



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:45 PM UTC

PDB ID : 6DCQ / pdb_00006dcq
EMDB ID : EMD-7858
Title : Ectodomain of full length, wild type HIV-1 glycoprotein clone PC64M18C043
in complex with PGT151 Fab
Authors : Rantalainen, K.
Deposited on : 2018-05-08
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

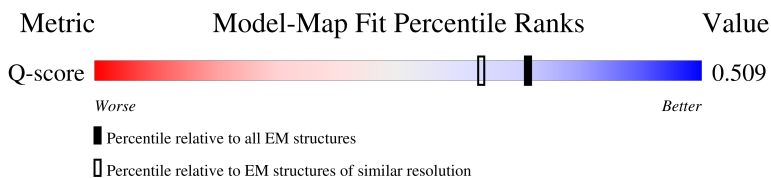
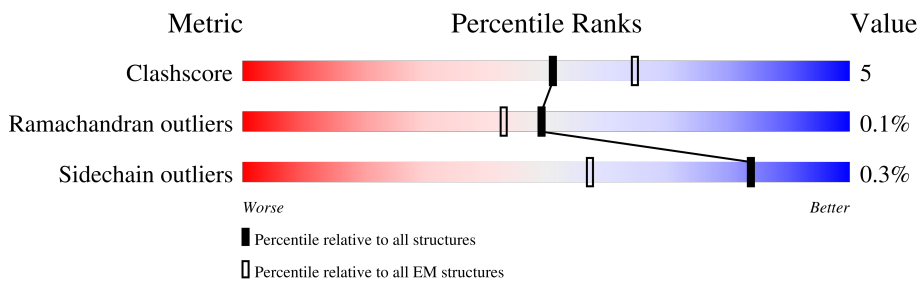
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

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

The reported resolution of this entry is 3.10 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.





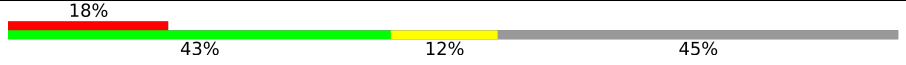
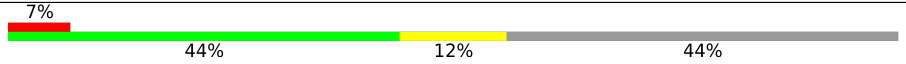
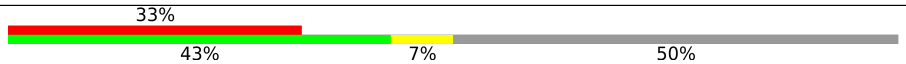
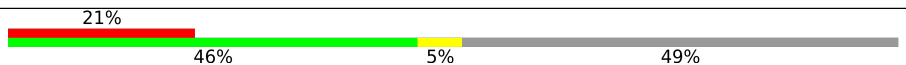
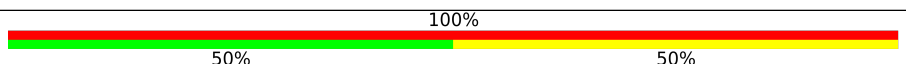
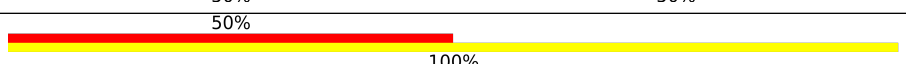
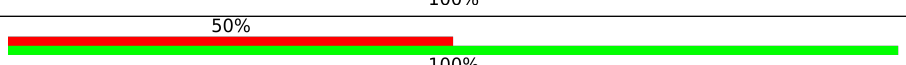
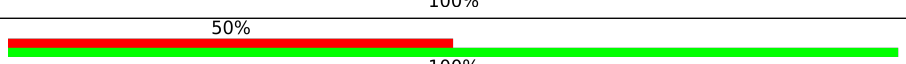
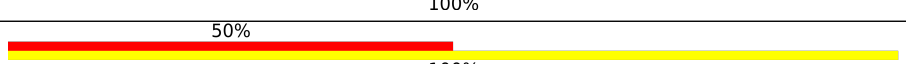
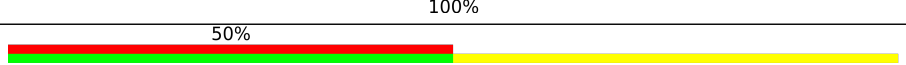

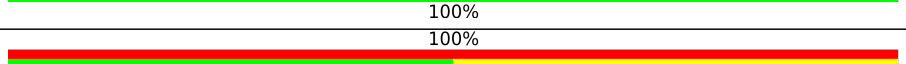




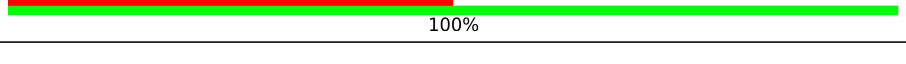
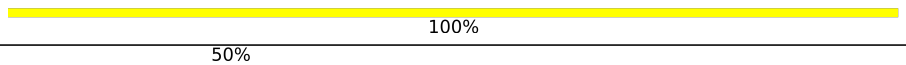
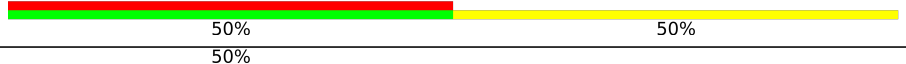
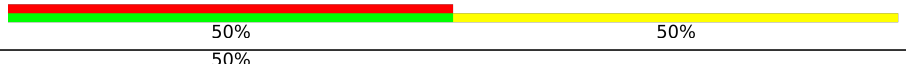
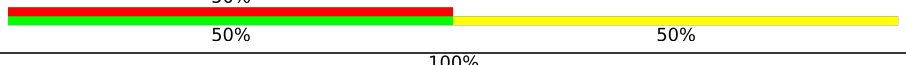
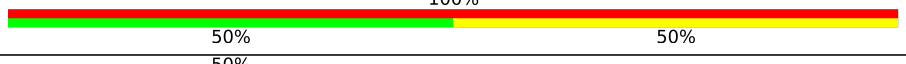
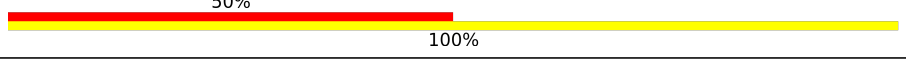
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	480	<div style="display: flex; justify-content: space-between; align-items: center;"> 12% 79% 12% 9% </div>
1	C	480	<div style="display: flex; justify-content: space-between; align-items: center;"> 11% 81% 13% 6% </div>
1	E	480	<div style="display: flex; justify-content: space-between; align-items: center;"> 10% 80% 13% 7% </div>
2	B	352	<div style="display: flex; justify-content: space-between; align-items: center;"> 32% 65% </div>

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Mol	Chain	Length	Quality of chain
2	D	352	
2	F	352	
3	H	240	
3	M	240	
4	L	219	
4	N	219	
5	G	2	
6	I	2	
6	J	2	
6	K	2	
6	O	2	
6	P	2	
6	Q	2	
6	R	2	
6	T	2	
6	U	2	
6	W	2	
6	X	2	
6	Y	2	
6	Z	2	
6	a	2	
6	b	2	
6	d	2	
6	e	2	
6	h	2	

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Mol	Chain	Length	Quality of chain
6	i	2	100%
6	j	2	50%
6	l	2	50%
6	m	2	50%
6	n	2	100%
6	o	2	100%
6	p	2	50%
6	q	2	50%
7	S	6	67%
8	V	3	67%
9	c	5	40%
10	f	10	30%
11	g	9	44%
11	r	9	44%
12	k	7	43%
13	s	9	33%

2 Entry composition i

There are 14 unique types of molecules in this entry. The entry contains 19300 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 gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	435	Total	C	N	O	S	1	0
			3413	2144	599	644	26		
1	C	452	Total	C	N	O	S	2	0
			3553	2232	626	669	26		
1	E	448	Total	C	N	O	S	2	0
			3536	2222	623	665	26		

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	122	Total	C	N	O	S	0	0
			950	605	160	181	4		
2	D	146	Total	C	N	O	S	0	0
			1167	740	201	222	4		
2	F	139	Total	C	N	O	S	0	0
			1095	698	186	207	4		

- Molecule 3 is a protein called Immunoglobulin G PGT151 Fab, Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	132	Total	C	N	O	S	0	0
			1050	670	182	192	6		
3	M	135	Total	C	N	O	S	0	0
			1067	679	185	197	6		

- Molecule 4 is a protein called Immunoglobulin G PGT151 Fab, Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	L	110	Total	C	N	O	S	0	0
			846	531	143	168	4		
4	N	112	Total	C	N	O	S	0	0
			866	545	149	168	4		

- Molecule 5 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	G	2	24	14	1	9	0	0

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



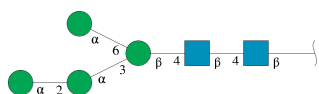
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	I	2	28	16	2	10	0	0
6	J	2	28	16	2	10	0	0
6	K	2	28	16	2	10	0	0
6	O	2	28	16	2	10	0	0
6	P	2	28	16	2	10	0	0
6	Q	2	28	16	2	10	0	0
6	R	2	28	16	2	10	0	0
6	T	2	28	16	2	10	0	0
6	U	2	28	16	2	10	0	0
6	W	2	28	16	2	10	0	0
6	X	2	28	16	2	10	0	0
6	Y	2	28	16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

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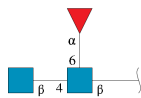
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	Z	2	28	16	2	10	0	0
6	a	2	28	16	2	10	0	0
6	b	2	28	16	2	10	0	0
6	d	2	28	16	2	10	0	0
6	e	2	28	16	2	10	0	0
6	h	2	28	16	2	10	0	0
6	i	2	28	16	2	10	0	0
6	j	2	28	16	2	10	0	0
6	l	2	28	16	2	10	0	0
6	m	2	28	16	2	10	0	0
6	n	2	28	16	2	10	0	0
6	o	2	28	16	2	10	0	0
6	p	2	28	16	2	10	0	0
6	q	2	28	16	2	10	0	0

- Molecule 7 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.



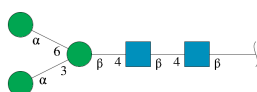
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	S	6	72	40	2	30	0	0

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



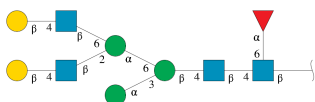
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	V	3	38	22	2	14	0	0

- 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.



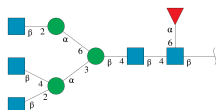
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	c	5	61	34	2	25	0	0

- Molecule 10 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(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)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



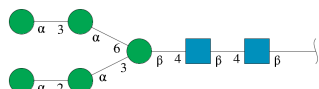
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	f	10	121	68	4	49	0	0

- Molecule 11 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



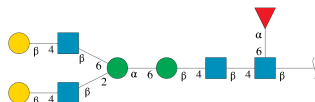
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	g	9	113	64	5	44	0	0
11	r	9	113	64	5	44	0	0

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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
			Total	C	N	O		
12	k	7	83	46	2	35	0	0

- Molecule 13 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	s	9	110	62	4	44	0	0

- Molecule 14 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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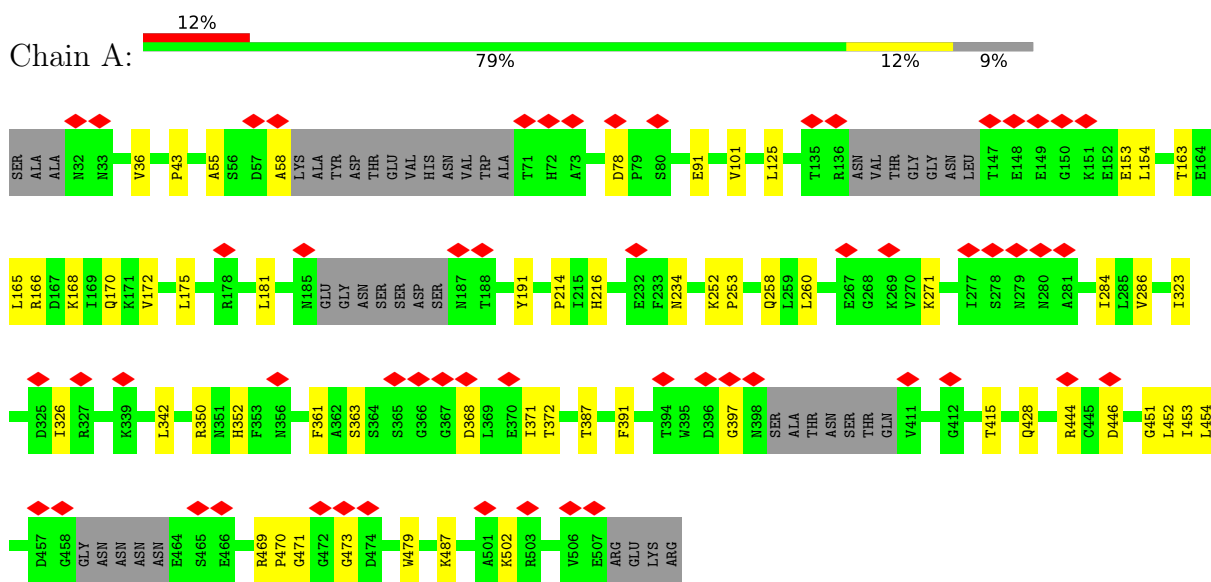
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
14	E	1	Total 14	8	1	5	0
14	E	1	Total 14	8	1	5	0
14	E	1	Total 14	8	1	5	0
14	E	1	Total 14	8	1	5	0
14	E	1	Total 14	8	1	5	0
14	F	1	Total 14	8	1	5	0
14	F	1	Total 14	8	1	5	0

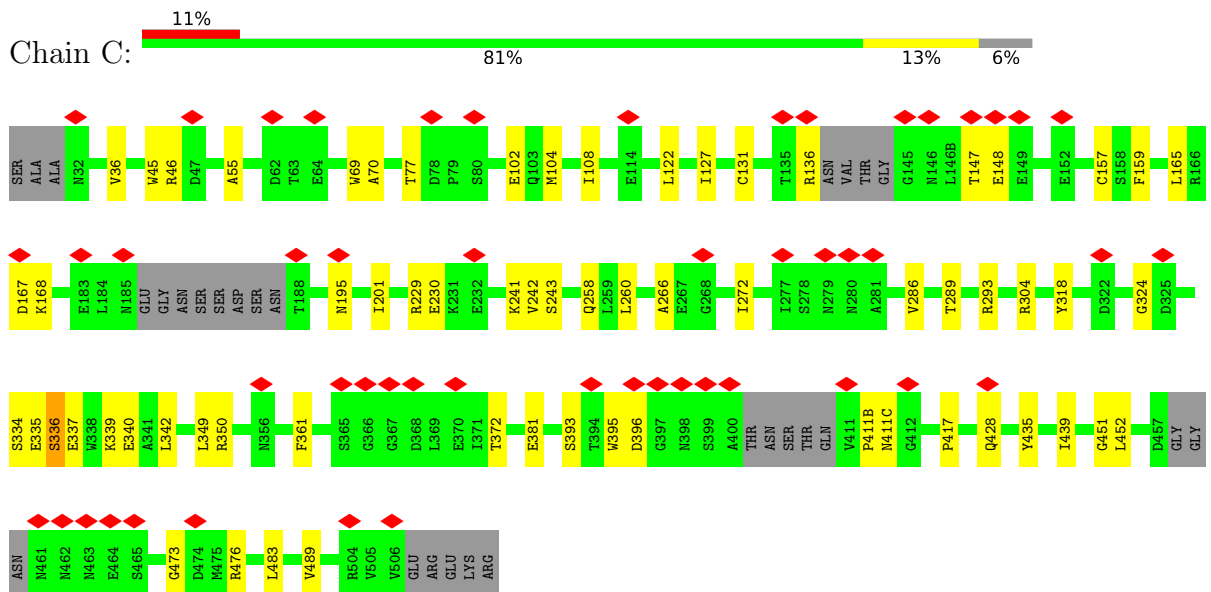
3 Residue-property plots [i](#)

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

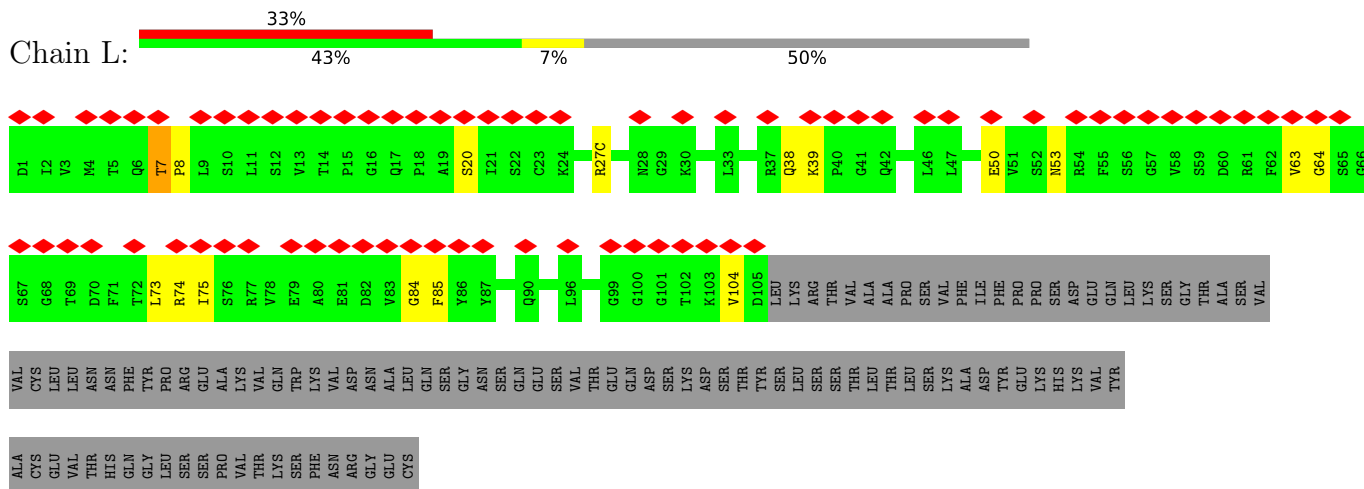
- Molecule 1: Envelope glycoprotein gp160



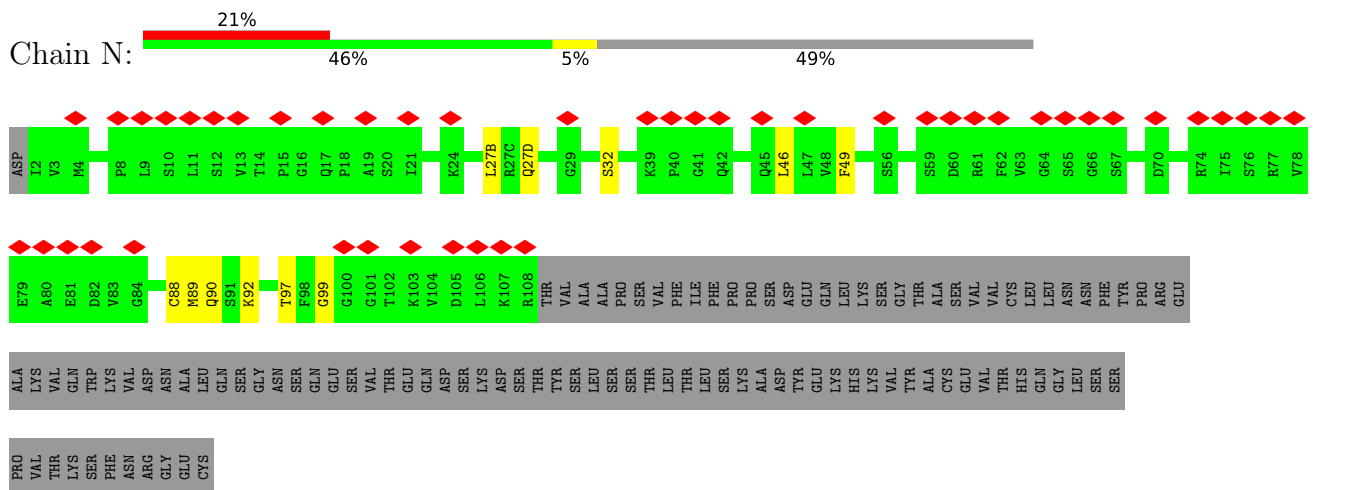
- Molecule 1: Envelope glycoprotein gp160



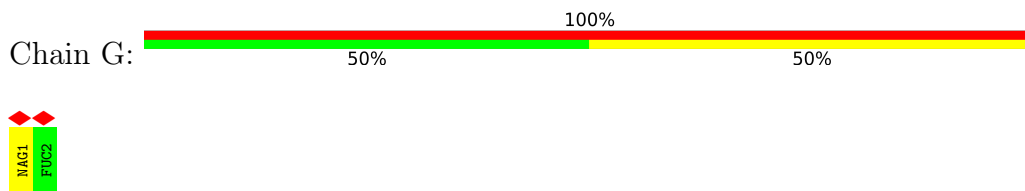
• Molecule 4: Immunoglobulin G PGT151 Fab, Light chain



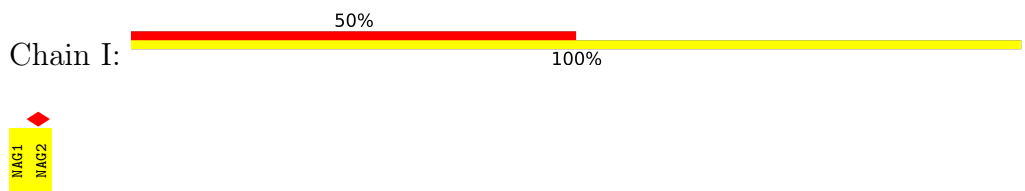
• Molecule 4: Immunoglobulin G PGT151 Fab, Light chain



• Molecule 5: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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



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





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



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



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

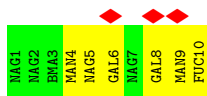


- Molecule 9: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(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)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose





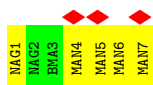
- Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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



- Molecule 13: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-[beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	236179	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 ($e^-/\text{\AA}^2$)	1.885	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	0.301	Depositor
Minimum map value	-0.147	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0583	Depositor
Map size (Å)	329.59998, 329.59998, 329.59998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, MAN, GAL, 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	0.28	0/3481	0.56	0/4719
1	C	0.30	0/3632	0.55	0/4928
1	E	0.31	0/3609	0.59	0/4897
2	B	0.31	0/967	0.48	0/1313
2	D	0.31	0/1188	0.53	0/1614
2	F	0.33	0/1114	0.55	0/1513
3	H	0.32	0/1079	0.63	0/1466
3	M	0.29	0/1096	0.55	0/1489
4	L	0.21	0/864	0.51	0/1167
4	N	0.20	0/884	0.43	0/1192
All	All	0.29	0/17914	0.55	0/24298

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3413	0	3361	37	0
1	C	3553	0	3500	48	0
1	E	3536	0	3477	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	950	0	935	7	0
2	D	1167	0	1154	15	0
2	F	1095	0	1087	15	0
3	H	1050	0	1014	19	0
3	M	1067	0	1029	22	0
4	L	846	0	824	9	0
4	N	866	0	854	6	0
5	G	24	0	22	0	0
6	I	28	0	25	1	0
6	J	28	0	24	0	0
6	K	28	0	25	0	0
6	O	28	0	25	0	0
6	P	28	0	25	0	0
6	Q	28	0	25	0	0
6	R	28	0	25	0	0
6	T	28	0	25	1	0
6	U	28	0	25	0	0
6	W	28	0	25	0	0
6	X	28	0	25	0	0
6	Y	28	0	25	0	0
6	Z	28	0	25	0	0
6	a	28	0	25	1	0
6	b	28	0	25	0	0
6	d	28	0	25	0	0
6	e	28	0	25	1	0
6	h	28	0	24	0	0
6	i	28	0	25	0	0
6	j	28	0	24	1	0
6	l	28	0	25	0	0
6	m	28	0	23	0	0
6	n	28	0	25	0	0
6	o	28	0	25	0	0
6	p	28	0	25	1	0
6	q	28	0	25	4	0
7	S	72	0	61	0	0
8	V	38	0	34	0	0
9	c	61	0	52	0	0
10	f	121	0	103	2	0
11	g	113	0	97	1	0
11	r	113	0	97	1	0
12	k	83	0	70	0	0
13	s	110	0	94	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	A	56	0	51	1	0
14	B	42	0	39	0	0
14	C	70	0	65	0	0
14	D	28	0	26	0	0
14	E	70	0	65	1	0
14	F	28	0	26	0	0
All	All	19300	0	18782	209	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 5.

The worst 5 of 209 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:335:GLU:CD	1:C:411(C):ASN:HB2	1.39	1.41
1:C:335:GLU:OE1	1:C:411(C):ASN:C	1.82	1.23
1:C:335:GLU:OE1	1:C:411(C):ASN:CB	1.86	1.22
1:E:258:GLN:C	1:E:259:LEU:HD22	1.68	1.17
1:C:335:GLU:OE1	1:C:411(C):ASN:CA	1.96	1.12

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	424/480 (88%)	397 (94%)	27 (6%)	0	100	100
1	C	444/480 (92%)	402 (90%)	41 (9%)	1 (0%)	43	73
1	E	440/480 (92%)	401 (91%)	38 (9%)	1 (0%)	43	73
2	B	118/352 (34%)	110 (93%)	8 (7%)	0	100	100
2	D	144/352 (41%)	138 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	135/352 (38%)	127 (94%)	8 (6%)	0	100	100
3	H	130/240 (54%)	106 (82%)	24 (18%)	0	100	100
3	M	133/240 (55%)	122 (92%)	11 (8%)	0	100	100
4	L	108/219 (49%)	94 (87%)	14 (13%)	0	100	100
4	N	110/219 (50%)	105 (96%)	5 (4%)	0	100	100
All	All	2186/3414 (64%)	2002 (92%)	182 (8%)	2 (0%)	49	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	133	ASN
1	C	336	SER

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	387/422 (92%)	386 (100%)	1 (0%)	86	87
1	C	402/422 (95%)	402 (100%)	0	100	100
1	E	400/422 (95%)	398 (100%)	2 (0%)	81	85
2	B	102/298 (34%)	102 (100%)	0	100	100
2	D	127/298 (43%)	127 (100%)	0	100	100
2	F	118/298 (40%)	118 (100%)	0	100	100
3	H	113/207 (55%)	112 (99%)	1 (1%)	70	80
3	M	115/207 (56%)	115 (100%)	0	100	100
4	L	97/195 (50%)	96 (99%)	1 (1%)	68	79
4	N	99/195 (51%)	99 (100%)	0	100	100
All	All	1960/2964 (66%)	1955 (100%)	5 (0%)	84	87

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

Mol	Chain	Res	Type
1	A	166	ARG
1	E	259	LEU
1	E	308	ARG
3	H	51	ILE
4	L	7	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	39	GLN
4	L	38	GLN
4	N	27(D)	GLN
1	C	195	ASN
1	C	146	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

112 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	$\# Z > 2$
5	NAG	G	1	1,5	14,14,15	0.34	0	17,19,21	1.11	2 (11%)
5	FUC	G	2	5	10,10,11	0.73	0	14,14,16	0.71	0
6	NAG	I	1	1,6	14,14,15	0.51	0	17,19,21	0.84	0
6	NAG	I	2	6	14,14,15	0.28	0	17,19,21	0.64	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	J	1	1,6	14,14,15	0.37	0	17,19,21	0.55	0
6	NAG	J	2	6	14,14,15	0.31	0	17,19,21	0.51	0
6	NAG	K	1	1,6	14,14,15	0.51	0	17,19,21	0.70	0
6	NAG	K	2	6	14,14,15	0.48	0	17,19,21	0.49	0
6	NAG	O	1	1,6	14,14,15	0.27	0	17,19,21	0.64	1 (5%)
6	NAG	O	2	6	14,14,15	0.39	0	17,19,21	0.64	1 (5%)
6	NAG	P	1	1,6	14,14,15	0.33	0	17,19,21	0.55	0
6	NAG	P	2	6	14,14,15	0.37	0	17,19,21	0.60	1 (5%)
6	NAG	Q	1	1,6	14,14,15	0.27	0	17,19,21	0.62	0
6	NAG	Q	2	6	14,14,15	0.47	0	17,19,21	0.40	0
6	NAG	R	1	1,6	14,14,15	0.37	0	17,19,21	1.01	1 (5%)
6	NAG	R	2	6	14,14,15	0.53	0	17,19,21	0.53	0
7	NAG	S	1	1,7	14,14,15	0.35	0	17,19,21	0.66	0
7	NAG	S	2	7	14,14,15	0.26	0	17,19,21	0.44	0
7	BMA	S	3	7	11,11,12	0.83	0	15,15,17	1.07	1 (6%)
7	MAN	S	4	7	11,11,12	0.82	1 (9%)	15,15,17	1.30	2 (13%)
7	MAN	S	5	7	11,11,12	0.75	0	15,15,17	1.29	2 (13%)
7	MAN	S	6	7	11,11,12	0.81	0	15,15,17	1.10	2 (13%)
6	NAG	T	1	1,6	14,14,15	0.24	0	17,19,21	0.59	0
6	NAG	T	2	6	14,14,15	0.31	0	17,19,21	0.58	0
6	NAG	U	1	6,2	14,14,15	0.45	0	17,19,21	1.14	1 (5%)
6	NAG	U	2	6	14,14,15	0.47	0	17,19,21	0.37	0
8	NAG	V	1	1,8	14,14,15	0.43	0	17,19,21	0.83	1 (5%)
8	NAG	V	2	8	14,14,15	0.42	0	17,19,21	0.35	0
8	FUC	V	3	8	10,10,11	0.81	0	14,14,16	0.92	1 (7%)
6	NAG	W	1	1,6	14,14,15	0.23	0	17,19,21	0.52	0
6	NAG	W	2	6	14,14,15	0.33	0	17,19,21	0.47	0
6	NAG	X	1	1,6	14,14,15	0.26	0	17,19,21	0.50	0
6	NAG	X	2	6	14,14,15	0.29	0	17,19,21	0.56	0
6	NAG	Y	1	1,6	14,14,15	0.63	0	17,19,21	2.43	3 (17%)
6	NAG	Y	2	6	14,14,15	0.81	1 (7%)	17,19,21	2.35	3 (17%)
6	NAG	Z	1	1,6	14,14,15	0.21	0	17,19,21	0.63	1 (5%)
6	NAG	Z	2	6	14,14,15	0.32	0	17,19,21	0.56	0
6	NAG	a	1	1,6	14,14,15	0.44	0	17,19,21	0.42	0
6	NAG	a	2	6	14,14,15	0.44	0	17,19,21	0.50	0
6	NAG	b	1	1,6	14,14,15	0.26	0	17,19,21	0.63	1 (5%)
6	NAG	b	2	6	14,14,15	0.32	0	17,19,21	0.53	0
9	NAG	c	1	1,9	14,14,15	0.32	0	17,19,21	0.63	1 (5%)
9	NAG	c	2	9	14,14,15	0.21	0	17,19,21	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	BMA	c	3	9	11,11,12	0.59	0	15,15,17	0.92	1 (6%)
9	MAN	c	4	9	11,11,12	0.87	0	15,15,17	1.09	2 (13%)
9	MAN	c	5	9	11,11,12	0.86	0	15,15,17	1.03	2 (13%)
6	NAG	d	1	1,6	14,14,15	0.84	1 (7%)	17,19,21	2.36	3 (17%)
6	NAG	d	2	6	14,14,15	0.33	0	17,19,21	0.48	0
6	NAG	e	1	1,6	14,14,15	0.22	0	17,19,21	0.44	0
6	NAG	e	2	6	14,14,15	0.37	0	17,19,21	0.69	1 (5%)
10	NAG	f	1	10,2	14,14,15	0.31	0	17,19,21	0.52	0
10	FUC	f	10	10	10,10,11	0.78	0	14,14,16	0.77	0
10	NAG	f	2	10	14,14,15	0.20	0	17,19,21	0.65	0
10	BMA	f	3	10	11,11,12	1.02	0	15,15,17	0.83	0
10	MAN	f	4	10	11,11,12	0.75	0	15,15,17	1.34	2 (13%)
10	NAG	f	5	10	14,14,15	0.29	0	17,19,21	0.65	1 (5%)
10	GAL	f	6	10	11,11,12	0.75	0	15,15,17	0.85	0
10	NAG	f	7	10	14,14,15	0.22	0	17,19,21	0.55	0
10	GAL	f	8	10	11,11,12	0.59	0	15,15,17	1.16	1 (6%)
10	MAN	f	9	10	11,11,12	0.70	0	15,15,17	1.03	2 (13%)
11	NAG	g	1	11,2	14,14,15	0.33	0	17,19,21	1.28	2 (11%)
11	NAG	g	2	11	14,14,15	0.73	1 (7%)	17,19,21	0.73	0
11	BMA	g	3	11	11,11,12	0.81	0	15,15,17	1.34	2 (13%)
11	MAN	g	4	11	11,11,12	0.77	0	15,15,17	1.39	2 (13%)
11	NAG	g	5	11	14,14,15	0.36	0	17,19,21	0.53	0
11	NAG	g	6	11	14,14,15	0.42	0	17,19,21	0.55	0
11	MAN	g	7	11	11,11,12	0.65	0	15,15,17	1.21	2 (13%)
11	NAG	g	8	11	14,14,15	0.28	0	17,19,21	0.49	0
11	FUC	g	9	11	10,10,11	0.65	0	14,14,16	0.82	1 (7%)
6	NAG	h	1	1,6	14,14,15	0.60	0	17,19,21	0.65	0
6	NAG	h	2	6	14,14,15	0.42	0	17,19,21	0.50	0
6	NAG	i	1	1,6	14,14,15	0.27	0	17,19,21	0.68	1 (5%)
6	NAG	i	2	6	14,14,15	0.37	0	17,19,21	0.38	0
6	NAG	j	1	1,6	14,14,15	0.77	1 (7%)	17,19,21	2.45	4 (23%)
6	NAG	j	2	6	14,14,15	0.96	1 (7%)	17,19,21	2.36	3 (17%)
12	NAG	k	1	1,12	14,14,15	0.30	0	17,19,21	0.68	1 (5%)
12	NAG	k	2	12	14,14,15	0.41	0	17,19,21	0.51	0
12	BMA	k	3	12	11,11,12	0.66	0	15,15,17	0.81	0
12	MAN	k	4	12	11,11,12	0.80	0	15,15,17	1.59	2 (13%)
12	MAN	k	5	12	11,11,12	0.75	0	15,15,17	1.07	2 (13%)
12	MAN	k	6	12	11,11,12	0.64	0	15,15,17	1.14	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	MAN	k	7	12	11,11,12	0.78	0	15,15,17	1.00	1 (6%)
6	NAG	l	1	1,6	14,14,15	0.30	0	17,19,21	0.82	1 (5%)
6	NAG	l	2	6	14,14,15	0.38	0	17,19,21	0.48	0
6	NAG	m	1	1,6	14,14,15	0.23	0	17,19,21	0.56	0
6	NAG	m	2	6	14,14,15	0.38	0	17,19,21	0.47	0
6	NAG	n	1	1,6	14,14,15	0.50	0	17,19,21	0.64	0
6	NAG	n	2	6	14,14,15	0.42	0	17,19,21	0.42	0
6	NAG	o	1	1,6	14,14,15	0.65	1 (7%)	17,19,21	0.47	0
6	NAG	o	2	6	14,14,15	0.31	0	17,19,21	0.53	0
6	NAG	p	1	1,6	14,14,15	0.19	0	17,19,21	0.59	0
6	NAG	p	2	6	14,14,15	0.34	0	17,19,21	0.58	0
6	NAG	q	1	6	14,14,15	0.58	1 (7%)	17,19,21	0.59	0
6	NAG	q	2	6	14,14,15	0.28	0	17,19,21	0.49	0
11	NAG	r	1	11,2	14,14,15	0.24	0	17,19,21	1.18	1 (5%)
11	NAG	r	2	11	14,14,15	0.51	0	17,19,21	0.66	0
11	BMA	r	3	11	11,11,12	0.76	0	15,15,17	1.07	2 (13%)
11	MAN	r	4	11	11,11,12	0.73	0	15,15,17	1.44	1 (6%)
11	NAG	r	5	11	14,14,15	0.46	0	17,19,21	0.54	0
11	NAG	r	6	11	14,14,15	0.38	0	17,19,21	0.48	0
11	MAN	r	7	11	11,11,12	0.66	0	15,15,17	1.44	2 (13%)
11	NAG	r	8	11	14,14,15	0.28	0	17,19,21	0.56	0
11	FUC	r	9	11	10,10,11	0.82	0	14,14,16	0.83	0
13	NAG	s	1	13,2	14,14,15	0.28	0	17,19,21	0.49	0
13	NAG	s	2	13	14,14,15	0.25	0	17,19,21	0.62	0
13	BMA	s	3	13	11,11,12	0.91	0	15,15,17	0.87	0
13	MAN	s	4	13	11,11,12	0.83	0	15,15,17	1.24	2 (13%)
13	NAG	s	5	13	14,14,15	0.37	0	17,19,21	0.60	0
13	GAL	s	6	13	11,11,12	0.69	0	15,15,17	0.84	0
13	NAG	s	7	13	14,14,15	0.24	0	17,19,21	0.53	0
13	GAL	s	8	13	11,11,12	0.72	0	15,15,17	1.16	1 (6%)
13	FUC	s	9	13	10,10,11	0.57	0	14,14,16	0.74	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
5	NAG	G	1	1,5	-	2/6/23/26	0/1/1/1
5	FUC	G	2	5	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	I	1	1,6	-	4/6/23/26	0/1/1/1
6	NAG	I	2	6	-	2/6/23/26	0/1/1/1
6	NAG	J	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	J	2	6	-	2/6/23/26	0/1/1/1
6	NAG	K	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	K	2	6	-	2/6/23/26	0/1/1/1
6	NAG	O	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	O	2	6	-	2/6/23/26	0/1/1/1
6	NAG	P	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	P	2	6	-	1/6/23/26	0/1/1/1
6	NAG	Q	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	2/6/23/26	0/1/1/1
6	NAG	R	1	1,6	-	4/6/23/26	0/1/1/1
6	NAG	R	2	6	-	1/6/23/26	0/1/1/1
7	NAG	S	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	S	2	7	-	2/6/23/26	0/1/1/1
7	BMA	S	3	7	-	0/2/19/22	0/1/1/1
7	MAN	S	4	7	-	0/2/19/22	0/1/1/1
7	MAN	S	5	7	-	0/2/19/22	0/1/1/1
7	MAN	S	6	7	-	2/2/19/22	0/1/1/1
6	NAG	T	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	T	2	6	-	0/6/23/26	0/1/1/1
6	NAG	U	1	6,2	-	4/6/23/26	0/1/1/1
6	NAG	U	2	6	-	0/6/23/26	0/1/1/1
8	NAG	V	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	V	2	8	-	2/6/23/26	0/1/1/1
8	FUC	V	3	8	-	-	0/1/1/1
6	NAG	W	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	W	2	6	-	0/6/23/26	0/1/1/1
6	NAG	X	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	X	2	6	-	2/6/23/26	0/1/1/1
6	NAG	Y	1	1,6	-	6/6/23/26	0/1/1/1
6	NAG	Y	2	6	-	5/6/23/26	0/1/1/1
6	NAG	Z	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	Z	2	6	-	2/6/23/26	0/1/1/1
6	NAG	a	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	a	2	6	-	2/6/23/26	0/1/1/1
6	NAG	b	1	1,6	-	1/6/23/26	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	MAN	k	4	12	-	2/2/19/22	0/1/1/1
12	MAN	k	5	12	-	2/2/19/22	0/1/1/1
12	MAN	k	6	12	-	2/2/19/22	0/1/1/1
12	MAN	k	7	12	-	1/2/19/22	0/1/1/1
6	NAG	l	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	l	2	6	-	0/6/23/26	0/1/1/1
6	NAG	m	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	m	2	6	-	2/6/23/26	0/1/1/1
6	NAG	n	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	n	2	6	-	2/6/23/26	0/1/1/1
6	NAG	o	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	o	2	6	-	2/6/23/26	0/1/1/1
6	NAG	p	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	p	2	6	-	3/6/23/26	0/1/1/1
6	NAG	q	1	6	-	2/6/23/26	0/1/1/1
6	NAG	q	2	6	-	0/6/23/26	0/1/1/1
11	NAG	r	1	11,2	-	4/6/23/26	0/1/1/1
11	NAG	r	2	11	-	2/6/23/26	0/1/1/1
11	BMA	r	3	11	-	0/2/19/22	0/1/1/1
11	MAN	r	4	11	-	0/2/19/22	0/1/1/1
11	NAG	r	5	11	-	0/6/23/26	0/1/1/1
11	NAG	r	6	11	-	2/6/23/26	0/1/1/1
11	MAN	r	7	11	-	2/2/19/22	0/1/1/1
11	NAG	r	8	11	-	2/6/23/26	0/1/1/1
11	FUC	r	9	11	-	-	0/1/1/1
13	NAG	s	1	13,2	-	0/6/23/26	0/1/1/1
13	NAG	s	2	13	-	0/6/23/26	0/1/1/1
13	BMA	s	3	13	-	2/2/19/22	0/1/1/1
13	MAN	s	4	13	-	0/2/19/22	0/1/1/1
13	NAG	s	5	13	-	2/6/23/26	0/1/1/1
13	GAL	s	6	13	-	0/2/19/22	0/1/1/1
13	NAG	s	7	13	-	0/6/23/26	0/1/1/1
13	GAL	s	8	13	-	0/2/19/22	0/1/1/1
13	FUC	s	9	13	-	-	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	j	2	NAG	C1-C2	2.91	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	g	2	NAG	O5-C1	-2.55	1.39	1.43
6	d	1	NAG	C1-C2	2.42	1.55	1.52
6	Y	2	NAG	C1-C2	2.36	1.55	1.52
6	o	1	NAG	C1-C2	2.23	1.55	1.52

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Y	1	NAG	C2-N2-C7	8.36	134.11	122.90
6	j	1	NAG	C2-N2-C7	8.35	134.09	122.90
6	d	1	NAG	C2-N2-C7	8.34	134.07	122.90
6	j	2	NAG	C2-N2-C7	8.28	133.99	122.90
6	Y	2	NAG	C2-N2-C7	8.24	133.95	122.90

There are no chirality outliers.

5 of 155 torsion outliers are listed below:

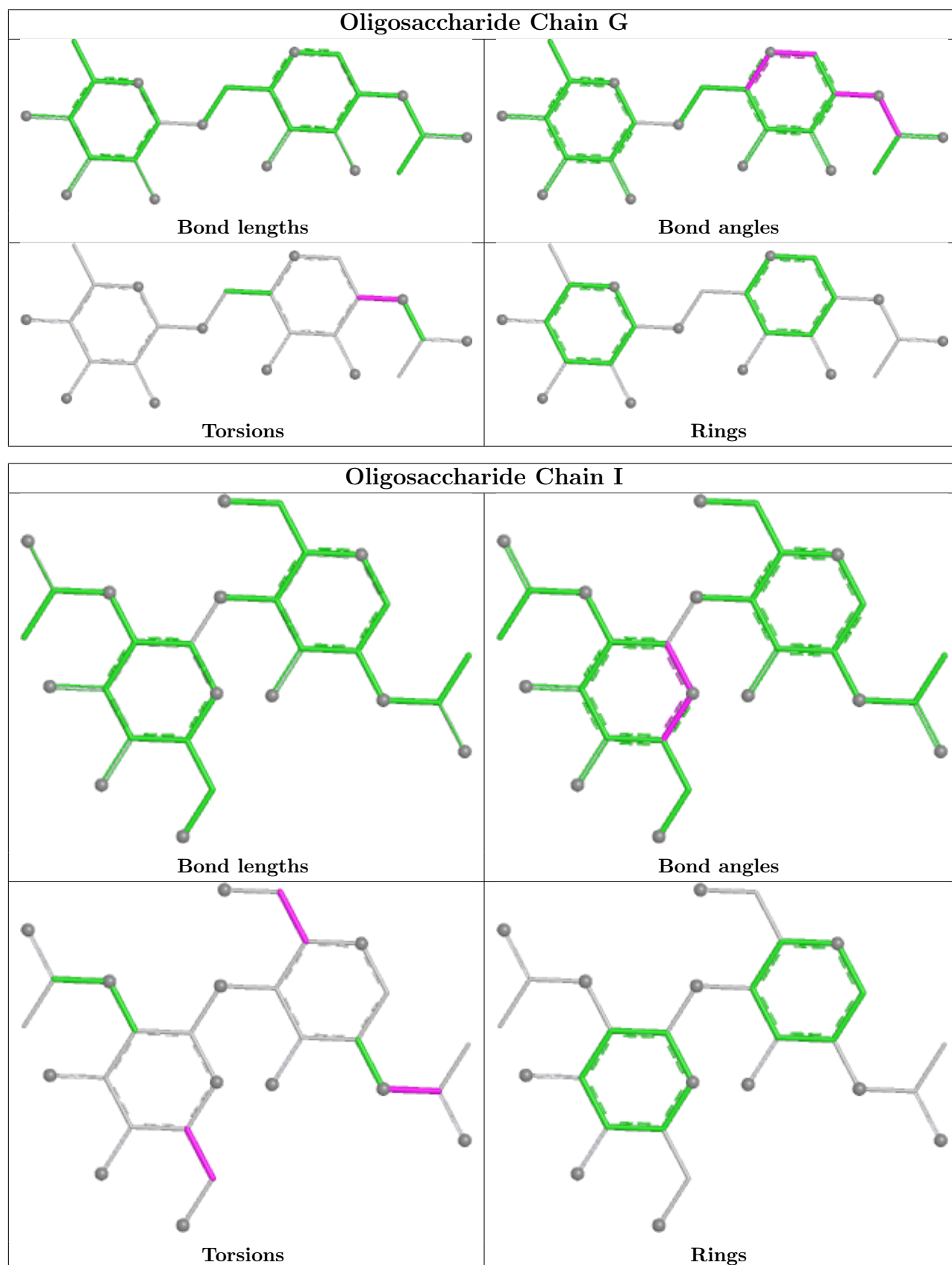
Mol	Chain	Res	Type	Atoms
6	o	2	NAG	O5-C5-C6-O6
6	i	1	NAG	O5-C5-C6-O6
6	I	1	NAG	O5-C5-C6-O6
11	r	8	NAG	O5-C5-C6-O6
6	K	2	NAG	C4-C5-C6-O6

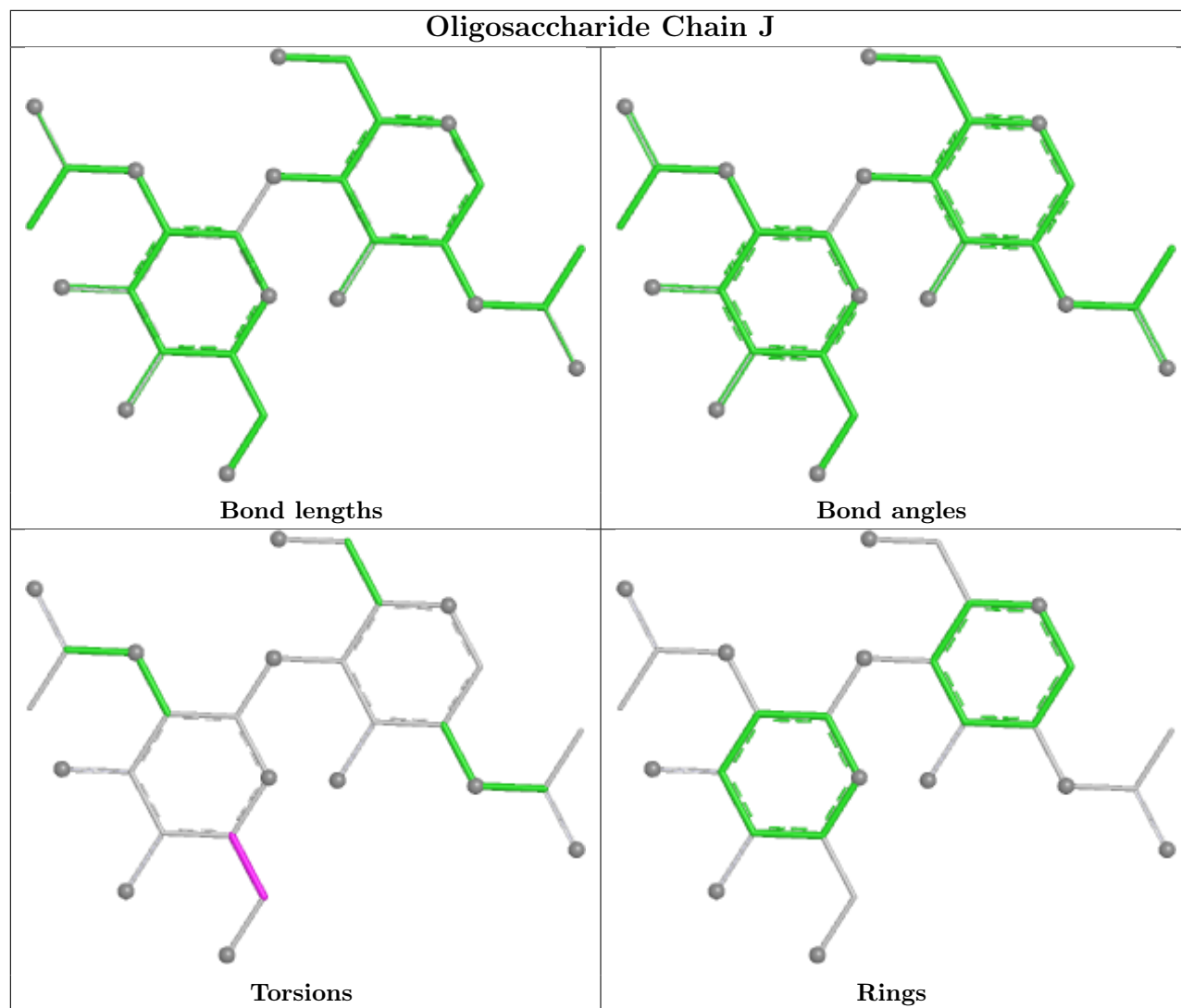
There are no ring outliers.

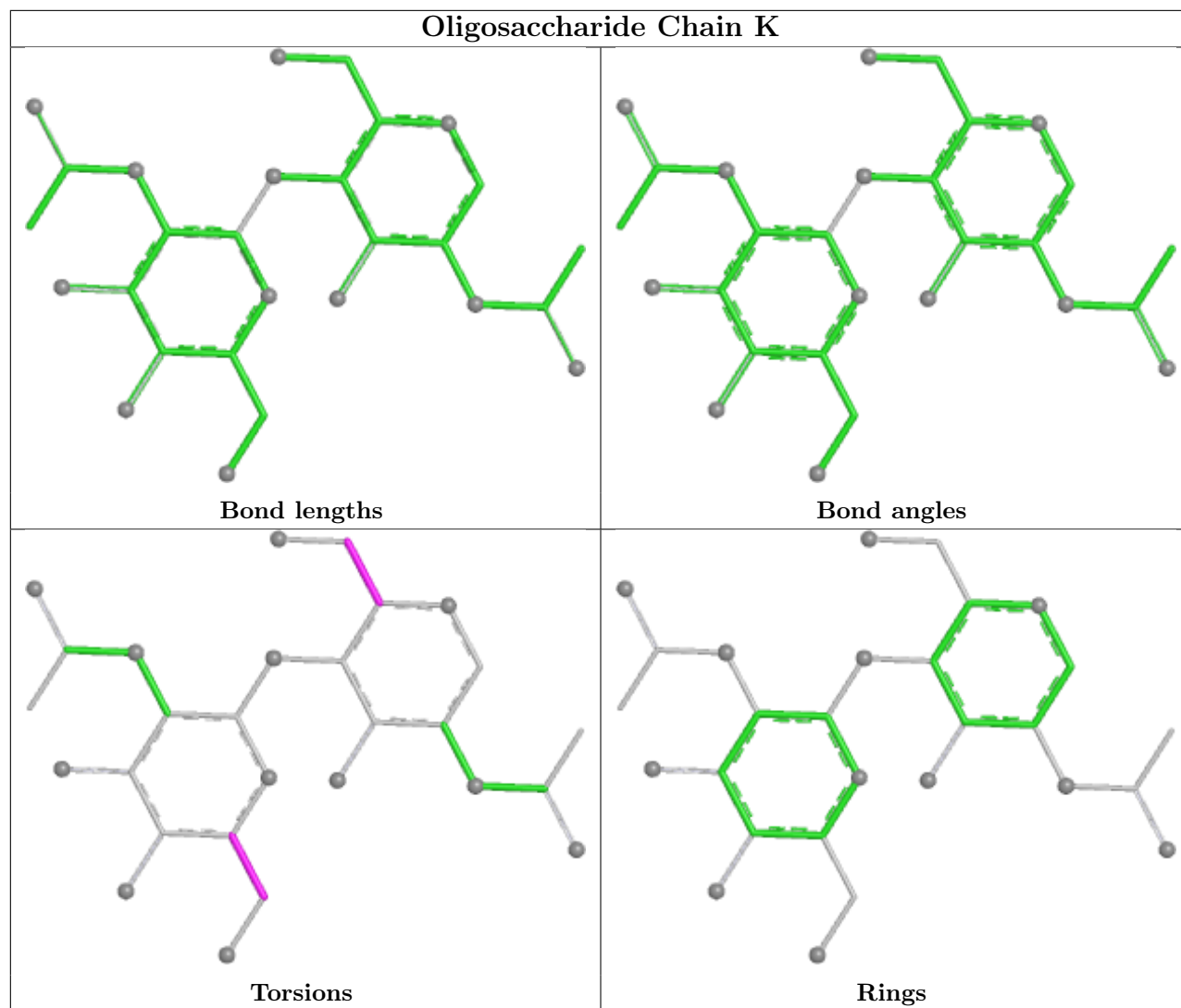
12 monomers are involved in 15 short contacts:

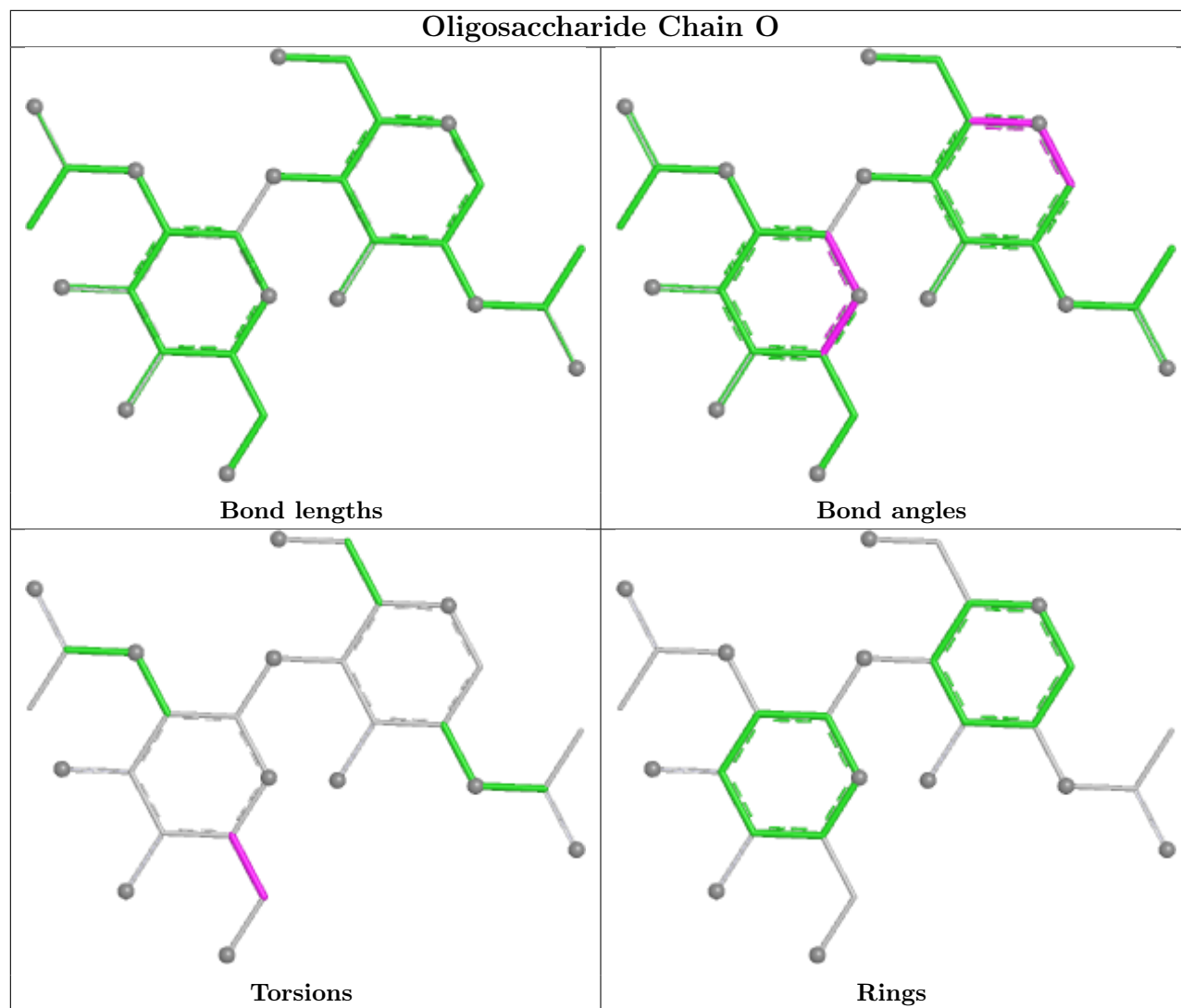
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	T	1	NAG	1	0
11	r	2	NAG	1	0
6	p	1	NAG	1	0
6	e	1	NAG	1	0
10	f	10	FUC	1	0
13	s	7	NAG	1	0
6	q	1	NAG	4	0
6	I	1	NAG	1	0
11	g	5	NAG	1	0
10	f	6	GAL	1	0
6	j	1	NAG	1	0
6	a	1	NAG	1	0

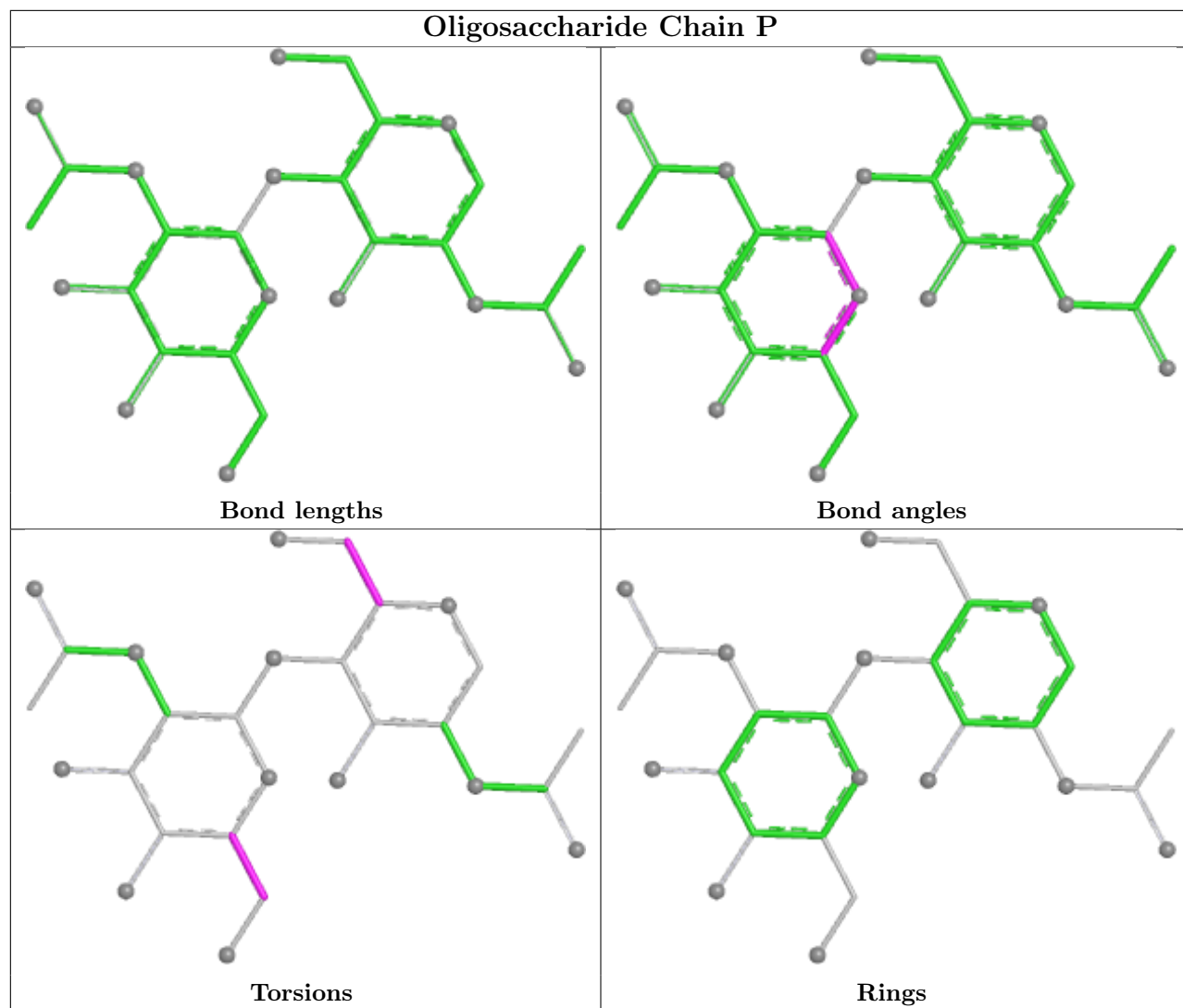
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

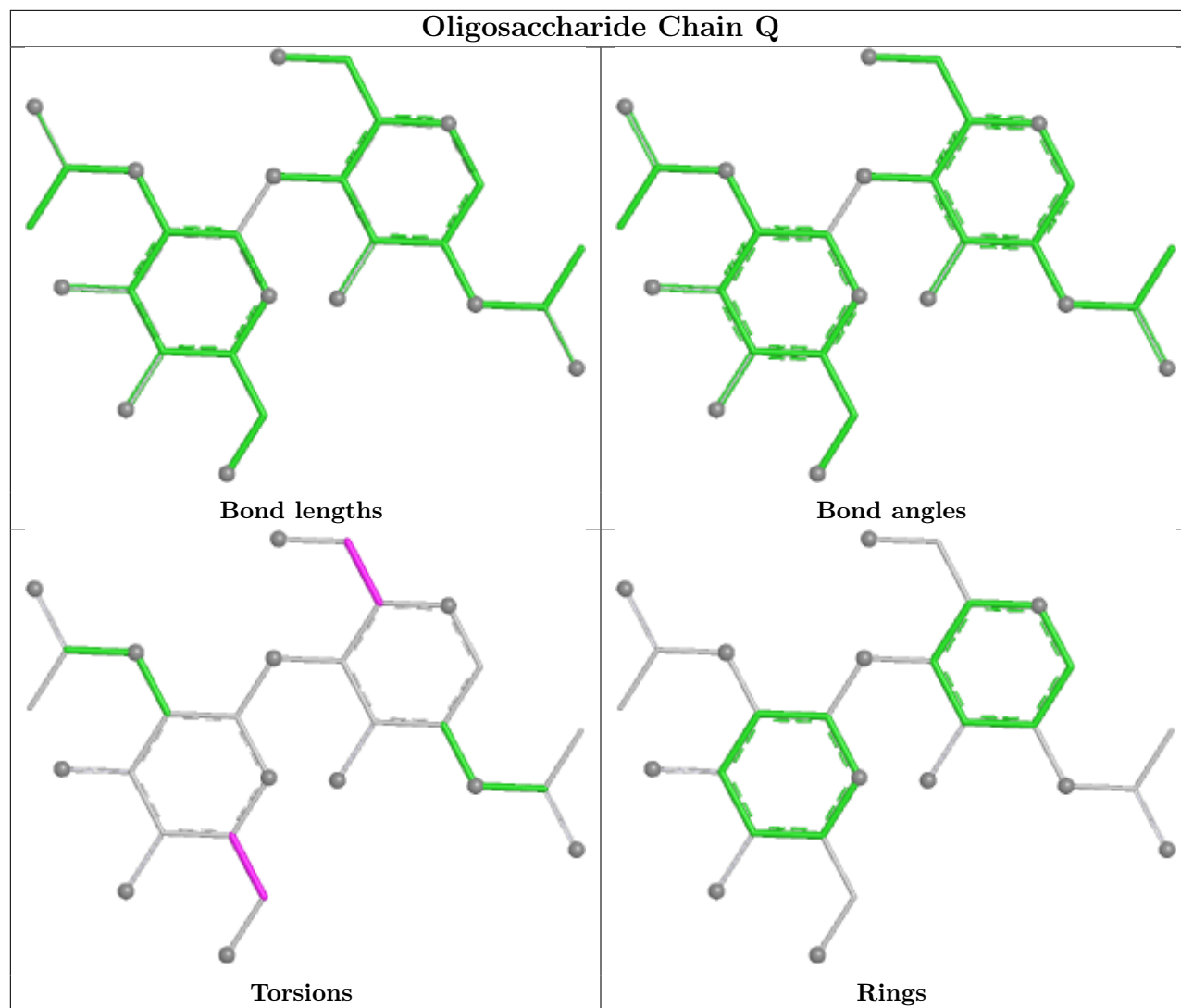


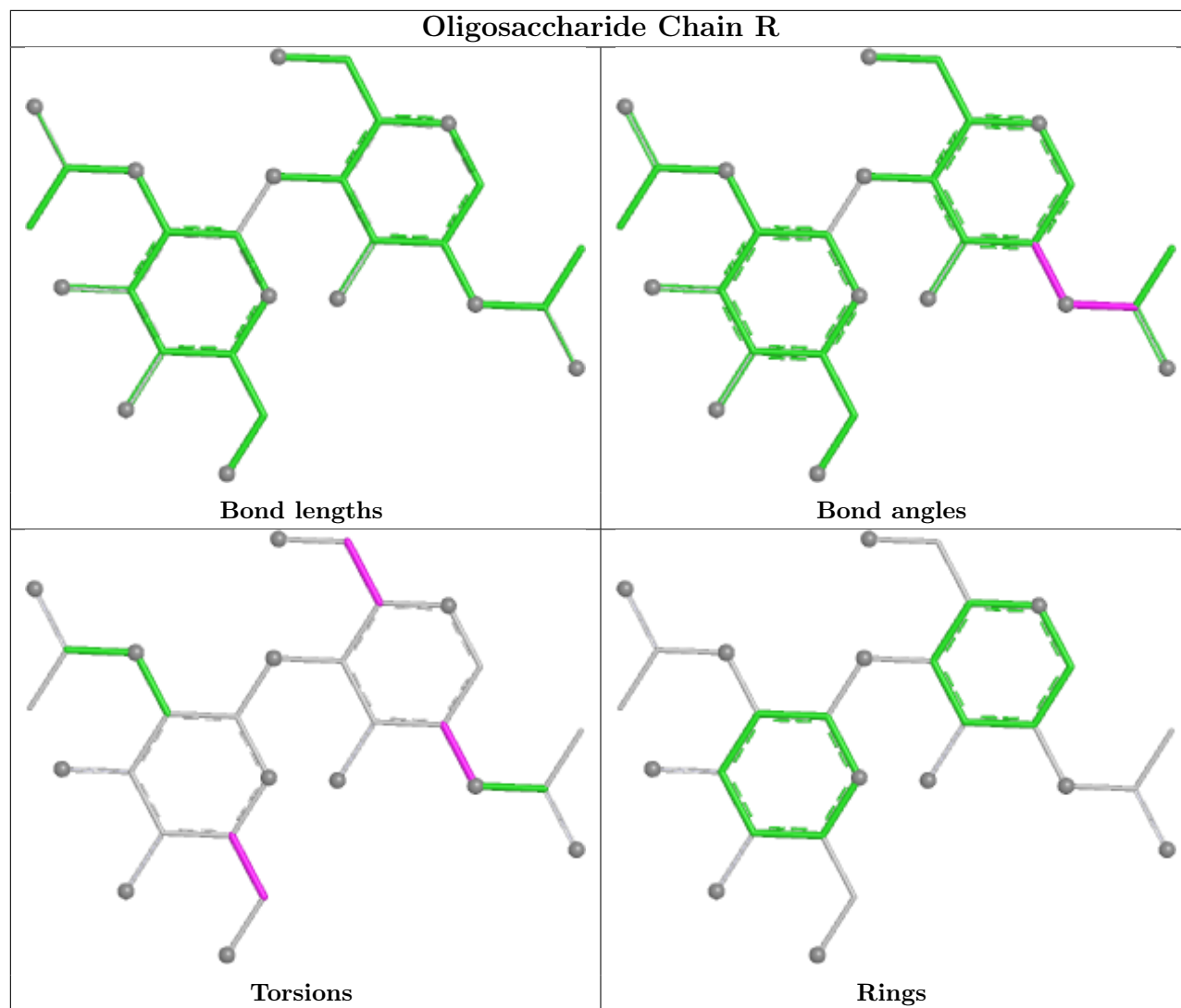


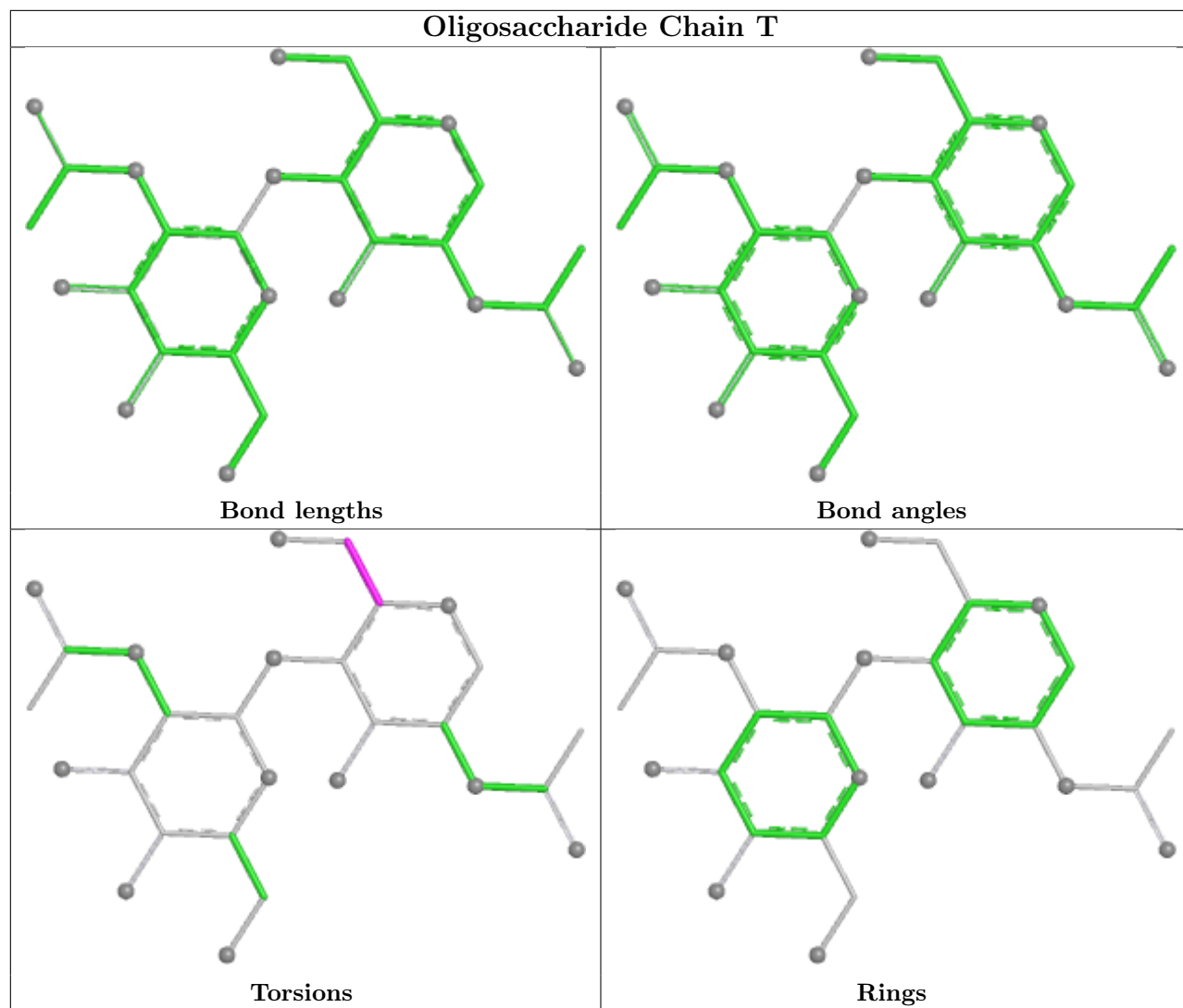


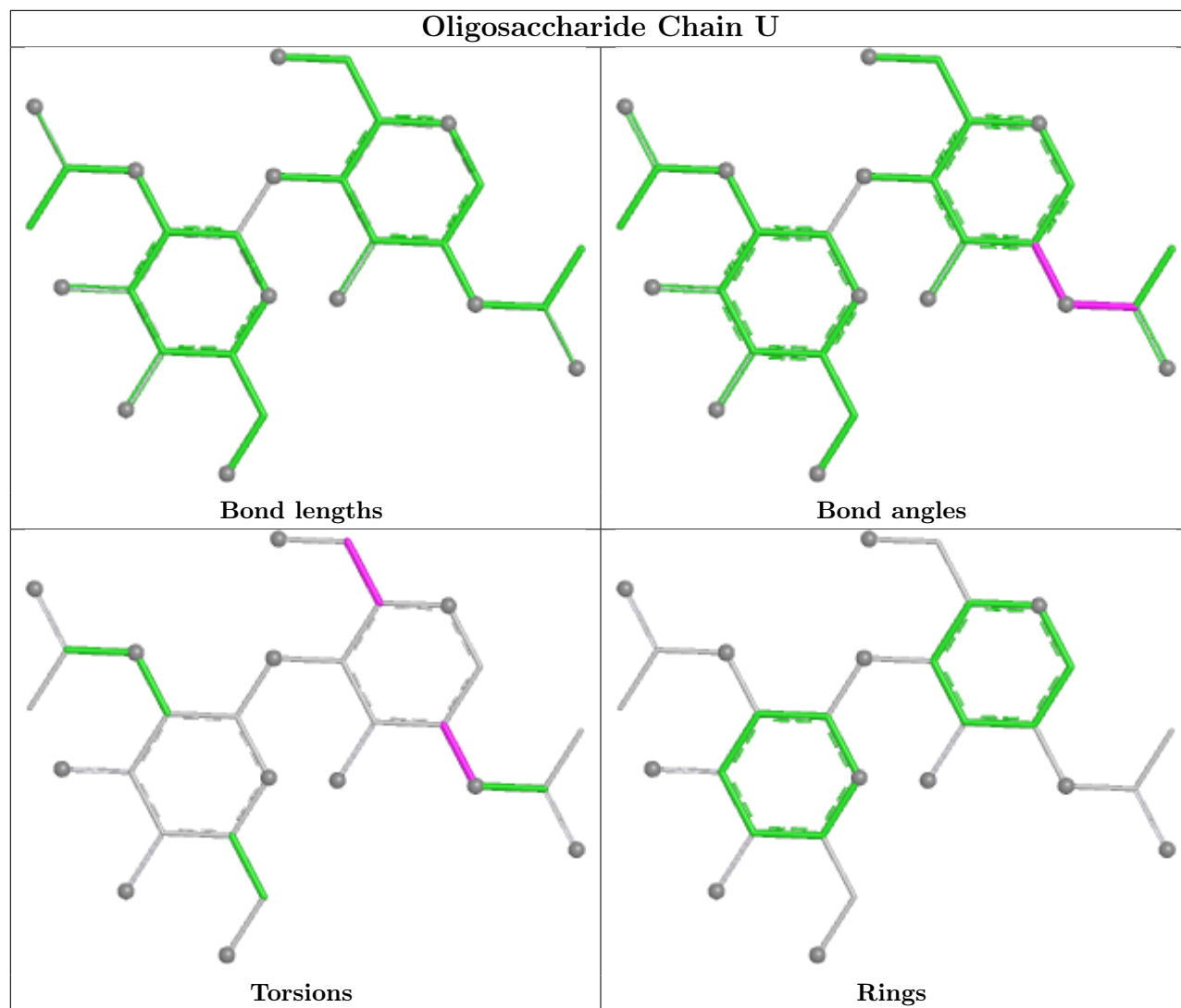


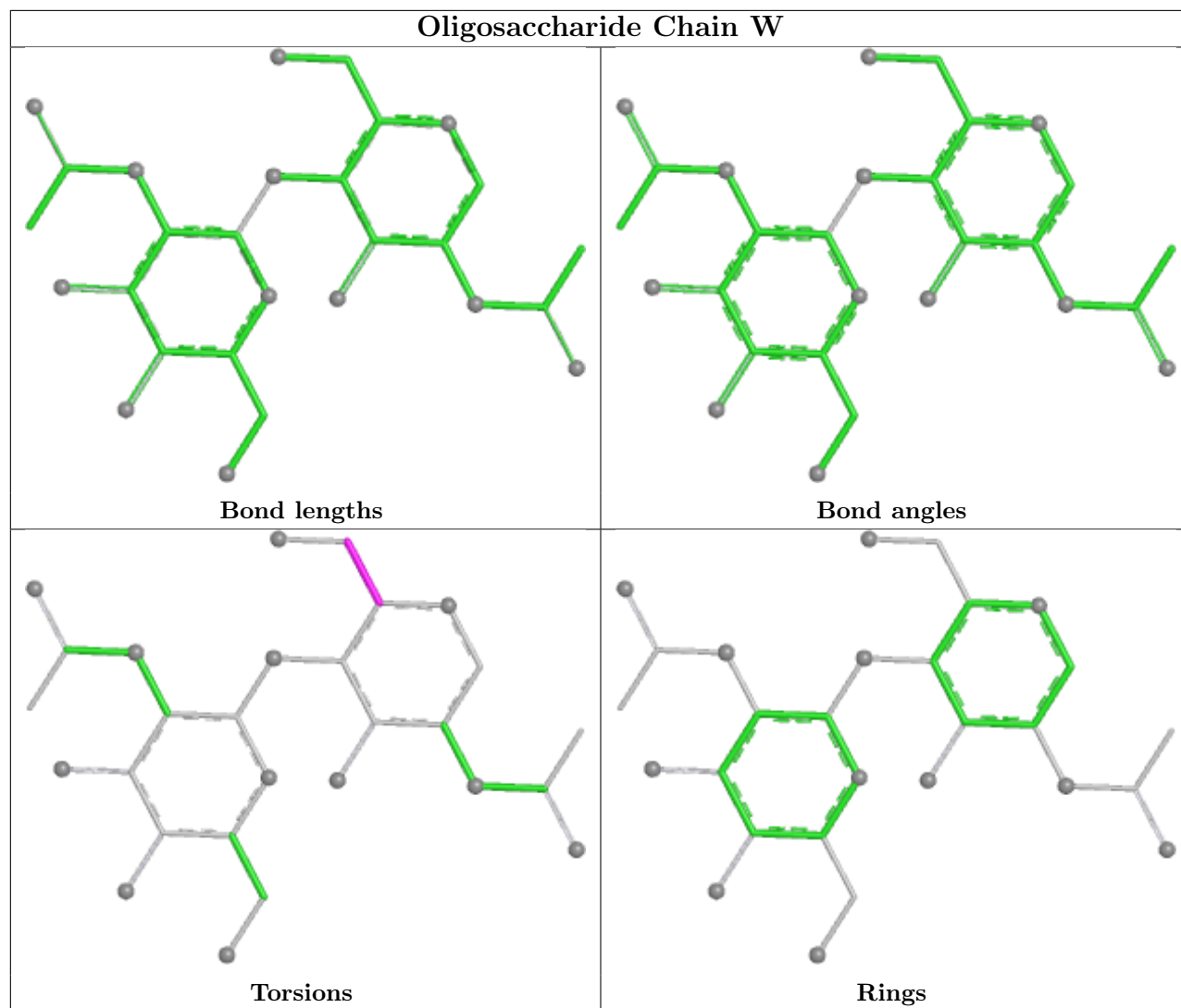


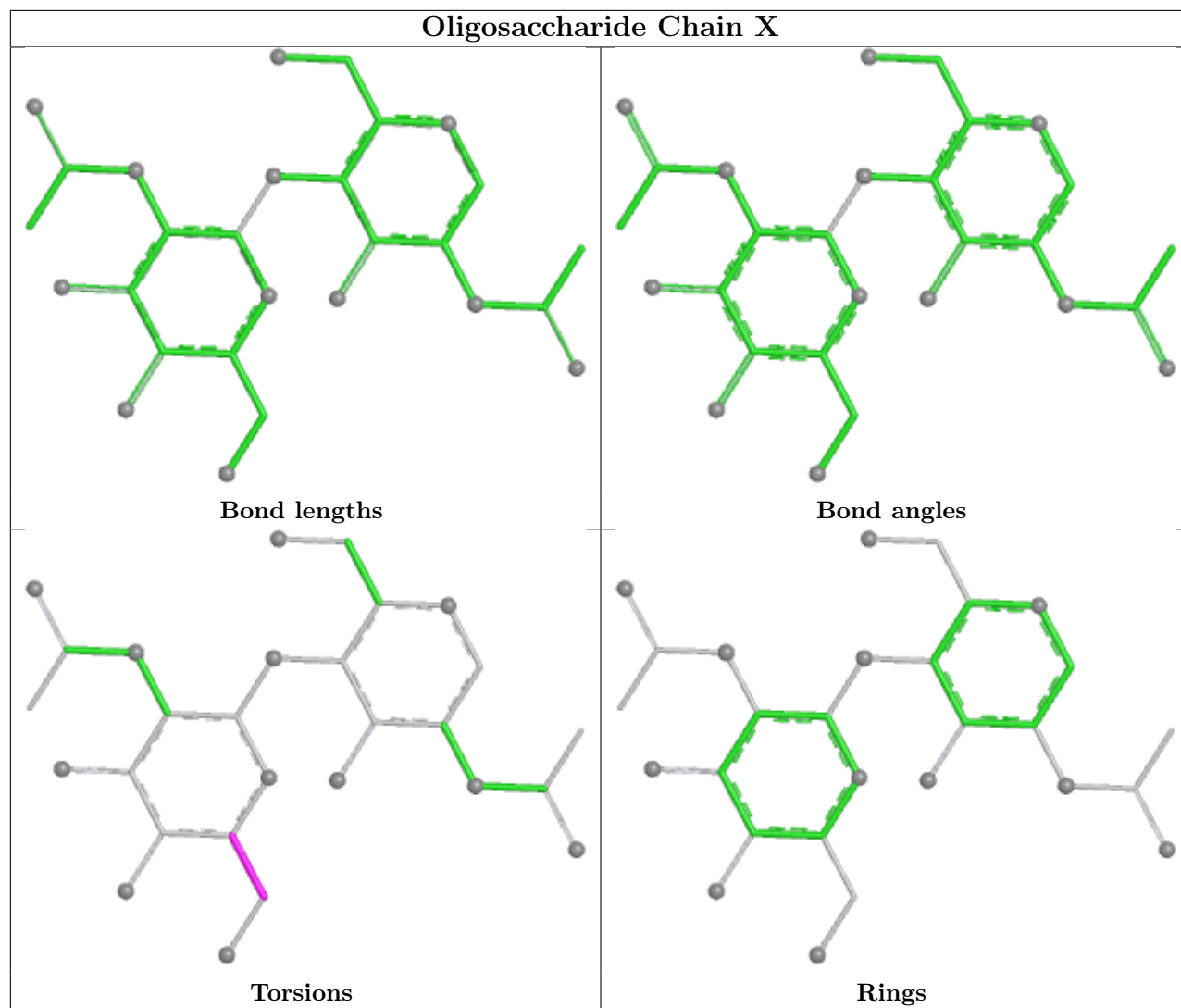


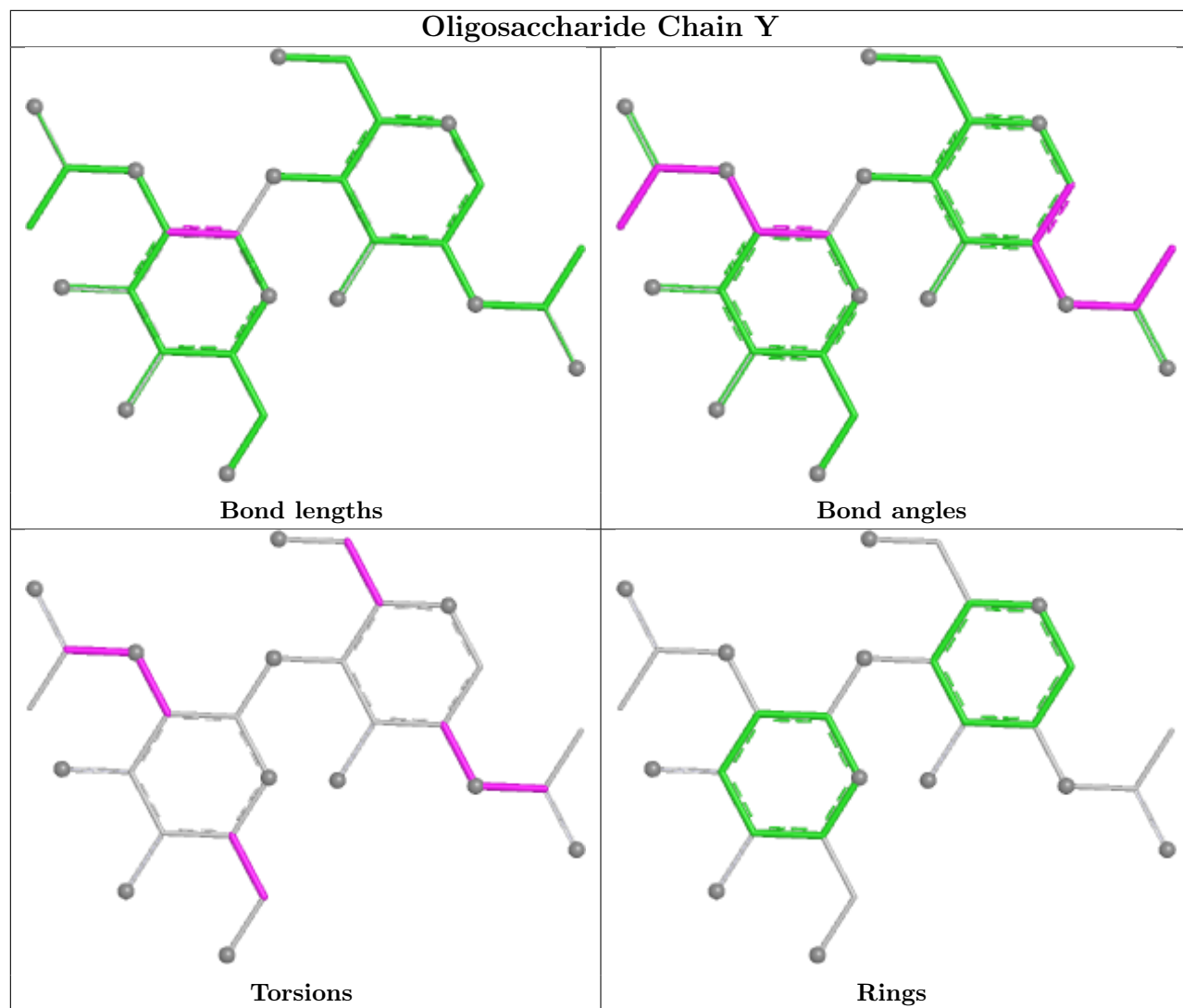


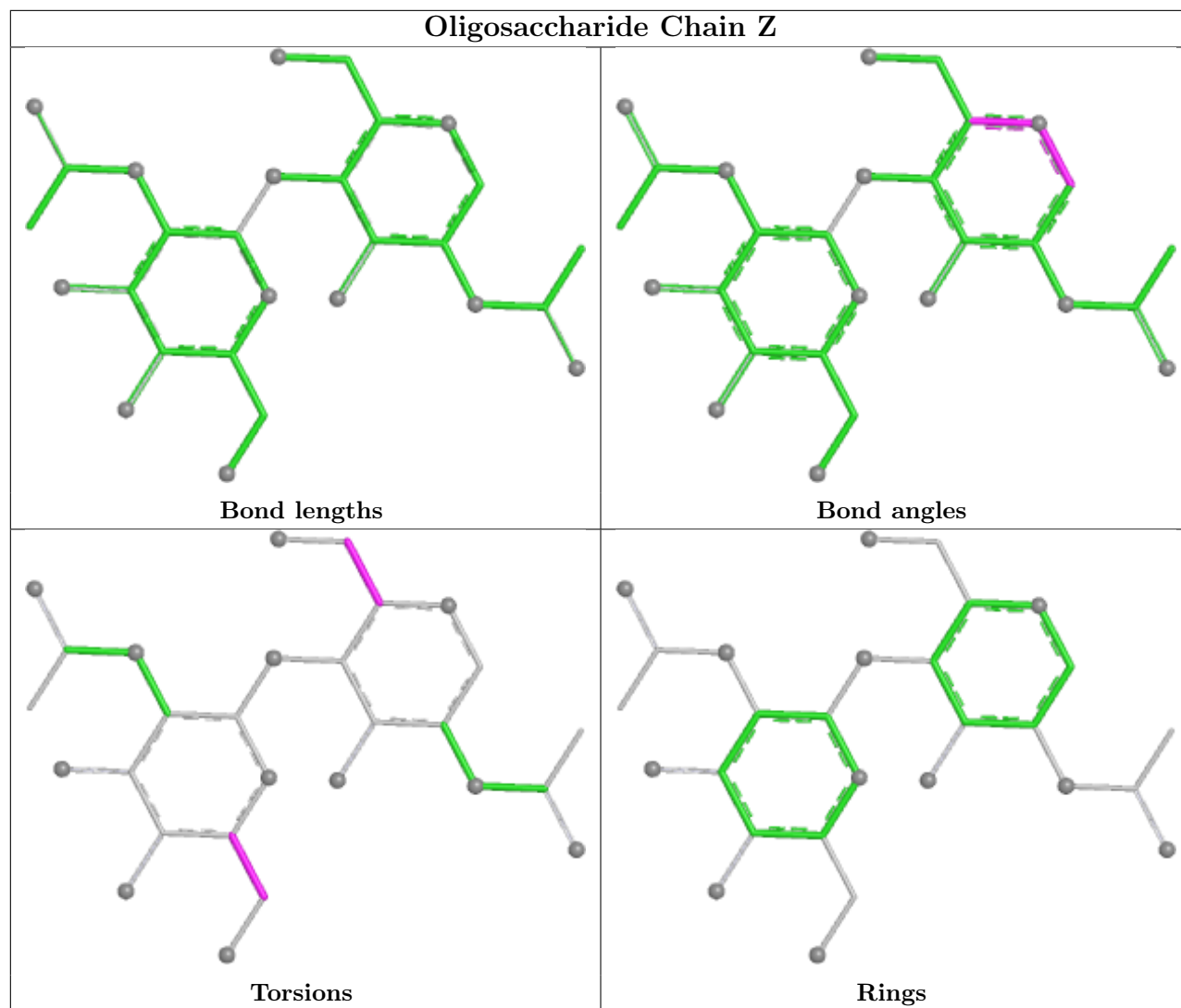


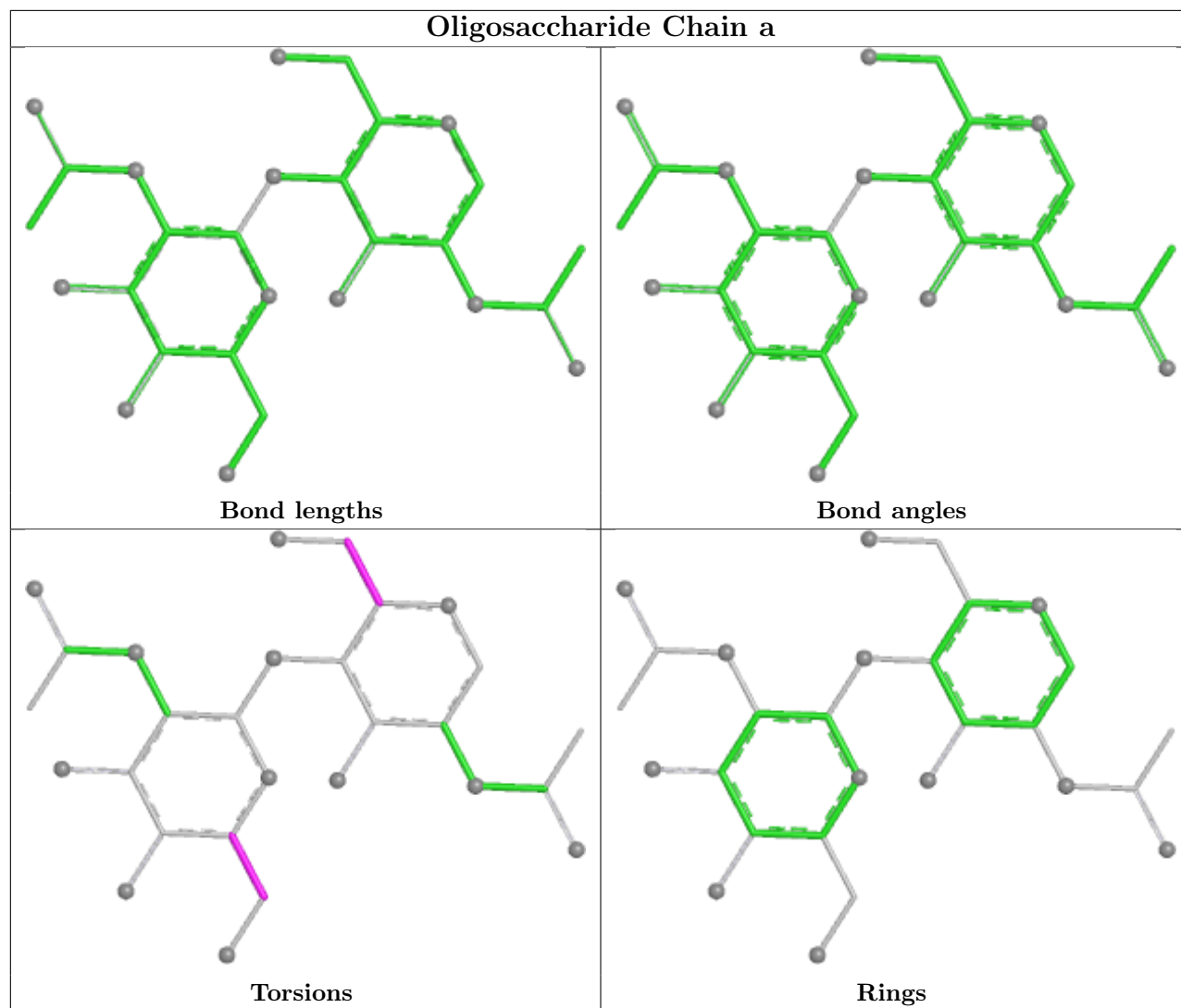


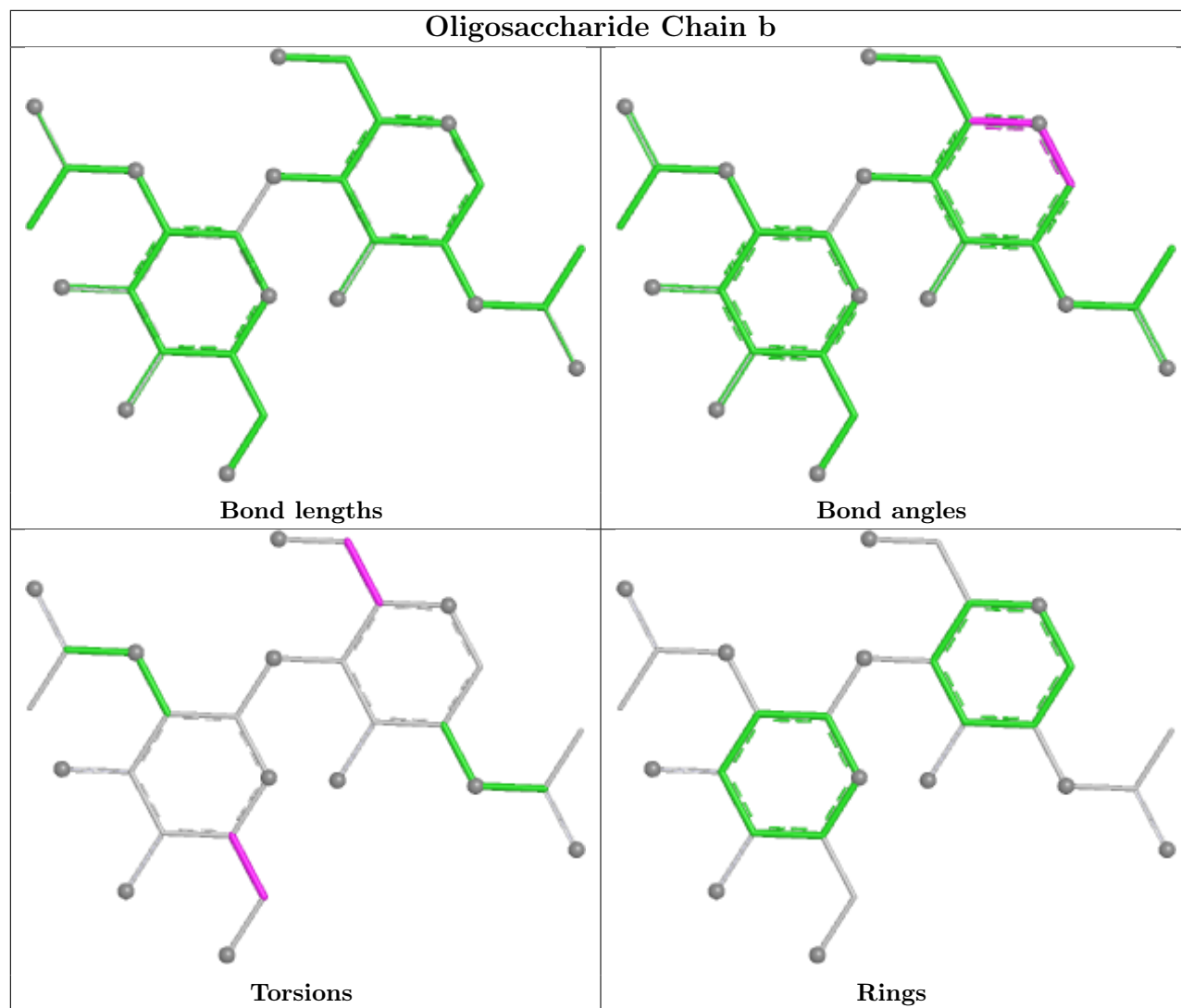


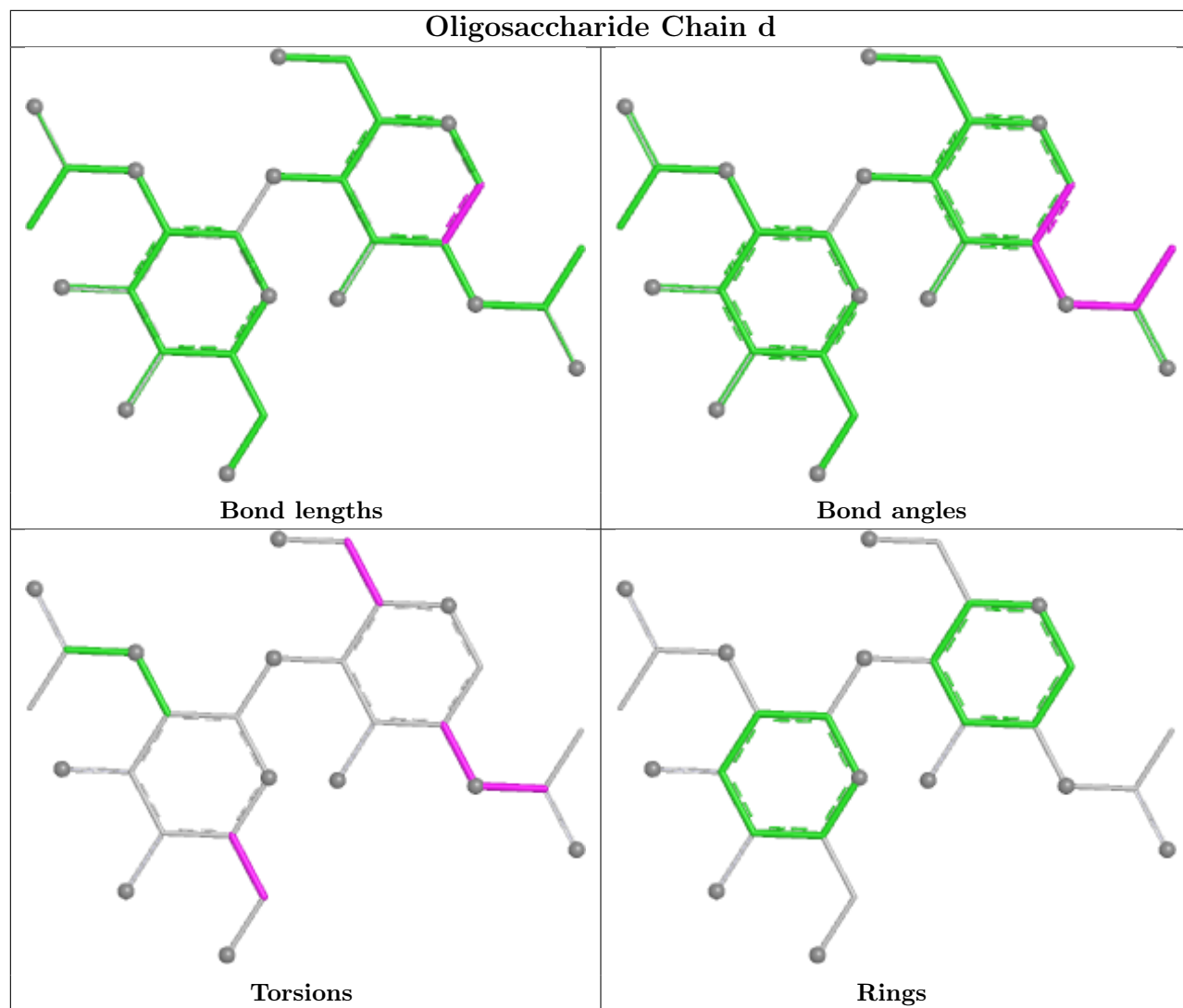


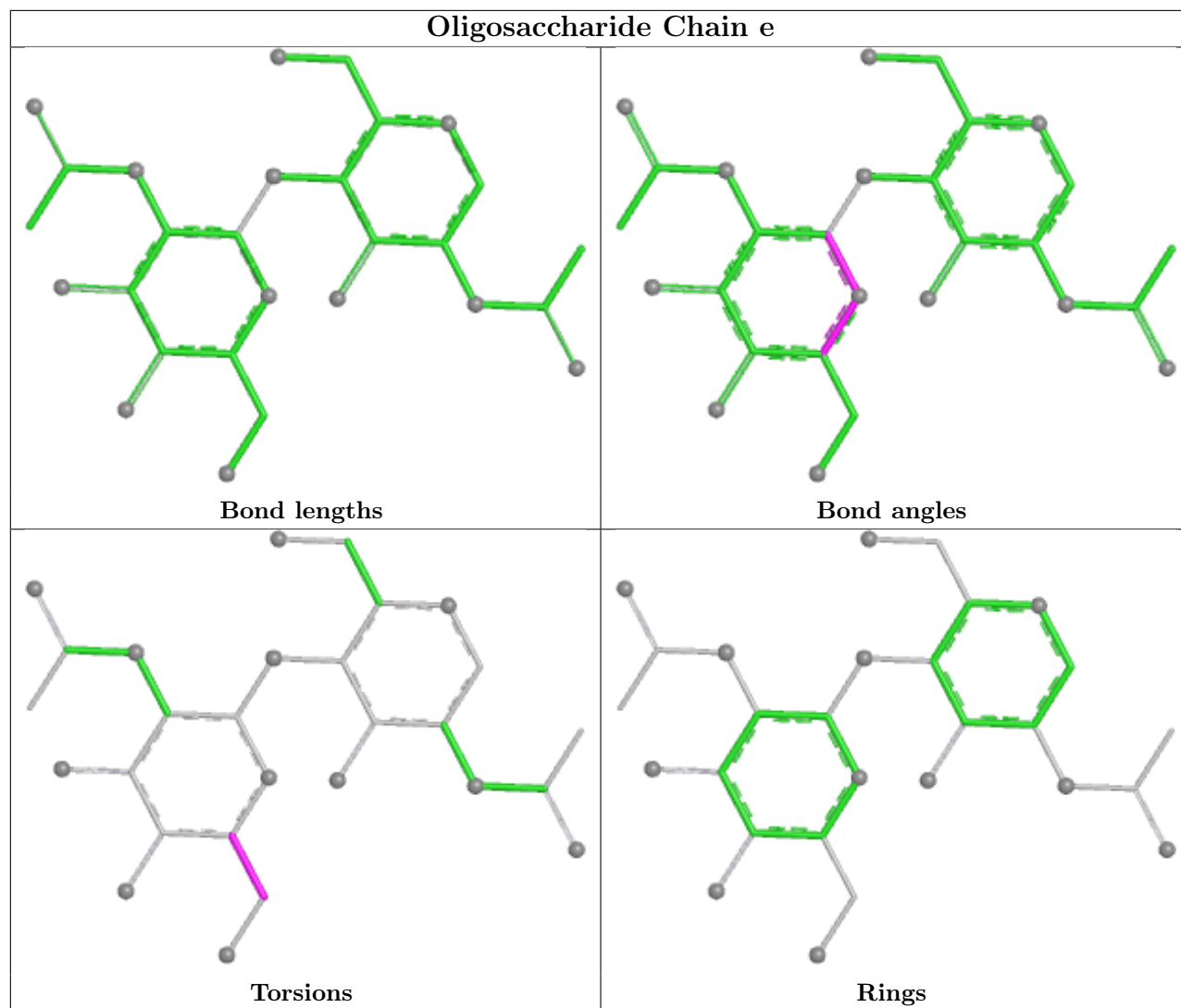


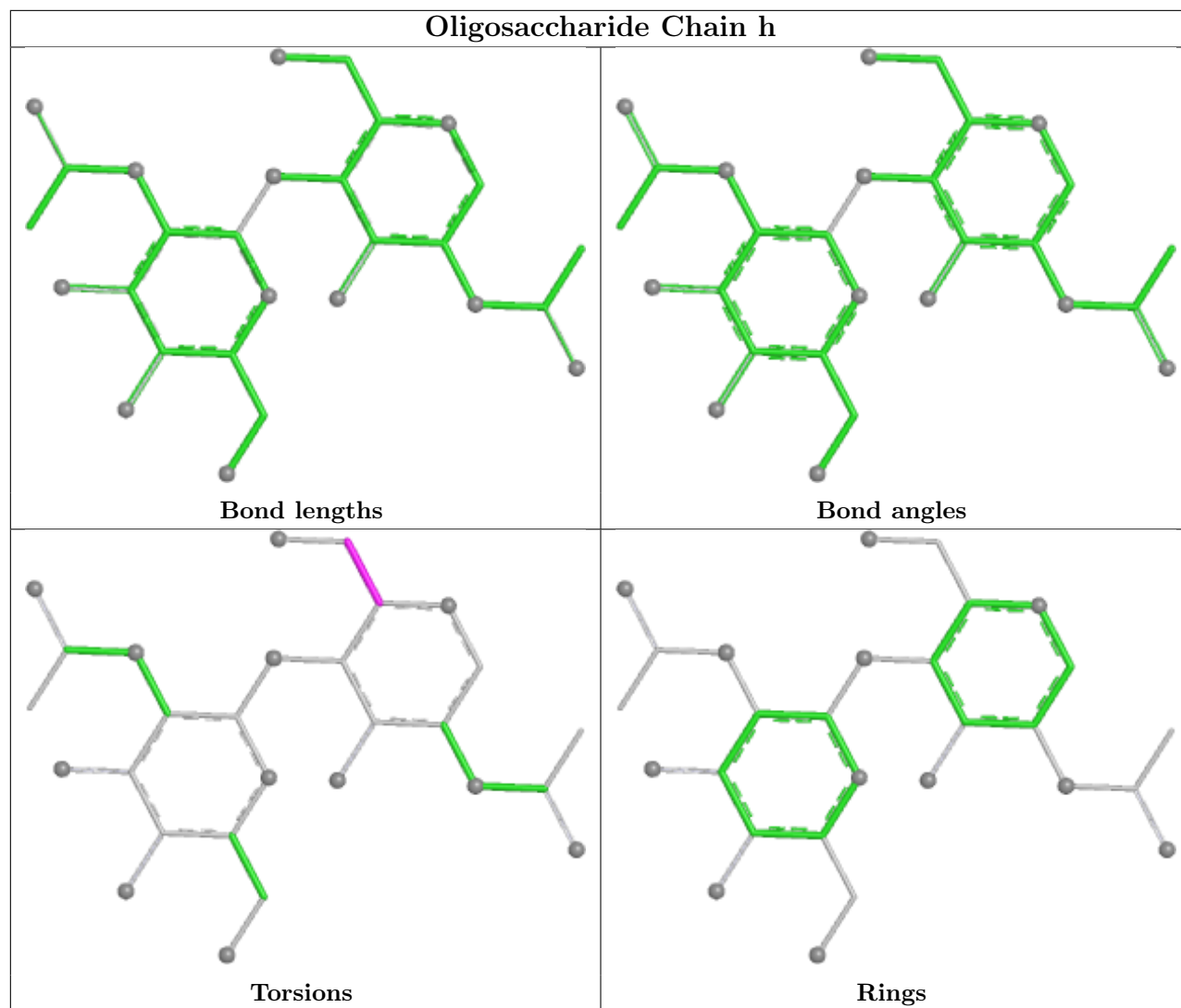


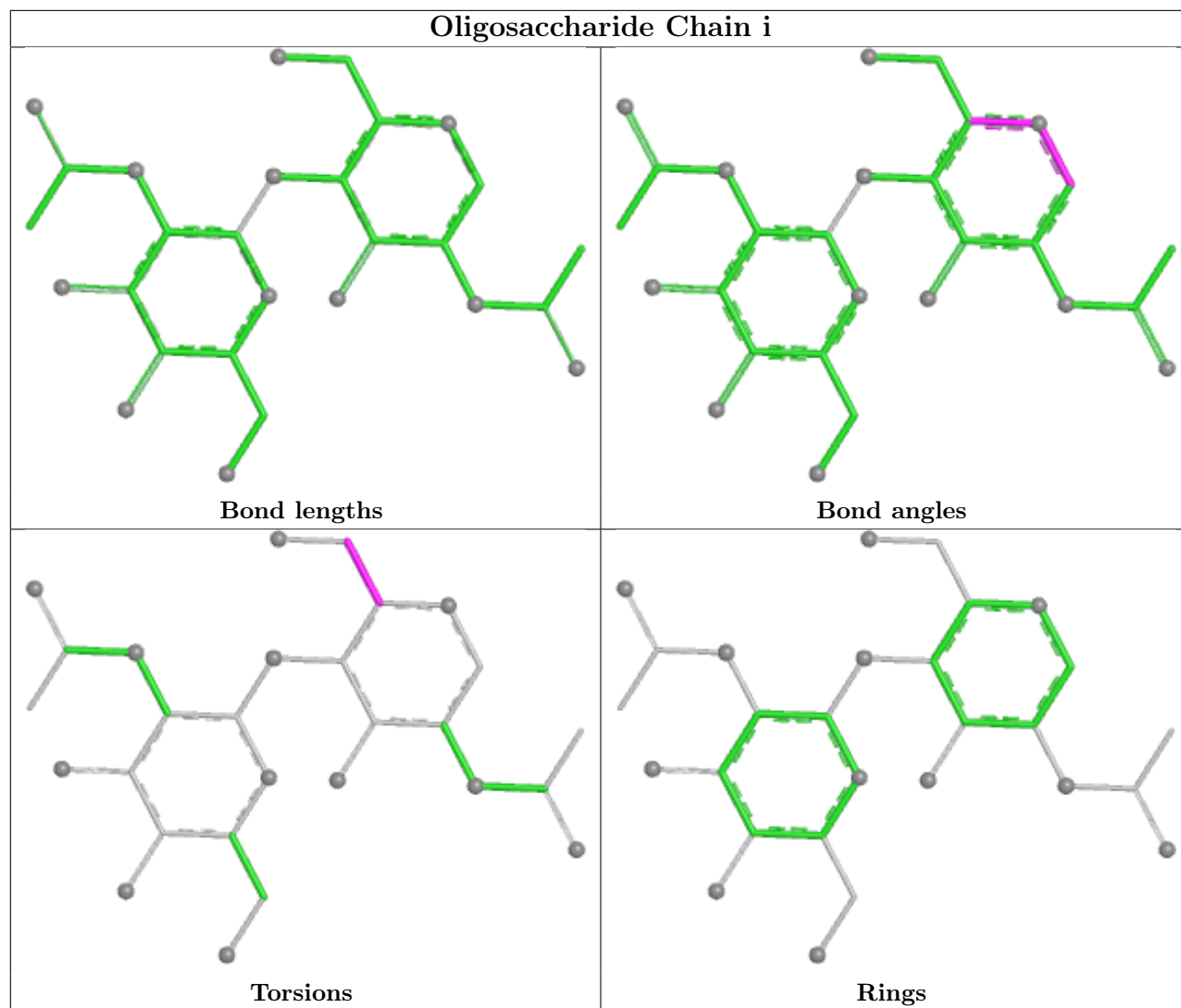


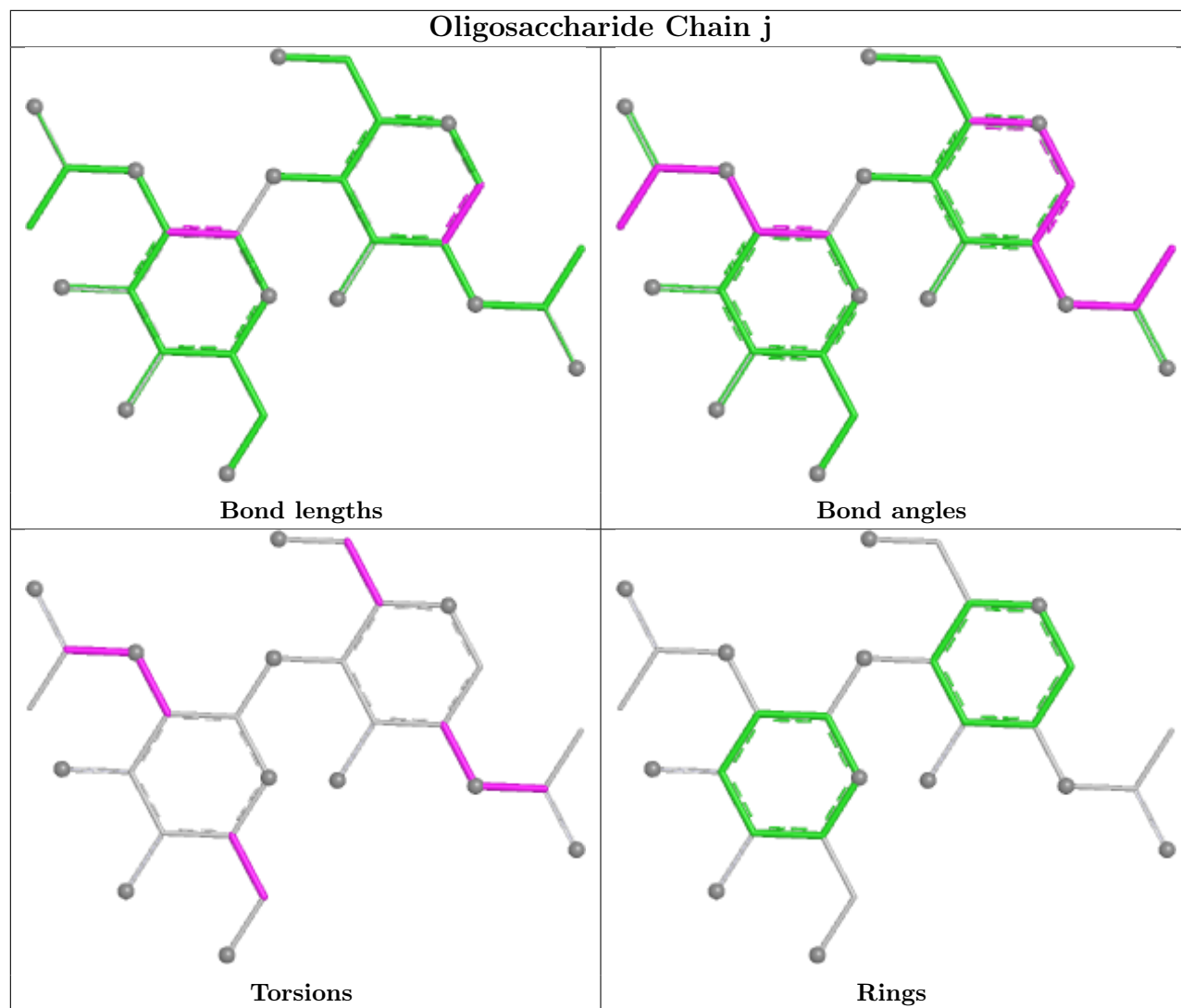


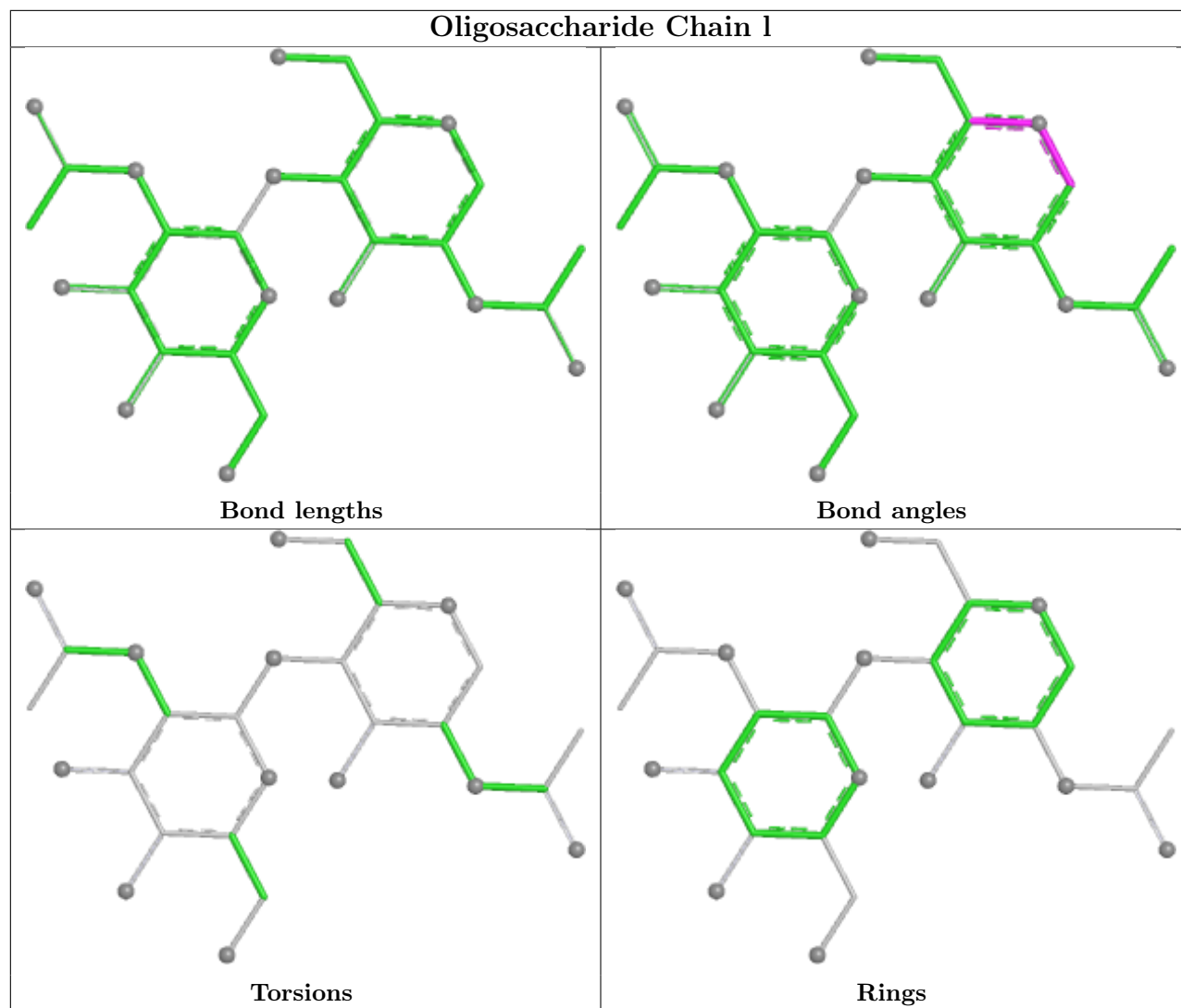


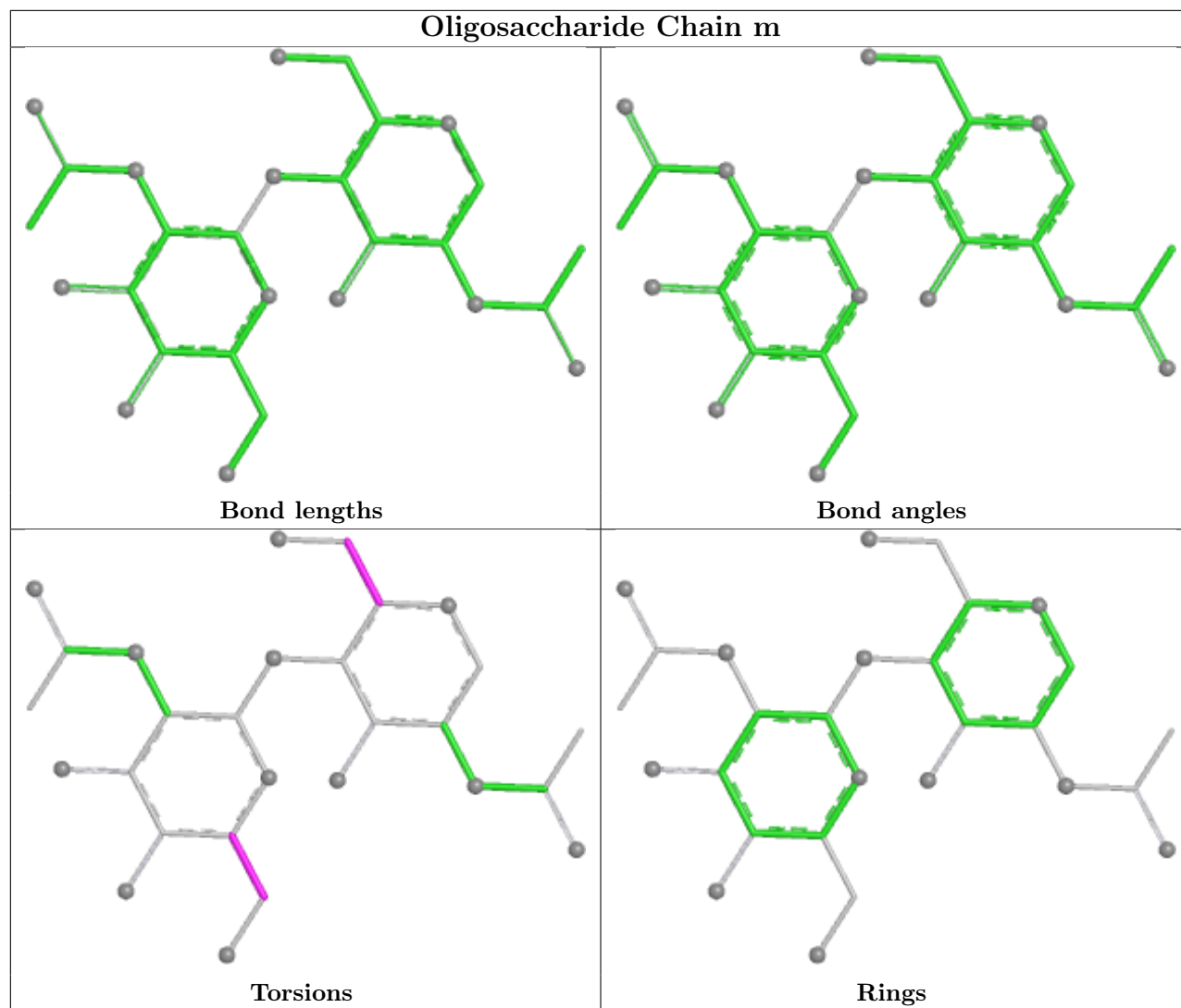


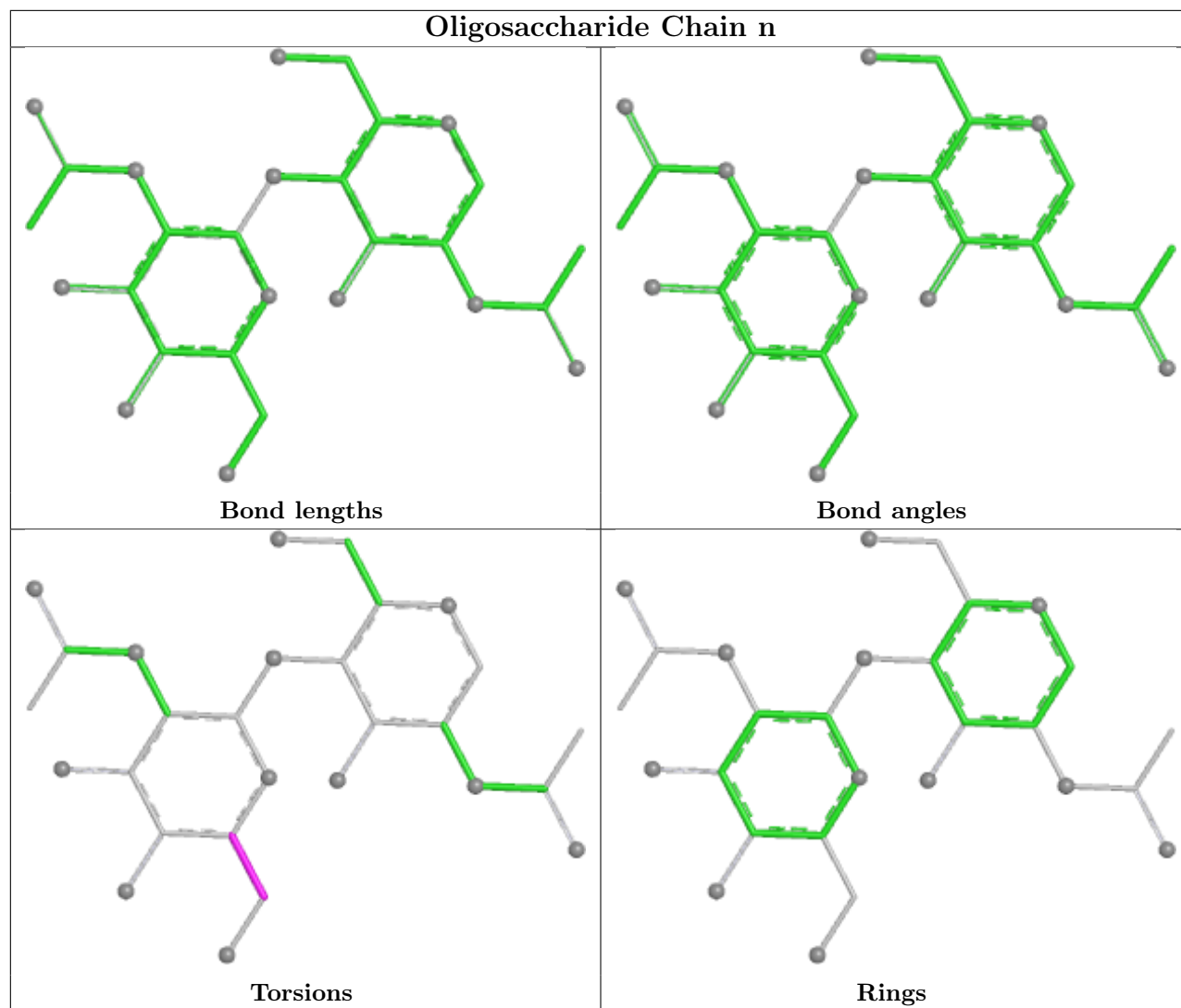


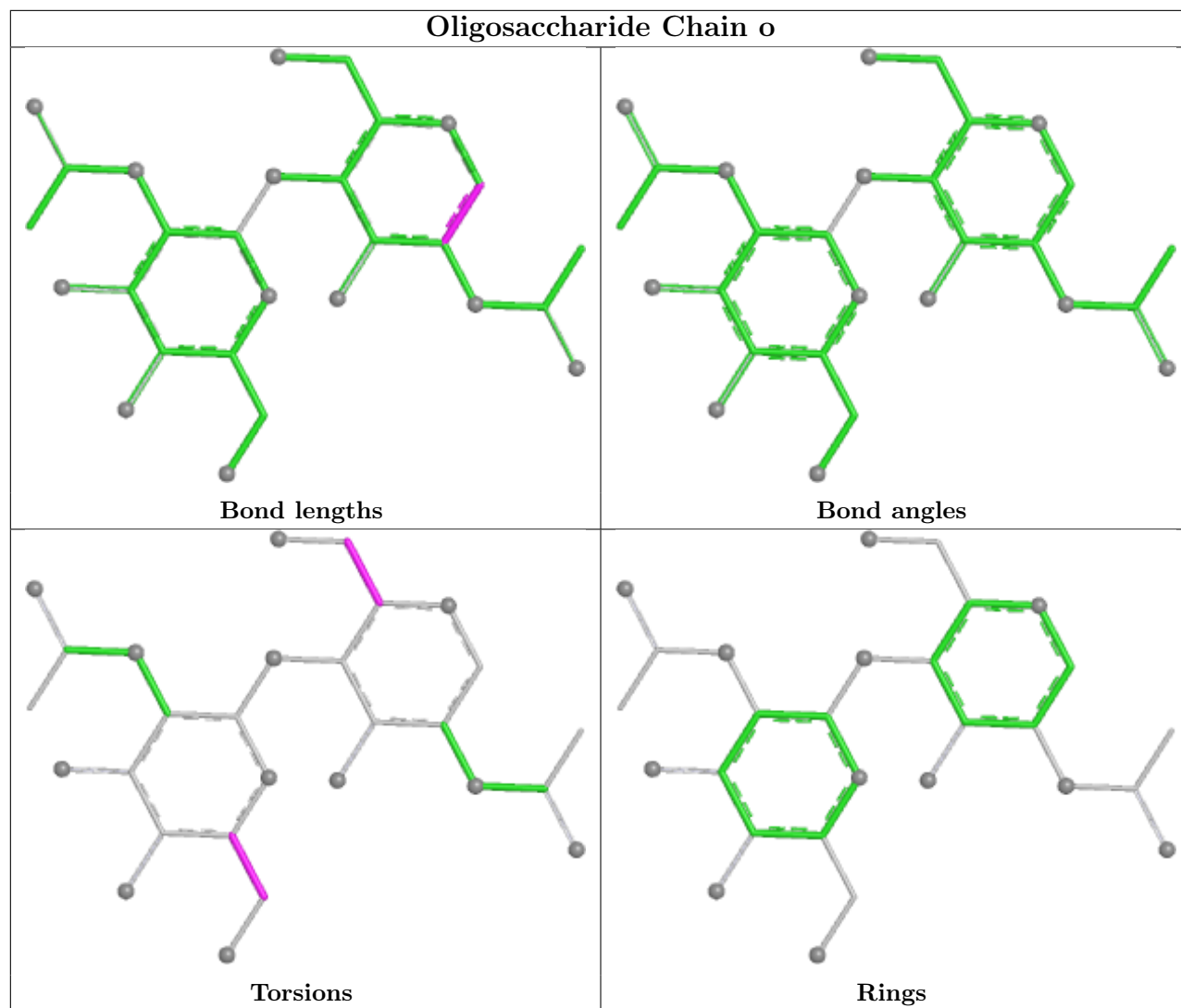


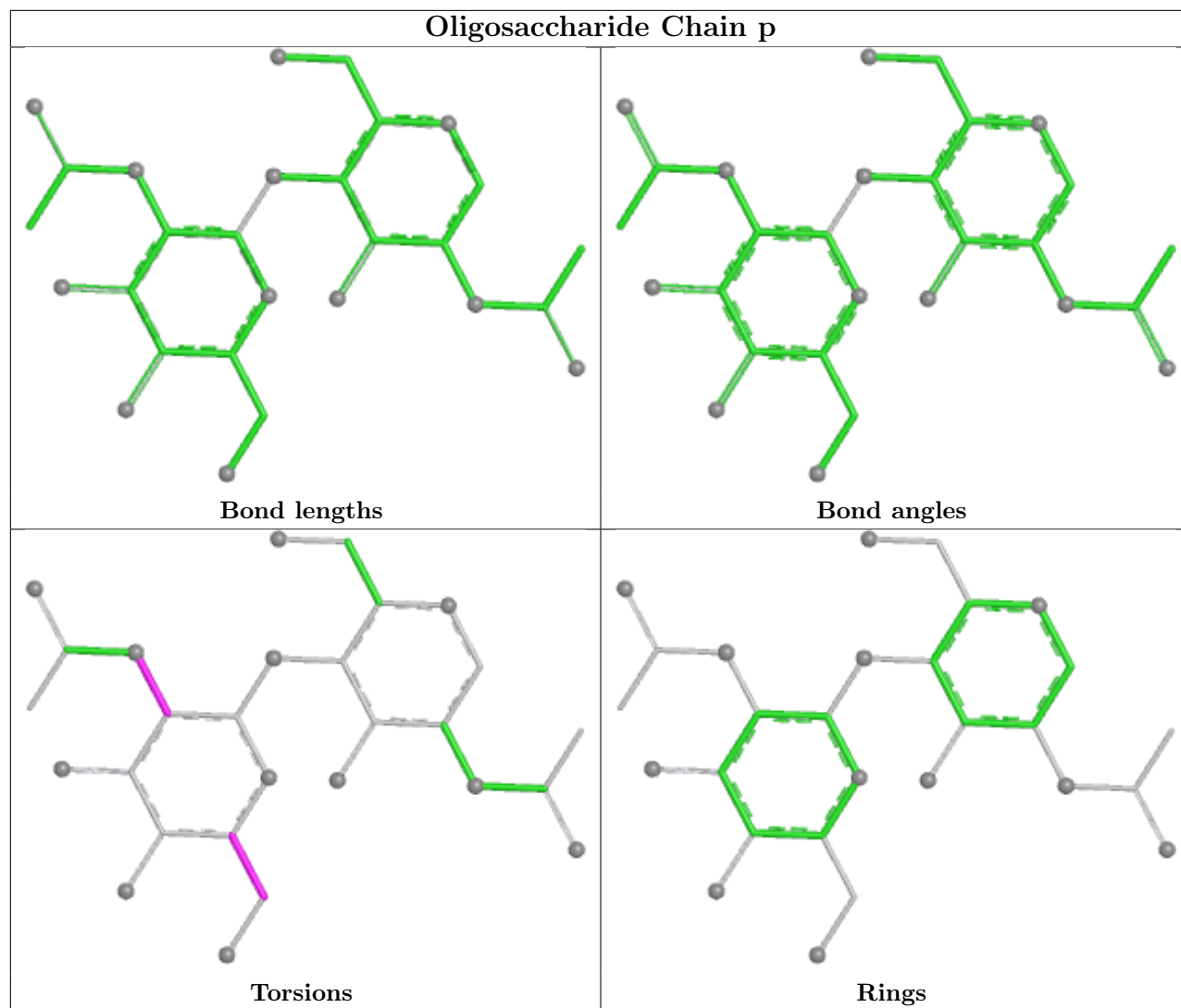


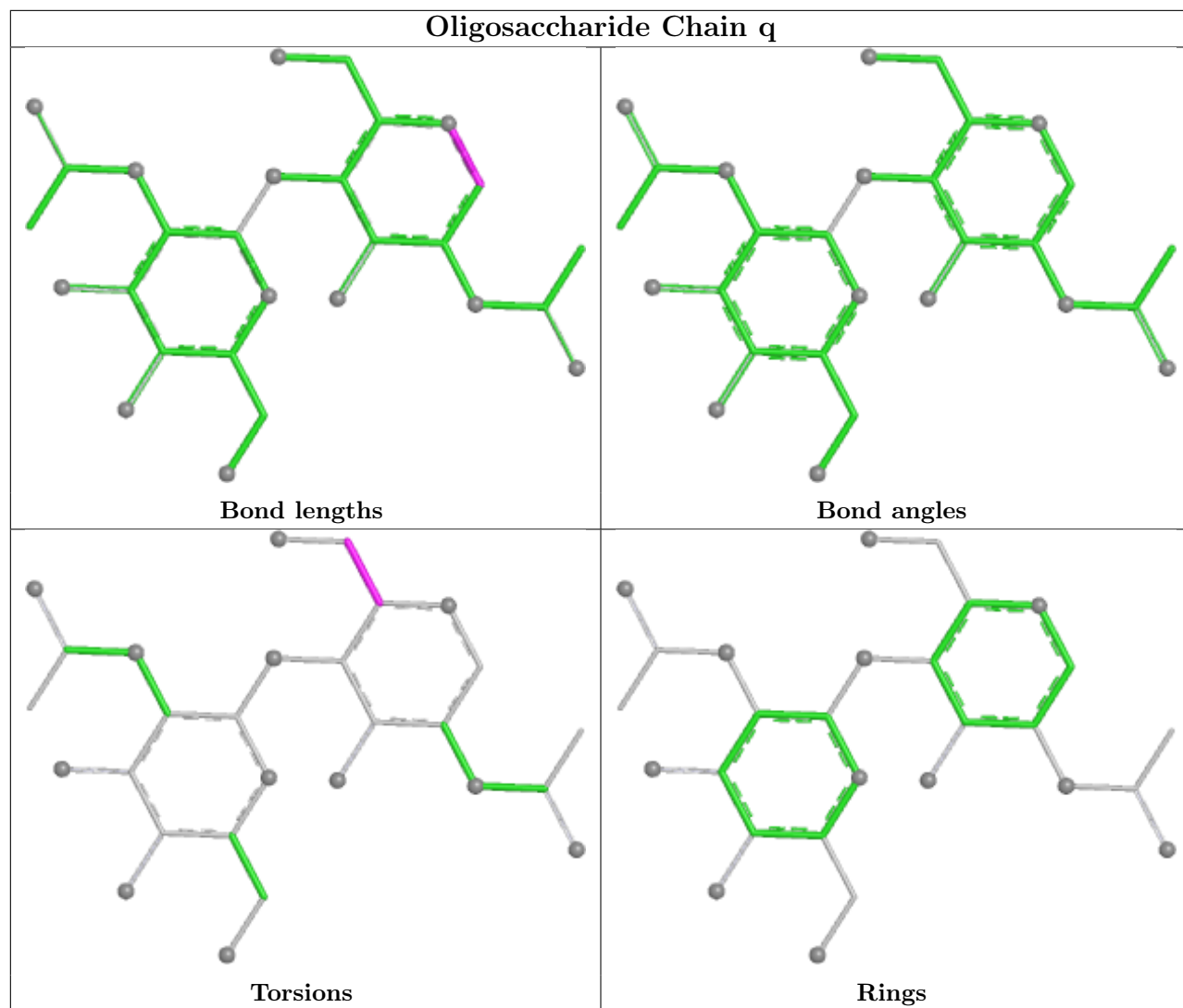


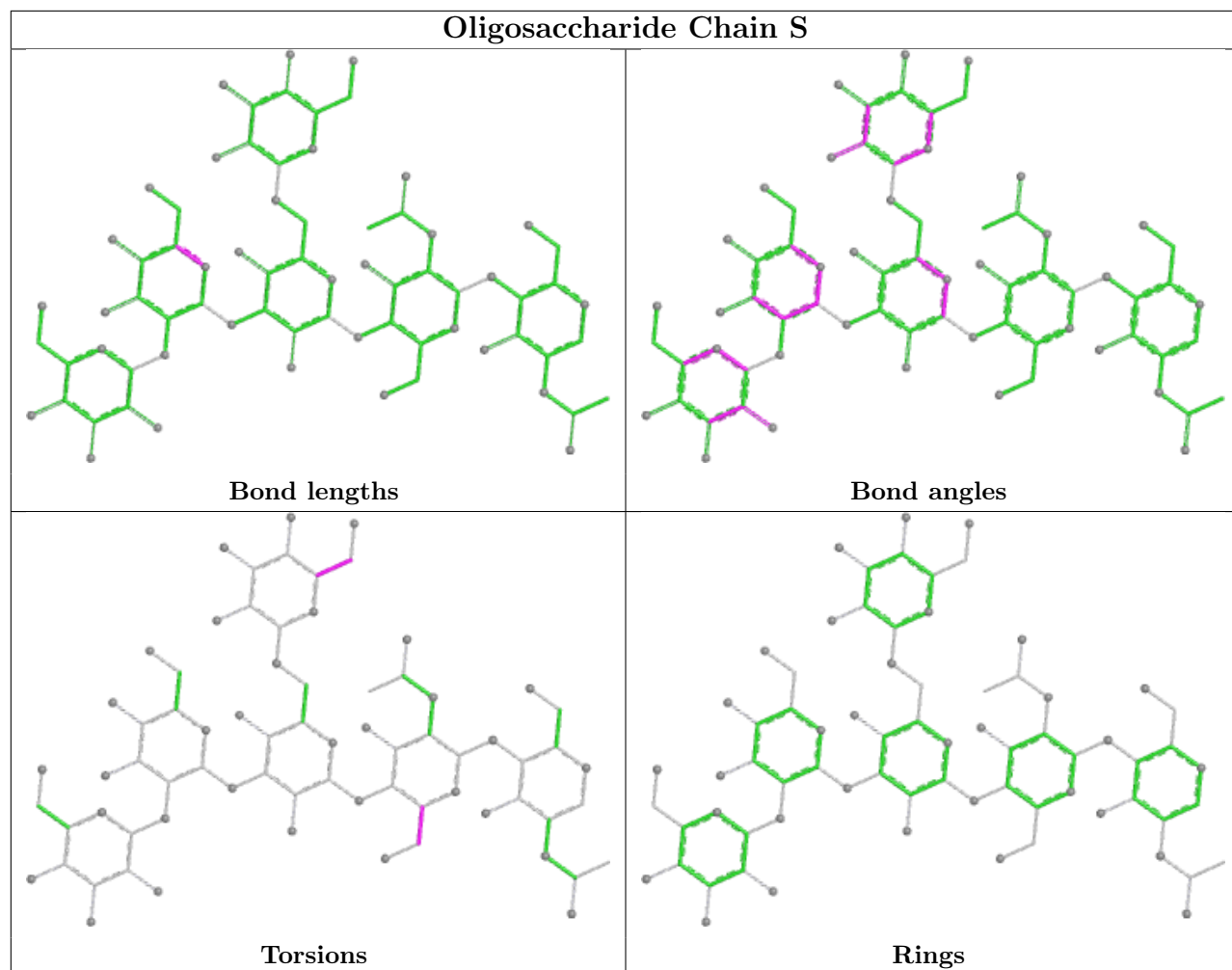


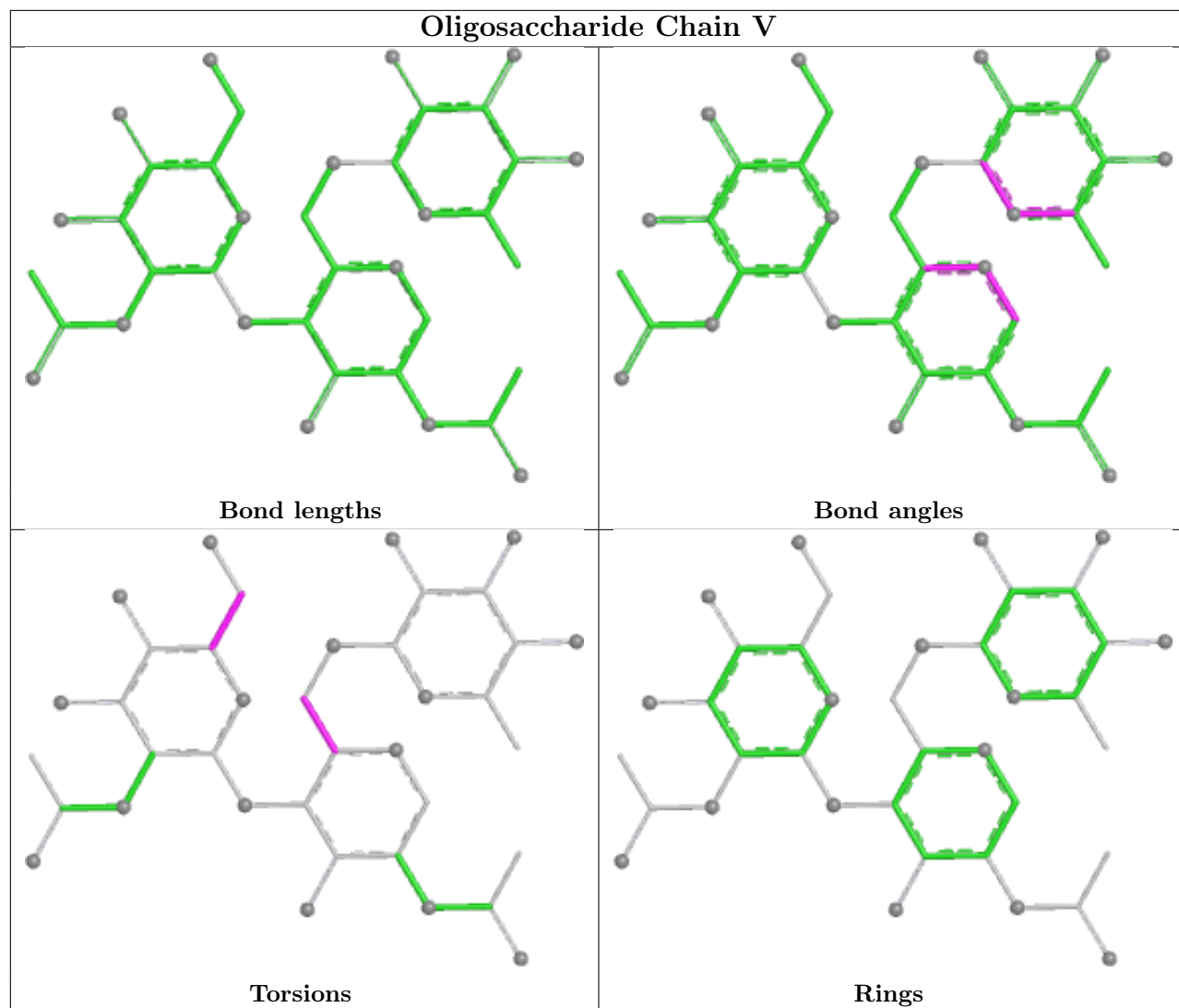


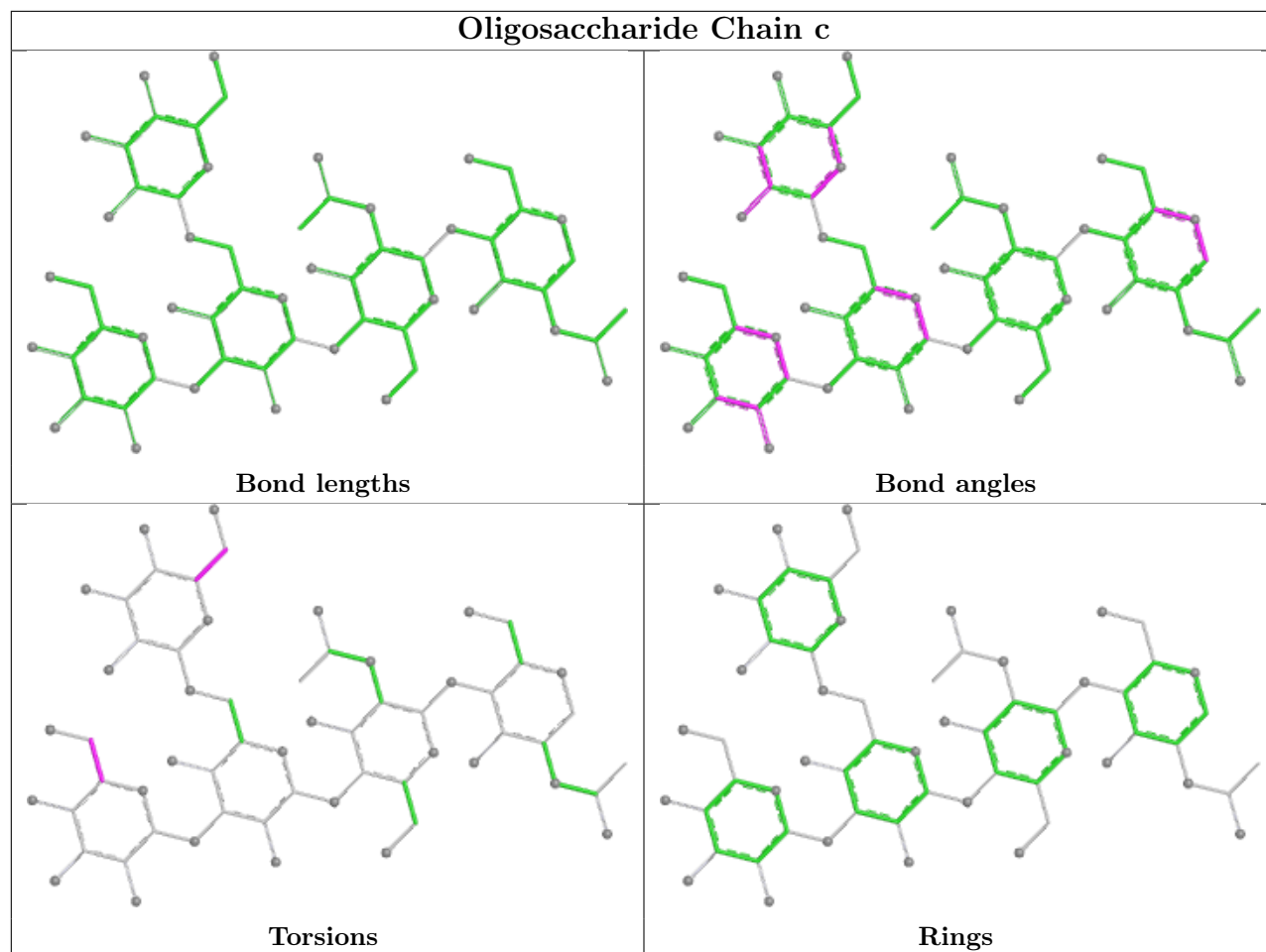


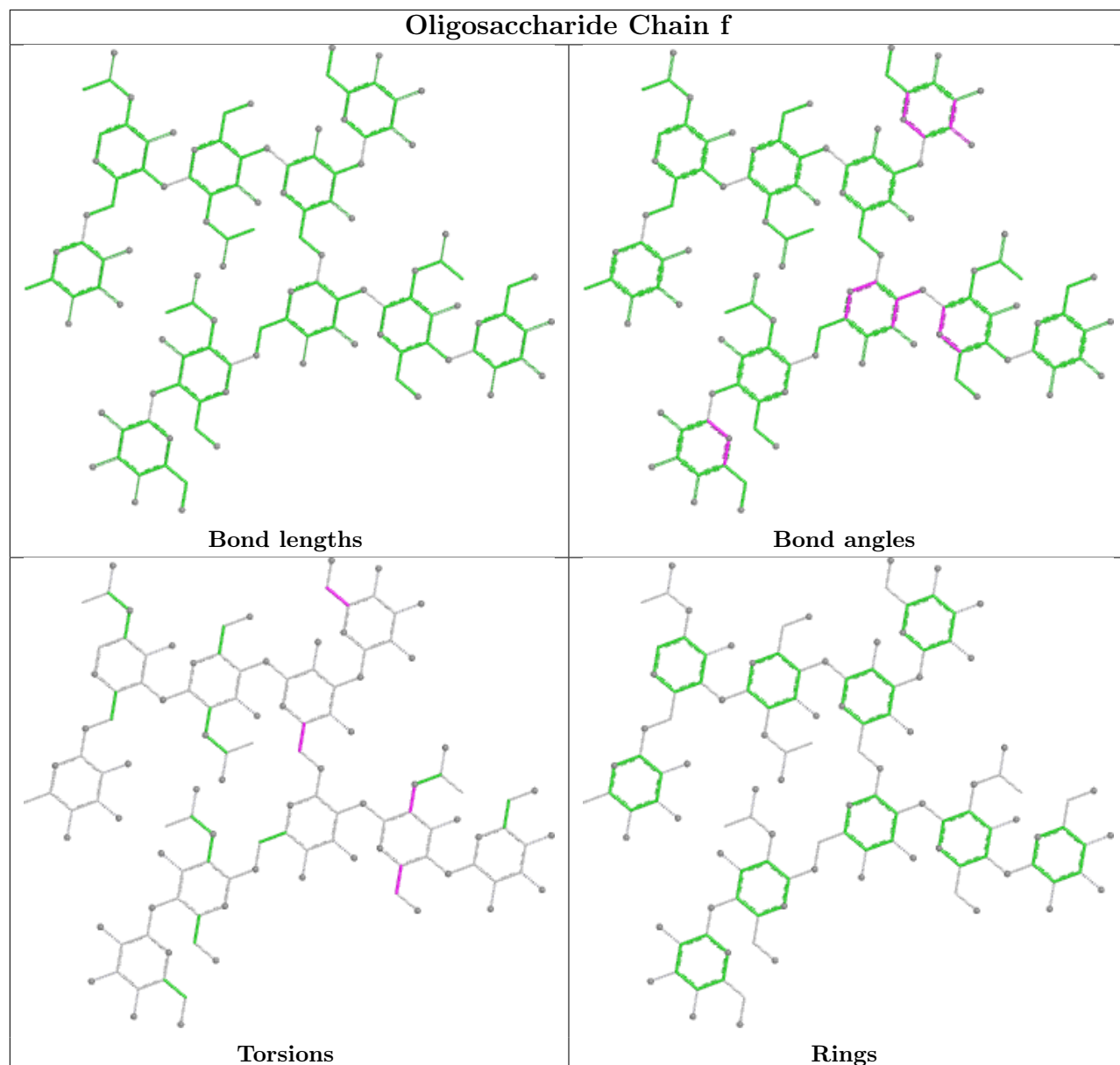


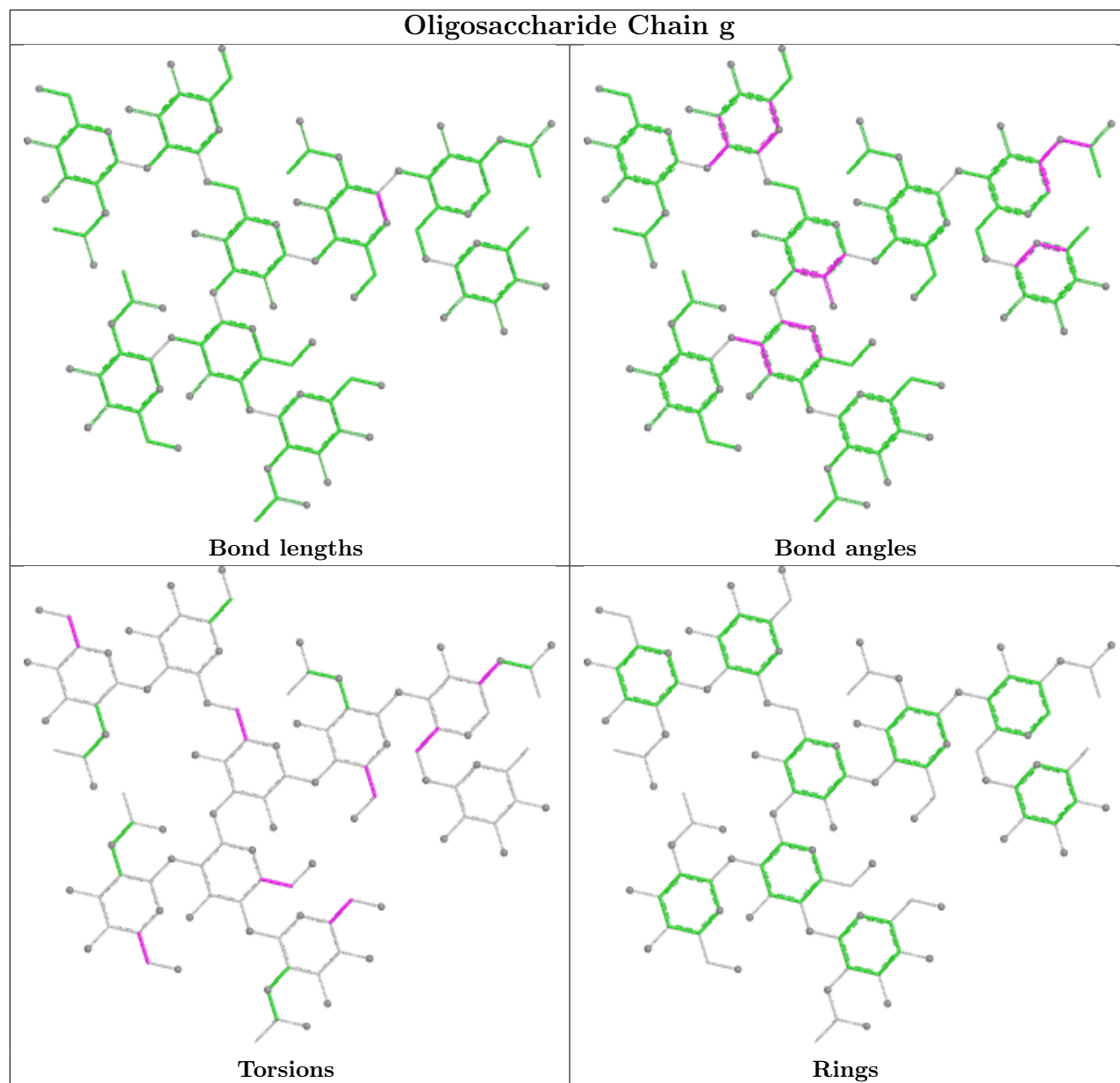


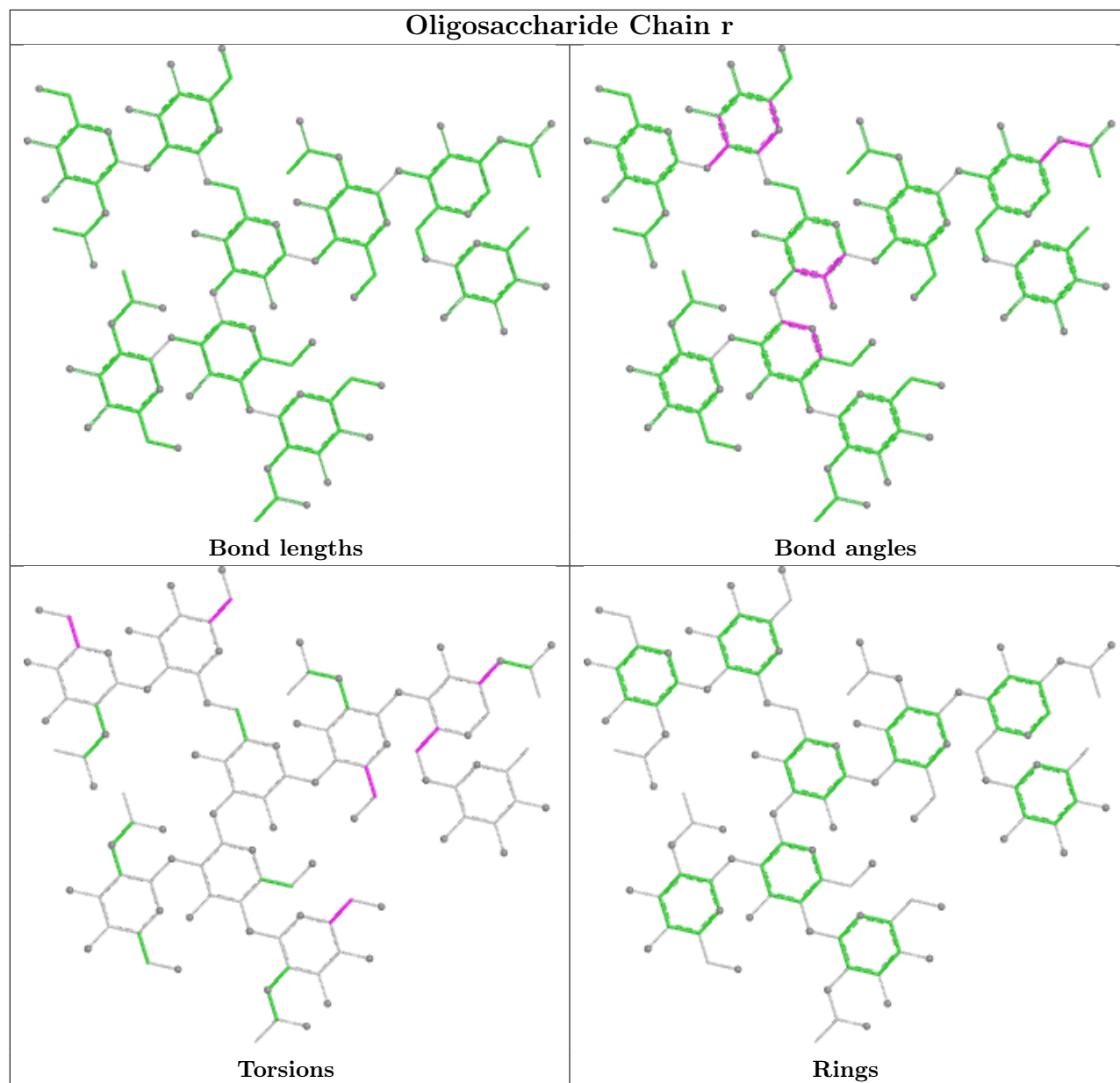


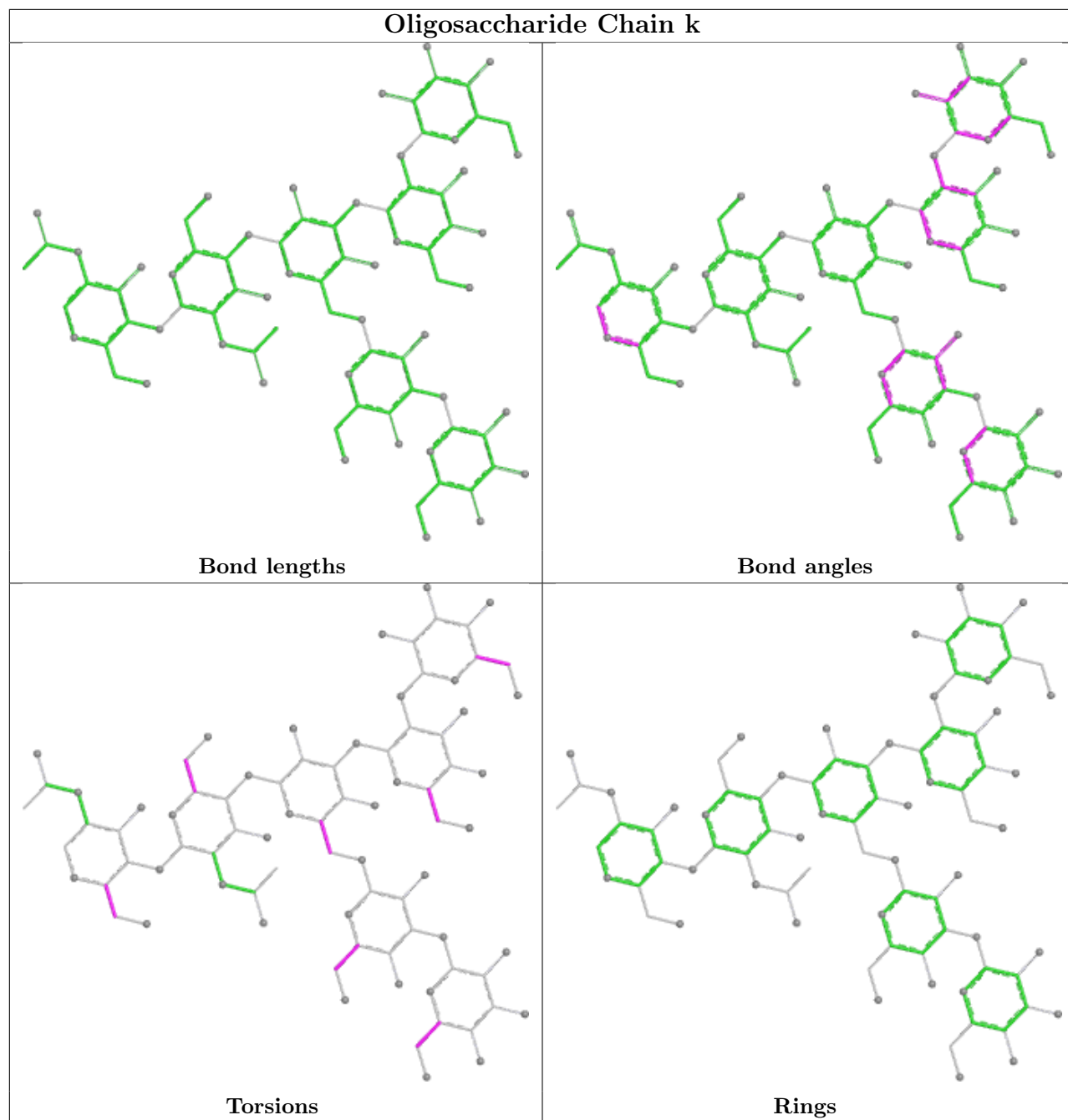


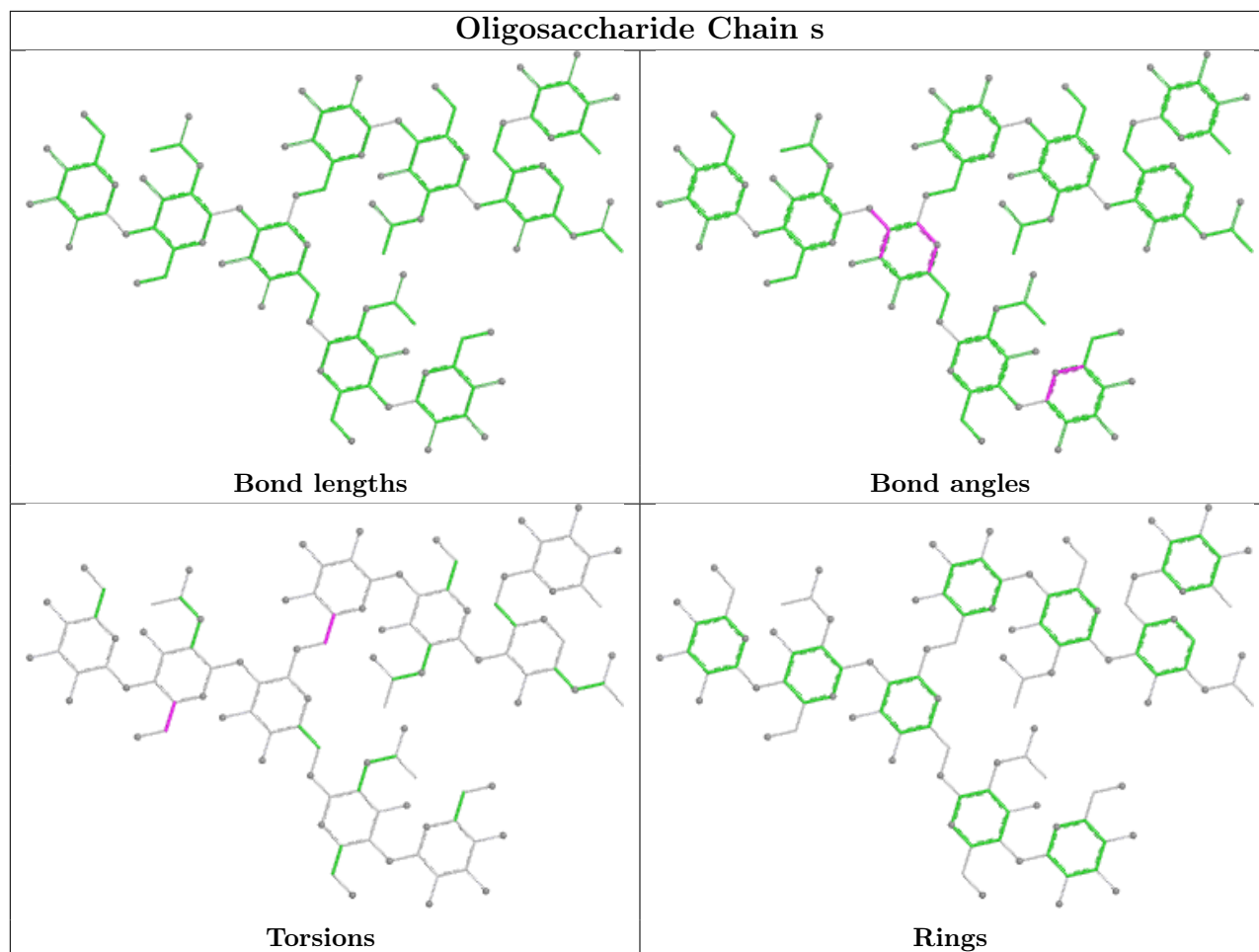












5.6 Ligand geometry [i](#)

21 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	$\# Z > 2$
14	NAG	C	611	1	14,14,15	0.33	0	17,19,21	0.84	1 (5%)
14	NAG	E	623	1	14,14,15	0.32	0	17,19,21	0.39	0
14	NAG	F	902	2	14,14,15	0.27	0	17,19,21	0.63	1 (5%)
14	NAG	D	1019	2	14,14,15	0.36	0	17,19,21	0.54	0
14	NAG	B	1000	2	14,14,15	0.26	0	17,19,21	0.45	0
14	NAG	C	614	1	14,14,15	0.28	0	17,19,21	0.61	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	NAG	A	628	1	14,14,15	0.94	1 (7%)	17,19,21	2.39	4 (23%)
14	NAG	A	612	1	14,14,15	0.33	0	17,19,21	0.53	0
14	NAG	A	607	1	14,14,15	0.27	0	17,19,21	0.46	0
14	NAG	E	619	1	14,14,15	0.26	0	17,19,21	0.65	1 (5%)
14	NAG	C	613	1	14,14,15	0.25	0	17,19,21	0.50	0
14	NAG	C	612	1	14,14,15	0.50	0	17,19,21	0.72	1 (5%)
14	NAG	C	601	1	14,14,15	0.60	0	17,19,21	0.74	1 (5%)
14	NAG	E	630	1	14,14,15	0.49	0	17,19,21	0.82	1 (5%)
14	NAG	A	617	1	14,14,15	0.61	0	17,19,21	0.50	0
14	NAG	B	1003	2	14,14,15	0.38	0	17,19,21	0.49	0
14	NAG	B	1004	2	14,14,15	0.52	0	17,19,21	0.44	0
14	NAG	F	901	2	14,14,15	0.44	0	17,19,21	0.54	0
14	NAG	E	620	1	14,14,15	0.51	0	17,19,21	0.61	1 (5%)
14	NAG	D	1020	2	14,14,15	0.53	0	17,19,21	0.75	1 (5%)
14	NAG	E	618	1	14,14,15	0.49	0	17,19,21	0.96	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
14	NAG	C	611	1	-	2/6/23/26	0/1/1/1
14	NAG	E	623	1	-	2/6/23/26	0/1/1/1
14	NAG	F	902	2	-	2/6/23/26	0/1/1/1
14	NAG	D	1019	2	-	0/6/23/26	0/1/1/1
14	NAG	B	1000	2	-	2/6/23/26	0/1/1/1
14	NAG	C	614	1	-	0/6/23/26	0/1/1/1
14	NAG	A	628	1	-	6/6/23/26	0/1/1/1
14	NAG	A	612	1	-	2/6/23/26	0/1/1/1
14	NAG	A	607	1	-	0/6/23/26	0/1/1/1
14	NAG	E	619	1	-	2/6/23/26	0/1/1/1
14	NAG	C	613	1	-	3/6/23/26	0/1/1/1
14	NAG	C	612	1	-	2/6/23/26	0/1/1/1
14	NAG	C	601	1	-	0/6/23/26	0/1/1/1
14	NAG	E	630	1	-	4/6/23/26	0/1/1/1
14	NAG	A	617	1	-	0/6/23/26	0/1/1/1
14	NAG	B	1003	2	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	NAG	B	1004	2	-	0/6/23/26	0/1/1/1
14	NAG	F	901	2	-	2/6/23/26	0/1/1/1
14	NAG	E	620	1	-	2/6/23/26	0/1/1/1
14	NAG	D	1020	2	-	2/6/23/26	0/1/1/1
14	NAG	E	618	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	A	628	NAG	C1-C2	2.96	1.56	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	A	628	NAG	C2-N2-C7	8.24	133.94	122.90
14	A	628	NAG	C1-C2-N2	3.96	116.68	110.43
14	E	618	NAG	C1-O5-C5	3.63	117.05	112.19
14	C	611	NAG	C1-O5-C5	3.14	116.40	112.19
14	E	630	NAG	C1-O5-C5	2.78	115.92	112.19

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	628	NAG	C4-C5-C6-O6
14	E	630	NAG	C4-C5-C6-O6
14	E	630	NAG	O5-C5-C6-O6
14	A	628	NAG	O5-C5-C6-O6
14	E	619	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	A	612	NAG	1	0
14	E	619	NAG	1	0

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.

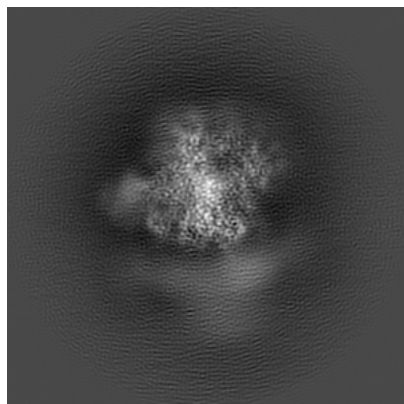
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7858. These allow visual inspection of the internal detail of the map and identification of artifacts.

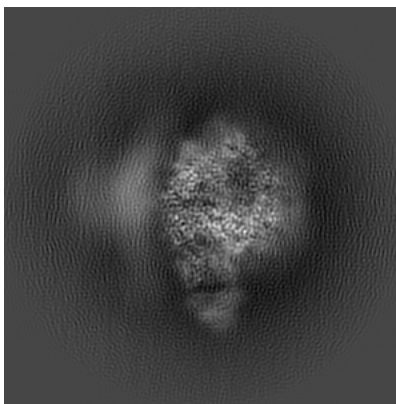
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

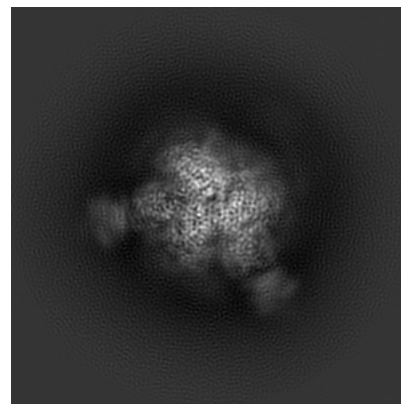
6.1.1 Primary map



X

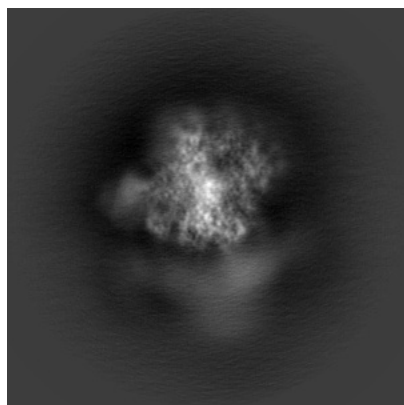


Y

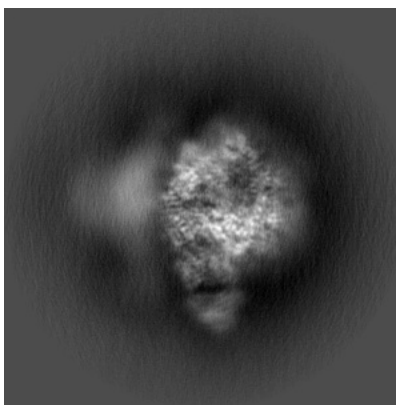


Z

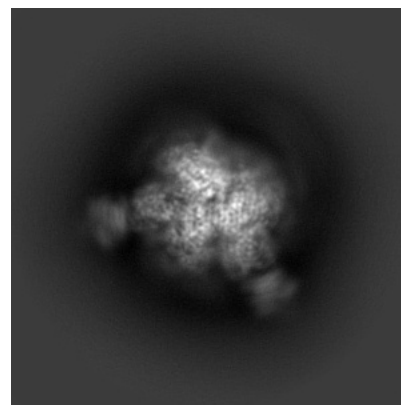
6.1.2 Raw map



X



Y

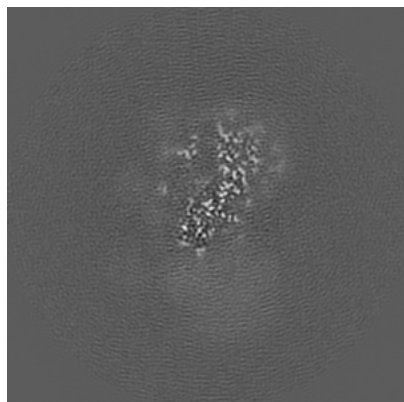


Z

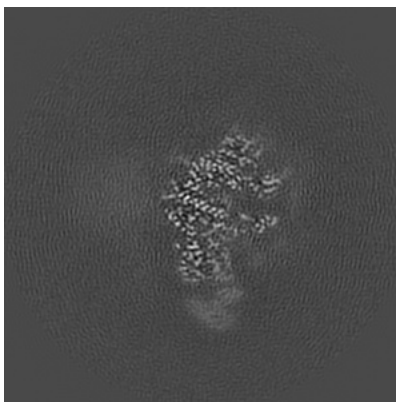
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

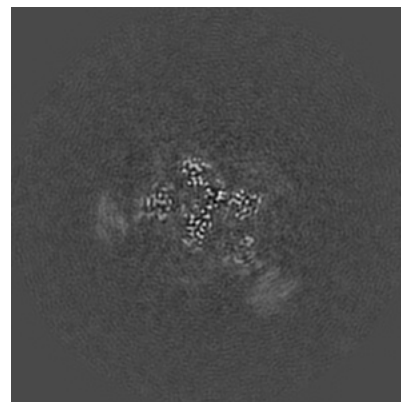
6.2.1 Primary map



X Index: 160

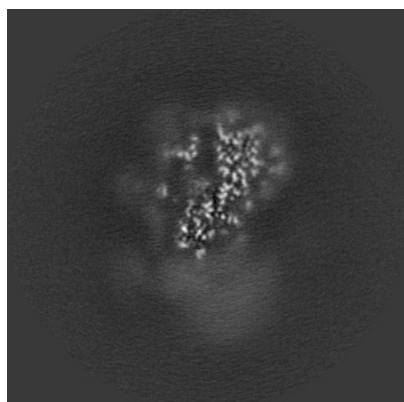


Y Index: 160

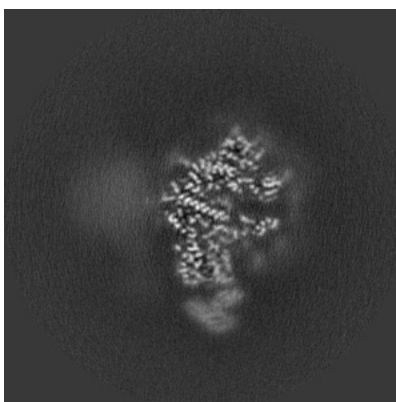


Z Index: 160

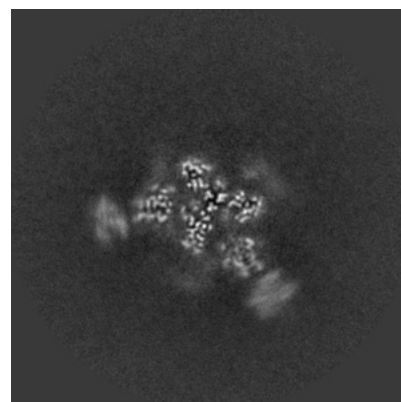
6.2.2 Raw map



X Index: 160



Y Index: 160

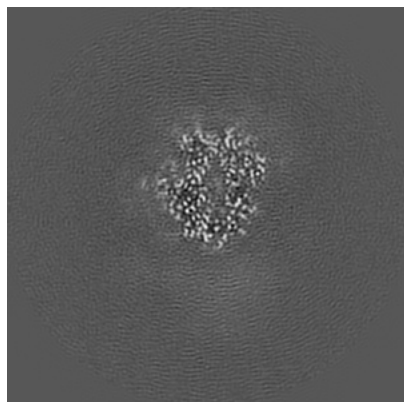


Z Index: 160

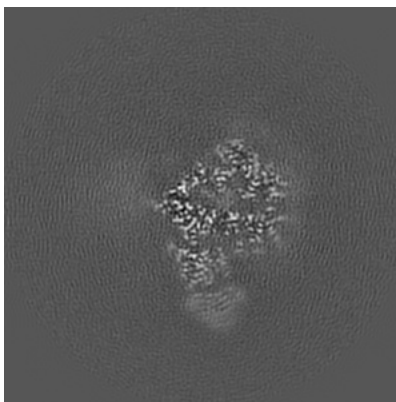
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

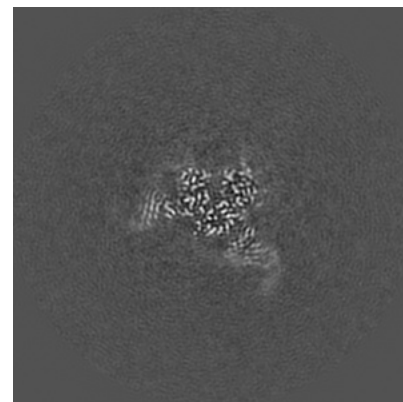
6.3.1 Primary map



X Index: 150

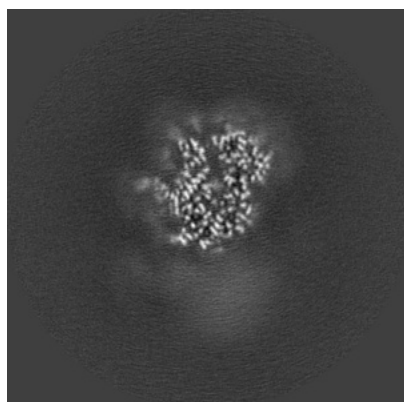


Y Index: 153

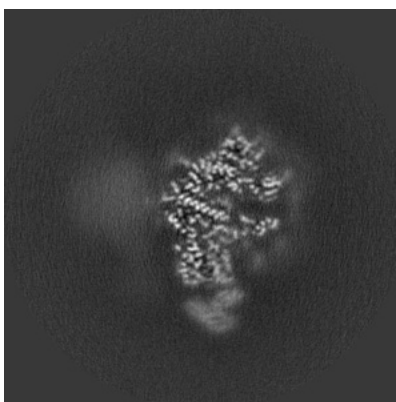


Z Index: 144

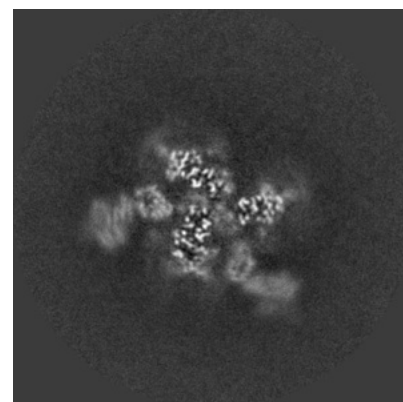
6.3.2 Raw map



X Index: 153



Y Index: 160

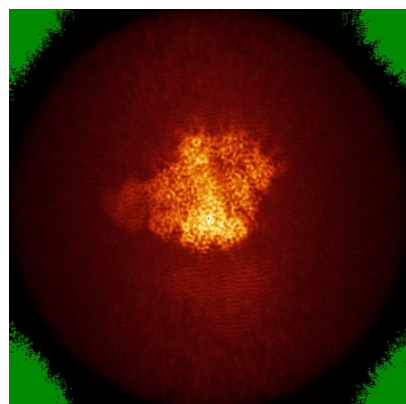


Z Index: 177

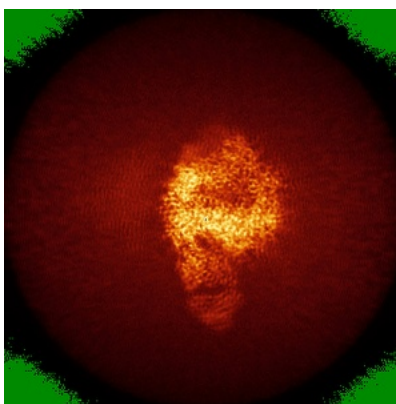
The images above show the largest variance slices of the map in three orthogonal directions.

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

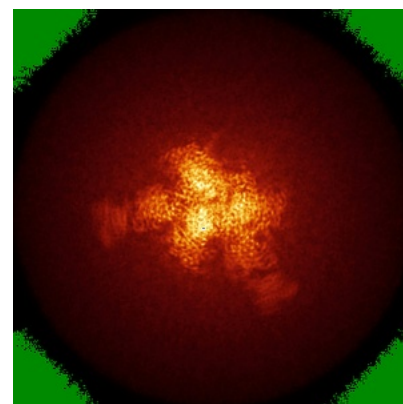
6.4.1 Primary map



X

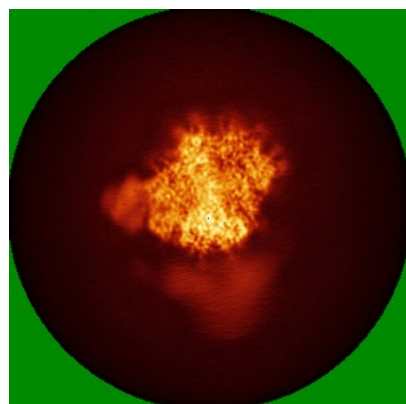


Y

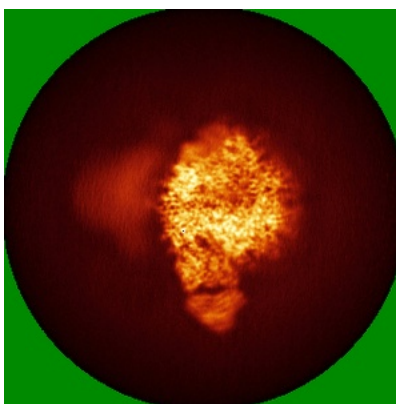


Z

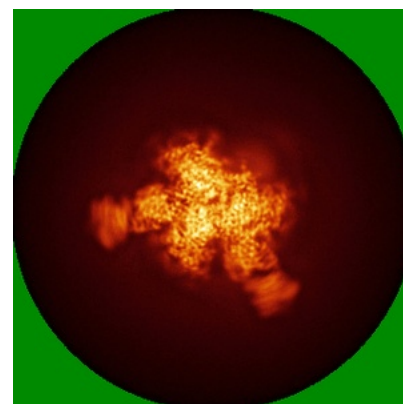
6.4.2 Raw map



X



Y

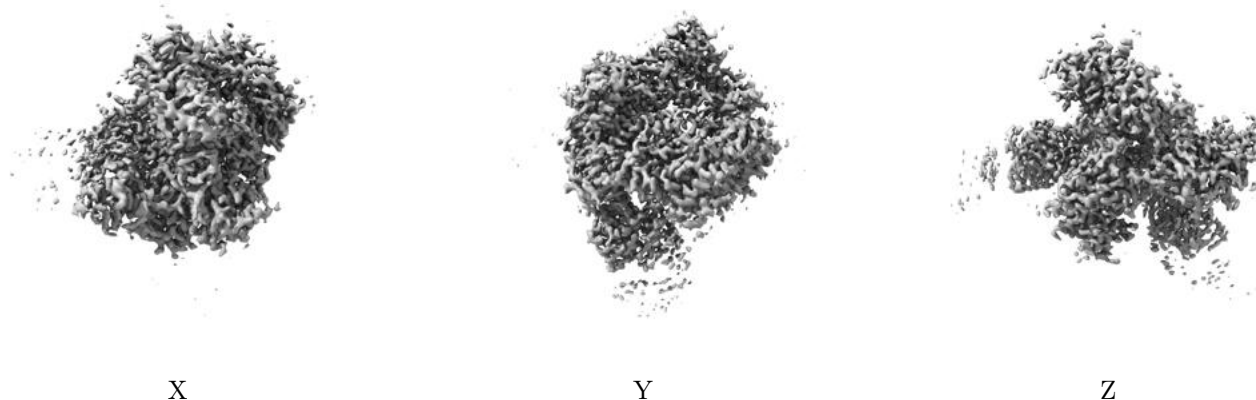


Z

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 0.0583. 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.

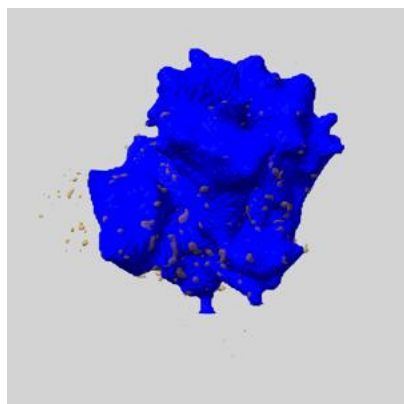
6.6 Mask visualisation [i](#)

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

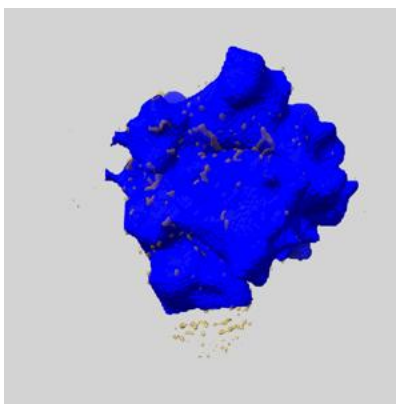
A mask typically either:

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

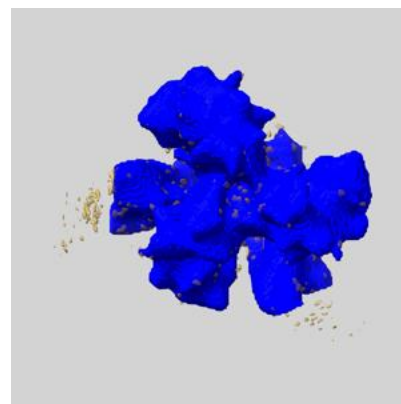
6.6.1 emd_7858_msk_1.map [i](#)



X



Y

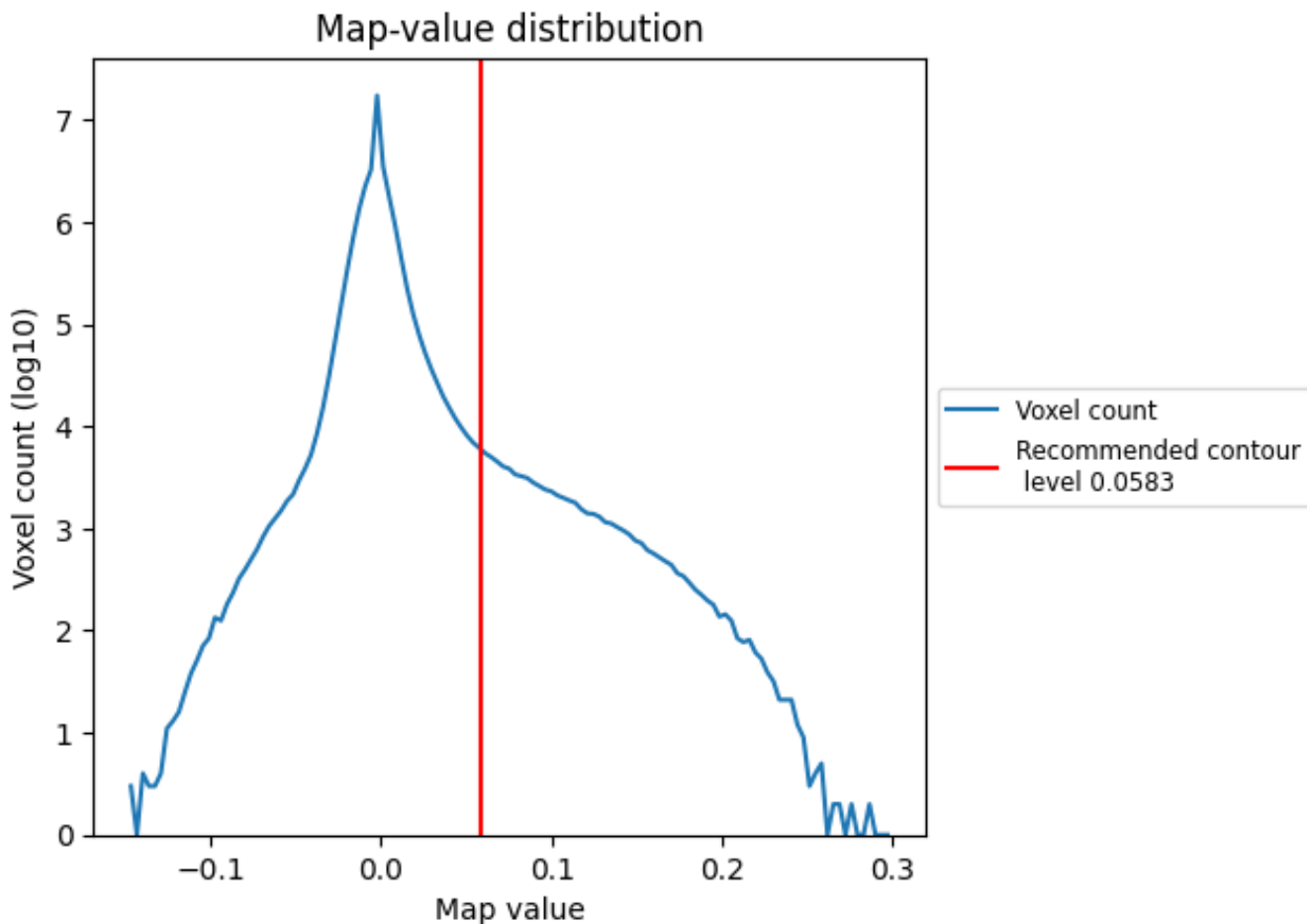


Z

7 Map analysis [i](#)

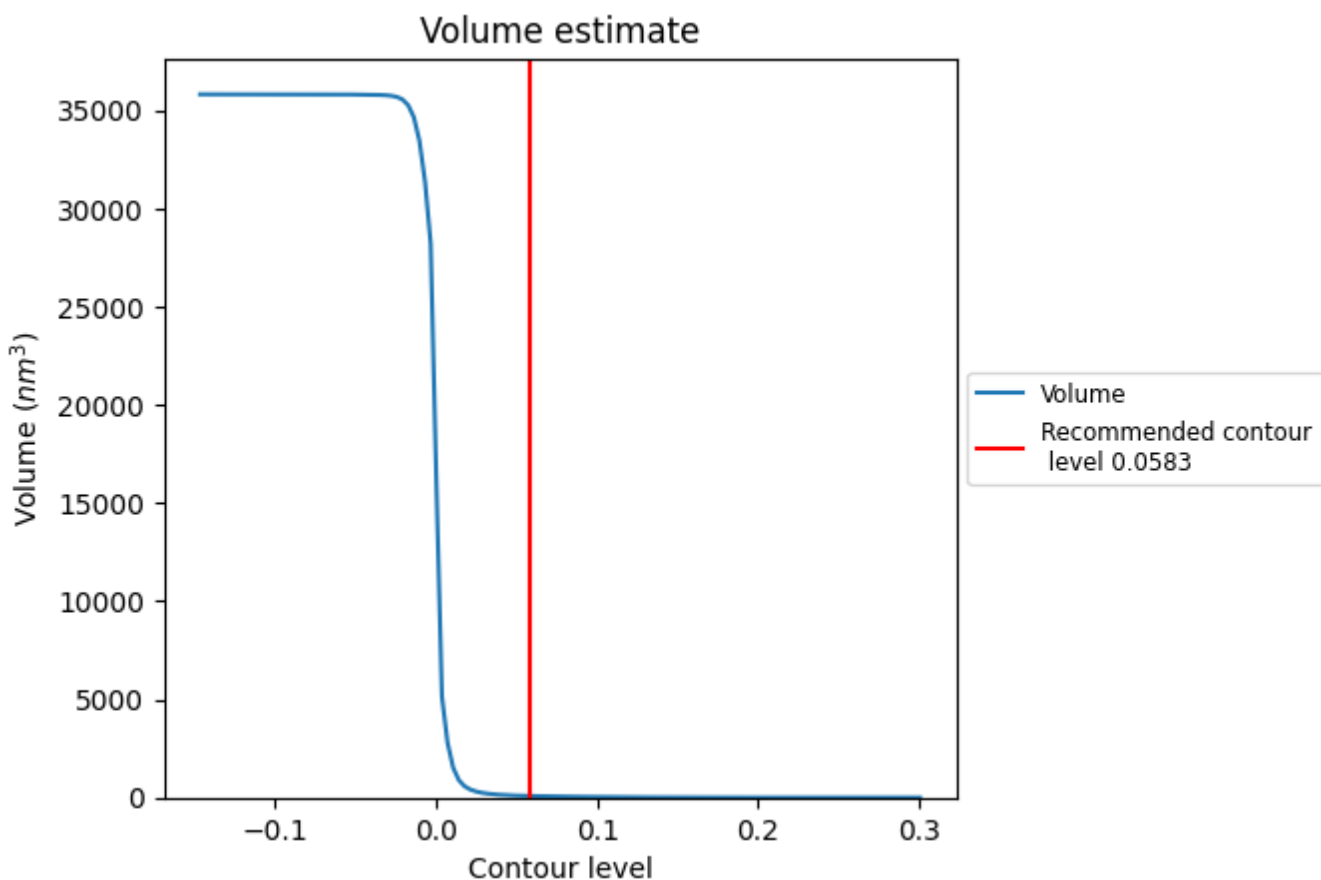
This section contains the results of statistical analysis of the map.

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.

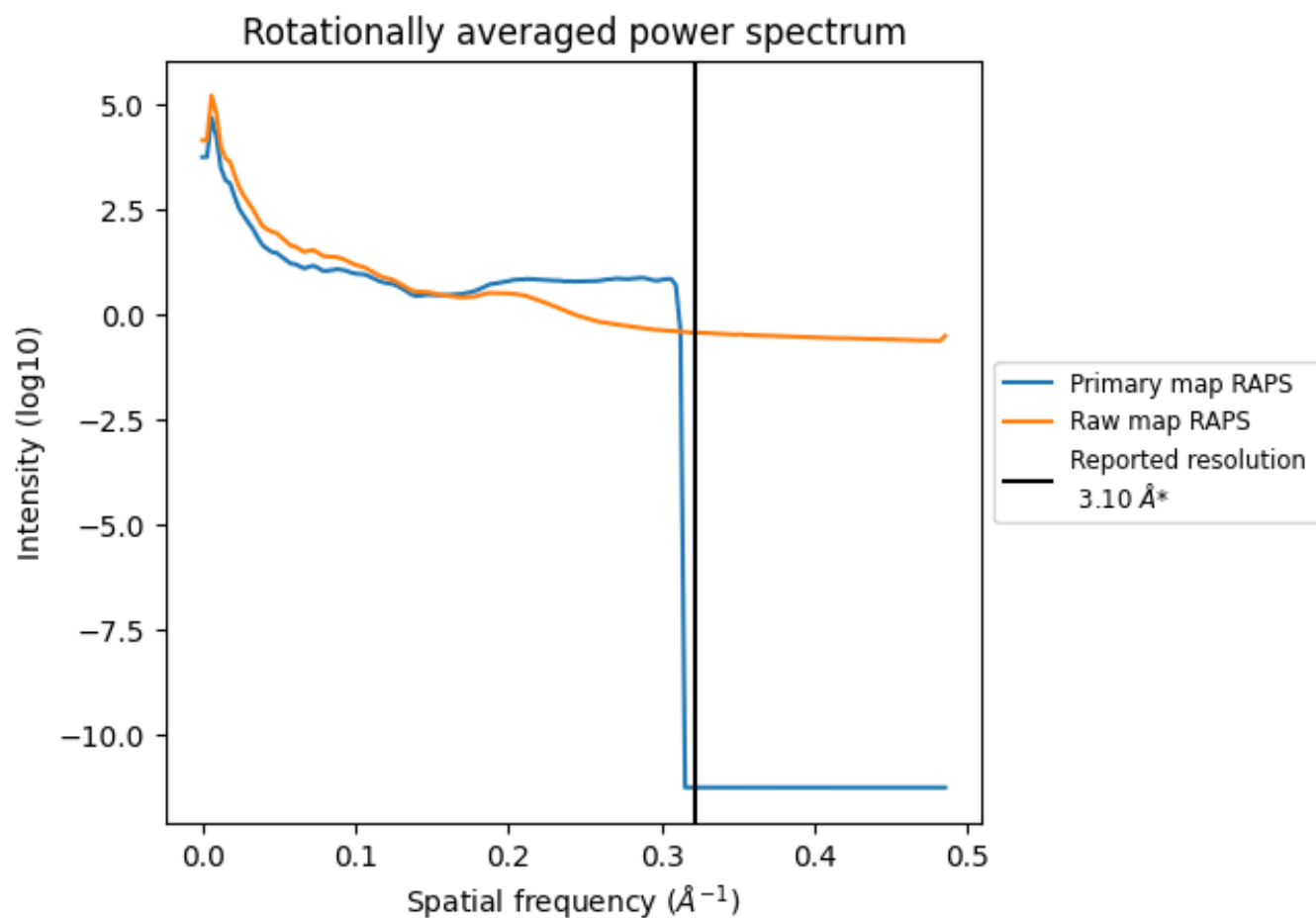
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 80 nm³; this corresponds to an approximate mass of 72 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](#)

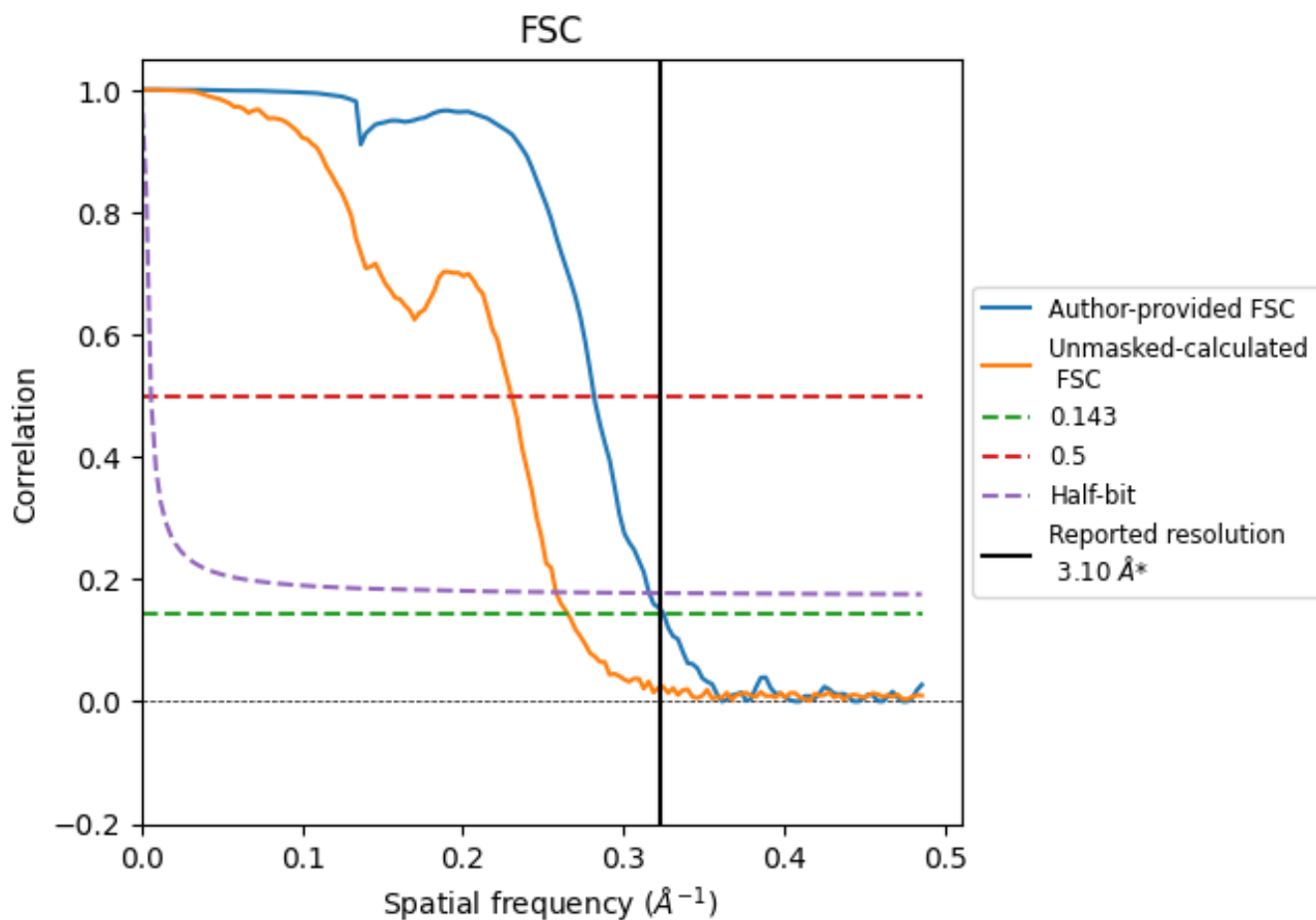


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.08	3.55	3.17
Unmasked-calculated*	3.77	4.34	3.88

*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 3.77 differs from the reported value 3.1 by more than 10 %

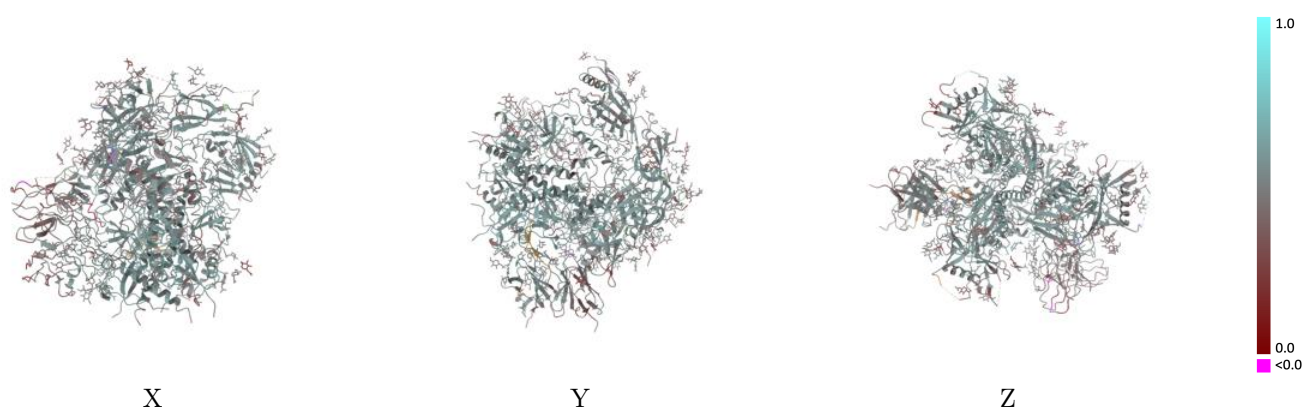
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7858 and PDB model 6DCQ. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

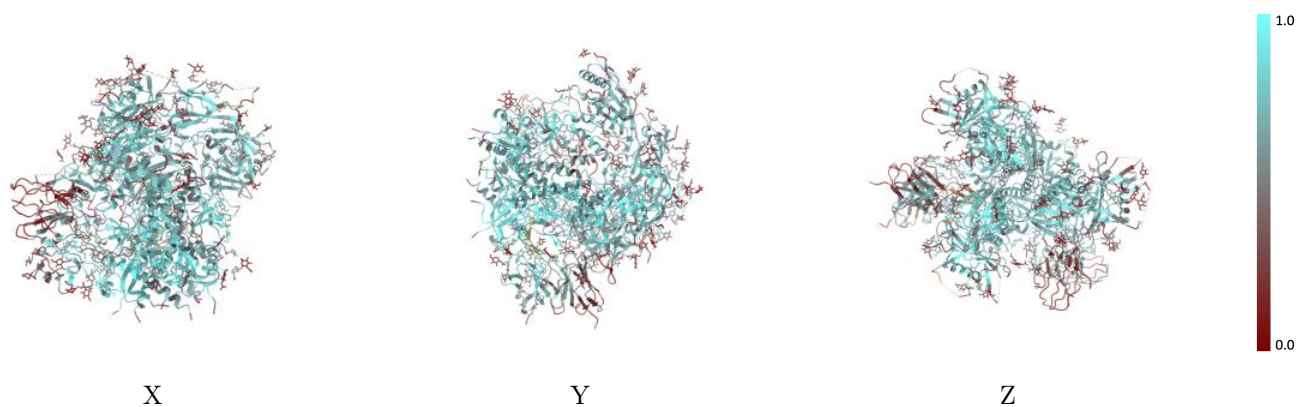
This section was not generated.

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



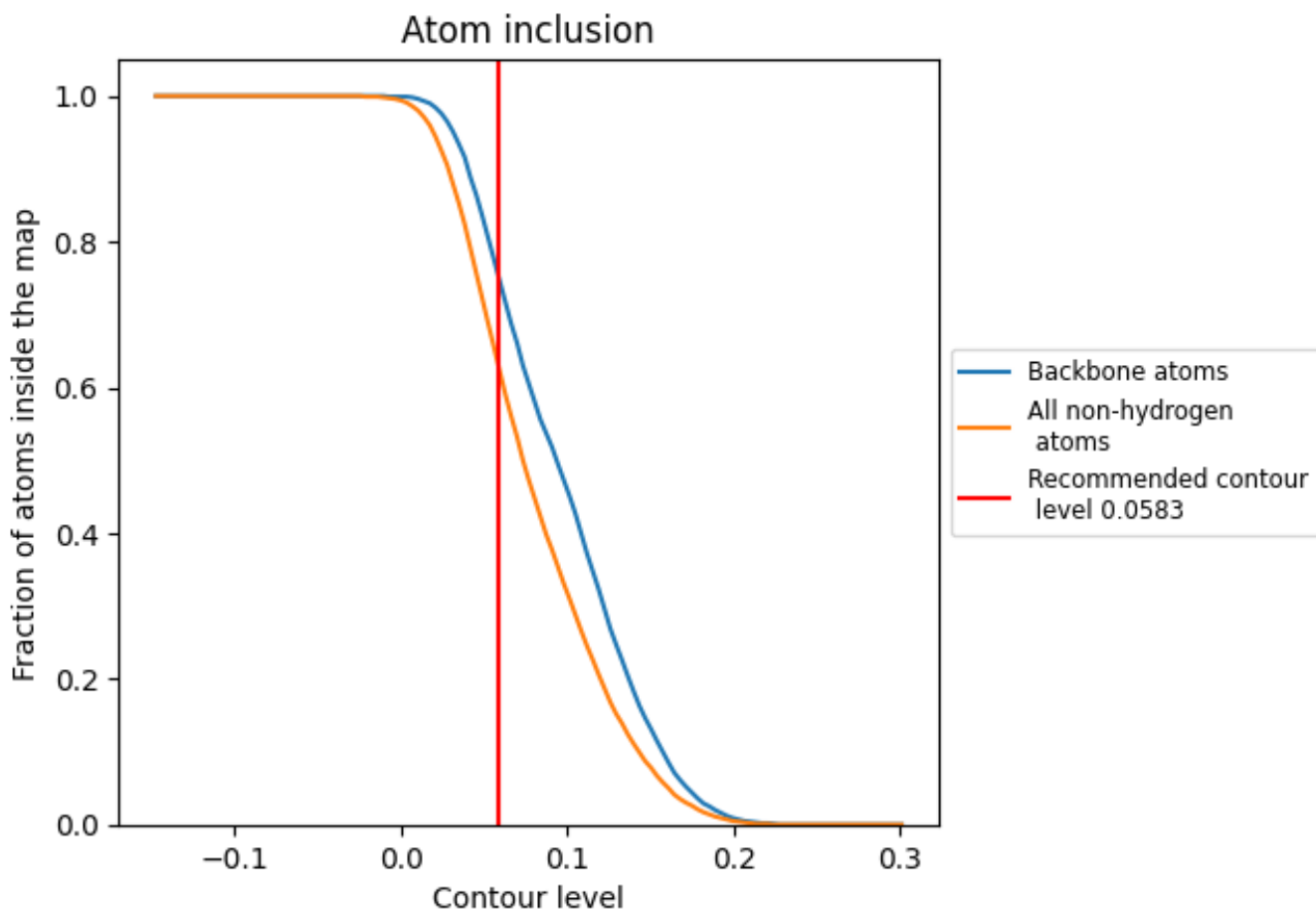
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0583).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 63% 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 (0.0583) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6340	 0.5090
A	 0.6480	 0.5140
B	 0.7110	 0.5370
C	 0.6870	 0.5260
D	 0.7090	 0.5320
E	 0.7010	 0.5270
F	 0.7720	 0.5550
G	 0.2920	 0.3780
H	 0.5580	 0.4530
I	 0.3930	 0.4050
J	 0.3210	 0.4300
K	 0.2500	 0.3380
L	 0.2850	 0.4000
M	 0.6780	 0.5090
N	 0.4620	 0.4590
O	 0.2500	 0.4490
P	 0.3210	 0.4760
Q	 0.2500	 0.4670
R	 0.0710	 0.3920
S	 0.3060	 0.4810
T	 0.4290	 0.4470
U	 0.2860	 0.3030
V	 0.3420	 0.4390
W	 0.3930	 0.5230
X	 0.2500	 0.4190
Y	 0.5000	 0.4880
Z	 0.4290	 0.5200
a	 0.3930	 0.3890
b	 0.2860	 0.4140
c	 0.5410	 0.5090
d	 0.1070	 0.3120
e	 0.2140	 0.4040
f	 0.5790	 0.5420
g	 0.5220	 0.5140
h	 0.6070	 0.5220



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Chain	Atom inclusion	Q-score
i	 0.1790	 0.4700
j	 0.5000	 0.4880
k	 0.5180	 0.4880
l	 0.3210	 0.4870
m	 0.4290	 0.5100
n	 0.3930	 0.4140
o	 0.2500	 0.3500
p	 0.3210	 0.4780
q	 0.3570	 0.3570
r	 0.4780	 0.5030
s	 0.5730	 0.5280