



## Full wwPDB EM Validation Report ⓘ

May 10, 2025 – 01:59 PM EDT

PDB ID : 9N13 / pdb\_00009n13  
EMDB ID : EMD-48804  
Title : Cryo-EM structure of HCoV-HKU1 glycoprotein D1 Domain (mutant T31VPR34 to GGGG)  
Authors : Jin, M.; Rini, J.M.  
Deposited on : 2025-01-24  
Resolution : 3.34 Å(reported)

This is a Full wwPDB EM Validation 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 : 2022.3.0, CSD as543be (2022)  
MolProbity : **FAILED**  
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 3.34 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4578 atoms, of which 2237 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	269	Total	C	H	N	O	S	0	0
			4265	1419	2083	344	410	9		

There are 67 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	34	GLY	ARG	engineered mutation	UNP Q5MQD0
B	1026	PRO	THR	conflict	UNP Q5MQD0
B	1071	PRO	ALA	conflict	UNP Q5MQD0
B	1072	PRO	LEU	conflict	UNP Q5MQD0
B	1299	SER	-	expression tag	UNP Q5MQD0
B	1300	GLY	-	expression tag	UNP Q5MQD0
B	1301	GLY	-	expression tag	UNP Q5MQD0
B	1302	TYR	-	expression tag	UNP Q5MQD0
B	1303	ILE	-	expression tag	UNP Q5MQD0
B	1304	PRO	-	expression tag	UNP Q5MQD0
B	1305	GLU	-	expression tag	UNP Q5MQD0
B	1306	ALA	-	expression tag	UNP Q5MQD0
B	1307	PRO	-	expression tag	UNP Q5MQD0
B	1308	ARG	-	expression tag	UNP Q5MQD0
B	1309	ASP	-	expression tag	UNP Q5MQD0
B	1310	GLY	-	expression tag	UNP Q5MQD0
B	1311	GLN	-	expression tag	UNP Q5MQD0
B	1312	ALA	-	expression tag	UNP Q5MQD0
B	1313	TYR	-	expression tag	UNP Q5MQD0
B	1314	VAL	-	expression tag	UNP Q5MQD0
B	1315	ARG	-	expression tag	UNP Q5MQD0
B	1316	LYS	-	expression tag	UNP Q5MQD0
B	1317	ASP	-	expression tag	UNP Q5MQD0
B	1318	GLY	-	expression tag	UNP Q5MQD0
B	1319	GLU	-	expression tag	UNP Q5MQD0
B	1320	TRP	-	expression tag	UNP Q5MQD0
B	1321	VAL	-	expression tag	UNP Q5MQD0
B	1322	LEU	-	expression tag	UNP Q5MQD0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1323	LEU	-	expression tag	UNP Q5MQD0
B	1324	SER	-	expression tag	UNP Q5MQD0
B	1325	THR	-	expression tag	UNP Q5MQD0
B	1326	PHE	-	expression tag	UNP Q5MQD0
B	1327	LEU	-	expression tag	UNP Q5MQD0
B	1328	ASN	-	expression tag	UNP Q5MQD0
B	1329	SER	-	expression tag	UNP Q5MQD0
B	1330	GLY	-	expression tag	UNP Q5MQD0
B	1331	ARG	-	expression tag	UNP Q5MQD0
B	1332	ALA	-	expression tag	UNP Q5MQD0
B	1333	HIS	-	expression tag	UNP Q5MQD0
B	1334	HIS	-	expression tag	UNP Q5MQD0
B	1335	HIS	-	expression tag	UNP Q5MQD0
B	1336	HIS	-	expression tag	UNP Q5MQD0
B	1337	HIS	-	expression tag	UNP Q5MQD0
B	1338	HIS	-	expression tag	UNP Q5MQD0
B	1339	GLY	-	expression tag	UNP Q5MQD0
B	1340	ALA	-	expression tag	UNP Q5MQD0
B	1341	GLY	-	expression tag	UNP Q5MQD0
B	1342	GLY	-	expression tag	UNP Q5MQD0
B	1343	LEU	-	expression tag	UNP Q5MQD0
B	1344	ASN	-	expression tag	UNP Q5MQD0
B	1345	ASP	-	expression tag	UNP Q5MQD0
B	1346	ILE	-	expression tag	UNP Q5MQD0
B	1347	PHE	-	expression tag	UNP Q5MQD0
B	1348	GLU	-	expression tag	UNP Q5MQD0
B	1349	ALA	-	expression tag	UNP Q5MQD0
B	1350	GLN	-	expression tag	UNP Q5MQD0
B	1351	LYS	-	expression tag	UNP Q5MQD0
B	1352	ILE	-	expression tag	UNP Q5MQD0
B	1353	GLU	-	expression tag	UNP Q5MQD0
B	1354	TRP	-	expression tag	UNP Q5MQD0
B	1355	HIS	-	expression tag	UNP Q5MQD0
B	1356	GLU	-	expression tag	UNP Q5MQD0
B	1357	ASP	-	expression tag	UNP Q5MQD0
B	1358	THR	-	expression tag	UNP Q5MQD0
B	1359	ALA	-	expression tag	UNP Q5MQD0
B	1360	ALA	-	expression tag	UNP Q5MQD0
B	1361	ALA	-	expression tag	UNP Q5MQD0

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



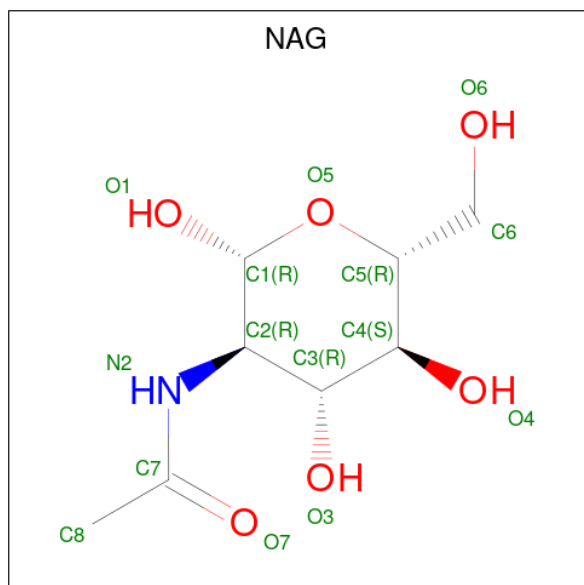
Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	5	Total	C	H	N	O	0	0
			118	34	57	2	25		

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	2	Total	C	H	N	O	0	0
			55	16	27	2	10		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	

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Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	

MolProbity failed to run properly - this section is therefore empty.

### 3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	302976	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	36	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	92000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.351	Depositor
Minimum map value	-0.536	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	288.0, 288.0, 288.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.125, 1.125, 1.125	Depositor

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 4.5 Carbohydrates [i](#)

7 monosaccharides 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
2	NAG	A	1	2,1	14,14,15	0.26	0	17,19,21	0.44	0
2	NAG	A	2	2	14,14,15	0.21	0	17,19,21	0.47	0
2	BMA	A	3	2	11,11,12	0.49	0	15,15,17	0.73	0
2	MAN	A	4	2	11,11,12	0.60	0	15,15,17	0.93	2 (13%)
2	MAN	A	5	2	11,11,12	0.63	0	15,15,17	0.97	2 (13%)
3	NAG	C	1	1,3	14,14,15	0.23	0	17,19,21	0.45	0
3	NAG	C	2	3	14,14,15	0.23	0	17,19,21	0.47	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
2	NAG	A	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	A	2	2	-	1/6/23/26	0/1/1/1
2	BMA	A	3	2	-	0/2/19/22	0/1/1/1
2	MAN	A	4	2	-	1/2/19/22	0/1/1/1
2	MAN	A	5	2	-	0/2/19/22	0/1/1/1
3	NAG	C	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5	MAN	C1-O5-C5	2.27	115.22	112.19
2	A	4	MAN	C1-O5-C5	2.26	115.21	112.19
2	A	5	MAN	O2-C2-C3	-2.20	105.60	110.15
2	A	4	MAN	O2-C2-C3	-2.16	105.68	110.15

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	4	MAN	O5-C5-C6-O6
3	C	1	NAG	C1-C2-N2-C7
3	C	2	NAG	C1-C2-N2-C7
3	C	1	NAG	C3-C2-N2-C7
3	C	2	NAG	C3-C2-N2-C7

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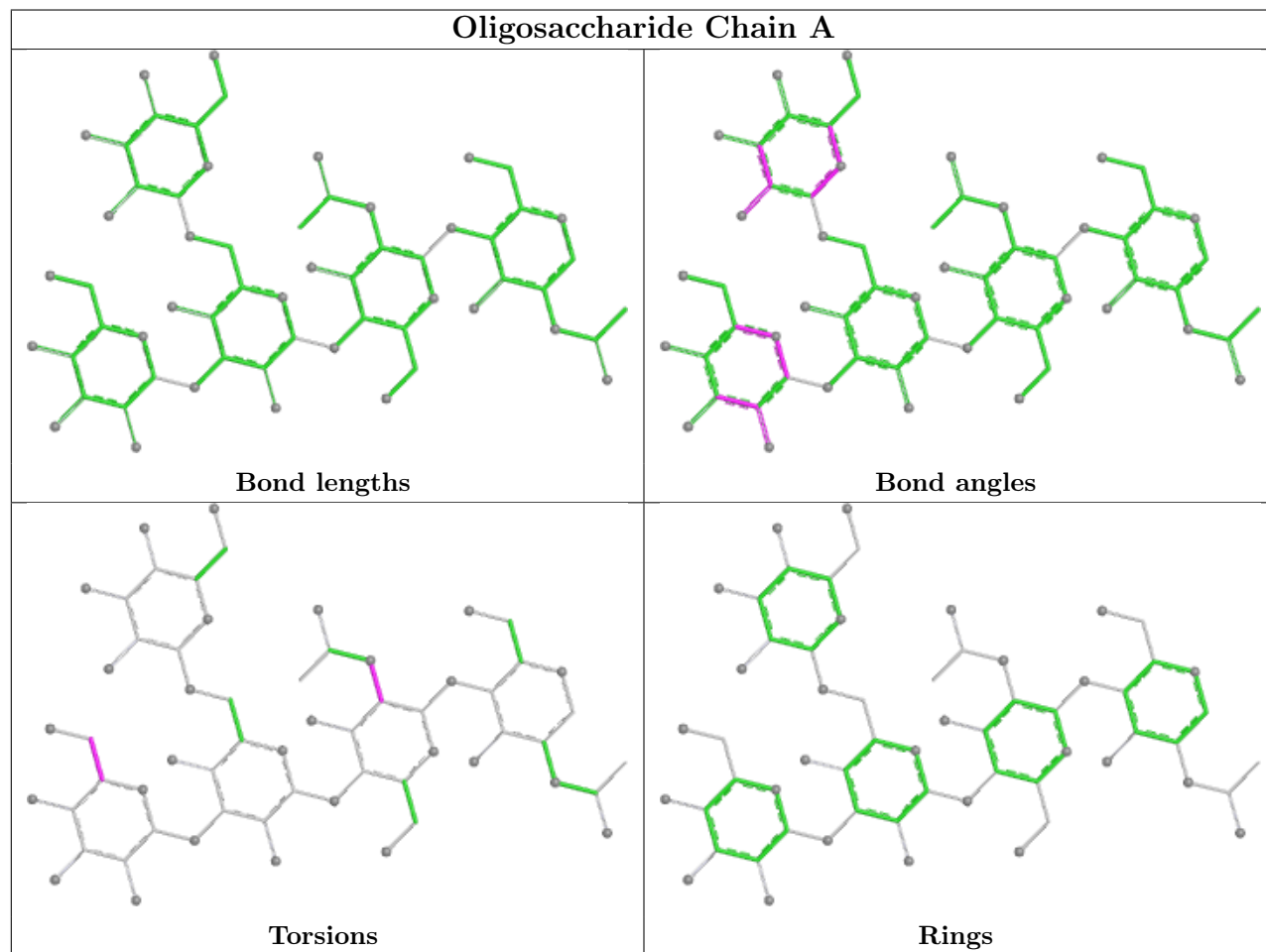
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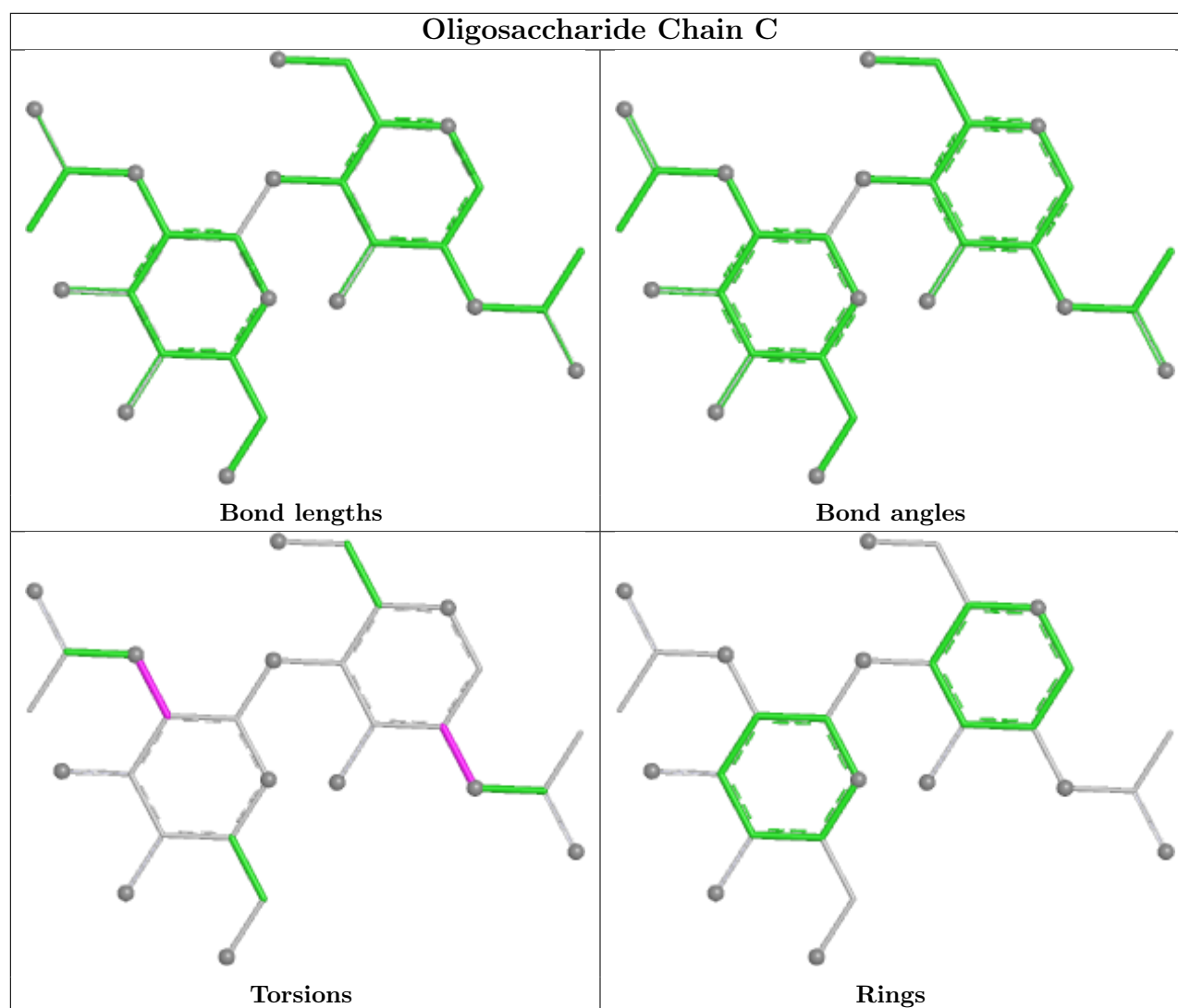
Mol	Chain	Res	Type	Atoms
2	A	2	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





## 4.6 Ligand geometry [i](#)

5 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	NAG	B	1404	1	14,14,15	0.22	0	17,19,21	0.50	0
4	NAG	B	1403	1	14,14,15	0.21	0	17,19,21	0.44	0
4	NAG	B	1401	1	14,14,15	0.20	0	17,19,21	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	B	1405	1	14,14,15	0.19	0	17,19,21	0.44	0
4	NAG	B	1402	1	14,14,15	0.27	0	17,19,21	0.46	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	NAG	B	1404	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1403	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1401	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1405	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1402	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 4.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

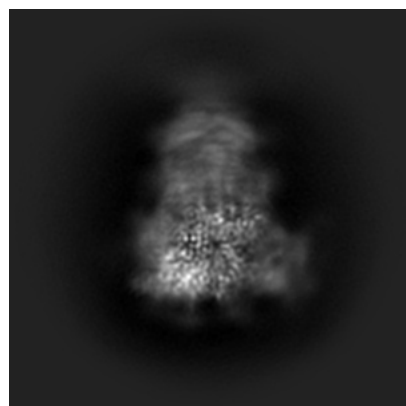
## 5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48804. These allow visual inspection of the internal detail of the map and identification of artifacts.

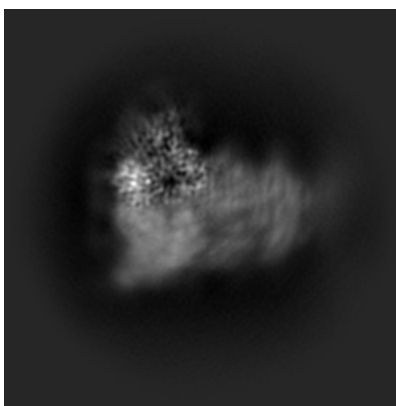
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

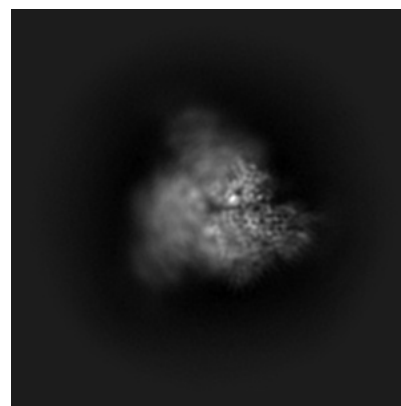
#### 5.1.1 Primary map



X

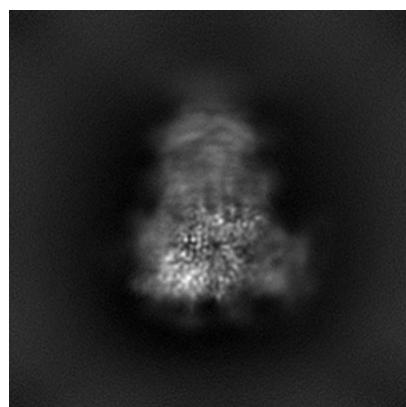


Y

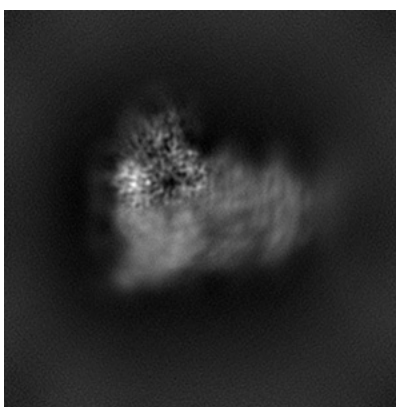


Z

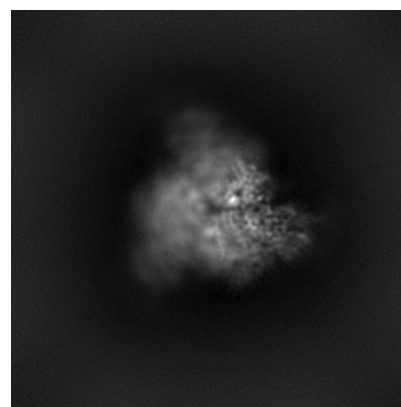
#### 5.1.2 Raw map



X



Y

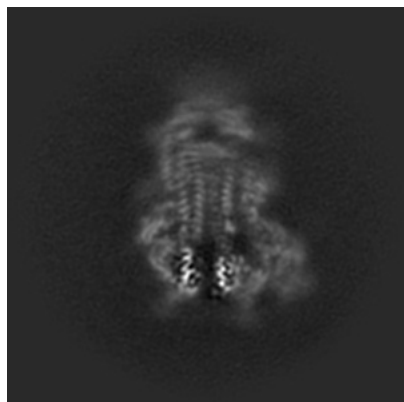


Z

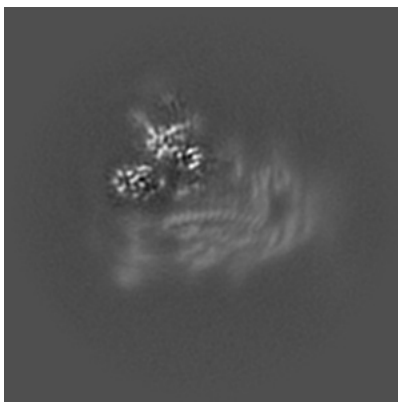
The images above show the map projected in three orthogonal directions.

## 5.2 Central slices [i](#)

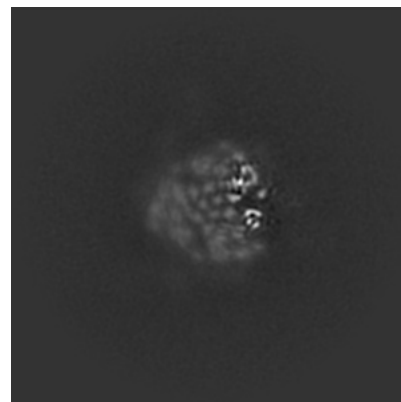
### 5.2.1 Primary map



X Index: 128

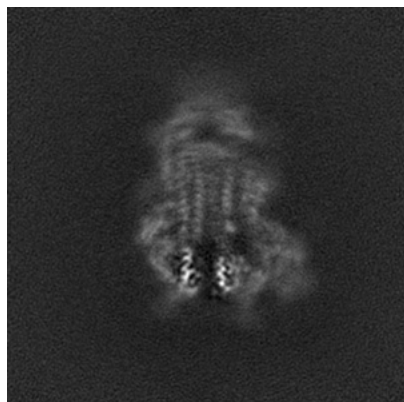


Y Index: 128

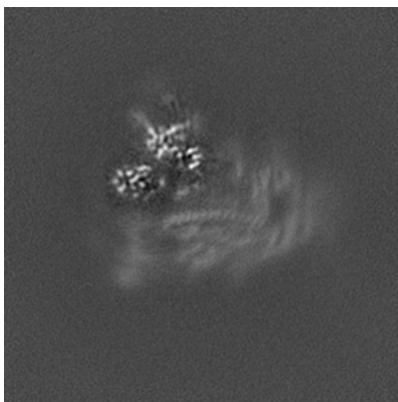


Z Index: 128

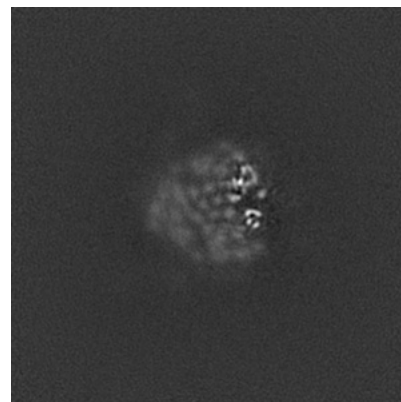
### 5.2.2 Raw map



X Index: 128



Y Index: 128

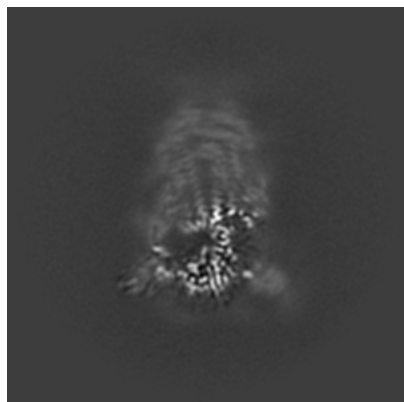


Z Index: 128

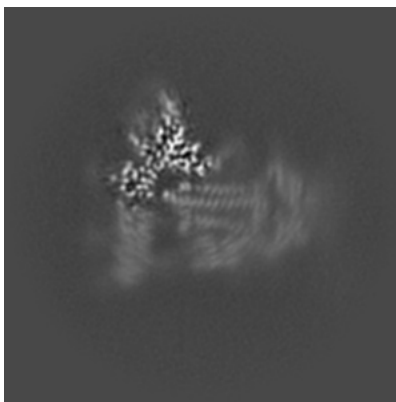
The images above show central slices of the map in three orthogonal directions.

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

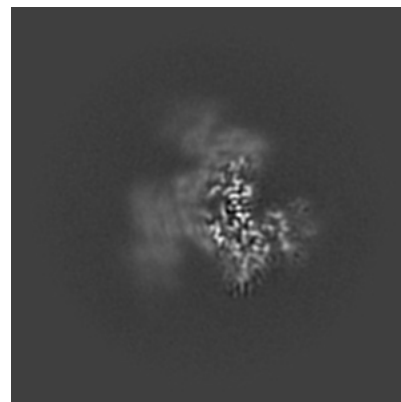
### 5.3.1 Primary map



X Index: 141

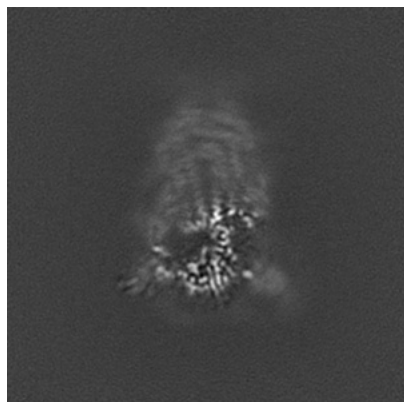


Y Index: 121

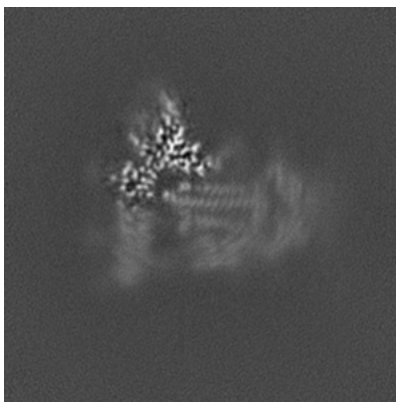


Z Index: 83

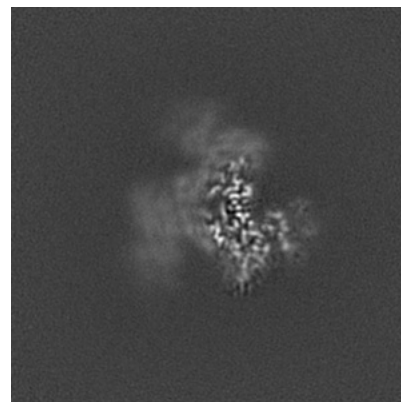
### 5.3.2 Raw map



X Index: 141



Y Index: 121

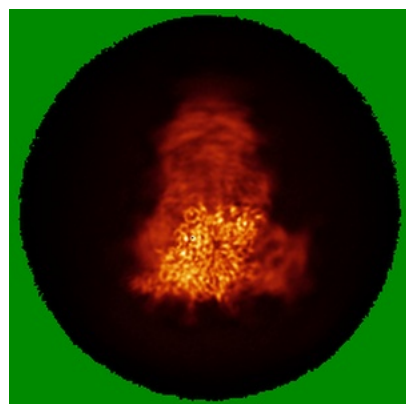


Z Index: 83

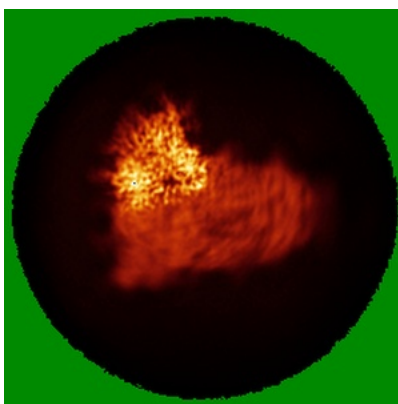
The images above show the largest variance slices of the map in three orthogonal directions.

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

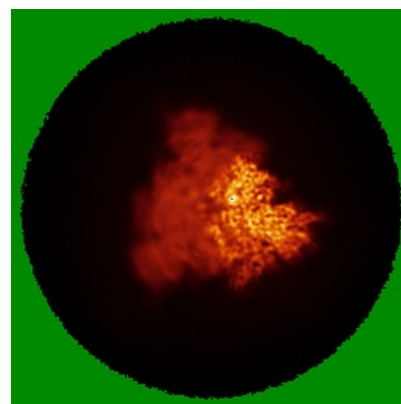
### 5.4.1 Primary map



X

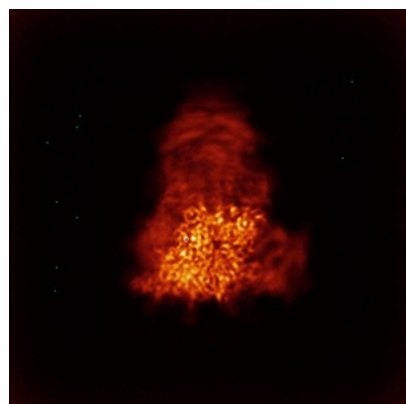


Y

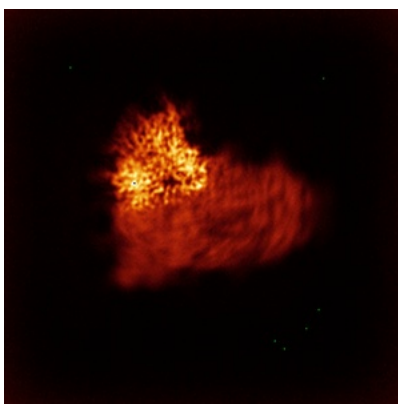


Z

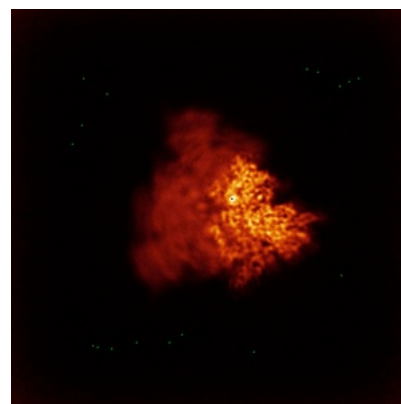
### 5.4.2 Raw map



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.



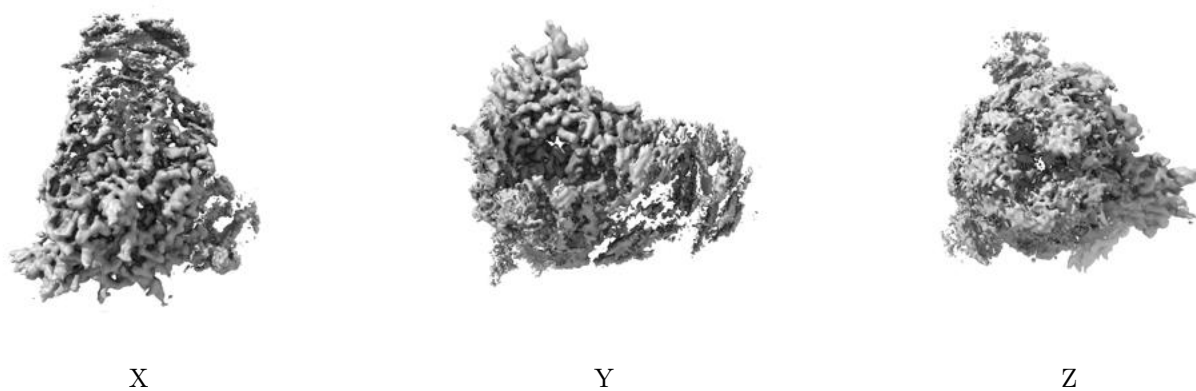
## 5.5 Orthogonal surface views [i](#)

### 5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 5.5.2 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.

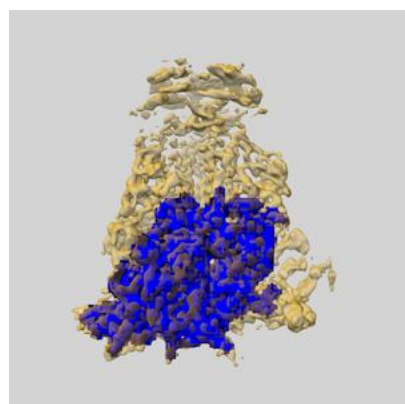
## 5.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

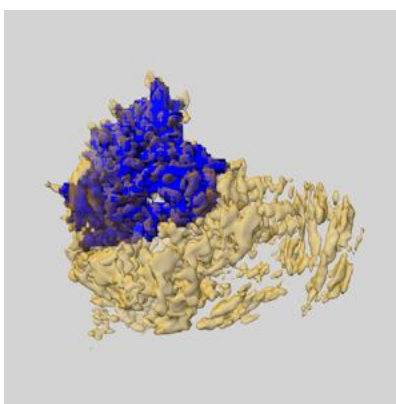
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

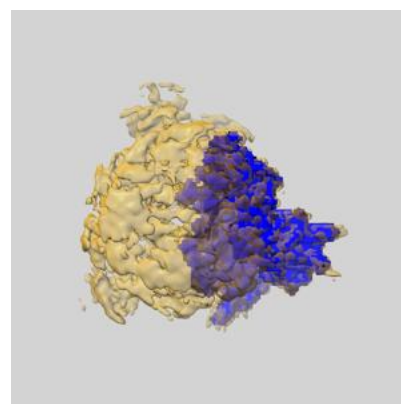
### 5.6.1 emd\_48804\_msk\_1.map [i](#)



X



Y

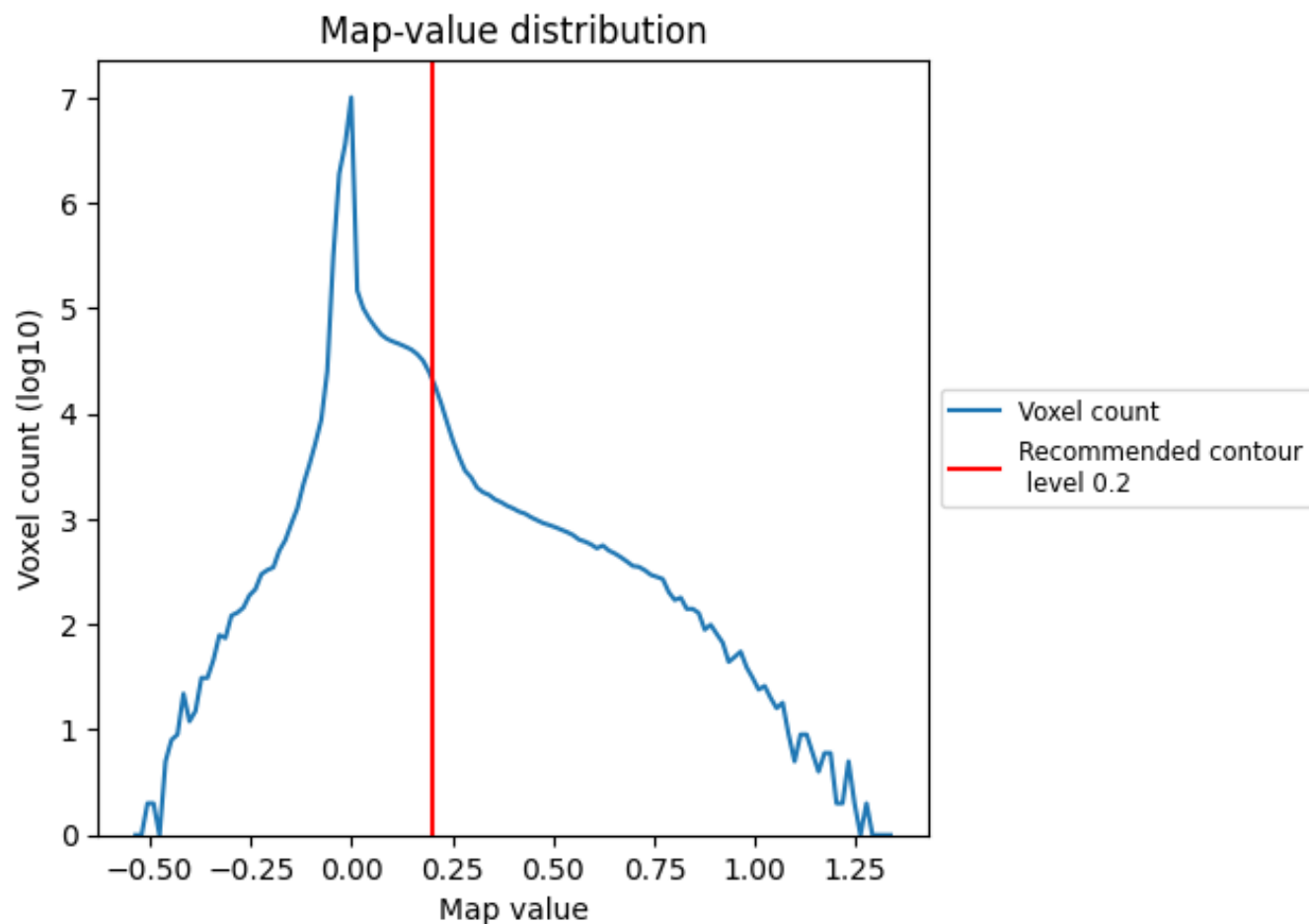


Z

## 6 Map analysis [i](#)

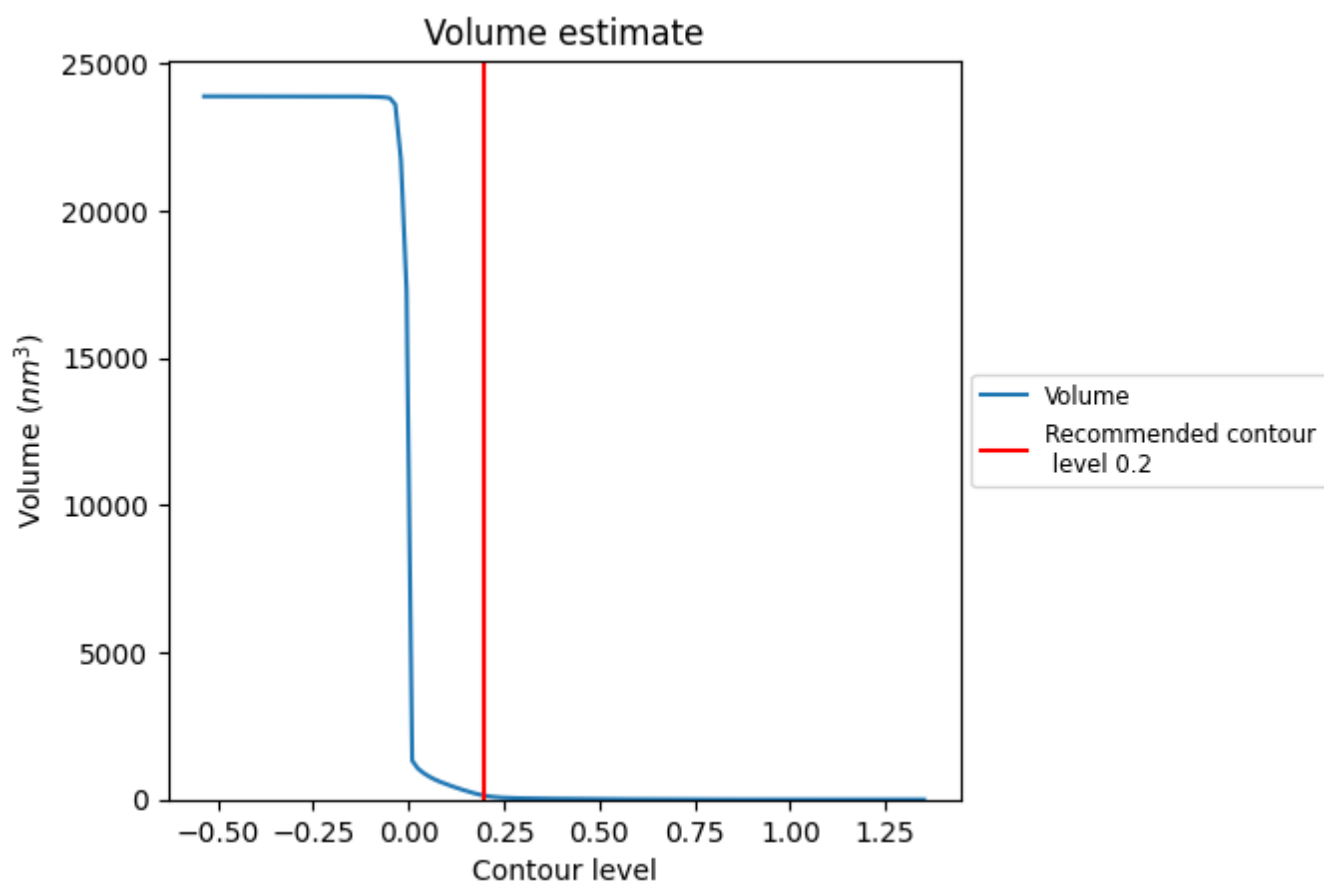
This section contains the results of statistical analysis of the map.

### 6.1 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.

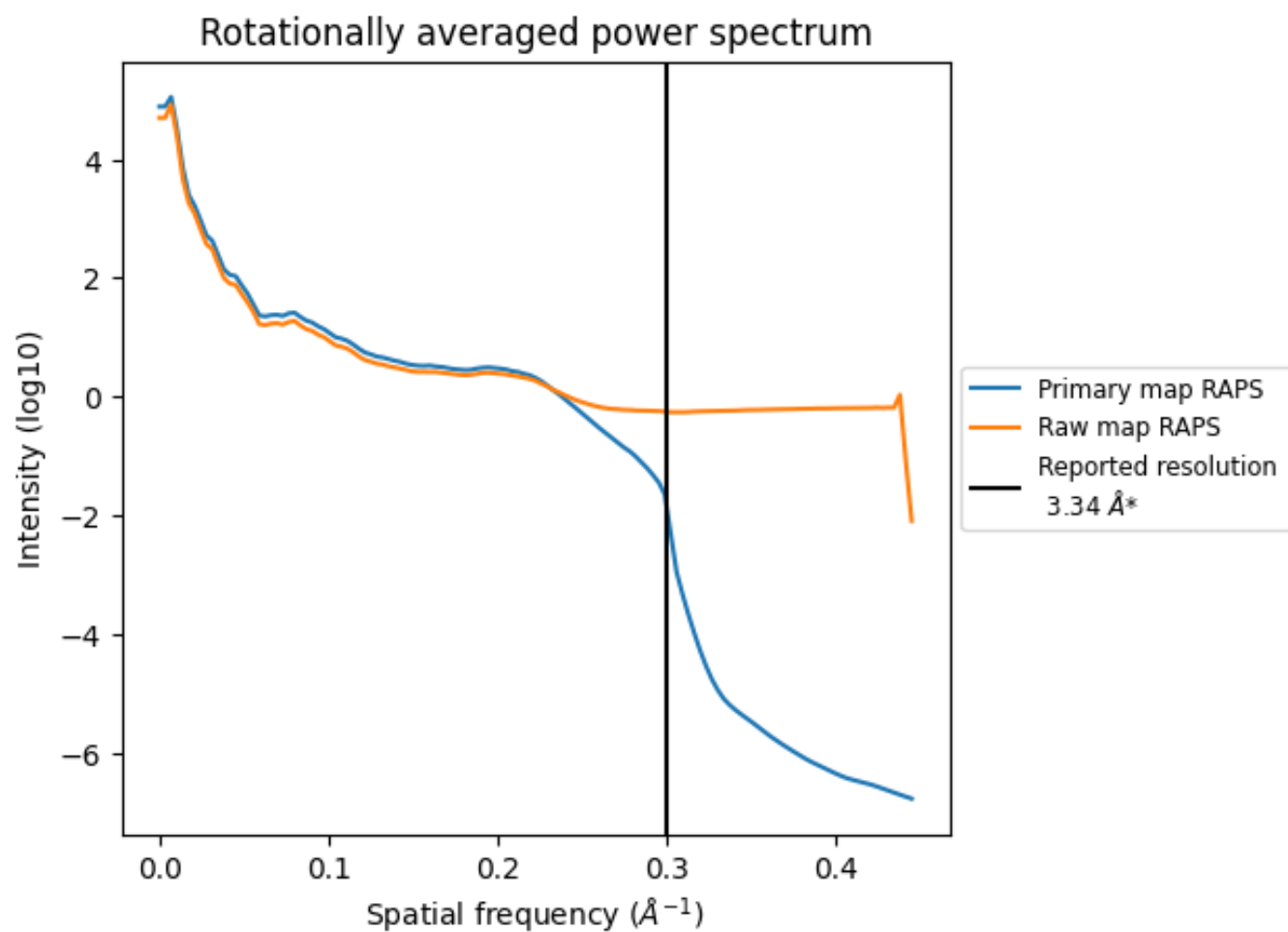
## 6.2 Volume estimate [i](#)



The volume at the recommended contour level is 132 nm<sup>3</sup>; this corresponds to an approximate mass of 120 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.

### 6.3 Rotationally averaged power spectrum ⓘ

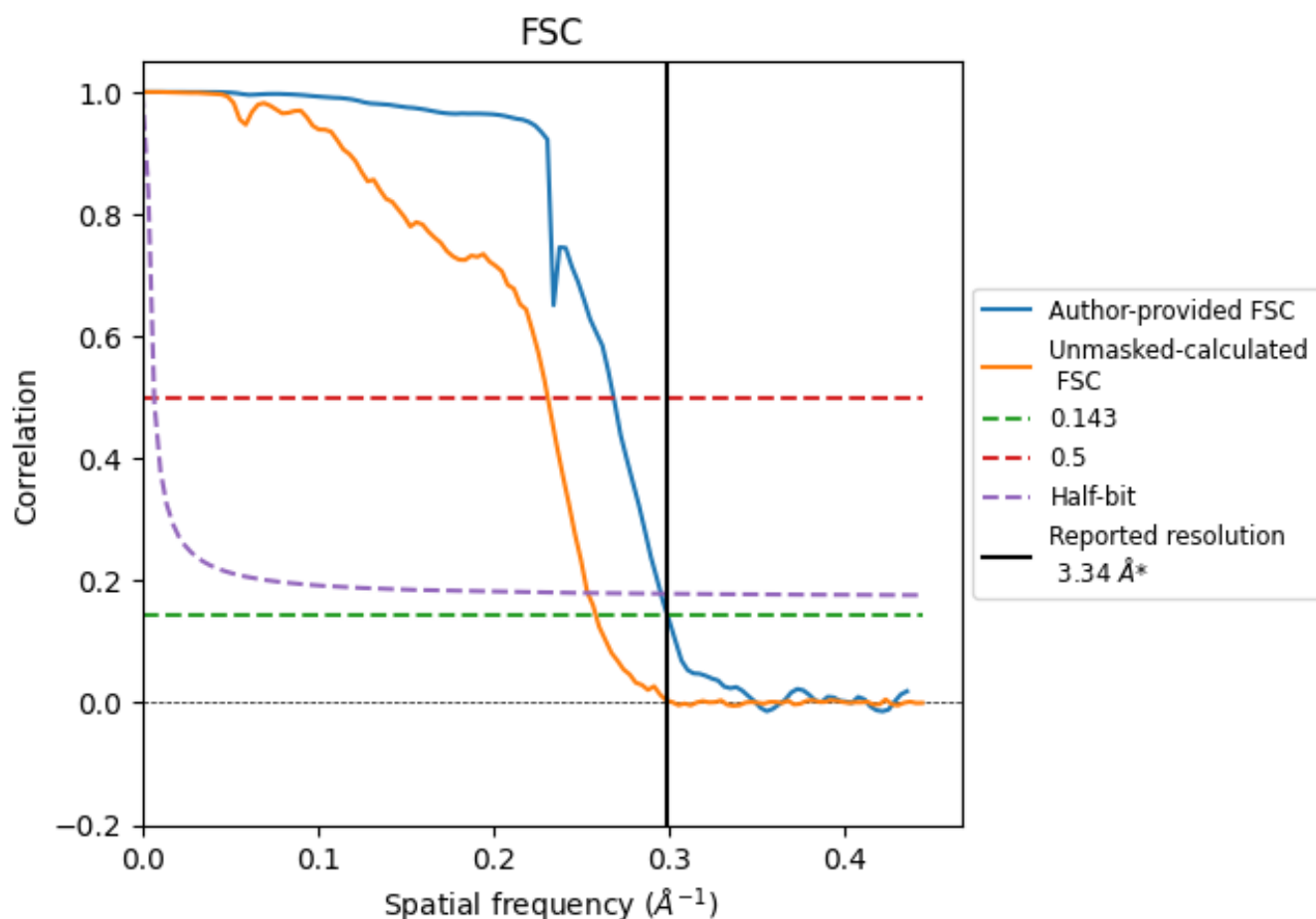


\*Reported resolution corresponds to spatial frequency of 0.299 Å<sup>-1</sup>

## 7 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.

### 7.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.299  $\text{\AA}^{-1}$

## 7.2 Resolution estimates [i](#)

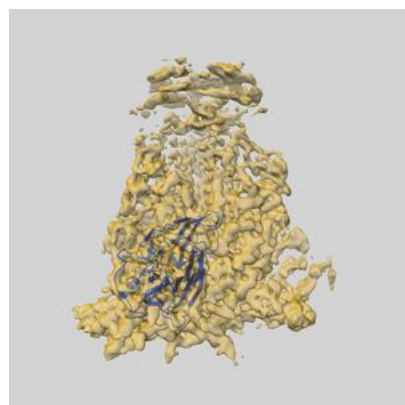
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.34	-	-
Author-provided FSC curve	3.34	3.72	3.38
Unmasked-calculated*	3.87	4.33	3.94

\*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 3.87 differs from the reported value 3.34 by more than 10 %

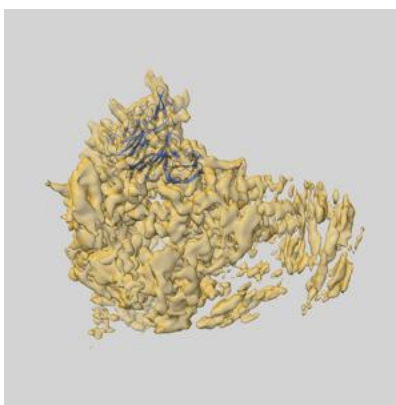
## 8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48804 and PDB model 9N13. Per-residue inclusion information can be found in section ?? on page ??.

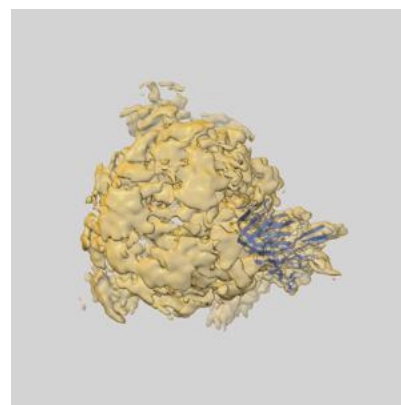
### 8.1 Map-model overlay [i](#)



X



Y

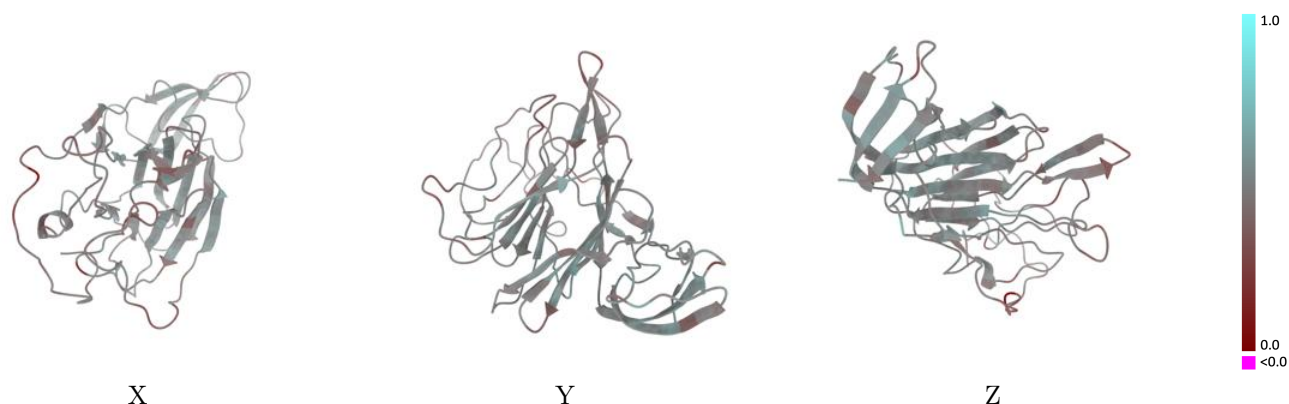


Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

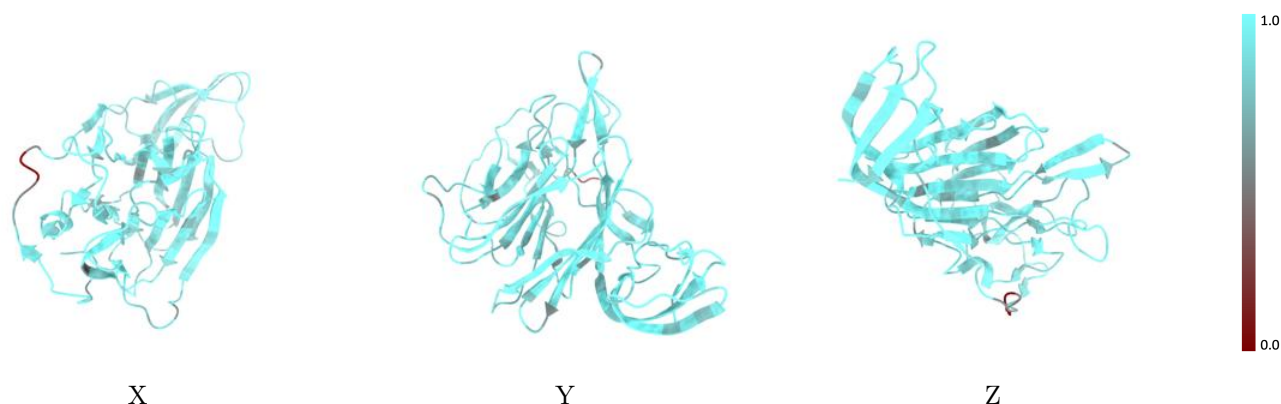


## 8.2 Q-score mapped to coordinate model [i](#)



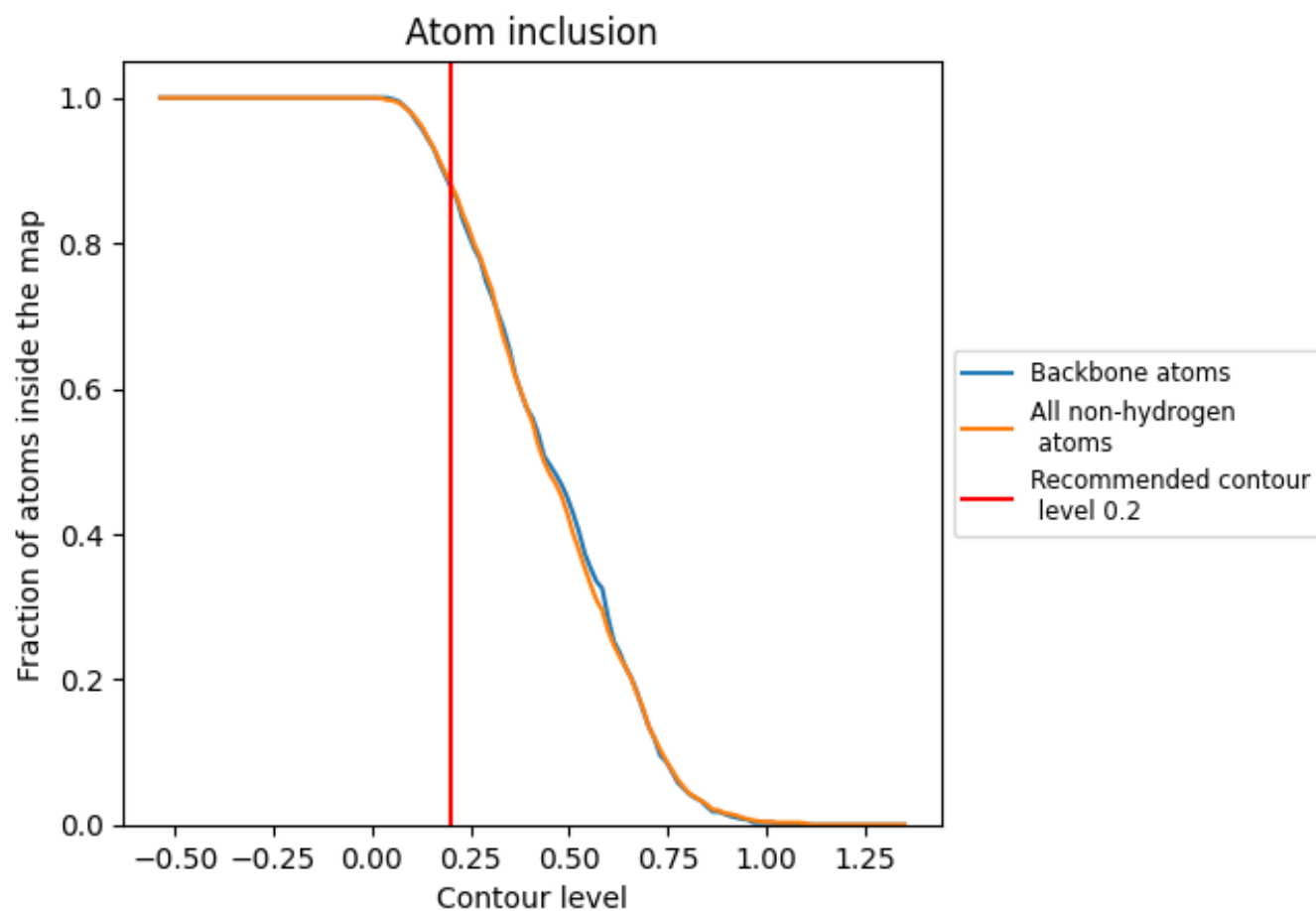
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 8.3 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 (0.2).

## 8.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8820	<div><div></div></div> 0.4650
A	<div><div></div></div> 0.8850	<div><div></div></div> 0.4310
B	<div><div></div></div> 0.8880	<div><div></div></div> 0.4660
C	<div><div></div></div> 0.8570	<div><div></div></div> 0.4140

