



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 03:46 AM UTC

PDB ID : 9DD7 / pdb_00009dd7
EMDB ID : EMD-46759
Title : Cryo-EM structure of neutralizing human antibody D48 in complex with HSV-1 glycoprotein B trimer gB-Ecto.516P.531E.DS
Authors : Roark, R.S.; Shapiro, L.; Kwong, P.D.
Deposited on : 2024-08-27
Resolution : 4.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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:

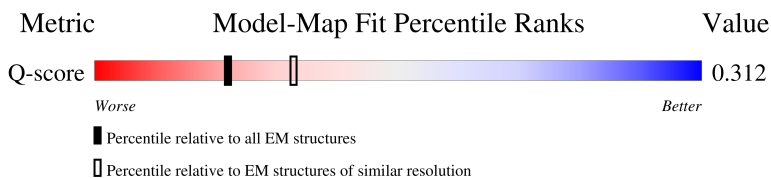
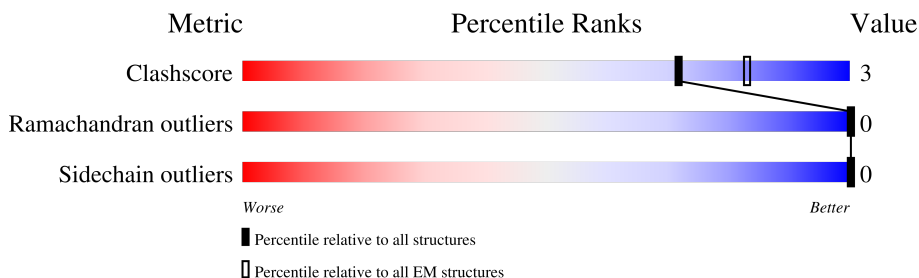
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13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

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

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	E	808	<div> <div>5%</div> <div>56%</div> <div>6%</div> <div>38%</div> </div>
1	F	808	<div> <div>6%</div> <div>55%</div> <div>7%</div> <div>38%</div> </div>
1	G	808	<div> <div>6%</div> <div>56%</div> <div>5%</div> <div>38%</div> </div>
2	I	120	<div> <div>22%</div> <div>92%</div> <div>8%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	J	120	<div> <div>22%</div> <div>88%</div> <div>12%</div> </div>
2	K	120	<div> <div>22%</div> <div>92%</div> <div>8%</div> </div>
3	M	107	<div> <div>33%</div> <div>90%</div> <div>10%</div> </div>
3	N	107	<div> <div>31%</div> <div>93%</div> <div>7%</div> </div>
3	O	107	<div> <div>30%</div> <div>93%</div> <div>7%</div> </div>
4	A	5	<div> <div>20%</div> <div>80%</div> </div>
4	C	5	<div> <div>20%</div> <div>80%</div> </div>
4	H	5	<div> <div>20%</div> <div>80%</div> </div>
5	B	2	<div> <div>50%</div> <div>100%</div> </div>
5	D	2	<div> <div>50%</div> <div>50%</div> <div>50%</div> </div>
5	L	2	<div> <div>50%</div> <div>50%</div> <div>50%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17502 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 Glycoprotein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	498	Total	C	N	O	S	0	0
			3973	2499	695	757	22		
1	F	498	Total	C	N	O	S	0	0
			3973	2499	695	757	22		
1	G	498	Total	C	N	O	S	0	0
			3973	2499	695	757	22		

There are 252 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	240	CYS	ALA	conflict	UNP A1Z0P6
E	516	PRO	HIS	engineered mutation	UNP A1Z0P6
E	531	GLU	LEU	engineered mutation	UNP A1Z0P6
E	607	CYS	GLU	conflict	UNP A1Z0P6
E	729	GLY	-	expression tag	UNP A1Z0P6
E	730	SER	-	expression tag	UNP A1Z0P6
E	731	GLY	-	expression tag	UNP A1Z0P6
E	732	TYR	-	expression tag	UNP A1Z0P6
E	733	ILE	-	expression tag	UNP A1Z0P6
E	734	PRO	-	expression tag	UNP A1Z0P6
E	735	GLU	-	expression tag	UNP A1Z0P6
E	736	ALA	-	expression tag	UNP A1Z0P6
E	737	PRO	-	expression tag	UNP A1Z0P6
E	738	ARG	-	expression tag	UNP A1Z0P6
E	739	ASP	-	expression tag	UNP A1Z0P6
E	740	GLY	-	expression tag	UNP A1Z0P6
E	741	GLN	-	expression tag	UNP A1Z0P6
E	742	ALA	-	expression tag	UNP A1Z0P6
E	743	TYR	-	expression tag	UNP A1Z0P6
E	744	VAL	-	expression tag	UNP A1Z0P6
E	745	ARG	-	expression tag	UNP A1Z0P6
E	746	LYS	-	expression tag	UNP A1Z0P6
E	747	ASP	-	expression tag	UNP A1Z0P6
E	748	GLY	-	expression tag	UNP A1Z0P6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	749	GLU	-	expression tag	UNP A1Z0P6
E	750	TRP	-	expression tag	UNP A1Z0P6
E	751	VAL	-	expression tag	UNP A1Z0P6
E	752	LEU	-	expression tag	UNP A1Z0P6
E	753	LEU	-	expression tag	UNP A1Z0P6
E	754	SER	-	expression tag	UNP A1Z0P6
E	755	THR	-	expression tag	UNP A1Z0P6
E	756	PHE	-	expression tag	UNP A1Z0P6
E	757	LEU	-	expression tag	UNP A1Z0P6
E	758	GLY	-	expression tag	UNP A1Z0P6
E	759	ARG	-	expression tag	UNP A1Z0P6
E	760	SER	-	expression tag	UNP A1Z0P6
E	761	LEU	-	expression tag	UNP A1Z0P6
E	762	GLU	-	expression tag	UNP A1Z0P6
E	763	VAL	-	expression tag	UNP A1Z0P6
E	764	LEU	-	expression tag	UNP A1Z0P6
E	765	PHE	-	expression tag	UNP A1Z0P6
E	766	GLN	-	expression tag	UNP A1Z0P6
E	767	GLY	-	expression tag	UNP A1Z0P6
E	768	PRO	-	expression tag	UNP A1Z0P6
E	769	GLY	-	expression tag	UNP A1Z0P6
E	770	HIS	-	expression tag	UNP A1Z0P6
E	771	HIS	-	expression tag	UNP A1Z0P6
E	772	HIS	-	expression tag	UNP A1Z0P6
E	773	HIS	-	expression tag	UNP A1Z0P6
E	774	HIS	-	expression tag	UNP A1Z0P6
E	775	HIS	-	expression tag	UNP A1Z0P6
E	776	HIS	-	expression tag	UNP A1Z0P6
E	777	HIS	-	expression tag	UNP A1Z0P6
E	778	SER	-	expression tag	UNP A1Z0P6
E	779	ALA	-	expression tag	UNP A1Z0P6
E	780	TRP	-	expression tag	UNP A1Z0P6
E	781	SER	-	expression tag	UNP A1Z0P6
E	782	HIS	-	expression tag	UNP A1Z0P6
E	783	PRO	-	expression tag	UNP A1Z0P6
E	784	GLN	-	expression tag	UNP A1Z0P6
E	785	PHE	-	expression tag	UNP A1Z0P6
E	786	GLU	-	expression tag	UNP A1Z0P6
E	787	LYS	-	expression tag	UNP A1Z0P6
E	788	GLY	-	expression tag	UNP A1Z0P6
E	789	GLY	-	expression tag	UNP A1Z0P6
E	790	GLY	-	expression tag	UNP A1Z0P6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	791	SER	-	expression tag	UNP A1Z0P6
E	792	GLY	-	expression tag	UNP A1Z0P6
E	793	GLY	-	expression tag	UNP A1Z0P6
E	794	GLY	-	expression tag	UNP A1Z0P6
E	795	GLY	-	expression tag	UNP A1Z0P6
E	796	SER	-	expression tag	UNP A1Z0P6
E	797	GLY	-	expression tag	UNP A1Z0P6
E	798	GLY	-	expression tag	UNP A1Z0P6
E	799	SER	-	expression tag	UNP A1Z0P6
E	800	ALA	-	expression tag	UNP A1Z0P6
E	801	TRP	-	expression tag	UNP A1Z0P6
E	802	SER	-	expression tag	UNP A1Z0P6
E	803	HIS	-	expression tag	UNP A1Z0P6
E	804	PRO	-	expression tag	UNP A1Z0P6
E	805	GLN	-	expression tag	UNP A1Z0P6
E	806	PHE	-	expression tag	UNP A1Z0P6
E	807	GLU	-	expression tag	UNP A1Z0P6
E	808	LYS	-	expression tag	UNP A1Z0P6
F	240	CYS	ALA	conflict	UNP A1Z0P6
F	516	PRO	HIS	engineered mutation	UNP A1Z0P6
F	531	GLU	LEU	engineered mutation	UNP A1Z0P6
F	607	CYS	GLU	conflict	UNP A1Z0P6
F	729	GLY	-	expression tag	UNP A1Z0P6
F	730	SER	-	expression tag	UNP A1Z0P6
F	731	GLY	-	expression tag	UNP A1Z0P6
F	732	TYR	-	expression tag	UNP A1Z0P6
F	733	ILE	-	expression tag	UNP A1Z0P6
F	734	PRO	-	expression tag	UNP A1Z0P6
F	735	GLU	-	expression tag	UNP A1Z0P6
F	736	ALA	-	expression tag	UNP A1Z0P6
F	737	PRO	-	expression tag	UNP A1Z0P6
F	738	ARG	-	expression tag	UNP A1Z0P6
F	739	ASP	-	expression tag	UNP A1Z0P6
F	740	GLY	-	expression tag	UNP A1Z0P6
F	741	GLN	-	expression tag	UNP A1Z0P6
F	742	ALA	-	expression tag	UNP A1Z0P6
F	743	TYR	-	expression tag	UNP A1Z0P6
F	744	VAL	-	expression tag	UNP A1Z0P6
F	745	ARG	-	expression tag	UNP A1Z0P6
F	746	LYS	-	expression tag	UNP A1Z0P6
F	747	ASP	-	expression tag	UNP A1Z0P6
F	748	GLY	-	expression tag	UNP A1Z0P6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	749	GLU	-	expression tag	UNP A1Z0P6
F	750	TRP	-	expression tag	UNP A1Z0P6
F	751	VAL	-	expression tag	UNP A1Z0P6
F	752	LEU	-	expression tag	UNP A1Z0P6
F	753	LEU	-	expression tag	UNP A1Z0P6
F	754	SER	-	expression tag	UNP A1Z0P6
F	755	THR	-	expression tag	UNP A1Z0P6
F	756	PHE	-	expression tag	UNP A1Z0P6
F	757	LEU	-	expression tag	UNP A1Z0P6
F	758	GLY	-	expression tag	UNP A1Z0P6
F	759	ARG	-	expression tag	UNP A1Z0P6
F	760	SER	-	expression tag	UNP A1Z0P6
F	761	LEU	-	expression tag	UNP A1Z0P6
F	762	GLU	-	expression tag	UNP A1Z0P6
F	763	VAL	-	expression tag	UNP A1Z0P6
F	764	LEU	-	expression tag	UNP A1Z0P6
F	765	PHE	-	expression tag	UNP A1Z0P6
F	766	GLN	-	expression tag	UNP A1Z0P6
F	767	GLY	-	expression tag	UNP A1Z0P6
F	768	PRO	-	expression tag	UNP A1Z0P6
F	769	GLY	-	expression tag	UNP A1Z0P6
F	770	HIS	-	expression tag	UNP A1Z0P6
F	771	HIS	-	expression tag	UNP A1Z0P6
F	772	HIS	-	expression tag	UNP A1Z0P6
F	773	HIS	-	expression tag	UNP A1Z0P6
F	774	HIS	-	expression tag	UNP A1Z0P6
F	775	HIS	-	expression tag	UNP A1Z0P6
F	776	HIS	-	expression tag	UNP A1Z0P6
F	777	HIS	-	expression tag	UNP A1Z0P6
F	778	SER	-	expression tag	UNP A1Z0P6
F	779	ALA	-	expression tag	UNP A1Z0P6
F	780	TRP	-	expression tag	UNP A1Z0P6
F	781	SER	-	expression tag	UNP A1Z0P6
F	782	HIS	-	expression tag	UNP A1Z0P6
F	783	PRO	-	expression tag	UNP A1Z0P6
F	784	GLN	-	expression tag	UNP A1Z0P6
F	785	PHE	-	expression tag	UNP A1Z0P6
F	786	GLU	-	expression tag	UNP A1Z0P6
F	787	LYS	-	expression tag	UNP A1Z0P6
F	788	GLY	-	expression tag	UNP A1Z0P6
F	789	GLY	-	expression tag	UNP A1Z0P6
F	790	GLY	-	expression tag	UNP A1Z0P6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	791	SER	-	expression tag	UNP A1Z0P6
F	792	GLY	-	expression tag	UNP A1Z0P6
F	793	GLY	-	expression tag	UNP A1Z0P6
F	794	GLY	-	expression tag	UNP A1Z0P6
F	795	GLY	-	expression tag	UNP A1Z0P6
F	796	SER	-	expression tag	UNP A1Z0P6
F	797	GLY	-	expression tag	UNP A1Z0P6
F	798	GLY	-	expression tag	UNP A1Z0P6
F	799	SER	-	expression tag	UNP A1Z0P6
F	800	ALA	-	expression tag	UNP A1Z0P6
F	801	TRP	-	expression tag	UNP A1Z0P6
F	802	SER	-	expression tag	UNP A1Z0P6
F	803	HIS	-	expression tag	UNP A1Z0P6
F	804	PRO	-	expression tag	UNP A1Z0P6
F	805	GLN	-	expression tag	UNP A1Z0P6
F	806	PHE	-	expression tag	UNP A1Z0P6
F	807	GLU	-	expression tag	UNP A1Z0P6
F	808	LYS	-	expression tag	UNP A1Z0P6
G	240	CYS	ALA	conflict	UNP A1Z0P6
G	516	PRO	HIS	engineered mutation	UNP A1Z0P6
G	531	GLU	LEU	engineered mutation	UNP A1Z0P6
G	607	CYS	GLU	conflict	UNP A1Z0P6
G	729	GLY	-	expression tag	UNP A1Z0P6
G	730	SER	-	expression tag	UNP A1Z0P6
G	731	GLY	-	expression tag	UNP A1Z0P6
G	732	TYR	-	expression tag	UNP A1Z0P6
G	733	ILE	-	expression tag	UNP A1Z0P6
G	734	PRO	-	expression tag	UNP A1Z0P6
G	735	GLU	-	expression tag	UNP A1Z0P6
G	736	ALA	-	expression tag	UNP A1Z0P6
G	737	PRO	-	expression tag	UNP A1Z0P6
G	738	ARG	-	expression tag	UNP A1Z0P6
G	739	ASP	-	expression tag	UNP A1Z0P6
G	740	GLY	-	expression tag	UNP A1Z0P6
G	741	GLN	-	expression tag	UNP A1Z0P6
G	742	ALA	-	expression tag	UNP A1Z0P6
G	743	TYR	-	expression tag	UNP A1Z0P6
G	744	VAL	-	expression tag	UNP A1Z0P6
G	745	ARG	-	expression tag	UNP A1Z0P6
G	746	LYS	-	expression tag	UNP A1Z0P6
G	747	ASP	-	expression tag	UNP A1Z0P6
G	748	GLY	-	expression tag	UNP A1Z0P6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	749	GLU	-	expression tag	UNP A1Z0P6
G	750	TRP	-	expression tag	UNP A1Z0P6
G	751	VAL	-	expression tag	UNP A1Z0P6
G	752	LEU	-	expression tag	UNP A1Z0P6
G	753	LEU	-	expression tag	UNP A1Z0P6
G	754	SER	-	expression tag	UNP A1Z0P6
G	755	THR	-	expression tag	UNP A1Z0P6
G	756	PHE	-	expression tag	UNP A1Z0P6
G	757	LEU	-	expression tag	UNP A1Z0P6
G	758	GLY	-	expression tag	UNP A1Z0P6
G	759	ARG	-	expression tag	UNP A1Z0P6
G	760	SER	-	expression tag	UNP A1Z0P6
G	761	LEU	-	expression tag	UNP A1Z0P6
G	762	GLU	-	expression tag	UNP A1Z0P6
G	763	VAL	-	expression tag	UNP A1Z0P6
G	764	LEU	-	expression tag	UNP A1Z0P6
G	765	PHE	-	expression tag	UNP A1Z0P6
G	766	GLN	-	expression tag	UNP A1Z0P6
G	767	GLY	-	expression tag	UNP A1Z0P6
G	768	PRO	-	expression tag	UNP A1Z0P6
G	769	GLY	-	expression tag	UNP A1Z0P6
G	770	HIS	-	expression tag	UNP A1Z0P6
G	771	HIS	-	expression tag	UNP A1Z0P6
G	772	HIS	-	expression tag	UNP A1Z0P6
G	773	HIS	-	expression tag	UNP A1Z0P6
G	774	HIS	-	expression tag	UNP A1Z0P6
G	775	HIS	-	expression tag	UNP A1Z0P6
G	776	HIS	-	expression tag	UNP A1Z0P6
G	777	HIS	-	expression tag	UNP A1Z0P6
G	778	SER	-	expression tag	UNP A1Z0P6
G	779	ALA	-	expression tag	UNP A1Z0P6
G	780	TRP	-	expression tag	UNP A1Z0P6
G	781	SER	-	expression tag	UNP A1Z0P6
G	782	HIS	-	expression tag	UNP A1Z0P6
G	783	PRO	-	expression tag	UNP A1Z0P6
G	784	GLN	-	expression tag	UNP A1Z0P6
G	785	PHE	-	expression tag	UNP A1Z0P6
G	786	GLU	-	expression tag	UNP A1Z0P6
G	787	LYS	-	expression tag	UNP A1Z0P6
G	788	GLY	-	expression tag	UNP A1Z0P6
G	789	GLY	-	expression tag	UNP A1Z0P6
G	790	GLY	-	expression tag	UNP A1Z0P6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	791	SER	-	expression tag	UNP A1Z0P6
G	792	GLY	-	expression tag	UNP A1Z0P6
G	793	GLY	-	expression tag	UNP A1Z0P6
G	794	GLY	-	expression tag	UNP A1Z0P6
G	795	GLY	-	expression tag	UNP A1Z0P6
G	796	SER	-	expression tag	UNP A1Z0P6
G	797	GLY	-	expression tag	UNP A1Z0P6
G	798	GLY	-	expression tag	UNP A1Z0P6
G	799	SER	-	expression tag	UNP A1Z0P6
G	800	ALA	-	expression tag	UNP A1Z0P6
G	801	TRP	-	expression tag	UNP A1Z0P6
G	802	SER	-	expression tag	UNP A1Z0P6
G	803	HIS	-	expression tag	UNP A1Z0P6
G	804	PRO	-	expression tag	UNP A1Z0P6
G	805	GLN	-	expression tag	UNP A1Z0P6
G	806	PHE	-	expression tag	UNP A1Z0P6
G	807	GLU	-	expression tag	UNP A1Z0P6
G	808	LYS	-	expression tag	UNP A1Z0P6

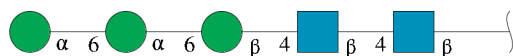
- Molecule 2 is a protein called D48 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	120	Total	C	N	O	S	0	0
			935	592	166	171	6		
2	J	120	Total	C	N	O	S	0	0
			935	592	166	171	6		
2	K	120	Total	C	N	O	S	0	0
			935	592	166	171	6		

- Molecule 3 is a protein called D48 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	107	Total	C	N	O	S	0	0
			823	521	138	160	4		
3	N	107	Total	C	N	O	S	0	0
			823	521	138	160	4		
3	O	107	Total	C	N	O	S	0	0
			823	521	138	160	4		

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-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
4	A	5	Total	C	N	O	0	0
			61	34	2	25		
4	C	5	Total	C	N	O	0	0
			61	34	2	25		
4	H	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 5 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
5	B	2	Total	C	N	O	0	0
			28	16	2	10		
5	D	2	Total	C	N	O	0	0
			28	16	2	10		
5	L	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



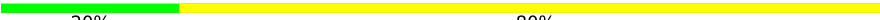
Mol	Chain	Residues	Atoms				AltConf
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	F	1	Total	C	N	O	0
			14	8	1	5	
6	G	1	Total	C	N	O	0
			14	8	1	5	

nose

Chain A:  20% 80%



• Molecule 4: alpha-D-mannopyranose-(1-6)-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

Chain C:  20% 80%



• Molecule 4: alpha-D-mannopyranose-(1-6)-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

Chain H:  20% 80%



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:  50% 100%



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  50% 50% 50%



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  50% 50% 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73388	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.560	Depositor
Minimum map value	-0.263	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.1	Depositor
Map size (\AA)	318.72, 318.72, 318.72	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, BMA, 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	E	0.19	0/4067	0.52	1/5527 (0.0%)
1	F	0.19	0/4067	0.50	0/5527
1	G	0.19	0/4067	0.52	1/5527 (0.0%)
2	I	0.23	0/957	0.55	0/1298
2	J	0.21	0/957	0.53	0/1298
2	K	0.23	0/957	0.56	0/1298
3	M	0.21	0/843	0.56	0/1147
3	N	0.19	0/843	0.52	0/1147
3	O	0.22	0/843	0.56	0/1147
All	All	0.20	0/17601	0.52	2/23916 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	429	TYR	N-CA-C	6.24	117.93	110.44
1	G	327	ALA	N-CA-C	5.57	122.67	110.80

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	E	3973	0	3807	30	0
1	F	3973	0	3807	33	0
1	G	3973	0	3807	26	0
2	I	935	0	913	6	0
2	J	935	0	913	10	0
2	K	935	0	913	6	0
3	M	823	0	806	6	0
3	N	823	0	806	4	0
3	O	823	0	806	4	0
4	A	61	0	52	0	0
4	C	61	0	52	0	0
4	H	61	0	52	0	0
5	B	28	0	25	0	0
5	D	28	0	25	1	0
5	L	28	0	25	1	0
6	E	14	0	13	0	0
6	F	14	0	13	0	0
6	G	14	0	13	0	0
All	All	17502	0	16848	116	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.

The worst 5 of 116 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:G:297:MET:HE3	1:G:345:LEU:HD13	1.71	0.73
1:F:200:LYS:O	1:F:205:GLY:N	2.26	0.69
1:E:249:THR:OG1	1:E:270:ASN:OD1	2.10	0.69
2:K:35:HIS:CD2	2:K:50:VAL:HG23	2.28	0.69
1:E:673:LEU:HD12	1:G:524:VAL:HG22	1.76	0.68

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	E	488/808 (60%)	446 (91%)	42 (9%)	0	100	100
1	F	488/808 (60%)	455 (93%)	33 (7%)	0	100	100
1	G	488/808 (60%)	448 (92%)	40 (8%)	0	100	100
2	I	118/120 (98%)	111 (94%)	7 (6%)	0	100	100
2	J	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
2	K	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
3	M	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
3	N	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
3	O	105/107 (98%)	99 (94%)	6 (6%)	0	100	100
All	All	2133/3105 (69%)	1982 (93%)	151 (7%)	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	E	430/674 (64%)	430 (100%)	0	100	100
1	F	430/674 (64%)	430 (100%)	0	100	100
1	G	430/674 (64%)	430 (100%)	0	100	100
2	I	101/101 (100%)	101 (100%)	0	100	100
2	J	101/101 (100%)	101 (100%)	0	100	100
2	K	101/101 (100%)	101 (100%)	0	100	100
3	M	89/89 (100%)	89 (100%)	0	100	100
3	N	89/89 (100%)	89 (100%)	0	100	100
3	O	89/89 (100%)	89 (100%)	0	100	100
All	All	1860/2592 (72%)	1860 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	580	ASN
2	I	35	HIS
2	J	82(A)	ASN
1	F	580	ASN
1	G	129	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

21 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	$\# Z > 2$
4	NAG	A	1	1,4	14,14,15	0.69	0	17,19,21	1.33	3 (17%)
4	NAG	A	2	4	14,14,15	0.75	0	17,19,21	0.95	0
4	BMA	A	3	4	11,11,12	0.87	0	15,15,17	2.50	6 (40%)
4	MAN	A	4	4	11,11,12	0.71	0	15,15,17	0.97	1 (6%)
4	MAN	A	5	4	11,11,12	0.66	0	15,15,17	1.25	1 (6%)
5	NAG	B	1	5,1	14,14,15	0.67	0	17,19,21	1.15	2 (11%)
5	NAG	B	2	5	14,14,15	0.72	0	17,19,21	1.18	1 (5%)
4	NAG	C	1	1,4	14,14,15	0.68	0	17,19,21	1.34	3 (17%)
4	NAG	C	2	4	14,14,15	0.74	0	17,19,21	0.99	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BMA	C	3	4	11,11,12	0.87	0	15,15,17	2.48	6 (40%)
4	MAN	C	4	4	11,11,12	0.69	0	15,15,17	0.98	1 (6%)
4	MAN	C	5	4	11,11,12	0.66	0	15,15,17	1.24	1 (6%)
5	NAG	D	1	5,1	14,14,15	0.71	0	17,19,21	1.14	2 (11%)
5	NAG	D	2	5	14,14,15	0.74	0	17,19,21	1.17	1 (5%)
4	NAG	H	1	1,4	14,14,15	0.67	0	17,19,21	1.29	3 (17%)
4	NAG	H	2	4	14,14,15	0.76	0	17,19,21	0.98	0
4	BMA	H	3	4	11,11,12	0.85	0	15,15,17	2.47	6 (40%)
4	MAN	H	4	4	11,11,12	0.71	0	15,15,17	0.93	1 (6%)
4	MAN	H	5	4	11,11,12	0.66	0	15,15,17	1.27	1 (6%)
5	NAG	L	1	5,1	14,14,15	0.69	0	17,19,21	1.14	2 (11%)
5	NAG	L	2	5	14,14,15	0.73	0	17,19,21	1.17	1 (5%)

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	A	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	2	4	-	0/6/23/26	0/1/1/1
4	BMA	A	3	4	-	1/2/19/22	0/1/1/1
4	MAN	A	4	4	-	2/2/19/22	0/1/1/1
4	MAN	A	5	4	-	1/2/19/22	0/1/1/1
5	NAG	B	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	B	2	5	-	1/6/23/26	0/1/1/1
4	NAG	C	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	2	4	-	0/6/23/26	0/1/1/1
4	BMA	C	3	4	-	1/2/19/22	0/1/1/1
4	MAN	C	4	4	-	2/2/19/22	0/1/1/1
4	MAN	C	5	4	-	1/2/19/22	0/1/1/1
5	NAG	D	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	D	2	5	-	1/6/23/26	0/1/1/1
4	NAG	H	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	1/2/19/22	0/1/1/1
4	MAN	H	4	4	-	2/2/19/22	0/1/1/1
4	MAN	H	5	4	-	1/2/19/22	0/1/1/1
5	NAG	L	1	5,1	-	1/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	L	2	5	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	3	BMA	C1-O5-C5	6.43	120.81	112.19
4	A	3	BMA	C1-O5-C5	6.42	120.79	112.19
4	C	3	BMA	C1-O5-C5	6.42	120.79	112.19
4	H	3	BMA	C3-C4-C5	4.27	117.97	110.23
4	A	3	BMA	C3-C4-C5	4.27	117.97	110.23

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

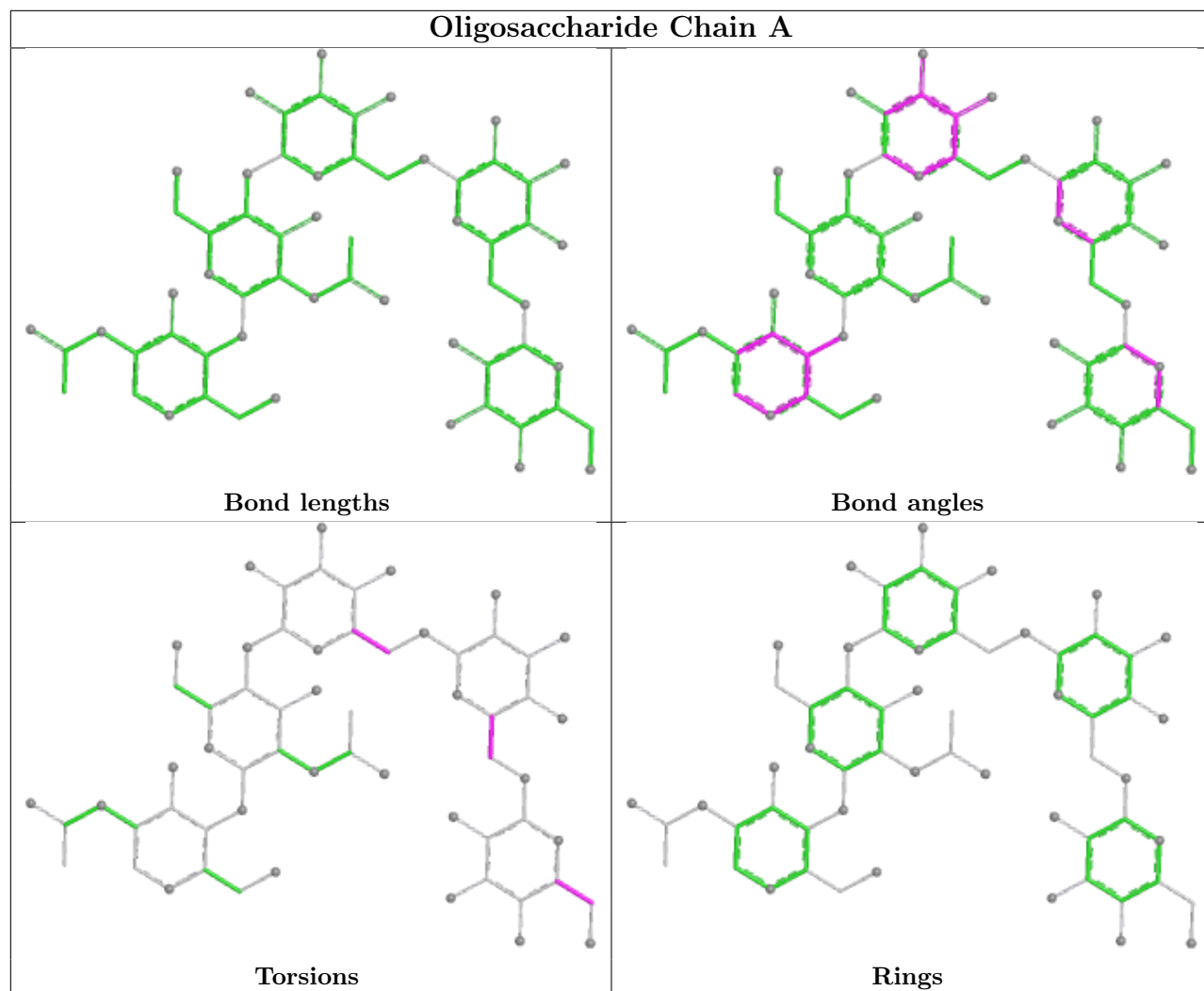
Mol	Chain	Res	Type	Atoms
4	C	4	MAN	O5-C5-C6-O6
4	A	4	MAN	O5-C5-C6-O6
4	H	4	MAN	O5-C5-C6-O6
4	C	3	BMA	O5-C5-C6-O6
5	B	2	NAG	O5-C5-C6-O6

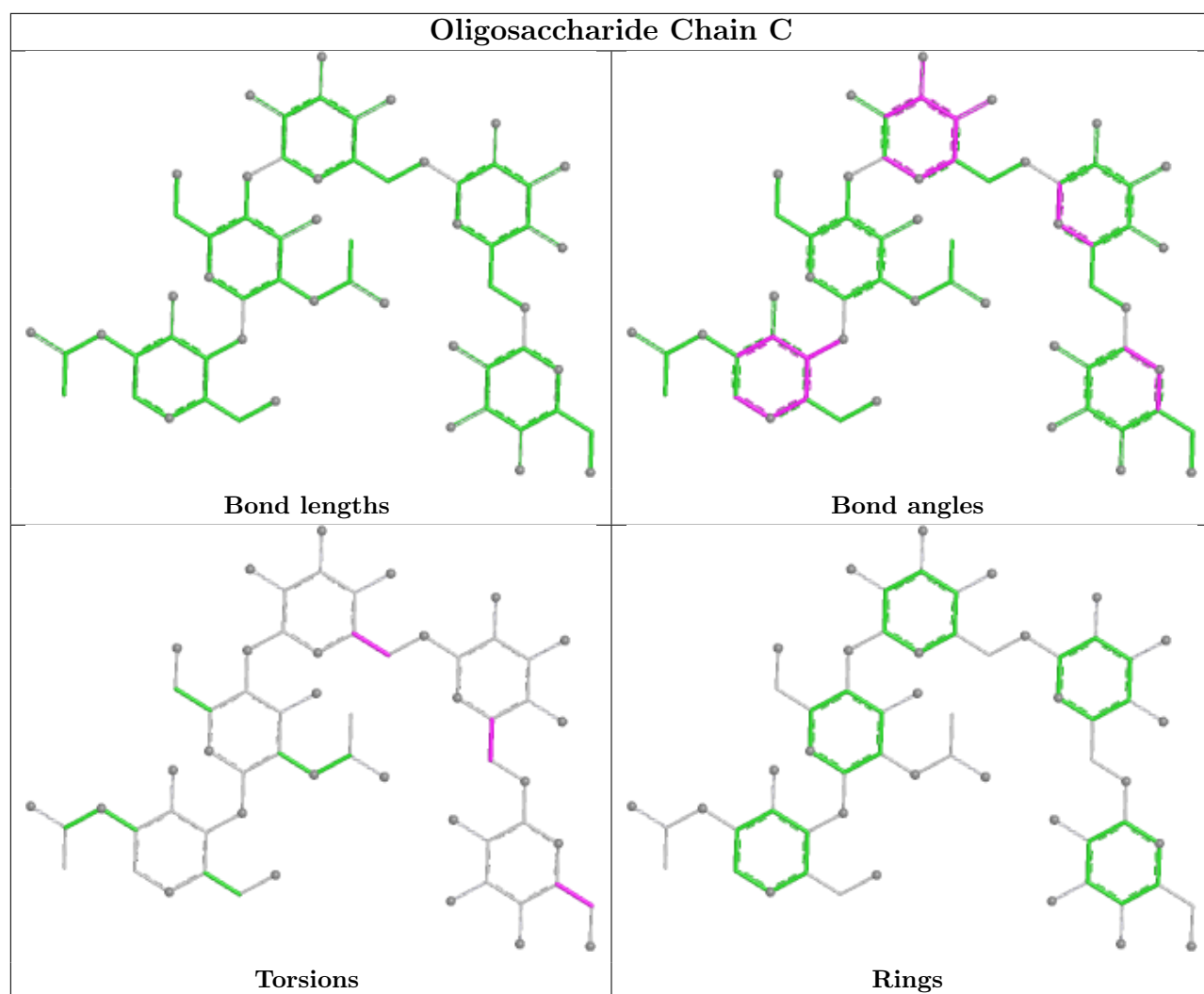
There are no ring outliers.

2 monomers are involved in 2 short contacts:

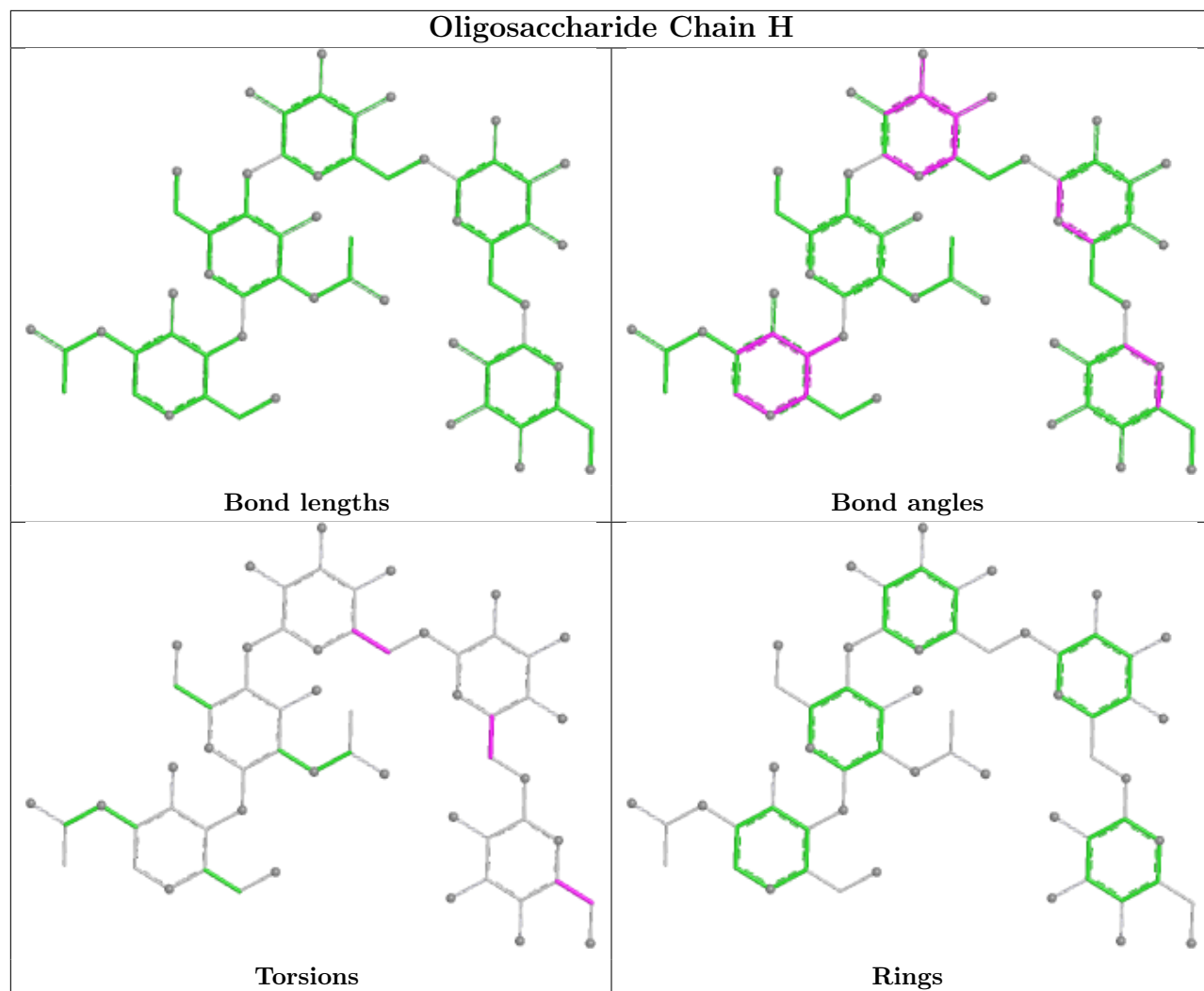
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1	NAG	1	0
5	L	1	NAG	1	0

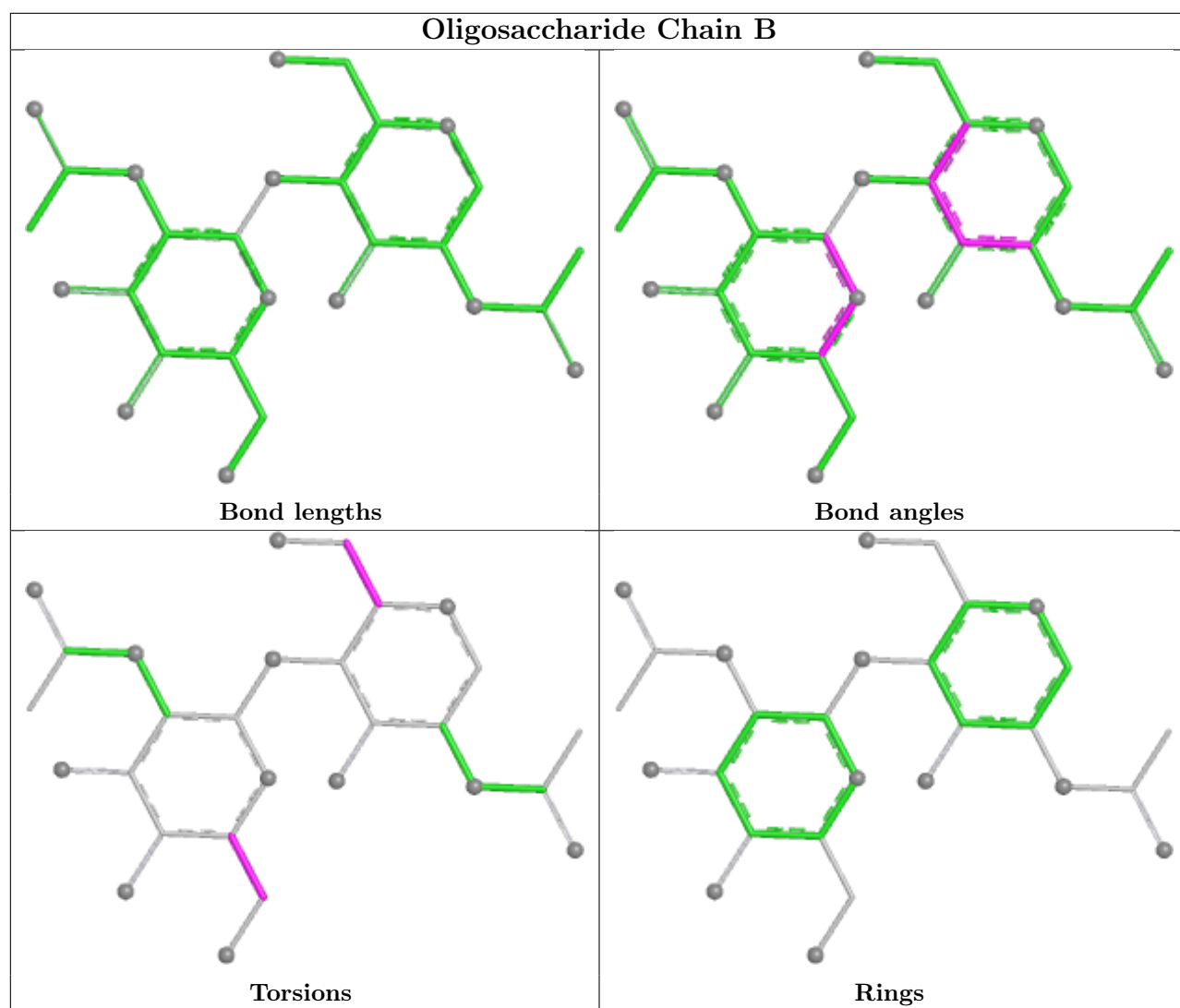
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

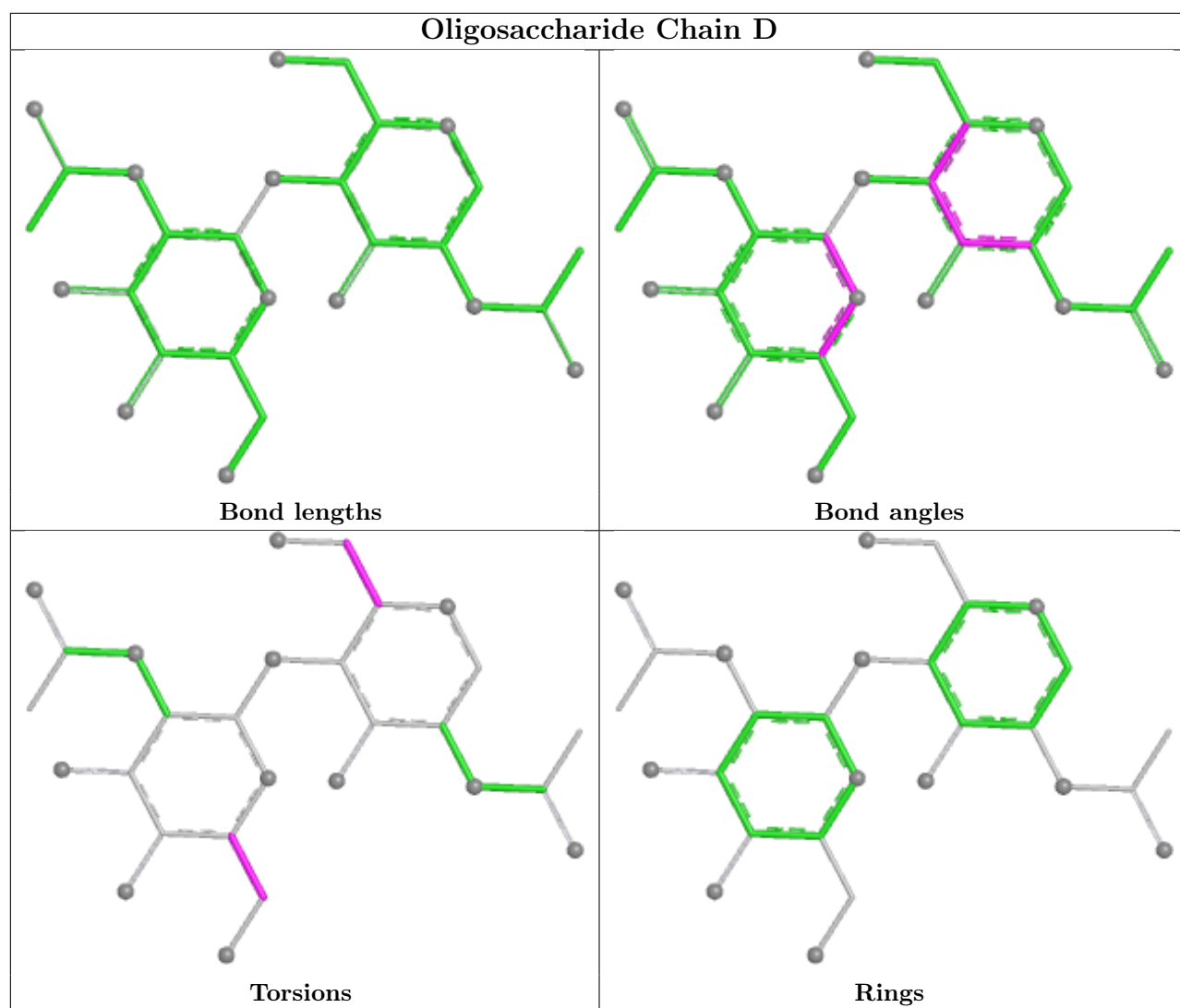


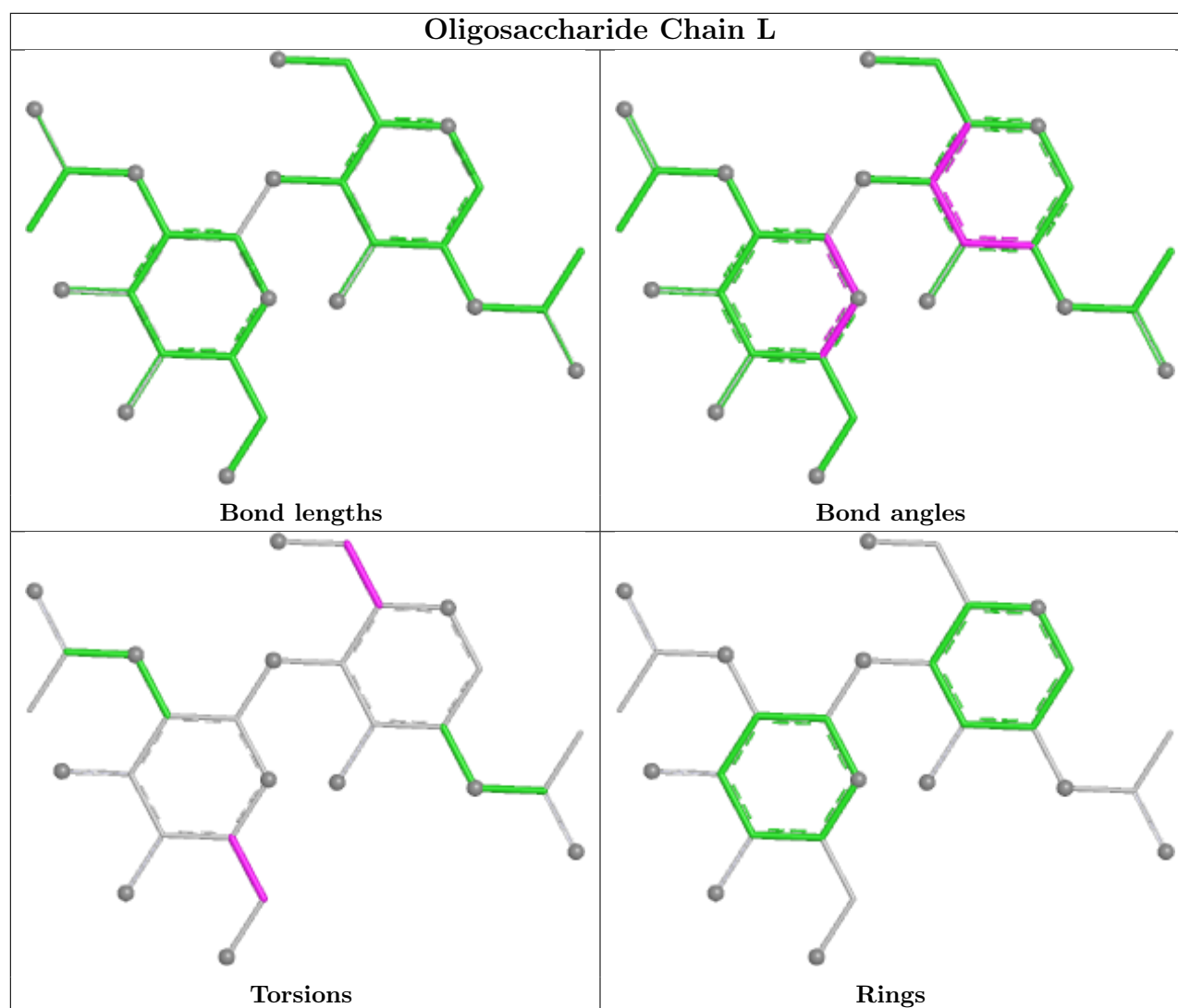


Oligosaccharide Chain H









5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
6	NAG	F	901	1	14,14,15	0.73	0	17,19,21	0.99	1 (5%)
6	NAG	E	901	1	14,14,15	0.74	0	17,19,21	1.03	1 (5%)
6	NAG	G	901	1	14,14,15	0.75	0	17,19,21	1.06	1 (5%)

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
6	NAG	F	901	1	-	0/6/23/26	0/1/1/1
6	NAG	E	901	1	-	0/6/23/26	0/1/1/1
6	NAG	G	901	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	901	NAG	C2-N2-C7	2.23	125.89	122.90
6	E	901	NAG	C2-N2-C7	2.19	125.84	122.90
6	F	901	NAG	C2-N2-C7	2.00	125.58	122.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

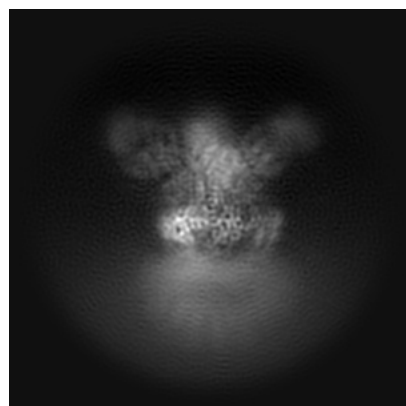
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46759. These allow visual inspection of the internal detail of the map and identification of artifacts.

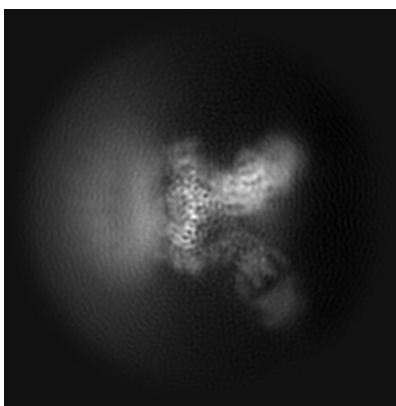
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

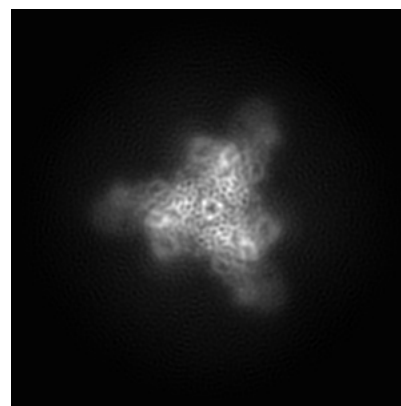
6.1.1 Primary map



X

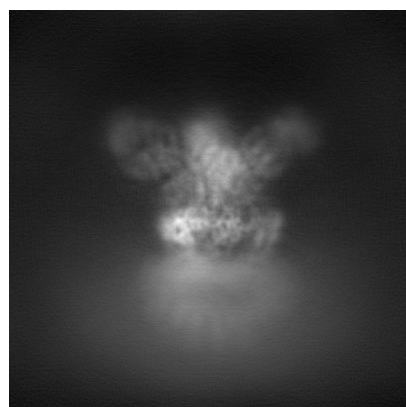


Y

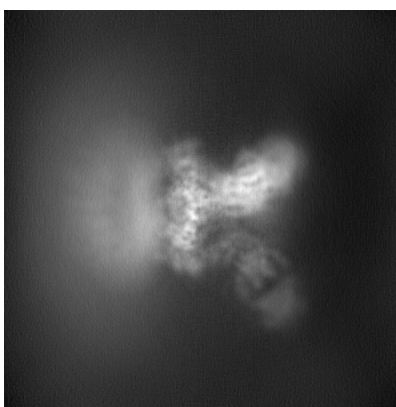


Z

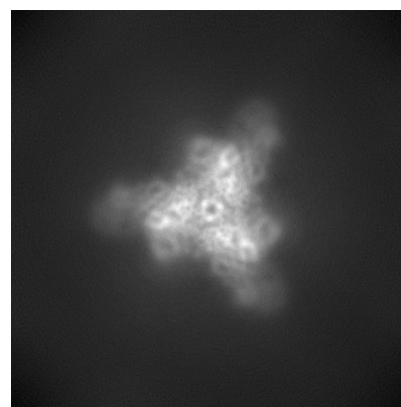
6.1.2 Raw map



X



Y

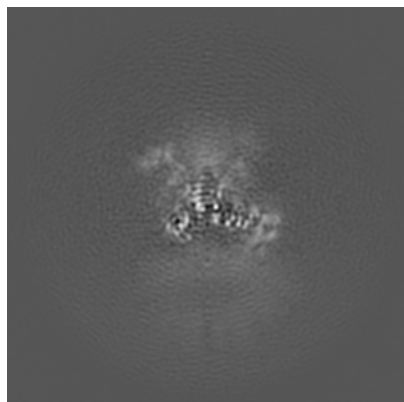


Z

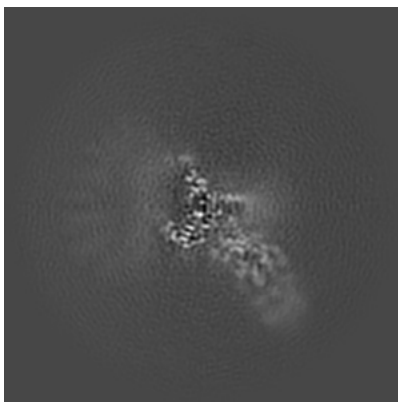
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

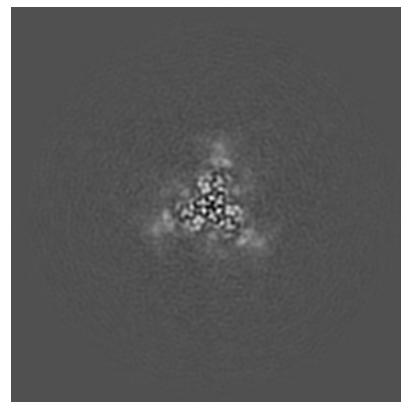
6.2.1 Primary map



X Index: 192

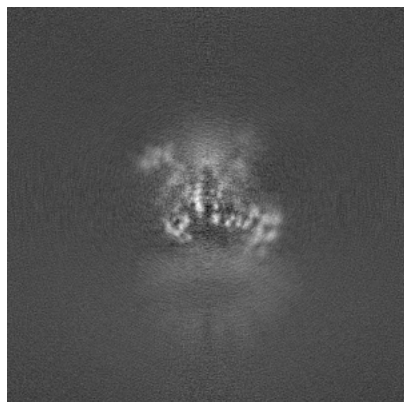


Y Index: 192

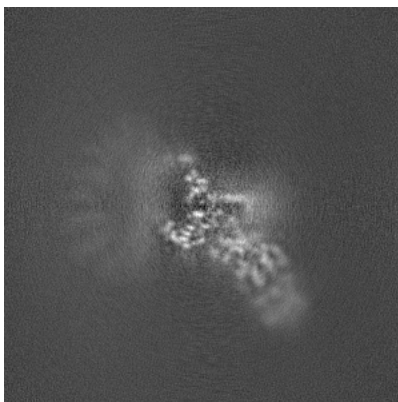


Z Index: 192

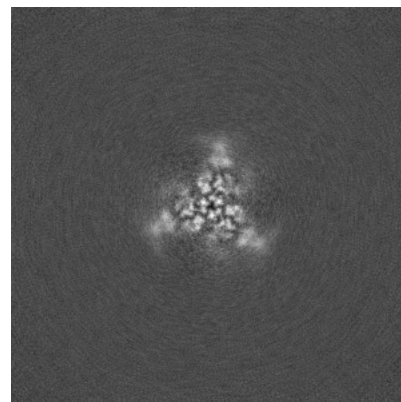
6.2.2 Raw map



X Index: 192



Y Index: 192

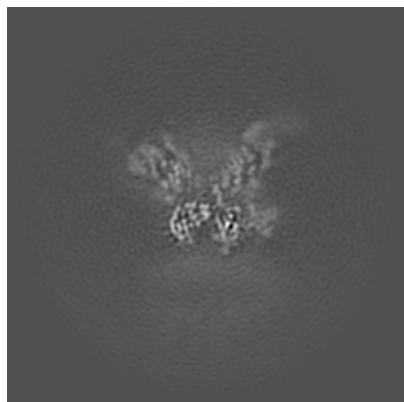


Z Index: 192

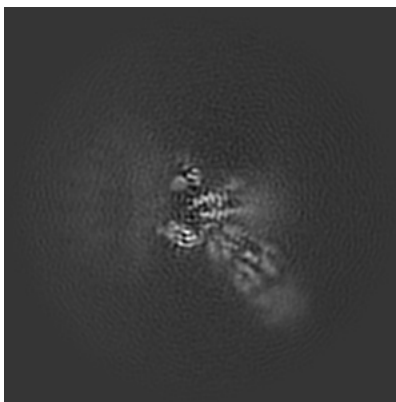
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

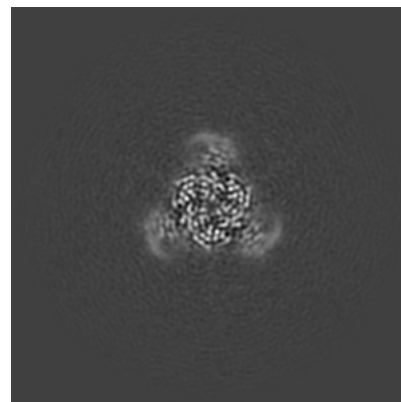
6.3.1 Primary map



X Index: 208

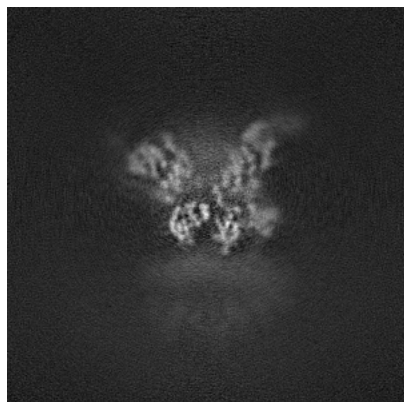


Y Index: 197

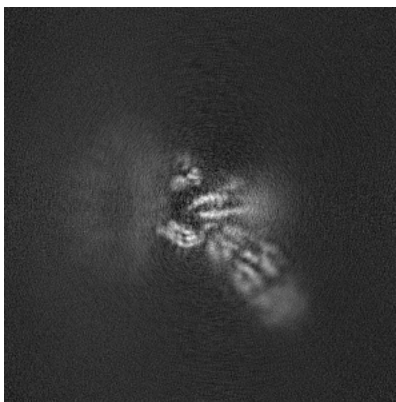


Z Index: 181

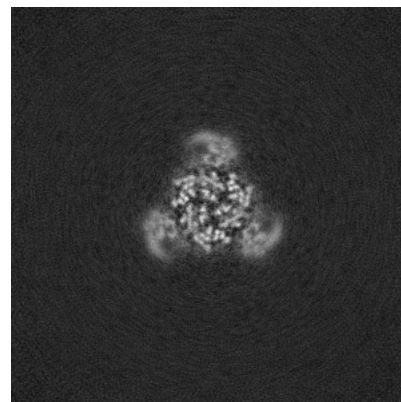
6.3.2 Raw map



X Index: 208



Y Index: 197

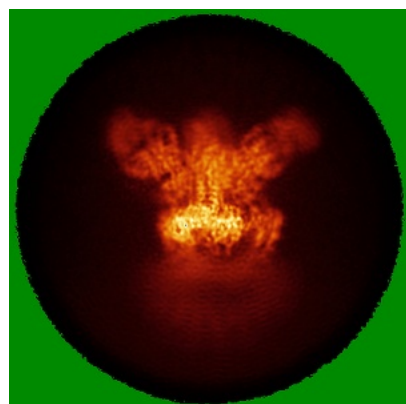


Z Index: 181

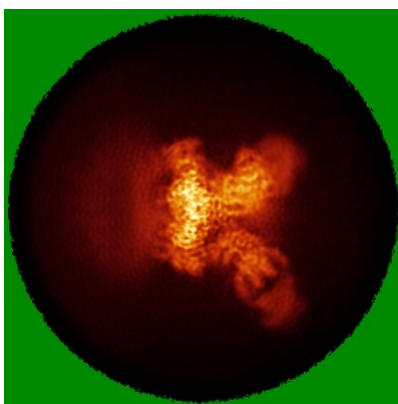
The images above show the largest variance slices of the map in three orthogonal directions.

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

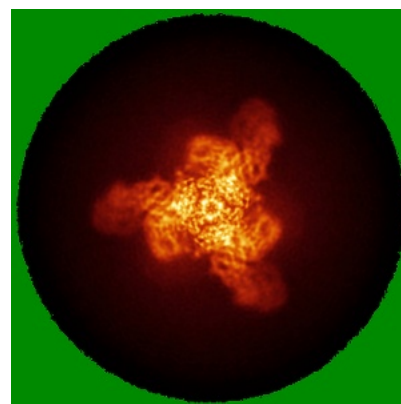
6.4.1 Primary map



X

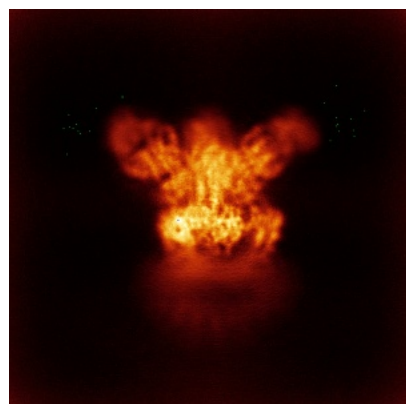


Y

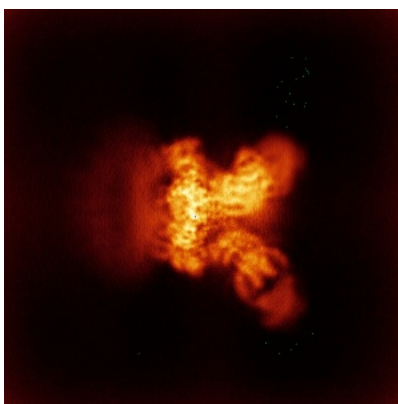


Z

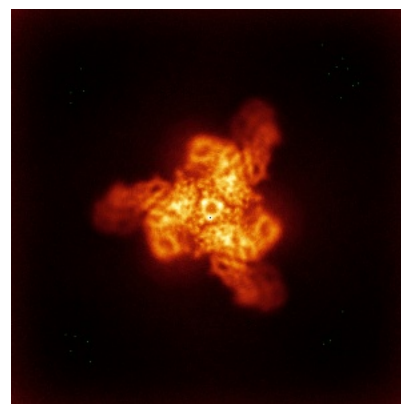
6.4.2 Raw map



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.

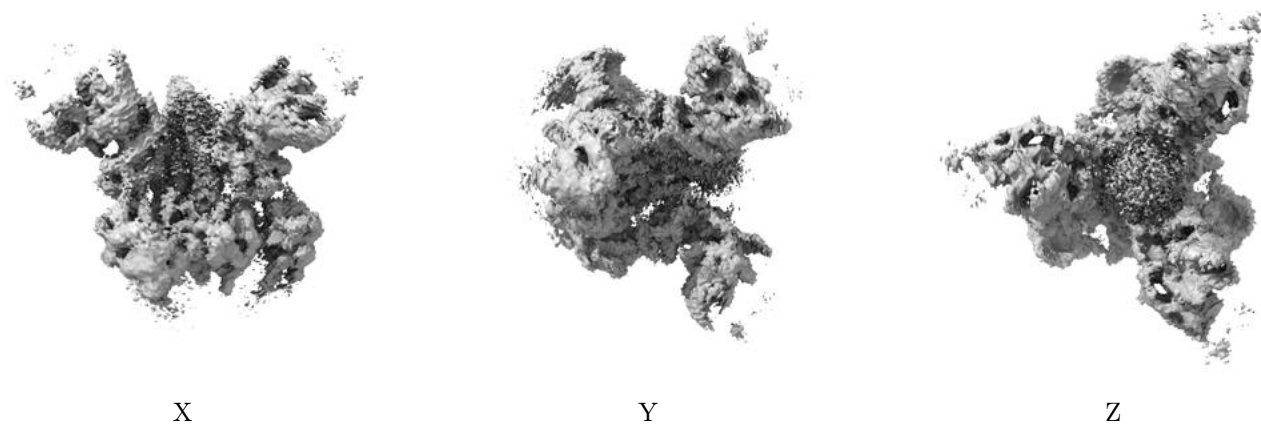
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

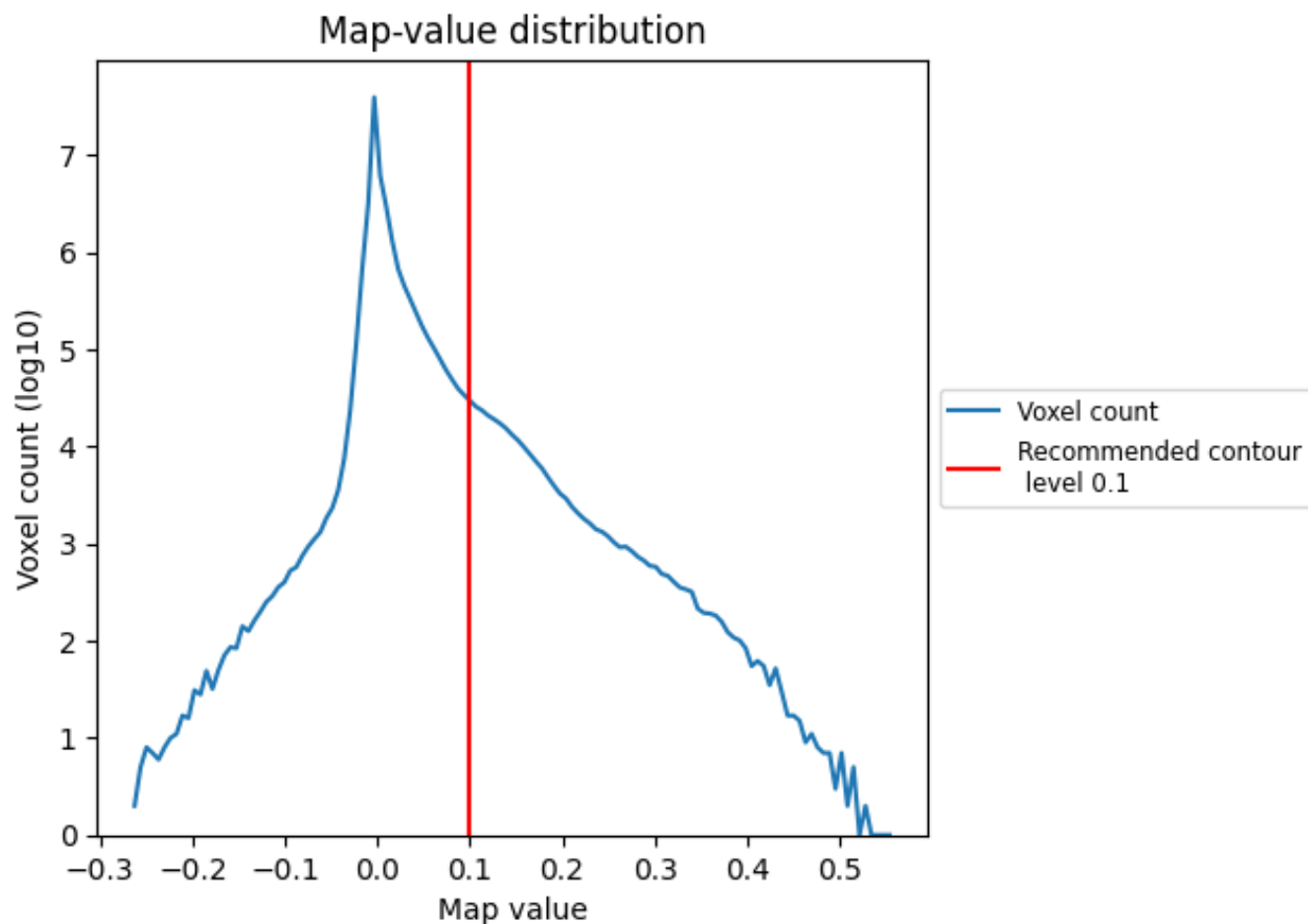
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

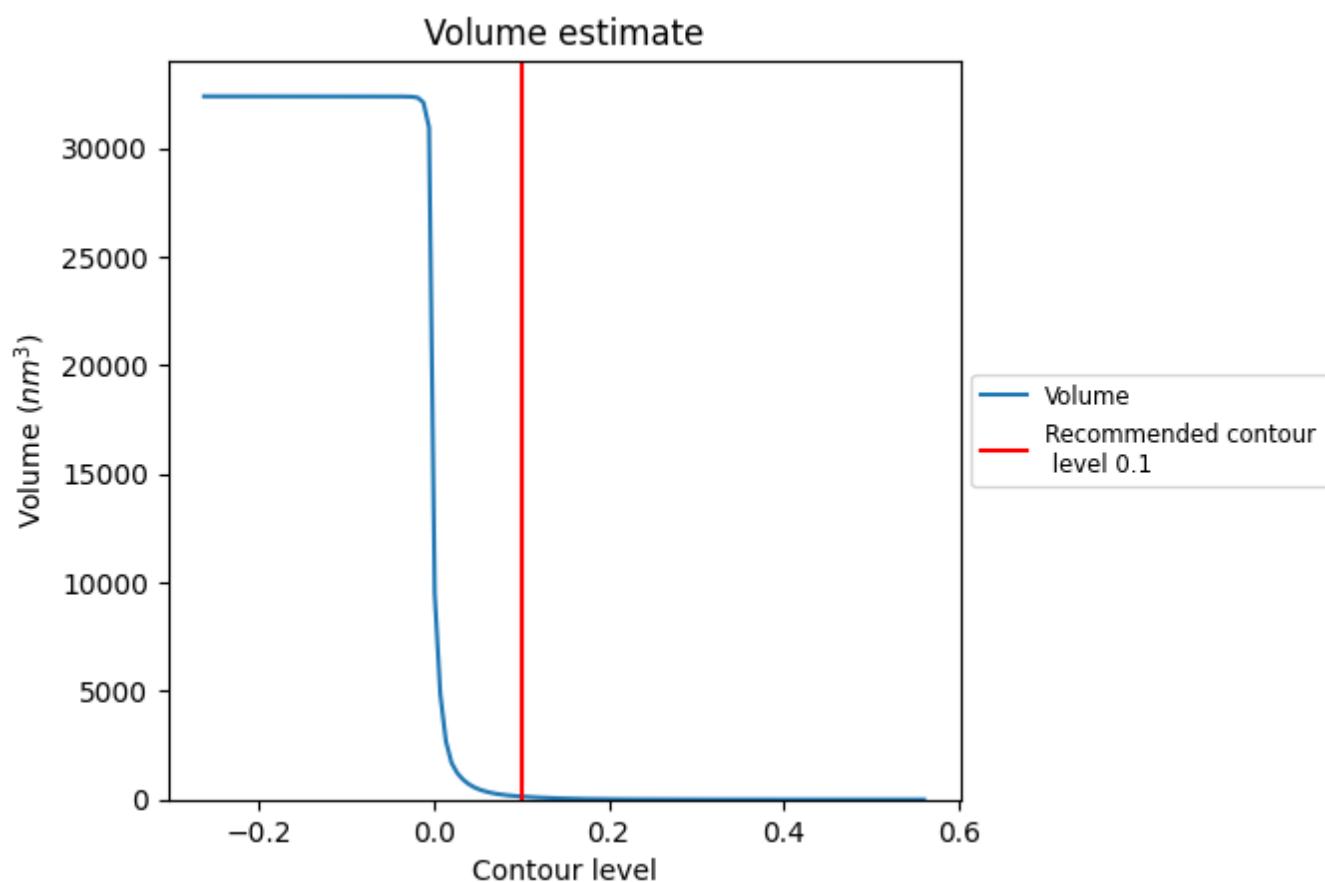
This section contains the results of statistical analysis of the map.

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.

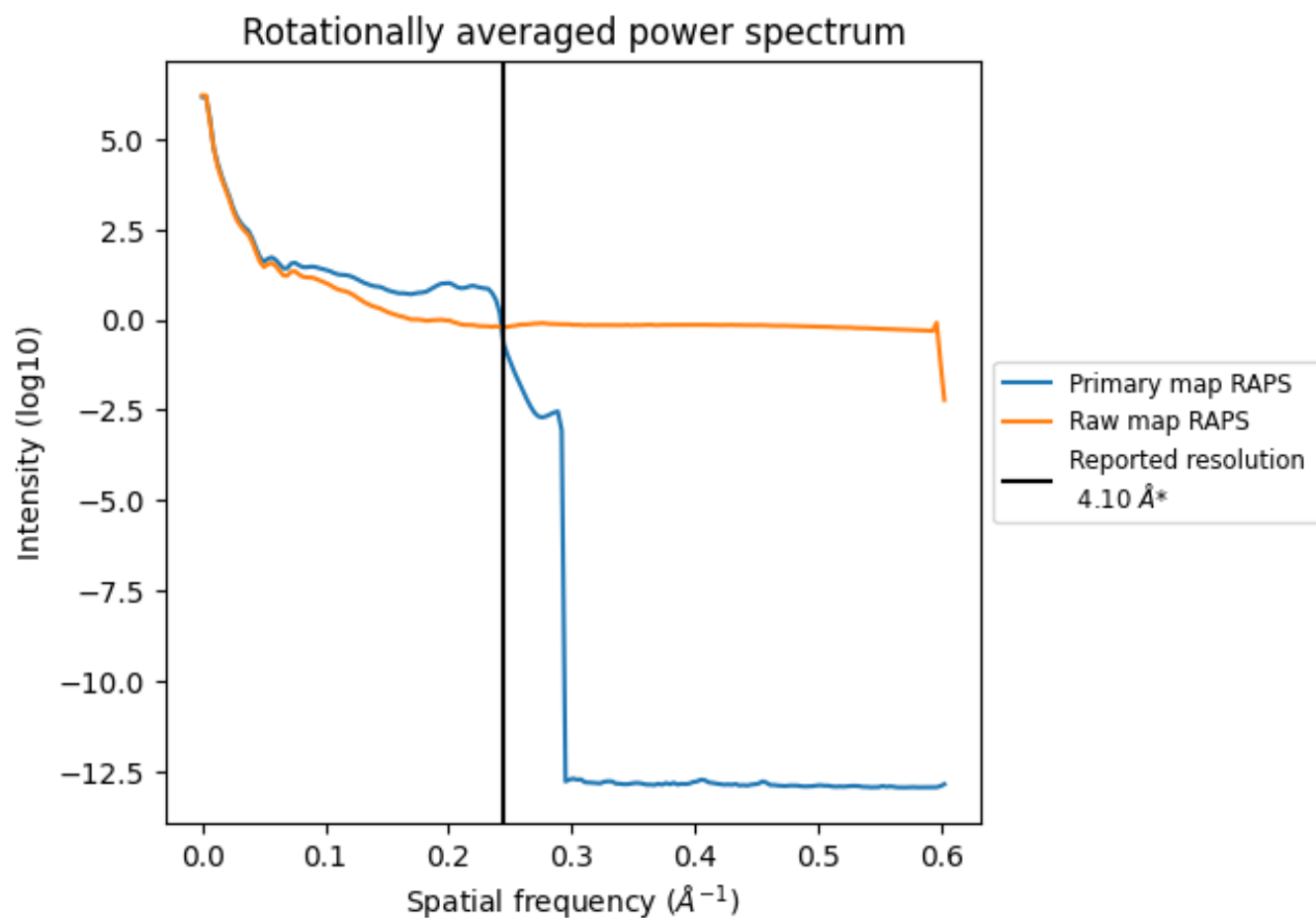
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 141 nm³; this corresponds to an approximate mass of 128 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 ⓘ

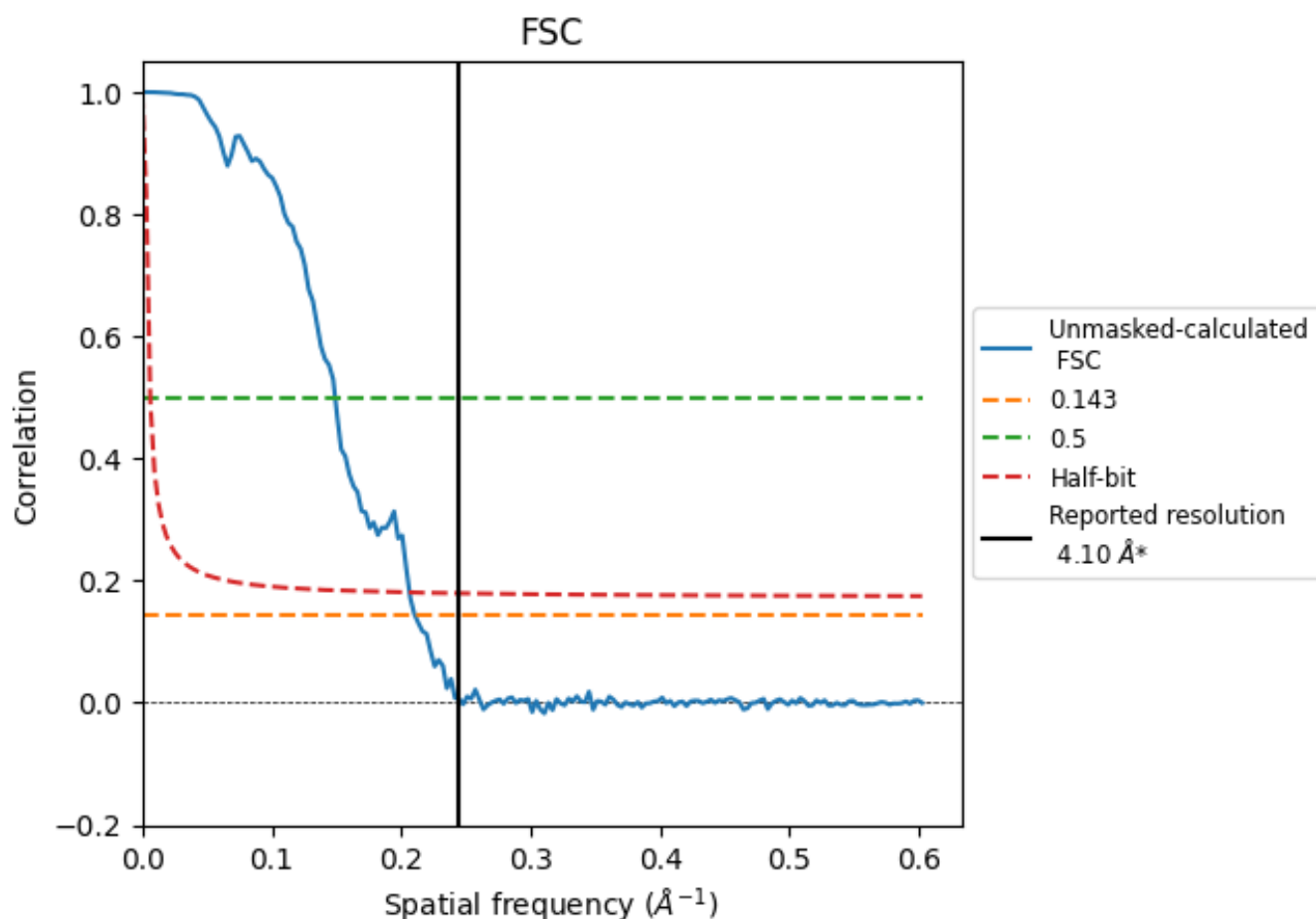


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

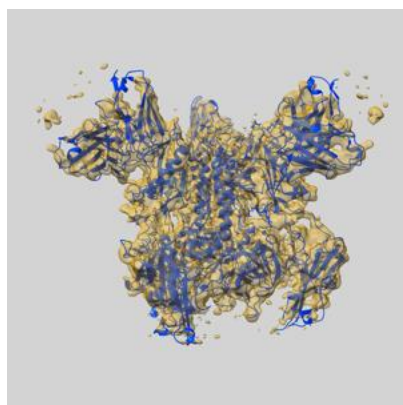
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.75	6.71	4.84

*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 4.75 differs from the reported value 4.1 by more than 10 %

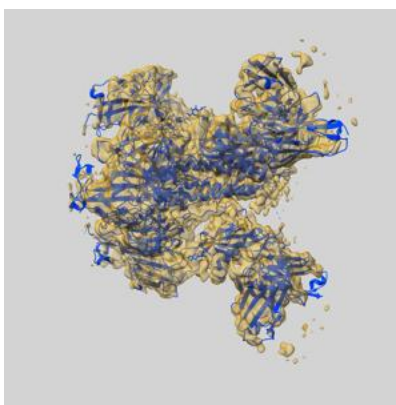
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46759 and PDB model 9DD7. Per-residue inclusion information can be found in section 3 on page 13.

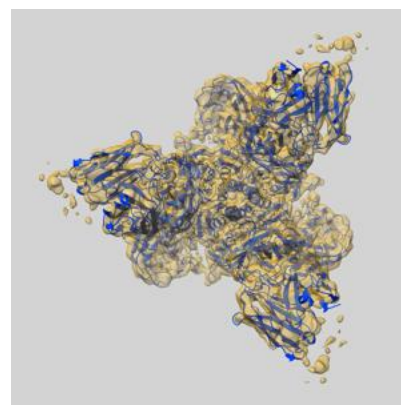
9.1 Map-model overlay [i](#)



X



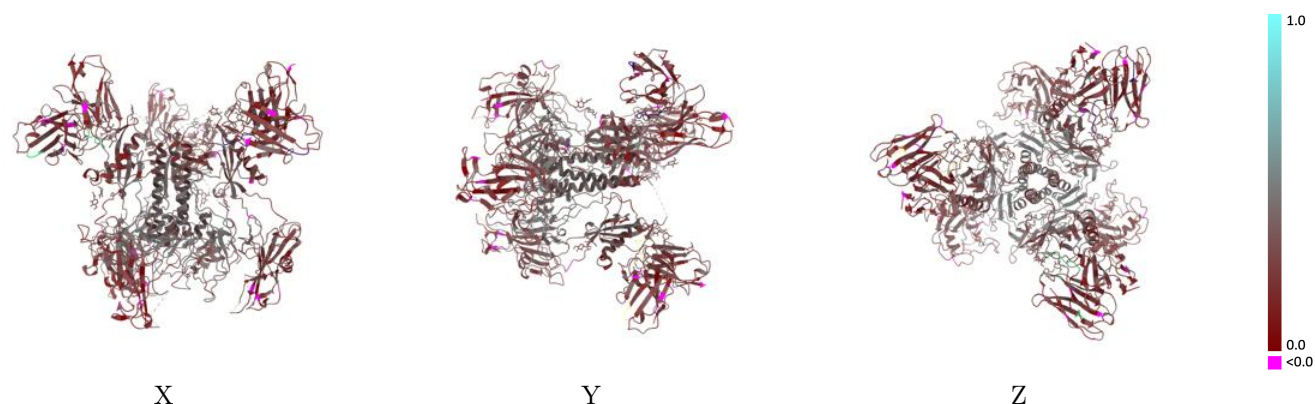
Y



Z

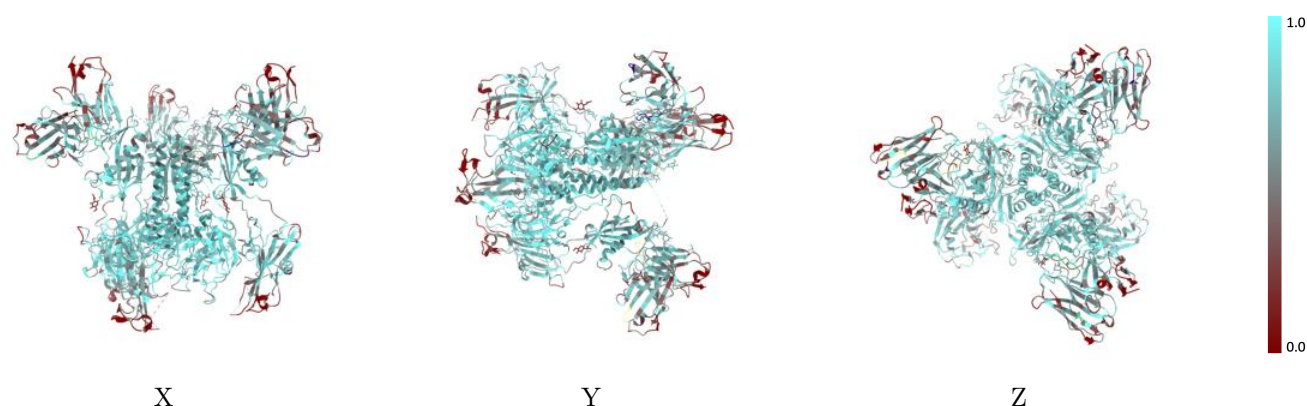
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



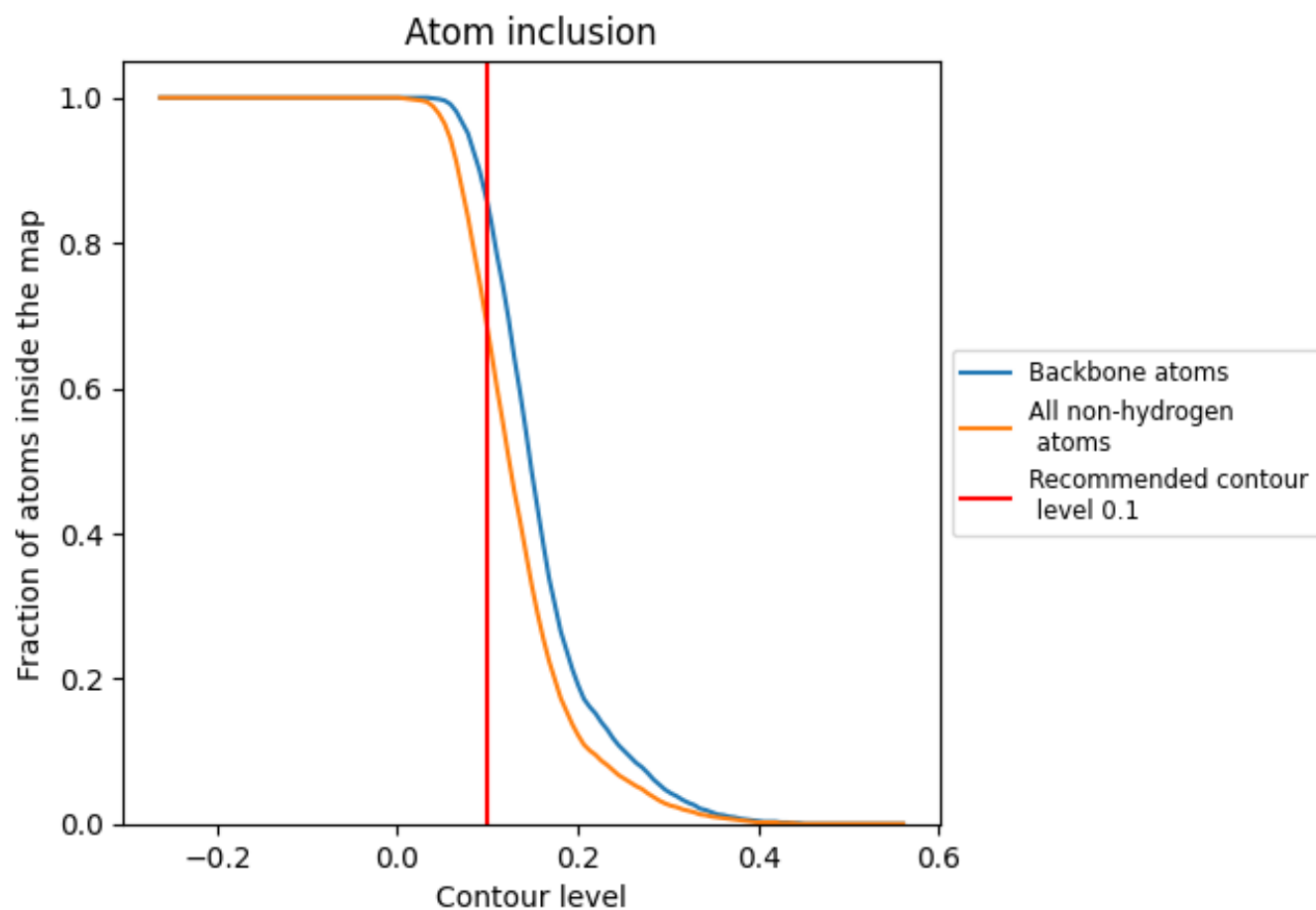
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 68% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.3120
A	 0.6720	 0.3680
B	 0.4640	 0.3260
C	 0.6560	 0.3690
D	 0.3930	 0.3370
E	 0.7310	 0.3360
F	 0.7340	 0.3360
G	 0.7330	 0.3370
H	 0.6560	 0.3660
I	 0.5840	 0.2430
J	 0.5870	 0.2410
K	 0.5870	 0.2450
L	 0.4290	 0.3280
M	 0.5440	 0.2690
N	 0.5420	 0.2650
O	 0.5490	 0.2640

