



## wwPDB EM Validation Summary Report ⓘ

May 26, 2026 – 04:36 PM JST

PDB ID : 9WHU / pdb\_00009whu  
EMDB ID : EMD-65977  
Title : Structure of Klebsiella pneumoniae trypsin-HamAB bound with DNA, trimer  
Authors : Huang, P.P.; Liu, J.X.; Shen, L.B.; Chen, M.R.; Xiao, Y.B.  
Deposited on : 2025-08-27  
Resolution : 3.50 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  
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

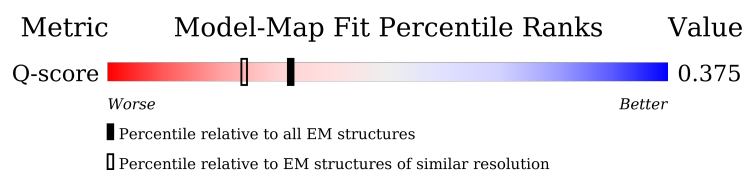
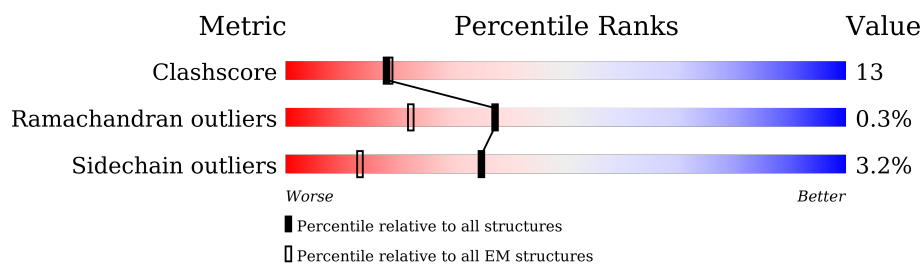
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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.



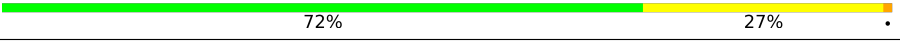

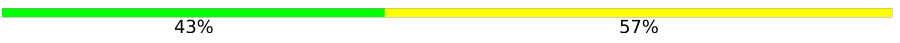
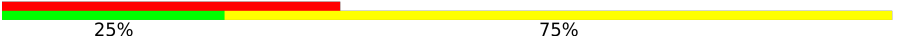

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 ( 3.00 - 4.00 )

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	528	
1	D	528	
1	G	528	
2	B	853	

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Mol	Chain	Length	Quality of chain
2	E	853	 72% 27%
2	H	853	 69% 30%
3	F	7	 43% 57%
4	C	8	 25% 38% 75%
4	I	8	 25% 50% 75%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 28311 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 Anti-bacteriophage protein A/HamA C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	284	Total	C	N	O	S	0	0
			2303	1472	388	432	11		
1	D	284	Total	C	N	O	S	0	0
			2303	1472	388	432	11		
1	G	284	Total	C	N	O	S	0	0
			2303	1472	388	432	11		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	ASN	THR	conflict	UNP A0A486PDC8
D	66	ASN	THR	conflict	UNP A0A486PDC8
G	66	ASN	THR	conflict	UNP A0A486PDC8

- Molecule 2 is a protein called DNA polymerase theta (Helicase domain only).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	851	Total	C	N	O	S	0	0
			6973	4494	1157	1304	18		
2	E	851	Total	C	N	O	S	0	0
			6973	4494	1157	1304	18		
2	H	851	Total	C	N	O	S	0	0
			6973	4494	1157	1304	18		

- Molecule 3 is a DNA chain called DNA (5'-D(P\*AP\*AP\*AP\*AP\*AP\*AP\*A)-3').

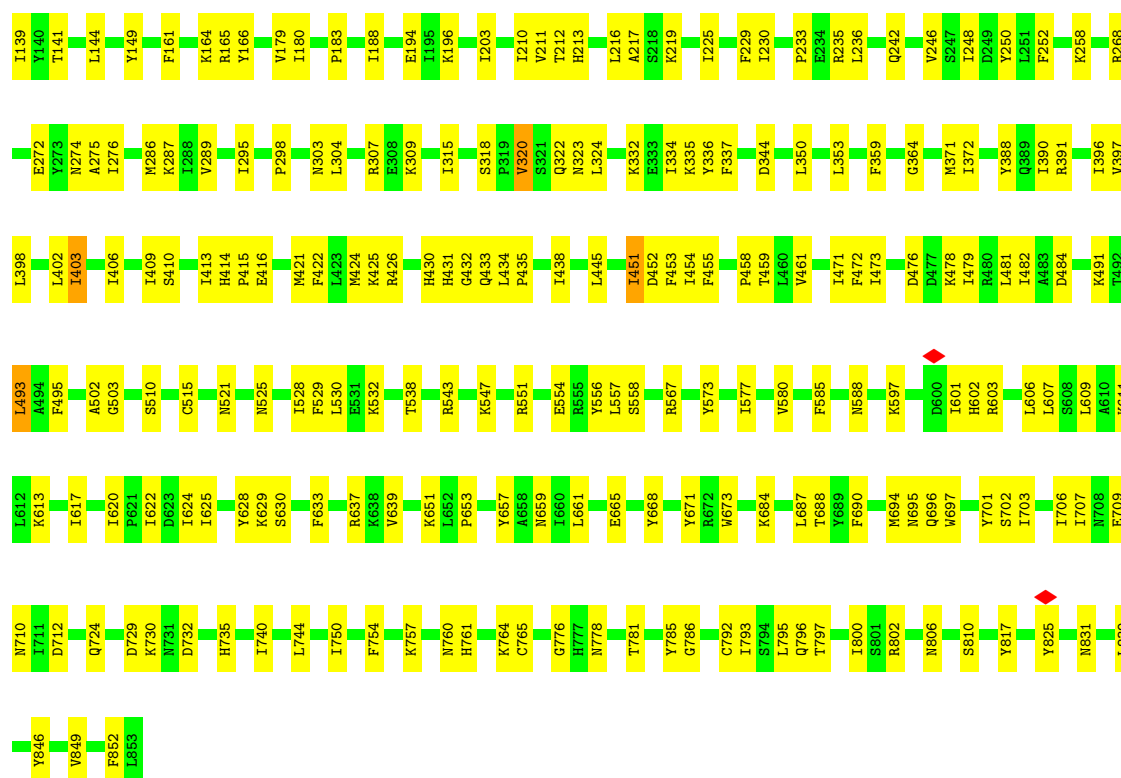
Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	7	Total	C	N	O	P	0	0
			147	70	35	35	7		

- Molecule 4 is a DNA chain called DNA (5'-D(P\*AP\*AP\*AP\*AP\*AP\*AP\*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	8	Total 168	C 80	N 40	O 40	P 8	0	0
4	C	8	Total 168	C 80	N 40	O 40	P 8	0	0

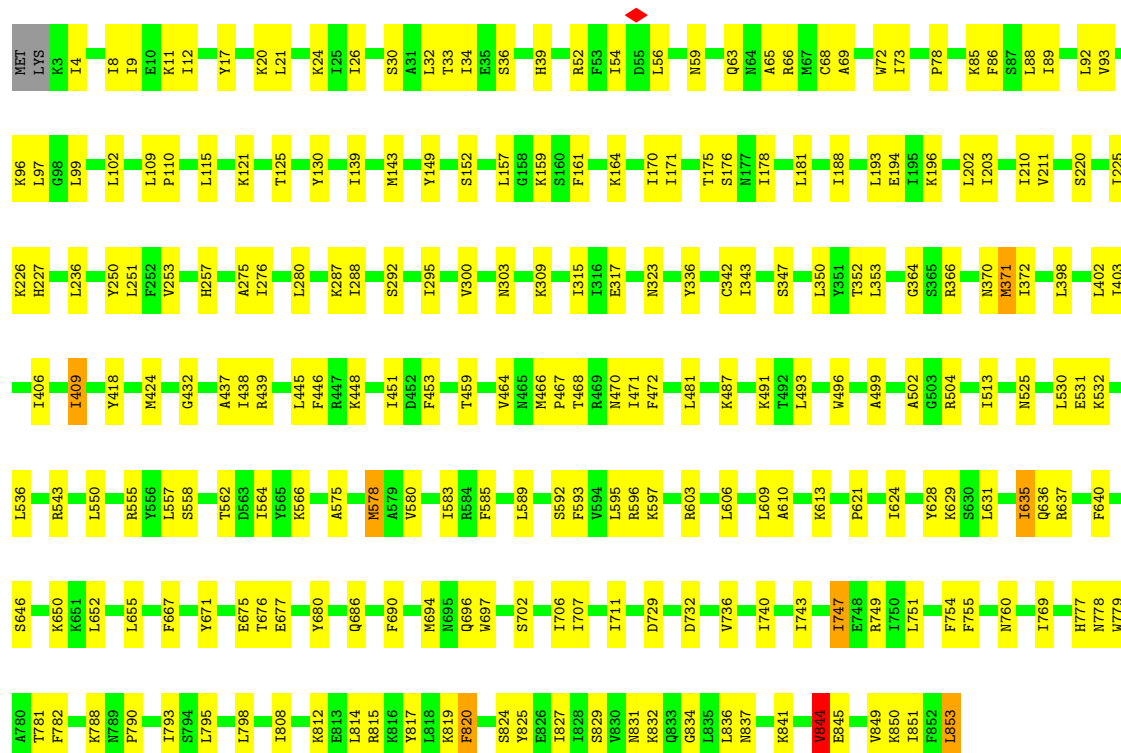






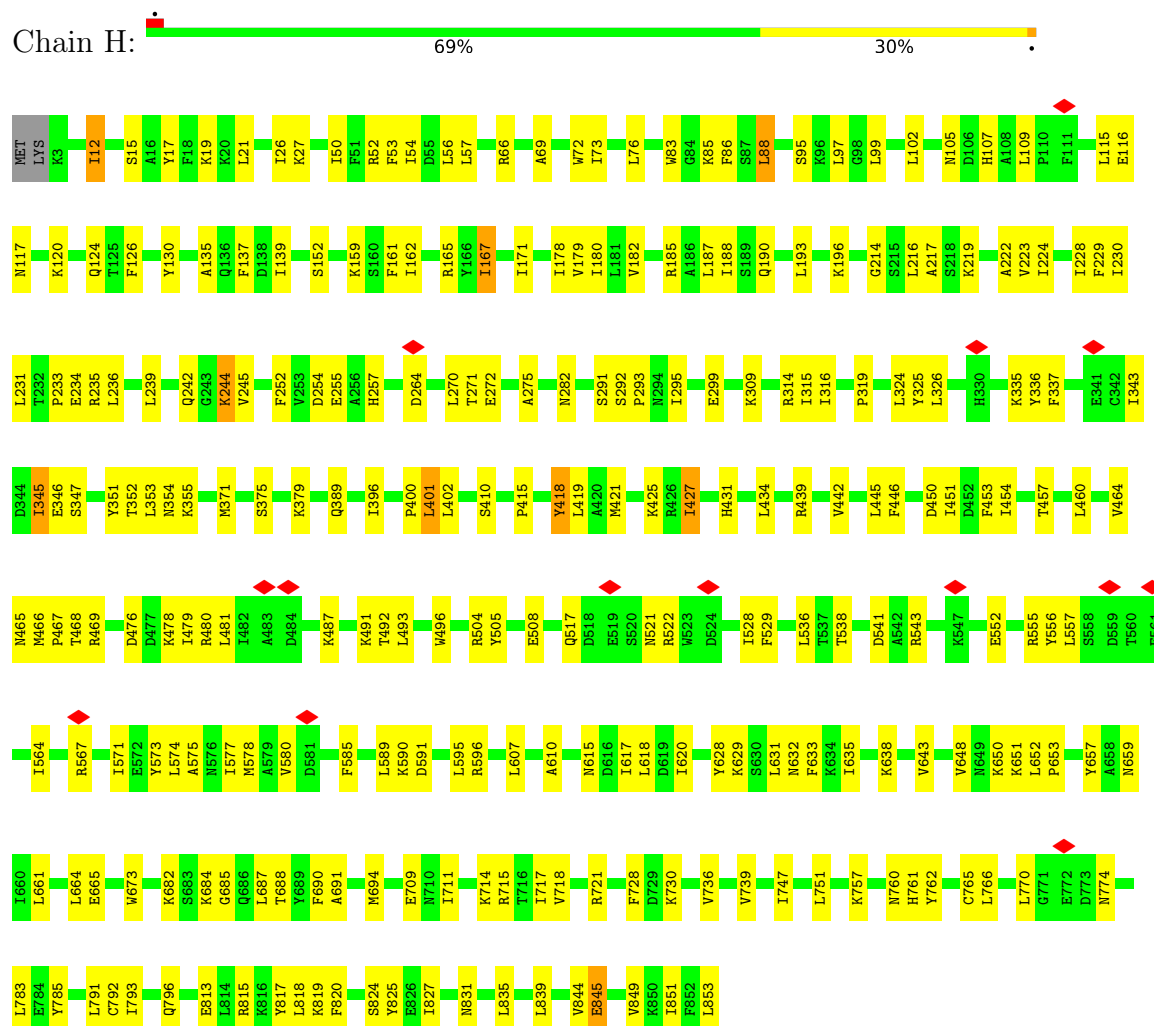
• Molecule 2: DNA polymerase theta (Helicase domain only)

Chain E: 72% 27%

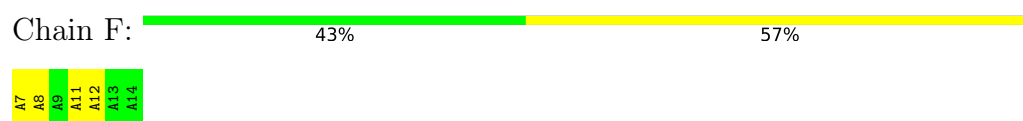


• Molecule 2: DNA polymerase theta (Helicase domain only)





- Molecule 3: DNA (5'-D(P\*AP\*AP\*AP\*AP\*AP\*AP\*A)-3')



- Molecule 4: DNA (5'-D(P\*AP\*AP\*AP\*AP\*AP\*AP\*A)-3')



- Molecule 4: DNA (5'-D(P\*AP\*AP\*AP\*AP\*AP\*AP\*A)-3')



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50060	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.517	Depositor
Minimum map value	-0.236	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	477.184, 477.184, 477.184	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	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	0.15	0/2344	0.46	0/3154
1	D	0.15	0/2344	0.40	0/3154
1	G	0.13	0/2344	0.43	1/3154 (0.0%)
2	B	0.10	0/7123	0.29	0/9625
2	E	0.11	0/7123	0.32	0/9625
2	H	0.11	0/7123	0.32	0/9625
3	F	0.20	0/166	0.32	0/251
4	C	0.18	0/190	0.29	0/288
4	I	0.13	0/190	0.25	0/288
All	All	0.12	0/28947	0.34	1/39164 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	255	MET	CB-CG-SD	5.03	127.80	112.70

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	2303	0	2298	68	0
1	D	2303	0	2298	84	0
1	G	2303	0	2298	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	6973	0	6973	167	0
2	E	6973	0	6973	166	0
2	H	6973	0	6973	183	0
3	F	147	0	79	4	0
4	C	168	0	90	5	0
4	I	168	0	90	10	0
All	All	28311	0	28072	749	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 13.

The worst 5 of 749 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)
2:E:292:SER:HB3	2:E:295:ILE:HD12	1.56	0.86
2:H:336:TYR:HB2	2:H:345:ILE:HD11	1.59	0.84
1:D:271:ARG:HD3	1:D:481:VAL:HG11	1.60	0.82
1:D:266:ILE:HG22	1:D:268:ASN:H	1.43	0.82
2:H:324:LEU:HD22	2:H:337:PHE:HB2	1.64	0.79

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	282/528 (53%)	242 (86%)	37 (13%)	3 (1%)	11	43
1	D	282/528 (53%)	251 (89%)	31 (11%)	0	100	100
1	G	282/528 (53%)	250 (89%)	29 (10%)	3 (1%)	11	43
2	B	849/853 (100%)	801 (94%)	46 (5%)	2 (0%)	43	74
2	E	849/853 (100%)	798 (94%)	50 (6%)	1 (0%)	48	79

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	849/853 (100%)	789 (93%)	58 (7%)	2 (0%)	43	74
All	All	3393/4143 (82%)	3131 (92%)	251 (7%)	11 (0%)	37	67

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	251	CYS
1	G	457	ILE
2	H	223	VAL
1	A	263	LYS
1	A	313	LYS

### 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	256/477 (54%)	243 (95%)	13 (5%)	21	48
1	D	256/477 (54%)	242 (94%)	14 (6%)	19	46
1	G	256/477 (54%)	243 (95%)	13 (5%)	21	48
2	B	780/782 (100%)	761 (98%)	19 (2%)	43	64
2	E	780/782 (100%)	761 (98%)	19 (2%)	43	64
2	H	780/782 (100%)	760 (97%)	20 (3%)	40	62
All	All	3108/3777 (82%)	3010 (97%)	98 (3%)	35	59

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	583	ILE
1	G	398	LEU
2	E	675	GLU
1	G	252	PHE
1	G	463	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	426	GLN
2	H	615	ASN
1	G	516	ASN
2	H	257	HIS
2	H	796	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	I	1
4	C	1
3	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	9:DA	O3'	11:DA	P	10.31
1	C	9:DA	O3'	12:DA	P	10.21
1	F	9:DA	O3'	11:DA	P	8.87

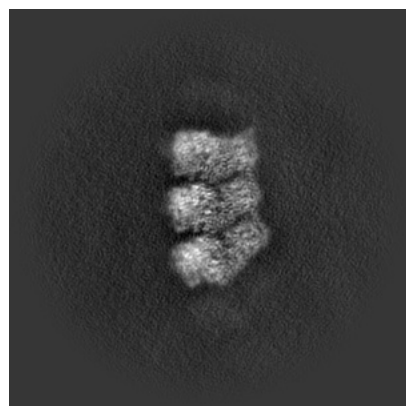
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65977. These allow visual inspection of the internal detail of the map and identification of artifacts.

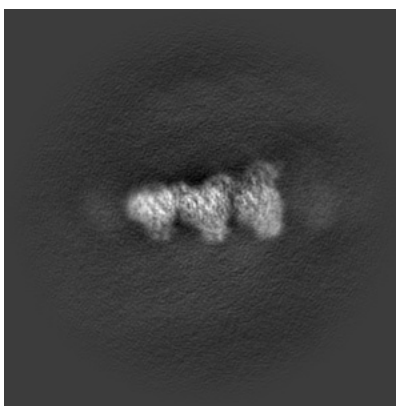
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

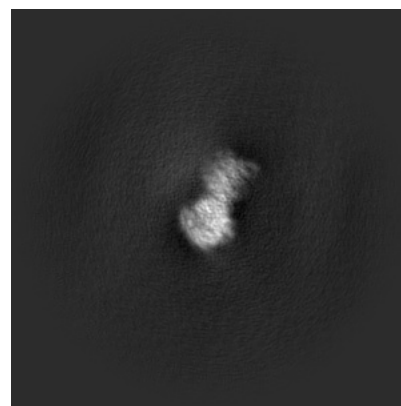
#### 6.1.1 Primary map



X

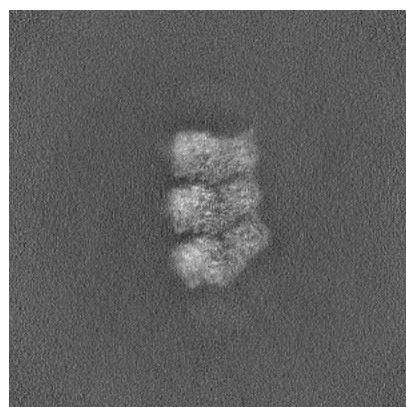


Y

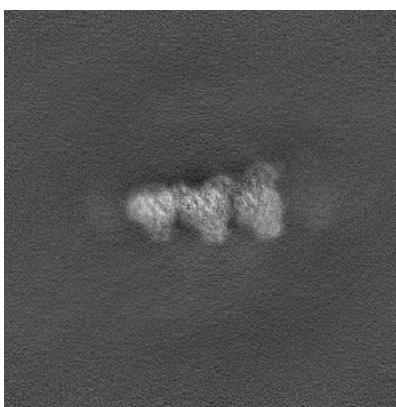


Z

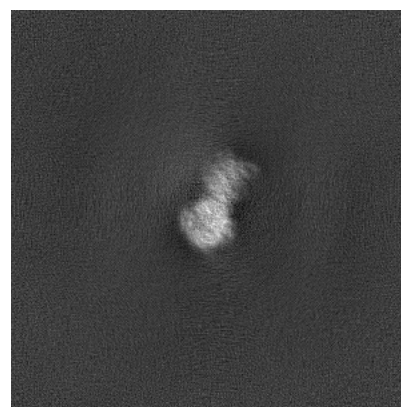
#### 6.1.2 Raw map



X



Y



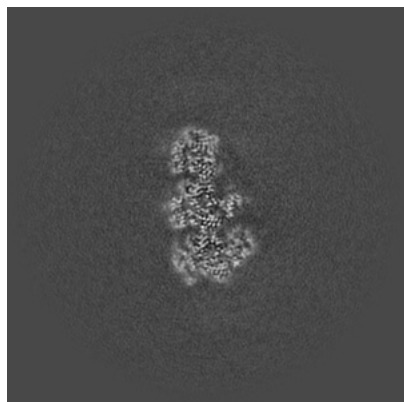
Z

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



## 6.2 Central slices [i](#)

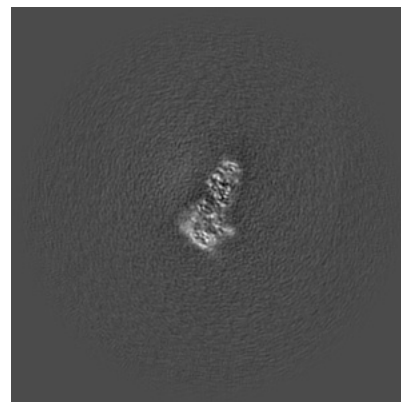
### 6.2.1 Primary map



X Index: 256

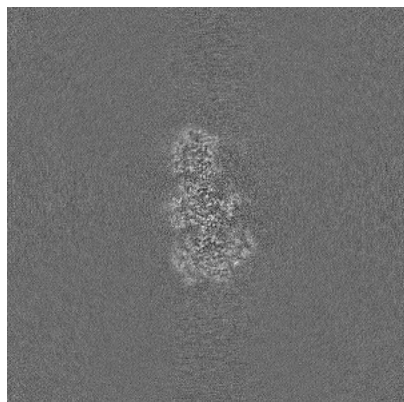


Y Index: 256

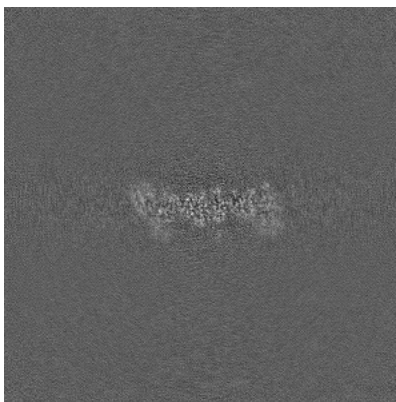


Z Index: 256

### 6.2.2 Raw map



X Index: 256



Y Index: 256

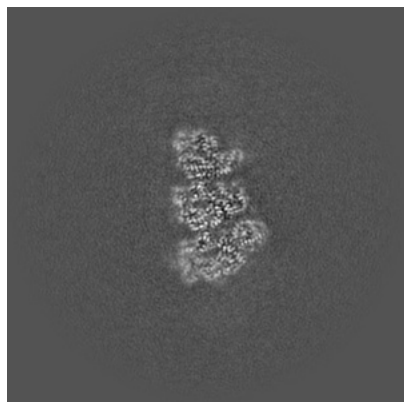


Z Index: 256

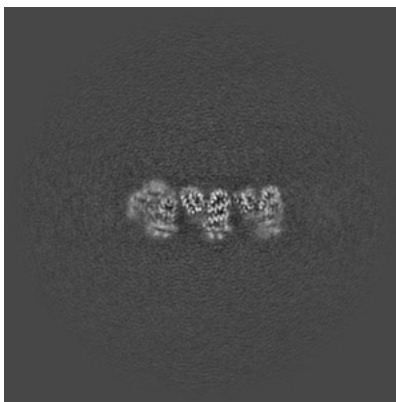
The images above show central slices of the map in three orthogonal directions.

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

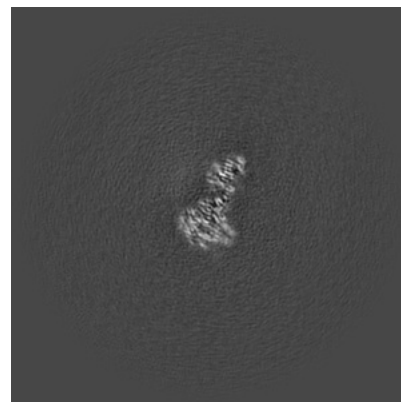
### 6.3.1 Primary map



X Index: 267

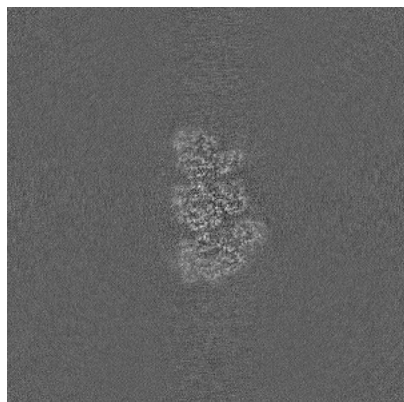


Y Index: 241

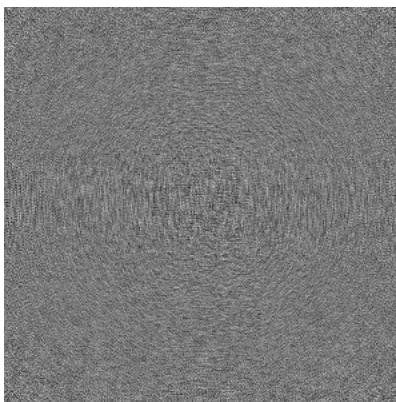


Z Index: 267

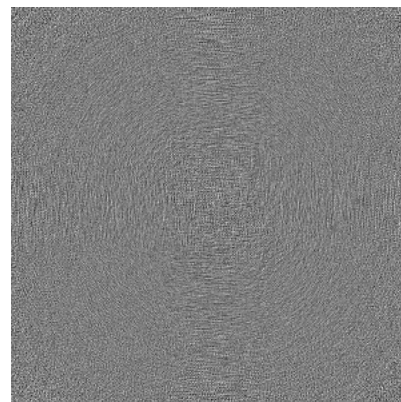
### 6.3.2 Raw map



X Index: 267



Y Index: 0

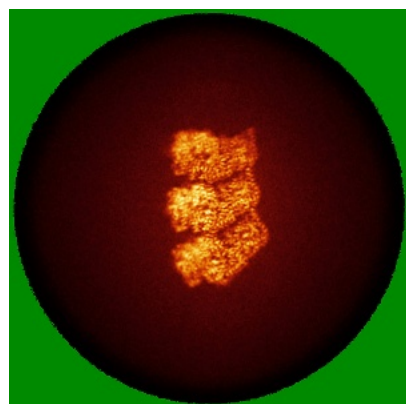


Z Index: 0

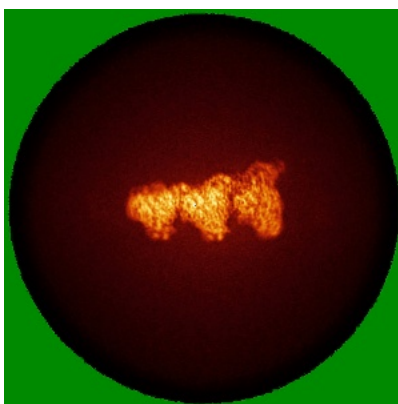
The images above show the largest variance slices of the map in three orthogonal directions.

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

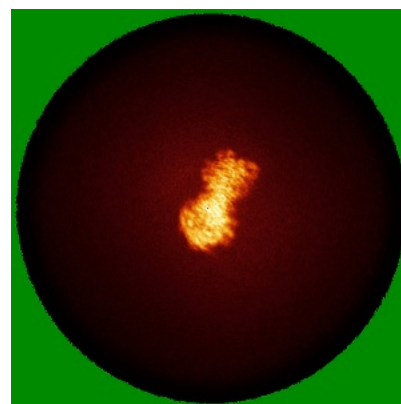
### 6.4.1 Primary map



X

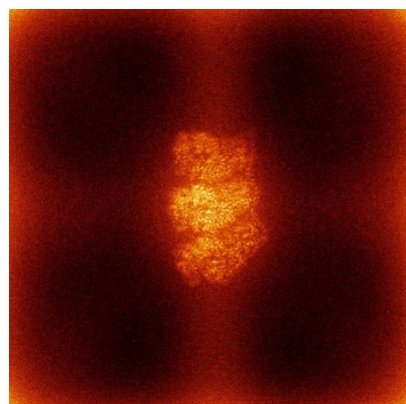


Y

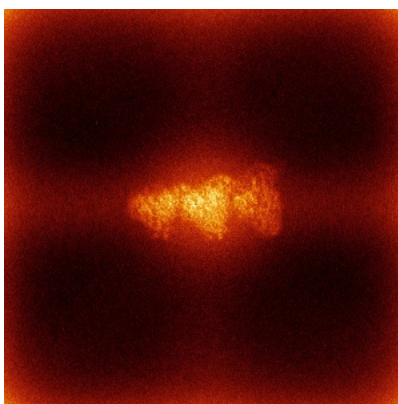


Z

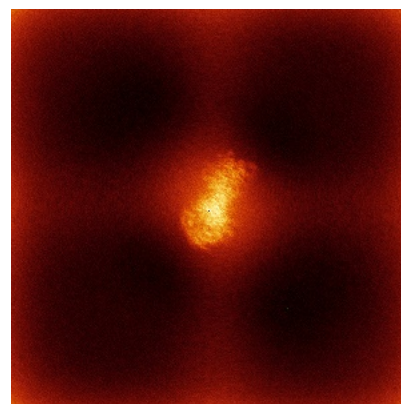
### 6.4.2 Raw map



X



Y

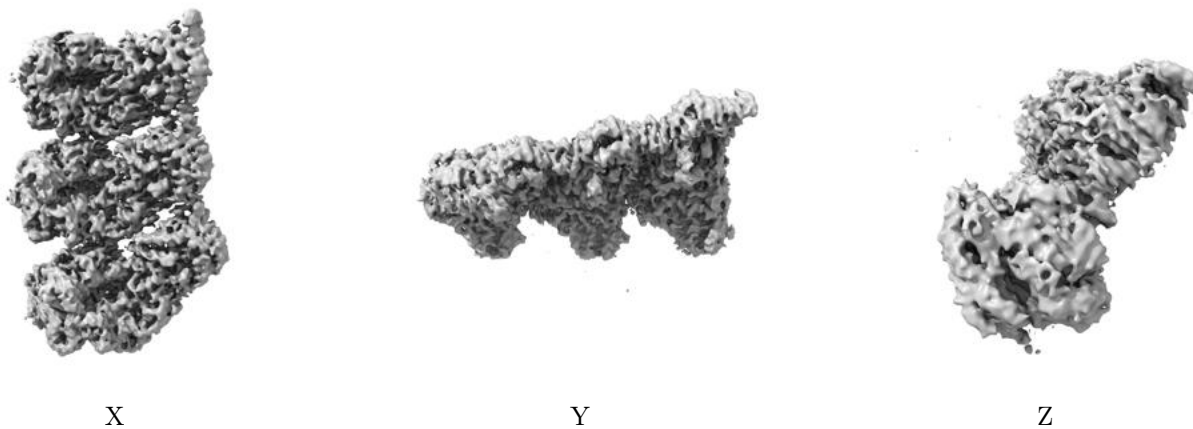


Z

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.

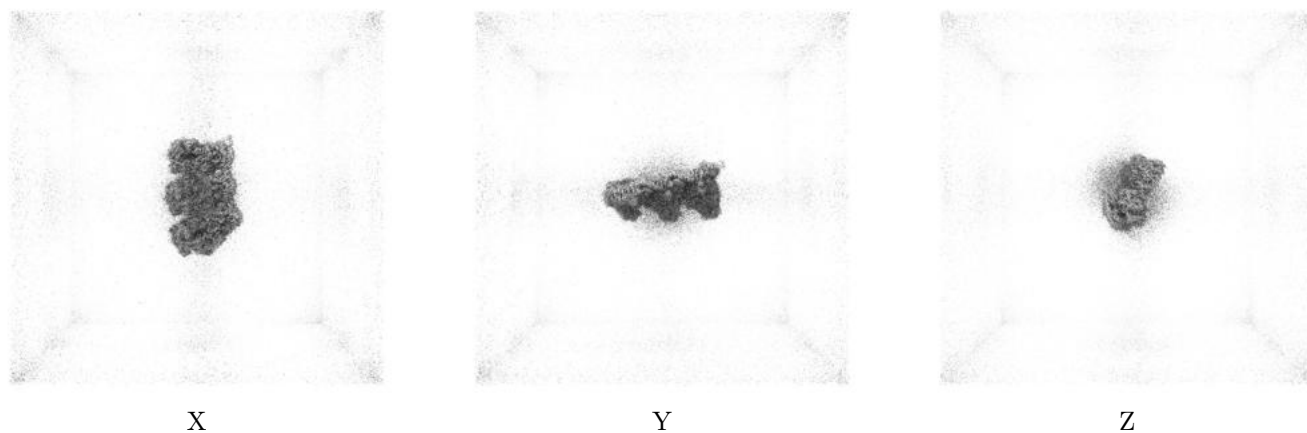
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. 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](#)

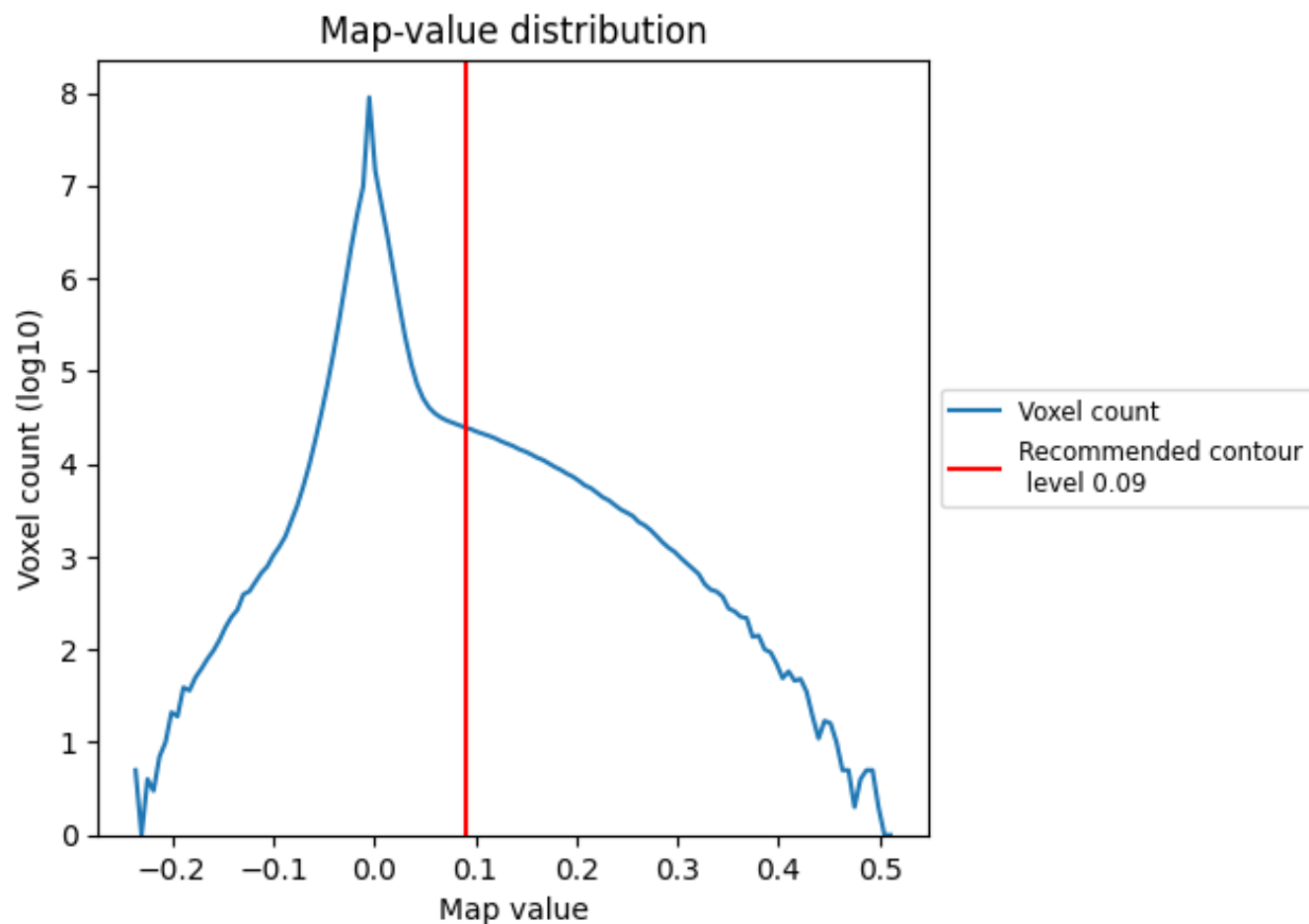
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

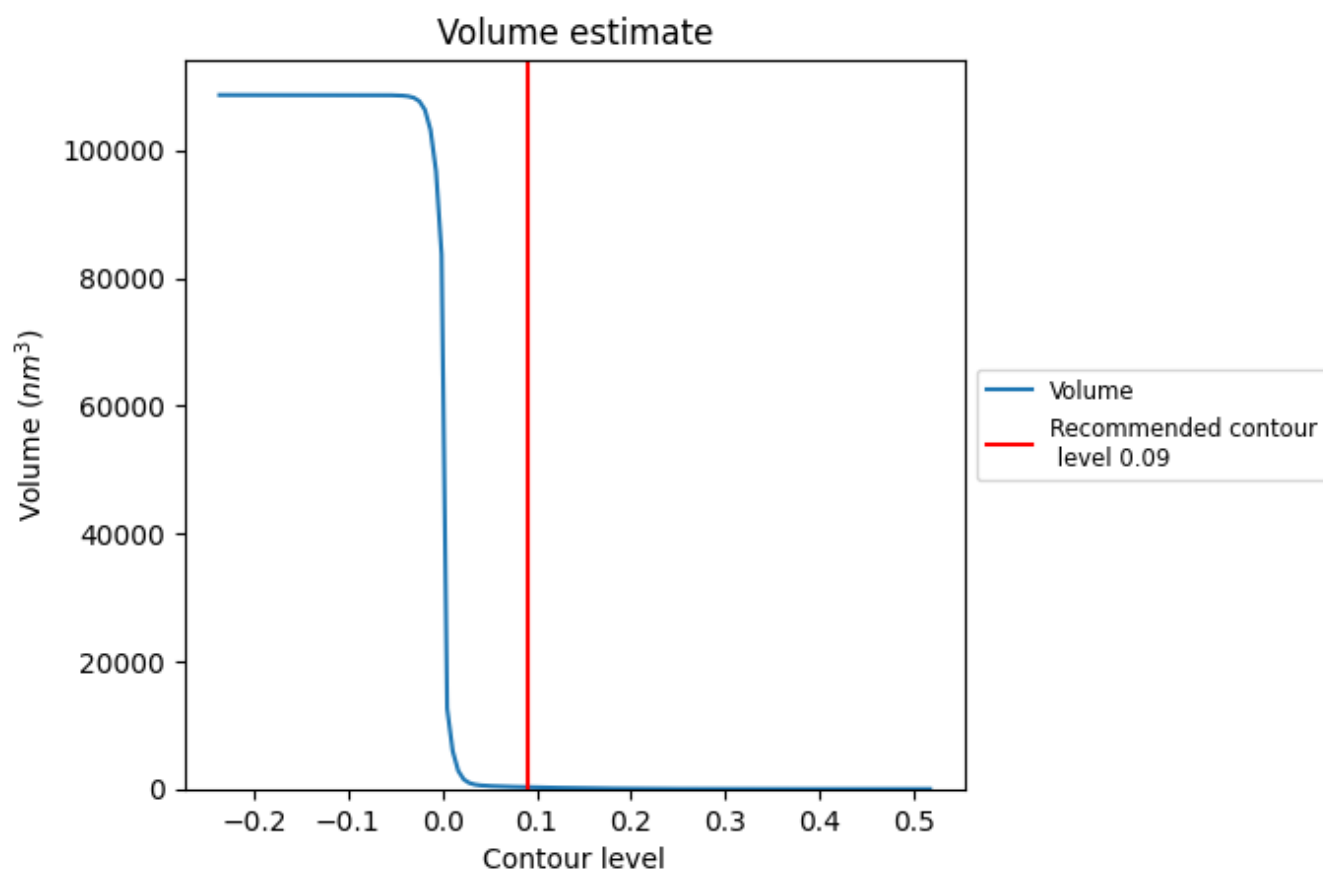
This section contains the results of statistical analysis of the map.

### 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.

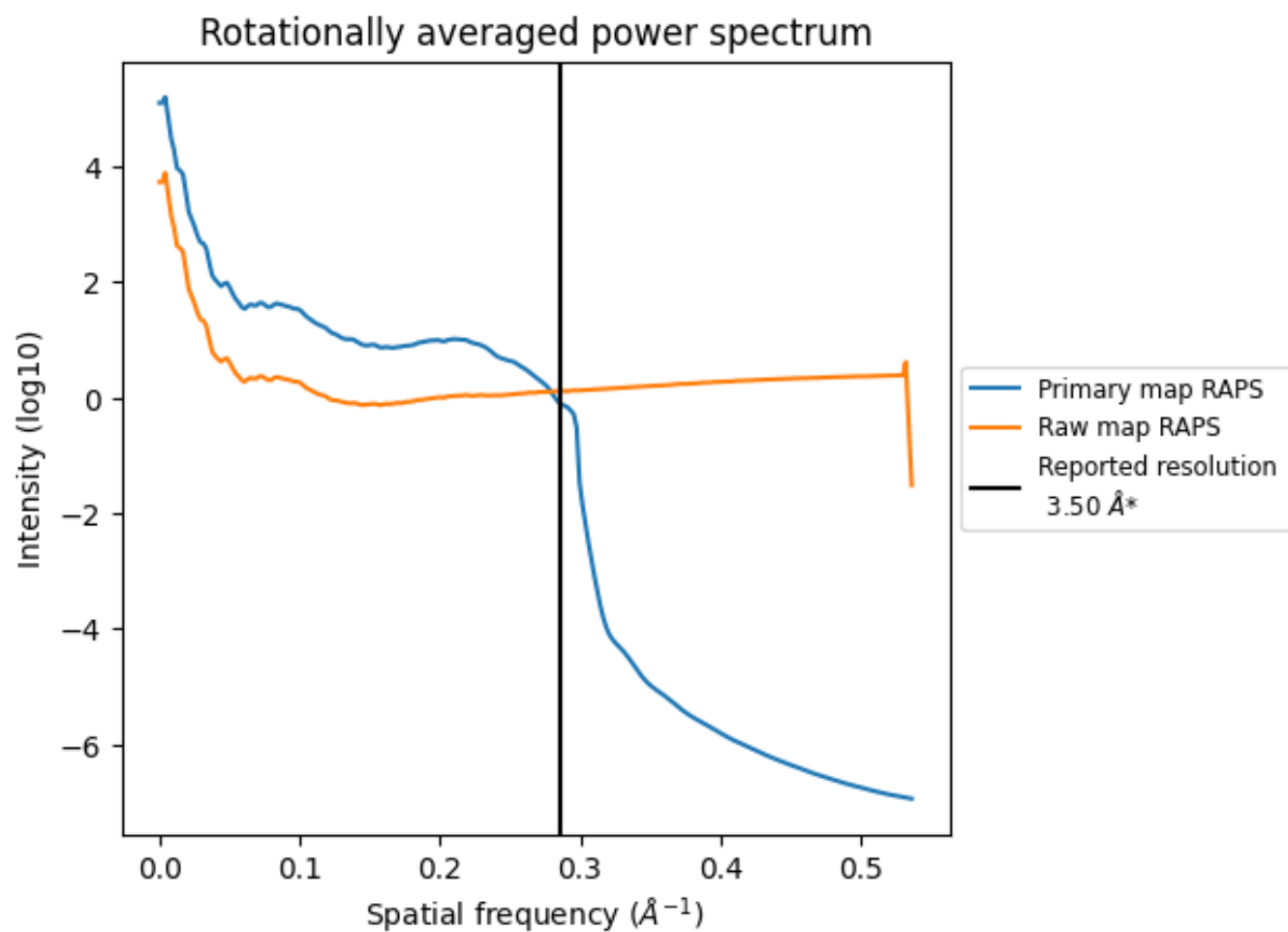
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 282 nm<sup>3</sup>; this corresponds to an approximate mass of 255 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 ⓘ

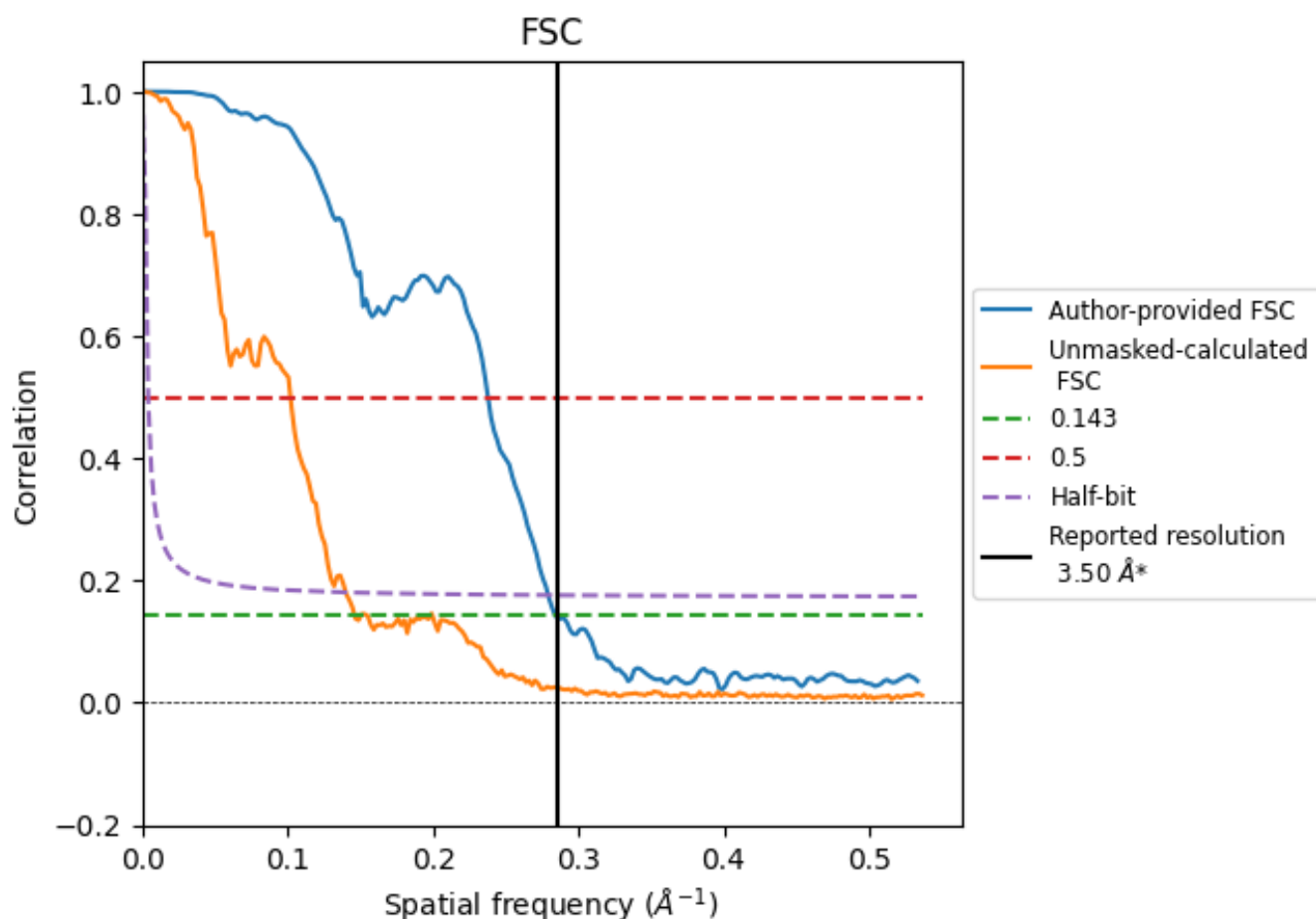


\*Reported resolution corresponds to spatial frequency of 0.286  $\text{\AA}^{-1}$

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



## 8.2 Resolution estimates [i](#)

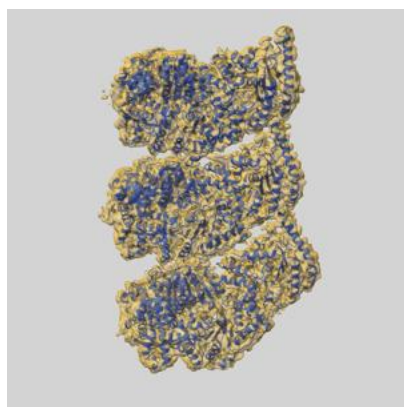
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.52	4.21	3.58
Unmasked-calculated*	6.84	9.80	7.14

\*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 6.84 differs from the reported value 3.5 by more than 10 %

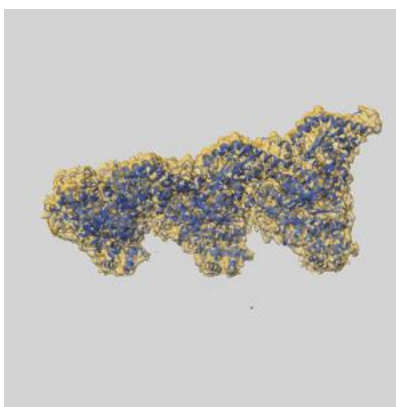
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65977 and PDB model 9WHU. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

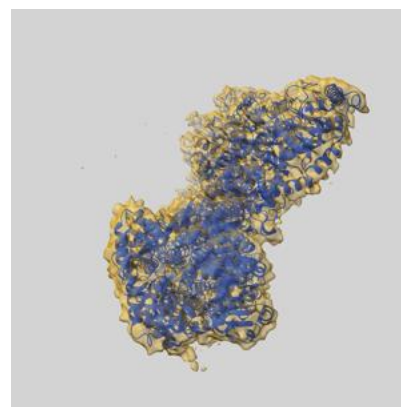
### 9.1 Map-model overlay [i](#)



X



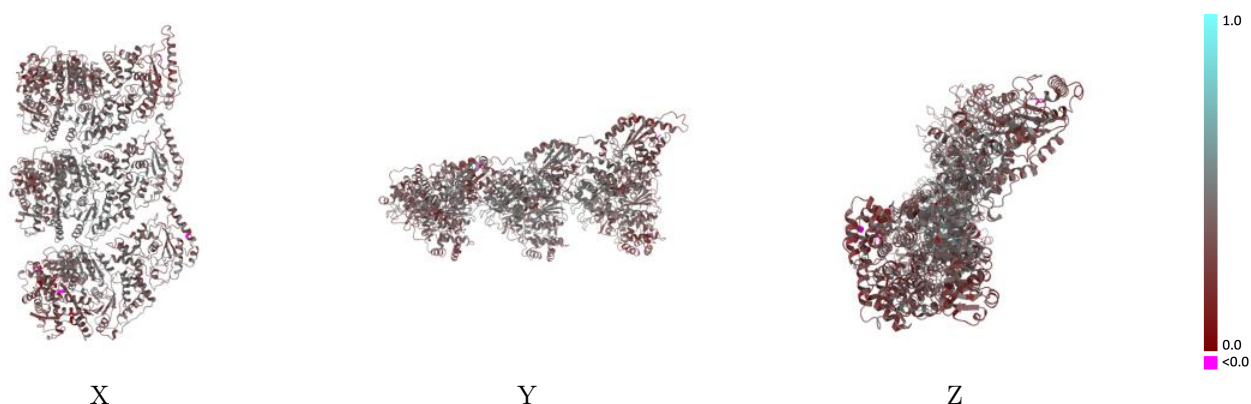
Y



Z

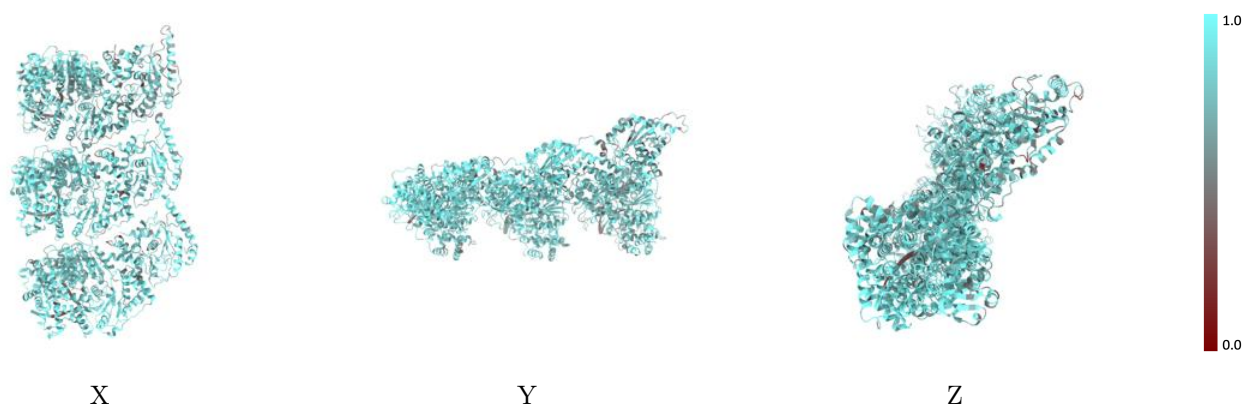
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



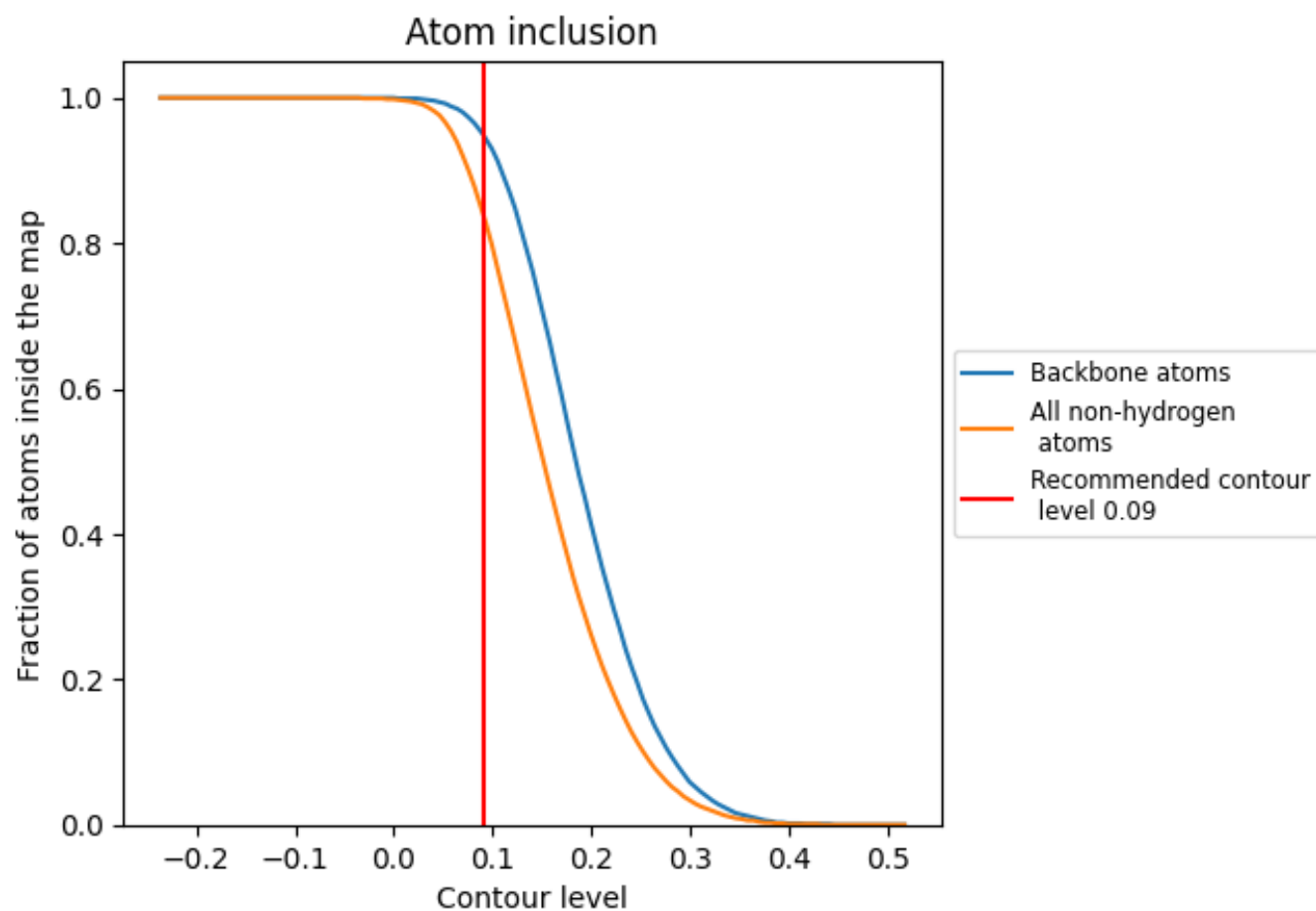
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 84% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8410</div>	<div><div></div>0.3750</div>
A	<div><div></div>0.8140</div>	<div><div></div>0.3690</div>
B	<div><div></div>0.8790</div>	<div><div></div>0.3560</div>
C	<div><div></div>0.5710</div>	<div><div></div>0.2600</div>
D	<div><div></div>0.8170</div>	<div><div></div>0.4020</div>
E	<div><div></div>0.8950</div>	<div><div></div>0.4150</div>
F	<div><div></div>0.6600</div>	<div><div></div>0.3330</div>
G	<div><div></div>0.7240</div>	<div><div></div>0.3450</div>
H	<div><div></div>0.8250</div>	<div><div></div>0.3640</div>
I	<div><div></div>0.5120</div>	<div><div></div>0.2410</div>

1.0

0.0

<0.0