



wwPDB EM Validation Summary Report ⓘ

Oct 14, 2024 – 06:41 PM JST

PDB ID : 7Y6T
EMDB ID : EMD-33647
Title : Cryo-EM map of IPEC-J2 cell-derived PEDV PT52 S protein one D0-down and two D0-up
Authors : Hsu, S.T.D.; Draczkowski, P.; Wang, Y.S.
Deposited on : 2022-06-21
Resolution : 4.20 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

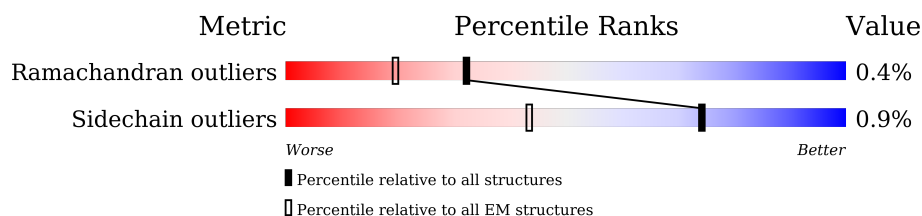
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


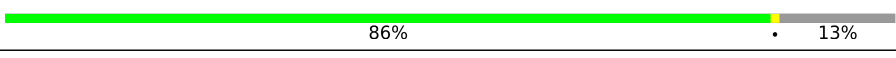

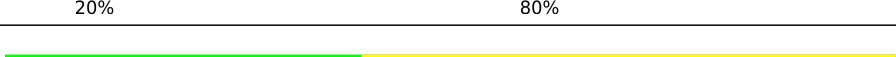
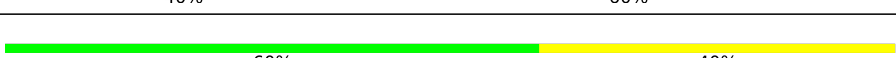
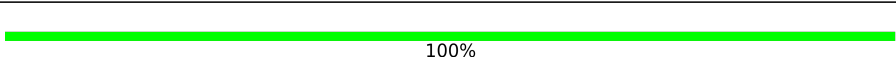
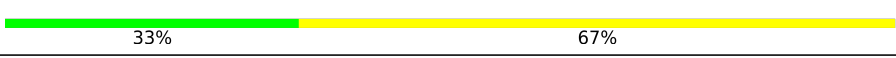
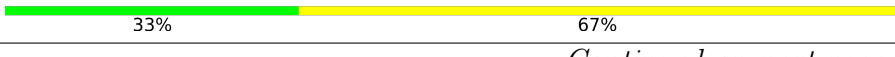

The reported resolution of this entry is 4.20 Å.

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1402	
1	B	1402	
1	C	1402	
2	D	5	
2	O	5	
2	b	5	
3	E	3	
3	F	3	
3	G	3	




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Mol	Chain	Length	Quality of chain
3	K	3	100%
3	Q	3	100%
3	T	3	33% 67%
3	V	3	33% 67%
3	X	3	33% 67%
3	d	3	100%
3	g	3	100%
3	h	3	67% 33%
3	j	3	100%
4	H	2	100%
4	I	2	50% 50%
4	J	2	50% 50%
4	L	2	100%
4	R	2	100%
4	U	2	100%
4	W	2	50% 50%
4	Y	2	100%
4	e	2	100%
4	i	2	50% 50%
5	M	3	100%
5	Z	3	33% 67%
6	N	4	50% 50%
6	a	4	100%
6	k	4	75% 25%
7	P	2	50% 50%

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Mol	Chain	Length	Quality of chain
7	S	2	 50%50%
7	c	2	 100%
7	f	2	 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 27988 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
1	A	1124	Total	C	N	O	S	0	0
			8648	5493	1442	1676	37		
1	C	1098	Total	C	N	O	S	0	0
			8440	5359	1407	1637	37		
1	B	1224	Total	C	N	O	S	0	0
			9398	5972	1556	1829	41		

There are 231 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1076	PRO	ILE	engineered mutation	UNP A0A1Y0DD46
A	1077	PRO	LEU	engineered mutation	UNP A0A1Y0DD46
A	1328	GLU	-	expression tag	UNP A0A1Y0DD46
A	1329	PHE	-	expression tag	UNP A0A1Y0DD46
A	1330	GLY	-	expression tag	UNP A0A1Y0DD46
A	1331	SER	-	expression tag	UNP A0A1Y0DD46
A	1332	GLY	-	expression tag	UNP A0A1Y0DD46
A	1333	GLY	-	expression tag	UNP A0A1Y0DD46
A	1334	TYR	-	expression tag	UNP A0A1Y0DD46
A	1335	ILE	-	expression tag	UNP A0A1Y0DD46
A	1336	PRO	-	expression tag	UNP A0A1Y0DD46
A	1337	GLU	-	expression tag	UNP A0A1Y0DD46
A	1338	ALA	-	expression tag	UNP A0A1Y0DD46
A	1339	PRO	-	expression tag	UNP A0A1Y0DD46
A	1340	ARG	-	expression tag	UNP A0A1Y0DD46
A	1341	ASP	-	expression tag	UNP A0A1Y0DD46
A	1342	GLY	-	expression tag	UNP A0A1Y0DD46
A	1343	GLN	-	expression tag	UNP A0A1Y0DD46
A	1344	ALA	-	expression tag	UNP A0A1Y0DD46
A	1345	TYR	-	expression tag	UNP A0A1Y0DD46
A	1346	VAL	-	expression tag	UNP A0A1Y0DD46
A	1347	ARG	-	expression tag	UNP A0A1Y0DD46
A	1348	LYS	-	expression tag	UNP A0A1Y0DD46
A	1349	ASP	-	expression tag	UNP A0A1Y0DD46

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1350	GLY	-	expression tag	UNP A0A1Y0DD46
A	1351	GLU	-	expression tag	UNP A0A1Y0DD46
A	1352	TRP	-	expression tag	UNP A0A1Y0DD46
A	1353	VAL	-	expression tag	UNP A0A1Y0DD46
A	1354	LEU	-	expression tag	UNP A0A1Y0DD46
A	1355	LEU	-	expression tag	UNP A0A1Y0DD46
A	1356	SER	-	expression tag	UNP A0A1Y0DD46
A	1357	THR	-	expression tag	UNP A0A1Y0DD46
A	1358	PHE	-	expression tag	UNP A0A1Y0DD46
A	1359	LEU	-	expression tag	UNP A0A1Y0DD46
A	1360	LYS	-	expression tag	UNP A0A1Y0DD46
A	1361	GLY	-	expression tag	UNP A0A1Y0DD46
A	1362	GLN	-	expression tag	UNP A0A1Y0DD46
A	1363	ASP	-	expression tag	UNP A0A1Y0DD46
A	1364	ASN	-	expression tag	UNP A0A1Y0DD46
A	1365	SER	-	expression tag	UNP A0A1Y0DD46
A	1366	ALA	-	expression tag	UNP A0A1Y0DD46
A	1367	ASP	-	expression tag	UNP A0A1Y0DD46
A	1368	ILE	-	expression tag	UNP A0A1Y0DD46
A	1369	GLN	-	expression tag	UNP A0A1Y0DD46
A	1370	HIS	-	expression tag	UNP A0A1Y0DD46
A	1371	SER	-	expression tag	UNP A0A1Y0DD46
A	1372	GLY	-	expression tag	UNP A0A1Y0DD46
A	1373	ARG	-	expression tag	UNP A0A1Y0DD46
A	1374	PRO	-	expression tag	UNP A0A1Y0DD46
A	1375	LEU	-	expression tag	UNP A0A1Y0DD46
A	1376	GLU	-	expression tag	UNP A0A1Y0DD46
A	1377	SER	-	expression tag	UNP A0A1Y0DD46
A	1378	ARG	-	expression tag	UNP A0A1Y0DD46
A	1379	GLY	-	expression tag	UNP A0A1Y0DD46
A	1380	PRO	-	expression tag	UNP A0A1Y0DD46
A	1381	PHE	-	expression tag	UNP A0A1Y0DD46
A	1382	GLU	-	expression tag	UNP A0A1Y0DD46
A	1383	GLN	-	expression tag	UNP A0A1Y0DD46
A	1384	LYS	-	expression tag	UNP A0A1Y0DD46
A	1385	LEU	-	expression tag	UNP A0A1Y0DD46
A	1386	ILE	-	expression tag	UNP A0A1Y0DD46
A	1387	SER	-	expression tag	UNP A0A1Y0DD46
A	1388	GLU	-	expression tag	UNP A0A1Y0DD46
A	1389	GLU	-	expression tag	UNP A0A1Y0DD46
A	1390	ASP	-	expression tag	UNP A0A1Y0DD46
A	1391	LEU	-	expression tag	UNP A0A1Y0DD46

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1392	ASN	-	expression tag	UNP A0A1Y0DD46
A	1393	MET	-	expression tag	UNP A0A1Y0DD46
A	1394	HIS	-	expression tag	UNP A0A1Y0DD46
A	1395	THR	-	expression tag	UNP A0A1Y0DD46
A	1396	GLY	-	expression tag	UNP A0A1Y0DD46
A	1397	HIS	-	expression tag	UNP A0A1Y0DD46
A	1398	HIS	-	expression tag	UNP A0A1Y0DD46
A	1399	HIS	-	expression tag	UNP A0A1Y0DD46
A	1400	HIS	-	expression tag	UNP A0A1Y0DD46
A	1401	HIS	-	expression tag	UNP A0A1Y0DD46
A	1402	HIS	-	expression tag	UNP A0A1Y0DD46
C	1076	PRO	ILE	conflict	UNP A0A1Y0DD46
C	1077	PRO	LEU	conflict	UNP A0A1Y0DD46
C	1328	GLU	-	expression tag	UNP A0A1Y0DD46
C	1329	PHE	-	expression tag	UNP A0A1Y0DD46
C	1330	GLY	-	expression tag	UNP A0A1Y0DD46
C	1331	SER	-	expression tag	UNP A0A1Y0DD46
C	1332	GLY	-	expression tag	UNP A0A1Y0DD46
C	1333	GLY	-	expression tag	UNP A0A1Y0DD46
C	1334	TYR	-	expression tag	UNP A0A1Y0DD46
C	1335	ILE	-	expression tag	UNP A0A1Y0DD46
C	1336	PRO	-	expression tag	UNP A0A1Y0DD46
C	1337	GLU	-	expression tag	UNP A0A1Y0DD46
C	1338	ALA	-	expression tag	UNP A0A1Y0DD46
C	1339	PRO	-	expression tag	UNP A0A1Y0DD46
C	1340	ARG	-	expression tag	UNP A0A1Y0DD46
C	1341	ASP	-	expression tag	UNP A0A1Y0DD46
C	1342	GLY	-	expression tag	UNP A0A1Y0DD46
C	1343	GLN	-	expression tag	UNP A0A1Y0DD46
C	1344	ALA	-	expression tag	UNP A0A1Y0DD46
C	1345	TYR	-	expression tag	UNP A0A1Y0DD46
C	1346	VAL	-	expression tag	UNP A0A1Y0DD46
C	1347	ARG	-	expression tag	UNP A0A1Y0DD46
C	1348	LYS	-	expression tag	UNP A0A1Y0DD46
C	1349	ASP	-	expression tag	UNP A0A1Y0DD46
C	1350	GLY	-	expression tag	UNP A0A1Y0DD46
C	1351	GLU	-	expression tag	UNP A0A1Y0DD46
C	1352	TRP	-	expression tag	UNP A0A1Y0DD46
C	1353	VAL	-	expression tag	UNP A0A1Y0DD46
C	1354	LEU	-	expression tag	UNP A0A1Y0DD46
C	1355	LEU	-	expression tag	UNP A0A1Y0DD46
C	1356	SER	-	expression tag	UNP A0A1Y0DD46

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1357	THR	-	expression tag	UNP A0A1Y0DD46
C	1358	PHE	-	expression tag	UNP A0A1Y0DD46
C	1359	LEU	-	expression tag	UNP A0A1Y0DD46
C	1360	LYS	-	expression tag	UNP A0A1Y0DD46
C	1361	GLY	-	expression tag	UNP A0A1Y0DD46
C	1362	GLN	-	expression tag	UNP A0A1Y0DD46
C	1363	ASP	-	expression tag	UNP A0A1Y0DD46
C	1364	ASN	-	expression tag	UNP A0A1Y0DD46
C	1365	SER	-	expression tag	UNP A0A1Y0DD46
C	1366	ALA	-	expression tag	UNP A0A1Y0DD46
C	1367	ASP	-	expression tag	UNP A0A1Y0DD46
C	1368	ILE	-	expression tag	UNP A0A1Y0DD46
C	1369	GLN	-	expression tag	UNP A0A1Y0DD46
C	1370	HIS	-	expression tag	UNP A0A1Y0DD46
C	1371	SER	-	expression tag	UNP A0A1Y0DD46
C	1372	GLY	-	expression tag	UNP A0A1Y0DD46
C	1373	ARG	-	expression tag	UNP A0A1Y0DD46
C	1374	PRO	-	expression tag	UNP A0A1Y0DD46
C	1375	LEU	-	expression tag	UNP A0A1Y0DD46
C	1376	GLU	-	expression tag	UNP A0A1Y0DD46
C	1377	SER	-	expression tag	UNP A0A1Y0DD46
C	1378	ARG	-	expression tag	UNP A0A1Y0DD46
C	1379	GLY	-	expression tag	UNP A0A1Y0DD46
C	1380	PRO	-	expression tag	UNP A0A1Y0DD46
C	1381	PHE	-	expression tag	UNP A0A1Y0DD46
C	1382	GLU	-	expression tag	UNP A0A1Y0DD46
C	1383	GLN	-	expression tag	UNP A0A1Y0DD46
C	1384	LYS	-	expression tag	UNP A0A1Y0DD46
C	1385	LEU	-	expression tag	UNP A0A1Y0DD46
C	1386	ILE	-	expression tag	UNP A0A1Y0DD46
C	1387	SER	-	expression tag	UNP A0A1Y0DD46
C	1388	GLU	-	expression tag	UNP A0A1Y0DD46
C	1389	GLU	-	expression tag	UNP A0A1Y0DD46
C	1390	ASP	-	expression tag	UNP A0A1Y0DD46
C	1391	LEU	-	expression tag	UNP A0A1Y0DD46
C	1392	ASN	-	expression tag	UNP A0A1Y0DD46
C	1393	MET	-	expression tag	UNP A0A1Y0DD46
C	1394	HIS	-	expression tag	UNP A0A1Y0DD46
C	1395	THR	-	expression tag	UNP A0A1Y0DD46
C	1396	GLY	-	expression tag	UNP A0A1Y0DD46
C	1397	HIS	-	expression tag	UNP A0A1Y0DD46
C	1398	HIS	-	expression tag	UNP A0A1Y0DD46

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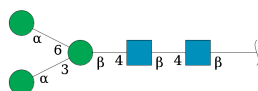
Chain	Residue	Modelled	Actual	Comment	Reference
C	1399	HIS	-	expression tag	UNP A0A1Y0DD46
C	1400	HIS	-	expression tag	UNP A0A1Y0DD46
C	1401	HIS	-	expression tag	UNP A0A1Y0DD46
C	1402	HIS	-	expression tag	UNP A0A1Y0DD46
B	1076	PRO	ILE	conflict	UNP A0A1Y0DD46
B	1077	PRO	LEU	conflict	UNP A0A1Y0DD46
B	1328	GLU	-	expression tag	UNP A0A1Y0DD46
B	1329	PHE	-	expression tag	UNP A0A1Y0DD46
B	1330	GLY	-	expression tag	UNP A0A1Y0DD46
B	1331	SER	-	expression tag	UNP A0A1Y0DD46
B	1332	GLY	-	expression tag	UNP A0A1Y0DD46
B	1333	GLY	-	expression tag	UNP A0A1Y0DD46
B	1334	TYR	-	expression tag	UNP A0A1Y0DD46
B	1335	ILE	-	expression tag	UNP A0A1Y0DD46
B	1336	PRO	-	expression tag	UNP A0A1Y0DD46
B	1337	GLU	-	expression tag	UNP A0A1Y0DD46
B	1338	ALA	-	expression tag	UNP A0A1Y0DD46
B	1339	PRO	-	expression tag	UNP A0A1Y0DD46
B	1340	ARG	-	expression tag	UNP A0A1Y0DD46
B	1341	ASP	-	expression tag	UNP A0A1Y0DD46
B	1342	GLY	-	expression tag	UNP A0A1Y0DD46
B	1343	GLN	-	expression tag	UNP A0A1Y0DD46
B	1344	ALA	-	expression tag	UNP A0A1Y0DD46
B	1345	TYR	-	expression tag	UNP A0A1Y0DD46
B	1346	VAL	-	expression tag	UNP A0A1Y0DD46
B	1347	ARG	-	expression tag	UNP A0A1Y0DD46
B	1348	LYS	-	expression tag	UNP A0A1Y0DD46
B	1349	ASP	-	expression tag	UNP A0A1Y0DD46
B	1350	GLY	-	expression tag	UNP A0A1Y0DD46
B	1351	GLU	-	expression tag	UNP A0A1Y0DD46
B	1352	TRP	-	expression tag	UNP A0A1Y0DD46
B	1353	VAL	-	expression tag	UNP A0A1Y0DD46
B	1354	LEU	-	expression tag	UNP A0A1Y0DD46
B	1355	LEU	-	expression tag	UNP A0A1Y0DD46
B	1356	SER	-	expression tag	UNP A0A1Y0DD46
B	1357	THR	-	expression tag	UNP A0A1Y0DD46
B	1358	PHE	-	expression tag	UNP A0A1Y0DD46
B	1359	LEU	-	expression tag	UNP A0A1Y0DD46
B	1360	LYS	-	expression tag	UNP A0A1Y0DD46
B	1361	GLY	-	expression tag	UNP A0A1Y0DD46
B	1362	GLN	-	expression tag	UNP A0A1Y0DD46
B	1363	ASP	-	expression tag	UNP A0A1Y0DD46

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1364	ASN	-	expression tag	UNP A0A1Y0DD46
B	1365	SER	-	expression tag	UNP A0A1Y0DD46
B	1366	ALA	-	expression tag	UNP A0A1Y0DD46
B	1367	ASP	-	expression tag	UNP A0A1Y0DD46
B	1368	ILE	-	expression tag	UNP A0A1Y0DD46
B	1369	GLN	-	expression tag	UNP A0A1Y0DD46
B	1370	HIS	-	expression tag	UNP A0A1Y0DD46
B	1371	SER	-	expression tag	UNP A0A1Y0DD46
B	1372	GLY	-	expression tag	UNP A0A1Y0DD46
B	1373	ARG	-	expression tag	UNP A0A1Y0DD46
B	1374	PRO	-	expression tag	UNP A0A1Y0DD46
B	1375	LEU	-	expression tag	UNP A0A1Y0DD46
B	1376	GLU	-	expression tag	UNP A0A1Y0DD46
B	1377	SER	-	expression tag	UNP A0A1Y0DD46
B	1378	ARG	-	expression tag	UNP A0A1Y0DD46
B	1379	GLY	-	expression tag	UNP A0A1Y0DD46
B	1380	PRO	-	expression tag	UNP A0A1Y0DD46
B	1381	PHE	-	expression tag	UNP A0A1Y0DD46
B	1382	GLU	-	expression tag	UNP A0A1Y0DD46
B	1383	GLN	-	expression tag	UNP A0A1Y0DD46
B	1384	LYS	-	expression tag	UNP A0A1Y0DD46
B	1385	LEU	-	expression tag	UNP A0A1Y0DD46
B	1386	ILE	-	expression tag	UNP A0A1Y0DD46
B	1387	SER	-	expression tag	UNP A0A1Y0DD46
B	1388	GLU	-	expression tag	UNP A0A1Y0DD46
B	1389	GLU	-	expression tag	UNP A0A1Y0DD46
B	1390	ASP	-	expression tag	UNP A0A1Y0DD46
B	1391	LEU	-	expression tag	UNP A0A1Y0DD46
B	1392	ASN	-	expression tag	UNP A0A1Y0DD46
B	1393	MET	-	expression tag	UNP A0A1Y0DD46
B	1394	HIS	-	expression tag	UNP A0A1Y0DD46
B	1395	THR	-	expression tag	UNP A0A1Y0DD46
B	1396	GLY	-	expression tag	UNP A0A1Y0DD46
B	1397	HIS	-	expression tag	UNP A0A1Y0DD46
B	1398	HIS	-	expression tag	UNP A0A1Y0DD46
B	1399	HIS	-	expression tag	UNP A0A1Y0DD46
B	1400	HIS	-	expression tag	UNP A0A1Y0DD46
B	1401	HIS	-	expression tag	UNP A0A1Y0DD46
B	1402	HIS	-	expression tag	UNP A0A1Y0DD46

- Molecule 2 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
2	D	5	Total	C	N	O	0	0
			61	34	2	25		
2	O	5	Total	C	N	O	0	0
			61	34	2	25		
2	b	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 3 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.



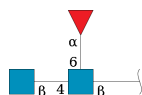
Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	3	Total	C	N	O	0	0
			39	22	2	15		
3	F	3	Total	C	N	O	0	0
			39	22	2	15		
3	G	3	Total	C	N	O	0	0
			39	22	2	15		
3	K	3	Total	C	N	O	0	0
			39	22	2	15		
3	Q	3	Total	C	N	O	0	0
			39	22	2	15		
3	T	3	Total	C	N	O	0	0
			39	22	2	15		
3	V	3	Total	C	N	O	0	0
			39	22	2	15		
3	X	3	Total	C	N	O	0	0
			39	22	2	15		
3	d	3	Total	C	N	O	0	0
			39	22	2	15		
3	g	3	Total	C	N	O	0	0
			39	22	2	15		
3	h	3	Total	C	N	O	0	0
			39	22	2	15		
3	j	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 4 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
4	H	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	J	2	Total	C	N	O	0	0
			28	16	2	10		
4	L	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		
4	W	2	Total	C	N	O	0	0
			28	16	2	10		
4	Y	2	Total	C	N	O	0	0
			28	16	2	10		
4	e	2	Total	C	N	O	0	0
			28	16	2	10		
4	i	2	Total	C	N	O	0	0
			28	16	2	10		

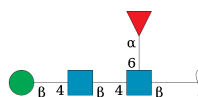
- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	3	Total	C	N	O	0	0
			38	22	2	14		
5	Z	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 6 is an oligosaccharide called 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.

ranose.



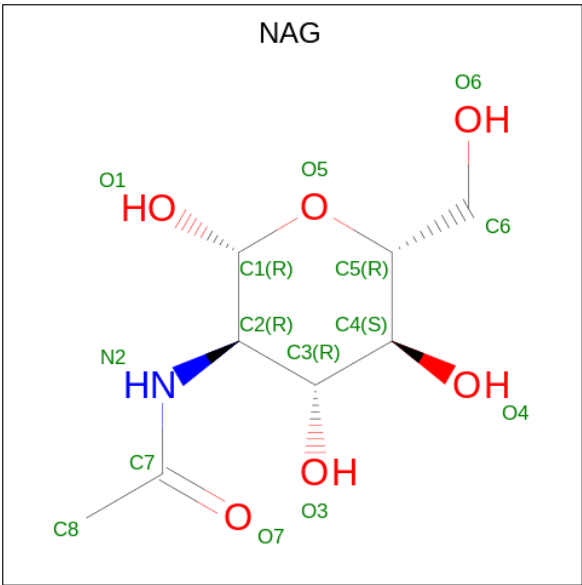
Mol	Chain	Residues	Atoms				AltConf	Trace
6	N	4	Total	C	N	O	0	0
			49	28	2	19		
6	a	4	Total	C	N	O	0	0
			49	28	2	19		
6	k	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 7 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
7	P	2	Total	C	N	O	0	0
			24	14	1	9		
7	S	2	Total	C	N	O	0	0
			24	14	1	9		
7	c	2	Total	C	N	O	0	0
			24	14	1	9		
7	f	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



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

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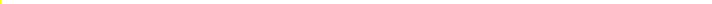
Mol	Chain	Residues	Atoms				AltConf
8	B	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 1: Spike glycoprotein

Chain B:  86% 13%

Position	Residue	Category	Annotation
1	LEU	Standard	
2	SER	Standard	
3	THR	Standard	
4	PHE	Standard	
5	LEU	Standard	
6	LEU	Standard	
7	LYS	Standard	
8	GLN	Standard	
9	ASP	Standard	
10	ASN	Standard	
11	ALA	Standard	
12	ASP	Standard	
13	ILE	Standard	
14	GLN	Standard	
15	HIS	Standard	
16	SER	Standard	
17	GLY	Standard	
18	ARG	Standard	
19	PRO	Standard	
20	LEU	Standard	
21	LEU	Standard	
22	GLU	Standard	
23	THR	Standard	
24	GLU	Standard	
25	GLY	Standard	
26	ASP	Standard	
27	GLY	Standard	
28	ILE	Standard	
29	THR	Standard	
30	HIS	Standard	
31	HIS	Standard	
32	HIS	Standard	
33	HIS	Standard	
34	HIS	Standard	
35	HIS	Standard	
36	ASP	Standard	
37	GLY	Standard	
38	GLU	Standard	
39	TRP	Standard	
40	VAL	Standard	
41	LEU	Standard	
42	LEU	Standard	
43	THR	Standard	
44	ASP	Standard	
45	GLN	Standard	
46	ASP	Standard	
47	VAL	Standard	
48	THR	Standard	
49	SER	Standard	
50	LEU	Standard	
51	PRO	Standard	
52	LEU	Standard	
53	SER	Standard	
54	LEU	Standard	
55	VAL	Standard	
56	PRO	Standard	
57	LEU	Standard	
58	PHE	Standard	
59	THR	Standard	
60	THR	Standard	
61	THR	Standard	
62	LYS	Standard	
63	ALA	Standard	
64	SER	Standard	
65	CYS	Standard	
66	ARG	Standard	
67	THR	Standard	
68	VAL	Standard	
69	LEU	Standard	
70	ASP	Standard	
71	ILE	Standard	
72	LYS	Standard	
73	TRP	Standard	
74	PRO	Standard	
75	SER	Standard	
76	GLU	Standard	
77	GLU	Standard	
78	ASP	Standard	
79	LEU	Standard	
80	LEU	Standard	
81	ASN	Standard	
82	GLY	Standard	
83	MET	Standard	
84	ASN	Standard	
85	GLY	Standard	
86	GLY	Standard	
87	THR	Standard	
88	THR	Standard	
89	ALA	Standard	
90	ASN	Standard	
91	PHE	Standard	
92	VAL	Standard	
93	ASP	Standard	
94	ASP	Standard	
95	LEU	Standard	
96	LEU	Standard	
97	ASP	Standard	
98	VAL	Standard	
99	ASN	Standard	
100	Tyr	Standard	
101	ILE	Standard	
102	ALA	Standard	
103	THR	Standard	
104	THR	Standard	
105	LEU	Standard	
106	ASN	Standard	
107	PRO	Standard	
108	ALA	Standard	
109	LEU	Standard	
110	LEU	Standard	
111	PRO	Standard	
112	THR	Standard	
113	THR	Standard	
114	GLY	Standard	
115	PRO	Standard	
116	LYS	Standard	
117	THR	Standard	
118	ARG	Standard	
119	ASN	Standard	
120	PRO	Standard	
121	THR	Standard	
122	ALA	Standard	
123	ASN	Standard	
124	PHE	Standard	
125	VAL	Standard	
126	ASP	Standard	
127	ASP	Standard	
128	PRO	Standard	
129	LEU	Standard	
130	LEU	Standard	
131	LEU	Standard	
132	THR	Standard	
133	VAL	Standard	
134	VAL	Standard	
135	ASP	Standard	
136	ASP	Standard	
137	PRO	Standard	
138	SER	Standard	
139	SER	Standard	
140	LEU	Standard	
141	LEU	Standard	
142	PRO	Standard	
143	PRO	Standard	
144	LEU	Standard	
145	LEU	Standard	

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

Chain D:  20% 80%

Category	Percentage
MAG1	0%
MAG2	20%
BMA3	0%
MAN4	0%
MAN5	80%

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

Chain O: 

Category	Percentage
MAN1	40%
MAN2	0%
MAN3	0%
MAN4	60%
MAN5	0%

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

Chain E:  100%

MAG1
MAG2
BMA3

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

Chain F:  33% 67%

MAG1
MAG2
BMA3

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

Chain G:  33% 67%

MAG1
MAG2
BMA3

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

Chain K:  100%

MAG1
MAG2
BMA3

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

Chain Q:  100%

MAG1
MAG2
BMA3

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

Chain T:  33% 67%

MAG1
MAG2
BMA3

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

Chain V:  33% 67%



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

Chain X:



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

Chain d:



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

Chain g:



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

Chain h:



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

Chain j:



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

Chain H:



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

Chain I:  50% 50%

MAG1
MAG2

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

Chain J:  50% 50%

MAG1
MAG2

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

Chain L:  100%

MAG1
MAG2

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

Chain R:  100%

MAG1
MAG2

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

Chain U:  100%

MAG1
MAG2

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

Chain W:  50% 50%

MAG1
MAG2

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

Chain Y:  100%

MAG1
MAG2

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

Chain e:  100%

MAG1
MAG2

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

Chain i:  50% 50%

MAG1
MAG2

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

Chain M:  100%

MAG1
MAG2
FUC3

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

Chain Z:  33% 67%

MAG1
MAG2
FUC3

- Molecule 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

Chain N:  50% 50%

MAG1
MAG2
BMA3
FUC4

- Molecule 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

Chain a:  100%

MAG1
MAG2
BMA3
FUC4

- Molecule 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

Chain k:  75% 25%

MAG1
MAG2
BMA3
FUC4

- Molecule 7: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  50% 50%

MAG1
FUC2

- Molecule 7: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:  50% 50%

MAG1
FUC2

- Molecule 7: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:  100%

MAG1
FUC2

- Molecule 7: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:  100%

MAG1
FUC2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51124	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 ($e^-/\text{\AA}^2$)	55.4	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.810	Depositor
Minimum map value	-0.175	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	385.83997, 385.83997, 385.83997	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/8838	0.58	0/12039
1	B	0.44	0/9610	0.58	0/13097
1	C	0.45	0/8626	0.59	0/11756
All	All	0.44	0/27074	0.58	0/36892

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1116/1402 (80%)	1005 (90%)	109 (10%)	2 (0%)	44	77
1	B	1222/1402 (87%)	1112 (91%)	103 (8%)	7 (1%)	22	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	1094/1402 (78%)	985 (90%)	103 (9%)	6 (0%)	25	62
All	All	3432/4206 (82%)	3102 (90%)	315 (9%)	15 (0%)	32	67

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	369	VAL
1	C	689	VAL
1	A	142	VAL
1	C	142	VAL
1	B	129	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	962/1209 (80%)	957 (100%)	5 (0%)	86	90
1	B	1049/1209 (87%)	1034 (99%)	15 (1%)	62	75
1	C	938/1209 (78%)	931 (99%)	7 (1%)	81	86
All	All	2949/3627 (81%)	2922 (99%)	27 (1%)	74	83

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

Mol	Chain	Res	Type
1	B	130	SER
1	B	134	LEU
1	B	818	ARG
1	B	133	THR
1	B	137	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1095	ASN
1	B	1116	GLN
1	B	114	ASN
1	B	979	GLN
1	C	1120	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

97 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	2,1	14,14,15	0.41	0	17,19,21	1.30	2 (11%)
2	NAG	D	2	2	14,14,15	0.24	0	17,19,21	0.44	0
2	BMA	D	3	2	11,11,12	0.87	1 (9%)	15,15,17	1.30	2 (13%)
2	MAN	D	4	2	11,11,12	0.81	0	15,15,17	0.98	1 (6%)
2	MAN	D	5	2	11,11,12	0.60	0	15,15,17	1.01	2 (13%)
3	NAG	E	1	1,3	14,14,15	0.41	0	17,19,21	0.71	0
3	NAG	E	2	3	14,14,15	0.20	0	17,19,21	0.58	0
3	BMA	E	3	3	11,11,12	0.59	0	15,15,17	0.82	0
3	NAG	F	1	1,3	14,14,15	0.56	0	17,19,21	1.35	2 (11%)
3	NAG	F	2	3	14,14,15	0.15	0	17,19,21	0.43	0
3	BMA	F	3	3	11,11,12	0.87	0	15,15,17	1.48	1 (6%)
3	NAG	G	1	3	14,14,15	0.85	1 (7%)	17,19,21	0.68	0
3	NAG	G	2	3	14,14,15	0.43	0	17,19,21	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BMA	G	3	3	11,11,12	0.68	0	15,15,17	0.85	1 (6%)
4	NAG	H	1	4,1	14,14,15	1.47	1 (7%)	17,19,21	1.18	1 (5%)
4	NAG	H	2	4	14,14,15	0.62	0	17,19,21	0.89	1 (5%)
4	NAG	I	1	4,1	14,14,15	0.95	1 (7%)	17,19,21	1.58	2 (11%)
4	NAG	I	2	4	14,14,15	0.21	0	17,19,21	0.40	0
4	NAG	J	1	4,1	14,14,15	0.31	0	17,19,21	0.47	0
4	NAG	J	2	4	14,14,15	0.47	0	17,19,21	0.71	1 (5%)
3	NAG	K	1	1,3	14,14,15	0.81	1 (7%)	17,19,21	0.58	0
3	NAG	K	2	3	14,14,15	0.39	0	17,19,21	1.36	2 (11%)
3	BMA	K	3	3	11,11,12	0.69	0	15,15,17	0.93	1 (6%)
4	NAG	L	1	4,1	14,14,15	0.26	0	17,19,21	0.53	0
4	NAG	L	2	4	14,14,15	0.20	0	17,19,21	0.43	0
5	NAG	M	1	1,5	14,14,15	1.42	1 (7%)	17,19,21	1.01	1 (5%)
5	NAG	M	2	5	14,14,15	0.48	0	17,19,21	1.30	2 (11%)
5	FUC	M	3	5	10,10,11	0.96	0	14,14,16	1.28	2 (14%)
6	NAG	N	1	6,1	14,14,15	0.29	0	17,19,21	0.90	1 (5%)
6	NAG	N	2	6	14,14,15	0.23	0	17,19,21	0.45	0
6	BMA	N	3	6	11,11,12	0.53	0	15,15,17	0.82	0
6	FUC	N	4	6	10,10,11	0.48	0	14,14,16	0.87	1 (7%)
2	NAG	O	1	2,1	14,14,15	0.29	0	17,19,21	0.43	0
2	NAG	O	2	2	14,14,15	0.15	0	17,19,21	0.45	0
2	BMA	O	3	2	11,11,12	0.66	0	15,15,17	0.77	1 (6%)
2	MAN	O	4	2	11,11,12	0.75	1 (9%)	15,15,17	0.96	1 (6%)
2	MAN	O	5	2	11,11,12	0.66	0	15,15,17	0.99	1 (6%)
7	NAG	P	1	7,1	14,14,15	0.19	0	17,19,21	0.46	0
7	FUC	P	2	7	10,10,11	0.77	0	14,14,16	0.87	1 (7%)
3	NAG	Q	1	1,3	14,14,15	0.52	0	17,19,21	0.38	0
3	NAG	Q	2	3	14,14,15	0.17	0	17,19,21	0.54	0
3	BMA	Q	3	3	11,11,12	0.64	0	15,15,17	0.84	0
4	NAG	R	1	4,1	14,14,15	0.38	0	17,19,21	0.50	0
4	NAG	R	2	4	14,14,15	0.26	0	17,19,21	0.40	0
7	NAG	S	1	7,1	14,14,15	0.62	0	17,19,21	0.82	1 (5%)
7	FUC	S	2	7	10,10,11	0.57	0	14,14,16	0.81	0
3	NAG	T	1	1,3	14,14,15	1.50	1 (7%)	17,19,21	0.98	1 (5%)
3	NAG	T	2	3	14,14,15	0.27	0	17,19,21	0.48	0
3	BMA	T	3	3	11,11,12	0.52	0	15,15,17	0.89	1 (6%)
4	NAG	U	1	4,1	14,14,15	0.27	0	17,19,21	1.33	1 (5%)
4	NAG	U	2	4	14,14,15	0.60	0	17,19,21	0.95	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	V	1	1,3	14,14,15	1.44	1 (7%)	17,19,21	1.43	2 (11%)
3	NAG	V	2	3	14,14,15	0.28	0	17,19,21	0.77	1 (5%)
3	BMA	V	3	3	11,11,12	0.72	0	15,15,17	0.72	0
4	NAG	W	1	4,1	14,14,15	0.60	1 (7%)	17,19,21	0.73	0
4	NAG	W	2	4	14,14,15	0.25	0	17,19,21	0.44	0
3	NAG	X	1	1,3	14,14,15	0.40	0	17,19,21	0.80	1 (5%)
3	NAG	X	2	3	14,14,15	0.31	0	17,19,21	0.38	0
3	BMA	X	3	3	11,11,12	0.86	0	15,15,17	0.99	1 (6%)
4	NAG	Y	1	4,1	14,14,15	0.73	1 (7%)	17,19,21	1.29	1 (5%)
4	NAG	Y	2	4	14,14,15	0.45	0	17,19,21	1.18	1 (5%)
5	NAG	Z	1	1,5	14,14,15	0.31	0	17,19,21	0.83	1 (5%)
5	NAG	Z	2	5	14,14,15	0.28	0	17,19,21	0.36	0
5	FUC	Z	3	5	10,10,11	0.49	0	14,14,16	0.92	1 (7%)
6	NAG	a	1	6,1	14,14,15	0.63	0	17,19,21	0.67	0
6	NAG	a	2	6	14,14,15	0.23	0	17,19,21	0.48	0
6	BMA	a	3	6	11,11,12	0.52	0	15,15,17	0.73	0
6	FUC	a	4	6	10,10,11	0.53	0	14,14,16	0.76	0
2	NAG	b	1	2,1	14,14,15	0.19	0	17,19,21	0.37	0
2	NAG	b	2	2	14,14,15	0.22	0	17,19,21	0.46	0
2	BMA	b	3	2	11,11,12	0.67	0	15,15,17	0.95	0
2	MAN	b	4	2	11,11,12	0.86	1 (9%)	15,15,17	1.01	1 (6%)
2	MAN	b	5	2	11,11,12	0.61	0	15,15,17	1.04	2 (13%)
7	NAG	c	1	7,1	14,14,15	0.28	0	17,19,21	0.33	0
7	FUC	c	2	7	10,10,11	0.65	0	14,14,16	0.97	0
3	NAG	d	1	1,3	14,14,15	0.44	0	17,19,21	0.39	0
3	NAG	d	2	3	14,14,15	0.18	0	17,19,21	0.48	0
3	BMA	d	3	3	11,11,12	0.58	0	15,15,17	0.97	0
4	NAG	e	1	4,1	14,14,15	0.42	0	17,19,21	0.57	0
4	NAG	e	2	4	14,14,15	0.20	0	17,19,21	0.43	0
7	NAG	f	1	7,1	14,14,15	0.16	0	17,19,21	0.51	0
7	FUC	f	2	7	10,10,11	0.78	0	14,14,16	0.77	0
3	NAG	g	1	1,3	14,14,15	0.31	0	17,19,21	0.52	0
3	NAG	g	2	3	14,14,15	0.18	0	17,19,21	0.37	0
3	BMA	g	3	3	11,11,12	0.52	0	15,15,17	0.84	0
3	NAG	h	1	1,3	14,14,15	0.82	1 (7%)	17,19,21	0.59	0
3	NAG	h	2	3	14,14,15	0.29	0	17,19,21	0.50	0
3	BMA	h	3	3	11,11,12	0.57	0	15,15,17	0.76	0
4	NAG	i	1	4,1	14,14,15	0.65	0	17,19,21	1.24	1 (5%)
4	NAG	i	2	4	14,14,15	0.21	0	17,19,21	0.36	0
3	NAG	j	1	1,3	14,14,15	0.59	1 (7%)	17,19,21	1.22	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	j	2	3	14,14,15	0.31	0	17,19,21	1.25	1 (5%)
3	BMA	j	3	3	11,11,12	1.36	2 (18%)	15,15,17	1.03	1 (6%)
6	NAG	k	1	6,1	14,14,15	0.69	1 (7%)	17,19,21	1.10	1 (5%)
6	NAG	k	2	6	14,14,15	0.29	0	17,19,21	0.49	0
6	BMA	k	3	6	11,11,12	0.60	0	15,15,17	0.67	0
6	FUC	k	4	6	10,10,11	0.59	0	14,14,16	0.89	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
2	NAG	D	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1
2	MAN	D	5	2	-	2/2/19/22	0/1/1/1
3	NAG	E	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	F	2	3	-	4/6/23/26	0/1/1/1
3	BMA	F	3	3	-	2/2/19/22	0/1/1/1
3	NAG	G	1	3	-	4/6/23/26	0/1/1/1
3	NAG	G	2	3	-	1/6/23/26	0/1/1/1
3	BMA	G	3	3	-	2/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	5/6/23/26	0/1/1/1
4	NAG	I	2	4	-	1/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	3/6/23/26	0/1/1/1
3	NAG	K	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	K	2	3	-	5/6/23/26	0/1/1/1
3	BMA	K	3	3	-	0/2/19/22	0/1/1/1
4	NAG	L	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	L	2	4	-	4/6/23/26	0/1/1/1

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

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

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	1	NAG	O5-C1	-5.33	1.35	1.43
3	V	1	NAG	O5-C1	-5.29	1.35	1.43
5	M	1	NAG	O5-C1	-5.17	1.35	1.43
4	H	1	NAG	O5-C1	-4.98	1.35	1.43
3	j	3	BMA	C1-C2	3.39	1.59	1.52

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	i	1	NAG	C1-O5-C5	4.53	118.32	112.19
3	F	1	NAG	C2-N2-C7	4.42	129.20	122.90
4	U	1	NAG	C2-N2-C7	4.39	129.16	122.90
3	F	3	BMA	C1-O5-C5	4.38	118.13	112.19
3	j	2	NAG	C2-N2-C7	4.25	128.96	122.90

There are no chirality outliers.

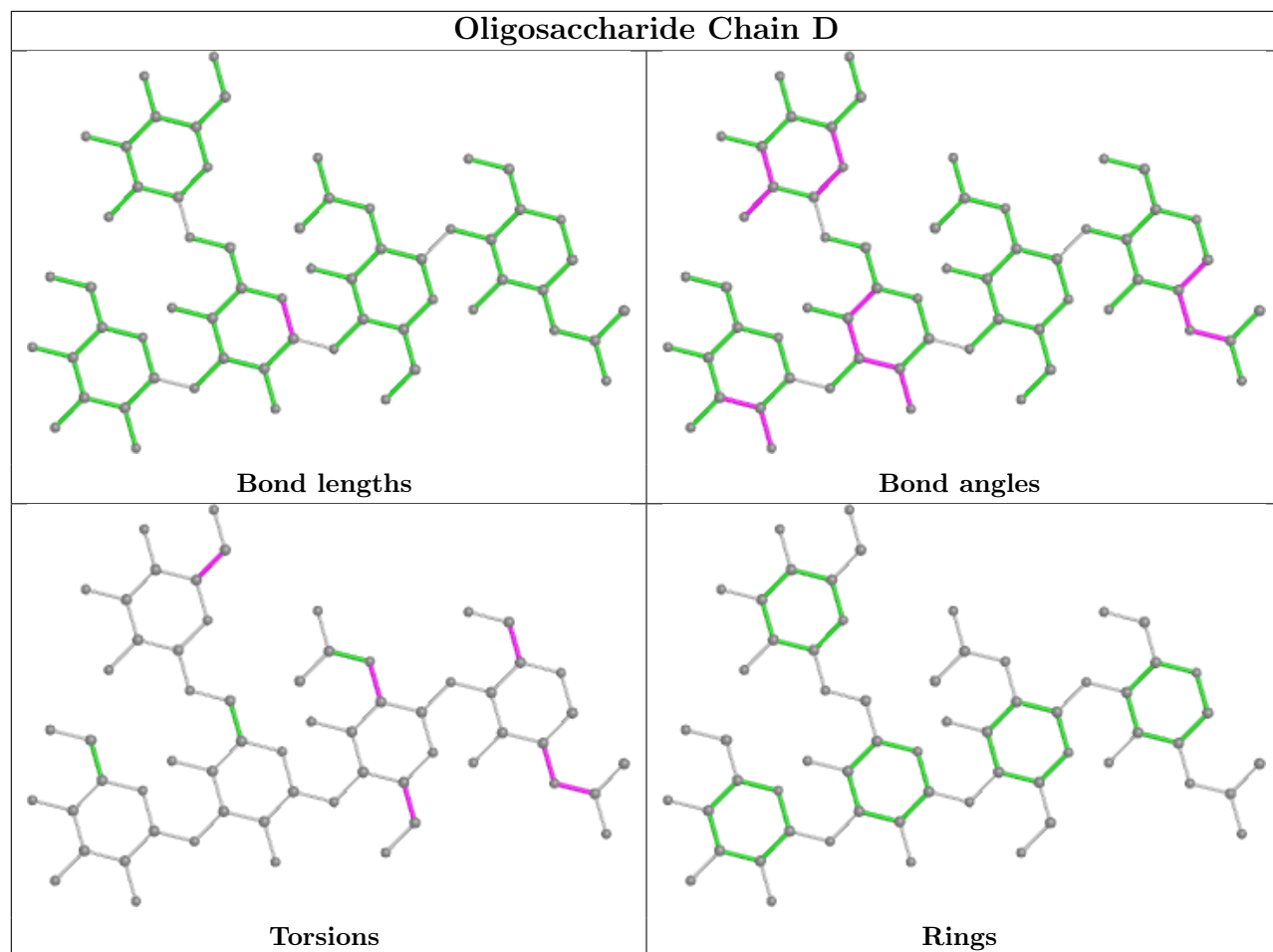
5 of 187 torsion outliers are listed below:

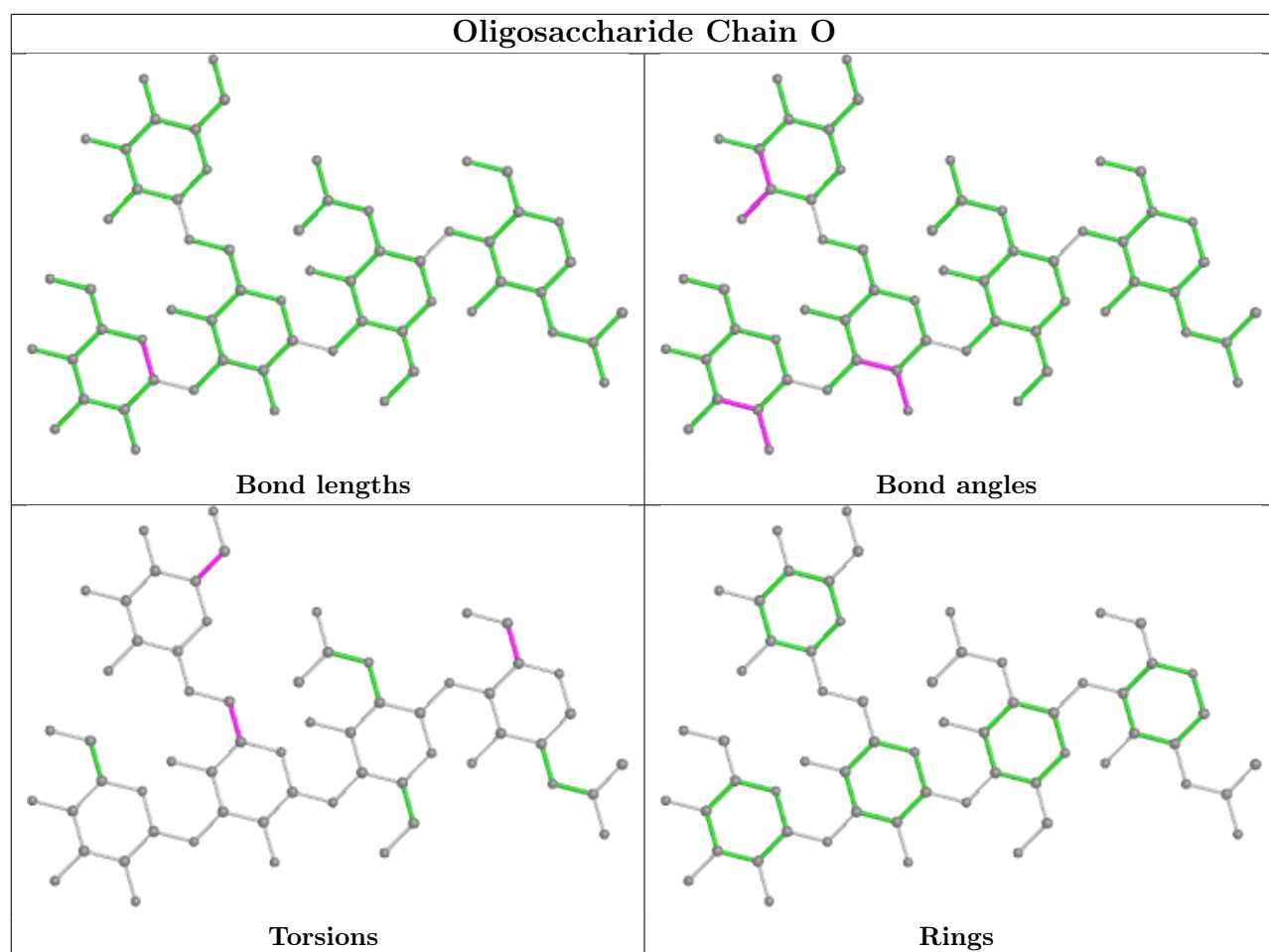
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C4-C5-C6-O6
4	U	1	NAG	C4-C5-C6-O6
7	c	1	NAG	C4-C5-C6-O6
2	O	5	MAN	O5-C5-C6-O6
3	X	1	NAG	O5-C5-C6-O6

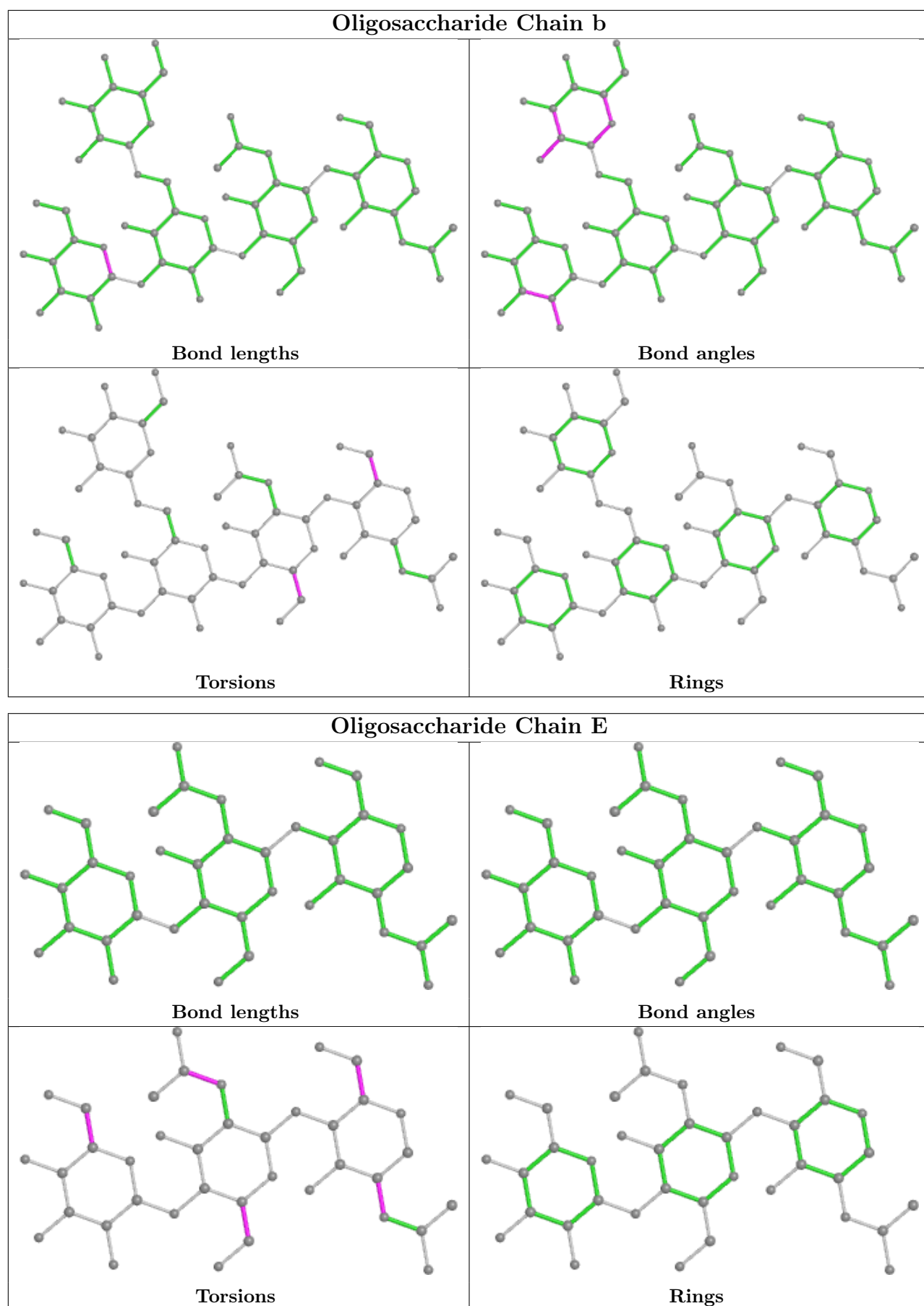
There are no ring outliers.

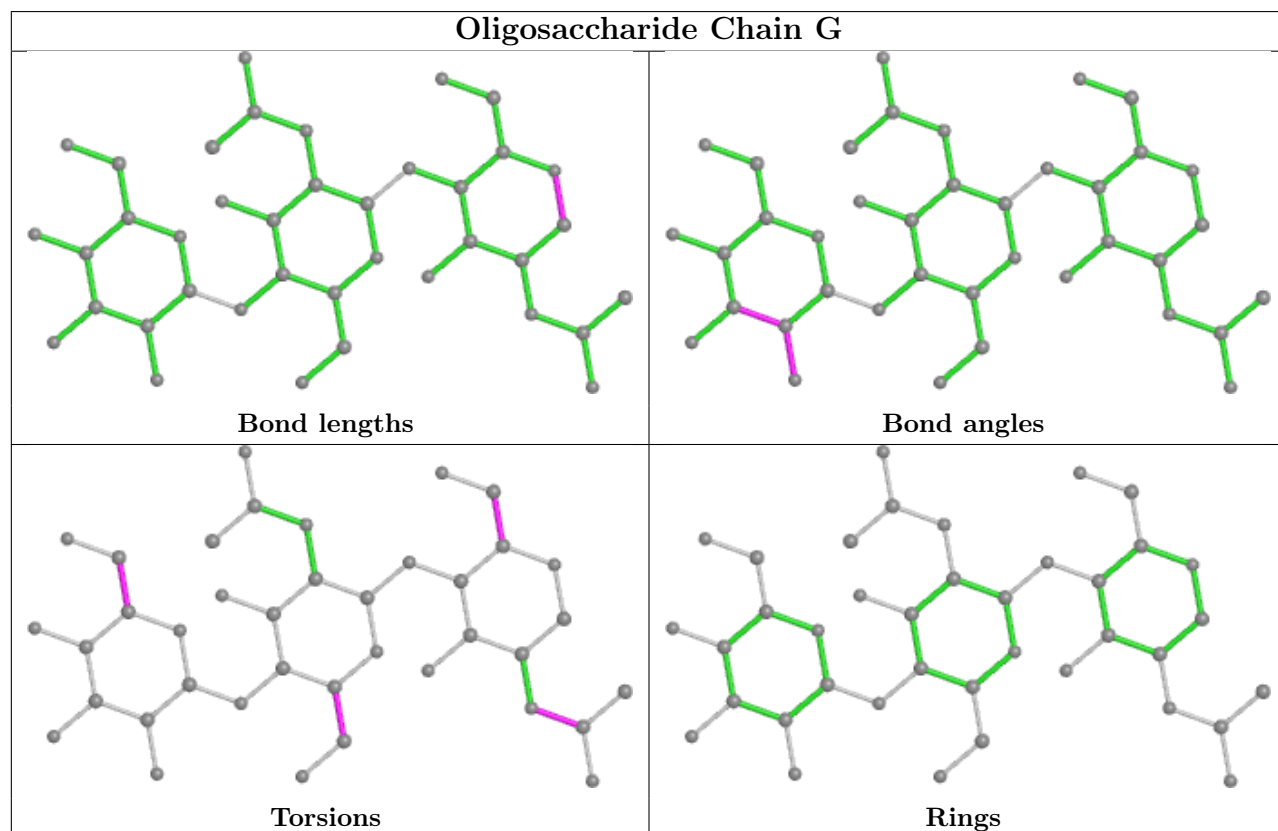
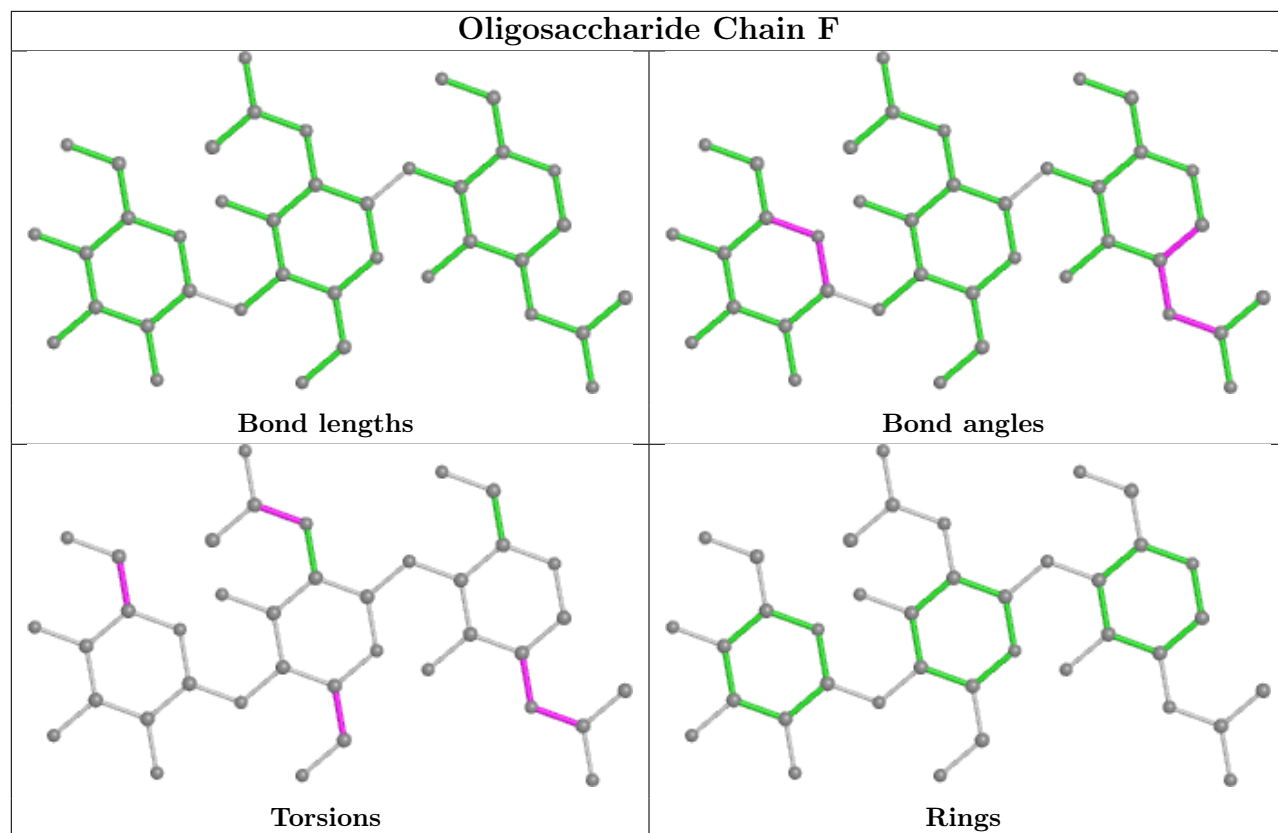
No monomer is involved in short contacts.

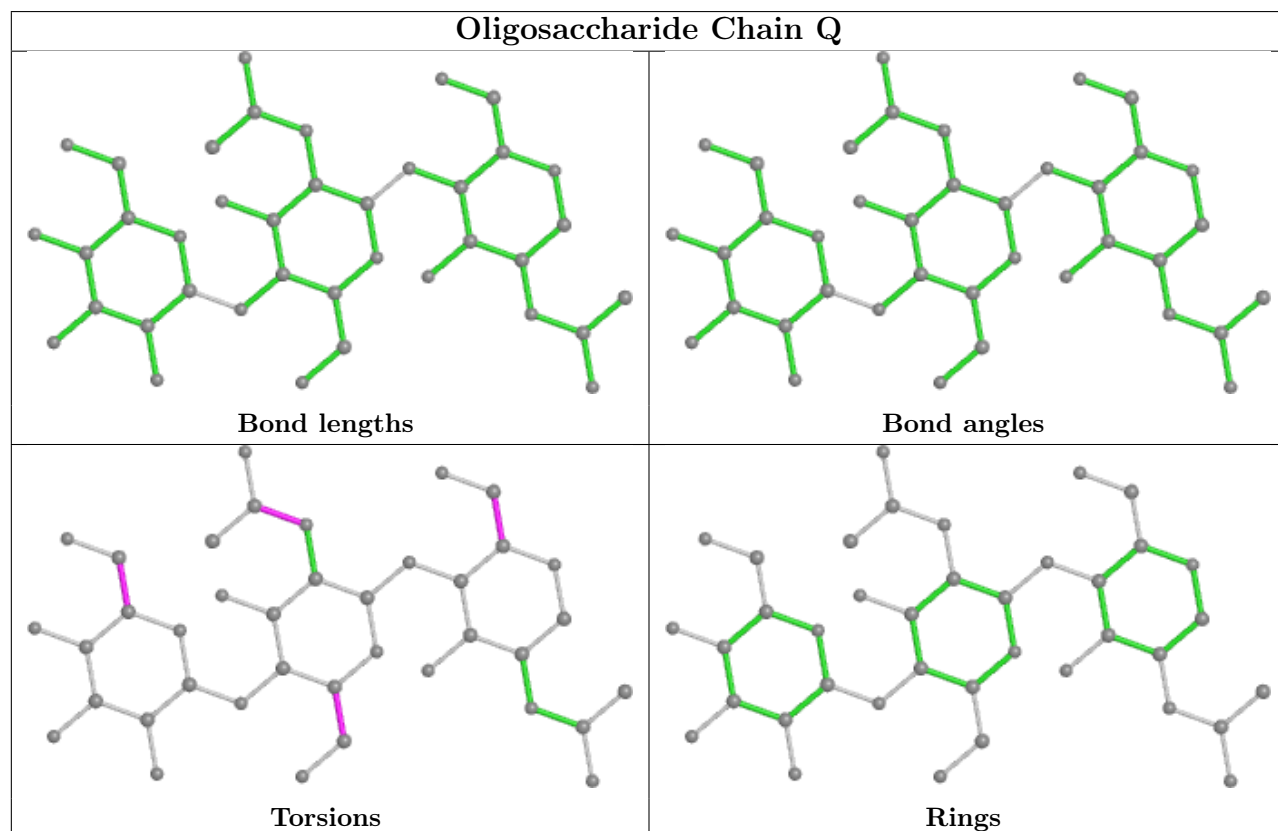
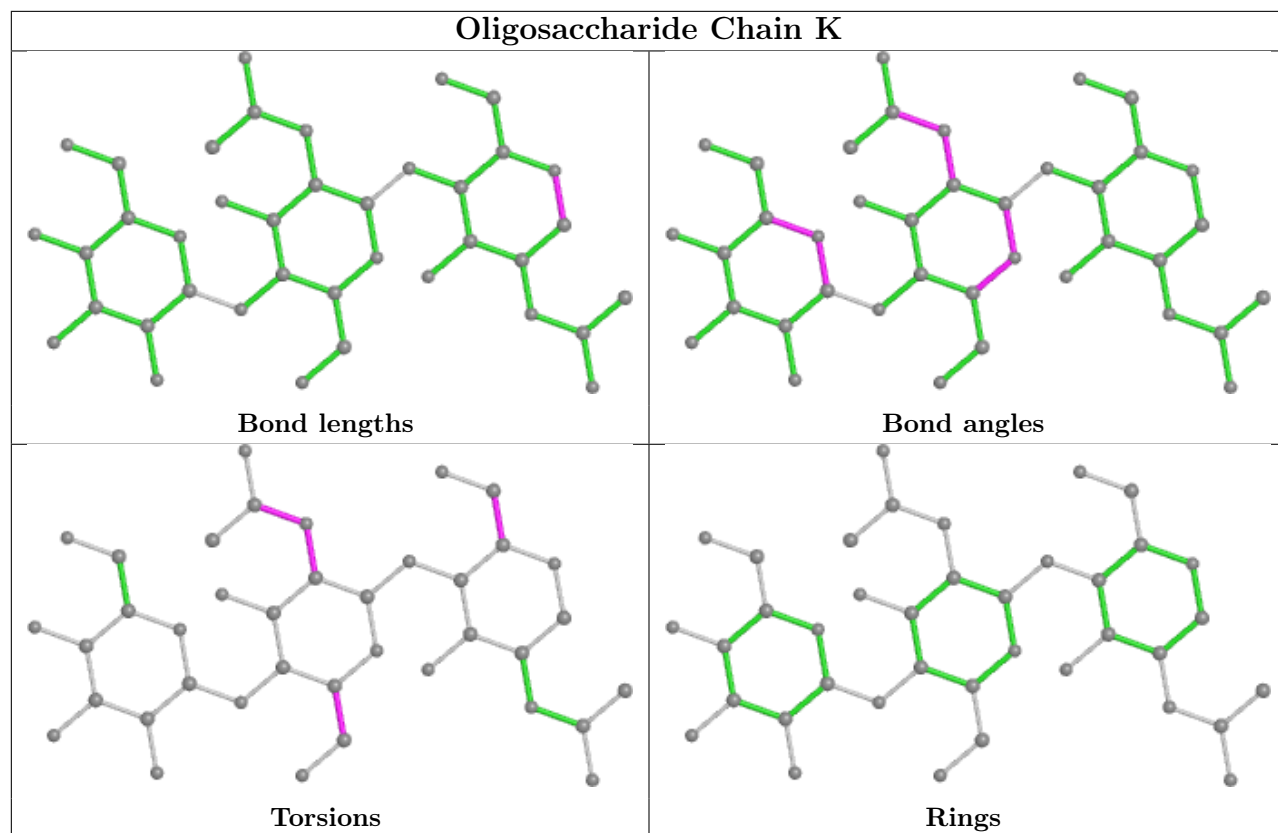
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

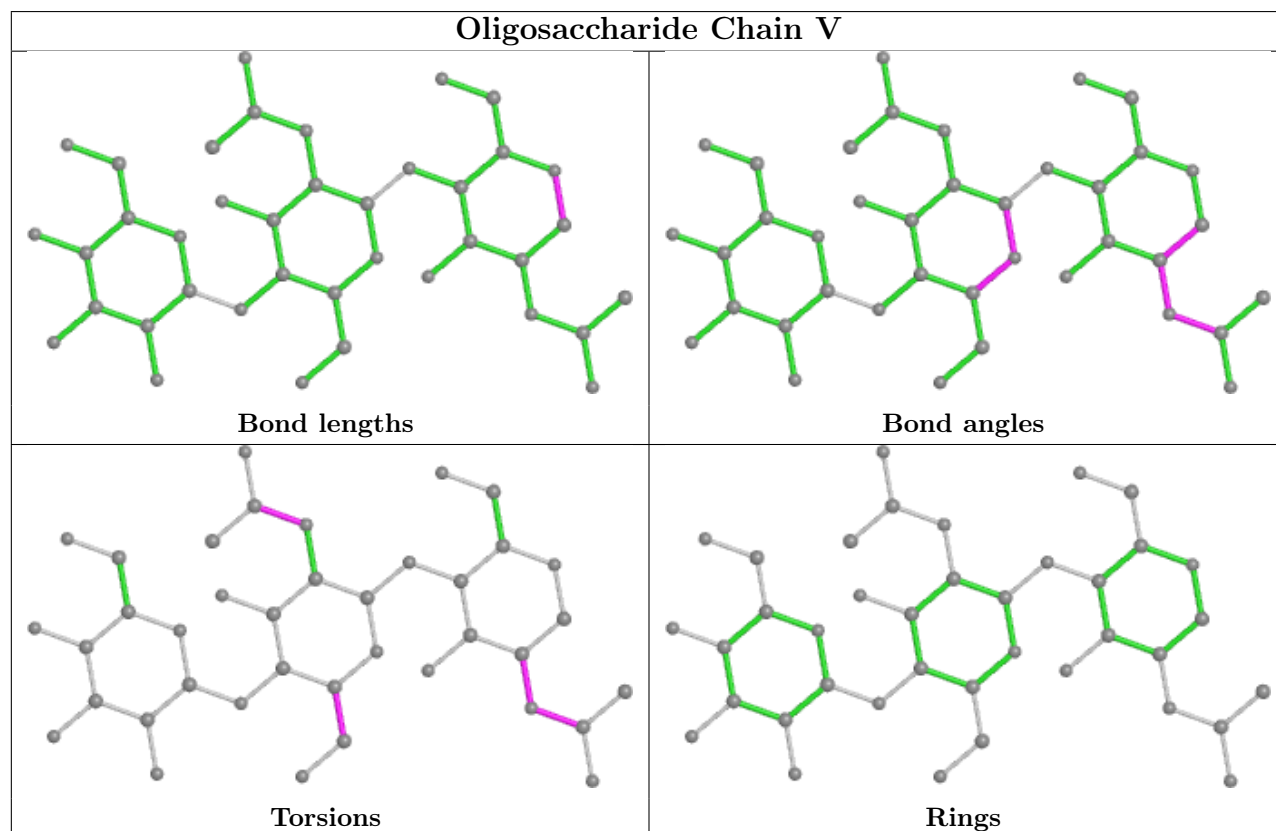
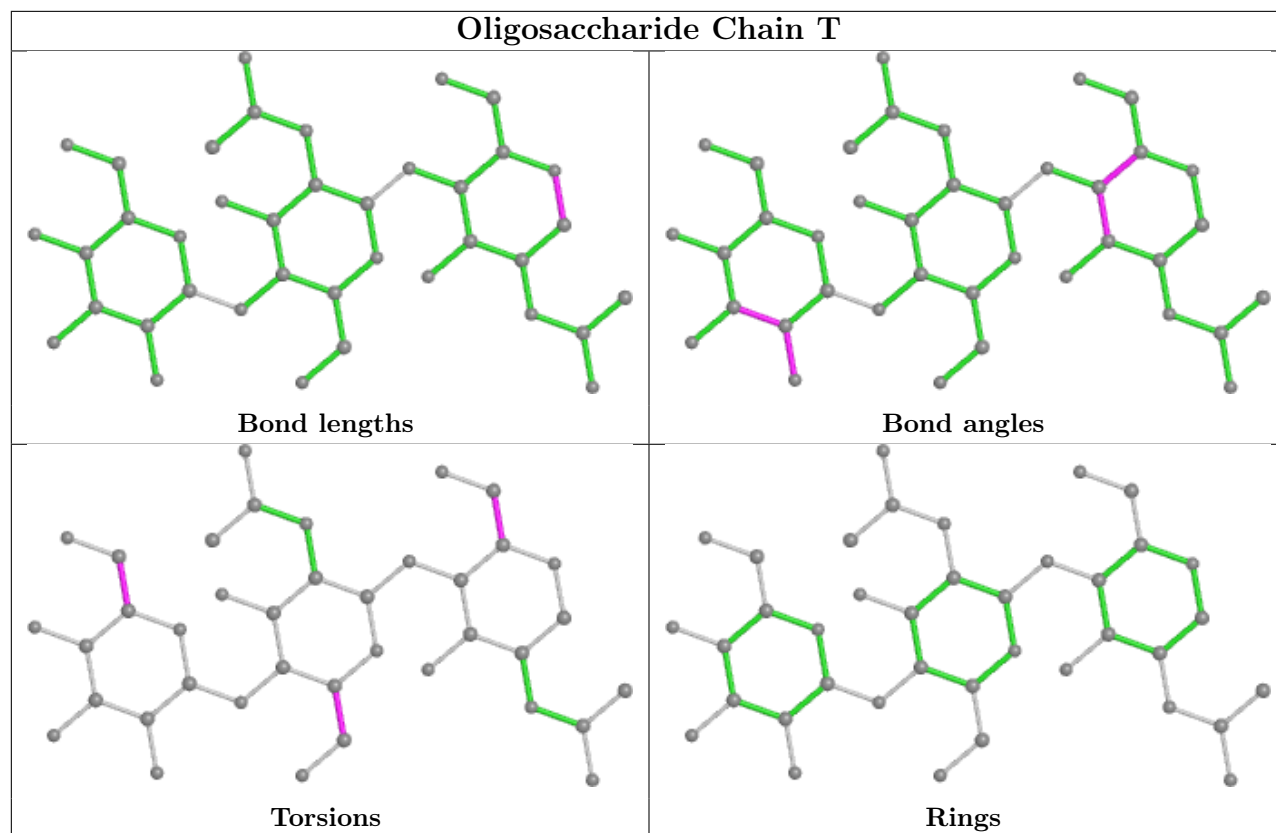


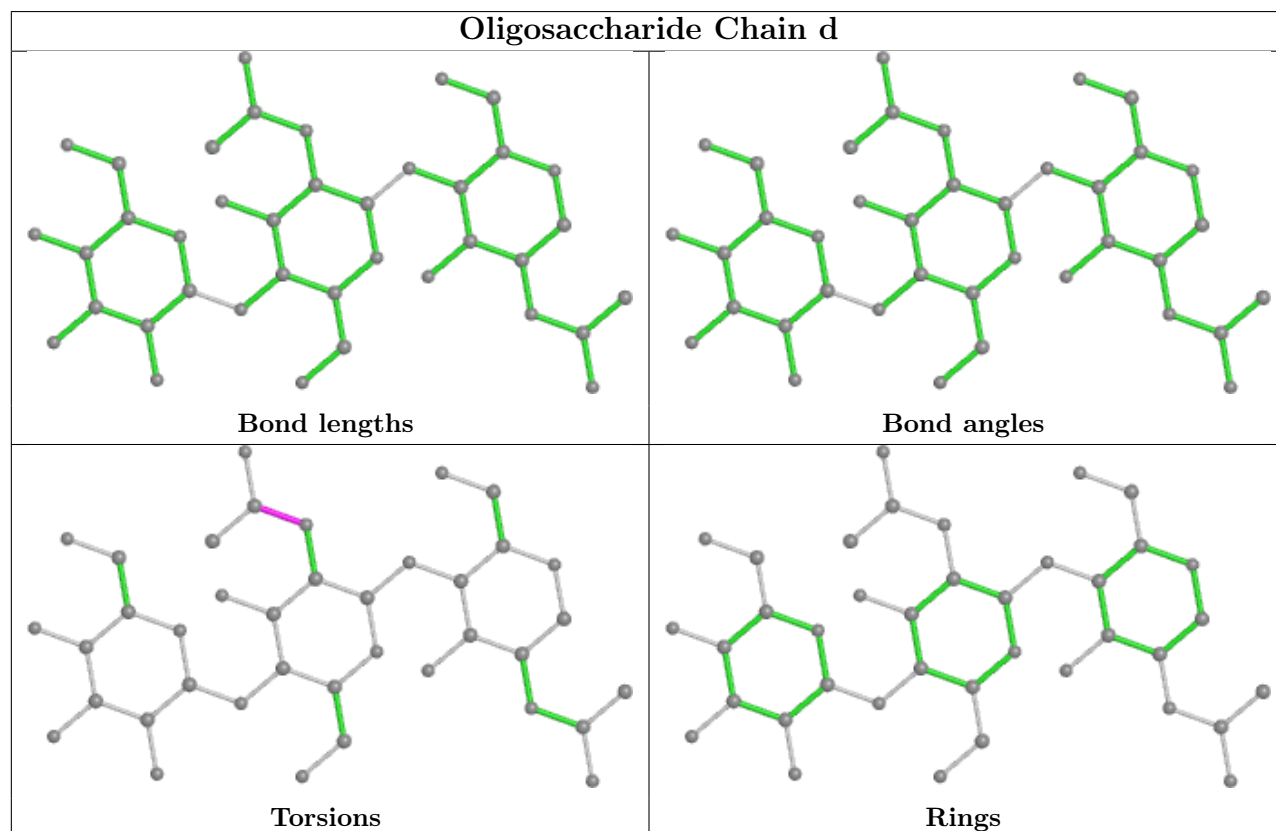
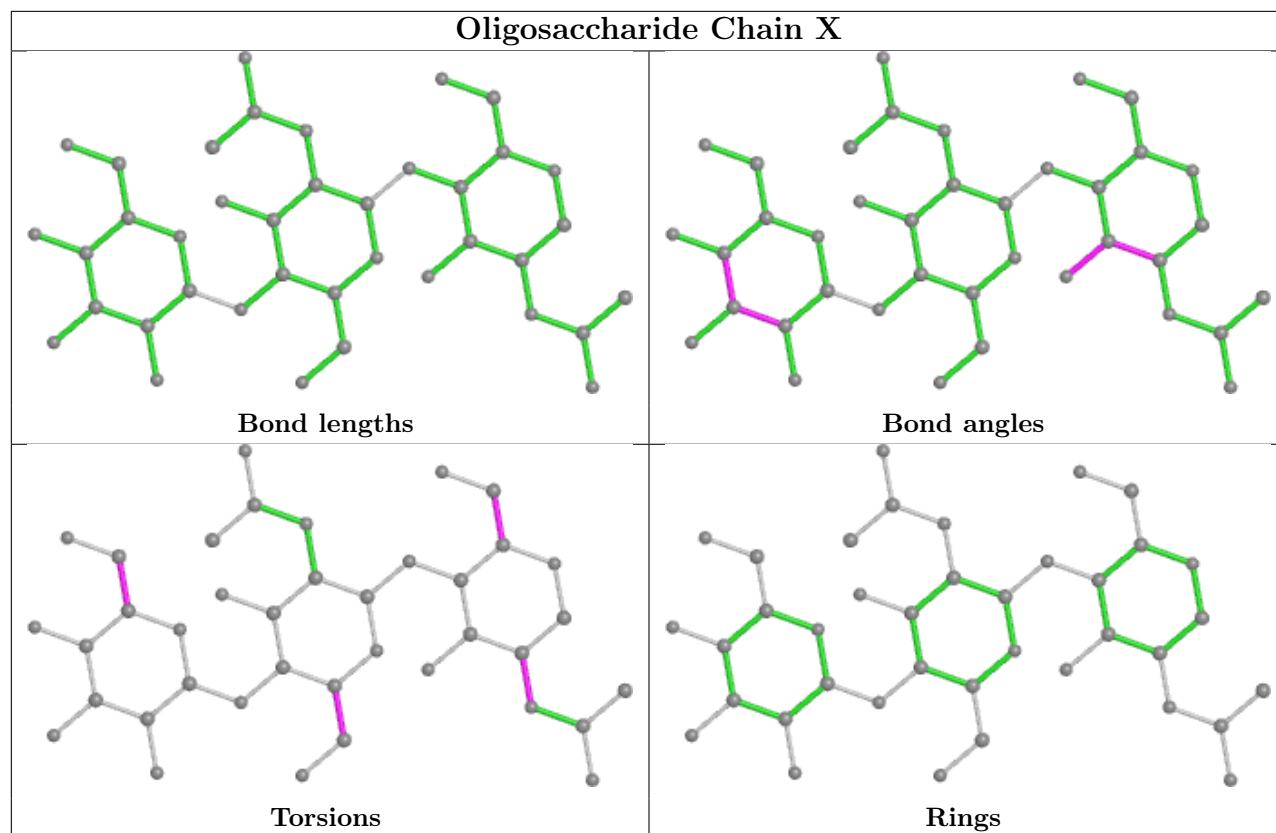


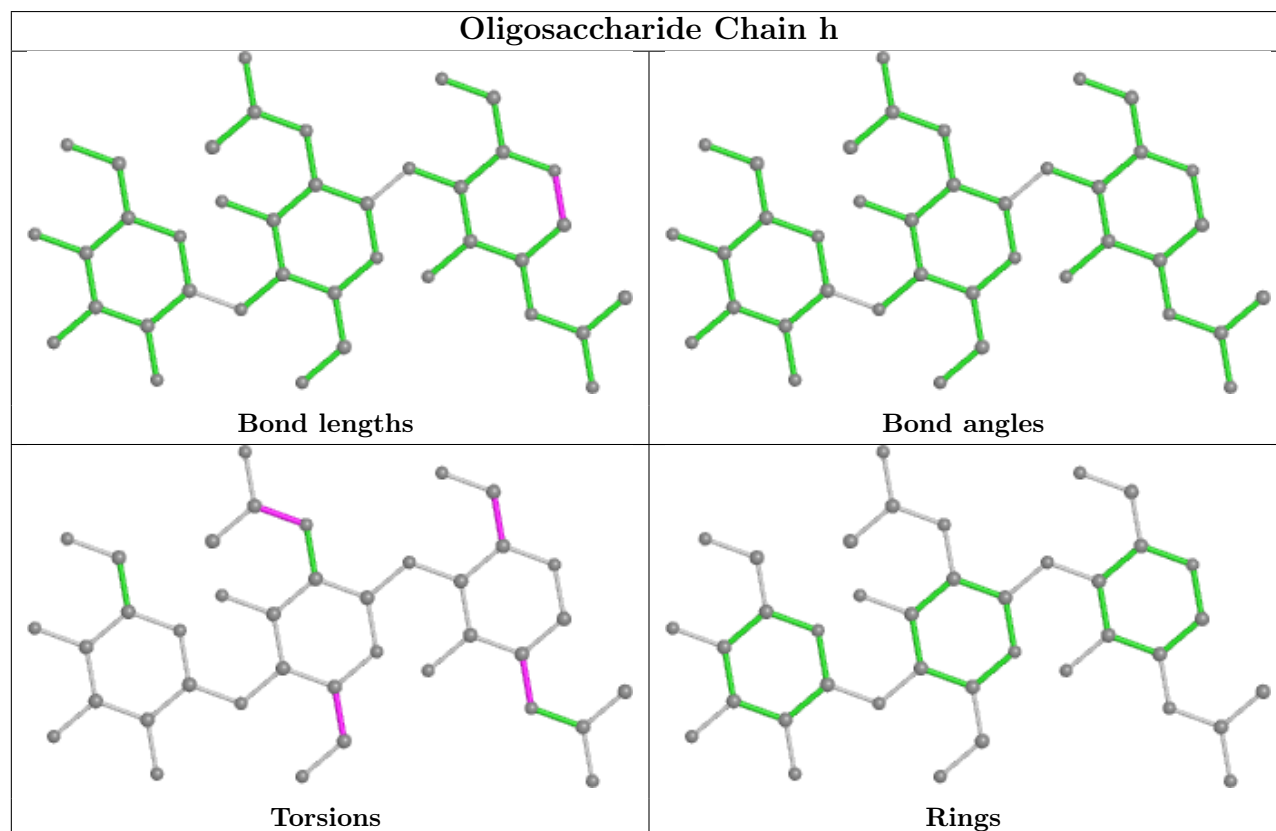
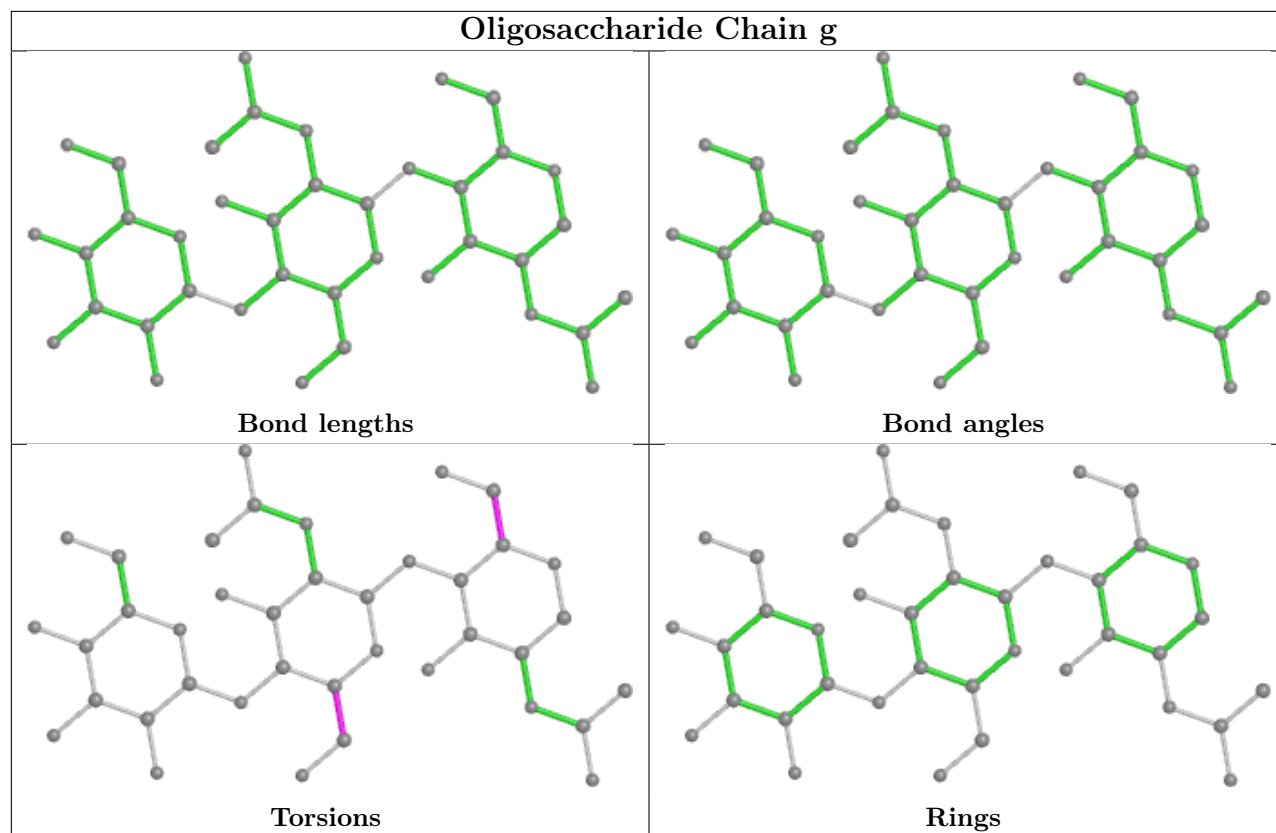


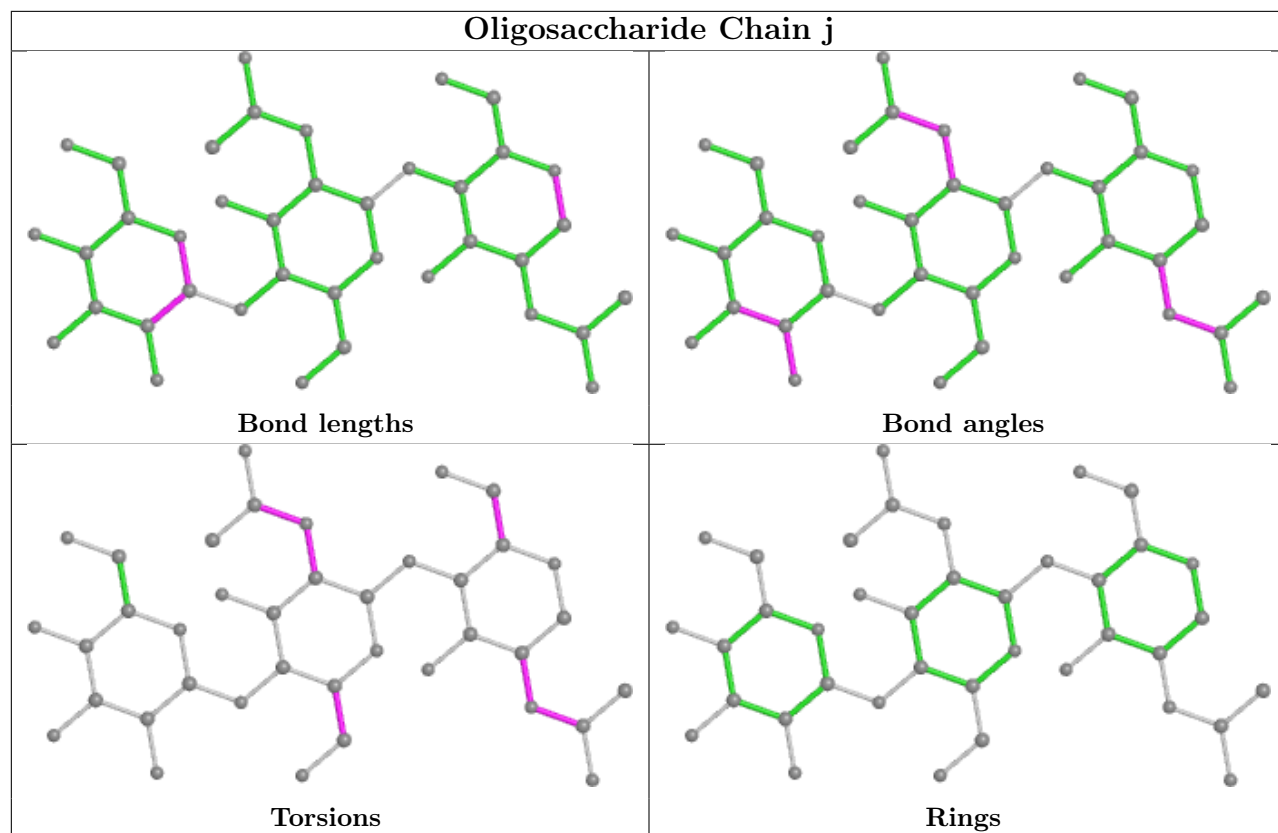


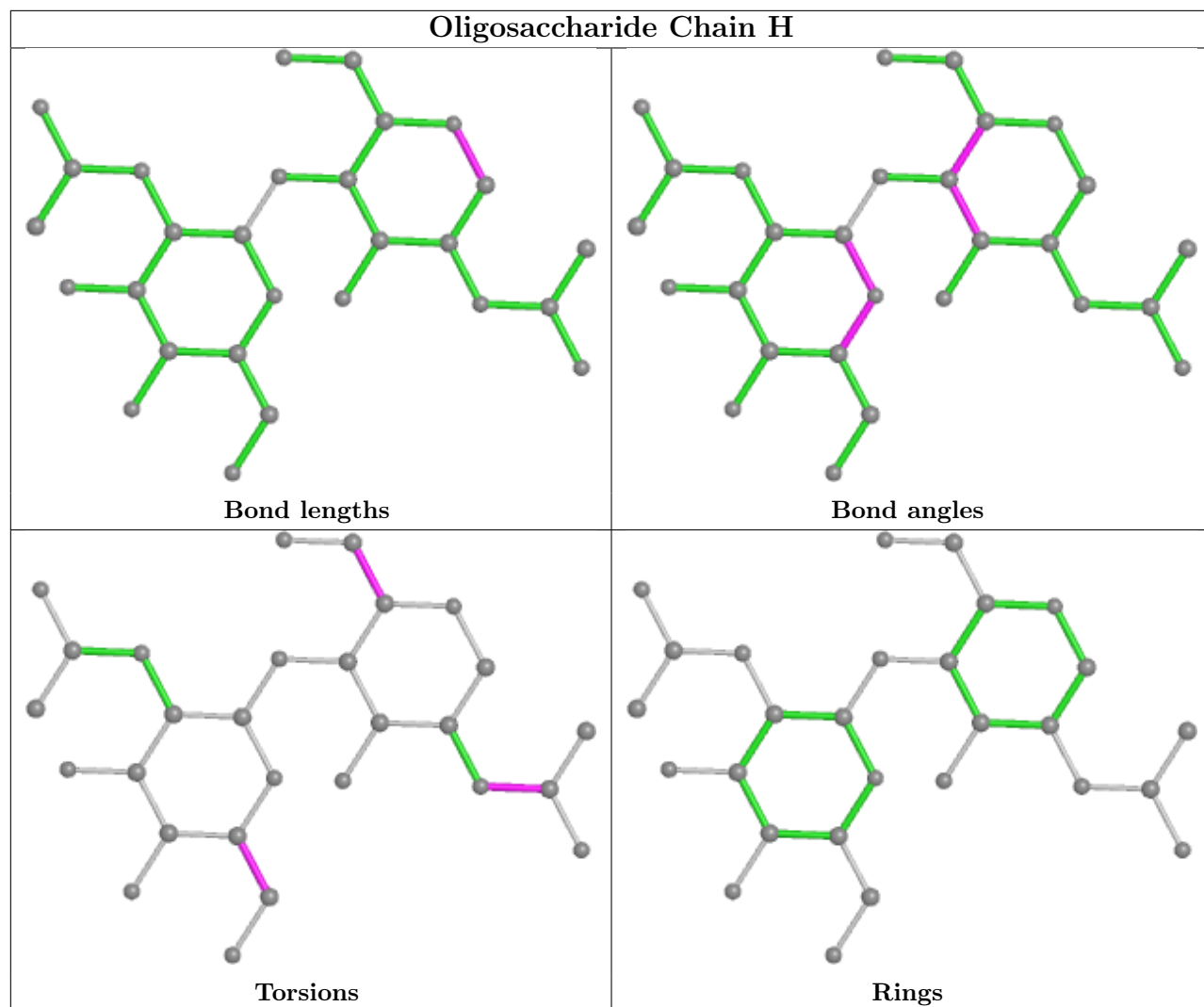


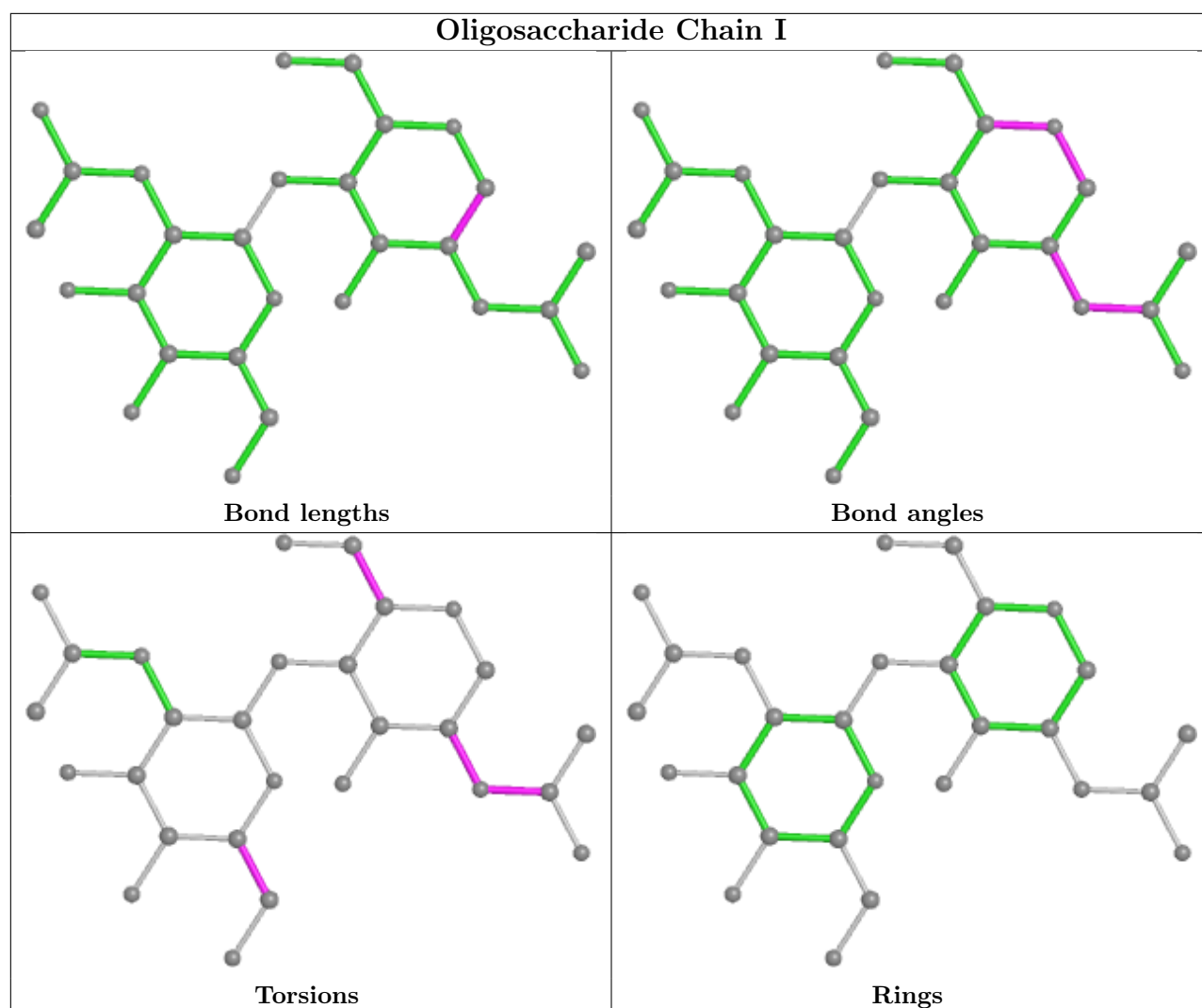


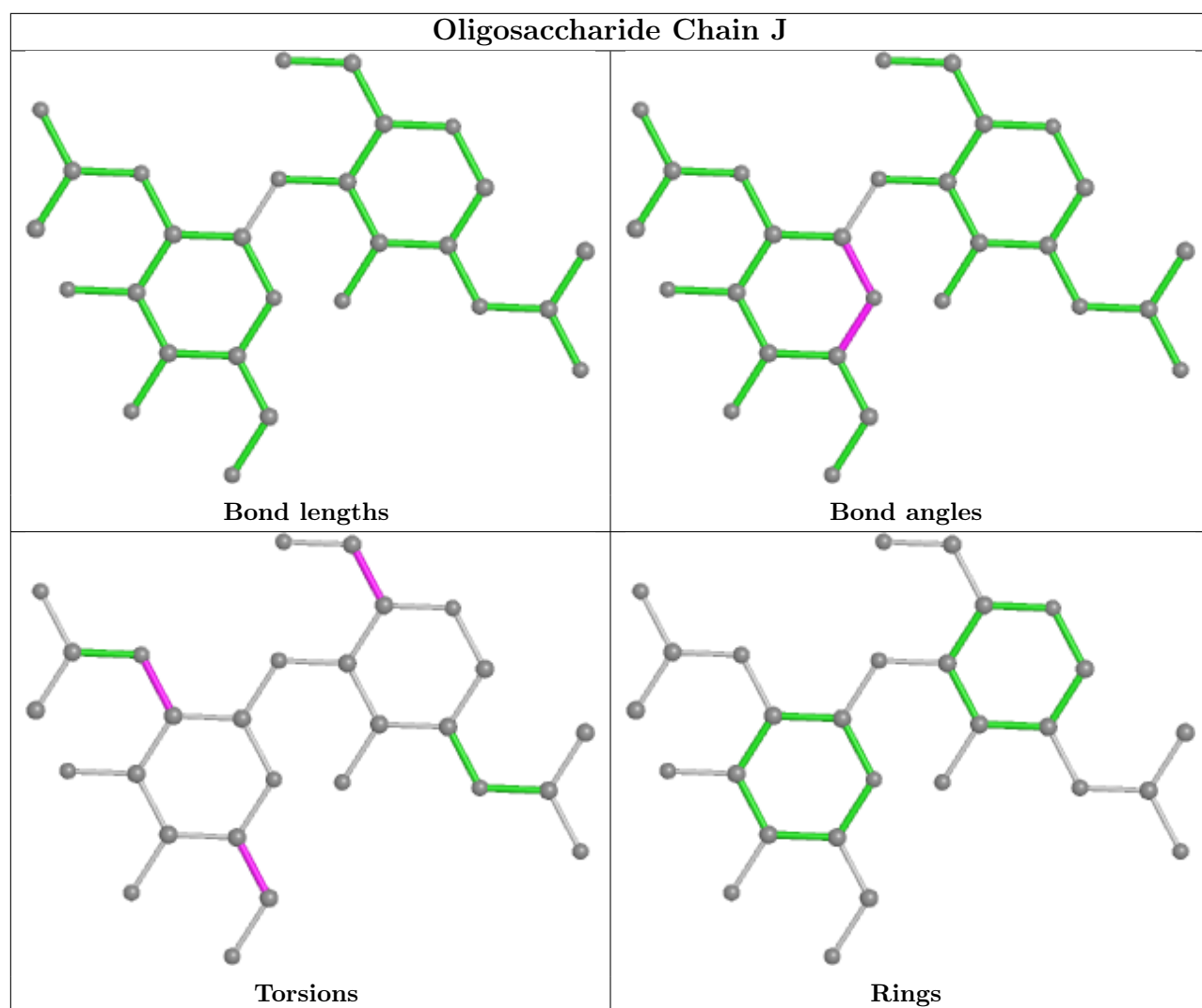


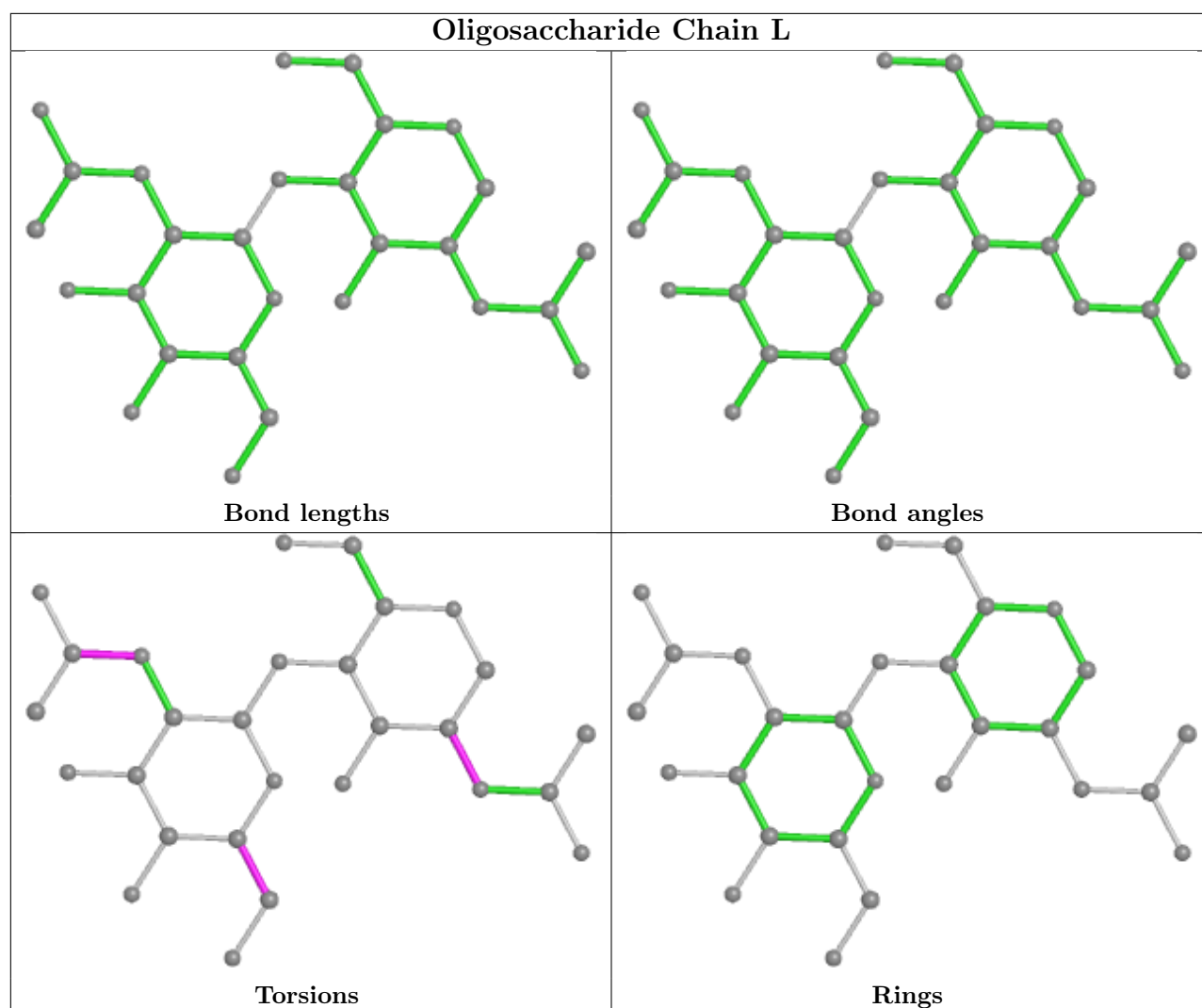


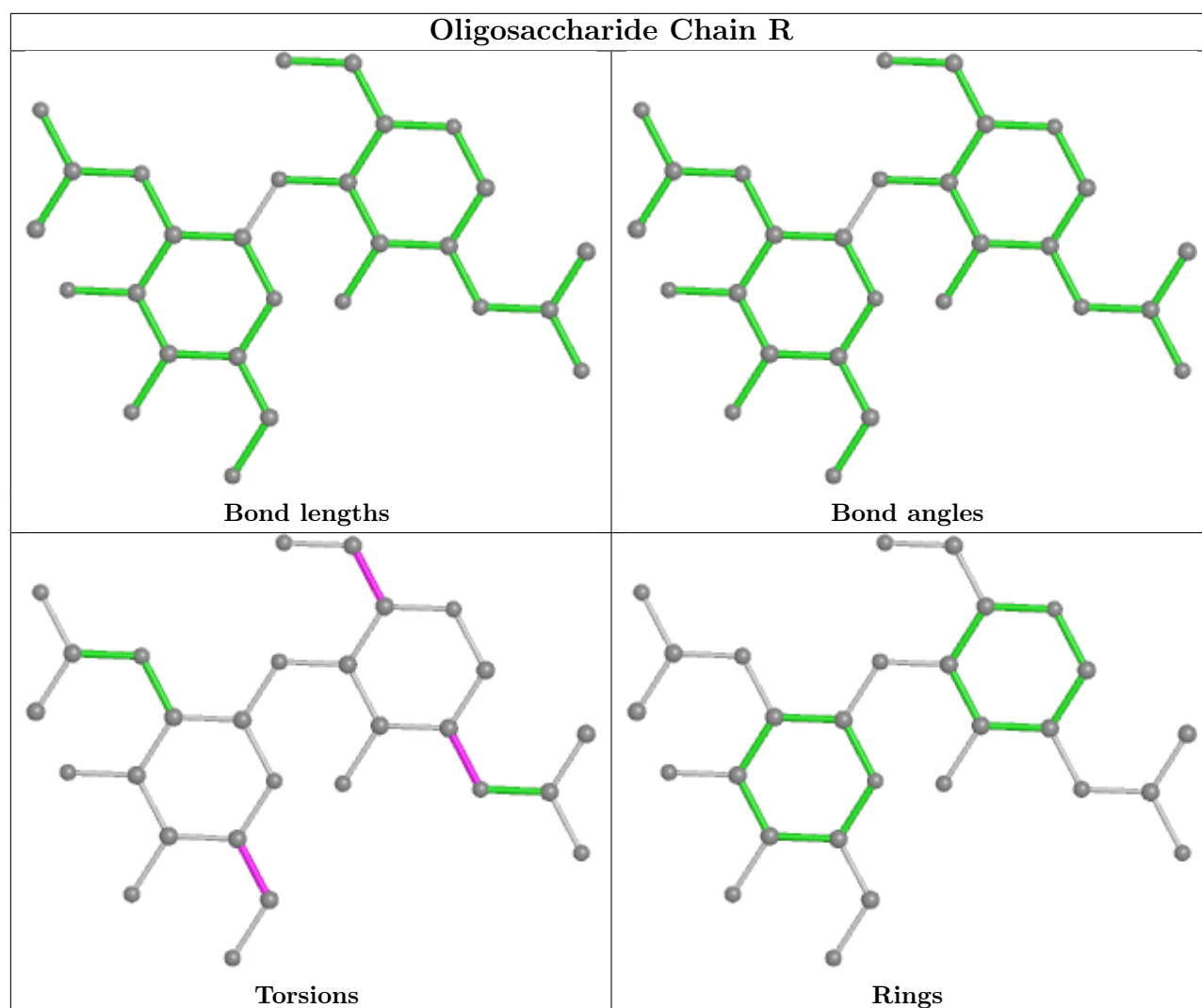


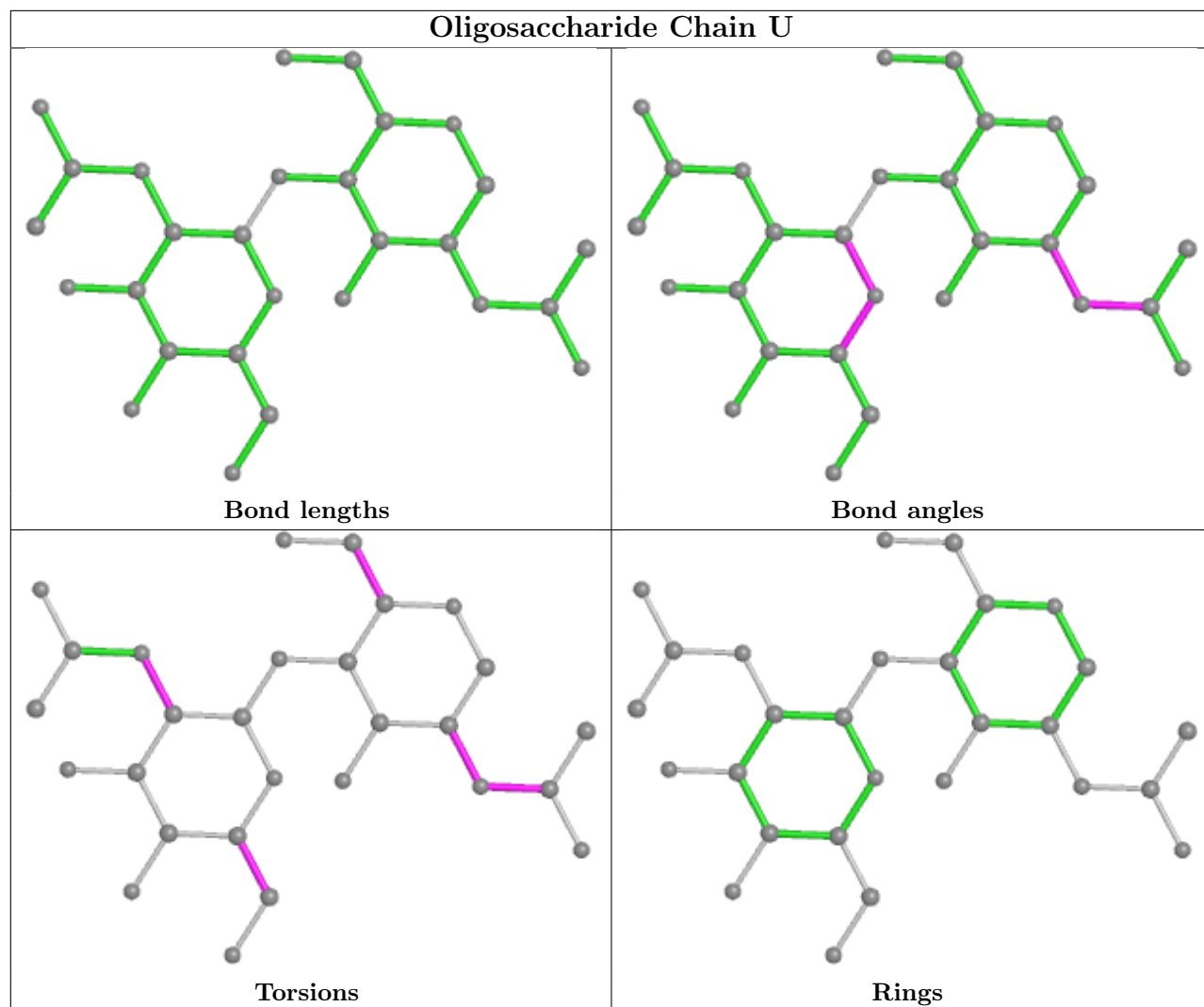


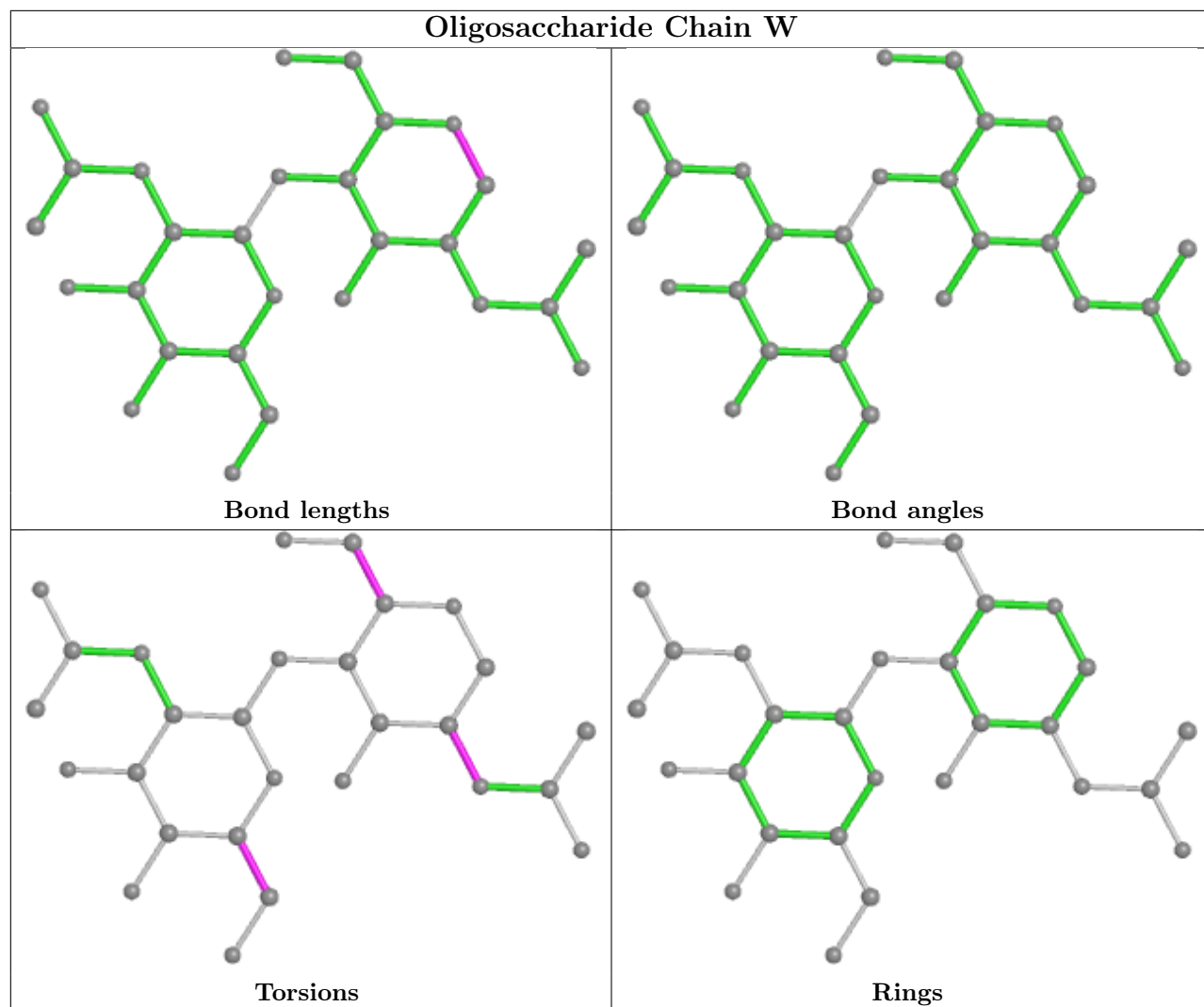


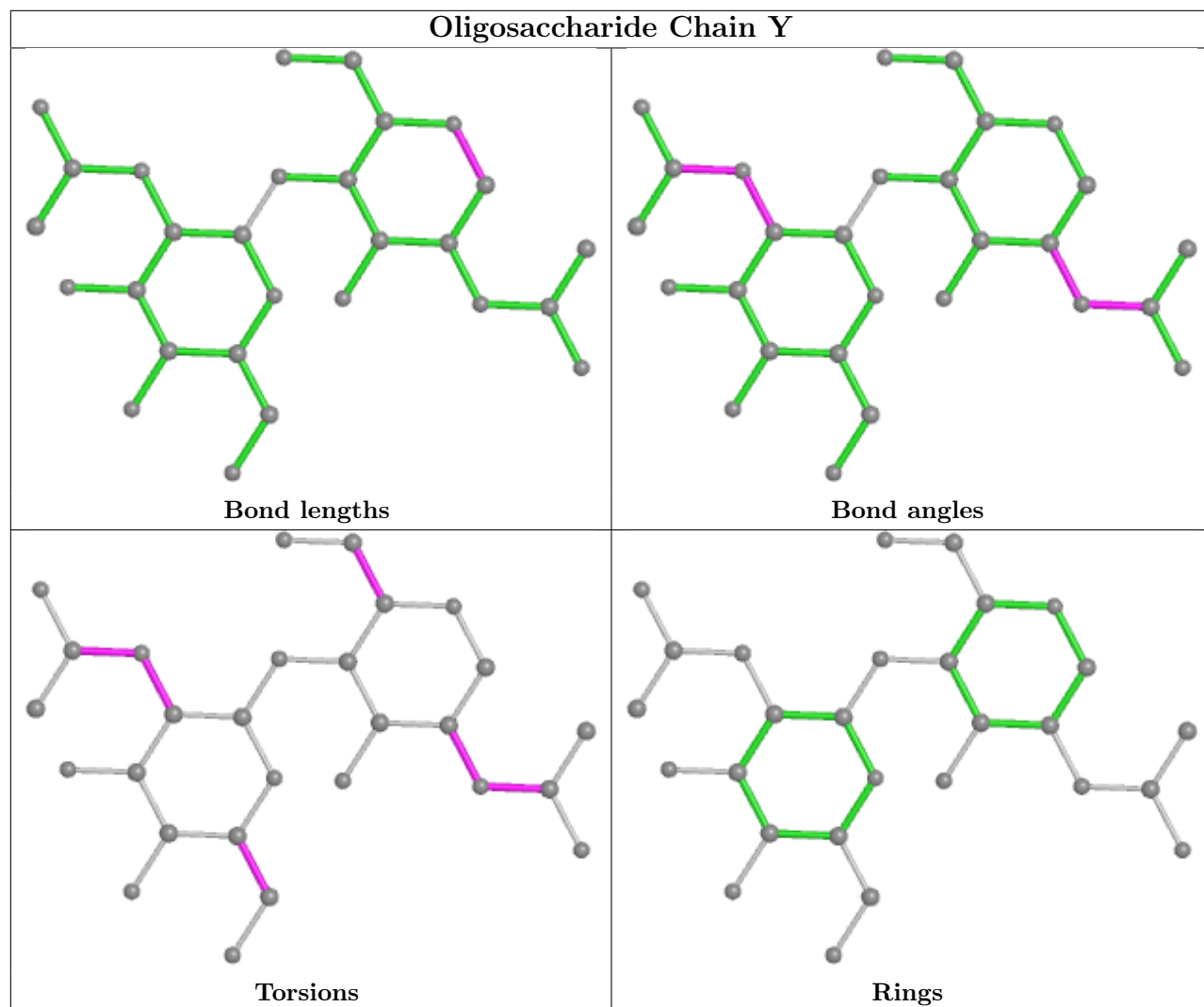


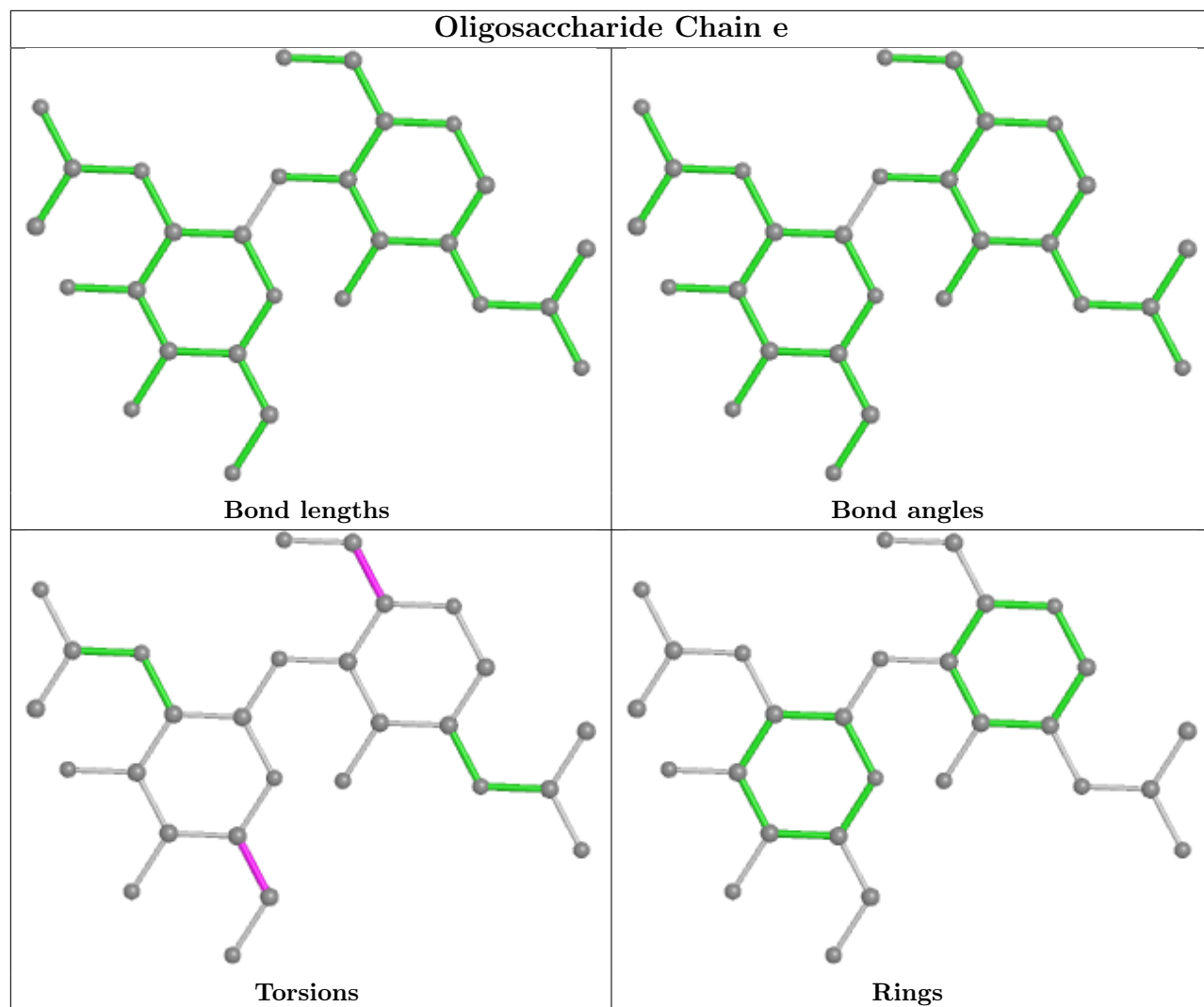


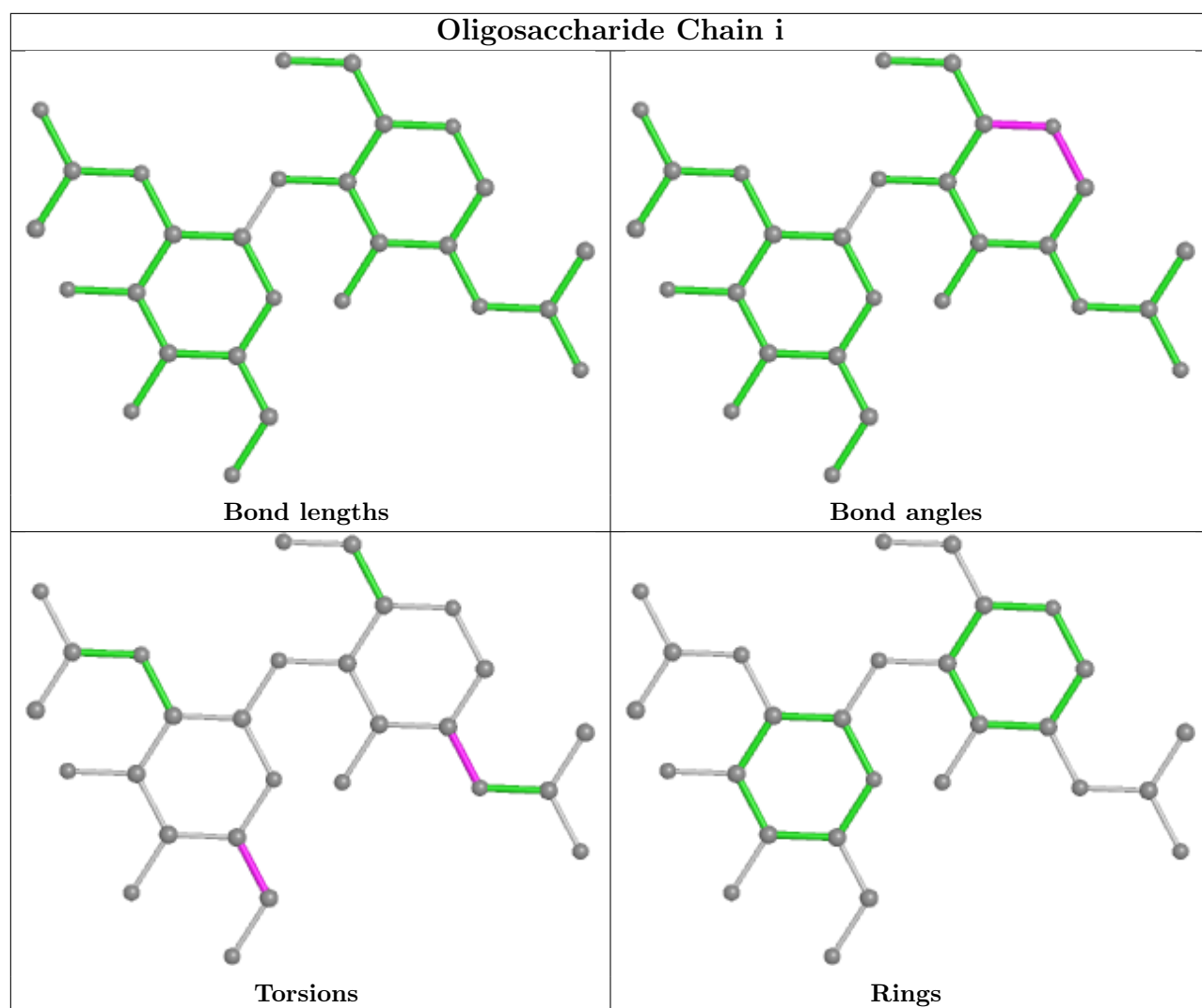


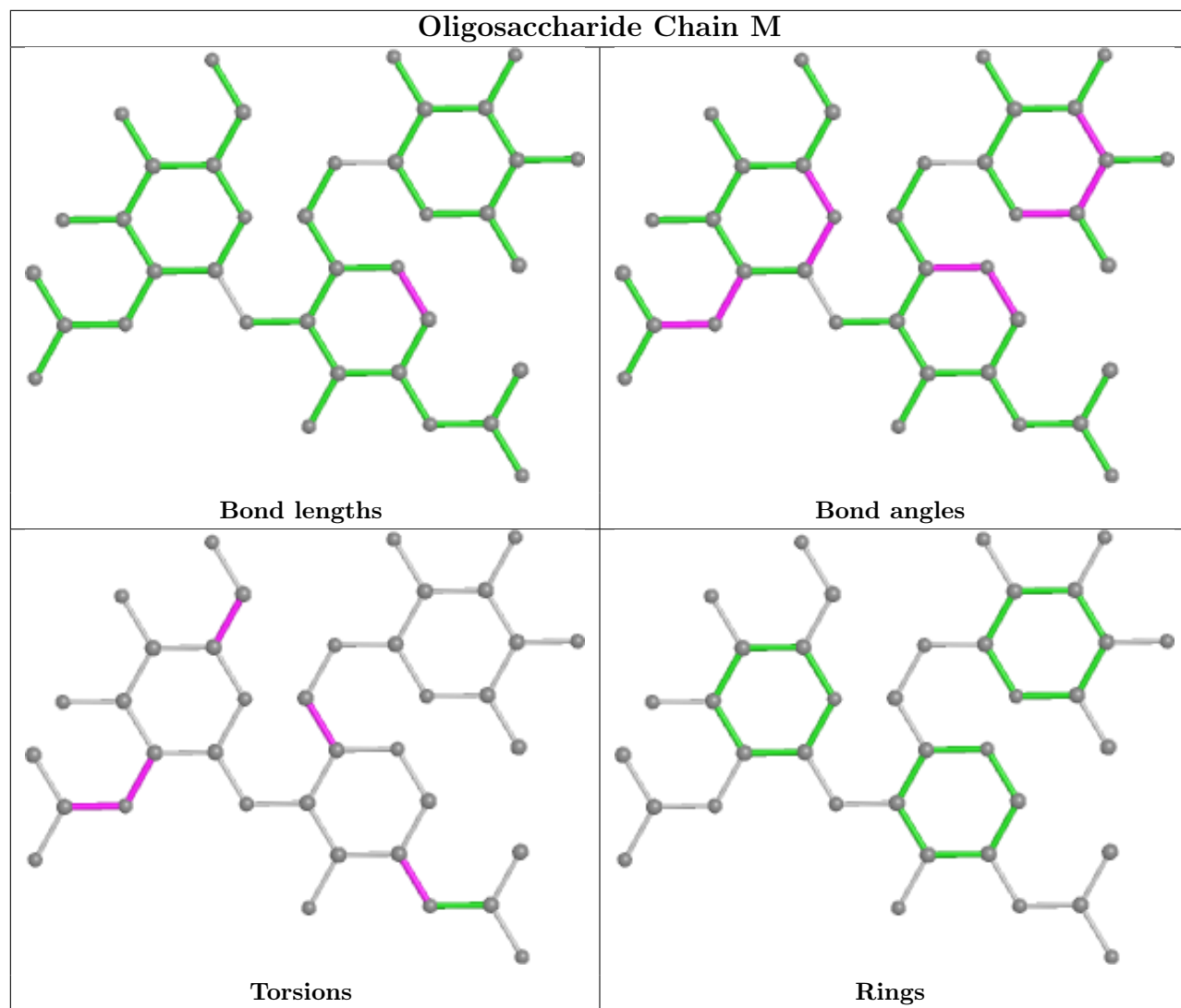


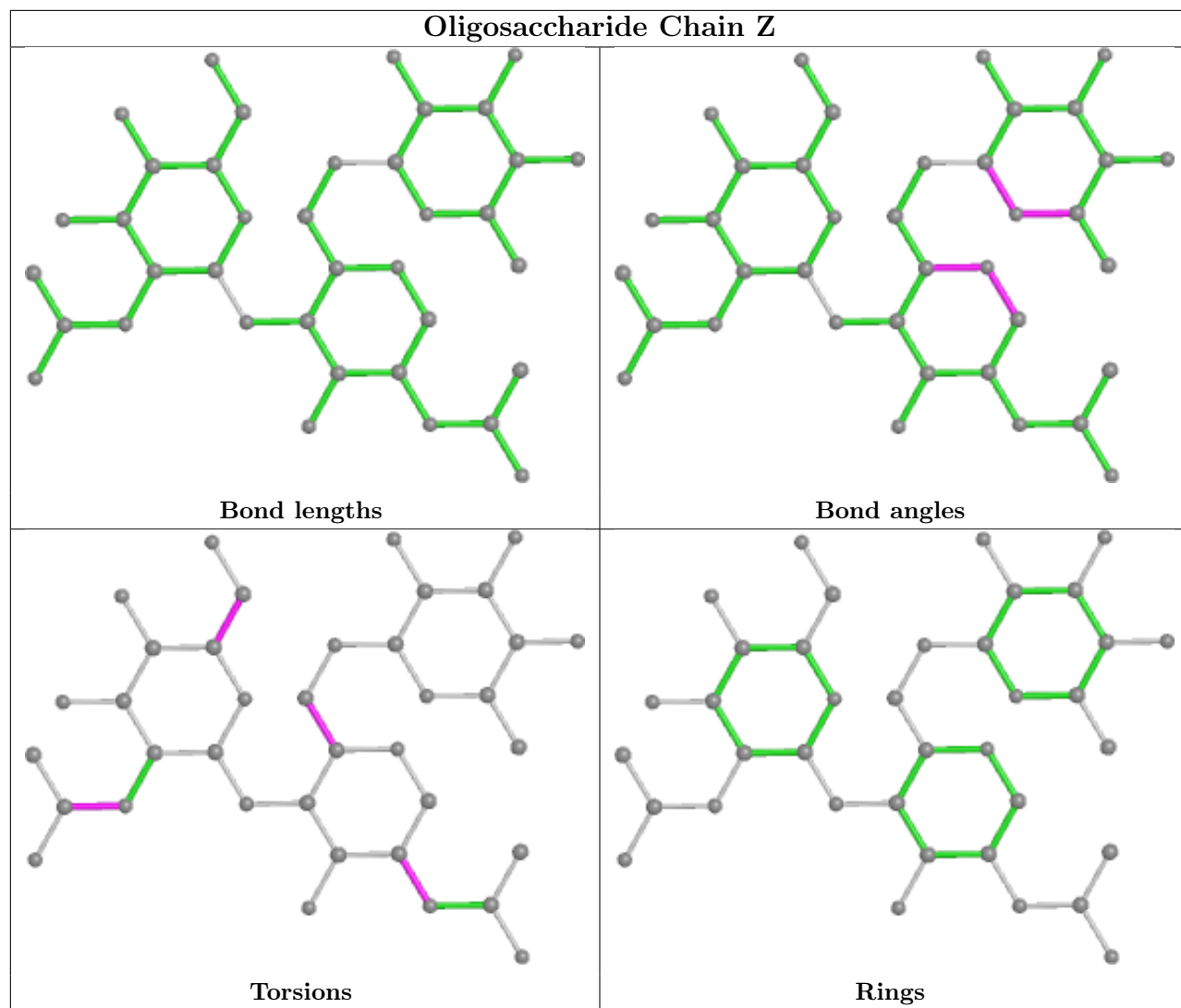


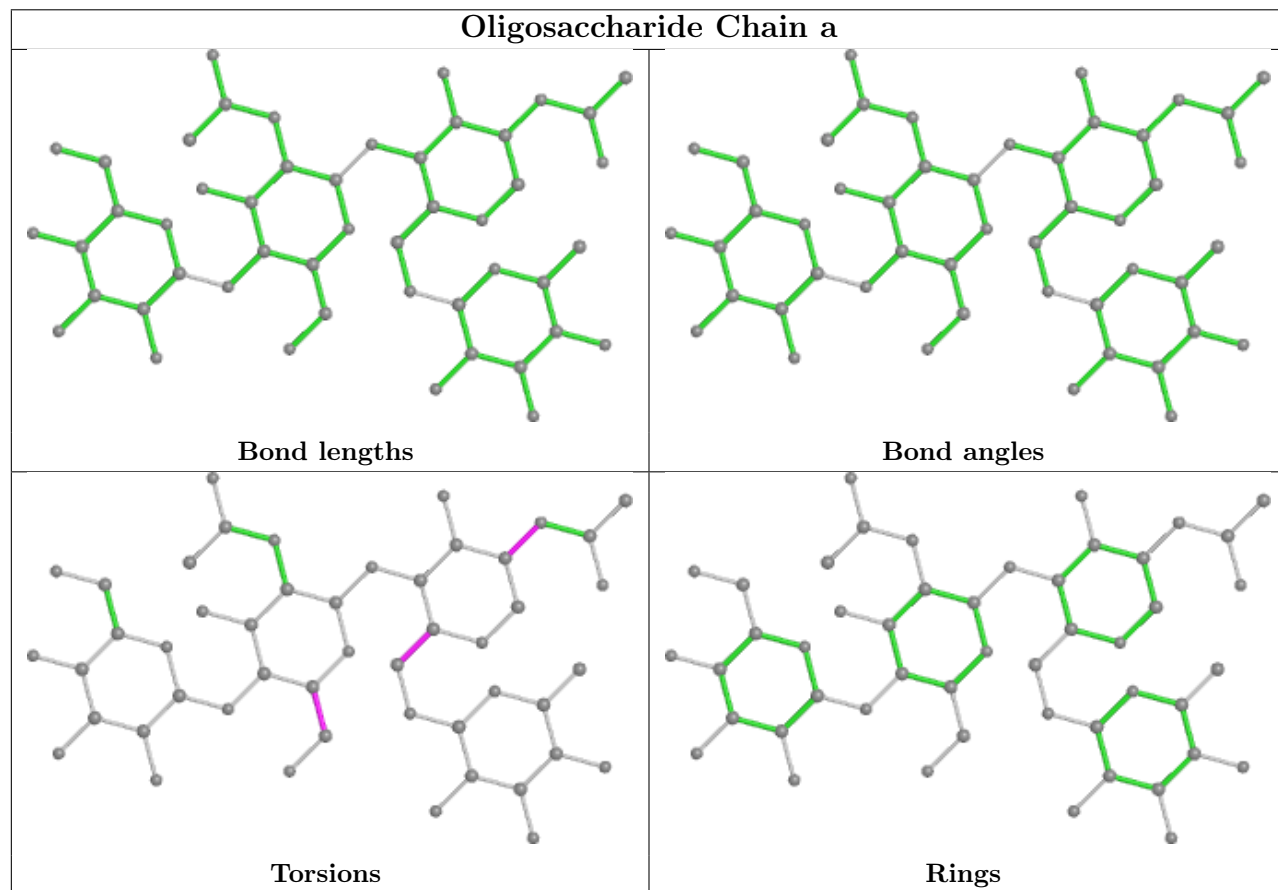
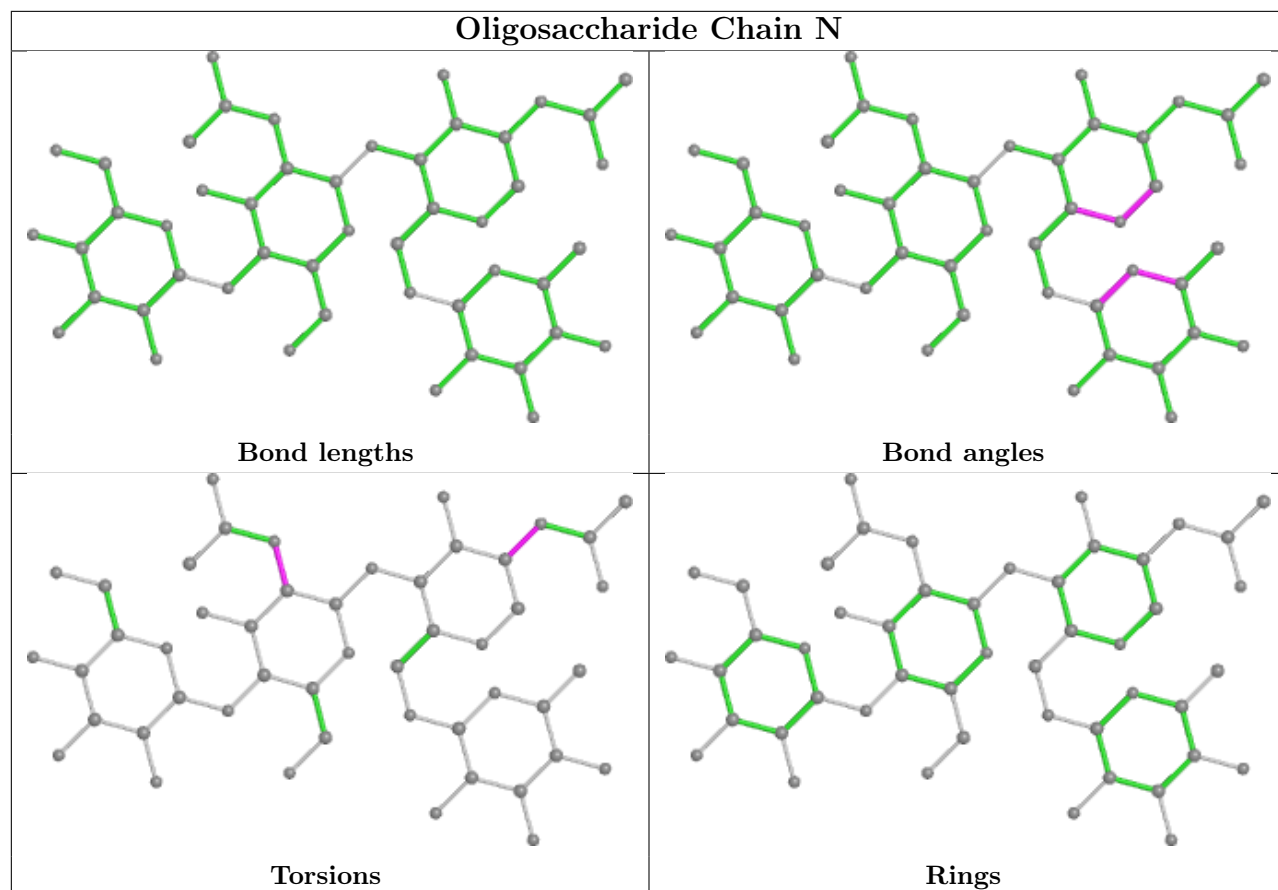


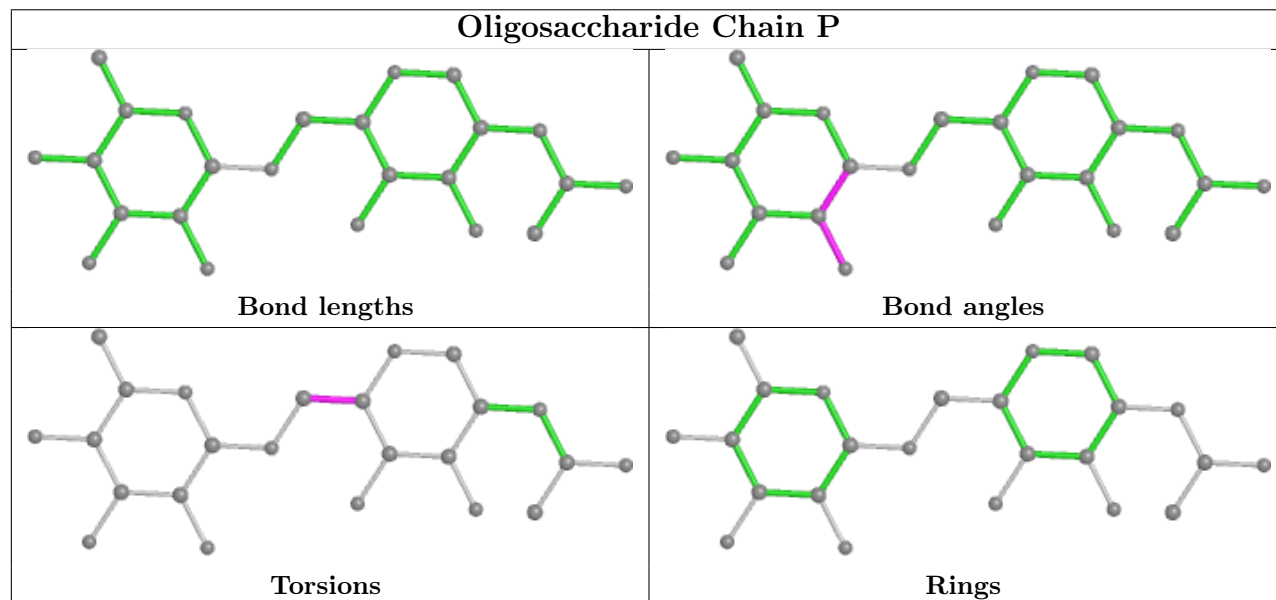
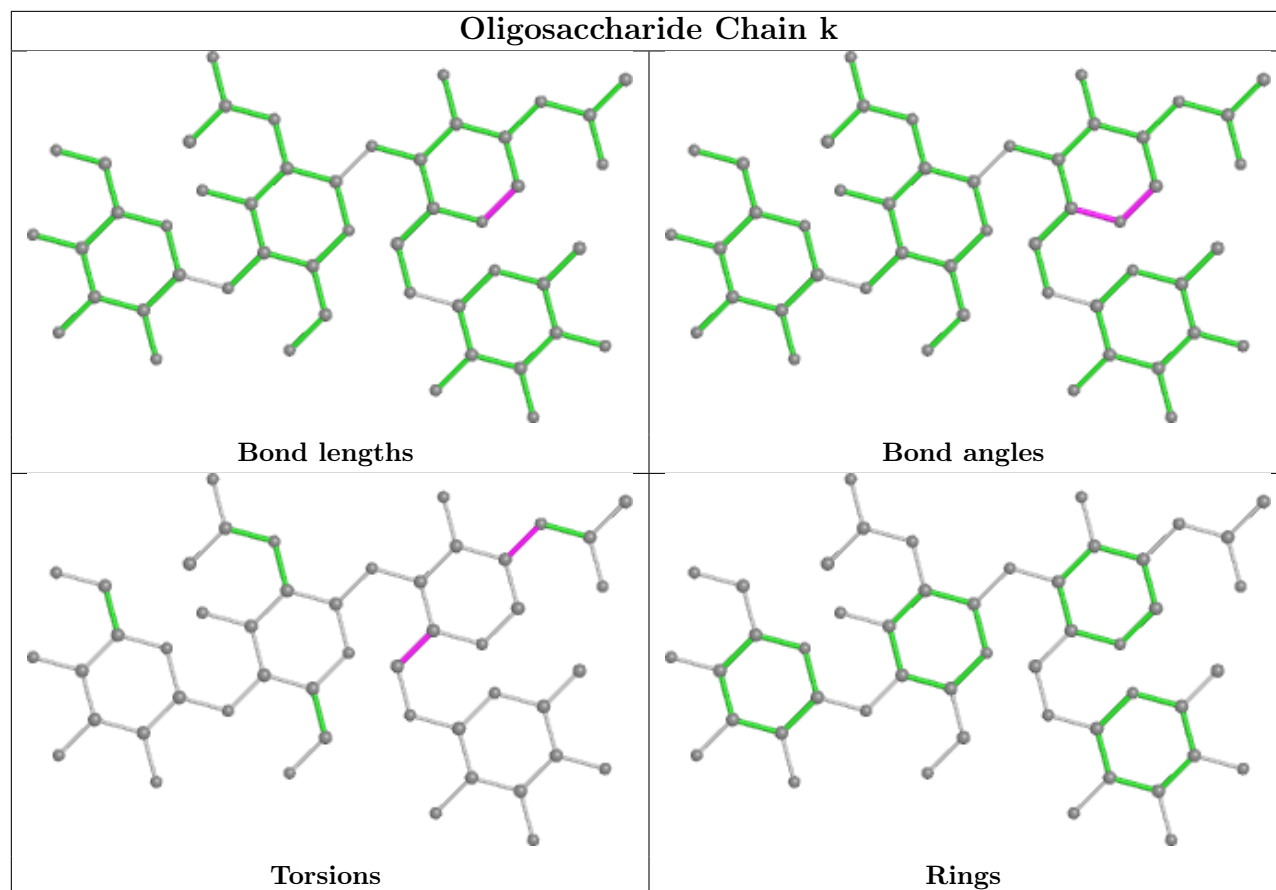


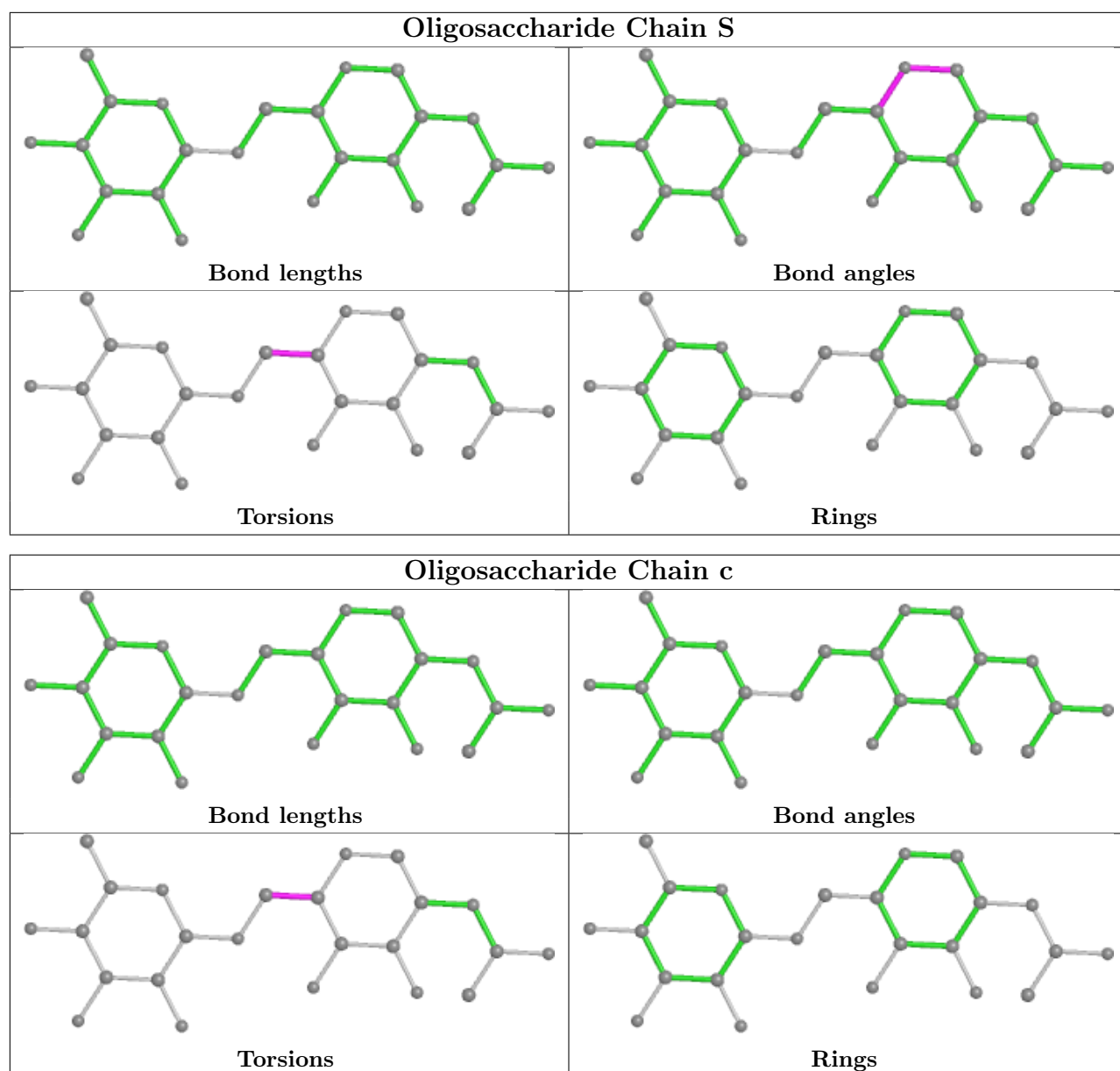


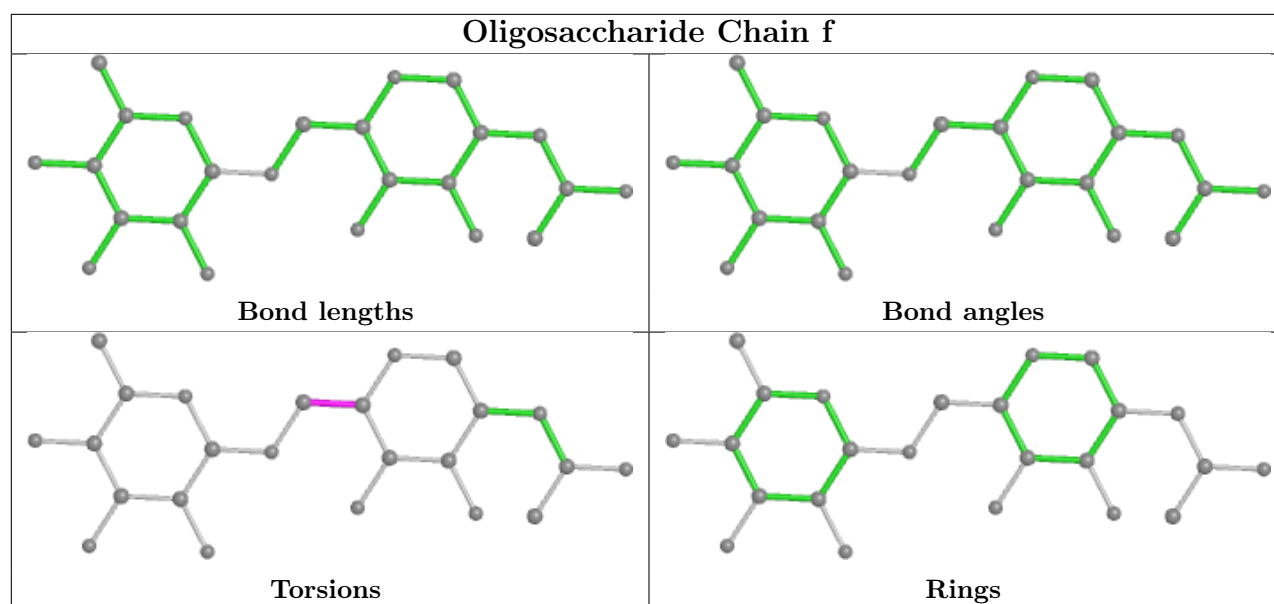












5.6 Ligand geometry [i](#)

18 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	NAG	B	1505	1	14,14,15	0.29	0	17,19,21	0.50	0
8	NAG	B	1502	1	14,14,15	0.30	0	17,19,21	0.41	0
8	NAG	A	1502	1	14,14,15	0.51	0	17,19,21	0.56	0
8	NAG	B	1501	1	14,14,15	0.27	0	17,19,21	0.38	0
8	NAG	B	1503	1	14,14,15	0.23	0	17,19,21	0.38	0
8	NAG	A	1503	1	14,14,15	0.34	0	17,19,21	0.55	0
8	NAG	B	1506	1	14,14,15	0.27	0	17,19,21	0.39	0
8	NAG	B	1507	1	14,14,15	0.22	0	17,19,21	0.41	0
8	NAG	A	1504	1	14,14,15	0.20	0	17,19,21	0.41	0
8	NAG	A	1506	1	14,14,15	0.44	0	17,19,21	0.59	0
8	NAG	C	1503	1	14,14,15	0.29	0	17,19,21	0.62	1 (5%)
8	NAG	B	1504	1	14,14,15	0.31	0	17,19,21	0.45	0
8	NAG	A	1505	1	14,14,15	0.69	0	17,19,21	1.15	1 (5%)
8	NAG	C	1505	1	14,14,15	0.96	1 (7%)	17,19,21	0.58	0
8	NAG	C	1504	1	14,14,15	0.24	0	17,19,21	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	C	1502	1	14,14,15	0.21	0	17,19,21	0.43	0
8	NAG	C	1501	1	14,14,15	0.28	0	17,19,21	0.38	0
8	NAG	A	1501	1	14,14,15	0.17	0	17,19,21	0.53	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	B	1505	1	-	2/6/23/26	0/1/1/1
8	NAG	B	1502	1	-	1/6/23/26	0/1/1/1
8	NAG	A	1502	1	-	3/6/23/26	0/1/1/1
8	NAG	B	1501	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1503	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1503	1	-	3/6/23/26	0/1/1/1
8	NAG	B	1506	1	-	0/6/23/26	0/1/1/1
8	NAG	B	1507	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1504	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1506	1	-	4/6/23/26	0/1/1/1
8	NAG	C	1503	1	-	2/6/23/26	0/1/1/1
8	NAG	B	1504	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1505	1	-	0/6/23/26	0/1/1/1
8	NAG	C	1505	1	-	2/6/23/26	0/1/1/1
8	NAG	C	1504	1	-	3/6/23/26	0/1/1/1
8	NAG	C	1502	1	-	2/6/23/26	0/1/1/1
8	NAG	C	1501	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1501	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)
8	C	1505	NAG	O5-C1	-3.31	1.38	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1505	NAG	C1-O5-C5	4.40	118.15	112.19
8	C	1503	NAG	C1-O5-C5	2.06	114.98	112.19

There are no chirality outliers.

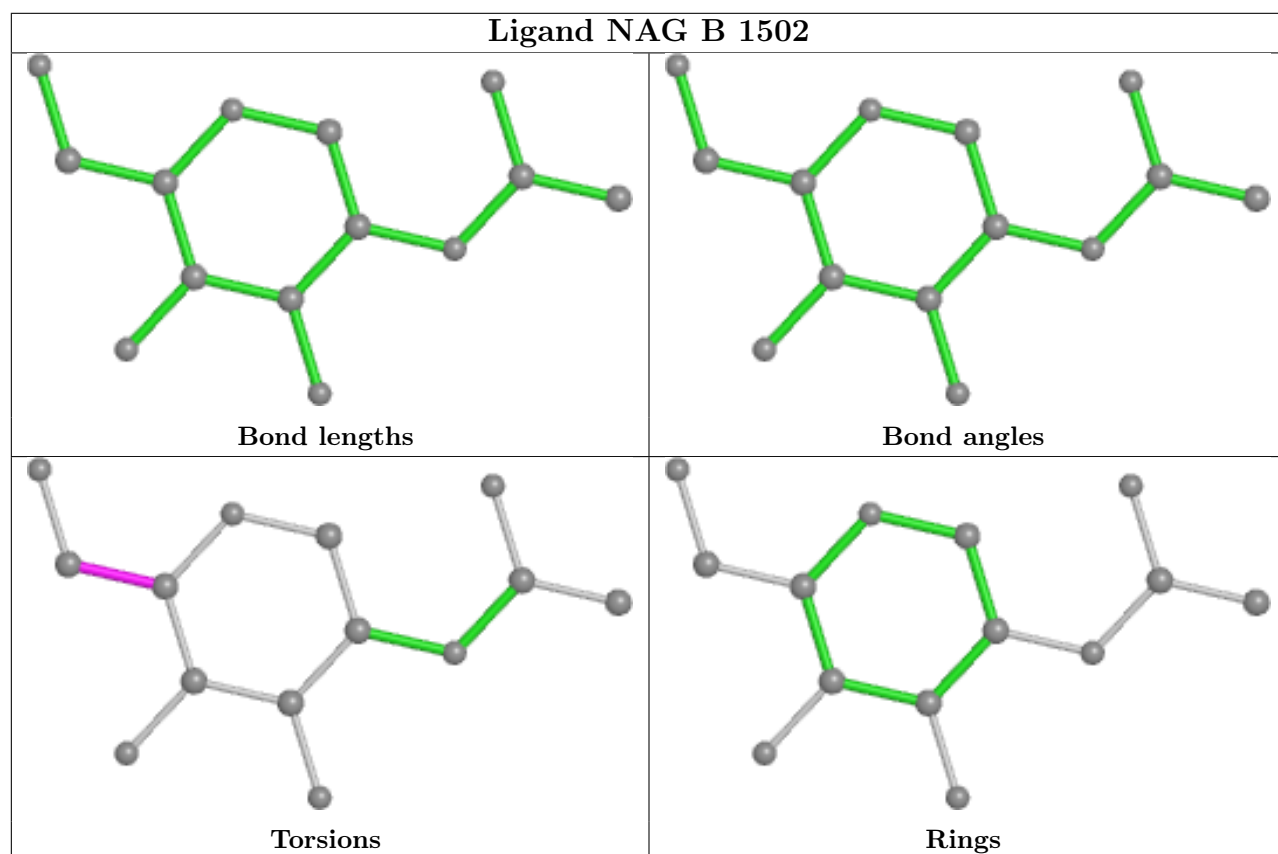
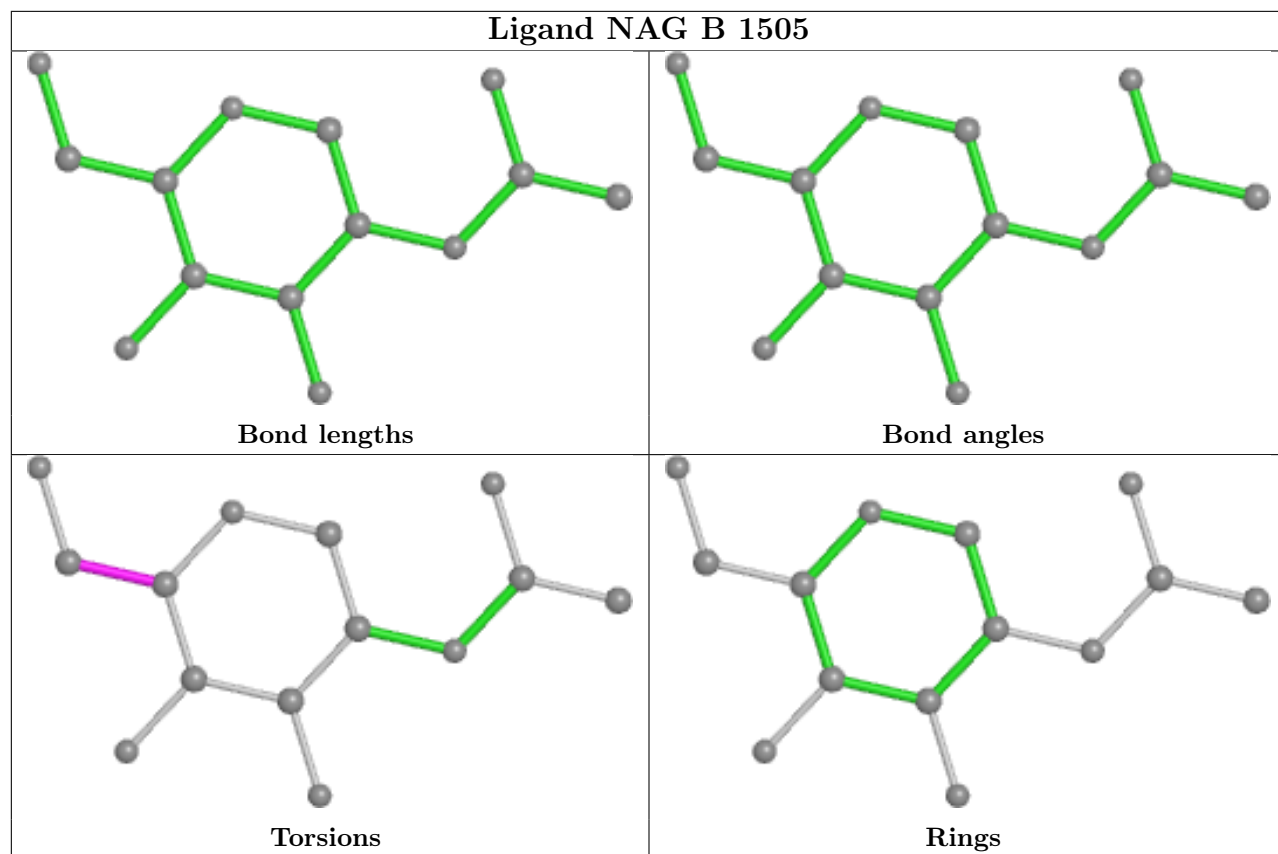
5 of 30 torsion outliers are listed below:

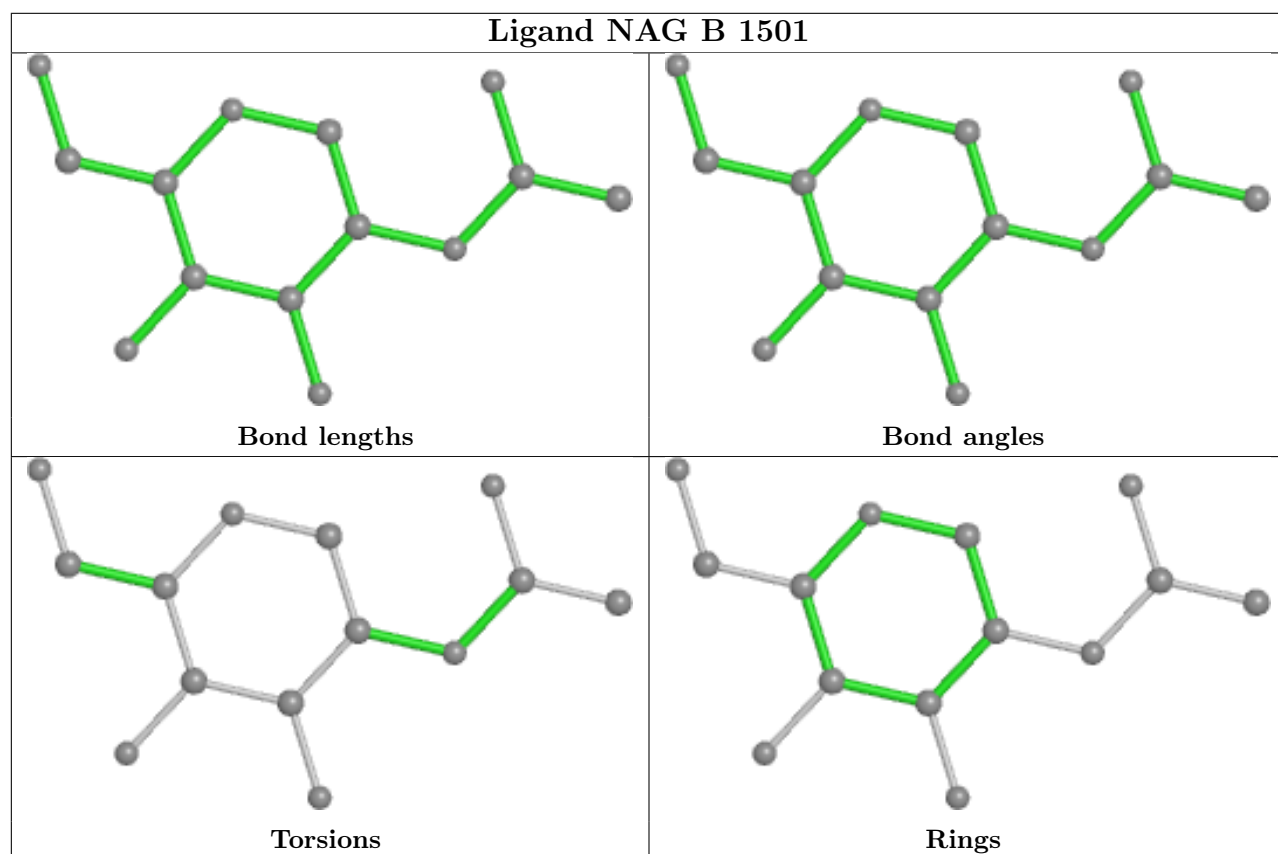
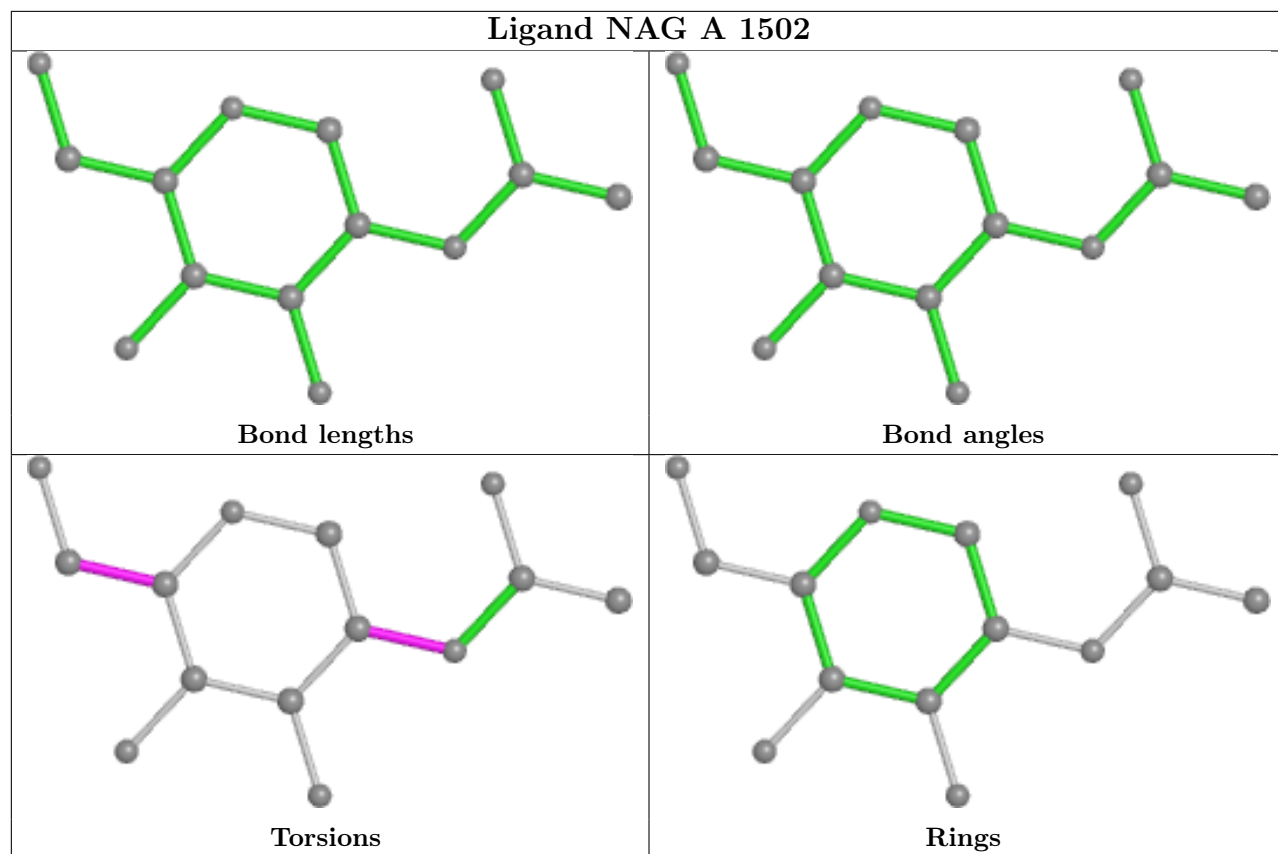
Mol	Chain	Res	Type	Atoms
8	A	1503	NAG	O5-C5-C6-O6
8	B	1503	NAG	O5-C5-C6-O6
8	B	1505	NAG	C4-C5-C6-O6
8	A	1506	NAG	C4-C5-C6-O6
8	C	1505	NAG	C4-C5-C6-O6

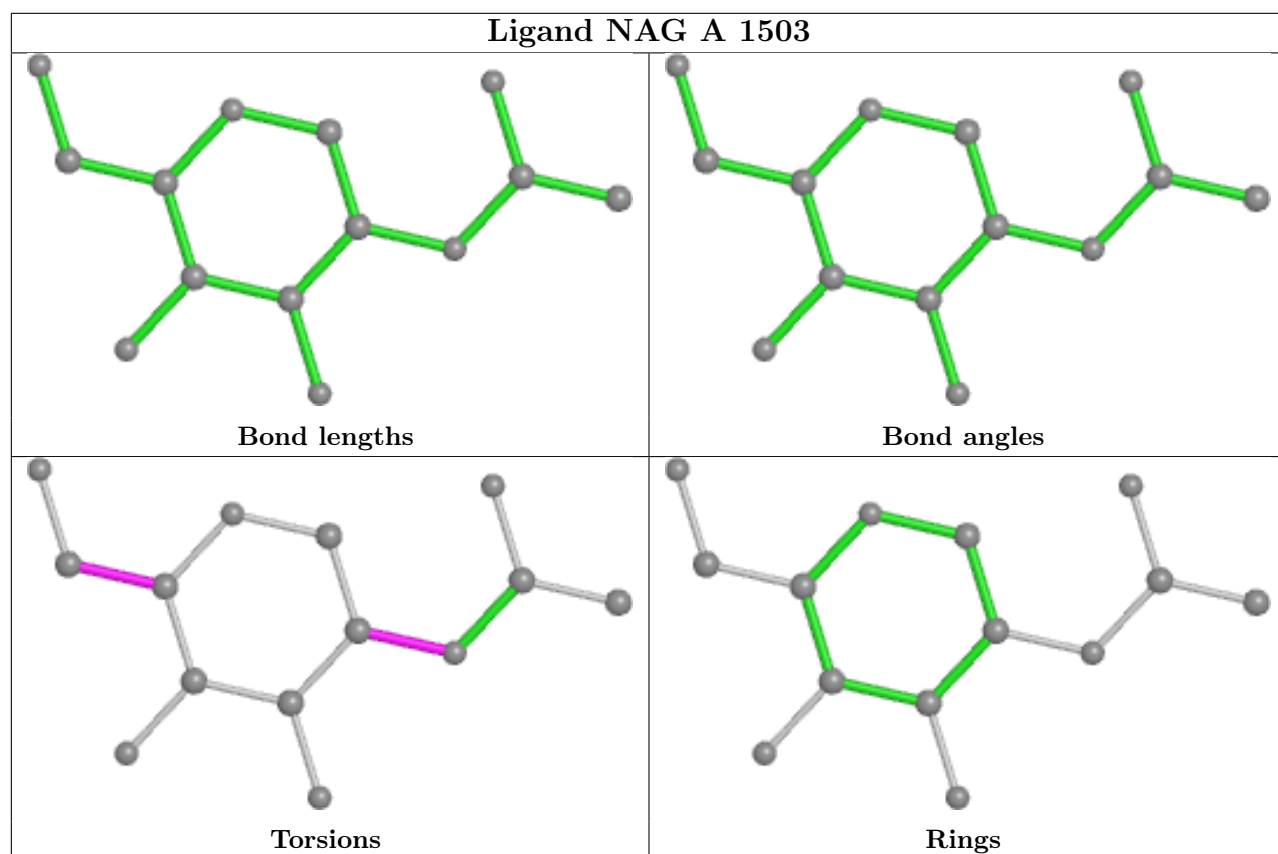
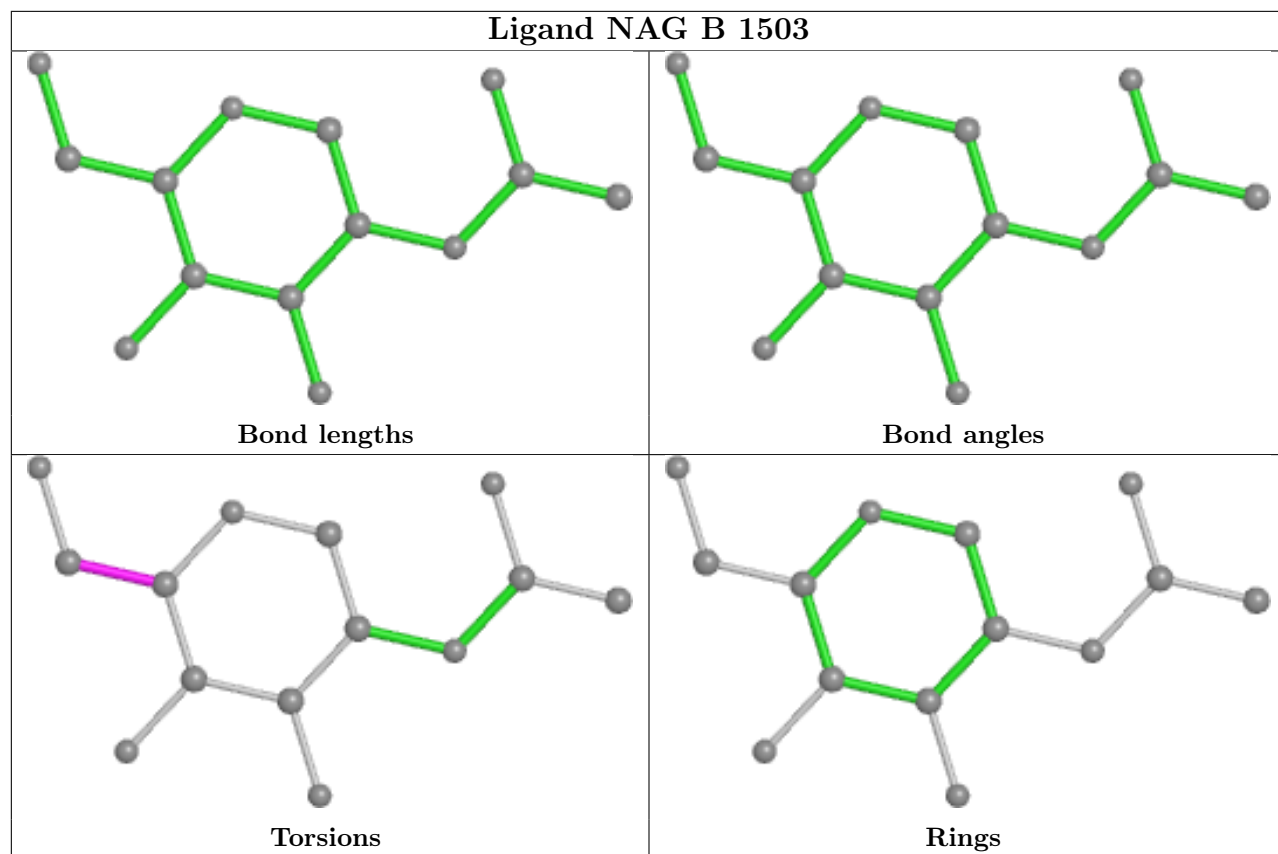
There are no ring outliers.

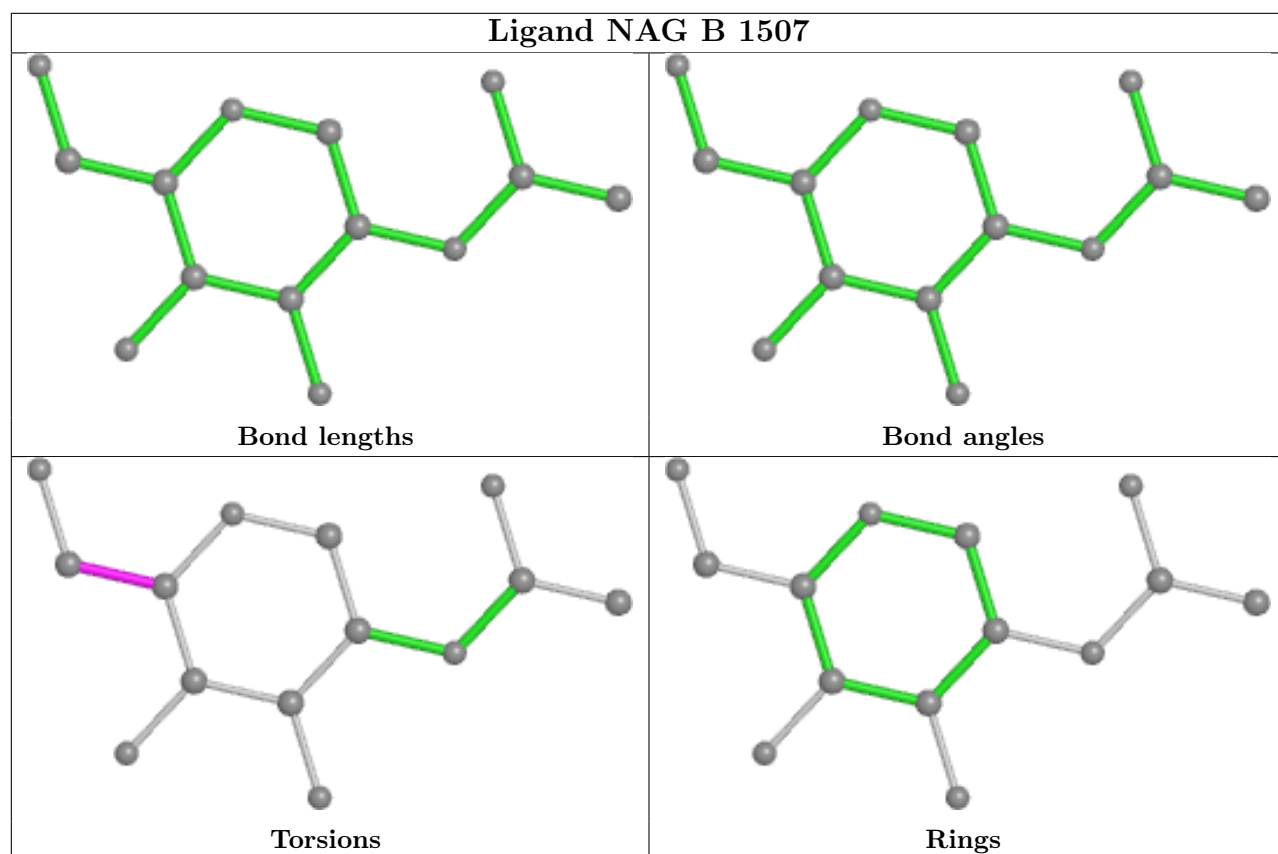
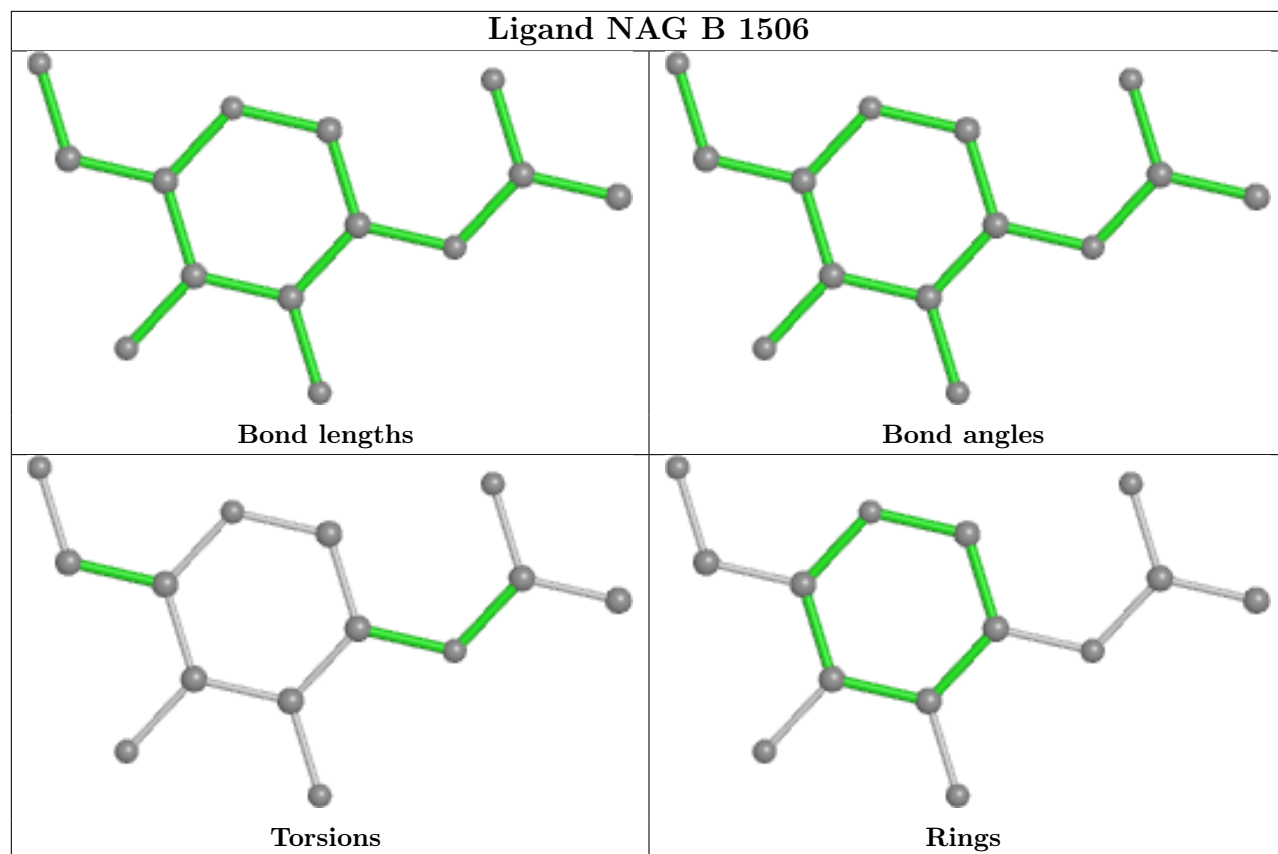
No monomer is involved in short contacts.

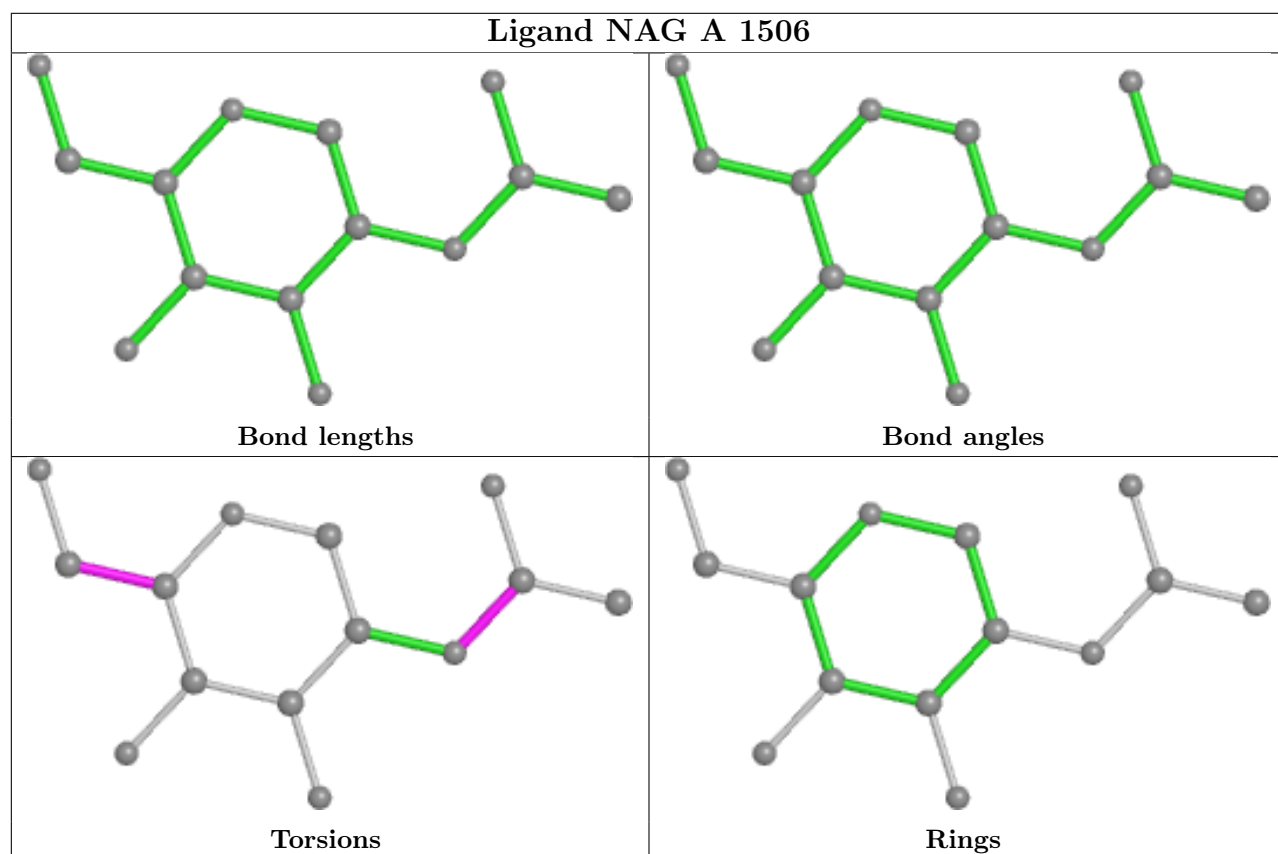
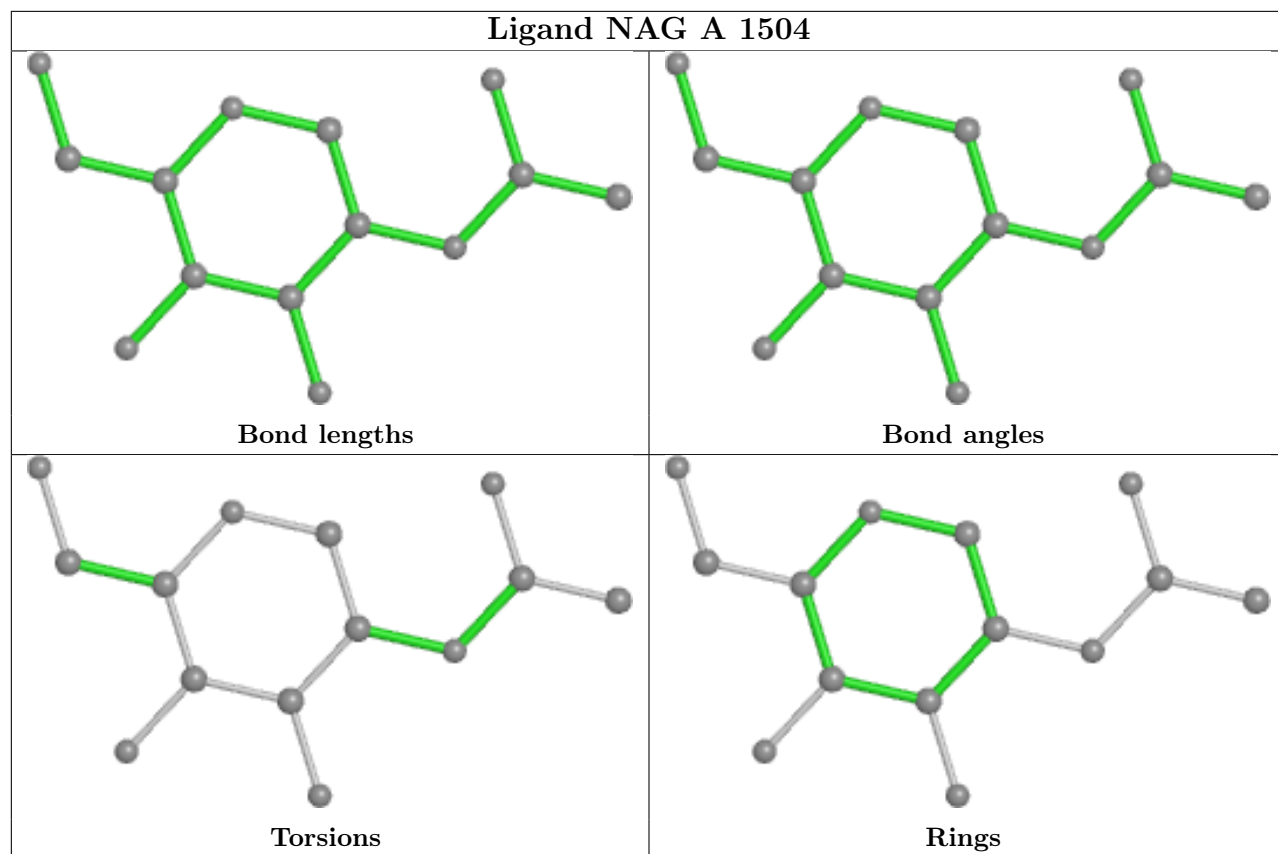
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

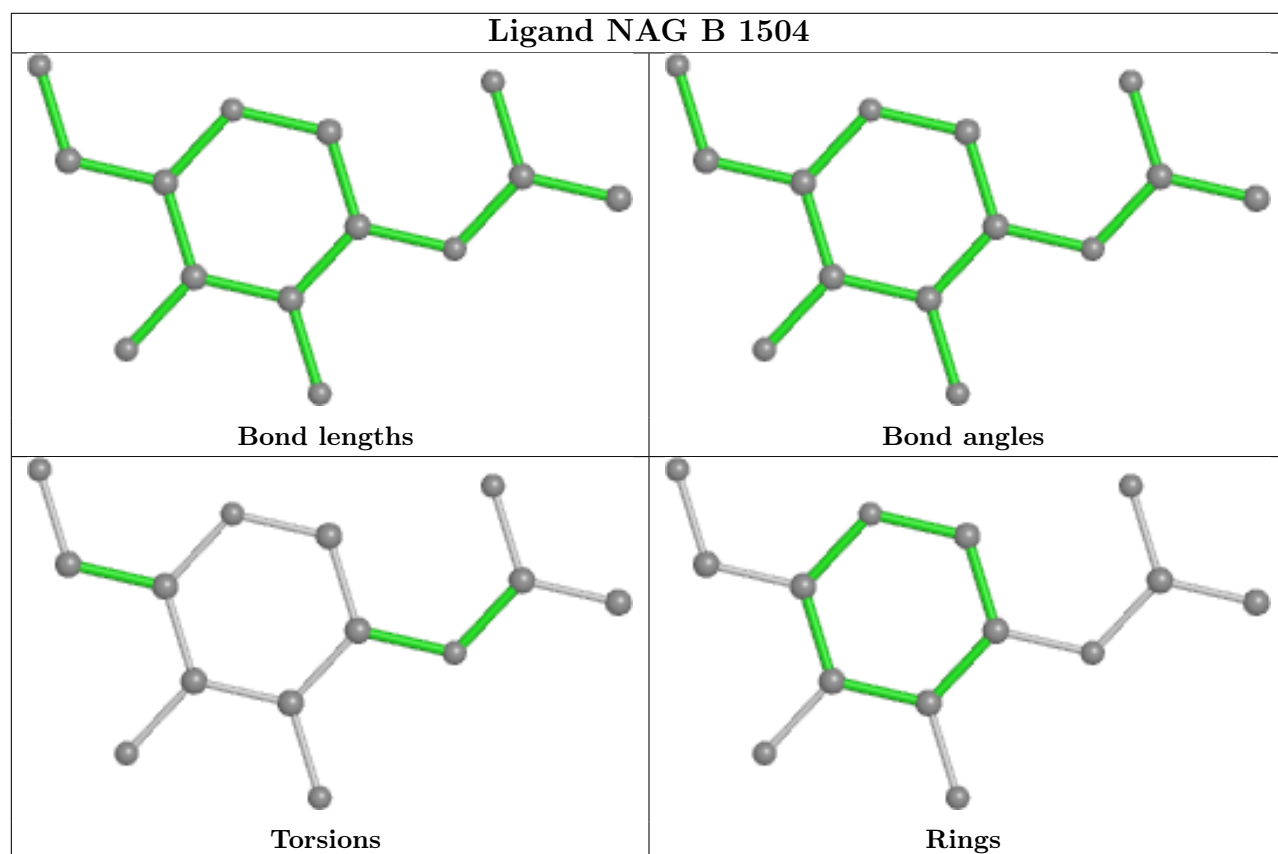
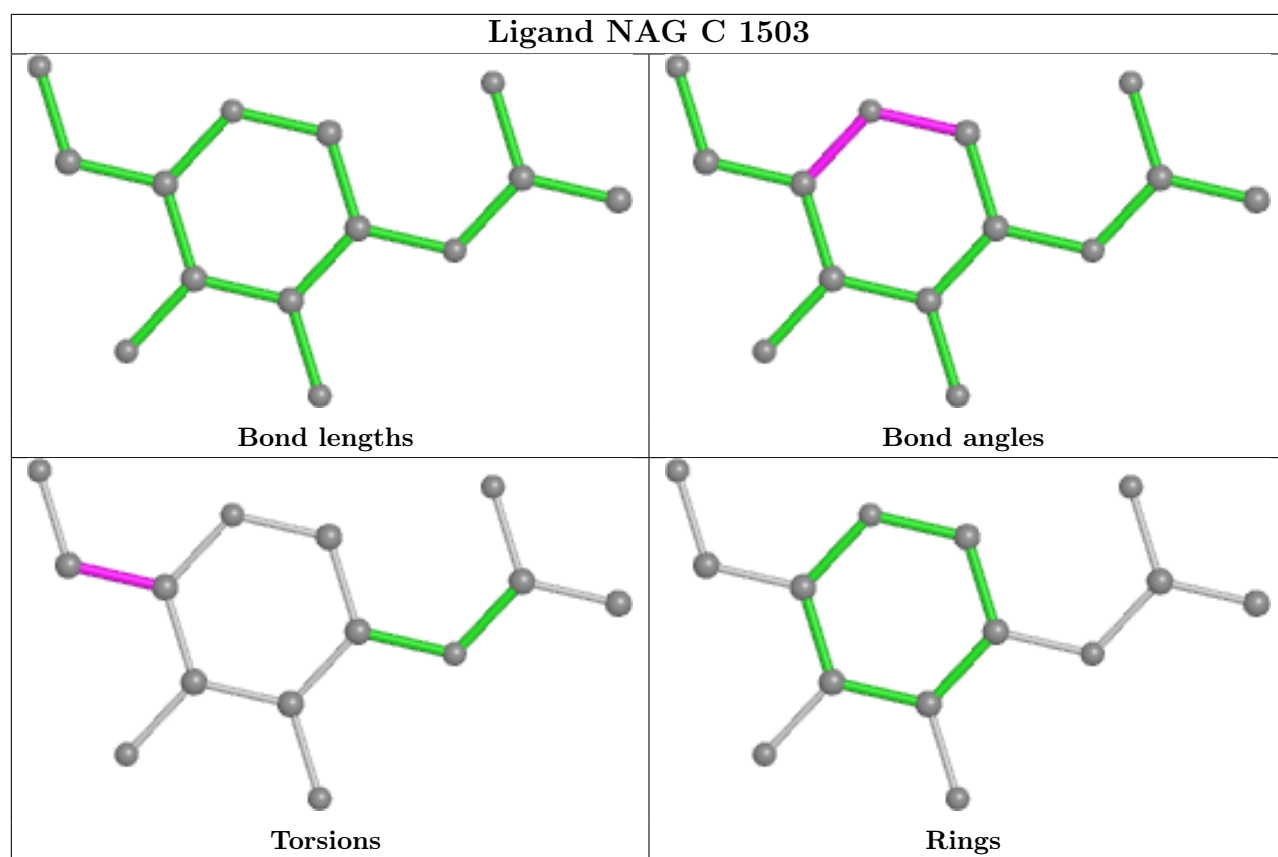


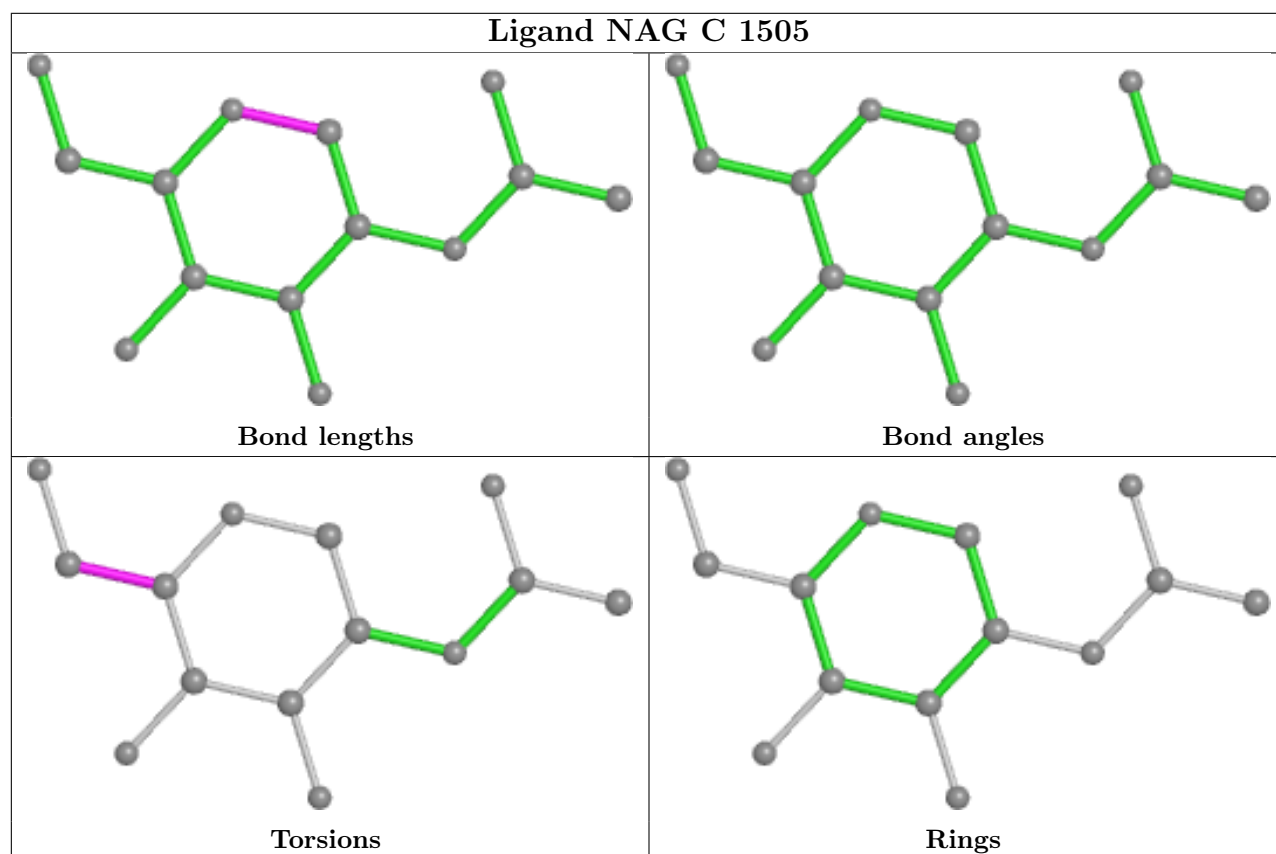
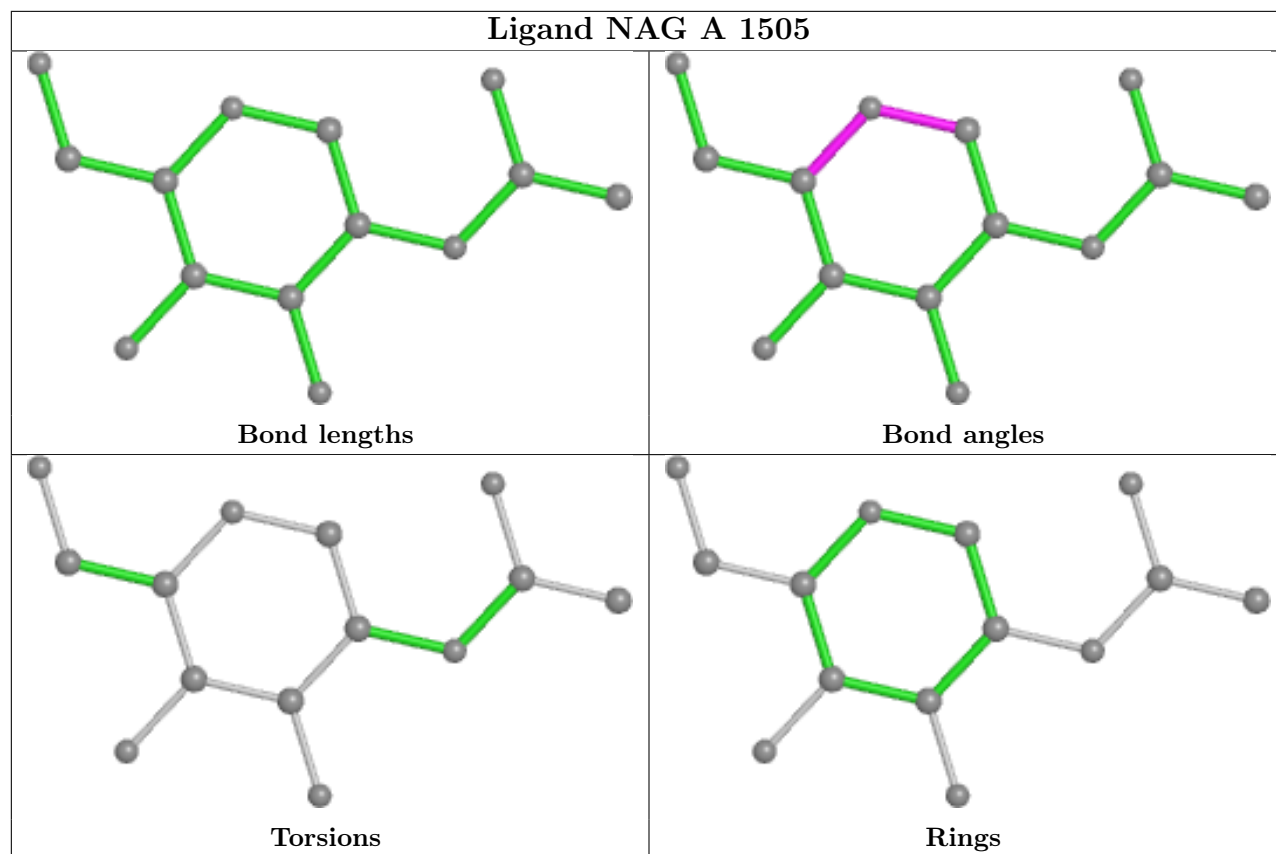


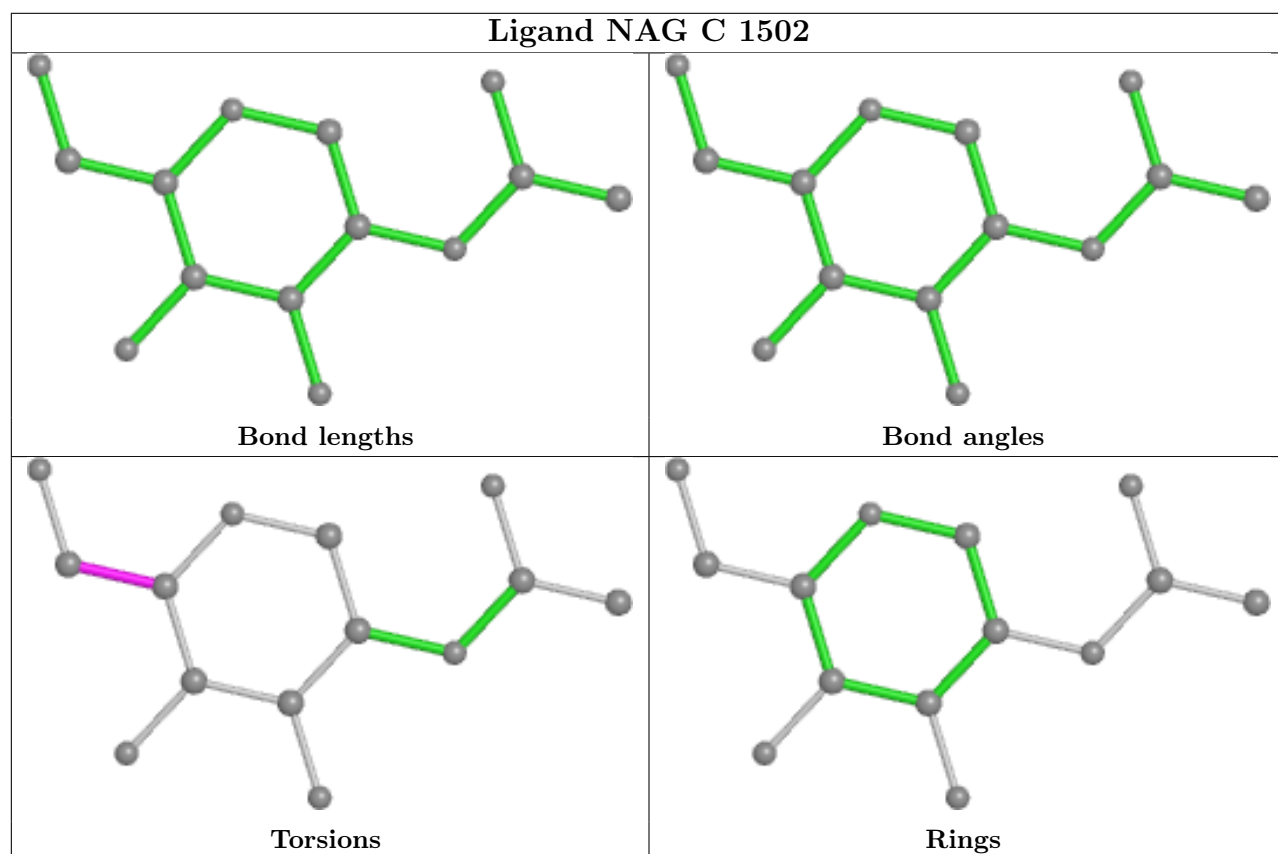
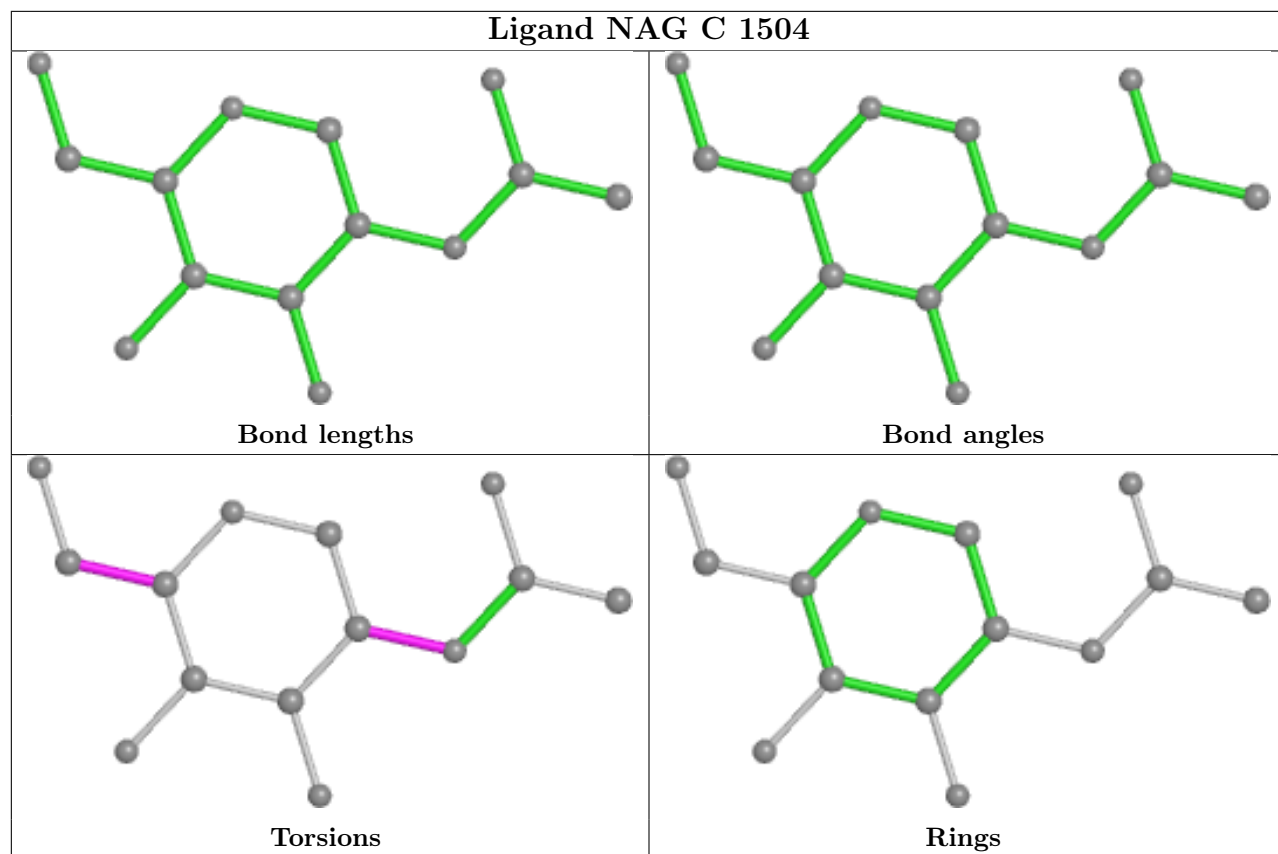


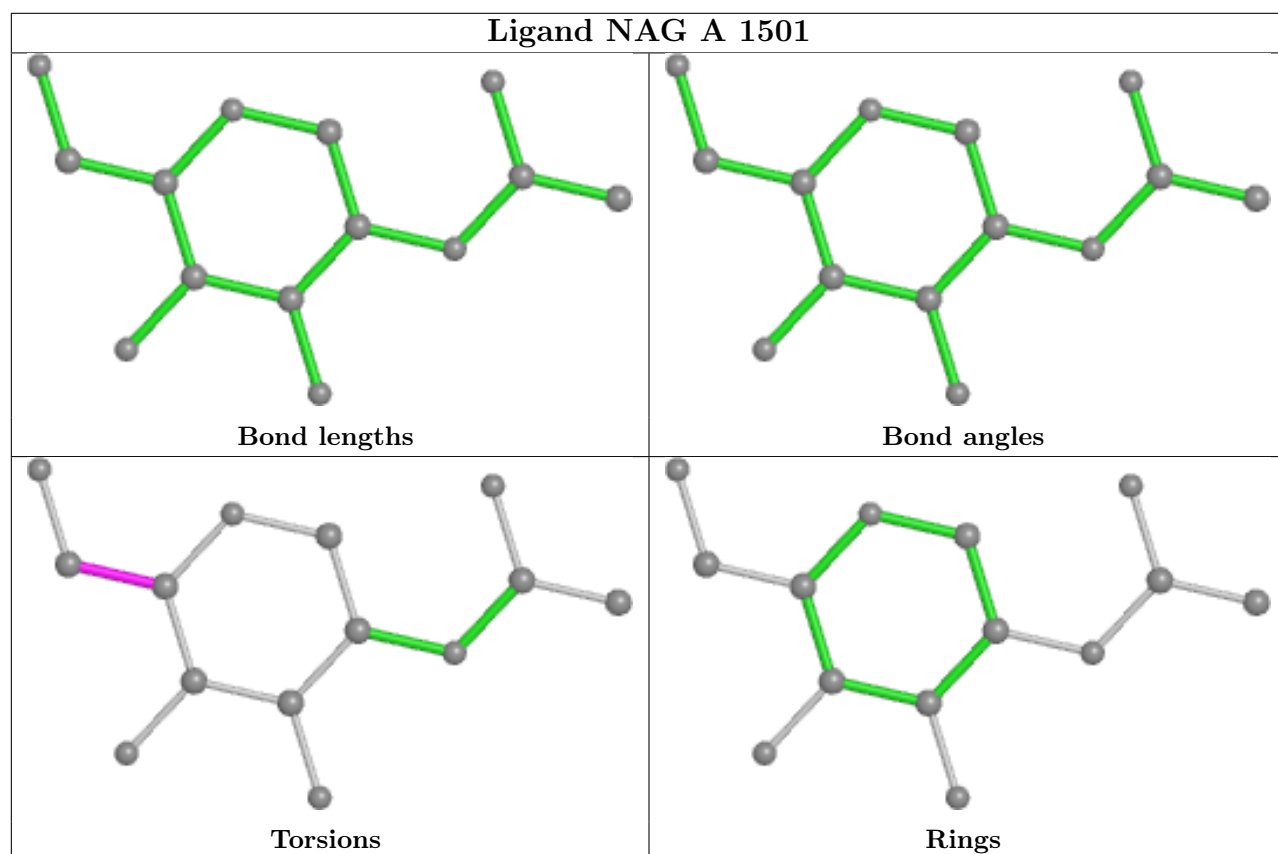
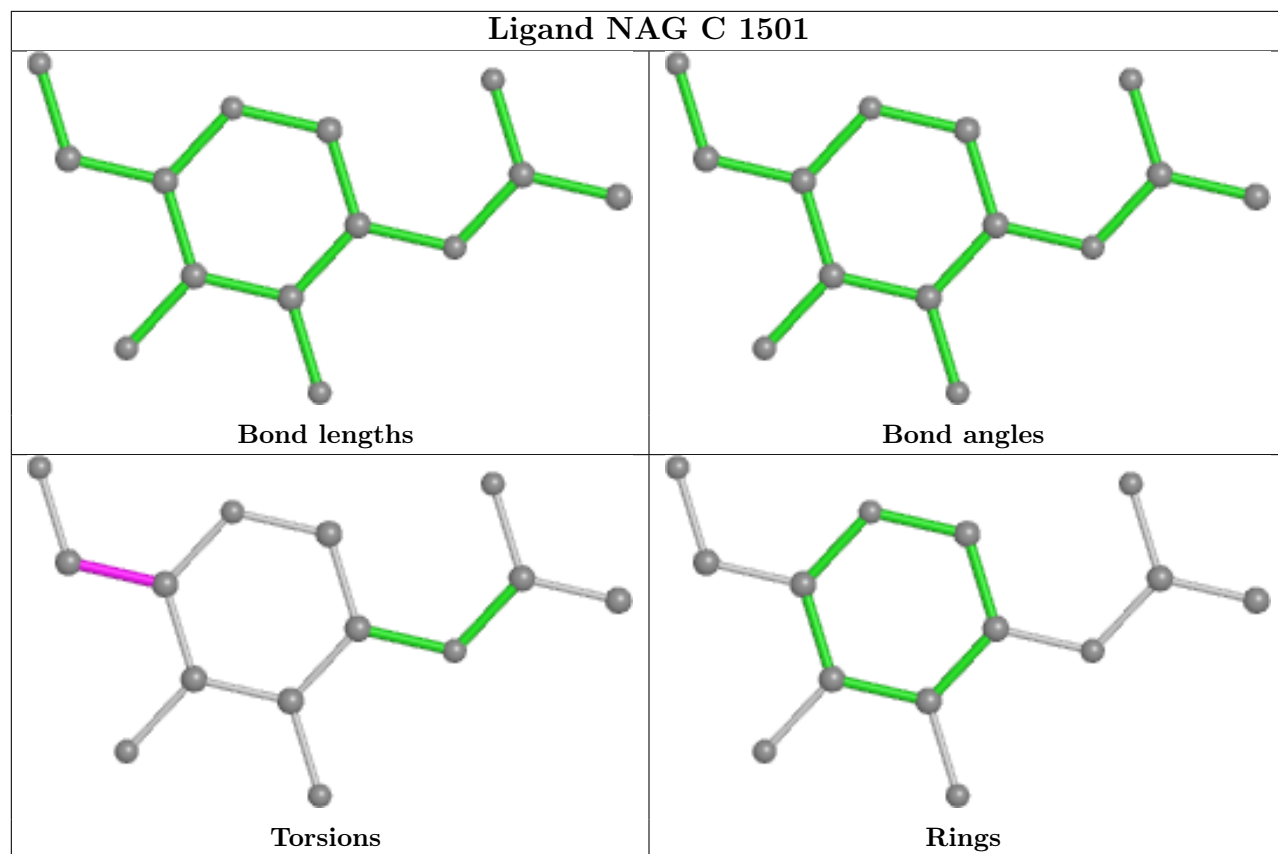












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

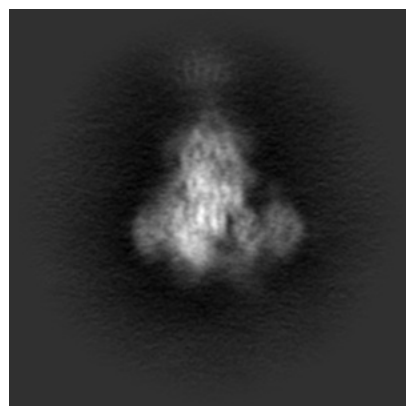
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33647. These allow visual inspection of the internal detail of the map and identification of artifacts.

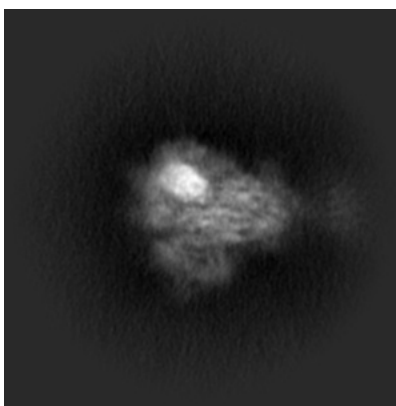
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

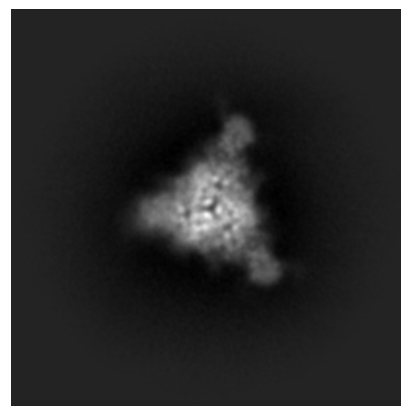
6.1.1 Primary map



X

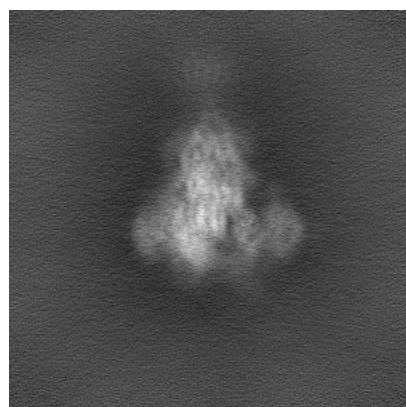


Y

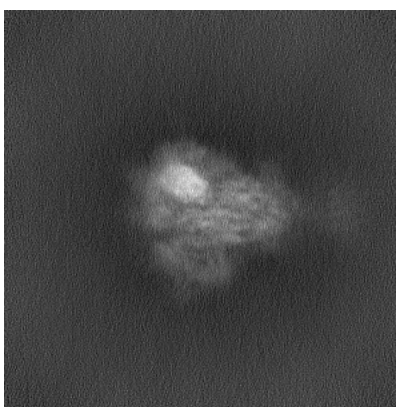


Z

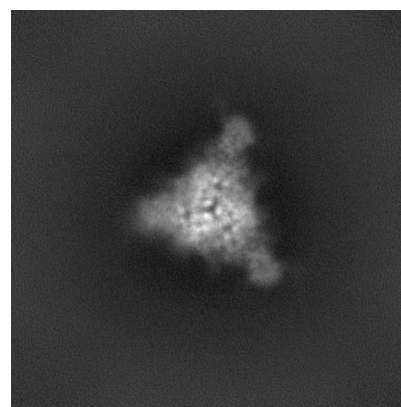
6.1.2 Raw map



X



Y

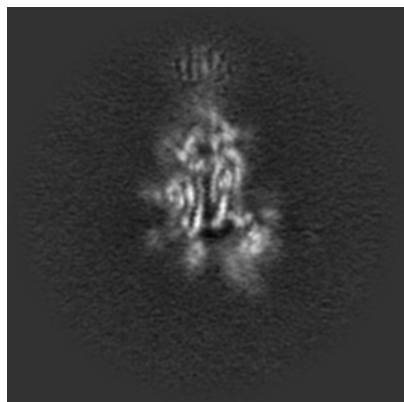


Z

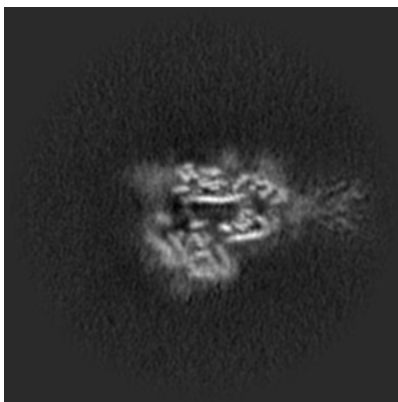
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

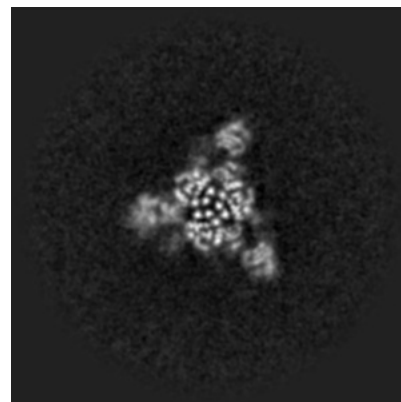
6.2.1 Primary map



X Index: 182

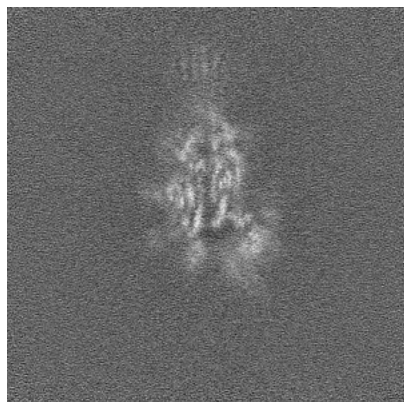


Y Index: 182



Z Index: 182

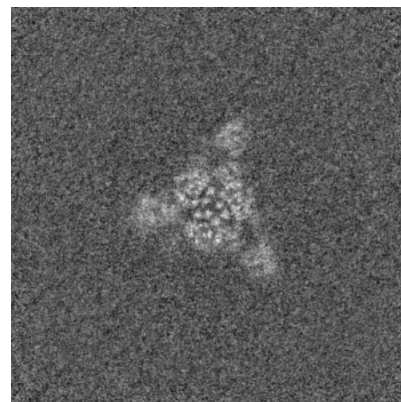
6.2.2 Raw map



X Index: 182



Y Index: 182

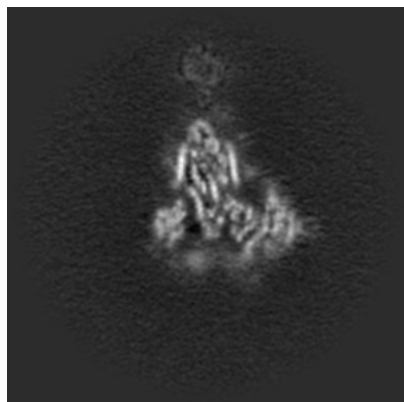


Z Index: 182

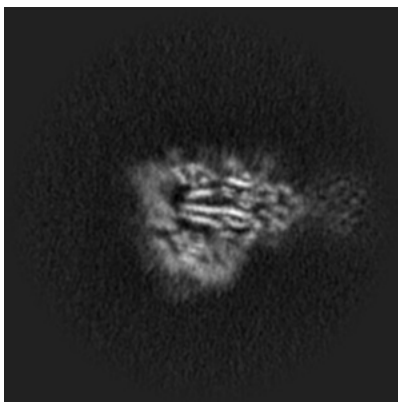
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

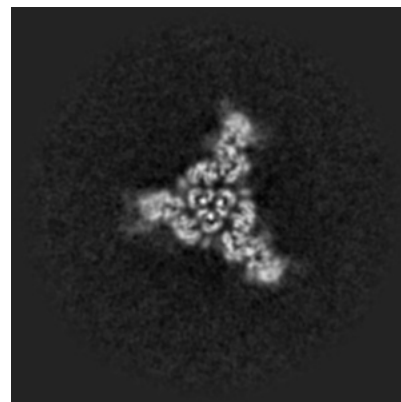
6.3.1 Primary map



X Index: 196

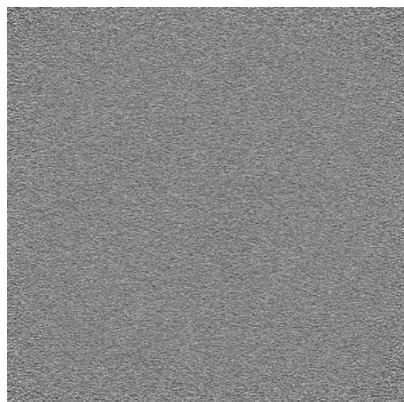


Y Index: 175

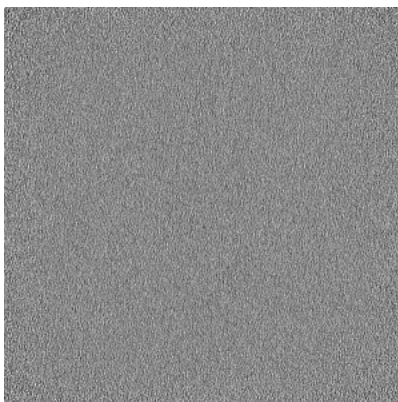


Z Index: 170

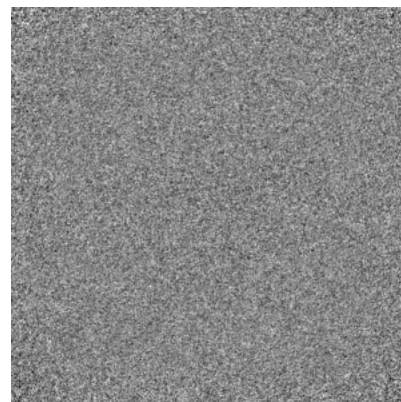
6.3.2 Raw map



X Index: 0



Y Index: 0

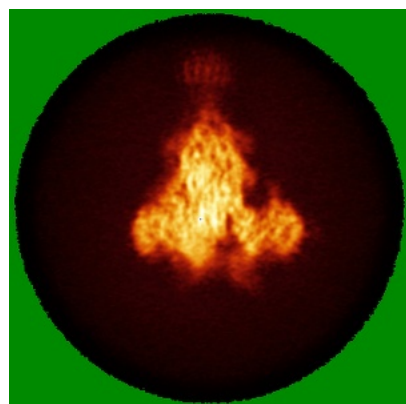


Z Index: 0

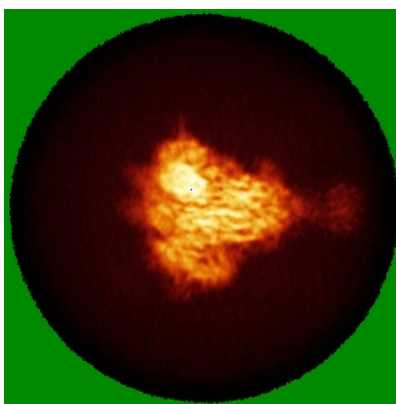
The images above show the largest variance slices of the map in three orthogonal directions.

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

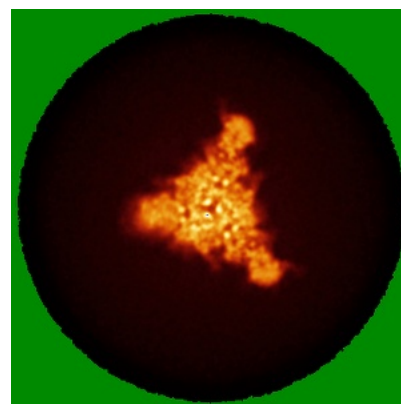
6.4.1 Primary map



X

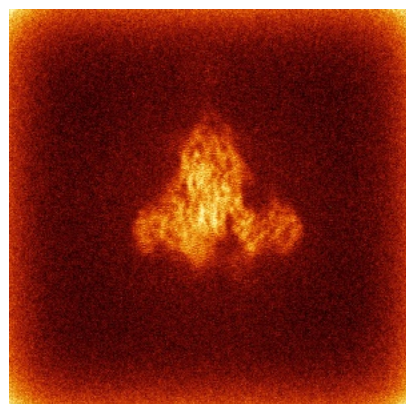


Y

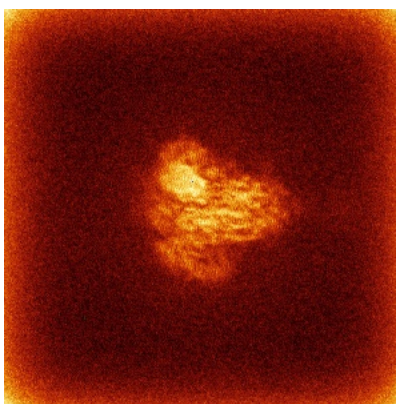


Z

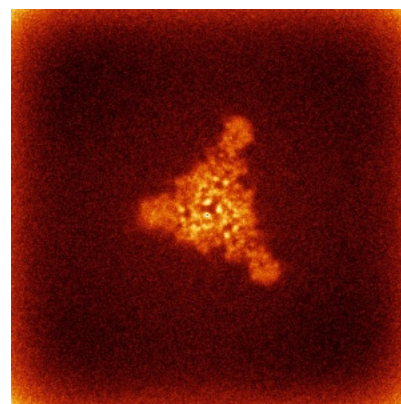
6.4.2 Raw map



X



Y

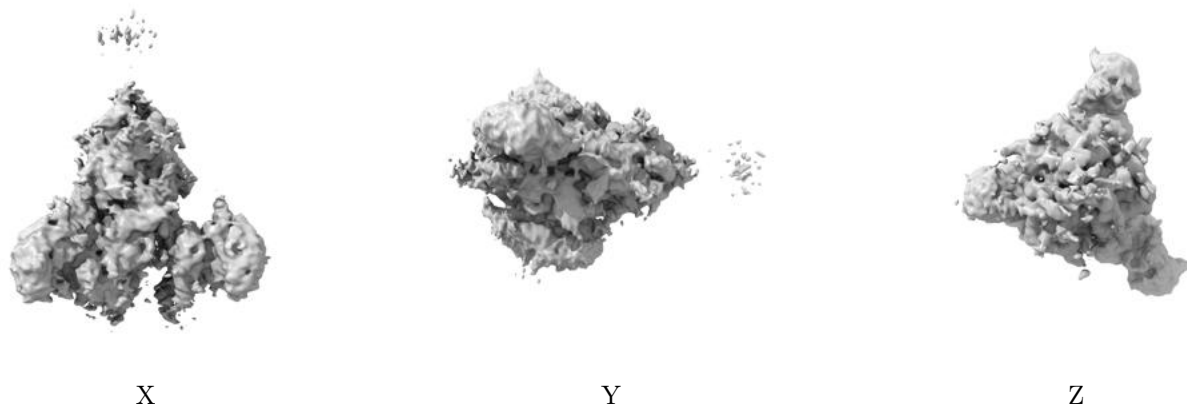


Z

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

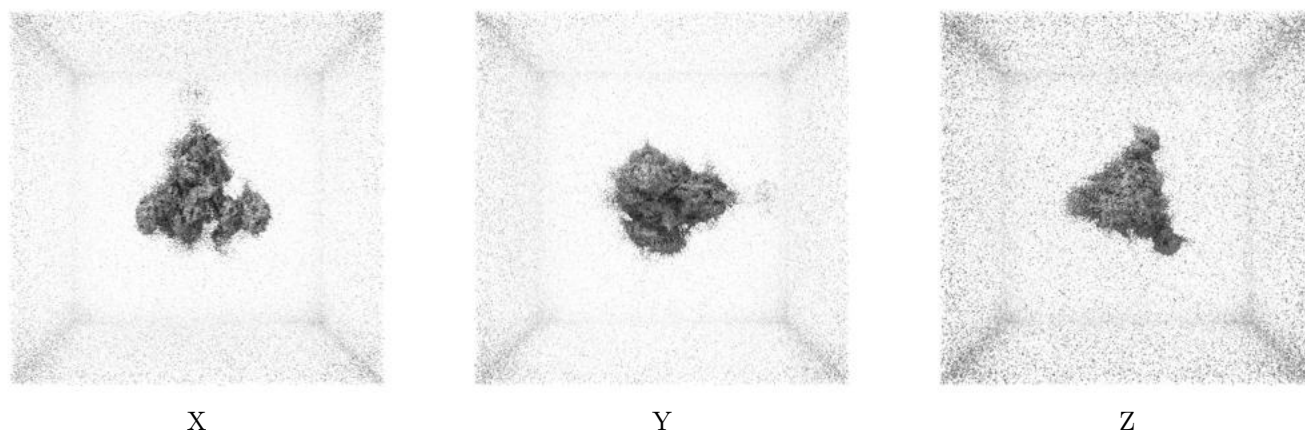
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

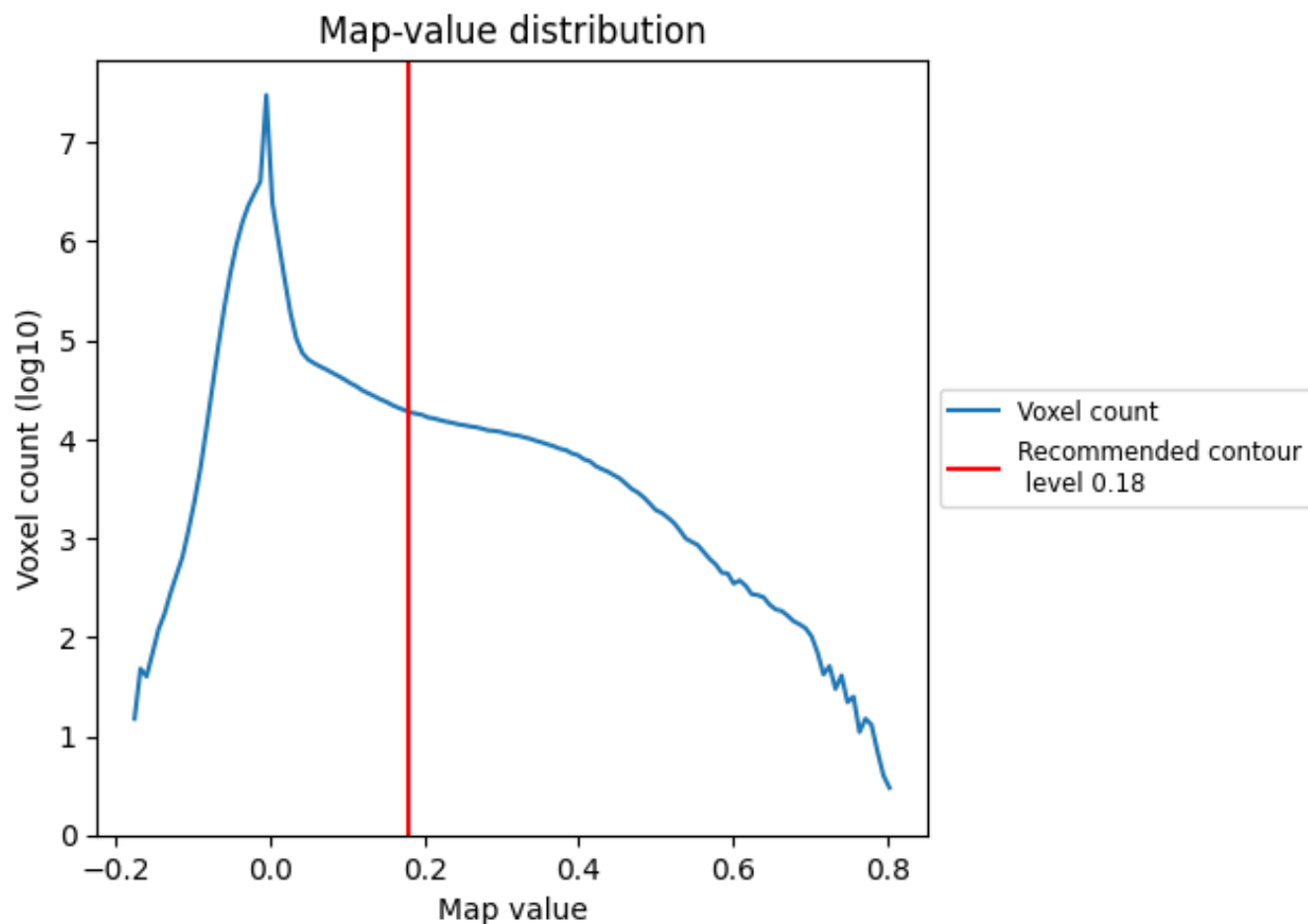
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

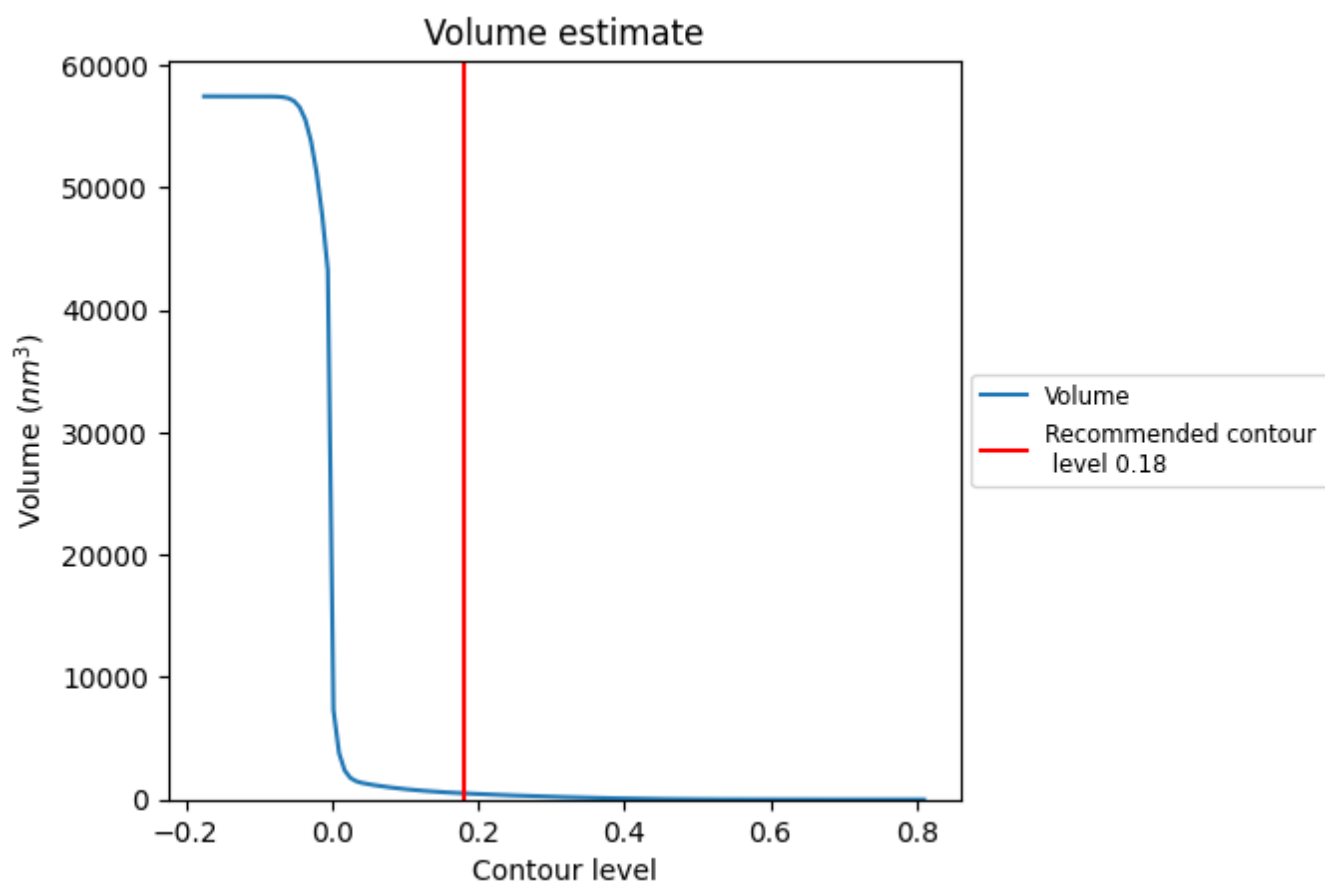
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

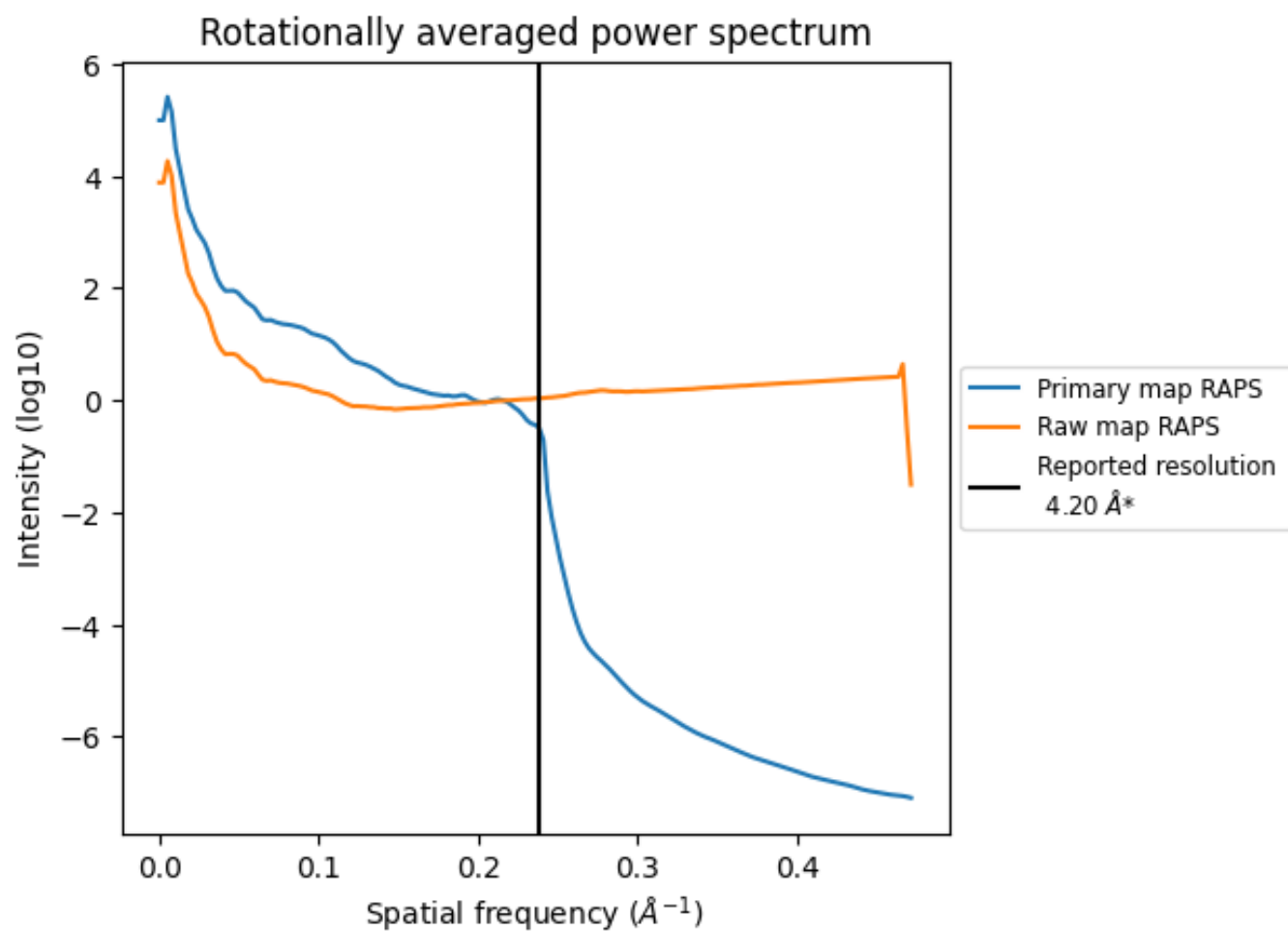
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 511 nm³; this corresponds to an approximate mass of 461 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

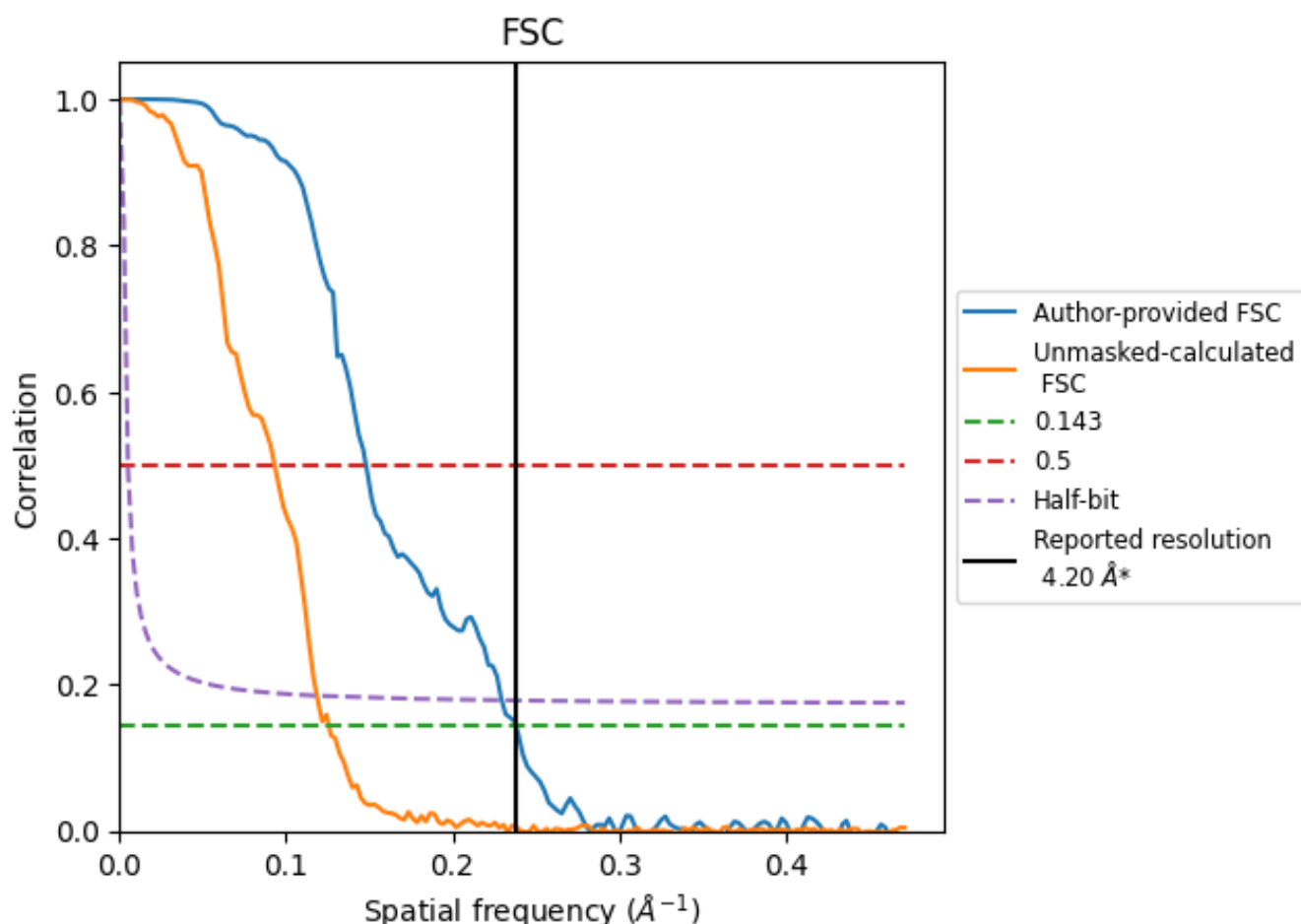


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

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 0.238 \AA^{-1}

8.2 Resolution estimates [i](#)

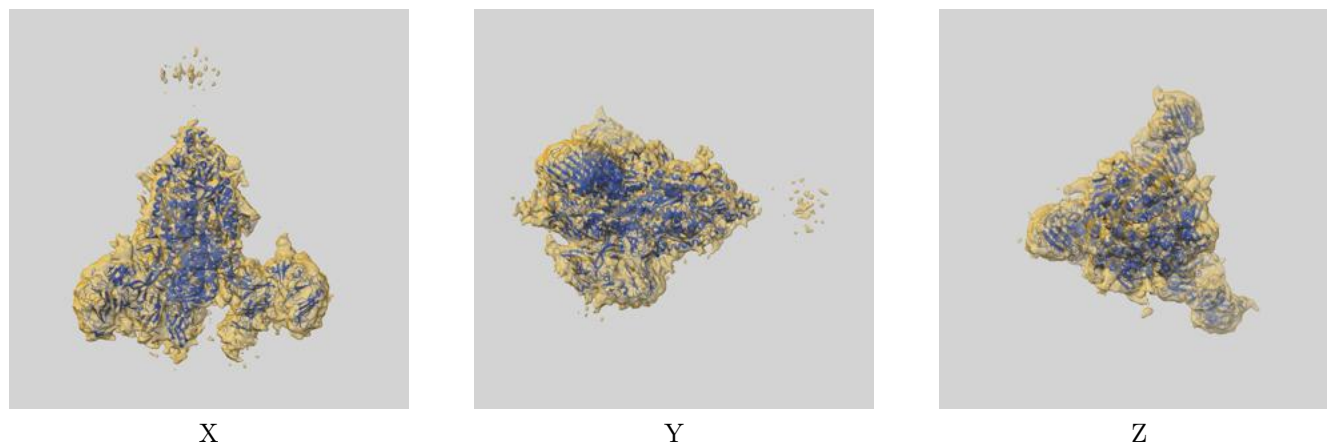
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.20	6.75	4.36
Unmasked-calculated*	7.95	10.74	8.43

*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 7.95 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

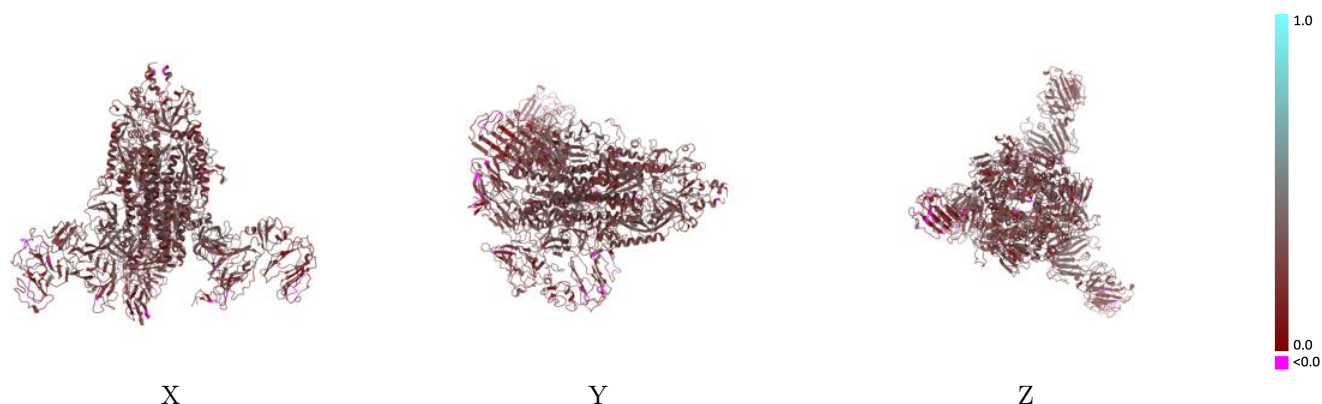
This section contains information regarding the fit between EMDB map EMD-33647 and PDB model 7Y6T. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



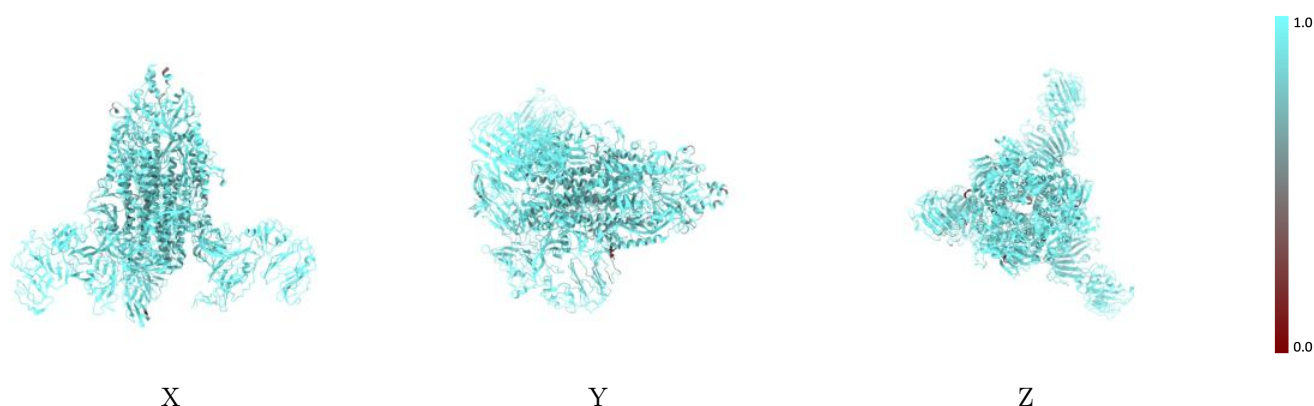
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



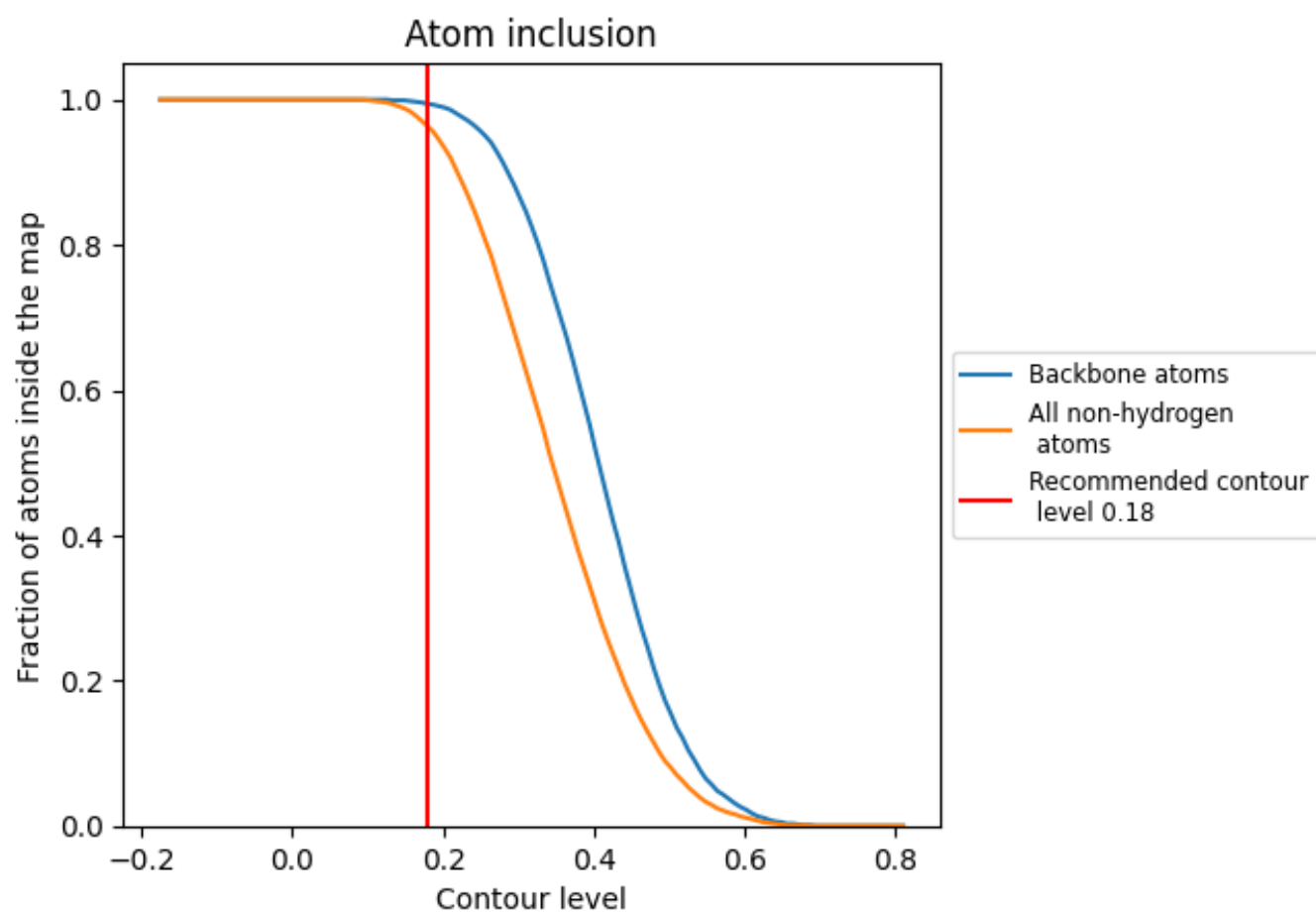
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 96% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9630	 0.2640
A	 0.9590	 0.2440
B	 0.9670	 0.2670
C	 0.9650	 0.2740
D	 0.9840	 0.3490
E	 0.9490	 0.2130
F	 1.0000	 0.3190
G	 0.9740	 0.3540
H	 0.7860	 0.3230
I	 0.9640	 0.3110
J	 0.9290	 0.3290
K	 0.9740	 0.3700
L	 0.7860	 0.2950
M	 0.9740	 0.2390
N	 0.9390	 0.3040
O	 1.0000	 0.3950
P	 0.8750	 0.1870
Q	 0.9490	 0.3760
R	 0.9640	 0.3060
S	 0.9580	 0.2530
T	 0.9740	 0.3620
U	 1.0000	 0.3300
V	 0.9740	 0.3270
W	 0.8930	 0.3130
X	 0.9230	 0.2980
Y	 0.9640	 0.3150
Z	 0.8680	 0.3110
a	 0.9590	 0.3200
b	 1.0000	 0.4180
c	 0.7920	 0.2190
d	 0.9740	 0.3350
e	 0.9290	 0.2700
f	 0.8750	 0.2570
g	 0.9740	 0.3680
h	 1.0000	 0.3410



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Chain	Atom inclusion	Q-score
i	 1.0000	 0.3800
j	 0.9740	 0.3870
k	 0.8160	 0.2890