



Full wwPDB EM Validation Report ⓘ

Sep 2, 2025 – 05:10 PM EDT

PDB ID : 9DD6 / pdb_00009dd6
EMDB ID : EMD-46758
Title : Cryo-EM structure of neutralizing murine antibody WS.HSV-1.24 in complex with HSV-1 glycoprotein B trimer gB-Ecto.516P.531E
Authors : Roark, R.S.; Shapiro, L.S.; Kwong, P.D.
Deposited on : 2024-08-27
Resolution : 3.10 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

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.dev126
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

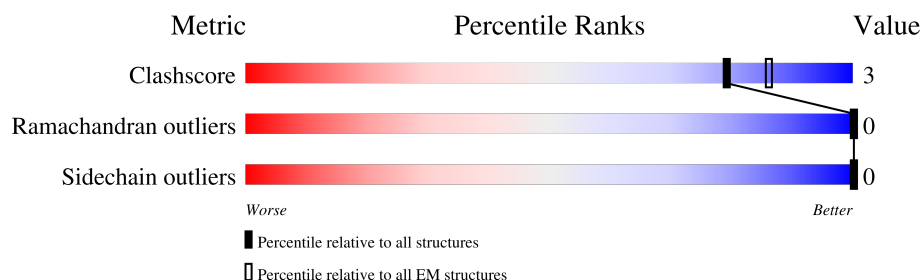
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	
1	F	808	
1	G	808	
2	H	218	
2	I	218	
2	J	218	
3	L	214	
3	M	214	

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Mol	Chain	Length	Quality of chain
3	N	214	 50% 50%
4	A	2	 100%
4	C	2	 100%
4	K	2	 100%
5	B	3	 67% 33%
5	D	3	 67% 33%
5	O	3	 67% 33%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18906 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	560	Total	C	N	O	S	0	0
			4512	2840	790	861	21		
1	F	560	Total	C	N	O	S	0	0
			4512	2840	790	861	21		
1	G	560	Total	C	N	O	S	0	0
			4512	2840	790	861	21		

There are 246 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	516	PRO	HIS	engineered mutation	UNP A1Z0P7
E	531	GLU	LEU	engineered mutation	UNP A1Z0P7
E	729	GLY	-	expression tag	UNP A1Z0P7
E	730	SER	-	expression tag	UNP A1Z0P7
E	731	GLY	-	expression tag	UNP A1Z0P7
E	732	TYR	-	expression tag	UNP A1Z0P7
E	733	ILE	-	expression tag	UNP A1Z0P7
E	734	PRO	-	expression tag	UNP A1Z0P7
E	735	GLU	-	expression tag	UNP A1Z0P7
E	736	ALA	-	expression tag	UNP A1Z0P7
E	737	PRO	-	expression tag	UNP A1Z0P7
E	738	ARG	-	expression tag	UNP A1Z0P7
E	739	ASP	-	expression tag	UNP A1Z0P7
E	740	GLY	-	expression tag	UNP A1Z0P7
E	741	GLN	-	expression tag	UNP A1Z0P7
E	742	ALA	-	expression tag	UNP A1Z0P7
E	743	TYR	-	expression tag	UNP A1Z0P7
E	744	VAL	-	expression tag	UNP A1Z0P7
E	745	ARG	-	expression tag	UNP A1Z0P7
E	746	LYS	-	expression tag	UNP A1Z0P7
E	747	ASP	-	expression tag	UNP A1Z0P7
E	748	GLY	-	expression tag	UNP A1Z0P7
E	749	GLU	-	expression tag	UNP A1Z0P7
E	750	TRP	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	751	VAL	-	expression tag	UNP A1Z0P7
E	752	LEU	-	expression tag	UNP A1Z0P7
E	753	LEU	-	expression tag	UNP A1Z0P7
E	754	SER	-	expression tag	UNP A1Z0P7
E	755	THR	-	expression tag	UNP A1Z0P7
E	756	PHE	-	expression tag	UNP A1Z0P7
E	757	LEU	-	expression tag	UNP A1Z0P7
E	758	GLY	-	expression tag	UNP A1Z0P7
E	759	ARG	-	expression tag	UNP A1Z0P7
E	760	SER	-	expression tag	UNP A1Z0P7
E	761	LEU	-	expression tag	UNP A1Z0P7
E	762	GLU	-	expression tag	UNP A1Z0P7
E	763	VAL	-	expression tag	UNP A1Z0P7
E	764	LEU	-	expression tag	UNP A1Z0P7
E	765	PHE	-	expression tag	UNP A1Z0P7
E	766	GLN	-	expression tag	UNP A1Z0P7
E	767	GLY	-	expression tag	UNP A1Z0P7
E	768	PRO	-	expression tag	UNP A1Z0P7
E	769	GLY	-	expression tag	UNP A1Z0P7
E	770	HIS	-	expression tag	UNP A1Z0P7
E	771	HIS	-	expression tag	UNP A1Z0P7
E	772	HIS	-	expression tag	UNP A1Z0P7
E	773	HIS	-	expression tag	UNP A1Z0P7
E	774	HIS	-	expression tag	UNP A1Z0P7
E	775	HIS	-	expression tag	UNP A1Z0P7
E	776	HIS	-	expression tag	UNP A1Z0P7
E	777	HIS	-	expression tag	UNP A1Z0P7
E	778	SER	-	expression tag	UNP A1Z0P7
E	779	ALA	-	expression tag	UNP A1Z0P7
E	780	TRP	-	expression tag	UNP A1Z0P7
E	781	SER	-	expression tag	UNP A1Z0P7
E	782	HIS	-	expression tag	UNP A1Z0P7
E	783	PRO	-	expression tag	UNP A1Z0P7
E	784	GLN	-	expression tag	UNP A1Z0P7
E	785	PHE	-	expression tag	UNP A1Z0P7
E	786	GLU	-	expression tag	UNP A1Z0P7
E	787	LYS	-	expression tag	UNP A1Z0P7
E	788	GLY	-	expression tag	UNP A1Z0P7
E	789	GLY	-	expression tag	UNP A1Z0P7
E	790	GLY	-	expression tag	UNP A1Z0P7
E	791	SER	-	expression tag	UNP A1Z0P7
E	792	GLY	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	793	GLY	-	expression tag	UNP A1Z0P7
E	794	GLY	-	expression tag	UNP A1Z0P7
E	795	GLY	-	expression tag	UNP A1Z0P7
E	796	SER	-	expression tag	UNP A1Z0P7
E	797	GLY	-	expression tag	UNP A1Z0P7
E	798	GLY	-	expression tag	UNP A1Z0P7
E	799	SER	-	expression tag	UNP A1Z0P7
E	800	ALA	-	expression tag	UNP A1Z0P7
E	801	TRP	-	expression tag	UNP A1Z0P7
E	802	SER	-	expression tag	UNP A1Z0P7
E	803	HIS	-	expression tag	UNP A1Z0P7
E	804	PRO	-	expression tag	UNP A1Z0P7
E	805	GLN	-	expression tag	UNP A1Z0P7
E	806	PHE	-	expression tag	UNP A1Z0P7
E	807	GLU	-	expression tag	UNP A1Z0P7
E	808	LYS	-	expression tag	UNP A1Z0P7
F	516	PRO	HIS	engineered mutation	UNP A1Z0P7
F	531	GLU	LEU	engineered mutation	UNP A1Z0P7
F	729	GLY	-	expression tag	UNP A1Z0P7
F	730	SER	-	expression tag	UNP A1Z0P7
F	731	GLY	-	expression tag	UNP A1Z0P7
F	732	TYR	-	expression tag	UNP A1Z0P7
F	733	ILE	-	expression tag	UNP A1Z0P7
F	734	PRO	-	expression tag	UNP A1Z0P7
F	735	GLU	-	expression tag	UNP A1Z0P7
F	736	ALA	-	expression tag	UNP A1Z0P7
F	737	PRO	-	expression tag	UNP A1Z0P7
F	738	ARG	-	expression tag	UNP A1Z0P7
F	739	ASP	-	expression tag	UNP A1Z0P7
F	740	GLY	-	expression tag	UNP A1Z0P7
F	741	GLN	-	expression tag	UNP A1Z0P7
F	742	ALA	-	expression tag	UNP A1Z0P7
F	743	TYR	-	expression tag	UNP A1Z0P7
F	744	VAL	-	expression tag	UNP A1Z0P7
F	745	ARG	-	expression tag	UNP A1Z0P7
F	746	LYS	-	expression tag	UNP A1Z0P7
F	747	ASP	-	expression tag	UNP A1Z0P7
F	748	GLY	-	expression tag	UNP A1Z0P7
F	749	GLU	-	expression tag	UNP A1Z0P7
F	750	TRP	-	expression tag	UNP A1Z0P7
F	751	VAL	-	expression tag	UNP A1Z0P7
F	752	LEU	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	753	LEU	-	expression tag	UNP A1Z0P7
F	754	SER	-	expression tag	UNP A1Z0P7
F	755	THR	-	expression tag	UNP A1Z0P7
F	756	PHE	-	expression tag	UNP A1Z0P7
F	757	LEU	-	expression tag	UNP A1Z0P7
F	758	GLY	-	expression tag	UNP A1Z0P7
F	759	ARG	-	expression tag	UNP A1Z0P7
F	760	SER	-	expression tag	UNP A1Z0P7
F	761	LEU	-	expression tag	UNP A1Z0P7
F	762	GLU	-	expression tag	UNP A1Z0P7
F	763	VAL	-	expression tag	UNP A1Z0P7
F	764	LEU	-	expression tag	UNP A1Z0P7
F	765	PHE	-	expression tag	UNP A1Z0P7
F	766	GLN	-	expression tag	UNP A1Z0P7
F	767	GLY	-	expression tag	UNP A1Z0P7
F	768	PRO	-	expression tag	UNP A1Z0P7
F	769	GLY	-	expression tag	UNP A1Z0P7
F	770	HIS	-	expression tag	UNP A1Z0P7
F	771	HIS	-	expression tag	UNP A1Z0P7
F	772	HIS	-	expression tag	UNP A1Z0P7
F	773	HIS	-	expression tag	UNP A1Z0P7
F	774	HIS	-	expression tag	UNP A1Z0P7
F	775	HIS	-	expression tag	UNP A1Z0P7
F	776	HIS	-	expression tag	UNP A1Z0P7
F	777	HIS	-	expression tag	UNP A1Z0P7
F	778	SER	-	expression tag	UNP A1Z0P7
F	779	ALA	-	expression tag	UNP A1Z0P7
F	780	TRP	-	expression tag	UNP A1Z0P7
F	781	SER	-	expression tag	UNP A1Z0P7
F	782	HIS	-	expression tag	UNP A1Z0P7
F	783	PRO	-	expression tag	UNP A1Z0P7
F	784	GLN	-	expression tag	UNP A1Z0P7
F	785	PHE	-	expression tag	UNP A1Z0P7
F	786	GLU	-	expression tag	UNP A1Z0P7
F	787	LYS	-	expression tag	UNP A1Z0P7
F	788	GLY	-	expression tag	UNP A1Z0P7
F	789	GLY	-	expression tag	UNP A1Z0P7
F	790	GLY	-	expression tag	UNP A1Z0P7
F	791	SER	-	expression tag	UNP A1Z0P7
F	792	GLY	-	expression tag	UNP A1Z0P7
F	793	GLY	-	expression tag	UNP A1Z0P7
F	794	GLY	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	795	GLY	-	expression tag	UNP A1Z0P7
F	796	SER	-	expression tag	UNP A1Z0P7
F	797	GLY	-	expression tag	UNP A1Z0P7
F	798	GLY	-	expression tag	UNP A1Z0P7
F	799	SER	-	expression tag	UNP A1Z0P7
F	800	ALA	-	expression tag	UNP A1Z0P7
F	801	TRP	-	expression tag	UNP A1Z0P7
F	802	SER	-	expression tag	UNP A1Z0P7
F	803	HIS	-	expression tag	UNP A1Z0P7
F	804	PRO	-	expression tag	UNP A1Z0P7
F	805	GLN	-	expression tag	UNP A1Z0P7
F	806	PHE	-	expression tag	UNP A1Z0P7
F	807	GLU	-	expression tag	UNP A1Z0P7
F	808	LYS	-	expression tag	UNP A1Z0P7
G	516	PRO	HIS	engineered mutation	UNP A1Z0P7
G	531	GLU	LEU	engineered mutation	UNP A1Z0P7
G	729	GLY	-	expression tag	UNP A1Z0P7
G	730	SER	-	expression tag	UNP A1Z0P7
G	731	GLY	-	expression tag	UNP A1Z0P7
G	732	TYR	-	expression tag	UNP A1Z0P7
G	733	ILE	-	expression tag	UNP A1Z0P7
G	734	PRO	-	expression tag	UNP A1Z0P7
G	735	GLU	-	expression tag	UNP A1Z0P7
G	736	ALA	-	expression tag	UNP A1Z0P7
G	737	PRO	-	expression tag	UNP A1Z0P7
G	738	ARG	-	expression tag	UNP A1Z0P7
G	739	ASP	-	expression tag	UNP A1Z0P7
G	740	GLY	-	expression tag	UNP A1Z0P7
G	741	GLN	-	expression tag	UNP A1Z0P7
G	742	ALA	-	expression tag	UNP A1Z0P7
G	743	TYR	-	expression tag	UNP A1Z0P7
G	744	VAL	-	expression tag	UNP A1Z0P7
G	745	ARG	-	expression tag	UNP A1Z0P7
G	746	LYS	-	expression tag	UNP A1Z0P7
G	747	ASP	-	expression tag	UNP A1Z0P7
G	748	GLY	-	expression tag	UNP A1Z0P7
G	749	GLU	-	expression tag	UNP A1Z0P7
G	750	TRP	-	expression tag	UNP A1Z0P7
G	751	VAL	-	expression tag	UNP A1Z0P7
G	752	LEU	-	expression tag	UNP A1Z0P7
G	753	LEU	-	expression tag	UNP A1Z0P7
G	754	SER	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
G	755	THR	-	expression tag	UNP A1Z0P7
G	756	PHE	-	expression tag	UNP A1Z0P7
G	757	LEU	-	expression tag	UNP A1Z0P7
G	758	GLY	-	expression tag	UNP A1Z0P7
G	759	ARG	-	expression tag	UNP A1Z0P7
G	760	SER	-	expression tag	UNP A1Z0P7
G	761	LEU	-	expression tag	UNP A1Z0P7
G	762	GLU	-	expression tag	UNP A1Z0P7
G	763	VAL	-	expression tag	UNP A1Z0P7
G	764	LEU	-	expression tag	UNP A1Z0P7
G	765	PHE	-	expression tag	UNP A1Z0P7
G	766	GLN	-	expression tag	UNP A1Z0P7
G	767	GLY	-	expression tag	UNP A1Z0P7
G	768	PRO	-	expression tag	UNP A1Z0P7
G	769	GLY	-	expression tag	UNP A1Z0P7
G	770	HIS	-	expression tag	UNP A1Z0P7
G	771	HIS	-	expression tag	UNP A1Z0P7
G	772	HIS	-	expression tag	UNP A1Z0P7
G	773	HIS	-	expression tag	UNP A1Z0P7
G	774	HIS	-	expression tag	UNP A1Z0P7
G	775	HIS	-	expression tag	UNP A1Z0P7
G	776	HIS	-	expression tag	UNP A1Z0P7
G	777	HIS	-	expression tag	UNP A1Z0P7
G	778	SER	-	expression tag	UNP A1Z0P7
G	779	ALA	-	expression tag	UNP A1Z0P7
G	780	TRP	-	expression tag	UNP A1Z0P7
G	781	SER	-	expression tag	UNP A1Z0P7
G	782	HIS	-	expression tag	UNP A1Z0P7
G	783	PRO	-	expression tag	UNP A1Z0P7
G	784	GLN	-	expression tag	UNP A1Z0P7
G	785	PHE	-	expression tag	UNP A1Z0P7
G	786	GLU	-	expression tag	UNP A1Z0P7
G	787	LYS	-	expression tag	UNP A1Z0P7
G	788	GLY	-	expression tag	UNP A1Z0P7
G	789	GLY	-	expression tag	UNP A1Z0P7
G	790	GLY	-	expression tag	UNP A1Z0P7
G	791	SER	-	expression tag	UNP A1Z0P7
G	792	GLY	-	expression tag	UNP A1Z0P7
G	793	GLY	-	expression tag	UNP A1Z0P7
G	794	GLY	-	expression tag	UNP A1Z0P7
G	795	GLY	-	expression tag	UNP A1Z0P7
G	796	SER	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
G	797	GLY	-	expression tag	UNP A1Z0P7
G	798	GLY	-	expression tag	UNP A1Z0P7
G	799	SER	-	expression tag	UNP A1Z0P7
G	800	ALA	-	expression tag	UNP A1Z0P7
G	801	TRP	-	expression tag	UNP A1Z0P7
G	802	SER	-	expression tag	UNP A1Z0P7
G	803	HIS	-	expression tag	UNP A1Z0P7
G	804	PRO	-	expression tag	UNP A1Z0P7
G	805	GLN	-	expression tag	UNP A1Z0P7
G	806	PHE	-	expression tag	UNP A1Z0P7
G	807	GLU	-	expression tag	UNP A1Z0P7
G	808	LYS	-	expression tag	UNP A1Z0P7

- Molecule 2 is a protein called WS.HSV-1.24 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	115	Total	C	N	O	S	0	0
			885	564	143	176	2		
2	I	115	Total	C	N	O	S	0	0
			885	564	143	176	2		
2	J	115	Total	C	N	O	S	0	0
			885	564	143	176	2		

- Molecule 3 is a protein called WS.HSV-1.24 light chain.

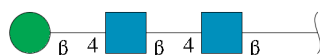
Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	107	Total	C	N	O	S	0	0
			810	502	135	170	3		
3	M	107	Total	C	N	O	S	0	0
			810	502	135	170	3		
3	N	107	Total	C	N	O	S	0	0
			810	502	135	170	3		

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



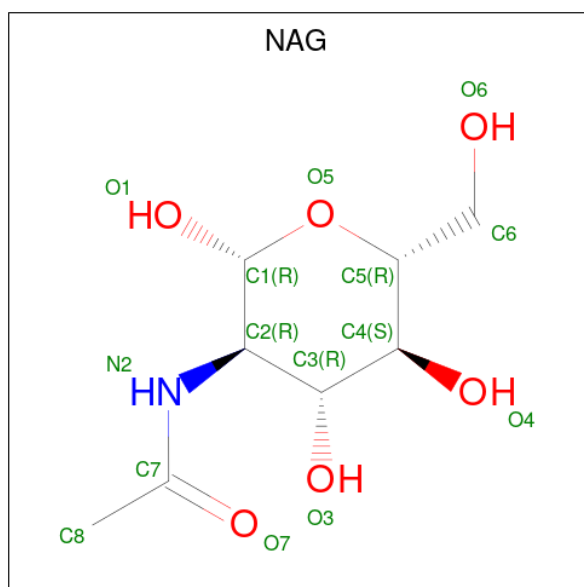
Mol	Chain	Residues	Atoms				AltConf	Trace
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	C	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 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.

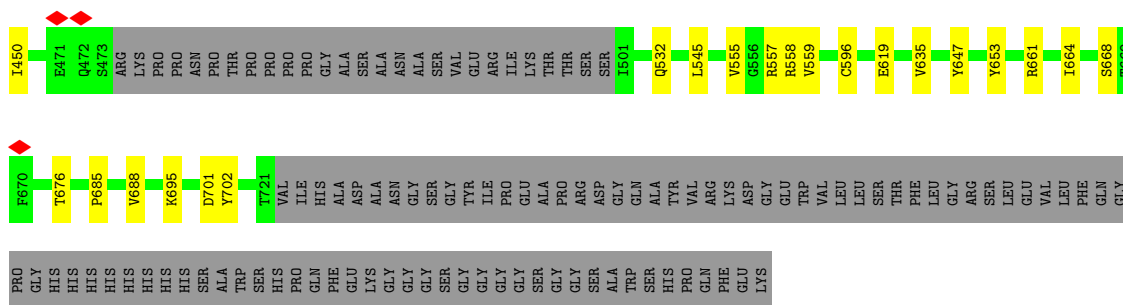


Mol	Chain	Residues	Atoms				AltConf	Trace
5	B	3	Total	C	N	O	0	0
			39	22	2	15		
5	D	3	Total	C	N	O	0	0
			39	22	2	15		
5	O	3	Total	C	N	O	0	0
			39	22	2	15		

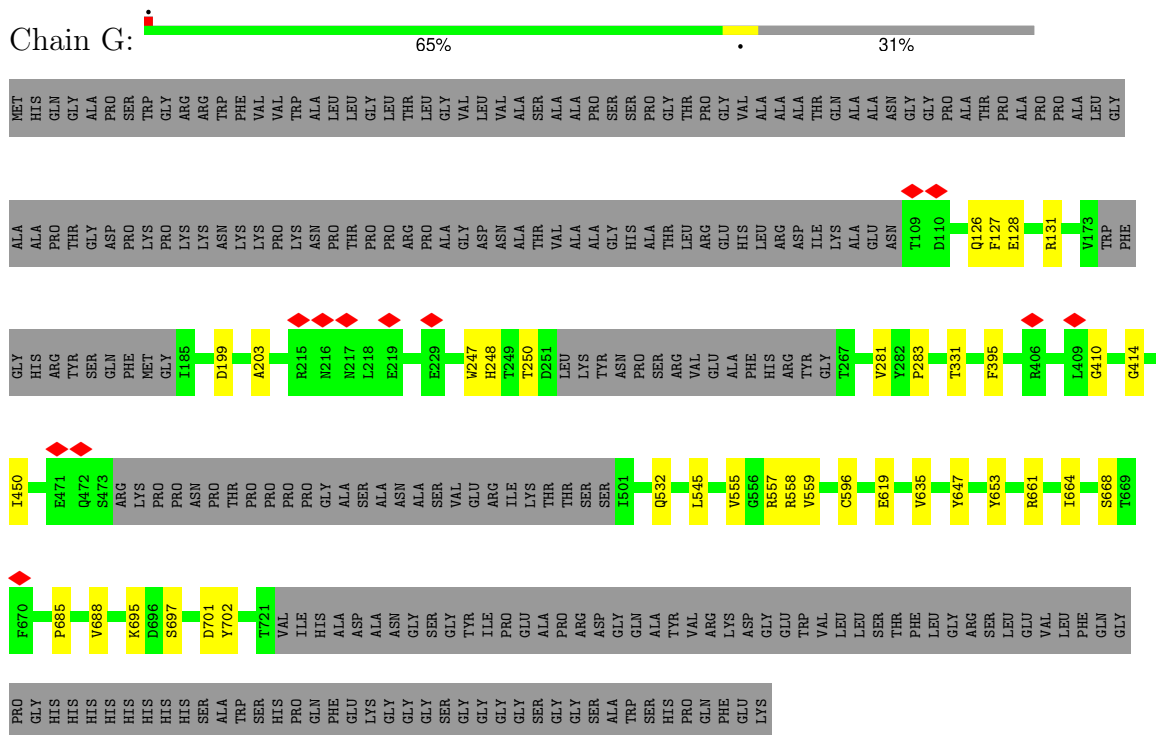
- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



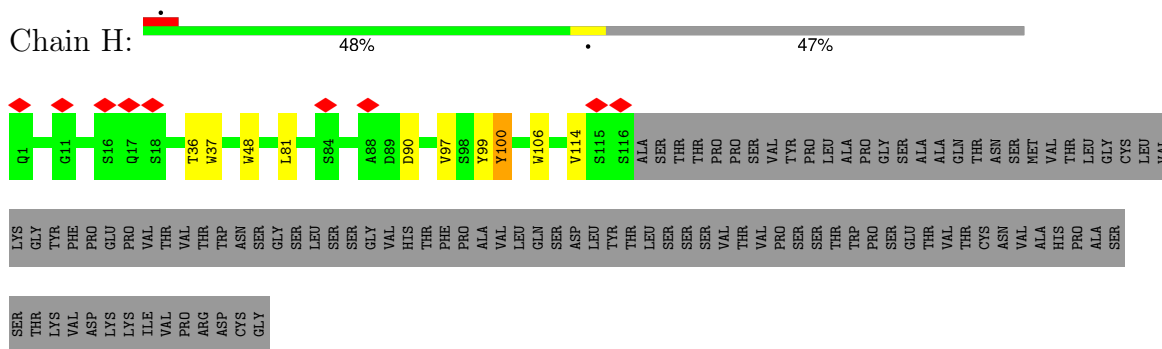
Mol	Chain	Residues	Atoms				AltConf
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	F	1	Total	C	N	O	0
			14	8	1	5	
6	F	1	Total	C	N	O	0
			14	8	1	5	
6	G	1	Total	C	N	O	0
			14	8	1	5	
6	G	1	Total	C	N	O	0
			14	8	1	5	



- Molecule 1: Glycoprotein B



- Molecule 2: WS.HSV-1.24 heavy chain



- Molecule 2: WS.HSV-1.24 heavy chain



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

Chain A:  100%

NAG1
NAG2

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

Chain C:  100%

NAG1
NAG2

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

Chain K:  100%

NAG1
NAG2

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

Chain B:  67% 33%

NAG1
NAG2
BMA3

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

Chain D:  67% 33%

NAG1
NAG2
BMA3

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

Chain O:  67% 33%

NAG1
NAG2
BMA3

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	127859	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)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.440	Depositor
Minimum map value	-0.214	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.08	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: 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	0.25	0/4618	0.51	2/6276 (0.0%)
1	F	0.25	0/4618	0.51	2/6276 (0.0%)
1	G	0.25	0/4618	0.51	2/6276 (0.0%)
2	H	0.34	0/908	0.66	1/1239 (0.1%)
2	I	0.34	0/908	0.66	1/1239 (0.1%)
2	J	0.34	0/908	0.66	1/1239 (0.1%)
3	L	0.16	0/824	0.45	0/1113
3	M	0.17	0/824	0.45	0/1113
3	N	0.17	0/824	0.45	0/1113
All	All	0.25	0/19050	0.53	9/25884 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	127	PHE	N-CA-CB	-9.77	93.63	111.13
1	E	127	PHE	N-CA-CB	-9.77	93.64	111.13
1	G	127	PHE	N-CA-CB	-9.75	93.67	111.13
1	E	127	PHE	CB-CA-C	9.11	127.86	109.38
1	G	127	PHE	CB-CA-C	9.10	127.85	109.38
1	F	127	PHE	CB-CA-C	9.09	127.83	109.38
2	J	100	TYR	N-CA-C	-7.62	102.11	111.33
2	H	100	TYR	N-CA-C	-7.61	102.12	111.33
2	I	100	TYR	N-CA-C	-7.60	102.13	111.33

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	4512	0	4328	27	0
1	F	4512	0	4328	25	0
1	G	4512	0	4328	24	0
2	H	885	0	854	9	0
2	I	885	0	854	10	0
2	J	885	0	854	10	0
3	L	810	0	792	0	0
3	M	810	0	792	0	0
3	N	810	0	792	1	0
4	A	28	0	25	0	0
4	C	28	0	25	0	0
4	K	28	0	25	0	0
5	B	39	0	34	0	0
5	D	39	0	34	0	0
5	O	39	0	34	0	0
6	E	28	0	26	0	0
6	F	28	0	26	0	0
6	G	28	0	26	0	0
All	All	18906	0	18177	96	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 (96) 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:E:545:LEU:HD11	1:F:545:LEU:CD1	2.20	0.70
1:F:701:ASP:OD1	1:F:702:TYR:N	2.29	0.66
1:E:701:ASP:OD1	1:E:702:TYR:N	2.29	0.65
2:I:36:THR:HG23	2:I:48:TRP:HE1	1.62	0.65
1:G:701:ASP:OD1	1:G:702:TYR:N	2.29	0.65
2:J:36:THR:HG23	2:J:48:TRP:HE1	1.61	0.64
2:H:36:THR:HG23	2:H:48:TRP:HE1	1.61	0.64
1:E:596:CYS:SG	1:E:653:TYR:CE1	2.92	0.62
1:F:619:GLU:OE1	1:F:619:GLU:N	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:596:CYS:SG	1:G:653:TYR:CE1	2.92	0.62
1:F:596:CYS:SG	1:F:653:TYR:CE1	2.92	0.62
1:E:619:GLU:N	1:E:619:GLU:OE1	2.33	0.61
2:H:36:THR:CG2	2:H:48:TRP:HE1	2.13	0.61
1:G:619:GLU:N	1:G:619:GLU:OE1	2.33	0.61
2:I:36:THR:CG2	2:I:48:TRP:HE1	2.13	0.61
2:J:36:THR:CG2	2:J:48:TRP:HE1	2.13	0.61
1:G:555:VAL:HG21	1:G:559:VAL:HG21	1.84	0.60
1:E:555:VAL:HG21	1:E:559:VAL:HG21	1.84	0.59
1:F:555:VAL:HG21	1:F:559:VAL:HG21	1.84	0.59
1:E:248:HIS:HD2	1:E:250:THR:O	1.86	0.58
1:E:545:LEU:HD11	1:F:545:LEU:HD11	1.86	0.58
1:F:248:HIS:HD2	1:F:250:THR:C	2.12	0.58
1:G:248:HIS:HD2	1:G:250:THR:C	2.12	0.58
1:G:248:HIS:HD2	1:G:250:THR:O	1.86	0.57
1:E:248:HIS:HD2	1:E:250:THR:C	2.12	0.57
1:F:248:HIS:HD2	1:F:250:THR:O	1.86	0.57
1:E:199:ASP:O	1:E:203:ALA:HB3	2.06	0.56
1:G:199:ASP:O	1:G:203:ALA:HB3	2.06	0.55
1:F:199:ASP:O	1:F:203:ALA:HB3	2.06	0.55
1:E:131:ARG:NH1	1:E:532:GLN:OE1	2.39	0.55
2:H:36:THR:HG23	2:H:48:TRP:NE1	2.22	0.54
2:J:36:THR:HG23	2:J:48:TRP:NE1	2.22	0.54
2:I:36:THR:HG23	2:I:48:TRP:NE1	2.22	0.54
1:E:545:LEU:HD13	1:G:545:LEU:HD11	1.92	0.51
1:G:647:TYR:OH	1:G:661:ARG:NH1	2.43	0.51
1:F:647:TYR:OH	1:F:661:ARG:NH1	2.43	0.51
1:E:647:TYR:OH	1:E:661:ARG:NH1	2.43	0.51
1:G:131:ARG:NH2	1:G:532:GLN:OE1	2.43	0.49
3:N:60:LYS:O	3:N:60:LYS:NZ	2.35	0.49
1:F:131:ARG:NH2	1:F:532:GLN:OE1	2.46	0.49
2:I:36:THR:CG2	2:I:48:TRP:NE1	2.77	0.48
2:J:36:THR:CG2	2:J:48:TRP:NE1	2.77	0.48
1:F:557:ARG:O	1:F:559:VAL:HG23	2.14	0.47
1:G:557:ARG:O	1:G:559:VAL:HG23	2.14	0.47
2:H:99:TYR:O	2:H:100:TYR:C	2.56	0.47
2:J:99:TYR:O	2:J:100:TYR:C	2.56	0.47
1:E:557:ARG:O	1:E:559:VAL:HG23	2.14	0.47
2:J:90:ASP:HB2	2:J:114:VAL:HG21	1.97	0.46
1:F:410:GLY:O	1:F:414:GLY:N	2.49	0.46
2:I:90:ASP:HB2	2:I:114:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:410:GLY:O	1:G:414:GLY:N	2.49	0.46
1:E:664:ILE:HG22	1:G:126:GLN:H	1.81	0.45
2:H:90:ASP:HB2	2:H:114:VAL:HG21	1.97	0.45
1:E:410:GLY:O	1:E:414:GLY:N	2.49	0.45
2:H:36:THR:CG2	2:H:48:TRP:NE1	2.77	0.45
1:G:281:VAL:HG23	1:G:283:PRO:HD2	2.00	0.44
1:E:128:GLU:HG3	1:F:668:SER:CB	2.46	0.44
1:F:558:ARG:C	1:F:559:VAL:HG23	2.43	0.44
1:E:558:ARG:C	1:E:559:VAL:HG23	2.43	0.44
1:F:281:VAL:HG23	1:F:283:PRO:HD2	1.99	0.44
2:I:99:TYR:O	2:I:100:TYR:C	2.56	0.44
1:E:281:VAL:HG23	1:E:283:PRO:HD2	1.99	0.44
1:G:558:ARG:C	1:G:559:VAL:HG23	2.43	0.43
1:F:128:GLU:HG3	1:G:668:SER:CB	2.48	0.43
1:F:126:GLN:H	1:G:664:ILE:HG22	1.83	0.43
1:E:248:HIS:CD2	1:E:250:THR:O	2.71	0.42
2:I:97:VAL:CG2	2:I:106:TRP:CE3	3.02	0.42
2:H:37:TRP:CE3	2:H:81:LEU:HD22	2.55	0.42
2:H:97:VAL:CG2	2:H:106:TRP:CE3	3.02	0.42
2:H:97:VAL:HG22	2:H:106:TRP:CE3	2.55	0.42
2:I:37:TRP:CE3	2:I:81:LEU:HD22	2.55	0.42
2:J:37:TRP:CE3	2:J:81:LEU:HD22	2.55	0.42
2:J:97:VAL:CG2	2:J:106:TRP:CE3	3.02	0.42
1:E:126:GLN:H	1:F:664:ILE:HG22	1.84	0.42
1:E:128:GLU:HG3	1:F:668:SER:HB2	2.01	0.41
1:G:697:SER:O	1:G:697:SER:OG	2.37	0.41
1:E:685:PRO:O	1:E:688:VAL:HG12	2.20	0.41
2:I:97:VAL:HG22	2:I:106:TRP:CE3	2.55	0.41
1:E:395:PHE:CG	1:E:450:ILE:HD11	2.56	0.41
1:G:635:VAL:HG22	1:G:695:LYS:HA	2.03	0.41
1:E:668:SER:CB	1:G:128:GLU:HG3	2.50	0.41
1:G:248:HIS:CD2	1:G:250:THR:O	2.71	0.41
1:E:247:TRP:HE1	1:E:331:THR:HG23	1.86	0.41
1:E:676:THR:O	1:E:676:THR:HG23	2.21	0.41
1:F:247:TRP:HE1	1:F:331:THR:HG23	1.86	0.41
1:G:685:PRO:O	1:G:688:VAL:HG12	2.20	0.41
1:F:635:VAL:HG22	1:F:695:LYS:HA	2.03	0.41
1:F:685:PRO:O	1:F:688:VAL:HG12	2.20	0.41
2:J:97:VAL:HG22	2:J:106:TRP:CE3	2.55	0.40
1:E:635:VAL:HG22	1:E:695:LYS:HA	2.03	0.40
1:G:395:PHE:CG	1:G:450:ILE:HD11	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:19:LEU:HB2	2:I:86:LEU:HD11	2.03	0.40
1:F:395:PHE:CG	1:F:450:ILE:HD11	2.56	0.40
1:G:247:TRP:HE1	1:G:331:THR:HG23	1.86	0.40
1:F:676:THR:HG23	1:F:676:THR:O	2.21	0.40
2:J:19:LEU:HB2	2:J:86:LEU:HD11	2.03	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	E	552/808 (68%)	529 (96%)	23 (4%)	0	100	100
1	F	552/808 (68%)	529 (96%)	23 (4%)	0	100	100
1	G	552/808 (68%)	529 (96%)	23 (4%)	0	100	100
2	H	113/218 (52%)	108 (96%)	5 (4%)	0	100	100
2	I	113/218 (52%)	108 (96%)	5 (4%)	0	100	100
2	J	113/218 (52%)	108 (96%)	5 (4%)	0	100	100
3	L	105/214 (49%)	102 (97%)	3 (3%)	0	100	100
3	M	105/214 (49%)	102 (97%)	3 (3%)	0	100	100
3	N	105/214 (49%)	102 (97%)	3 (3%)	0	100	100
All	All	2310/3720 (62%)	2217 (96%)	93 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	488/673 (72%)	488 (100%)	0	100	100
1	F	488/673 (72%)	488 (100%)	0	100	100
1	G	488/673 (72%)	488 (100%)	0	100	100
2	H	100/190 (53%)	100 (100%)	0	100	100
2	I	100/190 (53%)	100 (100%)	0	100	100
2	J	100/190 (53%)	100 (100%)	0	100	100
3	L	94/193 (49%)	94 (100%)	0	100	100
3	M	94/193 (49%)	94 (100%)	0	100	100
3	N	94/193 (49%)	94 (100%)	0	100	100
All	All	2046/3168 (65%)	2046 (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. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	129	GLN
1	E	238	ASN
1	E	248	HIS
1	F	129	GLN
1	F	248	HIS
1	G	129	GLN
1	G	248	HIS
2	H	105	HIS
2	H	108	GLN
2	I	105	HIS
2	J	108	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

15 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	0.72	0	17,19,21	1.01	1 (5%)
4	NAG	A	2	4	14,14,15	0.70	0	17,19,21	0.98	1 (5%)
5	NAG	B	1	1,5	14,14,15	0.73	0	17,19,21	0.93	0
5	NAG	B	2	5	14,14,15	0.71	0	17,19,21	0.82	0
5	BMA	B	3	5	11,11,12	0.84	0	15,15,17	2.57	6 (40%)
4	NAG	C	1	1,4	14,14,15	0.70	0	17,19,21	1.01	1 (5%)
4	NAG	C	2	4	14,14,15	0.70	0	17,19,21	0.98	1 (5%)
5	NAG	D	1	1,5	14,14,15	0.73	0	17,19,21	0.93	0
5	NAG	D	2	5	14,14,15	0.70	0	17,19,21	0.82	0
5	BMA	D	3	5	11,11,12	0.84	0	15,15,17	2.58	6 (40%)
4	NAG	K	1	1,4	14,14,15	0.72	0	17,19,21	1.00	1 (5%)
4	NAG	K	2	4	14,14,15	0.70	0	17,19,21	0.98	1 (5%)
5	NAG	O	1	1,5	14,14,15	0.73	0	17,19,21	0.92	0
5	NAG	O	2	5	14,14,15	0.70	0	17,19,21	0.82	0
5	BMA	O	3	5	11,11,12	0.83	0	15,15,17	2.57	6 (40%)

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	-	2/6/23/26	0/1/1/1
5	NAG	B	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	2	5	-	0/6/23/26	0/1/1/1
5	BMA	B	3	5	-	0/2/19/22	0/1/1/1
4	NAG	C	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	D	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	D	2	5	-	0/6/23/26	0/1/1/1
5	BMA	D	3	5	-	0/2/19/22	0/1/1/1
4	NAG	K	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
5	NAG	O	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1
5	BMA	O	3	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	3	BMA	C1-O5-C5	7.67	122.46	112.19
5	O	3	BMA	C1-O5-C5	7.63	122.41	112.19
5	B	3	BMA	C1-O5-C5	7.62	122.40	112.19
5	O	3	BMA	C3-C4-C5	3.51	116.59	110.23
5	D	3	BMA	C3-C4-C5	3.50	116.57	110.23
5	B	3	BMA	C3-C4-C5	3.50	116.57	110.23
5	O	3	BMA	C2-C3-C4	2.87	115.91	110.86
5	B	3	BMA	C2-C3-C4	2.86	115.89	110.86
5	D	3	BMA	C2-C3-C4	2.85	115.88	110.86
5	B	3	BMA	O3-C3-C2	-2.30	105.35	110.05
5	D	3	BMA	O3-C3-C2	-2.30	105.36	110.05
5	O	3	BMA	O3-C3-C2	-2.29	105.37	110.05
4	C	1	NAG	O5-C1-C2	-2.27	107.77	111.29
4	A	1	NAG	O5-C1-C2	-2.25	107.81	111.29
4	K	1	NAG	O5-C1-C2	-2.24	107.83	111.29
5	D	3	BMA	O4-C4-C3	-2.11	105.40	110.38
5	O	3	BMA	O4-C4-C3	-2.11	105.41	110.38
5	B	3	BMA	O4-C4-C3	-2.11	105.41	110.38
5	B	3	BMA	O5-C5-C4	2.07	115.87	110.83
5	D	3	BMA	O5-C5-C4	2.06	115.84	110.83
5	O	3	BMA	O5-C5-C4	2.06	115.84	110.83
4	C	2	NAG	C2-N2-C7	2.05	125.65	122.90
4	K	2	NAG	C2-N2-C7	2.05	125.64	122.90
4	A	2	NAG	C2-N2-C7	2.04	125.63	122.90

There are no chirality outliers.

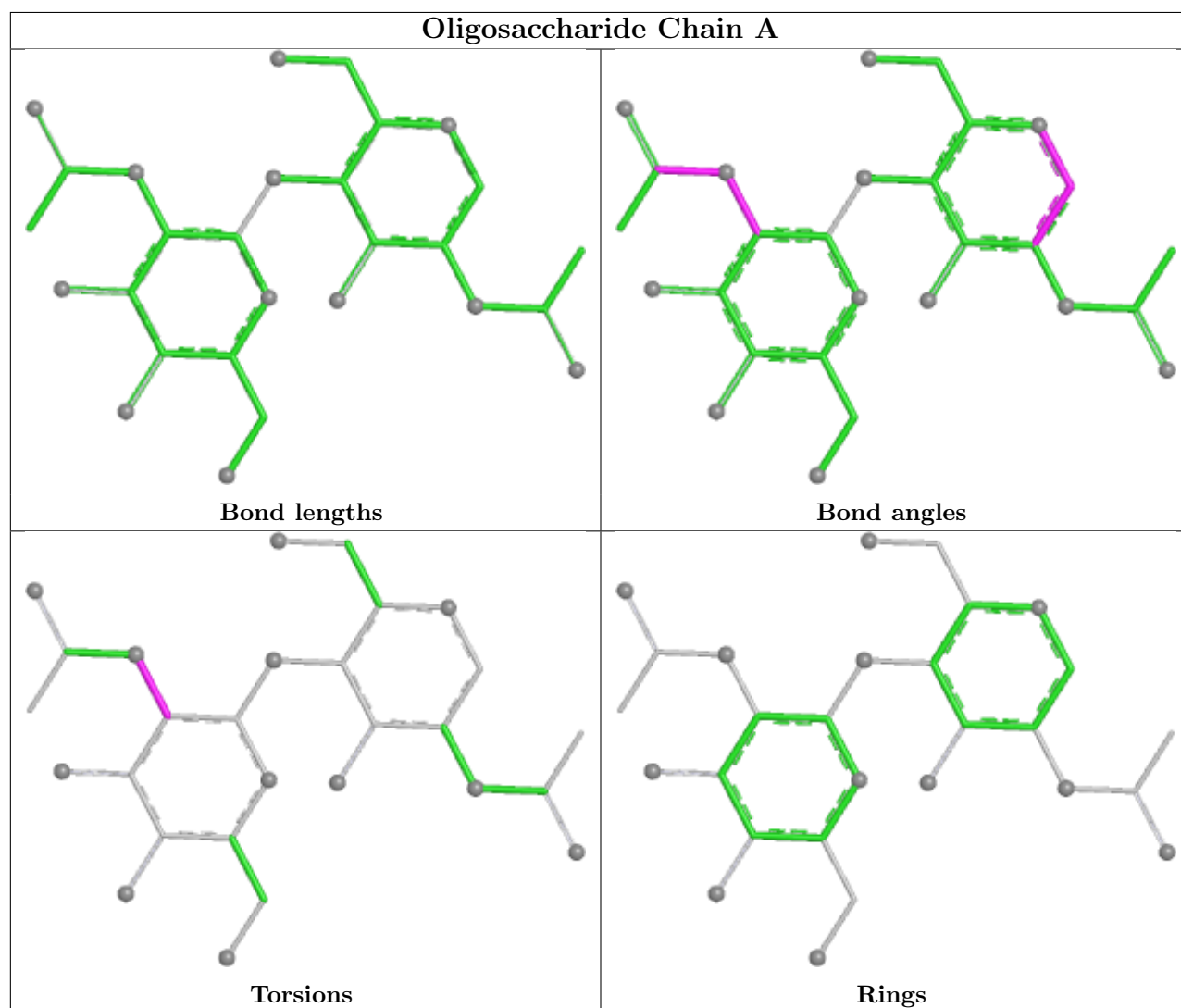
All (6) torsion outliers are listed below:

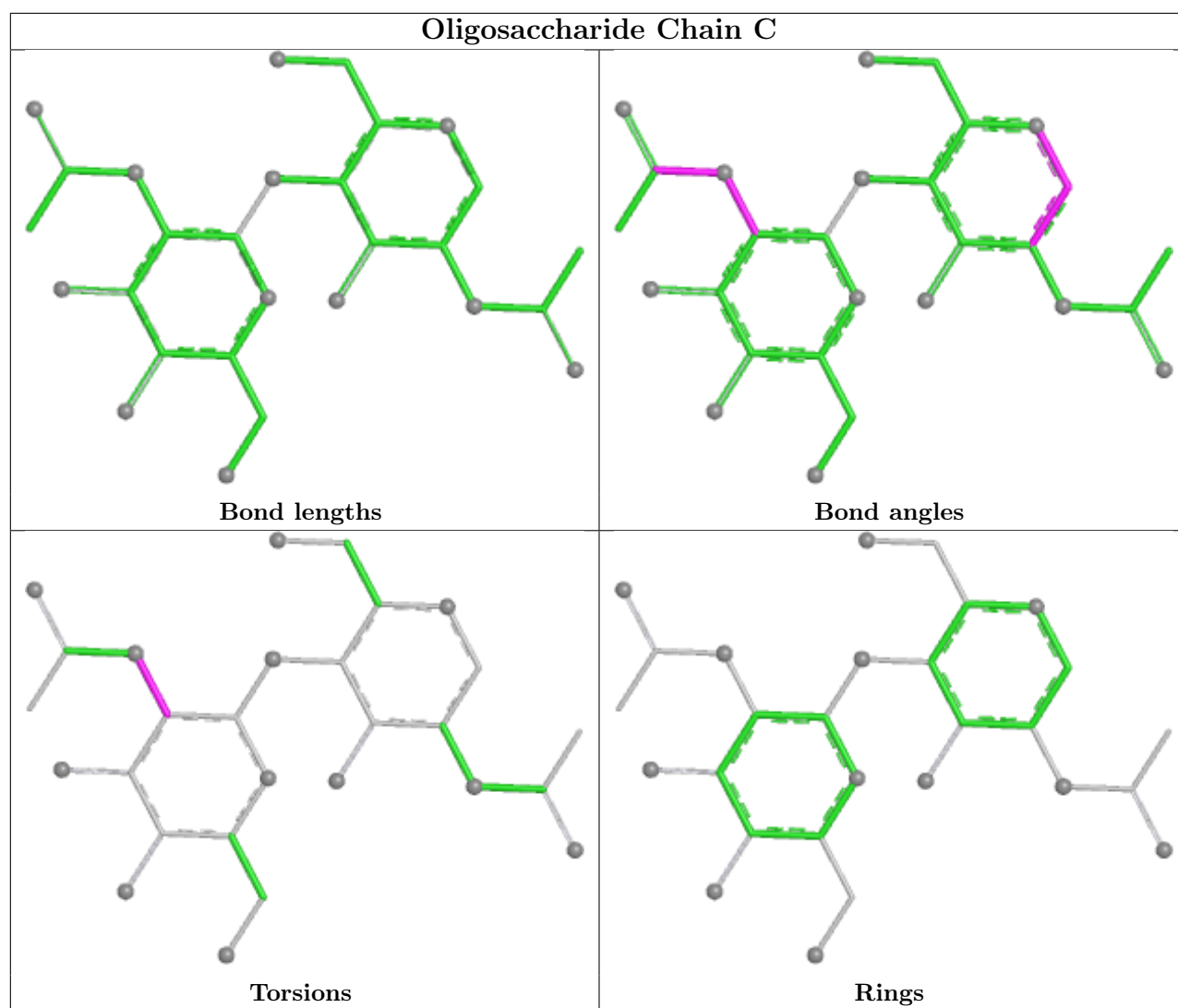
Mol	Chain	Res	Type	Atoms
4	A	2	NAG	C1-C2-N2-C7
4	C	2	NAG	C1-C2-N2-C7
4	K	2	NAG	C1-C2-N2-C7
4	A	2	NAG	C3-C2-N2-C7
4	C	2	NAG	C3-C2-N2-C7
4	K	2	NAG	C3-C2-N2-C7

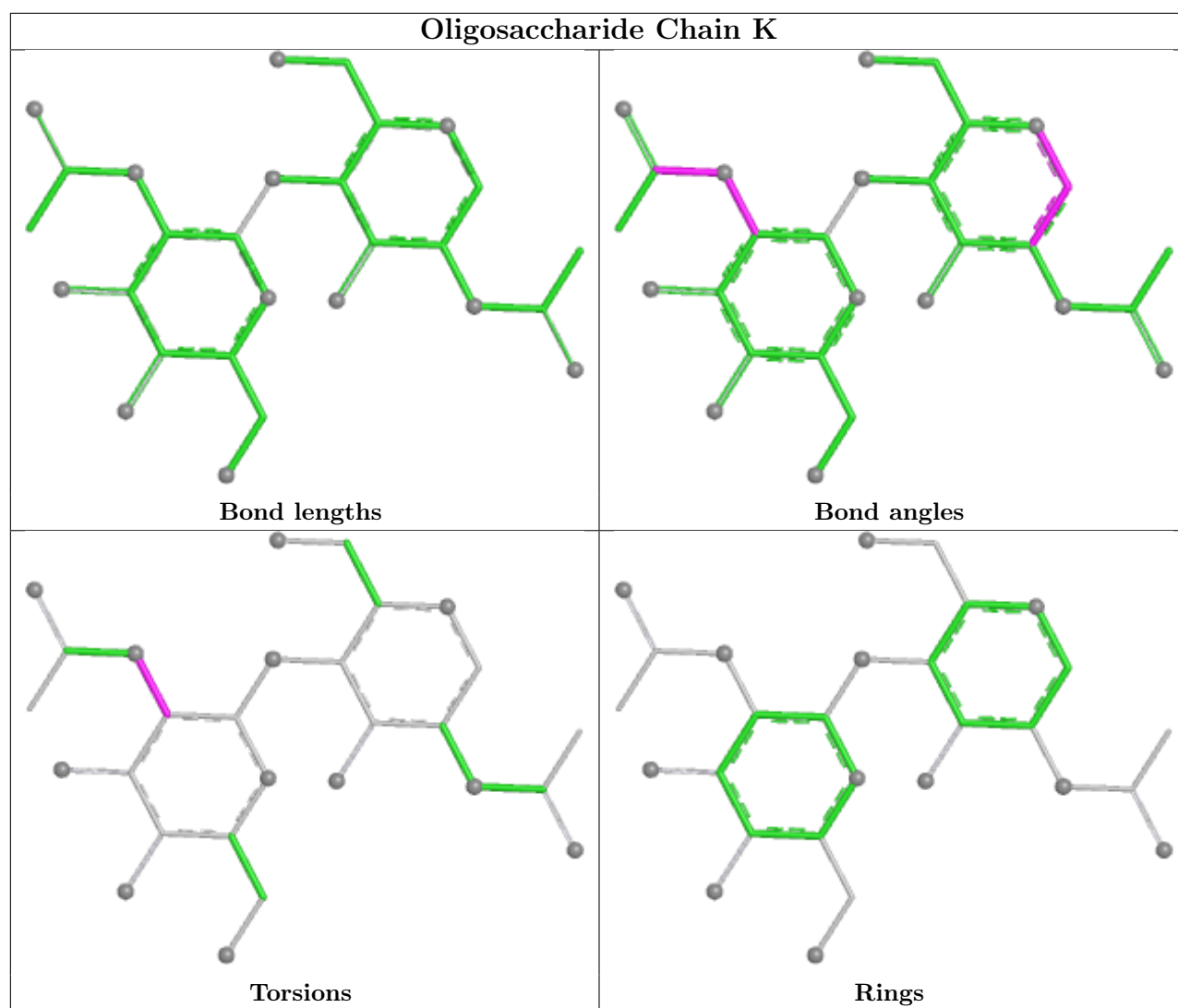
There are no ring outliers.

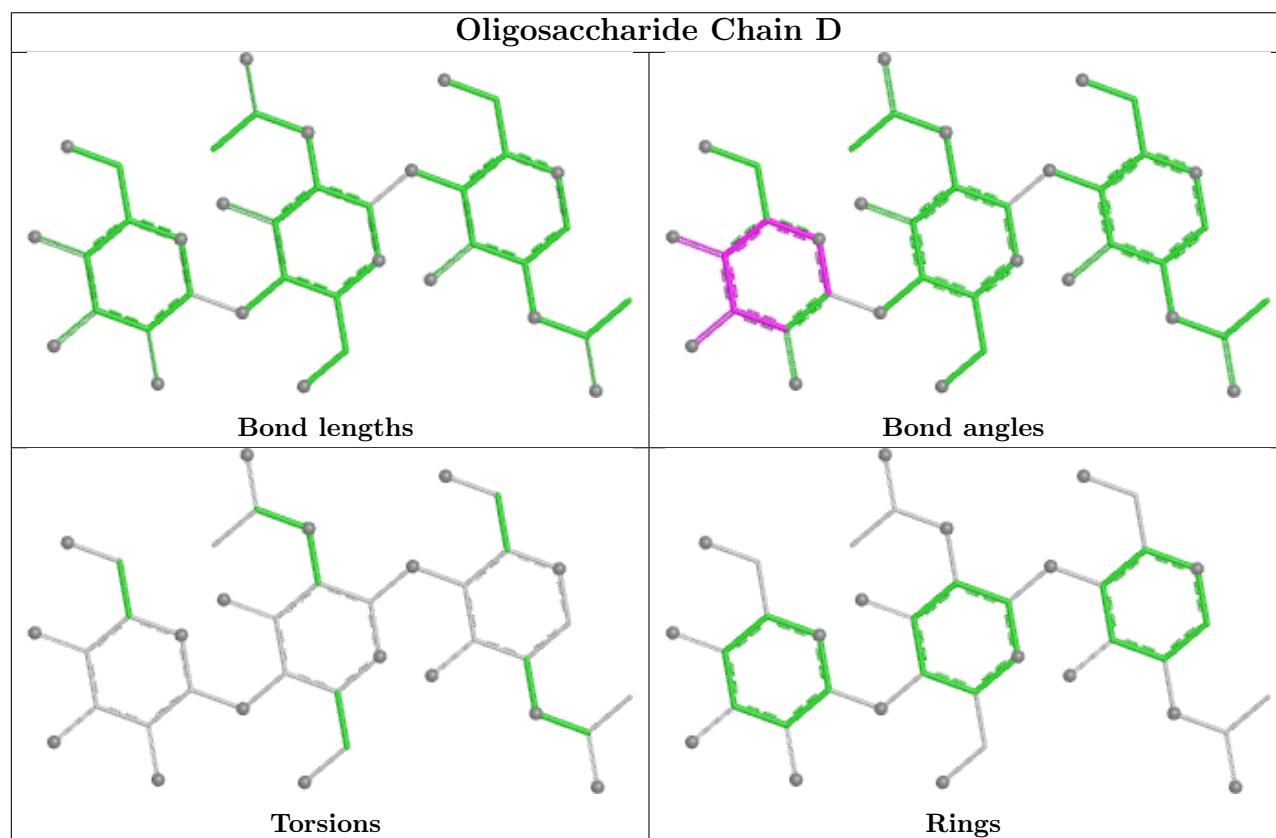
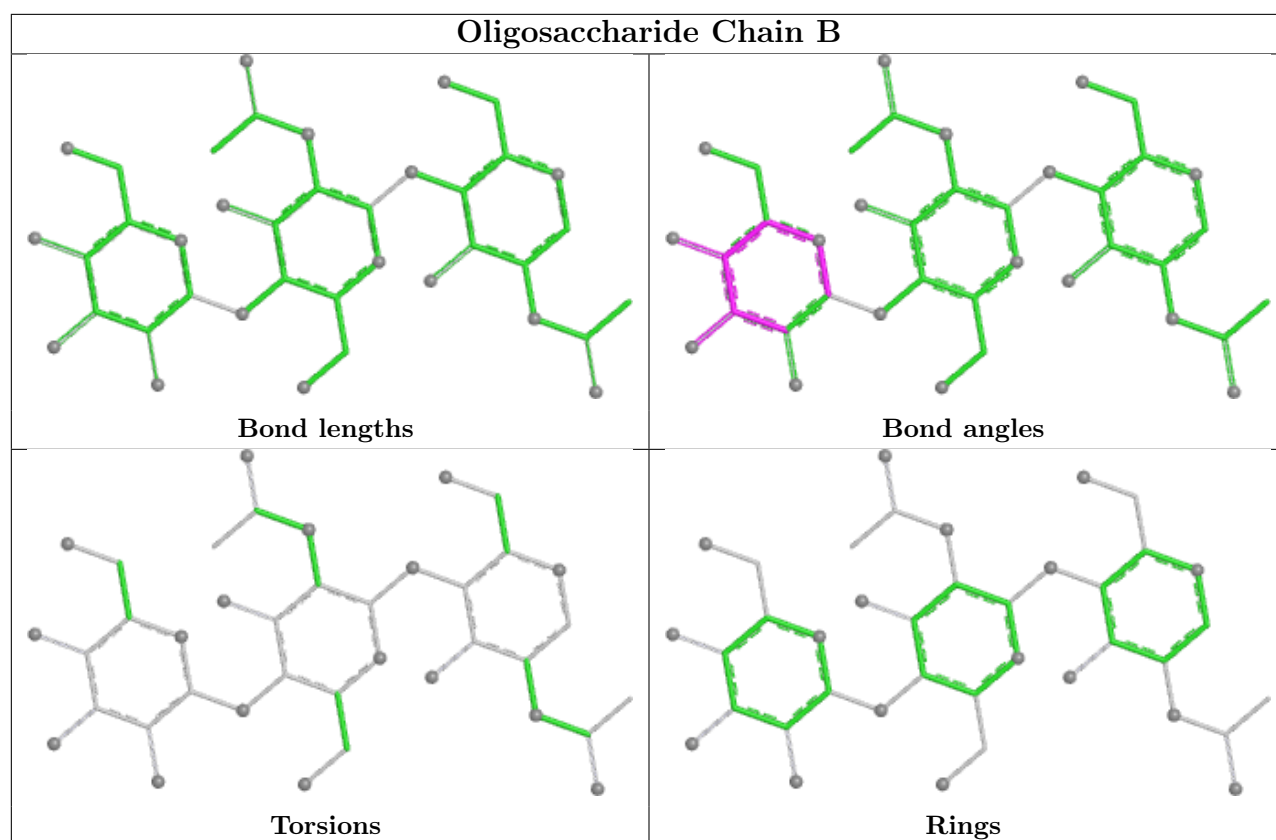
No monomer is involved in short contacts.

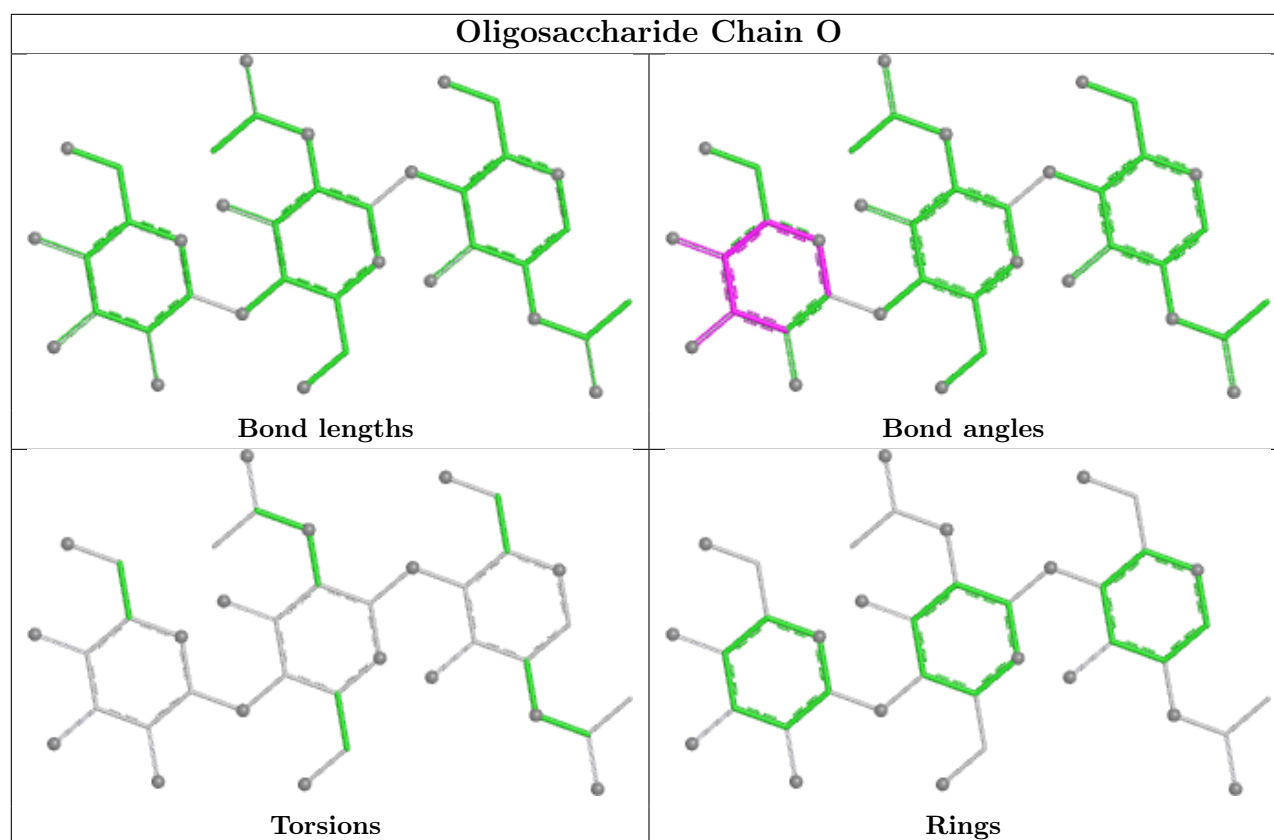
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

6 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	G	902	1	14,14,15	0.71	0	17,19,21	0.89	0
6	NAG	F	902	1	14,14,15	0.72	0	17,19,21	0.88	0
6	NAG	G	901	1	14,14,15	0.69	0	17,19,21	0.87	0
6	NAG	E	902	1	14,14,15	0.72	0	17,19,21	0.88	0
6	NAG	F	901	1	14,14,15	0.69	0	17,19,21	0.88	0
6	NAG	E	901	1	14,14,15	0.70	0	17,19,21	0.88	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
6	NAG	G	902	1	-	0/6/23/26	0/1/1/1
6	NAG	F	902	1	-	0/6/23/26	0/1/1/1
6	NAG	G	901	1	-	0/6/23/26	0/1/1/1
6	NAG	E	902	1	-	0/6/23/26	0/1/1/1
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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

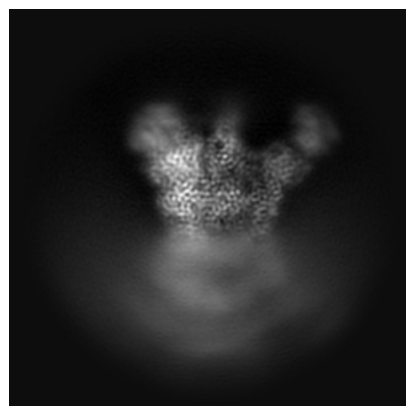
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46758. These allow visual inspection of the internal detail of the map and identification of artifacts.

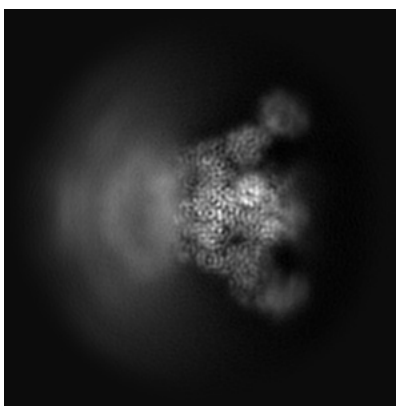
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

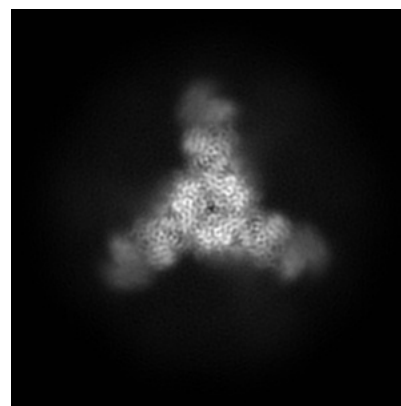
6.1.1 Primary map



X

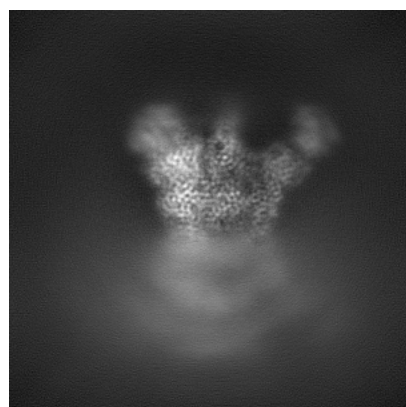


Y

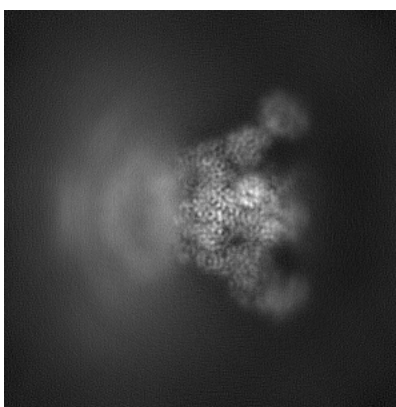


Z

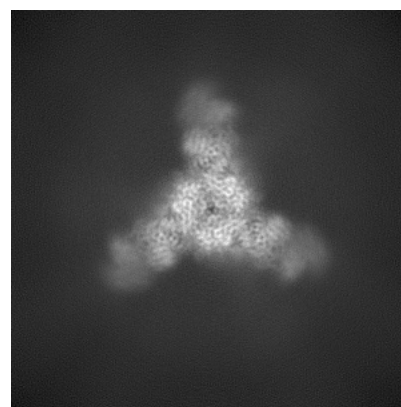
6.1.2 Raw map



X



Y

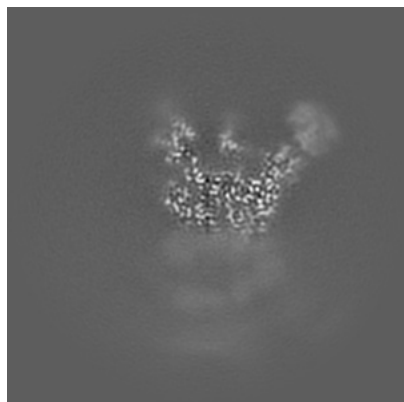


Z

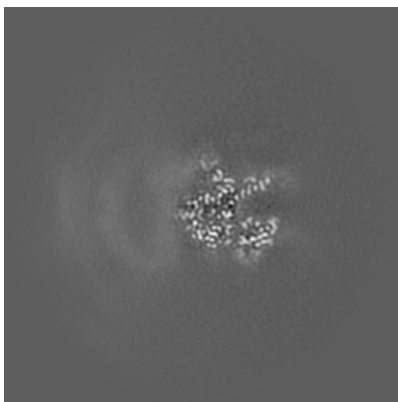
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

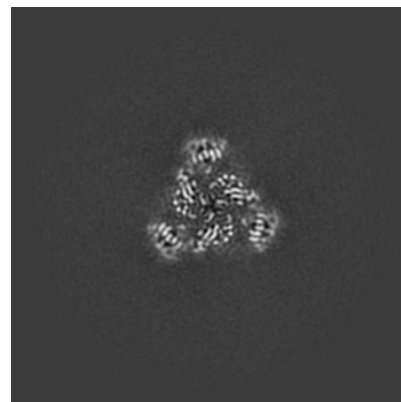
6.2.1 Primary map



X Index: 192

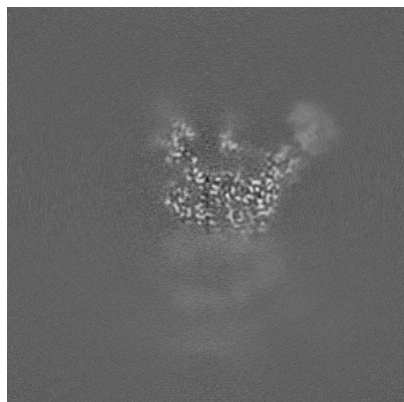


Y Index: 192

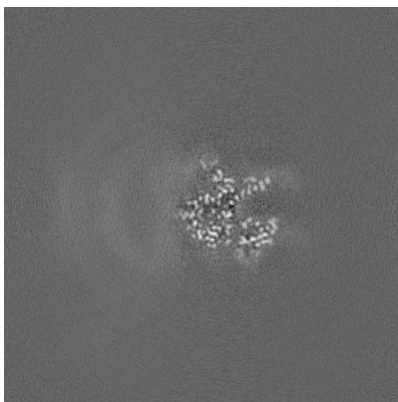


Z Index: 192

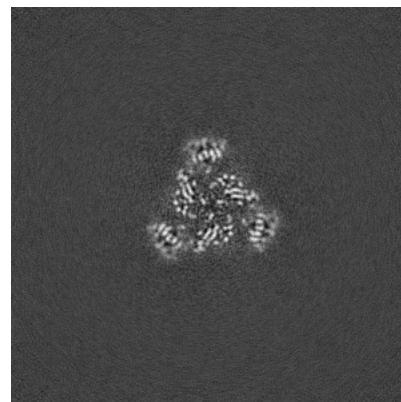
6.2.2 Raw map



X Index: 192



Y Index: 192

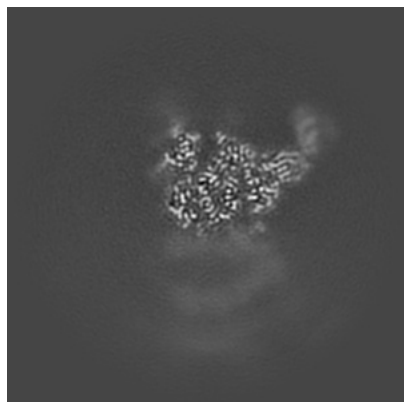


Z Index: 192

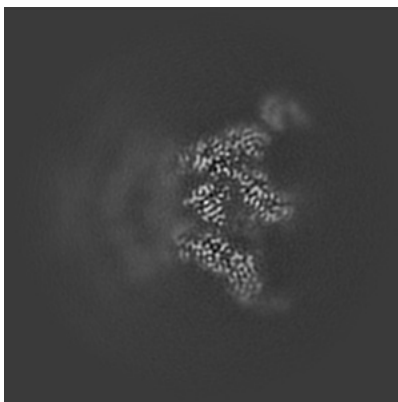
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

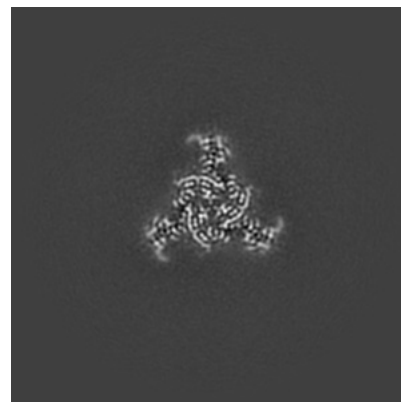
6.3.1 Primary map



X Index: 200

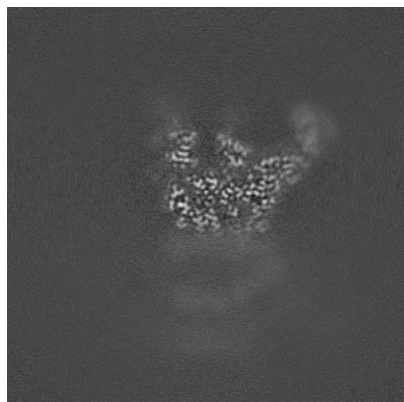


Y Index: 166

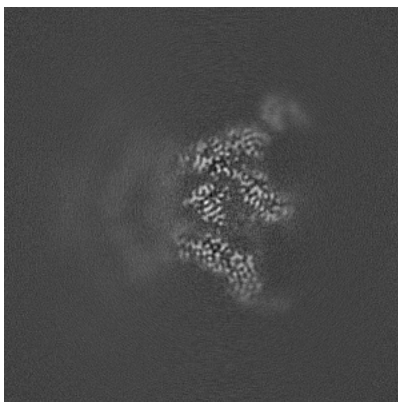


Z Index: 207

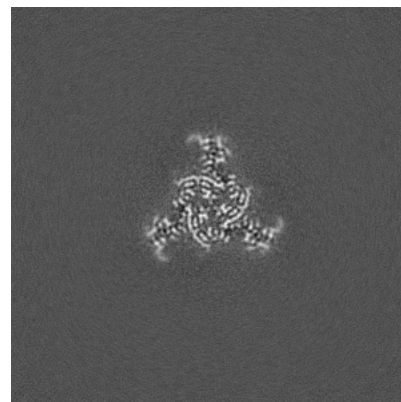
6.3.2 Raw map



X Index: 196



Y Index: 166

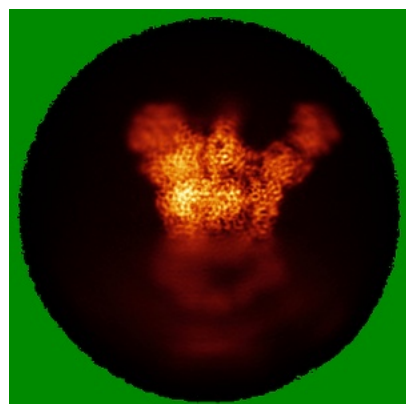


Z Index: 207

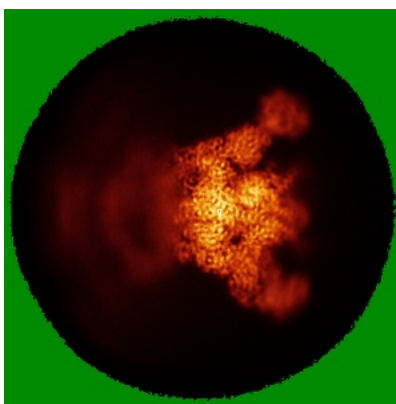
The images above show the largest variance slices of the map in three orthogonal directions.

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

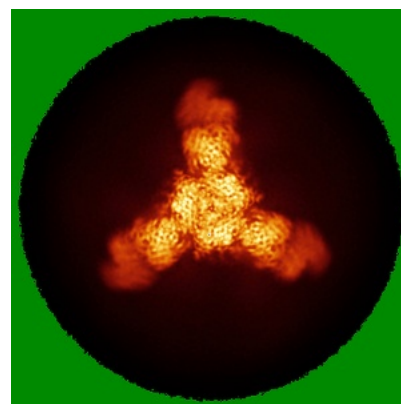
6.4.1 Primary map



X

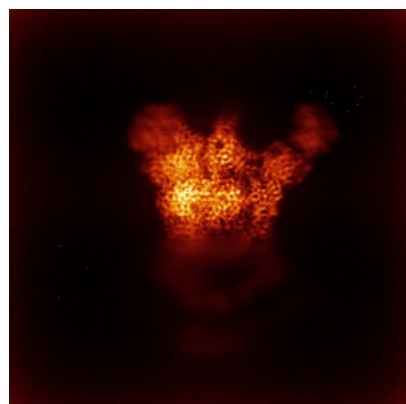


Y

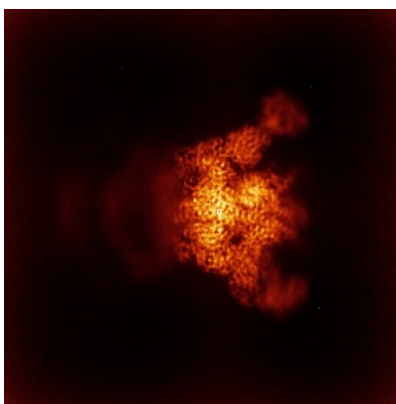


Z

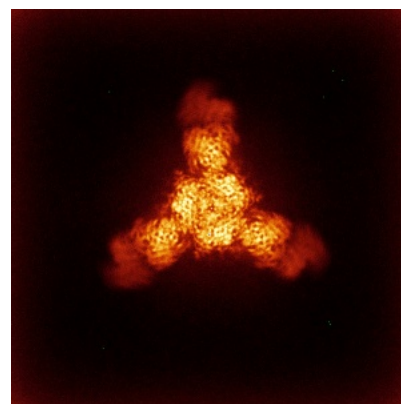
6.4.2 Raw map



X



Y

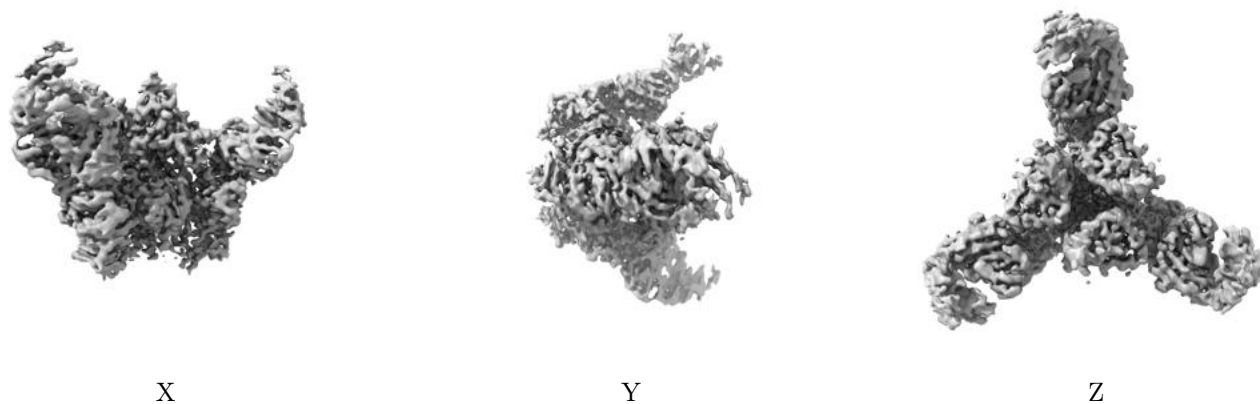


Z

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.

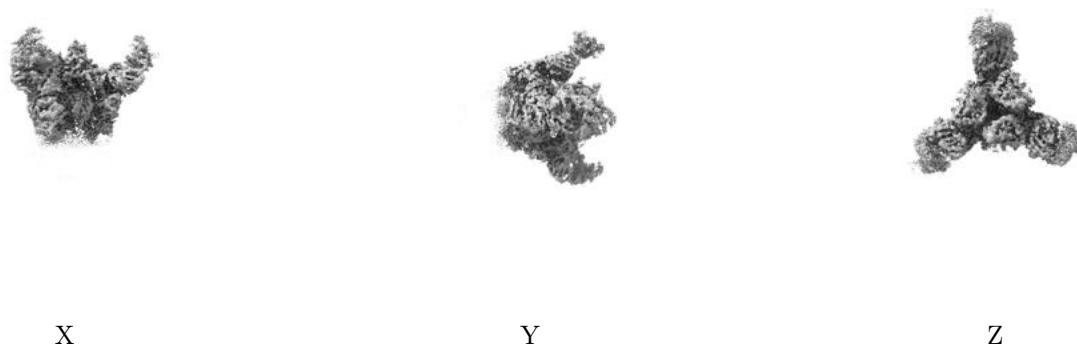
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. 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.

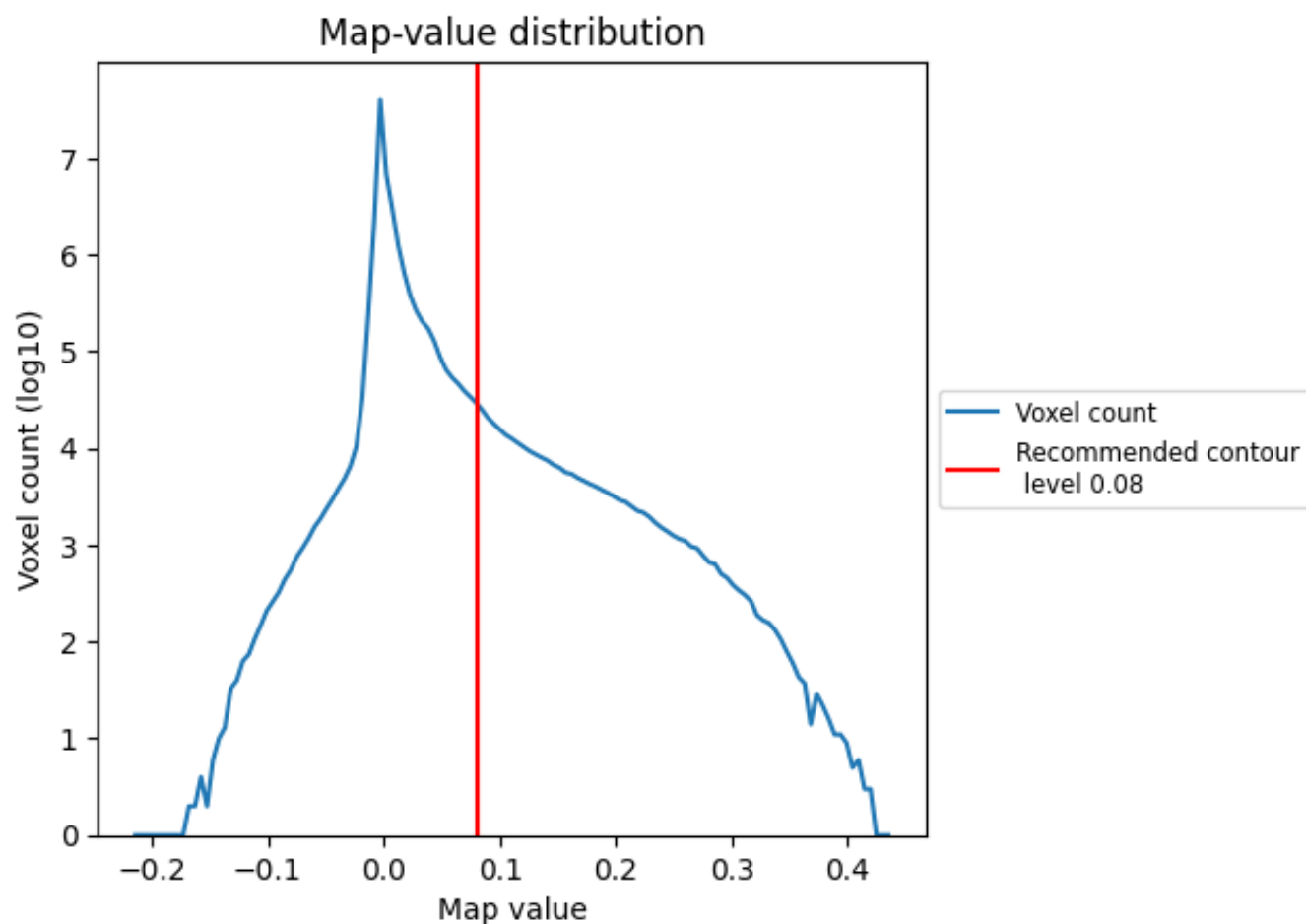
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

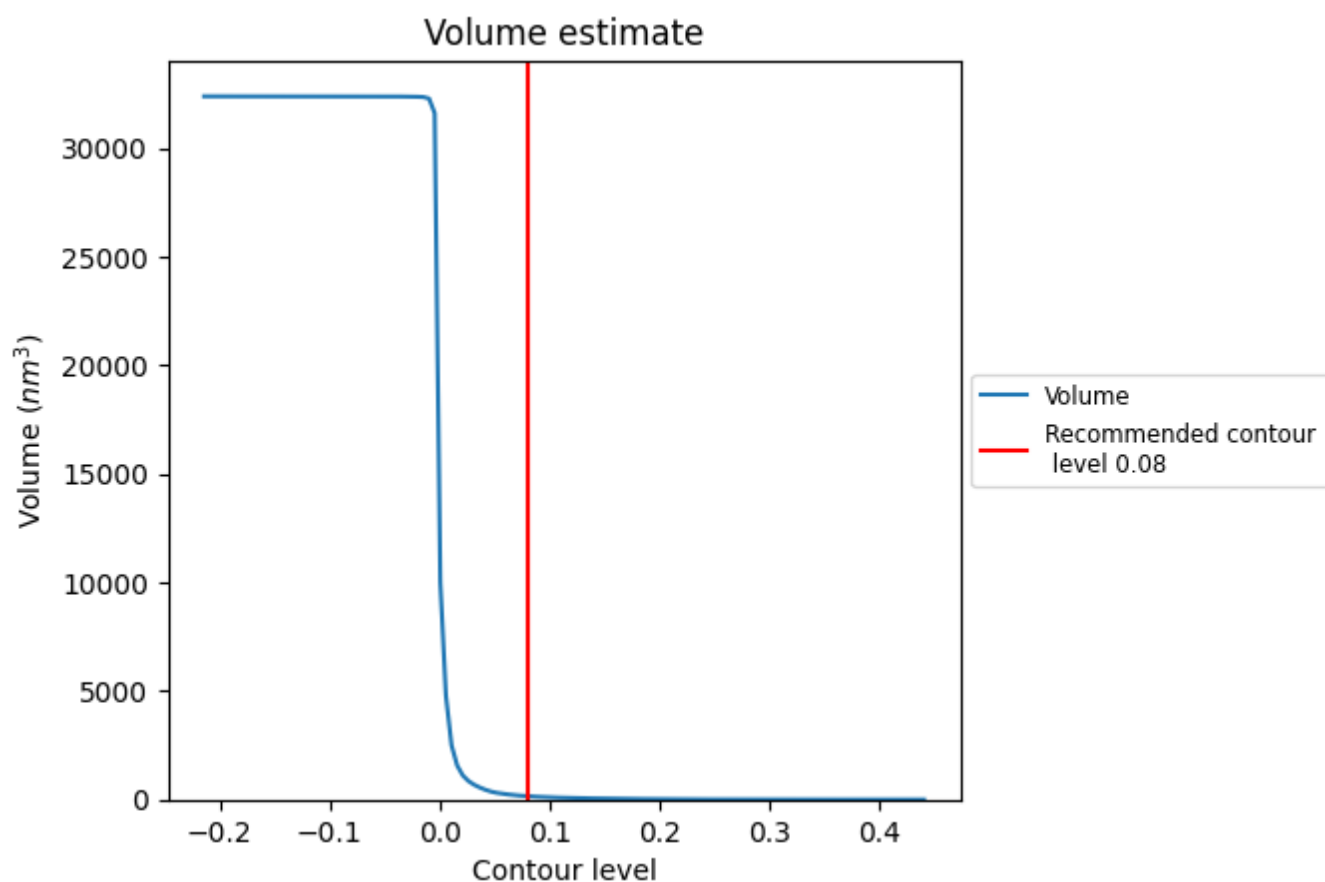
This section contains the results of statistical analysis of the map.

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.

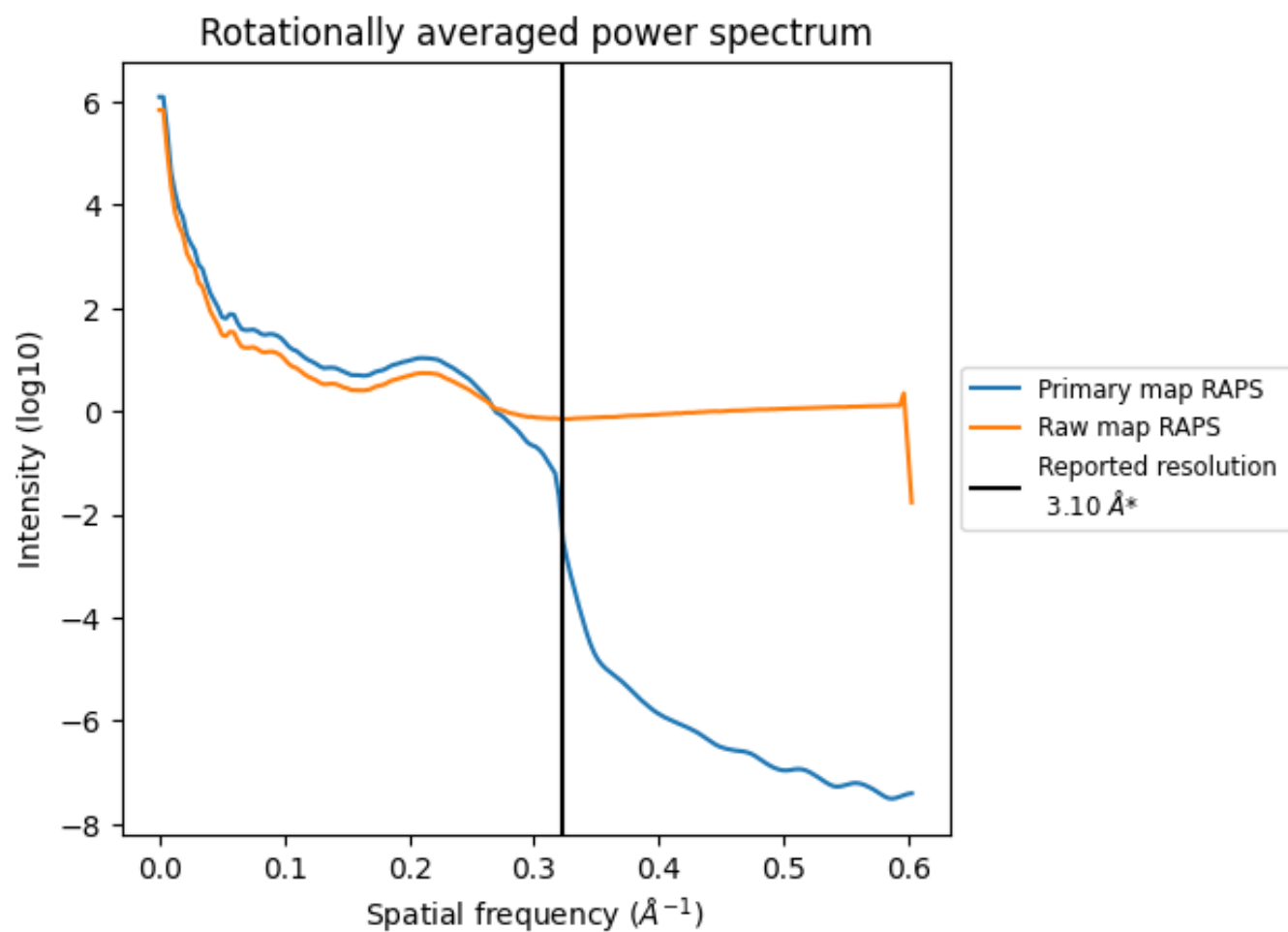
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 155 nm³; this corresponds to an approximate mass of 140 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 ⓘ

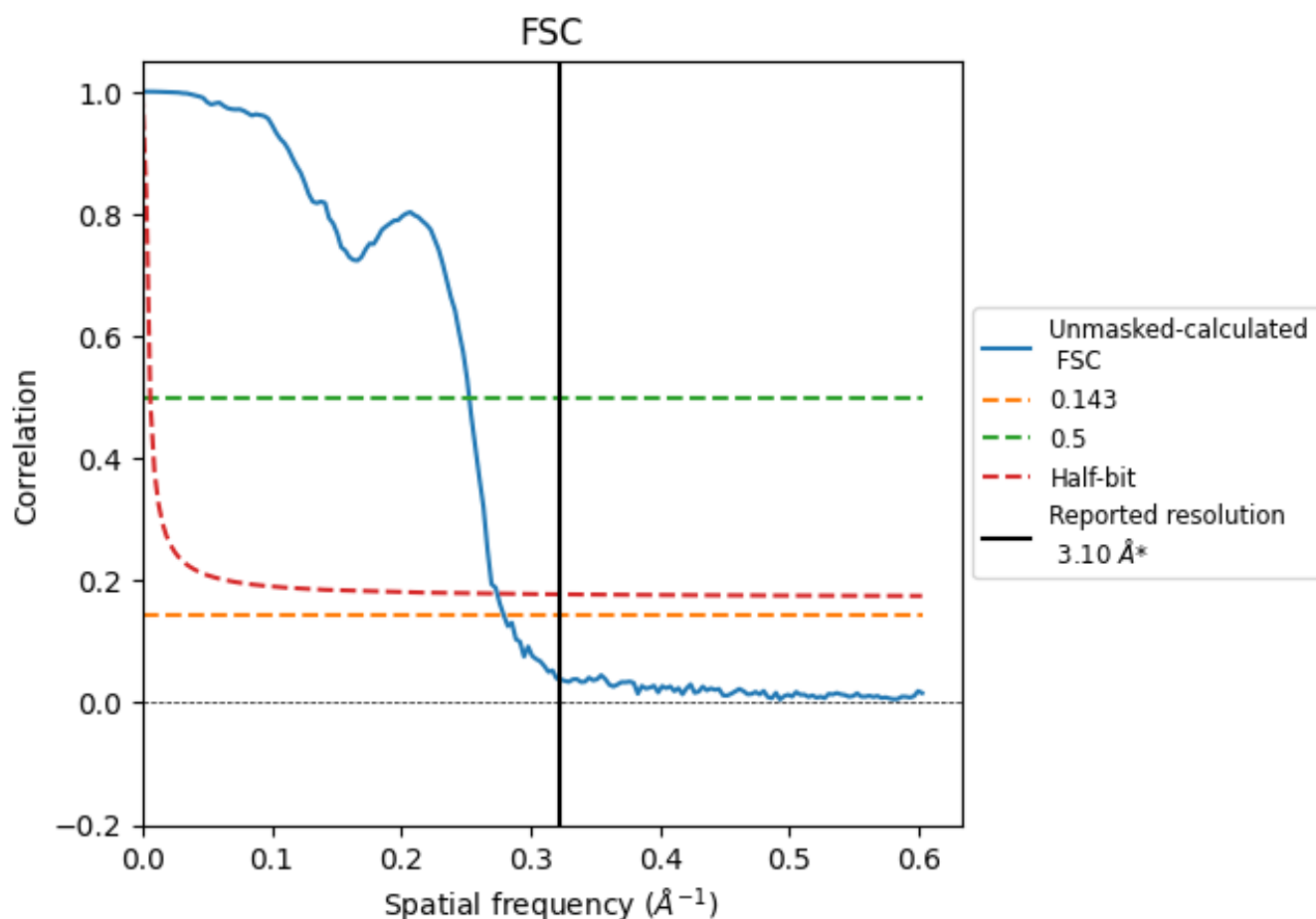


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

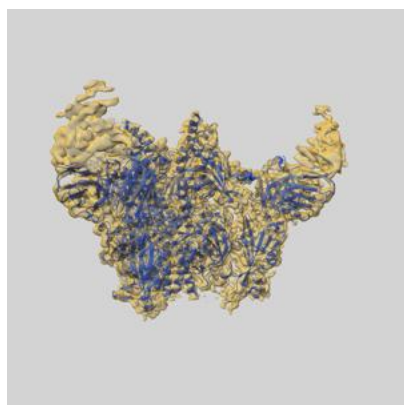
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.58	3.96	3.65

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

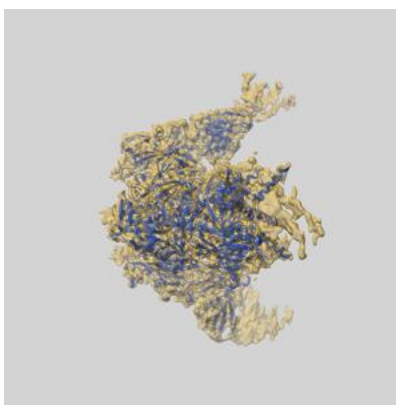
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46758 and PDB model 9DD6. Per-residue inclusion information can be found in section [3](#) on page [13](#).

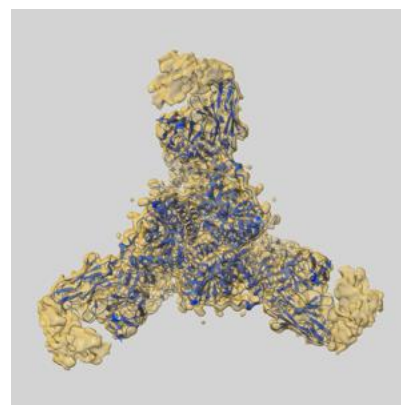
9.1 Map-model overlay [i](#)



X



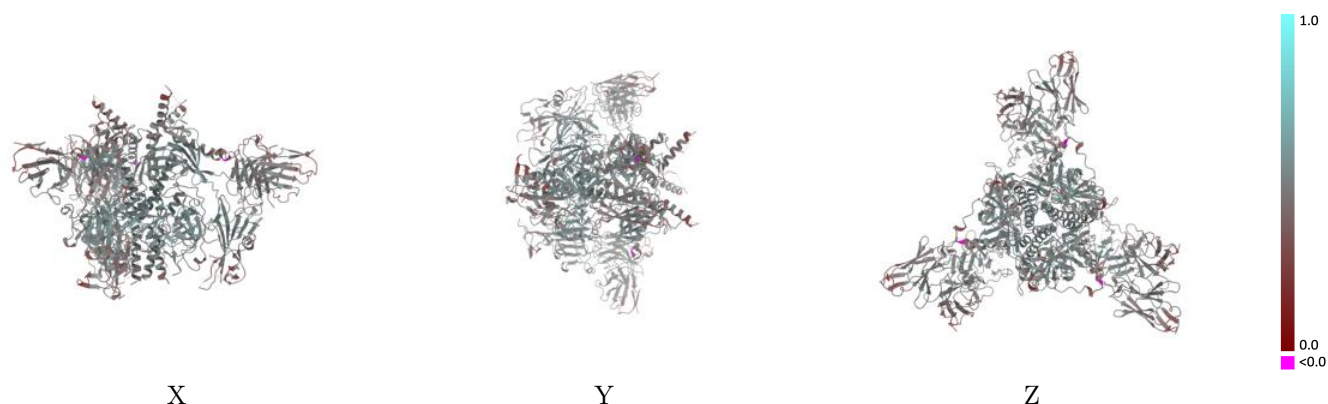
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08 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](#)



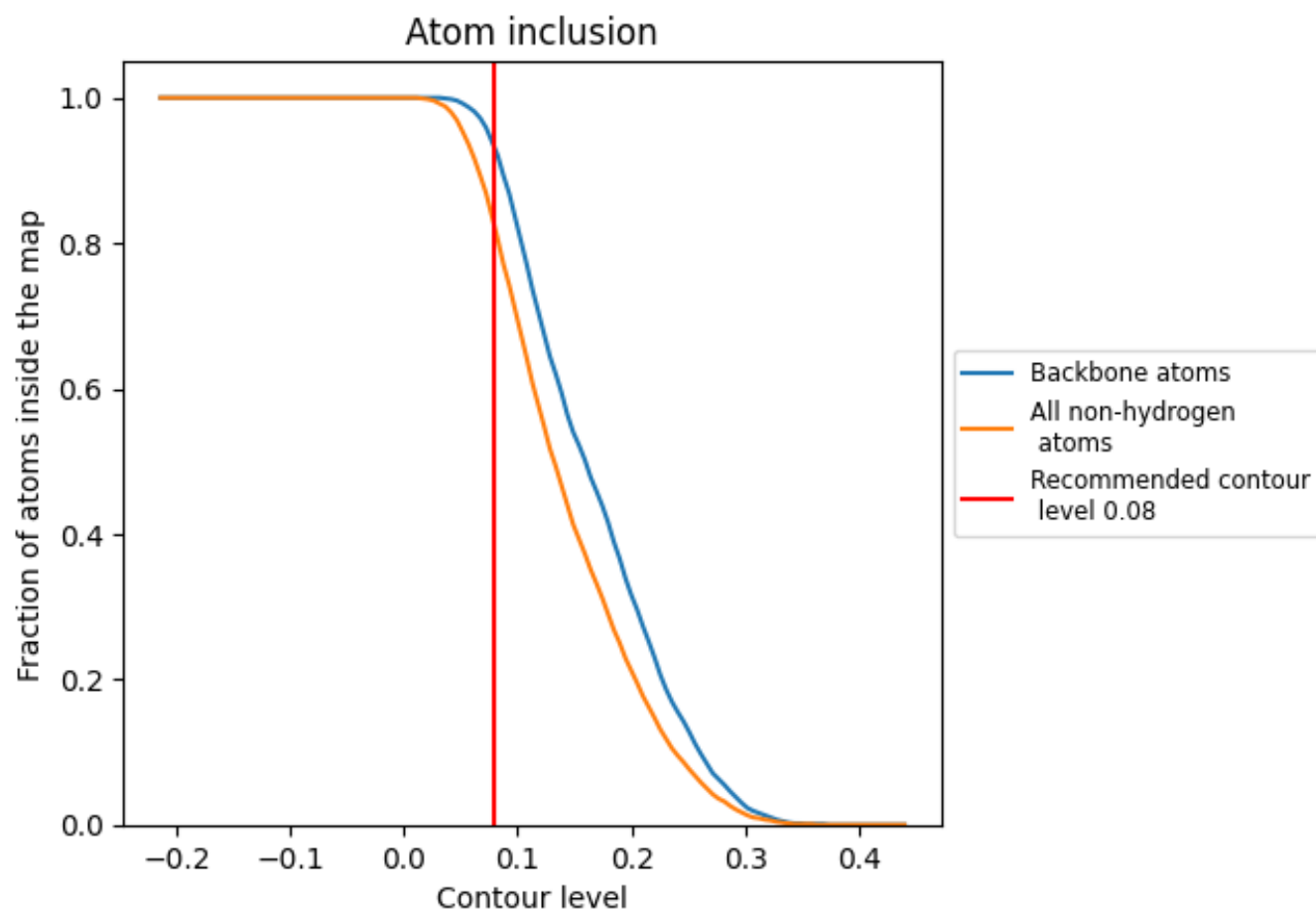
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 82% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8210	 0.4780
A	 0.7860	 0.4590
B	 0.3330	 0.3950
C	 0.7860	 0.4480
D	 0.3330	 0.4020
E	 0.8500	 0.4930
F	 0.8480	 0.4930
G	 0.8490	 0.4910
H	 0.7630	 0.4420
I	 0.7710	 0.4450
J	 0.7670	 0.4430
K	 0.7860	 0.4520
L	 0.7520	 0.4380
M	 0.7540	 0.4400
N	 0.7510	 0.4370
O	 0.3330	 0.3990

