



## Full wwPDB EM Validation Report ⓘ

May 19, 2026 – 10:36 AM EDT

PDB ID : 9ZVL / pdb\_00009zvl  
EMDB ID : EMD-74879  
Title : CryoEM structure of H5N1 A/Texas/37/2024 HA bound to Fab H83  
Authors : Morano, N.C.; Ho, D.D.; Shapiro, L.; Kwong, P.D.  
Deposited on : 2025-12-30  
Resolution : 3.48 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:

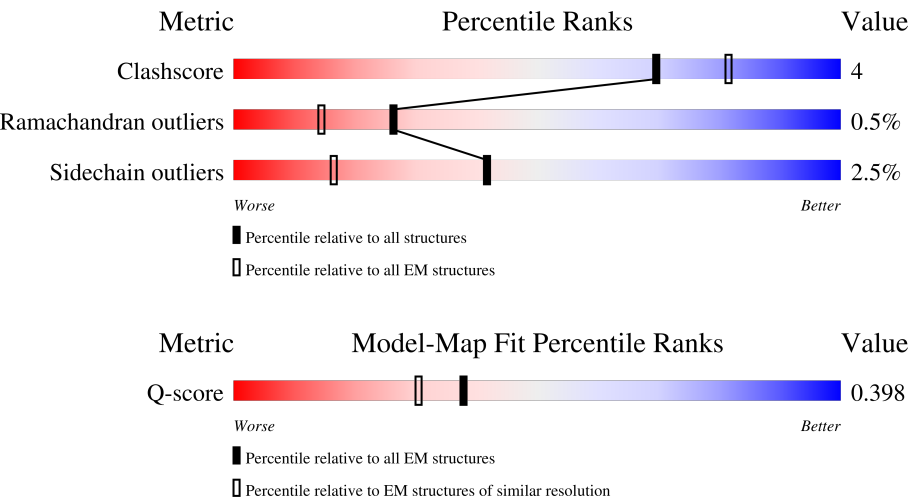
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 i

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

The reported resolution of this entry is 3.48 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	13672 ( 2.98 - 3.98 )

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	576	<div><div>15%</div><div>77%</div><div>8%</div><div>15%</div></div>
1	B	576	<div><div>17%</div><div>78%</div><div>7%</div><div>15%</div></div>
1	C	576	<div><div>15%</div><div>78%</div><div>7%</div><div>15%</div></div>
2	D	258	<div><div>38%</div><div>10%</div><div>52%</div></div>

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Mol	Chain	Length	Quality of chain
2	E	258	<div><div><div></div><div></div><div></div></div><div>40%9%52%</div></div>
2	H	258	<div><div><div></div><div></div><div></div></div><div>38%10%52%</div></div>
3	F	234	<div><div><div></div><div></div><div></div></div><div>7%37%9%54%</div></div>
3	G	234	<div><div><div></div><div></div><div></div></div><div>8%36%10%54%</div></div>
3	L	234	<div><div><div></div><div></div><div></div></div><div>7%38%8%54%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17372 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	491	Total	C	N	O	S	0	0
			3926	2470	683	750	23		
1	B	491	Total	C	N	O	S	0	0
			3927	2471	683	750	23		
1	C	491	Total	C	N	O	S	0	0
			3927	2471	683	750	23		

There are 195 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	ILE	THR	conflict	UNP A0AAX6NNG0
A	?	-	GLU	deletion	UNP A0AAX6NNG0
A	330	ARG	LYS	conflict	UNP A0AAX6NNG0
A	333	ARG	LYS	conflict	UNP A0AAX6NNG0
A	506	GLY	-	expression tag	UNP A0AAX6NNG0
A	507	SER	-	expression tag	UNP A0AAX6NNG0
A	508	SER	-	expression tag	UNP A0AAX6NNG0
A	509	GLY	-	expression tag	UNP A0AAX6NNG0
A	510	SER	-	expression tag	UNP A0AAX6NNG0
A	511	SER	-	expression tag	UNP A0AAX6NNG0
A	512	GLY	-	expression tag	UNP A0AAX6NNG0
A	513	TYR	-	expression tag	UNP A0AAX6NNG0
A	514	ILE	-	expression tag	UNP A0AAX6NNG0
A	515	PRO	-	expression tag	UNP A0AAX6NNG0
A	516	GLU	-	expression tag	UNP A0AAX6NNG0
A	517	ALA	-	expression tag	UNP A0AAX6NNG0
A	518	PRO	-	expression tag	UNP A0AAX6NNG0
A	519	ARG	-	expression tag	UNP A0AAX6NNG0
A	520	ASP	-	expression tag	UNP A0AAX6NNG0
A	521	GLY	-	expression tag	UNP A0AAX6NNG0
A	522	GLN	-	expression tag	UNP A0AAX6NNG0
A	523	ALA	-	expression tag	UNP A0AAX6NNG0
A	524	TYR	-	expression tag	UNP A0AAX6NNG0
A	525	VAL	-	expression tag	UNP A0AAX6NNG0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	526	ARG	-	expression tag	UNP A0AAX6NNG0
A	527	LYS	-	expression tag	UNP A0AAX6NNG0
A	528	ASP	-	expression tag	UNP A0AAX6NNG0
A	529	GLY	-	expression tag	UNP A0AAX6NNG0
A	530	GLU	-	expression tag	UNP A0AAX6NNG0
A	531	TRP	-	expression tag	UNP A0AAX6NNG0
A	532	VAL	-	expression tag	UNP A0AAX6NNG0
A	533	LEU	-	expression tag	UNP A0AAX6NNG0
A	534	LEU	-	expression tag	UNP A0AAX6NNG0
A	535	SER	-	expression tag	UNP A0AAX6NNG0
A	536	THR	-	expression tag	UNP A0AAX6NNG0
A	537	PHE	-	expression tag	UNP A0AAX6NNG0
A	538	LEU	-	expression tag	UNP A0AAX6NNG0
A	539	GLY	-	expression tag	UNP A0AAX6NNG0
A	540	HIS	-	expression tag	UNP A0AAX6NNG0
A	541	HIS	-	expression tag	UNP A0AAX6NNG0
A	542	HIS	-	expression tag	UNP A0AAX6NNG0
A	543	HIS	-	expression tag	UNP A0AAX6NNG0
A	544	HIS	-	expression tag	UNP A0AAX6NNG0
A	545	HIS	-	expression tag	UNP A0AAX6NNG0
A	546	HIS	-	expression tag	UNP A0AAX6NNG0
A	547	HIS	-	expression tag	UNP A0AAX6NNG0
A	548	HIS	-	expression tag	UNP A0AAX6NNG0
A	549	GLY	-	expression tag	UNP A0AAX6NNG0
A	550	GLY	-	expression tag	UNP A0AAX6NNG0
A	551	SER	-	expression tag	UNP A0AAX6NNG0
A	552	GLY	-	expression tag	UNP A0AAX6NNG0
A	553	LEU	-	expression tag	UNP A0AAX6NNG0
A	554	ASN	-	expression tag	UNP A0AAX6NNG0
A	555	ASP	-	expression tag	UNP A0AAX6NNG0
A	556	ILE	-	expression tag	UNP A0AAX6NNG0
A	557	PHE	-	expression tag	UNP A0AAX6NNG0
A	558	GLU	-	expression tag	UNP A0AAX6NNG0
A	559	ALA	-	expression tag	UNP A0AAX6NNG0
A	560	GLN	-	expression tag	UNP A0AAX6NNG0
A	561	LYS	-	expression tag	UNP A0AAX6NNG0
A	562	ILE	-	expression tag	UNP A0AAX6NNG0
A	563	GLU	-	expression tag	UNP A0AAX6NNG0
A	564	TRP	-	expression tag	UNP A0AAX6NNG0
A	565	HIS	-	expression tag	UNP A0AAX6NNG0
A	566	GLU	-	expression tag	UNP A0AAX6NNG0
B	199	ILE	THR	conflict	UNP A0AAX6NNG0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLU	deletion	UNP A0AAX6NNG0
B	338	ARG	LYS	conflict	UNP A0AAX6NNG0
B	341	ARG	LYS	conflict	UNP A0AAX6NNG0
B	514	GLY	-	expression tag	UNP A0AAX6NNG0
B	515	SER	-	expression tag	UNP A0AAX6NNG0
B	516	SER	-	expression tag	UNP A0AAX6NNG0
B	517	GLY	-	expression tag	UNP A0AAX6NNG0
B	518	SER	-	expression tag	UNP A0AAX6NNG0
B	519	SER	-	expression tag	UNP A0AAX6NNG0
B	520	GLY	-	expression tag	UNP A0AAX6NNG0
B	521	TYR	-	expression tag	UNP A0AAX6NNG0
B	522	ILE	-	expression tag	UNP A0AAX6NNG0
B	523	PRO	-	expression tag	UNP A0AAX6NNG0
B	524	GLU	-	expression tag	UNP A0AAX6NNG0
B	525	ALA	-	expression tag	UNP A0AAX6NNG0
B	526	PRO	-	expression tag	UNP A0AAX6NNG0
B	527	ARG	-	expression tag	UNP A0AAX6NNG0
B	528	ASP	-	expression tag	UNP A0AAX6NNG0
B	529	GLY	-	expression tag	UNP A0AAX6NNG0
B	530	GLN	-	expression tag	UNP A0AAX6NNG0
B	531	ALA	-	expression tag	UNP A0AAX6NNG0
B	532	TYR	-	expression tag	UNP A0AAX6NNG0
B	533	VAL	-	expression tag	UNP A0AAX6NNG0
B	534	ARG	-	expression tag	UNP A0AAX6NNG0
B	535	LYS	-	expression tag	UNP A0AAX6NNG0
B	536	ASP	-	expression tag	UNP A0AAX6NNG0
B	537	GLY	-	expression tag	UNP A0AAX6NNG0
B	538	GLU	-	expression tag	UNP A0AAX6NNG0
B	539	TRP	-	expression tag	UNP A0AAX6NNG0
B	540	VAL	-	expression tag	UNP A0AAX6NNG0
B	541	LEU	-	expression tag	UNP A0AAX6NNG0
B	542	LEU	-	expression tag	UNP A0AAX6NNG0
B	543	SER	-	expression tag	UNP A0AAX6NNG0
B	544	THR	-	expression tag	UNP A0AAX6NNG0
B	545	PHE	-	expression tag	UNP A0AAX6NNG0
B	546	LEU	-	expression tag	UNP A0AAX6NNG0
B	547	GLY	-	expression tag	UNP A0AAX6NNG0
B	548	HIS	-	expression tag	UNP A0AAX6NNG0
B	549	HIS	-	expression tag	UNP A0AAX6NNG0
B	550	HIS	-	expression tag	UNP A0AAX6NNG0
B	551	HIS	-	expression tag	UNP A0AAX6NNG0
B	552	HIS	-	expression tag	UNP A0AAX6NNG0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	553	HIS	-	expression tag	UNP A0AAX6NNG0
B	554	HIS	-	expression tag	UNP A0AAX6NNG0
B	555	HIS	-	expression tag	UNP A0AAX6NNG0
B	556	HIS	-	expression tag	UNP A0AAX6NNG0
B	557	GLY	-	expression tag	UNP A0AAX6NNG0
B	558	GLY	-	expression tag	UNP A0AAX6NNG0
B	559	SER	-	expression tag	UNP A0AAX6NNG0
B	560	GLY	-	expression tag	UNP A0AAX6NNG0
B	561	LEU	-	expression tag	UNP A0AAX6NNG0
B	562	ASN	-	expression tag	UNP A0AAX6NNG0
B	563	ASP	-	expression tag	UNP A0AAX6NNG0
B	564	ILE	-	expression tag	UNP A0AAX6NNG0
B	565	PHE	-	expression tag	UNP A0AAX6NNG0
B	566	GLU	-	expression tag	UNP A0AAX6NNG0
B	567	ALA	-	expression tag	UNP A0AAX6NNG0
B	568	GLN	-	expression tag	UNP A0AAX6NNG0
B	569	LYS	-	expression tag	UNP A0AAX6NNG0
B	570	ILE	-	expression tag	UNP A0AAX6NNG0
B	571	GLU	-	expression tag	UNP A0AAX6NNG0
B	572	TRP	-	expression tag	UNP A0AAX6NNG0
B	573	HIS	-	expression tag	UNP A0AAX6NNG0
B	574	GLU	-	expression tag	UNP A0AAX6NNG0
C	199	ILE	THR	conflict	UNP A0AAX6NNG0
C	?	-	GLU	deletion	UNP A0AAX6NNG0
C	338	ARG	LYS	conflict	UNP A0AAX6NNG0
C	341	ARG	LYS	conflict	UNP A0AAX6NNG0
C	514	GLY	-	expression tag	UNP A0AAX6NNG0
C	515	SER	-	expression tag	UNP A0AAX6NNG0
C	516	SER	-	expression tag	UNP A0AAX6NNG0
C	517	GLY	-	expression tag	UNP A0AAX6NNG0
C	518	SER	-	expression tag	UNP A0AAX6NNG0
C	519	SER	-	expression tag	UNP A0AAX6NNG0
C	520	GLY	-	expression tag	UNP A0AAX6NNG0
C	521	TYR	-	expression tag	UNP A0AAX6NNG0
C	522	ILE	-	expression tag	UNP A0AAX6NNG0
C	523	PRO	-	expression tag	UNP A0AAX6NNG0
C	524	GLU	-	expression tag	UNP A0AAX6NNG0
C	525	ALA	-	expression tag	UNP A0AAX6NNG0
C	526	PRO	-	expression tag	UNP A0AAX6NNG0
C	527	ARG	-	expression tag	UNP A0AAX6NNG0
C	528	ASP	-	expression tag	UNP A0AAX6NNG0
C	529	GLY	-	expression tag	UNP A0AAX6NNG0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	530	GLN	-	expression tag	UNP A0AAX6NNG0
C	531	ALA	-	expression tag	UNP A0AAX6NNG0
C	532	TYR	-	expression tag	UNP A0AAX6NNG0
C	533	VAL	-	expression tag	UNP A0AAX6NNG0
C	534	ARG	-	expression tag	UNP A0AAX6NNG0
C	535	LYS	-	expression tag	UNP A0AAX6NNG0
C	536	ASP	-	expression tag	UNP A0AAX6NNG0
C	537	GLY	-	expression tag	UNP A0AAX6NNG0
C	538	GLU	-	expression tag	UNP A0AAX6NNG0
C	539	TRP	-	expression tag	UNP A0AAX6NNG0
C	540	VAL	-	expression tag	UNP A0AAX6NNG0
C	541	LEU	-	expression tag	UNP A0AAX6NNG0
C	542	LEU	-	expression tag	UNP A0AAX6NNG0
C	543	SER	-	expression tag	UNP A0AAX6NNG0
C	544	THR	-	expression tag	UNP A0AAX6NNG0
C	545	PHE	-	expression tag	UNP A0AAX6NNG0
C	546	LEU	-	expression tag	UNP A0AAX6NNG0
C	547	GLY	-	expression tag	UNP A0AAX6NNG0
C	548	HIS	-	expression tag	UNP A0AAX6NNG0
C	549	HIS	-	expression tag	UNP A0AAX6NNG0
C	550	HIS	-	expression tag	UNP A0AAX6NNG0
C	551	HIS	-	expression tag	UNP A0AAX6NNG0
C	552	HIS	-	expression tag	UNP A0AAX6NNG0
C	553	HIS	-	expression tag	UNP A0AAX6NNG0
C	554	HIS	-	expression tag	UNP A0AAX6NNG0
C	555	HIS	-	expression tag	UNP A0AAX6NNG0
C	556	HIS	-	expression tag	UNP A0AAX6NNG0
C	557	GLY	-	expression tag	UNP A0AAX6NNG0
C	558	GLY	-	expression tag	UNP A0AAX6NNG0
C	559	SER	-	expression tag	UNP A0AAX6NNG0
C	560	GLY	-	expression tag	UNP A0AAX6NNG0
C	561	LEU	-	expression tag	UNP A0AAX6NNG0
C	562	ASN	-	expression tag	UNP A0AAX6NNG0
C	563	ASP	-	expression tag	UNP A0AAX6NNG0
C	564	ILE	-	expression tag	UNP A0AAX6NNG0
C	565	PHE	-	expression tag	UNP A0AAX6NNG0
C	566	GLU	-	expression tag	UNP A0AAX6NNG0
C	567	ALA	-	expression tag	UNP A0AAX6NNG0
C	568	GLN	-	expression tag	UNP A0AAX6NNG0
C	569	LYS	-	expression tag	UNP A0AAX6NNG0
C	570	ILE	-	expression tag	UNP A0AAX6NNG0
C	571	GLU	-	expression tag	UNP A0AAX6NNG0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	572	TRP	-	expression tag	UNP A0AAX6NNG0
C	573	HIS	-	expression tag	UNP A0AAX6NNG0
C	574	GLU	-	expression tag	UNP A0AAX6NNG0

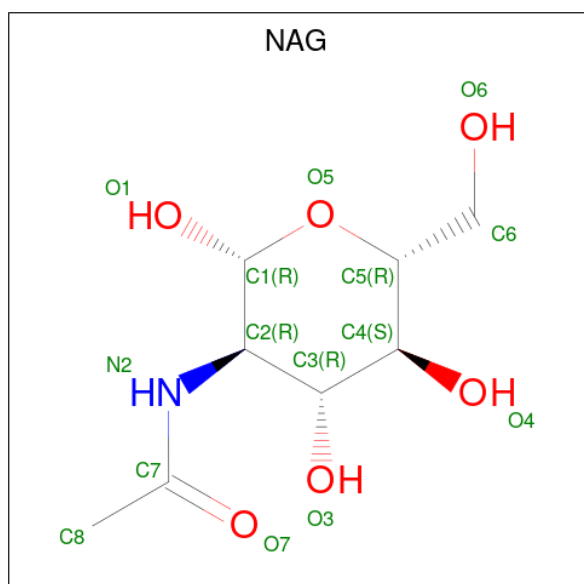
- Molecule 2 is a protein called Fab H83 Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	124	Total	C	N	O	S	0	0
			987	623	176	183	5		
2	D	124	Total	C	N	O	S	0	0
			987	623	176	183	5		
2	E	124	Total	C	N	O	S	0	0
			987	623	176	183	5		

- Molecule 3 is a protein called Fab H83 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	108	Total	C	N	O	S	0	0
			821	517	137	164	3		
3	F	108	Total	C	N	O	S	0	0
			821	517	137	164	3		
3	G	108	Total	C	N	O	S	0	0
			821	517	137	164	3		

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

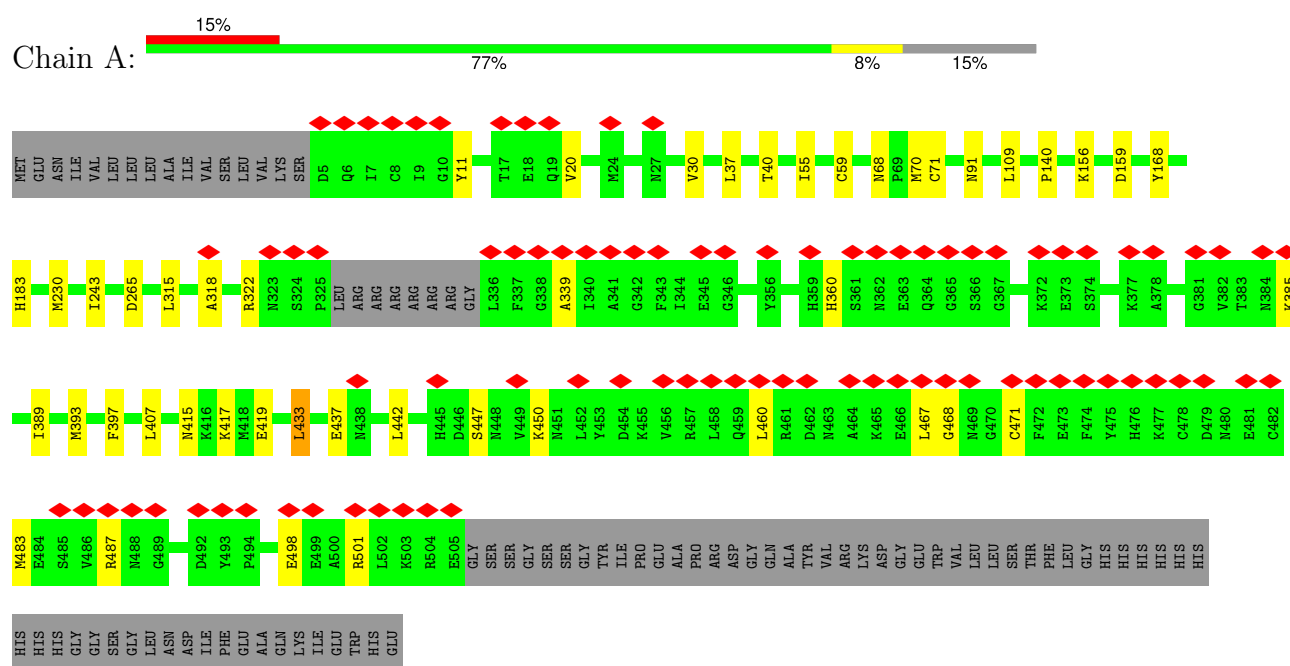


Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4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

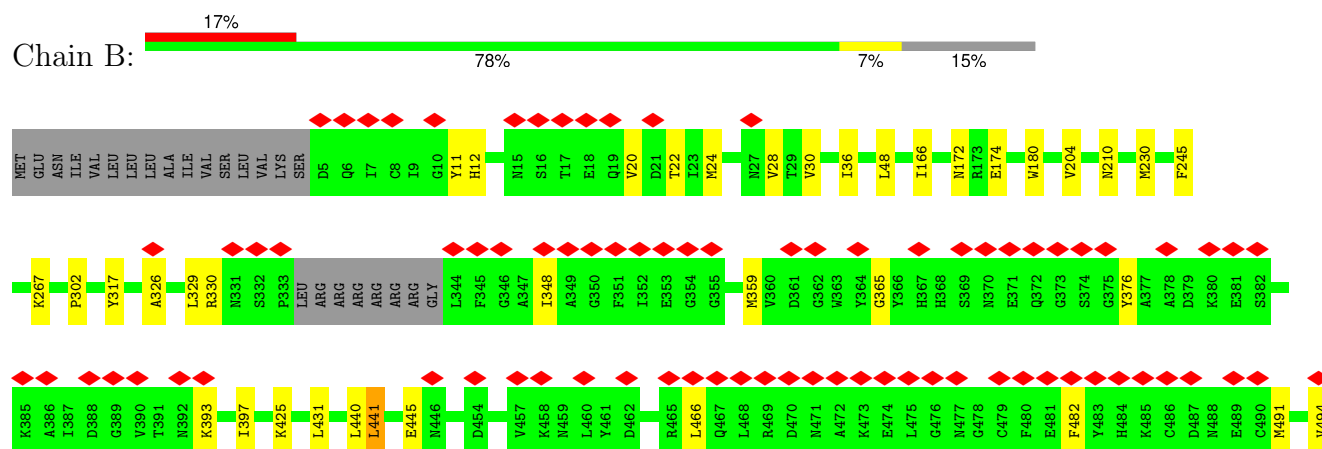
### 3 Residue-property plots

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.

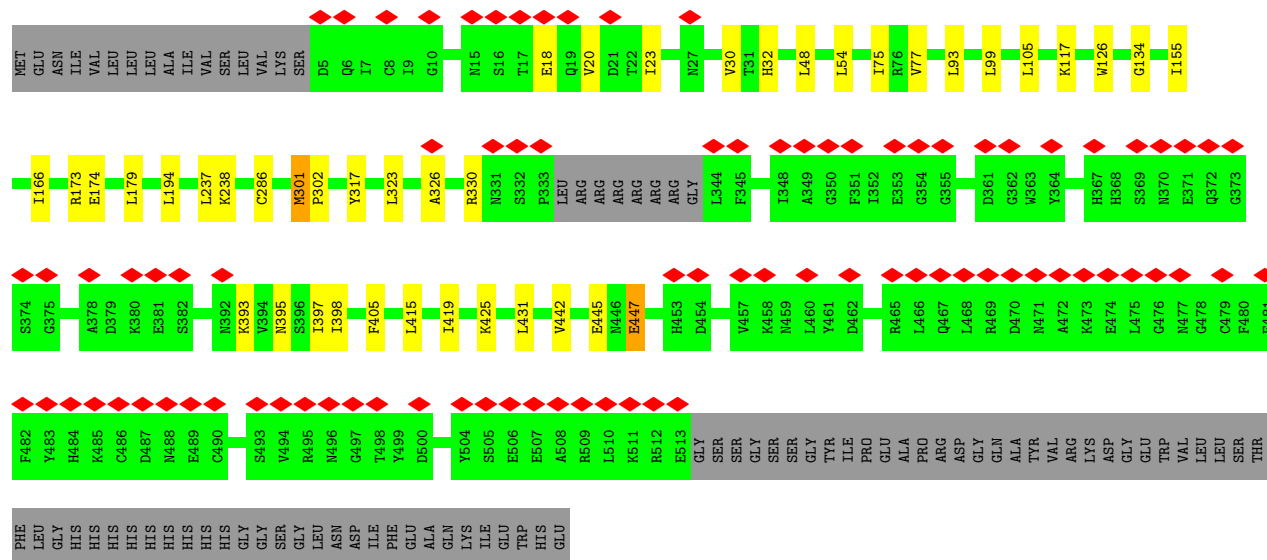
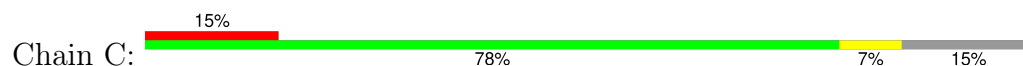
#### • Molecule 1: Hemagglutinin



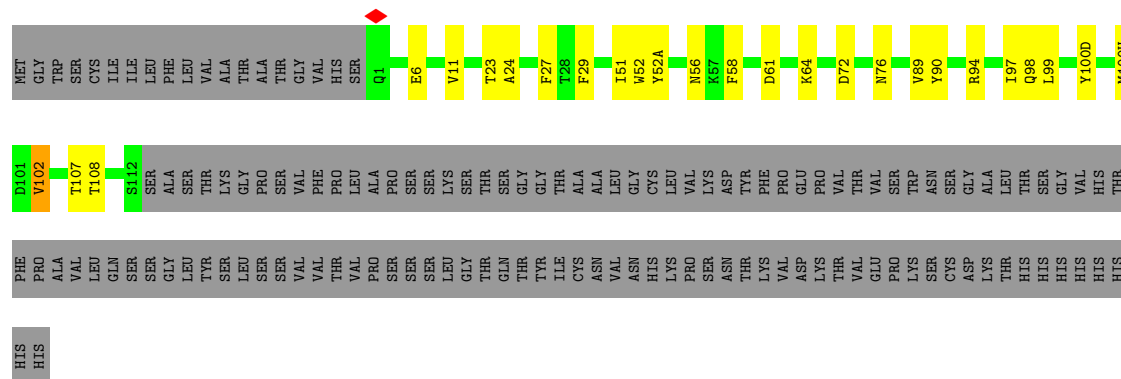
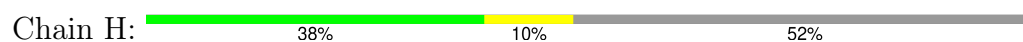
#### • Molecule 1: Hemagglutinin



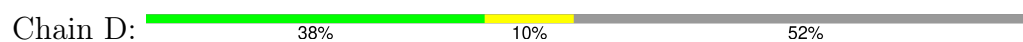
- Molecule 1: Hemagglutinin



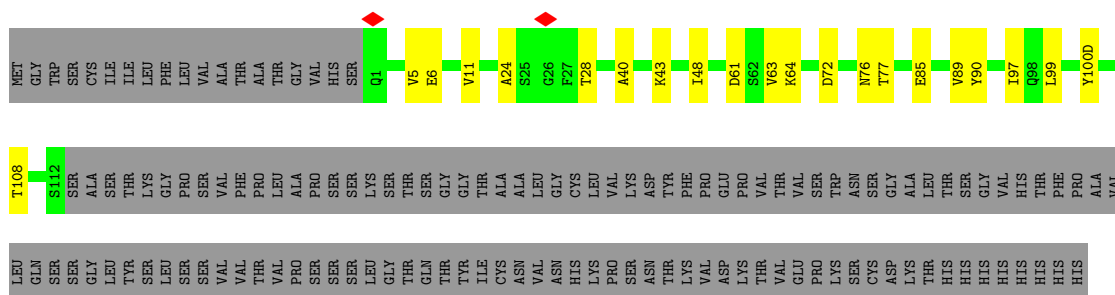
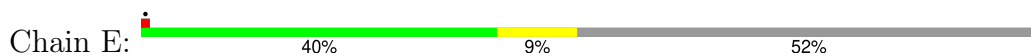
- Molecule 2: Fab H83 Heavy Chain



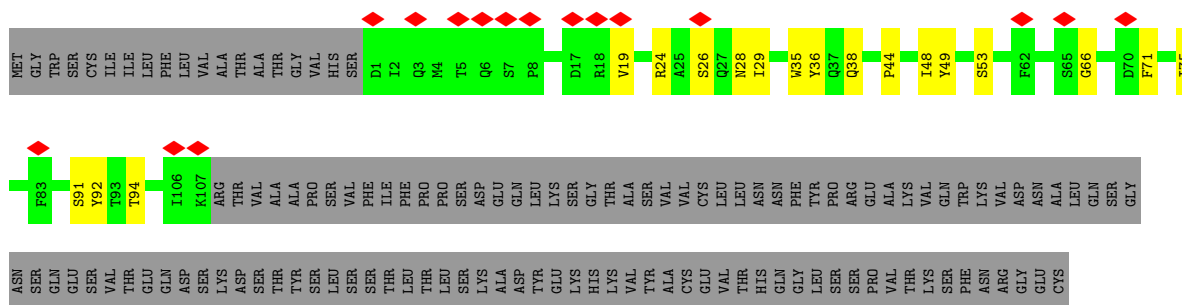
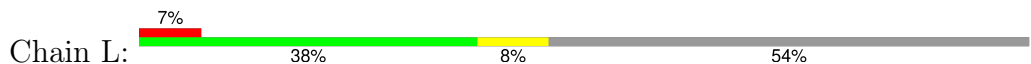
- Molecule 2: Fab H83 Heavy Chain



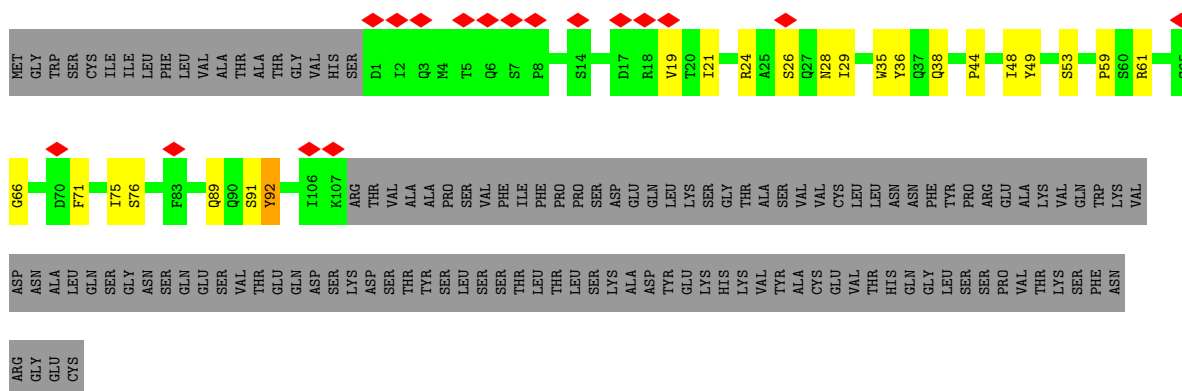
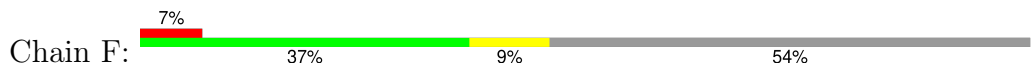
- Molecule 2: Fab H83 Heavy Chain



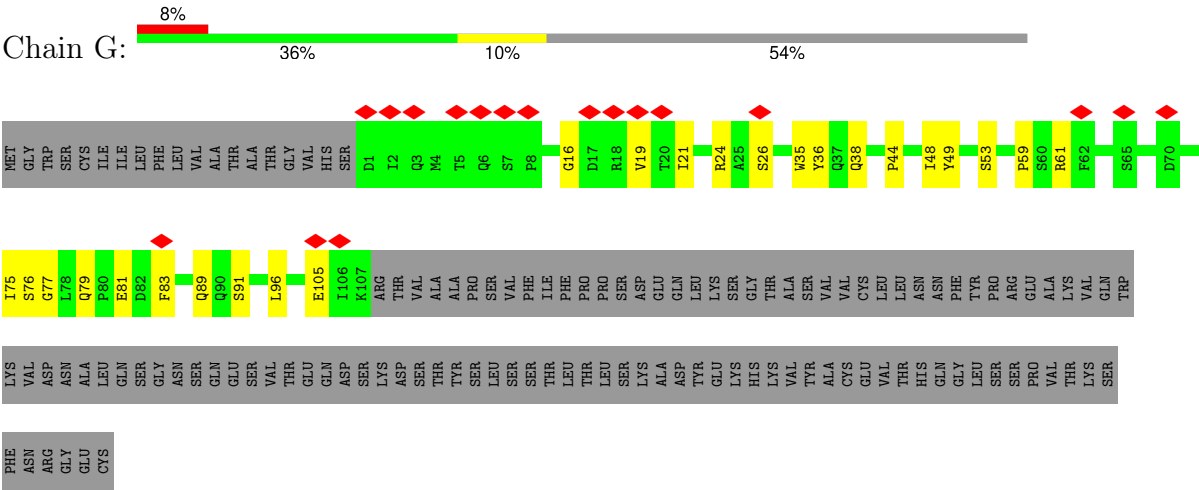
- Molecule 3: Fab H83 Light Chain



- Molecule 3: Fab H83 Light Chain



● Molecule 3: Fab H83 Light Chain



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT, POINT	Depositor
Number of particles used	30030, 30030, 30300, 30300, 30030, 30030, 30300, 30300, 30030, 30030, 30300, 30300, 30030, 30030, 30300, 30300	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	58	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.698	Depositor
Minimum map value	-0.435	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.0823	Depositor
Map size (Å)	495.0, 495.0, 495.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	0.17	0/4017	0.43	0/5439
1	B	0.16	0/4018	0.42	0/5441
1	C	0.18	0/4018	0.44	0/5441
2	D	0.22	0/1012	0.60	0/1371
2	E	0.21	0/1012	0.59	0/1371
2	H	0.22	0/1012	0.59	0/1371
3	F	0.22	0/839	0.63	2/1137 (0.2%)
3	G	0.20	0/839	0.63	2/1137 (0.2%)
3	L	0.21	0/839	0.63	2/1137 (0.2%)
All	All	0.19	0/17606	0.49	6/23845 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	G	91	SER	CA-C-N	6.18	133.35	121.54
3	G	91	SER	C-N-CA	6.18	133.35	121.54
3	F	91	SER	CA-C-N	5.17	131.42	121.54
3	F	91	SER	C-N-CA	5.17	131.42	121.54
3	L	91	SER	CA-C-N	5.14	131.37	121.54
3	L	91	SER	C-N-CA	5.14	131.37	121.54

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	3926	0	3776	25	0
1	B	3927	0	3780	20	0
1	C	3927	0	3780	26	0
2	D	987	0	944	9	0
2	E	987	0	944	7	0
2	H	987	0	944	12	0
3	F	821	0	804	10	0
3	G	821	0	804	11	0
3	L	821	0	804	10	0
4	A	56	0	52	0	0
4	B	56	0	52	0	0
4	C	56	0	52	2	0
All	All	17372	0	16736	124	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 4.

All (124) 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:C:395:ASN:HA	1:C:398:ILE:HD12	1.77	0.66
2:H:6:GLU:HB3	2:H:107:THR:HB	1.80	0.62
2:H:94:ARG:HG2	2:H:102:VAL:HG22	1.83	0.61
2:D:6:GLU:HB3	2:D:107:THR:HB	1.83	0.60
2:E:6:GLU:HB3	2:E:107:THR:HB	1.85	0.58
1:C:155:ILE:HD11	1:C:194:LEU:HD22	1.85	0.58
1:B:397:ILE:HG23	1:B:441:LEU:HD21	1.85	0.58
3:L:35:TRP:HB2	3:L:48:ILE:HB	1.86	0.58
2:E:89:VAL:HA	2:E:108:THR:HA	1.86	0.57
1:A:59:CYS:HA	1:A:91:ASN:HB2	1.88	0.56
1:C:23:ILE:HD12	1:C:447:GLU:HG3	1.87	0.56
1:C:30:VAL:HA	1:C:330:ARG:HA	1.87	0.56
1:C:134:GLY:HA2	2:H:99:LEU:HD12	1.86	0.56
2:D:89:VAL:HA	2:D:108:THR:HA	1.87	0.55
3:G:35:TRP:HB2	3:G:48:ILE:HB	1.87	0.55
1:A:20:VAL:HG11	1:A:318:ALA:HB2	1.89	0.55
2:H:61:ASP:HA	2:H:64:LYS:HD3	1.89	0.54
1:C:18:GLU:HB2	4:C:603:NAG:H61	1.88	0.54
1:C:20:VAL:HG11	1:C:326:ALA:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:GLY:HA2	1:B:466:LEU:HD22	1.90	0.54
2:D:61:ASP:HA	2:D:64:LYS:HD3	1.90	0.53
3:F:35:TRP:HB2	3:F:48:ILE:HB	1.89	0.53
2:E:61:ASP:HA	2:E:64:LYS:HD3	1.89	0.53
1:B:359:MET:HE2	1:B:365:GLY:HA3	1.90	0.53
1:B:425:LYS:HB3	1:C:405:PHE:HE1	1.74	0.53
2:H:89:VAL:HA	2:H:108:THR:HA	1.90	0.53
1:C:323:LEU:HB3	1:C:442:VAL:HG21	1.91	0.52
1:C:99:LEU:HD21	1:C:105:LEU:HD23	1.91	0.52
2:D:89:VAL:HG12	2:D:108:THR:HB	1.91	0.52
1:A:467:LEU:HD12	1:A:471:CYS:HB2	1.91	0.52
1:A:70:MET:HE2	1:A:140:PRO:HD2	1.93	0.51
1:B:172:ASN:HB3	1:B:267:LYS:HE3	1.92	0.51
1:B:329:LEU:HD11	1:B:348:ILE:HG21	1.91	0.51
2:D:27:PHE:HD1	2:D:29:PHE:H	1.59	0.51
3:G:49:TYR:HB3	3:G:53:SER:HB2	1.93	0.50
3:G:79:GLN:HB2	3:G:81:GLU:HG3	1.93	0.50
1:C:397:ILE:HD11	1:C:445:GLU:HG3	1.93	0.50
1:B:30:VAL:HA	1:B:330:ARG:HA	1.93	0.50
1:A:360:HIS:HB3	1:A:487:ARG:HH12	1.76	0.50
1:A:385:LYS:HD3	1:A:437:GLU:HB3	1.93	0.49
3:G:59:PRO:HB2	3:G:61:ARG:HH12	1.78	0.49
2:H:27:PHE:HD1	2:H:29:PHE:H	1.60	0.49
3:F:61:ARG:HB2	3:F:76:SER:HB3	1.94	0.49
1:B:20:VAL:HG11	1:B:326:ALA:HB2	1.94	0.49
1:B:36:ILE:HG23	1:B:302:PRO:HD2	1.95	0.49
2:D:24:ALA:HB3	2:D:76:ASN:HB3	1.95	0.49
1:B:482:PHE:HZ	1:B:494:VAL:HG21	1.78	0.48
3:F:59:PRO:HB2	3:F:61:ARG:HH12	1.78	0.48
3:G:61:ARG:HB2	3:G:76:SER:HB3	1.95	0.48
1:A:68:ASN:HB3	1:A:71:CYS:HB2	1.95	0.48
2:E:24:ALA:HB3	2:E:76:ASN:HB3	1.94	0.48
1:A:168:TYR:H	1:A:243:ILE:HG22	1.79	0.47
3:F:49:TYR:HB3	3:F:53:SER:HB2	1.96	0.47
1:A:389:ILE:HG23	1:A:433:LEU:HD21	1.95	0.47
1:A:30:VAL:HA	1:A:322:ARG:HA	1.95	0.47
1:B:24:MET:HG2	1:C:393:LYS:HD2	1.96	0.47
1:B:329:LEU:HD12	1:B:330:ARG:HG2	1.97	0.47
3:F:24:ARG:HE	3:F:26:SER:H	1.62	0.47
3:G:38:GLN:HB2	3:G:44:PRO:HG3	1.97	0.47
1:C:117:LYS:HZ2	1:C:117:LYS:HG3	1.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:56:ASN:HB3	2:H:58:PHE:HE1	1.80	0.47
3:L:24:ARG:HE	3:L:26:SER:H	1.63	0.47
3:F:36:TYR:HE2	3:F:89:GLN:HB2	1.80	0.47
1:C:317:TYR:HD2	1:C:431:LEU:HD22	1.80	0.46
3:L:49:TYR:HB3	3:L:53:SER:HB2	1.97	0.46
3:F:38:GLN:HB2	3:F:44:PRO:HG3	1.97	0.46
3:L:66:GLY:HA3	3:L:71:PHE:HA	1.98	0.46
1:A:360:HIS:HB2	1:A:483:MET:HE2	1.98	0.46
3:F:19:VAL:HB	3:F:75:ILE:HB	1.98	0.46
1:A:498:GLU:HA	1:A:501:ARG:HE	1.82	0.45
1:C:173:ARG:HA	1:C:173:ARG:HD3	1.87	0.45
2:D:38:ARG:HG3	2:D:48:ILE:HD11	1.97	0.45
3:G:24:ARG:HE	3:G:26:SER:H	1.64	0.45
2:D:56:ASN:HB3	2:D:58:PHE:HE1	1.82	0.45
2:H:24:ALA:HB3	2:H:76:ASN:HB3	1.99	0.45
2:E:43:LYS:HB3	2:E:43:LYS:HE3	1.81	0.45
1:C:32:HIS:HA	4:C:603:NAG:H4	1.99	0.44
3:G:36:TYR:HE2	3:G:89:GLN:HB2	1.82	0.44
1:B:22:THR:HG23	1:B:28:VAL:HG21	2.00	0.44
3:L:19:VAL:HB	3:L:75:ILE:HB	2.00	0.44
1:A:397:PHE:HE1	1:C:425:LYS:HB3	1.82	0.44
1:A:156:LYS:HE3	1:A:159:ASP:HA	1.99	0.43
1:C:48:LEU:HD12	1:C:48:LEU:HA	1.89	0.43
3:G:83:PHE:HD1	3:G:105:GLU:HA	1.82	0.43
1:A:415:ASN:O	1:A:419:GLU:HG2	2.19	0.43
1:B:393:LYS:HD3	1:B:445:GLU:HB3	2.00	0.43
1:A:433:LEU:O	1:A:437:GLU:HG2	2.19	0.43
1:C:237:LEU:HD12	1:C:237:LEU:HA	1.88	0.43
1:C:301:MET:HA	1:C:302:PRO:HD3	1.89	0.42
1:B:329:LEU:HD12	1:B:330:ARG:H	1.84	0.42
1:C:54:LEU:HD13	1:C:77:VAL:HG21	2.01	0.42
1:C:75:ILE:HD12	1:C:75:ILE:HA	1.93	0.42
1:A:447:SER:HA	1:A:450:LYS:HG2	2.00	0.42
1:B:48:LEU:HD12	1:B:48:LEU:HA	1.88	0.42
2:D:43:LYS:HB3	2:D:43:LYS:HE3	1.81	0.42
2:H:51:ILE:HD12	2:H:52:TRP:H	1.85	0.42
1:C:419:ILE:H	1:C:419:ILE:HG13	1.65	0.42
3:L:48:ILE:HD13	3:L:48:ILE:HA	1.88	0.42
1:C:238:LYS:HA	1:C:238:LYS:HD3	1.74	0.42
3:L:38:GLN:HB2	3:L:44:PRO:HG3	2.02	0.41
3:L:92:TYR:HE1	3:L:94:THR:HB	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:98:GLN:O	2:H:99:LEU:HD23	2.19	0.41
3:F:66:GLY:HA3	3:F:71:PHE:HA	2.02	0.41
3:G:16:GLY:HA2	3:G:77:GLY:HA2	2.01	0.41
1:A:393:MET:HE1	1:A:433:LEU:HD13	2.02	0.41
3:G:19:VAL:HB	3:G:75:ILE:HB	2.01	0.41
1:A:183:HIS:HB2	1:A:230:MET:HE2	2.02	0.41
1:B:166:ILE:HG22	1:B:245:PHE:HB2	2.01	0.41
1:B:317:TYR:HD2	1:B:431:LEU:HD22	1.86	0.41
3:L:29:ILE:HD13	3:L:29:ILE:HA	1.91	0.41
1:A:417:LYS:HD3	1:A:417:LYS:HA	1.82	0.41
1:B:359:MET:HG2	1:B:376:TYR:HB3	2.03	0.41
1:C:93:LEU:HD12	1:C:93:LEU:HA	1.86	0.41
1:C:126:TRP:HH2	1:C:166:ILE:HD13	1.86	0.41
2:E:48:ILE:HG23	2:E:63:VAL:HG21	2.03	0.41
1:A:37:LEU:HD22	1:A:315:LEU:HD12	2.03	0.40
1:A:339:ALA:HB2	1:A:450:LYS:HB3	2.02	0.40
1:A:389:ILE:HG12	1:A:433:LEU:HD21	2.03	0.40
2:H:89:VAL:HG12	2:H:108:THR:HB	2.04	0.40
2:E:40:ALA:HB3	2:E:43:LYS:HB2	2.04	0.40
3:F:29:ILE:HD13	3:F:29:ILE:HA	1.90	0.40
1:A:322:ARG:HD2	1:A:442:LEU:HD22	2.03	0.40
1:B:180:TRP:CE2	1:B:204:VAL:HG21	2.57	0.40
2:H:100(H):MET:HB2	3:L:36:TYR:OH	2.21	0.40

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	487/576 (84%)	465 (96%)	22 (4%)	0	100	100
1	B	487/576 (84%)	459 (94%)	28 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	487/576 (84%)	452 (93%)	35 (7%)	0	100	100
2	D	122/258 (47%)	102 (84%)	17 (14%)	3 (2%)	4	28
2	E	122/258 (47%)	106 (87%)	14 (12%)	2 (2%)	7	36
2	H	122/258 (47%)	108 (88%)	11 (9%)	3 (2%)	4	28
3	F	106/234 (45%)	95 (90%)	9 (8%)	2 (2%)	6	32
3	G	106/234 (45%)	94 (89%)	12 (11%)	0	100	100
3	L	106/234 (45%)	96 (91%)	9 (8%)	1 (1%)	14	47
All	All	2145/3204 (67%)	1977 (92%)	157 (7%)	11 (0%)	26	58

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	100(D)	TYR
2	D	100(D)	TYR
2	E	100(D)	TYR
2	H	90	TYR
2	D	90	TYR
2	E	90	TYR
2	H	52(A)	TYR
3	L	28	ASN
2	D	52(A)	TYR
3	F	28	ASN
3	F	92	TYR

### 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	431/502 (86%)	423 (98%)	8 (2%)	50	67
1	B	431/502 (86%)	422 (98%)	9 (2%)	47	66
1	C	431/502 (86%)	425 (99%)	6 (1%)	59	71
2	D	104/220 (47%)	97 (93%)	7 (7%)	15	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	104/220 (47%)	96 (92%)	8 (8%)	12	37
2	H	104/220 (47%)	99 (95%)	5 (5%)	23	49
3	F	92/203 (45%)	90 (98%)	2 (2%)	45	65
3	G	92/203 (45%)	90 (98%)	2 (2%)	45	65
3	L	92/203 (45%)	92 (100%)	0	100	100
All	All	1881/2775 (68%)	1834 (98%)	47 (2%)	42	63

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	TYR
1	A	40	THR
1	A	55	ILE
1	A	109	LEU
1	A	265	ASP
1	A	407	LEU
1	A	433	LEU
1	A	460	LEU
1	B	11	TYR
1	B	12	HIS
1	B	174	GLU
1	B	210	ASN
1	B	230	MET
1	B	440	LEU
1	B	441	LEU
1	B	491	MET
1	B	504	TYR
1	C	174	GLU
1	C	179	LEU
1	C	286	CYS
1	C	301	MET
1	C	415	LEU
1	C	447	GLU
2	H	11	VAL
2	H	23	THR
2	H	72	ASP
2	H	97	ILE
2	H	102	VAL
2	D	5	VAL
2	D	11	VAL

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Mol	Chain	Res	Type
2	D	28	THR
2	D	72	ASP
2	D	85	GLU
2	D	97	ILE
2	D	102	VAL
3	F	21	ILE
3	F	92	TYR
2	E	5	VAL
2	E	11	VAL
2	E	28	THR
2	E	72	ASP
2	E	77	THR
2	E	85	GLU
2	E	97	ILE
2	E	99	LEU
3	G	21	ILE
3	G	96	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	107	HIS
1	A	210	ASN
1	A	211	GLN
1	A	279	ASN
1	A	415	ASN
1	A	429	ASN
1	A	469	ASN
1	B	6	GLN
1	B	158	ASN
1	B	187	ASN
1	B	211	GLN
1	B	423	ASN
1	C	15	ASN
1	C	68	ASN
1	C	113	ASN
1	C	119	GLN
1	C	244	HIS
1	C	357	GLN
1	C	413	ASN
1	C	414	ASN

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Mol	Chain	Res	Type
1	C	423	ASN
2	H	73	ASN
3	L	34	ASN
3	L	89	GLN
3	F	34	ASN
3	F	89	GLN
2	E	73	ASN
2	E	76	ASN
3	G	34	ASN
3	G	38	GLN
3	G	55	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](#)

12 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	604	1	14,14,15	0.70	0	17,19,21	0.84	0
4	NAG	C	603	1	14,14,15	0.74	0	17,19,21	1.18	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	C	602	1	14,14,15	0.68	0	17,19,21	0.93	1 (5%)
4	NAG	A	602	1	14,14,15	0.67	0	17,19,21	0.93	1 (5%)
4	NAG	A	601	1	14,14,15	0.72	0	17,19,21	0.79	0
4	NAG	B	601	1	14,14,15	0.72	0	17,19,21	0.80	0
4	NAG	C	601	1	14,14,15	0.72	0	17,19,21	0.83	0
4	NAG	C	604	1	14,14,15	0.68	0	17,19,21	0.87	1 (5%)
4	NAG	B	603	1	14,14,15	0.71	1 (7%)	17,19,21	1.70	2 (11%)
4	NAG	A	604	1	14,14,15	0.70	0	17,19,21	0.85	0
4	NAG	B	602	1	14,14,15	0.67	0	17,19,21	0.89	1 (5%)
4	NAG	A	603	1	14,14,15	0.83	1 (7%)	17,19,21	2.03	3 (17%)

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	604	1	-	0/6/23/26	0/1/1/1
4	NAG	C	603	1	-	4/6/23/26	0/1/1/1
4	NAG	C	602	1	-	0/6/23/26	0/1/1/1
4	NAG	A	602	1	-	0/6/23/26	0/1/1/1
4	NAG	A	601	1	-	0/6/23/26	0/1/1/1
4	NAG	B	601	1	-	0/6/23/26	0/1/1/1
4	NAG	C	601	1	-	0/6/23/26	0/1/1/1
4	NAG	C	604	1	-	0/6/23/26	0/1/1/1
4	NAG	B	603	1	-	4/6/23/26	0/1/1/1
4	NAG	A	604	1	-	1/6/23/26	0/1/1/1
4	NAG	B	602	1	-	1/6/23/26	0/1/1/1
4	NAG	A	603	1	-	3/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	NAG	C1-C2	2.35	1.55	1.52
4	B	603	NAG	C1-C2	2.02	1.55	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	NAG	C1-O5-C5	5.72	119.86	112.19

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	NAG	C2-N2-C7	4.20	128.53	122.90
4	B	603	NAG	C2-N2-C7	4.09	128.38	122.90
4	B	603	NAG	O5-C5-C6	3.96	115.37	107.66
4	C	603	NAG	C2-N2-C7	3.58	127.70	122.90
4	A	602	NAG	O5-C1-C2	-2.34	107.67	111.29
4	A	603	NAG	O7-C7-N2	2.23	125.92	121.98
4	C	602	NAG	O5-C1-C2	-2.21	107.87	111.29
4	C	604	NAG	O5-C1-C2	-2.07	108.10	111.29
4	B	602	NAG	O5-C1-C2	-2.04	108.13	111.29

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	603	NAG	C4-C5-C6-O6
4	B	603	NAG	C4-C5-C6-O6
4	B	603	NAG	O5-C5-C6-O6
4	C	603	NAG	O5-C5-C6-O6
4	C	603	NAG	C8-C7-N2-C2
4	C	603	NAG	O7-C7-N2-C2
4	A	604	NAG	O5-C5-C6-O6
4	A	603	NAG	O5-C5-C6-O6
4	A	603	NAG	C1-C2-N2-C7
4	A	603	NAG	C3-C2-N2-C7
4	B	603	NAG	C1-C2-N2-C7
4	B	603	NAG	C3-C2-N2-C7
4	B	602	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	603	NAG	2	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

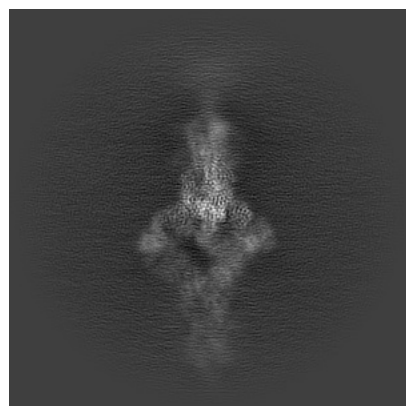
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74879. These allow visual inspection of the internal detail of the map and identification of artifacts.

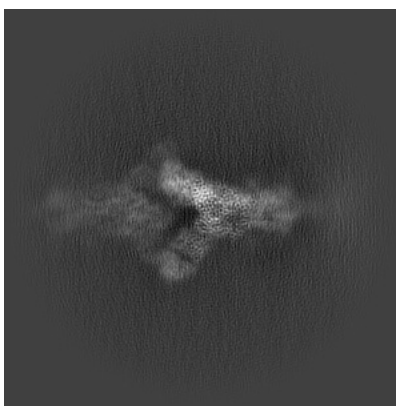
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

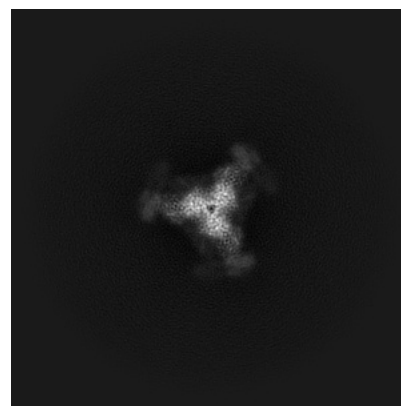
#### 6.1.1 Primary map



X

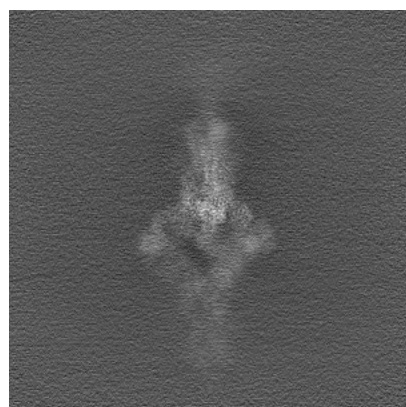


Y

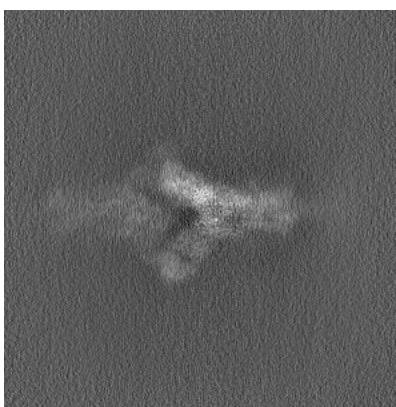


Z

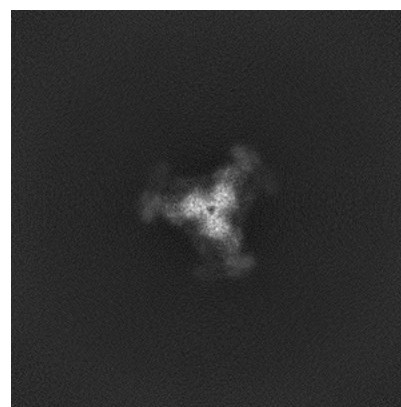
#### 6.1.2 Raw map



X



Y

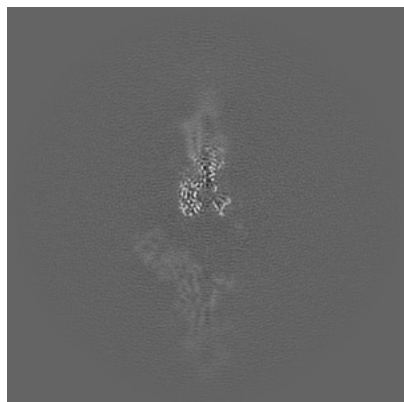


Z

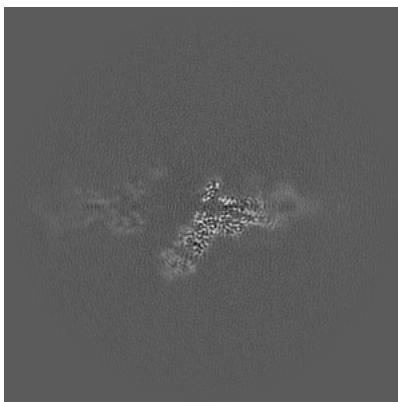
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

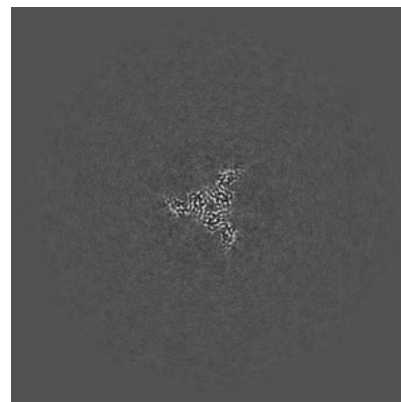
### 6.2.1 Primary map



X Index: 300

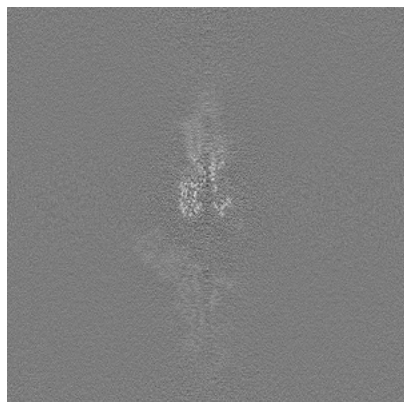


Y Index: 300

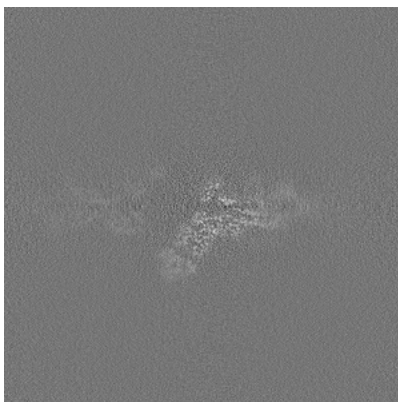


Z Index: 300

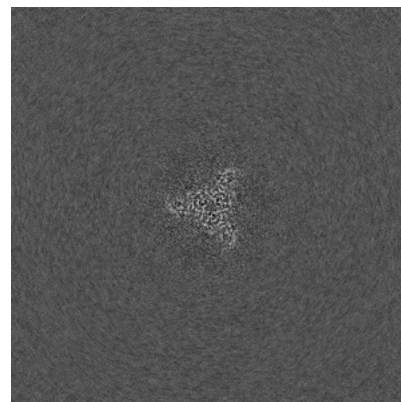
### 6.2.2 Raw map



X Index: 300



Y Index: 300

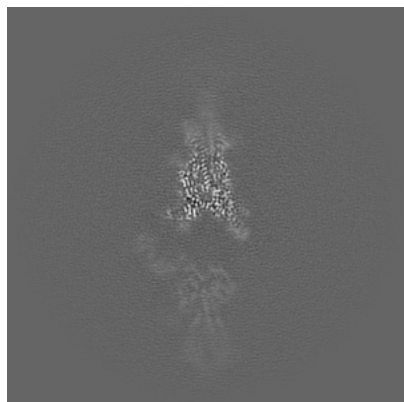


Z Index: 300

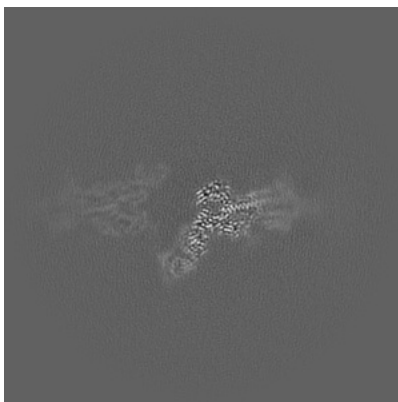
The images above show central slices of the map in three orthogonal directions.

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

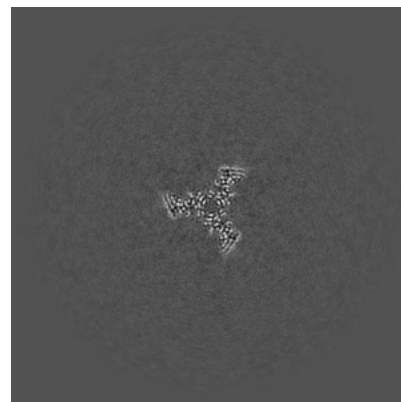
### 6.3.1 Primary map



X Index: 310

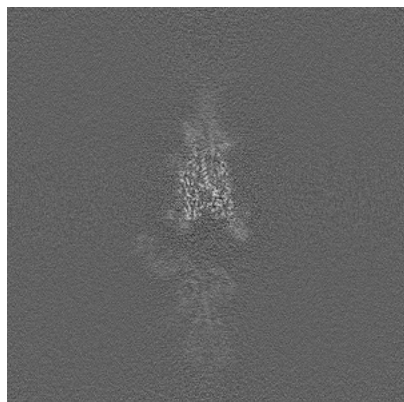


Y Index: 308

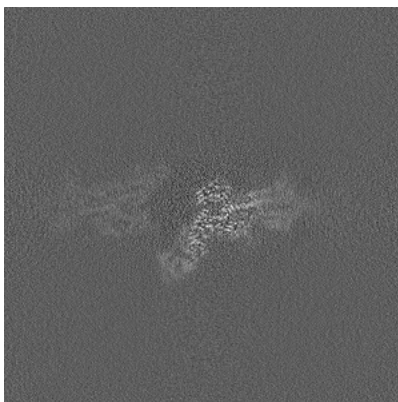


Z Index: 297

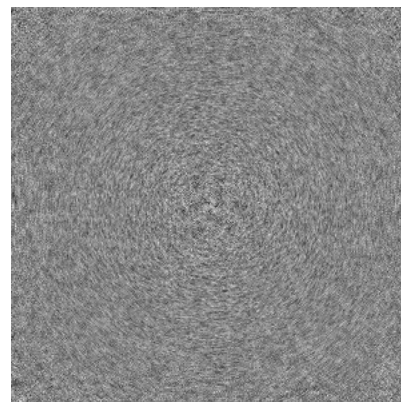
### 6.3.2 Raw map



X Index: 309



Y Index: 308

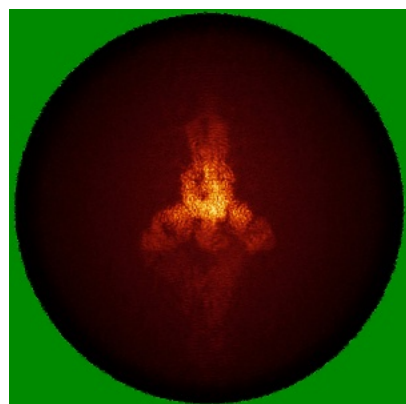


Z Index: 1

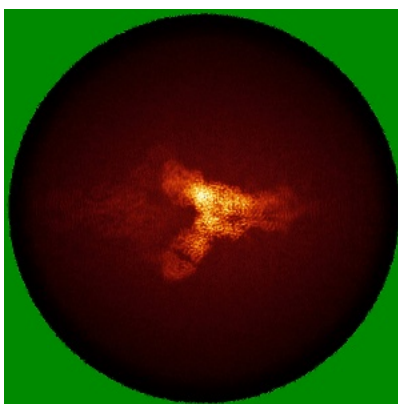
The images above show the largest variance slices of the map in three orthogonal directions.

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

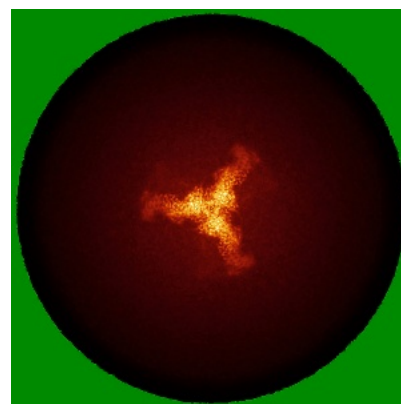
### 6.4.1 Primary map



X

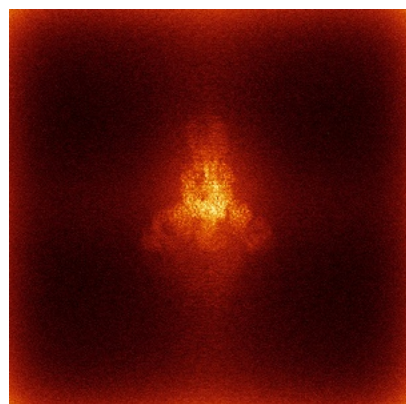


Y

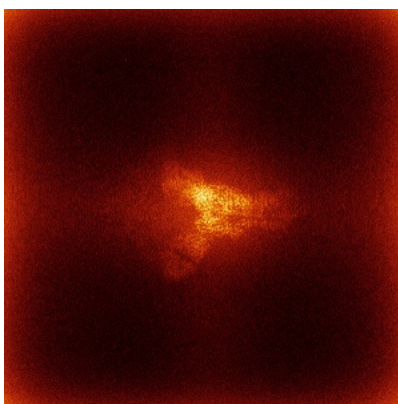


Z

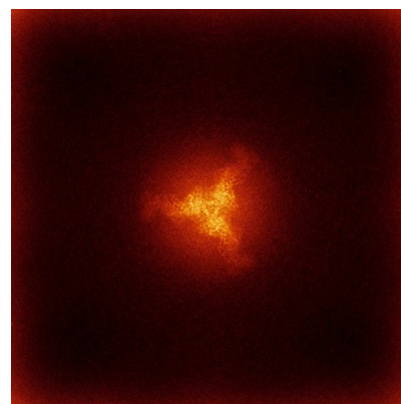
### 6.4.2 Raw map



X



Y

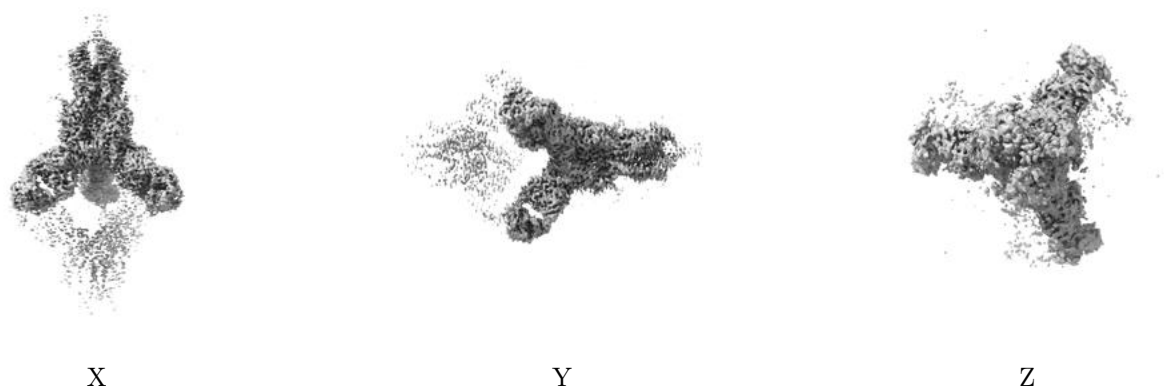


Z

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.

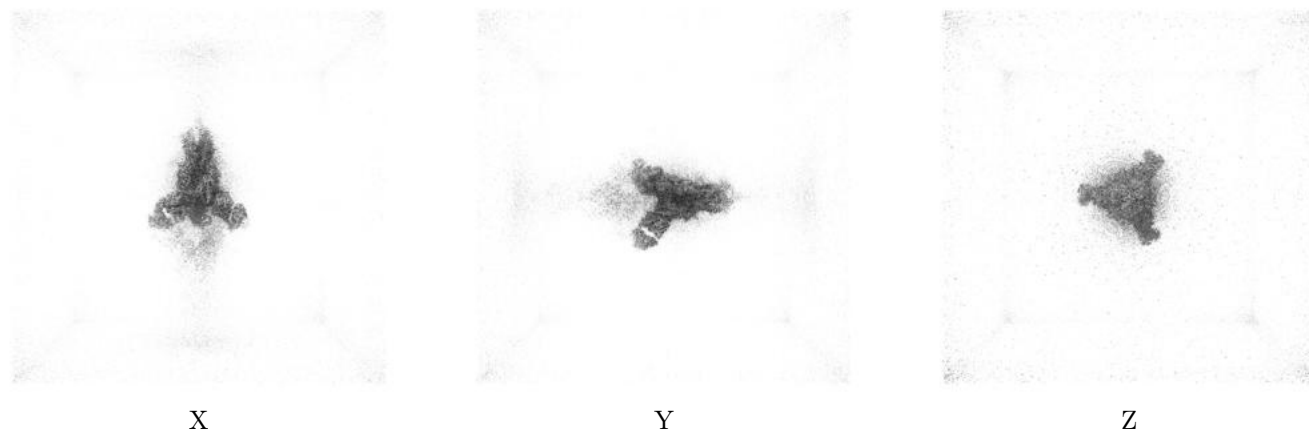
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0823. 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.

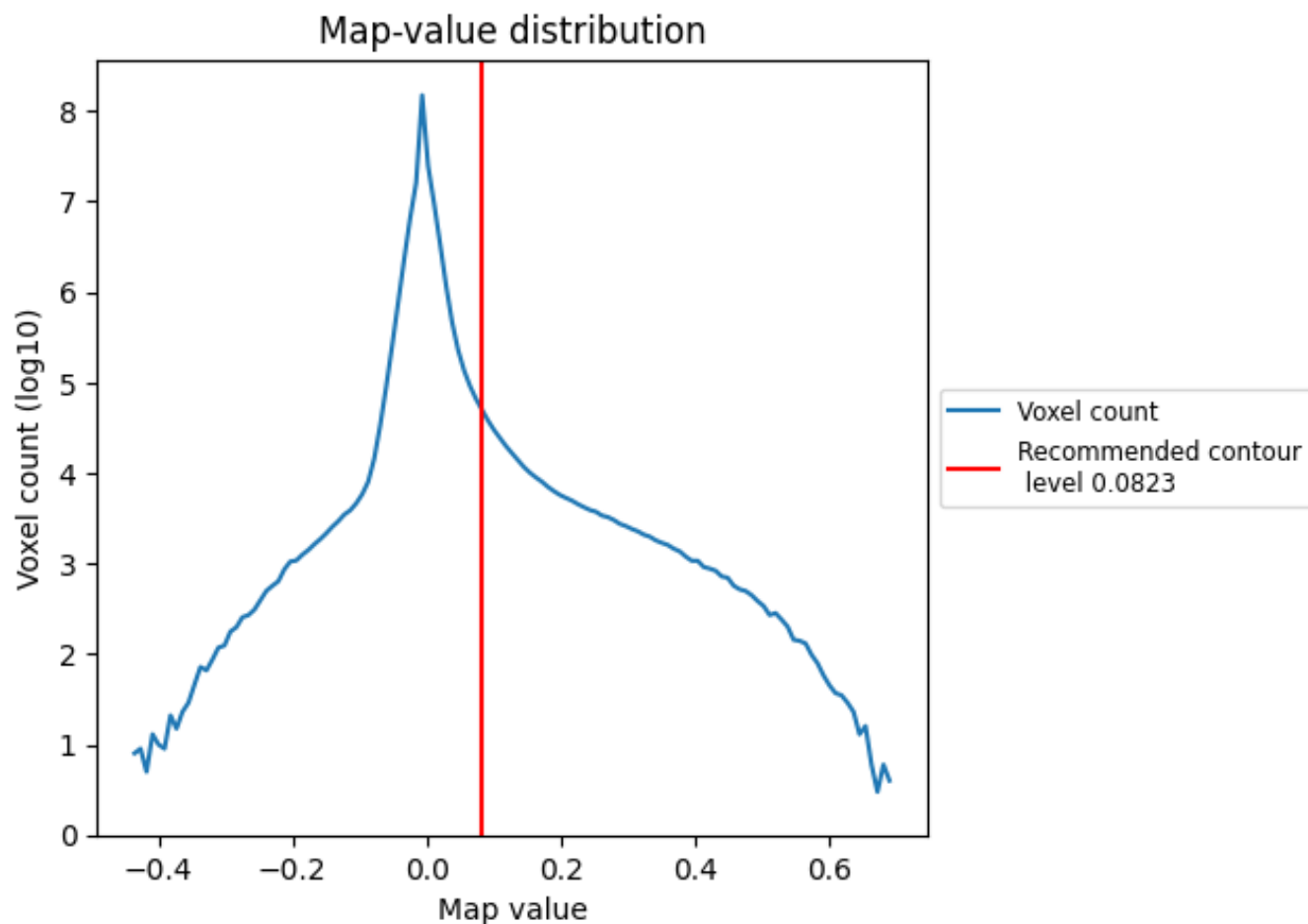
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

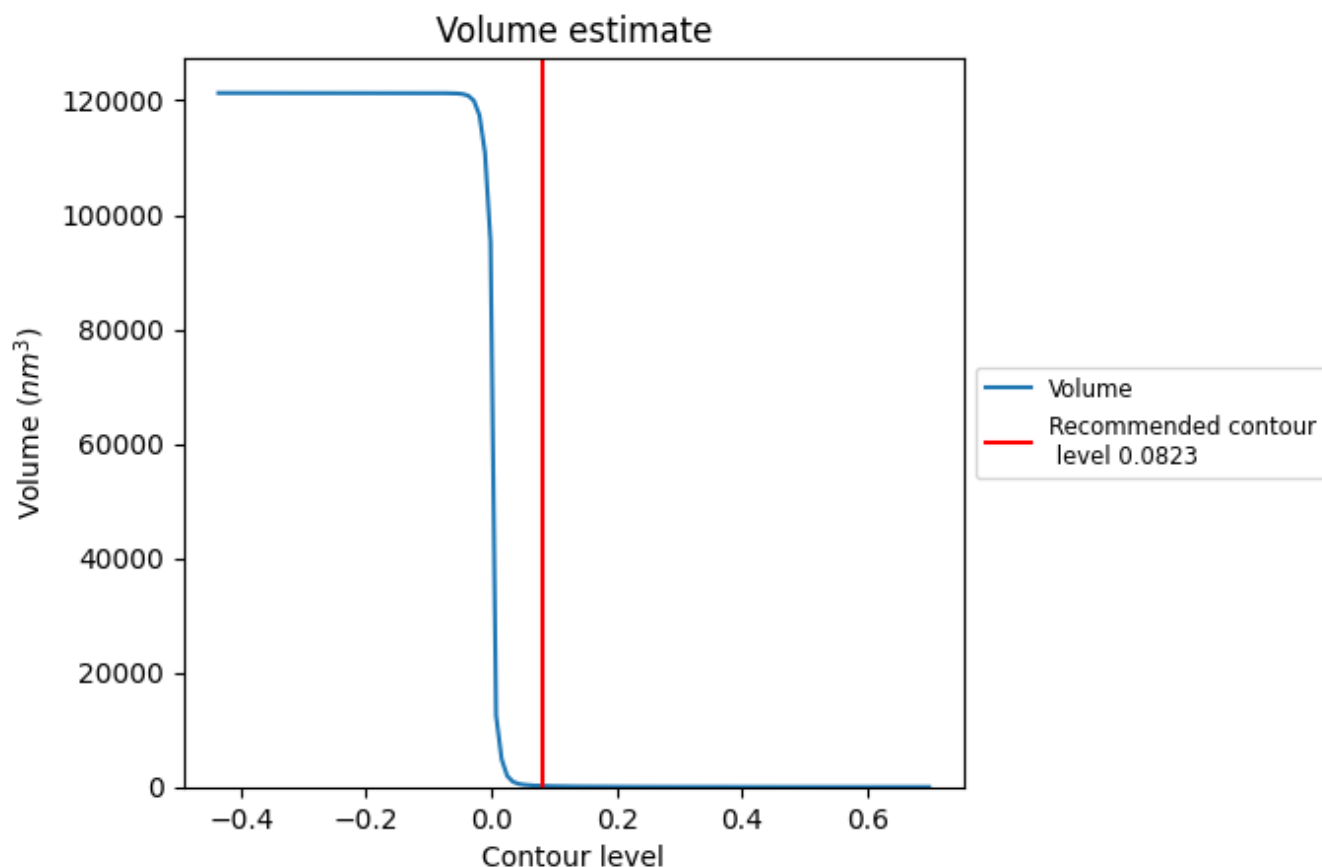
This section contains the results of statistical analysis of the map.

### 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.

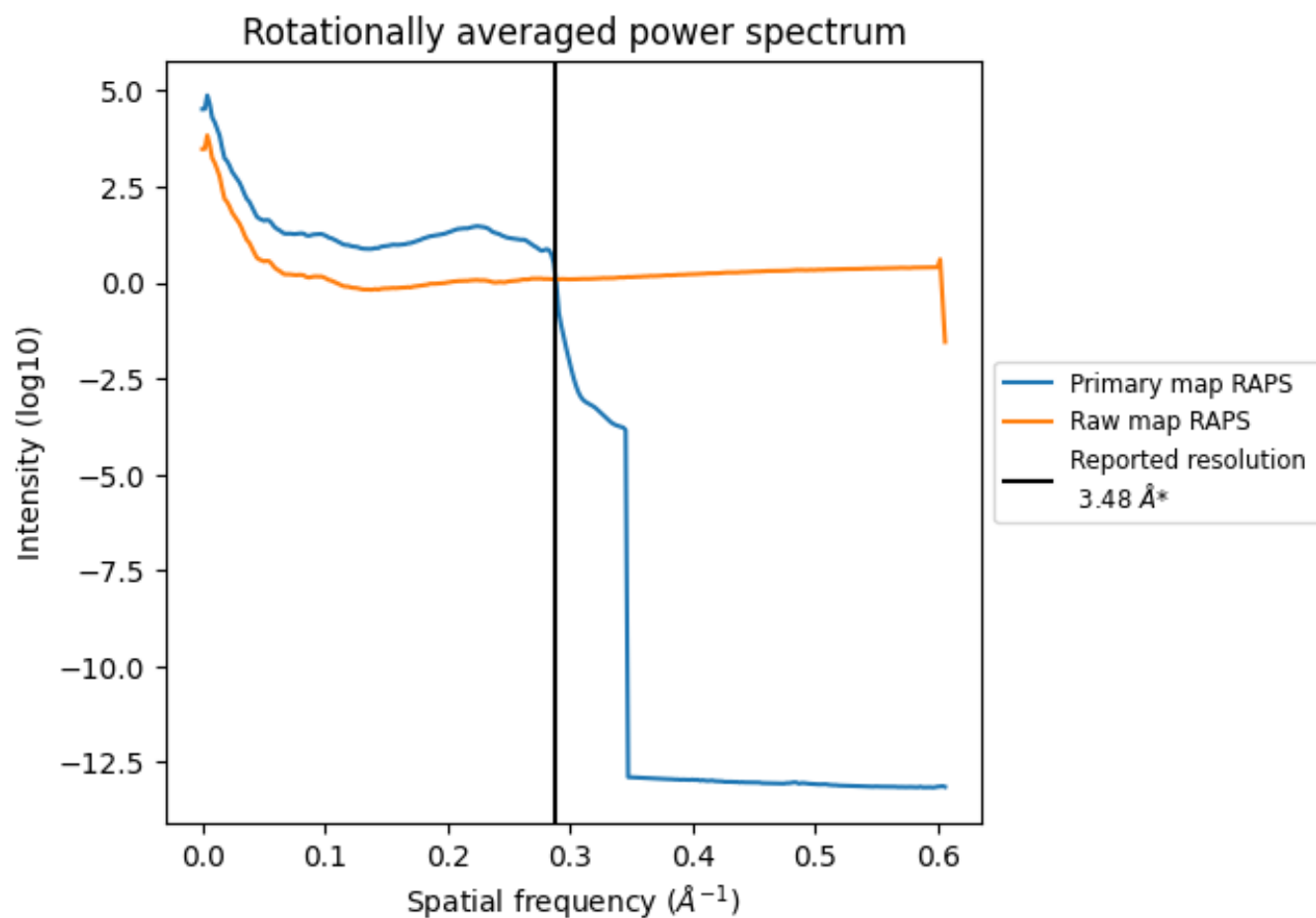
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 181 nm<sup>3</sup>; this corresponds to an approximate mass of 163 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 ⓘ

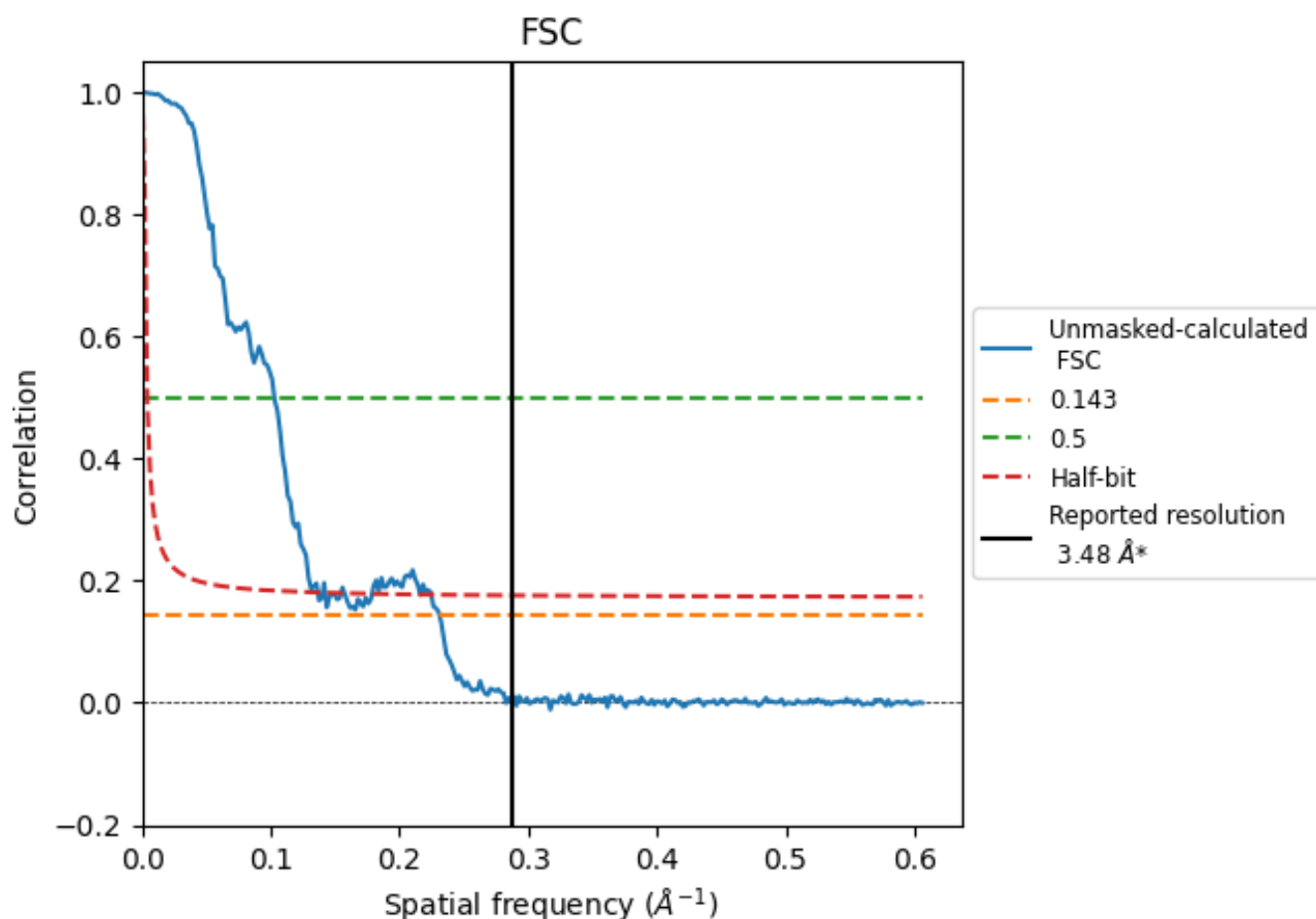


\*Reported resolution corresponds to spatial frequency of 0.287 Å<sup>-1</sup>

## 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  $0.287 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

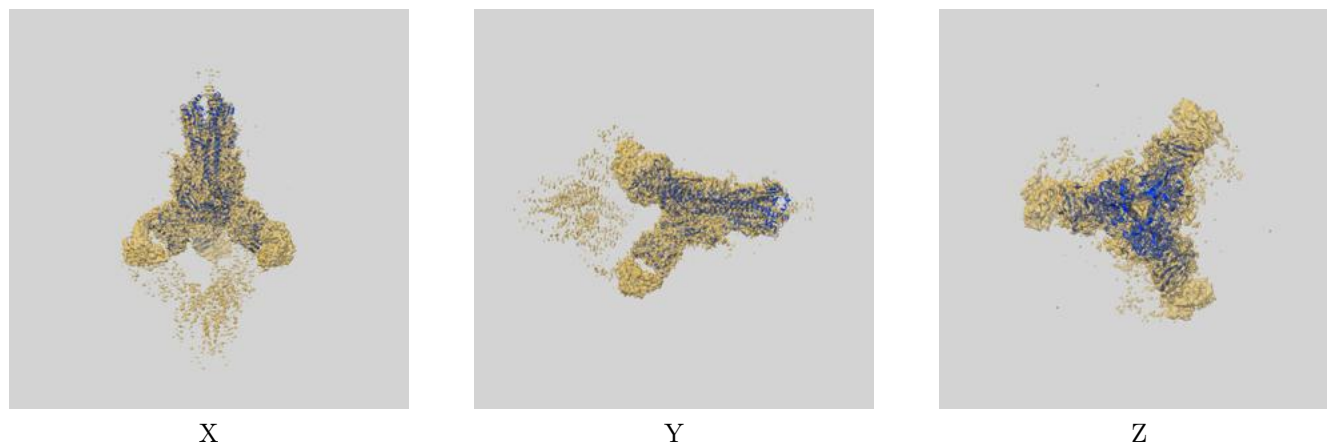
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.33	9.74	7.33

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

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

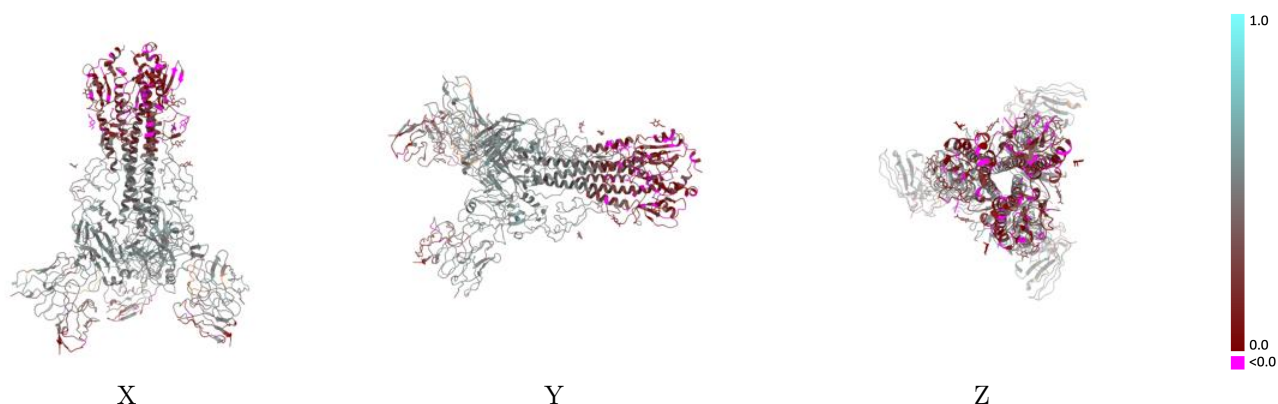
This section contains information regarding the fit between EMDB map EMD-74879 and PDB model 9ZVL. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

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



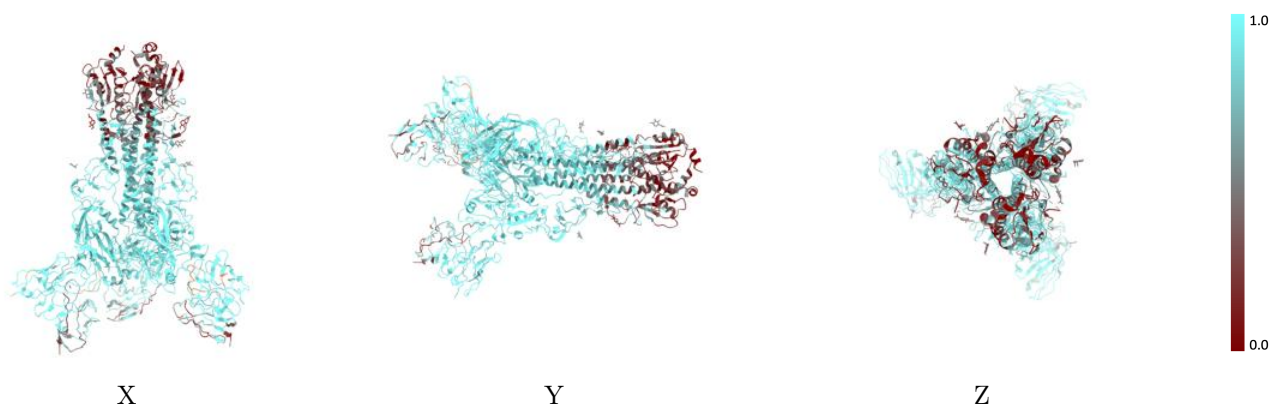
The images above show the 3D surface view of the map at the recommended contour level 0.0823 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



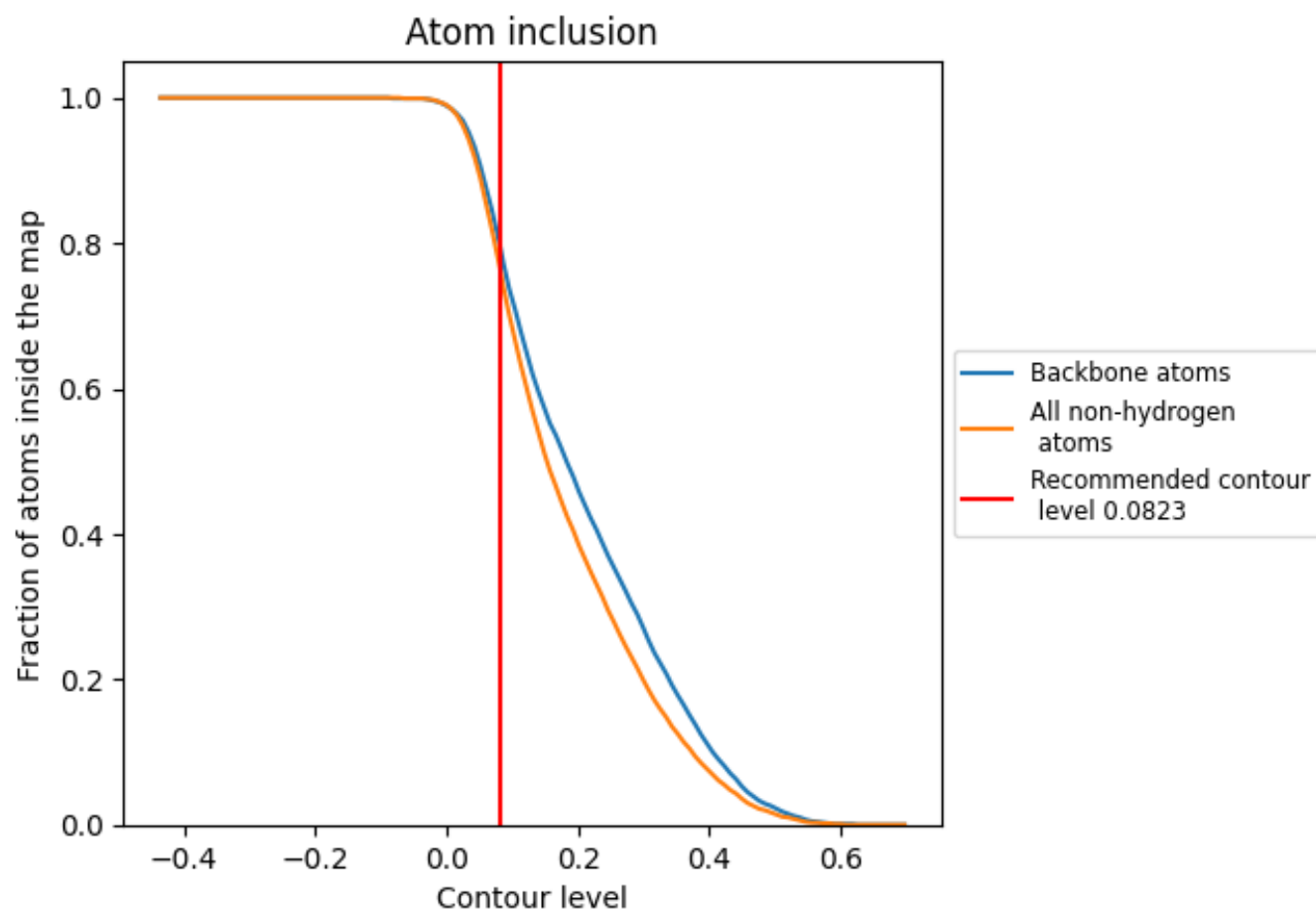
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0823).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 76% 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 (0.0823) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7630	<div></div> 0.3980
A	<div></div> 0.7440	<div></div> 0.3890
B	<div></div> 0.7370	<div></div> 0.3850
C	<div></div> 0.7480	<div></div> 0.3890
D	<div></div> 0.9100	<div></div> 0.4840
E	<div></div> 0.9090	<div></div> 0.4860
F	<div></div> 0.6800	<div></div> 0.3410
G	<div></div> 0.6740	<div></div> 0.3420
H	<div></div> 0.9180	<div></div> 0.4850
L	<div></div> 0.6840	<div></div> 0.3390

1.0

0.0

<0.0