



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:33 PM UTC

PDB ID : 6OSY / pdb_00006osy
EMDB ID : EMD-20189
Title : Cryo-EM structure of vaccine-elicited antibody 0PV-a.01 in complex with HIV-1 Env BG505 DS-SOSIP and antibodies VRC03 and PGT122
Authors : Gorman, J.; Kwong, P.D.
Deposited on : 2019-05-02
Resolution : 4.30 Å(reported)
Based on initial model : 6CDI

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

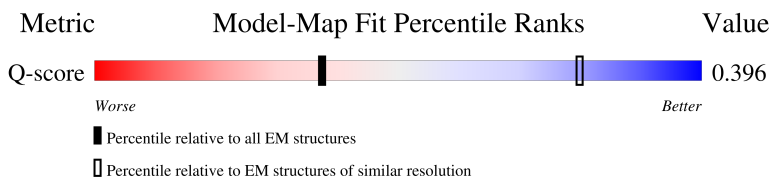
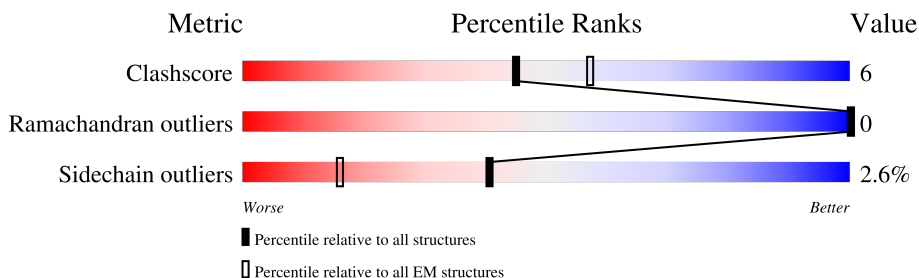
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.30 Å.

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



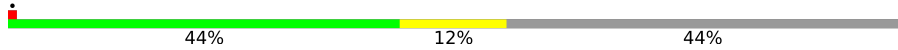
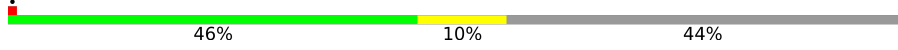
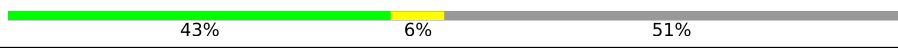
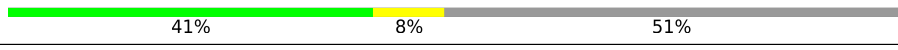
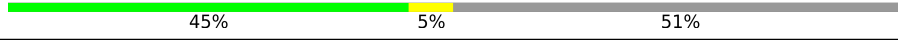
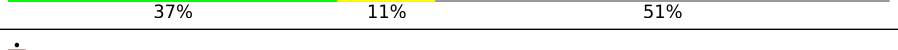
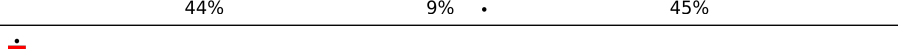
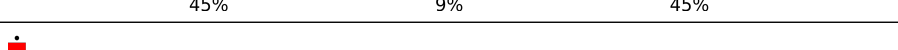
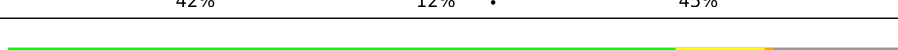
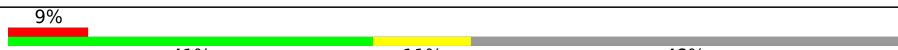
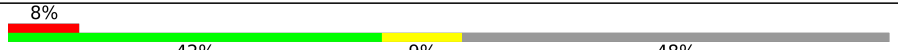
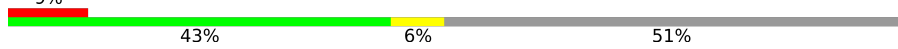
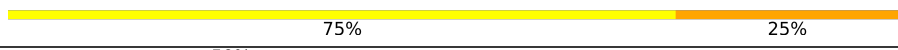
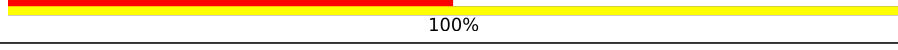
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	2	480	
1	B	480	
1	K	480	
2	5	235	

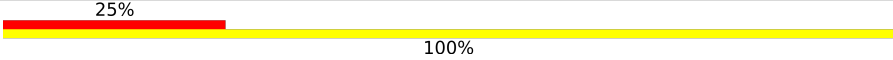
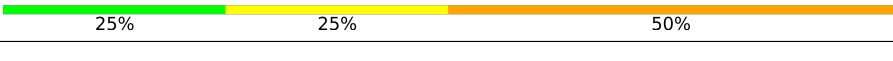
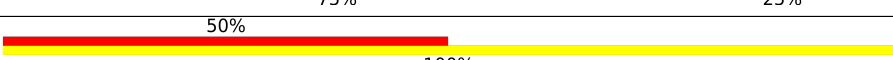
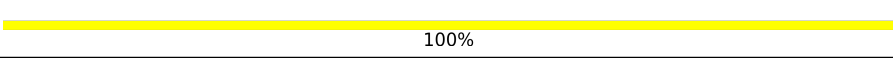
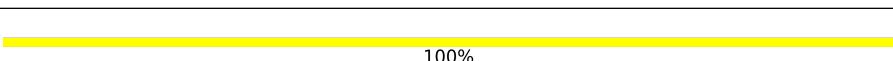
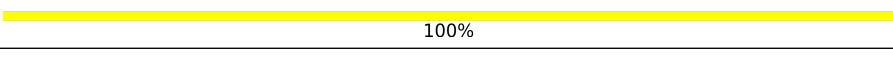
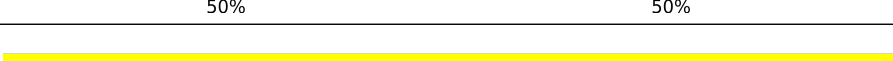
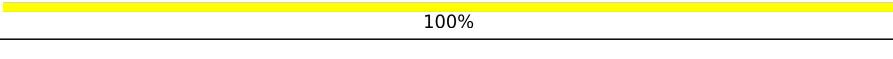
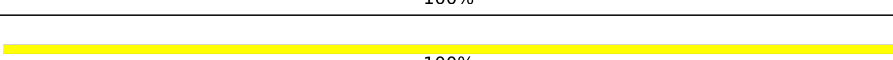
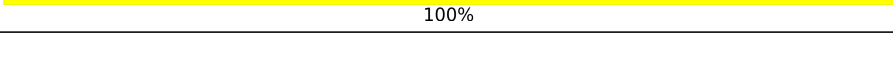
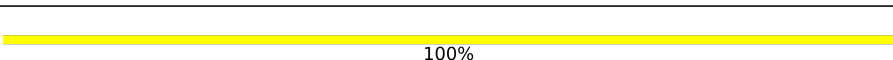
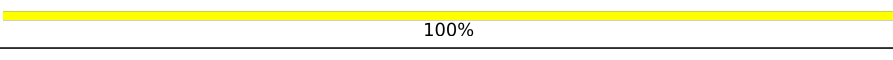
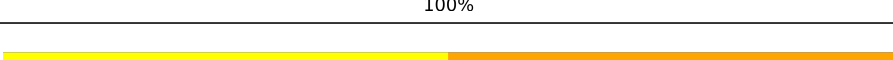
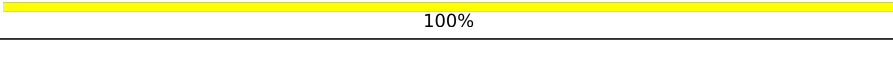
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Mol	Chain	Length	Quality of chain
2	C	235	
2	M	235	
3	6	213	
3	D	213	
3	N	213	
4	7	209	
4	E	209	
4	O	209	
5	8	233	
5	F	233	
5	P	233	
6	A	153	
6	G	153	
6	Q	153	
7	H	235	
7	I	235	
7	R	235	
8	J	213	
8	L	213	
8	S	213	
9	1	4	
9	JA	4	
9	T	4	
9	V	4	
9	i	4	

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Mol	Chain	Length	Quality of chain
9	j	4	
9	l	4	
9	y	4	
9	z	4	
10	0	2	
10	AA	2	
10	CA	2	
10	DA	2	
10	GA	2	
10	IA	2	
10	U	2	
10	Z	2	
10	b	2	
10	c	2	
10	f	2	
10	h	2	
10	k	2	
10	p	2	
10	r	2	
10	s	2	
10	v	2	
10	x	2	
11	3	5	
11	FA	5	
11	W	5	

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Mol	Chain	Length	Quality of chain
11	e	5	100%
11	m	5	20% 80%
11	u	5	100%
12	4	3	33% 33% 33%
12	EA	3	100%
12	X	3	100%
12	d	3	100%
12	n	3	67% 33%
12	t	3	100%
13	9	4	25% 75% 25%
13	Y	4	50% 75% 25%
13	o	4	25% 75% 25%
14	BA	6	17% 67% 17%
14	a	6	17% 67% 17%
14	q	6	17% 67% 17%
15	HA	9	100%
15	g	9	100%
15	w	9	100%

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 32463 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 BG505 gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	453	Total	C	N	O	S	0	0
			3564	2233	630	671	30		
1	B	453	Total	C	N	O	S	0	0
			3564	2233	630	671	30		
1	K	453	Total	C	N	O	S	0	0
			3564	2233	630	671	30		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	201	CYS	ILE	conflict	UNP Q2N0S6
2	332	ASN	THR	conflict	UNP Q2N0S6
2	433	CYS	ALA	conflict	UNP Q2N0S6
2	501	CYS	ALA	conflict	UNP Q2N0S6
2	506	GLY	VAL	conflict	UNP Q2N0S6
2	507	ARG	GLY	conflict	UNP Q2N0S6
2	509	ARG	GLU	conflict	UNP Q2N0S6
2	510	ARG	LYS	conflict	UNP Q2N0S6
2	512	ARG	-	expression tag	UNP Q2N0S6
B	201	CYS	ILE	conflict	UNP Q2N0S6
B	332	ASN	THR	conflict	UNP Q2N0S6
B	433	CYS	ALA	conflict	UNP Q2N0S6
B	501	CYS	ALA	conflict	UNP Q2N0S6
B	506	GLY	VAL	conflict	UNP Q2N0S6
B	507	ARG	GLY	conflict	UNP Q2N0S6
B	509	ARG	GLU	conflict	UNP Q2N0S6
B	510	ARG	LYS	conflict	UNP Q2N0S6
B	512	ARG	-	expression tag	UNP Q2N0S6
K	201	CYS	ILE	conflict	UNP Q2N0S6
K	332	ASN	THR	conflict	UNP Q2N0S6
K	433	CYS	ALA	conflict	UNP Q2N0S6
K	501	CYS	ALA	conflict	UNP Q2N0S6
K	506	GLY	VAL	conflict	UNP Q2N0S6
K	507	ARG	GLY	conflict	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
K	509	ARG	GLU	conflict	UNP Q2N0S6
K	510	ARG	LYS	conflict	UNP Q2N0S6
K	512	ARG	-	expression tag	UNP Q2N0S6

- Molecule 2 is a protein called PGT122 Heavy.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	132	Total	C	N	O	S	0	0
			1047	669	180	195	3		
2	C	132	Total	C	N	O	S	0	0
			1047	669	180	195	3		
2	M	132	Total	C	N	O	S	0	0
			1047	669	180	195	3		

- Molecule 3 is a protein called PGT122 Light.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	105	Total	C	N	O	S	0	0
			805	504	139	160	2		
3	D	105	Total	C	N	O	S	0	0
			805	504	139	160	2		
3	N	105	Total	C	N	O	S	0	0
			805	504	139	160	2		

- Molecule 4 is a protein called VRC03 Light.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	7	102	Total	C	N	O	S	0	0
			802	510	137	152	3		
4	E	102	Total	C	N	O	S	0	0
			802	510	137	152	3		
4	O	102	Total	C	N	O	S	0	0
			802	510	137	152	3		

- Molecule 5 is a protein called VRC03 Heavy.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	8	128	Total	C	N	O	S	0	0
			1023	657	175	185	6		
5	F	128	Total	C	N	O	S	0	0
			1023	657	175	185	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	128	Total	C	N	O	S	0	0
			1023	657	175	185	6		

- Molecule 6 is a protein called BG505 gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	132	Total	C	N	O	S	0	0
			1034	654	178	196	6		
6	G	132	Total	C	N	O	S	0	0
			1034	654	178	196	6		
6	Q	132	Total	C	N	O	S	0	0
			1034	654	178	196	6		

- Molecule 7 is a protein called 0PV-a.01 Heavy.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	122	Total	C	N	O	S	0	0
			957	609	160	184	4		
7	I	122	Total	C	N	O	S	0	0
			957	609	160	184	4		
7	R	122	Total	C	N	O	S	0	0
			957	609	160	184	4		

- Molecule 8 is a protein called 0PV-a.01 Light.

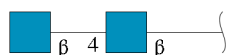
Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	104	Total	C	N	O	S	0	0
			802	498	138	162	4		
8	L	104	Total	C	N	O	S	0	0
			802	498	138	162	4		
8	S	104	Total	C	N	O	S	0	0
			802	498	138	162	4		

- Molecule 9 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
9	T	4	Total	C	N	O	0	0
			50	28	2	20		
9	V	4	Total	C	N	O	0	0
			50	28	2	20		
9	i	4	Total	C	N	O	0	0
			50	28	2	20		
9	j	4	Total	C	N	O	0	0
			50	28	2	20		
9	l	4	Total	C	N	O	0	0
			50	28	2	20		
9	y	4	Total	C	N	O	0	0
			50	28	2	20		
9	z	4	Total	C	N	O	0	0
			50	28	2	20		
9	1	4	Total	C	N	O	0	0
			50	28	2	20		
9	JA	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



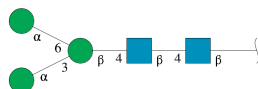
Mol	Chain	Residues	Atoms				AltConf	Trace
10	U	2	Total	C	N	O	0	0
			28	16	2	10		
10	Z	2	Total	C	N	O	0	0
			28	16	2	10		
10	b	2	Total	C	N	O	0	0
			28	16	2	10		
10	c	2	Total	C	N	O	0	0
			28	16	2	10		
10	f	2	Total	C	N	O	0	0
			28	16	2	10		
10	h	2	Total	C	N	O	0	0
			28	16	2	10		
10	k	2	Total	C	N	O	0	0
			28	16	2	10		
10	p	2	Total	C	N	O	0	0
			28	16	2	10		

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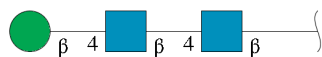
Mol	Chain	Residues	Atoms				AltConf	Trace
10	r	2	Total	C	N	O	0	0
			28	16	2	10		
10	s	2	Total	C	N	O	0	0
			28	16	2	10		
10	v	2	Total	C	N	O	0	0
			28	16	2	10		
10	x	2	Total	C	N	O	0	0
			28	16	2	10		
10	0	2	Total	C	N	O	0	0
			28	16	2	10		
10	AA	2	Total	C	N	O	0	0
			28	16	2	10		
10	CA	2	Total	C	N	O	0	0
			28	16	2	10		
10	DA	2	Total	C	N	O	0	0
			28	16	2	10		
10	GA	2	Total	C	N	O	0	0
			28	16	2	10		
10	IA	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 11 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
11	W	5	Total	C	N	O	0	0
			61	34	2	25		
11	e	5	Total	C	N	O	0	0
			61	34	2	25		
11	m	5	Total	C	N	O	0	0
			61	34	2	25		
11	u	5	Total	C	N	O	0	0
			61	34	2	25		
11	3	5	Total	C	N	O	0	0
			61	34	2	25		
11	FA	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 12 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.



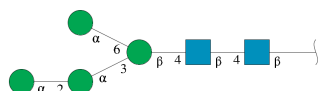
Mol	Chain	Residues	Atoms				AltConf	Trace
12	X	3	Total	C	N	O	0	0
			39	22	2	15		
12	d	3	Total	C	N	O	0	0
			39	22	2	15		
12	n	3	Total	C	N	O	0	0
			39	22	2	15		
12	t	3	Total	C	N	O	0	0
			39	22	2	15		
12	4	3	Total	C	N	O	0	0
			39	22	2	15		
12	EA	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 13 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.



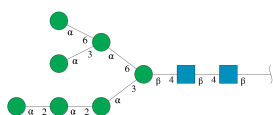
Mol	Chain	Residues	Atoms				AltConf	Trace
13	Y	4	Total	C	N	O	0	0
			50	28	2	20		
13	o	4	Total	C	N	O	0	0
			50	28	2	20		
13	9	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 14 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.



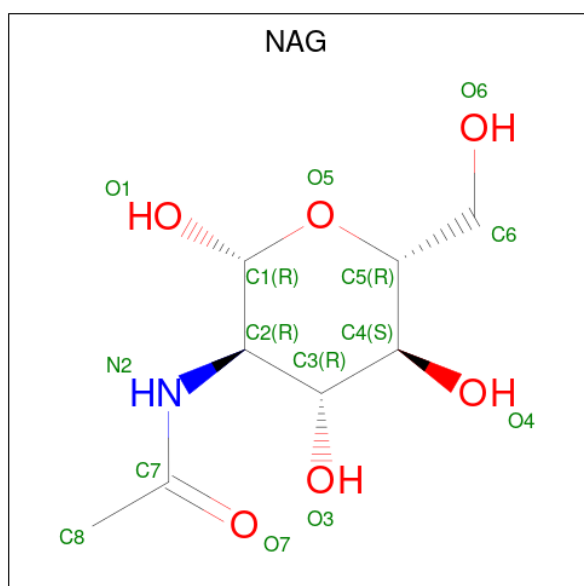
Mol	Chain	Residues	Atoms				AltConf	Trace
14	a	6	Total	C	N	O	0	0
			72	40	2	30		
14	q	6	Total	C	N	O	0	0
			72	40	2	30		
14	BA	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 15 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
15	g	9	Total	C	N	O	0	0
			105	58	2	45		
15	w	9	Total	C	N	O	0	0
			105	58	2	45		
15	HA	9	Total	C	N	O	0	0
			105	58	2	45		

- Molecule 16 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

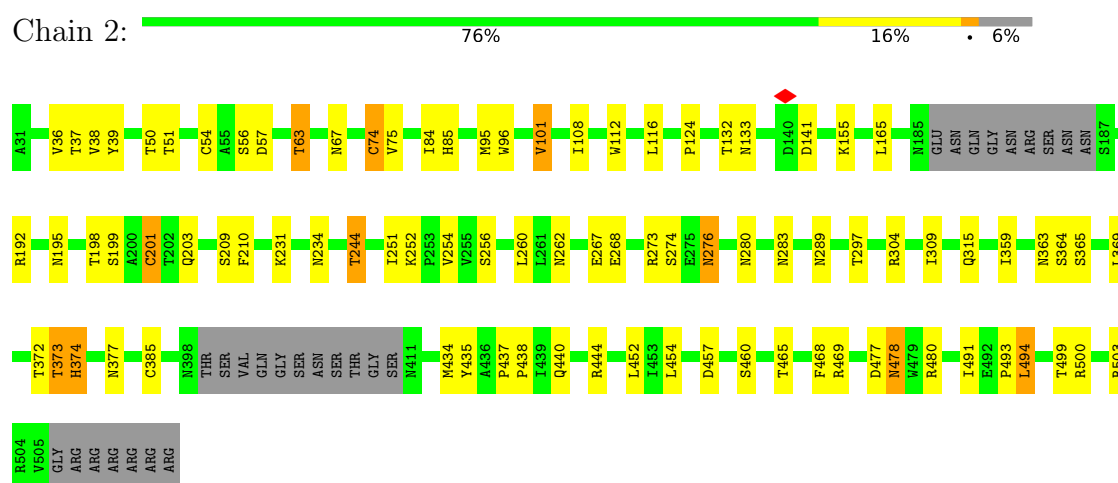


Mol	Chain	Residues	Atoms				AltConf
16	2	1	Total	C	N	O	0
			14	8	1	5	
16	A	1	Total	C	N	O	0
			14	8	1	5	
16	A	1	Total	C	N	O	0
			14	8	1	5	
16	B	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	G	1	Total	C	N	O	0
			14	8	1	5	
16	K	1	Total	C	N	O	0
			14	8	1	5	
16	Q	1	Total	C	N	O	0
			14	8	1	5	
16	Q	1	Total	C	N	O	0
			14	8	1	5	

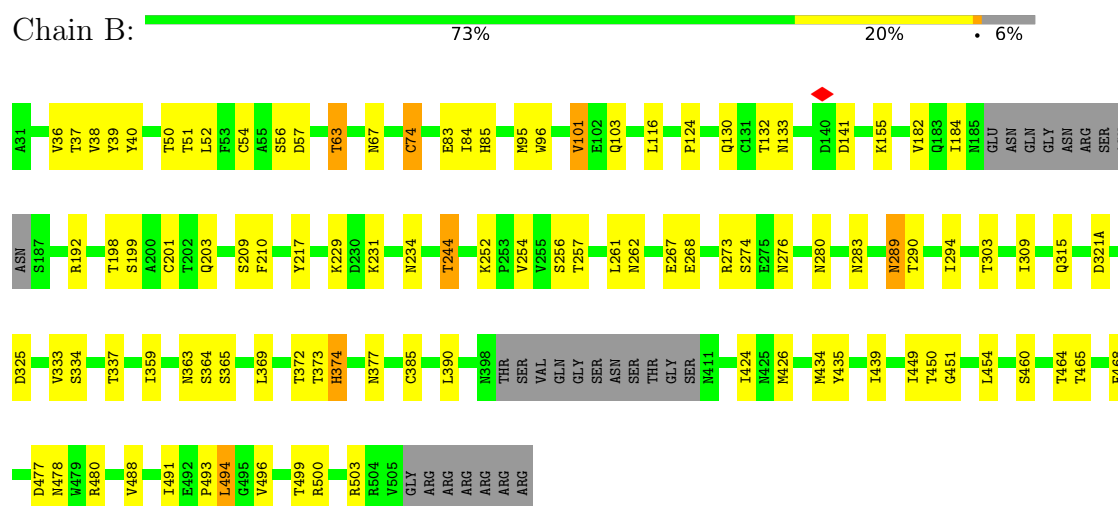
3 Residue-property plots

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: BG505 gp120



- Molecule 1: BG505 gp120



- Molecule 1: BG505 gp120



- Molecule 4: VRC03 Light

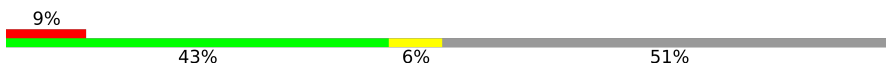
- Molecule 5: VRC03 Heavy

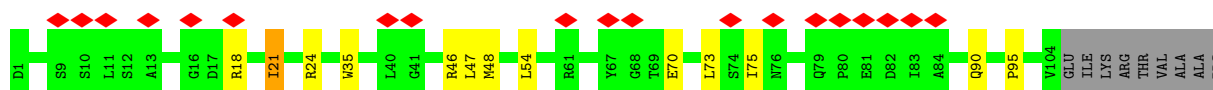
- Molecule 5: VRC03 Heavy

- Molecule 5: VRC03 Heavy

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

• Molecule 8: 0PV-a.01 Light

Chain S: 



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

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

• Molecule 9: 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 T: 



• Molecule 9: 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 V: 

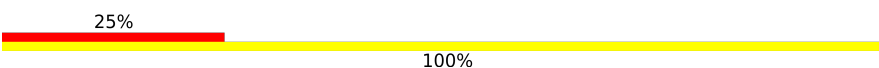


• Molecule 9: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain i: 



• Molecule 9: 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 j: 

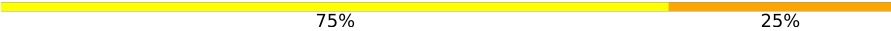


• Molecule 9: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain l:  25% 25% 50%



- Molecule 9: 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 y:  75% 25%



- Molecule 9: 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 z:  50% 100%



- Molecule 9: 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 1:  25% 25% 50%

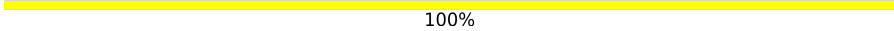


- Molecule 9: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain JA:  75% 25%



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

Chain U:  100%



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

Chain Z:  50% 50%



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

Chain b:  100%



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

Chain c:  100%



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

Chain f:  100%



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

Chain h:  50% 50%



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

Chain k:  100%



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

Chain p:  100%



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

Chain r:  100%

MAG1
MAG2

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

Chain s:  100%

MAG1
MAG2

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

Chain v:  100%

MAG1
MAG2

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

Chain x:  50%  50%

MAG1
MAG2

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

Chain 0:  100%

MAG1
MAG2

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

Chain AA:  50%  50%

MAG1
MAG2

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

Chain CA:  100%

MAG1
MAG2

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

Chain DA:  100%MAG1
MAG2

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

Chain GA:  100%MAG1
MAG2

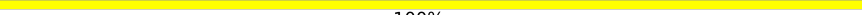
- Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain IA:  50% 50%MAG1
MAG2

- Molecule 11: 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 W:  20% 80%MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 11: 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 e:  100%MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 11: 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 m:  20% 80%



- Molecule 11: 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 u: 100%



- Molecule 11: 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 3: 20% 80%



- Molecule 11: 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 FA: 100%



- Molecule 12: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X: 100%



- Molecule 12: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d: 100%



- Molecule 12: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain n: 67% 33%



- Molecule 12: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain t:  100%

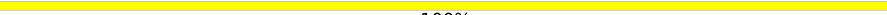


- Molecule 12: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain 4:  33% 33% 33%



- Molecule 12: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain EA:  100%



- Molecule 13: 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:  50% 75% 25%



- Molecule 13: 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 o:  25% 75% 25%



- Molecule 13: 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 9:  25% 75% 25%



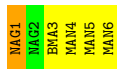
- Molecule 14: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a: 17% 67% 17%



- Molecule 14: 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 q: 17% 67% 17%



- Molecule 14: 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 BA: 17% 67% 17%



- Molecule 15: 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

Chain g: 100%



- Molecule 15: 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

Chain w: 100%



- Molecule 15: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] 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 HA:  100%

MAG1
MAG2
BKA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	55345	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 ($e^-/\text{\AA}^2$)	70.49	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	3.230	Depositor
Minimum map value	-1.878	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.138	Depositor
Recommended contour level	0.45	Depositor
Map size ($\text{\AA}$)	377.78403, 377.78403, 377.78403	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07325, 1.07325, 1.07325	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: BMA, NAG, MAN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.73	0/3638	0.92	3/4939 (0.1%)
1	B	0.73	0/3638	0.92	3/4939 (0.1%)
1	K	0.73	0/3638	0.92	6/4939 (0.1%)
2	5	0.46	0/1076	0.76	0/1465
2	C	0.46	0/1076	0.75	0/1465
2	M	0.46	0/1076	0.74	0/1465
3	6	0.54	0/826	0.80	2/1130 (0.2%)
3	D	0.54	0/826	0.79	2/1130 (0.2%)
3	N	0.53	0/826	0.79	2/1130 (0.2%)
4	7	0.56	0/820	0.91	2/1107 (0.2%)
4	E	0.56	0/820	0.90	2/1107 (0.2%)
4	O	0.55	0/820	0.89	2/1107 (0.2%)
5	8	0.63	0/1056	0.92	5/1439 (0.3%)
5	F	0.63	0/1056	0.89	5/1439 (0.3%)
5	P	0.63	0/1056	0.87	3/1439 (0.2%)
6	A	0.65	0/1052	0.89	3/1427 (0.2%)
6	G	0.64	0/1052	0.91	3/1427 (0.2%)
6	Q	0.63	0/1052	0.90	3/1427 (0.2%)
7	H	0.35	0/982	0.69	0/1341
7	I	0.34	0/982	0.66	0/1341
7	R	0.35	0/982	0.68	0/1341
8	J	0.30	0/819	0.69	0/1109
8	L	0.29	0/819	0.67	0/1109
8	S	0.30	0/819	0.67	0/1109
All	All	0.60	0/30807	0.85	46/41871 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2	0	3
1	B	0	2
1	K	0	2
4	7	0	1
4	E	0	1
4	O	0	1
6	A	0	1
6	G	0	1
6	Q	0	1
All	All	0	13

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	8	48	ILE	CA-C-N	-7.52	113.60	121.35
5	8	48	ILE	C-N-CA	-7.52	113.60	121.35
4	7	49	ASP	CA-C-N	7.37	135.61	121.54
4	7	49	ASP	C-N-CA	7.37	135.61	121.54
4	E	49	ASP	CA-C-N	7.28	135.45	121.54

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	201	CYS	Peptide
1	2	373	THR	Peptide
1	2	74	CYS	Peptide
4	7	88	GLN	Peptide
6	A	517	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	3564	0	3489	48	0
1	B	3564	0	3489	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	3564	0	3489	52	0
2	5	1047	0	1026	22	0
2	C	1047	0	1026	20	0
2	M	1047	0	1026	15	0
3	6	805	0	761	7	0
3	D	805	0	761	11	0
3	N	805	0	761	4	0
4	7	802	0	780	11	0
4	E	802	0	780	15	0
4	O	802	0	780	13	0
5	8	1023	0	971	15	0
5	F	1023	0	971	13	0
5	P	1023	0	971	18	0
6	A	1034	0	1013	9	0
6	G	1034	0	1013	16	0
6	Q	1034	0	1013	13	0
7	H	957	0	925	16	0
7	I	957	0	925	13	0
7	R	957	0	925	18	0
8	J	802	0	769	9	0
8	L	802	0	769	9	0
8	S	802	0	769	9	0
9	1	50	0	43	2	0
9	JA	50	0	43	1	0
9	T	50	0	43	0	0
9	V	50	0	43	2	0
9	i	50	0	43	1	0
9	j	50	0	43	0	0
9	l	50	0	43	2	0
9	y	50	0	43	1	0
9	z	50	0	43	0	0
10	0	28	0	25	0	0
10	AA	28	0	25	0	0
10	CA	28	0	25	0	0
10	DA	28	0	25	0	0
10	GA	28	0	25	0	0
10	IA	28	0	25	1	0
10	U	28	0	25	0	0
10	Z	28	0	25	0	0
10	b	28	0	25	0	0
10	c	28	0	25	0	0
10	f	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	h	28	0	25	1	0
10	k	28	0	25	0	0
10	p	28	0	25	0	0
10	r	28	0	25	0	0
10	s	28	0	25	0	0
10	v	28	0	25	0	0
10	x	28	0	25	1	0
11	3	61	0	52	0	0
11	FA	61	0	52	0	0
11	W	61	0	52	0	0
11	e	61	0	52	0	0
11	m	61	0	52	0	0
11	u	61	0	52	0	0
12	4	39	0	34	1	0
12	EA	39	0	34	0	0
12	X	39	0	34	0	0
12	d	39	0	34	0	0
12	n	39	0	34	1	0
12	t	39	0	34	0	0
13	9	50	0	43	1	0
13	Y	50	0	43	1	0
13	o	50	0	43	1	0
14	BA	72	0	61	1	0
14	a	72	0	61	1	0
14	q	72	0	61	1	0
15	HA	105	0	88	0	0
15	g	105	0	88	0	0
15	w	105	0	88	0	0
16	2	14	0	13	0	0
16	A	28	0	26	0	0
16	B	14	0	13	0	0
16	G	28	0	26	0	0
16	K	14	0	13	0	0
16	Q	28	0	26	0	0
All	All	32463	0	31248	403	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 6.

The worst 5 of 403 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)
7:H:90:TYR:O	7:H:106:GLY:HA2	1.72	0.88
7:I:90:TYR:O	7:I:106:GLY:HA2	1.74	0.86
7:R:90:TYR:O	7:R:106:GLY:HA2	1.77	0.85
8:S:18:ARG:HA	8:S:75:ILE:O	1.77	0.85
8:J:18:ARG:HA	8:J:75:ILE:O	1.80	0.81

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	2	447/480 (93%)	406 (91%)	41 (9%)	0	100	100
1	B	447/480 (93%)	405 (91%)	42 (9%)	0	100	100
1	K	447/480 (93%)	405 (91%)	42 (9%)	0	100	100
2	5	130/235 (55%)	117 (90%)	13 (10%)	0	100	100
2	C	130/235 (55%)	117 (90%)	13 (10%)	0	100	100
2	M	130/235 (55%)	115 (88%)	15 (12%)	0	100	100
3	6	103/213 (48%)	92 (89%)	11 (11%)	0	100	100
3	D	103/213 (48%)	91 (88%)	12 (12%)	0	100	100
3	N	103/213 (48%)	92 (89%)	11 (11%)	0	100	100
4	7	100/209 (48%)	89 (89%)	11 (11%)	0	100	100
4	E	100/209 (48%)	90 (90%)	10 (10%)	0	100	100
4	O	100/209 (48%)	89 (89%)	11 (11%)	0	100	100
5	8	126/233 (54%)	112 (89%)	14 (11%)	0	100	100
5	F	126/233 (54%)	112 (89%)	14 (11%)	0	100	100
5	P	126/233 (54%)	112 (89%)	14 (11%)	0	100	100
6	A	128/153 (84%)	118 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	G	128/153 (84%)	117 (91%)	11 (9%)	0	100	100
6	Q	128/153 (84%)	118 (92%)	10 (8%)	0	100	100
7	H	120/235 (51%)	110 (92%)	10 (8%)	0	100	100
7	I	120/235 (51%)	110 (92%)	10 (8%)	0	100	100
7	R	120/235 (51%)	107 (89%)	13 (11%)	0	100	100
8	J	102/213 (48%)	94 (92%)	8 (8%)	0	100	100
8	L	102/213 (48%)	94 (92%)	8 (8%)	0	100	100
8	S	102/213 (48%)	95 (93%)	7 (7%)	0	100	100
All	All	3768/5913 (64%)	3407 (90%)	361 (10%)	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	2	405/428 (95%)	388 (96%)	17 (4%)	26	48
1	B	405/428 (95%)	386 (95%)	19 (5%)	23	46
1	K	405/428 (95%)	390 (96%)	15 (4%)	30	51
2	5	116/205 (57%)	116 (100%)	0	100	100
2	C	116/205 (57%)	116 (100%)	0	100	100
2	M	116/205 (57%)	114 (98%)	2 (2%)	53	67
3	6	88/181 (49%)	88 (100%)	0	100	100
3	D	88/181 (49%)	87 (99%)	1 (1%)	65	74
3	N	88/181 (49%)	86 (98%)	2 (2%)	44	64
4	7	86/182 (47%)	83 (96%)	3 (4%)	32	54
4	E	86/182 (47%)	83 (96%)	3 (4%)	32	54
4	O	86/182 (47%)	83 (96%)	3 (4%)	32	54
5	8	108/199 (54%)	104 (96%)	4 (4%)	30	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	108/199 (54%)	107 (99%)	1 (1%)	70	76
5	P	108/199 (54%)	105 (97%)	3 (3%)	38	59
6	A	110/129 (85%)	108 (98%)	2 (2%)	51	67
6	G	110/129 (85%)	108 (98%)	2 (2%)	51	67
6	Q	110/129 (85%)	108 (98%)	2 (2%)	51	67
7	H	107/207 (52%)	107 (100%)	0	100	100
7	I	107/207 (52%)	103 (96%)	4 (4%)	30	51
7	R	107/207 (52%)	106 (99%)	1 (1%)	70	76
8	J	90/190 (47%)	90 (100%)	0	100	100
8	L	90/190 (47%)	90 (100%)	0	100	100
8	S	90/190 (47%)	89 (99%)	1 (1%)	65	74
All	All	3330/5163 (64%)	3245 (97%)	85 (3%)	41	60

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	38	VAL
2	M	83	THR
1	K	74	CYS
1	K	257	THR
4	O	42	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	478	ASN
6	Q	652	GLN
7	H	3	GLN
5	P	101	GLN
8	S	79	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 ⓘ

177 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
10	NAG	0	1	10,1	14,14,15	0.55	0	17,19,21	1.63	2 (11%)
10	NAG	0	2	10	14,14,15	1.04	2 (14%)	17,19,21	0.53	0
9	NAG	1	1	9,1	14,14,15	0.43	0	17,19,21	0.79	0
9	NAG	1	2	9	14,14,15	0.74	1 (7%)	17,19,21	1.16	2 (11%)
9	BMA	1	3	9	11,11,12	2.16	3 (27%)	15,15,17	2.18	3 (20%)
9	MAN	1	4	9	11,11,12	1.36	2 (18%)	15,15,17	2.02	2 (13%)
11	NAG	3	1	11,1	14,14,15	0.45	0	17,19,21	0.81	0
11	NAG	3	2	11	14,14,15	0.34	0	17,19,21	0.91	1 (5%)
11	BMA	3	3	11	11,11,12	1.46	2 (18%)	15,15,17	1.14	0
11	MAN	3	4	11	11,11,12	1.45	2 (18%)	15,15,17	1.41	3 (20%)
11	MAN	3	5	11	11,11,12	1.19	2 (18%)	15,15,17	1.27	1 (6%)
12	NAG	4	1	12,1	14,14,15	0.88	1 (7%)	17,19,21	1.59	2 (11%)
12	NAG	4	2	12	14,14,15	0.68	0	17,19,21	0.71	0
12	BMA	4	3	12	11,11,12	1.34	1 (9%)	15,15,17	1.22	2 (13%)
13	NAG	9	1	13,1	14,14,15	0.31	0	17,19,21	0.96	1 (5%)
13	NAG	9	2	13	14,14,15	0.38	0	17,19,21	0.85	1 (5%)
13	BMA	9	3	13	11,11,12	1.18	2 (18%)	15,15,17	1.74	1 (6%)
13	MAN	9	4	13	11,11,12	1.32	1 (9%)	15,15,17	1.85	2 (13%)
10	NAG	AA	1	10,1	14,14,15	0.64	0	17,19,21	0.81	0
10	NAG	AA	2	10	14,14,15	0.84	1 (7%)	17,19,21	0.62	1 (5%)
14	NAG	BA	1	14,1	14,14,15	0.46	0	17,19,21	0.75	1 (5%)
14	NAG	BA	2	14	14,14,15	0.42	0	17,19,21	0.69	0
14	BMA	BA	3	14	11,11,12	1.06	0	15,15,17	1.31	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	MAN	BA	4	14	11,11,12	0.94	1 (9%)	15,15,17	1.66	1 (6%)
14	MAN	BA	5	14	11,11,12	1.00	0	15,15,17	1.33	2 (13%)
14	MAN	BA	6	14	11,11,12	1.09	1 (9%)	15,15,17	1.35	2 (13%)
10	NAG	CA	1	10,1	14,14,15	0.56	0	17,19,21	0.86	1 (5%)
10	NAG	CA	2	10	14,14,15	0.74	1 (7%)	17,19,21	0.68	1 (5%)
10	NAG	DA	1	10,1	14,14,15	0.42	0	17,19,21	0.91	1 (5%)
10	NAG	DA	2	10	14,14,15	0.78	1 (7%)	17,19,21	0.82	1 (5%)
12	NAG	EA	1	12,1	14,14,15	0.77	0	17,19,21	0.91	1 (5%)
12	NAG	EA	2	12	14,14,15	0.54	0	17,19,21	1.14	1 (5%)
12	BMA	EA	3	12	11,11,12	1.59	3 (27%)	15,15,17	1.61	2 (13%)
11	NAG	FA	1	11,1	14,14,15	0.27	0	17,19,21	1.13	1 (5%)
11	NAG	FA	2	11	14,14,15	0.39	0	17,19,21	1.34	2 (11%)
11	BMA	FA	3	11	11,11,12	1.00	1 (9%)	15,15,17	1.85	3 (20%)
11	MAN	FA	4	11	11,11,12	1.16	1 (9%)	15,15,17	1.19	1 (6%)
11	MAN	FA	5	11	11,11,12	1.00	1 (9%)	15,15,17	1.43	2 (13%)
10	NAG	GA	1	10,1	14,14,15	0.35	0	17,19,21	0.88	1 (5%)
10	NAG	GA	2	10	14,14,15	0.85	1 (7%)	17,19,21	0.68	1 (5%)
15	NAG	HA	1	15,1	14,14,15	0.78	1 (7%)	17,19,21	0.90	1 (5%)
15	NAG	HA	2	15	14,14,15	0.38	0	17,19,21	1.76	3 (17%)
15	BMA	HA	3	15	11,11,12	2.01	6 (54%)	15,15,17	2.07	3 (20%)
15	MAN	HA	4	15	11,11,12	0.82	0	15,15,17	1.78	1 (6%)
15	MAN	HA	5	15	11,11,12	1.32	1 (9%)	15,15,17	2.20	2 (13%)
15	MAN	HA	6	15	11,11,12	1.15	1 (9%)	15,15,17	1.22	2 (13%)
15	MAN	HA	7	15	11,11,12	1.49	2 (18%)	15,15,17	1.74	3 (20%)
15	MAN	HA	8	15	11,11,12	1.30	1 (9%)	15,15,17	1.14	1 (6%)
15	MAN	HA	9	15	11,11,12	1.04	1 (9%)	15,15,17	1.57	2 (13%)
10	NAG	IA	1	10,1	14,14,15	0.48	0	17,19,21	1.60	3 (17%)
10	NAG	IA	2	10	14,14,15	0.60	0	17,19,21	1.24	1 (5%)
9	NAG	JA	1	9,1	14,14,15	0.95	1 (7%)	17,19,21	1.50	3 (17%)
9	NAG	JA	2	9	14,14,15	0.74	1 (7%)	17,19,21	1.04	1 (5%)
9	BMA	JA	3	9	11,11,12	1.72	3 (27%)	15,15,17	1.84	2 (13%)
9	MAN	JA	4	9	11,11,12	2.11	5 (45%)	15,15,17	2.44	5 (33%)
9	NAG	T	1	9,1	14,14,15	0.64	0	17,19,21	1.01	1 (5%)
9	NAG	T	2	9	14,14,15	0.84	1 (7%)	17,19,21	0.72	0
9	BMA	T	3	9	11,11,12	1.15	1 (9%)	15,15,17	1.00	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	MAN	T	4	9	11,11,12	1.16	1 (9%)	15,15,17	1.69	2 (13%)
10	NAG	U	1	10,1	14,14,15	0.53	0	17,19,21	1.63	2 (11%)
10	NAG	U	2	10	14,14,15	1.03	2 (14%)	17,19,21	0.54	0
9	NAG	V	1	9,1	14,14,15	0.44	0	17,19,21	0.77	0
9	NAG	V	2	9	14,14,15	0.72	1 (7%)	17,19,21	1.16	2 (11%)
9	BMA	V	3	9	11,11,12	2.13	3 (27%)	15,15,17	2.16	3 (20%)
9	MAN	V	4	9	11,11,12	1.36	2 (18%)	15,15,17	2.00	2 (13%)
11	NAG	W	1	11,1	14,14,15	0.44	0	17,19,21	0.78	0
11	NAG	W	2	11	14,14,15	0.35	0	17,19,21	0.87	1 (5%)
11	BMA	W	3	11	11,11,12	1.43	2 (18%)	15,15,17	1.14	0
11	MAN	W	4	11	11,11,12	1.45	2 (18%)	15,15,17	1.39	3 (20%)
11	MAN	W	5	11	11,11,12	1.20	2 (18%)	15,15,17	1.27	1 (6%)
12	NAG	X	1	12,1	14,14,15	0.90	1 (7%)	17,19,21	1.58	3 (17%)
12	NAG	X	2	12	14,14,15	0.70	0	17,19,21	0.73	1 (5%)
12	BMA	X	3	12	11,11,12	1.36	1 (9%)	15,15,17	1.22	2 (13%)
13	NAG	Y	1	13,1	14,14,15	0.32	0	17,19,21	0.87	1 (5%)
13	NAG	Y	2	13	14,14,15	0.37	0	17,19,21	0.87	1 (5%)
13	BMA	Y	3	13	11,11,12	1.18	2 (18%)	15,15,17	1.72	1 (6%)
13	MAN	Y	4	13	11,11,12	1.34	1 (9%)	15,15,17	1.86	2 (13%)
10	NAG	Z	1	10,1	14,14,15	0.61	0	17,19,21	0.81	0
10	NAG	Z	2	10	14,14,15	0.83	1 (7%)	17,19,21	0.62	1 (5%)
14	NAG	a	1	14,1	14,14,15	0.56	0	17,19,21	0.84	1 (5%)
14	NAG	a	2	14	14,14,15	0.39	0	17,19,21	0.71	0
14	BMA	a	3	14	11,11,12	1.03	0	15,15,17	1.26	2 (13%)
14	MAN	a	4	14	11,11,12	0.96	1 (9%)	15,15,17	1.65	1 (6%)
14	MAN	a	5	14	11,11,12	1.00	0	15,15,17	1.33	2 (13%)
14	MAN	a	6	14	11,11,12	1.08	1 (9%)	15,15,17	1.34	2 (13%)
10	NAG	b	1	10,1	14,14,15	0.49	0	17,19,21	0.87	1 (5%)
10	NAG	b	2	10	14,14,15	0.71	1 (7%)	17,19,21	0.69	1 (5%)
10	NAG	c	1	10,1	14,14,15	0.40	0	17,19,21	0.92	1 (5%)
10	NAG	c	2	10	14,14,15	0.82	1 (7%)	17,19,21	0.83	1 (5%)
12	NAG	d	1	12,1	14,14,15	0.73	0	17,19,21	0.89	1 (5%)
12	NAG	d	2	12	14,14,15	0.55	0	17,19,21	1.19	1 (5%)
12	BMA	d	3	12	11,11,12	1.58	2 (18%)	15,15,17	1.68	2 (13%)
11	NAG	e	1	11,1	14,14,15	0.28	0	17,19,21	1.13	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	NAG	e	2	11	14,14,15	0.36	0	17,19,21	1.34	2 (11%)
11	BMA	e	3	11	11,11,12	0.99	1 (9%)	15,15,17	1.83	3 (20%)
11	MAN	e	4	11	11,11,12	1.16	1 (9%)	15,15,17	1.21	1 (6%)
11	MAN	e	5	11	11,11,12	0.98	1 (9%)	15,15,17	1.44	2 (13%)
10	NAG	f	1	10,1	14,14,15	0.35	0	17,19,21	0.89	1 (5%)
10	NAG	f	2	10	14,14,15	0.82	1 (7%)	17,19,21	0.68	1 (5%)
15	NAG	g	1	15,1	14,14,15	0.78	1 (7%)	17,19,21	0.88	0
15	NAG	g	2	15	14,14,15	0.44	0	17,19,21	1.75	3 (17%)
15	BMA	g	3	15	11,11,12	1.99	5 (45%)	15,15,17	2.07	4 (26%)
15	MAN	g	4	15	11,11,12	0.87	1 (9%)	15,15,17	1.81	1 (6%)
15	MAN	g	5	15	11,11,12	1.29	1 (9%)	15,15,17	2.18	2 (13%)
15	MAN	g	6	15	11,11,12	1.12	1 (9%)	15,15,17	1.21	2 (13%)
15	MAN	g	7	15	11,11,12	1.47	2 (18%)	15,15,17	1.74	4 (26%)
15	MAN	g	8	15	11,11,12	1.28	1 (9%)	15,15,17	1.16	1 (6%)
15	MAN	g	9	15	11,11,12	1.04	1 (9%)	15,15,17	1.59	2 (13%)
10	NAG	h	1	10,1	14,14,15	0.46	0	17,19,21	1.60	3 (17%)
10	NAG	h	2	10	14,14,15	0.60	0	17,19,21	1.17	1 (5%)
9	NAG	i	1	9,1	14,14,15	1.84	1 (7%)	17,19,21	2.49	3 (17%)
9	NAG	i	2	9	14,14,15	0.38	0	17,19,21	1.33	1 (5%)
9	BMA	i	3	9	11,11,12	1.89	5 (45%)	15,15,17	1.99	3 (20%)
9	MAN	i	4	9	11,11,12	2.12	5 (45%)	15,15,17	2.49	5 (33%)
9	NAG	j	1	9,1	14,14,15	0.63	0	17,19,21	1.04	1 (5%)
9	NAG	j	2	9	14,14,15	0.84	1 (7%)	17,19,21	0.72	0
9	BMA	j	3	9	11,11,12	1.16	1 (9%)	15,15,17	1.00	2 (13%)
9	MAN	j	4	9	11,11,12	1.14	1 (9%)	15,15,17	1.66	2 (13%)
10	NAG	k	1	10,1	14,14,15	0.54	0	17,19,21	1.62	2 (11%)
10	NAG	k	2	10	14,14,15	1.02	2 (14%)	17,19,21	0.54	0
9	NAG	l	1	9,1	14,14,15	0.41	0	17,19,21	0.77	0
9	NAG	l	2	9	14,14,15	0.71	1 (7%)	17,19,21	1.18	2 (11%)
9	BMA	l	3	9	11,11,12	2.17	3 (27%)	15,15,17	2.17	4 (26%)
9	MAN	l	4	9	11,11,12	1.40	2 (18%)	15,15,17	2.03	2 (13%)
11	NAG	m	1	11,1	14,14,15	0.47	0	17,19,21	0.80	0
11	NAG	m	2	11	14,14,15	0.34	0	17,19,21	0.91	1 (5%)
11	BMA	m	3	11	11,11,12	1.46	2 (18%)	15,15,17	1.12	0
11	MAN	m	4	11	11,11,12	1.45	2 (18%)	15,15,17	1.41	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	MAN	m	5	11	11,11,12	1.18	2 (18%)	15,15,17	1.25	1 (6%)
12	NAG	n	1	12,1	14,14,15	0.91	1 (7%)	17,19,21	1.59	3 (17%)
12	NAG	n	2	12	14,14,15	0.70	0	17,19,21	0.72	1 (5%)
12	BMA	n	3	12	11,11,12	1.36	1 (9%)	15,15,17	1.24	2 (13%)
13	NAG	o	1	13,1	14,14,15	0.31	0	17,19,21	0.94	1 (5%)
13	NAG	o	2	13	14,14,15	0.38	0	17,19,21	0.85	1 (5%)
13	BMA	o	3	13	11,11,12	1.14	1 (9%)	15,15,17	1.73	1 (6%)
13	MAN	o	4	13	11,11,12	1.32	1 (9%)	15,15,17	1.86	2 (13%)
10	NAG	p	1	10,1	14,14,15	0.61	0	17,19,21	0.82	1 (5%)
10	NAG	p	2	10	14,14,15	0.84	1 (7%)	17,19,21	0.61	0
14	NAG	q	1	14,1	14,14,15	0.56	0	17,19,21	0.82	1 (5%)
14	NAG	q	2	14	14,14,15	0.40	0	17,19,21	0.72	0
14	BMA	q	3	14	11,11,12	1.04	0	15,15,17	1.25	2 (13%)
14	MAN	q	4	14	11,11,12	0.93	1 (9%)	15,15,17	1.62	1 (6%)
14	MAN	q	5	14	11,11,12	1.00	0	15,15,17	1.35	2 (13%)
14	MAN	q	6	14	11,11,12	1.08	1 (9%)	15,15,17	1.35	2 (13%)
10	NAG	r	1	10,1	14,14,15	0.50	0	17,19,21	0.85	1 (5%)
10	NAG	r	2	10	14,14,15	0.72	1 (7%)	17,19,21	0.69	1 (5%)
10	NAG	s	1	10,1	14,14,15	0.44	0	17,19,21	0.92	1 (5%)
10	NAG	s	2	10	14,14,15	0.79	1 (7%)	17,19,21	0.84	1 (5%)
12	NAG	t	1	12,1	14,14,15	0.71	0	17,19,21	0.85	1 (5%)
12	NAG	t	2	12	14,14,15	0.54	0	17,19,21	1.14	1 (5%)
12	BMA	t	3	12	11,11,12	1.56	2 (18%)	15,15,17	1.68	2 (13%)
11	NAG	u	1	11,1	14,14,15	0.27	0	17,19,21	1.10	1 (5%)
11	NAG	u	2	11	14,14,15	0.39	0	17,19,21	1.31	2 (11%)
11	BMA	u	3	11	11,11,12	0.98	1 (9%)	15,15,17	1.83	3 (20%)
11	MAN	u	4	11	11,11,12	1.18	1 (9%)	15,15,17	1.19	1 (6%)
11	MAN	u	5	11	11,11,12	0.98	1 (9%)	15,15,17	1.43	2 (13%)
10	NAG	v	1	10,1	14,14,15	0.36	0	17,19,21	0.89	1 (5%)
10	NAG	v	2	10	14,14,15	0.85	1 (7%)	17,19,21	0.67	0
15	NAG	w	1	15,1	14,14,15	0.83	1 (7%)	17,19,21	0.91	1 (5%)
15	NAG	w	2	15	14,14,15	0.42	0	17,19,21	1.79	3 (17%)
15	BMA	w	3	15	11,11,12	2.00	5 (45%)	15,15,17	2.07	3 (20%)
15	MAN	w	4	15	11,11,12	0.87	1 (9%)	15,15,17	1.82	1 (6%)
15	MAN	w	5	15	11,11,12	1.25	1 (9%)	15,15,17	2.17	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	MAN	w	6	15	11,11,12	1.15	1 (9%)	15,15,17	1.22	2 (13%)
15	MAN	w	7	15	11,11,12	1.51	2 (18%)	15,15,17	1.81	4 (26%)
15	MAN	w	8	15	11,11,12	1.30	2 (18%)	15,15,17	1.15	1 (6%)
15	MAN	w	9	15	11,11,12	1.07	0	15,15,17	1.55	2 (13%)
10	NAG	x	1	10,1	14,14,15	0.43	0	17,19,21	1.60	3 (17%)
10	NAG	x	2	10	14,14,15	0.58	0	17,19,21	1.20	1 (5%)
9	NAG	y	1	9,1	14,14,15	1.84	1 (7%)	17,19,21	2.42	3 (17%)
9	NAG	y	2	9	14,14,15	0.38	0	17,19,21	1.38	1 (5%)
9	BMA	y	3	9	11,11,12	1.82	4 (36%)	15,15,17	1.97	3 (20%)
9	MAN	y	4	9	11,11,12	2.21	5 (45%)	15,15,17	2.48	5 (33%)
9	NAG	z	1	9,1	14,14,15	0.63	0	17,19,21	1.01	1 (5%)
9	NAG	z	2	9	14,14,15	0.86	1 (7%)	17,19,21	0.73	0
9	BMA	z	3	9	11,11,12	1.17	1 (9%)	15,15,17	0.98	1 (6%)
9	MAN	z	4	9	11,11,12	1.18	1 (9%)	15,15,17	1.69	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	0	1	10,1	-	3/6/23/26	0/1/1/1
10	NAG	0	2	10	-	2/6/23/26	0/1/1/1
9	NAG	1	1	9,1	-	1/6/23/26	0/1/1/1
9	NAG	1	2	9	-	2/6/23/26	0/1/1/1
9	BMA	1	3	9	-	2/2/19/22	0/1/1/1
9	MAN	1	4	9	-	1/2/19/22	0/1/1/1
11	NAG	3	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	3	2	11	-	0/6/23/26	0/1/1/1
11	BMA	3	3	11	-	2/2/19/22	0/1/1/1
11	MAN	3	4	11	-	1/2/19/22	0/1/1/1
11	MAN	3	5	11	-	0/2/19/22	0/1/1/1
12	NAG	4	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	4	2	12	-	2/6/23/26	0/1/1/1
12	BMA	4	3	12	-	0/2/19/22	0/1/1/1
13	NAG	9	1	13,1	-	2/6/23/26	0/1/1/1
13	NAG	9	2	13	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	BMA	9	3	13	-	0/2/19/22	0/1/1/1
13	MAN	9	4	13	-	2/2/19/22	0/1/1/1
10	NAG	AA	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	AA	2	10	-	2/6/23/26	0/1/1/1
14	NAG	BA	1	14,1	-	2/6/23/26	0/1/1/1
14	NAG	BA	2	14	-	2/6/23/26	0/1/1/1
14	BMA	BA	3	14	-	0/2/19/22	0/1/1/1
14	MAN	BA	4	14	-	0/2/19/22	0/1/1/1
14	MAN	BA	5	14	-	2/2/19/22	0/1/1/1
14	MAN	BA	6	14	-	2/2/19/22	0/1/1/1
10	NAG	CA	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	CA	2	10	-	2/6/23/26	0/1/1/1
10	NAG	DA	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	DA	2	10	-	2/6/23/26	0/1/1/1
12	NAG	EA	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	EA	2	12	-	0/6/23/26	0/1/1/1
12	BMA	EA	3	12	-	2/2/19/22	0/1/1/1
11	NAG	FA	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	FA	2	11	-	0/6/23/26	0/1/1/1
11	BMA	FA	3	11	-	2/2/19/22	0/1/1/1
11	MAN	FA	4	11	-	2/2/19/22	0/1/1/1
11	MAN	FA	5	11	-	2/2/19/22	0/1/1/1
10	NAG	GA	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	GA	2	10	-	2/6/23/26	0/1/1/1
15	NAG	HA	1	15,1	-	2/6/23/26	0/1/1/1
15	NAG	HA	2	15	-	4/6/23/26	0/1/1/1
15	BMA	HA	3	15	-	1/2/19/22	0/1/1/1
15	MAN	HA	4	15	-	0/2/19/22	0/1/1/1
15	MAN	HA	5	15	-	1/2/19/22	0/1/1/1
15	MAN	HA	6	15	-	0/2/19/22	0/1/1/1
15	MAN	HA	7	15	-	0/2/19/22	0/1/1/1
15	MAN	HA	8	15	-	2/2/19/22	0/1/1/1
15	MAN	HA	9	15	-	2/2/19/22	0/1/1/1
10	NAG	IA	1	10,1	-	3/6/23/26	0/1/1/1
10	NAG	IA	2	10	-	0/6/23/26	0/1/1/1
9	NAG	JA	1	9,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	JA	2	9	-	2/6/23/26	0/1/1/1
9	BMA	JA	3	9	-	1/2/19/22	1/1/1/1
9	MAN	JA	4	9	-	0/2/19/22	0/1/1/1
9	NAG	T	1	9,1	-	1/6/23/26	0/1/1/1
9	NAG	T	2	9	-	2/6/23/26	0/1/1/1
9	BMA	T	3	9	-	2/2/19/22	0/1/1/1
9	MAN	T	4	9	-	2/2/19/22	0/1/1/1
10	NAG	U	1	10,1	-	3/6/23/26	0/1/1/1
10	NAG	U	2	10	-	2/6/23/26	0/1/1/1
9	NAG	V	1	9,1	-	1/6/23/26	0/1/1/1
9	NAG	V	2	9	-	2/6/23/26	0/1/1/1
9	BMA	V	3	9	-	2/2/19/22	0/1/1/1
9	MAN	V	4	9	-	1/2/19/22	0/1/1/1
11	NAG	W	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	W	2	11	-	0/6/23/26	0/1/1/1
11	BMA	W	3	11	-	2/2/19/22	0/1/1/1
11	MAN	W	4	11	-	1/2/19/22	0/1/1/1
11	MAN	W	5	11	-	0/2/19/22	0/1/1/1
12	NAG	X	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	X	2	12	-	2/6/23/26	0/1/1/1
12	BMA	X	3	12	-	0/2/19/22	0/1/1/1
13	NAG	Y	1	13,1	-	2/6/23/26	0/1/1/1
13	NAG	Y	2	13	-	0/6/23/26	0/1/1/1
13	BMA	Y	3	13	-	0/2/19/22	0/1/1/1
13	MAN	Y	4	13	-	2/2/19/22	0/1/1/1
10	NAG	Z	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	Z	2	10	-	2/6/23/26	0/1/1/1
14	NAG	a	1	14,1	-	2/6/23/26	0/1/1/1
14	NAG	a	2	14	-	2/6/23/26	0/1/1/1
14	BMA	a	3	14	-	0/2/19/22	0/1/1/1
14	MAN	a	4	14	-	0/2/19/22	0/1/1/1
14	MAN	a	5	14	-	2/2/19/22	0/1/1/1
14	MAN	a	6	14	-	2/2/19/22	0/1/1/1
10	NAG	b	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	b	2	10	-	2/6/23/26	0/1/1/1
10	NAG	c	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	c	2	10	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	d	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	d	2	12	-	0/6/23/26	0/1/1/1
12	BMA	d	3	12	-	2/2/19/22	0/1/1/1
11	NAG	e	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	e	2	11	-	0/6/23/26	0/1/1/1
11	BMA	e	3	11	-	2/2/19/22	0/1/1/1
11	MAN	e	4	11	-	2/2/19/22	0/1/1/1
11	MAN	e	5	11	-	2/2/19/22	0/1/1/1
10	NAG	f	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	f	2	10	-	2/6/23/26	0/1/1/1
15	NAG	g	1	15,1	-	2/6/23/26	0/1/1/1
15	NAG	g	2	15	-	4/6/23/26	0/1/1/1
15	BMA	g	3	15	-	1/2/19/22	0/1/1/1
15	MAN	g	4	15	-	0/2/19/22	0/1/1/1
15	MAN	g	5	15	-	1/2/19/22	0/1/1/1
15	MAN	g	6	15	-	0/2/19/22	0/1/1/1
15	MAN	g	7	15	-	0/2/19/22	0/1/1/1
15	MAN	g	8	15	-	2/2/19/22	0/1/1/1
15	MAN	g	9	15	-	2/2/19/22	0/1/1/1
10	NAG	h	1	10,1	-	4/6/23/26	0/1/1/1
10	NAG	h	2	10	-	0/6/23/26	0/1/1/1
9	NAG	i	1	9,1	-	0/6/23/26	0/1/1/1
9	NAG	i	2	9	-	2/6/23/26	0/1/1/1
9	BMA	i	3	9	-	1/2/19/22	1/1/1/1
9	MAN	i	4	9	-	0/2/19/22	0/1/1/1
9	NAG	j	1	9,1	-	1/6/23/26	0/1/1/1
9	NAG	j	2	9	-	2/6/23/26	0/1/1/1
9	BMA	j	3	9	-	2/2/19/22	0/1/1/1
9	MAN	j	4	9	-	2/2/19/22	0/1/1/1
10	NAG	k	1	10,1	-	3/6/23/26	0/1/1/1
10	NAG	k	2	10	-	2/6/23/26	0/1/1/1
9	NAG	l	1	9,1	-	1/6/23/26	0/1/1/1
9	NAG	l	2	9	-	2/6/23/26	0/1/1/1
9	BMA	l	3	9	-	2/2/19/22	0/1/1/1
9	MAN	l	4	9	-	1/2/19/22	0/1/1/1
11	NAG	m	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	m	2	11	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	BMA	m	3	11	-	2/2/19/22	0/1/1/1
11	MAN	m	4	11	-	1/2/19/22	0/1/1/1
11	MAN	m	5	11	-	0/2/19/22	0/1/1/1
12	NAG	n	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	n	2	12	-	2/6/23/26	0/1/1/1
12	BMA	n	3	12	-	0/2/19/22	0/1/1/1
13	NAG	o	1	13,1	-	2/6/23/26	0/1/1/1
13	NAG	o	2	13	-	0/6/23/26	0/1/1/1
13	BMA	o	3	13	-	0/2/19/22	0/1/1/1
13	MAN	o	4	13	-	2/2/19/22	0/1/1/1
10	NAG	p	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	p	2	10	-	2/6/23/26	0/1/1/1
14	NAG	q	1	14,1	-	2/6/23/26	0/1/1/1
14	NAG	q	2	14	-	2/6/23/26	0/1/1/1
14	BMA	q	3	14	-	0/2/19/22	0/1/1/1
14	MAN	q	4	14	-	0/2/19/22	0/1/1/1
14	MAN	q	5	14	-	2/2/19/22	0/1/1/1
14	MAN	q	6	14	-	1/2/19/22	0/1/1/1
10	NAG	r	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	r	2	10	-	2/6/23/26	0/1/1/1
10	NAG	s	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	s	2	10	-	2/6/23/26	0/1/1/1
12	NAG	t	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	t	2	12	-	0/6/23/26	0/1/1/1
12	BMA	t	3	12	-	2/2/19/22	0/1/1/1
11	NAG	u	1	11,1	-	2/6/23/26	0/1/1/1
11	NAG	u	2	11	-	0/6/23/26	0/1/1/1
11	BMA	u	3	11	-	2/2/19/22	0/1/1/1
11	MAN	u	4	11	-	2/2/19/22	0/1/1/1
11	MAN	u	5	11	-	2/2/19/22	0/1/1/1
10	NAG	v	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	v	2	10	-	2/6/23/26	0/1/1/1
15	NAG	w	1	15,1	-	2/6/23/26	0/1/1/1
15	NAG	w	2	15	-	4/6/23/26	0/1/1/1
15	BMA	w	3	15	-	1/2/19/22	0/1/1/1
15	MAN	w	4	15	-	1/2/19/22	0/1/1/1
15	MAN	w	5	15	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	MAN	w	6	15	-	0/2/19/22	0/1/1/1
15	MAN	w	7	15	-	0/2/19/22	0/1/1/1
15	MAN	w	8	15	-	2/2/19/22	0/1/1/1
15	MAN	w	9	15	-	0/2/19/22	0/1/1/1
10	NAG	x	1	10,1	-	4/6/23/26	0/1/1/1
10	NAG	x	2	10	-	0/6/23/26	0/1/1/1
9	NAG	y	1	9,1	-	0/6/23/26	0/1/1/1
9	NAG	y	2	9	-	2/6/23/26	0/1/1/1
9	BMA	y	3	9	-	1/2/19/22	1/1/1/1
9	MAN	y	4	9	-	0/2/19/22	0/1/1/1
9	NAG	z	1	9,1	-	1/6/23/26	0/1/1/1
9	NAG	z	2	9	-	2/6/23/26	0/1/1/1
9	BMA	z	3	9	-	2/2/19/22	0/1/1/1
9	MAN	z	4	9	-	2/2/19/22	0/1/1/1

The worst 5 of 169 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	i	1	NAG	O5-C1	6.78	1.55	1.43
9	y	1	NAG	O5-C1	6.77	1.55	1.43
9	y	4	MAN	C1-C2	5.39	1.65	1.52
9	i	4	MAN	C1-C2	4.86	1.63	1.52
9	JA	4	MAN	C1-C2	4.77	1.63	1.52

The worst 5 of 273 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	i	1	NAG	C1-O5-C5	9.11	124.39	112.19
9	y	1	NAG	C1-O5-C5	8.89	124.10	112.19
15	g	5	MAN	C1-O5-C5	7.56	122.32	112.19
15	HA	5	MAN	C1-O5-C5	7.53	122.28	112.19
15	w	5	MAN	C1-O5-C5	7.50	122.23	112.19

There are no chirality outliers.

5 of 258 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	w	1	NAG	C4-C5-C6-O6
12	EA	3	BMA	C4-C5-C6-O6
15	g	1	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
15	HA	1	NAG	C4-C5-C6-O6
9	y	2	NAG	O5-C5-C6-O6

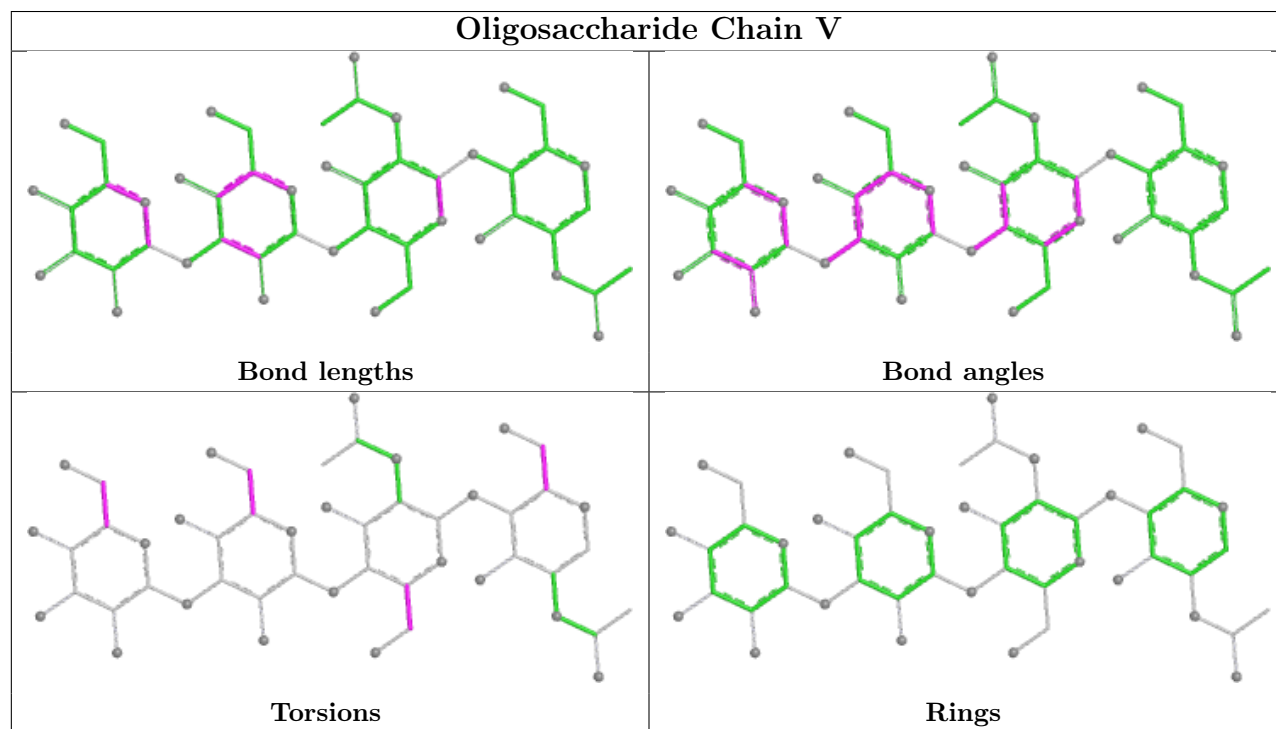
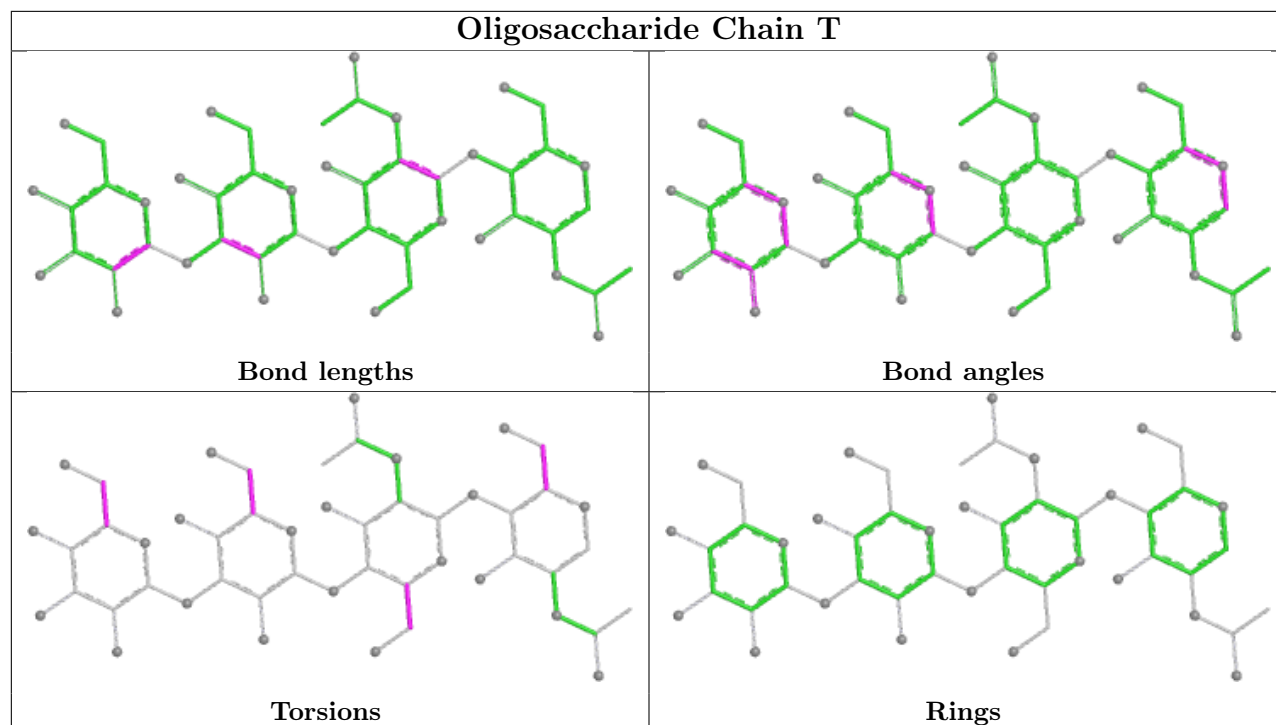
All (3) ring outliers are listed below:

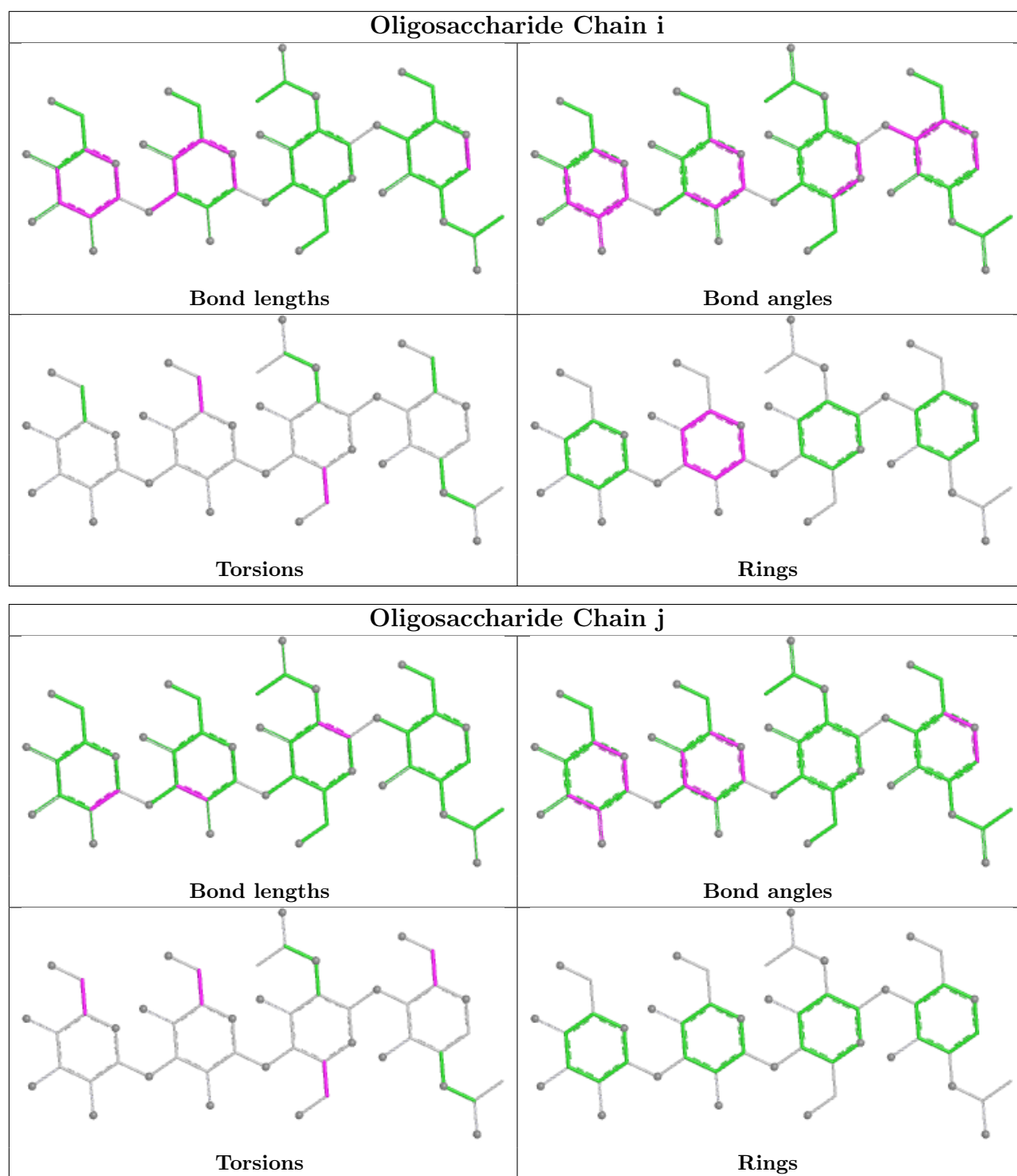
Mol	Chain	Res	Type	Atoms
9	i	3	BMA	C1-C2-C3-C4-C5-O5
9	y	3	BMA	C1-C2-C3-C4-C5-O5
9	JA	3	BMA	C1-C2-C3-C4-C5-O5

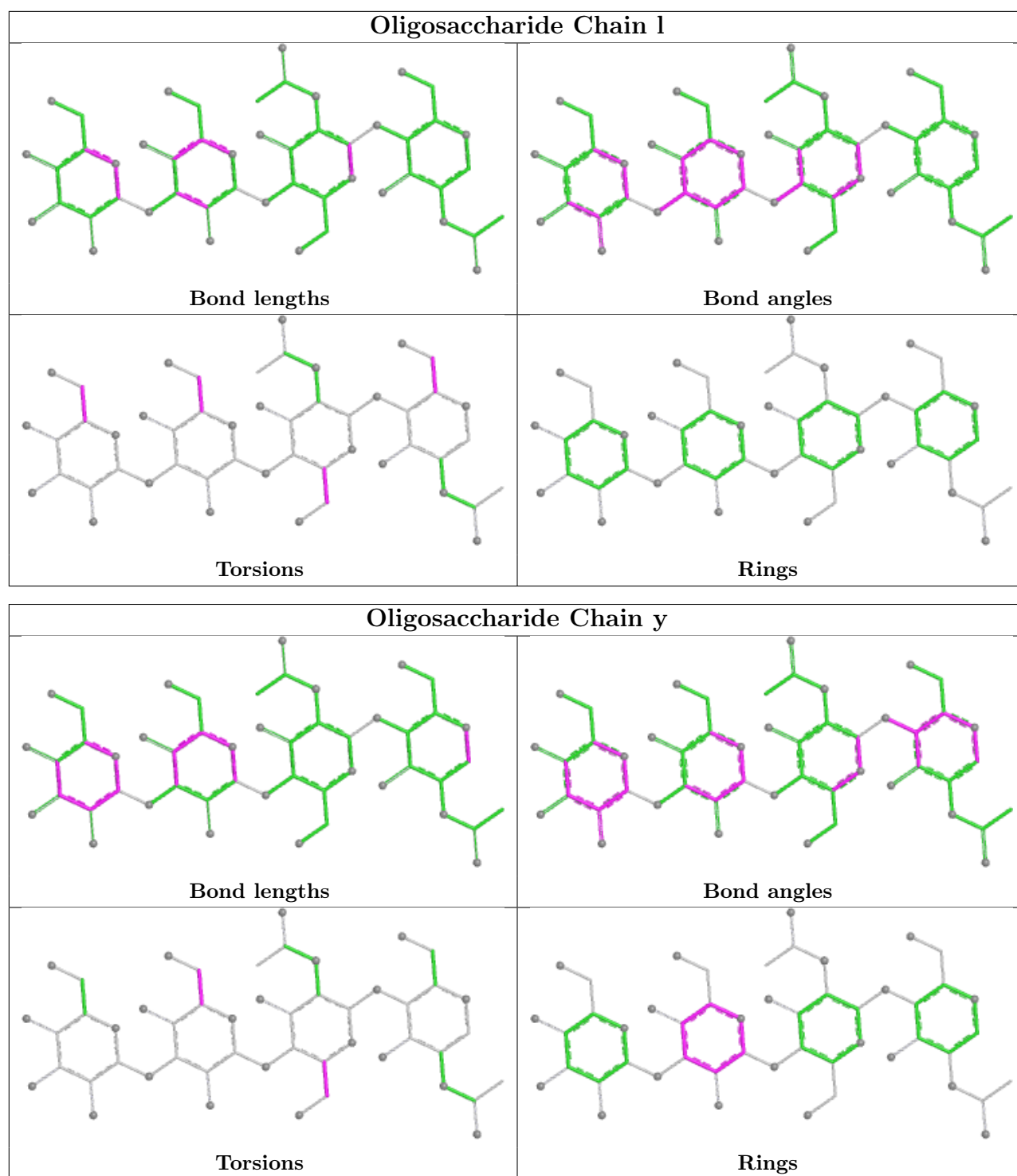
20 monomers are involved in 17 short contacts:

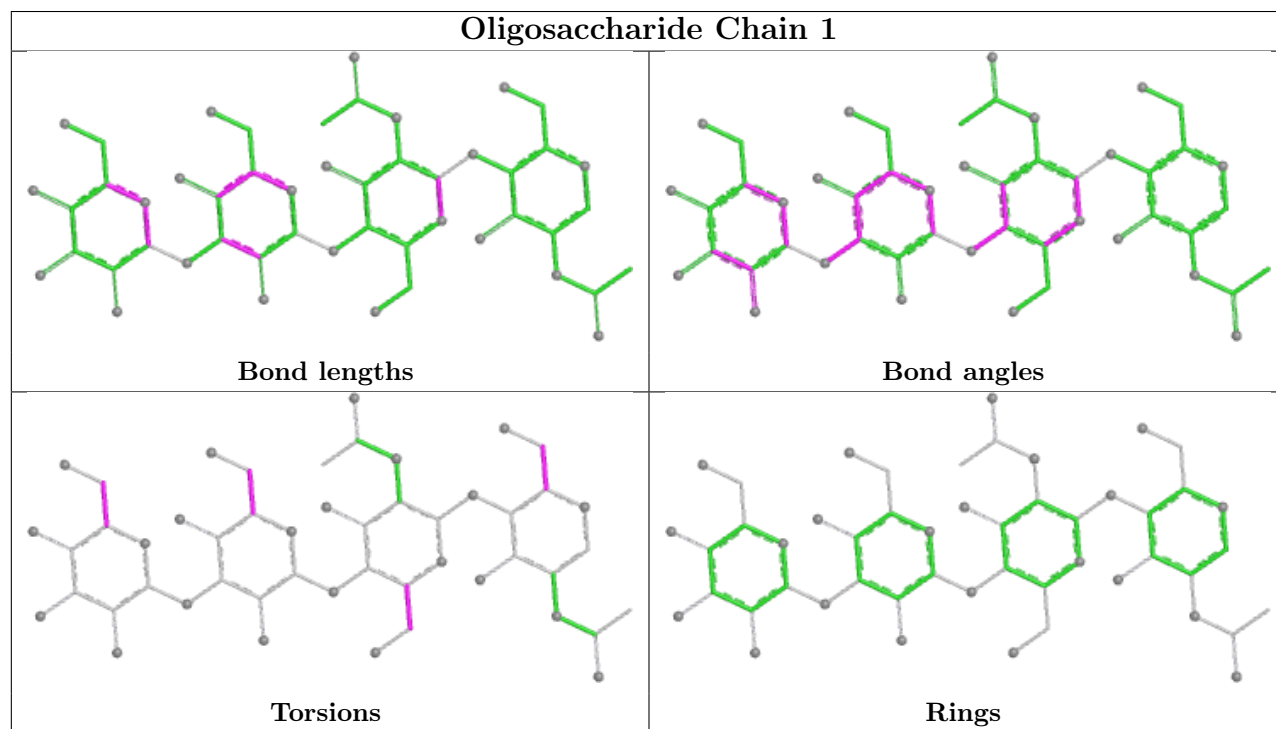
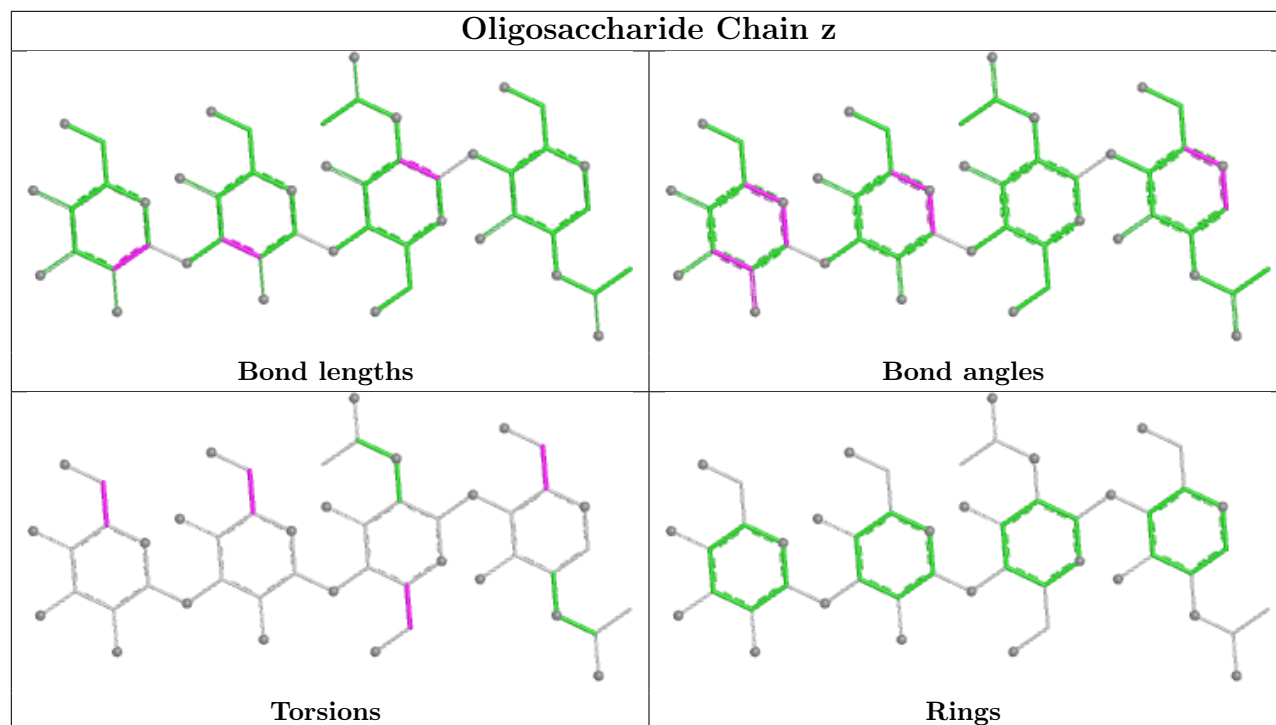
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	y	2	NAG	1	0
13	Y	1	NAG	1	0
9	V	2	NAG	1	0
9	i	2	NAG	1	0
9	1	2	NAG	1	0
13	9	1	NAG	1	0
10	x	1	NAG	1	0
9	1	3	BMA	1	0
10	IA	1	NAG	1	0
10	h	1	NAG	1	0
9	V	3	BMA	1	0
9	l	3	BMA	1	0
14	a	1	NAG	1	0
13	o	1	NAG	1	0
12	4	1	NAG	1	0
9	JA	2	NAG	1	0
14	q	1	NAG	1	0
12	n	1	NAG	1	0
14	BA	1	NAG	1	0
9	l	2	NAG	1	0

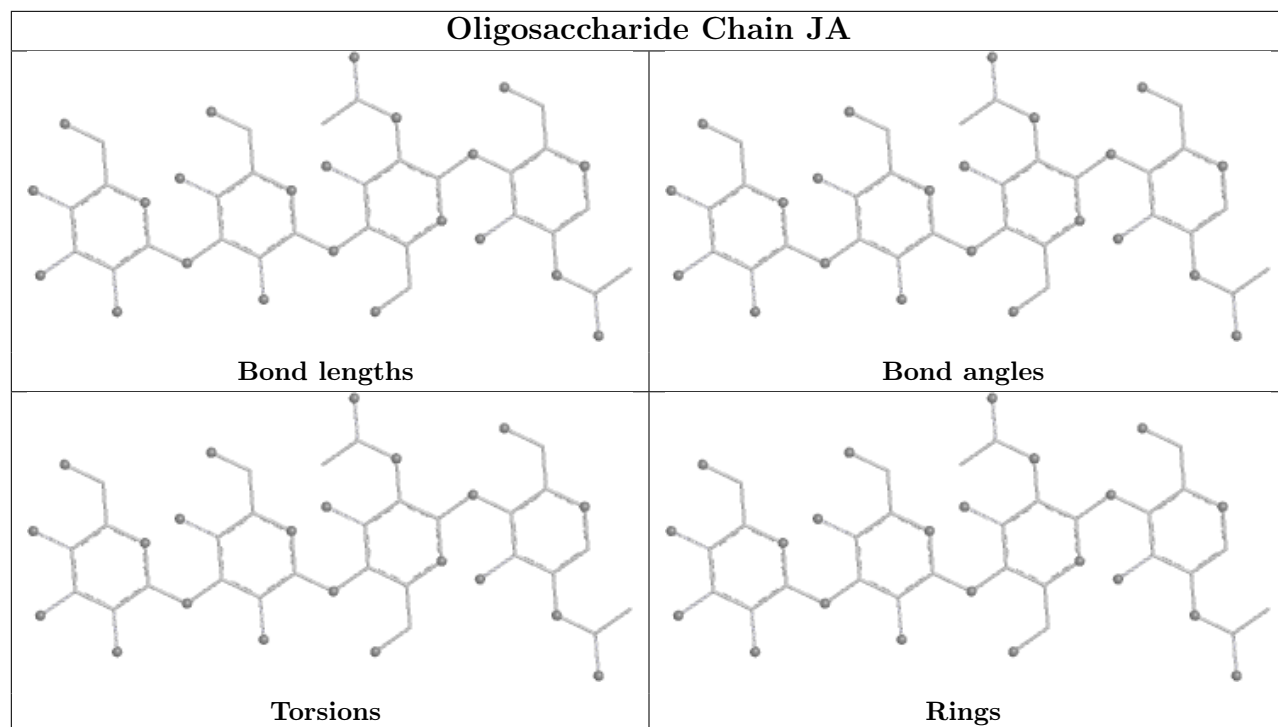
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

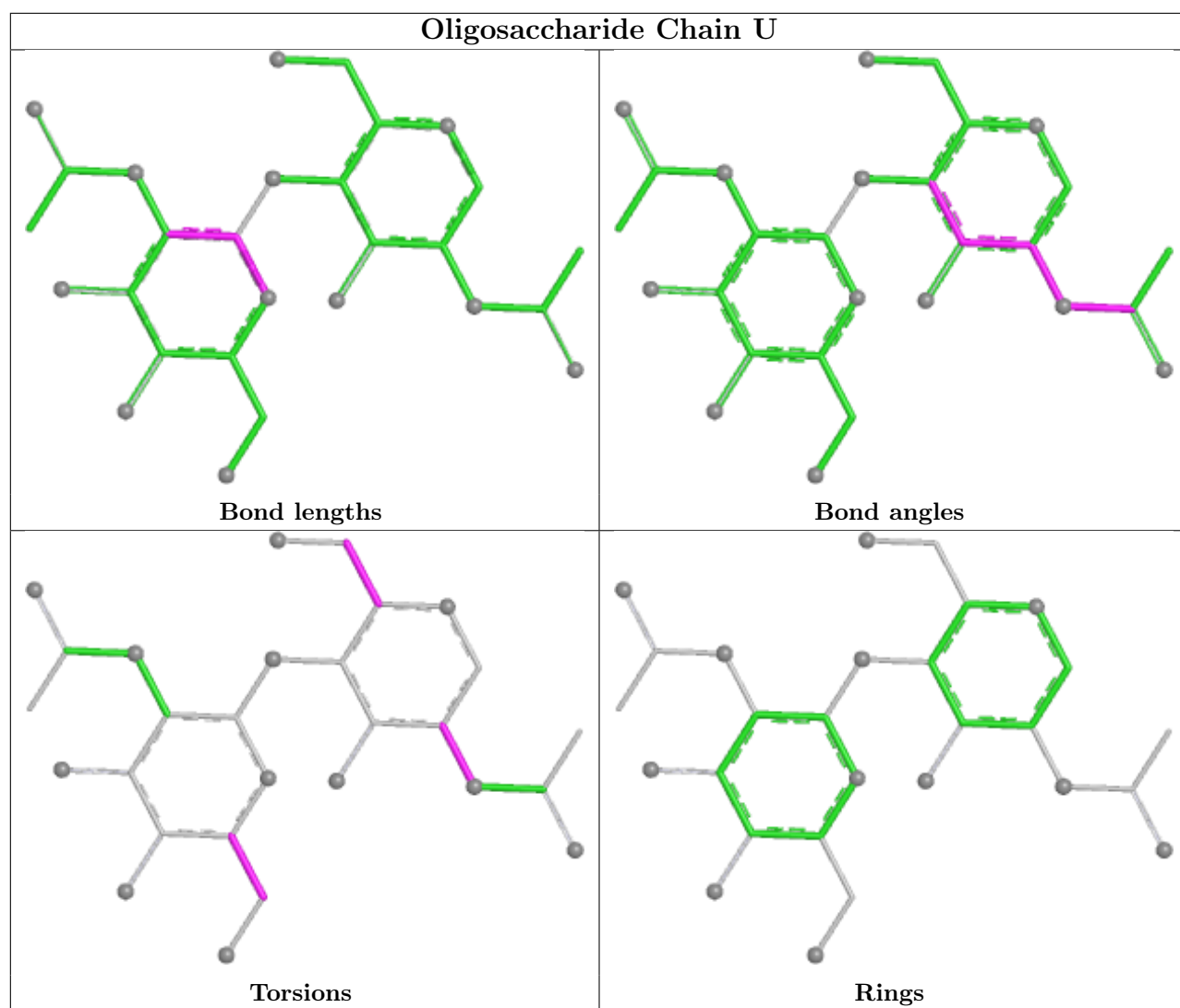


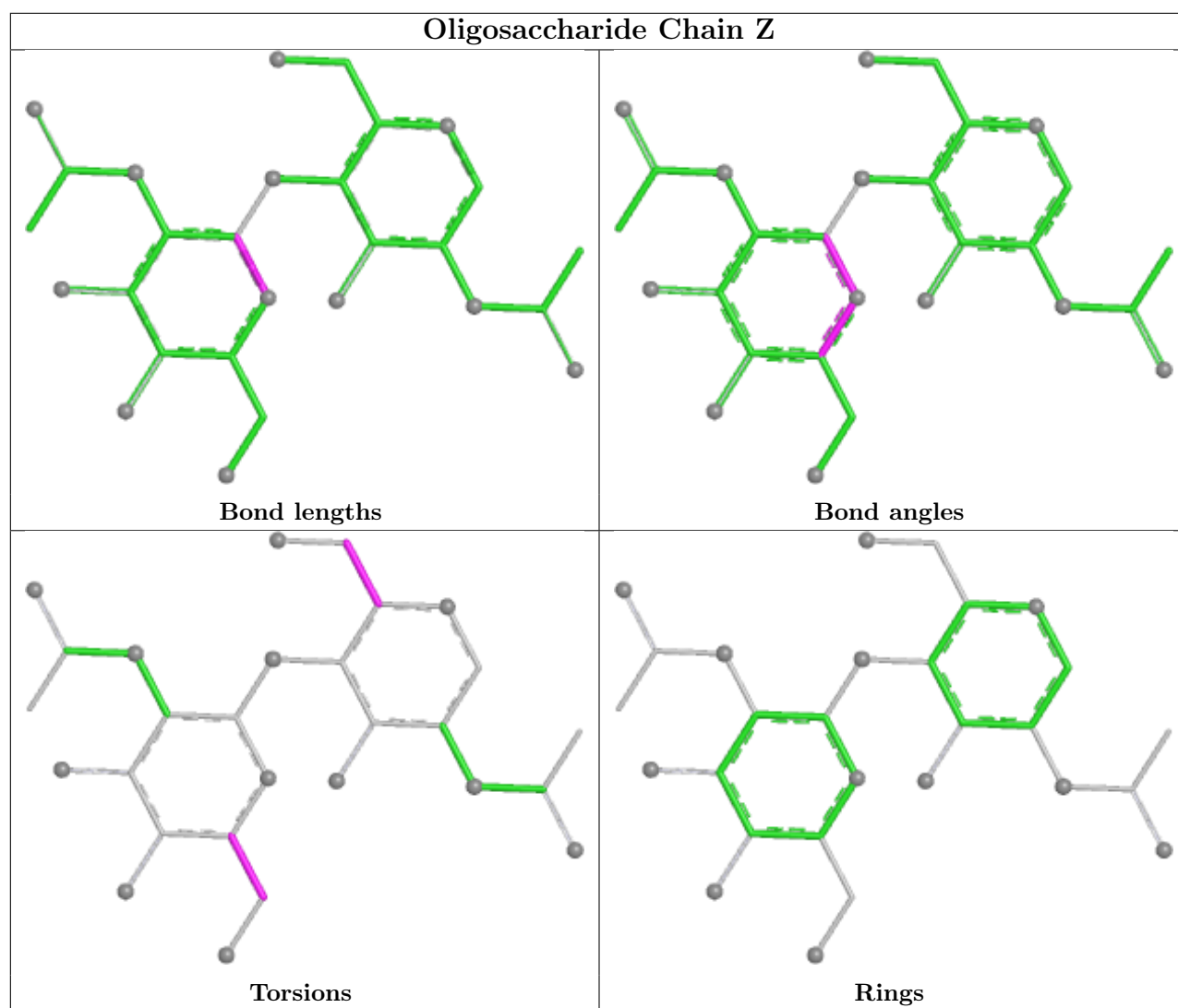


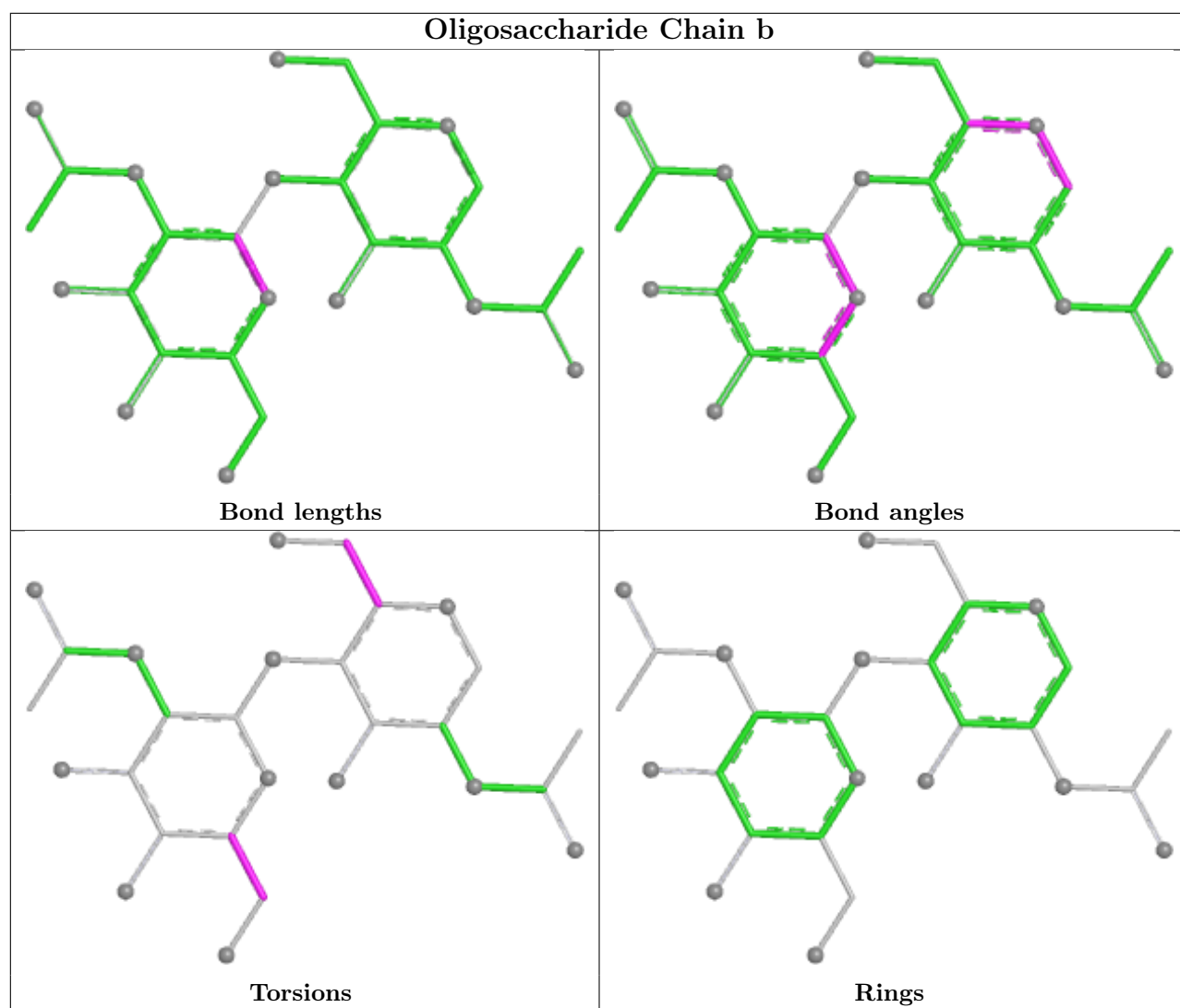


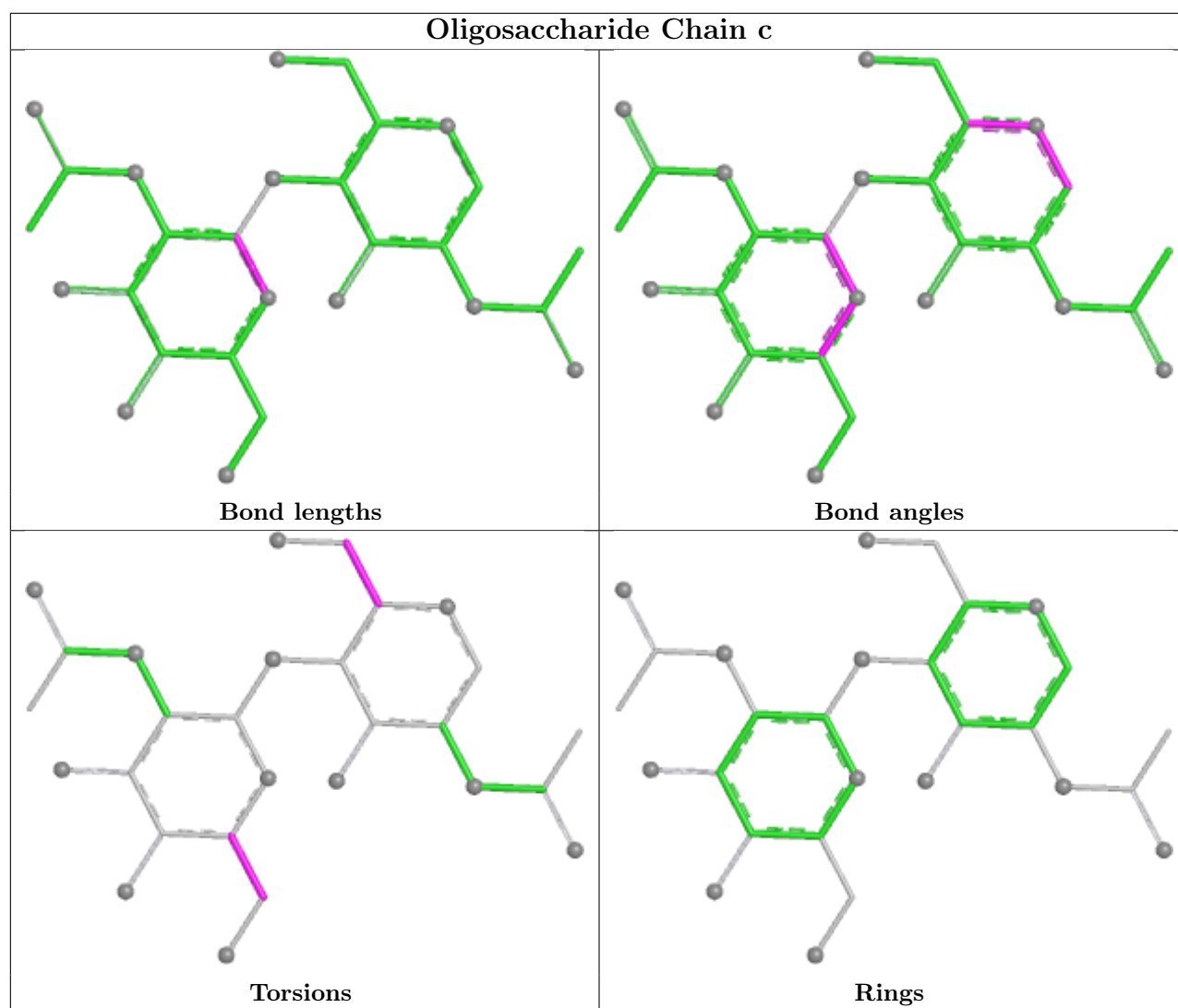


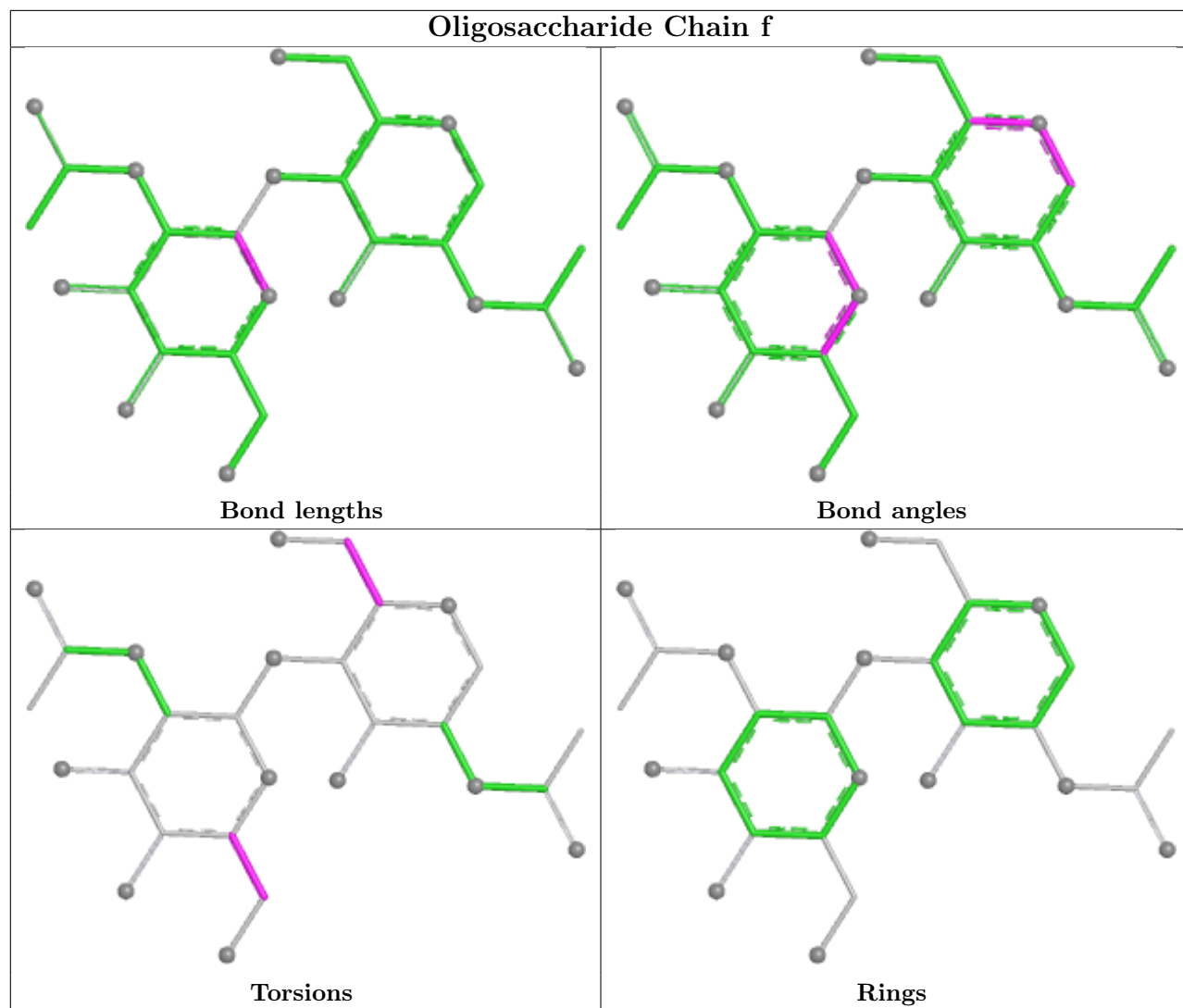


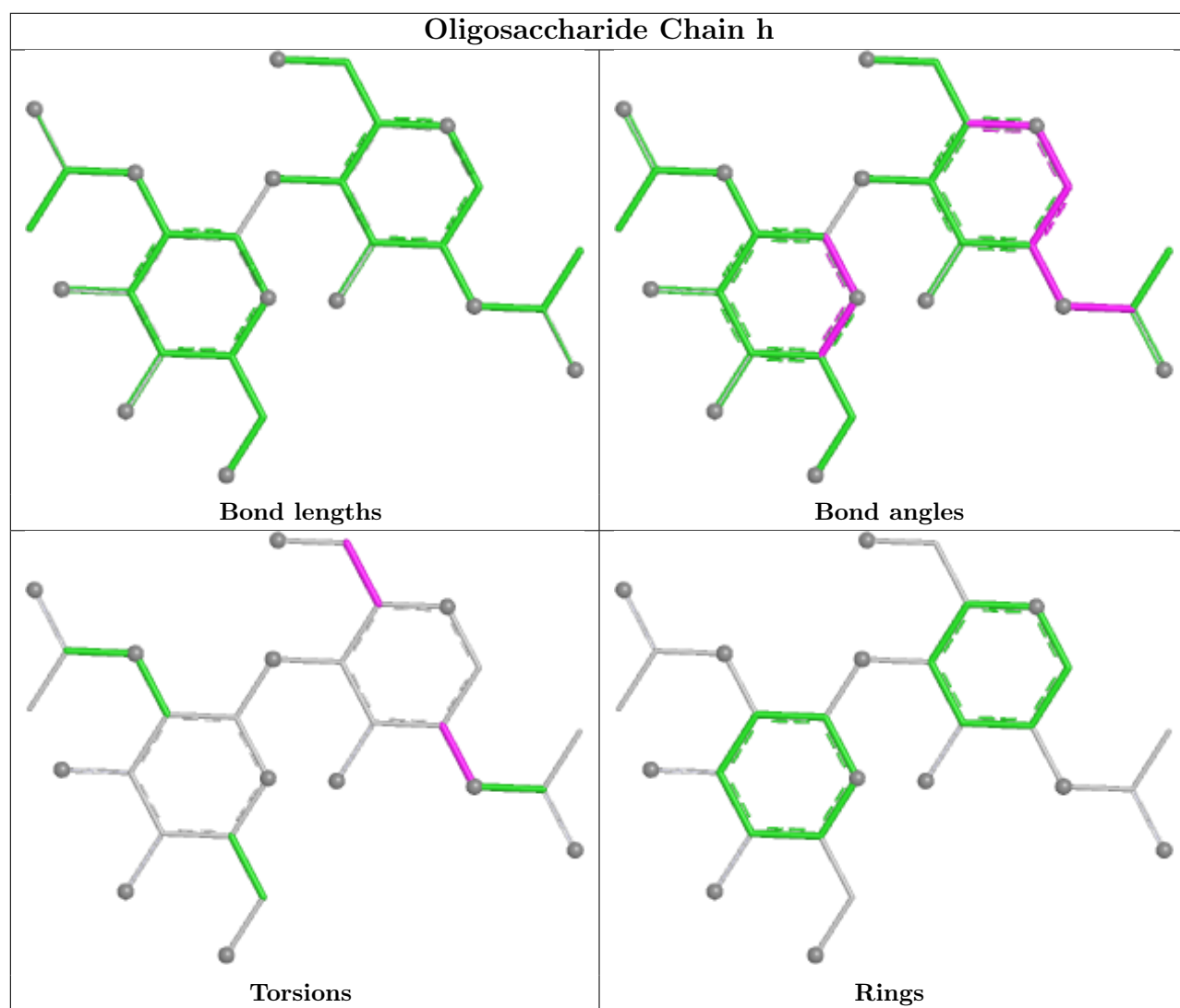


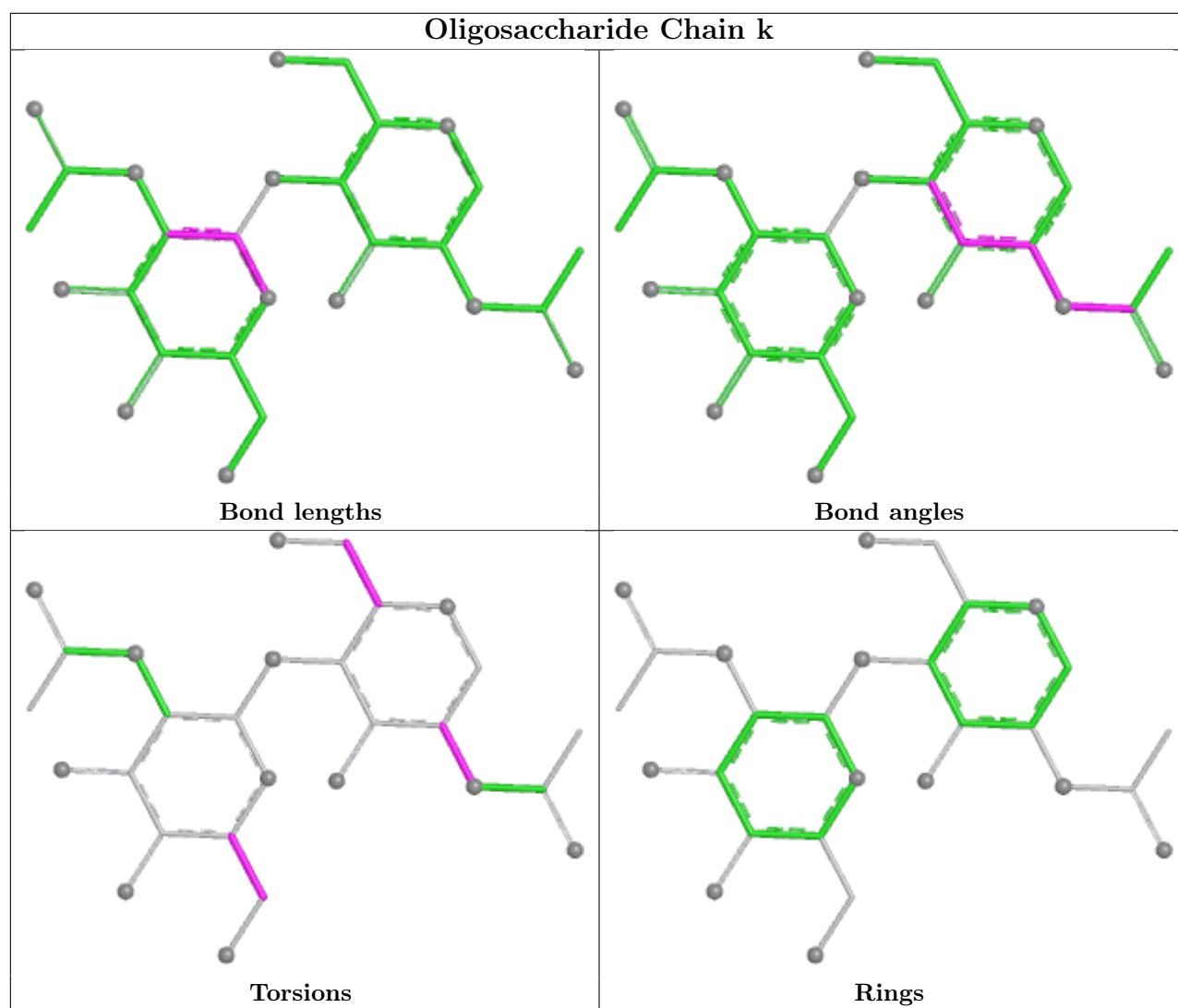


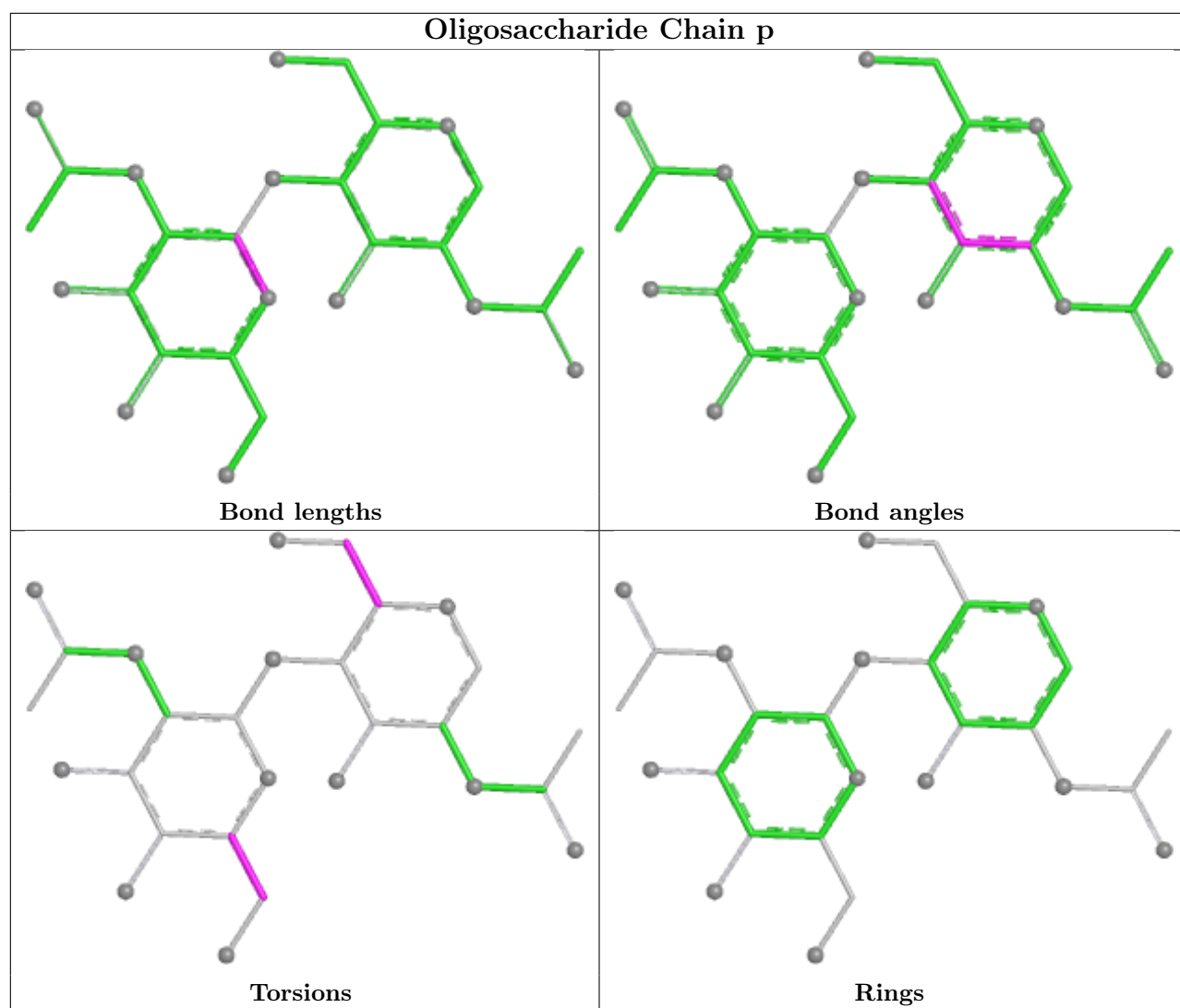


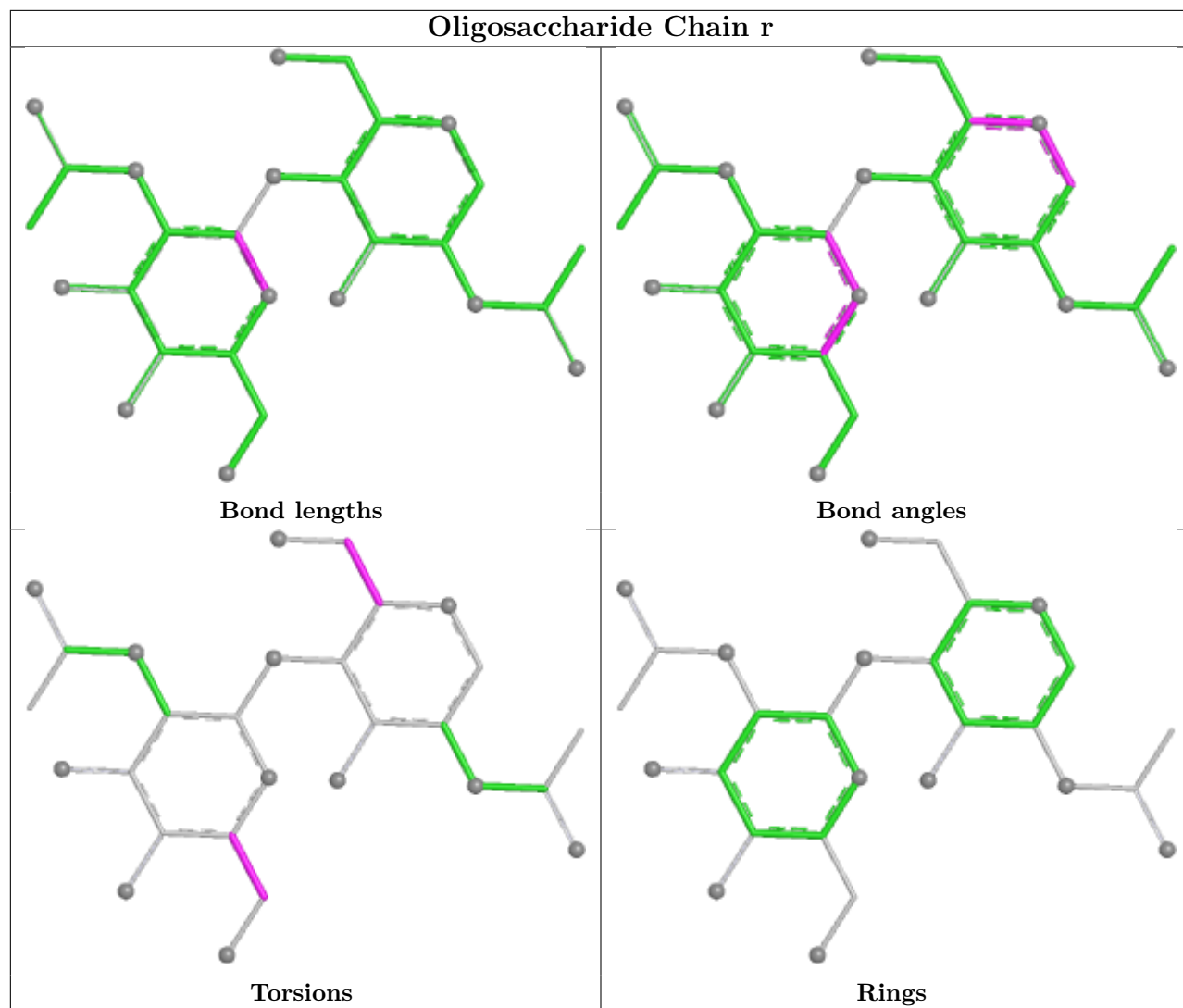


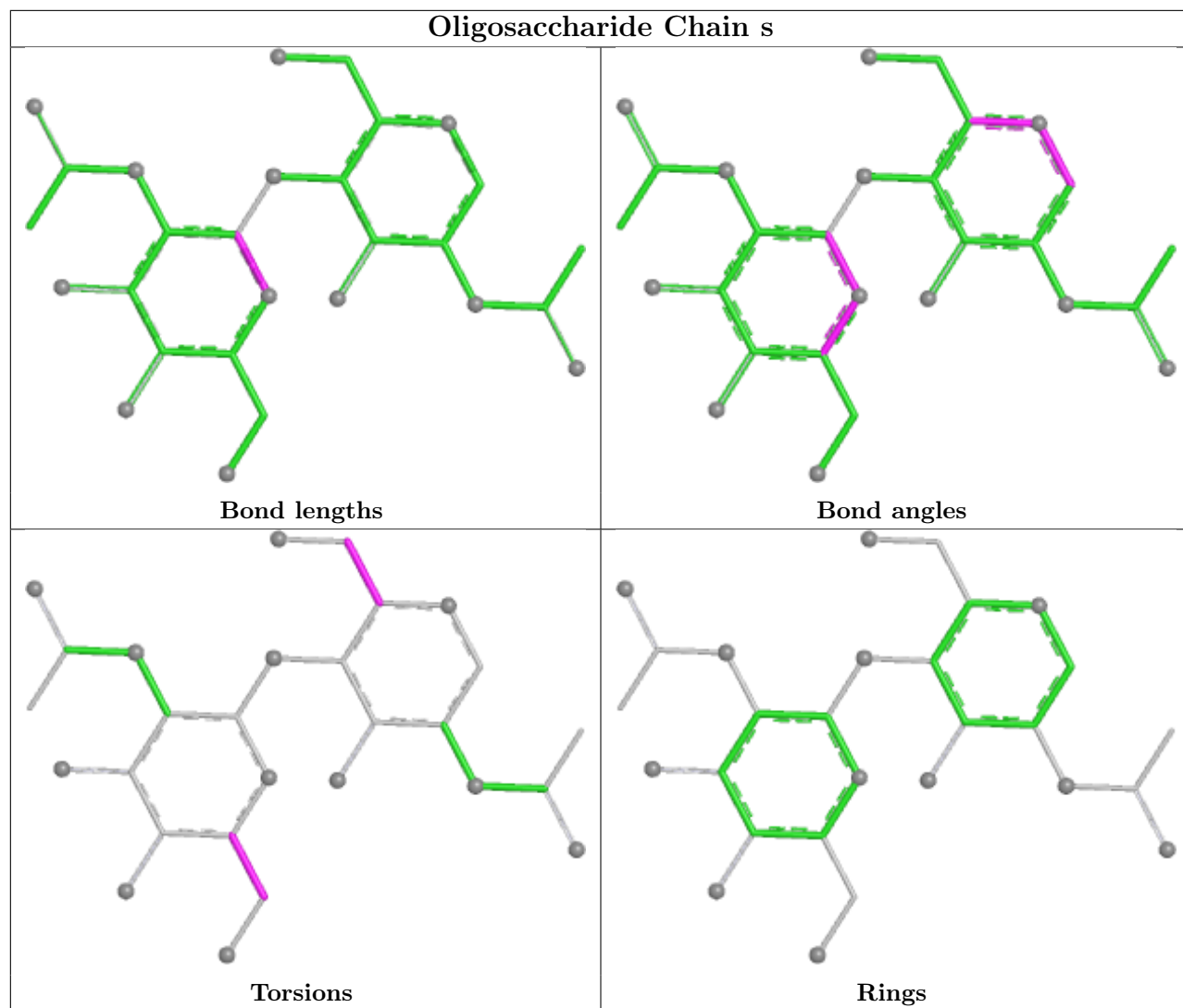


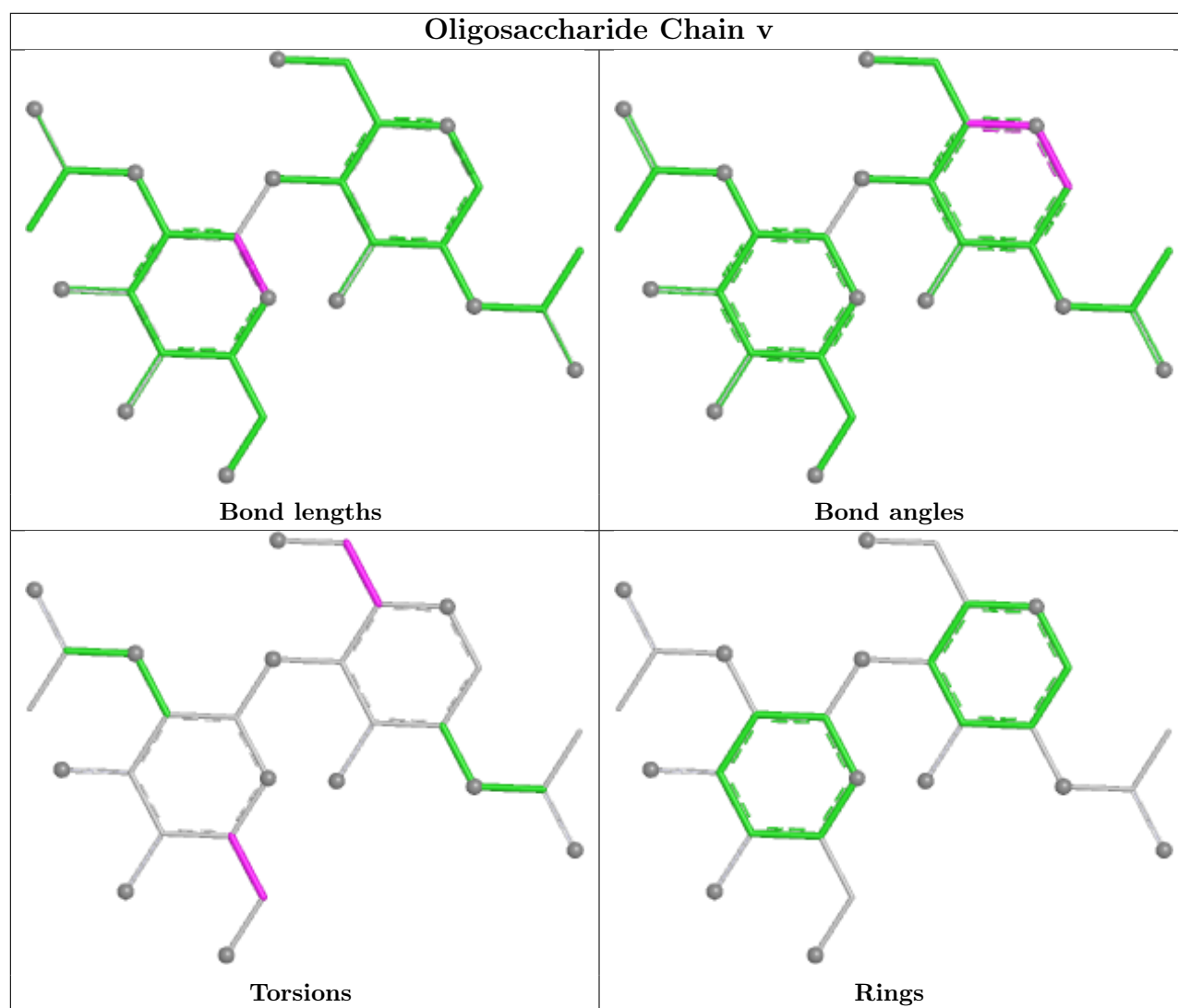


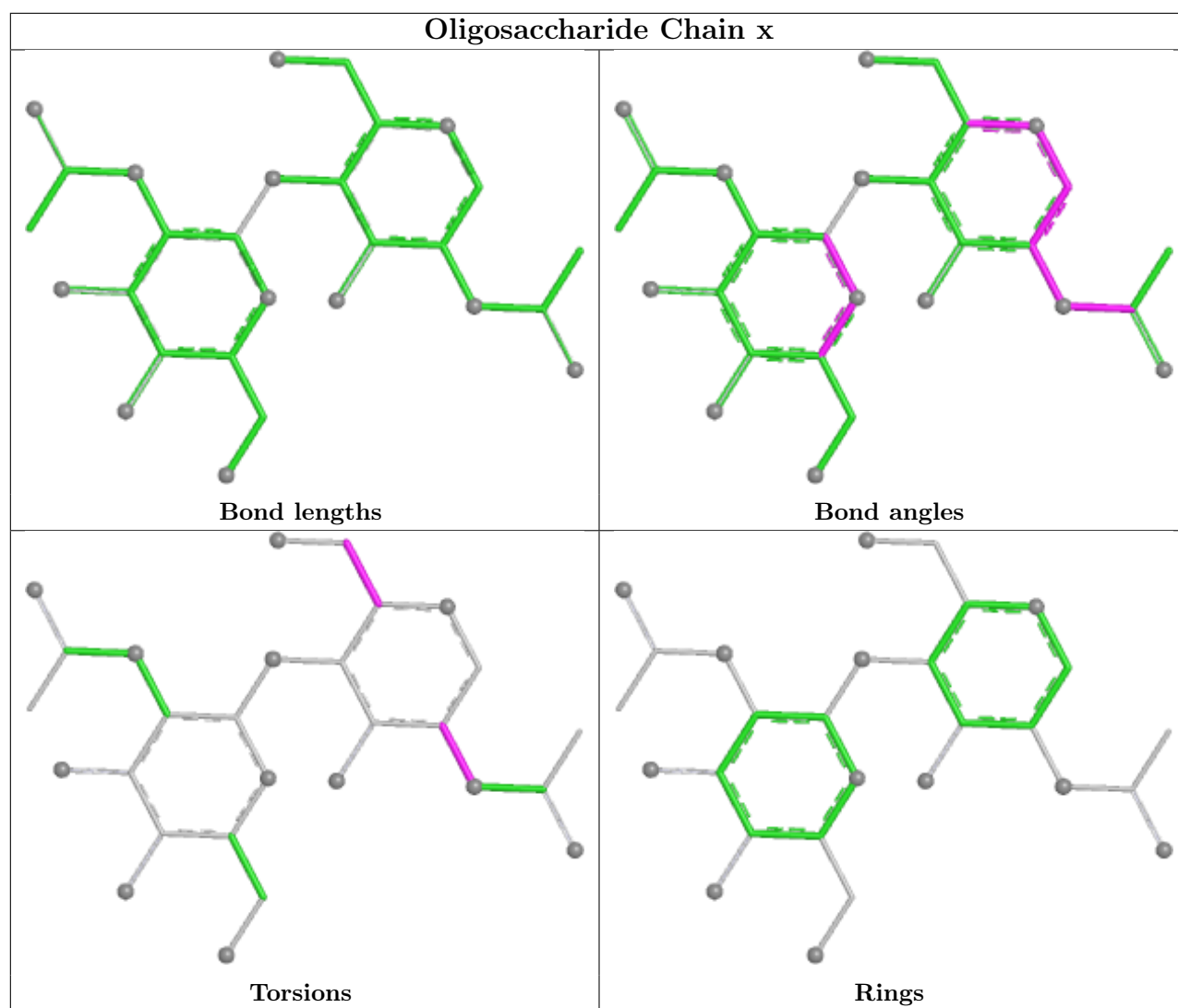


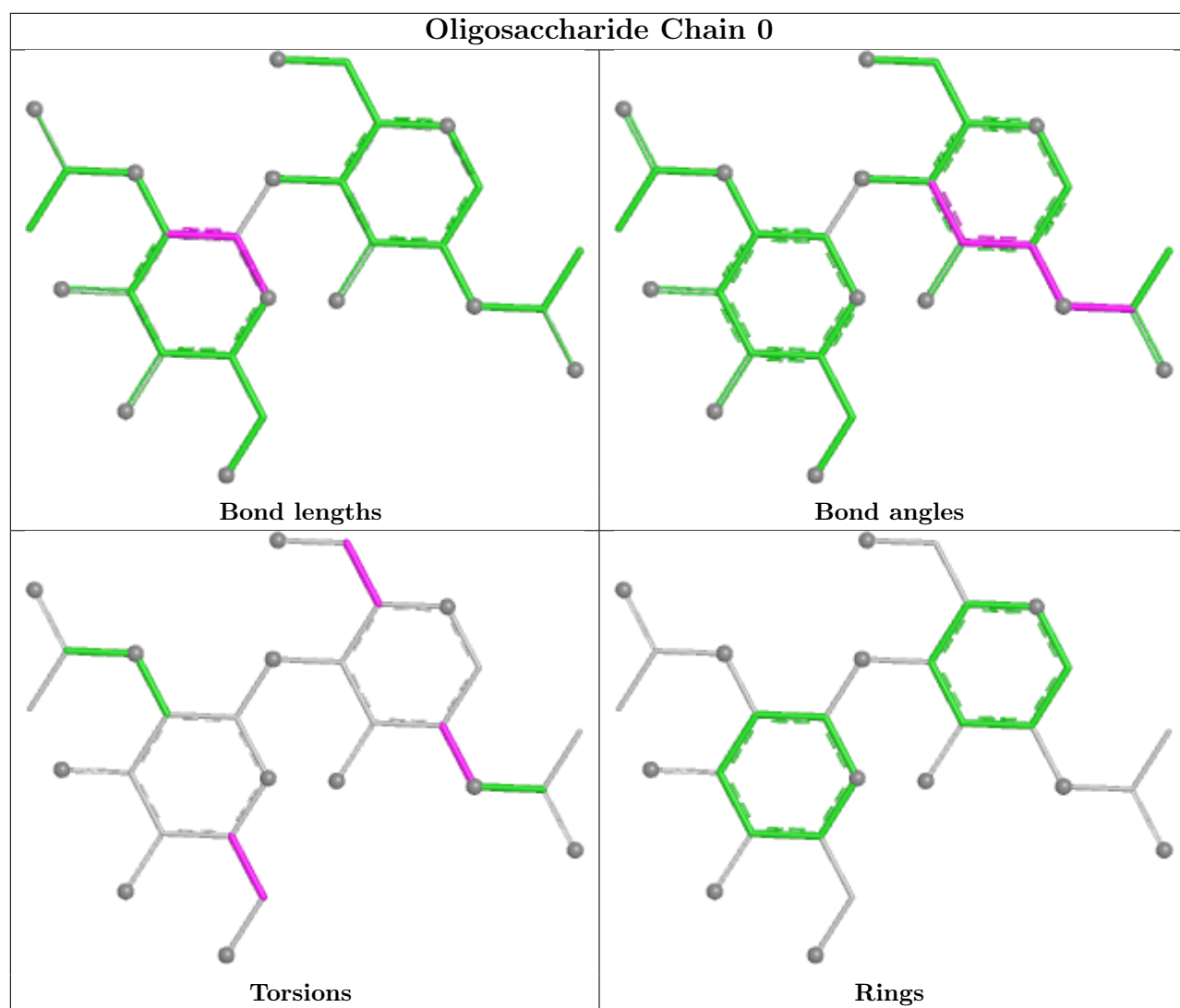


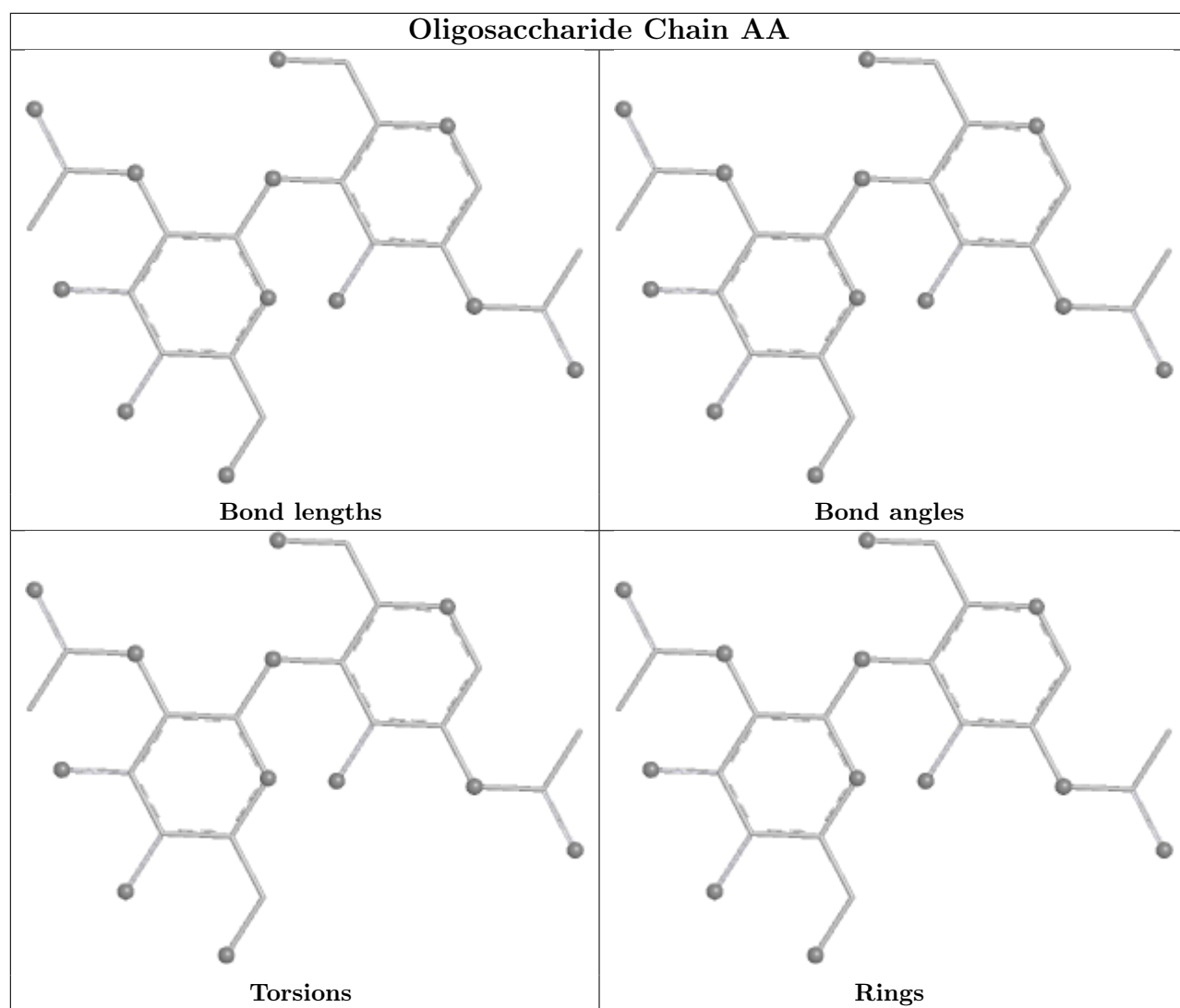


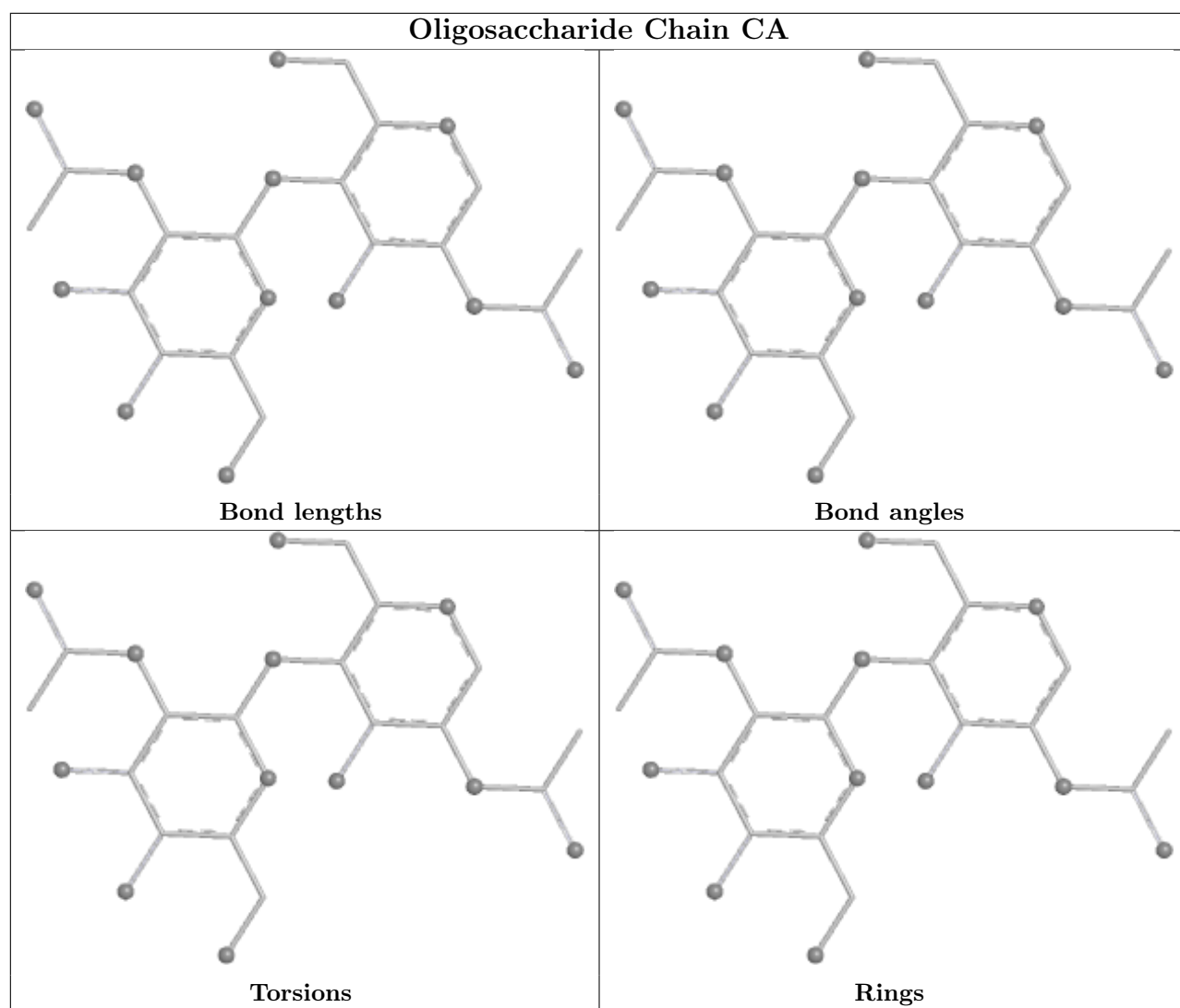


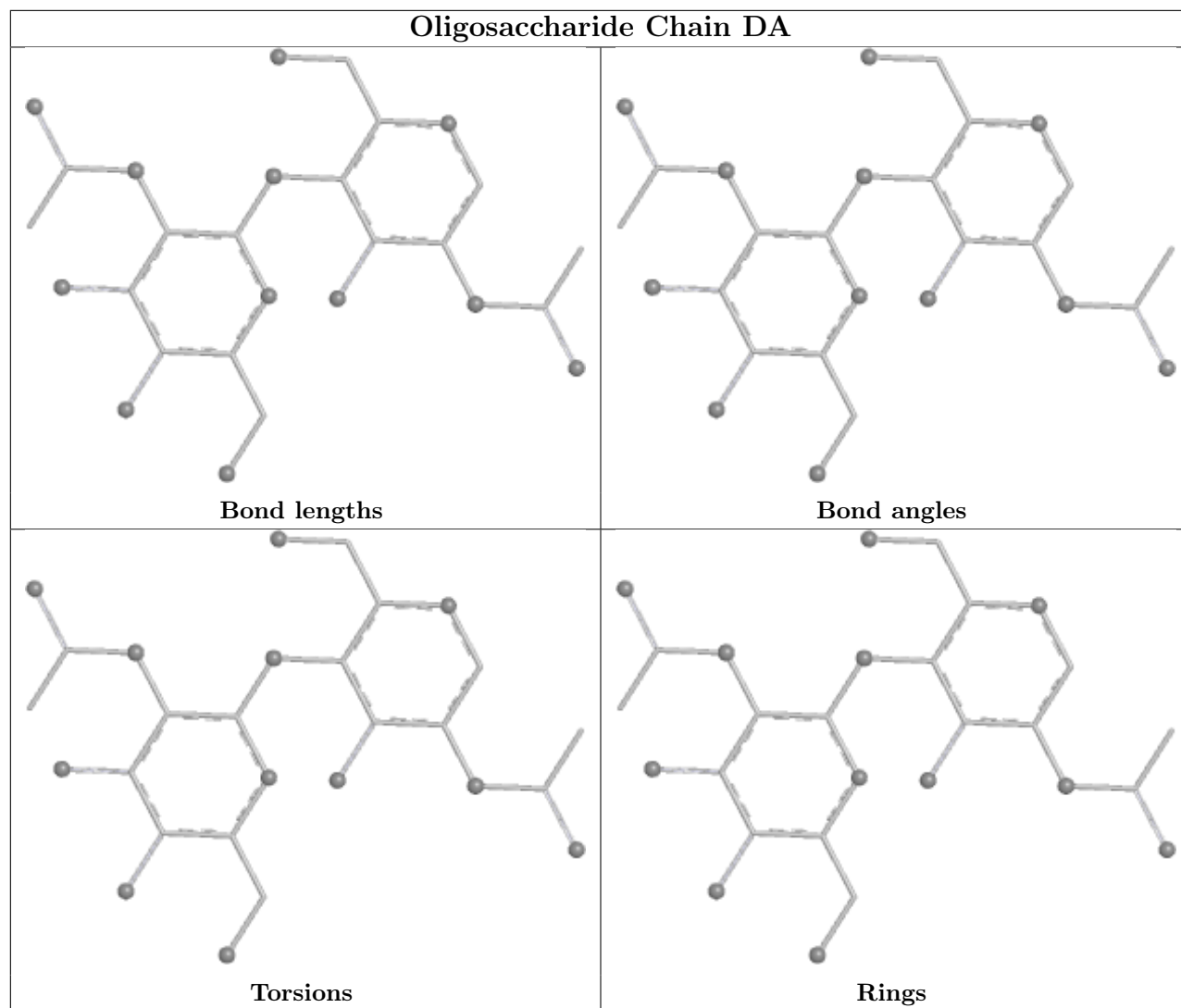


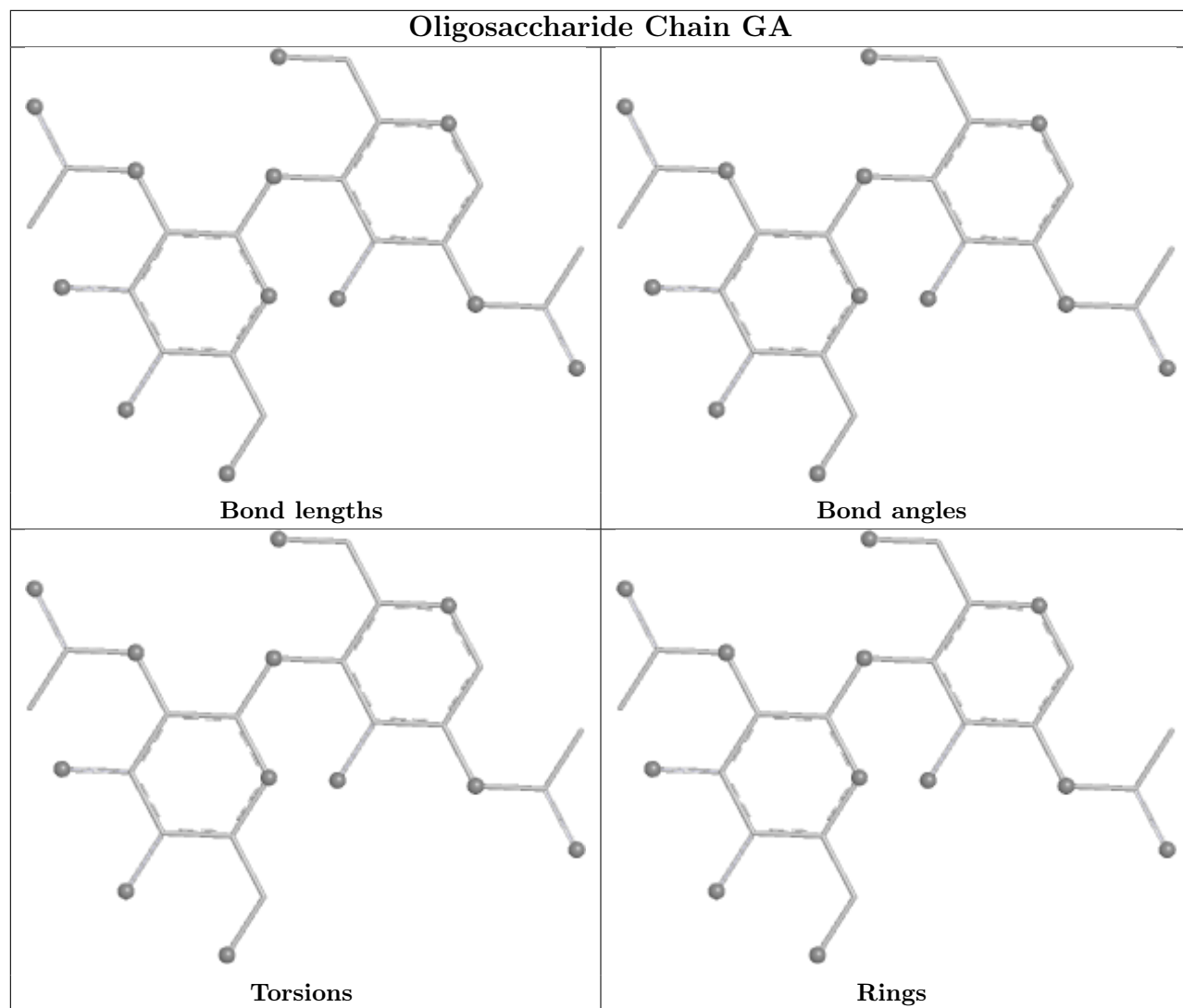


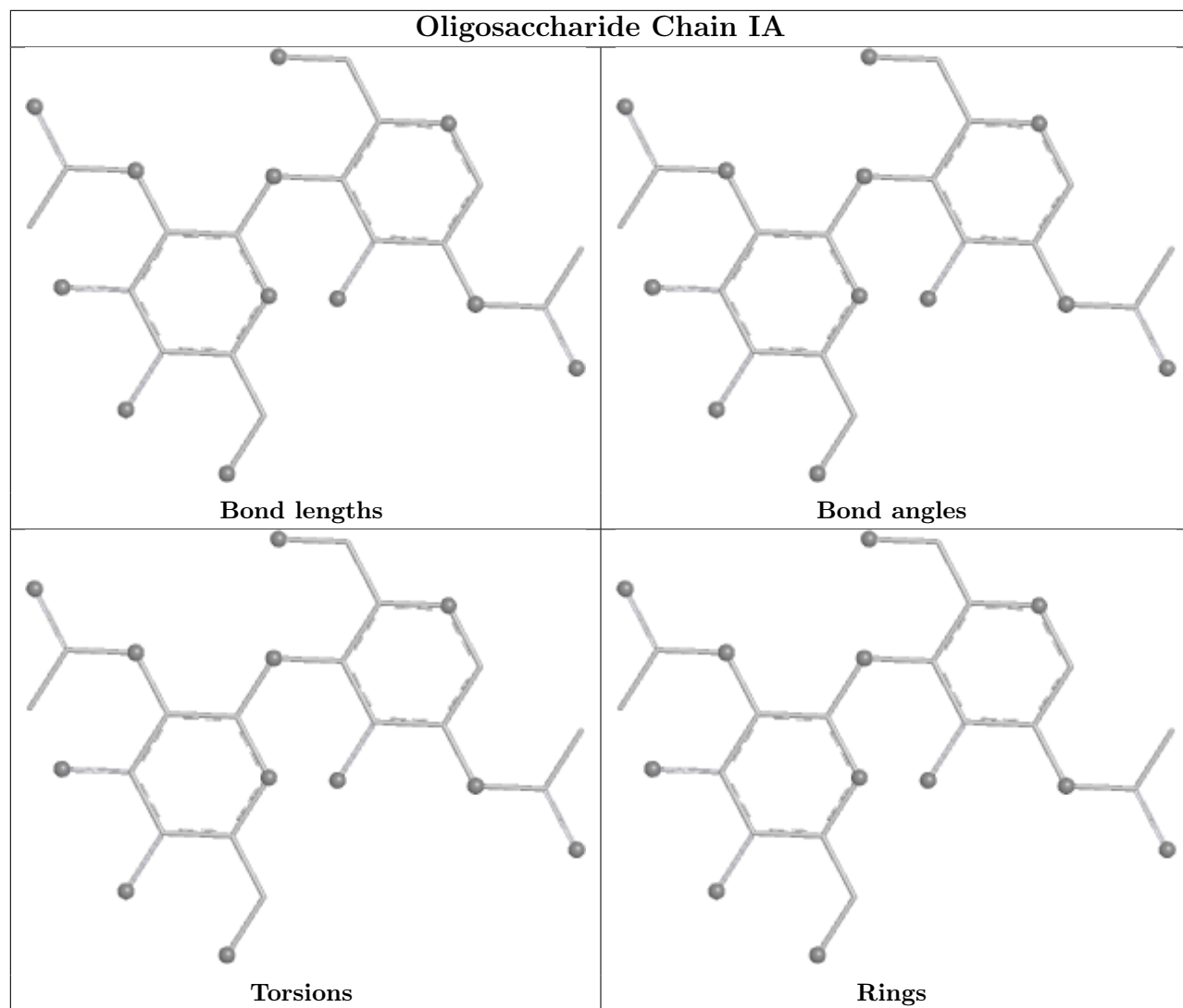


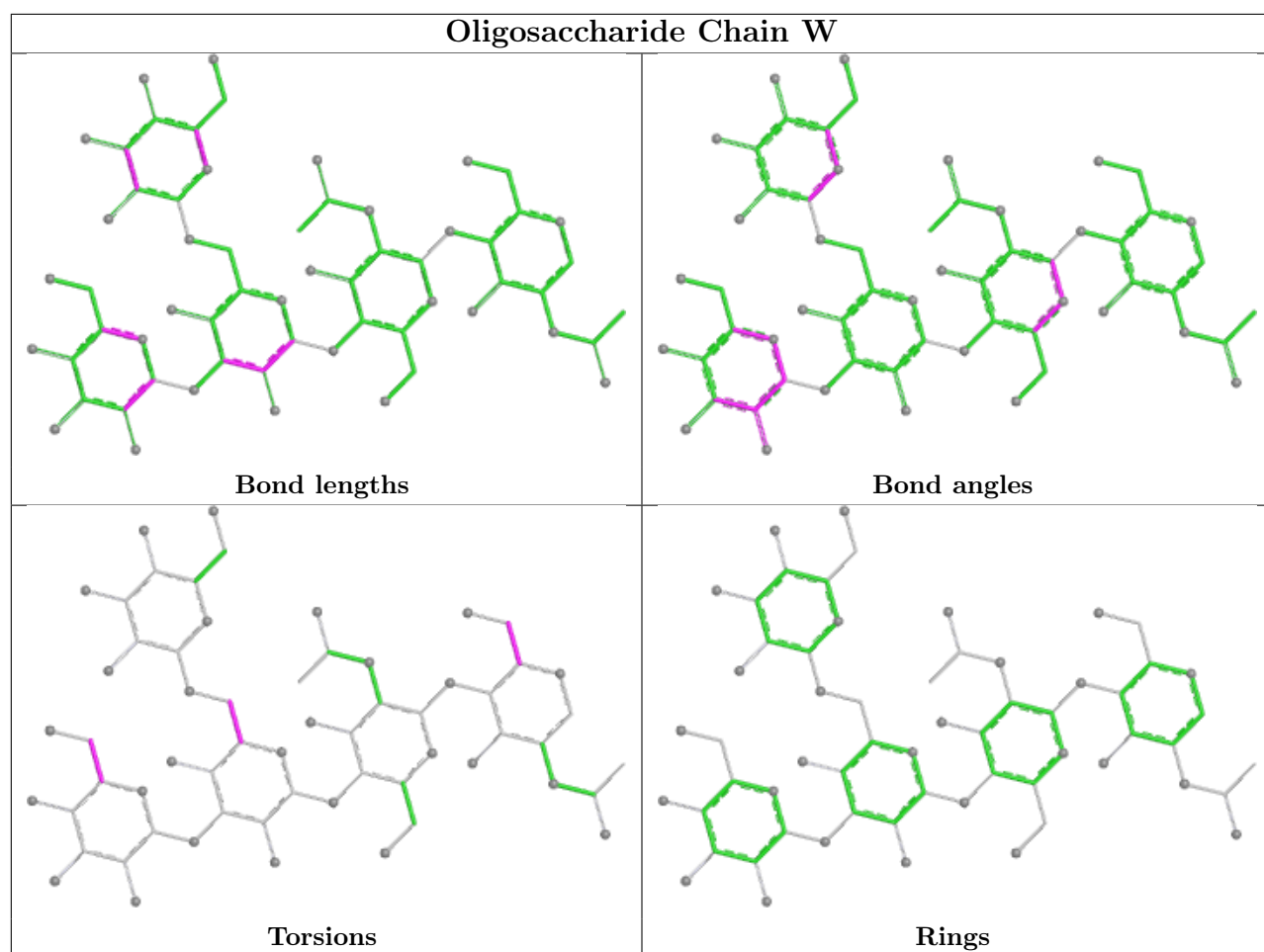


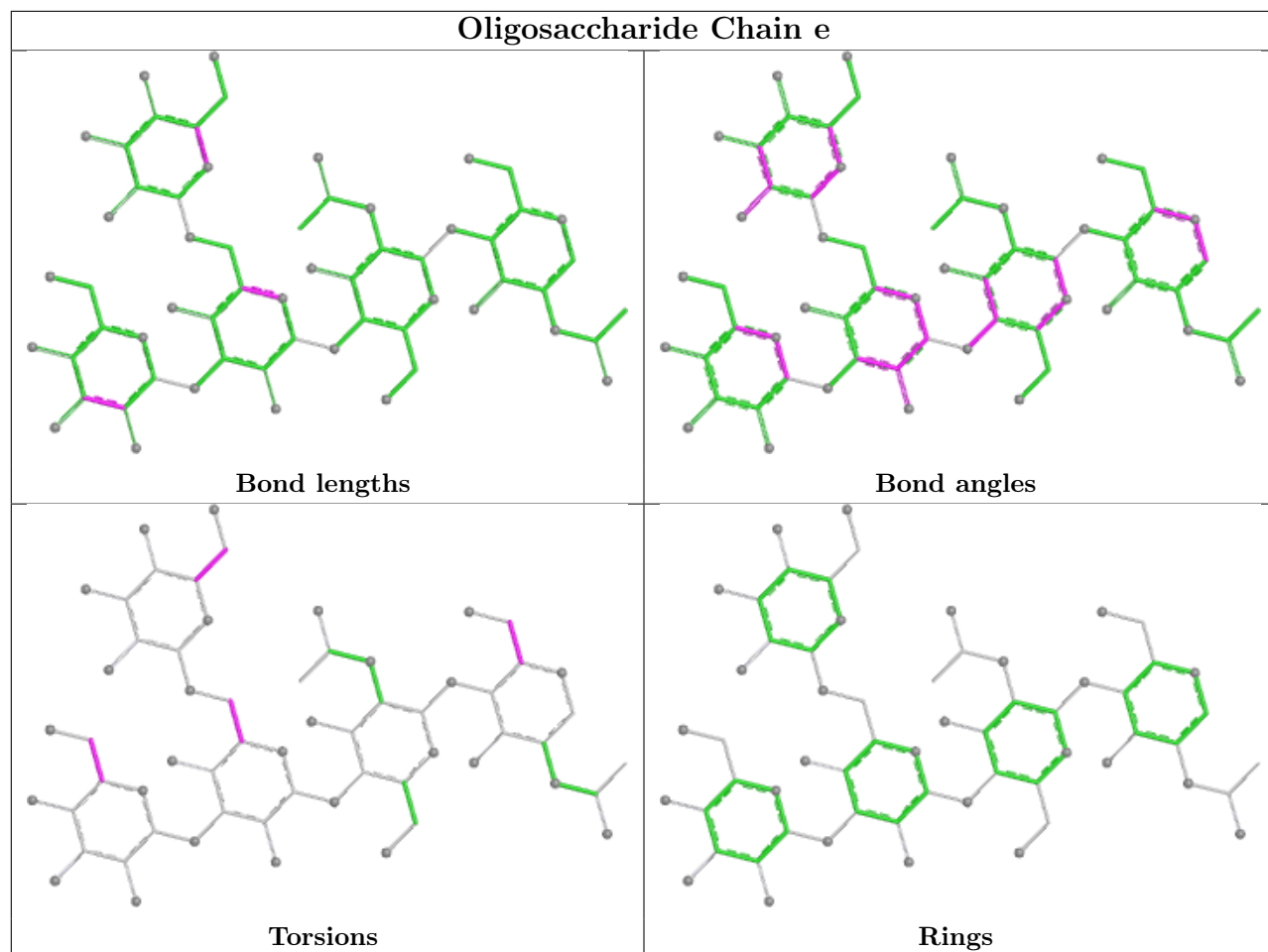


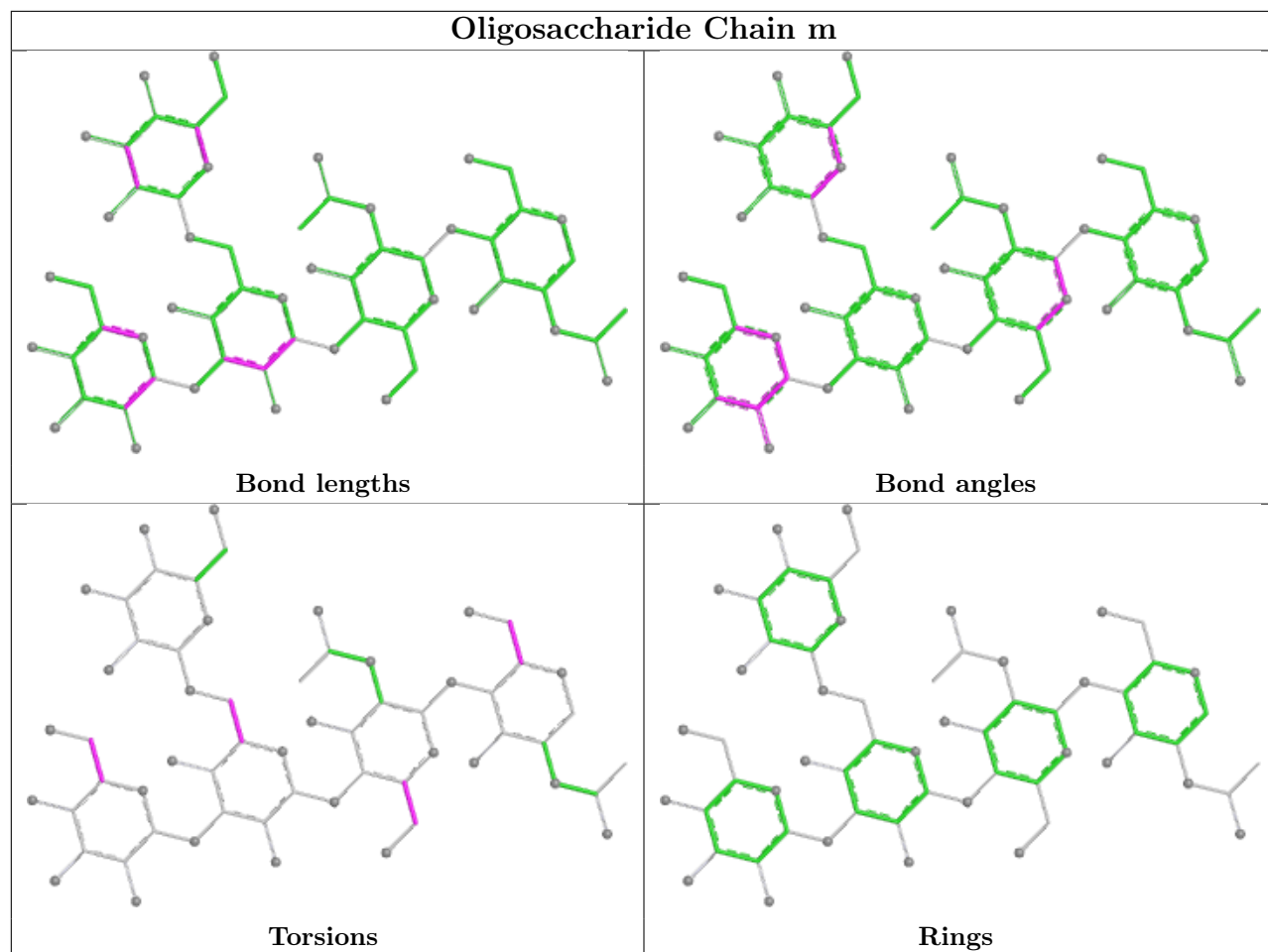


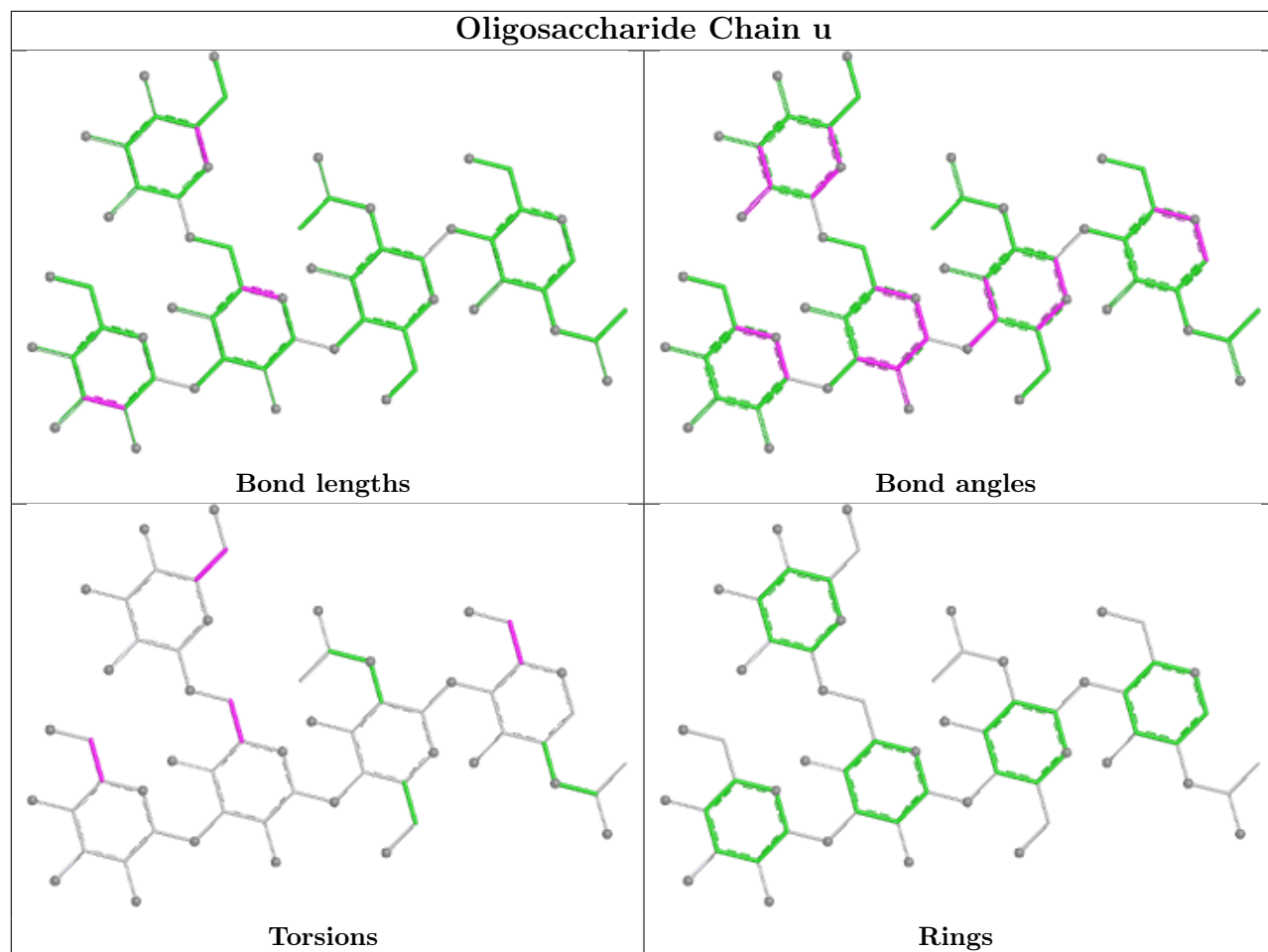


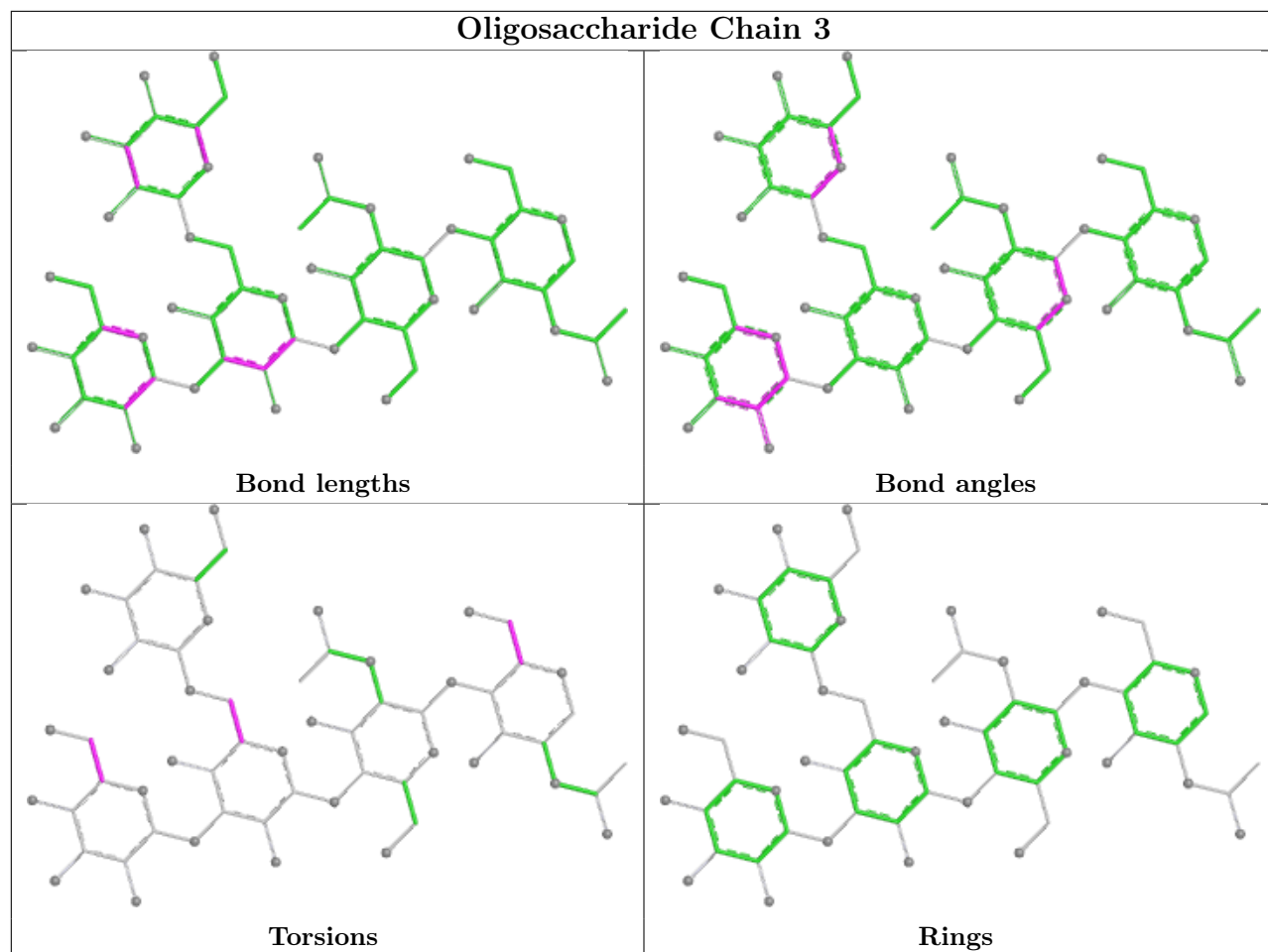


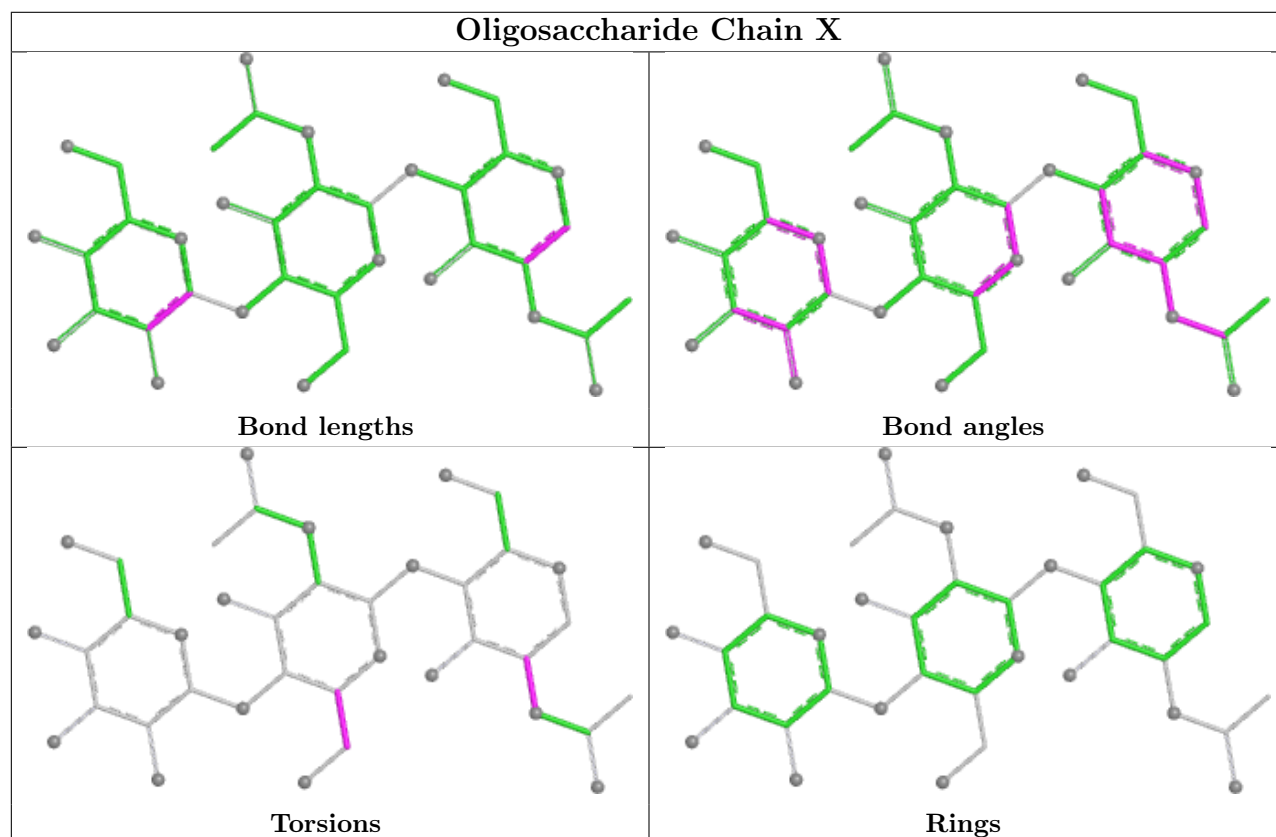
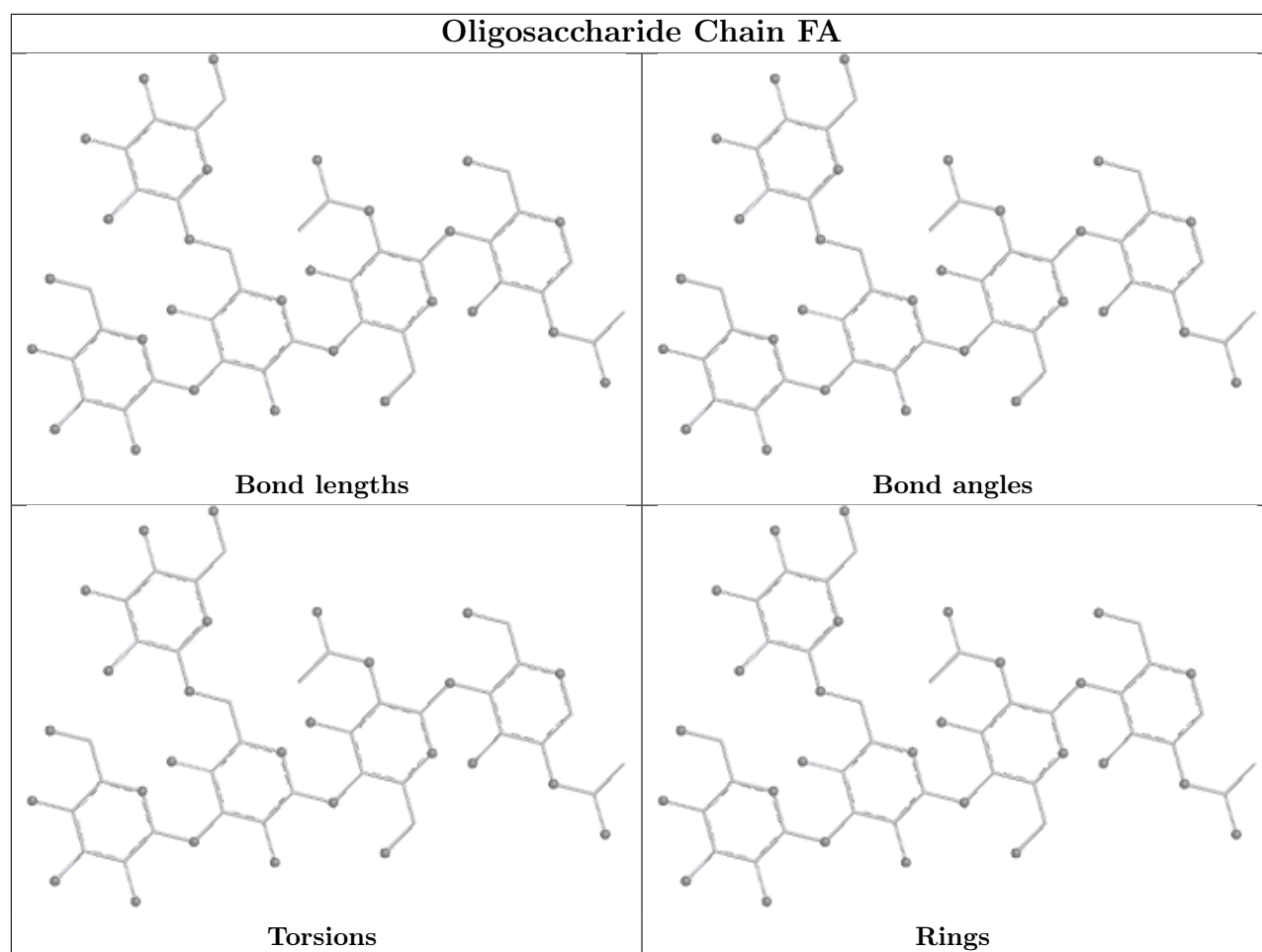


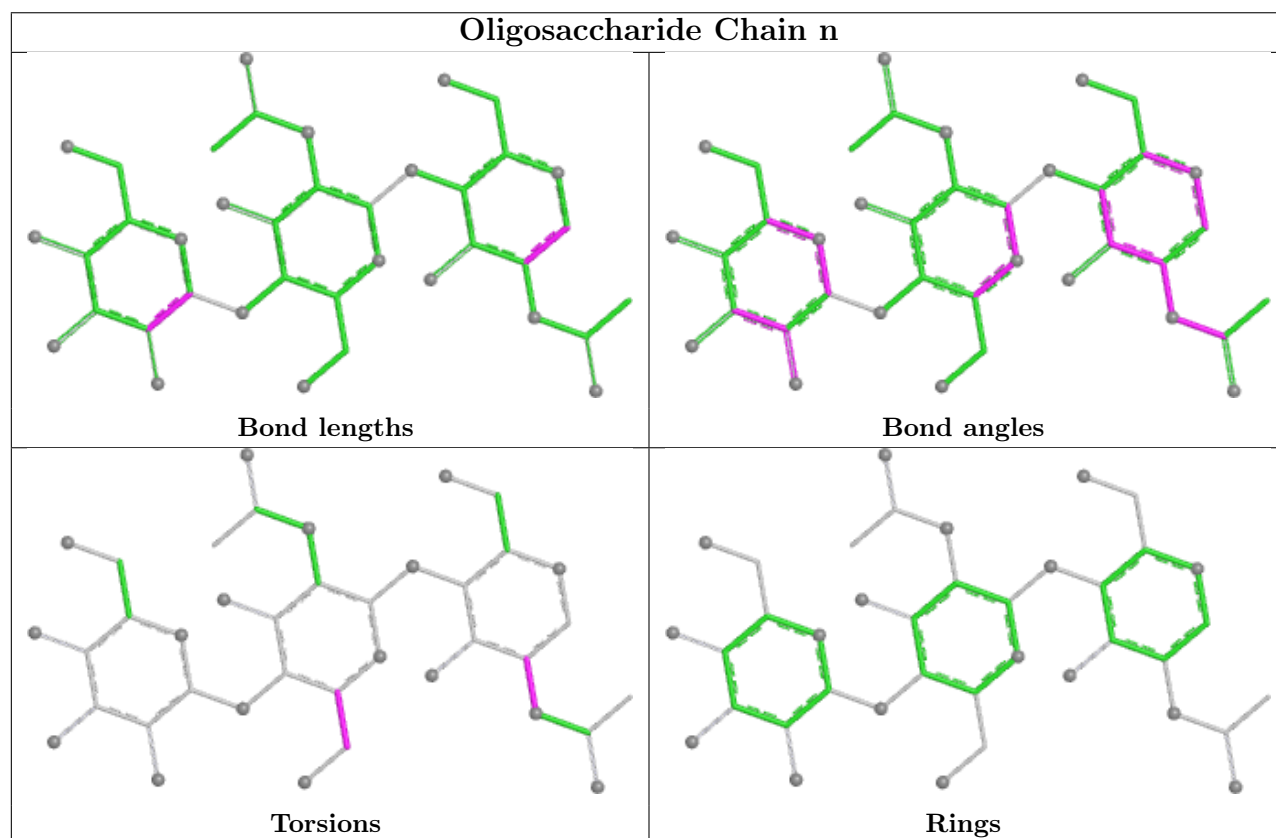
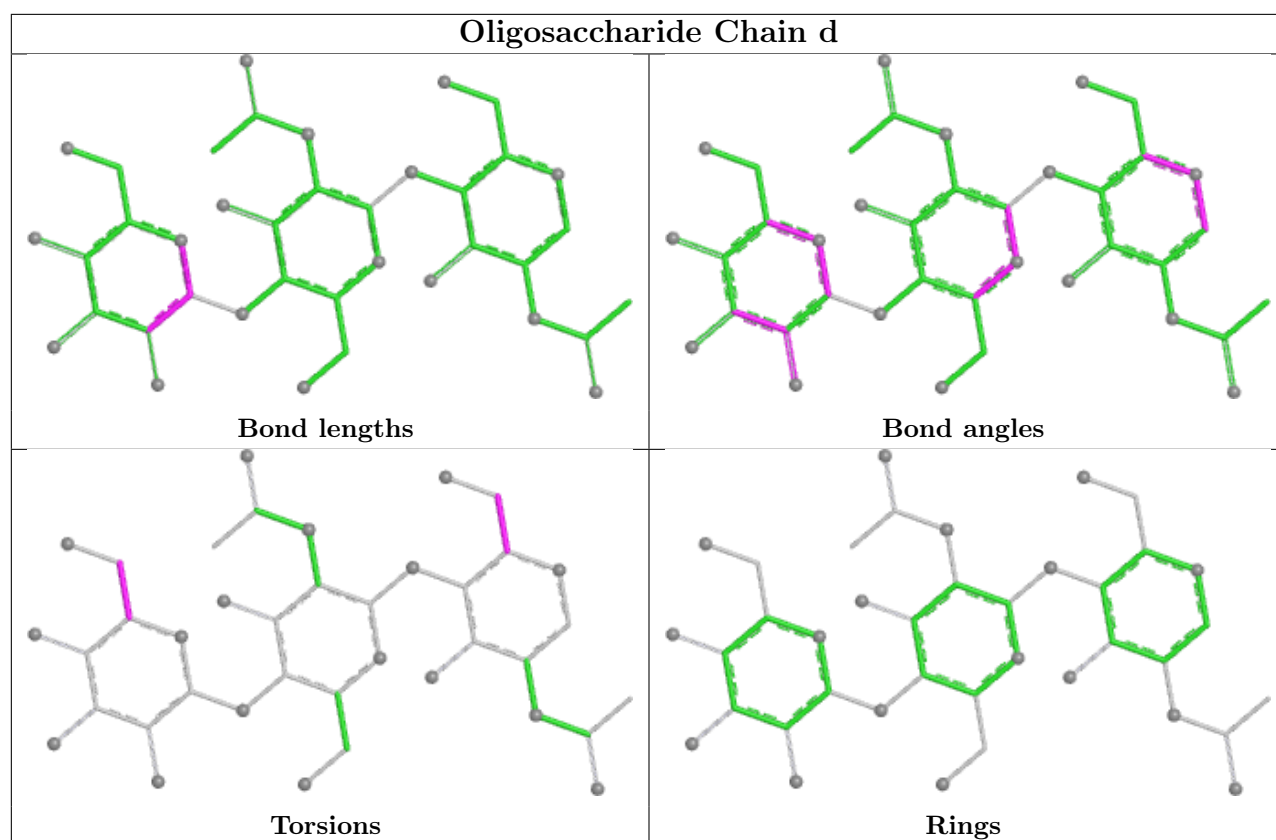


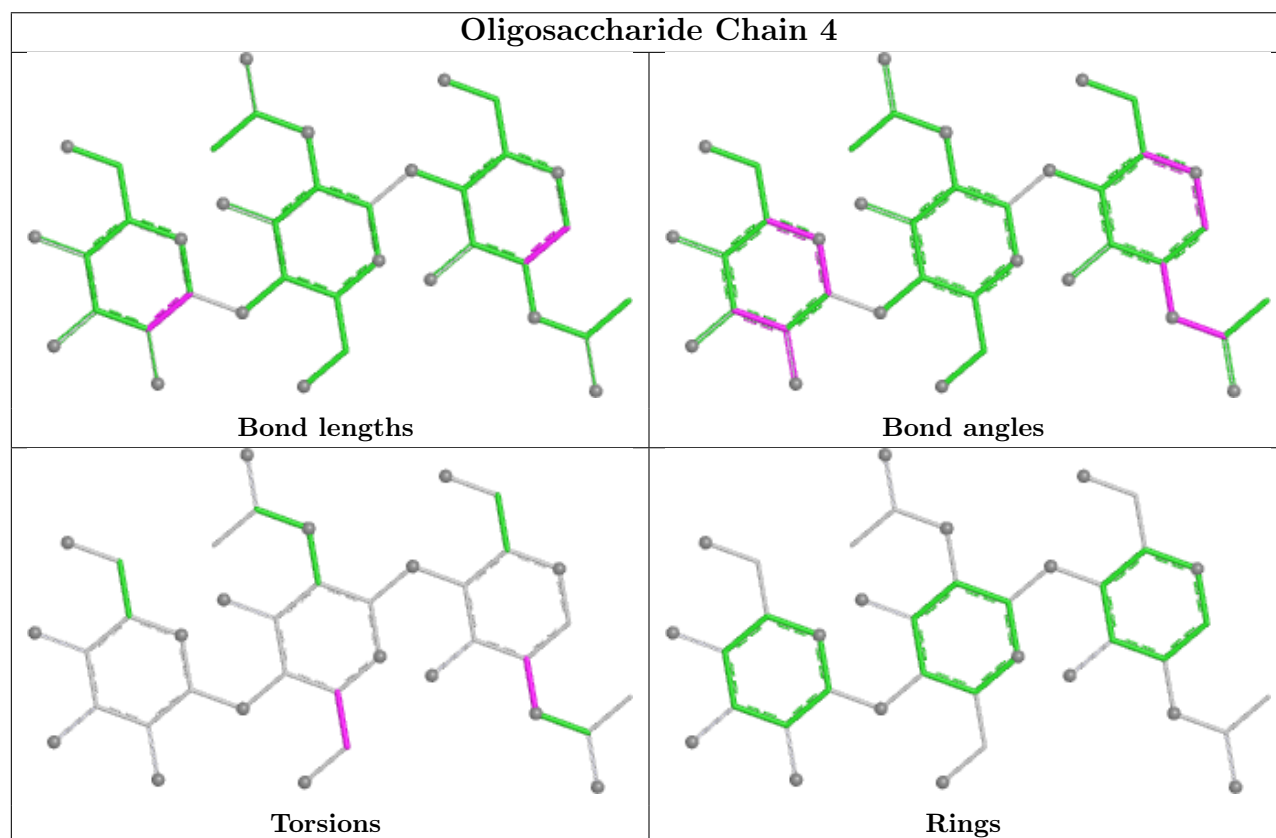
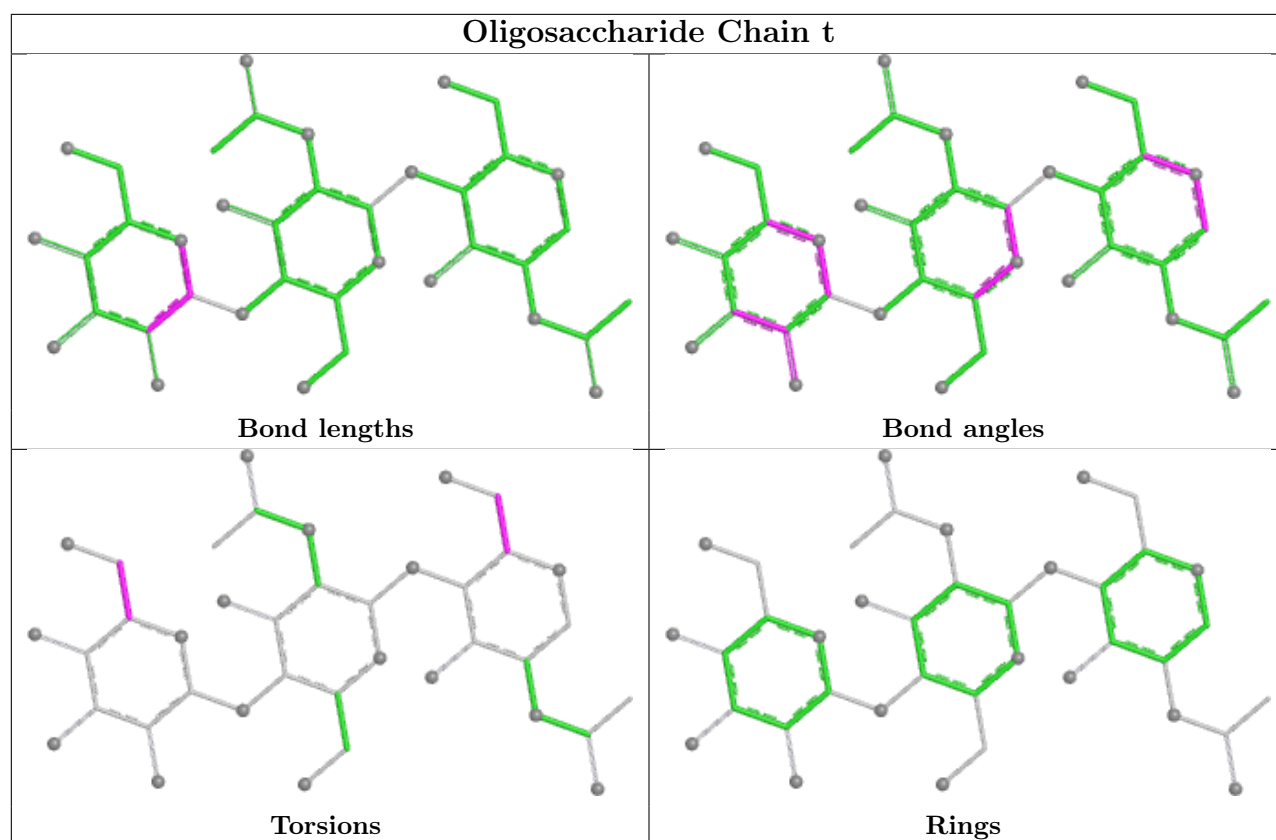


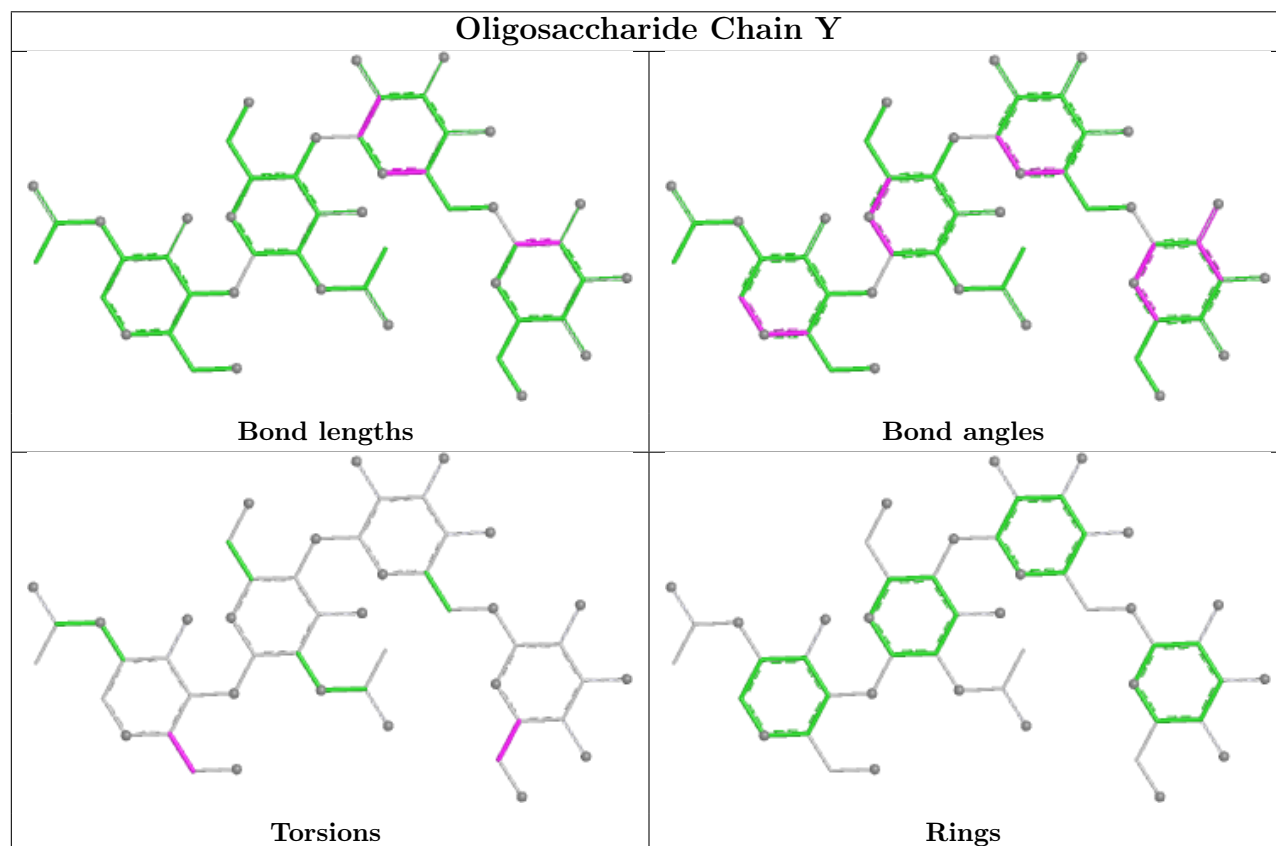
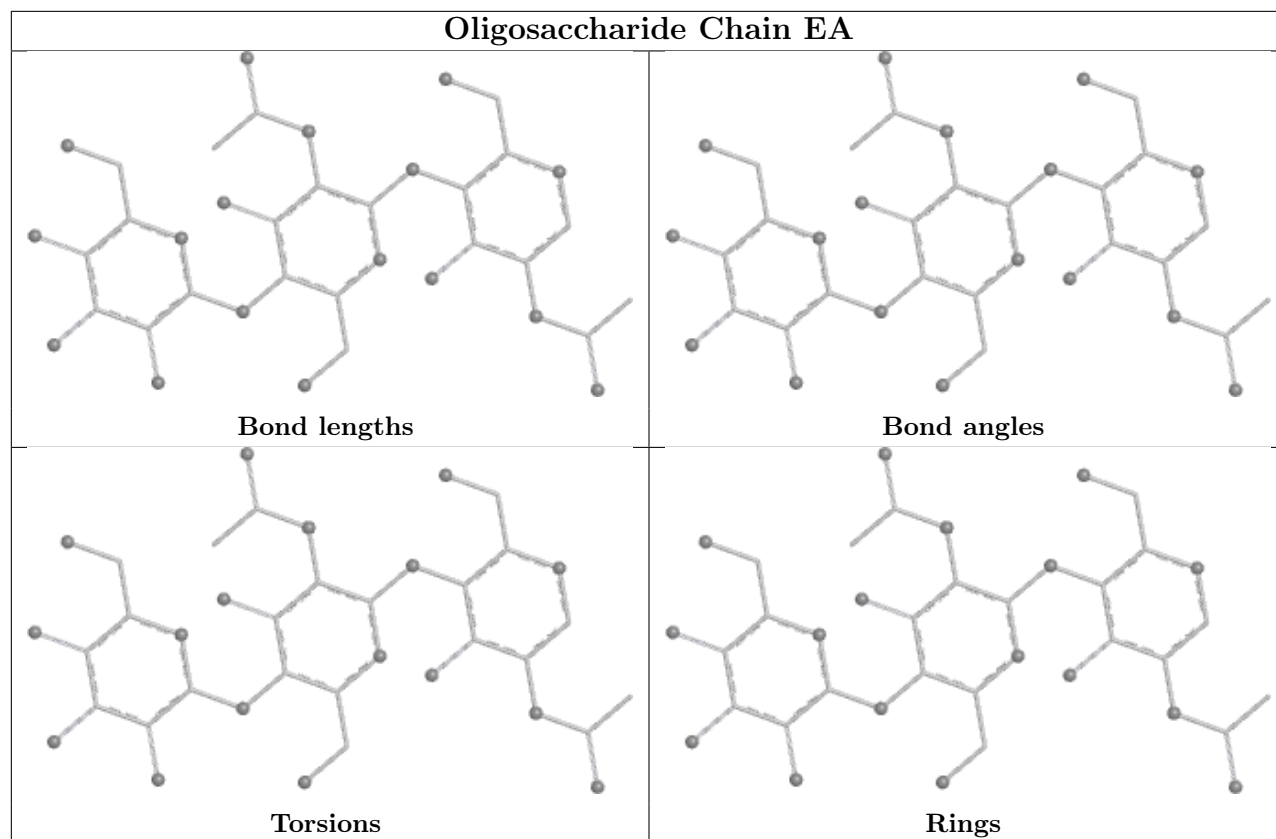


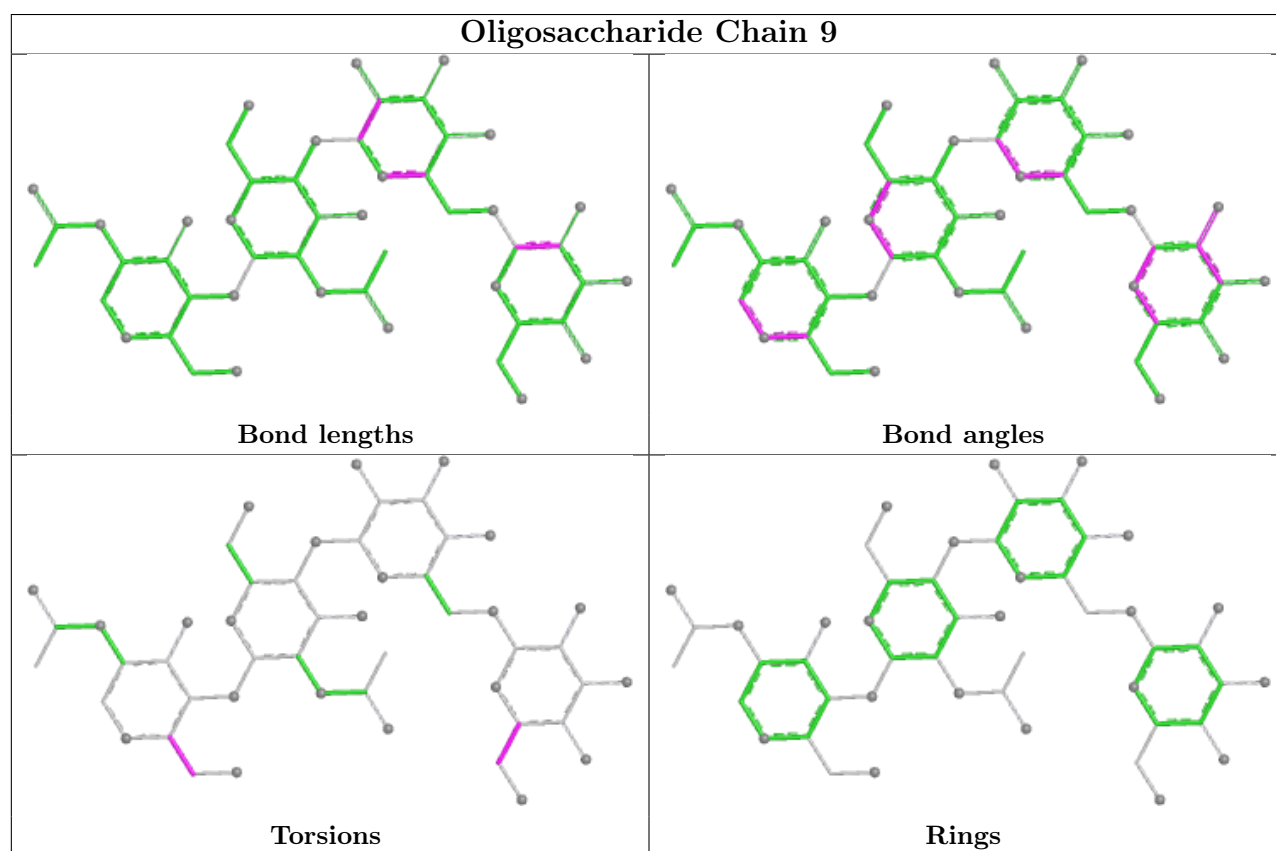
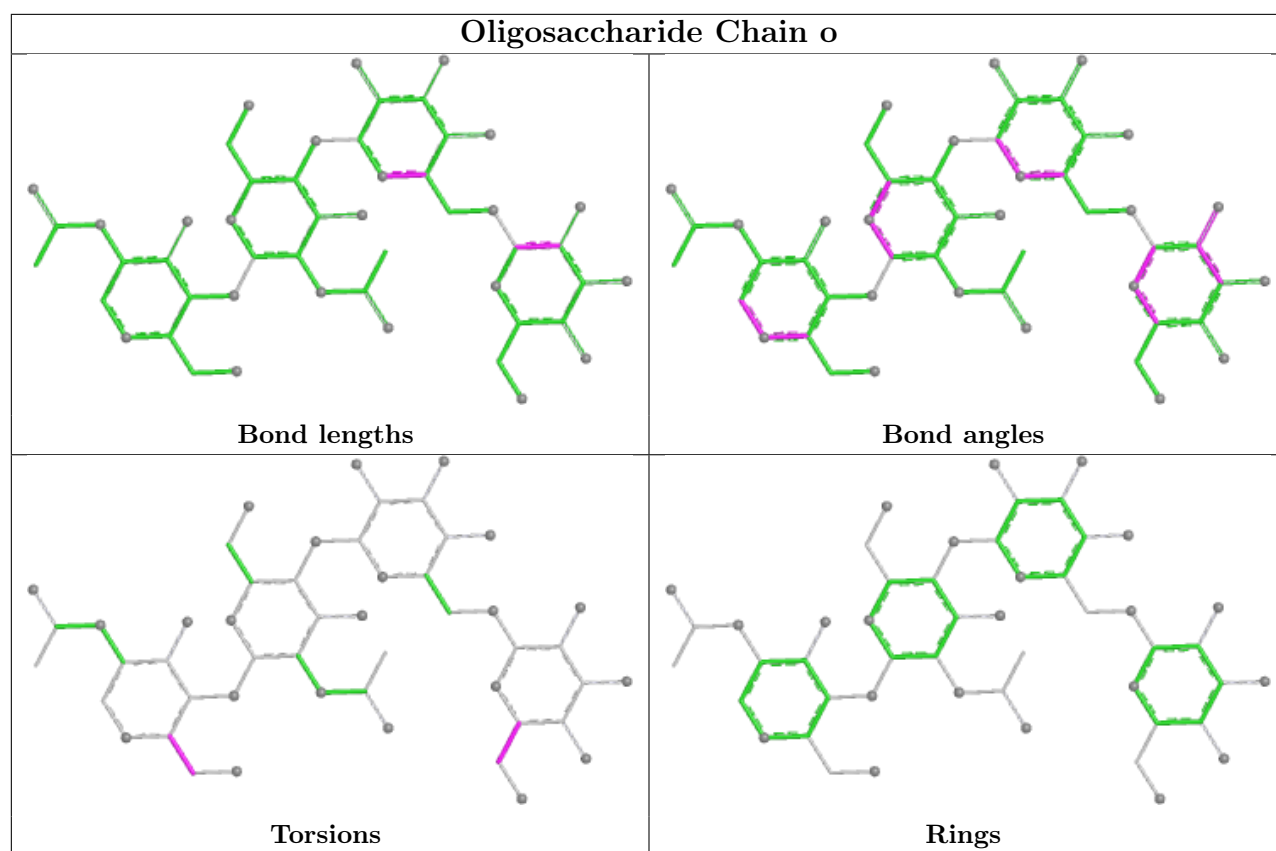


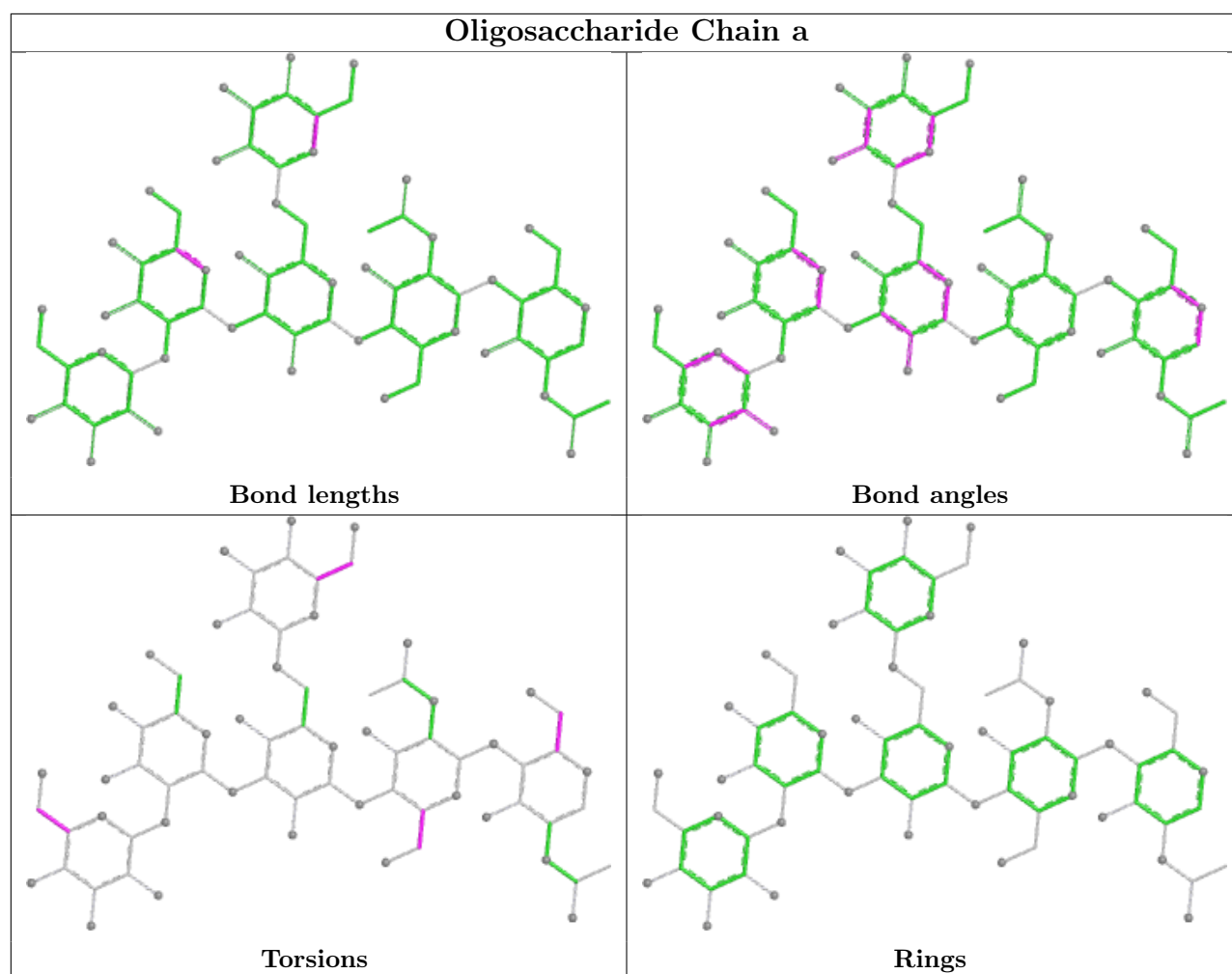


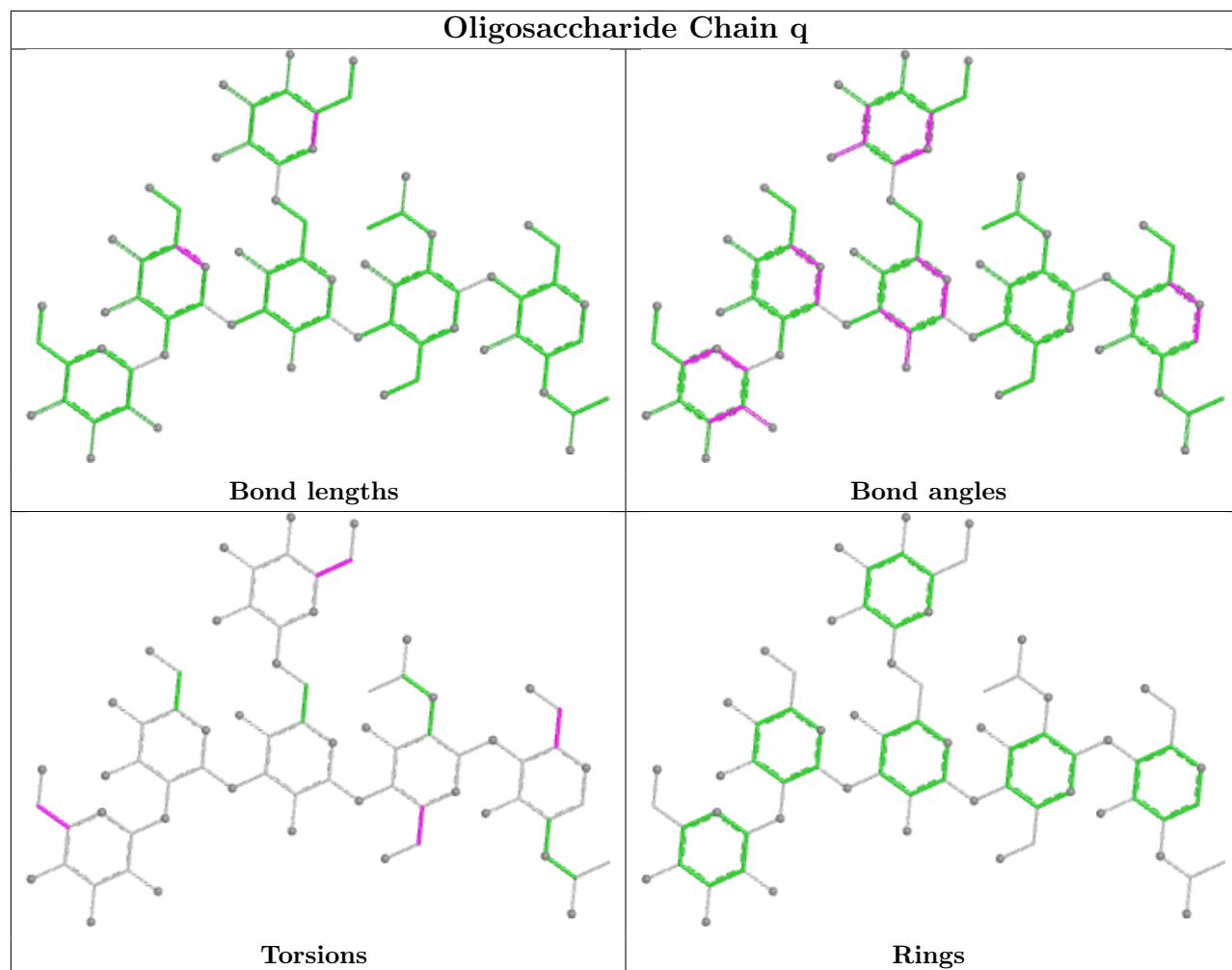


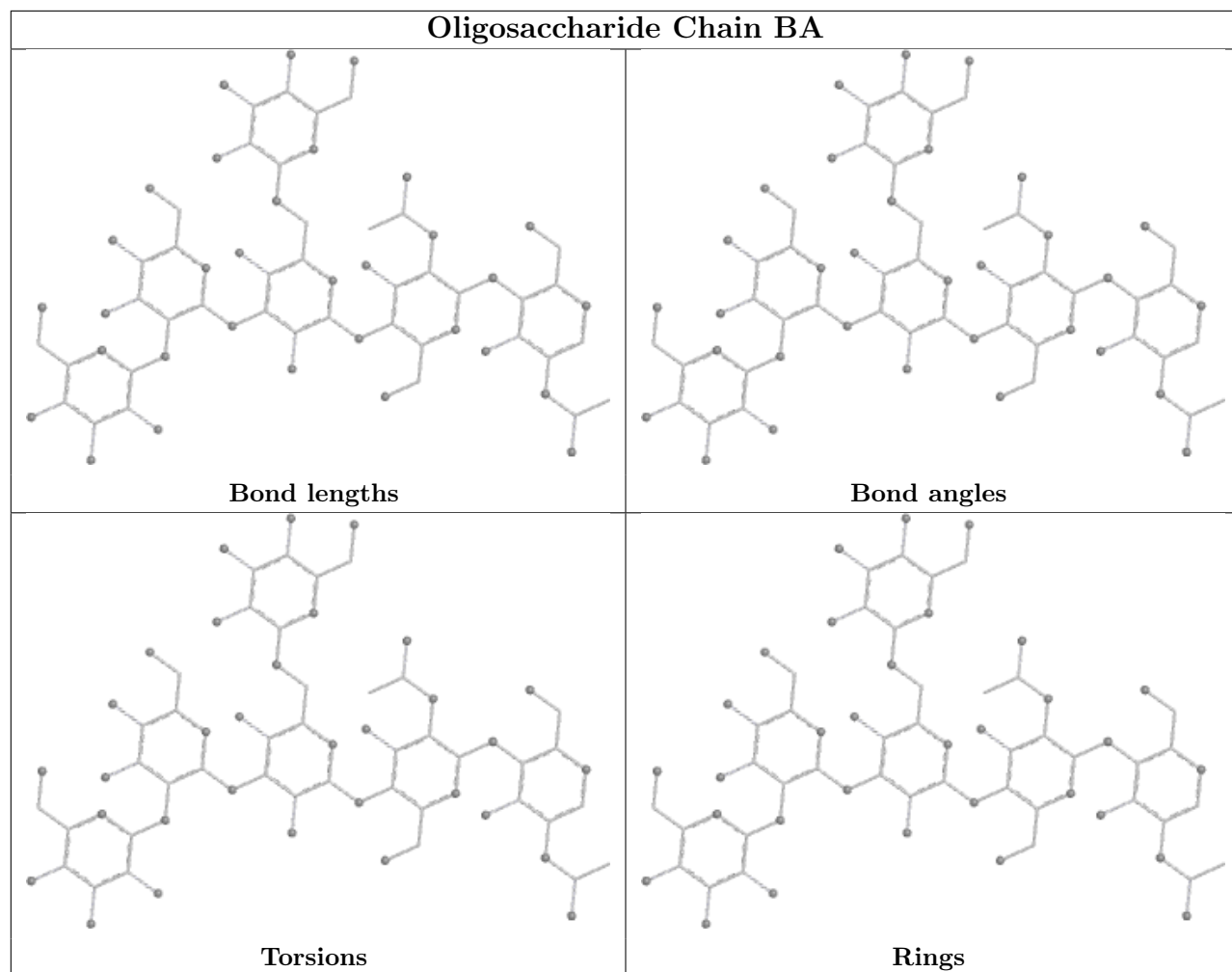


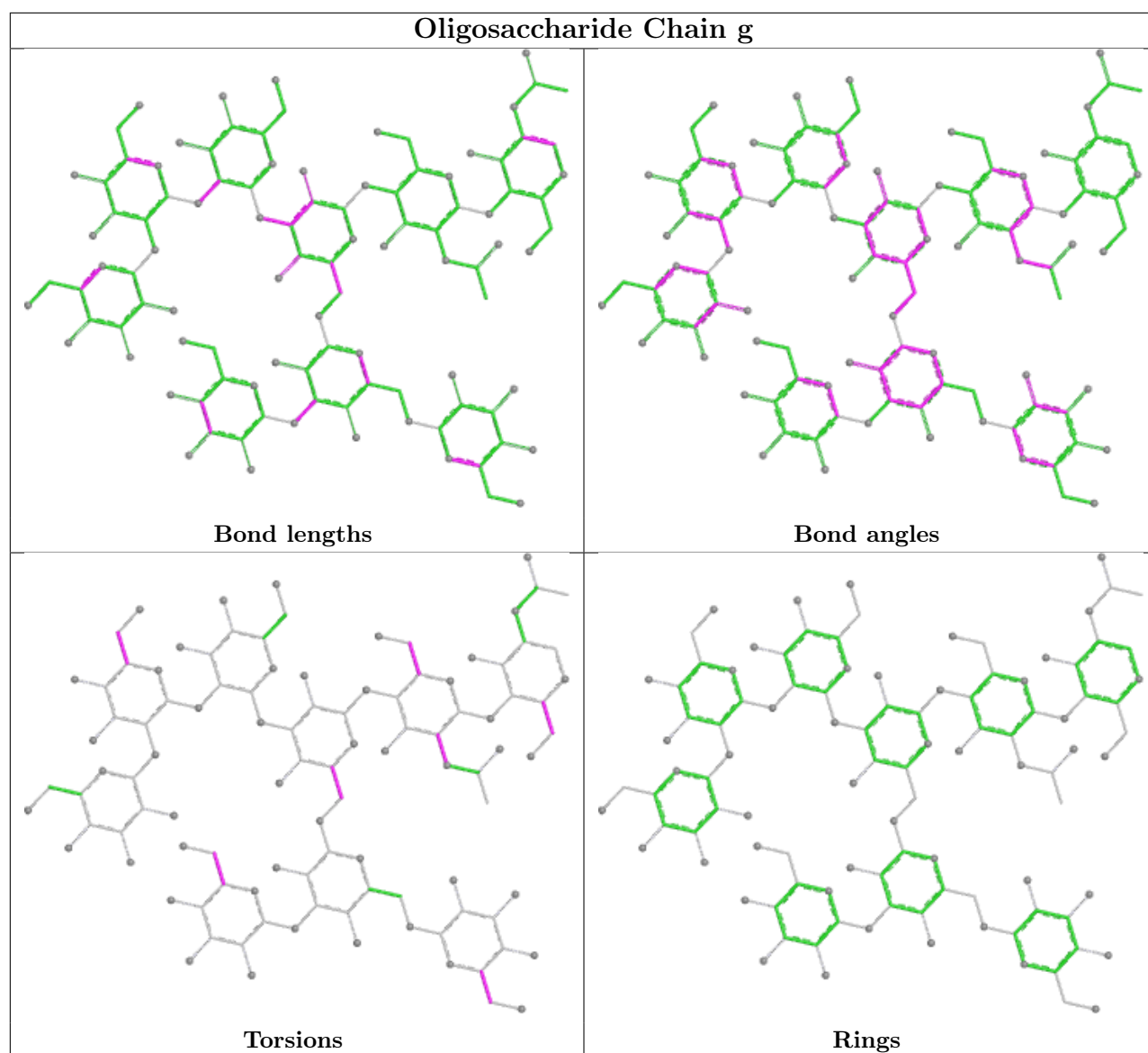


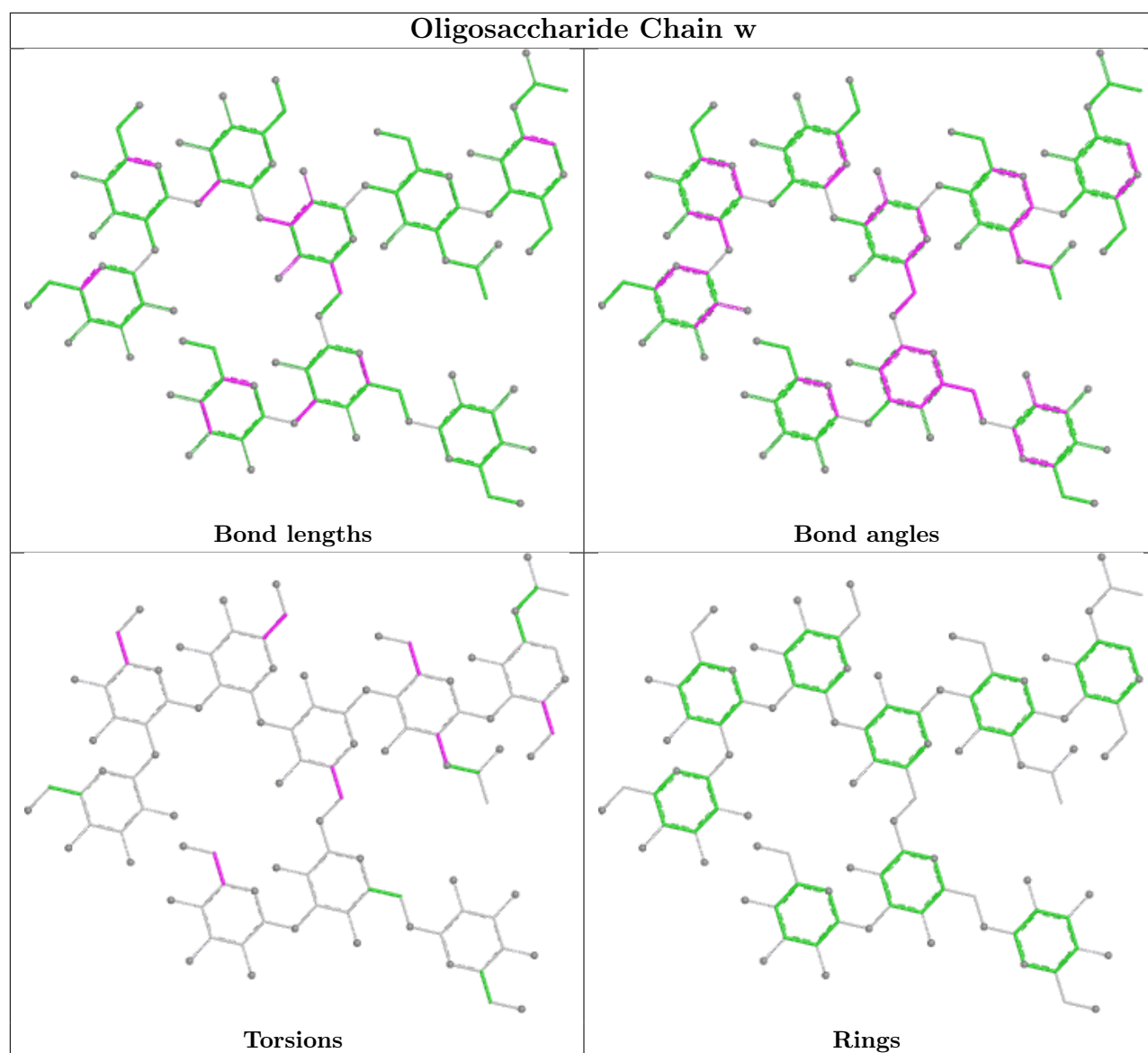


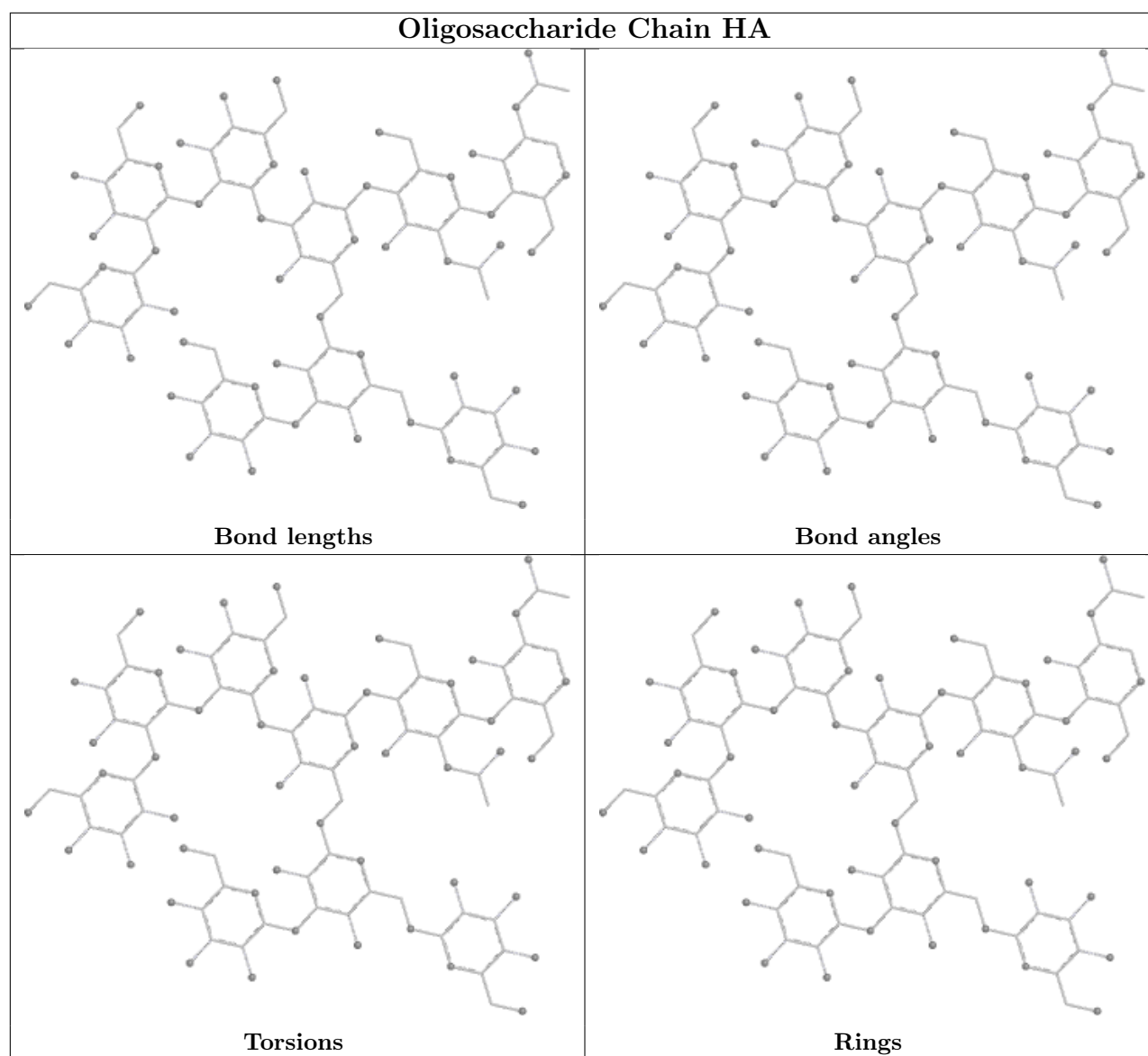




Oligosaccharide Chain BA







5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
16	NAG	G	701	6	14,14,15	0.85	2 (14%)	17,19,21	0.87	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	NAG	B	635	1	14,14,15	0.78	1 (7%)	17,19,21	0.86	1 (5%)
16	NAG	2	635	1	14,14,15	0.76	1 (7%)	17,19,21	0.86	1 (5%)
16	NAG	G	702	6	14,14,15	0.57	0	17,19,21	0.99	1 (5%)
16	NAG	A	702	6	14,14,15	0.54	0	17,19,21	0.98	1 (5%)
16	NAG	Q	701	6	14,14,15	0.79	1 (7%)	17,19,21	0.85	1 (5%)
16	NAG	K	635	1	14,14,15	0.76	1 (7%)	17,19,21	0.90	1 (5%)
16	NAG	A	701	6	14,14,15	0.82	1 (7%)	17,19,21	0.87	1 (5%)
16	NAG	Q	702	6	14,14,15	0.56	0	17,19,21	0.97	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
16	NAG	G	701	6	-	2/6/23/26	0/1/1/1
16	NAG	B	635	1	-	1/6/23/26	0/1/1/1
16	NAG	2	635	1	-	0/6/23/26	0/1/1/1
16	NAG	G	702	6	-	3/6/23/26	0/1/1/1
16	NAG	A	702	6	-	3/6/23/26	0/1/1/1
16	NAG	Q	701	6	-	2/6/23/26	0/1/1/1
16	NAG	K	635	1	-	1/6/23/26	0/1/1/1
16	NAG	A	701	6	-	2/6/23/26	0/1/1/1
16	NAG	Q	702	6	-	3/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	B	635	NAG	O5-C1	2.66	1.48	1.43
16	K	635	NAG	O5-C1	2.59	1.48	1.43
16	2	635	NAG	O5-C1	2.58	1.48	1.43
16	G	701	NAG	O5-C1	2.09	1.47	1.43
16	G	701	NAG	C1-C2	2.06	1.55	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	702	NAG	C1-O5-C5	3.75	117.22	112.19
16	A	702	NAG	C1-O5-C5	3.66	117.08	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	702	NAG	C1-O5-C5	3.63	117.06	112.19
16	K	635	NAG	C1-O5-C5	3.42	116.78	112.19
16	2	635	NAG	C1-O5-C5	3.21	116.49	112.19

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	G	702	NAG	O5-C5-C6-O6
16	A	702	NAG	O5-C5-C6-O6
16	Q	702	NAG	O5-C5-C6-O6
16	A	702	NAG	C4-C5-C6-O6
16	Q	702	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

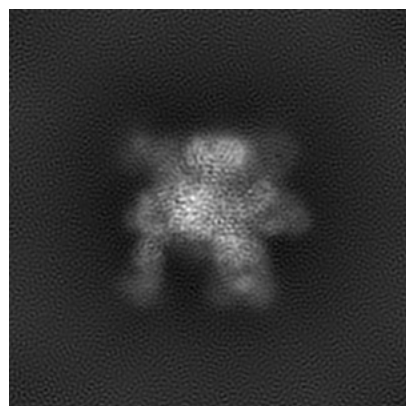
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20189. These allow visual inspection of the internal detail of the map and identification of artifacts.

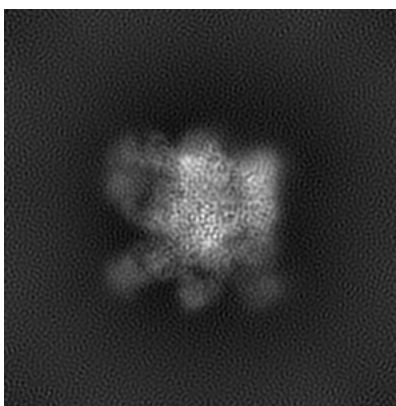
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

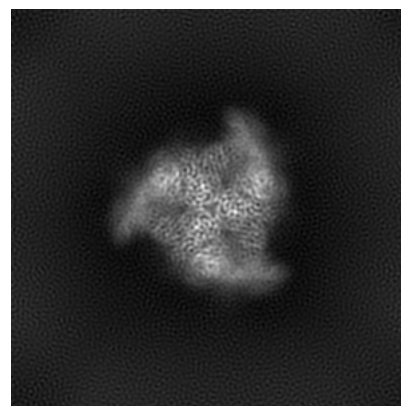
6.1.1 Primary map



X

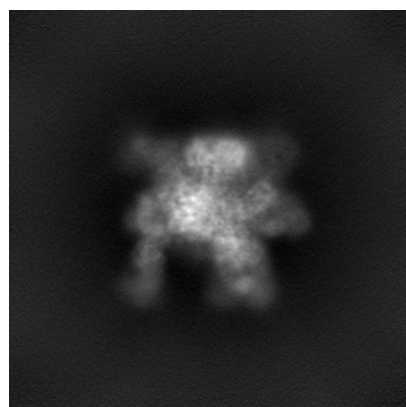


Y

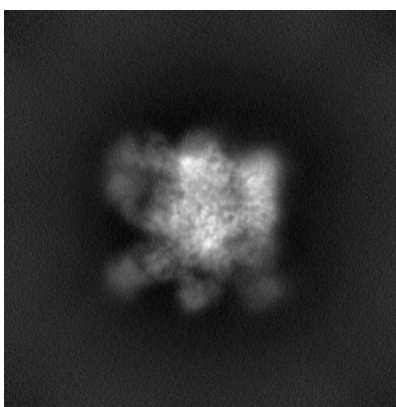


Z

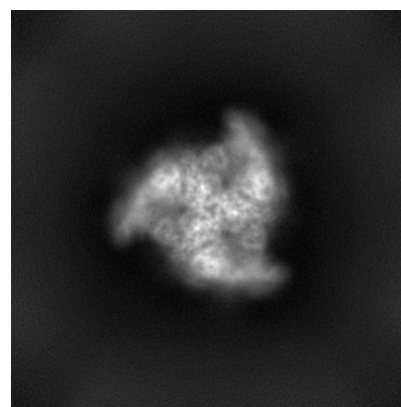
6.1.2 Raw map



X



Y

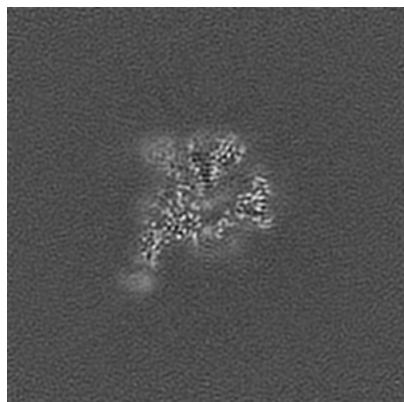


Z

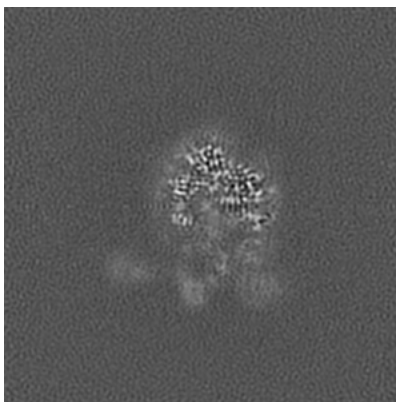
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

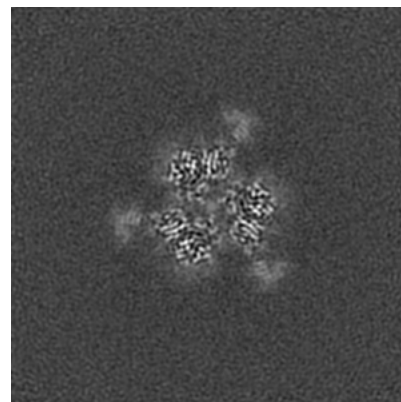
6.2.1 Primary map



X Index: 176

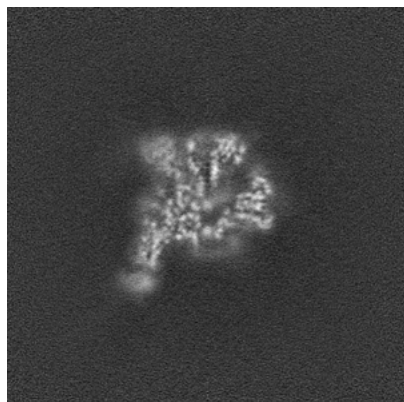


Y Index: 176

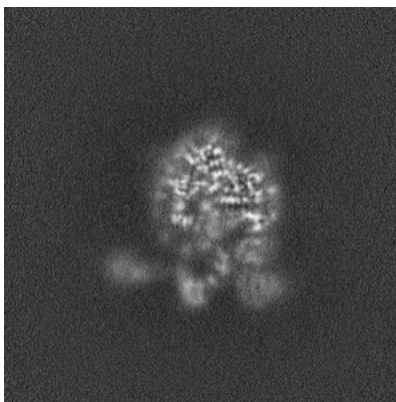


Z Index: 176

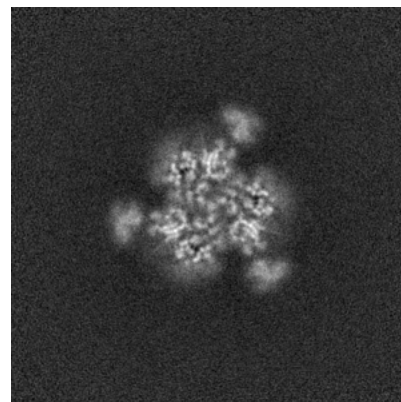
6.2.2 Raw map



X Index: 176



Y Index: 176

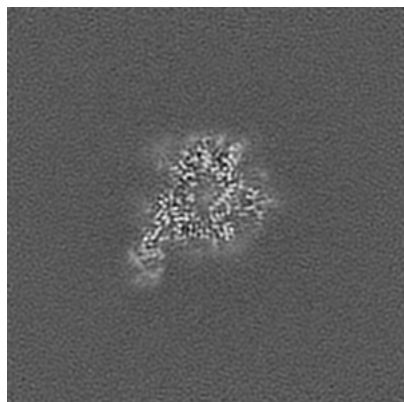


Z Index: 176

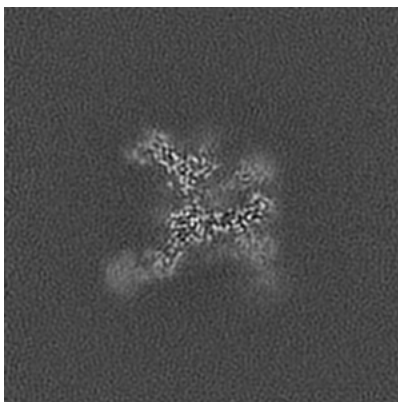
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

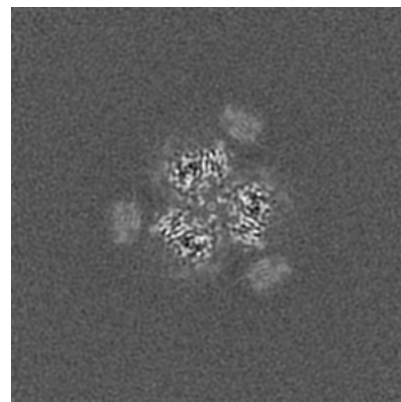
6.3.1 Primary map



X Index: 168

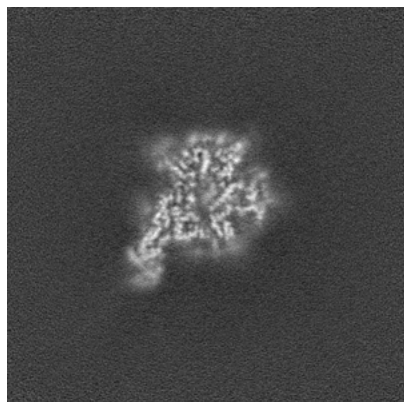


Y Index: 193

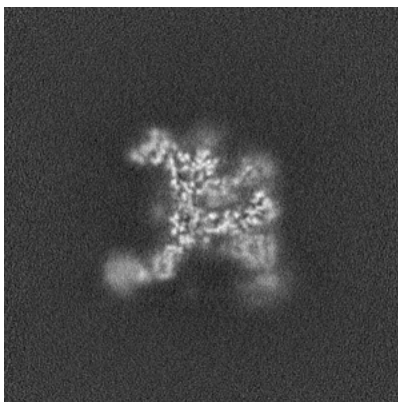


Z Index: 174

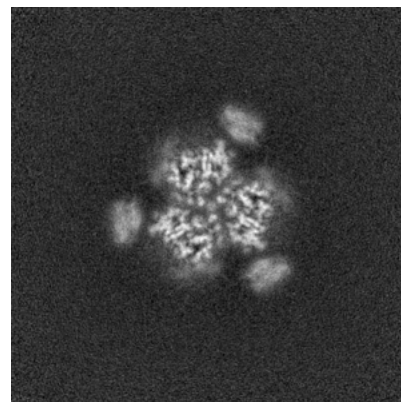
6.3.2 Raw map



X Index: 169



Y Index: 189

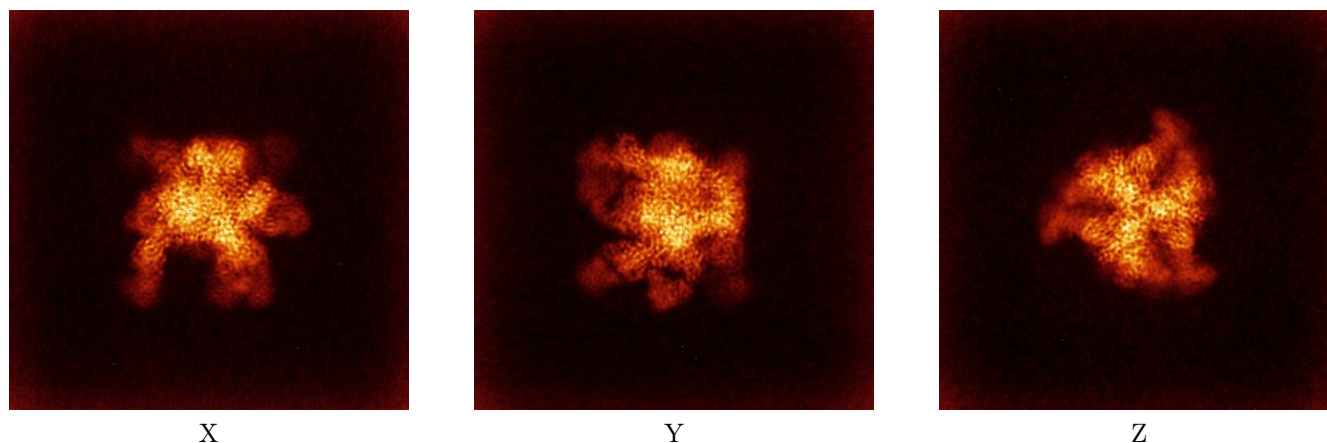


Z Index: 174

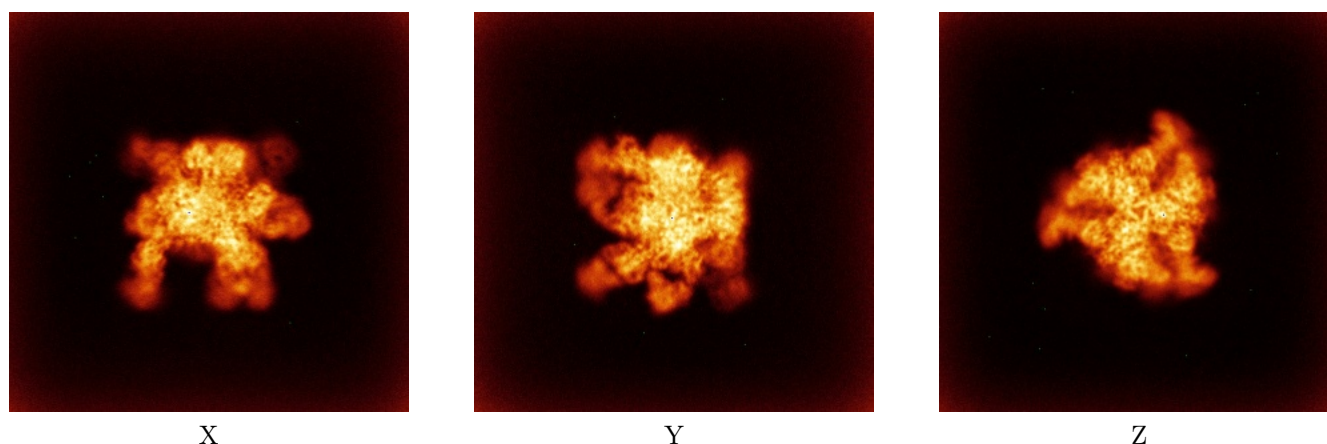
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

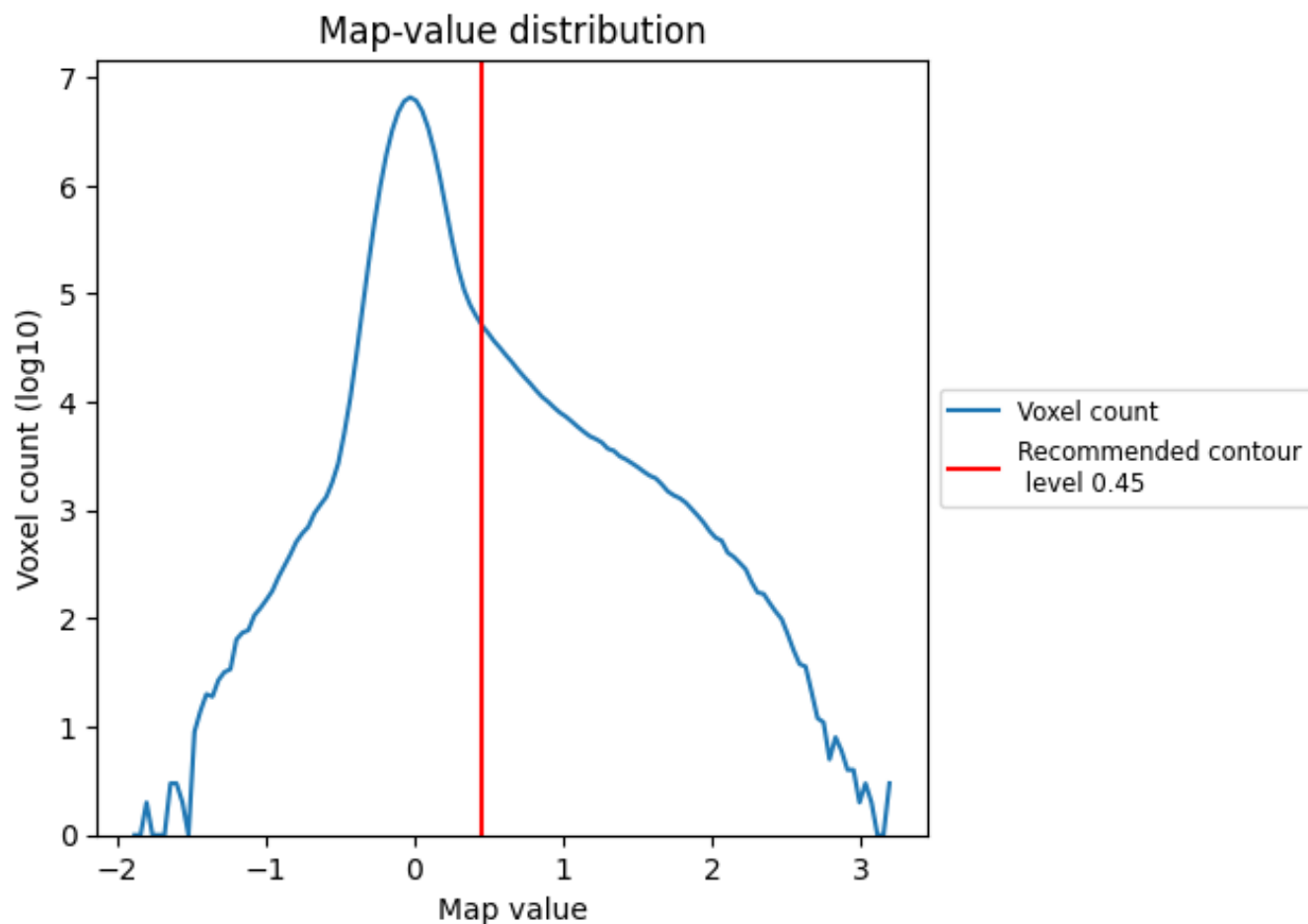
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

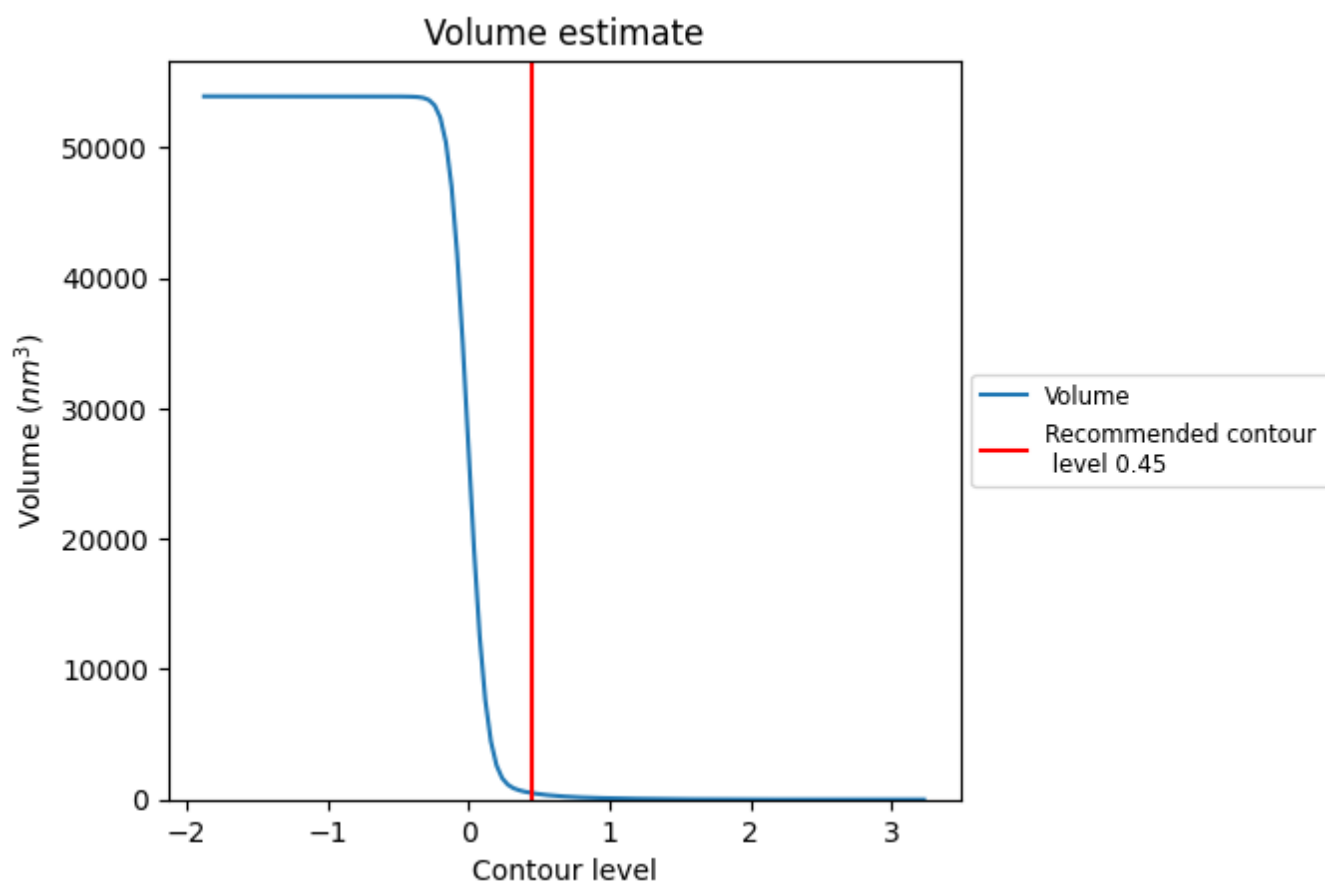
This section contains the results of statistical analysis of the map.

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.

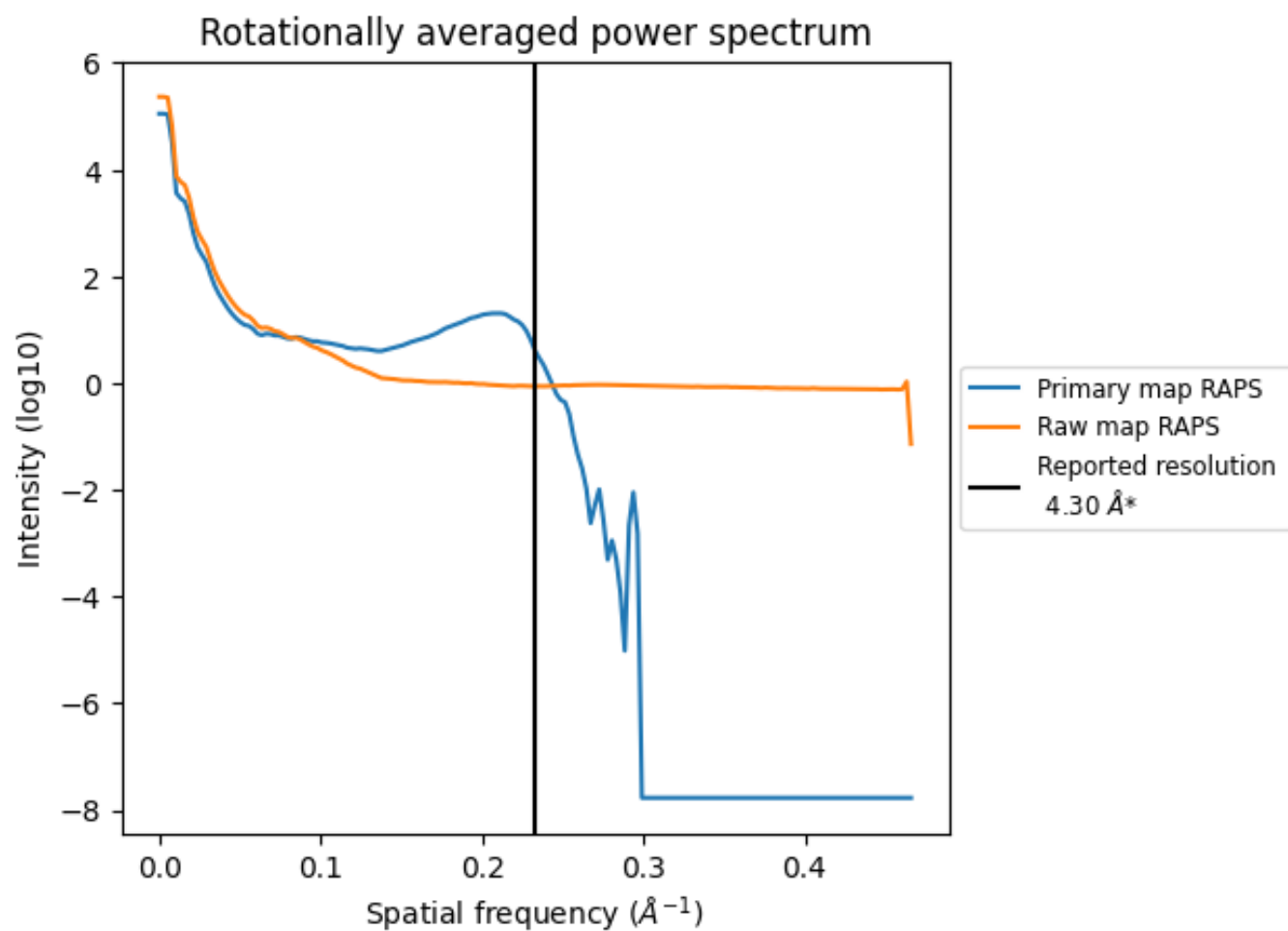
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 497 nm³; this corresponds to an approximate mass of 449 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 ⓘ

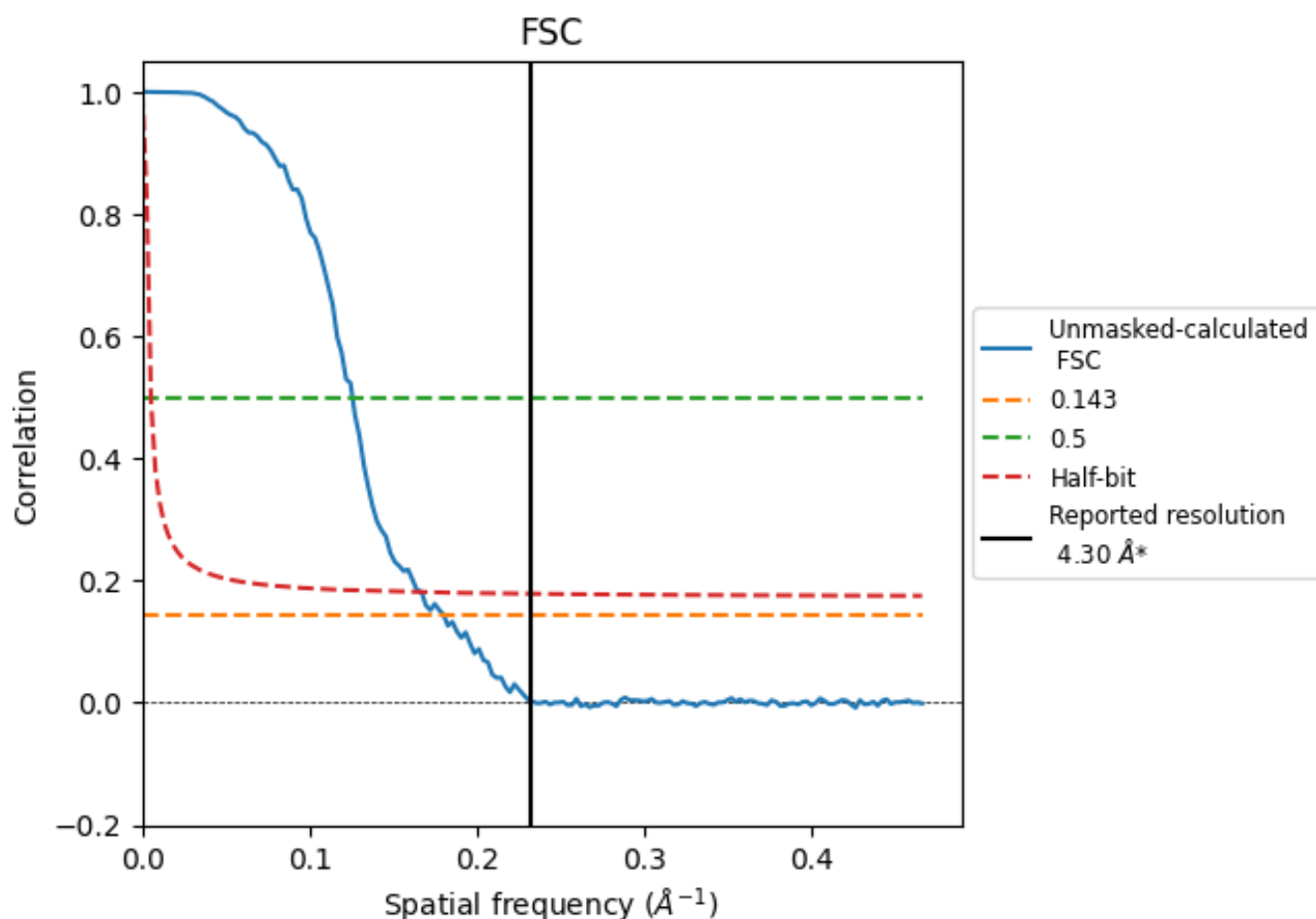


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

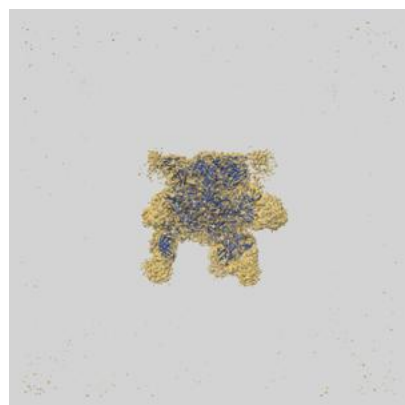
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.55	7.96	6.00

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.55 differs from the reported value 4.3 by more than 10 %

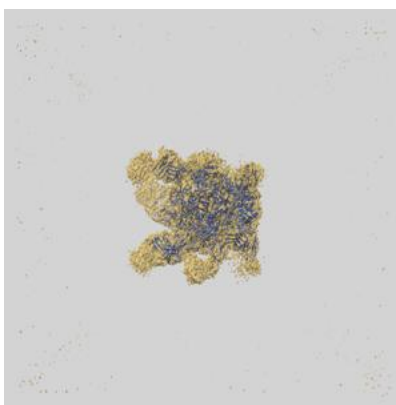
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20189 and PDB model 6OSY. Per-residue inclusion information can be found in section [3](#) on page [14](#).

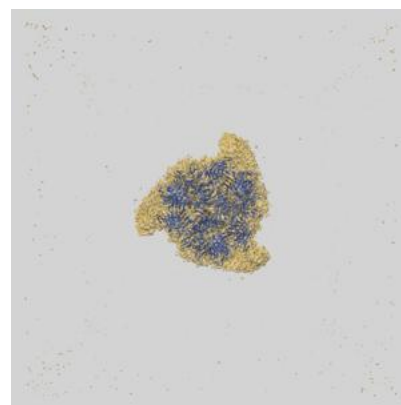
9.1 Map-model overlay [i](#)



X



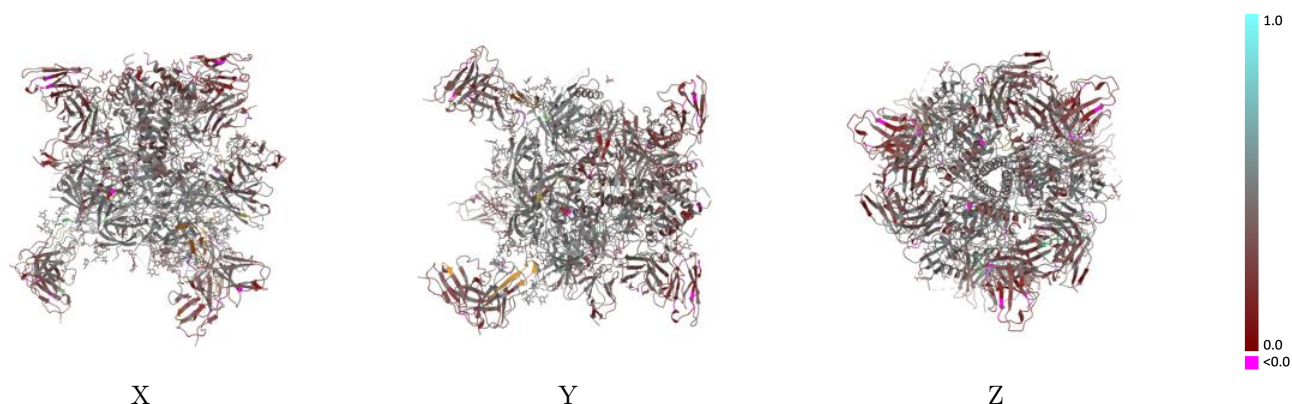
Y



Z

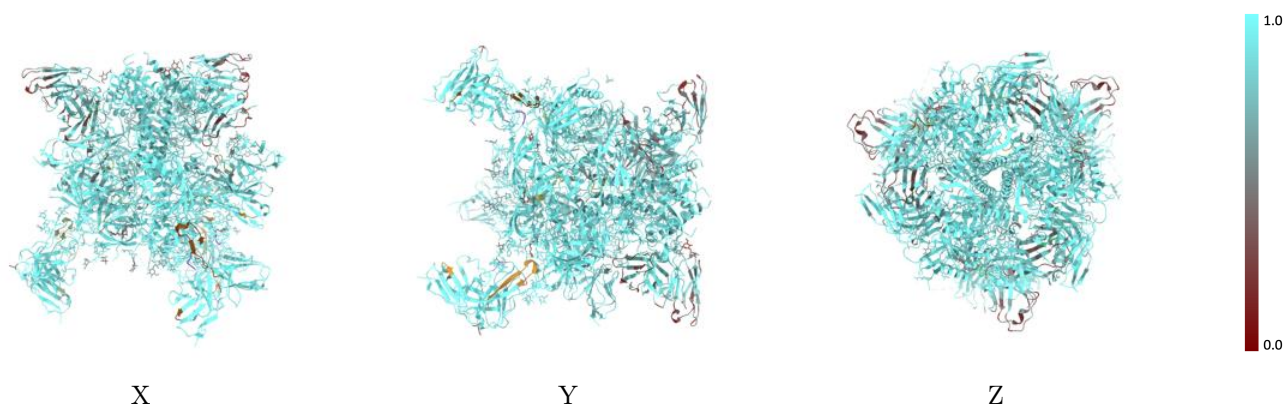
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



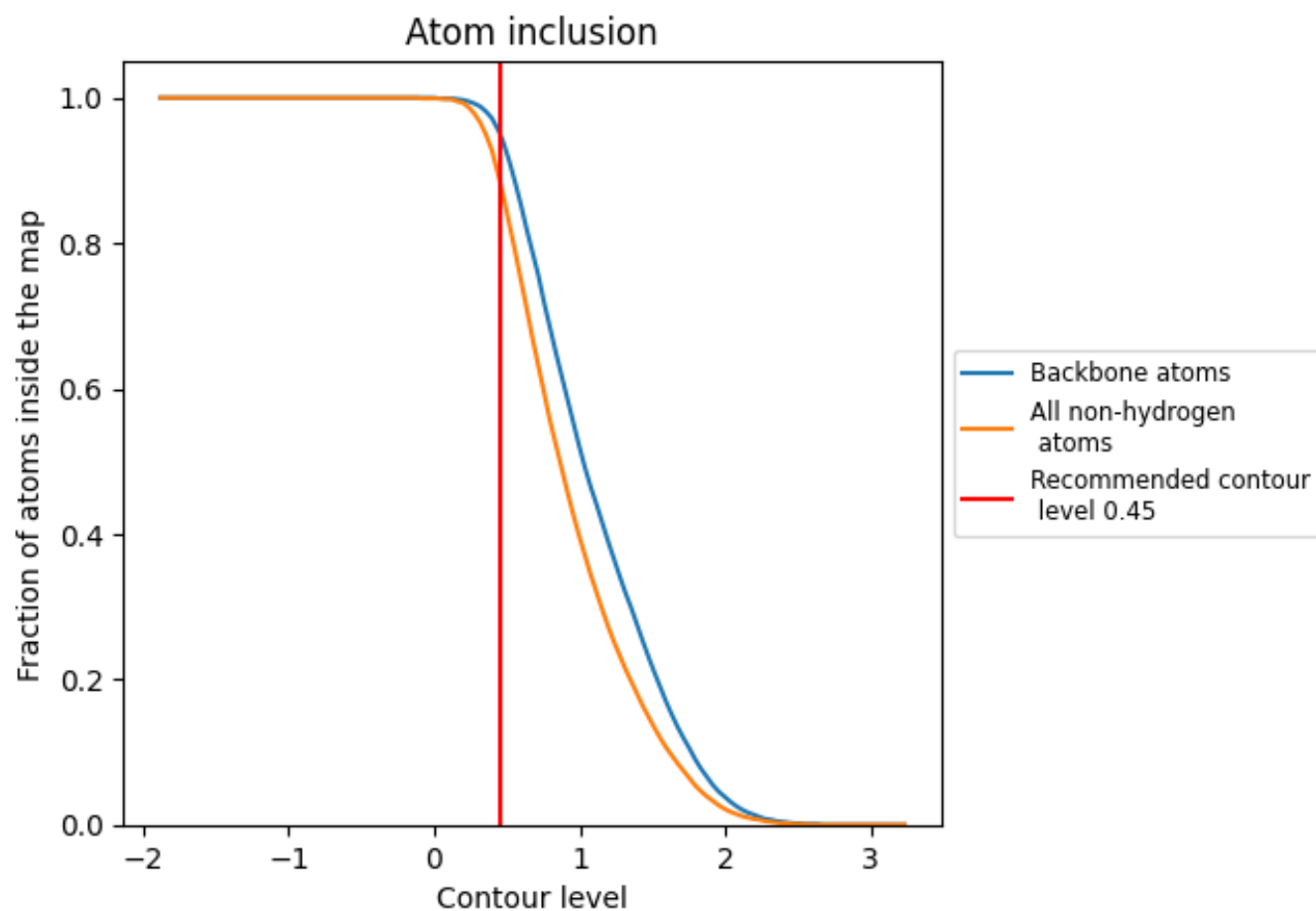
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 89% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8870	 0.3960
0	 0.8930	 0.3550
1	 0.9200	 0.4370
2	 0.9450	 0.4520
3	 0.7870	 0.4140
4	 0.6670	 0.3220
5	 0.9300	 0.3550
6	 0.9210	 0.3910
7	 0.9080	 0.3680
8	 0.8800	 0.4030
9	 0.5000	 0.3690
A	 0.9300	 0.3840
AA	 0.7860	 0.4360
B	 0.9450	 0.4500
BA	 0.9030	 0.4680
C	 0.9260	 0.3540
CA	 0.9290	 0.4820
D	 0.9250	 0.3870
DA	 0.9640	 0.4880
E	 0.9210	 0.3710
EA	 0.9230	 0.4770
F	 0.8780	 0.4030
FA	 0.9340	 0.4720
G	 0.9280	 0.3870
GA	 0.8570	 0.4010
H	 0.7320	 0.3520
HA	 0.9240	 0.4610
I	 0.7280	 0.3480
IA	 0.8210	 0.4050
J	 0.7150	 0.2720
JA	 0.8000	 0.3830
K	 0.9430	 0.4510
L	 0.7100	 0.2750
M	 0.9250	 0.3540
N	 0.9300	 0.3870



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Chain	Atom inclusion	Q-score
O	 0.9130	 0.3690
P	 0.8890	 0.4010
Q	 0.9290	 0.3880
R	 0.7240	 0.3460
S	 0.7060	 0.2720
T	 0.5600	 0.3390
U	 0.8930	 0.3720
V	 0.9400	 0.4420
W	 0.7870	 0.4150
X	 0.6670	 0.3290
Y	 0.4800	 0.3750
Z	 0.8210	 0.4360
a	 0.9310	 0.4730
b	 0.9290	 0.4860
c	 0.9640	 0.4690
d	 0.9230	 0.4680
e	 0.9180	 0.4650
f	 0.8570	 0.3960
g	 0.9330	 0.4620
h	 0.8210	 0.4060
i	 0.8200	 0.3790
j	 0.5800	 0.3610
k	 0.8930	 0.3640
l	 0.9400	 0.4370
m	 0.7700	 0.4170
n	 0.6670	 0.3220
o	 0.5000	 0.3850
p	 0.7860	 0.4430
q	 0.9310	 0.4710
r	 0.9290	 0.4820
s	 0.9640	 0.4730
t	 0.9490	 0.4750
u	 0.9180	 0.4650
v	 0.8570	 0.4080
w	 0.9240	 0.4590
x	 0.8210	 0.4120
y	 0.8400	 0.3750
z	 0.5400	 0.3530