



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 05:49 AM UTC

PDB ID : 8ULU / pdb_00008ulu
EMDB ID : EMD-42366
Title : Cryo-EM structure of the BG505 SOSIPv2 in complex with bNAb 04_A06 and PGDM1400 Fabs
Authors : DeLaitch, A.T.; Bjorkman, P.J.
Deposited on : 2023-10-16
Resolution : 3.80 Å (reported)
Based on initial models : 4RQQ, 6UDJ, 8UKI

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:

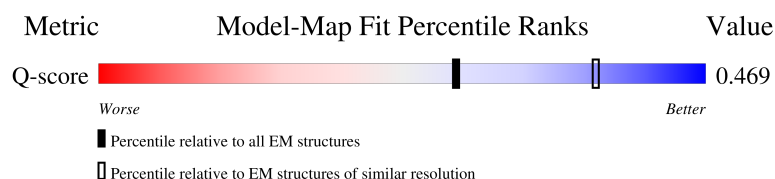
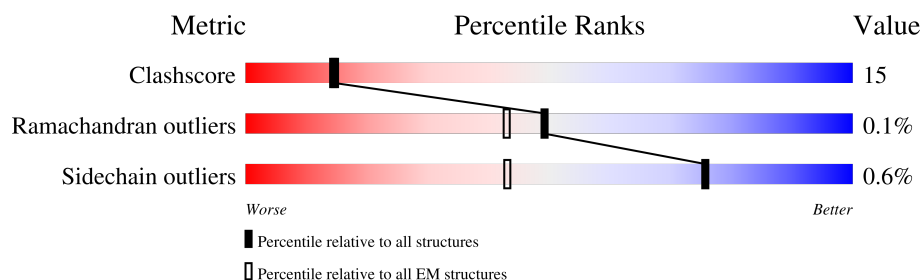
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.80 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	10198 (3.30 - 4.30)

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	479	 6% 64% 27% 8%
1	C	479	 7% 62% 29% 8%
1	E	479	 6% 59% 33% 8%
2	B	153	 10% 56% 25% 18%

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Mol	Chain	Length	Quality of chain
2	D	153	
2	F	153	
3	G	219	
4	H	245	
4	I	245	
4	J	245	
5	K	253	
6	L	211	
6	M	211	
6	N	211	
7	O	2	
7	R	2	
7	S	2	
7	U	2	
7	V	2	
7	W	2	
7	X	2	
7	Y	2	
7	Z	2	
7	a	2	
7	c	2	
7	d	2	
7	e	2	
7	f	2	
7	g	2	

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Mol	Chain	Length	Quality of chain
7	i	2	50%
7	o	2	50% 100%
7	q	2	50% 100%
7	r	2	50% 100%
7	s	2	50% 50%
7	t	2	50% 100%
7	u	2	100%
7	v	2	100%
7	w	2	50% 50%
8	P	3	33% 100%
8	h	3	67% 33%
8	k	3	67% 33%
8	l	3	67% 33%
8	n	3	33% 67% 33%
9	Q	5	20% 60% 20%
9	T	5	40% 60% 40%
9	j	5	60% 40%
10	b	7	29% 71%
11	m	6	50% 50%
12	p	4	25% 75% 25%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 22029 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 Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	440	Total	C	N	O	S	0	0
			3450	2170	614	638	28		
1	C	440	Total	C	N	O	S	0	0
			3450	2170	614	638	28		
1	E	440	Total	C	N	O	S	0	0
			3446	2167	613	638	28		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	332	ASN	THR	conflict	UNP Q2N0S6
A	501	CYS	ALA	conflict	UNP Q2N0S6
A	505	VAL	-	expression tag	UNP Q2N0S6
A	506	VAL	-	expression tag	UNP Q2N0S6
A	507	GLY	-	expression tag	UNP Q2N0S6
A	508	ARG	-	expression tag	UNP Q2N0S6
A	509	ARG	-	expression tag	UNP Q2N0S6
A	510	ARG	-	expression tag	UNP Q2N0S6
A	511	ARG	-	expression tag	UNP Q2N0S6
A	512	ARG	-	expression tag	UNP Q2N0S6
A	513	ARG	-	expression tag	UNP Q2N0S6
C	332	ASN	THR	conflict	UNP Q2N0S6
C	501	CYS	ALA	conflict	UNP Q2N0S6
C	505	VAL	-	expression tag	UNP Q2N0S6
C	506	VAL	-	expression tag	UNP Q2N0S6
C	507	GLY	-	expression tag	UNP Q2N0S6
C	508	ARG	-	expression tag	UNP Q2N0S6
C	509	ARG	-	expression tag	UNP Q2N0S6
C	510	ARG	-	expression tag	UNP Q2N0S6
C	511	ARG	-	expression tag	UNP Q2N0S6
C	512	ARG	-	expression tag	UNP Q2N0S6
C	513	ARG	-	expression tag	UNP Q2N0S6
E	332	ASN	THR	conflict	UNP Q2N0S6
E	501	CYS	ALA	conflict	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	505	VAL	-	expression tag	UNP Q2N0S6
E	506	VAL	-	expression tag	UNP Q2N0S6
E	507	GLY	-	expression tag	UNP Q2N0S6
E	508	ARG	-	expression tag	UNP Q2N0S6
E	509	ARG	-	expression tag	UNP Q2N0S6
E	510	ARG	-	expression tag	UNP Q2N0S6
E	511	ARG	-	expression tag	UNP Q2N0S6
E	512	ARG	-	expression tag	UNP Q2N0S6
E	513	ARG	-	expression tag	UNP Q2N0S6

- Molecule 2 is a protein called Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	125	Total	C	N	O	S	0	0
			982	619	170	187	6		
2	D	125	Total	C	N	O	S	0	0
			982	619	170	187	6		
2	F	125	Total	C	N	O	S	0	0
			982	619	170	187	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S5
B	605	CYS	THR	engineered mutation	UNP Q2N0S5
D	559	PRO	ILE	engineered mutation	UNP Q2N0S5
D	605	CYS	THR	engineered mutation	UNP Q2N0S5
F	559	PRO	ILE	engineered mutation	UNP Q2N0S5
F	605	CYS	THR	engineered mutation	UNP Q2N0S5

- Molecule 3 is a protein called PGDM1400 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	110	Total	C	N	O	S	0	0
			848	529	149	167	3		

- Molecule 4 is a protein called 04_A06 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	132	Total	C	N	O	S	0	0
			1024	654	177	191	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	132	Total	C	N	O	S	0	0
			1024	654	177	191	2		
4	J	132	Total	C	N	O	S	0	0
			1024	654	177	191	2		

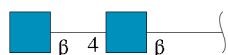
- Molecule 5 is a protein called PGDM1400 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	139	Total	C	N	O	S	0	0
			1091	689	189	209	4		

- Molecule 6 is a protein called 04_A06 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	103	Total	C	N	O	S	0	0
			791	502	139	148	2		
6	M	103	Total	C	N	O	S	0	0
			791	502	139	148	2		
6	N	103	Total	C	N	O	S	0	0
			791	502	139	148	2		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



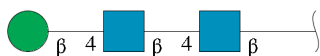
Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	2	Total	C	N	O	0	0
			28	16	2	10		
7	R	2	Total	C	N	O	0	0
			28	16	2	10		
7	S	2	Total	C	N	O	0	0
			28	16	2	10		
7	U	2	Total	C	N	O	0	0
			28	16	2	10		
7	V	2	Total	C	N	O	0	0
			28	16	2	10		
7	W	2	Total	C	N	O	0	0
			28	16	2	10		

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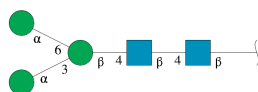
Mol	Chain	Residues	Atoms				AltConf	Trace
7	X	2	Total	C	N	O	0	0
			28	16	2	10		
7	Y	2	Total	C	N	O	0	0
			28	16	2	10		
7	Z	2	Total	C	N	O	0	0
			28	16	2	10		
7	a	2	Total	C	N	O	0	0
			28	16	2	10		
7	c	2	Total	C	N	O	0	0
			28	16	2	10		
7	d	2	Total	C	N	O	0	0
			28	16	2	10		
7	e	2	Total	C	N	O	0	0
			28	16	2	10		
7	f	2	Total	C	N	O	0	0
			28	16	2	10		
7	g	2	Total	C	N	O	0	0
			28	16	2	10		
7	i	2	Total	C	N	O	0	0
			28	16	2	10		
7	o	2	Total	C	N	O	0	0
			28	16	2	10		
7	q	2	Total	C	N	O	0	0
			28	16	2	10		
7	r	2	Total	C	N	O	0	0
			28	16	2	10		
7	s	2	Total	C	N	O	0	0
			28	16	2	10		
7	t	2	Total	C	N	O	0	0
			28	16	2	10		
7	u	2	Total	C	N	O	0	0
			28	16	2	10		
7	v	2	Total	C	N	O	0	0
			28	16	2	10		
7	w	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 8 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.



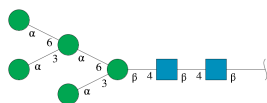
Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	3	Total	C	N	O	0	0
			39	22	2	15		
8	h	3	Total	C	N	O	0	0
			39	22	2	15		
8	k	3	Total	C	N	O	0	0
			39	22	2	15		
8	l	3	Total	C	N	O	0	0
			39	22	2	15		
8	n	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 9 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.



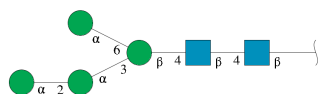
Mol	Chain	Residues	Atoms				AltConf	Trace
9	Q	5	Total	C	N	O	0	0
			61	34	2	25		
9	T	5	Total	C	N	O	0	0
			61	34	2	25		
9	j	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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.



Mol	Chain	Residues	Atoms				AltConf	Trace
10	b	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 11 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.



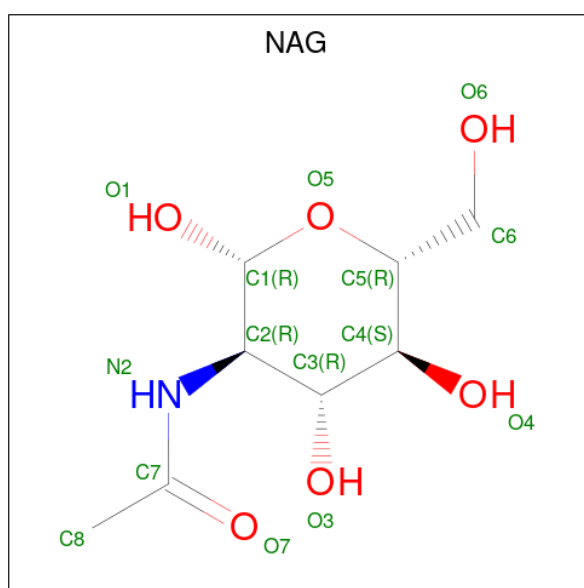
Mol	Chain	Residues	Atoms				AltConf	Trace
11	m	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 12 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
12	p	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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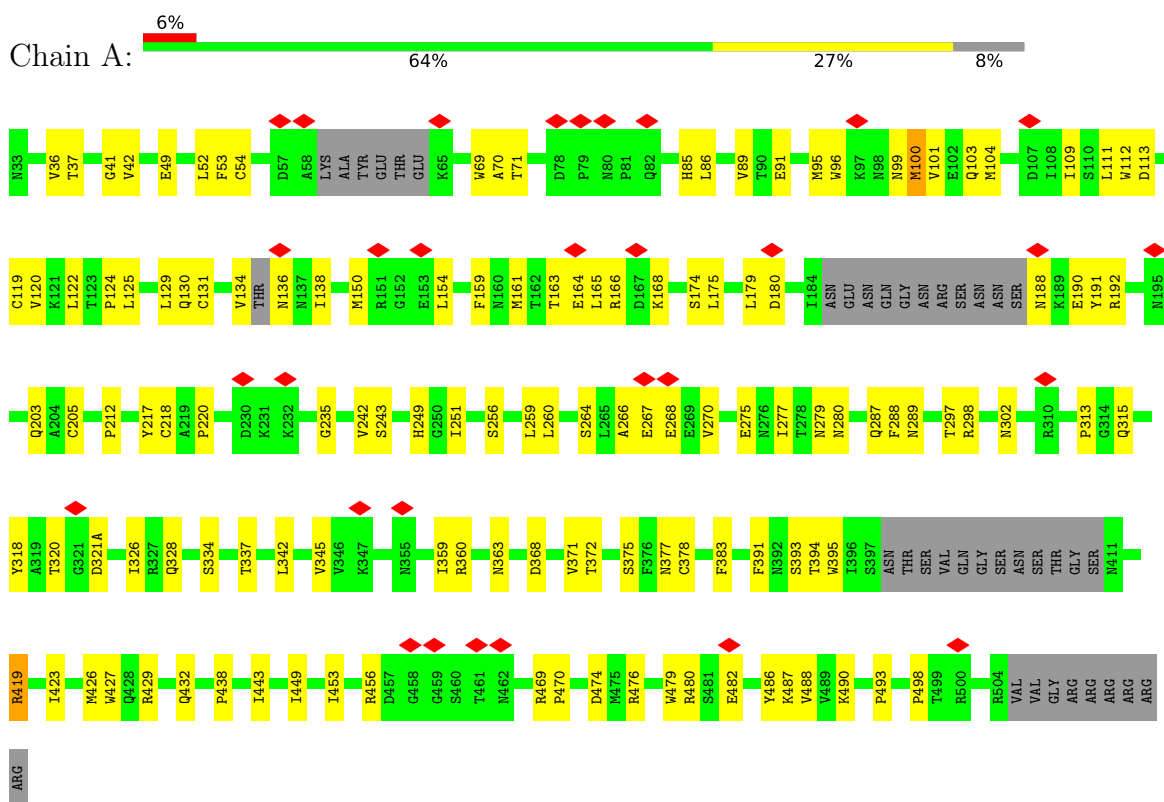
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Mol	Chain	Residues	Atoms				AltConf
13	C	1	Total 14	C 8	N 1	O 5	0
13	C	1	Total 14	C 8	N 1	O 5	0
13	C	1	Total 14	C 8	N 1	O 5	0
13	E	1	Total 14	C 8	N 1	O 5	0
13	E	1	Total 14	C 8	N 1	O 5	0

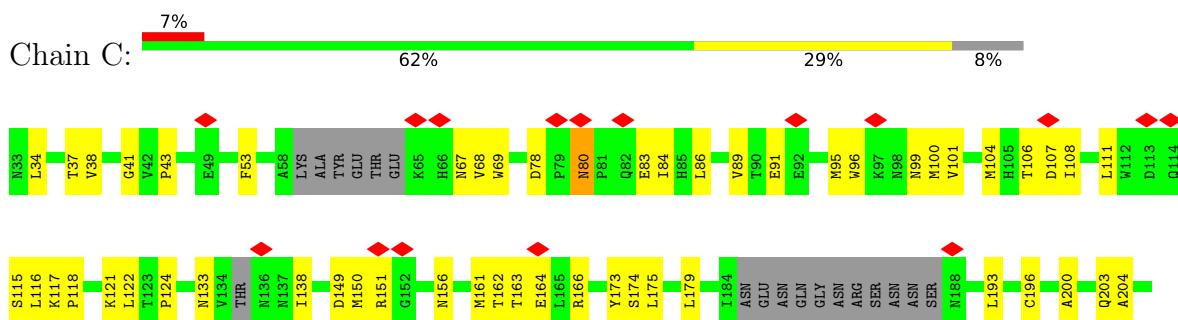
3 Residue-property plots

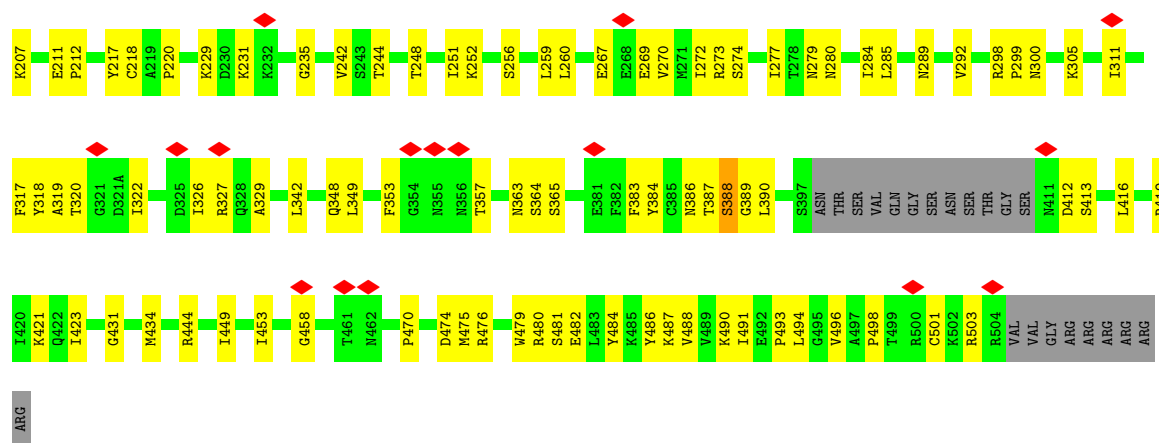
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Envelope glycoprotein gp120

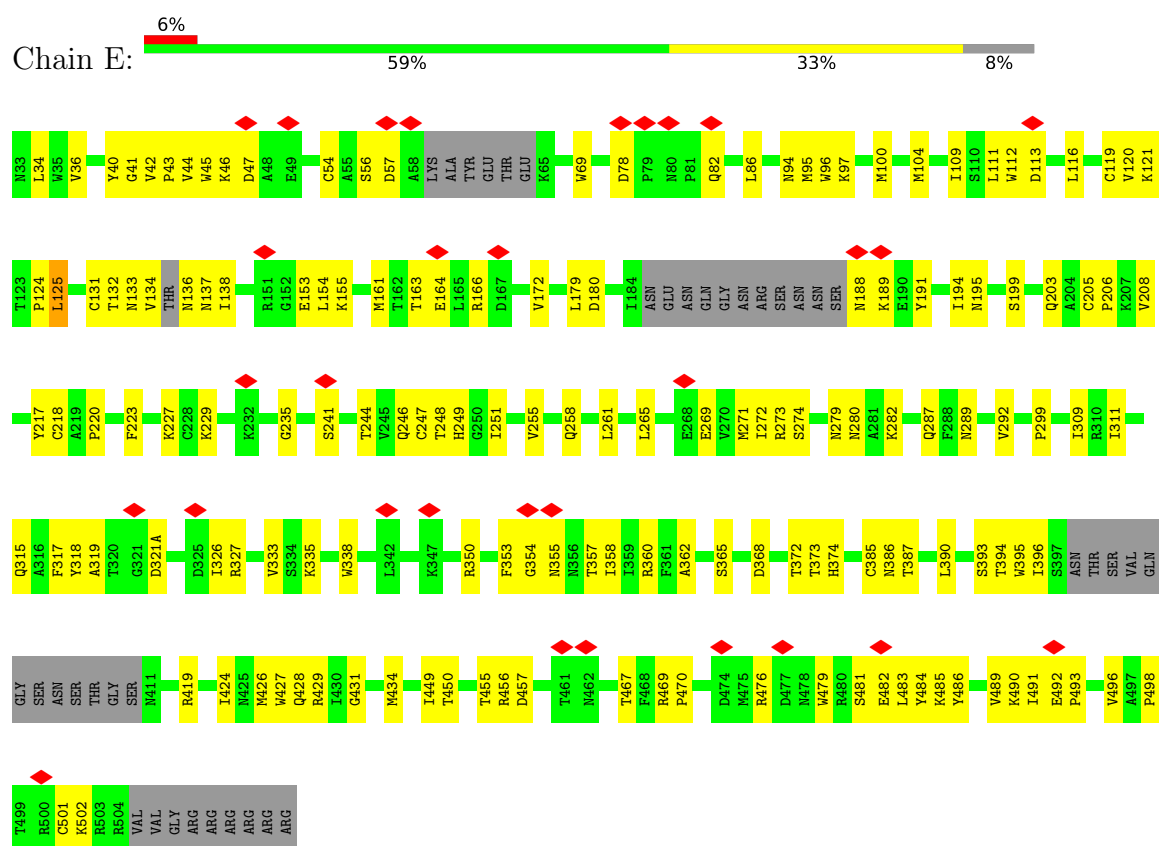


• Molecule 1: Envelope glycoprotein gp120

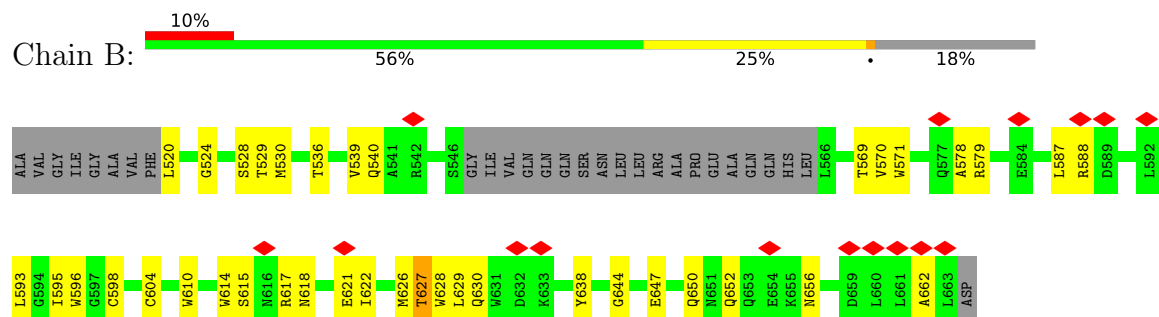


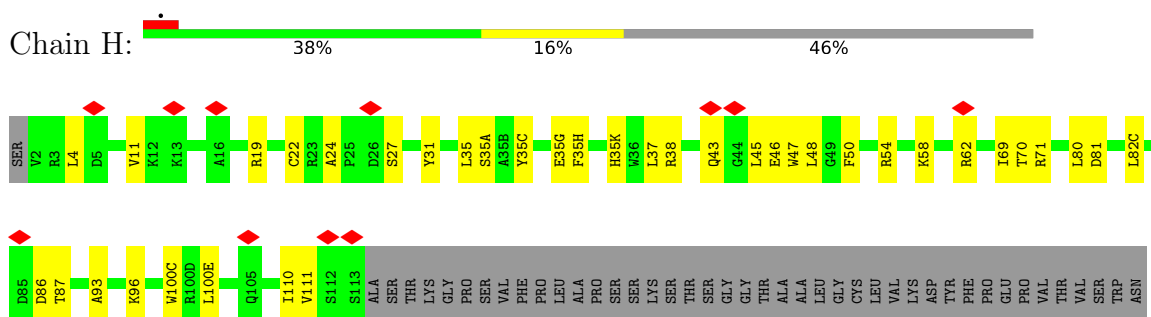


• Molecule 1: Envelope glycoprotein gp120



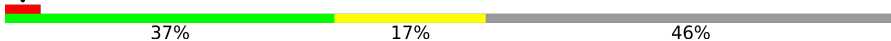
• Molecule 2: Envelope glycoprotein gp41





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

• Molecule 4: 04_A06 Fab Heavy Chain

Chain I: 

ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP	GLY	SER	ASP</
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• Molecule 4: 04_A06 Fab Heavy Chain

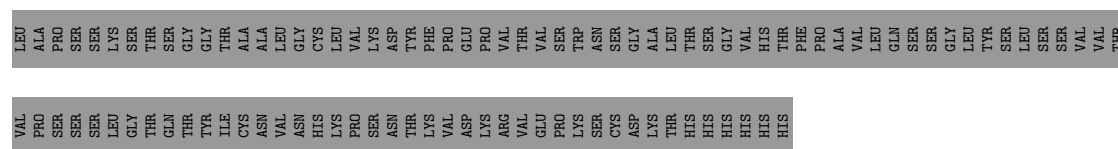
Chain J: 

CYS	ASN	VAL	ASN	HIS	LYS	PRO	PRO	SER	ASN	THR	LYS	VAL	ASP	LYS	ARG	VAL	GLU	PRO	LYS	SER	ASN	CYS	ASP	LYS	THR	HIS	HIS	HIS	HIS	HIS	HIS														
ALA	ALA	LEU	GLY	CYS	LEU	VAL	VAL	LYS	ASP	TYR	PHE	PRO	GLU	PRO	VAL	THR	VAL	SER	TRP	ASN	SER	GLY	ALA	LEU	THR	THR	THR	THR	THR	THR	THR														
R71	D72	E76	T77	L80	D81	L82	L82C	K83	A84	D85	D86	T89	Y90	Y91	C92	D95	K96	N97	V98	M100A	L100E	D101	S102	L108	V109	I110	V111	S112	S113	ALA															
SER	V2	R3	L4	D5	Q6	T9	A10	V11	K12	K13	A16	R19	R23	D26	S27	F28	Y31	R32	P33	R34	L35	F35D	W36	L37	R38	Q39	G42	Q43	Q44	L45	E46	W47	L48	G49	F50	I52A	F53	R54	K58	S61	R62	F63	R66	I69	T70

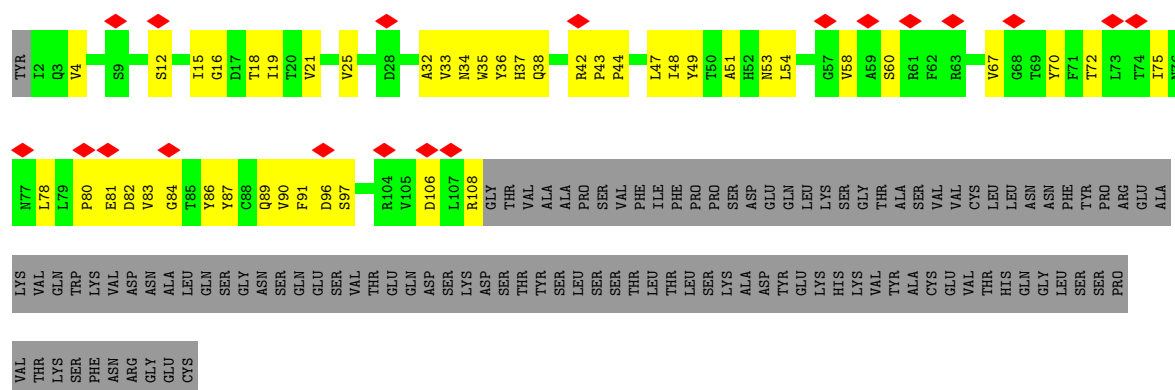
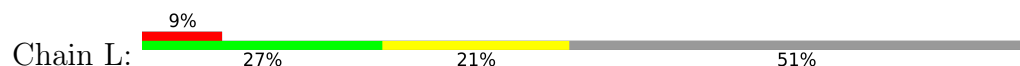
• Molecule 5: PGDM1400 Fab Heavy Chain

Chain K: 

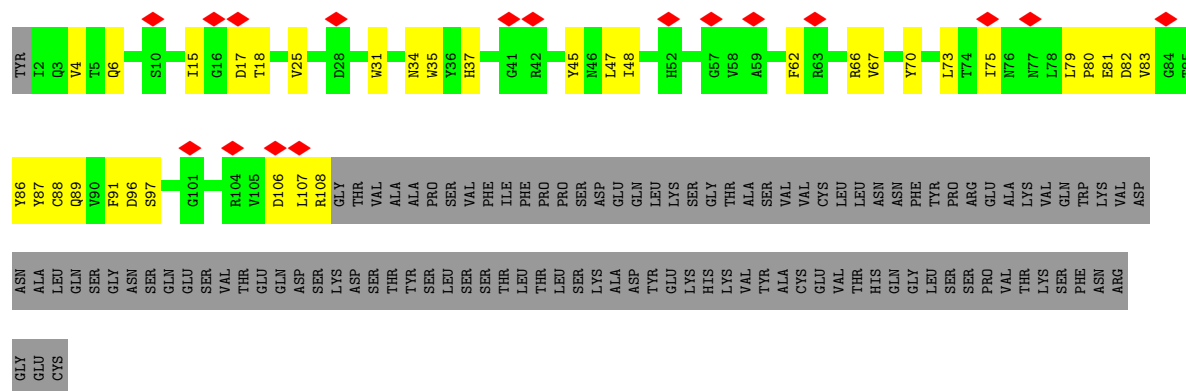
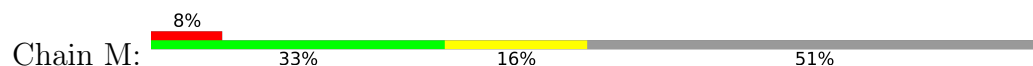
GLN	ALA	Q3	Q6	E10	V11	K12	K13	P14	G15	T16	S17	V18	K19	K23	A24	P25	G26	N27	T28	L29	K30	L34	H35	W36	V37	R38	S39	V40	P41	G42	L45	M48	G49	W50	I51	S52	D55	K56	K57	E61	K64	A65	K66	I69	D70	W71	D72	N76				
Y79	L82	L82C	T83	S84	G85	D86	T87	A88	V89	Y90	Y91	C92	A93	K94	R99	L100E	Y100F	D100G	D100H	D100I	G100J	A100K	L100L	N100M	W100N	A100O	V100P	D100Q	S100R	P100S	Y100T	L100U	S100V	N100W	L100X	E101	F102	Q105	T110	V111	S112	S113	ALA	SER	THR	LYS	GLY	PRO	SER	VAL	PHE	PRO
GLN	ALA	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
CYS	ASP	THR	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	



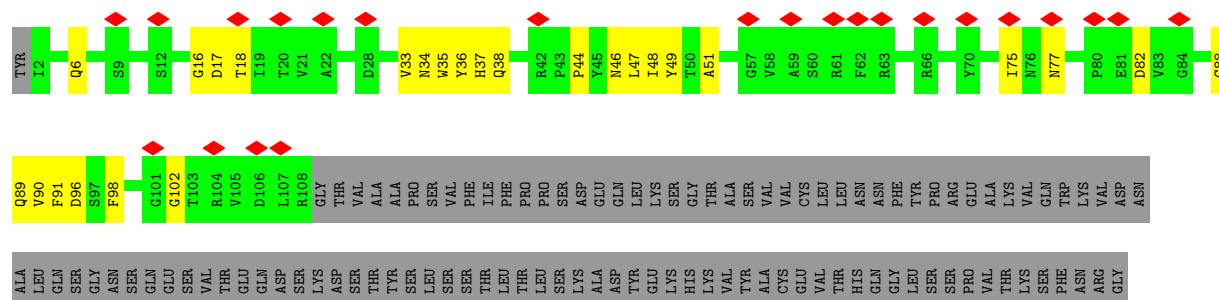
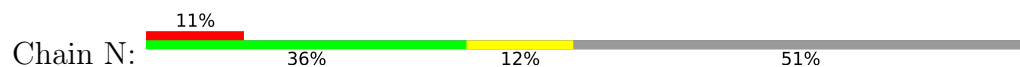
• Molecule 6: 04_A06 Fab Light Chain



• Molecule 6: 04_A06 Fab Light Chain



• Molecule 6: 04_A06 Fab Light Chain



GLU
CYS

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

NAG1
NAG2

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

NAG1
NAG2

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

NAG1
NAG2

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

NAG1
NAG2

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

NAG1
NAG2

- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



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

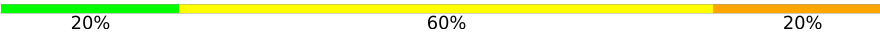


- Molecule 8: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

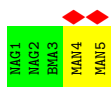


- Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

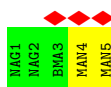
nose

Chain Q: 

• Molecule 9: 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 T: 

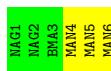
• Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j: 

• Molecule 10: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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: 

• Molecule 11: 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 m: 

• Molecule 12: 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 p: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46972	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.428	Depositor
Minimum map value	-0.240	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	346.112, 346.112, 346.112	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	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: TYS, MAN, NAG, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.22	0/3521	0.32	0/4778
1	C	0.23	0/3521	0.36	0/4778
1	E	0.23	0/3517	0.35	0/4774
2	B	0.21	0/999	0.36	0/1357
2	D	0.19	0/999	0.31	0/1357
2	F	0.20	0/999	0.34	0/1357
3	G	0.18	0/868	0.39	0/1175
4	H	0.23	0/1051	0.37	0/1432
4	I	0.23	0/1051	0.34	0/1432
4	J	0.22	0/1051	0.39	0/1432
5	K	0.18	0/1100	0.34	0/1494
6	L	0.20	0/813	0.47	1/1115 (0.1%)
6	M	0.21	0/813	0.44	0/1115
6	N	0.20	0/813	0.42	0/1115
All	All	0.22	0/21116	0.36	1/28711 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	80	PRO	CA-N-CD	-5.04	104.94	112.00

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	3450	0	3395	99	0
1	C	3450	0	3395	116	0
1	E	3446	0	3384	119	0
2	B	982	0	948	35	0
2	D	982	0	948	32	0
2	F	982	0	948	37	0
3	G	848	0	822	30	0
4	H	1024	0	977	33	0
4	I	1024	0	977	30	0
4	J	1024	0	977	47	0
5	K	1091	0	1054	48	0
6	L	791	0	755	39	0
6	M	791	0	755	32	0
6	N	791	0	755	24	0
7	O	28	0	25	0	0
7	R	28	0	25	1	0
7	S	28	0	25	0	0
7	U	28	0	25	0	0
7	V	28	0	25	0	0
7	W	28	0	25	0	0
7	X	28	0	25	0	0
7	Y	28	0	25	0	0
7	Z	28	0	25	0	0
7	a	28	0	25	0	0
7	c	28	0	25	0	0
7	d	28	0	25	1	0
7	e	28	0	25	1	0
7	f	28	0	25	0	0
7	g	28	0	25	1	0
7	i	28	0	25	1	0
7	o	28	0	25	0	0
7	q	28	0	25	0	0
7	r	28	0	25	0	0
7	s	28	0	25	1	0
7	t	28	0	25	0	0
7	u	28	0	25	0	0
7	v	28	0	25	0	0
7	w	28	0	25	1	0
8	P	39	0	34	0	0
8	h	39	0	34	0	0
8	k	39	0	34	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	l	39	0	34	1	0
8	n	39	0	34	1	0
9	Q	61	0	52	2	0
9	T	61	0	52	0	0
9	j	61	0	52	0	0
10	b	83	0	70	1	0
11	m	72	0	61	0	0
12	p	50	0	43	0	0
13	A	28	0	26	0	0
13	C	42	0	39	0	0
13	E	28	0	26	0	0
All	All	22029	0	21281	658	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 15.

The worst 5 of 658 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)
1:C:124:PRO:HA	1:E:166:ARG:HH12	1.23	1.01
1:C:300:ASN:HD21	1:C:326:ILE:HG23	1.43	0.84
1:A:277:ILE:O	1:A:456:ARG:NH2	2.12	0.83
5:K:13:LYS:HD3	5:K:14:PRO:HD2	1.64	0.80
4:J:2:VAL:N	4:J:102:SER:HG	1.79	0.79

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	430/479 (90%)	405 (94%)	24 (6%)	1 (0%)	43 73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	430/479 (90%)	388 (90%)	41 (10%)	1 (0%)	43	73
1	E	430/479 (90%)	402 (94%)	28 (6%)	0	100	100
2	B	121/153 (79%)	118 (98%)	3 (2%)	0	100	100
2	D	121/153 (79%)	117 (97%)	4 (3%)	0	100	100
2	F	121/153 (79%)	116 (96%)	5 (4%)	0	100	100
3	G	108/219 (49%)	97 (90%)	11 (10%)	0	100	100
4	H	130/245 (53%)	124 (95%)	6 (5%)	0	100	100
4	I	130/245 (53%)	120 (92%)	10 (8%)	0	100	100
4	J	130/245 (53%)	123 (95%)	7 (5%)	0	100	100
5	K	136/253 (54%)	127 (93%)	9 (7%)	0	100	100
6	L	101/211 (48%)	95 (94%)	6 (6%)	0	100	100
6	M	101/211 (48%)	95 (94%)	6 (6%)	0	100	100
6	N	101/211 (48%)	95 (94%)	6 (6%)	0	100	100
All	All	2590/3736 (69%)	2422 (94%)	166 (6%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	388	SER
1	A	449	ILE

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	389/427 (91%)	387 (100%)	2 (0%)	81	81
1	C	389/427 (91%)	388 (100%)	1 (0%)	86	84
1	E	388/427 (91%)	385 (99%)	3 (1%)	73	76
2	B	104/129 (81%)	103 (99%)	1 (1%)	68	74
2	D	104/129 (81%)	102 (98%)	2 (2%)	50	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	104/129 (81%)	103 (99%)	1 (1%)	68	74
3	G	96/194 (50%)	95 (99%)	1 (1%)	68	74
4	H	106/210 (50%)	106 (100%)	0	100	100
4	I	106/210 (50%)	104 (98%)	2 (2%)	50	66
4	J	106/210 (50%)	106 (100%)	0	100	100
5	K	115/215 (54%)	115 (100%)	0	100	100
6	L	85/183 (46%)	85 (100%)	0	100	100
6	M	85/183 (46%)	85 (100%)	0	100	100
6	N	85/183 (46%)	85 (100%)	0	100	100
All	All	2262/3256 (70%)	2249 (99%)	13 (1%)	76	79

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	455	THR
1	E	457	ASP
4	I	101	ASP
3	G	70	ASP
4	I	64	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	315	GLN
3	G	31	ASN
1	E	356	ASN
3	G	90	GLN
1	C	85	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	TYS	K	100(F)	5	15,16,17	1.59	3 (20%)	15,22,24	3.34	5 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	TYS	K	100(F)	5	-	6/10/11/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	K	100(F)	TYS	O2-S	4.25	1.63	1.45
5	K	100(F)	TYS	OH-CZ	-3.37	1.37	1.42
5	K	100(F)	TYS	OH-S	-2.08	1.54	1.58

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	100(F)	TYS	OH-S-O2	-7.34	85.21	107.56
5	K	100(F)	TYS	O2-S-O1	-6.87	85.75	112.24
5	K	100(F)	TYS	O3-S-O2	-6.03	87.47	108.56
5	K	100(F)	TYS	OH-S-O1	4.21	120.39	107.56
5	K	100(F)	TYS	O3-S-O1	2.87	118.61	108.56

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	K	100(F)	TYS	CE1-CZ-OH-S
5	K	100(F)	TYS	CE2-CZ-OH-S
5	K	100(F)	TYS	CZ-OH-S-O2

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Mol	Chain	Res	Type	Atoms
5	K	100(F)	TYS	CZ-OH-S-O3
5	K	100(F)	TYS	CA-CB-CG-CD1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	K	100(F)	TYS	1	0

5.5 Carbohydrates ⓘ

95 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	$\# Z > 2$
7	NAG	O	1	7,1	14,14,15	0.15	0	17,19,21	0.72	0
7	NAG	O	2	7	14,14,15	0.24	0	17,19,21	0.47	0
8	NAG	P	1	8,1	14,14,15	0.37	0	17,19,21	0.46	0
8	NAG	P	2	8	14,14,15	0.20	0	17,19,21	0.54	0
8	BMA	P	3	8	11,11,12	0.56	0	15,15,17	0.75	0
9	NAG	Q	1	9,1	14,14,15	0.33	0	17,19,21	0.42	0
9	NAG	Q	2	9	14,14,15	0.24	0	17,19,21	0.42	0
9	BMA	Q	3	9	11,11,12	0.50	0	15,15,17	0.85	0
9	MAN	Q	4	9	11,11,12	0.66	0	15,15,17	0.96	2 (13%)
9	MAN	Q	5	9	11,11,12	0.67	0	15,15,17	0.94	1 (6%)
7	NAG	R	1	7,1	14,14,15	0.22	0	17,19,21	0.46	0
7	NAG	R	2	7	14,14,15	0.21	0	17,19,21	0.40	0
7	NAG	S	1	7,1	14,14,15	0.23	0	17,19,21	0.48	0
7	NAG	S	2	7	14,14,15	0.26	0	17,19,21	0.37	0
9	NAG	T	1	9,1	14,14,15	0.29	0	17,19,21	0.41	0
9	NAG	T	2	9	14,14,15	0.17	0	17,19,21	0.55	0
9	BMA	T	3	9	11,11,12	0.60	0	15,15,17	0.88	0
9	MAN	T	4	9	11,11,12	0.70	0	15,15,17	0.87	1 (6%)
9	MAN	T	5	9	11,11,12	0.56	0	15,15,17	1.00	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	U	1	7,1	14,14,15	0.25	0	17,19,21	0.68	0
7	NAG	U	2	7	14,14,15	0.64	1 (7%)	17,19,21	0.50	0
7	NAG	V	1	7,1	14,14,15	0.45	0	17,19,21	0.42	0
7	NAG	V	2	7	14,14,15	0.26	0	17,19,21	0.50	0
7	NAG	W	1	7,1	14,14,15	0.30	0	17,19,21	0.43	0
7	NAG	W	2	7	14,14,15	0.28	0	17,19,21	0.41	0
7	NAG	X	1	7,1	14,14,15	0.31	0	17,19,21	0.44	0
7	NAG	X	2	7	14,14,15	0.27	0	17,19,21	0.52	0
7	NAG	Y	1	7,1	14,14,15	0.25	0	17,19,21	0.46	0
7	NAG	Y	2	7	14,14,15	0.24	0	17,19,21	0.46	0
7	NAG	Z	1	7,1	14,14,15	0.18	0	17,19,21	0.59	0
7	NAG	Z	2	7	14,14,15	0.21	0	17,19,21	0.43	0
7	NAG	a	1	7,1	14,14,15	0.22	0	17,19,21	0.44	0
7	NAG	a	2	7	14,14,15	0.26	0	17,19,21	0.50	0
10	NAG	b	1	1,10	14,14,15	0.23	0	17,19,21	0.46	0
10	NAG	b	2	10	14,14,15	0.25	0	17,19,21	0.54	0
10	BMA	b	3	10	11,11,12	0.46	0	15,15,17	0.70	0
10	MAN	b	4	10	11,11,12	0.70	0	15,15,17	0.97	1 (6%)
10	MAN	b	5	10	11,11,12	0.62	0	15,15,17	0.94	1 (6%)
10	MAN	b	6	10	11,11,12	0.61	0	15,15,17	0.85	1 (6%)
10	MAN	b	7	10	11,11,12	0.61	0	15,15,17	0.89	1 (6%)
7	NAG	c	1	7,1	14,14,15	0.21	0	17,19,21	0.37	0
7	NAG	c	2	7	14,14,15	0.19	0	17,19,21	0.45	0
7	NAG	d	1	7,1	14,14,15	0.69	1 (7%)	17,19,21	0.69	0
7	NAG	d	2	7	14,14,15	0.23	0	17,19,21	0.59	0
7	NAG	e	1	7,1	14,14,15	0.20	0	17,19,21	0.43	0
7	NAG	e	2	7	14,14,15	0.18	0	17,19,21	0.47	0
7	NAG	f	1	7,1	14,14,15	0.40	0	17,19,21	0.52	0
7	NAG	f	2	7	14,14,15	0.27	0	17,19,21	0.41	0
7	NAG	g	1	7,1	14,14,15	0.31	0	17,19,21	0.46	0
7	NAG	g	2	7	14,14,15	0.41	0	17,19,21	1.30	2 (11%)
8	NAG	h	1	8,1	14,14,15	0.95	1 (7%)	17,19,21	0.80	0
8	NAG	h	2	8	14,14,15	0.22	0	17,19,21	0.60	0
8	BMA	h	3	8	11,11,12	0.51	0	15,15,17	0.68	0
7	NAG	i	1	7,1	14,14,15	0.27	0	17,19,21	0.49	0
7	NAG	i	2	7	14,14,15	0.17	0	17,19,21	0.53	0
9	NAG	j	1	9,1	14,14,15	0.26	0	17,19,21	0.43	0
9	NAG	j	2	9	14,14,15	0.25	0	17,19,21	0.43	0
9	BMA	j	3	9	11,11,12	0.83	0	15,15,17	0.89	0
9	MAN	j	4	9	11,11,12	0.52	0	15,15,17	1.07	2 (13%)
9	MAN	j	5	9	11,11,12	0.65	0	15,15,17	0.92	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	k	1	8,1	14,14,15	0.25	0	17,19,21	0.49	0
8	NAG	k	2	8	14,14,15	0.24	0	17,19,21	0.47	0
8	BMA	k	3	8	11,11,12	0.57	0	15,15,17	0.94	0
8	NAG	l	1	8,1	14,14,15	0.50	0	17,19,21	0.55	0
8	NAG	l	2	8	14,14,15	0.42	0	17,19,21	0.47	0
8	BMA	l	3	8	11,11,12	0.55	0	15,15,17	0.78	0
11	NAG	m	1	1,11	14,14,15	0.37	0	17,19,21	0.51	0
11	NAG	m	2	11	14,14,15	0.20	0	17,19,21	0.55	0
11	BMA	m	3	11	11,11,12	0.63	0	15,15,17	0.95	0
11	MAN	m	4	11	11,11,12	0.64	0	15,15,17	1.02	1 (6%)
11	MAN	m	5	11	11,11,12	0.87	0	15,15,17	0.97	1 (6%)
11	MAN	m	6	11	11,11,12	0.52	0	15,15,17	0.98	2 (13%)
8	NAG	n	1	8,1	14,14,15	0.21	0	17,19,21	0.54	0
8	NAG	n	2	8	14,14,15	0.24	0	17,19,21	0.36	0
8	BMA	n	3	8	11,11,12	0.55	0	15,15,17	0.83	0
7	NAG	o	1	7,1	14,14,15	0.21	0	17,19,21	0.46	0
7	NAG	o	2	7	14,14,15	0.19	0	17,19,21	0.46	0
12	NAG	p	1	12,1	14,14,15	0.38	0	17,19,21	0.45	0
12	NAG	p	2	12	14,14,15	0.32	0	17,19,21	0.54	0
12	BMA	p	3	12	11,11,12	0.55	0	15,15,17	0.80	0
12	MAN	p	4	12	11,11,12	0.65	0	15,15,17	0.98	2 (13%)
7	NAG	q	1	7,1	14,14,15	0.47	0	17,19,21	0.59	0
7	NAG	q	2	7	14,14,15	0.27	0	17,19,21	0.45	0
7	NAG	r	1	7,1	14,14,15	0.28	0	17,19,21	0.53	0
7	NAG	r	2	7	14,14,15	0.20	0	17,19,21	0.44	0
7	NAG	s	1	7,1	14,14,15	0.42	0	17,19,21	1.36	2 (11%)
7	NAG	s	2	7	14,14,15	0.25	0	17,19,21	0.50	0
7	NAG	t	1	7,1	14,14,15	0.24	0	17,19,21	0.43	0
7	NAG	t	2	7	14,14,15	0.19	0	17,19,21	0.56	0
7	NAG	u	1	7,1	14,14,15	0.31	0	17,19,21	0.43	0
7	NAG	u	2	7	14,14,15	0.16	0	17,19,21	0.48	0
7	NAG	v	1	7,1	14,14,15	0.23	0	17,19,21	0.56	0
7	NAG	v	2	7	14,14,15	0.18	0	17,19,21	0.43	0
7	NAG	w	1	7,1	14,14,15	0.37	0	17,19,21	1.39	2 (11%)
7	NAG	w	2	7	14,14,15	0.21	0	17,19,21	0.40	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
7	NAG	O	1	7,1	-	4/6/23/26	0/1/1/1
7	NAG	O	2	7	-	2/6/23/26	0/1/1/1
8	NAG	P	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	P	2	8	-	3/6/23/26	0/1/1/1
8	BMA	P	3	8	-	1/2/19/22	0/1/1/1
9	NAG	Q	1	9,1	-	2/6/23/26	0/1/1/1
9	NAG	Q	2	9	-	2/6/23/26	0/1/1/1
9	BMA	Q	3	9	-	2/2/19/22	0/1/1/1
9	MAN	Q	4	9	-	0/2/19/22	0/1/1/1
9	MAN	Q	5	9	-	0/2/19/22	0/1/1/1
7	NAG	R	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	R	2	7	-	1/6/23/26	0/1/1/1
7	NAG	S	1	7,1	-	1/6/23/26	0/1/1/1
7	NAG	S	2	7	-	2/6/23/26	0/1/1/1
9	NAG	T	1	9,1	-	2/6/23/26	0/1/1/1
9	NAG	T	2	9	-	4/6/23/26	0/1/1/1
9	BMA	T	3	9	-	0/2/19/22	0/1/1/1
9	MAN	T	4	9	-	0/2/19/22	0/1/1/1
9	MAN	T	5	9	-	0/2/19/22	0/1/1/1
7	NAG	U	1	7,1	-	4/6/23/26	0/1/1/1
7	NAG	U	2	7	-	1/6/23/26	0/1/1/1
7	NAG	V	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	V	2	7	-	2/6/23/26	0/1/1/1
7	NAG	W	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	W	2	7	-	3/6/23/26	0/1/1/1
7	NAG	X	1	7,1	-	1/6/23/26	0/1/1/1
7	NAG	X	2	7	-	4/6/23/26	0/1/1/1
7	NAG	Y	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	Y	2	7	-	2/6/23/26	0/1/1/1
7	NAG	Z	1	7,1	-	3/6/23/26	0/1/1/1
7	NAG	Z	2	7	-	2/6/23/26	0/1/1/1
7	NAG	a	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	a	2	7	-	2/6/23/26	0/1/1/1
10	NAG	b	1	1,10	-	4/6/23/26	0/1/1/1
10	NAG	b	2	10	-	2/6/23/26	0/1/1/1
10	BMA	b	3	10	-	2/2/19/22	0/1/1/1
10	MAN	b	4	10	-	0/2/19/22	0/1/1/1
10	MAN	b	5	10	-	0/2/19/22	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	o	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	o	2	7	-	0/6/23/26	0/1/1/1
12	NAG	p	1	12,1	-	2/6/23/26	0/1/1/1
12	NAG	p	2	12	-	4/6/23/26	0/1/1/1
12	BMA	p	3	12	-	0/2/19/22	0/1/1/1
12	MAN	p	4	12	-	1/2/19/22	0/1/1/1
7	NAG	q	1	7,1	-	3/6/23/26	0/1/1/1
7	NAG	q	2	7	-	2/6/23/26	0/1/1/1
7	NAG	r	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	r	2	7	-	2/6/23/26	0/1/1/1
7	NAG	s	1	7,1	-	4/6/23/26	0/1/1/1
7	NAG	s	2	7	-	4/6/23/26	0/1/1/1
7	NAG	t	1	7,1	-	2/6/23/26	0/1/1/1
7	NAG	t	2	7	-	4/6/23/26	0/1/1/1
7	NAG	u	1	7,1	-	3/6/23/26	0/1/1/1
7	NAG	u	2	7	-	2/6/23/26	0/1/1/1
7	NAG	v	1	7,1	-	3/6/23/26	0/1/1/1
7	NAG	v	2	7	-	0/6/23/26	0/1/1/1
7	NAG	w	1	7,1	-	5/6/23/26	0/1/1/1
7	NAG	w	2	7	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	h	1	NAG	O5-C1	-3.28	1.38	1.43
7	d	1	NAG	O5-C1	-2.33	1.39	1.43
7	U	2	NAG	C1-C2	2.02	1.55	1.52

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	s	1	NAG	C2-N2-C7	4.60	129.06	122.90
7	w	1	NAG	C2-N2-C7	4.55	129.00	122.90
7	g	2	NAG	C2-N2-C7	4.54	128.98	122.90
9	j	4	MAN	C1-O5-C5	3.02	116.24	112.19
10	b	4	MAN	O2-C2-C3	-2.62	104.72	110.15

There are no chirality outliers.

5 of 170 torsion outliers are listed below:

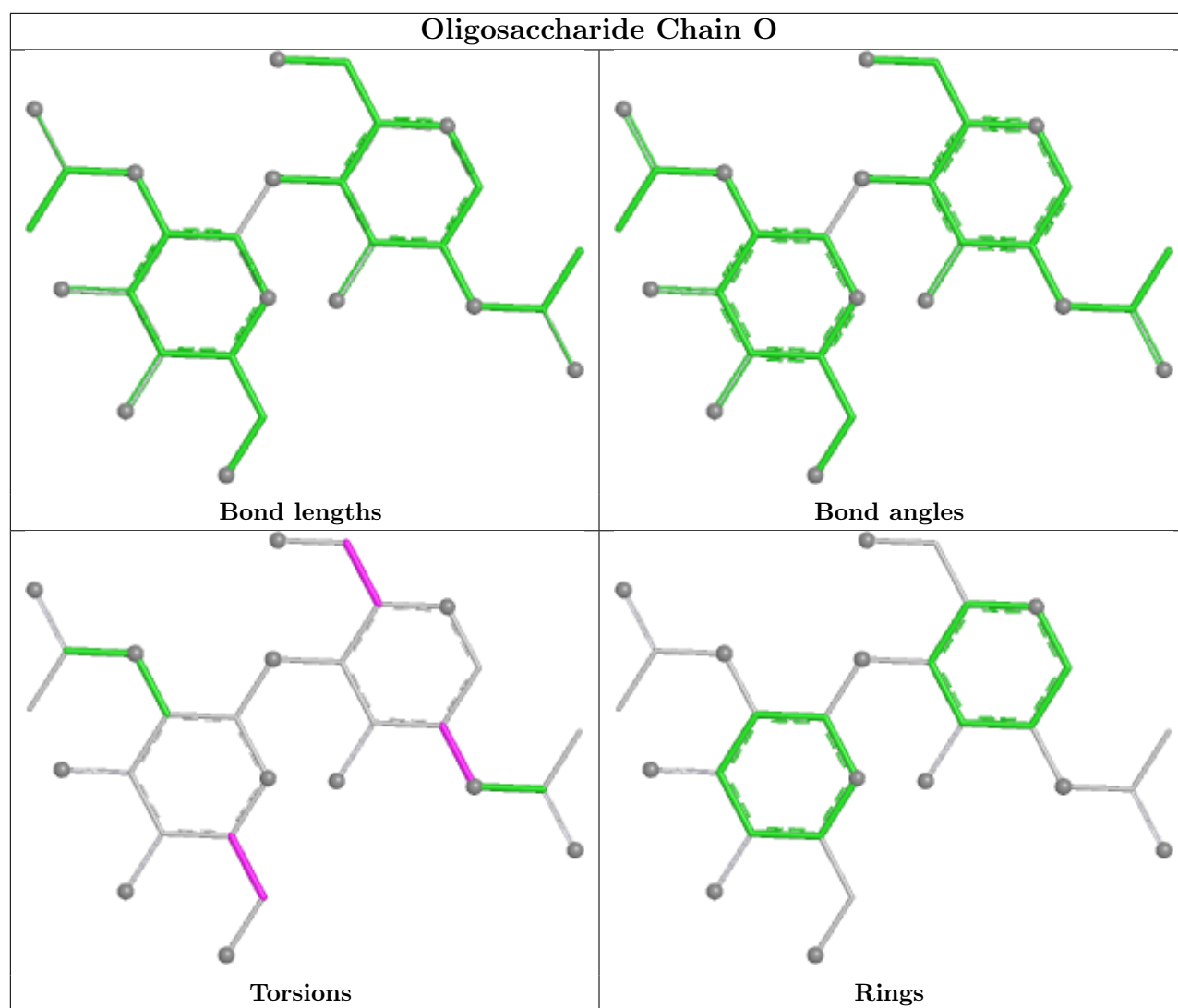
Mol	Chain	Res	Type	Atoms
7	d	2	NAG	C1-C2-N2-C7
12	p	2	NAG	C4-C5-C6-O6
7	S	2	NAG	O5-C5-C6-O6
7	U	1	NAG	O5-C5-C6-O6
7	c	2	NAG	O5-C5-C6-O6

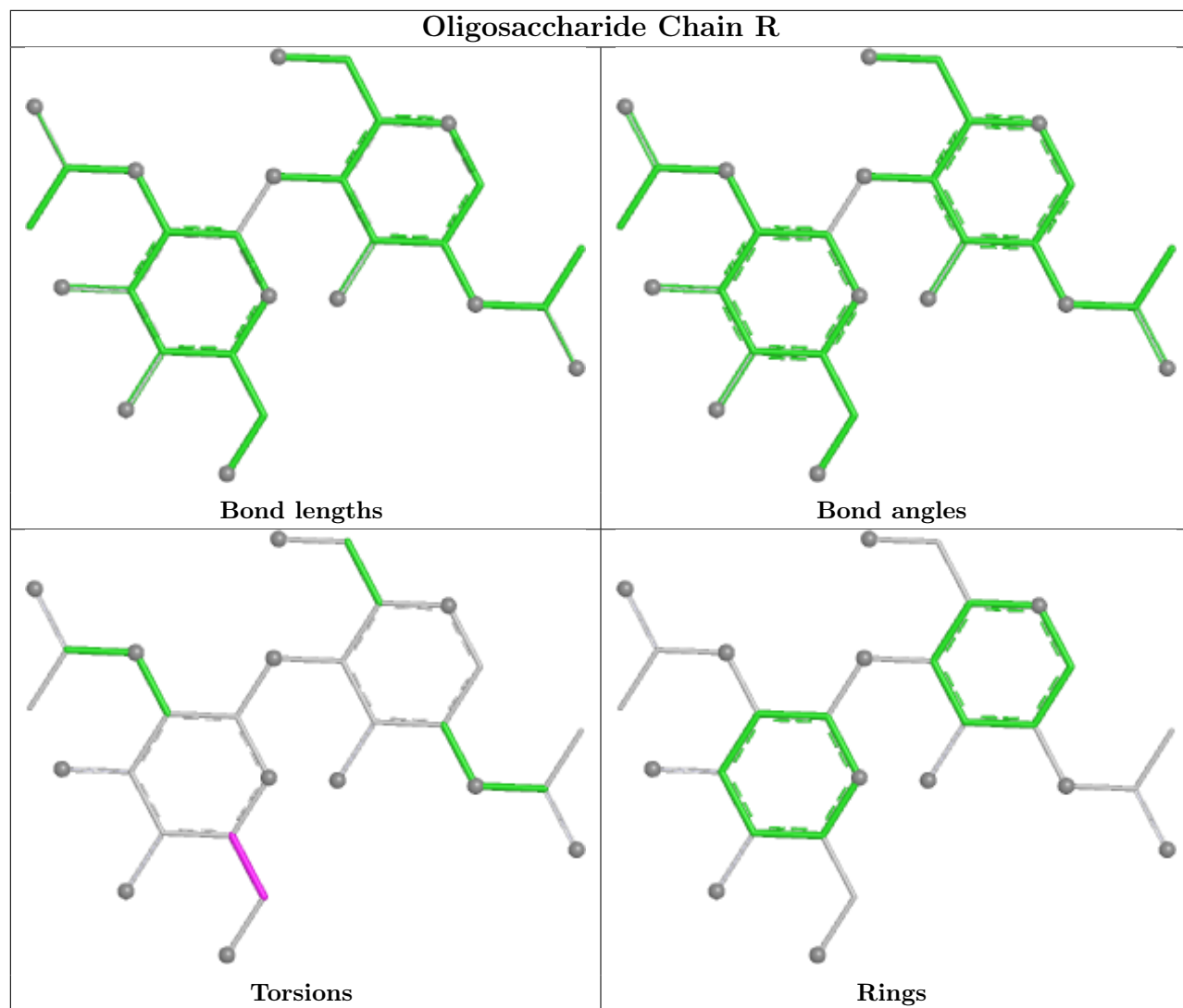
There are no ring outliers.

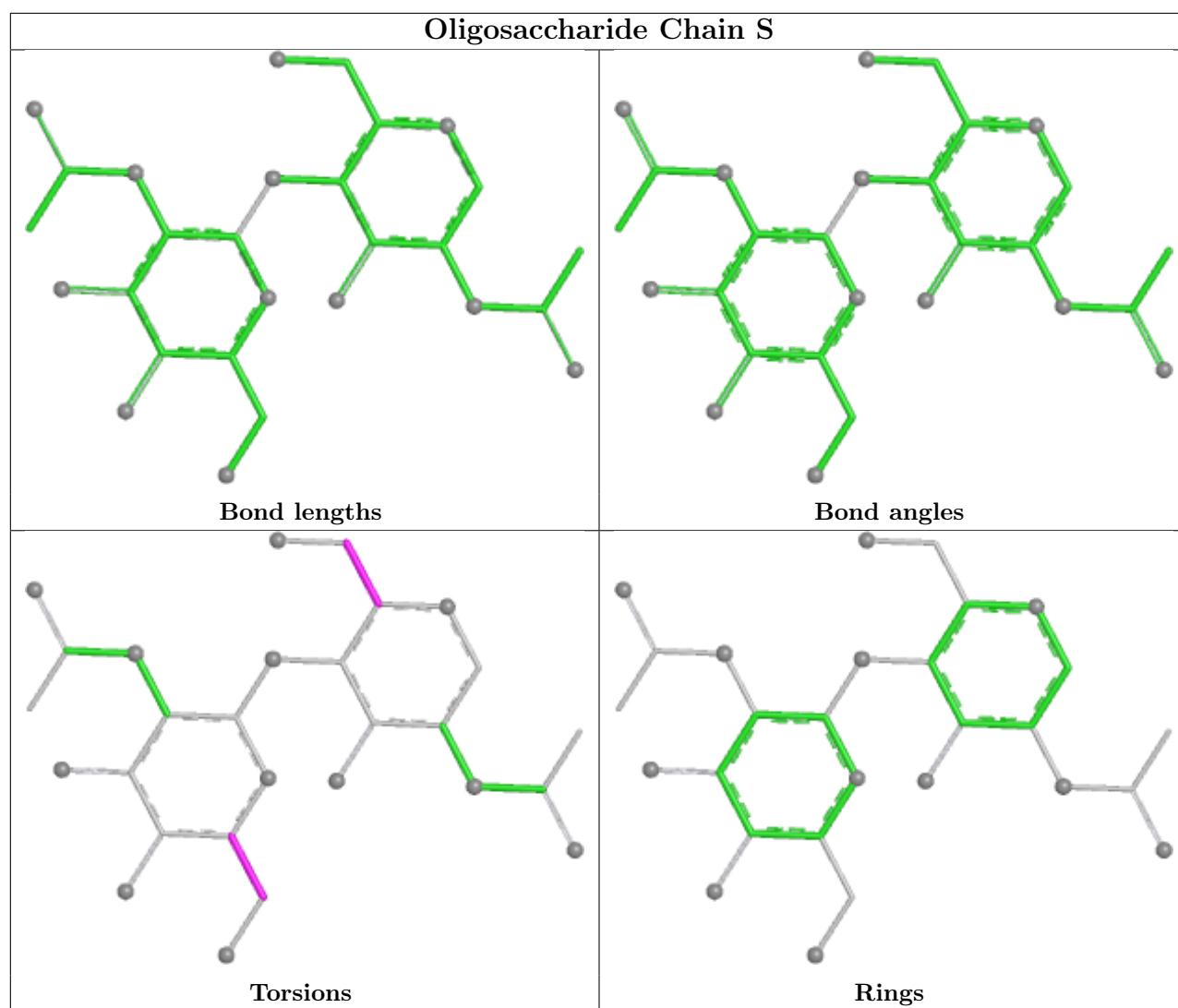
15 monomers are involved in 14 short contacts:

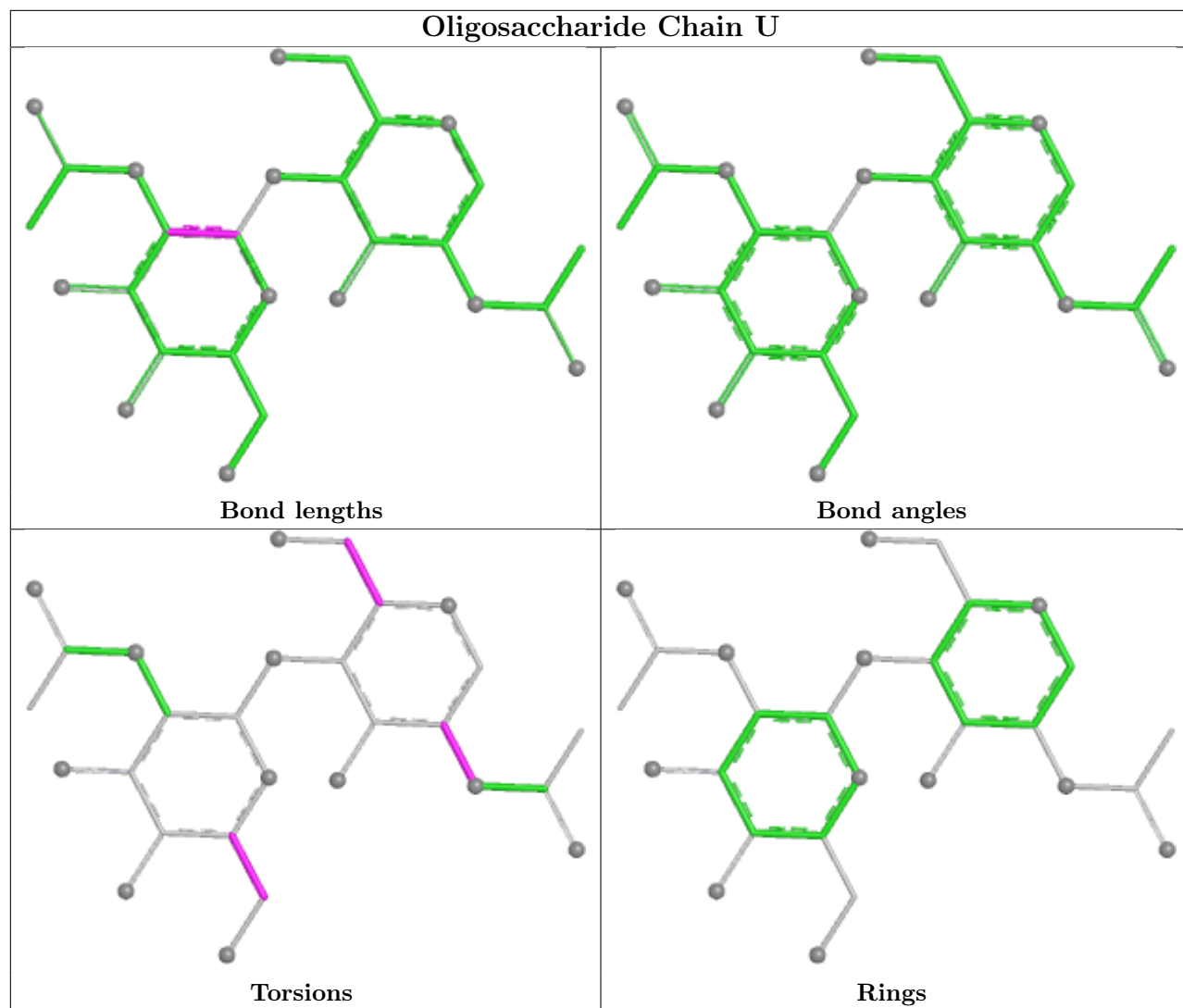
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	d	1	NAG	1	0
7	d	2	NAG	1	0
9	Q	5	MAN	1	0
9	Q	1	NAG	1	0
8	l	2	NAG	1	0
7	e	1	NAG	1	0
7	g	2	NAG	1	0
7	s	1	NAG	1	0
7	R	1	NAG	1	0
8	k	3	BMA	2	0
9	Q	3	BMA	1	0
8	n	1	NAG	1	0
10	b	2	NAG	1	0
7	i	1	NAG	1	0
7	w	1	NAG	1	0

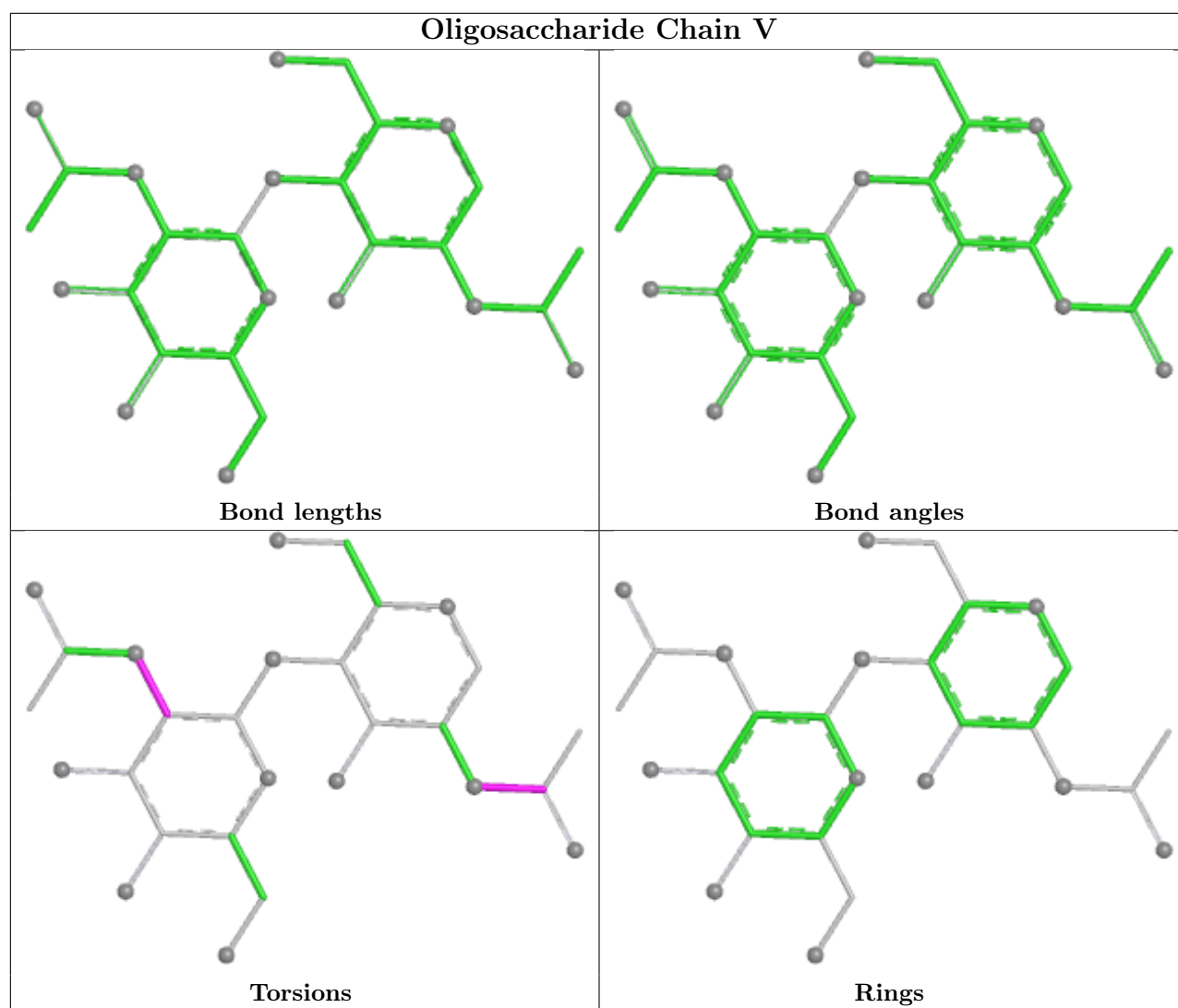
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

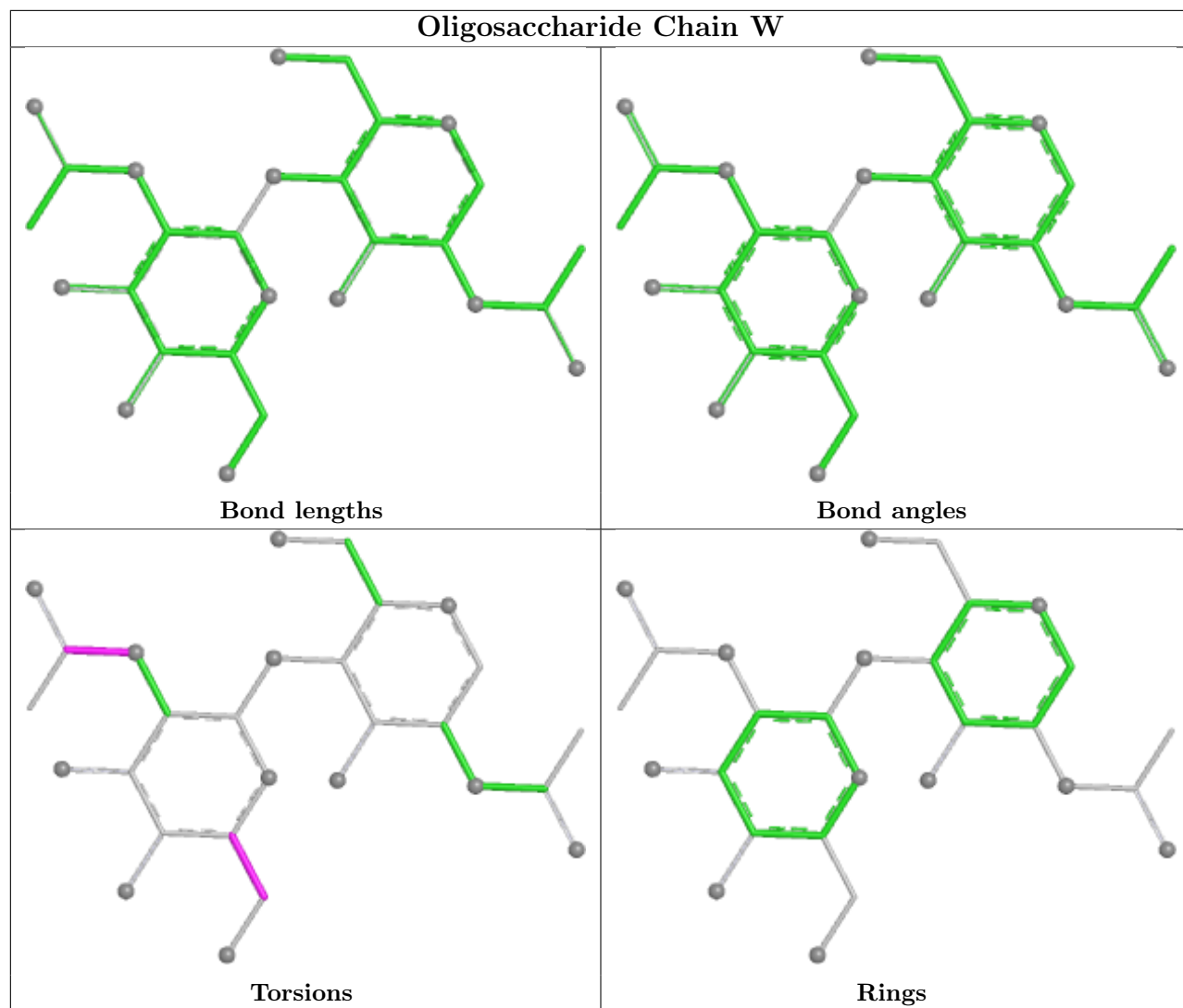


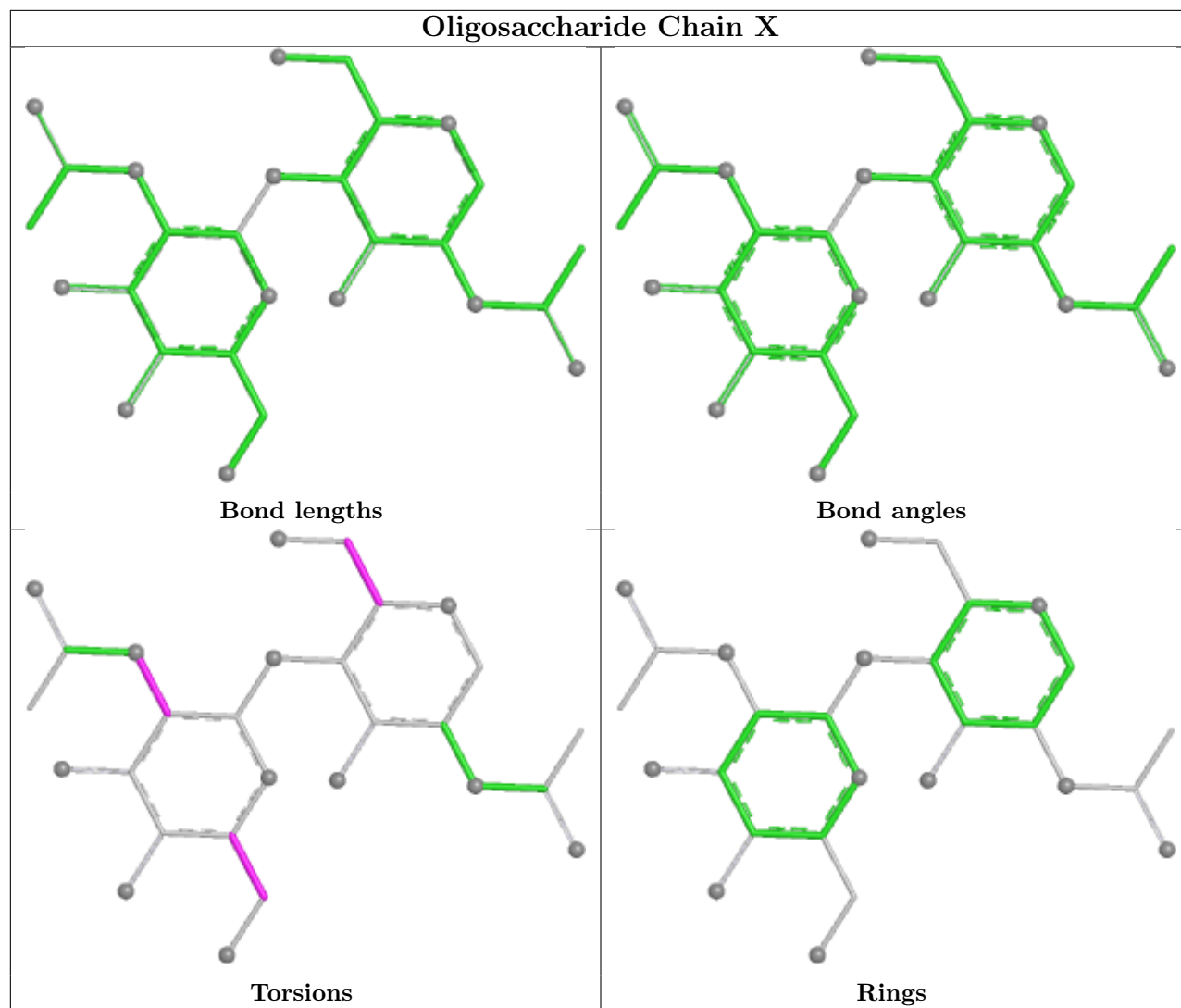


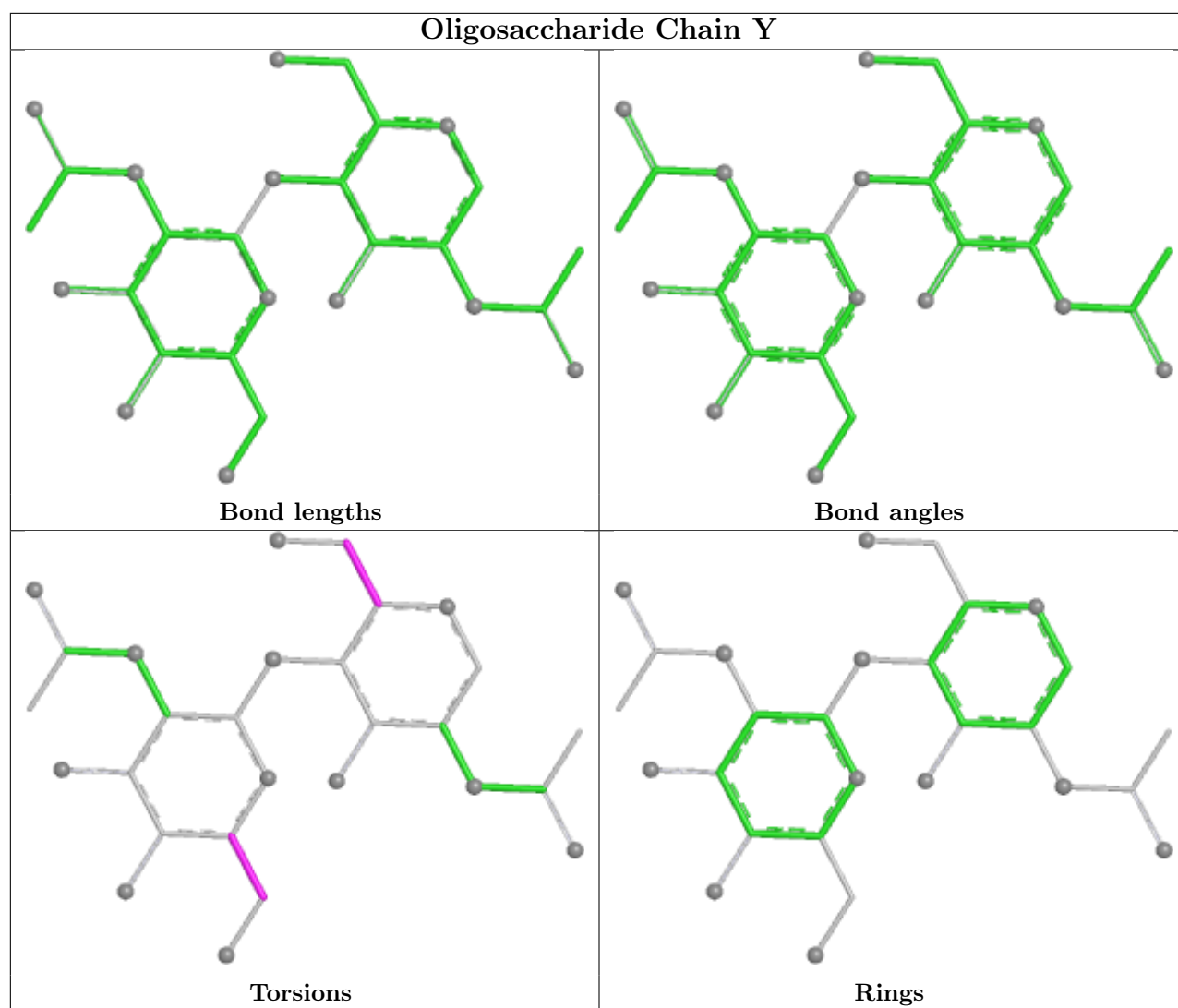


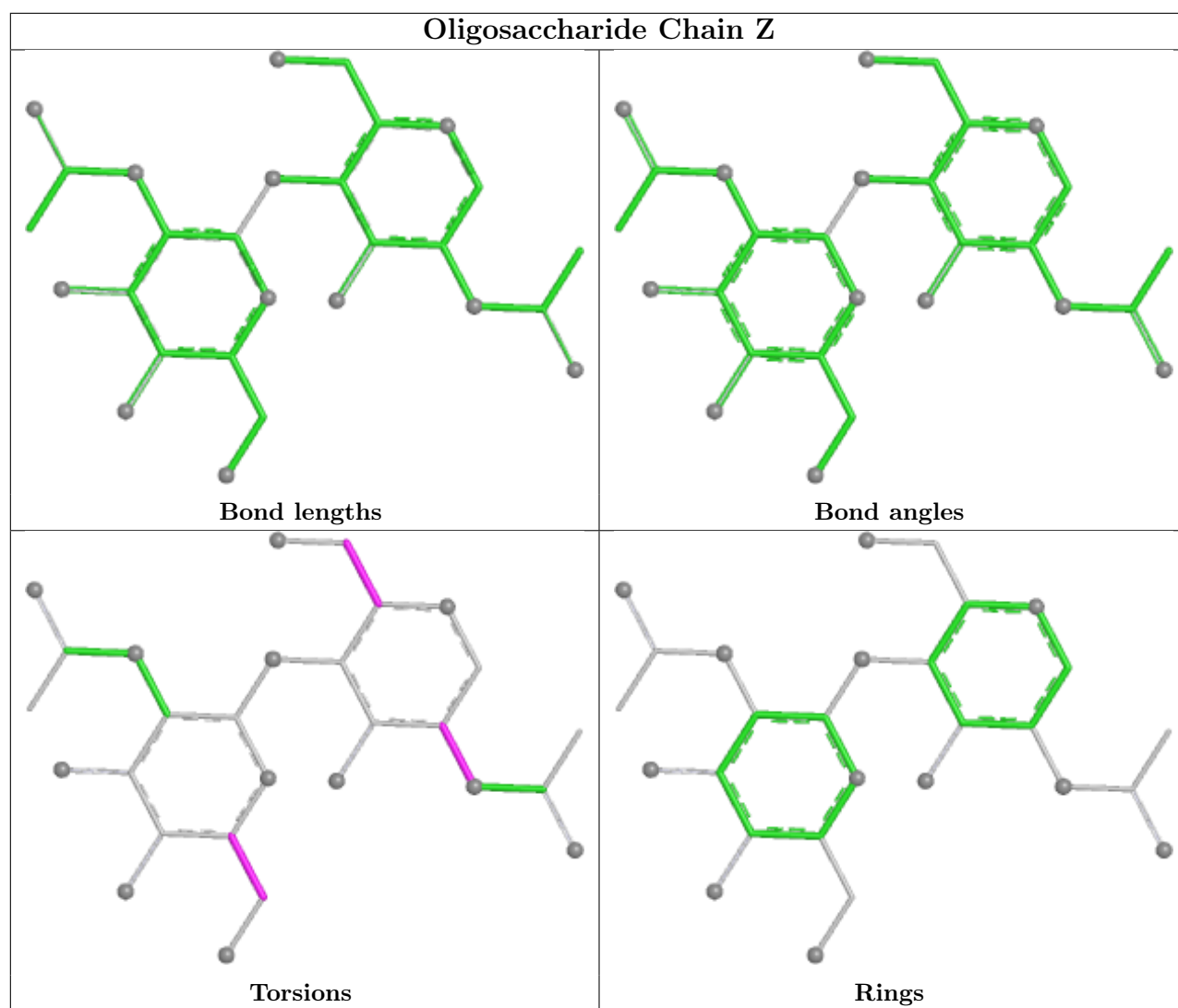


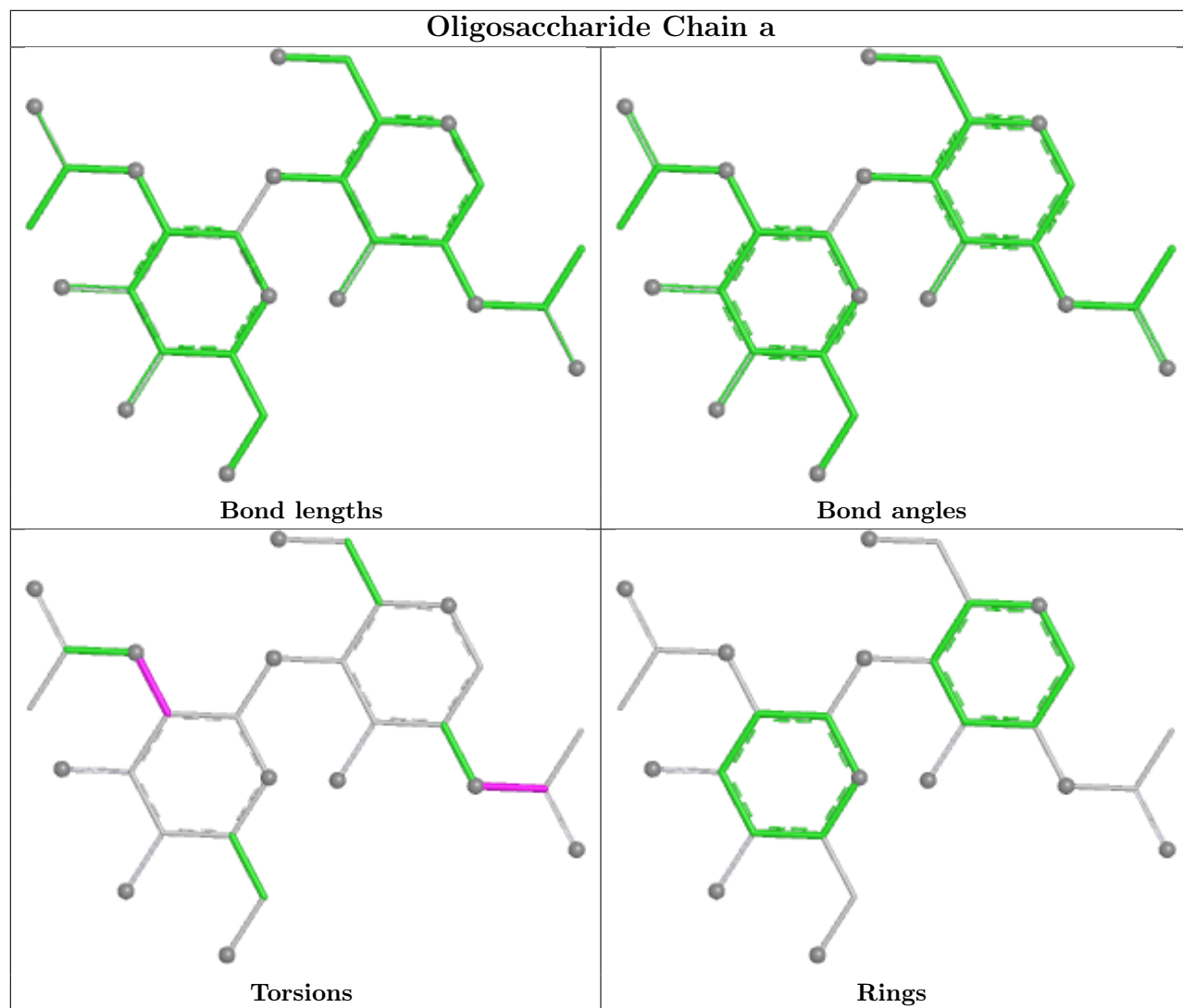


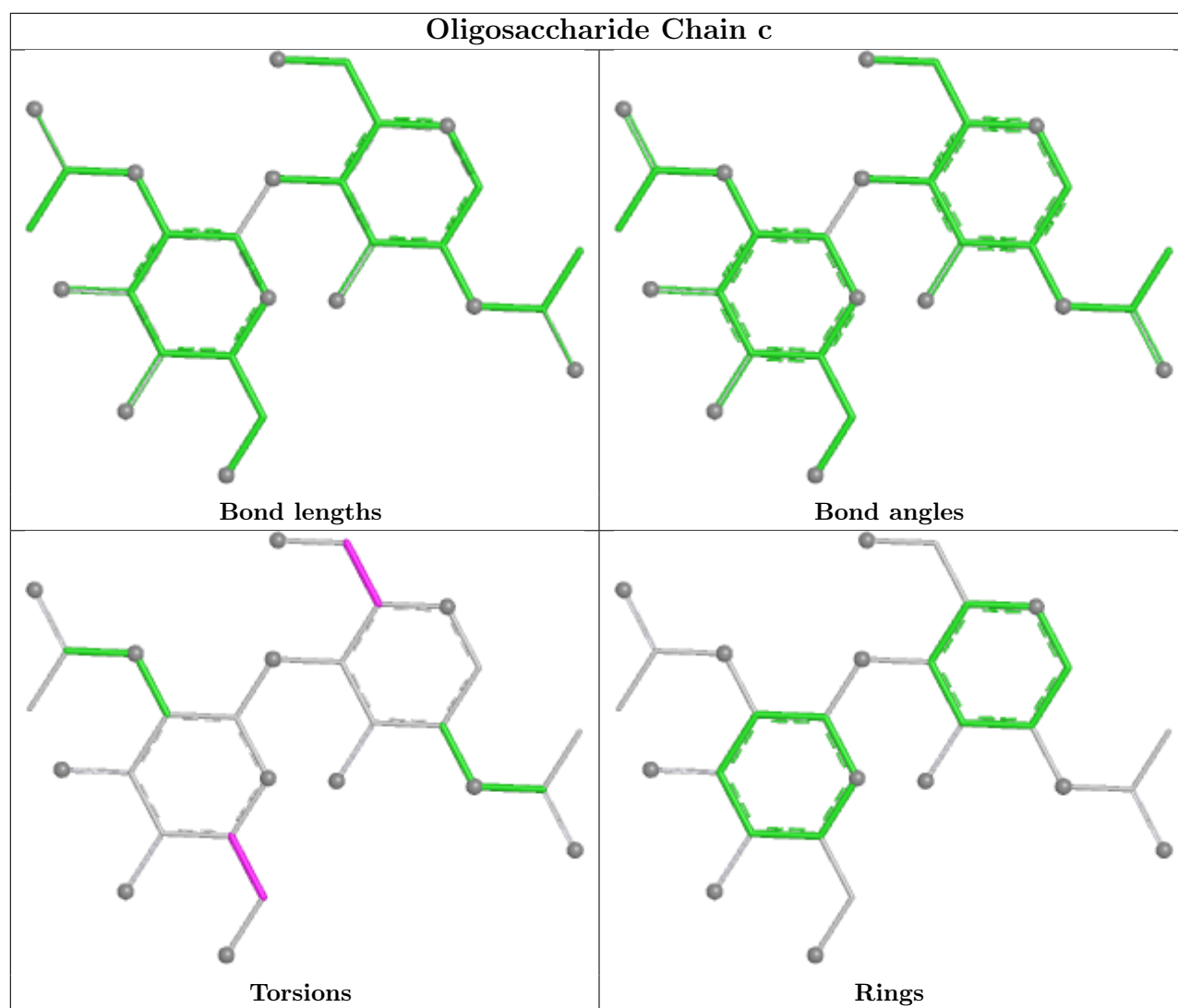


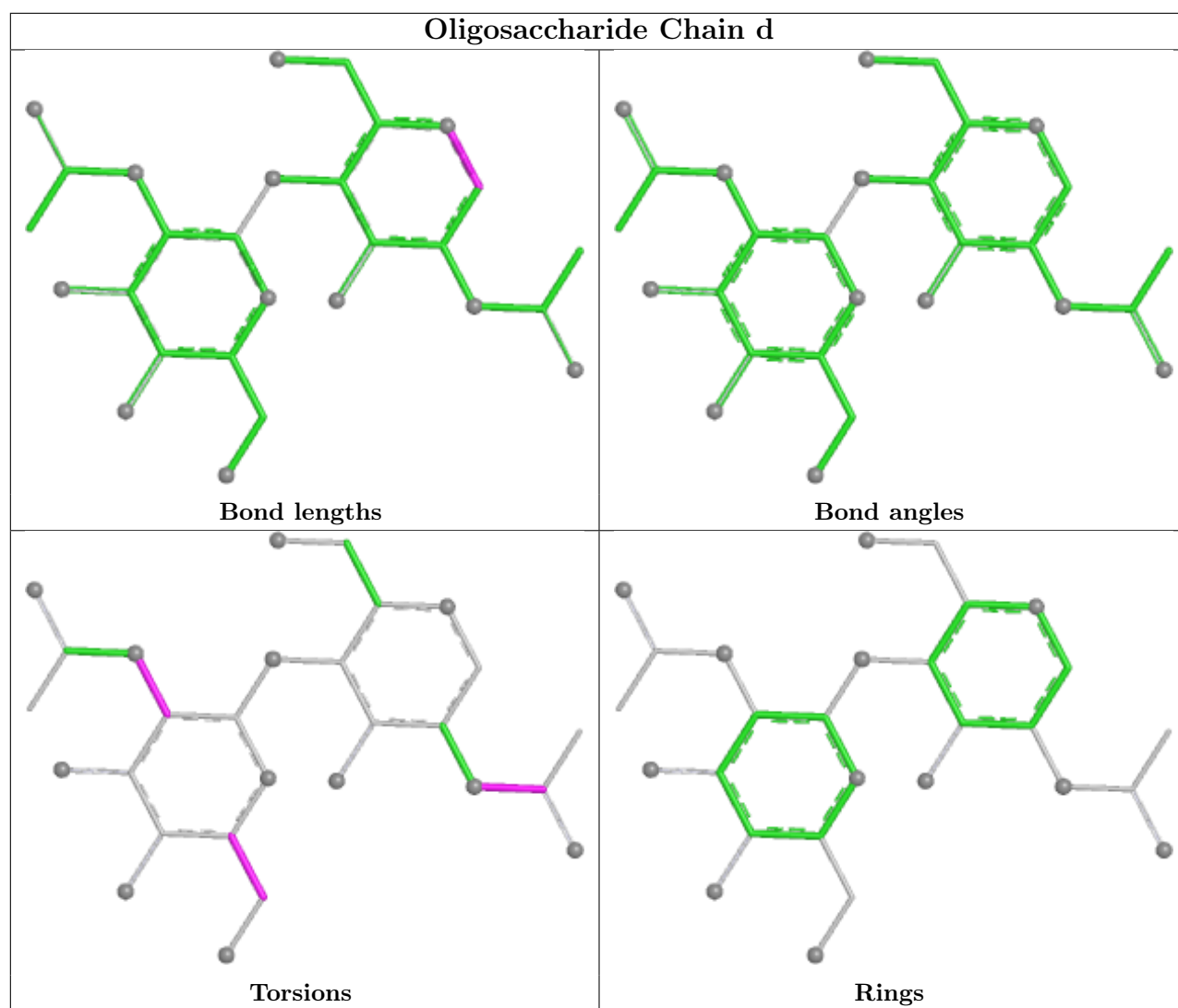


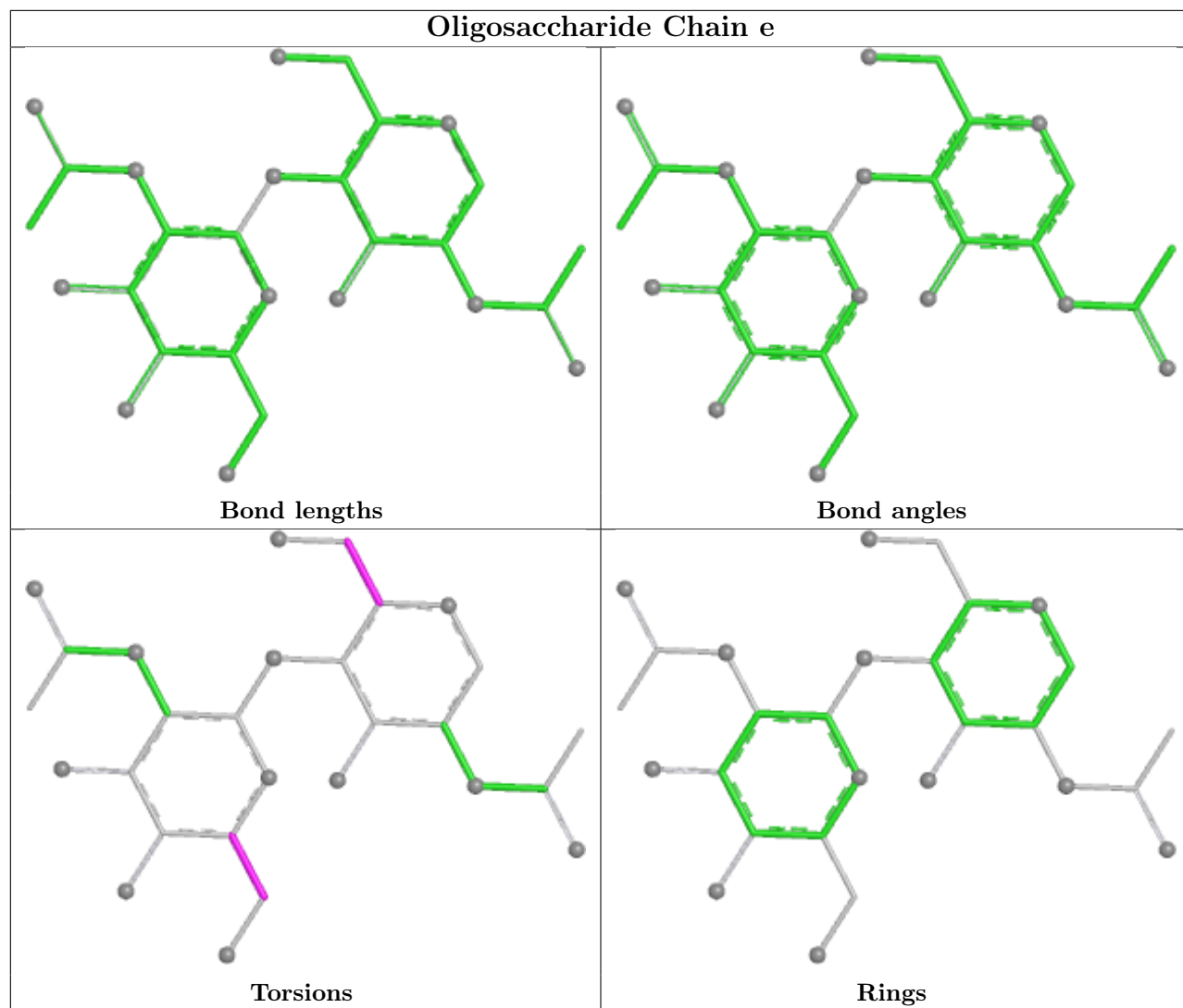


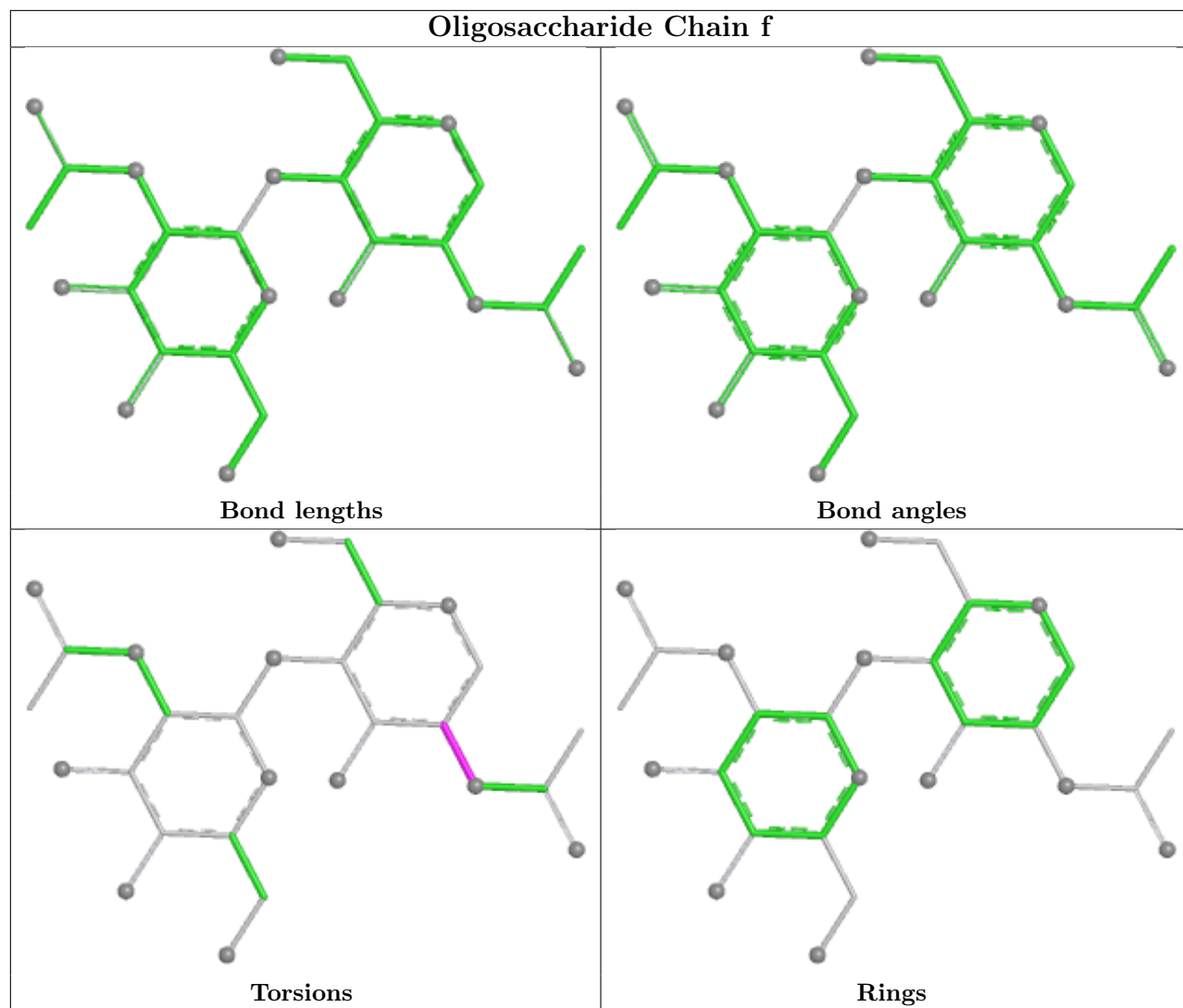


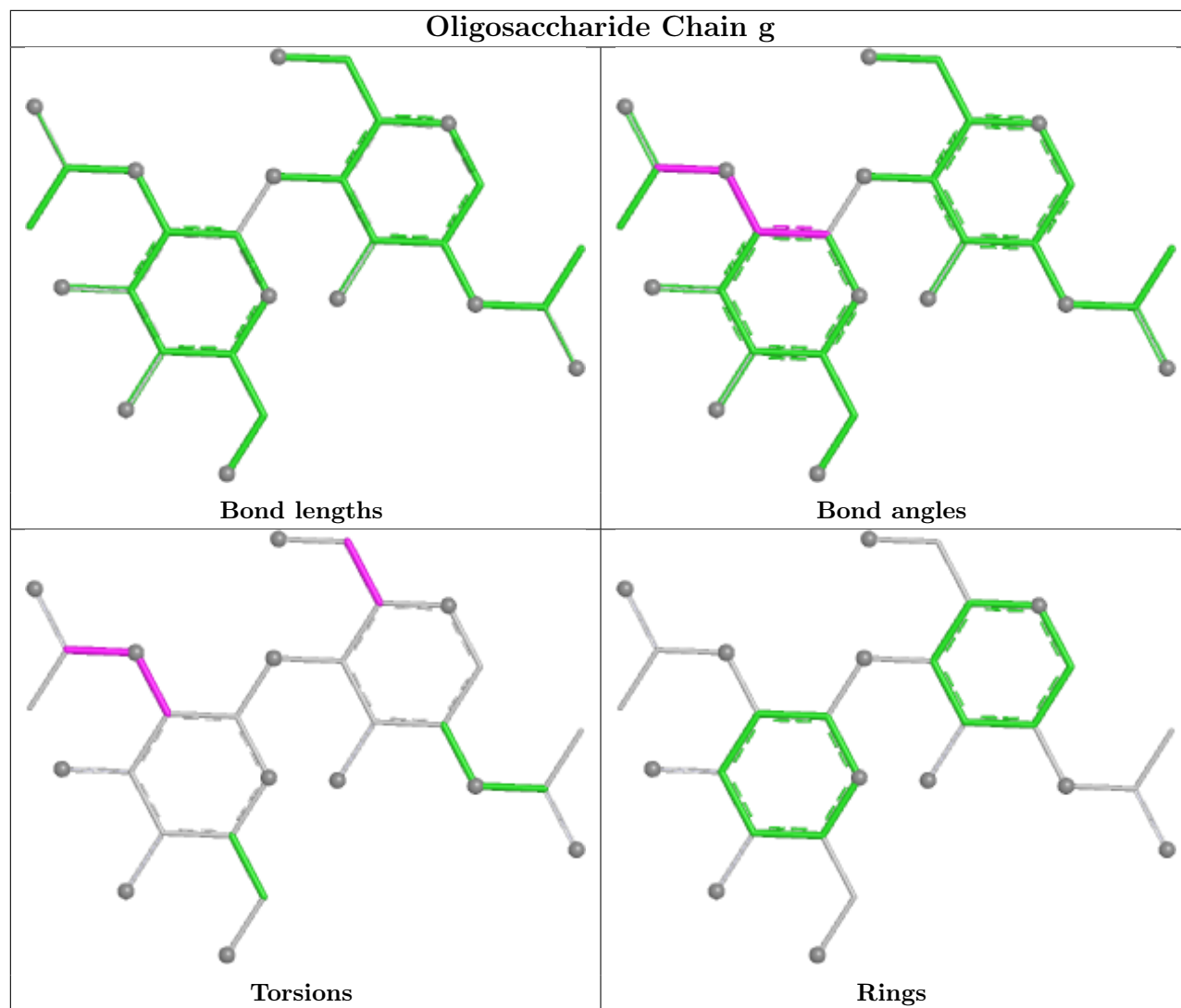


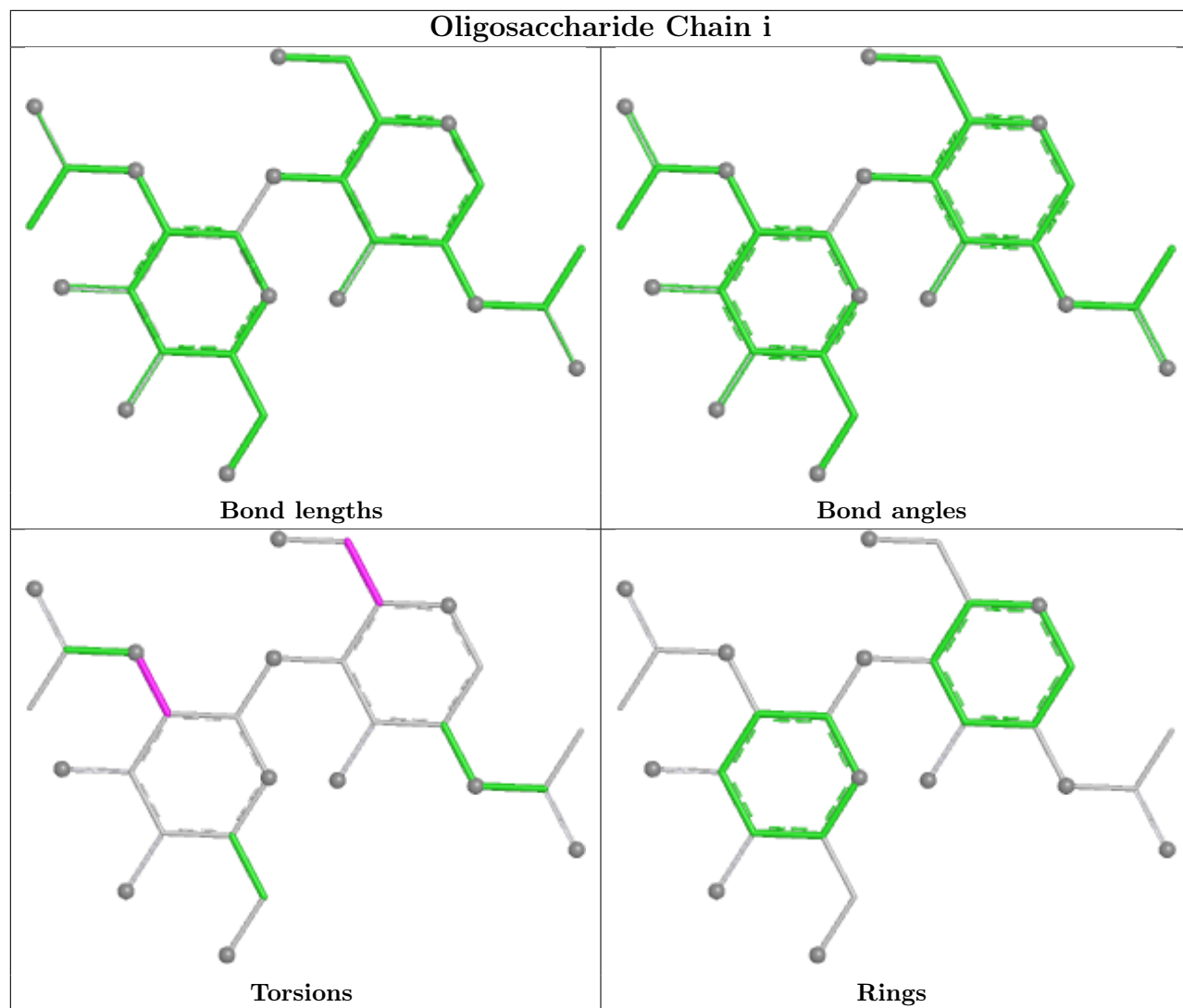


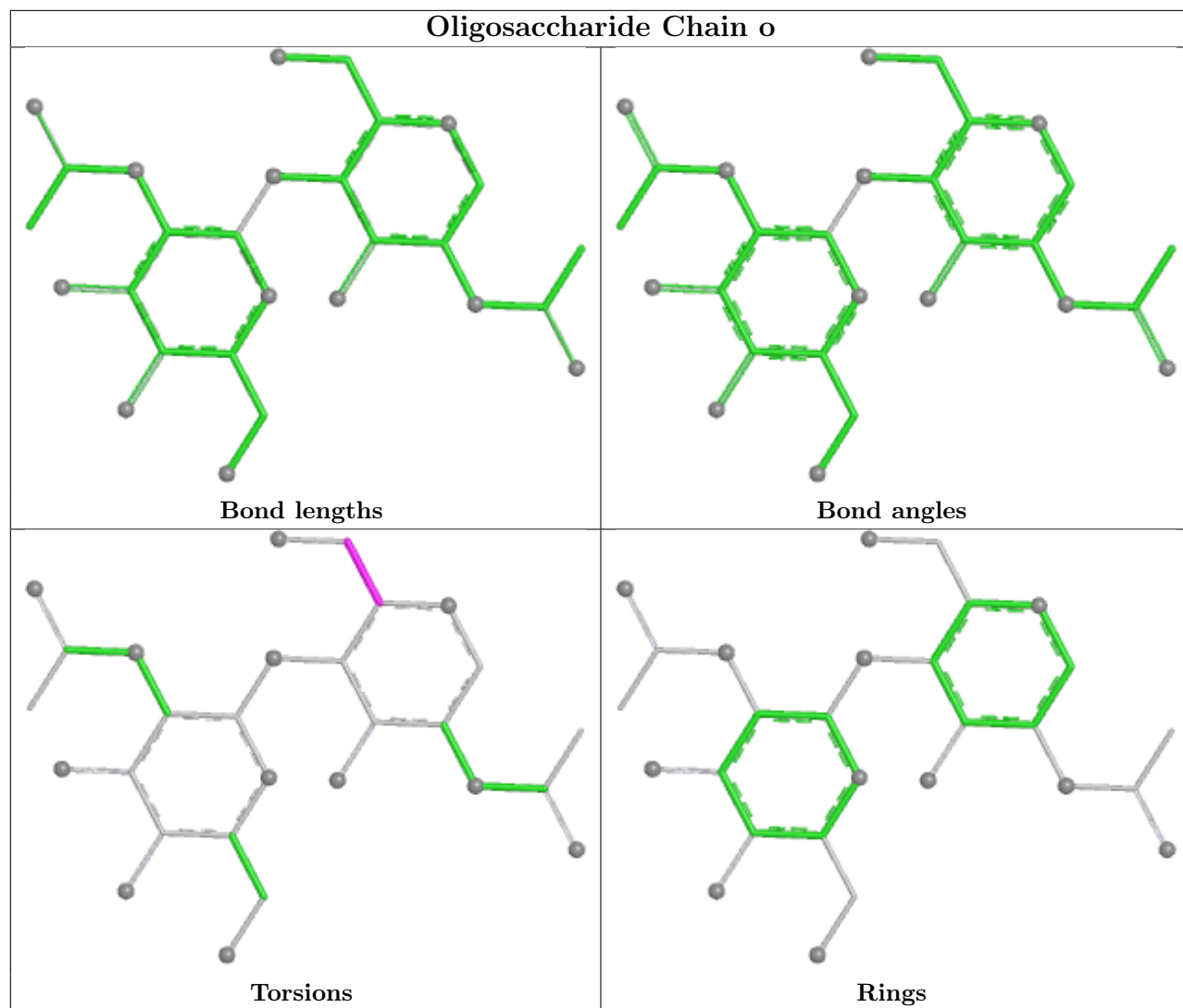


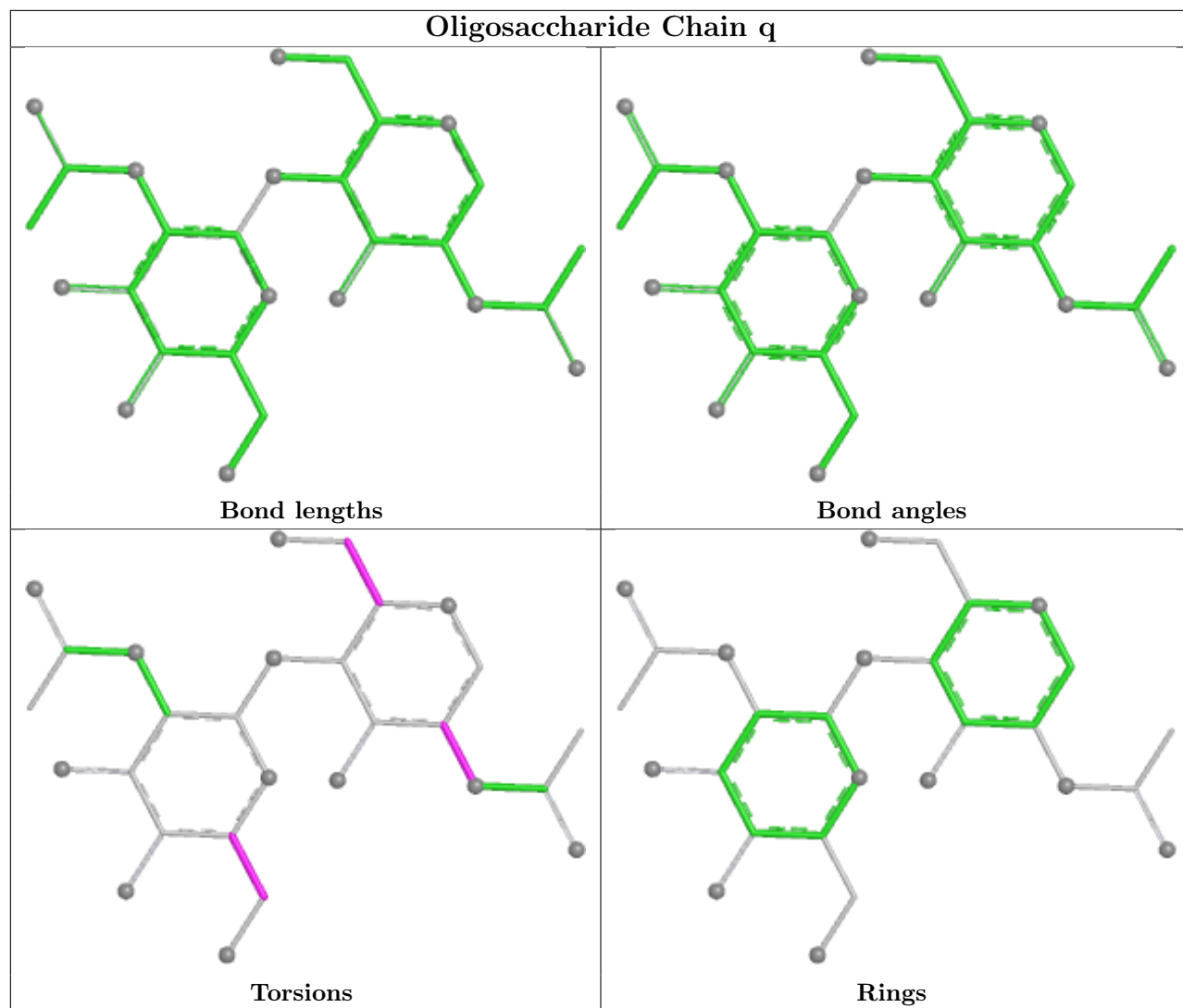


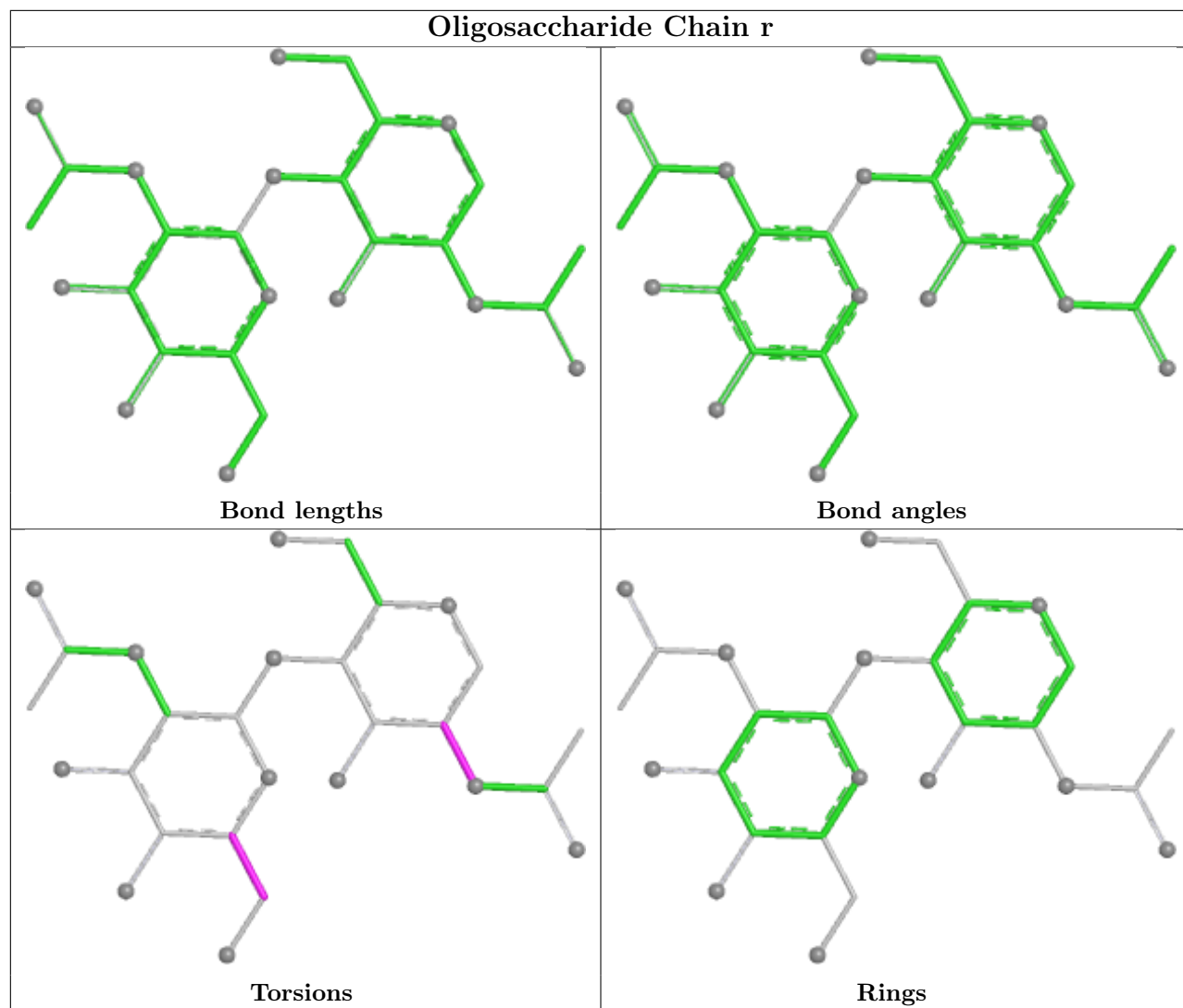


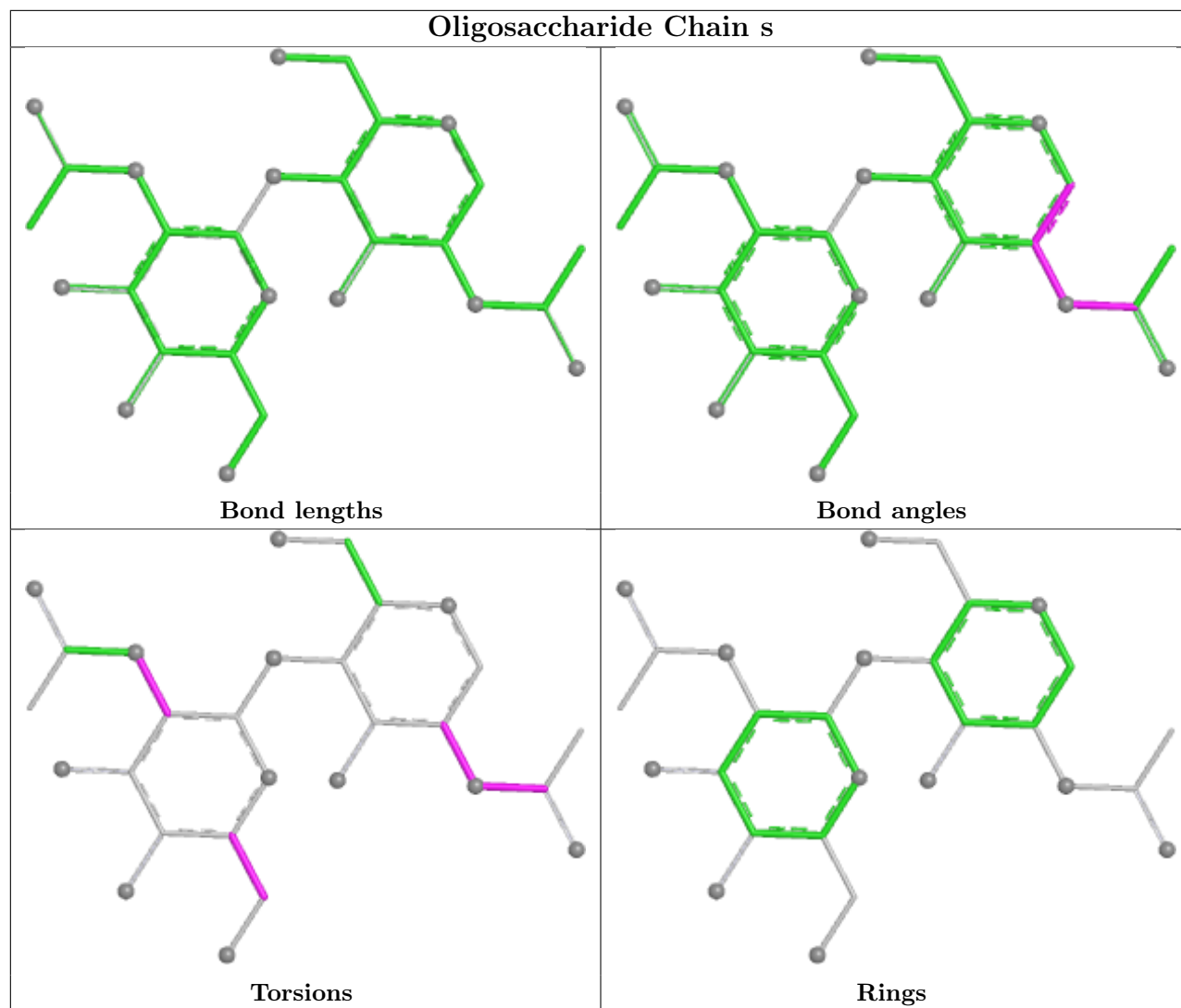


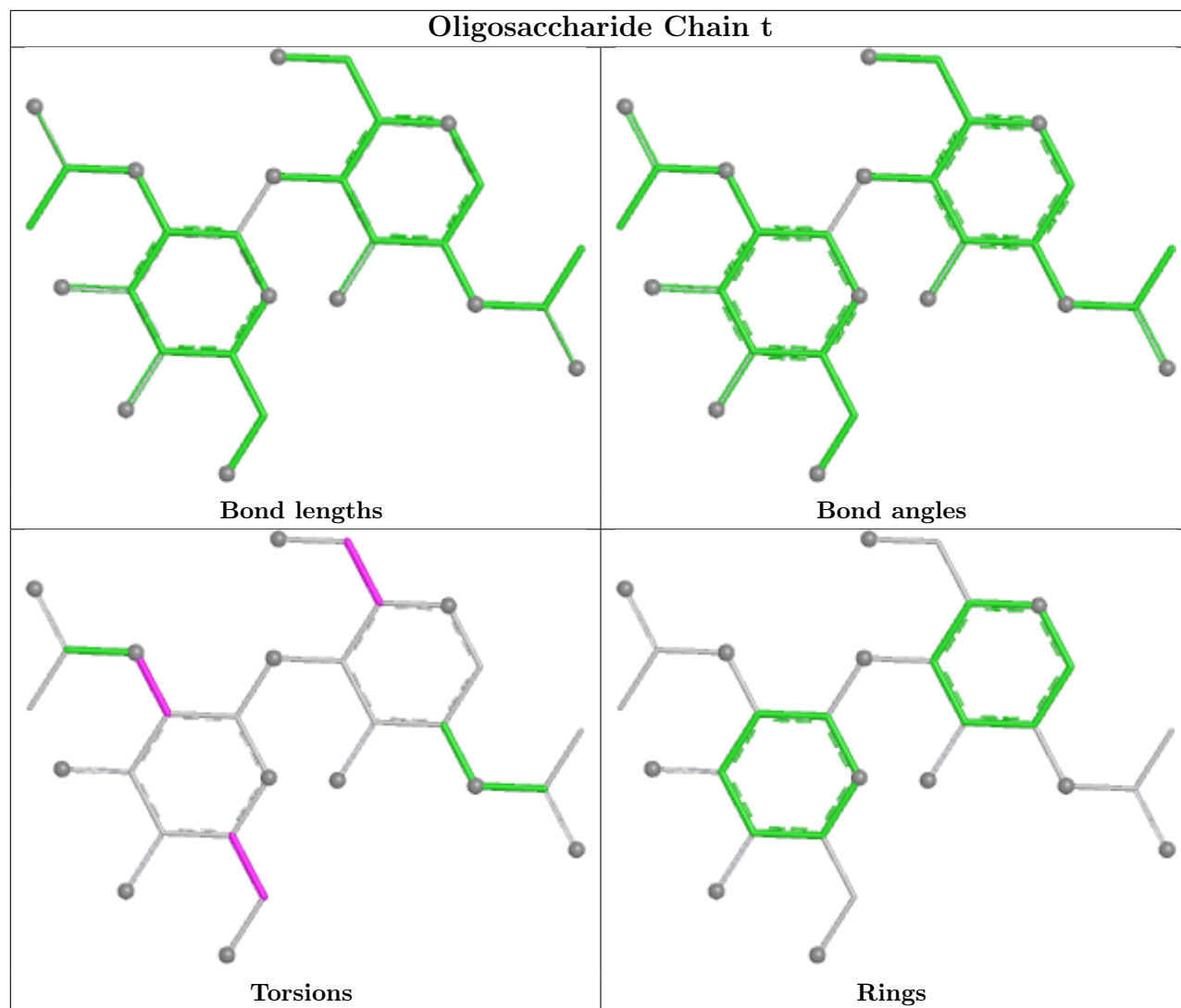


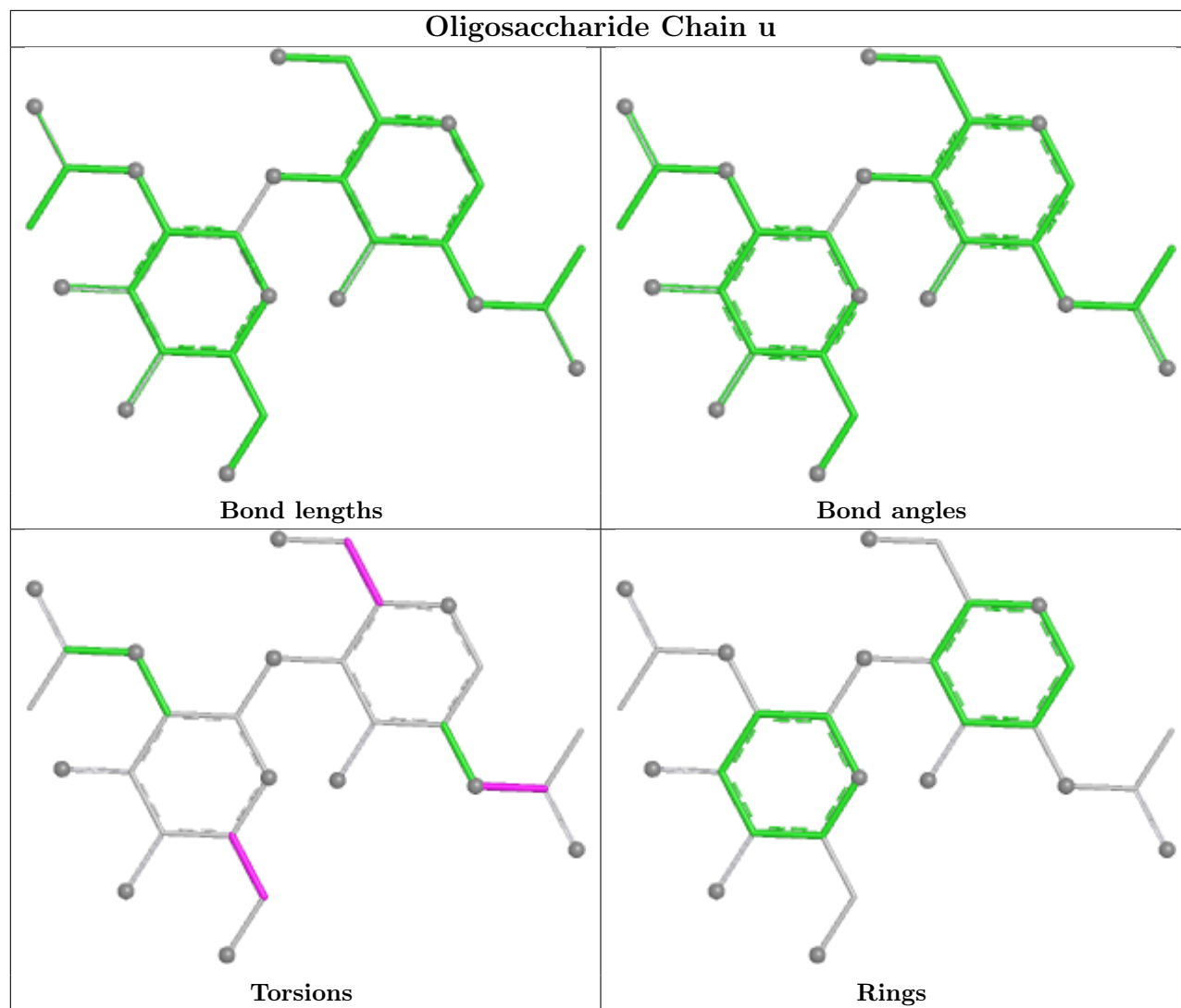


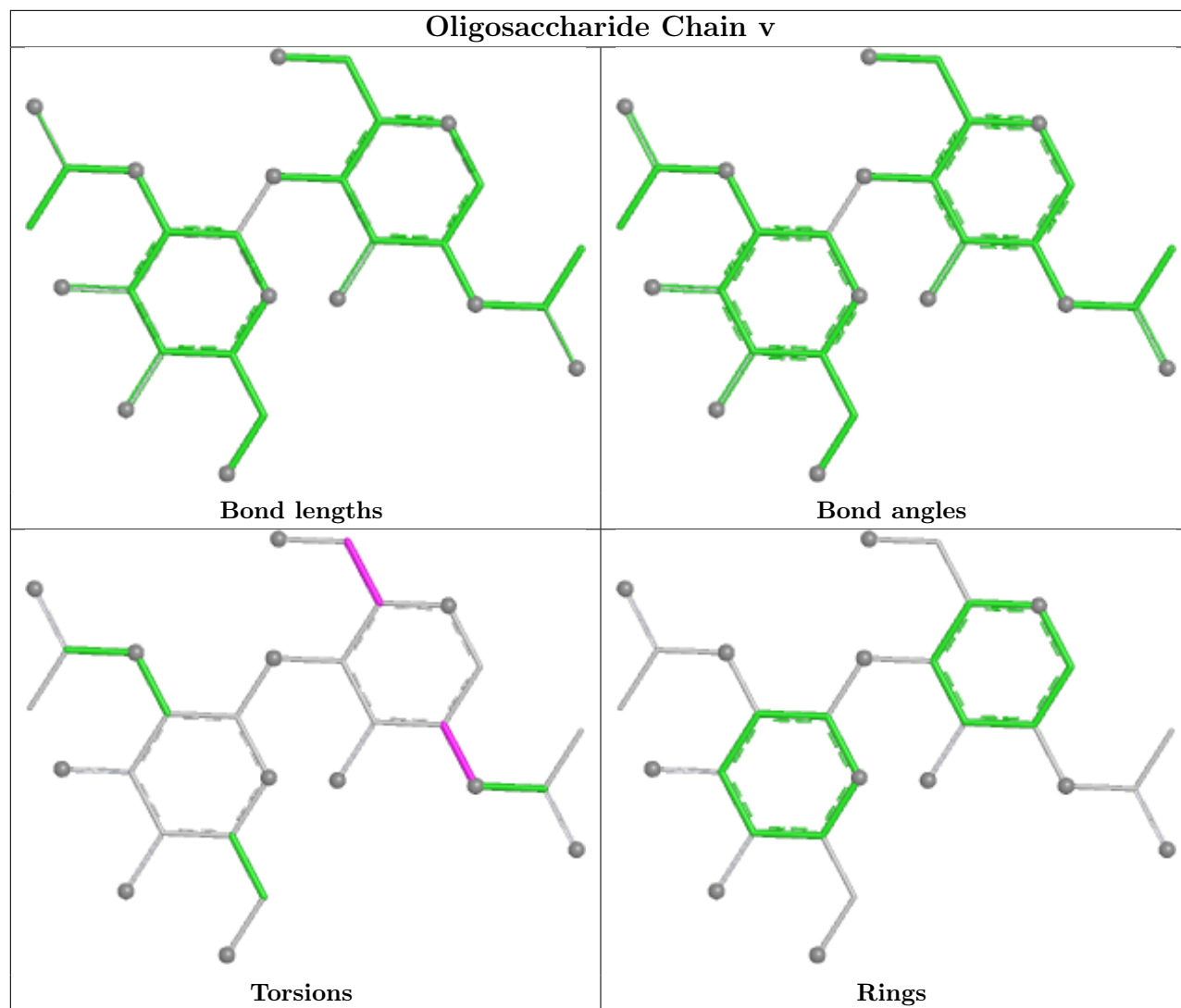


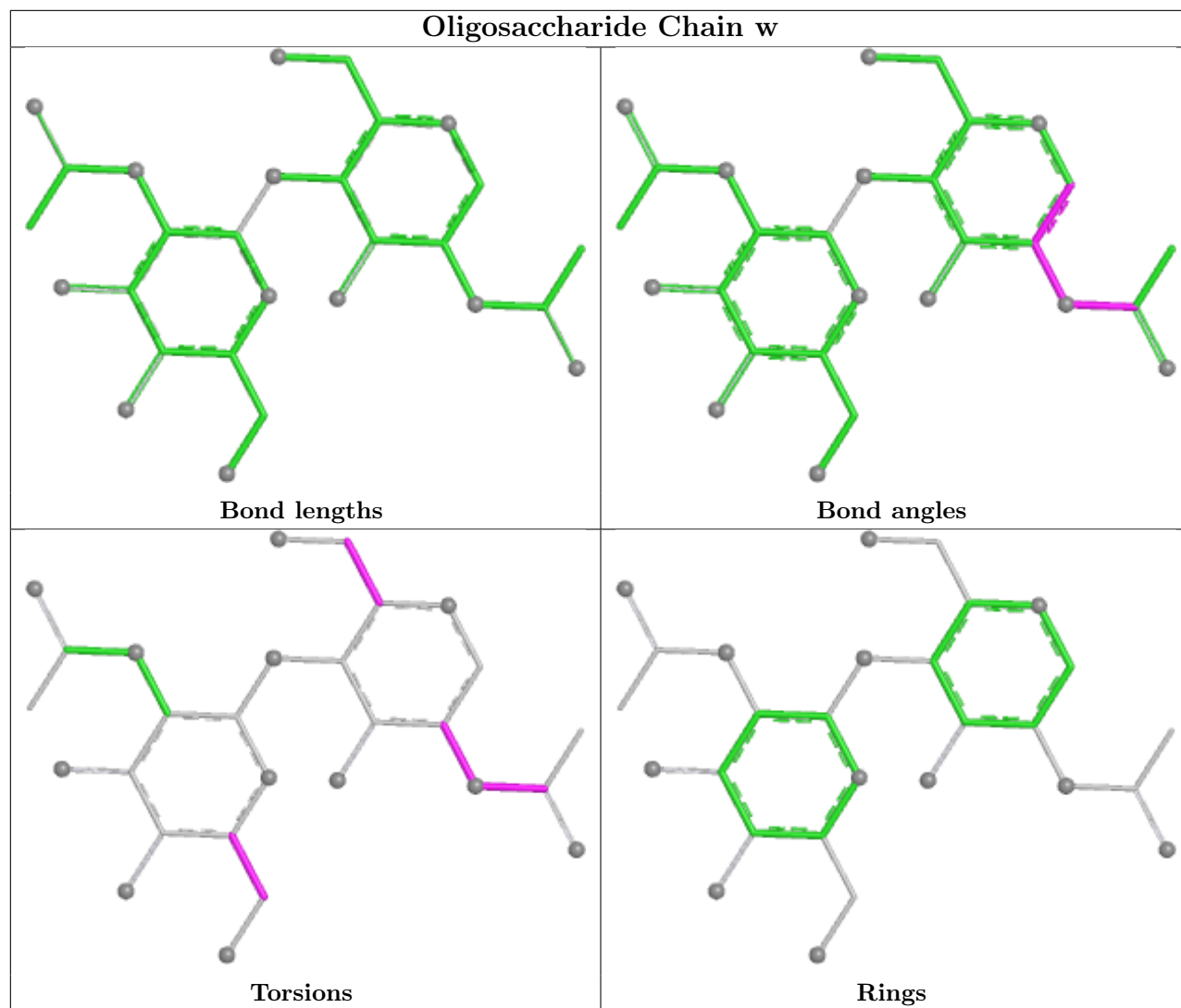


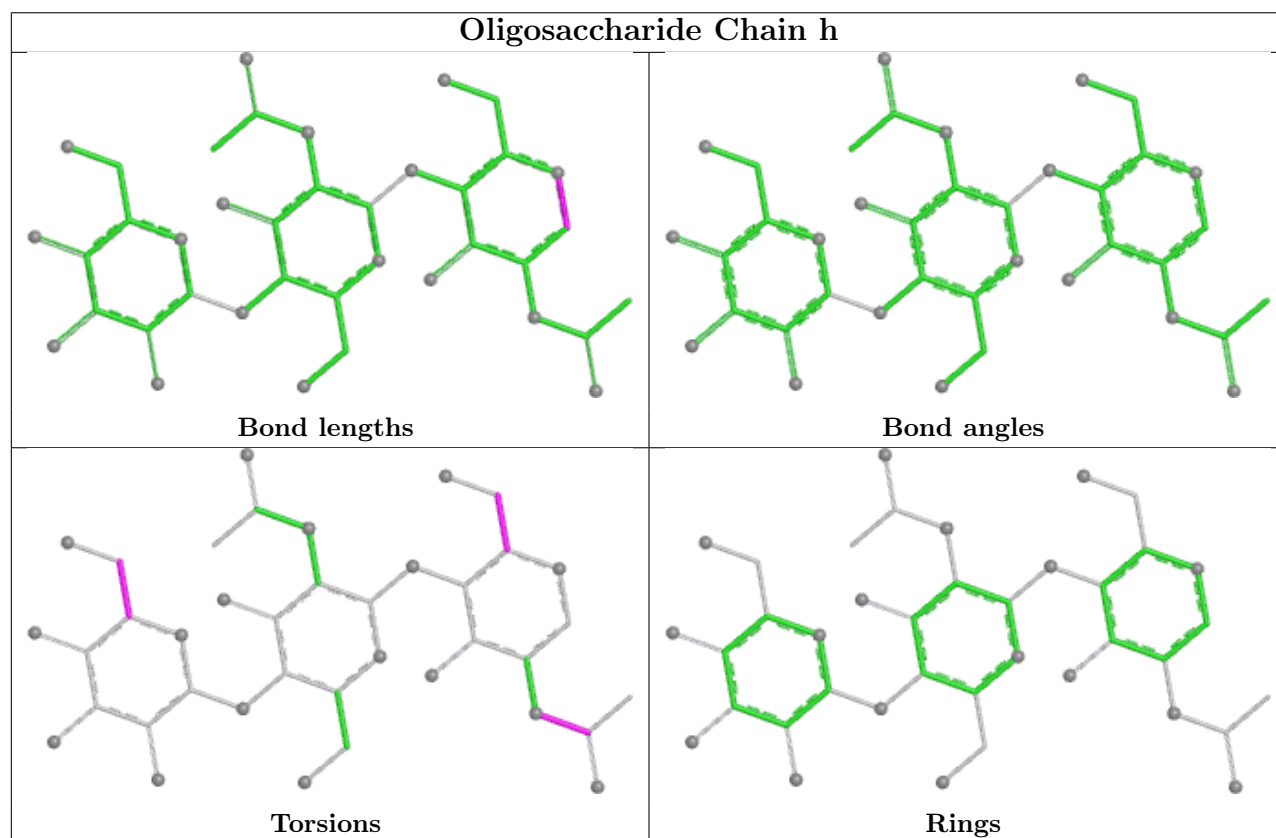
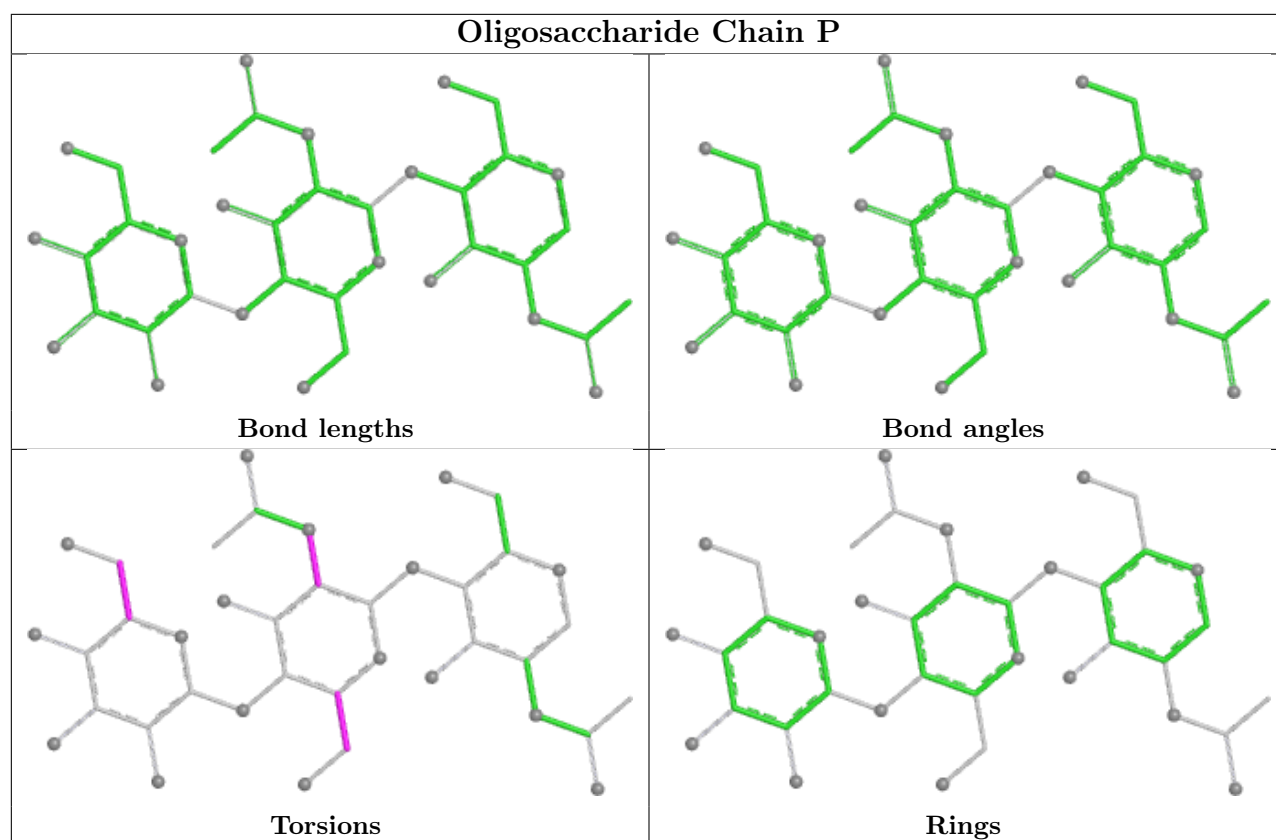


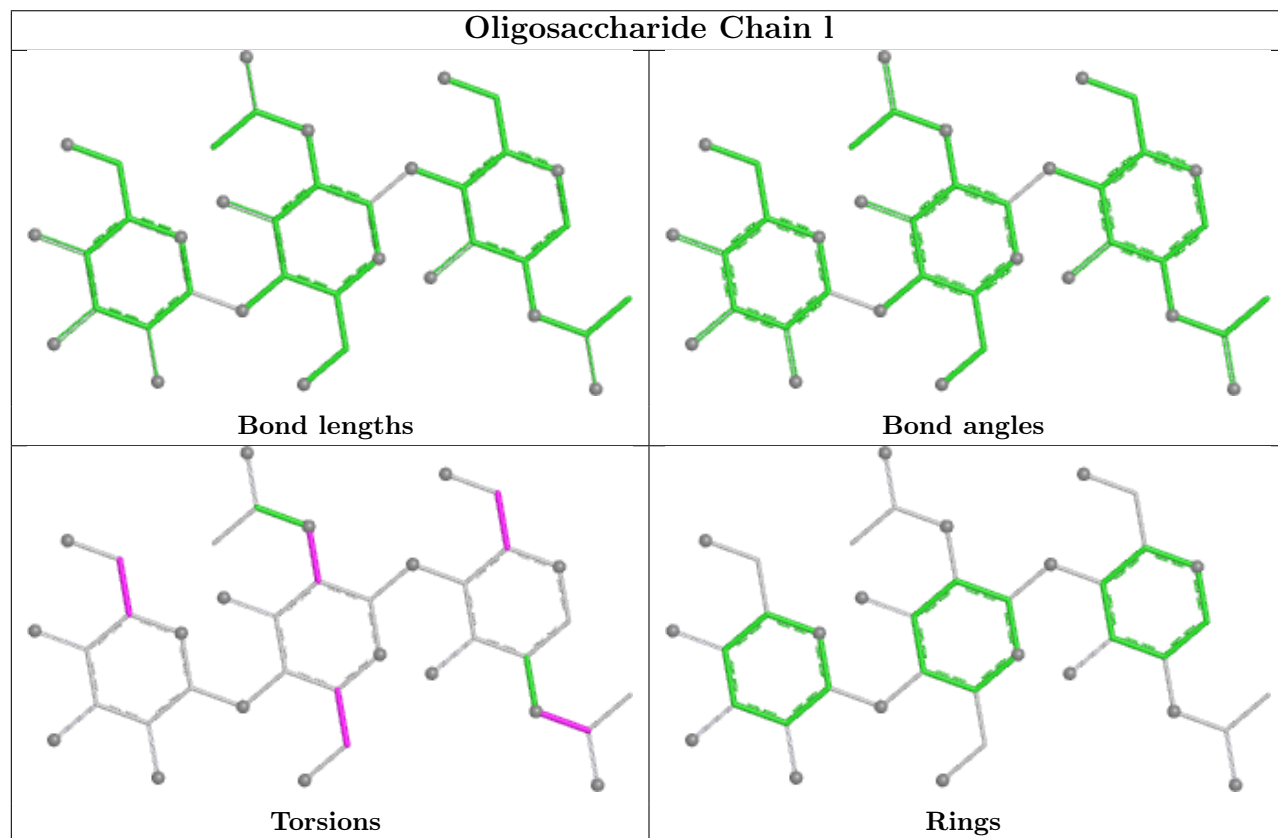
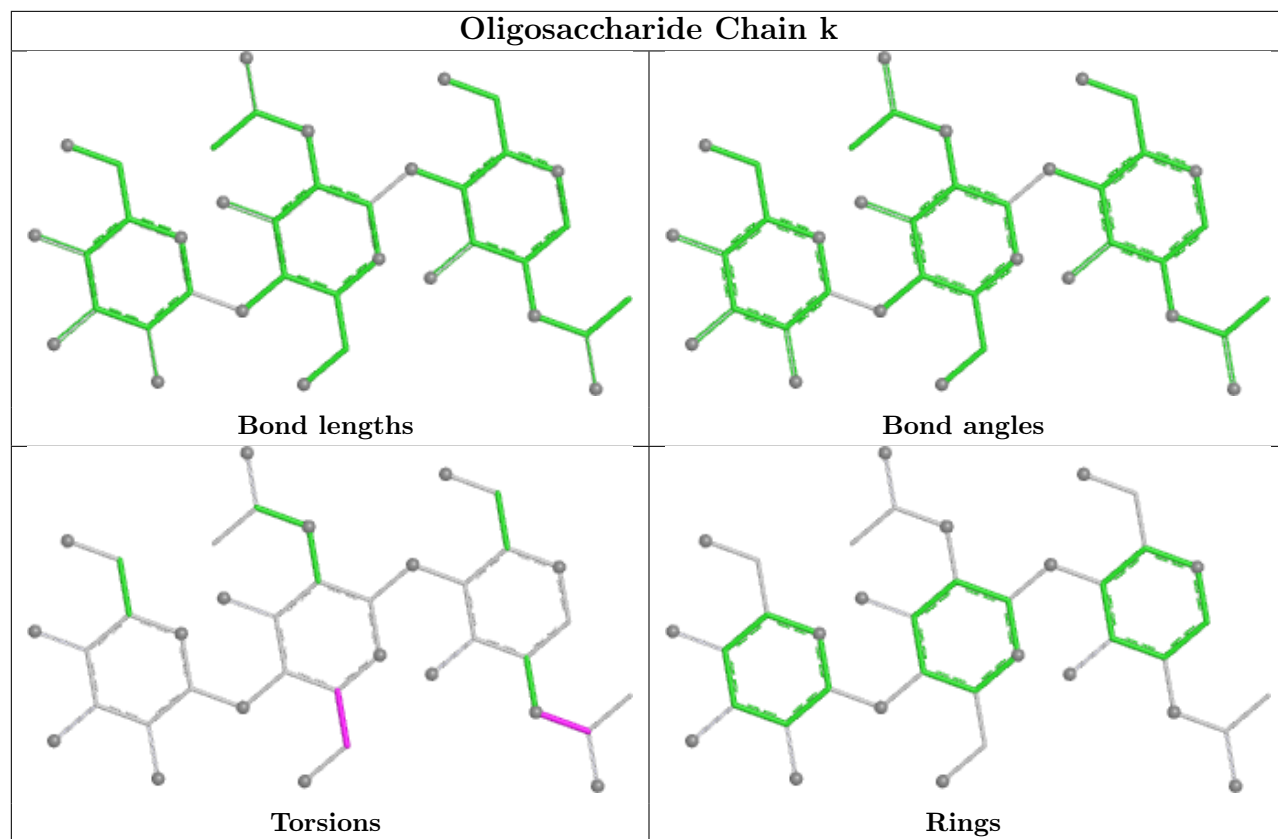


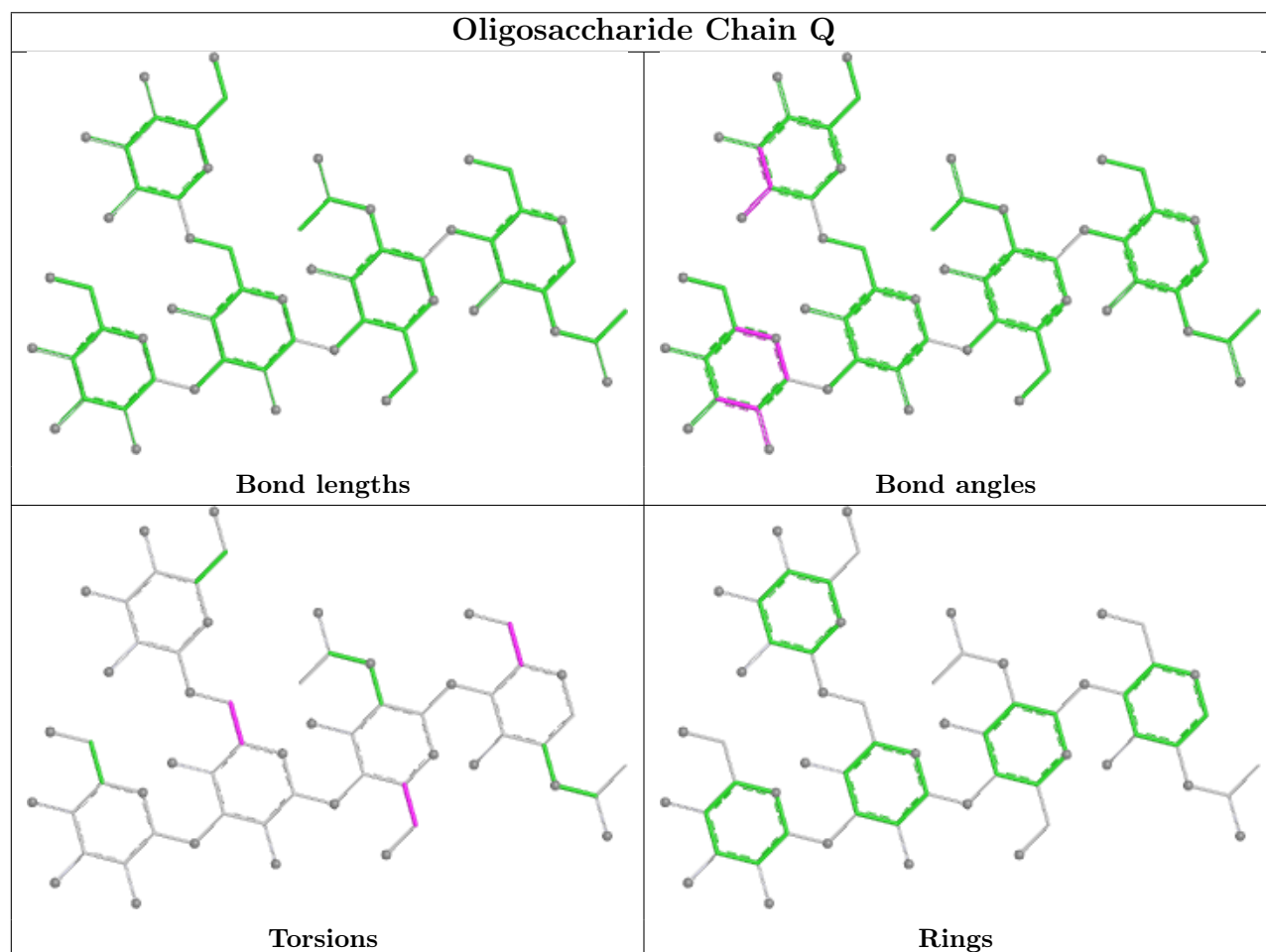
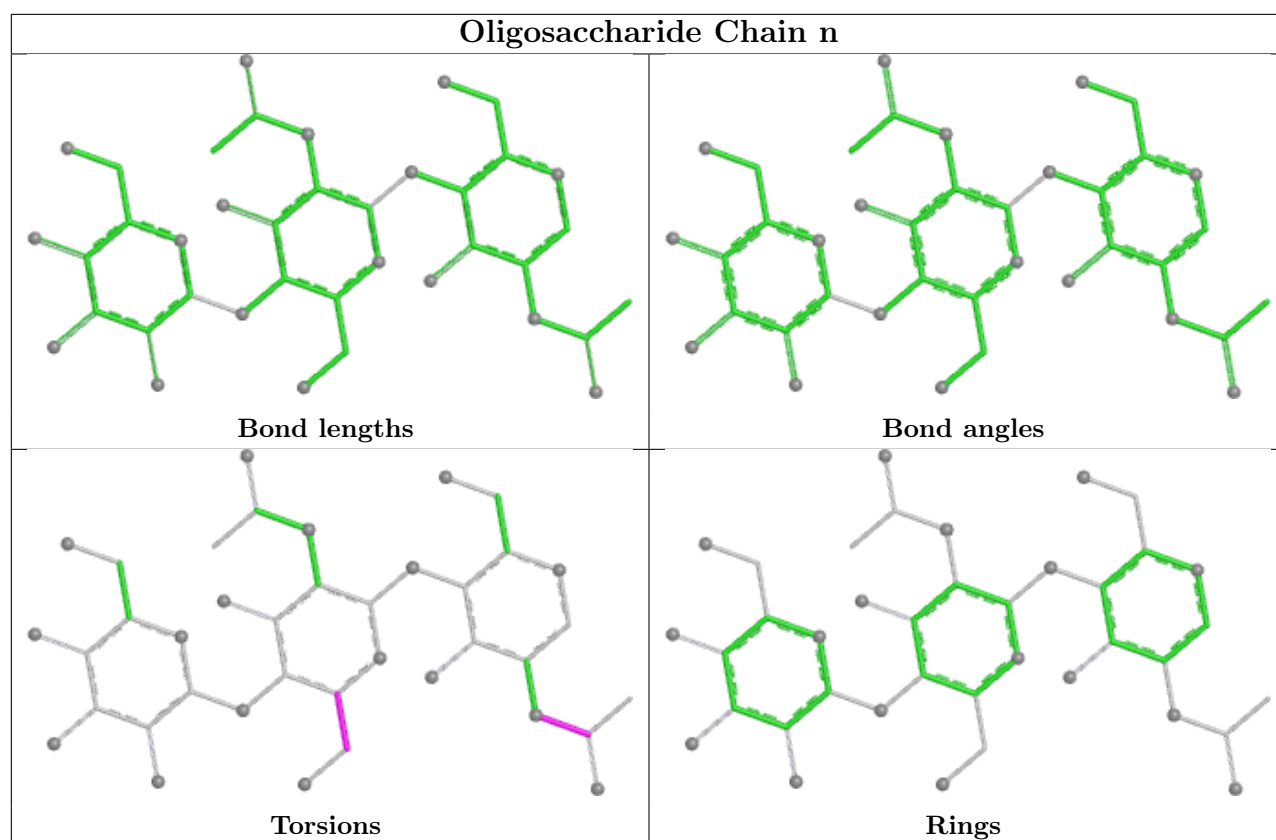


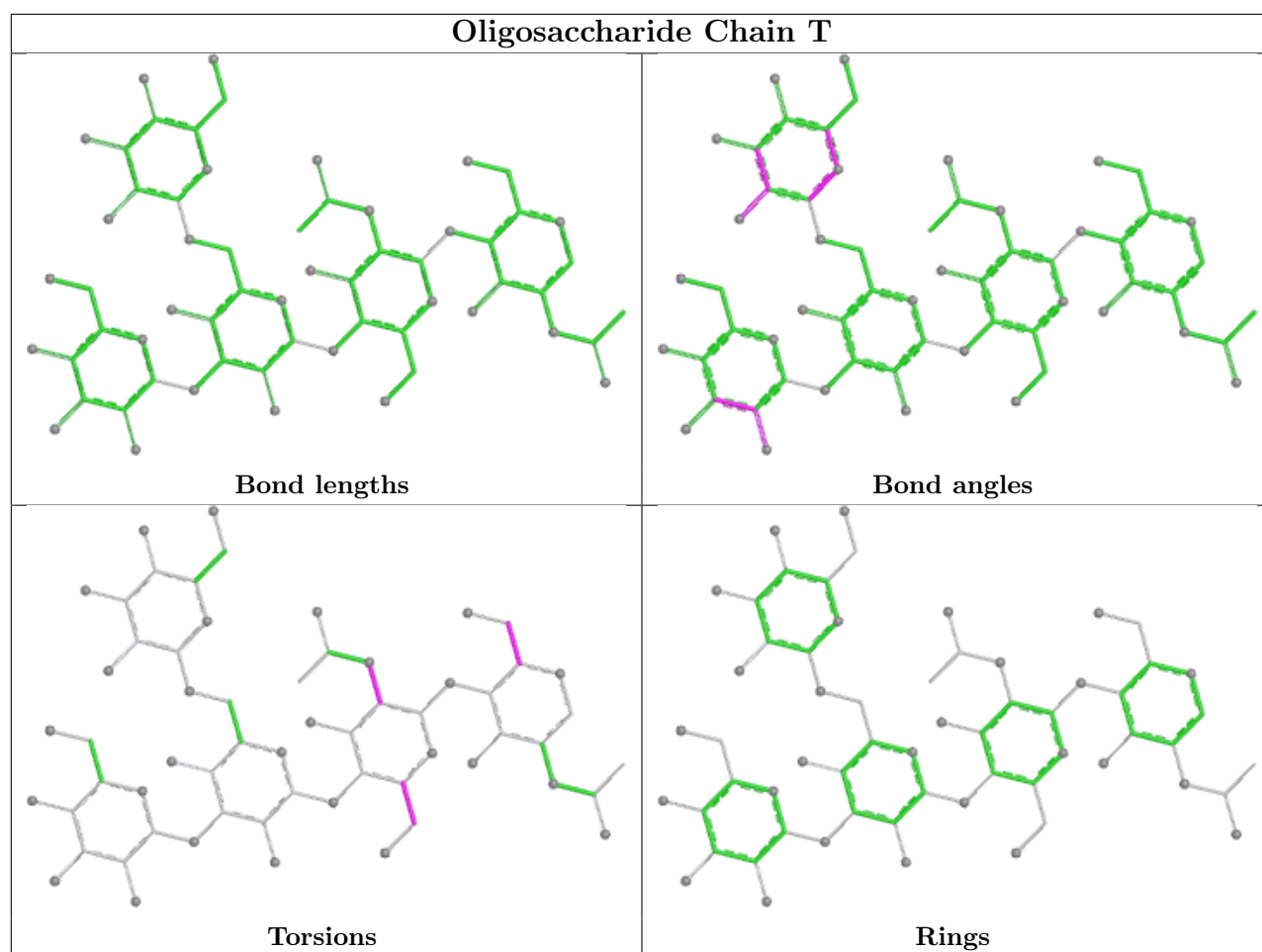


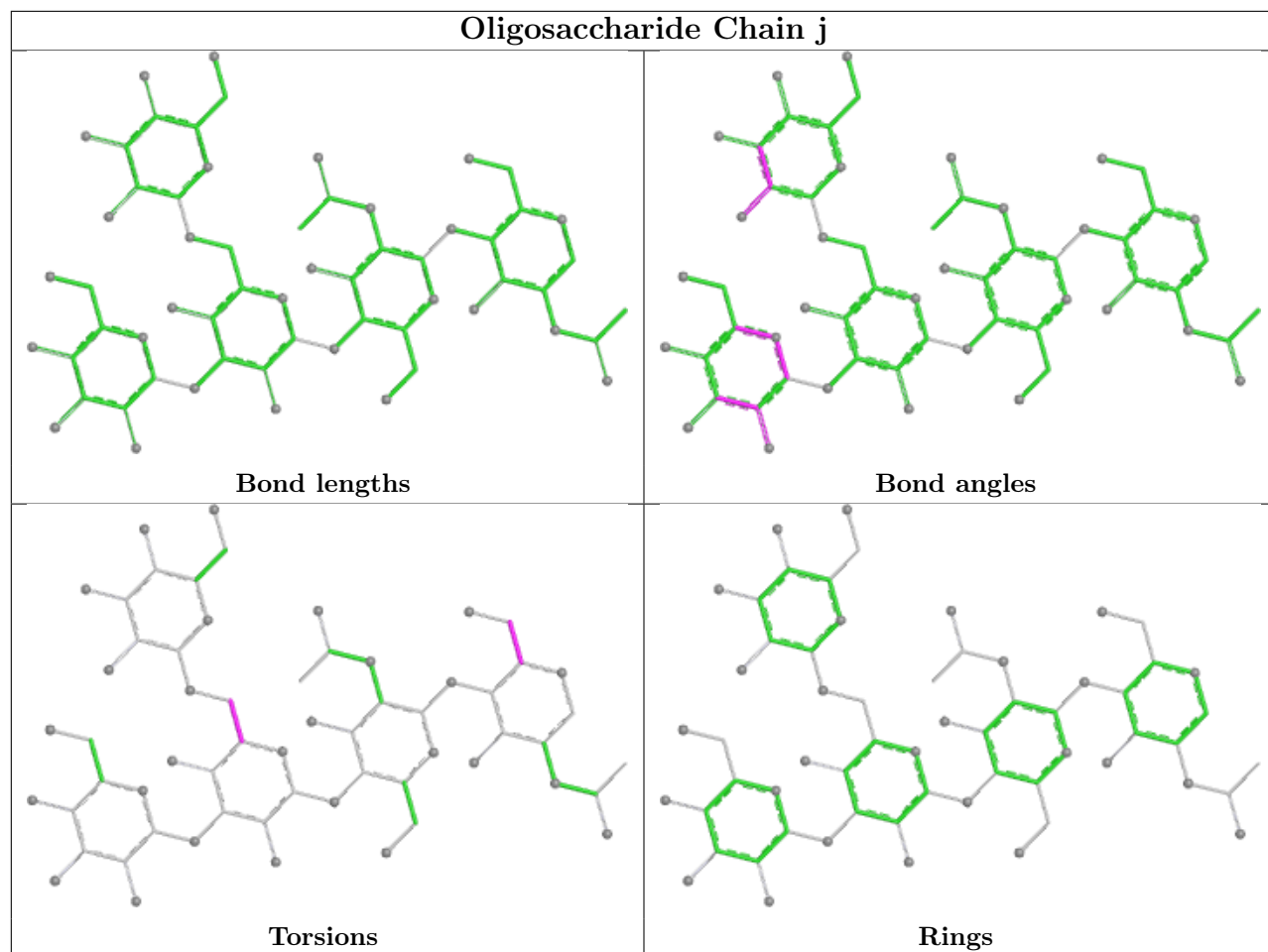


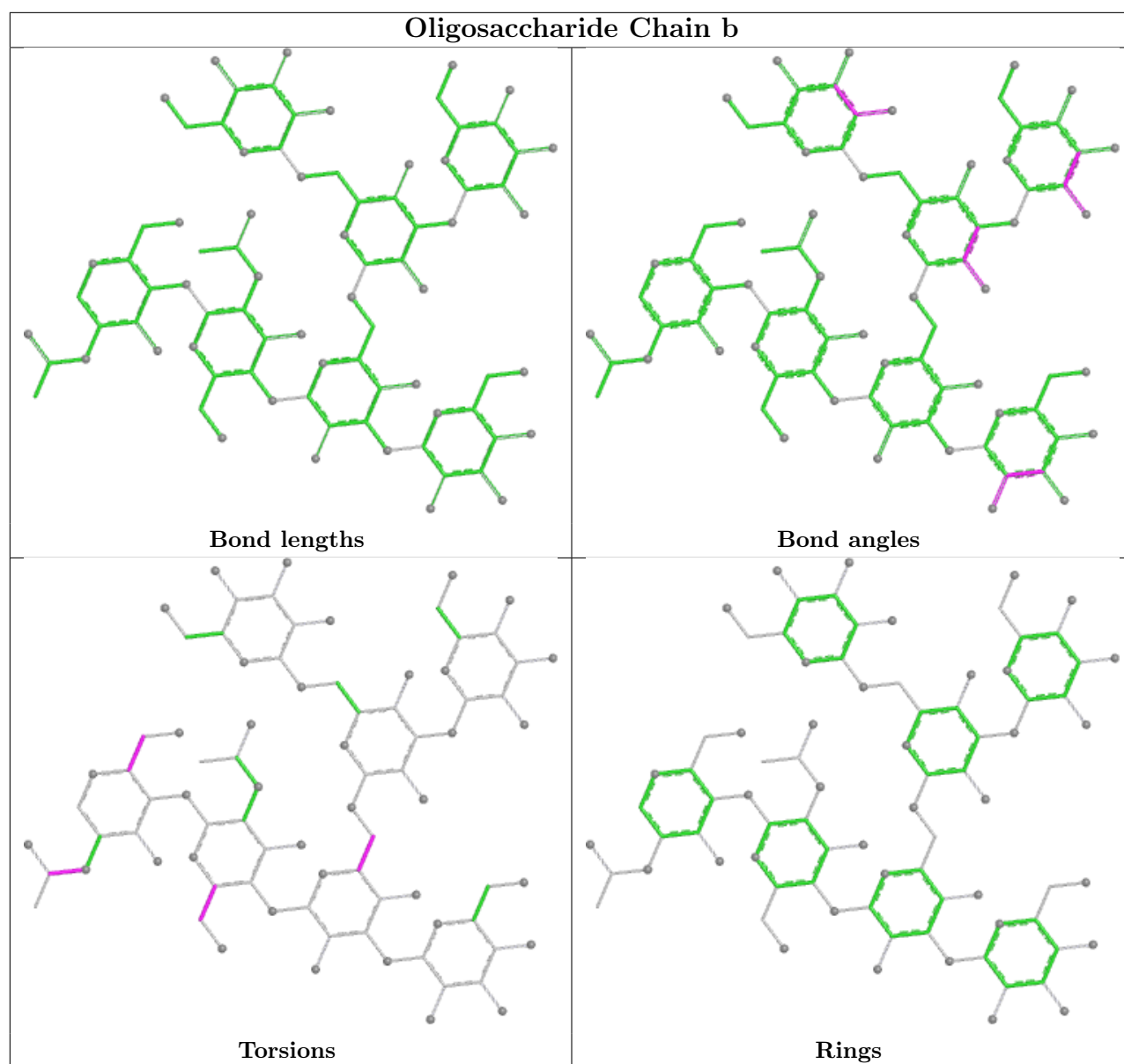


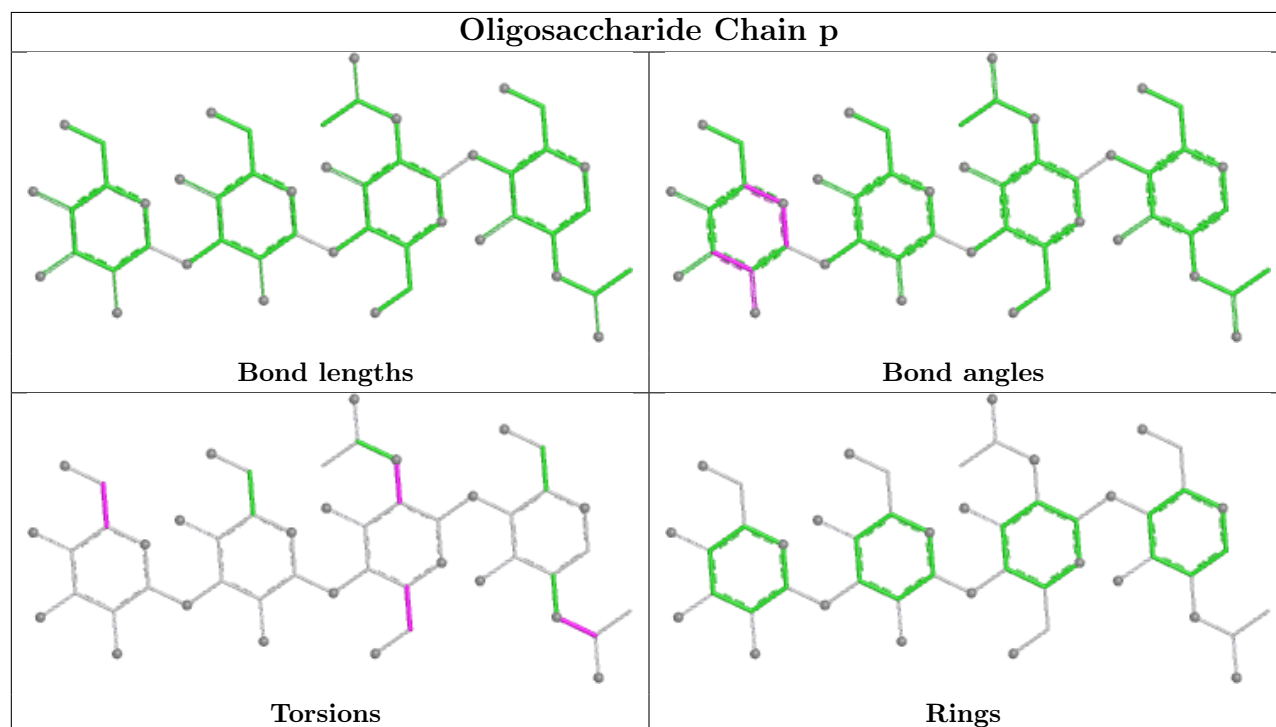
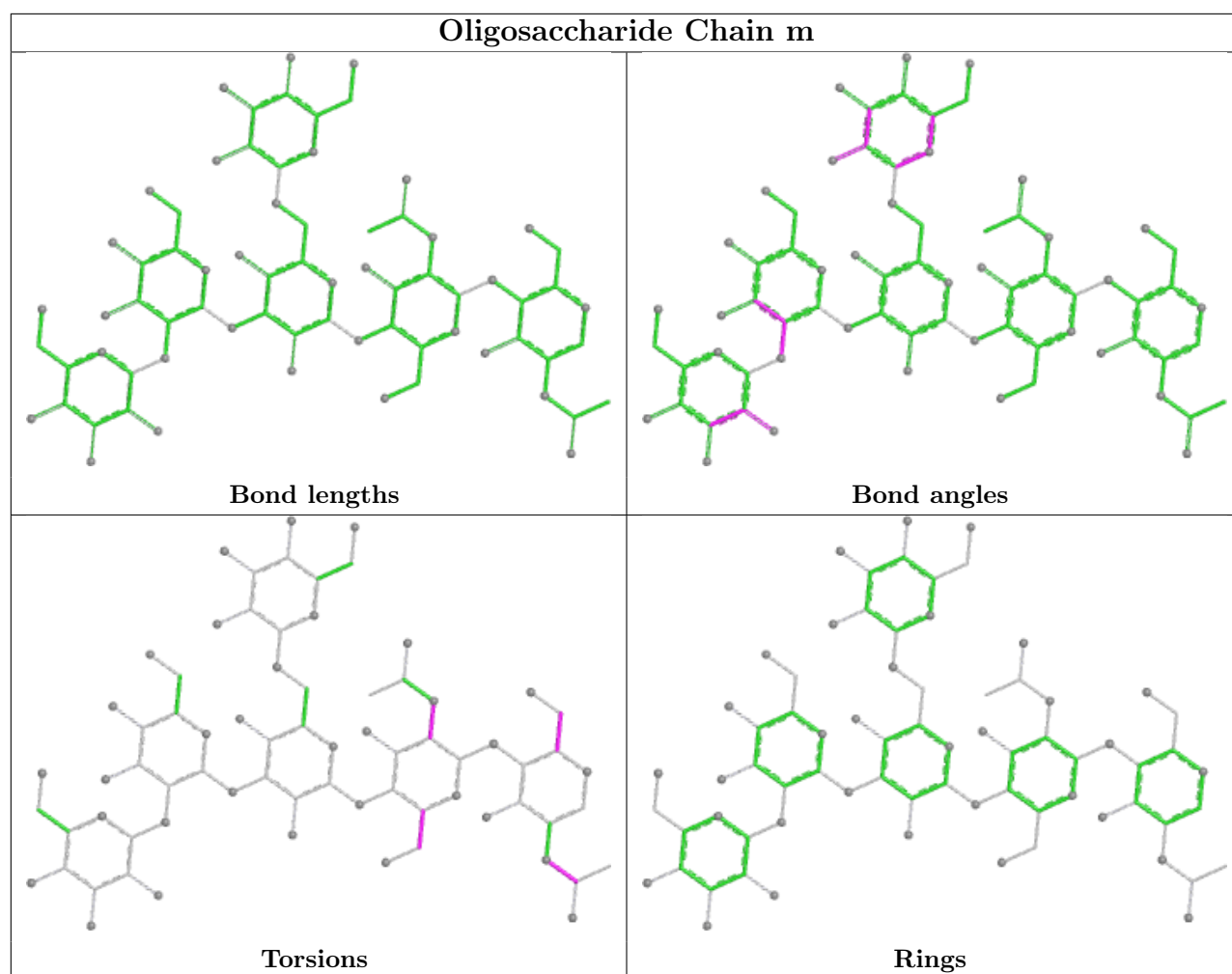












5.6 Ligand geometry

7 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	$\# Z > 2$
13	NAG	C	601	1	14,14,15	0.23	0	17,19,21	0.66	0
13	NAG	E	602	1	14,14,15	0.23	0	17,19,21	0.46	0
13	NAG	A	601	1	14,14,15	0.21	0	17,19,21	0.50	0
13	NAG	E	601	1	14,14,15	0.22	0	17,19,21	0.54	0
13	NAG	C	602	1	14,14,15	0.25	0	17,19,21	0.43	0
13	NAG	C	603	1	14,14,15	0.20	0	17,19,21	0.45	0
13	NAG	A	602	1	14,14,15	0.24	0	17,19,21	0.56	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
13	NAG	C	601	1	-	4/6/23/26	0/1/1/1
13	NAG	E	602	1	-	4/6/23/26	0/1/1/1
13	NAG	A	601	1	-	4/6/23/26	0/1/1/1
13	NAG	E	601	1	-	1/6/23/26	0/1/1/1
13	NAG	C	602	1	-	1/6/23/26	0/1/1/1
13	NAG	C	603	1	-	1/6/23/26	0/1/1/1
13	NAG	A	602	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	C	601	NAG	C4-C5-C6-O6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
13	E	602	NAG	C4-C5-C6-O6
13	C	601	NAG	O5-C5-C6-O6
13	E	602	NAG	O5-C5-C6-O6
13	E	602	NAG	C8-C7-N2-C2

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.

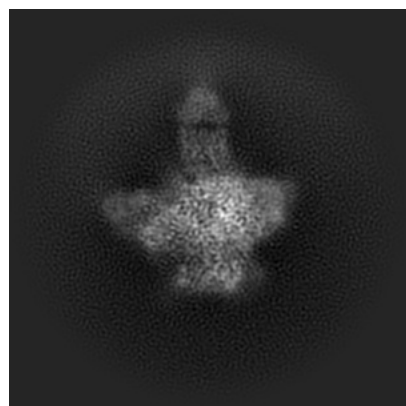
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42366. These allow visual inspection of the internal detail of the map and identification of artifacts.

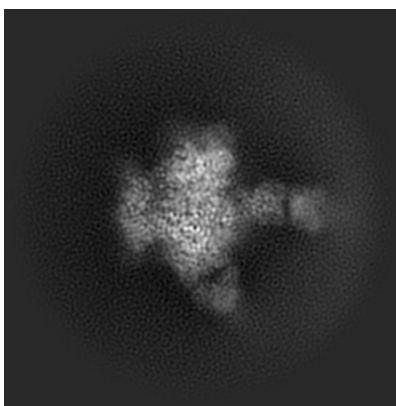
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

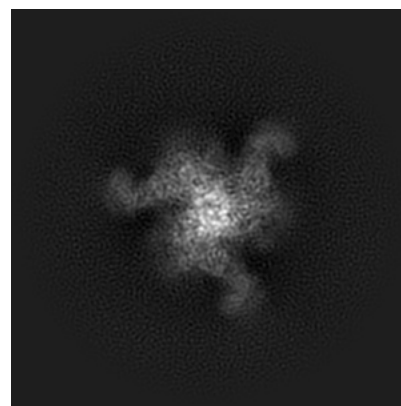
6.1.1 Primary map



X

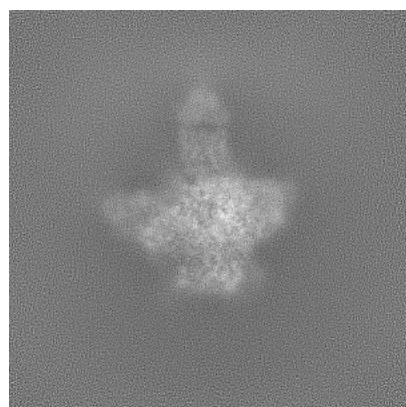


Y

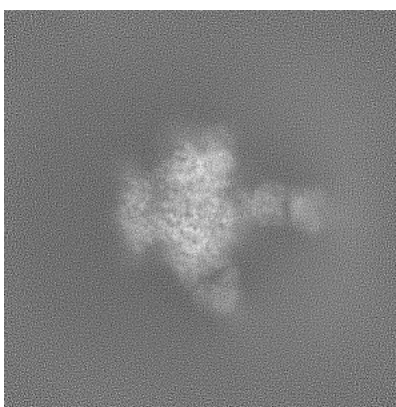


Z

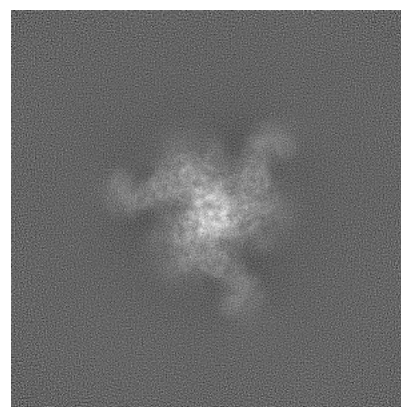
6.1.2 Raw map



X



Y

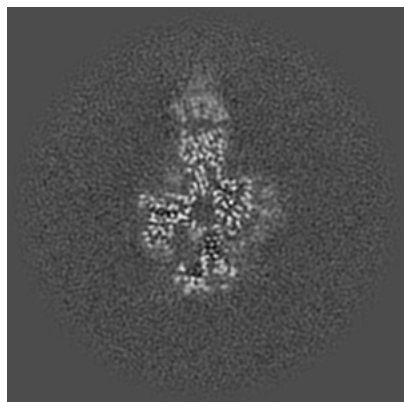


Z

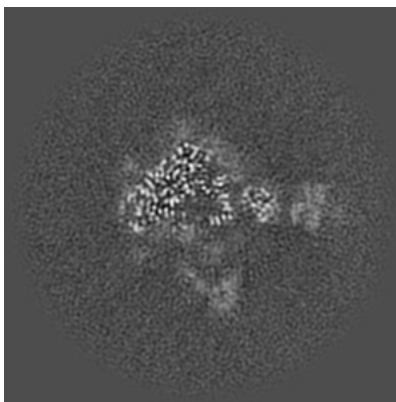
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

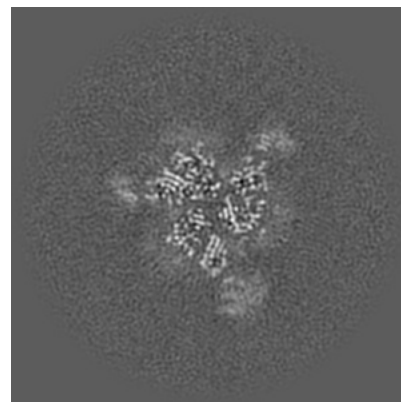
6.2.1 Primary map



X Index: 208

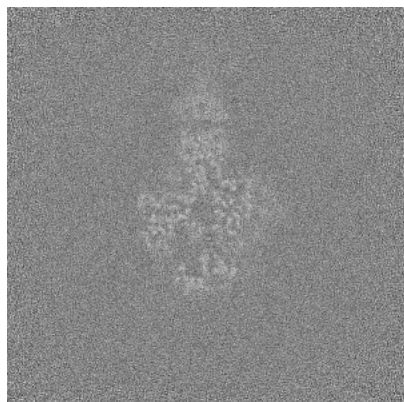


Y Index: 208

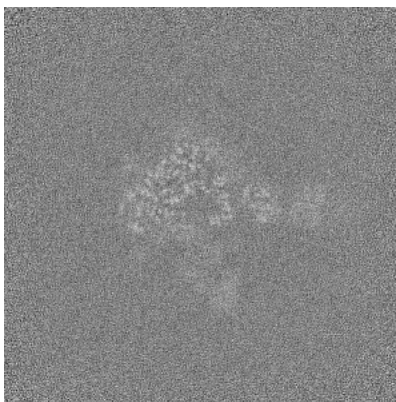


Z Index: 208

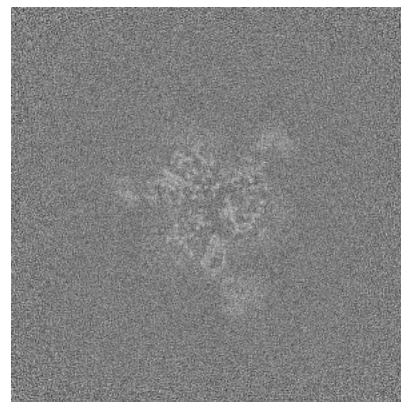
6.2.2 Raw map



X Index: 208



Y Index: 208

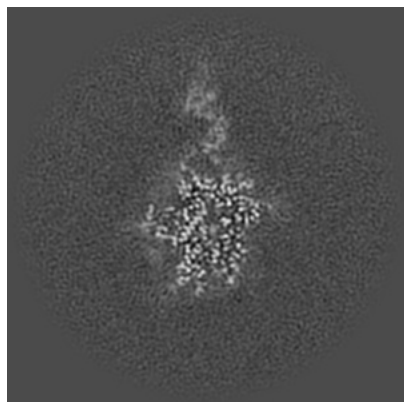


Z Index: 208

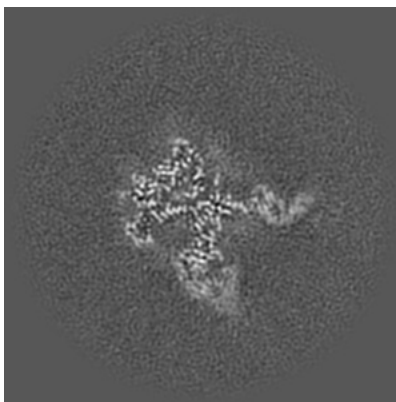
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

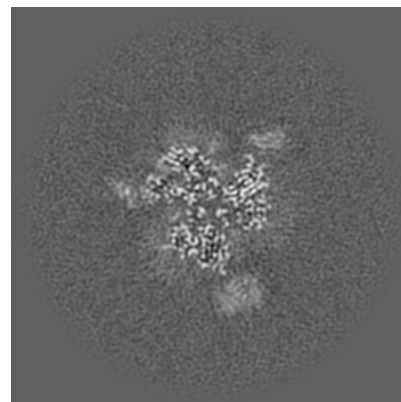
6.3.1 Primary map



X Index: 197

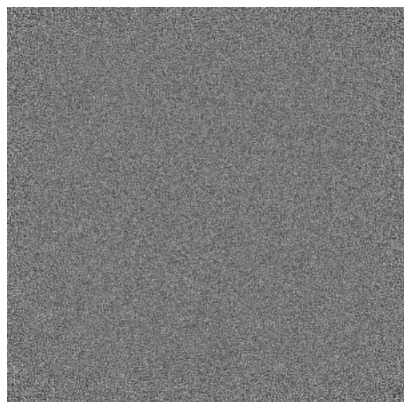


Y Index: 220

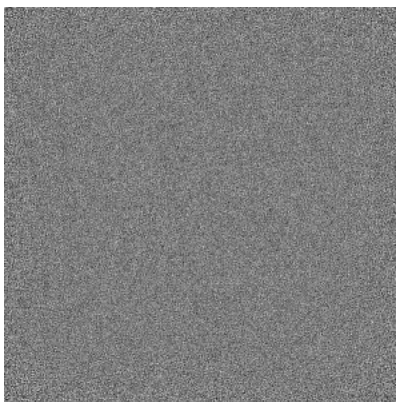


Z Index: 201

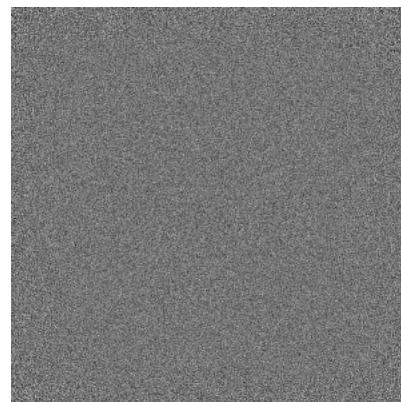
6.3.2 Raw map



X Index: 0



Y Index: 0

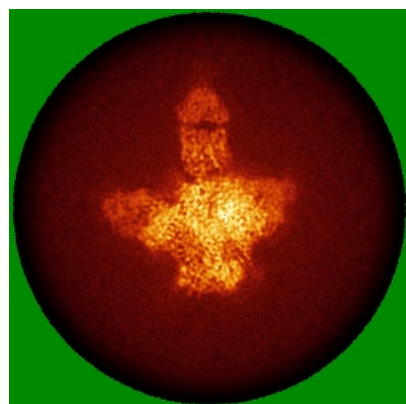


Z Index: 0

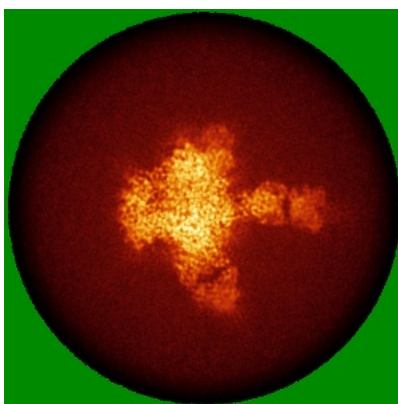
The images above show the largest variance slices of the map in three orthogonal directions.

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

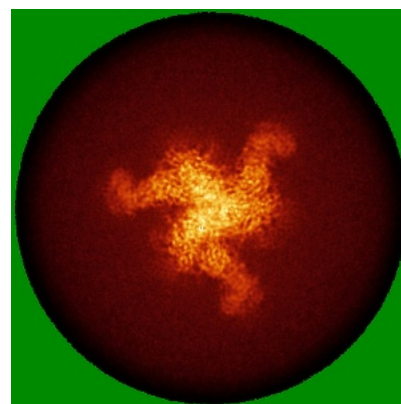
6.4.1 Primary map



X

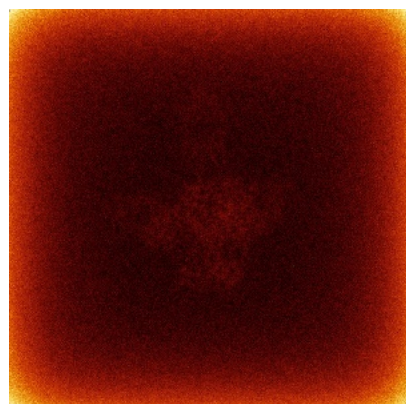


Y

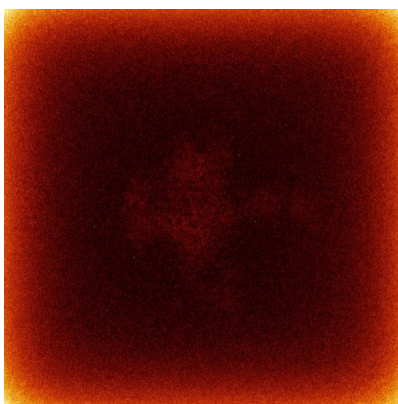


Z

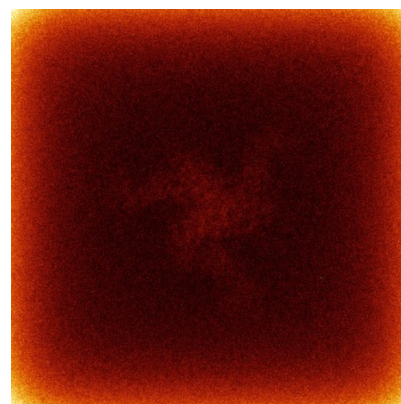
6.4.2 Raw map



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.

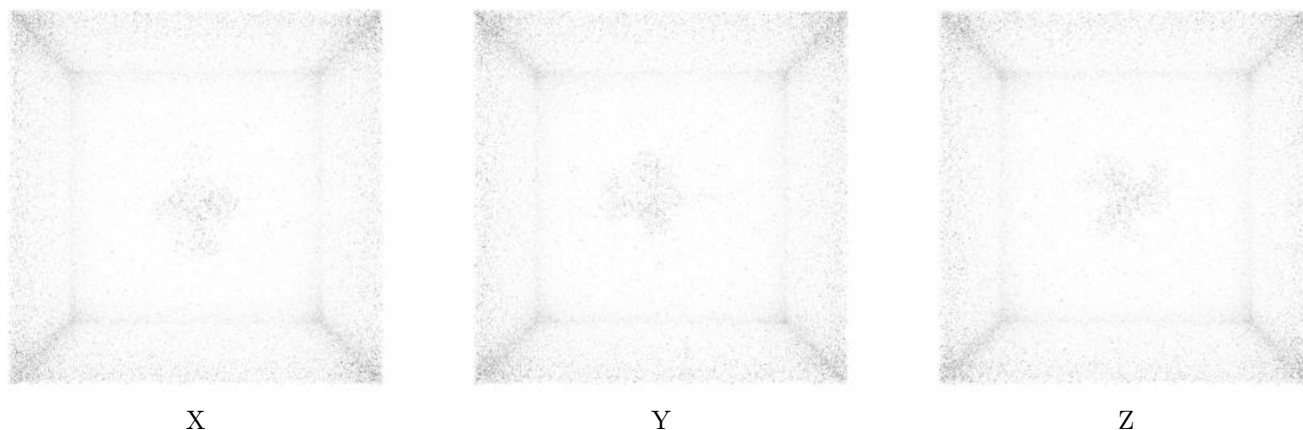
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.14. 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.

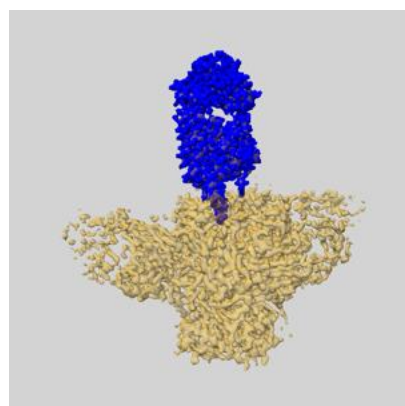
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

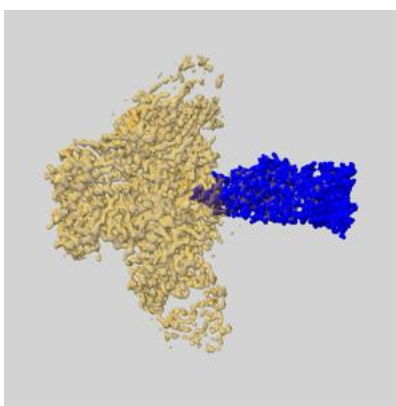
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

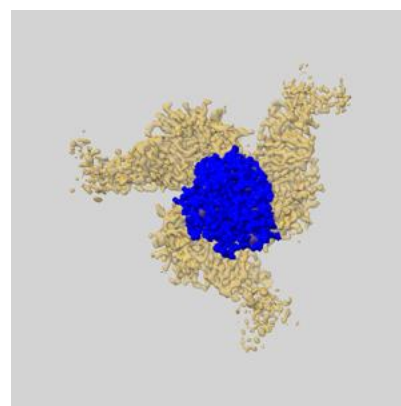
6.6.1 emd_42366_msk_1.map [i](#)



X

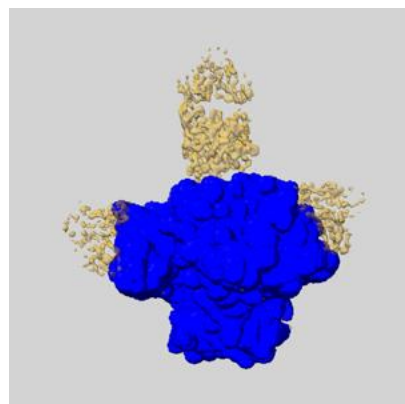


Y

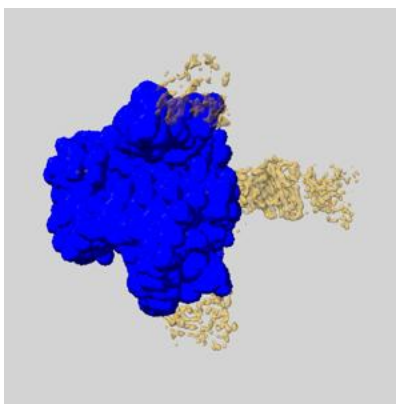


Z

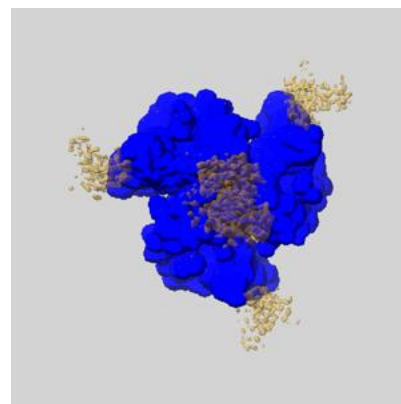
6.6.2 emd_42366_msk_2.map [i](#)



X



Y

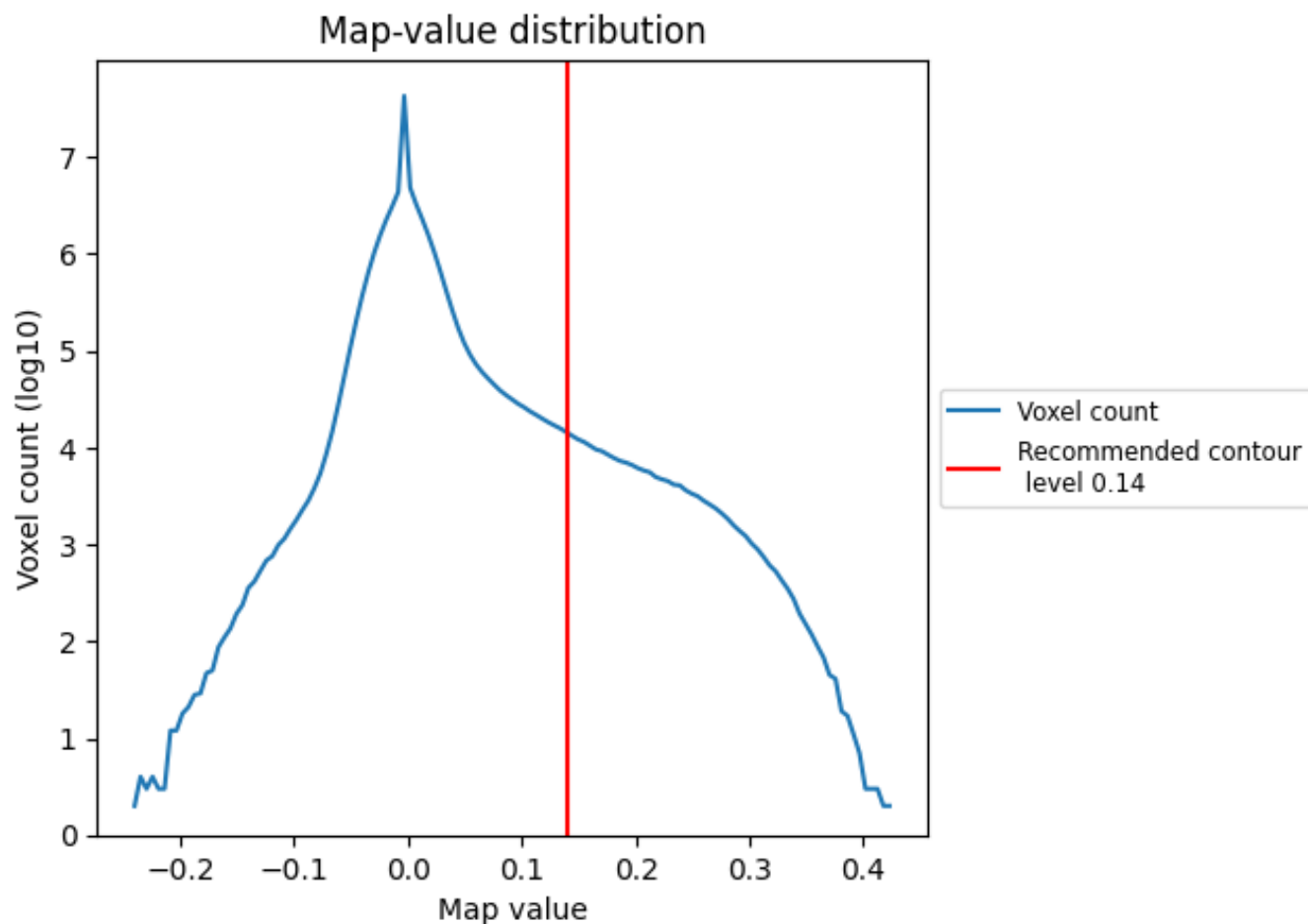


Z

7 Map analysis [i](#)

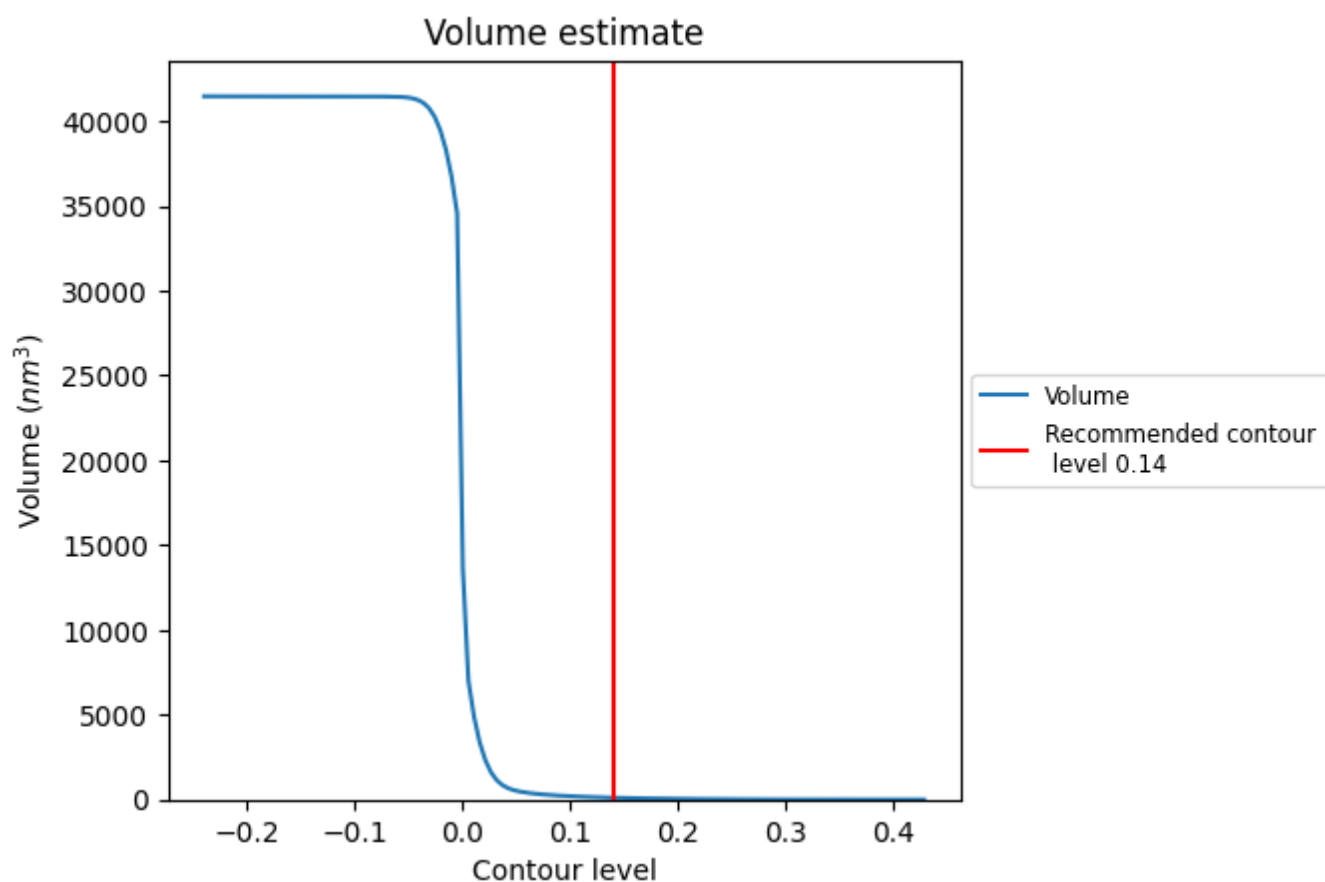
This section contains the results of statistical analysis of the map.

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.

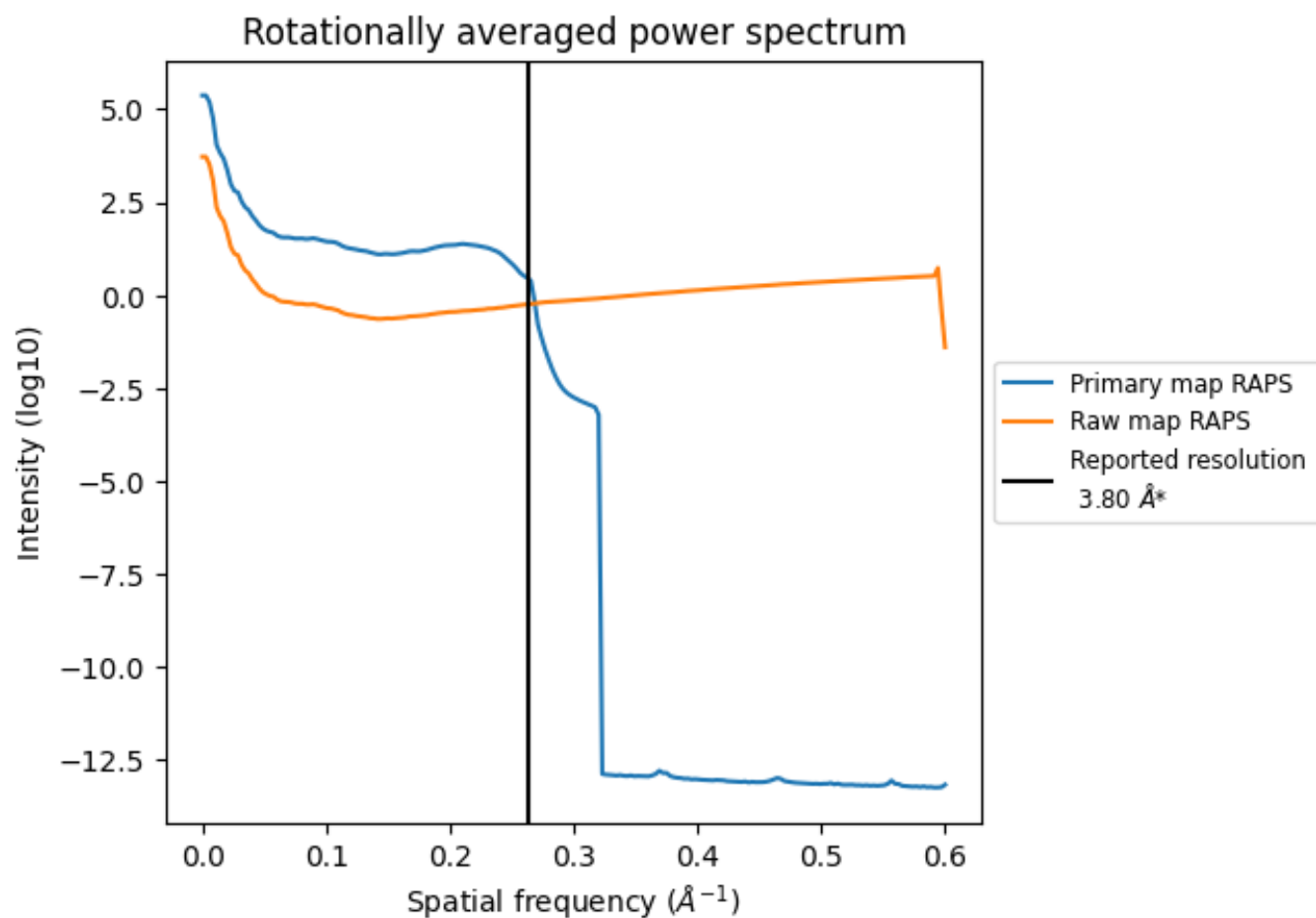
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 107 nm^3 ; this corresponds to an approximate mass of 97 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

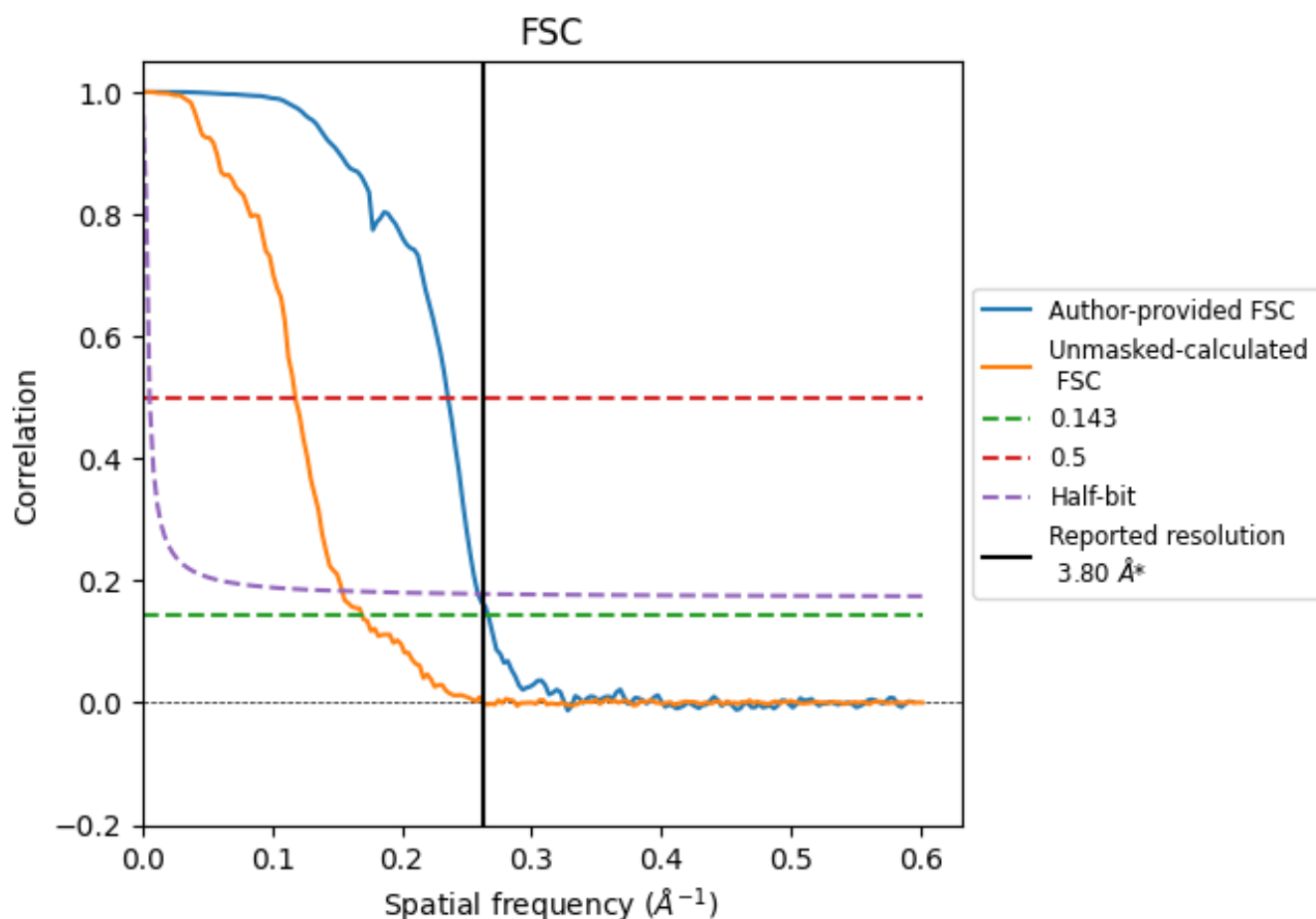


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

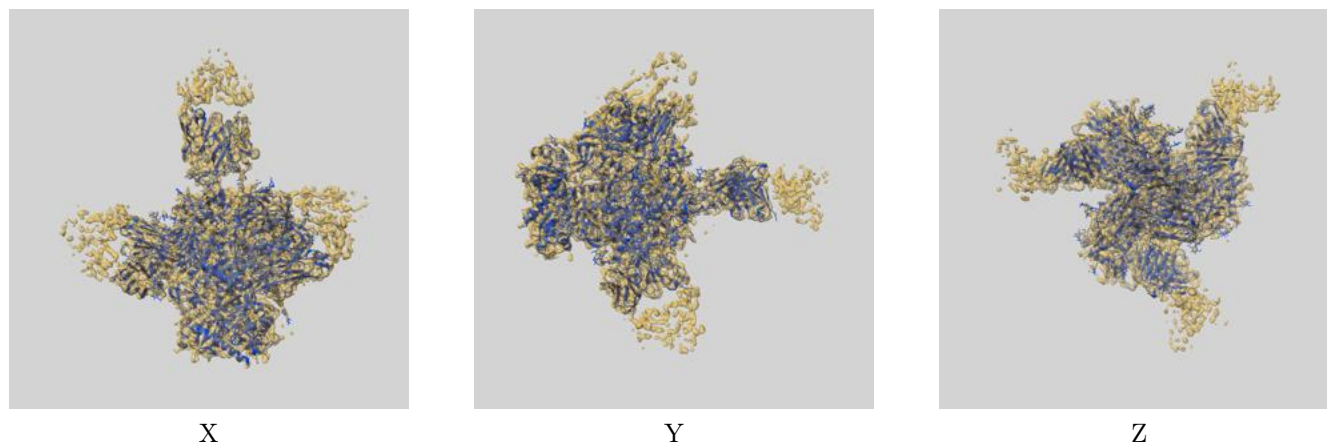
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.75	4.25	3.87
Unmasked-calculated*	5.90	8.47	6.49

*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 5.90 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

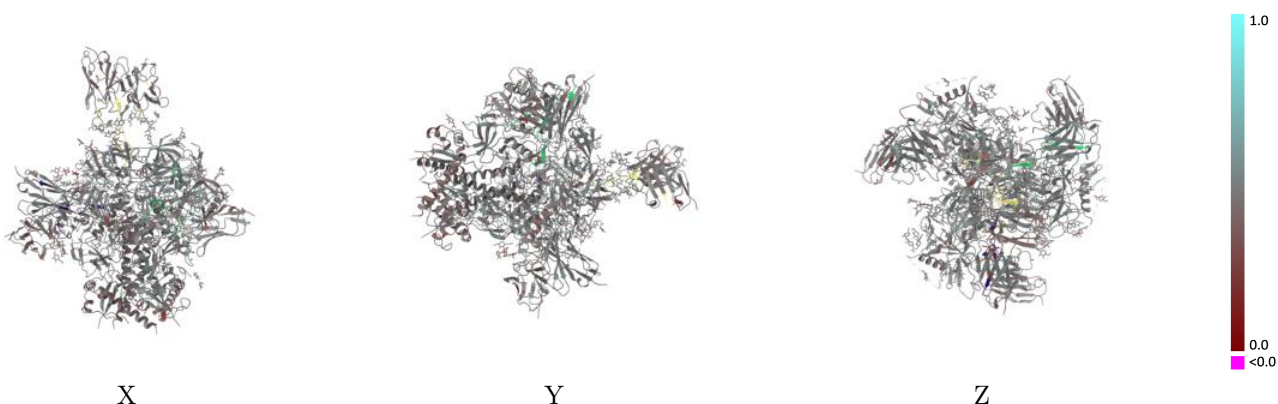
This section contains information regarding the fit between EMDB map EMD-42366 and PDB model 8ULU. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



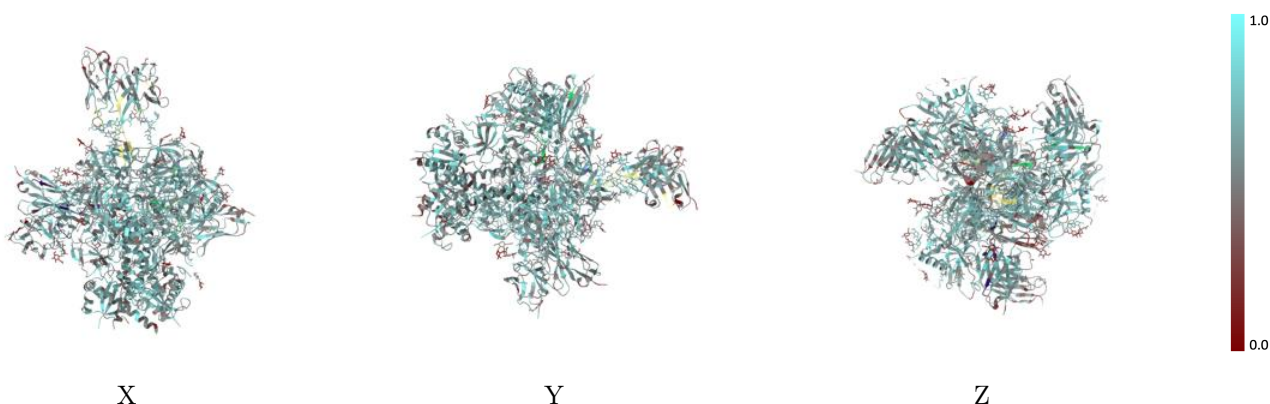
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



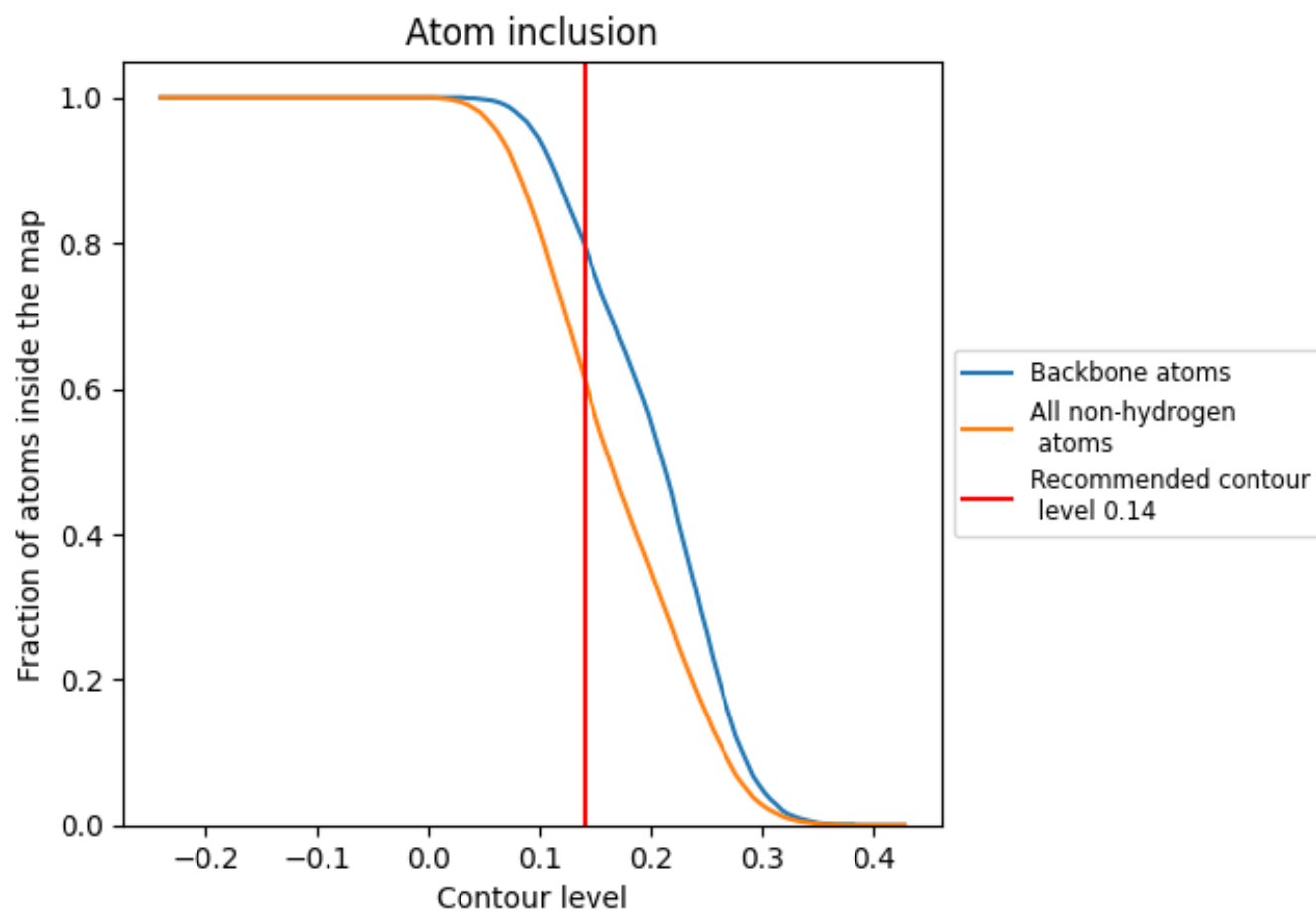
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 62% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6160	 0.4690
A	 0.6400	 0.4850
B	 0.6180	 0.4500
C	 0.6440	 0.4780
D	 0.6190	 0.4460
E	 0.6500	 0.4830
F	 0.6100	 0.4460
G	 0.5320	 0.4390
H	 0.6360	 0.4830
I	 0.6650	 0.4890
J	 0.6510	 0.4800
K	 0.5670	 0.4530
L	 0.5850	 0.4560
M	 0.5930	 0.4570
N	 0.5720	 0.4430
O	 0.2860	 0.4180
P	 0.3850	 0.4420
Q	 0.6890	 0.4740
R	 0.4290	 0.4970
S	 0.2140	 0.4110
T	 0.3770	 0.4570
U	 0.3570	 0.3190
V	 0.4290	 0.4560
W	 0.3210	 0.4170
X	 0.5000	 0.4560
Y	 0.5710	 0.4700
Z	 0.5360	 0.4540
a	 0.5000	 0.4940
b	 0.6510	 0.4650
c	 0.3210	 0.4490
d	 0.3930	 0.3410
e	 0.4640	 0.4480
f	 0.2860	 0.4080
g	 0.5360	 0.4610
h	 0.5380	 0.4070



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Chain	Atom inclusion	Q-score
i	 0.5000	 0.4250
j	 0.4100	 0.4340
k	 0.2050	 0.2770
l	 0.3330	 0.4040
m	 0.6670	 0.4590
n	 0.4620	 0.4910
o	 0.2860	 0.4330
p	 0.5000	 0.4530
q	 0.4640	 0.3770
r	 0.3570	 0.4220
s	 0.4290	 0.4550
t	 0.4640	 0.4430
u	 0.5360	 0.4460
v	 0.5710	 0.4390
w	 0.5000	 0.4690