



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2024 – 05:51 AM EST

PDB ID : 7LXM
EMDB ID : EMD-23571
Title : Cryo-EM structure of ConM SOSIP.v7 (ConM) in complex with bNAb PGT122
Authors : Martin, G.M.; Ward, A.B.; Sattentau, Q.J.
Deposited on : 2021-03-04
Resolution : 3.41 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:

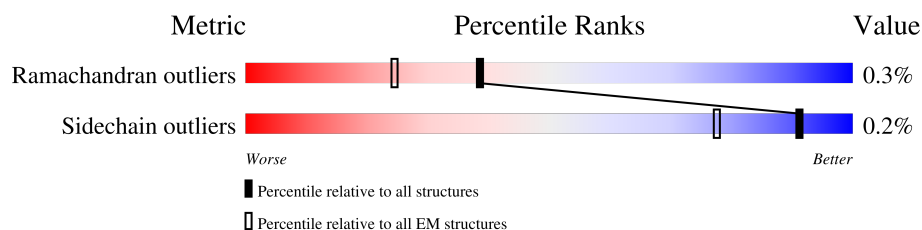
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 3.41 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.





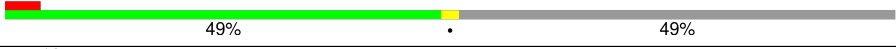
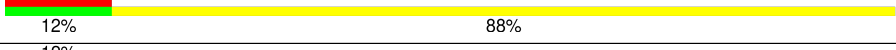
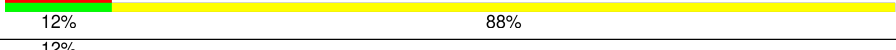
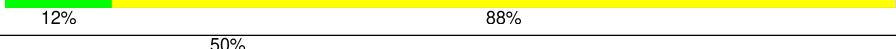
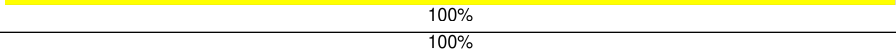
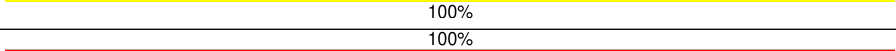


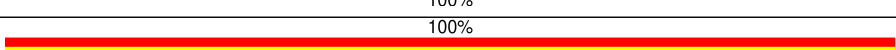
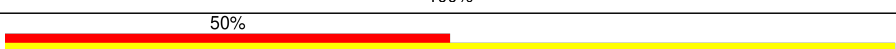

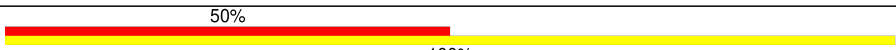
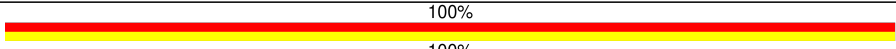



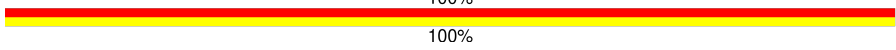

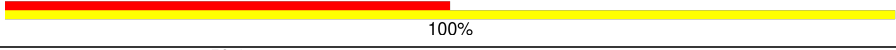
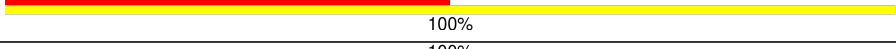
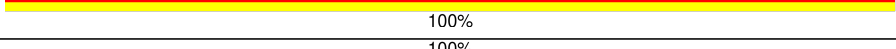
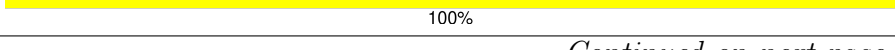

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	493	
1	C	493	
1	E	493	
2	B	153	
2	D	153	
2	F	153	
3	H	235	
3	N	235	
3	P	235	

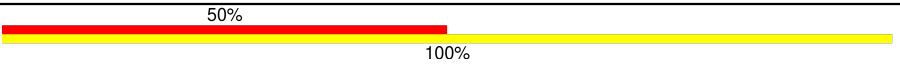
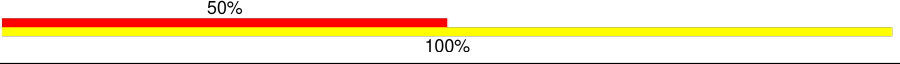
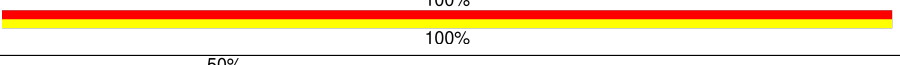
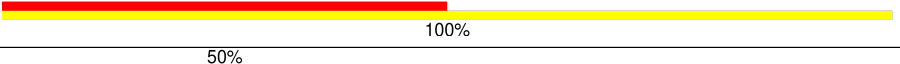
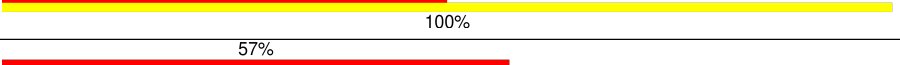

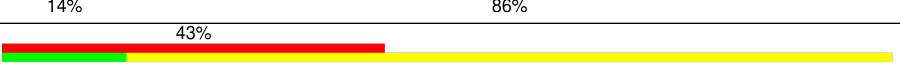



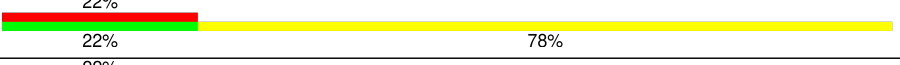
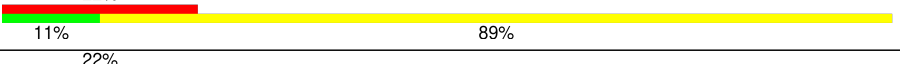

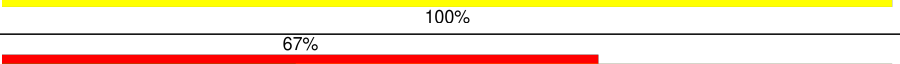

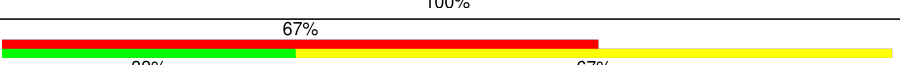
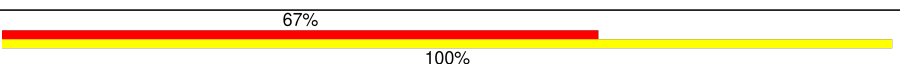



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Mol	Chain	Length	Quality of chain
4	L	213	
4	M	213	
4	O	213	
5	G	8	
5	a	8	
5	o	8	
6	0	2	
6	1	2	
6	I	2	
6	J	2	
6	K	2	
6	Q	2	
6	R	2	
6	T	2	
6	Y	2	
6	Z	2	
6	b	2	
6	c	2	
6	d	2	
6	e	2	
6	f	2	
6	h	2	
6	m	2	
6	n	2	
6	p	2	

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Mol	Chain	Length	Quality of chain
6	q	2	
6	r	2	
6	s	2	
6	t	2	
6	v	2	
7	S	7	
7	g	7	
7	u	7	
8	U	4	
8	i	4	
8	w	4	
9	V	9	
9	j	9	
9	x	9	
10	W	3	
10	X	3	
10	k	3	
10	l	3	
10	y	3	
10	z	3	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 20820 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 Env glycoprotein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	434	Total	C	N	O	S	0	0
			3450	2170	605	649	26		
1	C	434	Total	C	N	O	S	0	0
			3450	2170	605	649	26		
1	E	434	Total	C	N	O	S	0	0
			3450	2170	605	649	26		

- Molecule 2 is a protein called HIV-1 Env glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	118	Total	C	N	O	S	0	0
			950	598	160	185	7		
2	D	118	Total	C	N	O	S	0	0
			950	598	160	185	7		
2	F	118	Total	C	N	O	S	0	0
			950	598	160	185	7		

- Molecule 3 is a protein called PGT122 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	131	Total	C	N	O	S	0	0
			1041	666	179	193	3		
3	N	131	Total	C	N	O	S	0	0
			1041	666	179	193	3		
3	P	131	Total	C	N	O	S	0	0
			1041	666	179	193	3		

- Molecule 4 is a protein called PGT122 Fab light chain.

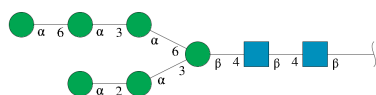
Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	108	Total	C	N	O	S	0	0
			823	515	142	164	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	108	Total	C	N	O	S	0	0
			823	515	142	164	2		
4	O	108	Total	C	N	O	S	0	0
			823	515	142	164	2		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	8	Total	C	N	O	0	0
			94	52	2	40		
5	a	8	Total	C	N	O	0	0
			94	52	2	40		
5	o	8	Total	C	N	O	0	0
			94	52	2	40		

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



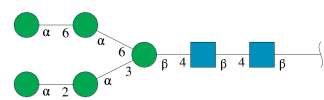
Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	2	Total	C	N	O	0	0
			28	16	2	10		
6	J	2	Total	C	N	O	0	0
			28	16	2	10		
6	K	2	Total	C	N	O	0	0
			28	16	2	10		
6	Q	2	Total	C	N	O	0	0
			28	16	2	10		
6	R	2	Total	C	N	O	0	0
			28	16	2	10		
6	T	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	Y	2	Total	C	N	O	0	0
			28	16	2	10		
6	Z	2	Total	C	N	O	0	0
			28	16	2	10		
6	b	2	Total	C	N	O	0	0
			28	16	2	10		
6	c	2	Total	C	N	O	0	0
			28	16	2	10		
6	d	2	Total	C	N	O	0	0
			28	16	2	10		
6	e	2	Total	C	N	O	0	0
			28	16	2	10		
6	f	2	Total	C	N	O	0	0
			28	16	2	10		
6	h	2	Total	C	N	O	0	0
			28	16	2	10		
6	m	2	Total	C	N	O	0	0
			28	16	2	10		
6	n	2	Total	C	N	O	0	0
			28	16	2	10		
6	p	2	Total	C	N	O	0	0
			28	16	2	10		
6	q	2	Total	C	N	O	0	0
			28	16	2	10		
6	r	2	Total	C	N	O	0	0
			28	16	2	10		
6	s	2	Total	C	N	O	0	0
			28	16	2	10		
6	t	2	Total	C	N	O	0	0
			28	16	2	10		
6	v	2	Total	C	N	O	0	0
			28	16	2	10		
6	0	2	Total	C	N	O	0	0
			28	16	2	10		
6	1	2	Total	C	N	O	0	0
			28	16	2	10		

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



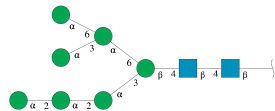
Mol	Chain	Residues	Atoms				AltConf	Trace
7	S	7	Total	C	N	O	0	0
			83	46	2	35		
7	g	7	Total	C	N	O	0	0
			83	46	2	35		
7	u	7	Total	C	N	O	0	0
			83	46	2	35		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
8	U	4	Total	C	N	O	0	0
			50	28	2	20		
8	i	4	Total	C	N	O	0	0
			50	28	2	20		
8	w	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[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.



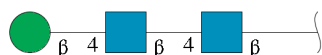
Mol	Chain	Residues	Atoms				AltConf	Trace
9	V	9	Total	C	N	O	0	0
			105	58	2	45		
9	j	9	Total	C	N	O	0	0
			105	58	2	45		

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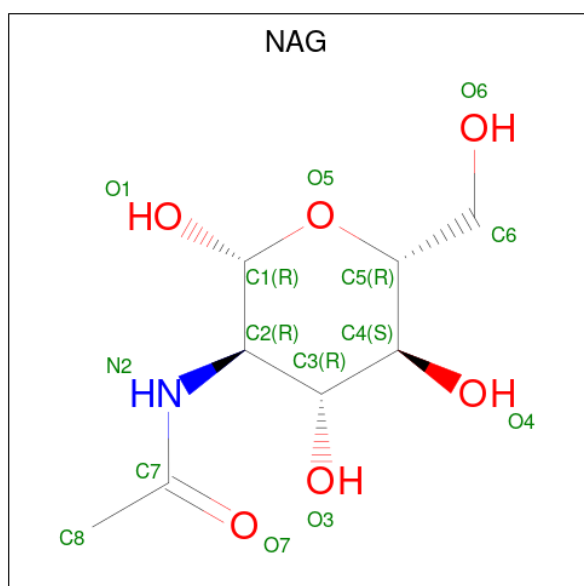
Mol	Chain	Residues	Atoms				AltConf	Trace
9	x	9	Total	C	N	O	0	0
			105	58	2	45		

- Molecule 10 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
10	W	3	Total	C	N	O	0	0
			39	22	2	15		
10	X	3	Total	C	N	O	0	0
			39	22	2	15		
10	k	3	Total	C	N	O	0	0
			39	22	2	15		
10	l	3	Total	C	N	O	0	0
			39	22	2	15		
10	y	3	Total	C	N	O	0	0
			39	22	2	15		
10	z	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

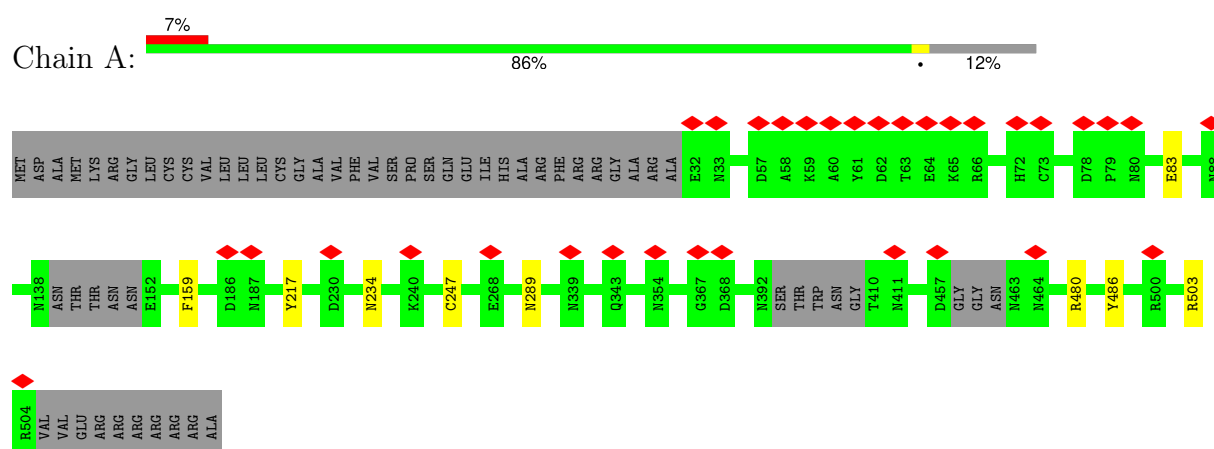


Mol	Chain	Residues	Atoms				AltConf
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	A	1	Total	C	N	O	0
			14	8	1	5	
11	B	1	Total	C	N	O	0
			14	8	1	5	
11	C	1	Total	C	N	O	0
			14	8	1	5	
11	C	1	Total	C	N	O	0
			14	8	1	5	
11	D	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14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

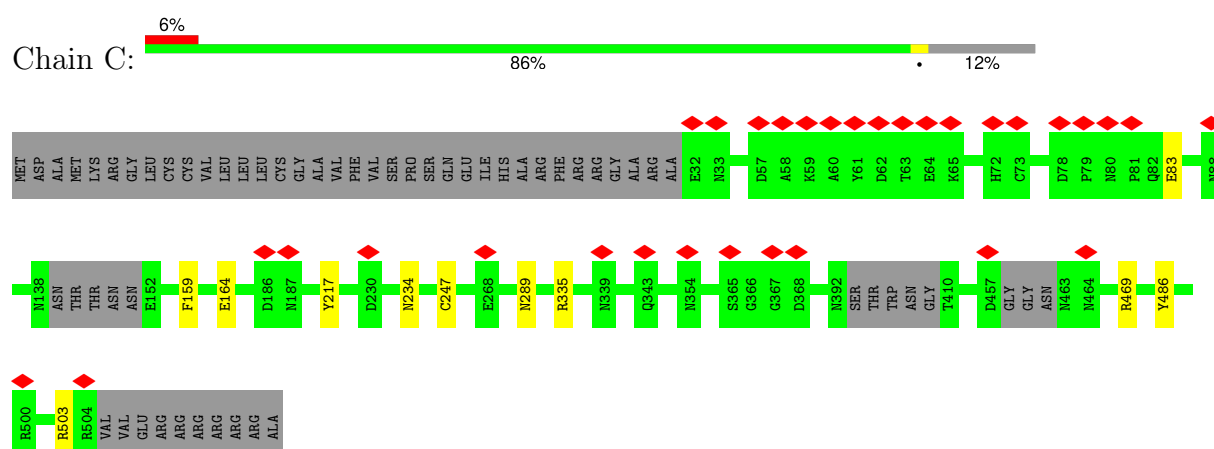
3 Residue-property plots [i](#)

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

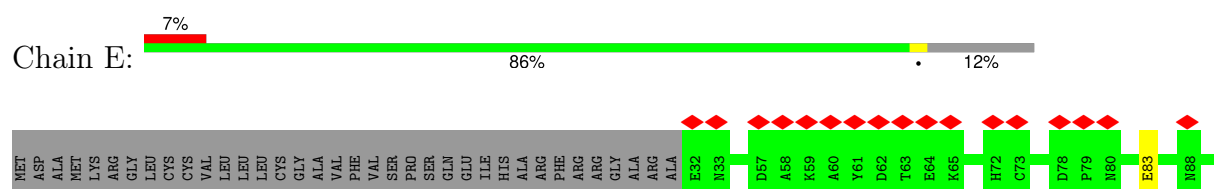
• Molecule 1: HIV-1 Env glycoprotein gp120



• Molecule 1: HIV-1 Env glycoprotein gp120



• Molecule 1: HIV-1 Env glycoprotein gp120



THR
LYS
VAL
ASP
LYS
LYS
ARG
VAL
GLU
PRO
LYS
SER
CYS

• Molecule 3: PGT122 Fab heavy chain



Q1 G10 S15 G26 D31 N32 Y33 W34 S54 G55 D72 K73 S74 K75 Y91 R100 S110
SER ALA SER THR LYS GLY PRO SER VAL PHE PRO SER LEU ALA PRO SER SER LYS THR GLY THR THR ALA ALA LEU GLY CYS LEU VAL LYS ASP THR PHE

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

VAL
ASP
LYS
ARG
VAL
GLU
PRO
LYS
SER
CYS

• Molecule 3: PGT122 Fab heavy chain



Q1 E6 G10 S15 G26 D31 N32 Y33 W34 K43 Y50 S54 G55 D72 K73 S74 K75 Y91 S110
SER ALA SER THR LYS GLY PRO SER VAL PHE PRO SER LEU ALA PRO SER SER LYS THR GLY THR THR ALA ALA LEU GLY CYS LEU VAL LYS

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

SER
ASN
THR
LYS
VAL
ASP
LYS
ARG
VAL
GLU
PRO
LYS
SER
CYS

• Molecule 4: PGT122 Fab light chain



A6 P7 G16 Q17 R39 R61 Y87 F98 I105 V106 L107 S108
GLN PRO LYS THR ALA ALA PRO SER VAL THR LEU PHE PRO PRO SER GLU SER GLN TRP LYS SER HIS TYR CYS THR ILE ASP PHE THR PRO GLU VAL THR VAL ALA THR VAL TRP LYS

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

GLU
CYS
SER

• Molecule 4: PGT122 Fab light chain



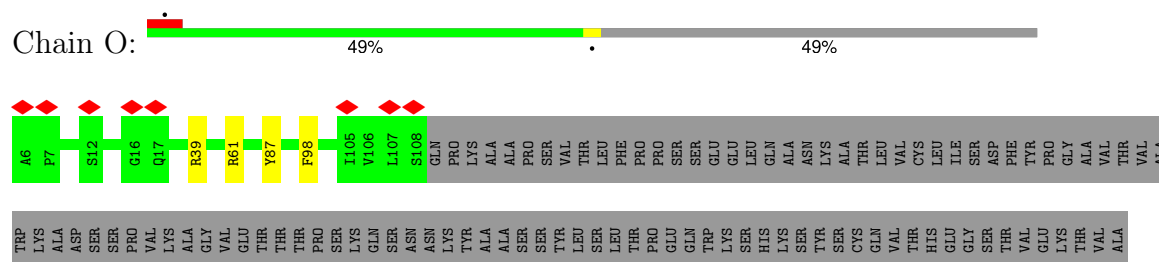
A6 P7 G16 Q17 R39 R61 Y87 I105 V106 L107 S108
GLN PRO LYS THR ALA ALA PRO SER VAL THR LEU PHE PRO PRO SER GLU SER GLN TRP LYS SER HIS TYR CYS THR ILE ASP PHE THR PRO GLU VAL THR VAL ALA THR VAL TRP LYS ASP

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

SER

- Molecule 4: PGT122 Fab light chain

Chain O:

PRO
THR
GLU
CYS
SER

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

Chain G:

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8

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

Chain a:

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8

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

Chain o:

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8

- 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 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



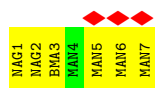
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



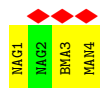
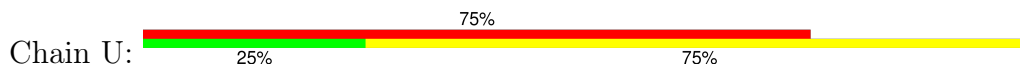
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



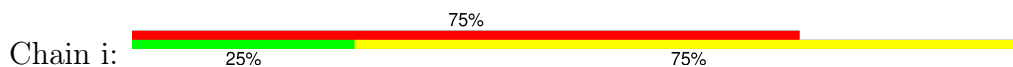
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



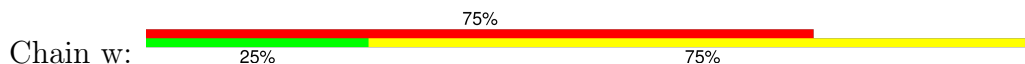
- Molecule 8: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: alpha-D-mannopyranose-(1-6)-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-(1-6)-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-(1-3)-[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



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



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



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: 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	144741	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.676	Depositor
Minimum map value	-2.248	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.103	Depositor
Recommended contour level	0.4	Depositor
Map size (\AA)	225.72, 225.72, 225.72	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.026, 1.026, 1.026	Depositor

5 Model quality

5.1 Standard geometry

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	1.07	4/3520 (0.1%)	0.90	7/4779 (0.1%)
1	C	1.07	5/3520 (0.1%)	0.92	9/4779 (0.2%)
1	E	1.04	4/3520 (0.1%)	0.89	6/4779 (0.1%)
2	B	1.14	3/967 (0.3%)	0.78	0/1310
2	D	1.16	4/967 (0.4%)	0.77	0/1310
2	F	1.16	3/967 (0.3%)	0.77	0/1310
3	H	1.20	4/1070 (0.4%)	0.94	4/1457 (0.3%)
3	N	1.19	2/1070 (0.2%)	0.96	3/1457 (0.2%)
3	P	1.21	3/1070 (0.3%)	0.91	2/1457 (0.1%)
4	L	1.11	0/845	0.99	4/1157 (0.3%)
4	M	1.10	0/845	1.00	3/1157 (0.3%)
4	O	1.12	0/845	1.01	4/1157 (0.3%)
All	All	1.10	32/19206 (0.2%)	0.91	42/26109 (0.2%)

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	247	CYS	CB-SG	-12.06	1.61	1.82
1	A	247	CYS	CB-SG	-11.95	1.61	1.82
1	C	159	PHE	CB-CG	-7.34	1.38	1.51
1	E	159	PHE	CB-CG	-7.32	1.39	1.51
3	H	34	TRP	CB-CG	-7.26	1.37	1.50

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	100	ARG	NE-CZ-NH2	-10.36	115.12	120.30
1	C	217	TYR	CB-CG-CD2	-9.96	115.03	121.00
1	A	217	TYR	CB-CG-CD2	-9.84	115.10	121.00
1	A	503	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	E	503	ARG	NE-CZ-NH2	-9.59	115.50	120.30

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	426/493 (86%)	421 (99%)	5 (1%)	0	100	100
1	C	426/493 (86%)	421 (99%)	5 (1%)	0	100	100
1	E	426/493 (86%)	422 (99%)	4 (1%)	0	100	100
2	B	114/153 (74%)	111 (97%)	1 (1%)	2 (2%)	7	27
2	D	114/153 (74%)	110 (96%)	2 (2%)	2 (2%)	7	27
2	F	114/153 (74%)	110 (96%)	2 (2%)	2 (2%)	7	27
3	H	129/235 (55%)	127 (98%)	2 (2%)	0	100	100
3	N	129/235 (55%)	127 (98%)	2 (2%)	0	100	100
3	P	129/235 (55%)	127 (98%)	2 (2%)	0	100	100
4	L	106/213 (50%)	105 (99%)	1 (1%)	0	100	100
4	M	106/213 (50%)	105 (99%)	1 (1%)	0	100	100
4	O	106/213 (50%)	105 (99%)	1 (1%)	0	100	100
All	All	2325/3282 (71%)	2291 (98%)	28 (1%)	6 (0%)	38	67

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	636	ASN
2	D	636	ASN
2	F	636	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	608	VAL
2	D	608	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	393/440 (89%)	391 (100%)	2 (0%)	86	92
1	C	393/440 (89%)	391 (100%)	2 (0%)	86	92
1	E	393/440 (89%)	392 (100%)	1 (0%)	91	95
2	B	104/131 (79%)	104 (100%)	0	100	100
2	D	104/131 (79%)	104 (100%)	0	100	100
2	F	104/131 (79%)	104 (100%)	0	100	100
3	H	115/205 (56%)	115 (100%)	0	100	100
3	N	115/205 (56%)	115 (100%)	0	100	100
3	P	115/205 (56%)	115 (100%)	0	100	100
4	L	90/181 (50%)	90 (100%)	0	100	100
4	M	90/181 (50%)	90 (100%)	0	100	100
4	O	90/181 (50%)	90 (100%)	0	100	100
All	All	2106/2871 (73%)	2101 (100%)	5 (0%)	91	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	ASN
1	A	289	ASN
1	C	234	ASN
1	C	289	ASN
1	E	289	ASN

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

Mol	Chain	Res	Type
1	C	422	GLN
1	E	422	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

150 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$
6	NAG	0	1	1,6	14,14,15	1.13	1 (7%)	17,19,21	1.19	2 (11%)
6	NAG	0	2	6	14,14,15	0.75	1 (7%)	17,19,21	0.93	1 (5%)
6	NAG	1	1	1,6	14,14,15	1.17	1 (7%)	17,19,21	1.70	4 (23%)
6	NAG	1	2	6	14,14,15	0.74	1 (7%)	17,19,21	0.87	1 (5%)
5	NAG	G	1	1,5	14,14,15	0.93	1 (7%)	17,19,21	1.49	3 (17%)
5	NAG	G	2	5	14,14,15	0.90	1 (7%)	17,19,21	1.26	2 (11%)
5	BMA	G	3	5	11,11,12	0.58	0	15,15,17	1.68	2 (13%)
5	MAN	G	4	5	11,11,12	0.81	0	15,15,17	1.73	4 (26%)
5	MAN	G	5	5	11,11,12	0.78	0	15,15,17	1.15	2 (13%)
5	MAN	G	6	5	11,11,12	0.68	0	15,15,17	0.81	0
5	MAN	G	7	5	11,11,12	0.70	0	15,15,17	1.35	3 (20%)
5	MAN	G	8	5	11,11,12	0.81	0	15,15,17	1.24	1 (6%)
6	NAG	I	1	1,6	14,14,15	1.05	1 (7%)	17,19,21	0.95	1 (5%)
6	NAG	I	2	6	14,14,15	0.80	1 (7%)	17,19,21	0.79	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	J	1	1,6	14,14,15	1.07	1 (7%)	17,19,21	1.29	3 (17%)
6	NAG	J	2	6	14,14,15	0.80	1 (7%)	17,19,21	0.83	1 (5%)
6	NAG	K	1	1,6	14,14,15	0.99	1 (7%)	17,19,21	1.08	1 (5%)
6	NAG	K	2	6	14,14,15	0.81	1 (7%)	17,19,21	0.95	1 (5%)
6	NAG	Q	1	1,6	14,14,15	1.01	1 (7%)	17,19,21	1.58	2 (11%)
6	NAG	Q	2	6	14,14,15	1.37	1 (7%)	17,19,21	0.96	2 (11%)
6	NAG	R	1	1,6	14,14,15	1.00	1 (7%)	17,19,21	0.92	0
6	NAG	R	2	6	14,14,15	0.78	1 (7%)	17,19,21	0.72	1 (5%)
7	NAG	S	1	1,7	14,14,15	1.02	1 (7%)	17,19,21	0.86	1 (5%)
7	NAG	S	2	7	14,14,15	0.80	1 (7%)	17,19,21	0.87	0
7	BMA	S	3	7	11,11,12	0.56	0	15,15,17	0.81	1 (6%)
7	MAN	S	4	7	11,11,12	0.63	0	15,15,17	0.77	0
7	MAN	S	5	7	11,11,12	0.63	0	15,15,17	0.74	1 (6%)
7	MAN	S	6	7	11,11,12	0.70	0	15,15,17	0.85	1 (6%)
7	MAN	S	7	7	11,11,12	0.68	0	15,15,17	0.85	1 (6%)
6	NAG	T	1	1,6	14,14,15	0.92	1 (7%)	17,19,21	1.01	1 (5%)
6	NAG	T	2	6	14,14,15	0.71	1 (7%)	17,19,21	0.80	1 (5%)
8	NAG	U	1	8,1	14,14,15	1.00	1 (7%)	17,19,21	0.79	0
8	NAG	U	2	8	14,14,15	0.74	0	17,19,21	0.76	0
8	BMA	U	3	8	11,11,12	0.61	0	15,15,17	0.81	1 (6%)
8	MAN	U	4	8	11,11,12	0.69	0	15,15,17	0.97	1 (6%)
9	NAG	V	1	1,9	14,14,15	0.79	1 (7%)	17,19,21	1.18	0
9	NAG	V	2	9	14,14,15	0.67	0	17,19,21	1.47	2 (11%)
9	BMA	V	3	9	11,11,12	0.42	0	15,15,17	0.94	1 (6%)
9	MAN	V	4	9	11,11,12	0.39	0	15,15,17	0.86	0
9	MAN	V	5	9	11,11,12	0.56	0	15,15,17	0.93	1 (6%)
9	MAN	V	6	9	11,11,12	0.55	0	15,15,17	0.85	0
9	MAN	V	7	9	11,11,12	0.60	0	15,15,17	0.71	1 (6%)
9	MAN	V	8	9	11,11,12	0.65	0	15,15,17	0.85	1 (6%)
9	MAN	V	9	9	11,11,12	0.64	0	15,15,17	0.77	1 (6%)
10	NAG	W	1	1,10	14,14,15	0.99	1 (7%)	17,19,21	0.71	1 (5%)
10	NAG	W	2	10	14,14,15	0.77	1 (7%)	17,19,21	0.72	0
10	BMA	W	3	10	11,11,12	0.59	0	15,15,17	0.74	1 (6%)
10	NAG	X	1	1,10	14,14,15	1.07	1 (7%)	17,19,21	1.10	2 (11%)
10	NAG	X	2	10	14,14,15	0.78	1 (7%)	17,19,21	0.86	1 (5%)
10	BMA	X	3	10	11,11,12	0.62	0	15,15,17	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	Y	1	1,6	14,14,15	1.25	1 (7%)	17,19,21	0.91	1 (5%)
6	NAG	Y	2	6	14,14,15	0.76	1 (7%)	17,19,21	0.97	1 (5%)
6	NAG	Z	1	1,6	14,14,15	1.16	1 (7%)	17,19,21	1.81	4 (23%)
6	NAG	Z	2	6	14,14,15	0.75	1 (7%)	17,19,21	0.87	1 (5%)
5	NAG	a	1	1,5	14,14,15	0.94	1 (7%)	17,19,21	1.56	4 (23%)
5	NAG	a	2	5	14,14,15	1.00	1 (7%)	17,19,21	1.53	3 (17%)
5	BMA	a	3	5	11,11,12	0.65	0	15,15,17	1.63	2 (13%)
5	MAN	a	4	5	11,11,12	0.73	0	15,15,17	1.72	2 (13%)
5	MAN	a	5	5	11,11,12	0.75	0	15,15,17	1.07	2 (13%)
5	MAN	a	6	5	11,11,12	0.64	0	15,15,17	0.78	0
5	MAN	a	7	5	11,11,12	0.65	0	15,15,17	1.45	3 (20%)
5	MAN	a	8	5	11,11,12	0.79	0	15,15,17	1.26	1 (6%)
6	NAG	b	1	1,6	14,14,15	1.04	1 (7%)	17,19,21	0.95	1 (5%)
6	NAG	b	2	6	14,14,15	0.81	1 (7%)	17,19,21	0.79	1 (5%)
6	NAG	c	1	1,6	14,14,15	1.08	1 (7%)	17,19,21	1.33	2 (11%)
6	NAG	c	2	6	14,14,15	0.81	1 (7%)	17,19,21	0.82	1 (5%)
6	NAG	d	1	1,6	14,14,15	1.01	1 (7%)	17,19,21	1.07	1 (5%)
6	NAG	d	2	6	14,14,15	0.79	1 (7%)	17,19,21	0.93	1 (5%)
6	NAG	e	1	1,6	14,14,15	1.10	1 (7%)	17,19,21	1.58	2 (11%)
6	NAG	e	2	6	14,14,15	1.41	1 (7%)	17,19,21	1.02	2 (11%)
6	NAG	f	1	1,6	14,14,15	1.00	1 (7%)	17,19,21	0.89	0
6	NAG	f	2	6	14,14,15	0.78	1 (7%)	17,19,21	0.72	1 (5%)
7	NAG	g	1	1,7	14,14,15	1.02	1 (7%)	17,19,21	0.98	1 (5%)
7	NAG	g	2	7	14,14,15	0.82	1 (7%)	17,19,21	0.82	1 (5%)
7	BMA	g	3	7	11,11,12	0.56	0	15,15,17	0.85	1 (6%)
7	MAN	g	4	7	11,11,12	0.65	0	15,15,17	0.79	0
7	MAN	g	5	7	11,11,12	0.63	0	15,15,17	0.74	1 (6%)
7	MAN	g	6	7	11,11,12	0.70	0	15,15,17	0.85	1 (6%)
7	MAN	g	7	7	11,11,12	0.67	0	15,15,17	0.85	1 (6%)
6	NAG	h	1	1,6	14,14,15	0.93	1 (7%)	17,19,21	1.05	1 (5%)
6	NAG	h	2	6	14,14,15	0.70	1 (7%)	17,19,21	0.80	1 (5%)
8	NAG	i	1	8,1	14,14,15	1.00	1 (7%)	17,19,21	0.79	0
8	NAG	i	2	8	14,14,15	0.72	0	17,19,21	0.75	0
8	BMA	i	3	8	11,11,12	0.60	0	15,15,17	0.81	1 (6%)
8	MAN	i	4	8	11,11,12	0.68	0	15,15,17	0.97	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	j	1	1,9	14,14,15	0.80	1 (7%)	17,19,21	1.12	0
9	NAG	j	2	9	14,14,15	0.69	0	17,19,21	1.46	2 (11%)
9	BMA	j	3	9	11,11,12	0.45	0	15,15,17	0.99	1 (6%)
9	MAN	j	4	9	11,11,12	0.40	0	15,15,17	0.95	1 (6%)
9	MAN	j	5	9	11,11,12	0.51	0	15,15,17	1.02	1 (6%)
9	MAN	j	6	9	11,11,12	0.54	0	15,15,17	0.85	0
9	MAN	j	7	9	11,11,12	0.62	0	15,15,17	0.73	1 (6%)
9	MAN	j	8	9	11,11,12	0.65	0	15,15,17	0.86	1 (6%)
9	MAN	j	9	9	11,11,12	0.66	0	15,15,17	0.82	1 (6%)
10	NAG	k	1	1,10	14,14,15	0.99	1 (7%)	17,19,21	0.74	1 (5%)
10	NAG	k	2	10	14,14,15	0.78	1 (7%)	17,19,21	0.73	0
10	BMA	k	3	10	11,11,12	0.59	0	15,15,17	0.74	1 (6%)
10	NAG	l	1	1,10	14,14,15	0.97	1 (7%)	17,19,21	0.94	1 (5%)
10	NAG	l	2	10	14,14,15	0.78	1 (7%)	17,19,21	0.85	1 (5%)
10	BMA	l	3	10	11,11,12	0.63	0	15,15,17	0.68	0
6	NAG	m	1	1,6	14,14,15	1.23	1 (7%)	17,19,21	0.88	0
6	NAG	m	2	6	14,14,15	0.77	1 (7%)	17,19,21	0.97	1 (5%)
6	NAG	n	1	1,6	14,14,15	1.18	1 (7%)	17,19,21	1.71	4 (23%)
6	NAG	n	2	6	14,14,15	0.72	1 (7%)	17,19,21	0.87	1 (5%)
5	NAG	o	1	1,5	14,14,15	0.92	1 (7%)	17,19,21	1.69	4 (23%)
5	NAG	o	2	5	14,14,15	0.93	1 (7%)	17,19,21	1.31	2 (11%)
5	BMA	o	3	5	11,11,12	0.57	0	15,15,17	1.71	3 (20%)
5	MAN	o	4	5	11,11,12	0.81	0	15,15,17	1.85	4 (26%)
5	MAN	o	5	5	11,11,12	0.78	1 (9%)	15,15,17	1.13	2 (13%)
5	MAN	o	6	5	11,11,12	0.64	0	15,15,17	0.81	0
5	MAN	o	7	5	11,11,12	0.67	0	15,15,17	1.44	3 (20%)
5	MAN	o	8	5	11,11,12	0.84	0	15,15,17	1.46	3 (20%)
6	NAG	p	1	1,6	14,14,15	1.05	1 (7%)	17,19,21	0.94	1 (5%)
6	NAG	p	2	6	14,14,15	0.81	1 (7%)	17,19,21	0.79	1 (5%)
6	NAG	q	1	1,6	14,14,15	1.08	1 (7%)	17,19,21	1.28	2 (11%)
6	NAG	q	2	6	14,14,15	0.81	1 (7%)	17,19,21	0.81	1 (5%)
6	NAG	r	1	1,6	14,14,15	0.99	1 (7%)	17,19,21	1.08	1 (5%)
6	NAG	r	2	6	14,14,15	0.81	1 (7%)	17,19,21	0.94	1 (5%)
6	NAG	s	1	1,6	14,14,15	1.06	1 (7%)	17,19,21	1.88	4 (23%)
6	NAG	s	2	6	14,14,15	1.48	1 (7%)	17,19,21	0.97	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	t	1	1,6	14,14,15	1.00	1 (7%)	17,19,21	0.91	0
6	NAG	t	2	6	14,14,15	0.77	1 (7%)	17,19,21	0.73	1 (5%)
7	NAG	u	1	1,7	14,14,15	1.01	1 (7%)	17,19,21	0.99	1 (5%)
7	NAG	u	2	7	14,14,15	0.82	1 (7%)	17,19,21	0.83	0
7	BMA	u	3	7	11,11,12	0.60	0	15,15,17	0.85	1 (6%)
7	MAN	u	4	7	11,11,12	0.69	0	15,15,17	0.81	0
7	MAN	u	5	7	11,11,12	0.63	0	15,15,17	0.75	1 (6%)
7	MAN	u	6	7	11,11,12	0.71	0	15,15,17	0.87	1 (6%)
7	MAN	u	7	7	11,11,12	0.68	0	15,15,17	0.84	1 (6%)
6	NAG	v	1	1,6	14,14,15	0.91	1 (7%)	17,19,21	1.07	1 (5%)
6	NAG	v	2	6	14,14,15	0.72	1 (7%)	17,19,21	0.81	1 (5%)
8	NAG	w	1	8,1	14,14,15	1.00	1 (7%)	17,19,21	0.79	0
8	NAG	w	2	8	14,14,15	0.73	0	17,19,21	0.75	0
8	BMA	w	3	8	11,11,12	0.62	0	15,15,17	0.81	1 (6%)
8	MAN	w	4	8	11,11,12	0.69	0	15,15,17	0.96	1 (6%)
9	NAG	x	1	1,9	14,14,15	0.81	1 (7%)	17,19,21	1.13	0
9	NAG	x	2	9	14,14,15	0.68	0	17,19,21	1.46	2 (11%)
9	BMA	x	3	9	11,11,12	0.45	0	15,15,17	0.99	1 (6%)
9	MAN	x	4	9	11,11,12	0.46	0	15,15,17	0.79	0
9	MAN	x	5	9	11,11,12	0.60	0	15,15,17	0.99	1 (6%)
9	MAN	x	6	9	11,11,12	0.55	0	15,15,17	0.85	0
9	MAN	x	7	9	11,11,12	0.59	0	15,15,17	0.71	1 (6%)
9	MAN	x	8	9	11,11,12	0.64	0	15,15,17	0.85	1 (6%)
9	MAN	x	9	9	11,11,12	0.64	0	15,15,17	0.75	1 (6%)
10	NAG	y	1	1,10	14,14,15	0.97	1 (7%)	17,19,21	0.75	1 (5%)
10	NAG	y	2	10	14,14,15	0.77	1 (7%)	17,19,21	0.72	0
10	BMA	y	3	10	11,11,12	0.59	0	15,15,17	0.74	1 (6%)
10	NAG	z	1	1,10	14,14,15	1.00	1 (7%)	17,19,21	0.90	1 (5%)
10	NAG	z	2	10	14,14,15	0.79	1 (7%)	17,19,21	0.86	1 (5%)
10	BMA	z	3	10	11,11,12	0.65	0	15,15,17	0.69	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	0	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	0	2	6	-	2/6/23/26	0/1/1/1
6	NAG	1	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	1	2	6	-	1/6/23/26	0/1/1/1
5	NAG	G	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	MAN	G	4	5	-	1/2/19/22	0/1/1/1
5	MAN	G	5	5	-	2/2/19/22	0/1/1/1
5	MAN	G	6	5	-	1/2/19/22	0/1/1/1
5	MAN	G	7	5	-	1/2/19/22	0/1/1/1
5	MAN	G	8	5	-	1/2/19/22	0/1/1/1
6	NAG	I	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	1/6/23/26	0/1/1/1
6	NAG	J	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	J	2	6	-	1/6/23/26	0/1/1/1
6	NAG	K	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	K	2	6	-	1/6/23/26	0/1/1/1
6	NAG	Q	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	1/6/23/26	0/1/1/1
6	NAG	R	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	R	2	6	-	2/6/23/26	0/1/1/1
7	NAG	S	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	S	2	7	-	0/6/23/26	0/1/1/1
7	BMA	S	3	7	-	0/2/19/22	0/1/1/1
7	MAN	S	4	7	-	1/2/19/22	0/1/1/1
7	MAN	S	5	7	-	1/2/19/22	0/1/1/1
7	MAN	S	6	7	-	1/2/19/22	0/1/1/1
7	MAN	S	7	7	-	1/2/19/22	0/1/1/1
6	NAG	T	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	T	2	6	-	1/6/23/26	0/1/1/1
8	NAG	U	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	U	2	8	-	0/6/23/26	0/1/1/1
8	BMA	U	3	8	-	0/2/19/22	0/1/1/1
8	MAN	U	4	8	-	1/2/19/22	0/1/1/1
9	NAG	V	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	V	2	9	-	1/6/23/26	0/1/1/1
9	BMA	V	3	9	-	0/2/19/22	0/1/1/1
9	MAN	V	4	9	-	0/2/19/22	0/1/1/1
9	MAN	V	5	9	-	1/2/19/22	0/1/1/1
9	MAN	V	6	9	-	1/2/19/22	0/1/1/1
9	MAN	V	7	9	-	0/2/19/22	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	i	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	i	2	8	-	0/6/23/26	0/1/1/1
8	BMA	i	3	8	-	0/2/19/22	0/1/1/1
8	MAN	i	4	8	-	1/2/19/22	0/1/1/1
9	NAG	j	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	j	2	9	-	1/6/23/26	0/1/1/1
9	BMA	j	3	9	-	0/2/19/22	0/1/1/1
9	MAN	j	4	9	-	2/2/19/22	0/1/1/1
9	MAN	j	5	9	-	1/2/19/22	0/1/1/1
9	MAN	j	6	9	-	1/2/19/22	0/1/1/1
9	MAN	j	7	9	-	0/2/19/22	0/1/1/1
9	MAN	j	8	9	-	1/2/19/22	0/1/1/1
9	MAN	j	9	9	-	1/2/19/22	0/1/1/1
10	NAG	k	1	1,10	-	1/6/23/26	0/1/1/1
10	NAG	k	2	10	-	1/6/23/26	0/1/1/1
10	BMA	k	3	10	-	1/2/19/22	0/1/1/1
10	NAG	l	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	l	2	10	-	1/6/23/26	0/1/1/1
10	BMA	l	3	10	-	1/2/19/22	0/1/1/1
6	NAG	m	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	m	2	6	-	2/6/23/26	0/1/1/1
6	NAG	n	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	n	2	6	-	1/6/23/26	0/1/1/1
5	NAG	o	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	o	2	5	-	0/6/23/26	0/1/1/1
5	BMA	o	3	5	-	0/2/19/22	0/1/1/1
5	MAN	o	4	5	-	1/2/19/22	0/1/1/1
5	MAN	o	5	5	-	2/2/19/22	0/1/1/1
5	MAN	o	6	5	-	2/2/19/22	0/1/1/1
5	MAN	o	7	5	-	1/2/19/22	0/1/1/1
5	MAN	o	8	5	-	1/2/19/22	0/1/1/1
6	NAG	p	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	p	2	6	-	1/6/23/26	0/1/1/1
6	NAG	q	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	q	2	6	-	1/6/23/26	0/1/1/1
6	NAG	r	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	r	2	6	-	1/6/23/26	0/1/1/1
6	NAG	s	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	s	2	6	-	2/6/23/26	0/1/1/1
6	NAG	t	1	1,6	-	0/6/23/26	0/1/1/1

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

The worst 5 of 79 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	s	2	NAG	C1-C2	5.34	1.59	1.52
6	e	2	NAG	C1-C2	5.07	1.59	1.52
6	Q	2	NAG	C1-C2	4.89	1.59	1.52
6	Y	1	NAG	C1-C2	4.46	1.58	1.52
6	m	1	NAG	C1-C2	4.37	1.58	1.52

The worst 5 of 178 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	a	4	MAN	O3-C3-C4	5.01	122.18	110.38
6	s	1	NAG	C4-C3-C2	-4.92	103.80	111.02
5	o	4	MAN	O3-C3-C4	4.87	121.85	110.38
5	G	4	MAN	O3-C3-C4	4.61	121.23	110.38
6	e	1	NAG	C4-C3-C2	-4.61	104.27	111.02

There are no chirality outliers.

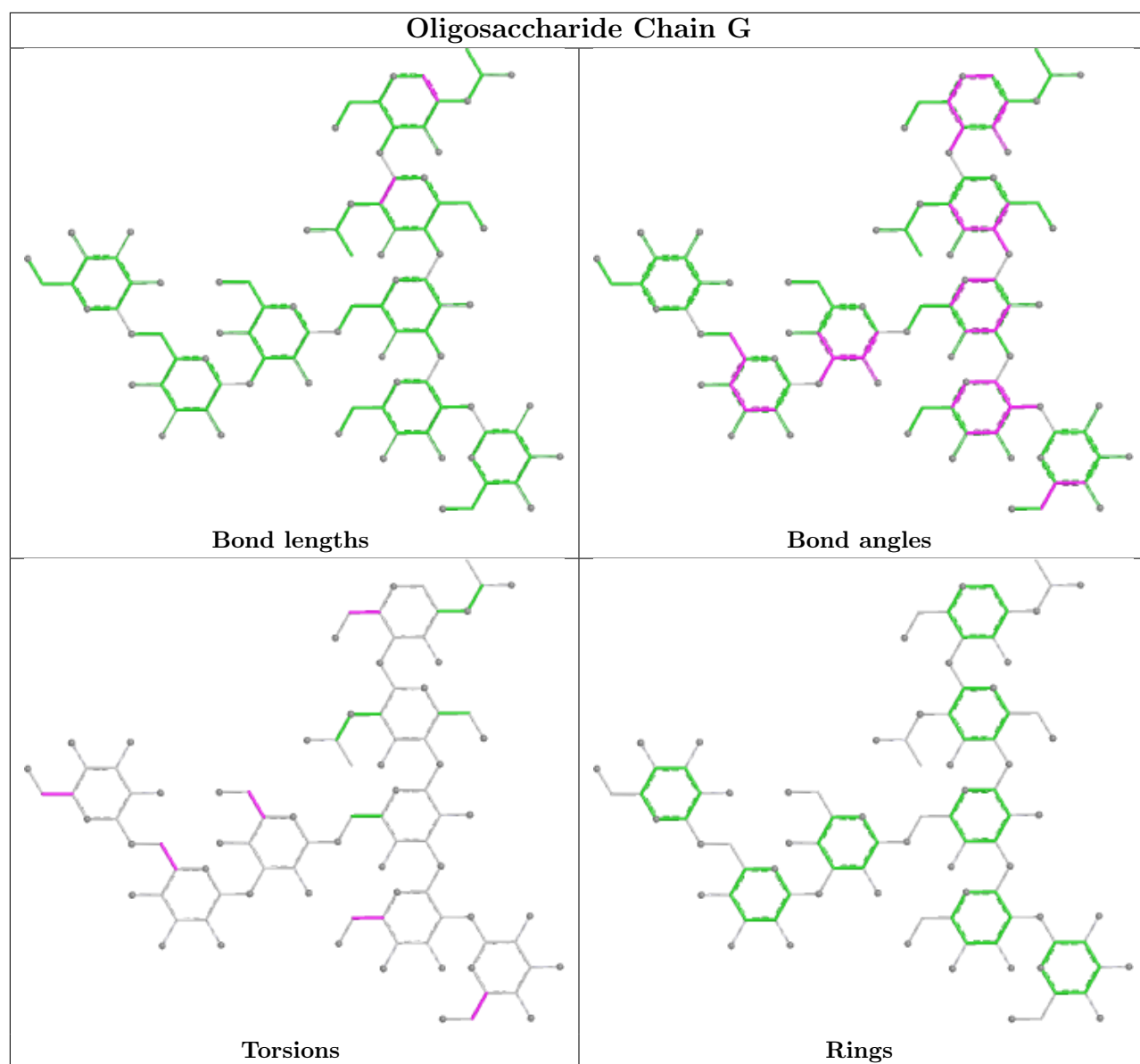
5 of 146 torsion outliers are listed below:

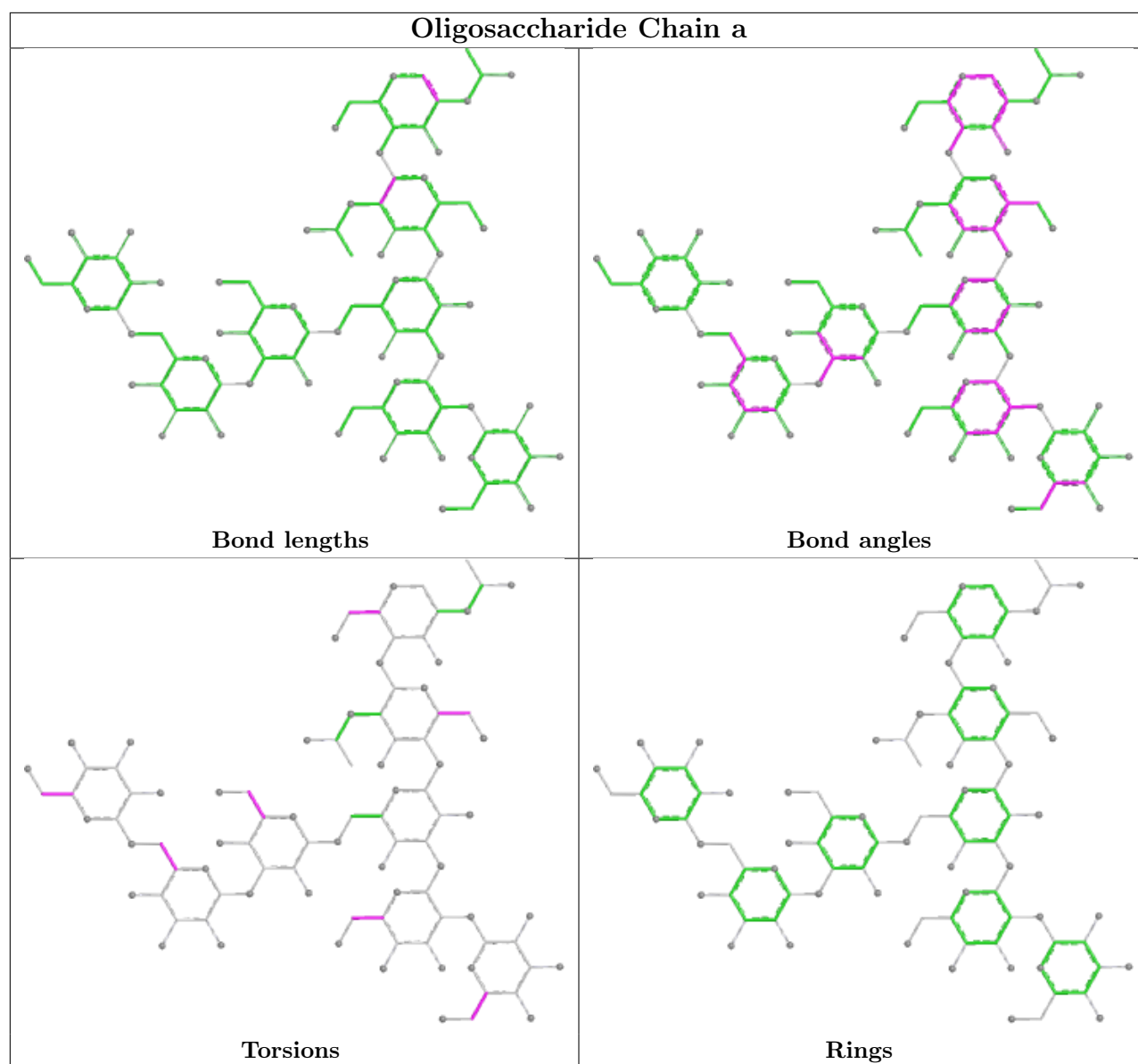
Mol	Chain	Res	Type	Atoms
6	s	1	NAG	C3-C2-N2-C7
6	J	1	NAG	O5-C5-C6-O6
6	c	1	NAG	O5-C5-C6-O6
6	q	1	NAG	O5-C5-C6-O6
5	a	5	MAN	C4-C5-C6-O6

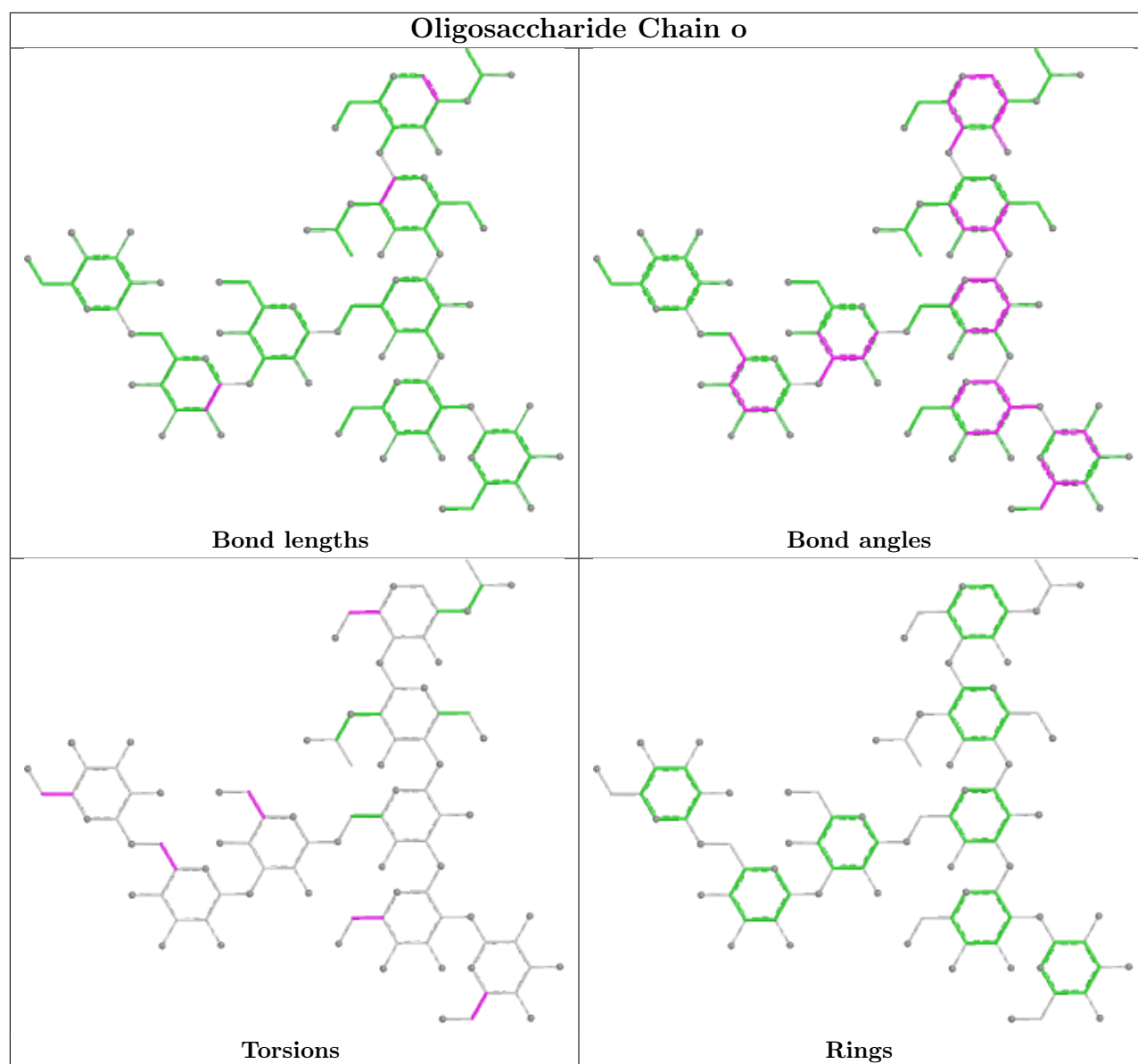
There are no ring outliers.

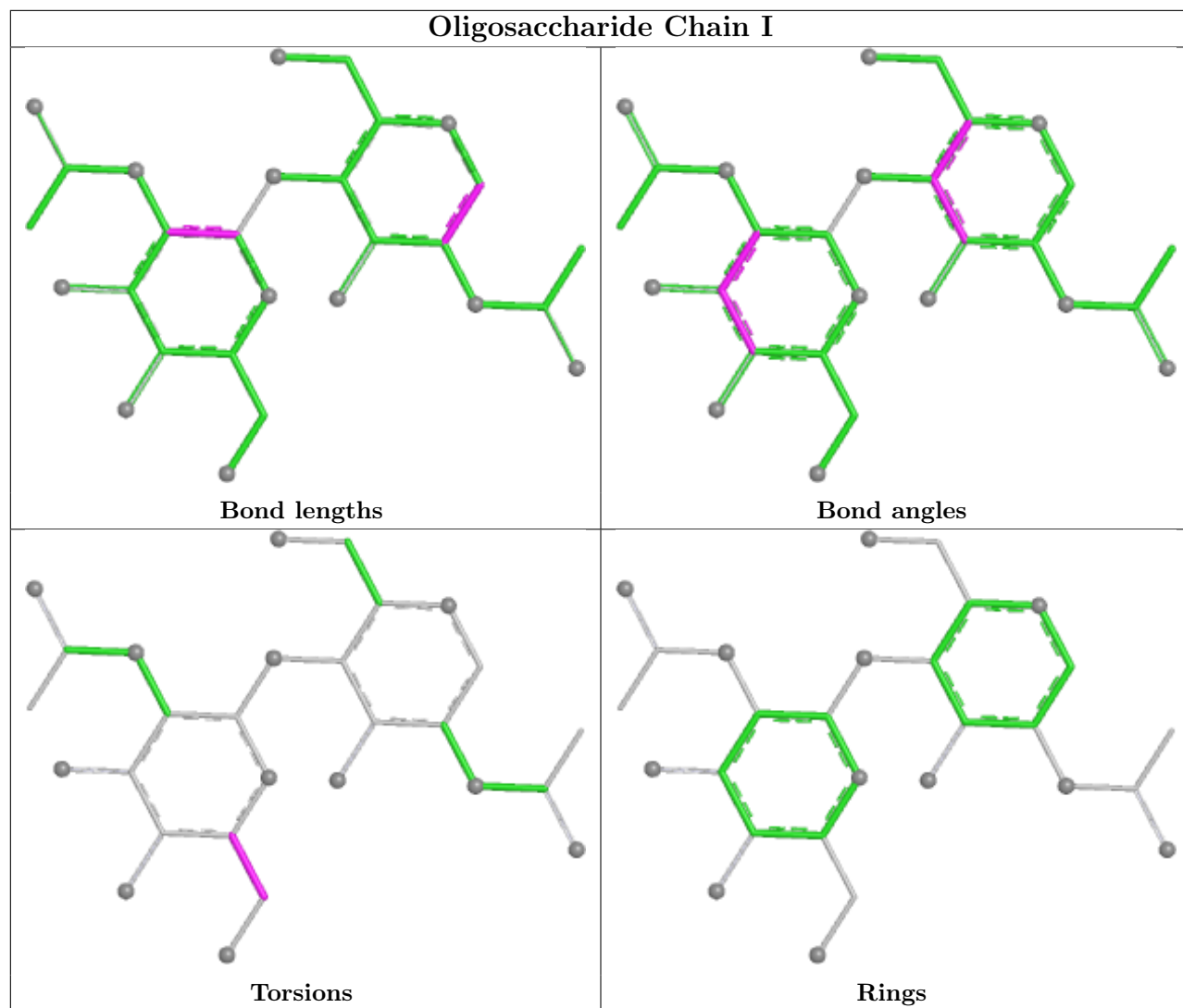
No monomer is involved in short contacts.

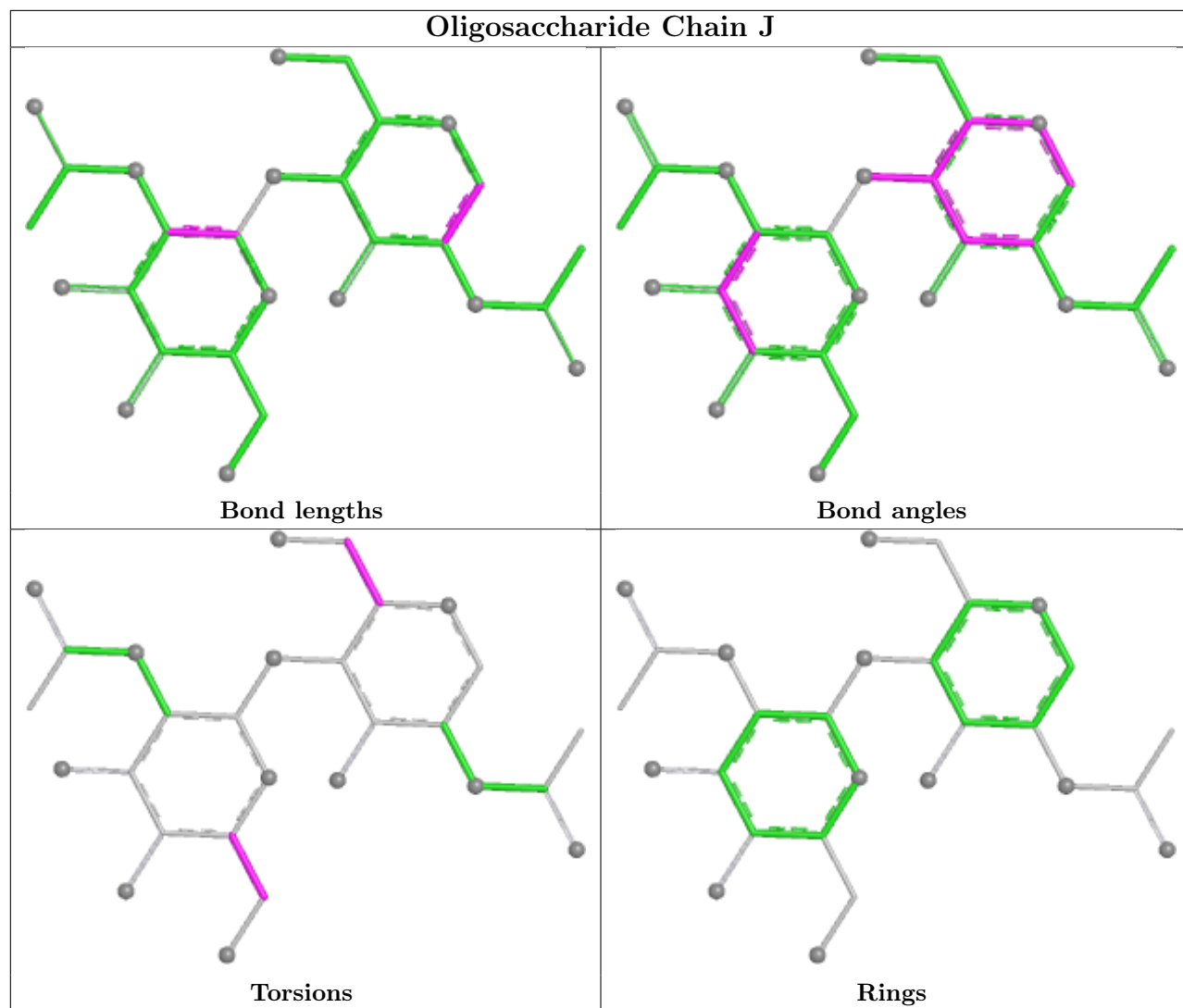
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

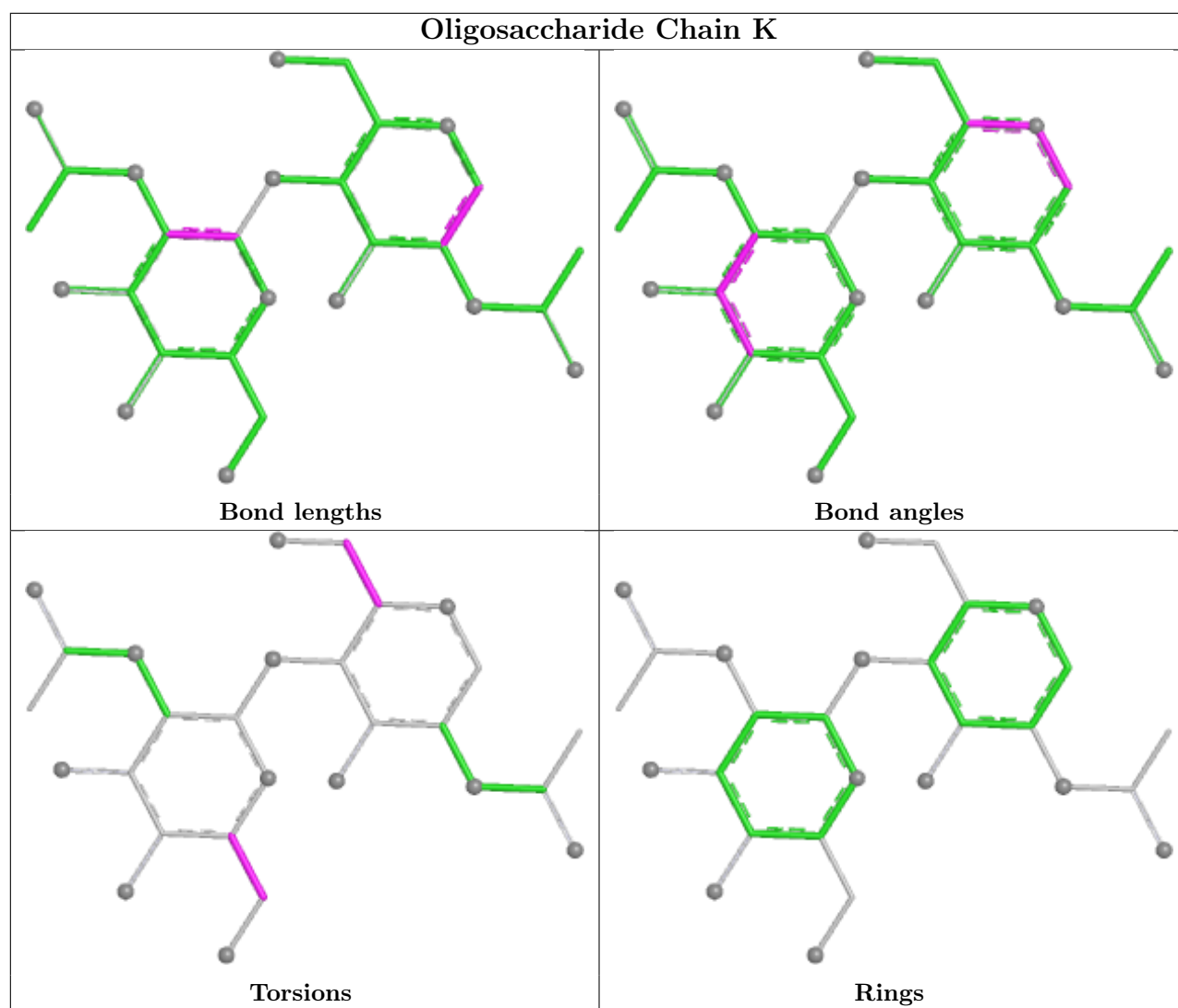


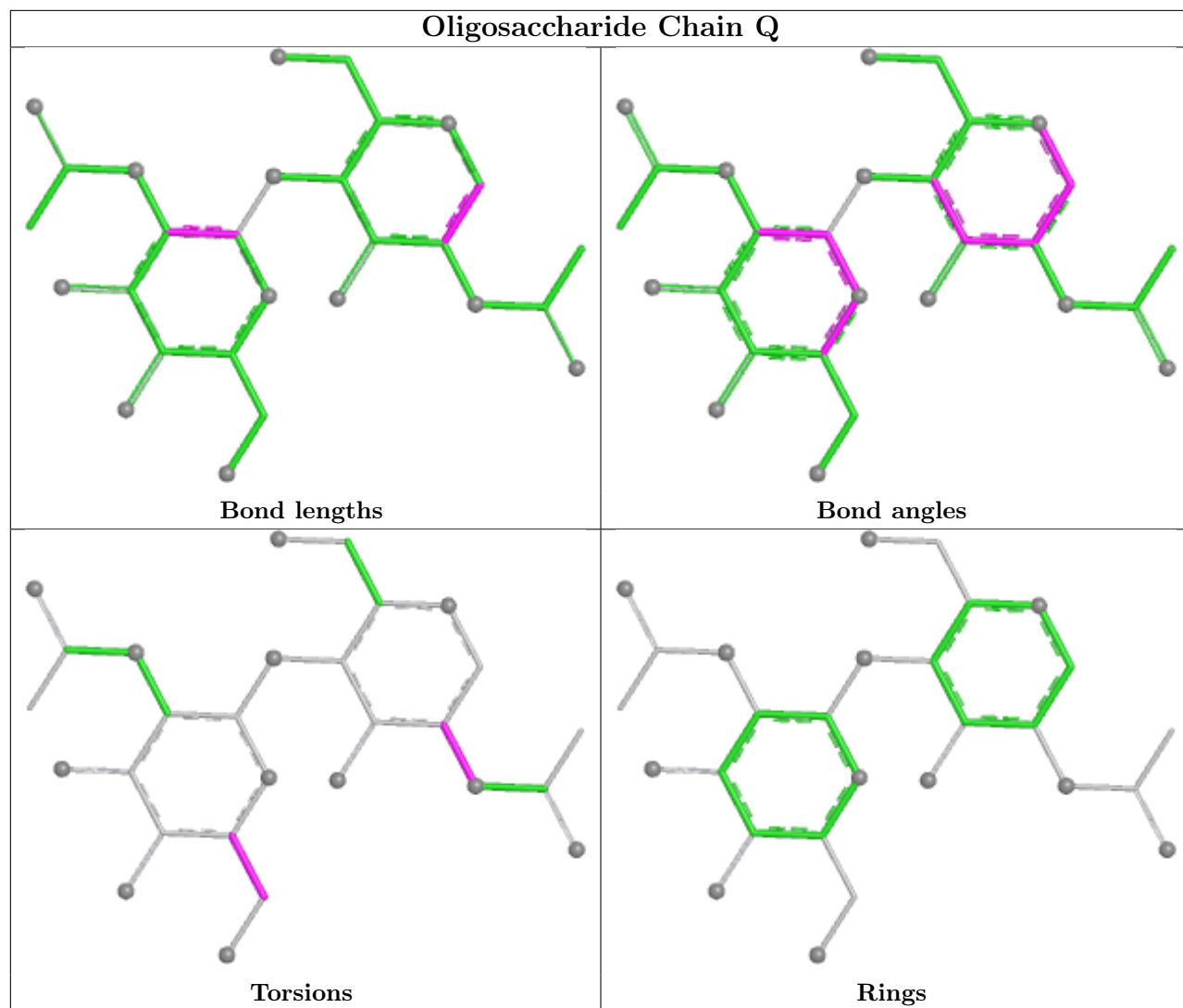


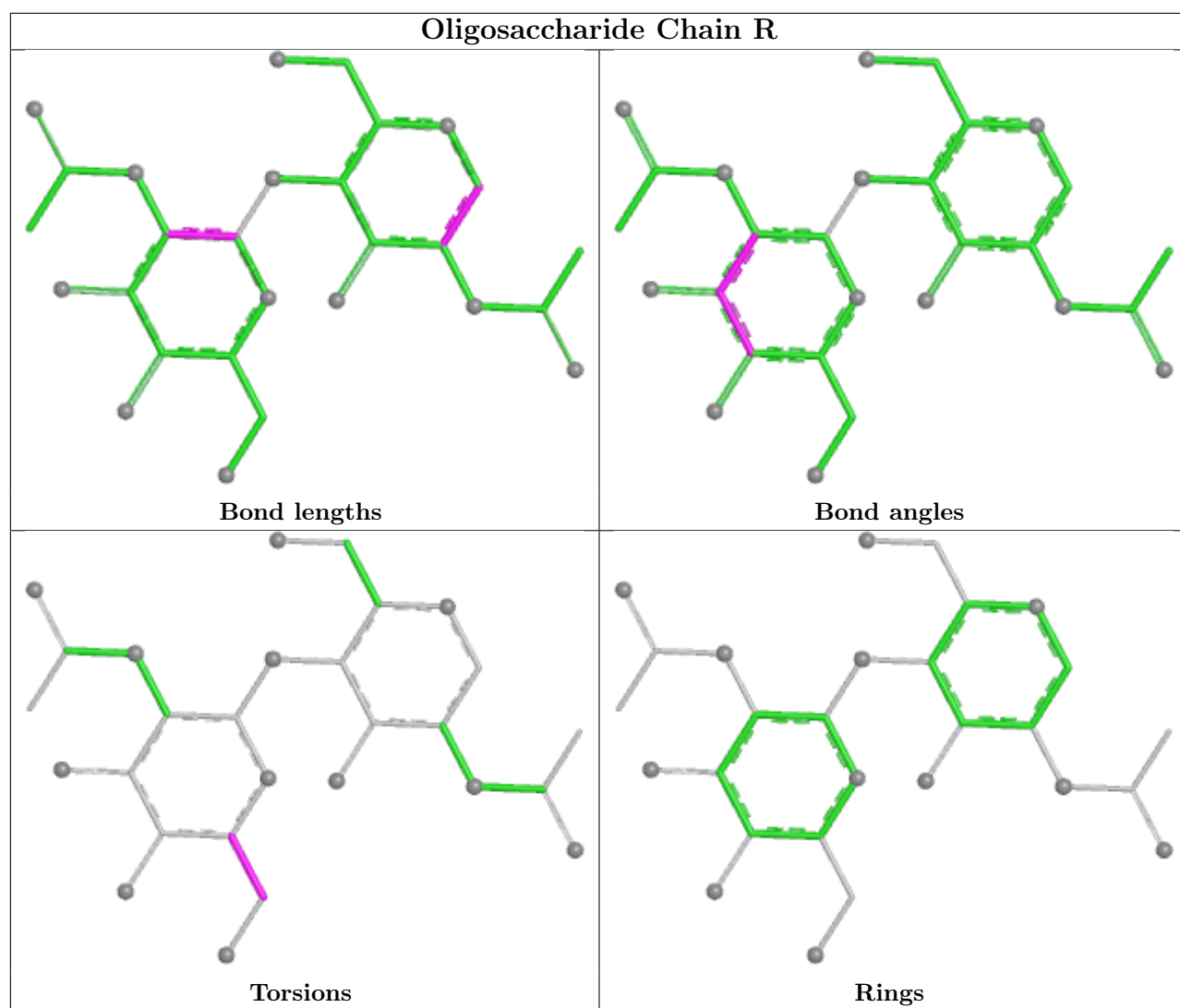


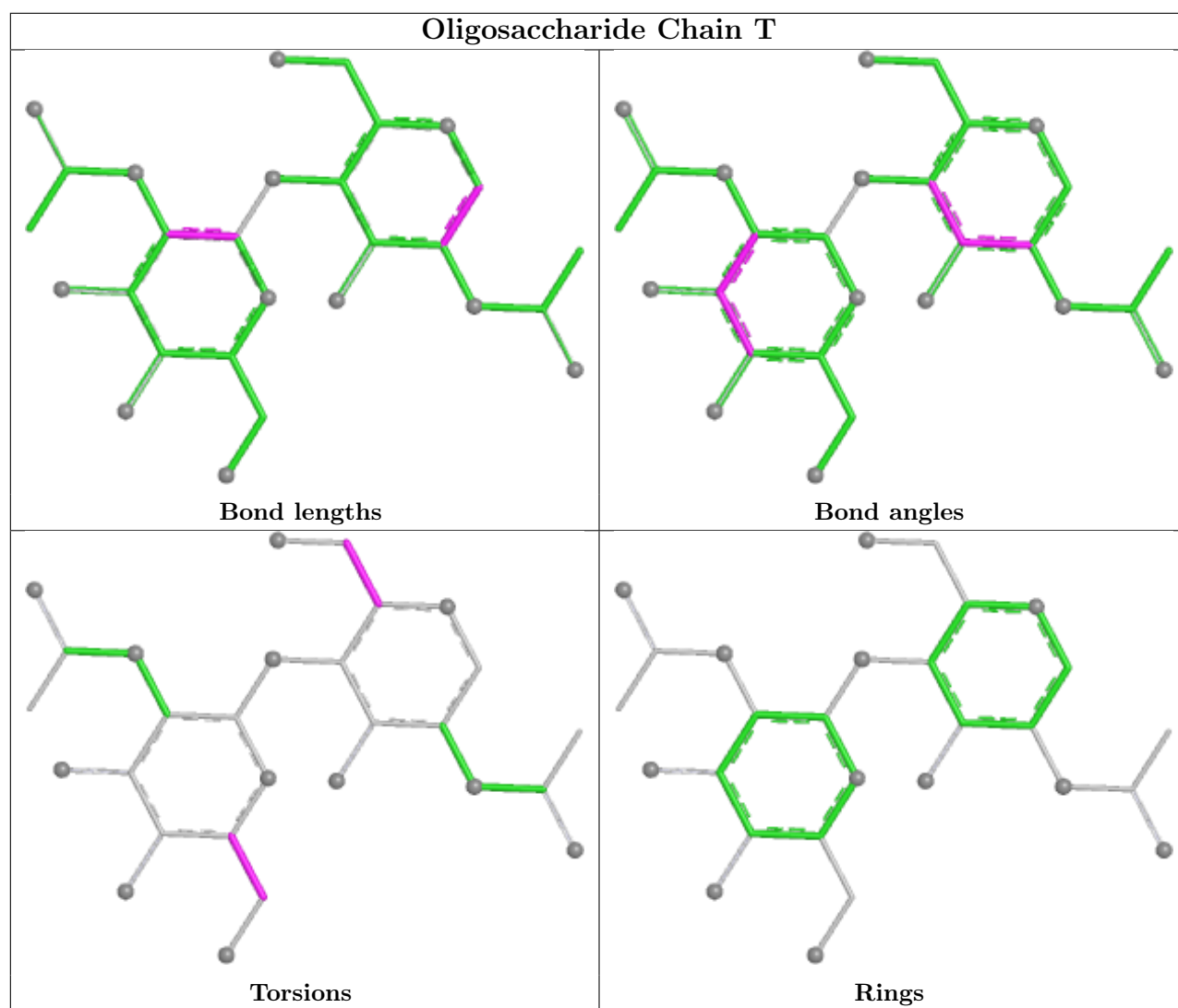


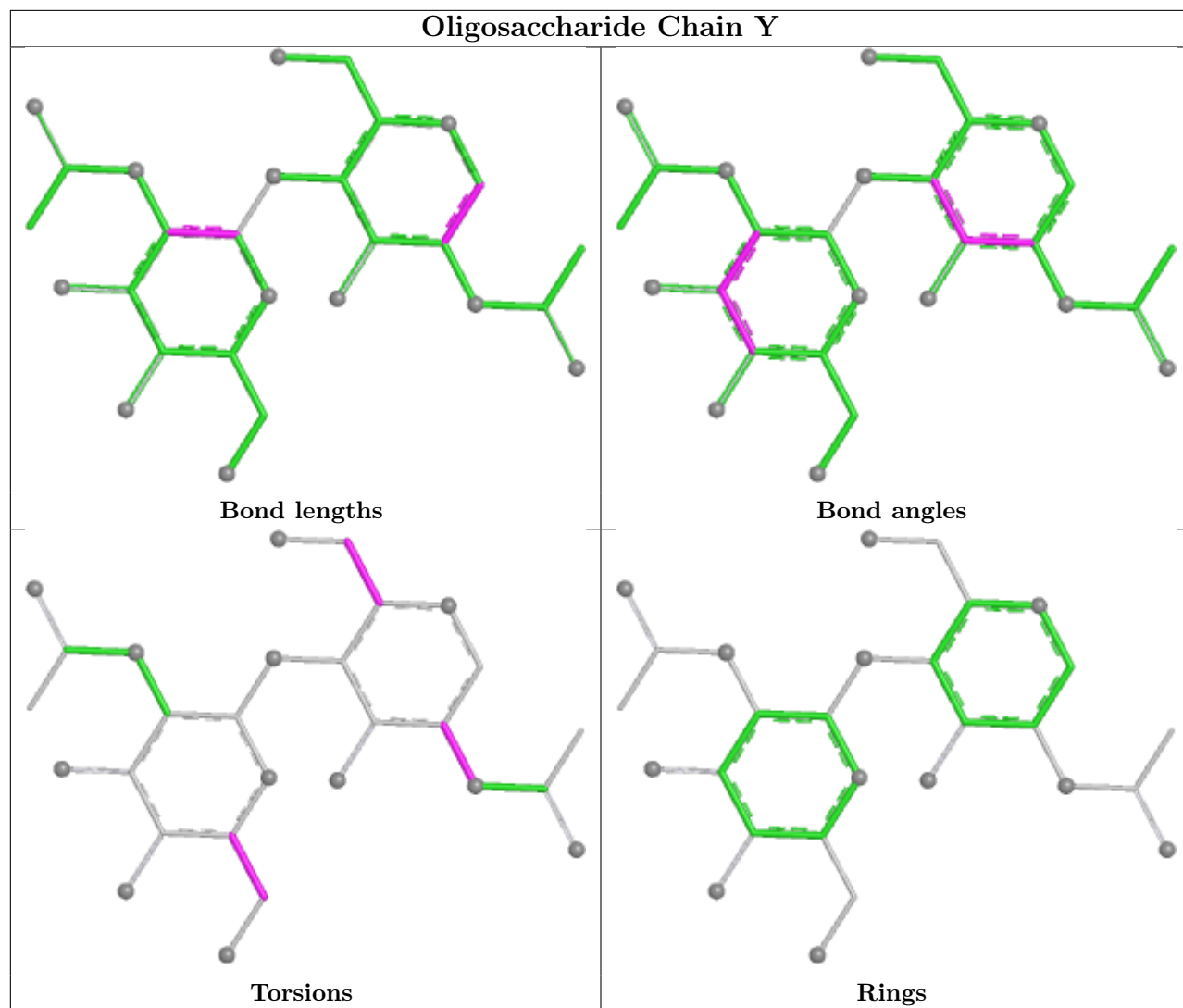


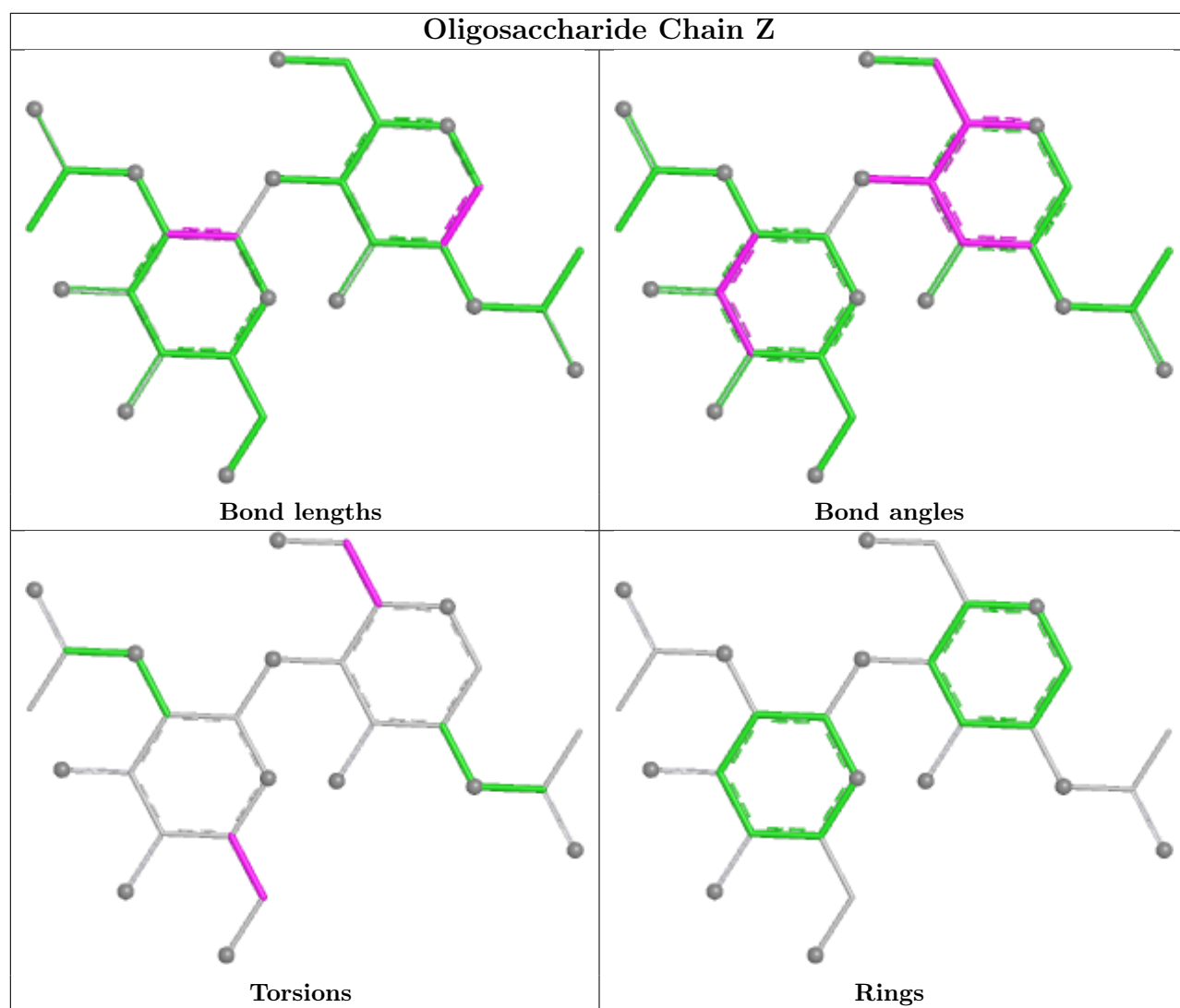


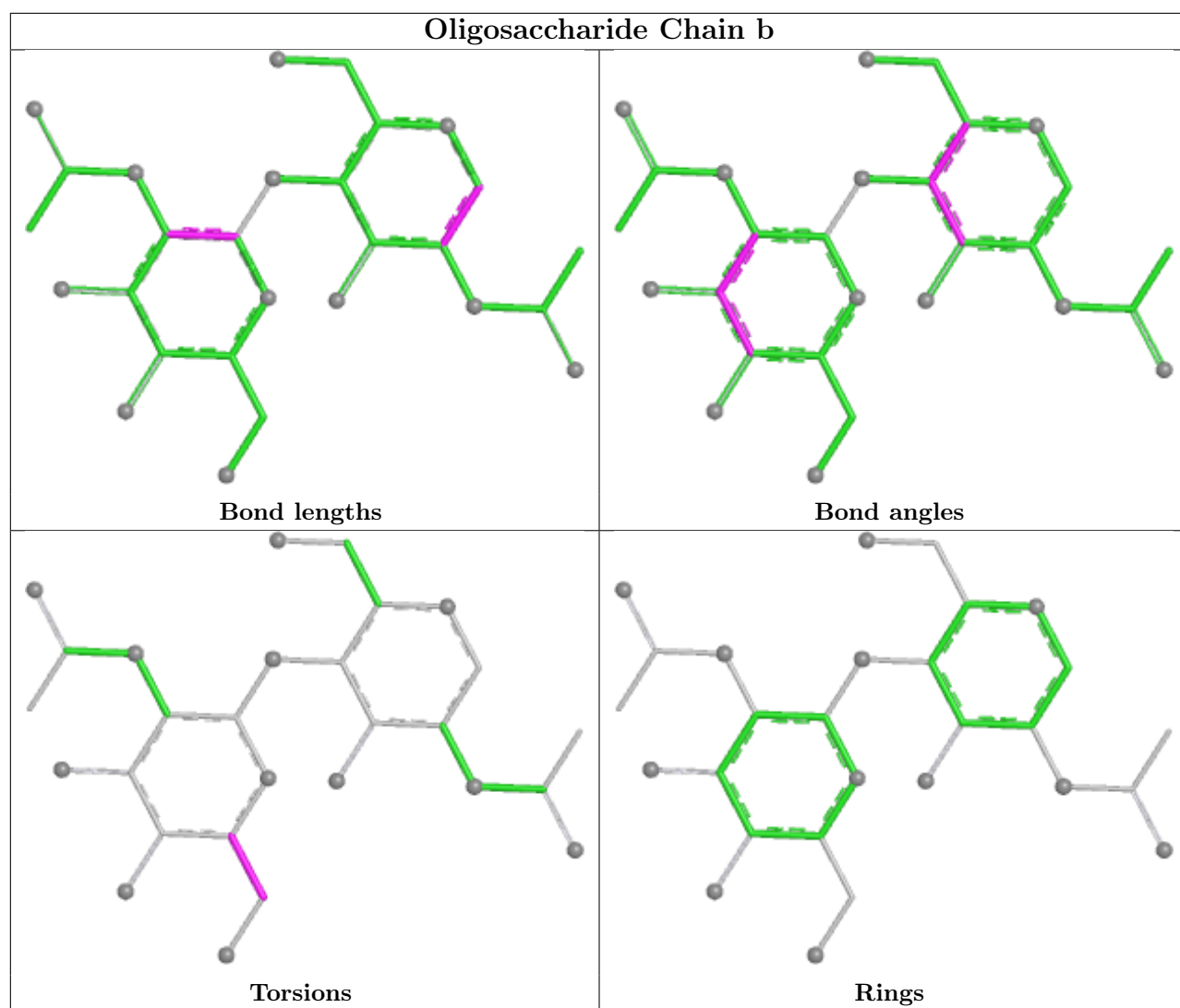


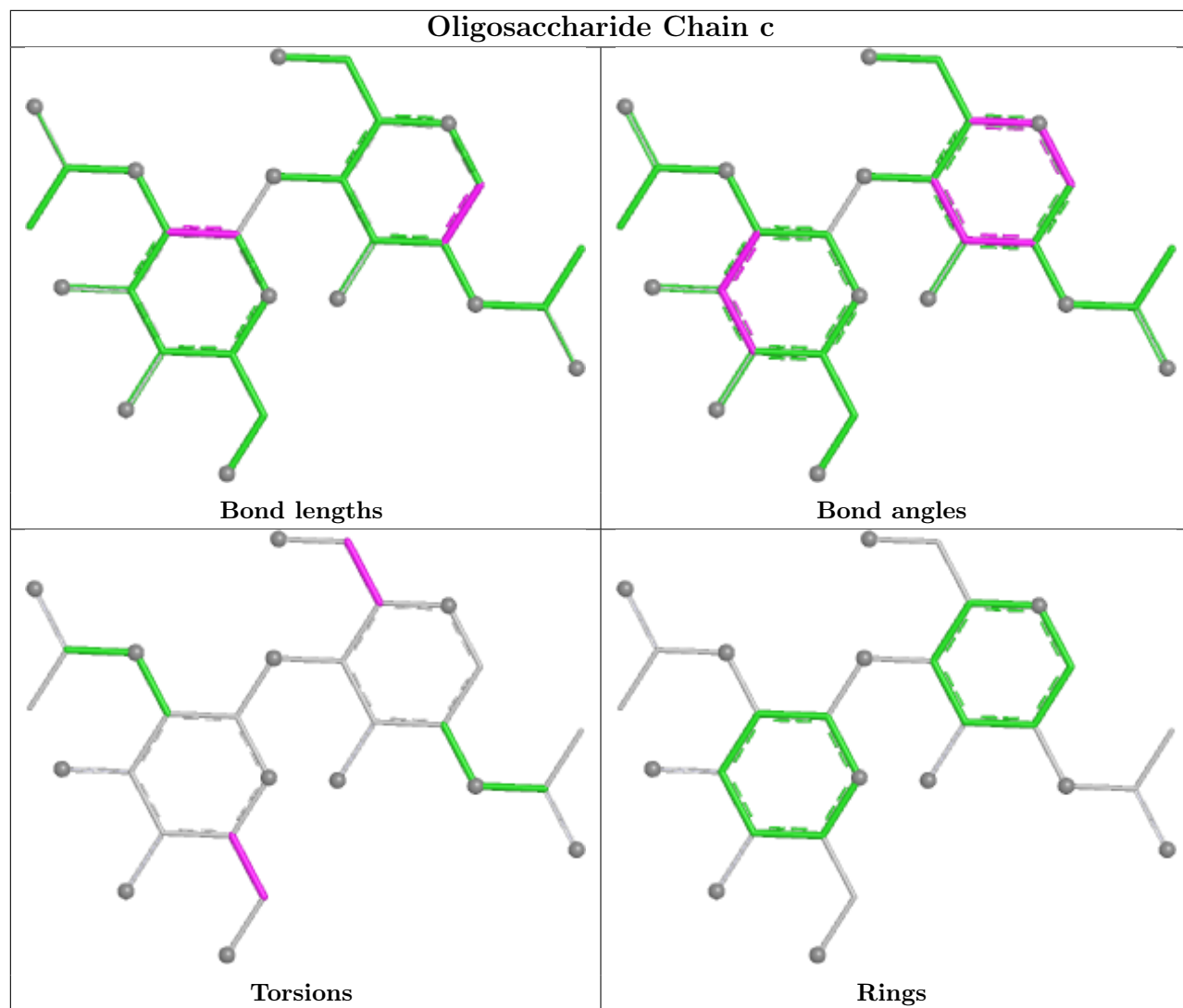


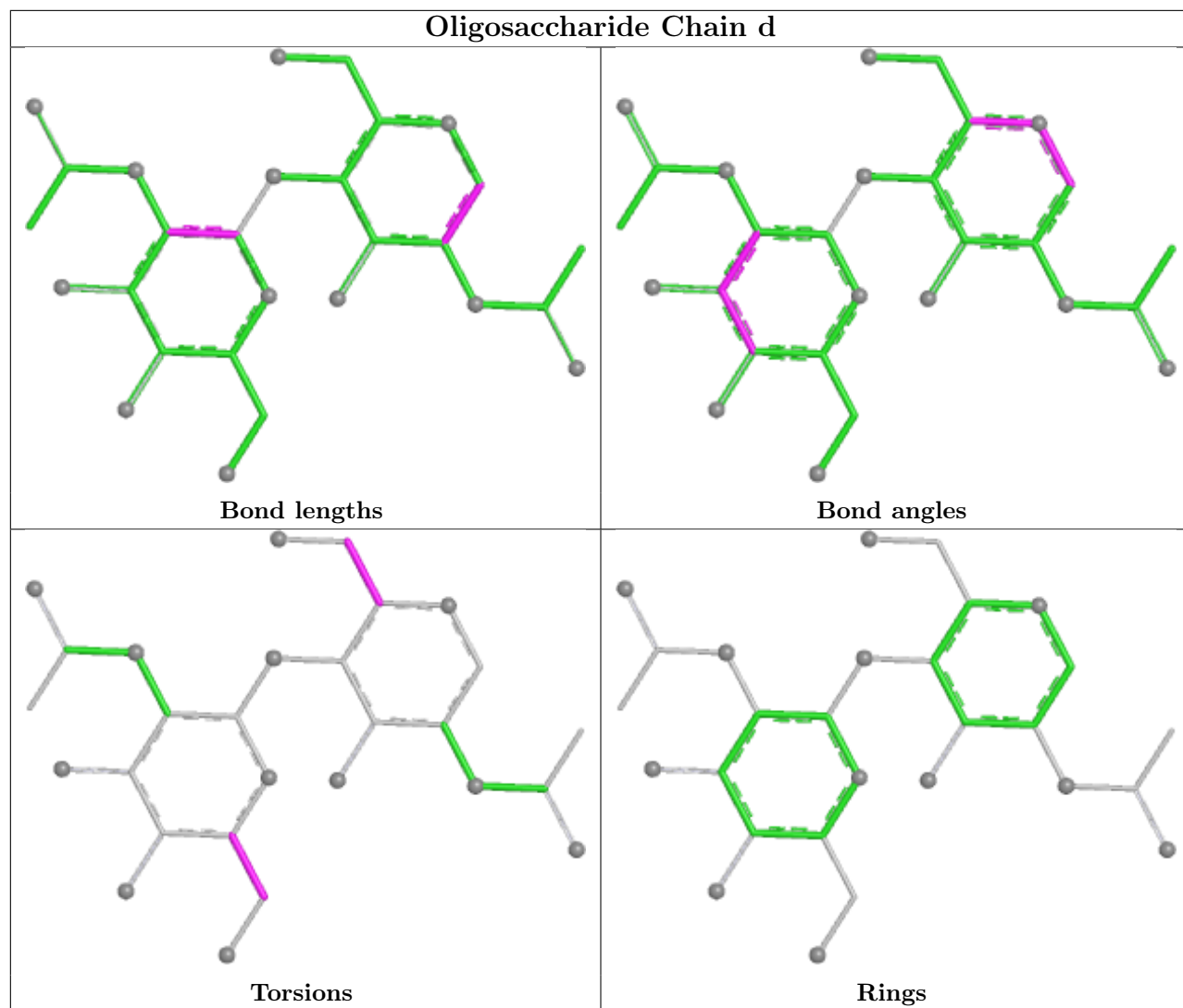


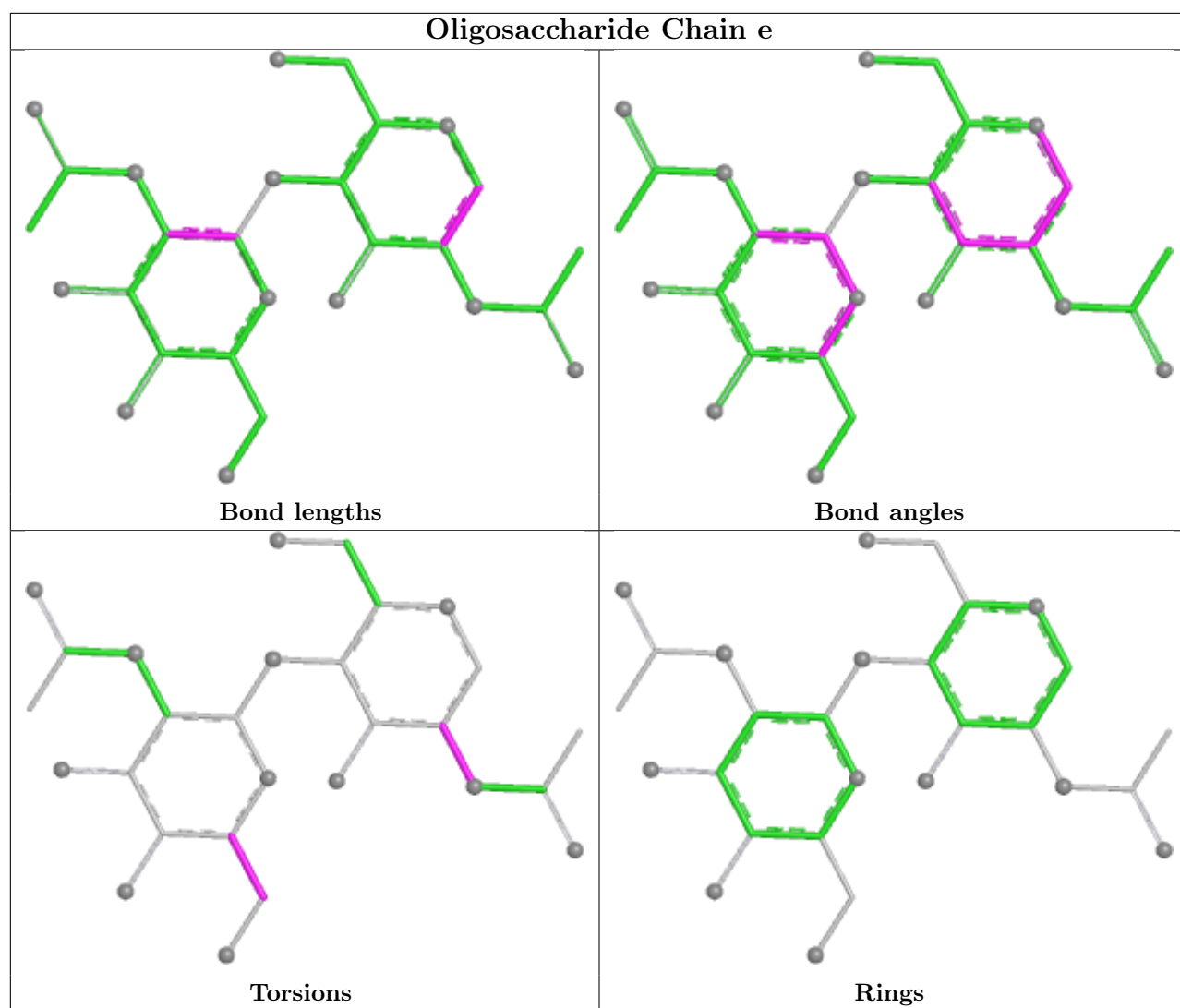


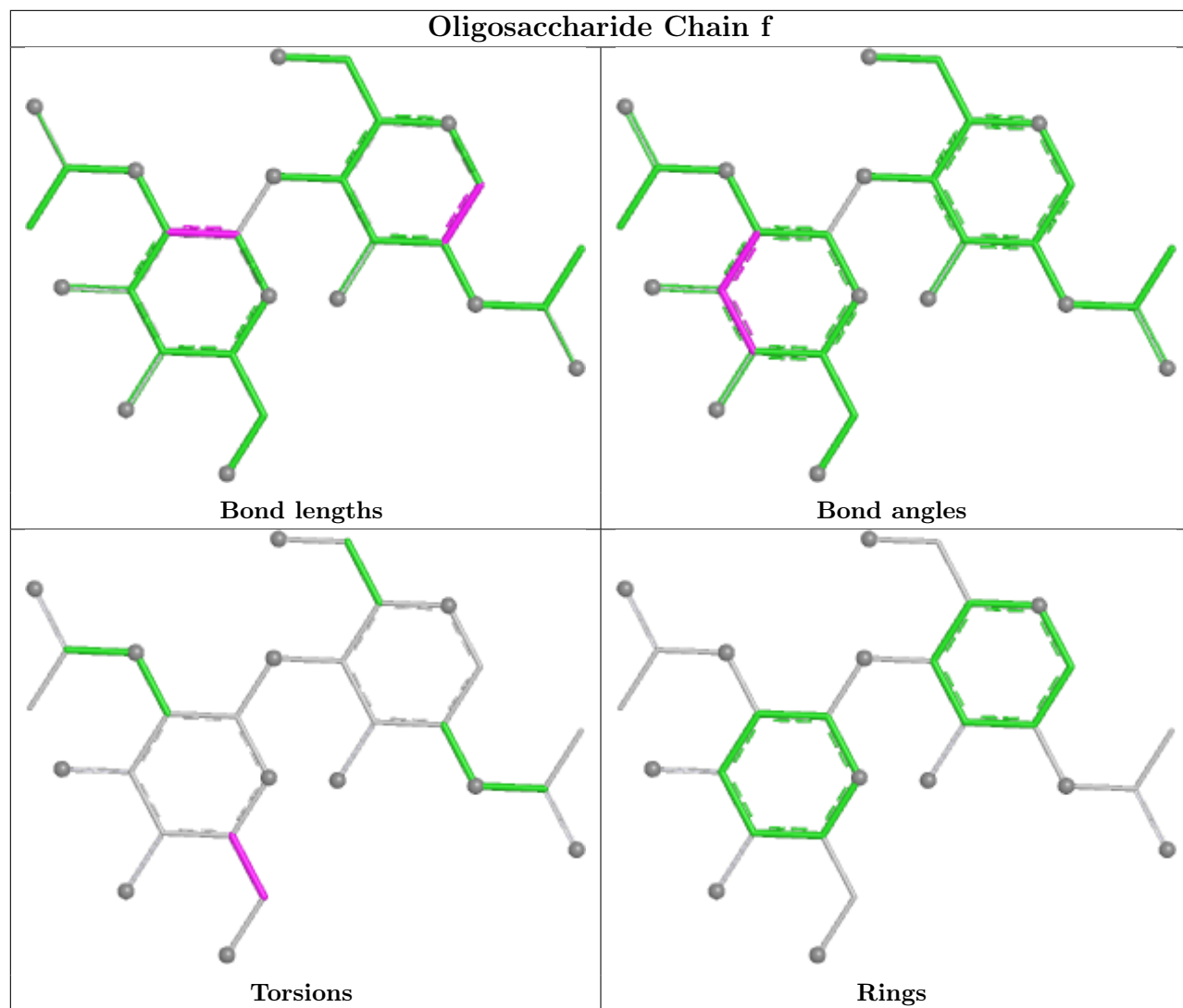


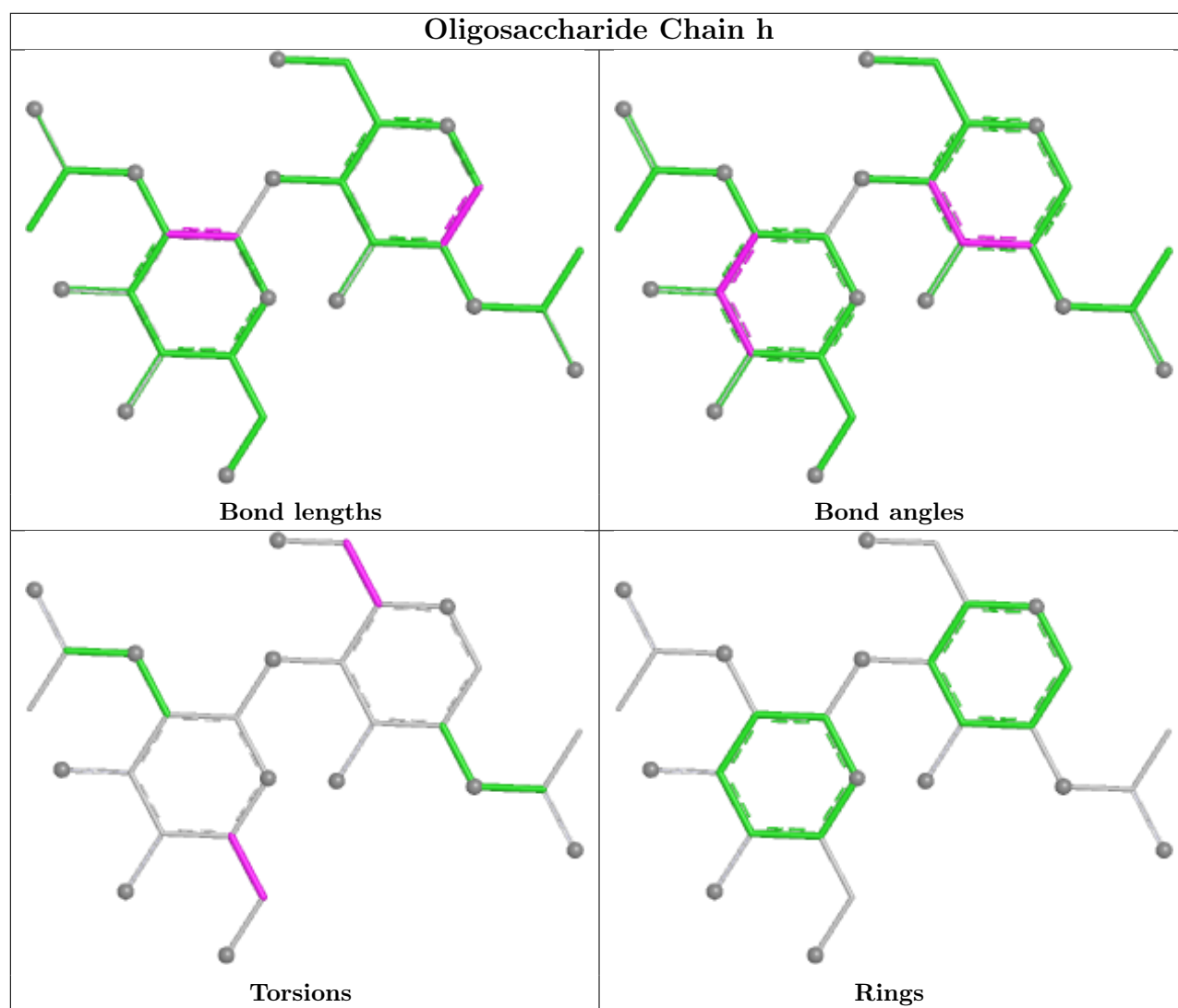


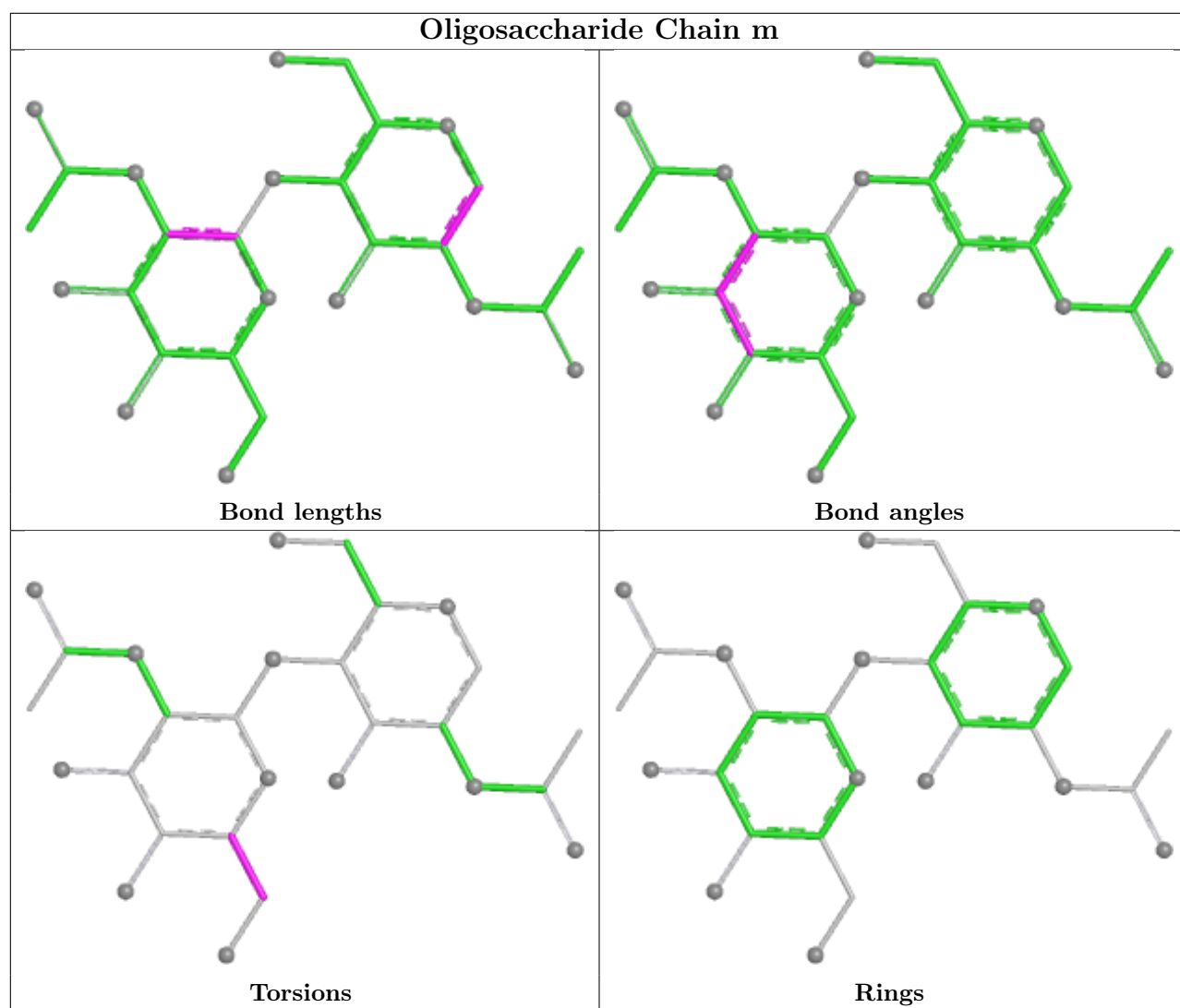


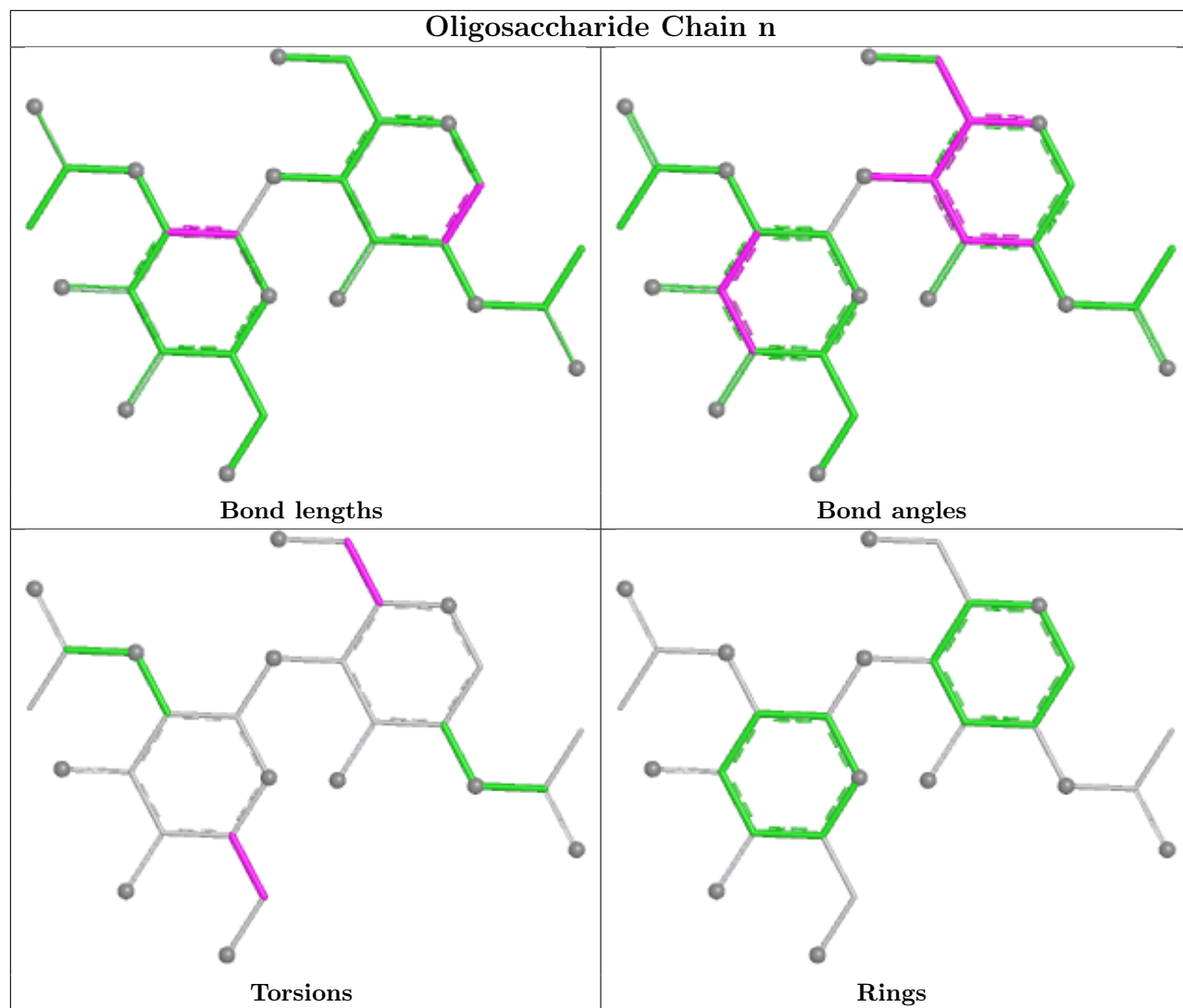


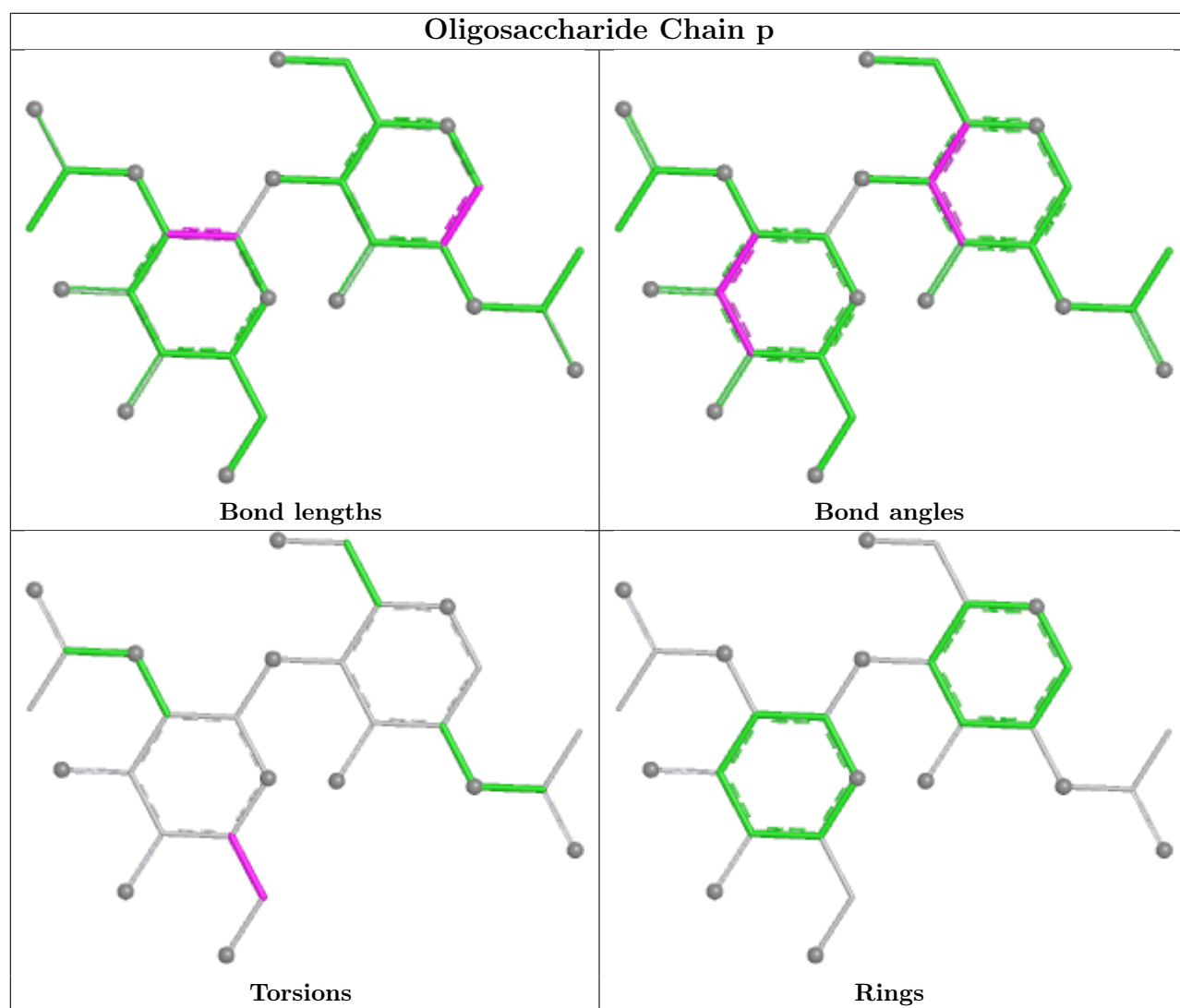


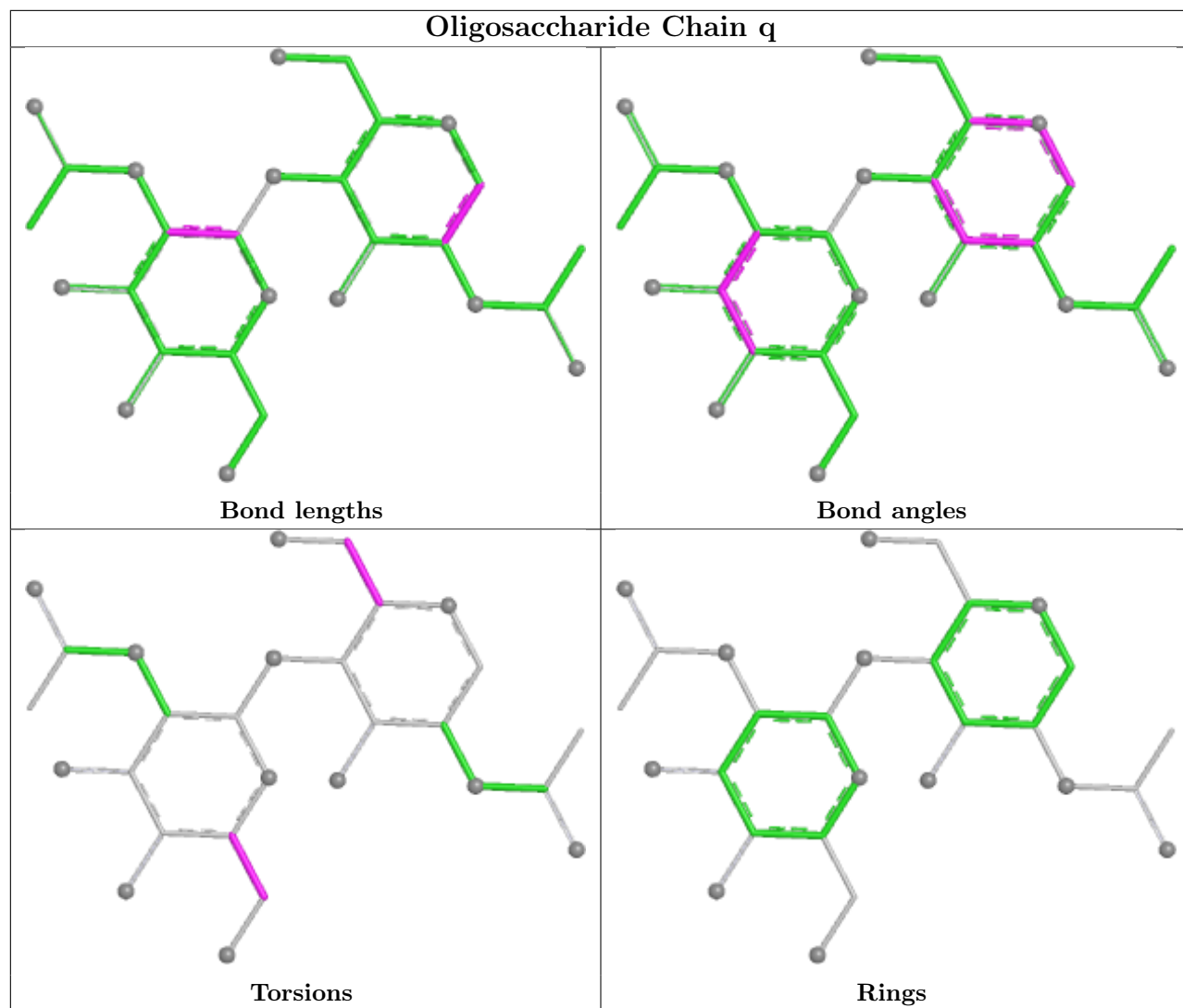


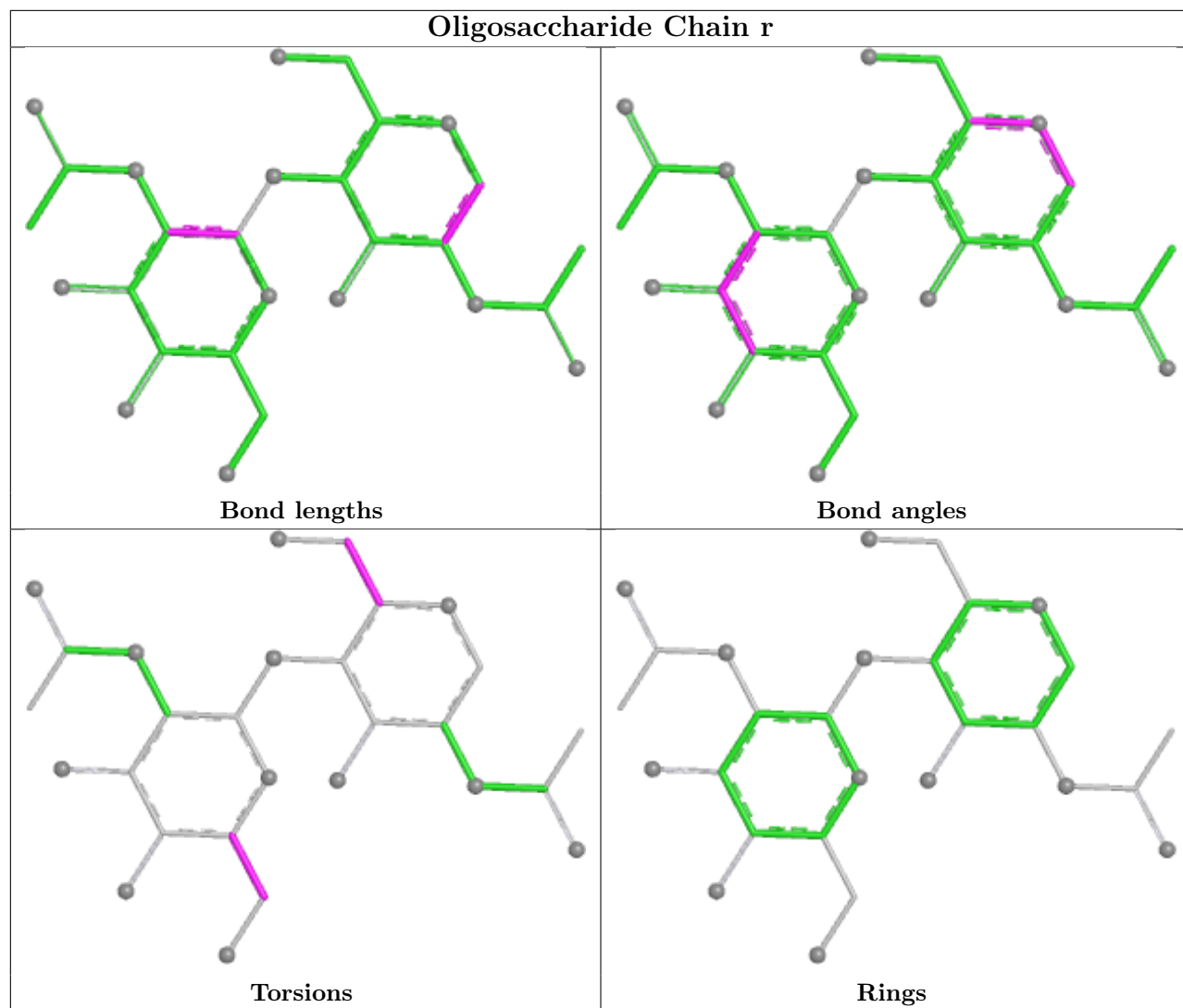


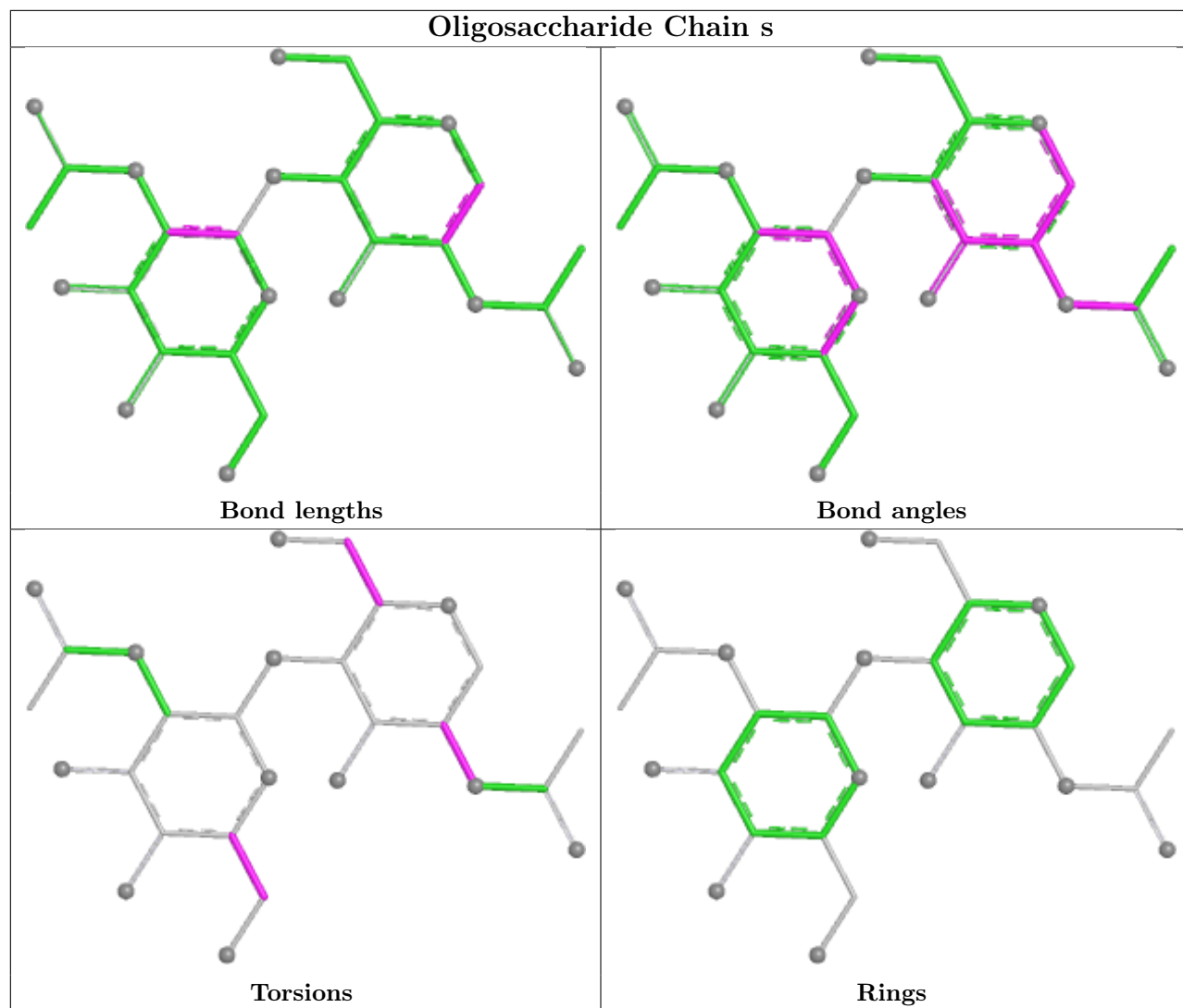


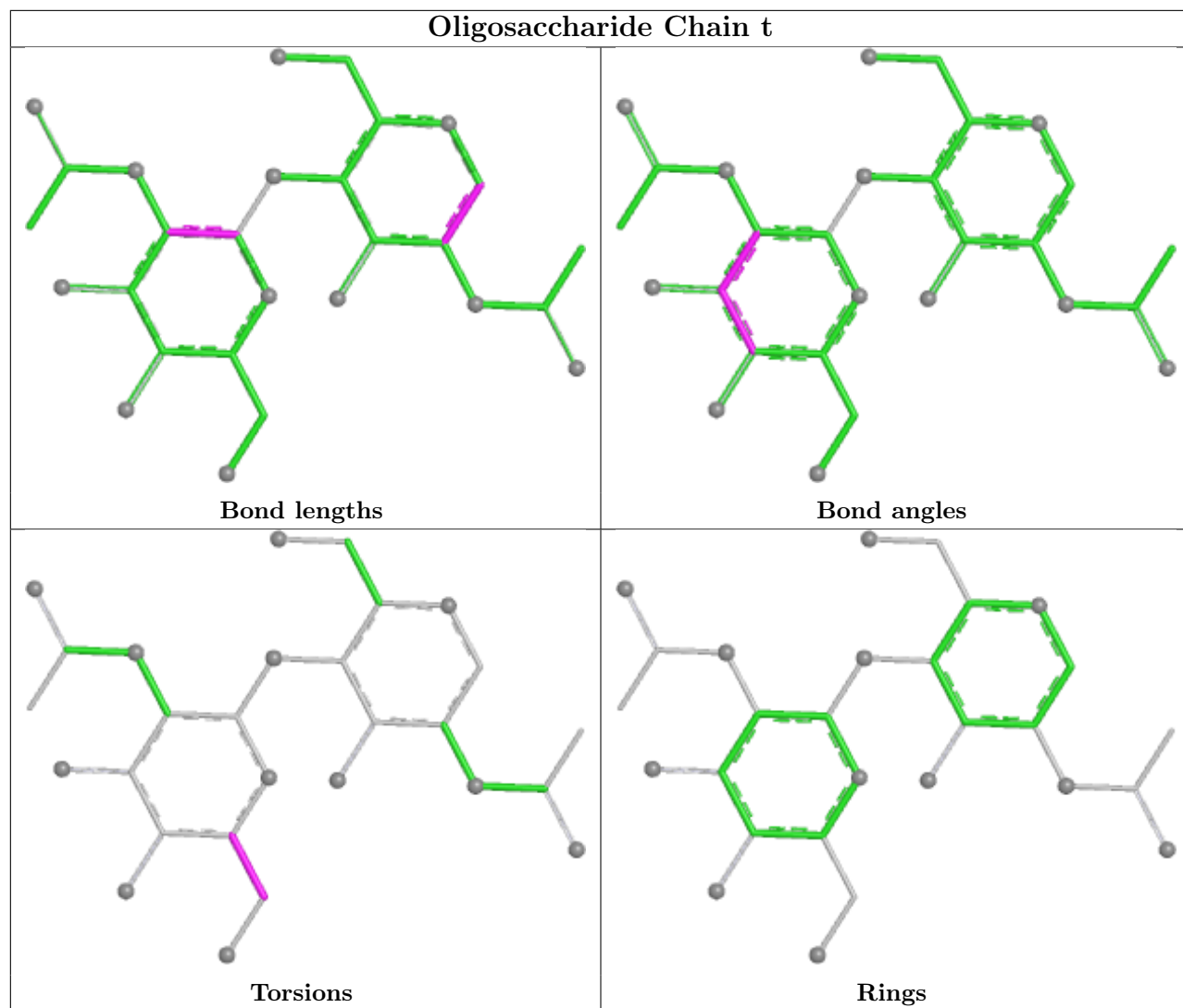


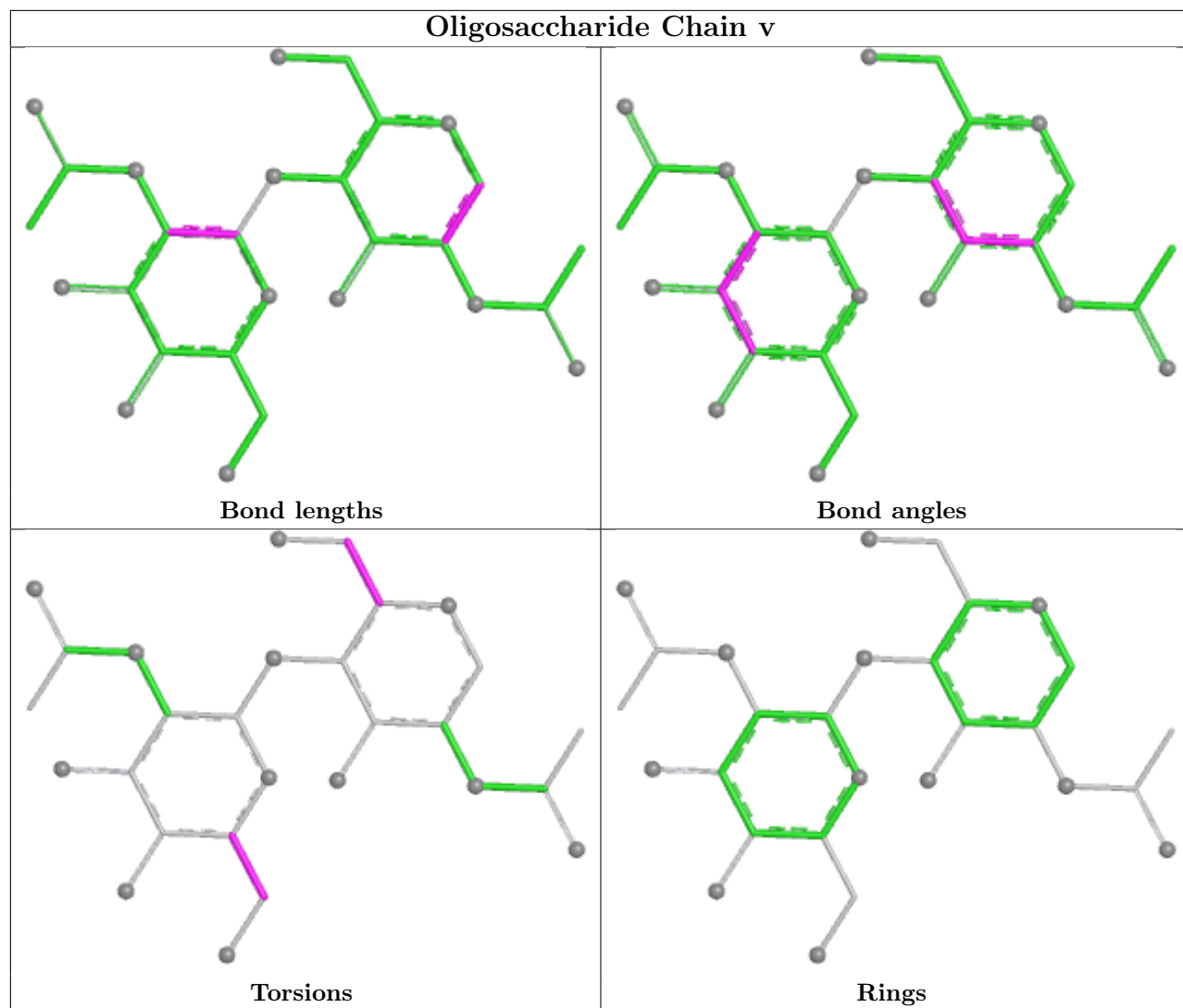


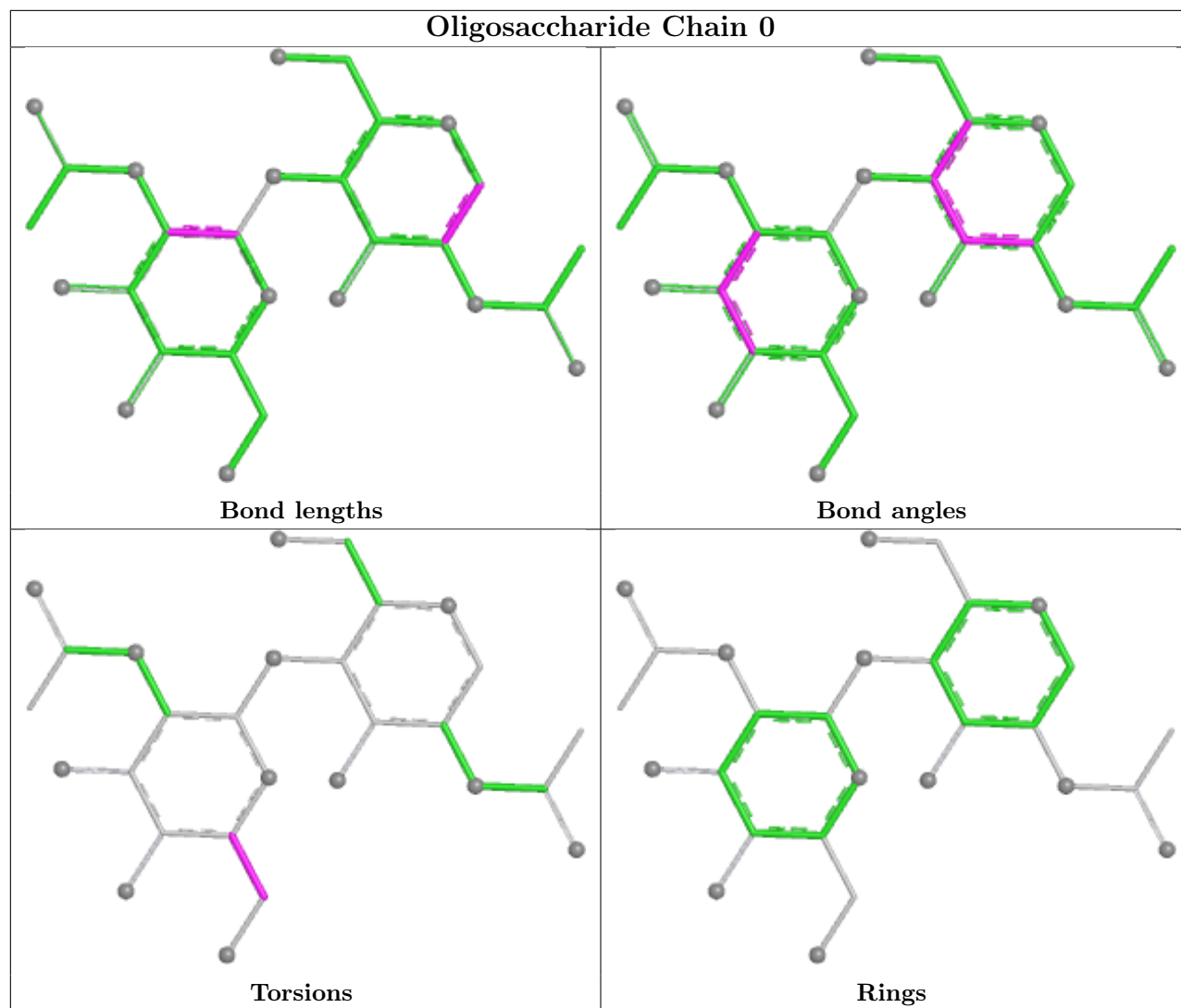


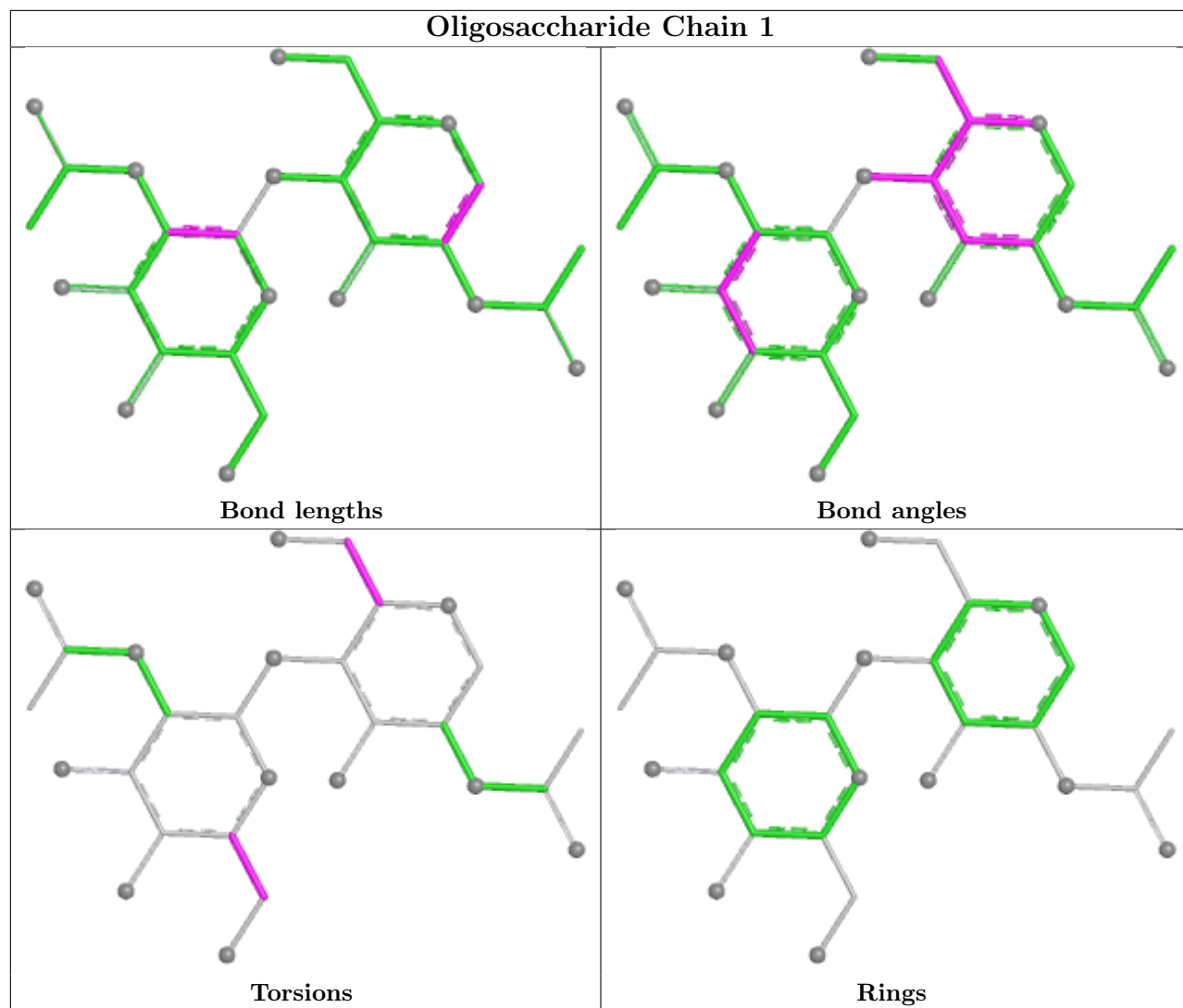


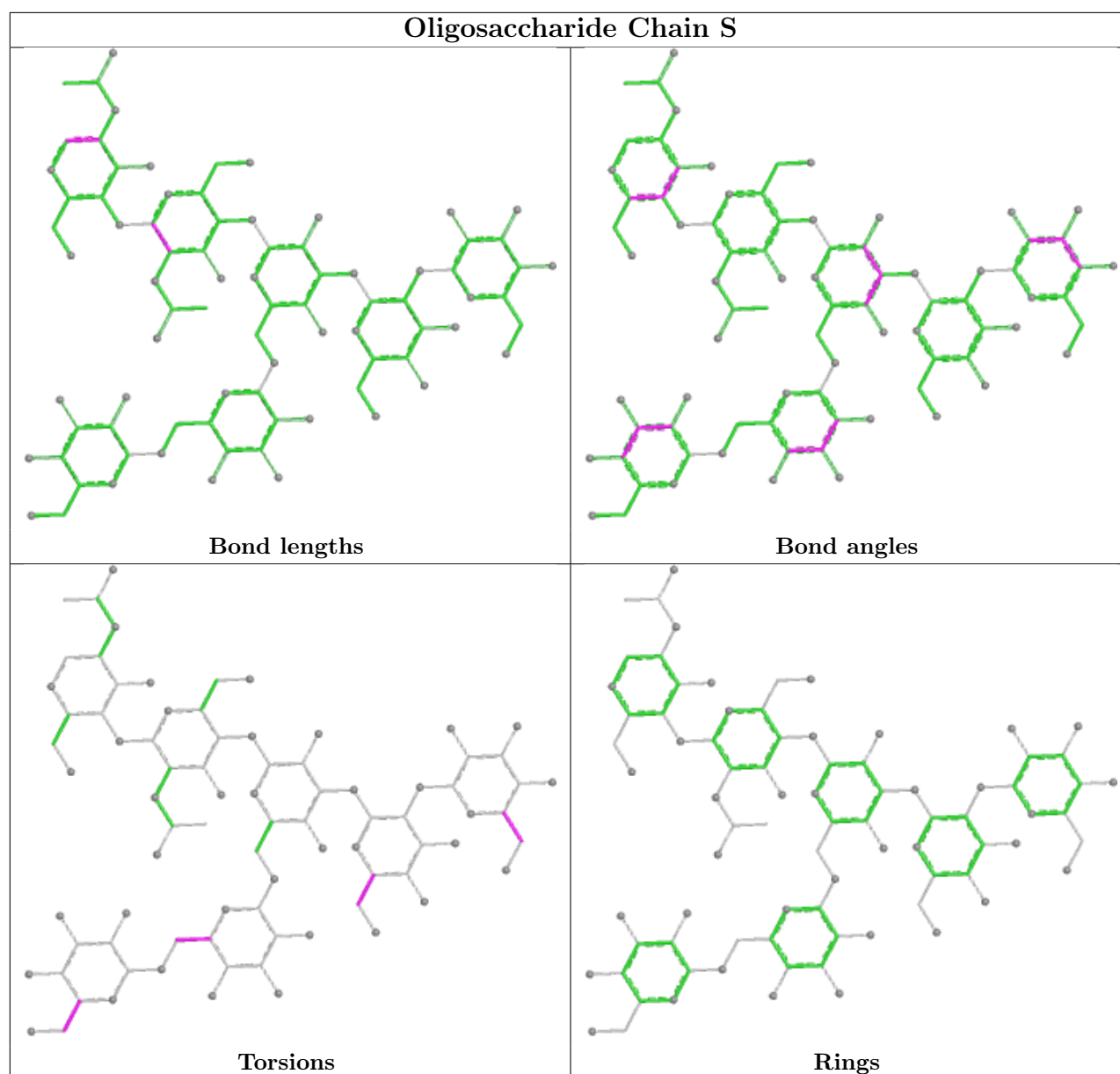


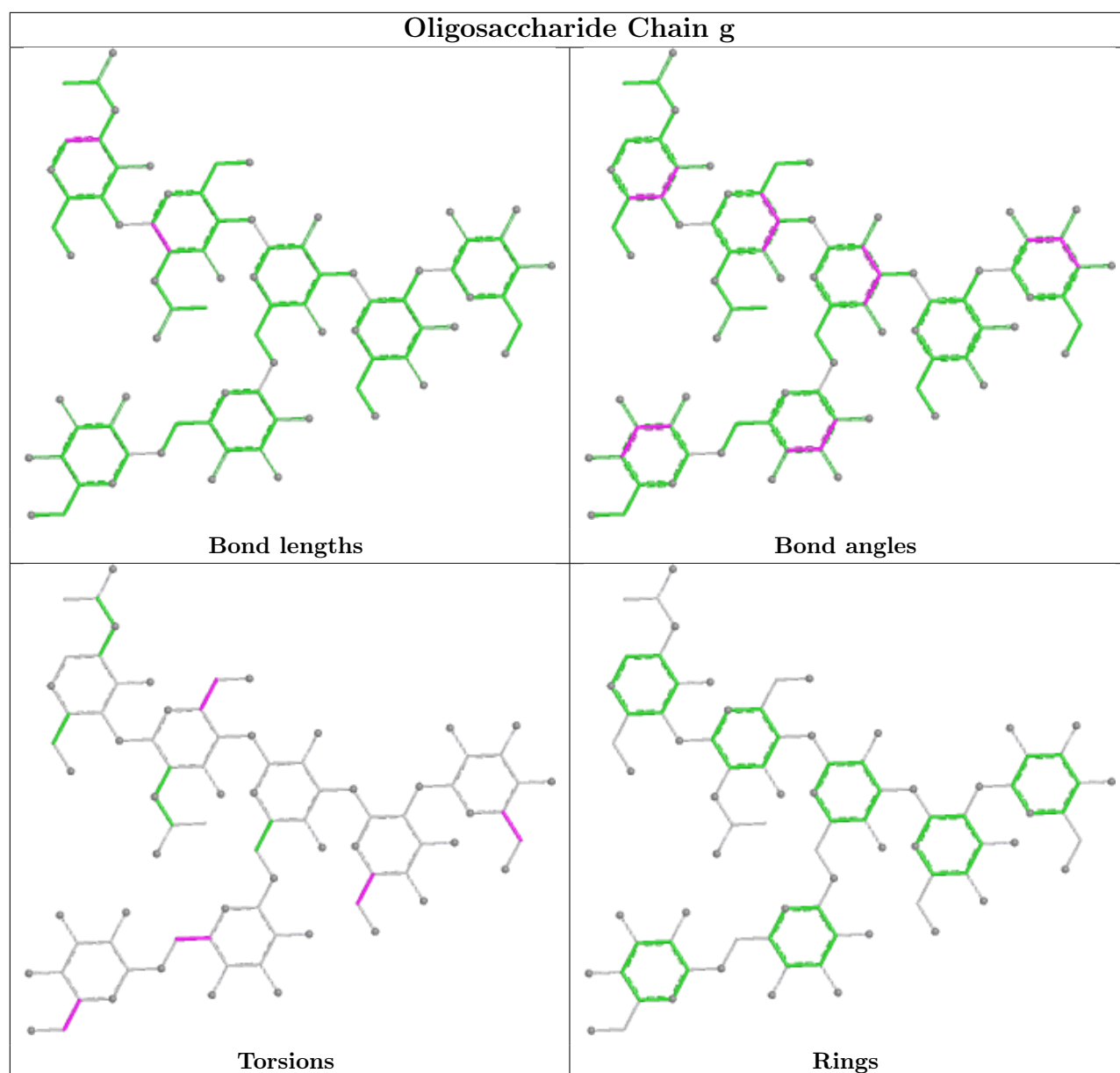


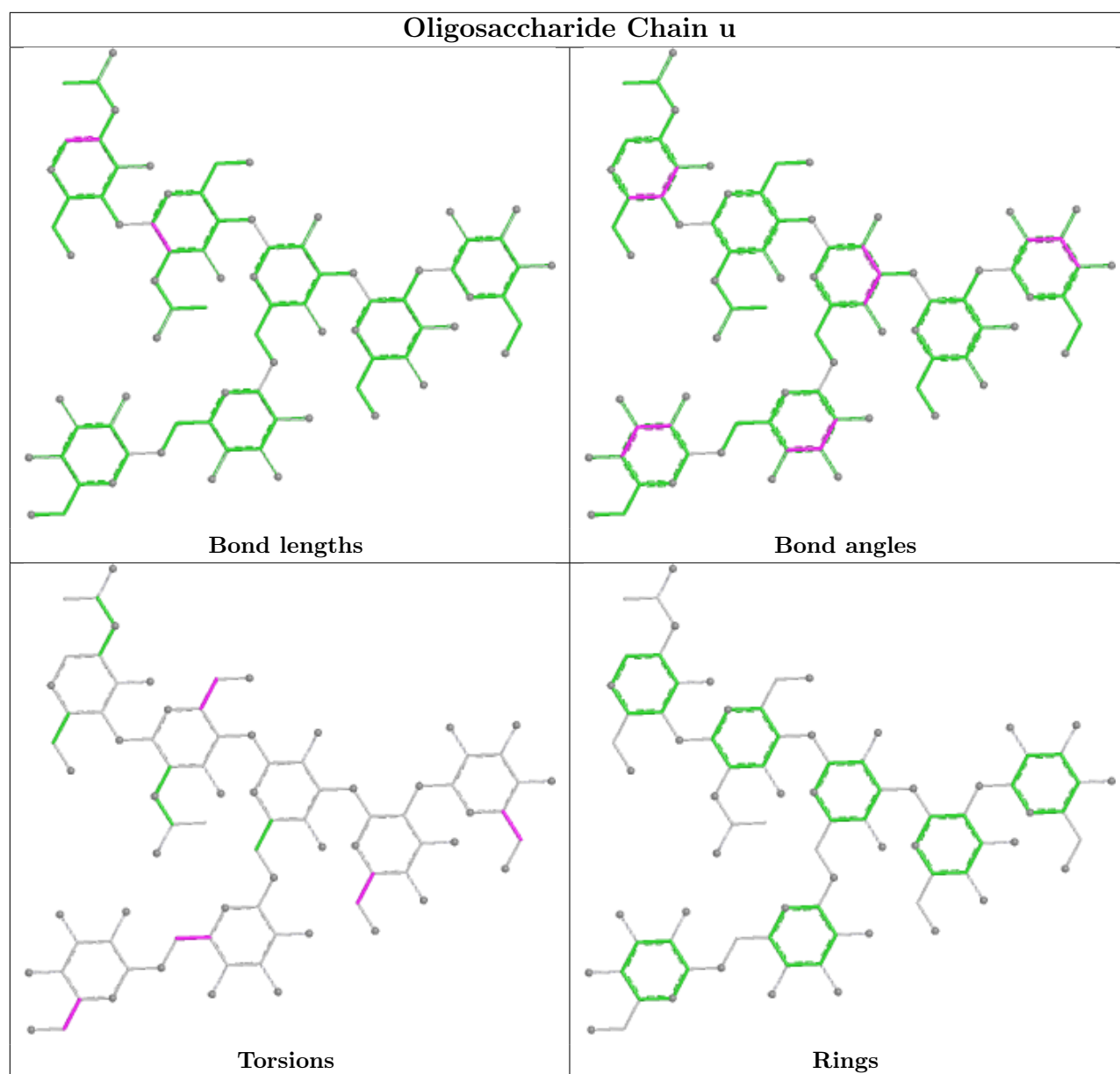


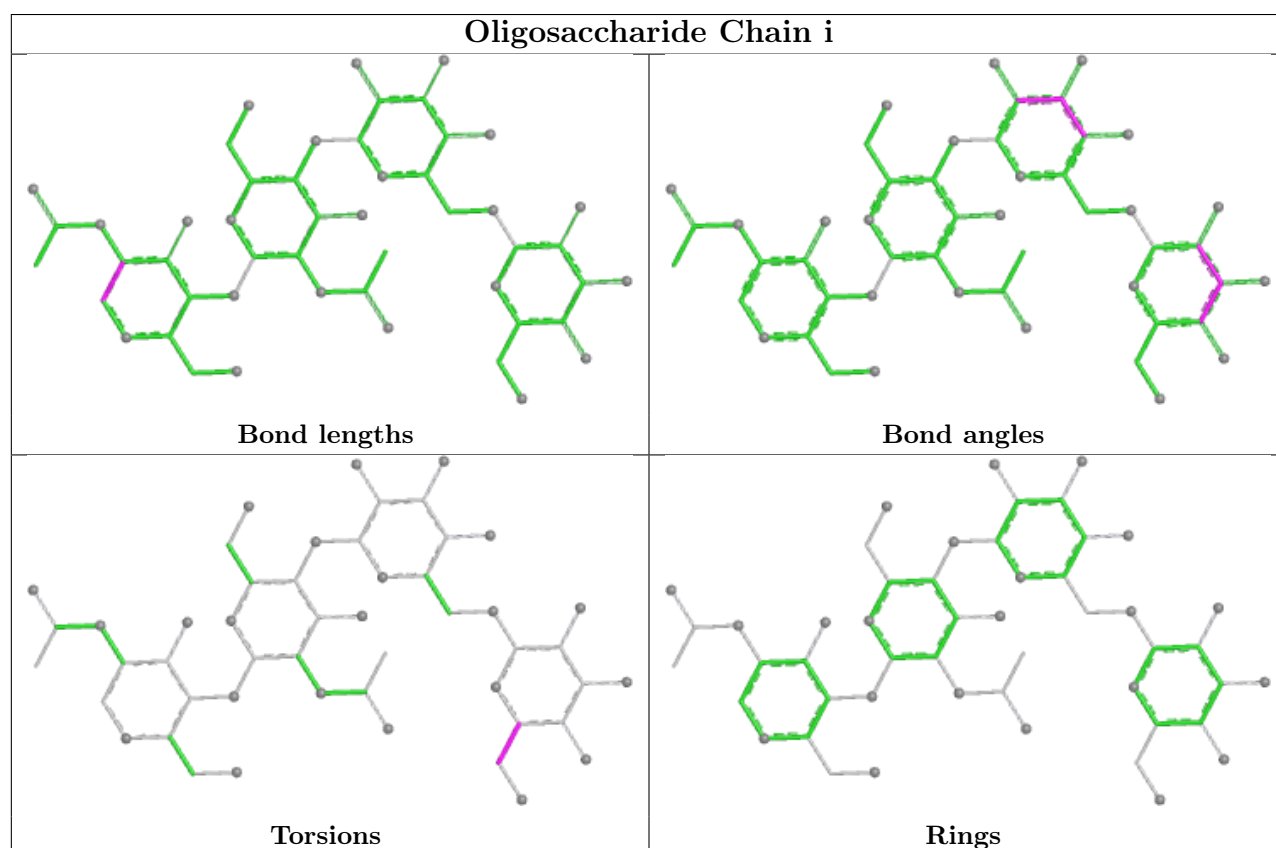
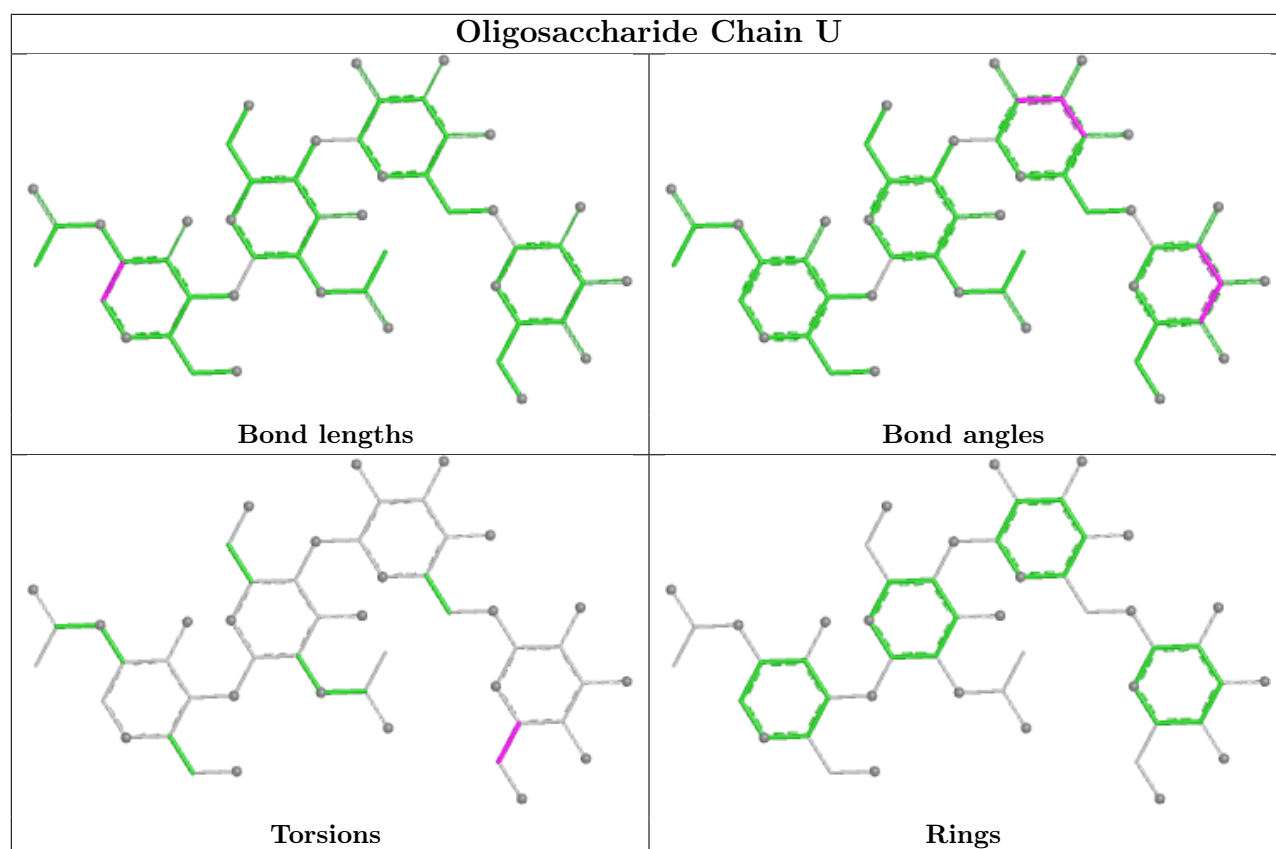


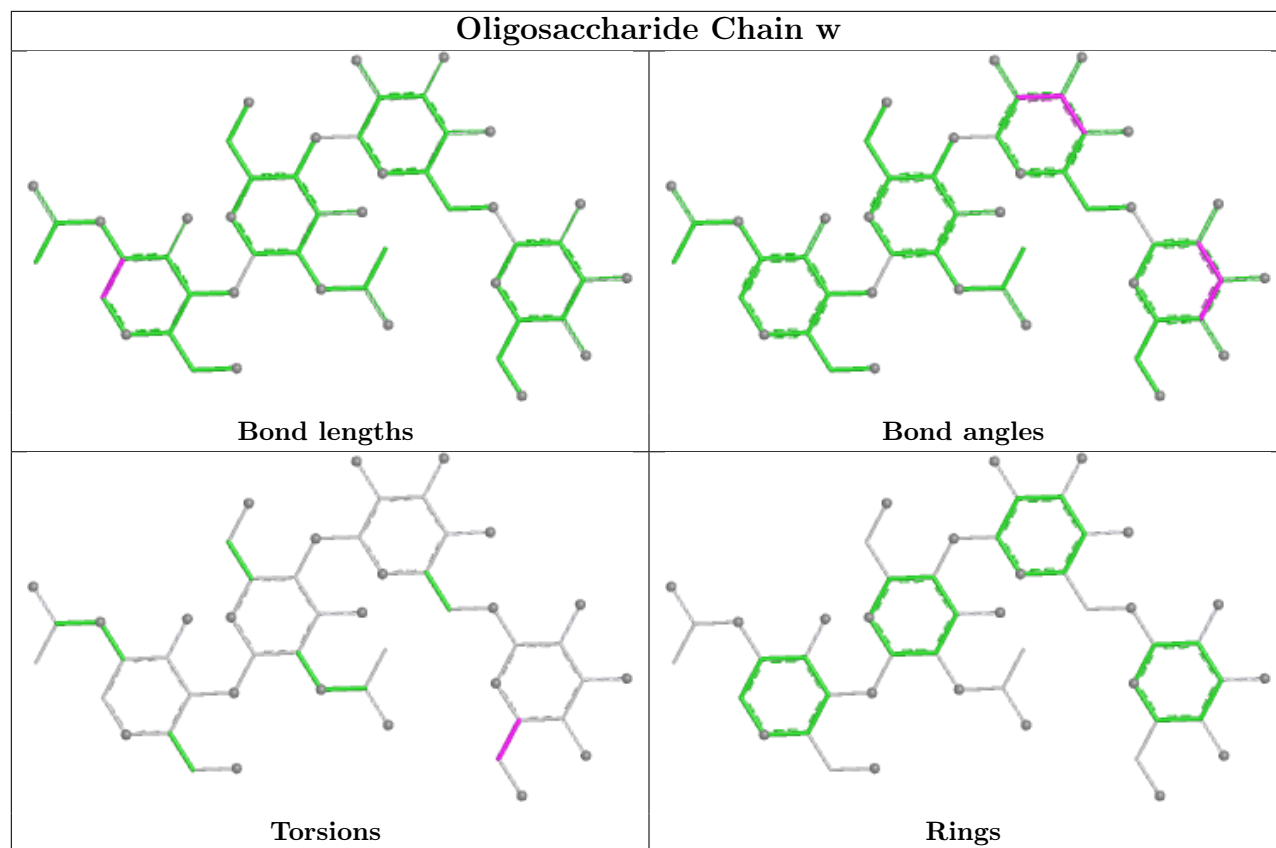


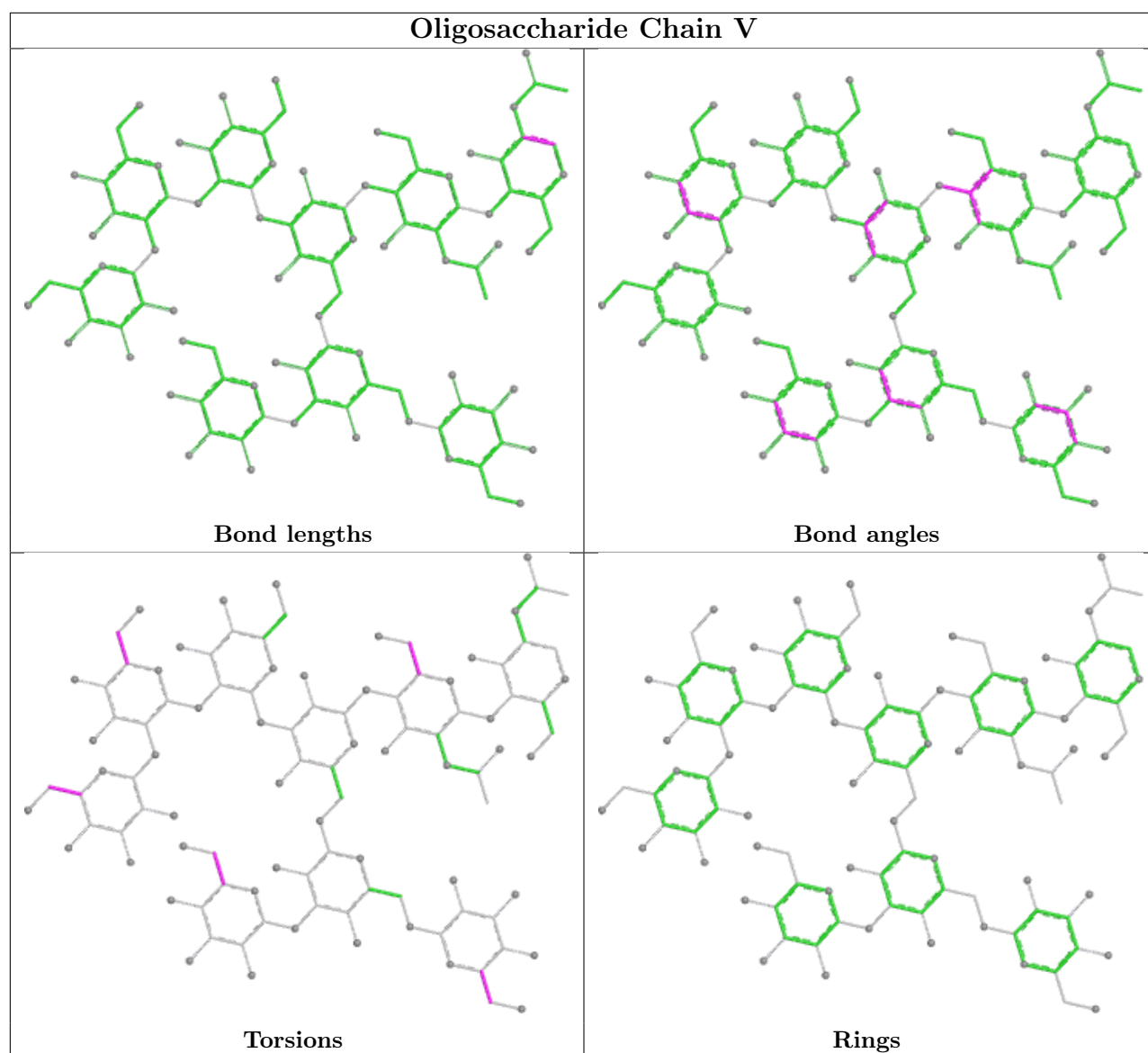


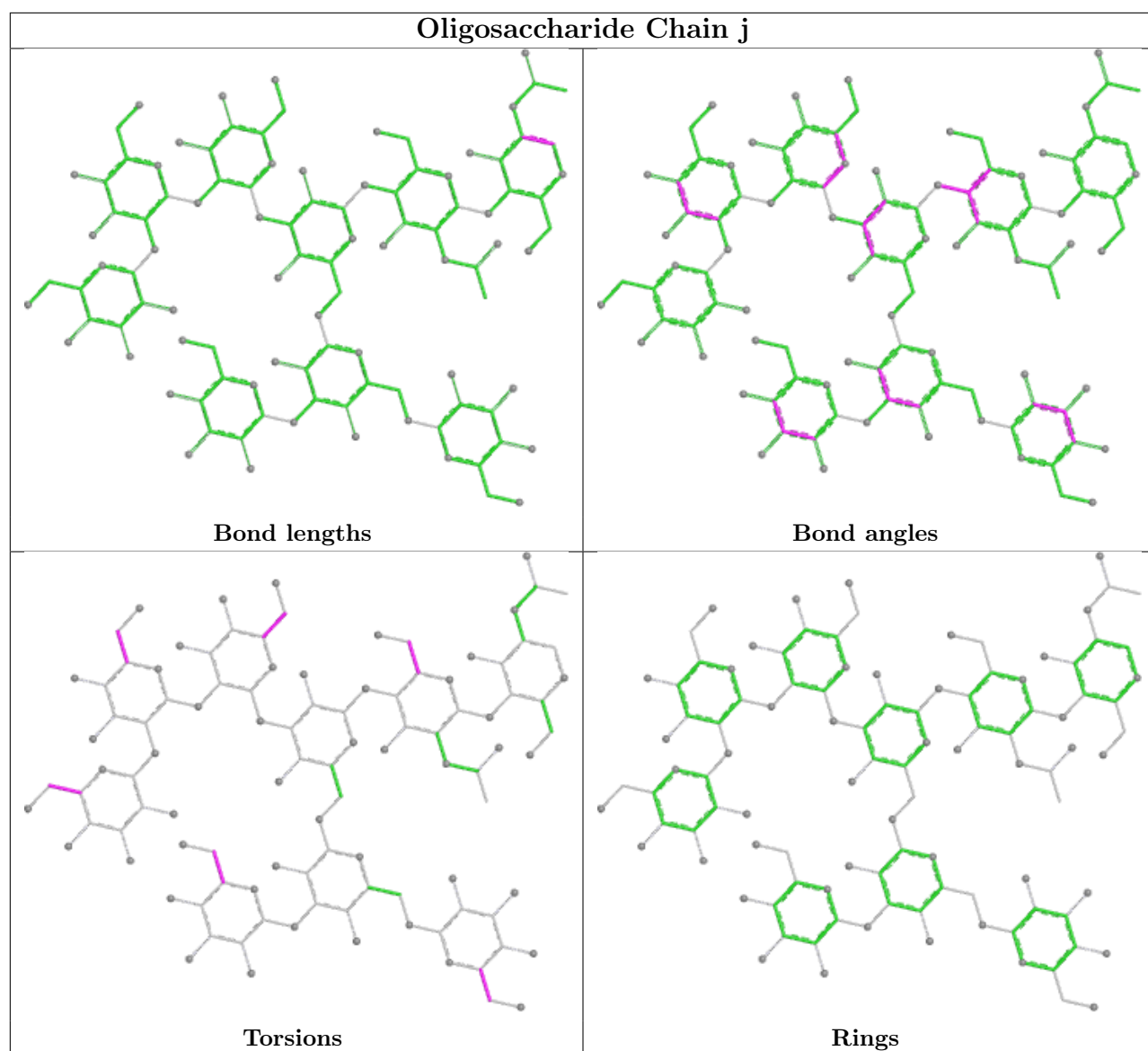


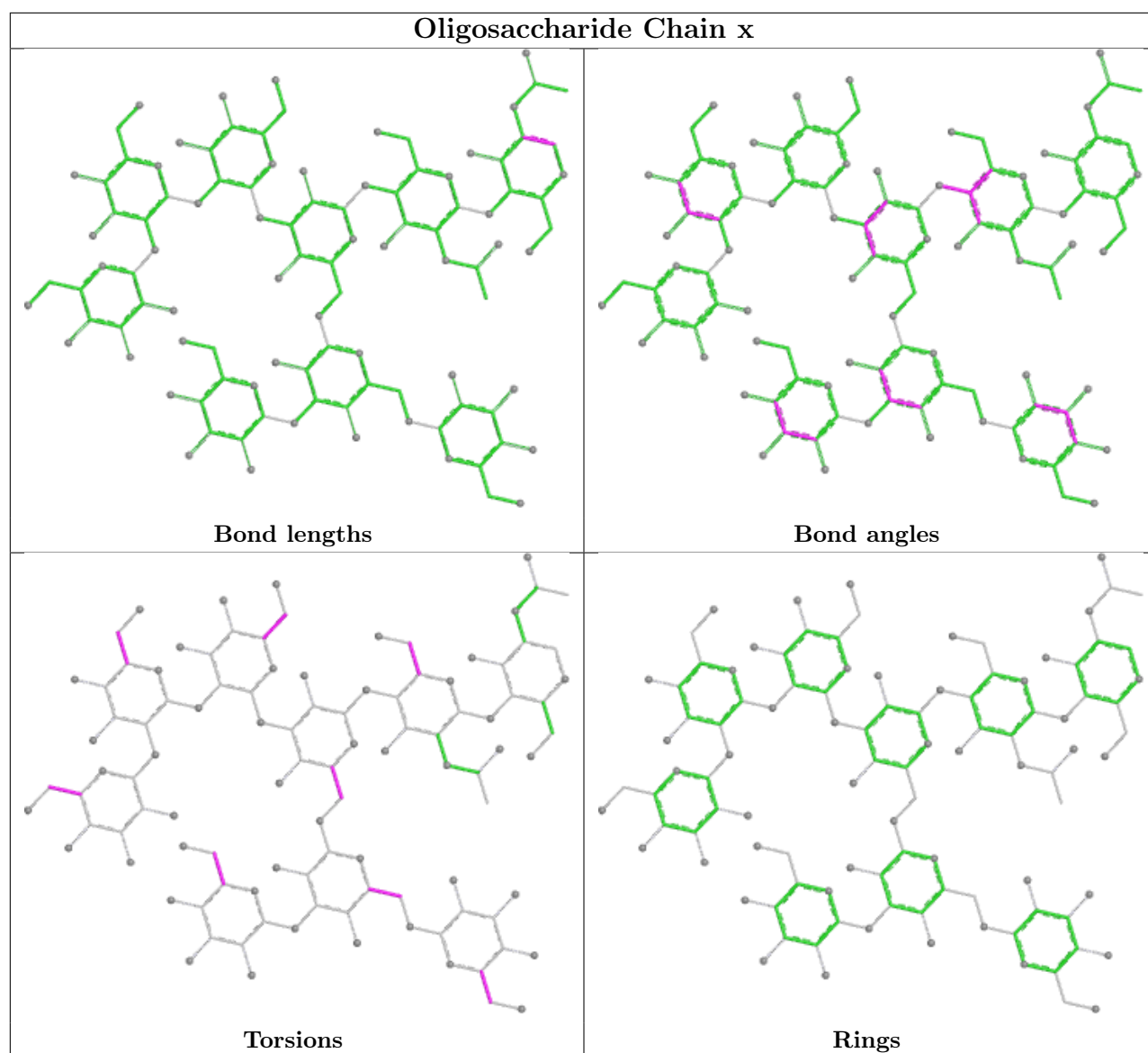


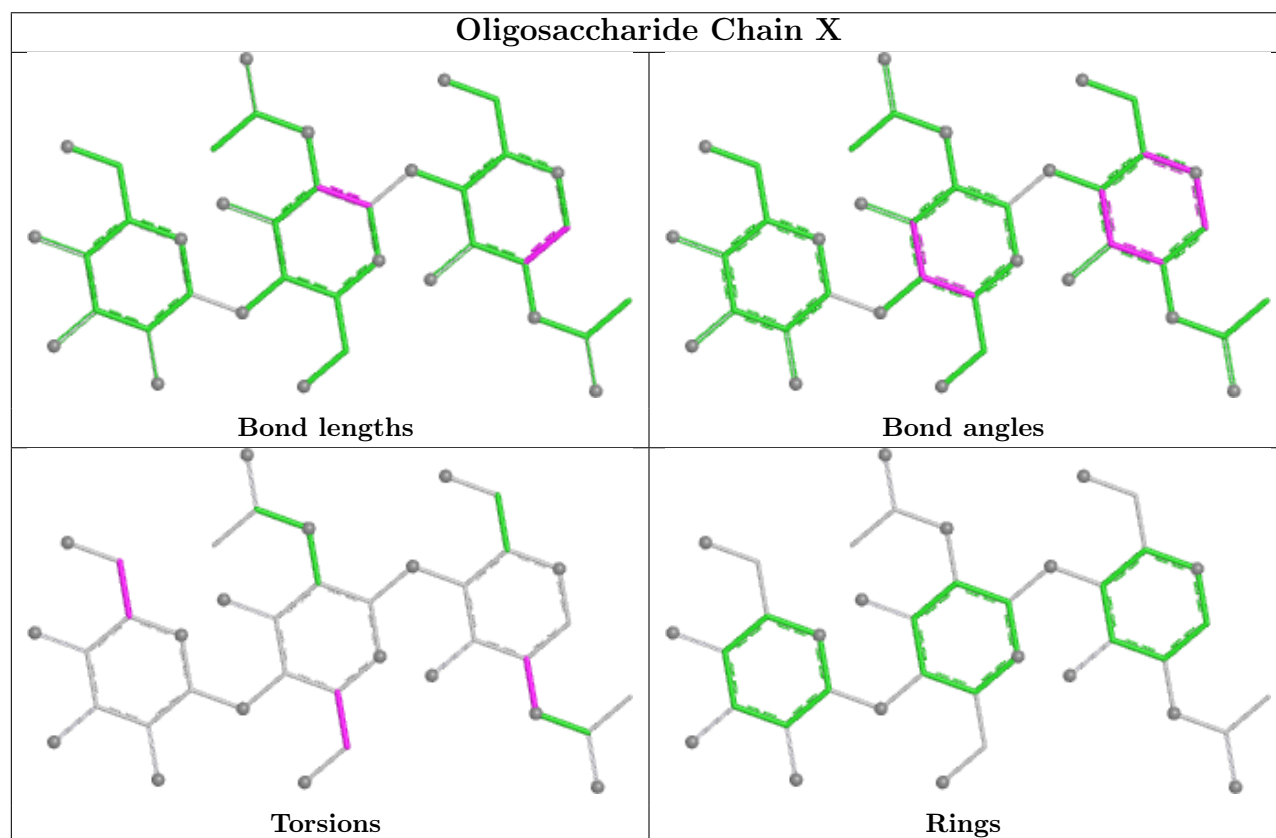
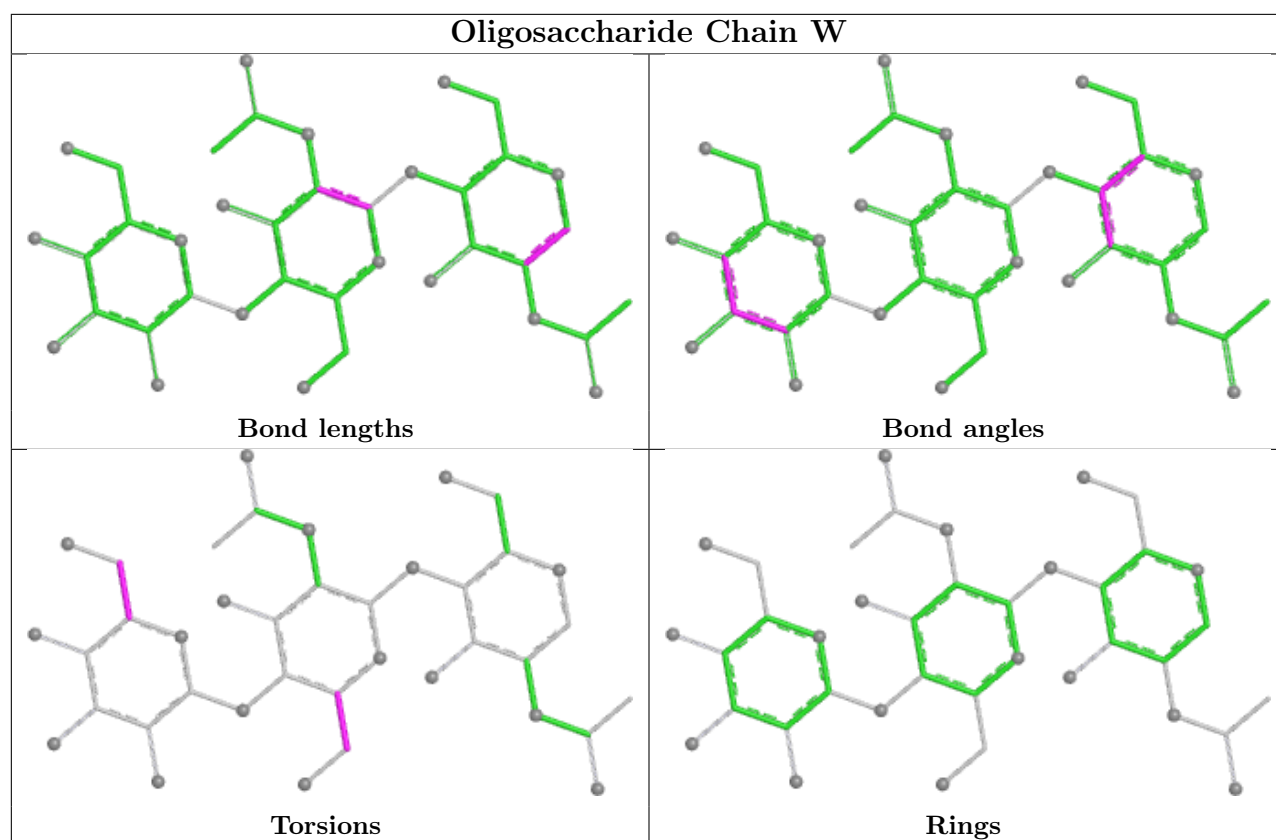


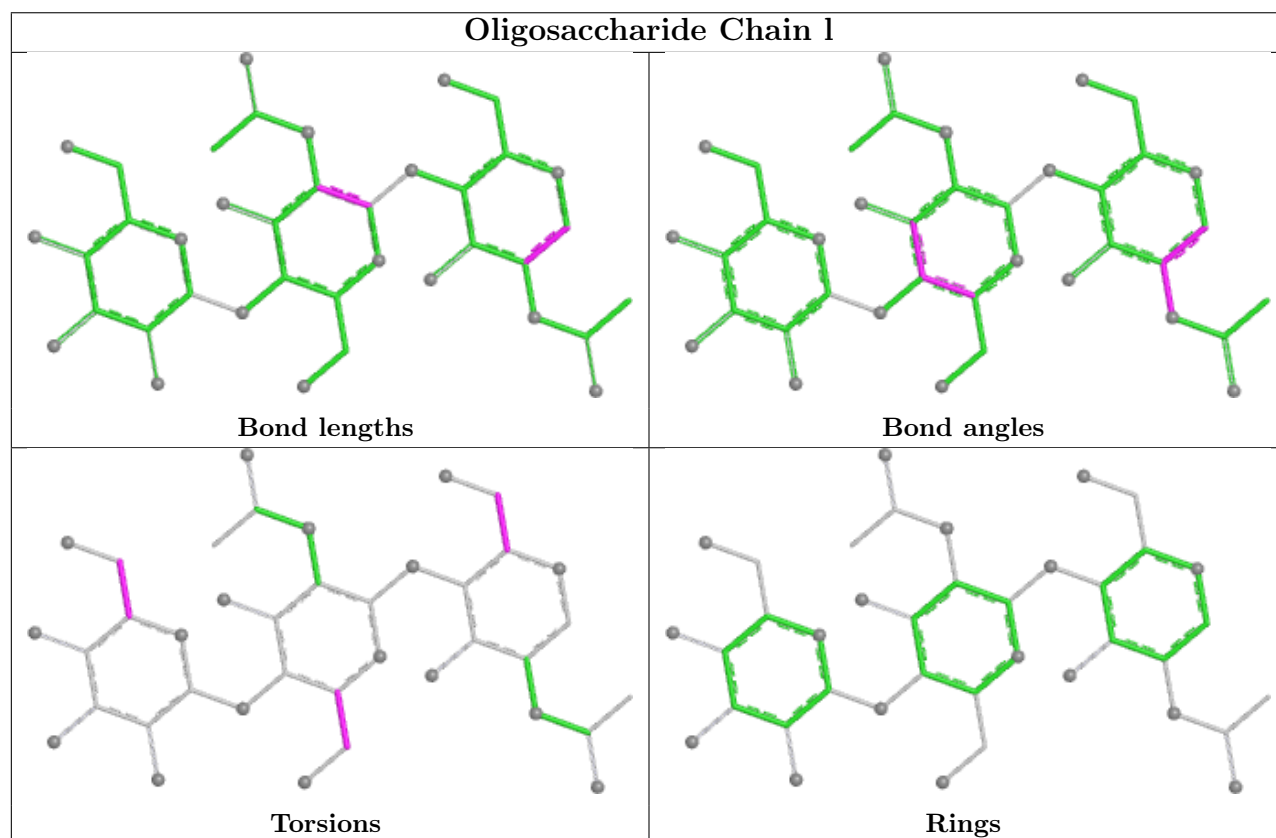
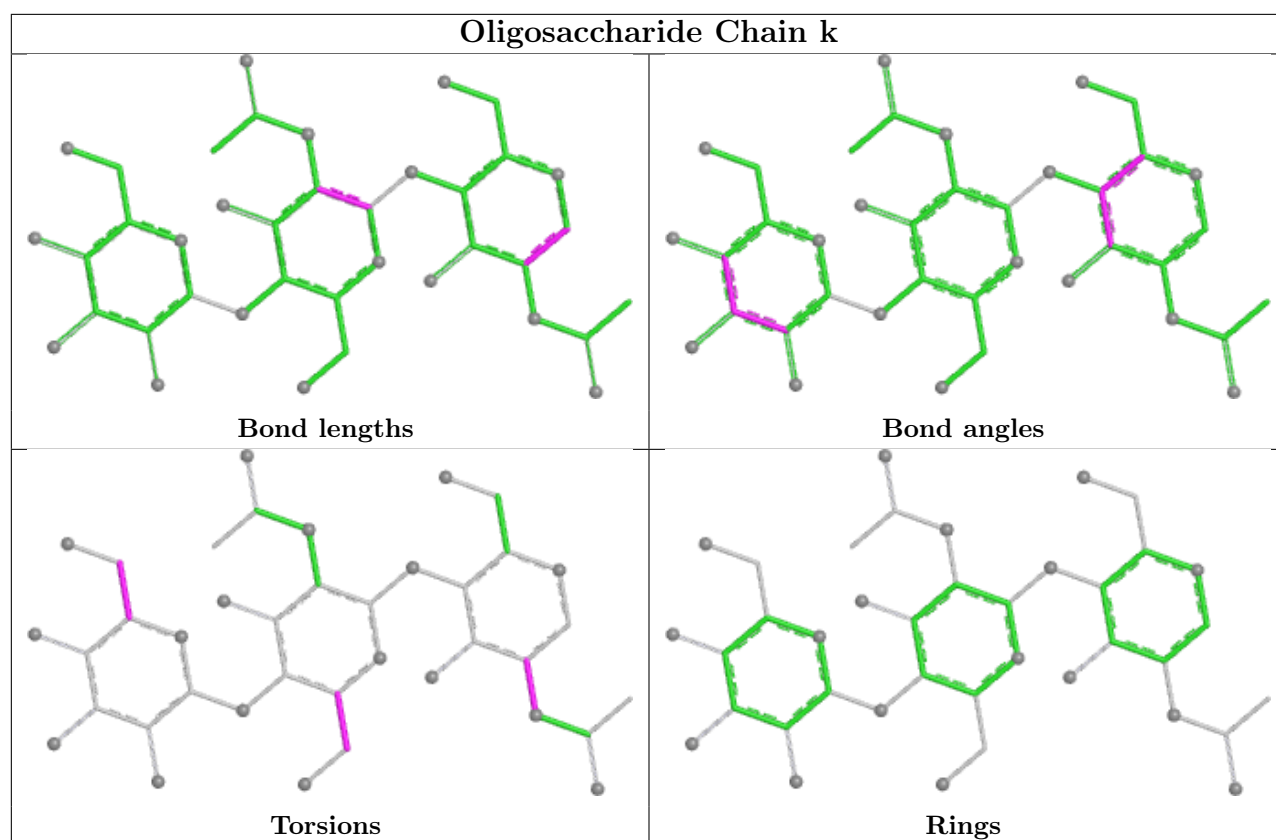


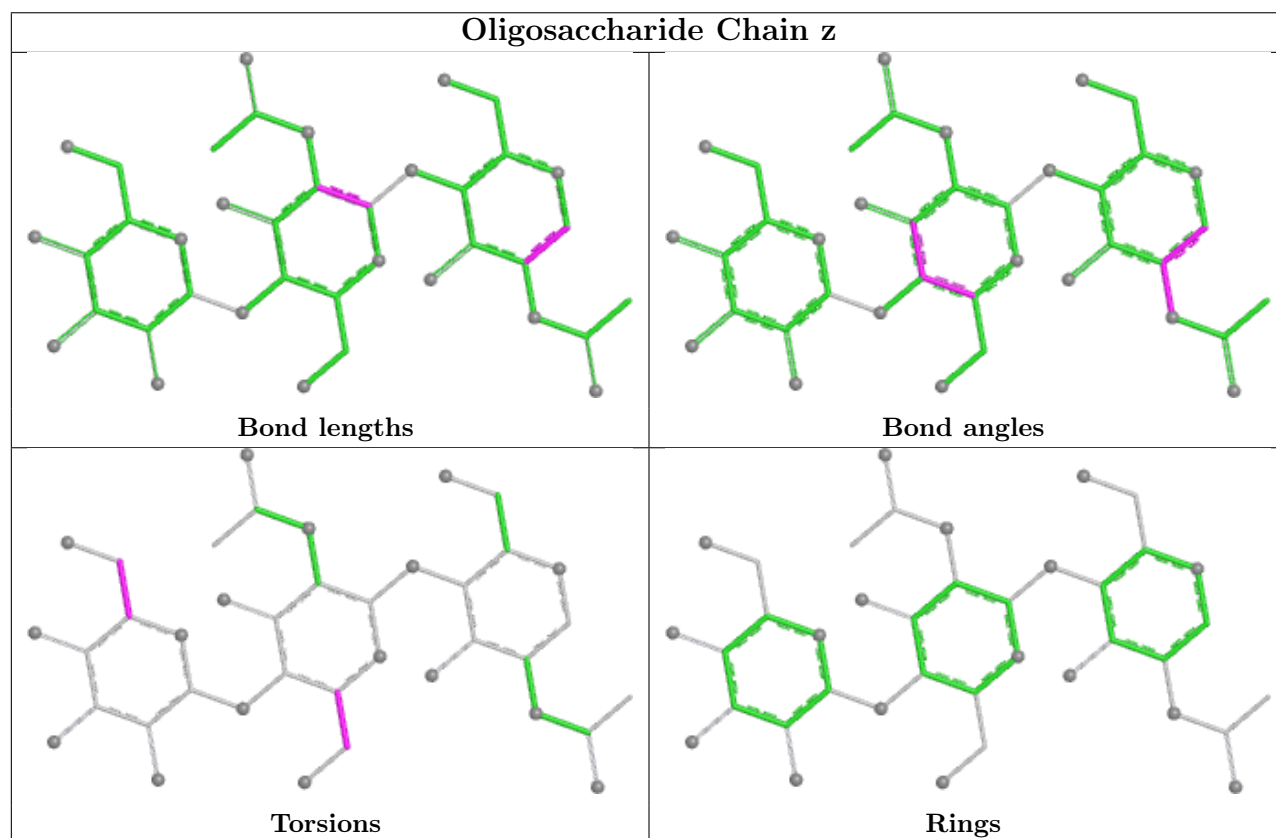
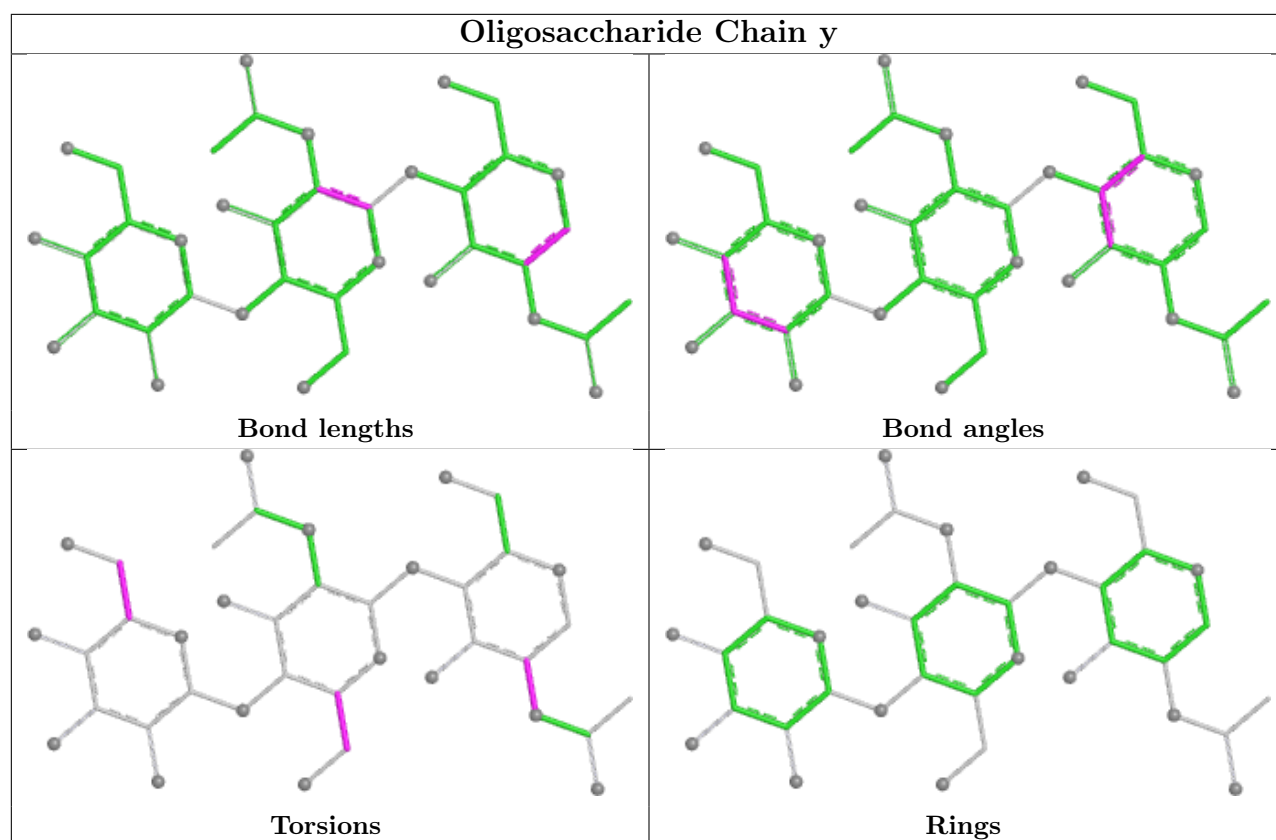












5.6 Ligand geometry

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
11	NAG	D	701	2	14,14,15	0.95	1 (7%)	17,19,21	1.24	1 (5%)
11	NAG	C	602	1	14,14,15	1.13	1 (7%)	17,19,21	0.92	1 (5%)
11	NAG	A	602	1	14,14,15	1.11	1 (7%)	17,19,21	0.92	2 (11%)
11	NAG	E	601	1	14,14,15	0.92	1 (7%)	17,19,21	1.06	1 (5%)
11	NAG	B	701	2	14,14,15	0.95	1 (7%)	17,19,21	1.22	1 (5%)
11	NAG	C	601	1	14,14,15	0.91	1 (7%)	17,19,21	1.09	1 (5%)
11	NAG	E	602	1	14,14,15	1.14	1 (7%)	17,19,21	0.92	1 (5%)
11	NAG	A	601	1	14,14,15	0.92	1 (7%)	17,19,21	1.04	1 (5%)
11	NAG	F	701	2	14,14,15	0.96	1 (7%)	17,19,21	1.24	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	D	701	2	-	1/6/23/26	0/1/1/1
11	NAG	C	602	1	-	1/6/23/26	0/1/1/1
11	NAG	A	602	1	-	1/6/23/26	0/1/1/1
11	NAG	E	601	1	-	1/6/23/26	0/1/1/1
11	NAG	B	701	2	-	1/6/23/26	0/1/1/1
11	NAG	C	601	1	-	1/6/23/26	0/1/1/1
11	NAG	E	602	1	-	1/6/23/26	0/1/1/1
11	NAG	A	601	1	-	1/6/23/26	0/1/1/1
11	NAG	F	701	2	-	1/6/23/26	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	E	602	NAG	C1-C2	4.00	1.57	1.52
11	C	602	NAG	C1-C2	3.96	1.57	1.52
11	A	602	NAG	C1-C2	3.89	1.57	1.52
11	F	701	NAG	C1-C2	3.18	1.56	1.52
11	B	701	NAG	C1-C2	3.17	1.56	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	701	NAG	C4-C3-C2	-3.89	105.31	111.02
11	D	701	NAG	C4-C3-C2	-3.80	105.45	111.02
11	B	701	NAG	C4-C3-C2	-3.70	105.60	111.02
11	E	602	NAG	C4-C3-C2	-2.61	107.20	111.02
11	C	602	NAG	C4-C3-C2	-2.56	107.26	111.02

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	D	701	NAG	O5-C5-C6-O6
11	F	701	NAG	O5-C5-C6-O6
11	C	602	NAG	O5-C5-C6-O6
11	E	602	NAG	O5-C5-C6-O6
11	E	601	NAG	O5-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.

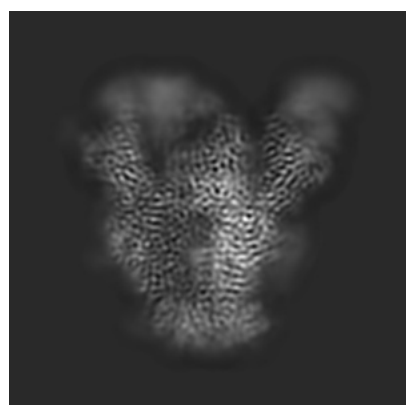
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23571. These allow visual inspection of the internal detail of the map and identification of artifacts.

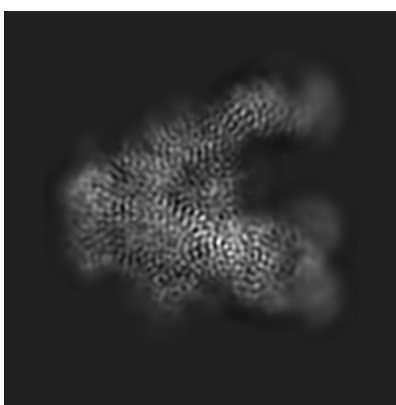
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

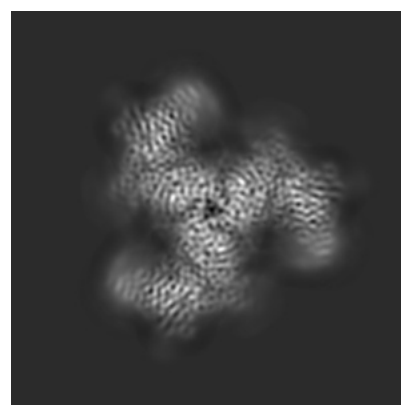
6.1.1 Primary map



X



Y



Z

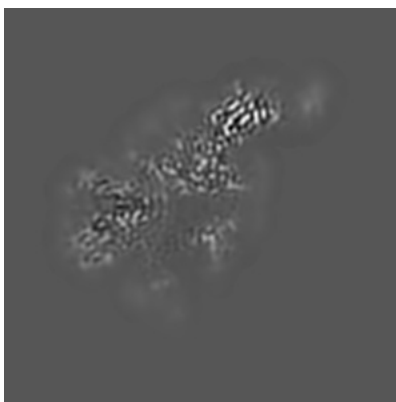
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 110



Y Index: 110



Z Index: 110

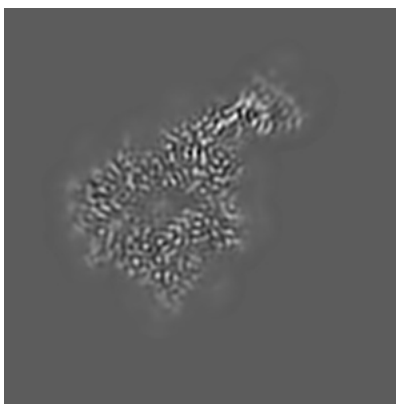
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

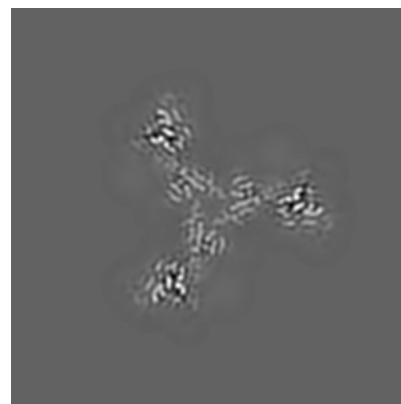
6.3.1 Primary map



X Index: 86



Y Index: 120

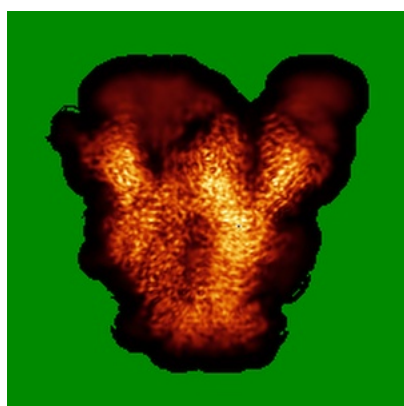


Z Index: 124

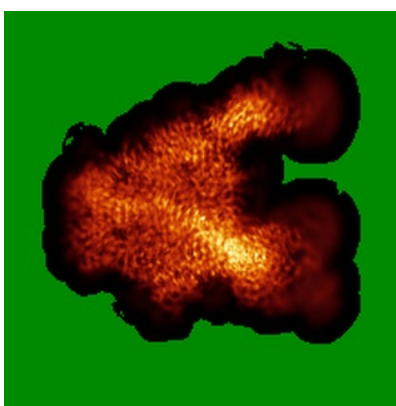
The images above show the largest variance slices of the map in three orthogonal directions.

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

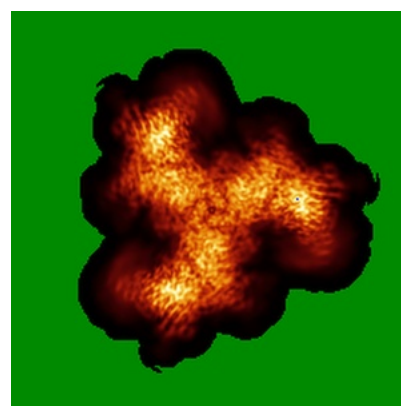
6.4.1 Primary map



X



Y

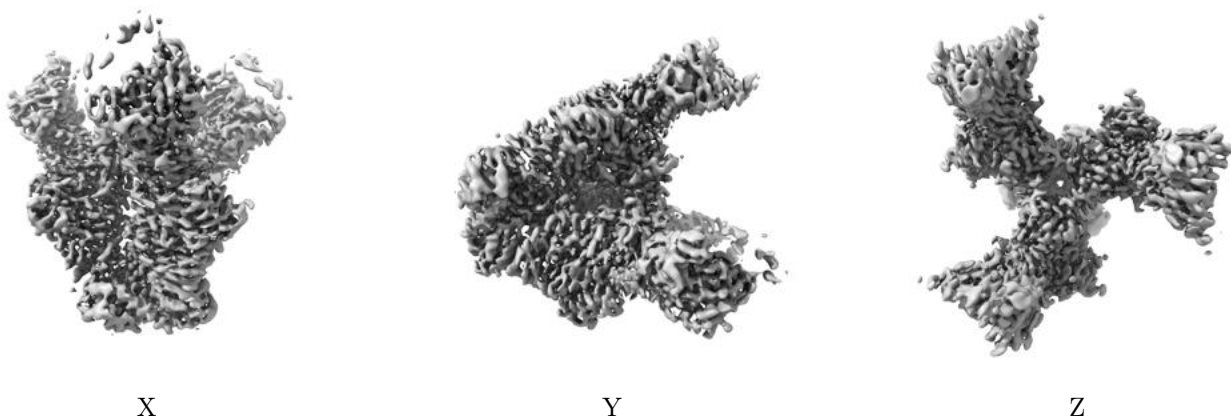


Z

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

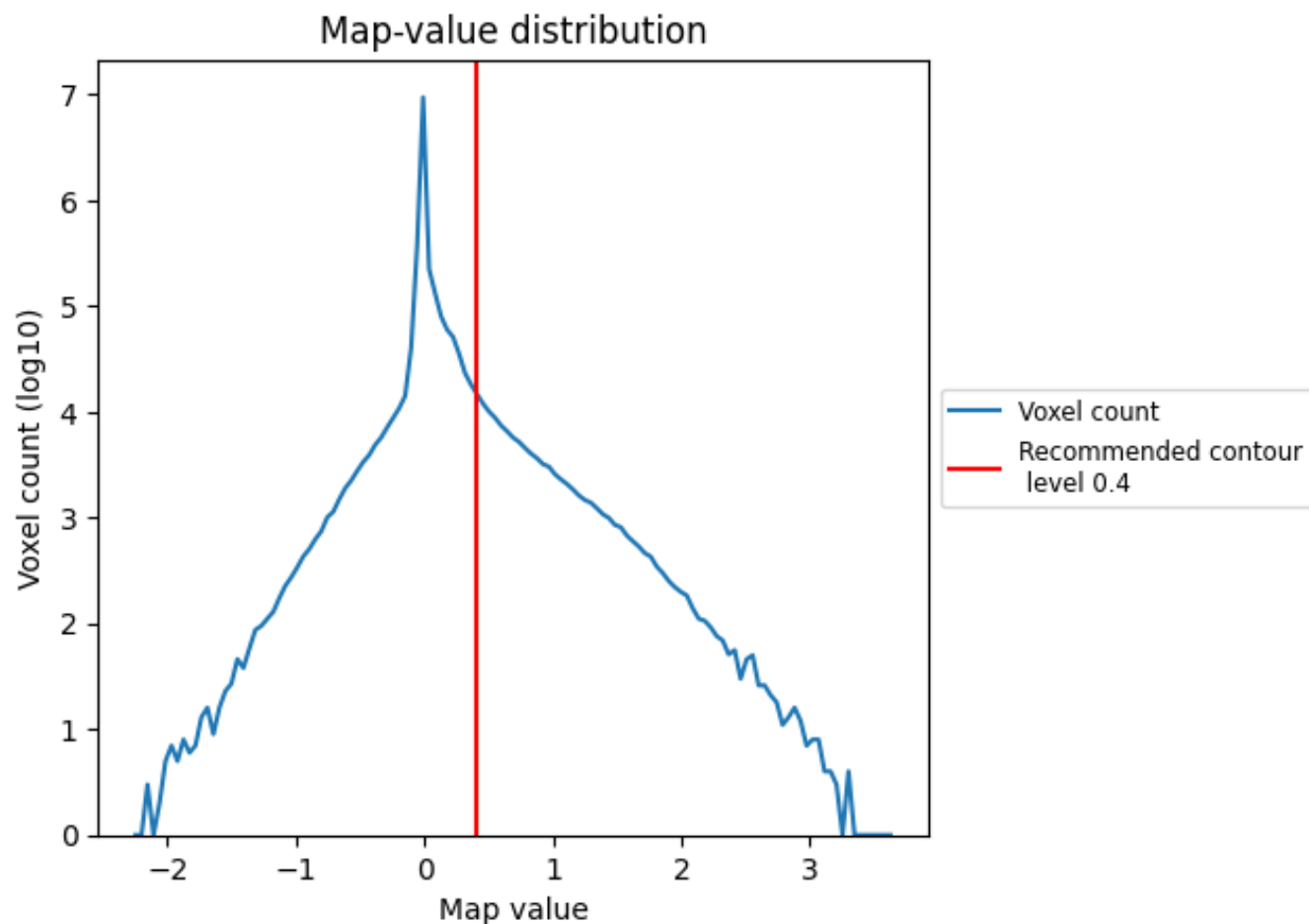
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

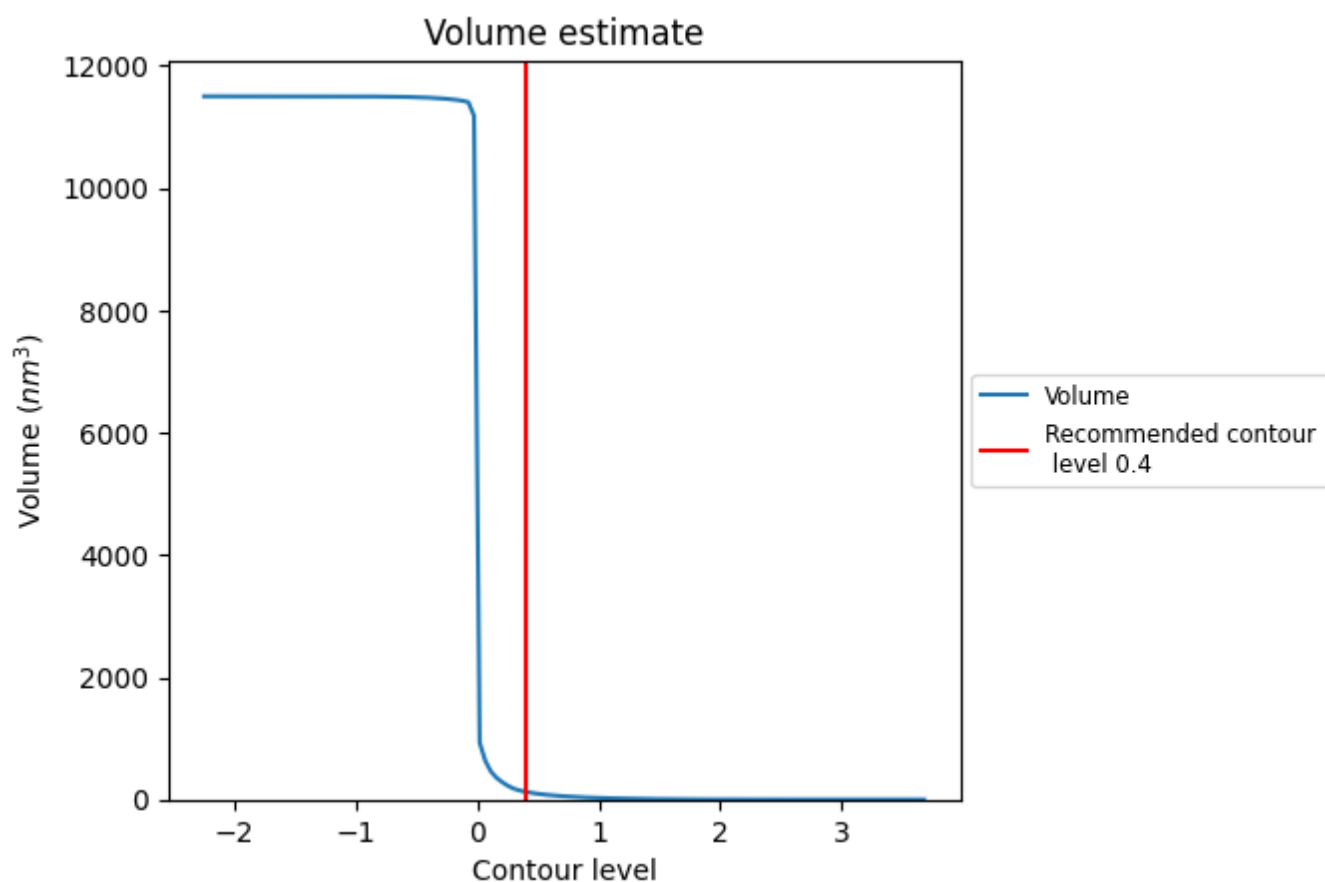
This section contains the results of statistical analysis of the map.

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.

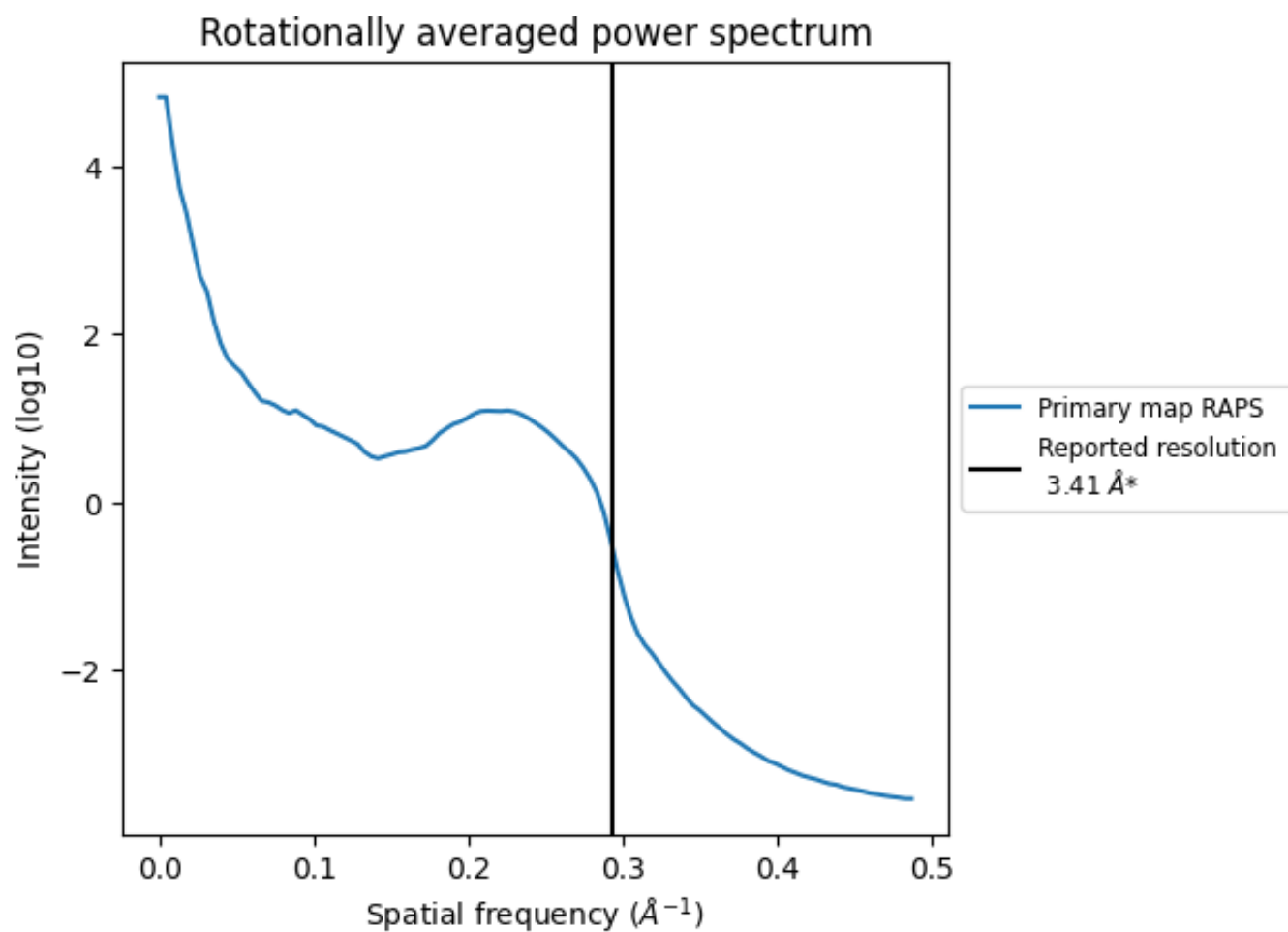
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 126 nm³; this corresponds to an approximate mass of 114 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.293 Å⁻¹

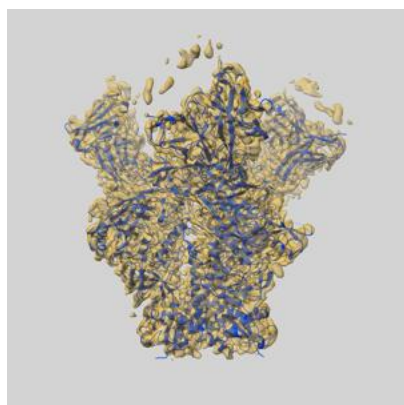
8 Fourier-Shell correlation ⓘ

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

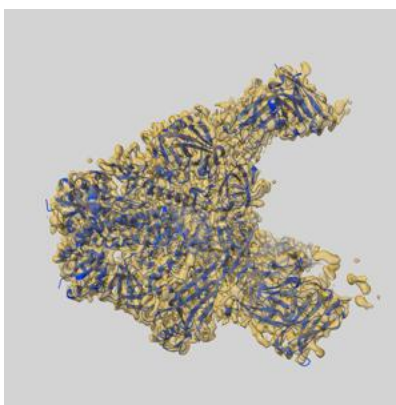
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23571 and PDB model 7LXM. Per-residue inclusion information can be found in section [3](#) on page [11](#).

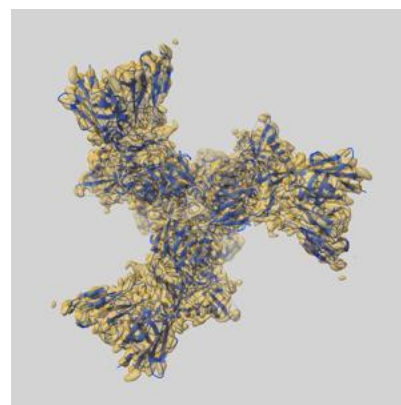
9.1 Map-model overlay [i](#)



X



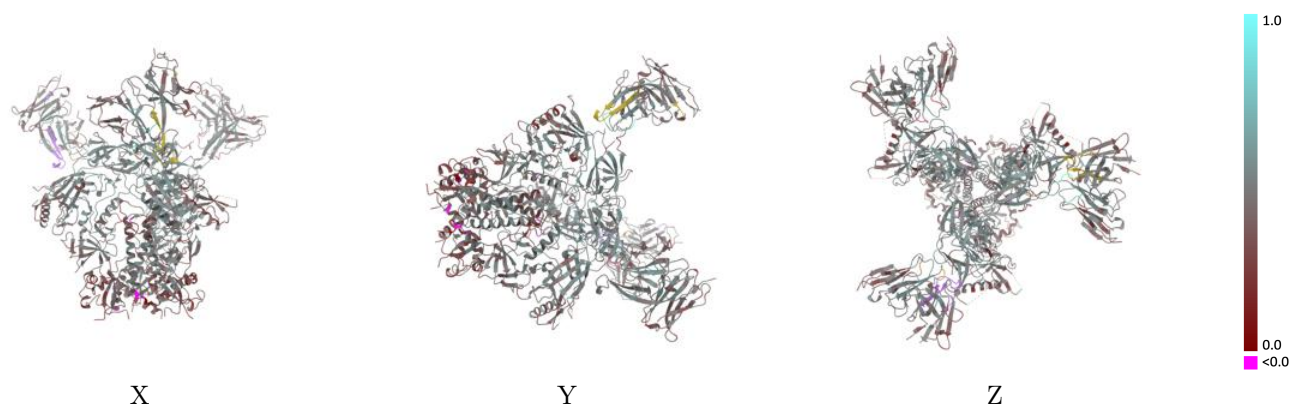
Y



Z

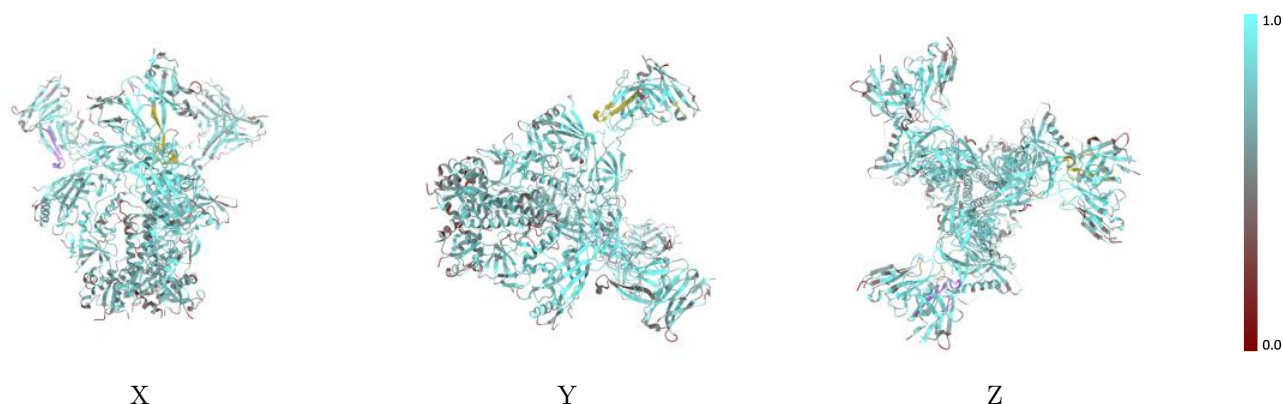
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



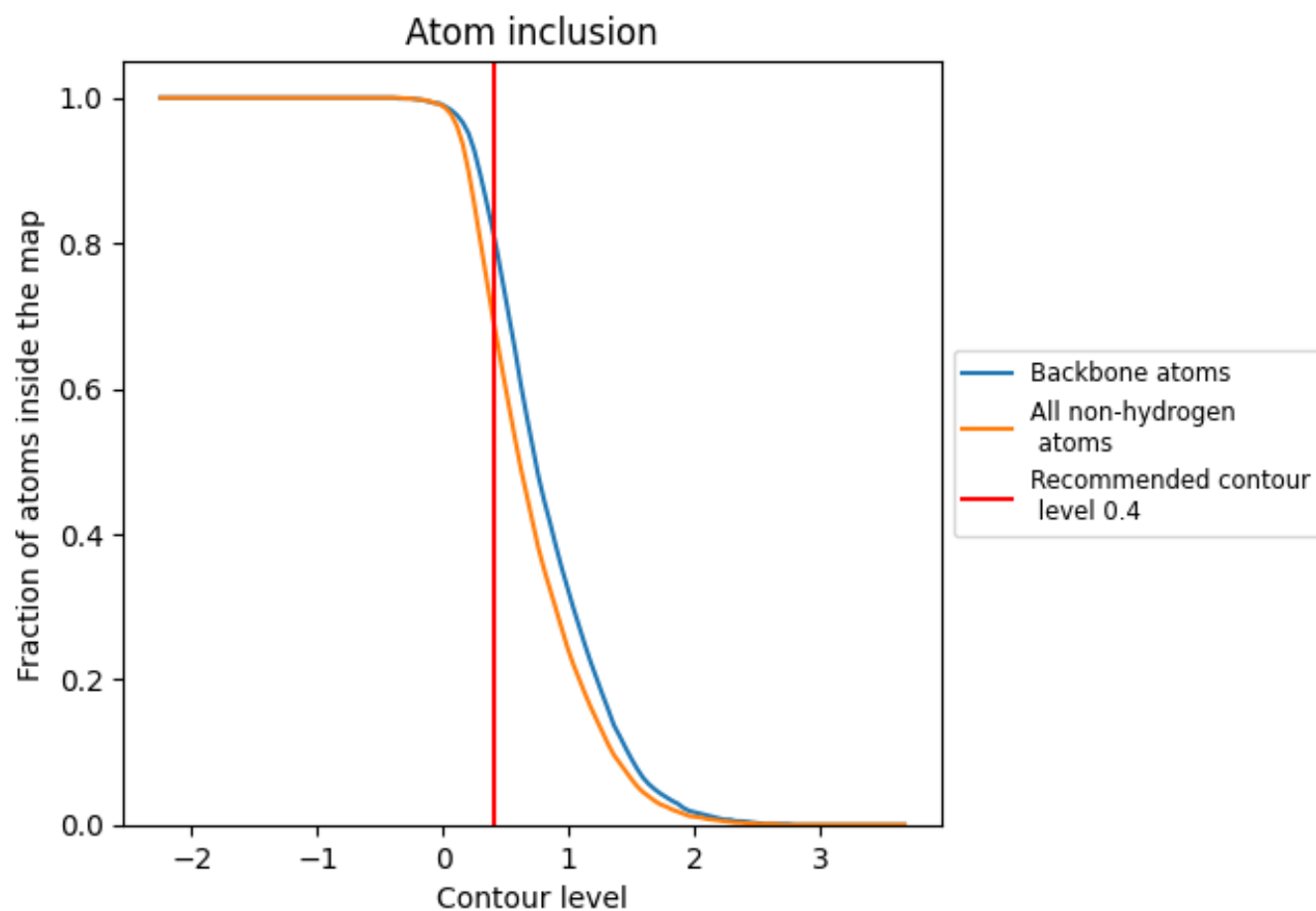
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 70% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6960	 0.4410
0	 0.3930	 0.3500
1	 0.0360	 0.3340
A	 0.7430	 0.4620
B	 0.6340	 0.3690
C	 0.7400	 0.4590
D	 0.6310	 0.3690
E	 0.7410	 0.4610
F	 0.6300	 0.3710
G	 0.6280	 0.3330
H	 0.7360	 0.4520
I	 0.0710	 0.3180
J	 0.2140	 0.3180
K	 0.2860	 0.3090
L	 0.7490	 0.4630
M	 0.7510	 0.4660
N	 0.7350	 0.4570
O	 0.7560	 0.4610
P	 0.7360	 0.4540
Q	 0.1430	 0.2310
R	 0.3930	 0.4270
S	 0.4460	 0.4530
T	 0.3930	 0.4830
U	 0.2800	 0.4580
V	 0.6860	 0.4660
W	 0.3330	 0.4270
X	 0.2560	 0.3520
Y	 0.4640	 0.3690
Z	 0.0360	 0.3310
a	 0.6170	 0.3400
b	 0.0710	 0.3060
c	 0.2500	 0.3180
d	 0.3210	 0.3220
e	 0.1070	 0.2550
f	 0.3930	 0.4420



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Chain	Atom inclusion	Q-score
g	 0.4700	 0.4560
h	 0.4290	 0.4590
i	 0.3200	 0.4470
j	 0.6950	 0.4790
k	 0.3330	 0.4180
l	 0.2560	 0.3800
m	 0.4640	 0.3570
n	 0.0360	 0.3340
o	 0.6060	 0.3410
p	 0.0710	 0.3190
q	 0.2500	 0.3300
r	 0.2860	 0.3210
s	 0.1790	 0.2140
t	 0.3930	 0.4510
u	 0.4700	 0.4510
v	 0.3930	 0.4690
w	 0.3200	 0.4610
x	 0.6860	 0.4770
y	 0.3330	 0.4290
z	 0.2560	 0.3700