



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:09 PM UTC

PDB ID : 6IDL / pdb_00006idl
EMDB ID : EMD-9651
Title : Cryo-EM structure of Immature Dengue virus serotype 3 in complex with human antibody 1H10 Fab at pH 5.0 (Class II particle)
Authors : Wirawan, M.; Fibriansah, G.; Ng, T.S.; Zhang, Q.; Kostyuchenko, V.A.; Shi, J.; Lok, S.M.
Deposited on : 2018-09-10
Resolution : 25.00 Å (reported)
Based on initial model : 3IYA

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

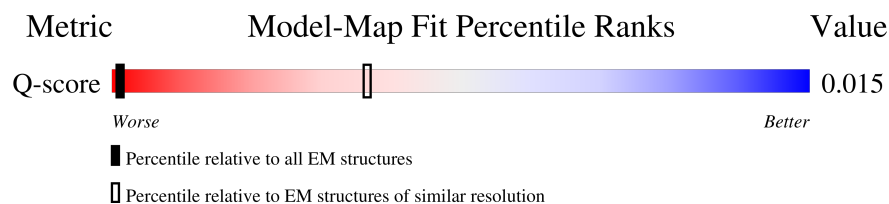
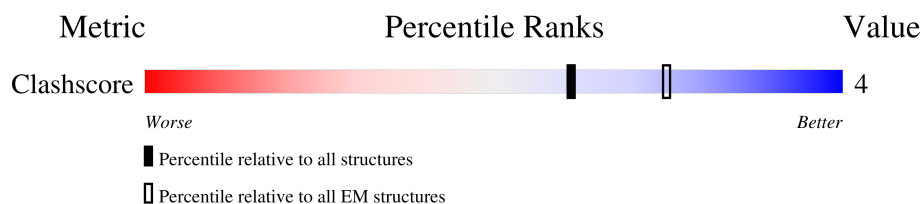
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

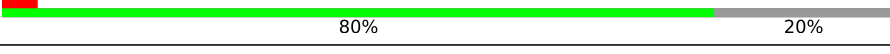
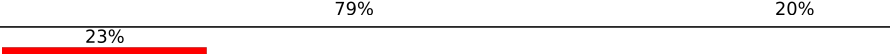
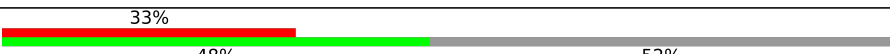
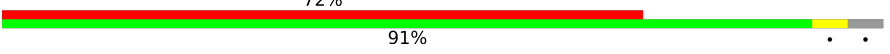
The reported resolution of this entry is 25.00 Å.

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	-
Q-score	-	25397	11 (25.00 - 25.00)

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	493	
1	B	493	
1	C	493	
2	E	166	
2	F	166	
3	I	137	

Continued on next page...

Mol	Chain	Length	Quality of chain
3	M	137	17% 91% • •
4	J	116	28% 96% •
4	N	116	• 96% •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1821 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.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	393	Total C 393 393	0	393
1	B	393	Total C 393 393	0	393
1	C	393	Total C 393 393	0	393

- Molecule 2 is a protein called Premembrane protein.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	E	79	Total C 79 79	0	79
2	F	79	Total C 79 79	0	79

- Molecule 3 is a protein called Fab 1H10 heavy chain (V-region).

Mol	Chain	Residues	Atoms	AltConf	Trace
3	I	131	Total C 131 131	0	131
3	M	131	Total C 131 131	0	131

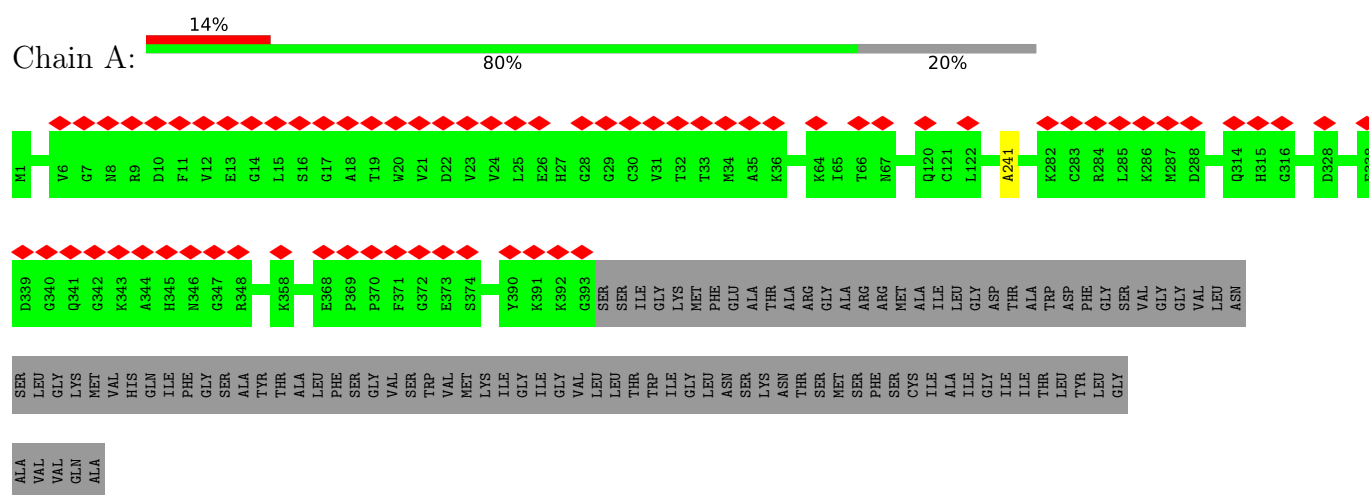
- Molecule 4 is a protein called Fab 1H10 light chain (V-region).

Mol	Chain	Residues	Atoms	AltConf	Trace
4	J	111	Total C 111 111	0	111
4	N	111	Total C 111 111	0	111

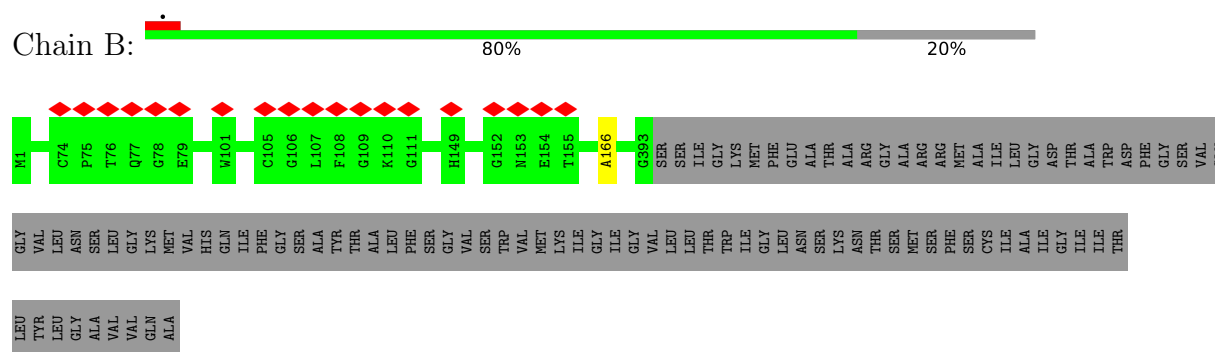
3 Residue-property plots

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.

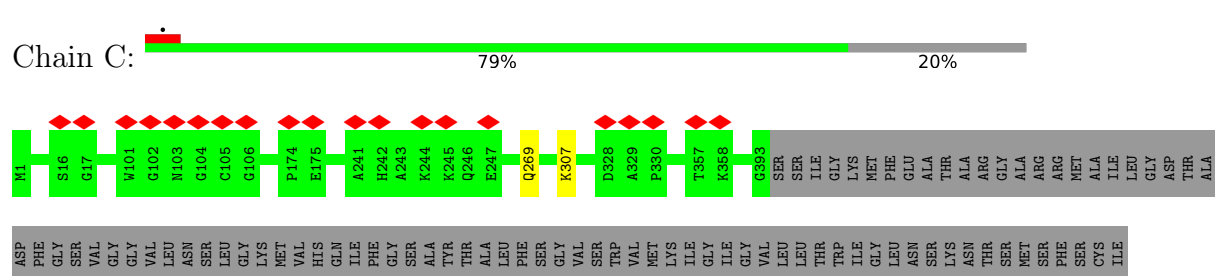
• Molecule 1: Envelope protein



• Molecule 1: Envelope protein



• Molecule 1: Envelope protein



ALA
ILE
GLY
ILE
ILE
THR
LEU
LEU
TYR
GLY
ALA
VAL
GLN
ALA

• Molecule 2: Premembrane protein

Chain E: 

FI R19 G20 K21 S22 L23 L24 F25 K26 T27 A28 S29 G30 I31 N32 M33 C34 T35 L36 I37 A38 M39 D40 L41 H55 I56 T57 E58 V59 E60 P61 D65 C66 W67 C68 N69 L70 T71 S72 T79 CYS ASN GLN GLY HIS ARG ASP LYS SER VAL ALA LEU

ALA PRO HIS VAL MET LEU VAL THR PRO SER MET THR

ILE
LEU
LEU
MET
LEU
VAL
THR
PRO
SER
MET
THR

• Molecule 2: Premembrane protein

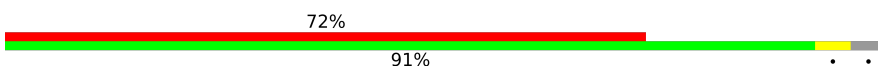
Chain F: 

FI G15 K16 R19 G20 K21 S22 L23 S29 G30 I31 N32 M33 C34 T35 L36 I37 A38 M39 D40 L41 G42 E43 D47 T48 V49 T50 Y51 K52 C53 P54 H55 I56 T57 E58 V59 E60 P61 E62 D63 I64 D65 C66 W67 C68 N69 L70 T71 S72 T73 W74 V75 T76 G78 T79

CYS ASN GLN ALA GLY HIS ARG ASP LYS ARG SER VAL ALA ALA LEU LEU LEU VAL THR PRO SER MET THR

LEU
ALA
HIS
TYR
ILE
GLY
THR
SER
LEU
THR
GLN
LYS
VAL
VAL
PHE
ILE
LEU
LEU
MET
VAL
THR
PRO
SER
MET
THR

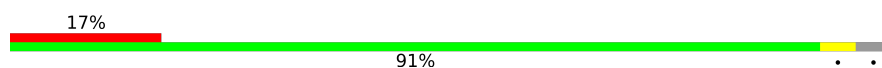
• Molecule 3: Fab 1H10 heavy chain (V-region)

Chain I: 

Q1 V2 Q3 L4 V5 E6 S7 G8 G9 G10 V11 V12 Q13 P14 G15 R16 S17 L18 R19 L20 S21 C22 A23 A24 A25 S26 G26 F27 T28 F29 N31 N32 F32 A33 M34 H35 W36 E46 W47 V48 S49 L50 L51 S52 S53 D54 G55 S56 N57 X58 Y59 N60 A61 D62 S63 V64 R65 G66 R67 F68

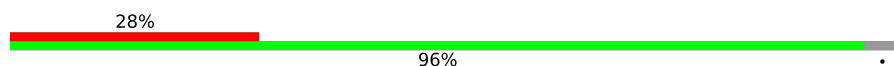
S69 I70 S71 R72 D73 W74 S75 K76 N77 T78 L79 Y80 L81 Q82 M83 H84 S85 L86 R87 L88 E89 D90 T91 C96 V97 T104 Q105 A106 W107 S108 T109 N110 Y111 F112 Y113 V126 T127 V128 S129 S130 A131 SER THR LYS GLY PRO SER

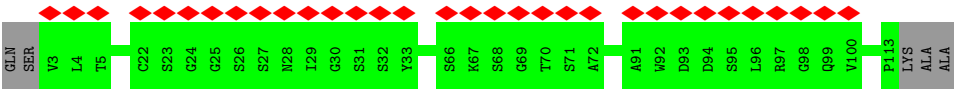
• Molecule 3: Fab 1H10 heavy chain (V-region)

Chain M: 

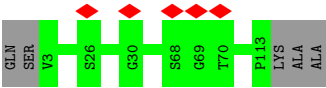
Q1 G8 G9 G10 V11 V12 Q13 P14 G15 R16 S17 L18 R19 G66 R67 Q82 M83 N84 S85 L86 R87 T104 Q105 T109 N110 V128 S129 S130 A131 SER THR LYS GLY PRO SER

• Molecule 4: Fab 1H10 light chain (V-region)

Chain J: 



• Molecule 4: Fab 1H10 light chain (V-region)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	3106	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	18	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	47000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	7.592	Depositor
Minimum map value	-3.298	Depositor
Average map value	0.043	Depositor
Map value standard deviation	0.993	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	870.4, 870.4, 870.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.7, 1.7, 1.7	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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	393	0	0	1	0
1	B	393	0	0	1	0
1	C	393	0	0	2	0
2	E	79	0	0	0	0
2	F	79	0	0	0	0
3	I	131	0	0	3	0
3	M	131	0	0	3	0
4	J	111	0	0	0	0
4	N	111	0	0	0	0
All	All	1821	0	0	8	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 4.

The worst 5 of 8 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:241:ALA:CA	1:C:269:GLN:CA	2.61	0.79
3:M:104:THR:CA	3:M:105:GLN:CA	2.85	0.55
3:M:109:THR:CA	3:M:110:ASN:CA	2.85	0.54
3:I:104:THR:CA	3:I:105:GLN:CA	2.85	0.54
3:I:109:THR:CA	3:I:110:ASN:CA	2.85	0.54

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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 ⓘ

There are no chain breaks in this entry.

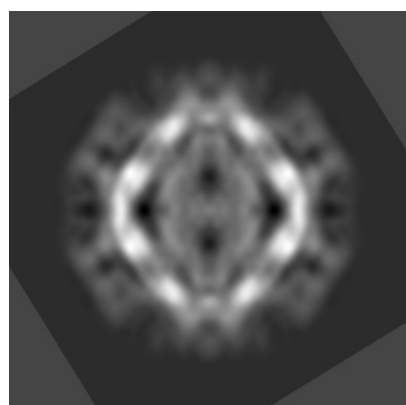
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9651. These allow visual inspection of the internal detail of the map and identification of artifacts.

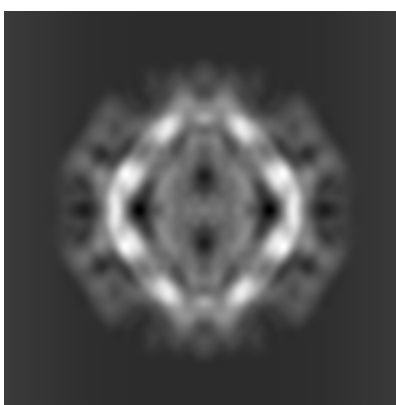
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

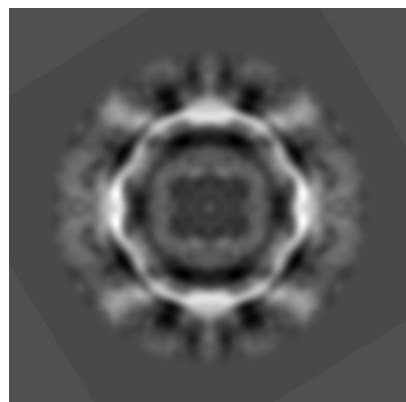


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256



Y Index: 256



Z Index: 256

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: 207



Y Index: 207

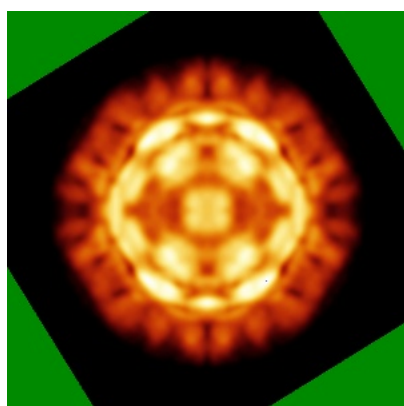


Z Index: 305

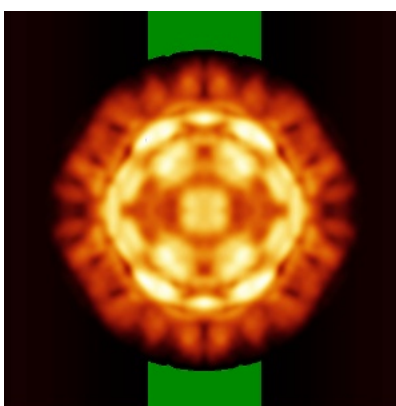
The images above show the largest variance slices of the map in three orthogonal directions.

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

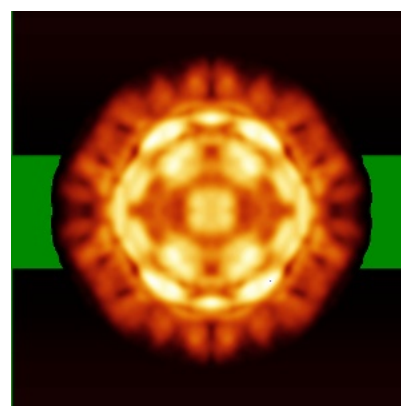
6.4.1 Primary map



X



Y

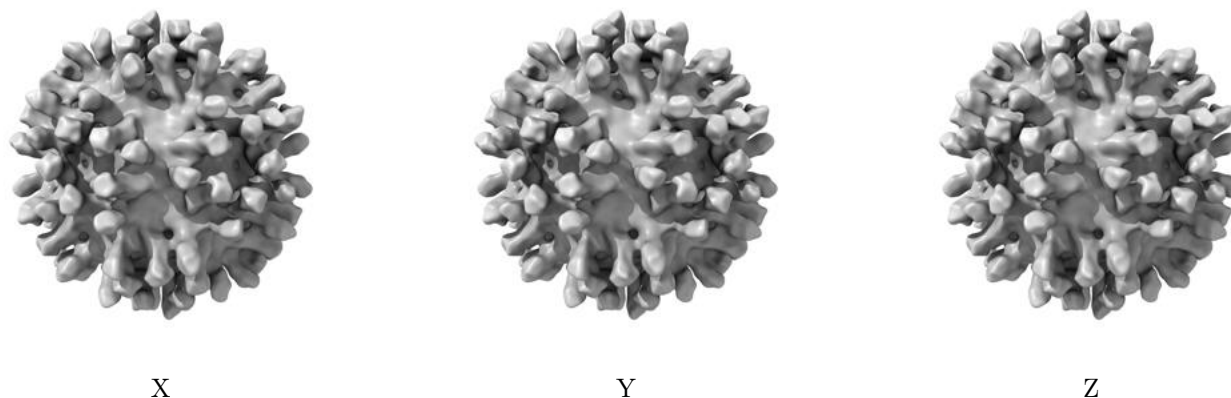


Z

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 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

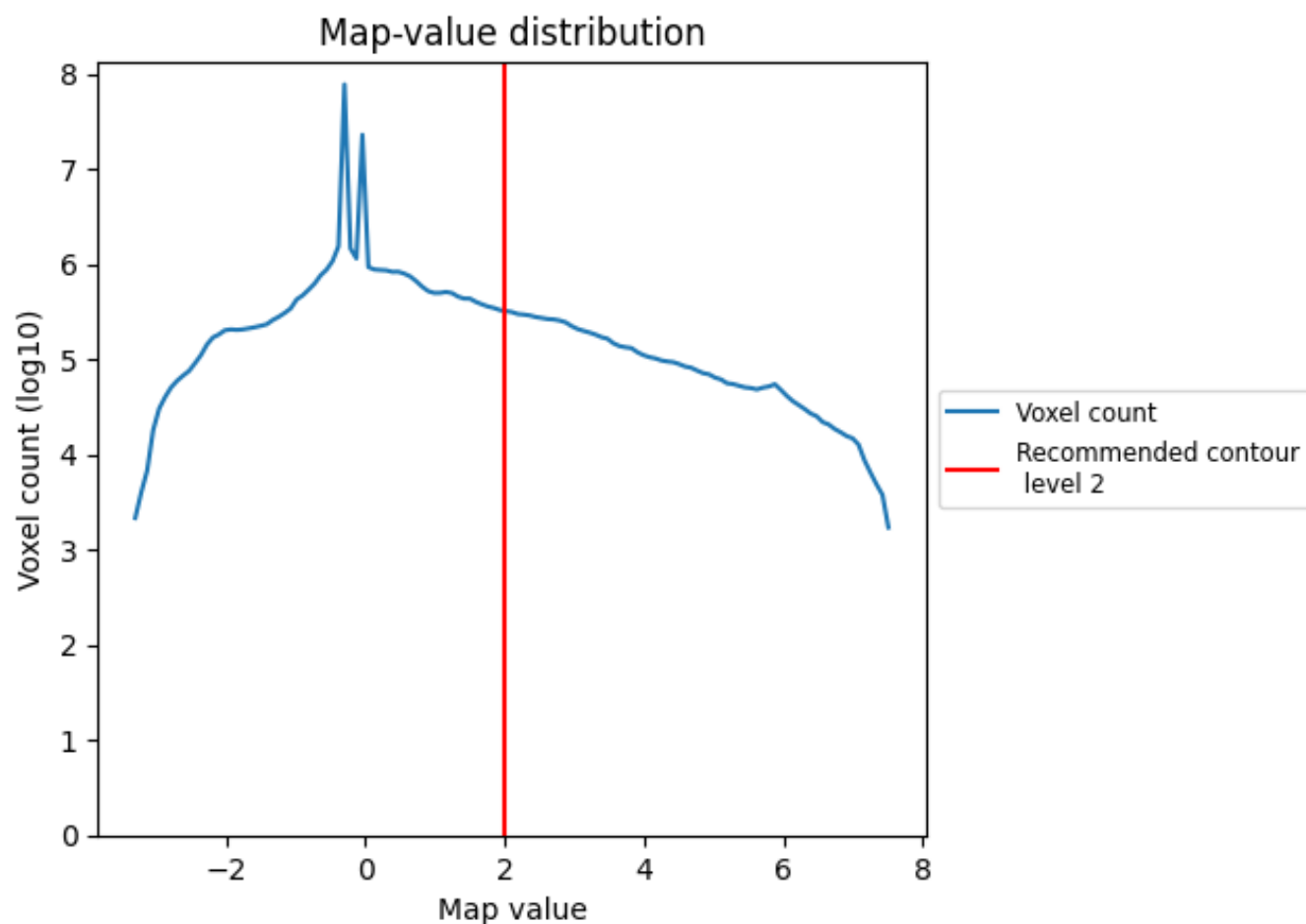
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

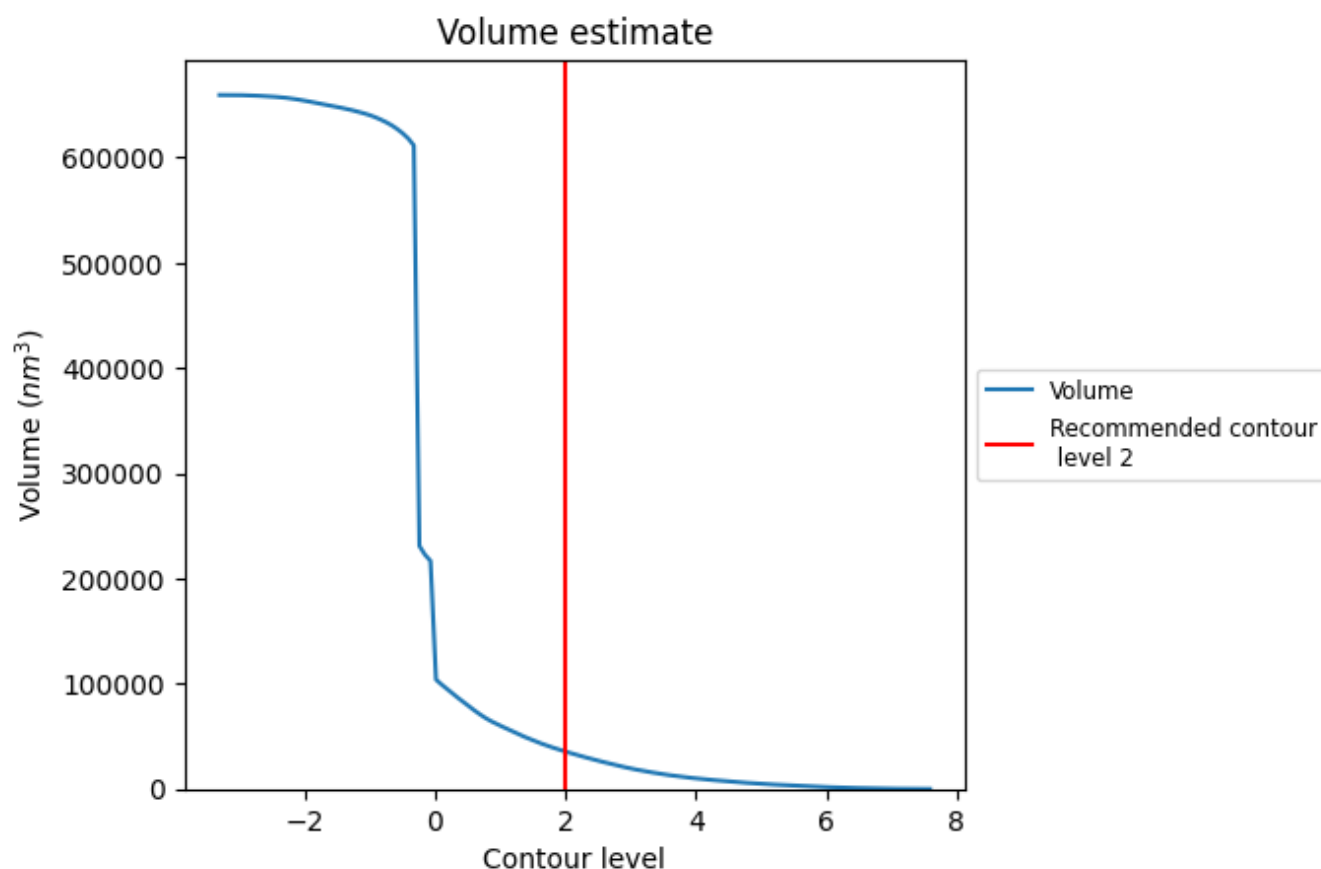
This section contains the results of statistical analysis of the map.

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.

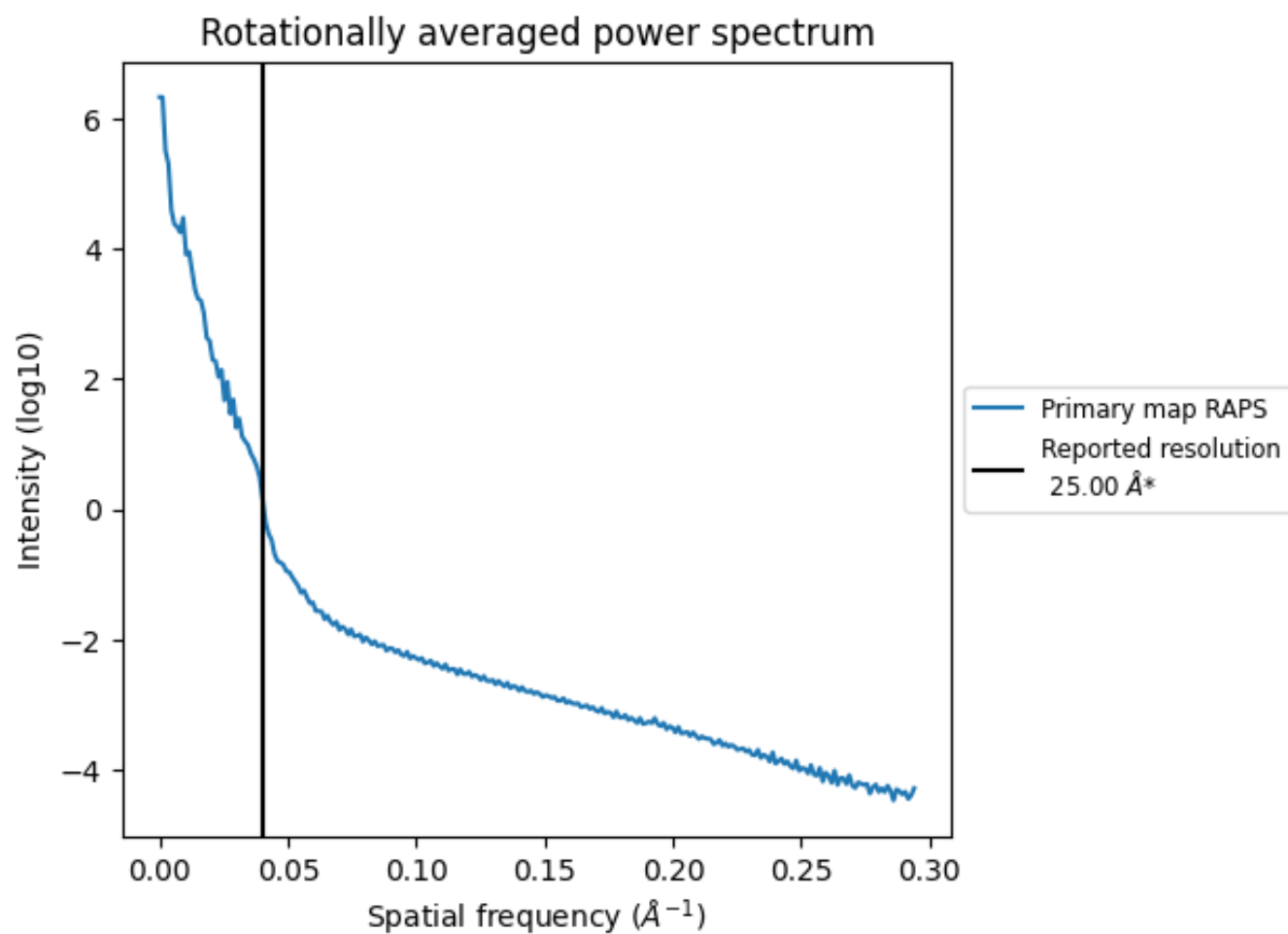
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 35599 nm^3 ; this corresponds to an approximate mass of 32157 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 ⓘ

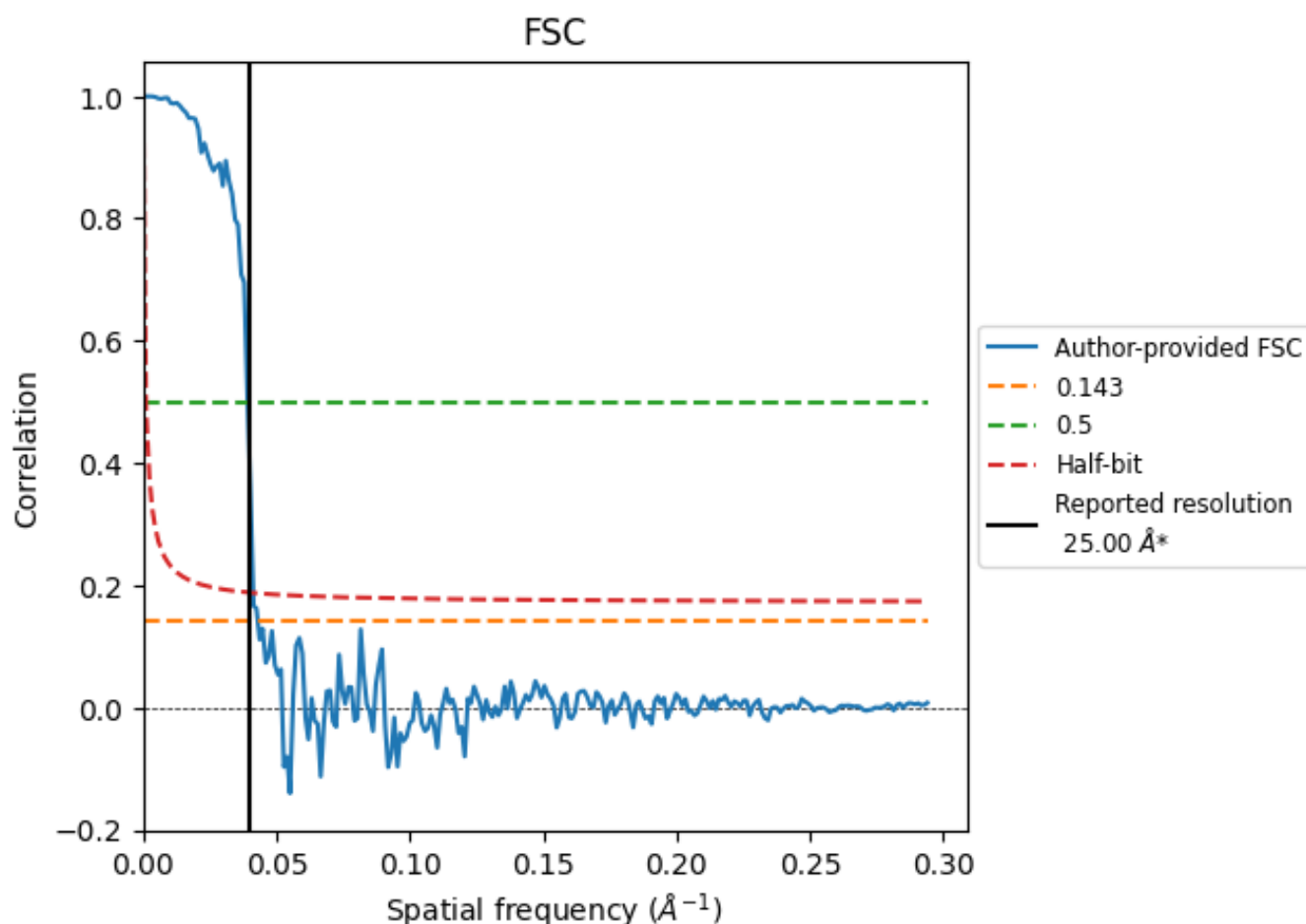


*Reported resolution corresponds to spatial frequency of 0.040 Å⁻¹

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 0.040 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	25.00	-
Author-provided FSC curve	23.31	25.58	24.27
Unmasked-calculated*	-	-	-

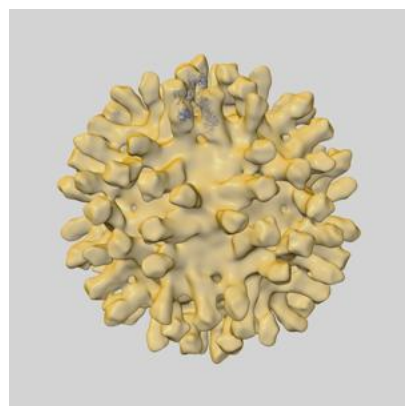
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

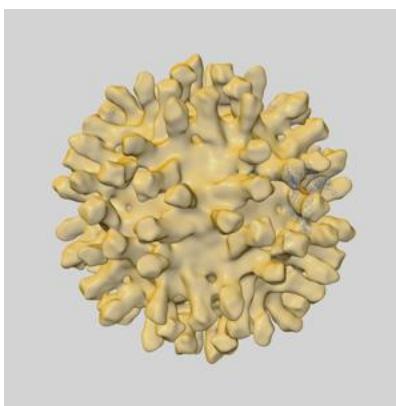
This section contains information regarding the fit between EMDB map EMD-9651 and PDB model 6IDL. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

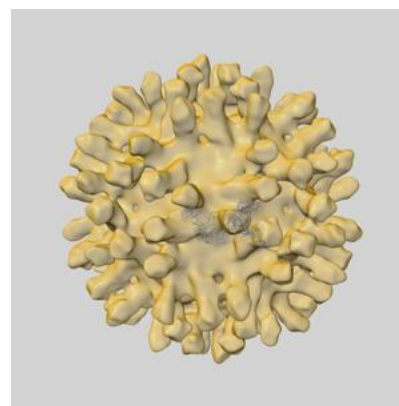
9.1.1 Map-model overlay [i](#)



X

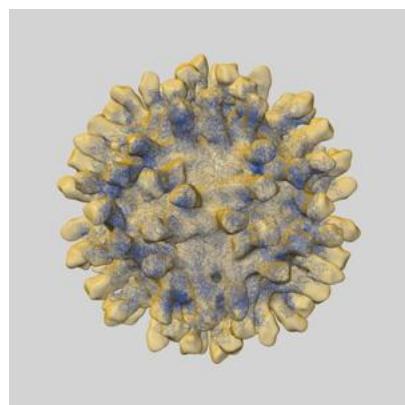


Y

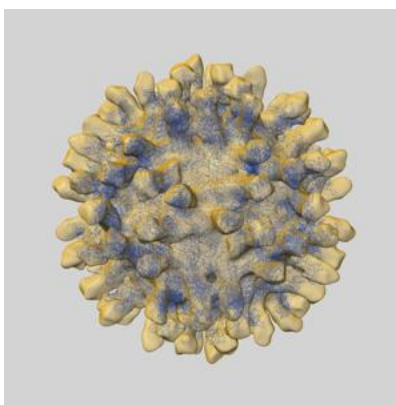


Z

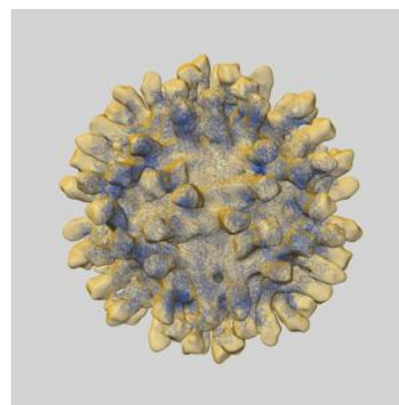
9.1.2 Map-model assembly overlay [i](#)



X



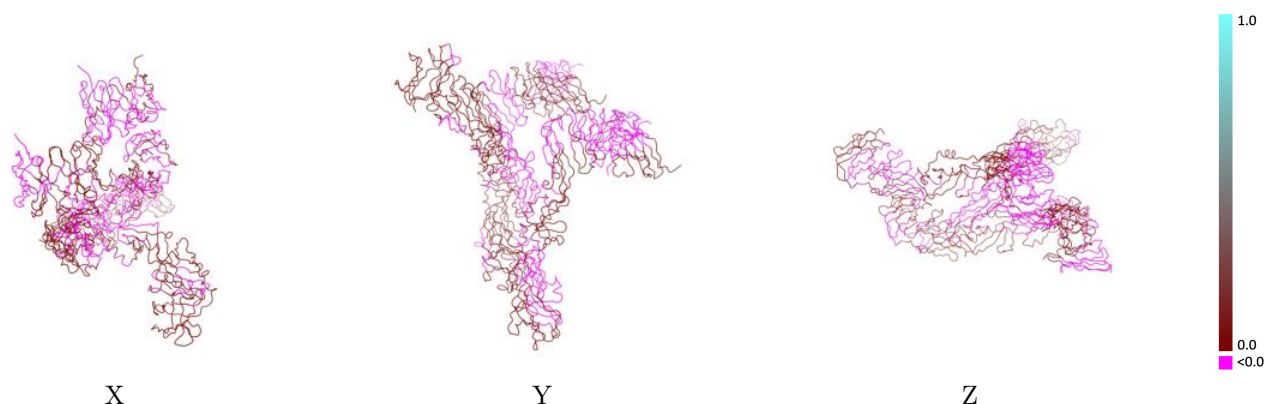
Y



Z

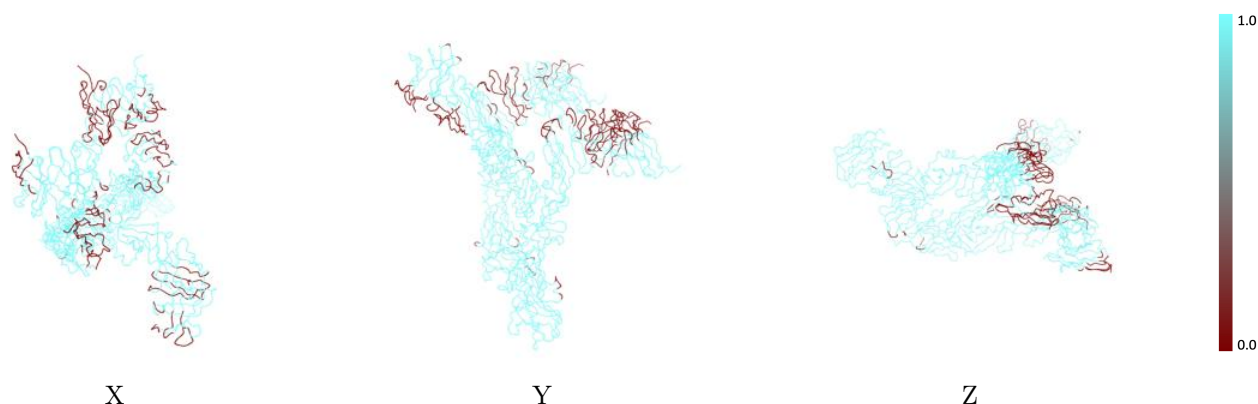
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



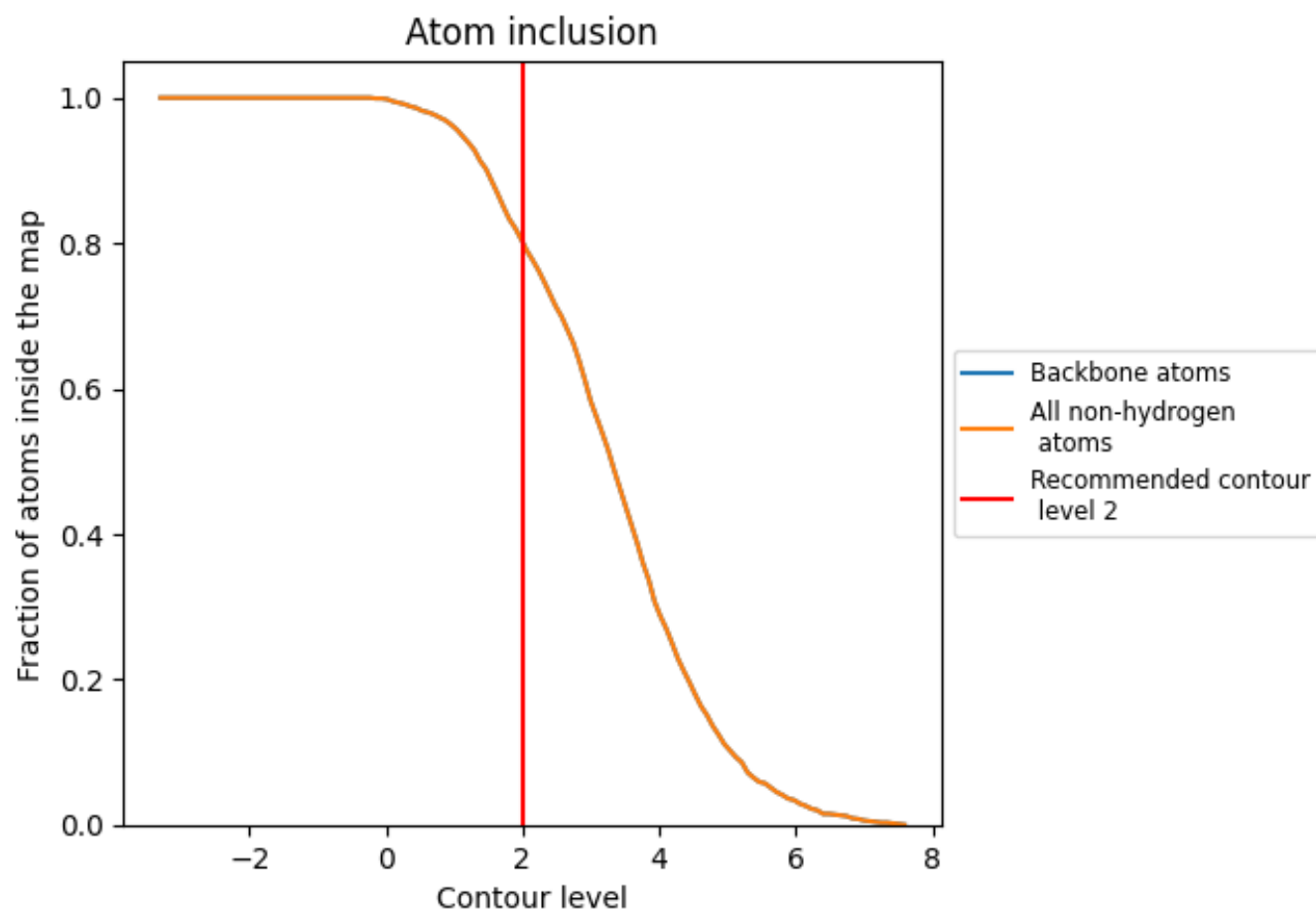
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8020	0.0150
A	0.8240	0.0280
B	0.9520	0.0130
C	0.9490	0.0320
E	0.5190	-0.0060
F	0.3040	-0.0210
I	0.2440	-0.0420
J	0.7120	0.0150
M	0.8240	0.0080
N	0.9550	0.0270

1.0

0.0

<0.0