



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 11:30 AM UTC

PDB ID : 7VH2 / pdb_00007vh2
EMDB ID : EMD-31984
Title : Cryo-EM structure of Machupo virus dimeric polymerase L
Authors : Zhang, X.; Ma, J.; Zhang, S.
Deposited on : 2021-09-20
Resolution : 5.10 Å(reported)

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

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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

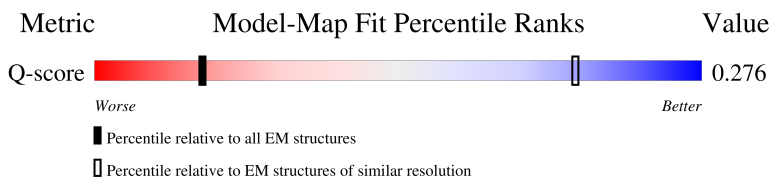
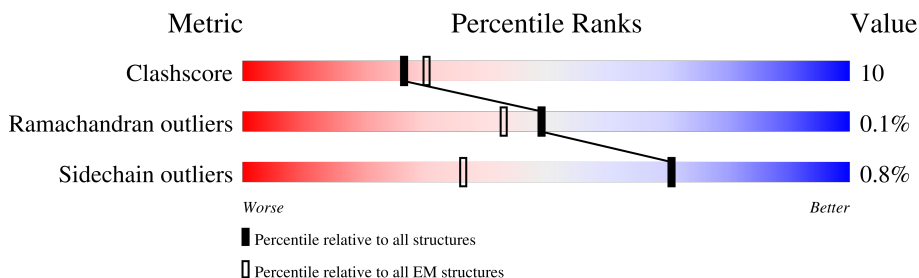
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.10 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	844 (4.60 - 5.60)

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	2238	12% 53% 19% • 28%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12749 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	1612	Total	C	N	O	S	0	0
			12749	8144	2129	2389	87		

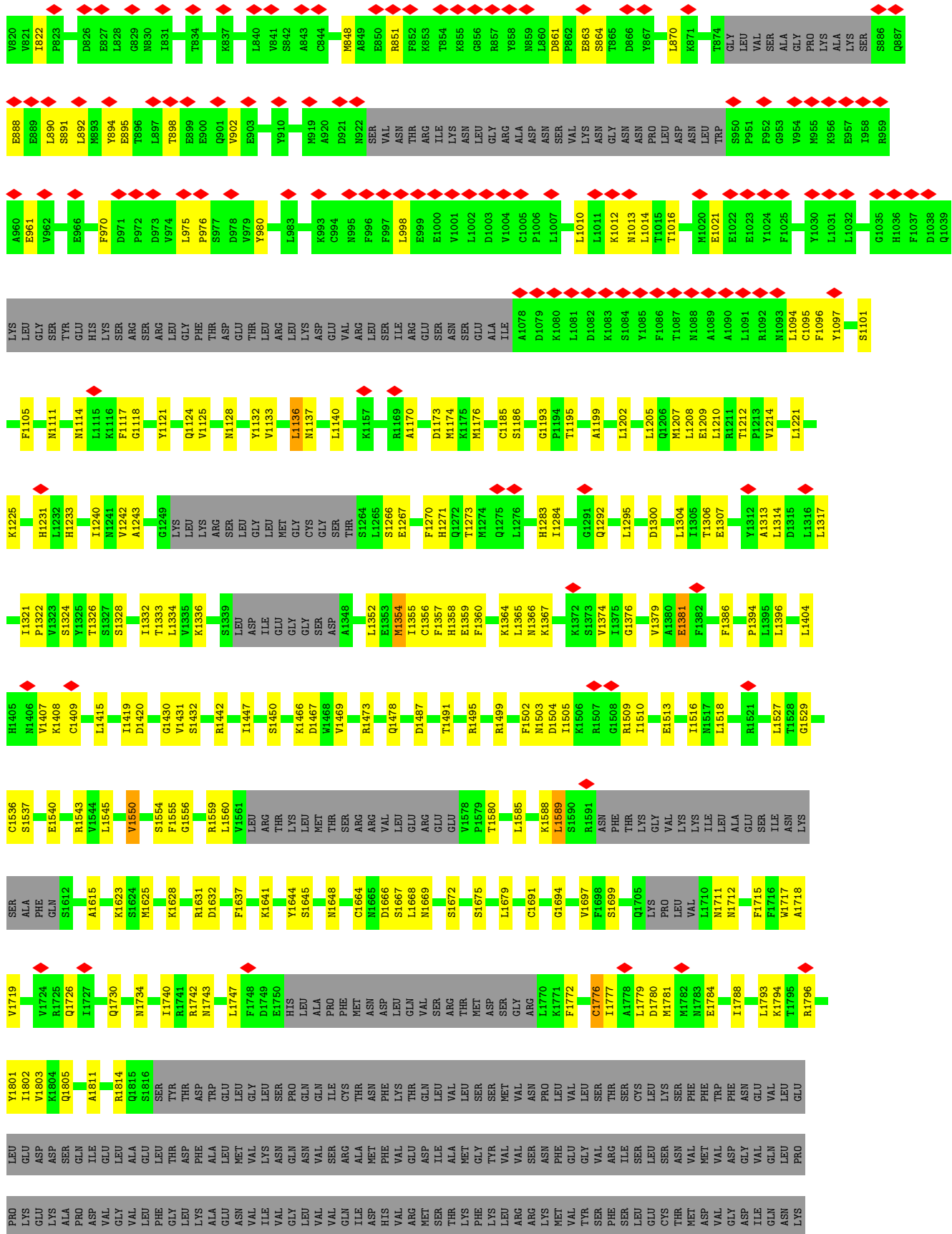
There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2210	TRP	-	expression tag	UNP Q6IUF8
A	2211	SER	-	expression tag	UNP Q6IUF8
A	2212	HIS	-	expression tag	UNP Q6IUF8
A	2213	PRO	-	expression tag	UNP Q6IUF8
A	2214	GLN	-	expression tag	UNP Q6IUF8
A	2215	PHE	-	expression tag	UNP Q6IUF8
A	2216	GLU	-	expression tag	UNP Q6IUF8
A	2217	LYS	-	expression tag	UNP Q6IUF8
A	2218	GLY	-	expression tag	UNP Q6IUF8
A	2219	GLY	-	expression tag	UNP Q6IUF8
A	2220	GLY	-	expression tag	UNP Q6IUF8
A	2221	SER	-	expression tag	UNP Q6IUF8
A	2222	GLY	-	expression tag	UNP Q6IUF8
A	2223	GLY	-	expression tag	UNP Q6IUF8
A	2224	GLY	-	expression tag	UNP Q6IUF8
A	2225	SER	-	expression tag	UNP Q6IUF8
A	2226	GLY	-	expression tag	UNP Q6IUF8
A	2227	GLY	-	expression tag	UNP Q6IUF8
A	2228	SER	-	expression tag	UNP Q6IUF8
A	2229	SER	-	expression tag	UNP Q6IUF8
A	2230	ALA	-	expression tag	UNP Q6IUF8
A	2231	TRP	-	expression tag	UNP Q6IUF8
A	2232	SER	-	expression tag	UNP Q6IUF8
A	2233	HIS	-	expression tag	UNP Q6IUF8
A	2234	PRO	-	expression tag	UNP Q6IUF8
A	2235	GLN	-	expression tag	UNP Q6IUF8
A	2236	PHE	-	expression tag	UNP Q6IUF8
A	2237	GLU	-	expression tag	UNP Q6IUF8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2238	LYS	-	expression tag	UNP Q6IUF8



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52947	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.137	Depositor
Minimum map value	-0.073	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0225	Depositor
Map size (Å)	262.4, 262.4, 262.4	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.64, 1.64, 1.64	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	0.37	1/12967 (0.0%)	0.77	12/17487 (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	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1467	ASP	CA-C	-5.00	1.45	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1777	ILE	N-CA-C	-7.90	102.25	113.07
1	A	1694	GLY	N-CA-C	6.22	117.68	111.21
1	A	388	LEU	CA-C-N	5.93	128.54	120.77
1	A	388	LEU	C-N-CA	5.93	128.54	120.77
1	A	389	VAL	N-CA-C	5.88	116.35	110.23

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	388	LEU	Peptide
1	A	390	ASN	Peptide
1	A	392	ARG	Peptide
1	A	395	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	A	710	THR	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	12749	0	12784	255	0
All	All	12749	0	12784	255	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 10.

The worst 5 of 255 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:218:LEU:O	1:A:222:LEU:HB2	1.66	0.95
1:A:1322:PRO:HA	1:A:1334:LEU:O	1.68	0.91
1:A:1354:MET:O	1:A:1357:PHE:HB3	1.73	0.89
1:A:1118:GLY:H	1:A:1133:VAL:H	1.37	0.72
1:A:245:TRP:O	1:A:249:GLU:HB2	1.89	0.71

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	1582/2238 (71%)	1363 (86%)	217 (14%)	2 (0%)	48 83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	475	PHE
1	A	711	PRO

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	1441/2026 (71%)	1430 (99%)	11 (1%)	73 78

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1284	ILE
1	A	1550	VAL
1	A	1589	LEU
1	A	1560	LEU
1	A	580	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1124	GLN
1	A	1444	ASN
1	A	1292	GLN
1	A	1478	GLN
1	A	431	GLN

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.

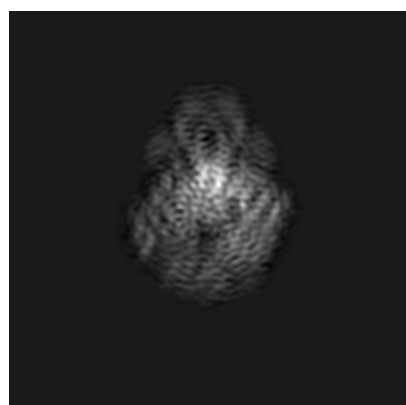
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31984. These allow visual inspection of the internal detail of the map and identification of artifacts.

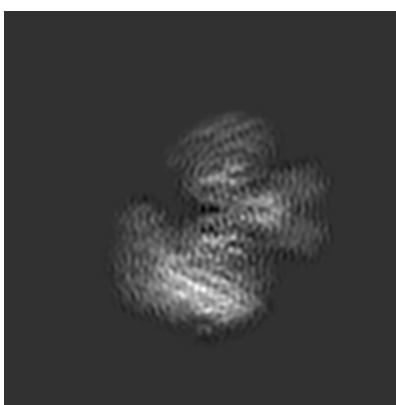
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

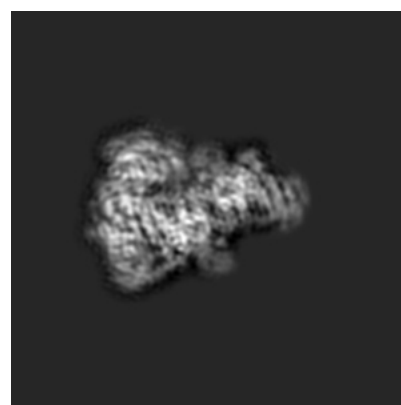
6.1.1 Primary map



X



Y



Z

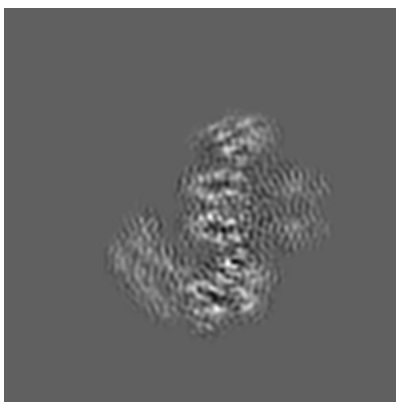
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

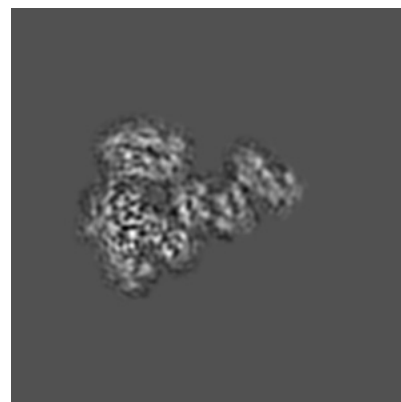
6.2.1 Primary map



X Index: 80



Y Index: 80

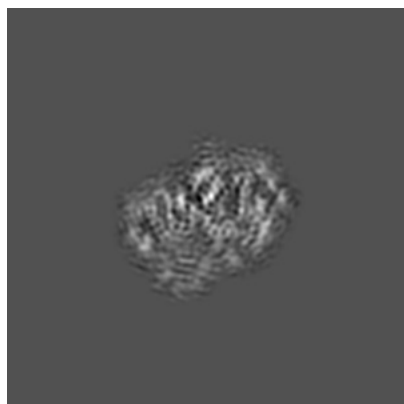


Z Index: 80

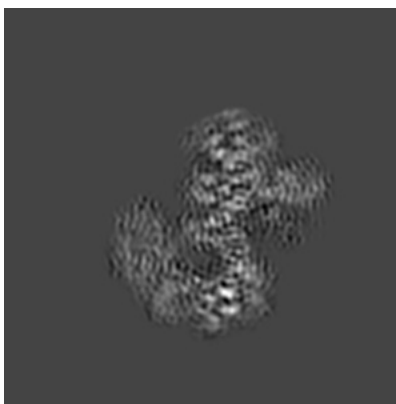
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

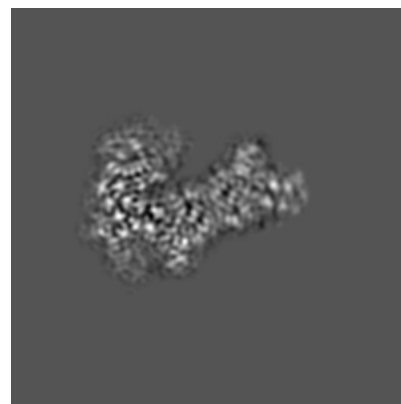
6.3.1 Primary map



X Index: 47



Y Index: 83

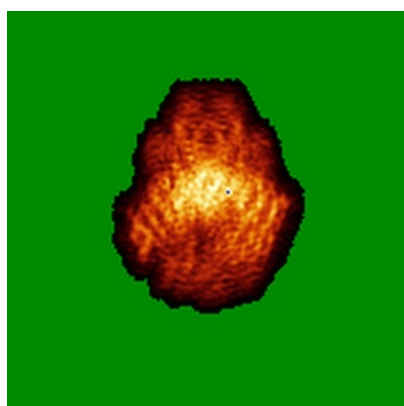


Z Index: 87

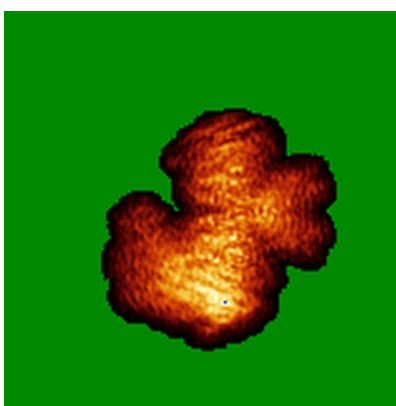
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

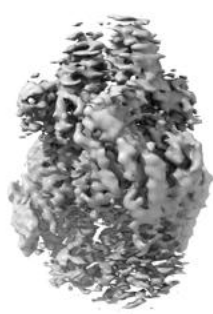


Z

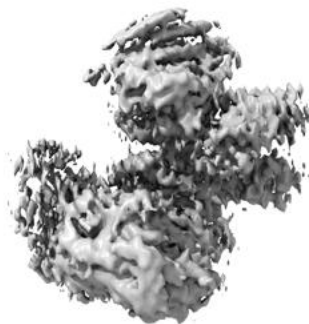
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

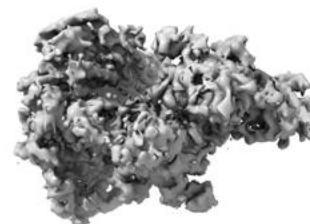
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0225. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

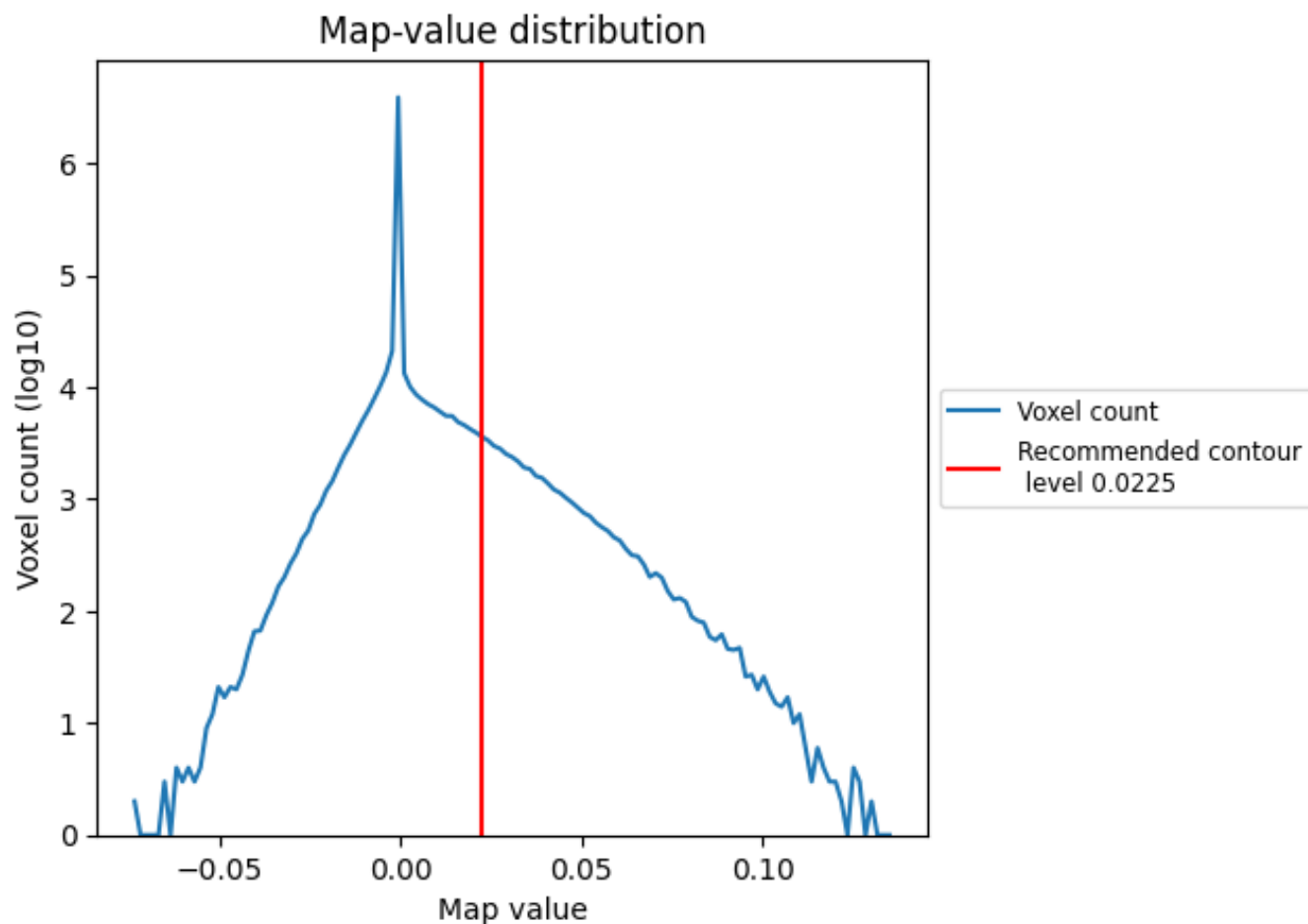
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

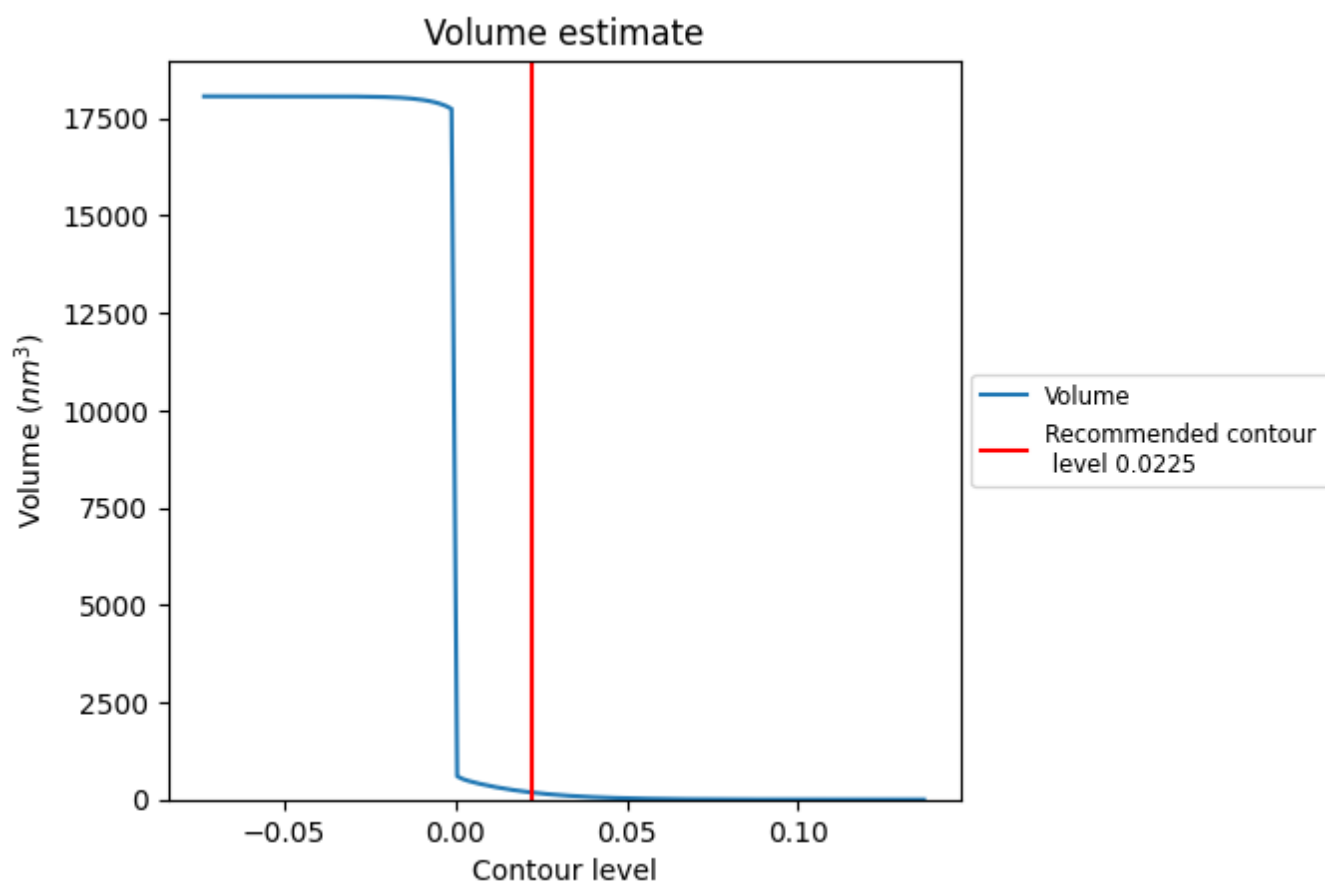
This section contains the results of statistical analysis of the map.

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.

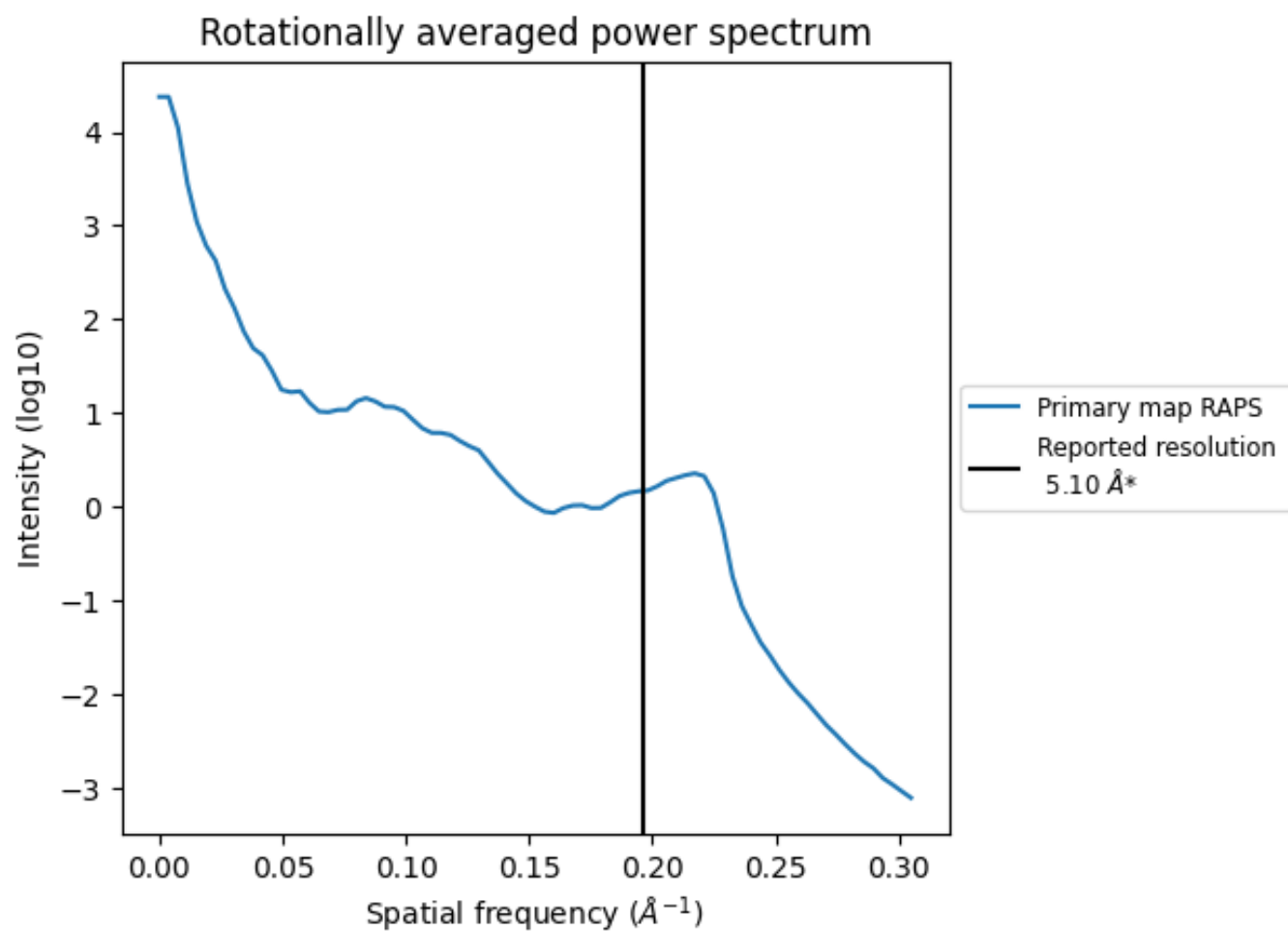
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm³; this corresponds to an approximate mass of 162 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 0.196 Å⁻¹

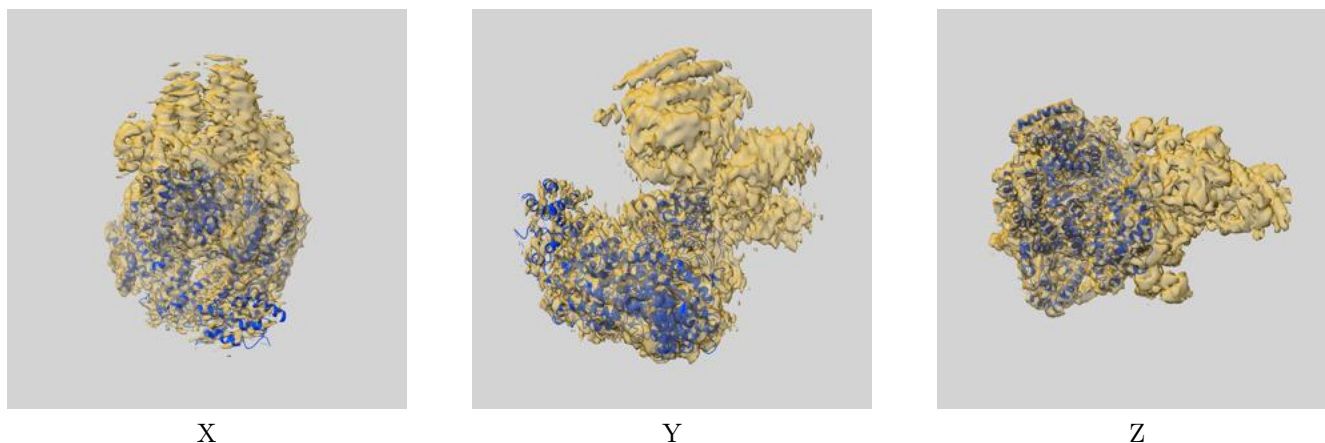
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

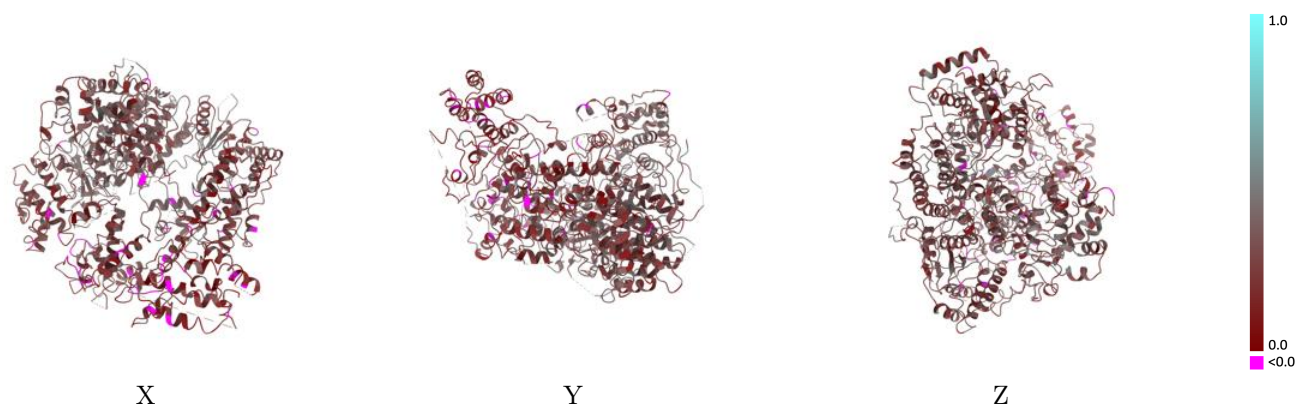
This section contains information regarding the fit between EMDB map EMD-31984 and PDB model 7VH2. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



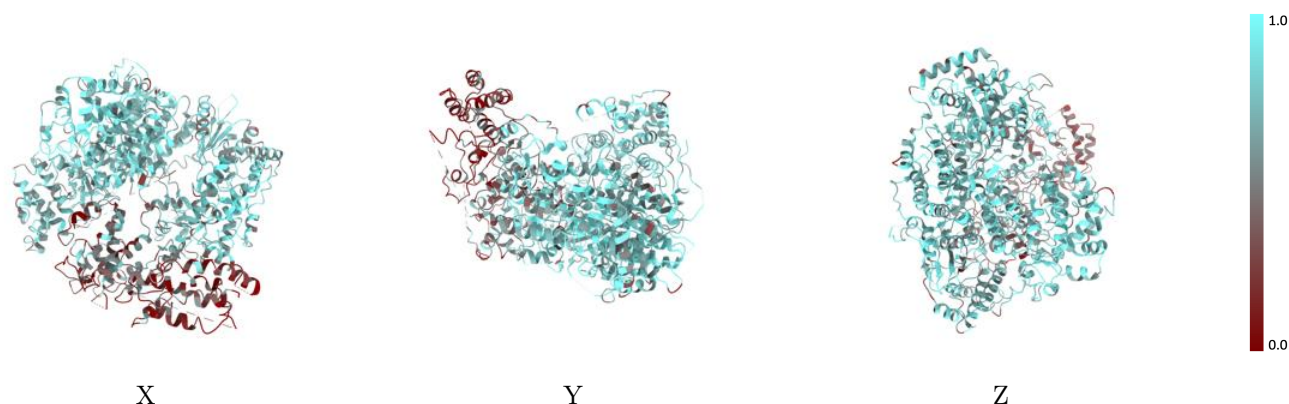
The images above show the 3D surface view of the map at the recommended contour level 0.0225 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



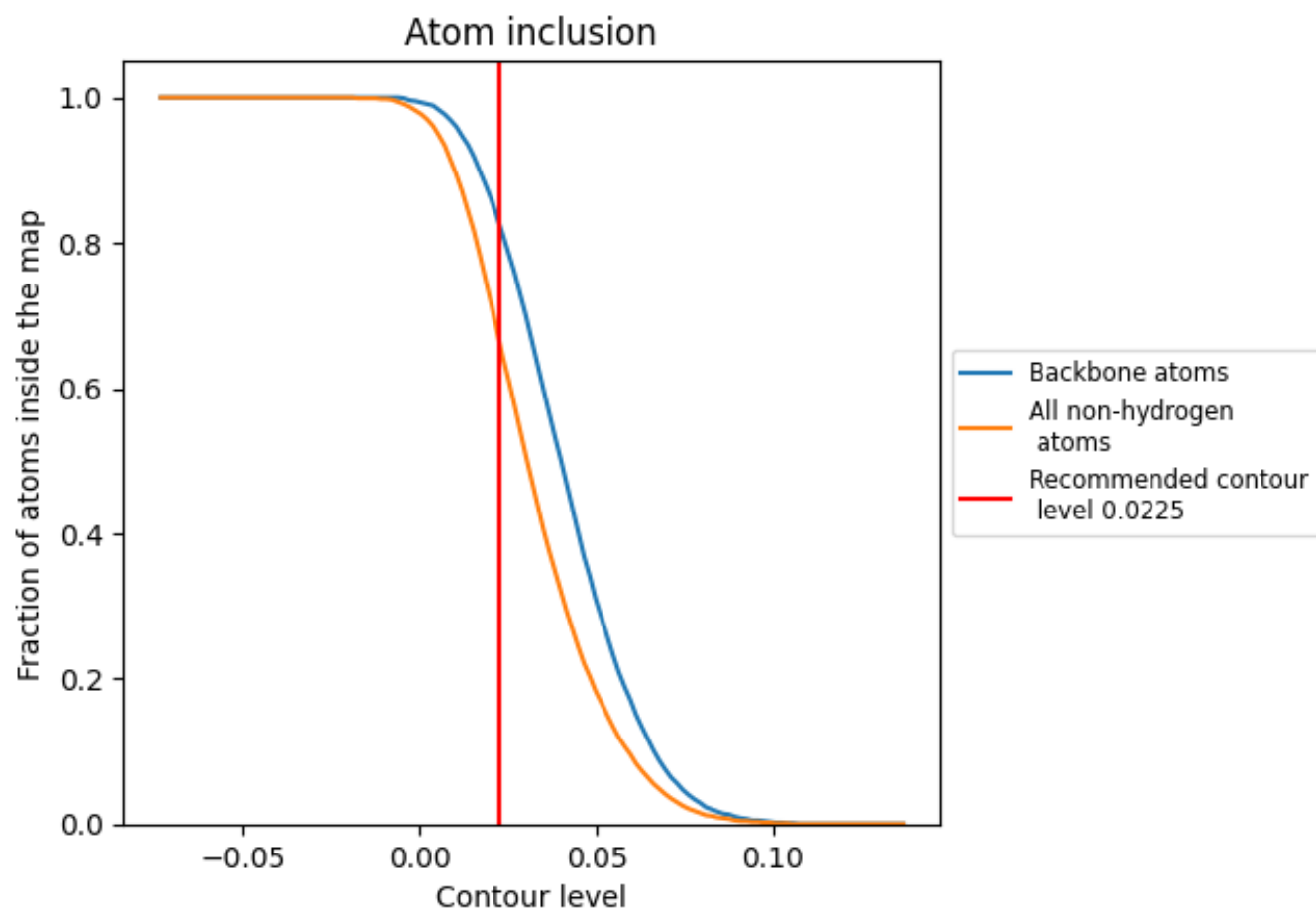
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0225).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 66% 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 (0.0225) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6650	0.2760
A	0.6650	0.2760

