



wwPDB EM Validation Summary Report ⓘ

Sep 29, 2024 – 01:57 AM EDT

PDB ID : 8TGW
EMDB ID : EMD-41246
Title : Cryo-EM structure of 1059 SOSIP trimer purified via Galanthus nivalis lectin chromatography
Authors : Parsons, R.J.; Pothula, K.; Acharya, P.
Deposited on : 2023-07-13
Resolution : 3.60 Å(reported)
Based on initial model : 7LX2

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:

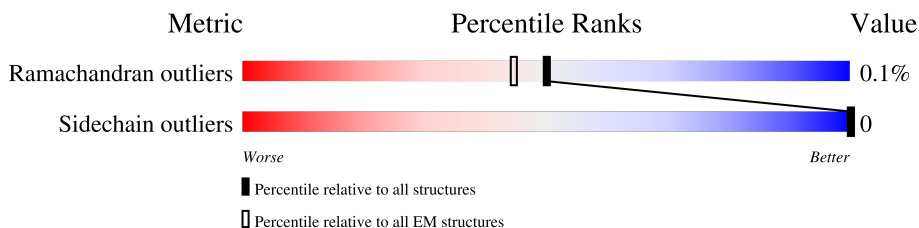
EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.60 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.





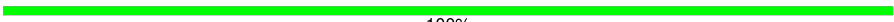










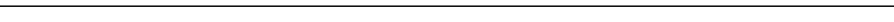



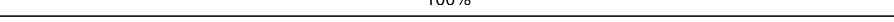
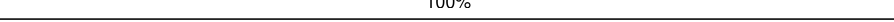
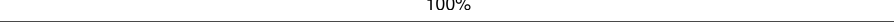



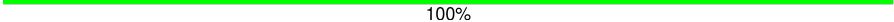

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	491	78% 21%
1	B	491	79% 21%
1	C	491	79% 21%
2	a	153	71% 29%
2	b	153	71% 29%
2	c	153	71% 29%
3	0	2	50% 50%
3	2	2	50% 50%
3	3	2	100%





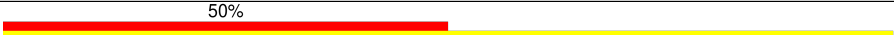
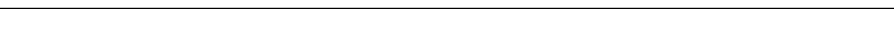
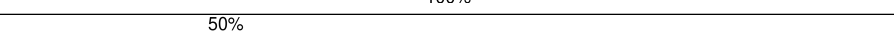
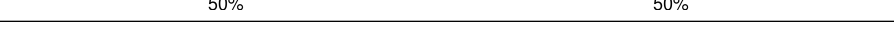

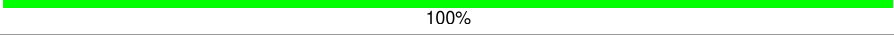

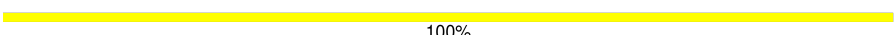



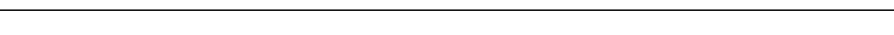
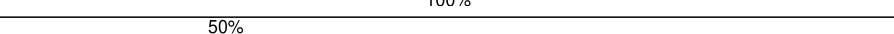
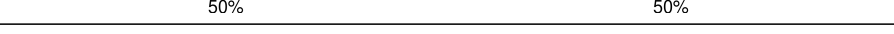




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Mol	Chain	Length	Quality of chain
3	D	2	 100%
3	E	2	 50% 50%
3	F	2	 100%
3	G	2	 100%
3	H	2	 100%
3	I	2	 100%
3	J	2	 50% 100%
3	L	2	 100%
3	M	2	 50% 50%
3	N	2	 100%
3	O	2	 100%
3	P	2	 100%
3	Q	2	 100%
3	R	2	 100%
3	S	2	 100%
3	T	2	 50% 50%
3	U	2	 100%
3	V	2	 100%
3	W	2	 100%
3	X	2	 50% 50%
3	Y	2	 50% 50%
3	Z	2	 50% 50%
3	d	2	 100%
3	e	2	 100%
3	h	2	 50% 50%

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Mol	Chain	Length	Quality of chain
3	j	2	 50% 50%
3	k	2	 50% 50%
3	l	2	 50% 100%
3	n	2	 50% 100%
3	o	2	 50% 100%
3	p	2	 100%
3	r	2	 50% 50%
3	s	2	 50% 50%
3	t	2	 50% 100%
3	u	2	 50% 100%
3	v	2	 100%
3	w	2	 100%
3	x	2	 100%
3	y	2	 50% 50%
3	z	2	 100%
4	K	2	 50% 50%
5	l	3	 67% 33%
5	f	3	 67% 33%
5	g	3	 33% 67% 33%
5	i	3	 33% 67% 33%
5	m	3	 33% 67% 33%
5	q	3	 100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13443 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 1059 SOSIP Surface protein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	387	Total 3079	C 1958	N 527	O 569	S 25	0	0
1	B	387	Total 3079	C 1958	N 527	O 569	S 25	0	0
1	C	387	Total 3079	C 1958	N 527	O 569	S 25	0	0

- Molecule 2 is a protein called 1059 SOSIP Transmembrane protein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	a	109	Total 864	C 548	N 150	O 159	S 7	0	0
2	b	109	Total 864	C 548	N 150	O 159	S 7	0	0
2	c	109	Total 864	C 548	N 150	O 159	S 7	0	0

- Molecule 3 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		
3	D	2	Total 28	C 16	N 2	O 10	0	0
3	E	2	Total 28	C 16	N 2	O 10	0	0
3	F	2	Total 28	C 16	N 2	O 10	0	0
3	G	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		
3	H	2	28	16	2	10	0	0
3	I	2	28	16	2	10	0	0
3	J	2	28	16	2	10	0	0
3	L	2	28	16	2	10	0	0
3	M	2	28	16	2	10	0	0
3	N	2	28	16	2	10	0	0
3	O	2	28	16	2	10	0	0
3	P	2	28	16	2	10	0	0
3	Q	2	28	16	2	10	0	0
3	R	2	28	16	2	10	0	0
3	S	2	28	16	2	10	0	0
3	T	2	28	16	2	10	0	0
3	U	2	28	16	2	10	0	0
3	V	2	28	16	2	10	0	0
3	W	2	28	16	2	10	0	0
3	X	2	28	16	2	10	0	0
3	Y	2	28	16	2	10	0	0
3	Z	2	28	16	2	10	0	0
3	2	2	28	16	2	10	0	0
3	3	2	28	16	2	10	0	0
3	d	2	28	16	2	10	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	e	2	28	16	2	10	0	0
3	h	2	28	16	2	10	0	0
3	j	2	28	16	2	10	0	0
3	k	2	28	16	2	10	0	0
3	l	2	28	16	2	10	0	0
3	n	2	28	16	2	10	0	0
3	o	2	28	16	2	10	0	0
3	p	2	28	16	2	10	0	0
3	r	2	28	16	2	10	0	0
3	s	2	28	16	2	10	0	0
3	t	2	28	16	2	10	0	0
3	u	2	28	16	2	10	0	0
3	v	2	28	16	2	10	0	0
3	w	2	28	16	2	10	0	0
3	x	2	28	16	2	10	0	0
3	y	2	28	16	2	10	0	0
3	z	2	28	16	2	10	0	0
3	0	2	28	16	2	10	0	0

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-beta-D-mannopyranos e.



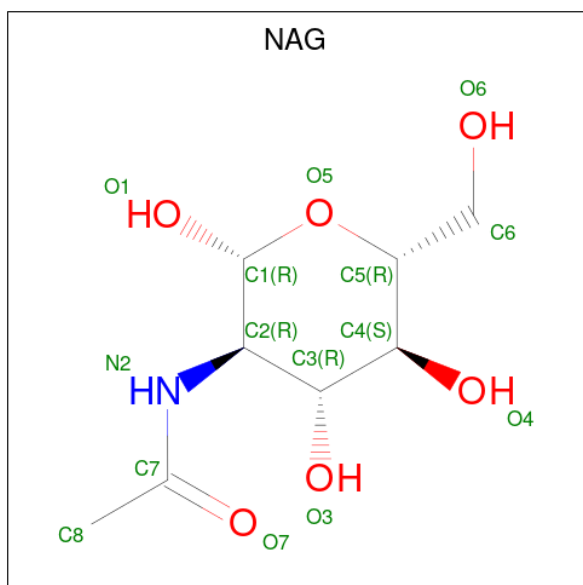
Mol	Chain	Residues	Atoms			AltConf	Trace
4	K	2	Total	C	O	0	0
			22	12	10		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
5	1	3	Total	C	N	O	0	0
			39	22	2	15		
5	f	3	Total	C	N	O	0	0
			39	22	2	15		
5	g	3	Total	C	N	O	0	0
			39	22	2	15		
5	i	3	Total	C	N	O	0	0
			39	22	2	15		
5	m	3	Total	C	N	O	0	0
			39	22	2	15		
5	q	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

GLN
ARG
ARG
ARG
ARG
ARG
ARG

- Molecule 2: 1059 SOSIP Transmembrane protein gp41

Chain a:  71% 29%

ALA VAL GLY ILE GLY ALA VAL F519 L520 L523 I548 VAL GLN GLN ASN GLN ASN GLN LEU LEU ARG ARG ALA PRO GLN ALA GLN GLN HIS LEU LEU LEU LEU LEU LEU LEU LEU THR VAL ILE K574 Q652 GLN LYS ASN GLN LEU LEU LEU LEU LEU ASP

- Molecule 2: 1059 SOSIP Transmembrane protein gp41

Chain b:  71% 29%

ALA VAL GLY ILE GLY ALA VAL F519 I548 VAL GLN GLN ASN GLN ASN GLN LEU LEU ARG ARG ALA PRO GLN ALA GLN GLN HIS LEU LEU LEU LEU LEU LEU LEU LEU THR VAL TRP LEU LEU ILE K574 C598 K601 I602 I603 C604 I635 Q652 GLN LYS ASN GLN LEU LEU LEU LEU LEU ASP

- Molecule 2: 1059 SOSIP Transmembrane protein gp41

Chain c:  71% 29%

ALA VAL GLY ILE GLY ALA VAL F519 G547 I548 VAL GLN GLN ASN GLN ASN GLN LEU LEU ARG ARG ALA PRO GLN ALA GLN GLN HIS LEU LEU LEU LEU LEU LEU LEU LEU THR VAL TRP LEU LEU ILE K574 Q652 GLN LYS ASN GLN LEU LEU LEU LEU LEU ASP

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

Chain D:  100%

NAG1
NAG2

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

Chain E:  50% 50%

NAG1
NAG2

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

Chain F:  100%

NAG1
NAG2

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

Chain G:  100%

MAG1
MAG2

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

Chain H:  100%

MAG1
MAG2

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

Chain I:  100%


MAG1
MAG2

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

Chain J:  50% 100%

MAG1
MAG2

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

Chain L:  100%

MAG1
MAG2

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

Chain M:  50% 50%

MAG1
MAG2

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

Chain N:  100%

MAG1
MAG2

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

Chain O:  100%MAG1
MAG2

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

Chain P:  100%MAG1
MAG2

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

Chain Q:  100%MAG1
MAG2

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

Chain R:  100%MAG1
MAG2

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

Chain S:  100%MAG1
MAG2

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

Chain T:  50% 50%MAG1
MAG2

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

Chain U:  100%



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

Chain V:  100%



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

Chain W:  100%



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

Chain X:  50% 50%



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

Chain Y:  50% 50%



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

Chain Z:  50% 50%



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

Chain 2:  50% 50%

MAG1
MAG2

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

Chain 3:  100%

MAG1
MAG2

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

Chain d:  100%

MAG1
MAG2

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

Chain e:  100%

MAG1
MAG2

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

Chain h:  50% 50%

MAG1
MAG2

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

Chain j:  50% 50%

MAG1
MAG2

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

Chain k:  50% 50%



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



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



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



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



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



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



MAG1
MAG2

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

MAG1
MAG2

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

MAG1
MAG2

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

MAG1
MAG2

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

MAG1
MAG2

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

MAG1
MAG2

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

MAG1
MAG2

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

Chain z:  100%

 NAG1
NAG2

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

Chain 0:  50%
50%

 NAG1
NAG2

- Molecule 4: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose

Chain K:  50%
50%

 BMA1
BMA2

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

Chain 1:  67% 33%

 NAG1
NAG2
BMA3

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

Chain f:  67% 33%

 NAG1
NAG2
BMA3

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

Chain g:  33% 67% 33%

 NAG1
NAG2
BMA3

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



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



- Molecule 5: 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, Not provided	
Number of particles used	737588	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CryoSPARCv4.01 Patch motion correction and CTF estimation jobs	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.1	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.110	Depositor
Minimum map value	-1.469	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	302.40002, 302.40002, 302.40002	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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

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	0.30	0/3138	0.58	1/4254 (0.0%)
1	B	0.30	0/3138	0.57	0/4254
1	C	0.28	0/3138	0.55	0/4254
2	a	0.28	0/880	0.55	1/1193 (0.1%)
2	b	0.35	0/880	0.63	1/1193 (0.1%)
2	c	0.28	0/880	0.54	0/1193
All	All	0.30	0/12054	0.57	3/16341 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	ASP	CB-CG-OD1	9.06	126.45	118.30
2	b	635	ILE	CG1-CB-CG2	-7.87	94.10	111.40
2	a	523	LEU	CA-CB-CG	5.32	127.54	115.30

There are no chirality outliers.

There are no planarity outliers.

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	373/491 (76%)	353 (95%)	19 (5%)	1 (0%)	37	67
1	B	373/491 (76%)	361 (97%)	12 (3%)	0	100	100
1	C	373/491 (76%)	362 (97%)	11 (3%)	0	100	100
2	a	105/153 (69%)	102 (97%)	3 (3%)	0	100	100
2	b	105/153 (69%)	101 (96%)	4 (4%)	0	100	100
2	c	105/153 (69%)	104 (99%)	1 (1%)	0	100	100
All	All	1434/1932 (74%)	1383 (96%)	50 (4%)	1 (0%)	50	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	VAL

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	354/440 (80%)	354 (100%)	0	100	100
1	B	354/440 (80%)	354 (100%)	0	100	100
1	C	354/440 (80%)	354 (100%)	0	100	100
2	a	92/129 (71%)	92 (100%)	0	100	100
2	b	92/129 (71%)	92 (100%)	0	100	100
2	c	92/129 (71%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1338/1707 (78%)	1338 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
2	b	644	ASN

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](#)

106 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
3	NAG	0	1	3,1	14,14,15	0.36	0	17,19,21	1.12	2 (11%)
3	NAG	0	2	3	14,14,15	0.42	0	17,19,21	0.58	0
5	NAG	1	1	5,1	14,14,15	0.32	0	17,19,21	0.62	0
5	NAG	1	2	5	14,14,15	0.25	0	17,19,21	0.53	0
5	BMA	1	3	5	11,11,12	1.08	1 (9%)	15,15,17	0.79	0
3	NAG	2	1	3,1	14,14,15	0.37	0	17,19,21	0.57	0
3	NAG	2	2	3	14,14,15	0.52	0	17,19,21	1.01	1 (5%)
3	NAG	3	1	3	14,14,15	0.36	0	17,19,21	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	3	2	3	14,14,15	0.63	0	17,19,21	0.41	0
3	NAG	D	1	3	14,14,15	0.21	0	17,19,21	0.56	0
3	NAG	D	2	3	14,14,15	0.36	0	17,19,21	0.58	0
3	NAG	E	1	3	14,14,15	0.35	0	17,19,21	1.06	1 (5%)
3	NAG	E	2	3	14,14,15	0.36	0	17,19,21	0.52	0
3	NAG	F	1	3,1	14,14,15	0.31	0	17,19,21	0.57	0
3	NAG	F	2	3	14,14,15	0.36	0	17,19,21	0.50	0
3	NAG	G	1	3,1	14,14,15	0.26	0	17,19,21	0.51	0
3	NAG	G	2	3	14,14,15	0.31	0	17,19,21	0.50	0
3	NAG	H	1	3,1	14,14,15	0.30	0	17,19,21	0.56	0
3	NAG	H	2	3	14,14,15	0.38	0	17,19,21	0.48	0
3	NAG	I	1	3,1	14,14,15	0.23	0	17,19,21	0.45	0
3	NAG	I	2	3	14,14,15	0.33	0	17,19,21	0.53	0
3	NAG	J	1	3	14,14,15	0.43	0	17,19,21	0.68	0
3	NAG	J	2	3	14,14,15	0.51	0	17,19,21	0.41	0
4	BMA	K	1	4	11,11,12	0.75	0	15,15,17	0.88	1 (6%)
4	BMA	K	2	4	11,11,12	0.72	0	15,15,17	0.75	0
3	NAG	L	1	3	14,14,15	0.50	0	17,19,21	1.03	1 (5%)
3	NAG	L	2	3	14,14,15	0.69	0	17,19,21	1.01	1 (5%)
3	NAG	M	1	3,1	14,14,15	0.23	0	17,19,21	0.51	0
3	NAG	M	2	3	14,14,15	0.44	0	17,19,21	1.05	1 (5%)
3	NAG	N	1	3,1	14,14,15	0.31	0	17,19,21	0.57	0
3	NAG	N	2	3	14,14,15	0.37	0	17,19,21	0.51	0
3	NAG	O	1	3,1	14,14,15	0.26	0	17,19,21	0.50	0
3	NAG	O	2	3	14,14,15	0.35	0	17,19,21	0.49	0
3	NAG	P	1	3,1	14,14,15	0.29	0	17,19,21	0.52	0
3	NAG	P	2	3	14,14,15	0.33	0	17,19,21	0.51	0
3	NAG	Q	1	3,1	14,14,15	0.26	0	17,19,21	0.49	0
3	NAG	Q	2	3	14,14,15	0.35	0	17,19,21	0.50	0
3	NAG	R	1	3,1	14,14,15	0.27	0	17,19,21	0.50	0
3	NAG	R	2	3	14,14,15	0.33	0	17,19,21	0.50	0
3	NAG	S	1	3,1	14,14,15	0.24	0	17,19,21	0.52	0
3	NAG	S	2	3	14,14,15	0.36	0	17,19,21	0.49	0
3	NAG	T	1	3,1	14,14,15	0.42	0	17,19,21	0.68	1 (5%)
3	NAG	T	2	3	14,14,15	0.40	0	17,19,21	0.45	0
3	NAG	U	1	3,1	14,14,15	0.35	0	17,19,21	0.60	0
3	NAG	U	2	3	14,14,15	0.53	0	17,19,21	0.43	0
3	NAG	V	1	3,1	14,14,15	0.34	0	17,19,21	0.58	0
3	NAG	V	2	3	14,14,15	0.39	0	17,19,21	0.49	0
3	NAG	W	1	3,1	14,14,15	0.32	0	17,19,21	0.56	0
3	NAG	W	2	3	14,14,15	0.36	0	17,19,21	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	X	1	3,1	14,14,15	0.32	0	17,19,21	1.12	1 (5%)
3	NAG	X	2	3	14,14,15	0.35	0	17,19,21	0.57	0
3	NAG	Y	1	3,1	14,14,15	0.45	0	17,19,21	0.71	0
3	NAG	Y	2	3	14,14,15	0.51	0	17,19,21	1.09	2 (11%)
3	NAG	Z	1	3,1	14,14,15	0.40	0	17,19,21	0.78	0
3	NAG	Z	2	3	14,14,15	0.81	1 (7%)	17,19,21	1.10	2 (11%)
3	NAG	d	1	3,1	14,14,15	0.30	0	17,19,21	0.57	0
3	NAG	d	2	3	14,14,15	0.38	0	17,19,21	0.51	0
3	NAG	e	1	3,1	14,14,15	0.26	0	17,19,21	0.52	0
3	NAG	e	2	3	14,14,15	0.32	0	17,19,21	0.49	0
5	NAG	f	1	5,1	14,14,15	0.26	0	17,19,21	0.47	0
5	NAG	f	2	5	14,14,15	0.30	0	17,19,21	0.59	1 (5%)
5	BMA	f	3	5	11,11,12	0.79	0	15,15,17	0.81	0
5	NAG	g	1	5,1	14,14,15	0.32	0	17,19,21	0.57	0
5	NAG	g	2	5	14,14,15	0.34	0	17,19,21	0.45	0
5	BMA	g	3	5	11,11,12	0.76	0	15,15,17	0.93	1 (6%)
3	NAG	h	1	3,1	14,14,15	0.39	0	17,19,21	1.06	1 (5%)
3	NAG	h	2	3	14,14,15	0.35	0	17,19,21	0.50	0
5	NAG	i	1	5,1	14,14,15	0.27	0	17,19,21	0.53	0
5	NAG	i	2	5	14,14,15	0.36	0	17,19,21	0.59	0
5	BMA	i	3	5	11,11,12	0.75	0	15,15,17	0.83	1 (6%)
3	NAG	j	1	3,1	14,14,15	0.41	0	17,19,21	1.07	1 (5%)
3	NAG	j	2	3	14,14,15	0.37	0	17,19,21	0.50	0
3	NAG	k	1	3,1	14,14,15	0.75	1 (7%)	17,19,21	1.17	2 (11%)
3	NAG	k	2	3	14,14,15	0.37	0	17,19,21	0.54	0
3	NAG	l	1	3,1	14,14,15	0.25	0	17,19,21	0.50	0
3	NAG	l	2	3	14,14,15	0.33	0	17,19,21	0.52	0
5	NAG	m	1	5,1	14,14,15	0.33	0	17,19,21	0.61	0
5	NAG	m	2	5	14,14,15	0.31	0	17,19,21	0.44	0
5	BMA	m	3	5	11,11,12	0.76	0	15,15,17	0.91	1 (6%)
3	NAG	n	1	3	14,14,15	0.24	0	17,19,21	0.50	0
3	NAG	n	2	3	14,14,15	0.33	0	17,19,21	0.50	0
3	NAG	o	1	3	14,14,15	0.32	0	17,19,21	0.75	1 (5%)
3	NAG	o	2	3	14,14,15	1.41	2 (14%)	17,19,21	1.05	1 (5%)
3	NAG	p	1	3,1	14,14,15	0.22	0	17,19,21	0.51	0
3	NAG	p	2	3	14,14,15	0.33	0	17,19,21	0.52	0
5	NAG	q	1	5,1	14,14,15	0.31	0	17,19,21	0.61	0
5	NAG	q	2	5	14,14,15	0.27	0	17,19,21	0.48	0
5	BMA	q	3	5	11,11,12	0.74	0	15,15,17	0.83	0
3	NAG	r	1	3,1	14,14,15	0.45	0	17,19,21	1.03	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	r	2	3	14,14,15	0.37	0	17,19,21	0.48	0
3	NAG	s	1	3,1	14,14,15	0.32	0	17,19,21	0.53	0
3	NAG	s	2	3	14,14,15	0.52	0	17,19,21	1.07	1 (5%)
3	NAG	t	1	3,1	14,14,15	0.30	0	17,19,21	0.58	0
3	NAG	t	2	3	14,14,15	0.36	0	17,19,21	0.49	0
3	NAG	u	1	3,1	14,14,15	0.26	0	17,19,21	0.53	0
3	NAG	u	2	3	14,14,15	0.38	0	17,19,21	0.49	0
3	NAG	v	1	3,1	14,14,15	0.32	0	17,19,21	1.10	1 (5%)
3	NAG	v	2	3	14,14,15	0.32	0	17,19,21	0.61	1 (5%)
3	NAG	w	1	3,1	14,14,15	0.31	0	17,19,21	0.53	0
3	NAG	w	2	3	14,14,15	0.39	0	17,19,21	0.47	0
3	NAG	x	1	3,1	14,14,15	0.27	0	17,19,21	0.51	0
3	NAG	x	2	3	14,14,15	0.36	0	17,19,21	0.48	0
3	NAG	y	1	3,1	14,14,15	0.27	0	17,19,21	0.60	1 (5%)
3	NAG	y	2	3	14,14,15	0.37	0	17,19,21	0.49	0
3	NAG	z	1	3,1	14,14,15	0.29	0	17,19,21	0.56	0
3	NAG	z	2	3	14,14,15	0.37	0	17,19,21	0.49	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
3	NAG	0	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	0	2	3	-	0/6/23/26	0/1/1/1
5	NAG	1	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	1	2	5	-	0/6/23/26	0/1/1/1
5	BMA	1	3	5	-	0/2/19/22	0/1/1/1
3	NAG	2	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	2	2	3	-	4/6/23/26	0/1/1/1
3	NAG	3	1	3	-	2/6/23/26	0/1/1/1
3	NAG	3	2	3	-	2/6/23/26	0/1/1/1
3	NAG	D	1	3	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	NAG	E	1	3	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	NAG	H	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
3	NAG	J	1	3	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
4	BMA	K	1	4	-	1/2/19/22	0/1/1/1
4	BMA	K	2	4	-	0/2/19/22	0/1/1/1
3	NAG	L	1	3	-	4/6/23/26	0/1/1/1
3	NAG	L	2	3	-	4/6/23/26	0/1/1/1
3	NAG	M	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	M	2	3	-	2/6/23/26	0/1/1/1
3	NAG	N	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	0/6/23/26	0/1/1/1
3	NAG	O	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	0/6/23/26	0/1/1/1
3	NAG	P	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	P	2	3	-	0/6/23/26	0/1/1/1
3	NAG	Q	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	0/6/23/26	0/1/1/1
3	NAG	R	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	R	2	3	-	1/6/23/26	0/1/1/1
3	NAG	S	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	S	2	3	-	0/6/23/26	0/1/1/1
3	NAG	T	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	T	2	3	-	0/6/23/26	0/1/1/1
3	NAG	U	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	U	2	3	-	2/6/23/26	0/1/1/1
3	NAG	V	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	V	2	3	-	2/6/23/26	0/1/1/1
3	NAG	W	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	W	2	3	-	0/6/23/26	0/1/1/1
3	NAG	X	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	X	2	3	-	2/6/23/26	0/1/1/1
3	NAG	Y	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	Y	2	3	-	4/6/23/26	0/1/1/1
3	NAG	Z	1	3,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	Z	2	3	-	4/6/23/26	0/1/1/1
3	NAG	d	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	d	2	3	-	2/6/23/26	0/1/1/1
3	NAG	e	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	e	2	3	-	0/6/23/26	0/1/1/1
5	NAG	f	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	f	2	5	-	2/6/23/26	0/1/1/1
5	BMA	f	3	5	-	0/2/19/22	0/1/1/1
5	NAG	g	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	g	2	5	-	0/6/23/26	0/1/1/1
5	BMA	g	3	5	-	0/2/19/22	0/1/1/1
3	NAG	h	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	h	2	3	-	2/6/23/26	0/1/1/1
5	NAG	i	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	i	2	5	-	2/6/23/26	0/1/1/1
5	BMA	i	3	5	-	0/2/19/22	0/1/1/1
3	NAG	j	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	j	2	3	-	1/6/23/26	0/1/1/1
3	NAG	k	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	k	2	3	-	2/6/23/26	0/1/1/1
3	NAG	l	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	l	2	3	-	2/6/23/26	0/1/1/1
5	NAG	m	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	m	2	5	-	0/6/23/26	0/1/1/1
5	BMA	m	3	5	-	0/2/19/22	0/1/1/1
3	NAG	n	1	3	-	0/6/23/26	0/1/1/1
3	NAG	n	2	3	-	0/6/23/26	0/1/1/1
3	NAG	o	1	3	-	2/6/23/26	0/1/1/1
3	NAG	o	2	3	-	2/6/23/26	0/1/1/1
3	NAG	p	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	p	2	3	-	2/6/23/26	0/1/1/1
5	NAG	q	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	q	2	5	-	0/6/23/26	0/1/1/1
5	BMA	q	3	5	-	0/2/19/22	0/1/1/1
3	NAG	r	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	r	2	3	-	0/6/23/26	0/1/1/1
3	NAG	s	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	s	2	3	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	t	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	t	2	3	-	2/6/23/26	0/1/1/1
3	NAG	u	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	u	2	3	-	2/6/23/26	0/1/1/1
3	NAG	v	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	v	2	3	-	2/6/23/26	0/1/1/1
3	NAG	w	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	w	2	3	-	2/6/23/26	0/1/1/1
3	NAG	x	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	x	2	3	-	0/6/23/26	0/1/1/1
3	NAG	y	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	y	2	3	-	0/6/23/26	0/1/1/1
3	NAG	z	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	z	2	3	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	o	2	NAG	O5-C1	3.79	1.50	1.43
3	o	2	NAG	C1-C2	3.58	1.57	1.52
5	1	3	BMA	C1-C2	2.77	1.58	1.52
3	Z	2	NAG	C1-C2	2.70	1.56	1.52
3	k	1	NAG	C1-C2	2.47	1.55	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	X	1	NAG	C2-N2-C7	3.33	127.36	122.90
3	0	1	NAG	C2-N2-C7	3.31	127.33	122.90
3	M	2	NAG	C2-N2-C7	3.30	127.32	122.90
3	2	2	NAG	C2-N2-C7	3.28	127.30	122.90
3	v	1	NAG	C2-N2-C7	3.28	127.30	122.90

There are no chirality outliers.

5 of 127 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	V	2	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	Z	1	NAG	O5-C5-C6-O6

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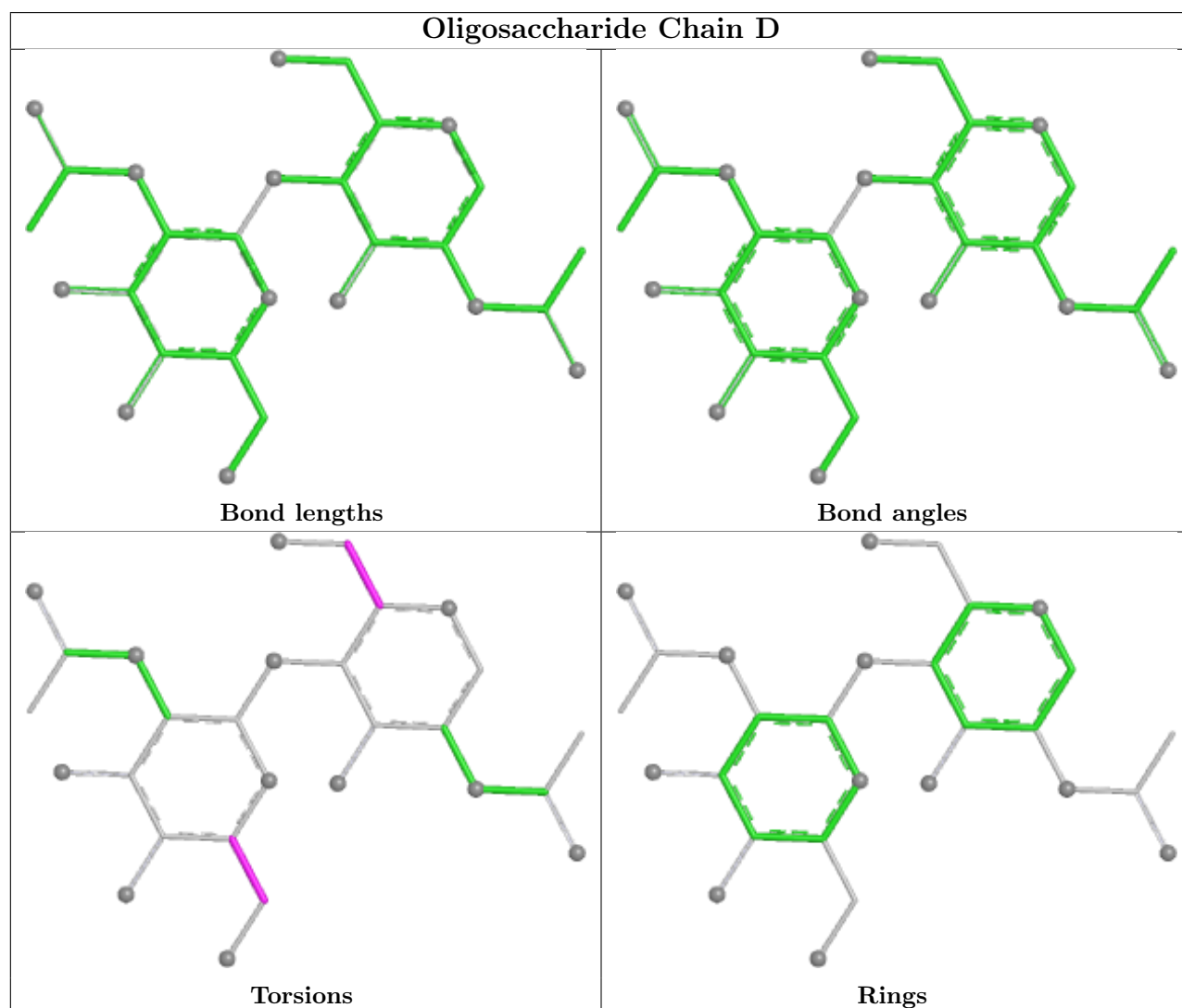
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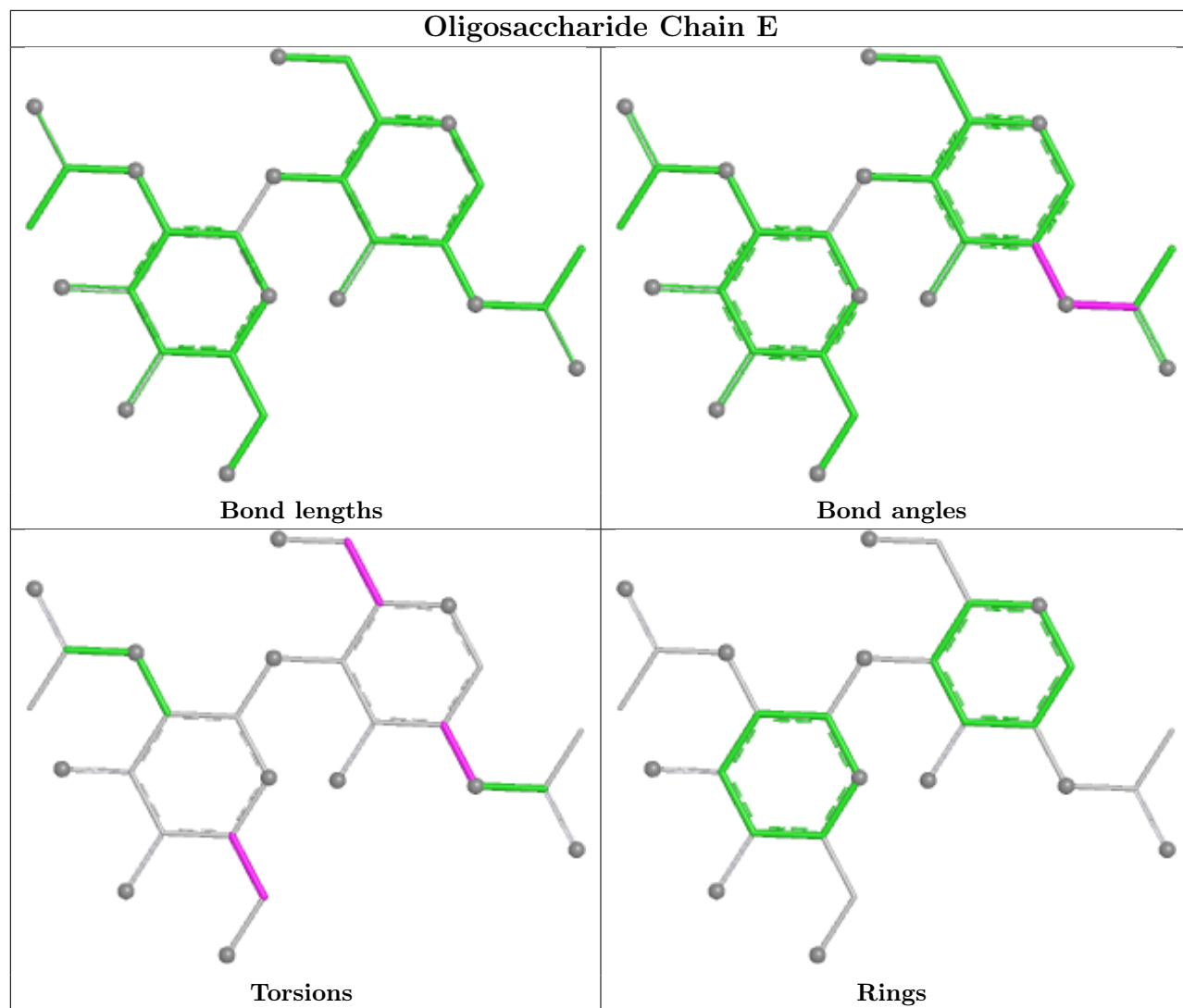
Mol	Chain	Res	Type	Atoms
3	X	1	NAG	O5-C5-C6-O6
3	L	2	NAG	O5-C5-C6-O6

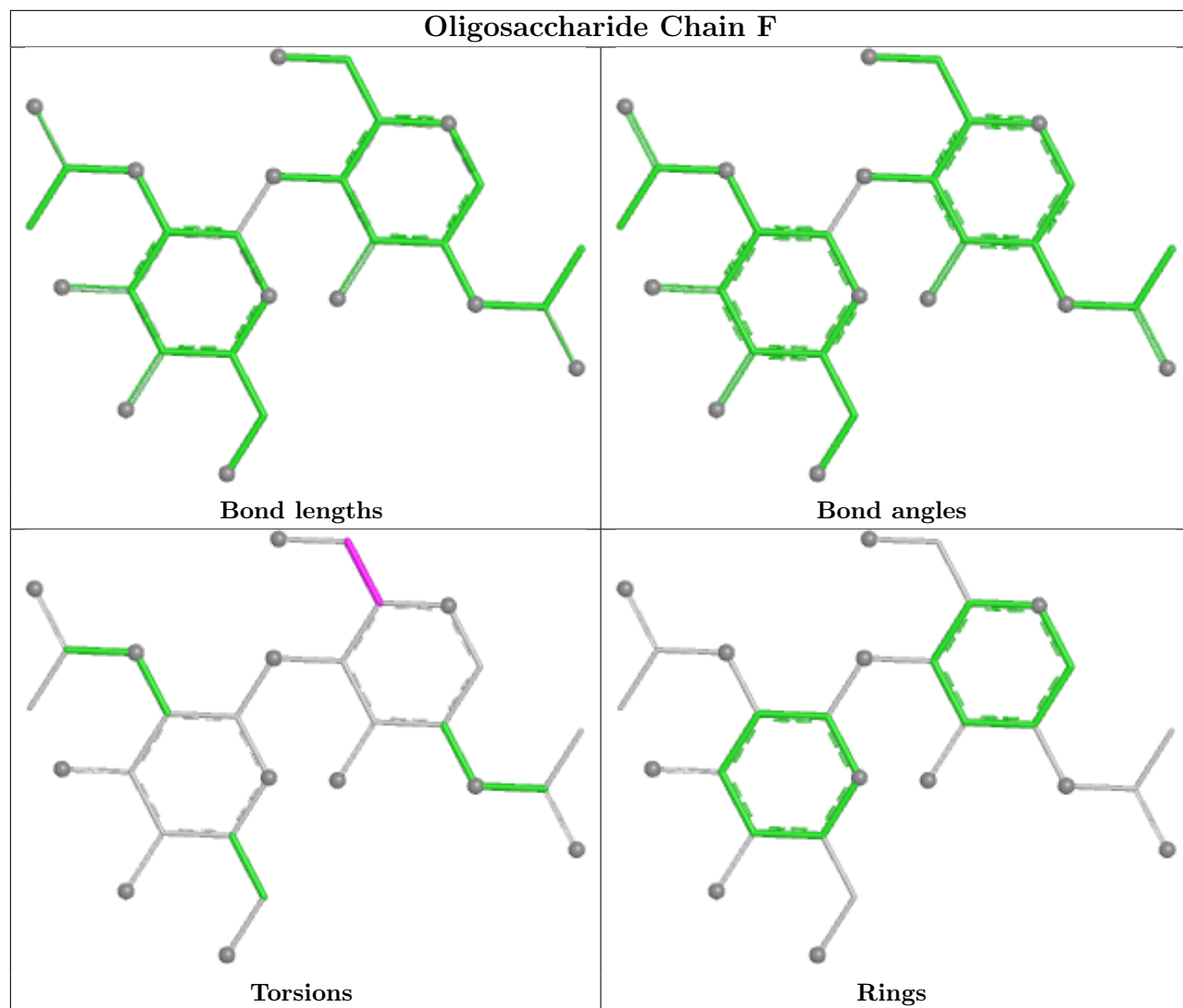
There are no ring outliers.

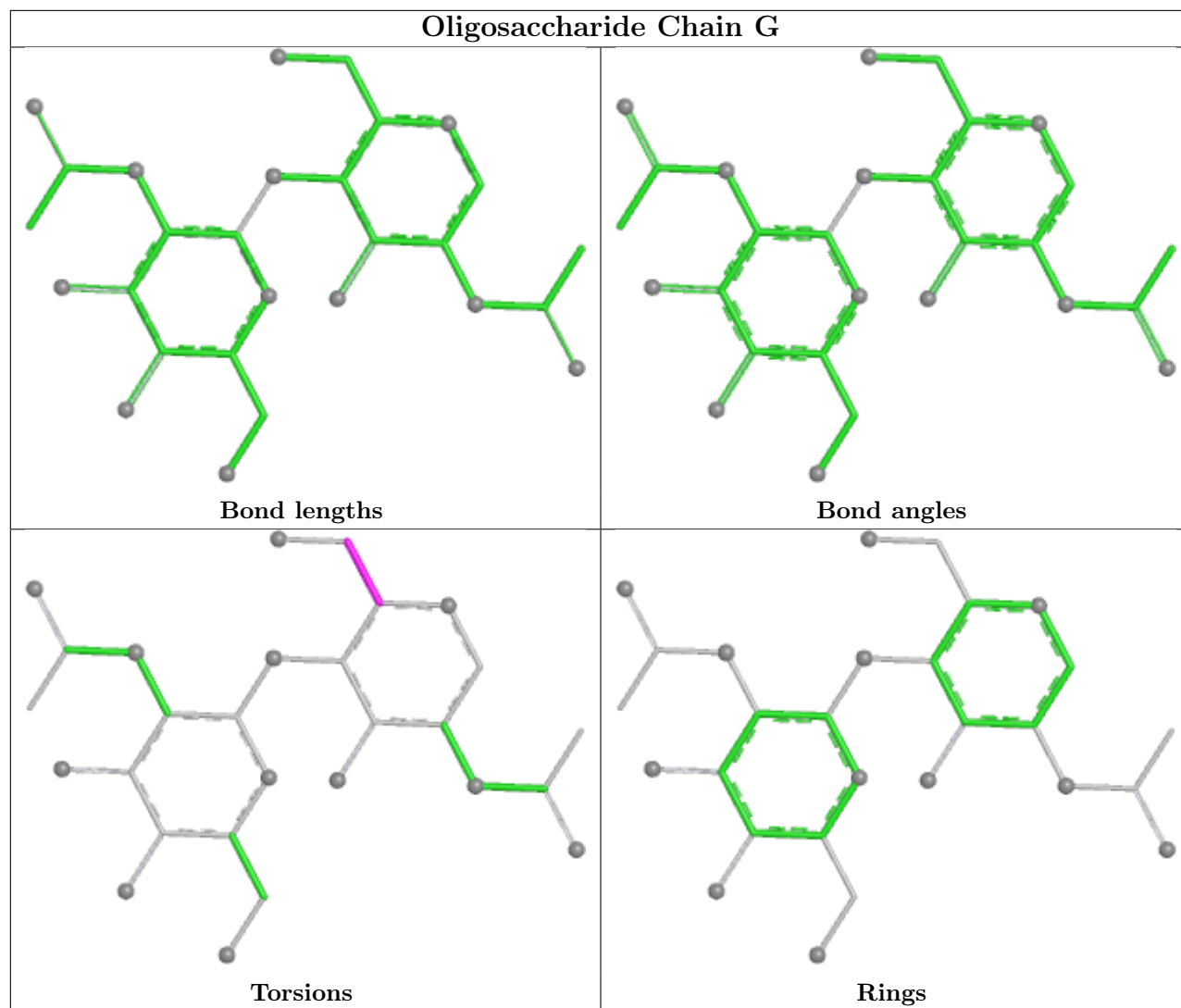
No monomer is involved in short contacts.

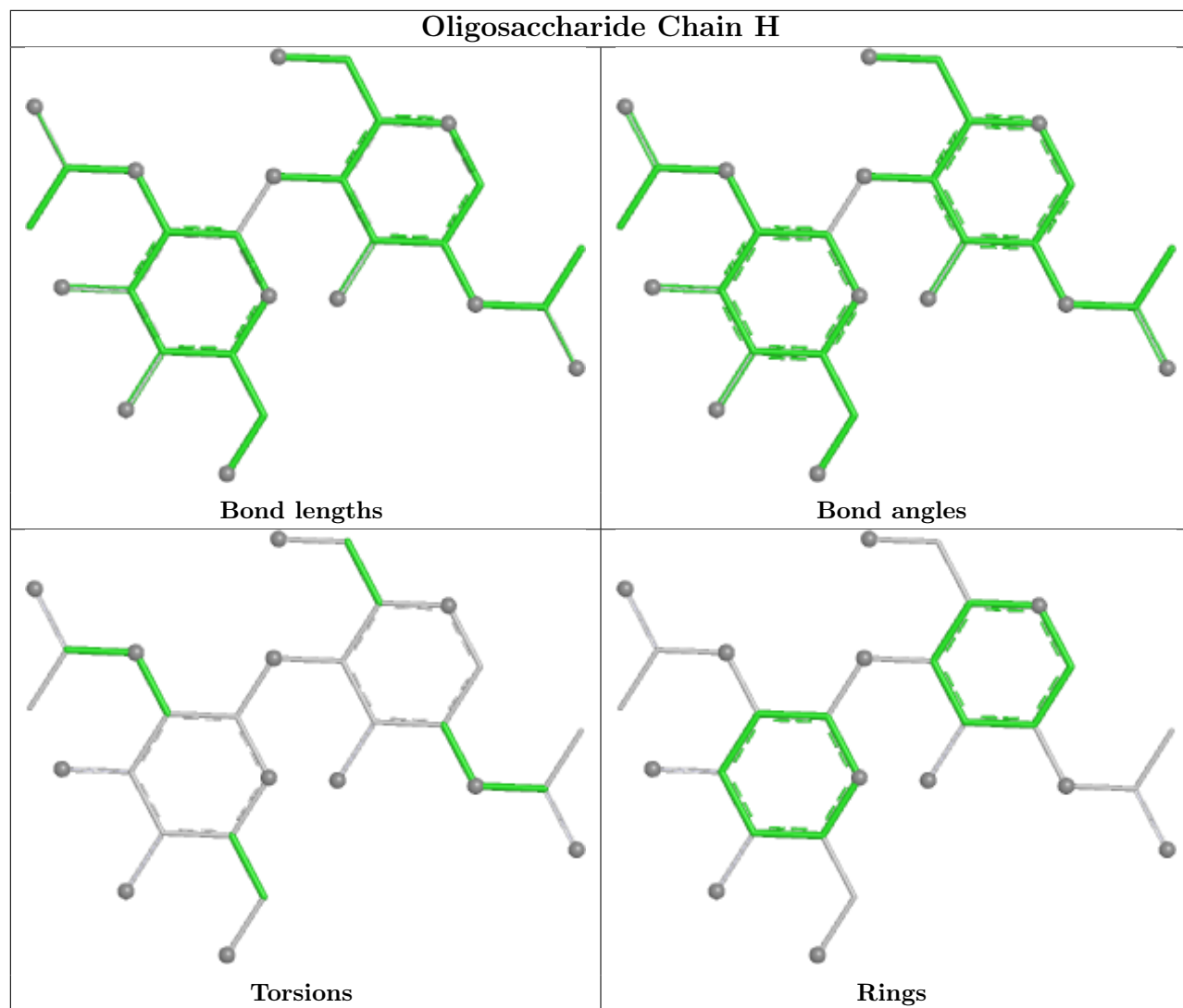
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

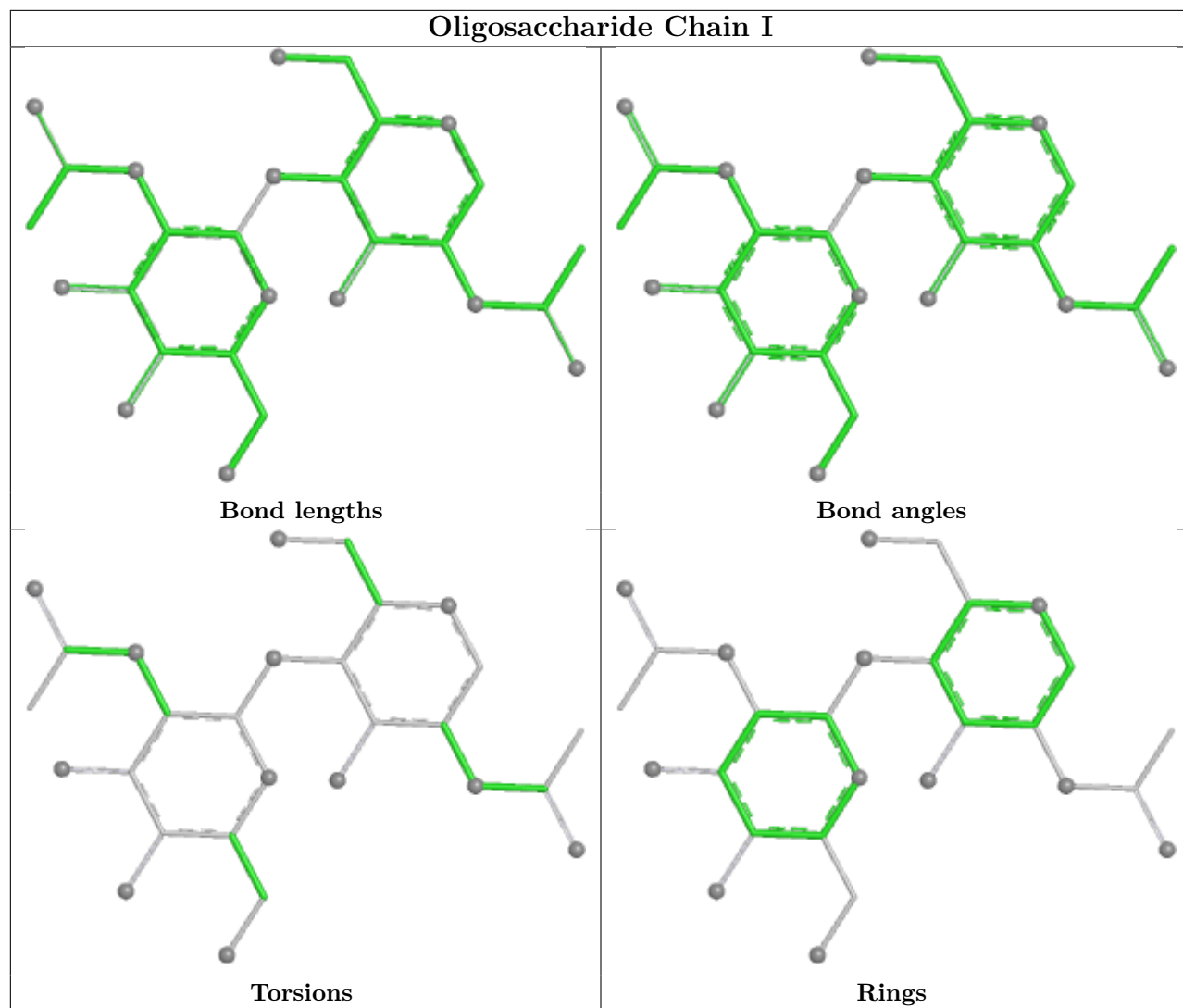


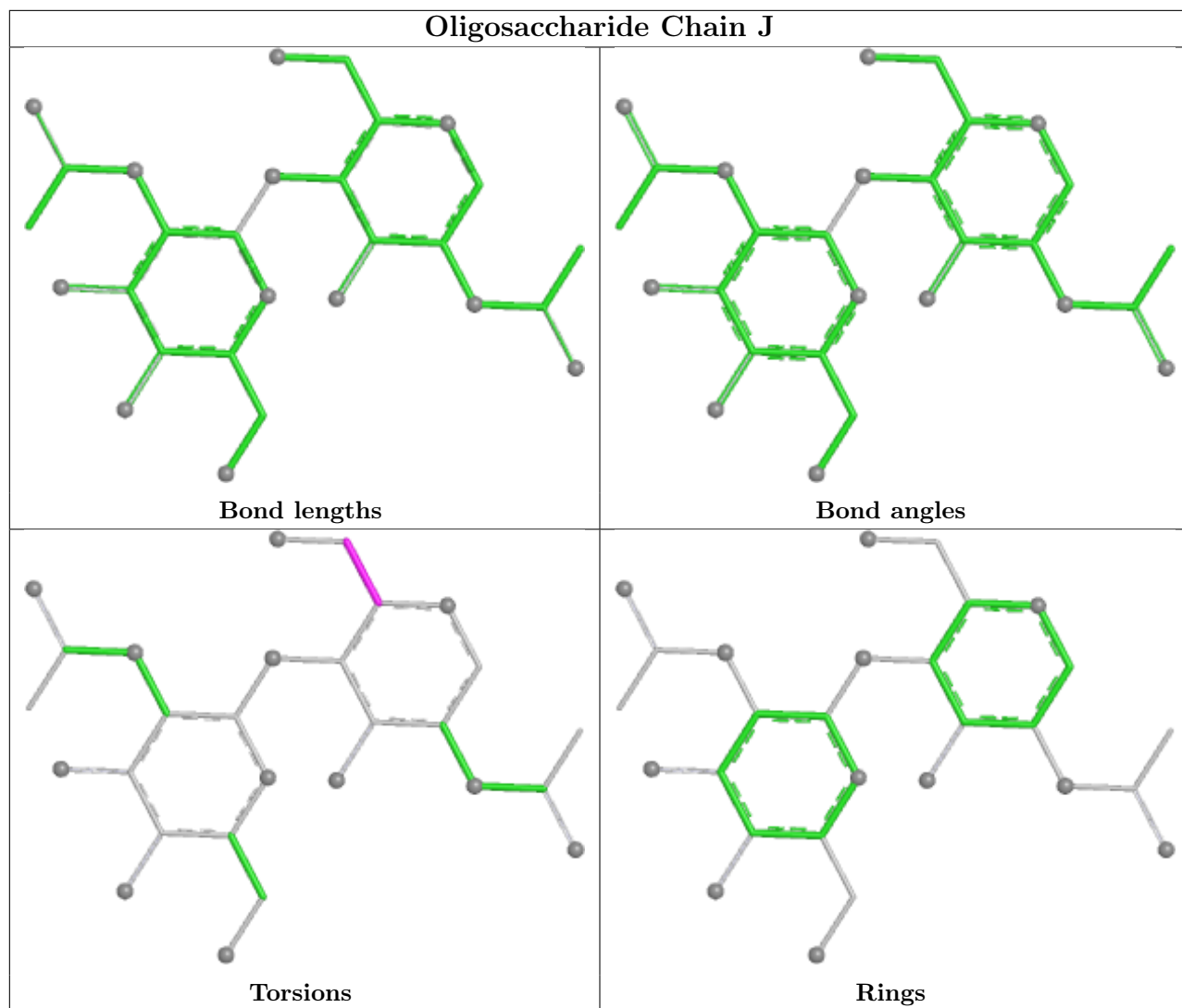


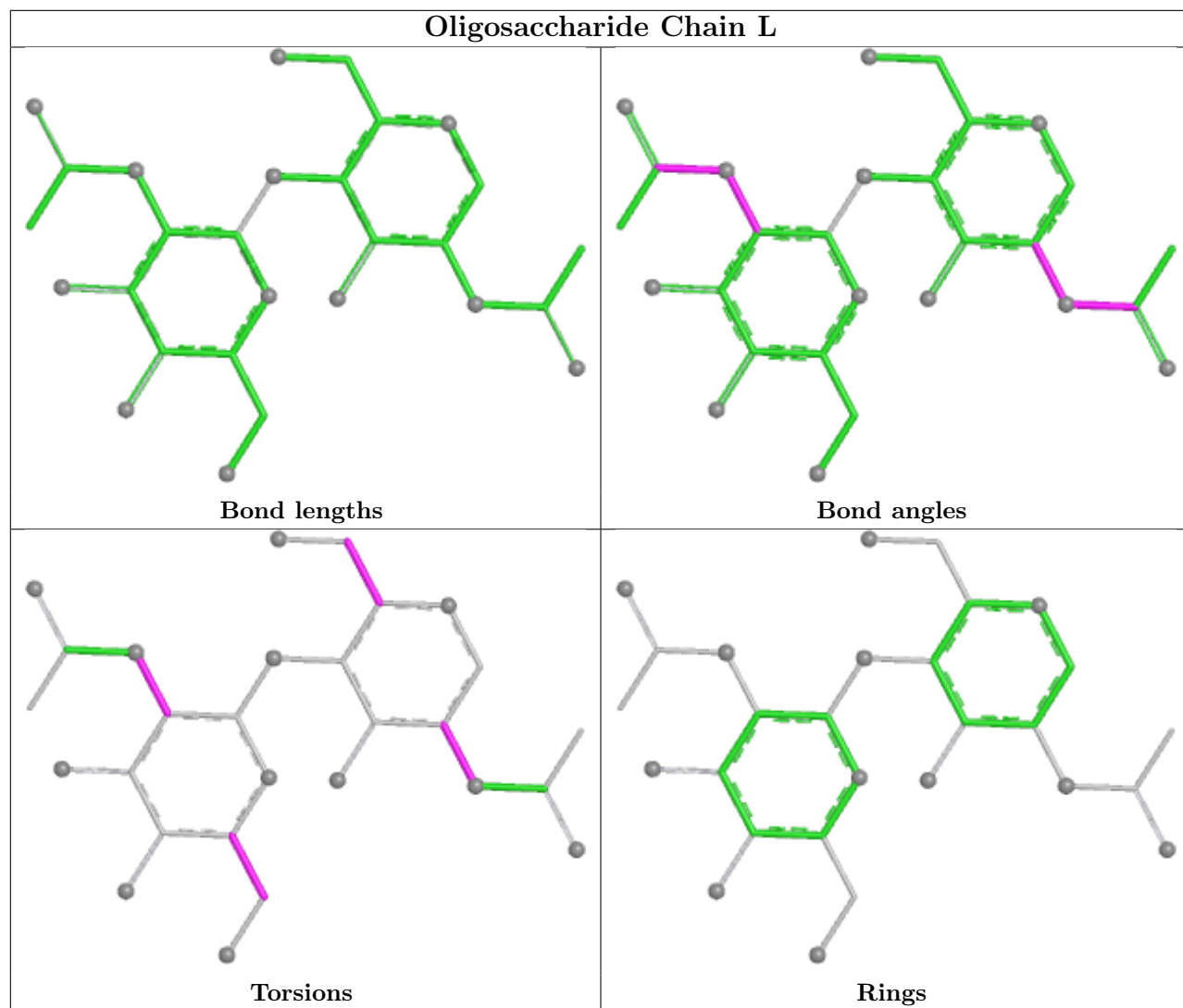


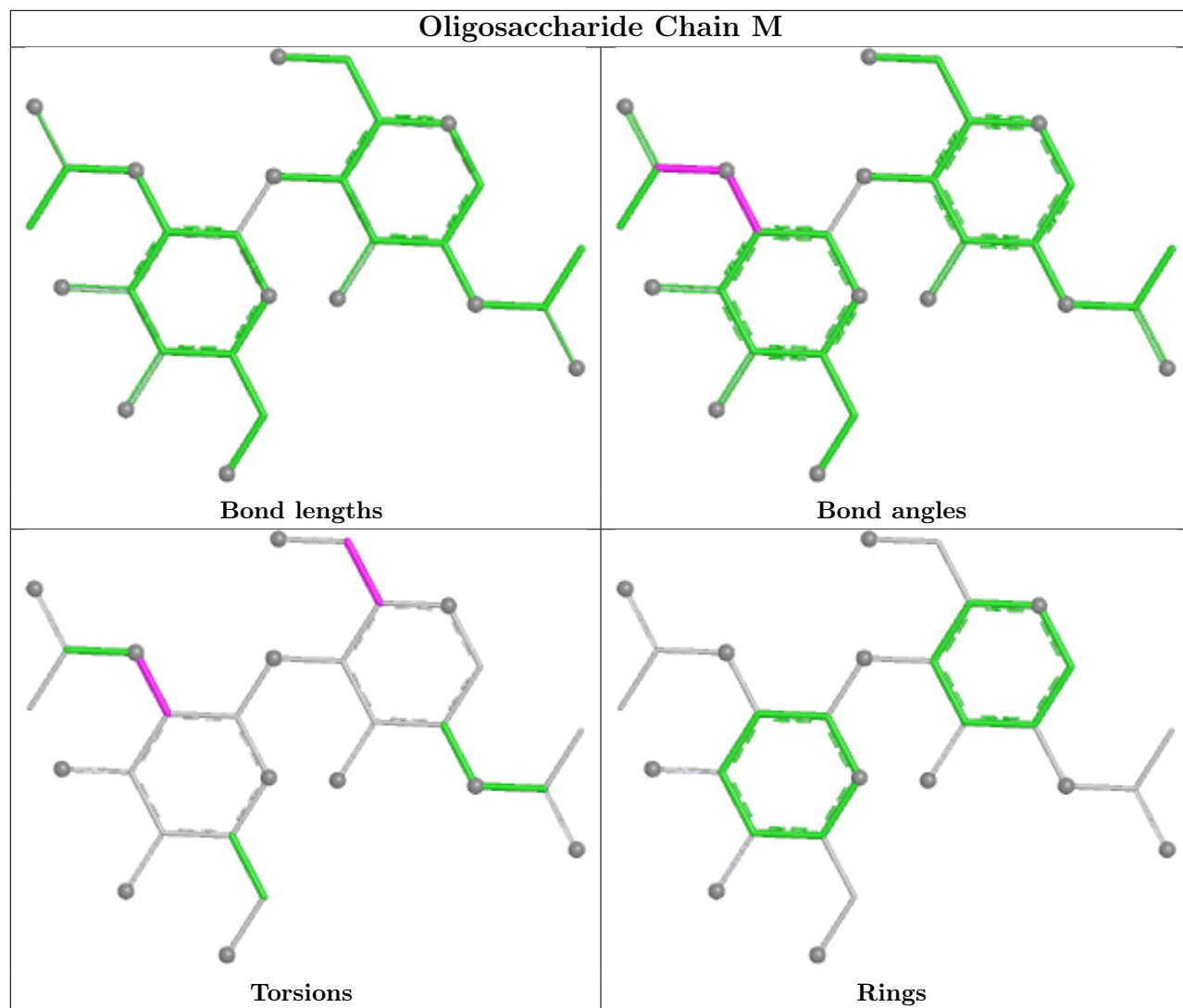


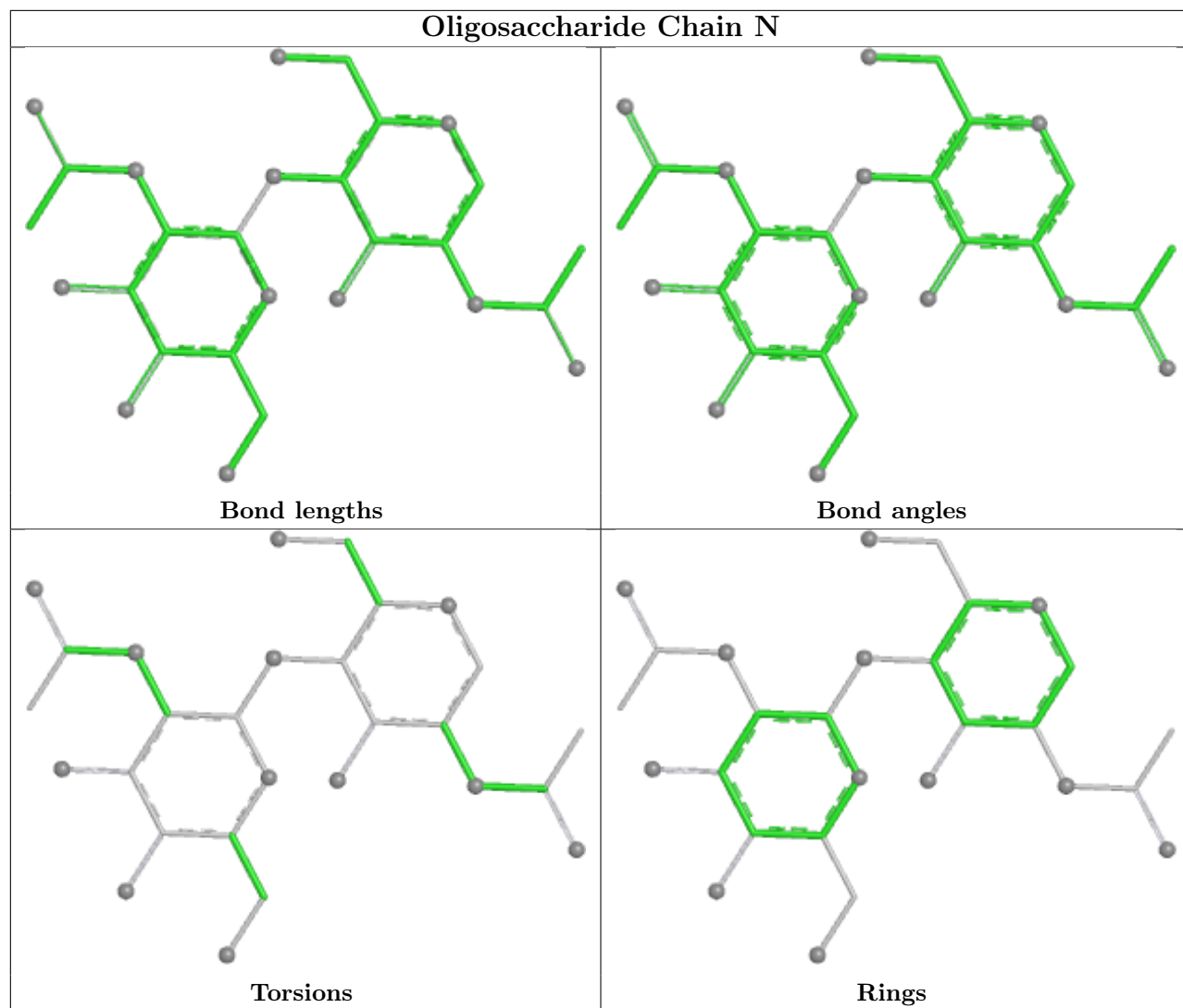


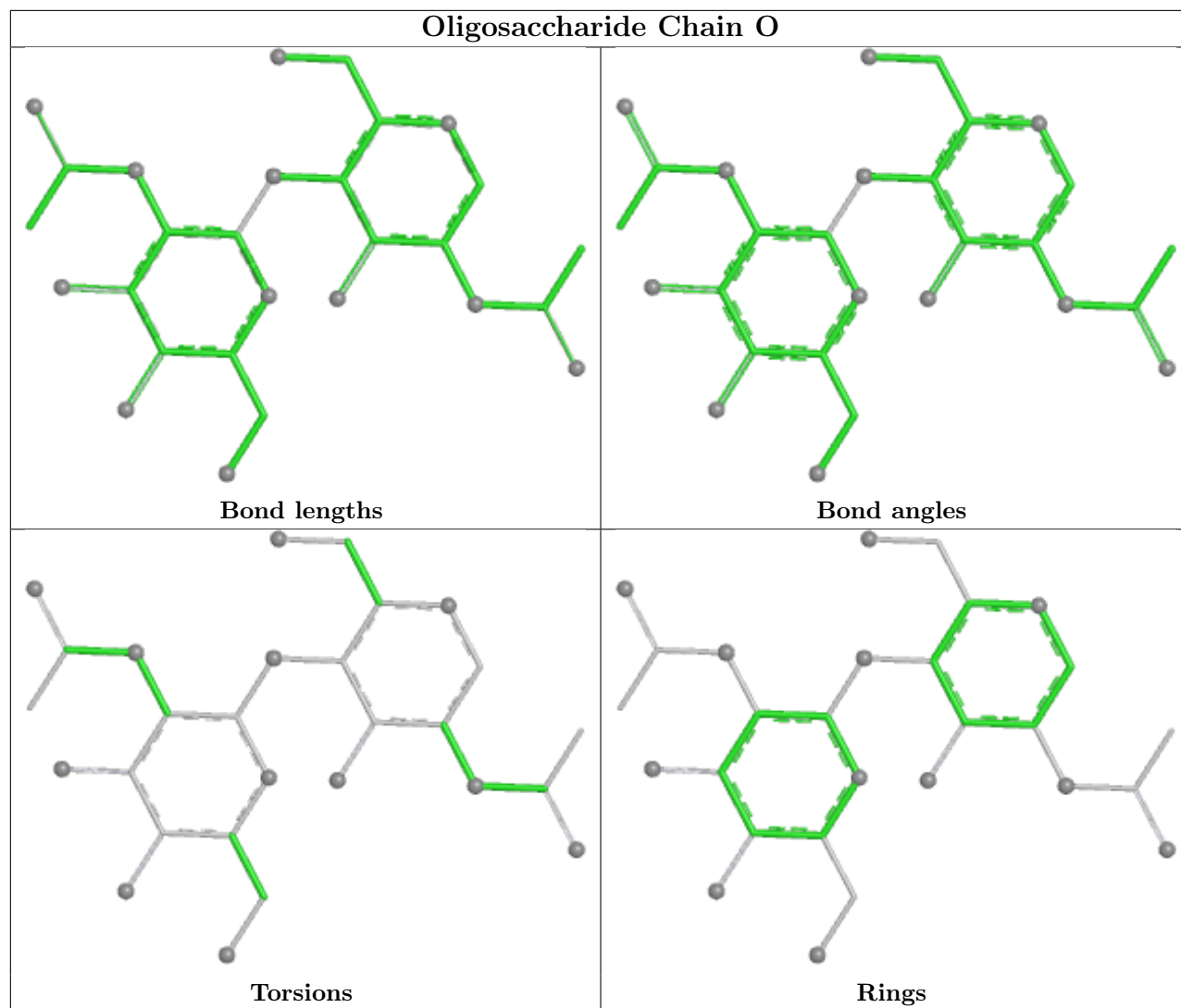


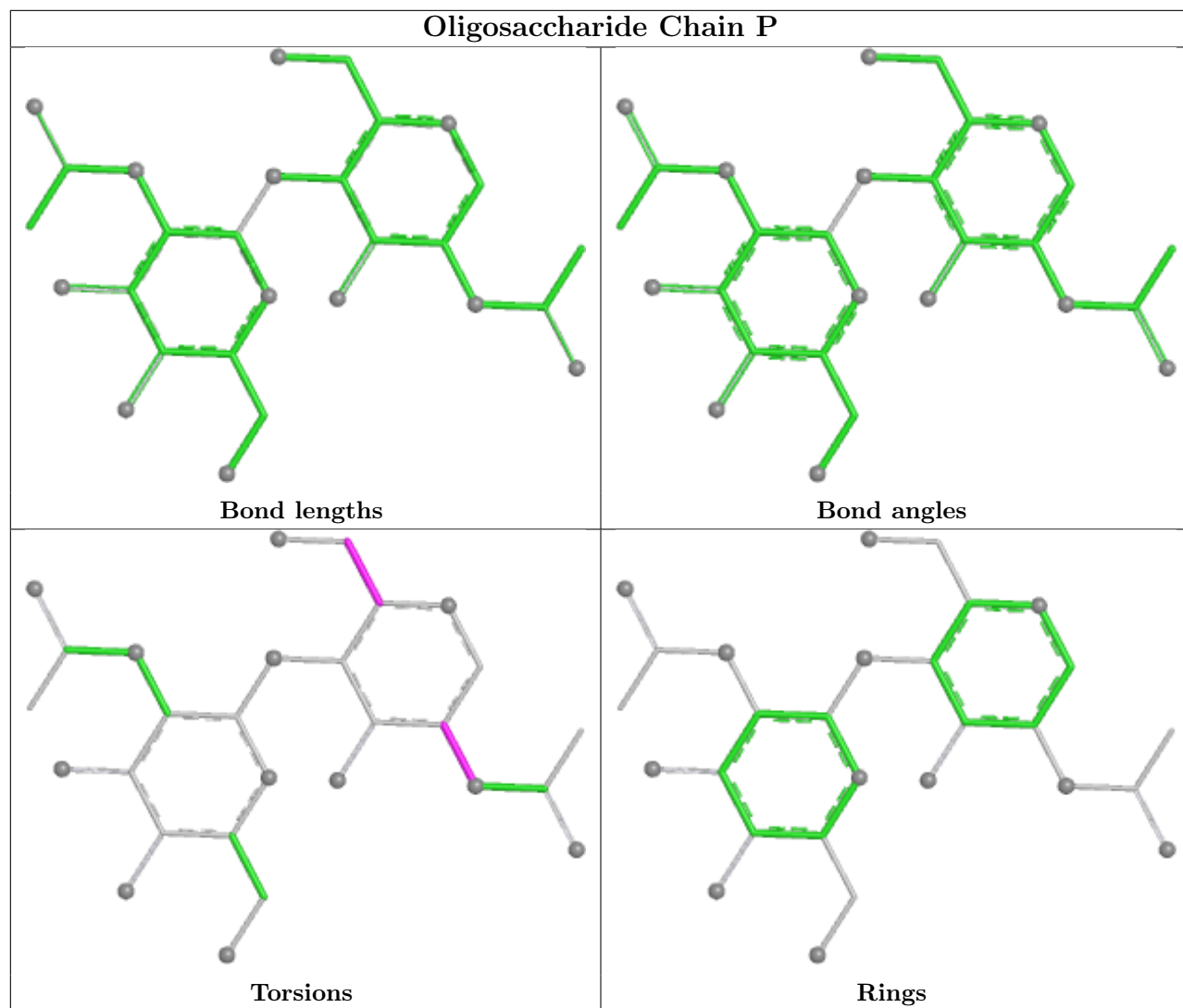


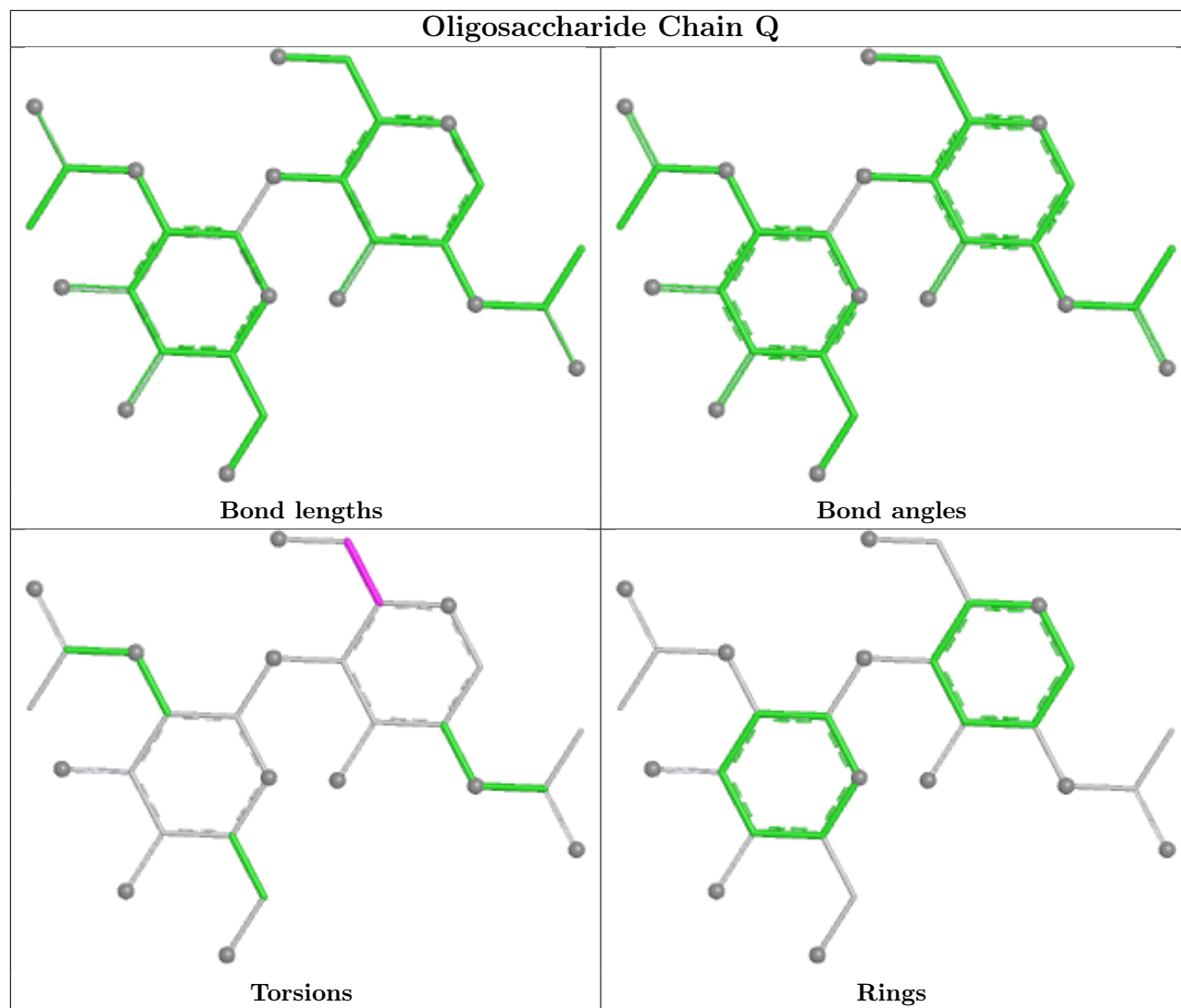


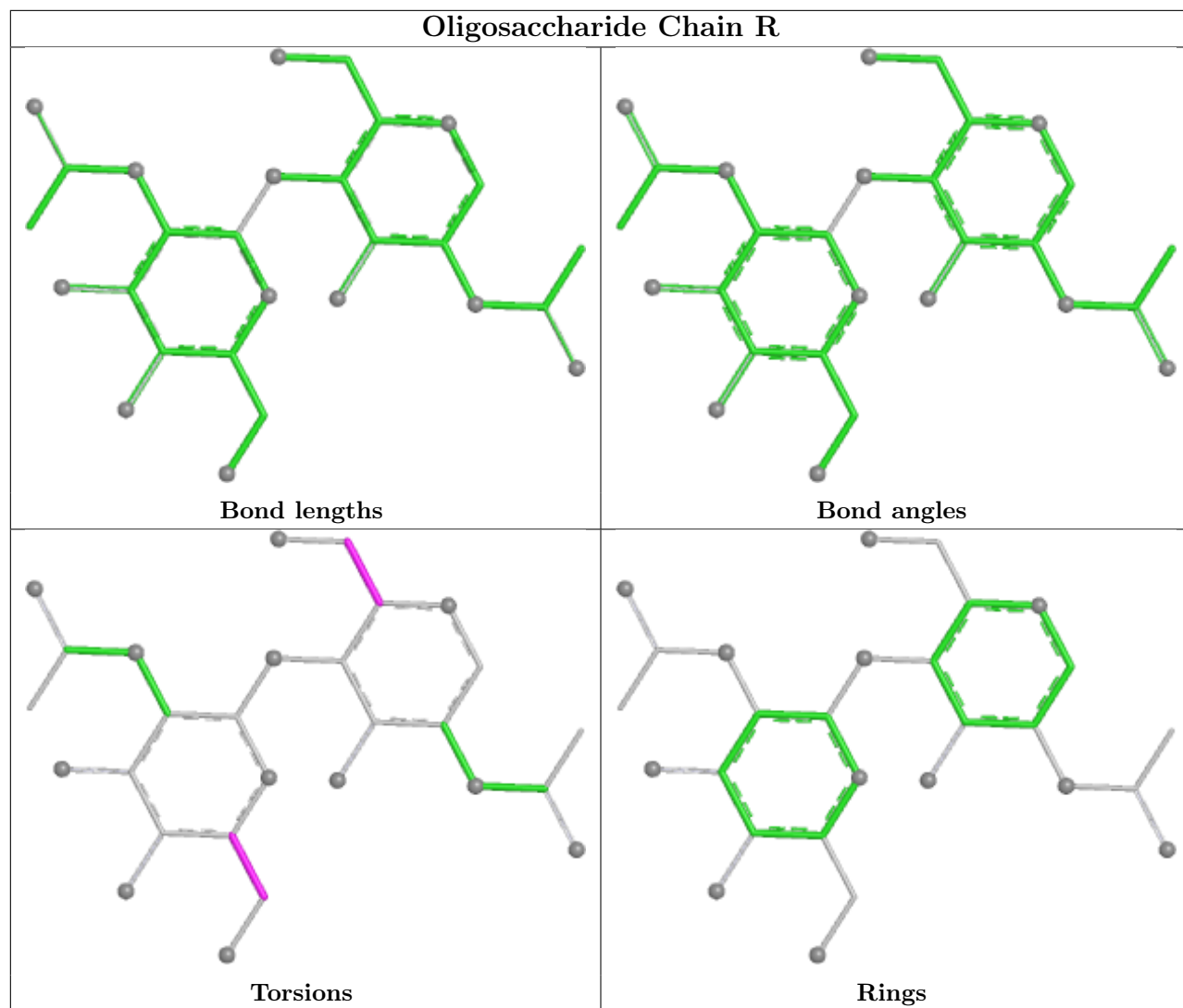


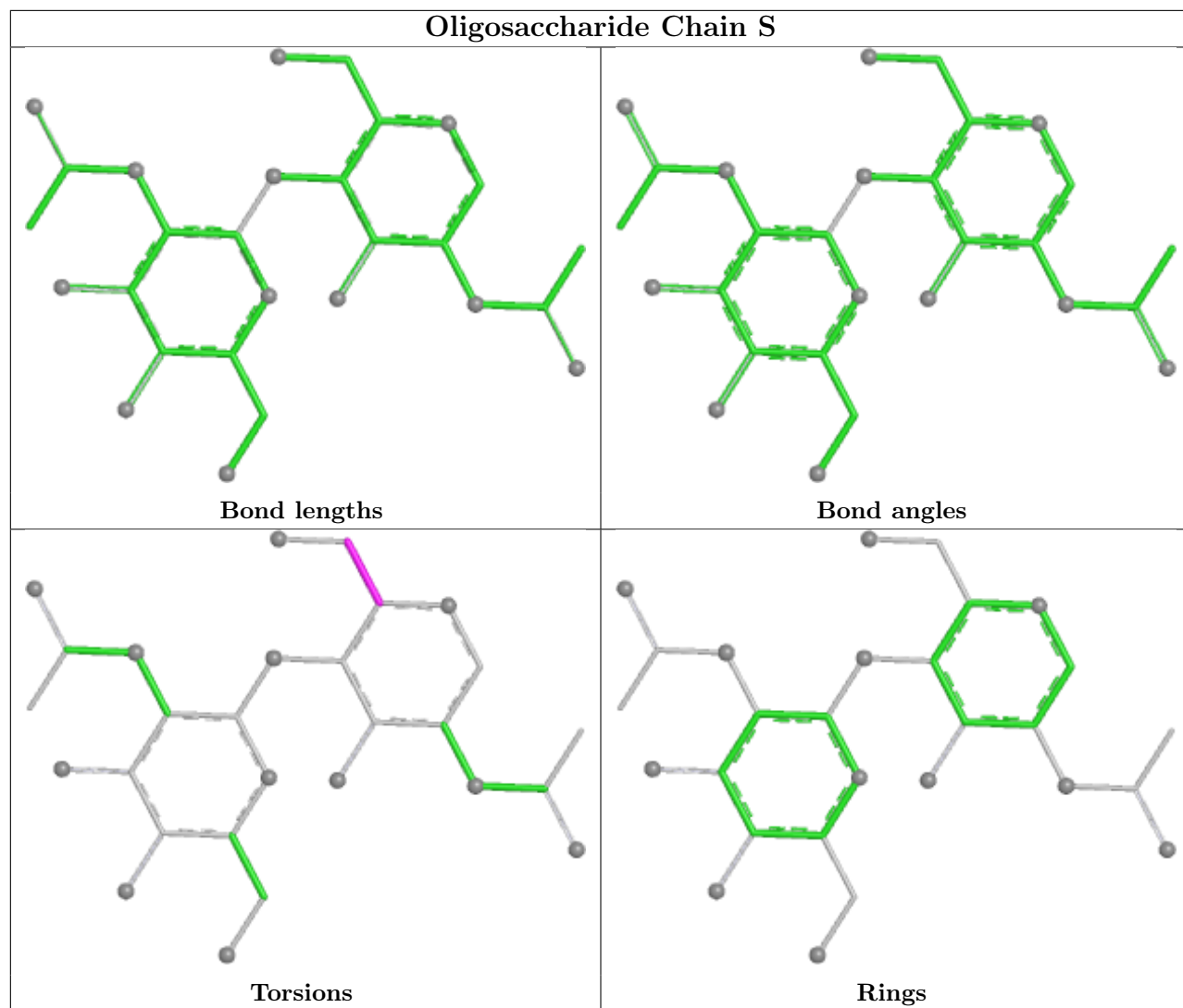


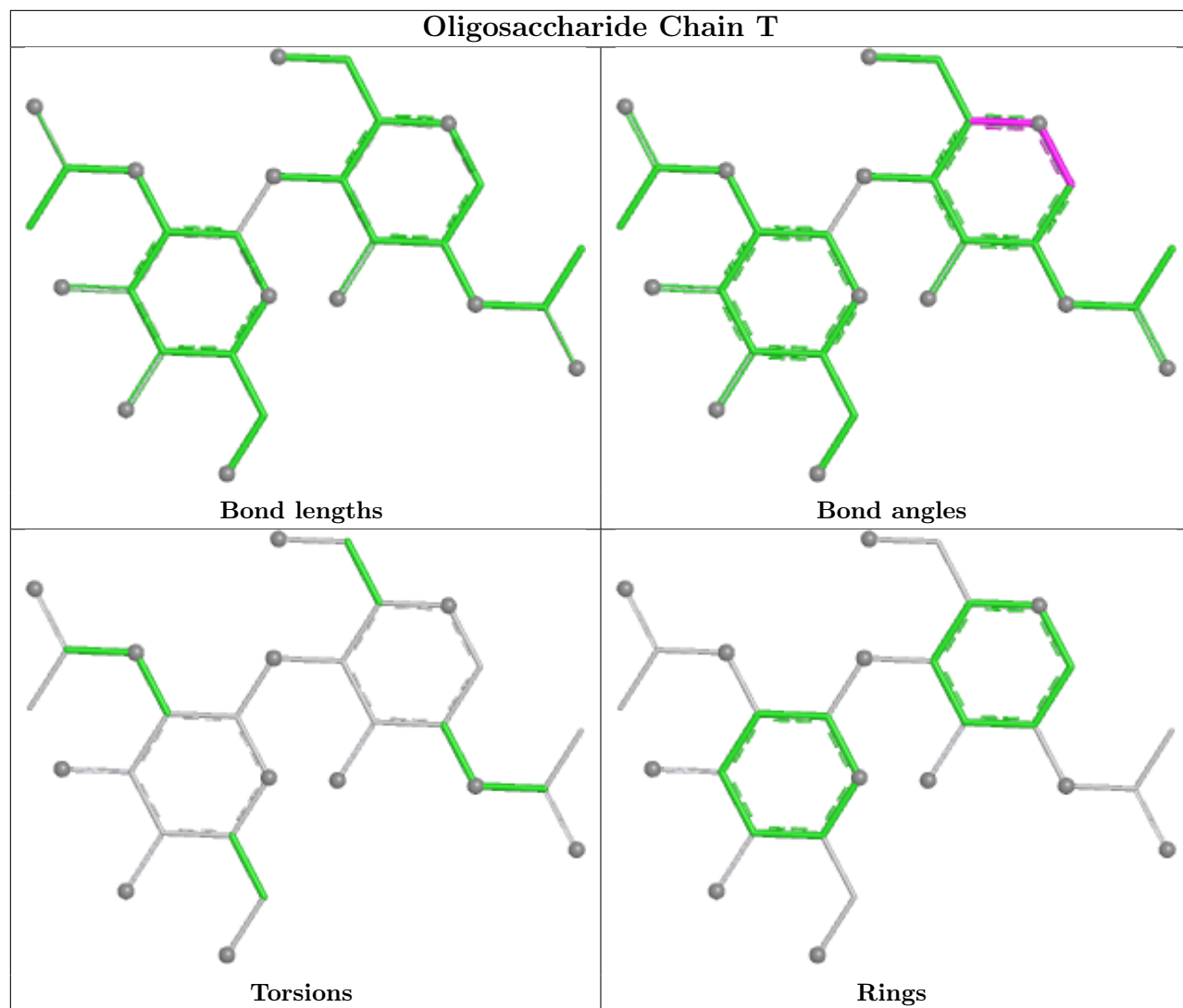


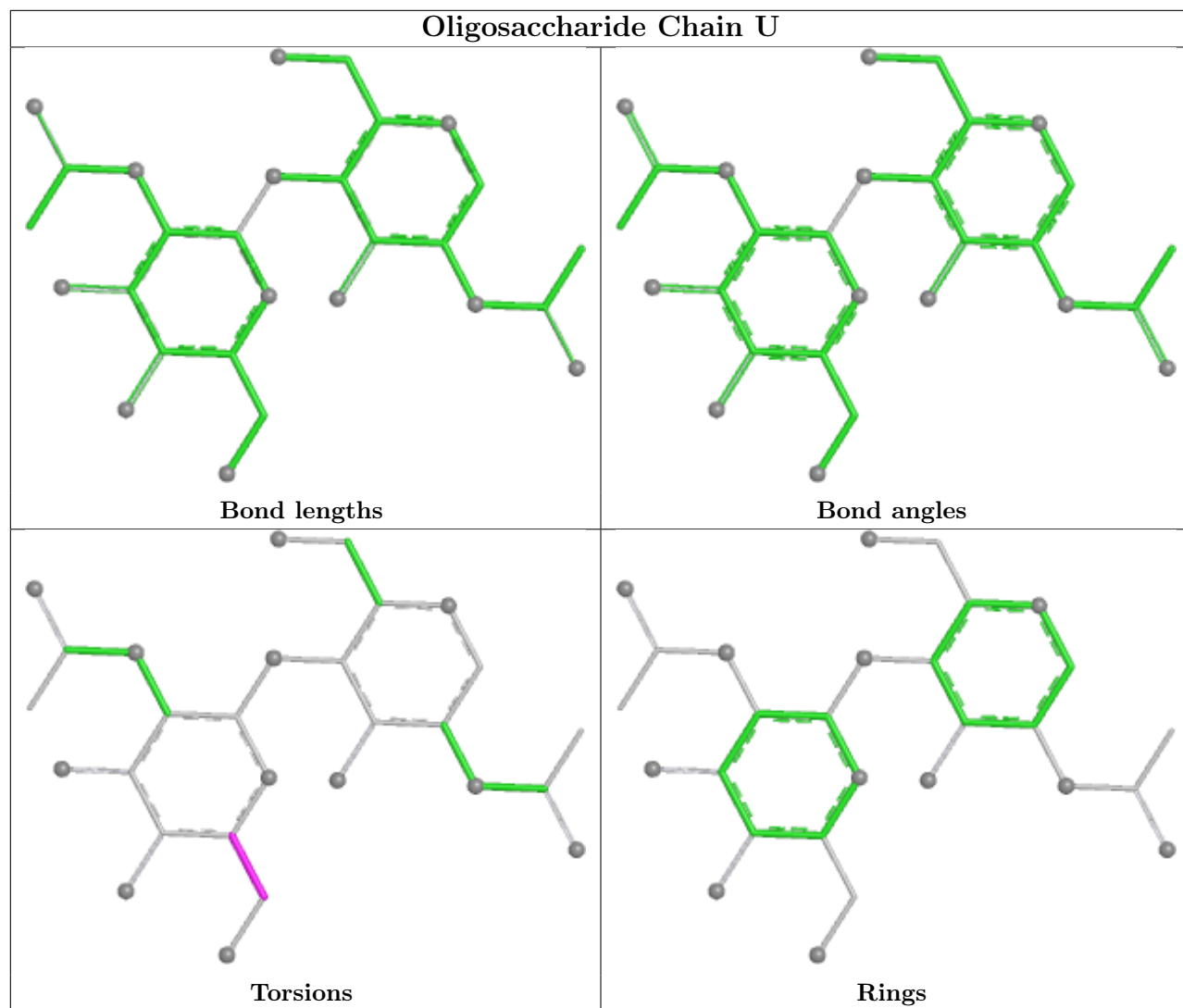


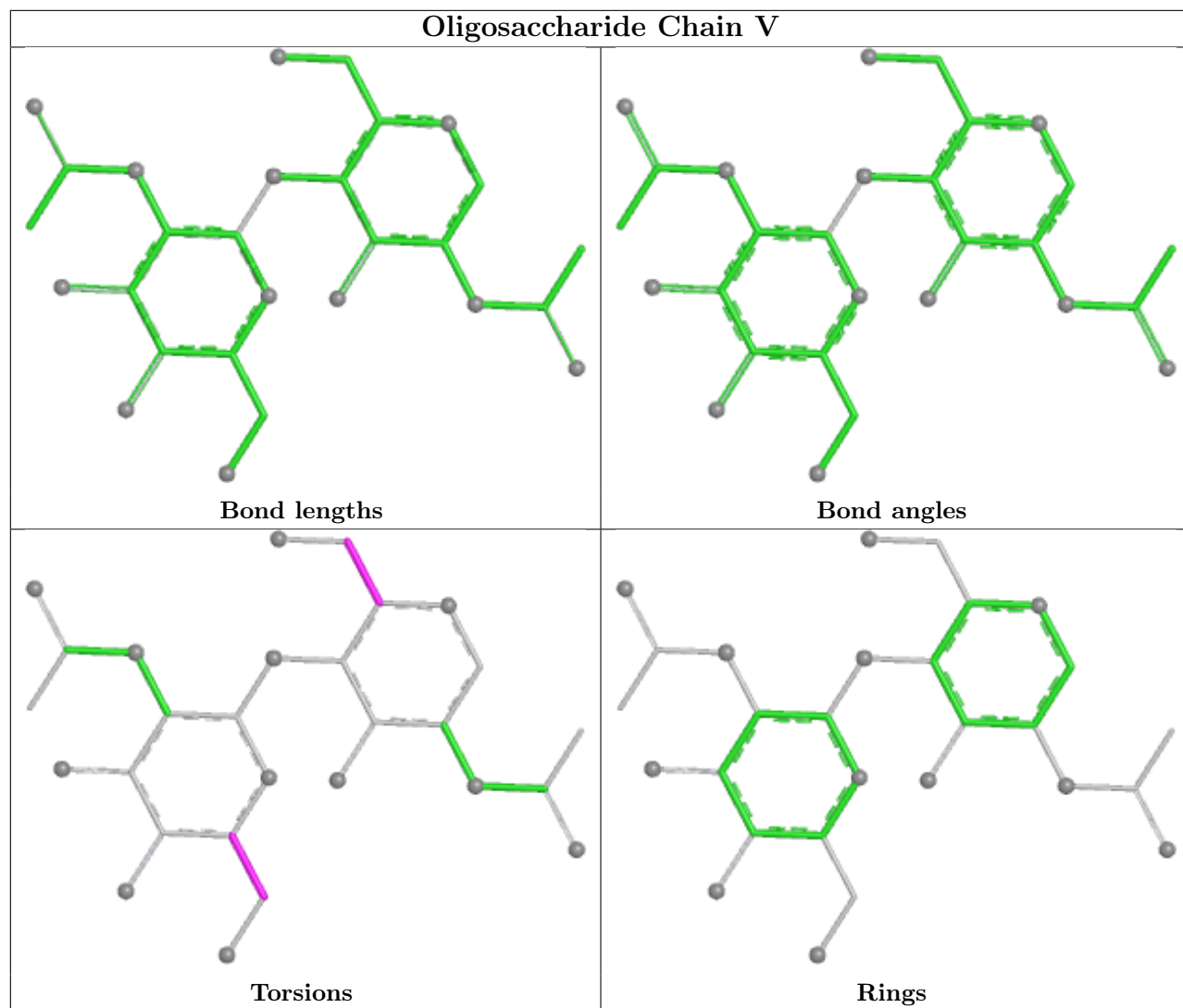


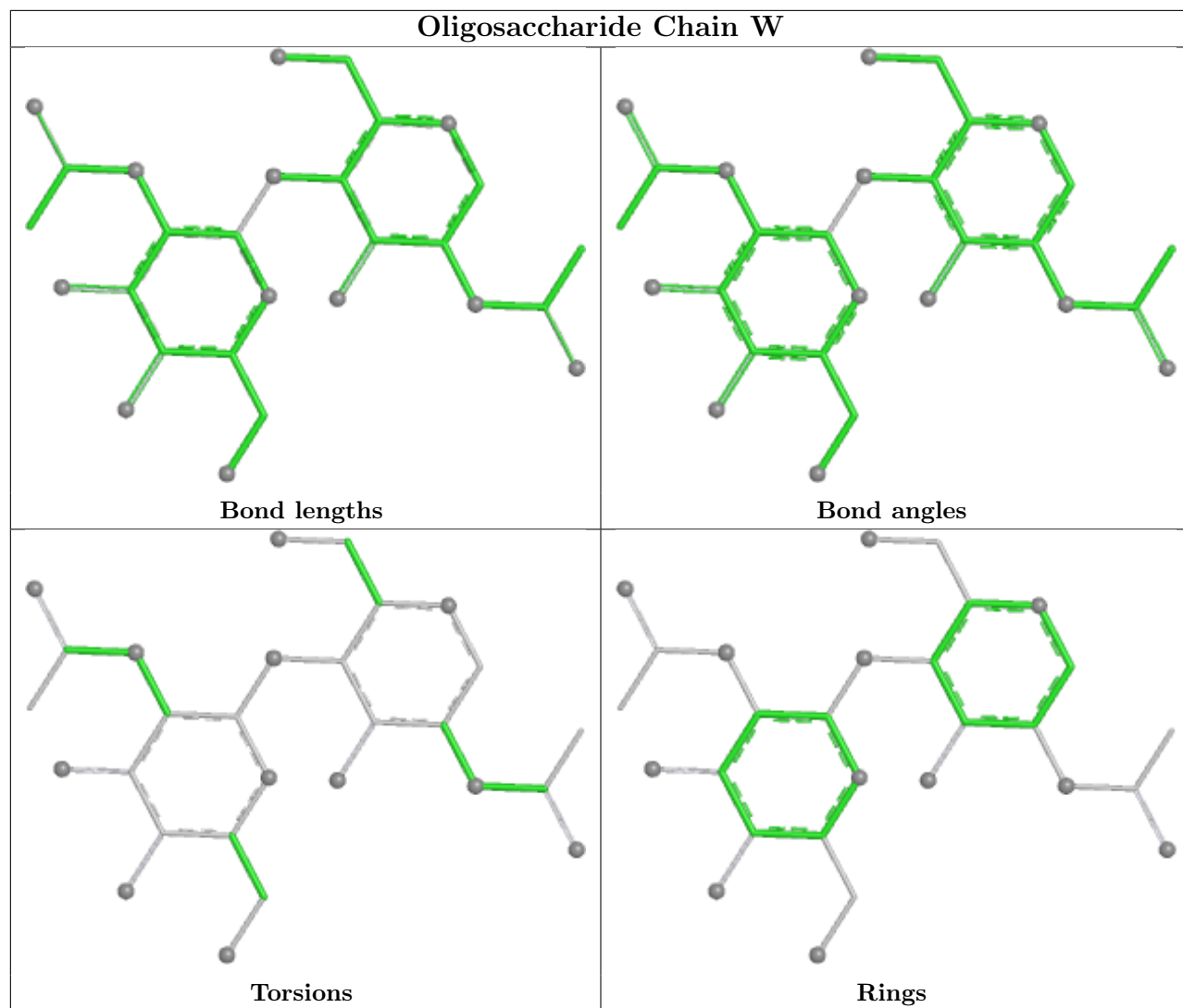


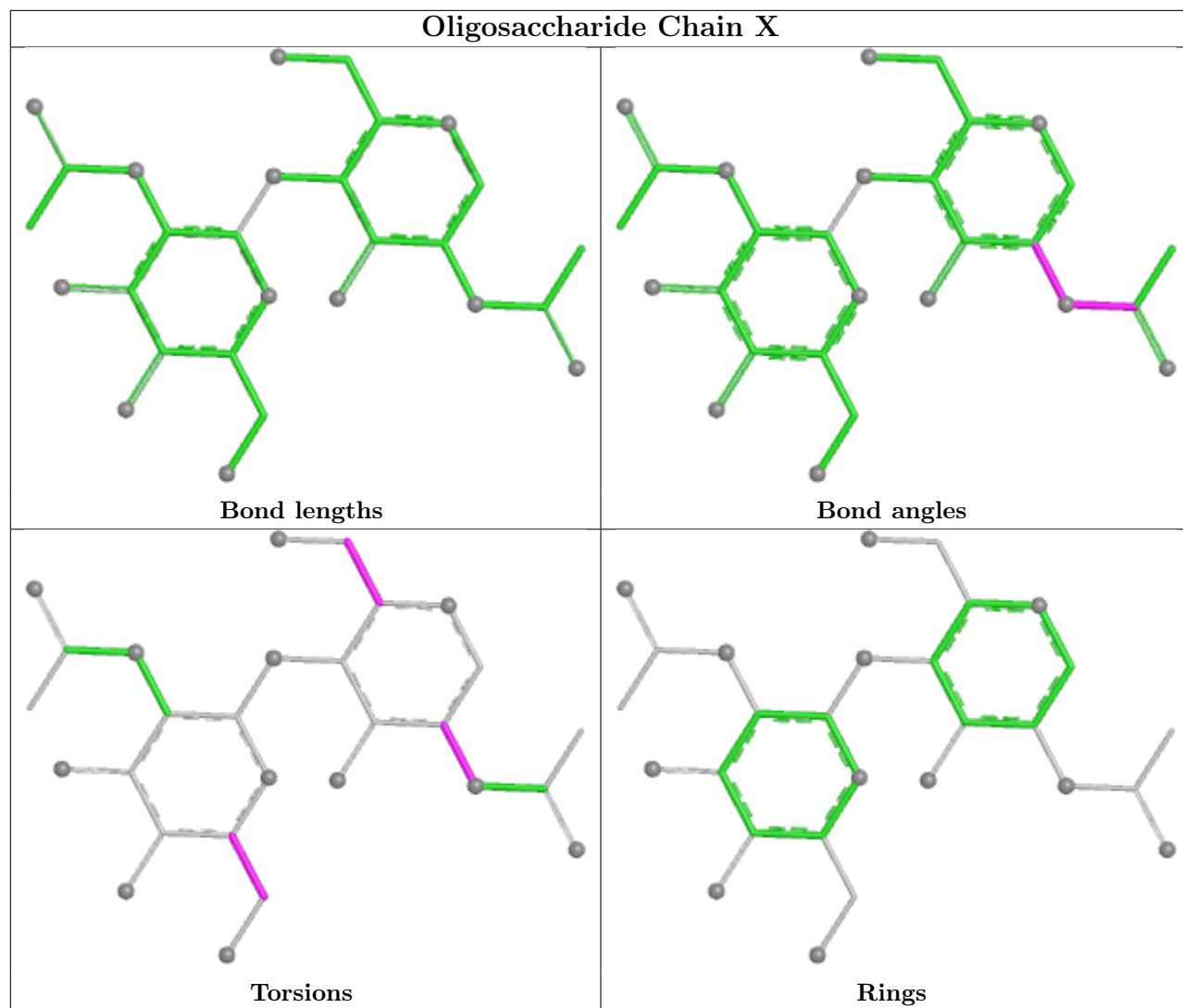


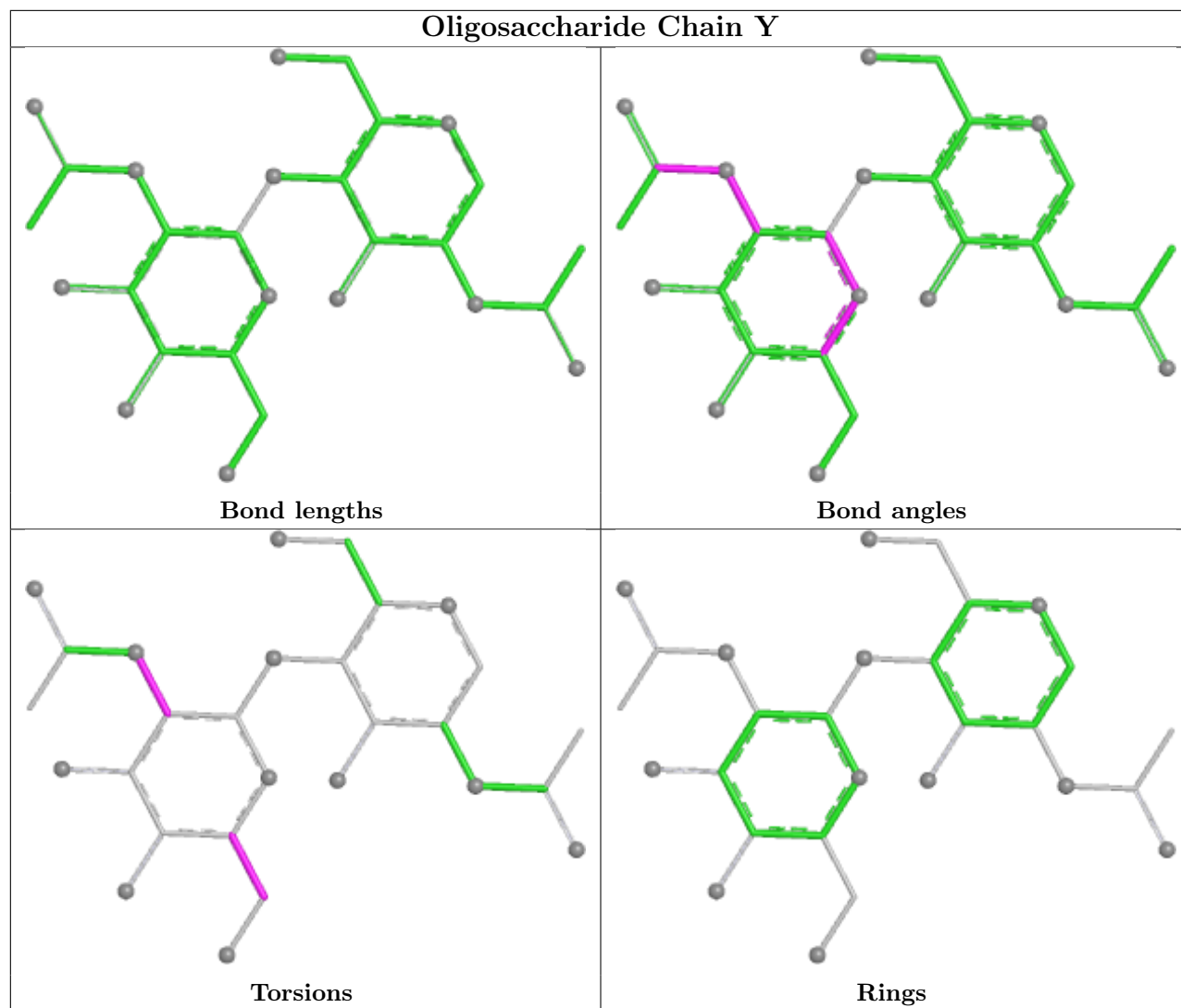


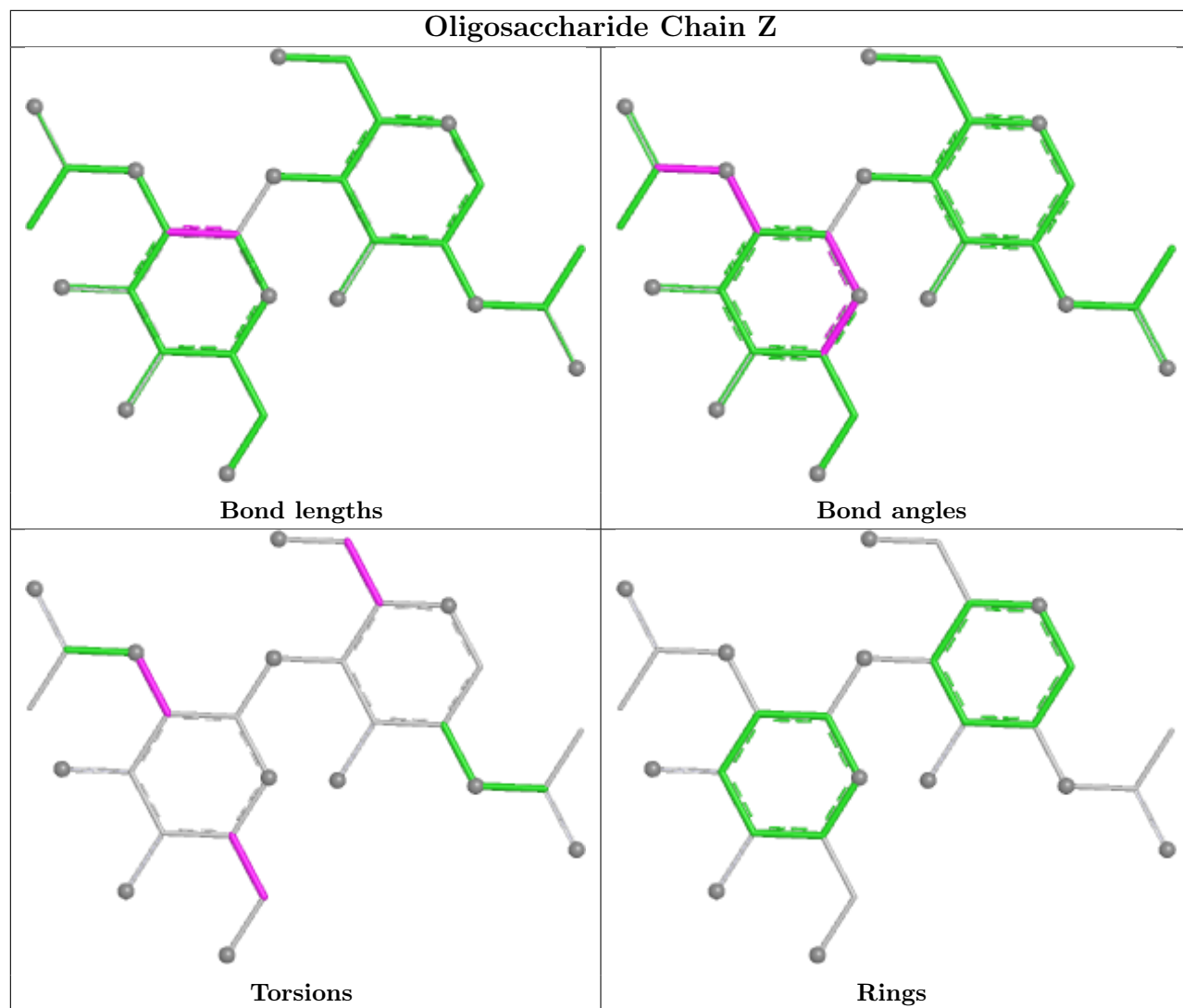


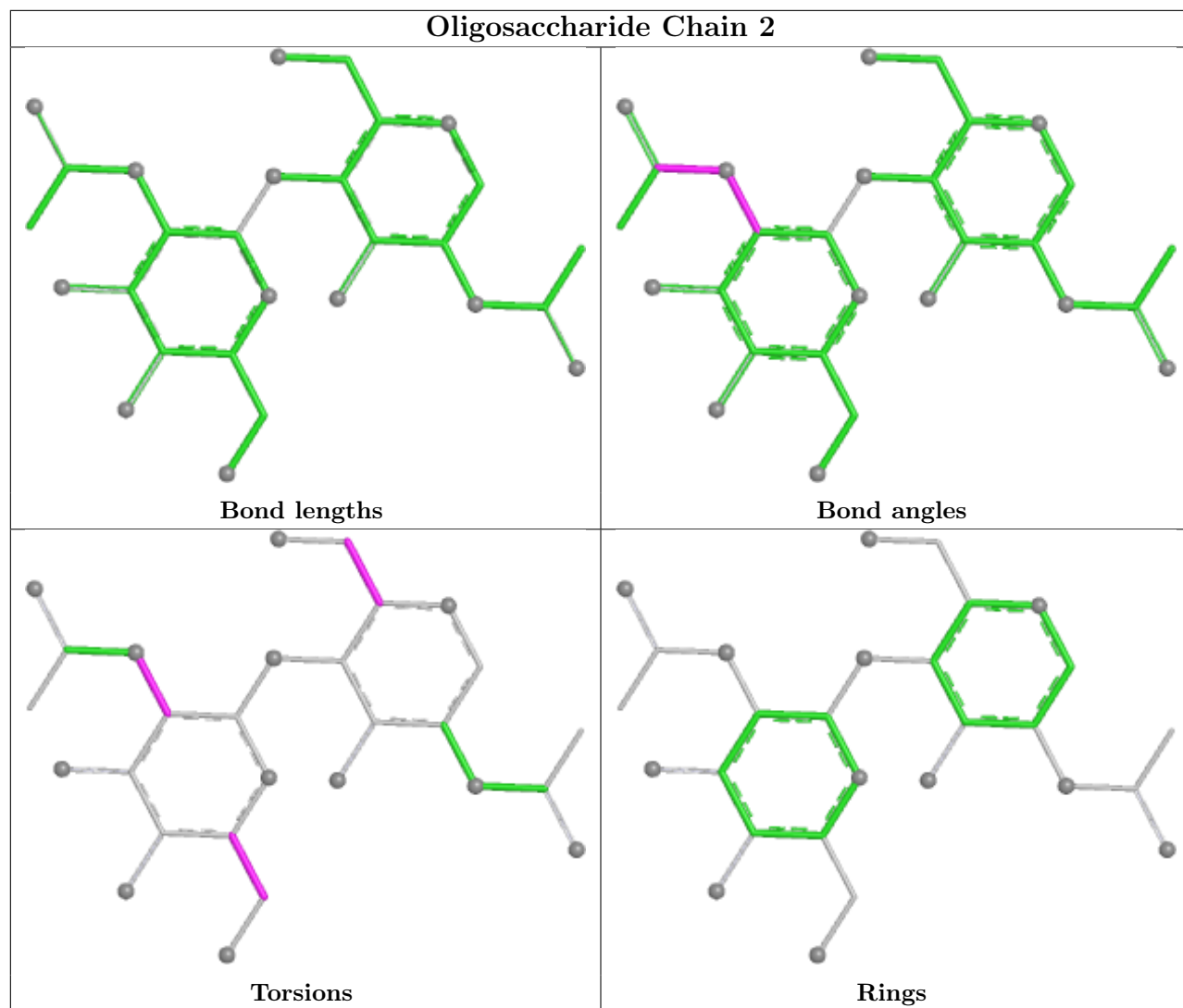


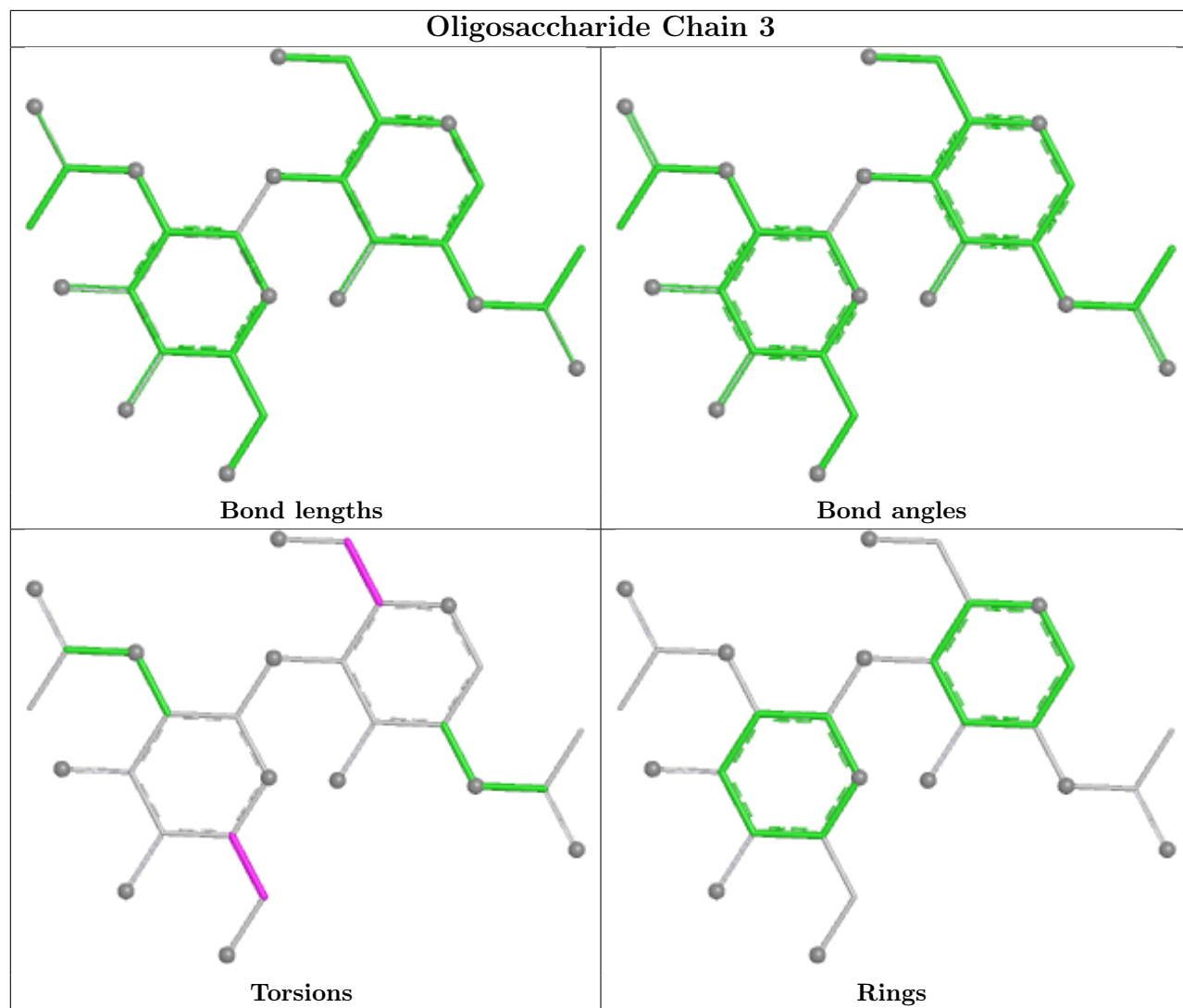


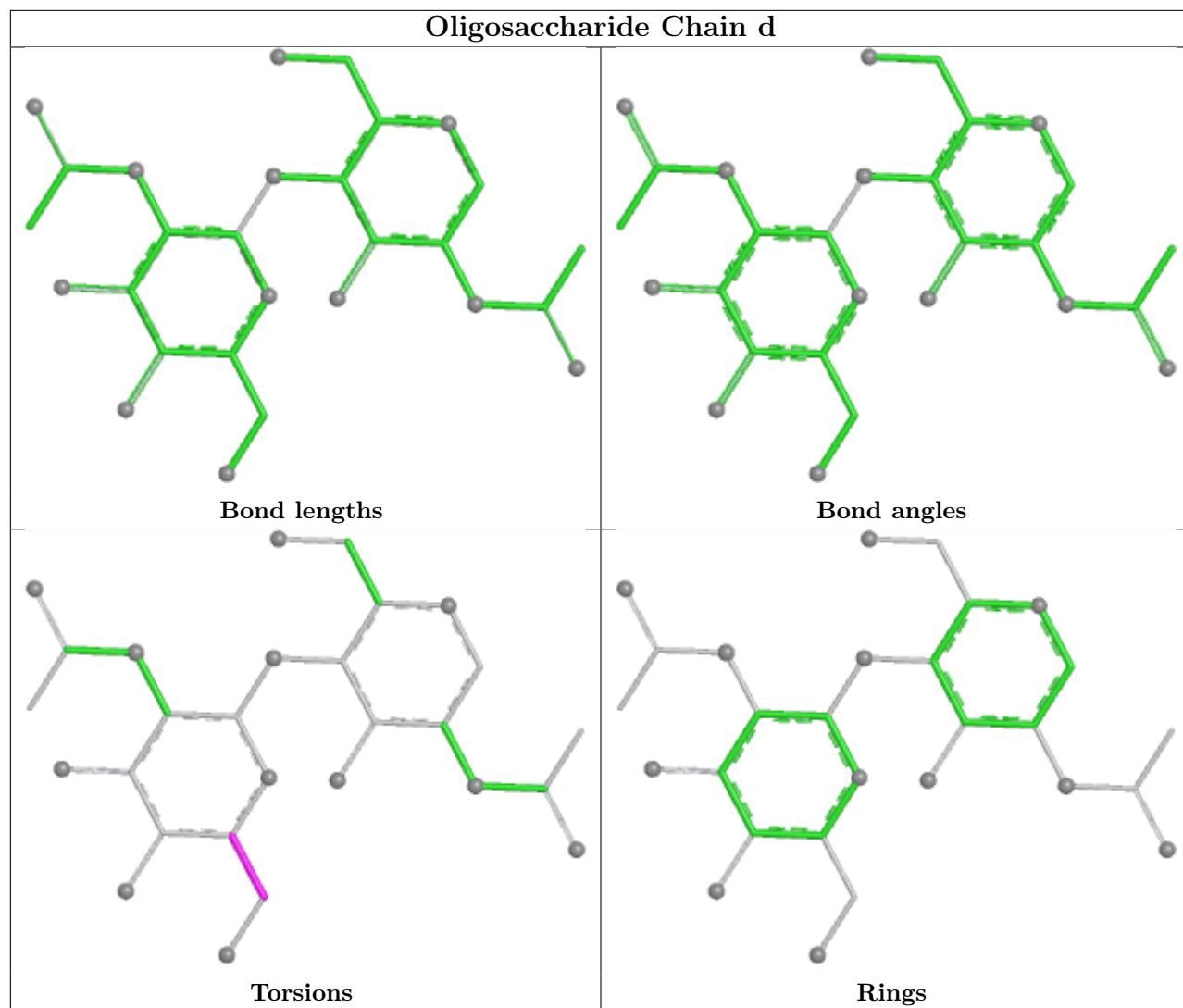


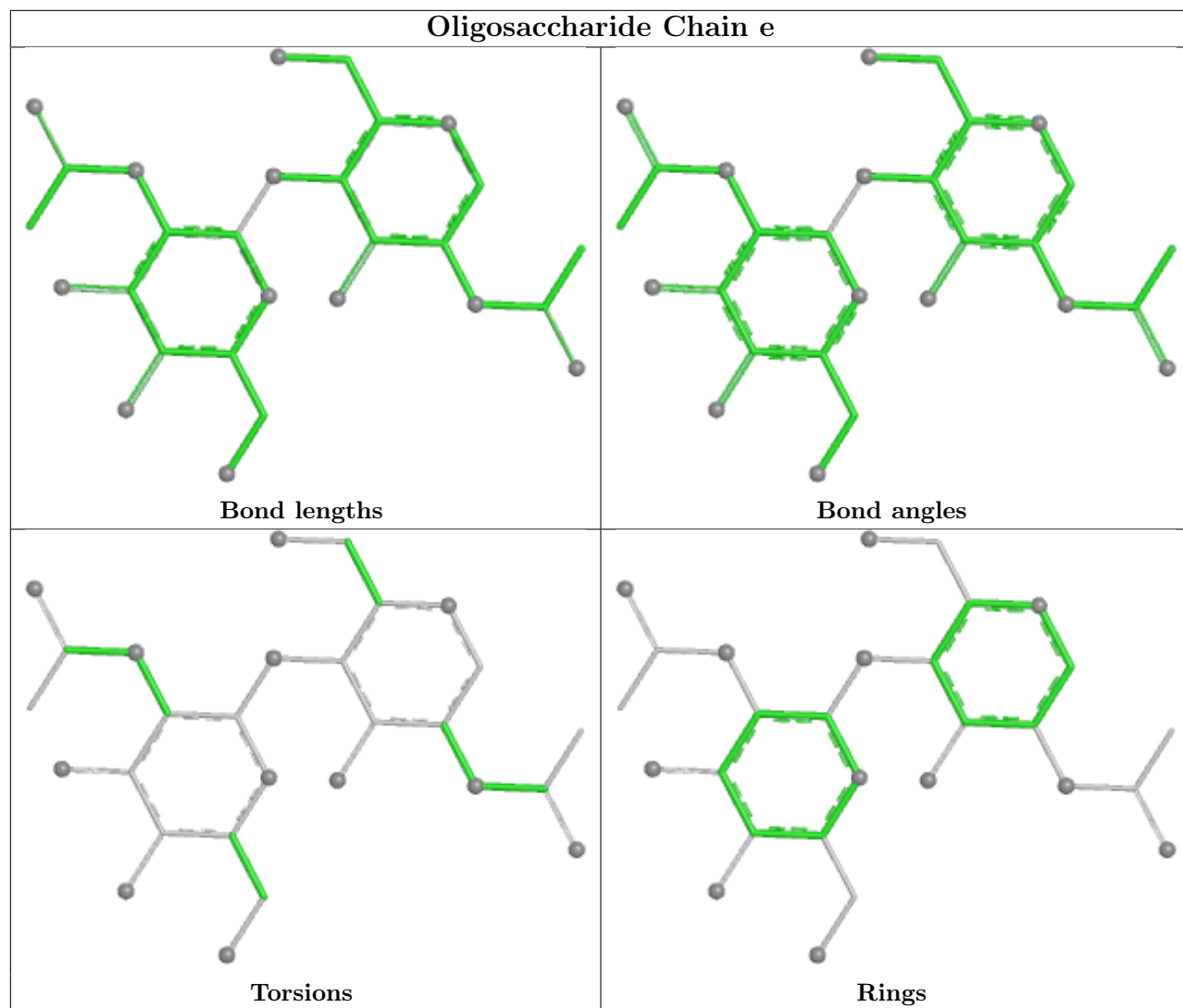


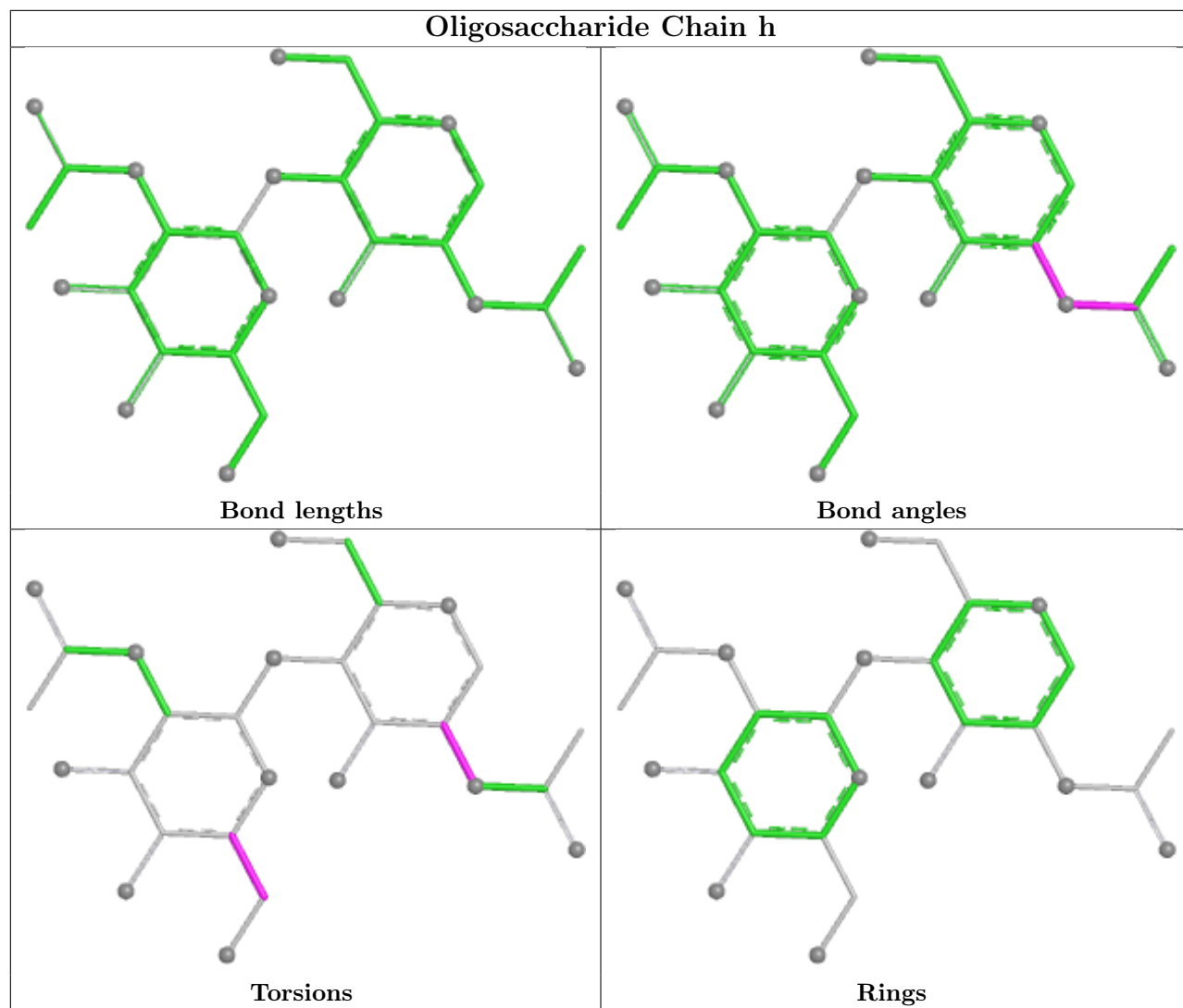


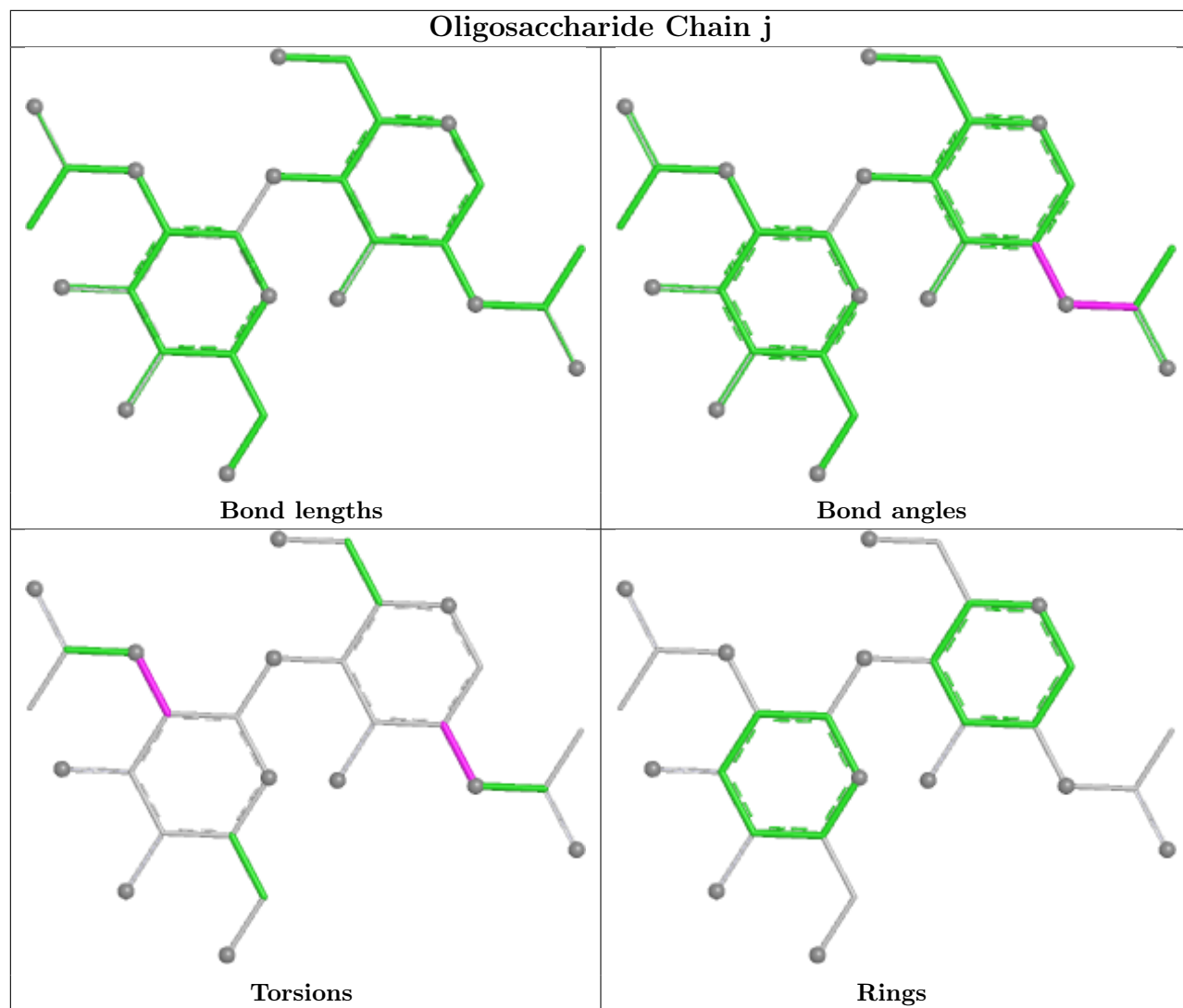


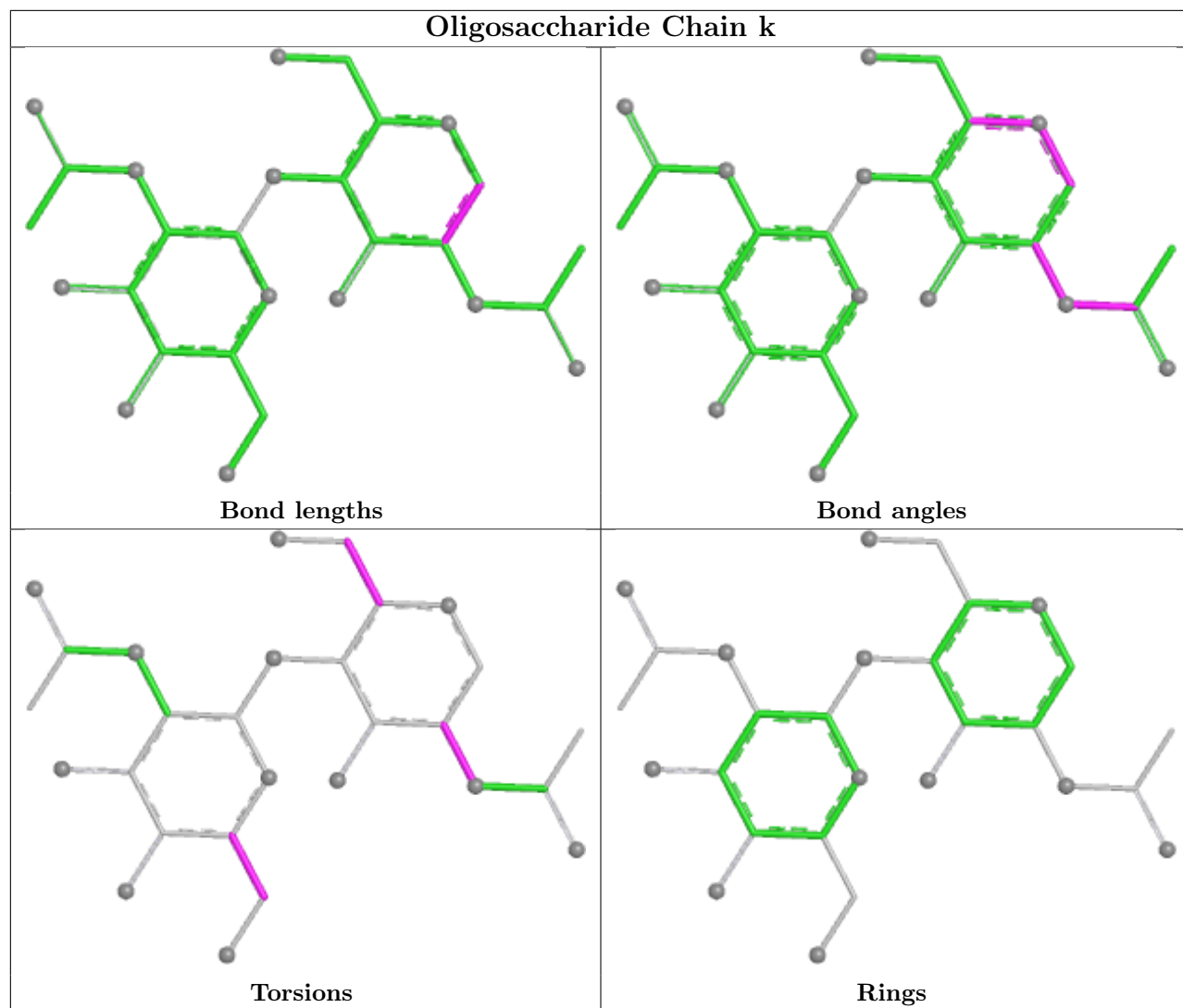


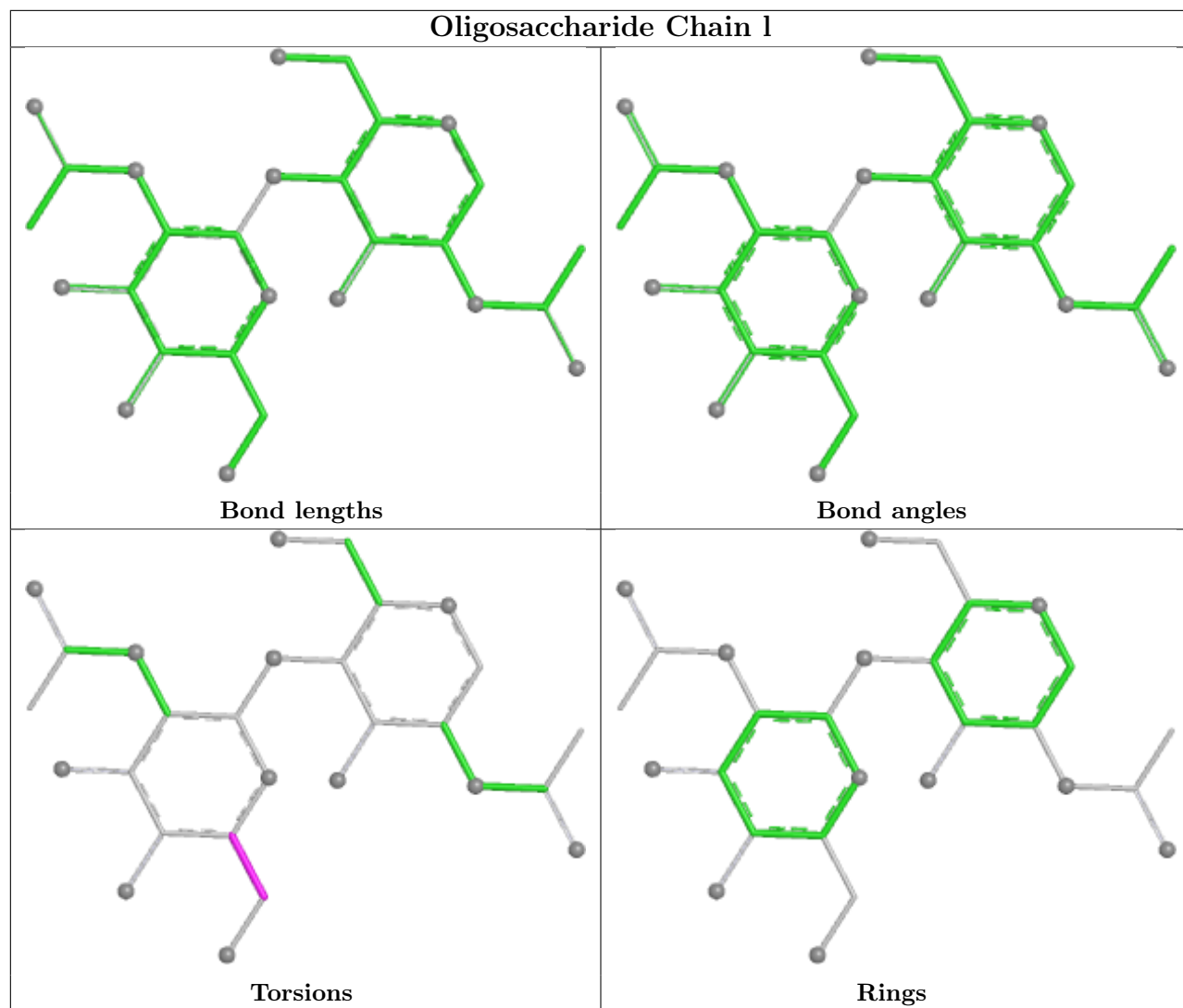


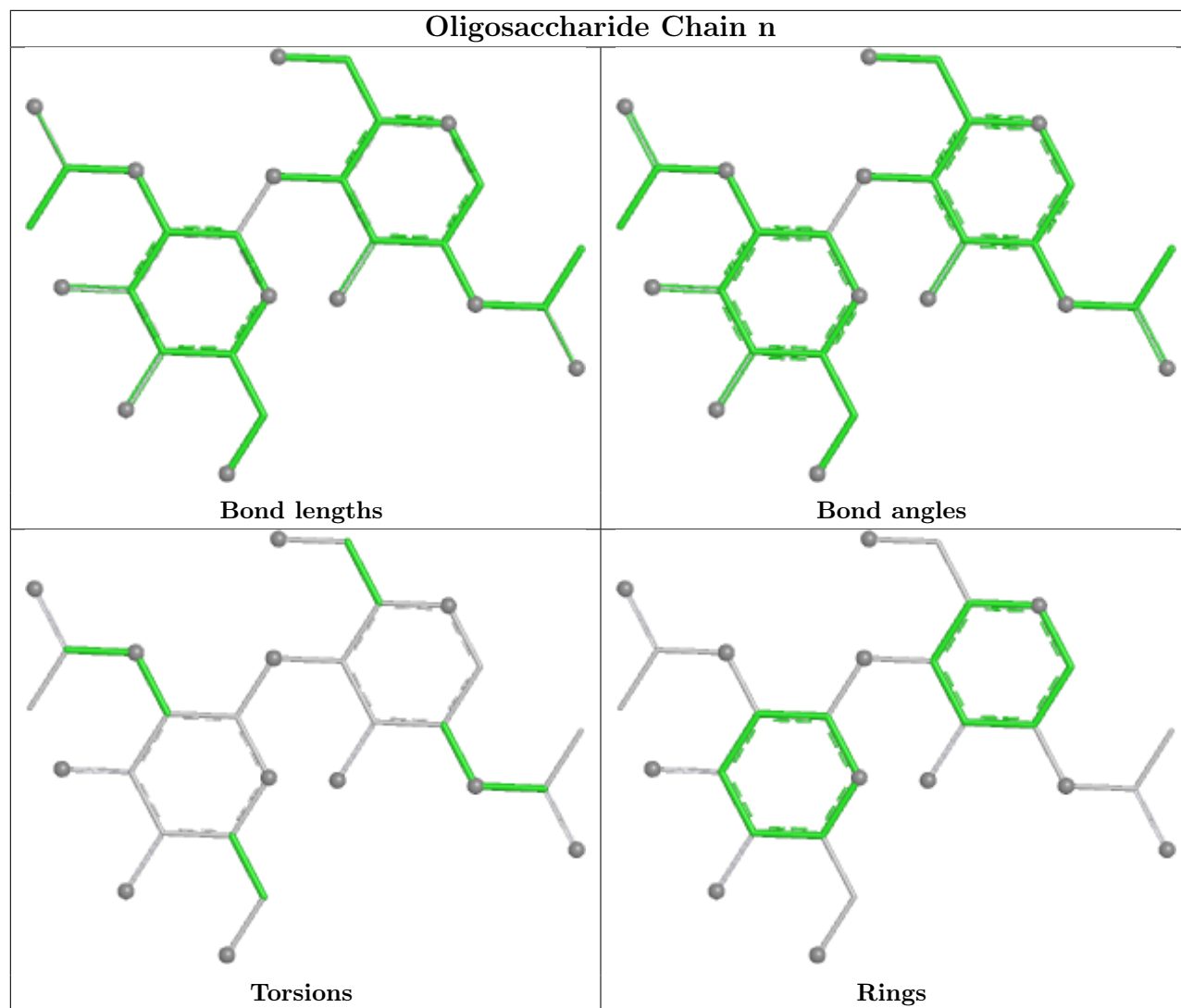


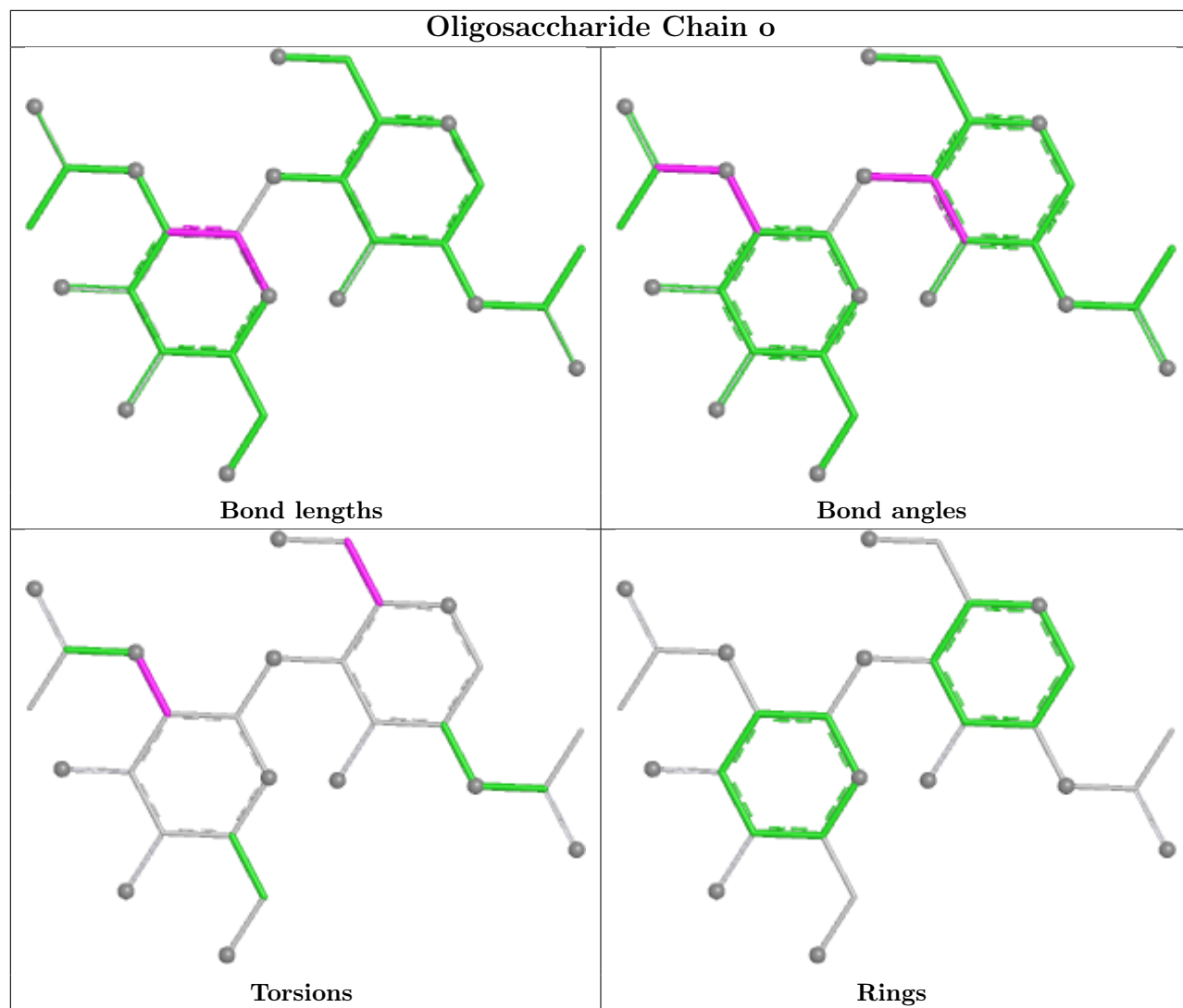


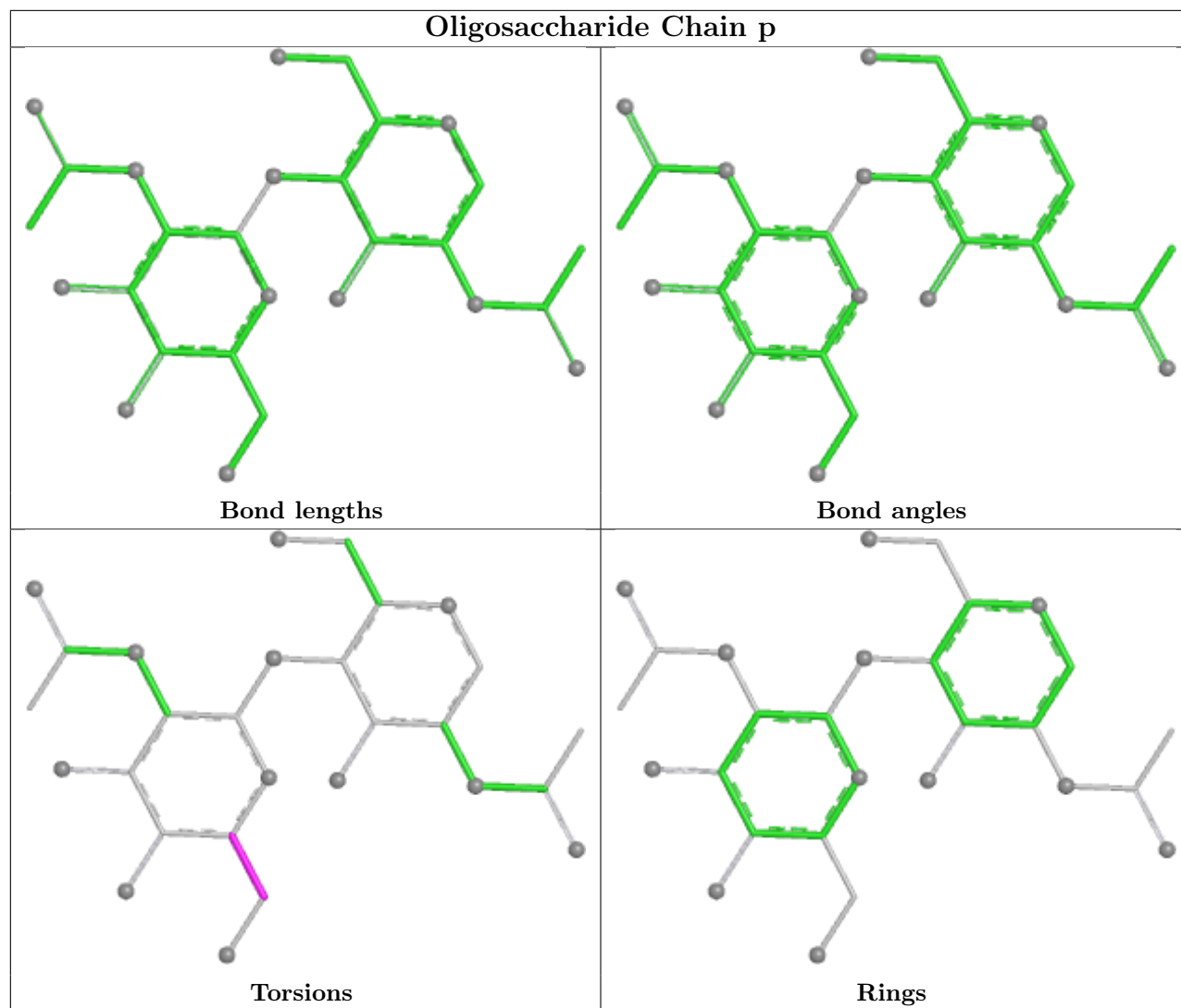


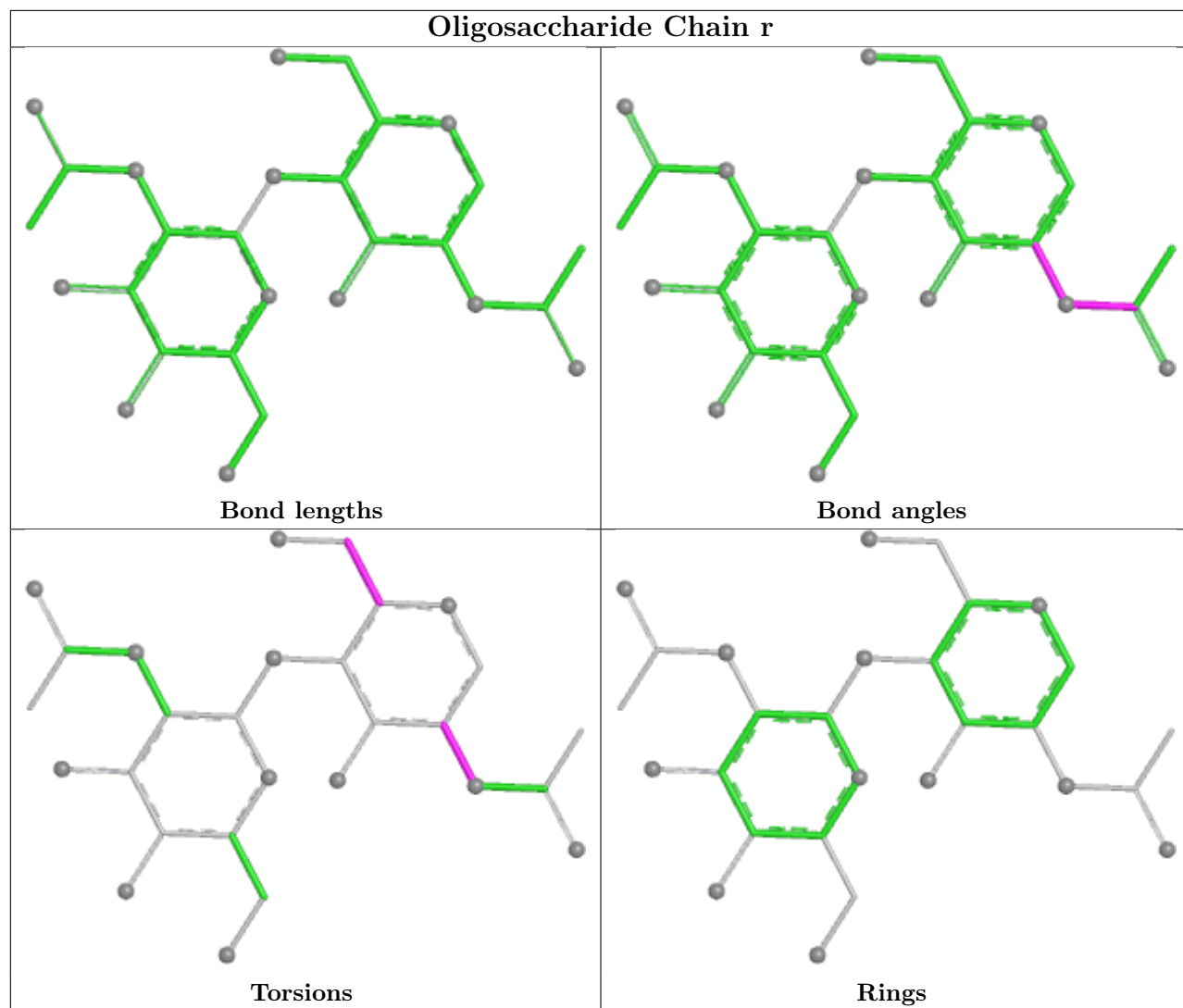


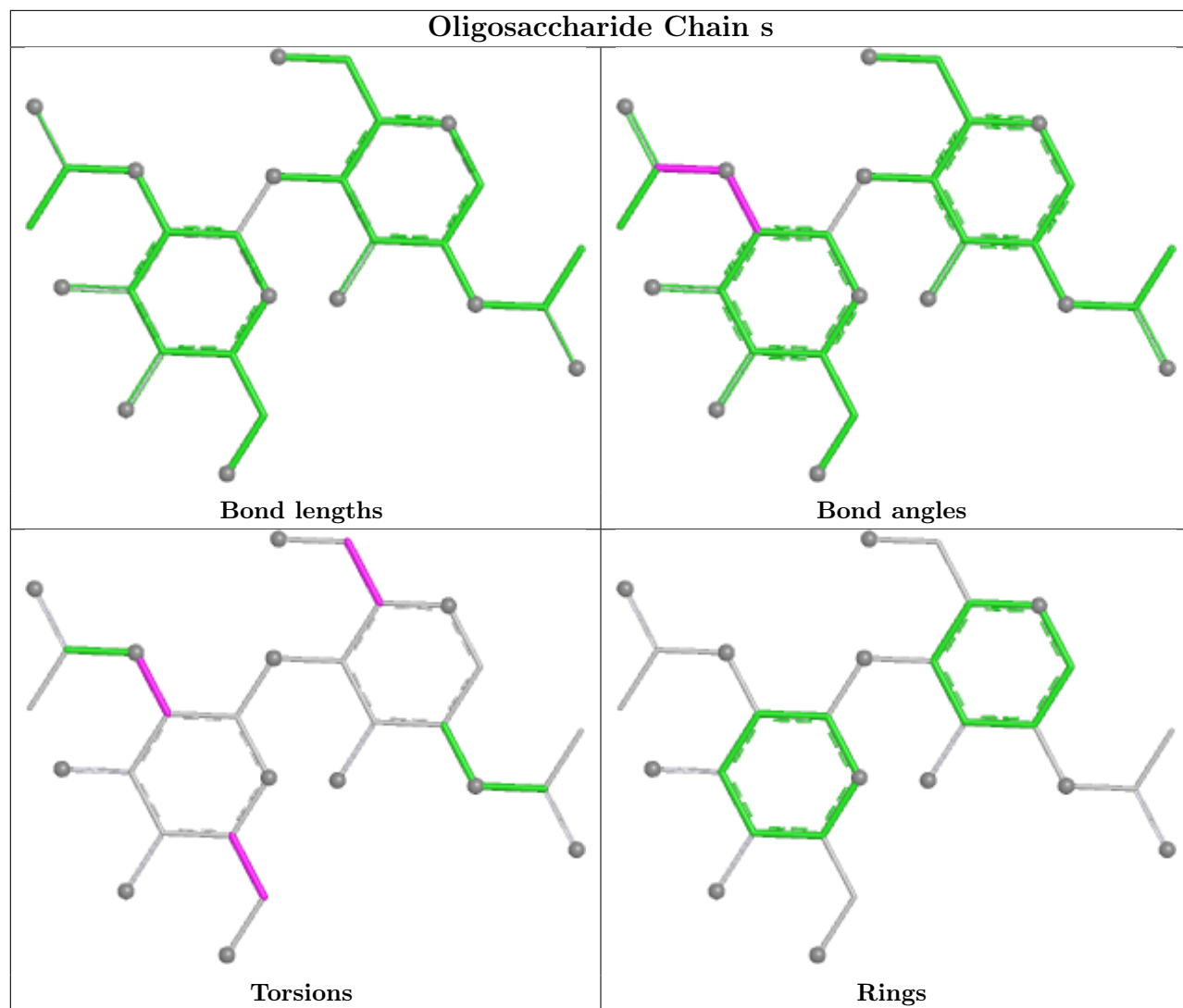


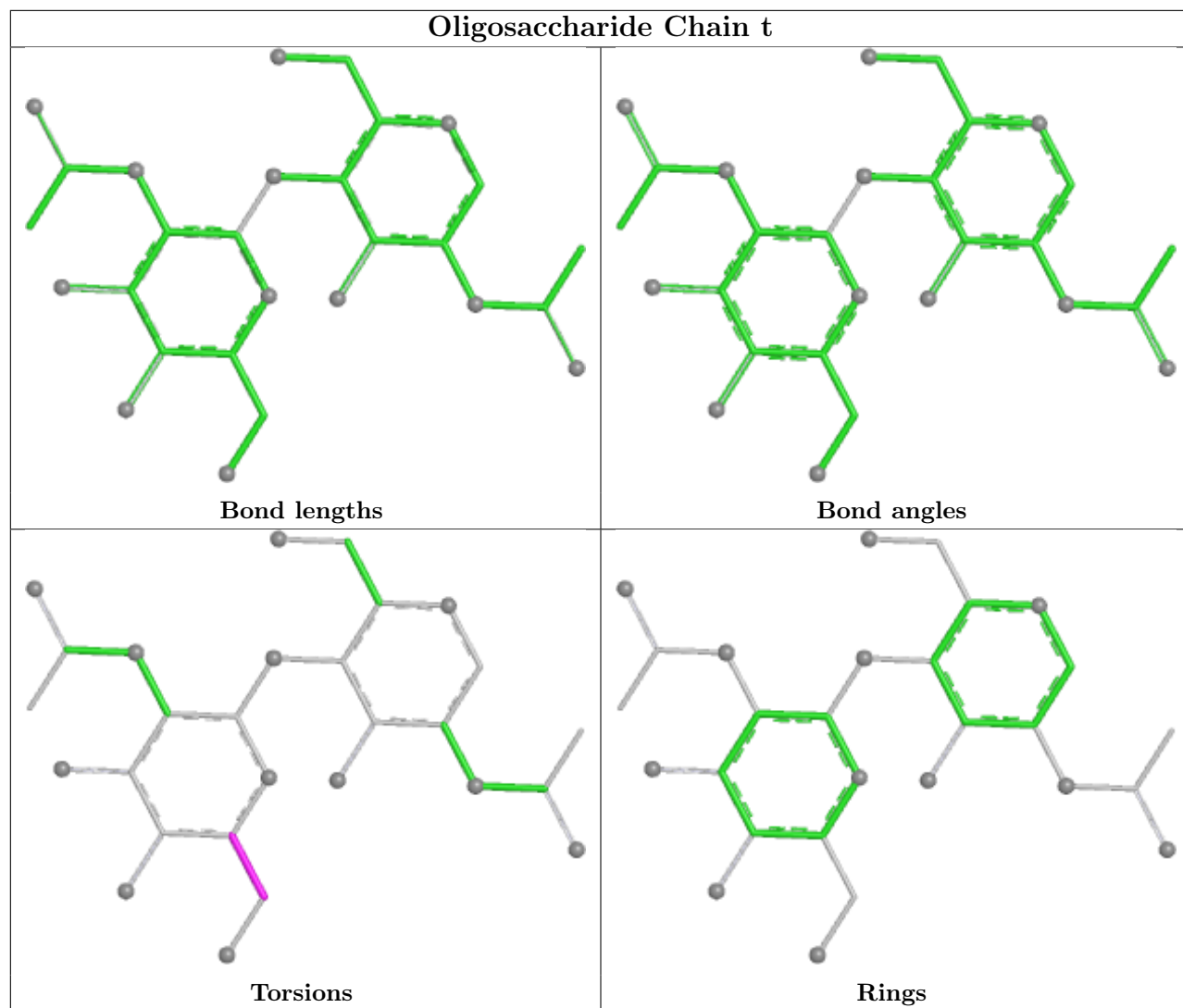


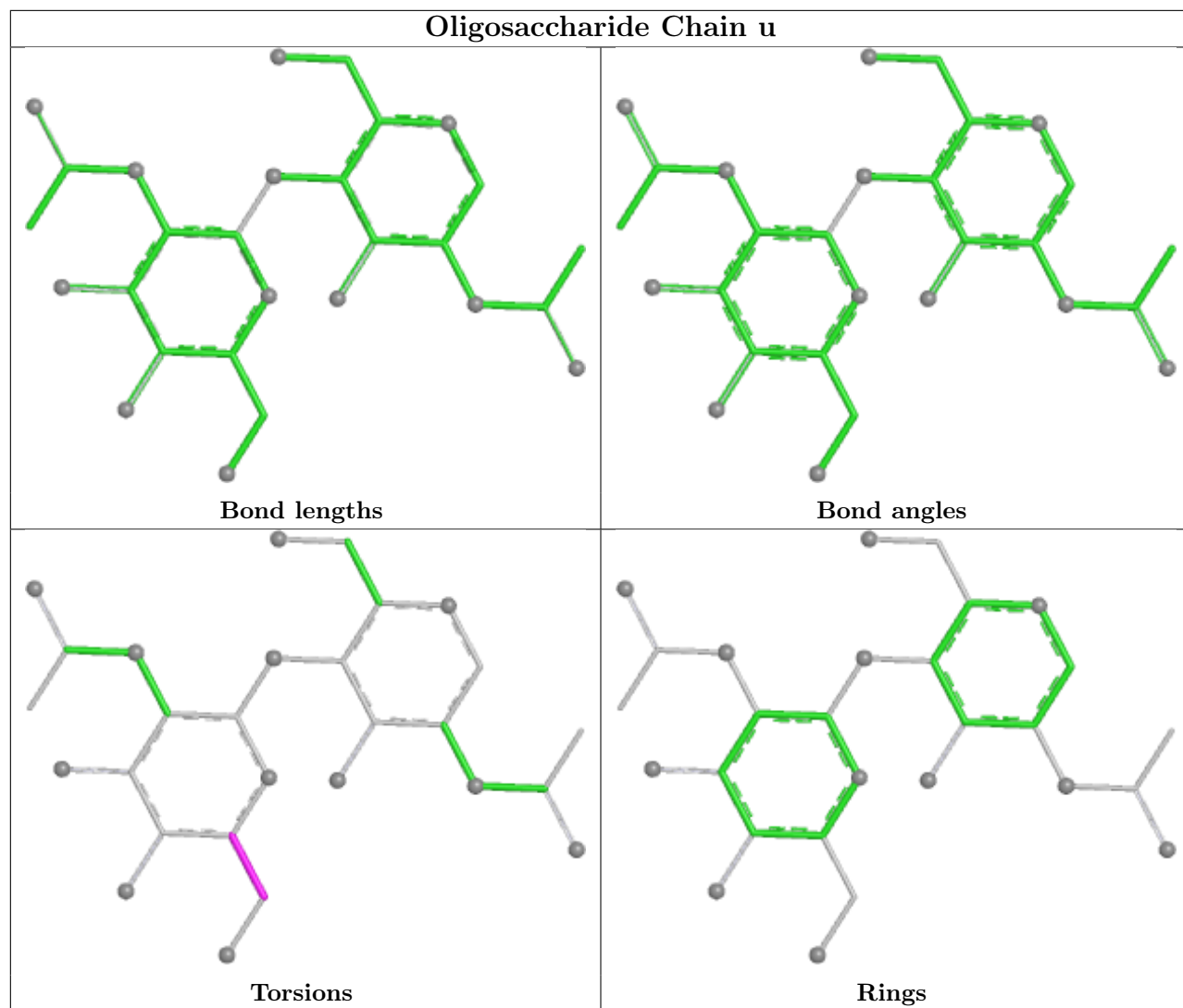


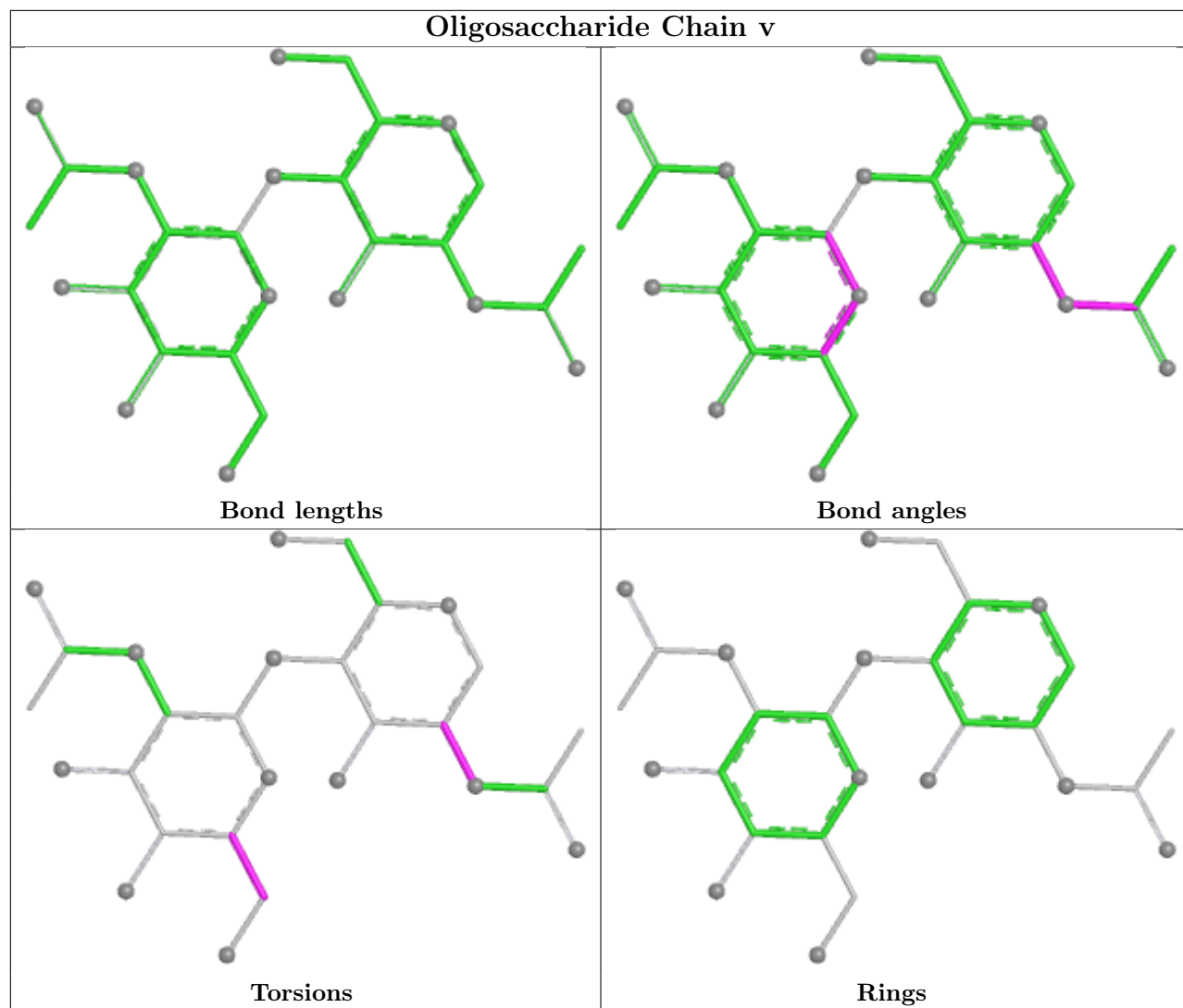


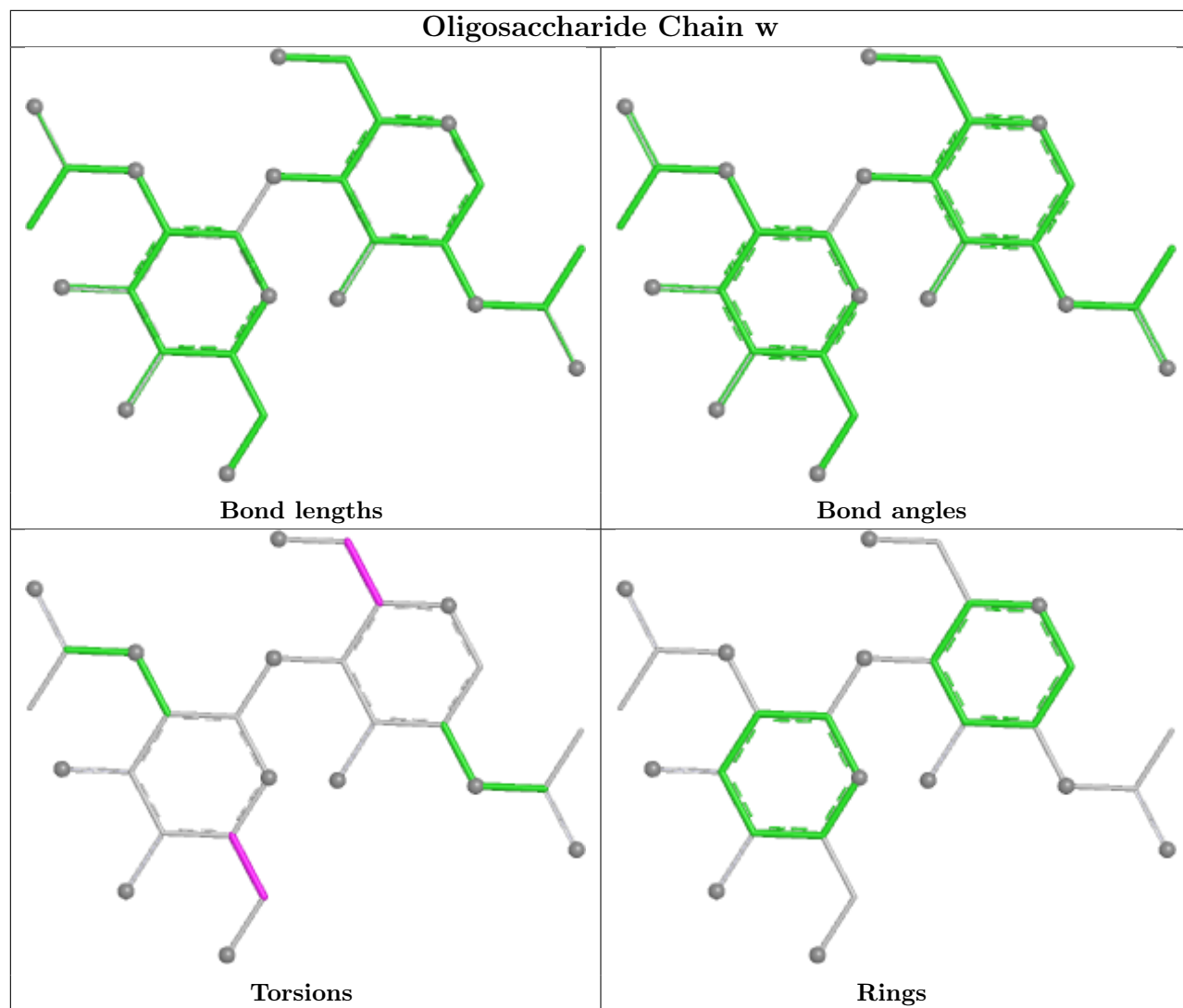


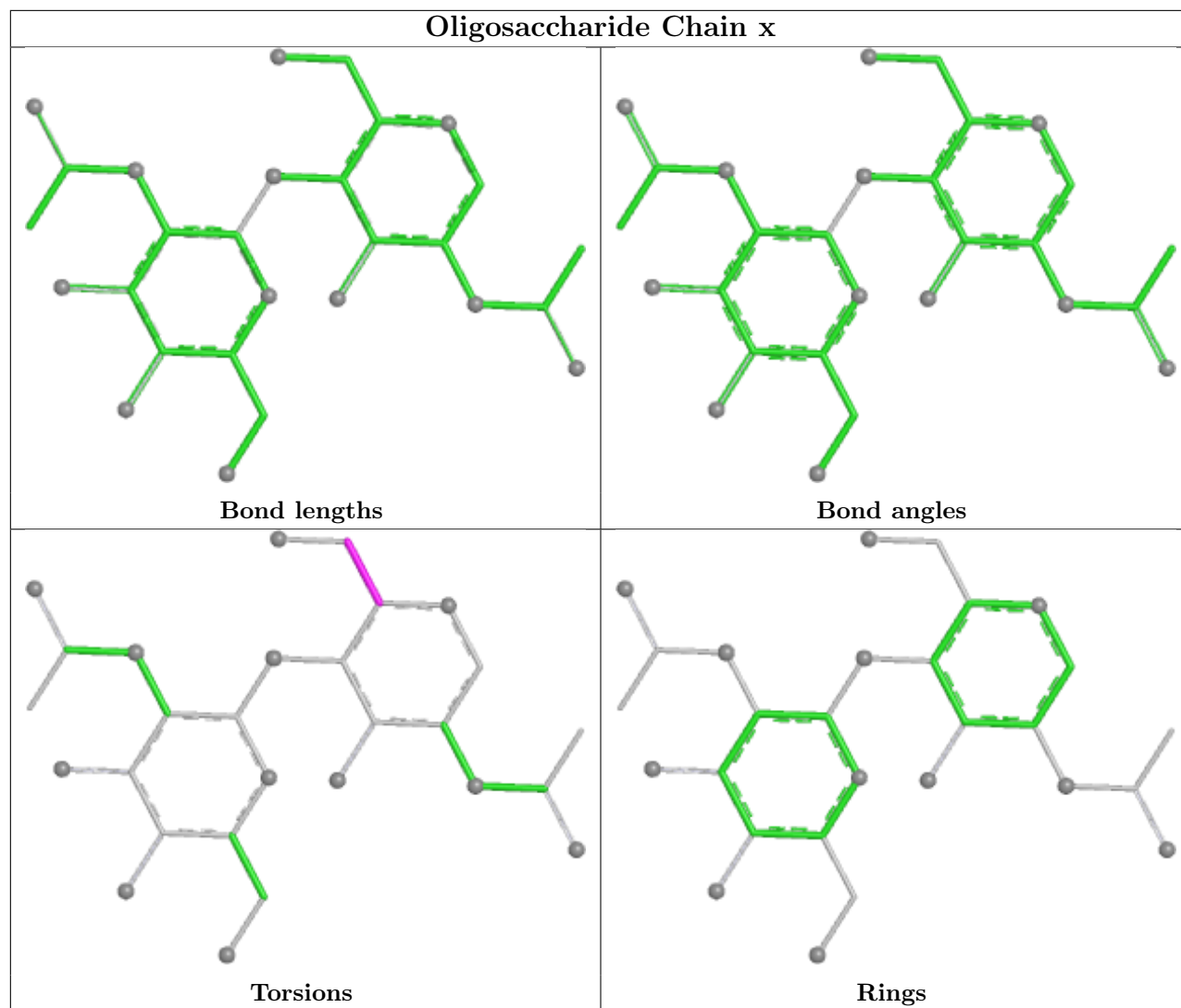


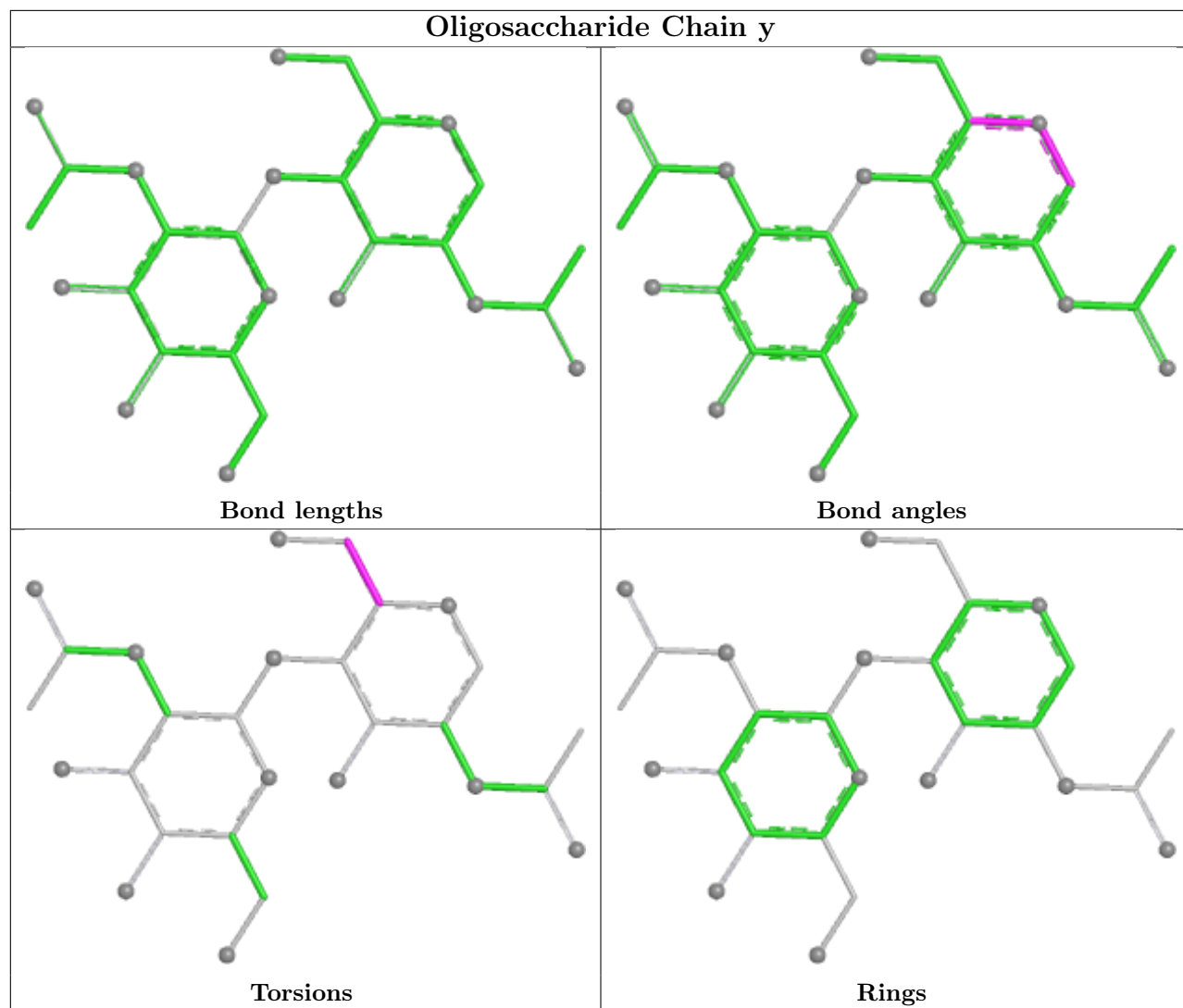


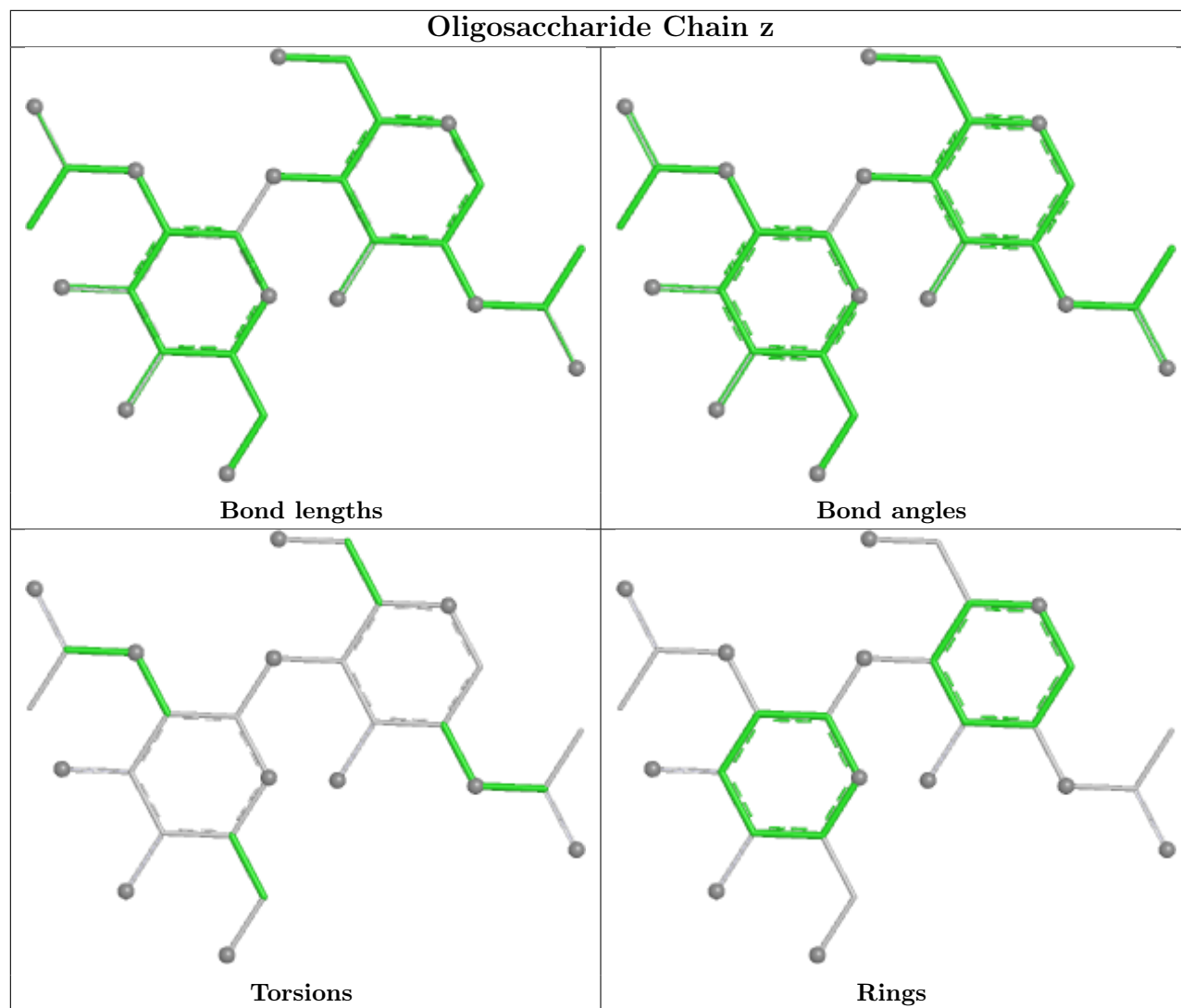


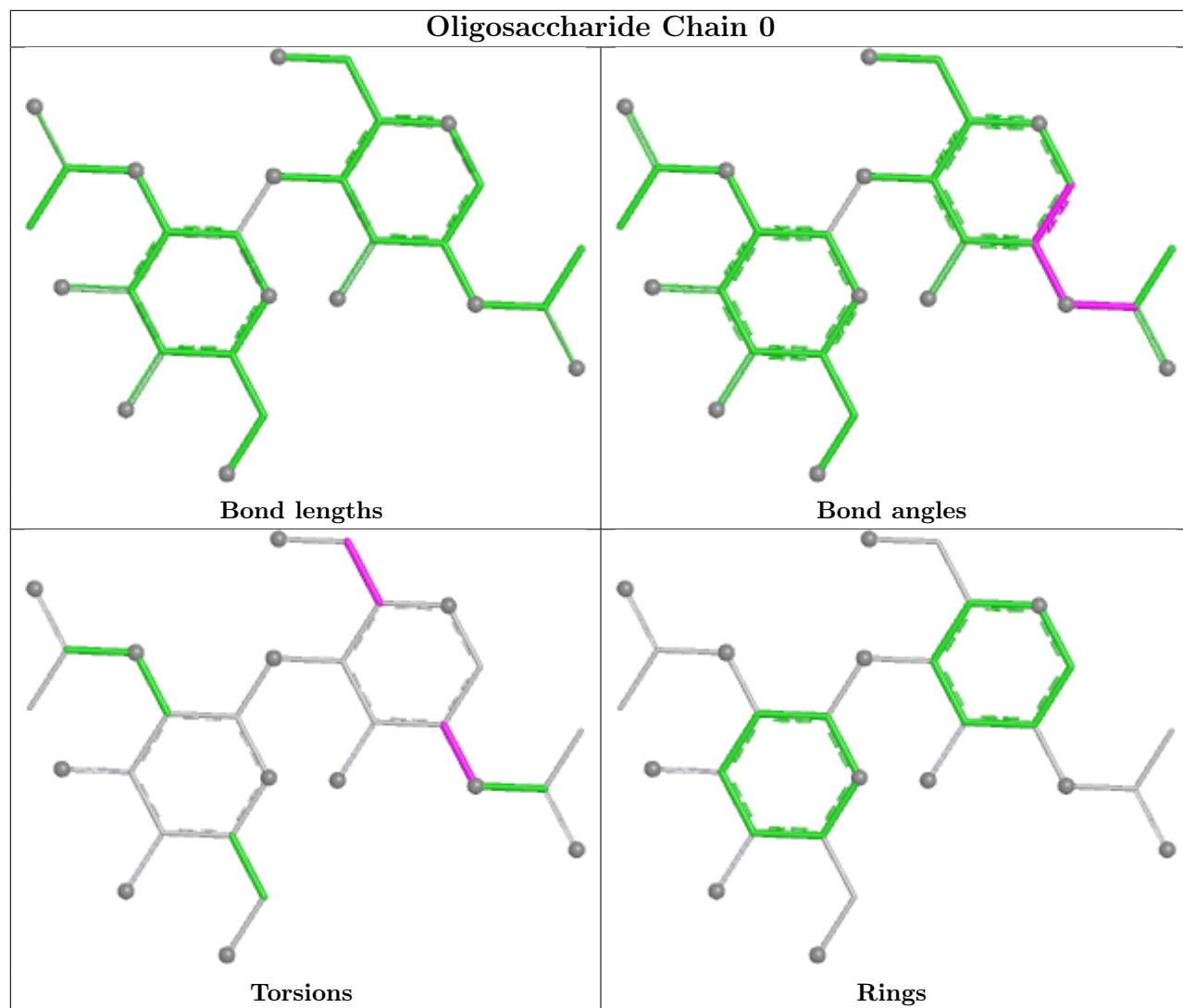


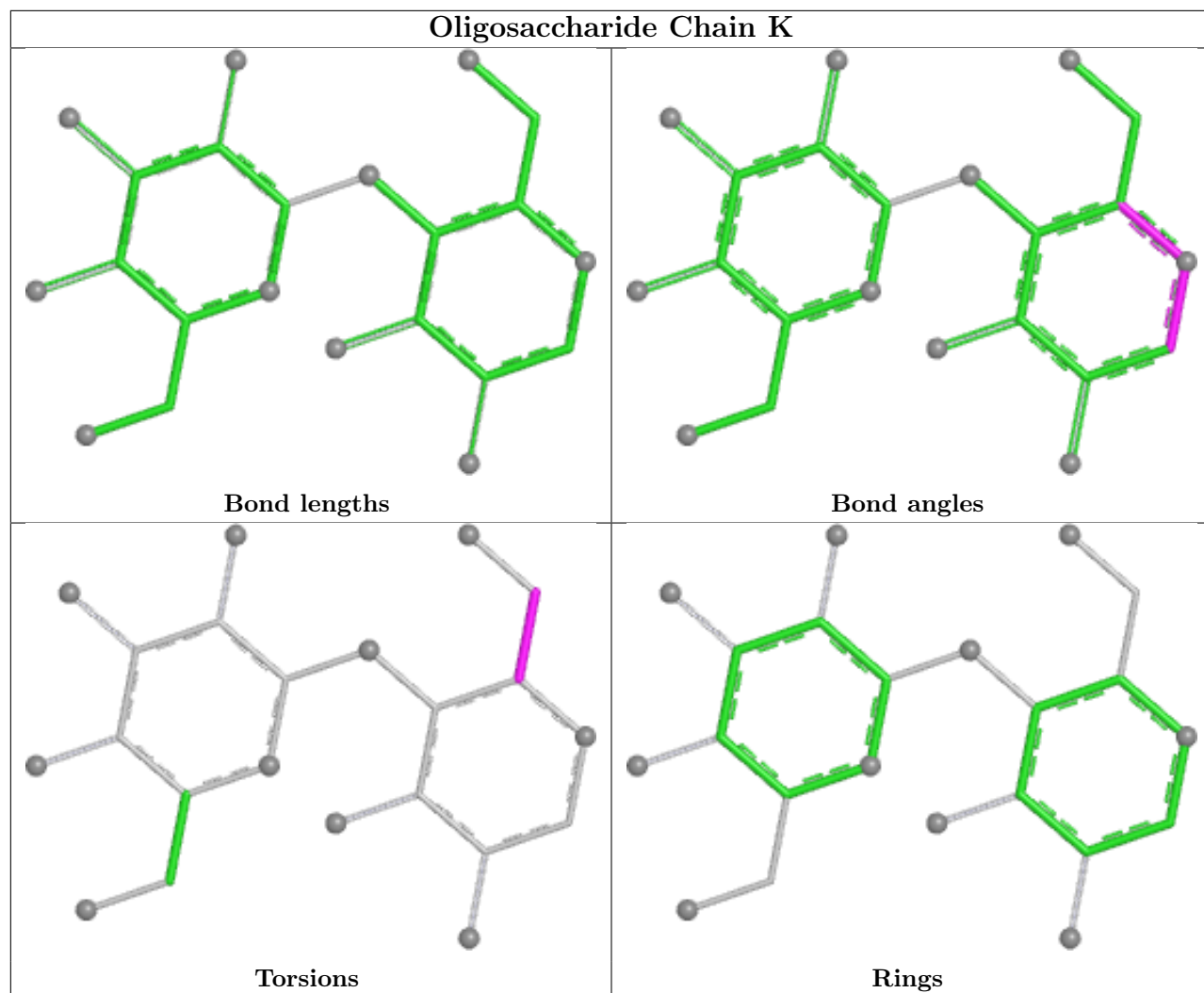


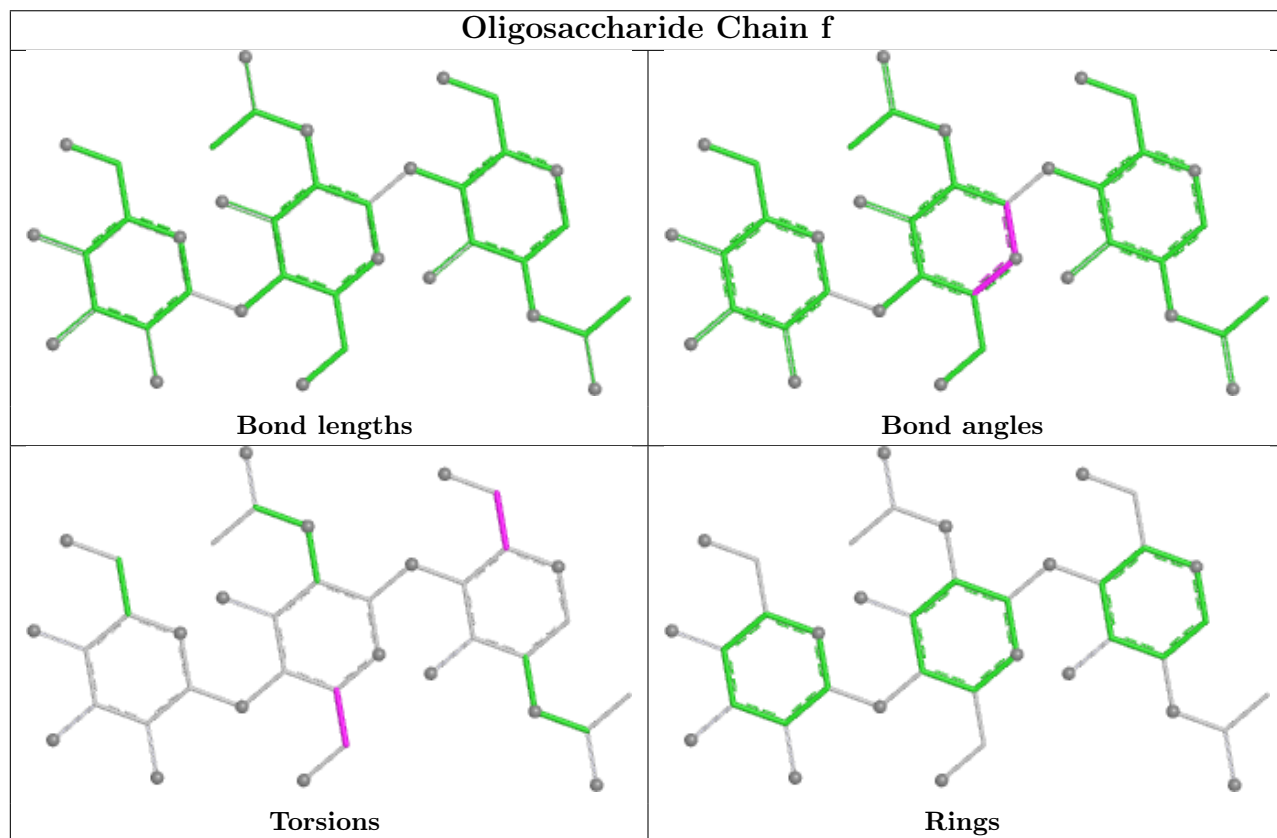
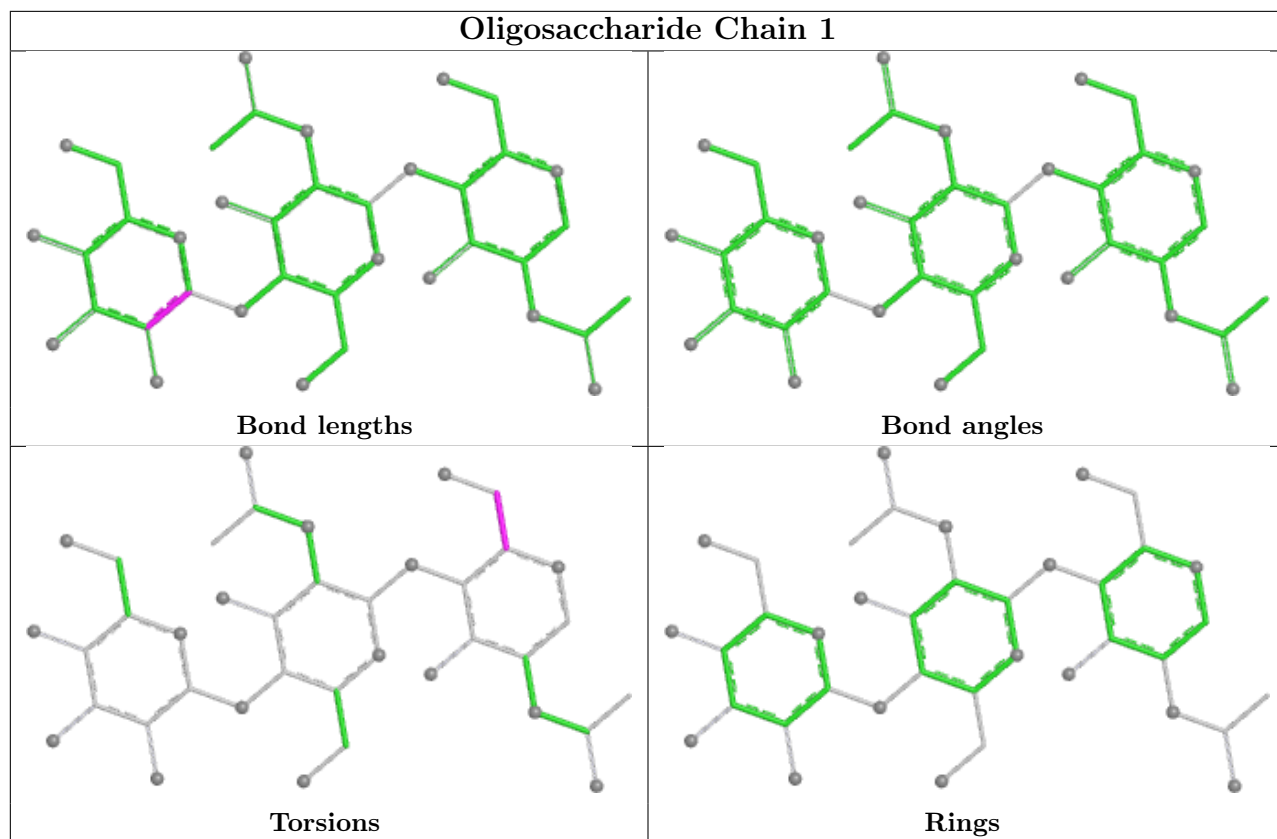


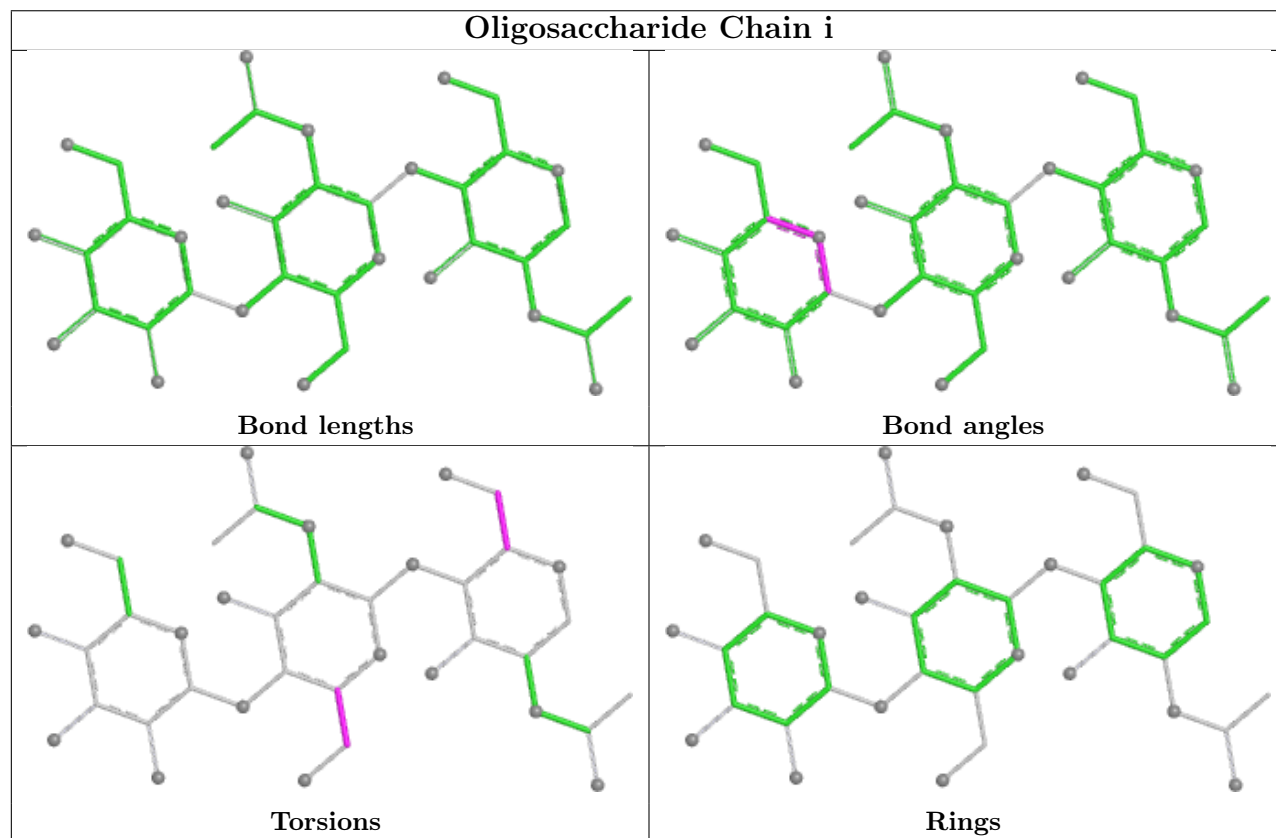
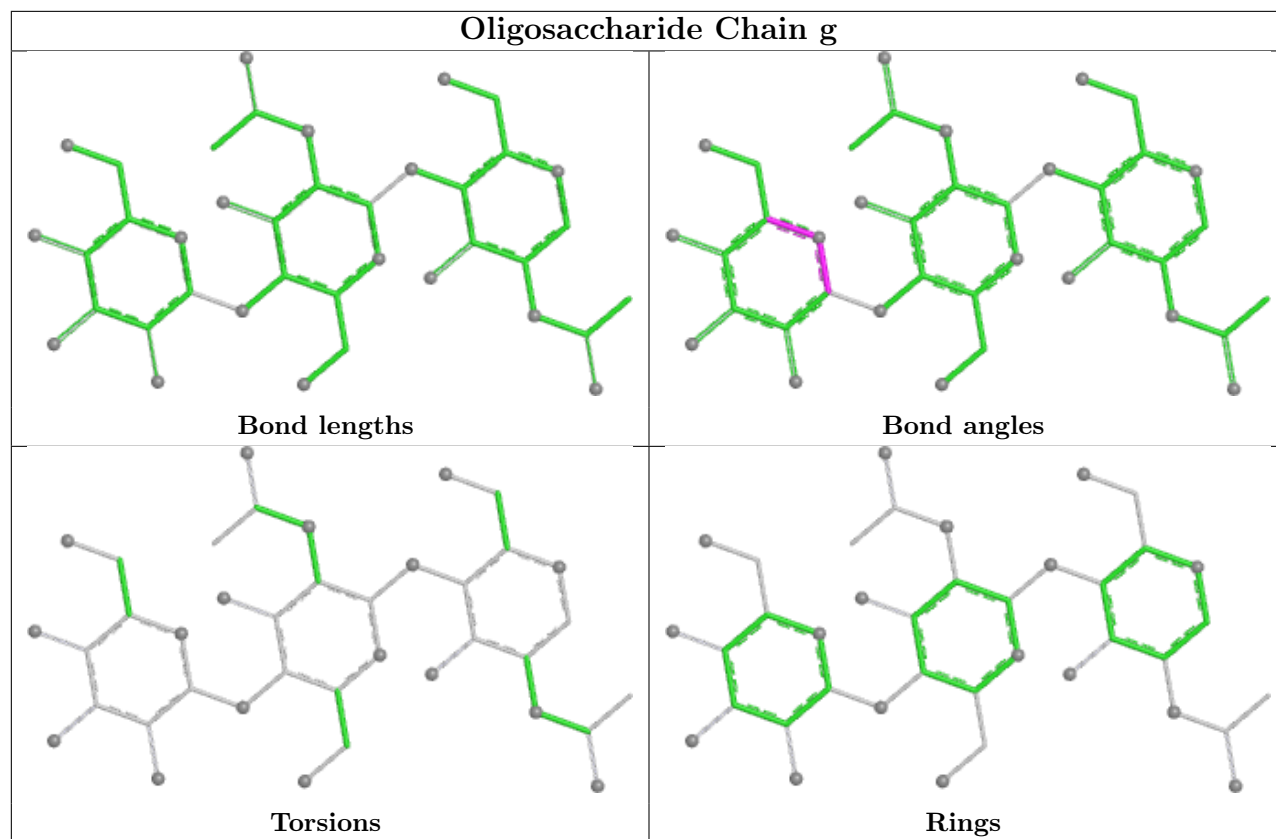


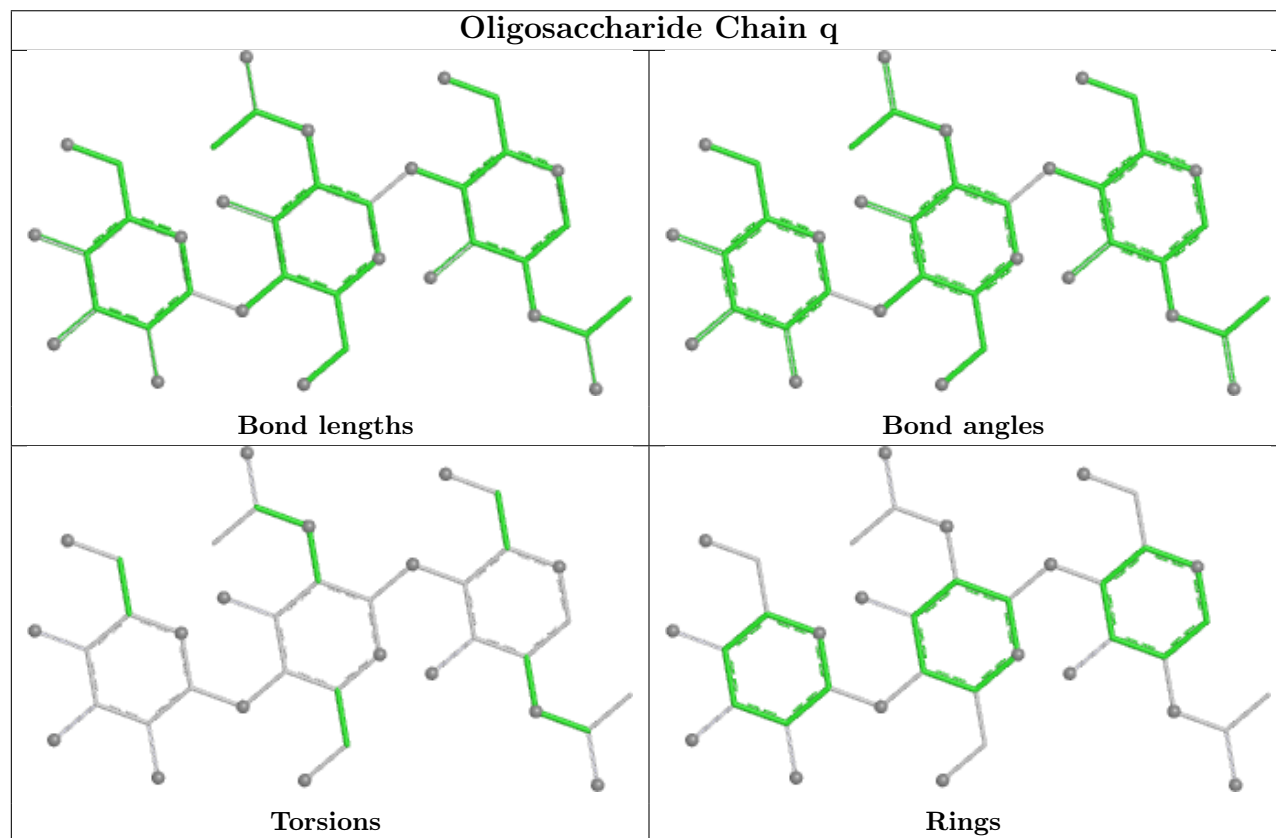
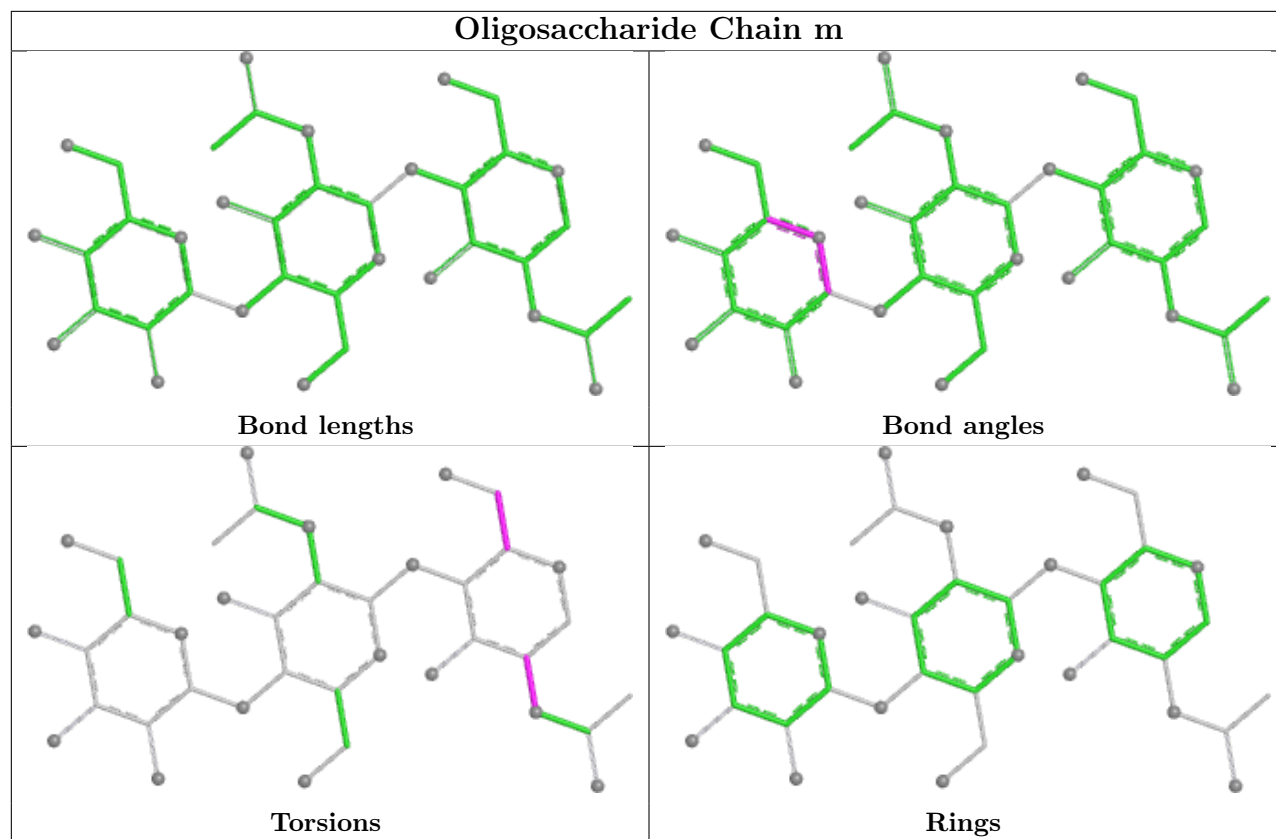












5.6 Ligand geometry

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	a	701	2	14,14,15	0.34	0	17,19,21	0.51	0
6	NAG	c	701	2	14,14,15	0.39	0	17,19,21	0.59	1 (5%)
6	NAG	A	602	1	14,14,15	0.33	0	17,19,21	0.61	1 (5%)
6	NAG	b	701	2	14,14,15	0.37	0	17,19,21	0.53	0
6	NAG	B	601	1	14,14,15	0.53	0	17,19,21	1.05	1 (5%)
6	NAG	A	603	-	14,14,15	0.24	0	17,19,21	0.51	0
6	NAG	a	702	2	14,14,15	0.38	0	17,19,21	0.48	0
6	NAG	A	601	1	14,14,15	0.52	0	17,19,21	1.05	1 (5%)
6	NAG	c	702	2	14,14,15	0.34	0	17,19,21	0.49	0
6	NAG	b	702	2	14,14,15	0.37	0	17,19,21	0.56	0
6	NAG	C	601	1	14,14,15	0.37	0	17,19,21	0.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	a	701	2	-	2/6/23/26	0/1/1/1
6	NAG	c	701	2	-	1/6/23/26	0/1/1/1
6	NAG	A	602	1	-	2/6/23/26	0/1/1/1
6	NAG	b	701	2	-	2/6/23/26	0/1/1/1
6	NAG	B	601	1	-	4/6/23/26	0/1/1/1
6	NAG	A	603	-	-	2/6/23/26	0/1/1/1
6	NAG	a	702	2	-	0/6/23/26	0/1/1/1
6	NAG	A	601	1	-	2/6/23/26	0/1/1/1
6	NAG	c	702	2	-	0/6/23/26	0/1/1/1
6	NAG	b	702	2	-	0/6/23/26	0/1/1/1
6	NAG	C	601	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	601	NAG	C2-N2-C7	3.25	127.26	122.90
6	A	601	NAG	C2-N2-C7	3.23	127.23	122.90
6	A	602	NAG	C1-O5-C5	2.08	114.97	112.19
6	c	701	NAG	C1-O5-C5	2.03	114.90	112.19

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	603	NAG	O5-C5-C6-O6
6	A	603	NAG	C4-C5-C6-O6
6	B	601	NAG	O5-C5-C6-O6
6	b	701	NAG	O5-C5-C6-O6
6	B	601	NAG	C4-C5-C6-O6

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.

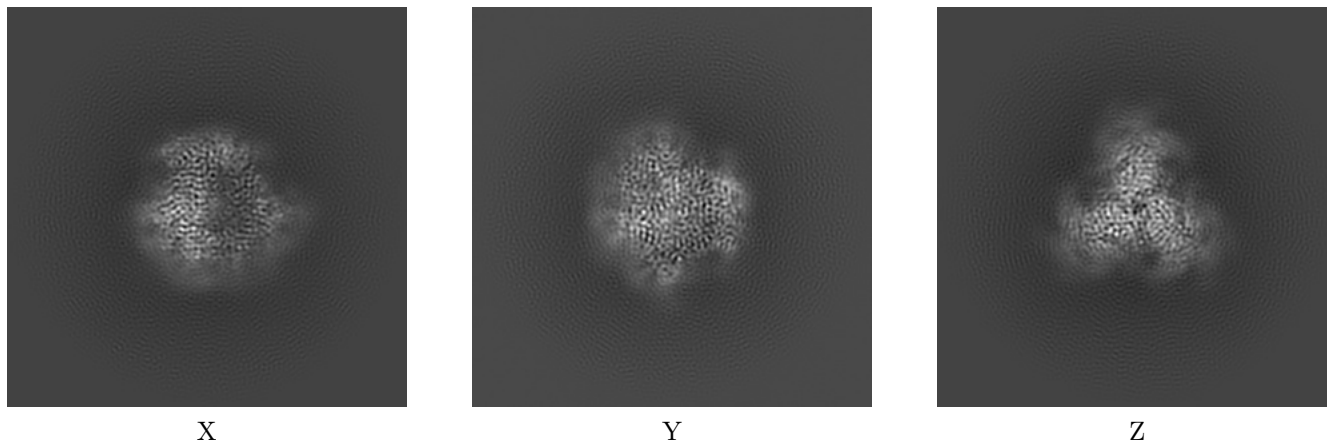
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41246. These allow visual inspection of the internal detail of the map and identification of artifacts.

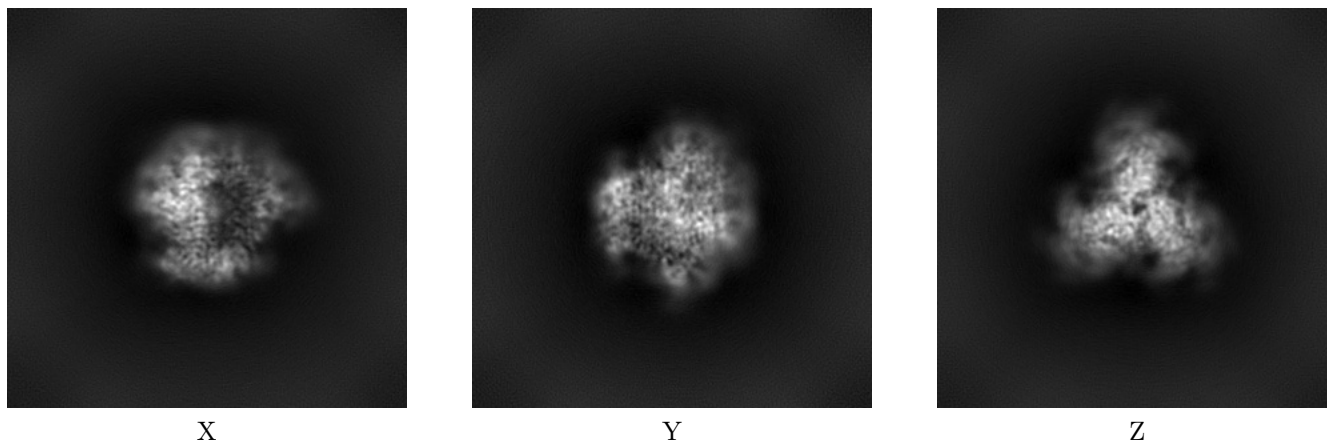
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



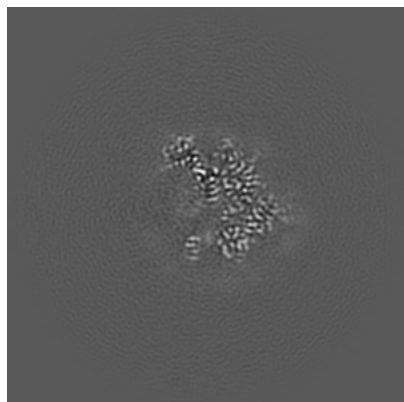
6.1.2 Raw map



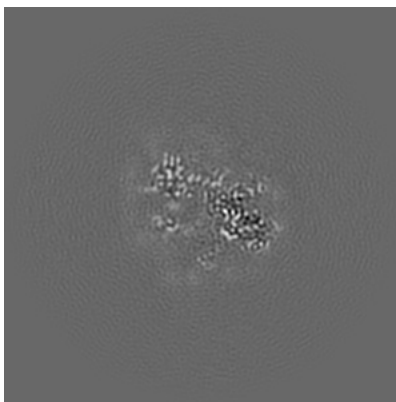
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

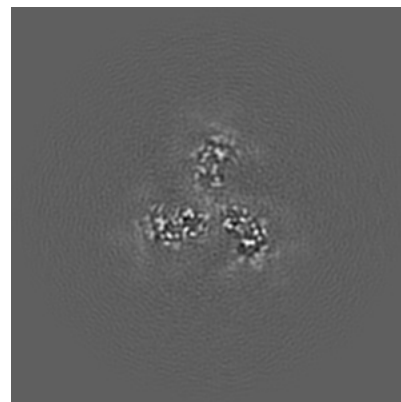
6.2.1 Primary map



X Index: 140

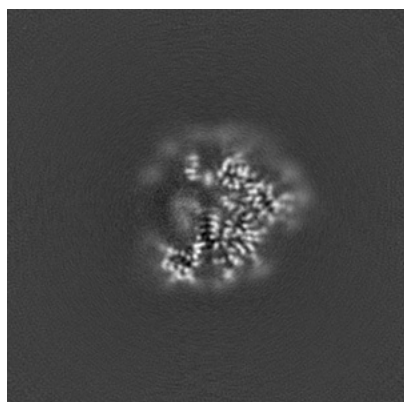


Y Index: 140

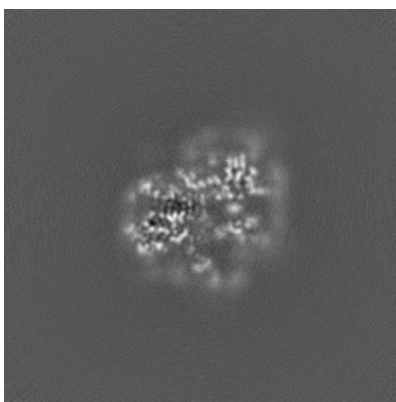


Z Index: 140

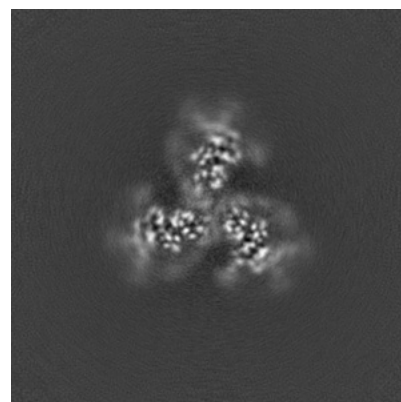
6.2.2 Raw map



X Index: 140



Y Index: 140

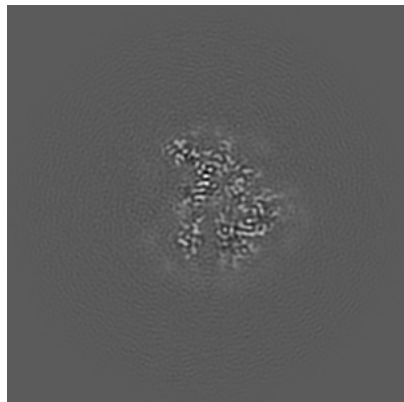


Z Index: 140

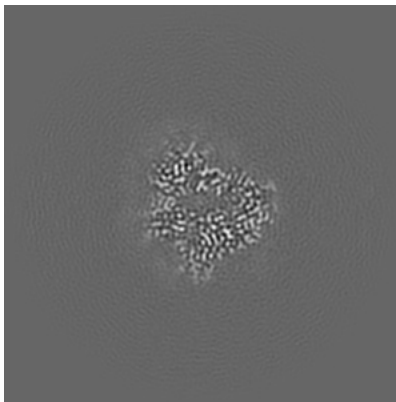
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

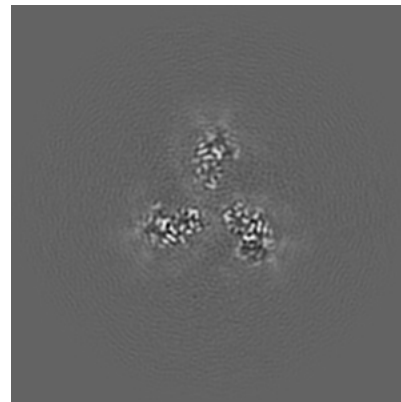
6.3.1 Primary map



X Index: 136

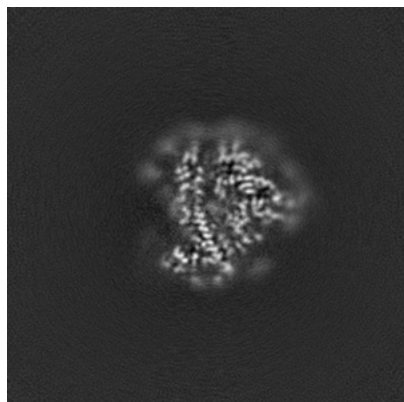


Y Index: 130

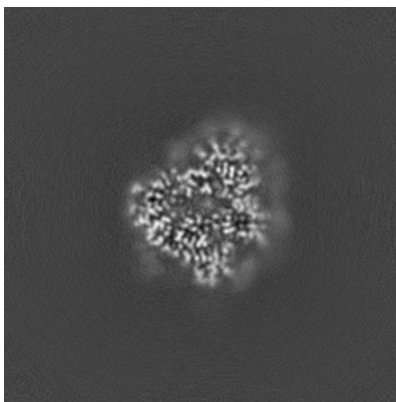


Z Index: 136

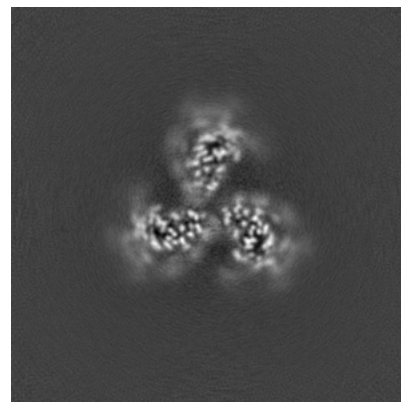
6.3.2 Raw map



X Index: 135



Y Index: 130

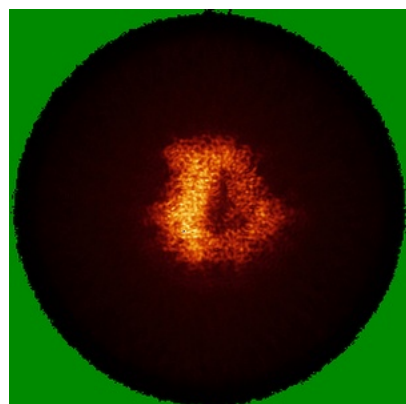


Z Index: 144

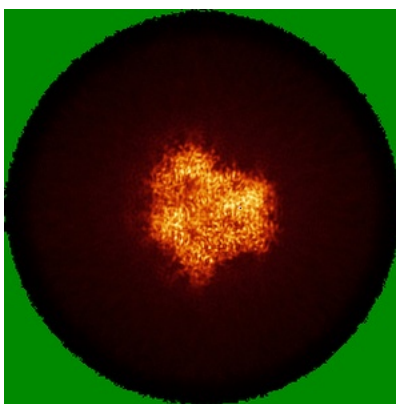
The images above show the largest variance slices of the map in three orthogonal directions.

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

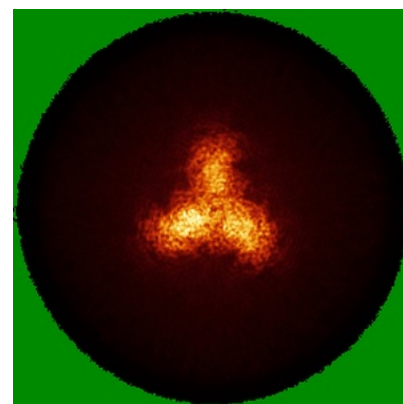
6.4.1 Primary map



X

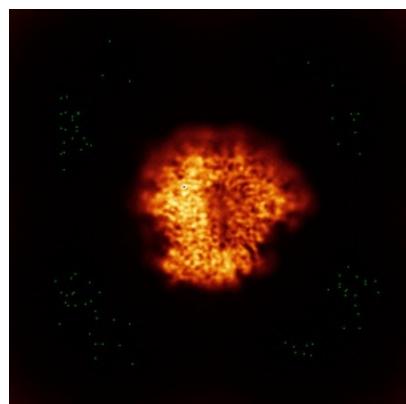


Y

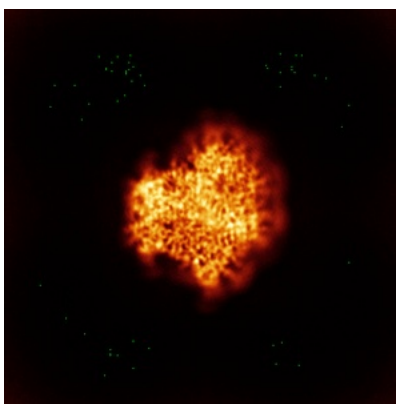


Z

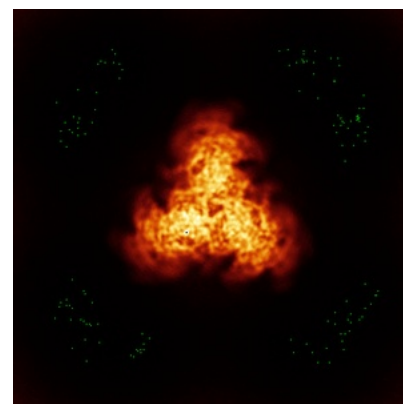
6.4.2 Raw map



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.

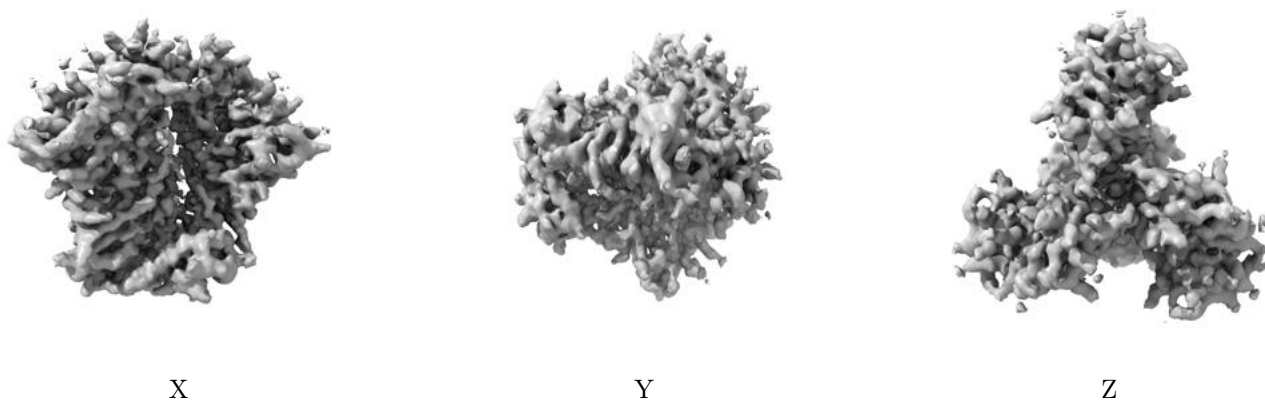
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

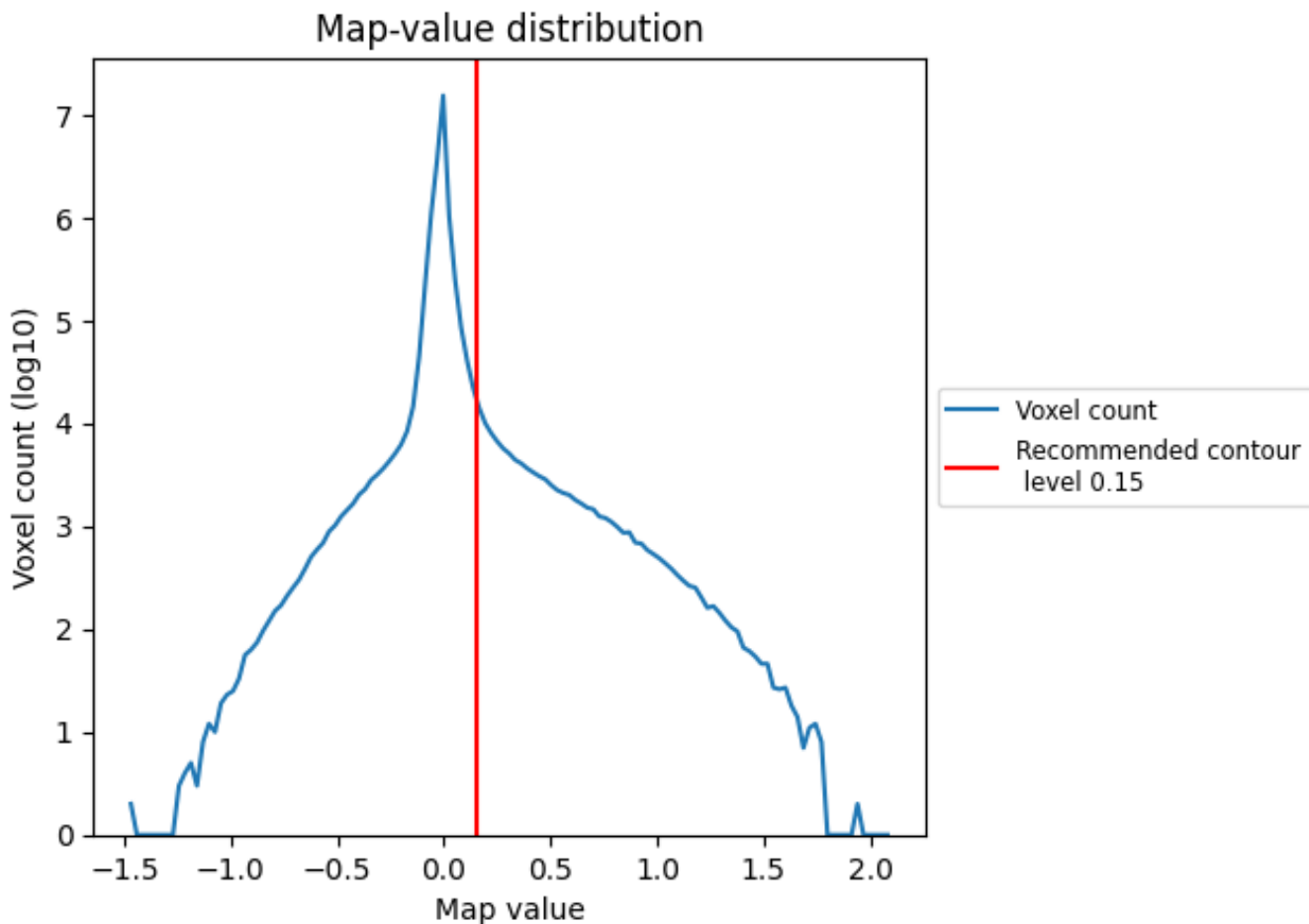
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

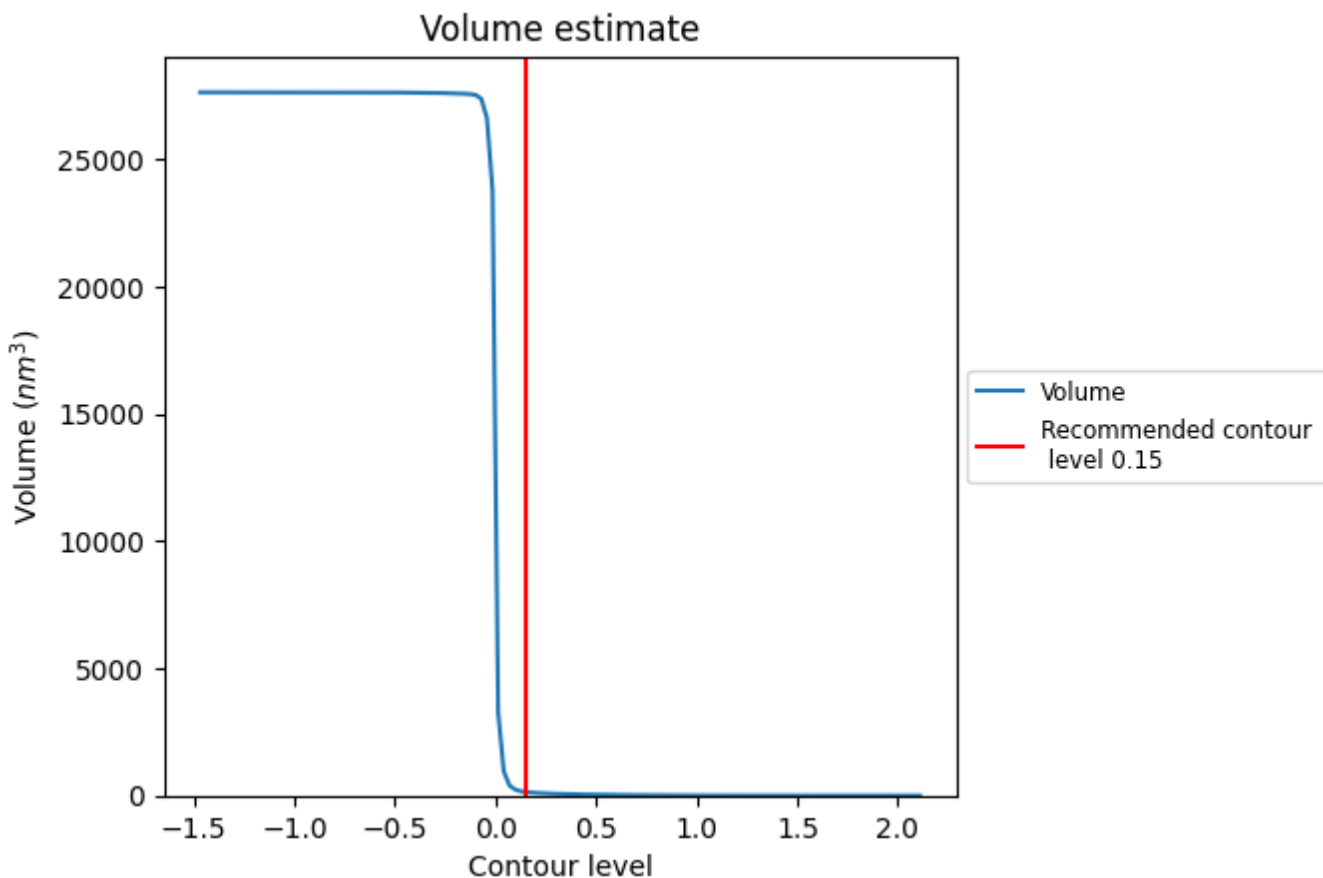
This section contains the results of statistical analysis of the map.

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.

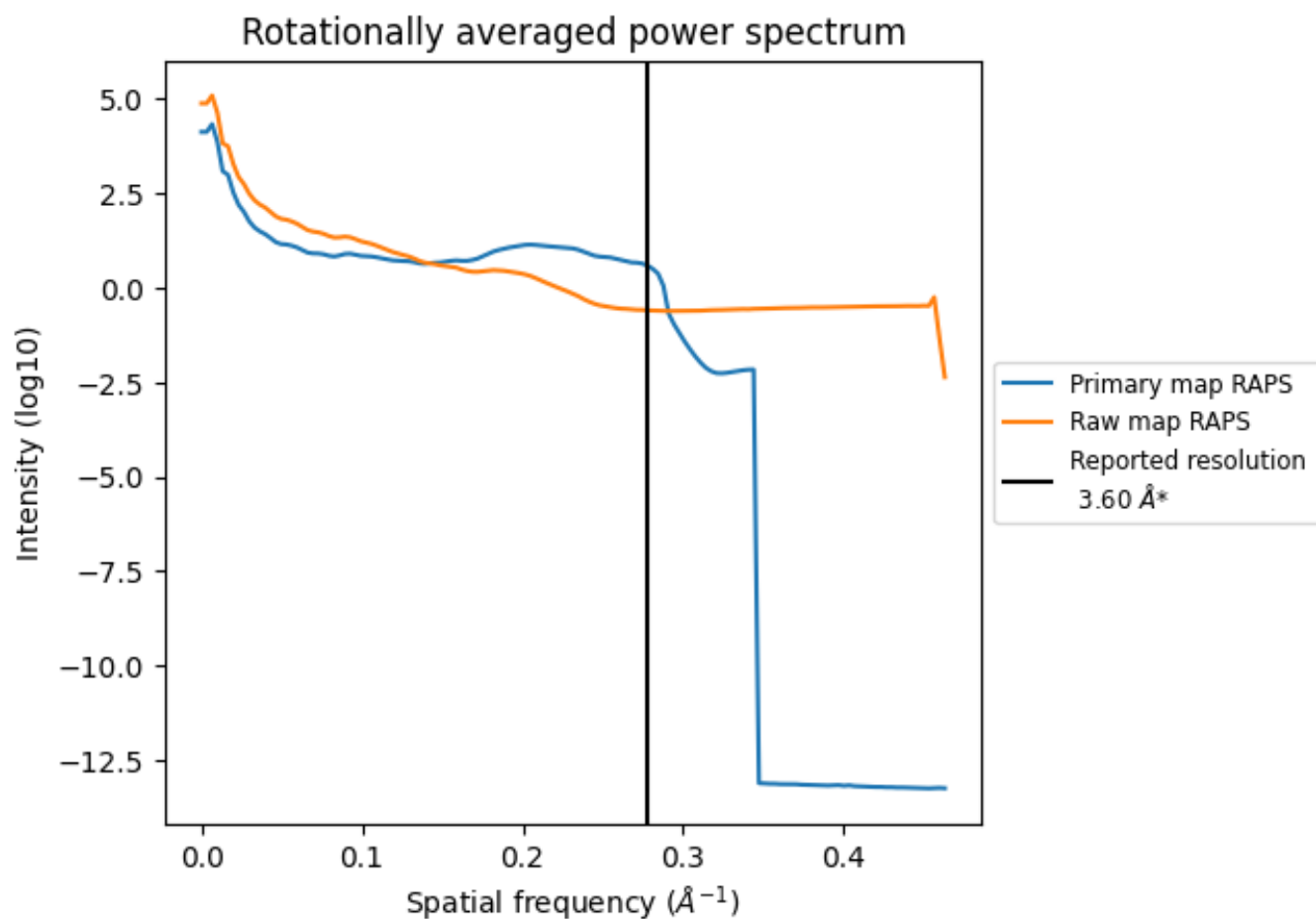
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm^3 ; this corresponds to an approximate mass of 126 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](#)

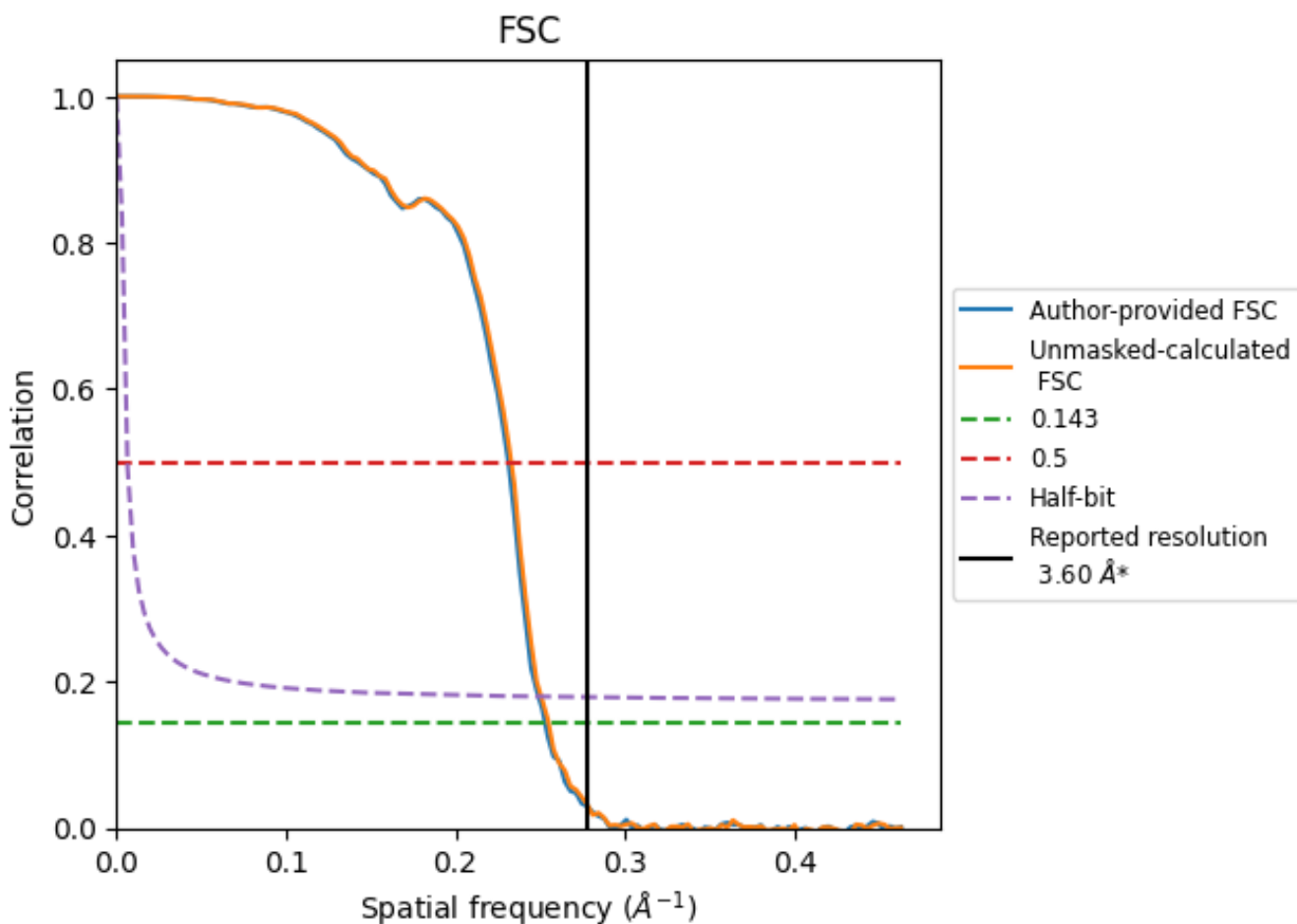


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	3.60	-
Author-provided FSC curve	3.95	4.32	4.01
Unmasked-calculated*	3.92	4.29	3.99

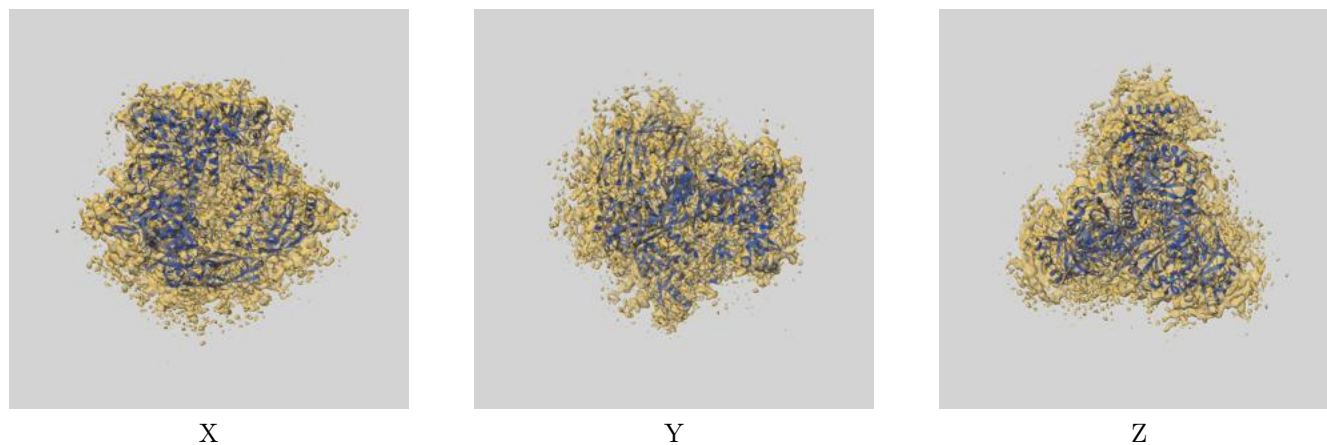
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.5 CUT-OFF 4.32 differs from the reported value 3.6 by more than 10 %

The value from deposited half-maps intersecting FSC 0.5 CUT-OFF 4.29 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

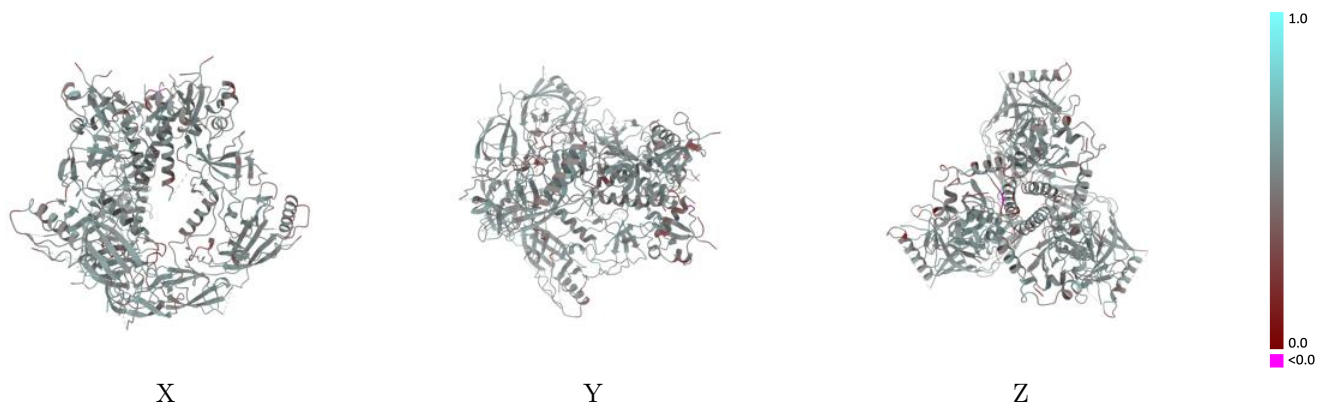
This section contains information regarding the fit between EMDB map EMD-41246 and PDB model 8TGW. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.15 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](#)



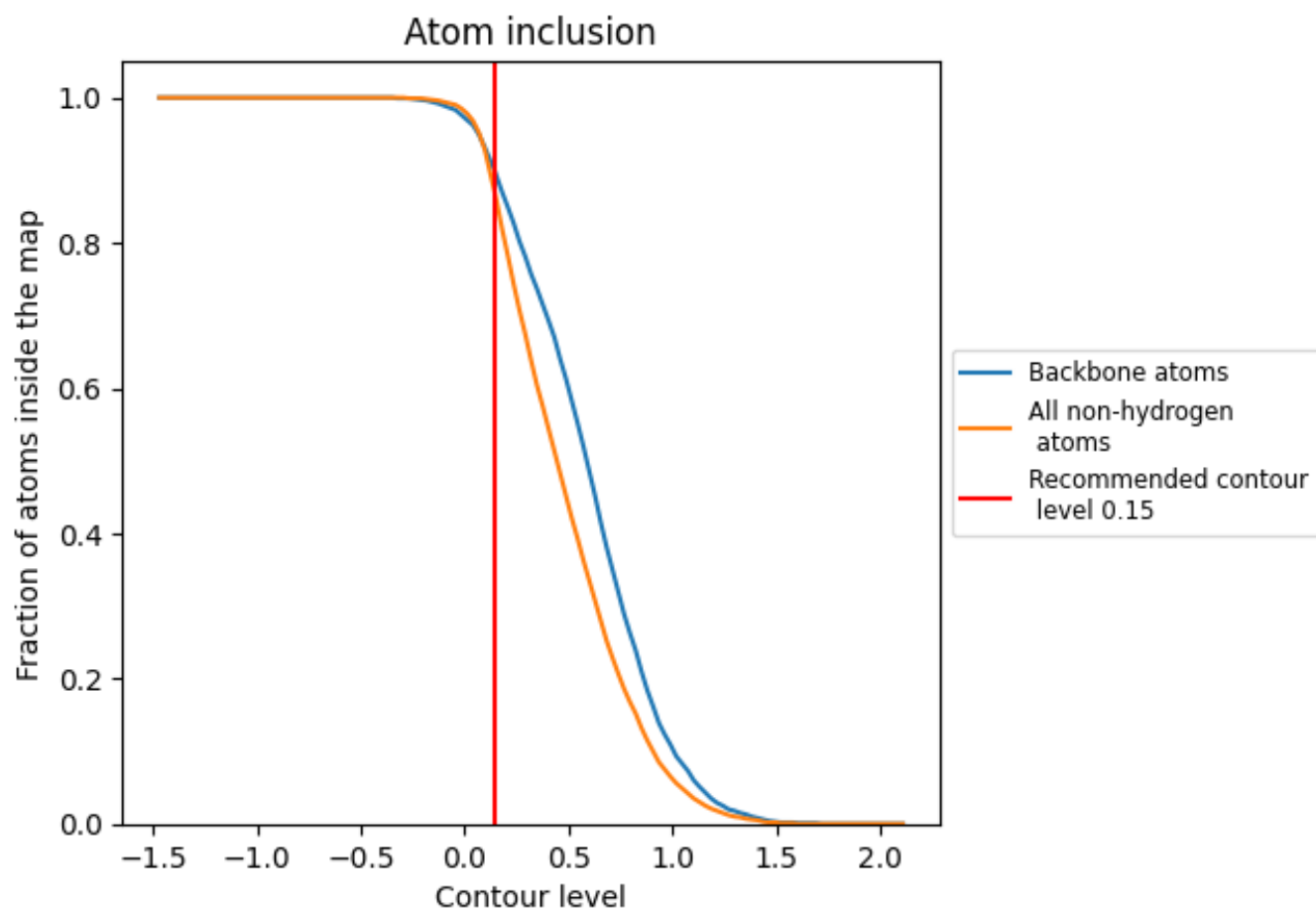
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8640	 0.4860
0	 0.3570	 0.2810
1	 0.7690	 0.3900
2	 0.5710	 0.3440
3	 0.6790	 0.3390
A	 0.8950	 0.5040
B	 0.8910	 0.5110
C	 0.8860	 0.5020
D	 0.6790	 0.4670
E	 0.6430	 0.3340
F	 0.8210	 0.4650
G	 0.8930	 0.5140
H	 0.6070	 0.3300
I	 0.7500	 0.4020
J	 0.5000	 0.2490
K	 0.4550	 0.2790
L	 0.6430	 0.3200
M	 0.6430	 0.3090
N	 0.8210	 0.5010
O	 0.8210	 0.4520
P	 0.8210	 0.4580
Q	 0.8210	 0.4290
R	 0.7500	 0.3980
S	 0.7140	 0.3800
T	 0.8210	 0.3940
U	 0.7860	 0.4220
V	 0.5710	 0.3300
W	 0.9290	 0.5060
X	 0.3210	 0.1740
Y	 0.5360	 0.3110
Z	 0.6430	 0.3640
a	 0.8770	 0.4910
b	 0.8590	 0.4610
c	 0.8980	 0.4870
d	 0.6790	 0.3700



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Chain	Atom inclusion	Q-score
e	 0.7500	 0.4210
f	 0.8210	 0.4320
g	 0.6920	 0.3750
h	 0.7860	 0.4240
i	 0.6670	 0.3650
j	 0.7500	 0.3620
k	 0.4290	 0.1630
l	 0.5360	 0.3800
m	 0.5900	 0.3290
n	 0.3930	 0.2190
o	 0.2500	 0.1250
p	 0.7140	 0.3800
q	 0.9230	 0.4820
r	 0.4640	 0.2170
s	 0.7500	 0.4690
t	 0.5360	 0.3650
u	 0.5360	 0.3010
v	 0.9640	 0.4420
w	 0.6790	 0.3590
x	 0.7140	 0.4350
y	 0.6430	 0.3930
z	 0.6790	 0.3530