



wwPDB EM Validation Summary Report ⓘ

Oct 15, 2025 – 01:35 am BST

PDB ID : 9QT9 / pdb_00009qt9
EMDB ID : EMD-53348
Title : Cryo-EM structure of the core of the Arabidopsis thaliana
UBR4/DI19/CALM1 complex
Authors : Grabarczyk, D.B.; Clausen, T.
Deposited on : 2025-04-08
Resolution : 3.90 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

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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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

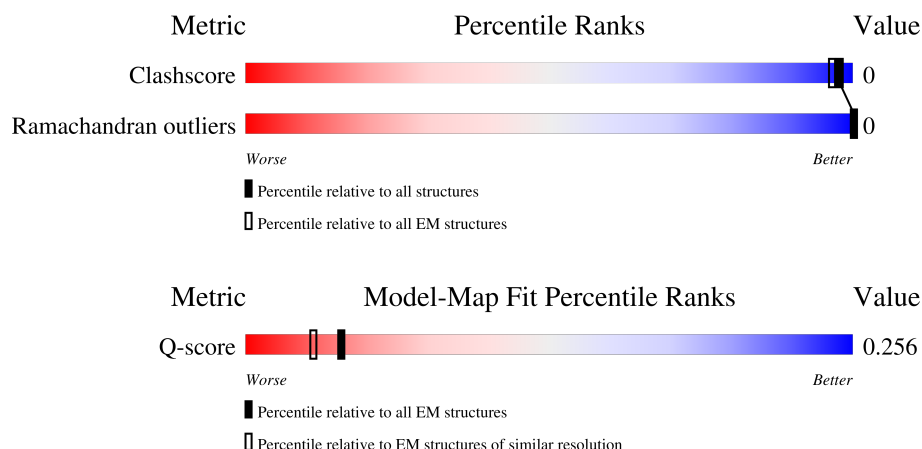
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	5141	
1	B	5141	
2	E	177	
2	F	177	
3	C	221	

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Mol	Chain	Length	Quality of chain
3	D	221	 11% 89%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9662 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 Auxin transport protein (BIG).

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	834	Total	C	N	O	0	0
			4137	2469	834	834		
1	B	834	Total	C	N	O	0	0
			4137	2469	834	834		

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5099	GLY	-	expression tag	UNP A0A1I9LSK4
A	5100	SER	-	expression tag	UNP A0A1I9LSK4
A	5101	LEU	-	expression tag	UNP A0A1I9LSK4
A	5102	GLU	-	expression tag	UNP A0A1I9LSK4
A	5103	VAL	-	expression tag	UNP A0A1I9LSK4
A	5104	LEU	-	expression tag	UNP A0A1I9LSK4
A	5105	PHE	-	expression tag	UNP A0A1I9LSK4
A	5106	GLN	-	expression tag	UNP A0A1I9LSK4
A	5107	GLY	-	expression tag	UNP A0A1I9LSK4
A	5108	PRO	-	expression tag	UNP A0A1I9LSK4
A	5109	ALA	-	expression tag	UNP A0A1I9LSK4
A	5110	GLU	-	expression tag	UNP A0A1I9LSK4
A	5111	ALA	-	expression tag	UNP A0A1I9LSK4
A	5112	ALA	-	expression tag	UNP A0A1I9LSK4
A	5113	ALA	-	expression tag	UNP A0A1I9LSK4
A	5114	LYS	-	expression tag	UNP A0A1I9LSK4
A	5115	GLU	-	expression tag	UNP A0A1I9LSK4
A	5116	ALA	-	expression tag	UNP A0A1I9LSK4
A	5117	ALA	-	expression tag	UNP A0A1I9LSK4
A	5118	ALA	-	expression tag	UNP A0A1I9LSK4
A	5119	LYS	-	expression tag	UNP A0A1I9LSK4
A	5120	GLU	-	expression tag	UNP A0A1I9LSK4
A	5121	ALA	-	expression tag	UNP A0A1I9LSK4
A	5122	ALA	-	expression tag	UNP A0A1I9LSK4
A	5123	ALA	-	expression tag	UNP A0A1I9LSK4
A	5124	LYS	-	expression tag	UNP A0A1I9LSK4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	5125	GLU	-	expression tag	UNP A0A1I9LSK4
A	5126	ALA	-	expression tag	UNP A0A1I9LSK4
A	5127	ALA	-	expression tag	UNP A0A1I9LSK4
A	5128	ALA	-	expression tag	UNP A0A1I9LSK4
A	5129	LYS	-	expression tag	UNP A0A1I9LSK4
A	5130	ALA	-	expression tag	UNP A0A1I9LSK4
A	5131	LEU	-	expression tag	UNP A0A1I9LSK4
A	5132	GLU	-	expression tag	UNP A0A1I9LSK4
A	5133	ALA	-	expression tag	UNP A0A1I9LSK4
A	5134	GLU	-	expression tag	UNP A0A1I9LSK4
A	5135	ALA	-	expression tag	UNP A0A1I9LSK4
A	5136	ALA	-	expression tag	UNP A0A1I9LSK4
A	5137	ALA	-	expression tag	UNP A0A1I9LSK4
A	5138	LYS	-	expression tag	UNP A0A1I9LSK4
A	5139	GLU	-	expression tag	UNP A0A1I9LSK4
A	5140	ALA	-	expression tag	UNP A0A1I9LSK4
A	5141	ALA	-	expression tag	UNP A0A1I9LSK4
A	5142	ALA	-	expression tag	UNP A0A1I9LSK4
A	5143	LYS	-	expression tag	UNP A0A1I9LSK4
A	5144	GLU	-	expression tag	UNP A0A1I9LSK4
A	5145	ALA	-	expression tag	UNP A0A1I9LSK4
A	5146	ALA	-	expression tag	UNP A0A1I9LSK4
A	5147	ALA	-	expression tag	UNP A0A1I9LSK4
A	5148	LYS	-	expression tag	UNP A0A1I9LSK4
A	5149	GLU	-	expression tag	UNP A0A1I9LSK4
A	5150	ALA	-	expression tag	UNP A0A1I9LSK4
A	5151	ALA	-	expression tag	UNP A0A1I9LSK4
A	5152	ALA	-	expression tag	UNP A0A1I9LSK4
A	5153	LYS	-	expression tag	UNP A0A1I9LSK4
A	5154	ALA	-	expression tag	UNP A0A1I9LSK4
A	5155	HIS	-	expression tag	UNP A0A1I9LSK4
A	5156	HIS	-	expression tag	UNP A0A1I9LSK4
A	5157	HIS	-	expression tag	UNP A0A1I9LSK4
A	5158	HIS	-	expression tag	UNP A0A1I9LSK4
A	5159	HIS	-	expression tag	UNP A0A1I9LSK4
A	5160	HIS	-	expression tag	UNP A0A1I9LSK4
A	5161	HIS	-	expression tag	UNP A0A1I9LSK4
A	5162	HIS	-	expression tag	UNP A0A1I9LSK4
B	5099	GLY	-	expression tag	UNP A0A1I9LSK4
B	5100	SER	-	expression tag	UNP A0A1I9LSK4
B	5101	LEU	-	expression tag	UNP A0A1I9LSK4
B	5102	GLU	-	expression tag	UNP A0A1I9LSK4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5103	VAL	-	expression tag	UNP A0A1I9LSK4
B	5104	LEU	-	expression tag	UNP A0A1I9LSK4
B	5105	PHE	-	expression tag	UNP A0A1I9LSK4
B	5106	GLN	-	expression tag	UNP A0A1I9LSK4
B	5107	GLY	-	expression tag	UNP A0A1I9LSK4
B	5108	PRO	-	expression tag	UNP A0A1I9LSK4
B	5109	ALA	-	expression tag	UNP A0A1I9LSK4
B	5110	GLU	-	expression tag	UNP A0A1I9LSK4
B	5111	ALA	-	expression tag	UNP A0A1I9LSK4
B	5112	ALA	-	expression tag	UNP A0A1I9LSK4
B	5113	ALA	-	expression tag	UNP A0A1I9LSK4
B	5114	LYS	-	expression tag	UNP A0A1I9LSK4
B	5115	GLU	-	expression tag	UNP A0A1I9LSK4
B	5116	ALA	-	expression tag	UNP A0A1I9LSK4
B	5117	ALA	-	expression tag	UNP A0A1I9LSK4
B	5118	ALA	-	expression tag	UNP A0A1I9LSK4
B	5119	LYS	-	expression tag	UNP A0A1I9LSK4
B	5120	GLU	-	expression tag	UNP A0A1I9LSK4
B	5121	ALA	-	expression tag	UNP A0A1I9LSK4
B	5122	ALA	-	expression tag	UNP A0A1I9LSK4
B	5123	ALA	-	expression tag	UNP A0A1I9LSK4
B	5124	LYS	-	expression tag	UNP A0A1I9LSK4
B	5125	GLU	-	expression tag	UNP A0A1I9LSK4
B	5126	ALA	-	expression tag	UNP A0A1I9LSK4
B	5127	ALA	-	expression tag	UNP A0A1I9LSK4
B	5128	ALA	-	expression tag	UNP A0A1I9LSK4
B	5129	LYS	-	expression tag	UNP A0A1I9LSK4
B	5130	ALA	-	expression tag	UNP A0A1I9LSK4
B	5131	LEU	-	expression tag	UNP A0A1I9LSK4
B	5132	GLU	-	expression tag	UNP A0A1I9LSK4
B	5133	ALA	-	expression tag	UNP A0A1I9LSK4
B	5134	GLU	-	expression tag	UNP A0A1I9LSK4
B	5135	ALA	-	expression tag	UNP A0A1I9LSK4
B	5136	ALA	-	expression tag	UNP A0A1I9LSK4
B	5137	ALA	-	expression tag	UNP A0A1I9LSK4
B	5138	LYS	-	expression tag	UNP A0A1I9LSK4
B	5139	GLU	-	expression tag	UNP A0A1I9LSK4
B	5140	ALA	-	expression tag	UNP A0A1I9LSK4
B	5141	ALA	-	expression tag	UNP A0A1I9LSK4
B	5142	ALA	-	expression tag	UNP A0A1I9LSK4
B	5143	LYS	-	expression tag	UNP A0A1I9LSK4
B	5144	GLU	-	expression tag	UNP A0A1I9LSK4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5145	ALA	-	expression tag	UNP A0A1I9LSK4
B	5146	ALA	-	expression tag	UNP A0A1I9LSK4
B	5147	ALA	-	expression tag	UNP A0A1I9LSK4
B	5148	LYS	-	expression tag	UNP A0A1I9LSK4
B	5149	GLU	-	expression tag	UNP A0A1I9LSK4
B	5150	ALA	-	expression tag	UNP A0A1I9LSK4
B	5151	ALA	-	expression tag	UNP A0A1I9LSK4
B	5152	ALA	-	expression tag	UNP A0A1I9LSK4
B	5153	LYS	-	expression tag	UNP A0A1I9LSK4
B	5154	ALA	-	expression tag	UNP A0A1I9LSK4
B	5155	HIS	-	expression tag	UNP A0A1I9LSK4
B	5156	HIS	-	expression tag	UNP A0A1I9LSK4
B	5157	HIS	-	expression tag	UNP A0A1I9LSK4
B	5158	HIS	-	expression tag	UNP A0A1I9LSK4
B	5159	HIS	-	expression tag	UNP A0A1I9LSK4
B	5160	HIS	-	expression tag	UNP A0A1I9LSK4
B	5161	HIS	-	expression tag	UNP A0A1I9LSK4
B	5162	HIS	-	expression tag	UNP A0A1I9LSK4

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	E	115	Total	C	N	O	0	0
			569	339	115	115		
2	F	115	Total	C	N	O	0	0
			569	339	115	115		

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-27	MET	-	initiating methionine	UNP P0DH95
E	-26	ASP	-	expression tag	UNP P0DH95
E	-25	TYR	-	expression tag	UNP P0DH95
E	-24	LYS	-	expression tag	UNP P0DH95
E	-23	ASP	-	expression tag	UNP P0DH95
E	-22	HIS	-	expression tag	UNP P0DH95
E	-21	ASP	-	expression tag	UNP P0DH95
E	-20	GLY	-	expression tag	UNP P0DH95
E	-19	ASP	-	expression tag	UNP P0DH95
E	-18	TYR	-	expression tag	UNP P0DH95
E	-17	LYS	-	expression tag	UNP P0DH95
E	-16	ASP	-	expression tag	UNP P0DH95

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-15	HIS	-	expression tag	UNP P0DH95
E	-14	ASP	-	expression tag	UNP P0DH95
E	-13	ILE	-	expression tag	UNP P0DH95
E	-12	ASP	-	expression tag	UNP P0DH95
E	-11	TYR	-	expression tag	UNP P0DH95
E	-10	LYS	-	expression tag	UNP P0DH95
E	-9	ASP	-	expression tag	UNP P0DH95
E	-8	ASP	-	expression tag	UNP P0DH95
E	-7	ASP	-	expression tag	UNP P0DH95
E	-6	ASP	-	expression tag	UNP P0DH95
E	-5	LYS	-	expression tag	UNP P0DH95
E	-4	GLY	-	expression tag	UNP P0DH95
E	-3	GLY	-	expression tag	UNP P0DH95
E	-2	SER	-	expression tag	UNP P0DH95
E	-1	GLY	-	expression tag	UNP P0DH95
E	0	GLY	-	expression tag	UNP P0DH95
F	-27	MET	-	initiating methionine	UNP P0DH95
F	-26	ASP	-	expression tag	UNP P0DH95
F	-25	TYR	-	expression tag	UNP P0DH95
F	-24	LYS	-	expression tag	UNP P0DH95
F	-23	ASP	-	expression tag	UNP P0DH95
F	-22	HIS	-	expression tag	UNP P0DH95
F	-21	ASP	-	expression tag	UNP P0DH95
F	-20	GLY	-	expression tag	UNP P0DH95
F	-19	ASP	-	expression tag	UNP P0DH95
F	-18	TYR	-	expression tag	UNP P0DH95
F	-17	LYS	-	expression tag	UNP P0DH95
F	-16	ASP	-	expression tag	UNP P0DH95
F	-15	HIS	-	expression tag	UNP P0DH95
F	-14	ASP	-	expression tag	UNP P0DH95
F	-13	ILE	-	expression tag	UNP P0DH95
F	-12	ASP	-	expression tag	UNP P0DH95
F	-11	TYR	-	expression tag	UNP P0DH95
F	-10	LYS	-	expression tag	UNP P0DH95
F	-9	ASP	-	expression tag	UNP P0DH95
F	-8	ASP	-	expression tag	UNP P0DH95
F	-7	ASP	-	expression tag	UNP P0DH95
F	-6	ASP	-	expression tag	UNP P0DH95
F	-5	LYS	-	expression tag	UNP P0DH95
F	-4	GLY	-	expression tag	UNP P0DH95
F	-3	GLY	-	expression tag	UNP P0DH95
F	-2	SER	-	expression tag	UNP P0DH95

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	GLY	-	expression tag	UNP P0DH95
F	0	GLY	-	expression tag	UNP P0DH95

- Molecule 3 is a protein called Protein DEHYDRATION-INDUCED 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	25	Total	C	N	O	0	0
			125	75	25	25		
3	D	25	Total	C	N	O	0	0
			125	75	25	25		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	207	GLY	-	expression tag	UNP Q39083
C	208	GLY	-	expression tag	UNP Q39083
C	209	SER	-	expression tag	UNP Q39083
C	210	GLY	-	expression tag	UNP Q39083
C	211	GLY	-	expression tag	UNP Q39083
C	212	SER	-	expression tag	UNP Q39083
C	213	ALA	-	expression tag	UNP Q39083
C	214	TRP	-	expression tag	UNP Q39083
C	215	SER	-	expression tag	UNP Q39083
C	216	HIS	-	expression tag	UNP Q39083
C	217	PRO	-	expression tag	UNP Q39083
C	218	GLN	-	expression tag	UNP Q39083
C	219	PHE	-	expression tag	UNP Q39083
C	220	GLU	-	expression tag	UNP Q39083
C	221	LYS	-	expression tag	UNP Q39083
D	207	GLY	-	expression tag	UNP Q39083
D	208	GLY	-	expression tag	UNP Q39083
D	209	SER	-	expression tag	UNP Q39083
D	210	GLY	-	expression tag	UNP Q39083
D	211	GLY	-	expression tag	UNP Q39083
D	212	SER	-	expression tag	UNP Q39083
D	213	ALA	-	expression tag	UNP Q39083
D	214	TRP	-	expression tag	UNP Q39083
D	215	SER	-	expression tag	UNP Q39083
D	216	HIS	-	expression tag	UNP Q39083
D	217	PRO	-	expression tag	UNP Q39083
D	218	GLN	-	expression tag	UNP Q39083
D	219	PHE	-	expression tag	UNP Q39083

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Chain	Residue	Modelled	Actual	Comment	Reference
D	220	GLU	-	expression tag	UNP Q39083
D	221	LYS	-	expression tag	UNP Q39083







ALA
ALA
LYS
GLU
ALA
ALA
ALA
LYS
GLU
ALA
ALA
ALA
LYS
GLU
ALA
ALA
ALA
LYS
ALA
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS

- Molecule 1: Auxin transport protein (BIG)

[illegible]







D204	GLU
	VAL
	GLY
	GLY
	SER
	GLY
	SER
	GLY
	ALA
	TRP
	SER
	HIS
	PRO
	GLN
	PHE
	GLU
	LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67226	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)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.920	Depositor
Minimum map value	-0.486	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	486.912, 486.912, 486.912	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.268, 1.268, 1.268	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	0.14	0/4126	0.39	0/5739
1	B	0.14	0/4126	0.39	0/5739
2	E	0.19	0/564	0.61	0/778
2	F	0.19	0/564	0.61	0/778
3	C	0.12	0/124	0.31	0/172
3	D	0.12	0/124	0.31	0/172
All	All	0.15	0/9628	0.42	0/13378

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	4137	0	1814	2	0
1	B	4137	0	1814	2	0
2	E	569	0	253	1	0
2	F	569	0	253	1	0
3	C	125	0	52	0	0
3	D	125	0	52	0	0
All	All	9662	0	4238	6	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 0.

The worst 5 of 6 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:3399:ASN:HA	1:B:3441:CYS:H	1.70	0.56
1:A:3399:ASN:HA	1:A:3441:CYS:H	1.70	0.56
1:B:3874:TRP:HA	1:B:3878:ALA:HB3	1.96	0.48
1:A:3874:TRP:HA	1:A:3878:ALA:HB3	1.96	0.47
2:E:38:ARG:HA	2:E:42:GLN:O	2.20	0.41

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	812/5141 (16%)	798 (98%)	14 (2%)	0	100	100
1	B	812/5141 (16%)	798 (98%)	14 (2%)	0	100	100
2	E	105/177 (59%)	105 (100%)	0	0	100	100
2	F	105/177 (59%)	105 (100%)	0	0	100	100
3	C	23/221 (10%)	23 (100%)	0	0	100	100
3	D	23/221 (10%)	23 (100%)	0	0	100	100
All	All	1880/11078 (17%)	1852 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

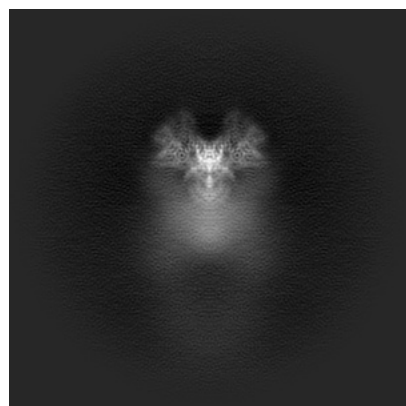
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53348. These allow visual inspection of the internal detail of the map and identification of artifacts.

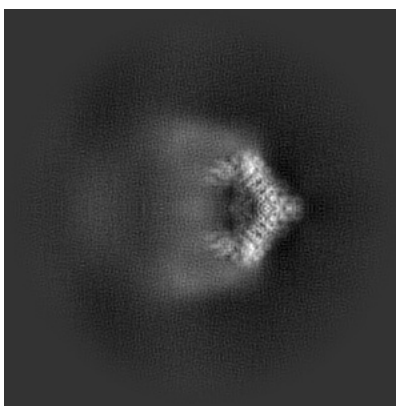
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

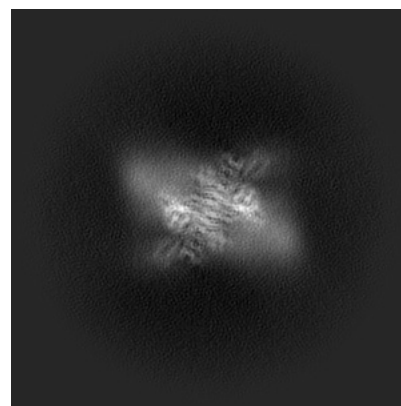
6.1.1 Primary map



X

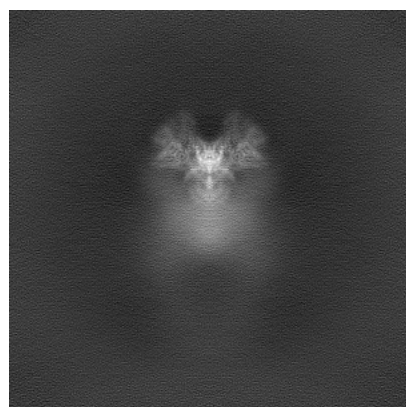


Y

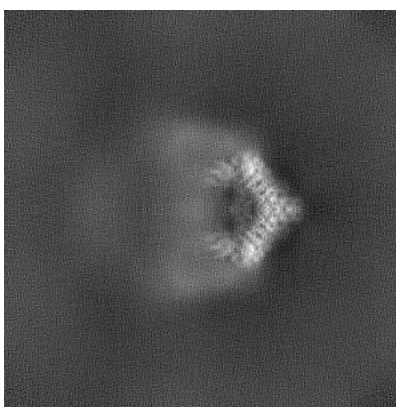


Z

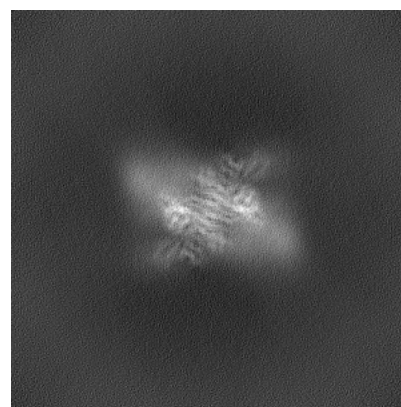
6.1.2 Raw map



X



Y

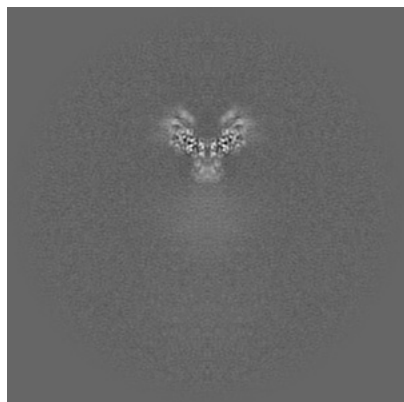


Z

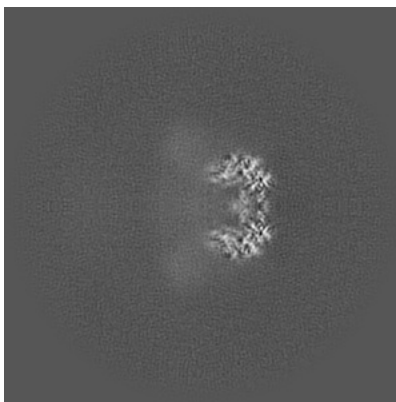
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

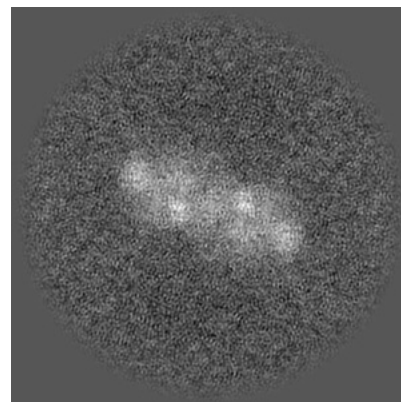
6.2.1 Primary map



X Index: 192

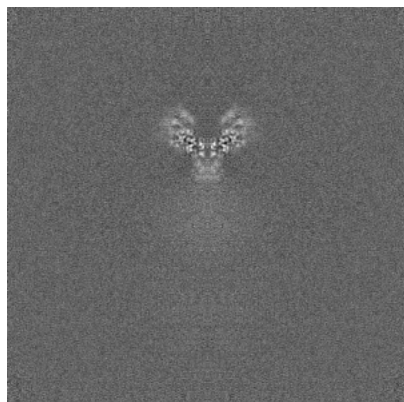


Y Index: 192

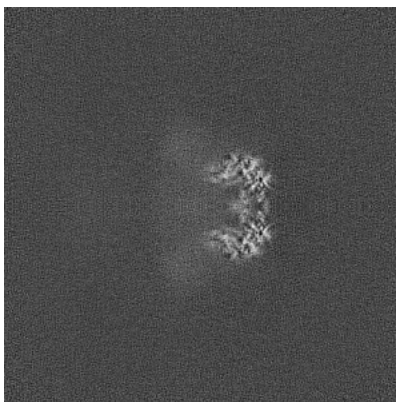


Z Index: 192

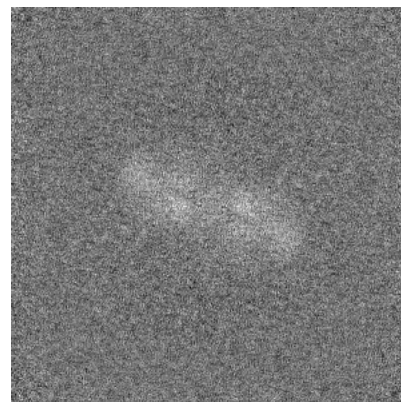
6.2.2 Raw map



X Index: 192



Y Index: 192

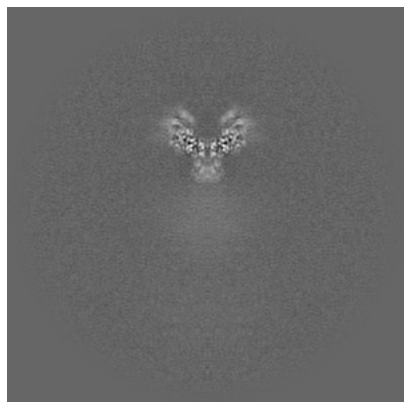


Z Index: 192

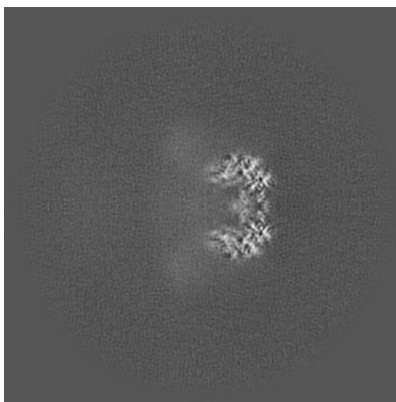
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

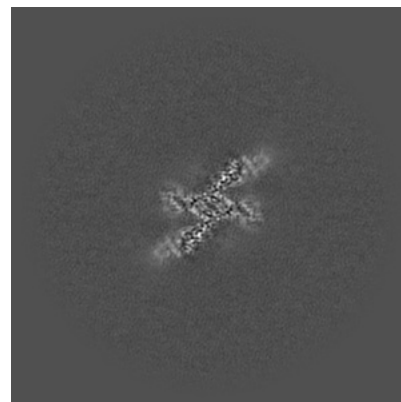
6.3.1 Primary map



X Index: 192

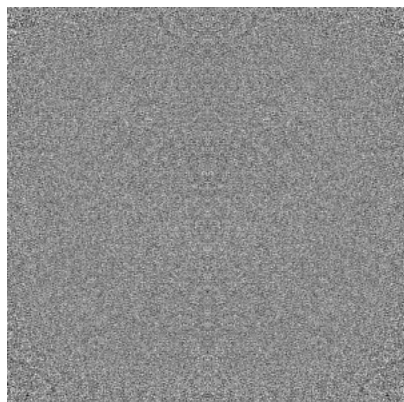


Y Index: 192

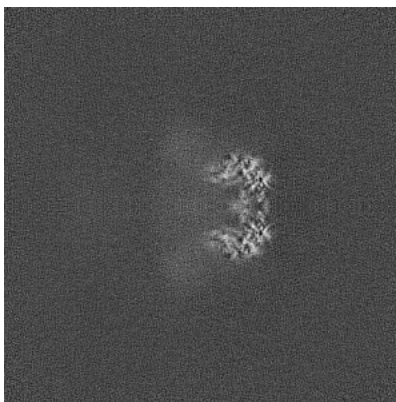


Z Index: 245

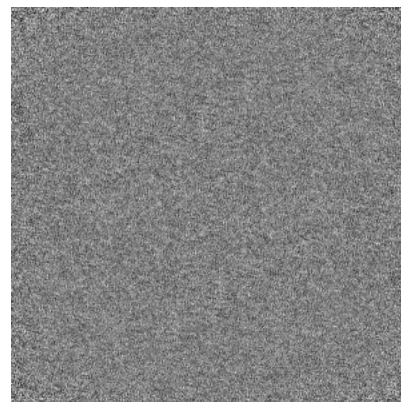
6.3.2 Raw map



X Index: 0



Y Index: 192

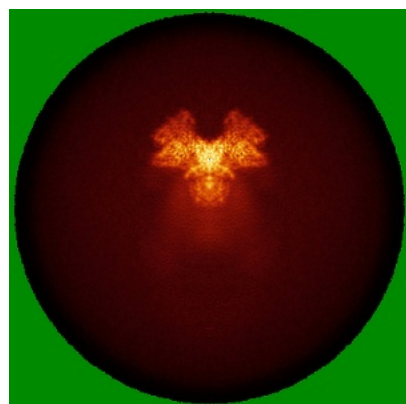


Z Index: 0

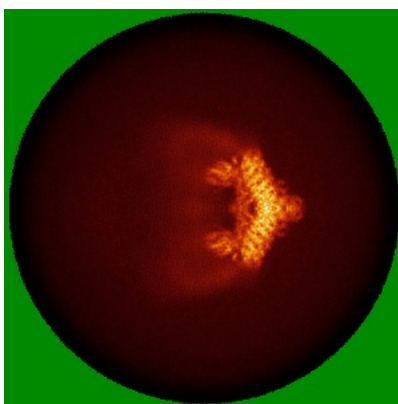
The images above show the largest variance slices of the map in three orthogonal directions.

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

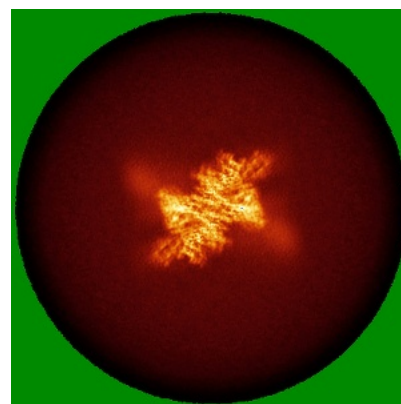
6.4.1 Primary map



X

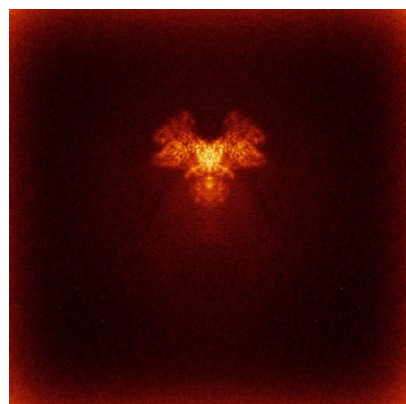


Y

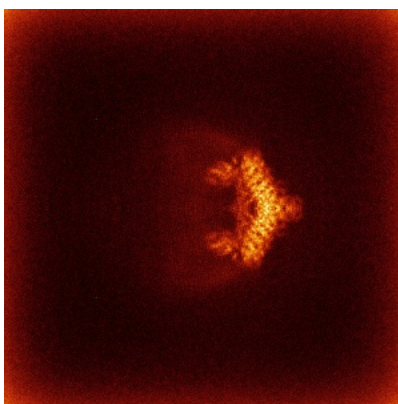


Z

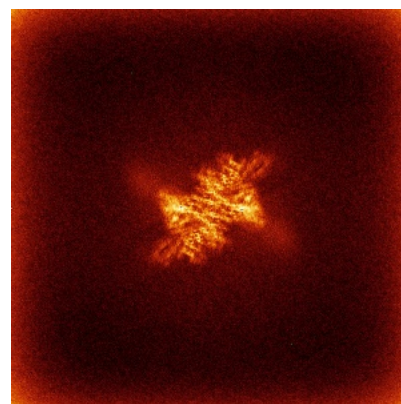
6.4.2 Raw map



X



Y

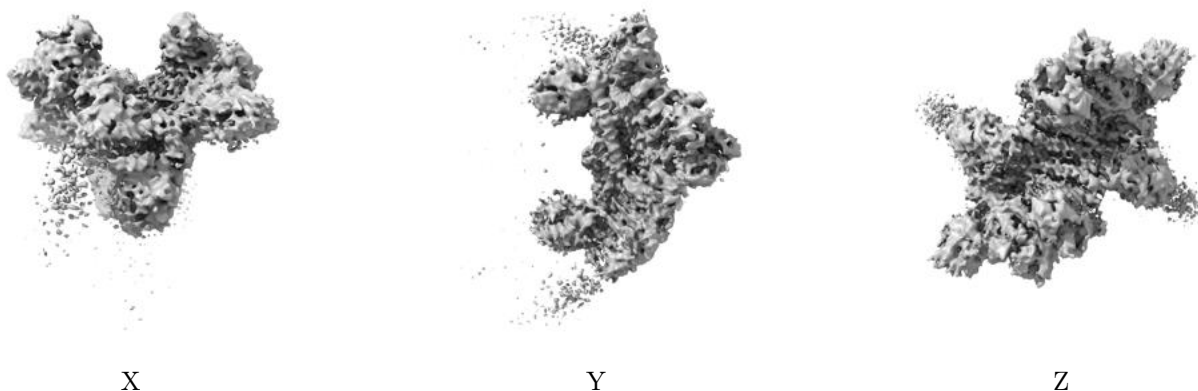


Z

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.

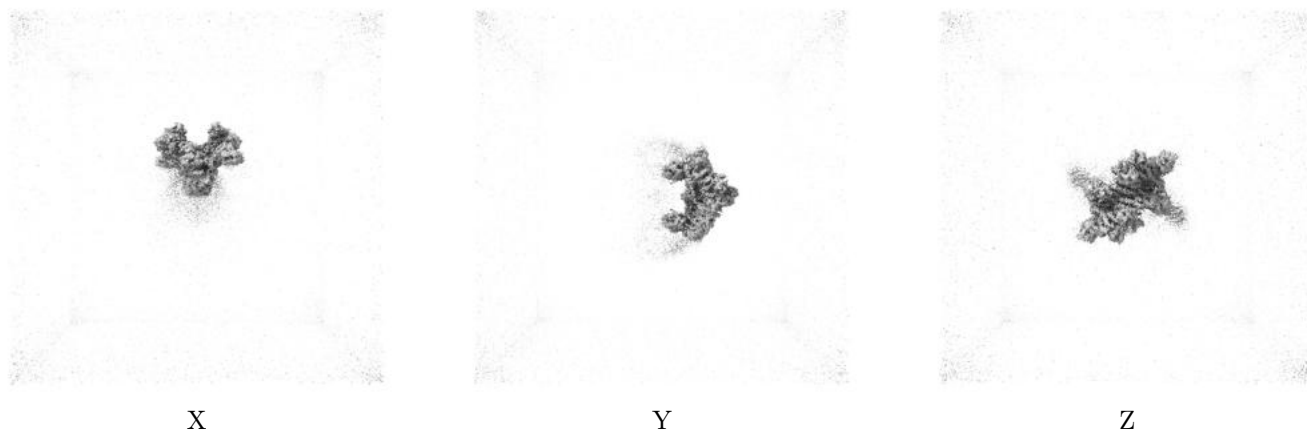
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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.

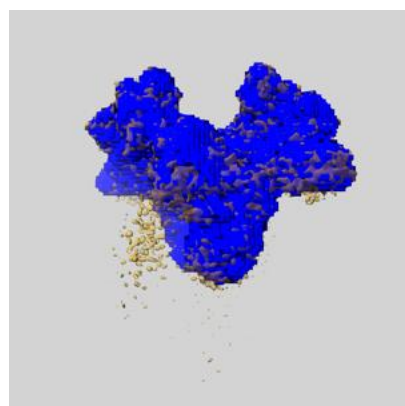
6.6 Mask visualisation [i](#)

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

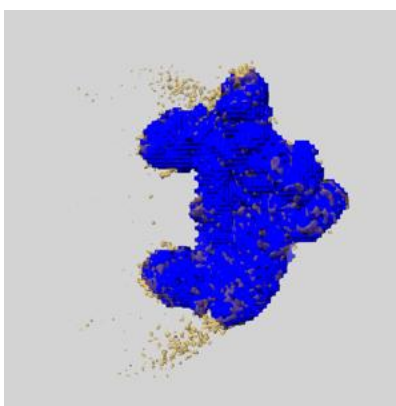
A mask typically either:

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

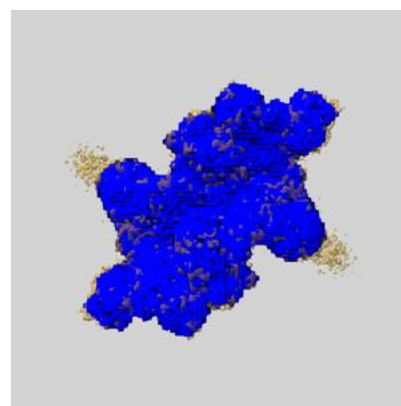
6.6.1 emd_53348_msk_1.map [i](#)



X



Y

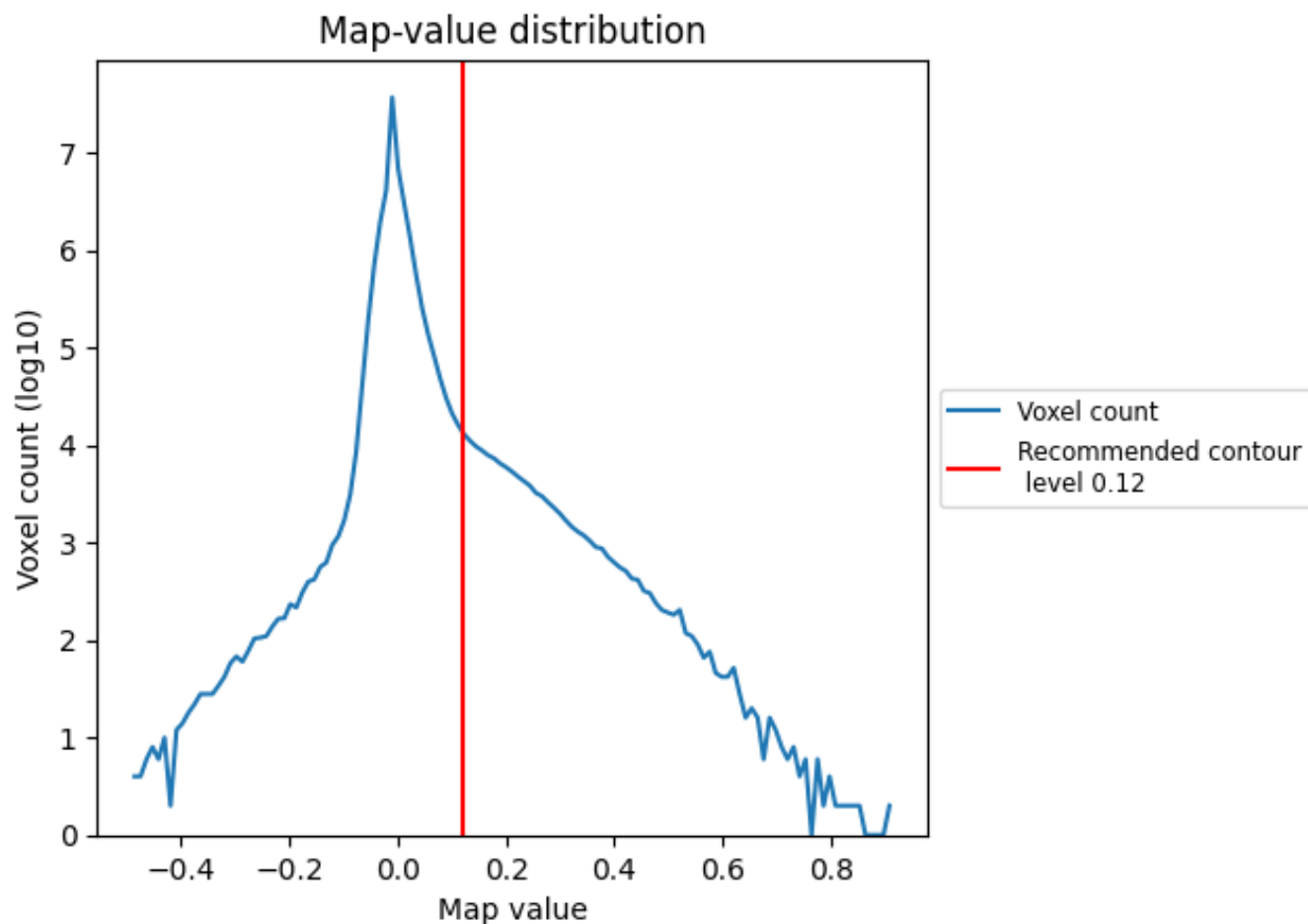


Z

7 Map analysis [i](#)

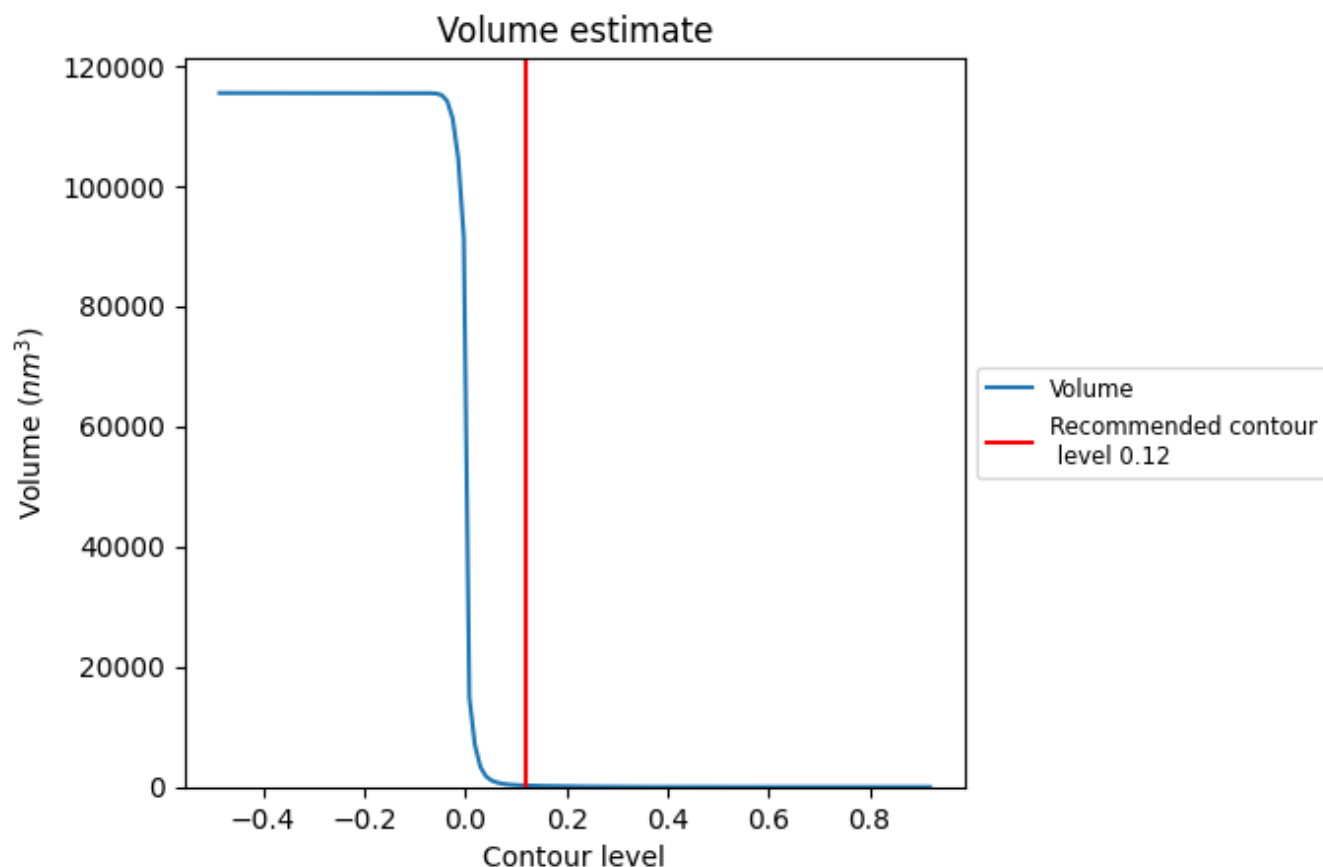
This section contains the results of statistical analysis of the map.

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.

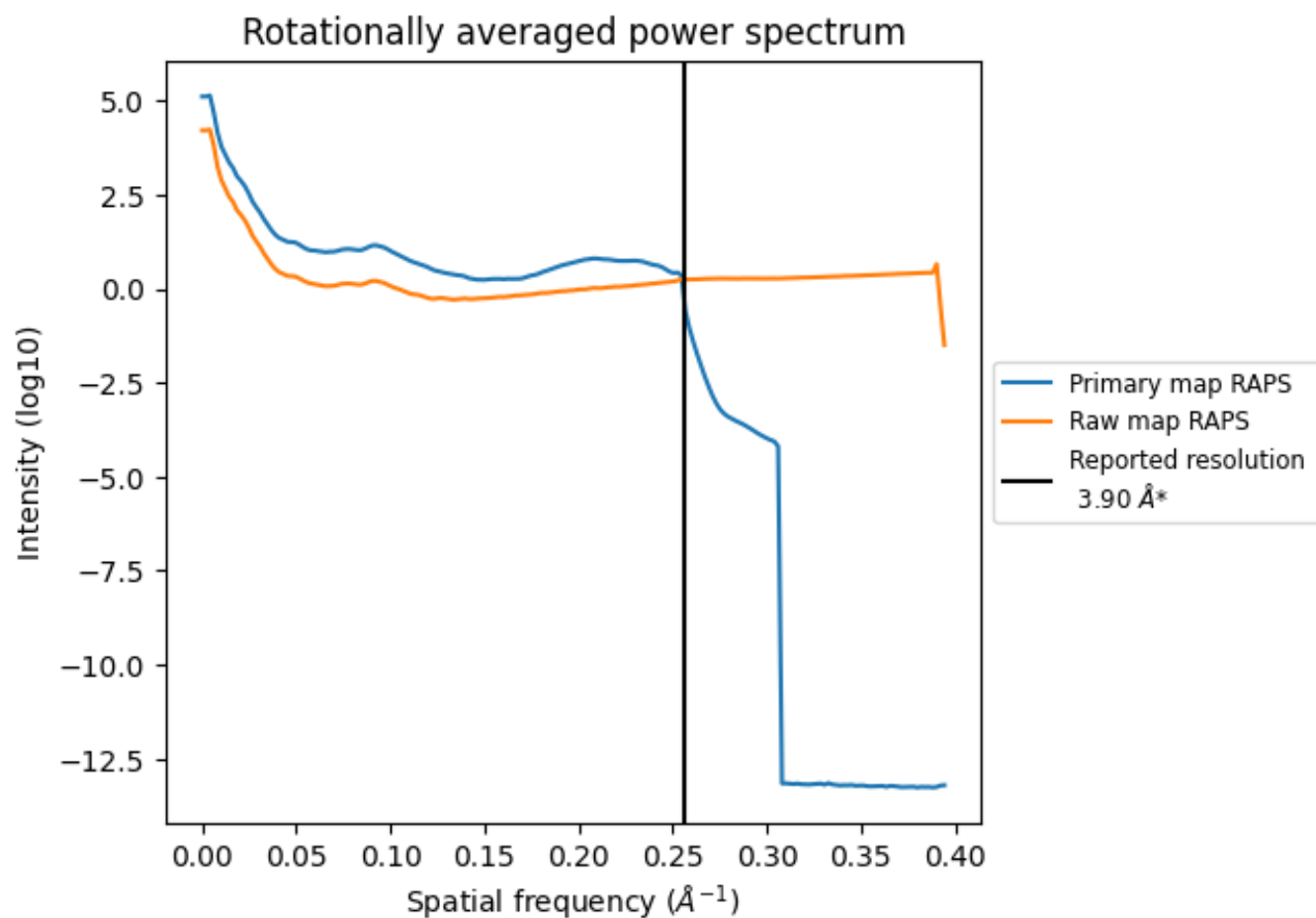
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 244 nm³; this corresponds to an approximate mass of 220 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 ⓘ

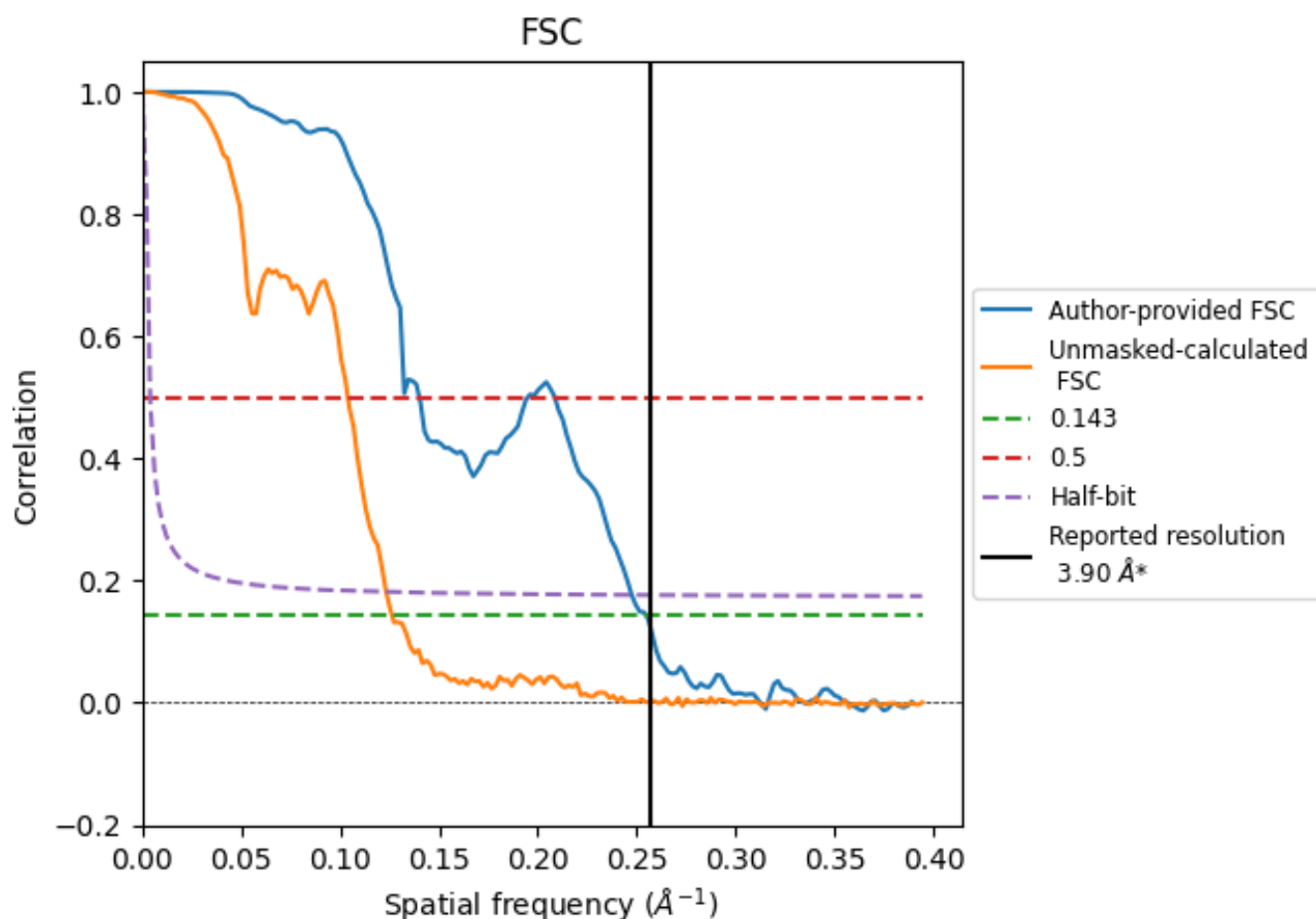


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 \AA^{-1}

8.2 Resolution estimates [i](#)

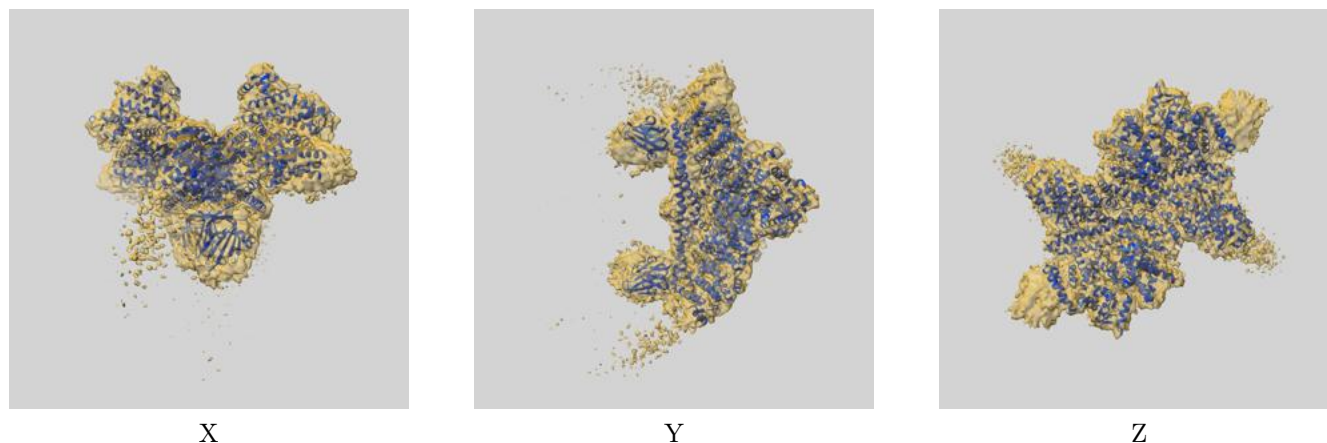
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.93	7.14	4.04
Unmasked-calculated*	7.92	9.62	8.10

*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 7.92 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53348 and PDB model 9QT9. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



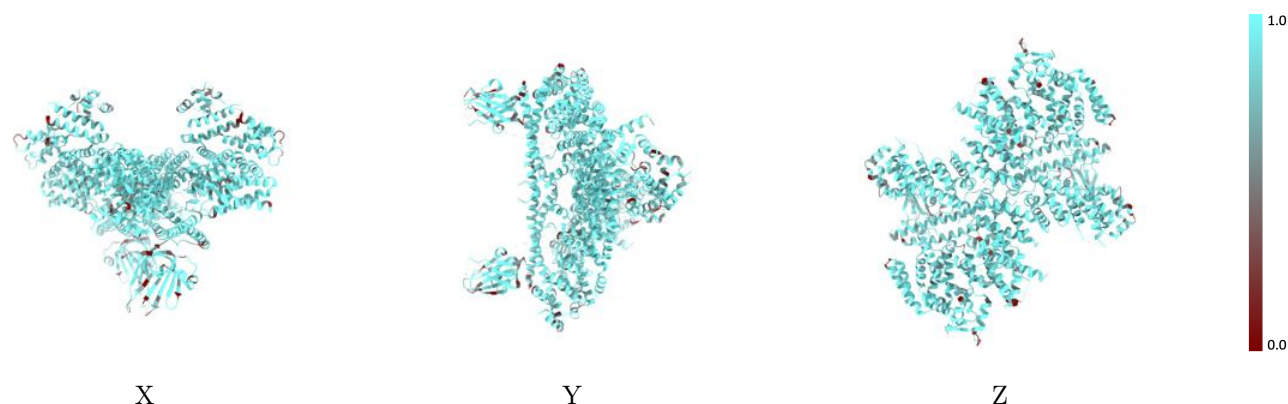
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



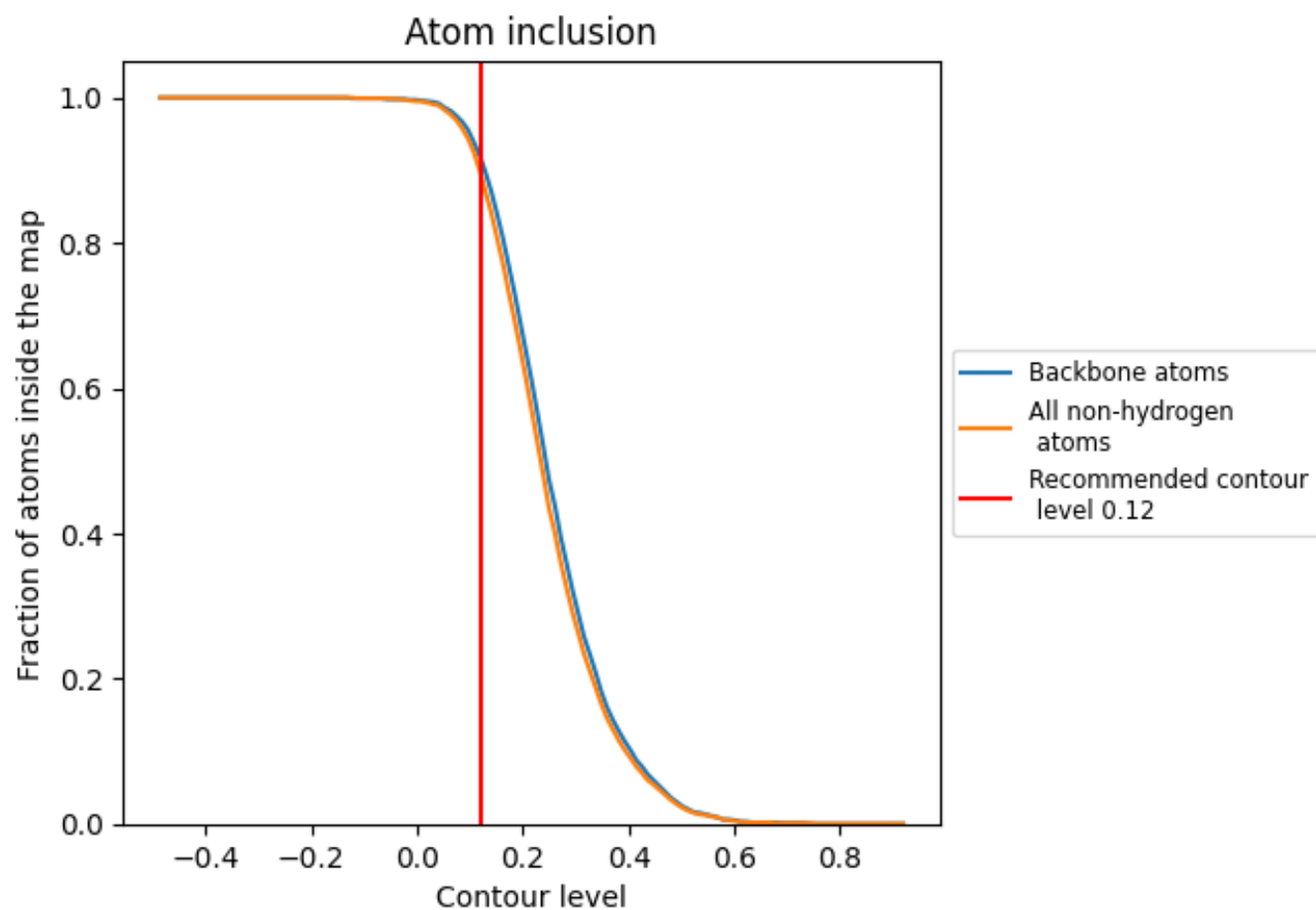
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8960</div>	<div><div></div>0.2560</div>
A	<div><div></div>0.9060</div>	<div><div></div>0.2570</div>
B	<div><div></div>0.9080</div>	<div><div></div>0.2590</div>
C	<div><div></div>0.9280</div>	<div><div></div>0.2970</div>
D	<div><div></div>0.9280</div>	<div><div></div>0.3000</div>
E	<div><div></div>0.8120</div>	<div><div></div>0.2320</div>
F	<div><div></div>0.8070</div>	<div><div></div>0.2320</div>

1.0

0.0

<0.0