



wwPDB EM Validation Summary Report ⓘ

Apr 7, 2025 – 04:53 PM EDT

PDB ID : 8ULR / pdb_00008ulr
EMDB ID : EMD-42363
Title : Cryo-EM structure of the BG505 SOSIPv2 in complex with bNAb 05_B08 Fabs
Authors : DeLaitch, A.T.; Bjorkman, P.J.
Deposited on : 2023-10-16
Resolution : 3.30 Å (reported)
Based on initial models : 6UDJ, 8UKI

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

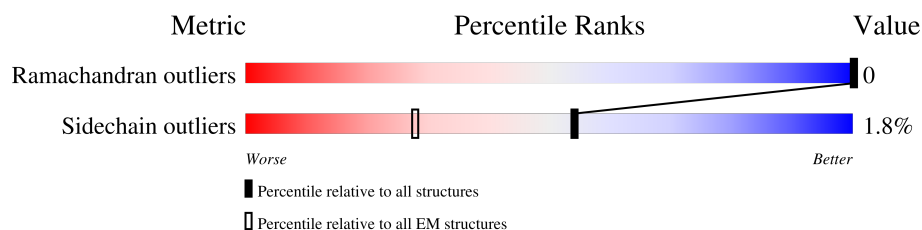
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

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 3.30 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)
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	A	479	 91% 8%
1	C	479	 90% 8%
1	E	479	 91% 8%
2	B	153	 23% 79% 20%
2	D	153	 24% 80% 20%
2	F	153	 24% 80% 20%
3	H	232	 50% 49%
3	I	232	 49% 49%
3	J	232	 50% 49%

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Mol	Chain	Length	Quality of chain
4	L	210	
4	M	210	
4	N	210	
5	G	2	
5	K	2	
5	R	2	
5	S	2	
5	U	2	
5	V	2	
5	W	2	
5	a	2	
5	b	2	
5	d	2	
5	e	2	
5	g	2	
5	k	2	
5	l	2	
5	n	2	
6	O	3	
6	X	3	
6	f	3	
7	P	4	
7	Y	4	
7	h	4	
7	i	4	

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Mol	Chain	Length	Quality of chain
8	Q	6	<div><div>33%</div><div>50%</div><div>50%</div></div>
8	Z	6	<div><div>50%</div><div>50%</div><div>50%</div></div>
9	T	5	<div><div>40%</div><div>60%</div><div>40%</div></div>
9	c	5	<div><div>40%</div><div>60%</div><div>40%</div></div>
9	m	5	<div><div>40%</div><div>60%</div><div>40%</div></div>
10	j	5	<div><div>40%</div><div>60%</div><div>40%</div></div>

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 19837 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	440	Total	C	N	O	S	0	0
			3455	2171	614	642	28		
1	C	440	Total	C	N	O	S	0	0
			3455	2171	614	642	28		
1	E	440	Total	C	N	O	S	0	0
			3455	2171	614	642	28		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	332	ASN	THR	conflict	UNP Q2N0S6
A	501	CYS	ALA	conflict	UNP Q2N0S6
A	505	VAL	-	expression tag	UNP Q2N0S6
A	506	VAL	-	expression tag	UNP Q2N0S6
A	507	GLY	-	expression tag	UNP Q2N0S6
A	508	ARG	-	expression tag	UNP Q2N0S6
A	509	ARG	-	expression tag	UNP Q2N0S6
A	510	ARG	-	expression tag	UNP Q2N0S6
A	511	ARG	-	expression tag	UNP Q2N0S6
A	512	ARG	-	expression tag	UNP Q2N0S6
A	513	ARG	-	expression tag	UNP Q2N0S6
C	332	ASN	THR	conflict	UNP Q2N0S6
C	501	CYS	ALA	conflict	UNP Q2N0S6
C	505	VAL	-	expression tag	UNP Q2N0S6
C	506	VAL	-	expression tag	UNP Q2N0S6
C	507	GLY	-	expression tag	UNP Q2N0S6
C	508	ARG	-	expression tag	UNP Q2N0S6
C	509	ARG	-	expression tag	UNP Q2N0S6
C	510	ARG	-	expression tag	UNP Q2N0S6
C	511	ARG	-	expression tag	UNP Q2N0S6
C	512	ARG	-	expression tag	UNP Q2N0S6
C	513	ARG	-	expression tag	UNP Q2N0S6
E	332	ASN	THR	conflict	UNP Q2N0S6
E	501	CYS	ALA	conflict	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	505	VAL	-	expression tag	UNP Q2N0S6
E	506	VAL	-	expression tag	UNP Q2N0S6
E	507	GLY	-	expression tag	UNP Q2N0S6
E	508	ARG	-	expression tag	UNP Q2N0S6
E	509	ARG	-	expression tag	UNP Q2N0S6
E	510	ARG	-	expression tag	UNP Q2N0S6
E	511	ARG	-	expression tag	UNP Q2N0S6
E	512	ARG	-	expression tag	UNP Q2N0S6
E	513	ARG	-	expression tag	UNP Q2N0S6

- Molecule 2 is a protein called BG505 DS-SOSIP glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	123	Total	C	N	O	S	0	0
			983	622	170	185	6		
2	D	123	Total	C	N	O	S	0	0
			983	622	170	185	6		
2	F	123	Total	C	N	O	S	0	0
			983	622	170	185	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S5
B	605	CYS	THR	engineered mutation	UNP Q2N0S5
D	559	PRO	ILE	engineered mutation	UNP Q2N0S5
D	605	CYS	THR	engineered mutation	UNP Q2N0S5
F	559	PRO	ILE	engineered mutation	UNP Q2N0S5
F	605	CYS	THR	engineered mutation	UNP Q2N0S5

- Molecule 3 is a protein called 05_B08 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	119	Total	C	N	O	S	0	0
			956	603	166	180	7		
3	I	119	Total	C	N	O	S	0	0
			956	603	166	180	7		
3	J	119	Total	C	N	O	S	0	0
			956	603	166	180	7		

- Molecule 4 is a protein called 05_B08 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	101	Total	C	N	O	S	0	0
			778	494	128	153	3		
4	M	101	Total	C	N	O	S	0	0
			778	494	128	153	3		
4	N	101	Total	C	N	O	S	0	0
			778	494	128	153	3		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



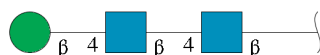
Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	2	Total	C	N	O	0	0
			28	16	2	10		
5	K	2	Total	C	N	O	0	0
			28	16	2	10		
5	R	2	Total	C	N	O	0	0
			28	16	2	10		
5	S	2	Total	C	N	O	0	0
			28	16	2	10		
5	U	2	Total	C	N	O	0	0
			28	16	2	10		
5	V	2	Total	C	N	O	0	0
			28	16	2	10		
5	W	2	Total	C	N	O	0	0
			28	16	2	10		
5	a	2	Total	C	N	O	0	0
			28	16	2	10		
5	b	2	Total	C	N	O	0	0
			28	16	2	10		
5	d	2	Total	C	N	O	0	0
			28	16	2	10		
5	e	2	Total	C	N	O	0	0
			28	16	2	10		
5	g	2	Total	C	N	O	0	0
			28	16	2	10		
5	k	2	Total	C	N	O	0	0
			28	16	2	10		
5	l	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	n	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 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.



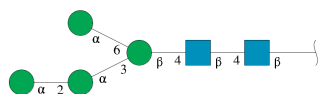
Mol	Chain	Residues	Atoms				AltConf	Trace
6	O	3	Total	C	N	O	0	0
			39	22	2	15		
6	X	3	Total	C	N	O	0	0
			39	22	2	15		
6	f	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 7 is an oligosaccharide called 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.



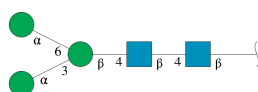
Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	4	Total	C	N	O	0	0
			50	28	2	20		
7	Y	4	Total	C	N	O	0	0
			50	28	2	20		
7	h	4	Total	C	N	O	0	0
			50	28	2	20		
7	i	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(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.



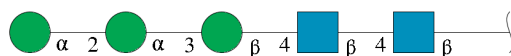
Mol	Chain	Residues	Atoms				AltConf	Trace
8	Q	6	Total	C	N	O	0	0
			72	40	2	30		
8	Z	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 9 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
9	T	5	Total	C	N	O	0	0
			61	34	2	25		
9	c	5	Total	C	N	O	0	0
			61	34	2	25		
9	m	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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
10	j	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

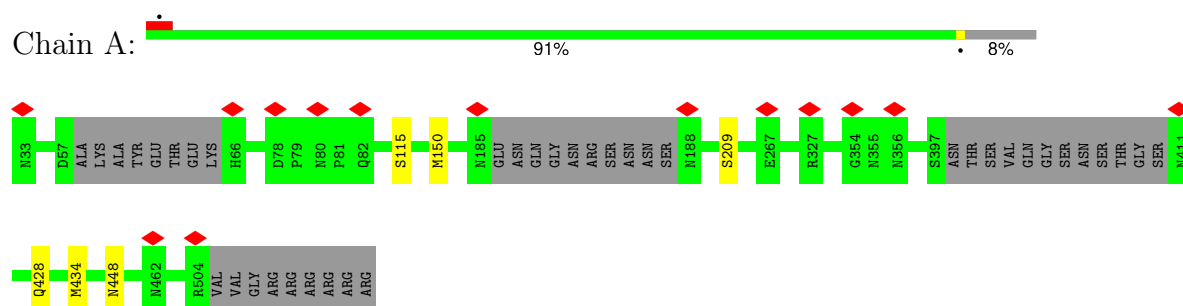


Mol	Chain	Residues	Atoms				AltConf
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	C	1	Total	C	N	O	0
			14	8	1	5	
11	C	1	Total	C	N	O	0
			14	8	1	5	
11	C	1	Total	C	N	O	0
			14	8	1	5	
11	C	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	

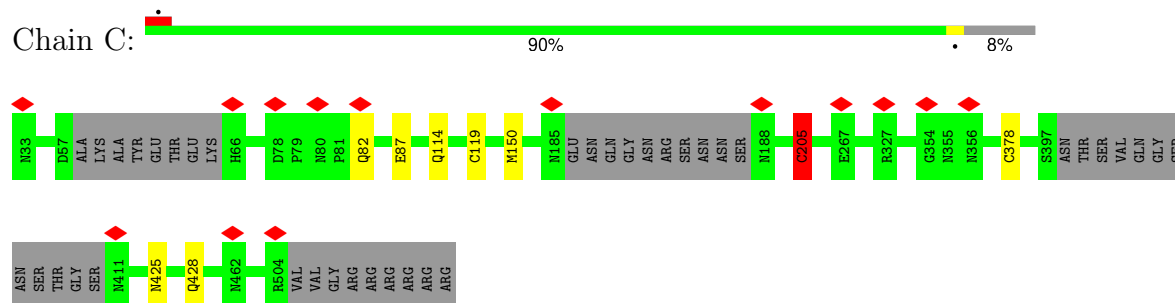
3 Residue-property plots [i](#)

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.

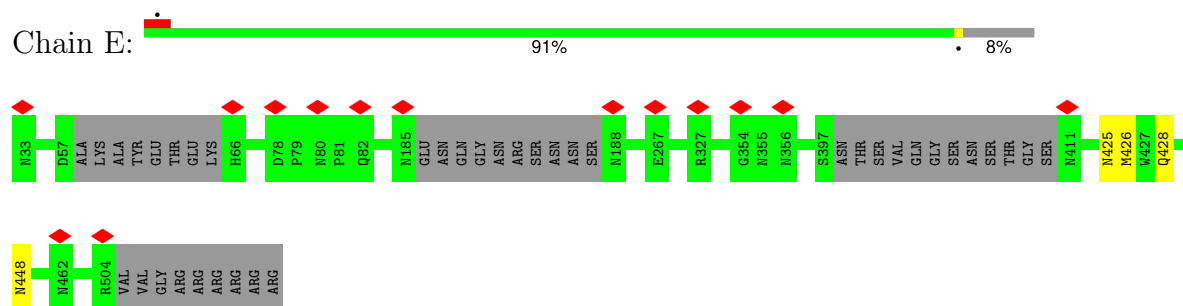
- Molecule 1: Envelope glycoprotein gp160



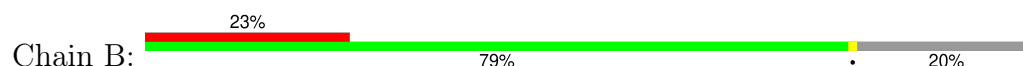
- Molecule 1: Envelope glycoprotein gp160

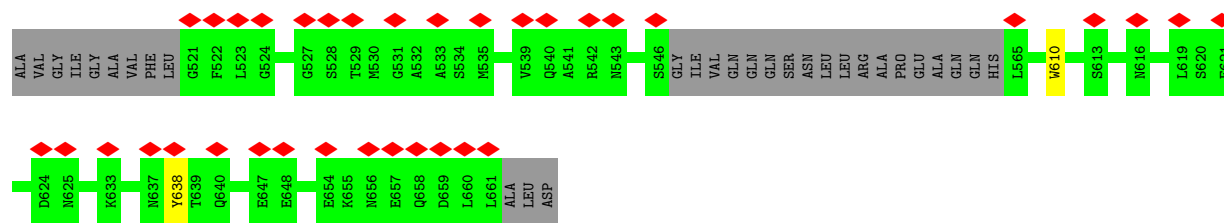


- Molecule 1: Envelope glycoprotein gp160

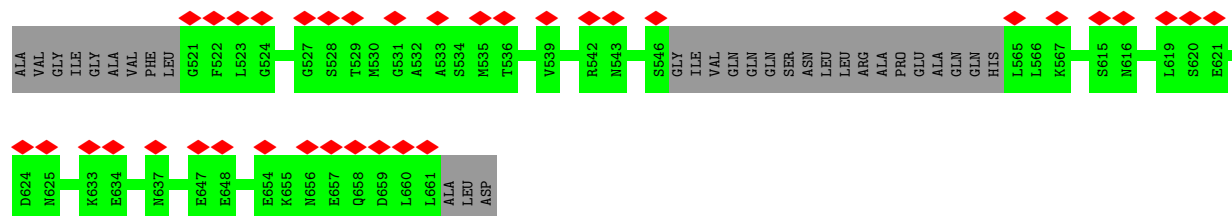
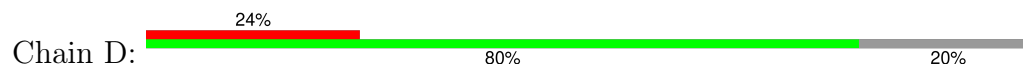


- Molecule 2: BG505 DS-SOSIP glycoprotein gp41

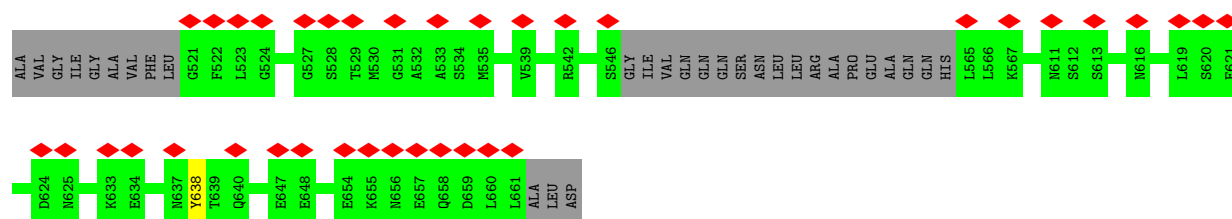
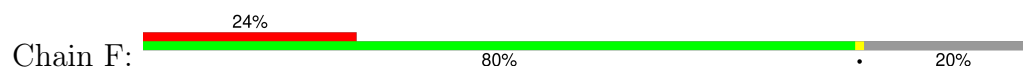




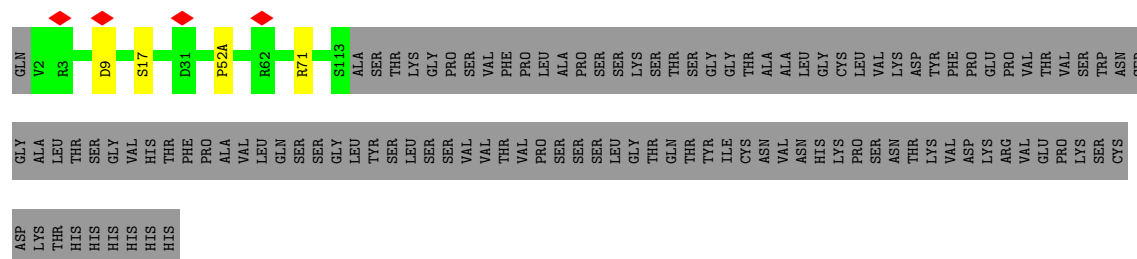
- Molecule 2: BG505 DS-SOSIP glycoprotein gp41



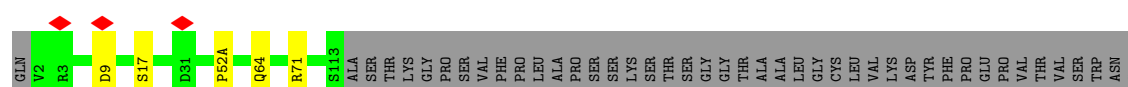
- Molecule 2: BG505 DS-SOSIP glycoprotein gp41



- Molecule 3: 05_B08 Fab Heavy Chain



- Molecule 3: 05_B08 Fab Heavy Chain



ASP	GLY
LYS	LEU
THR	ALA
HIS	THR
HIS	SER
HIS	GLY
HIS	VAL
HIS	HIS
HIS	THR
HIS	PHE
	PRO
	ALA
	VAL
	LEU
	GLN
	SER
	SER
	GLY
	LEU
	THR
	THR
	VAL
	VAL
	PRO
	SER
	SER
	SER
	LEU
	GLY
	THR
	GLN
	THR
	TYR
	ILE
	ILE
	CYS
	ASN
	VAL
	ASN
	HIS
	LYS
	PRO
	SER
	ASN
	THR
	LYS
	VAL
	ASP
	LYS
	ARG
	VAL
	GLU
	PRO
	LYS
	SER
	CYS

- Molecule 3: 05 B08 Fab Heavy Chain

Chain J: 50% 49%

THR	THR	LEU
HIS	GLN	THR
HIS	V2	THR
HIS	R3	GLY
HIS	L4	VAL
HIS	M5	HIS
HIS	S17	THR
HIS	D31	PHE
	R71	PRO
	M95	ALA
	S113	VAL
	ALA	LEU
	THR	TVR
	THR	SER
	LYS	SER
	GLY	LEU
	PRO	SER
	PHE	VAL
	SER	VAL
	VAL	THR
	THR	VAL
	PRO	PRO
	ALA	SER
	PRO	SER
	SER	SER
	SER	LEU
	LYS	GLY
	SER	THR
	THR	GLN
	SER	THR
	GLY	TYR
	GLY	ILE
	THR	CYS
	ALA	ASN
	ALA	VAL
	LEU	ASN
	GLY	HIS
	CYS	LYS
	LEU	PRO
	VAL	SER
	VAL	ASN
	ASP	THR
	LYS	LYS
	THR	VAL
	ASP	ASP
	LYS	LYS
	ARG	VAL
	VAL	VAL
	GLU	GLU
	PRO	PRO
	LYS	LYS
	SER	SER
	CYS	CYS
	ASP	ASP
	LYS	LYS

- Molecule 4: 05 B08 Light Chain

Chain L: 

[illegible]

- Molecule 4: 05 B08 Light Chain

Chain M: 

THR	ASN	ASP
HIS	ASN	SER
GLN	PHE	P3
LEU	TYR	
GLY	PRO	S10
SER	ARG	L11
SER	GLU	S12
PRO	ALA	I13
PRO	VAL	
THR	VAL	G16
LYS	GLN	
SER	TRP	T20
PHE	LYS	
ASN	VAL	
ARG	ASP	G57
GLY	ASN	V58
GLU	ALA	P59
GLY	LEU	S60
CYS	GLN	R61
	SER	
	GLY	
	ASN	I75
	SER	
	GLN	P80
	GLU	E81
	SER	D82
	VAL	V83
	THR	
	GLU	
	GLN	R103
	ASP	L104
	SER	E105
	LYS	I106
	ASP	I107
	SER	
	THR	ARG
	THR	THR
	TYR	VAL
	SER	LYS
	LEU	ALA
	SER	ALA
	SER	PRO
	THR	VAL
	LEU	PHE
	THR	ILE
	LEU	PHE
	SER	PRO
	LYS	PRO
	SER	SER
	ASP	ASP
	TYR	GLU
	GLU	GLN
	LYS	LEU
	HIS	LYS
	LYS	LYS
	VAL	GLY
	TYR	THR
	ALA	ALA
	CYS	SER
	GLU	VAL
	VAL	VAL
		CYS
		LEU
		THR

- Molecule 4: 05 B08 Light Chain

Chain N:  6% 48% 52%

[illegible]



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



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



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



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



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



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



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



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



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



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



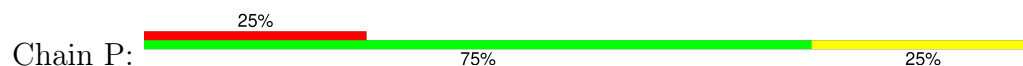
- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



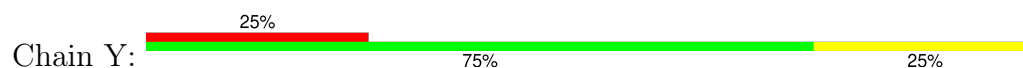
- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



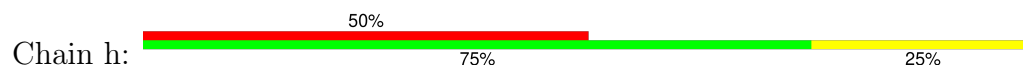
- Molecule 7: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



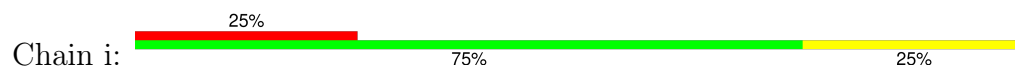
- Molecule 7: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 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



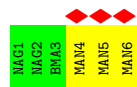
- Molecule 7: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



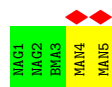
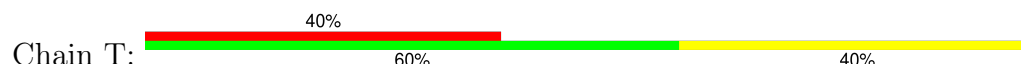
- Molecule 8: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



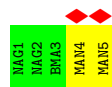
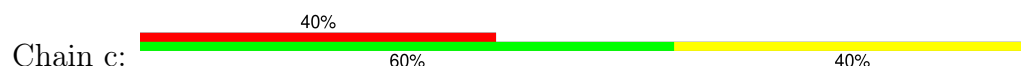
- Molecule 8: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



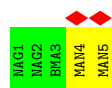
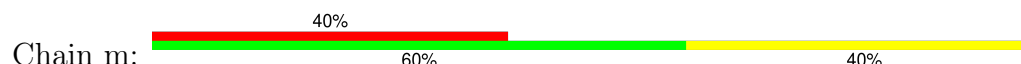
- Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



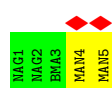
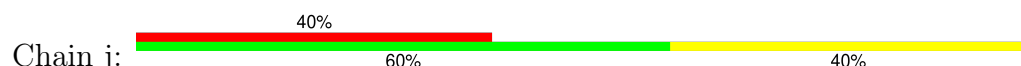
- Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 9: 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



- Molecule 10: alpha-D-mannopyranose-(1-2)-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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	129686	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.897	Depositor
Minimum map value	-0.505	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	326.144, 326.144, 326.144	wwPDB
Map dimensions	392, 392, 392	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	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, MAN

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	0.28	0/3527	0.50	0/4789
1	C	0.28	0/3527	0.50	1/4789 (0.0%)
1	E	0.28	0/3527	0.50	0/4789
2	B	0.24	0/1000	0.45	0/1355
2	D	0.24	0/1000	0.44	0/1355
2	F	0.24	0/1000	0.46	0/1355
3	H	0.28	0/978	0.57	0/1319
3	I	0.28	0/978	0.56	0/1319
3	J	0.27	0/978	0.56	0/1319
4	L	0.28	0/799	0.50	0/1086
4	M	0.31	0/799	0.56	2/1086 (0.2%)
4	N	0.28	0/799	0.52	0/1086
All	All	0.27	0/18912	0.51	3/25647 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	59	PRO	CA-N-CD	-5.85	103.31	111.50
1	C	205	CYS	CA-CB-SG	5.31	123.56	114.00
4	M	59	PRO	N-CD-CG	-5.25	95.32	103.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	119	CYS	Peptide
1	C	205	CYS	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	432/479 (90%)	417 (96%)	15 (4%)	0	100	100
1	C	432/479 (90%)	416 (96%)	16 (4%)	0	100	100
1	E	432/479 (90%)	418 (97%)	14 (3%)	0	100	100
2	B	119/153 (78%)	113 (95%)	6 (5%)	0	100	100
2	D	119/153 (78%)	111 (93%)	8 (7%)	0	100	100
2	F	119/153 (78%)	114 (96%)	5 (4%)	0	100	100
3	H	117/232 (50%)	109 (93%)	8 (7%)	0	100	100
3	I	117/232 (50%)	109 (93%)	8 (7%)	0	100	100
3	J	117/232 (50%)	109 (93%)	8 (7%)	0	100	100
4	L	99/210 (47%)	91 (92%)	8 (8%)	0	100	100
4	M	99/210 (47%)	90 (91%)	9 (9%)	0	100	100
4	N	99/210 (47%)	90 (91%)	9 (9%)	0	100	100
All	All	2301/3222 (71%)	2187 (95%)	114 (5%)	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	391/427 (92%)	385 (98%)	6 (2%)	60	77
1	C	391/427 (92%)	383 (98%)	8 (2%)	50	71
1	E	391/427 (92%)	387 (99%)	4 (1%)	73	84
2	B	107/129 (83%)	105 (98%)	2 (2%)	52	72
2	D	107/129 (83%)	107 (100%)	0	100	100
2	F	107/129 (83%)	106 (99%)	1 (1%)	75	85
3	H	103/203 (51%)	99 (96%)	4 (4%)	27	55
3	I	103/203 (51%)	98 (95%)	5 (5%)	21	49
3	J	103/203 (51%)	99 (96%)	4 (4%)	27	55
4	L	85/186 (46%)	84 (99%)	1 (1%)	67	80
4	M	85/186 (46%)	84 (99%)	1 (1%)	67	80
4	N	85/186 (46%)	84 (99%)	1 (1%)	67	80
All	All	2058/2835 (73%)	2021 (98%)	37 (2%)	54	74

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	64	GLN
4	M	61	ARG
3	I	71	ARG
3	J	71	ARG
1	C	205	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	577	GLN
3	I	89	GLN
3	J	6	GLN
2	B	630	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	577	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 ⓘ

87 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	G	1	1,5	14,14,15	0.34	0	17,19,21	0.47	0
5	NAG	G	2	5	14,14,15	0.29	0	17,19,21	0.50	0
5	NAG	K	1	1,5	14,14,15	0.27	0	17,19,21	0.49	0
5	NAG	K	2	5	14,14,15	0.26	0	17,19,21	0.42	0
6	NAG	O	1	6,1	14,14,15	0.23	0	17,19,21	0.51	0
6	NAG	O	2	6	14,14,15	0.21	0	17,19,21	0.40	0
6	BMA	O	3	6	11,11,12	0.54	0	15,15,17	0.77	0
7	NAG	P	1	7,1	14,14,15	0.20	0	17,19,21	0.42	0
7	NAG	P	2	7	14,14,15	0.18	0	17,19,21	0.42	0
7	BMA	P	3	7	11,11,12	0.56	0	15,15,17	0.80	0
7	MAN	P	4	7	11,11,12	0.63	0	15,15,17	0.99	2 (13%)
8	NAG	Q	1	8,1	14,14,15	0.26	0	17,19,21	0.49	0
8	NAG	Q	2	8	14,14,15	0.19	0	17,19,21	0.40	0
8	BMA	Q	3	8	11,11,12	0.59	0	15,15,17	0.86	0
8	MAN	Q	4	8	11,11,12	0.62	0	15,15,17	1.06	1 (6%)
8	MAN	Q	5	8	11,11,12	0.75	1 (9%)	15,15,17	1.36	2 (13%)
8	MAN	Q	6	8	11,11,12	0.62	0	15,15,17	1.01	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	R	1	1,5	14,14,15	0.66	1 (7%)	17,19,21	0.57	0
5	NAG	R	2	5	14,14,15	0.79	1 (7%)	17,19,21	1.50	2 (11%)
5	NAG	S	1	1,5	14,14,15	0.32	0	17,19,21	0.64	0
5	NAG	S	2	5	14,14,15	0.32	0	17,19,21	0.56	0
9	NAG	T	1	1,9	14,14,15	0.22	0	17,19,21	0.41	0
9	NAG	T	2	9	14,14,15	0.19	0	17,19,21	0.46	0
9	BMA	T	3	9	11,11,12	0.56	0	15,15,17	0.72	0
9	MAN	T	4	9	11,11,12	0.65	0	15,15,17	0.87	1 (6%)
9	MAN	T	5	9	11,11,12	0.57	0	15,15,17	0.96	2 (13%)
5	NAG	U	1	1,5	14,14,15	0.23	0	17,19,21	0.56	0
5	NAG	U	2	5	14,14,15	0.28	0	17,19,21	0.45	0
5	NAG	V	1	1,5	14,14,15	0.34	0	17,19,21	0.50	0
5	NAG	V	2	5	14,14,15	0.29	0	17,19,21	0.50	0
5	NAG	W	1	1,5	14,14,15	0.28	0	17,19,21	0.49	0
5	NAG	W	2	5	14,14,15	0.24	0	17,19,21	0.42	0
6	NAG	X	1	6,1	14,14,15	0.21	0	17,19,21	0.50	0
6	NAG	X	2	6	14,14,15	0.21	0	17,19,21	0.40	0
6	BMA	X	3	6	11,11,12	0.55	0	15,15,17	0.73	0
7	NAG	Y	1	7,1	14,14,15	0.20	0	17,19,21	0.42	0
7	NAG	Y	2	7	14,14,15	0.18	0	17,19,21	0.42	0
7	BMA	Y	3	7	11,11,12	0.56	0	15,15,17	0.79	0
7	MAN	Y	4	7	11,11,12	0.64	0	15,15,17	0.99	2 (13%)
8	NAG	Z	1	8,1	14,14,15	0.27	0	17,19,21	0.49	0
8	NAG	Z	2	8	14,14,15	0.19	0	17,19,21	0.40	0
8	BMA	Z	3	8	11,11,12	0.60	0	15,15,17	0.87	0
8	MAN	Z	4	8	11,11,12	0.63	0	15,15,17	1.08	1 (6%)
8	MAN	Z	5	8	11,11,12	0.76	1 (9%)	15,15,17	1.38	2 (13%)
8	MAN	Z	6	8	11,11,12	0.63	0	15,15,17	1.01	2 (13%)
5	NAG	a	1	1,5	14,14,15	0.34	0	17,19,21	0.45	0
5	NAG	a	2	5	14,14,15	0.25	0	17,19,21	0.38	0
5	NAG	b	1	1,5	14,14,15	0.22	0	17,19,21	0.58	0
5	NAG	b	2	5	14,14,15	0.21	0	17,19,21	0.48	0
9	NAG	c	1	1,9	14,14,15	0.18	0	17,19,21	0.42	0
9	NAG	c	2	9	14,14,15	0.18	0	17,19,21	0.47	0
9	BMA	c	3	9	11,11,12	0.53	0	15,15,17	0.77	0
9	MAN	c	4	9	11,11,12	0.61	0	15,15,17	0.89	1 (6%)
9	MAN	c	5	9	11,11,12	0.58	0	15,15,17	0.96	2 (13%)
5	NAG	d	1	1,5	14,14,15	0.26	0	17,19,21	0.57	0
5	NAG	d	2	5	14,14,15	0.27	0	17,19,21	0.45	0
5	NAG	e	1	1,5	14,14,15	0.29	0	17,19,21	0.58	0
5	NAG	e	2	5	14,14,15	0.27	0	17,19,21	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	f	1	6,1	14,14,15	0.29	0	17,19,21	0.45	0
6	NAG	f	2	6	14,14,15	0.26	0	17,19,21	0.50	0
6	BMA	f	3	6	11,11,12	0.58	0	15,15,17	0.75	0
5	NAG	g	1	1,5	14,14,15	0.30	0	17,19,21	0.48	0
5	NAG	g	2	5	14,14,15	0.22	0	17,19,21	0.40	0
7	NAG	h	1	7,1	14,14,15	0.22	0	17,19,21	0.50	0
7	NAG	h	2	7	14,14,15	0.22	0	17,19,21	0.40	0
7	BMA	h	3	7	11,11,12	0.55	0	15,15,17	0.75	0
7	MAN	h	4	7	11,11,12	0.64	0	15,15,17	0.98	2 (13%)
7	NAG	i	1	7,1	14,14,15	0.21	0	17,19,21	0.43	0
7	NAG	i	2	7	14,14,15	0.19	0	17,19,21	0.42	0
7	BMA	i	3	7	11,11,12	0.54	0	15,15,17	0.80	0
7	MAN	i	4	7	11,11,12	0.67	0	15,15,17	1.00	2 (13%)
10	NAG	j	1	10,1	14,14,15	0.26	0	17,19,21	0.49	0
10	NAG	j	2	10	14,14,15	0.20	0	17,19,21	0.40	0
10	BMA	j	3	10	11,11,12	0.55	0	15,15,17	0.83	0
10	MAN	j	4	10	11,11,12	0.61	0	15,15,17	1.01	2 (13%)
10	MAN	j	5	10	11,11,12	0.70	0	15,15,17	0.89	1 (6%)
5	NAG	k	1	1,5	14,14,15	0.33	0	17,19,21	0.67	1 (5%)
5	NAG	k	2	5	14,14,15	0.32	0	17,19,21	0.39	0
5	NAG	l	1	1,5	14,14,15	0.21	0	17,19,21	0.56	0
5	NAG	l	2	5	14,14,15	0.20	0	17,19,21	0.47	0
9	NAG	m	1	1,9	14,14,15	0.19	0	17,19,21	0.41	0
9	NAG	m	2	9	14,14,15	0.19	0	17,19,21	0.46	0
9	BMA	m	3	9	11,11,12	0.56	0	15,15,17	0.71	0
9	MAN	m	4	9	11,11,12	0.62	0	15,15,17	0.89	1 (6%)
9	MAN	m	5	9	11,11,12	0.61	0	15,15,17	1.03	2 (13%)
5	NAG	n	1	1,5	14,14,15	0.27	0	17,19,21	0.56	0
5	NAG	n	2	5	14,14,15	0.26	0	17,19,21	0.45	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
5	NAG	G	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	G	2	5	-	3/6/23/26	0/1/1/1
5	NAG	K	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	K	2	5	-	0/6/23/26	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	MAN	Z	4	8	-	0/2/19/22	0/1/1/1
8	MAN	Z	5	8	-	0/2/19/22	0/1/1/1
8	MAN	Z	6	8	-	0/2/19/22	0/1/1/1
5	NAG	a	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	a	2	5	-	0/6/23/26	0/1/1/1
5	NAG	b	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	b	2	5	-	0/6/23/26	0/1/1/1
9	NAG	c	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	c	2	9	-	1/6/23/26	0/1/1/1
9	BMA	c	3	9	-	2/2/19/22	0/1/1/1
9	MAN	c	4	9	-	1/2/19/22	0/1/1/1
9	MAN	c	5	9	-	0/2/19/22	0/1/1/1
5	NAG	d	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	d	2	5	-	2/6/23/26	0/1/1/1
5	NAG	e	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	e	2	5	-	2/6/23/26	0/1/1/1
6	NAG	f	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	f	2	6	-	3/6/23/26	0/1/1/1
6	BMA	f	3	6	-	1/2/19/22	0/1/1/1
5	NAG	g	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	g	2	5	-	0/6/23/26	0/1/1/1
7	NAG	h	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	h	2	7	-	0/6/23/26	0/1/1/1
7	BMA	h	3	7	-	0/2/19/22	0/1/1/1
7	MAN	h	4	7	-	1/2/19/22	0/1/1/1
7	NAG	i	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	i	2	7	-	2/6/23/26	0/1/1/1
7	BMA	i	3	7	-	0/2/19/22	0/1/1/1
7	MAN	i	4	7	-	1/2/19/22	0/1/1/1
10	NAG	j	1	10,1	-	4/6/23/26	0/1/1/1
10	NAG	j	2	10	-	1/6/23/26	0/1/1/1
10	BMA	j	3	10	-	2/2/19/22	0/1/1/1
10	MAN	j	4	10	-	0/2/19/22	0/1/1/1
10	MAN	j	5	10	-	1/2/19/22	0/1/1/1
5	NAG	k	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	k	2	5	-	0/6/23/26	0/1/1/1
5	NAG	l	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	l	2	5	-	0/6/23/26	0/1/1/1
9	NAG	m	1	1,9	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	m	2	9	-	2/6/23/26	0/1/1/1
9	BMA	m	3	9	-	0/2/19/22	0/1/1/1
9	MAN	m	4	9	-	1/2/19/22	0/1/1/1
9	MAN	m	5	9	-	1/2/19/22	0/1/1/1
5	NAG	n	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	n	2	5	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	2	NAG	C1-C2	2.66	1.56	1.52
5	R	1	NAG	O5-C1	-2.26	1.39	1.43
8	Z	5	MAN	C1-C2	2.19	1.57	1.52
8	Q	5	MAN	C1-C2	2.14	1.57	1.52

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	2	NAG	C2-N2-C7	4.91	129.48	122.90
8	Z	5	MAN	C1-O5-C5	4.30	117.95	112.19
8	Q	5	MAN	C1-O5-C5	4.22	117.84	112.19
8	Z	4	MAN	C1-O5-C5	2.95	116.14	112.19
8	Q	4	MAN	C1-O5-C5	2.90	116.07	112.19

There are no chirality outliers.

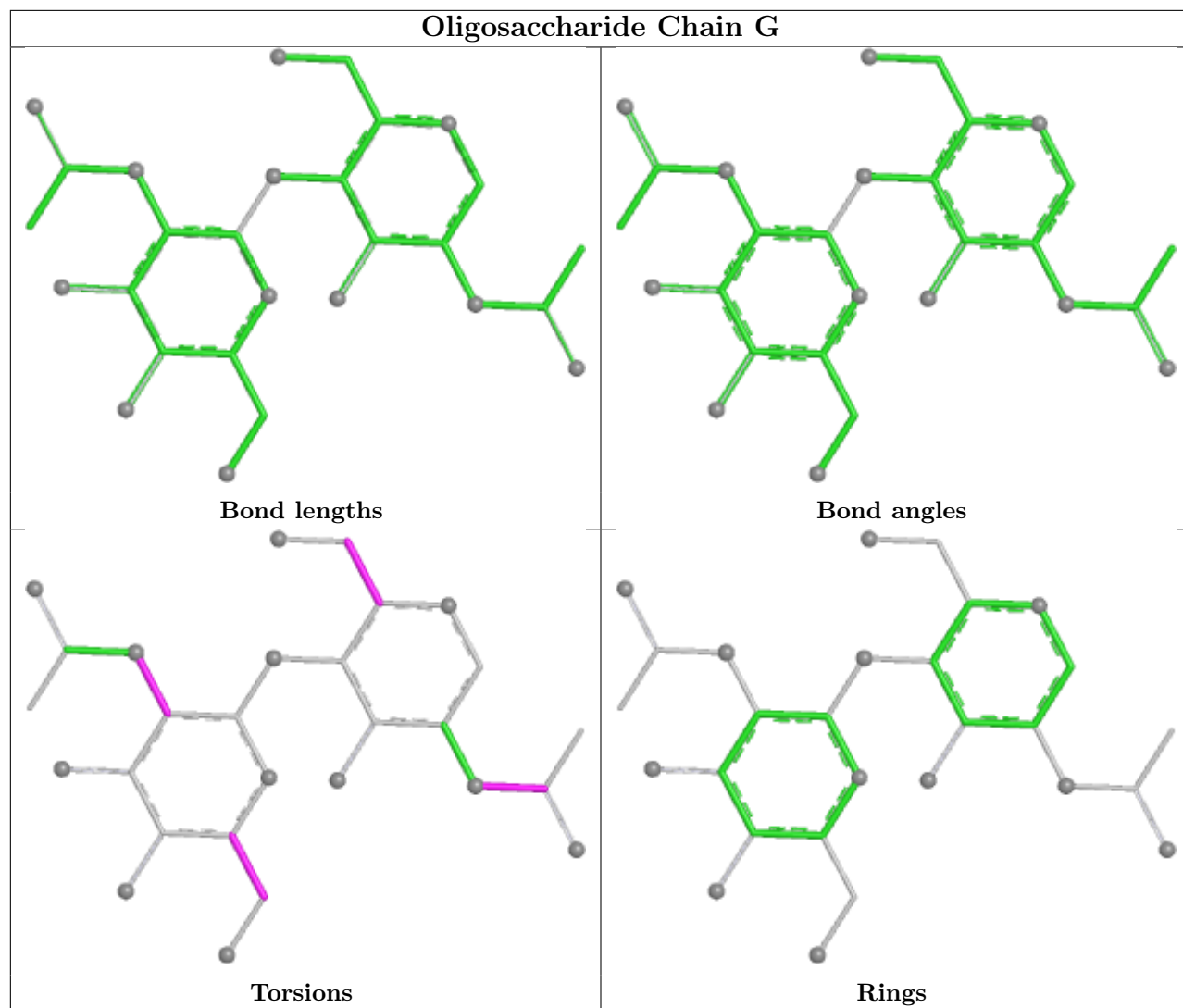
5 of 111 torsion outliers are listed below:

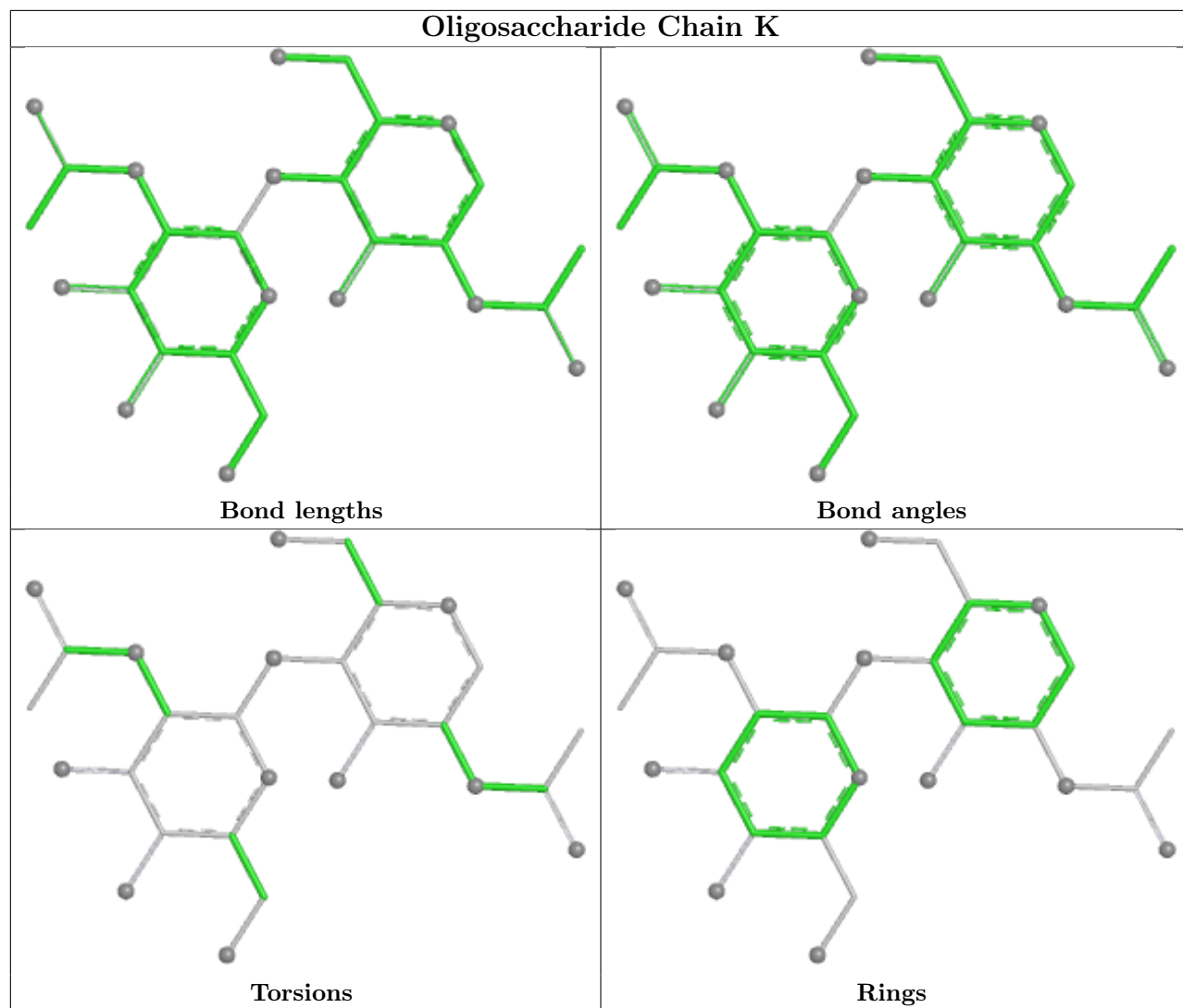
Mol	Chain	Res	Type	Atoms
5	U	1	NAG	O5-C5-C6-O6
10	j	3	BMA	O5-C5-C6-O6
9	m	2	NAG	O5-C5-C6-O6
5	U	1	NAG	C4-C5-C6-O6
5	V	1	NAG	O5-C5-C6-O6

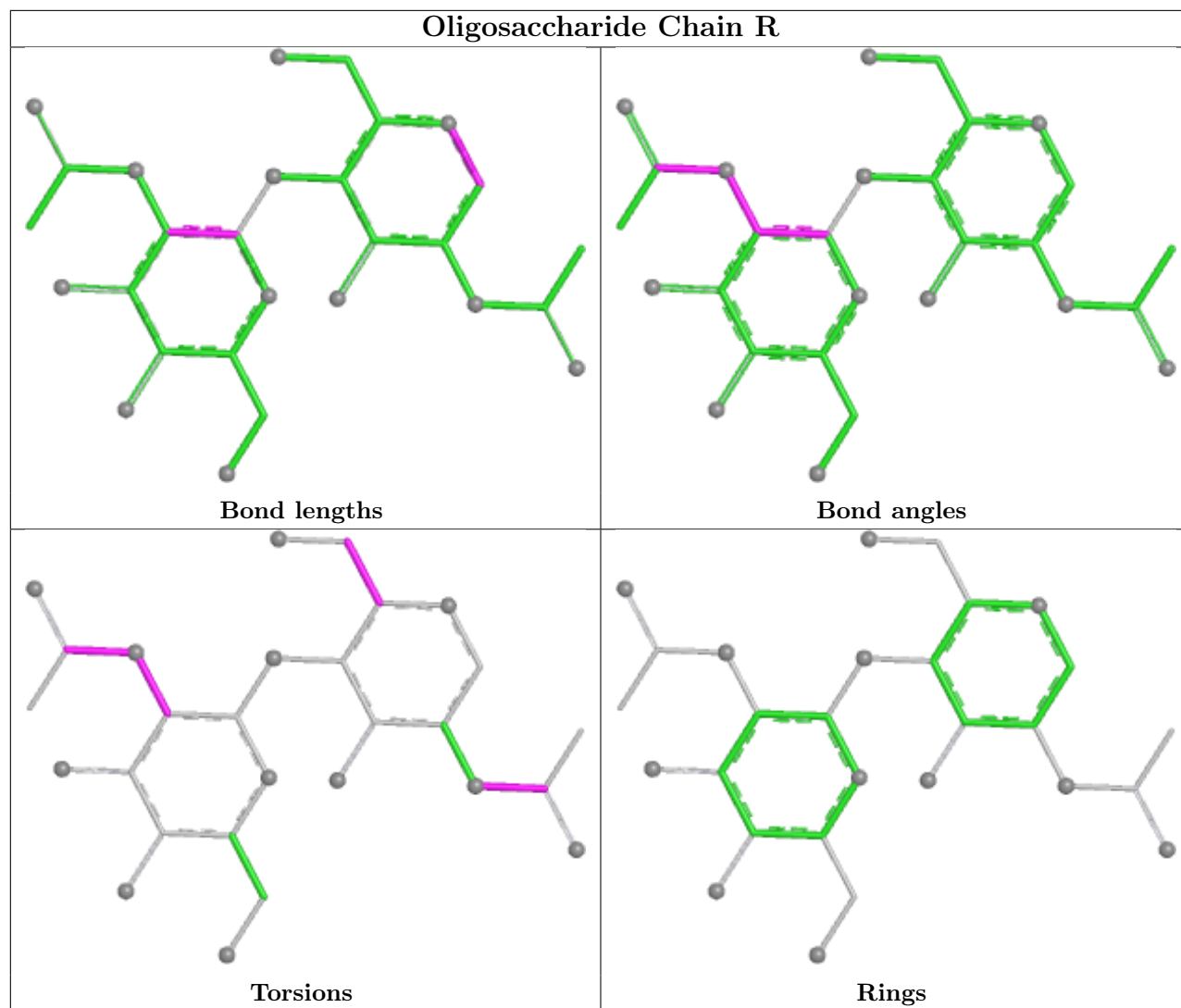
There are no ring outliers.

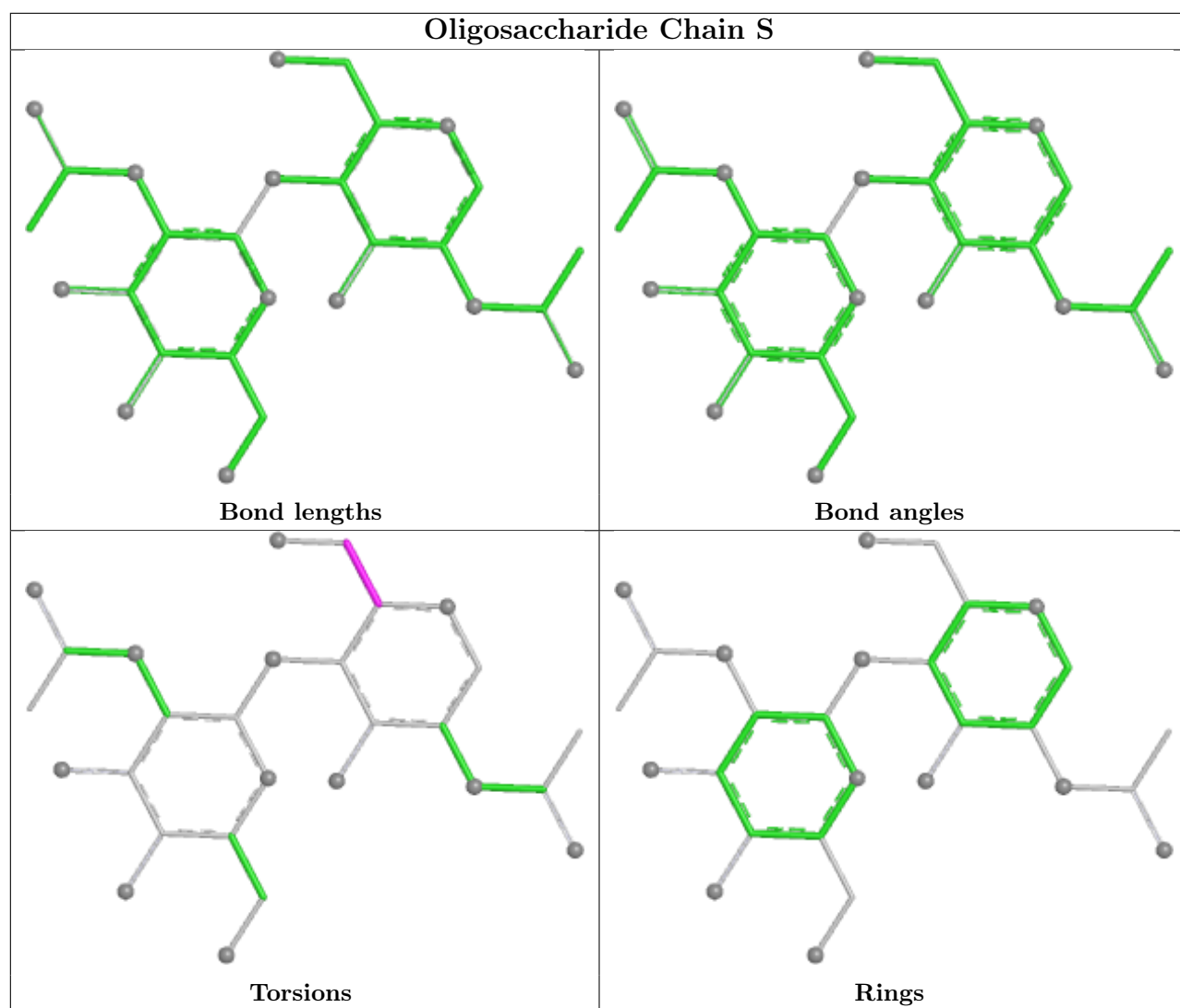
No monomer is involved in short contacts.

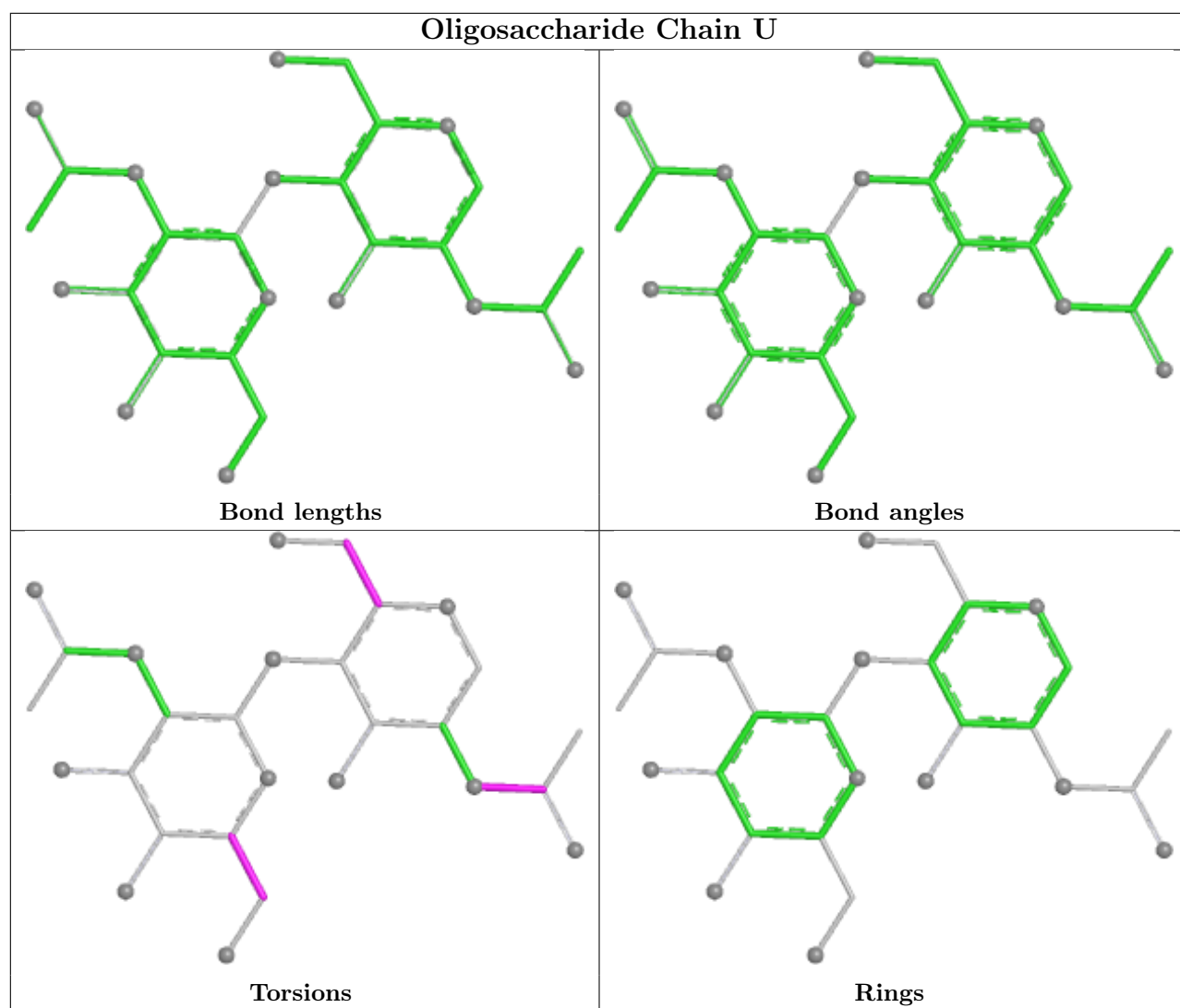
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

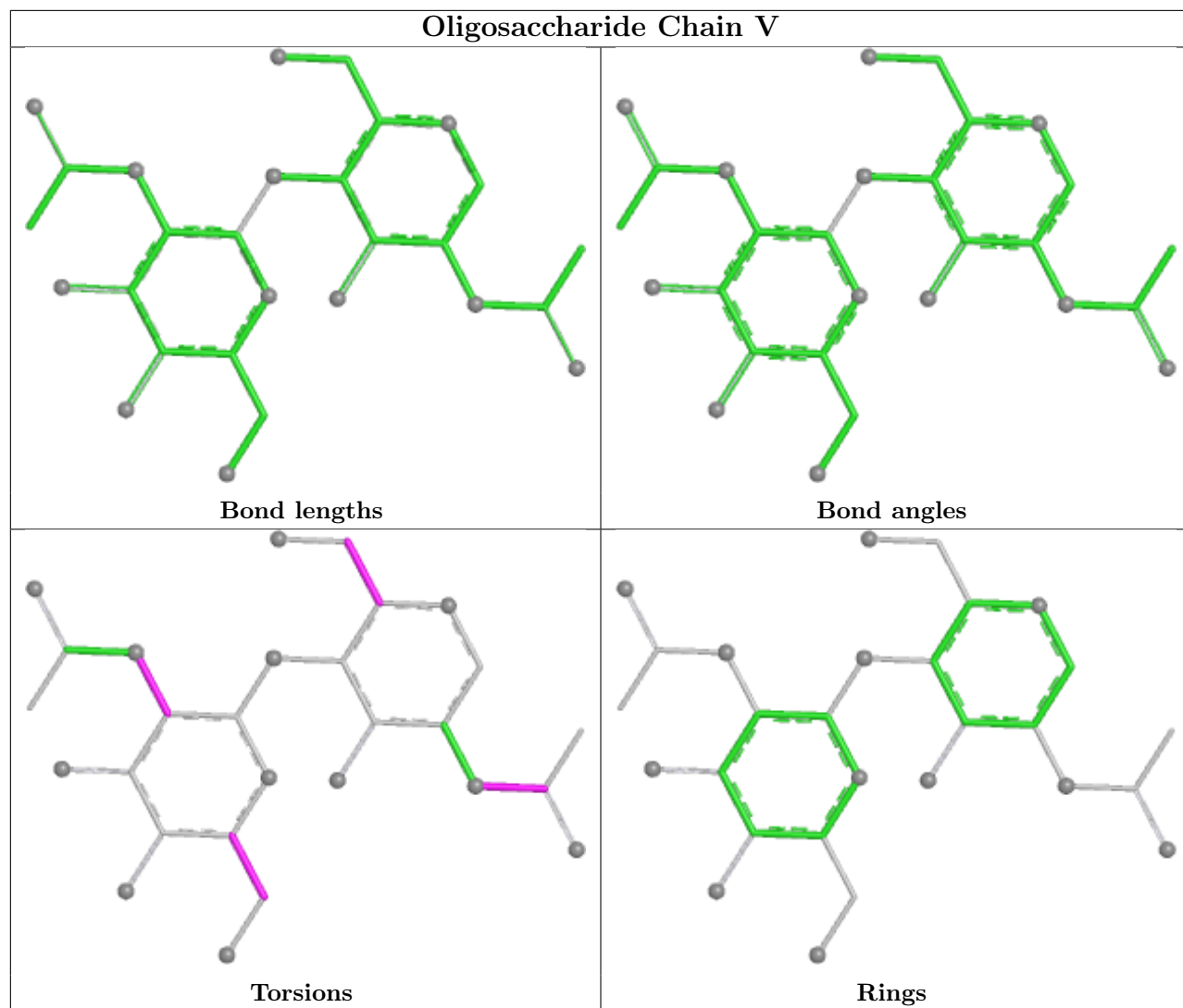


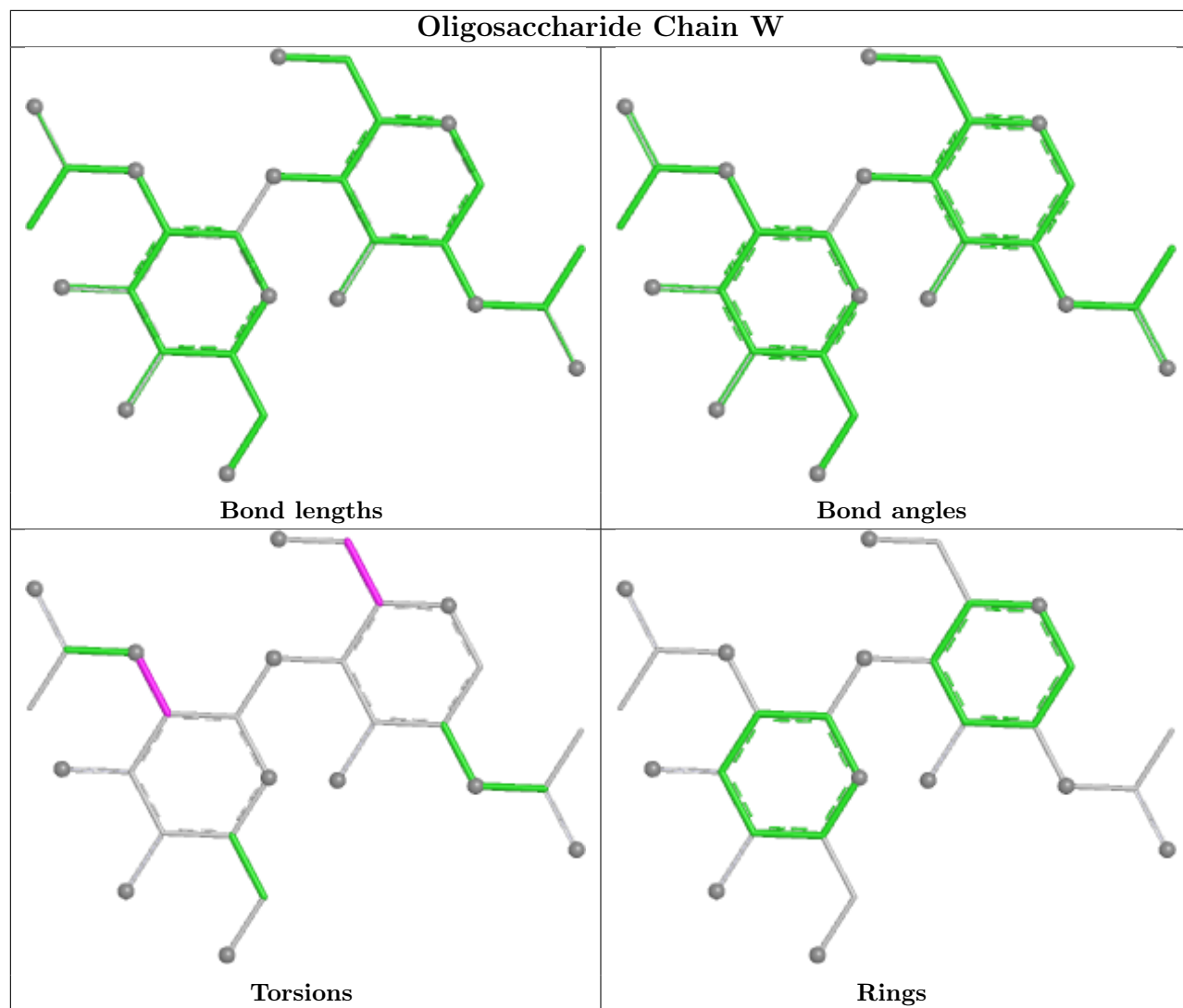


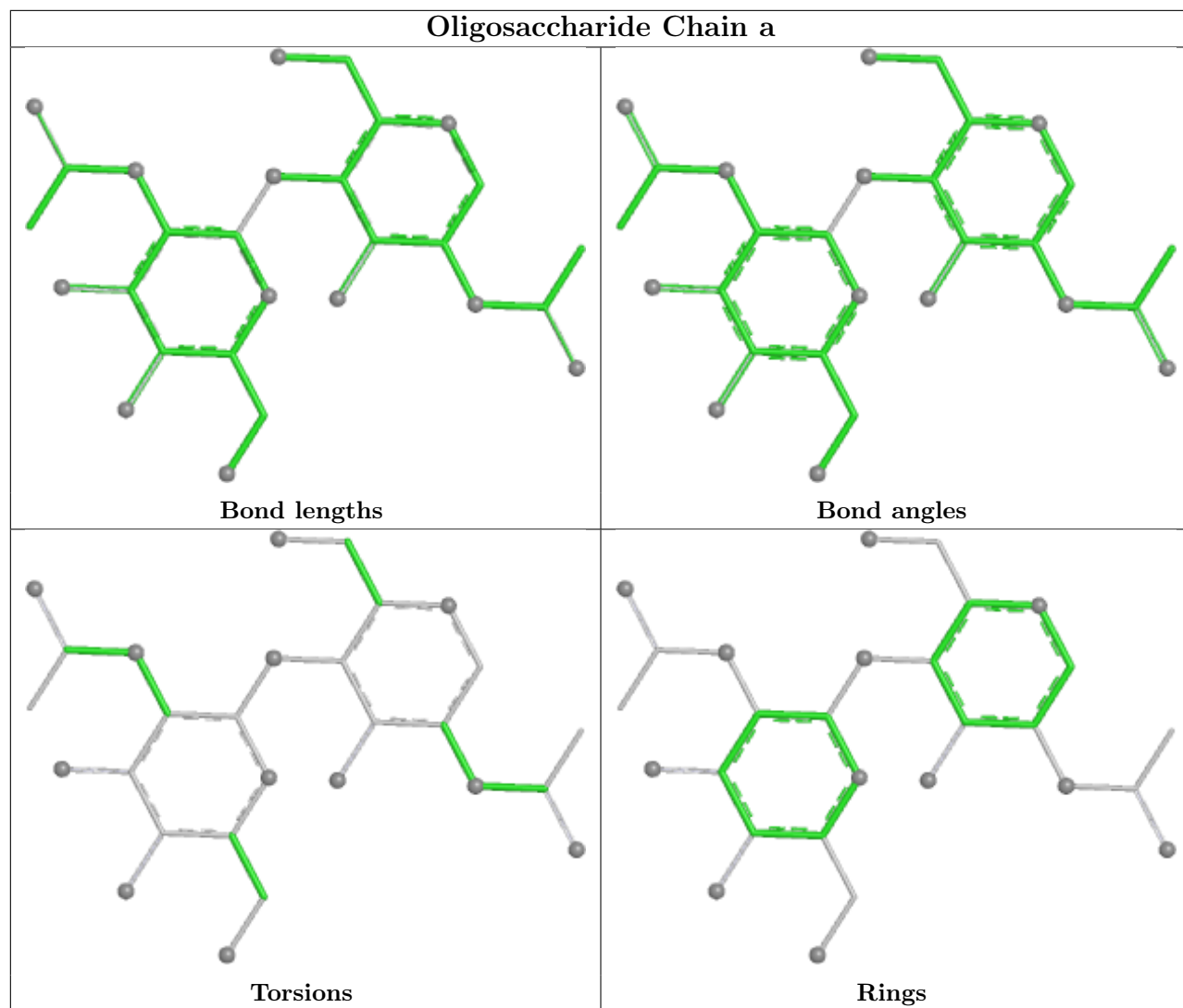


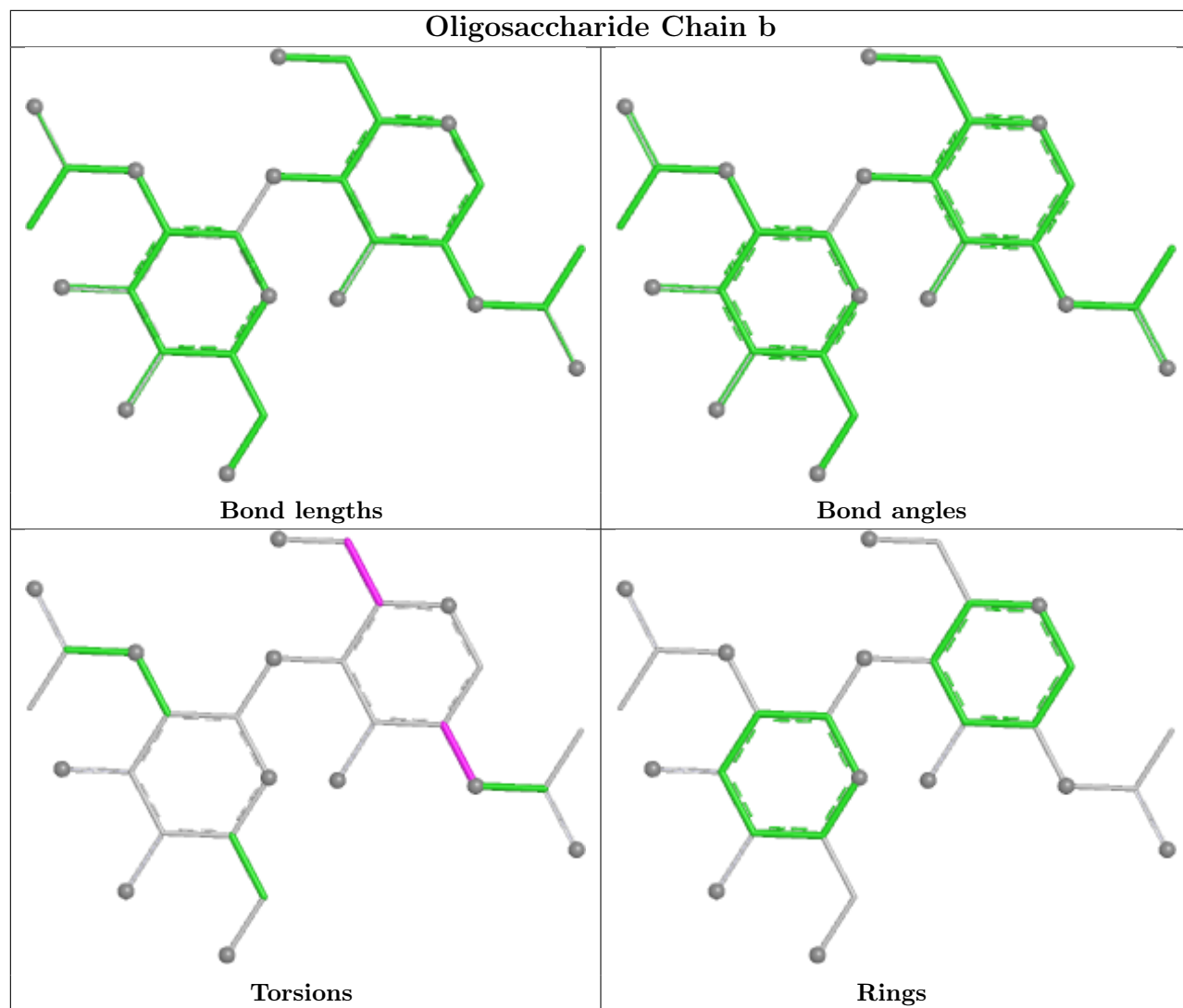


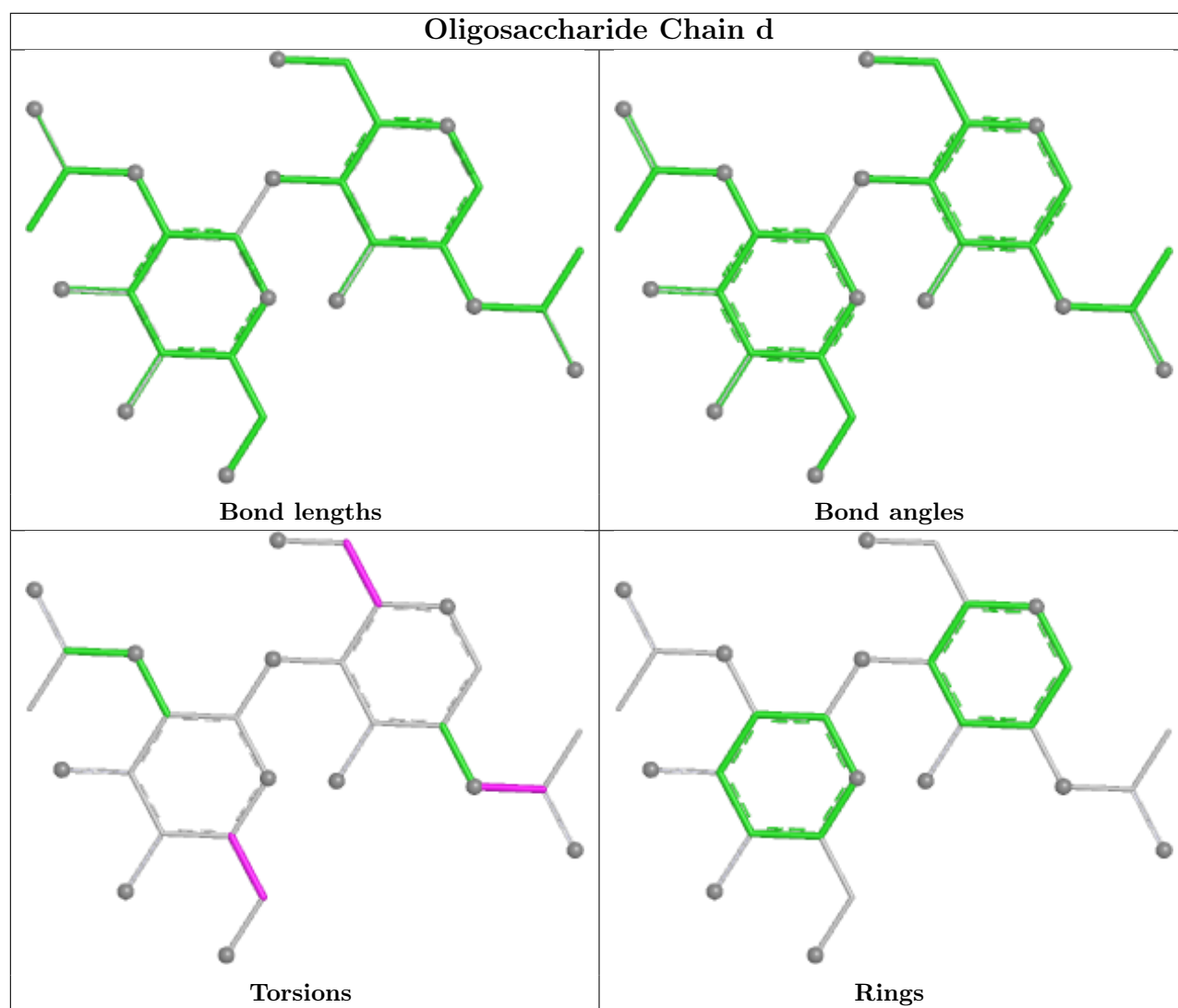


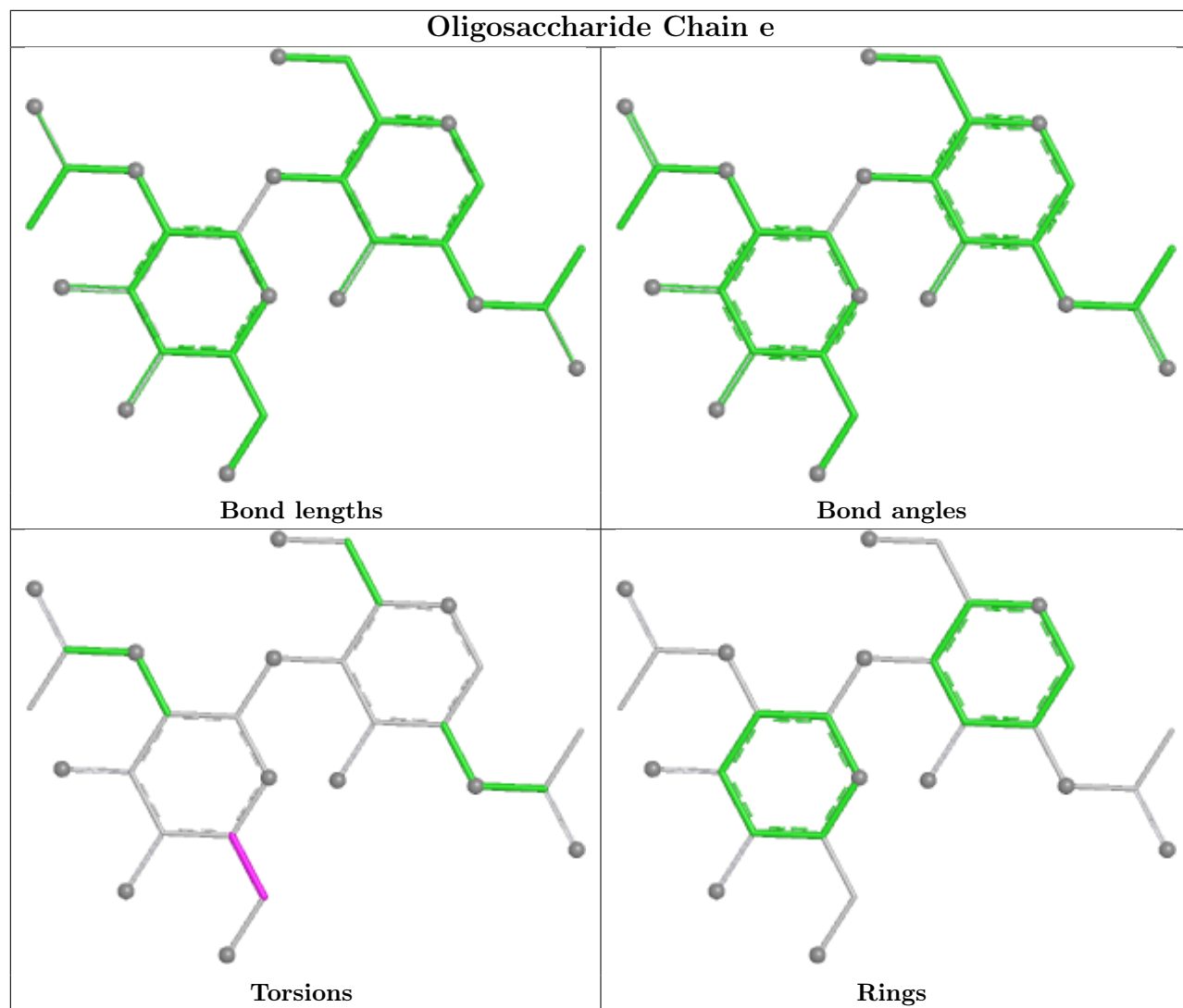


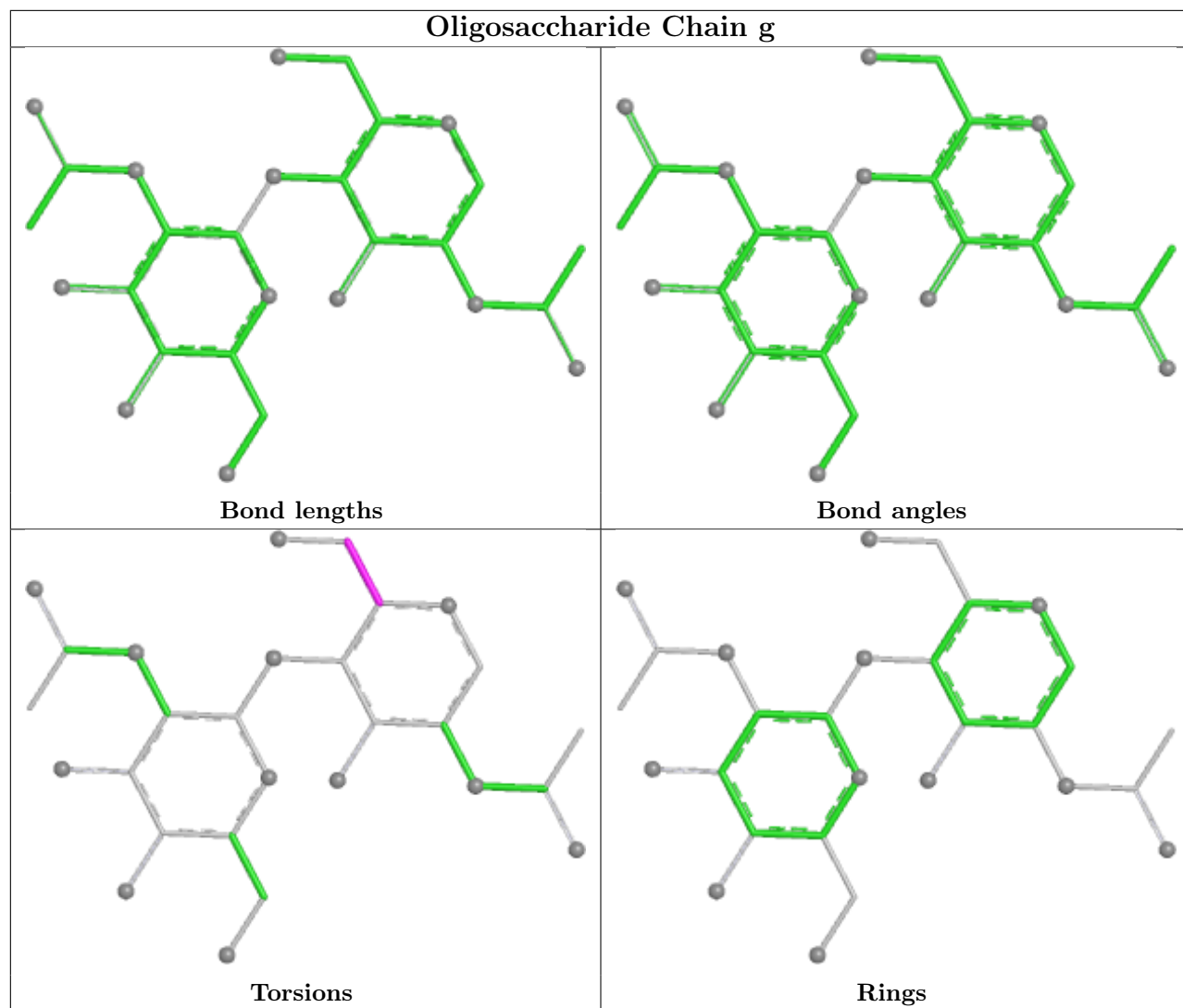


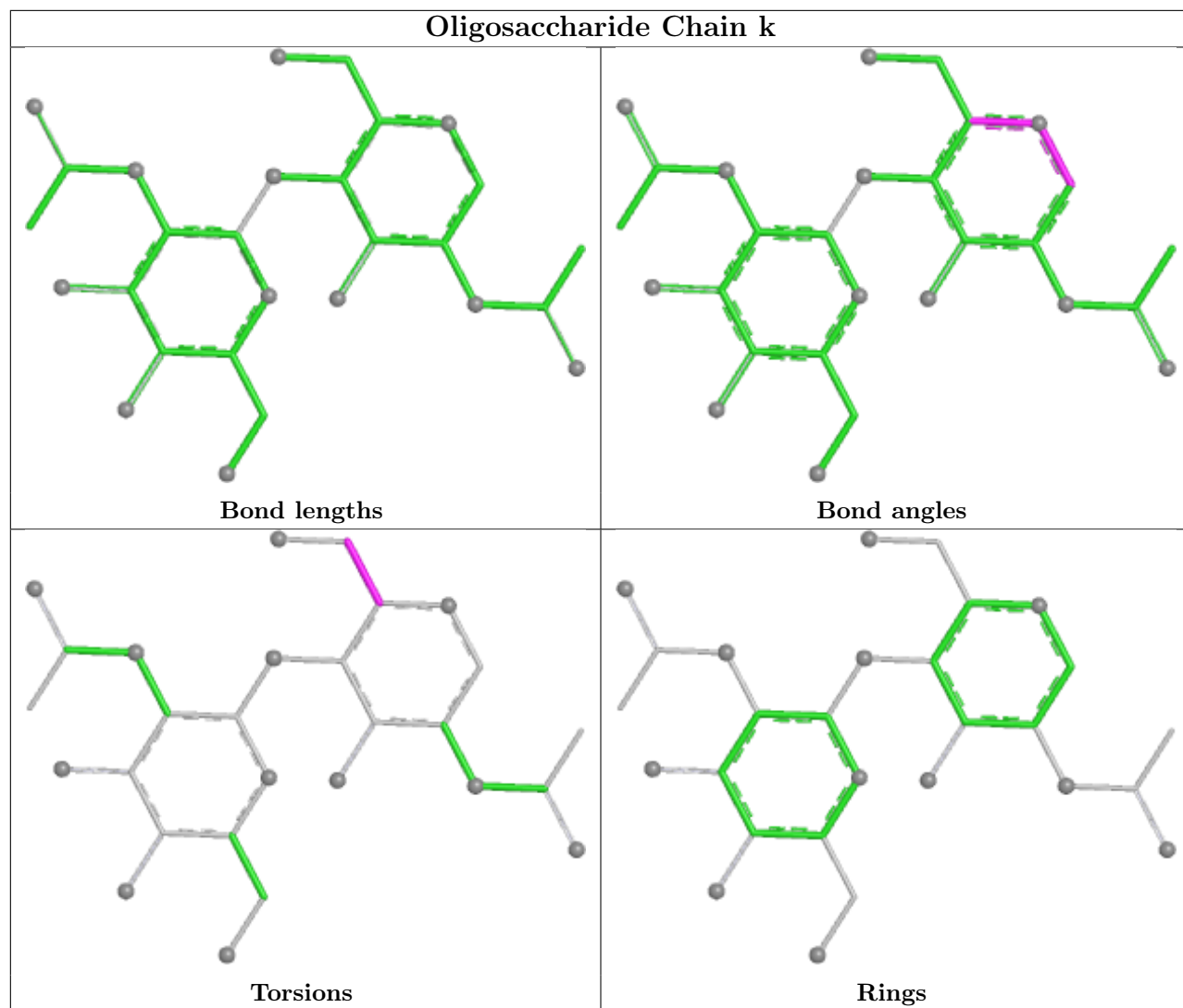


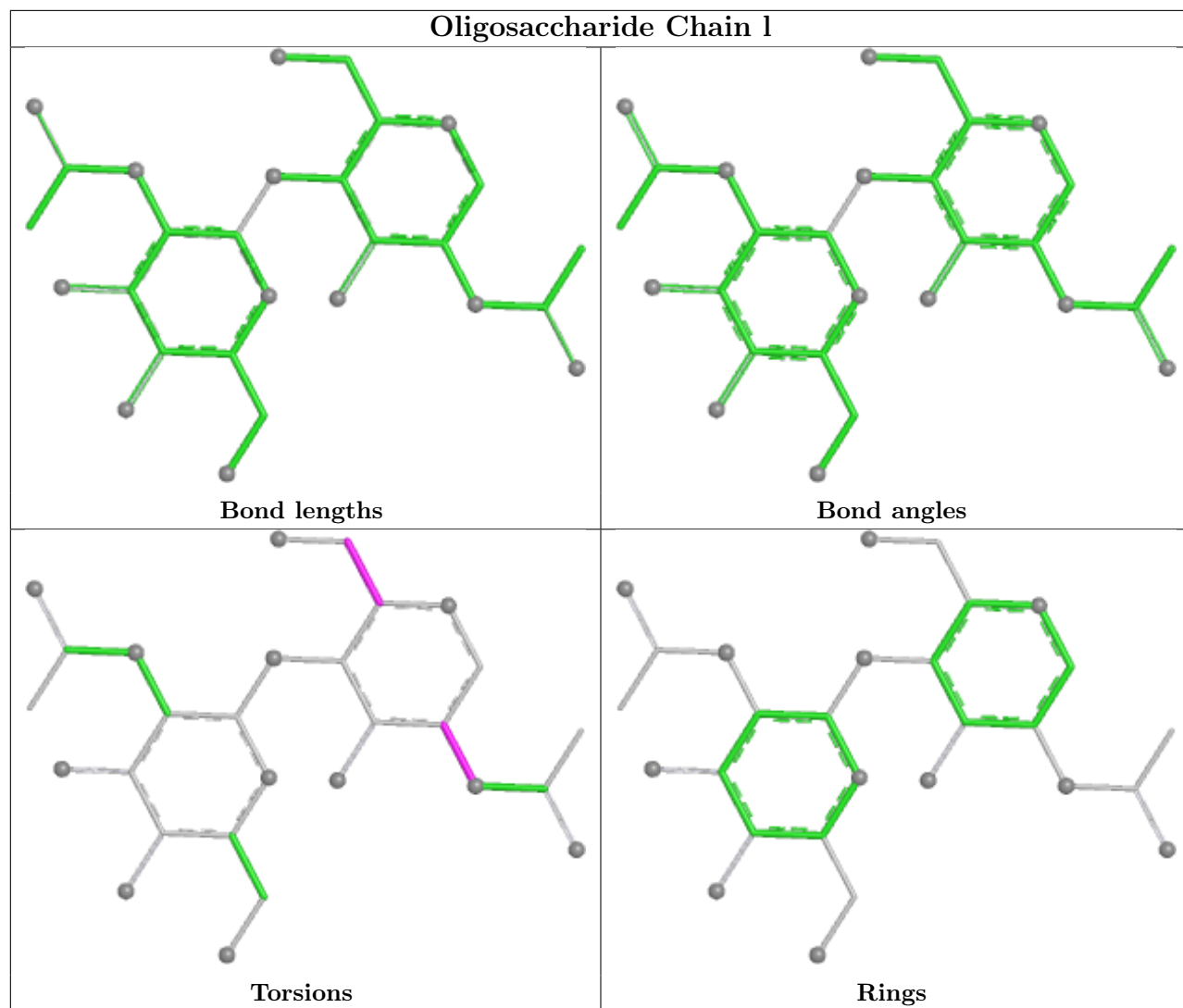


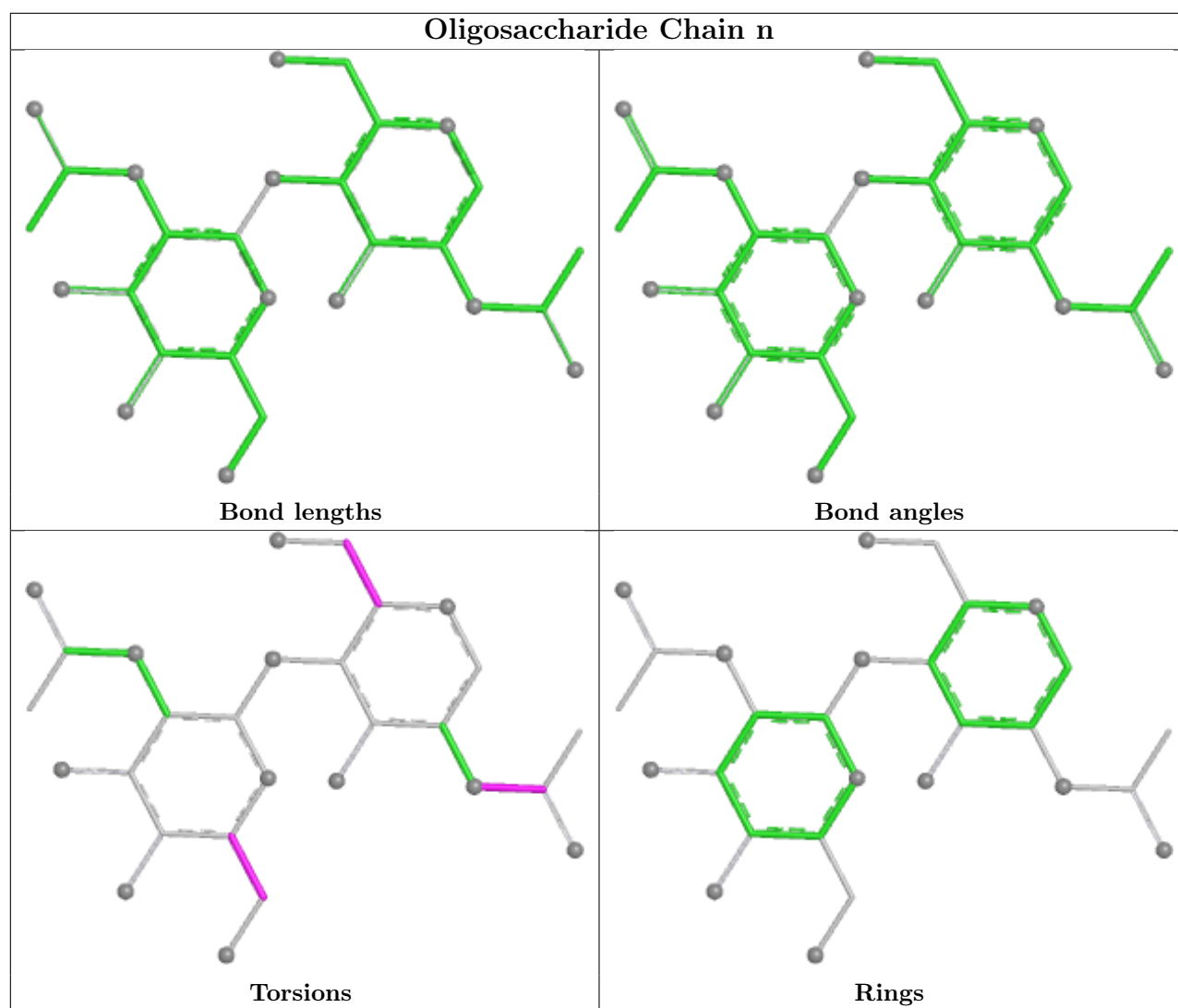


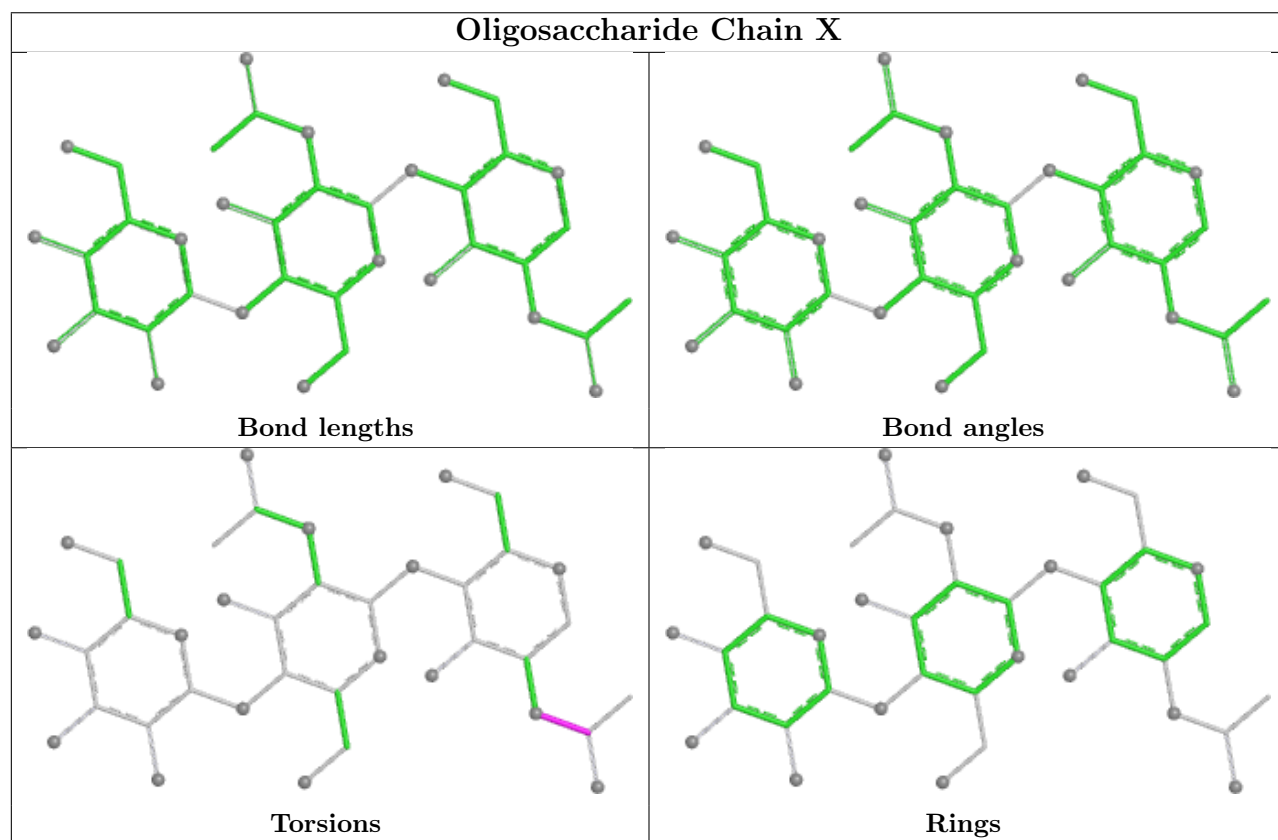
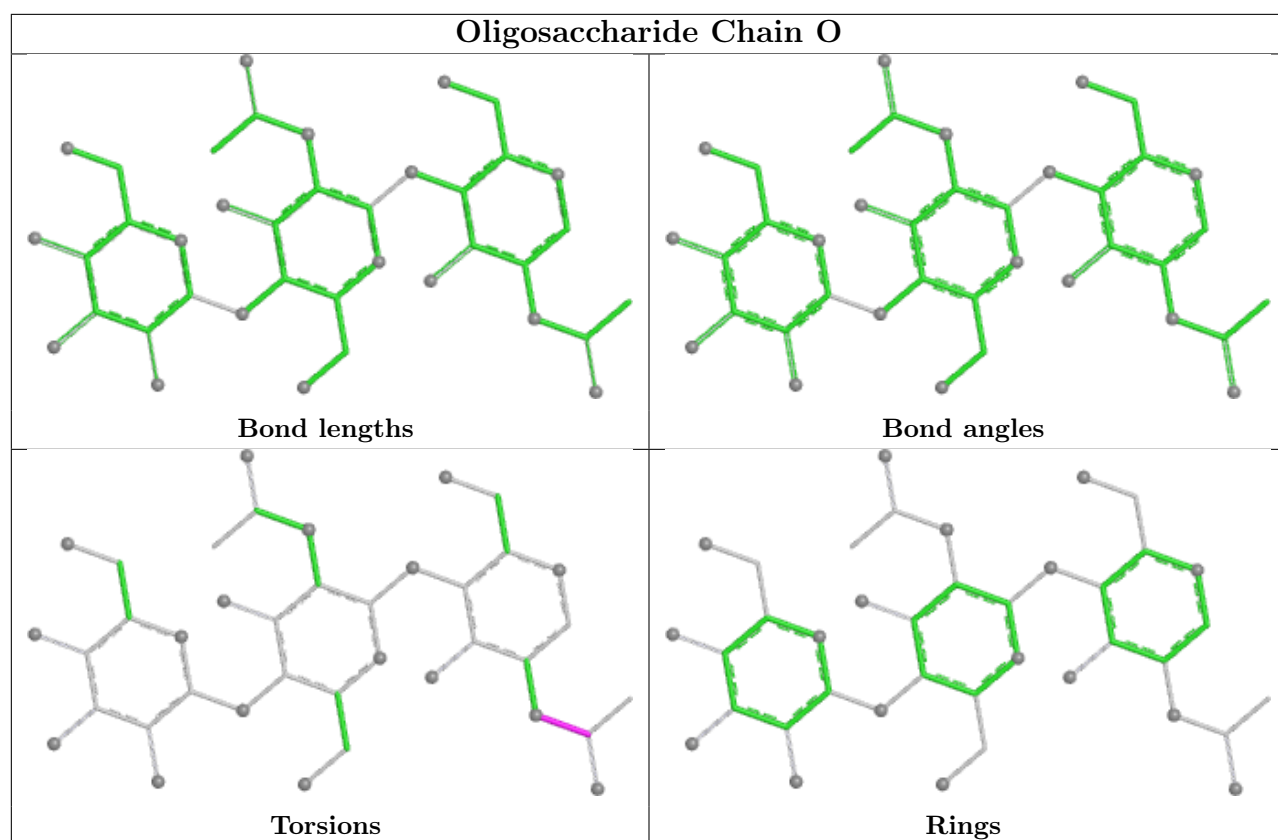


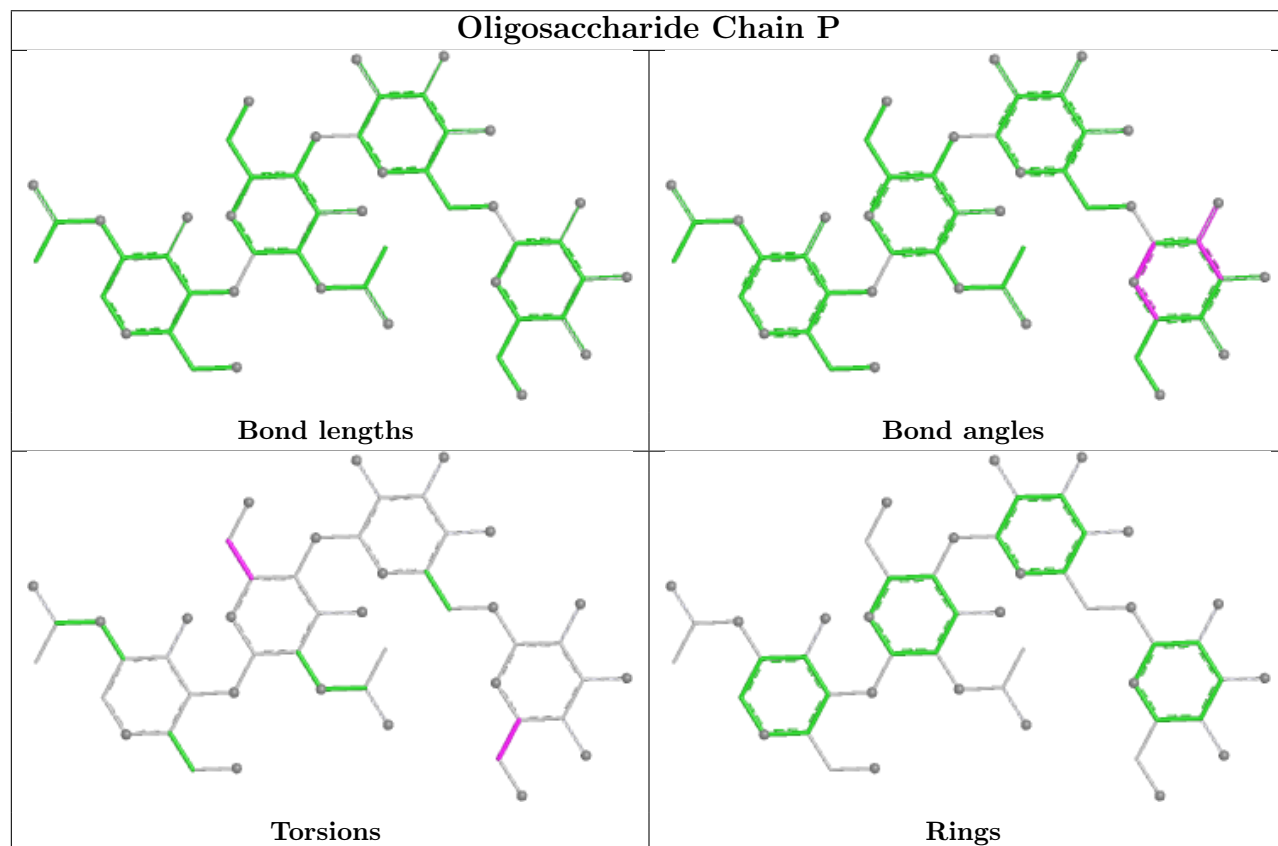
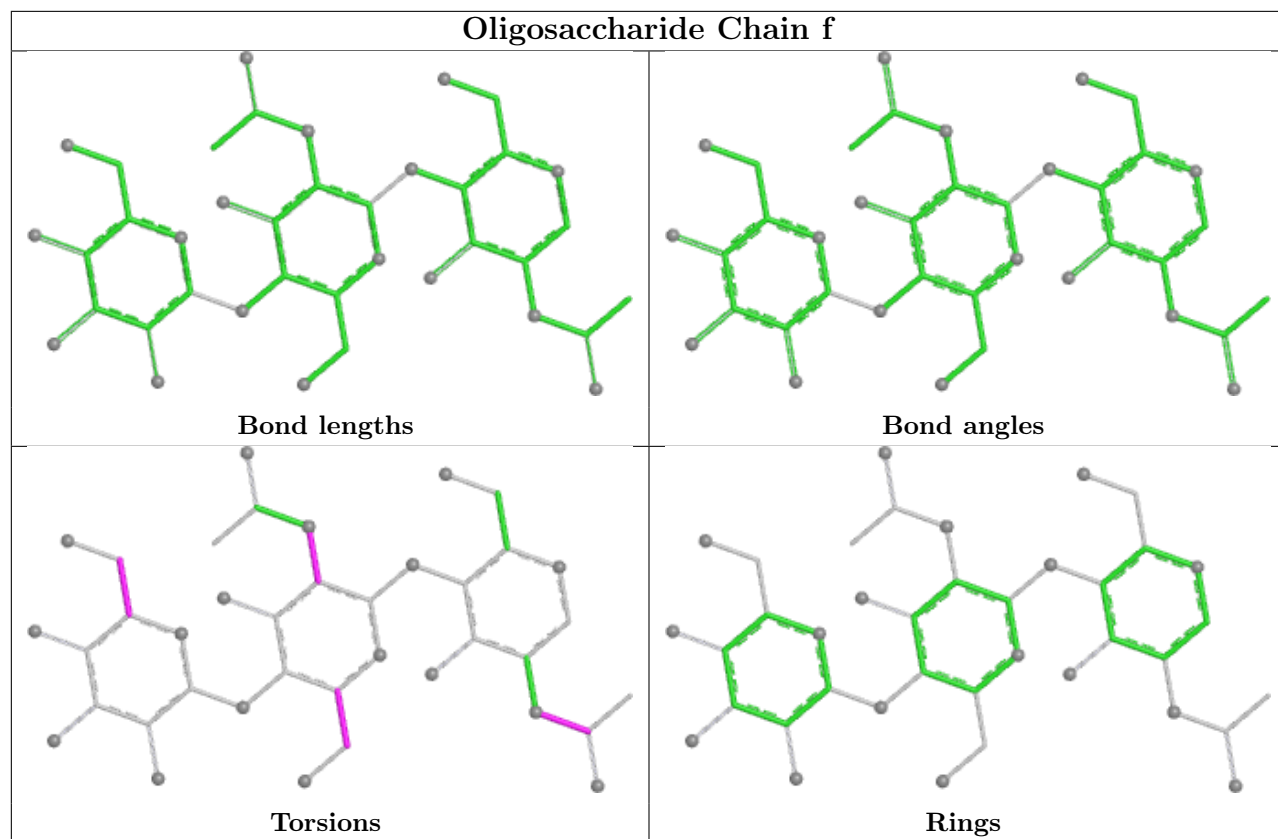


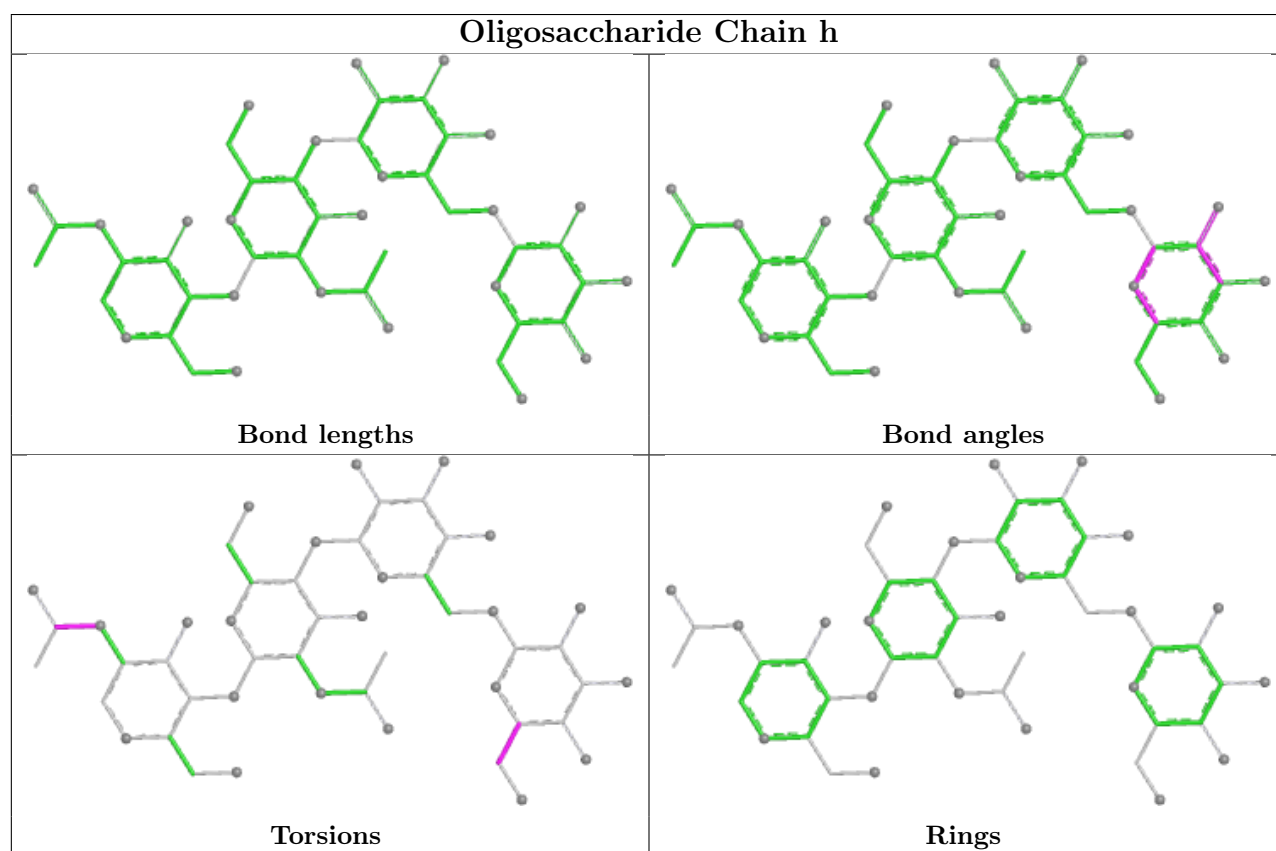
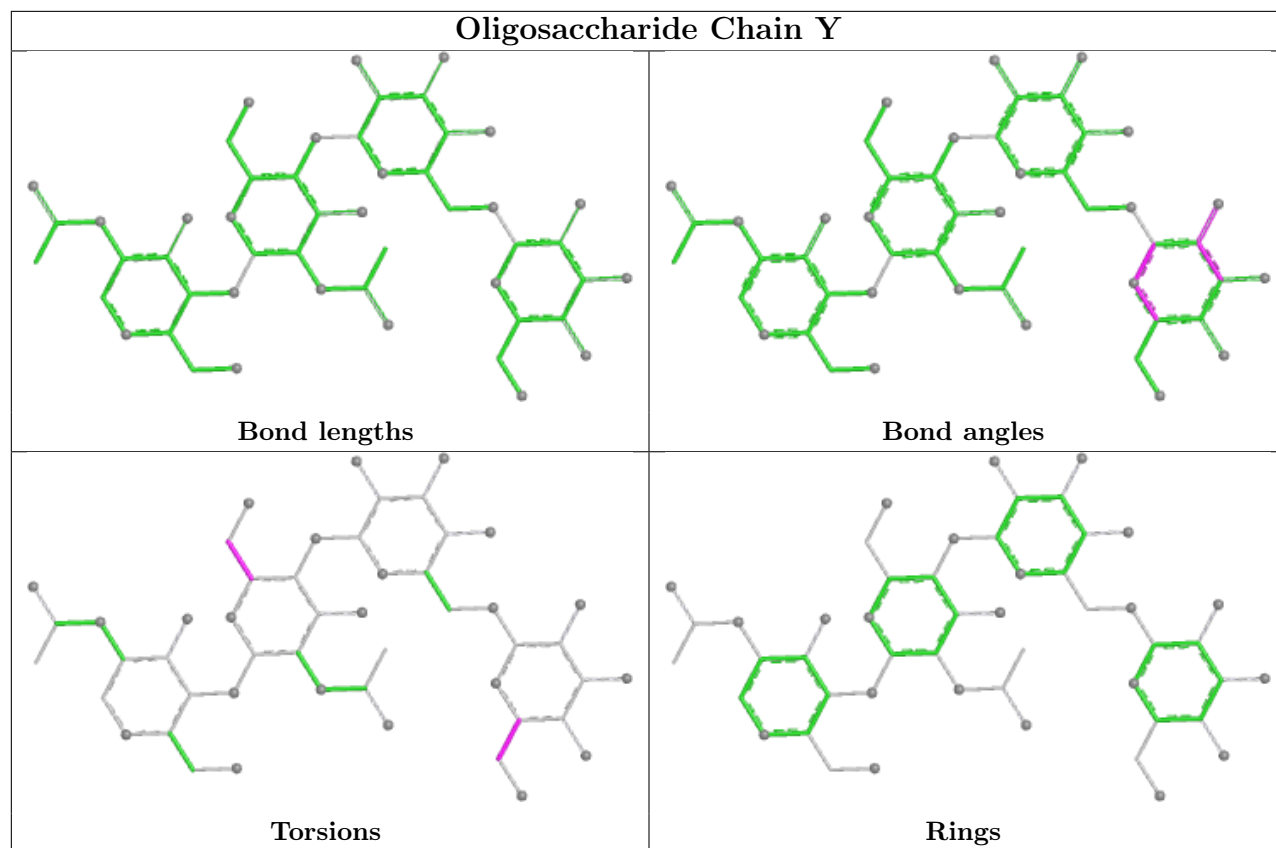


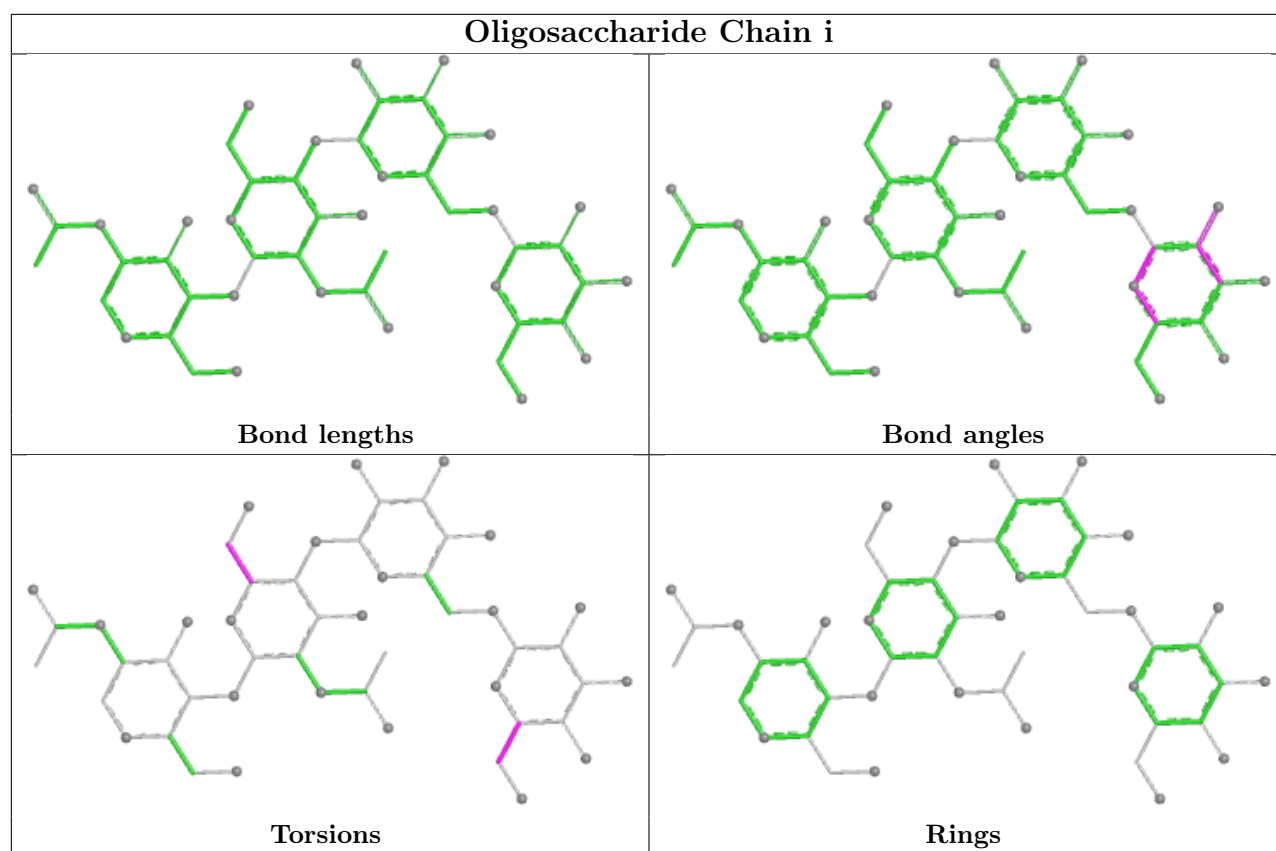


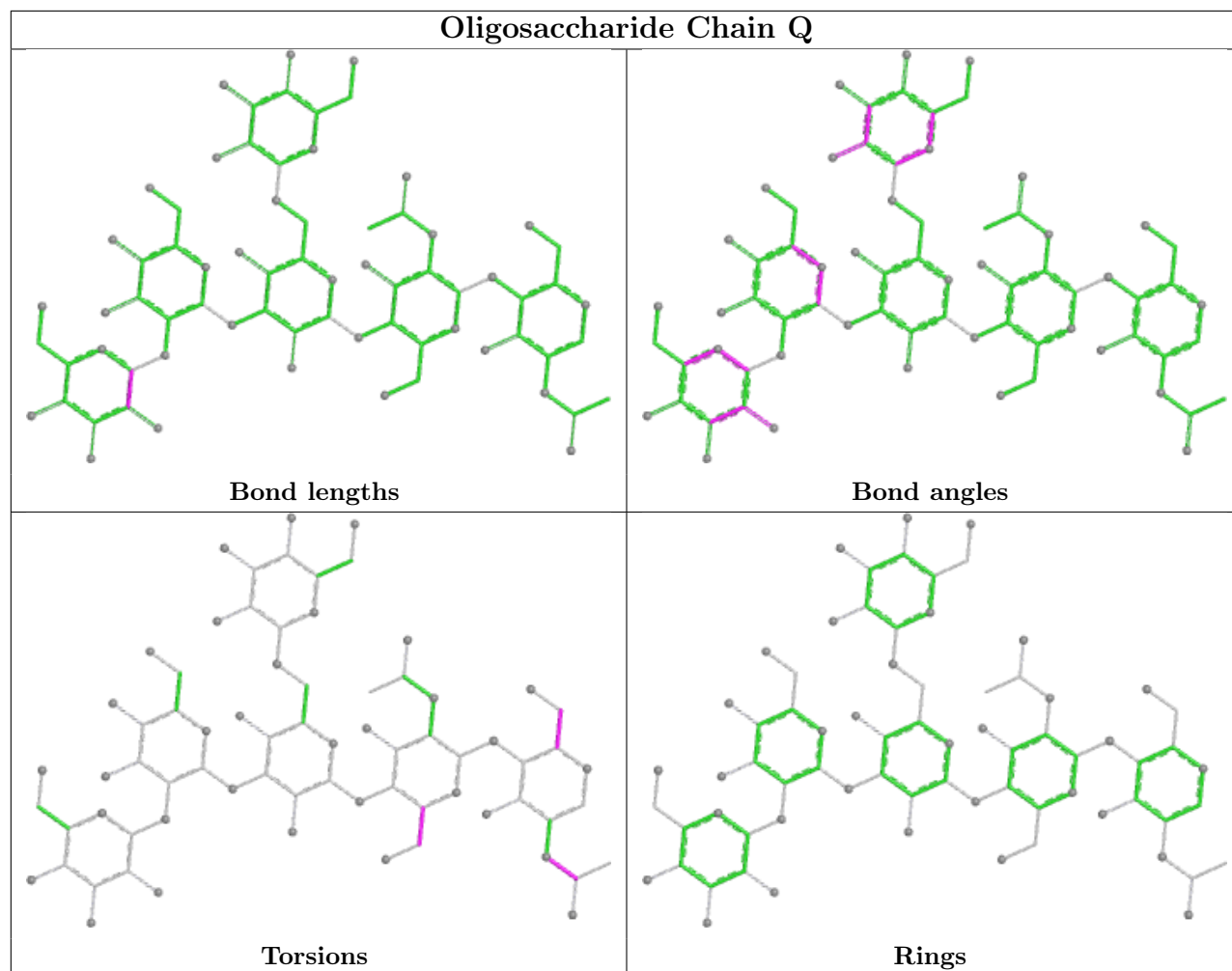


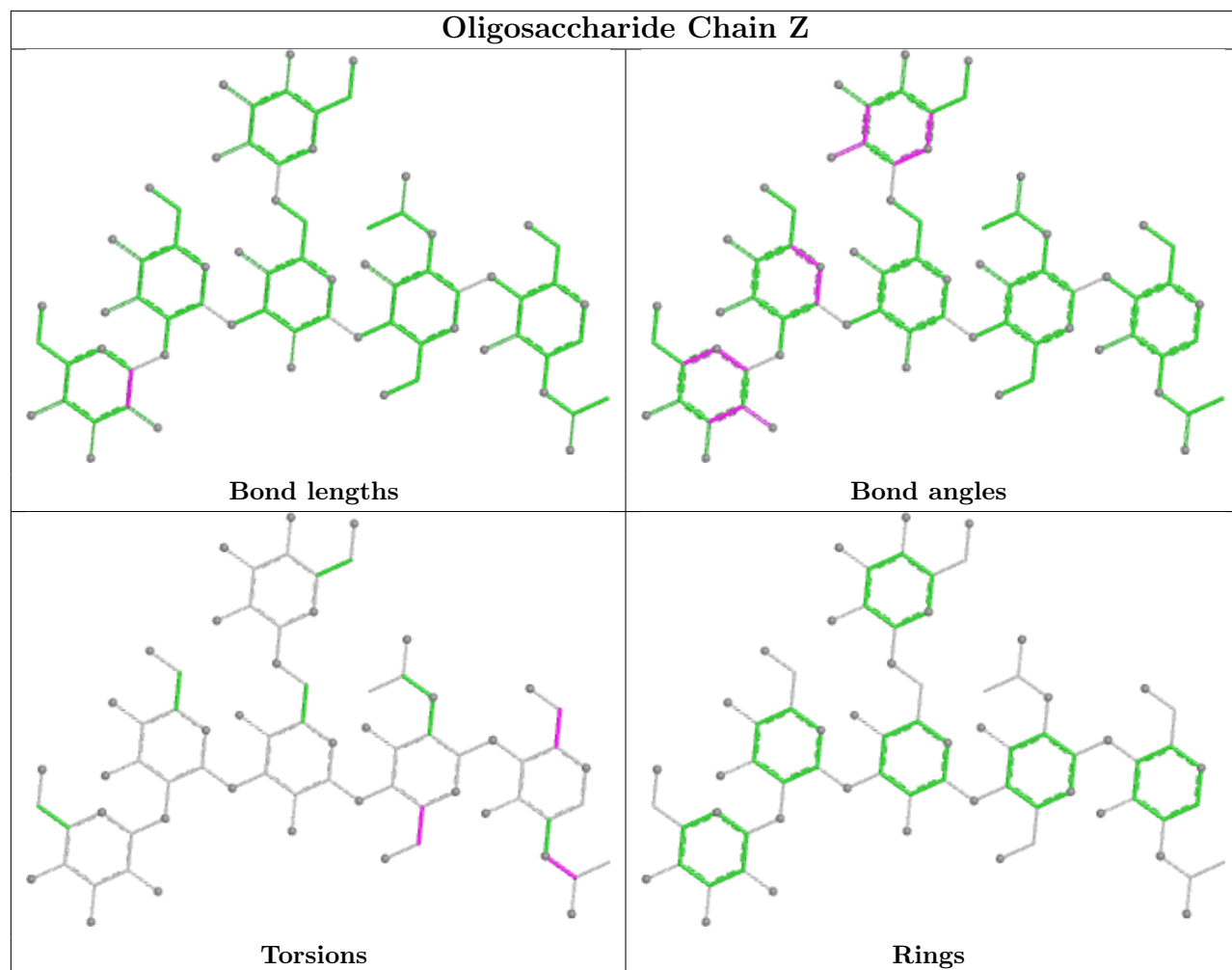


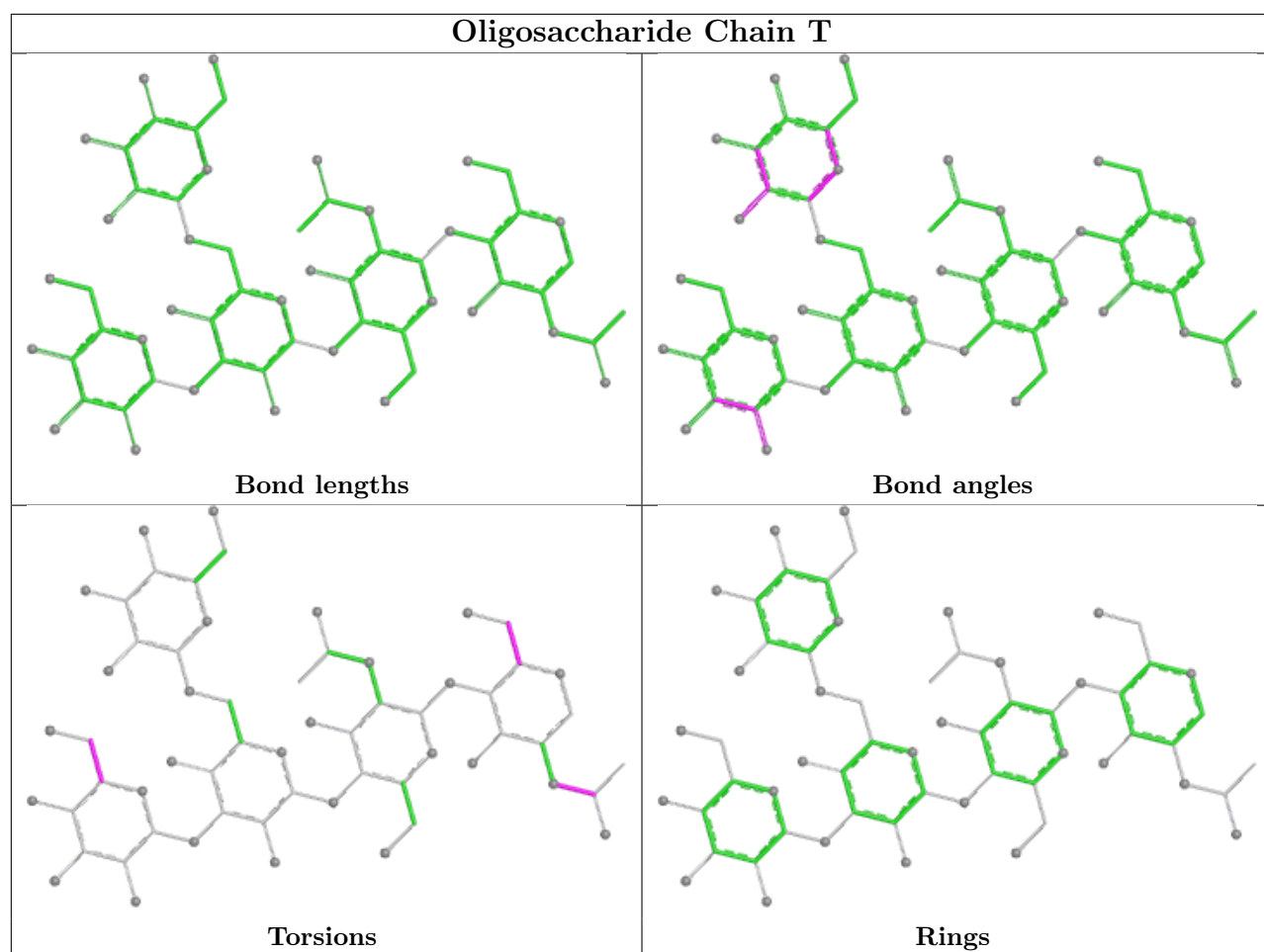


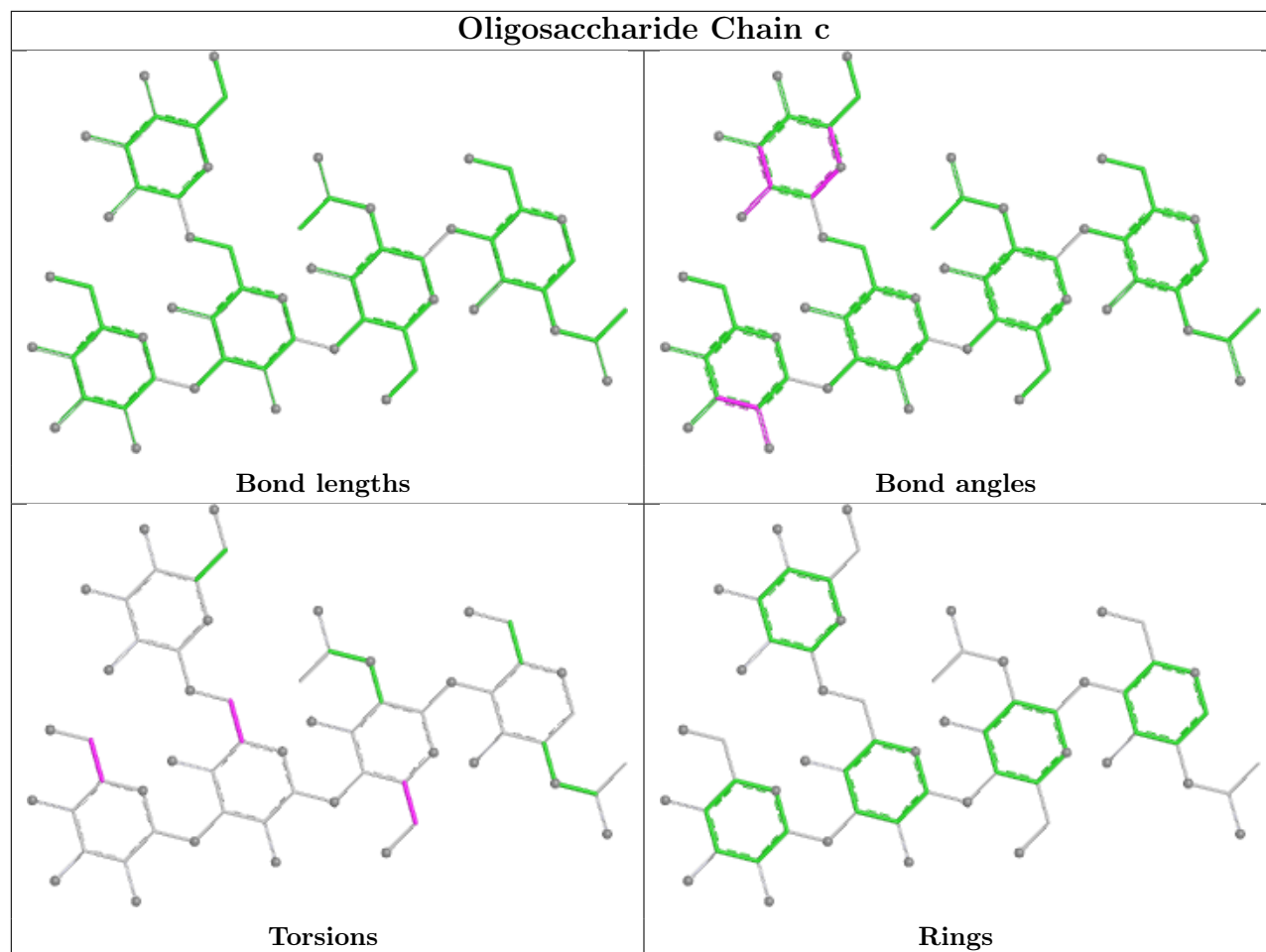


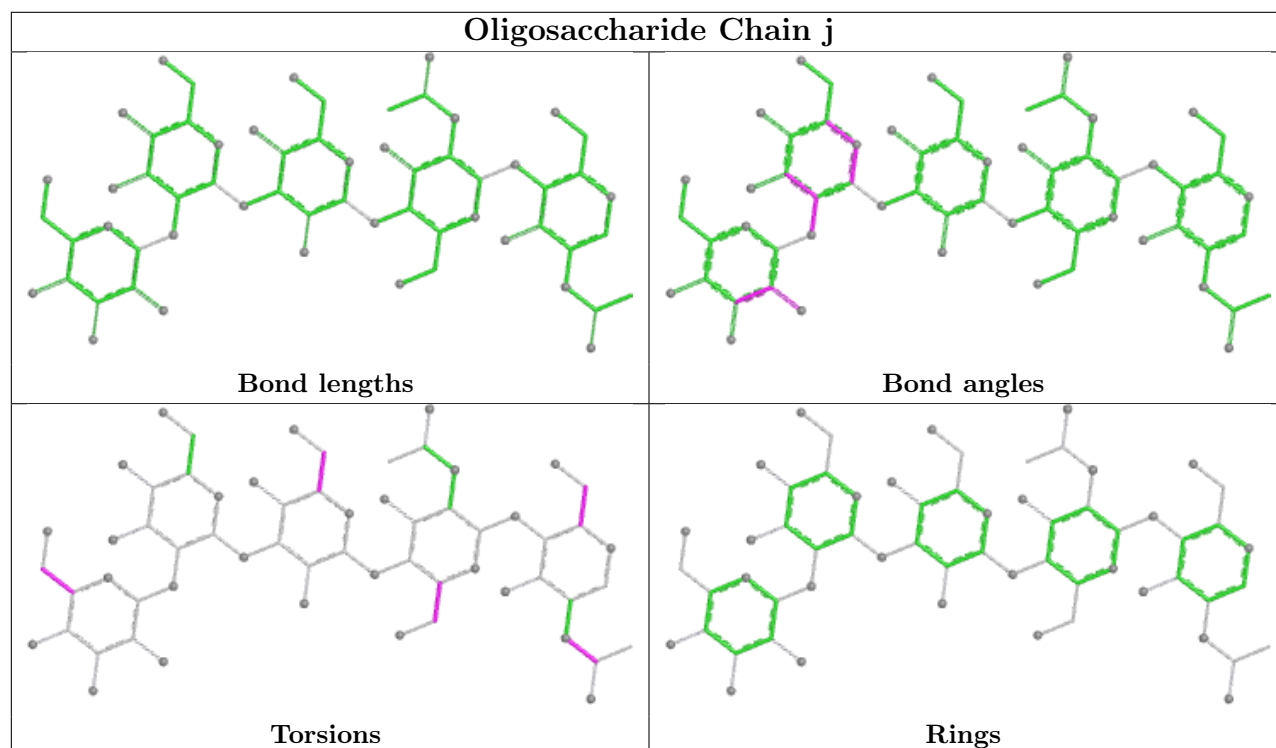
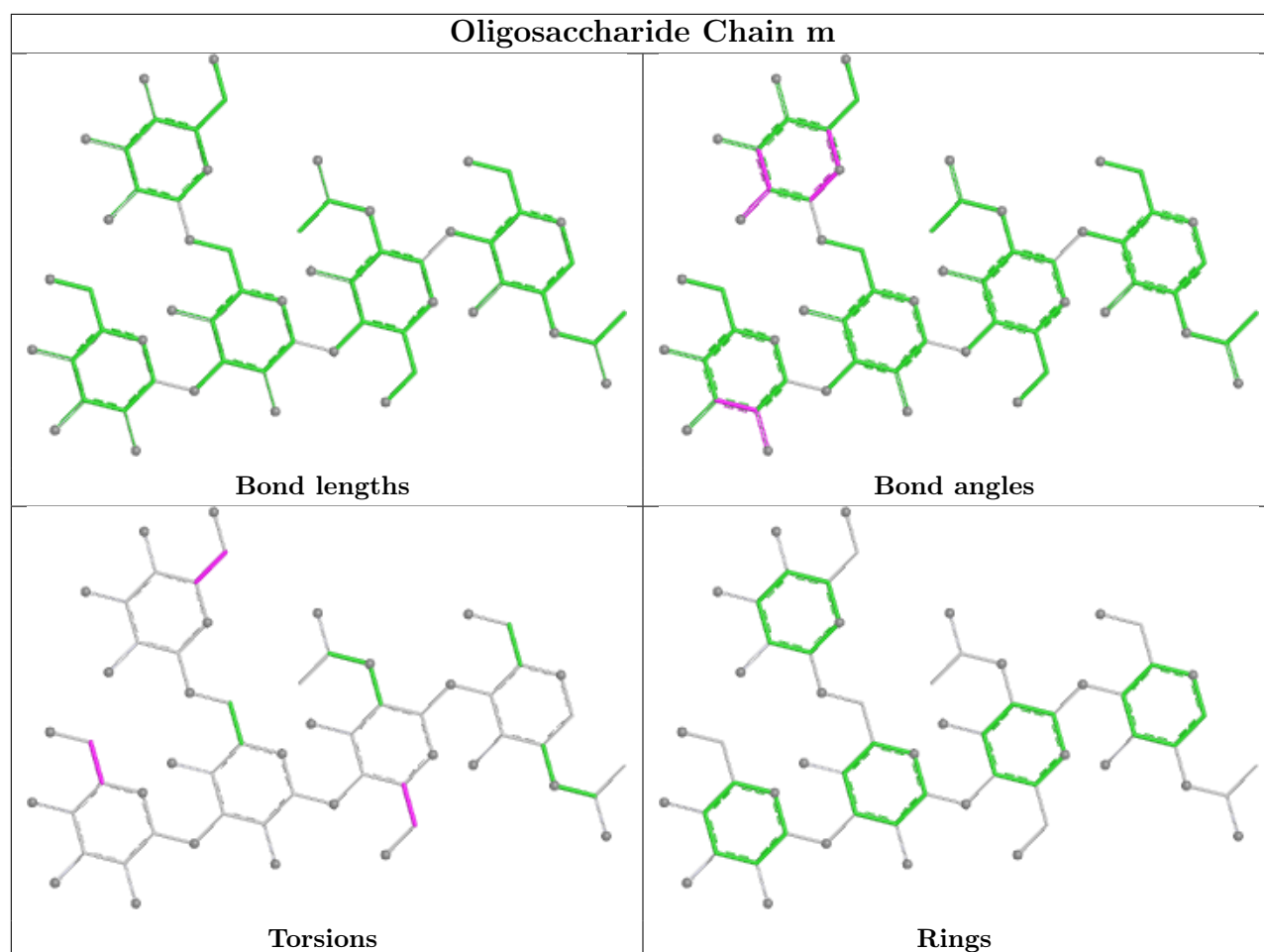












5.6 Ligand geometry

14 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$
11	NAG	A	603	1	14,14,15	0.24	0	17,19,21	0.48	0
11	NAG	A	605	1	14,14,15	0.25	0	17,19,21	0.45	0
11	NAG	C	601	1	14,14,15	0.21	0	17,19,21	0.43	0
11	NAG	E	601	1	14,14,15	0.21	0	17,19,21	0.42	0
11	NAG	E	604	1	14,14,15	0.23	0	17,19,21	0.48	0
11	NAG	C	602	1	14,14,15	0.18	0	17,19,21	0.41	0
11	NAG	C	603	1	14,14,15	0.23	0	17,19,21	0.46	0
11	NAG	A	602	1	14,14,15	0.19	0	17,19,21	0.40	0
11	NAG	C	604	1	14,14,15	0.22	0	17,19,21	0.48	0
11	NAG	E	603	1	14,14,15	0.23	0	17,19,21	0.46	0
11	NAG	A	604	1	14,14,15	0.22	0	17,19,21	0.48	0
11	NAG	E	602	1	14,14,15	0.19	0	17,19,21	0.42	0
11	NAG	A	601	1	14,14,15	0.21	0	17,19,21	0.43	0
11	NAG	E	605	1	14,14,15	0.25	0	17,19,21	0.45	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
11	NAG	A	603	1	-	0/6/23/26	0/1/1/1
11	NAG	A	605	1	-	0/6/23/26	0/1/1/1
11	NAG	C	601	1	-	2/6/23/26	0/1/1/1
11	NAG	E	601	1	-	2/6/23/26	0/1/1/1
11	NAG	E	604	1	-	0/6/23/26	0/1/1/1
11	NAG	C	602	1	-	1/6/23/26	0/1/1/1
11	NAG	C	603	1	-	2/6/23/26	0/1/1/1
11	NAG	A	602	1	-	2/6/23/26	0/1/1/1
11	NAG	C	604	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	E	603	1	-	2/6/23/26	0/1/1/1
11	NAG	A	604	1	-	2/6/23/26	0/1/1/1
11	NAG	E	602	1	-	2/6/23/26	0/1/1/1
11	NAG	A	601	1	-	2/6/23/26	0/1/1/1
11	NAG	E	605	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.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	601	NAG	C8-C7-N2-C2
11	A	601	NAG	O7-C7-N2-C2
11	A	604	NAG	C8-C7-N2-C2
11	A	604	NAG	O7-C7-N2-C2
11	C	601	NAG	C8-C7-N2-C2

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.

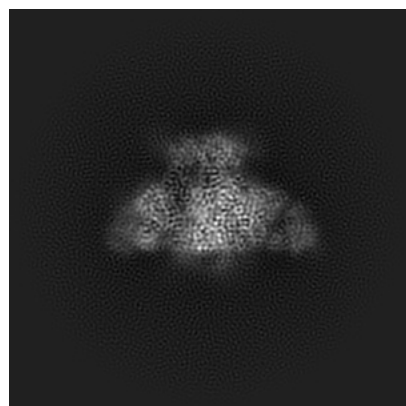
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42363. These allow visual inspection of the internal detail of the map and identification of artifacts.

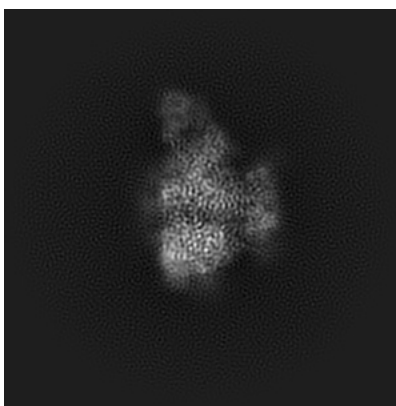
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

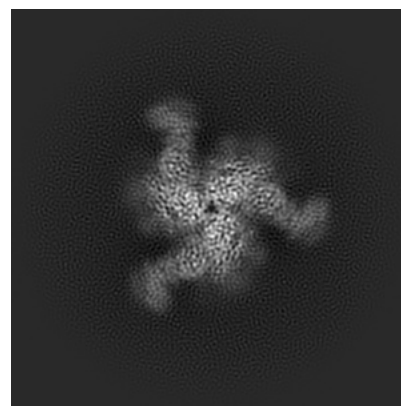
6.1.1 Primary map



X

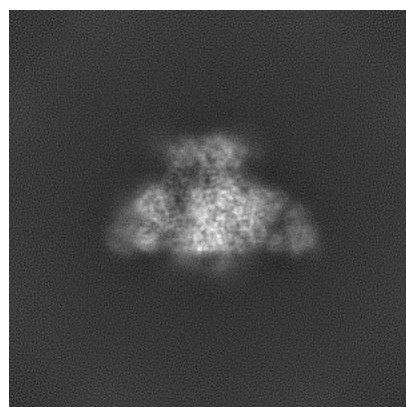


Y

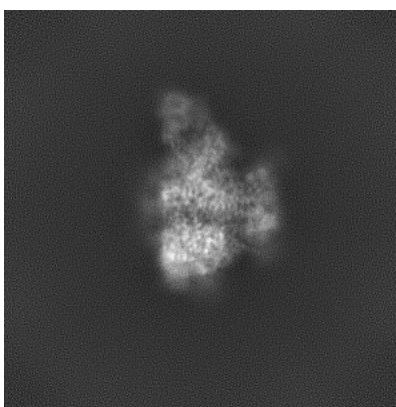


Z

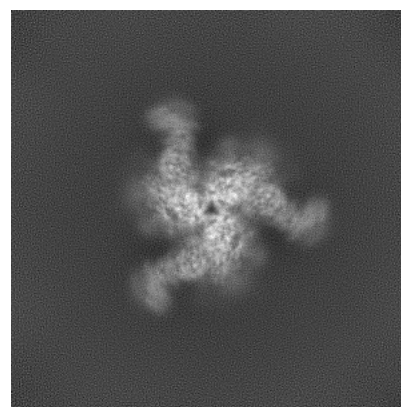
6.1.2 Raw map



X



Y

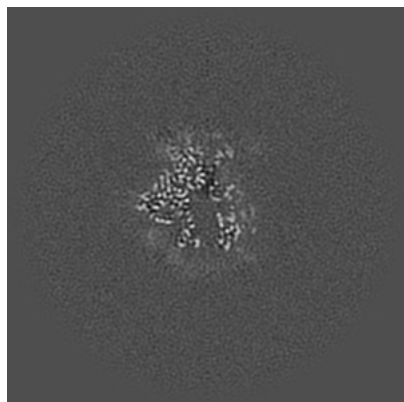


Z

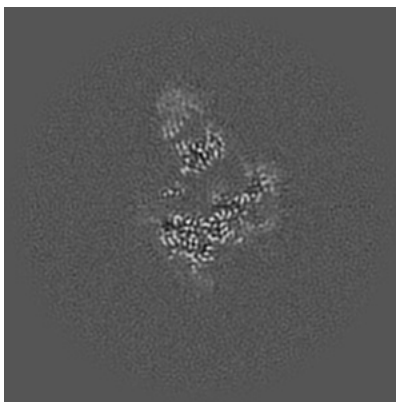
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

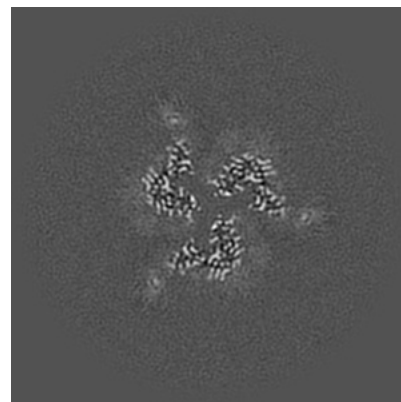
6.2.1 Primary map



X Index: 196

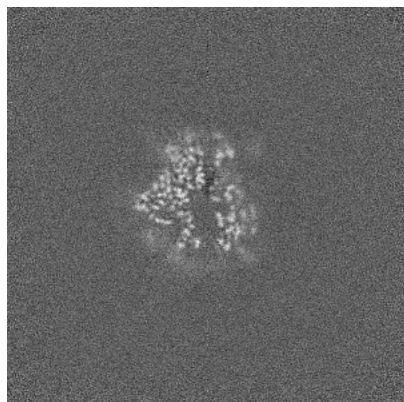


Y Index: 196

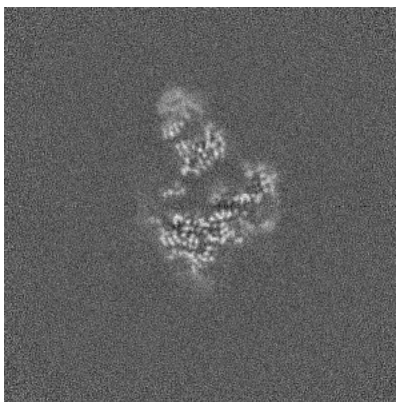


Z Index: 196

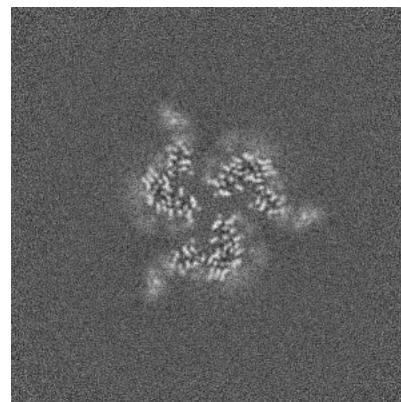
6.2.2 Raw map



X Index: 196



Y Index: 196

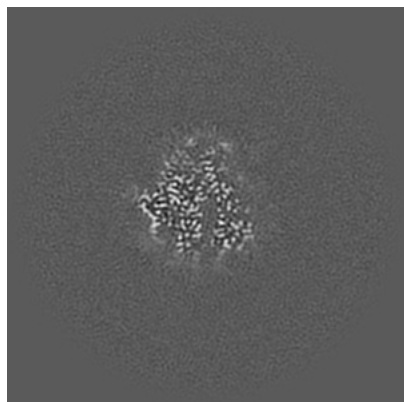


Z Index: 196

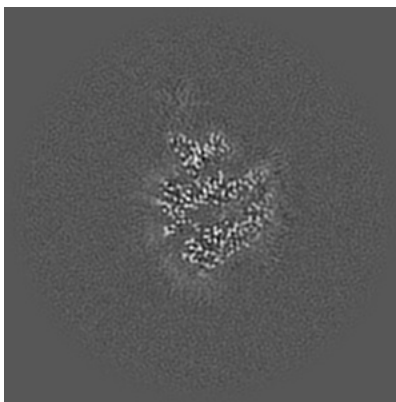
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

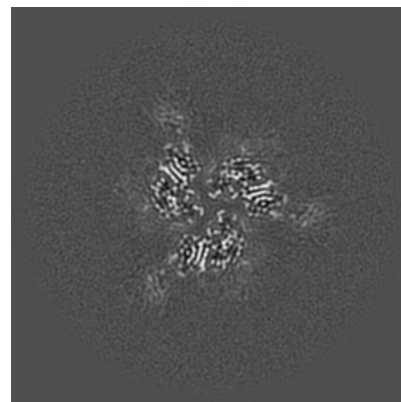
6.3.1 Primary map



X Index: 203

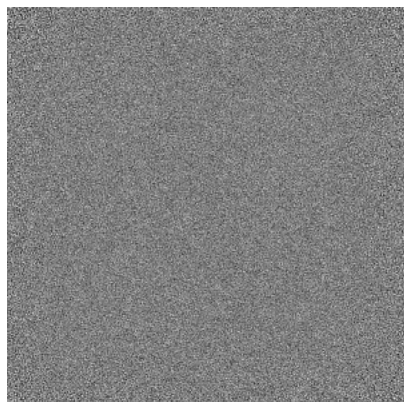


Y Index: 209

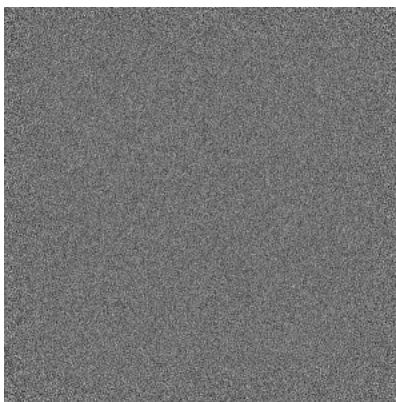


Z Index: 187

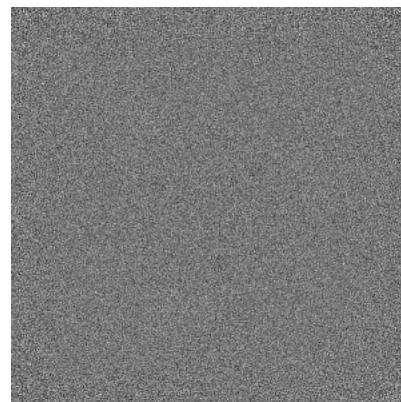
6.3.2 Raw map



X Index: 0



Y Index: 0

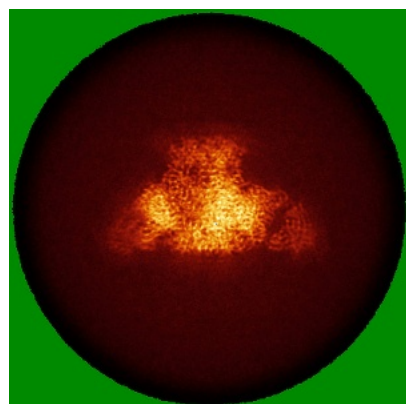


Z Index: 391

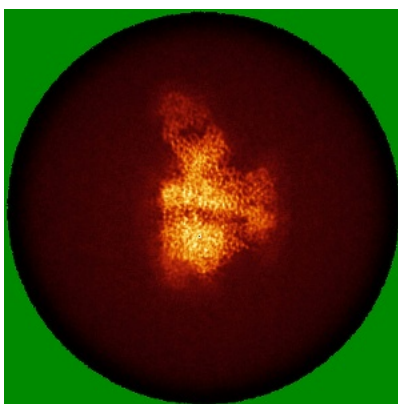
The images above show the largest variance slices of the map in three orthogonal directions.

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

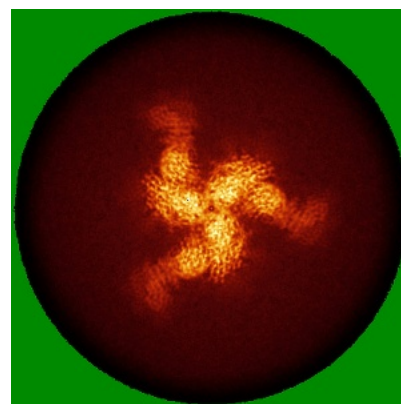
6.4.1 Primary map



X

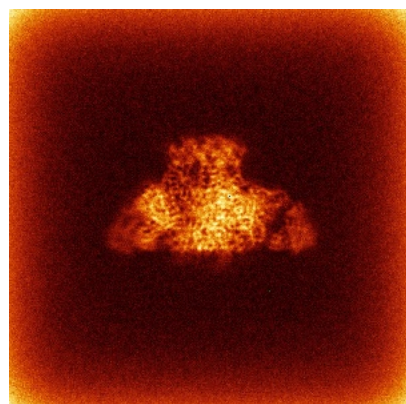


Y

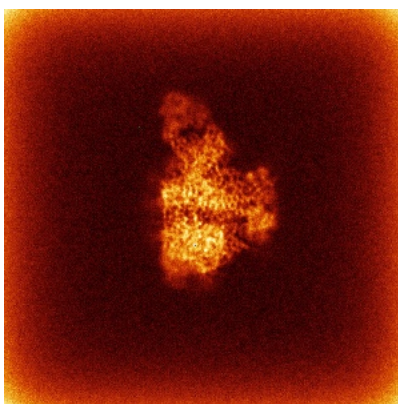


Z

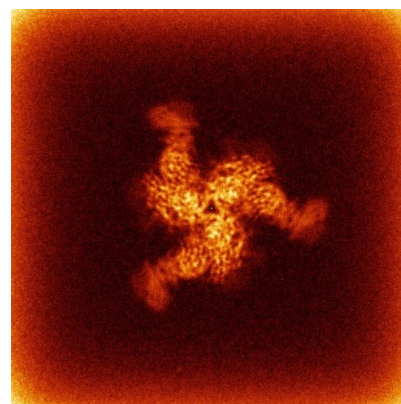
6.4.2 Raw map



X



Y

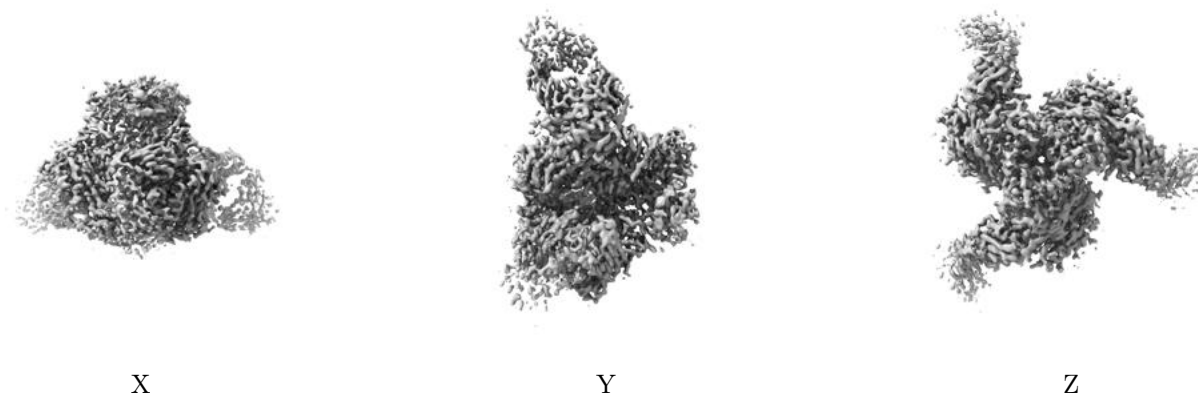


Z

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.

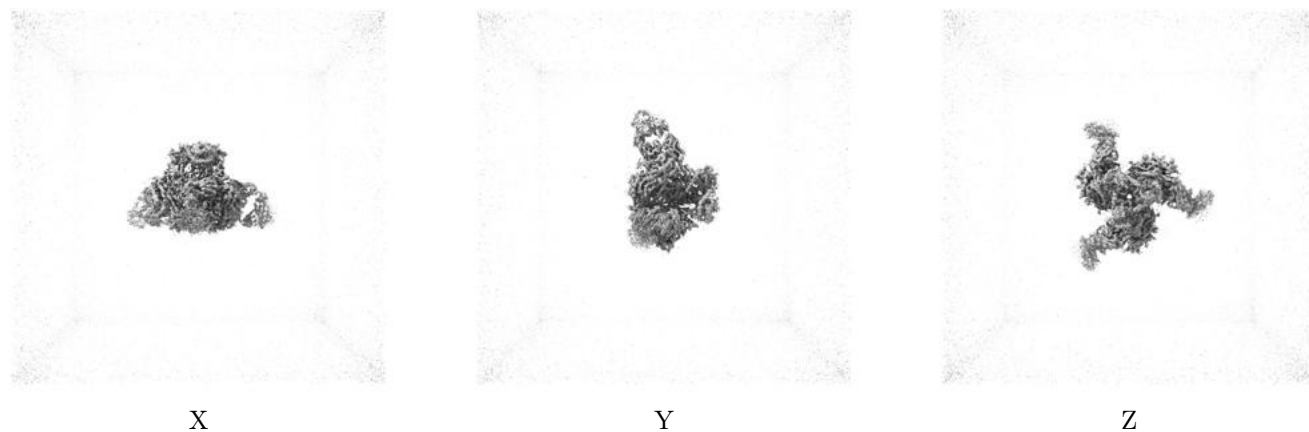
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. 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.

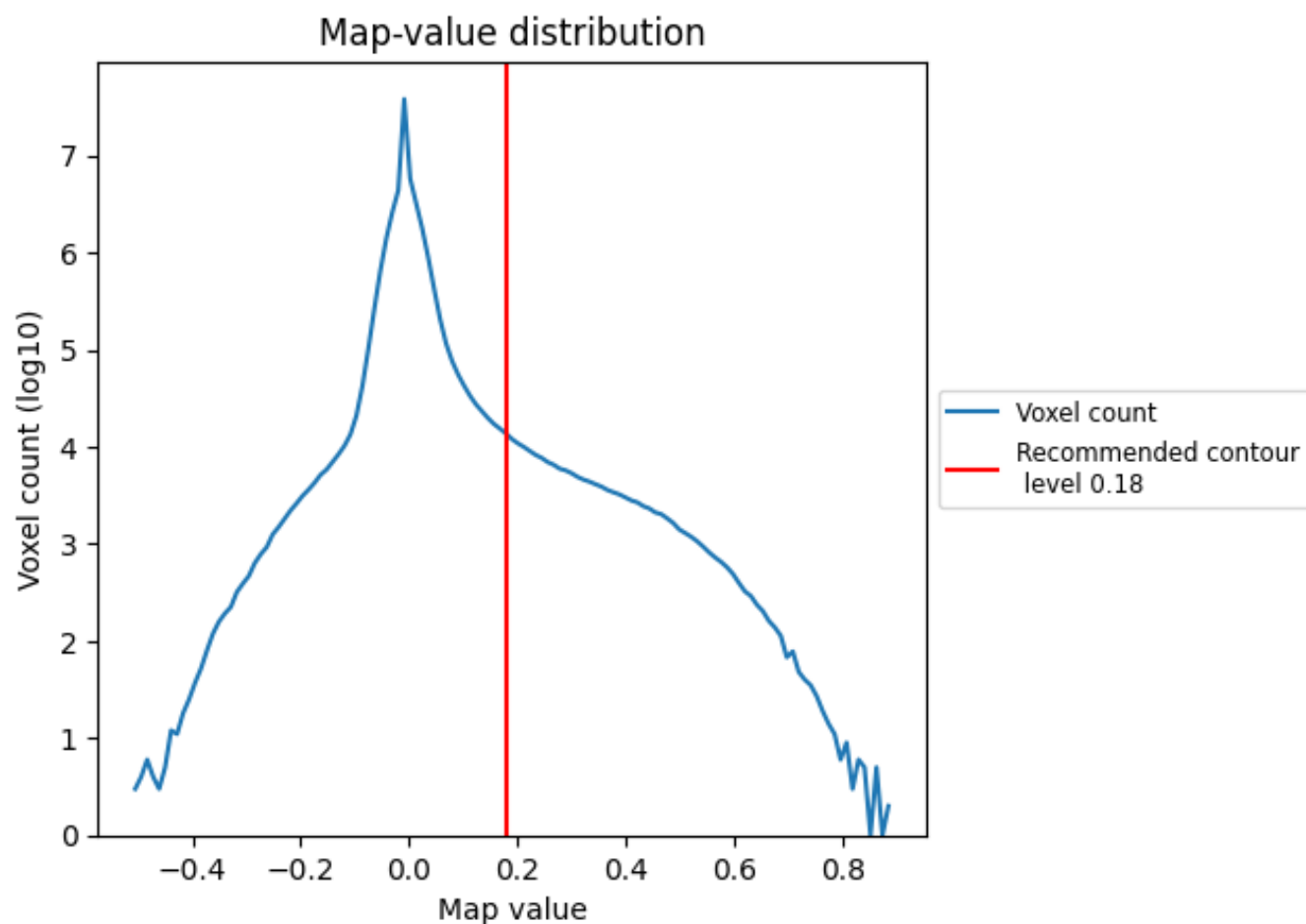
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

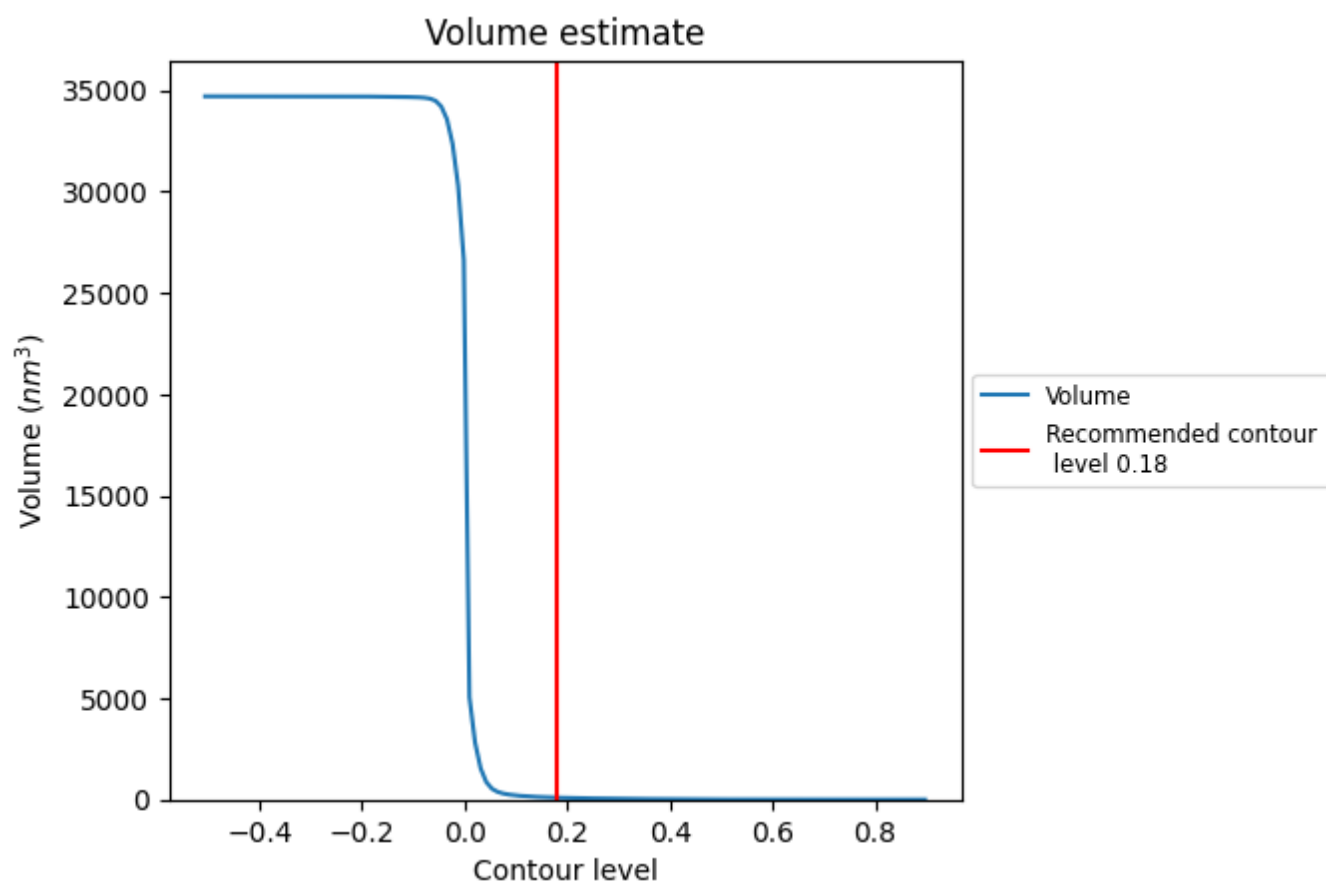
This section contains the results of statistical analysis of the map.

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.

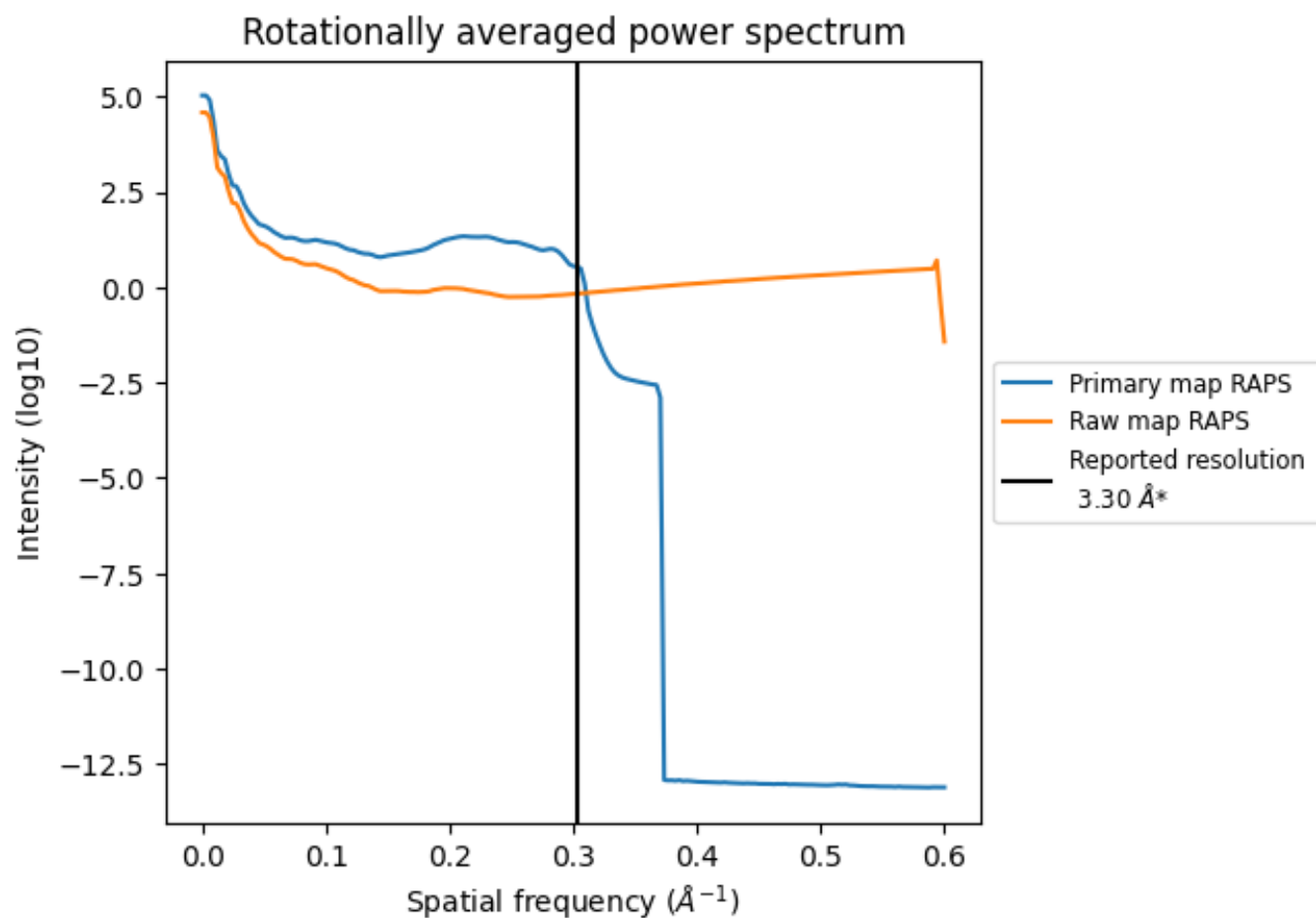
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 95 nm³; this corresponds to an approximate mass of 86 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 ⓘ

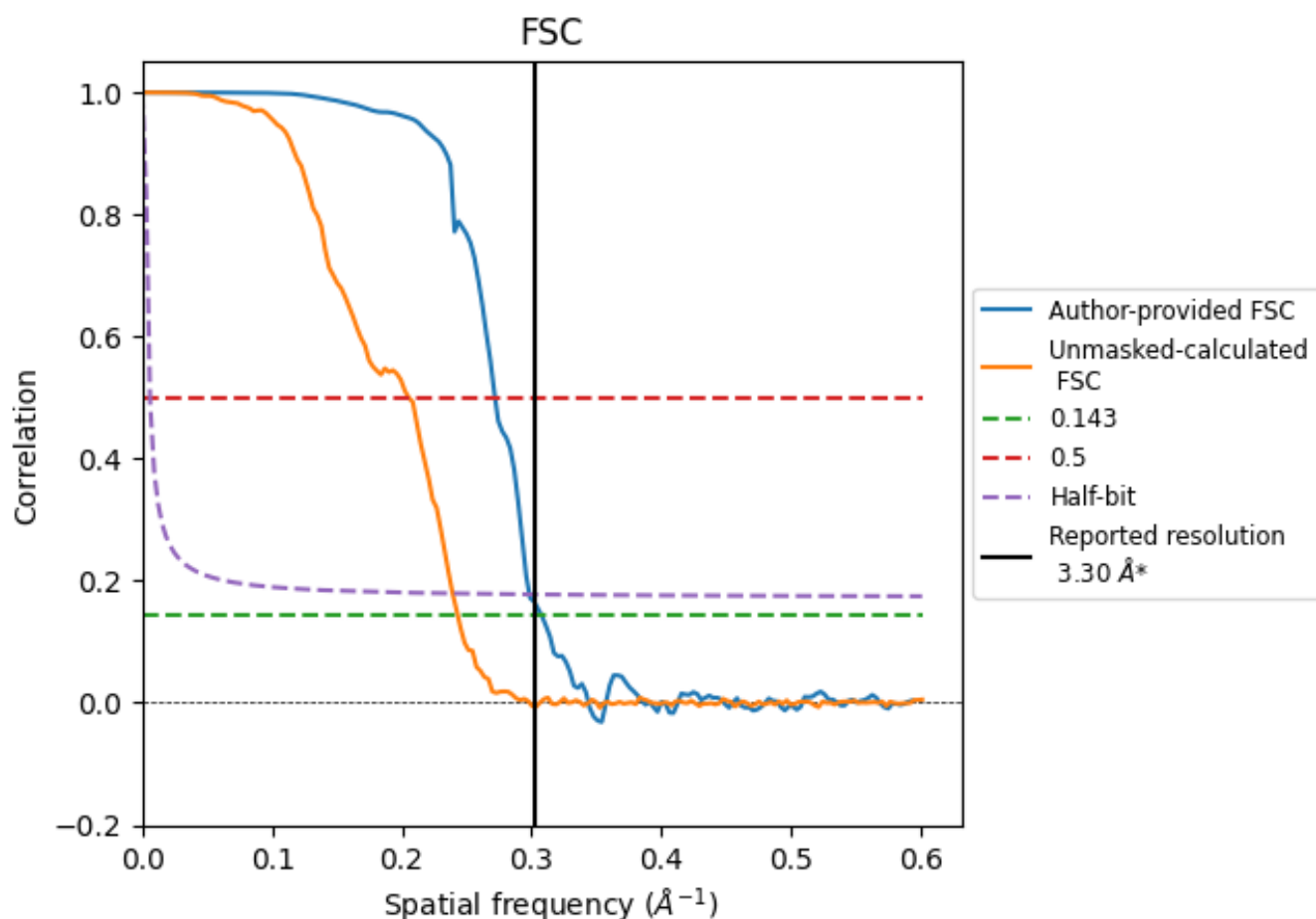


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 \AA^{-1}

8.2 Resolution estimates [i](#)

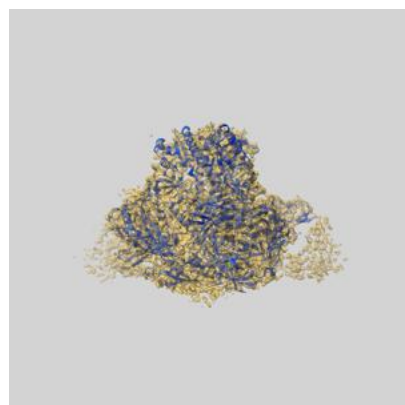
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.25	3.68	3.35
Unmasked-calculated*	4.11	4.87	4.18

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.11 differs from the reported value 3.3 by more than 10 %

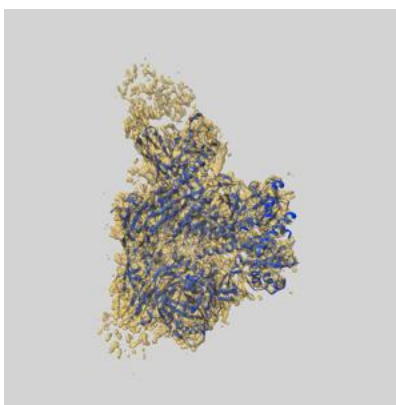
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42363 and PDB model 8ULR. Per-residue inclusion information can be found in section 3 on page 11.

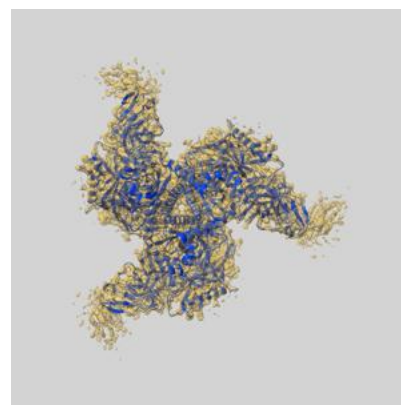
9.1 Map-model overlay [i](#)



X



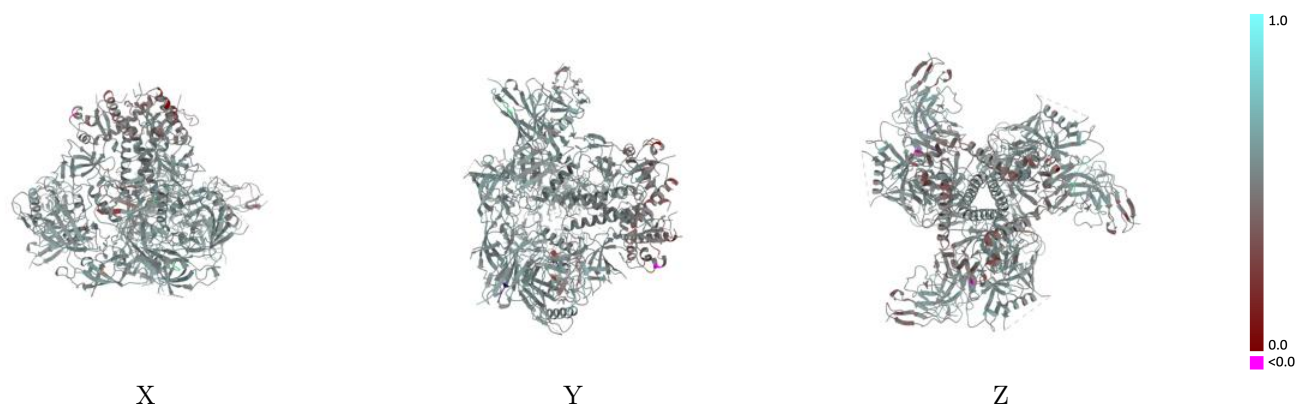
Y



Z

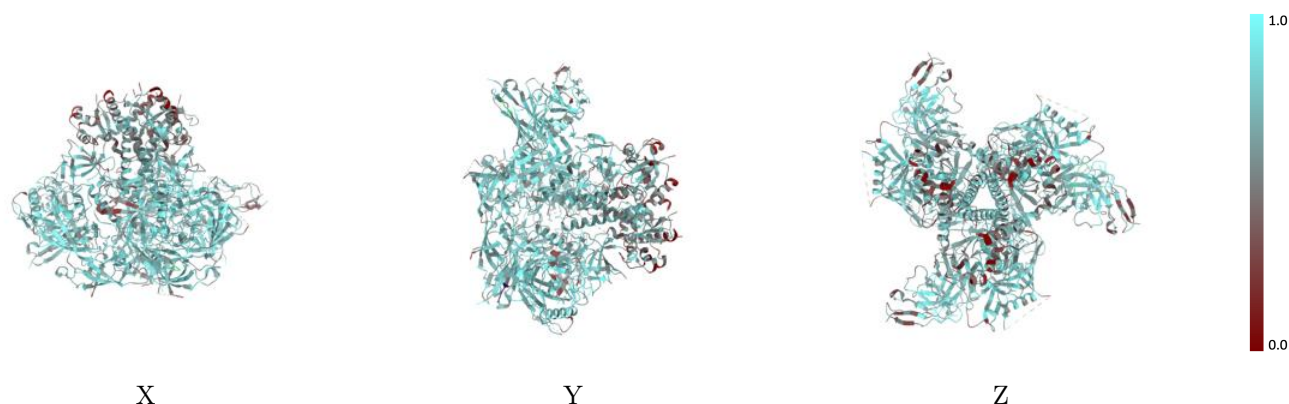
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



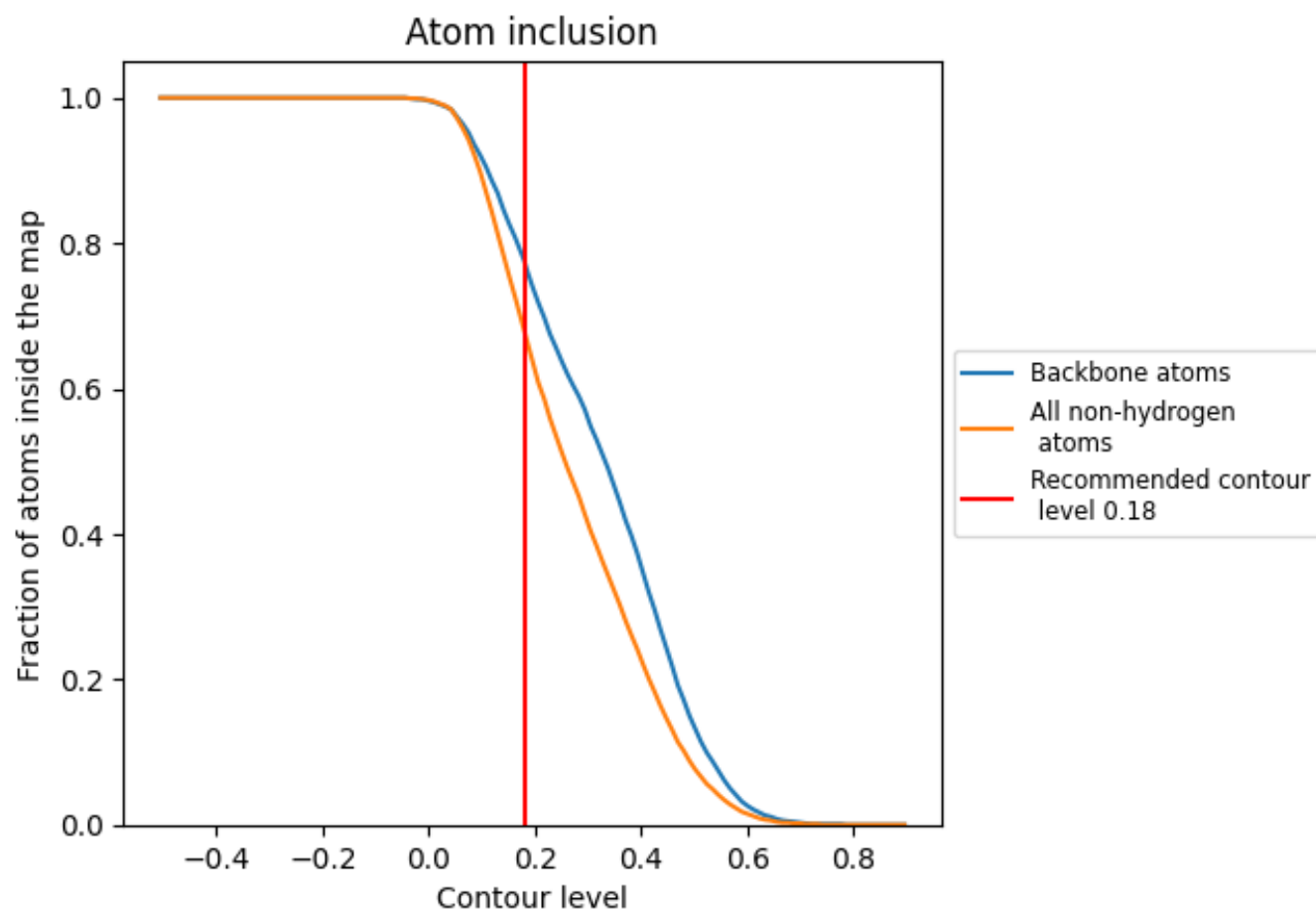
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ













The table lists the average atom inclusion at the recommended contour level (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.5220
A	 0.7210	 0.5370
B	 0.5490	 0.4680
C	 0.7190	 0.5380
D	 0.5490	 0.4710
E	 0.7210	 0.5380
F	 0.5480	 0.4660
G	 0.3930	 0.4400
H	 0.7510	 0.5480
I	 0.7470	 0.5490
J	 0.7570	 0.5470
K	 0.2860	 0.4080
L	 0.6920	 0.5080
M	 0.6920	 0.5140
N	 0.6900	 0.5100
O	 0.4100	 0.5240
P	 0.4800	 0.4810
Q	 0.5420	 0.4900
R	 0.3210	 0.5050
S	 0.5000	 0.4620
T	 0.4750	 0.4780
U	 0.6430	 0.5060
V	 0.3930	 0.4280
W	 0.2860	 0.4250
X	 0.3850	 0.5150
Y	 0.4800	 0.4770
Z	 0.5280	 0.4910
a	 0.2860	 0.4650
b	 0.4640	 0.4710
c	 0.4590	 0.4700
d	 0.6430	 0.4970
e	 0.3570	 0.4190
f	 0.2820	 0.4070
g	 0.2500	 0.4140
h	 0.3200	 0.5020



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Chain	Atom inclusion	Q-score
i	 0.4800	 0.4930
j	 0.5080	 0.4780
k	 0.2860	 0.4790
l	 0.4640	 0.4550
m	 0.4590	 0.4930
n	 0.6430	 0.4770