



## wwPDB EM Validation Summary Report ⓘ

Jun 9, 2025 – 05:55 PM JST

PDB ID : 8YGE / pdb\_00008yge  
EMDB ID : EMD-39245  
Title : pP1192R-DNA-m-AMSA complex DNA binding/cleavage domain  
Authors : Sun, J.Q.; Liu, R.L.  
Deposited on : 2024-02-26  
Resolution : 2.76 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](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.dev118  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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) : 2.43.1

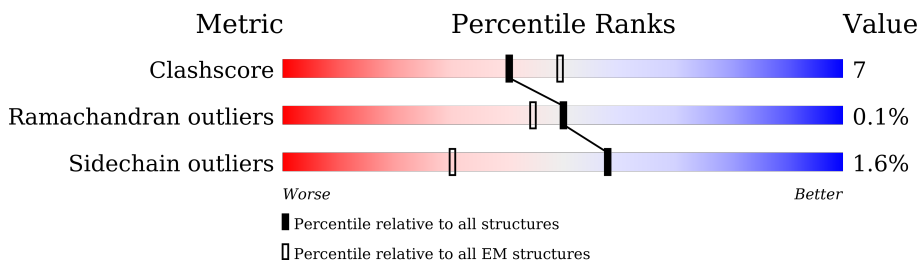
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.76 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	1194	
1	B	1194	
2	C	20	
3	D	8	
4	E	12	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13479 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 DNA topoisomerase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	779	Total	C	N	O	S	0	0
			6303	4038	1087	1149	29		
1	B	779	Total	C	N	O	S	0	0
			6303	4038	1087	1149	29		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1193	HIS	-	expression tag	UNP A0A0C5B080
A	1194	HIS	-	expression tag	UNP A0A0C5B080
B	1193	HIS	-	expression tag	UNP A0A0C5B080
B	1194	HIS	-	expression tag	UNP A0A0C5B080

- Molecule 2 is a DNA chain called DNA (20-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	20	Total	C	N	O	P	0	0
			411	197	76	119	19		

- Molecule 3 is a DNA chain called DNA (8-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	8	Total	C	N	O	P	0	0
			161	78	30	46	7		

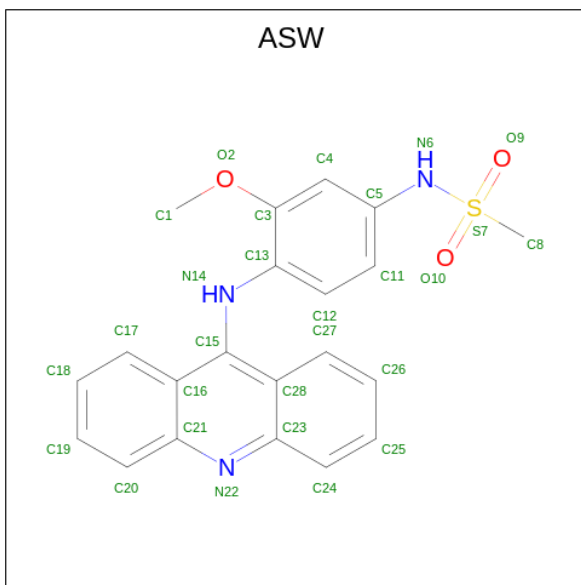
- Molecule 4 is a DNA chain called DNA (12-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	12	Total	C	N	O	P	0	0
			242	116	43	71	12		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Mg	0
			1	1	
5	B	2	Total	Mg	0
			2	2	

- Molecule 6 is N-[4-(acridin-9-ylamino)-3-methoxyphenyl]methanesulfonamide (CCD ID: ASW) (formula: C<sub>21</sub>H<sub>19</sub>N<sub>3</sub>O<sub>3</sub>S).

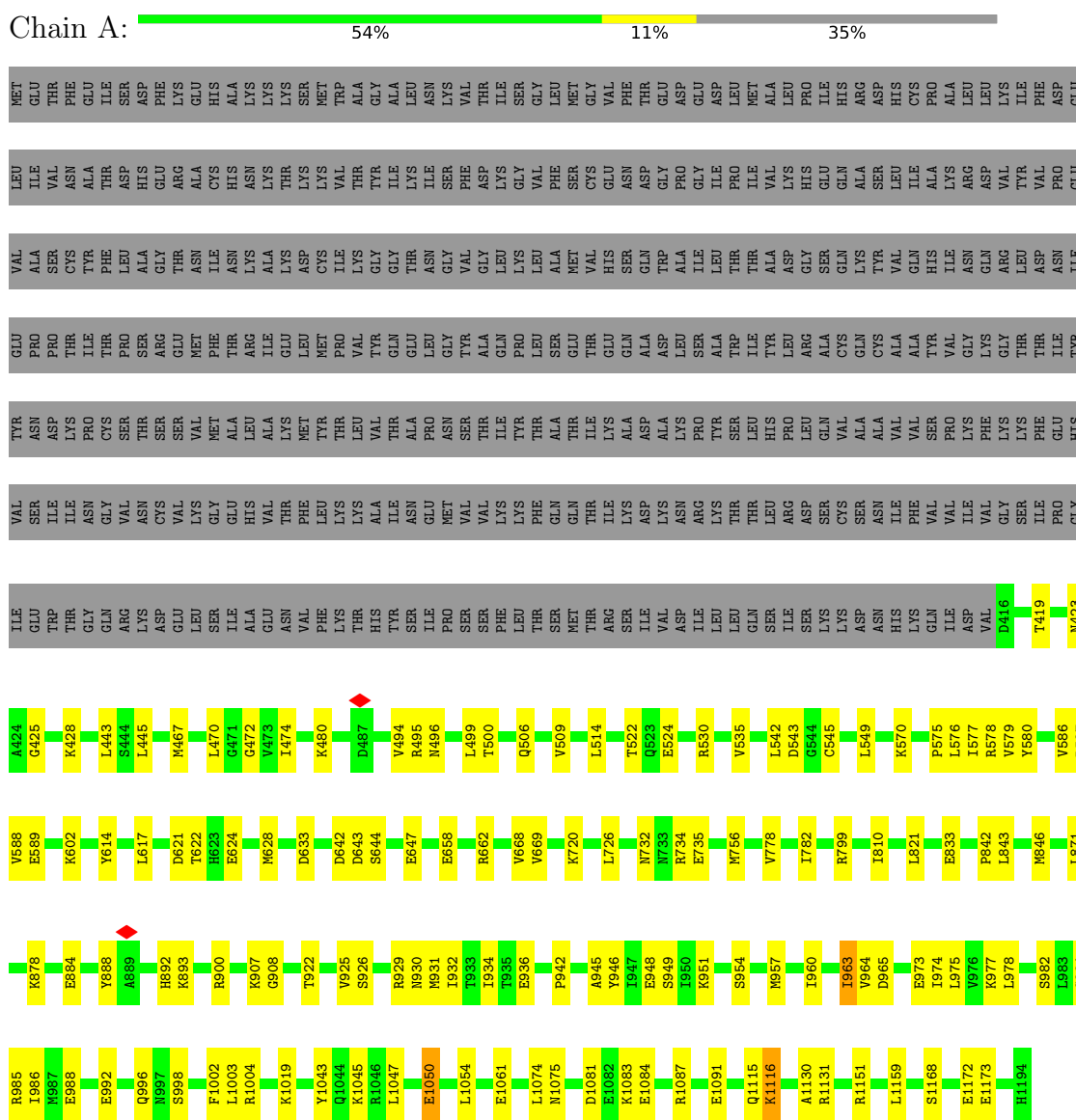


Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	S	0
			28	21	3	3	1	
6	C	1	Total	C	N	O	S	0
			28	21	3	3	1	

### 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: DNA topoisomerase 2



- Molecule 1: DNA topoisomerase 2

35%

E1082	K1083		Y917	V625		E438
L1101		Y920	L641			L443
P1105		G921	D642	D643		L452
E1106		T922	Y923			N456
F1107		Y924	R660			S461
A1108		V925	V668			F462
T1109		V669				D463
I1110			T674			G466
K1116		N931				M467
L1126		T932				T468
S1127		T933				S469
L1128		T934				M475
K1154		T935				N476
L1158		E936				T482
S1168		Y946				D487
E1172		R956				R495
H1194		N957				L499
		I960				V509
		T963				L514
		V964				V535
		D965				V538
		Y966				K570
		S969				V579
		E970				V588
		E973				V592
		I974				E595
		L975				F596
		V976				D597
		K977				A598
		L978				K601
		S982				N608
		L983				H609
		S984				T610
		R985				V611
		V986				D621
		H987				
		E988				
		K991				
		L1003				
		P1018				
		K1019				
		R1039				
		K1045				
		D1081				

- 50%

50%

WORLDWIDE  
**PDB**  
PROTEIN DATA BANK

Chain E:



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	271076	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.223	Depositor
Minimum map value	-0.379	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.124	Depositor
Map size ( $\text{\AA}$ )	255.0, 255.0, 255.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.85, 0.85, 0.85	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: ASW, MG

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	0.16	0/6450	0.32	0/8713
1	B	0.16	0/6450	0.30	0/8713
2	C	0.29	0/461	0.47	0/711
3	D	0.29	0/180	0.45	0/276
4	E	0.28	0/270	0.43	0/413
All	All	0.17	0/13811	0.32	0/18826

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	6303	0	6302	92	0
1	B	6303	0	6302	79	0
2	C	411	0	228	7	0
3	D	161	0	92	4	0
4	E	242	0	136	2	0
5	A	1	0	0	0	0
5	B	2	0	0	0	0
6	A	28	0	19	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	28	0	19	1	0
All	All	13479	0	13098	181	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 7.

The worst 5 of 181 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:B:929:ARG:O	1:B:929:ARG:NH1	2.07	0.87
1:B:873:ARG:O	1:B:877:ASP:HB2	1.78	0.84
3:D:11:DA:H2''	3:D:12:DA:H5''	1.62	0.80
1:A:929:ARG:O	1:A:929:ARG:NH1	2.13	0.77
1:B:932:ILE:HG23	1:B:976:VAL:HB	1.69	0.75

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	777/1194 (65%)	743 (96%)	34 (4%)	0	100	100
1	B	777/1194 (65%)	737 (95%)	39 (5%)	1 (0%)	48	70
All	All	1554/2388 (65%)	1480 (95%)	73 (5%)	1 (0%)	50	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1105	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	681/1045 (65%)	668 (98%)	13 (2%)	52	71
1	B	681/1045 (65%)	672 (99%)	9 (1%)	65	80
All	All	1362/2090 (65%)	1340 (98%)	22 (2%)	58	75

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	595	GLU
1	B	668	VAL
1	B	625	VAL
1	B	669	VAL
1	A	871	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	650	HIS
1	B	1012	HIS
1	A	1099	GLN
1	A	1115	GLN
1	A	1129	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](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z  > 2$
6	ASW	A	1202	-	31,31,31	3.59	6 (19%)	45,45,45	1.48	6 (13%)
6	ASW	C	101	-	31,31,31	3.60	6 (19%)	45,45,45	1.55	5 (11%)

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
6	ASW	A	1202	-	-	4/11/11/11	0/4/4/4
6	ASW	C	101	-	-	1/11/11/11	0/4/4/4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1202	ASW	O9-S7	12.64	1.65	1.43
6	C	101	ASW	O9-S7	12.57	1.65	1.43
6	C	101	ASW	O10-S7	12.34	1.65	1.43
6	A	1202	ASW	O10-S7	12.25	1.64	1.43
6	C	101	ASW	S7-N6	6.37	1.71	1.63

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	101	ASW	O10-S7-O9	-6.95	108.85	118.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1202	ASW	O10-S7-O9	-6.14	110.03	118.85
6	C	101	ASW	O2-C3-C13	3.91	119.59	114.80
6	A	1202	ASW	O2-C3-C13	3.72	119.36	114.80
6	C	101	ASW	O2-C3-C4	-2.20	120.33	124.12

There are no chirality outliers.

All (5) torsion outliers are listed below:

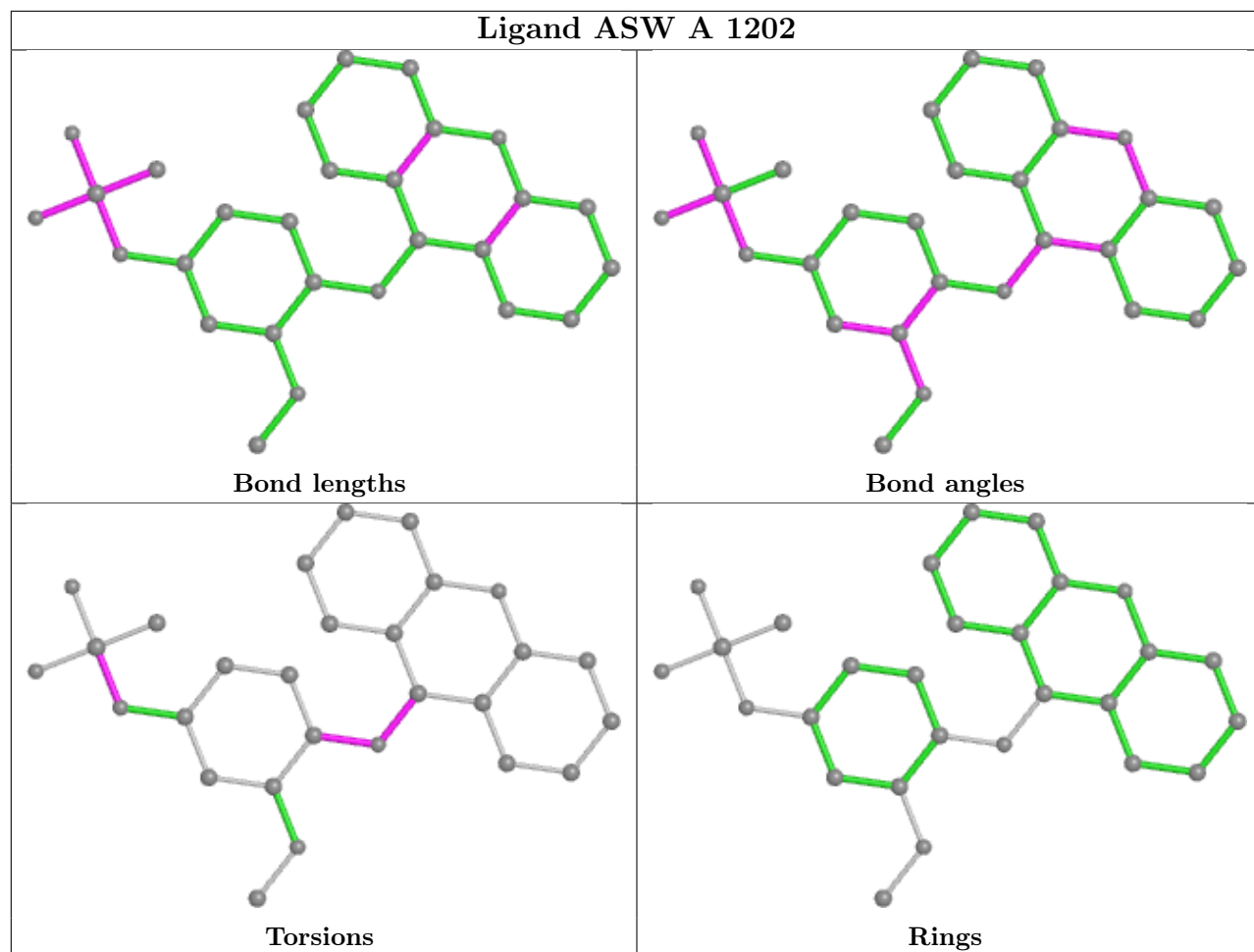
Mol	Chain	Res	Type	Atoms
6	A	1202	ASW	C5-N6-S7-C8
6	A	1202	ASW	C5-N6-S7-O10
6	A	1202	ASW	C12-C13-N14-C15
6	A	1202	ASW	C28-C15-N14-C13
6	C	101	ASW	C5-N6-S7-O9

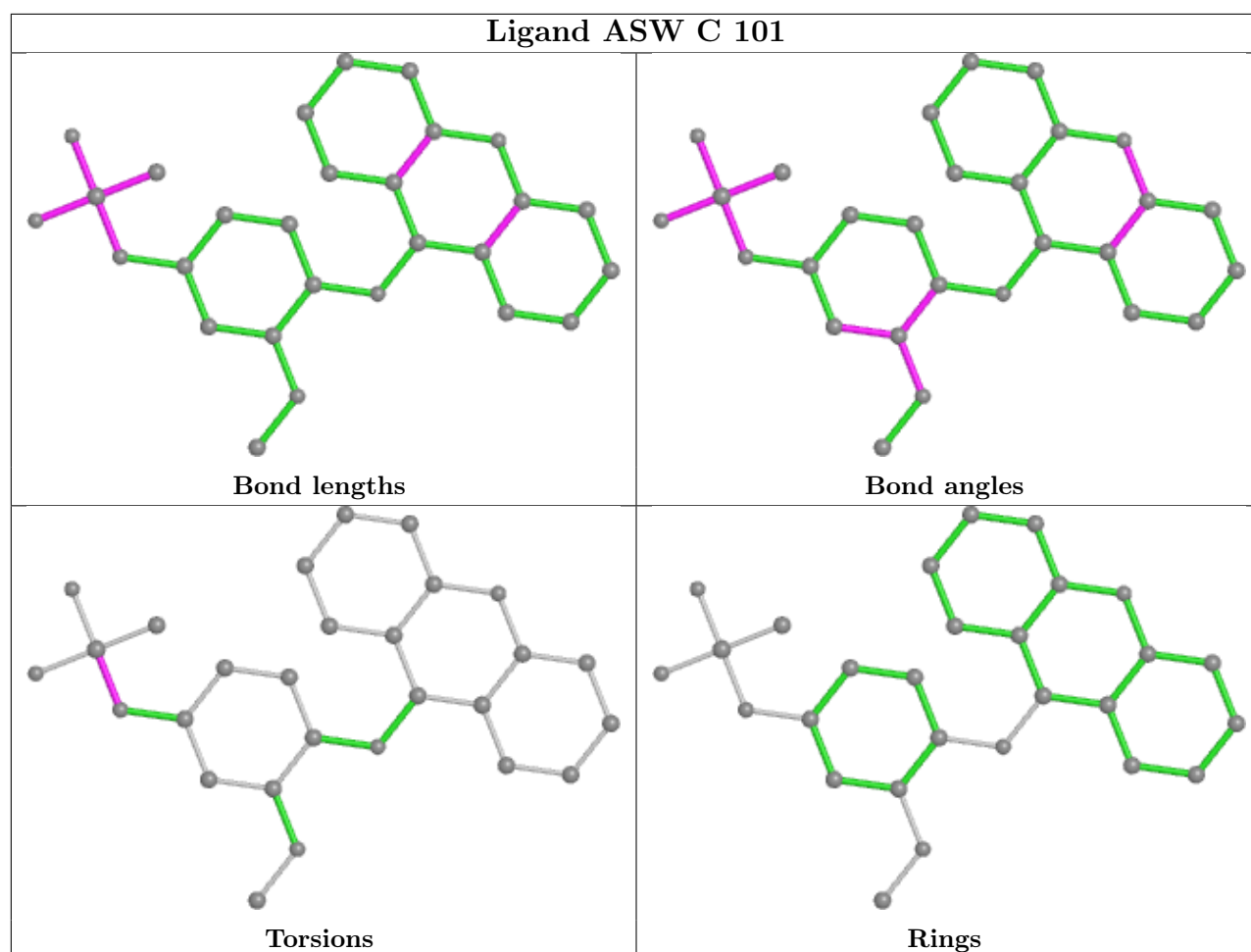
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1202	ASW	3	0
6	C	101	ASW	1	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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

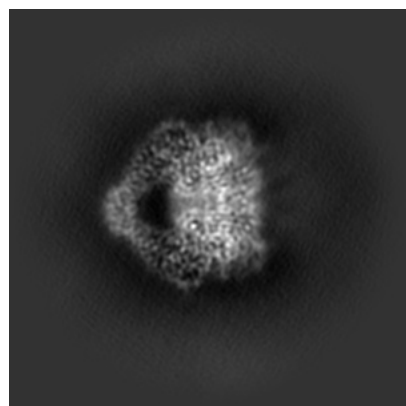
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39245. These allow visual inspection of the internal detail of the map and identification of artifacts.

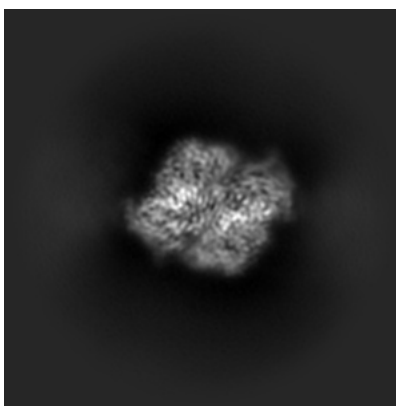
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

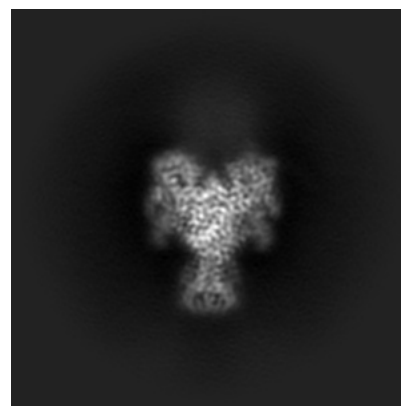
#### 6.1.1 Primary map



X

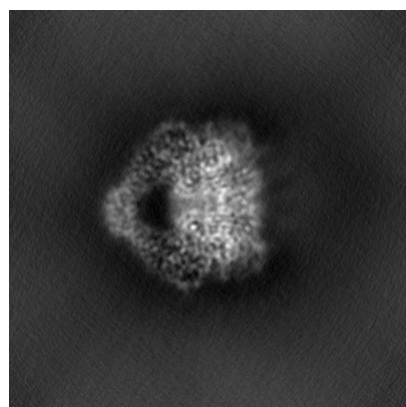


Y

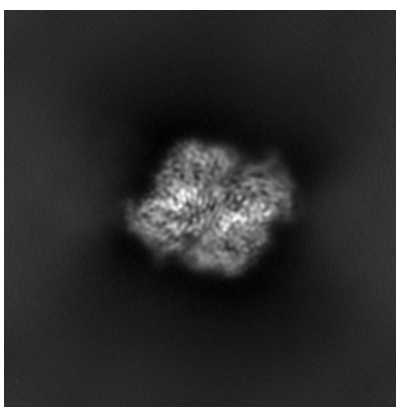


Z

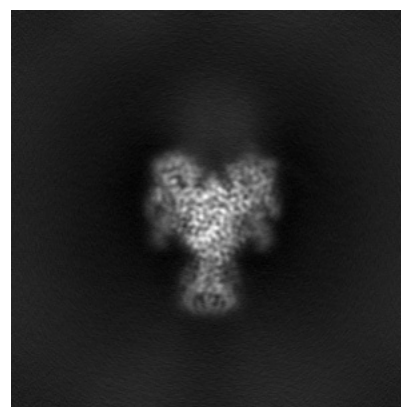
#### 6.1.2 Raw map



X



Y



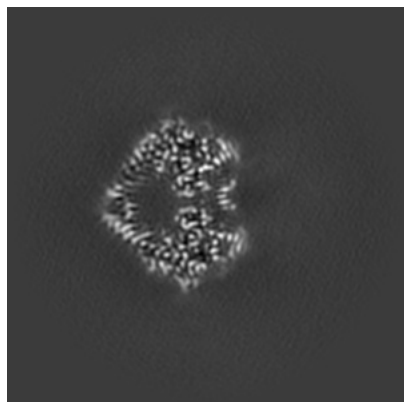
Z

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

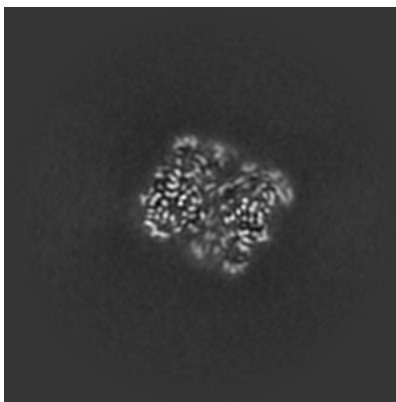


## 6.2 Central slices [i](#)

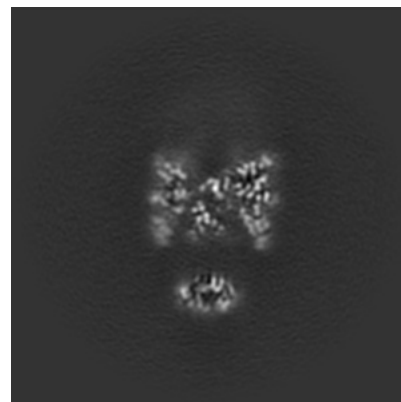
### 6.2.1 Primary map



X Index: 150

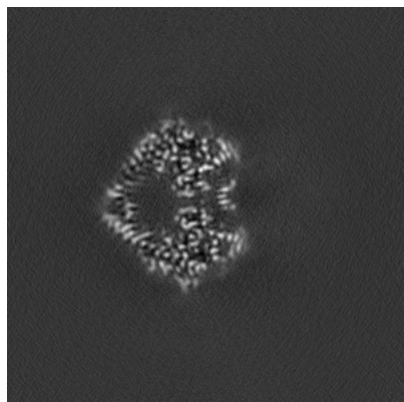


Y Index: 150

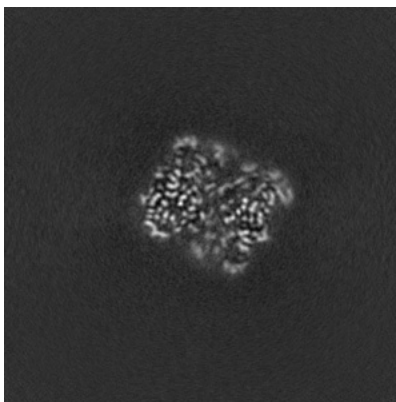


Z Index: 150

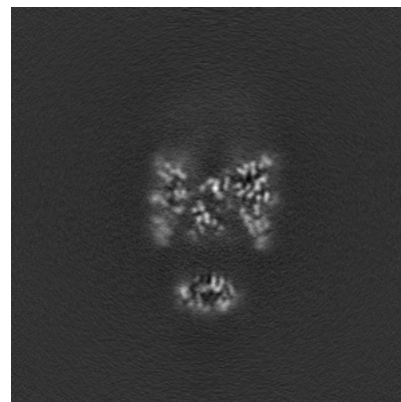
### 6.2.2 Raw map



X Index: 150



Y Index: 150

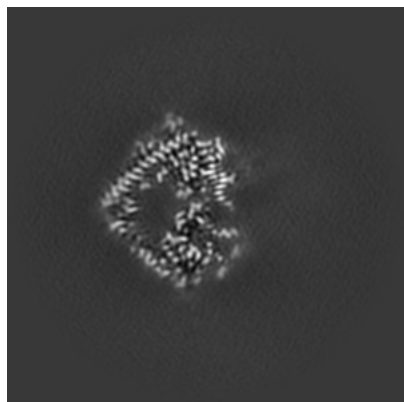


Z Index: 150

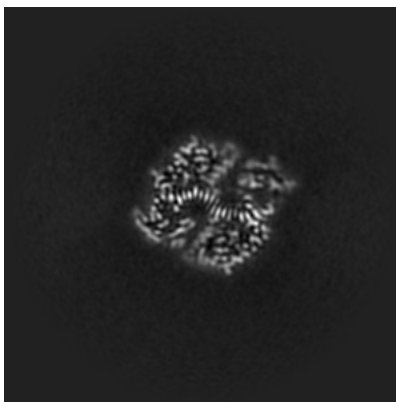
The images above show central slices of the map in three orthogonal directions.

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

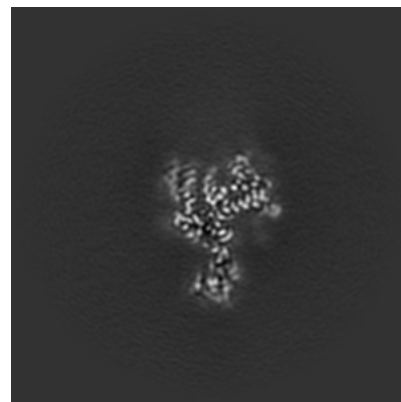
### 6.3.1 Primary map



X Index: 146

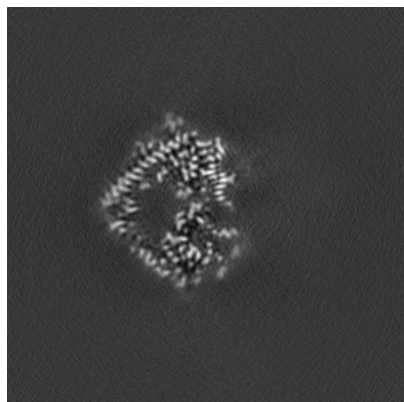


Y Index: 158

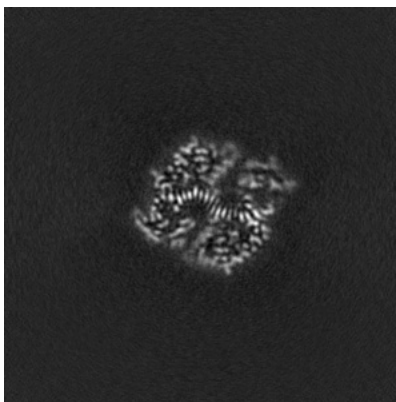


Z Index: 130

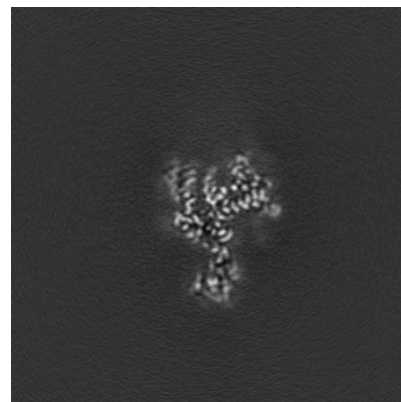
### 6.3.2 Raw map



X Index: 146



Y Index: 158

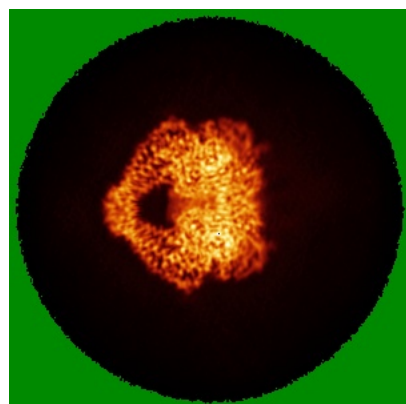


Z Index: 130

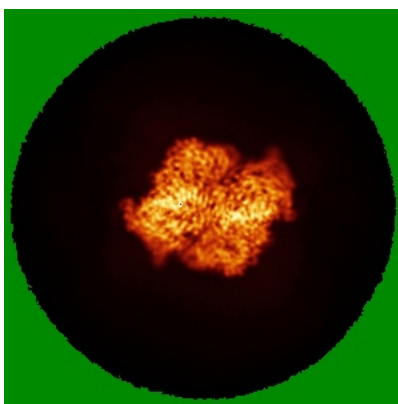
The images above show the largest variance slices of the map in three orthogonal directions.

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

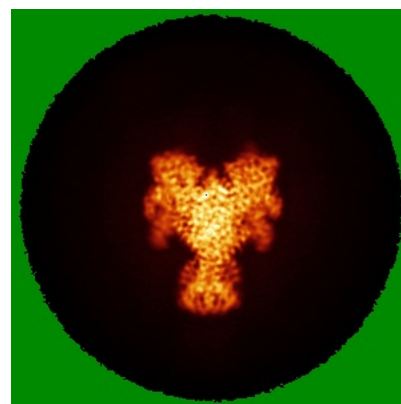
### 6.4.1 Primary map



X

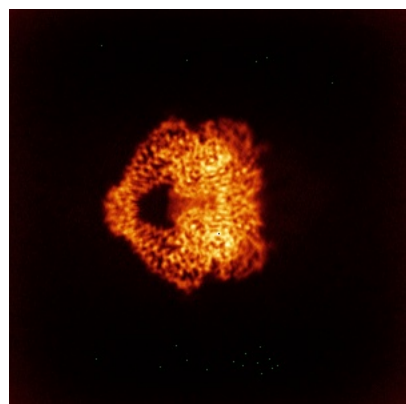


Y

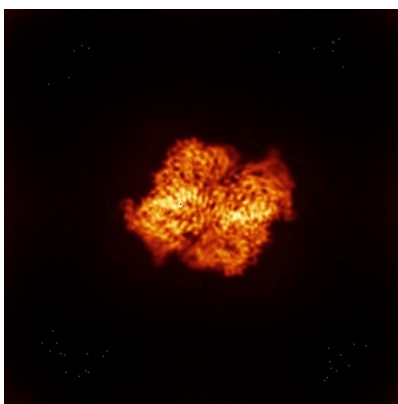


Z

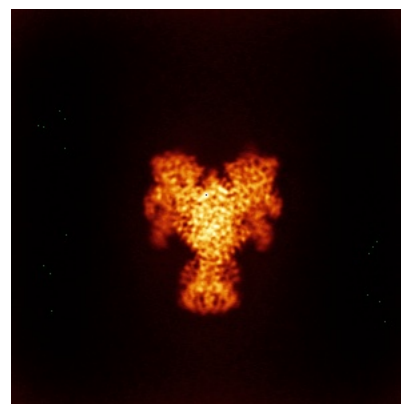
### 6.4.2 Raw map



X



Y

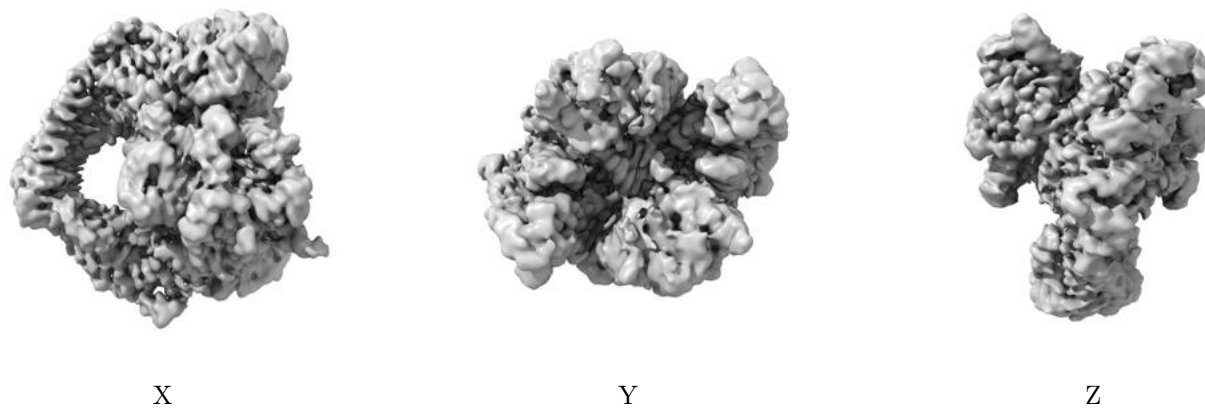


Z

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.

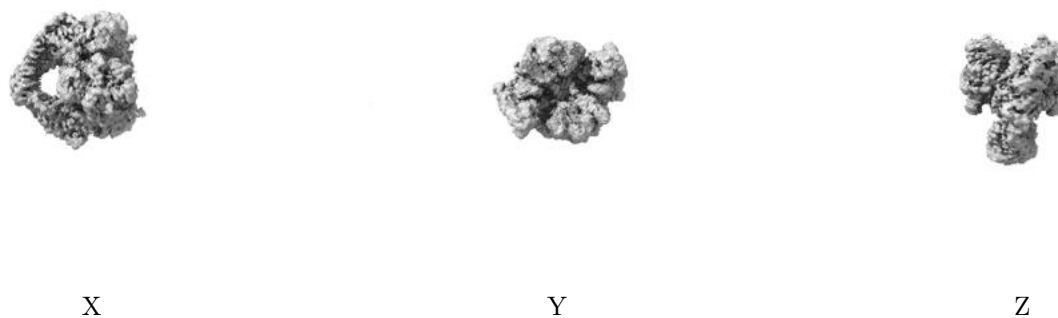
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.124. 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.

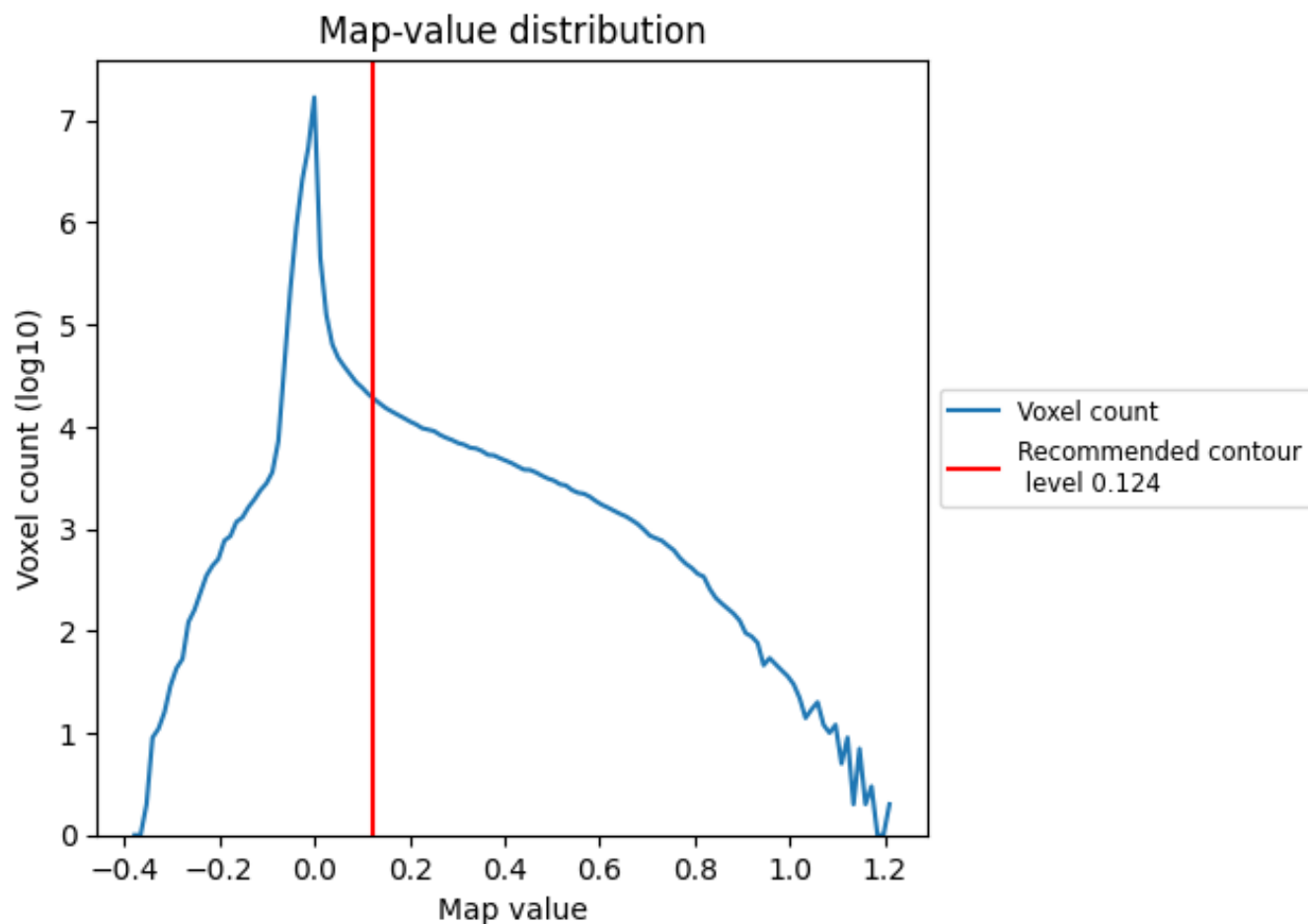
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

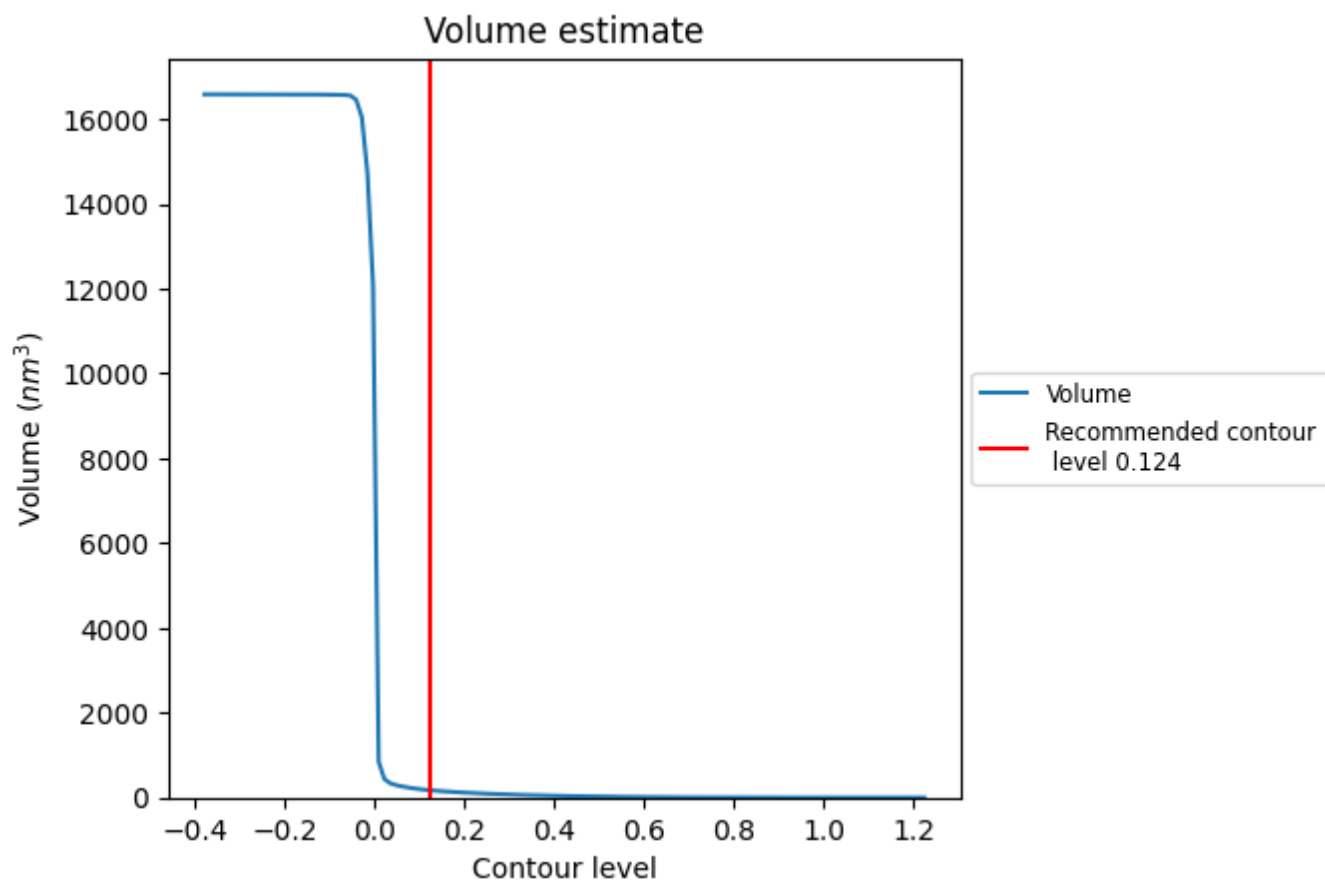
This section contains the results of statistical analysis of the map.

### 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.

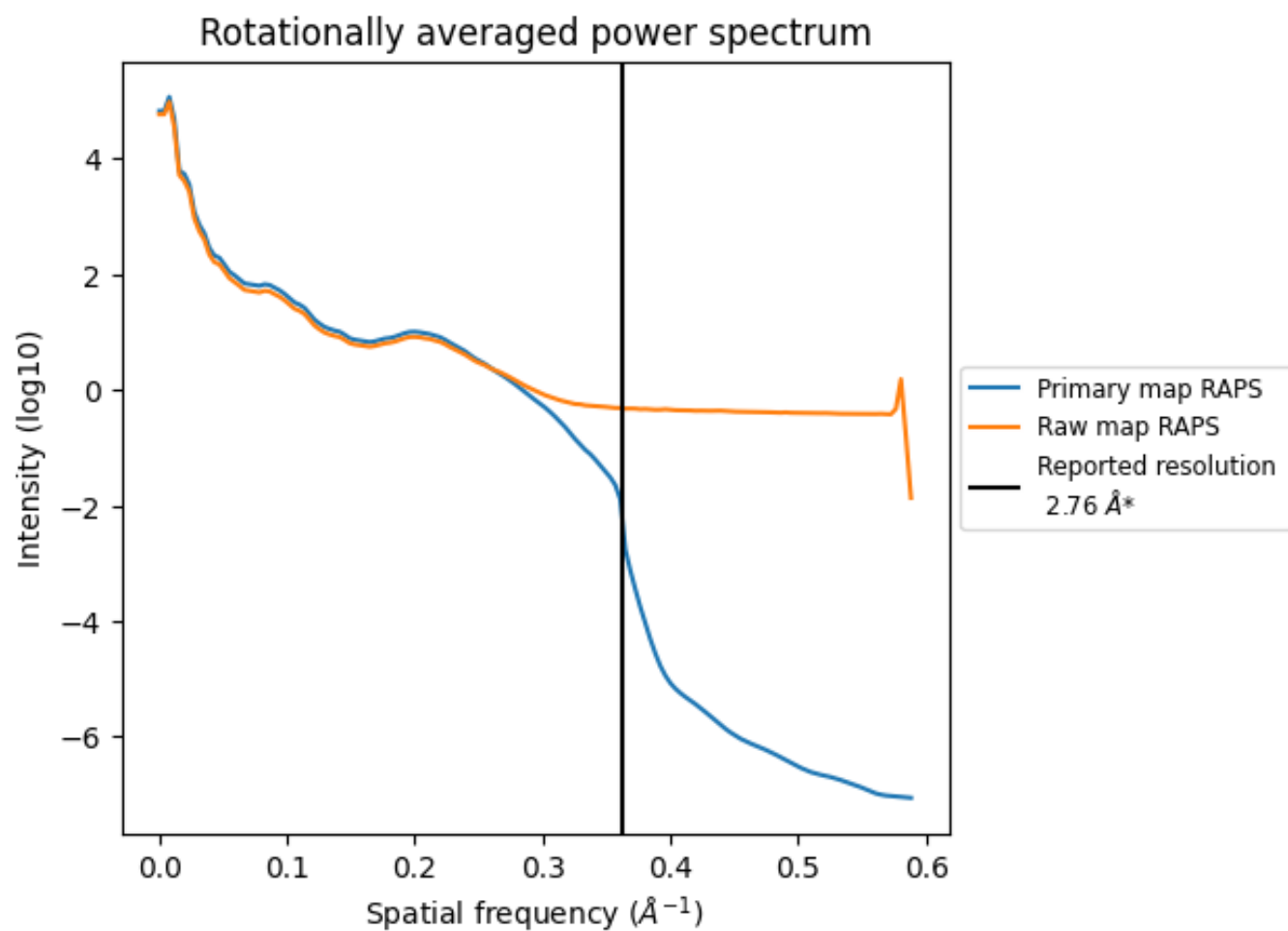
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 172 nm<sup>3</sup>; this corresponds to an approximate mass of 155 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 ⓘ

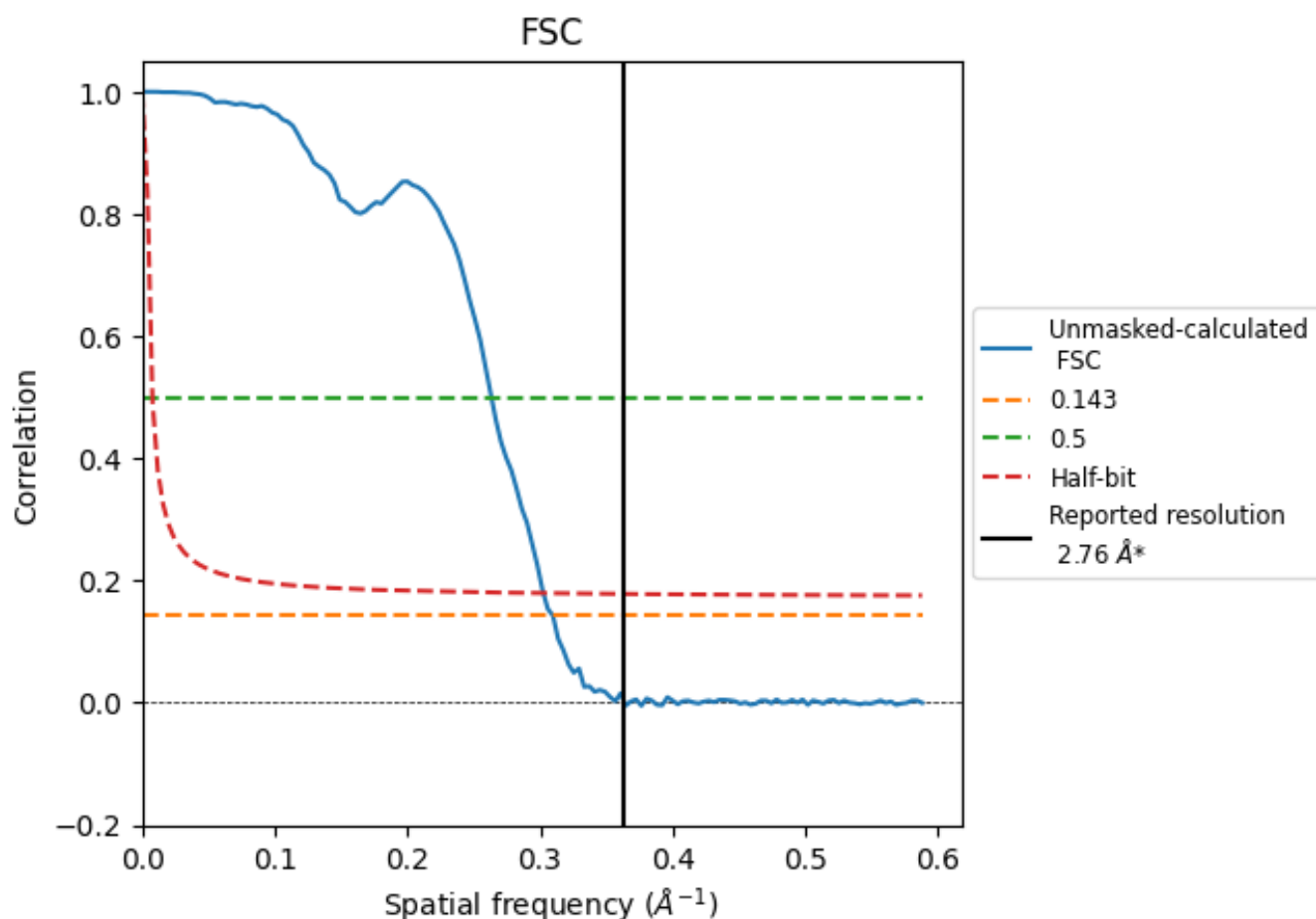


\*Reported resolution corresponds to spatial frequency of 0.362  $\text{\AA}^{-1}$

## 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 0.362 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

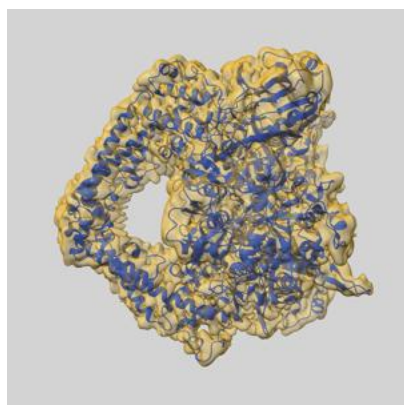
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.23	3.80	3.31

\*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 3.23 differs from the reported value 2.76 by more than 10 %

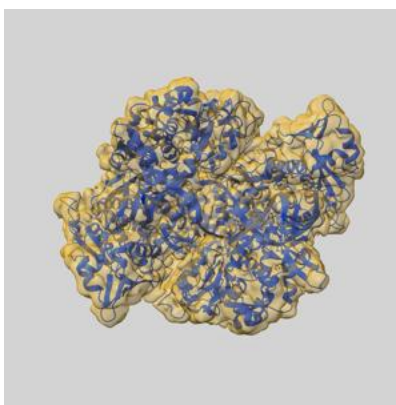
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39245 and PDB model 8YGE. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

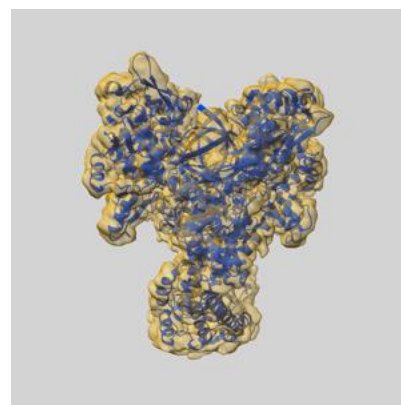
### 9.1 Map-model overlay [i](#)



X



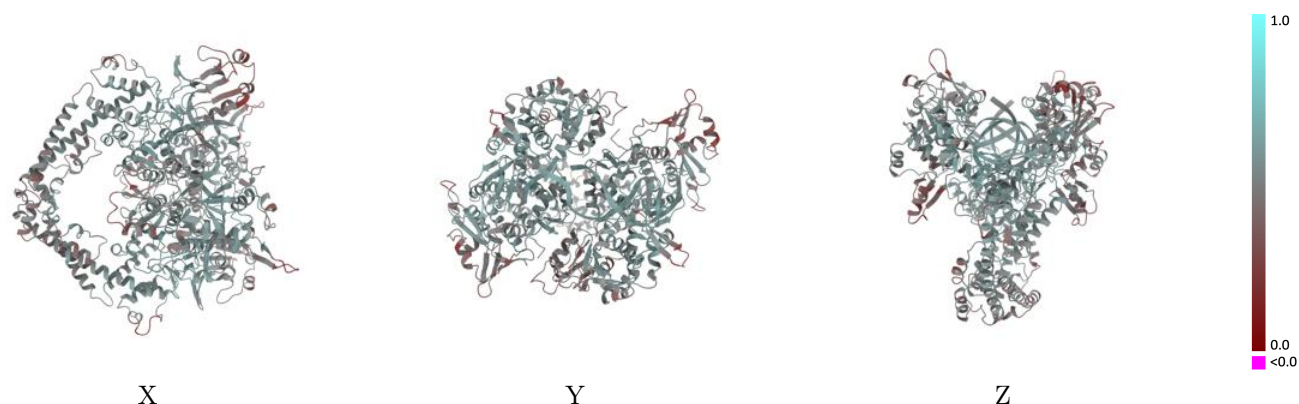
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.124 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](#)



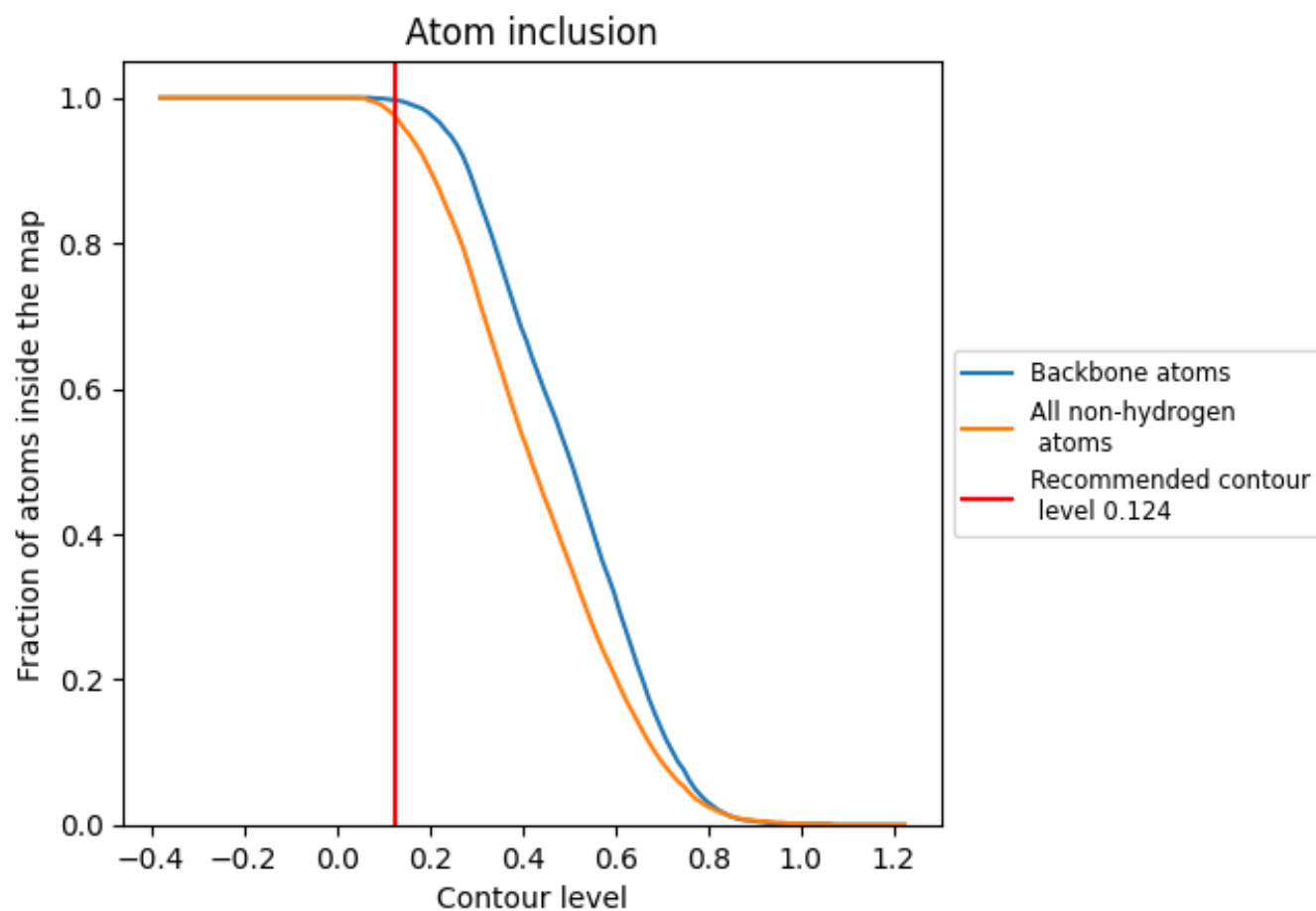
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.124).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% 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 (0.124) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9760	<div></div> 0.5130
A	<div></div> 0.9740	<div></div> 0.5030
B	<div></div> 0.9750	<div></div> 0.5150
C	<div></div> 0.9950	<div></div> 0.5750
D	<div></div> 0.9940	<div></div> 0.5680
E	<div></div> 1.0000	<div></div> 0.5730

