



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:18 AM UTC

PDB ID : 8TH3 / pdb\_00008th3  
EMDB ID : EMD-41248  
Title : Structure of AT118-H Nanobody Antagonist in Complex with the Angiotensin II Type I Receptor  
Authors : Skiba, M.A.; Kruse, A.C.  
Deposited on : 2023-07-13  
Resolution : 3.00 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:

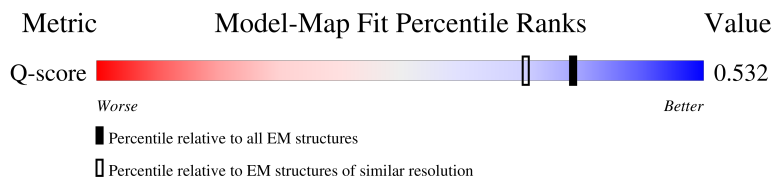
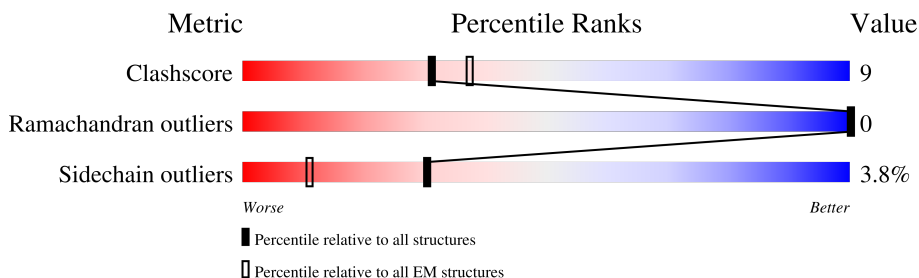
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (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

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 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	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 ( 2.50 - 3.50 )

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  $\geq 3$ , 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	582	<p>18% (red), 53% (green), 14% (yellow), 32% (grey)</p>
1	B	582	<p>8% (red), 12% (green), 83% (grey)</p>
2	C	231	<p>30% (red), 39% (green), 13% (yellow), 47% (grey)</p>
3	D	215	<p>7% (red), 37% (green), 12% (yellow), 51% (grey)</p>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5770 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 AT118-H nanobody, Type-1 angiotensin II receptor, Soluble cytochrome b562 complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	393	3160	2096	511	535	18	0	0
1	B	99	785	490	145	146	4	0	0

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	TRP	MET	engineered mutation	UNP P0ABE7
A	327	ILE	HIS	engineered mutation	UNP P0ABE7
A	331	LEU	-	linker	UNP P0ABE7
A	332	GLU	-	linker	UNP P0ABE7
A	333	ARG	-	linker	UNP P0ABE7
A	334	ALA	-	linker	UNP P0ABE7
A	335	ARG	-	linker	UNP P0ABE7
A	336	SER	-	linker	UNP P0ABE7
A	337	THR	-	linker	UNP P0ABE7
A	338	LEU	-	linker	UNP P0ABE7
A	339	ASP	-	linker	UNP P0ABE7
A	340	LYS	-	linker	UNP P0ABE7
A	341	LEU	-	linker	UNP P0ABE7
A	1320	GLY	-	expression tag	UNP P30556
A	1321	GLY	-	expression tag	UNP P30556
A	1322	SER	-	expression tag	UNP P30556
A	1323	SER	-	expression tag	UNP P30556
A	1324	LEU	-	expression tag	UNP P30556
A	1325	GLU	-	expression tag	UNP P30556
A	1326	VAL	-	expression tag	UNP P30556
A	1327	LEU	-	expression tag	UNP P30556
A	1328	PHE	-	expression tag	UNP P30556
A	1329	GLN	-	expression tag	UNP P30556
A	1330	GLY	-	expression tag	UNP P30556
A	1331	PRO	-	expression tag	UNP P30556

*Continued on next page...*

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1332	THR	-	expression tag	UNP P30556
A	1333	GLU	-	expression tag	UNP P30556
A	1334	THR	-	expression tag	UNP P30556
A	1335	SER	-	expression tag	UNP P30556
A	1336	GLN	-	expression tag	UNP P30556
A	1337	VAL	-	expression tag	UNP P30556
A	1338	ALA	-	expression tag	UNP P30556
A	1339	PRO	-	expression tag	UNP P30556
A	1340	ALA	-	expression tag	UNP P30556
B	367	TRP	MET	engineered mutation	UNP P0ABE7
B	462	ILE	HIS	engineered mutation	UNP P0ABE7
B	466	LEU	-	linker	UNP P0ABE7
B	467	GLU	-	linker	UNP P0ABE7
B	468	ARG	-	linker	UNP P0ABE7
B	469	ALA	-	linker	UNP P0ABE7
B	470	ARG	-	linker	UNP P0ABE7
B	471	SER	-	linker	UNP P0ABE7
B	472	THR	-	linker	UNP P0ABE7
B	473	LEU	-	linker	UNP P0ABE7
B	474	ASP	-	linker	UNP P0ABE7
B	475	LYS	-	linker	UNP P0ABE7
B	476	LEU	-	linker	UNP P0ABE7
B	562	GLY	-	expression tag	UNP P30556
B	563	GLY	-	expression tag	UNP P30556
B	564	SER	-	expression tag	UNP P30556
B	565	SER	-	expression tag	UNP P30556
B	566	LEU	-	expression tag	UNP P30556
B	567	GLU	-	expression tag	UNP P30556
B	568	VAL	-	expression tag	UNP P30556
B	569	LEU	-	expression tag	UNP P30556
B	570	PHE	-	expression tag	UNP P30556
B	571	GLN	-	expression tag	UNP P30556
B	572	GLY	-	expression tag	UNP P30556
B	573	PRO	-	expression tag	UNP P30556
B	574	THR	-	expression tag	UNP P30556
B	575	GLU	-	expression tag	UNP P30556
B	576	THR	-	expression tag	UNP P30556
B	577	SER	-	expression tag	UNP P30556
B	578	GLN	-	expression tag	UNP P30556
B	579	VAL	-	expression tag	UNP P30556
B	580	ALA	-	expression tag	UNP P30556
B	581	PRO	-	expression tag	UNP P30556

*Continued on next page...*







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

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	478571	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 ( $e^-/\text{\AA}^2$ )	64.2	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.245	Depositor
Minimum map value	-1.636	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.398	Depositor
Map size (Å)	239.04, 239.04, 239.04	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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: Y01

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	0.15	0/3233	0.29	0/4387
1	B	0.13	0/802	0.24	0/1083
2	C	0.11	0/973	0.28	0/1327
3	D	0.16	0/829	0.33	0/1126
All	All	0.14	0/5837	0.29	0/7923

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	3160	0	3273	53	0
1	B	785	0	758	17	0
2	C	944	0	886	18	0
3	D	811	0	787	21	0
4	A	70	0	98	2	0
All	All	5770	0	5802	102	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 9.

The worst 5 of 102 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:38:ARG:NH1	1:B:89:ASP:OD2	2.22	0.71
3:D:38:GLN:HB2	3:D:48:LEU:HD11	1.75	0.69
1:A:1244:ALA:HB2	4:A:1402:Y01:HAD3	1.78	0.64
1:A:258:MET:HE1	1:A:319:LEU:HD13	1.80	0.64
3:D:7:GLN:H	3:D:102:GLN:HE22	1.42	0.64

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	389/582 (67%)	372 (96%)	17 (4%)	0	100	100
1	B	97/582 (17%)	88 (91%)	9 (9%)	0	100	100
2	C	120/231 (52%)	114 (95%)	6 (5%)	0	100	100
3	D	104/215 (48%)	98 (94%)	6 (6%)	0	100	100
All	All	710/1610 (44%)	672 (95%)	38 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	340/496 (68%)	329 (97%)	11 (3%)	34	67
1	B	80/496 (16%)	74 (92%)	6 (8%)	12	41
2	C	97/192 (50%)	94 (97%)	3 (3%)	35	68
3	D	92/190 (48%)	89 (97%)	3 (3%)	33	67
All	All	609/1374 (44%)	586 (96%)	23 (4%)	30	63

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	70	SER
2	C	41	ARG
1	B	101	VAL
2	C	49	GLU
1	A	1240	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1294	ASN
2	C	31	ASN
3	D	102	GLN
2	C	87	ASN
1	A	238	ASN

### 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

2 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
4	Y01	A	1402	-	38,38,38	0.56	0	57,57,57	0.58	0
4	Y01	A	1401	-	38,38,38	0.57	0	57,57,57	0.71	0

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
4	Y01	A	1402	-	-	3/19/77/77	0/4/4/4
4	Y01	A	1401	-	-	5/19/77/77	0/4/4/4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

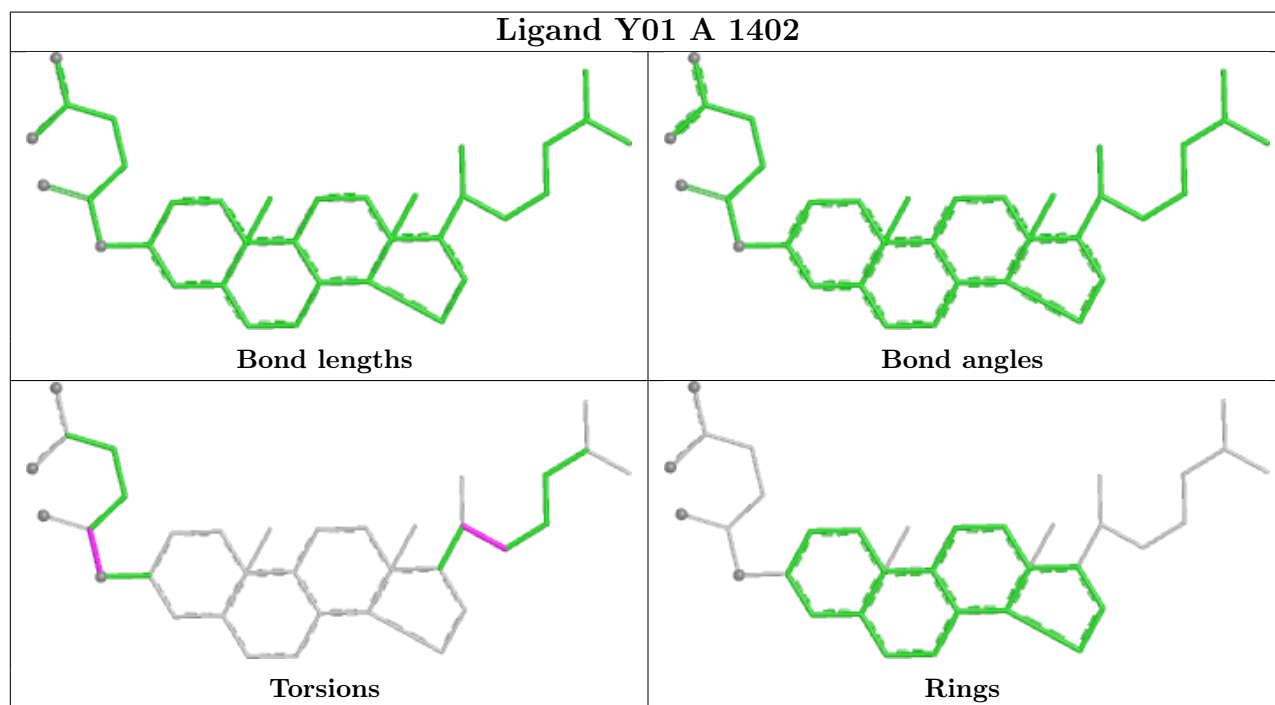
Mol	Chain	Res	Type	Atoms
4	A	1402	Y01	CAM-CAY-OAW-CBC
4	A	1402	Y01	OAG-CAY-OAW-CBC
4	A	1401	Y01	CAJ-CAO-CBB-CBE
4	A	1402	Y01	CAJ-CAO-CBB-CBE
4	A	1401	Y01	CAN-CAJ-CAO-CBB

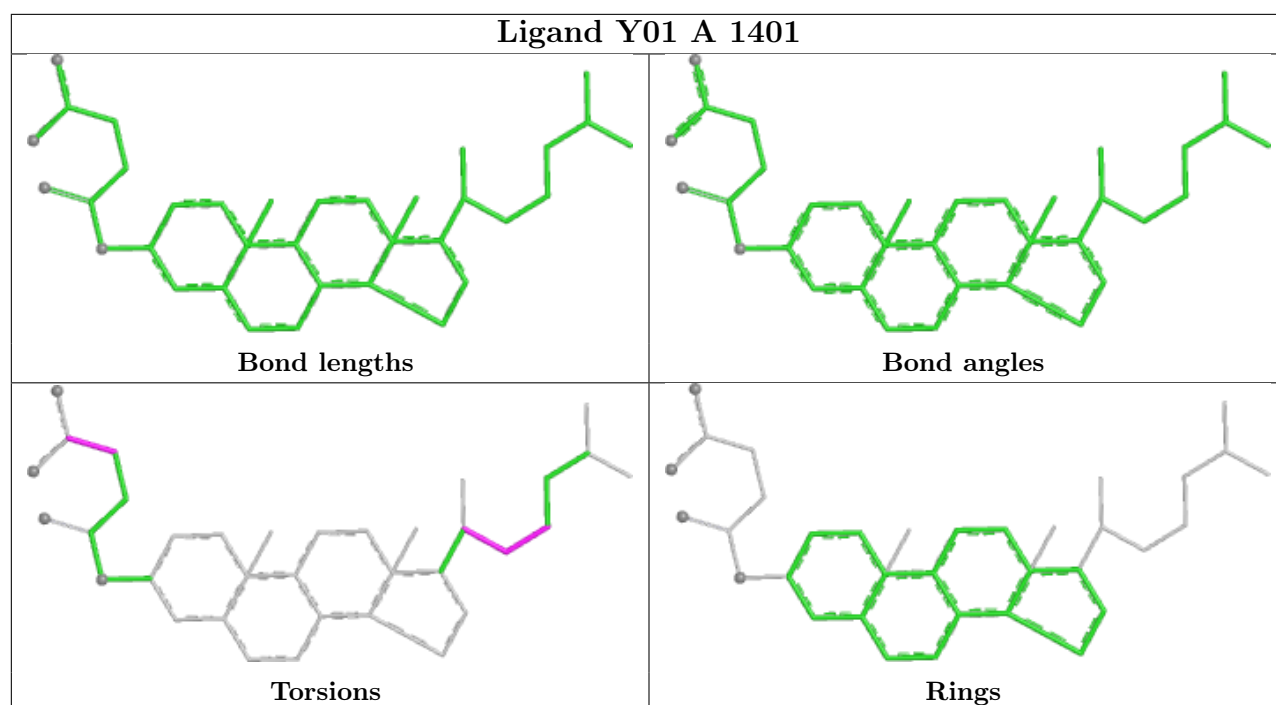
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1402	Y01	2	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.

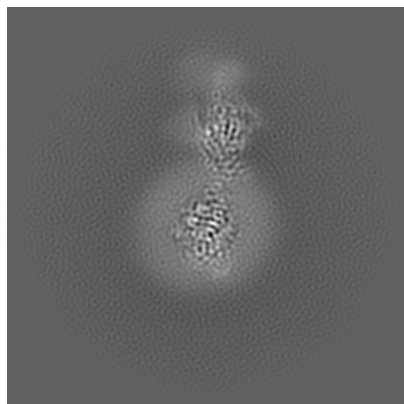
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41248. These allow visual inspection of the internal detail of the map and identification of artifacts.

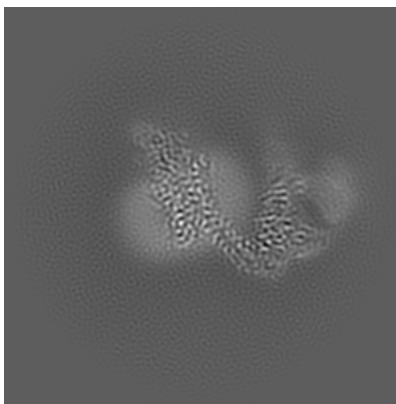
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

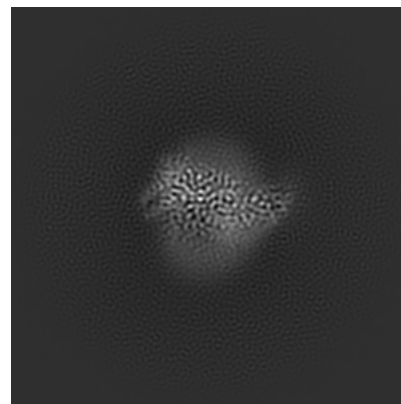
#### 6.1.1 Primary map



X

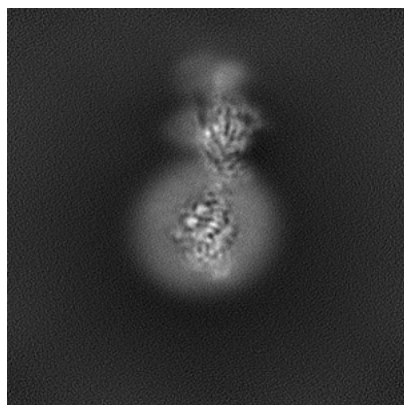


Y

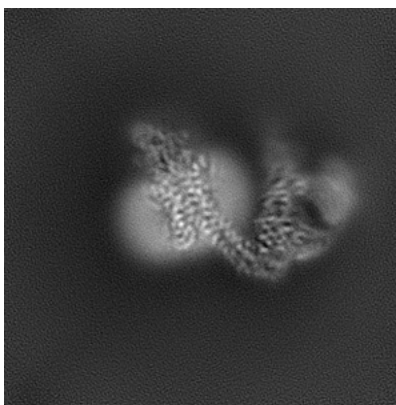


Z

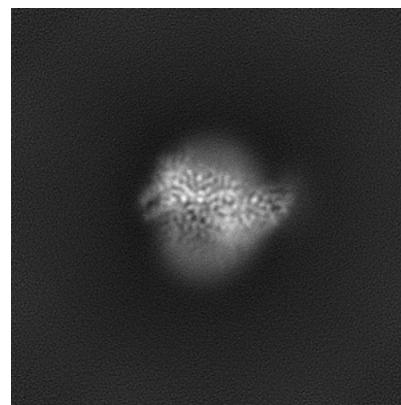
#### 6.1.2 Raw map



X



Y

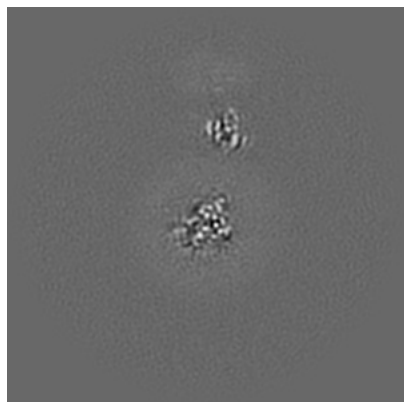


Z

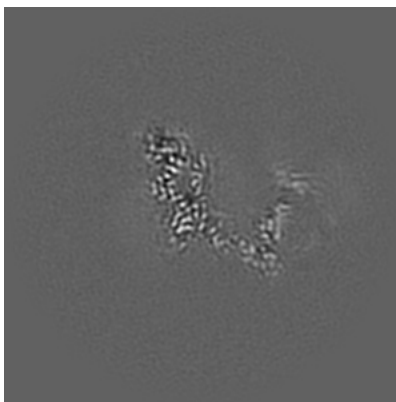
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

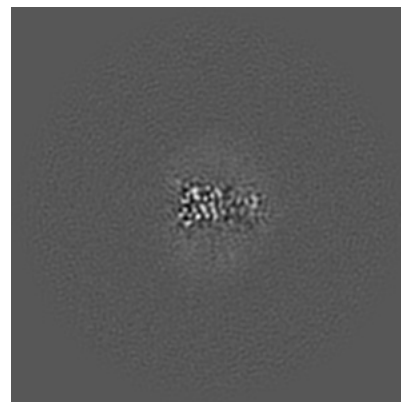
### 6.2.1 Primary map



X Index: 144

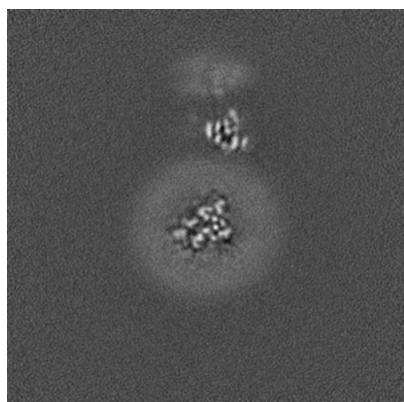


Y Index: 144

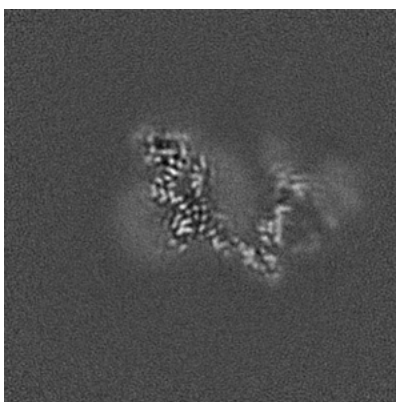


Z Index: 144

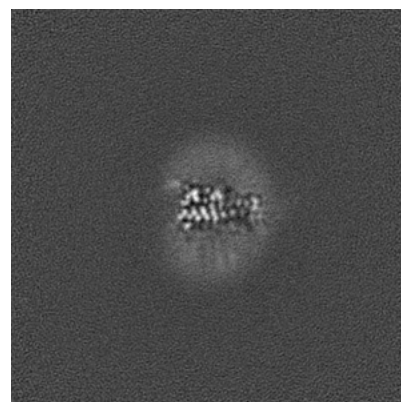
### 6.2.2 Raw map



X Index: 144



Y Index: 144

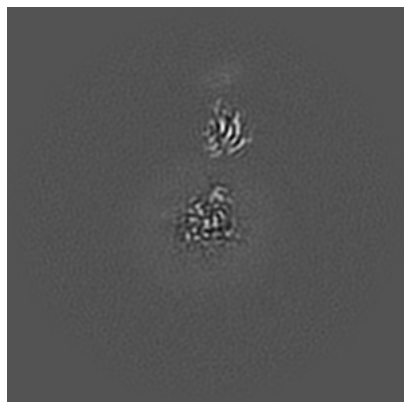


Z Index: 144

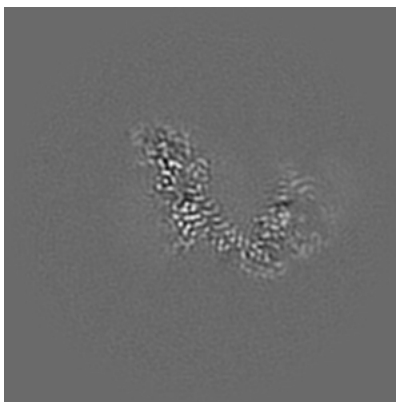
The images above show central slices of the map in three orthogonal directions.

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

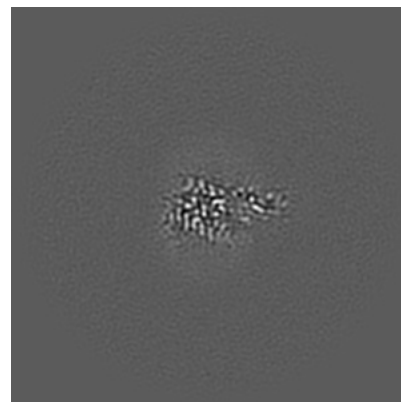
### 6.3.1 Primary map



X Index: 135

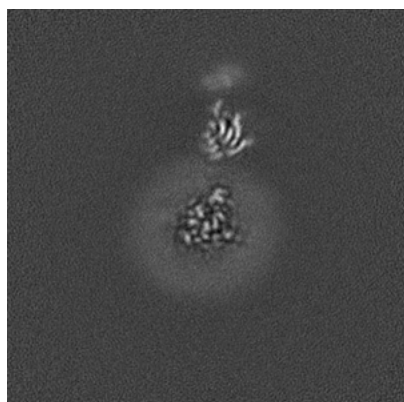


Y Index: 149

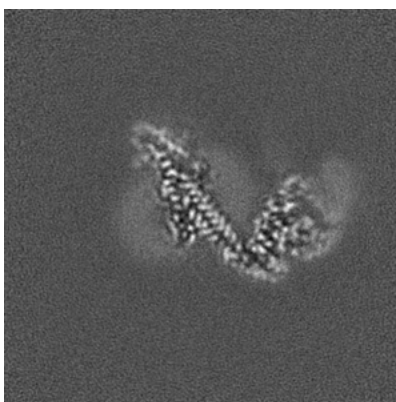


Z Index: 126

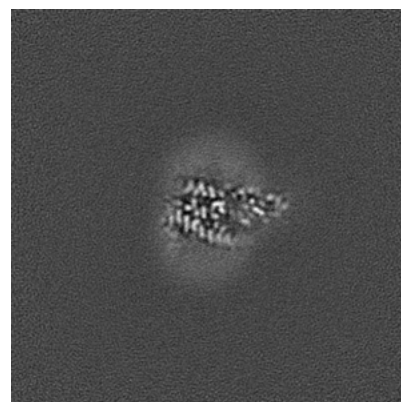
### 6.3.2 Raw map



X Index: 135



Y Index: 152

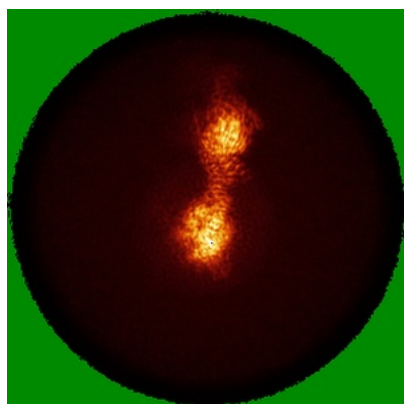


Z Index: 126

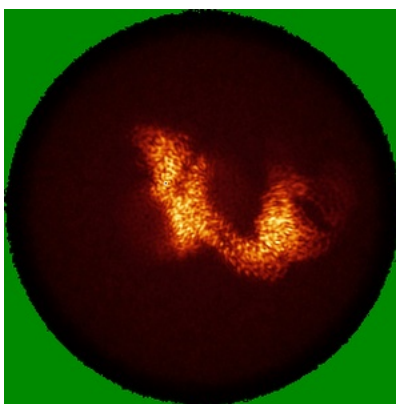
The images above show the largest variance slices of the map in three orthogonal directions.

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

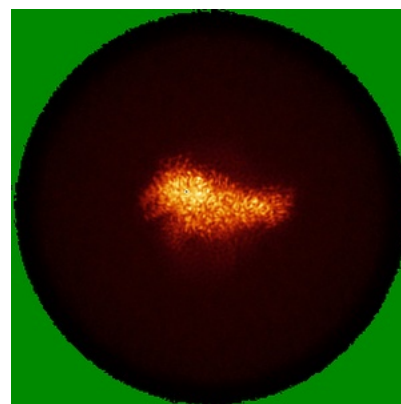
### 6.4.1 Primary map



X

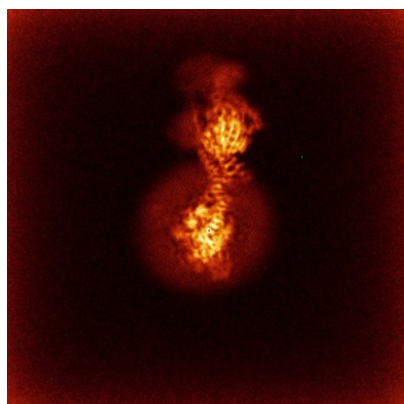


Y

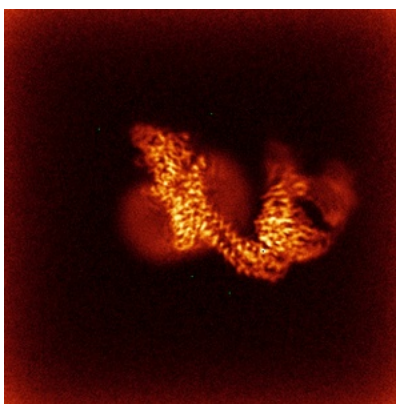


Z

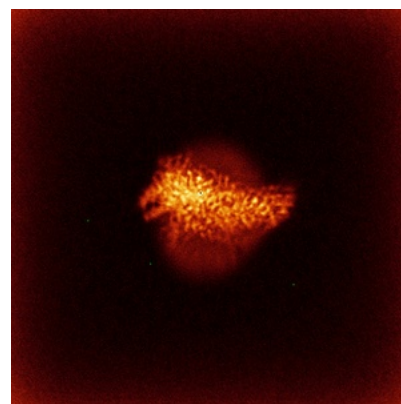
### 6.4.2 Raw map



X



Y

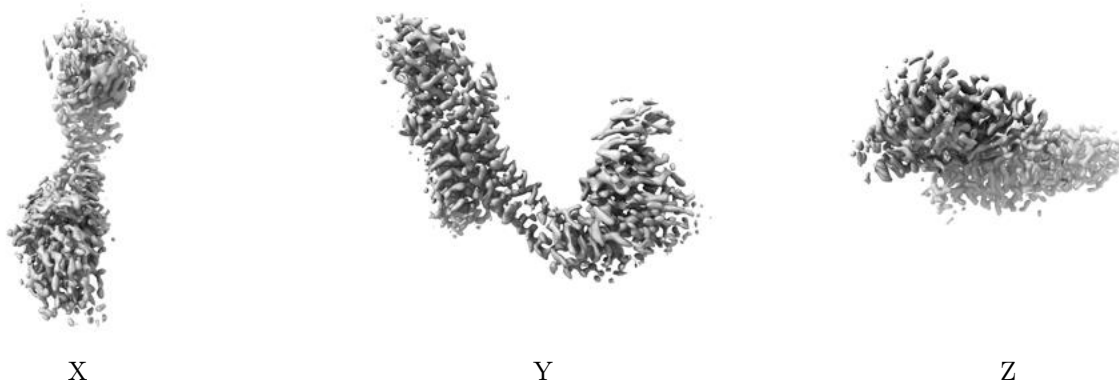


Z

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.

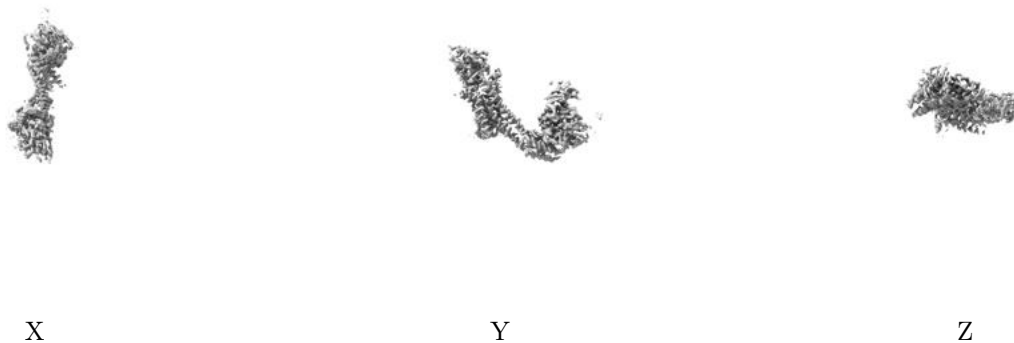
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.398. 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.

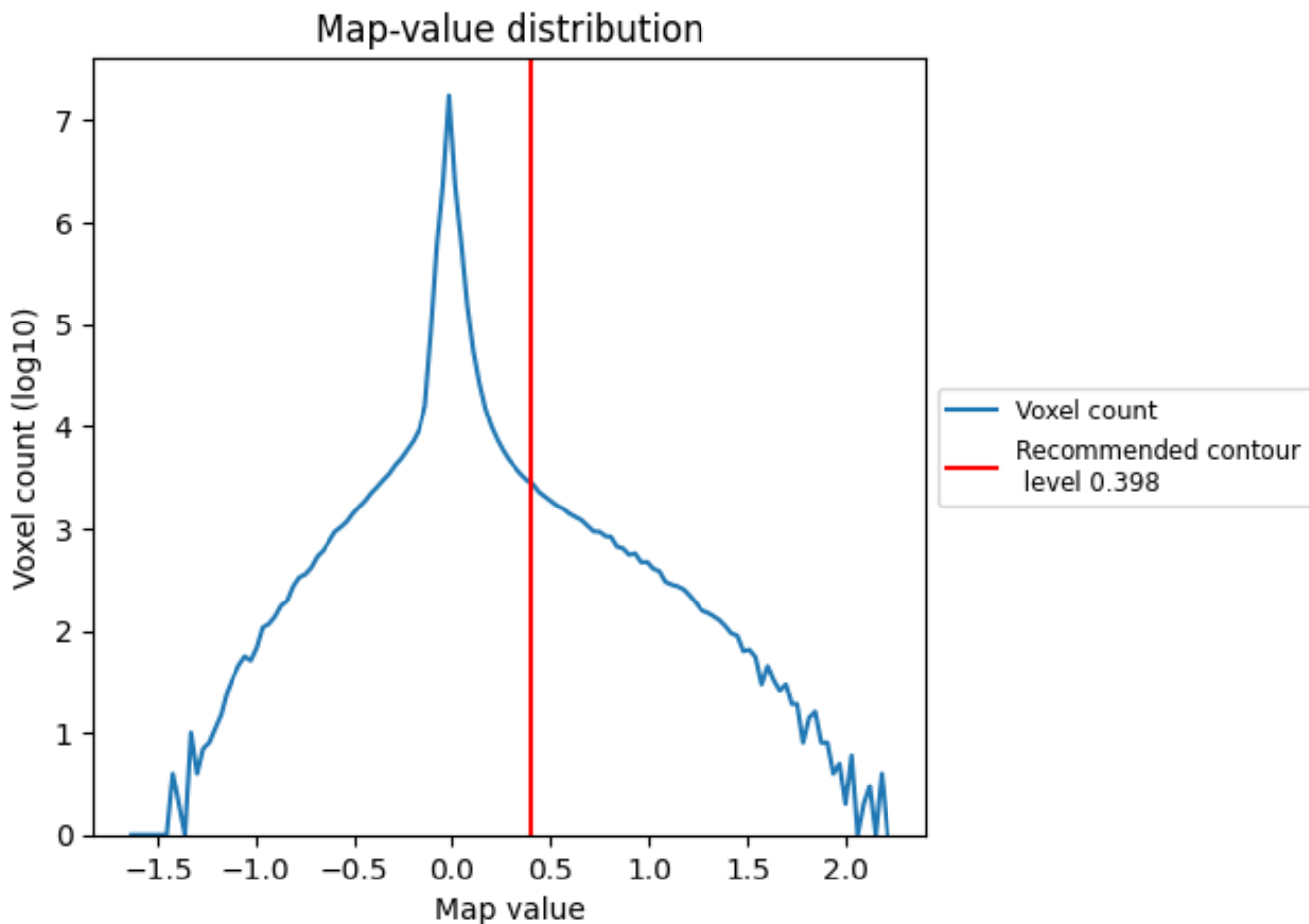
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

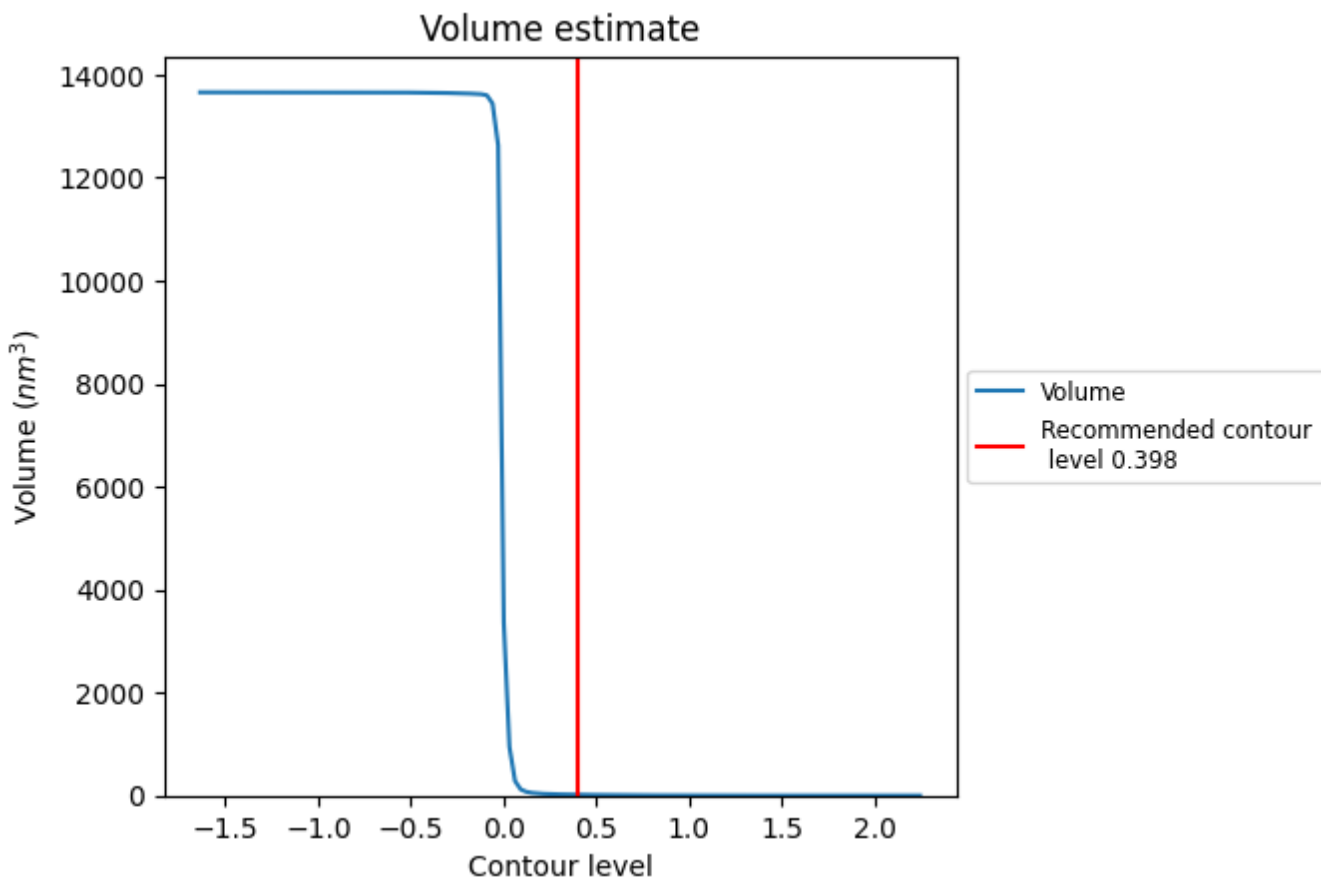
This section contains the results of statistical analysis of the map.

### 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.

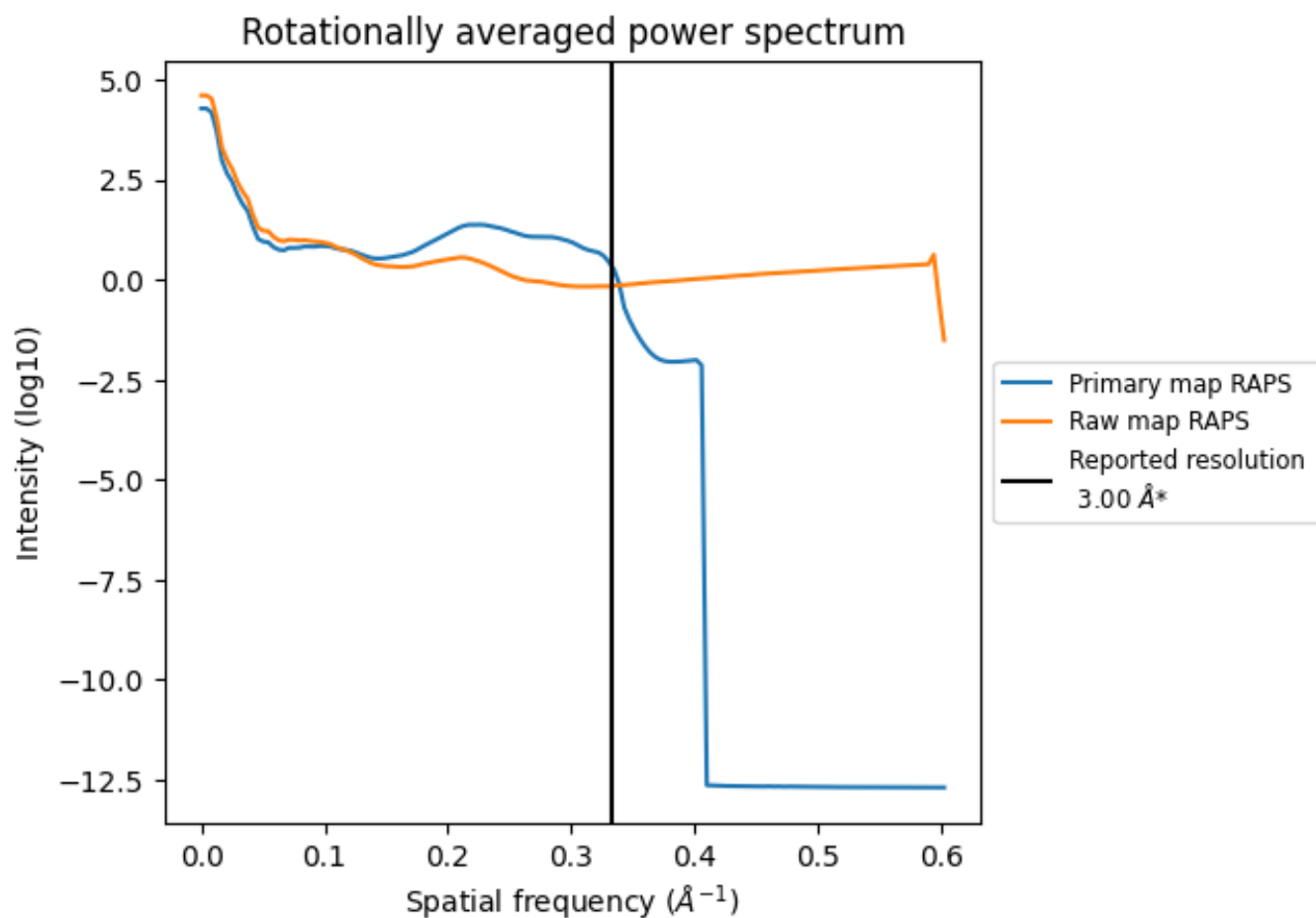
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 17 nm<sup>3</sup>; this corresponds to an approximate mass of 15 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 [i](#)

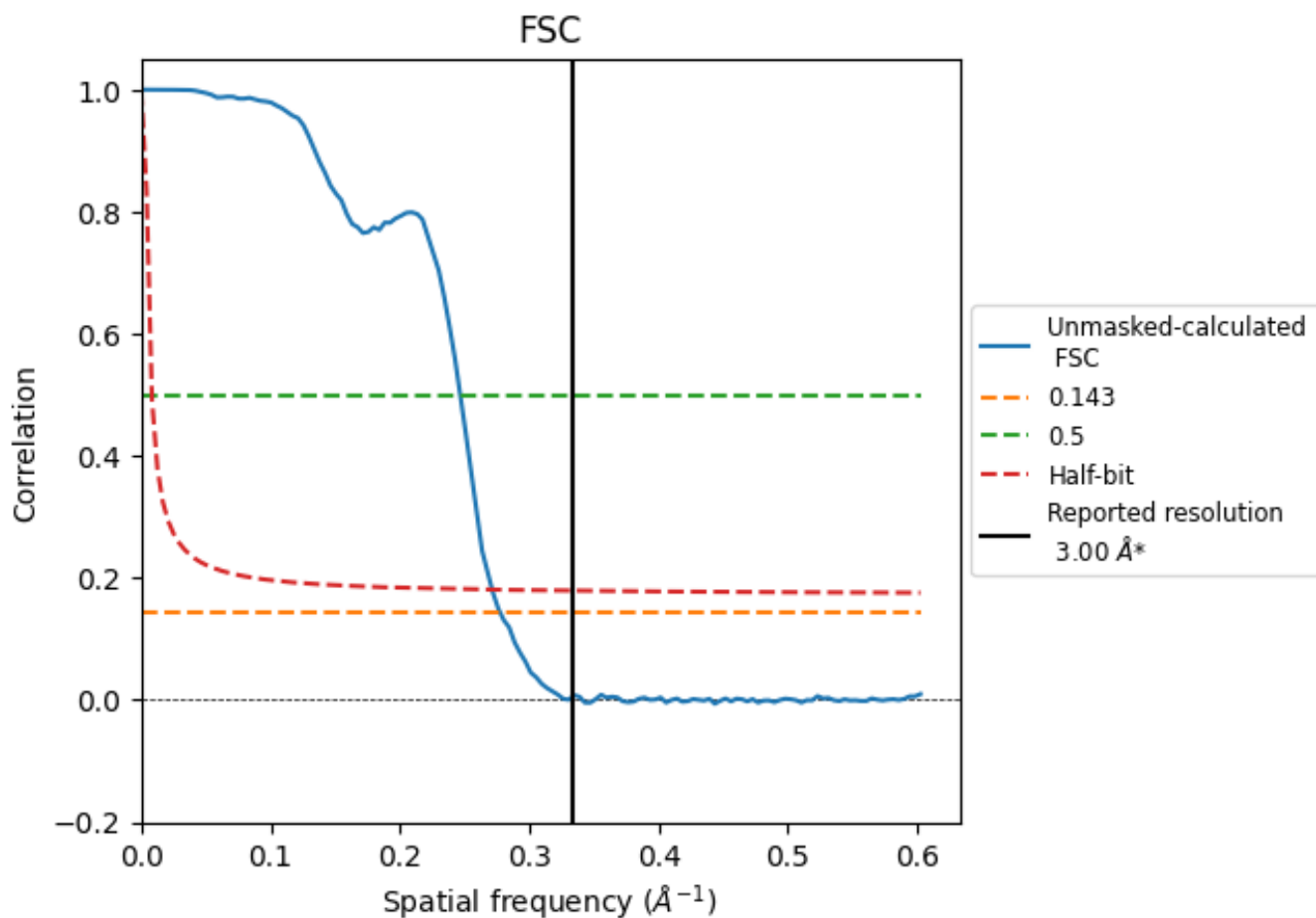


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 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 0.333 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

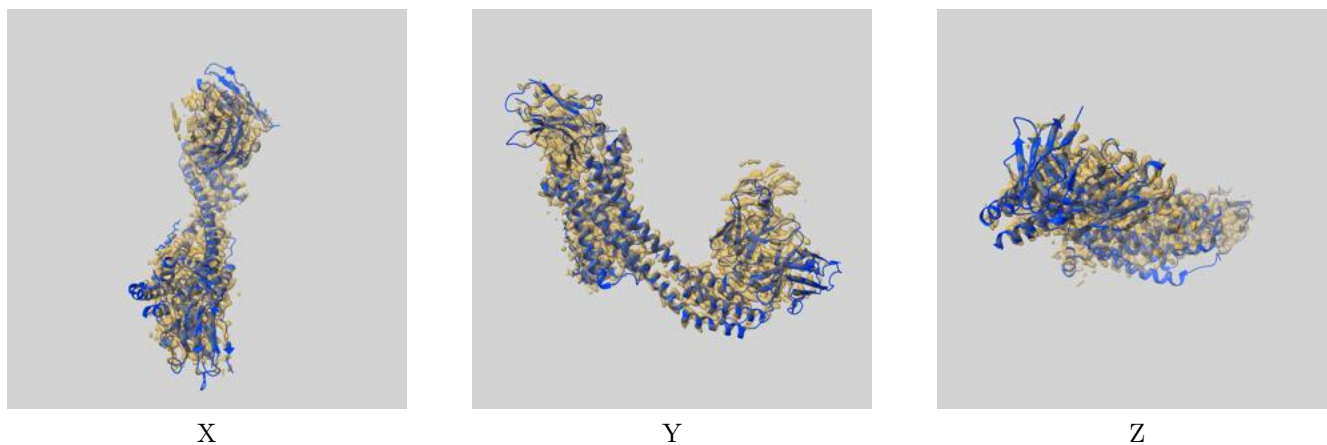
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.60	4.05	3.68

\*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 3.60 differs from the reported value 3.0 by more than 10 %

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

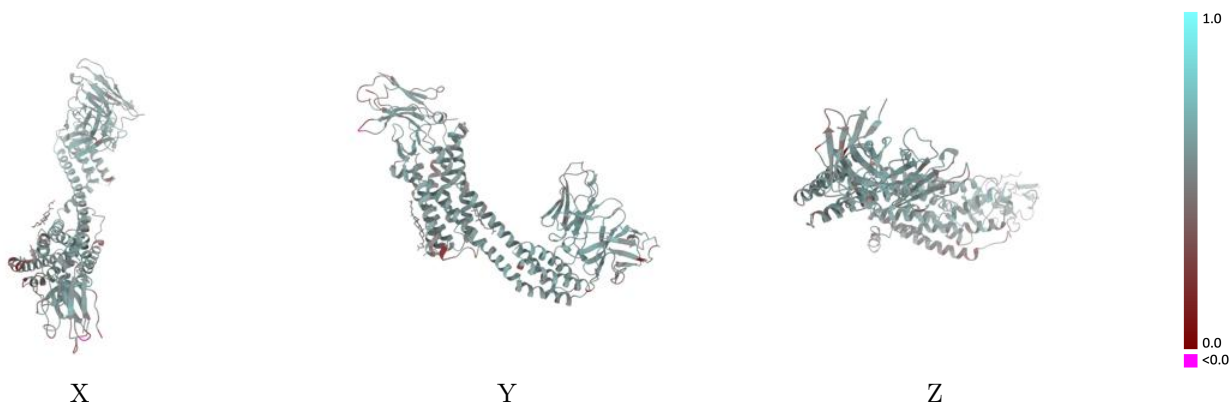
This section contains information regarding the fit between EMDB map EMD-41248 and PDB model 8TH3. Per-residue inclusion information can be found in section 3 on page 6.

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



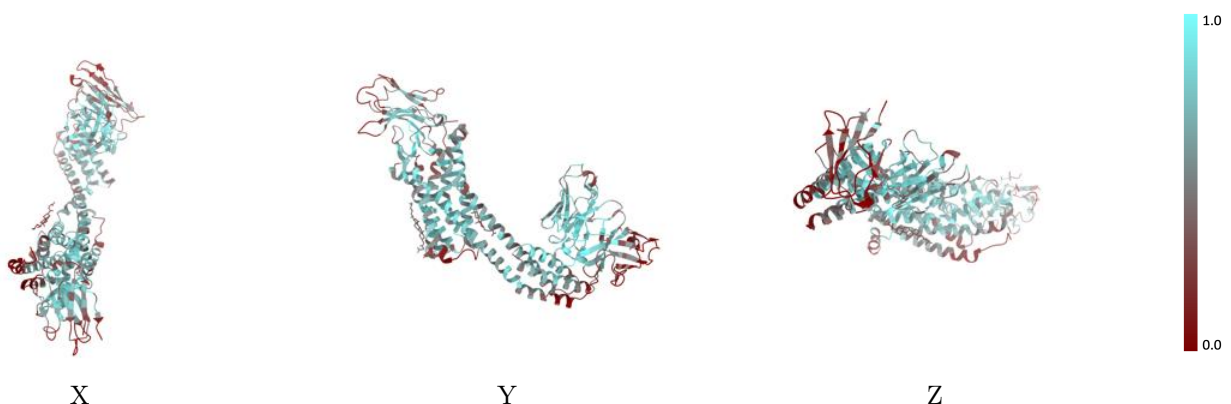
The images above show the 3D surface view of the map at the recommended contour level 0.398 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



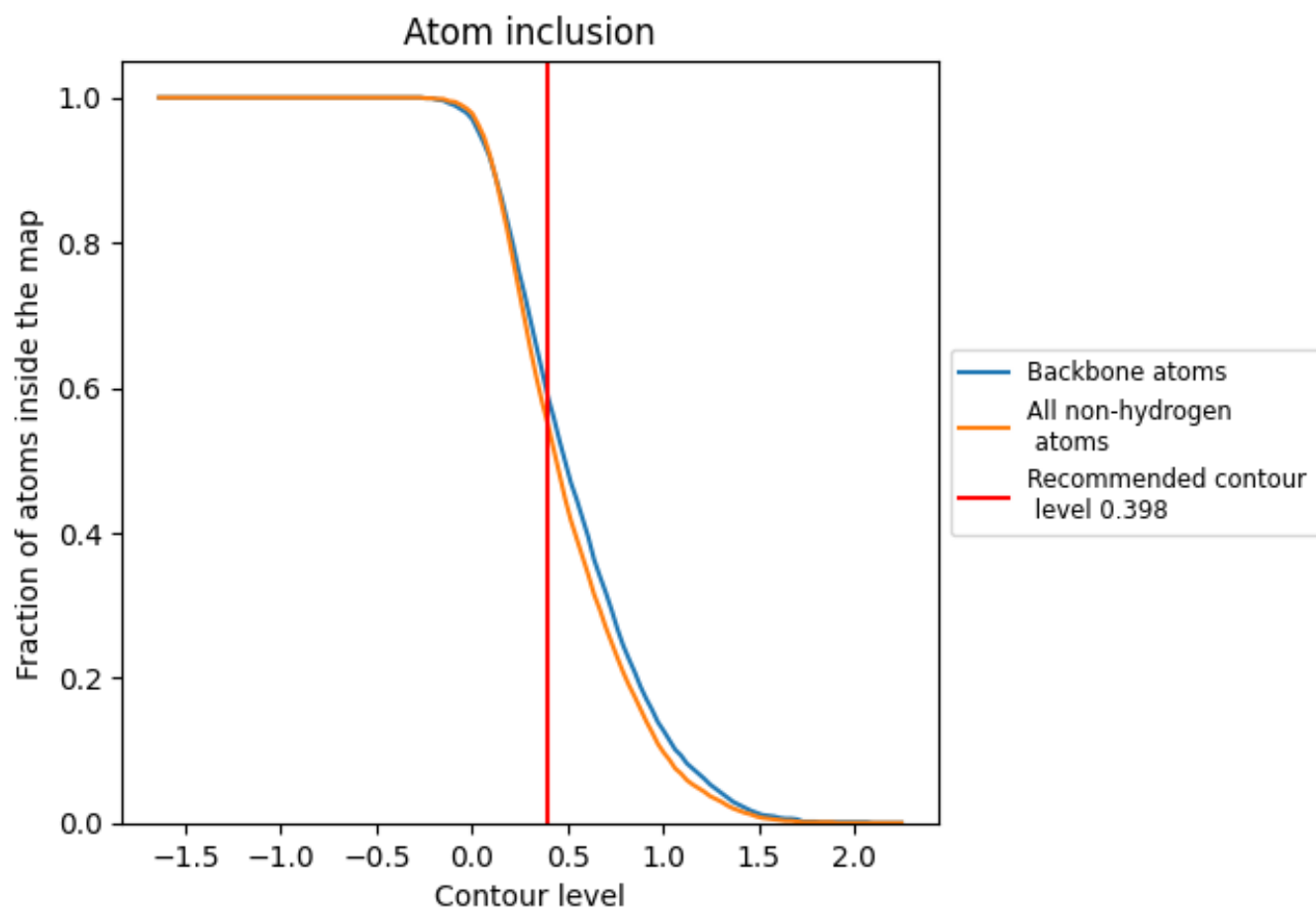
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.398).











## 9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 55% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.398) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5480	 0.5320
A	 0.5580	 0.5320
B	 0.4940	 0.5020
C	 0.4260	 0.5330
D	 0.6980	 0.5610

