



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:58 AM UTC

PDB ID : 8ZPV / pdb_00008zpv
EMDB ID : EMD-60355
Title : Nipah virus polymerase complex
Authors : Wang, Y.R.; Zhang, H.Q.
Deposited on : 2024-05-31
Resolution : 2.90 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

<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:

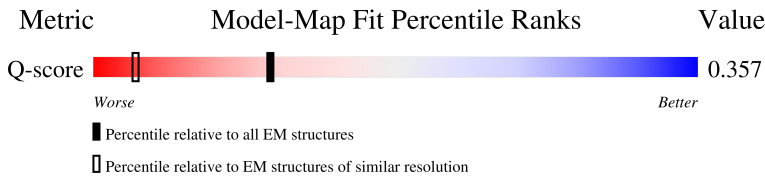
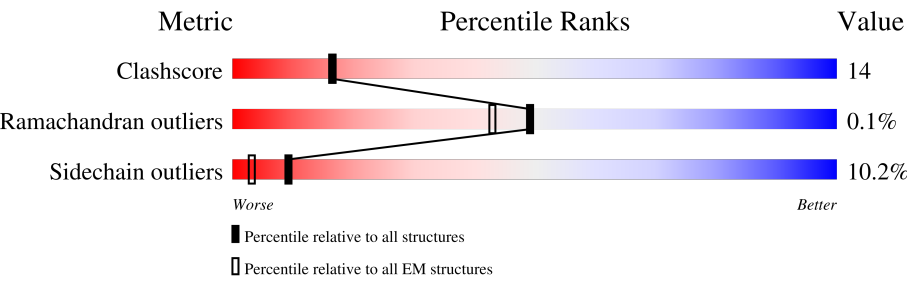
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 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	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	2244	41%14%•43%
2	B	709	•••93%
2	C	709	•••92%
2	D	709	7%8%•83%

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Mol	Chain	Length	Quality of chain
2	E	709	 92%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12440 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1275	Total	C	N	O	S	0	0
			10260	6533	1758	1903	66		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	581	THR	GLU	conflict	UNP Q997F0

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	51	Total	C	N	O	S	0	0
			400	252	70	77	1		
2	C	54	Total	C	N	O	S	0	0
			425	269	75	80	1		
2	D	117	Total	C	N	O	S	0	0
			922	573	161	183	5		
2	E	55	Total	C	N	O	S	0	0
			431	272	76	82	1		

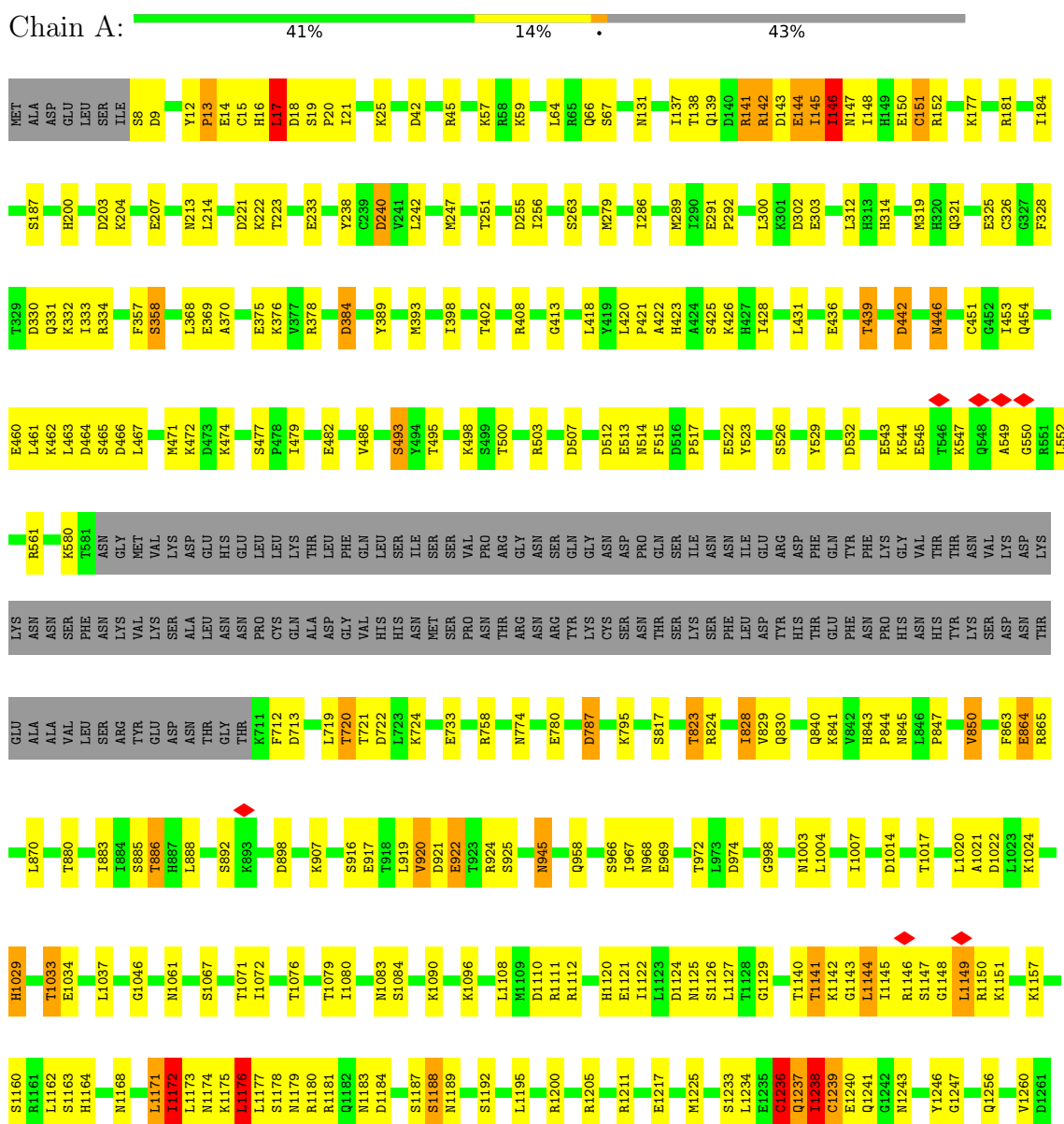
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

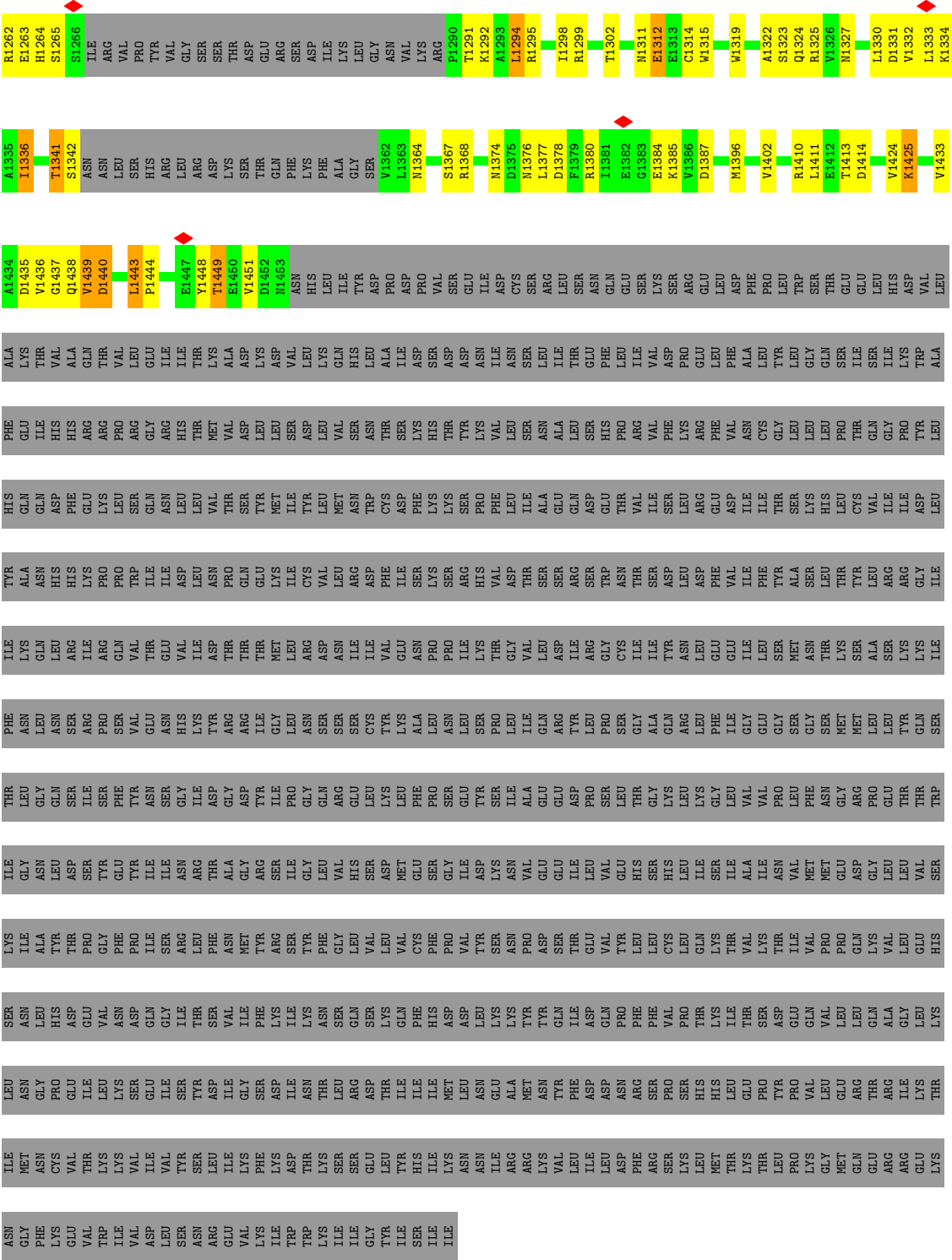
Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

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.

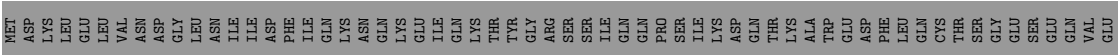
• Molecule 1: RNA-directed RNA polymerase L





● Molecule 2: Phosphoprotein

Chain B: ● ● ● ● 93%



GLN	ASN	ASP	LEU	GLY	GLY	MET
PRO	LYS	ASP	THR	THR	GLU	ASP
PRO	SER	GLU	THR	THR	LYS	LYS
TYR	THR	GLU	GLY	GLY	SER	GLU
HIS	ASP	ALA	THR	THR	LYS	LEU
TRP	VAL	ASP	LEU	TYR	ASP	LEU
SER	PRO	GLN	ASN	GLY	ASP	VAL
ILE	PRO	LEU	PRO	PHE	GLY	ASN
GLU	GLY	GLU	THR	GLU	ARG	ILE
ARG	ALA	PHE	LEU	GLY	ASN	ASP
GLY	ASP	PHE	THR	GLY	LEU	ASP
ALA	ALA	ALA	LEU	ARG	GLU	PHE
LYS	VAL	GLY	ARG	LYS	THR	ASN
THR	LYS	SER	ASN	SER	ASP	ILE
GLU	GLU	SER	LEU	THR	LEU	GLN
ILE	GLU	SER	SER	TYR	SER	LYS
VAL	PRO	GLU	ASP	THR	SER	ASN
ASN	PRO	VAL	PRO	GLY	THR	GLN
GLY	GLN	ILE	ALA	GLY	SER	LYS
ALA	LYS	VAL	LYS	ALA	PRO	GLU
VAL	ARG	GLY	ASP	ASN	THR	ILE
GLN	LEU	ILE	SER	ASN	ASP	GLN
THR	PRO	PRO	PRO	ASN	GLY	LYS
ALA	MET	PRO	VAL	VAL	ILE	TYR
ASP	LEU	GLU	ILE	GLU	GLY	GLY
ARG	ALA	ASP	ALA	LEU	LYS	ARG
GLN	GLU	GLU	GLU	LEU	ARG	GLN
ARG	GLU	GLU	HIS	VAL	ARG	SER
PRO	PHE	PRO	TYR	THR	VAL	SER
GLY	CYS	SER	GLY	ALA	SER	ILE
THR	SER	VAL	LEU	ALA	ASN	GLN
PRO	SER	VAL	GLY	LYS	THR	GLN
MET	GLY	GLY	GLY	MET	ARG	PRO
PRO	SER	GLY	VAL	LEU	ASP	SER
LYS	ASP	LYS	LYS	TYR	TRP	ILE
SER	GLU	PRO	GLU	TYR	ALA	LYS
ARG	PRO	ASN	GLN	ALA	ASN	GLU
GLY	ILE	GLU	ASN	PRO	GLY	GLN
ILE	ILE	SER	VAL	GLU	SER	THR
PRO	ARG	ILE	GLY	ILE	ASP	LYS
ILE	GLU	GLY	PRO	ALA	ASP	ALA
LYS	LEU	ARG	GLN	VAL	ILE	TRP
LYS	LEU	THR	THR	SER	GLN	GLU
GLY	LYS	ILE	SER	LYS	LEU	ASP
THR	GLU	GLY	ARG	GLU	ASP	PHE
ASP	ASN	GLY	ASN	ASP	PRO	LEU
ALA	SER	GLN	VAL	VAL	GLN	GLN
LYS	LEU	SER	ASN	GLU	VAL	CYS
TYR	ILE	ILE	LEU	THR	THR	THR
PRO	ASN	ARG	ASP	ASP	SER	SER
SER	CYS	ASP	SER	LEU	GLY	GLY
ALA	GLN	ASN	ILE	VAL	VAL	GLU
GLY	GLN	LEU	LYS	HIS	TYR	SER
THR	GLY	LEU	LEU	GLU	HIS	GLU
GLU	LYS	ALA	TYR	GLU	ASP	GLN
ASN	ASP	LYS	THR	ASN	HIS	GLN
ALA	ALA	ASP	SER	LYS	CYS	GLU

- Molecule 2: Phosphoprotein

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	523611	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.364	Depositor
Minimum map value	-0.523	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.178	Depositor
Map size (Å)	270.004, 270.004, 270.004	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9643, 0.9643, 0.9643	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.50	14/10470 (0.1%)	0.54	19/14152 (0.1%)
2	B	0.21	0/401	0.59	0/539
2	C	0.21	0/427	0.60	0/575
2	D	0.18	0/926	0.47	0/1245
2	E	0.19	0/433	0.56	0/583
All	All	0.46	14/12657 (0.1%)	0.54	19/17094 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
2	B	0	1
All	All	0	6

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	13	PRO	N-CA	18.33	1.68	1.47
1	A	1175	LYS	C-O	-16.00	1.05	1.24
1	A	1176	LEU	C-O	-15.49	1.05	1.24
1	A	1172	ILE	C-O	-12.08	1.10	1.24
1	A	1171	LEU	C-O	-10.27	1.12	1.24

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	TYR	CA-C-N	17.56	138.72	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	TYR	C-N-CA	17.56	138.72	119.93
1	A	13	PRO	N-CA-C	-9.50	95.78	111.26
1	A	1175	LYS	CA-C-O	-8.32	111.73	120.55
1	A	13	PRO	CA-N-CD	-7.46	101.55	112.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1172	ILE	Mainchain
1	A	1237	GLN	Peptide
1	A	1238	ILE	Peptide
1	A	145	ILE	Peptide
1	A	828	ILE	Peptide

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	10260	0	10301	226	0
2	B	400	0	433	40	0
2	C	425	0	460	34	0
2	D	922	0	959	55	0
2	E	431	0	465	38	0
3	A	2	0	0	0	0
All	All	12440	0	12618	354	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 14.

The worst 5 of 354 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:A:13:PRO:N	1:A:13:PRO:CA	1.68	1.47
1:A:1236:CYS:HB3	1:A:1239:CYS:HA	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:LYS:H	1:A:426:LYS:CE	1.90	0.85
2:C:532:ARG:HG3	2:D:533:LEU:HD23	1.57	0.85
2:C:543:ILE:HG13	2:C:544:PRO:HD3	1.58	0.85

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	1267/2244 (56%)	1166 (92%)	99 (8%)	2 (0%)	43	72
2	B	49/709 (7%)	40 (82%)	9 (18%)	0	100	100
2	C	52/709 (7%)	45 (86%)	7 (14%)	0	100	100
2	D	113/709 (16%)	105 (93%)	8 (7%)	0	100	100
2	E	53/709 (8%)	50 (94%)	3 (6%)	0	100	100
All	All	1534/5080 (30%)	1406 (92%)	126 (8%)	2 (0%)	49	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	146	ILE
1	A	922	GLU

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	1144/2046 (56%)	1047 (92%)	97 (8%)	10	31
2	B	47/625 (8%)	35 (74%)	12 (26%)	0	2
2	C	50/625 (8%)	43 (86%)	7 (14%)	3	11
2	D	107/625 (17%)	86 (80%)	21 (20%)	1	5
2	E	51/625 (8%)	45 (88%)	6 (12%)	5	17
All	All	1399/4546 (31%)	1256 (90%)	143 (10%)	9	23

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	570	HIS
2	D	560	THR
2	D	680	GLU
1	A	917	GLU
1	A	892	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1169	GLN
1	A	1327	ASN
2	E	522	ASN
1	A	1256	GLN
1	A	1394	GLN

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

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

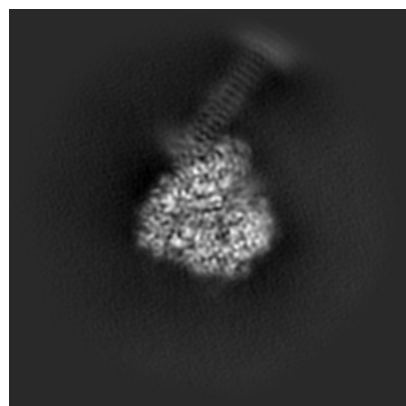
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60355. These allow visual inspection of the internal detail of the map and identification of artifacts.

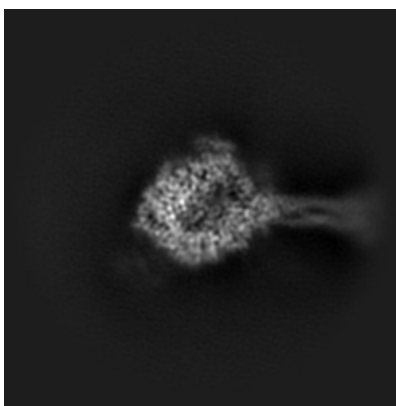
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

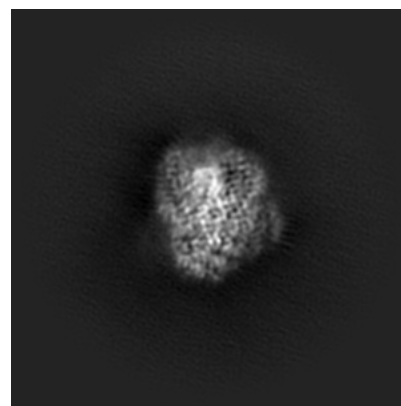
6.1.1 Primary map



X

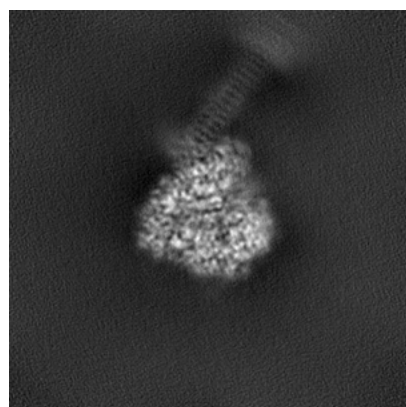


Y

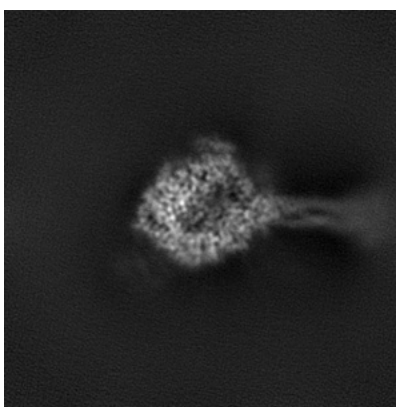


Z

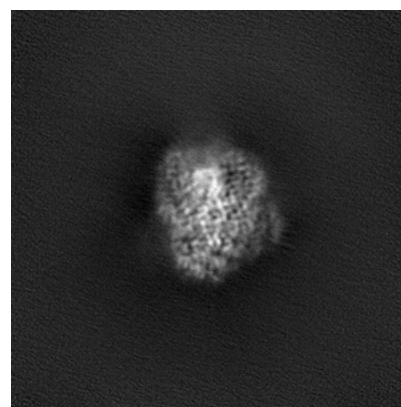
6.1.2 Raw map



X



Y

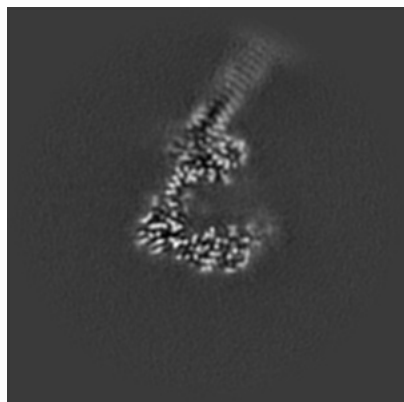


Z

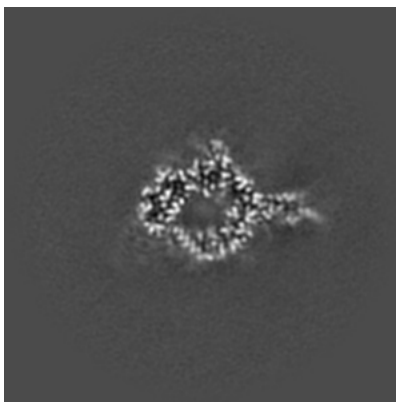
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

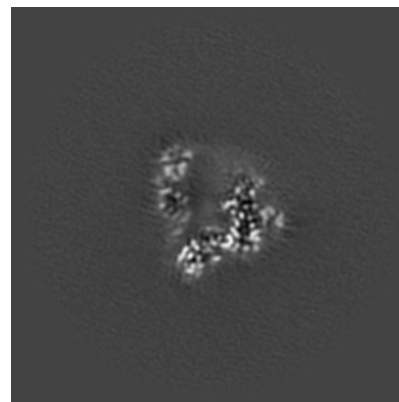
6.2.1 Primary map



X Index: 140

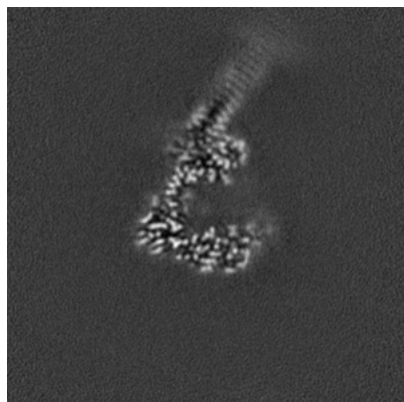


Y Index: 140

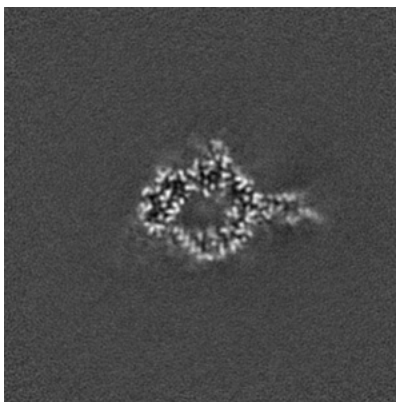


Z Index: 140

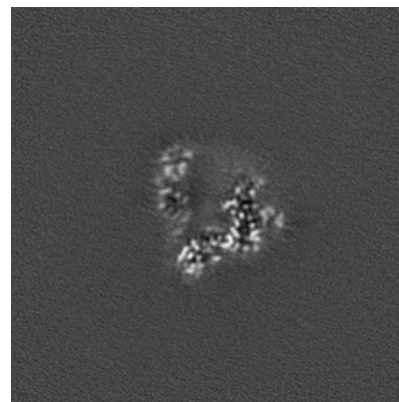
6.2.2 Raw map



X Index: 140



Y Index: 140

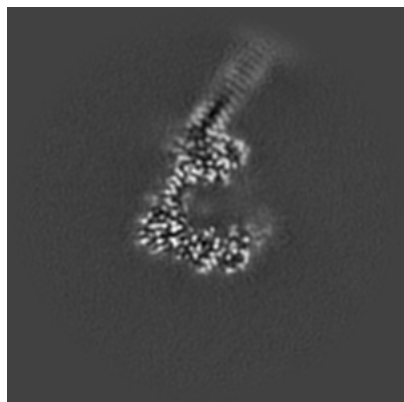


Z Index: 140

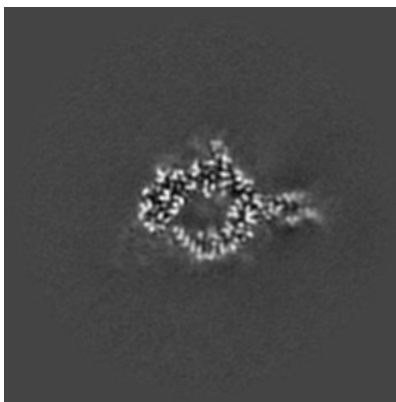
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

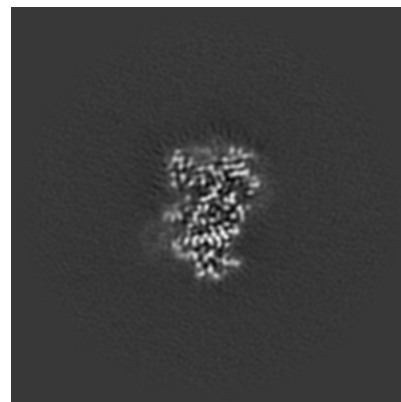
6.3.1 Primary map



X Index: 139

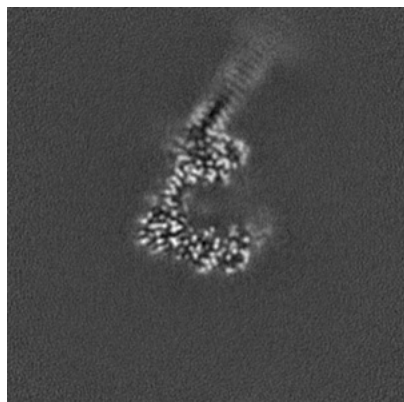


Y Index: 141

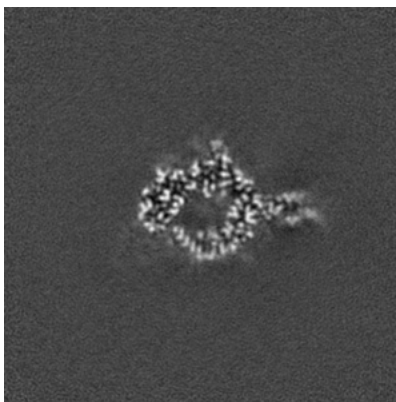


Z Index: 116

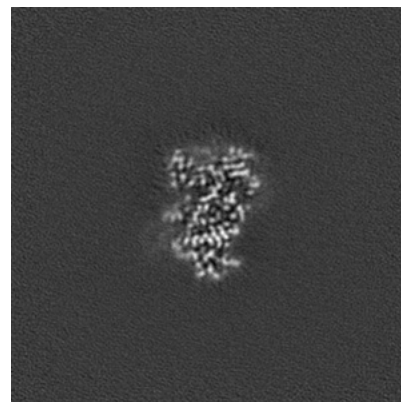
6.3.2 Raw map



X Index: 139



Y Index: 141

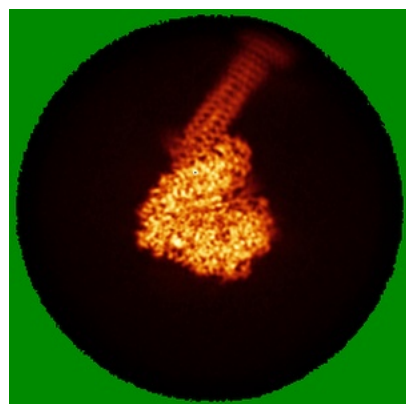


Z Index: 116

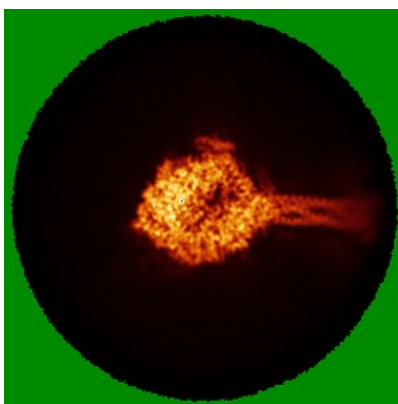
The images above show the largest variance slices of the map in three orthogonal directions.

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

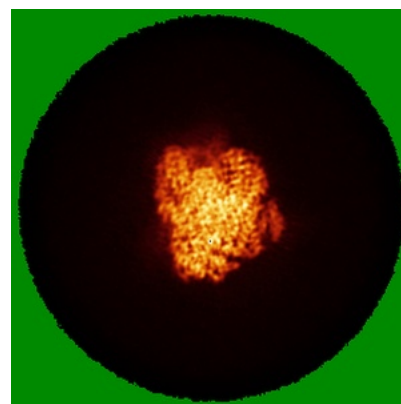
6.4.1 Primary map



X

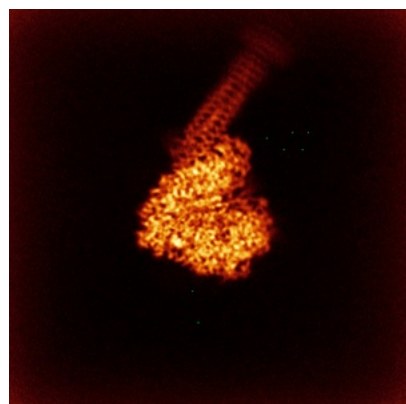


Y

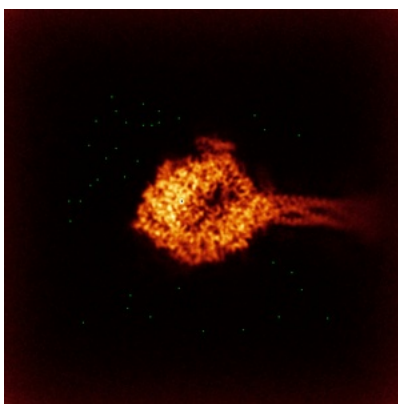


Z

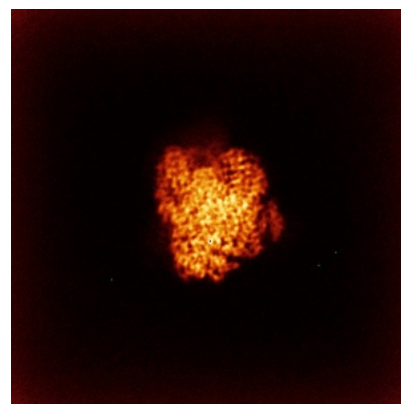
6.4.2 Raw map



X



Y

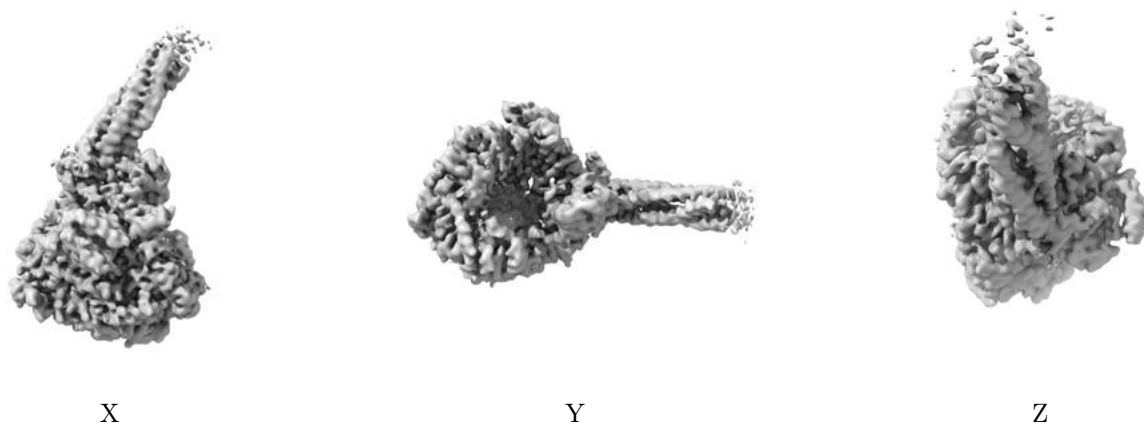


Z

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.

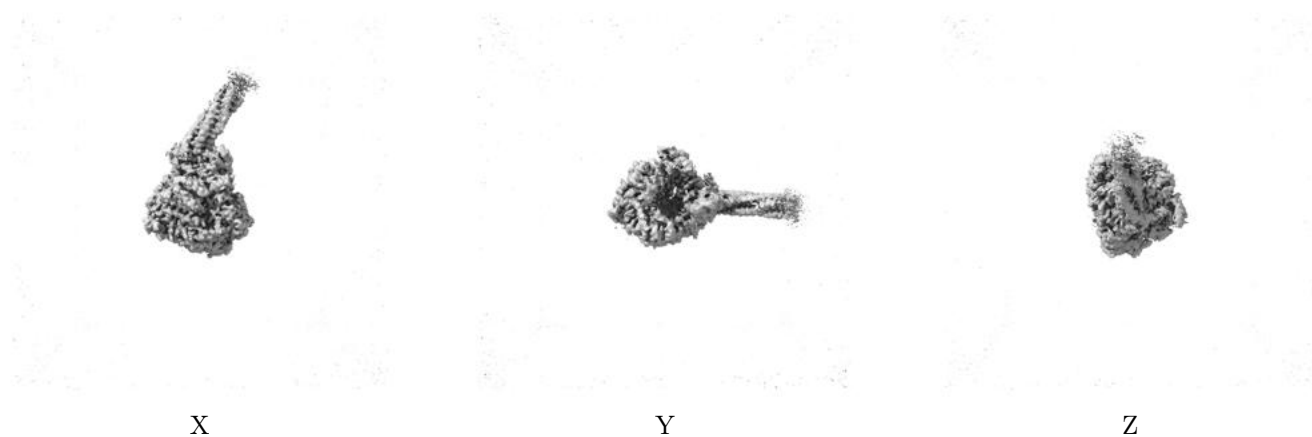
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.178. 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.

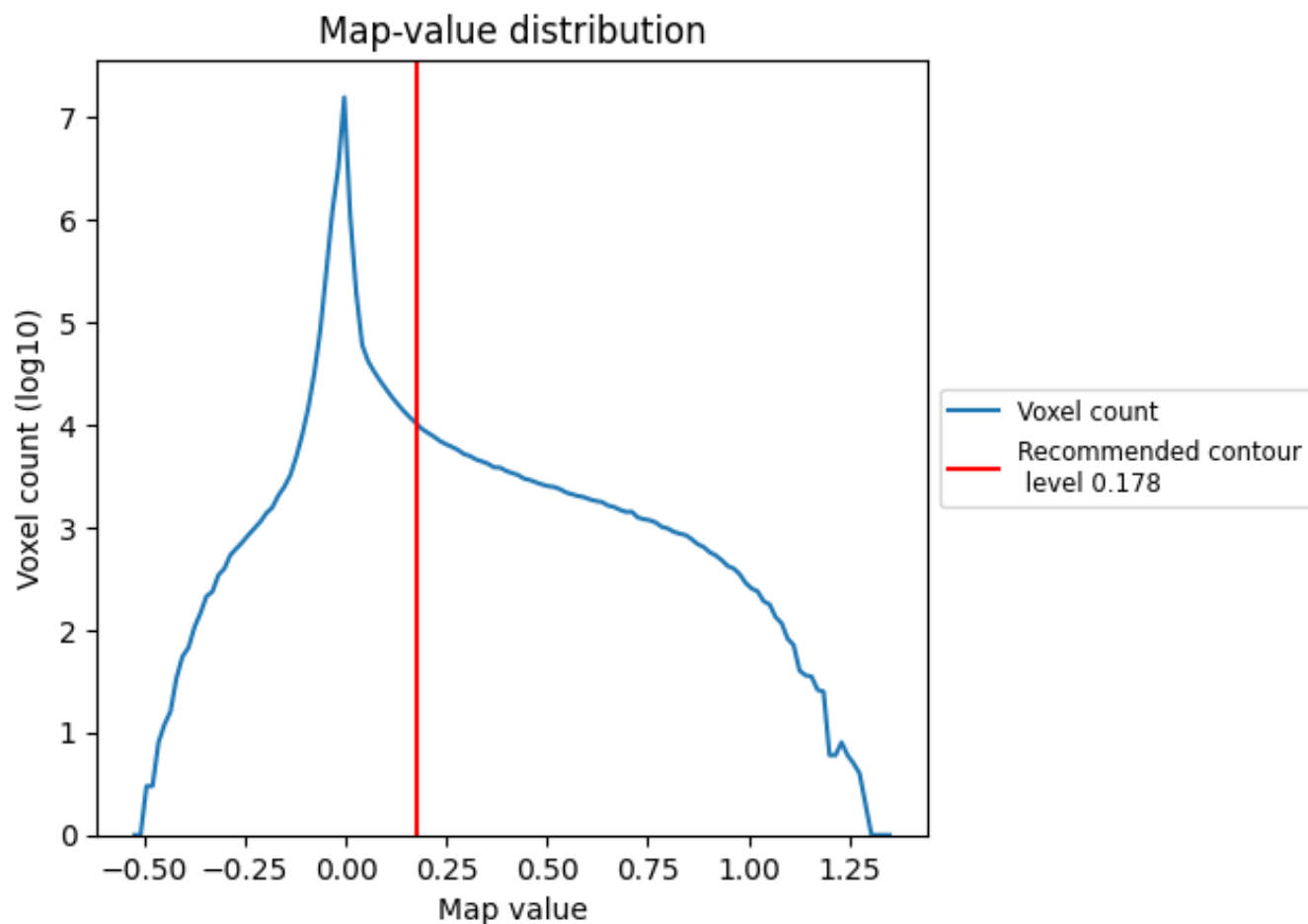
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

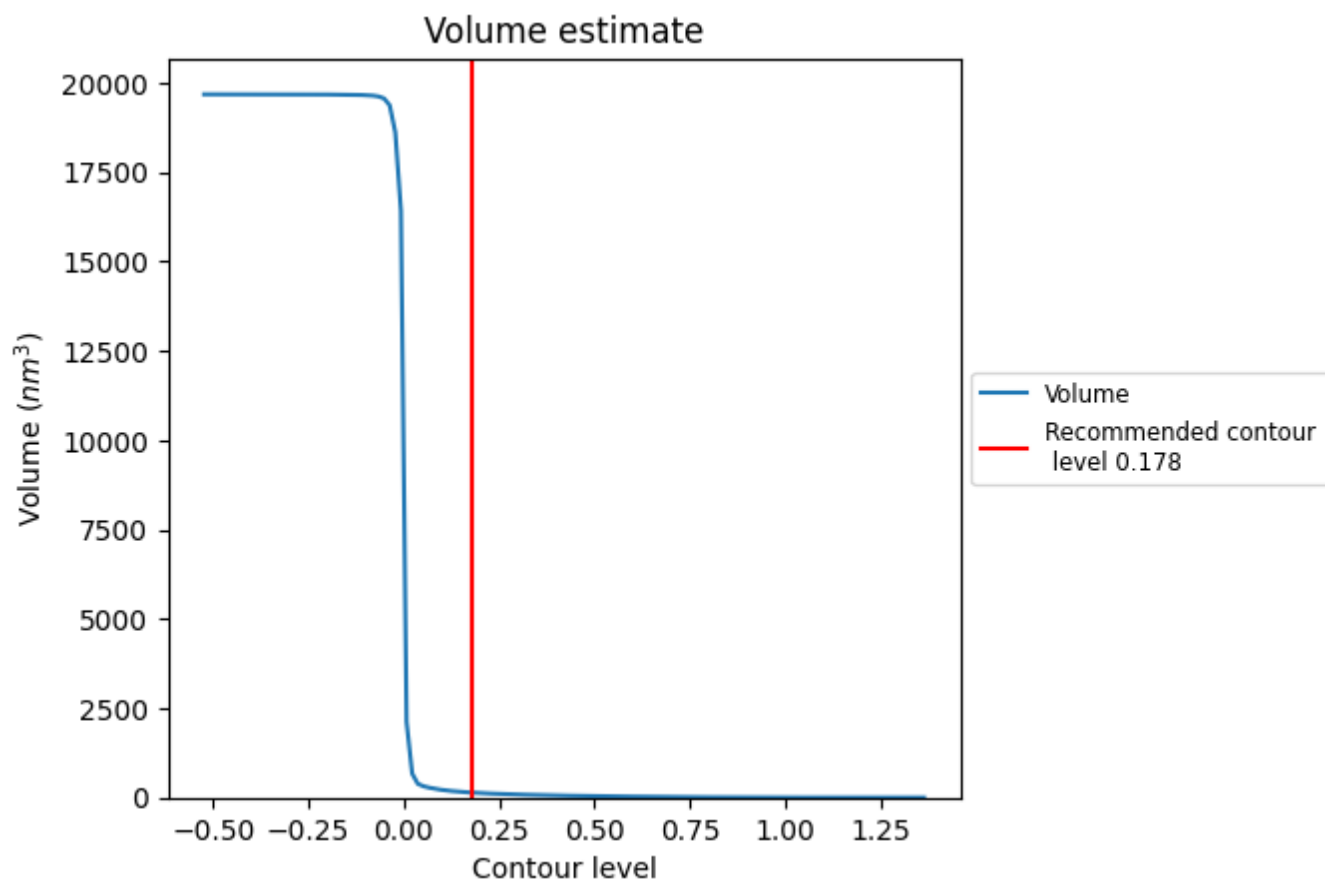
This section contains the results of statistical analysis of the map.

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.

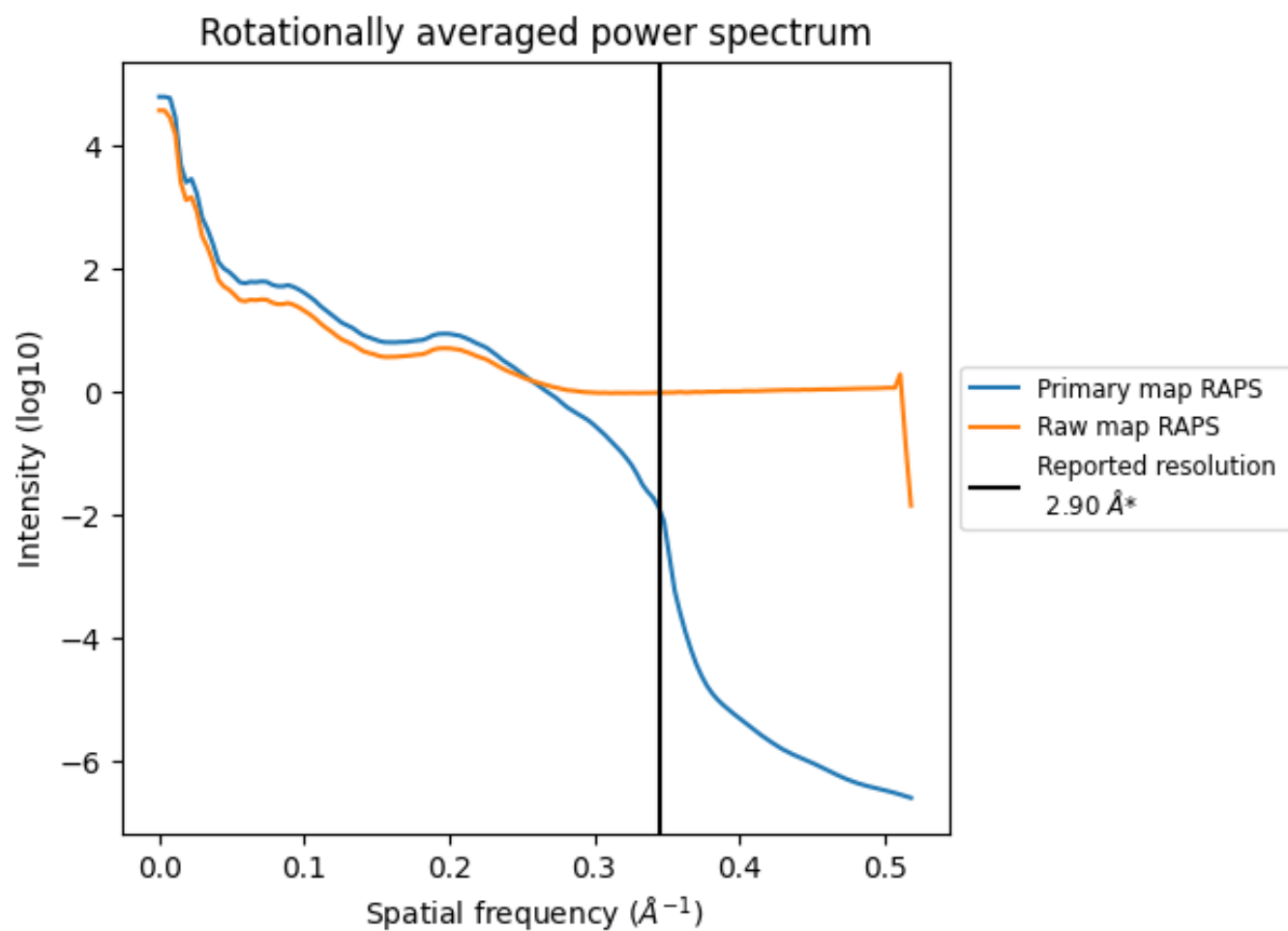
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm^3 ; this corresponds to an approximate mass of 126 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 ⓘ

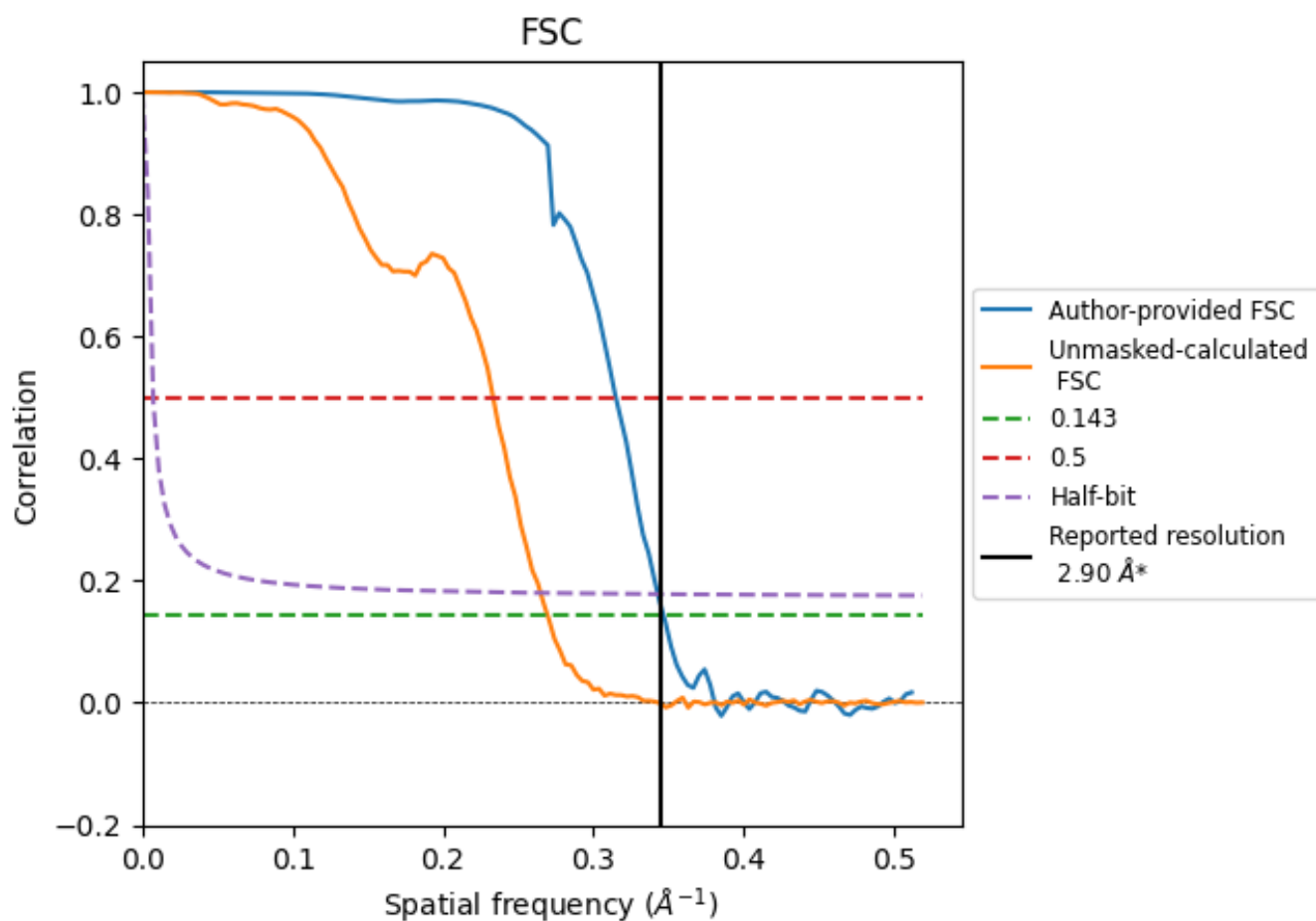


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

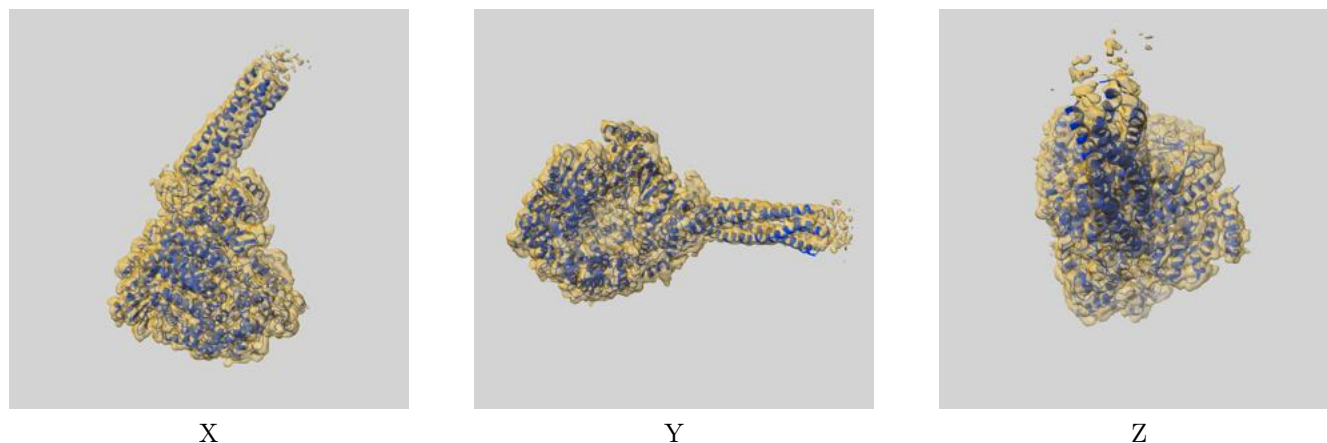
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.89	3.18	2.92
Unmasked-calculated*	3.71	4.28	3.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.71 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

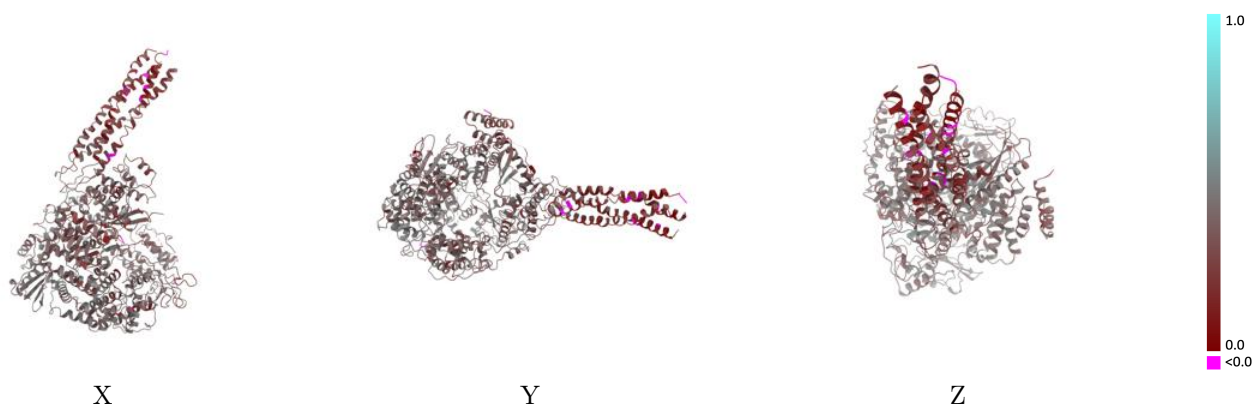
This section contains information regarding the fit between EMDB map EMD-60355 and PDB model 8ZPV. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



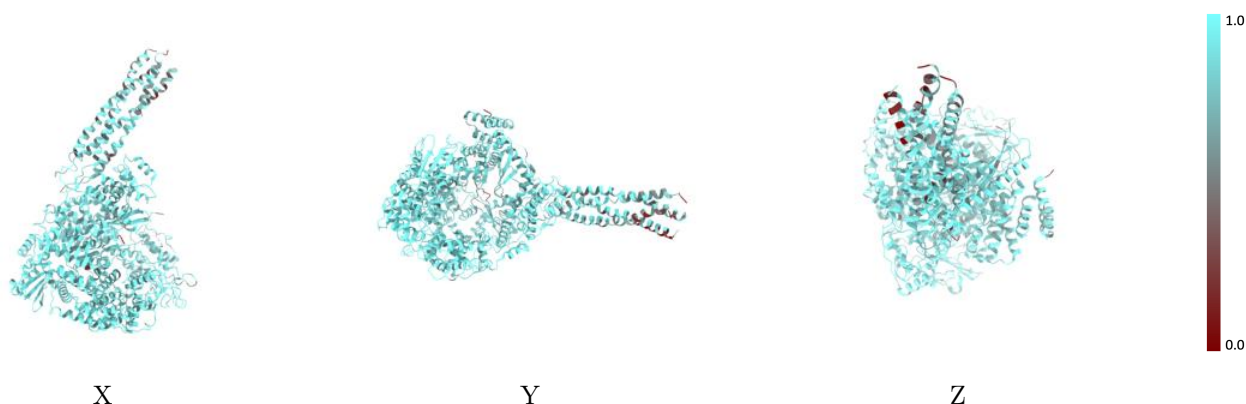
The images above show the 3D surface view of the map at the recommended contour level 0.178 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



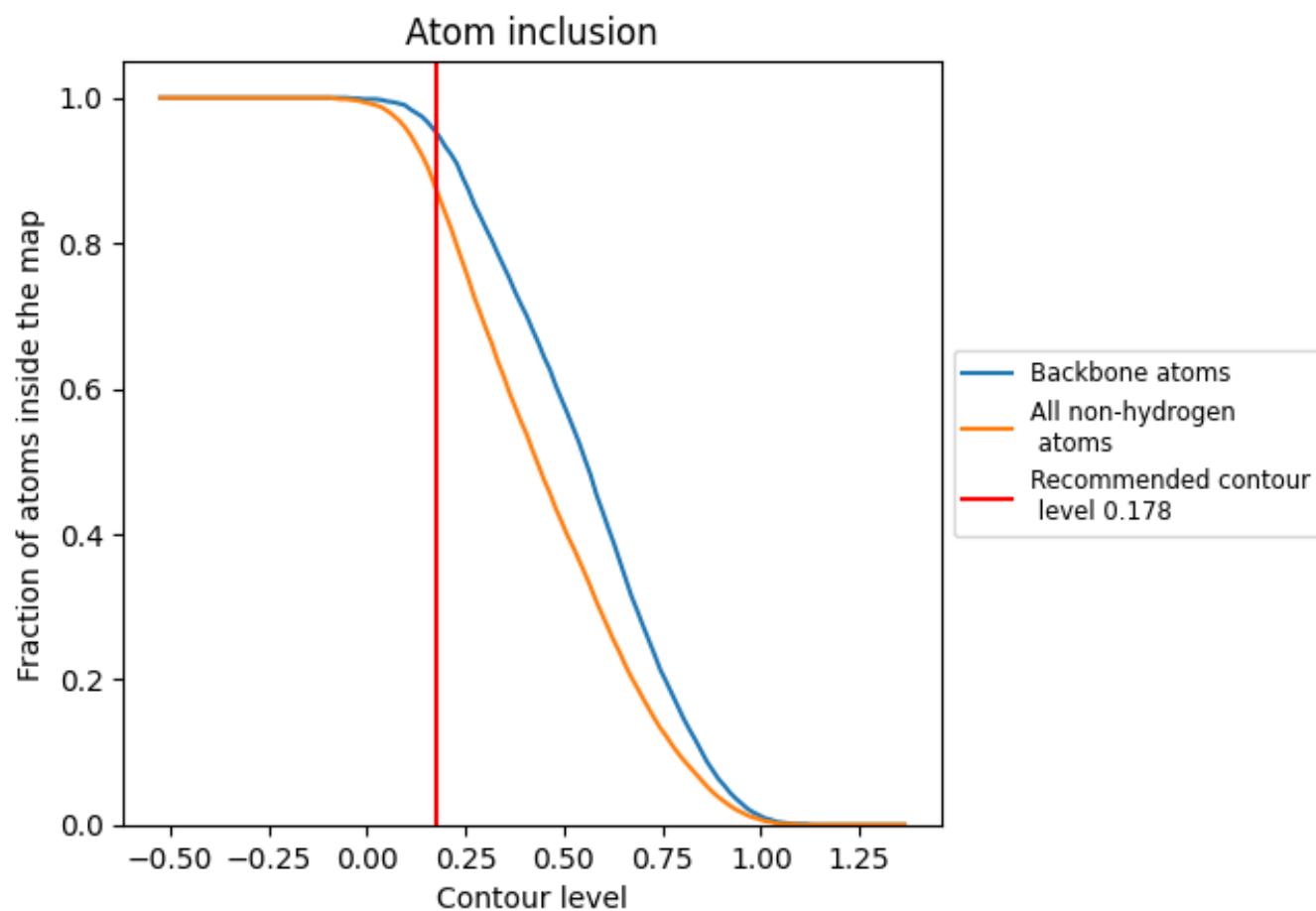
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.178).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 87% 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 (0.178) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8720	0.3570
A	0.9000	0.3840
B	0.7550	0.1610
C	0.7340	0.2180
D	0.7570	0.2520
E	0.6960	0.2470

