



## wwPDB EM Validation Summary Report ⓘ

Sep 14, 2025 – 12:23 PM EDT

PDB ID : 9MHE / pdb\_00009mhe  
EMDB ID : EMD-48275  
Title : Native tagless Lassa virus spike complex bound to ARN-75039 at pH 8.0  
Authors : Cohen-Dvashi, H.; Katz, M.; Diskin, R.  
Deposited on : 2024-12-11  
Resolution : 2.01 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
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

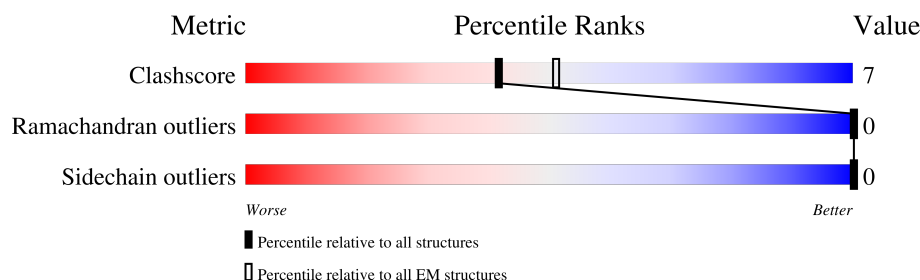
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.01 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.









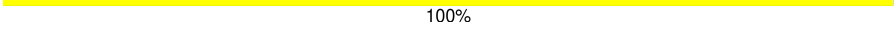
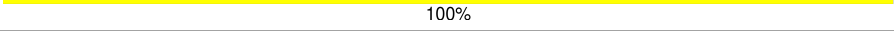
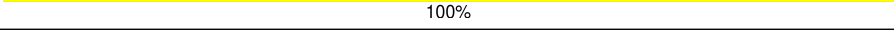
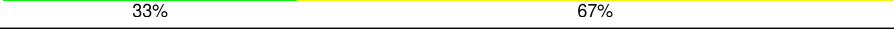

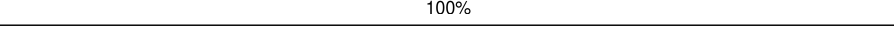

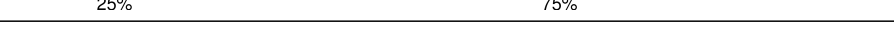



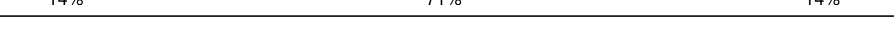
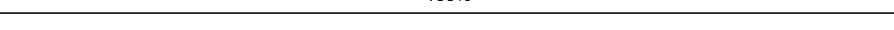


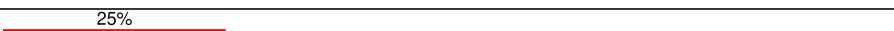


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	232	
1	b	232	
1	c	232	
2	A	259	
2	B	259	
2	C	259	
3	D	249	
3	F	249	

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Mol	Chain	Length	Quality of chain
3	H	249	
4	E	214	
4	G	214	
4	L	214	
5	I	6	
5	f	6	
6	J	2	
6	Q	2	
7	K	3	
7	N	3	
7	T	3	
7	Y	3	
8	M	4	
8	S	4	
8	X	4	
9	O	7	
9	U	7	
9	Z	7	
10	P	5	
10	V	5	
10	d	5	
11	R	4	
11	W	4	
12	e	5	

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 17624 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 G2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	184	Total	C	N	O	S	0	0
			1495	955	246	280	14		
1	b	186	Total	C	N	O	S	0	0
			1513	967	250	282	14		
1	c	186	Total	C	N	O	S	0	0
			1513	967	250	282	14		

- Molecule 2 is a protein called Glycoprotein G1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	229	Total	C	N	O	S	0	0
			1827	1161	309	341	16		
2	B	229	Total	C	N	O	S	0	0
			1827	1161	309	341	16		
2	C	229	Total	C	N	O	S	0	0
			1827	1161	309	341	16		

- Molecule 3 is a protein called 12.1F Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	123	Total	C	N	O	S	2	0
			969	622	158	187	2		
3	D	123	Total	C	N	O	S	2	0
			969	622	158	187	2		
3	F	123	Total	C	N	O	S	2	0
			969	622	158	187	2		

- Molecule 4 is a protein called 12.1F Light chain.

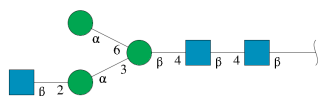
Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	106	Total	C	N	O	S	0	0
			817	512	144	159	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	106	Total	C	N	O	S	0	0
			817	512	144	159	2		
4	G	106	Total	C	N	O	S	0	0
			817	512	144	159	2		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



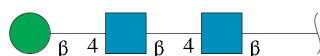
Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	6	Total	C	N	O		0	0
			75	42	3	30			
5	f	6	Total	C	N	O		0	0
			75	42	3	30			

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



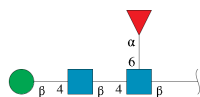
Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	2	Total	C	N	O		0	0
			28	16	2	10			
6	Q	2	Total	C	N	O		0	0
			28	16	2	10			

- Molecule 7 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.



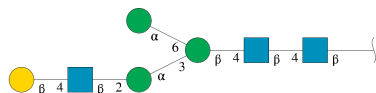
Mol	Chain	Residues	Atoms				AltConf	Trace
7	K	3	Total	C	N	O	0	0
			39	22	2	15		
7	N	3	Total	C	N	O	0	0
			39	22	2	15		
7	T	3	Total	C	N	O	0	0
			39	22	2	15		
7	Y	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 8 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
8	M	4	Total	C	N	O	0	0
			49	28	2	19		
8	S	4	Total	C	N	O	0	0
			49	28	2	19		
8	X	4	Total	C	N	O	0	0
			49	28	2	19		

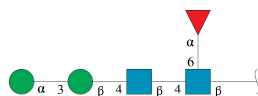
- Molecule 9 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
9	O	7	Total	C	N	O	0	0
			86	48	3	35		
9	U	7	Total	C	N	O	0	0
			86	48	3	35		
9	Z	7	Total	C	N	O	0	0
			86	48	3	35		

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyran

ose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



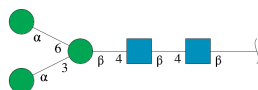
Mol	Chain	Residues	Atoms				AltConf	Trace
10	P	5	Total	C	N	O	0	0
			60	34	2	24		
10	V	5	Total	C	N	O	0	0
			60	34	2	24		
10	d	5	Total	C	N	O	0	0
			60	34	2	24		

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-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
11	R	4	Total	C	N	O	0	0
			50	28	2	20		
11	W	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
12	e	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				AltConf
13	a	1	Total	C	N	O	0
			14	8	1	5	
13	a	1	Total	C	N	O	0
			14	8	1	5	
13	A	1	Total	C	N	O	0
			14	8	1	5	
13	B	1	Total	C	N	O	0
			14	8	1	5	
13	C	1	Total	C	N	O	0
			14	8	1	5	
13	C	1	Total	C	N	O	0
			14	8	1	5	
13	b	1	Total	C	N	O	0
			14	8	1	5	
13	b	1	Total	C	N	O	0
			14	8	1	5	
13	c	1	Total	C	N	O	0
			14	8	1	5	
13	c	1	Total	C	N	O	0
			14	8	1	5	

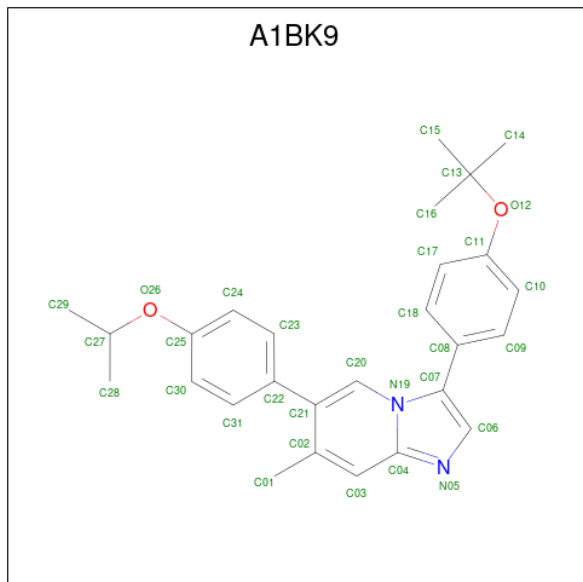
- Molecule 14 is UNKNOWN LIGAND (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		AltConf
14	a	2	Total	X	0
			2	2	

- Molecule 15 is (4S)-3-(4-tert-butoxyphenyl)-7-methyl-6-{4-[(propan-2-yl)oxy]phenyl}imidaz



o[1,2-a]pyridine (CCD ID: A1BK9) (formula:  $C_{27}H_{30}N_2O_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
15	c	1	Total	C	N	O	0
			31	27	2	2	

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		AltConf
16	a	97	Total	O	0
			97	97	
16	A	163	Total	O	0
			163	163	
16	B	160	Total	O	0
			160	160	
16	C	165	Total	O	0
			165	165	
16	b	85	Total	O	0
			85	85	
16	c	110	Total	O	0
			110	110	
16	H	34	Total	O	0
			34	34	
16	L	30	Total	O	0
			30	30	
16	E	26	Total	O	0
			26	26	

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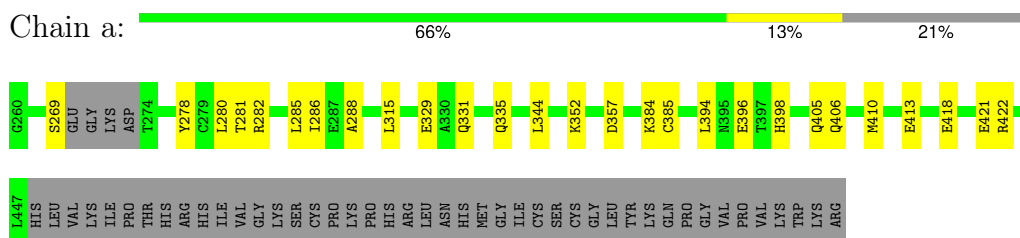
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Mol	Chain	Residues	Atoms		AltConf
16	G	30	Total 30	O 30	0
16	D	42	Total 42	O 42	0
16	F	41	Total 41	O 41	0

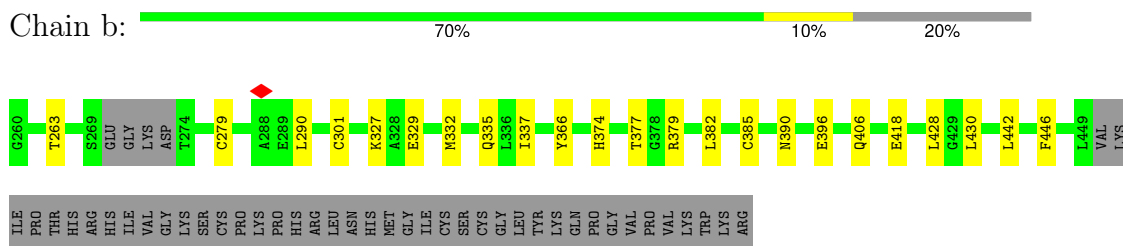
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

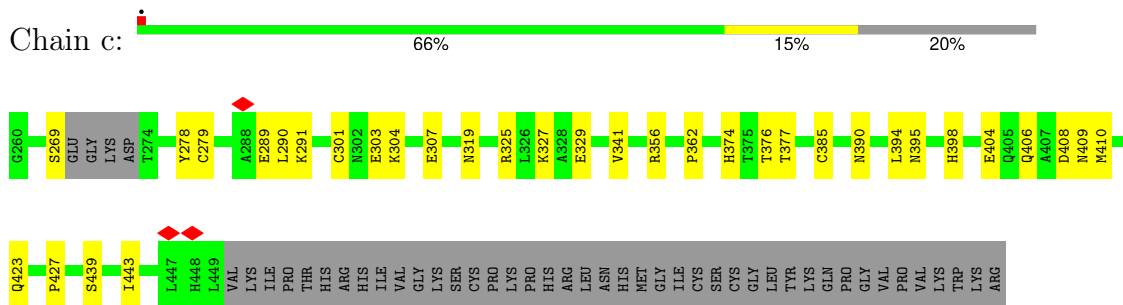
#### • Molecule 1: Glycoprotein G2



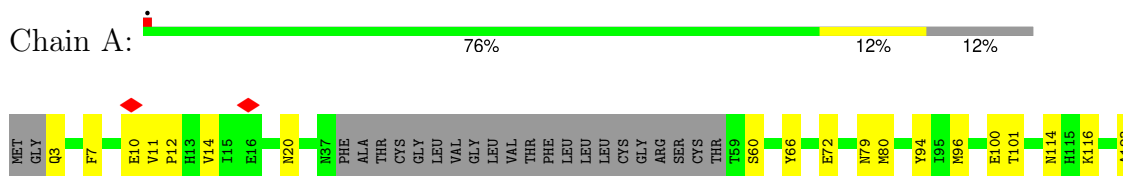
#### • Molecule 1: Glycoprotein G2

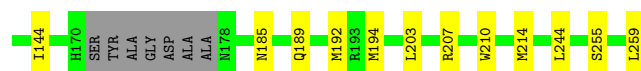


#### • Molecule 1: Glycoprotein G2

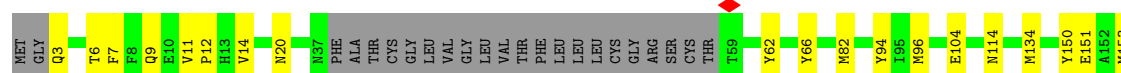
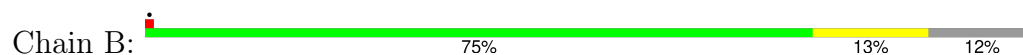


#### • Molecule 2: Glycoprotein G1

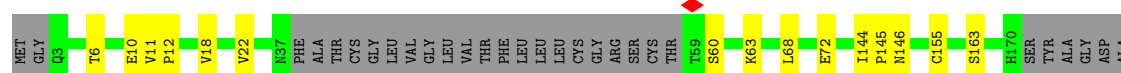
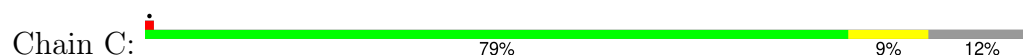




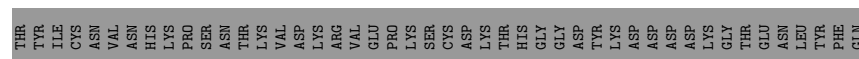
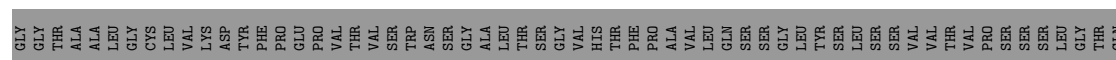
• Molecule 2: Glycoprotein G1



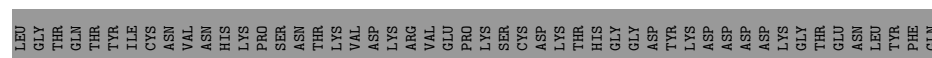
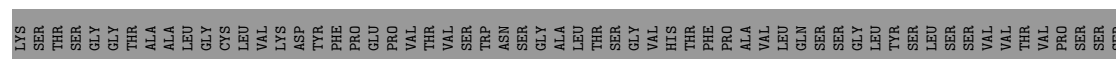
• Molecule 2: Glycoprotein G1




• Molecule 3: 12.1F Heavy chain



• Molecule 3: 12.1F Heavy chain



• Molecule 3: 12.1F Heavy chain

Chain F:  39% 11% 51%

Q1	V2	Q3	L4	Q5	L12	R13	P14	D25	E27	S28	F29	R30	R38	W47	I48	I51	Y59	R66	I69	S70	V71	F78	T83	T90	R97	W105	P106	V113	T121	V122	S123	SER	ALA	SER	LEU	THR	LYS	GLY	PRO	VAL	PHE	PRO	THR	LEU	
ALA	PRO	SER	SER	LEU	THR	SER	GLY	THR	ALA	ALA	LEU	CYS	LEU	VAL	ASP	THR	LYS	PHE	PRO	GLU	PRO	ASN	GLY	ALA	THR	GLY	VAL	HIS	THR	PHE	PRO	SER	GLY	LEU	THR	LYS	GLY	LEU	SER	PRO	VAL	PHE	PRO	THR	LEU
PRO	SER	SER	SER	LEU	GLY	THR	THR	ILE	CYS	ASN	VAL	ASN	LYS	PRO	ASN	THR	LYS	VAL	VAL	GLU	PRO	LYS	SER	CYS	ASP	LYS	TYR	ASP	ASP	ASP	ASP	LYS	THR	GLY	ASN	LEU	THR	PHE	GLN						

• Molecule 4: 12.1F Light chain

Chain L:  41% 8% 50%

ALA	CYS	GLU	VAL	THR	HIS	GLN	GLY	LEU	SER	PRO	VAL	THR	LYS	SER	PHE	ASN	ARG	GLY	GLU	CYS																																		
VAL	CYS	LEU	VAL	ASN	ASN	PHE	TYR	PRO	ARG	GLU	ALA	LYS	VAL	GLN	TRP	LYS	VAL	ASP	ASN	ALA	LEU	GLN	SER	GLY	ASN	SER	GLN	GLU	SER	VAL	THR	THR	GLN	GLU	ASP	SER	LYS	ASP	SER	THR	THR	LEU	SER	LEU	LYS	ASP	ALA	TYR	GLU	LYS	HIS	LYS	VAL	THR
E1	I2	V3	P8	L11	R24	A25	S26	Q27	Q37	R45	L46	L47	T56	R61	D70	E81	D82	F83	Y86	L104	E105	I106	LYS	ARG	THR	VAL	ALA	ALA	PRO	SER	SER	VAL	PHE	ILE	PHE	PRO	PRO	SER	SER	ASP	GLU	GLN	LEU	LYS	LYS	THR	ALA	VAL						

• Molecule 4: 12.1F Light chain

Chain E:  42% 8% 50%

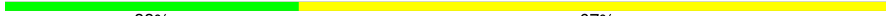
CYS	GLU	VAL	THR	HIS	GLN	GLY	LEU	SER	PRO	THR	VAL	LYS	GLN	TRP	LYS	VAL	ASP	ASN	ALA	LEU	GLN	SER	GLY	ASN	SER	GLN	SER	GLY	VAL	THR	ASP	SER	LYS	VAL	THR	ARG	LYS	LYS	ASP	GLN	LEU	SER	THR	VAL	ALA		
E1	R24	L33	Q37	R45	L46	L47	T56	S57	I58	T69	F83	Y86	H90	W94	R95	F98	R103	I104	E105	I106	LYS	ARG	THR	VAL	ALA	ALA	PRO	SER	VAL	PHE	ILE	PHE	PRO	PRO	SER	THR	ASP	GLU	GLN	LEU	LYS	ASP	TYR	GLY	THR	ALA	VAL

• Molecule 4: 12.1F Light chain

Chain G:  41% 9% 50%

VAL	TYR	ALA	CYS	GLU	VAL	THR	HIS	GLN	GLY	THR	PRO	VAL	THR	LYS	SER	PHE	ASN	ARG	GLY	GLU	CYS																										
SER	VAL	CYS	LEU	ASN	ASN	PHE	THR	PRO	ARG	GLU	ALA	LYS	VAL	GLN	TRP	LYS	VAL	ASP	ASN	ALA	LEU	GLN	SER	GLY	THR	VAL	ALA	PRO	SER	VAL	PHE	ILE	PHE	PRO	PRO	SER	SER	ASP	GLU	GLN	LEU	LYS	ASP	TYR	GLY	THR	ALA
E1	I2	V3	L11	P15	R24	A25	S26	Q37	L47	T56	G57	I58	G66	D70	F71	L78	Y86	H90	T96	L104	E105	I106	LYS	ARG	THR	VAL	ALA	ALA	PRO	SER	VAL	PHE	PHE	PRO	PRO	SER	ASP	GLU	GLN	LEU	LYS	ASP	TYR	GLY	THR	ALA	

• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  33% 67%

NAG1  
NAG2  
BMA3  
MAN4  
NAG5  
MAN6

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:  17% 83%

NAG1  
NAG2  
BMA3  
MAN4  
NAG5  
MAN6

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%


NAG1  
NAG2

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  100%


NAG1  
NAG2

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%

NAG1  
NAG2  
BMA3

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  33% 67%

NAG1  
NAG2  
BMA3

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  33% 67%



- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:

100%



- Molecule 8: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

50%

50%



- Molecule 8: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:

25%

75%



- Molecule 8: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:

75%

25%



- Molecule 9: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

71%

29%



- Molecule 9: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:

86%

14%



- Molecule 9: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z: 



- Molecule 10: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P: 




- Molecule 10: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V: 



- Molecule 10: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d: 



- Molecule 11: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R: 



- Molecule 11: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W: 





- Molecule 12:  $\alpha$ -D-mannopyranose-(1-3)-[ $\alpha$ -D-mannopyranose-(1-6)] $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose

Chain e:

100%

MAG1  
MAG2  
EMJ3  
MAN4  
MAN5

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	523003	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	38	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.458	Depositor
Minimum map value	-0.213	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	296.712, 296.712, 296.712	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82420003, 0.82420003, 0.82420003	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: MAN, BMA, FUC, GAL, A1BK9, NAG, UNX

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	0.22	0/1527	0.40	0/2062
1	b	0.22	0/1546	0.38	0/2088
1	c	0.23	0/1546	0.38	0/2088
2	A	0.23	0/1865	0.41	0/2526
2	B	0.23	0/1865	0.40	0/2526
2	C	0.23	0/1865	0.40	0/2526
3	D	0.19	0/1003	0.40	0/1369
3	F	0.18	0/1003	0.38	0/1369
3	H	0.19	0/1003	0.39	0/1369
4	E	0.20	0/837	0.40	0/1136
4	G	0.18	0/837	0.39	0/1136
4	L	0.17	0/837	0.39	0/1136
All	All	0.21	0/15734	0.39	0/21331

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	1495	0	1453	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	1513	0	1471	23	0
1	c	1513	0	1471	29	0
2	A	1827	0	1782	29	0
2	B	1827	0	1782	29	0
2	C	1827	0	1782	19	0
3	D	969	0	931	17	0
3	F	969	0	931	17	0
3	H	969	0	931	14	0
4	E	817	0	794	17	0
4	G	817	0	794	12	0
4	L	817	0	794	11	0
5	I	75	0	64	0	0
5	f	75	0	64	0	0
6	J	28	0	25	0	0
6	Q	28	0	25	0	0
7	K	39	0	34	0	0
7	N	39	0	34	0	0
7	T	39	0	34	0	0
7	Y	39	0	34	0	0
8	M	49	0	43	0	0
8	S	49	0	43	0	0
8	X	49	0	43	0	0
9	O	86	0	73	3	0
9	U	86	0	73	3	0
9	Z	86	0	73	1	0
10	P	60	0	52	0	0
10	V	60	0	52	0	0
10	d	60	0	52	1	0
11	R	50	0	43	0	0
11	W	50	0	43	0	0
12	e	61	0	52	0	0
13	A	14	0	13	0	0
13	B	14	0	13	0	0
13	C	28	0	26	0	0
13	a	28	0	26	0	0
13	b	28	0	26	1	0
13	c	28	0	26	0	0
14	a	2	0	0	0	0
15	c	31	0	0	0	0
16	A	163	0	0	6	0
16	B	160	0	0	7	0
16	C	165	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	D	42	0	0	3	0
16	E	26	0	0	1	0
16	F	41	0	0	0	0
16	G	30	0	0	0	0
16	H	34	0	0	4	0
16	L	30	0	0	0	0
16	a	97	0	0	8	0
16	b	85	0	0	5	0
16	c	110	0	0	11	0
All	All	17624	0	16002	214	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 7.

The worst 5 of 214 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:b:374:HIS:HD2	1:b:377:THR:H	1.11	0.95
2:A:100:GLU:HG2	2:A:101:THR:HG23	1.55	0.89
2:C:63:LYS:NZ	1:c:408:ASP:OD1	2.14	0.80
1:b:385:CYS:SG	16:b:607:HOH:O	2.44	0.76
1:c:385:CYS:SG	16:c:621:HOH:O	2.43	0.76

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	180/232 (78%)	178 (99%)	2 (1%)	0	100	100
1	b	182/232 (78%)	181 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	c	182/232 (78%)	180 (99%)	2 (1%)	0	100	100
2	A	223/259 (86%)	218 (98%)	5 (2%)	0	100	100
2	B	223/259 (86%)	218 (98%)	5 (2%)	0	100	100
2	C	223/259 (86%)	215 (96%)	8 (4%)	0	100	100
3	D	123/249 (49%)	122 (99%)	1 (1%)	0	100	100
3	F	123/249 (49%)	122 (99%)	1 (1%)	0	100	100
3	H	123/249 (49%)	121 (98%)	2 (2%)	0	100	100
4	E	104/214 (49%)	97 (93%)	7 (7%)	0	100	100
4	G	104/214 (49%)	99 (95%)	5 (5%)	0	100	100
4	L	104/214 (49%)	98 (94%)	6 (6%)	0	100	100
All	All	1894/2862 (66%)	1849 (98%)	45 (2%)	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	166/209 (79%)	166 (100%)	0	100	100
1	b	168/209 (80%)	168 (100%)	0	100	100
1	c	168/209 (80%)	168 (100%)	0	100	100
2	A	207/228 (91%)	207 (100%)	0	100	100
2	B	207/228 (91%)	207 (100%)	0	100	100
2	C	207/228 (91%)	207 (100%)	0	100	100
3	D	106/213 (50%)	106 (100%)	0	100	100
3	F	106/213 (50%)	106 (100%)	0	100	100
3	H	106/213 (50%)	106 (100%)	0	100	100
4	E	89/186 (48%)	89 (100%)	0	100	100
4	G	89/186 (48%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L	89/186 (48%)	89 (100%)	0	100	100
All	All	1708/2508 (68%)	1708 (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 30 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	158	ASN
3	D	39	GLN
1	b	374	HIS
3	F	39	GLN
3	H	3	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 ⓘ

89 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	$\# Z  > 2$
5	NAG	I	1	5,1	14,14,15	0.84	0	17,19,21	0.63	0
5	NAG	I	2	5	14,14,15	0.94	0	17,19,21	0.92	0
5	BMA	I	3	5	11,11,12	1.05	1 (9%)	15,15,17	2.34	4 (26%)
5	MAN	I	4	5	11,11,12	0.70	0	15,15,17	1.28	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	I	5	5	14,14,15	0.72	0	17,19,21	1.19	1 (5%)
5	MAN	I	6	5	11,11,12	0.71	0	15,15,17	1.20	1 (6%)
6	NAG	J	1	2,6	14,14,15	0.75	0	17,19,21	0.98	1 (5%)
6	NAG	J	2	6	14,14,15	0.74	0	17,19,21	0.91	1 (5%)
7	NAG	K	1	2,7	14,14,15	0.80	0	17,19,21	1.25	3 (17%)
7	NAG	K	2	7	14,14,15	0.77	1 (7%)	17,19,21	1.44	2 (11%)
7	BMA	K	3	7	11,11,12	0.84	0	15,15,17	2.15	3 (20%)
8	NAG	M	1	2,8	14,14,15	0.83	0	17,19,21	1.02	2 (11%)
8	NAG	M	2	8	14,14,15	0.76	0	17,19,21	0.85	0
8	BMA	M	3	8	11,11,12	0.85	0	15,15,17	2.14	3 (20%)
8	FUC	M	4	8	10,10,11	0.75	0	14,14,16	1.03	0
7	NAG	N	1	2,7	14,14,15	0.81	0	17,19,21	0.92	1 (5%)
7	NAG	N	2	7	14,14,15	0.79	0	17,19,21	0.92	0
7	BMA	N	3	7	11,11,12	0.82	0	15,15,17	2.06	3 (20%)
9	NAG	O	1	2,9	14,14,15	0.92	1 (7%)	17,19,21	0.88	1 (5%)
9	NAG	O	2	9	14,14,15	0.75	0	17,19,21	1.17	1 (5%)
9	BMA	O	3	9	11,11,12	0.92	0	15,15,17	1.75	2 (13%)
9	MAN	O	4	9	11,11,12	0.78	0	15,15,17	1.32	1 (6%)
9	NAG	O	5	9	14,14,15	0.87	0	17,19,21	1.04	1 (5%)
9	GAL	O	6	9	11,11,12	0.76	0	15,15,17	1.04	0
9	MAN	O	7	9	11,11,12	0.65	0	15,15,17	2.38	5 (33%)
10	NAG	P	1	2,10	14,14,15	0.79	0	17,19,21	1.34	2 (11%)
10	NAG	P	2	10	14,14,15	0.80	0	17,19,21	0.90	1 (5%)
10	BMA	P	3	10	11,11,12	0.79	0	15,15,17	2.17	4 (26%)
10	MAN	P	4	10	11,11,12	0.74	0	15,15,17	1.18	1 (6%)
10	FUC	P	5	10	10,10,11	0.77	0	14,14,16	1.16	2 (14%)
6	NAG	Q	1	2,6	14,14,15	0.76	0	17,19,21	1.47	3 (17%)
6	NAG	Q	2	6	14,14,15	0.66	0	17,19,21	1.16	2 (11%)
11	NAG	R	1	2,11	14,14,15	0.77	0	17,19,21	1.09	1 (5%)
11	NAG	R	2	11	14,14,15	0.77	0	17,19,21	1.12	1 (5%)
11	BMA	R	3	11	11,11,12	0.84	0	15,15,17	2.14	3 (20%)
11	MAN	R	4	11	11,11,12	0.71	0	15,15,17	1.09	1 (6%)
8	NAG	S	1	2,8	14,14,15	0.83	0	17,19,21	1.08	2 (11%)
8	NAG	S	2	8	14,14,15	0.77	0	17,19,21	1.11	0
8	BMA	S	3	8	11,11,12	0.86	0	15,15,17	2.11	3 (20%)
8	FUC	S	4	8	10,10,11	0.73	0	14,14,16	1.15	1 (7%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	NAG	T	1	2,7	14,14,15	0.75	0	17,19,21	1.12	1 (5%)
7	NAG	T	2	7	14,14,15	0.83	0	17,19,21	0.84	0
7	BMA	T	3	7	11,11,12	0.85	0	15,15,17	2.22	4 (26%)
9	NAG	U	1	2,9	14,14,15	0.76	0	17,19,21	1.20	2 (11%)
9	NAG	U	2	9	14,14,15	0.82	0	17,19,21	1.23	1 (5%)
9	BMA	U	3	9	11,11,12	0.86	0	15,15,17	2.35	6 (40%)
9	MAN	U	4	9	11,11,12	0.82	0	15,15,17	0.97	1 (6%)
9	NAG	U	5	9	14,14,15	0.74	0	17,19,21	1.01	1 (5%)
9	GAL	U	6	9	11,11,12	0.77	0	15,15,17	1.07	1 (6%)
9	MAN	U	7	9	11,11,12	0.83	0	15,15,17	0.93	0
10	NAG	V	1	2,10	14,14,15	0.71	0	17,19,21	1.61	1 (5%)
10	NAG	V	2	10	14,14,15	0.81	0	17,19,21	1.10	1 (5%)
10	BMA	V	3	10	11,11,12	0.86	0	15,15,17	2.41	4 (26%)
10	MAN	V	4	10	11,11,12	0.68	0	15,15,17	1.30	1 (6%)
10	FUC	V	5	10	10,10,11	0.82	0	14,14,16	0.97	0
11	NAG	W	1	2,11	14,14,15	0.89	1 (7%)	17,19,21	1.20	2 (11%)
11	NAG	W	2	11	14,14,15	0.80	0	17,19,21	1.32	1 (5%)
11	BMA	W	3	11	11,11,12	0.84	0	15,15,17	2.04	4 (26%)
11	MAN	W	4	11	11,11,12	0.71	0	15,15,17	1.15	1 (6%)
8	NAG	X	1	2,8	14,14,15	0.86	0	17,19,21	0.86	0
8	NAG	X	2	8	14,14,15	0.74	0	17,19,21	0.92	0
8	BMA	X	3	8	11,11,12	0.84	0	15,15,17	2.14	3 (20%)
8	FUC	X	4	8	10,10,11	0.79	0	14,14,16	0.89	0
7	NAG	Y	1	2,7	14,14,15	0.98	1 (7%)	17,19,21	1.32	2 (11%)
7	NAG	Y	2	7	14,14,15	0.76	0	17,19,21	1.06	1 (5%)
7	BMA	Y	3	7	11,11,12	0.84	0	15,15,17	2.00	3 (20%)
9	NAG	Z	1	2,9	14,14,15	0.77	0	17,19,21	0.77	0
9	NAG	Z	2	9	14,14,15	0.74	0	17,19,21	0.92	1 (5%)
9	BMA	Z	3	9	11,11,12	0.83	0	15,15,17	2.47	5 (33%)
9	MAN	Z	4	9	11,11,12	0.80	0	15,15,17	1.21	1 (6%)
9	NAG	Z	5	9	14,14,15	0.77	0	17,19,21	1.00	1 (5%)
9	GAL	Z	6	9	11,11,12	0.69	0	15,15,17	1.09	1 (6%)
9	MAN	Z	7	9	11,11,12	0.71	0	15,15,17	2.69	3 (20%)
10	NAG	d	1	2,10	14,14,15	0.80	0	17,19,21	1.33	1 (5%)
10	NAG	d	2	10	14,14,15	0.90	0	17,19,21	0.91	0
10	BMA	d	3	10	11,11,12	0.83	0	15,15,17	2.36	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
10	MAN	d	4	10	11,11,12	0.65	0	15,15,17	1.47	1 (6%)
10	FUC	d	5	10	10,10,11	0.90	0	14,14,16	0.84	0
12	NAG	e	1	12,1	14,14,15	0.85	0	17,19,21	0.96	1 (5%)
12	NAG	e	2	12	14,14,15	0.90	0	17,19,21	0.91	1 (5%)
12	BMA	e	3	12	11,11,12	1.02	1 (9%)	15,15,17	2.02	4 (26%)
12	MAN	e	4	12	11,11,12	0.71	0	15,15,17	1.07	1 (6%)
12	MAN	e	5	12	11,11,12	0.75	0	15,15,17	1.03	1 (6%)
5	NAG	f	1	5,1	14,14,15	0.83	0	17,19,21	0.94	0
5	NAG	f	2	5	14,14,15	0.97	1 (7%)	17,19,21	0.91	0
5	BMA	f	3	5	11,11,12	1.02	0	15,15,17	2.06	4 (26%)
5	MAN	f	4	5	11,11,12	0.67	0	15,15,17	1.21	1 (6%)
5	NAG	f	5	5	14,14,15	0.71	0	17,19,21	1.11	1 (5%)
5	MAN	f	6	5	11,11,12	0.64	0	15,15,17	1.37	1 (6%)

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
5	NAG	I	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	I	2	5	-	0/6/23/26	0/1/1/1
5	BMA	I	3	5	-	0/2/19/22	0/1/1/1
5	MAN	I	4	5	-	0/2/19/22	0/1/1/1
5	NAG	I	5	5	-	2/6/23/26	0/1/1/1
5	MAN	I	6	5	-	0/2/19/22	0/1/1/1
6	NAG	J	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	J	2	6	-	2/6/23/26	0/1/1/1
7	NAG	K	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	K	2	7	-	0/6/23/26	0/1/1/1
7	BMA	K	3	7	-	2/2/19/22	0/1/1/1
8	NAG	M	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	M	2	8	-	0/6/23/26	0/1/1/1
8	BMA	M	3	8	-	0/2/19/22	0/1/1/1
8	FUC	M	4	8	-	-	0/1/1/1
7	NAG	N	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	N	2	7	-	4/6/23/26	0/1/1/1
7	BMA	N	3	7	-	0/2/19/22	0/1/1/1
9	NAG	O	1	2,9	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	O	2	9	-	0/6/23/26	0/1/1/1
9	BMA	O	3	9	-	2/2/19/22	0/1/1/1
9	MAN	O	4	9	-	2/2/19/22	0/1/1/1
9	NAG	O	5	9	-	4/6/23/26	0/1/1/1
9	GAL	O	6	9	-	0/2/19/22	0/1/1/1
9	MAN	O	7	9	-	0/2/19/22	0/1/1/1
10	NAG	P	1	2,10	-	0/6/23/26	0/1/1/1
10	NAG	P	2	10	-	1/6/23/26	0/1/1/1
10	BMA	P	3	10	-	0/2/19/22	0/1/1/1
10	MAN	P	4	10	-	1/2/19/22	0/1/1/1
10	FUC	P	5	10	-	-	0/1/1/1
6	NAG	Q	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	2/6/23/26	0/1/1/1
11	NAG	R	1	2,11	-	0/6/23/26	0/1/1/1
11	NAG	R	2	11	-	0/6/23/26	0/1/1/1
11	BMA	R	3	11	-	1/2/19/22	0/1/1/1
11	MAN	R	4	11	-	1/2/19/22	0/1/1/1
8	NAG	S	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	S	2	8	-	2/6/23/26	0/1/1/1
8	BMA	S	3	8	-	1/2/19/22	0/1/1/1
8	FUC	S	4	8	-	-	0/1/1/1
7	NAG	T	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	T	2	7	-	4/6/23/26	0/1/1/1
7	BMA	T	3	7	-	0/2/19/22	0/1/1/1
9	NAG	U	1	2,9	-	0/6/23/26	0/1/1/1
9	NAG	U	2	9	-	0/6/23/26	0/1/1/1
9	BMA	U	3	9	-	1/2/19/22	0/1/1/1
9	MAN	U	4	9	-	2/2/19/22	0/1/1/1
9	NAG	U	5	9	-	2/6/23/26	0/1/1/1
9	GAL	U	6	9	-	0/2/19/22	0/1/1/1
9	MAN	U	7	9	-	2/2/19/22	0/1/1/1
10	NAG	V	1	2,10	-	0/6/23/26	0/1/1/1
10	NAG	V	2	10	-	0/6/23/26	0/1/1/1
10	BMA	V	3	10	-	0/2/19/22	0/1/1/1
10	MAN	V	4	10	-	0/2/19/22	0/1/1/1
10	FUC	V	5	10	-	-	0/1/1/1
11	NAG	W	1	2,11	-	0/6/23/26	0/1/1/1
11	NAG	W	2	11	-	0/6/23/26	0/1/1/1
11	BMA	W	3	11	-	0/2/19/22	0/1/1/1
11	MAN	W	4	11	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	X	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	X	2	8	-	0/6/23/26	0/1/1/1
8	BMA	X	3	8	-	0/2/19/22	0/1/1/1
8	FUC	X	4	8	-	-	0/1/1/1
7	NAG	Y	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	Y	2	7	-	2/6/23/26	0/1/1/1
7	BMA	Y	3	7	-	1/2/19/22	0/1/1/1
9	NAG	Z	1	2,9	-	0/6/23/26	0/1/1/1
9	NAG	Z	2	9	-	0/6/23/26	0/1/1/1
9	BMA	Z	3	9	-	2/2/19/22	0/1/1/1
9	MAN	Z	4	9	-	1/2/19/22	0/1/1/1
9	NAG	Z	5	9	-	4/6/23/26	0/1/1/1
9	GAL	Z	6	9	-	0/2/19/22	0/1/1/1
9	MAN	Z	7	9	-	0/2/19/22	0/1/1/1
10	NAG	d	1	2,10	-	0/6/23/26	0/1/1/1
10	NAG	d	2	10	-	0/6/23/26	0/1/1/1
10	BMA	d	3	10	-	1/2/19/22	0/1/1/1
10	MAN	d	4	10	-	1/2/19/22	0/1/1/1
10	FUC	d	5	10	-	-	0/1/1/1
12	NAG	e	1	12,1	-	0/6/23/26	0/1/1/1
12	NAG	e	2	12	-	0/6/23/26	0/1/1/1
12	BMA	e	3	12	-	0/2/19/22	0/1/1/1
12	MAN	e	4	12	-	0/2/19/22	0/1/1/1
12	MAN	e	5	12	-	0/2/19/22	0/1/1/1
5	NAG	f	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	f	2	5	-	0/6/23/26	0/1/1/1
5	BMA	f	3	5	-	0/2/19/22	0/1/1/1
5	MAN	f	4	5	-	0/2/19/22	0/1/1/1
5	NAG	f	5	5	-	2/6/23/26	0/1/1/1
5	MAN	f	6	5	-	0/2/19/22	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	Y	1	NAG	C1-C2	2.47	1.55	1.52
5	I	3	BMA	C2-C3	2.21	1.55	1.52
5	f	2	NAG	C1-C2	2.11	1.55	1.52
9	O	1	NAG	O5-C1	-2.11	1.40	1.43
11	W	1	NAG	O5-C1	-2.04	1.40	1.43

The worst 5 of 138 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
9	Z	7	MAN	C1-O5-C5	7.98	122.88	112.19
9	Z	3	BMA	C1-O5-C5	7.40	122.10	112.19
10	d	3	BMA	C1-O5-C5	7.09	121.69	112.19
10	V	3	BMA	C1-O5-C5	6.91	121.45	112.19
9	O	7	MAN	C1-O5-C5	6.83	121.34	112.19

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

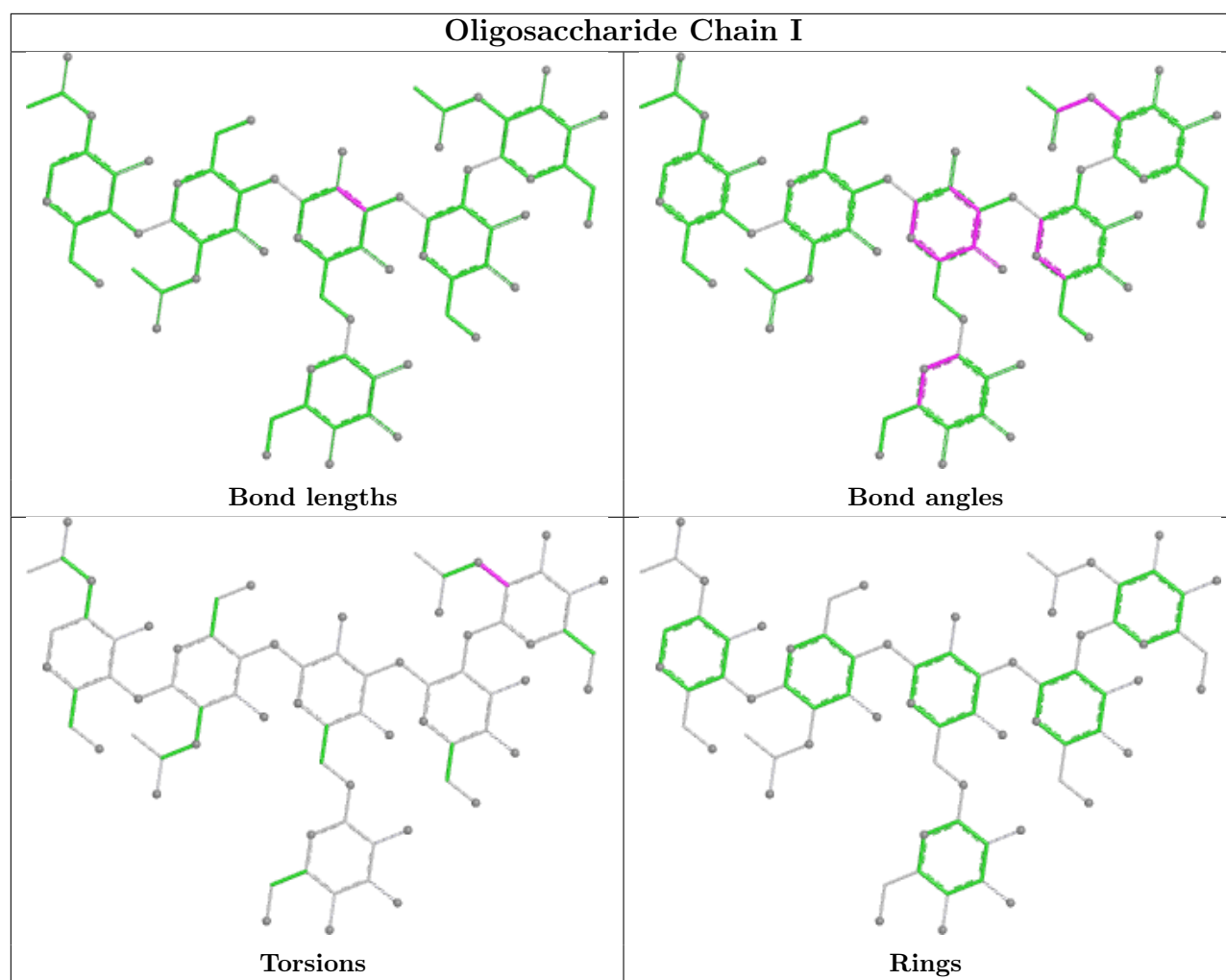
Mol	Chain	Res	Type	Atoms
6	J	1	NAG	O5-C5-C6-O6
6	Q	1	NAG	O5-C5-C6-O6
7	K	3	BMA	O5-C5-C6-O6
9	O	5	NAG	O5-C5-C6-O6
9	Z	5	NAG	O5-C5-C6-O6

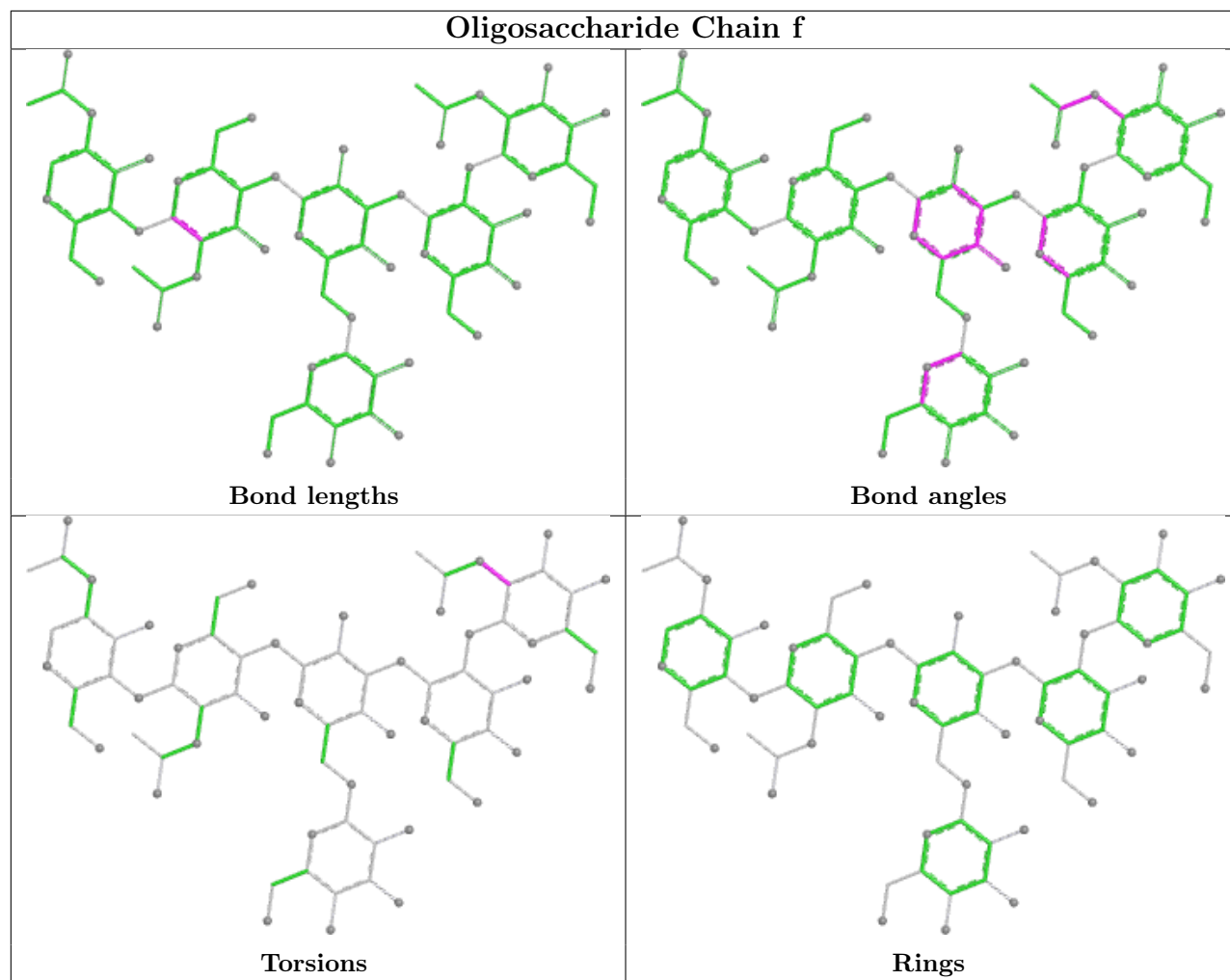
There are no ring outliers.

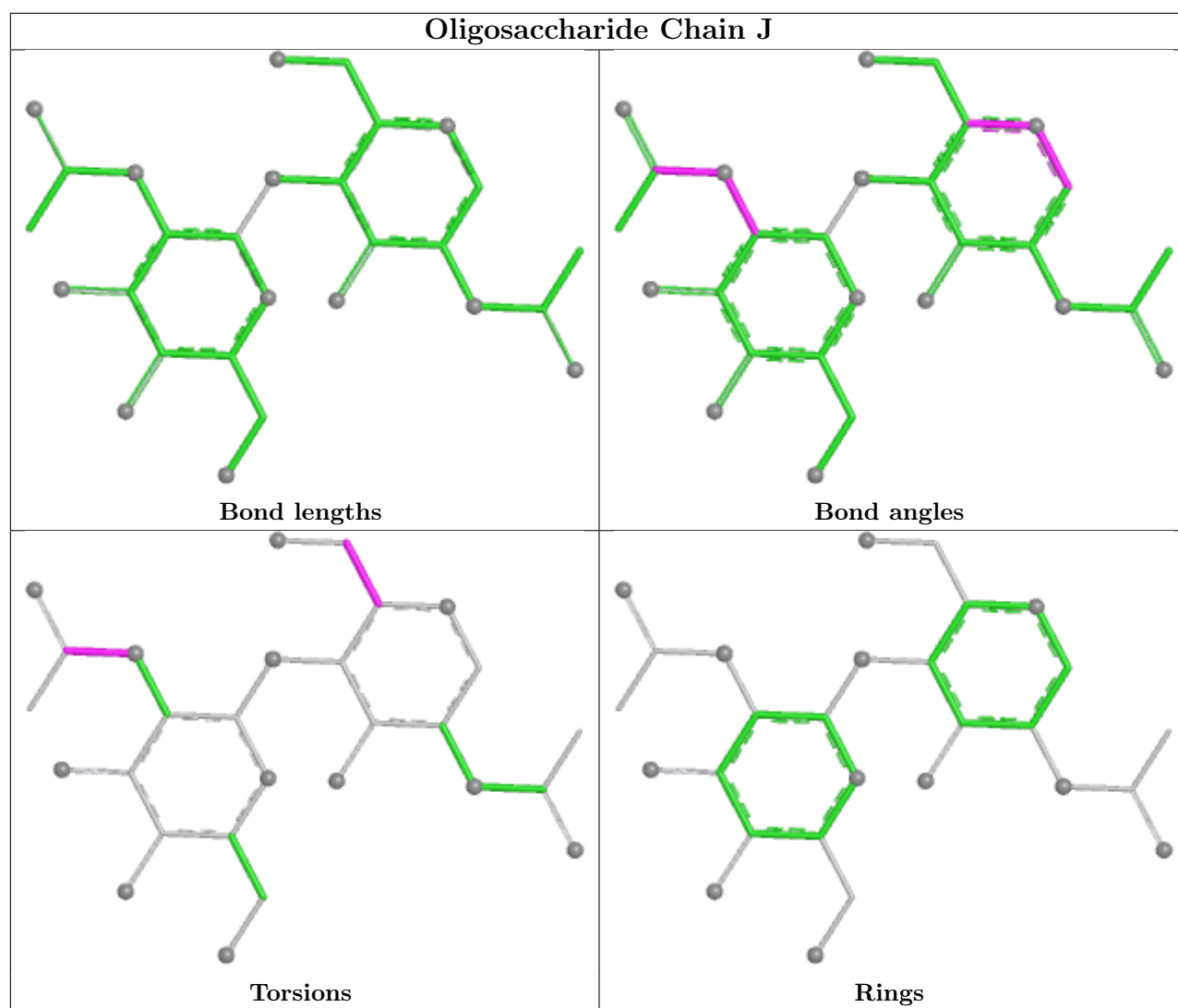
7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	O	6	GAL	1	0
9	Z	5	NAG	1	0
9	U	7	MAN	2	0
9	O	5	NAG	1	0
9	U	5	NAG	1	0
9	O	3	BMA	1	0
10	d	1	NAG	1	0

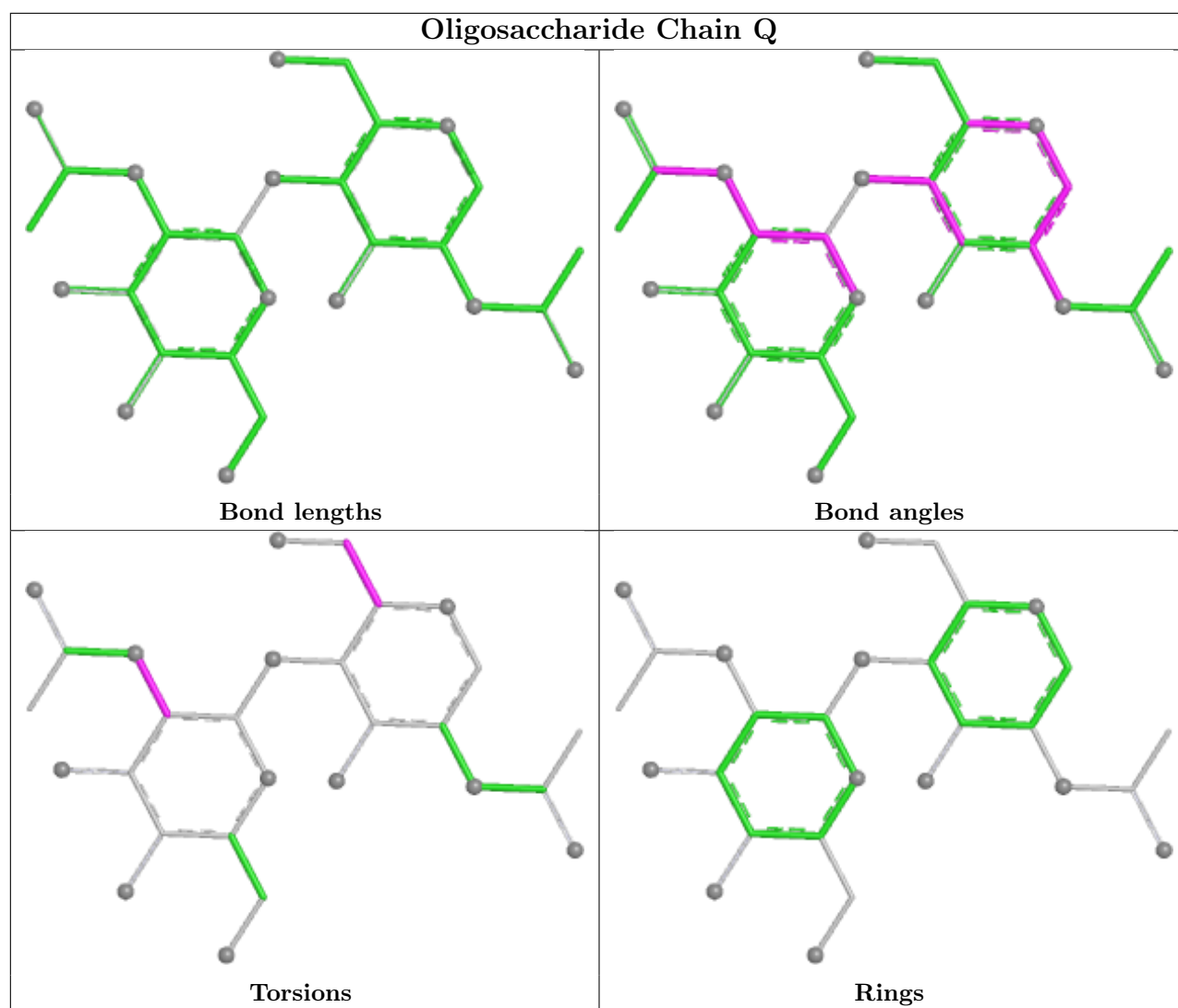
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

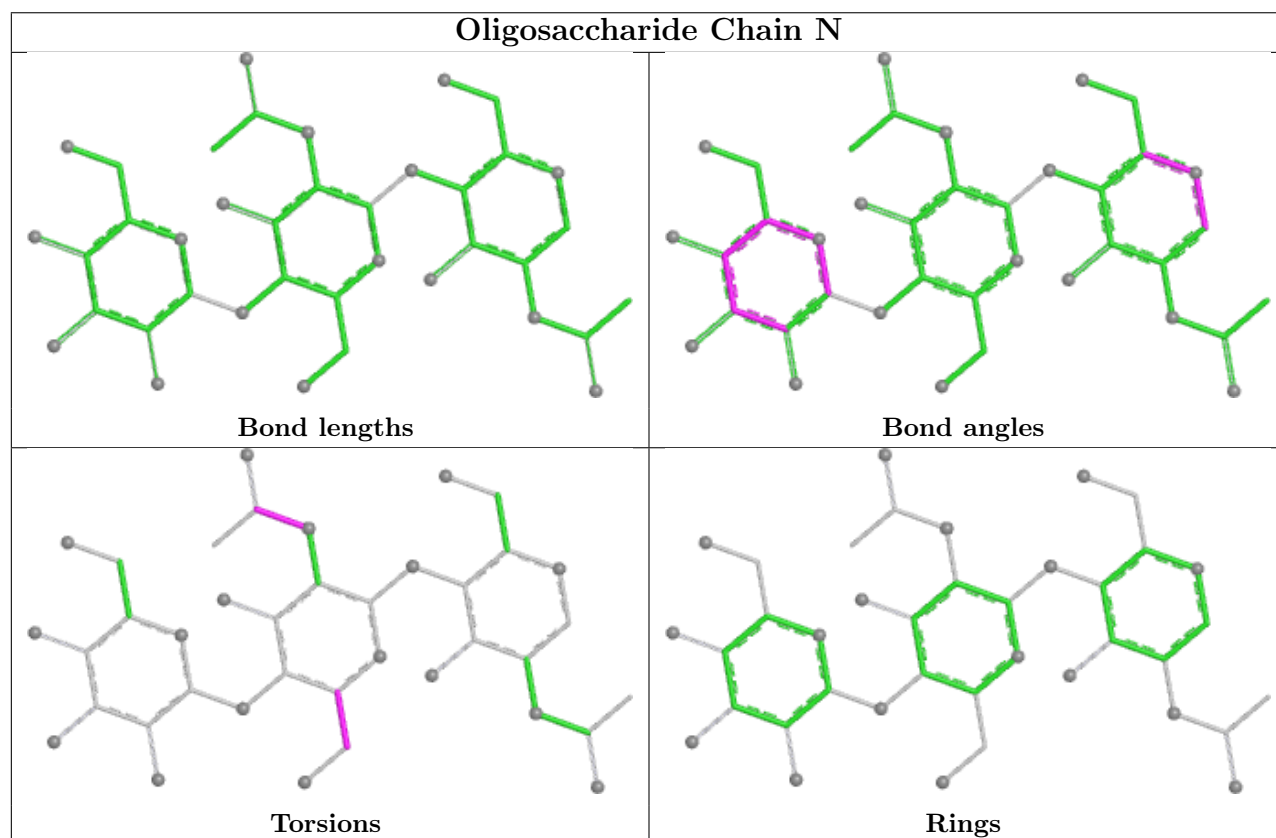
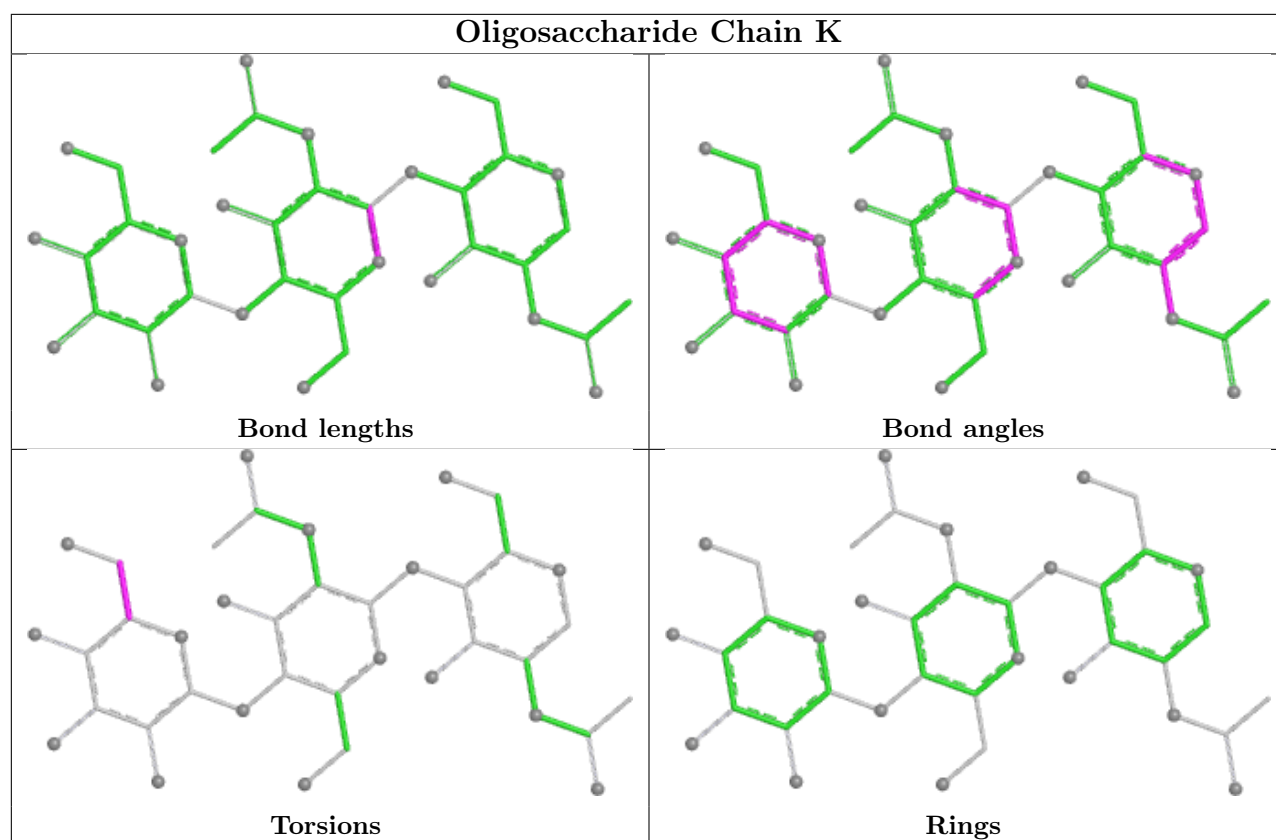


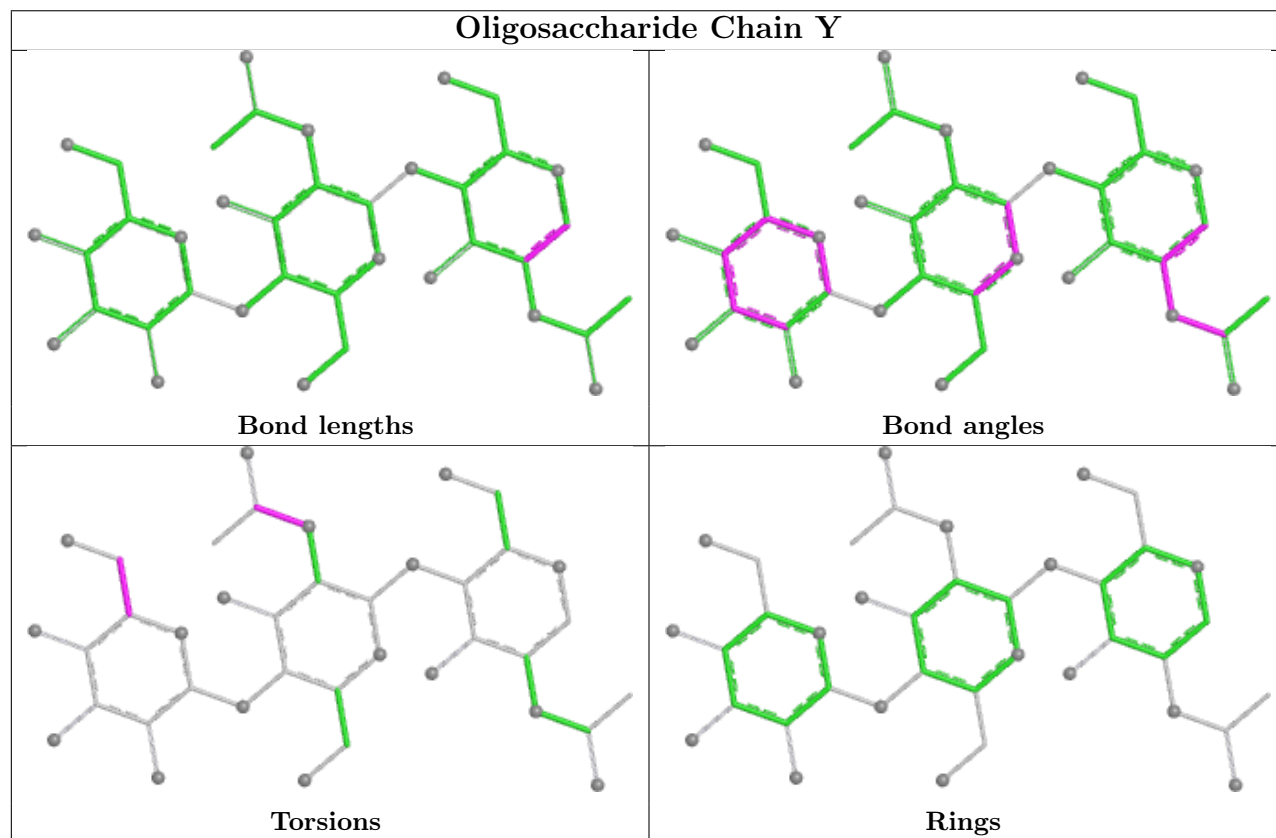
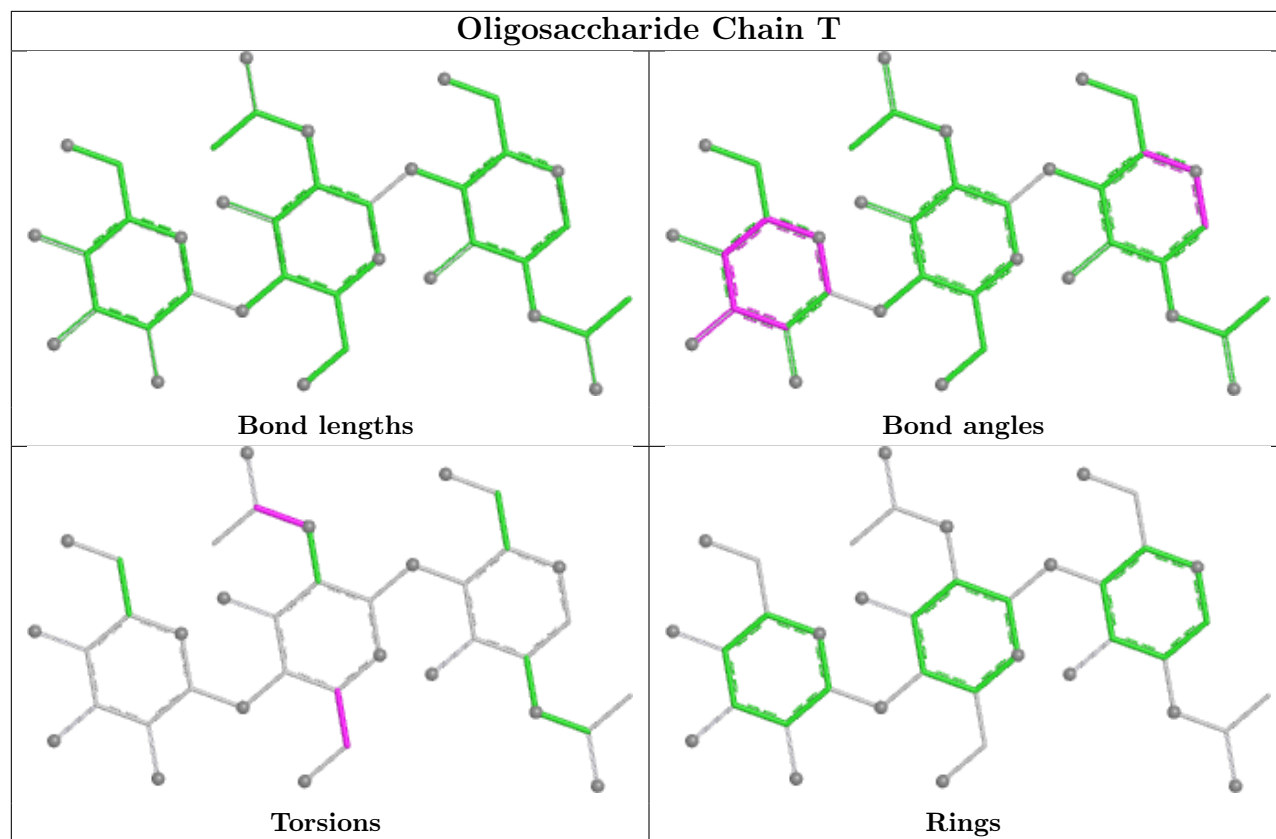


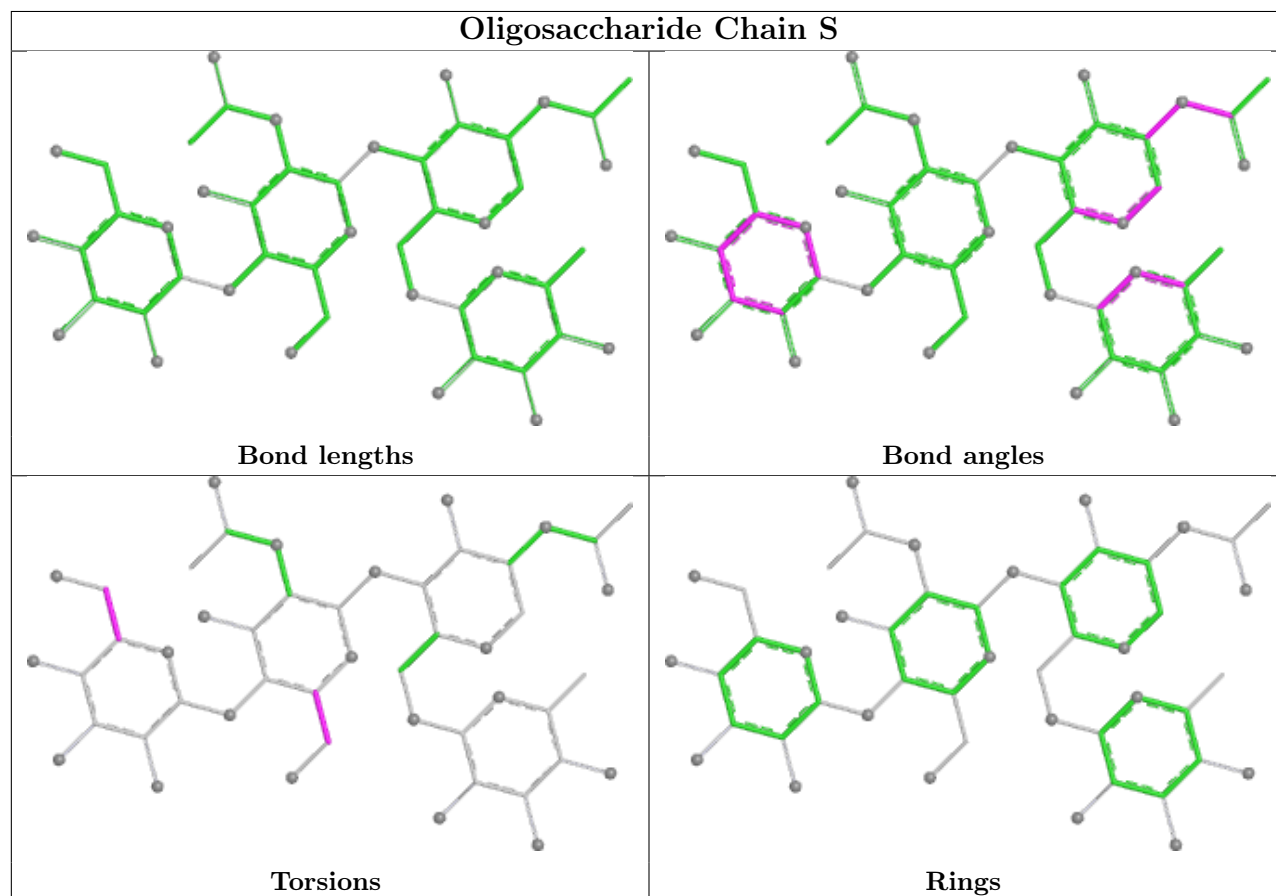
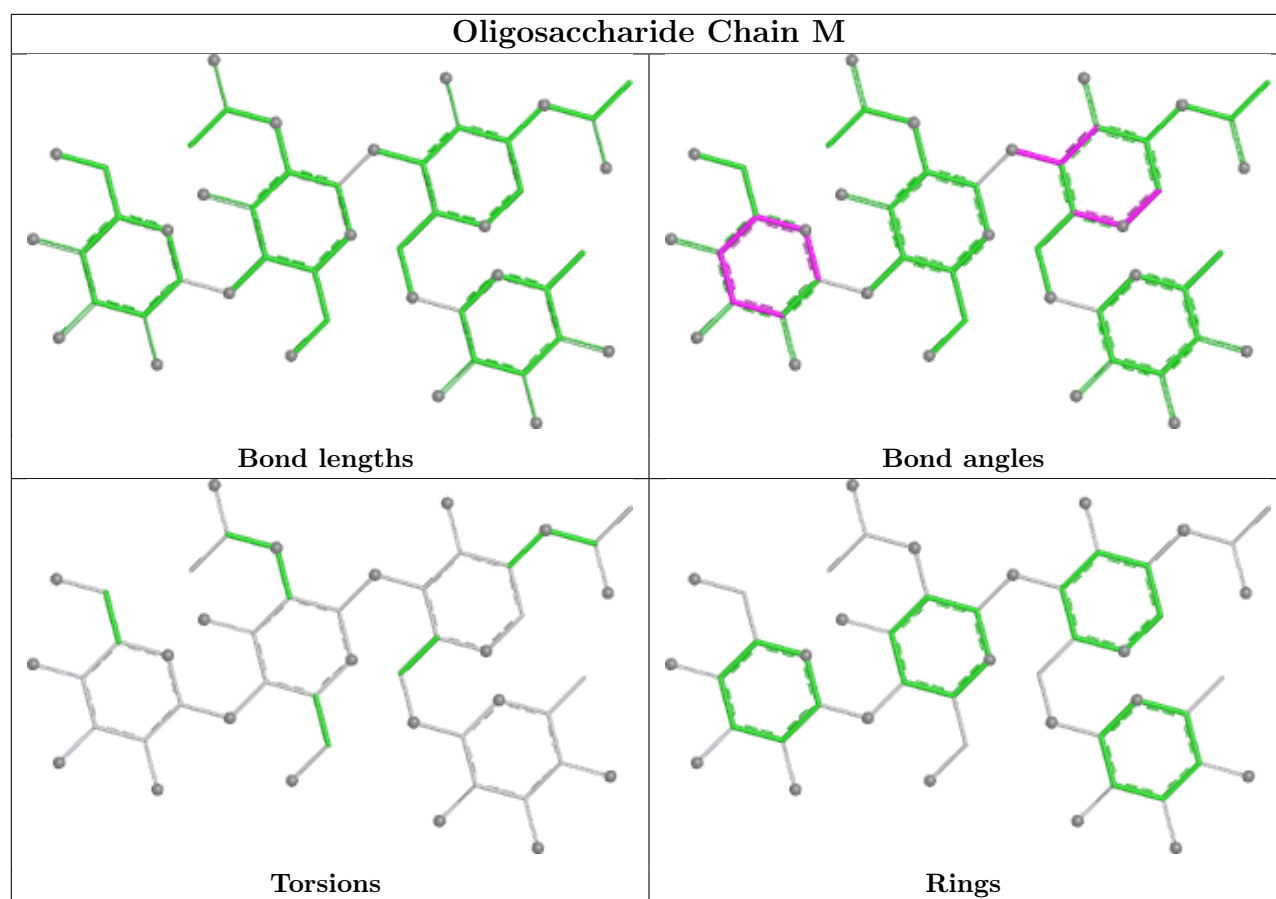


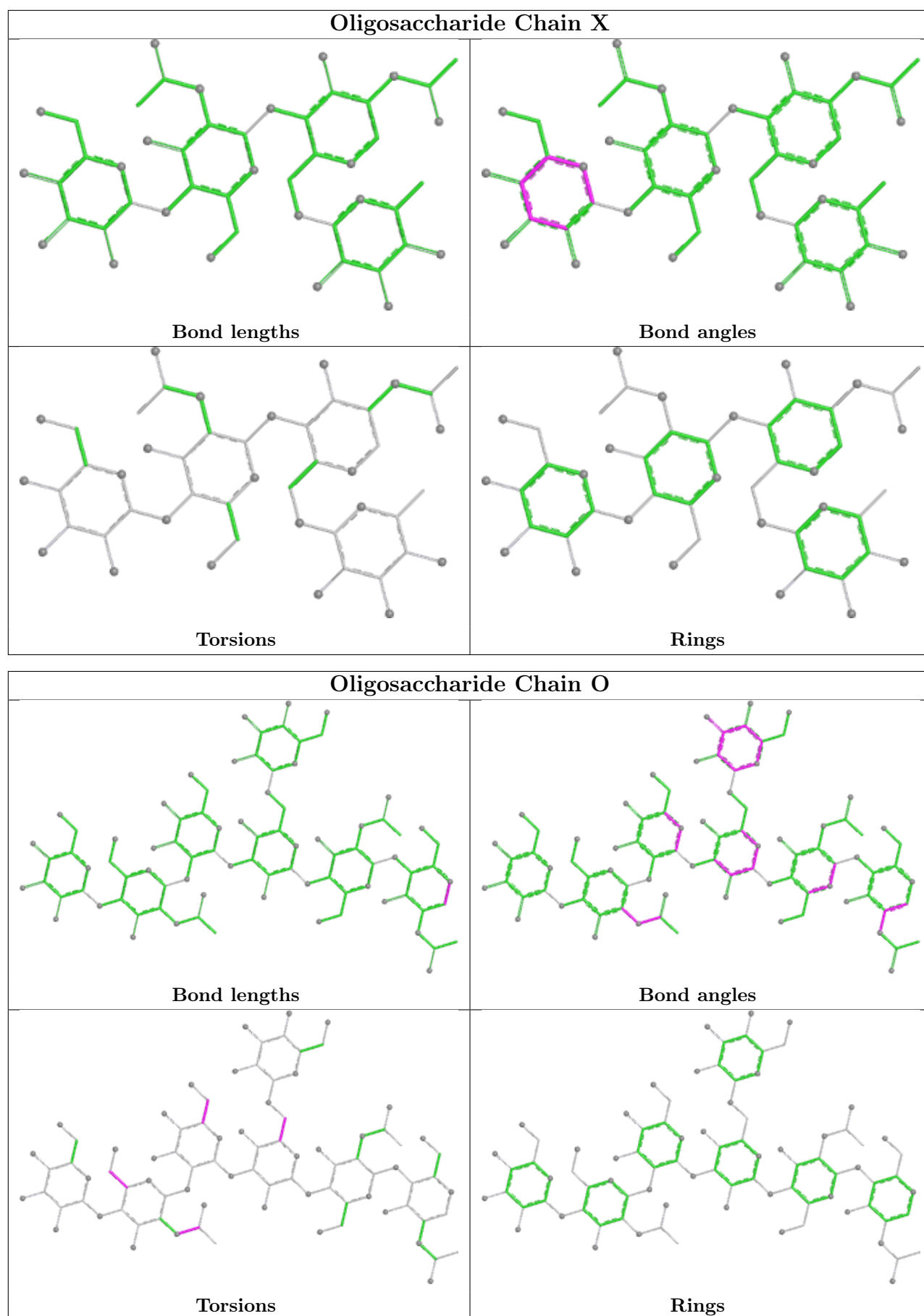


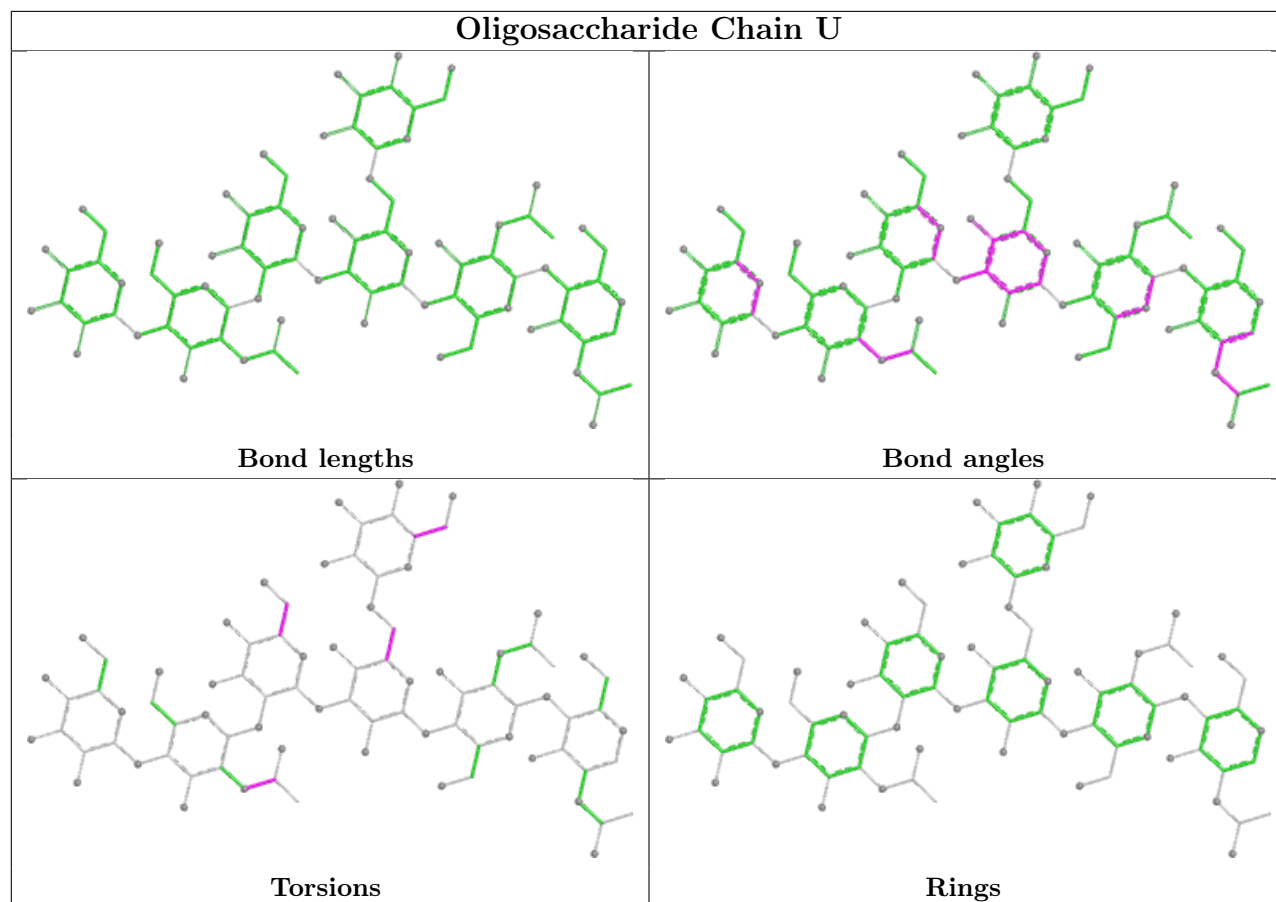


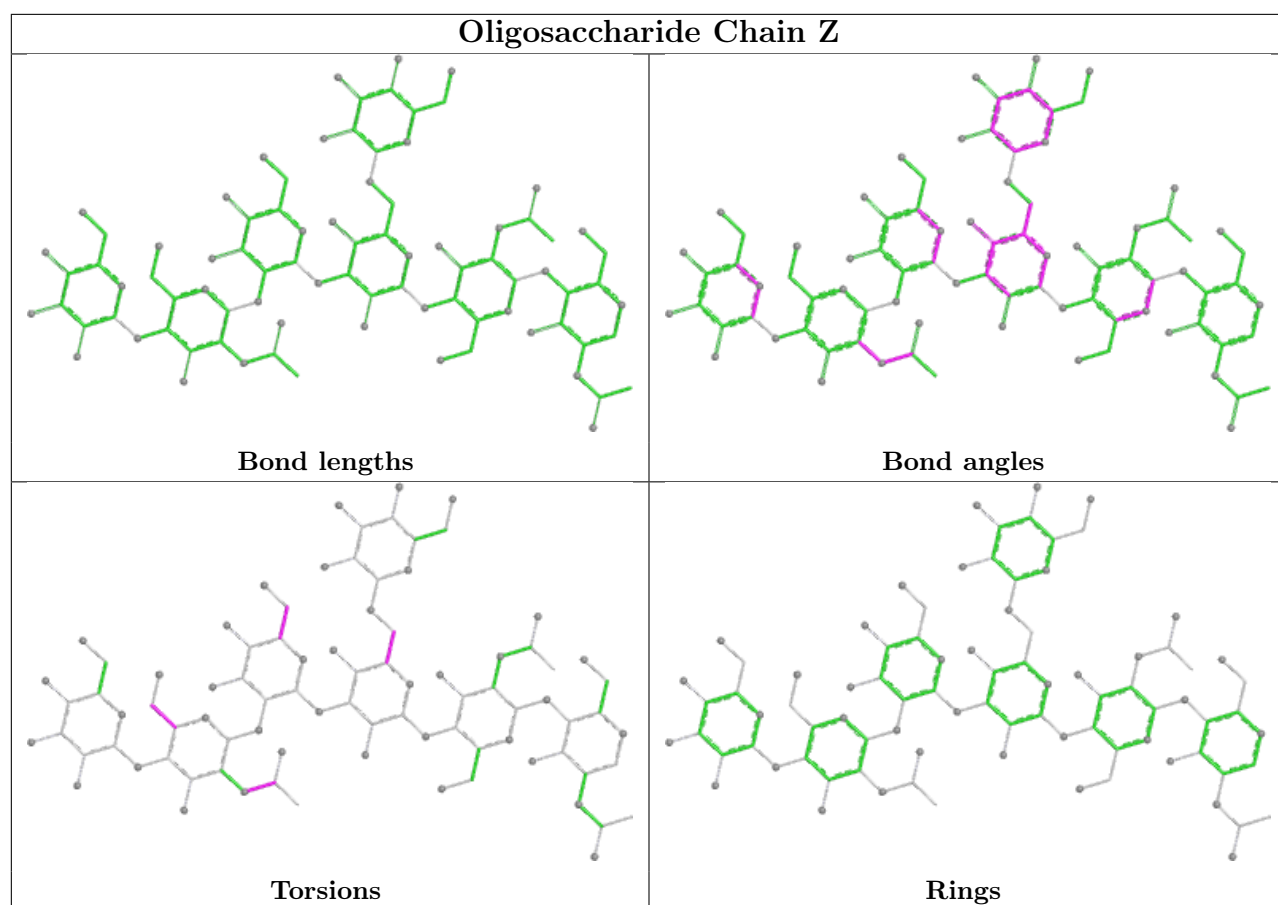


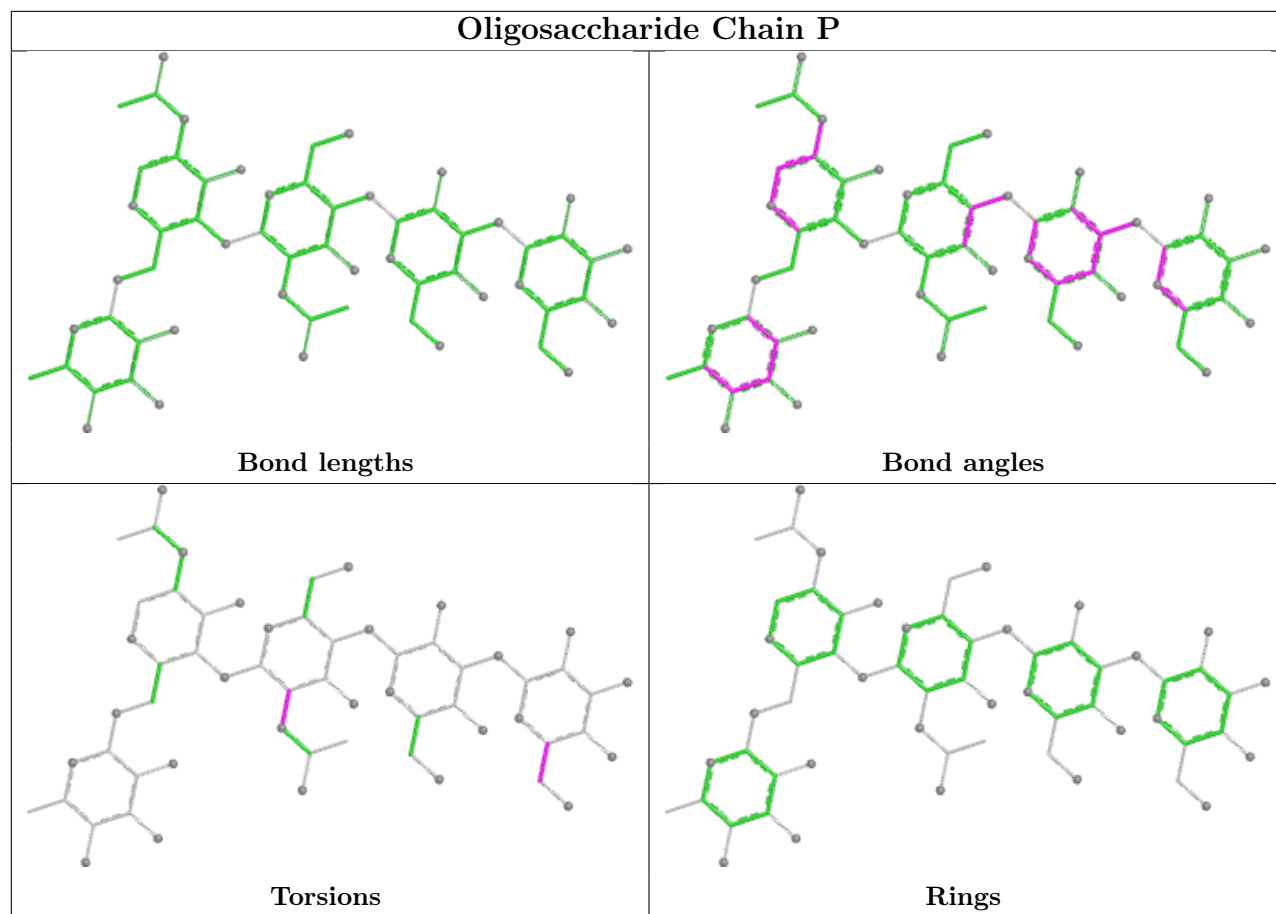




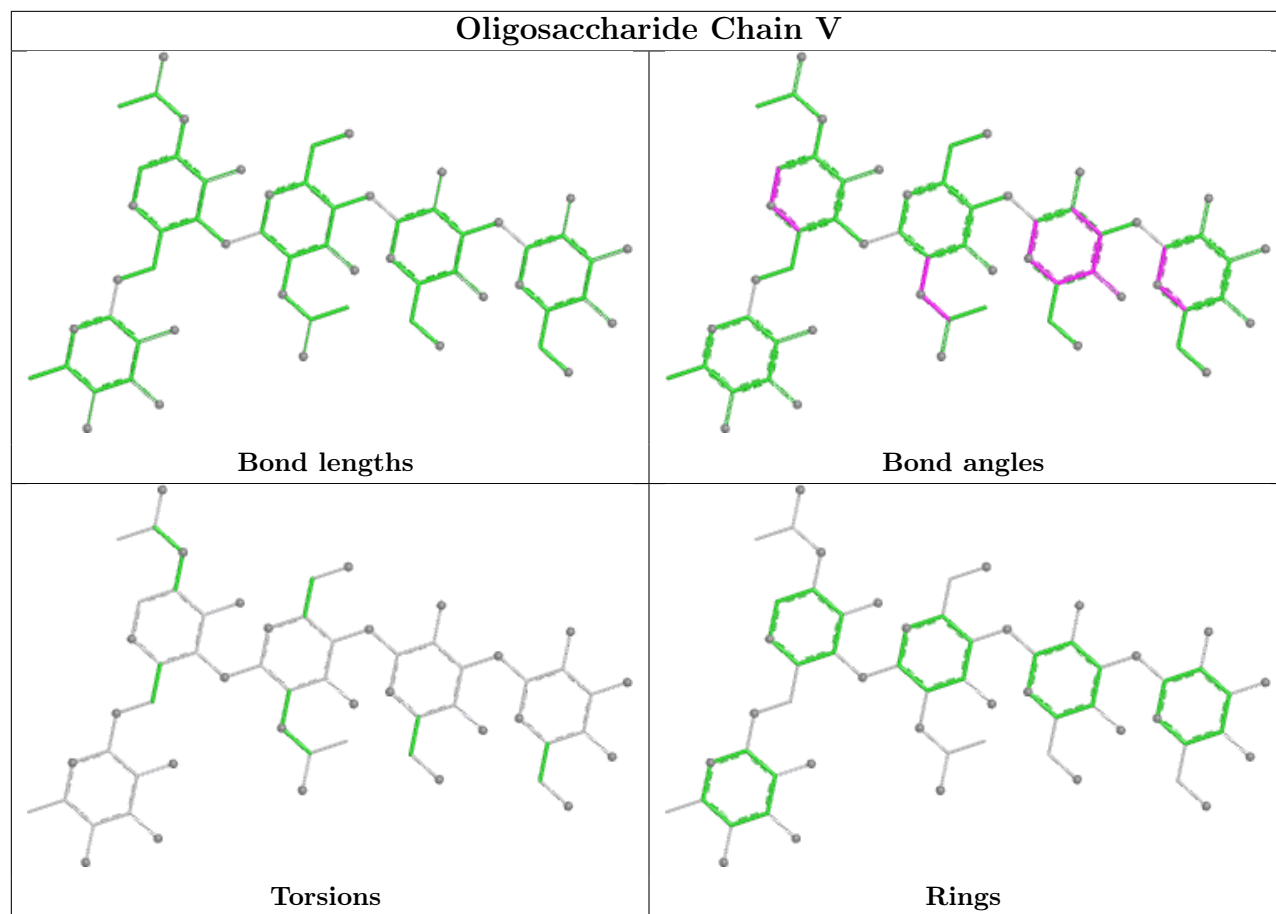


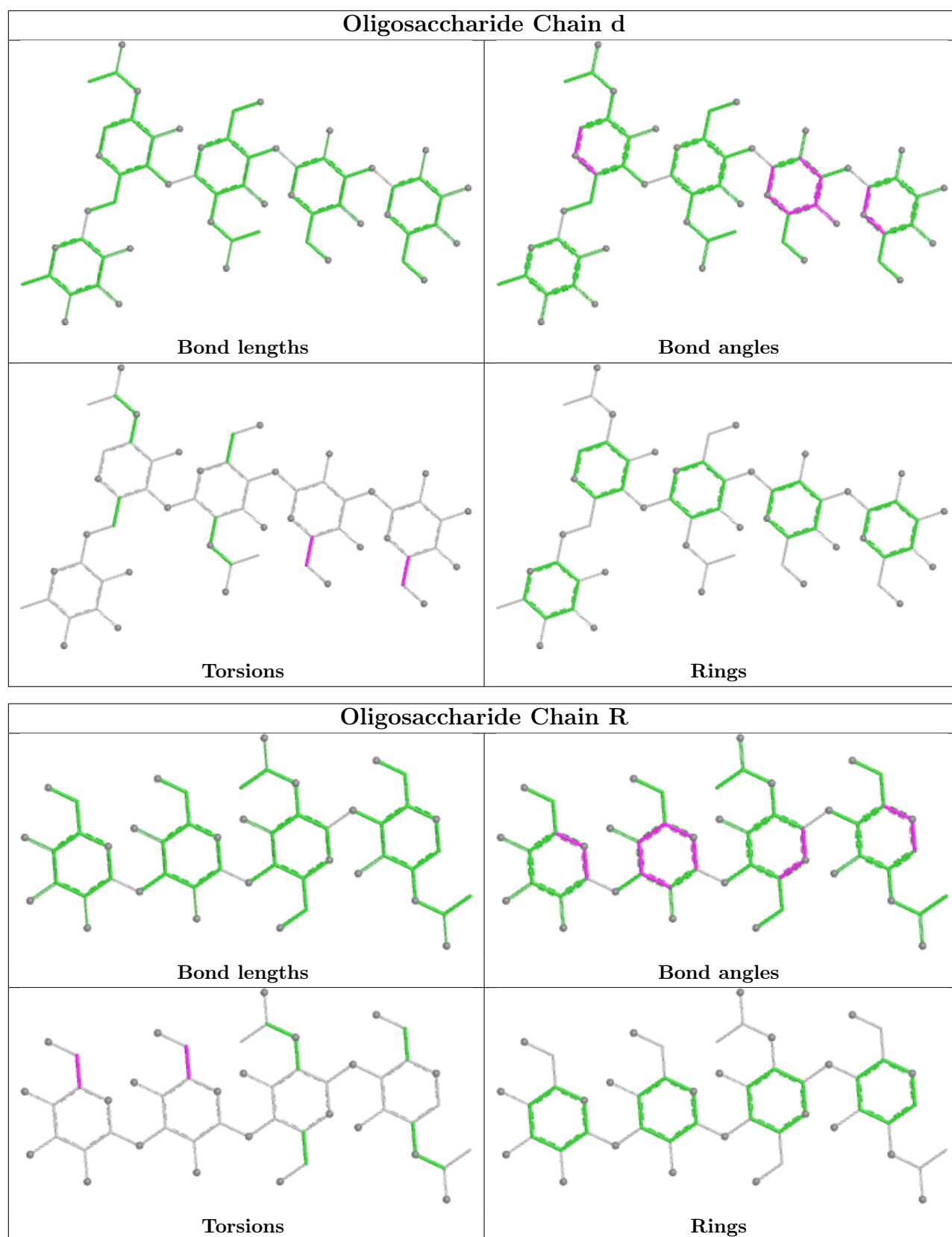


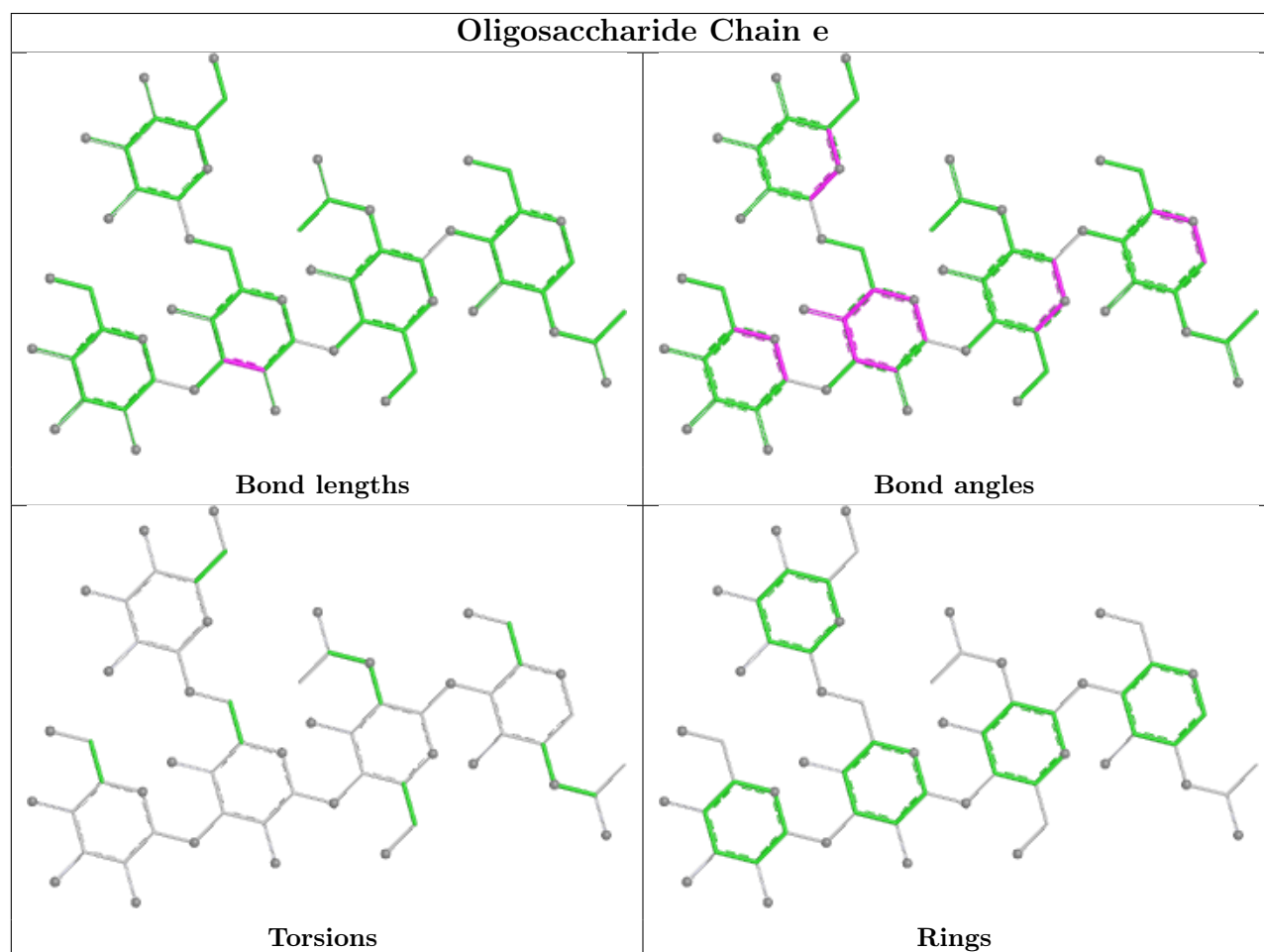
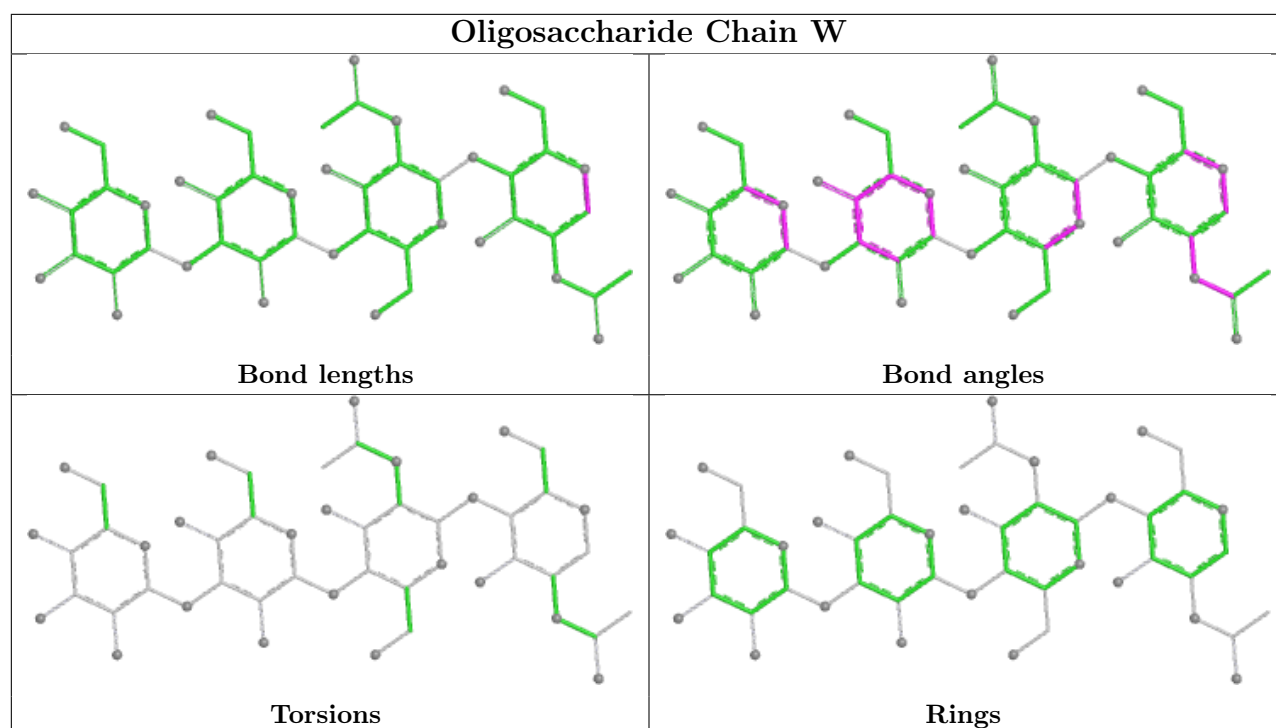












## 5.6 Ligand geometry

Of 13 ligands modelled in this entry, 2 are unknown - leaving 11 for Mogul analysis.

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
13	NAG	b	502	1	14,14,15	0.82	1 (7%)	17,19,21	1.42	2 (11%)
15	A1BK9	c	501	-	32,34,34	2.26	11 (34%)	43,50,50	1.37	6 (13%)
13	NAG	A	301	2	14,14,15	0.73	0	17,19,21	1.08	1 (5%)
13	NAG	b	501	1	14,14,15	0.85	0	17,19,21	0.94	1 (5%)
13	NAG	c	503	1	14,14,15	0.74	0	17,19,21	0.88	0
13	NAG	a	502	1	14,14,15	0.76	0	17,19,21	0.84	0
13	NAG	C	301	2	14,14,15	0.77	0	17,19,21	1.38	2 (11%)
13	NAG	c	502	1	14,14,15	0.86	0	17,19,21	1.14	2 (11%)
13	NAG	B	301	2	14,14,15	0.77	0	17,19,21	0.84	1 (5%)
13	NAG	a	501	1	14,14,15	0.81	0	17,19,21	0.94	1 (5%)
13	NAG	C	302	2	14,14,15	0.71	0	17,19,21	0.77	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
13	NAG	b	502	1	-	0/6/23/26	0/1/1/1
15	A1BK9	c	501	-	-	7/17/17/17	0/4/4/4
13	NAG	A	301	2	-	0/6/23/26	0/1/1/1
13	NAG	b	501	1	-	2/6/23/26	0/1/1/1
13	NAG	c	503	1	-	0/6/23/26	0/1/1/1
13	NAG	a	502	1	-	1/6/23/26	0/1/1/1
13	NAG	C	301	2	-	1/6/23/26	0/1/1/1
13	NAG	c	502	1	-	0/6/23/26	0/1/1/1
13	NAG	B	301	2	-	1/6/23/26	0/1/1/1
13	NAG	a	501	1	-	0/6/23/26	0/1/1/1
13	NAG	C	302	2	-	0/6/23/26	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	c	501	A1BK9	C04-N05	5.67	1.38	1.33
15	c	501	A1BK9	C08-C07	5.39	1.55	1.48
15	c	501	A1BK9	C21-C22	3.68	1.56	1.49
15	c	501	A1BK9	C20-N19	3.61	1.42	1.36
15	c	501	A1BK9	C14-C13	3.58	1.61	1.51

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	C	301	NAG	C1-O5-C5	4.01	117.56	112.19
15	c	501	A1BK9	C06-C07-C08	-3.94	123.85	128.62
13	b	502	NAG	C1-O5-C5	3.15	116.41	112.19
15	c	501	A1BK9	C25-O26-C27	-2.95	115.55	119.43
13	c	502	NAG	C1-O5-C5	2.94	116.13	112.19

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	a	502	NAG	O5-C5-C6-O6
13	B	301	NAG	O5-C5-C6-O6
15	c	501	A1BK9	C30-C25-O26-C27
15	c	501	A1BK9	C24-C25-O26-C27
15	c	501	A1BK9	C20-C21-C22-C23

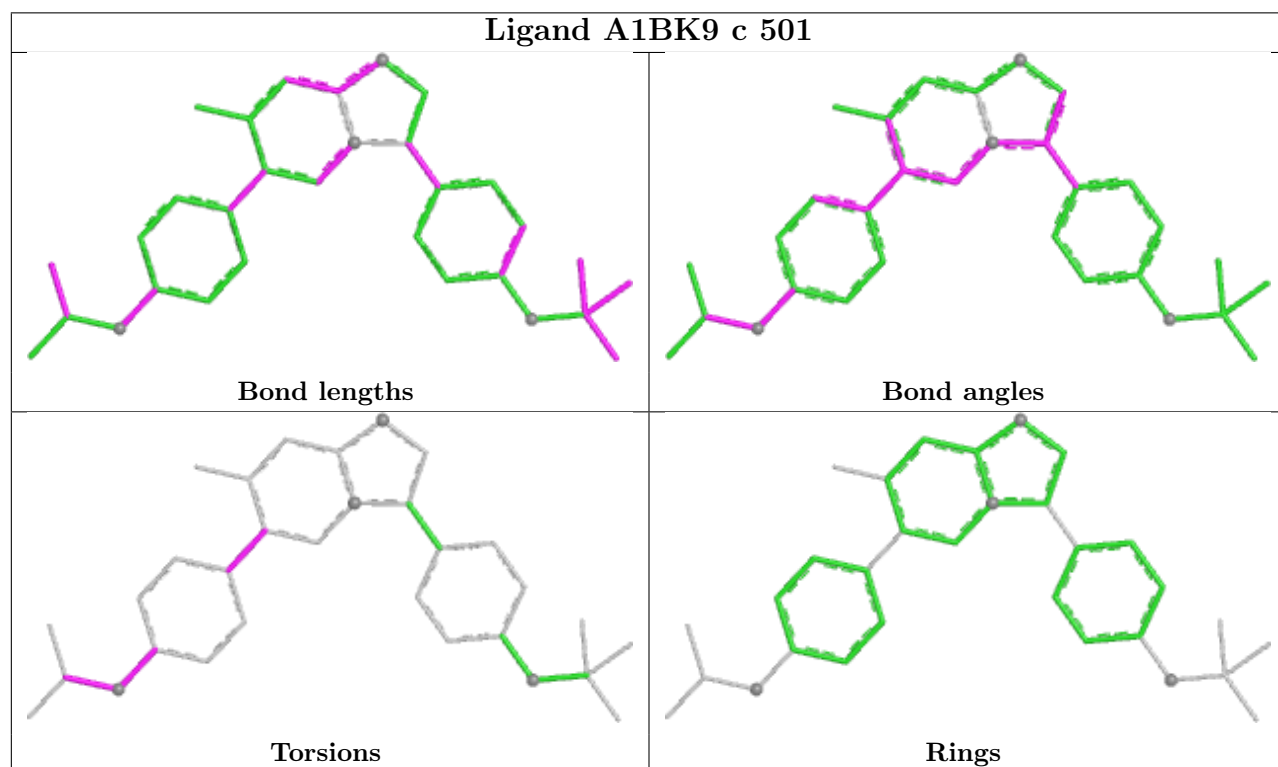
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	b	502	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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.

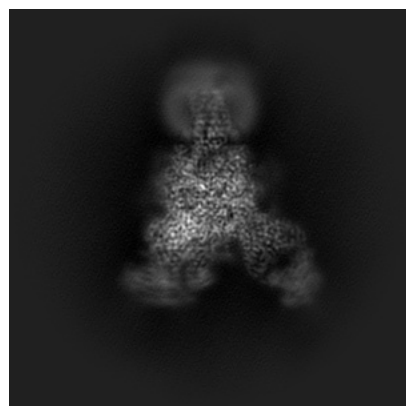
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48275. These allow visual inspection of the internal detail of the map and identification of artifacts.

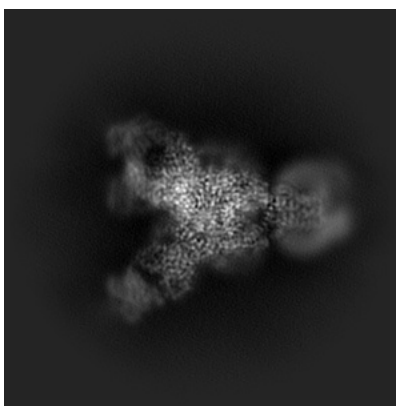
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

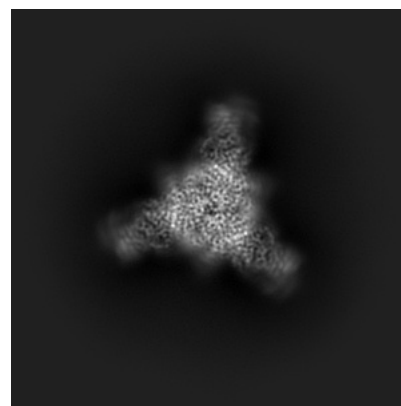
#### 6.1.1 Primary map



X

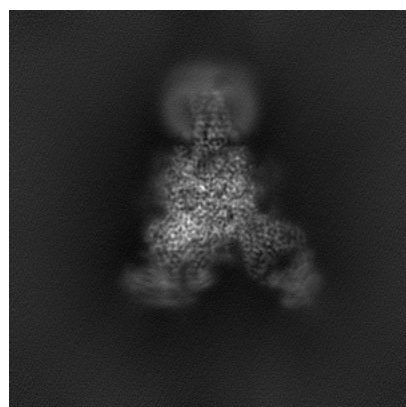


Y

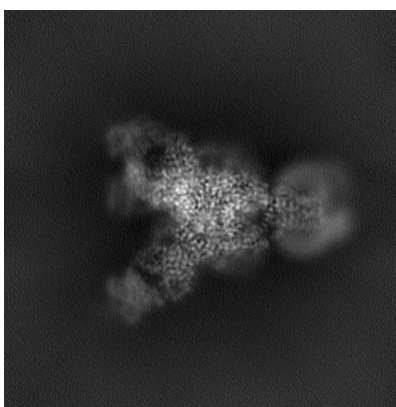


Z

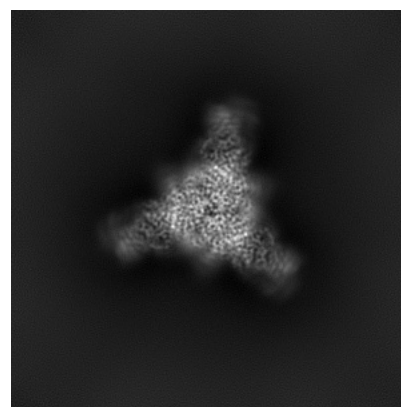
#### 6.1.2 Raw map



X



Y

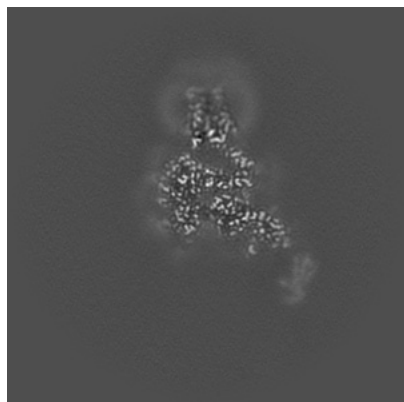


Z

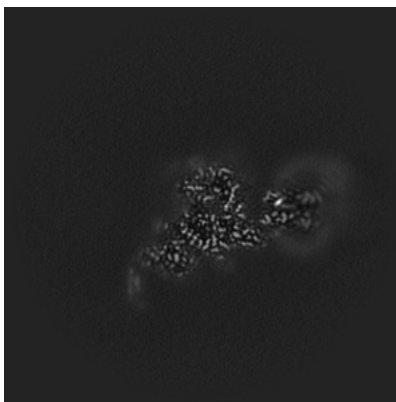
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

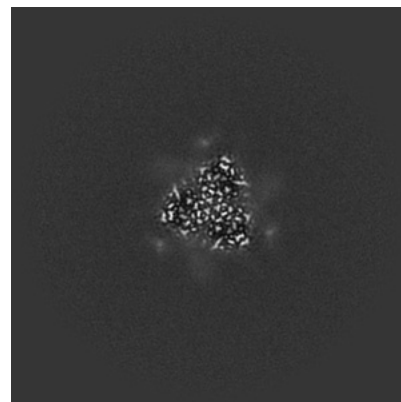
### 6.2.1 Primary map



X Index: 180

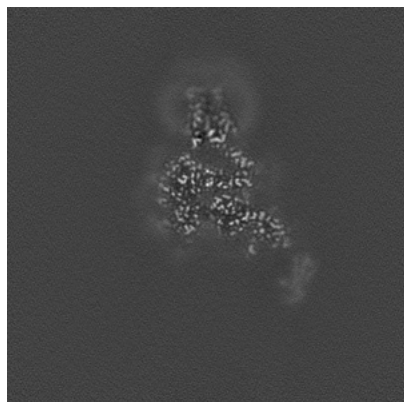


Y Index: 180

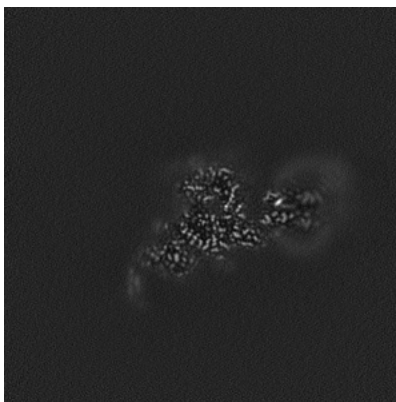


Z Index: 180

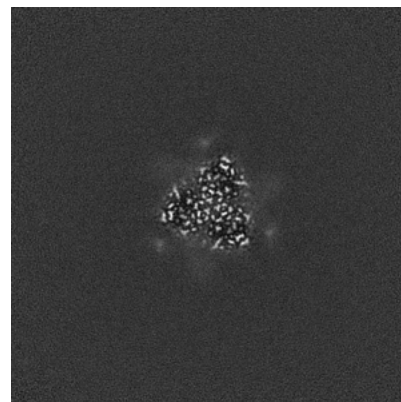
### 6.2.2 Raw map



X Index: 180



Y Index: 180



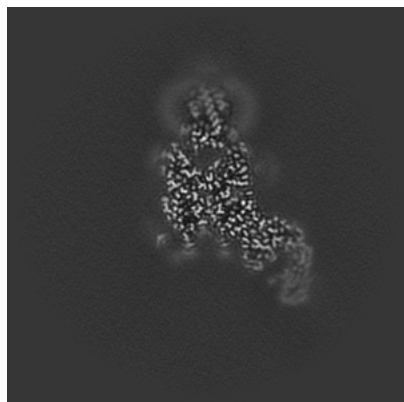
Z Index: 180

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

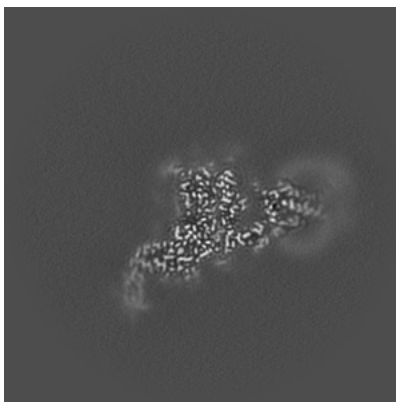


## 6.3 Largest variance slices [i](#)

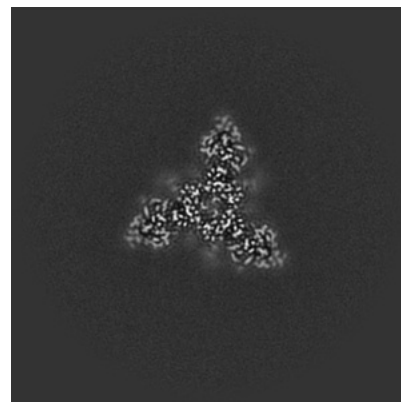
### 6.3.1 Primary map



X Index: 189

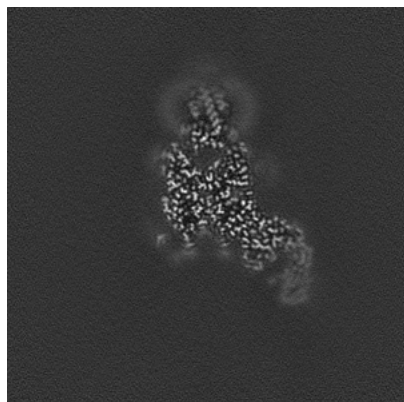


Y Index: 172

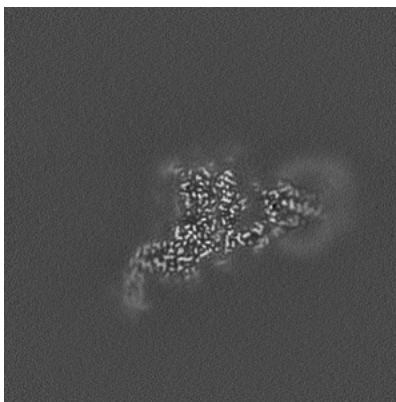


Z Index: 163

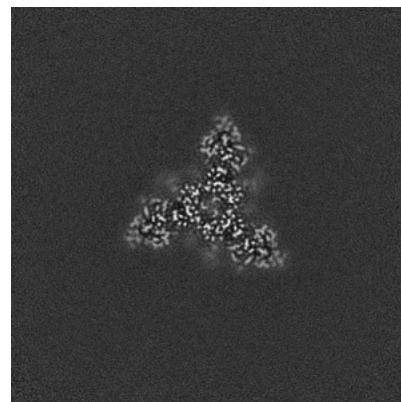
### 6.3.2 Raw map



X Index: 189



Y Index: 172

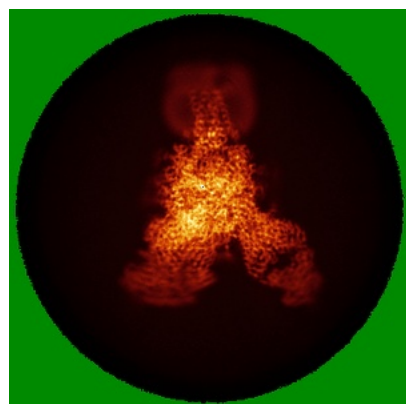


Z Index: 163

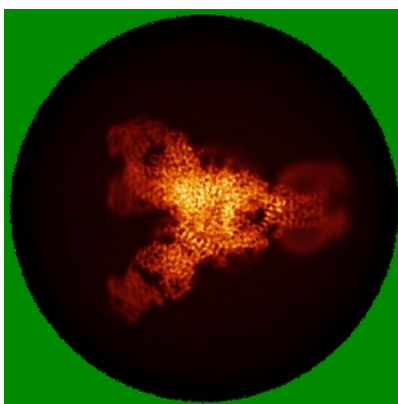
The images above show the largest variance slices of the map in three orthogonal directions.

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

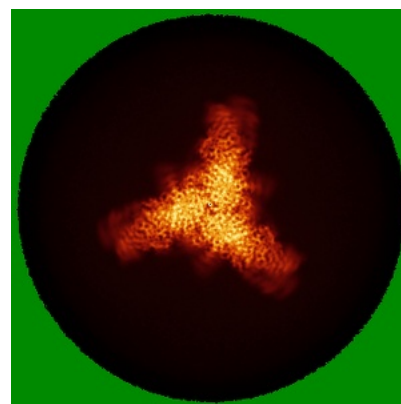
### 6.4.1 Primary map



X

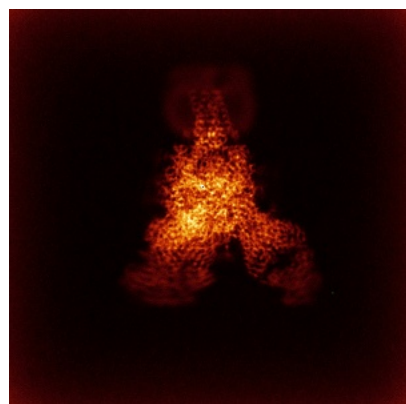


Y

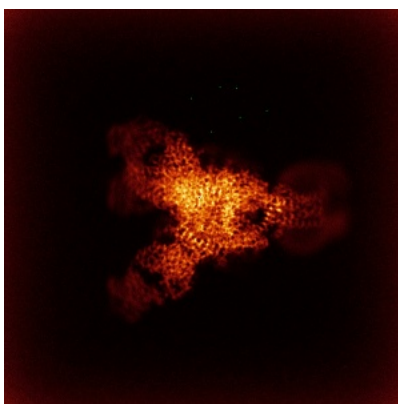


Z

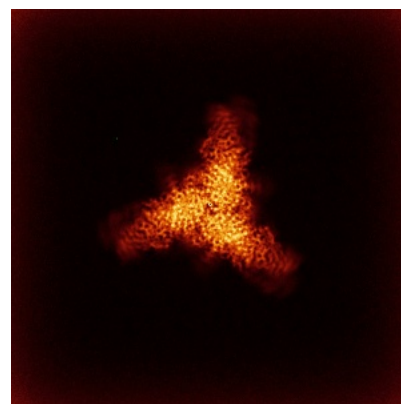
### 6.4.2 Raw map



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.

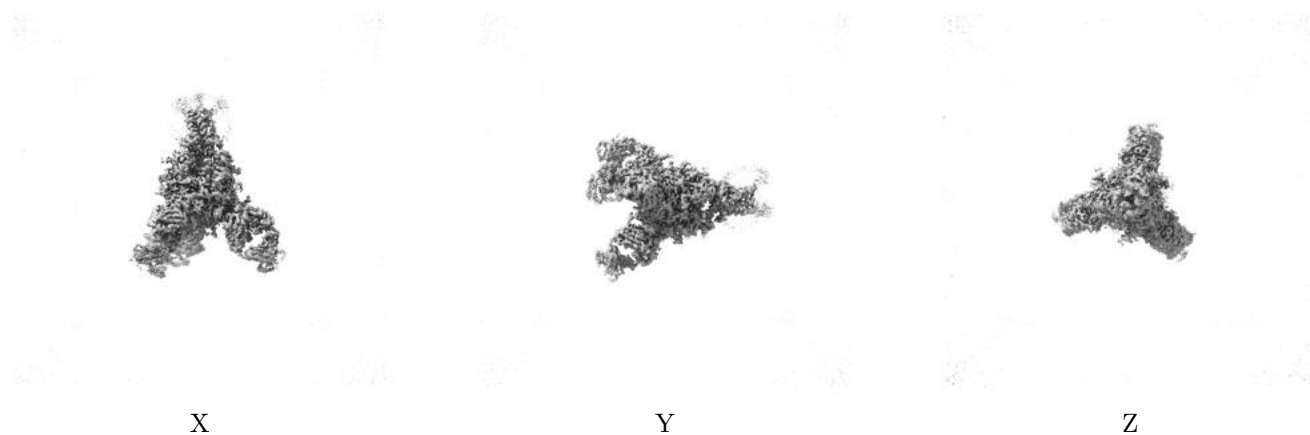
## 6.5 Orthogonal surface views [i](#)

### 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.

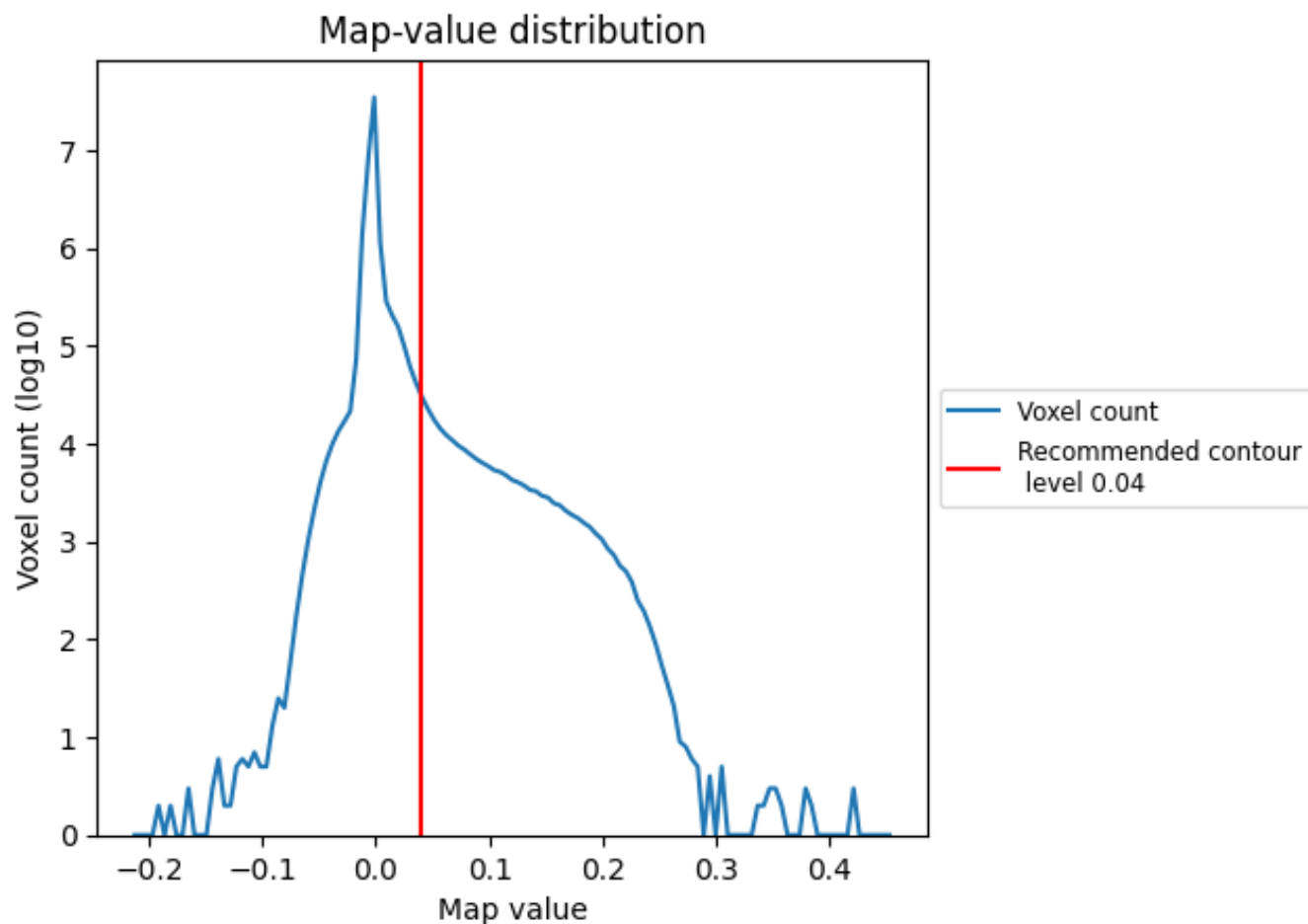
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

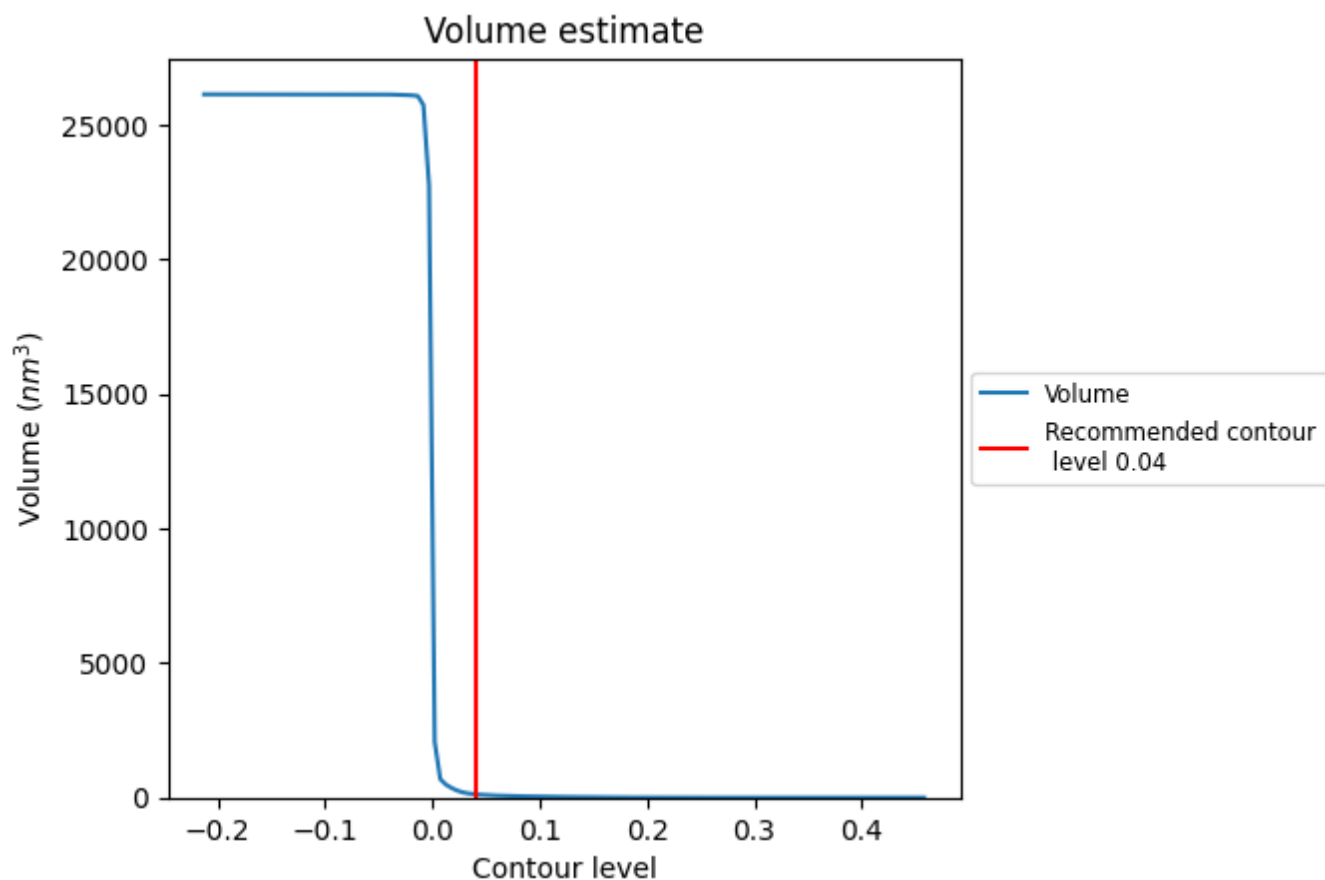
This section contains the results of statistical analysis of the map.

### 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.

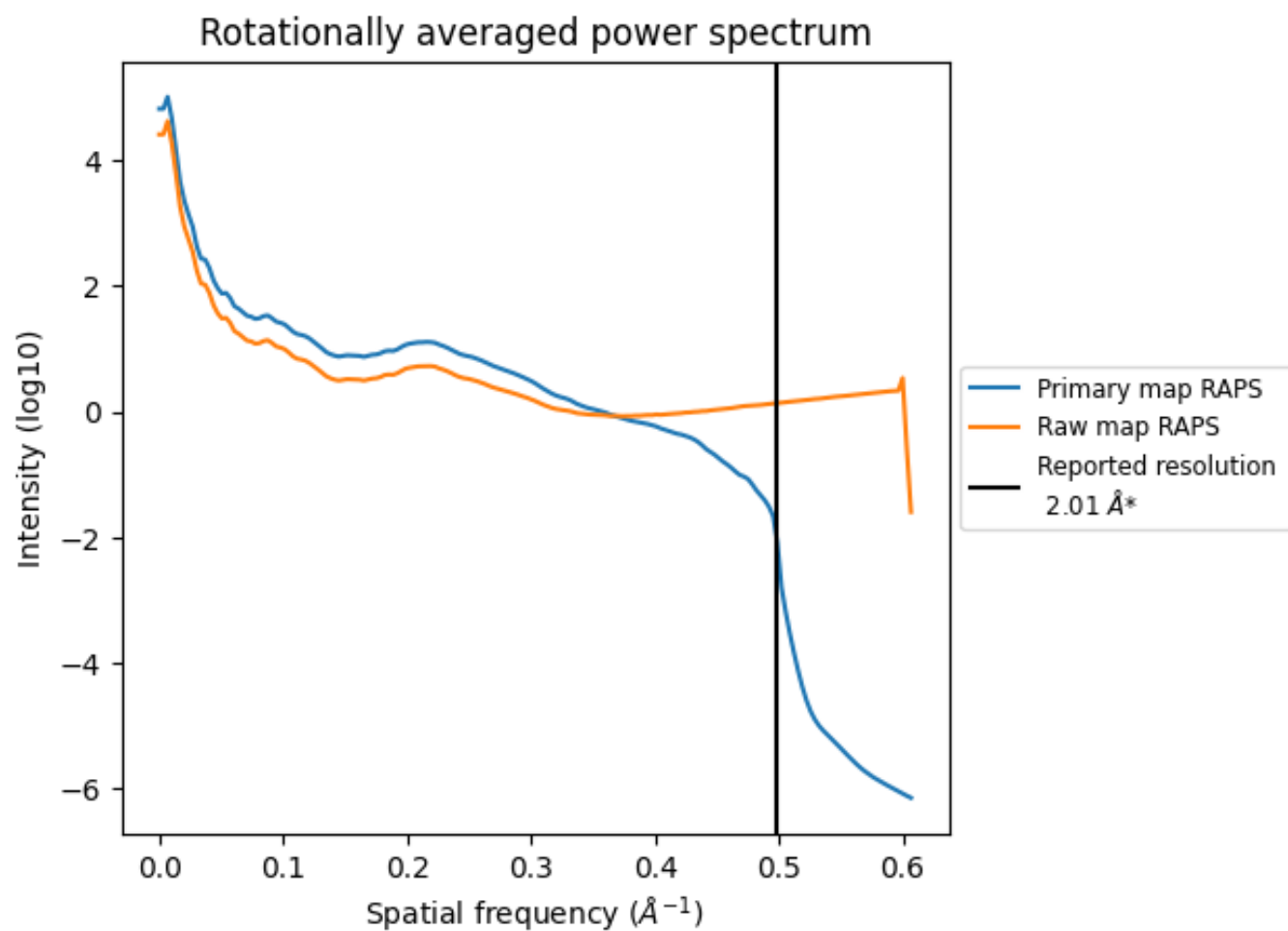
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123  $\text{nm}^3$ ; this corresponds to an approximate mass of 111 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 ⓘ

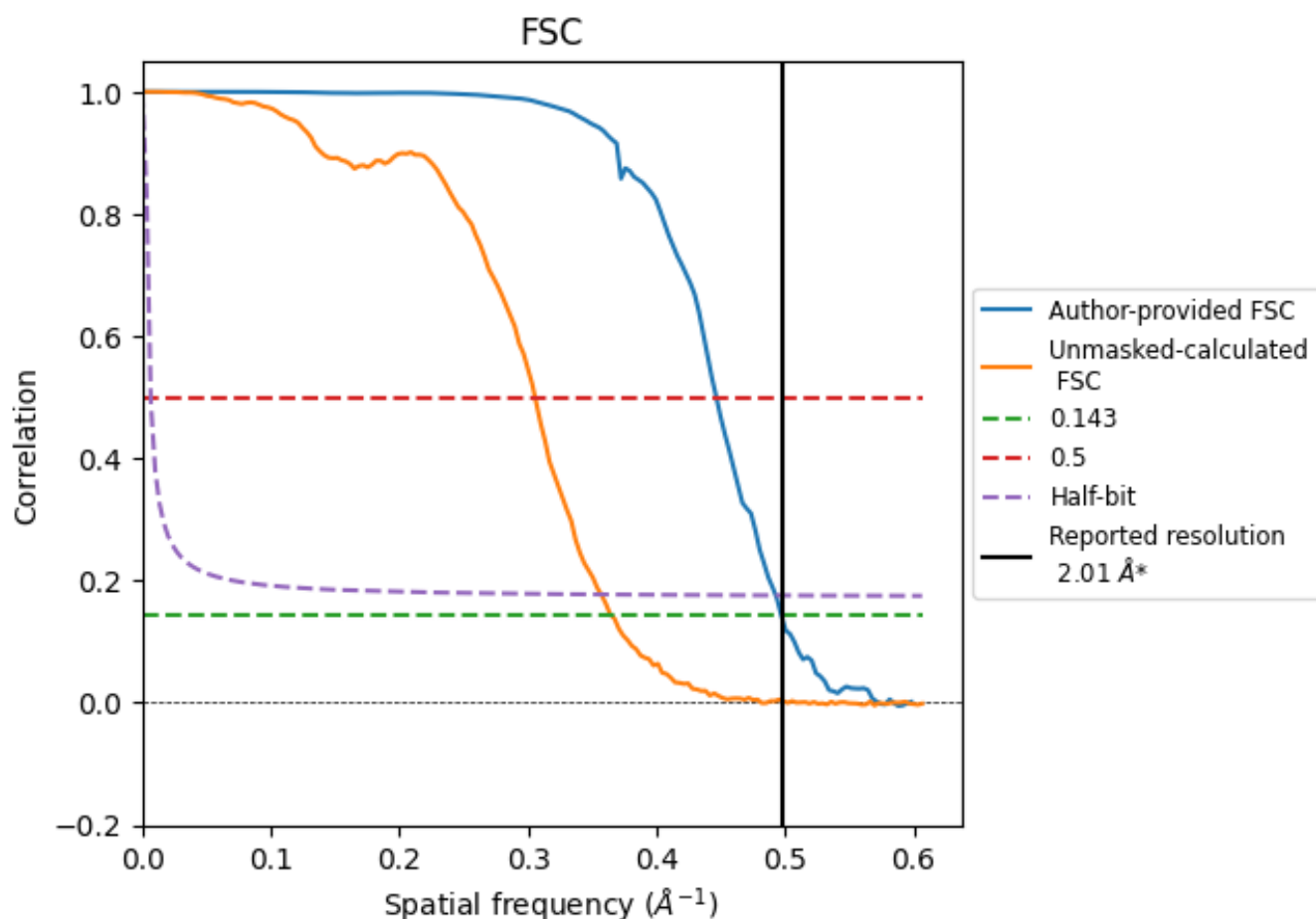


\*Reported resolution corresponds to spatial frequency of 0.498 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.498  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.01	-	-
Author-provided FSC curve	2.01	2.24	2.03
Unmasked-calculated*	2.74	3.27	2.80

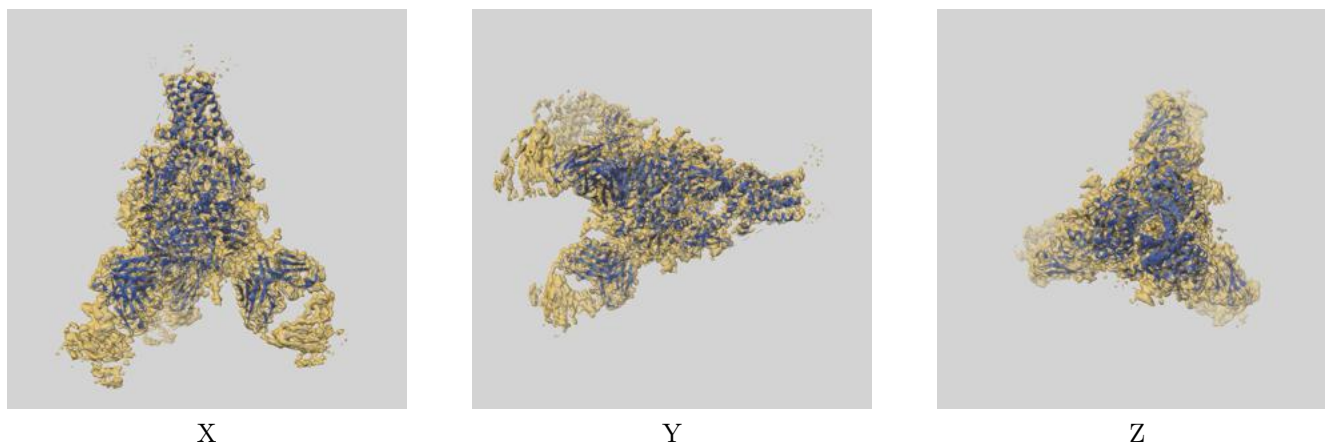
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.74 differs from the reported value 2.01 by more than 10 %



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

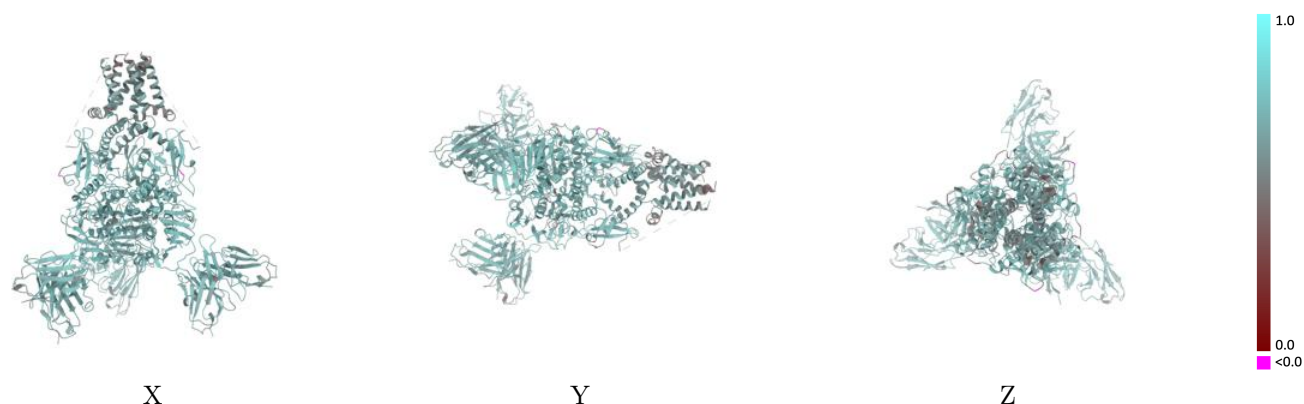
This section contains information regarding the fit between EMDB map EMD-48275 and PDB model 9MHE. Per-residue inclusion information can be found in section [3](#) on page [11](#).

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



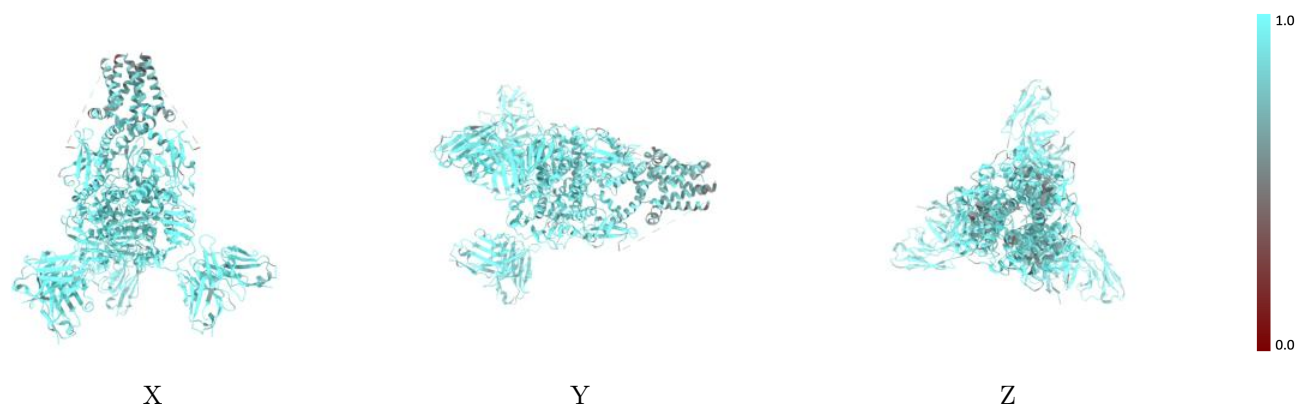
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



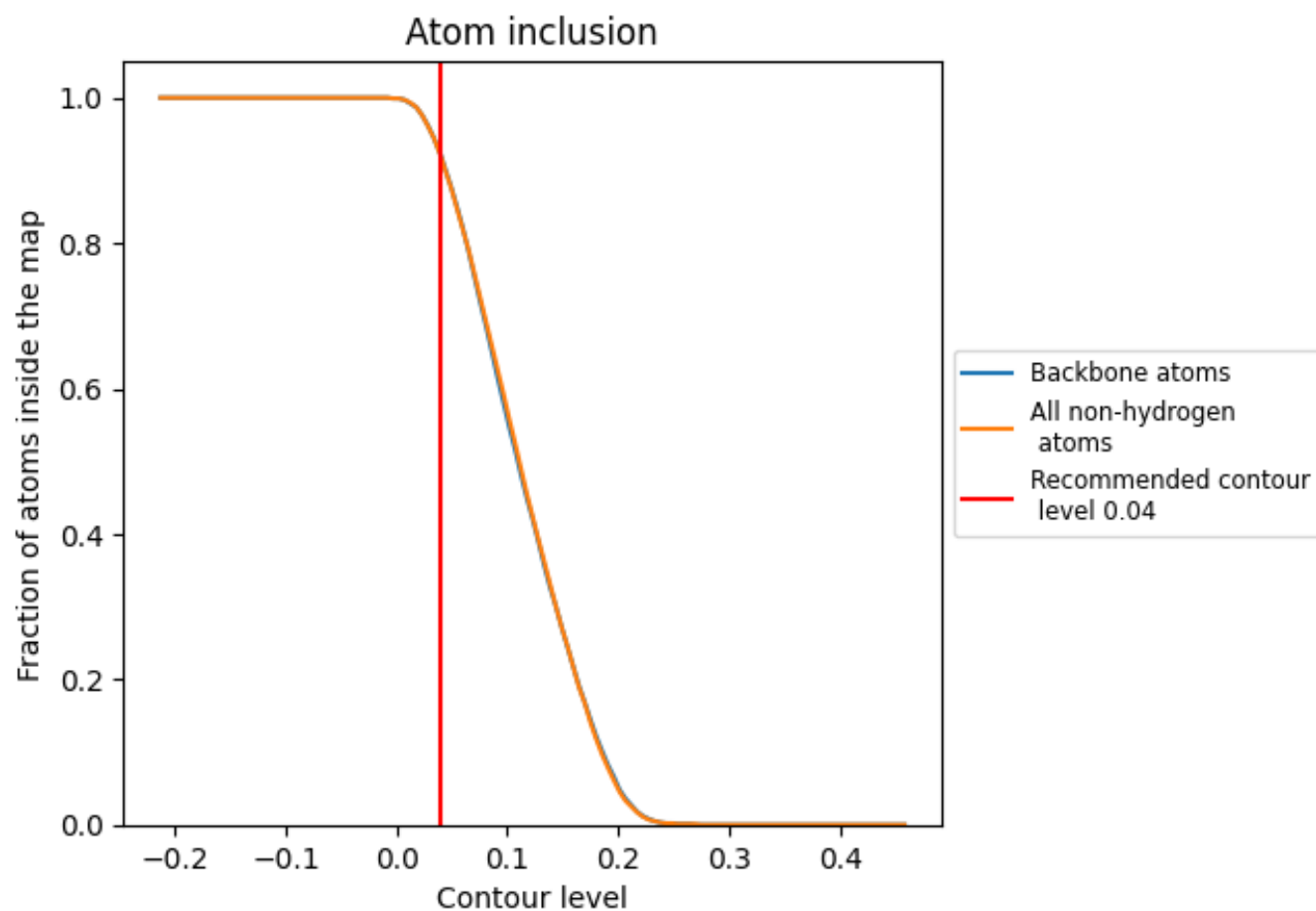
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 92% of all backbone atoms, 92% 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	 0.9200	 0.6470
A	 0.9190	 0.6560
B	 0.9220	 0.6610
C	 0.9230	 0.6610
D	 0.9230	 0.6500
E	 0.9220	 0.6270
F	 0.9220	 0.6460
G	 0.9290	 0.6330
H	 0.9180	 0.6420
I	 0.9200	 0.6040
J	 0.9290	 0.6060
K	 0.9490	 0.6010
L	 0.9260	 0.6250
M	 0.9180	 0.5930
N	 0.9230	 0.6110
O	 0.9650	 0.6240
P	 0.9170	 0.5980
Q	 0.8930	 0.5570
R	 0.8600	 0.5630
S	 0.9180	 0.5800
T	 0.9490	 0.5990
U	 0.9650	 0.6370
V	 0.9330	 0.5960
W	 0.8400	 0.5680
X	 0.9390	 0.5920
Y	 0.9490	 0.5940
Z	 0.9300	 0.6250
a	 0.9210	 0.6560
b	 0.9150	 0.6540
c	 0.9170	 0.6510
d	 0.9670	 0.6110
e	 1.0000	 0.6550
f	 0.8930	 0.6000

