



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 05:54 PM UTC

PDB ID : 9OAL / pdb_00009oal
EMDB ID : EMD-70288
Title : Cryo-EM structure of EBV gB prefusion construct C3-GT
Authors : McCool, R.S.; McLellan, J.S.
Deposited on : 2025-04-21
Resolution : 3.10 Å (reported)
Based on initial model : .

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at 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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

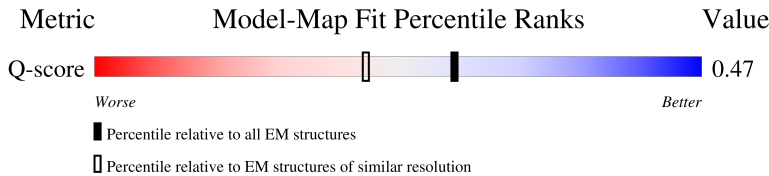
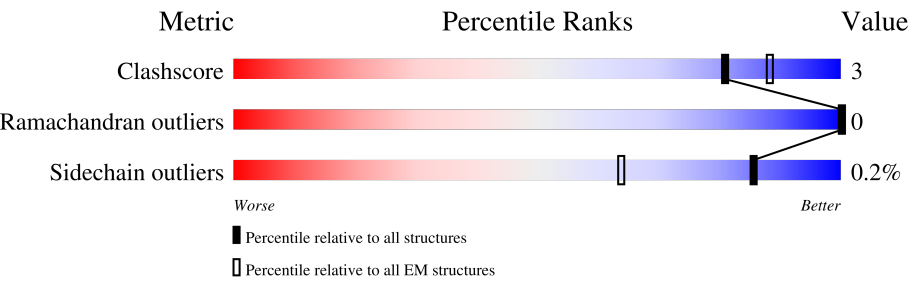
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.10 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	14724 (2.60 - 3.60)

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 ≥ 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	775	
1	B	775	
1	C	775	
2	D	3	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain	
2	E	3		33%
2	F	3		33%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13059 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 Envelope glycoprotein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	540	Total	C	N	O	S	0	0
			4314	2716	734	838	26		
1	B	540	Total	C	N	O	S	0	0
			4314	2716	734	838	26		
1	C	540	Total	C	N	O	S	0	0
			4314	2716	734	838	26		

There are 327 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	CYS	ILE	engineered mutation	UNP P0C762
A	112	HIS	TRP	engineered mutation	UNP P0C762
A	113	ARG	TYR	engineered mutation	UNP P0C762
A	128	GLU	ASP	conflict	UNP P0C762
A	175	CYS	ALA	engineered mutation	UNP P0C762
A	193	ARG	TRP	engineered mutation	UNP P0C762
A	194	VAL	LEU	engineered mutation	UNP P0C762
A	195	GLU	ILE	engineered mutation	UNP P0C762
A	196	ALA	TRP	engineered mutation	UNP P0C762
A	220	GLU	ASP	engineered mutation	UNP P0C762
A	241	THR	LYS	conflict	UNP P0C762
A	316	ILE	HIS	engineered mutation	UNP P0C762
A	320	GLN	ASP	engineered mutation	UNP P0C762
A	325	LEU	SER	engineered mutation	UNP P0C762
A	428	GLY	ARG	engineered mutation	UNP P0C762
A	429	GLY	ARG	engineered mutation	UNP P0C762
A	430	SER	ARG	conflict	UNP P0C762
A	431	GLY	ARG	engineered mutation	UNP P0C762
A	432	GLY	ARG	engineered mutation	UNP P0C762
A	433	ASN	ASP	conflict	UNP P0C762
A	628A	GLY	-	insertion	UNP P0C762
A	628B	CYS	-	insertion	UNP P0C762
A	628C	GLY	LEU	conflict	UNP P0C762
A	634	CYS	GLU	engineered mutation	UNP P0C762

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	689	GLY	-	expression tag	UNP P0C762
A	690	GLY	-	expression tag	UNP P0C762
A	691	SER	-	expression tag	UNP P0C762
A	692	GLY	-	expression tag	UNP P0C762
A	693	TYR	-	expression tag	UNP P0C762
A	694	ILE	-	expression tag	UNP P0C762
A	695	PRO	-	expression tag	UNP P0C762
A	696	GLU	-	expression tag	UNP P0C762
A	697	ALA	-	expression tag	UNP P0C762
A	698	PRO	-	expression tag	UNP P0C762
A	699	ARG	-	expression tag	UNP P0C762
A	700	ASP	-	expression tag	UNP P0C762
A	701	GLY	-	expression tag	UNP P0C762
A	702	GLN	-	expression tag	UNP P0C762
A	703	ALA	-	expression tag	UNP P0C762
A	704	TYR	-	expression tag	UNP P0C762
A	705	VAL	-	expression tag	UNP P0C762
A	706	ARG	-	expression tag	UNP P0C762
A	707	LYS	-	expression tag	UNP P0C762
A	708	ASP	-	expression tag	UNP P0C762
A	709	GLY	-	expression tag	UNP P0C762
A	710	GLU	-	expression tag	UNP P0C762
A	711	TRP	-	expression tag	UNP P0C762
A	712	VAL	-	expression tag	UNP P0C762
A	713	LEU	-	expression tag	UNP P0C762
A	714	LEU	-	expression tag	UNP P0C762
A	715	SER	-	expression tag	UNP P0C762
A	716	THR	-	expression tag	UNP P0C762
A	717	PHE	-	expression tag	UNP P0C762
A	718	LEU	-	expression tag	UNP P0C762
A	719	GLY	-	expression tag	UNP P0C762
A	720	ARG	-	expression tag	UNP P0C762
A	721	ALA	-	expression tag	UNP P0C762
A	722	ALA	-	expression tag	UNP P0C762
A	723	ALA	-	expression tag	UNP P0C762
A	724	SER	-	expression tag	UNP P0C762
A	725	SER	-	expression tag	UNP P0C762
A	726	LEU	-	expression tag	UNP P0C762
A	727	GLU	-	expression tag	UNP P0C762
A	728	VAL	-	expression tag	UNP P0C762
A	729	LEU	-	expression tag	UNP P0C762
A	730	PHE	-	expression tag	UNP P0C762

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	731	GLN	-	expression tag	UNP P0C762
A	732	GLY	-	expression tag	UNP P0C762
A	733	PRO	-	expression tag	UNP P0C762
A	734	GLY	-	expression tag	UNP P0C762
A	735	HIS	-	expression tag	UNP P0C762
A	736	HIS	-	expression tag	UNP P0C762
A	737	HIS	-	expression tag	UNP P0C762
A	738	HIS	-	expression tag	UNP P0C762
A	739	HIS	-	expression tag	UNP P0C762
A	740	HIS	-	expression tag	UNP P0C762
A	741	HIS	-	expression tag	UNP P0C762
A	742	HIS	-	expression tag	UNP P0C762
A	743	SER	-	expression tag	UNP P0C762
A	744	ALA	-	expression tag	UNP P0C762
A	745	TRP	-	expression tag	UNP P0C762
A	746	SER	-	expression tag	UNP P0C762
A	747	HIS	-	expression tag	UNP P0C762
A	748	PRO	-	expression tag	UNP P0C762
A	749	GLN	-	expression tag	UNP P0C762
A	750	PHE	-	expression tag	UNP P0C762
A	751	GLU	-	expression tag	UNP P0C762
A	752	LYS	-	expression tag	UNP P0C762
A	753	GLY	-	expression tag	UNP P0C762
A	754	GLY	-	expression tag	UNP P0C762
A	755	GLY	-	expression tag	UNP P0C762
A	756	SER	-	expression tag	UNP P0C762
A	757	GLY	-	expression tag	UNP P0C762
A	758	GLY	-	expression tag	UNP P0C762
A	759	GLY	-	expression tag	UNP P0C762
A	760	GLY	-	expression tag	UNP P0C762
A	761	SER	-	expression tag	UNP P0C762
A	762	GLY	-	expression tag	UNP P0C762
A	763	GLY	-	expression tag	UNP P0C762
A	764	SER	-	expression tag	UNP P0C762
A	765	ALA	-	expression tag	UNP P0C762
A	766	TRP	-	expression tag	UNP P0C762
A	767	SER	-	expression tag	UNP P0C762
A	768	HIS	-	expression tag	UNP P0C762
A	769	PRO	-	expression tag	UNP P0C762
A	770	GLN	-	expression tag	UNP P0C762
A	771	PHE	-	expression tag	UNP P0C762
A	772	GLU	-	expression tag	UNP P0C762

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	773	LYS	-	expression tag	UNP P0C762
B	89	CYS	ILE	engineered mutation	UNP P0C762
B	112	HIS	TRP	engineered mutation	UNP P0C762
B	113	ARG	TYR	engineered mutation	UNP P0C762
B	128	GLU	ASP	conflict	UNP P0C762
B	175	CYS	ALA	engineered mutation	UNP P0C762
B	193	ARG	TRP	engineered mutation	UNP P0C762
B	194	VAL	LEU	engineered mutation	UNP P0C762
B	195	GLU	ILE	engineered mutation	UNP P0C762
B	196	ALA	TRP	engineered mutation	UNP P0C762
B	220	GLU	ASP	engineered mutation	UNP P0C762
B	241	THR	LYS	conflict	UNP P0C762
B	316	ILE	HIS	engineered mutation	UNP P0C762
B	320	GLN	ASP	engineered mutation	UNP P0C762
B	325	LEU	SER	engineered mutation	UNP P0C762
B	428	GLY	ARG	engineered mutation	UNP P0C762
B	429	GLY	ARG	engineered mutation	UNP P0C762
B	430	SER	ARG	conflict	UNP P0C762
B	431	GLY	ARG	engineered mutation	UNP P0C762
B	432	GLY	ARG	engineered mutation	UNP P0C762
B	433	ASN	ASP	conflict	UNP P0C762
B	628A	GLY	-	insertion	UNP P0C762
B	628B	CYS	-	insertion	UNP P0C762
B	628C	GLY	LEU	conflict	UNP P0C762
B	634	CYS	GLU	engineered mutation	UNP P0C762
B	689	GLY	-	expression tag	UNP P0C762
B	690	GLY	-	expression tag	UNP P0C762
B	691	SER	-	expression tag	UNP P0C762
B	692	GLY	-	expression tag	UNP P0C762
B	693	TYR	-	expression tag	UNP P0C762
B	694	ILE	-	expression tag	UNP P0C762
B	695	PRO	-	expression tag	UNP P0C762
B	696	GLU	-	expression tag	UNP P0C762
B	697	ALA	-	expression tag	UNP P0C762
B	698	PRO	-	expression tag	UNP P0C762
B	699	ARG	-	expression tag	UNP P0C762
B	700	ASP	-	expression tag	UNP P0C762
B	701	GLY	-	expression tag	UNP P0C762
B	702	GLN	-	expression tag	UNP P0C762
B	703	ALA	-	expression tag	UNP P0C762
B	704	TYR	-	expression tag	UNP P0C762
B	705	VAL	-	expression tag	UNP P0C762

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	706	ARG	-	expression tag	UNP P0C762
B	707	LYS	-	expression tag	UNP P0C762
B	708	ASP	-	expression tag	UNP P0C762
B	709	GLY	-	expression tag	UNP P0C762
B	710	GLU	-	expression tag	UNP P0C762
B	711	TRP	-	expression tag	UNP P0C762
B	712	VAL	-	expression tag	UNP P0C762
B	713	LEU	-	expression tag	UNP P0C762
B	714	LEU	-	expression tag	UNP P0C762
B	715	SER	-	expression tag	UNP P0C762
B	716	THR	-	expression tag	UNP P0C762
B	717	PHE	-	expression tag	UNP P0C762
B	718	LEU	-	expression tag	UNP P0C762
B	719	GLY	-	expression tag	UNP P0C762
B	720	ARG	-	expression tag	UNP P0C762
B	721	ALA	-	expression tag	UNP P0C762
B	722	ALA	-	expression tag	UNP P0C762
B	723	ALA	-	expression tag	UNP P0C762
B	724	SER	-	expression tag	UNP P0C762
B	725	SER	-	expression tag	UNP P0C762
B	726	LEU	-	expression tag	UNP P0C762
B	727	GLU	-	expression tag	UNP P0C762
B	728	VAL	-	expression tag	UNP P0C762
B	729	LEU	-	expression tag	UNP P0C762
B	730	PHE	-	expression tag	UNP P0C762
B	731	GLN	-	expression tag	UNP P0C762
B	732	GLY	-	expression tag	UNP P0C762
B	733	PRO	-	expression tag	UNP P0C762
B	734	GLY	-	expression tag	UNP P0C762
B	735	HIS	-	expression tag	UNP P0C762
B	736	HIS	-	expression tag	UNP P0C762
B	737	HIS	-	expression tag	UNP P0C762
B	738	HIS	-	expression tag	UNP P0C762
B	739	HIS	-	expression tag	UNP P0C762
B	740	HIS	-	expression tag	UNP P0C762
B	741	HIS	-	expression tag	UNP P0C762
B	742	HIS	-	expression tag	UNP P0C762
B	743	SER	-	expression tag	UNP P0C762
B	744	ALA	-	expression tag	UNP P0C762
B	745	TRP	-	expression tag	UNP P0C762
B	746	SER	-	expression tag	UNP P0C762
B	747	HIS	-	expression tag	UNP P0C762

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	748	PRO	-	expression tag	UNP P0C762
B	749	GLN	-	expression tag	UNP P0C762
B	750	PHE	-	expression tag	UNP P0C762
B	751	GLU	-	expression tag	UNP P0C762
B	752	LYS	-	expression tag	UNP P0C762
B	753	GLY	-	expression tag	UNP P0C762
B	754	GLY	-	expression tag	UNP P0C762
B	755	GLY	-	expression tag	UNP P0C762
B	756	SER	-	expression tag	UNP P0C762
B	757	GLY	-	expression tag	UNP P0C762
B	758	GLY	-	expression tag	UNP P0C762
B	759	GLY	-	expression tag	UNP P0C762
B	760	GLY	-	expression tag	UNP P0C762
B	761	SER	-	expression tag	UNP P0C762
B	762	GLY	-	expression tag	UNP P0C762
B	763	GLY	-	expression tag	UNP P0C762
B	764	SER	-	expression tag	UNP P0C762
B	765	ALA	-	expression tag	UNP P0C762
B	766	TRP	-	expression tag	UNP P0C762
B	767	SER	-	expression tag	UNP P0C762
B	768	HIS	-	expression tag	UNP P0C762
B	769	PRO	-	expression tag	UNP P0C762
B	770	GLN	-	expression tag	UNP P0C762
B	771	PHE	-	expression tag	UNP P0C762
B	772	GLU	-	expression tag	UNP P0C762
B	773	LYS	-	expression tag	UNP P0C762
C	89	CYS	ILE	engineered mutation	UNP P0C762
C	112	HIS	TRP	engineered mutation	UNP P0C762
C	113	ARG	TYR	engineered mutation	UNP P0C762
C	128	GLU	ASP	conflict	UNP P0C762
C	175	CYS	ALA	engineered mutation	UNP P0C762
C	193	ARG	TRP	engineered mutation	UNP P0C762
C	194	VAL	LEU	engineered mutation	UNP P0C762
C	195	GLU	ILE	engineered mutation	UNP P0C762
C	196	ALA	TRP	engineered mutation	UNP P0C762
C	220	GLU	ASP	engineered mutation	UNP P0C762
C	241	THR	LYS	conflict	UNP P0C762
C	316	ILE	HIS	engineered mutation	UNP P0C762
C	320	GLN	ASP	engineered mutation	UNP P0C762
C	325	LEU	SER	engineered mutation	UNP P0C762
C	428	GLY	ARG	engineered mutation	UNP P0C762
C	429	GLY	ARG	engineered mutation	UNP P0C762

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	430	SER	ARG	conflict	UNP P0C762
C	431	GLY	ARG	engineered mutation	UNP P0C762
C	432	GLY	ARG	engineered mutation	UNP P0C762
C	433	ASN	ASP	conflict	UNP P0C762
C	628A	GLY	-	insertion	UNP P0C762
C	628B	CYS	-	insertion	UNP P0C762
C	628C	GLY	LEU	conflict	UNP P0C762
C	634	CYS	GLU	engineered mutation	UNP P0C762
C	689	GLY	-	expression tag	UNP P0C762
C	690	GLY	-	expression tag	UNP P0C762
C	691	SER	-	expression tag	UNP P0C762
C	692	GLY	-	expression tag	UNP P0C762
C	693	TYR	-	expression tag	UNP P0C762
C	694	ILE	-	expression tag	UNP P0C762
C	695	PRO	-	expression tag	UNP P0C762
C	696	GLU	-	expression tag	UNP P0C762
C	697	ALA	-	expression tag	UNP P0C762
C	698	PRO	-	expression tag	UNP P0C762
C	699	ARG	-	expression tag	UNP P0C762
C	700	ASP	-	expression tag	UNP P0C762
C	701	GLY	-	expression tag	UNP P0C762
C	702	GLN	-	expression tag	UNP P0C762
C	703	ALA	-	expression tag	UNP P0C762
C	704	TYR	-	expression tag	UNP P0C762
C	705	VAL	-	expression tag	UNP P0C762
C	706	ARG	-	expression tag	UNP P0C762
C	707	LYS	-	expression tag	UNP P0C762
C	708	ASP	-	expression tag	UNP P0C762
C	709	GLY	-	expression tag	UNP P0C762
C	710	GLU	-	expression tag	UNP P0C762
C	711	TRP	-	expression tag	UNP P0C762
C	712	VAL	-	expression tag	UNP P0C762
C	713	LEU	-	expression tag	UNP P0C762
C	714	LEU	-	expression tag	UNP P0C762
C	715	SER	-	expression tag	UNP P0C762
C	716	THR	-	expression tag	UNP P0C762
C	717	PHE	-	expression tag	UNP P0C762
C	718	LEU	-	expression tag	UNP P0C762
C	719	GLY	-	expression tag	UNP P0C762
C	720	ARG	-	expression tag	UNP P0C762
C	721	ALA	-	expression tag	UNP P0C762
C	722	ALA	-	expression tag	UNP P0C762

Continued on next page...

Continued from previous page...

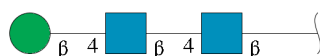
Chain	Residue	Modelled	Actual	Comment	Reference
C	723	ALA	-	expression tag	UNP P0C762
C	724	SER	-	expression tag	UNP P0C762
C	725	SER	-	expression tag	UNP P0C762
C	726	LEU	-	expression tag	UNP P0C762
C	727	GLU	-	expression tag	UNP P0C762
C	728	VAL	-	expression tag	UNP P0C762
C	729	LEU	-	expression tag	UNP P0C762
C	730	PHE	-	expression tag	UNP P0C762
C	731	GLN	-	expression tag	UNP P0C762
C	732	GLY	-	expression tag	UNP P0C762
C	733	PRO	-	expression tag	UNP P0C762
C	734	GLY	-	expression tag	UNP P0C762
C	735	HIS	-	expression tag	UNP P0C762
C	736	HIS	-	expression tag	UNP P0C762
C	737	HIS	-	expression tag	UNP P0C762
C	738	HIS	-	expression tag	UNP P0C762
C	739	HIS	-	expression tag	UNP P0C762
C	740	HIS	-	expression tag	UNP P0C762
C	741	HIS	-	expression tag	UNP P0C762
C	742	HIS	-	expression tag	UNP P0C762
C	743	SER	-	expression tag	UNP P0C762
C	744	ALA	-	expression tag	UNP P0C762
C	745	TRP	-	expression tag	UNP P0C762
C	746	SER	-	expression tag	UNP P0C762
C	747	HIS	-	expression tag	UNP P0C762
C	748	PRO	-	expression tag	UNP P0C762
C	749	GLN	-	expression tag	UNP P0C762
C	750	PHE	-	expression tag	UNP P0C762
C	751	GLU	-	expression tag	UNP P0C762
C	752	LYS	-	expression tag	UNP P0C762
C	753	GLY	-	expression tag	UNP P0C762
C	754	GLY	-	expression tag	UNP P0C762
C	755	GLY	-	expression tag	UNP P0C762
C	756	SER	-	expression tag	UNP P0C762
C	757	GLY	-	expression tag	UNP P0C762
C	758	GLY	-	expression tag	UNP P0C762
C	759	GLY	-	expression tag	UNP P0C762
C	760	GLY	-	expression tag	UNP P0C762
C	761	SER	-	expression tag	UNP P0C762
C	762	GLY	-	expression tag	UNP P0C762
C	763	GLY	-	expression tag	UNP P0C762
C	764	SER	-	expression tag	UNP P0C762

Continued on next page...

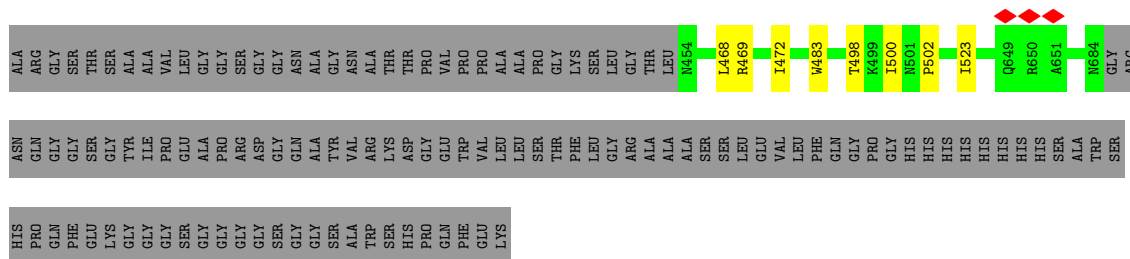
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	765	ALA	-	expression tag	UNP P0C762
C	766	TRP	-	expression tag	UNP P0C762
C	767	SER	-	expression tag	UNP P0C762
C	768	HIS	-	expression tag	UNP P0C762
C	769	PRO	-	expression tag	UNP P0C762
C	770	GLN	-	expression tag	UNP P0C762
C	771	PHE	-	expression tag	UNP P0C762
C	772	GLU	-	expression tag	UNP P0C762
C	773	LYS	-	expression tag	UNP P0C762

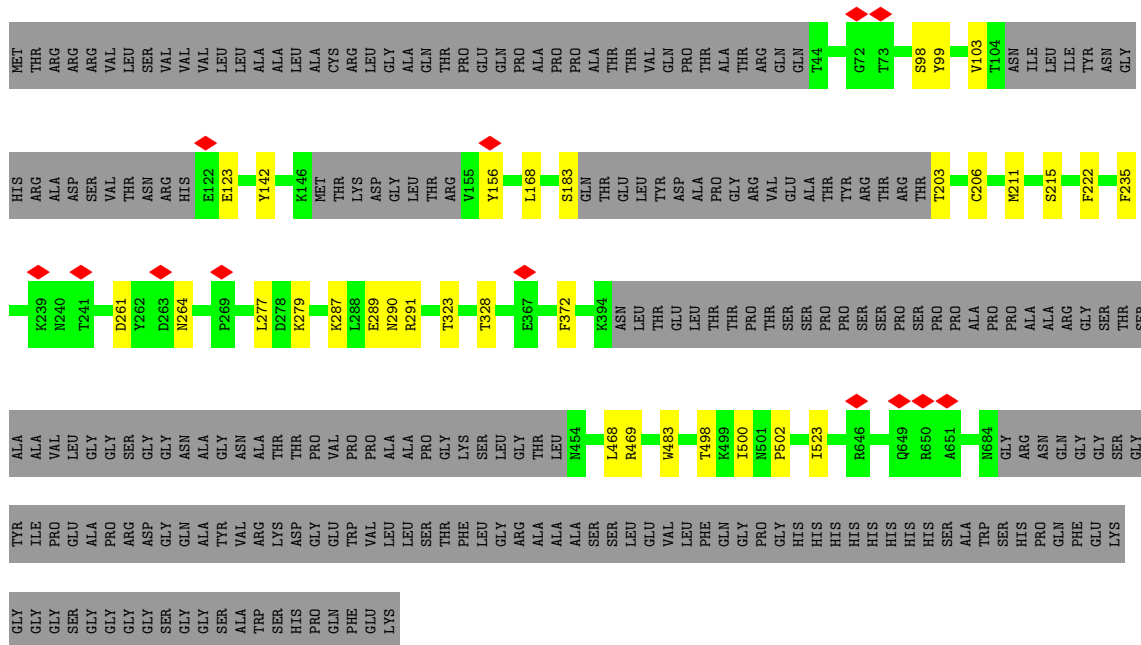
- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	3	Total	C	N	O	0	0
			39	22	2	15		
2	E	3	Total	C	N	O	0	0
			39	22	2	15		
2	F	3	Total	C	N	O	0	0
			39	22	2	15		



- Molecule 1: Envelope glycoprotein B



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

67%

33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	162928	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 ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	150000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.392	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	358.272, 358.272, 358.272	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.933, 0.933, 0.933	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.24	0/4398	0.49	0/5951
1	B	0.24	0/4398	0.50	0/5951
1	C	0.24	0/4398	0.49	0/5951
All	All	0.24	0/13194	0.49	0/17853

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4314	0	4183	25	0
1	B	4314	0	4183	25	0
1	C	4314	0	4183	24	0
2	D	39	0	34	2	0
2	E	39	0	34	2	0
2	F	39	0	34	2	0
All	All	13059	0	12651	67	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 3.

All (67) 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:498:THR:HG21	1:C:523:ILE:HD11	1.48	0.95
1:B:103:VAL:HG11	1:B:156:TYR:OH	1.67	0.95
1:C:103:VAL:HG11	1:C:156:TYR:OH	1.67	0.94
1:B:498:THR:HG21	1:B:523:ILE:HD11	1.48	0.94
1:A:103:VAL:HG11	1:A:156:TYR:OH	1.67	0.94
1:A:498:THR:HG21	1:A:523:ILE:HD11	1.48	0.93
1:B:103:VAL:CG1	1:B:156:TYR:OH	2.23	0.86
1:C:103:VAL:CG1	1:C:156:TYR:OH	2.23	0.86
1:A:103:VAL:CG1	1:A:156:TYR:OH	2.23	0.85
1:C:323:THR:HG1	1:C:483:TRP:CG	2.17	0.63
1:C:168:LEU:HA	1:C:183:SER:HB2	1.80	0.63
1:B:168:LEU:HA	1:B:183:SER:HB2	1.80	0.62
1:B:323:THR:HG1	1:B:483:TRP:CG	2.18	0.61
1:A:287:LYS:HE3	1:A:289:GLU:HG2	1.82	0.61
1:A:168:LEU:HA	1:A:183:SER:HB2	1.80	0.61
1:A:323:THR:HG1	1:A:483:TRP:CG	2.19	0.60
1:A:142:TYR:CZ	2:D:1:NAG:H61	2.37	0.59
1:C:168:LEU:HD21	1:C:206:CYS:HB2	1.85	0.59
1:B:142:TYR:CZ	2:E:1:NAG:H61	2.37	0.58
1:C:142:TYR:CZ	2:F:1:NAG:H61	2.37	0.58
1:B:103:VAL:HB	1:B:123:GLU:HG3	1.85	0.58
1:B:168:LEU:HD21	1:B:206:CYS:HB2	1.85	0.58
1:A:103:VAL:HB	1:A:123:GLU:HG3	1.85	0.58
1:A:168:LEU:HD21	1:A:206:CYS:HB2	1.85	0.58
1:B:498:THR:HG23	1:B:502:PRO:HB3	1.86	0.58
1:A:498:THR:HG23	1:A:502:PRO:HB3	1.86	0.57
1:A:469:ARG:HD2	1:C:468:LEU:HD21	1.86	0.57
1:C:103:VAL:HB	1:C:123:GLU:HG3	1.85	0.57
1:C:498:THR:HG23	1:C:502:PRO:HB3	1.86	0.56
1:A:498:THR:HG21	1:A:523:ILE:CD1	2.30	0.56
1:B:498:THR:HG21	1:B:523:ILE:CD1	2.30	0.56
1:C:498:THR:HG21	1:C:523:ILE:CD1	2.30	0.55
1:A:468:LEU:HD21	1:B:469:ARG:HD2	1.88	0.55
1:C:287:LYS:HE3	1:C:289:GLU:HG2	1.88	0.54
1:B:468:LEU:HD21	1:C:469:ARG:HD2	1.87	0.54
1:C:235:PHE:CD1	1:C:291:ARG:HA	2.43	0.53
1:B:235:PHE:CD1	1:B:291:ARG:HA	2.43	0.53
1:C:142:TYR:CE1	2:F:1:NAG:H61	2.44	0.53
1:A:142:TYR:CE1	2:D:1:NAG:H61	2.44	0.52
1:B:142:TYR:CE1	2:E:1:NAG:H61	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:289:GLU:O	1:C:290:ASN:C	2.54	0.51
1:A:235:PHE:CD1	1:A:291:ARG:HA	2.46	0.50
1:B:287:LYS:HE3	1:B:289:GLU:HG2	1.93	0.49
1:B:289:GLU:O	1:B:290:ASN:C	2.56	0.48
1:A:215:SER:HB3	1:A:222:PHE:HB3	1.95	0.48
1:C:215:SER:HB3	1:C:222:PHE:HB3	1.95	0.47
1:B:215:SER:HB3	1:B:222:PHE:HB3	1.95	0.46
1:B:103:VAL:HA	1:B:203:THR:O	2.15	0.46
1:C:103:VAL:HA	1:C:203:THR:O	2.15	0.46
1:A:103:VAL:HA	1:A:203:THR:O	2.15	0.46
1:A:500:ILE:HD11	1:B:500:ILE:HD11	1.97	0.46
1:C:98:SER:HB2	1:C:211:MET:HE2	1.98	0.45
1:B:500:ILE:HD11	1:C:500:ILE:HD11	1.98	0.45
1:B:98:SER:HB2	1:B:211:MET:HE2	1.98	0.45
1:A:98:SER:HB2	1:A:211:MET:HE2	1.98	0.45
1:B:261:ASP:HB3	1:B:264:ASN:HB2	1.99	0.45
1:A:261:ASP:HB3	1:A:264:ASN:HB2	1.99	0.45
1:C:261:ASP:HB3	1:C:264:ASN:HB2	1.99	0.45
1:A:500:ILE:HD11	1:C:500:ILE:HD11	1.99	0.44
1:A:289:GLU:O	1:A:290:ASN:C	2.60	0.44
1:A:328:THR:HG21	1:A:372:PHE:CD1	2.54	0.43
1:C:328:THR:HG21	1:C:372:PHE:CD1	2.54	0.43
1:B:328:THR:HG21	1:B:372:PHE:CD1	2.54	0.43
1:A:277:LEU:HD21	1:A:279:LYS:HD3	2.01	0.42
1:C:277:LEU:HD21	1:C:279:LYS:HD3	2.01	0.42
1:B:277:LEU:HD21	1:B:279:LYS:HD3	2.01	0.41
1:A:475:MET:CE	1:B:472:ILE:HG23	2.51	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	530/775 (68%)	513 (97%)	17 (3%)	0	100	100
1	B	530/775 (68%)	513 (97%)	17 (3%)	0	100	100
1	C	530/775 (68%)	512 (97%)	18 (3%)	0	100	100
All	All	1590/2325 (68%)	1538 (97%)	52 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	483/662 (73%)	482 (100%)	1 (0%)	87	89
1	B	483/662 (73%)	482 (100%)	1 (0%)	87	89
1	C	483/662 (73%)	482 (100%)	1 (0%)	87	89
All	All	1449/1986 (73%)	1446 (100%)	3 (0%)	85	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	TYR
1	B	99	TYR
1	C	99	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	167	ASN
1	A	320	GLN
1	A	462	GLN
1	A	491	ASN
1	A	606	ASN
1	A	610	HIS
1	B	167	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	320	GLN
1	B	462	GLN
1	B	487	GLN
1	B	491	ASN
1	B	606	ASN
1	B	610	HIS
1	C	167	ASN
1	C	320	GLN
1	C	491	ASN
1	C	606	ASN
1	C	610	HIS

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](#)

9 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	D	1	1,2	14,14,15	0.42	0	17,19,21	1.41	2 (11%)
2	NAG	D	2	2	14,14,15	0.42	0	17,19,21	0.87	0
2	BMA	D	3	2	11,11,12	0.68	0	15,15,17	0.56	0
2	NAG	E	1	1,2	14,14,15	0.42	0	17,19,21	1.41	2 (11%)
2	NAG	E	2	2	14,14,15	0.44	0	17,19,21	0.87	0
2	BMA	E	3	2	11,11,12	0.68	0	15,15,17	0.55	0
2	NAG	F	1	1,2	14,14,15	0.42	0	17,19,21	1.40	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	F	2	2	14,14,15	0.42	0	17,19,21	0.87	0
2	BMA	F	3	2	11,11,12	0.68	0	15,15,17	0.55	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	D	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	NAG	E	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	E	2	2	-	3/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	NAG	F	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	F	2	2	-	3/6/23/26	0/1/1/1
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	NAG	C1-C2-N2	4.53	117.57	110.43
2	E	1	NAG	C1-C2-N2	4.52	117.56	110.43
2	D	1	NAG	C1-C2-N2	4.50	117.52	110.43
2	D	1	NAG	C2-N2-C7	2.96	126.87	122.90
2	E	1	NAG	C2-N2-C7	2.94	126.84	122.90
2	F	1	NAG	C2-N2-C7	2.91	126.80	122.90

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C1-C2-N2-C7
2	D	1	NAG	O7-C7-N2-C2
2	E	1	NAG	C1-C2-N2-C7
2	E	1	NAG	O7-C7-N2-C2
2	F	1	NAG	C1-C2-N2-C7
2	F	1	NAG	O7-C7-N2-C2

Continued on next page...

Continued from previous page...

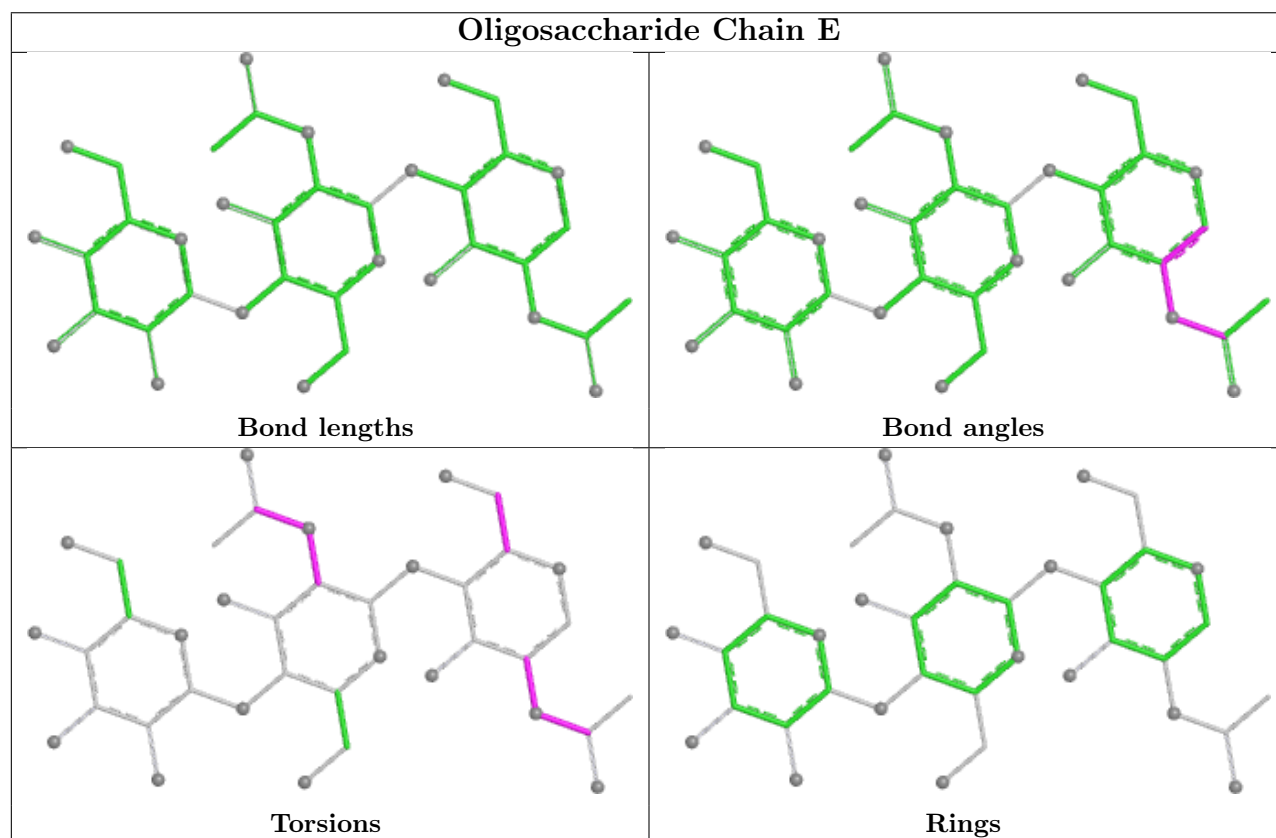
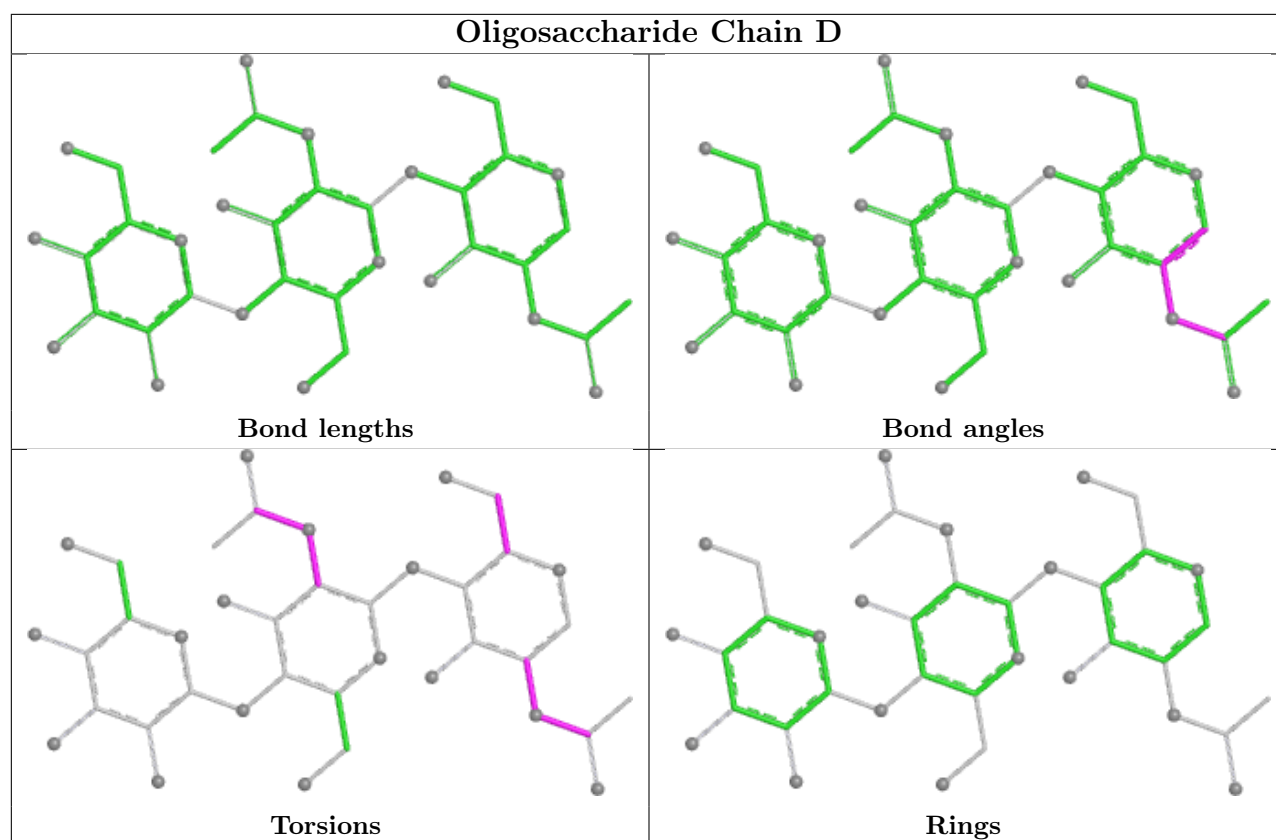
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	E	1	NAG	C8-C7-N2-C2
2	F	1	NAG	C8-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	E	2	NAG	C8-C7-N2-C2
2	F	2	NAG	C8-C7-N2-C2
2	D	1	NAG	O5-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
2	D	2	NAG	C3-C2-N2-C7
2	E	2	NAG	C3-C2-N2-C7
2	F	2	NAG	C3-C2-N2-C7
2	D	2	NAG	O7-C7-N2-C2
2	E	2	NAG	O7-C7-N2-C2
2	F	2	NAG	O7-C7-N2-C2

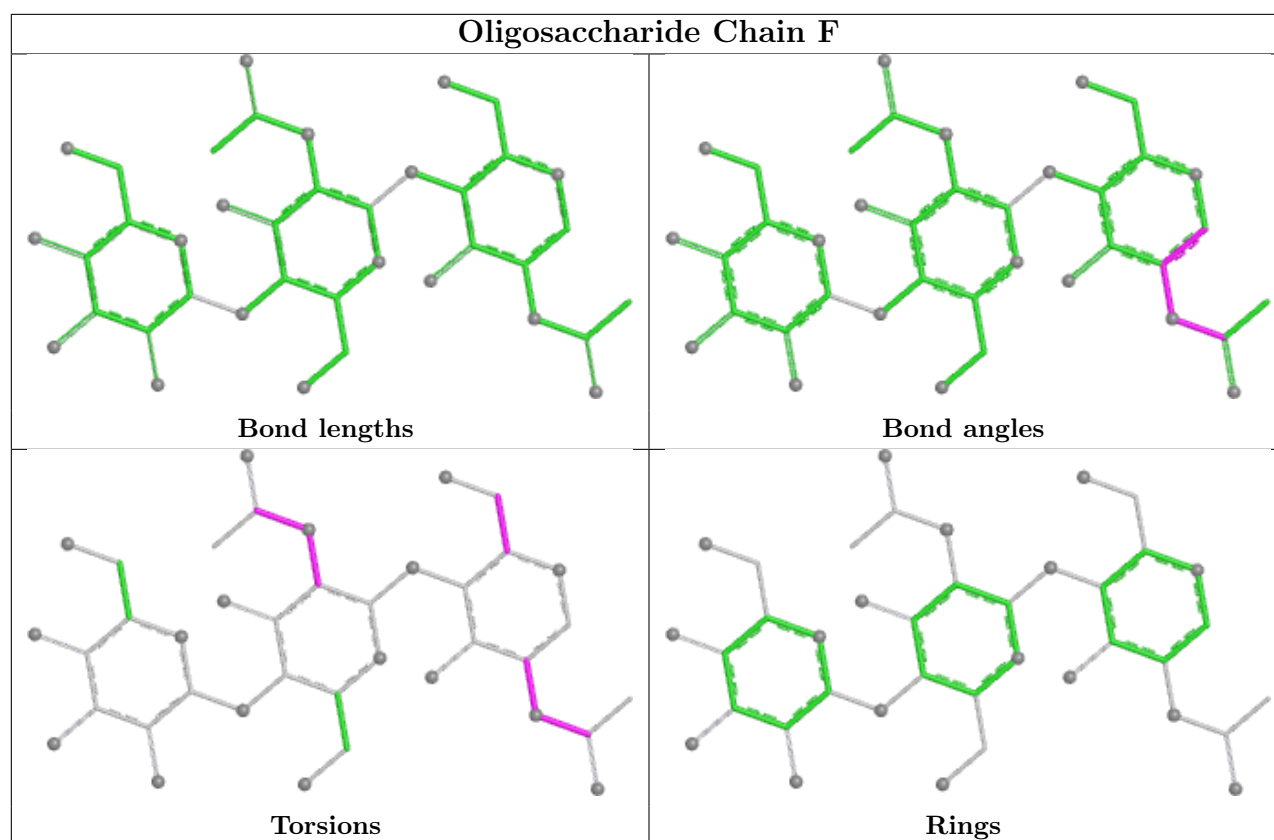
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	2	0
2	F	1	NAG	2	0
2	D	1	NAG	2	0

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





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](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70288. These allow visual inspection of the internal detail of the map and identification of artifacts.

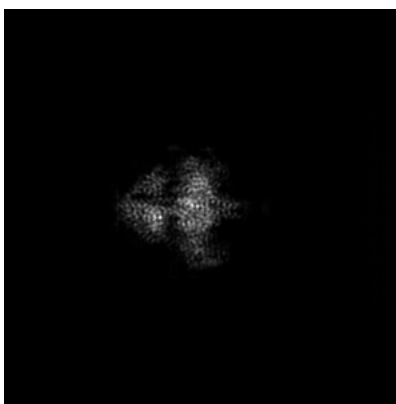
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

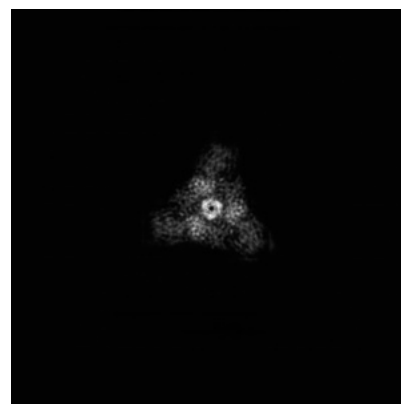
6.1.1 Primary map



X

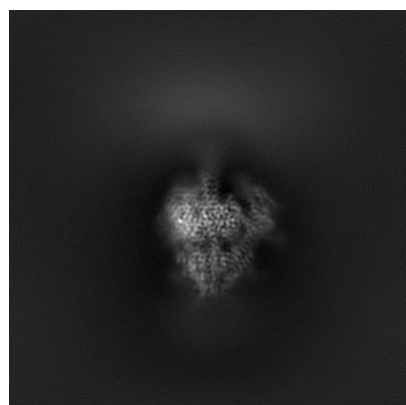


Y

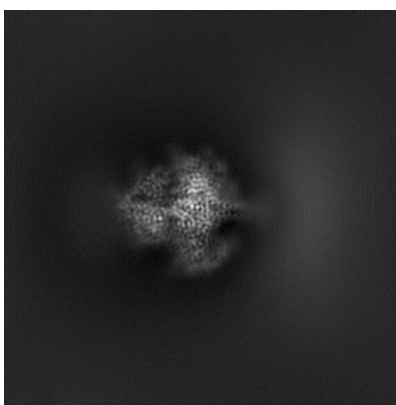


Z

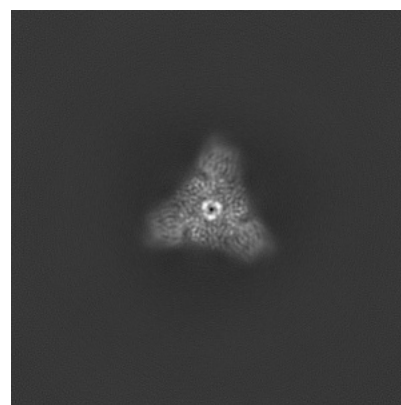
6.1.2 Raw map



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: 192

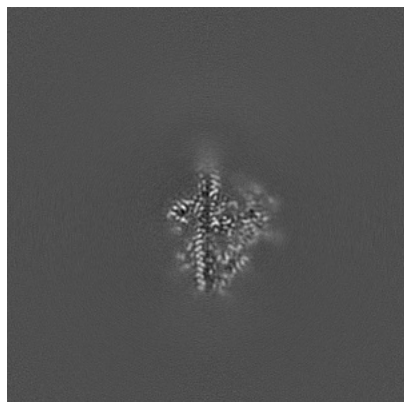


Y Index: 192

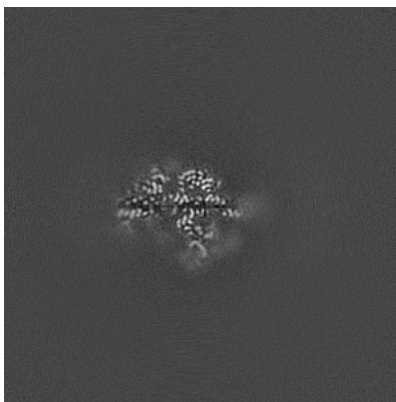


Z Index: 192

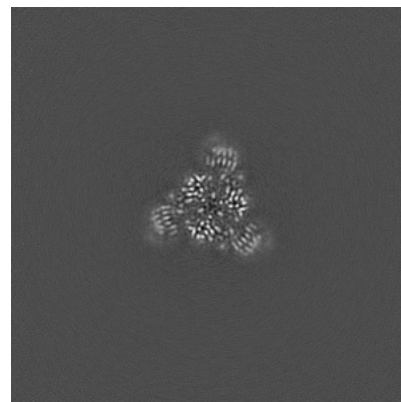
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

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: 185

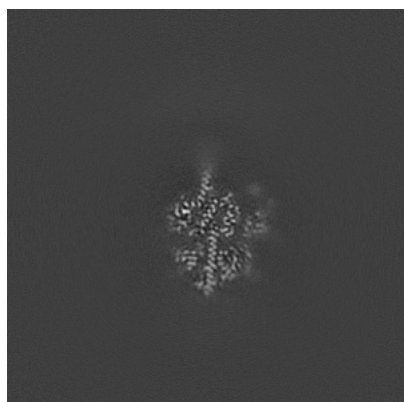


Y Index: 187

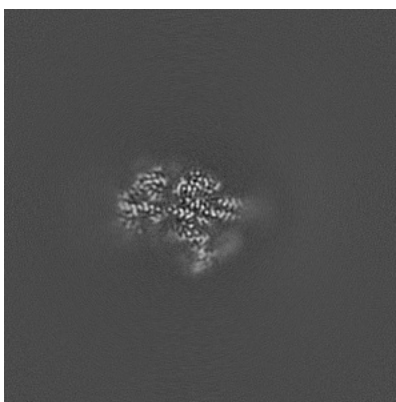


Z Index: 185

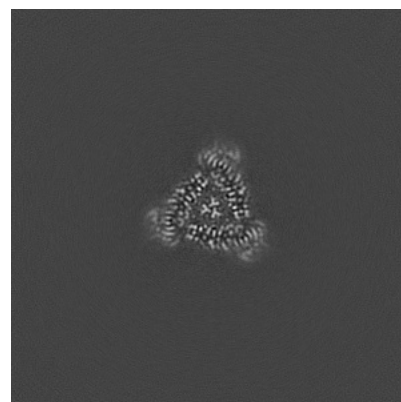
6.3.2 Raw map



X Index: 185



Y Index: 187

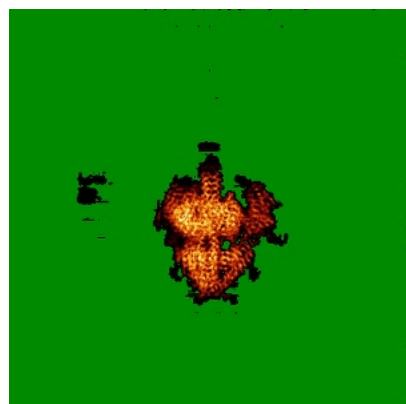


Z Index: 185

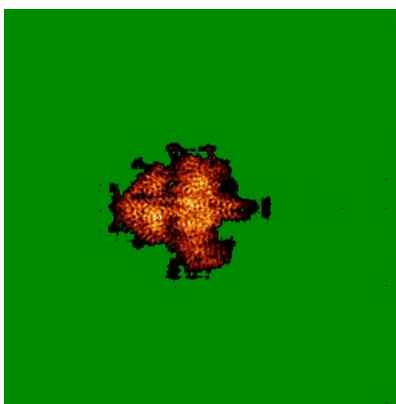
The images above show the largest variance slices of the map in three orthogonal directions.

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

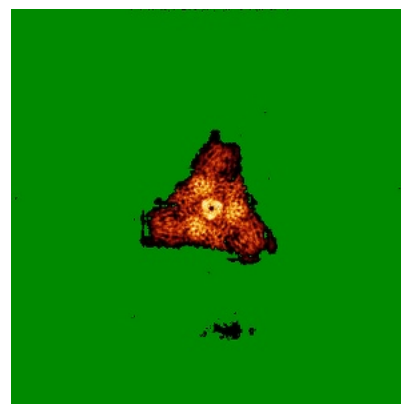
6.4.1 Primary map



X

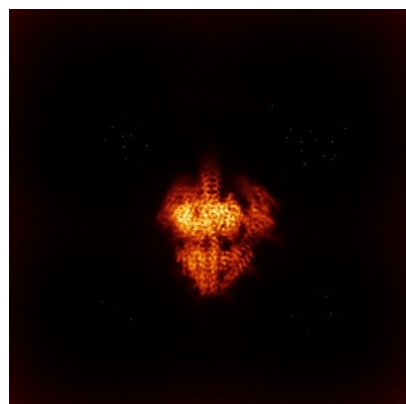


Y

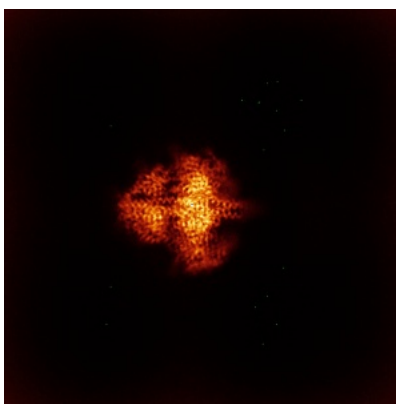


Z

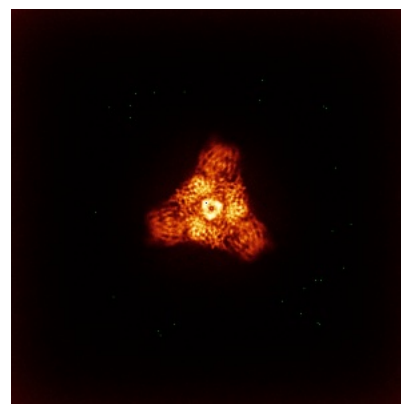
6.4.2 Raw map



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.

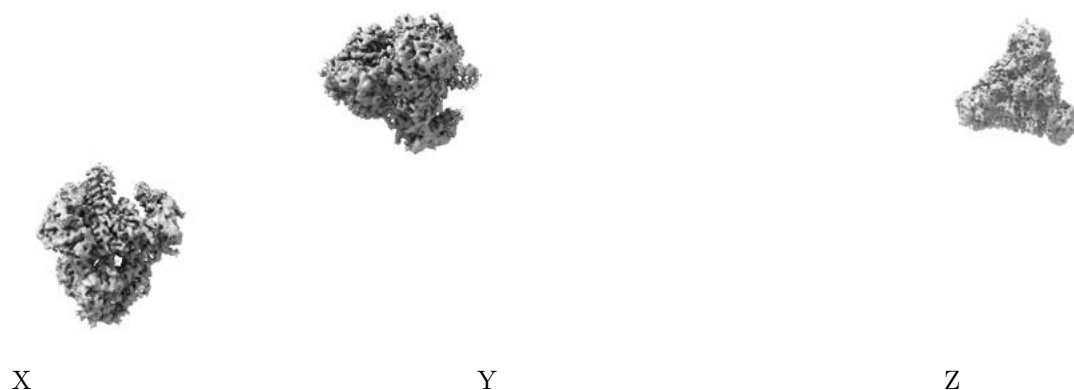
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

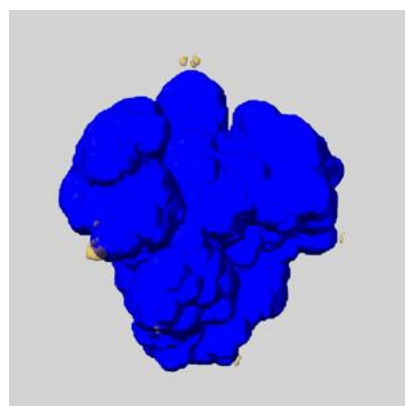
6.6 Mask visualisation [i](#)

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

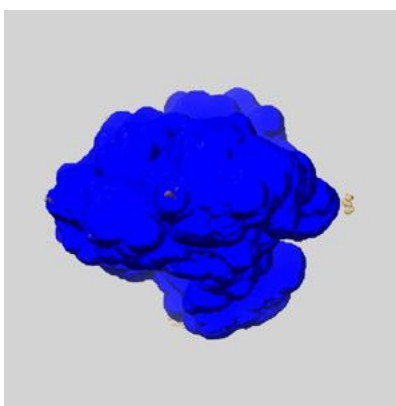
A mask typically either:

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

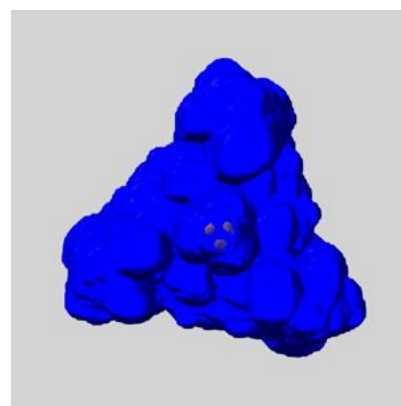
6.6.1 emd_70288_msk_1.map [i](#)



X



Y

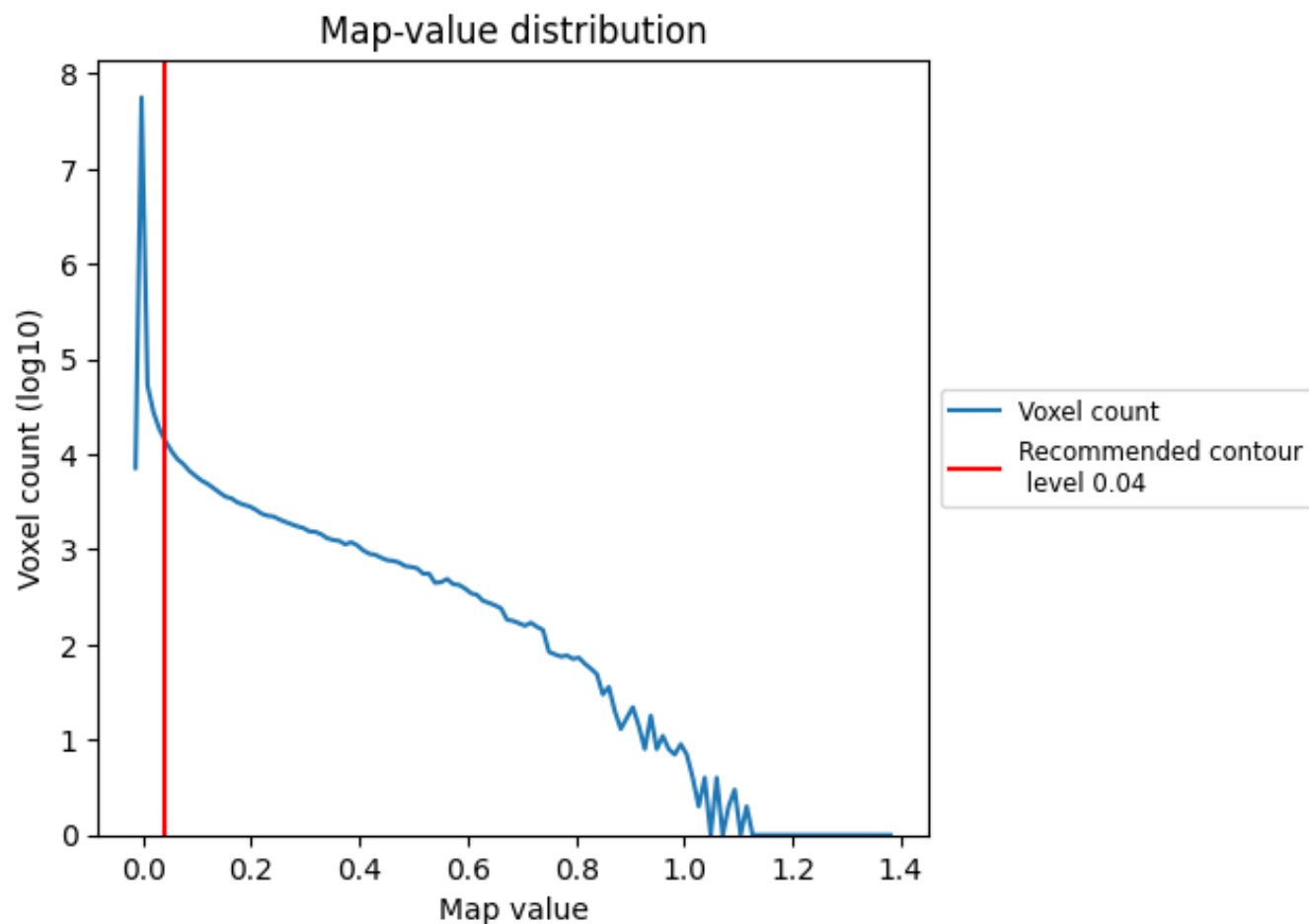


Z

7 Map analysis [i](#)

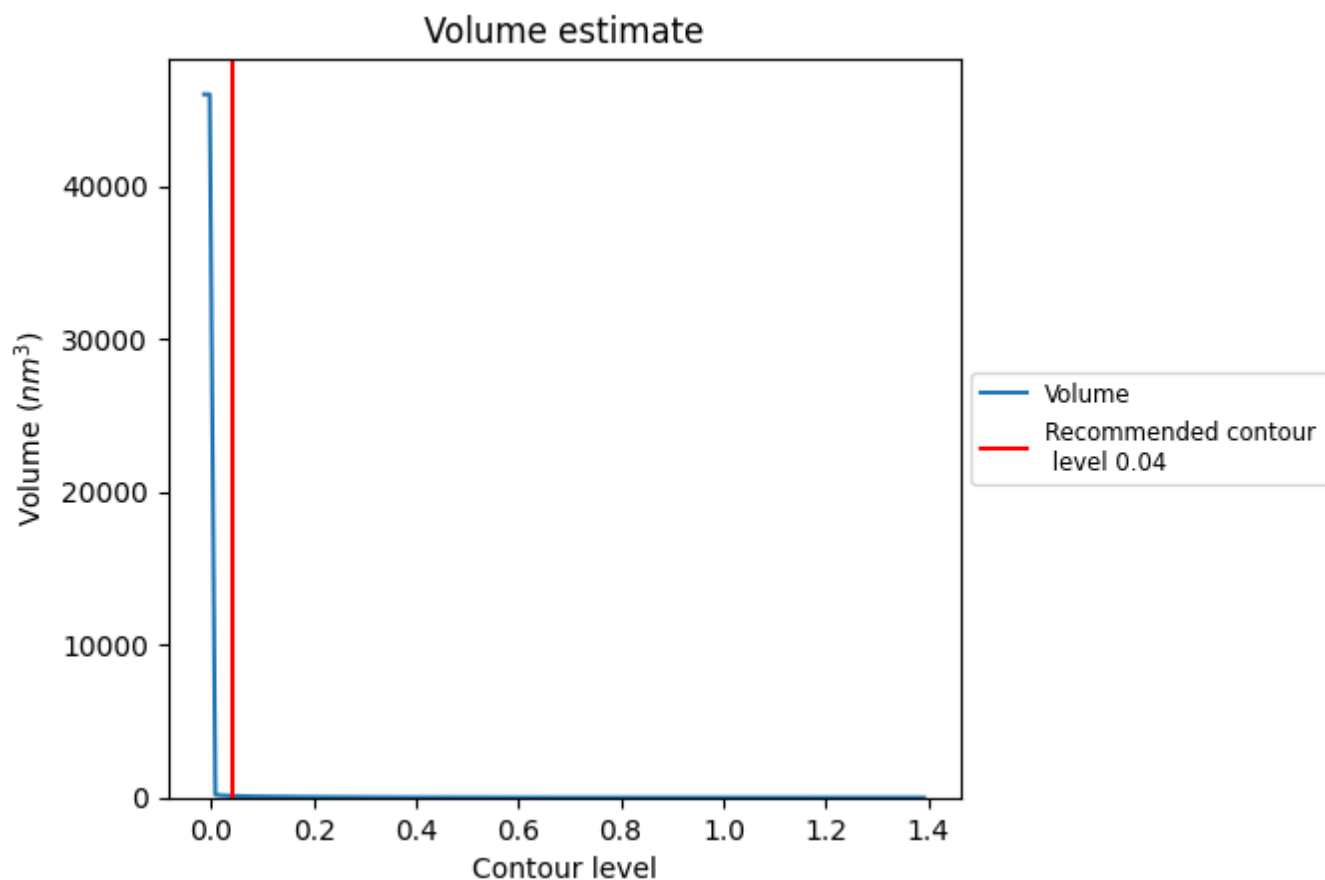
This section contains the results of statistical analysis of the map.

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.

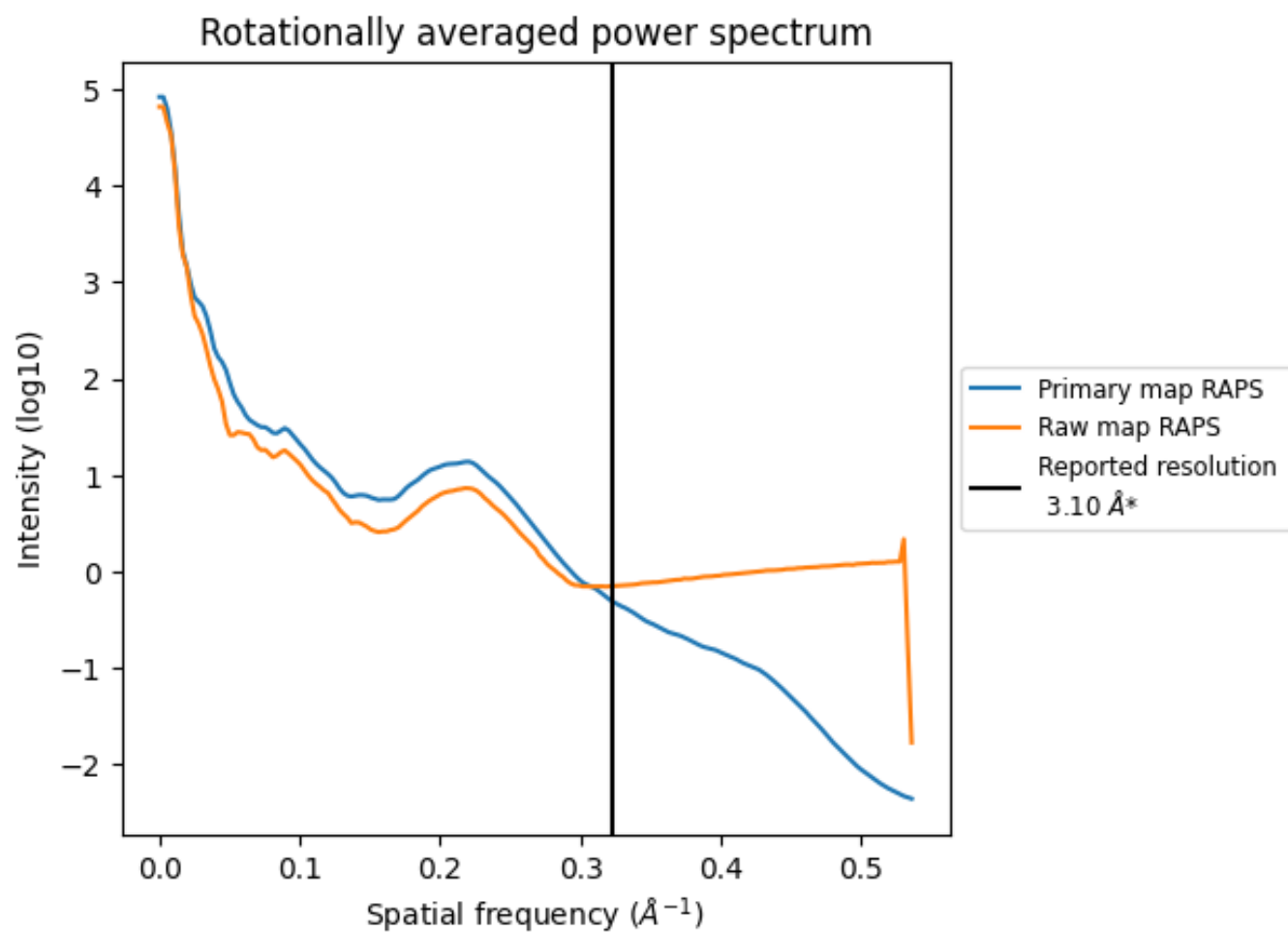
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 111 nm^3 ; this corresponds to an approximate mass of 101 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 ⓘ

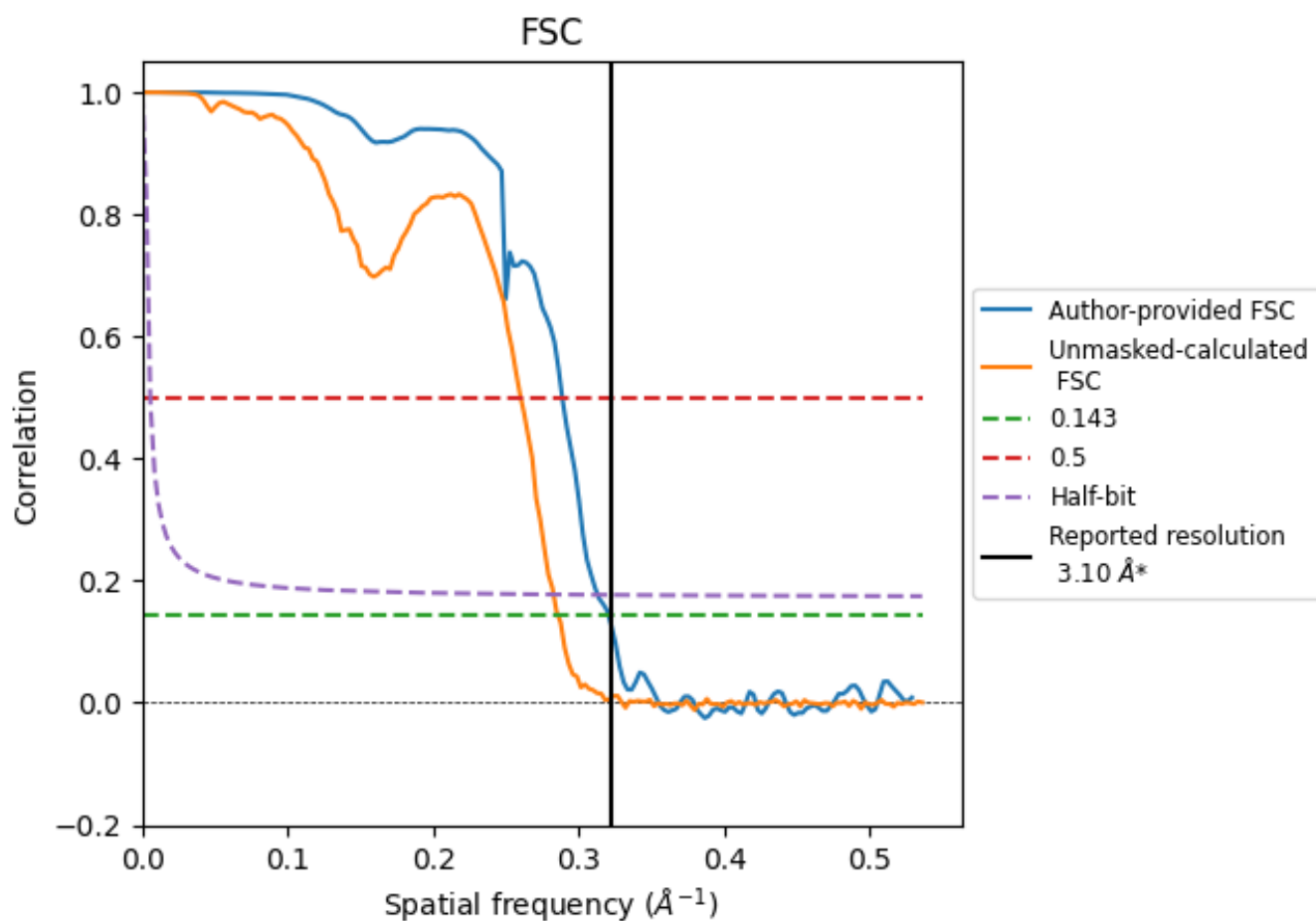


*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

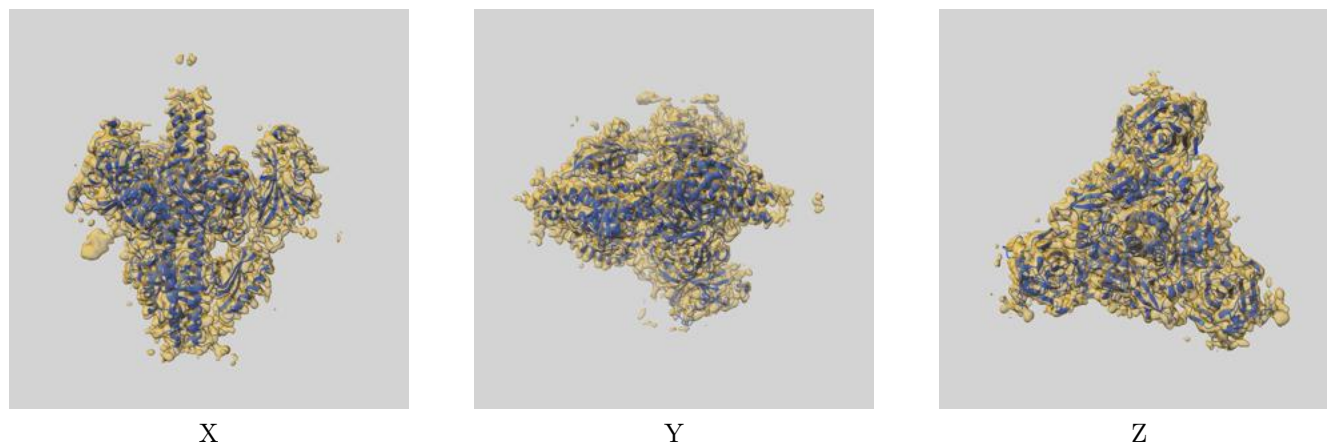
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.47	3.19
Unmasked-calculated*	3.50	3.84	3.54

*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 3.50 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

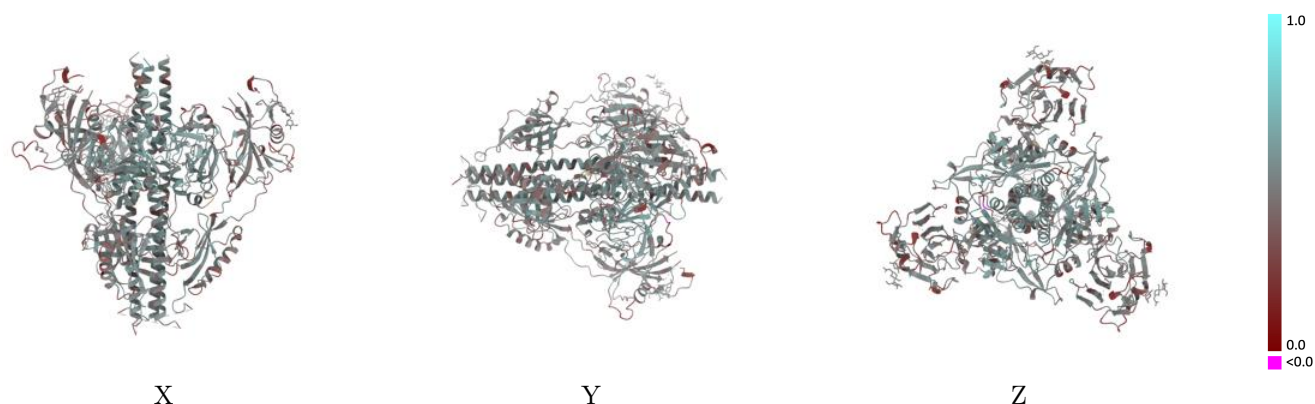
This section contains information regarding the fit between EMDB map EMD-70288 and PDB model 9OAL. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



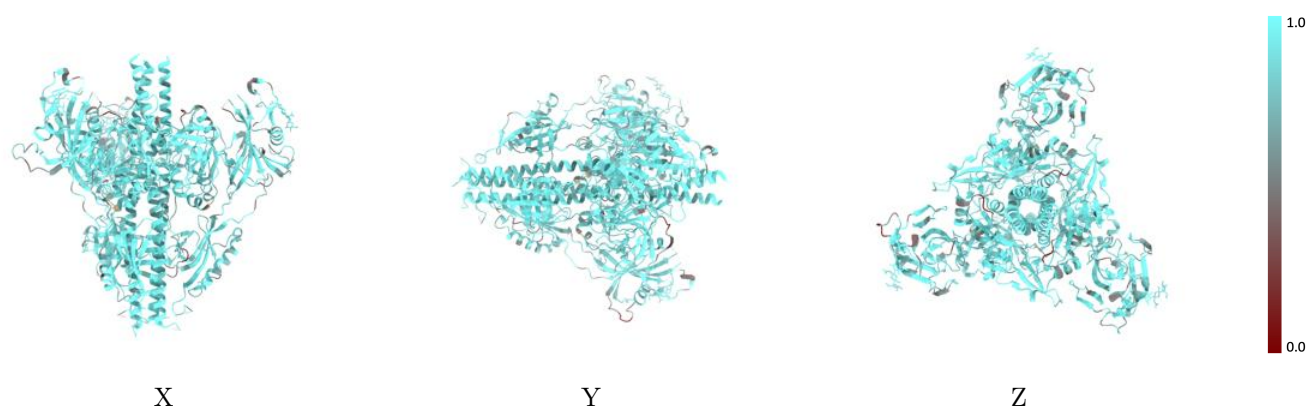
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



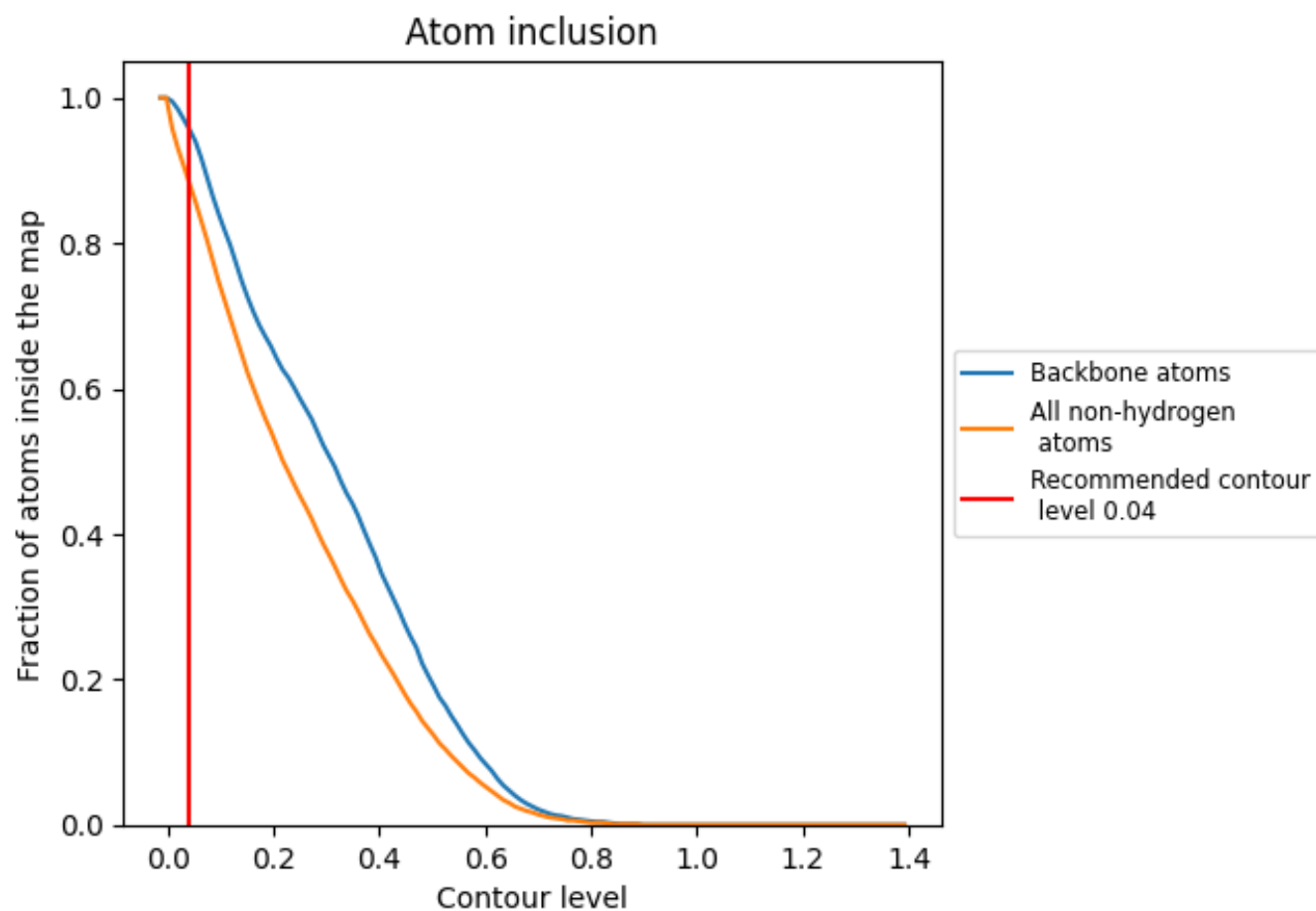
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 88% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8840	0.4700
A	0.8800	0.4710
B	0.8840	0.4700
C	0.8880	0.4710
D	0.9490	0.4720
E	0.8970	0.4470
F	0.8720	0.4490

1.0

0.0

<0.0