



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 11:16 PM UTC

PDB ID : 3IYK / pdb_00003iyk
EMDB ID : EMD-5147
Title : Bluetongue virus structure reveals a sialic acid binding domain, amphipathic helices and a central coiled coil in the outer capsid proteins
Authors : Zhang, X.; Boyce, M.; Bhattacharya, B.; Zhang, X.; Schein, S.; Roy, P.; Zhou, Z.H.
Deposited on : 2010-01-25
Resolution : 7.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

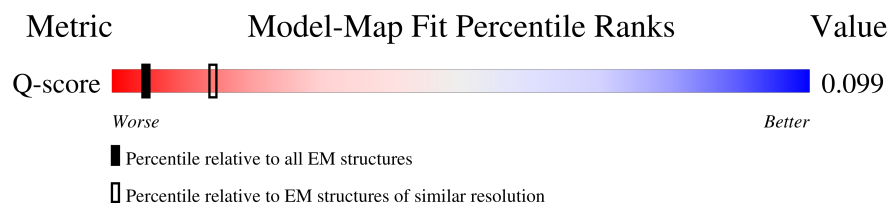
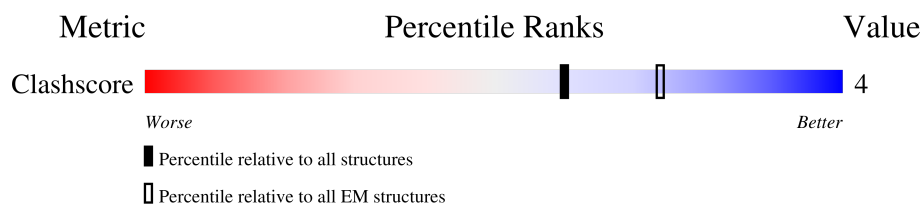
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.00 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	483 (6.50 - 7.50)

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	526		
1	B	526		
1	C	526		
1	D	526		
1	E	526		
1	F	526		

Continued on next page...

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Mol	Chain	Length	Quality of chain
2	G	600	 23%76%
2	I	600	 23%76%
2	K	600	 23%76%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2331 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.

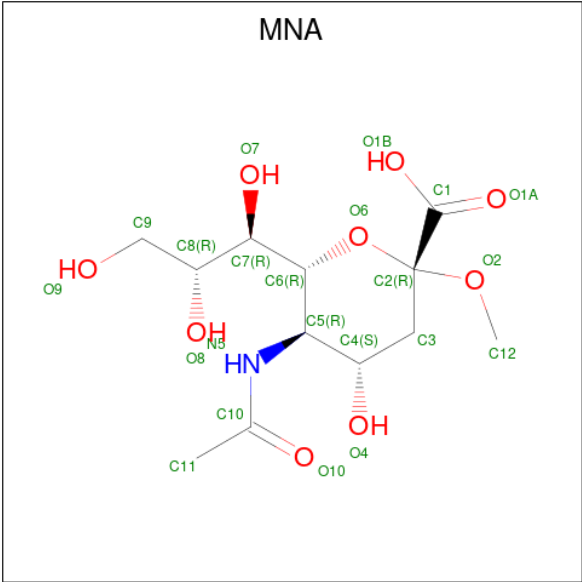
- Molecule 1 is a protein called VP5.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	307	Total C 307 307	0	307
1	B	307	Total C 307 307	0	307
1	C	307	Total C 307 307	0	307
1	D	307	Total C 307 307	0	307
1	E	307	Total C 307 307	0	307
1	F	307	Total C 307 307	0	307

- Molecule 2 is a protein called VP2.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	G	141	Total C 141 141	0	141
2	I	141	Total C 141 141	0	141
2	K	141	Total C 141 141	0	141

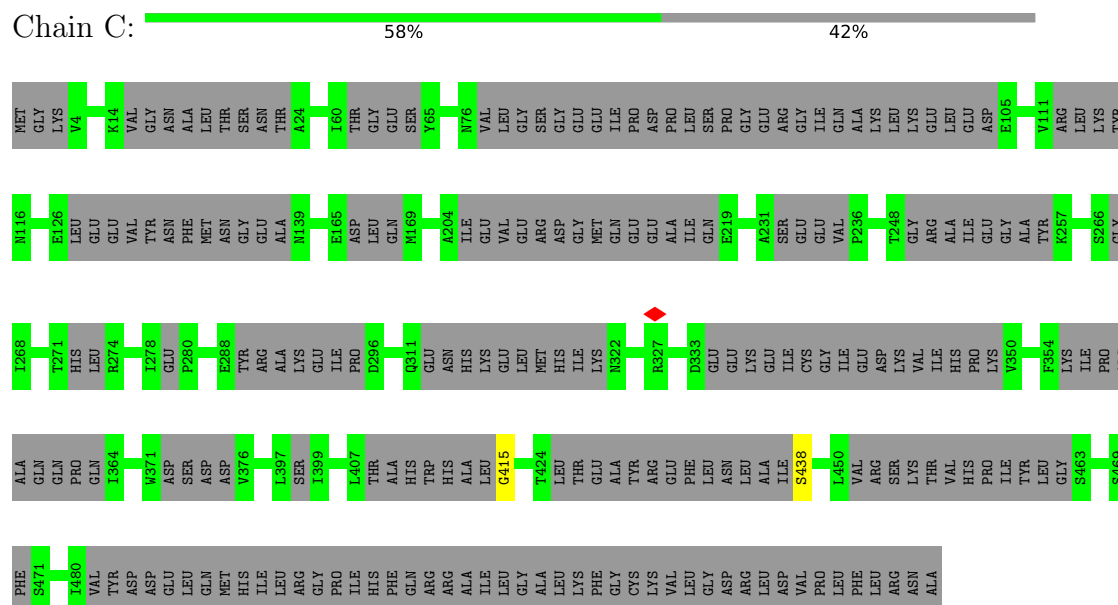
- Molecule 3 is 2-O-methyl-5-N-acetyl-alpha-D-neuraminic acid (CCD ID: MNA) (formula: C₁₂H₂₁NO₉).



Mol	Chain	Residues	Atoms				AltConf
3	G	1	Total	C	N	O	1
			22	12	1	9	
3	I	1	Total	C	N	O	1
			22	12	1	9	
3	K	1	Total	C	N	O	1
			22	12	1	9	

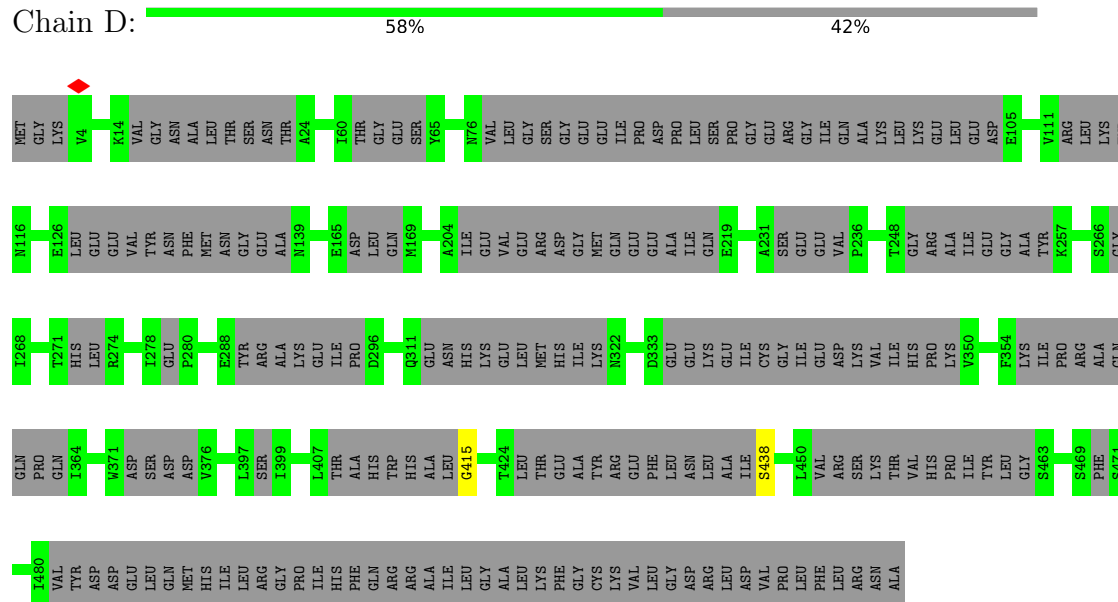
- Molecule 1: VP5

Chain C:



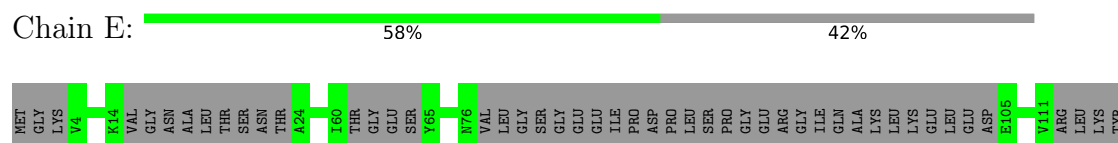
- Molecule 1: VP5

Chain D:

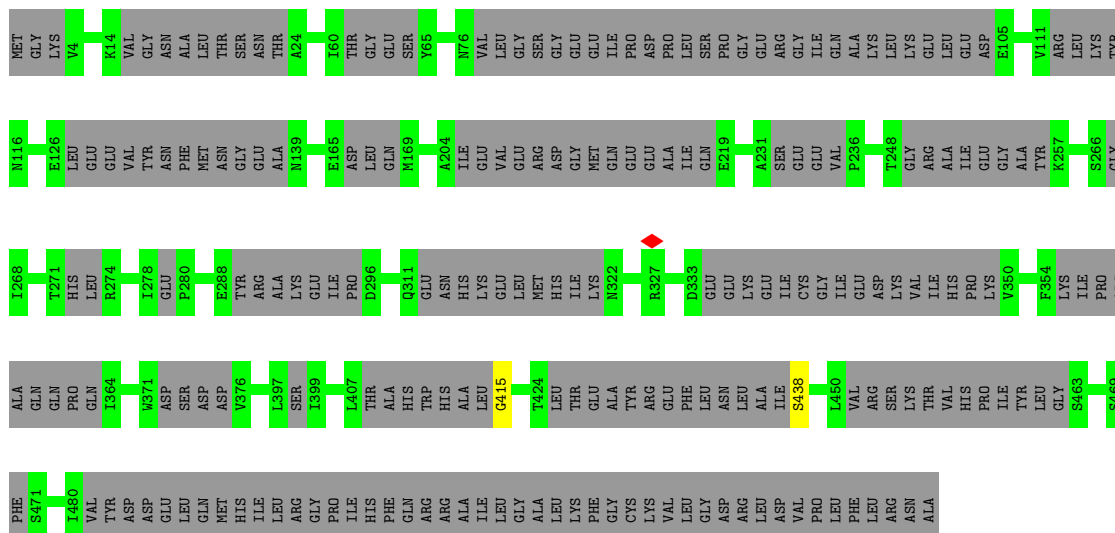


- Molecule 1: VP5

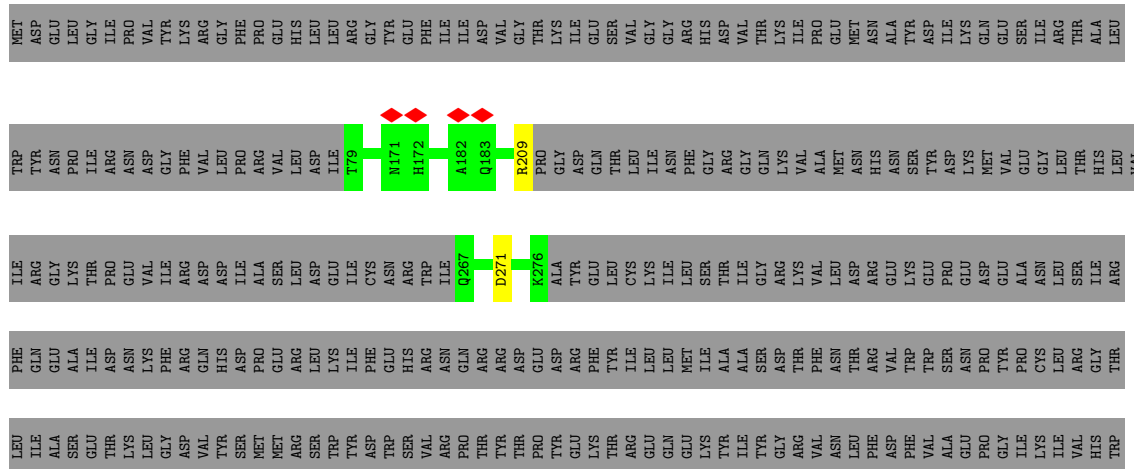
Chain E:



- Molecule 1: VP5



- Molecule 2: VP2



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

SER
PRO
ILE
THR
ALA
ASP
PRO
ILE
GLU
LEU
GLN
ARG
LEU
THR
LEU
ALA
ARG
PHE
TYR
ASP
ILE
ARG
PRO
ALA
LEU
ARG
GLY
GLN
ALA
LEU
SER
ARG
GLN
GLN
ALA
GLN
SER
THR
TYR
ASP
GLU
GLU
ILE
SER
LYS
GLN
ARG
ASP
TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	3400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	79787	Depositor
Image detector	GENERIC CCD	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.080	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.019	Depositor
Map size ($\text{\AA}$)	940.0, 940.0, 940.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.88, 1.88, 1.88	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	307	0	0	1	0
1	B	307	0	0	1	0
1	C	307	0	0	1	0
1	D	307	0	0	1	0
1	E	307	0	0	1	0
1	F	307	0	0	1	0
2	G	141	0	0	2	0
2	I	141	0	0	2	0
2	K	141	0	0	2	0
3	G	22	0	20	0	0
3	I	22	0	20	0	0
3	K	22	0	20	0	0
All	All	2331	0	60	9	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.

All (9) 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:C:415:GLY:CA	1:C:438:SER:CA	2.38	1.02
1:D:415:GLY:CA	1:D:438:SER:CA	2.38	1.02
1:E:415:GLY:CA	1:E:438:SER:CA	2.38	1.02
1:B:415:GLY:CA	1:B:438:SER:CA	2.38	1.01
1:A:415:GLY:CA	1:A:438:SER:CA	2.38	1.01
1:F:415:GLY:CA	1:F:438:SER:CA	2.38	1.00
2:G:271:ASP:CA	2:K:209:ARG:CA	2.50	0.89
2:I:209:ARG:CA	2:K:271:ASP:CA	2.62	0.78
2:G:209:ARG:CA	2:I:271:ASP:CA	2.64	0.75

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

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MNA	K	1000[C]	-	22,22,22	0.86	2 (9%)	26,32,32	0.81	1 (3%)
3	MNA	I	1000[B]	-	22,22,22	0.85	2 (9%)	26,32,32	0.80	1 (3%)
3	MNA	G	1000[A]	-	22,22,22	0.84	2 (9%)	26,32,32	0.80	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MNA	K	1000[C]	-	-	4/23/41/41	0/1/1/1
3	MNA	I	1000[B]	-	-	4/23/41/41	0/1/1/1
3	MNA	G	1000[A]	-	-	4/23/41/41	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	1000[C]	MNA	C4-C5	2.17	1.55	1.53
3	G	1000[A]	MNA	C4-C5	2.12	1.55	1.53
3	I	1000[B]	MNA	C4-C5	2.12	1.55	1.53
3	I	1000[B]	MNA	C3-C2	2.06	1.55	1.52
3	K	1000[C]	MNA	C3-C2	2.04	1.55	1.52
3	G	1000[A]	MNA	C3-C2	2.01	1.55	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	1000[C]	MNA	O1A-C1-C2	-2.12	117.40	123.79
3	G	1000[A]	MNA	O1A-C1-C2	-2.12	117.41	123.79
3	I	1000[B]	MNA	O1A-C1-C2	-2.10	117.46	123.79

There are no chirality outliers.

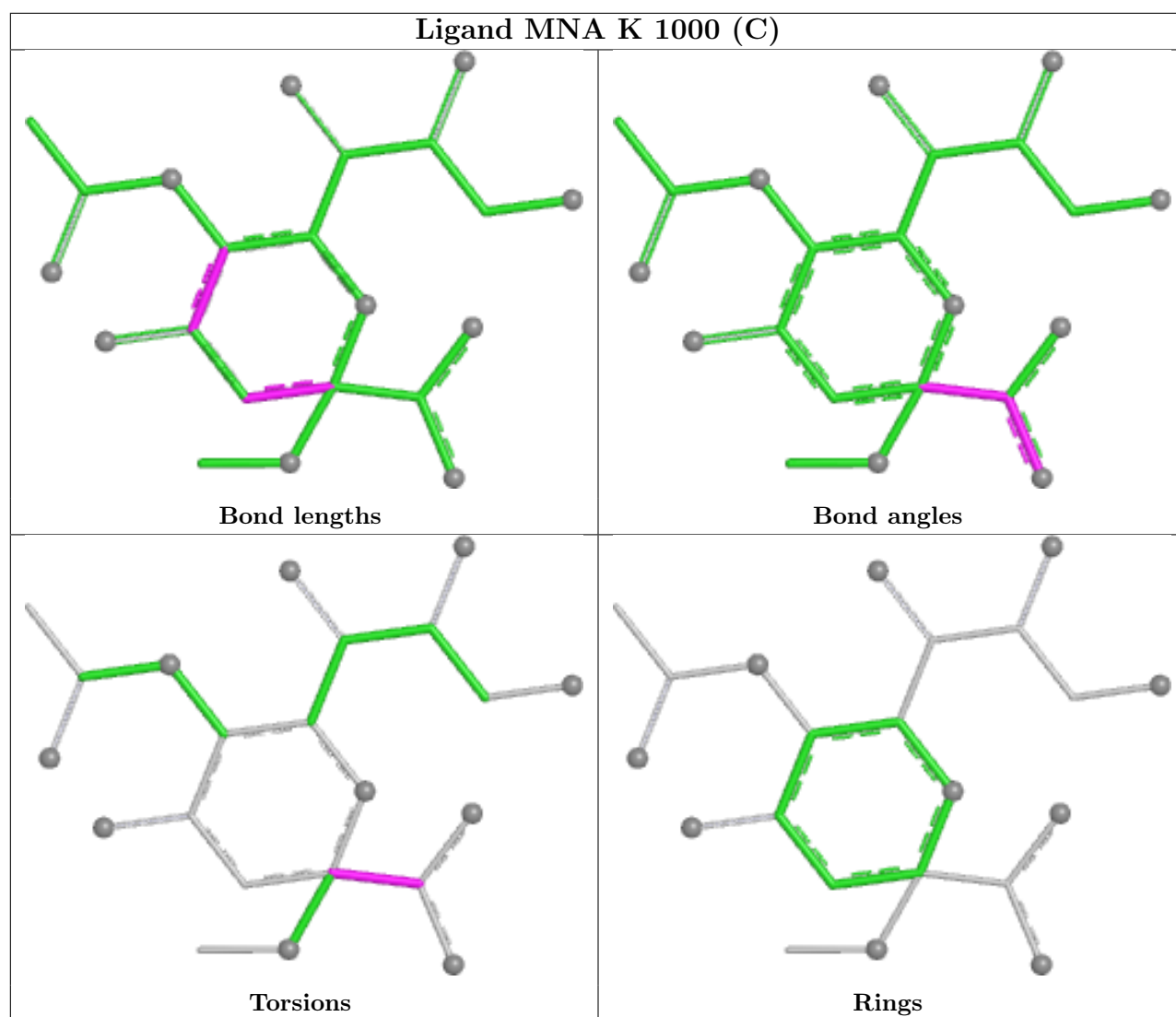
All (12) torsion outliers are listed below:

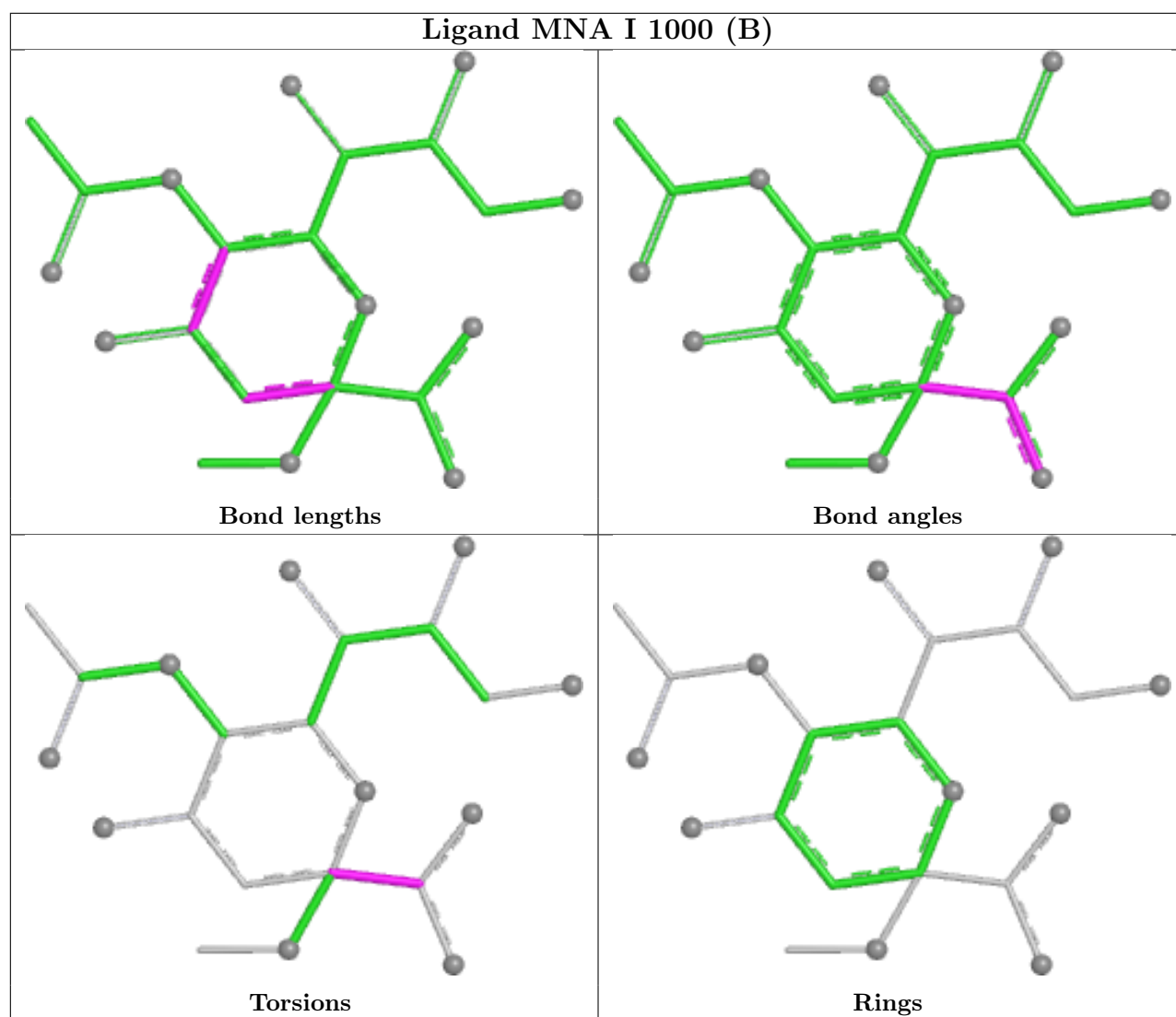
Mol	Chain	Res	Type	Atoms
3	G	1000[A]	MNA	O1B-C1-C2-O2
3	G	1000[A]	MNA	O1B-C1-C2-O6
3	I	1000[B]	MNA	O1B-C1-C2-O2
3	I	1000[B]	MNA	O1B-C1-C2-O6
3	K	1000[C]	MNA	O1B-C1-C2-O2
3	K	1000[C]	MNA	O1B-C1-C2-O6
3	G	1000[A]	MNA	O1A-C1-C2-O2
3	I	1000[B]	MNA	O1A-C1-C2-O2
3	K	1000[C]	MNA	O1A-C1-C2-O2
3	G	1000[A]	MNA	O1A-C1-C2-C3
3	I	1000[B]	MNA	O1A-C1-C2-C3
3	K	1000[C]	MNA	O1A-C1-C2-C3

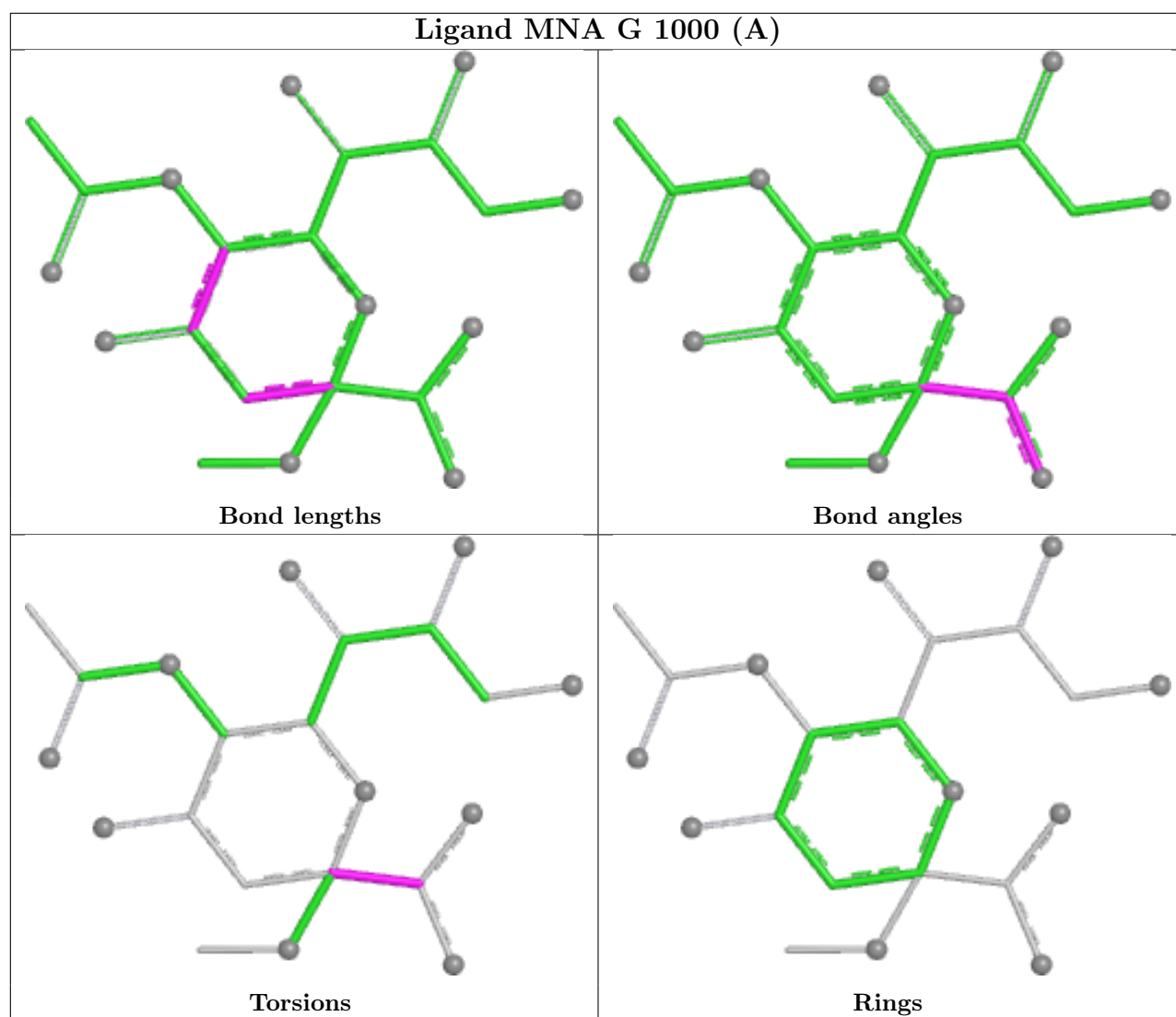
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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.

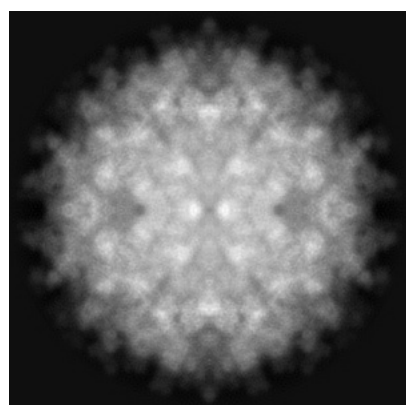
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5147. These allow visual inspection of the internal detail of the map and identification of artifacts.

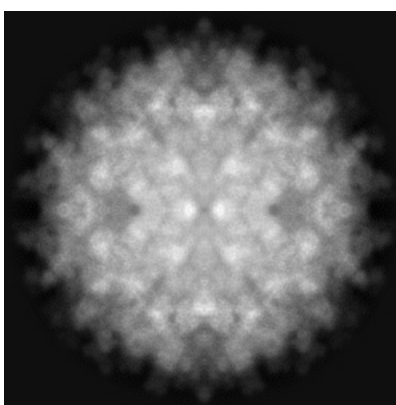
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

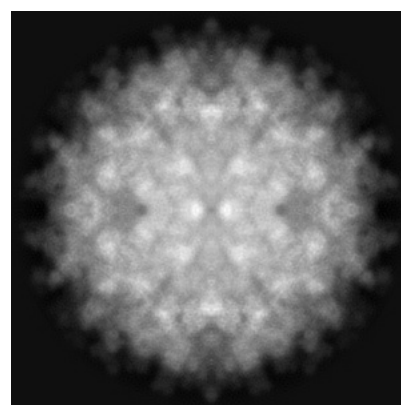
6.1.1 Primary map



X



Y

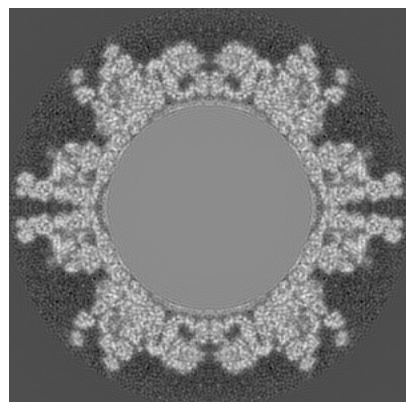


Z

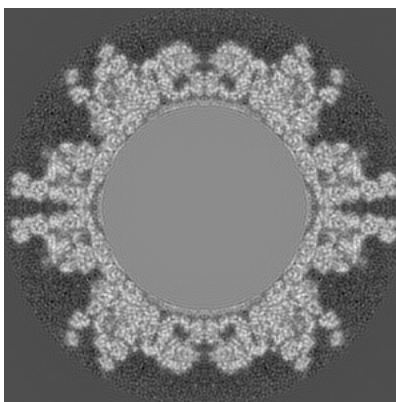
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

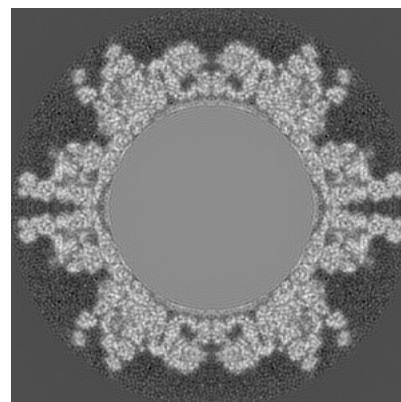
6.2.1 Primary map



X Index: 250



Y Index: 250

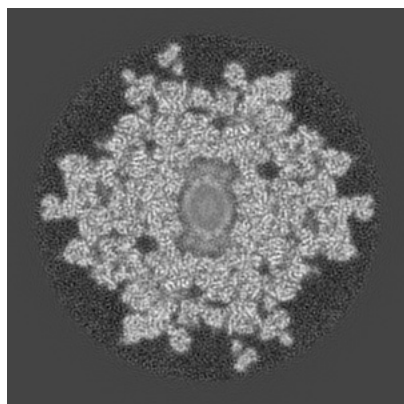


Z Index: 250

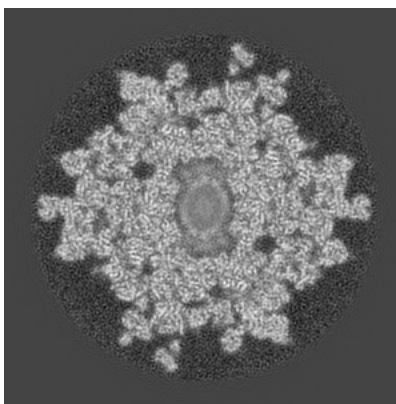
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

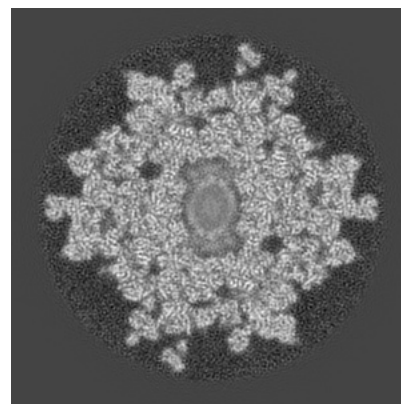
6.3.1 Primary map



X Index: 375



Y Index: 125

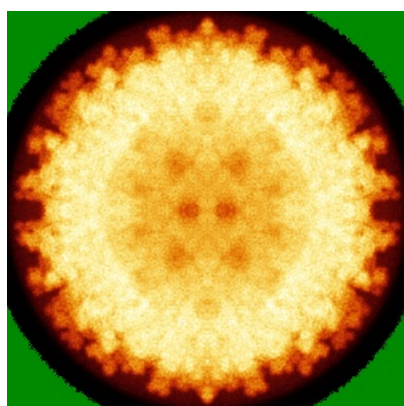


Z Index: 125

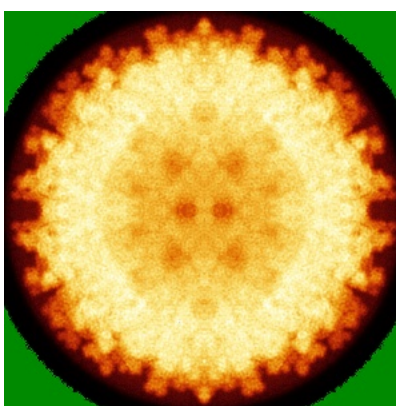
The images above show the largest variance slices of the map in three orthogonal directions.

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

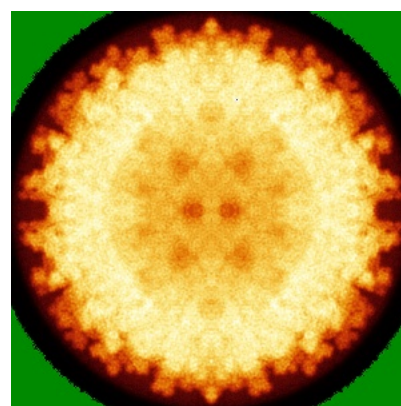
6.4.1 Primary map



X



Y

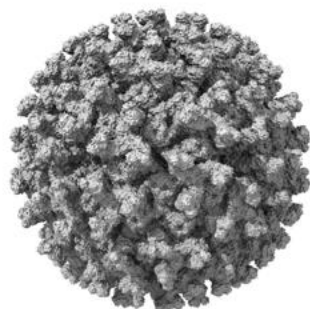


Z

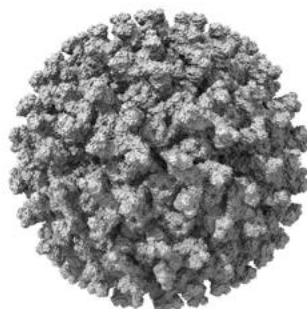
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

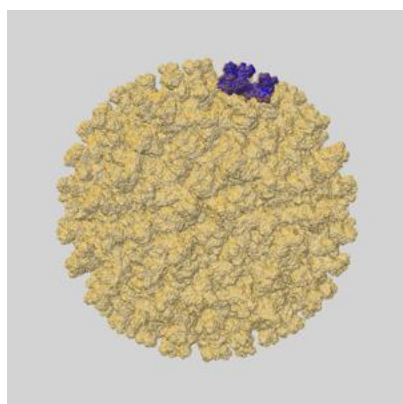
6.6 Mask visualisation [i](#)

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

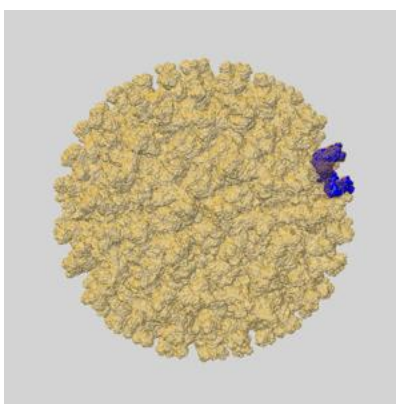
A mask typically either:

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

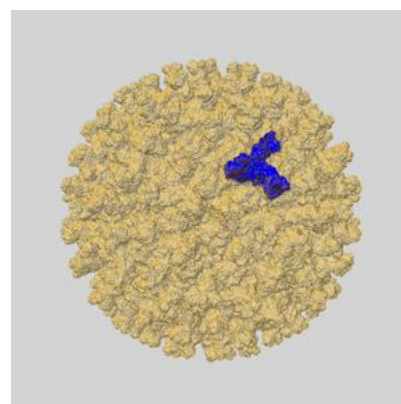
6.6.1 emd_5147_msk_1.map [i](#)



X

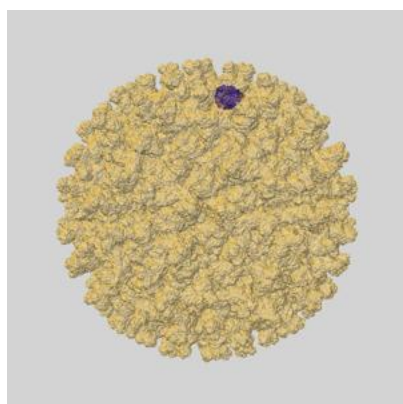


Y

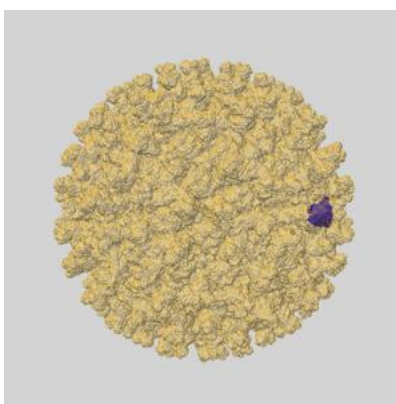


Z

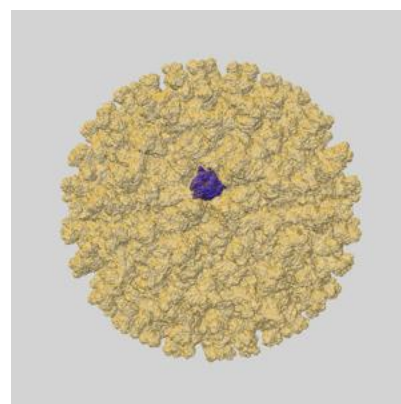
6.6.2 emd_5147_msk_2.map [i](#)



X



Y

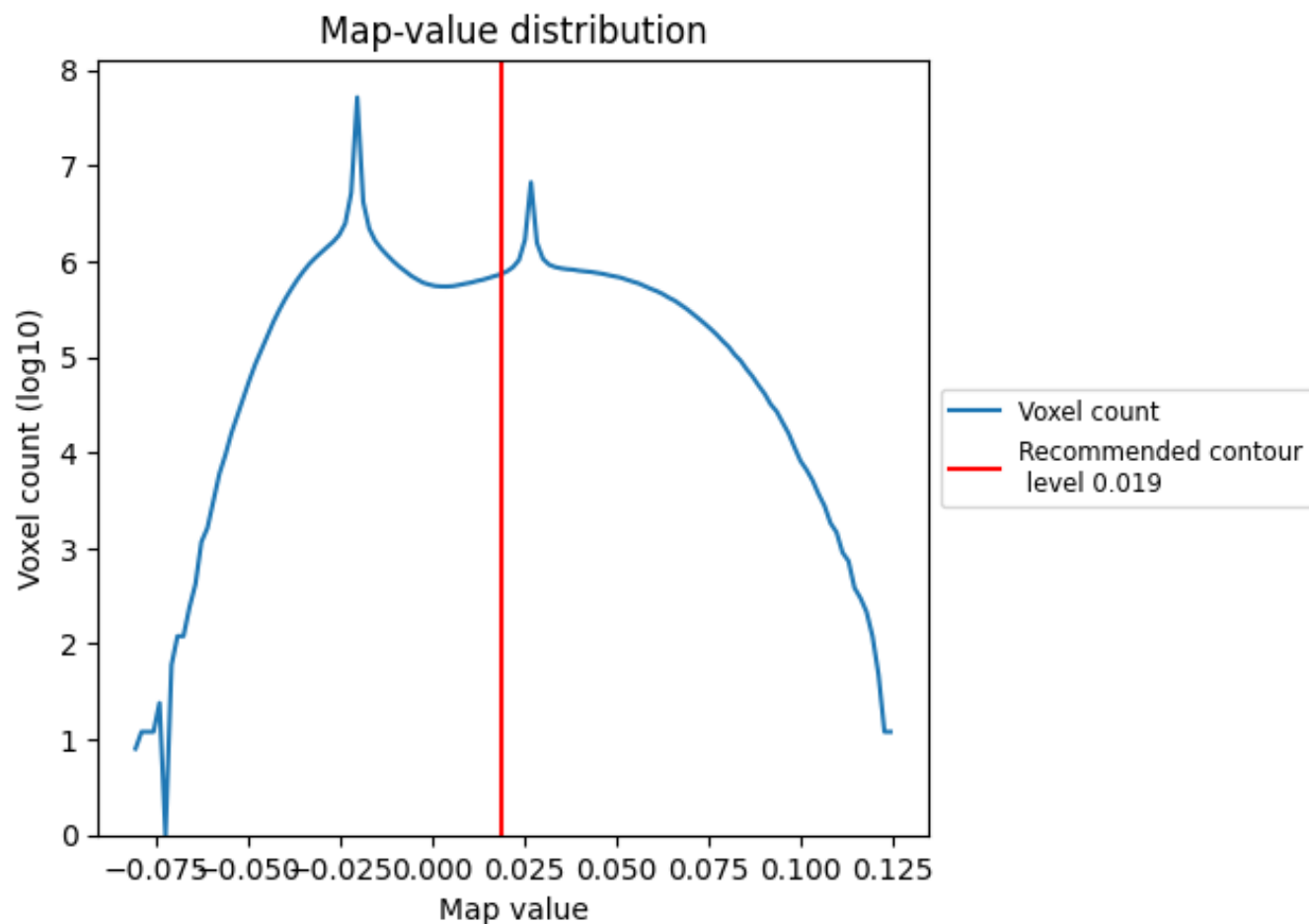


Z

7 Map analysis [i](#)

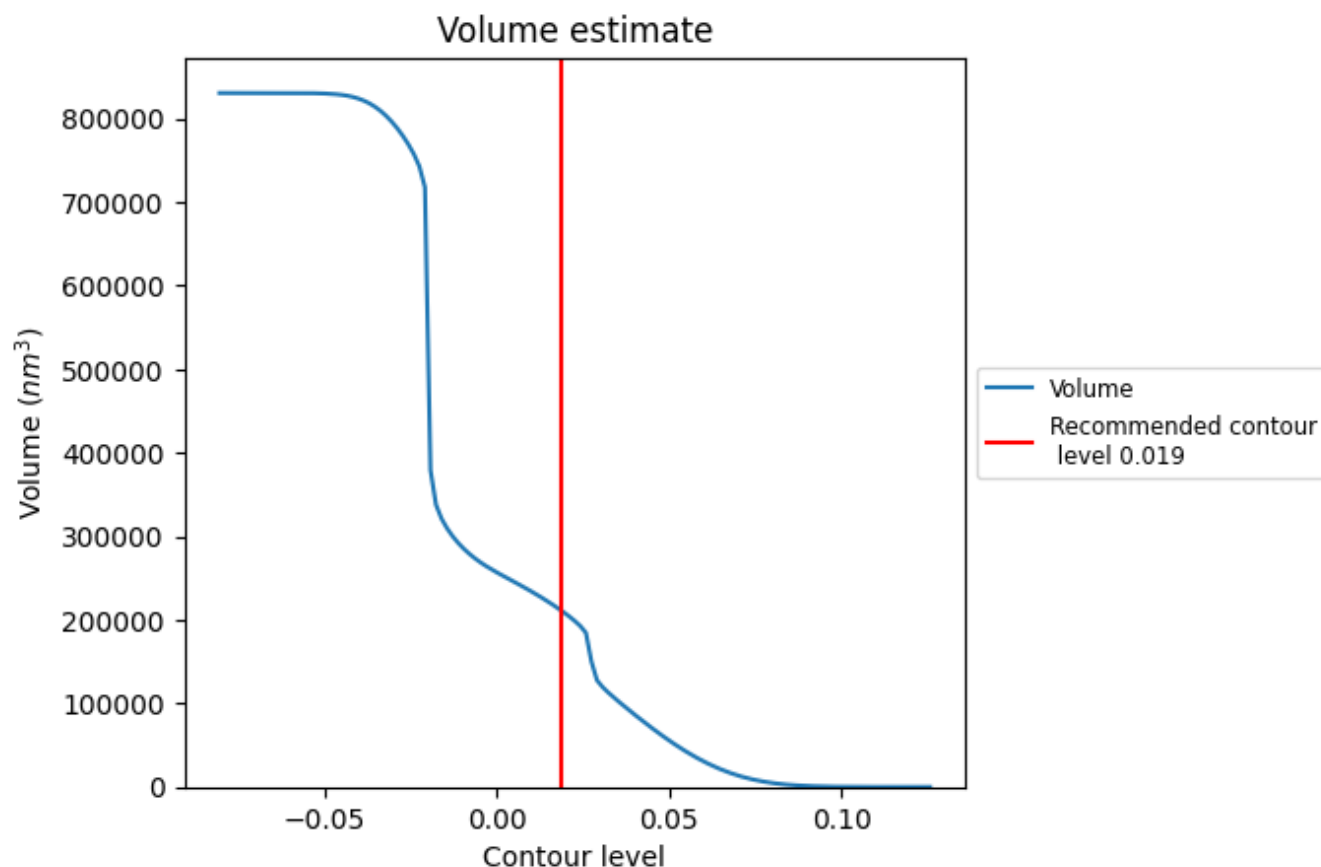
This section contains the results of statistical analysis of the map.

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.

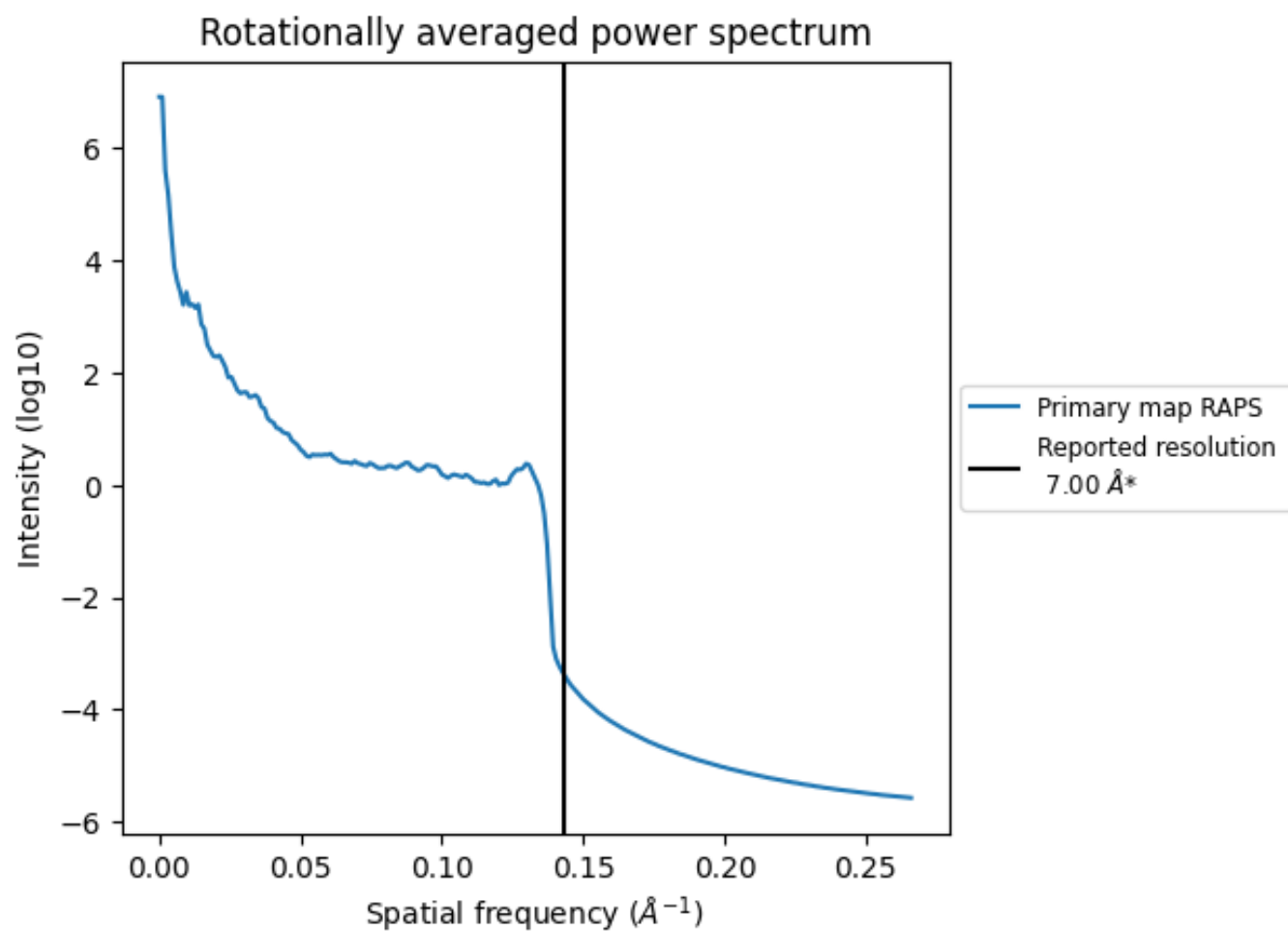
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 210568 nm^3 ; this corresponds to an approximate mass of 190212 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 0.143 Å⁻¹

8 Fourier-Shell correlation

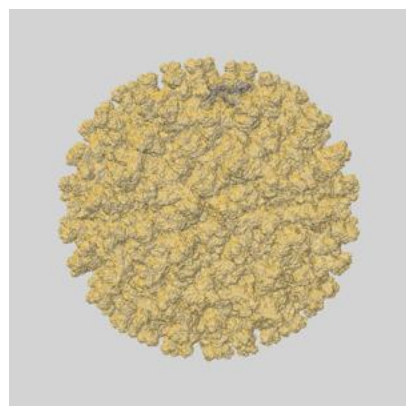
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

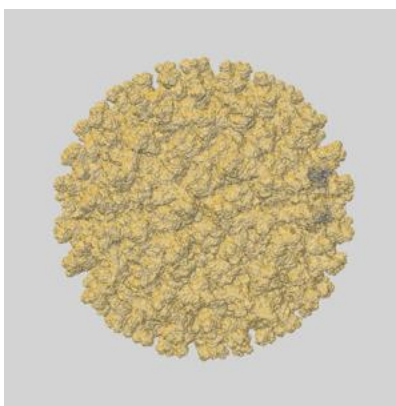
This section contains information regarding the fit between EMDB map EMD-5147 and PDB model 3IYK. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlays

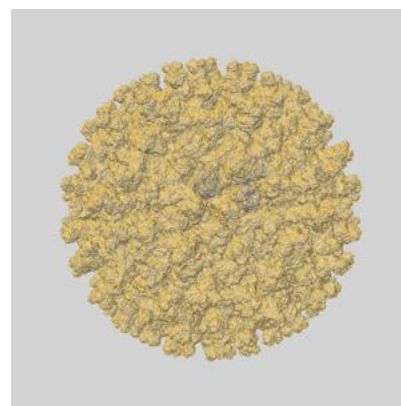
9.1.1 Map-model overlay [i](#)



X

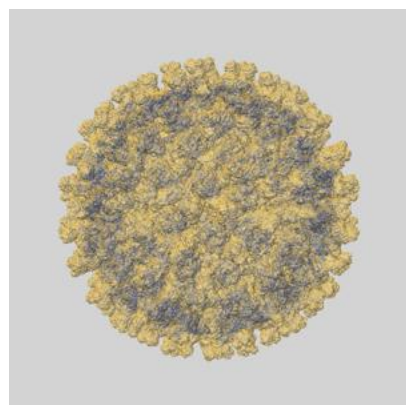


Y

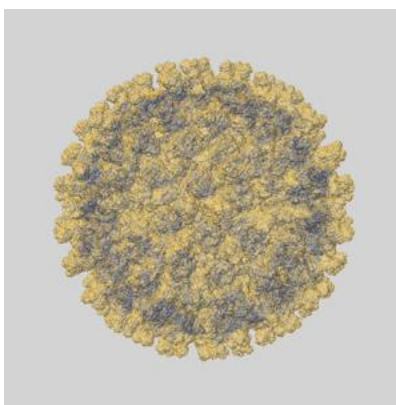


Z

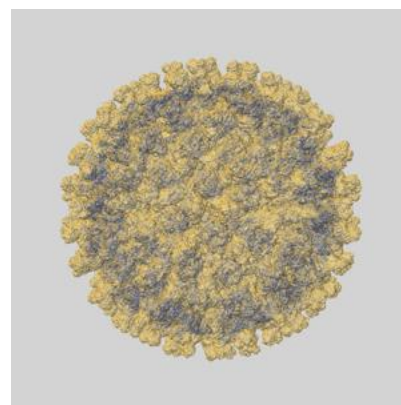
9.1.2 Map-model assembly overlay [i](#)



X



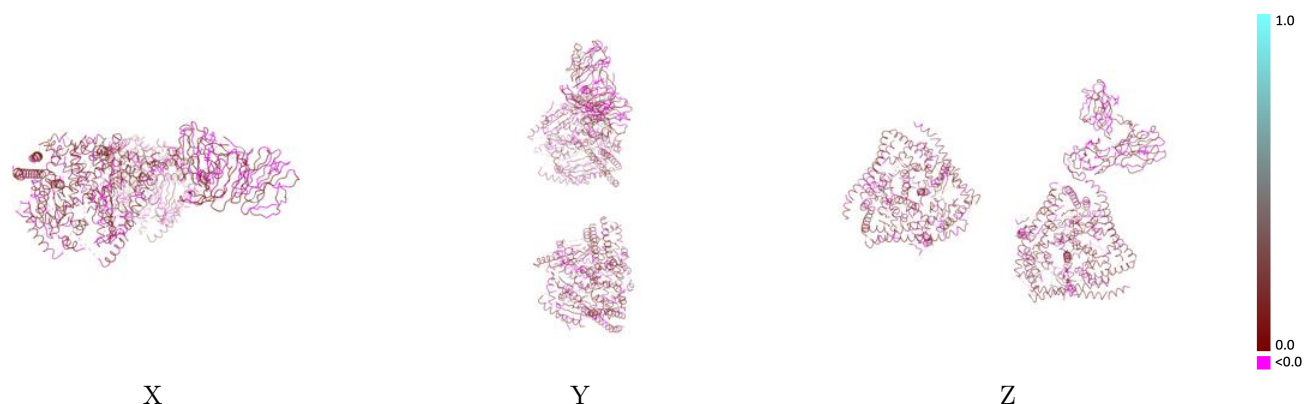
Y



Z

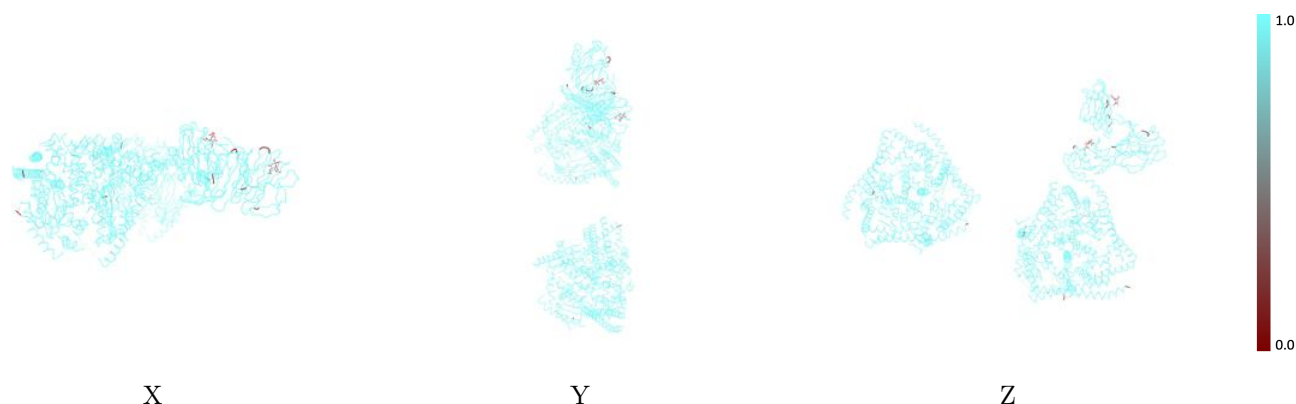
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



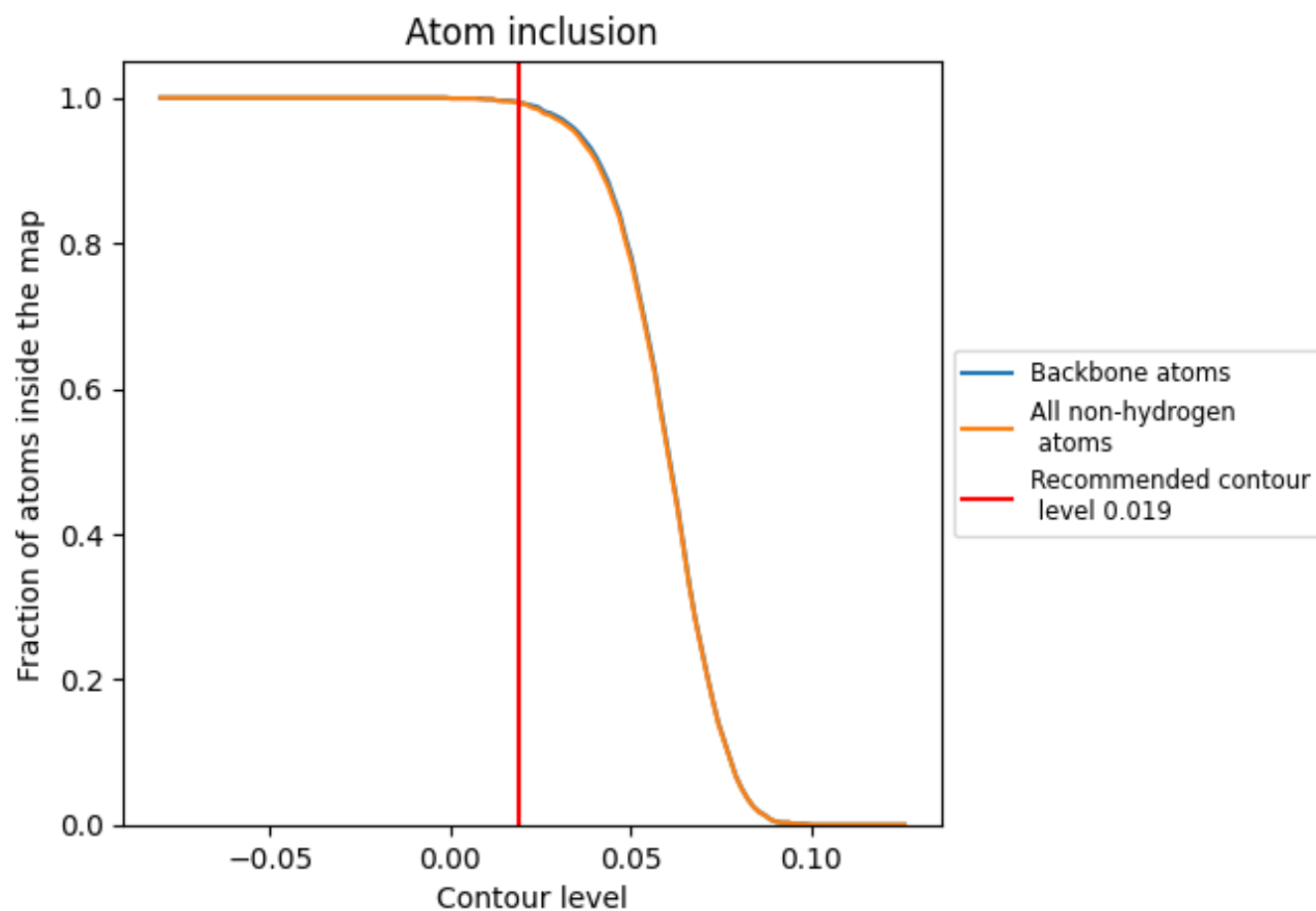
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.019).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9930	0.0990
A	0.9940	0.1290
B	1.0000	0.1080
C	0.9970	0.1120
D	0.9970	0.1140
E	1.0000	0.1150
F	0.9970	0.1120
G	0.9630	0.0320
I	0.9720	0.0390
K	0.9930	0.0370

1.0

0.0

<0.0