



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:23 PM UTC

PDB ID : 5ACO / pdb_00005aco
EMDB ID : EMD-3121
Title : Cryo-EM structure of PGT128 Fab in complex with BG505 SOSIP.664 Env trimer
Authors : Lee, J.H.; Ward, A.B.
Deposited on : 2015-08-17
Resolution : 4.36 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

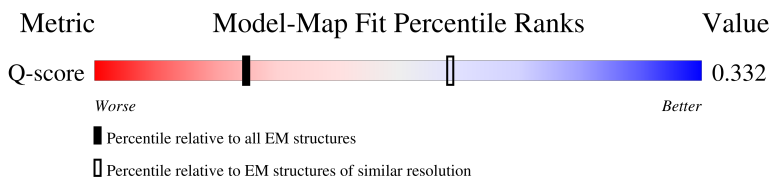
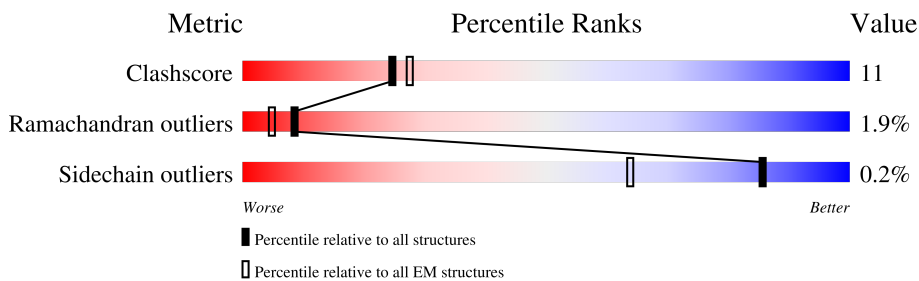
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.36 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3737 (3.87 - 4.86)

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	476	
1	C	476	
1	D	476	
2	B	153	

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Mol	Chain	Length	Quality of chain
2	E	153	
2	F	153	
3	G	239	
3	H	239	
3	I	239	
4	J	211	
4	K	211	
4	L	211	
5	0	3	
5	5	3	
5	6	3	
5	M	3	
5	O	3	
5	P	3	
5	T	3	
5	Y	3	
5	Z	3	
5	d	3	
5	f	3	
5	g	3	
5	k	3	
5	p	3	
5	q	3	
5	t	3	
5	v	3	

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Mol	Chain	Length	Quality of chain
5	w	3	67%
6	4	2	100%
6	7	2	100%
6	8	2	50%
6	9	2	100%
6	AA	2	100%
6	N	2	50%
6	Q	2	50%
6	R	2	50%
6	X	2	100%
6	a	2	100%
6	b	2	50%
6	c	2	100%
6	e	2	50%
6	h	2	50%
6	i	2	50%
6	o	2	100%
6	r	2	100%
6	s	2	50%
6	u	2	50%
6	x	2	50%
6	y	2	50%
7	2	7	29%
7	S	7	57%
7	V	7	29%

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Mol	Chain	Length	Quality of chain
7	j	7	 57% 43%
7	m	7	 29% 71% 29%
7	z	7	 57% 43%
8	1	5	 60% 100%
8	U	5	 60% 100%
8	l	5	 60% 100%
9	3	10	 10% 60% 30%
9	W	10	 10% 60% 30%
9	n	10	 20% 10% 60% 30%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	M	1	-	-	X	-
5	NAG	d	1	-	-	X	-
5	NAG	t	1	-	-	X	-
6	NAG	s	1	-	-	X	-
9	NAG	3	1	-	-	X	-
9	MAN	3	6	-	-	X	-
9	NAG	W	1	-	-	X	-
9	MAN	W	6	-	-	X	-
9	NAG	n	1	-	-	X	-
9	MAN	n	6	-	-	X	-

2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 21297 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 HIV-1 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	438	3453	2170	610	645	28	0	0
1	C	438	3453	2170	610	645	28	0	0
1	D	438	3453	2170	610	645	28	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	332	ASN	THR	engineered mutation	UNP Q2N0S6
A	501	CYS	ALA	engineered mutation	UNP Q2N0S6
C	332	ASN	THR	engineered mutation	UNP Q2N0S6
C	501	CYS	ALA	engineered mutation	UNP Q2N0S6
D	332	ASN	THR	engineered mutation	UNP Q2N0S6
D	501	CYS	ALA	engineered mutation	UNP Q2N0S6

- Molecule 2 is a protein called HIV-1 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	132	1051	667	180	198	6	0	0
2	E	132	1051	667	180	198	6	0	0
2	F	132	1051	667	180	198	6	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S6
B	605	CYS	THR	engineered mutation	UNP Q2N0S6
E	559	PRO	ILE	engineered mutation	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	605	CYS	THR	engineered mutation	UNP Q2N0S6
F	559	PRO	ILE	engineered mutation	UNP Q2N0S6
F	605	CYS	THR	engineered mutation	UNP Q2N0S6

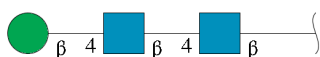
- Molecule 3 is a protein called PGT128 FAB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	132	Total	C	N	O	S	0	0
			1028	659	175	190	4		
3	H	132	Total	C	N	O	S	0	0
			1028	659	175	190	4		
3	I	132	Total	C	N	O	S	0	0
			1028	659	175	190	4		

- Molecule 4 is a protein called PGT128 FAB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	103	Total	C	N	O	S	0	0
			752	469	128	153	2		
4	K	103	Total	C	N	O	S	0	0
			752	469	128	153	2		
4	L	103	Total	C	N	O	S	0	0
			752	469	128	153	2		

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



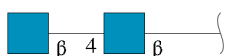
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	M	3	Total	C	N	O	0	0
			39	22	2	15		
5	O	3	Total	C	N	O	0	0
			39	22	2	15		
5	P	3	Total	C	N	O	0	0
			39	22	2	15		
5	T	3	Total	C	N	O	0	0
			39	22	2	15		
5	Y	3	Total	C	N	O	0	0
			39	22	2	15		

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	Z	3	Total 39	C 22	N 2	O 15	0	0
5	d	3	Total 39	C 22	N 2	O 15	0	0
5	f	3	Total 39	C 22	N 2	O 15	0	0
5	g	3	Total 39	C 22	N 2	O 15	0	0
5	k	3	Total 39	C 22	N 2	O 15	0	0
5	p	3	Total 39	C 22	N 2	O 15	0	0
5	q	3	Total 39	C 22	N 2	O 15	0	0
5	t	3	Total 39	C 22	N 2	O 15	0	0
5	v	3	Total 39	C 22	N 2	O 15	0	0
5	w	3	Total 39	C 22	N 2	O 15	0	0
5	0	3	Total 39	C 22	N 2	O 15	0	0
5	5	3	Total 39	C 22	N 2	O 15	0	0
5	6	3	Total 39	C 22	N 2	O 15	0	0

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



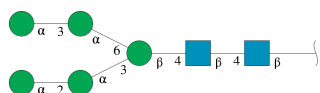
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	N	2	Total 28	C 16	N 2	O 10	0	0
6	Q	2	Total 28	C 16	N 2	O 10	0	0
6	R	2	Total 28	C 16	N 2	O 10	0	0
6	X	2	Total 28	C 16	N 2	O 10	0	0

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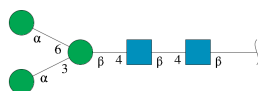
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	a	2	28	16	2	10	0	0
6	b	2	28	16	2	10	0	0
6	c	2	28	16	2	10	0	0
6	e	2	28	16	2	10	0	0
6	h	2	28	16	2	10	0	0
6	i	2	28	16	2	10	0	0
6	o	2	28	16	2	10	0	0
6	r	2	28	16	2	10	0	0
6	s	2	28	16	2	10	0	0
6	u	2	28	16	2	10	0	0
6	x	2	28	16	2	10	0	0
6	y	2	28	16	2	10	0	0
6	4	2	28	16	2	10	0	0
6	7	2	28	16	2	10	0	0
6	8	2	28	16	2	10	0	0
6	9	2	28	16	2	10	0	0
6	AA	2	28	16	2	10	0	0

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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.



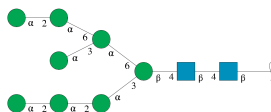
Mol	Chain	Residues	Atoms				AltConf	Trace
7	S	7	Total	C	N	O	0	0
			83	46	2	35		
7	V	7	Total	C	N	O	0	0
			83	46	2	35		
7	j	7	Total	C	N	O	0	0
			83	46	2	35		
7	m	7	Total	C	N	O	0	0
			83	46	2	35		
7	z	7	Total	C	N	O	0	0
			83	46	2	35		
7	2	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 8 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
8	U	5	Total	C	N	O	0	0
			61	34	2	25		
8	1	5	Total	C	N	O	0	0
			61	34	2	25		
8	1	5	Total	C	N	O	0	0
			61	34	2	25		

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



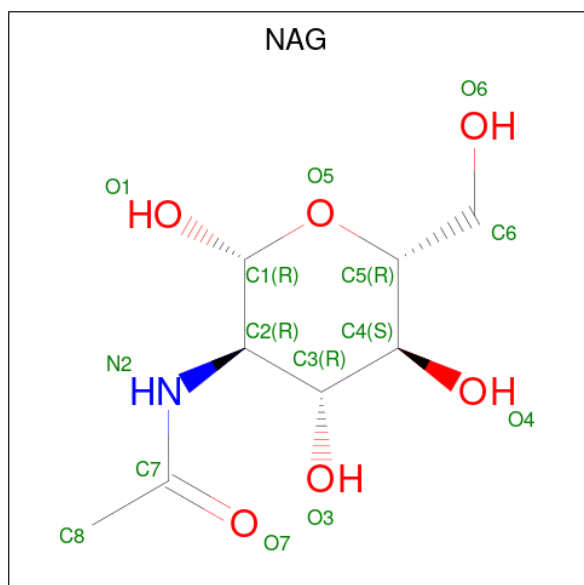
Mol	Chain	Residues	Atoms				AltConf	Trace
9	W	10	Total	C	N	O	0	0
			116	64	2	50		

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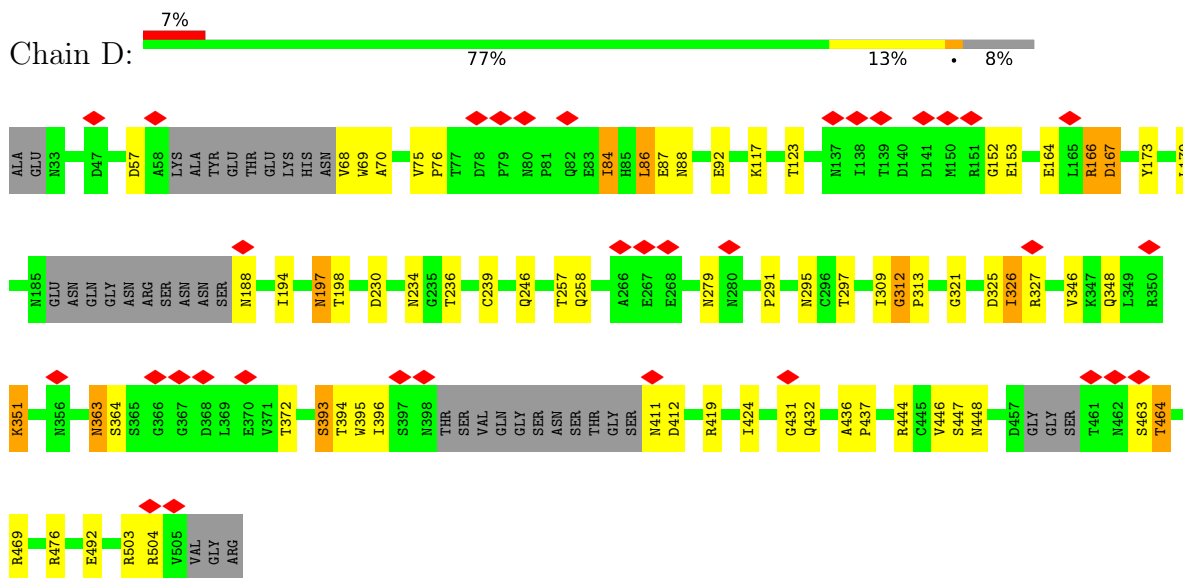
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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	n	10	116	64	2	50	0	0
9	3	10	116	64	2	50	0	0

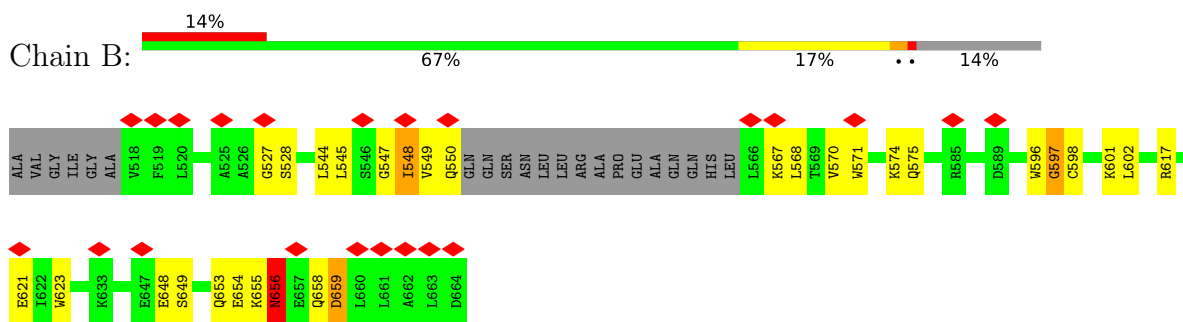
- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



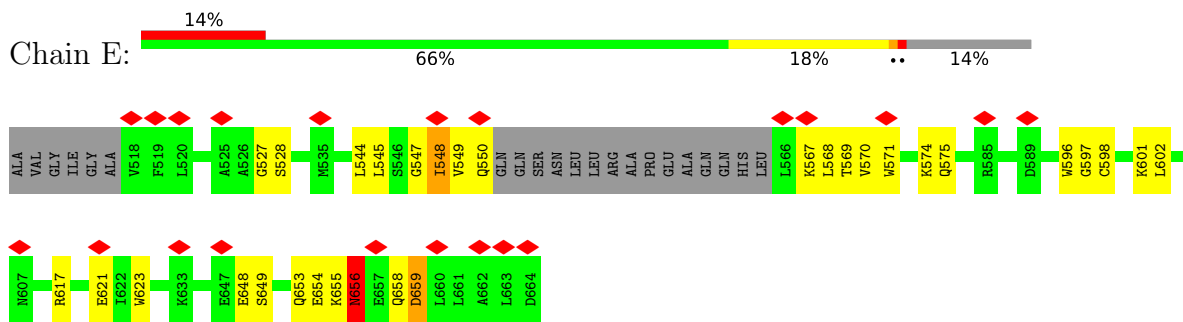
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
10	A	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	B	1	14	8	1	5	0
10	C	1	14	8	1	5	0
10	D	1	14	8	1	5	0
10	E	1	14	8	1	5	0
10	E	1	14	8	1	5	0
10	F	1	14	8	1	5	0
10	F	1	14	8	1	5	0



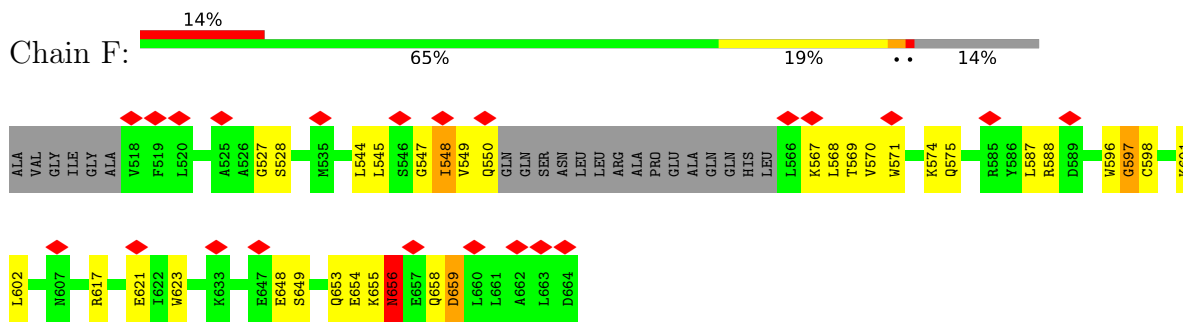
• Molecule 2: HIV-1 ENVELOPE GLYCOPROTEIN

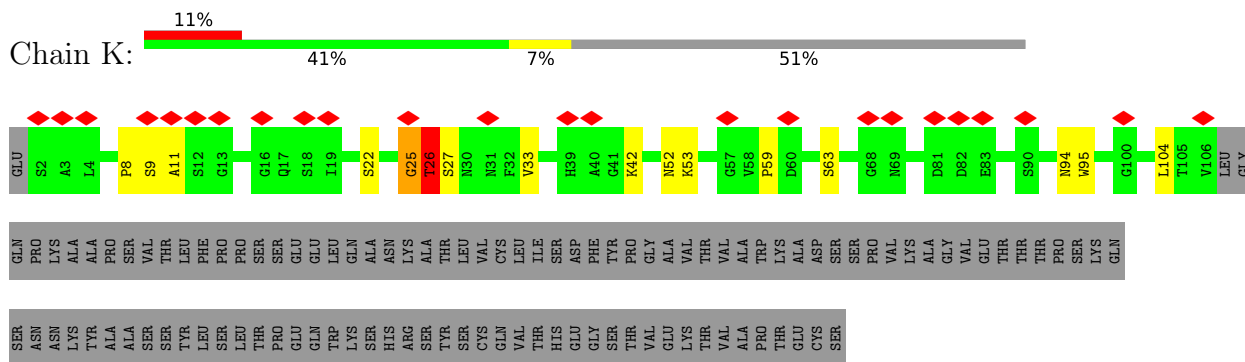


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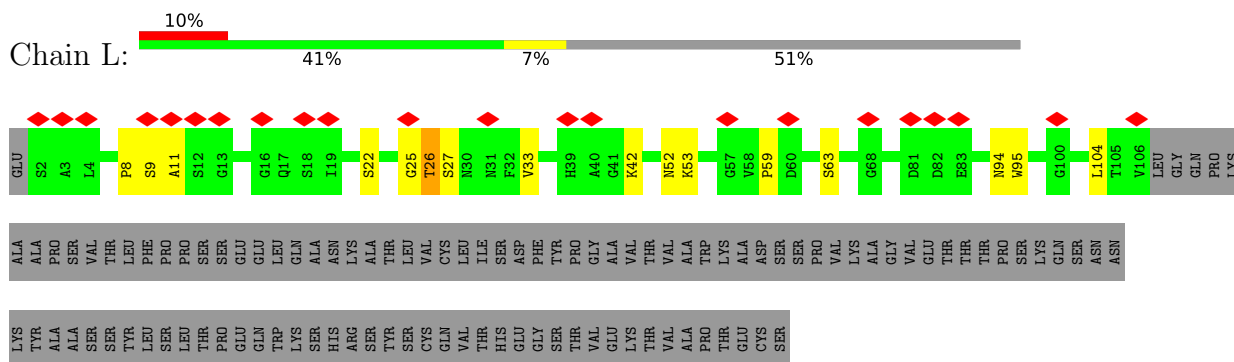


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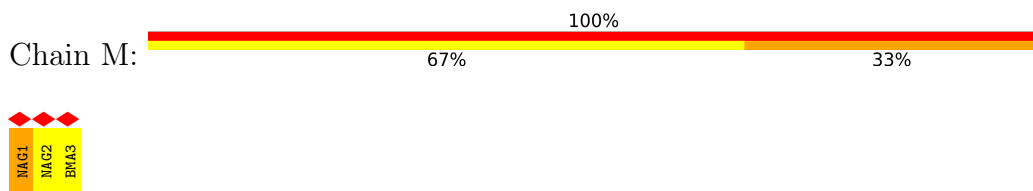




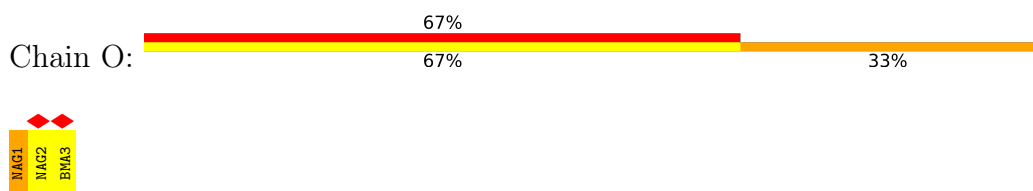
• Molecule 4: PGT128 FAB



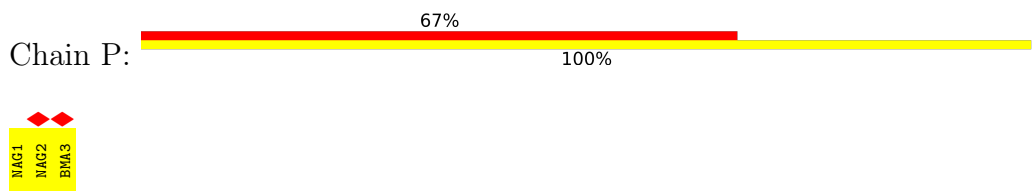
• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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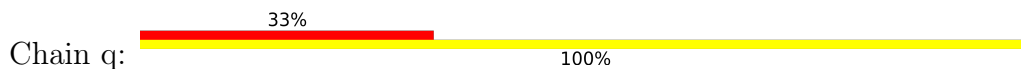
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- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



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



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



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



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



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



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



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



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



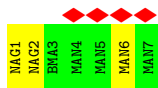
- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



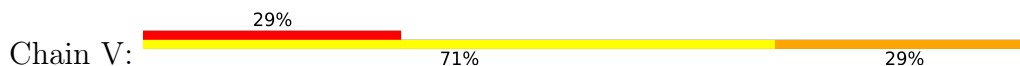
- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



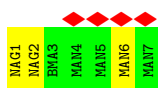
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



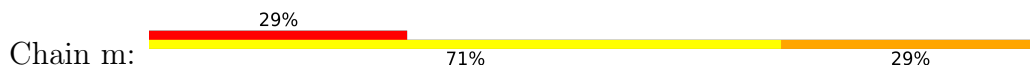
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



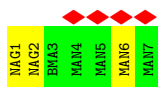
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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-(1-3)-[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-(1-3)-[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

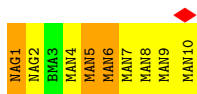
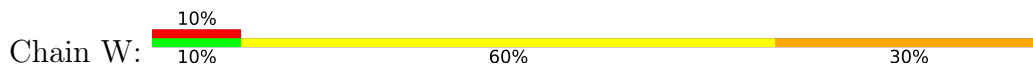


- Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

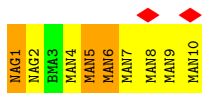
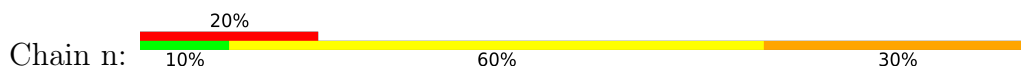




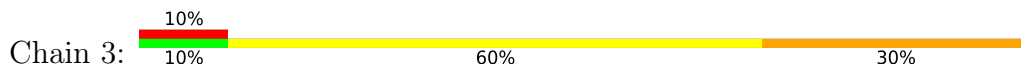
- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	92095	Depositor
Resolution determination method	Not provided	
CTF correction method	WHOLE MICROGRAPH	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.144	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.041	Depositor
Map size (\AA)	335.36, 335.36, 335.36	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.31, 1.31, 1.31	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, 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	0.69	10/3523 (0.3%)	1.12	34/4783 (0.7%)
1	C	0.69	10/3523 (0.3%)	1.12	35/4783 (0.7%)
1	D	0.69	10/3523 (0.3%)	1.12	35/4783 (0.7%)
2	B	0.83	1/1069 (0.1%)	1.21	14/1448 (1.0%)
2	E	0.83	1/1069 (0.1%)	1.21	14/1448 (1.0%)
2	F	0.83	1/1069 (0.1%)	1.20	14/1448 (1.0%)
3	G	0.86	0/1061	1.14	2/1455 (0.1%)
3	H	0.86	0/1061	1.14	2/1455 (0.1%)
3	I	0.85	0/1061	1.13	2/1455 (0.1%)
4	J	1.22	4/769 (0.5%)	1.47	17/1048 (1.6%)
4	K	1.22	4/769 (0.5%)	1.47	17/1048 (1.6%)
4	L	1.22	3/769 (0.4%)	1.47	17/1048 (1.6%)
All	All	0.82	44/19266 (0.2%)	1.18	203/26202 (0.8%)

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	A	0	1
1	C	0	1
1	D	0	1
All	All	0	3

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	8	PRO	C-N	20.61	1.58	1.33
4	J	8	PRO	C-N	20.58	1.58	1.33
4	K	8	PRO	C-N	20.58	1.58	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	658	GLN	C-N	20.45	1.61	1.33
2	B	658	GLN	C-N	20.45	1.61	1.33

The worst 5 of 203 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	648	GLU	N-CA-C	18.04	149.23	110.80
2	B	648	GLU	N-CA-C	18.04	149.22	110.80
2	F	648	GLU	N-CA-C	18.02	149.18	110.80
1	D	86	LEU	O-C-N	-16.57	102.49	122.87
1	A	86	LEU	O-C-N	-16.57	102.49	122.87

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	86	LEU	Mainchain
1	C	86	LEU	Mainchain
1	D	86	LEU	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3453	0	3390	75	0
1	C	3453	0	3390	80	0
1	D	3453	0	3390	76	0
2	B	1051	0	1037	35	0
2	E	1051	0	1037	34	0
2	F	1051	0	1037	36	0
3	G	1028	0	990	28	0
3	H	1028	0	990	25	0
3	I	1028	0	990	28	0
4	J	752	0	724	10	0
4	K	752	0	724	9	0
4	L	752	0	724	7	0
5	0	39	0	34	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	5	39	0	34	1	0
5	6	39	0	34	0	0
5	M	39	0	34	8	0
5	O	39	0	34	1	0
5	P	39	0	34	0	0
5	T	39	0	34	5	0
5	Y	39	0	34	1	0
5	Z	39	0	34	0	0
5	d	39	0	34	8	0
5	f	39	0	34	1	0
5	g	39	0	34	0	0
5	k	39	0	34	5	0
5	p	39	0	34	1	0
5	q	39	0	34	0	0
5	t	39	0	34	8	0
5	v	39	0	34	1	0
5	w	39	0	34	0	0
6	4	28	0	25	0	0
6	7	28	0	25	0	0
6	8	28	0	25	6	0
6	9	28	0	25	0	0
6	AA	28	0	25	0	0
6	N	28	0	25	0	0
6	Q	28	0	25	3	0
6	R	28	0	25	1	0
6	X	28	0	25	0	0
6	a	28	0	25	0	0
6	b	28	0	25	6	0
6	c	28	0	25	0	0
6	e	28	0	25	0	0
6	h	28	0	25	3	0
6	i	28	0	25	1	0
6	o	28	0	25	0	0
6	r	28	0	25	0	0
6	s	28	0	25	7	0
6	u	28	0	25	0	0
6	x	28	0	25	3	0
6	y	28	0	25	1	0
7	2	83	0	70	2	0
7	S	83	0	70	2	0
7	V	83	0	70	2	0
7	j	83	0	70	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	m	83	0	70	2	0
7	z	83	0	70	2	0
8	1	61	0	52	0	0
8	U	61	0	52	0	0
8	l	61	0	52	0	0
9	3	116	0	97	41	0
9	W	116	0	97	37	0
9	n	116	0	97	42	0
10	A	14	0	13	0	0
10	B	28	0	26	1	0
10	C	14	0	13	0	0
10	D	14	0	13	0	0
10	E	28	0	26	1	0
10	F	28	0	26	1	0
All	All	21297	0	20544	443	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 11.

The worst 5 of 443 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)
2:B:528:SER:HB3	5:M:1:NAG:H81	1.24	1.15
2:F:528:SER:HB3	5:t:1:NAG:H81	1.25	1.14
1:A:194:ILE:HD11	6:Q:1:NAG:O6	1.48	1.14
1:D:194:ILE:HD11	6:x:1:NAG:O6	1.48	1.14
2:E:528:SER:HB3	5:d:1:NAG:H81	1.24	1.10

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	428/476 (90%)	386 (90%)	33 (8%)	9 (2%)	5	30
1	C	428/476 (90%)	386 (90%)	33 (8%)	9 (2%)	5	30
1	D	428/476 (90%)	386 (90%)	33 (8%)	9 (2%)	5	30
2	B	128/153 (84%)	102 (80%)	22 (17%)	4 (3%)	3	22
2	E	128/153 (84%)	102 (80%)	22 (17%)	4 (3%)	3	22
2	F	128/153 (84%)	102 (80%)	22 (17%)	4 (3%)	3	22
3	G	130/239 (54%)	121 (93%)	9 (7%)	0	100	100
3	H	130/239 (54%)	121 (93%)	9 (7%)	0	100	100
3	I	130/239 (54%)	121 (93%)	9 (7%)	0	100	100
4	J	101/211 (48%)	91 (90%)	8 (8%)	2 (2%)	6	31
4	K	101/211 (48%)	91 (90%)	8 (8%)	2 (2%)	6	31
4	L	101/211 (48%)	91 (90%)	8 (8%)	2 (2%)	6	31
All	All	2361/3237 (73%)	2100 (89%)	216 (9%)	45 (2%)	8	32

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	ASP
1	A	396	ILE
1	C	167	ASP
1	C	396	ILE
1	D	167	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	5/423 (1%)	5 (100%)	0	100	100
1	C	393/423 (93%)	391 (100%)	2 (0%)	81	81
1	D	393/423 (93%)	391 (100%)	2 (0%)	81	81
2	B	95/129 (74%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	114/129 (88%)	114 (100%)	0	100	100
2	F	114/129 (88%)	114 (100%)	0	100	100
3	G	110/203 (54%)	110 (100%)	0	100	100
3	H	110/203 (54%)	110 (100%)	0	100	100
3	I	110/203 (54%)	110 (100%)	0	100	100
4	J	84/177 (48%)	84 (100%)	0	100	100
4	K	84/177 (48%)	84 (100%)	0	100	100
4	L	84/177 (48%)	84 (100%)	0	100	100
All	All	1696/2796 (61%)	1692 (100%)	4 (0%)	85	85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	197	ASN
1	C	363	ASN
1	D	197	ASN
1	D	363	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	59	HIS
3	I	59	HIS
4	L	94	ASN
4	K	37	GLN
4	L	37	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates i

183 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	0	1	5,1	14,14,15	0.49	0	17,19,21	2.28	3 (17%)
5	NAG	0	2	5	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
5	BMA	0	3	5	11,11,12	0.62	0	15,15,17	1.43	3 (20%)
8	NAG	1	1	8,1	14,14,15	0.48	0	17,19,21	2.28	3 (17%)
8	NAG	1	2	8	14,14,15	0.50	0	17,19,21	1.33	3 (17%)
8	BMA	1	3	8	11,11,12	0.63	0	15,15,17	1.42	3 (20%)
8	MAN	1	4	8	11,11,12	0.54	0	15,15,17	1.50	3 (20%)
8	MAN	1	5	8	11,11,12	0.61	0	15,15,17	2.21	3 (20%)
7	NAG	2	1	1,7	14,14,15	0.32	0	17,19,21	0.91	1 (5%)
7	NAG	2	2	7	14,14,15	0.33	0	17,19,21	2.56	4 (23%)
7	BMA	2	3	7	11,11,12	0.43	0	15,15,17	1.16	2 (13%)
7	MAN	2	4	7	11,11,12	0.44	0	15,15,17	0.88	1 (6%)
7	MAN	2	5	7	11,11,12	0.42	0	15,15,17	0.81	1 (6%)
7	MAN	2	6	7	11,11,12	0.47	0	15,15,17	0.77	1 (6%)
7	MAN	2	7	7	11,11,12	0.34	0	15,15,17	1.21	1 (6%)
9	NAG	3	1	9,1	14,14,15	0.33	0	17,19,21	0.91	1 (5%)
9	MAN	3	10	9	11,11,12	0.33	0	15,15,17	0.87	1 (6%)
9	NAG	3	2	9	14,14,15	0.35	0	17,19,21	0.92	1 (5%)
9	BMA	3	3	9	11,11,12	0.41	0	15,15,17	0.58	0
9	MAN	3	4	9	11,11,12	0.42	0	15,15,17	1.08	1 (6%)
9	MAN	3	5	9	11,11,12	0.45	0	15,15,17	1.03	2 (13%)
9	MAN	3	6	9	11,11,12	0.47	0	15,15,17	1.06	1 (6%)
9	MAN	3	7	9	11,11,12	0.28	0	15,15,17	1.11	1 (6%)
9	MAN	3	8	9	11,11,12	0.38	0	15,15,17	1.26	1 (6%)
9	MAN	3	9	9	11,11,12	0.34	0	15,15,17	0.71	0
6	NAG	4	1	1,6	14,14,15	0.51	0	17,19,21	2.28	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	4	2	6	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
5	NAG	5	1	5,1	14,14,15	0.49	0	17,19,21	2.28	3 (17%)
5	NAG	5	2	5	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
5	BMA	5	3	5	11,11,12	0.64	0	15,15,17	1.43	3 (20%)
5	NAG	6	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	6	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	6	3	5	11,11,12	0.65	0	15,15,17	1.43	3 (20%)
6	NAG	7	1	1,6	14,14,15	0.51	0	17,19,21	2.27	3 (17%)
6	NAG	7	2	6	14,14,15	0.52	0	17,19,21	1.33	3 (17%)
6	NAG	8	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	8	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
6	NAG	9	1	2,6	14,14,15	0.52	0	17,19,21	2.27	3 (17%)
6	NAG	9	2	6	14,14,15	0.52	0	17,19,21	1.33	3 (17%)
6	NAG	AA	1	2,6	14,14,15	0.51	0	17,19,21	2.27	3 (17%)
6	NAG	AA	2	6	14,14,15	0.52	0	17,19,21	1.32	3 (17%)
5	NAG	M	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	M	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	M	3	5	11,11,12	0.63	0	15,15,17	1.43	3 (20%)
6	NAG	N	1	1,6	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
6	NAG	N	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	NAG	O	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	O	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	O	3	5	11,11,12	0.64	0	15,15,17	1.42	3 (20%)
5	NAG	P	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	P	2	5	14,14,15	0.51	0	17,19,21	1.31	3 (17%)
5	BMA	P	3	5	11,11,12	0.65	0	15,15,17	1.43	3 (20%)
6	NAG	Q	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	Q	2	6	14,14,15	0.52	0	17,19,21	1.32	3 (17%)
6	NAG	R	1	1,6	14,14,15	0.51	0	17,19,21	2.27	3 (17%)
6	NAG	R	2	6	14,14,15	0.50	0	17,19,21	1.33	3 (17%)
7	NAG	S	1	1,7	14,14,15	0.58	0	17,19,21	0.67	0
7	NAG	S	2	7	14,14,15	0.56	0	17,19,21	0.86	0
7	BMA	S	3	7	11,11,12	0.64	0	15,15,17	0.72	0
7	MAN	S	4	7	11,11,12	0.60	0	15,15,17	0.56	0
7	MAN	S	5	7	11,11,12	0.52	0	15,15,17	0.65	0
7	MAN	S	6	7	11,11,12	0.64	0	15,15,17	0.93	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MAN	S	7	7	11,11,12	0.60	0	15,15,17	0.53	0
5	NAG	T	1	5,1	14,14,15	0.49	0	17,19,21	2.27	3 (17%)
5	NAG	T	2	5	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
5	BMA	T	3	5	11,11,12	0.63	0	15,15,17	1.43	3 (20%)
8	NAG	U	1	8,1	14,14,15	0.49	0	17,19,21	2.27	3 (17%)
8	NAG	U	2	8	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
8	BMA	U	3	8	11,11,12	0.64	0	15,15,17	1.42	3 (20%)
8	MAN	U	4	8	11,11,12	0.54	0	15,15,17	1.50	3 (20%)
8	MAN	U	5	8	11,11,12	0.61	0	15,15,17	2.21	3 (20%)
7	NAG	V	1	1,7	14,14,15	0.32	0	17,19,21	0.91	1 (5%)
7	NAG	V	2	7	14,14,15	0.33	0	17,19,21	2.56	4 (23%)
7	BMA	V	3	7	11,11,12	0.42	0	15,15,17	1.17	2 (13%)
7	MAN	V	4	7	11,11,12	0.44	0	15,15,17	0.88	1 (6%)
7	MAN	V	5	7	11,11,12	0.43	0	15,15,17	0.80	1 (6%)
7	MAN	V	6	7	11,11,12	0.47	0	15,15,17	0.78	1 (6%)
7	MAN	V	7	7	11,11,12	0.34	0	15,15,17	1.21	1 (6%)
9	NAG	W	1	9,1	14,14,15	0.32	0	17,19,21	0.91	1 (5%)
9	MAN	W	10	9	11,11,12	0.33	0	15,15,17	0.88	1 (6%)
9	NAG	W	2	9	14,14,15	0.34	0	17,19,21	0.92	1 (5%)
9	BMA	W	3	9	11,11,12	0.40	0	15,15,17	0.58	0
9	MAN	W	4	9	11,11,12	0.42	0	15,15,17	1.08	1 (6%)
9	MAN	W	5	9	11,11,12	0.45	0	15,15,17	1.03	2 (13%)
9	MAN	W	6	9	11,11,12	0.47	0	15,15,17	1.06	1 (6%)
9	MAN	W	7	9	11,11,12	0.28	0	15,15,17	1.11	1 (6%)
9	MAN	W	8	9	11,11,12	0.38	0	15,15,17	1.26	1 (6%)
9	MAN	W	9	9	11,11,12	0.33	0	15,15,17	0.71	0
6	NAG	X	1	1,6	14,14,15	0.51	0	17,19,21	2.27	3 (17%)
6	NAG	X	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	NAG	Y	1	5,1	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
5	NAG	Y	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	Y	3	5	11,11,12	0.64	0	15,15,17	1.43	3 (20%)
5	NAG	Z	1	5,1	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
5	NAG	Z	2	5	14,14,15	0.50	0	17,19,21	1.33	3 (17%)
5	BMA	Z	3	5	11,11,12	0.64	0	15,15,17	1.43	3 (20%)
6	NAG	a	1	1,6	14,14,15	0.50	0	17,19,21	2.27	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	a	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
6	NAG	b	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	b	2	6	14,14,15	0.52	0	17,19,21	1.33	3 (17%)
6	NAG	c	1	2,6	14,14,15	0.51	0	17,19,21	2.27	3 (17%)
6	NAG	c	2	6	14,14,15	0.52	0	17,19,21	1.33	3 (17%)
5	NAG	d	1	5,1	14,14,15	0.49	0	17,19,21	2.27	3 (17%)
5	NAG	d	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	d	3	5	11,11,12	0.63	0	15,15,17	1.43	3 (20%)
6	NAG	e	1	1,6	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
6	NAG	e	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	NAG	f	1	5,1	14,14,15	0.51	0	17,19,21	2.28	3 (17%)
5	NAG	f	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	f	3	5	11,11,12	0.63	0	15,15,17	1.42	3 (20%)
5	NAG	g	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	g	2	5	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
5	BMA	g	3	5	11,11,12	0.64	0	15,15,17	1.42	3 (20%)
6	NAG	h	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	h	2	6	14,14,15	0.54	0	17,19,21	1.32	3 (17%)
6	NAG	i	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	i	2	6	14,14,15	0.49	0	17,19,21	1.33	3 (17%)
7	NAG	j	1	1,7	14,14,15	0.58	0	17,19,21	0.67	0
7	NAG	j	2	7	14,14,15	0.55	0	17,19,21	0.86	0
7	BMA	j	3	7	11,11,12	0.64	0	15,15,17	0.72	0
7	MAN	j	4	7	11,11,12	0.60	0	15,15,17	0.56	0
7	MAN	j	5	7	11,11,12	0.52	0	15,15,17	0.64	0
7	MAN	j	6	7	11,11,12	0.64	0	15,15,17	0.93	2 (13%)
7	MAN	j	7	7	11,11,12	0.61	0	15,15,17	0.54	0
5	NAG	k	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	k	2	5	14,14,15	0.50	0	17,19,21	1.33	3 (17%)
5	BMA	k	3	5	11,11,12	0.63	0	15,15,17	1.42	3 (20%)
8	NAG	l	1	8,1	14,14,15	0.49	0	17,19,21	2.27	3 (17%)
8	NAG	l	2	8	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
8	BMA	l	3	8	11,11,12	0.64	0	15,15,17	1.42	3 (20%)
8	MAN	l	4	8	11,11,12	0.54	0	15,15,17	1.50	3 (20%)
8	MAN	l	5	8	11,11,12	0.63	0	15,15,17	2.21	3 (20%)
7	NAG	m	1	1,7	14,14,15	0.32	0	17,19,21	0.91	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	m	2	7	14,14,15	0.33	0	17,19,21	2.56	4 (23%)
7	BMA	m	3	7	11,11,12	0.43	0	15,15,17	1.16	2 (13%)
7	MAN	m	4	7	11,11,12	0.43	0	15,15,17	0.88	1 (6%)
7	MAN	m	5	7	11,11,12	0.44	0	15,15,17	0.79	1 (6%)
7	MAN	m	6	7	11,11,12	0.47	0	15,15,17	0.78	1 (6%)
7	MAN	m	7	7	11,11,12	0.33	0	15,15,17	1.21	1 (6%)
9	NAG	n	1	9,1	14,14,15	0.33	0	17,19,21	0.92	1 (5%)
9	MAN	n	10	9	11,11,12	0.32	0	15,15,17	0.88	1 (6%)
9	NAG	n	2	9	14,14,15	0.34	0	17,19,21	0.91	1 (5%)
9	BMA	n	3	9	11,11,12	0.40	0	15,15,17	0.58	0
9	MAN	n	4	9	11,11,12	0.43	0	15,15,17	1.08	1 (6%)
9	MAN	n	5	9	11,11,12	0.45	0	15,15,17	1.03	2 (13%)
9	MAN	n	6	9	11,11,12	0.47	0	15,15,17	1.06	1 (6%)
9	MAN	n	7	9	11,11,12	0.29	0	15,15,17	1.11	1 (6%)
9	MAN	n	8	9	11,11,12	0.38	0	15,15,17	1.26	1 (6%)
9	MAN	n	9	9	11,11,12	0.33	0	15,15,17	0.72	0
6	NAG	o	1	1,6	14,14,15	0.51	0	17,19,21	2.28	3 (17%)
6	NAG	o	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	NAG	p	1	5,1	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
5	NAG	p	2	5	14,14,15	0.52	0	17,19,21	1.33	3 (17%)
5	BMA	p	3	5	11,11,12	0.64	0	15,15,17	1.43	3 (20%)
5	NAG	q	1	5,1	14,14,15	0.49	0	17,19,21	2.28	3 (17%)
5	NAG	q	2	5	14,14,15	0.50	0	17,19,21	1.33	3 (17%)
5	BMA	q	3	5	11,11,12	0.64	0	15,15,17	1.43	3 (20%)
6	NAG	r	1	1,6	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
6	NAG	r	2	6	14,14,15	0.51	0	17,19,21	1.34	3 (17%)
6	NAG	s	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	s	2	6	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	NAG	t	1	5,1	14,14,15	0.49	0	17,19,21	2.27	3 (17%)
5	NAG	t	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)
5	BMA	t	3	5	11,11,12	0.63	0	15,15,17	1.43	3 (20%)
6	NAG	u	1	1,6	14,14,15	0.49	0	17,19,21	2.28	3 (17%)
6	NAG	u	2	6	14,14,15	0.51	0	17,19,21	1.32	3 (17%)
5	NAG	v	1	5,1	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
5	NAG	v	2	5	14,14,15	0.51	0	17,19,21	1.33	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BMA	v	3	5	11,11,12	0.64	0	15,15,17	1.42	3 (20%)
5	NAG	w	1	5,1	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
5	NAG	w	2	5	14,14,15	0.50	0	17,19,21	1.31	3 (17%)
5	BMA	w	3	5	11,11,12	0.65	0	15,15,17	1.43	3 (20%)
6	NAG	x	1	1,6	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
6	NAG	x	2	6	14,14,15	0.52	0	17,19,21	1.32	3 (17%)
6	NAG	y	1	1,6	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
6	NAG	y	2	6	14,14,15	0.50	0	17,19,21	1.33	3 (17%)
7	NAG	z	1	1,7	14,14,15	0.58	0	17,19,21	0.67	0
7	NAG	z	2	7	14,14,15	0.56	0	17,19,21	0.85	0
7	BMA	z	3	7	11,11,12	0.66	0	15,15,17	0.71	0
7	MAN	z	4	7	11,11,12	0.58	0	15,15,17	0.56	0
7	MAN	z	5	7	11,11,12	0.52	0	15,15,17	0.65	0
7	MAN	z	6	7	11,11,12	0.65	0	15,15,17	0.93	2 (13%)
7	MAN	z	7	7	11,11,12	0.61	0	15,15,17	0.54	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	0	1	5,1	-	3/6/23/26	0/1/1/1
5	NAG	0	2	5	-	0/6/23/26	0/1/1/1
5	BMA	0	3	5	-	2/2/19/22	0/1/1/1
8	NAG	1	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	1	2	8	-	0/6/23/26	0/1/1/1
8	BMA	1	3	8	-	2/2/19/22	0/1/1/1
8	MAN	1	4	8	-	0/2/19/22	0/1/1/1
8	MAN	1	5	8	-	0/2/19/22	0/1/1/1
7	NAG	2	1	1,7	-	3/6/23/26	0/1/1/1
7	NAG	2	2	7	-	1/6/23/26	0/1/1/1
7	BMA	2	3	7	-	0/2/19/22	0/1/1/1
7	MAN	2	4	7	-	2/2/19/22	0/1/1/1
7	MAN	2	5	7	-	0/2/19/22	0/1/1/1
7	MAN	2	6	7	-	2/2/19/22	0/1/1/1
7	MAN	2	7	7	-	1/2/19/22	0/1/1/1
9	NAG	3	1	9,1	-	0/6/23/26	0/1/1/1
9	MAN	3	10	9	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	3	2	9	-	1/6/23/26	0/1/1/1
9	BMA	3	3	9	-	0/2/19/22	0/1/1/1
9	MAN	3	4	9	-	1/2/19/22	0/1/1/1
9	MAN	3	5	9	-	0/2/19/22	0/1/1/1
9	MAN	3	6	9	-	0/2/19/22	0/1/1/1
9	MAN	3	7	9	-	0/2/19/22	0/1/1/1
9	MAN	3	8	9	-	0/2/19/22	0/1/1/1
9	MAN	3	9	9	-	1/2/19/22	0/1/1/1
6	NAG	4	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	4	2	6	-	0/6/23/26	0/1/1/1
5	NAG	5	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	5	2	5	-	0/6/23/26	0/1/1/1
5	BMA	5	3	5	-	2/2/19/22	0/1/1/1
5	NAG	6	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	6	2	5	-	0/6/23/26	0/1/1/1
5	BMA	6	3	5	-	2/2/19/22	0/1/1/1
6	NAG	7	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	7	2	6	-	0/6/23/26	0/1/1/1
6	NAG	8	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	8	2	6	-	0/6/23/26	0/1/1/1
6	NAG	9	1	2,6	-	1/6/23/26	0/1/1/1
6	NAG	9	2	6	-	0/6/23/26	0/1/1/1
6	NAG	AA	1	2,6	-	1/6/23/26	0/1/1/1
6	NAG	AA	2	6	-	0/6/23/26	0/1/1/1
5	NAG	M	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	M	2	5	-	0/6/23/26	0/1/1/1
5	BMA	M	3	5	-	2/2/19/22	0/1/1/1
6	NAG	N	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	N	2	6	-	0/6/23/26	0/1/1/1
5	NAG	O	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1
5	BMA	O	3	5	-	2/2/19/22	0/1/1/1
5	NAG	P	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	P	2	5	-	0/6/23/26	0/1/1/1
5	BMA	P	3	5	-	2/2/19/22	0/1/1/1
6	NAG	Q	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	0/6/23/26	0/1/1/1
6	NAG	R	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	R	2	6	-	0/6/23/26	0/1/1/1
7	NAG	S	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	S	2	7	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BMA	S	3	7	-	2/2/19/22	0/1/1/1
7	MAN	S	4	7	-	0/2/19/22	0/1/1/1
7	MAN	S	5	7	-	2/2/19/22	0/1/1/1
7	MAN	S	6	7	-	2/2/19/22	0/1/1/1
7	MAN	S	7	7	-	0/2/19/22	0/1/1/1
5	NAG	T	1	5,1	-	3/6/23/26	0/1/1/1
5	NAG	T	2	5	-	0/6/23/26	0/1/1/1
5	BMA	T	3	5	-	2/2/19/22	0/1/1/1
8	NAG	U	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	U	2	8	-	0/6/23/26	0/1/1/1
8	BMA	U	3	8	-	2/2/19/22	0/1/1/1
8	MAN	U	4	8	-	0/2/19/22	0/1/1/1
8	MAN	U	5	8	-	0/2/19/22	0/1/1/1
7	NAG	V	1	1,7	-	3/6/23/26	0/1/1/1
7	NAG	V	2	7	-	1/6/23/26	0/1/1/1
7	BMA	V	3	7	-	0/2/19/22	0/1/1/1
7	MAN	V	4	7	-	2/2/19/22	0/1/1/1
7	MAN	V	5	7	-	0/2/19/22	0/1/1/1
7	MAN	V	6	7	-	2/2/19/22	0/1/1/1
7	MAN	V	7	7	-	1/2/19/22	0/1/1/1
9	NAG	W	1	9,1	-	0/6/23/26	0/1/1/1
9	MAN	W	10	9	-	1/2/19/22	0/1/1/1
9	NAG	W	2	9	-	1/6/23/26	0/1/1/1
9	BMA	W	3	9	-	0/2/19/22	0/1/1/1
9	MAN	W	4	9	-	1/2/19/22	0/1/1/1
9	MAN	W	5	9	-	0/2/19/22	0/1/1/1
9	MAN	W	6	9	-	0/2/19/22	0/1/1/1
9	MAN	W	7	9	-	0/2/19/22	0/1/1/1
9	MAN	W	8	9	-	0/2/19/22	0/1/1/1
9	MAN	W	9	9	-	1/2/19/22	0/1/1/1
6	NAG	X	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	X	2	6	-	0/6/23/26	0/1/1/1
5	NAG	Y	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	Y	2	5	-	0/6/23/26	0/1/1/1
5	BMA	Y	3	5	-	2/2/19/22	0/1/1/1
5	NAG	Z	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	Z	2	5	-	0/6/23/26	0/1/1/1
5	BMA	Z	3	5	-	2/2/19/22	0/1/1/1
6	NAG	a	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	a	2	6	-	0/6/23/26	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	m	6	7	-	2/2/19/22	0/1/1/1
7	MAN	m	7	7	-	1/2/19/22	0/1/1/1
9	NAG	n	1	9,1	-	0/6/23/26	0/1/1/1
9	MAN	n	10	9	-	1/2/19/22	0/1/1/1
9	NAG	n	2	9	-	1/6/23/26	0/1/1/1
9	BMA	n	3	9	-	0/2/19/22	0/1/1/1
9	MAN	n	4	9	-	1/2/19/22	0/1/1/1
9	MAN	n	5	9	-	0/2/19/22	0/1/1/1
9	MAN	n	6	9	-	0/2/19/22	0/1/1/1
9	MAN	n	7	9	-	0/2/19/22	0/1/1/1
9	MAN	n	8	9	-	0/2/19/22	0/1/1/1
9	MAN	n	9	9	-	1/2/19/22	0/1/1/1
6	NAG	o	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	o	2	6	-	0/6/23/26	0/1/1/1
5	NAG	p	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	p	2	5	-	0/6/23/26	0/1/1/1
5	BMA	p	3	5	-	2/2/19/22	0/1/1/1
5	NAG	q	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	q	2	5	-	0/6/23/26	0/1/1/1
5	BMA	q	3	5	-	2/2/19/22	0/1/1/1
6	NAG	r	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	r	2	6	-	0/6/23/26	0/1/1/1
6	NAG	s	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	s	2	6	-	0/6/23/26	0/1/1/1
5	NAG	t	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	t	2	5	-	0/6/23/26	0/1/1/1
5	BMA	t	3	5	-	2/2/19/22	0/1/1/1
6	NAG	u	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	u	2	6	-	0/6/23/26	0/1/1/1
5	NAG	v	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	v	2	5	-	0/6/23/26	0/1/1/1
5	BMA	v	3	5	-	2/2/19/22	0/1/1/1
5	NAG	w	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	w	2	5	-	0/6/23/26	0/1/1/1
5	BMA	w	3	5	-	2/2/19/22	0/1/1/1
6	NAG	x	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	x	2	6	-	0/6/23/26	0/1/1/1
6	NAG	y	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	y	2	6	-	0/6/23/26	0/1/1/1
7	NAG	z	1	1,7	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	z	2	7	-	2/6/23/26	0/1/1/1
7	BMA	z	3	7	-	2/2/19/22	0/1/1/1
7	MAN	z	4	7	-	0/2/19/22	0/1/1/1
7	MAN	z	5	7	-	2/2/19/22	0/1/1/1
7	MAN	z	6	7	-	2/2/19/22	0/1/1/1
7	MAN	z	7	7	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 399 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	2	2	NAG	C1-C2-N2	9.13	124.82	110.43
7	V	2	NAG	C1-C2-N2	9.13	124.81	110.43
7	m	2	NAG	C1-C2-N2	9.12	124.80	110.43
6	u	1	NAG	O5-C1-C2	-7.55	99.60	111.29
5	q	1	NAG	O5-C1-C2	-7.55	99.62	111.29

There are no chirality outliers.

5 of 159 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	V	1	NAG	C1-C2-N2-C7
7	V	2	NAG	C1-C2-N2-C7
7	m	1	NAG	C1-C2-N2-C7
7	m	2	NAG	C1-C2-N2-C7
7	2	1	NAG	C1-C2-N2-C7

There are no ring outliers.

54 monomers are involved in 209 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	V	1	NAG	1	0
9	W	9	MAN	4	0
5	p	1	NAG	1	0
7	S	1	NAG	2	0
9	W	5	MAN	3	0
6	x	1	NAG	3	0
7	z	1	NAG	2	0
7	2	6	MAN	1	0
9	n	1	NAG	15	0

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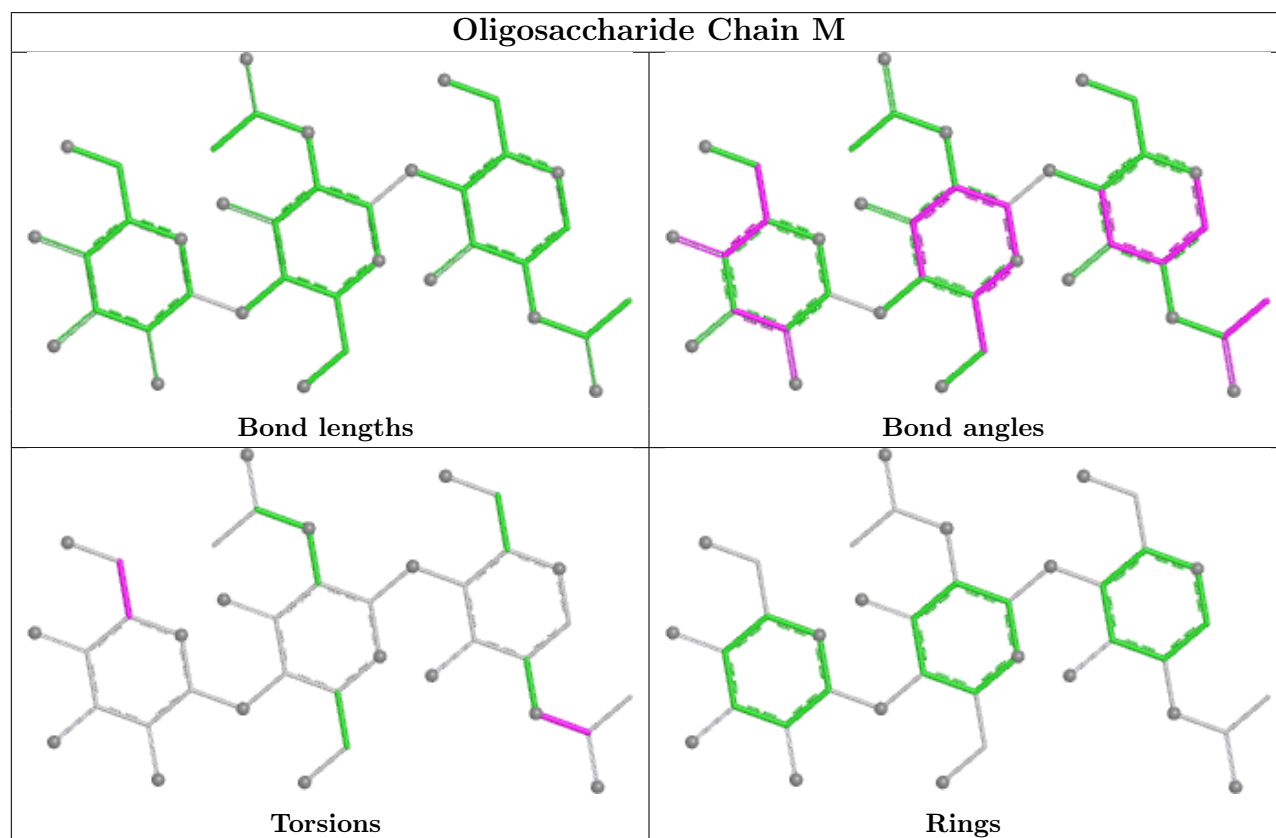
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	Y	1	NAG	1	0
5	k	2	NAG	2	0
6	b	1	NAG	6	0
7	z	2	NAG	1	0
5	k	1	NAG	5	0
5	M	1	NAG	8	0
6	Q	1	NAG	3	0
9	n	9	MAN	4	0
7	V	6	MAN	1	0
6	i	1	NAG	1	0
9	3	6	MAN	19	0
5	t	1	NAG	8	0
5	0	2	NAG	2	0
9	W	6	MAN	16	0
5	T	1	NAG	5	0
9	n	5	MAN	3	0
9	3	5	MAN	3	0
7	2	1	NAG	1	0
6	8	1	NAG	6	0
9	3	1	NAG	15	0
7	S	2	NAG	1	0
6	R	1	NAG	1	0
6	y	2	NAG	1	0
5	d	1	NAG	8	0
7	j	2	NAG	1	0
9	W	1	NAG	14	0
5	O	1	NAG	1	0
6	i	2	NAG	1	0
5	T	2	NAG	2	0
6	y	1	NAG	1	0
5	f	1	NAG	1	0
7	m	1	NAG	1	0
5	5	1	NAG	1	0
9	3	9	MAN	4	0
9	n	6	MAN	20	0
6	Q	2	NAG	1	0
7	m	6	MAN	1	0
6	h	2	NAG	1	0
6	R	2	NAG	1	0
6	s	1	NAG	7	0
5	v	1	NAG	1	0
6	h	1	NAG	3	0

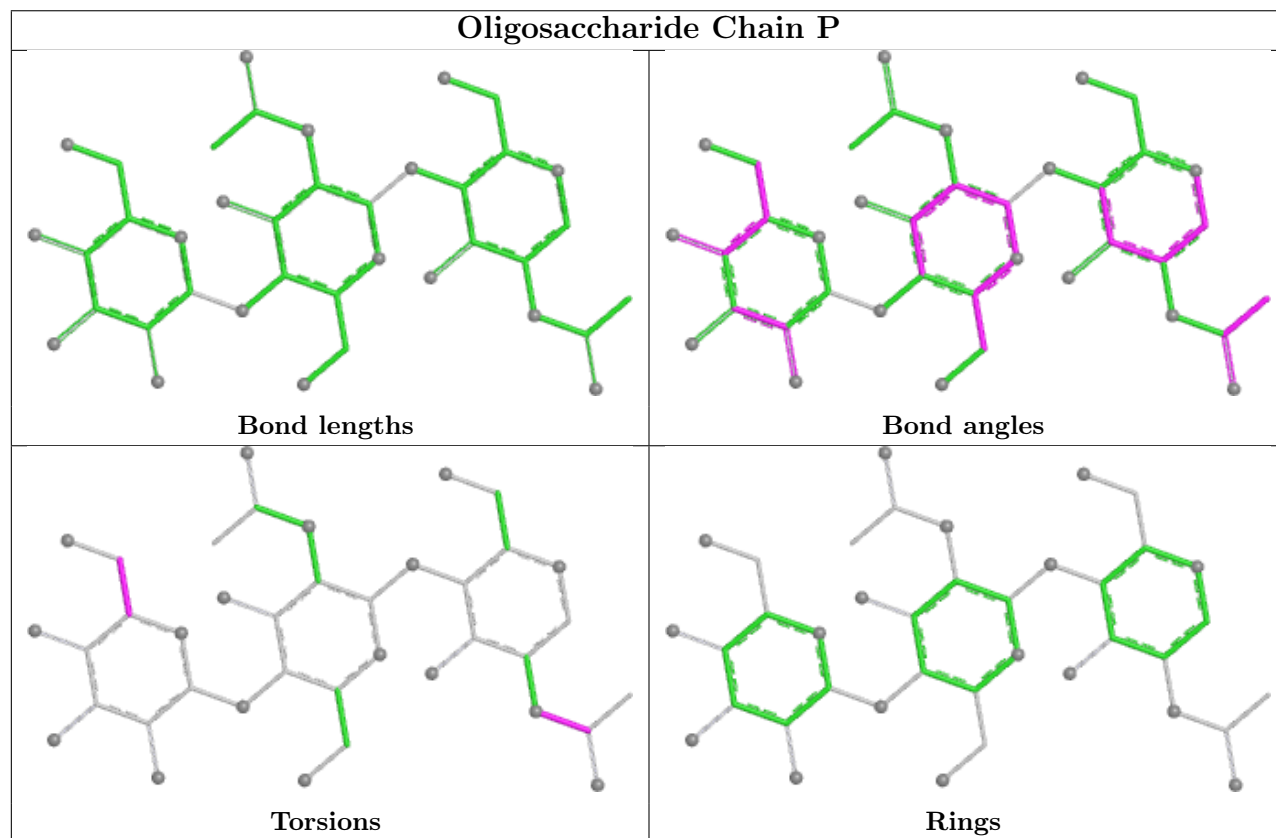
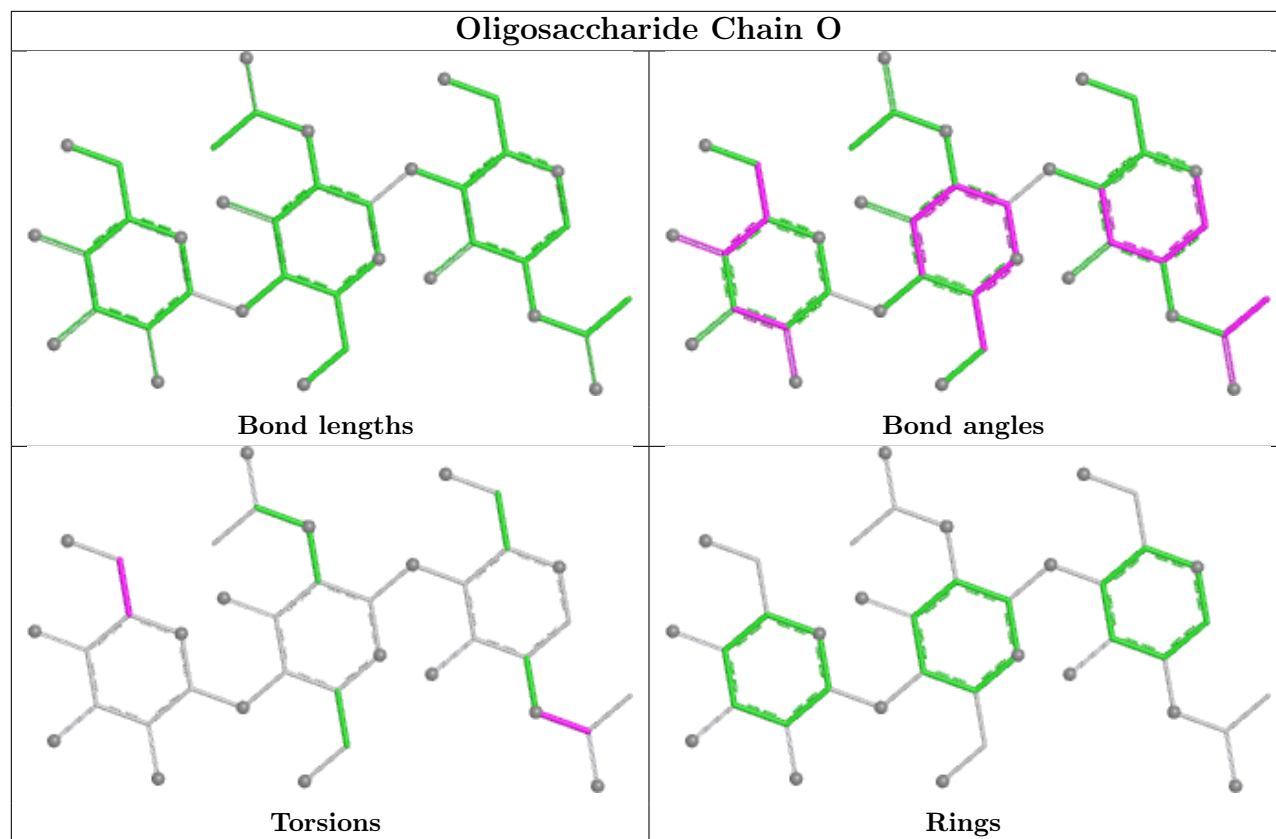
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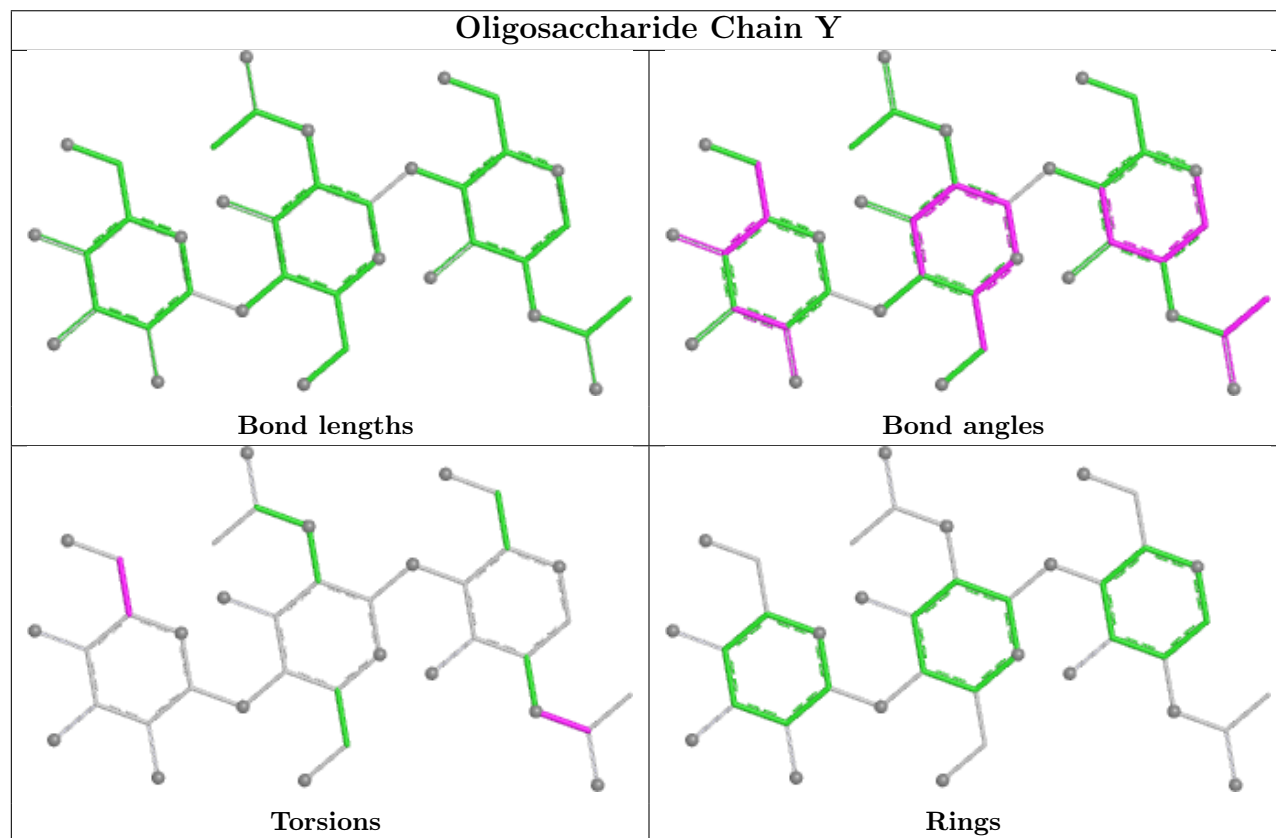
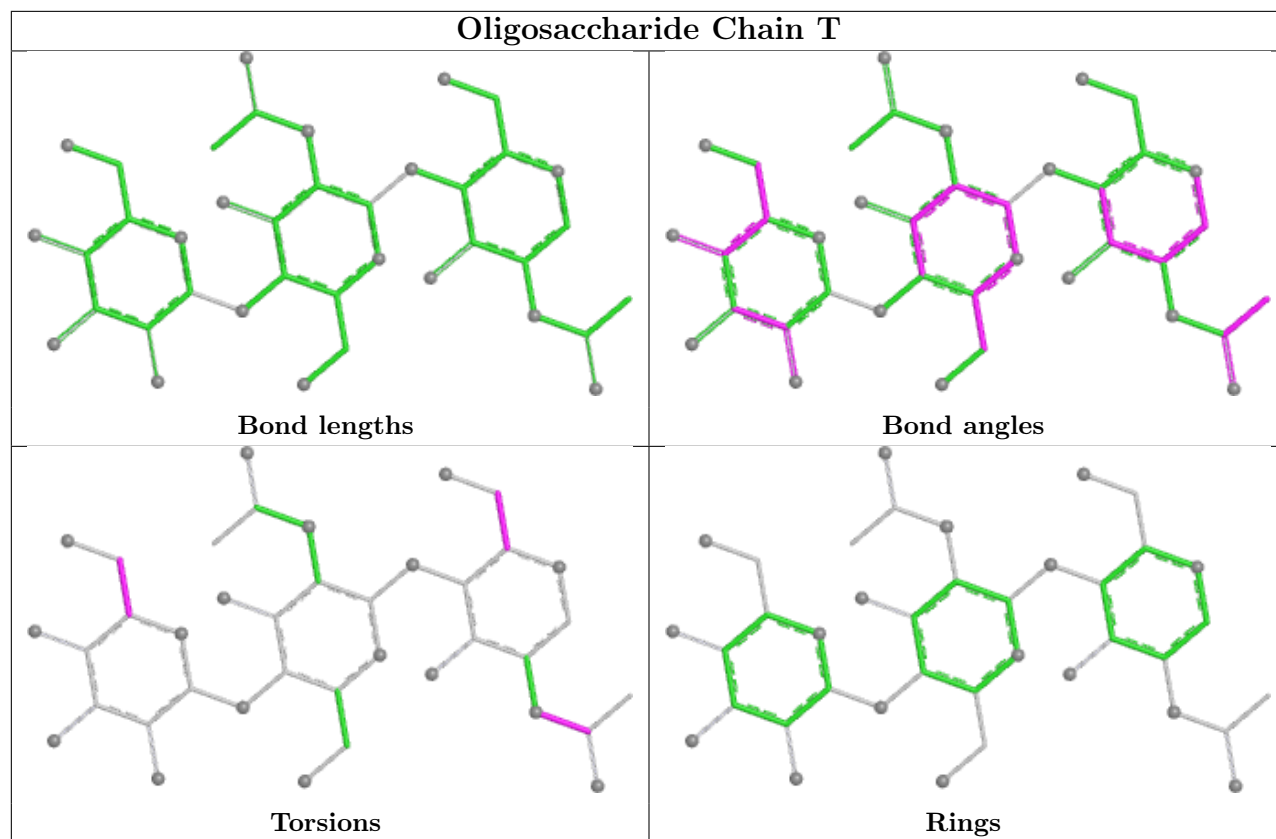
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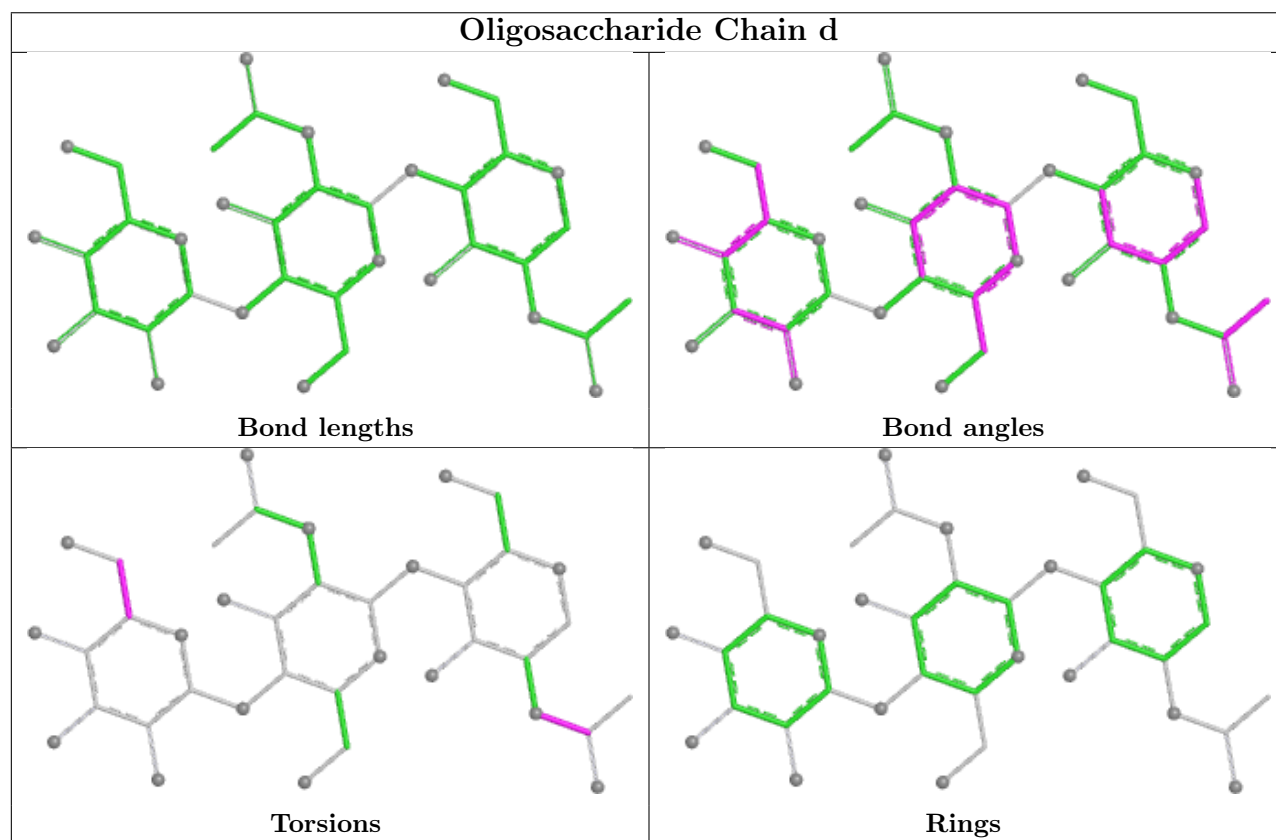
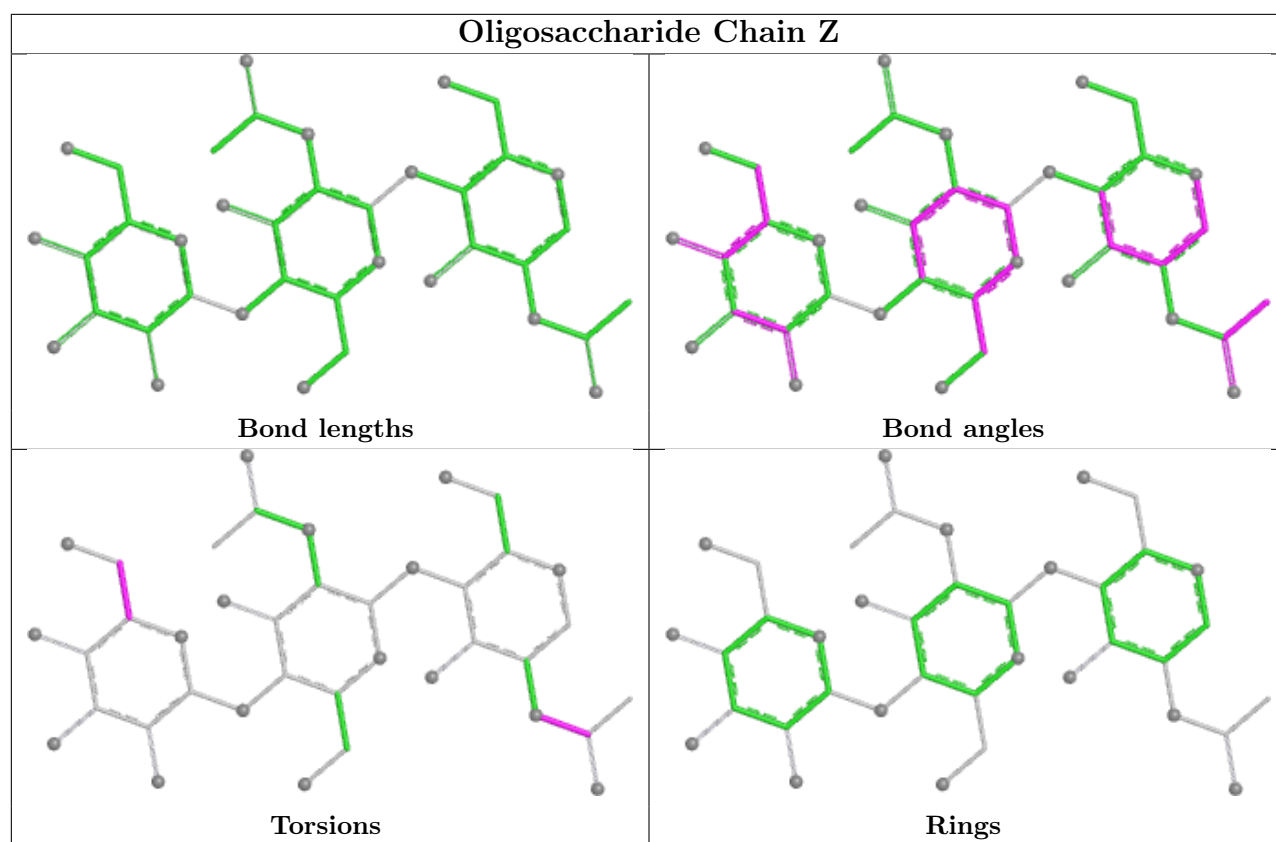
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	j	1	NAG	3	0
6	x	2	NAG	1	0
5	0	1	NAG	5	0

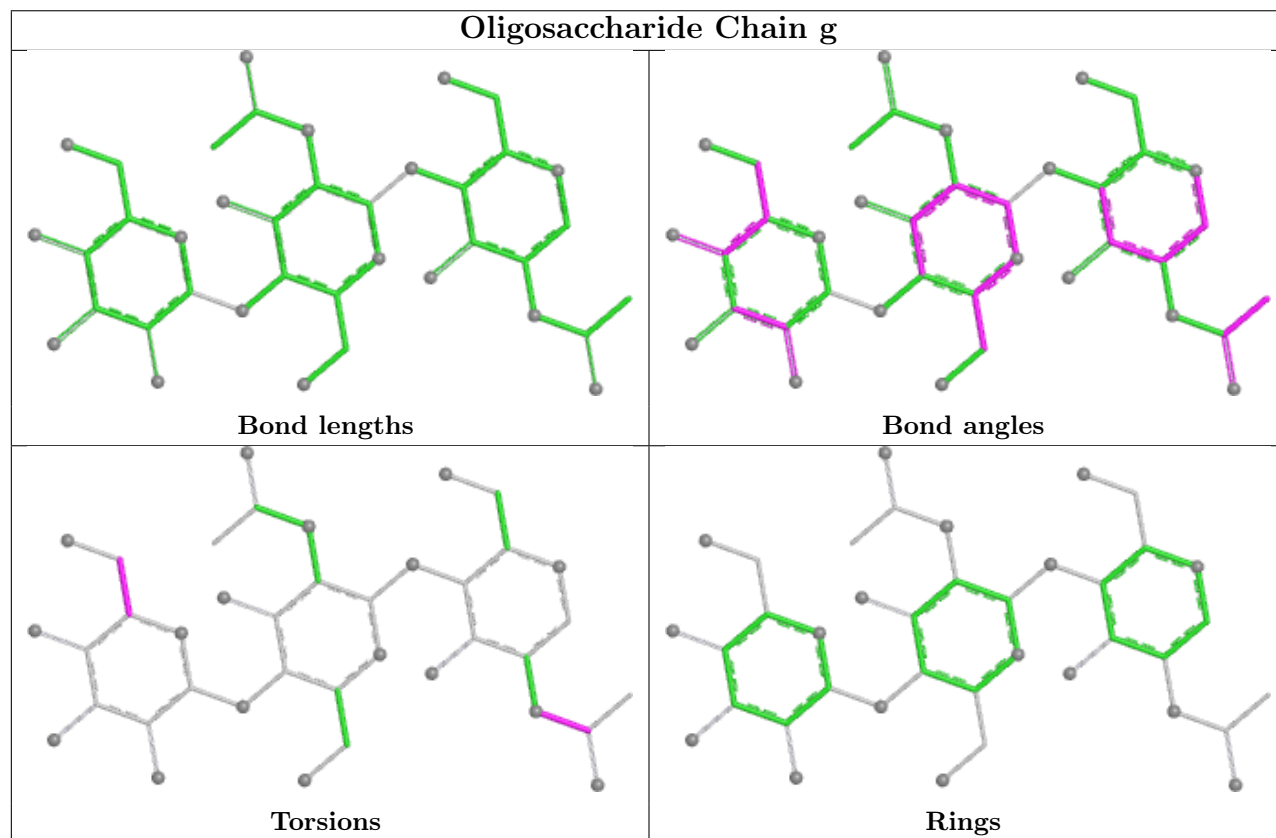
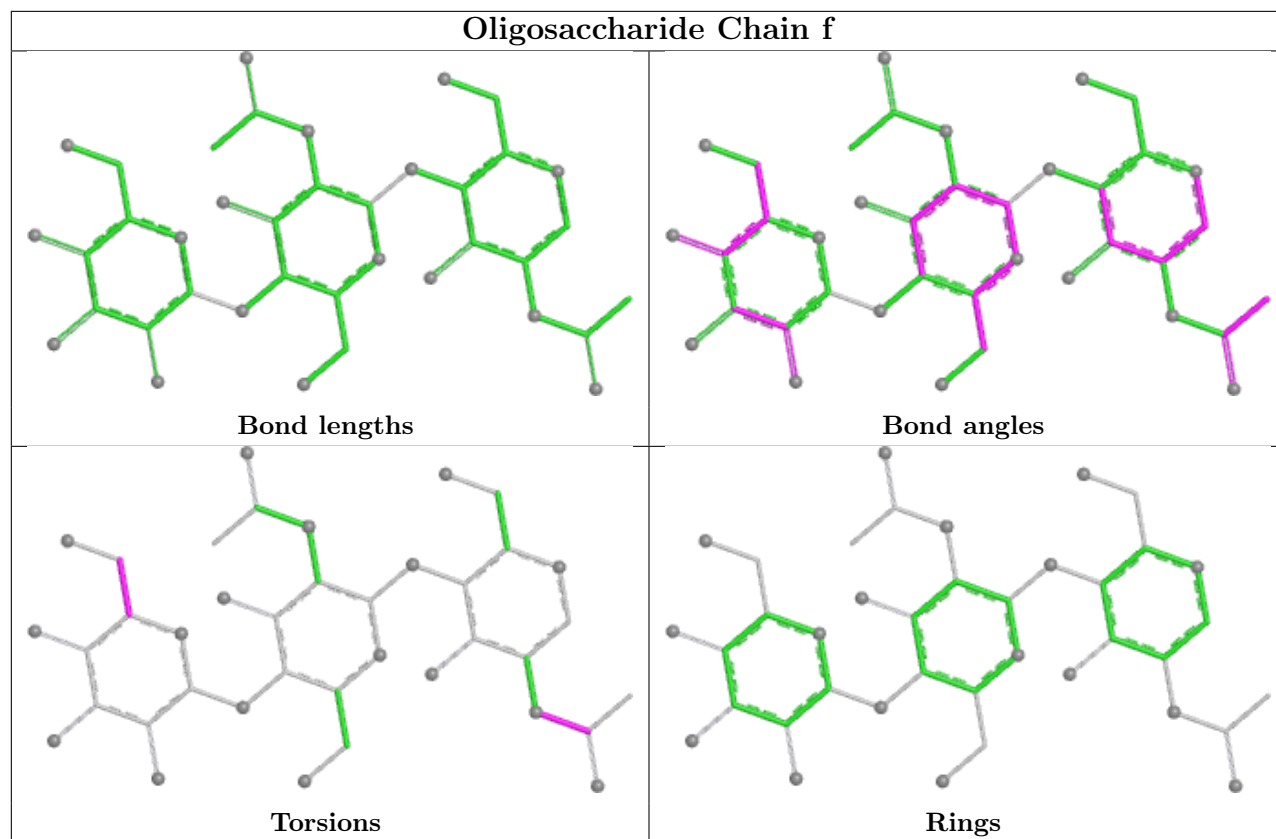
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

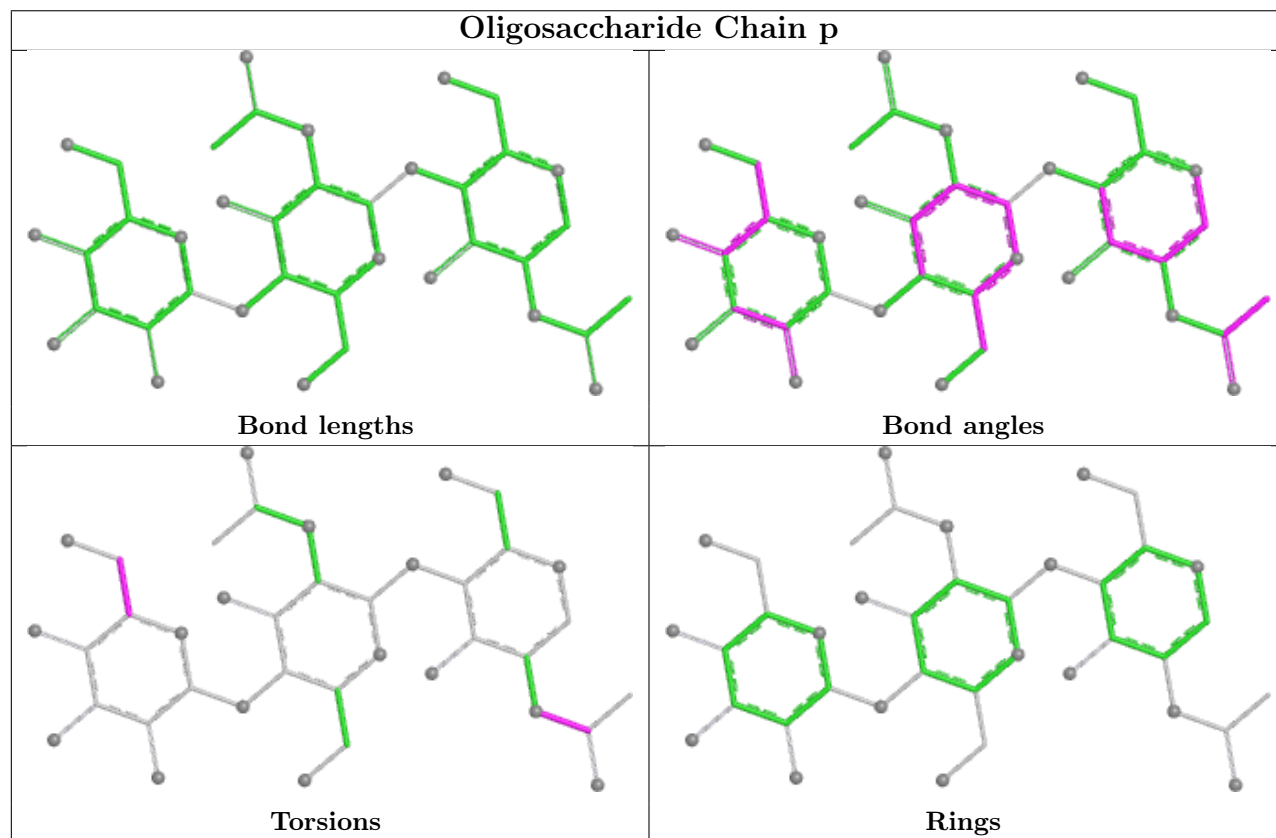
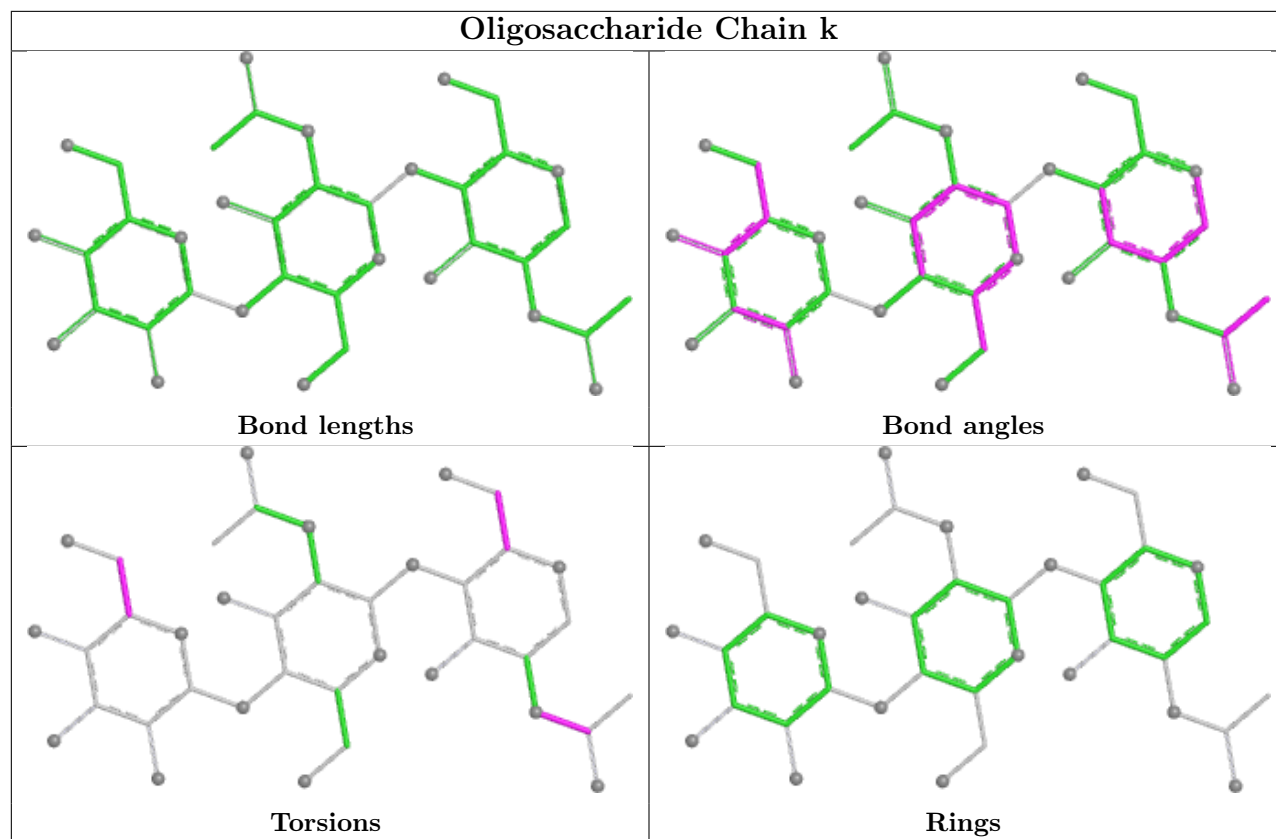


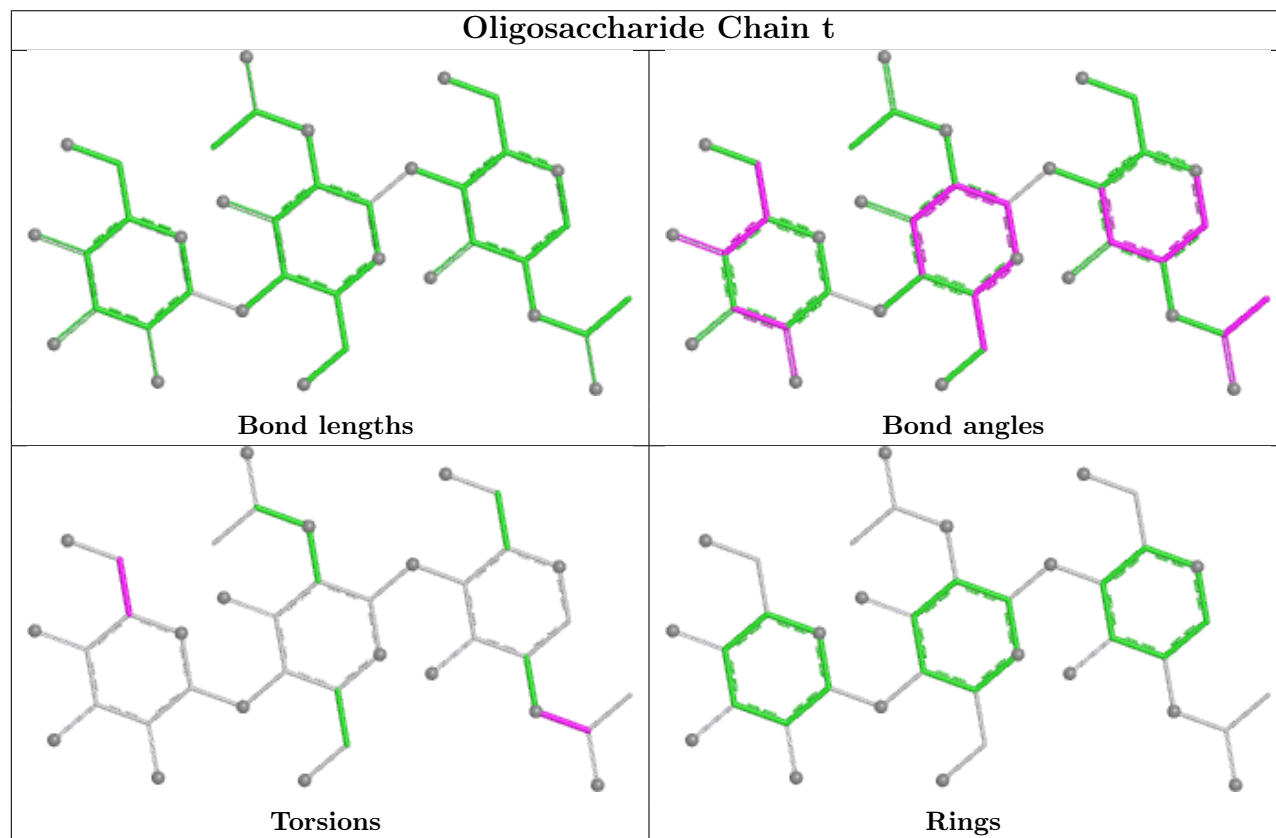
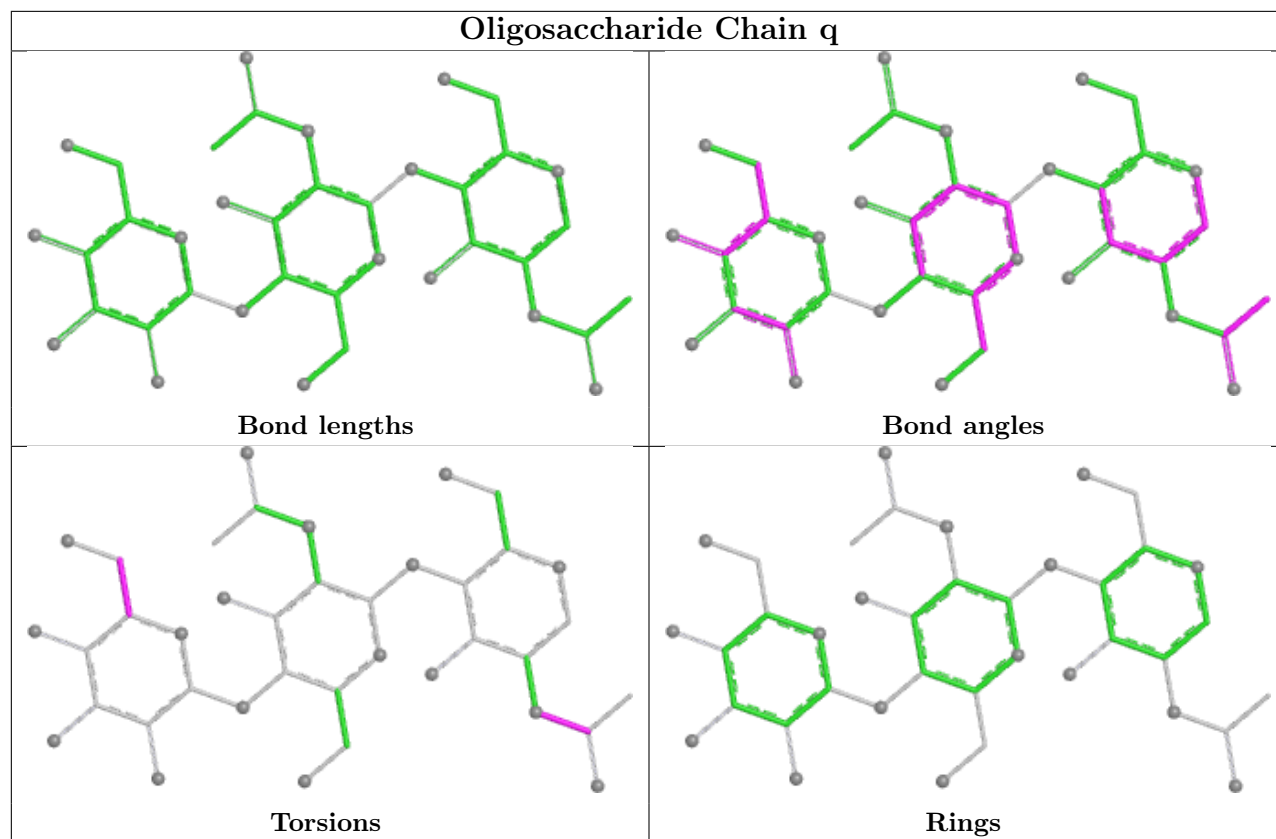


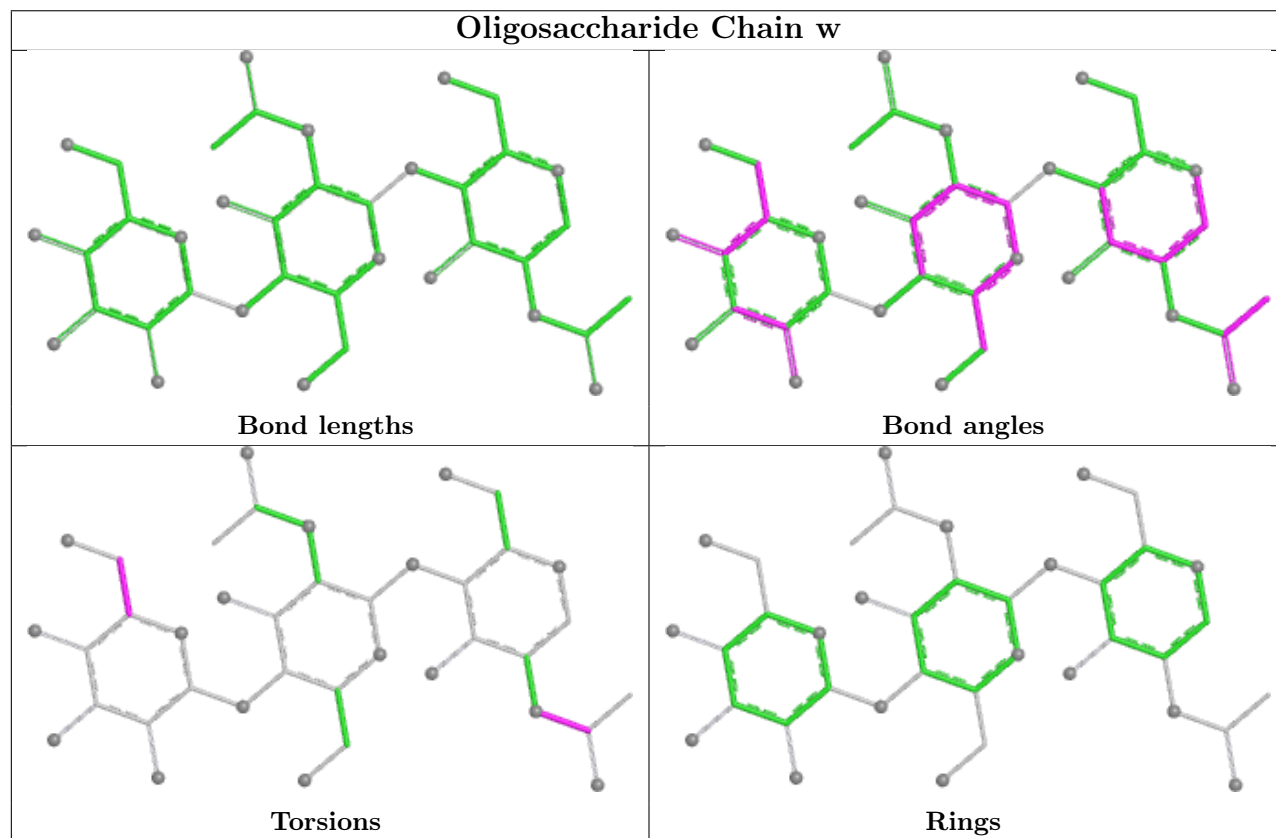
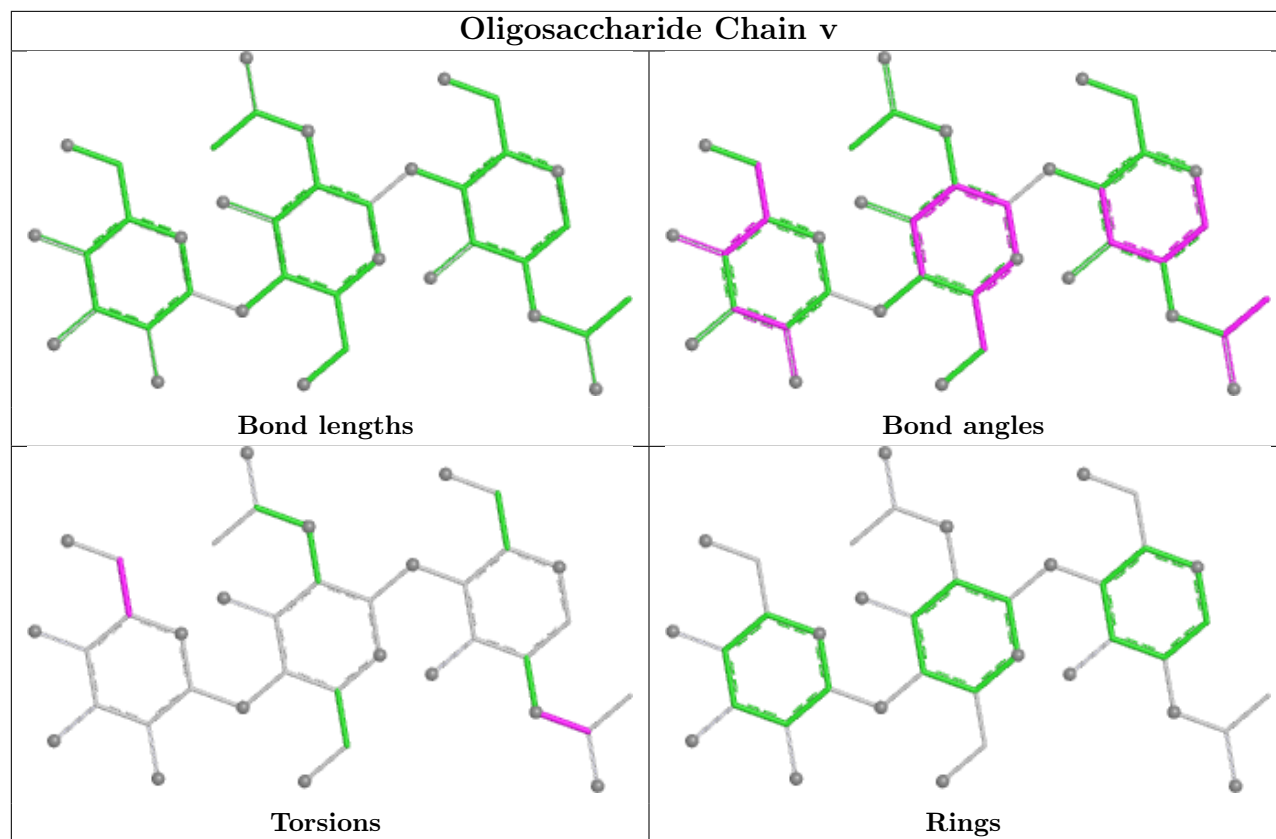


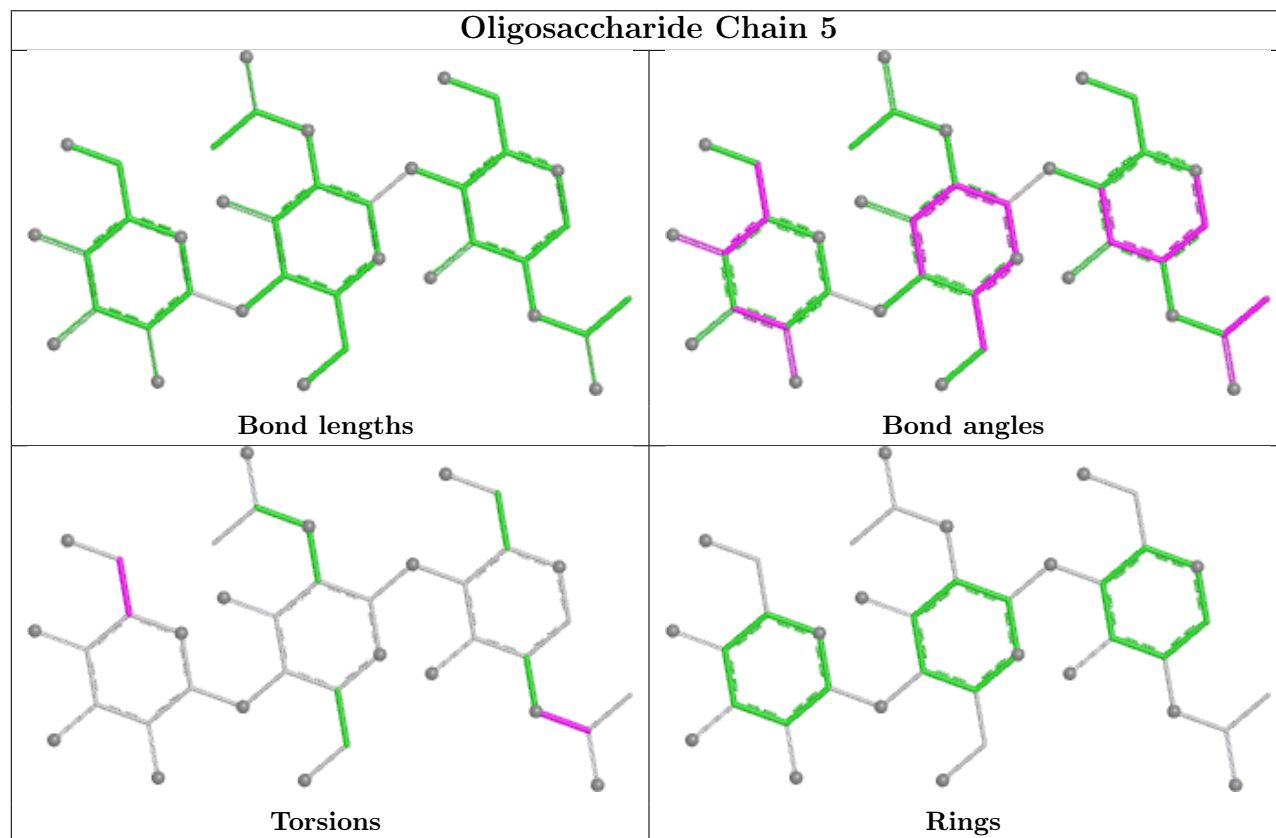
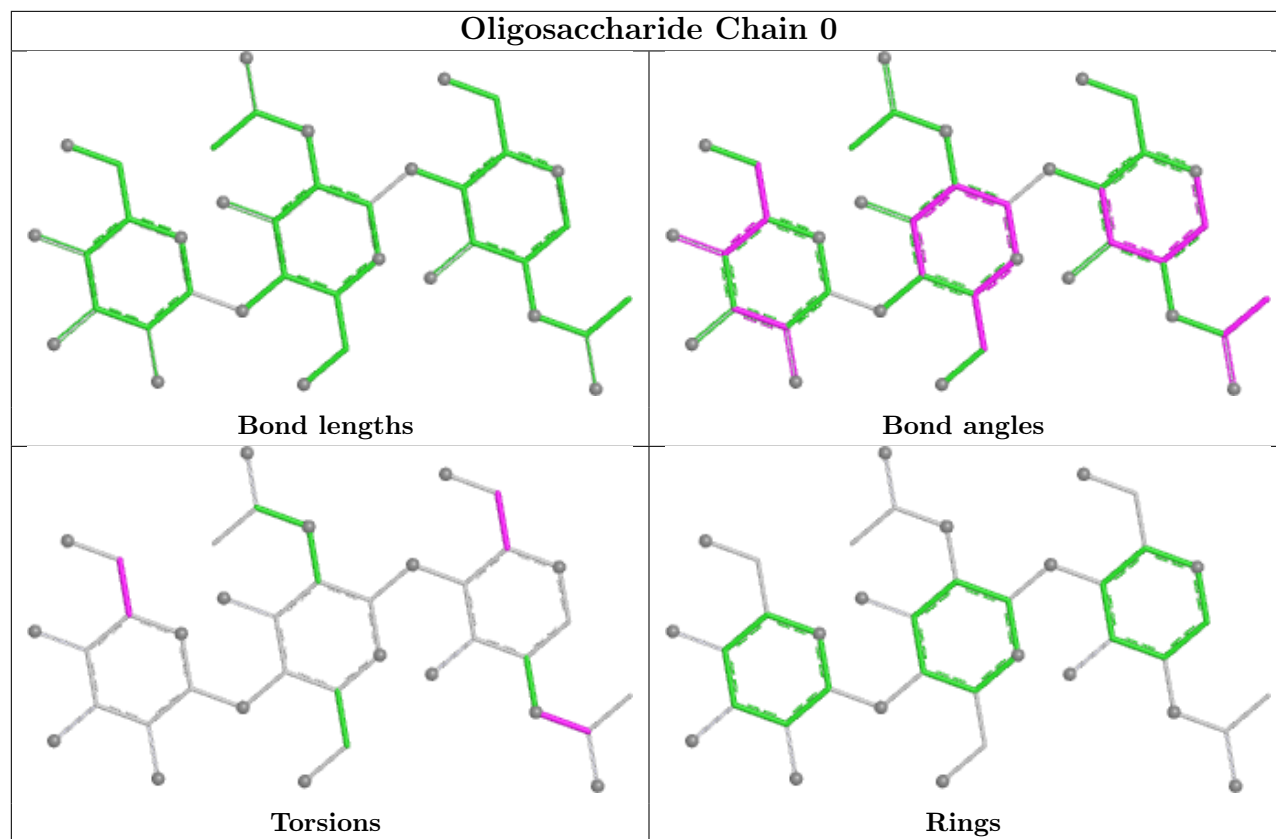


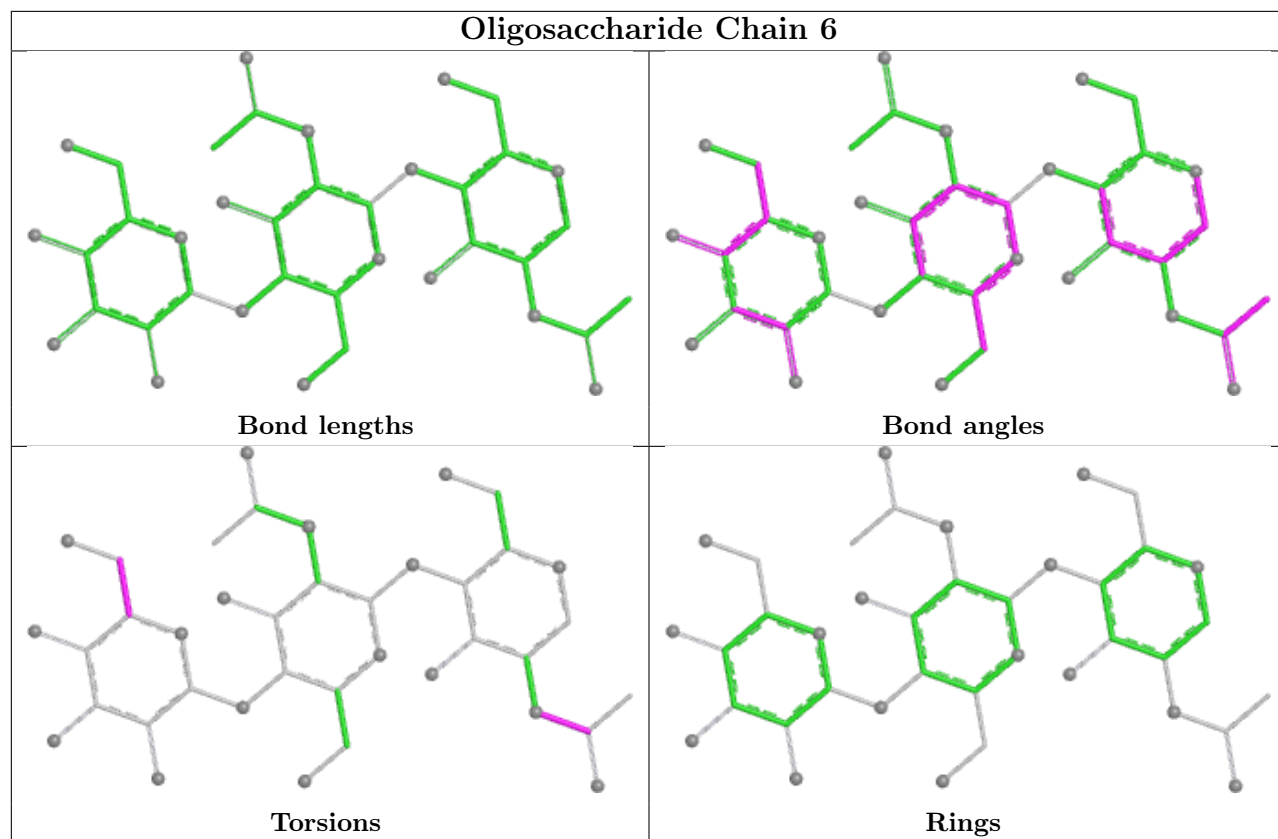


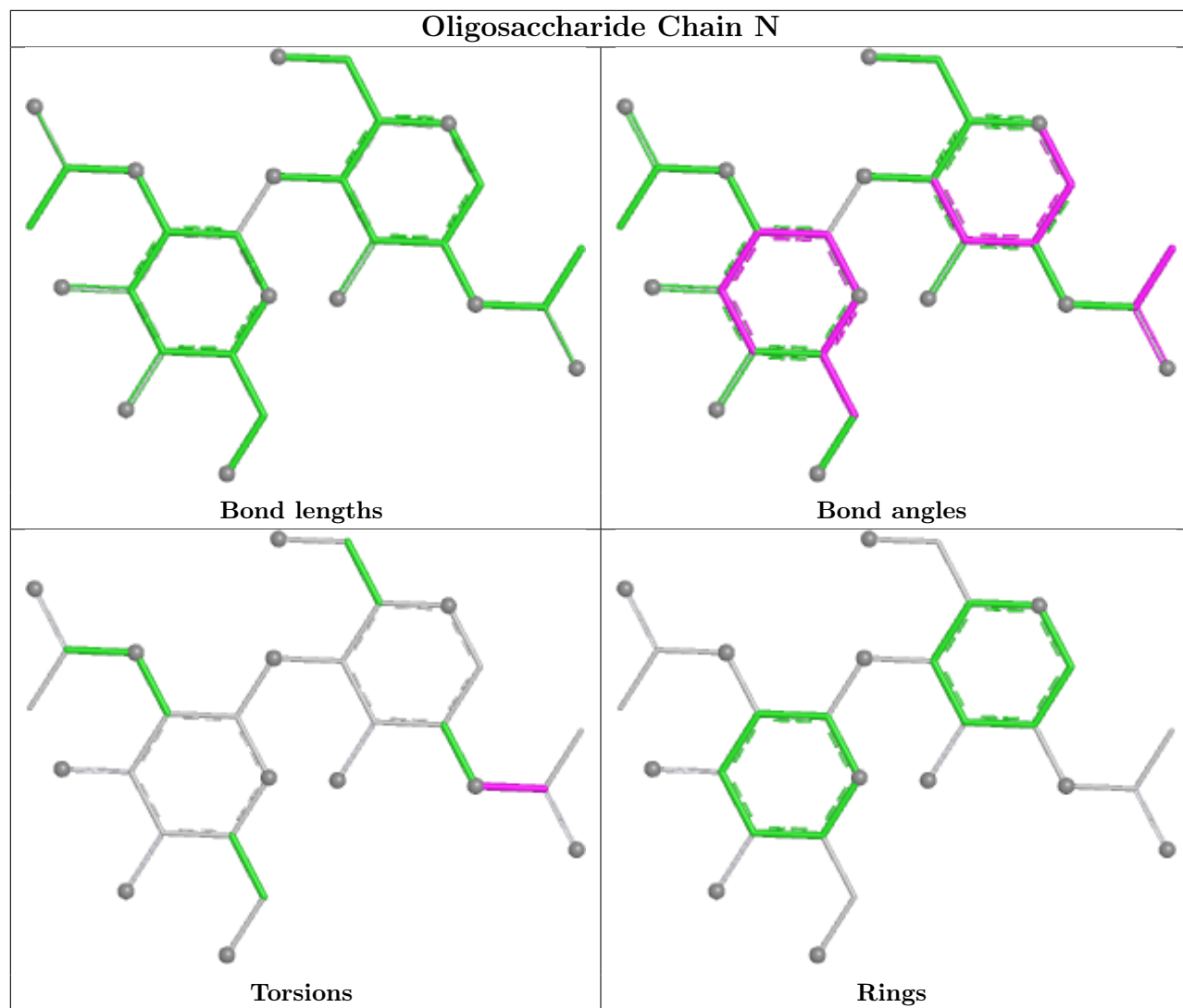


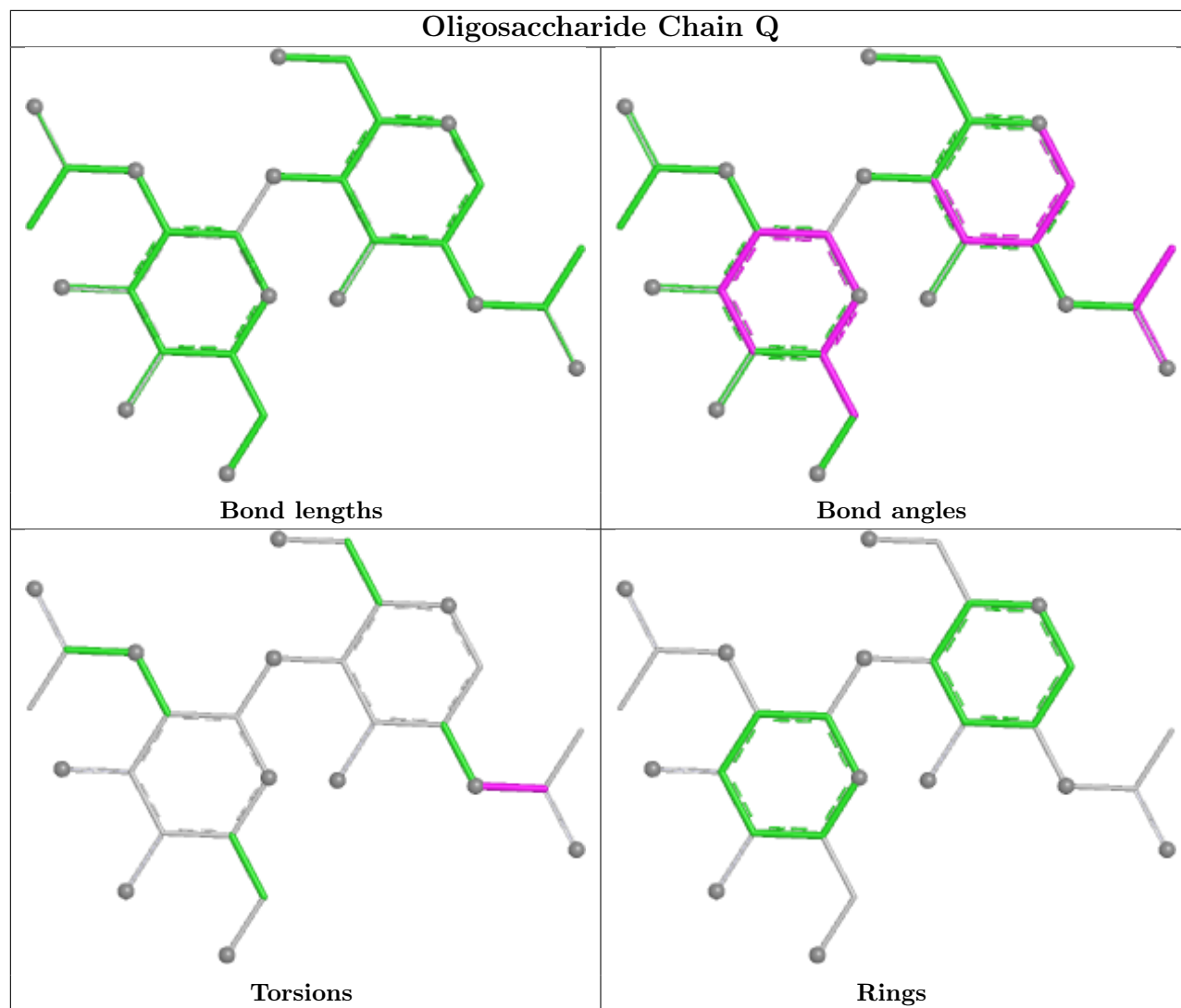


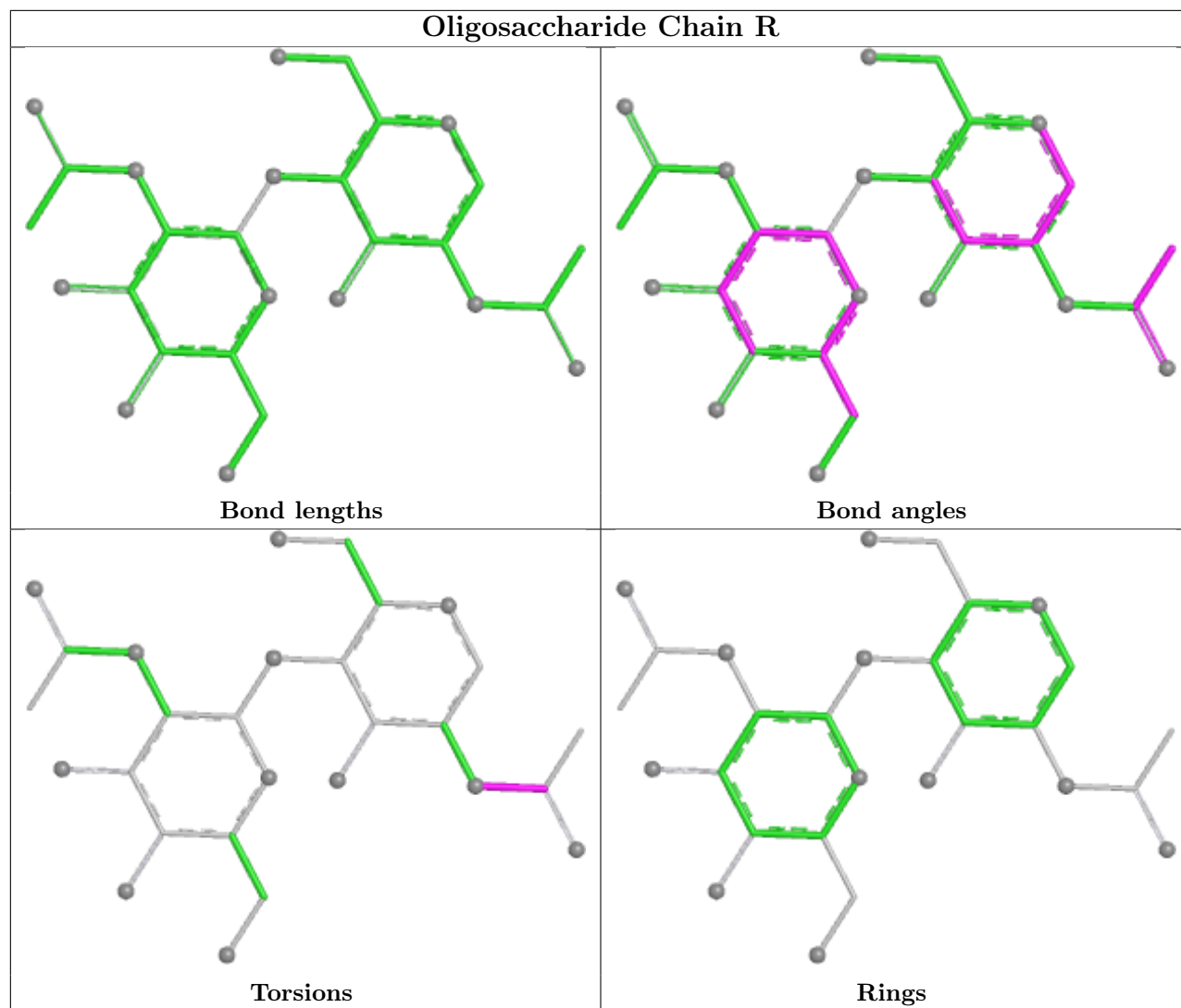


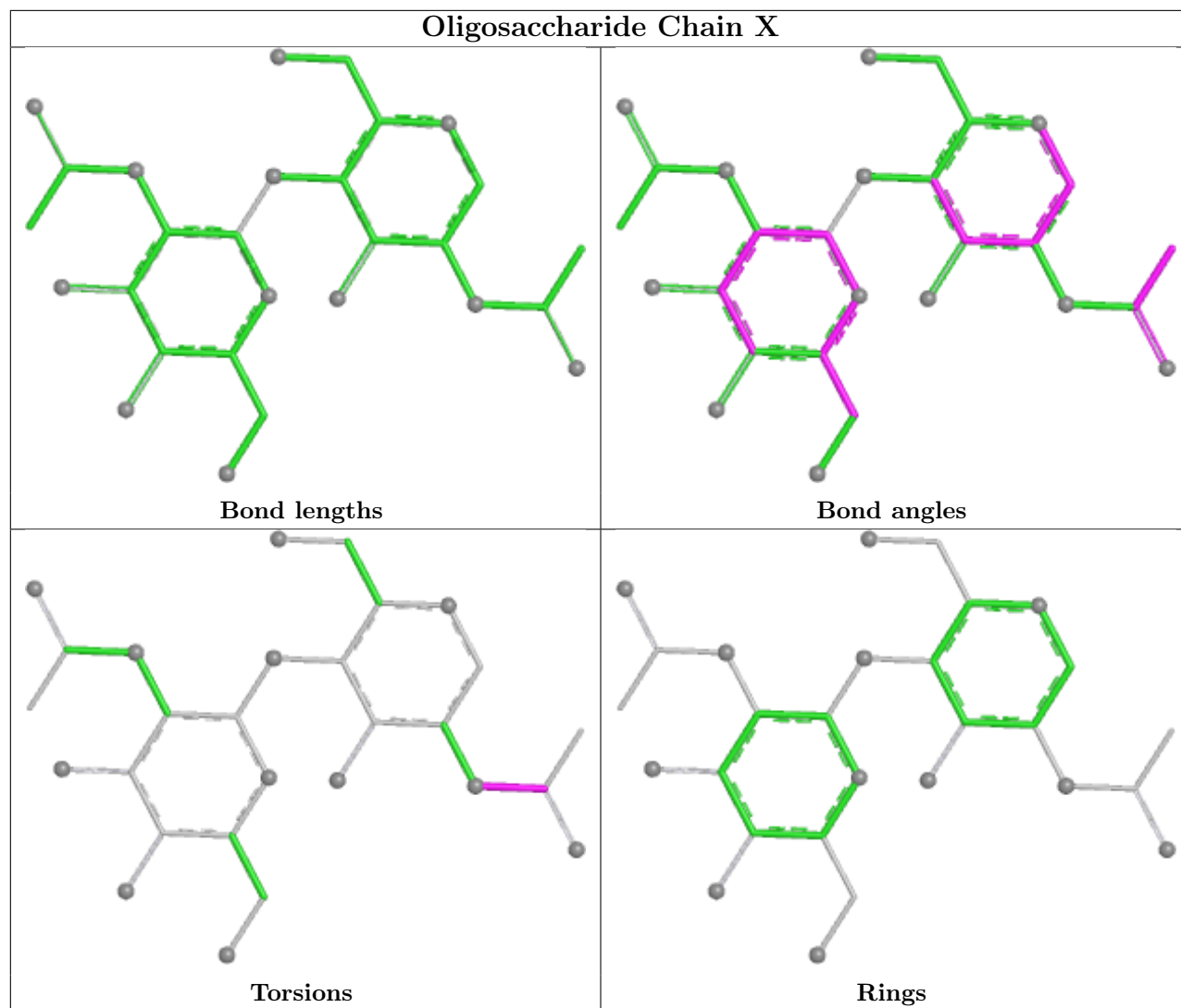


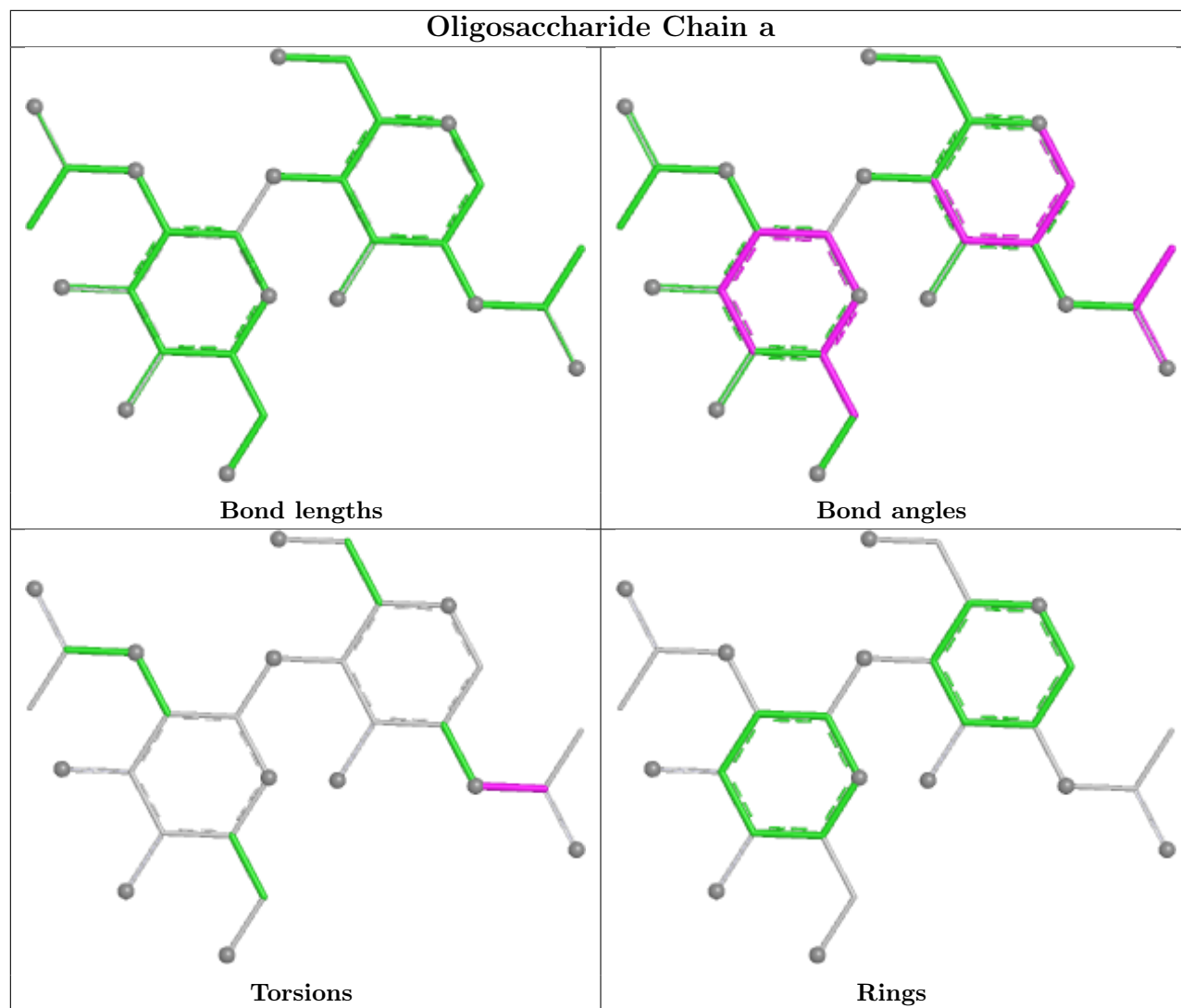


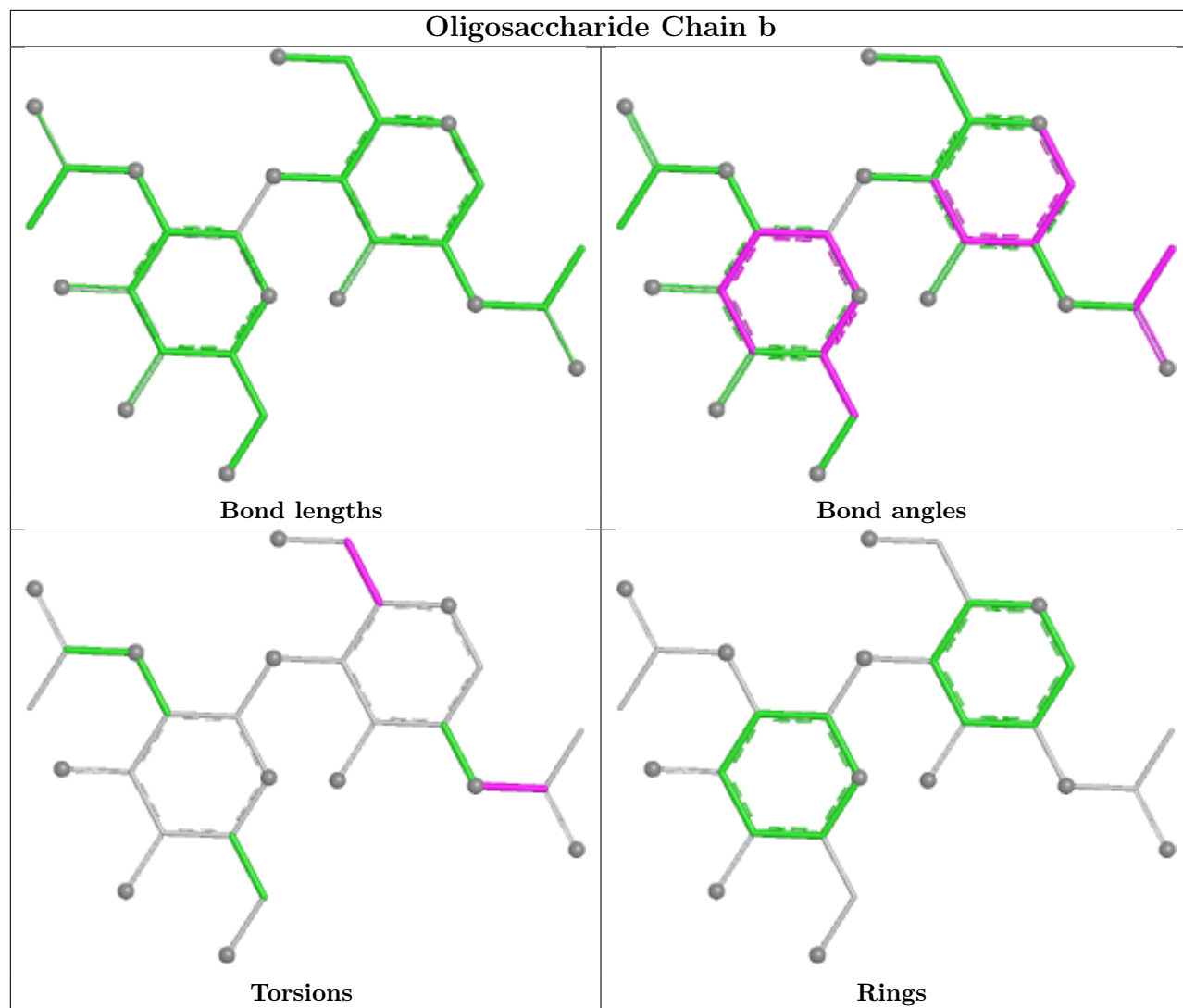


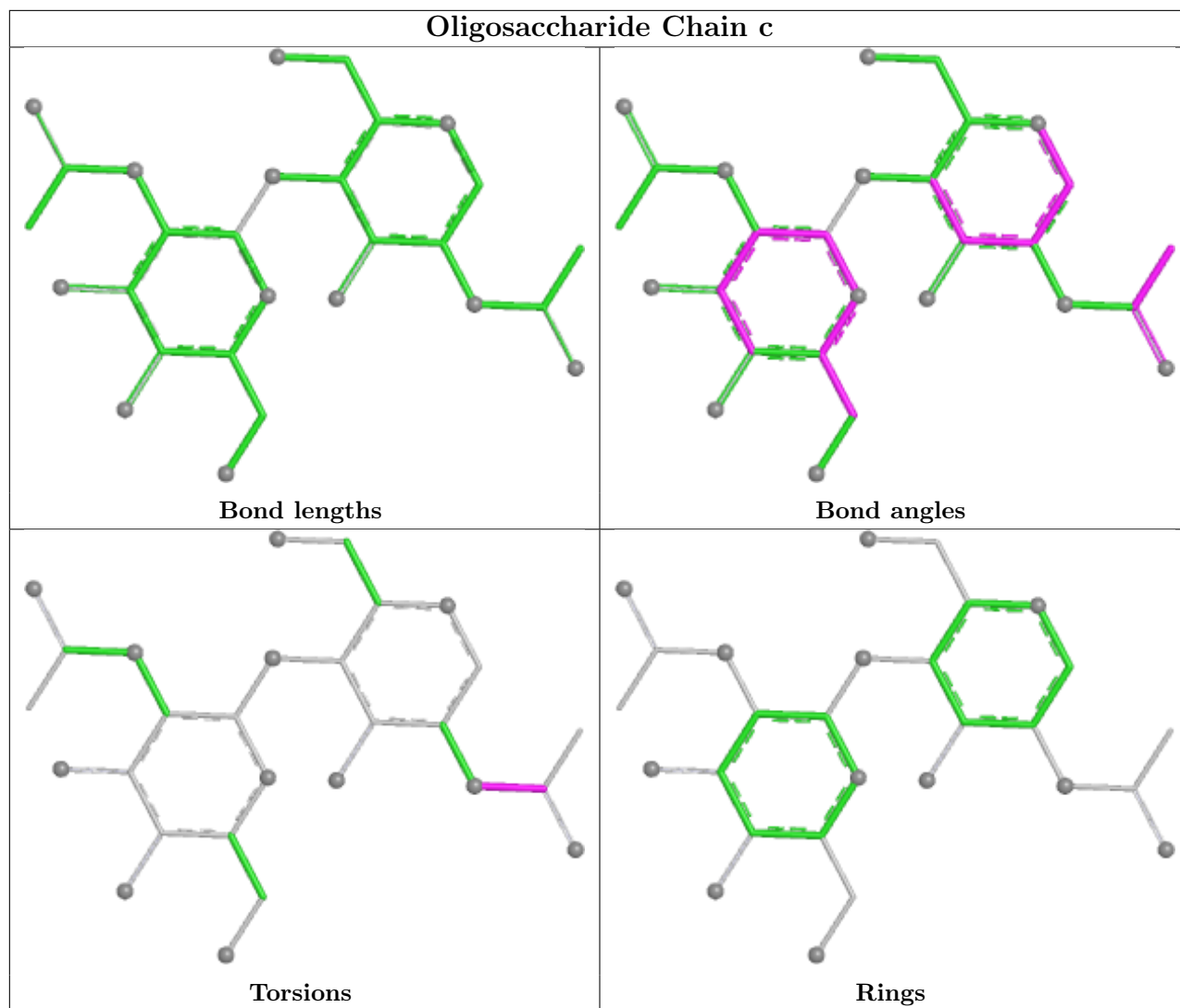


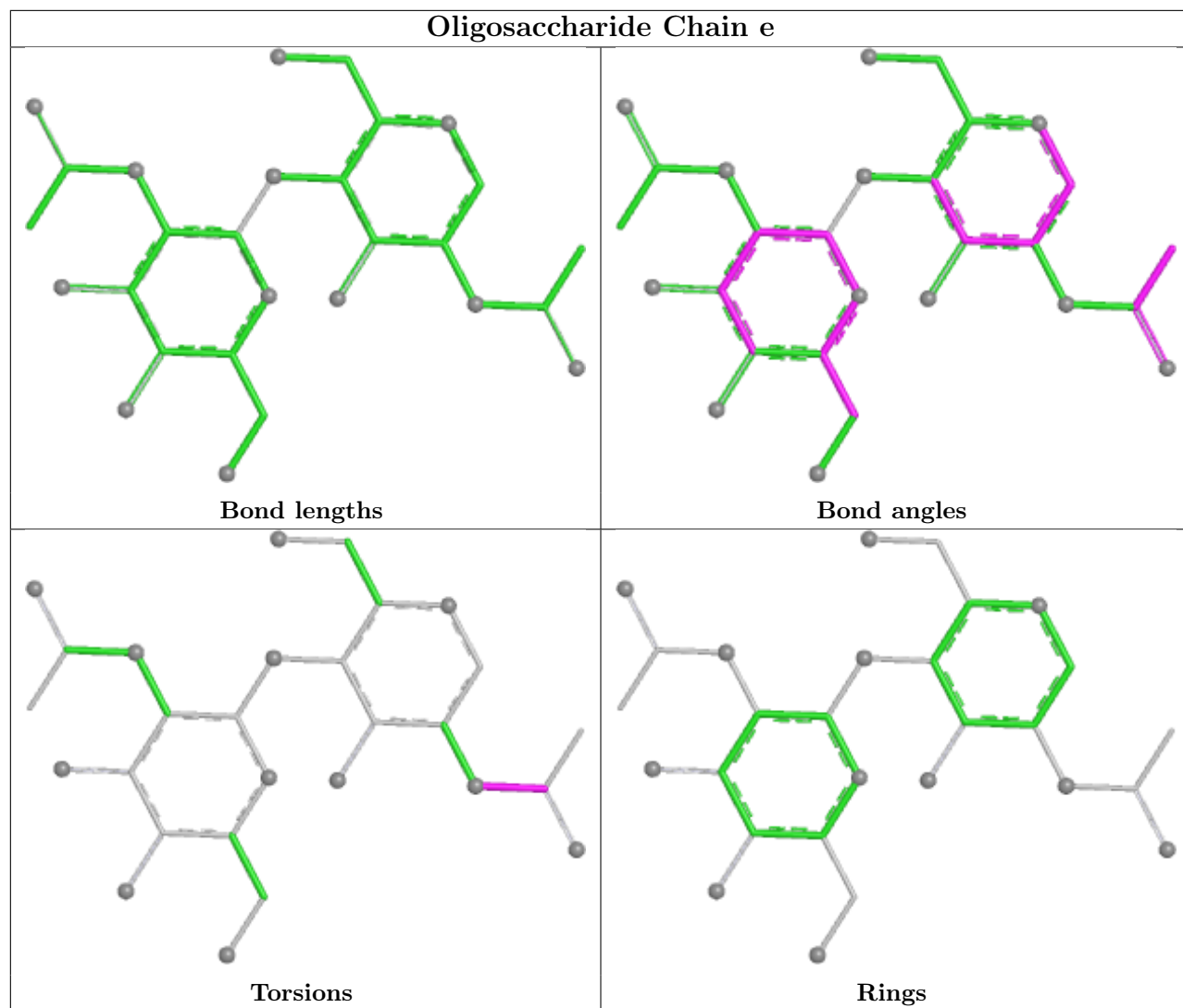


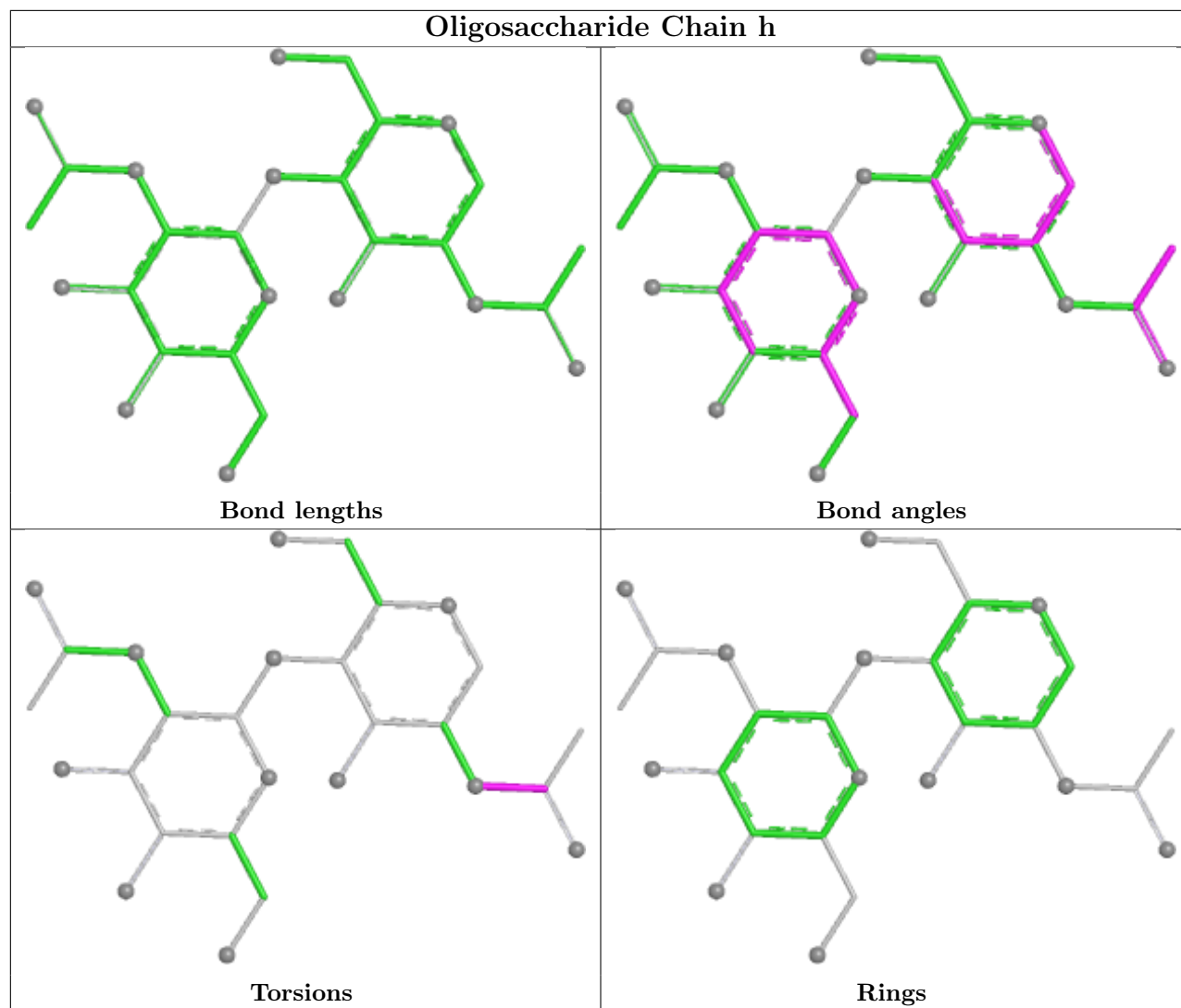


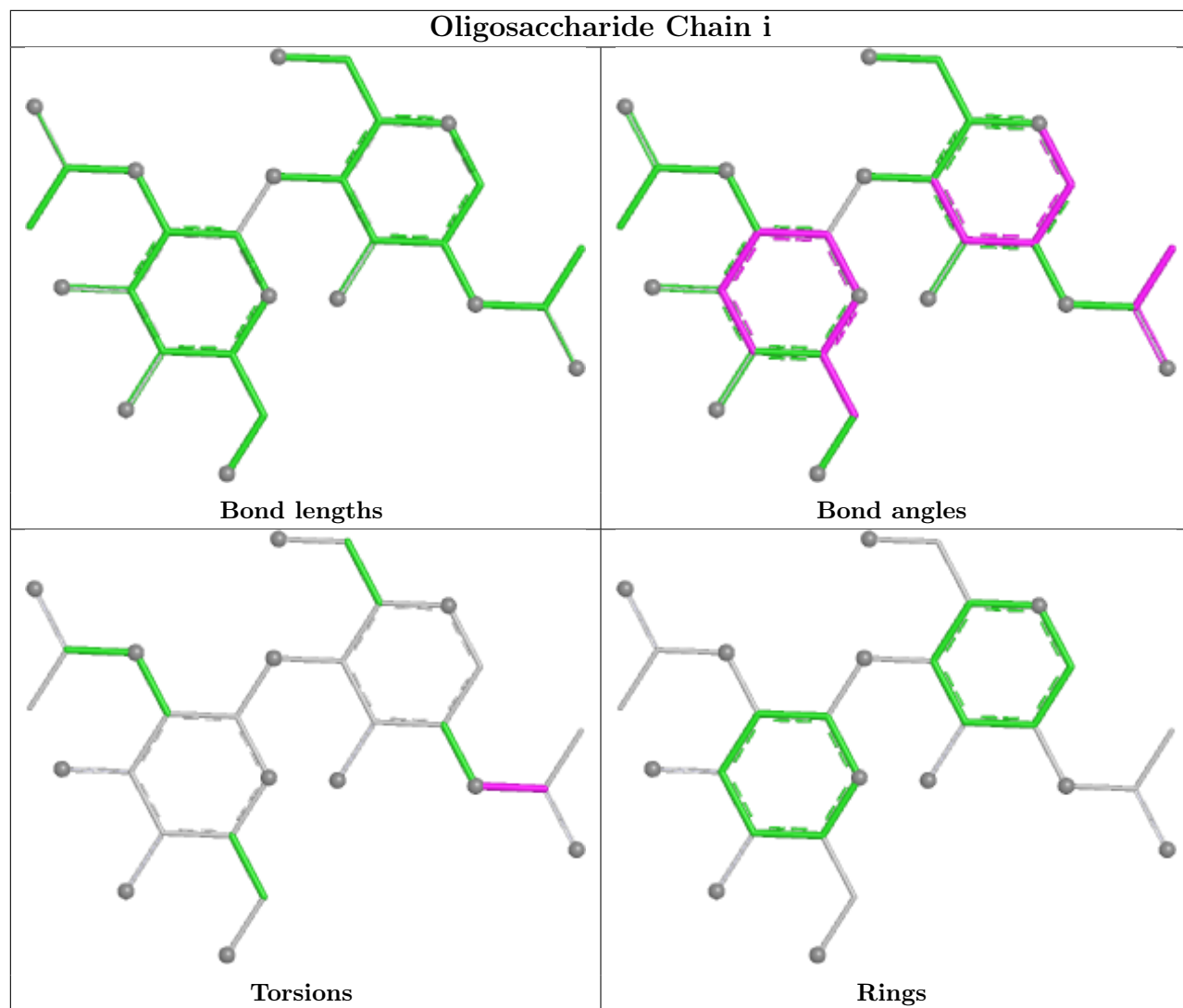


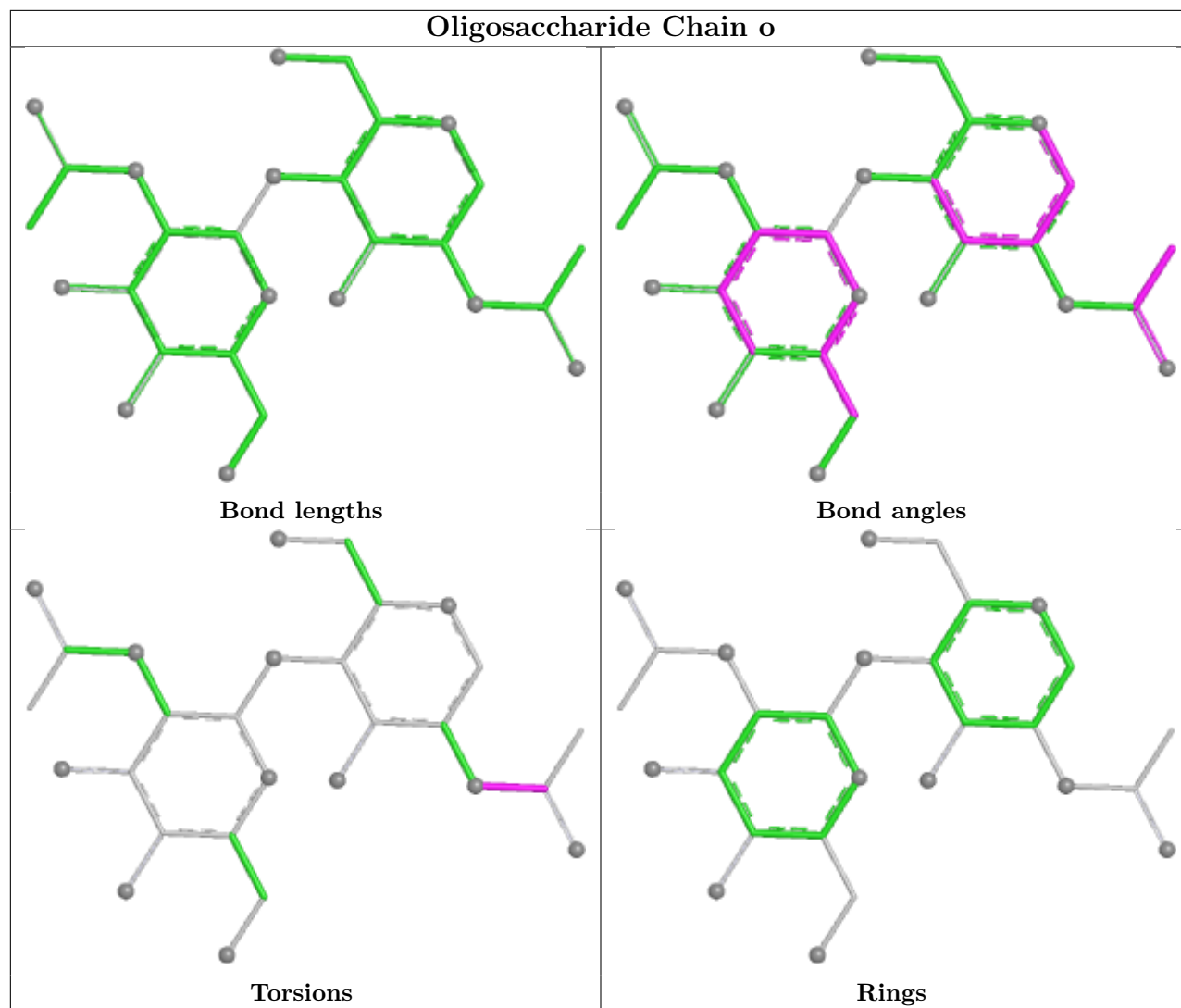


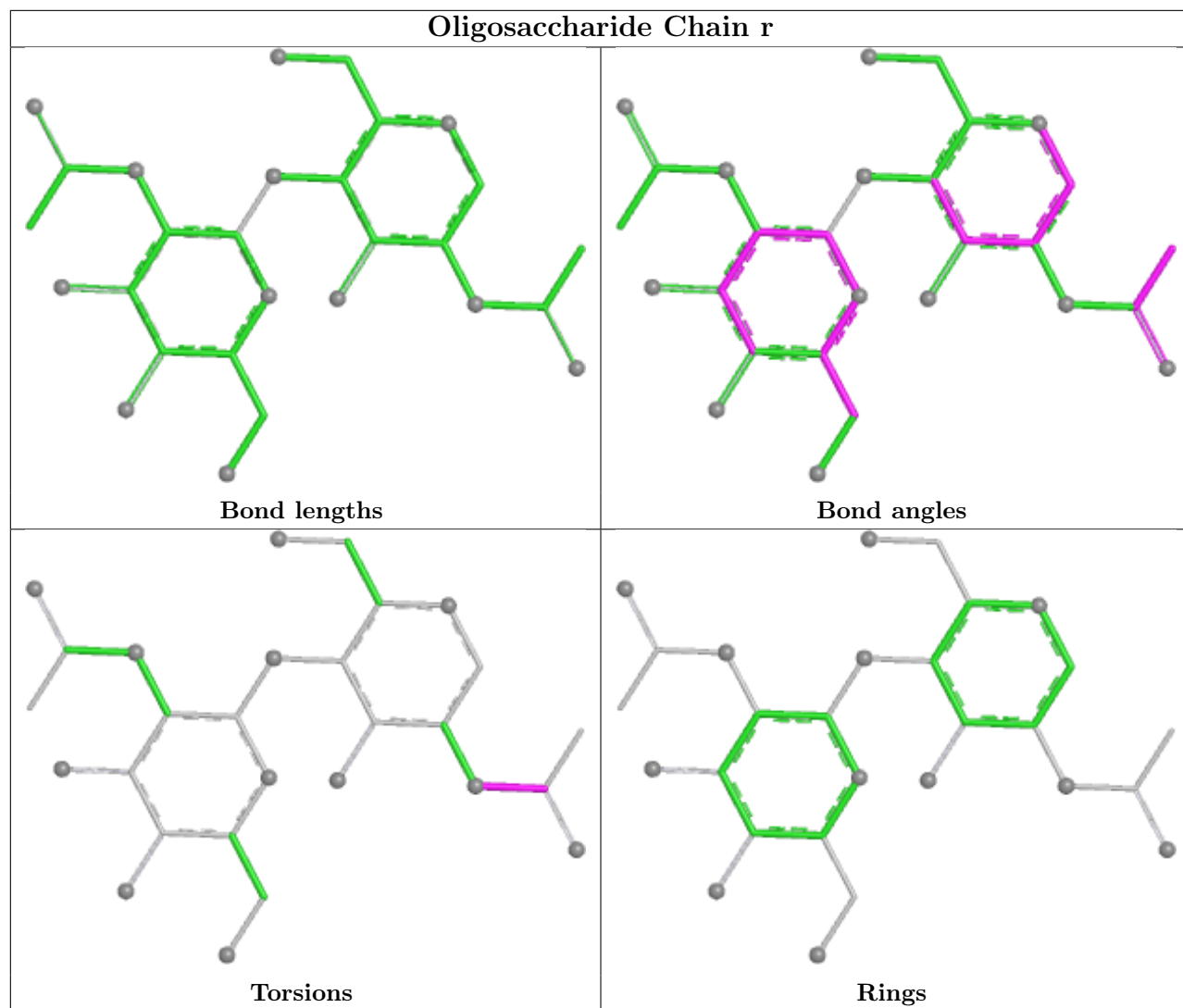


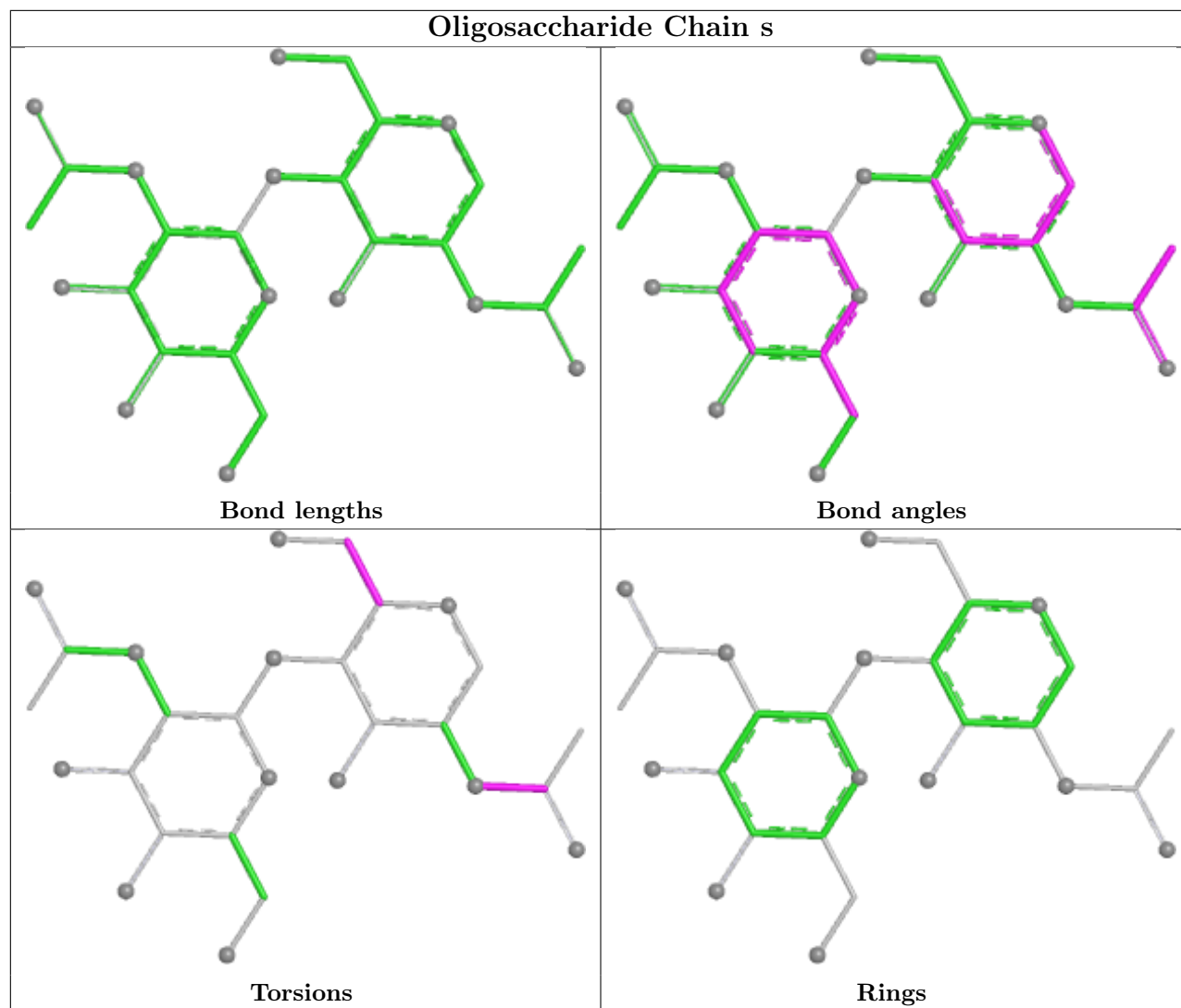


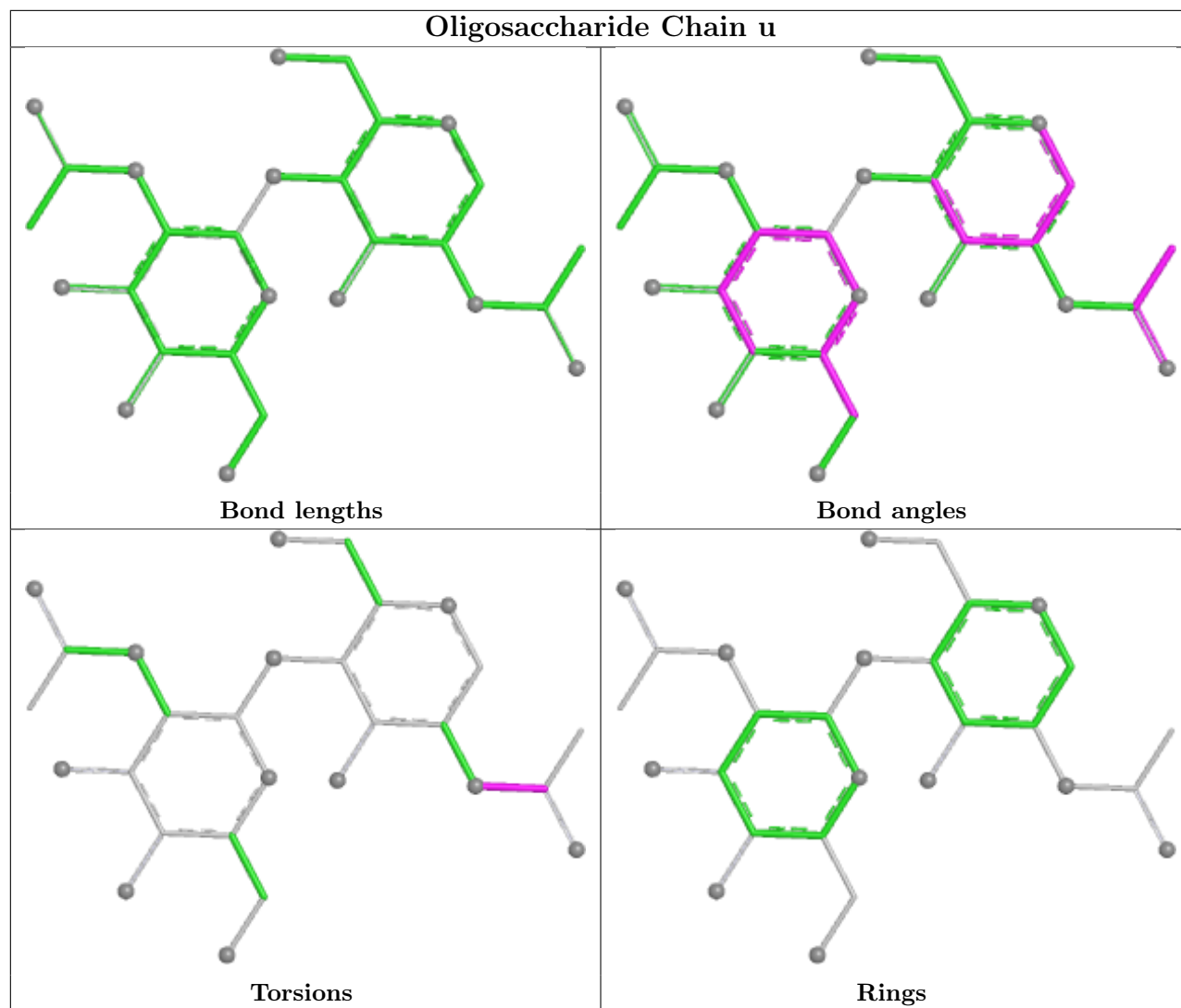


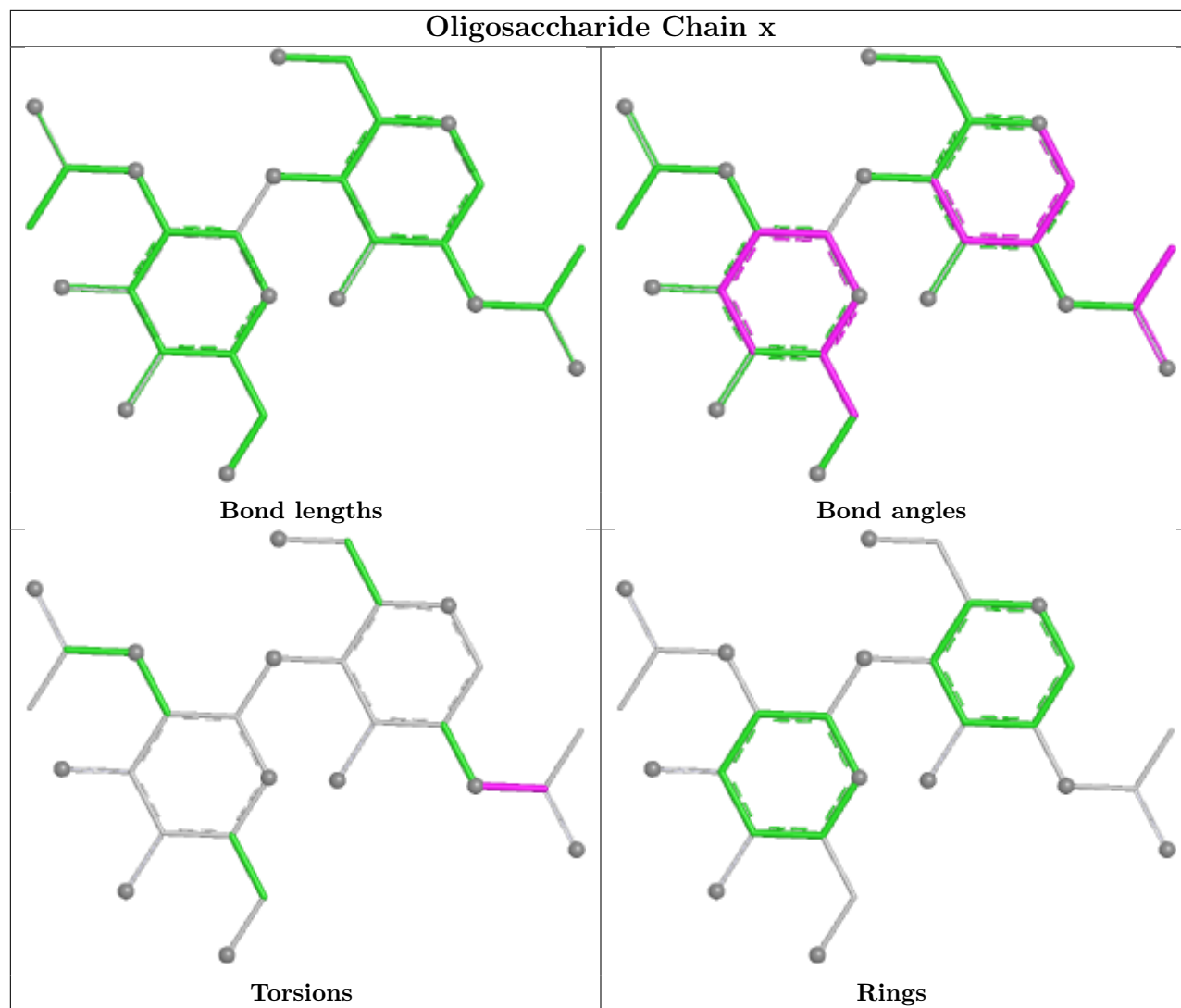


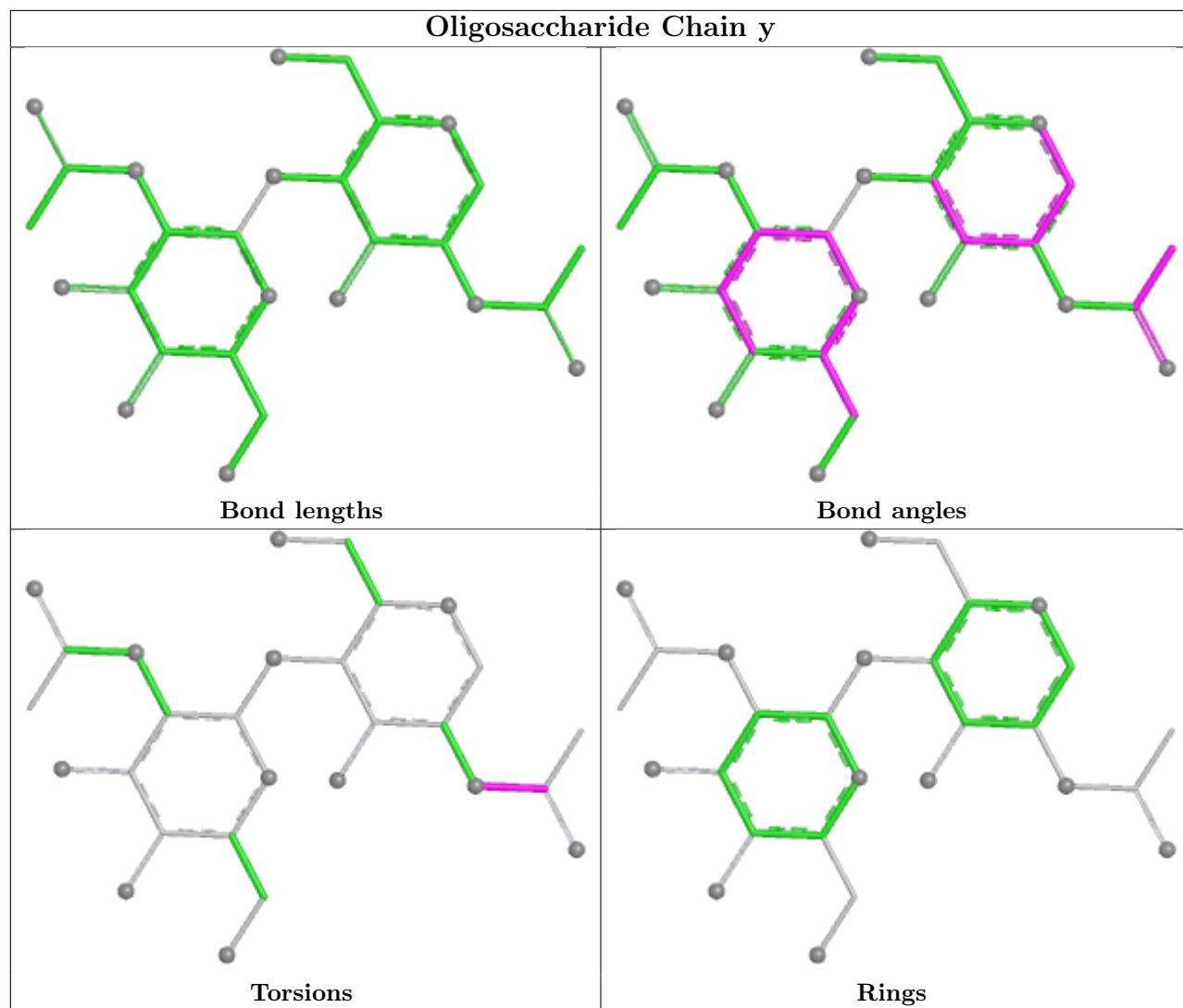


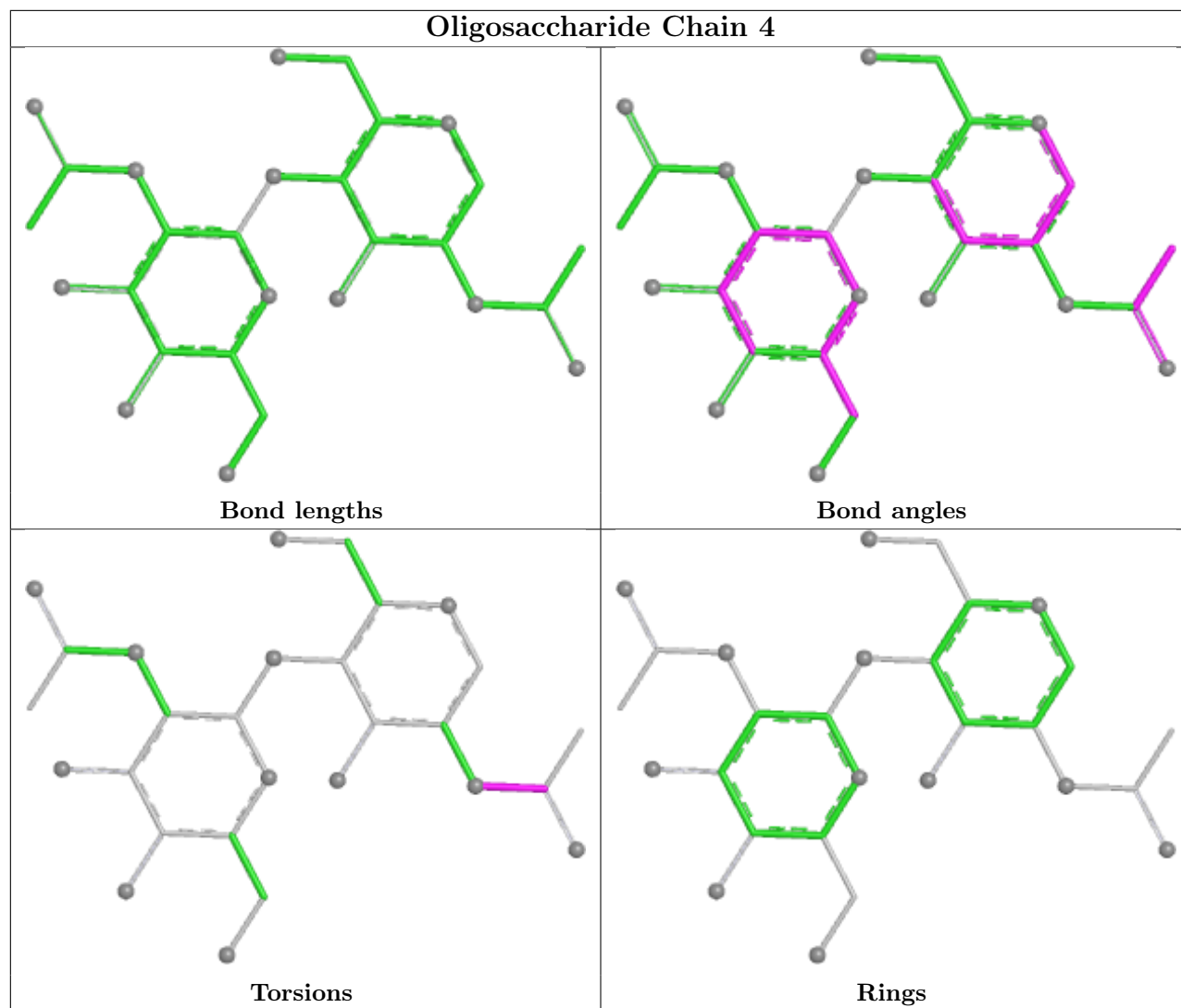


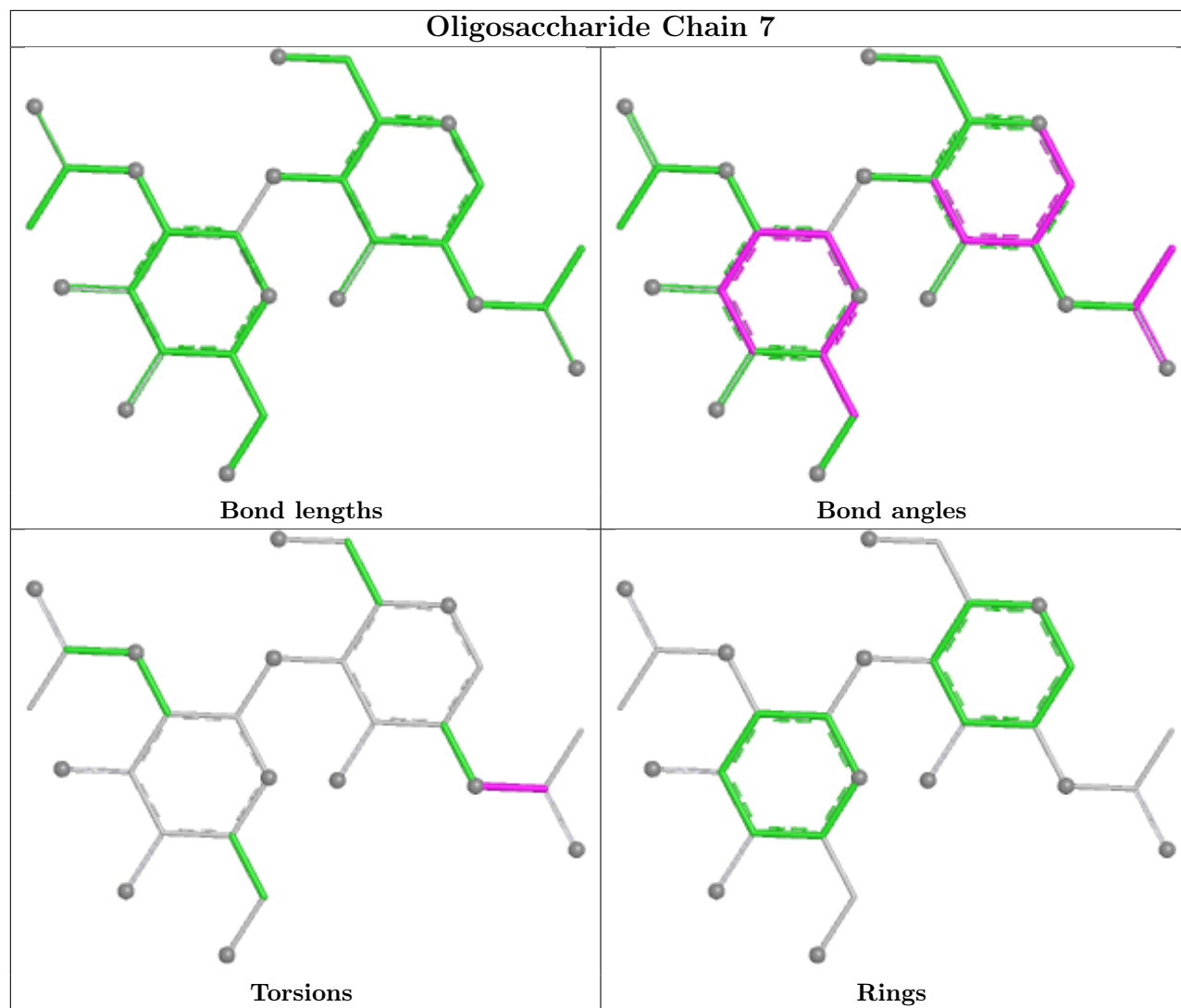


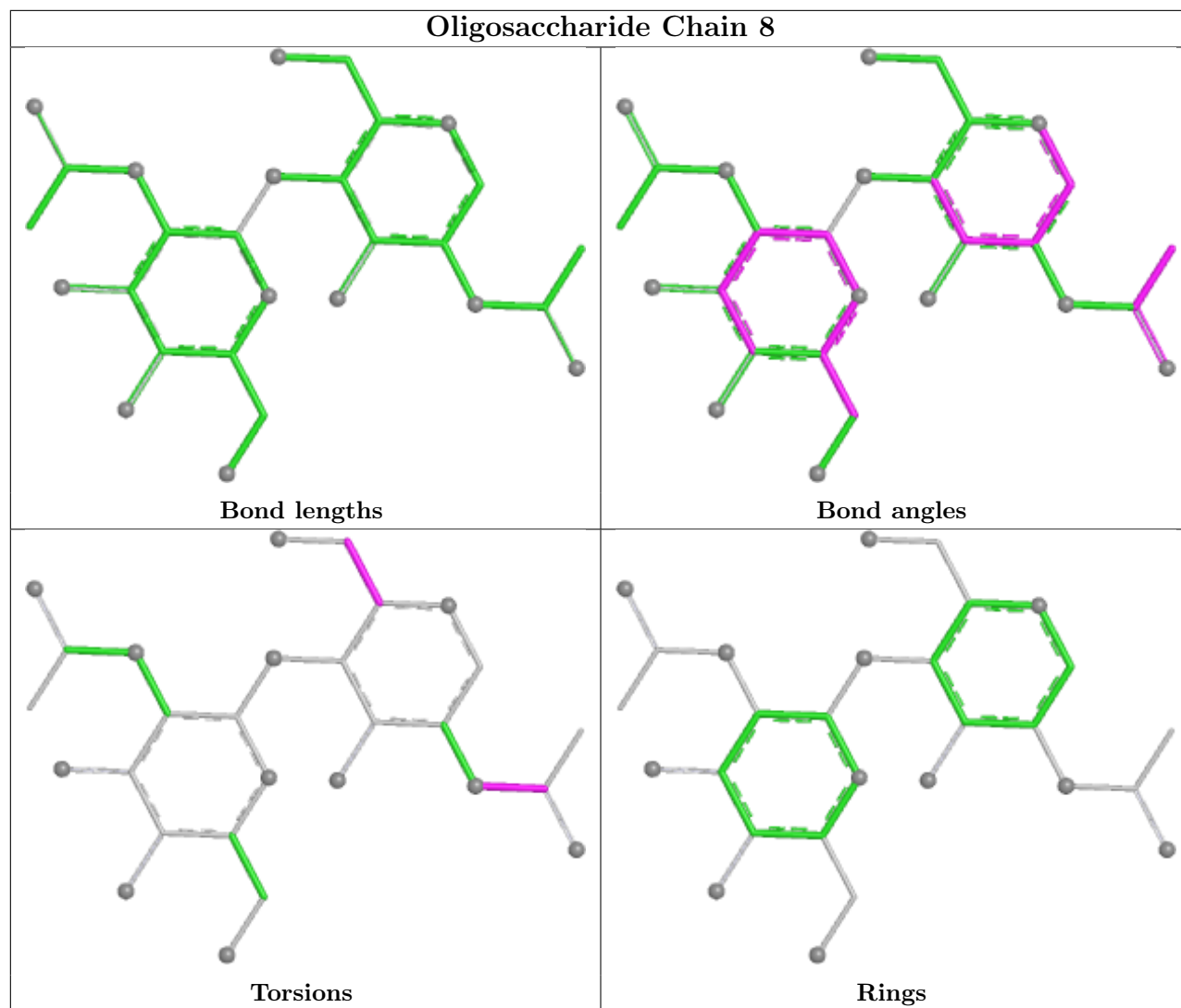


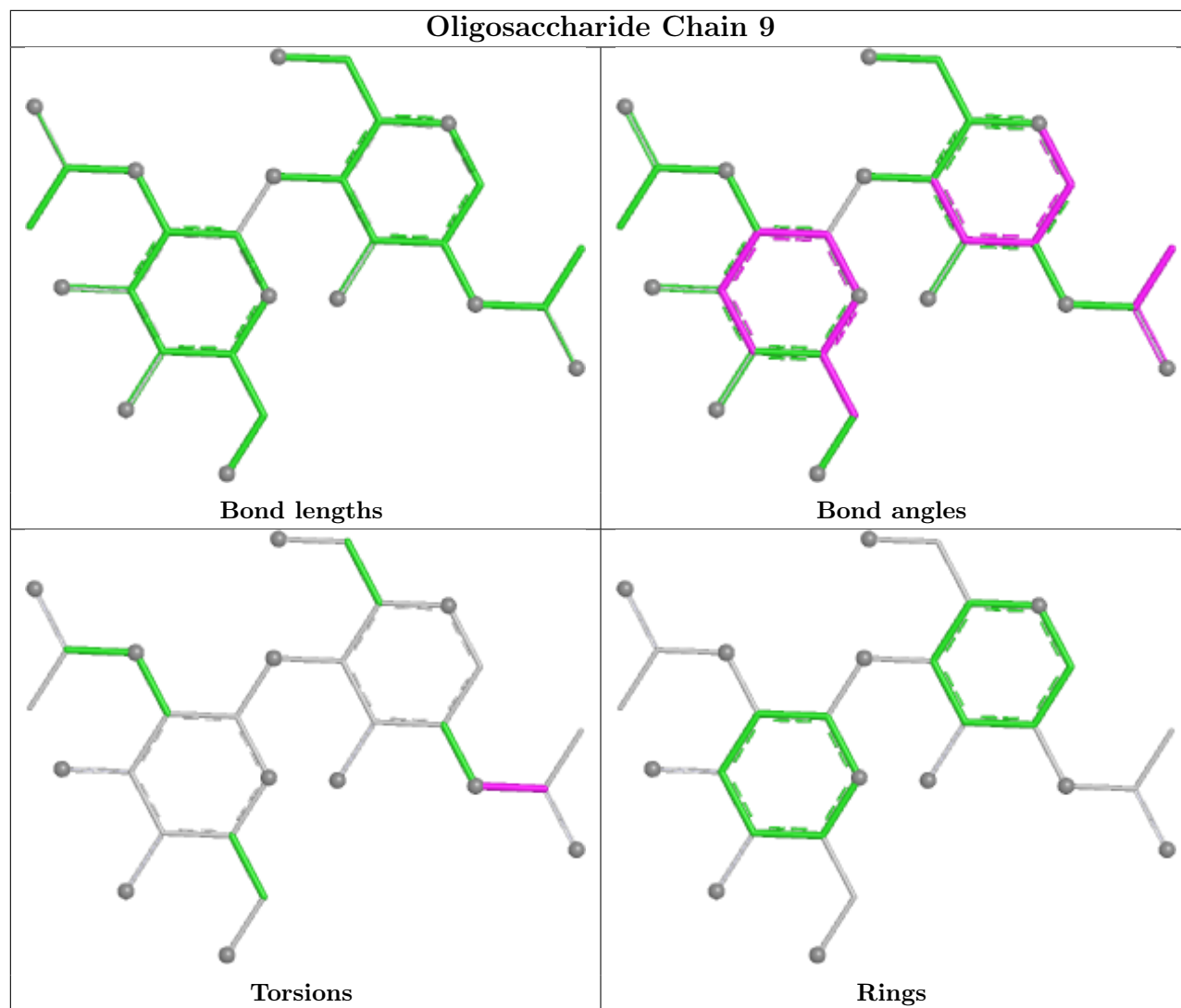


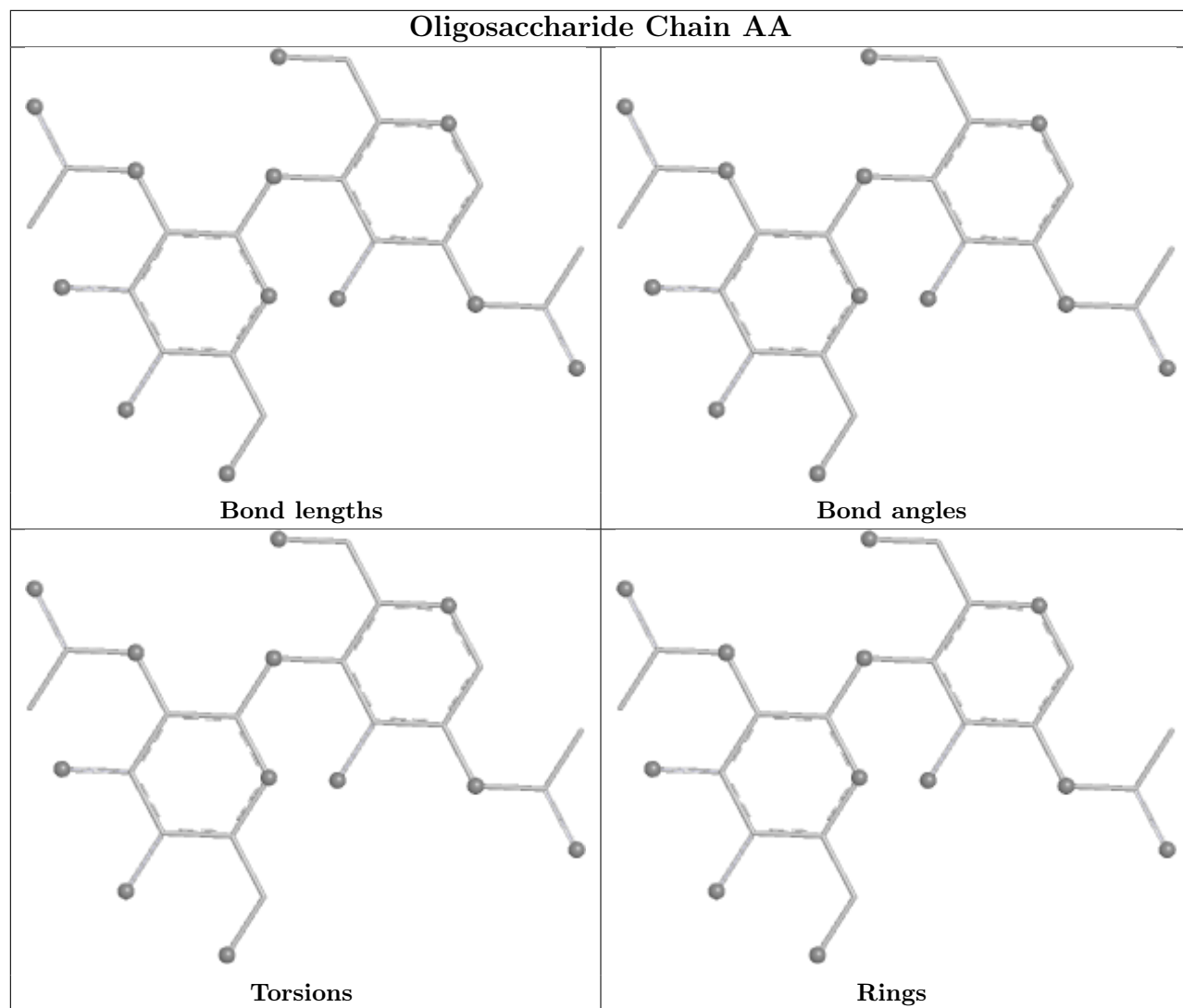


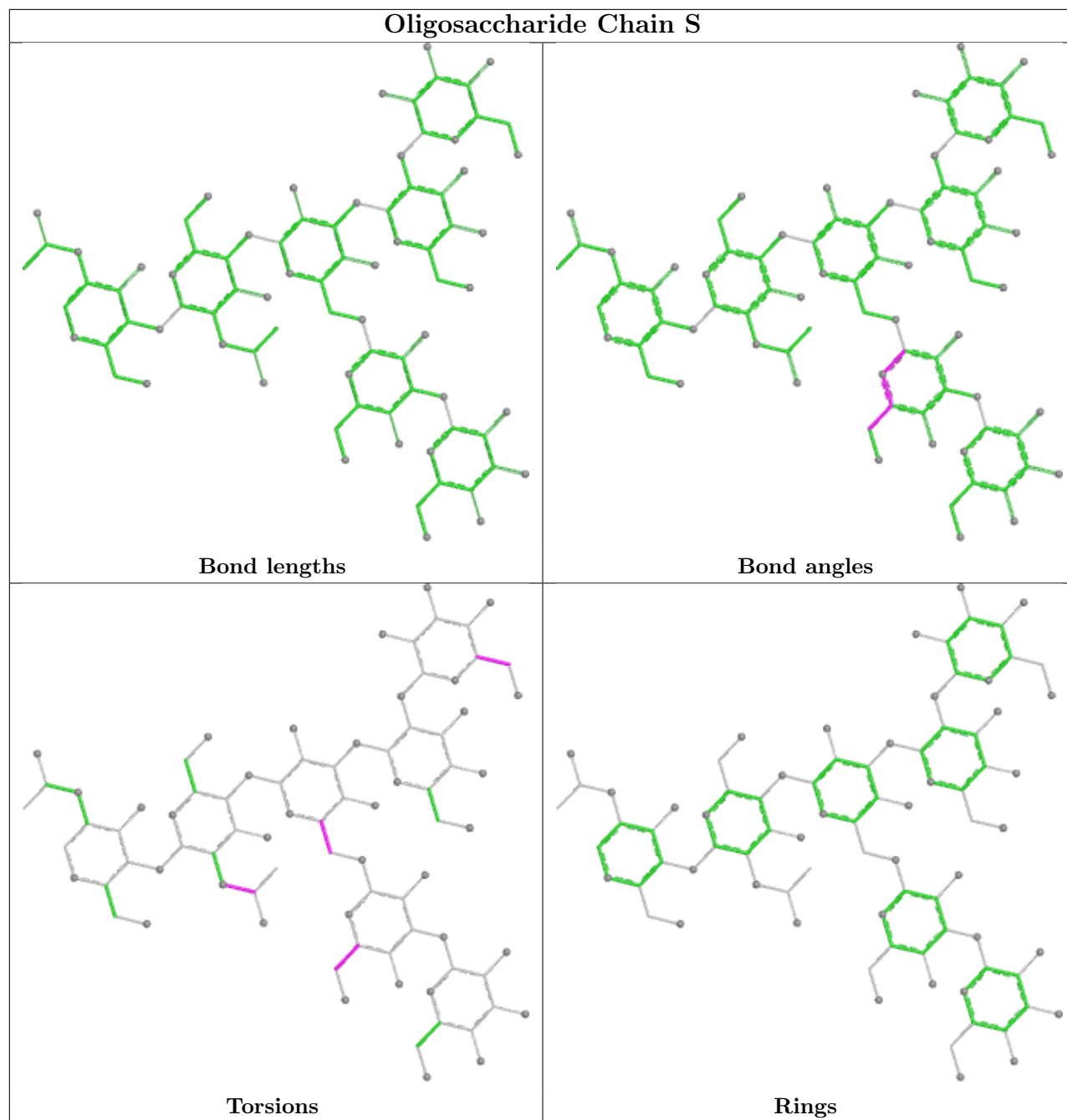


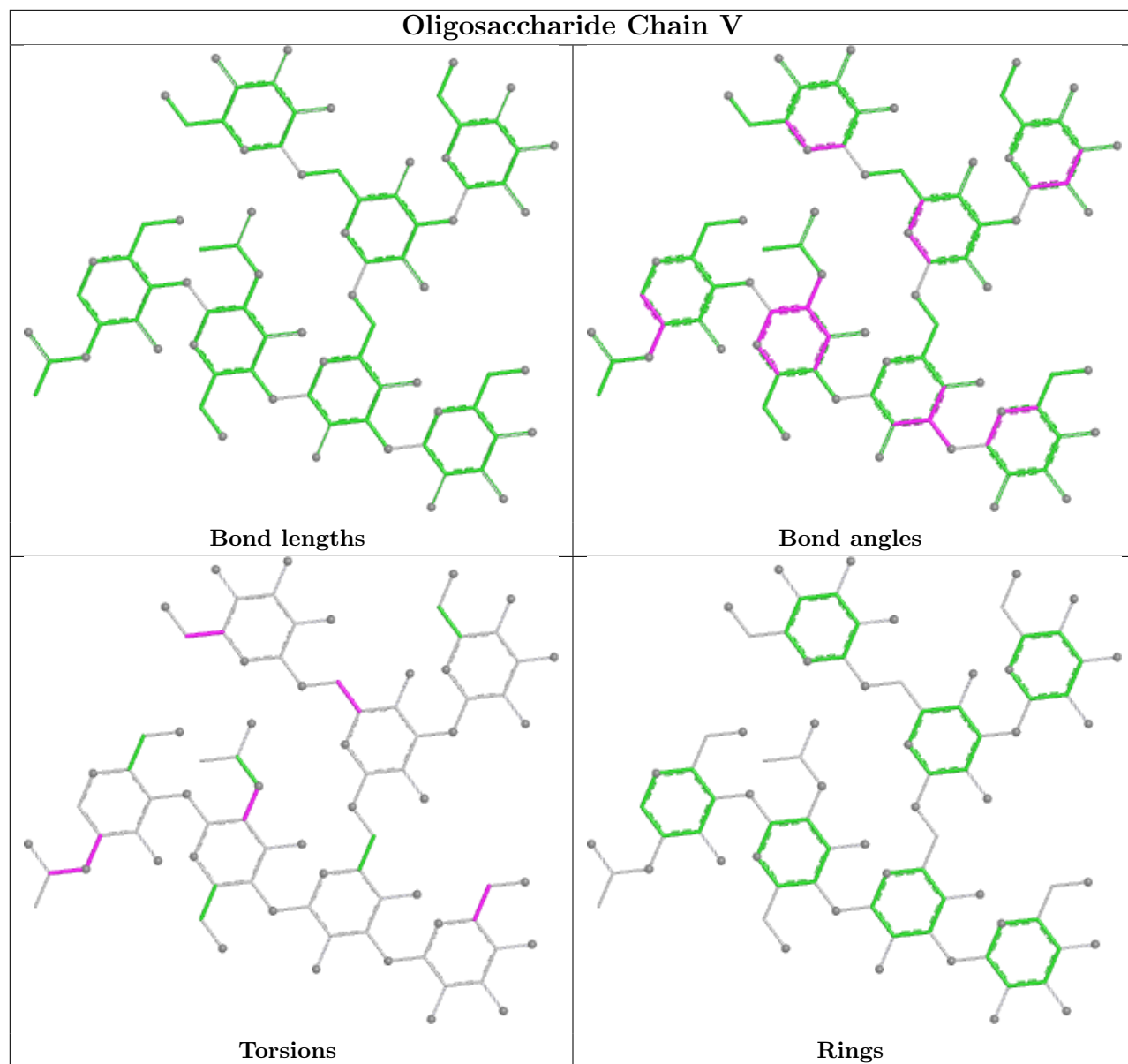


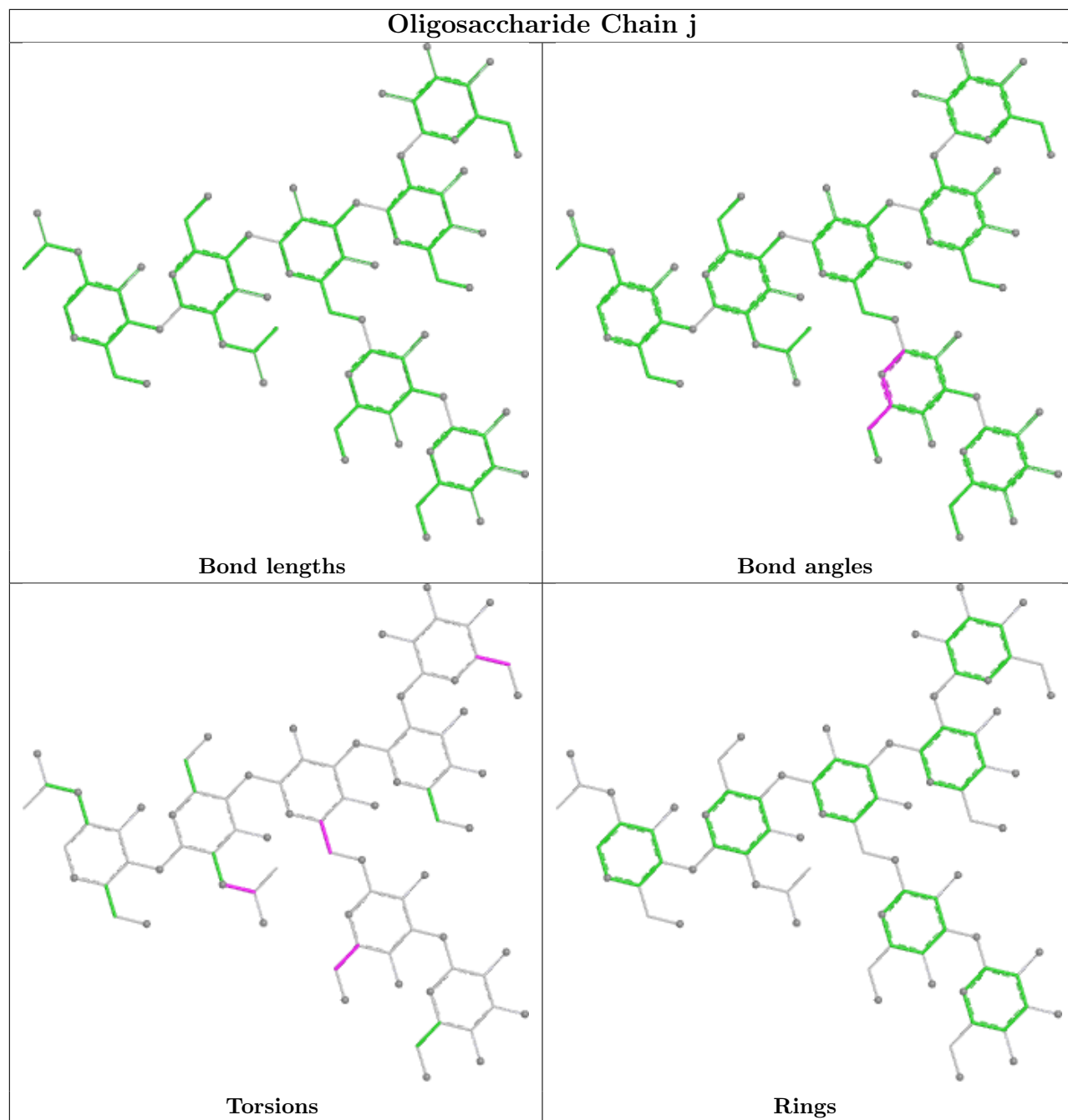


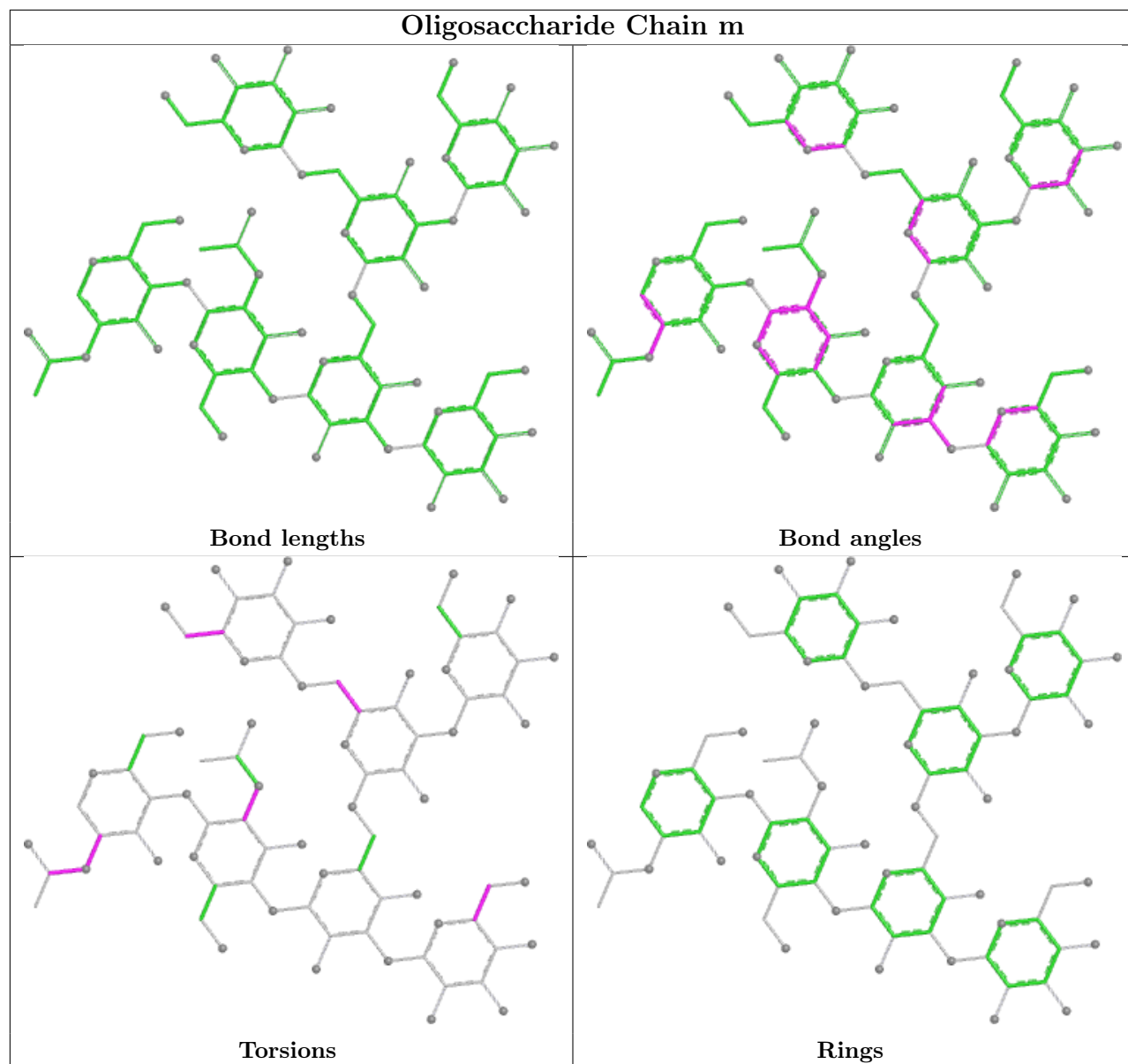


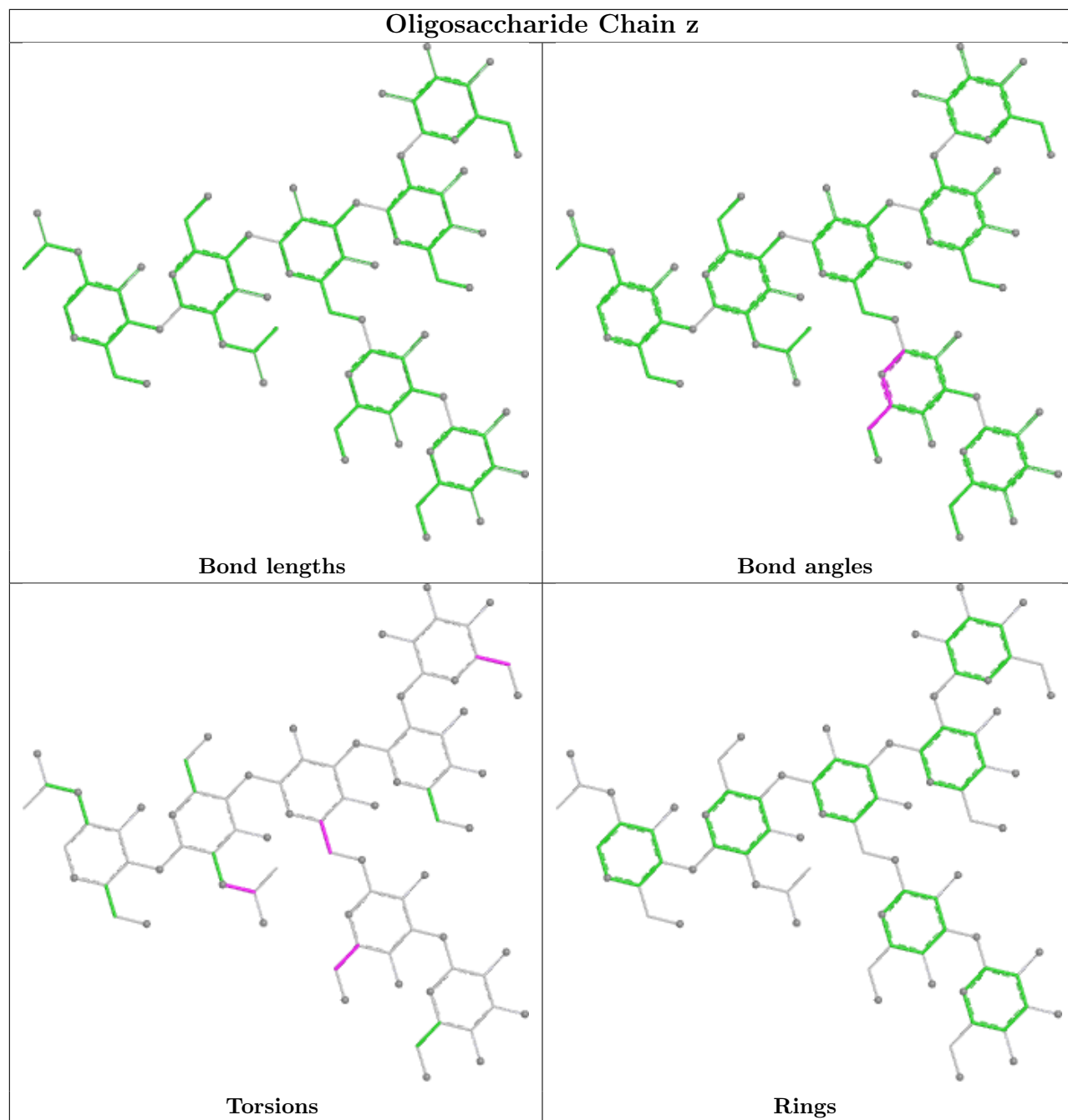


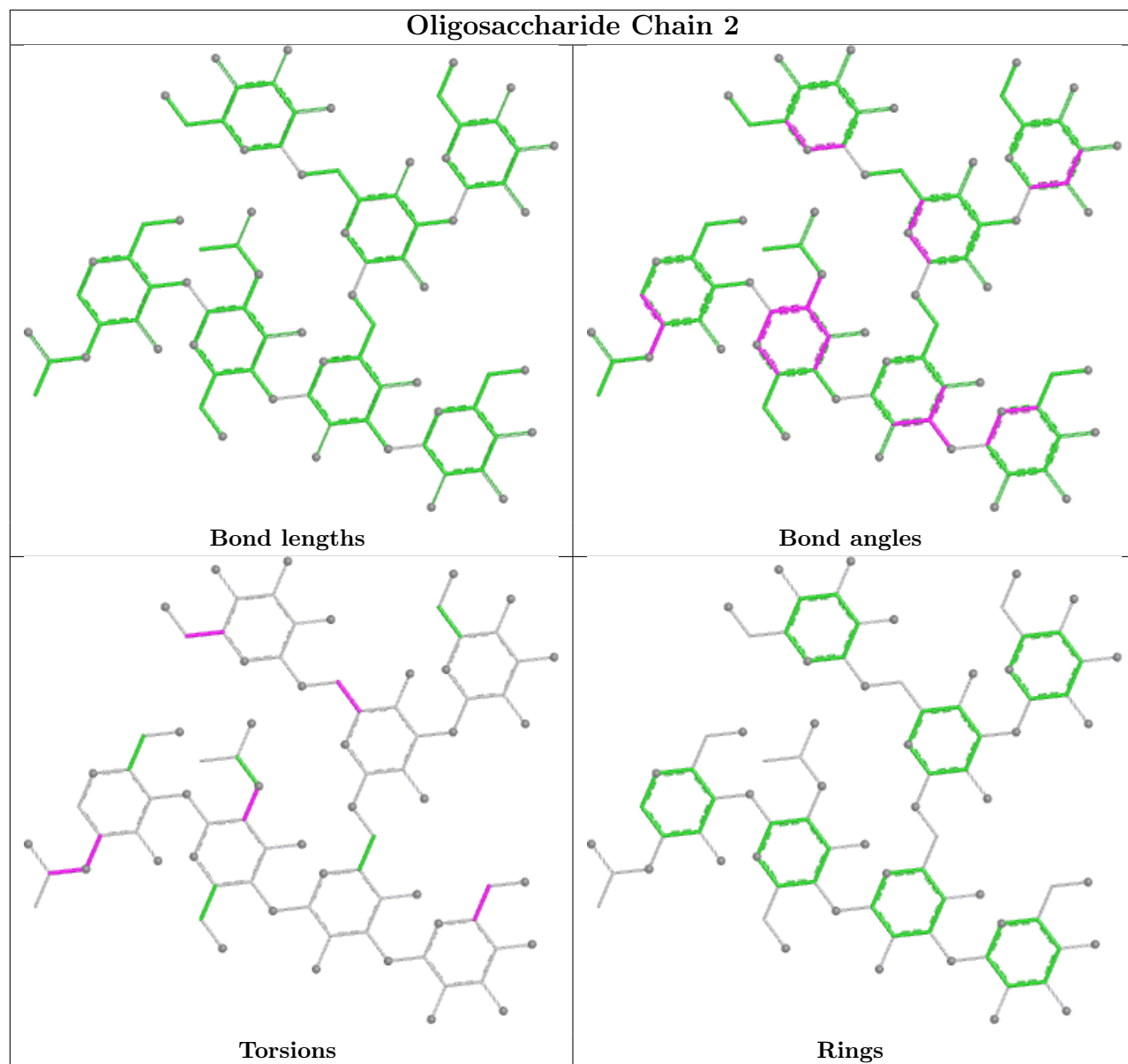


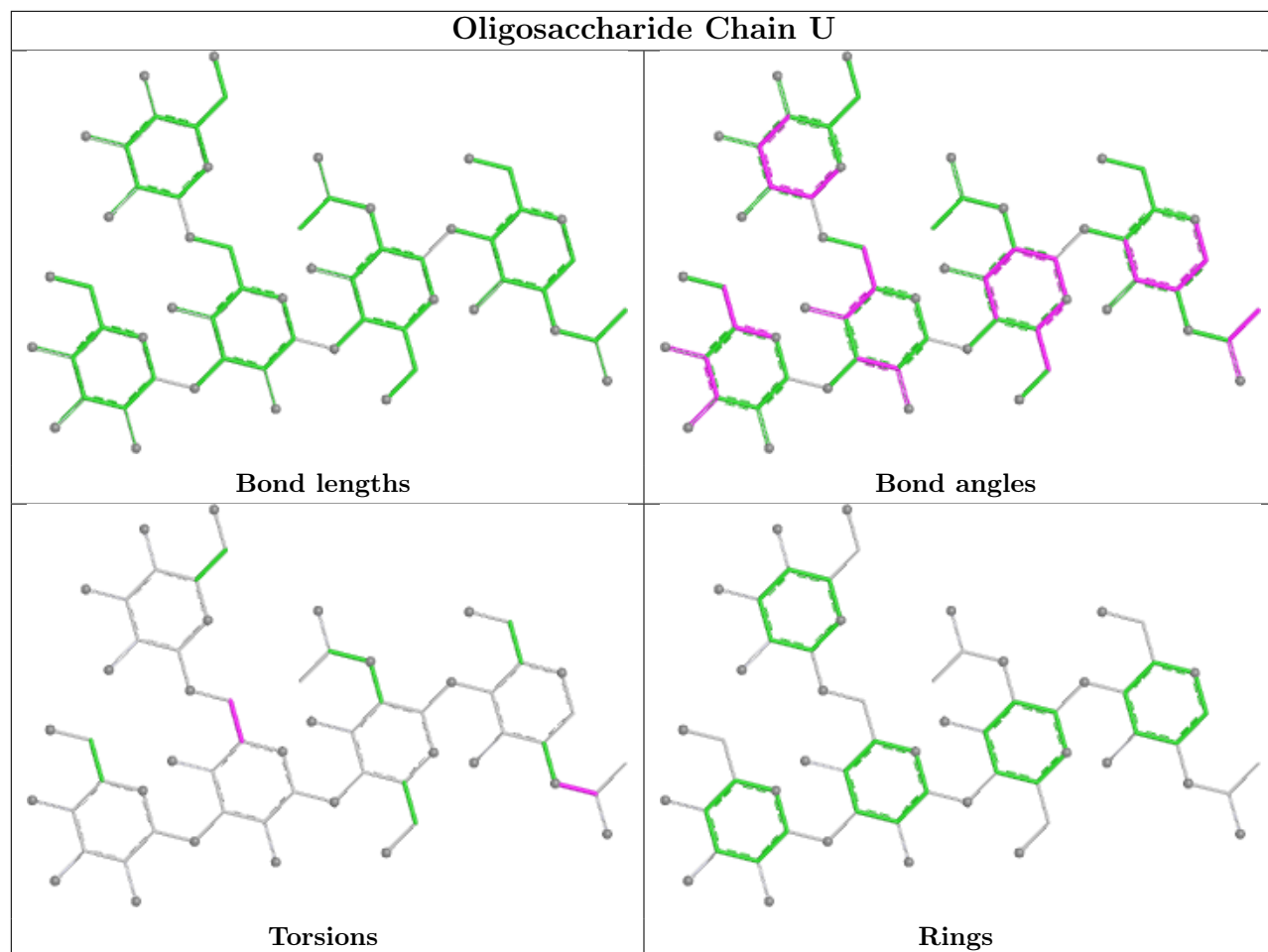


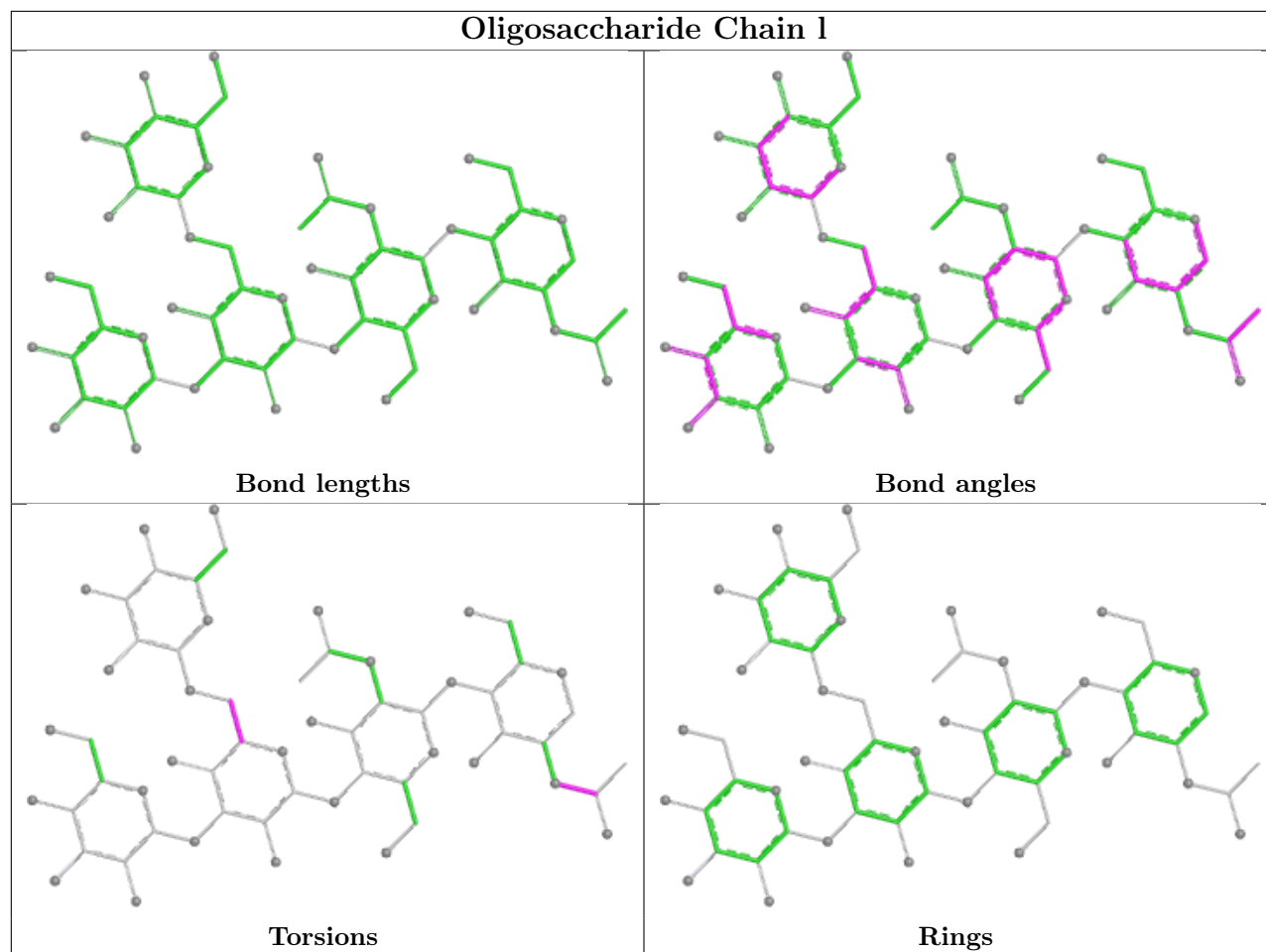


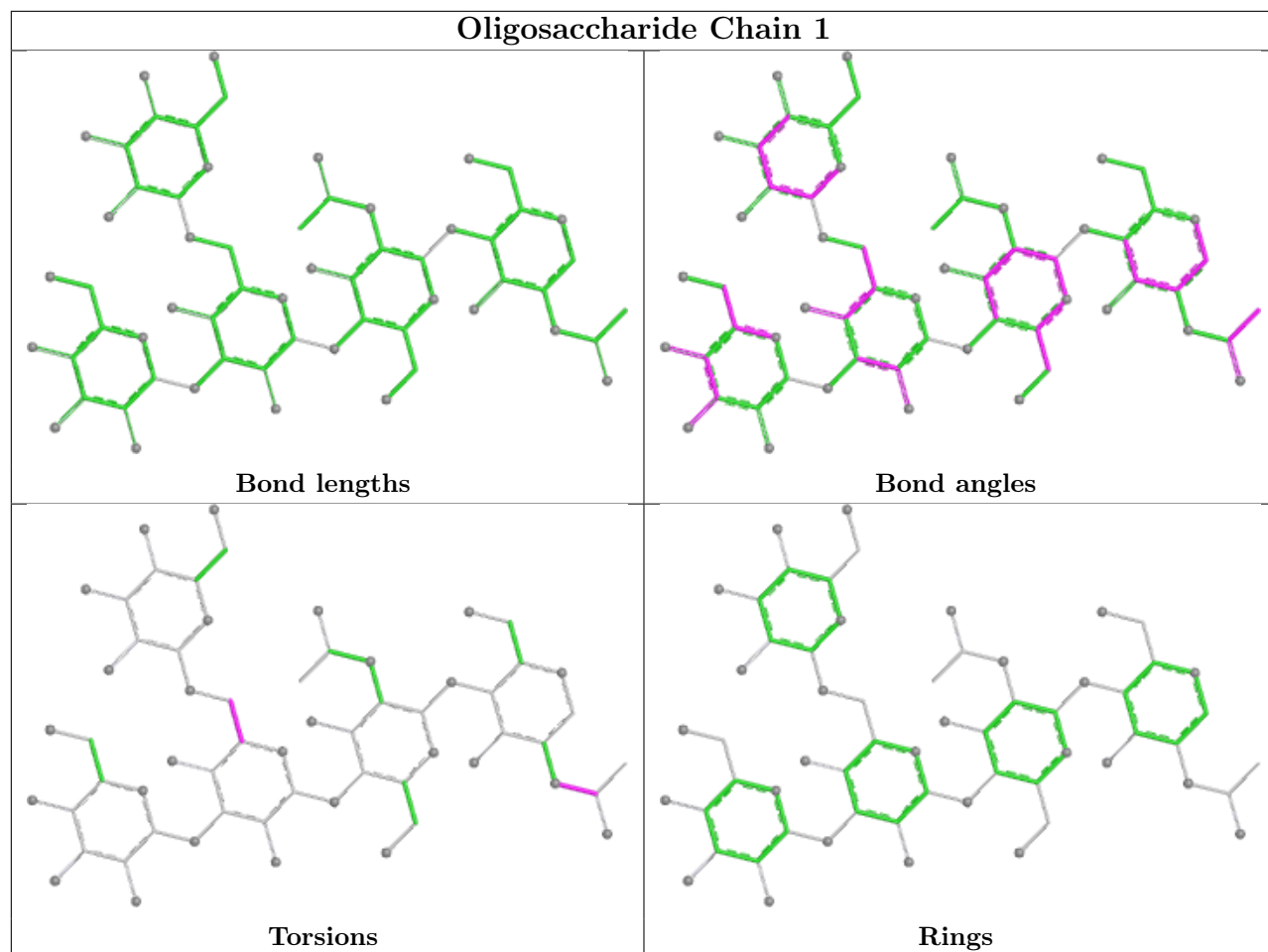


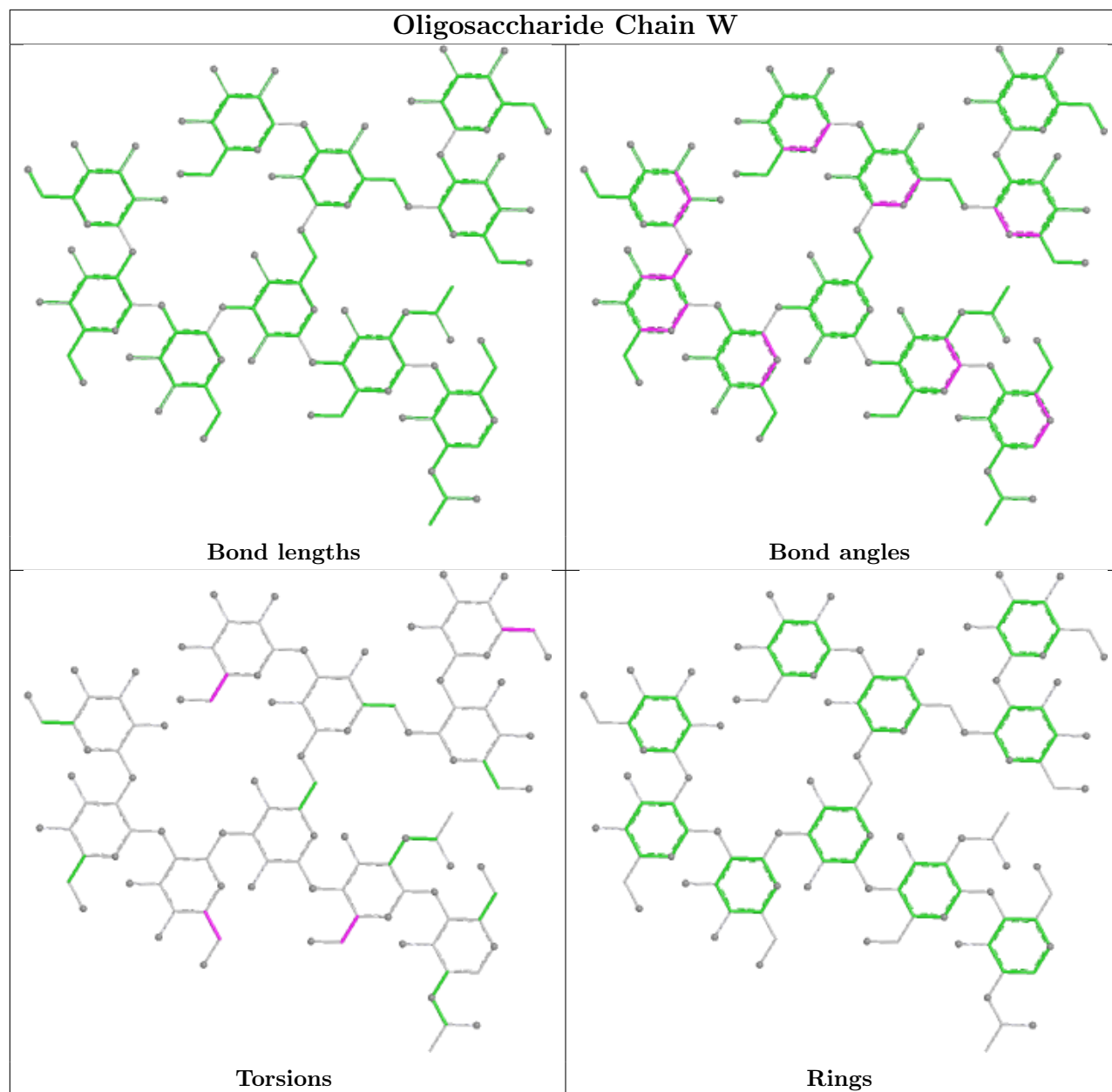


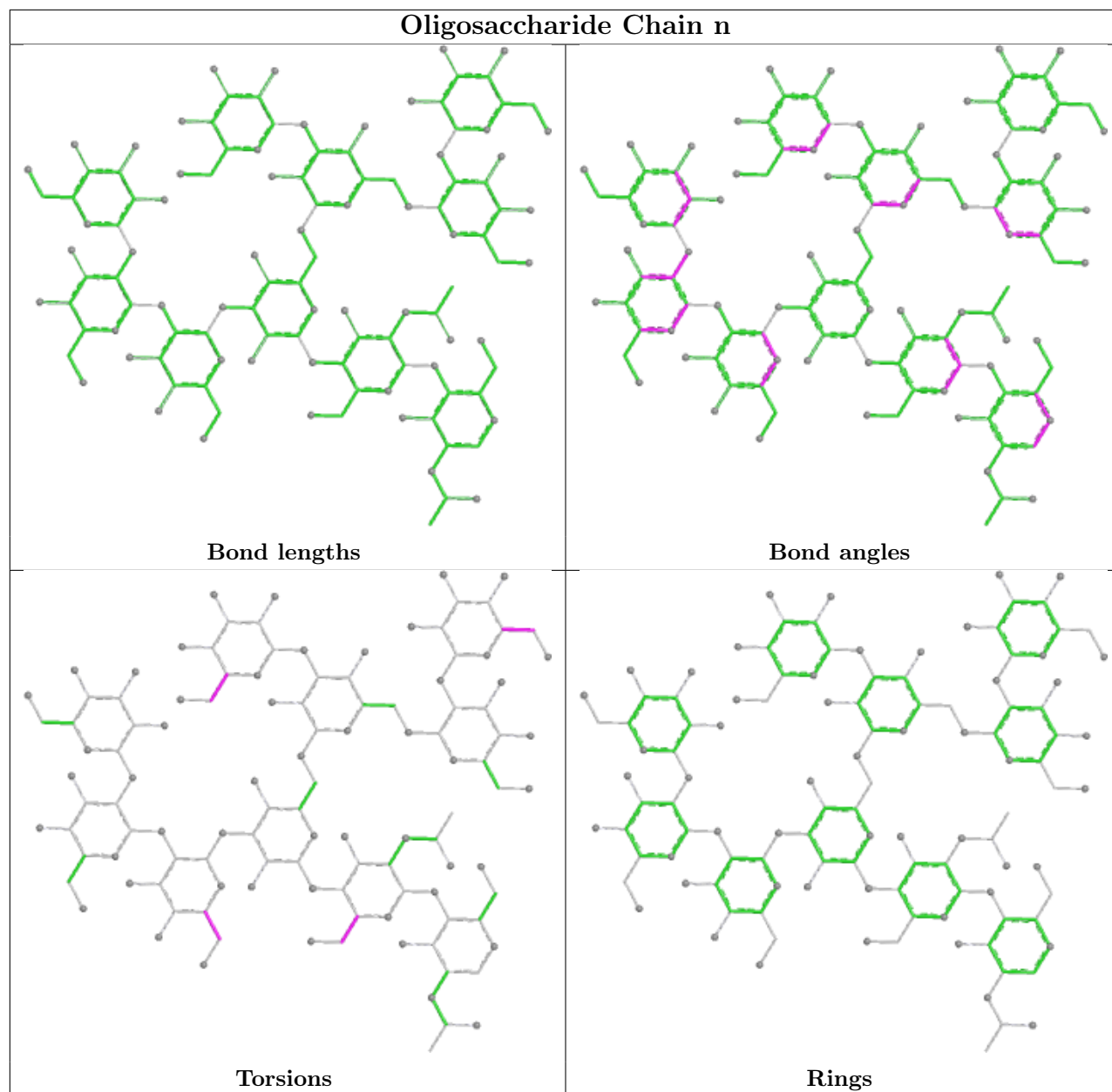


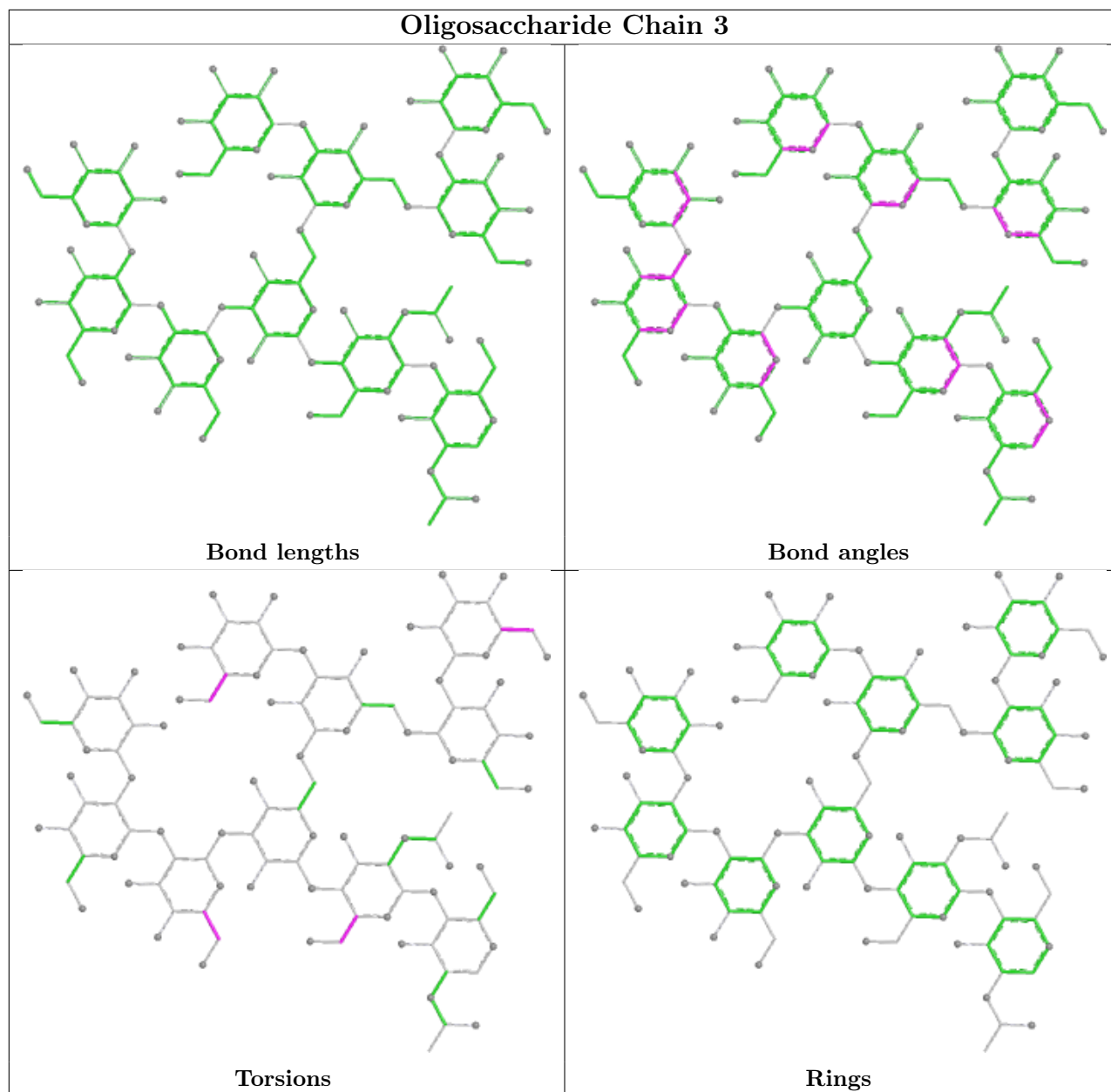












5.6 Ligand geometry [i](#)

9 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
10	NAG	B	1637	2	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
10	NAG	D	1343	1	14,14,15	0.52	0	17,19,21	2.27	3 (17%)
10	NAG	E	1618	2	14,14,15	0.51	0	17,19,21	2.28	3 (17%)
10	NAG	F	1637	2	14,14,15	0.50	0	17,19,21	2.27	3 (17%)
10	NAG	E	1637	2	14,14,15	0.49	0	17,19,21	2.28	3 (17%)
10	NAG	F	1618	2	14,14,15	0.50	0	17,19,21	2.28	3 (17%)
10	NAG	B	1618	2	14,14,15	0.51	0	17,19,21	2.28	3 (17%)
10	NAG	C	1343	1	14,14,15	0.50	0	17,19,21	2.29	3 (17%)
10	NAG	A	1343	1	14,14,15	0.51	0	17,19,21	2.28	3 (17%)

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
10	NAG	B	1637	2	-	1/6/23/26	0/1/1/1
10	NAG	D	1343	1	-	1/6/23/26	0/1/1/1
10	NAG	E	1618	2	-	2/6/23/26	0/1/1/1
10	NAG	F	1637	2	-	1/6/23/26	0/1/1/1
10	NAG	E	1637	2	-	1/6/23/26	0/1/1/1
10	NAG	F	1618	2	-	2/6/23/26	0/1/1/1
10	NAG	B	1618	2	-	2/6/23/26	0/1/1/1
10	NAG	C	1343	1	-	1/6/23/26	0/1/1/1
10	NAG	A	1343	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	C	1343	NAG	O5-C1-C2	-7.55	99.61	111.29
10	B	1618	NAG	O5-C1-C2	-7.54	99.62	111.29
10	E	1637	NAG	O5-C1-C2	-7.53	99.63	111.29
10	F	1618	NAG	O5-C1-C2	-7.53	99.64	111.29
10	A	1343	NAG	O5-C1-C2	-7.53	99.64	111.29

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	1618	NAG	C3-C2-N2-C7
10	E	1618	NAG	C3-C2-N2-C7
10	F	1618	NAG	C3-C2-N2-C7
10	B	1618	NAG	O7-C7-N2-C2
10	E	1618	NAG	O7-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	E	1618	NAG	1	0
10	F	1618	NAG	1	0
10	B	1618	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1
2	E	1
2	F	1
1	A	1
1	C	1
1	D	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	658:GLN	C	659:ASP	N	1.61
1	E	658:GLN	C	659:ASP	N	1.61
1	F	658:GLN	C	659:ASP	N	1.61
1	A	92:GLU	C	93:PHE	N	1.19
1	C	92:GLU	C	93:PHE	N	1.19

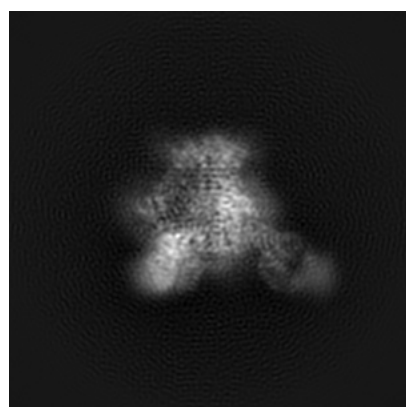
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3121. These allow visual inspection of the internal detail of the map and identification of artifacts.

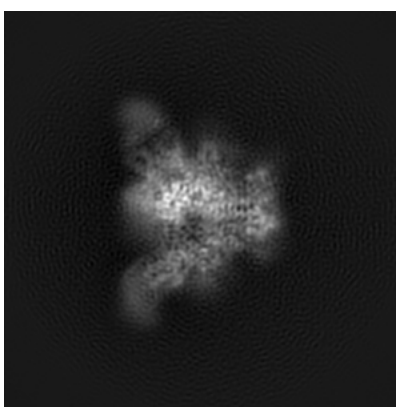
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

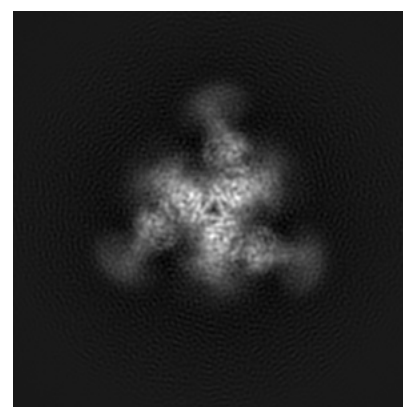
6.1.1 Primary map



X



Y

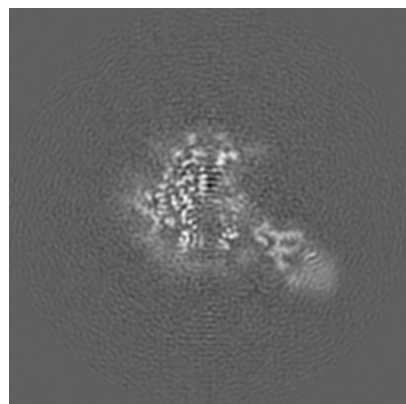


Z

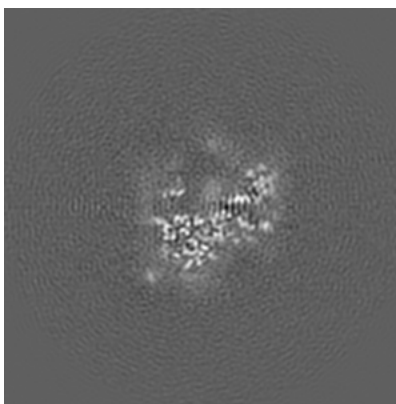
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

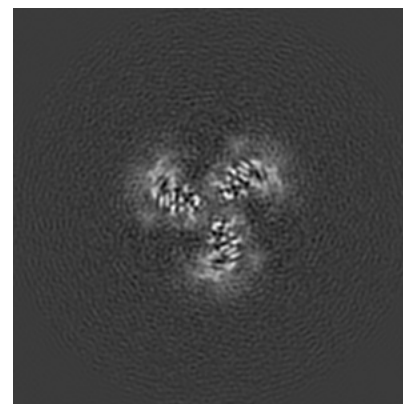
6.2.1 Primary map



X Index: 128



Y Index: 128

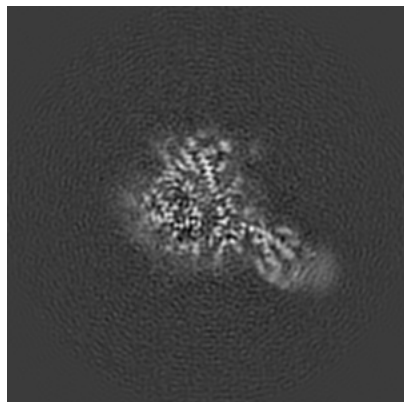


Z Index: 128

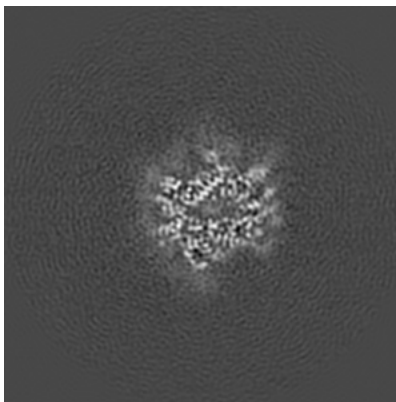
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

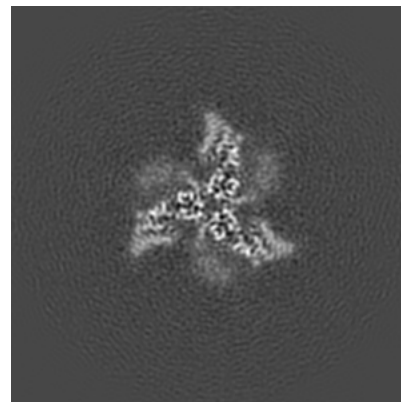
6.3.1 Primary map



X Index: 133



Y Index: 136

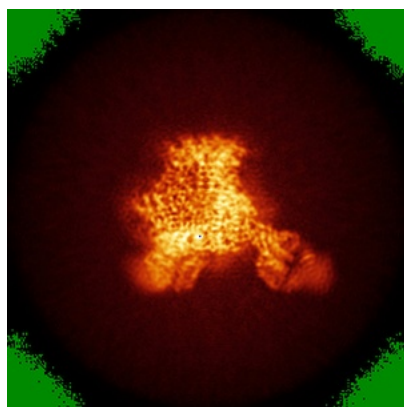


Z Index: 110

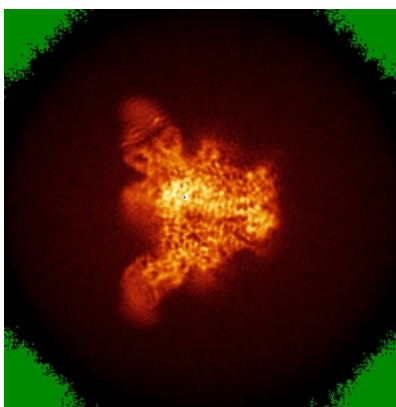
The images above show the largest variance slices of the map in three orthogonal directions.

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

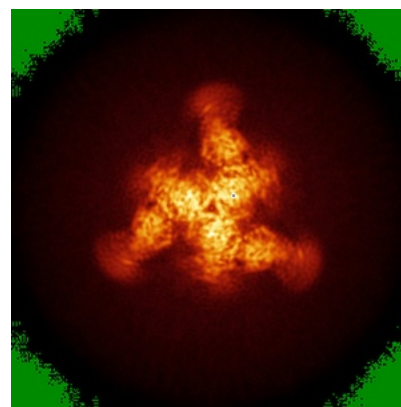
6.4.1 Primary map



X



Y

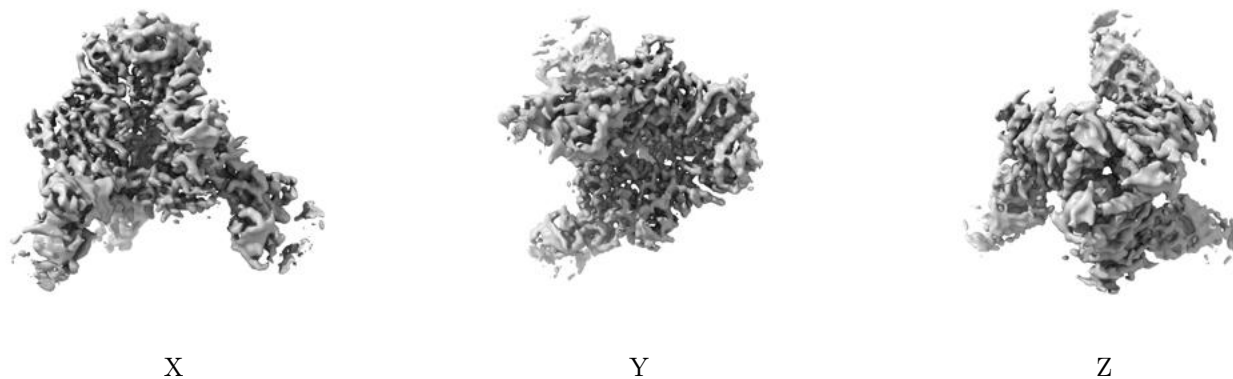


Z

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 0.041. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

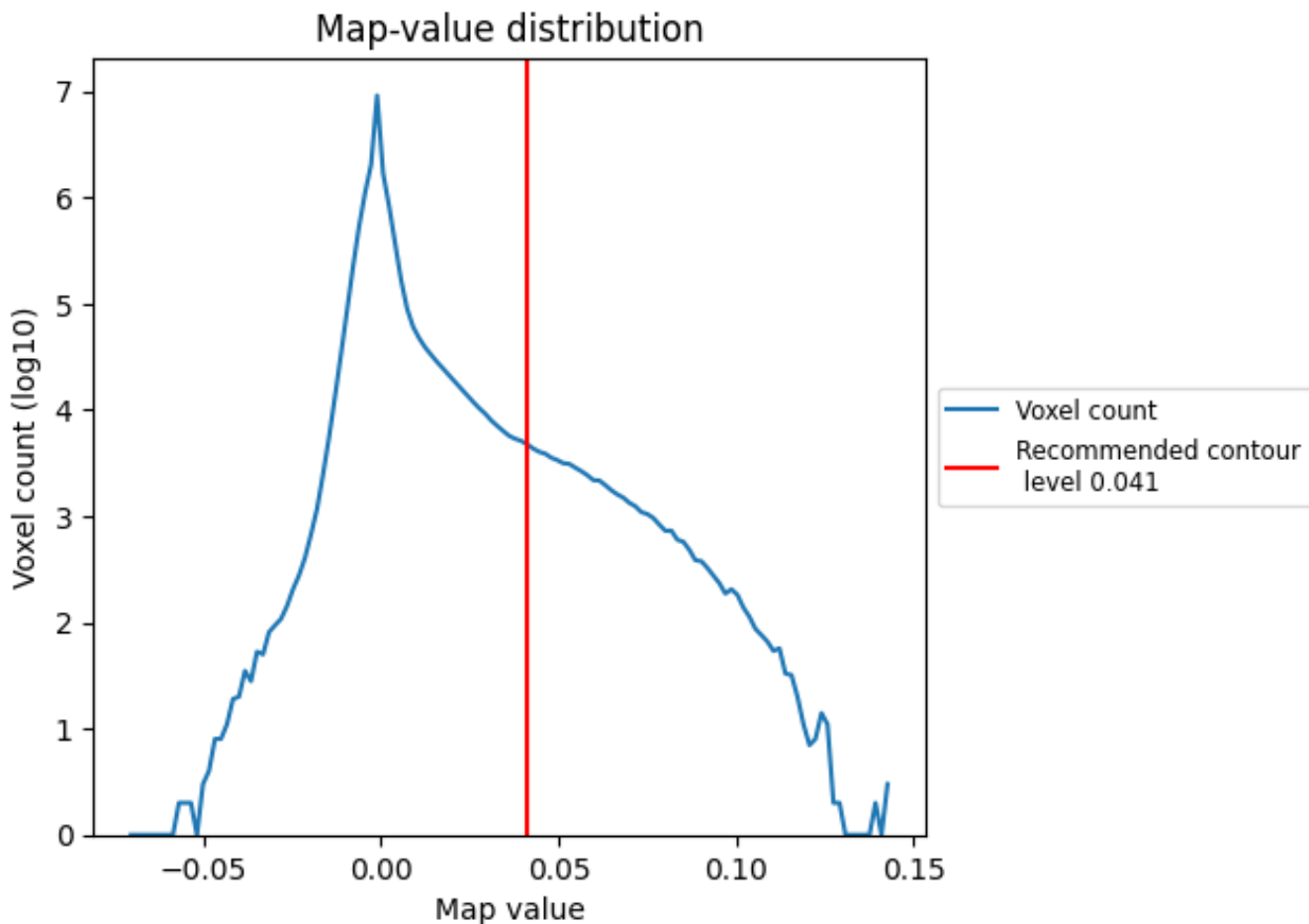
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

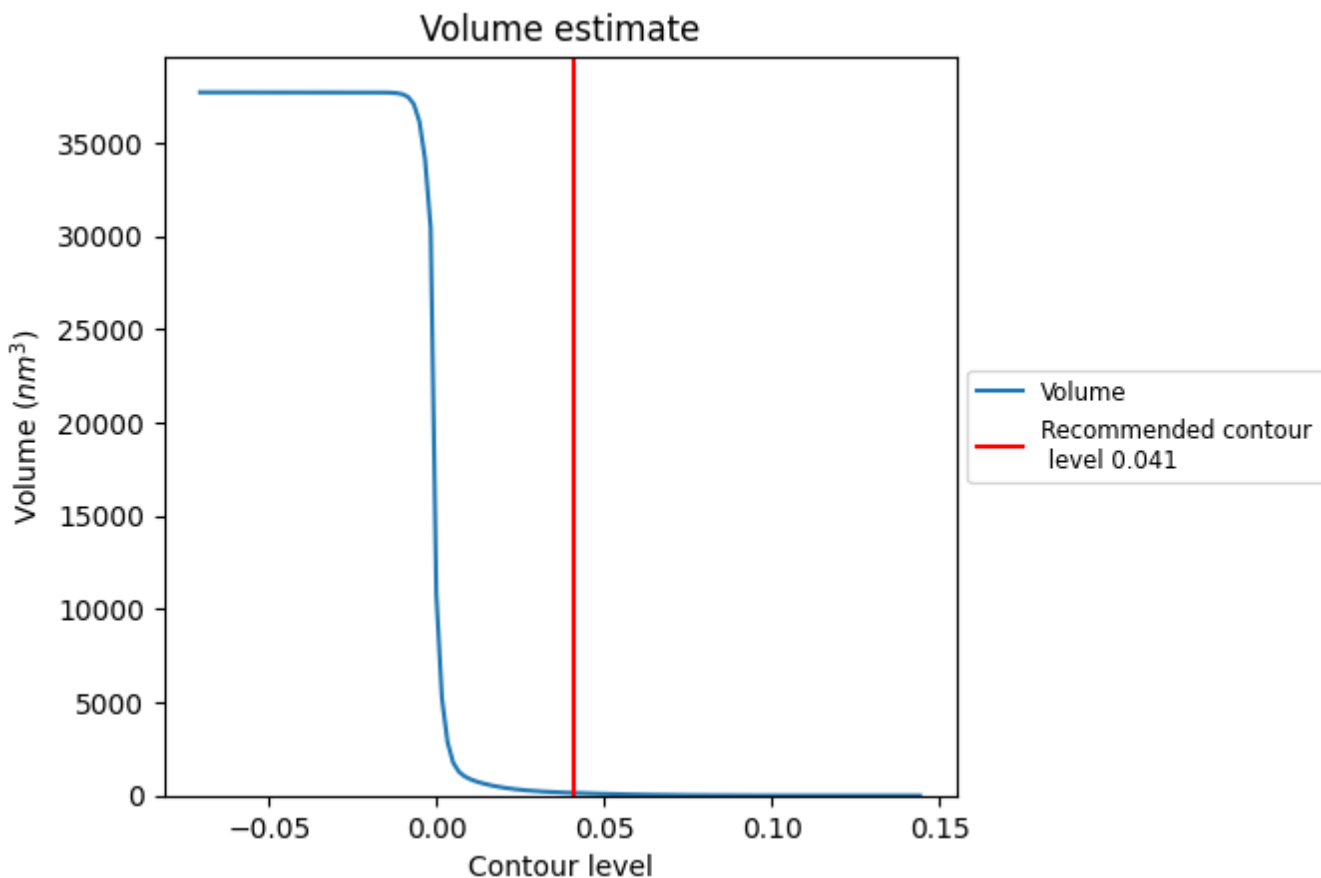
This section contains the results of statistical analysis of the map.

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.

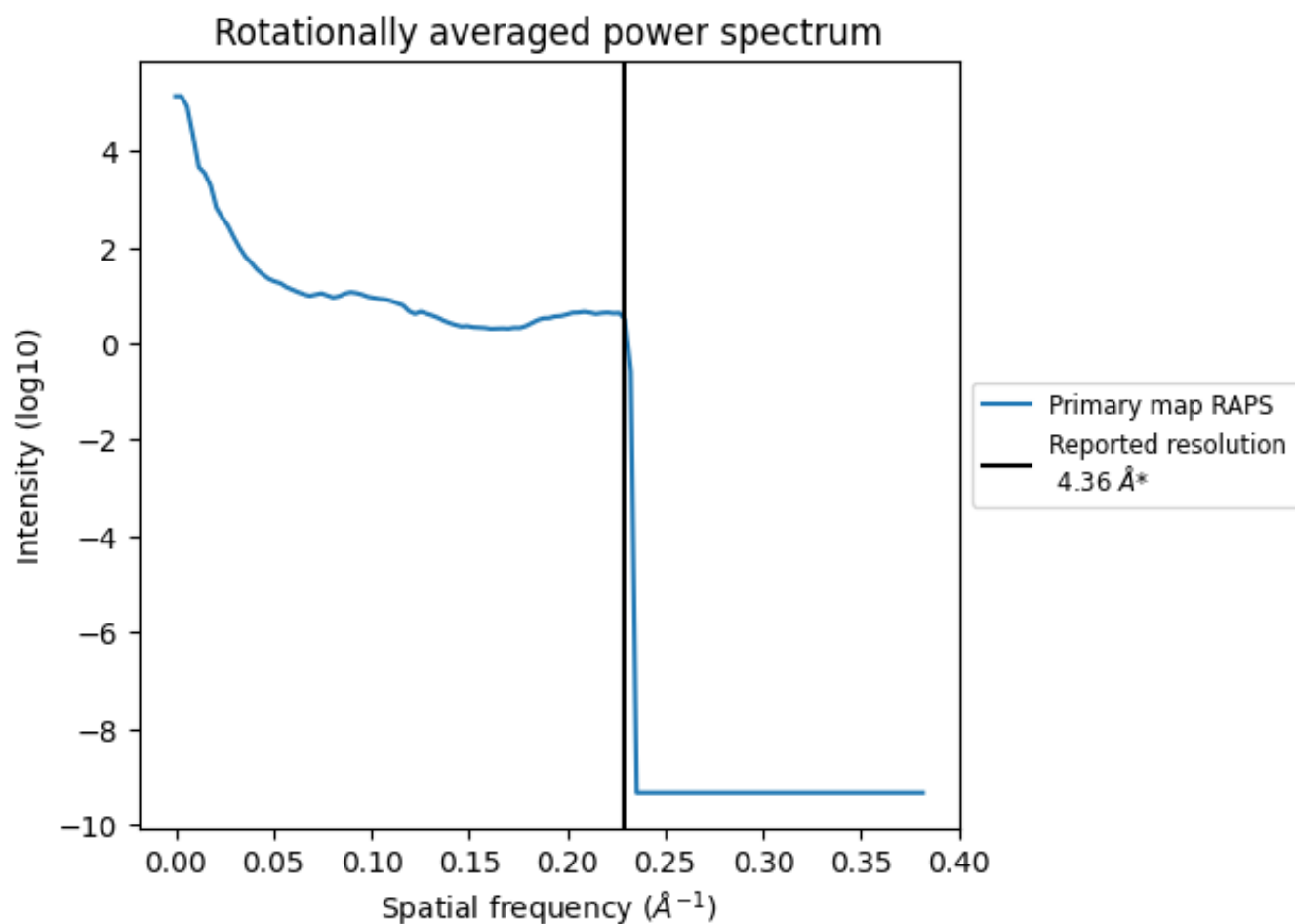
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 140 nm³; this corresponds to an approximate mass of 127 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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.229 Å⁻¹

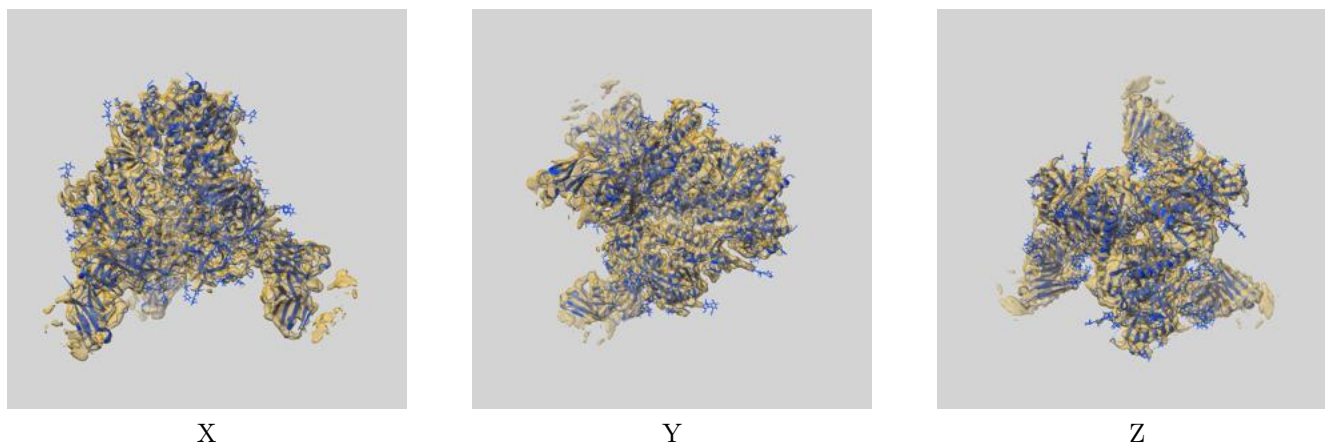
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

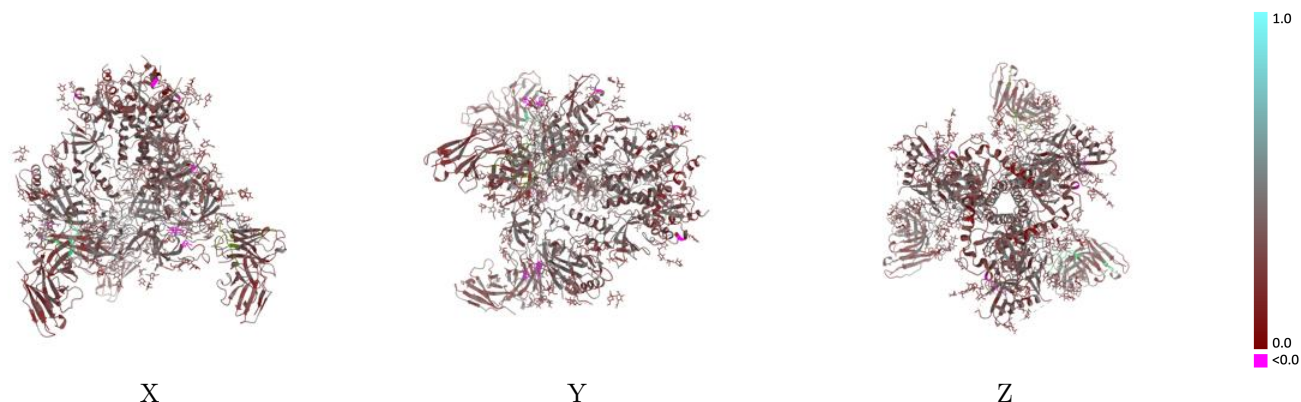
This section contains information regarding the fit between EMDB map EMD-3121 and PDB model 5ACO. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



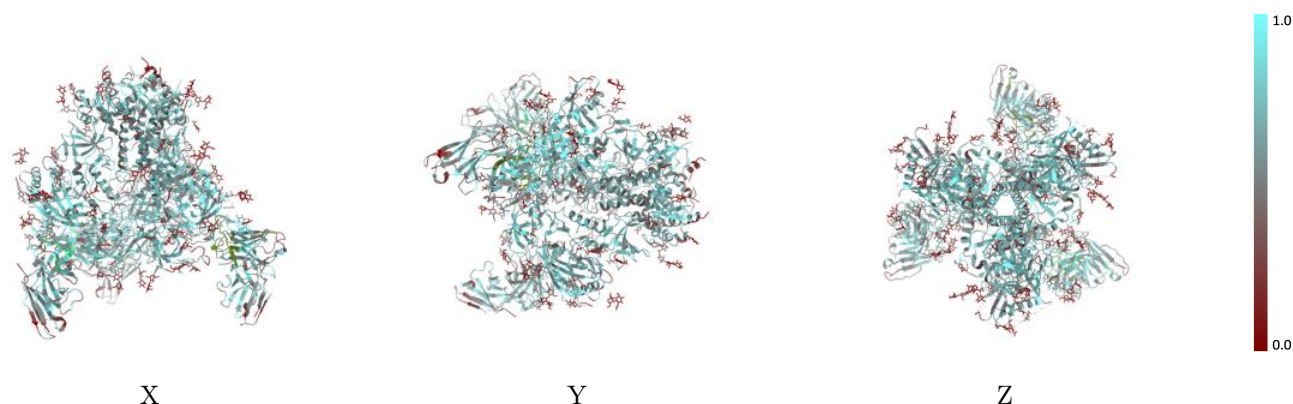
The images above show the 3D surface view of the map at the recommended contour level 0.041 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



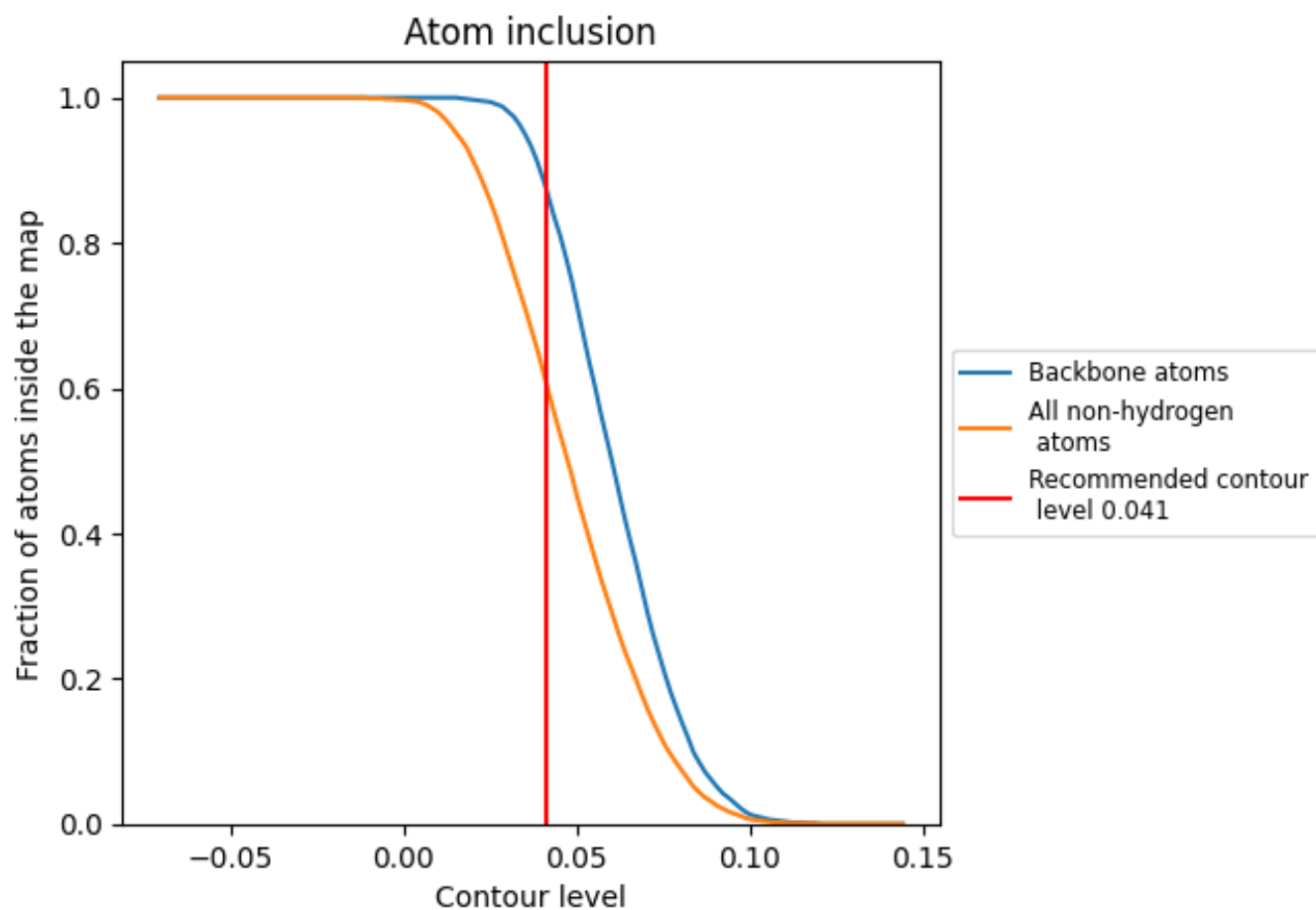
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.041).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 61% 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 (0.041) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6120	 0.3320
0	 0.1540	 0.2740
1	 0.2460	 0.2430
2	 0.4700	 0.3210
3	 0.6720	 0.3810
4	 0.0000	 0.2270
5	 0.2310	 0.1350
6	 0.3850	 0.1600
7	 0.0710	 0.2440
8	 0.3930	 0.2620
9	 0.1070	 0.2370
A	 0.6860	 0.3690
AA	 0.0710	 0.2290
B	 0.5840	 0.2980
C	 0.6860	 0.3690
D	 0.6840	 0.3690
E	 0.5900	 0.3000
F	 0.5880	 0.2990
G	 0.6290	 0.3150
H	 0.6320	 0.3160
I	 0.6320	 0.3170
J	 0.5780	 0.2900
K	 0.5770	 0.2850
L	 0.5760	 0.2890
M	 0.1280	 0.2900
N	 0.2140	 0.2910
O	 0.3330	 0.2100
P	 0.2560	 0.3290
Q	 0.3210	 0.2740
R	 0.2140	 0.2670
S	 0.3610	 0.2860
T	 0.1540	 0.2570
U	 0.2460	 0.2370
V	 0.4700	 0.3220
W	 0.6720	 0.3740



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Chain	Atom inclusion	Q-score
X	 0.0360	 0.2450
Y	 0.2310	 0.1310
Z	 0.3850	 0.1680
a	 0.0710	 0.2230
b	 0.3930	 0.2500
c	 0.0710	 0.2230
d	 0.1280	 0.2750
e	 0.2500	 0.3020
f	 0.3330	 0.2020
g	 0.2310	 0.3240
h	 0.3210	 0.2760
i	 0.2140	 0.2970
j	 0.3730	 0.2830
k	 0.1280	 0.2610
l	 0.2460	 0.2380
m	 0.4700	 0.3210
n	 0.6720	 0.3670
o	 0.0000	 0.2290
p	 0.2310	 0.1450
q	 0.4100	 0.1620
r	 0.0710	 0.2330
s	 0.3930	 0.2440
t	 0.1280	 0.2900
u	 0.2140	 0.2980
v	 0.3330	 0.2120
w	 0.2050	 0.3370
x	 0.3210	 0.2700
y	 0.2500	 0.2800
z	 0.3730	 0.2830