



## wwPDB EM Validation Summary Report ⓘ

Aug 25, 2025 – 02:10 PM EDT

PDB ID : 9D30 / pdb\_00009d30  
EMDB ID : EMD-46506  
Title : Cryo-EM structure of mycocerosic acid synthase with a single DH-ACP crosslink using C16 alpha-bromoamide. Complex C  
Authors : Heberlig, G.W.; Jiang, Z.; Burkart, M.D.  
Deposited on : 2024-08-09  
Resolution : 3.74 Å(reported)  
Based on initial model : .

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

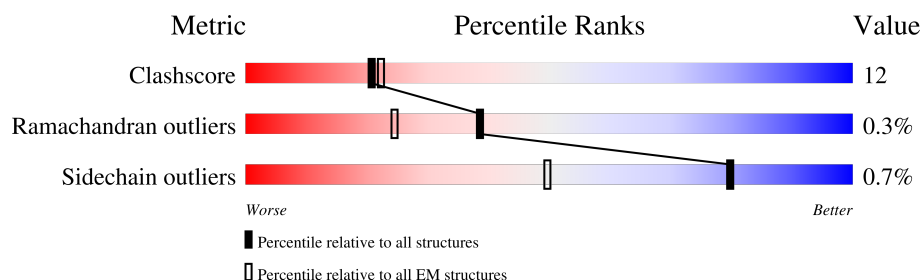
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.74 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	2124	
1	B	2124	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 34840 atoms, of which 17255 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.

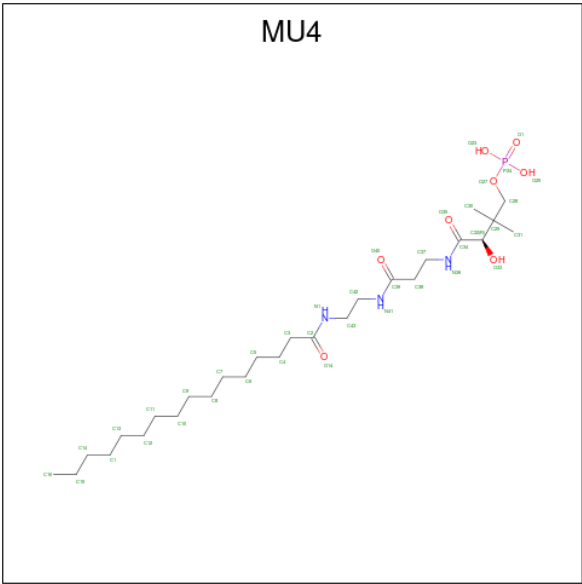
- Molecule 1 is a protein called Mycocerosic acid synthase.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1215	Total	C	H	N	O	S	0	0
			18247	5745	9050	1663	1760	29		
1	B	1109	Total	C	H	N	O	S	0	0
			16567	5227	8205	1509	1601	25		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2112	LYS	-	expression tag	UNP A0A0E8V6Y3
A	2113	LEU	-	expression tag	UNP A0A0E8V6Y3
A	2114	ALA	-	expression tag	UNP A0A0E8V6Y3
A	2115	ALA	-	expression tag	UNP A0A0E8V6Y3
A	2116	ALA	-	expression tag	UNP A0A0E8V6Y3
A	2117	LEU	-	expression tag	UNP A0A0E8V6Y3
A	2118	GLU	-	expression tag	UNP A0A0E8V6Y3
A	2119	HIS	-	expression tag	UNP A0A0E8V6Y3
A	2120	HIS	-	expression tag	UNP A0A0E8V6Y3
A	2121	HIS	-	expression tag	UNP A0A0E8V6Y3
A	2122	HIS	-	expression tag	UNP A0A0E8V6Y3
A	2123	HIS	-	expression tag	UNP A0A0E8V6Y3
A	2124	HIS	-	expression tag	UNP A0A0E8V6Y3
B	2112	LYS	-	expression tag	UNP A0A0E8V6Y3
B	2113	LEU	-	expression tag	UNP A0A0E8V6Y3
B	2114	ALA	-	expression tag	UNP A0A0E8V6Y3
B	2115	ALA	-	expression tag	UNP A0A0E8V6Y3
B	2116	ALA	-	expression tag	UNP A0A0E8V6Y3
B	2117	LEU	-	expression tag	UNP A0A0E8V6Y3
B	2118	GLU	-	expression tag	UNP A0A0E8V6Y3
B	2119	HIS	-	expression tag	UNP A0A0E8V6Y3
B	2120	HIS	-	expression tag	UNP A0A0E8V6Y3
B	2121	HIS	-	expression tag	UNP A0A0E8V6Y3
B	2122	HIS	-	expression tag	UNP A0A0E8V6Y3
B	2123	HIS	-	expression tag	UNP A0A0E8V6Y3
B	2124	HIS	-	expression tag	UNP A0A0E8V6Y3

- Molecule 2 is N-[2-(hexadecanoylamino)ethyl]-N 3 -[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alaninamide (CCD ID: MU4) (formula: C<sub>27</sub>H<sub>54</sub>N<sub>3</sub>O<sub>8</sub>P).

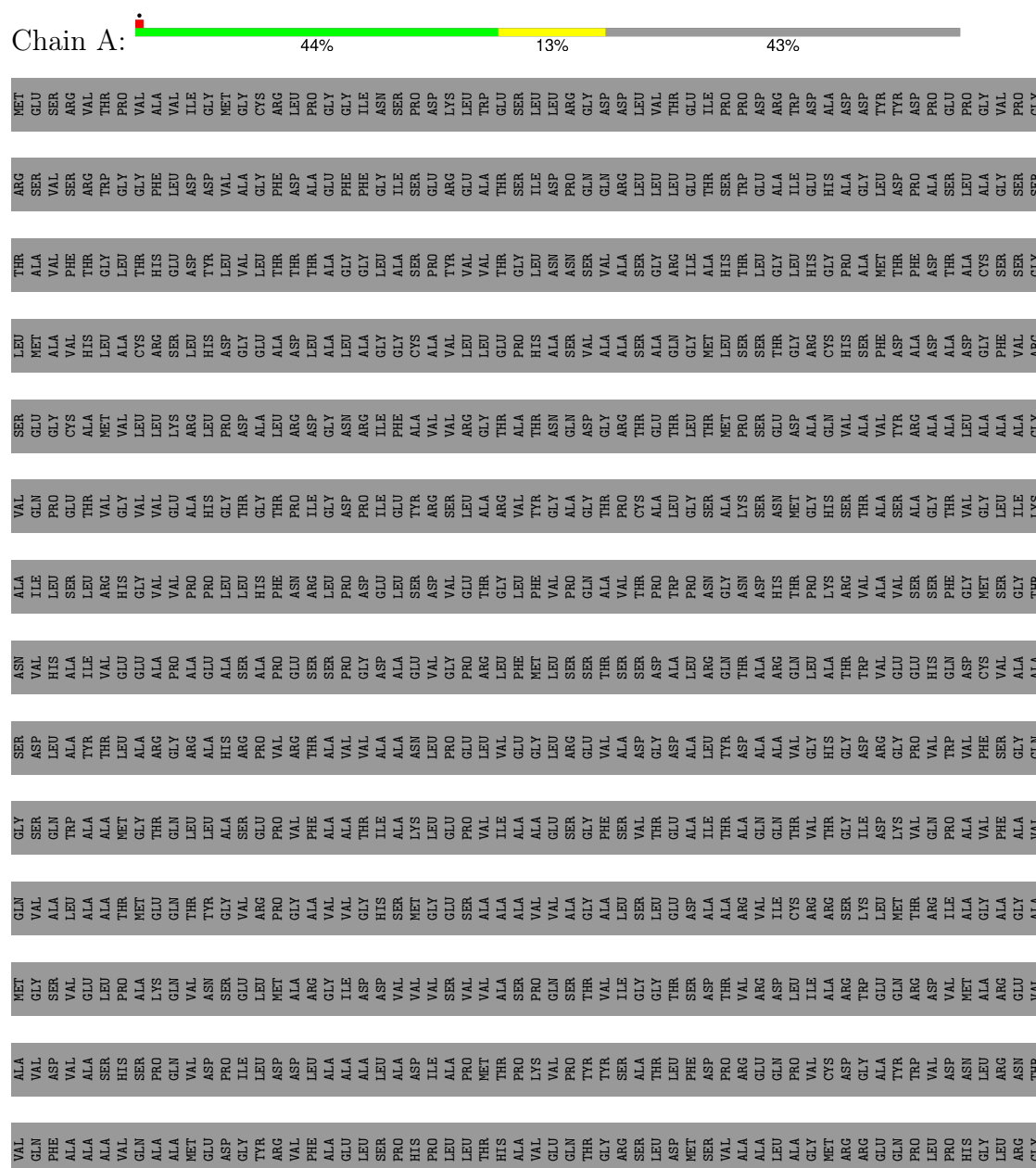


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	26	15	3	7	1	0

### 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.

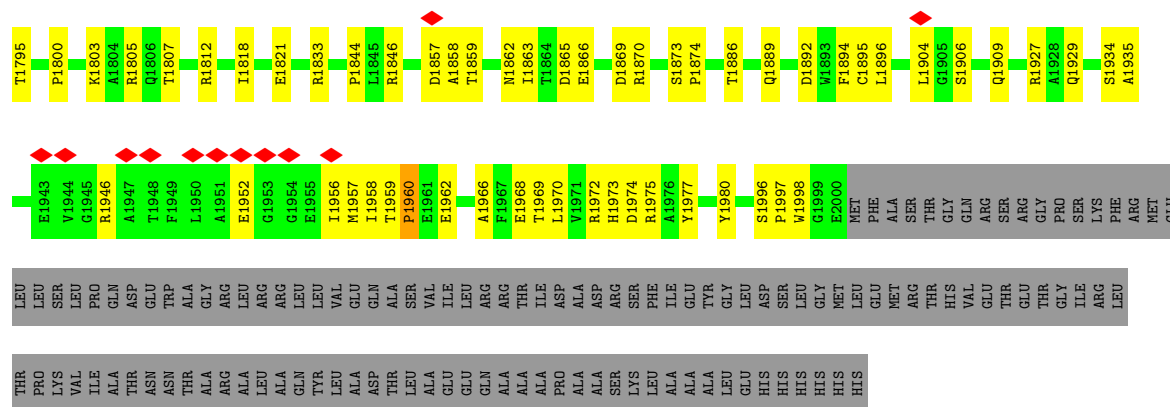
#### • Molecule 1: Mycocerosic acid synthase





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







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35969	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)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.552	Depositor
Minimum map value	-0.267	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	341.376, 341.376, 341.376	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.889, 0.889, 0.889	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MU4

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	0.20	0/9380	0.38	4/12768 (0.0%)
1	B	0.14	0/8534	0.31	1/11626 (0.0%)
All	All	0.18	0/17914	0.35	5/24394 (0.0%)

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	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	2061	LEU	N-CA-C	-7.82	103.70	113.55
1	B	1960	PRO	CA-N-CD	-6.77	102.52	112.00
1	A	2062	GLY	N-CA-C	-6.31	104.92	113.37
1	A	2060	SER	N-CA-C	-6.15	106.19	113.38
1	A	926	LEU	N-CA-C	-5.39	104.81	111.33

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1189	ARG	Sidechain
1	A	2045	ARG	Sidechain

## 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	9197	9050	9053	229	0
1	B	8362	8205	8206	189	0
2	A	26	0	0	8	0
All	All	17585	17255	17259	411	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 12.

The worst 5 of 411 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:1116:LEU:HD21	2:A:2201:MU4:C38	1.93	0.99
1:A:1095:ASP:OD1	2:A:2201:MU4:C5	2.12	0.97
1:A:2035:LEU:HD21	1:A:2092:LEU:HD22	1.50	0.92
1:A:1636:THR:OG1	1:A:1660:ASP:OD1	1.95	0.83
1:A:1070:VAL:O	1:A:1134:TYR:OH	1.96	0.82

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	1213/2124 (57%)	1099 (91%)	109 (9%)	5 (0%)	30 62
1	B	1107/2124 (52%)	1005 (91%)	99 (9%)	3 (0%)	37 67
All	All	2320/4248 (55%)	2104 (91%)	208 (9%)	8 (0%)	38 67

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	928	ASP
1	A	1148	ARG
1	B	1670	PHE
1	A	930	GLN
1	A	1089	ILE

### 5.3.2 Protein sidechains ⓘ

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	942/1634 (58%)	931 (99%)	11 (1%)	67	79
1	B	854/1634 (52%)	852 (100%)	2 (0%)	92	95
All	All	1796/3268 (55%)	1783 (99%)	13 (1%)	80	88

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1507	PHE
1	A	1998	TRP
1	B	1760	LEU
1	A	2060	SER
1	B	1636	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1218	ASN
1	A	1565	HIS
1	B	1459	ASN
1	B	1252	GLN
1	B	1300	HIS

### 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](#)

1 ligand is 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	$\# Z  > 2$
2	MU4	A	2201	1	21,25,38	0.22	0	25,32,47	0.64	1 (4%)

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
2	MU4	A	2201	1	-	12/30/32/45	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2201	MU4	C31-C29-C28	2.47	112.31	108.22

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

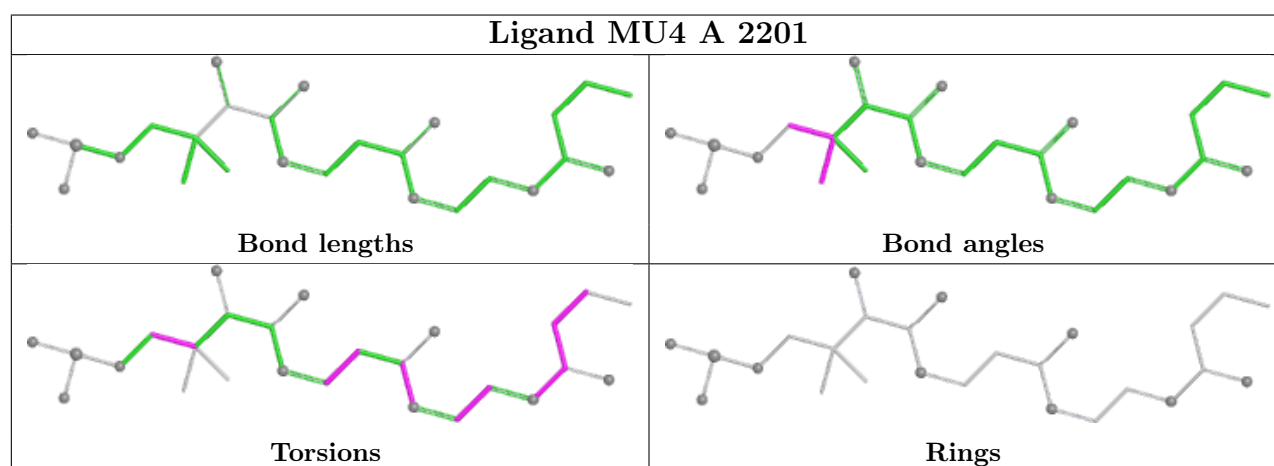
Mol	Chain	Res	Type	Atoms
2	A	2201	MU4	O27-C28-C29-C30
2	A	2201	MU4	O27-C28-C29-C31
2	A	2201	MU4	O27-C28-C29-C32
2	A	2201	MU4	N36-C37-C38-C39
2	A	2201	MU4	C38-C39-N41-C42

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2201	MU4	8	0

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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

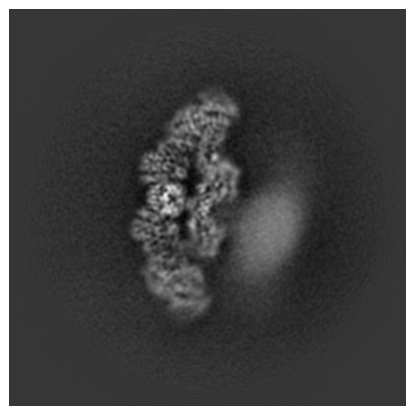
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46506. These allow visual inspection of the internal detail of the map and identification of artifacts.

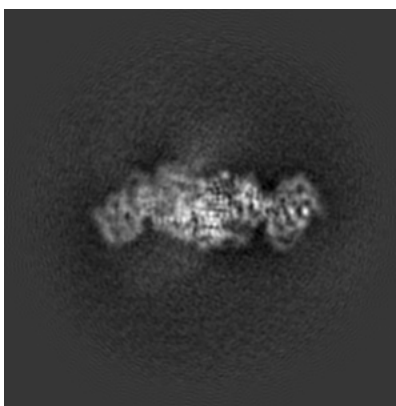
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

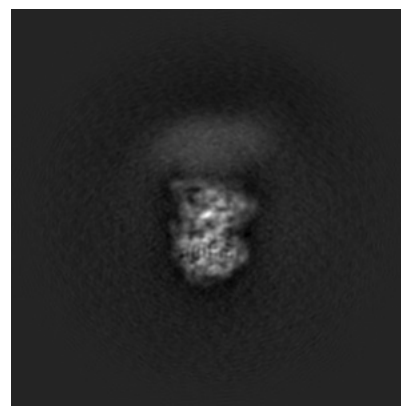
#### 6.1.1 Primary map



X



Y

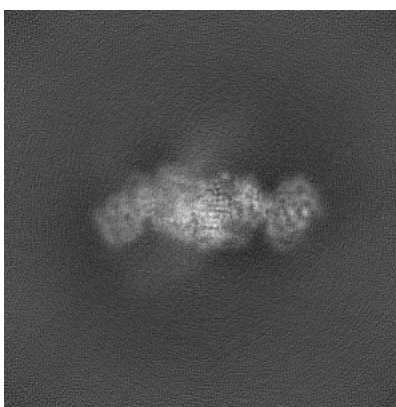


Z

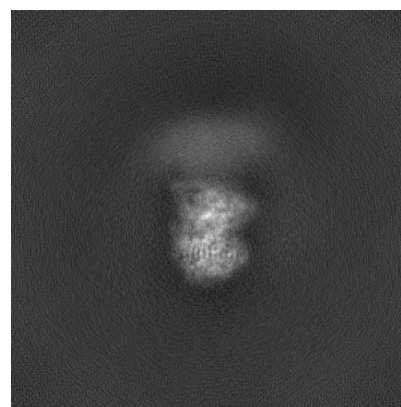
#### 6.1.2 Raw map



X



Y



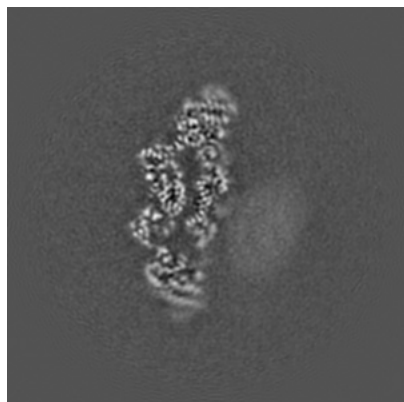
Z

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

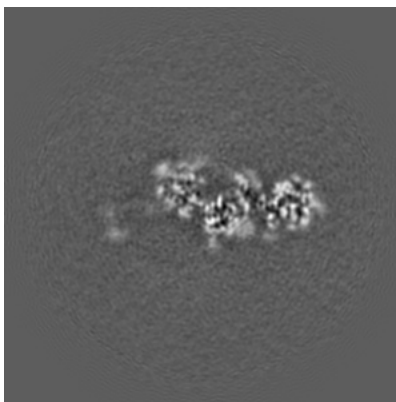


## 6.2 Central slices [i](#)

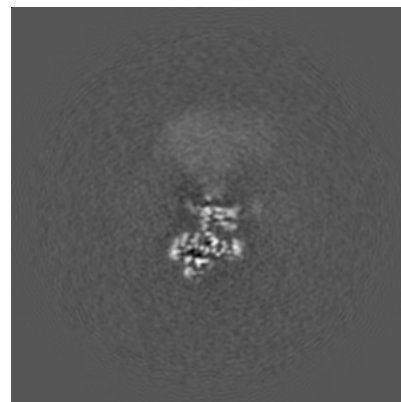
### 6.2.1 Primary map



X Index: 192

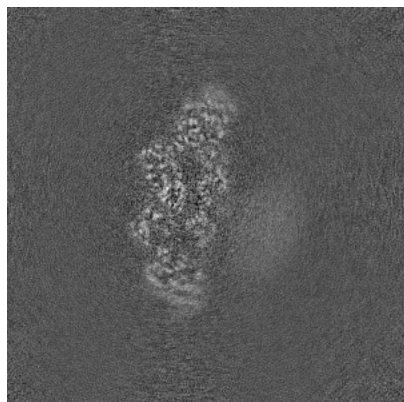


Y Index: 192

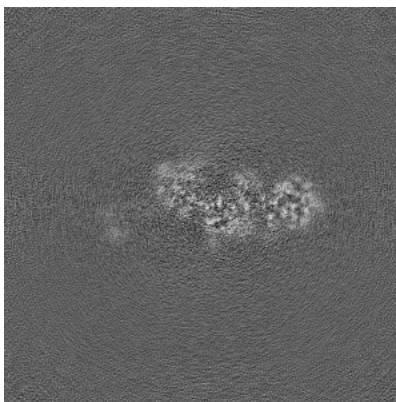


Z Index: 192

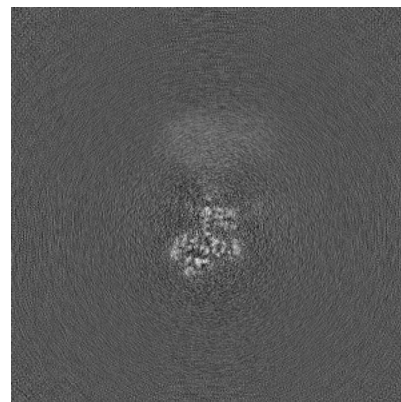
### 6.2.2 Raw map



X Index: 192



Y Index: 192

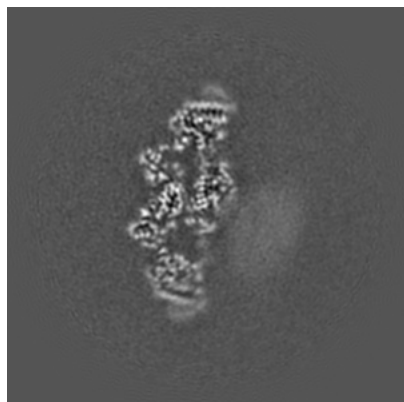


Z Index: 192

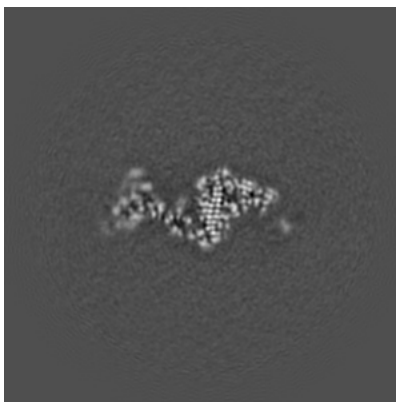
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

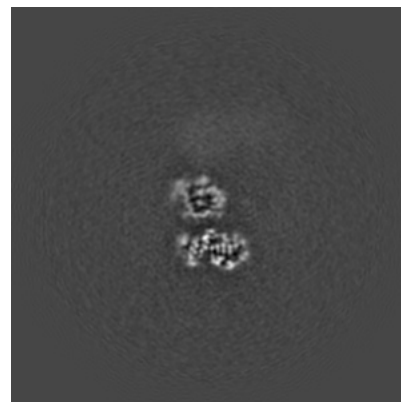
### 6.3.1 Primary map



X Index: 188

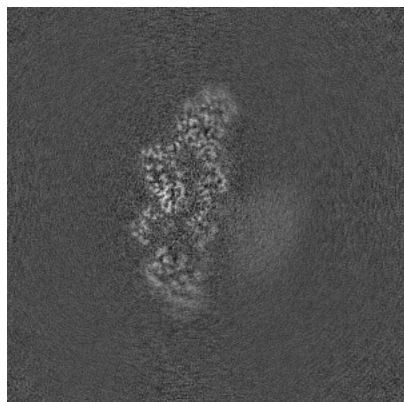


Y Index: 150

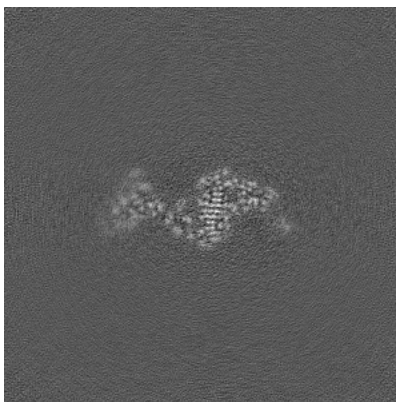


Z Index: 208

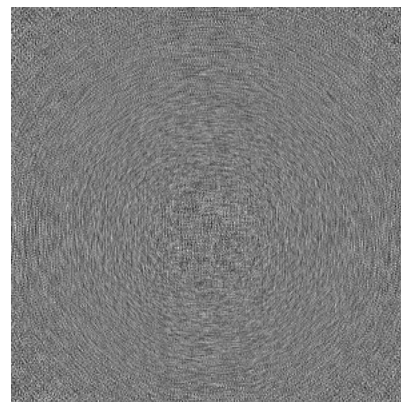
### 6.3.2 Raw map



X Index: 193



Y Index: 151

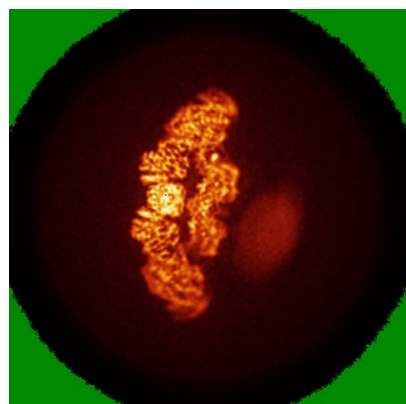


Z Index: 0

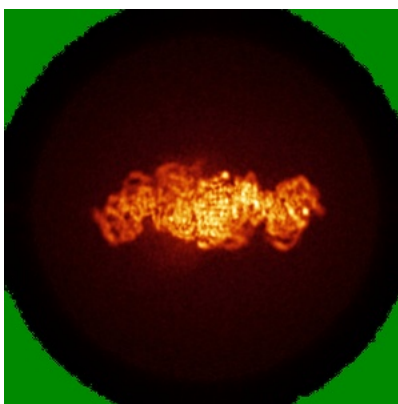
The images above show the largest variance slices of the map in three orthogonal directions.

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

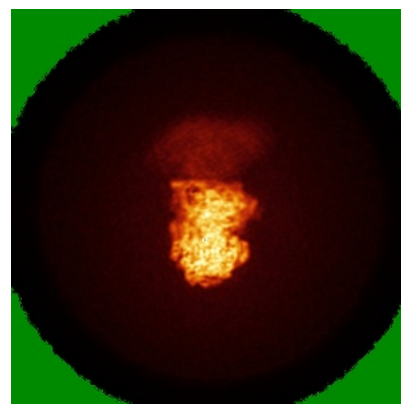
### 6.4.1 Primary map



X

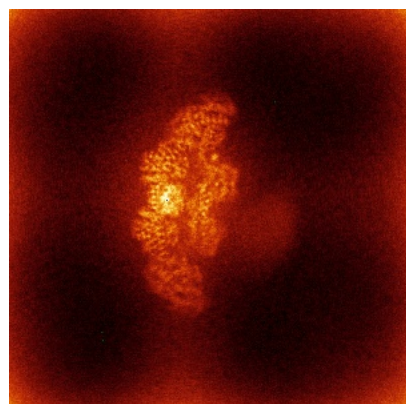


Y

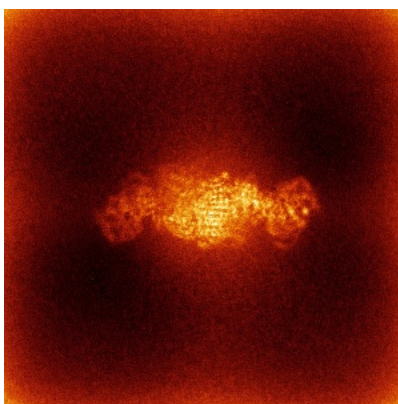


Z

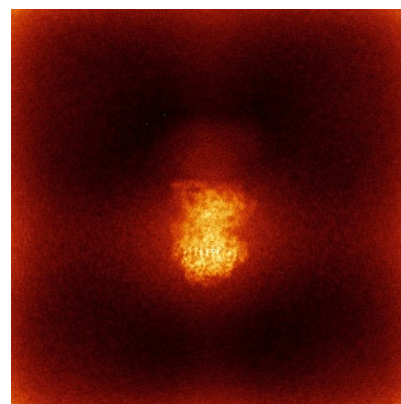
### 6.4.2 Raw map



X



Y

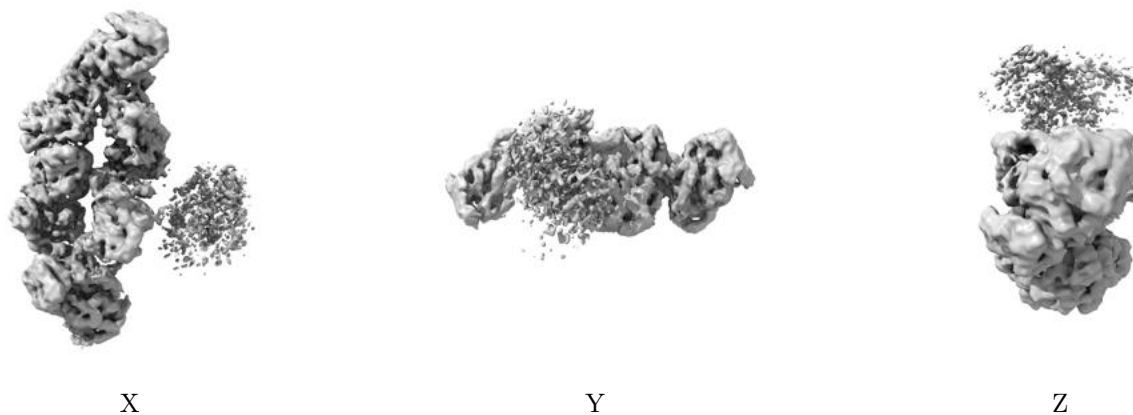


Z

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.

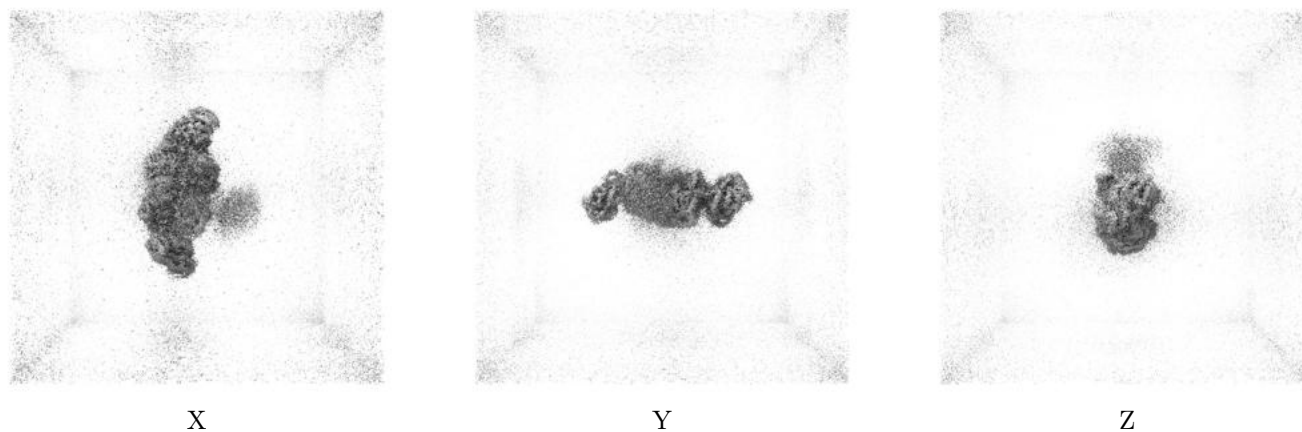
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. 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](#)

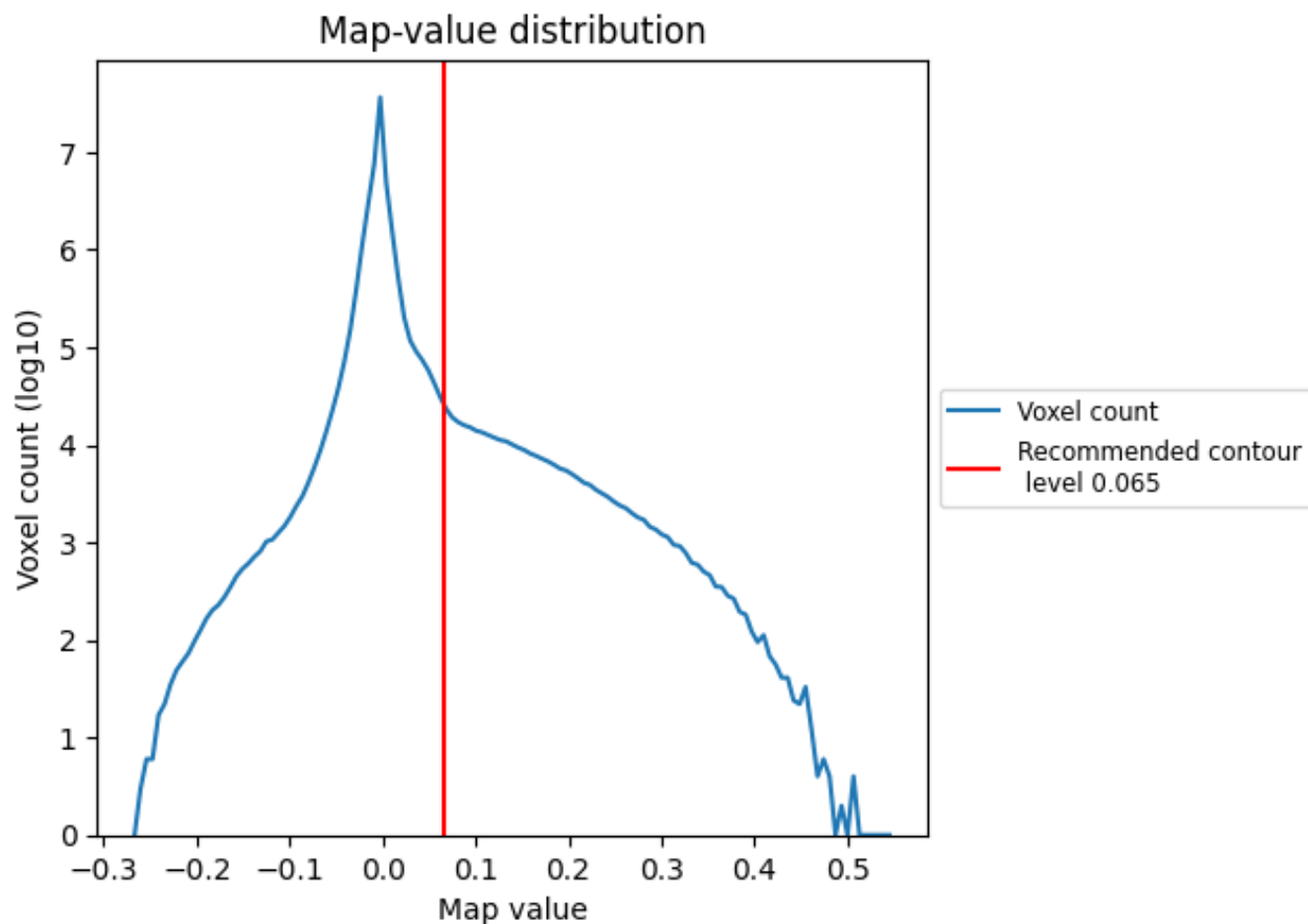
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

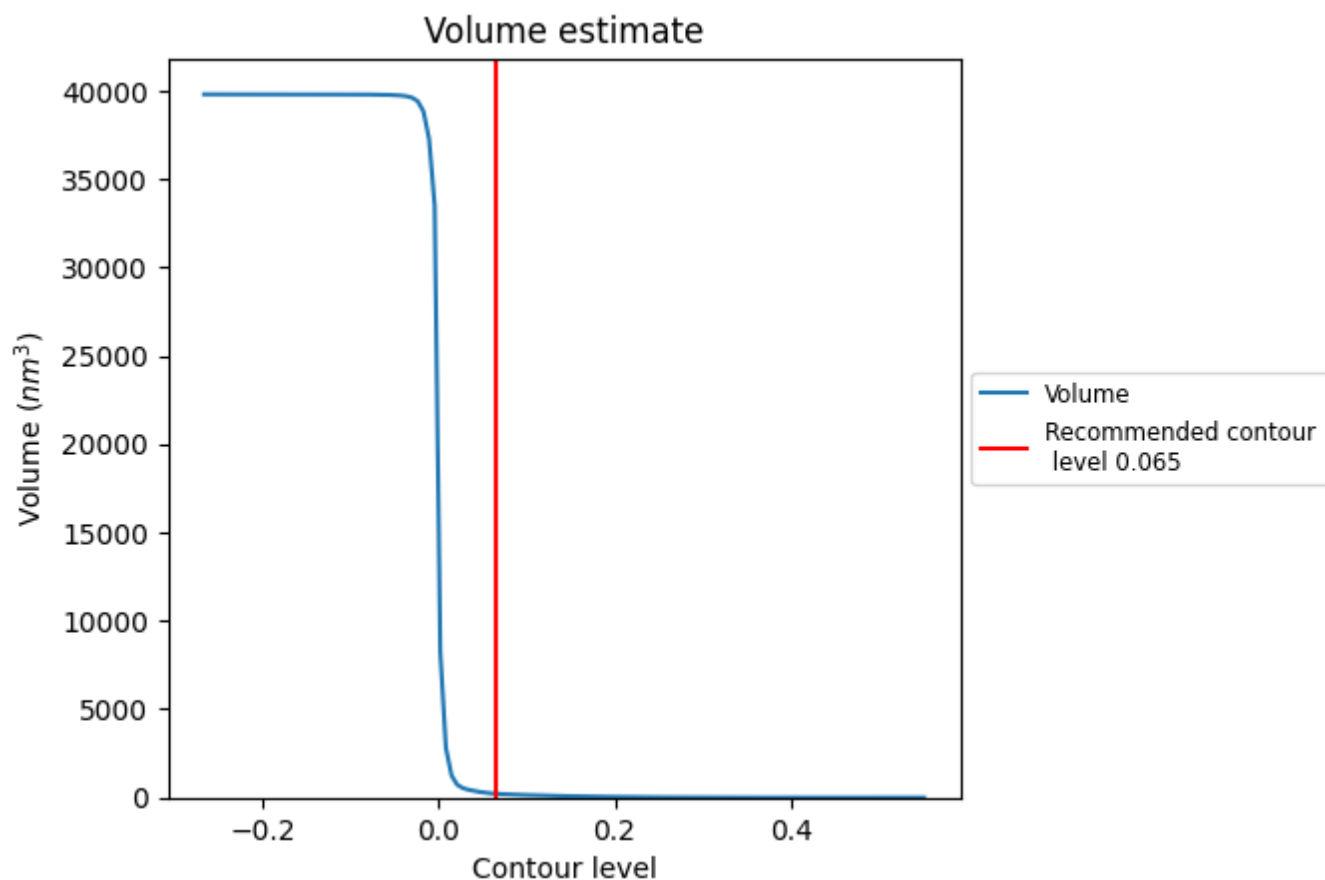
This section contains the results of statistical analysis of the map.

### 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.

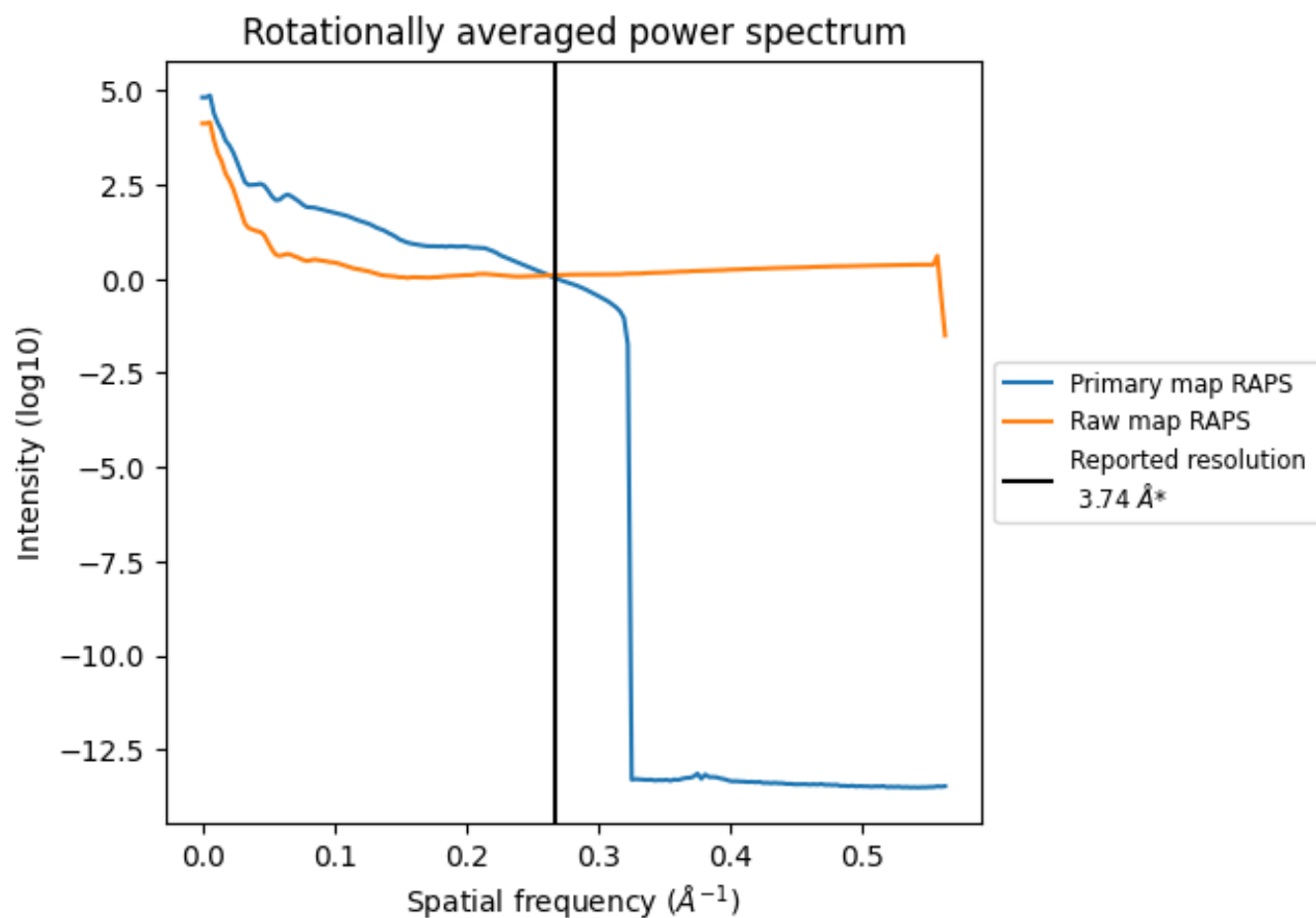
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 216  $\text{nm}^3$ ; this corresponds to an approximate mass of 195 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 ⓘ

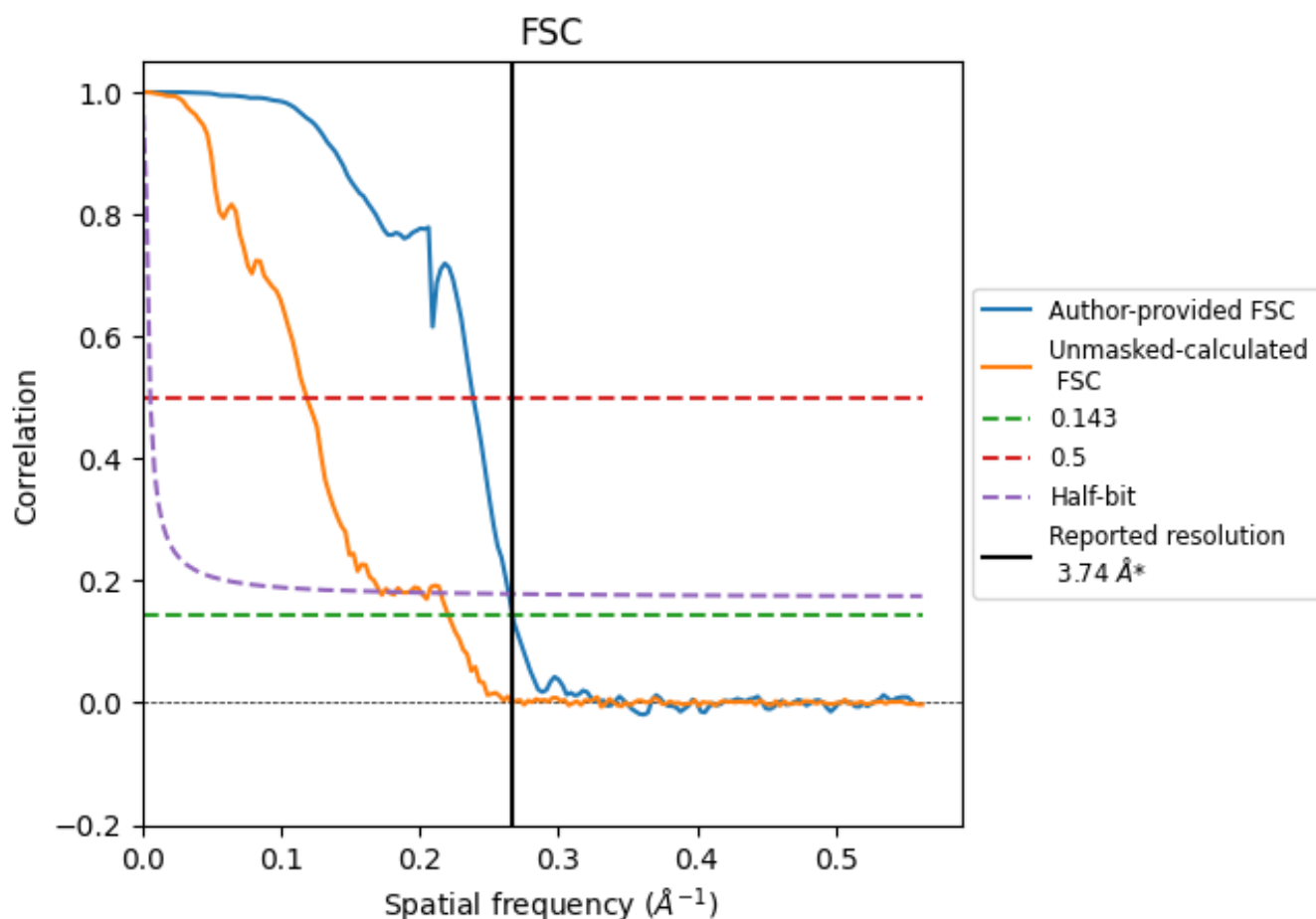


\*Reported resolution corresponds to spatial frequency of 0.267 Å<sup>-1</sup>

## 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 0.267  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

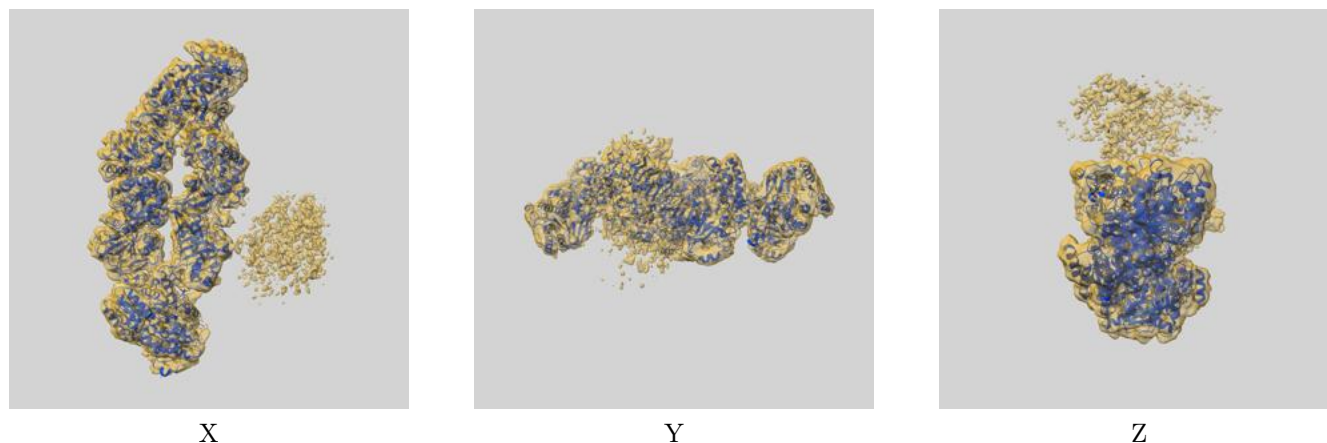
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.74	-	-
Author-provided FSC curve	3.74	4.19	3.78
Unmasked-calculated*	4.53	8.43	5.83

\*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 4.53 differs from the reported value 3.74 by more than 10 %

## 9 Map-model fit [i](#)

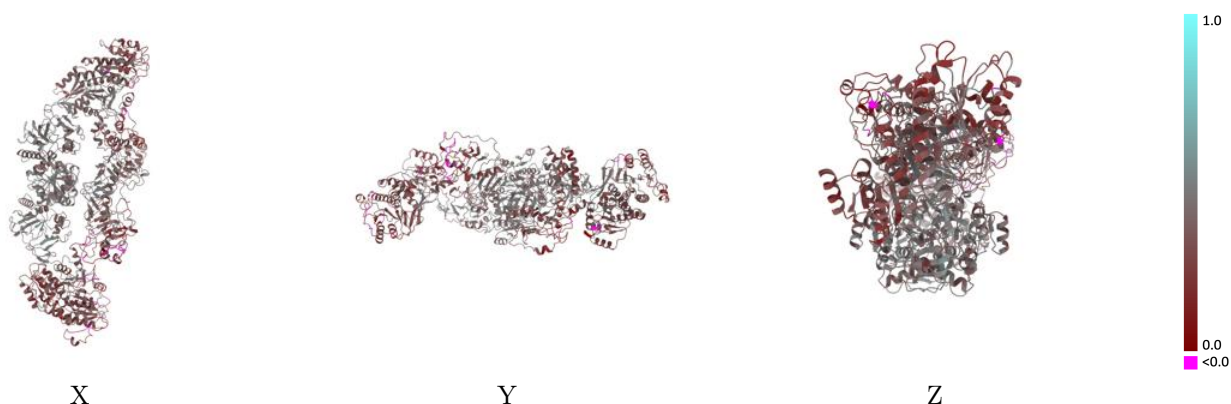
This section contains information regarding the fit between EMDB map EMD-46506 and PDB model 9D30. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

### 9.1 Map-model overlay [i](#)



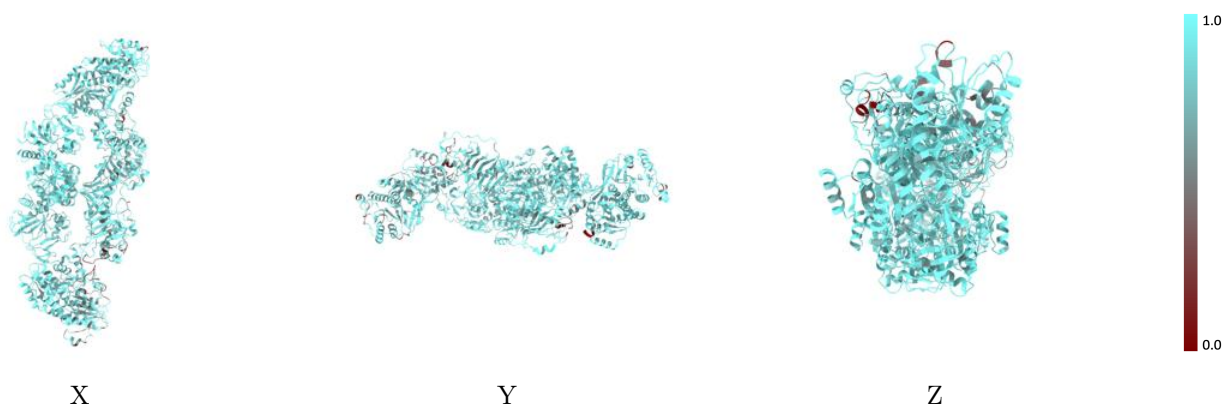
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



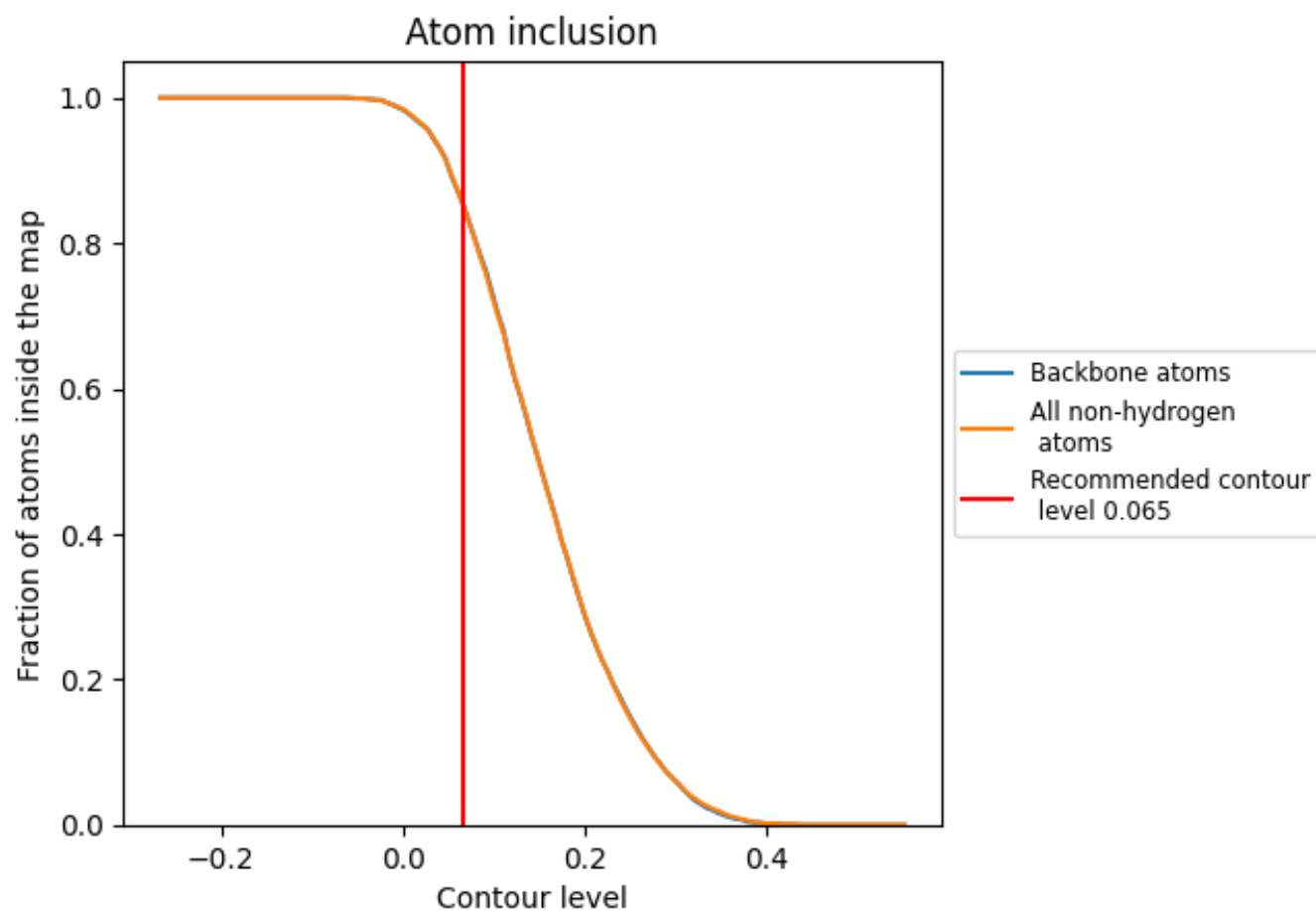
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8560	<div></div> 0.3520
A	<div></div> 0.8780	<div></div> 0.3680
B	<div></div> 0.8390	<div></div> 0.3350

