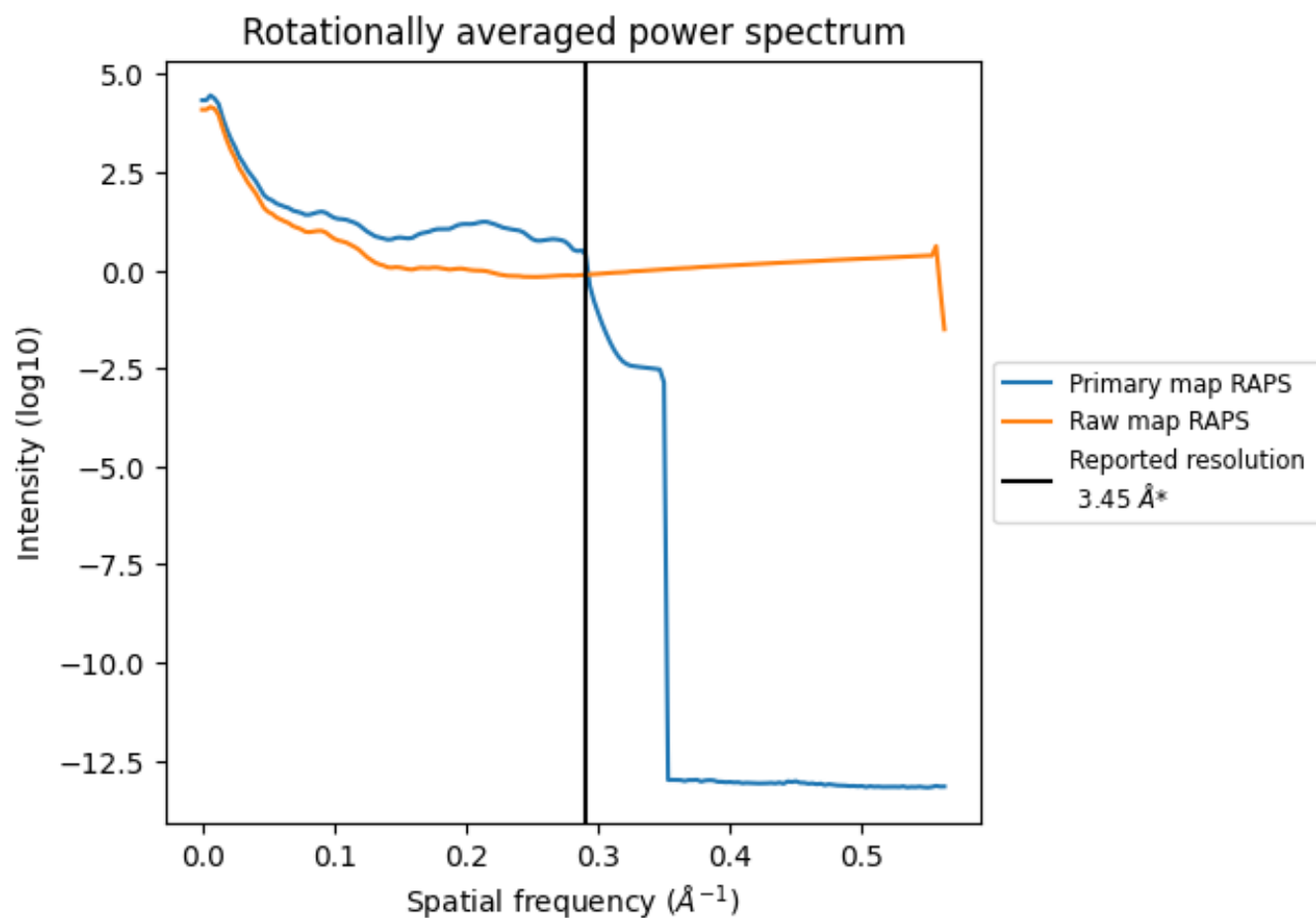
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 125 nm³; this corresponds to an approximate mass of 113 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 [i](#)

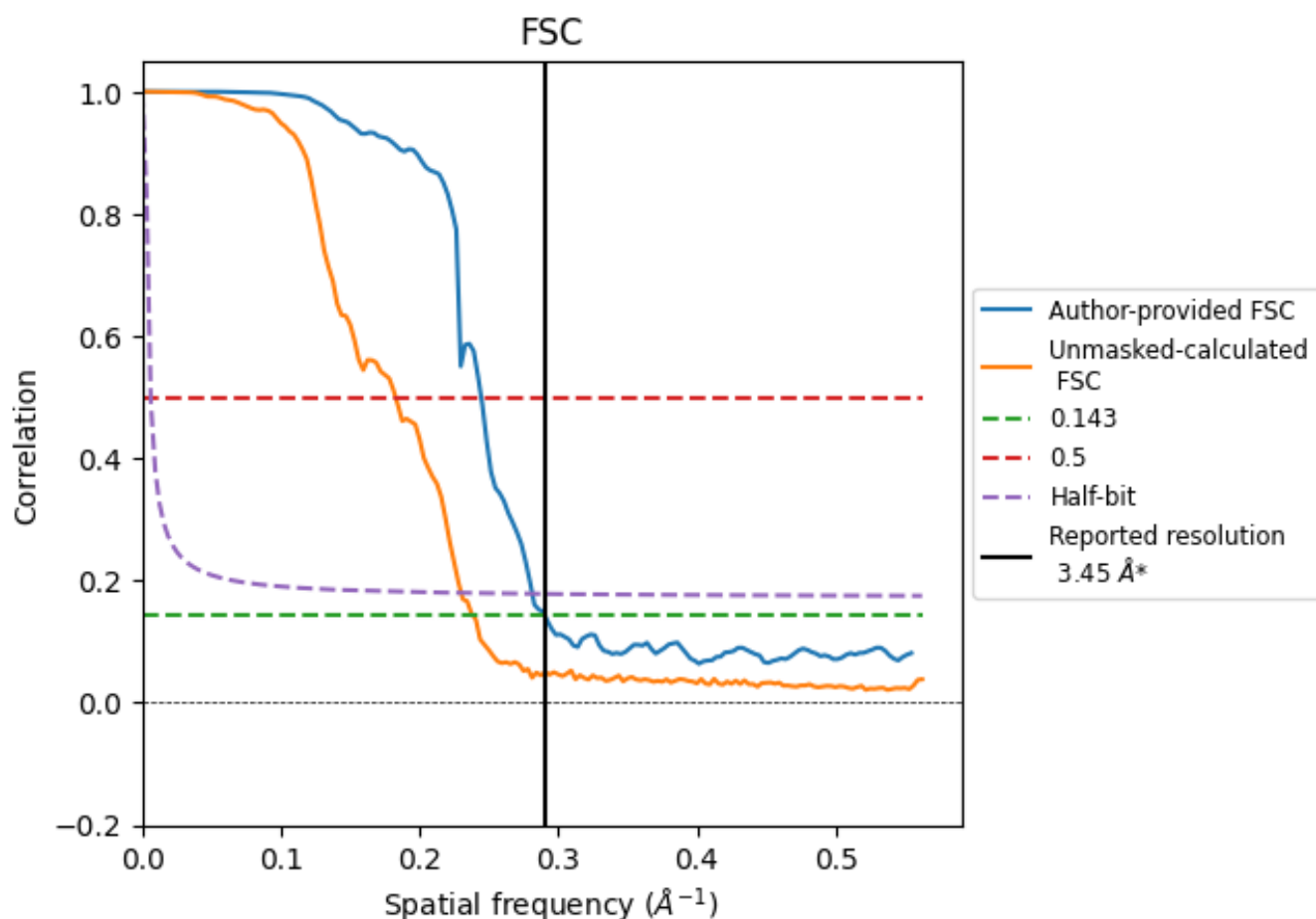


*Reported resolution corresponds to spatial frequency of 0.290 $\text{\AA}^{-1}$

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 $0.290 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

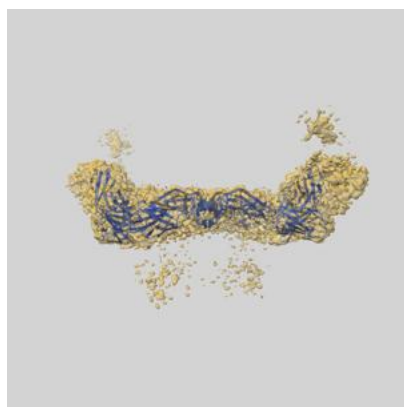
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.45	-	-
Author-provided FSC curve	3.44	4.09	3.55
Unmasked-calculated*	4.20	5.47	4.35

*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 4.20 differs from the reported value 3.45 by more than 10 %

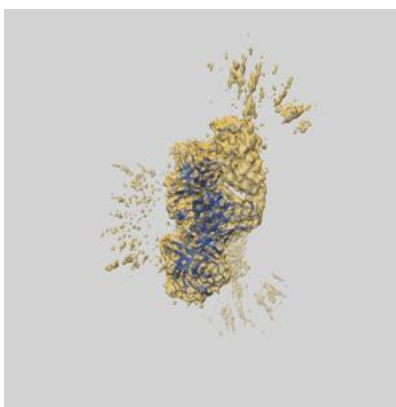
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-71728 and PDB model 9PM6. Per-residue inclusion information can be found in section [3](#) on page [7](#).

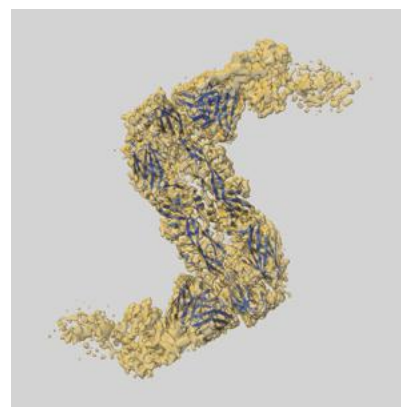
9.1 Map-model overlay [i](#)



X



Y



Z

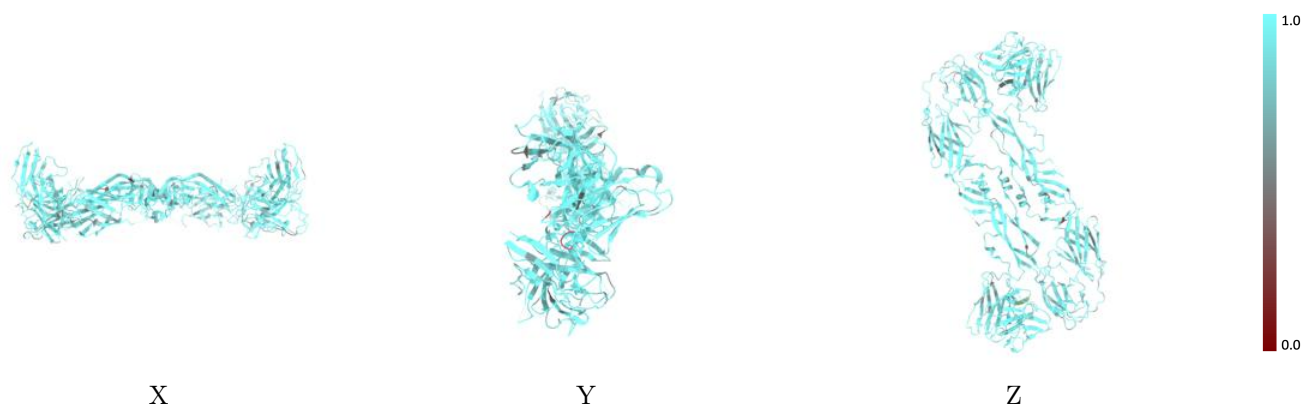
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



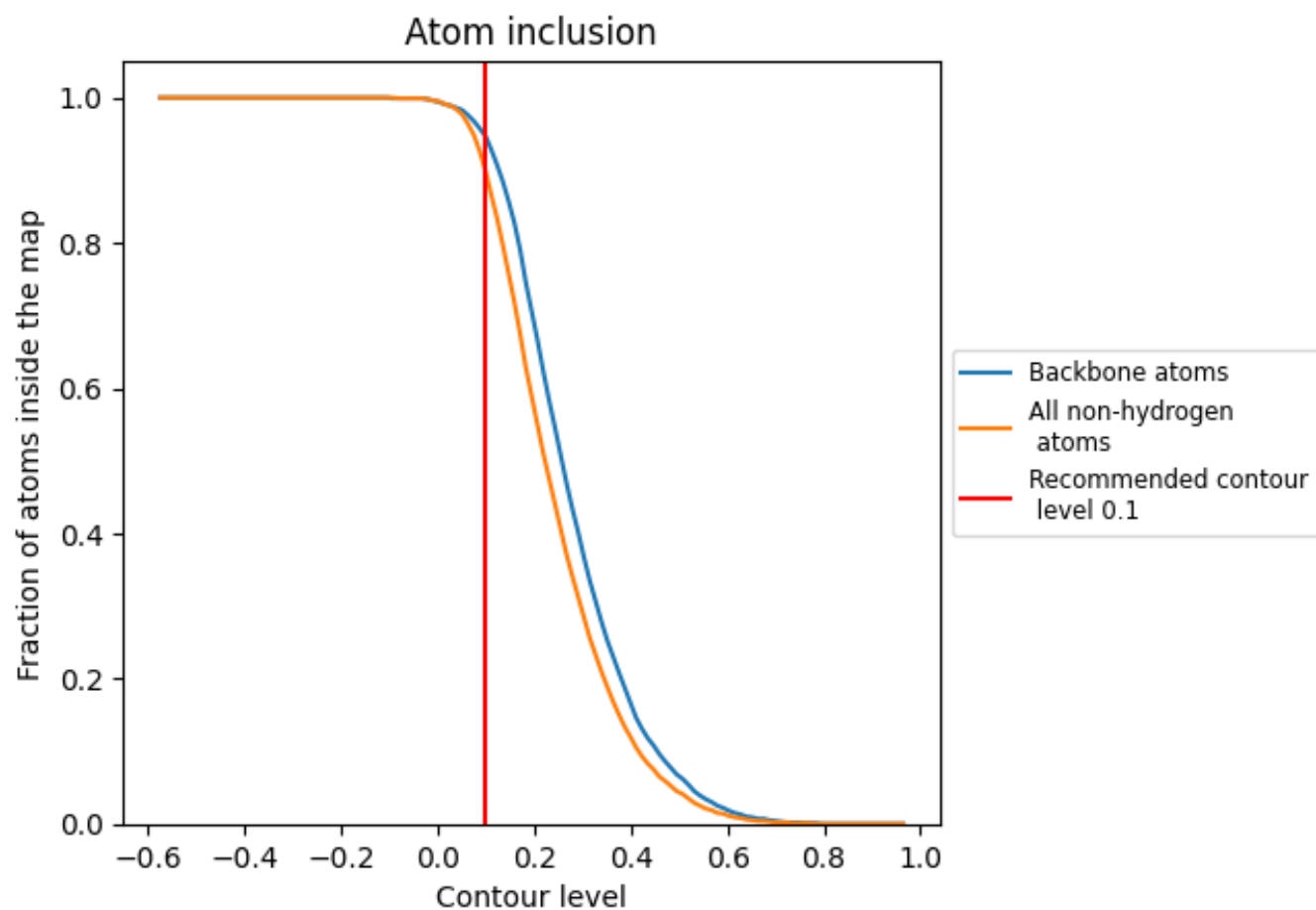
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8970	0.4350
A	0.8920	0.4260
B	0.8840	0.4260
C	0.8900	0.4430
D	0.9360	0.4550
H	0.9060	0.4510
L	0.9190	0.4540

