



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 11:29 AM UTC

PDB ID : 6Q04 / pdb_00006q04
EMDB ID : EMD-20542
Title : MERS-CoV S structure in complex with 5-N-acetyl neuraminic acid
Authors : Park, Y.J.; Walls, A.C.; Wang, Z.; Sauer, M.; Li, W.; Tortorici, M.A.; Bosch, B.J.; DiMaio, F.D.; Veessler, D.; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2019-08-01
Resolution : 2.50 Å (reported)
Based on initial model : 6BN3

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:

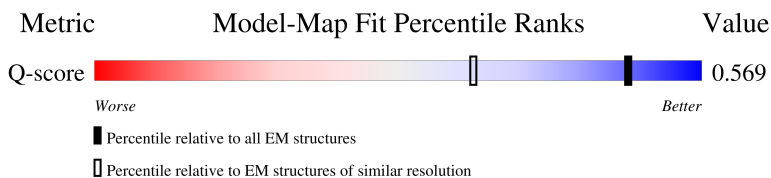
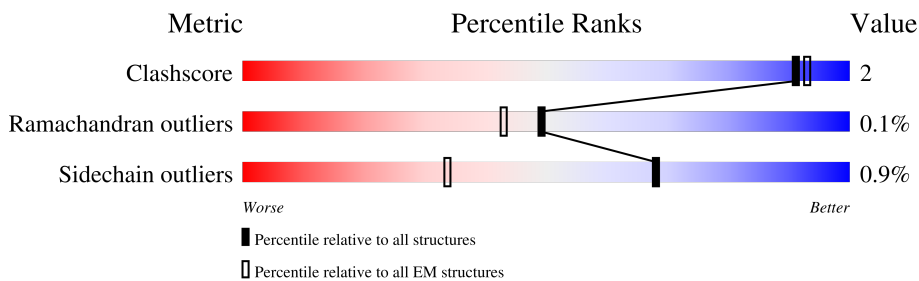
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.50 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	7115 (2.00 - 3.00)

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	1359	 77% 7% 15%
1	B	1359	 77% 7% 15%
1	C	1359	 77% 7% 15%


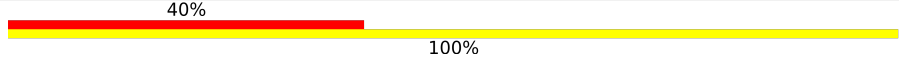

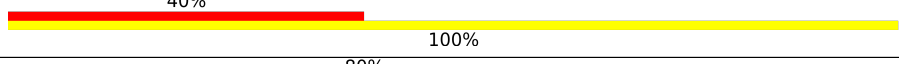

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Mol	Chain	Length	Quality of chain
2	D	4	50% 100%
2	H	4	75% 100%
2	N	4	50% 100%
2	R	4	75% 100%
2	X	4	50% 100%
2	b	4	75% 100%
3	E	2	100%
3	I	2	50% 100%
3	J	2	100%
3	M	2	50% 100%
3	O	2	100%
3	S	2	50% 100%
3	T	2	100%
3	W	2	50% 100%
3	Y	2	100%
3	c	2	50% 100%
3	d	2	100%
3	g	2	50% 100%
4	F	7	71% 43% 57%
4	P	7	71% 43% 57%
4	Z	7	71% 43% 57%
5	G	3	100%
5	Q	3	100%
5	a	3	100%
6	K	5	40% 100%

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Mol	Chain	Length	Quality of chain
6	L	5	 <p>80% 20% 80%</p>
6	U	5	 <p>40% 100%</p>
6	V	5	 <p>60% 20% 80%</p>
6	e	5	 <p>40% 100%</p>
6	f	5	 <p>80% 20% 80%</p>

2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 28911 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1159	8952	5694	1476	1733	49	0	0
1	B	1159	8952	5694	1476	1733	49	0	0
1	C	1159	8952	5694	1476	1733	49	0	0

There are 261 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP K0BRG7
A	-12	GLY	-	expression tag	UNP K0BRG7
A	-11	ILE	-	expression tag	UNP K0BRG7
A	-10	LEU	-	expression tag	UNP K0BRG7
A	-9	PRO	-	expression tag	UNP K0BRG7
A	-8	SER	-	expression tag	UNP K0BRG7
A	-7	PRO	-	expression tag	UNP K0BRG7
A	-6	GLY	-	expression tag	UNP K0BRG7
A	-5	MET	-	expression tag	UNP K0BRG7
A	-4	PRO	-	expression tag	UNP K0BRG7
A	-3	ALA	-	expression tag	UNP K0BRG7
A	-2	LEU	-	expression tag	UNP K0BRG7
A	-1	LEU	-	expression tag	UNP K0BRG7
A	0	SER	-	expression tag	UNP K0BRG7
A	1	LEU	-	expression tag	UNP K0BRG7
A	2	VAL	-	expression tag	UNP K0BRG7
A	3	SER	-	expression tag	UNP K0BRG7
A	4	LEU	-	expression tag	UNP K0BRG7
A	5	LEU	-	expression tag	UNP K0BRG7
A	6	SER	-	expression tag	UNP K0BRG7
A	7	VAL	-	expression tag	UNP K0BRG7
A	8	LEU	-	expression tag	UNP K0BRG7
A	9	LEU	-	expression tag	UNP K0BRG7
A	10	MET	-	expression tag	UNP K0BRG7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	11	GLY	-	expression tag	UNP K0BRG7
A	12	CYS	-	expression tag	UNP K0BRG7
A	13	VAL	-	expression tag	UNP K0BRG7
A	14	ALA	-	expression tag	UNP K0BRG7
A	15	GLU	-	expression tag	UNP K0BRG7
A	16	THR	-	expression tag	UNP K0BRG7
A	17	GLY	-	expression tag	UNP K0BRG7
A	18	THR	-	expression tag	UNP K0BRG7
A	748	ALA	ARG	conflict	UNP K0BRG7
A	751	GLY	ARG	conflict	UNP K0BRG7
A	1060	PRO	VAL	conflict	UNP K0BRG7
A	1061	PRO	LEU	conflict	UNP K0BRG7
A	1295	GLY	-	expression tag	UNP K0BRG7
A	1296	SER	-	expression tag	UNP K0BRG7
A	1297	GLY	-	expression tag	UNP K0BRG7
A	1298	ARG	-	expression tag	UNP K0BRG7
A	1299	GLU	-	expression tag	UNP K0BRG7
A	1300	ASN	-	expression tag	UNP K0BRG7
A	1301	LEU	-	expression tag	UNP K0BRG7
A	1302	TYR	-	expression tag	UNP K0BRG7
A	1303	PHE	-	expression tag	UNP K0BRG7
A	1304	GLN	-	expression tag	UNP K0BRG7
A	1305	GLY	-	expression tag	UNP K0BRG7
A	1306	GLY	-	expression tag	UNP K0BRG7
A	1307	GLY	-	expression tag	UNP K0BRG7
A	1308	GLY	-	expression tag	UNP K0BRG7
A	1309	SER	-	expression tag	UNP K0BRG7
A	1310	GLY	-	expression tag	UNP K0BRG7
A	1311	TYR	-	expression tag	UNP K0BRG7
A	1312	ILE	-	expression tag	UNP K0BRG7
A	1313	PRO	-	expression tag	UNP K0BRG7
A	1314	GLU	-	expression tag	UNP K0BRG7
A	1315	ALA	-	expression tag	UNP K0BRG7
A	1316	PRO	-	expression tag	UNP K0BRG7
A	1317	ARG	-	expression tag	UNP K0BRG7
A	1318	ASP	-	expression tag	UNP K0BRG7
A	1319	GLY	-	expression tag	UNP K0BRG7
A	1320	GLN	-	expression tag	UNP K0BRG7
A	1321	ALA	-	expression tag	UNP K0BRG7
A	1322	TYR	-	expression tag	UNP K0BRG7
A	1323	VAL	-	expression tag	UNP K0BRG7
A	1324	ARG	-	expression tag	UNP K0BRG7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1325	LYS	-	expression tag	UNP K0BRG7
A	1326	ASP	-	expression tag	UNP K0BRG7
A	1327	GLY	-	expression tag	UNP K0BRG7
A	1328	GLU	-	expression tag	UNP K0BRG7
A	1329	TRP	-	expression tag	UNP K0BRG7
A	1330	VAL	-	expression tag	UNP K0BRG7
A	1331	LEU	-	expression tag	UNP K0BRG7
A	1332	LEU	-	expression tag	UNP K0BRG7
A	1333	SER	-	expression tag	UNP K0BRG7
A	1334	THR	-	expression tag	UNP K0BRG7
A	1335	PHE	-	expression tag	UNP K0BRG7
A	1336	LEU	-	expression tag	UNP K0BRG7
A	1337	GLY	-	expression tag	UNP K0BRG7
A	1338	HIS	-	expression tag	UNP K0BRG7
A	1339	HIS	-	expression tag	UNP K0BRG7
A	1340	HIS	-	expression tag	UNP K0BRG7
A	1341	HIS	-	expression tag	UNP K0BRG7
A	1342	HIS	-	expression tag	UNP K0BRG7
A	1343	HIS	-	expression tag	UNP K0BRG7
A	1344	HIS	-	expression tag	UNP K0BRG7
A	1345	HIS	-	expression tag	UNP K0BRG7
B	-13	MET	-	initiating methionine	UNP K0BRG7
B	-12	GLY	-	expression tag	UNP K0BRG7
B	-11	ILE	-	expression tag	UNP K0BRG7
B	-10	LEU	-	expression tag	UNP K0BRG7
B	-9	PRO	-	expression tag	UNP K0BRG7
B	-8	SER	-	expression tag	UNP K0BRG7
B	-7	PRO	-	expression tag	UNP K0BRG7
B	-6	GLY	-	expression tag	UNP K0BRG7
B	-5	MET	-	expression tag	UNP K0BRG7
B	-4	PRO	-	expression tag	UNP K0BRG7
B	-3	ALA	-	expression tag	UNP K0BRG7
B	-2	LEU	-	expression tag	UNP K0BRG7
B	-1	LEU	-	expression tag	UNP K0BRG7
B	0	SER	-	expression tag	UNP K0BRG7
B	1	LEU	-	expression tag	UNP K0BRG7
B	2	VAL	-	expression tag	UNP K0BRG7
B	3	SER	-	expression tag	UNP K0BRG7
B	4	LEU	-	expression tag	UNP K0BRG7
B	5	LEU	-	expression tag	UNP K0BRG7
B	6	SER	-	expression tag	UNP K0BRG7
B	7	VAL	-	expression tag	UNP K0BRG7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	8	LEU	-	expression tag	UNP K0BRG7
B	9	LEU	-	expression tag	UNP K0BRG7
B	10	MET	-	expression tag	UNP K0BRG7
B	11	GLY	-	expression tag	UNP K0BRG7
B	12	CYS	-	expression tag	UNP K0BRG7
B	13	VAL	-	expression tag	UNP K0BRG7
B	14	ALA	-	expression tag	UNP K0BRG7
B	15	GLU	-	expression tag	UNP K0BRG7
B	16	THR	-	expression tag	UNP K0BRG7
B	17	GLY	-	expression tag	UNP K0BRG7
B	18	THR	-	expression tag	UNP K0BRG7
B	748	ALA	ARG	conflict	UNP K0BRG7
B	751	GLY	ARG	conflict	UNP K0BRG7
B	1060	PRO	VAL	conflict	UNP K0BRG7
B	1061	PRO	LEU	conflict	UNP K0BRG7
B	1295	GLY	-	expression tag	UNP K0BRG7
B	1296	SER	-	expression tag	UNP K0BRG7
B	1297	GLY	-	expression tag	UNP K0BRG7
B	1298	ARG	-	expression tag	UNP K0BRG7
B	1299	GLU	-	expression tag	UNP K0BRG7
B	1300	ASN	-	expression tag	UNP K0BRG7
B	1301	LEU	-	expression tag	UNP K0BRG7
B	1302	TYR	-	expression tag	UNP K0BRG7
B	1303	PHE	-	expression tag	UNP K0BRG7
B	1304	GLN	-	expression tag	UNP K0BRG7
B	1305	GLY	-	expression tag	UNP K0BRG7
B	1306	GLY	-	expression tag	UNP K0BRG7
B	1307	GLY	-	expression tag	UNP K0BRG7
B	1308	GLY	-	expression tag	UNP K0BRG7
B	1309	SER	-	expression tag	UNP K0BRG7
B	1310	GLY	-	expression tag	UNP K0BRG7
B	1311	TYR	-	expression tag	UNP K0BRG7
B	1312	ILE	-	expression tag	UNP K0BRG7
B	1313	PRO	-	expression tag	UNP K0BRG7
B	1314	GLU	-	expression tag	UNP K0BRG7
B	1315	ALA	-	expression tag	UNP K0BRG7
B	1316	PRO	-	expression tag	UNP K0BRG7
B	1317	ARG	-	expression tag	UNP K0BRG7
B	1318	ASP	-	expression tag	UNP K0BRG7
B	1319	GLY	-	expression tag	UNP K0BRG7
B	1320	GLN	-	expression tag	UNP K0BRG7
B	1321	ALA	-	expression tag	UNP K0BRG7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1322	TYR	-	expression tag	UNP K0BRG7
B	1323	VAL	-	expression tag	UNP K0BRG7
B	1324	ARG	-	expression tag	UNP K0BRG7
B	1325	LYS	-	expression tag	UNP K0BRG7
B	1326	ASP	-	expression tag	UNP K0BRG7
B	1327	GLY	-	expression tag	UNP K0BRG7
B	1328	GLU	-	expression tag	UNP K0BRG7
B	1329	TRP	-	expression tag	UNP K0BRG7
B	1330	VAL	-	expression tag	UNP K0BRG7
B	1331	LEU	-	expression tag	UNP K0BRG7
B	1332	LEU	-	expression tag	UNP K0BRG7
B	1333	SER	-	expression tag	UNP K0BRG7
B	1334	THR	-	expression tag	UNP K0BRG7
B	1335	PHE	-	expression tag	UNP K0BRG7
B	1336	LEU	-	expression tag	UNP K0BRG7
B	1337	GLY	-	expression tag	UNP K0BRG7
B	1338	HIS	-	expression tag	UNP K0BRG7
B	1339	HIS	-	expression tag	UNP K0BRG7
B	1340	HIS	-	expression tag	UNP K0BRG7
B	1341	HIS	-	expression tag	UNP K0BRG7
B	1342	HIS	-	expression tag	UNP K0BRG7
B	1343	HIS	-	expression tag	UNP K0BRG7
B	1344	HIS	-	expression tag	UNP K0BRG7
B	1345	HIS	-	expression tag	UNP K0BRG7
C	-13	MET	-	initiating methionine	UNP K0BRG7
C	-12	GLY	-	expression tag	UNP K0BRG7
C	-11	ILE	-	expression tag	UNP K0BRG7
C	-10	LEU	-	expression tag	UNP K0BRG7
C	-9	PRO	-	expression tag	UNP K0BRG7
C	-8	SER	-	expression tag	UNP K0BRG7
C	-7	PRO	-	expression tag	UNP K0BRG7
C	-6	GLY	-	expression tag	UNP K0BRG7
C	-5	MET	-	expression tag	UNP K0BRG7
C	-4	PRO	-	expression tag	UNP K0BRG7
C	-3	ALA	-	expression tag	UNP K0BRG7
C	-2	LEU	-	expression tag	UNP K0BRG7
C	-1	LEU	-	expression tag	UNP K0BRG7
C	0	SER	-	expression tag	UNP K0BRG7
C	1	LEU	-	expression tag	UNP K0BRG7
C	2	VAL	-	expression tag	UNP K0BRG7
C	3	SER	-	expression tag	UNP K0BRG7
C	4	LEU	-	expression tag	UNP K0BRG7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	5	LEU	-	expression tag	UNP K0BRG7
C	6	SER	-	expression tag	UNP K0BRG7
C	7	VAL	-	expression tag	UNP K0BRG7
C	8	LEU	-	expression tag	UNP K0BRG7
C	9	LEU	-	expression tag	UNP K0BRG7
C	10	MET	-	expression tag	UNP K0BRG7
C	11	GLY	-	expression tag	UNP K0BRG7
C	12	CYS	-	expression tag	UNP K0BRG7
C	13	VAL	-	expression tag	UNP K0BRG7
C	14	ALA	-	expression tag	UNP K0BRG7
C	15	GLU	-	expression tag	UNP K0BRG7
C	16	THR	-	expression tag	UNP K0BRG7
C	17	GLY	-	expression tag	UNP K0BRG7
C	18	THR	-	expression tag	UNP K0BRG7
C	748	ALA	ARG	conflict	UNP K0BRG7
C	751	GLY	ARG	conflict	UNP K0BRG7
C	1060	PRO	VAL	conflict	UNP K0BRG7
C	1061	PRO	LEU	conflict	UNP K0BRG7
C	1295	GLY	-	expression tag	UNP K0BRG7
C	1296	SER	-	expression tag	UNP K0BRG7
C	1297	GLY	-	expression tag	UNP K0BRG7
C	1298	ARG	-	expression tag	UNP K0BRG7
C	1299	GLU	-	expression tag	UNP K0BRG7
C	1300	ASN	-	expression tag	UNP K0BRG7
C	1301	LEU	-	expression tag	UNP K0BRG7
C	1302	TYR	-	expression tag	UNP K0BRG7
C	1303	PHE	-	expression tag	UNP K0BRG7
C	1304	GLN	-	expression tag	UNP K0BRG7
C	1305	GLY	-	expression tag	UNP K0BRG7
C	1306	GLY	-	expression tag	UNP K0BRG7
C	1307	GLY	-	expression tag	UNP K0BRG7
C	1308	GLY	-	expression tag	UNP K0BRG7
C	1309	SER	-	expression tag	UNP K0BRG7
C	1310	GLY	-	expression tag	UNP K0BRG7
C	1311	TYR	-	expression tag	UNP K0BRG7
C	1312	ILE	-	expression tag	UNP K0BRG7
C	1313	PRO	-	expression tag	UNP K0BRG7
C	1314	GLU	-	expression tag	UNP K0BRG7
C	1315	ALA	-	expression tag	UNP K0BRG7
C	1316	PRO	-	expression tag	UNP K0BRG7
C	1317	ARG	-	expression tag	UNP K0BRG7
C	1318	ASP	-	expression tag	UNP K0BRG7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1319	GLY	-	expression tag	UNP K0BRG7
C	1320	GLN	-	expression tag	UNP K0BRG7
C	1321	ALA	-	expression tag	UNP K0BRG7
C	1322	TYR	-	expression tag	UNP K0BRG7
C	1323	VAL	-	expression tag	UNP K0BRG7
C	1324	ARG	-	expression tag	UNP K0BRG7
C	1325	LYS	-	expression tag	UNP K0BRG7
C	1326	ASP	-	expression tag	UNP K0BRG7
C	1327	GLY	-	expression tag	UNP K0BRG7
C	1328	GLU	-	expression tag	UNP K0BRG7
C	1329	TRP	-	expression tag	UNP K0BRG7
C	1330	VAL	-	expression tag	UNP K0BRG7
C	1331	LEU	-	expression tag	UNP K0BRG7
C	1332	LEU	-	expression tag	UNP K0BRG7
C	1333	SER	-	expression tag	UNP K0BRG7
C	1334	THR	-	expression tag	UNP K0BRG7
C	1335	PHE	-	expression tag	UNP K0BRG7
C	1336	LEU	-	expression tag	UNP K0BRG7
C	1337	GLY	-	expression tag	UNP K0BRG7
C	1338	HIS	-	expression tag	UNP K0BRG7
C	1339	HIS	-	expression tag	UNP K0BRG7
C	1340	HIS	-	expression tag	UNP K0BRG7
C	1341	HIS	-	expression tag	UNP K0BRG7
C	1342	HIS	-	expression tag	UNP K0BRG7
C	1343	HIS	-	expression tag	UNP K0BRG7
C	1344	HIS	-	expression tag	UNP K0BRG7
C	1345	HIS	-	expression tag	UNP K0BRG7

- Molecule 2 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	
2	D	4	Total	C	N	O	0	0
			50	28	2	20		
2	H	4	Total	C	N	O	0	0
			50	28	2	20		

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	N	4	Total	C	N	O	0	0
			50	28	2	20		
2	R	4	Total	C	N	O	0	0
			50	28	2	20		
2	X	4	Total	C	N	O	0	0
			50	28	2	20		
2	b	4	Total	C	N	O	0	0
			50	28	2	20		

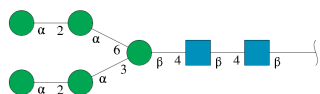
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		
3	J	2	Total	C	N	O	0	0
			28	16	2	10		
3	M	2	Total	C	N	O	0	0
			28	16	2	10		
3	O	2	Total	C	N	O	0	0
			28	16	2	10		
3	S	2	Total	C	N	O	0	0
			28	16	2	10		
3	T	2	Total	C	N	O	0	0
			28	16	2	10		
3	W	2	Total	C	N	O	0	0
			28	16	2	10		
3	Y	2	Total	C	N	O	0	0
			28	16	2	10		
3	c	2	Total	C	N	O	0	0
			28	16	2	10		
3	d	2	Total	C	N	O	0	0
			28	16	2	10		
3	g	2	Total	C	N	O	0	0
			28	16	2	10		

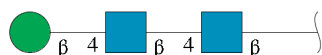
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyran

ose-(1-3)-[alpha-D-mannopyranose-(1-2)-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.



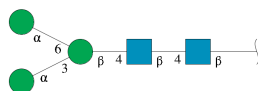
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	F	7	83	46	2	35	0	0
4	P	7	83	46	2	35	0	0
4	Z	7	83	46	2	35	0	0

- Molecule 5 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
			Total	C	N	O		
5	G	3	39	22	2	15	0	0
5	Q	3	39	22	2	15	0	0
5	a	3	39	22	2	15	0	0

- Molecule 6 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.



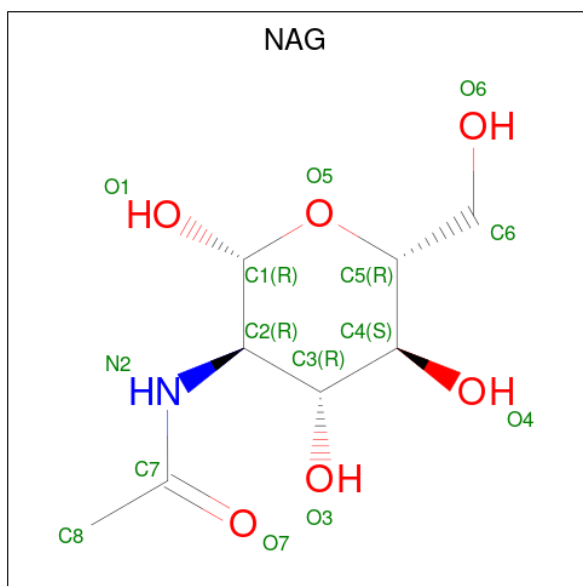
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	K	5	61	34	2	25	0	0
6	L	5	61	34	2	25	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	U	5	Total	C	N	O	0	0
			61	34	2	25		
6	V	5	Total	C	N	O	0	0
			61	34	2	25		
6	e	5	Total	C	N	O	0	0
			61	34	2	25		
6	f	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



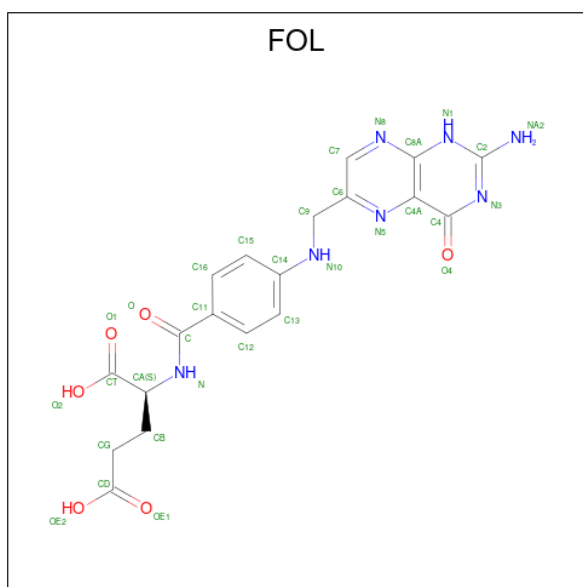
Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	

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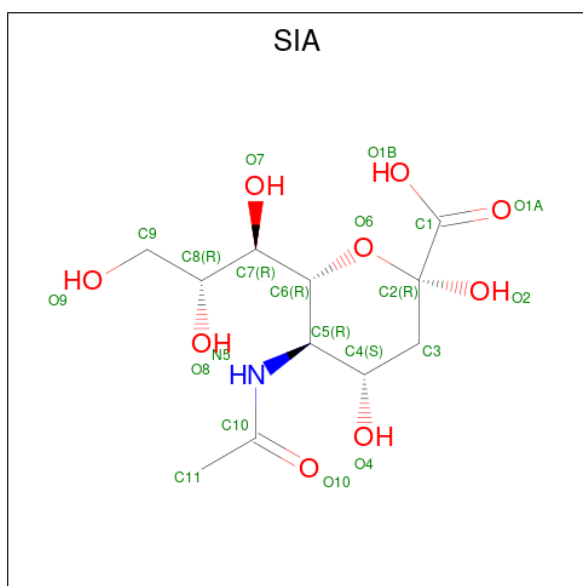
Mol	Chain	Residues	Atoms				AltConf
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	C	1	Total	C	N	O	0
			14	8	1	5	
7	C	1	Total	C	N	O	0
			14	8	1	5	
7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

- Molecule 8 is FOLIC ACID (CCD ID: FOL) (formula: $C_{19}H_{19}N_7O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf	
8	A	1	Total	C	N	O	0
			32	19	7	6	
8	B	1	Total	C	N	O	0
			32	19	7	6	
8	C	1	Total	C	N	O	0
			32	19	7	6	

- Molecule 9 is N-acetyl-alpha-neuraminic acid (CCD ID: SIA) (formula: C₁₁H₁₉NO₉) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
9	A	1	Total	C	N	O	0
			21	11	1	9	
9	B	1	Total	C	N	O	0
			21	11	1	9	
9	C	1	Total	C	N	O	0
			21	11	1	9	

- Molecule 10 is water.

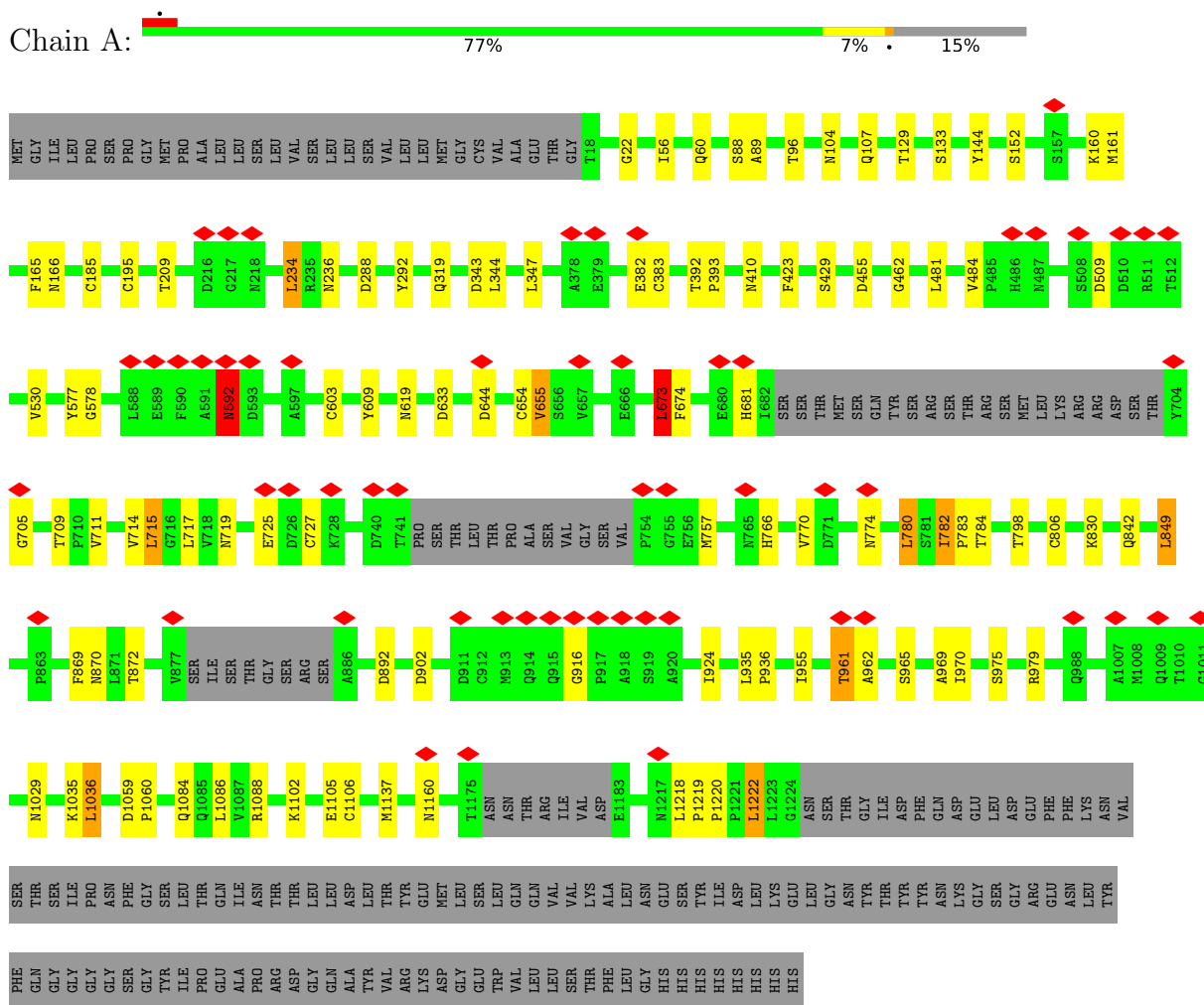
Mol	Chain	Residues	Atoms		AltConf
10	A	78	Total	O	0
			78	78	
10	B	78	Total	O	0
			78	78	
10	C	78	Total	O	0
			78	78	

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.

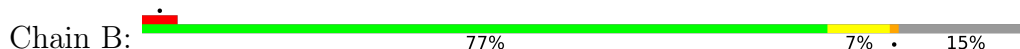
- Molecule 1: Spike glycoprotein

Chain A:



- Molecule 1: Spike glycoprotein

Chain B:

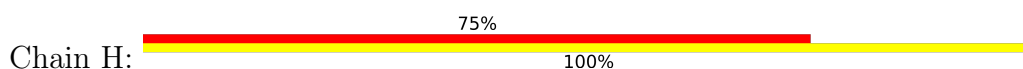




- Molecule 2: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



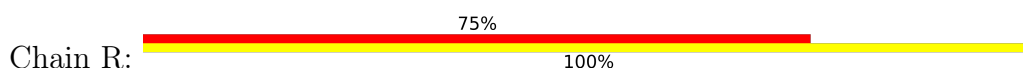
- Molecule 2: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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

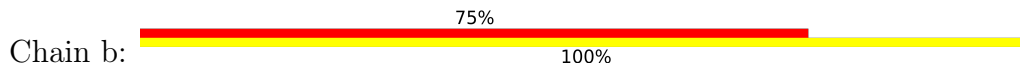


- Molecule 2: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





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



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



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



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



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



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



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



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



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



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



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



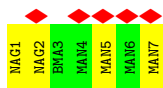
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



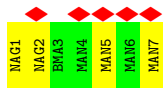
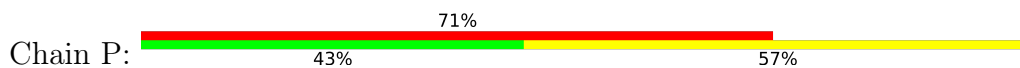
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



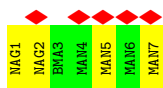
- Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



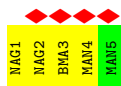
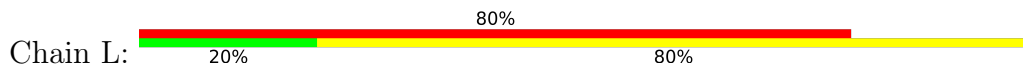
- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 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 6: 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

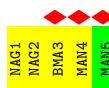


- Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





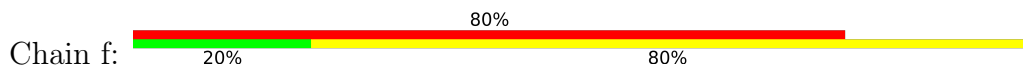
- Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 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 6: 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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	121443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	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	7.096	Depositor
Minimum map value	-3.870	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.101	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.37	38/9163 (0.4%)	1.37	105/12471 (0.8%)
1	B	1.37	38/9163 (0.4%)	1.37	105/12471 (0.8%)
1	C	1.37	38/9163 (0.4%)	1.37	105/12471 (0.8%)
All	All	1.37	114/27489 (0.4%)	1.37	315/37413 (0.8%)

The worst 5 of 114 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	383	CYS	C-O	-30.13	0.87	1.23
1	A	383	CYS	C-O	-30.13	0.87	1.23
1	B	383	CYS	C-O	-30.09	0.87	1.23
1	A	383	CYS	C-N	15.79	1.56	1.33
1	C	383	CYS	C-N	15.79	1.56	1.33

The worst 5 of 315 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	383	CYS	CA-C-O	18.55	142.25	120.92
1	C	383	CYS	CA-C-O	18.55	142.25	120.92
1	B	383	CYS	CA-C-O	18.50	142.20	120.92
1	C	382	GLU	CA-C-N	-12.98	102.88	122.09
1	C	382	GLU	C-N-CA	-12.98	102.88	122.09

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	8952	0	8632	31	0
1	B	8952	0	8632	32	0
1	C	8952	0	8632	33	0
2	D	50	0	43	0	0
2	H	50	0	43	0	0
2	N	50	0	43	0	0
2	R	50	0	43	0	0
2	X	50	0	43	0	0
2	b	50	0	43	0	0
3	E	28	0	25	0	0
3	I	28	0	25	0	0
3	J	28	0	25	0	0
3	M	28	0	25	0	0
3	O	28	0	25	0	0
3	S	28	0	25	0	0
3	T	28	0	25	0	0
3	W	28	0	25	0	0
3	Y	28	0	25	0	0
3	c	28	0	25	0	0
3	d	28	0	25	0	0
3	g	28	0	25	0	0
4	F	83	0	70	0	0
4	P	83	0	70	0	0
4	Z	83	0	70	0	0
5	G	39	0	34	0	0
5	Q	39	0	34	0	0
5	a	39	0	34	0	0
6	K	61	0	52	0	0
6	L	61	0	52	0	0
6	U	61	0	52	0	0
6	V	61	0	52	0	0
6	e	61	0	52	0	0
6	f	61	0	52	0	0
7	A	98	0	91	0	0
7	B	98	0	91	0	0
7	C	98	0	91	0	0
8	A	32	0	17	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	32	0	17	1	0
8	C	32	0	17	1	0
9	A	21	0	18	0	0
9	B	21	0	18	0	0
9	C	21	0	18	0	0
10	A	78	0	0	0	0
10	B	78	0	0	0	0
10	C	78	0	0	0	0
All	All	28911	0	27456	87	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 2.

The worst 5 of 87 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:673:LEU:HD13	1:C:714:VAL:HG22	1.57	0.87
1:B:673:LEU:HD13	1:B:714:VAL:HG22	1.57	0.86
1:A:673:LEU:HD13	1:A:714:VAL:HG22	1.57	0.85
1:B:107:GLN:HE21	1:B:160:LYS:HB3	1.42	0.84
1:C:673:LEU:HD21	1:C:711:VAL:HG23	1.59	0.83

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	1149/1359 (84%)	1130 (98%)	18 (2%)	1 (0%)	48 68
1	B	1149/1359 (84%)	1130 (98%)	18 (2%)	1 (0%)	48 68
1	C	1149/1359 (84%)	1130 (98%)	18 (2%)	1 (0%)	48 68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3447/4077 (84%)	3390 (98%)	54 (2%)	3 (0%)	49 68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	578	GLY
1	B	578	GLY
1	C	578	GLY

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	992/1167 (85%)	983 (99%)	9 (1%)	70 87
1	B	992/1167 (85%)	983 (99%)	9 (1%)	70 87
1	C	992/1167 (85%)	983 (99%)	9 (1%)	70 87
All	All	2976/3501 (85%)	2949 (99%)	27 (1%)	68 87

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	715	LEU
1	B	1222	LEU
1	C	849	LEU
1	B	1036	LEU
1	C	234	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	377	GLN
1	C	1084	GLN
1	C	636	GLN

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Mol	Chain	Res	Type
1	C	981	ASN
1	C	1208	GLN

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](#)

108 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$
2	NAG	D	1	1,2	14,14,15	1.42	4 (28%)	17,19,21	1.87	6 (35%)
2	NAG	D	2	2	14,14,15	1.25	2 (14%)	17,19,21	1.65	3 (17%)
2	BMA	D	3	2	11,11,12	1.50	2 (18%)	15,15,17	1.64	1 (6%)
2	MAN	D	4	2	11,11,12	1.12	1 (9%)	15,15,17	1.13	3 (20%)
3	NAG	E	1	1,3	14,14,15	1.53	3 (21%)	17,19,21	1.80	5 (29%)
3	NAG	E	2	3	14,14,15	1.16	1 (7%)	17,19,21	0.87	1 (5%)
4	NAG	F	1	1,4	14,14,15	1.34	1 (7%)	17,19,21	0.83	0
4	NAG	F	2	4	14,14,15	1.40	2 (14%)	17,19,21	0.76	0
4	BMA	F	3	4	11,11,12	1.03	0	15,15,17	0.61	0
4	MAN	F	4	4	11,11,12	0.69	0	15,15,17	0.61	0
4	MAN	F	5	4	11,11,12	1.41	3 (27%)	15,15,17	0.60	0
4	MAN	F	6	4	11,11,12	0.64	0	15,15,17	0.60	0
4	MAN	F	7	4	11,11,12	1.41	2 (18%)	15,15,17	0.57	0
5	NAG	G	1	1,5	14,14,15	1.55	4 (28%)	17,19,21	1.75	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	G	2	5	14,14,15	1.55	3 (21%)	17,19,21	1.25	1 (5%)
5	BMA	G	3	5	11,11,12	0.73	1 (9%)	15,15,17	0.81	0
2	NAG	H	1	1,2	14,14,15	1.78	4 (28%)	17,19,21	2.16	4 (23%)
2	NAG	H	2	2	14,14,15	1.67	3 (21%)	17,19,21	1.91	3 (17%)
2	BMA	H	3	2	11,11,12	1.43	2 (18%)	15,15,17	1.85	1 (6%)
2	MAN	H	4	2	11,11,12	1.15	2 (18%)	15,15,17	1.14	2 (13%)
3	NAG	I	1	1,3	14,14,15	1.53	4 (28%)	17,19,21	1.84	3 (17%)
3	NAG	I	2	3	14,14,15	1.16	1 (7%)	17,19,21	0.68	0
3	NAG	J	1	1,3	14,14,15	1.77	5 (35%)	17,19,21	1.74	2 (11%)
3	NAG	J	2	3	14,14,15	1.27	1 (7%)	17,19,21	0.77	0
6	NAG	K	1	1,6	14,14,15	1.46	4 (28%)	17,19,21	1.84	2 (11%)
6	NAG	K	2	6	14,14,15	1.40	2 (14%)	17,19,21	1.30	1 (5%)
6	BMA	K	3	6	11,11,12	2.09	3 (27%)	15,15,17	1.66	3 (20%)
6	MAN	K	4	6	11,11,12	1.07	1 (9%)	15,15,17	1.17	2 (13%)
6	MAN	K	5	6	11,11,12	1.05	1 (9%)	15,15,17	1.15	1 (6%)
6	NAG	L	1	1,6	14,14,15	0.83	1 (7%)	17,19,21	1.12	1 (5%)
6	NAG	L	2	6	14,14,15	0.78	1 (7%)	17,19,21	1.33	3 (17%)
6	BMA	L	3	6	11,11,12	0.68	0	15,15,17	0.94	1 (6%)
6	MAN	L	4	6	11,11,12	0.69	0	15,15,17	0.74	1 (6%)
6	MAN	L	5	6	11,11,12	0.70	0	15,15,17	0.73	0
3	NAG	M	1	1,3	14,14,15	1.59	5 (35%)	17,19,21	1.65	2 (11%)
3	NAG	M	2	3	14,14,15	1.24	1 (7%)	17,19,21	0.77	1 (5%)
2	NAG	N	1	1,2	14,14,15	1.41	4 (28%)	17,19,21	1.87	6 (35%)
2	NAG	N	2	2	14,14,15	1.25	2 (14%)	17,19,21	1.64	3 (17%)
2	BMA	N	3	2	11,11,12	1.50	2 (18%)	15,15,17	1.63	1 (6%)
2	MAN	N	4	2	11,11,12	1.13	1 (9%)	15,15,17	1.13	3 (20%)
3	NAG	O	1	1,3	14,14,15	1.53	3 (21%)	17,19,21	1.80	5 (29%)
3	NAG	O	2	3	14,14,15	1.16	1 (7%)	17,19,21	0.87	1 (5%)
4	NAG	P	1	1,4	14,14,15	1.35	1 (7%)	17,19,21	0.84	0
4	NAG	P	2	4	14,14,15	1.41	2 (14%)	17,19,21	0.76	0
4	BMA	P	3	4	11,11,12	1.04	0	15,15,17	0.61	0
4	MAN	P	4	4	11,11,12	0.70	0	15,15,17	0.61	0
4	MAN	P	5	4	11,11,12	1.41	3 (27%)	15,15,17	0.60	0
4	MAN	P	6	4	11,11,12	0.63	0	15,15,17	0.59	0
4	MAN	P	7	4	11,11,12	1.42	2 (18%)	15,15,17	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	Q	1	1,5	14,14,15	1.55	4 (28%)	17,19,21	1.75	3 (17%)
5	NAG	Q	2	5	14,14,15	1.56	3 (21%)	17,19,21	1.25	1 (5%)
5	BMA	Q	3	5	11,11,12	0.73	1 (9%)	15,15,17	0.81	0
2	NAG	R	1	1,2	14,14,15	1.77	4 (28%)	17,19,21	2.16	4 (23%)
2	NAG	R	2	2	14,14,15	1.67	3 (21%)	17,19,21	1.91	3 (17%)
2	BMA	R	3	2	11,11,12	1.44	2 (18%)	15,15,17	1.85	2 (13%)
2	MAN	R	4	2	11,11,12	1.16	2 (18%)	15,15,17	1.15	2 (13%)
3	NAG	S	1	1,3	14,14,15	1.53	4 (28%)	17,19,21	1.83	3 (17%)
3	NAG	S	2	3	14,14,15	1.17	1 (7%)	17,19,21	0.68	0
3	NAG	T	1	1,3	14,14,15	1.77	5 (35%)	17,19,21	1.74	2 (11%)
3	NAG	T	2	3	14,14,15	1.26	1 (7%)	17,19,21	0.76	0
6	NAG	U	1	1,6	14,14,15	1.47	4 (28%)	17,19,21	1.84	2 (11%)
6	NAG	U	2	6	14,14,15	1.41	2 (14%)	17,19,21	1.30	1 (5%)
6	BMA	U	3	6	11,11,12	2.08	3 (27%)	15,15,17	1.66	3 (20%)
6	MAN	U	4	6	11,11,12	1.06	1 (9%)	15,15,17	1.17	2 (13%)
6	MAN	U	5	6	11,11,12	1.06	1 (9%)	15,15,17	1.14	1 (6%)
6	NAG	V	1	1,6	14,14,15	0.83	1 (7%)	17,19,21	1.13	1 (5%)
6	NAG	V	2	6	14,14,15	0.78	1 (7%)	17,19,21	1.33	3 (17%)
6	BMA	V	3	6	11,11,12	0.67	0	15,15,17	0.94	1 (6%)
6	MAN	V	4	6	11,11,12	0.68	0	15,15,17	0.74	1 (6%)
6	MAN	V	5	6	11,11,12	0.70	0	15,15,17	0.73	0
3	NAG	W	1	1,3	14,14,15	1.59	5 (35%)	17,19,21	1.65	2 (11%)
3	NAG	W	2	3	14,14,15	1.23	1 (7%)	17,19,21	0.78	1 (5%)
2	NAG	X	1	1,2	14,14,15	1.42	4 (28%)	17,19,21	1.88	6 (35%)
2	NAG	X	2	2	14,14,15	1.26	2 (14%)	17,19,21	1.65	3 (17%)
2	BMA	X	3	2	11,11,12	1.50	2 (18%)	15,15,17	1.64	1 (6%)
2	MAN	X	4	2	11,11,12	1.12	1 (9%)	15,15,17	1.13	3 (20%)
3	NAG	Y	1	1,3	14,14,15	1.53	3 (21%)	17,19,21	1.80	5 (29%)
3	NAG	Y	2	3	14,14,15	1.16	1 (7%)	17,19,21	0.87	1 (5%)
4	NAG	Z	1	1,4	14,14,15	1.35	1 (7%)	17,19,21	0.83	0
4	NAG	Z	2	4	14,14,15	1.41	2 (14%)	17,19,21	0.76	0
4	BMA	Z	3	4	11,11,12	1.02	0	15,15,17	0.61	0
4	MAN	Z	4	4	11,11,12	0.70	0	15,15,17	0.62	0
4	MAN	Z	5	4	11,11,12	1.41	3 (27%)	15,15,17	0.60	0
4	MAN	Z	6	4	11,11,12	0.63	0	15,15,17	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	Z	7	4	11,11,12	1.42	2 (18%)	15,15,17	0.57	0
5	NAG	a	1	1,5	14,14,15	1.56	4 (28%)	17,19,21	1.75	3 (17%)
5	NAG	a	2	5	14,14,15	1.55	3 (21%)	17,19,21	1.25	1 (5%)
5	BMA	a	3	5	11,11,12	0.73	1 (9%)	15,15,17	0.81	0
2	NAG	b	1	1,2	14,14,15	1.78	4 (28%)	17,19,21	2.17	4 (23%)
2	NAG	b	2	2	14,14,15	1.67	3 (21%)	17,19,21	1.90	3 (17%)
2	BMA	b	3	2	11,11,12	1.45	2 (18%)	15,15,17	1.85	1 (6%)
2	MAN	b	4	2	11,11,12	1.16	2 (18%)	15,15,17	1.14	2 (13%)
3	NAG	c	1	1,3	14,14,15	1.53	4 (28%)	17,19,21	1.83	3 (17%)
3	NAG	c	2	3	14,14,15	1.15	1 (7%)	17,19,21	0.68	0
3	NAG	d	1	1,3	14,14,15	1.77	5 (35%)	17,19,21	1.74	2 (11%)
3	NAG	d	2	3	14,14,15	1.27	1 (7%)	17,19,21	0.76	0
6	NAG	e	1	1,6	14,14,15	1.46	4 (28%)	17,19,21	1.84	2 (11%)
6	NAG	e	2	6	14,14,15	1.40	2 (14%)	17,19,21	1.30	1 (5%)
6	BMA	e	3	6	11,11,12	2.10	3 (27%)	15,15,17	1.66	3 (20%)
6	MAN	e	4	6	11,11,12	1.08	1 (9%)	15,15,17	1.17	2 (13%)
6	MAN	e	5	6	11,11,12	1.05	1 (9%)	15,15,17	1.14	1 (6%)
6	NAG	f	1	1,6	14,14,15	0.83	1 (7%)	17,19,21	1.12	1 (5%)
6	NAG	f	2	6	14,14,15	0.78	1 (7%)	17,19,21	1.33	3 (17%)
6	BMA	f	3	6	11,11,12	0.68	0	15,15,17	0.94	1 (6%)
6	MAN	f	4	6	11,11,12	0.70	0	15,15,17	0.74	1 (6%)
6	MAN	f	5	6	11,11,12	0.69	0	15,15,17	0.74	0
3	NAG	g	1	1,3	14,14,15	1.59	5 (35%)	17,19,21	1.64	2 (11%)
3	NAG	g	2	3	14,14,15	1.23	1 (7%)	17,19,21	0.77	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
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	BMA	D	3	2	-	1/2/19/22	0/1/1/1
2	MAN	D	4	2	-	1/2/19/22	0/1/1/1
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	1/2/19/22	0/1/1/1
4	MAN	F	5	4	-	0/2/19/22	0/1/1/1
4	MAN	F	6	4	-	1/2/19/22	0/1/1/1
4	MAN	F	7	4	-	0/2/19/22	0/1/1/1
5	NAG	G	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	BMA	G	3	5	-	1/2/19/22	0/1/1/1
2	NAG	H	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	1/6/23/26	0/1/1/1
2	BMA	H	3	2	-	1/2/19/22	0/1/1/1
2	MAN	H	4	2	-	2/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	1/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	1/6/23/26	0/1/1/1
6	NAG	K	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	K	2	6	-	1/6/23/26	0/1/1/1
6	BMA	K	3	6	-	2/2/19/22	0/1/1/1
6	MAN	K	4	6	-	2/2/19/22	0/1/1/1
6	MAN	K	5	6	-	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	-	2/6/23/26	0/1/1/1
6	BMA	L	3	6	-	1/2/19/22	0/1/1/1
6	MAN	L	4	6	-	1/2/19/22	0/1/1/1
6	MAN	L	5	6	-	1/2/19/22	0/1/1/1
3	NAG	M	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	1/6/23/26	0/1/1/1
2	NAG	N	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	N	2	2	-	0/6/23/26	0/1/1/1
2	BMA	N	3	2	-	1/2/19/22	0/1/1/1
2	MAN	N	4	2	-	1/2/19/22	0/1/1/1
3	NAG	O	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	O	2	3	-	1/6/23/26	0/1/1/1
4	NAG	P	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	BMA	P	3	4	-	2/2/19/22	0/1/1/1
4	MAN	P	4	4	-	1/2/19/22	0/1/1/1

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

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

The worst 5 of 210 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	d	2	NAG	C1-C2	4.62	1.58	1.52
3	J	2	NAG	C1-C2	4.60	1.58	1.52
3	T	2	NAG	C1-C2	4.59	1.58	1.52
3	M	2	NAG	C1-C2	4.48	1.58	1.52
3	W	2	NAG	C1-C2	4.47	1.58	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	1	NAG	C3-C4-C5	-6.43	98.58	110.23
2	R	1	NAG	C3-C4-C5	-6.42	98.59	110.23
2	H	1	NAG	C3-C4-C5	-6.41	98.61	110.23
2	b	3	BMA	C2-C3-C4	-6.40	99.60	110.86
2	R	3	BMA	C2-C3-C4	-6.40	99.61	110.86

There are no chirality outliers.

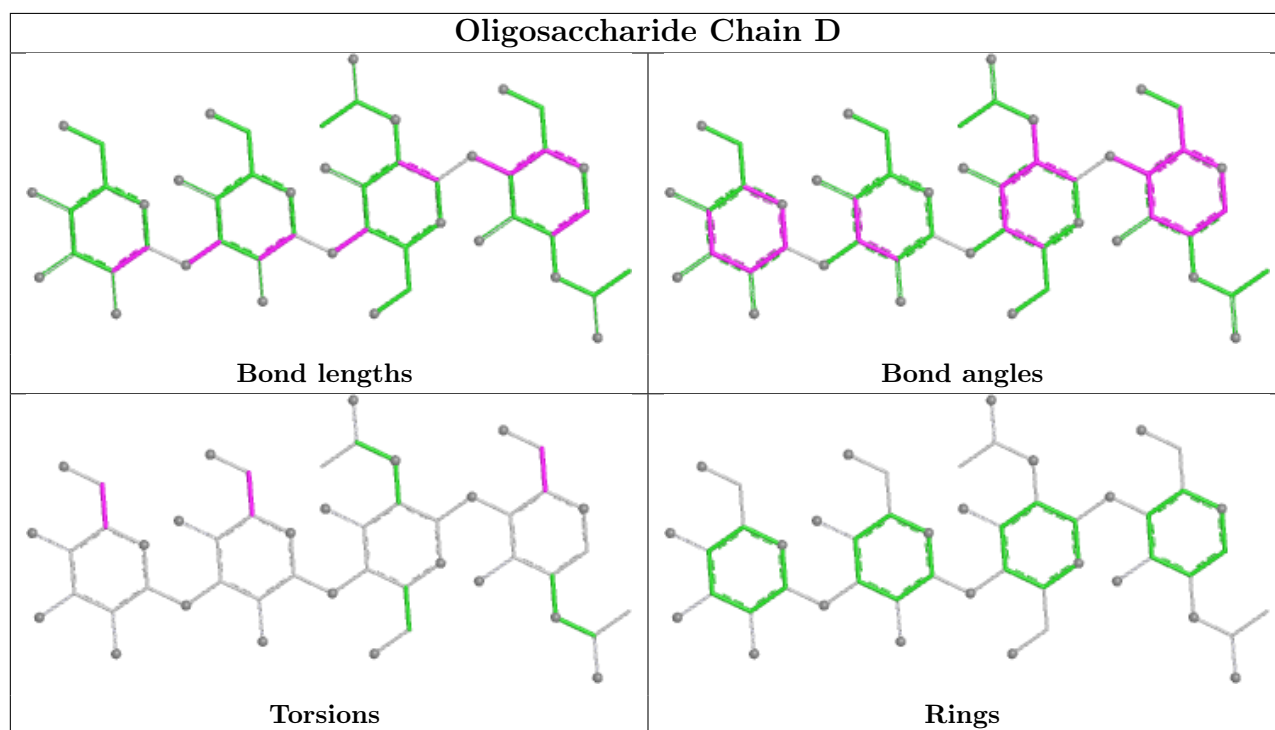
5 of 111 torsion outliers are listed below:

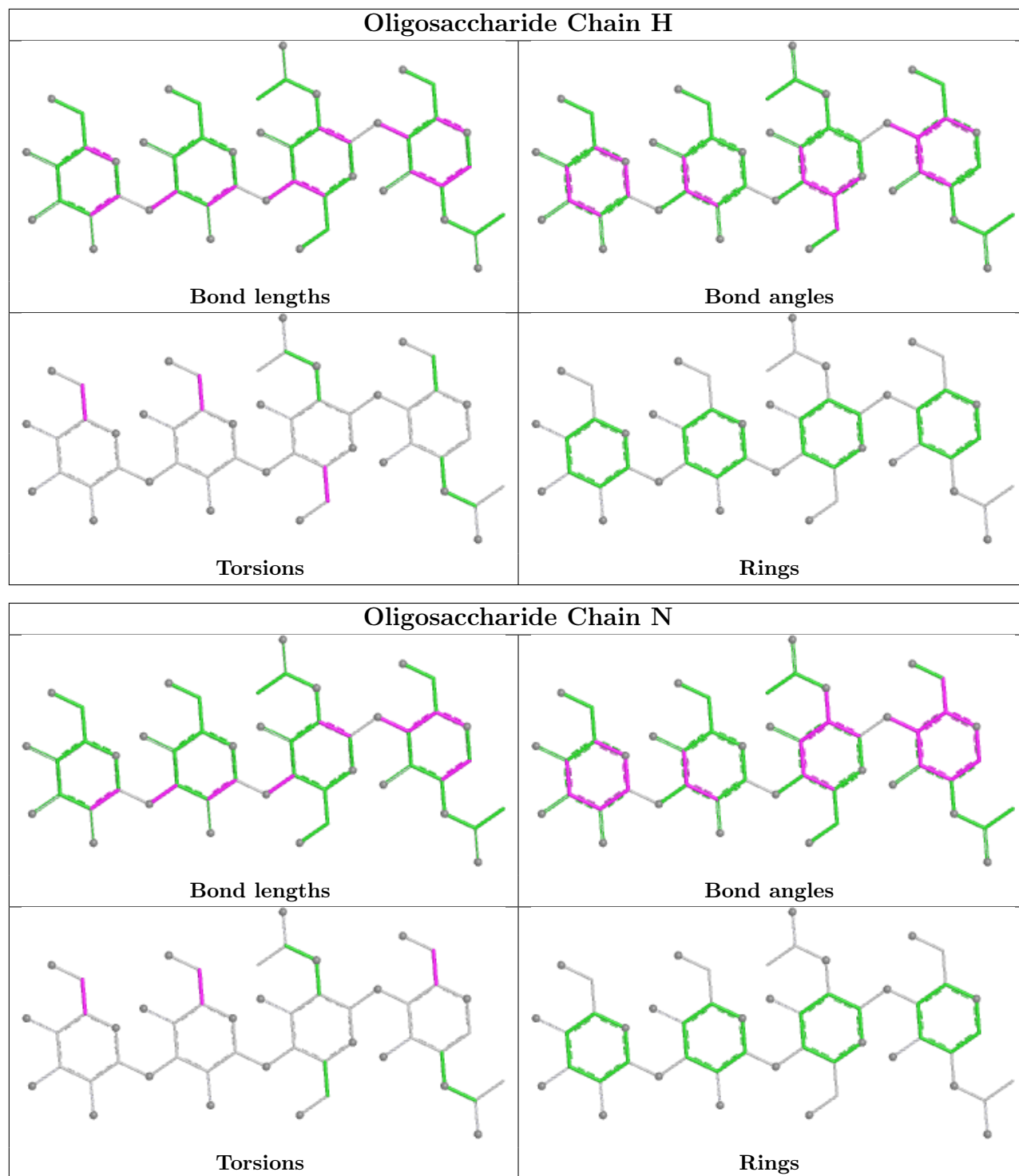
Mol	Chain	Res	Type	Atoms
4	F	3	BMA	C4-C5-C6-O6
4	P	3	BMA	C4-C5-C6-O6
4	Z	3	BMA	C4-C5-C6-O6
6	K	3	BMA	O5-C5-C6-O6
6	U	3	BMA	O5-C5-C6-O6

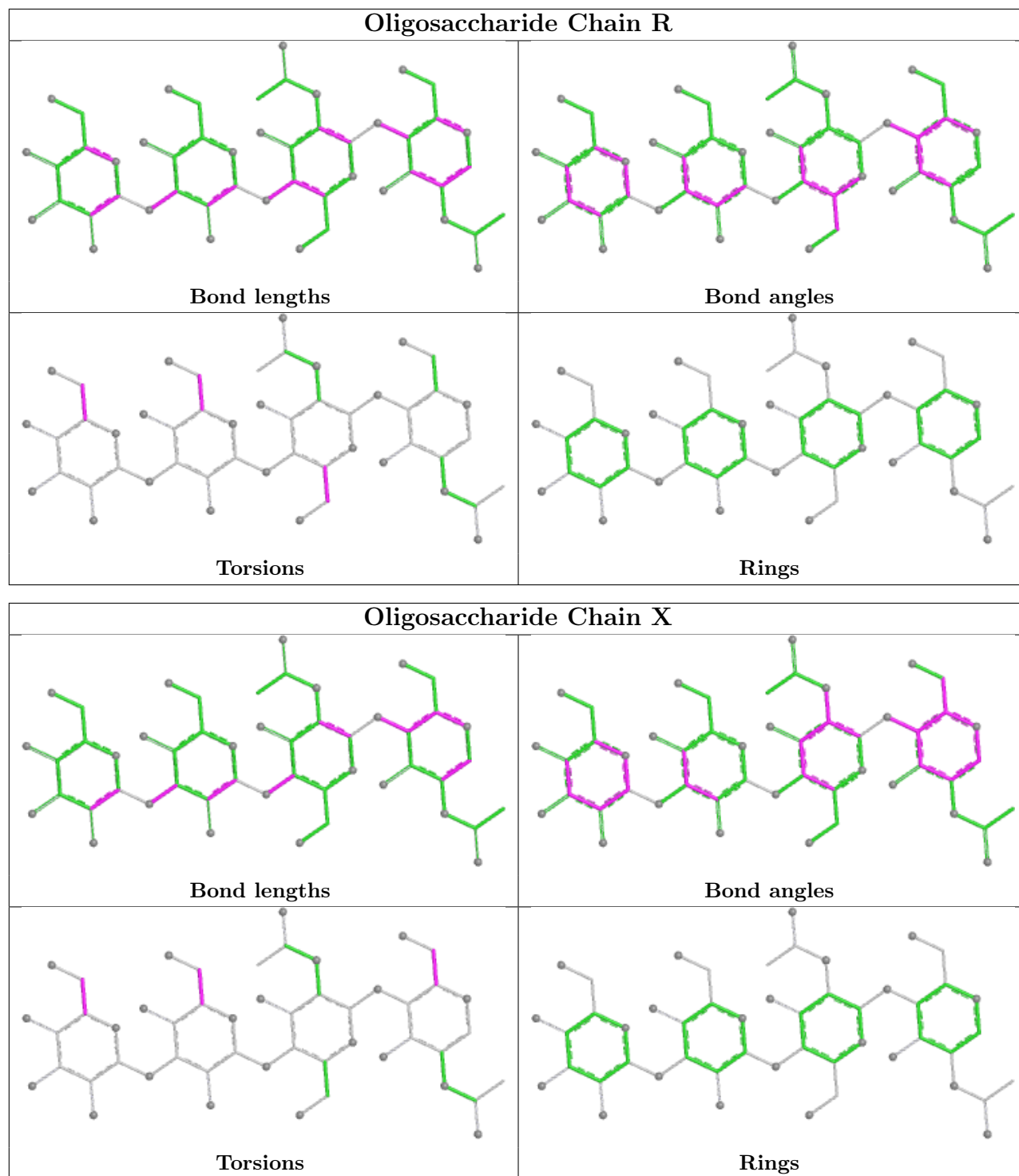
There are no ring outliers.

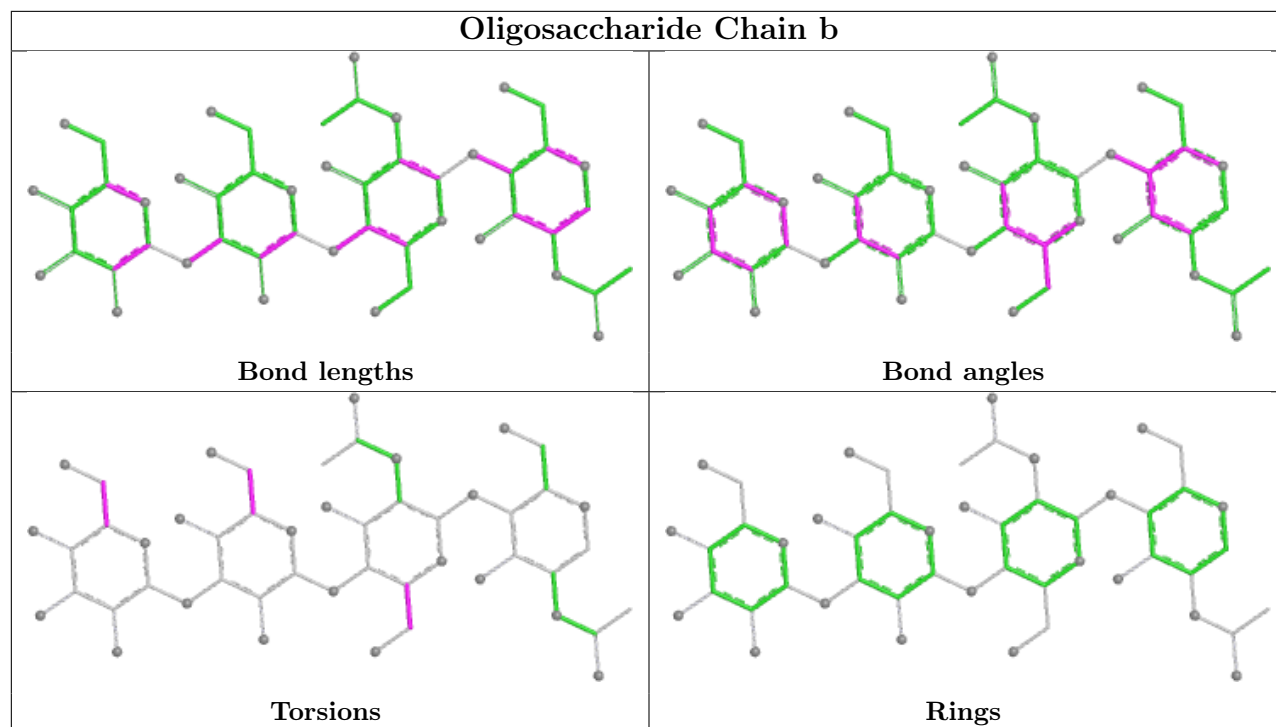
No monomer is involved in short contacts.

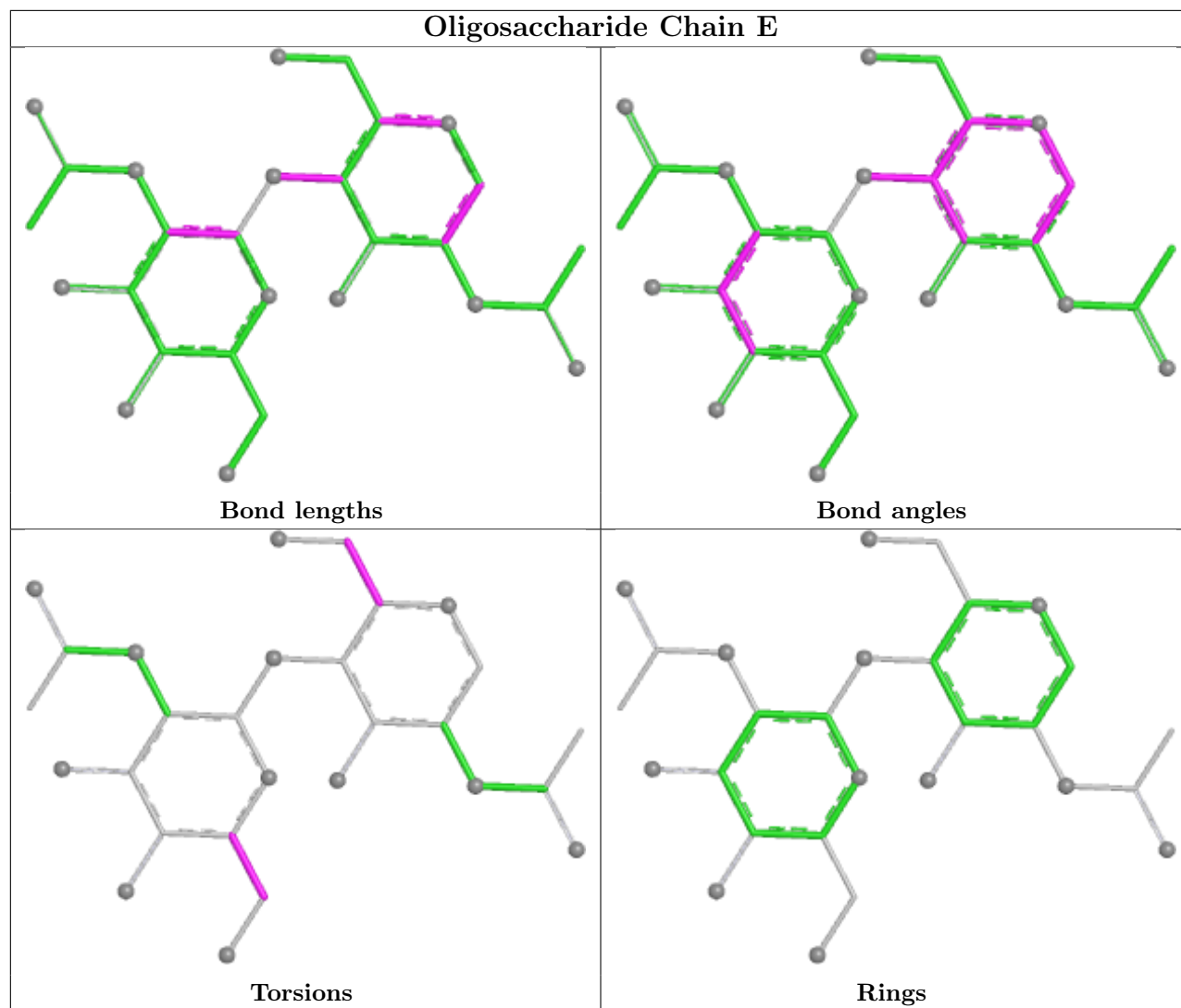
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

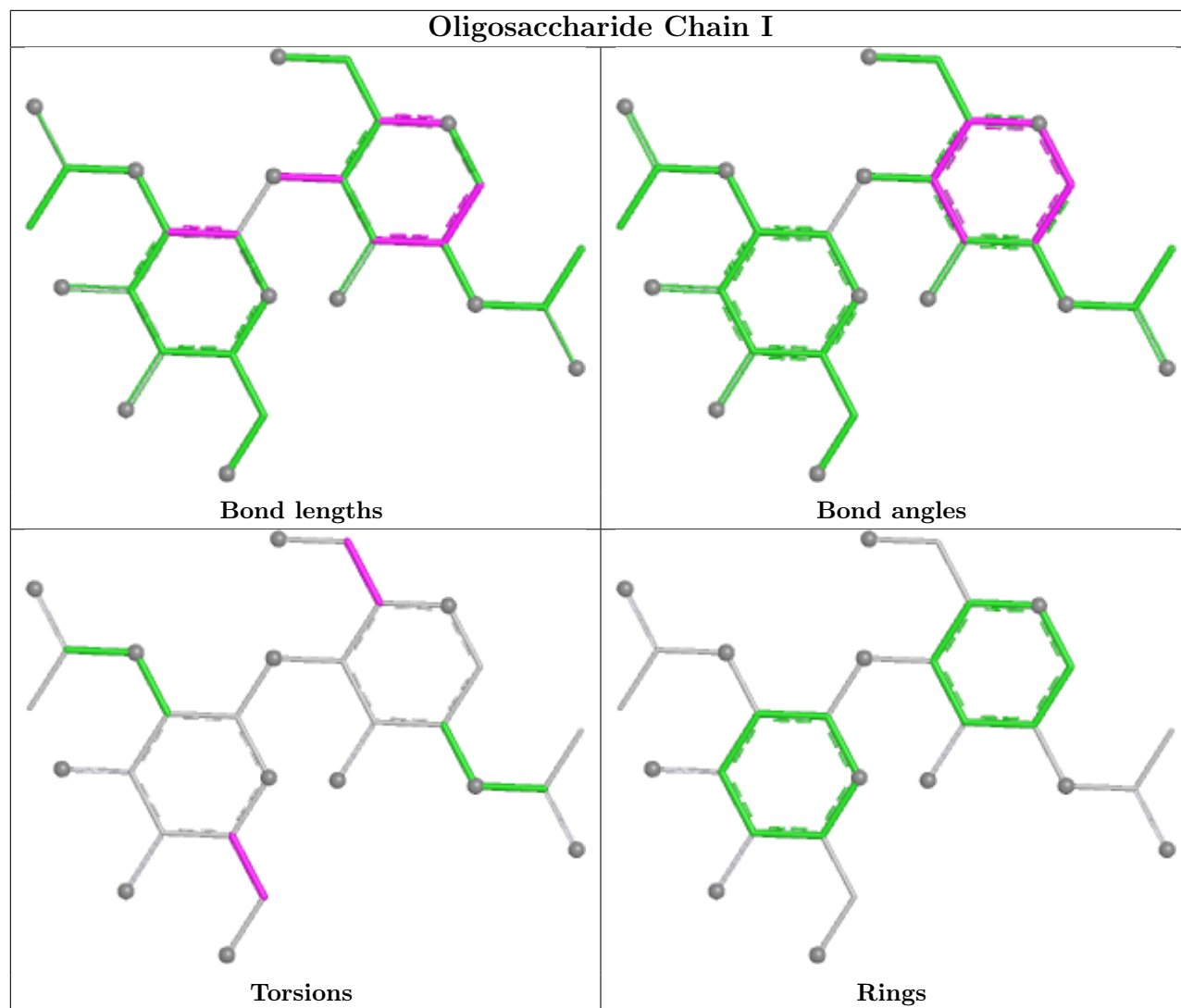


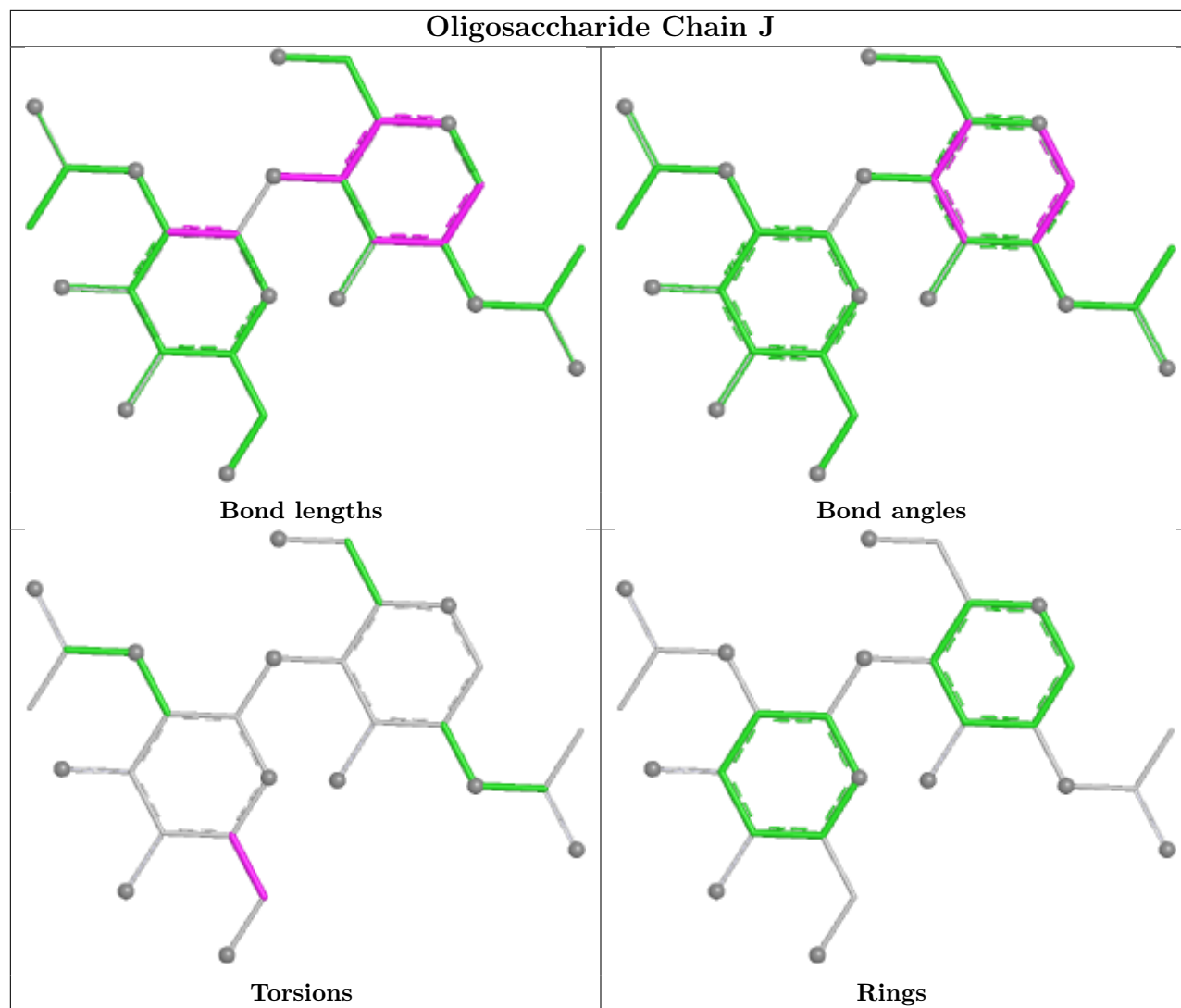


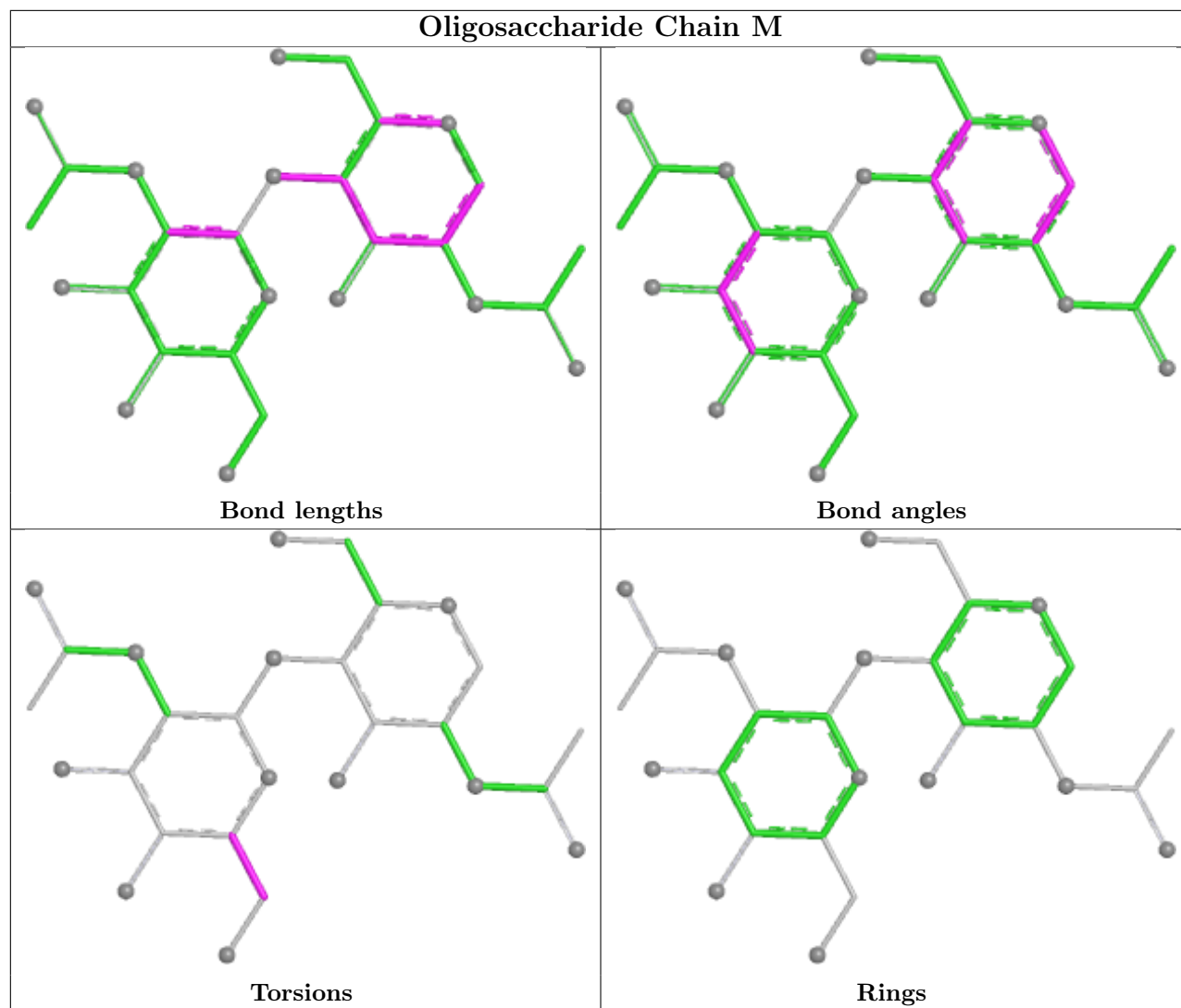


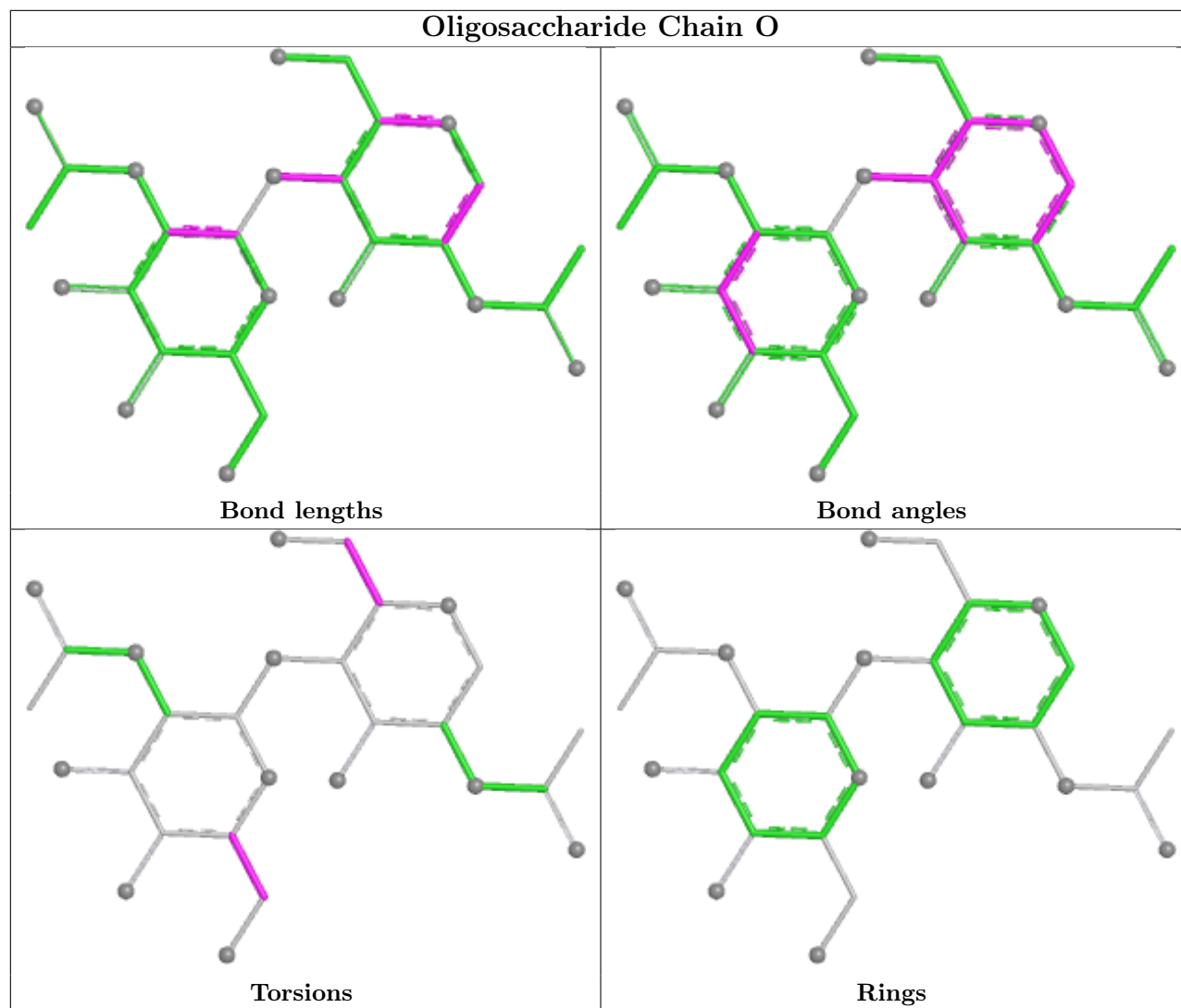


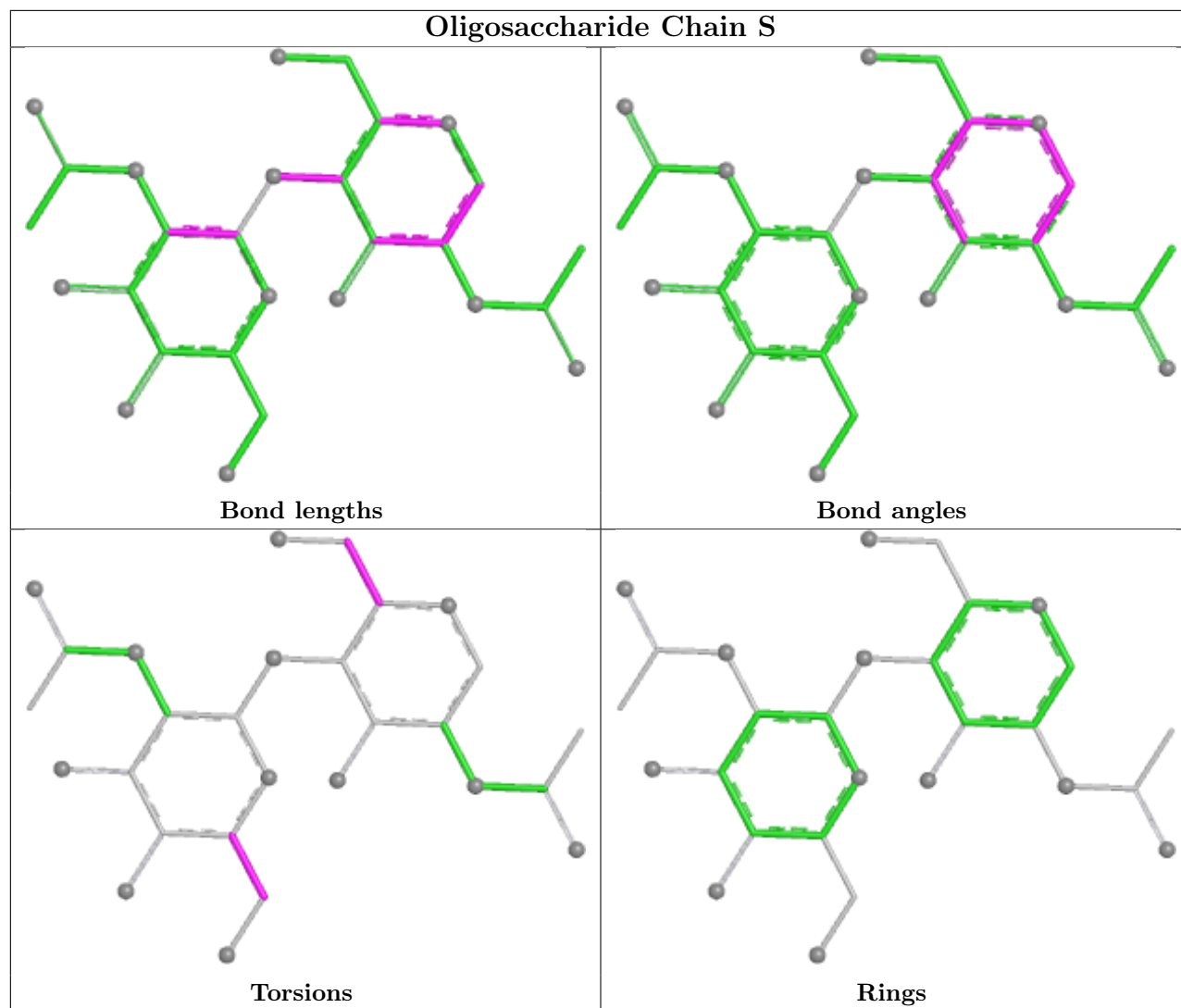


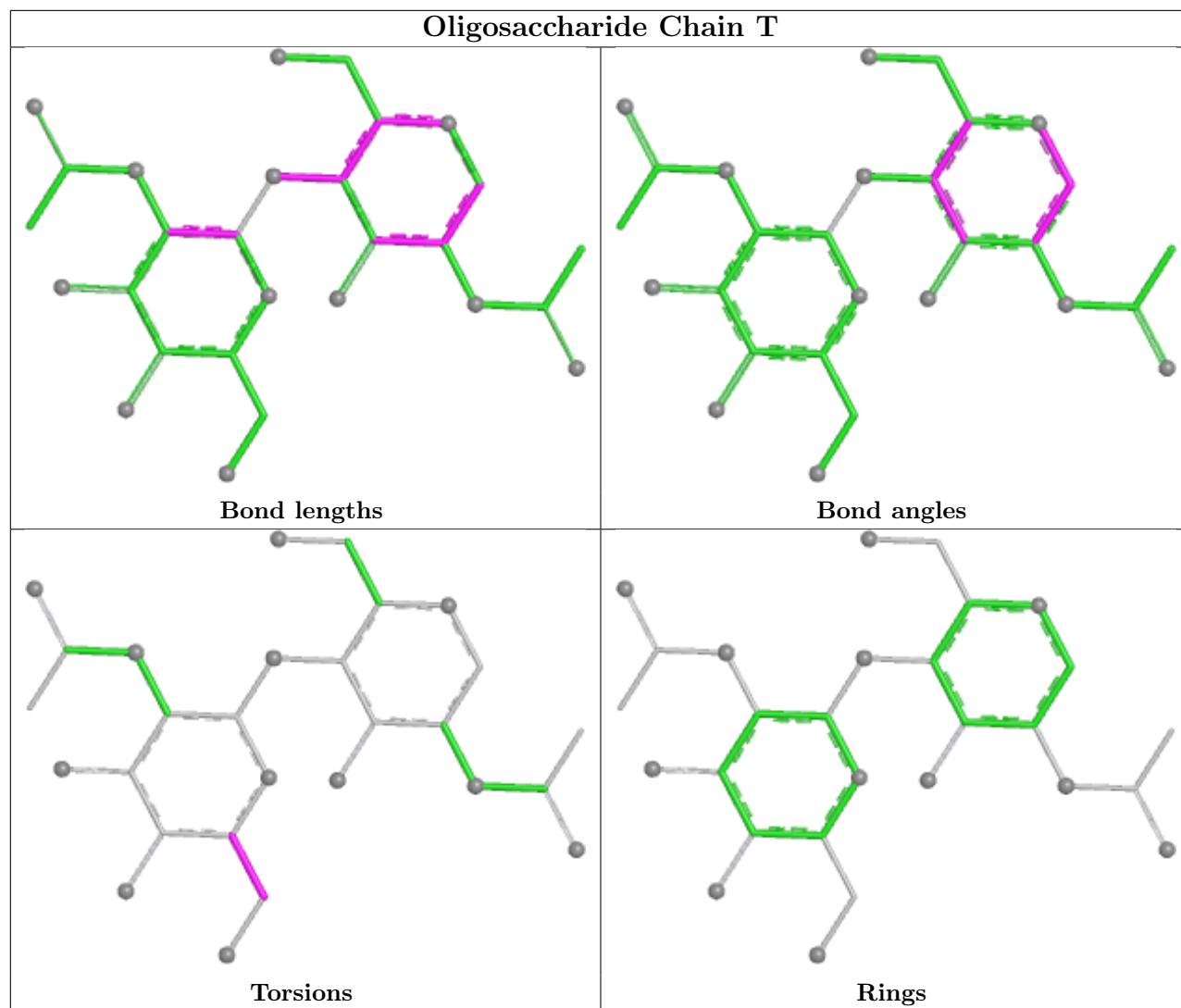


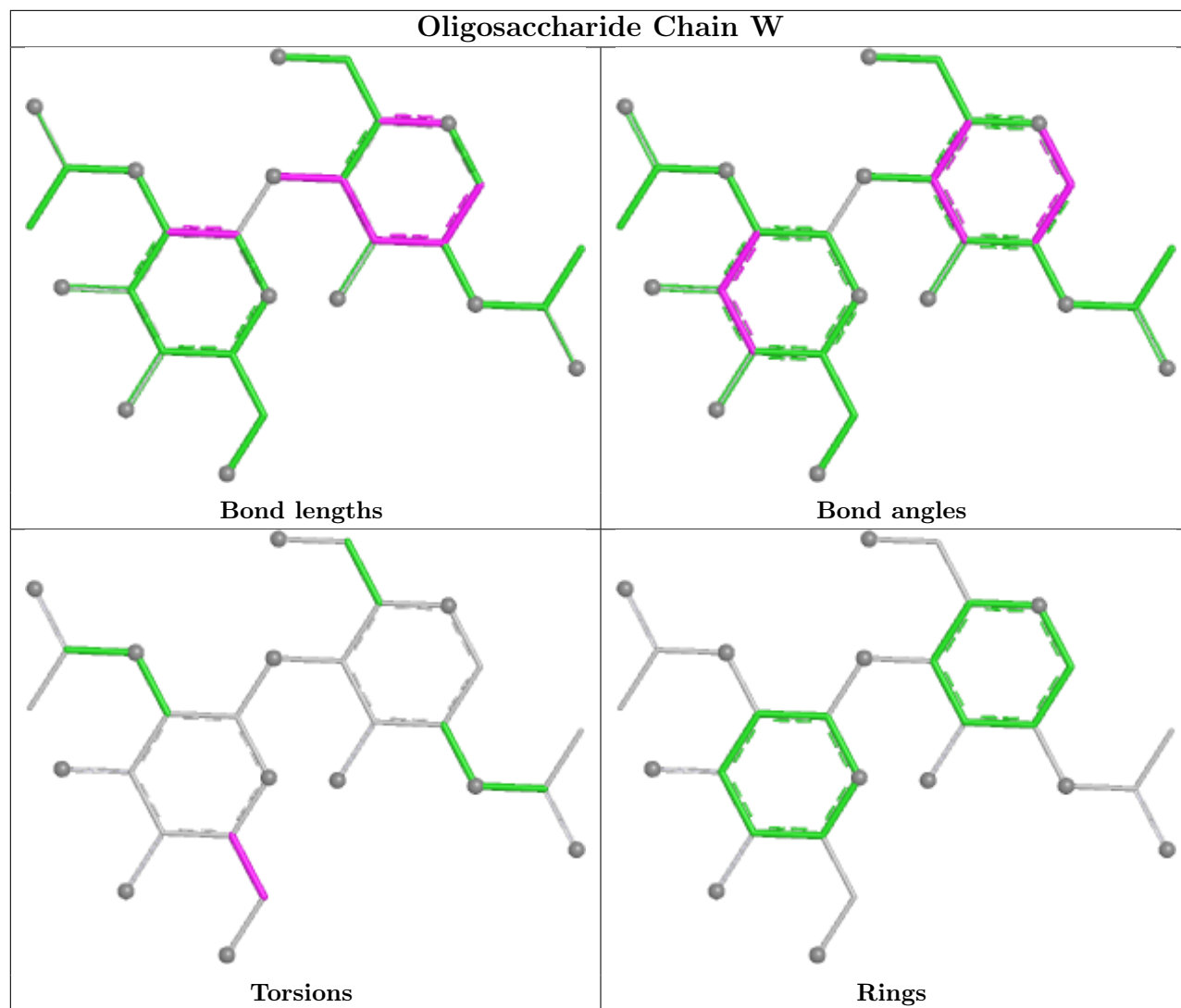


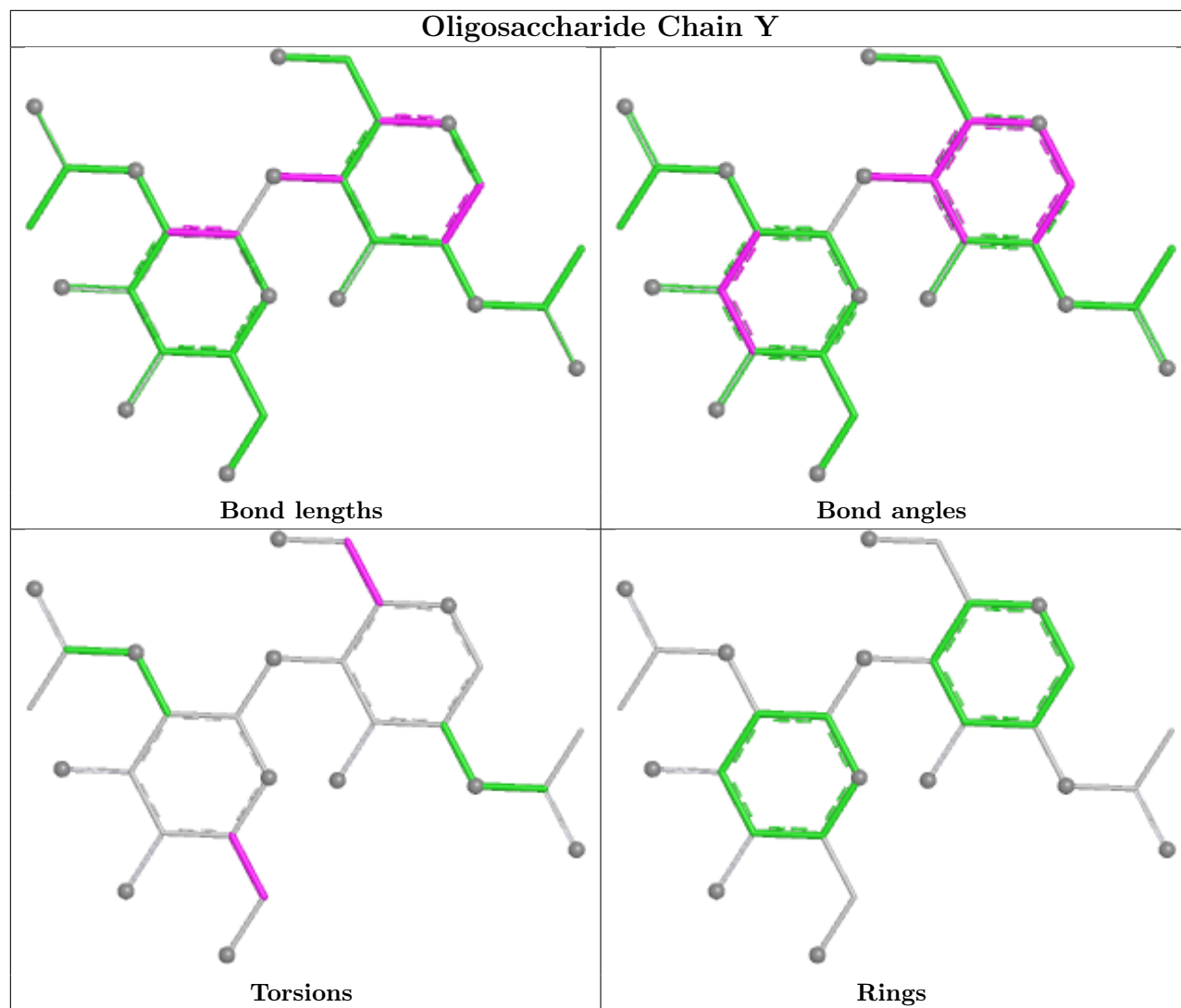


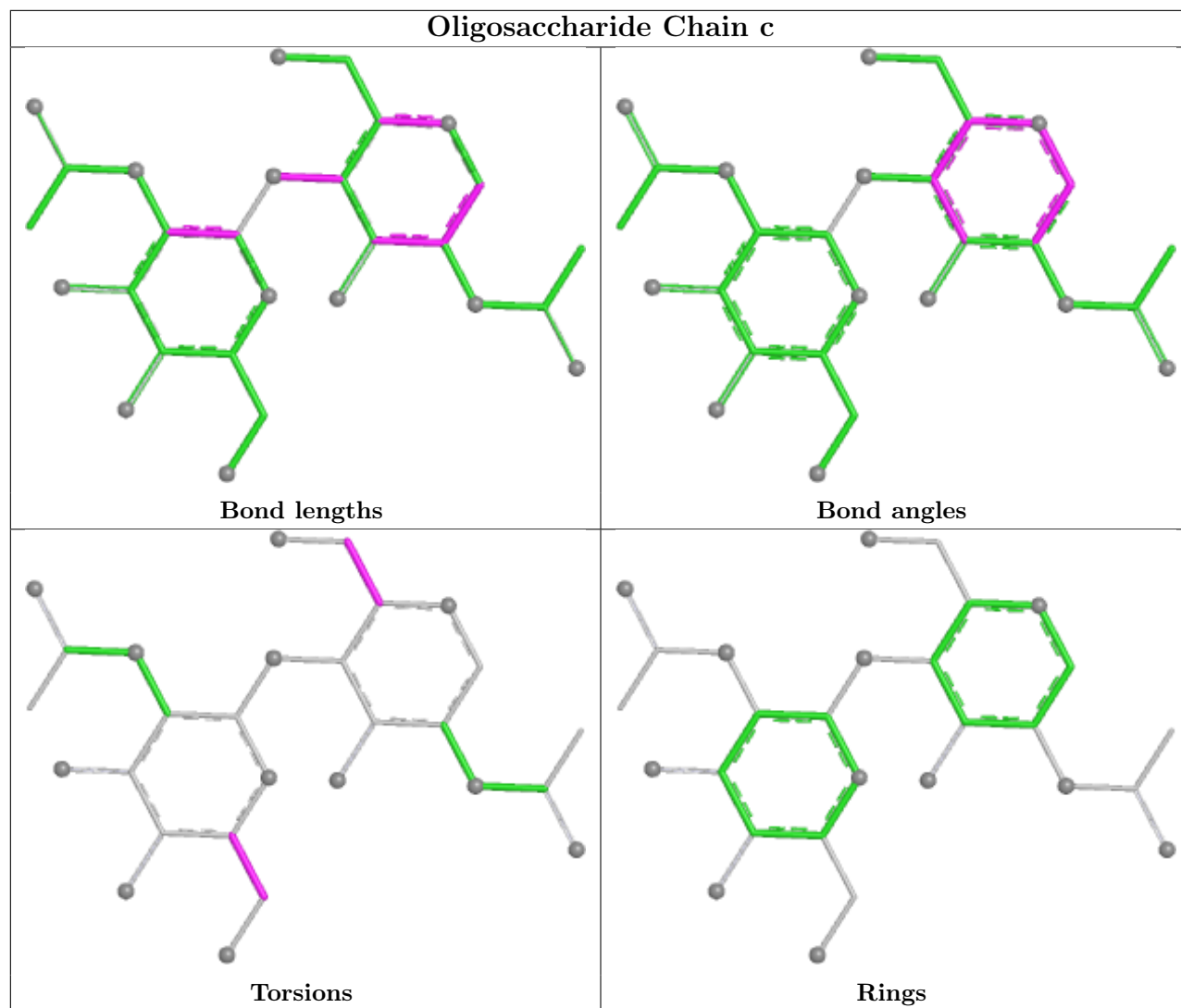


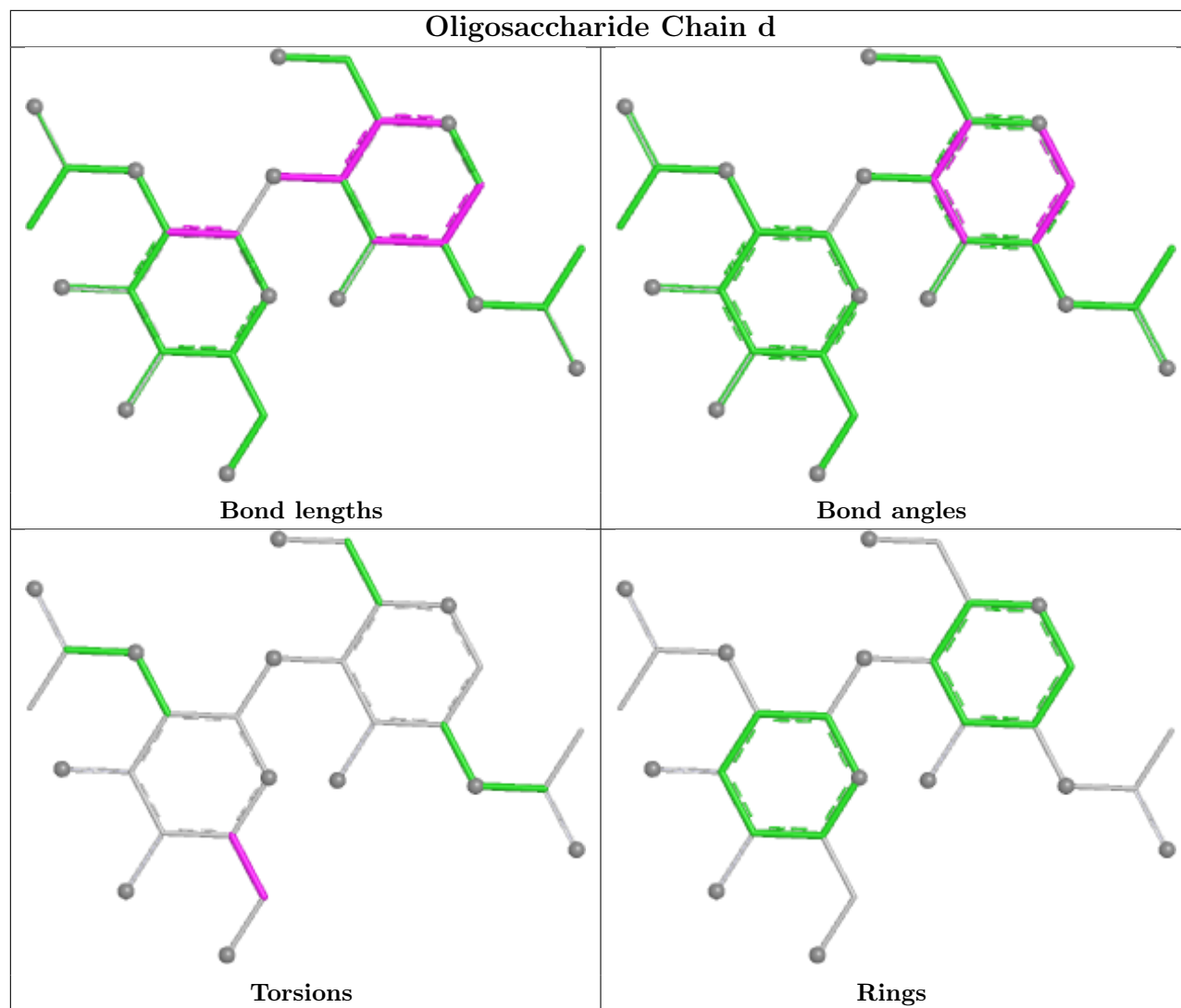


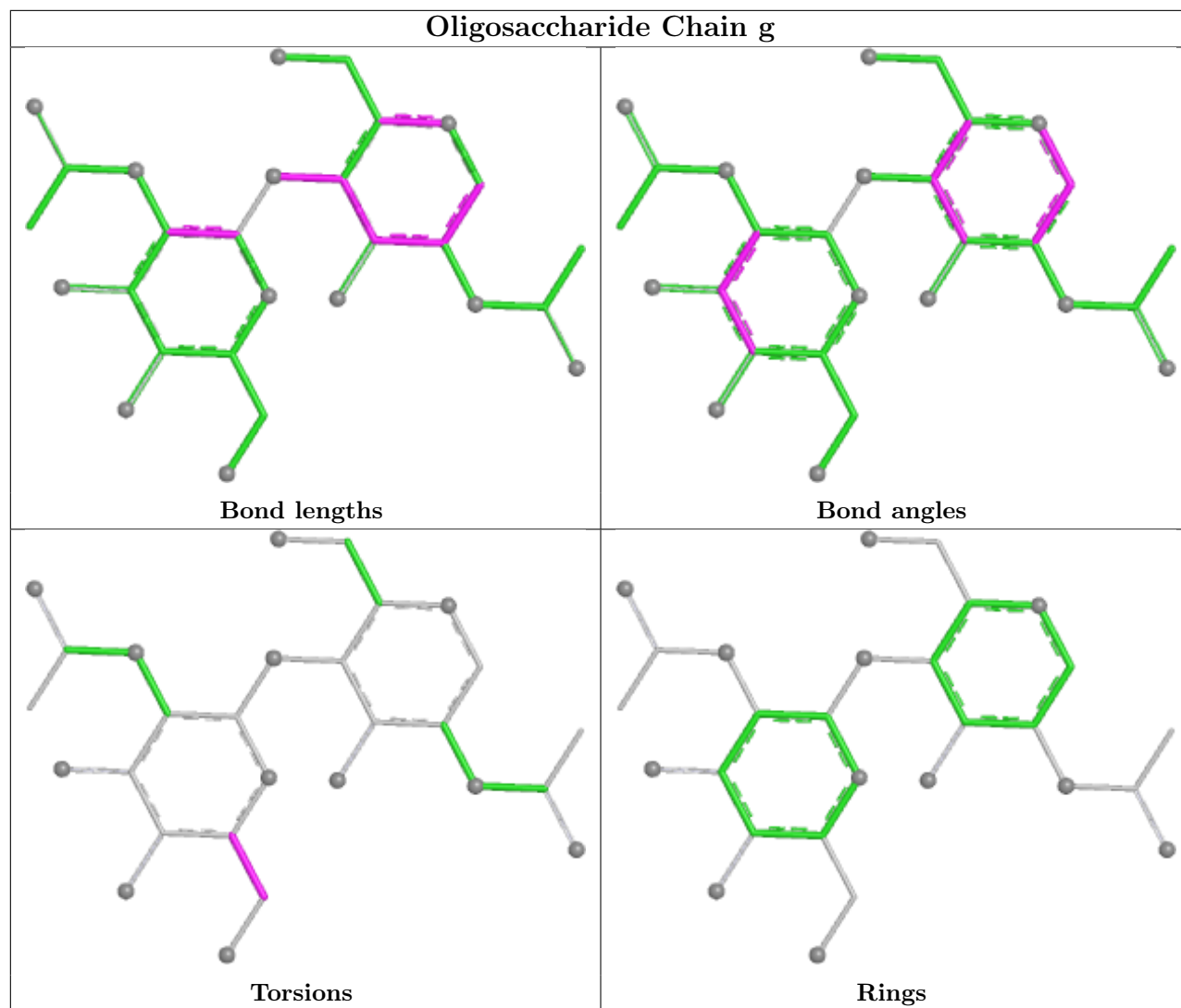


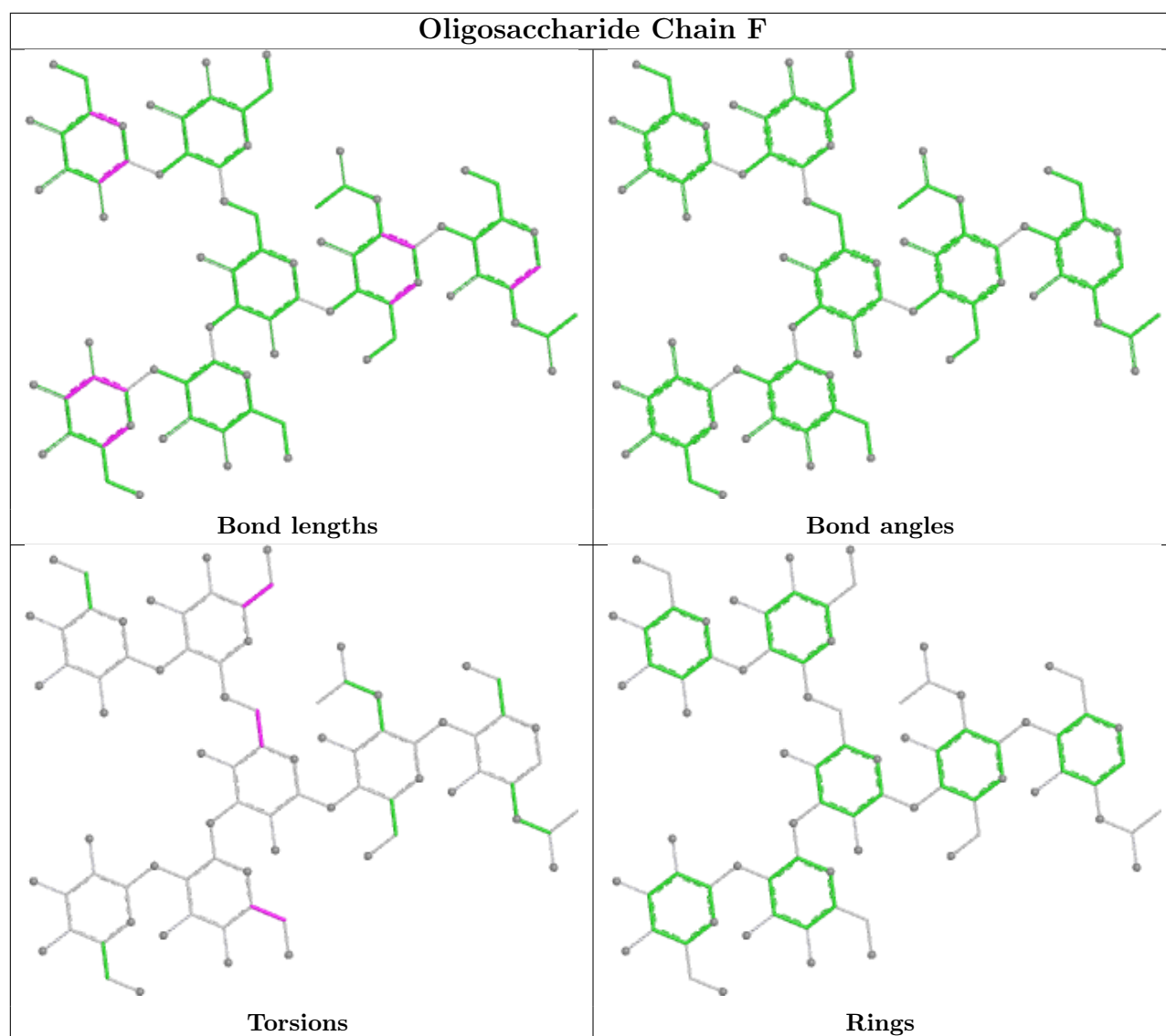


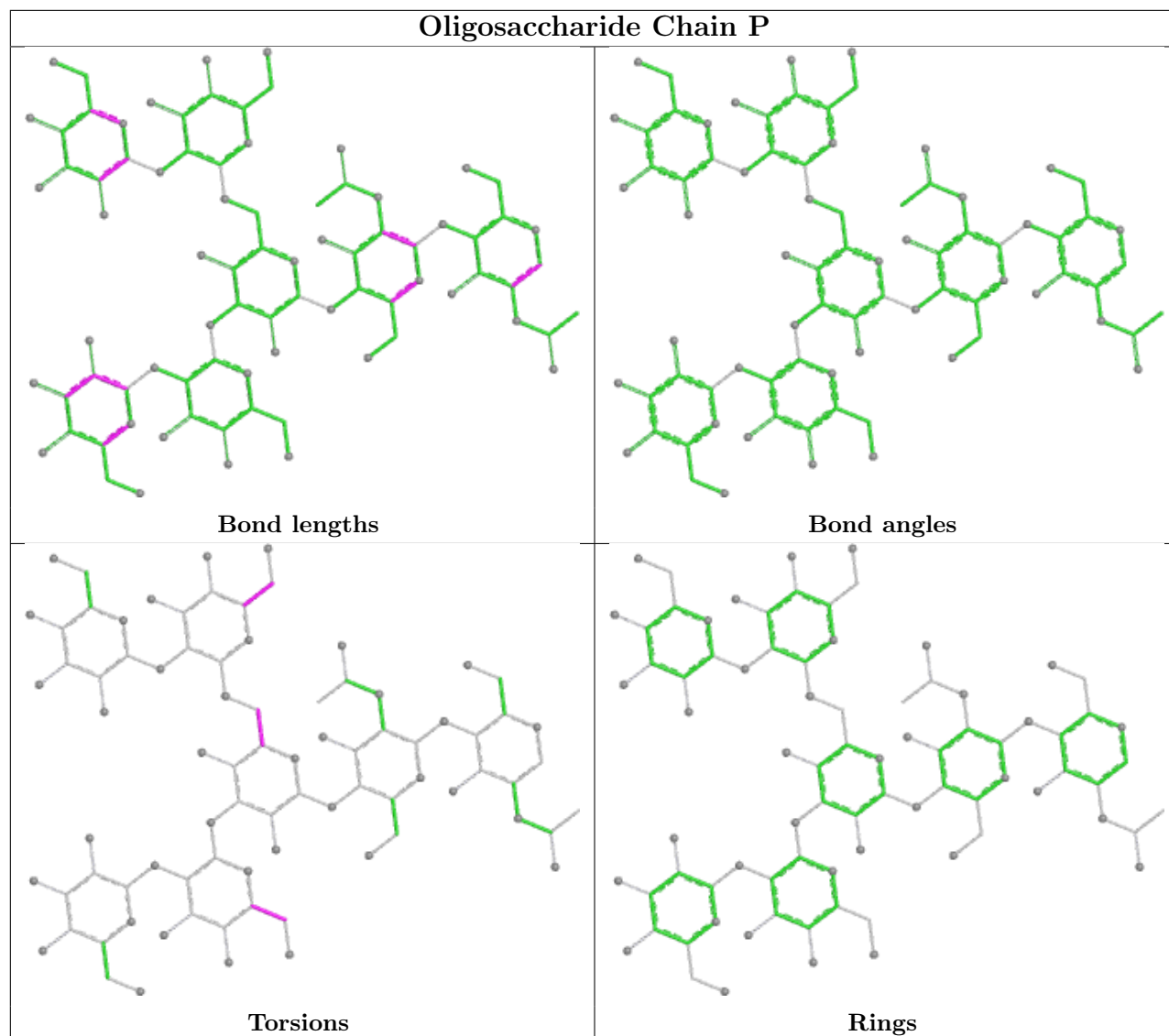


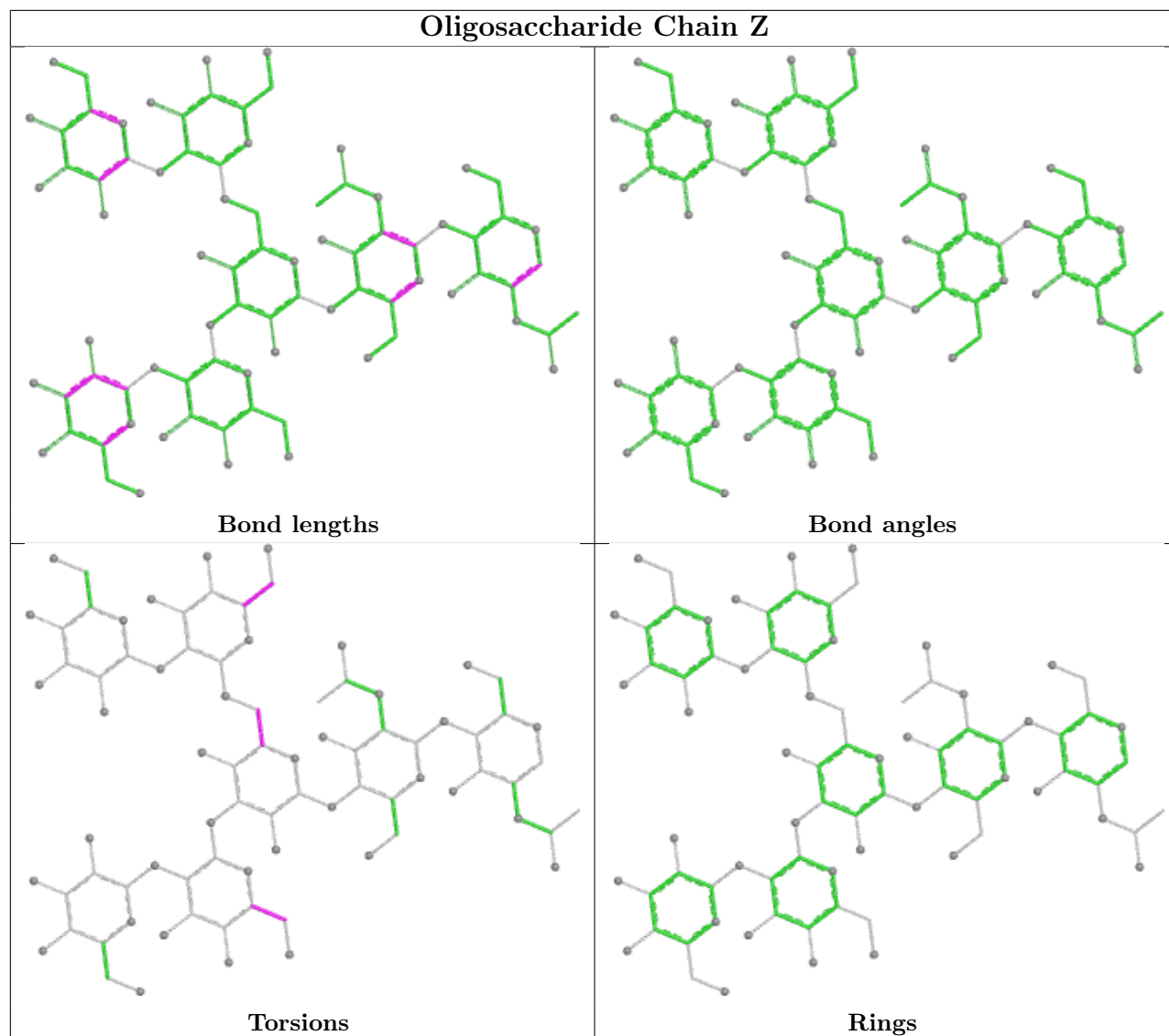


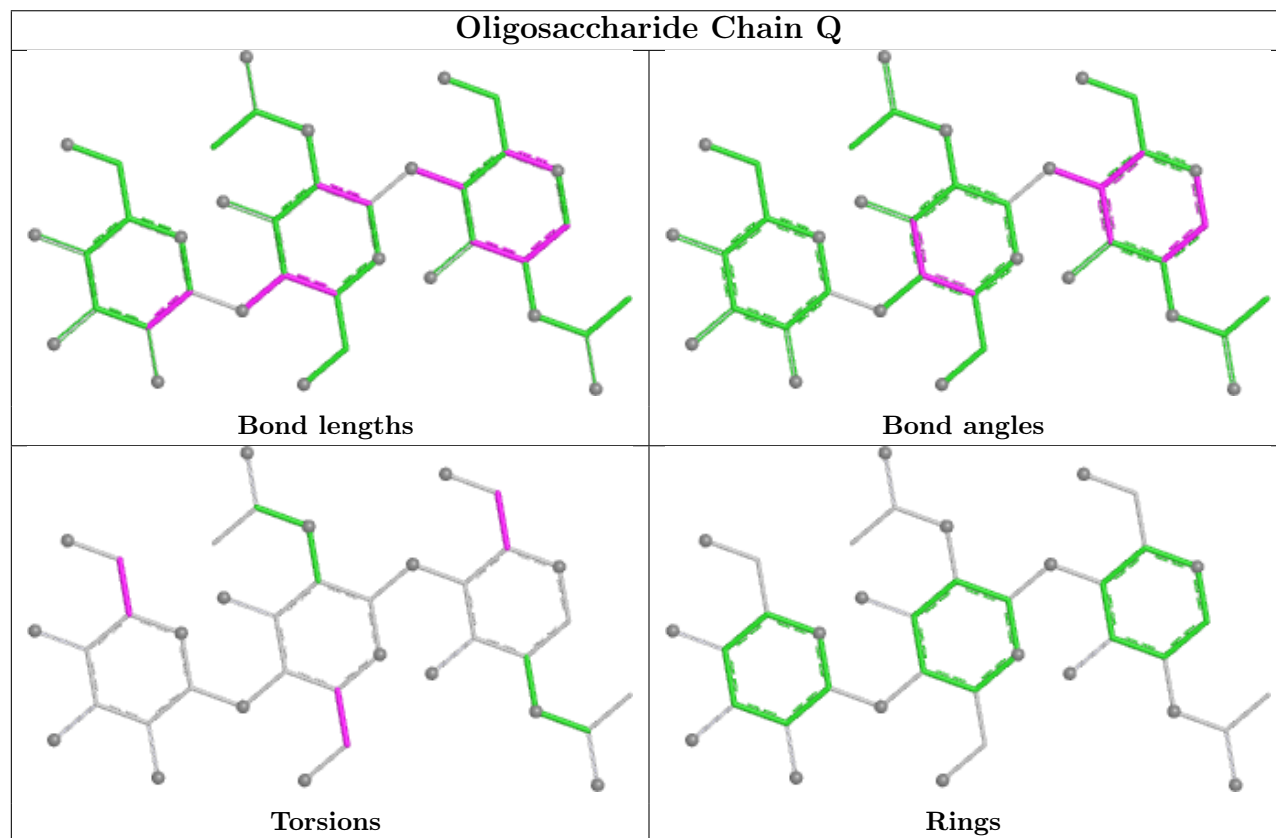
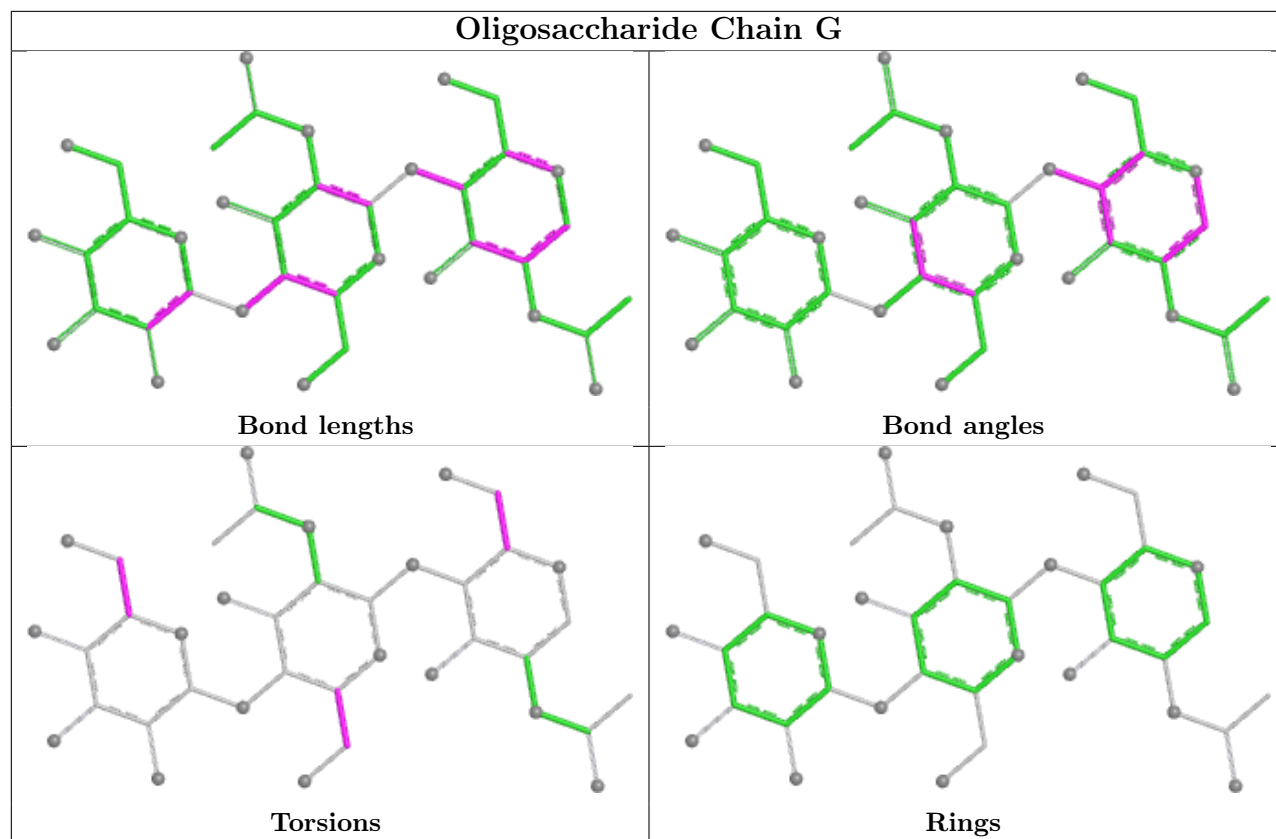


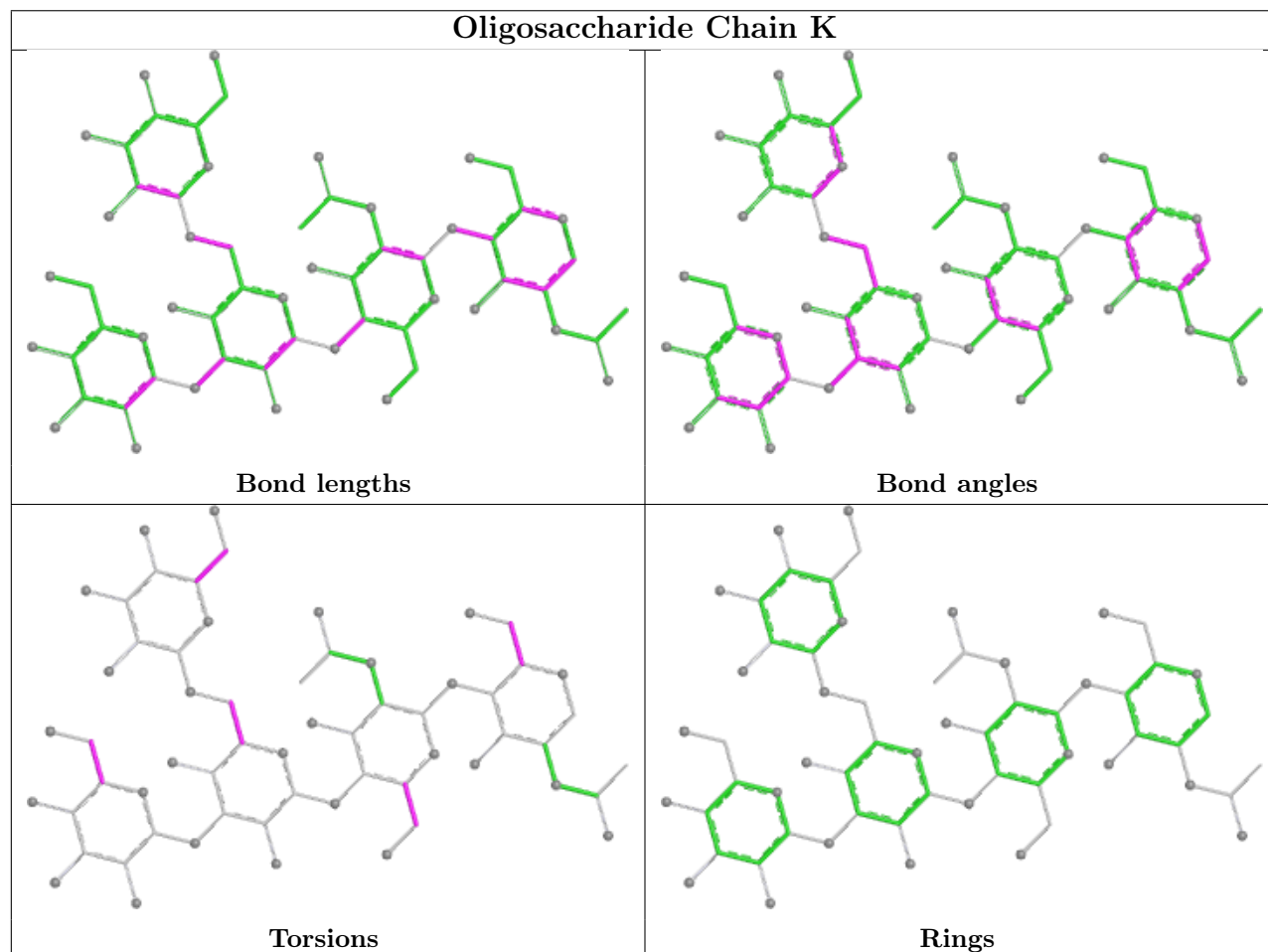
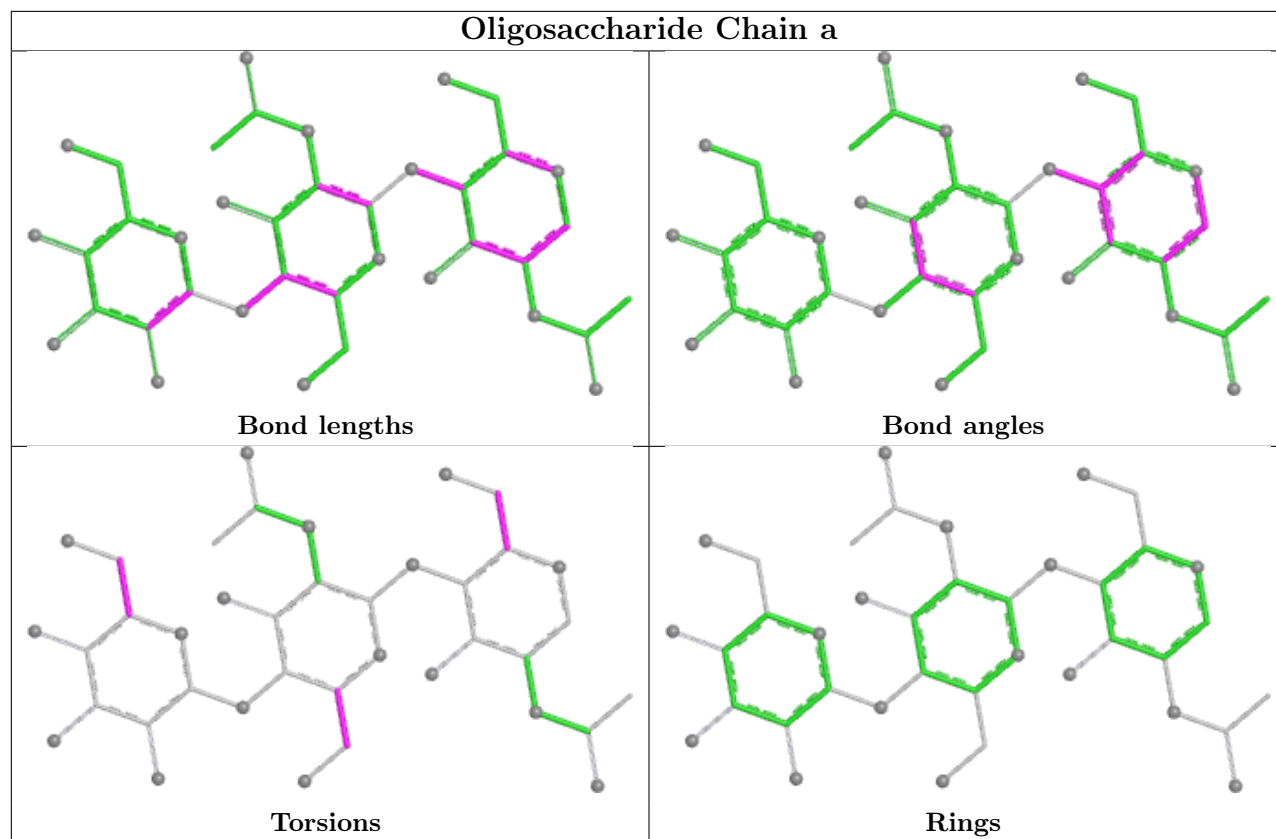


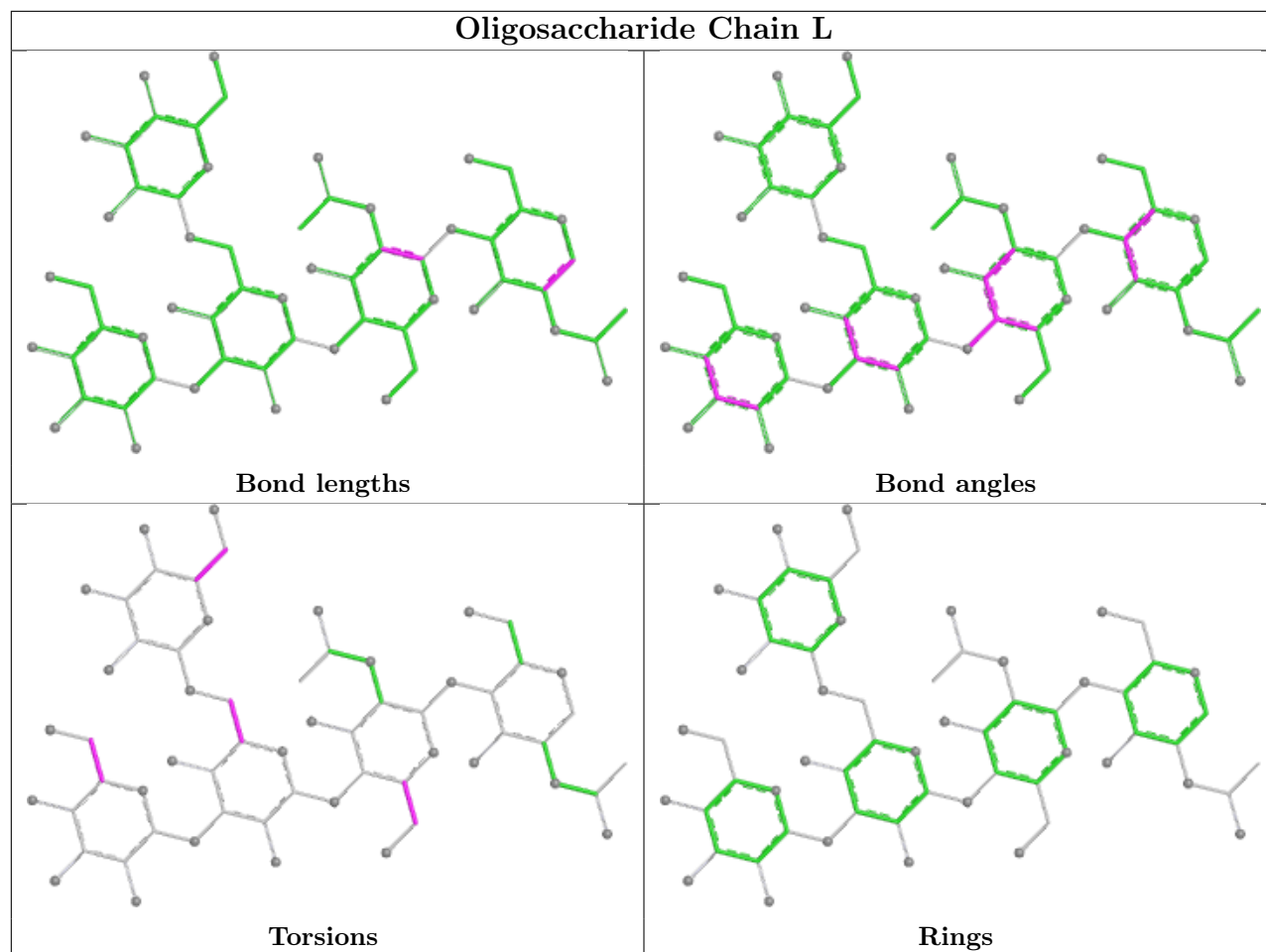


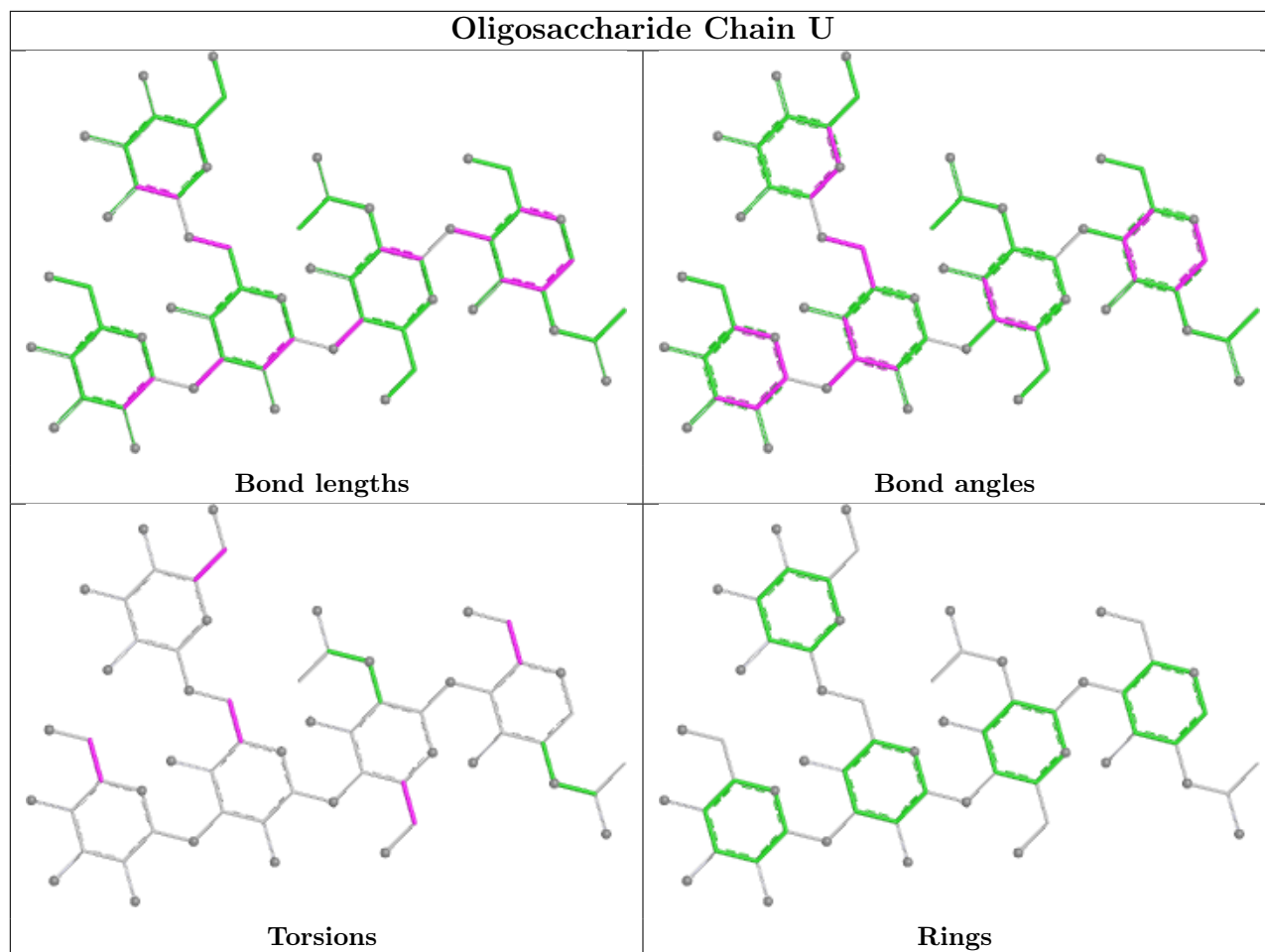


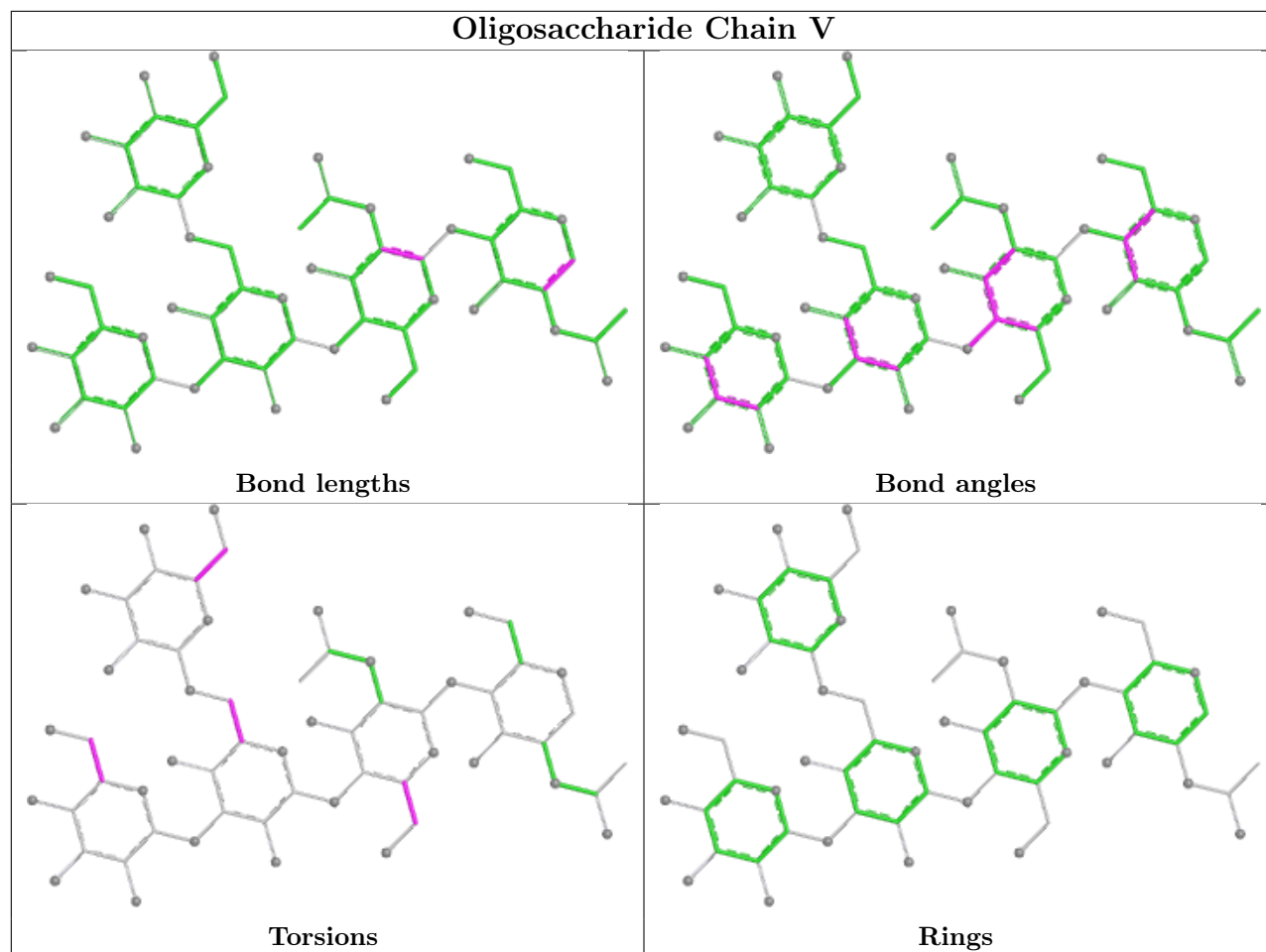


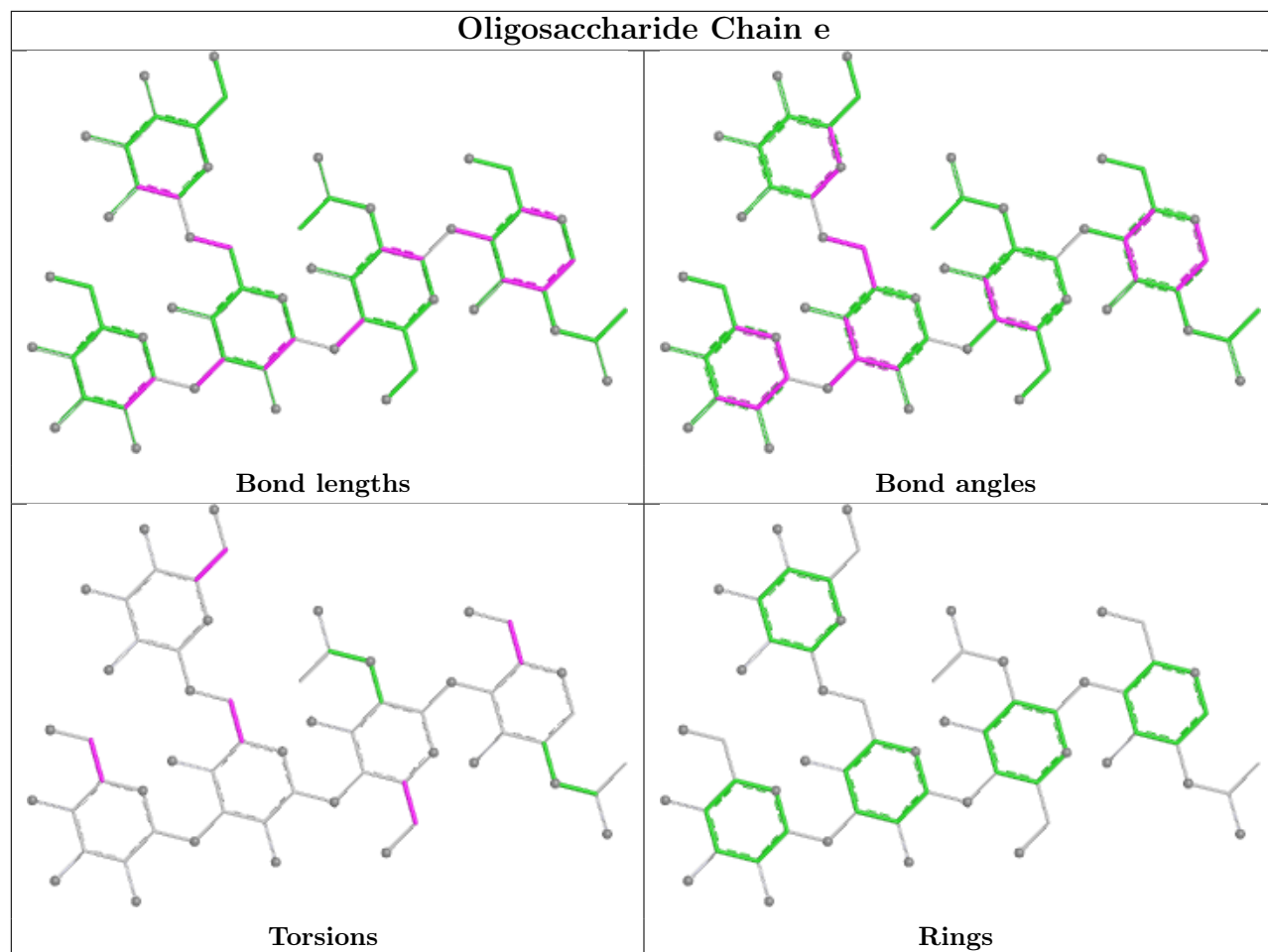


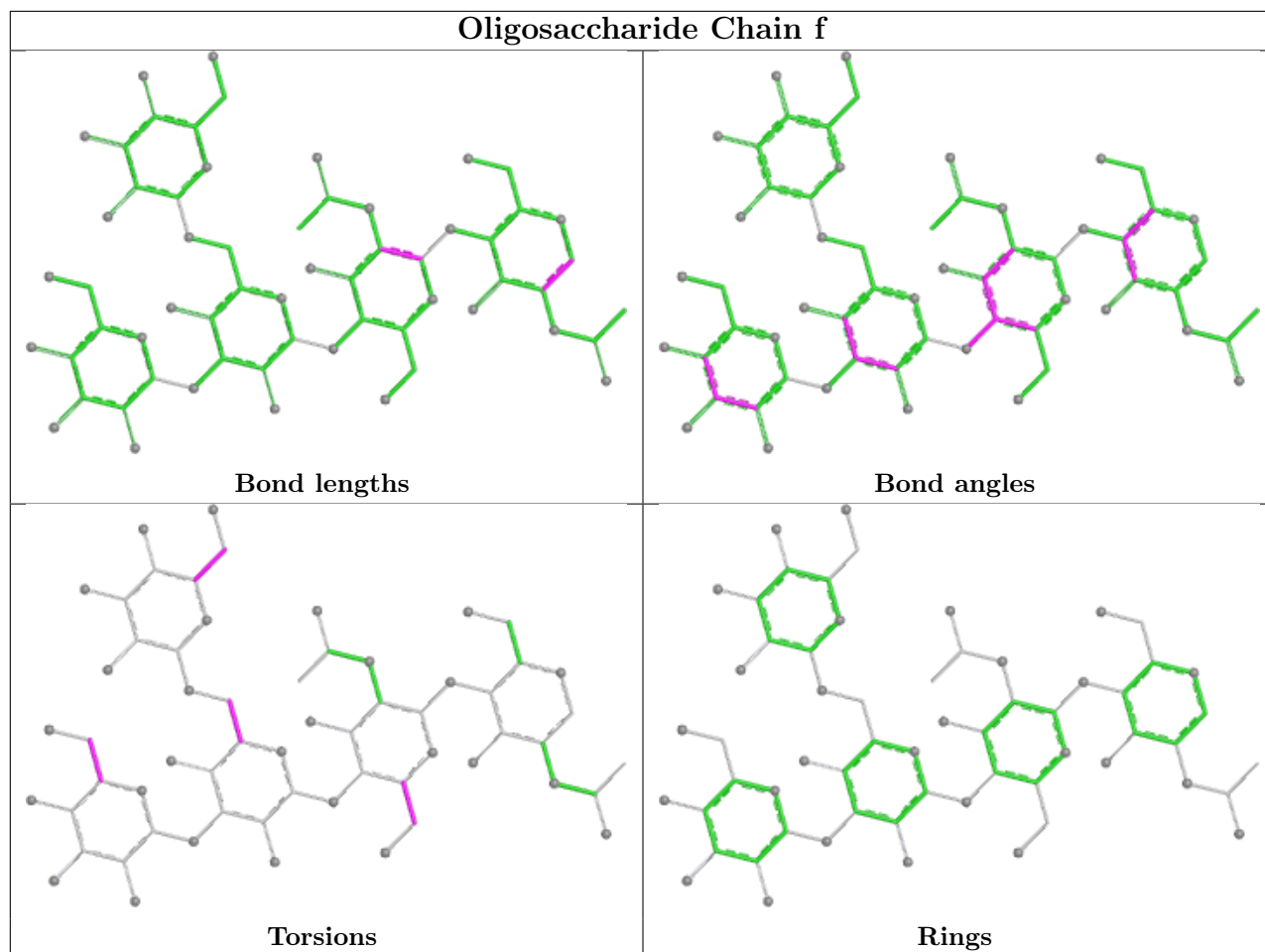












5.6 Ligand geometry [i](#)

27 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$
9	SIA	A	1445	-	21,21,21	2.20	6 (28%)	24,31,31	1.26	2 (8%)
7	NAG	C	1418	1	14,14,15	1.10	1 (7%)	17,19,21	1.14	1 (5%)
9	SIA	B	1445	-	21,21,21	2.20	6 (28%)	24,31,31	1.26	2 (8%)
7	NAG	B	1416	1	14,14,15	1.66	3 (21%)	17,19,21	1.76	5 (29%)
7	NAG	C	1414	1	14,14,15	1.19	1 (7%)	17,19,21	1.00	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	C	1436	1	14,14,15	1.65	5 (35%)	17,19,21	1.93	4 (23%)
7	NAG	A	1416	1	14,14,15	1.65	3 (21%)	17,19,21	1.77	5 (29%)
7	NAG	C	1417	1	14,14,15	1.06	1 (7%)	17,19,21	1.08	2 (11%)
7	NAG	B	1418	1	14,14,15	1.09	1 (7%)	17,19,21	1.14	1 (5%)
7	NAG	A	1417	1	14,14,15	1.06	1 (7%)	17,19,21	1.08	2 (11%)
7	NAG	B	1436	1	14,14,15	1.65	5 (35%)	17,19,21	1.93	4 (23%)
7	NAG	C	1416	1	14,14,15	1.66	3 (21%)	17,19,21	1.76	5 (29%)
8	FOL	B	1444	-	34,34,34	1.00	2 (5%)	43,47,47	1.39	4 (9%)
7	NAG	A	1436	1	14,14,15	1.65	5 (35%)	17,19,21	1.93	4 (23%)
8	FOL	C	1444	-	34,34,34	1.00	2 (5%)	43,47,47	1.39	4 (9%)
7	NAG	B	1419	1	14,14,15	1.16	1 (7%)	17,19,21	1.26	2 (11%)
7	NAG	A	1418	1	14,14,15	1.10	1 (7%)	17,19,21	1.14	1 (5%)
7	NAG	B	1415	1	14,14,15	1.26	1 (7%)	17,19,21	1.12	2 (11%)
7	NAG	A	1419	1	14,14,15	1.15	1 (7%)	17,19,21	1.26	2 (11%)
7	NAG	C	1415	1	14,14,15	1.26	1 (7%)	17,19,21	1.12	2 (11%)
9	SIA	C	1445	-	21,21,21	2.20	6 (28%)	24,31,31	1.26	2 (8%)
7	NAG	B	1414	1	14,14,15	1.20	2 (14%)	17,19,21	0.99	1 (5%)
7	NAG	A	1415	1	14,14,15	1.25	1 (7%)	17,19,21	1.12	2 (11%)
7	NAG	C	1419	1	14,14,15	1.15	1 (7%)	17,19,21	1.25	2 (11%)
8	FOL	A	1444	-	34,34,34	1.00	2 (5%)	43,47,47	1.39	4 (9%)
7	NAG	B	1417	1	14,14,15	1.07	1 (7%)	17,19,21	1.08	2 (11%)
7	NAG	A	1414	1	14,14,15	1.20	2 (14%)	17,19,21	1.00	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
9	SIA	A	1445	-	-	3/20/38/38	0/1/1/1
7	NAG	C	1418	1	-	1/6/23/26	0/1/1/1
9	SIA	B	1445	-	-	3/20/38/38	0/1/1/1
7	NAG	B	1416	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1414	1	-	1/6/23/26	0/1/1/1
7	NAG	C	1436	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1416	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	C	1417	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1418	1	-	1/6/23/26	0/1/1/1
7	NAG	A	1417	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1436	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1416	1	-	2/6/23/26	0/1/1/1
8	FOL	B	1444	-	-	2/22/22/22	0/3/3/3
7	NAG	A	1436	1	-	2/6/23/26	0/1/1/1
8	FOL	C	1444	-	-	2/22/22/22	0/3/3/3
7	NAG	B	1419	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1418	1	-	1/6/23/26	0/1/1/1
7	NAG	B	1415	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1419	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1415	1	-	2/6/23/26	0/1/1/1
9	SIA	C	1445	-	-	3/20/38/38	0/1/1/1
7	NAG	B	1414	1	-	1/6/23/26	0/1/1/1
7	NAG	A	1415	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1419	1	-	2/6/23/26	0/1/1/1
8	FOL	A	1444	-	-	2/22/22/22	0/3/3/3
7	NAG	B	1417	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1414	1	-	1/6/23/26	0/1/1/1

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1445	SIA	C6-C5	5.73	1.62	1.53
9	B	1445	SIA	C6-C5	5.71	1.62	1.53
9	C	1445	SIA	C6-C5	5.71	1.62	1.53
9	A	1445	SIA	C3-C2	4.98	1.58	1.51
9	C	1445	SIA	C3-C2	4.98	1.58	1.51

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	1436	NAG	C3-C4-C5	-5.08	101.01	110.23
7	A	1436	NAG	C3-C4-C5	-5.07	101.03	110.23
7	C	1436	NAG	C3-C4-C5	-5.06	101.06	110.23
7	A	1416	NAG	O4-C4-C5	4.35	120.04	109.32
7	B	1416	NAG	O4-C4-C5	4.34	120.02	109.32

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

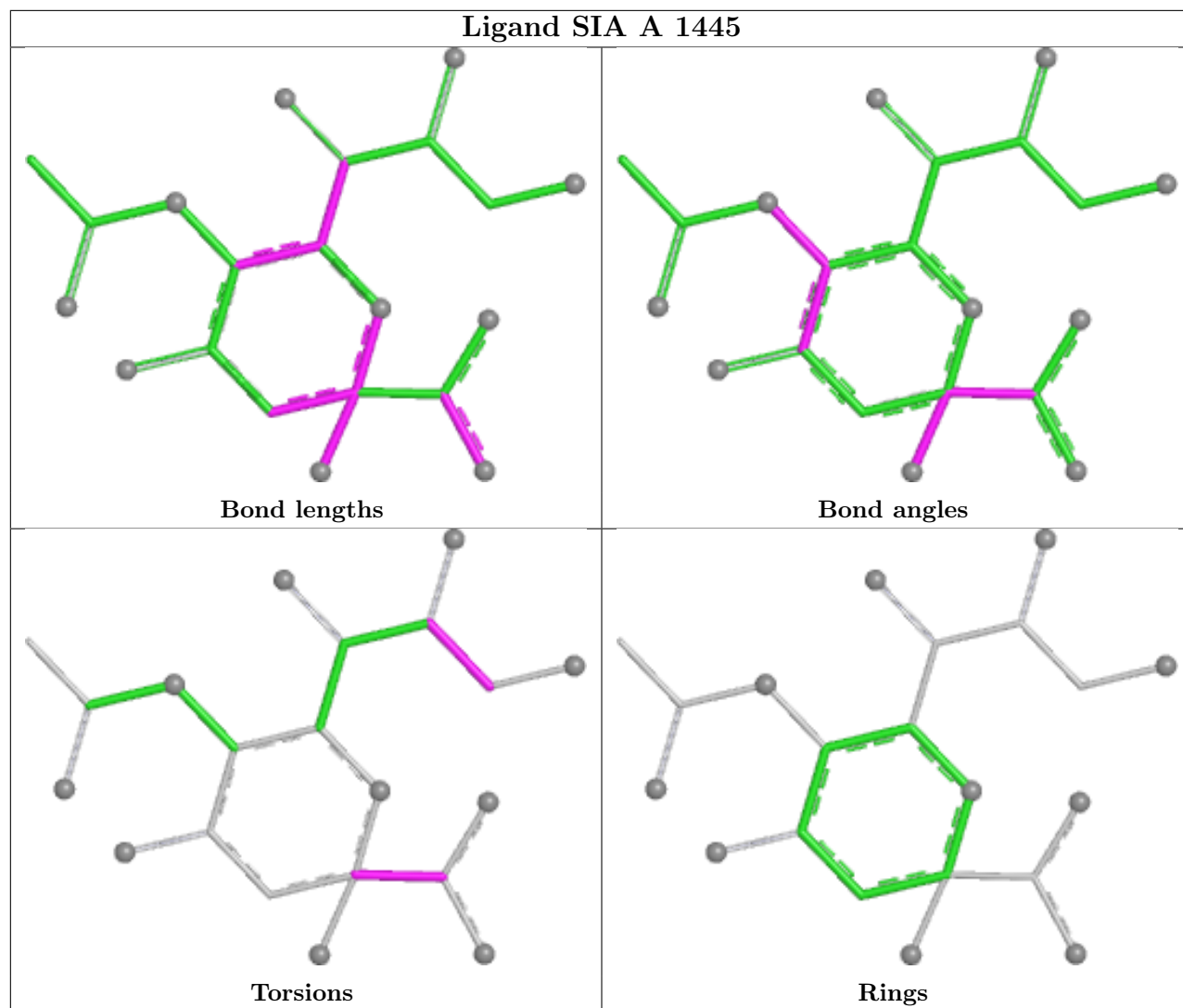
Mol	Chain	Res	Type	Atoms
9	A	1445	SIA	O8-C8-C9-O9
9	B	1445	SIA	O8-C8-C9-O9
9	C	1445	SIA	O8-C8-C9-O9
7	A	1436	NAG	O5-C5-C6-O6
7	B	1436	NAG	O5-C5-C6-O6

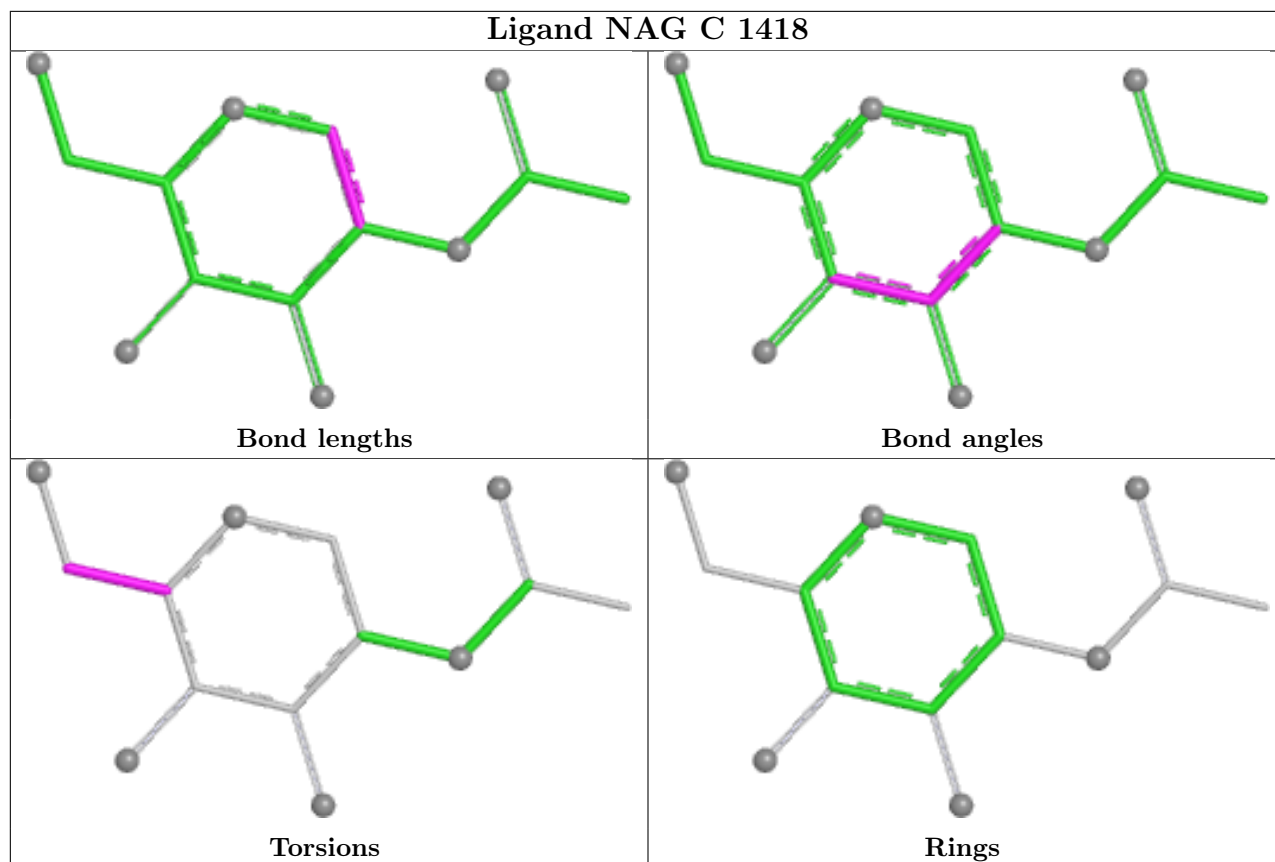
There are no ring outliers.

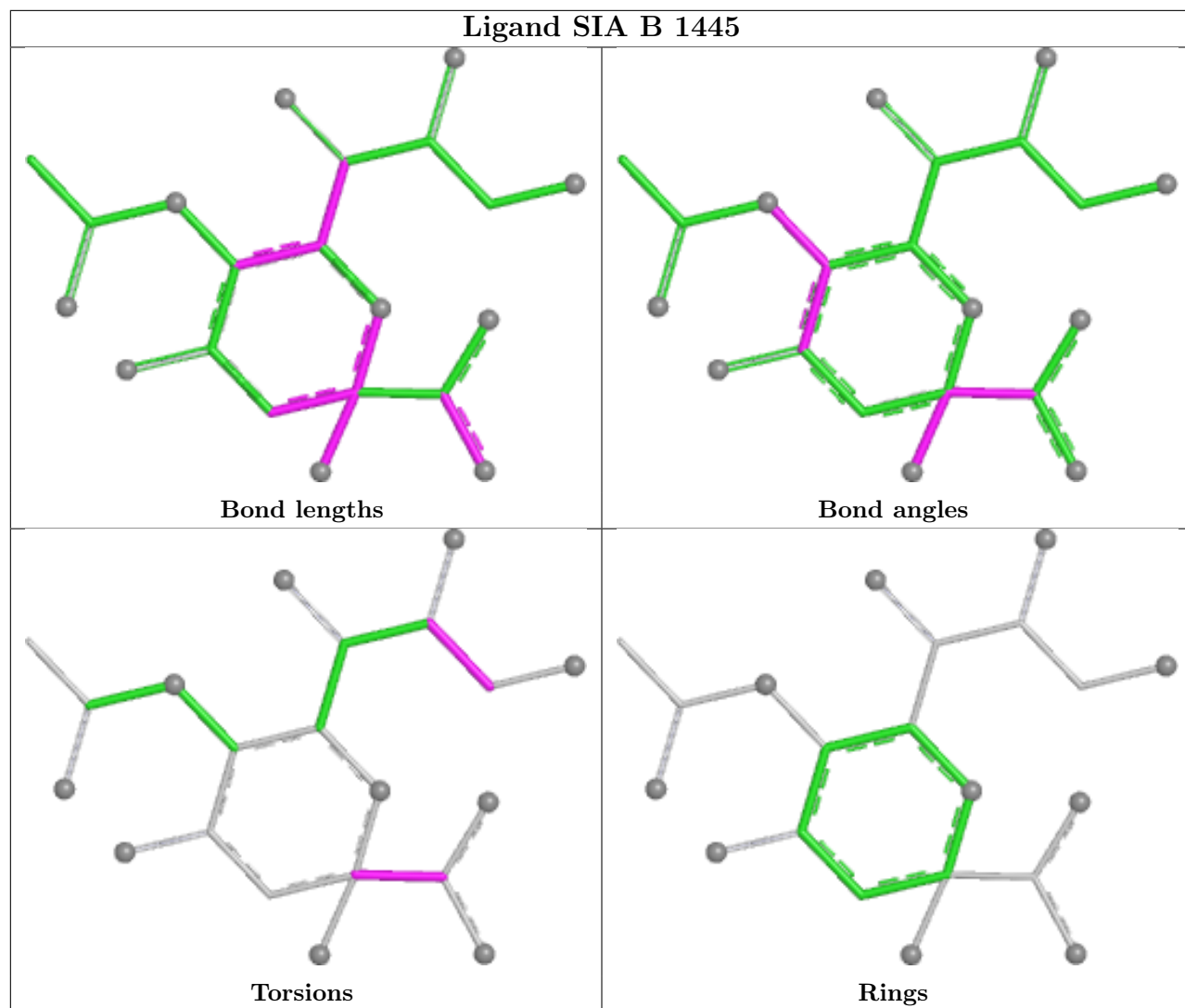
3 monomers are involved in 3 short contacts:

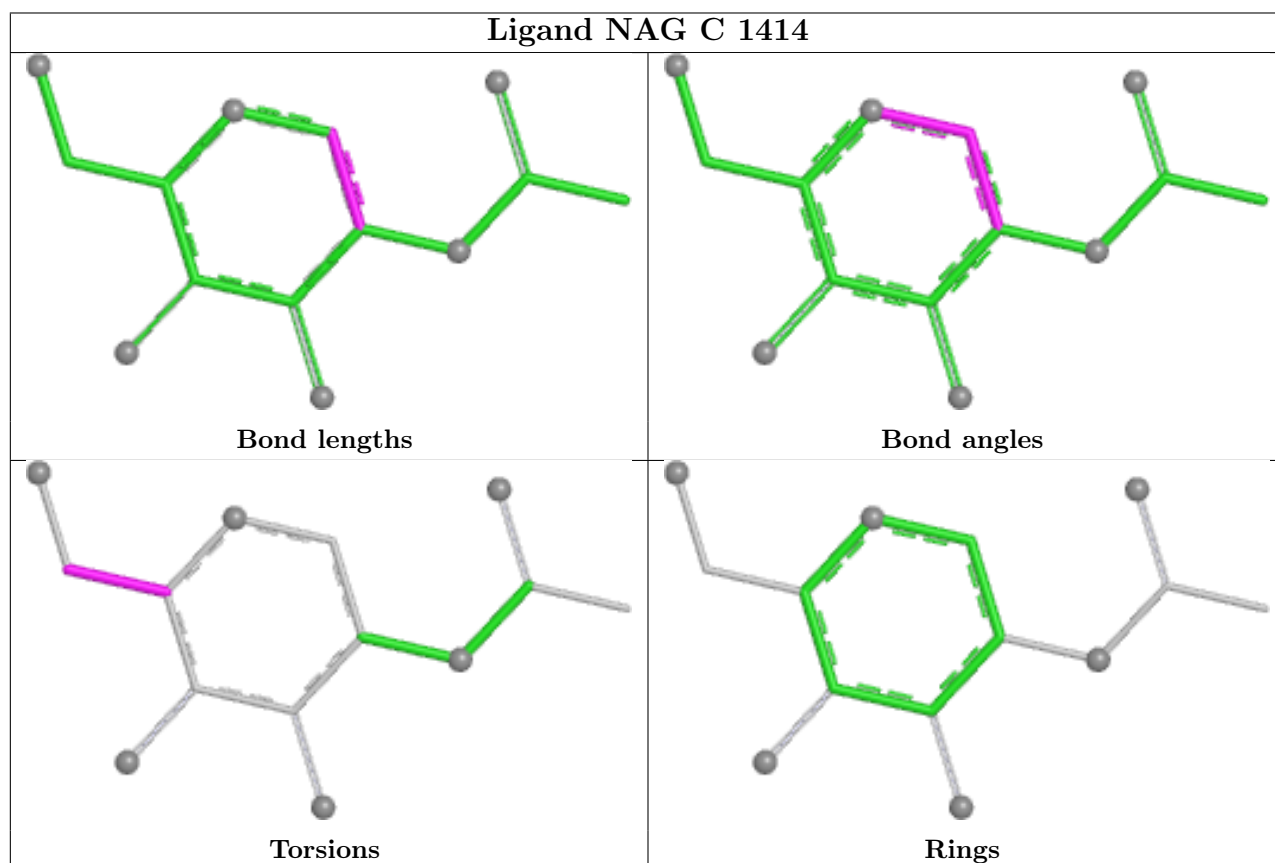
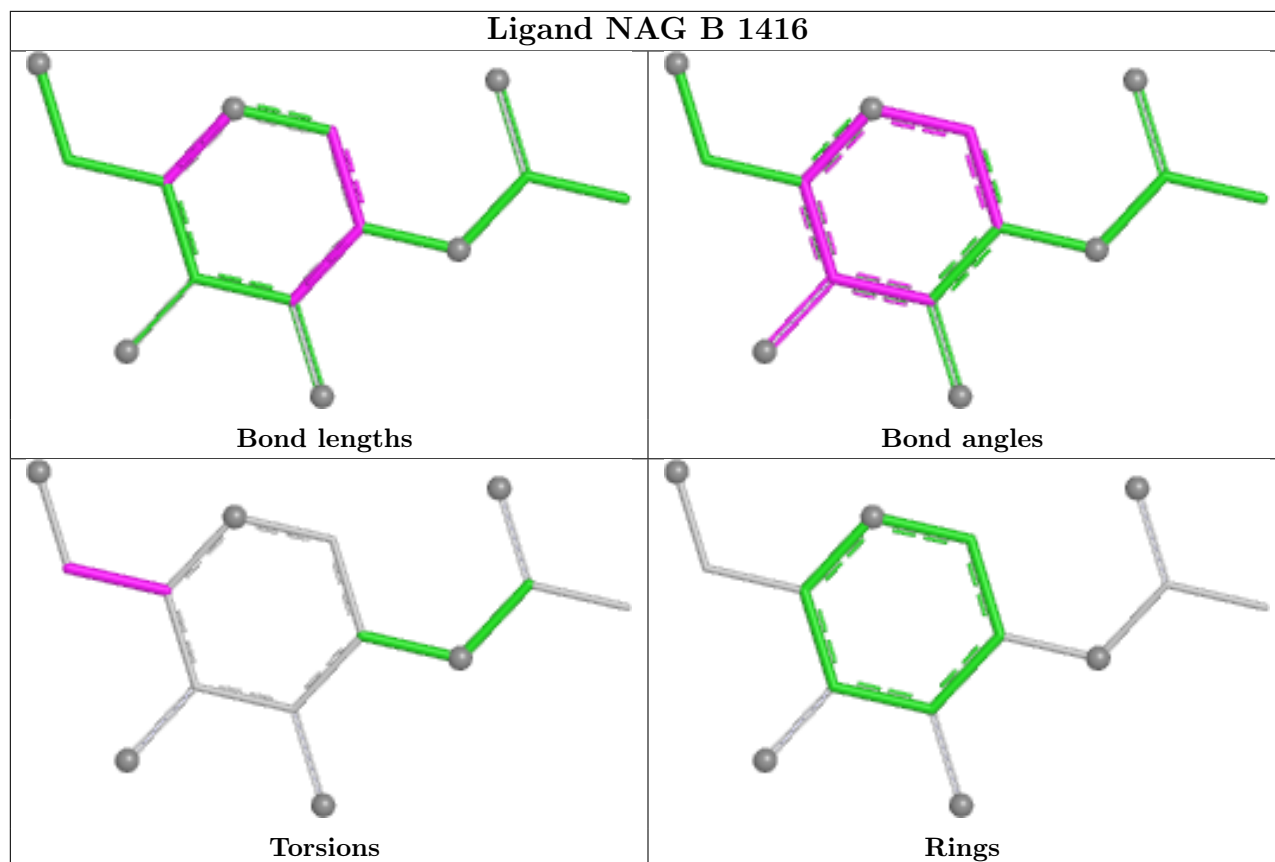
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	1444	FOL	1	0
8	C	1444	FOL	1	0
8	A	1444	FOL	1	0

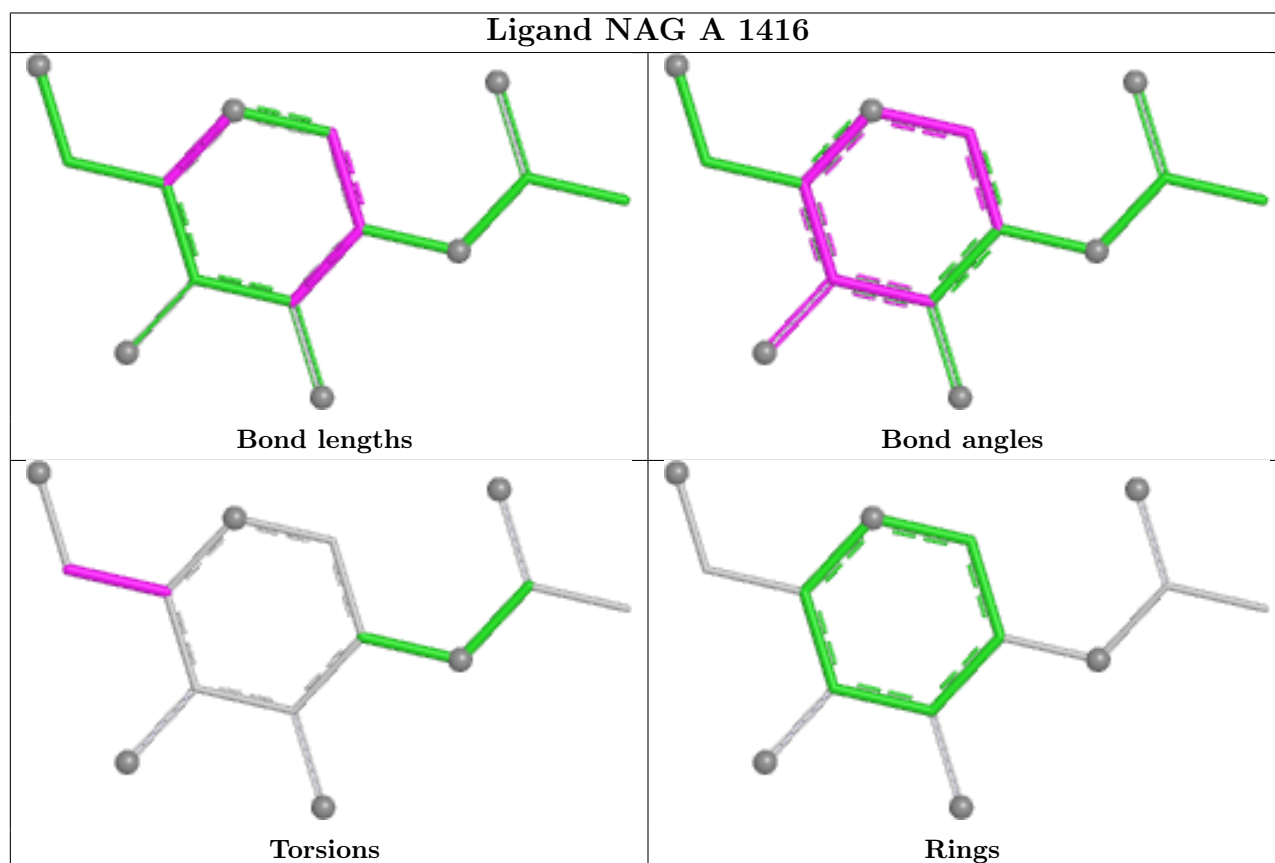
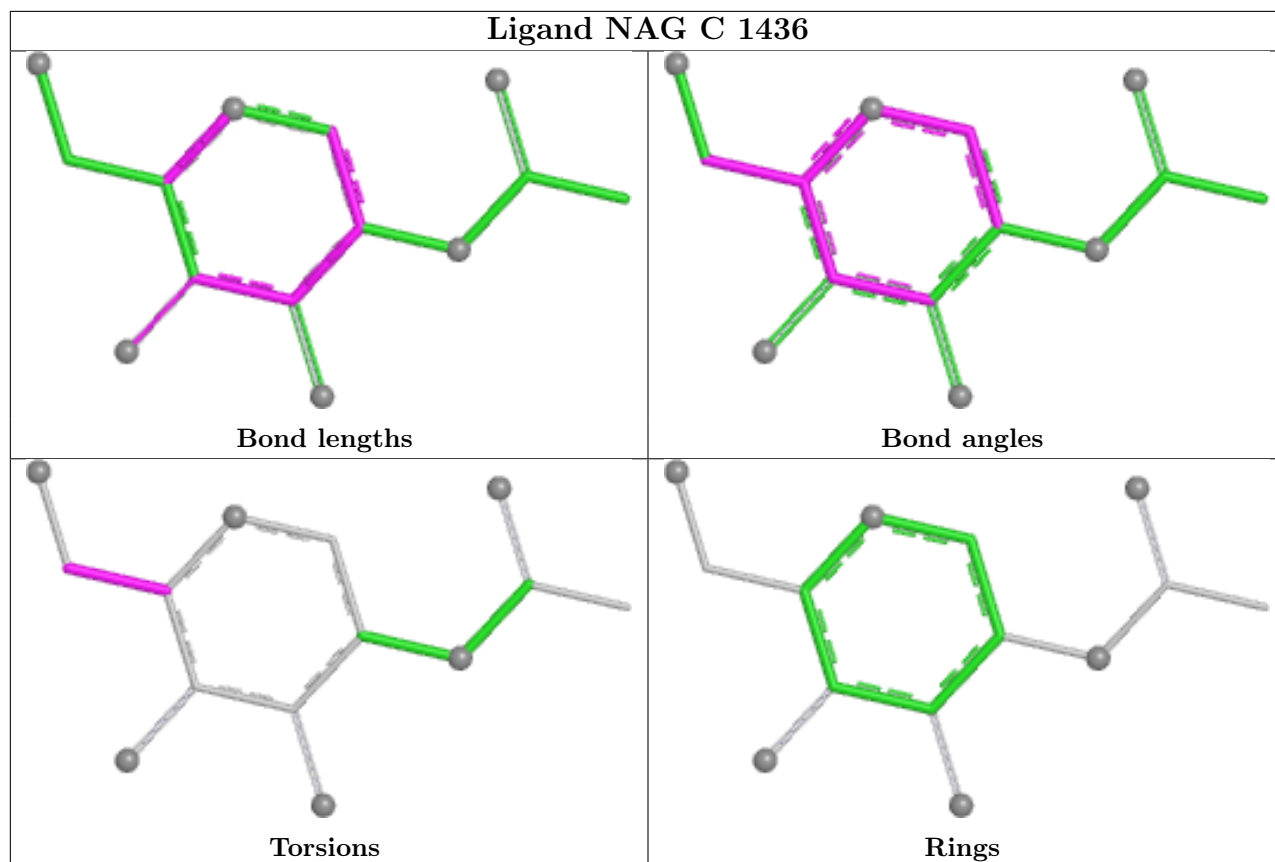
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

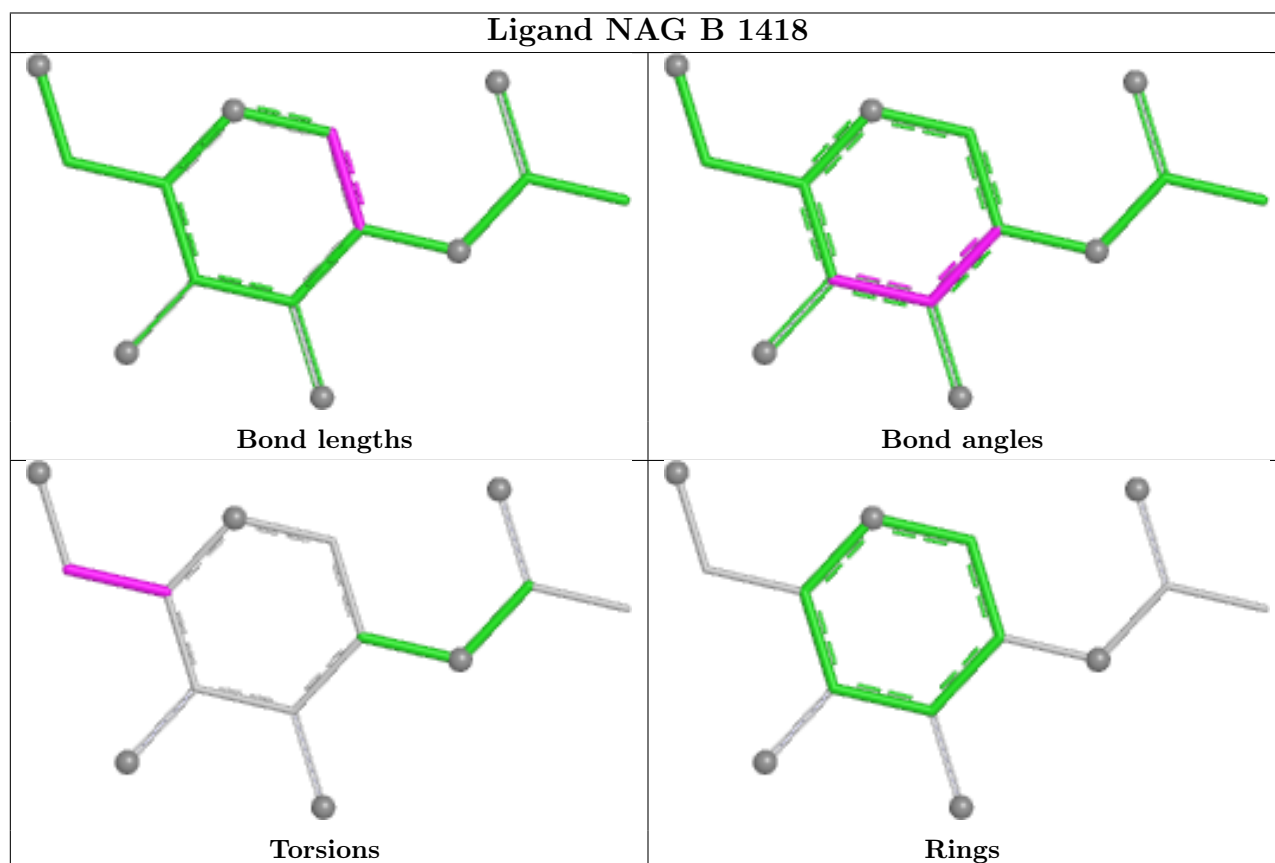
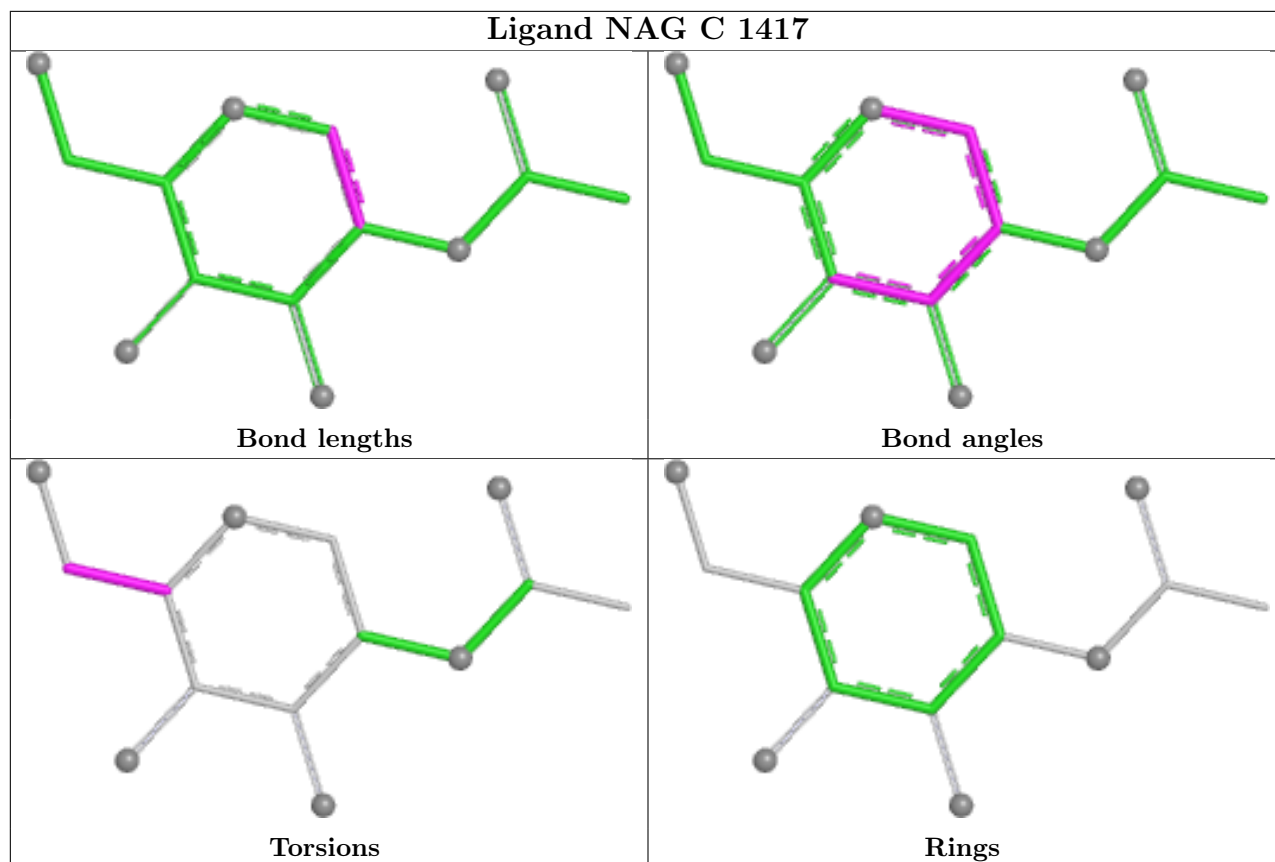


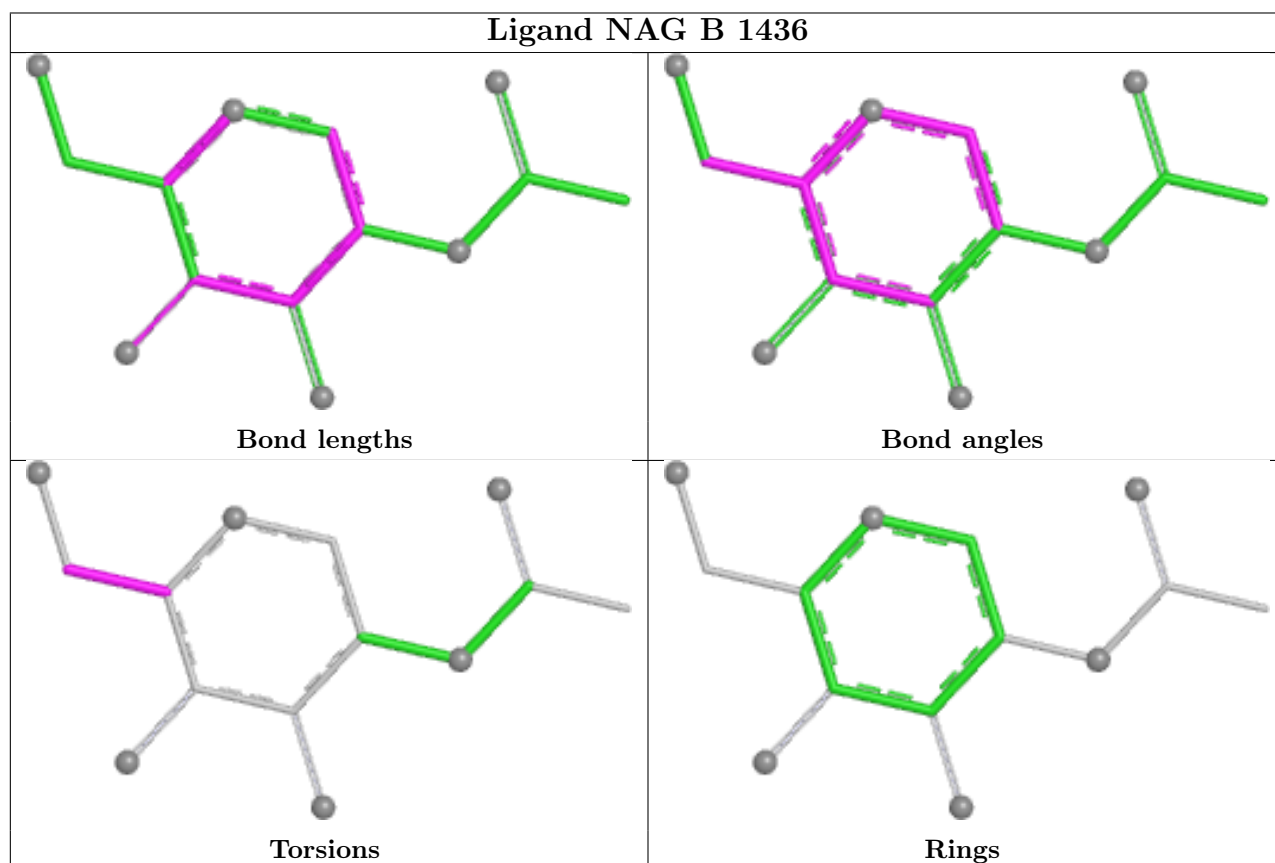
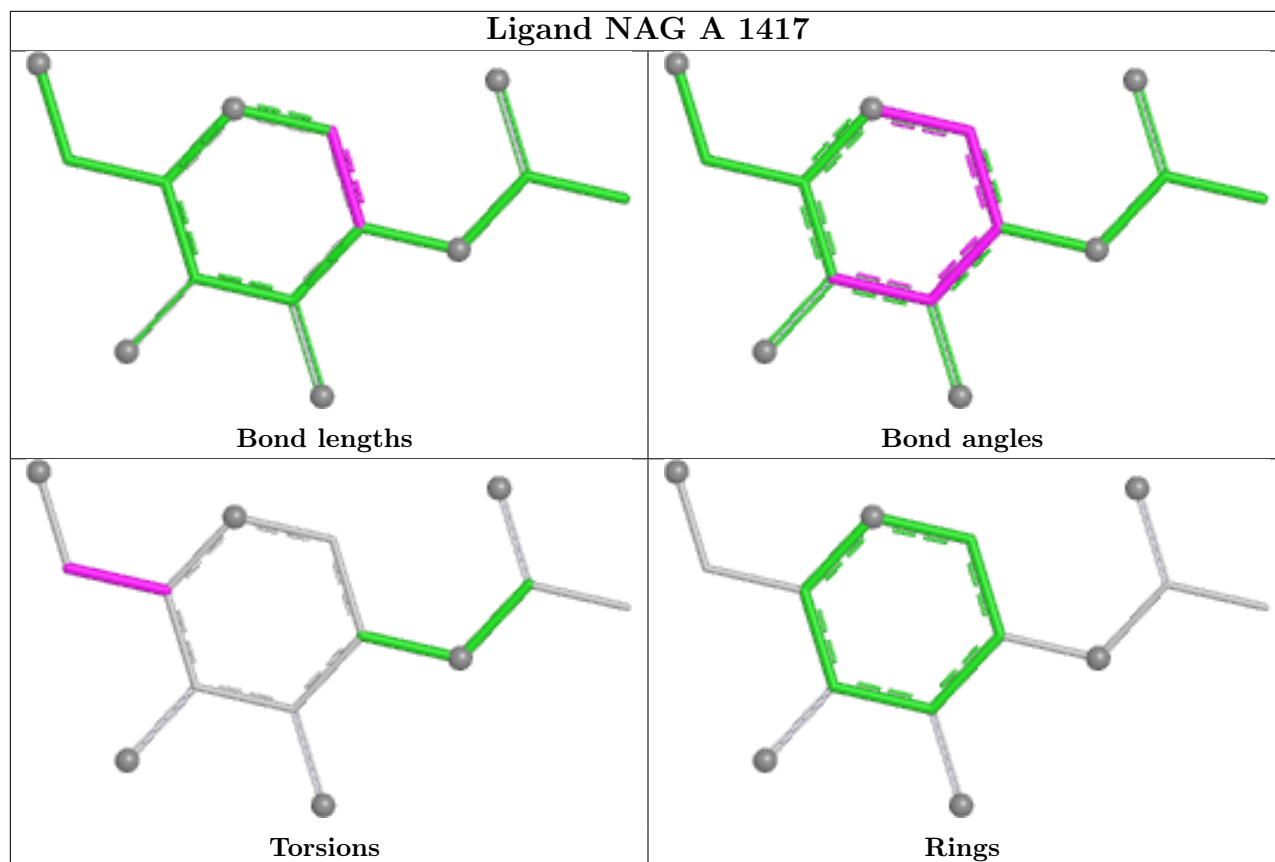


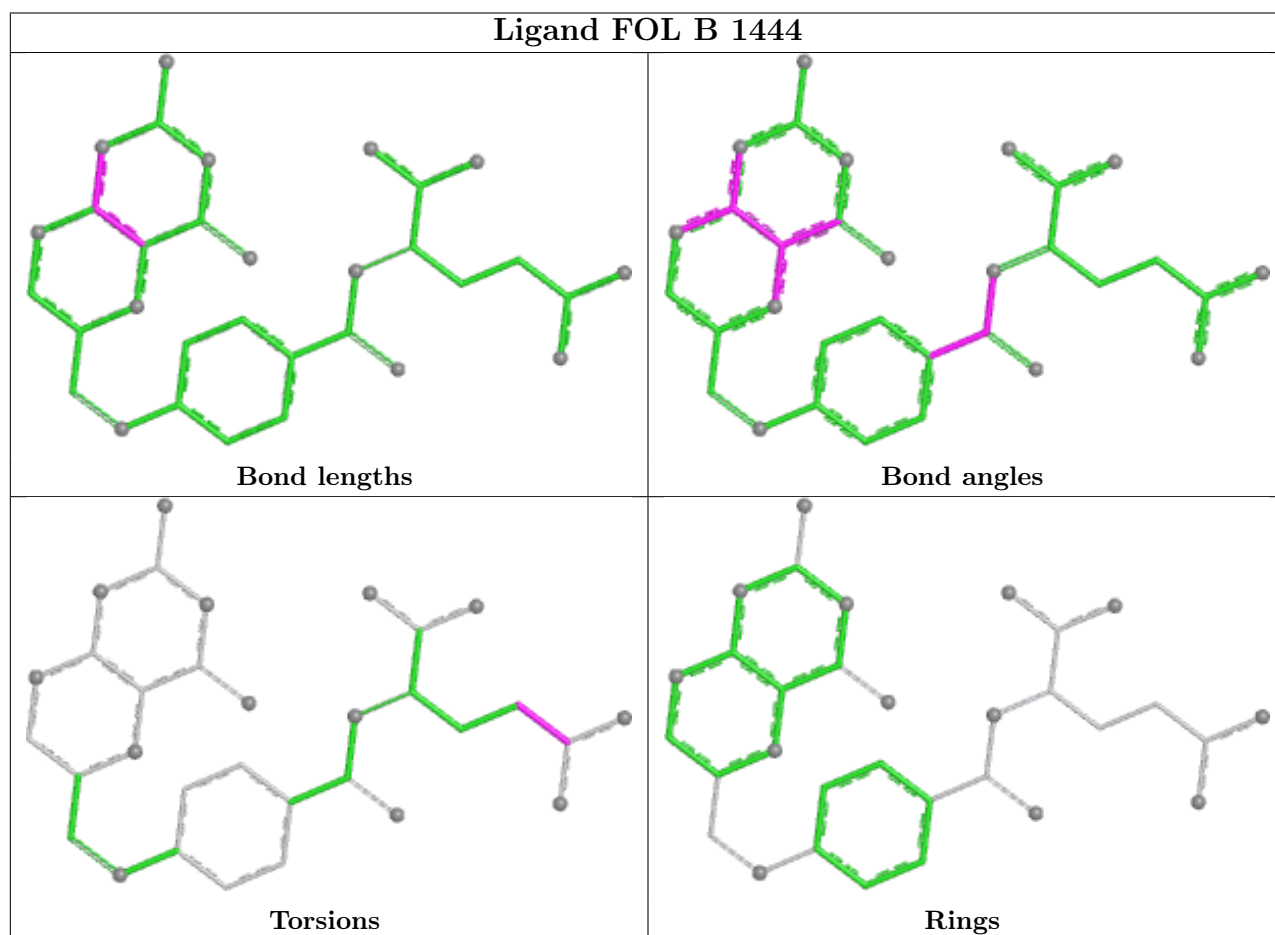
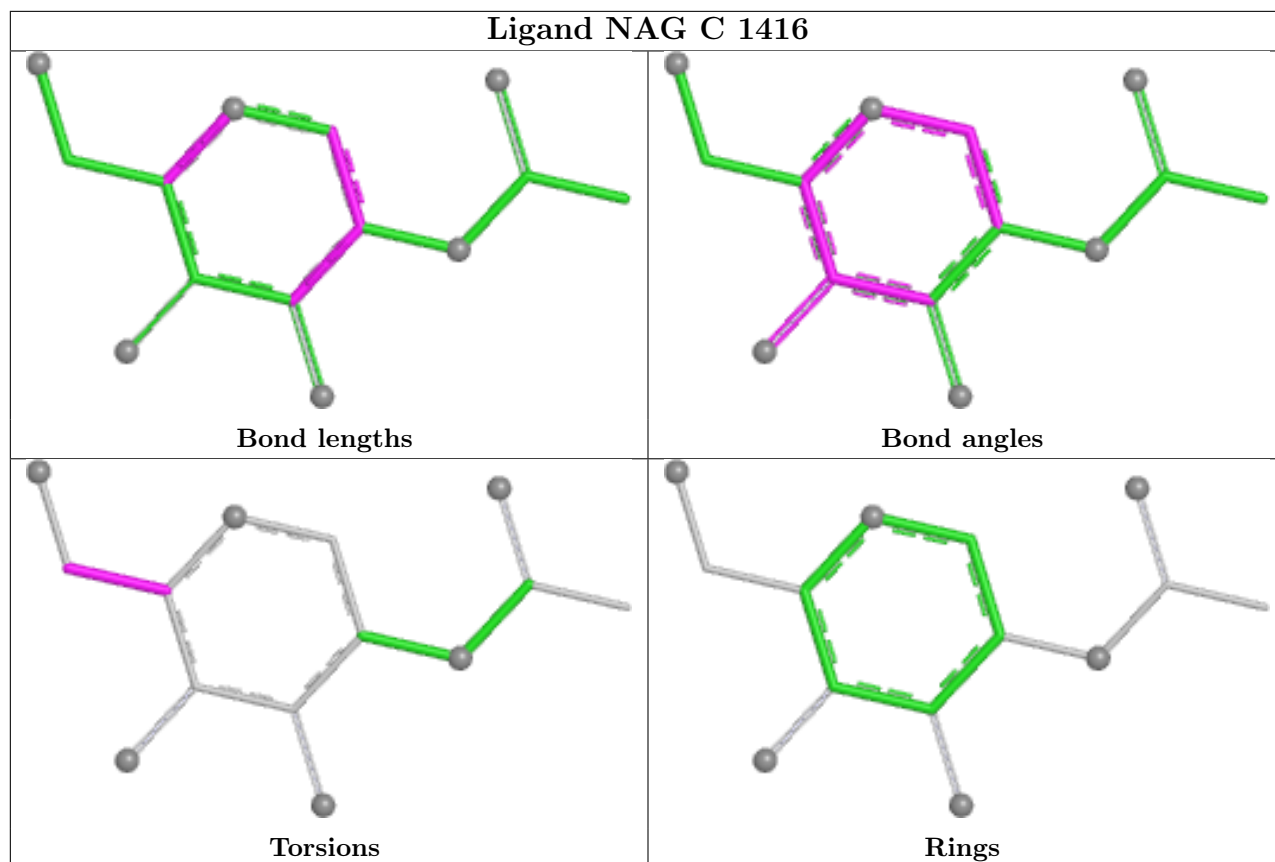


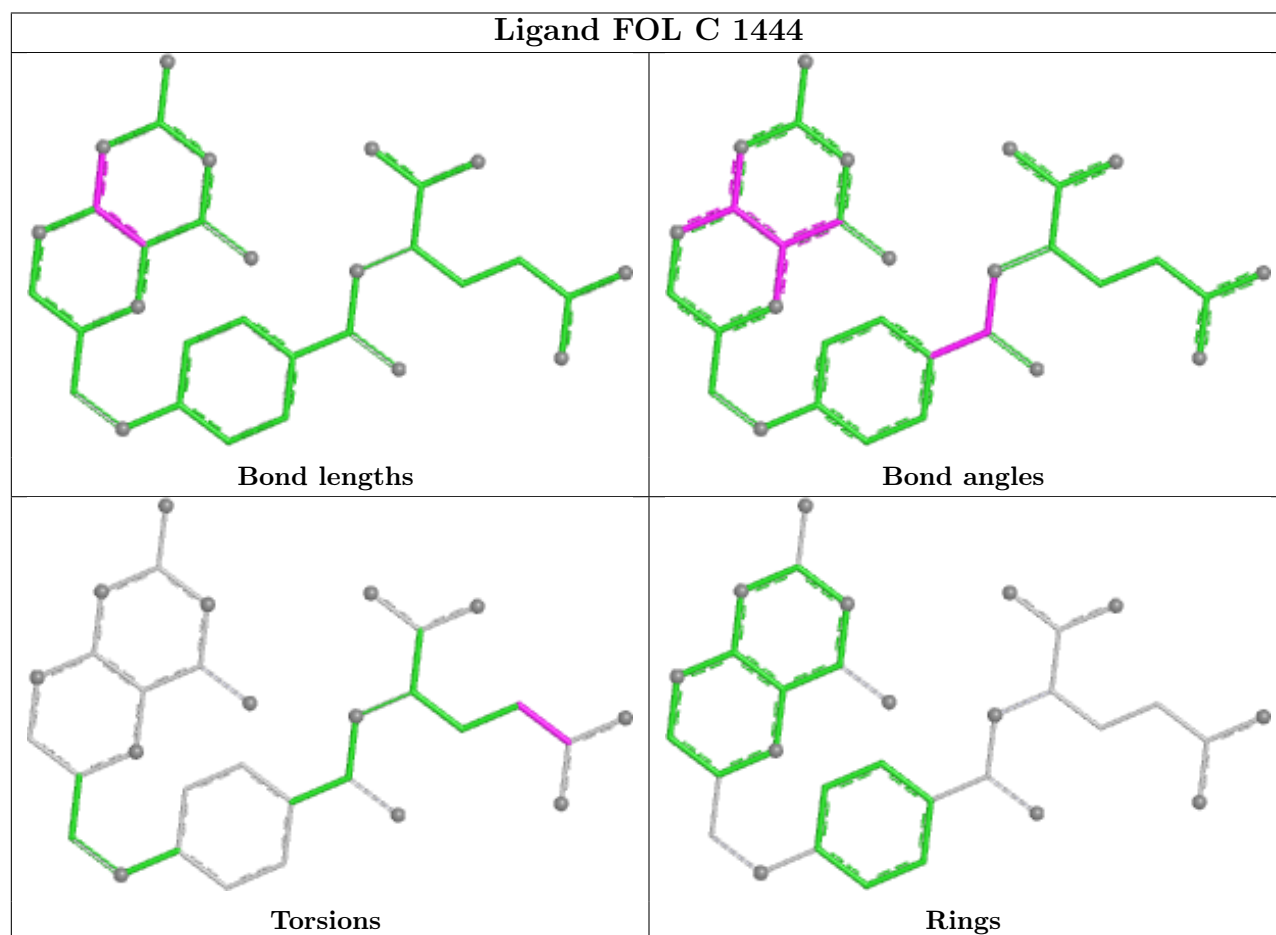
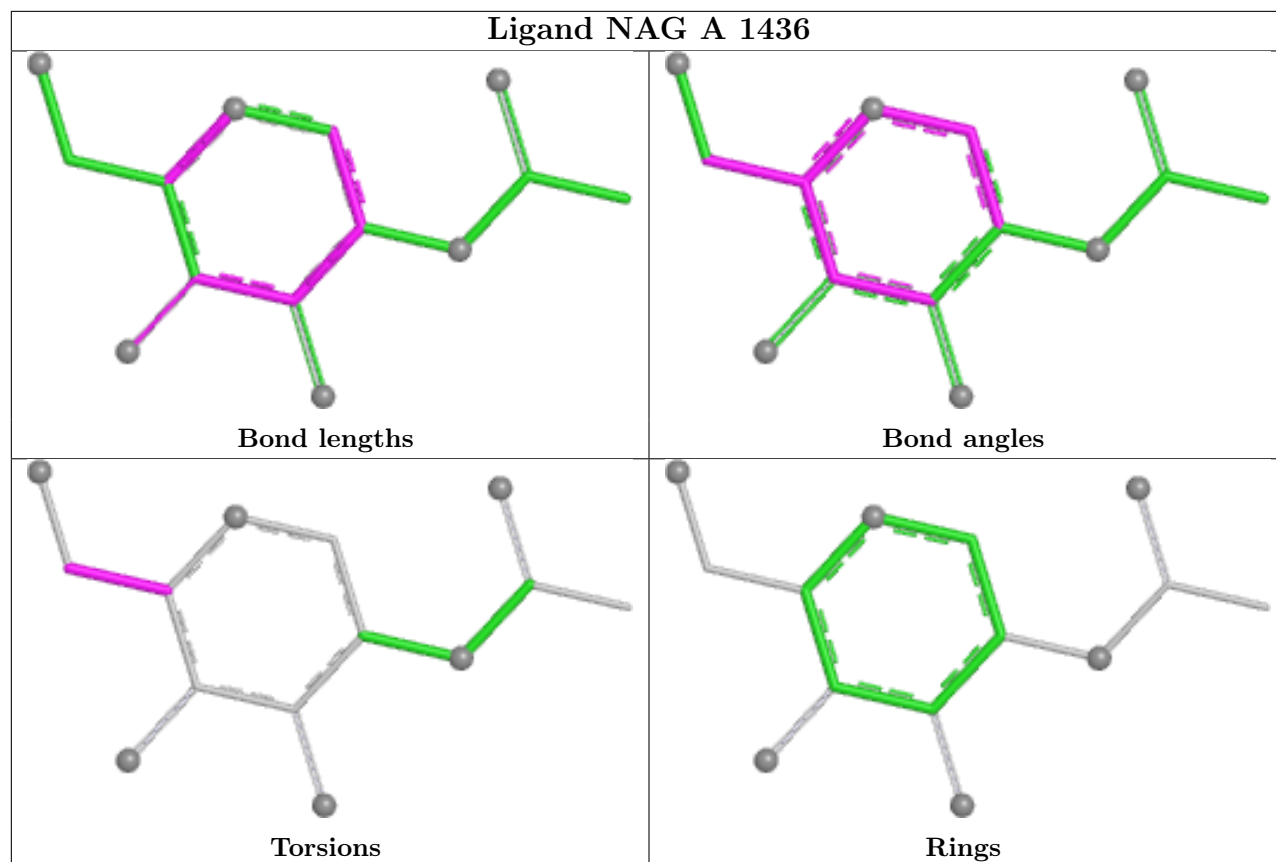


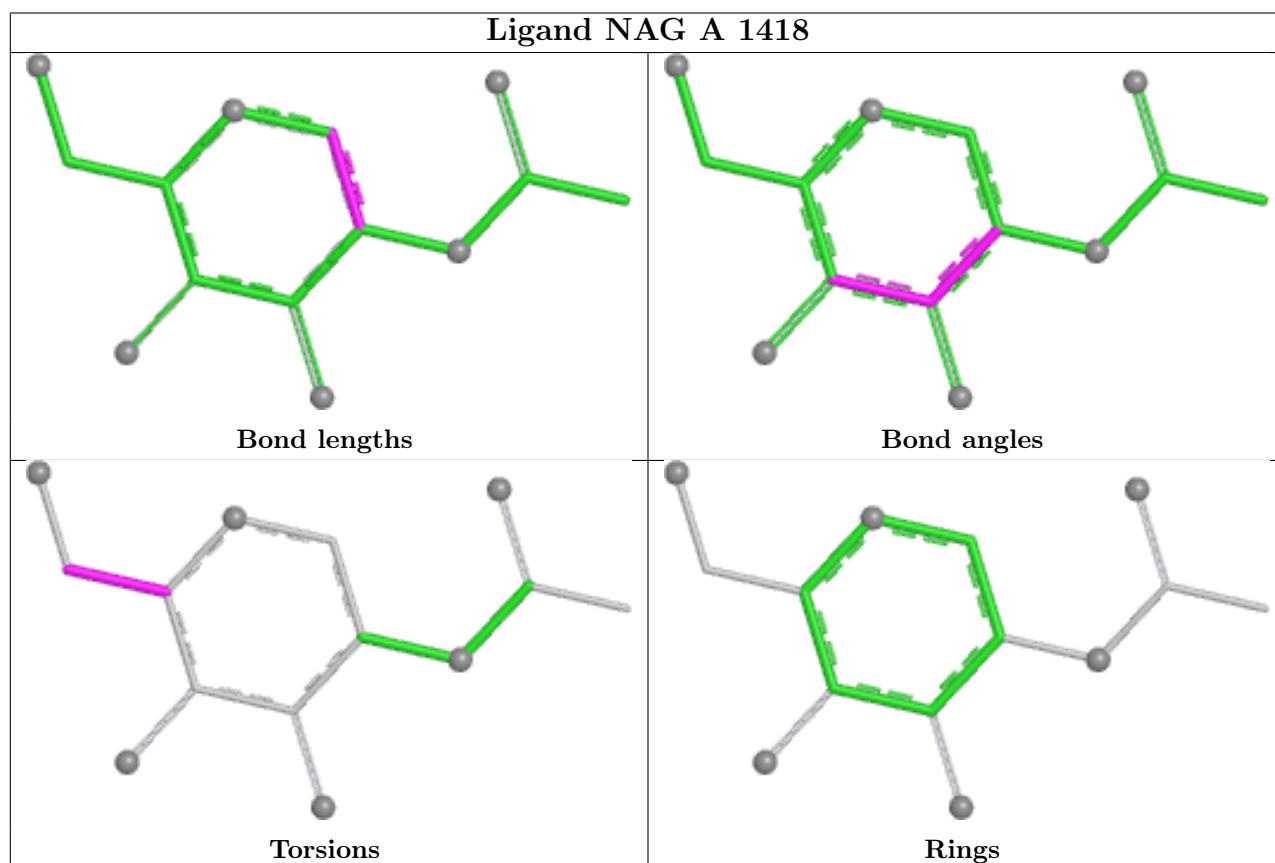
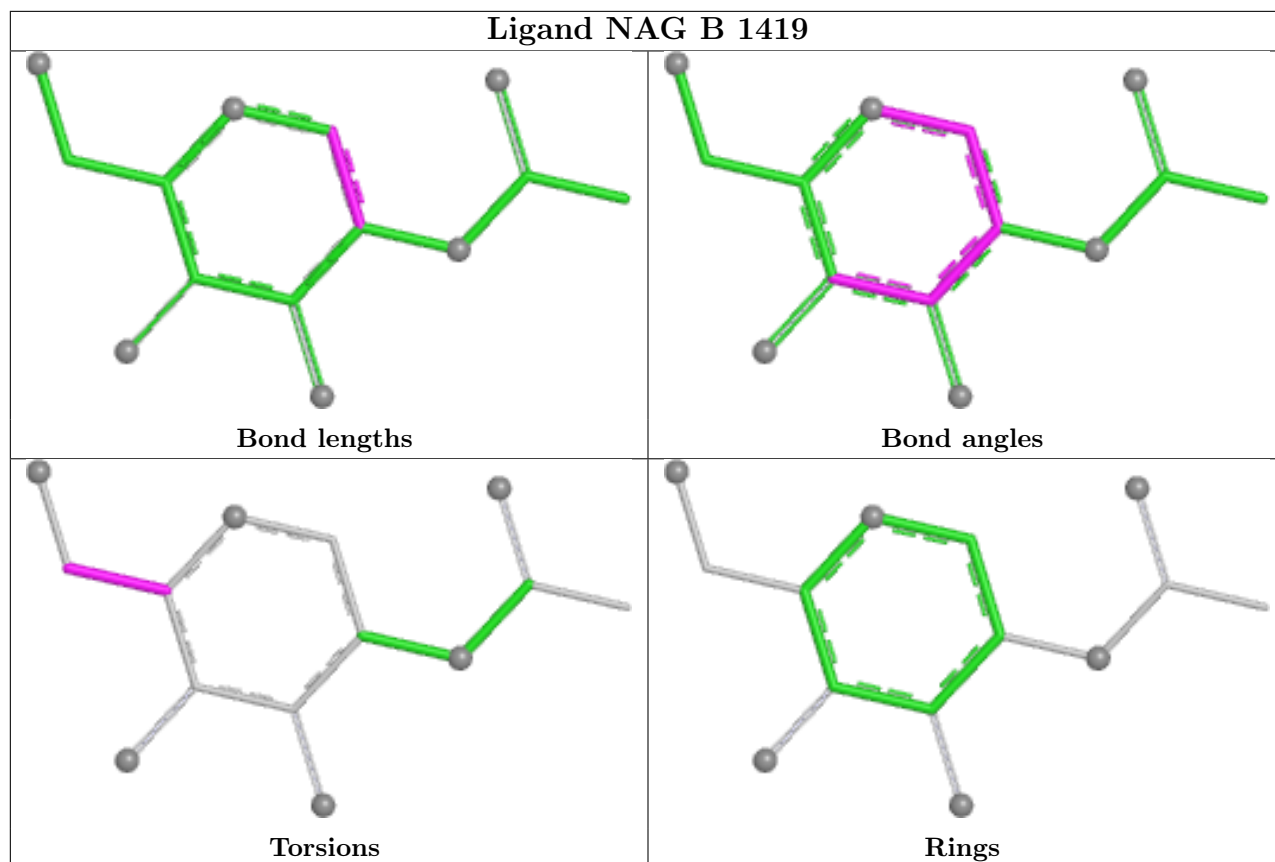


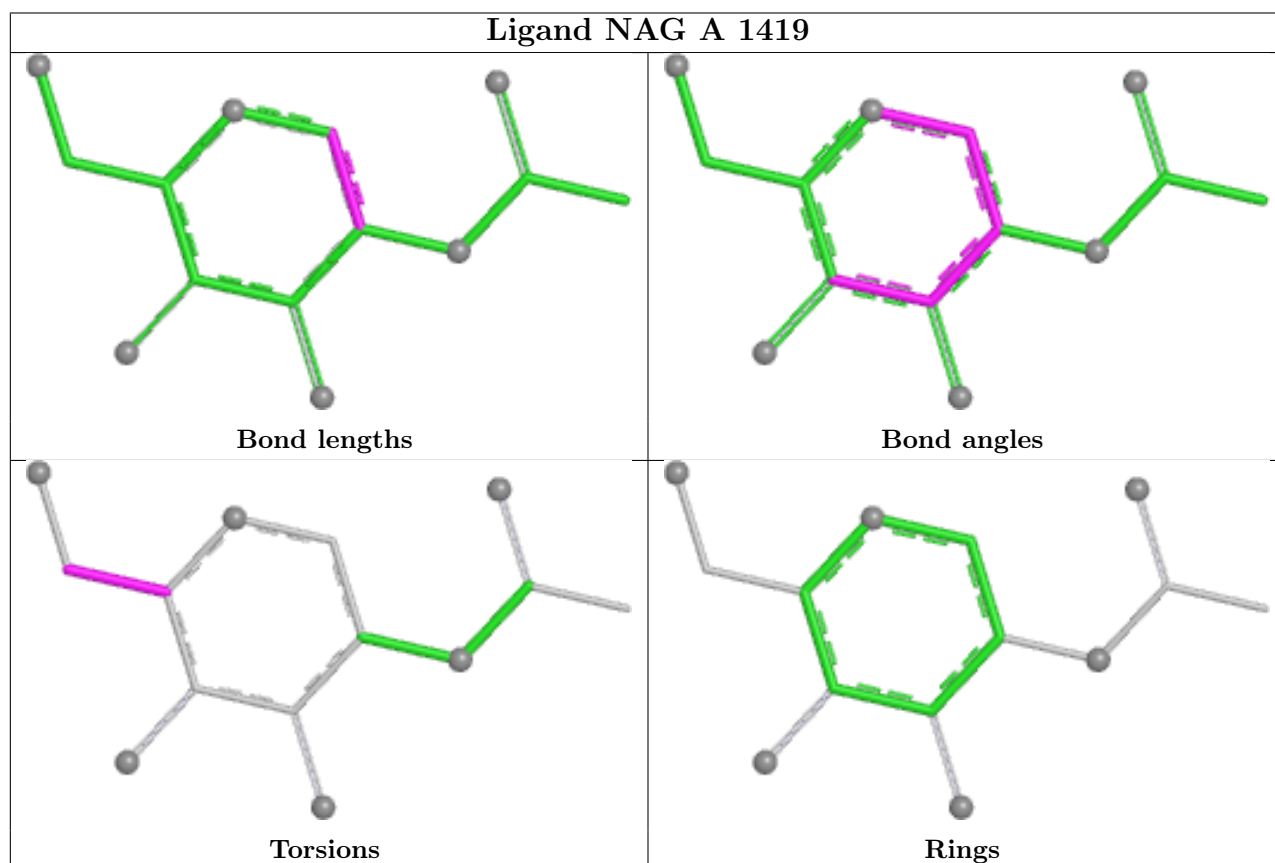
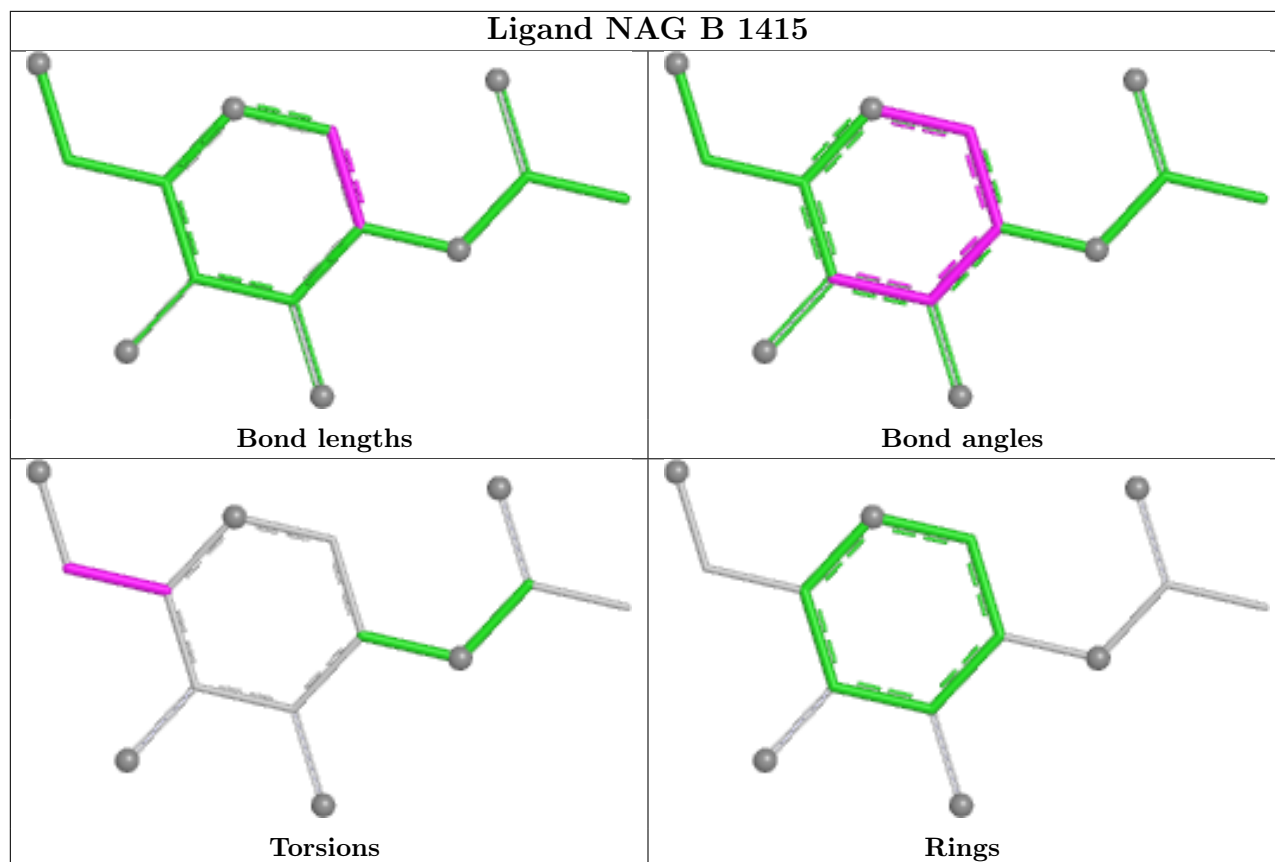


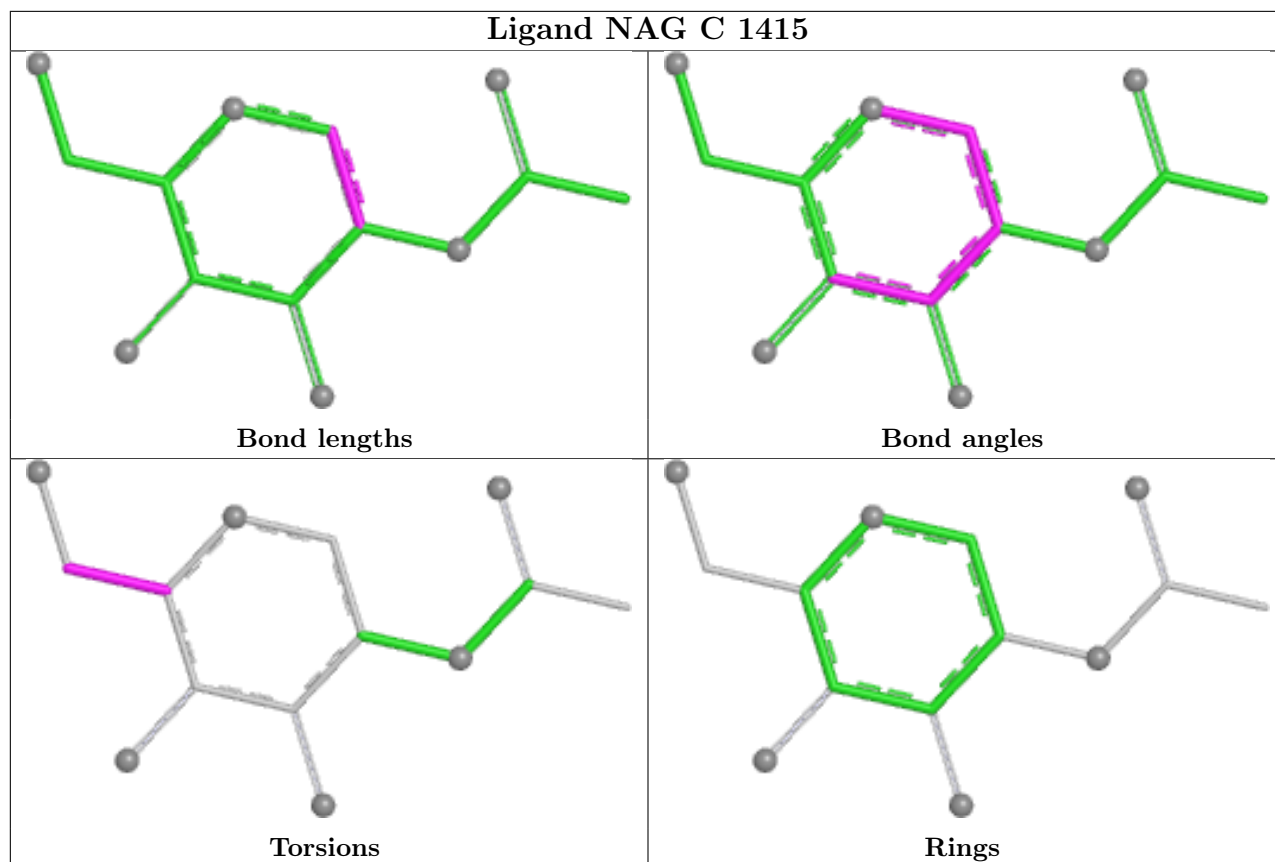


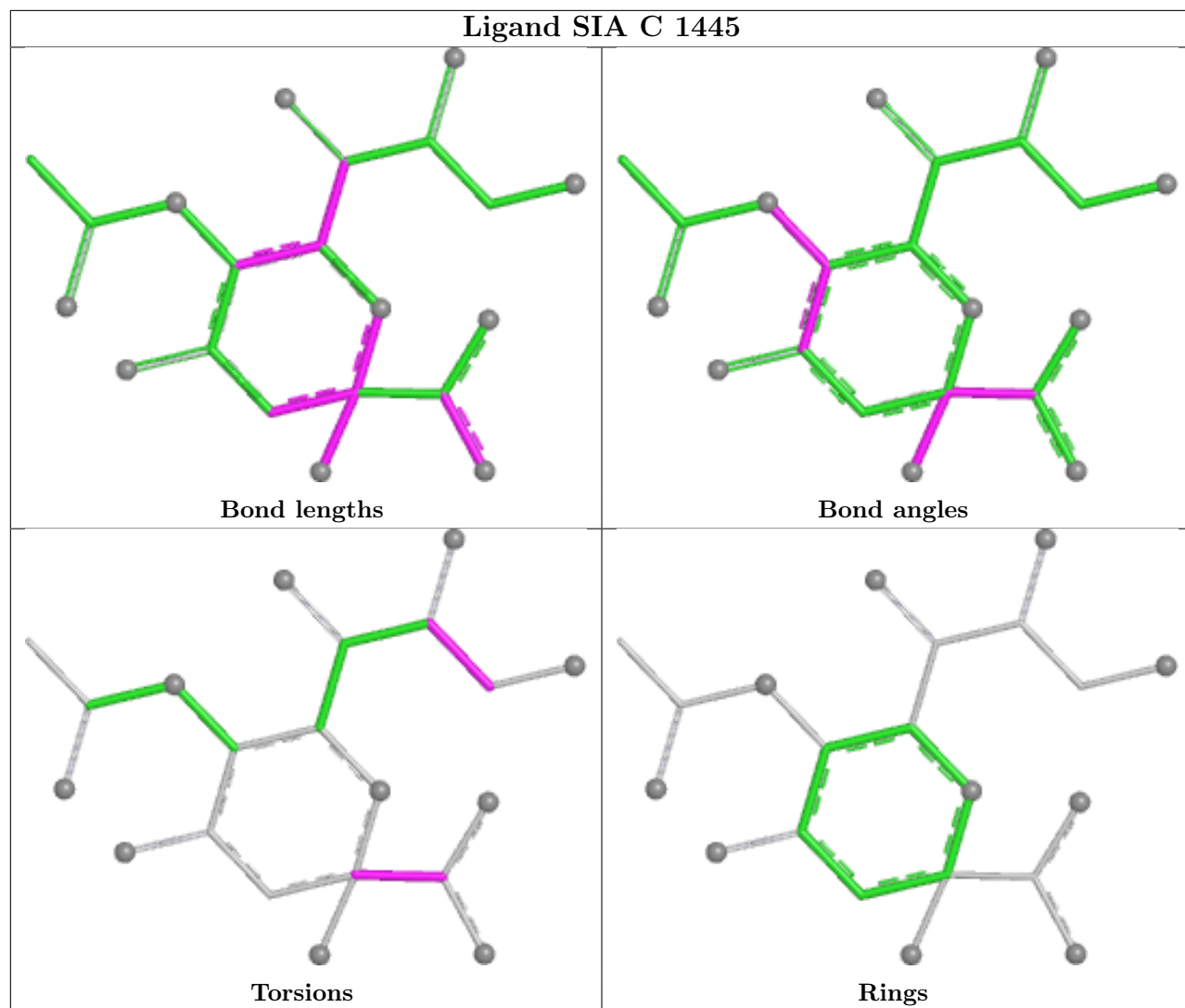


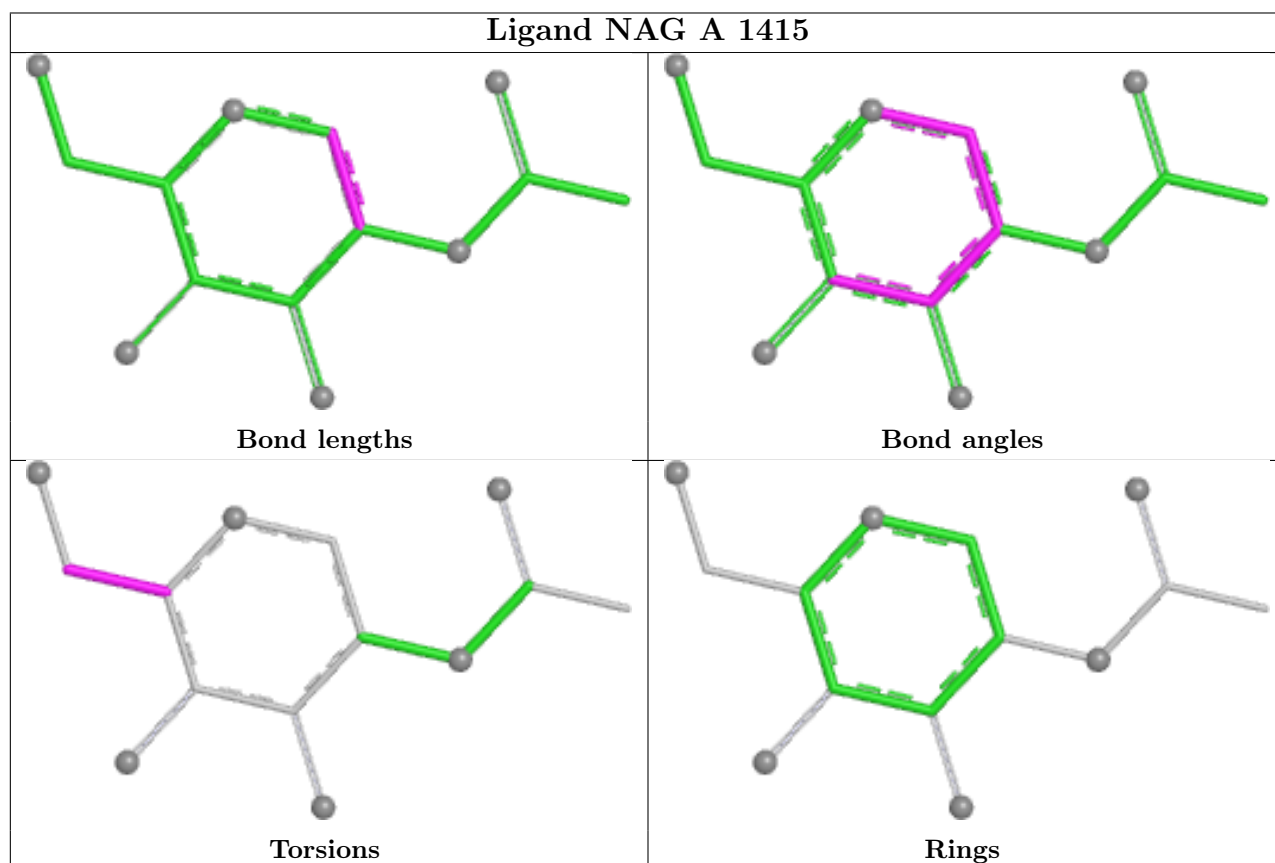
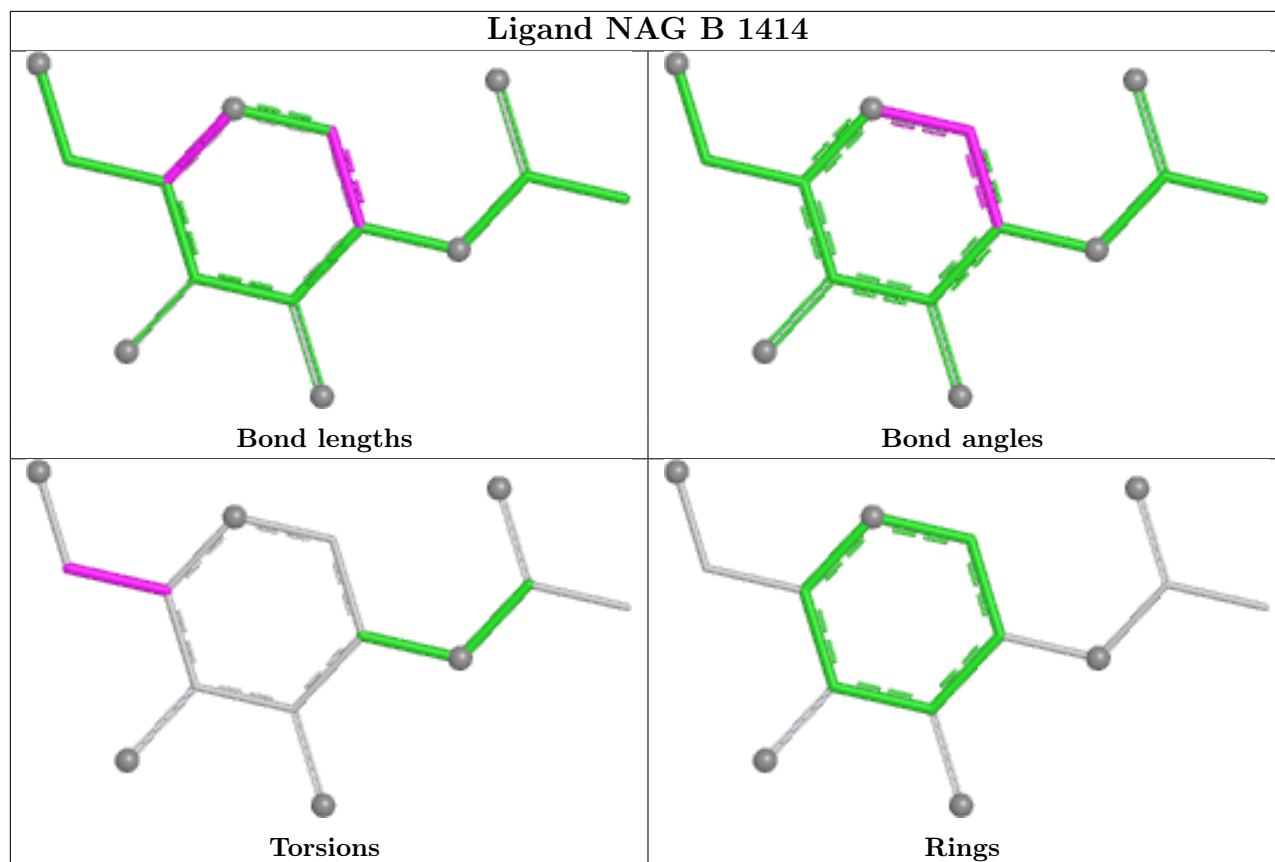


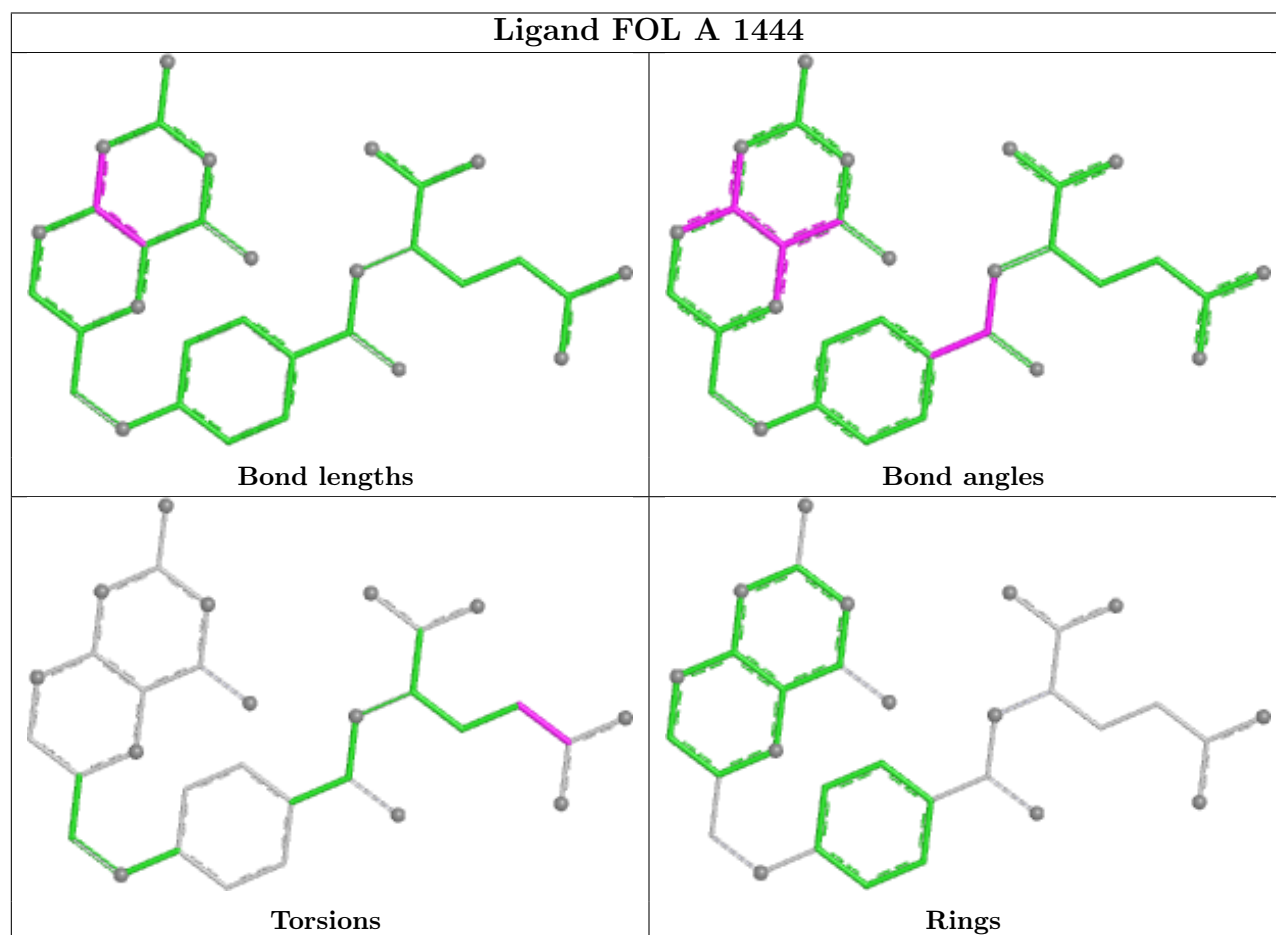
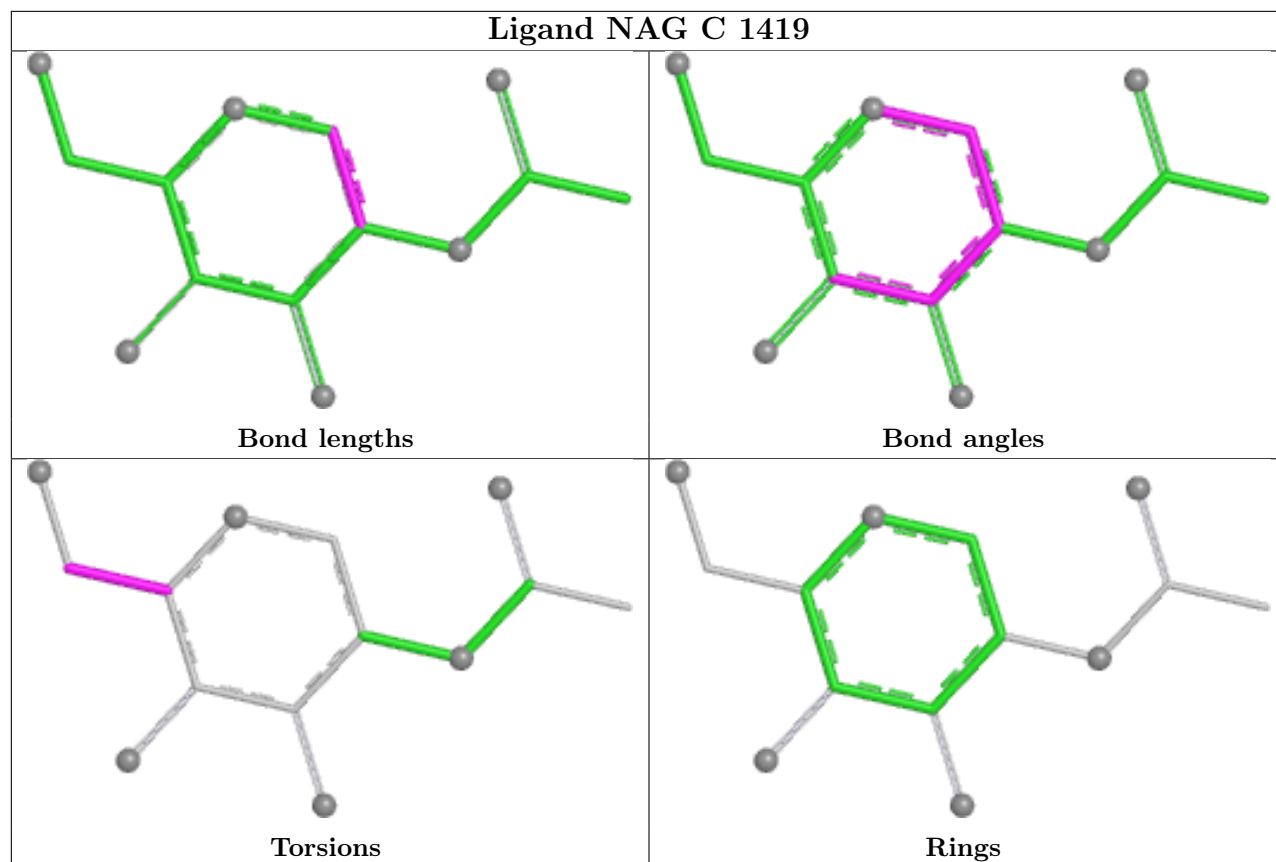


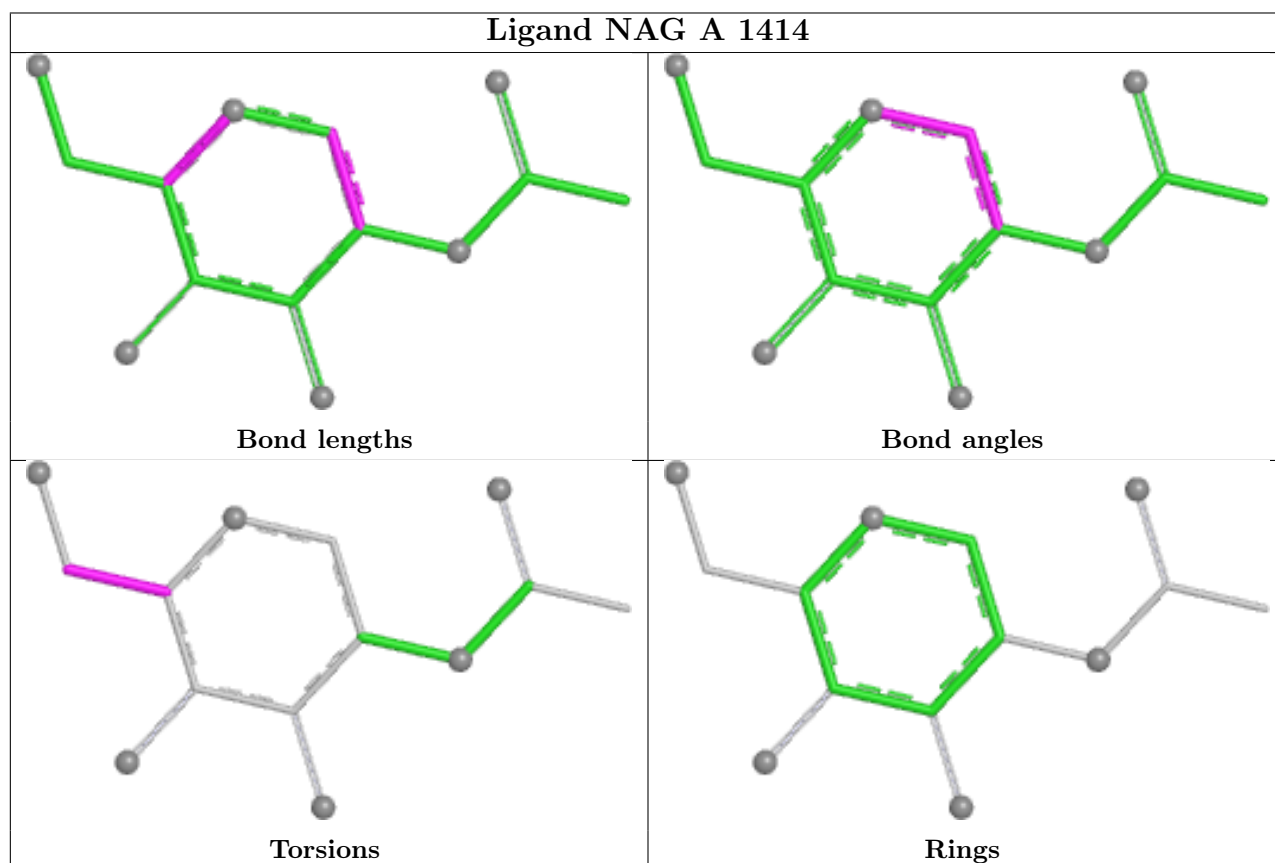
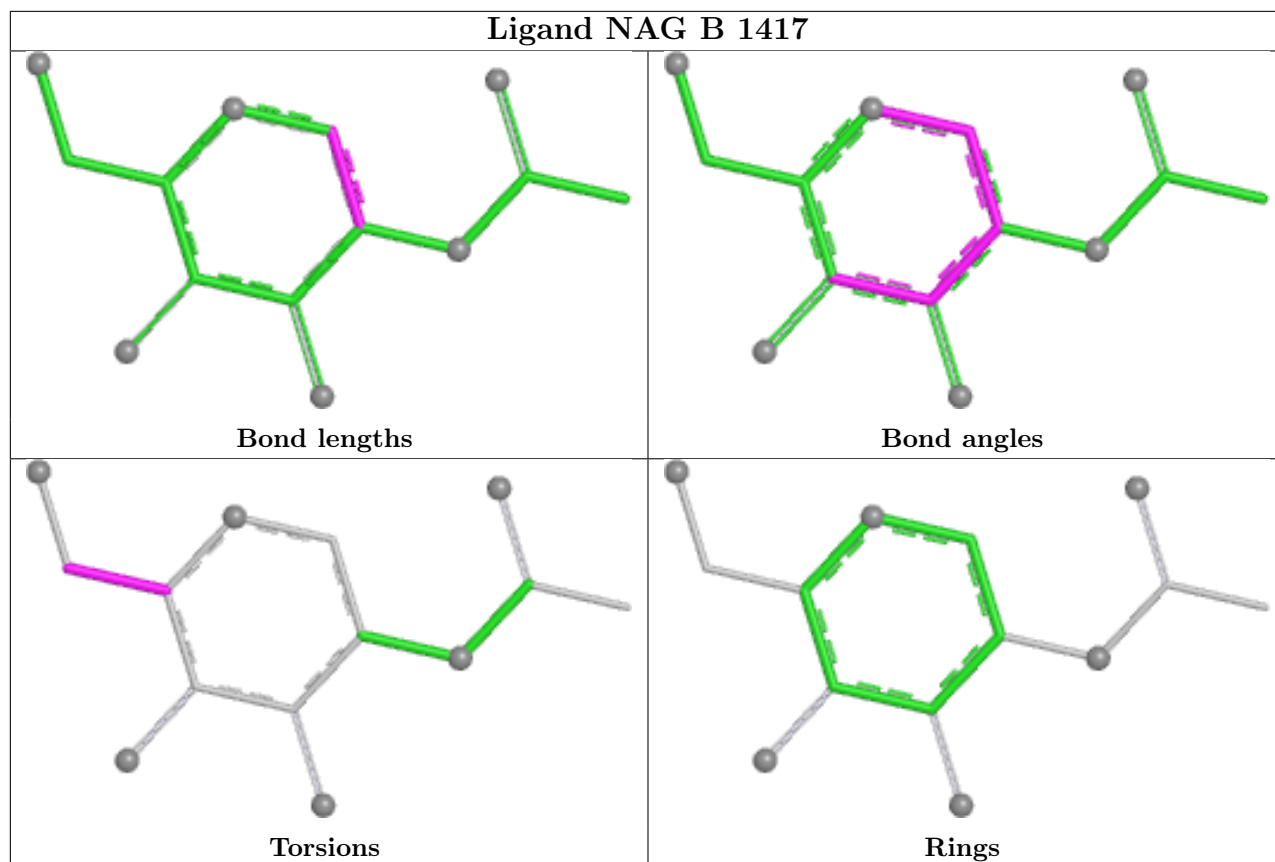












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

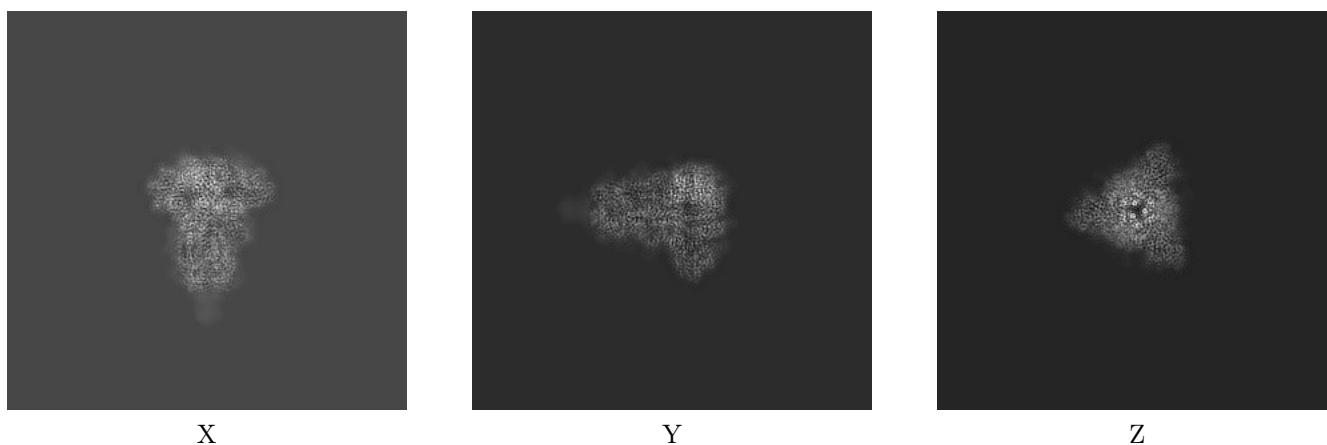
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20542. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

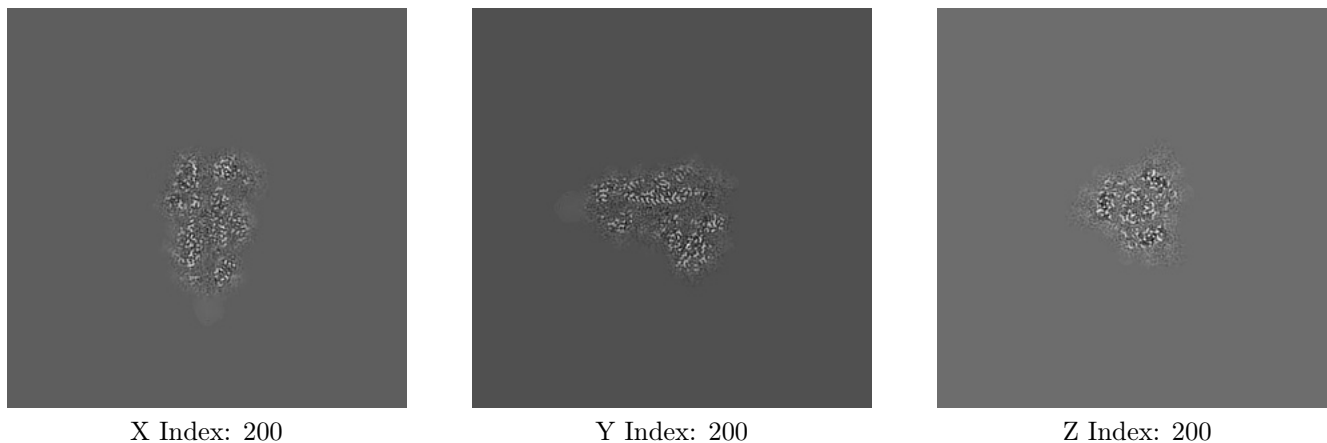
6.1.1 Primary map



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

6.2 Central slices [i](#)

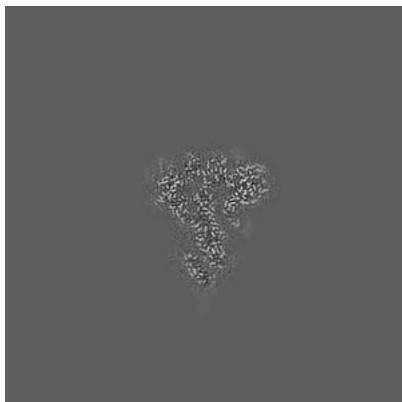
6.2.1 Primary map



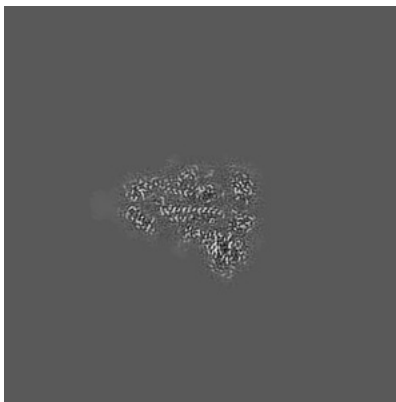
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

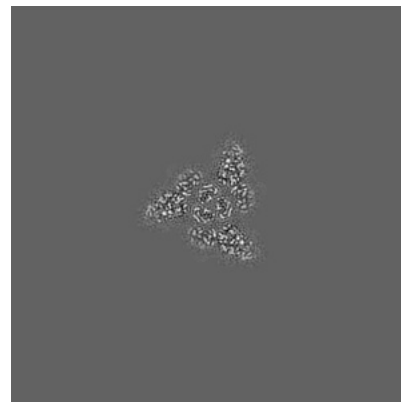
6.3.1 Primary map



X Index: 214



Y Index: 193

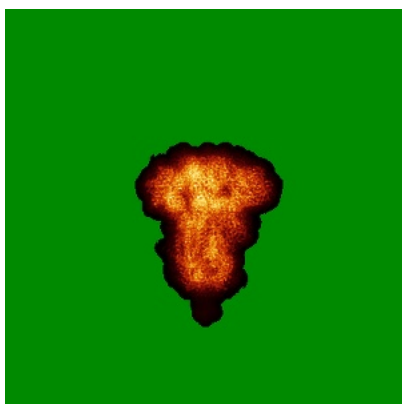


Z Index: 208

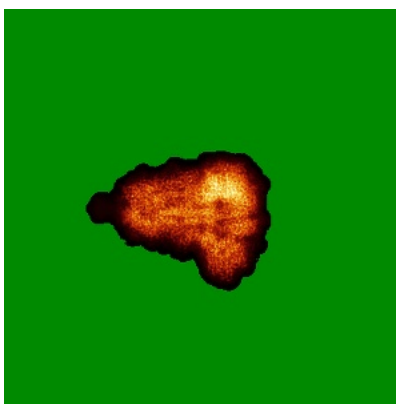
The images above show the largest variance slices of the map in three orthogonal directions.

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

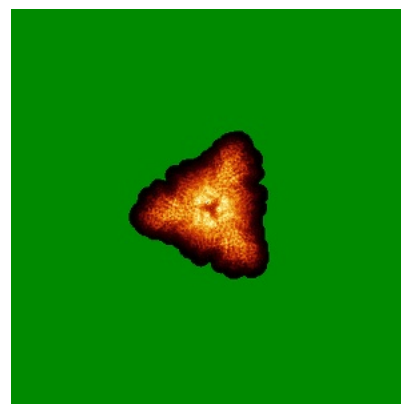
6.4.1 Primary map



X



Y

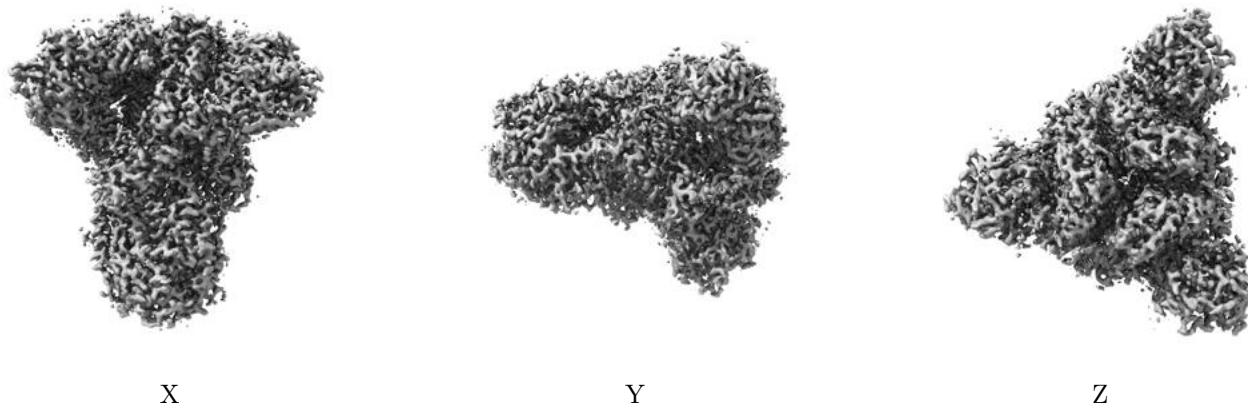


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

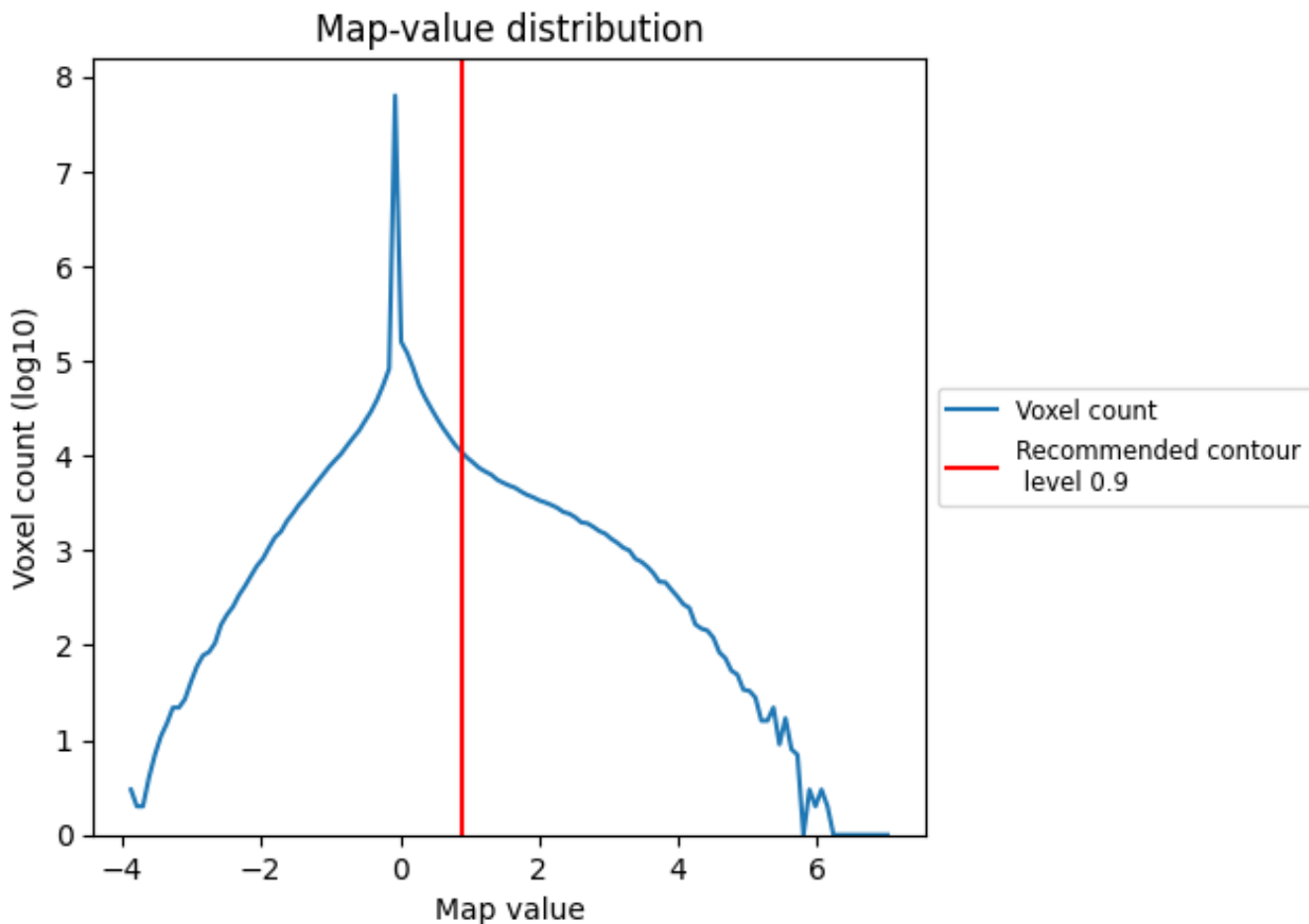
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

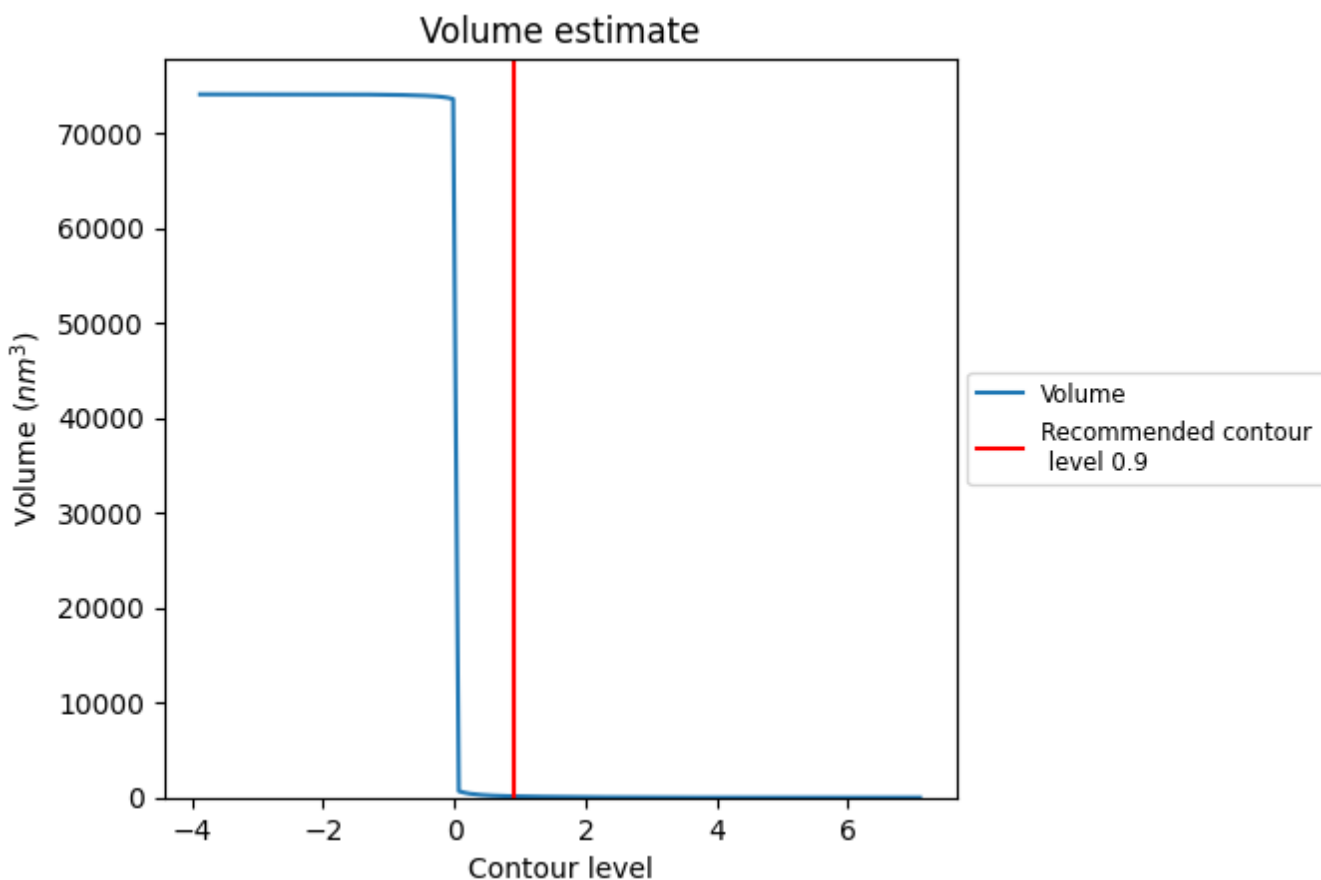
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

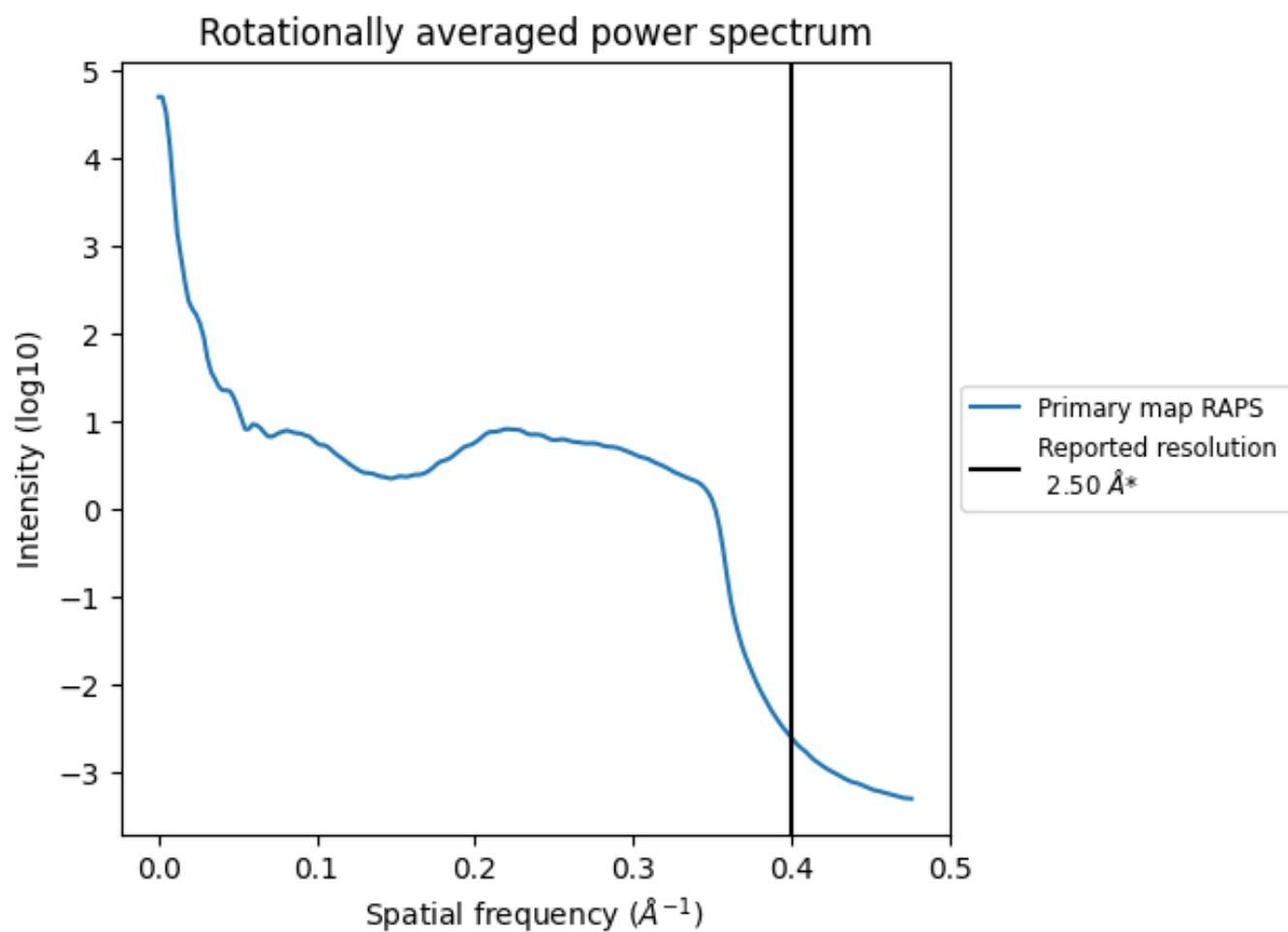
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 136 nm³; this corresponds to an approximate mass of 123 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 0.400 Å⁻¹

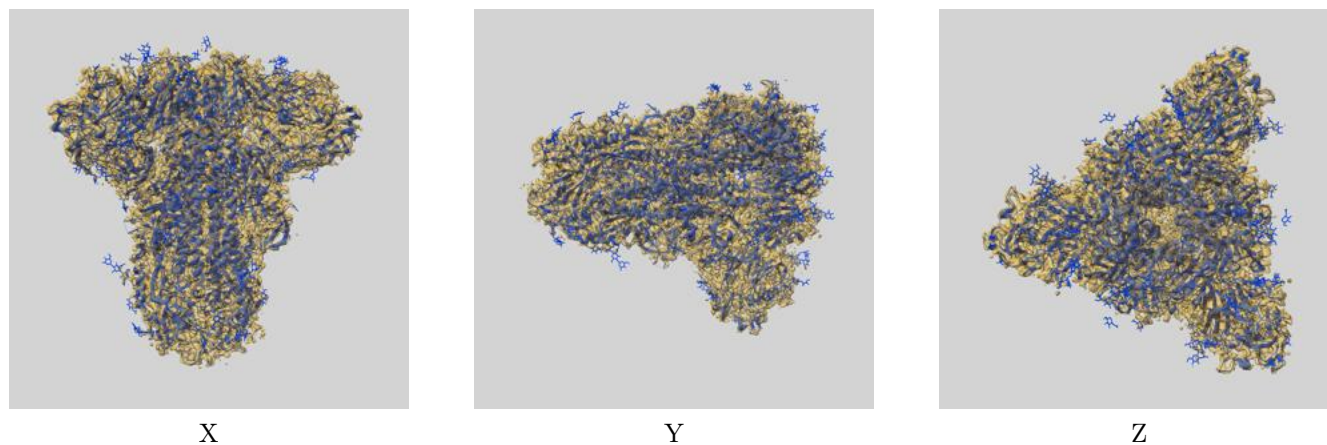
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

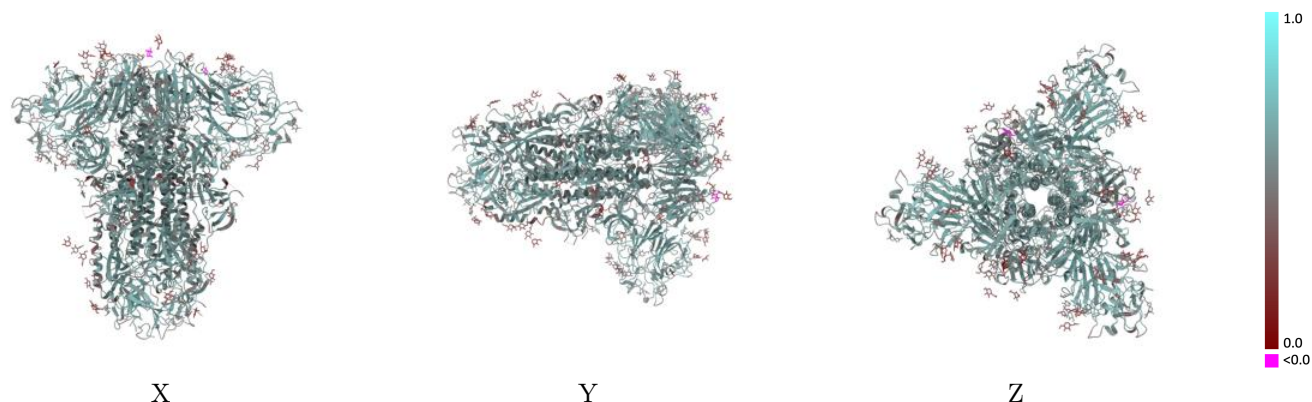
This section contains information regarding the fit between EMDB map EMD-20542 and PDB model 6Q04. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



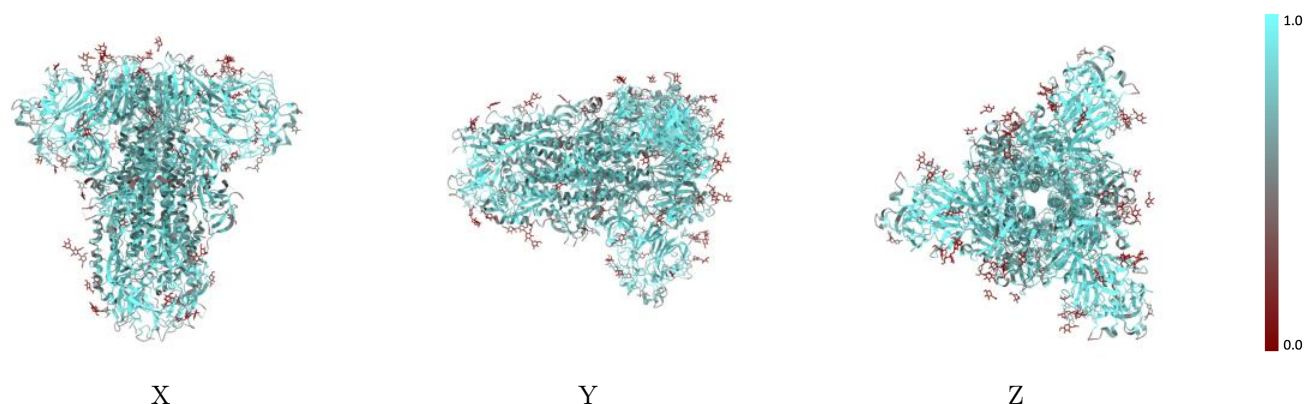
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



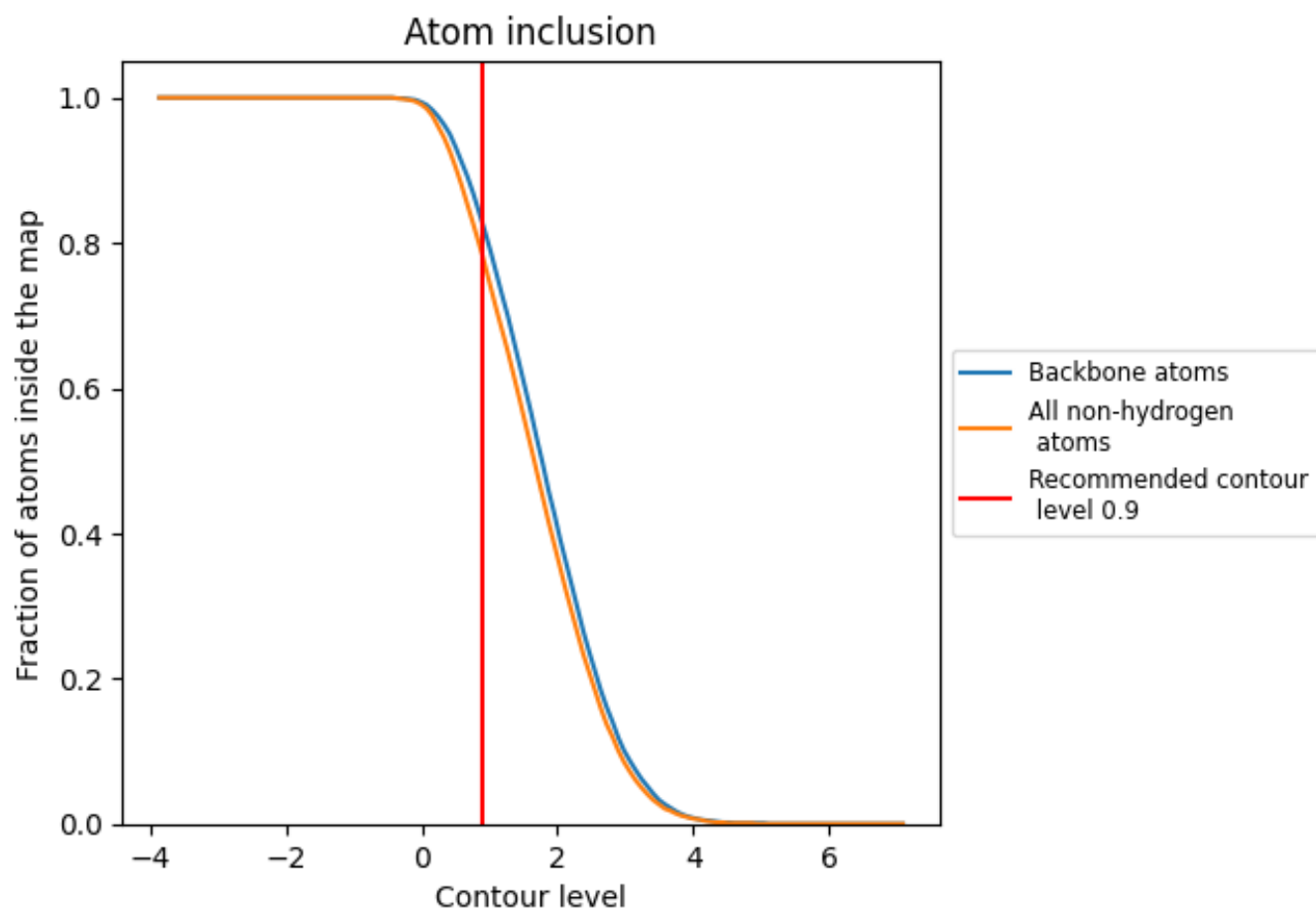
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.9).





































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.5690
A	 0.8080	 0.5780
B	 0.8070	 0.5780
C	 0.8100	 0.5790
D	 0.4600	 0.4210
E	 0.1790	 0.2930
F	 0.3010	 0.3630
G	 0.1030	 0.2570
H	 0.2600	 0.3540
I	 0.2860	 0.4750
J	 0.0710	 0.2940
K	 0.5250	 0.4650
L	 0.2950	 0.4000
M	 0.3570	 0.3660
N	 0.4200	 0.4040
O	 0.1790	 0.2950
P	 0.3130	 0.3540
Q	 0.1030	 0.2580
R	 0.2400	 0.3640
S	 0.3210	 0.4660
T	 0.0710	 0.3010
U	 0.5250	 0.4610
V	 0.3110	 0.3990
W	 0.3570	 0.3870
X	 0.4200	 0.4100
Y	 0.1790	 0.2970
Z	 0.2770	 0.3560
a	 0.1540	 0.2580
b	 0.2600	 0.3630
c	 0.2500	 0.4630
d	 0.0710	 0.2850
e	 0.5410	 0.4650
f	 0.2950	 0.3870
g	 0.3570	 0.3690

