



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2025 – 04:47 PM EST

PDB ID : 9PQ3 / pdb_00009pq3
EMDB ID : EMD-71782
Title : Cryo-EM structure of HIV-1 459C-ALT DS-SOSIP RnS Env trimer
Authors : Wang, S.; Zhou, T.; Kwong, P.D.; Morano, N.C.; Shapiro, L.
Deposited on : 2025-07-22
Resolution : 3.94 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:

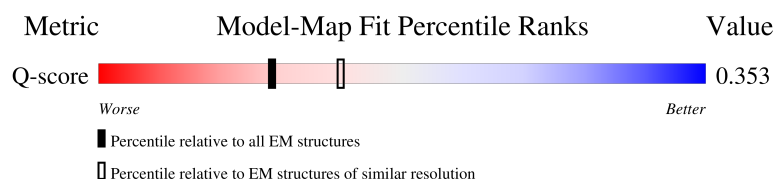
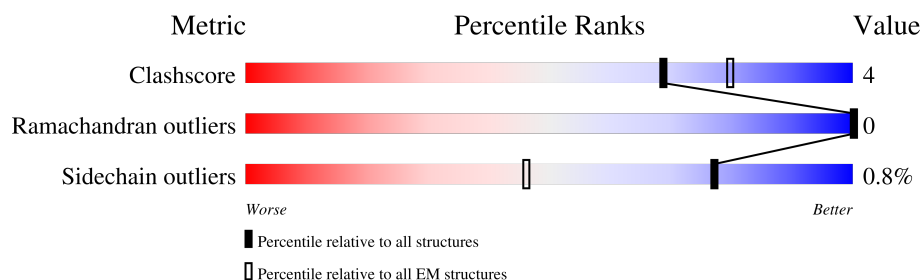
EMDB validation analysis : 0.0.1.dev129
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.47

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 3.94 Å.

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







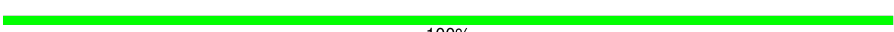

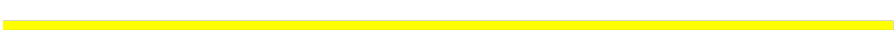





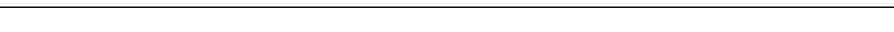

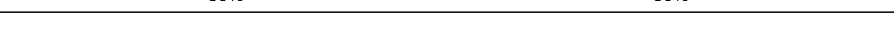
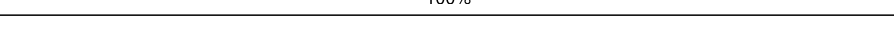
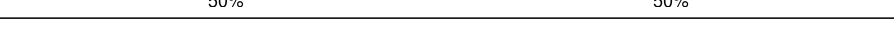
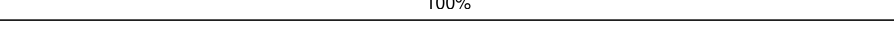




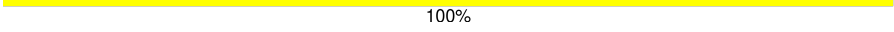

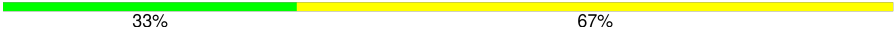
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	7757 (3.44 - 4.43)

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	153	
1	B	153	
1	F	153	
2	C	469	



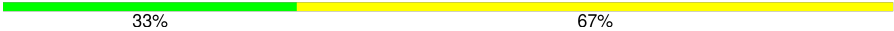
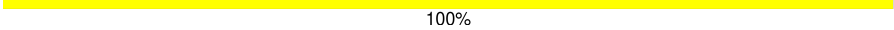






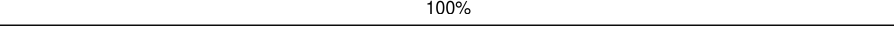
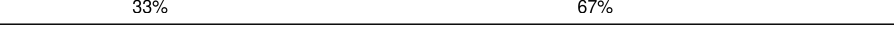
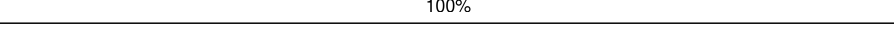



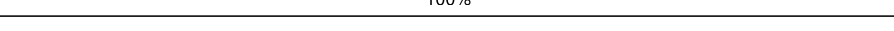
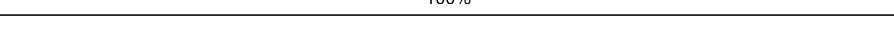
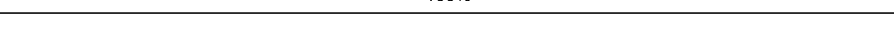
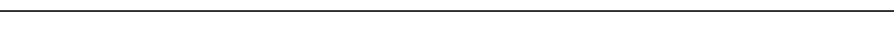

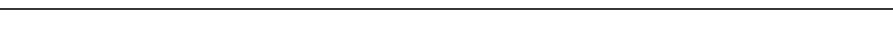
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	469	 85% 11%
2	I	469	 86% 10%
3	D	2	 50% 50%
3	E	2	 50% 50%
3	L	2	 100%
3	O	2	 50% 50%
3	T	2	 100%
3	V	2	 50% 50%
3	W	2	 50% 50%
3	a	2	 100%
3	d	2	 50% 50%
3	i	2	 100%
3	k	2	 50% 50%
3	l	2	 50% 50%
3	p	2	 100%
3	s	2	 50% 50%
3	x	2	 100%
4	H	3	 33% 67%
4	K	3	 67% 33%
4	P	3	 33% 67%
4	Q	3	 33% 67%
4	R	3	 100%
4	S	3	 33% 67%
4	U	3	 33% 67%
4	X	3	 33% 67%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	Z	3	 67% 33%
4	e	3	 33% 67%
4	f	3	 33% 67%
4	g	3	 100%
4	h	3	 33% 67%
4	j	3	 33% 67%
4	m	3	 33% 67%
4	o	3	 67% 33%
4	t	3	 33% 67%
4	u	3	 33% 67%
4	v	3	 100%
4	w	3	 33% 67%
4	y	3	 100%
5	J	6	 17% 83%
5	Y	6	 17% 83%
5	n	6	 17% 83%
6	M	4	 100%
6	b	4	 100%
6	q	4	 100%
7	N	5	 100%
7	c	5	 100%
7	r	5	 100%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 15684 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 459C-ALT RnS DS-SOSIP gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	126	Total	C	N	O	S	0	0
			1004	638	169	191	6		
1	B	126	Total	C	N	O	S	0	0
			1004	638	169	191	6		
1	F	126	Total	C	N	O	S	0	0
			1004	638	169	191	6		

- Molecule 2 is a protein called HIV-1 459C-ALT RnS DS-SOSIP gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	450	Total	C	N	O	S	0	0
			3558	2236	629	665	28		
2	G	450	Total	C	N	O	S	0	0
			3558	2236	629	665	28		
2	I	450	Total	C	N	O	S	0	0
			3558	2236	629	665	28		

- 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
3	D	2	Total	C	N	O	0	0
			28	16	2	10		
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	L	2	Total	C	N	O	0	0
			28	16	2	10		
3	O	2	Total	C	N	O	0	0
			28	16	2	10		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
3	T	2	Total	C	N	O	0	0
			28	16	2	10		
3	V	2	Total	C	N	O	0	0
			28	16	2	10		
3	W	2	Total	C	N	O	0	0
			28	16	2	10		
3	a	2	Total	C	N	O	0	0
			28	16	2	10		
3	d	2	Total	C	N	O	0	0
			28	16	2	10		
3	i	2	Total	C	N	O	0	0
			28	16	2	10		
3	k	2	Total	C	N	O	0	0
			28	16	2	10		
3	l	2	Total	C	N	O	0	0
			28	16	2	10		
3	p	2	Total	C	N	O	0	0
			28	16	2	10		
3	s	2	Total	C	N	O	0	0
			28	16	2	10		
3	x	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 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.



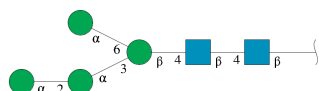
Mol	Chain	Residues	Atoms				AltConf	Trace
4	H	3	Total	C	N	O	0	0
			39	22	2	15		
4	K	3	Total	C	N	O	0	0
			39	22	2	15		
4	P	3	Total	C	N	O	0	0
			39	22	2	15		
4	Q	3	Total	C	N	O	0	0
			39	22	2	15		
4	R	3	Total	C	N	O	0	0
			39	22	2	15		
4	S	3	Total	C	N	O	0	0
			39	22	2	15		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
4	U	3	Total	C	N	O	0	0
			39	22	2	15		
4	X	3	Total	C	N	O	0	0
			39	22	2	15		
4	Z	3	Total	C	N	O	0	0
			39	22	2	15		
4	e	3	Total	C	N	O	0	0
			39	22	2	15		
4	f	3	Total	C	N	O	0	0
			39	22	2	15		
4	g	3	Total	C	N	O	0	0
			39	22	2	15		
4	h	3	Total	C	N	O	0	0
			39	22	2	15		
4	j	3	Total	C	N	O	0	0
			39	22	2	15		
4	m	3	Total	C	N	O	0	0
			39	22	2	15		
4	o	3	Total	C	N	O	0	0
			39	22	2	15		
4	t	3	Total	C	N	O	0	0
			39	22	2	15		
4	u	3	Total	C	N	O	0	0
			39	22	2	15		
4	v	3	Total	C	N	O	0	0
			39	22	2	15		
4	w	3	Total	C	N	O	0	0
			39	22	2	15		
4	y	3	Total	C	N	O	0	0
			39	22	2	15		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
5	J	6	Total	C	N	O	0	0
			72	40	2	30		

Continued on next page...

Continued from previous page...

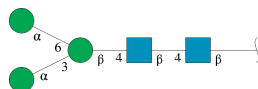
Mol	Chain	Residues	Atoms				AltConf	Trace
5	Y	6	Total	C	N	O	0	0
			72	40	2	30		
5	n	6	Total	C	N	O	0	0
			72	40	2	30		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	4	Total	C	N	O	0	0
			50	28	2	20		
6	b	4	Total	C	N	O	0	0
			50	28	2	20		
6	q	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
7	N	5	Total	C	N	O	0	0
			61	34	2	25		
7	c	5	Total	C	N	O	0	0
			61	34	2	25		
7	r	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
8	A	1	Total	C	N	O	0
			14	8	1	5	
8	A	1	Total	C	N	O	0
			14	8	1	5	
8	C	1	Total	C	N	O	0
			14	8	1	5	
8	C	1	Total	C	N	O	0
			14	8	1	5	
8	C	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	
8	G	1	Total	C	N	O	0
			14	8	1	5	
8	G	1	Total	C	N	O	0
			14	8	1	5	
8	G	1	Total	C	N	O	0
			14	8	1	5	
8	F	1	Total	C	N	O	0
			14	8	1	5	
8	F	1	Total	C	N	O	0
			14	8	1	5	
8	I	1	Total	C	N	O	0
			14	8	1	5	
8	I	1	Total	C	N	O	0
			14	8	1	5	

Continued on next page...

Continued from previous page...

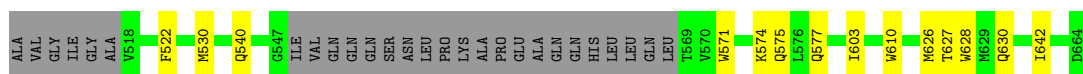
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
8	I	1	14	8	1	5	0

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.

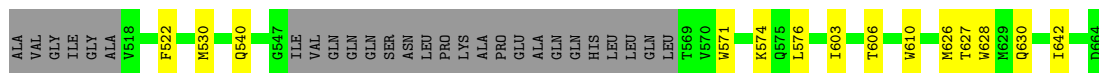
- Molecule 1: HIV-1 459C-ALT RnS DS-SOSIP gp41

Chain A: 



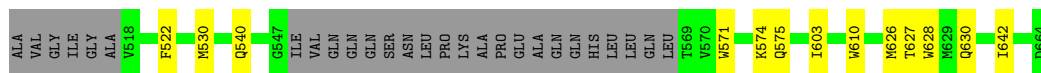
- Molecule 1: HIV-1 459C-ALT RnS DS-SOSIP gp41

Chain B: 




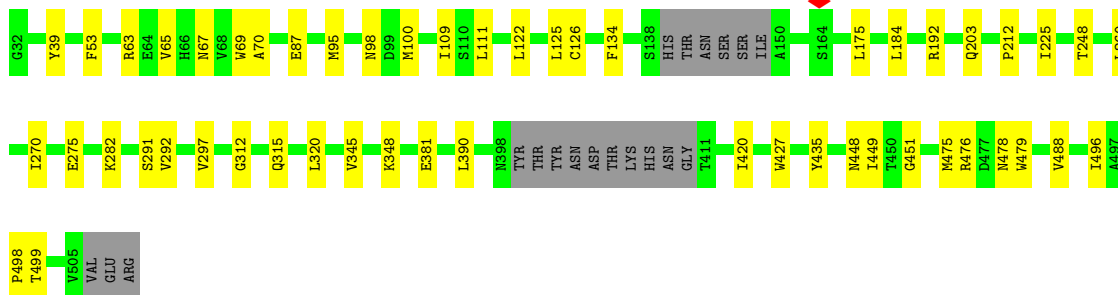
- Molecule 1: HIV-1 459C-ALT RnS DS-SOSIP gp41

Chain F: 



- Molecule 2: HIV-1 459C-ALT RnS DS-SOSIP gp120

Chain C: 



- Molecule 2: HIV-1 459C-ALT RnS DS-SOSIP gp120

T499	R503	R504	R505	VAL	GLU	ARG	T1270	G32	Y39	V65	H66	H67	V68	V69	A70	T71	H72	A73	E87	H95	N98	D99	M100	I109	S110	L111	L122	L125	C126	F134	S138	HIS	THR	ASN	SER	SER	ILE	A150	S164	L175	L184	R192	Q203	P212	I225	T248	L260
------	------	------	------	-----	-----	-----	-------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------

- [illegible]

- | | NAG1 | NAG2 |
|-----|--------|--------|
| 1 | 0.0000 | 0.0000 |
| 2 | 0.0000 | 0.0000 |
| 3 | 0.0000 | 0.0000 |
| 4 | 0.0000 | 0.0000 |
| 5 | 0.0000 | 0.0000 |
| 6 | 0.0000 | 0.0000 |
| 7 | 0.0000 | 0.0000 |
| 8 | 0.0000 | 0.0000 |
| 9 | 0.0000 | 0.0000 |
| 10 | 0.0000 | 0.0000 |
| 11 | 0.0000 | 0.0000 |
| 12 | 0.0000 | 0.0000 |
| 13 | 0.0000 | 0.0000 |
| 14 | 0.0000 | 0.0000 |
| 15 | 0.0000 | 0.0000 |
| 16 | 0.0000 | 0.0000 |
| 17 | 0.0000 | 0.0000 |
| 18 | 0.0000 | 0.0000 |
| 19 | 0.0000 | 0.0000 |
| 20 | 0.0000 | 0.0000 |
| 21 | 0.0000 | 0.0000 |
| 22 | 0.0000 | 0.0000 |
| 23 | 0.0000 | 0.0000 |
| 24 | 0.0000 | 0.0000 |
| 25 | 0.0000 | 0.0000 |
| 26 | 0.0000 | 0.0000 |
| 27 | 0.0000 | 0.0000 |
| 28 | 0.0000 | 0.0000 |
| 29 | 0.0000 | 0.0000 |
| 30 | 0.0000 | 0.0000 |
| 31 | 0.0000 | 0.0000 |
| 32 | 0.0000 | 0.0000 |
| 33 | 0.0000 | 0.0000 |
| 34 | 0.0000 | 0.0000 |
| 35 | 0.0000 | 0.0000 |
| 36 | 0.0000 | 0.0000 |
| 37 | 0.0000 | 0.0000 |
| 38 | 0.0000 | 0.0000 |
| 39 | 0.0000 | 0.0000 |
| 40 | 0.0000 | 0.0000 |
| 41 | 0.0000 | 0.0000 |
| 42 | 0.0000 | 0.0000 |
| 43 | 0.0000 | 0.0000 |
| 44 | 0.0000 | 0.0000 |
| 45 | 0.0000 | 0.0000 |
| 46 | 0.0000 | 0.0000 |
| 47 | 0.0000 | 0.0000 |
| 48 | 0.0000 | 0.0000 |
| 49 | 0.0000 | 0.0000 |
| 50 | 0.0000 | 0.0000 |
| 51 | 0.0000 | 0.0000 |
| 52 | 0.0000 | 0.0000 |
| 53 | 0.0000 | 0.0000 |
| 54 | 0.0000 | 0.0000 |
| 55 | 0.0000 | 0.0000 |
| 56 | 0.0000 | 0.0000 |
| 57 | 0.0000 | 0.0000 |
| 58 | 0.0000 | 0.0000 |
| 59 | 0.0000 | 0.0000 |
| 60 | 0.0000 | 0.0000 |
| 61 | 0.0000 | 0.0000 |
| 62 | 0.0000 | 0.0000 |
| 63 | 0.0000 | 0.0000 |
| 64 | 0.0000 | 0.0000 |
| 65 | 0.0000 | 0.0000 |
| 66 | 0.0000 | 0.0000 |
| 67 | 0.0000 | 0.0000 |
| 68 | 0.0000 | 0.0000 |
| 69 | 0.0000 | 0.0000 |
| 70 | 0.0000 | 0.0000 |
| 71 | 0.0000 | 0.0000 |
| 72 | 0.0000 | 0.0000 |
| 73 | 0.0000 | 0.0000 |
| 74 | 0.0000 | 0.0000 |
| 75 | 0.0000 | 0.0000 |
| 76 | 0.0000 | 0.0000 |
| 77 | 0.0000 | 0.0000 |
| 78 | 0.0000 | 0.0000 |
| 79 | 0.0000 | 0.0000 |
| 80 | 0.0000 | 0.0000 |
| 81 | 0.0000 | 0.0000 |
| 82 | 0.0000 | 0.0000 |
| 83 | 0.0000 | 0.0000 |
| 84 | 0.0000 | 0.0000 |
| 85 | 0.0000 | 0.0000 |
| 86 | 0.0000 | 0.0000 |
| 87 | 0.0000 | 0.0000 |
| 88 | 0.0000 | 0.0000 |
| 89 | 0.0000 | 0.0000 |
| 90 | 0.0000 | 0.0000 |
| 91 | 0.0000 | 0.0000 |
| 92 | 0.0000 | 0.0000 |
| 93 | 0.0000 | 0.0000 |
| 94 | 0.0000 | 0.0000 |
| 95 | 0.0000 | 0.0000 |
| 96 | 0.0000 | 0.0000 |
| 97 | 0.0000 | 0.0000 |
| 98 | 0.0000 | 0.0000 |
| 99 | 0.0000 | 0.0000 |
| 100 | 0.0000 | 0.0000 |

- NAG1
NAG2

- NAG1
NAG2

- 

Chain O:  50% 50%

MAG1
MAG2

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

Chain T:  100%

MAG1
MAG2

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

Chain V:  50% 50%

MAG1
MAG2

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

Chain W:  50% 50%

MAG1
MAG2

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

Chain a:  100%

MAG1
MAG2

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

Chain d:  50% 50%

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 k:  50% 50%

MAG1
MAG2

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

Chain l:  50% 50%

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 s:  50% 50%

MAG1
MAG2

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

Chain x:  100%

MAG1
MAG2

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

Chain H:  33% 67%

MAG1
MAG2
BNA3

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

Chain K:  67% 33%



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

Chain P:  33% 67%



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

Chain Q:  33% 67%



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

Chain R:  100%



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

Chain S:  33% 67%



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

Chain U:  33% 67%



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

Chain X:  33% 67%



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

Chain Z:  67% 33%



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

Chain e:  33% 67%



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

Chain f:  33% 67%



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

Chain g:  100%

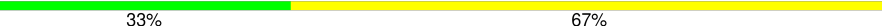


- Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h:  33% 67%



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

Chain j:  33% 67%



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

Chain m:  33% 67%


MAG1
MAG2
BMA3

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

Chain o:  67% 33%

MAG1
MAG2
BMA3

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

Chain t:  33% 67%

MAG1
MAG2
BMA3

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

Chain u:  33% 67%


MAG1
MAG2
BMA3

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

Chain v:  100%

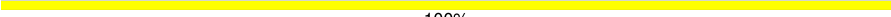
MAG1
MAG2
BMA3

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

Chain w:  33% 67%

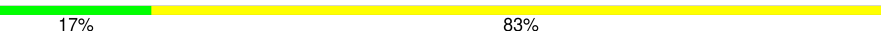
MAG1
MAG2
BMA3

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

Chain y:  100%

MAG1
MAG2
BMA3

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

Chain J:  17% 83%

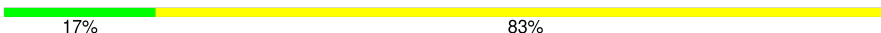
MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

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

Chain Y:  17% 83%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

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

Chain n:  17% 83%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

- Molecule 6: 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 M:  100%

MAG1
MAG2
BMA3
MAN4

- Molecule 6: 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 b:  100%

MAG1
MAG2
BMA3
MAN4

- Molecule 6: 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 q:  100%

MAG1
MAG2
BMA3
MAN4

● Molecule 7: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain N:  100%

MAG1
MAG2
BMA3
MAN4
MAN5

● Molecule 7: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain c:  100%

MAG1
MAG2
BMA3
MAN4
MAN5

● Molecule 7: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain r:  100%

MAG1
MAG2
BMA3
MAN4
MAN5

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	158204	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.249	Depositor
Minimum map value	-0.106	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0275	Depositor
Map size (Å)	356.4, 356.4, 356.4	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.26	0/1023	0.55	0/1390
1	B	0.26	0/1023	0.55	0/1390
1	F	0.26	0/1023	0.55	0/1390
2	C	0.15	0/3635	0.42	0/4938
2	G	0.15	0/3635	0.42	0/4938
2	I	0.15	0/3635	0.42	0/4938
All	All	0.18	0/13974	0.45	0/18984

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1004	0	978	11	0
1	B	1004	0	978	12	0
1	F	1004	0	978	10	0
2	C	3558	0	3484	30	0
2	G	3558	0	3484	30	0
2	I	3558	0	3484	28	0
3	D	28	0	25	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	28	0	25	1	0
3	L	28	0	25	0	0
3	O	28	0	25	0	0
3	T	28	0	25	0	0
3	V	28	0	25	1	0
3	W	28	0	25	1	0
3	a	28	0	25	0	0
3	d	28	0	25	0	0
3	i	28	0	25	0	0
3	k	28	0	25	1	0
3	l	28	0	25	1	0
3	p	28	0	25	0	0
3	s	28	0	25	0	0
3	x	28	0	25	0	0
4	H	39	0	34	0	0
4	K	39	0	34	0	0
4	P	39	0	34	0	0
4	Q	39	0	34	0	0
4	R	39	0	34	0	0
4	S	39	0	34	0	0
4	U	39	0	34	0	0
4	X	39	0	34	0	0
4	Z	39	0	34	0	0
4	e	39	0	34	0	0
4	f	39	0	34	0	0
4	g	39	0	34	0	0
4	h	39	0	34	0	0
4	j	39	0	34	0	0
4	m	39	0	34	0	0
4	o	39	0	34	0	0
4	t	39	0	34	0	0
4	u	39	0	34	0	0
4	v	39	0	34	0	0
4	w	39	0	34	0	0
4	y	39	0	34	0	0
5	J	72	0	61	0	0
5	Y	72	0	61	0	0
5	n	72	0	61	0	0
6	M	50	0	43	0	0
6	b	50	0	43	0	0
6	q	50	0	43	0	0
7	N	61	0	52	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	c	61	0	52	0	0
7	r	61	0	52	0	0
8	A	28	0	26	0	0
8	B	28	0	26	0	0
8	C	42	0	39	0	0
8	F	28	0	26	0	0
8	G	42	0	39	0	0
8	I	42	0	39	0	0
All	All	15684	0	15138	108	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 108 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:270:ILE:HB	2:C:348:LYS:HG3	1.87	0.57
2:I:270:ILE:HB	2:I:348:LYS:HG3	1.87	0.57
2:G:270:ILE:HB	2:G:348:LYS:HG3	1.87	0.57
1:F:603:ILE:HG22	2:I:39:TYR:HA	1.86	0.56
2:C:292:VAL:HB	2:C:449:ILE:HB	1.88	0.55

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	122/153 (80%)	120 (98%)	2 (2%)	0	100	100
1	B	122/153 (80%)	120 (98%)	2 (2%)	0	100	100
1	F	122/153 (80%)	120 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	444/469 (95%)	432 (97%)	12 (3%)	0	100	100
2	G	444/469 (95%)	432 (97%)	12 (3%)	0	100	100
2	I	444/469 (95%)	432 (97%)	12 (3%)	0	100	100
All	All	1698/1866 (91%)	1656 (98%)	42 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	109/130 (84%)	109 (100%)	0	100	100
1	B	109/130 (84%)	109 (100%)	0	100	100
1	F	109/130 (84%)	109 (100%)	0	100	100
2	C	403/421 (96%)	399 (99%)	4 (1%)	73	81
2	G	403/421 (96%)	399 (99%)	4 (1%)	73	81
2	I	403/421 (96%)	399 (99%)	4 (1%)	73	81
All	All	1536/1653 (93%)	1524 (99%)	12 (1%)	77	84

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	499	THR
2	I	65	VAL
2	I	499	THR
2	I	126	CYS
2	C	499	THR

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

Mol	Chain	Res	Type
2	G	66	HIS
2	G	279	ASN
2	I	478	ASN
1	F	656	ASN
2	I	66	HIS

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 ⓘ

138 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	D	1	2,3	14,14,15	0.69	0	17,19,21	1.03	1 (5%)
3	NAG	D	2	3	14,14,15	0.72	0	17,19,21	1.61	3 (17%)
3	NAG	E	1	2,3	14,14,15	0.69	0	17,19,21	1.26	3 (17%)
3	NAG	E	2	3	14,14,15	0.69	0	17,19,21	0.82	0
4	NAG	H	1	2,4	14,14,15	0.68	0	17,19,21	0.90	1 (5%)
4	NAG	H	2	4	14,14,15	0.69	0	17,19,21	0.94	0
4	BMA	H	3	4	11,11,12	0.90	1 (9%)	15,15,17	2.45	4 (26%)
5	NAG	J	1	2,5	14,14,15	0.72	0	17,19,21	0.98	0
5	NAG	J	2	5	14,14,15	0.73	0	17,19,21	1.01	1 (5%)
5	BMA	J	3	5	11,11,12	0.86	0	15,15,17	2.35	4 (26%)
5	MAN	J	4	5	11,11,12	0.63	0	15,15,17	1.46	1 (6%)
5	MAN	J	5	5	11,11,12	0.72	0	15,15,17	1.25	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MAN	J	6	5	11,11,12	0.69	0	15,15,17	1.24	1 (6%)
4	NAG	K	1	2,4	14,14,15	0.72	0	17,19,21	0.93	0
4	NAG	K	2	4	14,14,15	0.70	0	17,19,21	0.92	0
4	BMA	K	3	4	11,11,12	0.88	1 (9%)	15,15,17	2.52	5 (33%)
3	NAG	L	1	2,3	14,14,15	0.69	0	17,19,21	0.87	0
3	NAG	L	2	3	14,14,15	0.74	0	17,19,21	0.93	0
6	NAG	M	1	2,6	14,14,15	0.71	0	17,19,21	1.00	2 (11%)
6	NAG	M	2	6	14,14,15	0.68	0	17,19,21	1.55	2 (11%)
6	BMA	M	3	6	11,11,12	0.88	1 (9%)	15,15,17	2.45	5 (33%)
6	MAN	M	4	6	11,11,12	0.63	0	15,15,17	1.46	1 (6%)
7	NAG	N	1	2,7	14,14,15	0.70	0	17,19,21	1.16	1 (5%)
7	NAG	N	2	7	14,14,15	0.74	0	17,19,21	1.02	1 (5%)
7	BMA	N	3	7	11,11,12	0.87	0	15,15,17	2.40	6 (40%)
7	MAN	N	4	7	11,11,12	0.75	0	15,15,17	1.32	1 (6%)
7	MAN	N	5	7	11,11,12	0.71	0	15,15,17	1.16	1 (6%)
3	NAG	O	1	2,3	14,14,15	0.75	0	17,19,21	1.08	1 (5%)
3	NAG	O	2	3	14,14,15	0.70	0	17,19,21	0.86	0
4	NAG	P	1	2,4	14,14,15	0.79	0	17,19,21	2.94	4 (23%)
4	NAG	P	2	4	14,14,15	0.69	0	17,19,21	0.91	0
4	BMA	P	3	4	11,11,12	0.87	0	15,15,17	2.45	4 (26%)
4	NAG	Q	1	2,4	14,14,15	0.70	0	17,19,21	1.57	2 (11%)
4	NAG	Q	2	4	14,14,15	0.71	0	17,19,21	0.95	0
4	BMA	Q	3	4	11,11,12	0.89	1 (9%)	15,15,17	2.40	4 (26%)
4	NAG	R	1	2,4	14,14,15	0.77	0	17,19,21	1.11	1 (5%)
4	NAG	R	2	4	14,14,15	0.71	0	17,19,21	1.07	1 (5%)
4	BMA	R	3	4	11,11,12	0.89	1 (9%)	15,15,17	2.42	3 (20%)
4	NAG	S	1	2,4	14,14,15	0.72	0	17,19,21	0.92	1 (5%)
4	NAG	S	2	4	14,14,15	0.71	0	17,19,21	0.99	0
4	BMA	S	3	4	11,11,12	0.88	1 (9%)	15,15,17	2.39	4 (26%)
3	NAG	T	1	2,3	14,14,15	0.76	0	17,19,21	1.67	3 (17%)
3	NAG	T	2	3	14,14,15	0.70	0	17,19,21	0.84	1 (5%)
4	NAG	U	1	2,4	14,14,15	0.72	0	17,19,21	0.92	1 (5%)
4	NAG	U	2	4	14,14,15	0.73	0	17,19,21	1.21	0
4	BMA	U	3	4	11,11,12	0.88	0	15,15,17	2.28	4 (26%)
3	NAG	V	1	2,3	14,14,15	0.69	0	17,19,21	1.03	1 (5%)
3	NAG	V	2	3	14,14,15	0.73	0	17,19,21	1.61	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	W	1	2,3	14,14,15	0.70	0	17,19,21	1.27	3 (17%)
3	NAG	W	2	3	14,14,15	0.69	0	17,19,21	0.83	0
4	NAG	X	1	2,4	14,14,15	0.69	0	17,19,21	0.90	1 (5%)
4	NAG	X	2	4	14,14,15	0.68	0	17,19,21	0.94	0
4	BMA	X	3	4	11,11,12	0.91	1 (9%)	15,15,17	2.46	5 (33%)
5	NAG	Y	1	2,5	14,14,15	0.74	0	17,19,21	0.97	0
5	NAG	Y	2	5	14,14,15	0.72	0	17,19,21	1.00	1 (5%)
5	BMA	Y	3	5	11,11,12	0.86	0	15,15,17	2.35	4 (26%)
5	MAN	Y	4	5	11,11,12	0.64	0	15,15,17	1.46	1 (6%)
5	MAN	Y	5	5	11,11,12	0.71	0	15,15,17	1.24	1 (6%)
5	MAN	Y	6	5	11,11,12	0.68	0	15,15,17	1.23	1 (6%)
4	NAG	Z	1	2,4	14,14,15	0.70	0	17,19,21	0.93	0
4	NAG	Z	2	4	14,14,15	0.71	0	17,19,21	0.92	0
4	BMA	Z	3	4	11,11,12	0.87	0	15,15,17	2.51	5 (33%)
3	NAG	a	1	2,3	14,14,15	0.69	0	17,19,21	0.88	0
3	NAG	a	2	3	14,14,15	0.72	0	17,19,21	0.94	0
6	NAG	b	1	2,6	14,14,15	0.71	0	17,19,21	1.01	2 (11%)
6	NAG	b	2	6	14,14,15	0.68	0	17,19,21	1.55	2 (11%)
6	BMA	b	3	6	11,11,12	0.88	0	15,15,17	2.45	5 (33%)
6	MAN	b	4	6	11,11,12	0.63	0	15,15,17	1.47	1 (6%)
7	NAG	c	1	2,7	14,14,15	0.71	0	17,19,21	1.16	1 (5%)
7	NAG	c	2	7	14,14,15	0.74	0	17,19,21	1.02	1 (5%)
7	BMA	c	3	7	11,11,12	0.86	0	15,15,17	2.39	6 (40%)
7	MAN	c	4	7	11,11,12	0.74	0	15,15,17	1.33	1 (6%)
7	MAN	c	5	7	11,11,12	0.70	0	15,15,17	1.16	1 (6%)
3	NAG	d	1	2,3	14,14,15	0.76	0	17,19,21	1.08	1 (5%)
3	NAG	d	2	3	14,14,15	0.69	0	17,19,21	0.85	0
4	NAG	e	1	2,4	14,14,15	0.79	0	17,19,21	2.94	4 (23%)
4	NAG	e	2	4	14,14,15	0.70	0	17,19,21	0.90	0
4	BMA	e	3	4	11,11,12	0.86	1 (9%)	15,15,17	2.46	4 (26%)
4	NAG	f	1	2,4	14,14,15	0.69	0	17,19,21	1.57	2 (11%)
4	NAG	f	2	4	14,14,15	0.70	0	17,19,21	0.96	0
4	BMA	f	3	4	11,11,12	0.89	0	15,15,17	2.41	5 (33%)
4	NAG	g	1	2,4	14,14,15	0.77	0	17,19,21	1.11	1 (5%)
4	NAG	g	2	4	14,14,15	0.71	0	17,19,21	1.07	1 (5%)
4	BMA	g	3	4	11,11,12	0.89	1 (9%)	15,15,17	2.43	3 (20%)
4	NAG	h	1	2,4	14,14,15	0.71	0	17,19,21	0.91	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	h	2	4	14,14,15	0.71	0	17,19,21	0.98	0
4	BMA	h	3	4	11,11,12	0.87	1 (9%)	15,15,17	2.38	4 (26%)
3	NAG	i	1	2,3	14,14,15	0.76	0	17,19,21	1.67	3 (17%)
3	NAG	i	2	3	14,14,15	0.70	0	17,19,21	0.84	1 (5%)
4	NAG	j	1	2,4	14,14,15	0.73	0	17,19,21	0.92	1 (5%)
4	NAG	j	2	4	14,14,15	0.72	0	17,19,21	1.21	0
4	BMA	j	3	4	11,11,12	0.89	1 (9%)	15,15,17	2.28	4 (26%)
3	NAG	k	1	2,3	14,14,15	0.69	0	17,19,21	1.02	1 (5%)
3	NAG	k	2	3	14,14,15	0.74	0	17,19,21	1.61	3 (17%)
3	NAG	l	1	2,3	14,14,15	0.70	0	17,19,21	1.25	3 (17%)
3	NAG	l	2	3	14,14,15	0.68	0	17,19,21	0.82	0
4	NAG	m	1	2,4	14,14,15	0.69	0	17,19,21	0.90	1 (5%)
4	NAG	m	2	4	14,14,15	0.69	0	17,19,21	0.94	0
4	BMA	m	3	4	11,11,12	0.90	1 (9%)	15,15,17	2.45	4 (26%)
5	NAG	n	1	2,5	14,14,15	0.72	0	17,19,21	0.98	0
5	NAG	n	2	5	14,14,15	0.73	0	17,19,21	1.00	1 (5%)
5	BMA	n	3	5	11,11,12	0.87	0	15,15,17	2.35	4 (26%)
5	MAN	n	4	5	11,11,12	0.63	0	15,15,17	1.46	1 (6%)
5	MAN	n	5	5	11,11,12	0.72	0	15,15,17	1.25	1 (6%)
5	MAN	n	6	5	11,11,12	0.70	0	15,15,17	1.24	1 (6%)
4	NAG	o	1	2,4	14,14,15	0.71	0	17,19,21	0.92	0
4	NAG	o	2	4	14,14,15	0.70	0	17,19,21	0.92	0
4	BMA	o	3	4	11,11,12	0.88	1 (9%)	15,15,17	2.52	5 (33%)
3	NAG	p	1	2,3	14,14,15	0.70	0	17,19,21	0.87	0
3	NAG	p	2	3	14,14,15	0.73	0	17,19,21	0.94	0
6	NAG	q	1	2,6	14,14,15	0.72	0	17,19,21	1.00	2 (11%)
6	NAG	q	2	6	14,14,15	0.69	0	17,19,21	1.55	2 (11%)
6	BMA	q	3	6	11,11,12	0.88	0	15,15,17	2.45	5 (33%)
6	MAN	q	4	6	11,11,12	0.63	0	15,15,17	1.47	1 (6%)
7	NAG	r	1	2,7	14,14,15	0.70	0	17,19,21	1.16	1 (5%)
7	NAG	r	2	7	14,14,15	0.73	0	17,19,21	1.01	1 (5%)
7	BMA	r	3	7	11,11,12	0.85	0	15,15,17	2.40	6 (40%)
7	MAN	r	4	7	11,11,12	0.76	0	15,15,17	1.33	1 (6%)
7	MAN	r	5	7	11,11,12	0.71	0	15,15,17	1.17	1 (6%)
3	NAG	s	1	2,3	14,14,15	0.74	0	17,19,21	1.07	1 (5%)
3	NAG	s	2	3	14,14,15	0.70	0	17,19,21	0.86	0
4	NAG	t	1	2,4	14,14,15	0.78	0	17,19,21	2.94	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	t	2	4	14,14,15	0.70	0	17,19,21	0.91	0
4	BMA	t	3	4	11,11,12	0.86	0	15,15,17	2.46	4 (26%)
4	NAG	u	1	2,4	14,14,15	0.68	0	17,19,21	1.56	2 (11%)
4	NAG	u	2	4	14,14,15	0.71	0	17,19,21	0.96	0
4	BMA	u	3	4	11,11,12	0.89	0	15,15,17	2.40	5 (33%)
4	NAG	v	1	2,4	14,14,15	0.77	0	17,19,21	1.12	1 (5%)
4	NAG	v	2	4	14,14,15	0.70	0	17,19,21	1.07	1 (5%)
4	BMA	v	3	4	11,11,12	0.91	1 (9%)	15,15,17	2.42	3 (20%)
4	NAG	w	1	2,4	14,14,15	0.70	0	17,19,21	0.92	1 (5%)
4	NAG	w	2	4	14,14,15	0.71	0	17,19,21	0.98	0
4	BMA	w	3	4	11,11,12	0.88	1 (9%)	15,15,17	2.38	3 (20%)
3	NAG	x	1	2,3	14,14,15	0.76	0	17,19,21	1.67	3 (17%)
3	NAG	x	2	3	14,14,15	0.71	0	17,19,21	0.84	1 (5%)
4	NAG	y	1	2,4	14,14,15	0.73	0	17,19,21	0.92	1 (5%)
4	NAG	y	2	4	14,14,15	0.72	0	17,19,21	1.22	1 (5%)
4	BMA	y	3	4	11,11,12	0.90	1 (9%)	15,15,17	2.29	4 (26%)

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	D	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	3/6/23/26	0/1/1/1
3	NAG	E	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
4	NAG	H	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	0/2/19/22	0/1/1/1
5	NAG	J	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	J	2	5	-	0/6/23/26	0/1/1/1
5	BMA	J	3	5	-	2/2/19/22	0/1/1/1
5	MAN	J	4	5	-	2/2/19/22	0/1/1/1
5	MAN	J	5	5	-	0/2/19/22	0/1/1/1
5	MAN	J	6	5	-	0/2/19/22	0/1/1/1
4	NAG	K	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	0/6/23/26	0/1/1/1
4	BMA	K	3	4	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	y	3	4	-	1/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	v	3	BMA	C2-C3	2.12	1.55	1.52
4	X	3	BMA	C2-C3	2.07	1.55	1.52
4	m	3	BMA	C2-C3	2.05	1.55	1.52
4	R	3	BMA	C2-C3	2.04	1.55	1.52
4	h	3	BMA	C2-C3	2.04	1.55	1.52

The worst 5 of 240 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	t	1	NAG	C2-N2-C7	10.56	137.05	122.90
4	e	1	NAG	C2-N2-C7	10.56	137.05	122.90
4	P	1	NAG	C2-N2-C7	10.55	137.03	122.90
4	o	3	BMA	C1-O5-C5	7.84	122.69	112.19
4	K	3	BMA	C1-O5-C5	7.83	122.67	112.19

There are no chirality outliers.

5 of 87 torsion outliers are listed below:

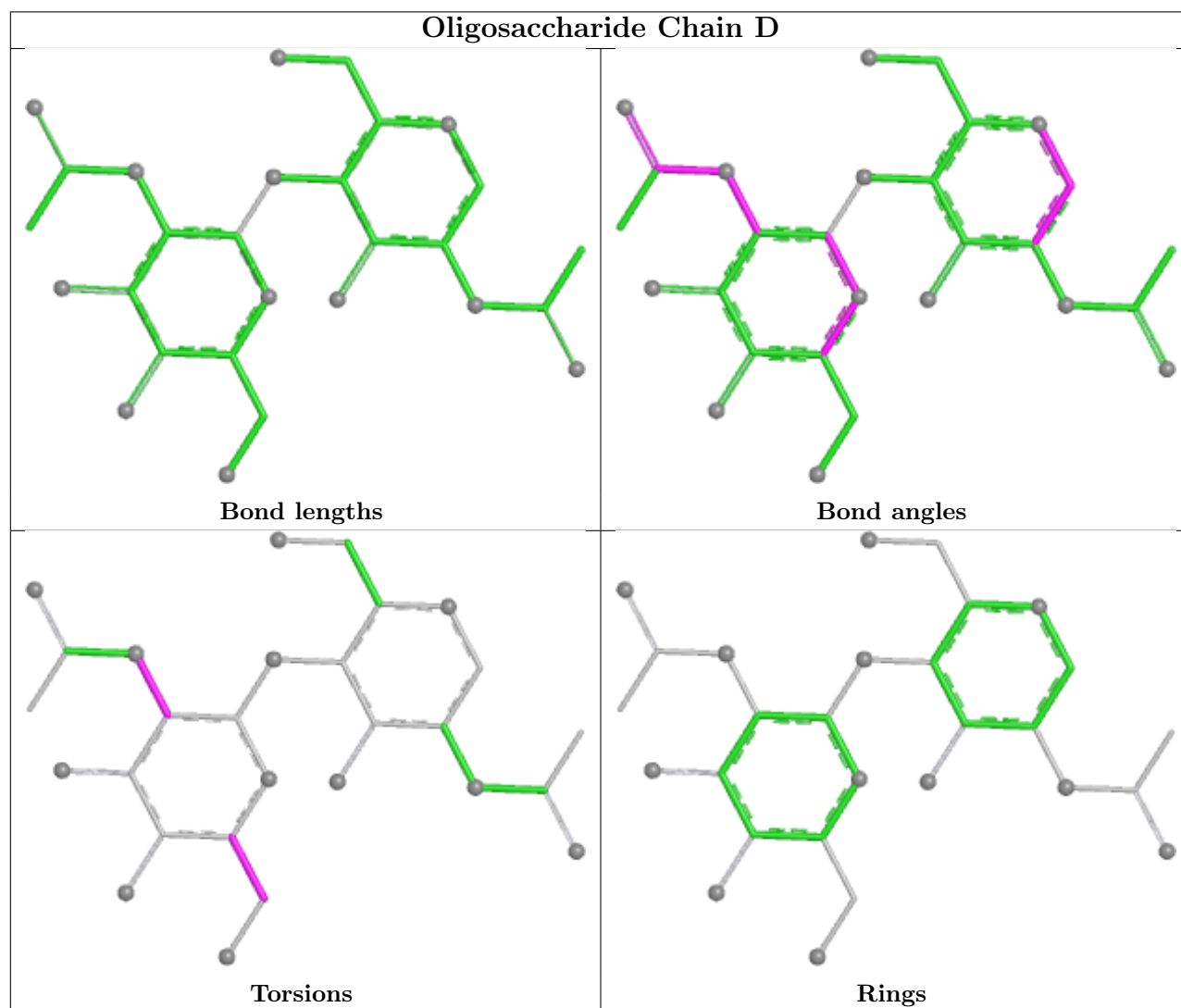
Mol	Chain	Res	Type	Atoms
5	J	3	BMA	O5-C5-C6-O6
5	Y	3	BMA	O5-C5-C6-O6
5	n	3	BMA	O5-C5-C6-O6
5	J	3	BMA	C4-C5-C6-O6
5	Y	3	BMA	C4-C5-C6-O6

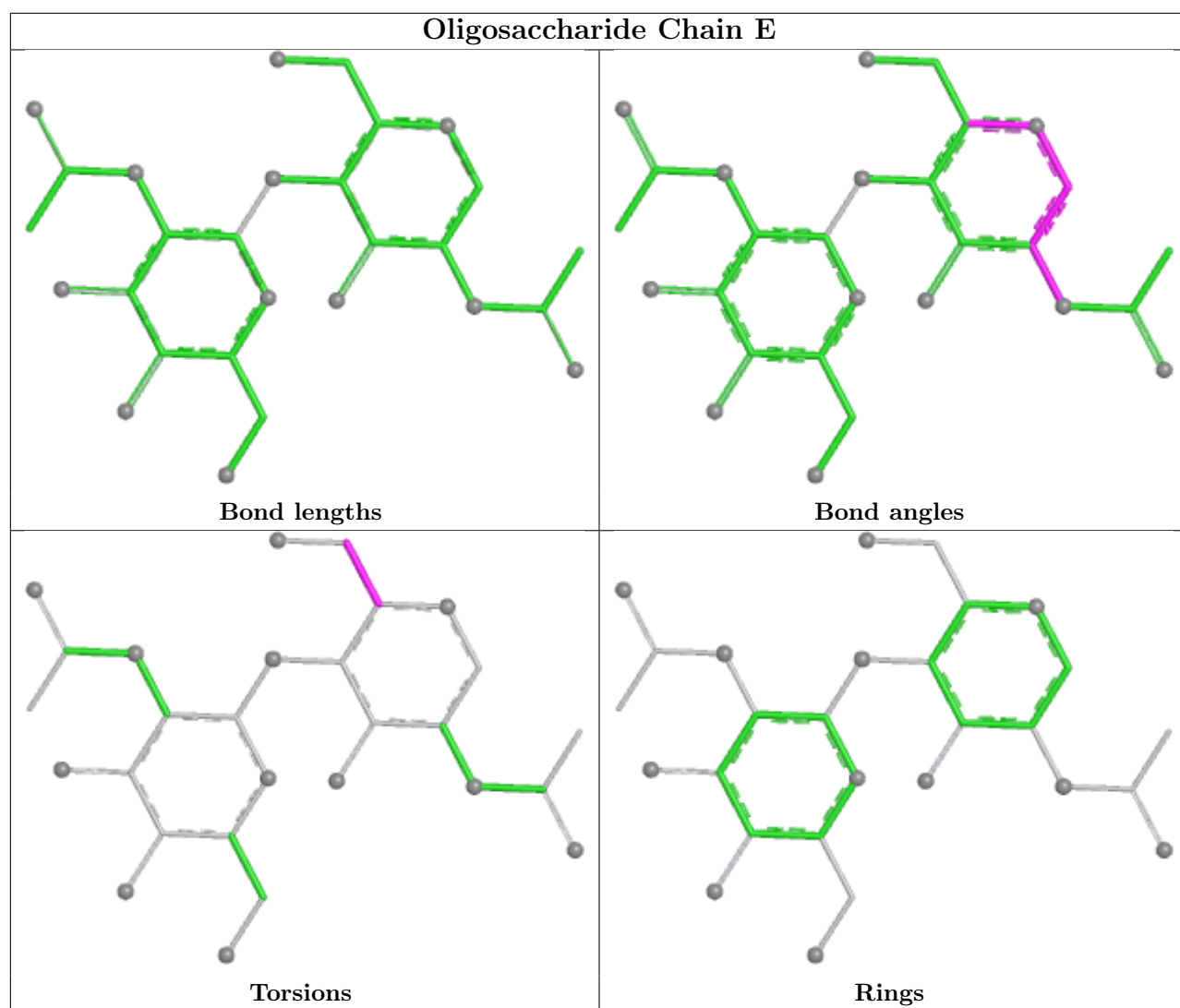
There are no ring outliers.

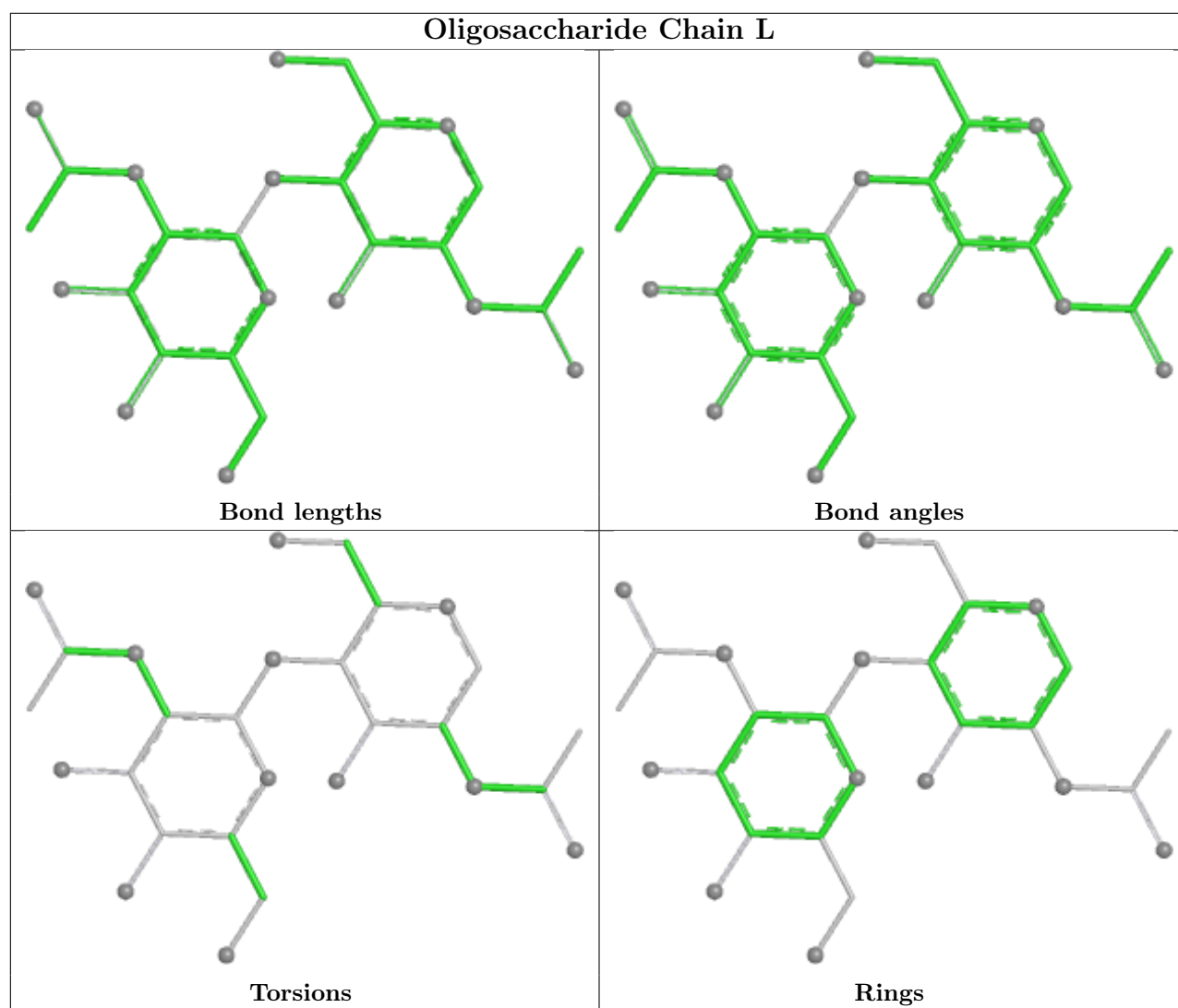
6 monomers are involved in 6 short contacts:

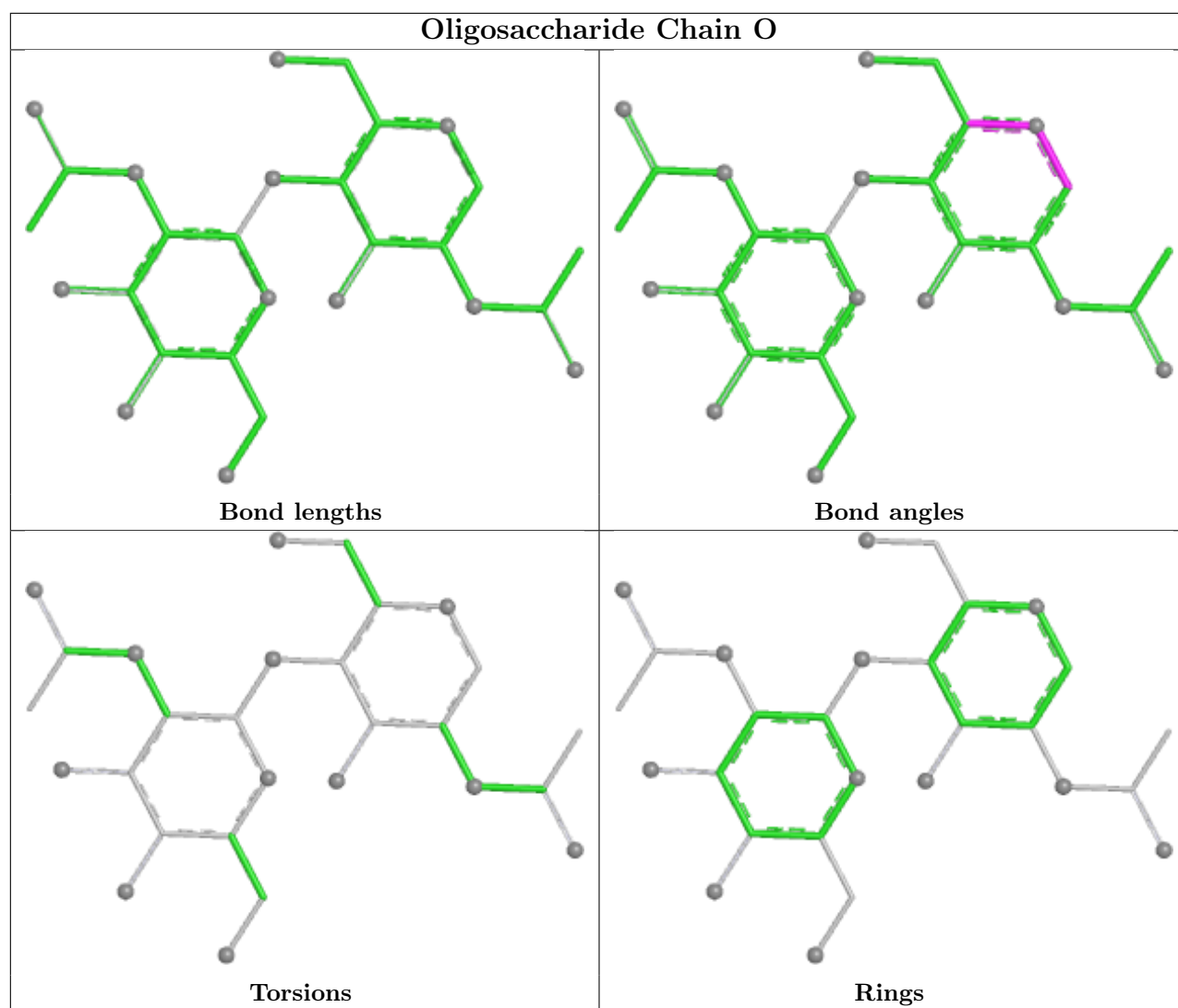
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1	NAG	1	0
3	E	1	NAG	1	0
3	k	1	NAG	1	0
3	W	1	NAG	1	0
3	l	1	NAG	1	0
3	V	1	NAG	1	0

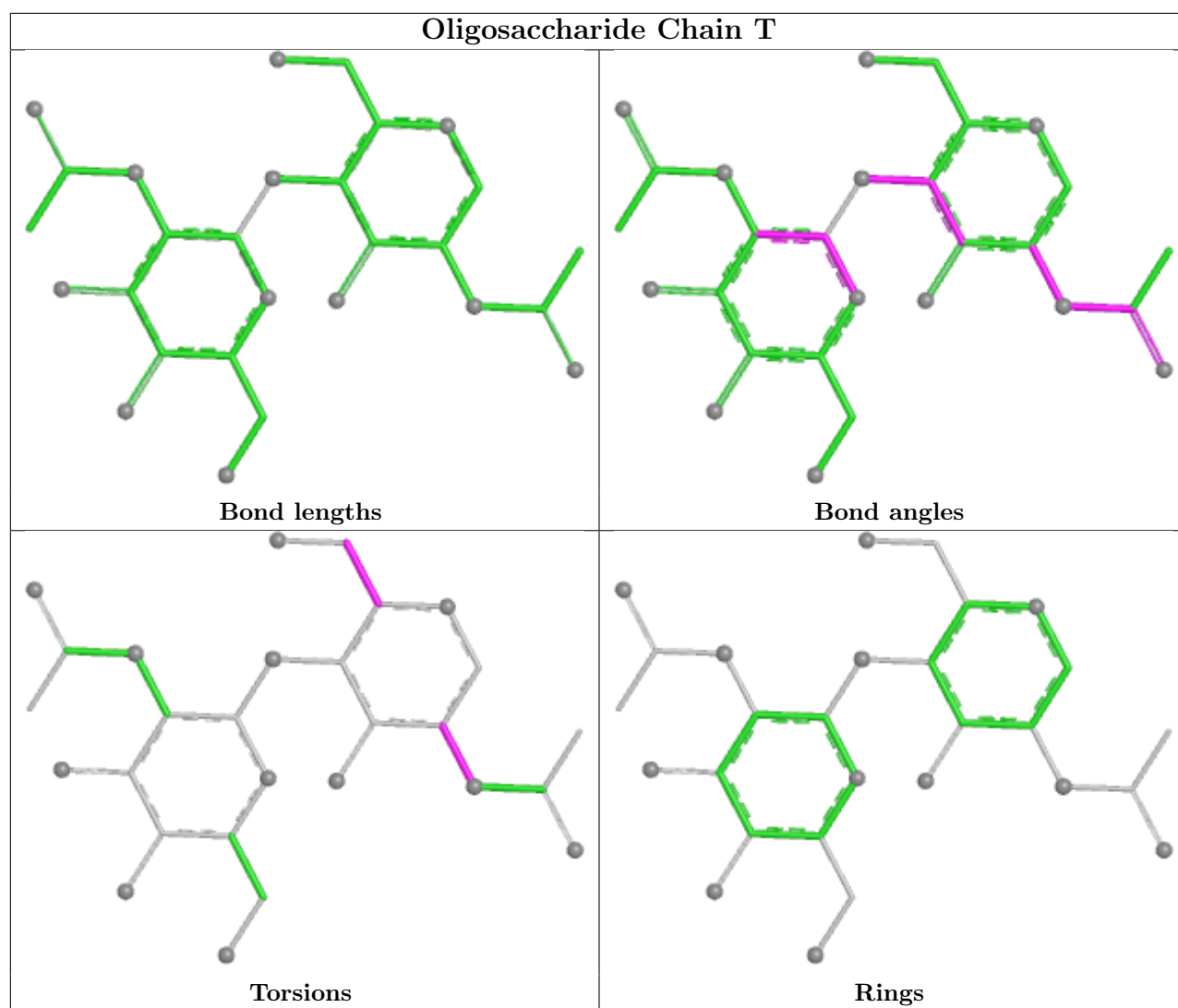
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

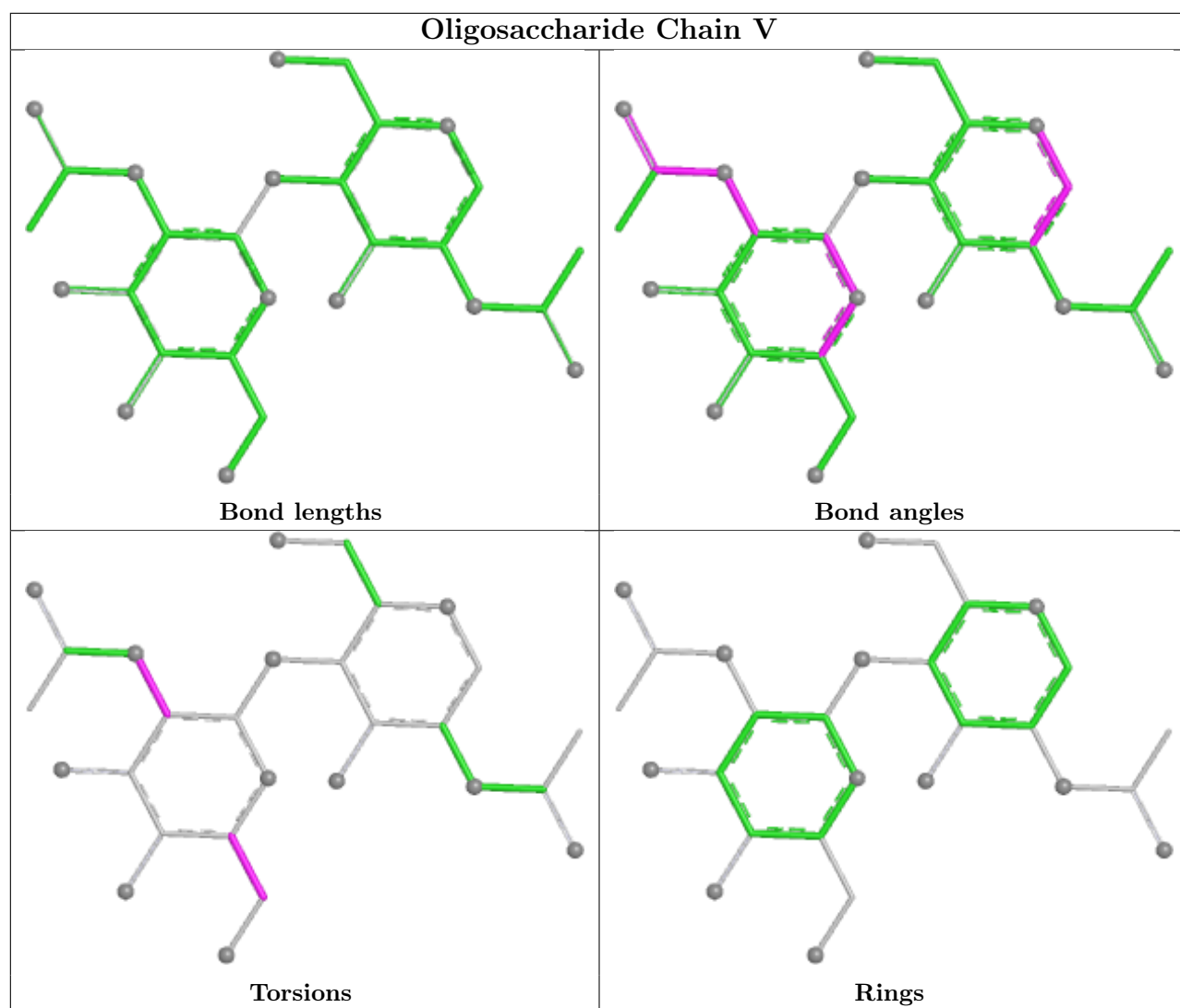


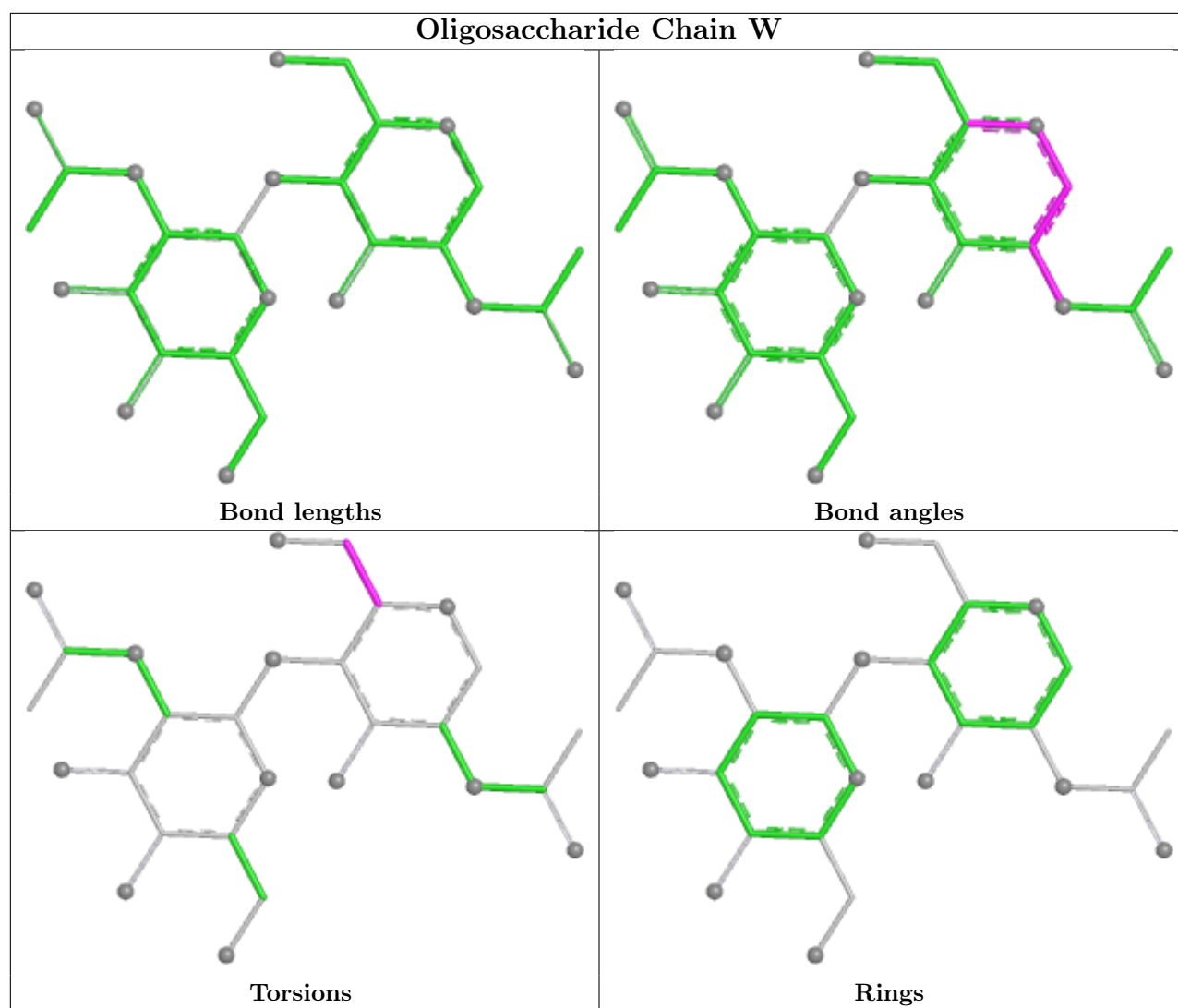


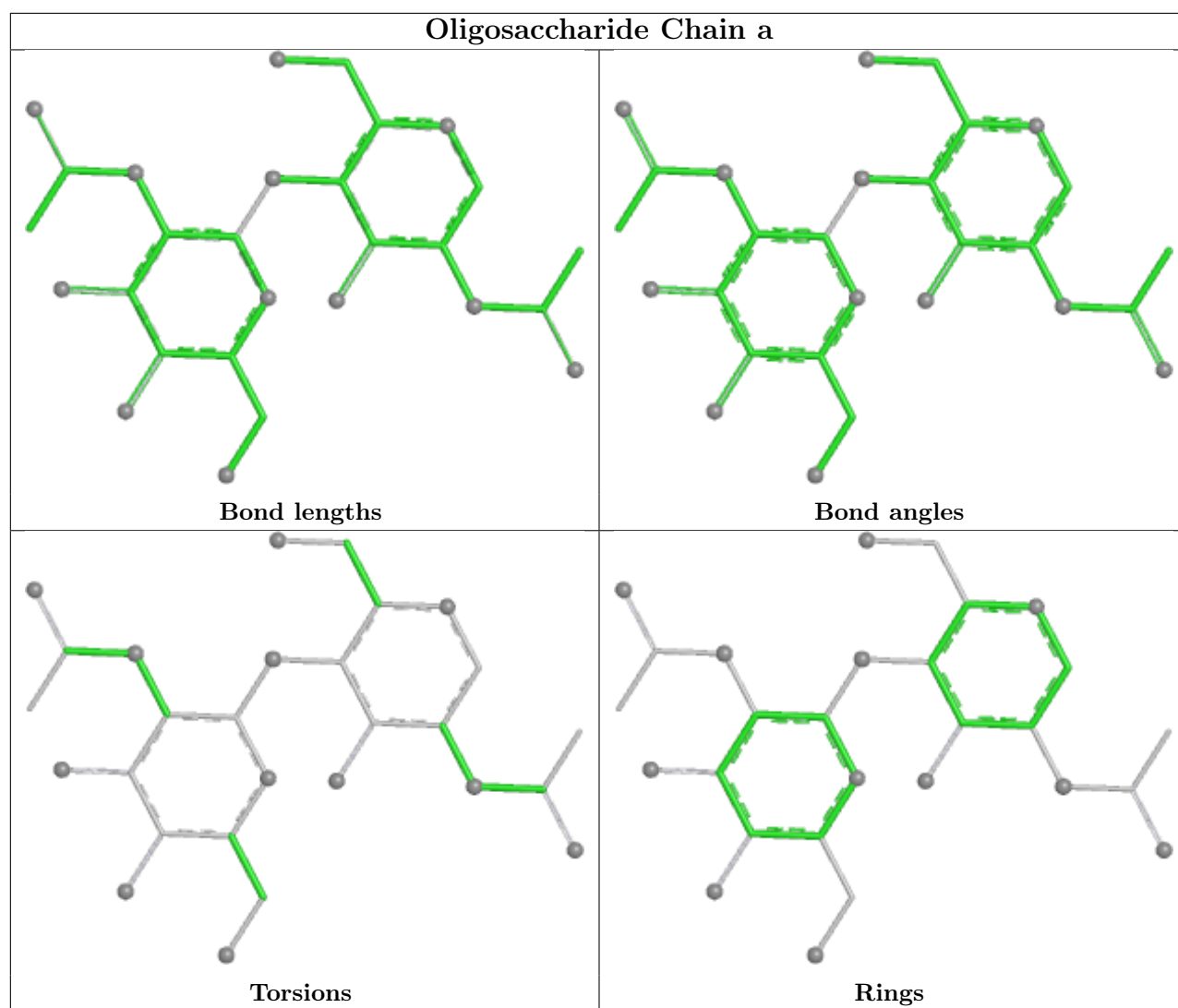


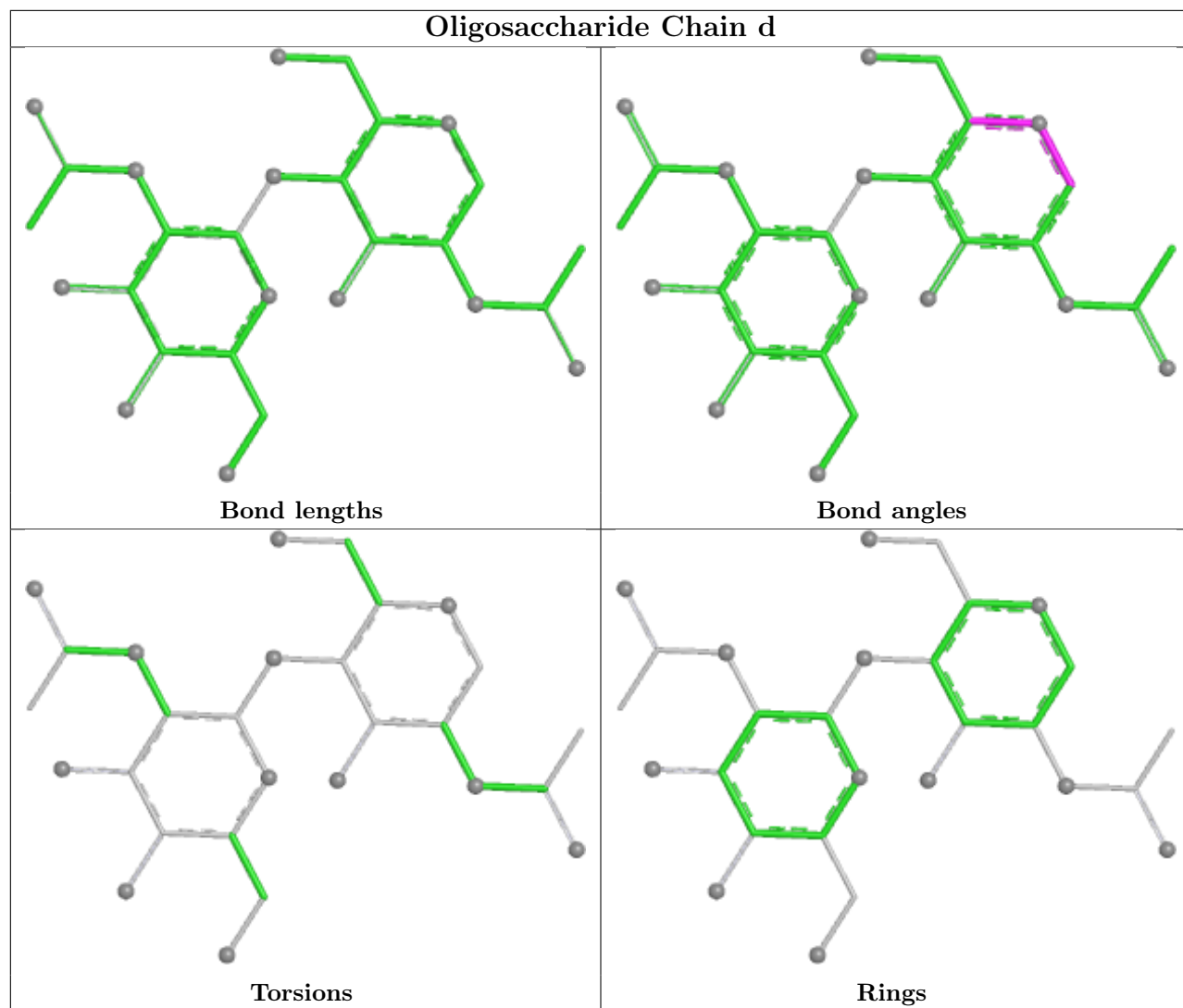


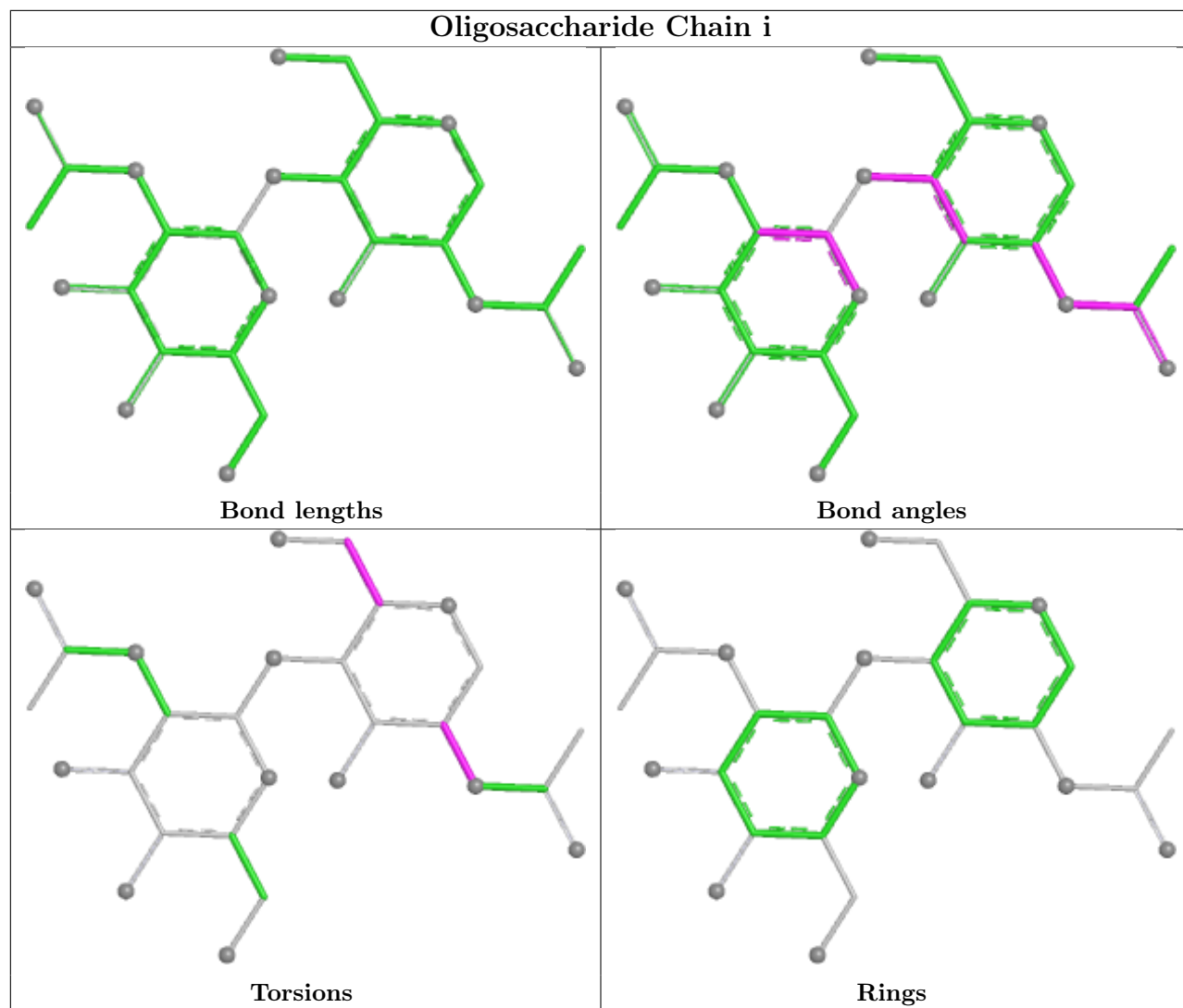


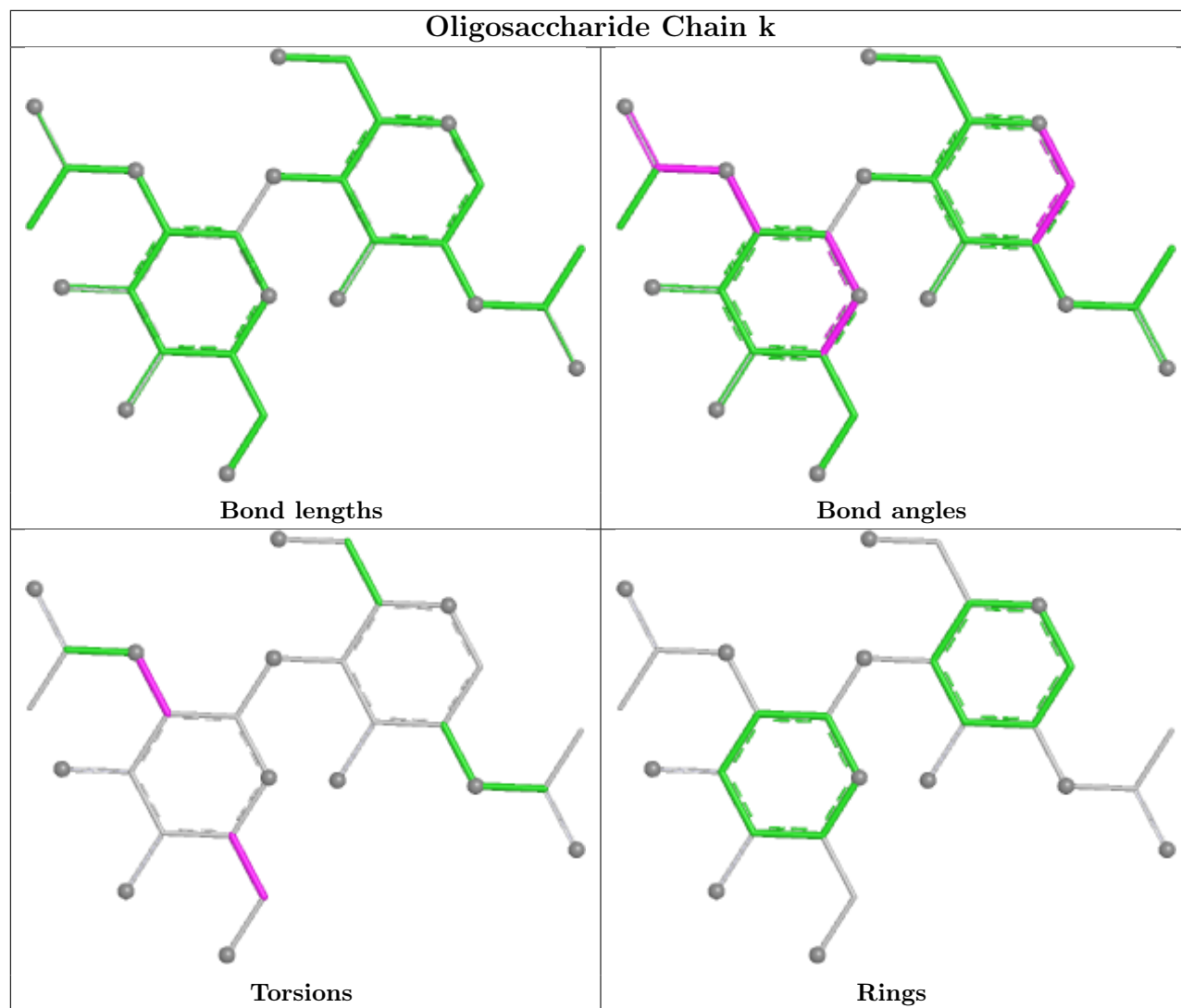


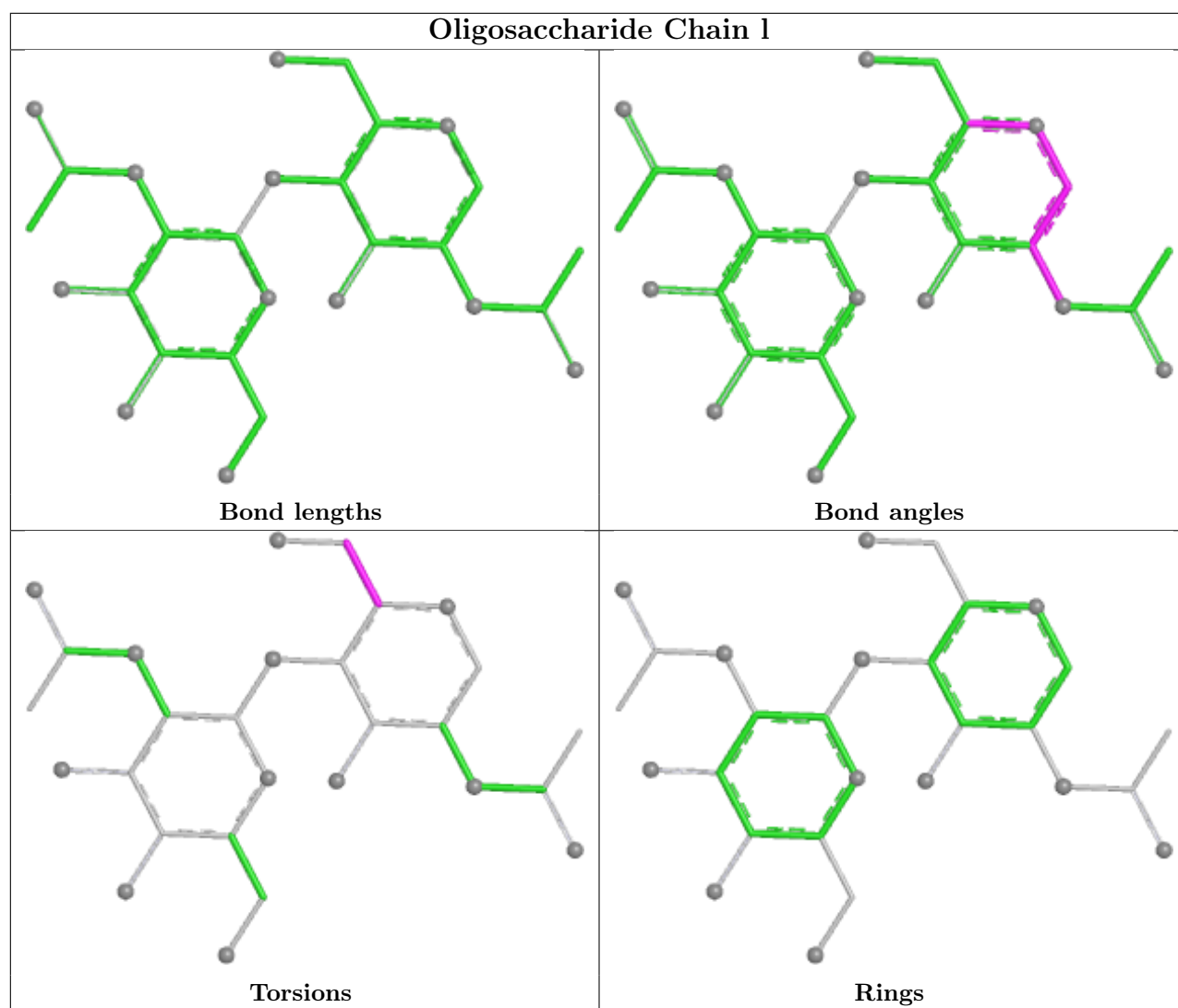


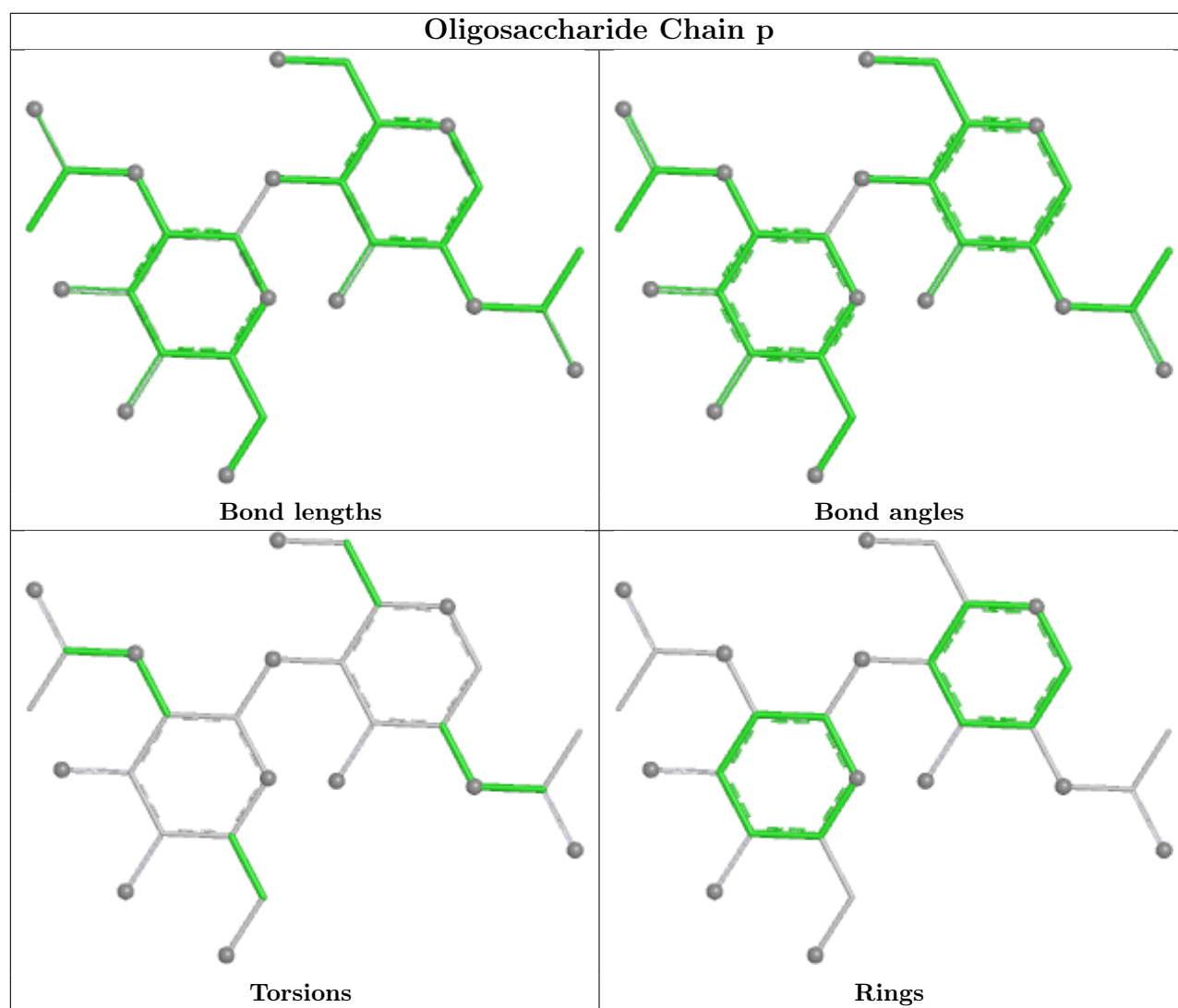


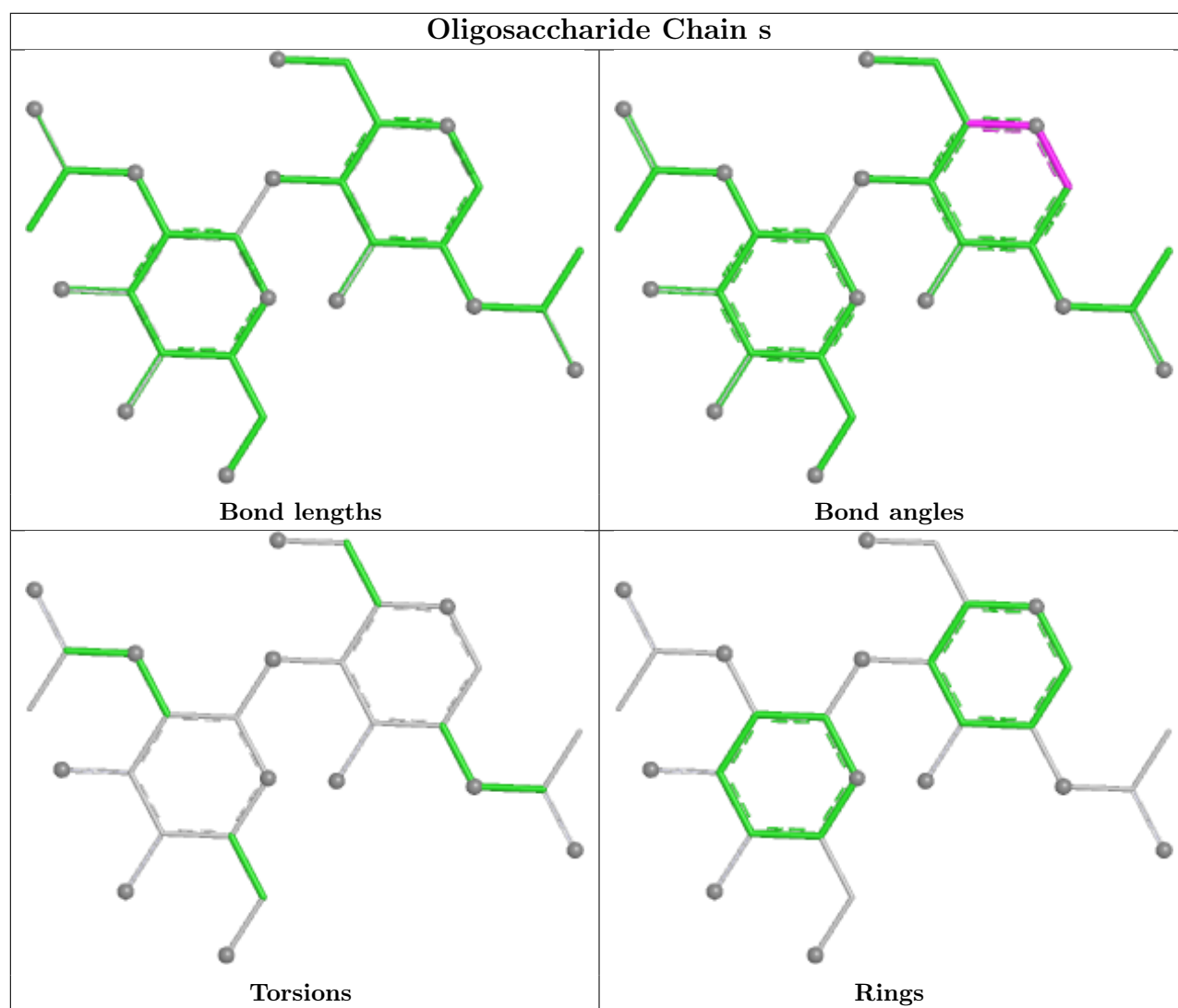


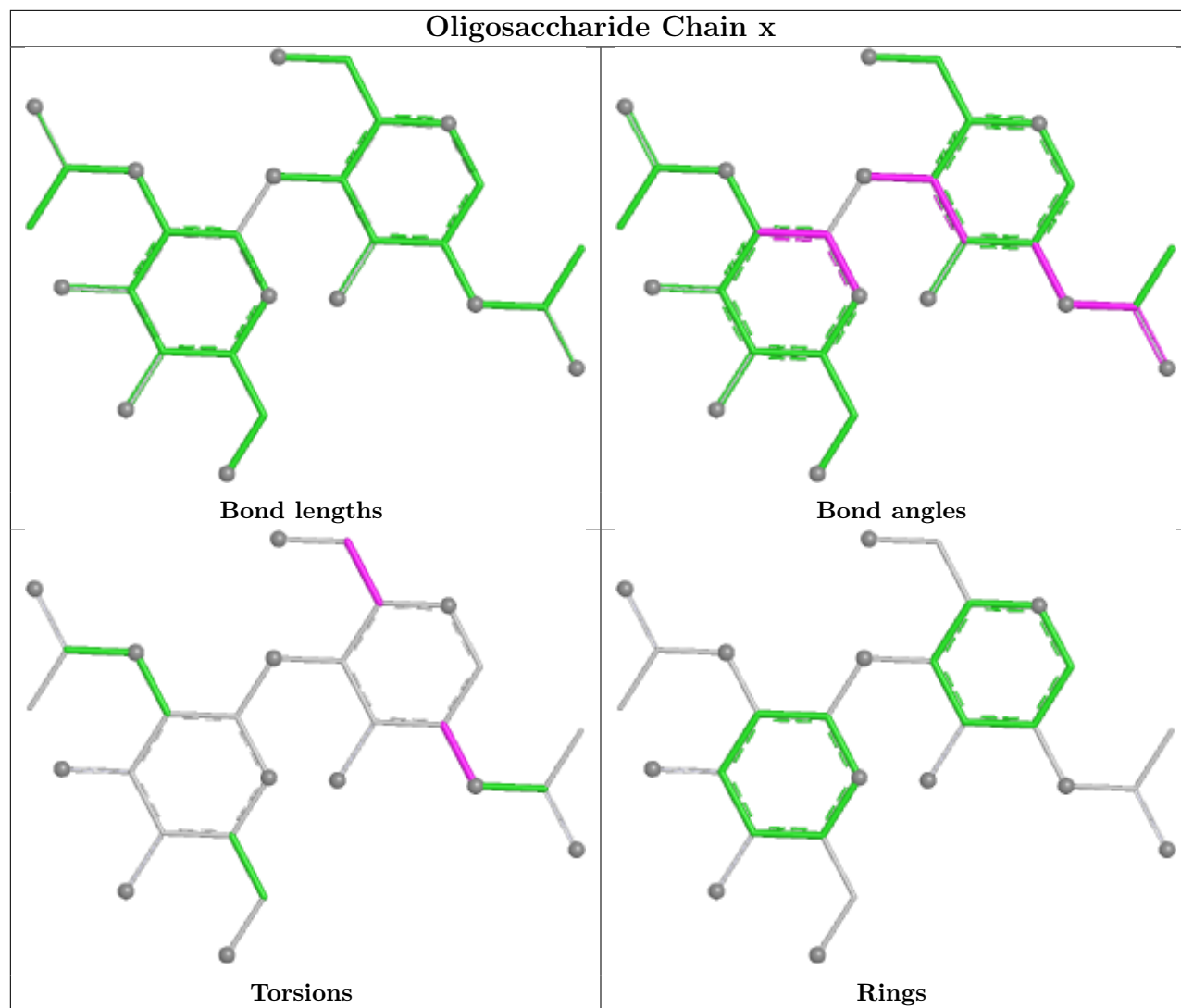


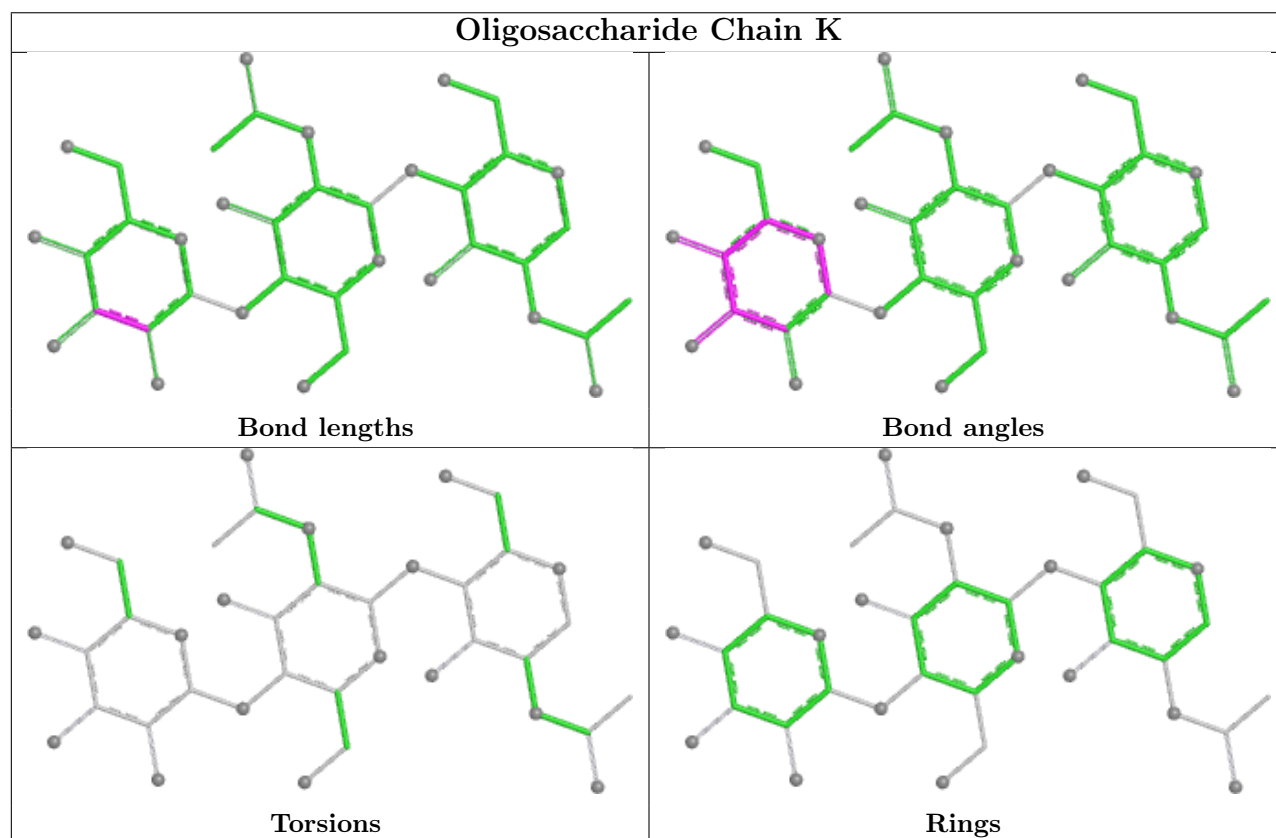
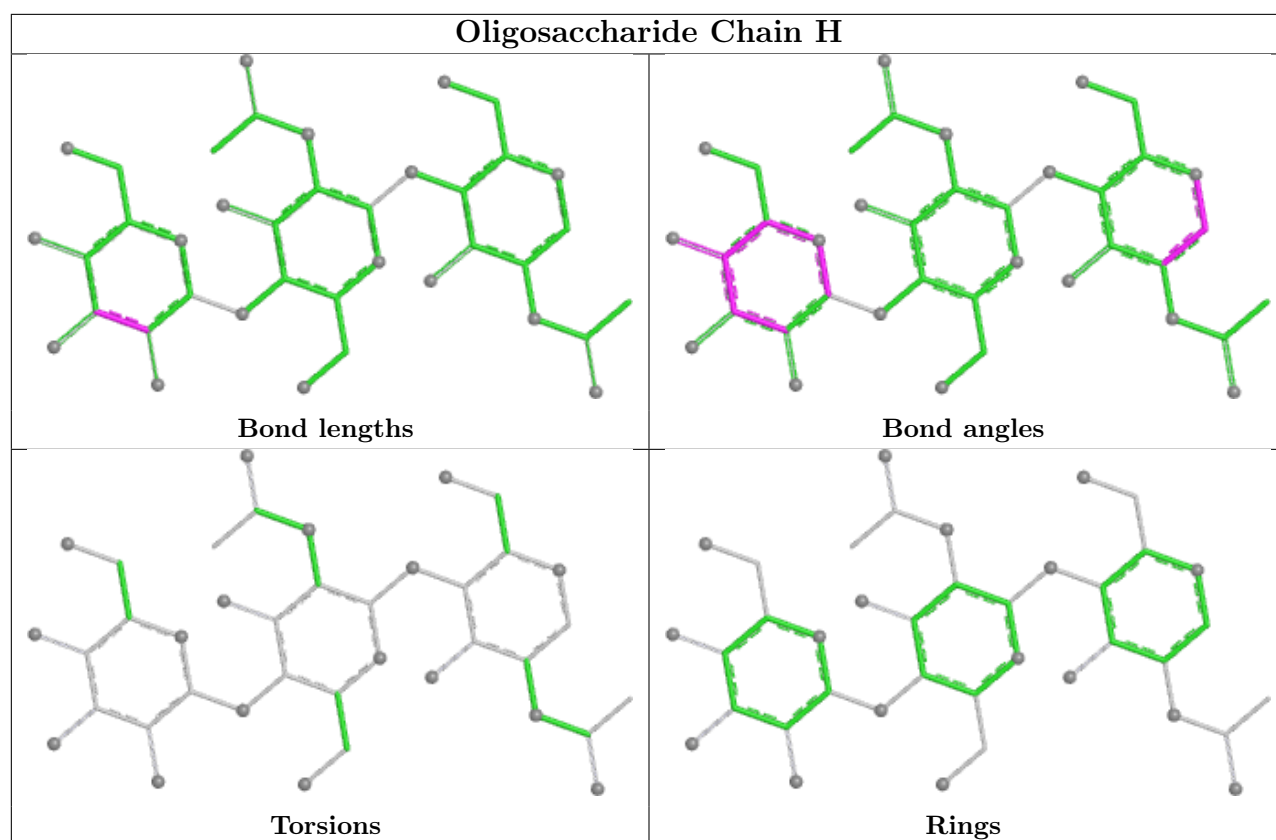


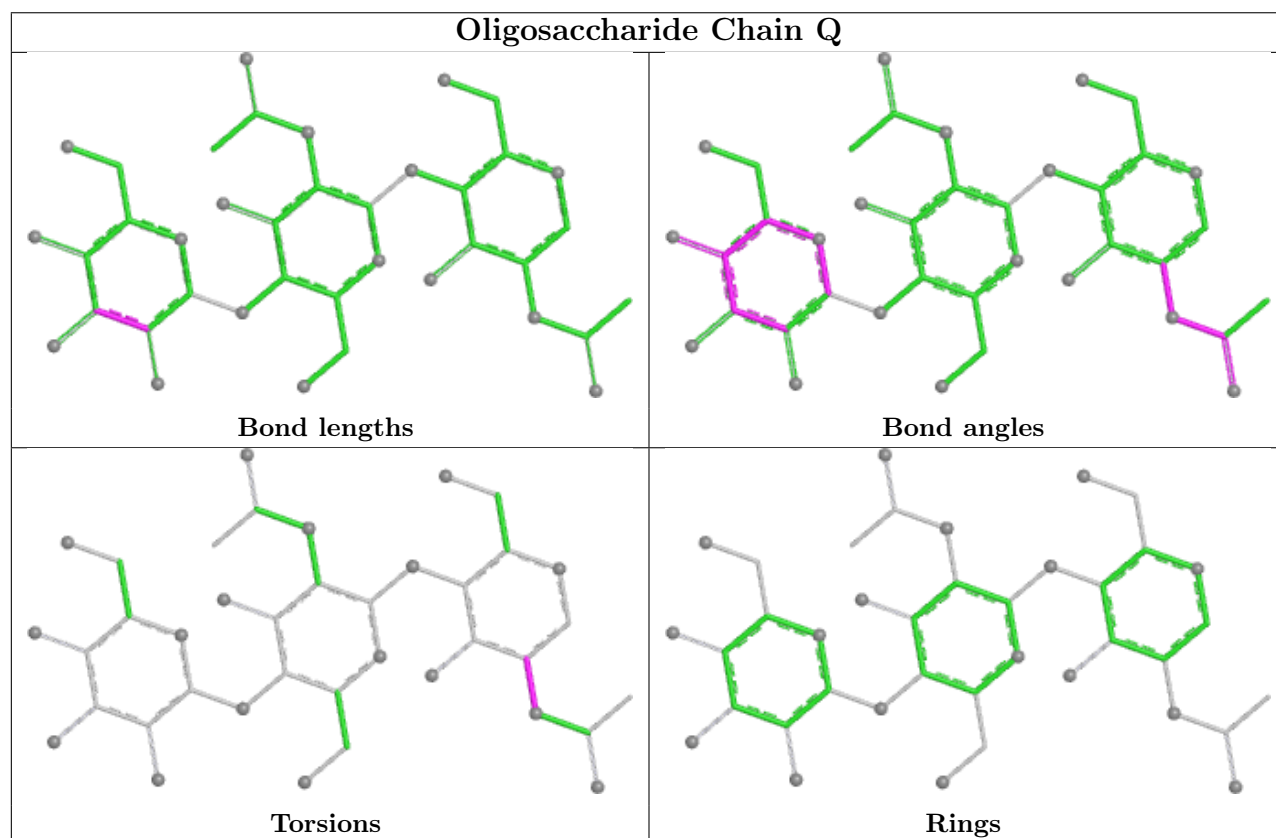
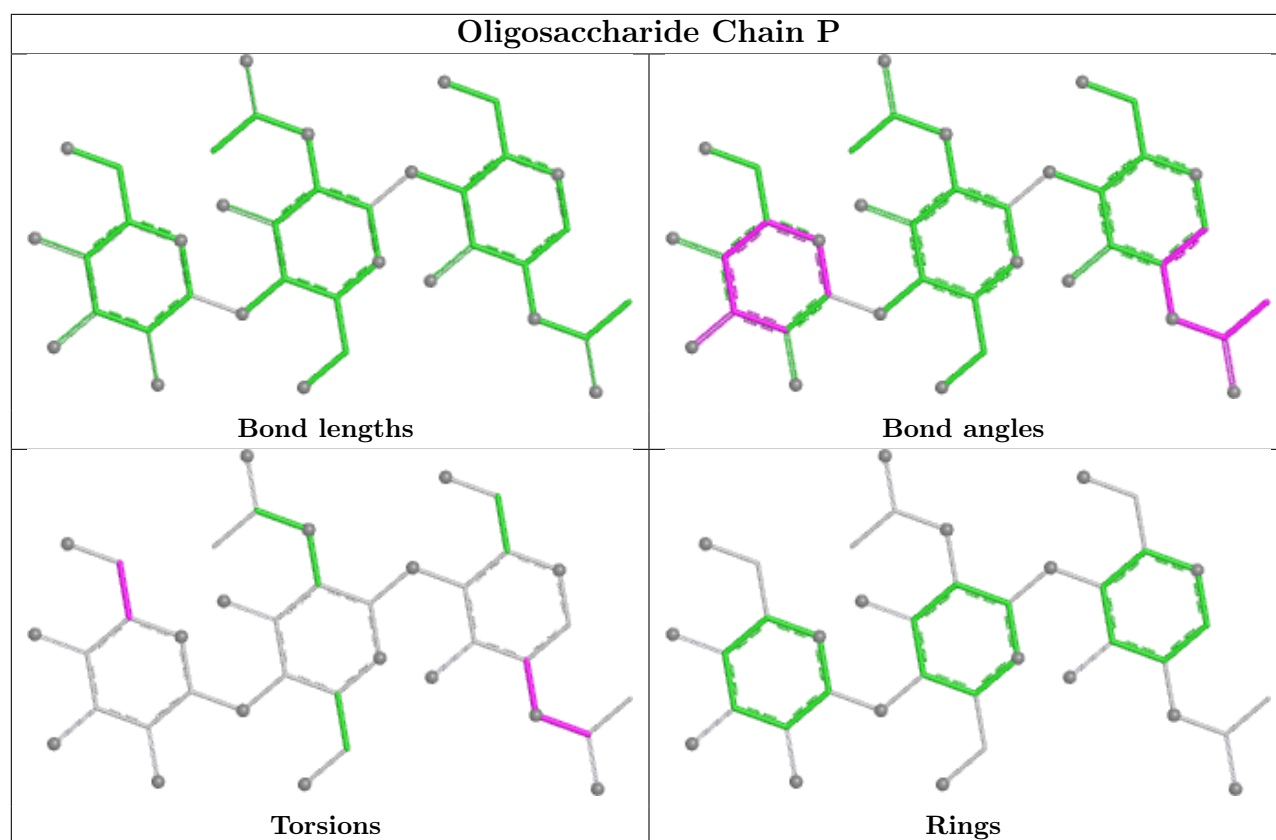


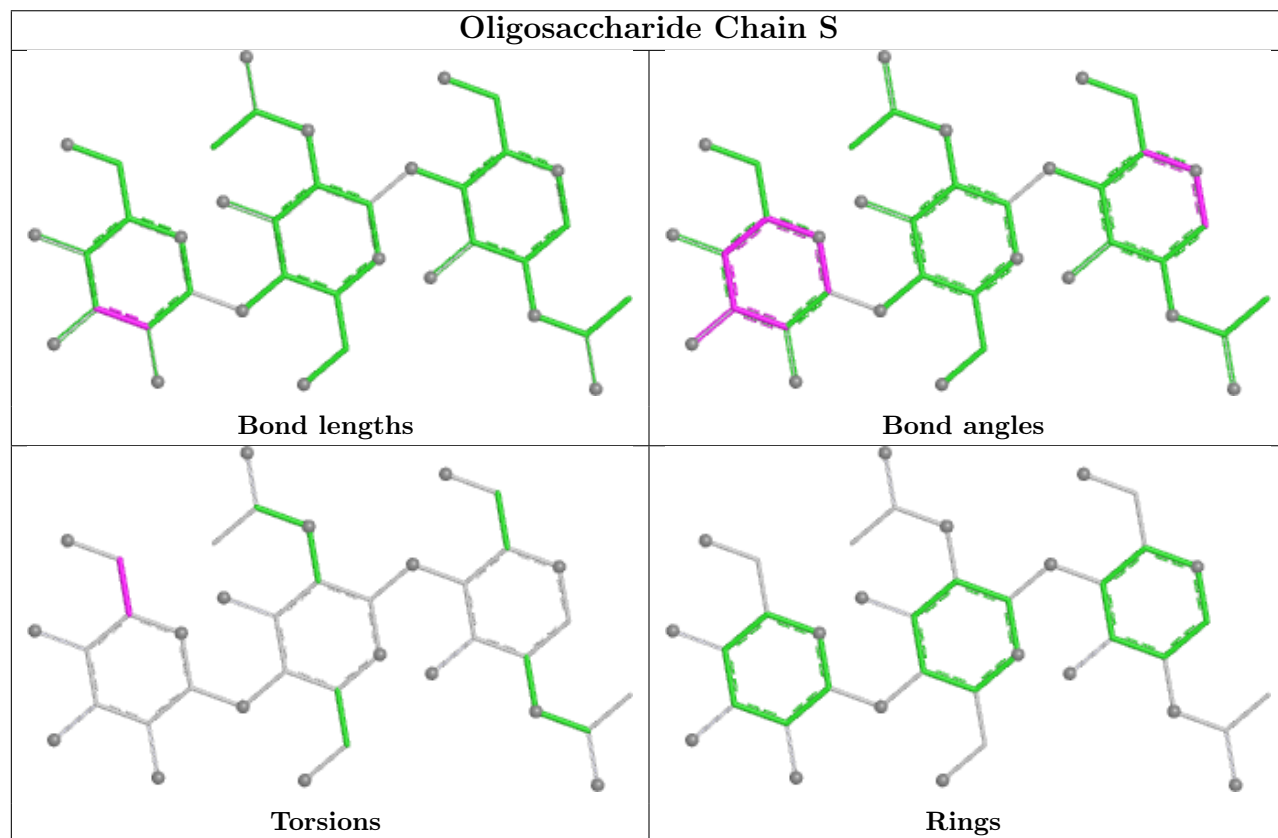
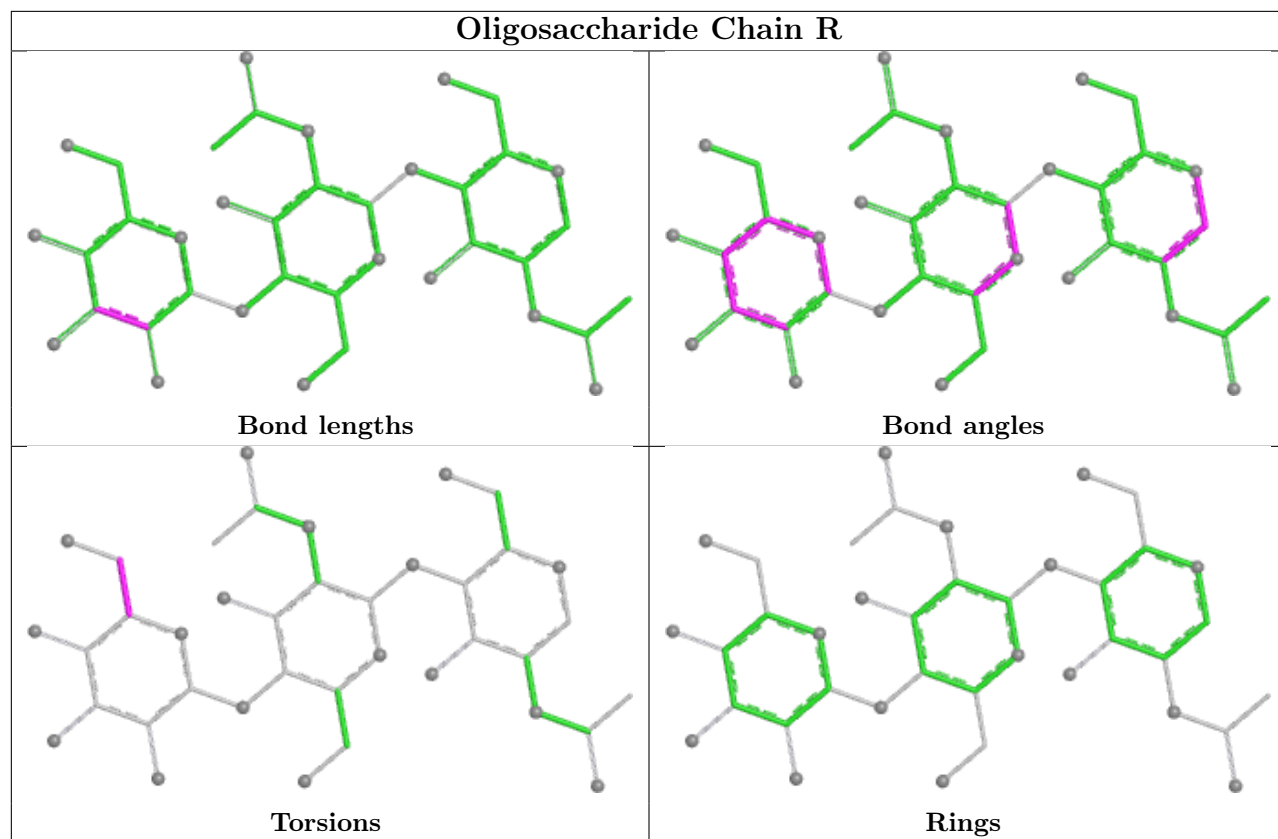


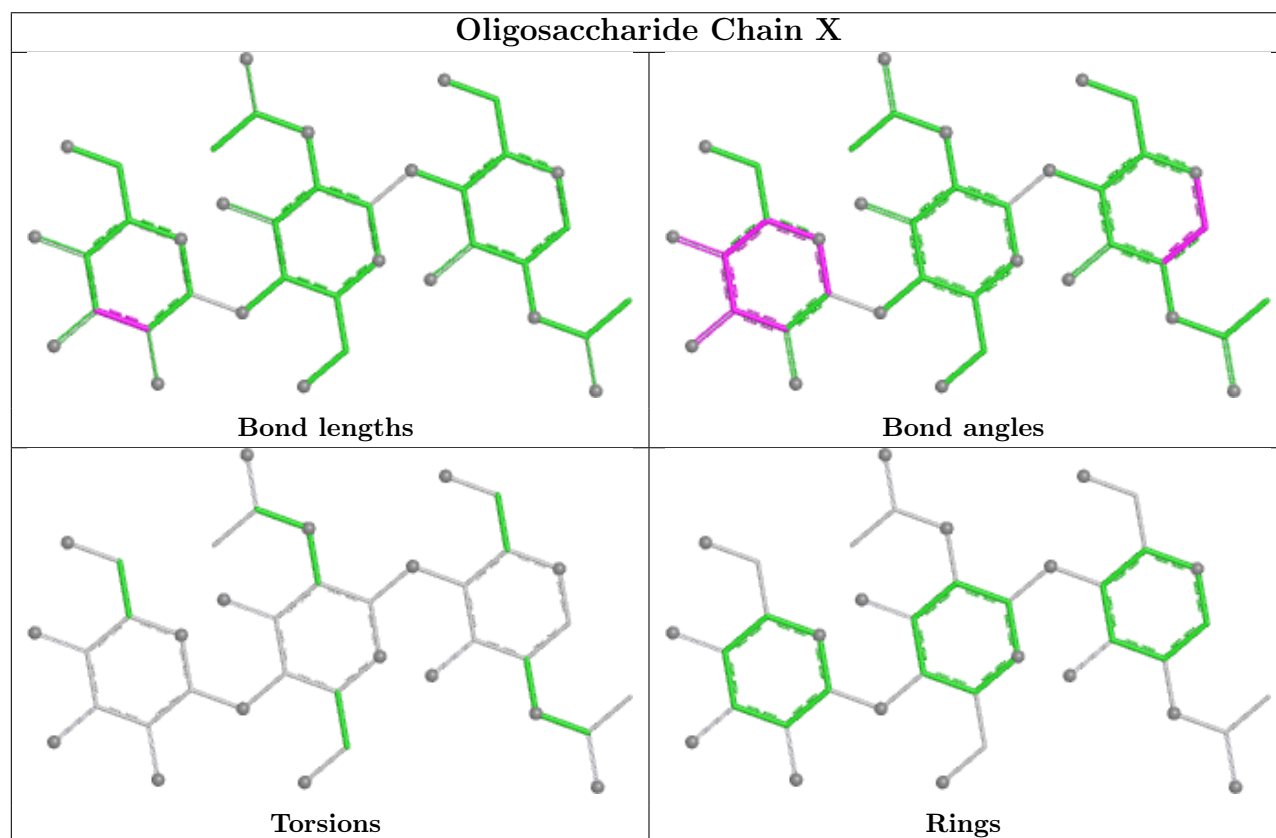
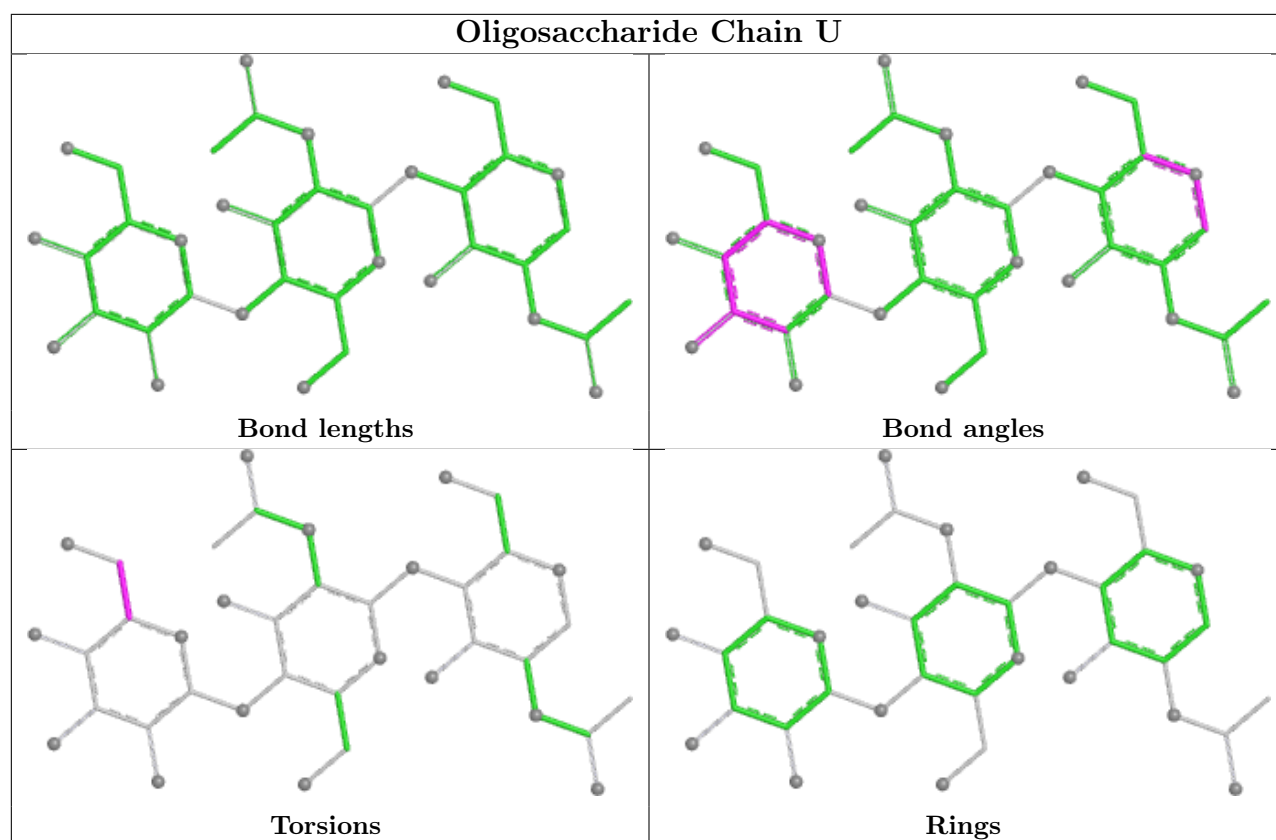


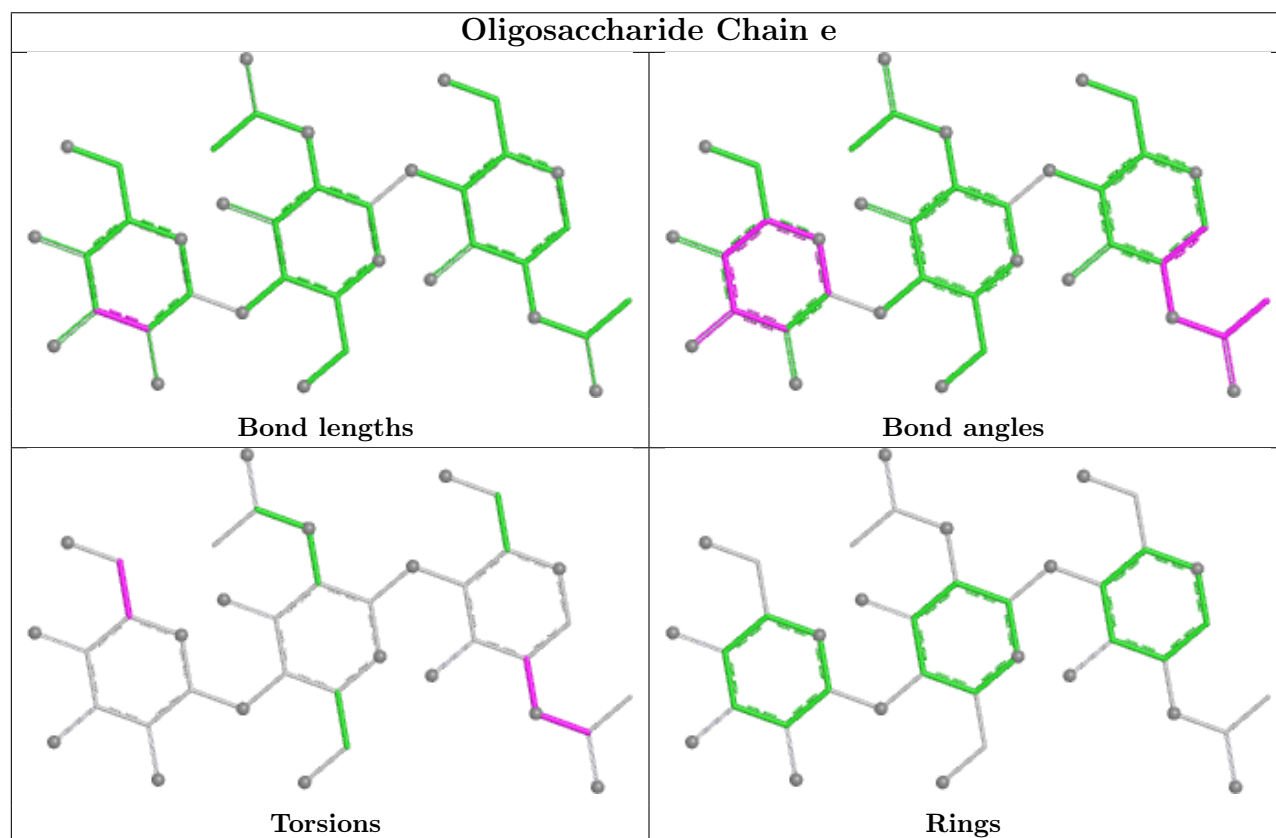
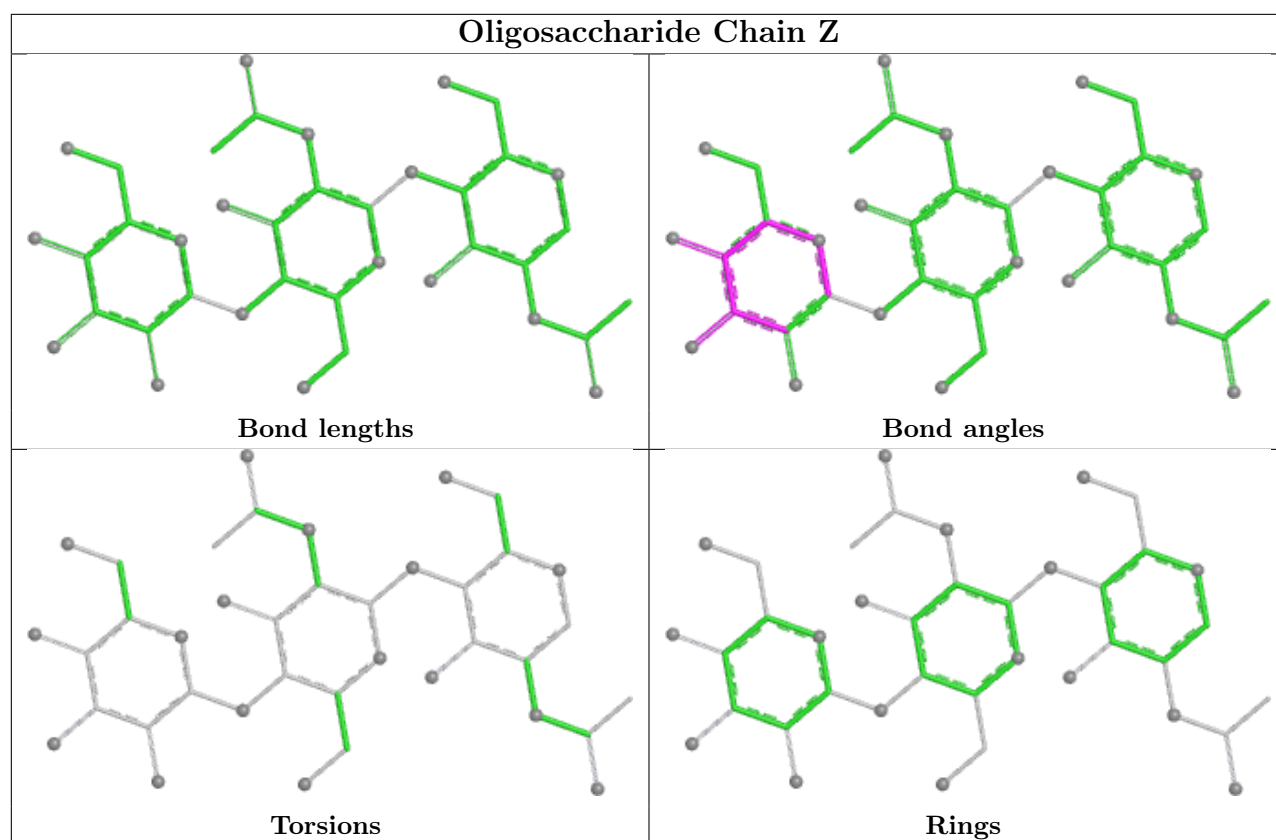


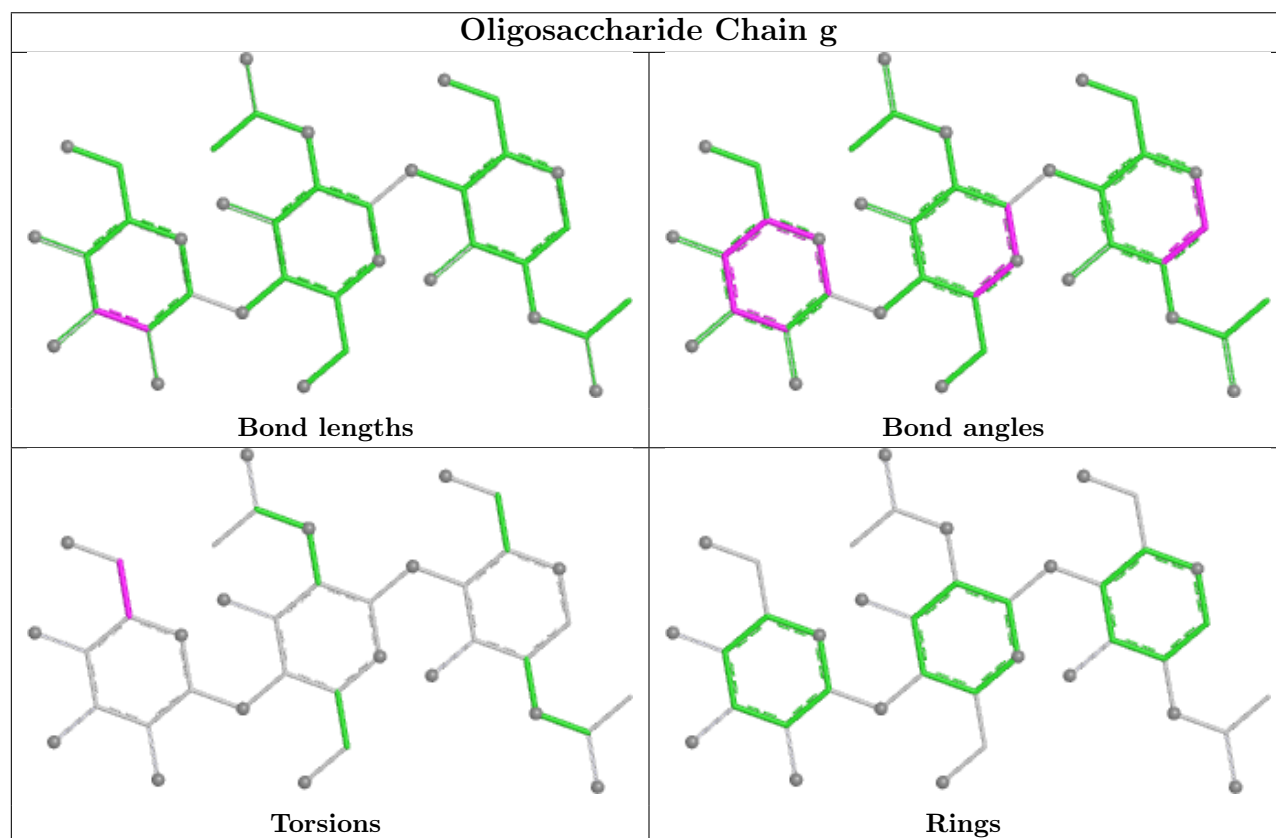
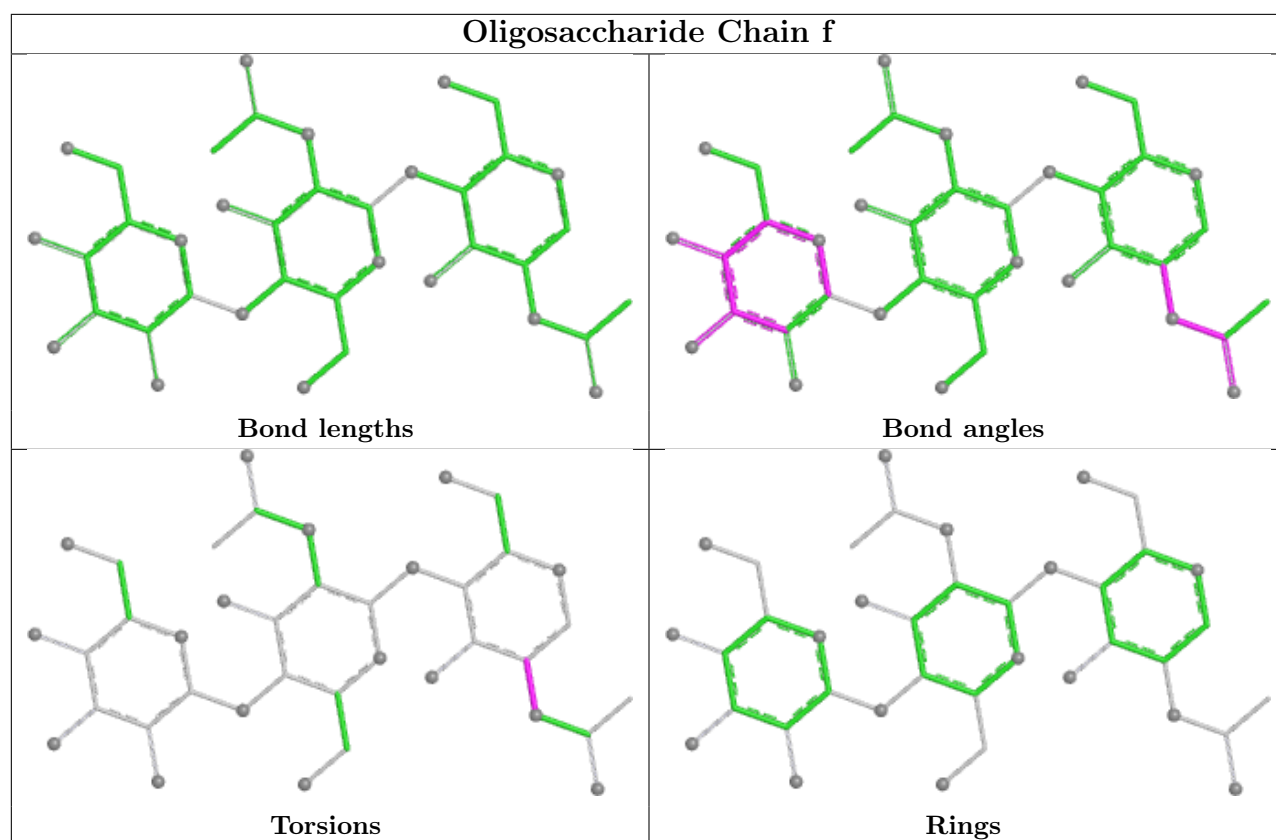


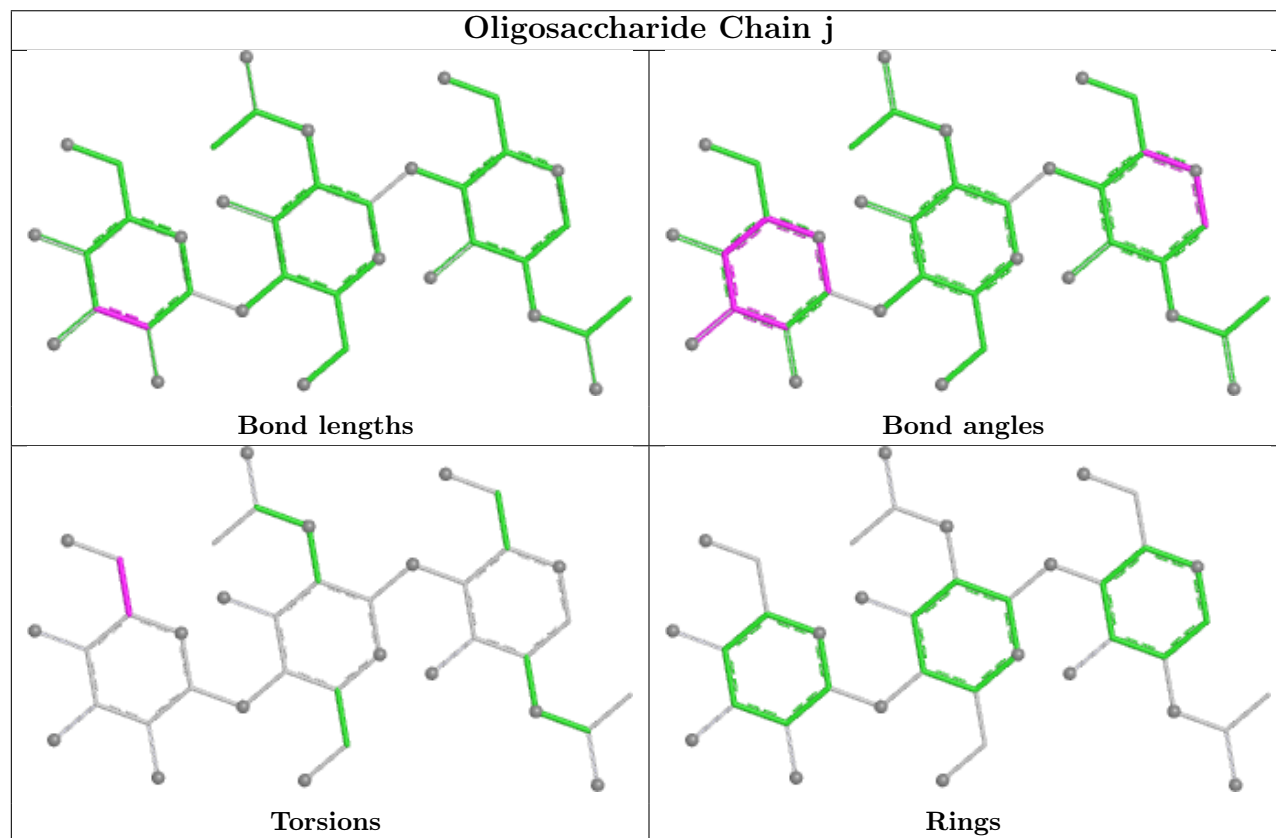
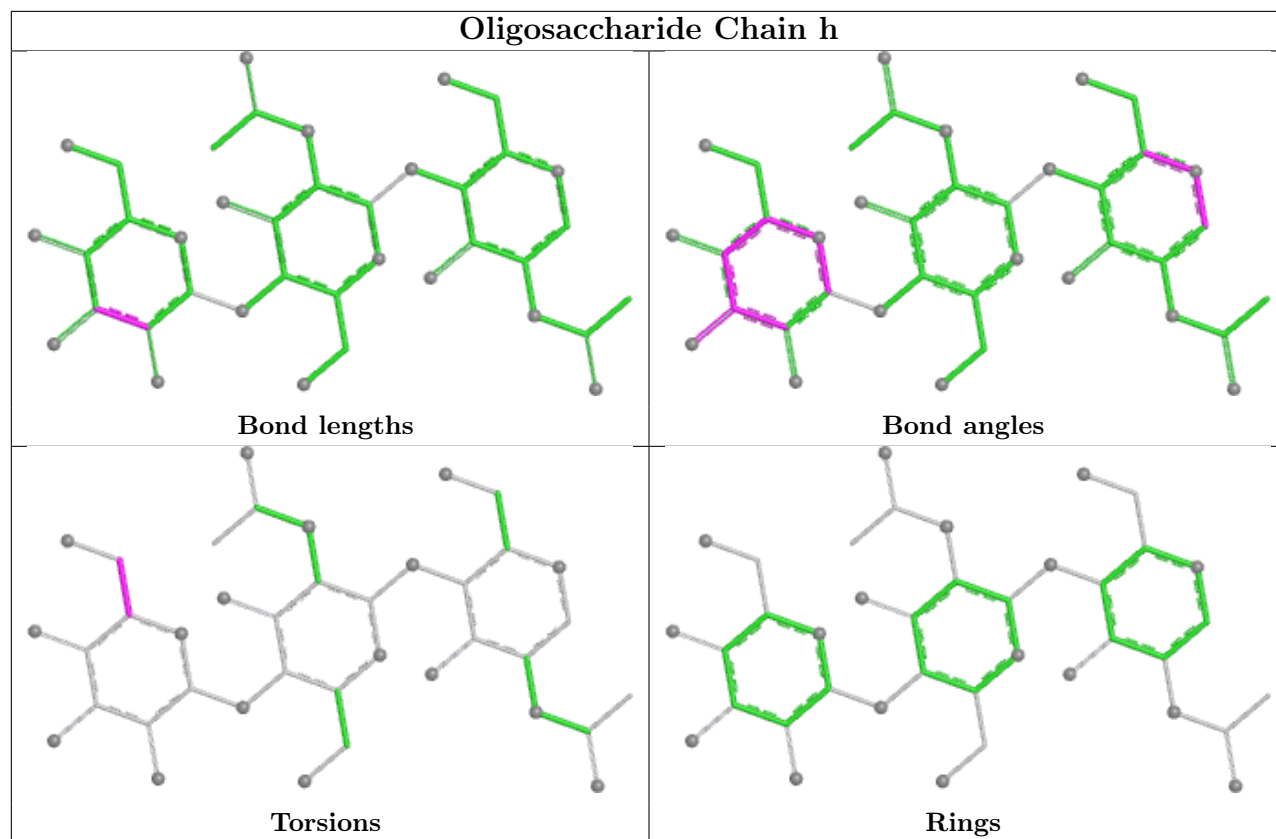


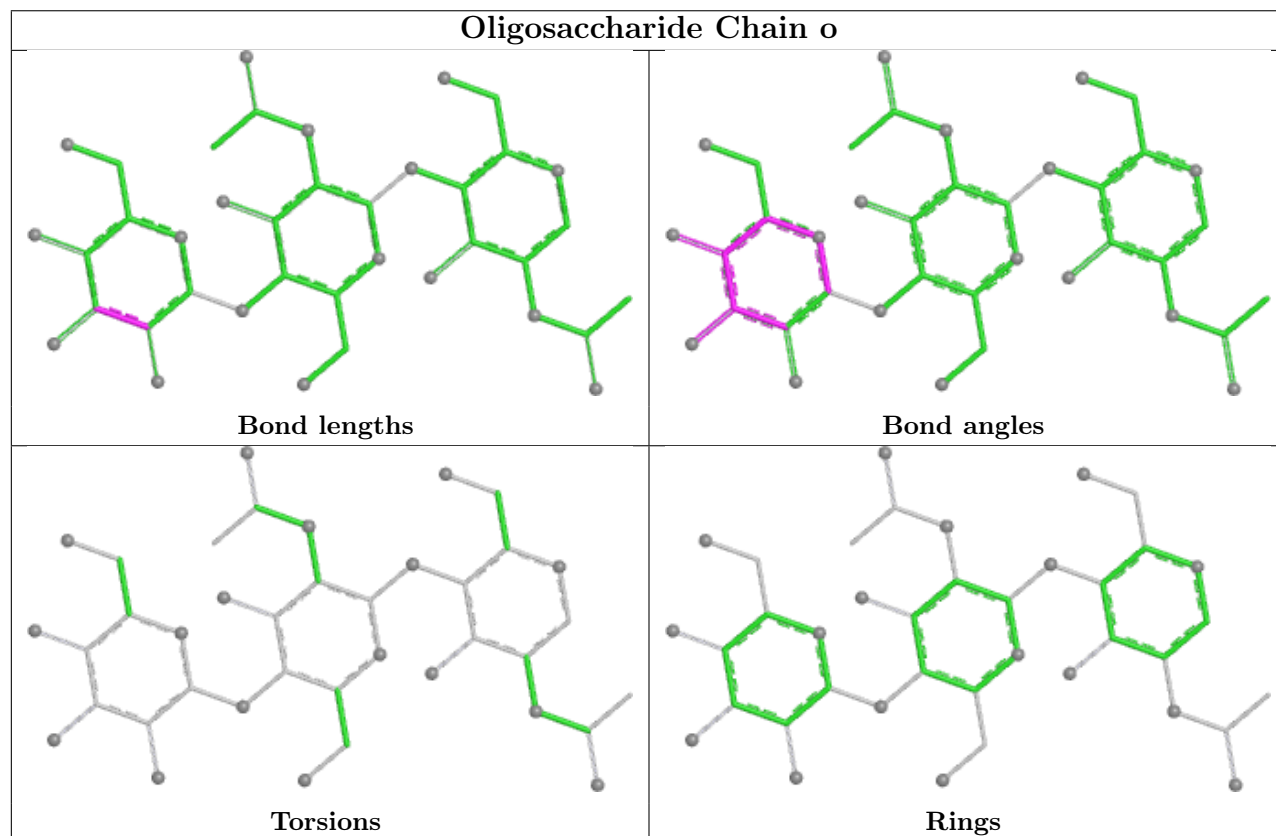
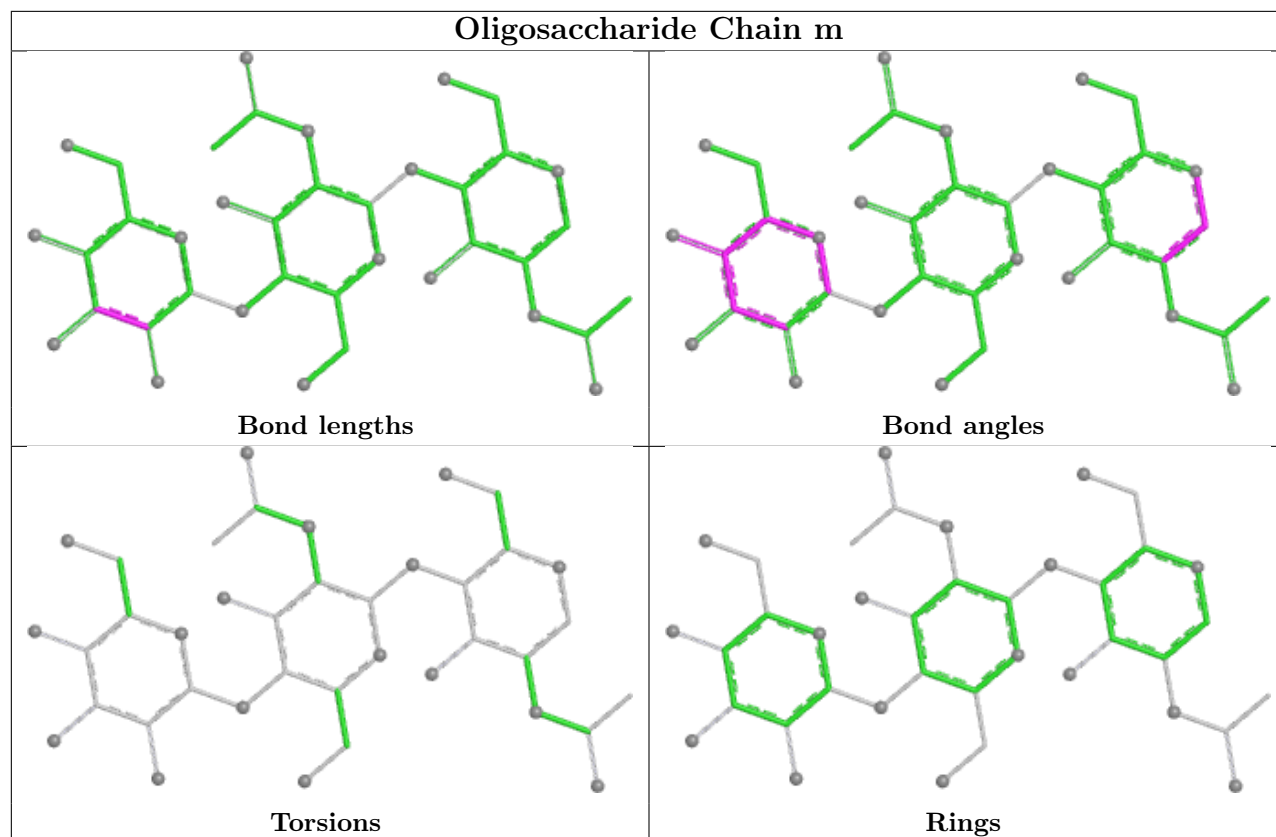


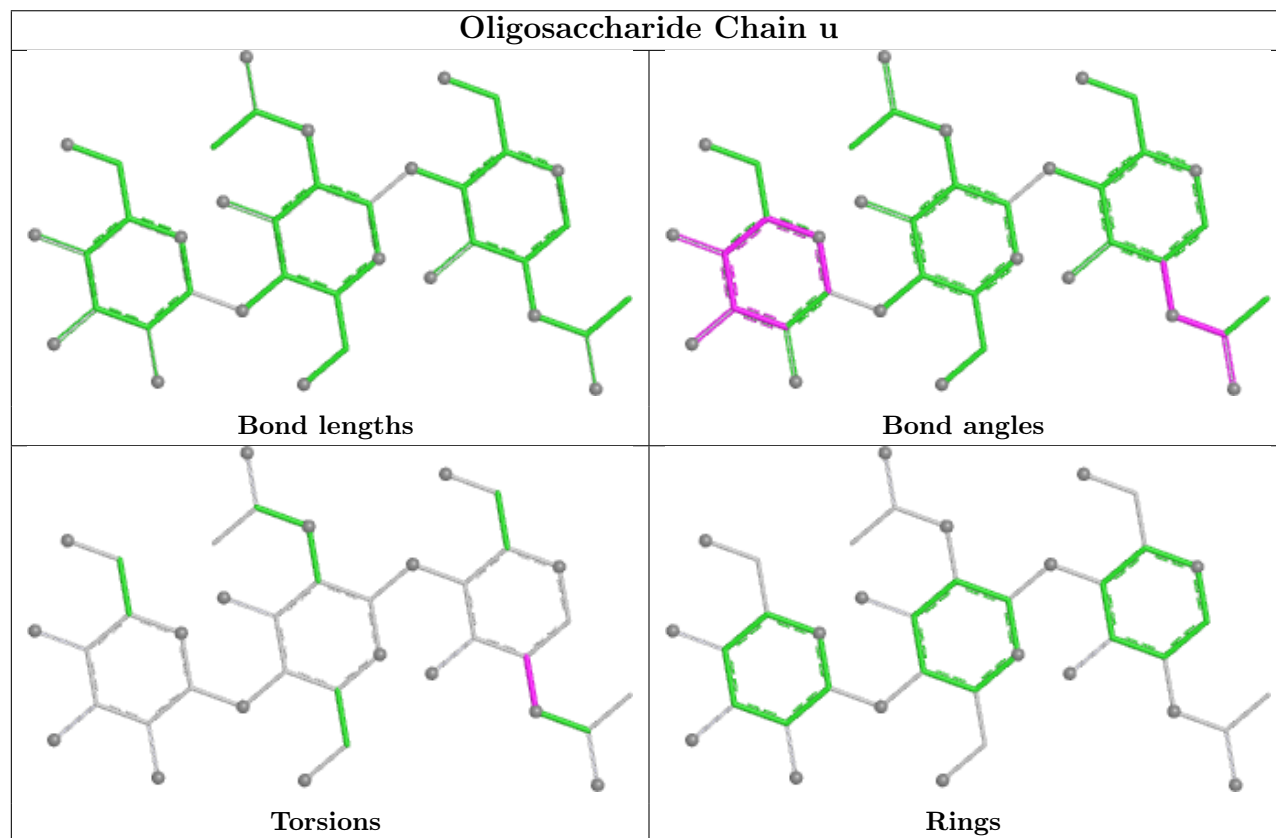
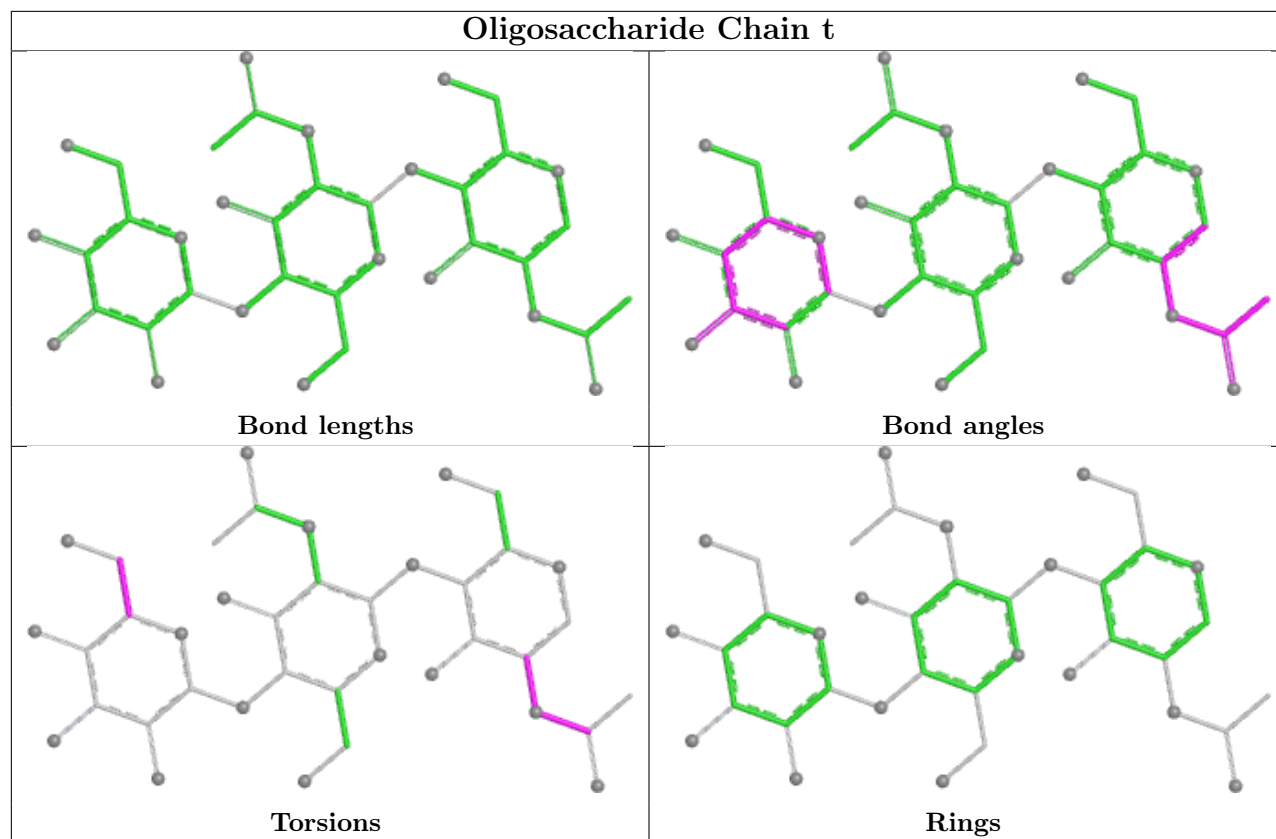


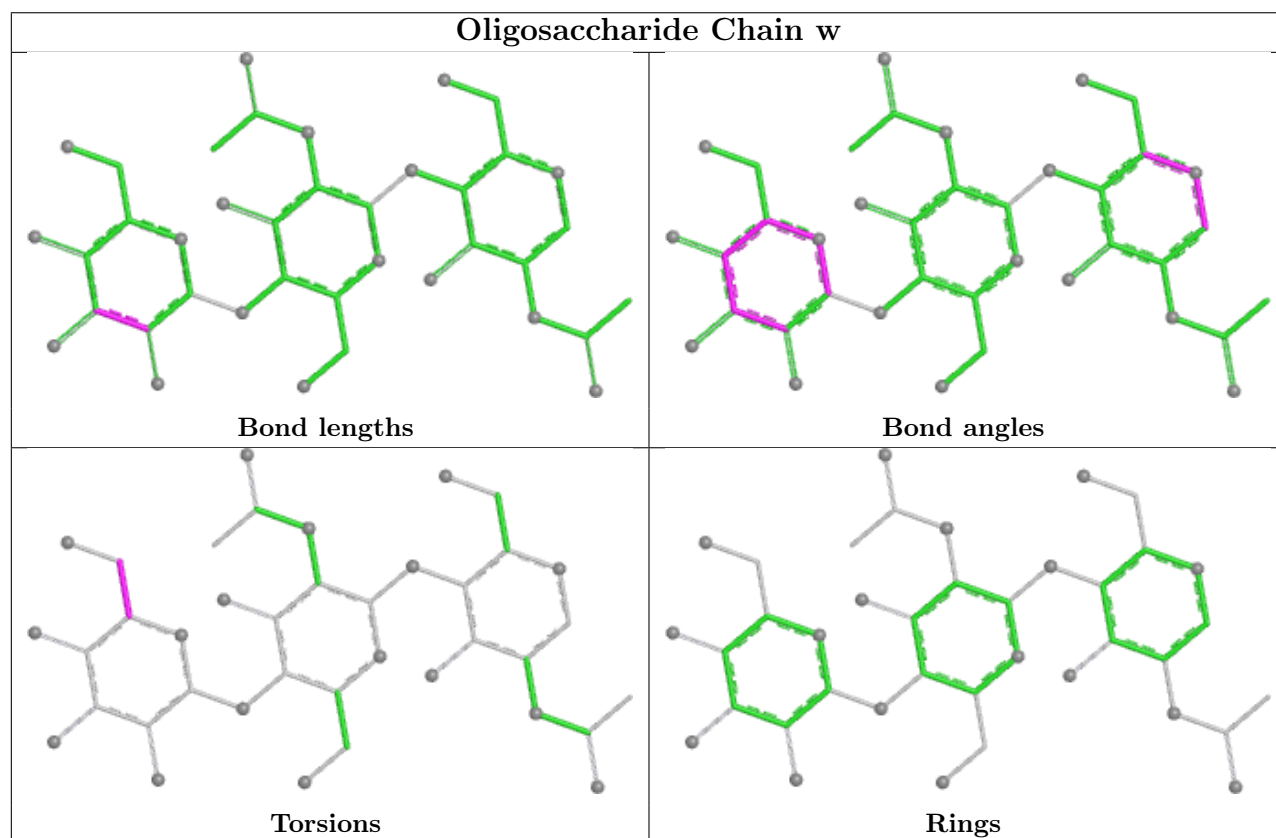
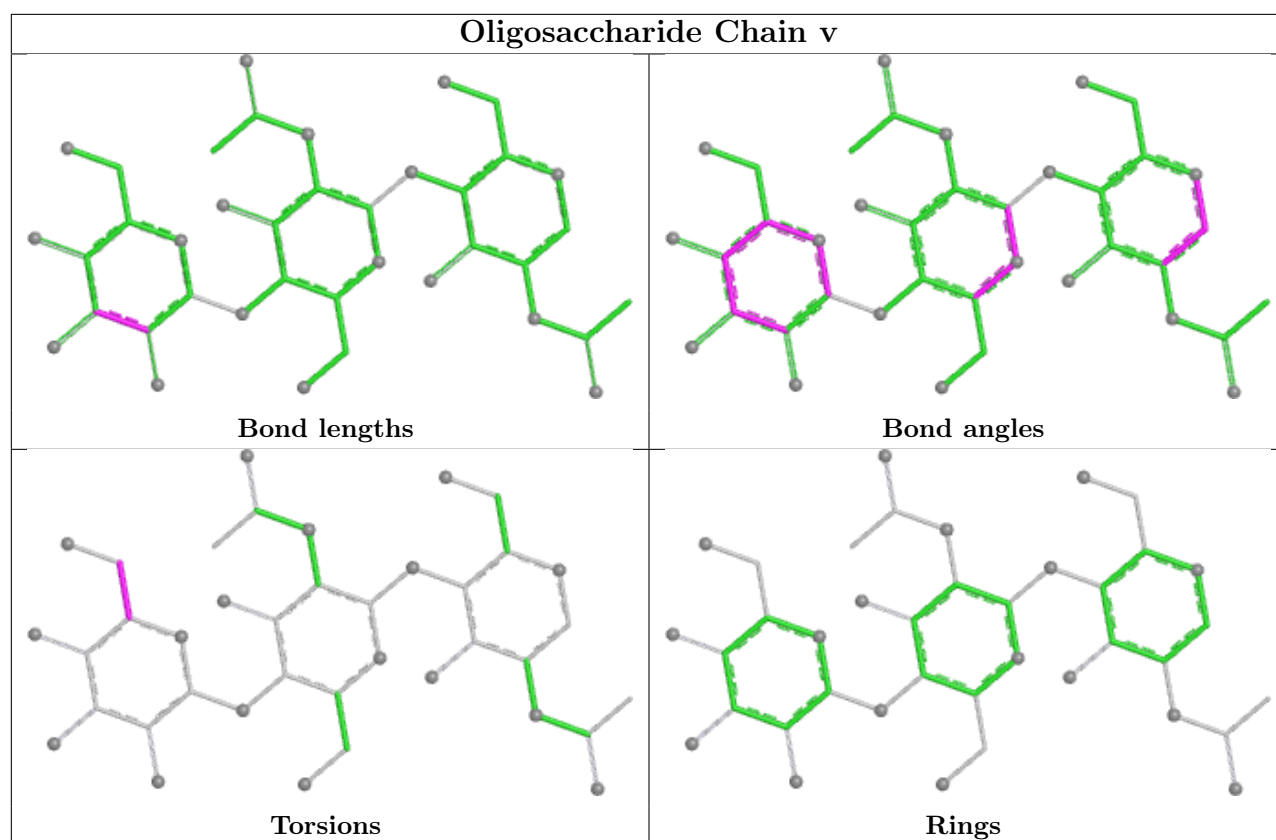


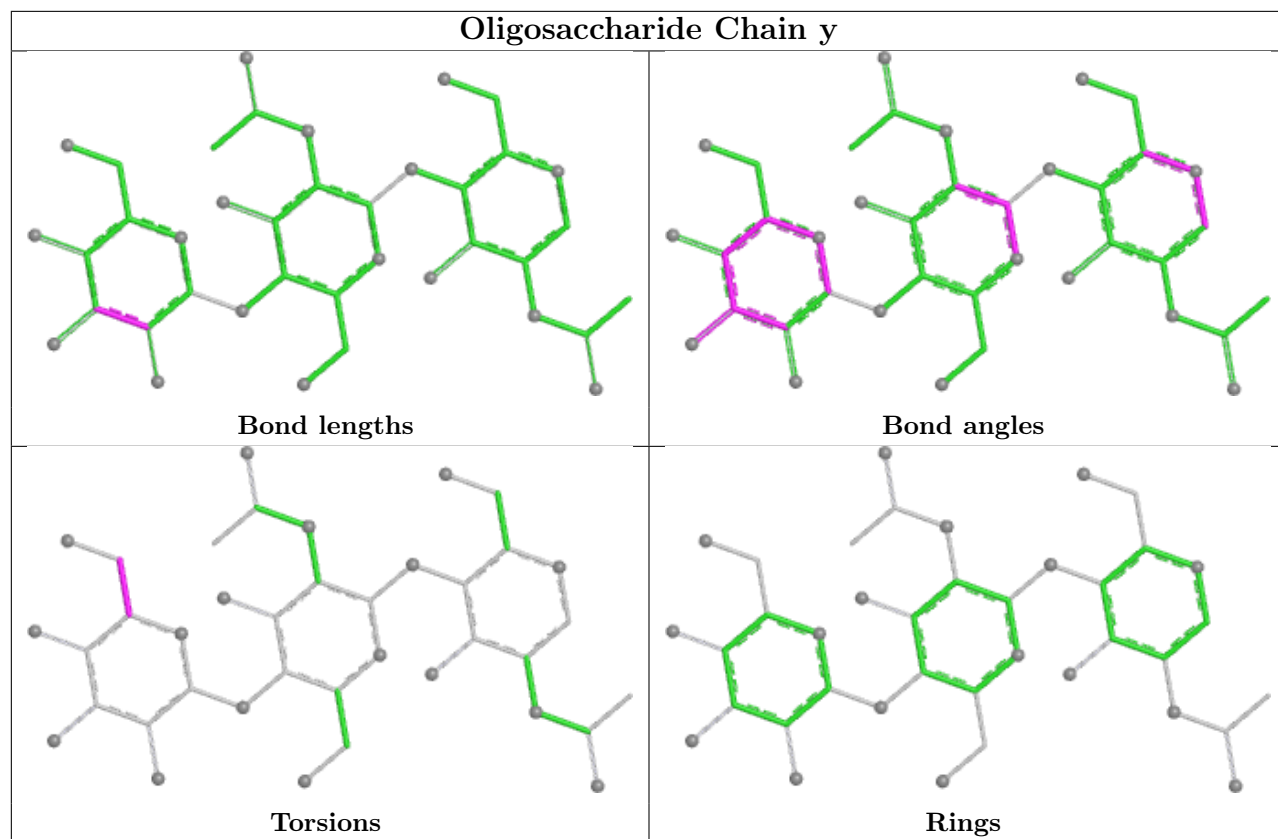


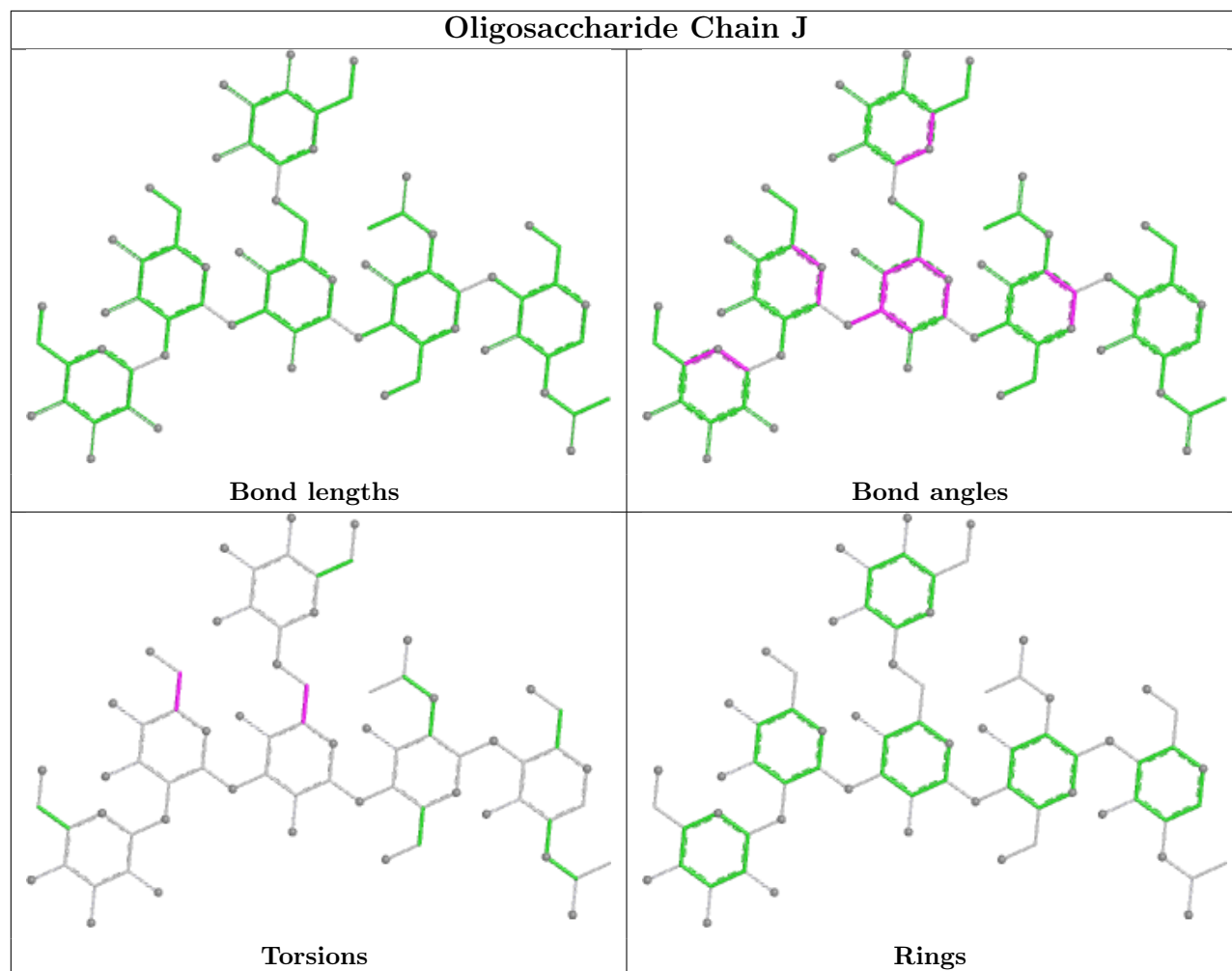


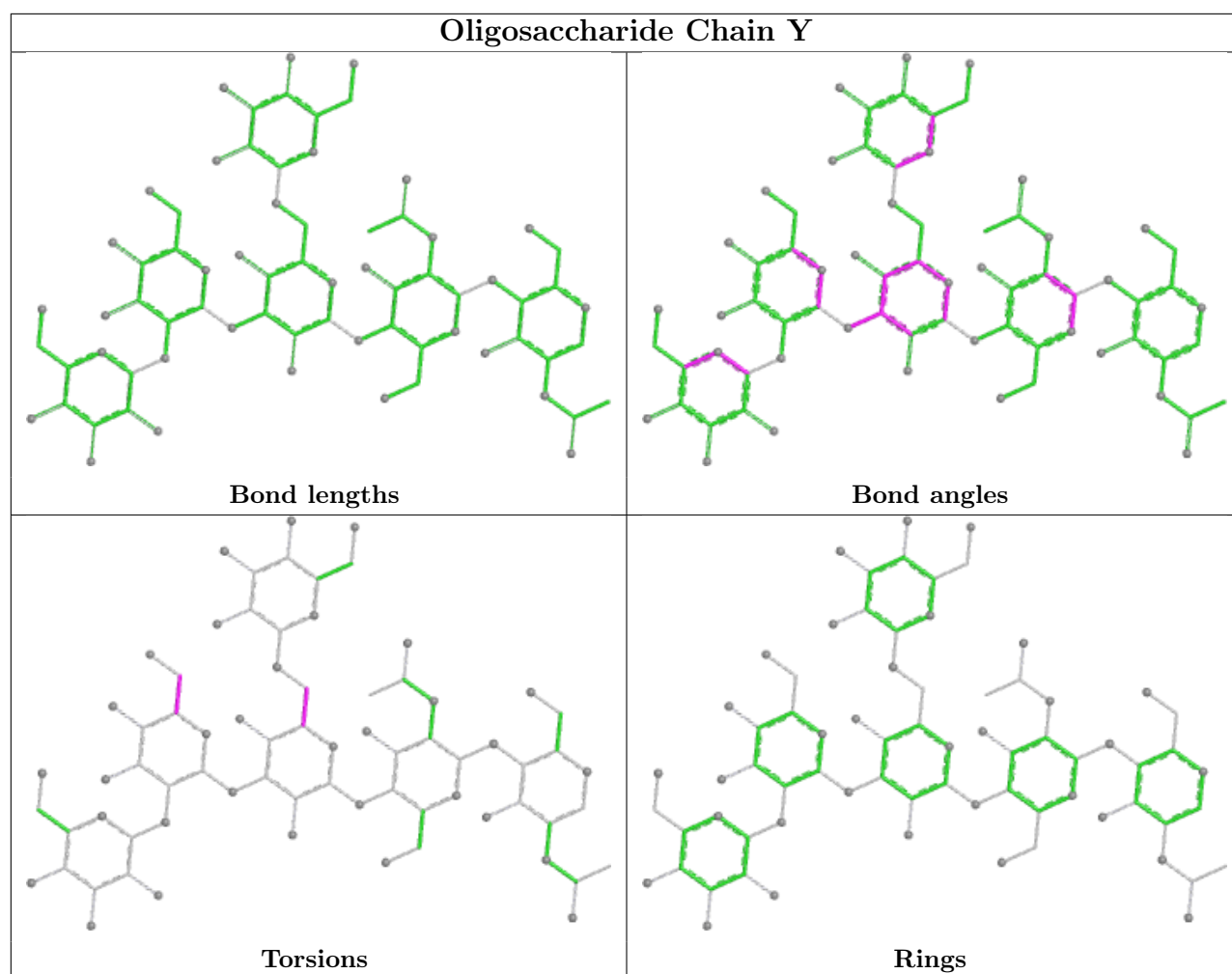


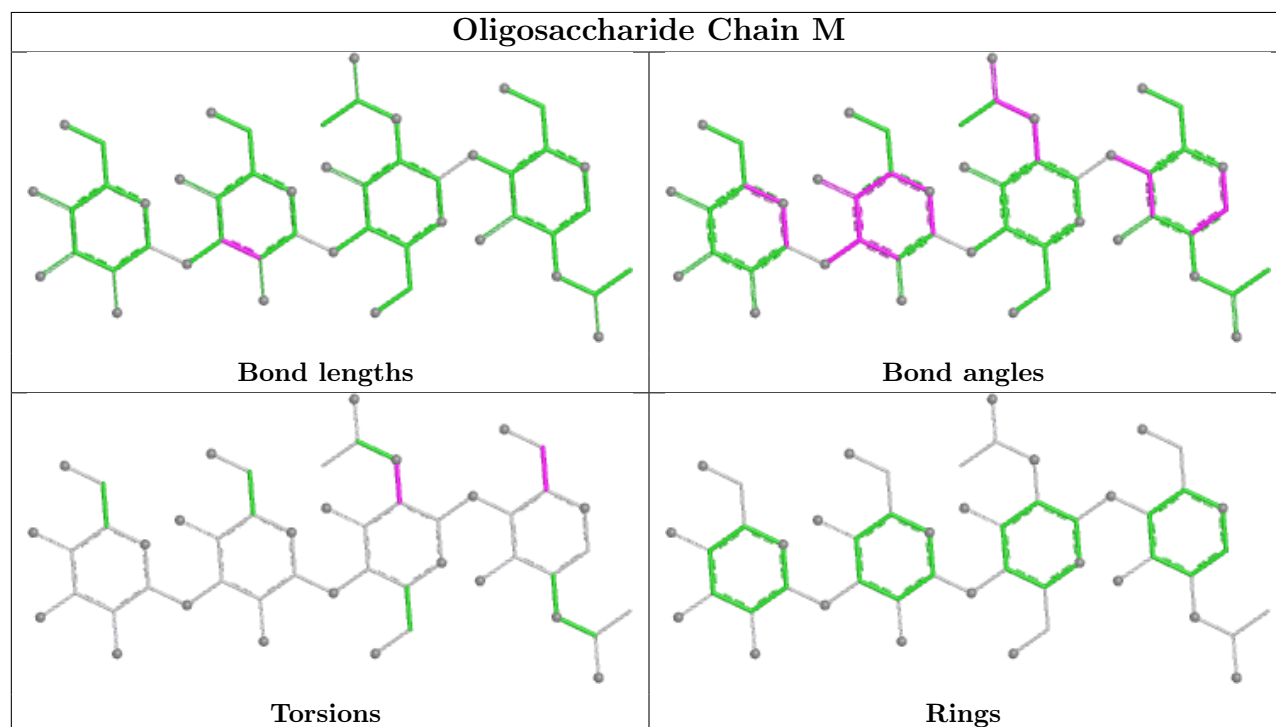
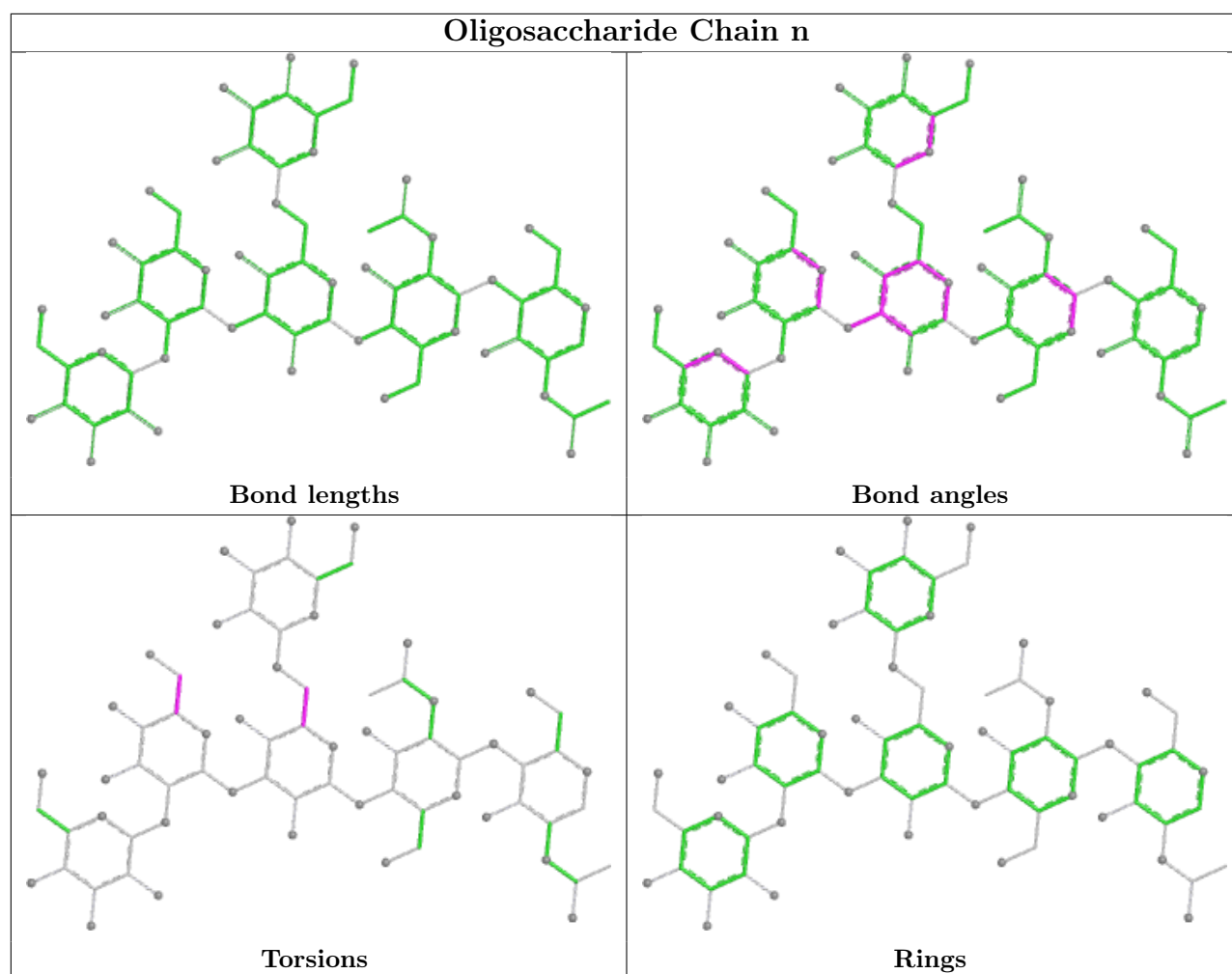


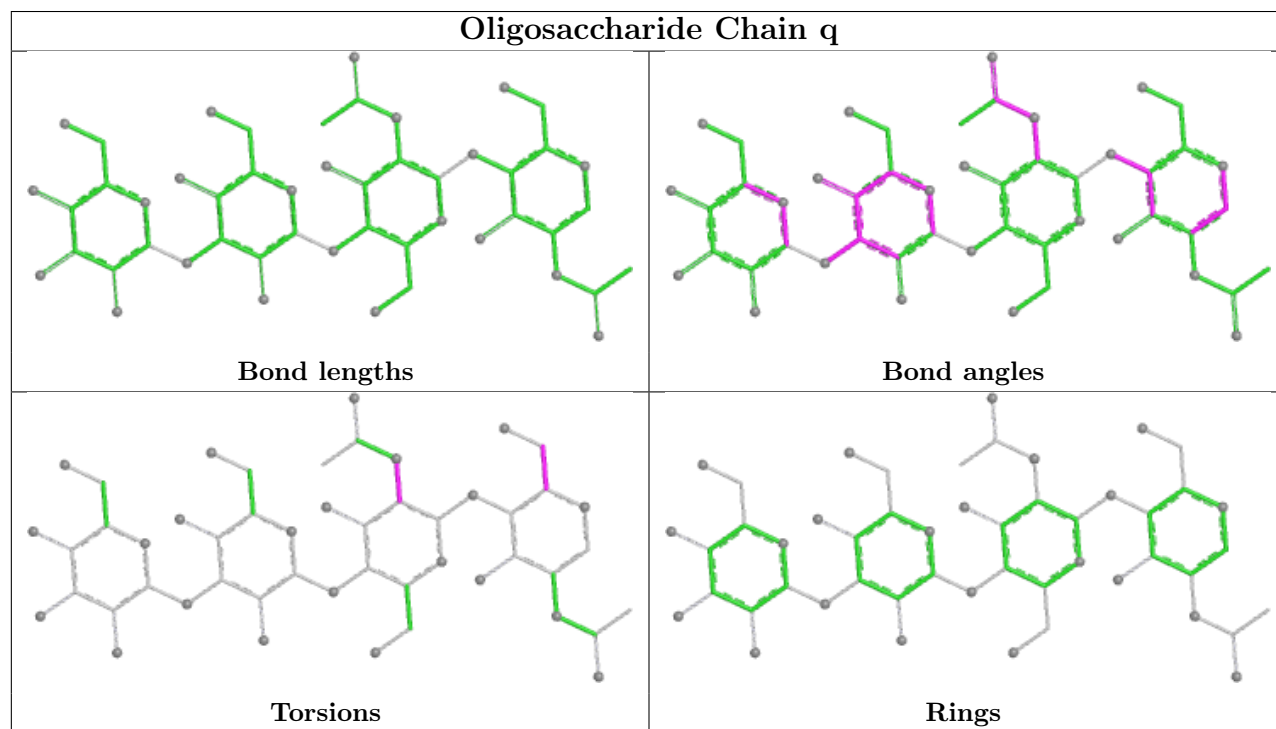
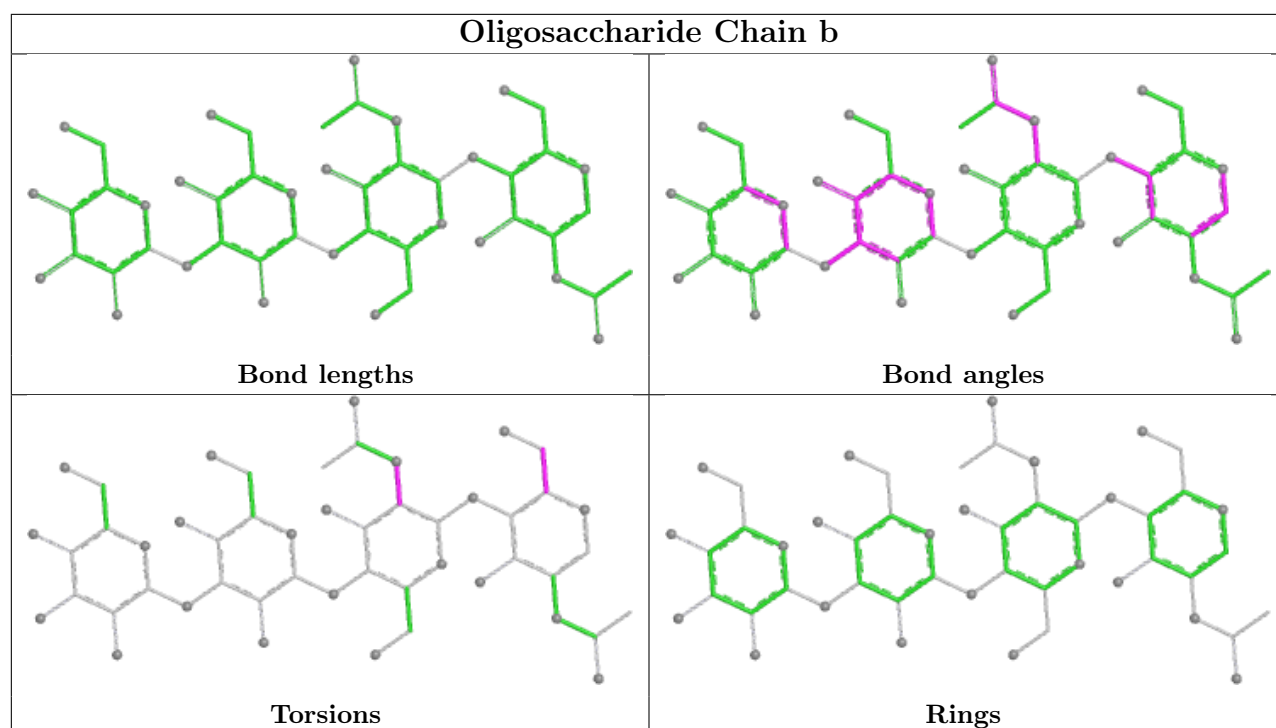


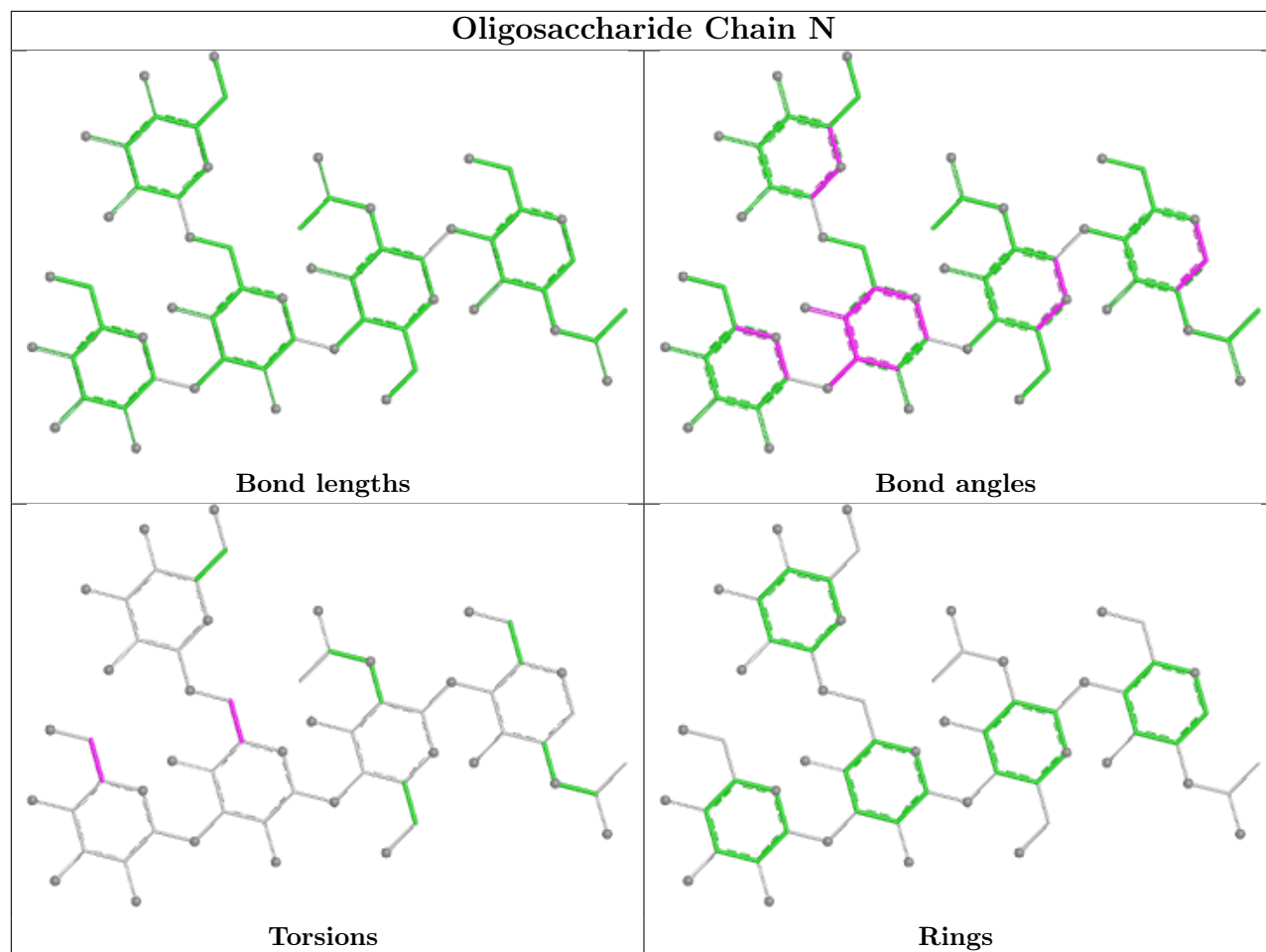


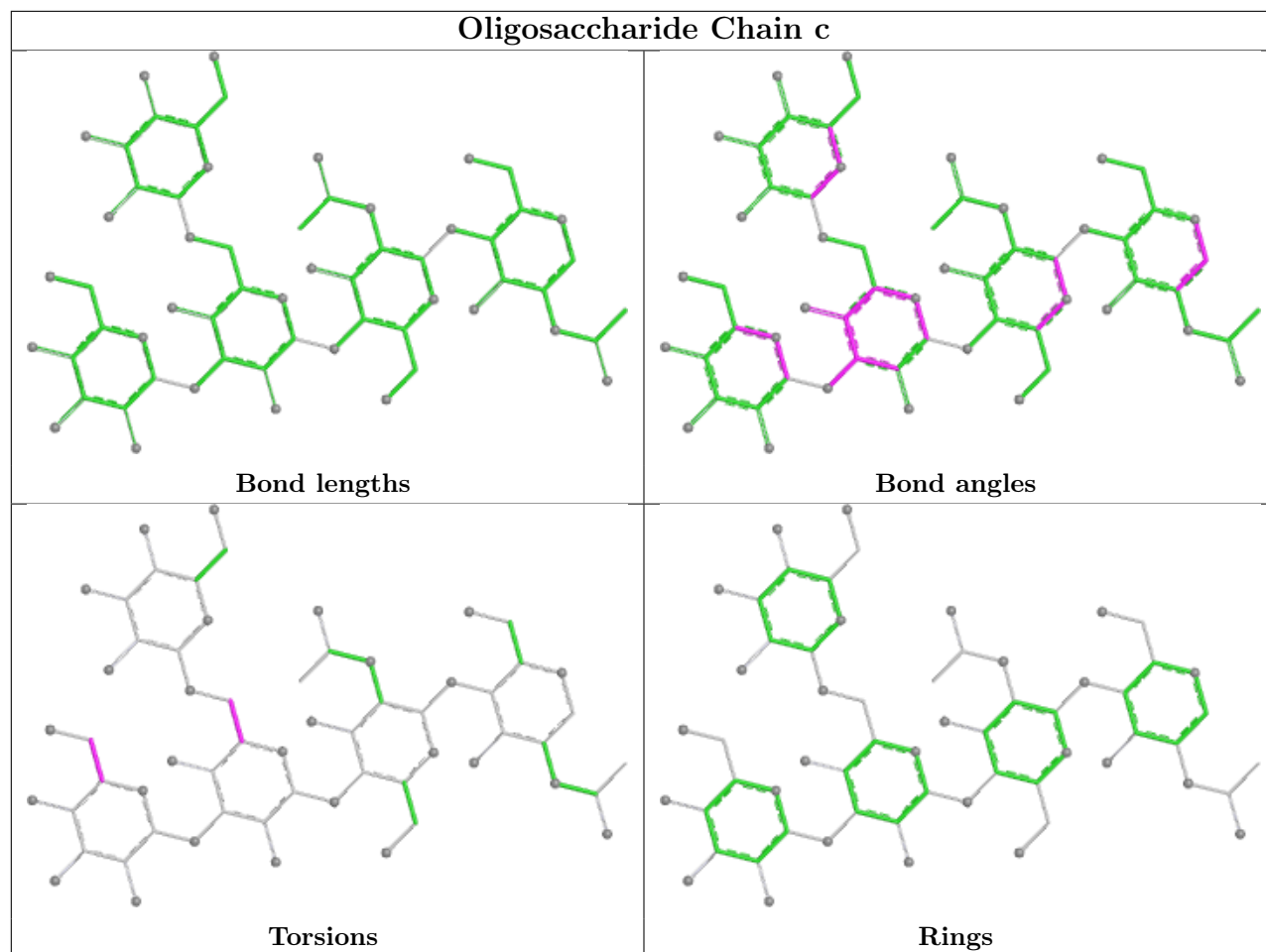


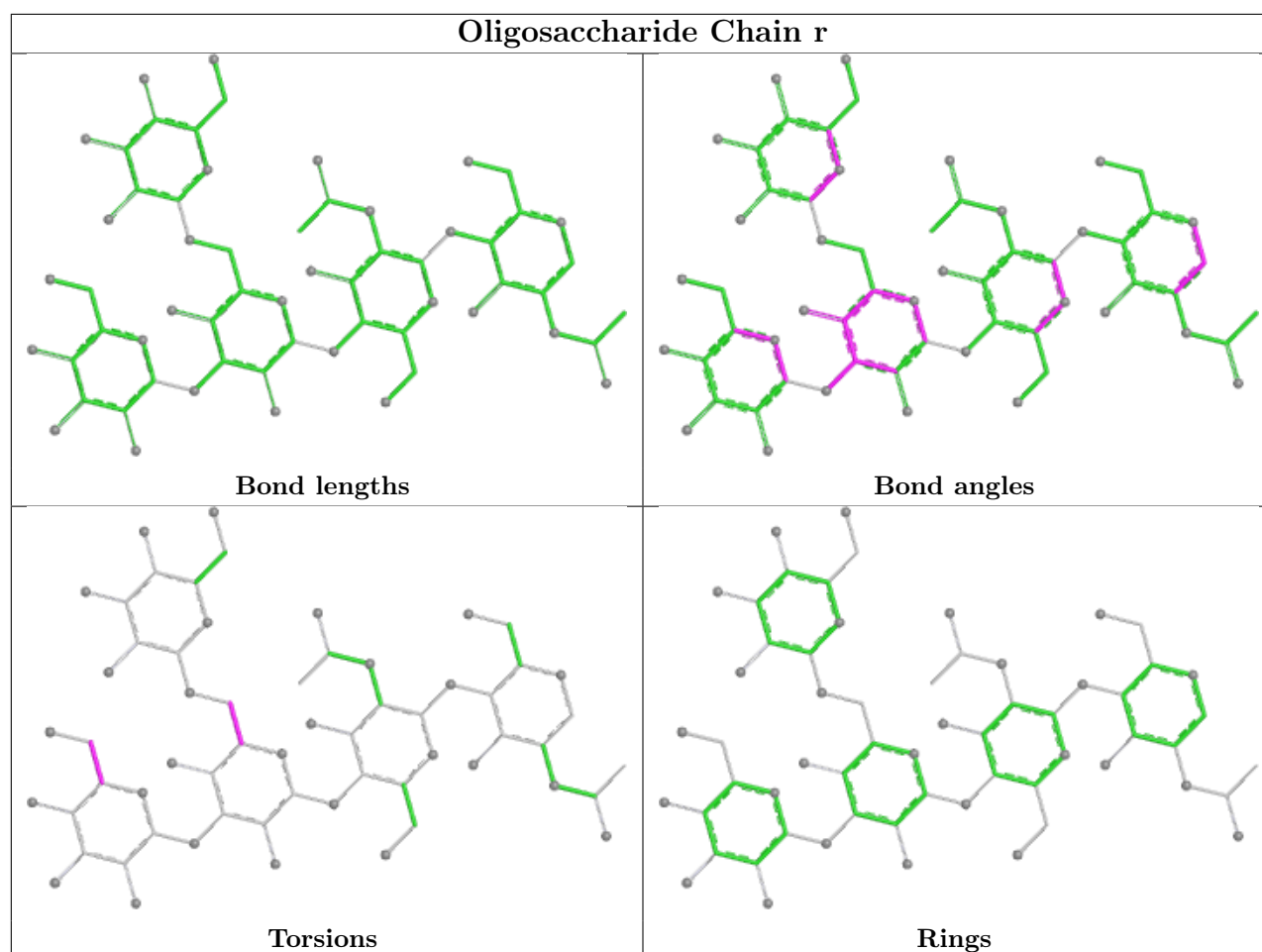












5.6 Ligand geometry [i](#)

15 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	$\# Z > 2$
8	NAG	G	602	2	14,14,15	0.71	0	17,19,21	0.88	0
8	NAG	C	602	2	14,14,15	0.71	0	17,19,21	0.88	0
8	NAG	C	601	2	14,14,15	0.73	0	17,19,21	0.90	0
8	NAG	I	602	2	14,14,15	0.71	0	17,19,21	0.88	0
8	NAG	B	701	1	14,14,15	0.70	0	17,19,21	0.83	0
8	NAG	G	603	2	14,14,15	0.71	0	17,19,21	0.92	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	F	702	1	14,14,15	0.71	0	17,19,21	0.86	0
8	NAG	F	701	1	14,14,15	0.69	0	17,19,21	0.83	0
8	NAG	I	601	2	14,14,15	0.71	0	17,19,21	0.90	0
8	NAG	A	701	1	14,14,15	0.69	0	17,19,21	0.84	0
8	NAG	I	603	2	14,14,15	0.70	0	17,19,21	0.91	0
8	NAG	G	601	2	14,14,15	0.71	0	17,19,21	0.90	0
8	NAG	A	702	1	14,14,15	0.71	0	17,19,21	0.86	0
8	NAG	B	702	1	14,14,15	0.71	0	17,19,21	0.87	0
8	NAG	C	603	2	14,14,15	0.72	0	17,19,21	0.92	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
8	NAG	G	602	2	-	0/6/23/26	0/1/1/1
8	NAG	C	602	2	-	0/6/23/26	0/1/1/1
8	NAG	C	601	2	-	0/6/23/26	0/1/1/1
8	NAG	I	602	2	-	0/6/23/26	0/1/1/1
8	NAG	B	701	1	-	0/6/23/26	0/1/1/1
8	NAG	G	603	2	-	1/6/23/26	0/1/1/1
8	NAG	F	702	1	-	0/6/23/26	0/1/1/1
8	NAG	F	701	1	-	0/6/23/26	0/1/1/1
8	NAG	I	601	2	-	0/6/23/26	0/1/1/1
8	NAG	A	701	1	-	0/6/23/26	0/1/1/1
8	NAG	I	603	2	-	1/6/23/26	0/1/1/1
8	NAG	G	601	2	-	0/6/23/26	0/1/1/1
8	NAG	A	702	1	-	0/6/23/26	0/1/1/1
8	NAG	B	702	1	-	0/6/23/26	0/1/1/1
8	NAG	C	603	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	C	603	NAG	O5-C5-C6-O6
8	G	603	NAG	O5-C5-C6-O6
8	I	603	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

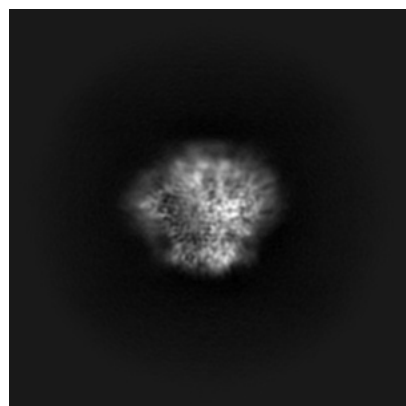
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71782. These allow visual inspection of the internal detail of the map and identification of artifacts.

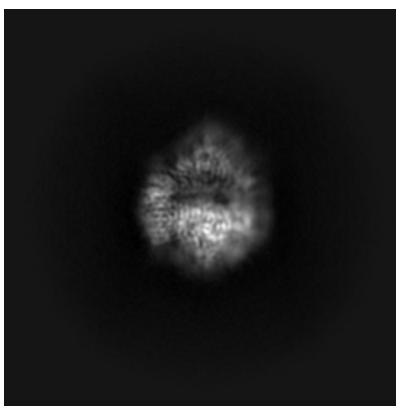
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

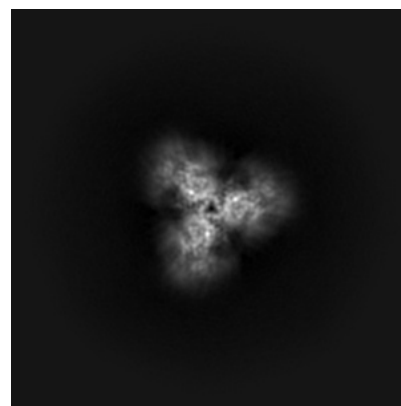
6.1.1 Primary map



X

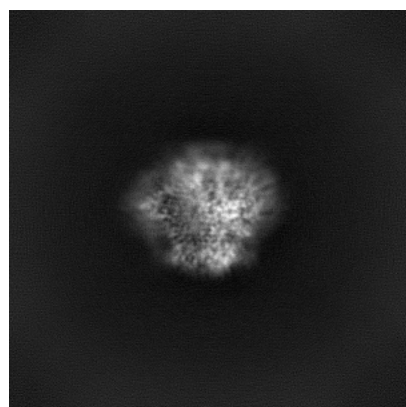


Y

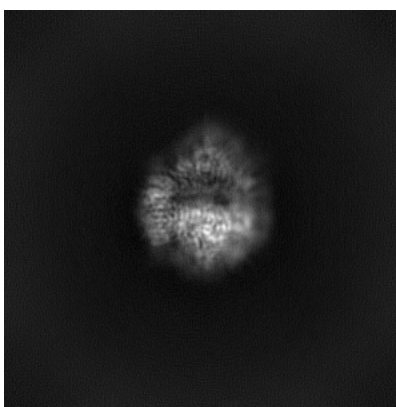


Z

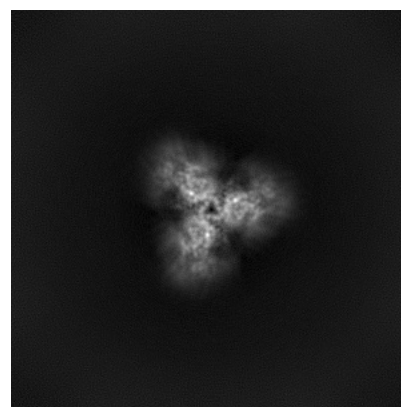
6.1.2 Raw map



X



Y

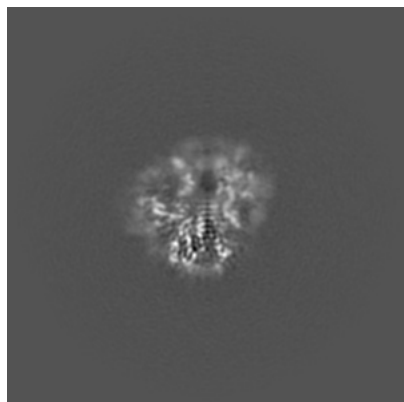


Z

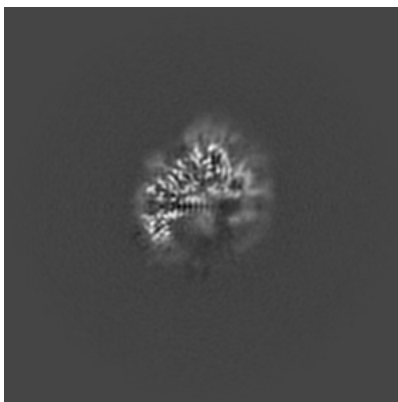
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

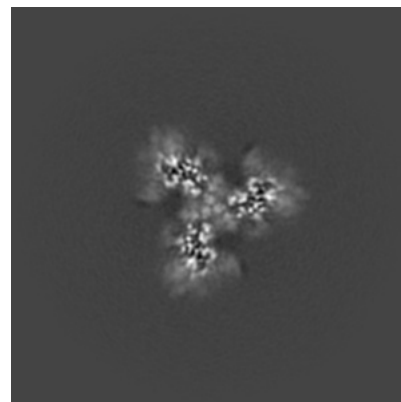
6.2.1 Primary map



X Index: 216

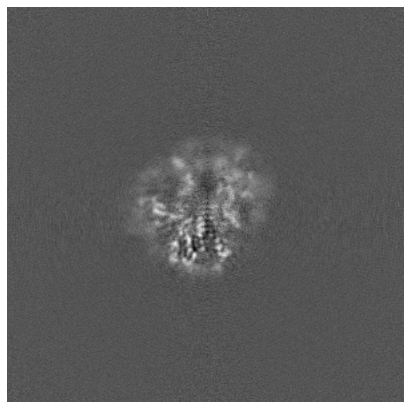


Y Index: 216

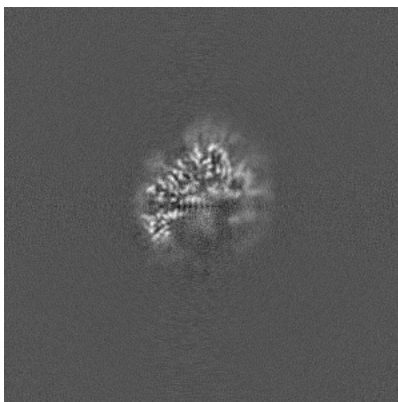


Z Index: 216

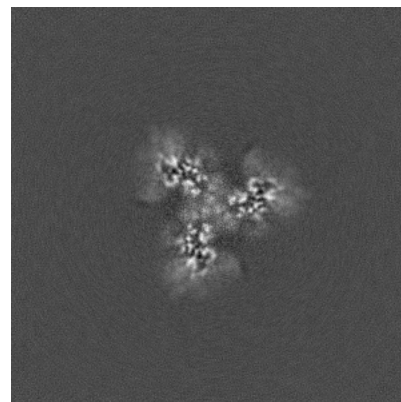
6.2.2 Raw map



X Index: 216



Y Index: 216

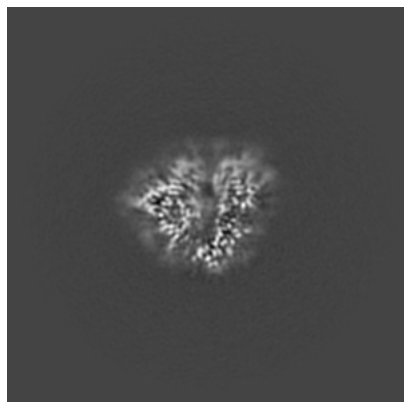


Z Index: 216

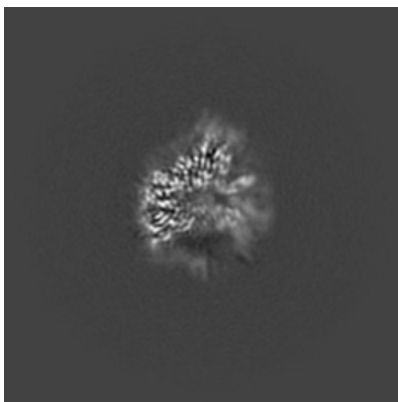
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

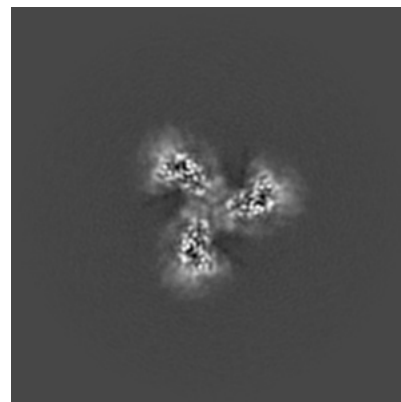
6.3.1 Primary map



X Index: 198

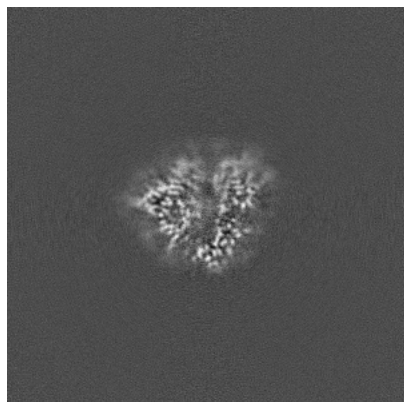


Y Index: 227

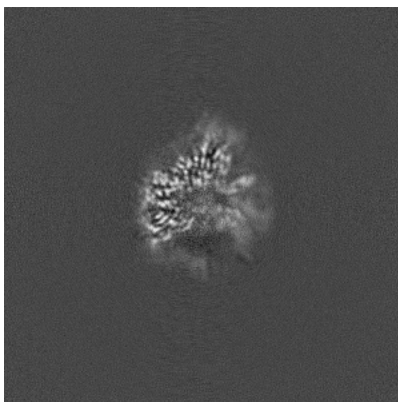


Z Index: 221

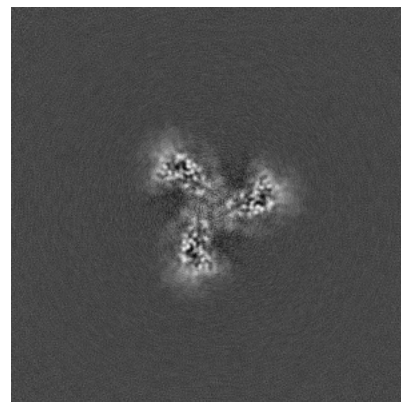
6.3.2 Raw map



X Index: 198



Y Index: 227

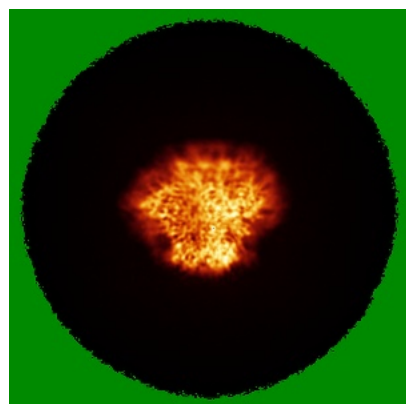


Z Index: 221

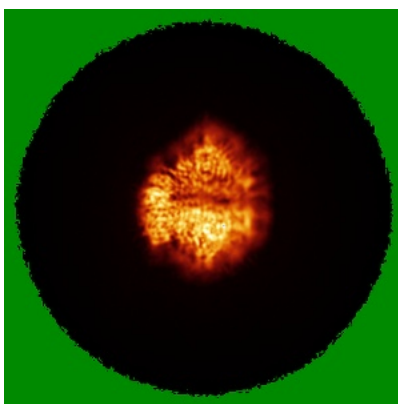
The images above show the largest variance slices of the map in three orthogonal directions.

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

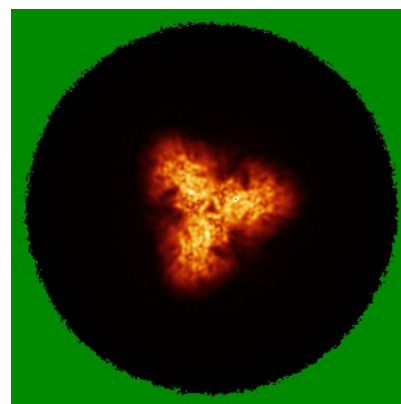
6.4.1 Primary map



X

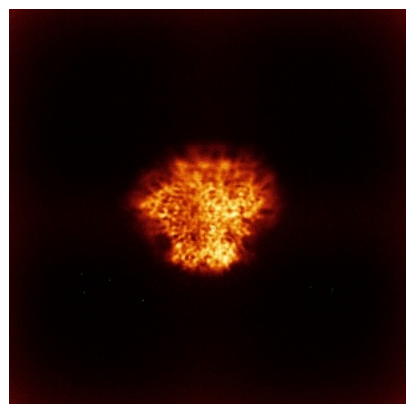


Y

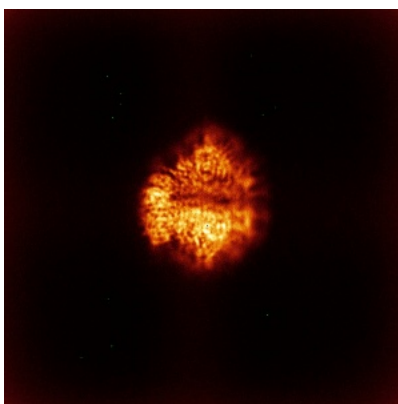


Z

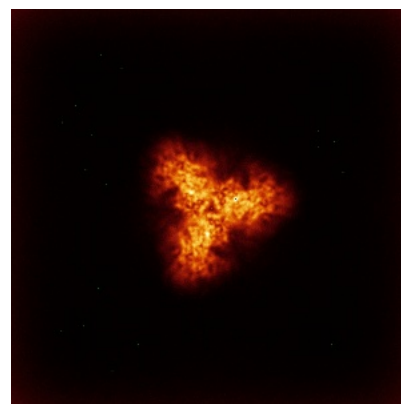
6.4.2 Raw map



X



Y

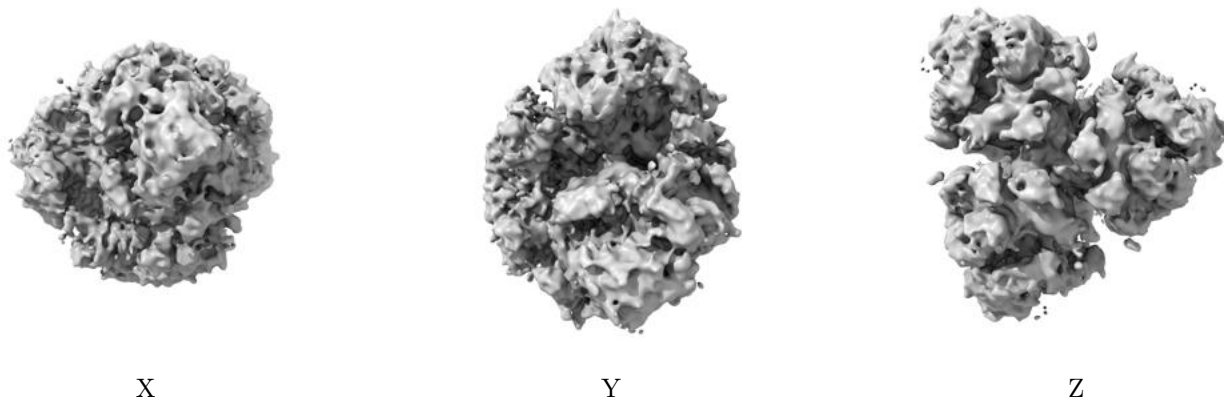


Z

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.

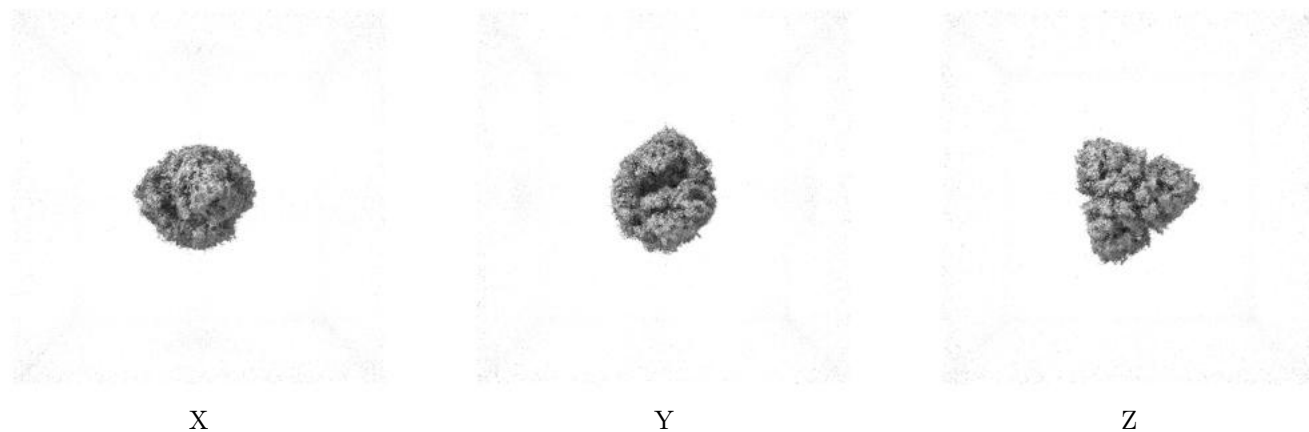
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0275. 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.

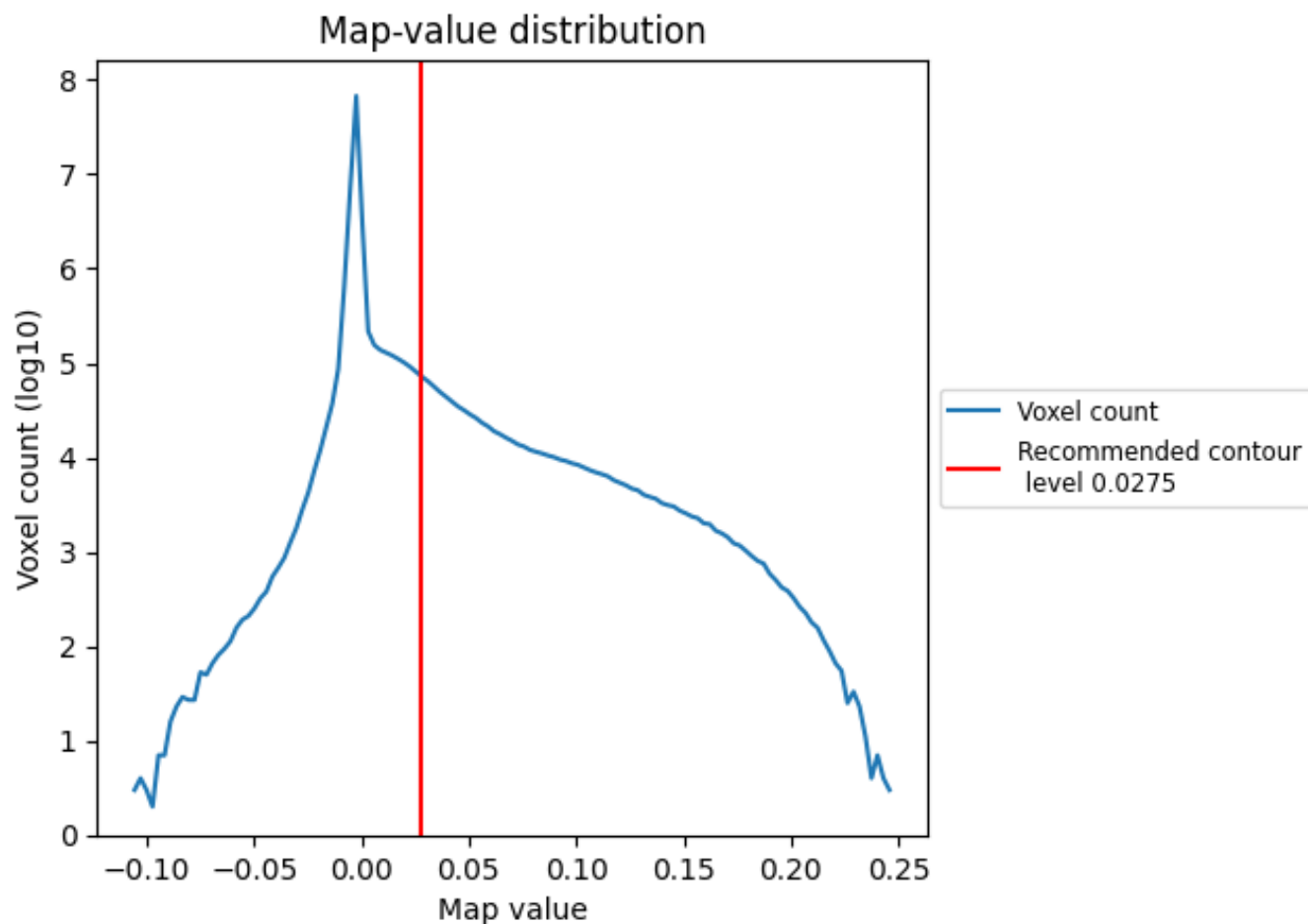
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

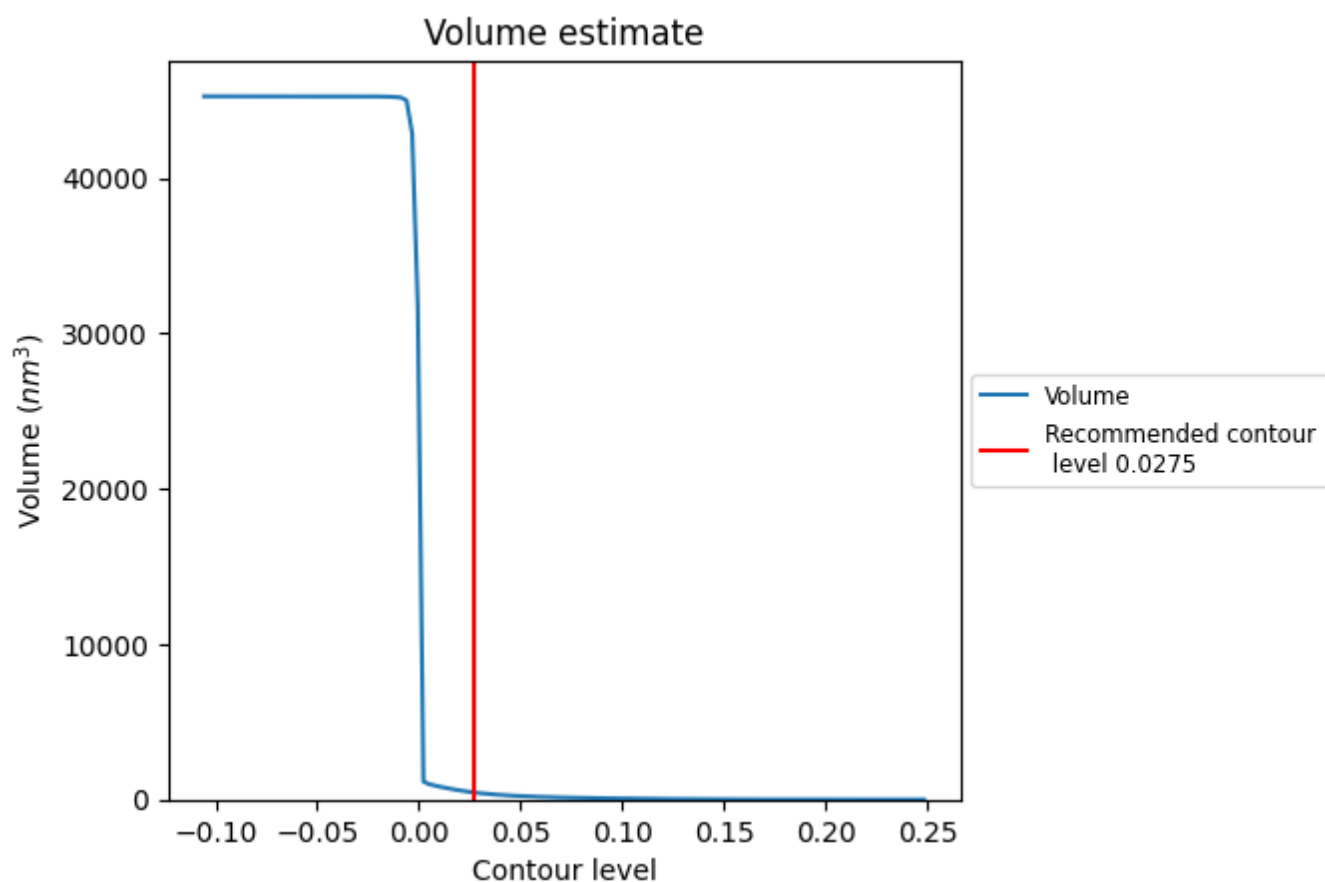
This section contains the results of statistical analysis of the map.

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.

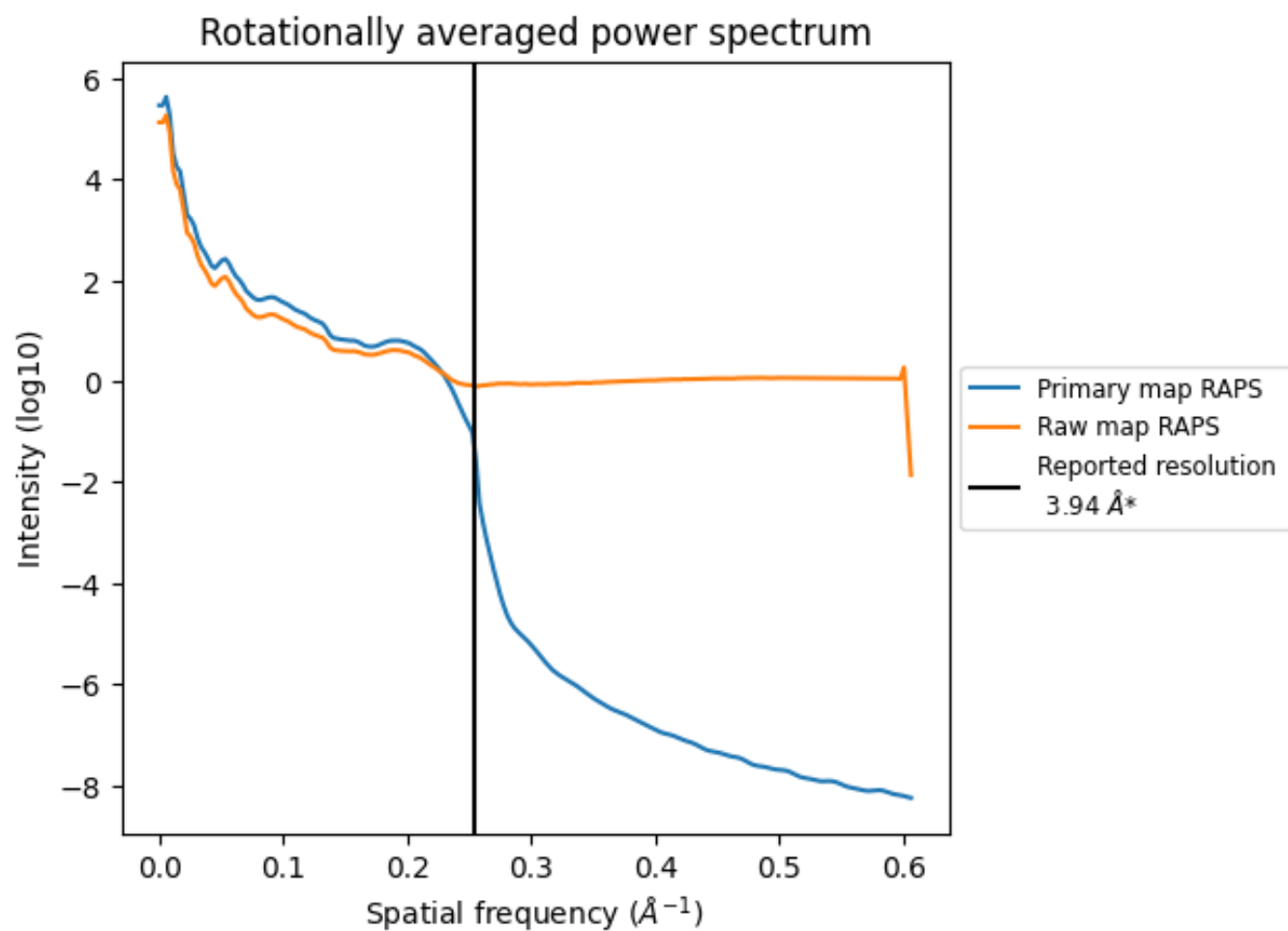
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 452 nm^3 ; this corresponds to an approximate mass of 408 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 ⓘ

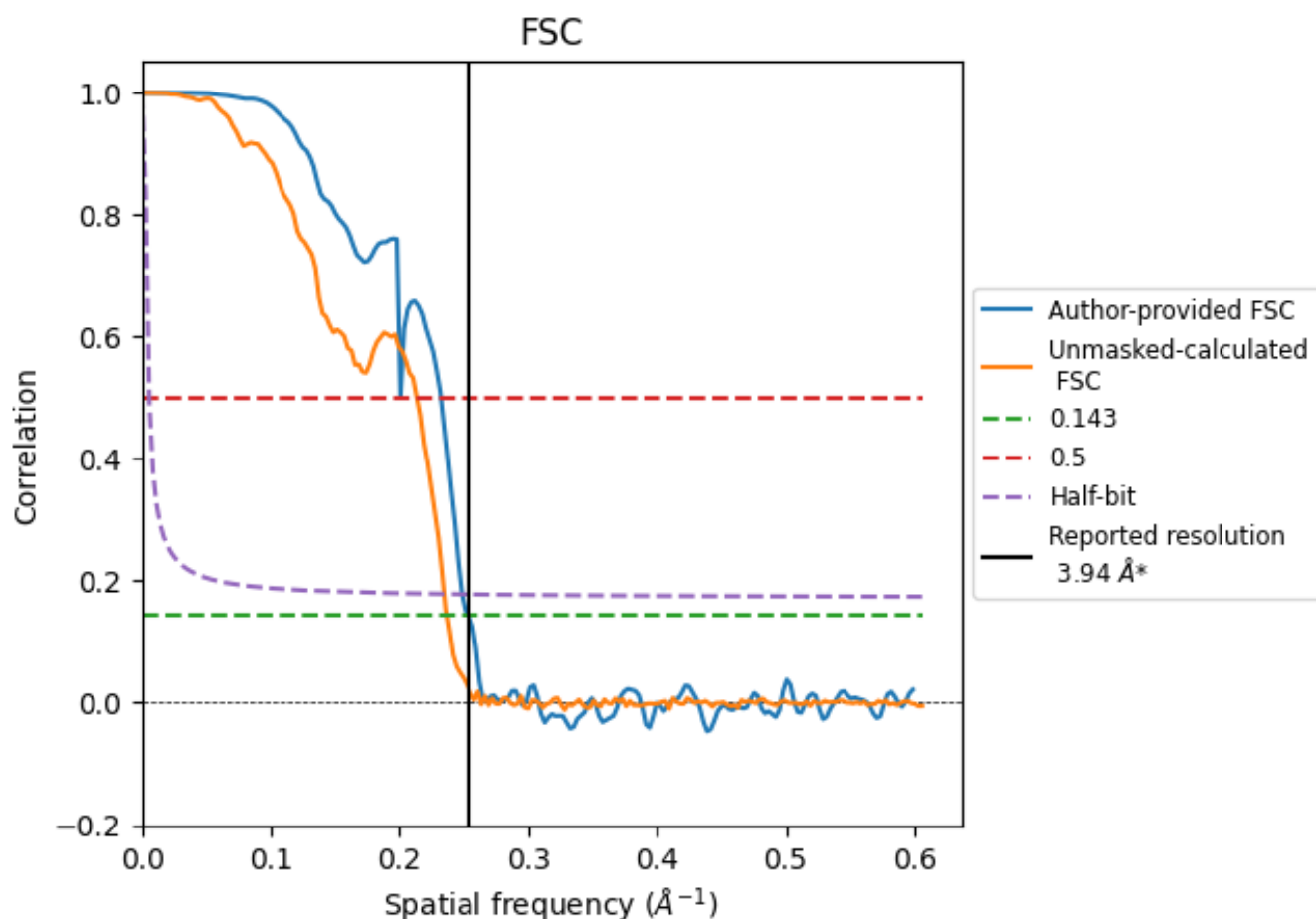


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 0.254 \AA^{-1}

8.2 Resolution estimates [i](#)

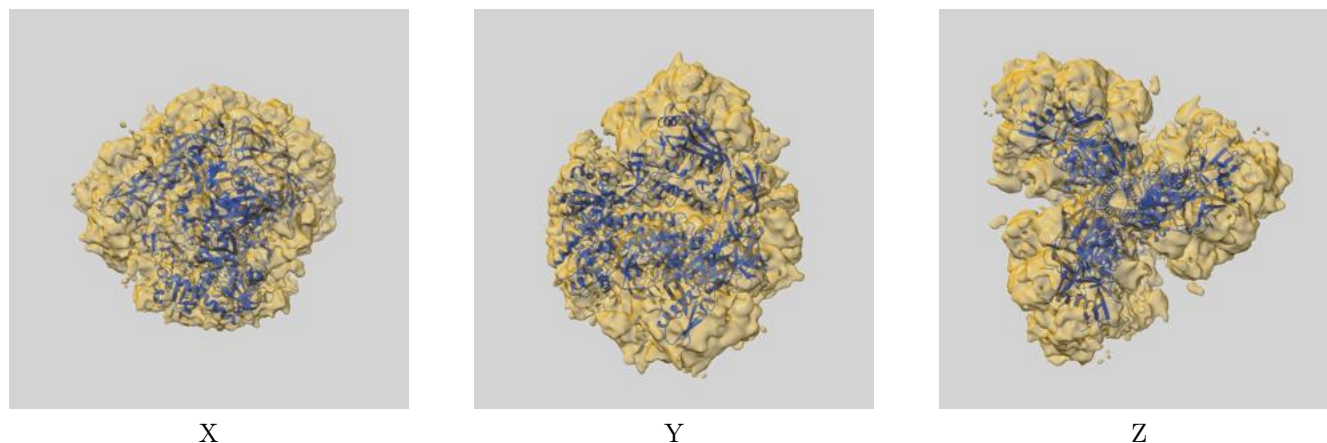
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.94	-	-
Author-provided FSC curve	3.94	4.31	4.03
Unmasked-calculated*	4.23	4.68	4.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

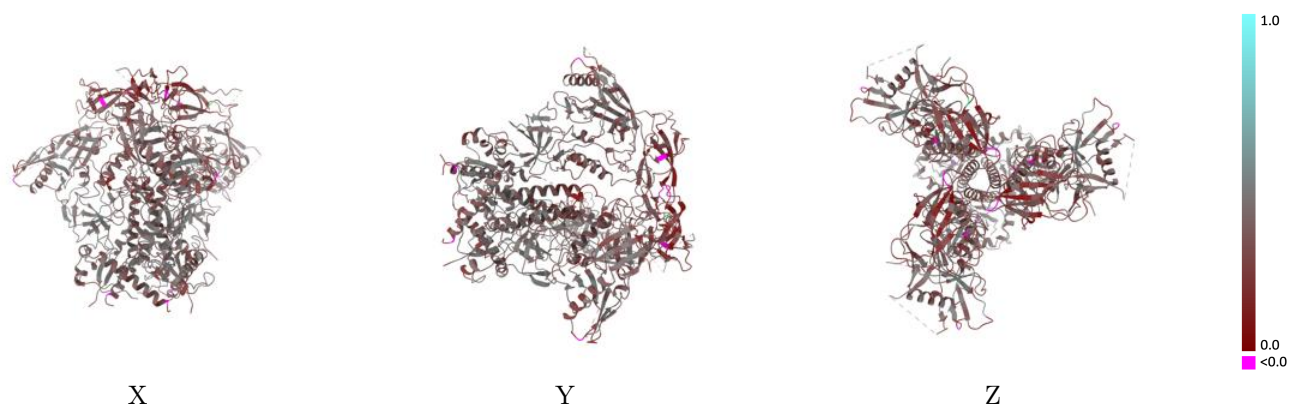
This section contains information regarding the fit between EMDB map EMD-71782 and PDB model 9PQ3. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0275 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](#)



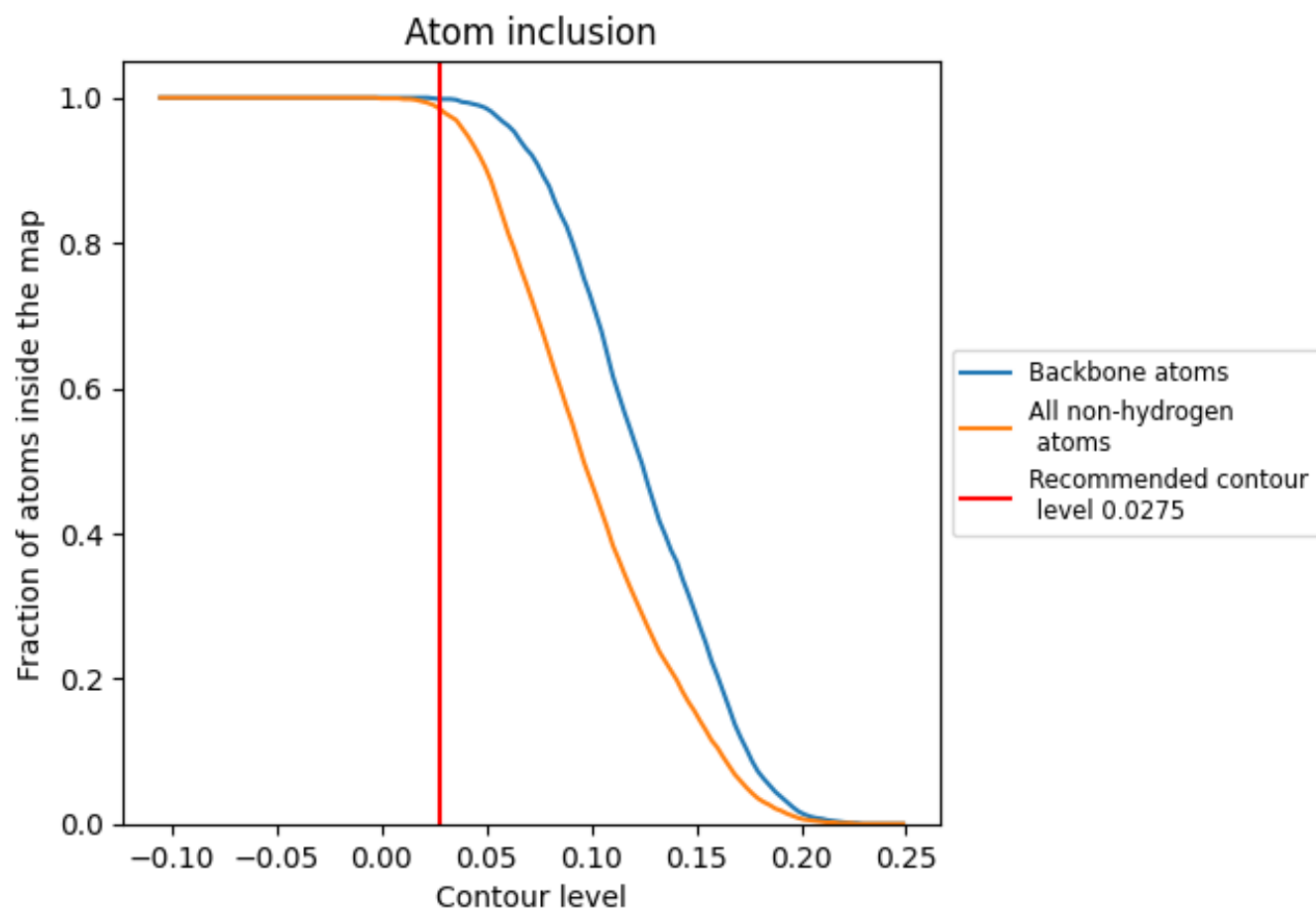
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0275).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% 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 (0.0275) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.3530
A	 0.9830	 0.3690
B	 0.9820	 0.3670
C	 0.9850	 0.3490
D	 1.0000	 0.3890
E	 1.0000	 0.2470
F	 0.9830	 0.3670
G	 0.9850	 0.3470
H	 0.9740	 0.4080
I	 0.9850	 0.3480
J	 1.0000	 0.3950
K	 1.0000	 0.3800
L	 1.0000	 0.3590
M	 0.9600	 0.3910
N	 0.9840	 0.3360
O	 1.0000	 0.2730
P	 1.0000	 0.3180
Q	 1.0000	 0.2970
R	 1.0000	 0.3590
S	 1.0000	 0.4430
T	 1.0000	 0.3320
U	 1.0000	 0.4210
V	 1.0000	 0.3780
W	 1.0000	 0.2460
X	 0.9740	 0.4040
Y	 1.0000	 0.4000
Z	 1.0000	 0.3840
a	 1.0000	 0.3800
b	 0.9600	 0.3820
c	 0.9840	 0.3360
d	 1.0000	 0.2720
e	 1.0000	 0.3340
f	 1.0000	 0.3000
g	 1.0000	 0.3630
h	 1.0000	 0.4390



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 1.0000	 0.3350
j	 1.0000	 0.4110
k	 1.0000	 0.3930
l	 1.0000	 0.2360
m	 0.9740	 0.4160
n	 1.0000	 0.3950
o	 1.0000	 0.3760
p	 1.0000	 0.3740
q	 0.9600	 0.3940
r	 0.9840	 0.3380
s	 1.0000	 0.2670
t	 1.0000	 0.3200
u	 1.0000	 0.3190
v	 1.0000	 0.3620
w	 1.0000	 0.4310
x	 1.0000	 0.3310
y	 1.0000	 0.4250