



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:57 AM EST

PDB ID : 7MY2  
EMDB ID : EMD-24077  
Title : CryoEM structure of neutralizing nanobody Nb30 in complex with SARS-CoV2 spike  
Authors : Xu, K.; Kwong, P.D.  
Deposited on : 2021-05-20  
Resolution : 2.65 Å(reported)  
Based on initial model : 6XKL

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

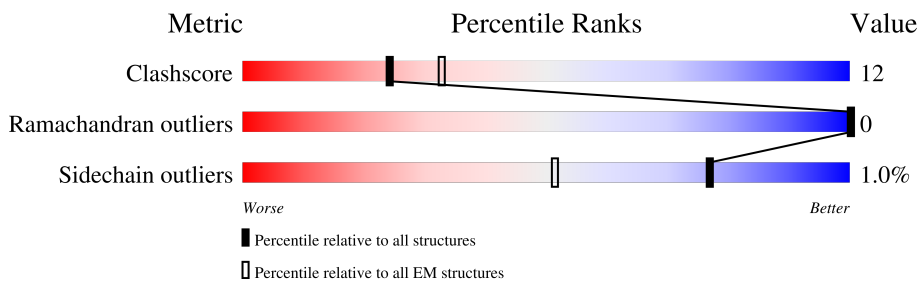
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.65 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	B	1288	62% 18% 20%
1	C	1288	60% 20% 19%
1	E	1288	63% 18% 19%
2	A	131	52% 40% 8%
2	D	131	49% 43% 8%
2	H	131	46% 46% 8%
3	F	2	100%
3	I	2	100%
3	J	2	50% 50%

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Mol	Chain	Length	Quality of chain
3	K	2	 100%
3	L	2	 100%
3	M	2	 100%
3	N	2	 100%
3	O	2	 100%
3	P	2	 100%
3	Q	2	 100%
3	T	2	 50% 50%
4	G	3	 100%
4	S	3	 100%
4	U	3	 100%
4	V	3	 100%
5	R	2	 100%

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 27884 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	B	1036	8062	5154	1339	1533	36	0	0
1	C	1038	8083	5168	1344	1535	36	0	0
1	E	1042	8114	5190	1348	1539	37	0	0

There are 267 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	817	PRO	PHE	engineered mutation	UNP P0DTC2
B	892	PRO	ALA	engineered mutation	UNP P0DTC2
B	899	PRO	ALA	engineered mutation	UNP P0DTC2
B	942	PRO	ALA	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLY	-	expression tag	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP P0DTC2
B	1240	SER	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2
B	1242	GLU	-	expression tag	UNP P0DTC2
B	1243	VAL	-	expression tag	UNP P0DTC2
B	1244	LEU	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	GLN	-	expression tag	UNP P0DTC2
B	1247	GLY	-	expression tag	UNP P0DTC2
B	1248	PRO	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	SER	-	expression tag	UNP P0DTC2
B	1259	ALA	-	expression tag	UNP P0DTC2
B	1260	TRP	-	expression tag	UNP P0DTC2
B	1261	SER	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
B	1263	PRO	-	expression tag	UNP P0DTC2
B	1264	GLN	-	expression tag	UNP P0DTC2
B	1265	PHE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1266	GLU	-	expression tag	UNP P0DTC2
B	1267	LYS	-	expression tag	UNP P0DTC2
B	1268	GLY	-	expression tag	UNP P0DTC2
B	1269	GLY	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	GLY	-	expression tag	UNP P0DTC2
B	1273	GLY	-	expression tag	UNP P0DTC2
B	1274	GLY	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	SER	-	expression tag	UNP P0DTC2
B	1277	GLY	-	expression tag	UNP P0DTC2
B	1278	GLY	-	expression tag	UNP P0DTC2
B	1279	SER	-	expression tag	UNP P0DTC2
B	1280	ALA	-	expression tag	UNP P0DTC2
B	1281	TRP	-	expression tag	UNP P0DTC2
B	1282	SER	-	expression tag	UNP P0DTC2
B	1283	HIS	-	expression tag	UNP P0DTC2
B	1284	PRO	-	expression tag	UNP P0DTC2
B	1285	GLN	-	expression tag	UNP P0DTC2
B	1286	PHE	-	expression tag	UNP P0DTC2
B	1287	GLU	-	expression tag	UNP P0DTC2
B	1288	LYS	-	expression tag	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	817	PRO	PHE	engineered mutation	UNP P0DTC2
C	892	PRO	ALA	engineered mutation	UNP P0DTC2
C	899	PRO	ALA	engineered mutation	UNP P0DTC2
C	942	PRO	ALA	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2
C	1237	LEU	-	expression tag	UNP P0DTC2
C	1238	GLY	-	expression tag	UNP P0DTC2
C	1239	ARG	-	expression tag	UNP P0DTC2
C	1240	SER	-	expression tag	UNP P0DTC2
C	1241	LEU	-	expression tag	UNP P0DTC2
C	1242	GLU	-	expression tag	UNP P0DTC2
C	1243	VAL	-	expression tag	UNP P0DTC2
C	1244	LEU	-	expression tag	UNP P0DTC2
C	1245	PHE	-	expression tag	UNP P0DTC2
C	1246	GLN	-	expression tag	UNP P0DTC2
C	1247	GLY	-	expression tag	UNP P0DTC2
C	1248	PRO	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	HIS	-	expression tag	UNP P0DTC2
C	1251	HIS	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	SER	-	expression tag	UNP P0DTC2
C	1259	ALA	-	expression tag	UNP P0DTC2
C	1260	TRP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1261	SER	-	expression tag	UNP P0DTC2
C	1262	HIS	-	expression tag	UNP P0DTC2
C	1263	PRO	-	expression tag	UNP P0DTC2
C	1264	GLN	-	expression tag	UNP P0DTC2
C	1265	PHE	-	expression tag	UNP P0DTC2
C	1266	GLU	-	expression tag	UNP P0DTC2
C	1267	LYS	-	expression tag	UNP P0DTC2
C	1268	GLY	-	expression tag	UNP P0DTC2
C	1269	GLY	-	expression tag	UNP P0DTC2
C	1270	GLY	-	expression tag	UNP P0DTC2
C	1271	SER	-	expression tag	UNP P0DTC2
C	1272	GLY	-	expression tag	UNP P0DTC2
C	1273	GLY	-	expression tag	UNP P0DTC2
C	1274	GLY	-	expression tag	UNP P0DTC2
C	1275	GLY	-	expression tag	UNP P0DTC2
C	1276	SER	-	expression tag	UNP P0DTC2
C	1277	GLY	-	expression tag	UNP P0DTC2
C	1278	GLY	-	expression tag	UNP P0DTC2
C	1279	SER	-	expression tag	UNP P0DTC2
C	1280	ALA	-	expression tag	UNP P0DTC2
C	1281	TRP	-	expression tag	UNP P0DTC2
C	1282	SER	-	expression tag	UNP P0DTC2
C	1283	HIS	-	expression tag	UNP P0DTC2
C	1284	PRO	-	expression tag	UNP P0DTC2
C	1285	GLN	-	expression tag	UNP P0DTC2
C	1286	PHE	-	expression tag	UNP P0DTC2
C	1287	GLU	-	expression tag	UNP P0DTC2
C	1288	LYS	-	expression tag	UNP P0DTC2
E	682	GLY	ARG	engineered mutation	UNP P0DTC2
E	683	SER	ARG	engineered mutation	UNP P0DTC2
E	685	SER	ARG	engineered mutation	UNP P0DTC2
E	817	PRO	PHE	engineered mutation	UNP P0DTC2
E	892	PRO	ALA	engineered mutation	UNP P0DTC2
E	899	PRO	ALA	engineered mutation	UNP P0DTC2
E	942	PRO	ALA	engineered mutation	UNP P0DTC2
E	986	PRO	LYS	engineered mutation	UNP P0DTC2
E	987	PRO	VAL	engineered mutation	UNP P0DTC2
E	1209	GLY	-	expression tag	UNP P0DTC2
E	1210	SER	-	expression tag	UNP P0DTC2
E	1211	GLY	-	expression tag	UNP P0DTC2
E	1212	TYR	-	expression tag	UNP P0DTC2
E	1213	ILE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1214	PRO	-	expression tag	UNP P0DTC2
E	1215	GLU	-	expression tag	UNP P0DTC2
E	1216	ALA	-	expression tag	UNP P0DTC2
E	1217	PRO	-	expression tag	UNP P0DTC2
E	1218	ARG	-	expression tag	UNP P0DTC2
E	1219	ASP	-	expression tag	UNP P0DTC2
E	1220	GLY	-	expression tag	UNP P0DTC2
E	1221	GLN	-	expression tag	UNP P0DTC2
E	1222	ALA	-	expression tag	UNP P0DTC2
E	1223	TYR	-	expression tag	UNP P0DTC2
E	1224	VAL	-	expression tag	UNP P0DTC2
E	1225	ARG	-	expression tag	UNP P0DTC2
E	1226	LYS	-	expression tag	UNP P0DTC2
E	1227	ASP	-	expression tag	UNP P0DTC2
E	1228	GLY	-	expression tag	UNP P0DTC2
E	1229	GLU	-	expression tag	UNP P0DTC2
E	1230	TRP	-	expression tag	UNP P0DTC2
E	1231	VAL	-	expression tag	UNP P0DTC2
E	1232	LEU	-	expression tag	UNP P0DTC2
E	1233	LEU	-	expression tag	UNP P0DTC2
E	1234	SER	-	expression tag	UNP P0DTC2
E	1235	THR	-	expression tag	UNP P0DTC2
E	1236	PHE	-	expression tag	UNP P0DTC2
E	1237	LEU	-	expression tag	UNP P0DTC2
E	1238	GLY	-	expression tag	UNP P0DTC2
E	1239	ARG	-	expression tag	UNP P0DTC2
E	1240	SER	-	expression tag	UNP P0DTC2
E	1241	LEU	-	expression tag	UNP P0DTC2
E	1242	GLU	-	expression tag	UNP P0DTC2
E	1243	VAL	-	expression tag	UNP P0DTC2
E	1244	LEU	-	expression tag	UNP P0DTC2
E	1245	PHE	-	expression tag	UNP P0DTC2
E	1246	GLN	-	expression tag	UNP P0DTC2
E	1247	GLY	-	expression tag	UNP P0DTC2
E	1248	PRO	-	expression tag	UNP P0DTC2
E	1249	GLY	-	expression tag	UNP P0DTC2
E	1250	HIS	-	expression tag	UNP P0DTC2
E	1251	HIS	-	expression tag	UNP P0DTC2
E	1252	HIS	-	expression tag	UNP P0DTC2
E	1253	HIS	-	expression tag	UNP P0DTC2
E	1254	HIS	-	expression tag	UNP P0DTC2
E	1255	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1256	HIS	-	expression tag	UNP P0DTC2
E	1257	HIS	-	expression tag	UNP P0DTC2
E	1258	SER	-	expression tag	UNP P0DTC2
E	1259	ALA	-	expression tag	UNP P0DTC2
E	1260	TRP	-	expression tag	UNP P0DTC2
E	1261	SER	-	expression tag	UNP P0DTC2
E	1262	HIS	-	expression tag	UNP P0DTC2
E	1263	PRO	-	expression tag	UNP P0DTC2
E	1264	GLN	-	expression tag	UNP P0DTC2
E	1265	PHE	-	expression tag	UNP P0DTC2
E	1266	GLU	-	expression tag	UNP P0DTC2
E	1267	LYS	-	expression tag	UNP P0DTC2
E	1268	GLY	-	expression tag	UNP P0DTC2
E	1269	GLY	-	expression tag	UNP P0DTC2
E	1270	GLY	-	expression tag	UNP P0DTC2
E	1271	SER	-	expression tag	UNP P0DTC2
E	1272	GLY	-	expression tag	UNP P0DTC2
E	1273	GLY	-	expression tag	UNP P0DTC2
E	1274	GLY	-	expression tag	UNP P0DTC2
E	1275	GLY	-	expression tag	UNP P0DTC2
E	1276	SER	-	expression tag	UNP P0DTC2
E	1277	GLY	-	expression tag	UNP P0DTC2
E	1278	GLY	-	expression tag	UNP P0DTC2
E	1279	SER	-	expression tag	UNP P0DTC2
E	1280	ALA	-	expression tag	UNP P0DTC2
E	1281	TRP	-	expression tag	UNP P0DTC2
E	1282	SER	-	expression tag	UNP P0DTC2
E	1283	HIS	-	expression tag	UNP P0DTC2
E	1284	PRO	-	expression tag	UNP P0DTC2
E	1285	GLN	-	expression tag	UNP P0DTC2
E	1286	PHE	-	expression tag	UNP P0DTC2
E	1287	GLU	-	expression tag	UNP P0DTC2
E	1288	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called Nanobody Nb30.

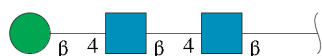
Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	N	O			S
2	H	120	Total	C	N	O	S	0	0
			910	571	157	176	6		
2	A	120	Total	C	N	O	S	0	0
			910	571	157	176	6		
2	D	120	Total	C	N	O	S	0	0
			910	571	157	176	6		

- 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
			Total	C	N	O		
3	F	2	28	16	2	10	0	0
3	I	2	28	16	2	10	0	0
3	J	2	28	16	2	10	0	0
3	K	2	28	16	2	10	0	0
3	L	2	28	16	2	10	0	0
3	M	2	28	16	2	10	0	0
3	N	2	28	16	2	10	0	0
3	O	2	28	16	2	10	0	0
3	P	2	28	16	2	10	0	0
3	Q	2	28	16	2	10	0	0
3	T	2	28	16	2	10	0	0

- Molecule 4 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		
4	G	3	39	22	2	15	0	0
4	S	3	39	22	2	15	0	0

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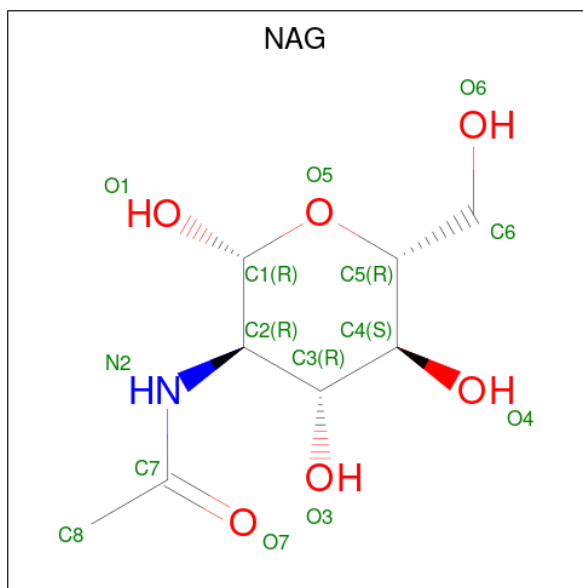
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	U	3	39	22	2	15	0	0
4	V	3	39	22	2	15	0	0

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	R	2	25	14	1	10	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	B	1	140	80	10	50	0
6	B	1	140	80	10	50	0
6	B	1	140	80	10	50	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	B	1	Total 140	C 80	N 10	O 50	0
6	B	1	Total 140	C 80	N 10	O 50	0
6	B	1	Total 140	C 80	N 10	O 50	0
6	B	1	Total 140	C 80	N 10	O 50	0
6	B	1	Total 140	C 80	N 10	O 50	0
6	B	1	Total 140	C 80	N 10	O 50	0
6	B	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	C	1	Total 140	C 80	N 10	O 50	0
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0

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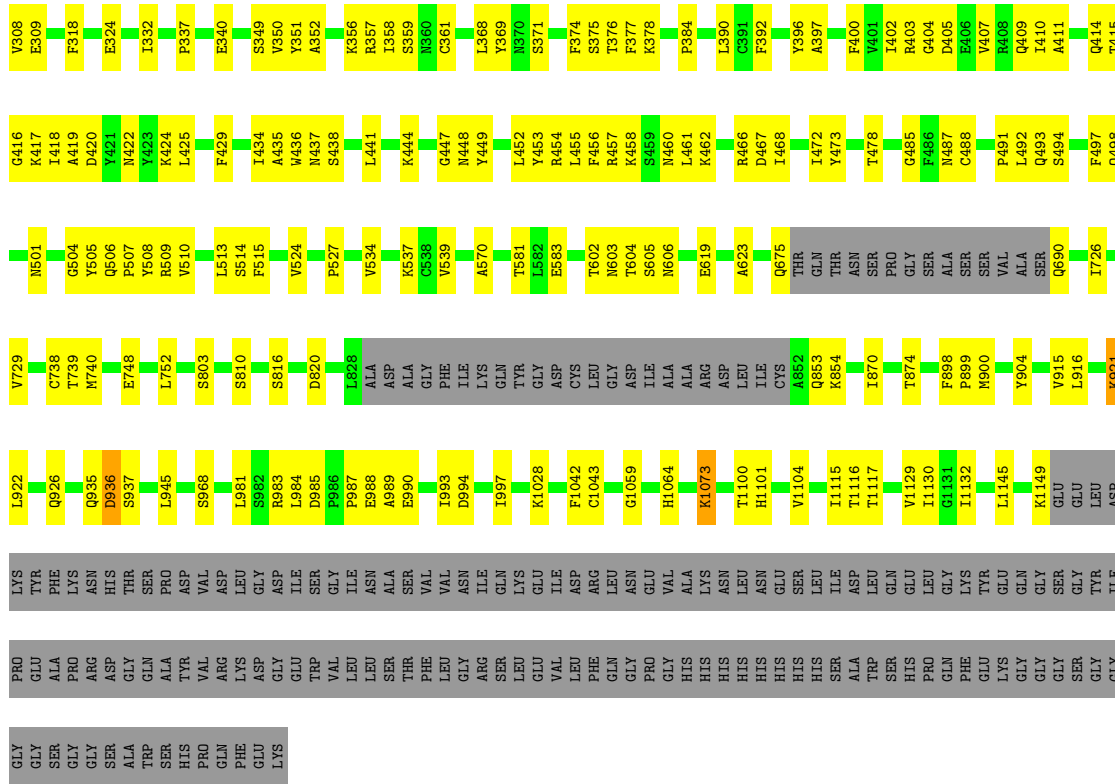
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0
6	E	1	Total 126	C 72	N 9	O 45	0

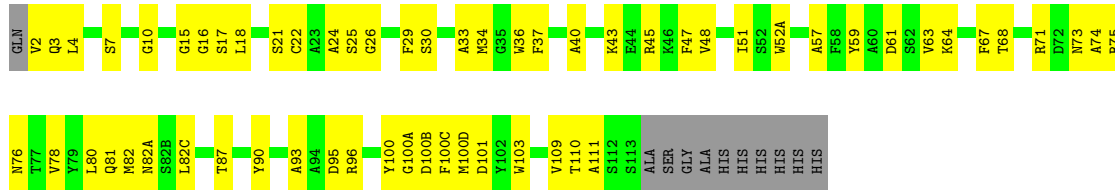




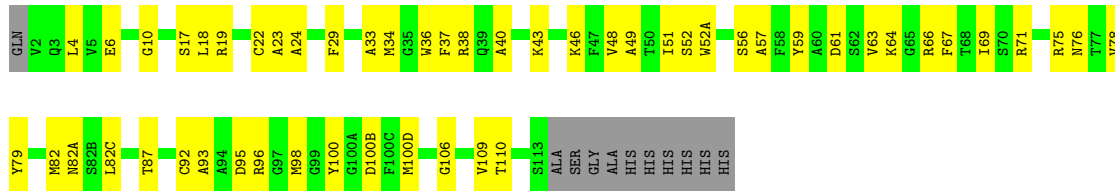




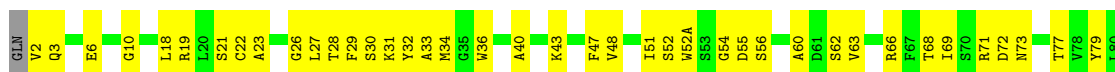
- Molecule 2: Nanobody Nb30

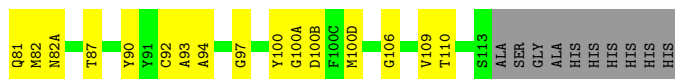


- Molecule 2: Nanobody Nb30



- Molecule 2: Nanobody Nb30





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

Chain F: 100%

NAG1  
NAG2

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

Chain I: 100%

NAG1  
NAG2

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

Chain J: 50% 50%

NAG1  
NAG2

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

Chain K: 100%

NAG1  
NAG2

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

Chain L: 100%

NAG1  
NAG2

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

Chain M: 100%

NAG1  
NAG2

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

Chain N:  100%

MAG1  
MAG2

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

Chain O:  100%

MAG1  
MAG2

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

Chain P:  100%

MAG1  
MAG2

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

Chain Q:  100%

MAG1  
MAG2

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

Chain T:  50% 50%

MAG1  
MAG2

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

Chain G:  100%

MAG1  
MAG2  
BMA3

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

Chain S:  100%



MAG1  
MAG2  
BHA3

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

Chain U:  100%



MAG1  
MAG2  
BHA3

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

Chain V:  100%



MAG1  
MAG2  
BHA3

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

Chain R:  100%



MAG1  
BHA2

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	333232	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 ( $e^-/\text{\AA}^2$ )	40.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	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

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	B	0.41	2/8251 (0.0%)	0.53	0/11238
1	C	0.42	2/8273 (0.0%)	0.56	2/11268 (0.0%)
1	E	0.41	2/8305 (0.0%)	0.54	1/11310 (0.0%)
2	A	0.27	0/930	0.52	0/1254
2	D	0.27	0/930	0.51	0/1254
2	H	0.27	0/930	0.51	0/1254
All	All	0.40	6/27619 (0.0%)	0.54	3/37578 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
All	All	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	803	SER	CA-CB	-6.02	1.44	1.52
1	E	816	SER	CA-CB	-5.91	1.44	1.52
1	C	803	SER	CA-CB	-5.86	1.44	1.52
1	E	803	SER	CA-CB	-5.42	1.44	1.52
1	C	816	SER	CA-CB	-5.18	1.45	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	904	TYR	CB-CA-C	-6.81	96.78	110.40
1	C	897	PRO	N-CA-CB	-5.63	96.41	102.60
1	E	904	TYR	CB-CA-C	-5.24	99.91	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	122	ASN	Peptide
1	C	617	CYS	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	8062	0	7839	186	0
1	C	8083	0	7857	183	0
1	E	8114	0	7889	163	0
2	A	910	0	864	43	0
2	D	910	0	864	44	0
2	H	910	0	864	49	0
3	F	28	0	25	0	0
3	I	28	0	25	0	0
3	J	28	0	25	1	0
3	K	28	0	25	0	0
3	L	28	0	25	0	0
3	M	28	0	25	0	0
3	N	28	0	25	0	0
3	O	28	0	25	0	0
3	P	28	0	25	0	0
3	Q	28	0	25	0	0
3	T	28	0	25	1	0
4	G	39	0	34	0	0
4	S	39	0	34	0	0
4	U	39	0	34	0	0
4	V	39	0	34	0	0
5	R	25	0	22	0	0
6	B	140	0	130	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	140	0	130	3	0
6	E	126	0	117	0	0
All	All	27884	0	26987	653	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 12.

The worst 5 of 653 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:E:402:ILE:O	1:E:507:PRO:HA	1.49	1.11
2:D:90:TYR:O	2:D:106:GLY:HA2	1.58	1.01
1:B:434:ILE:O	1:B:510:VAL:HA	1.64	0.98
1:E:411:ALA:HB3	1:E:414:GLN:HB3	1.55	0.88
1:B:318:PHE:HZ	1:B:615:VAL:HG21	1.41	0.86

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	B	1022/1288 (79%)	951 (93%)	71 (7%)	0	100	100
1	C	1024/1288 (80%)	947 (92%)	77 (8%)	0	100	100
1	E	1028/1288 (80%)	966 (94%)	62 (6%)	0	100	100
2	A	118/131 (90%)	106 (90%)	12 (10%)	0	100	100
2	D	118/131 (90%)	106 (90%)	12 (10%)	0	100	100
2	H	118/131 (90%)	112 (95%)	6 (5%)	0	100	100
All	All	3428/4257 (80%)	3188 (93%)	240 (7%)	0	100	100



There are no Ramachandran outliers to report.

### 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	B	898/1116 (80%)	893 (99%)	5 (1%)	86	92
1	C	900/1116 (81%)	887 (99%)	13 (1%)	67	81
1	E	903/1116 (81%)	892 (99%)	11 (1%)	71	84
2	A	92/100 (92%)	92 (100%)	0	100	100
2	D	92/100 (92%)	92 (100%)	0	100	100
2	H	92/100 (92%)	92 (100%)	0	100	100
All	All	2977/3648 (82%)	2948 (99%)	29 (1%)	77	86

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	939	SER
1	E	936	ASP
1	C	1073	LYS
1	E	916	LEU
1	C	943	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	804	GLN
1	C	901	GLN
1	E	448	ASN
1	E	501	ASN
1	E	506	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](#)

36 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	$\# Z  > 2$
3	NAG	F	1	1,3	14,14,15	0.21	0	17,19,21	0.50	0
3	NAG	F	2	3	14,14,15	0.20	0	17,19,21	0.43	0
4	NAG	G	1	1,4	14,14,15	0.23	0	17,19,21	0.50	0
4	NAG	G	2	4	14,14,15	0.24	0	17,19,21	0.46	0
4	BMA	G	3	4	11,11,12	0.58	0	15,15,17	0.69	0
3	NAG	I	1	1,3	14,14,15	0.25	0	17,19,21	0.46	0
3	NAG	I	2	3	14,14,15	0.20	0	17,19,21	0.45	0
3	NAG	J	1	1,3	14,14,15	0.44	0	17,19,21	0.44	0
3	NAG	J	2	3	14,14,15	0.28	0	17,19,21	0.52	0
3	NAG	K	1	1,3	14,14,15	0.17	0	17,19,21	0.43	0
3	NAG	K	2	3	14,14,15	0.19	0	17,19,21	0.46	0
3	NAG	L	1	1,3	14,14,15	0.26	0	17,19,21	0.51	0
3	NAG	L	2	3	14,14,15	0.19	0	17,19,21	0.41	0
3	NAG	M	1	1,3	14,14,15	0.22	0	17,19,21	0.49	0
3	NAG	M	2	3	14,14,15	0.19	0	17,19,21	0.43	0
3	NAG	N	1	1,3	14,14,15	0.24	0	17,19,21	0.48	0
3	NAG	N	2	3	14,14,15	0.19	0	17,19,21	0.49	0
3	NAG	O	1	1,3	14,14,15	0.17	0	17,19,21	0.46	0
3	NAG	O	2	3	14,14,15	0.21	0	17,19,21	0.45	0
3	NAG	P	1	1,3	14,14,15	0.31	0	17,19,21	0.59	0
3	NAG	P	2	3	14,14,15	0.29	0	17,19,21	0.51	0
3	NAG	Q	1	1,3	14,14,15	0.17	0	17,19,21	0.57	0
3	NAG	Q	2	3	14,14,15	0.19	0	17,19,21	0.42	0
5	NAG	R	1	1,5	14,14,15	0.30	0	17,19,21	0.46	0
5	BMA	R	2	5	11,11,12	0.61	0	15,15,17	0.65	0
4	NAG	S	1	1,4	14,14,15	0.27	0	17,19,21	0.49	0
4	NAG	S	2	4	14,14,15	0.26	0	17,19,21	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	BMA	S	3	4	11,11,12	0.56	0	15,15,17	0.74	0
3	NAG	T	1	1,3	14,14,15	0.28	0	17,19,21	0.50	0
3	NAG	T	2	3	14,14,15	0.42	0	17,19,21	1.26	1 (5%)
4	NAG	U	1	1,4	14,14,15	0.23	0	17,19,21	0.50	0
4	NAG	U	2	4	14,14,15	0.18	0	17,19,21	0.45	0
4	BMA	U	3	4	11,11,12	0.58	0	15,15,17	0.77	0
4	NAG	V	1	1,4	14,14,15	0.37	0	17,19,21	0.49	0
4	NAG	V	2	4	14,14,15	0.22	0	17,19,21	0.44	0
4	BMA	V	3	4	11,11,12	0.68	0	15,15,17	1.07	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. '2' means no outliers of that kind were identified.

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	S	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	2/6/23/26	0/1/1/1
4	BMA	S	3	4	-	2/2/19/22	0/1/1/1
3	NAG	T	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	T	2	3	-	5/6/23/26	0/1/1/1
4	NAG	U	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1
4	BMA	U	3	4	-	2/2/19/22	0/1/1/1
4	NAG	V	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	V	2	4	-	1/6/23/26	0/1/1/1
4	BMA	V	3	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	2	NAG	C2-N2-C7	4.33	129.07	122.90

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

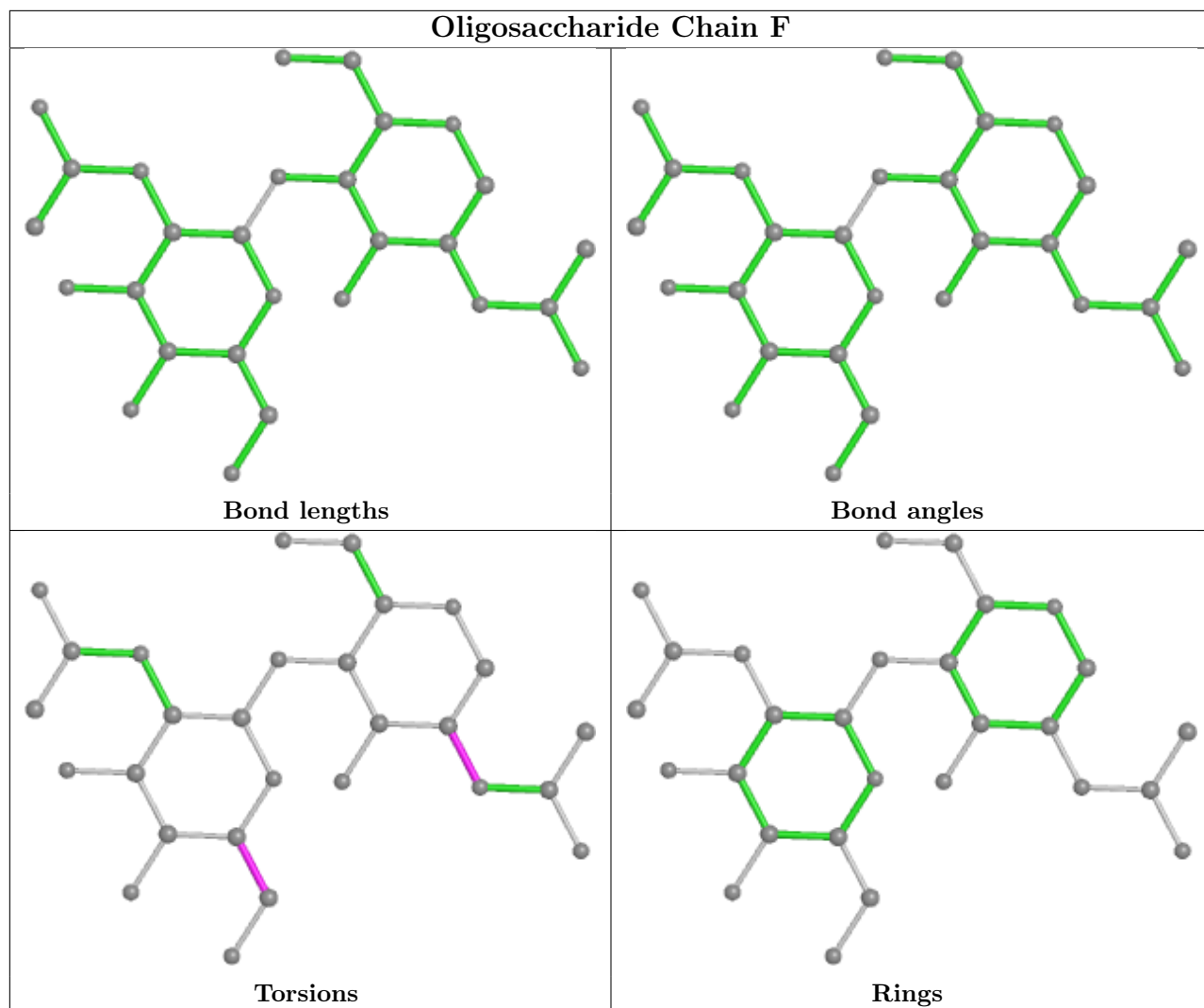
Mol	Chain	Res	Type	Atoms
3	J	1	NAG	C4-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
3	L	2	NAG	O5-C5-C6-O6
4	U	3	BMA	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6

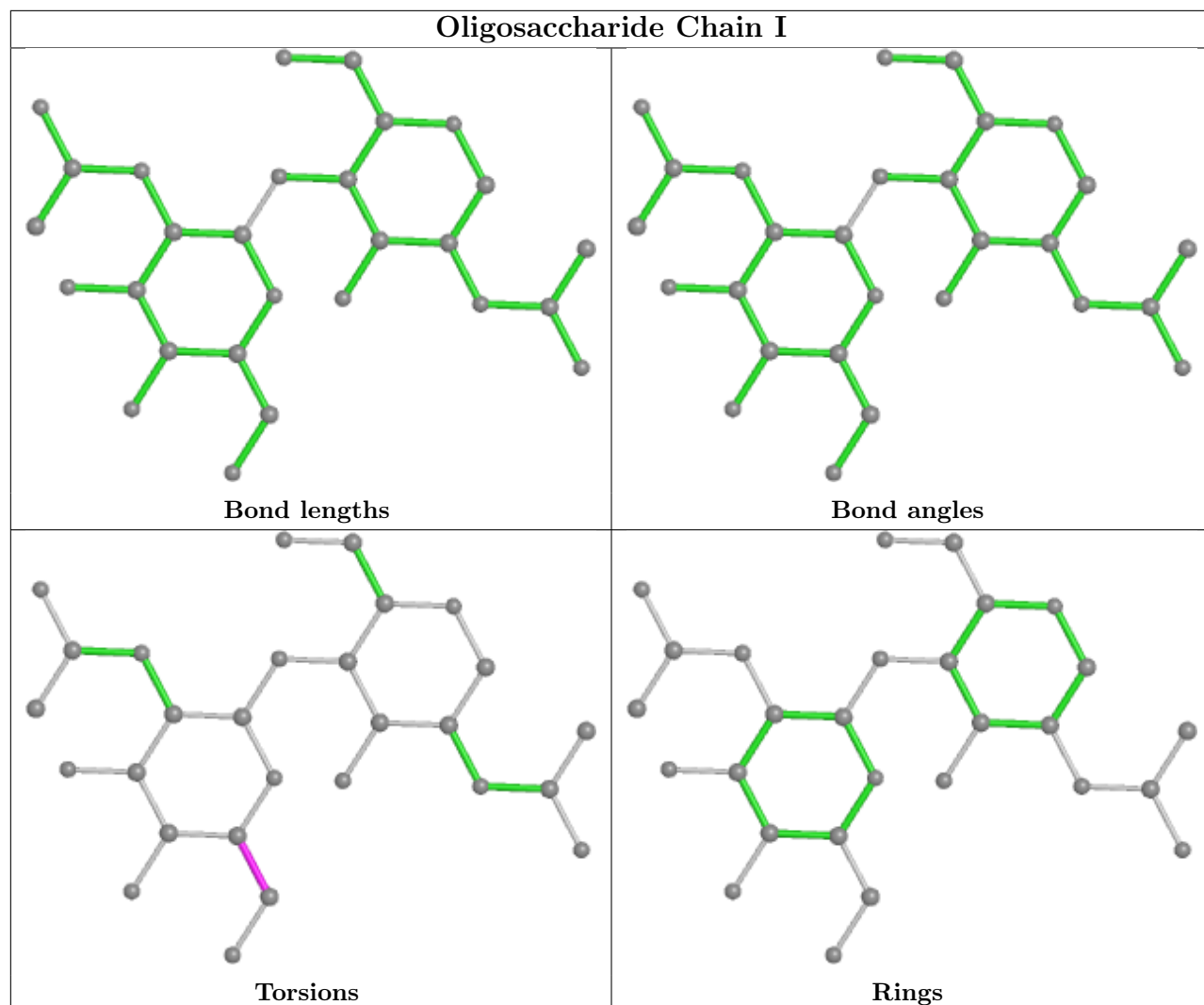
There are no ring outliers.

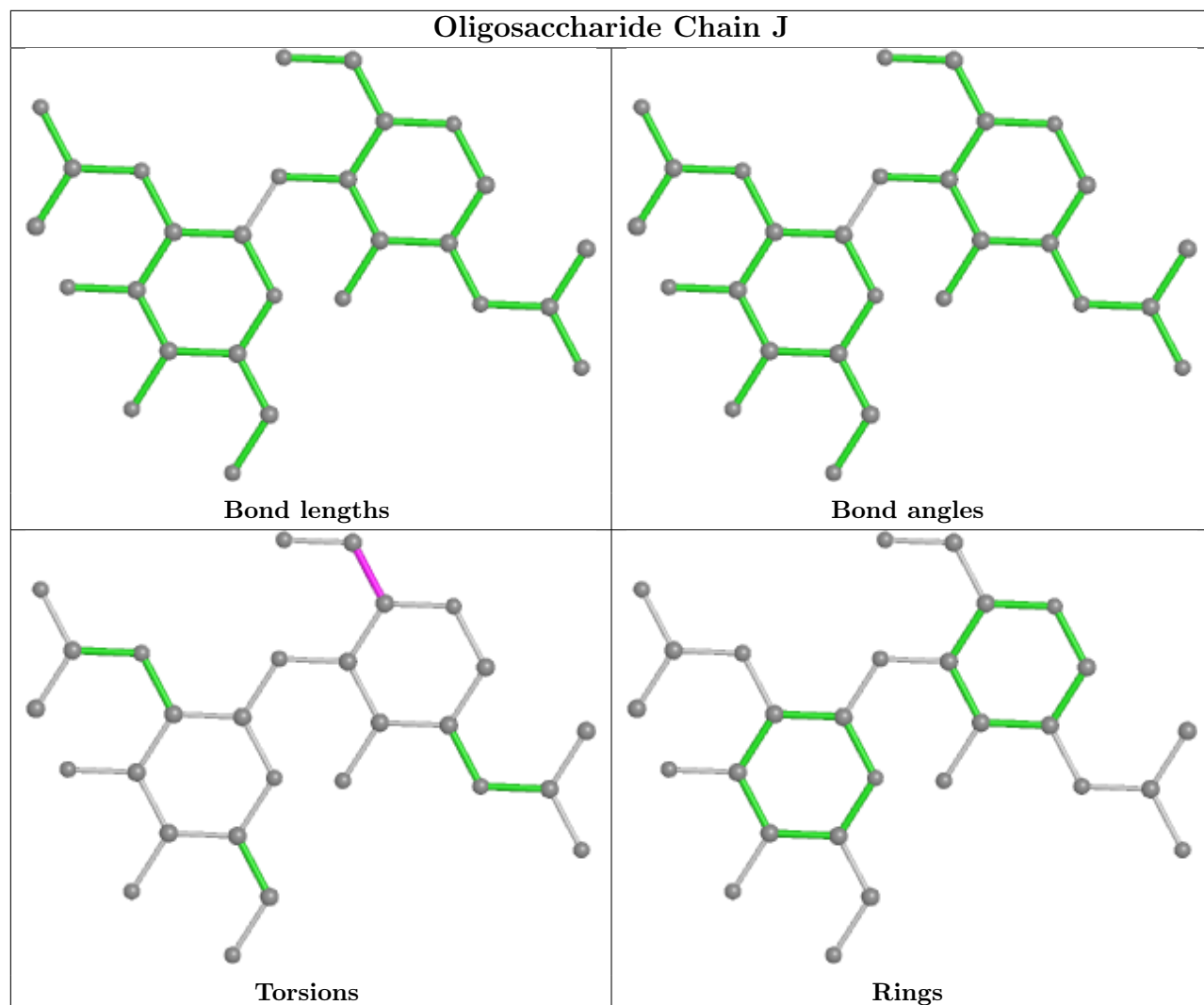
2 monomers are involved in 2 short contacts:

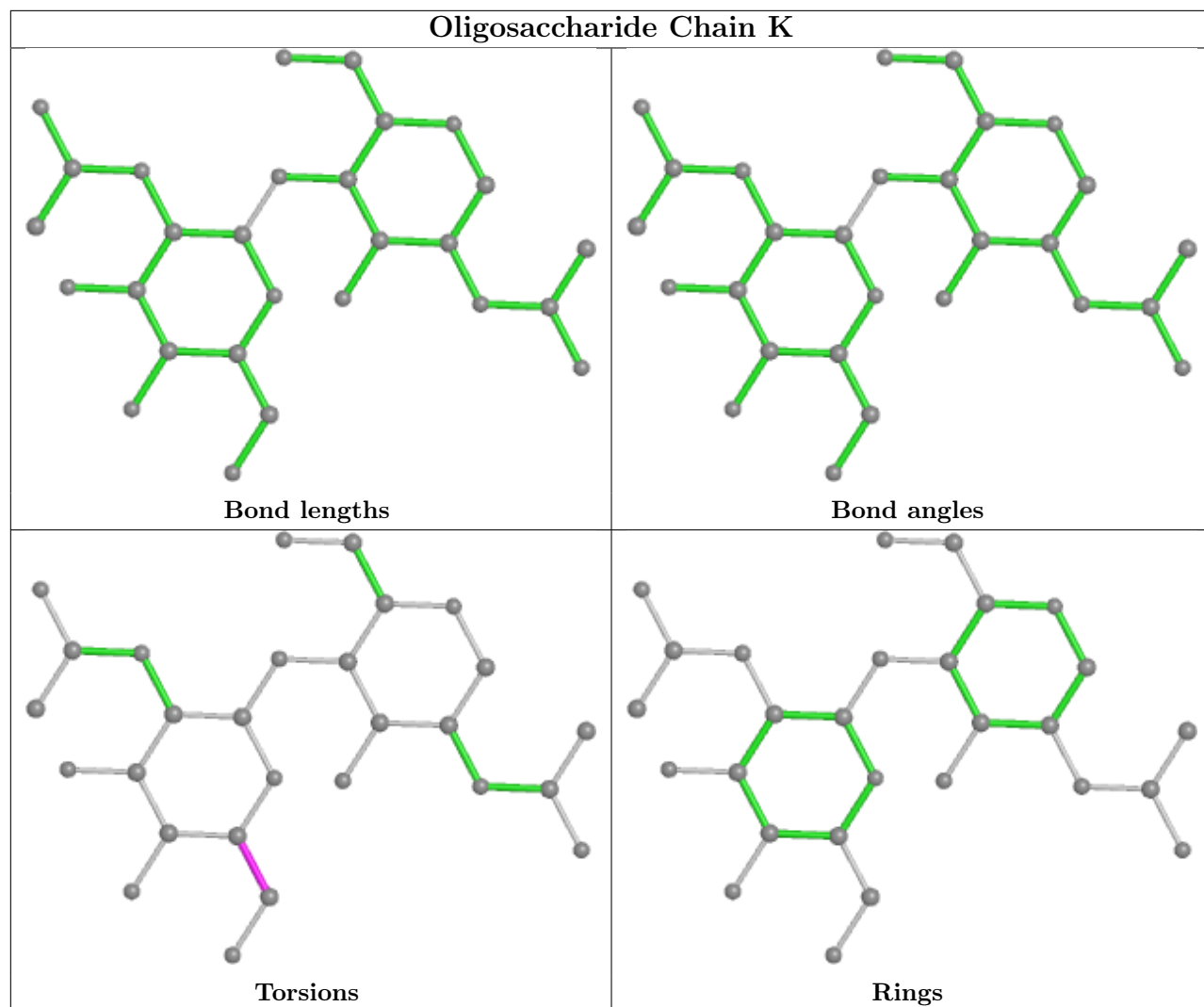
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	T	2	NAG	1	0
3	J	1	NAG	1	0

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

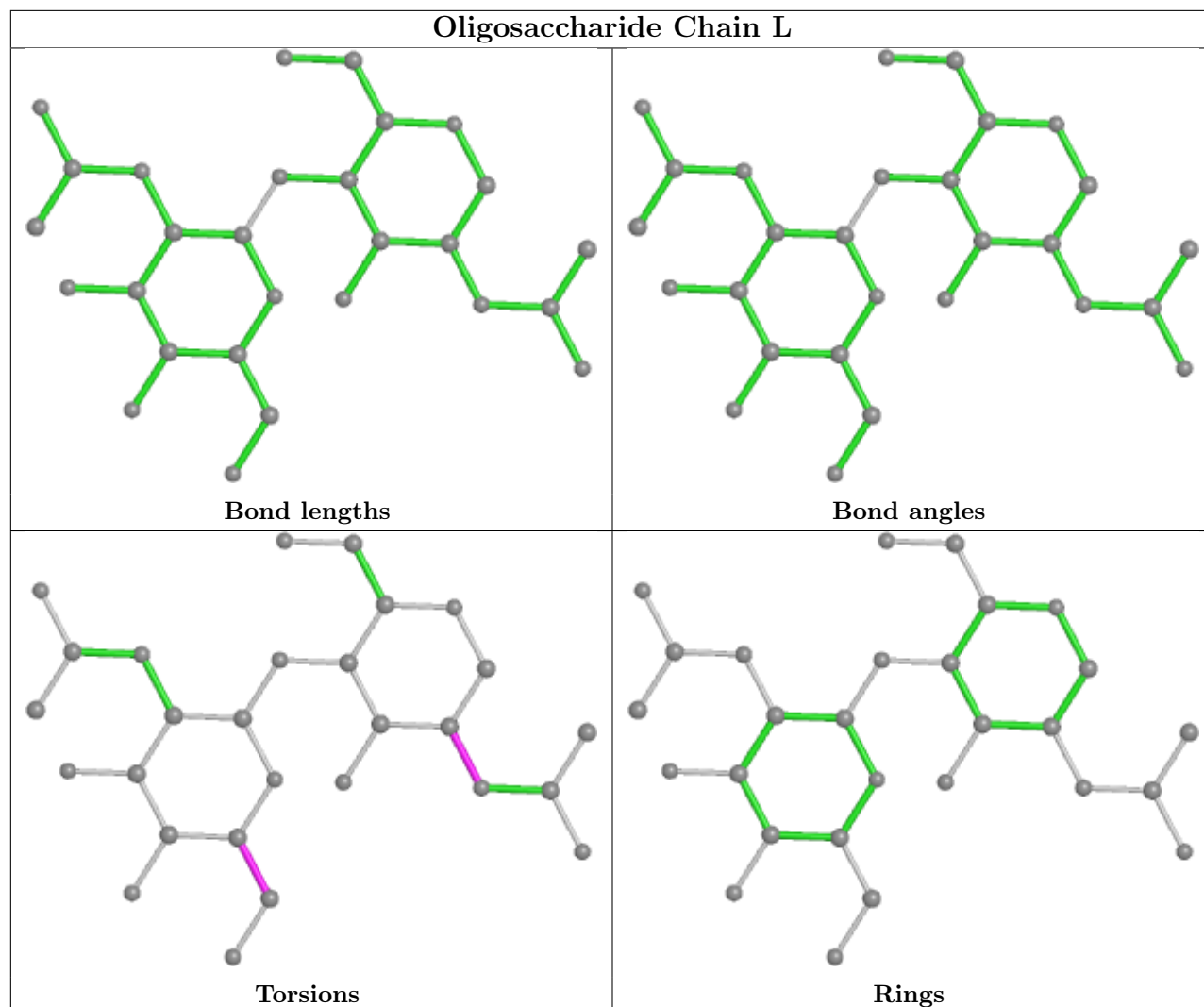


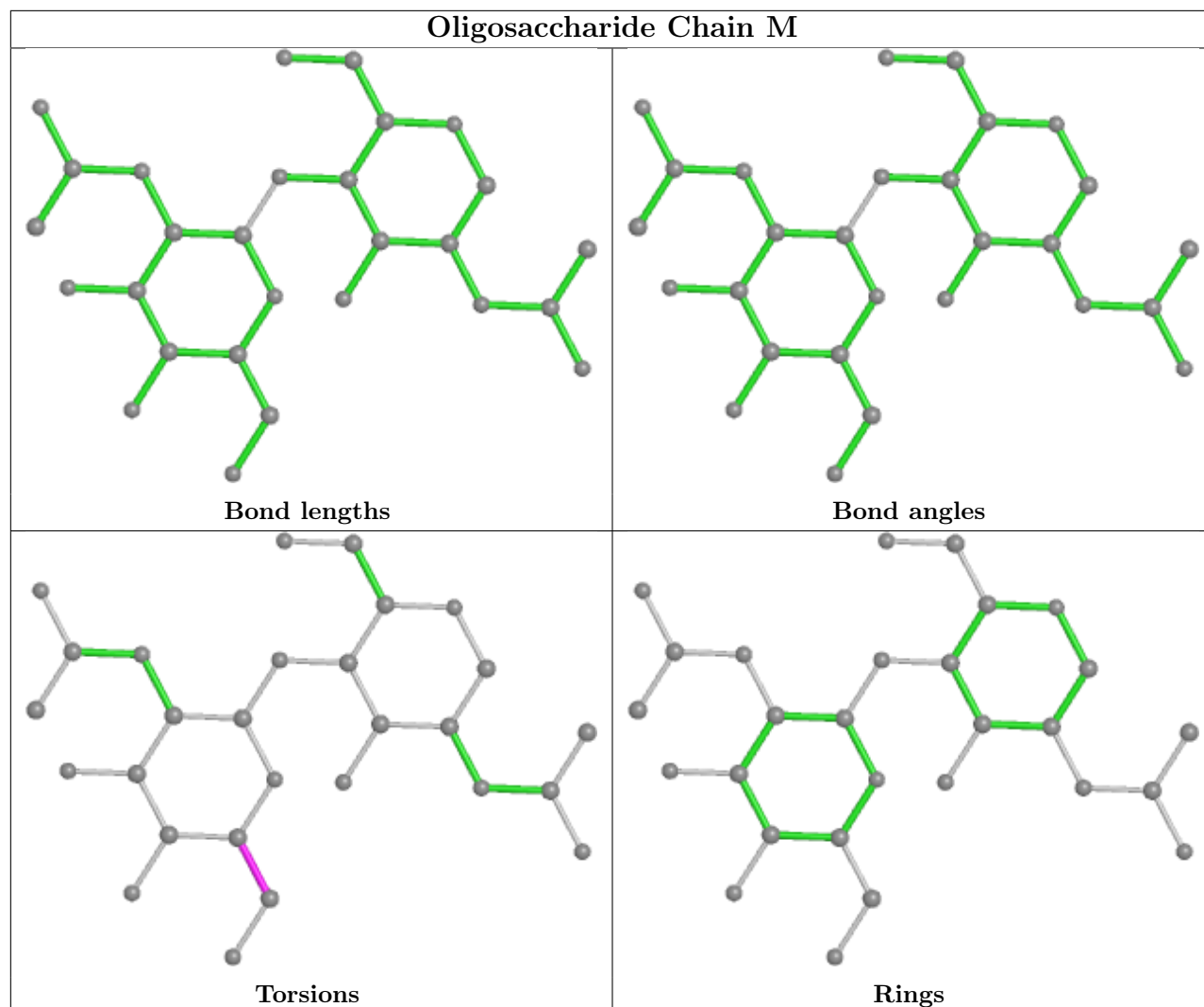


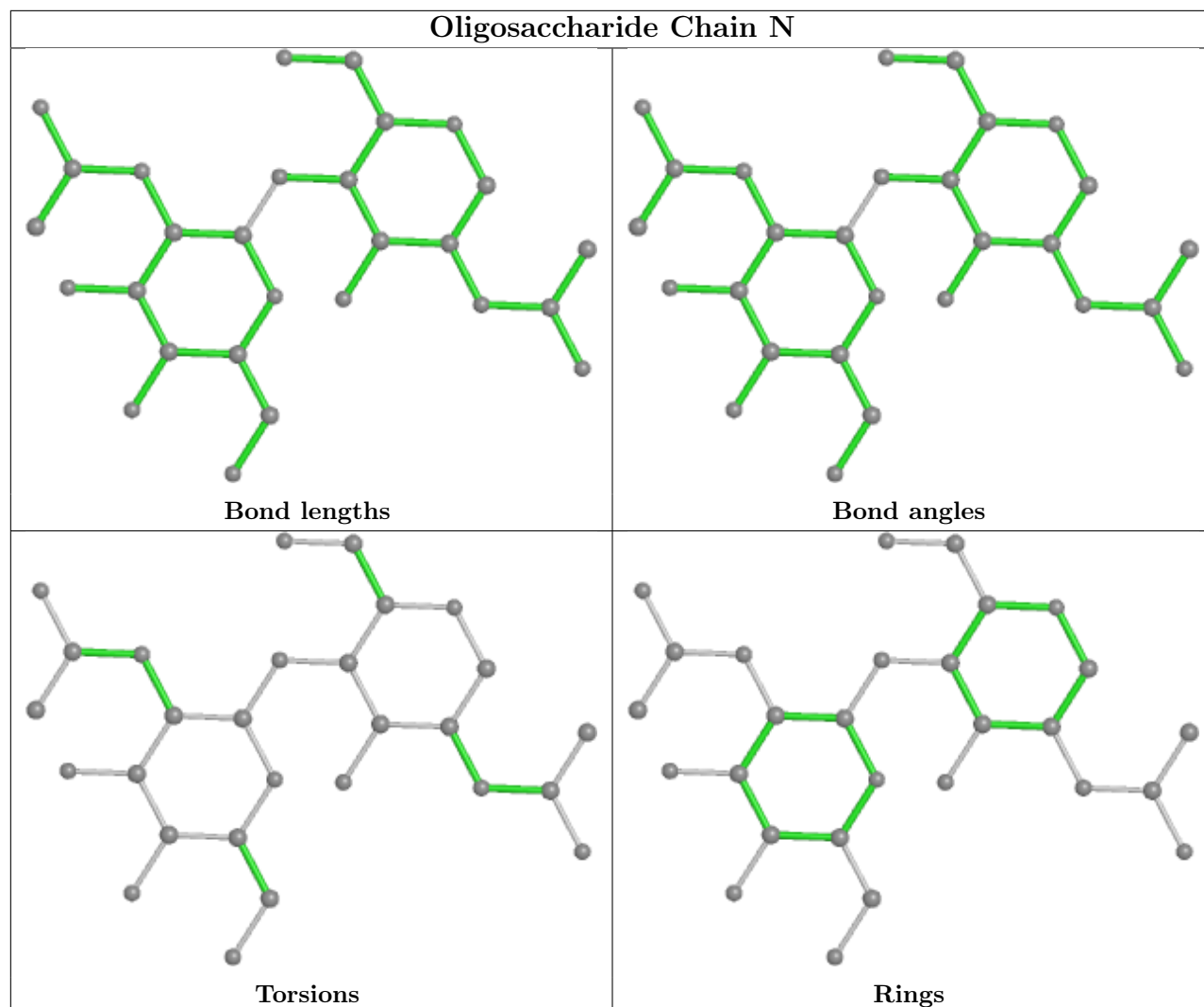


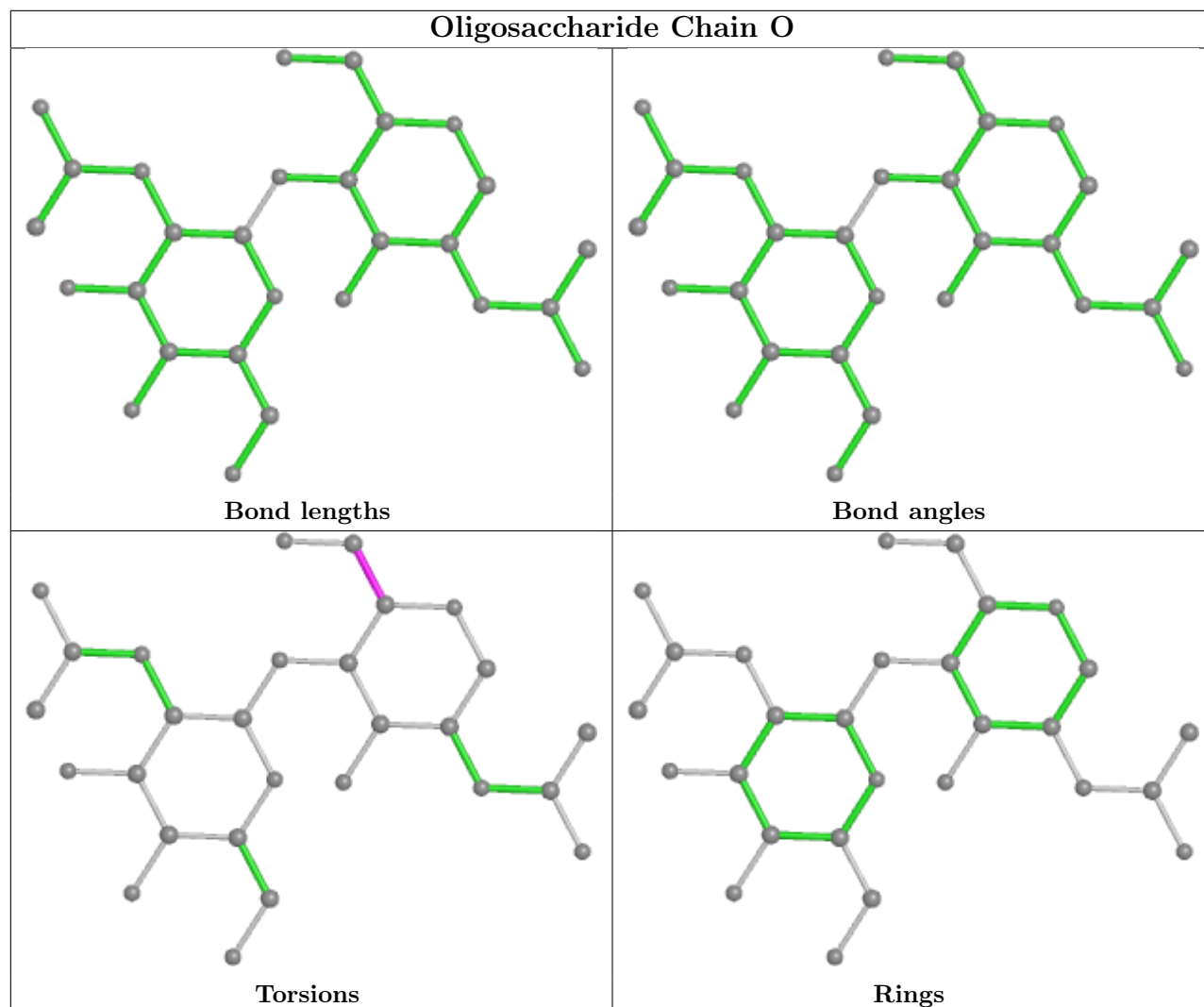


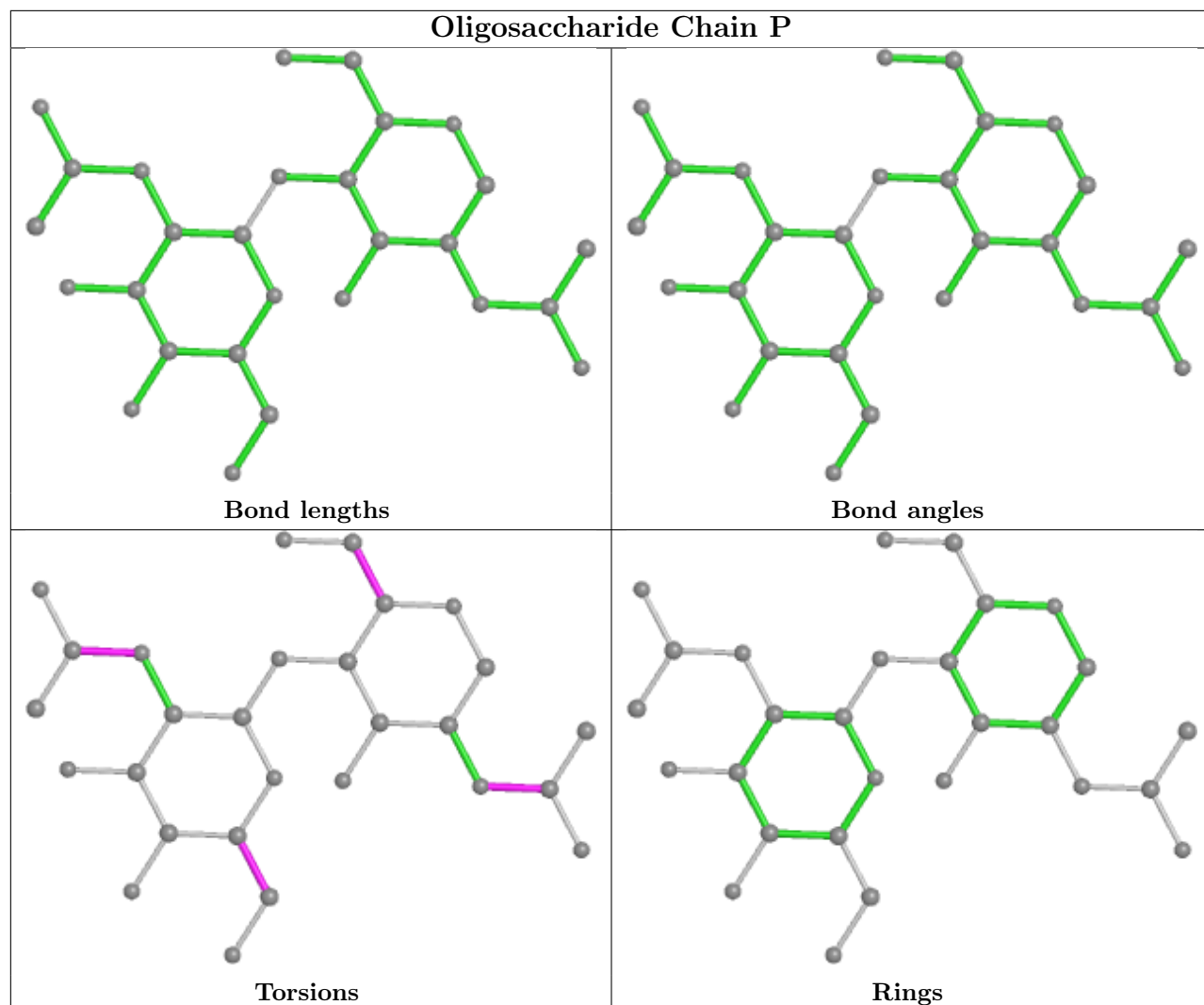


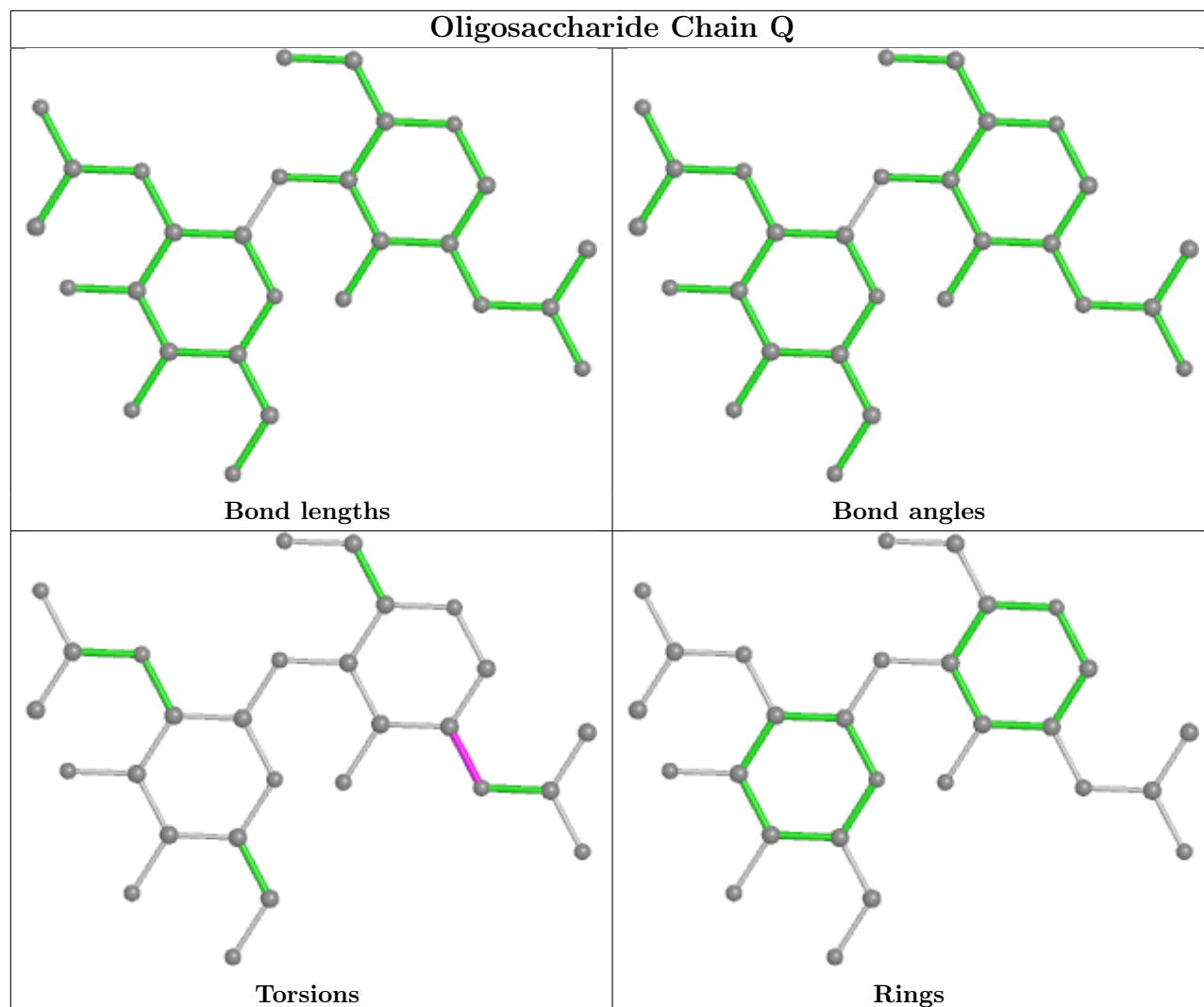


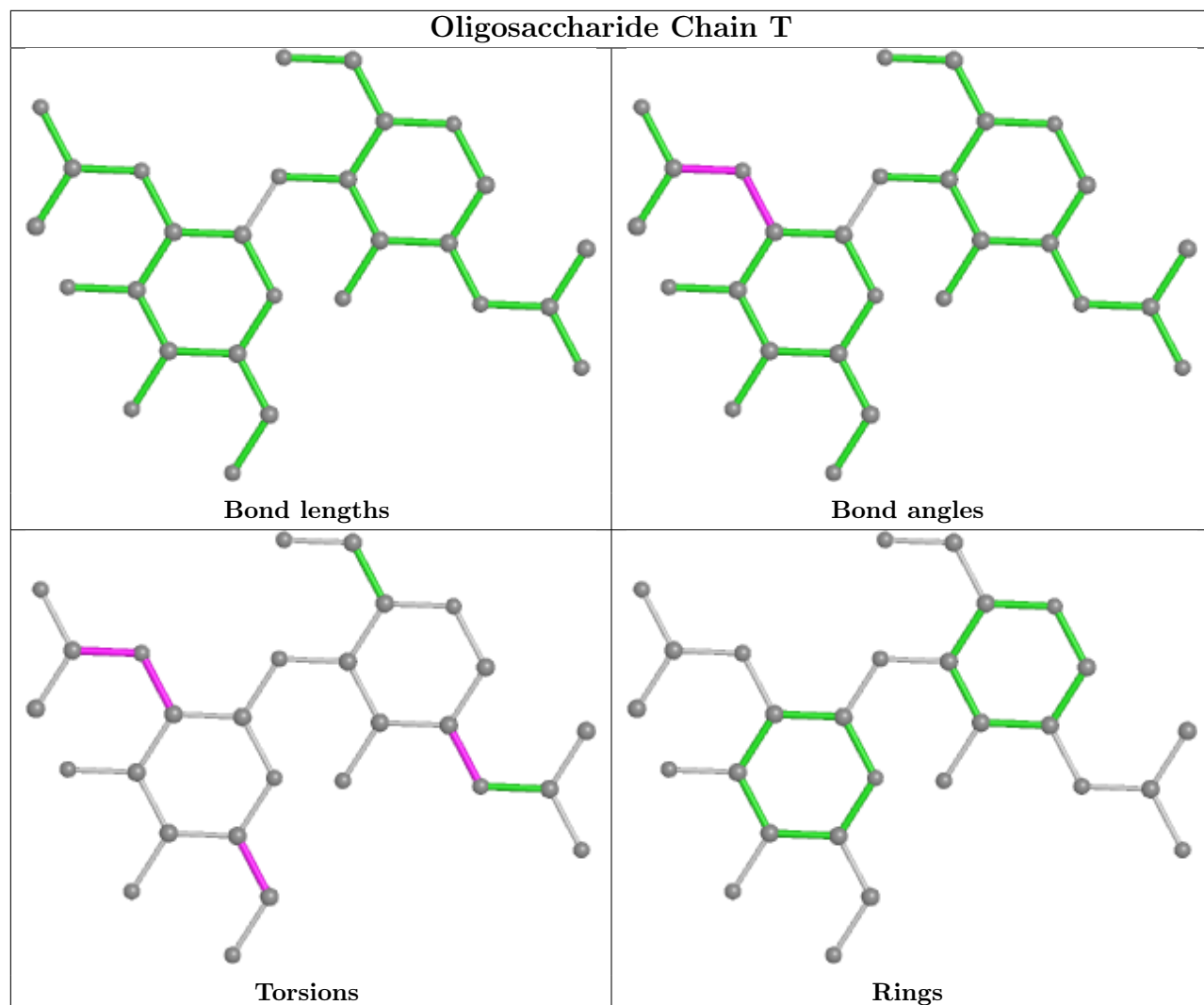


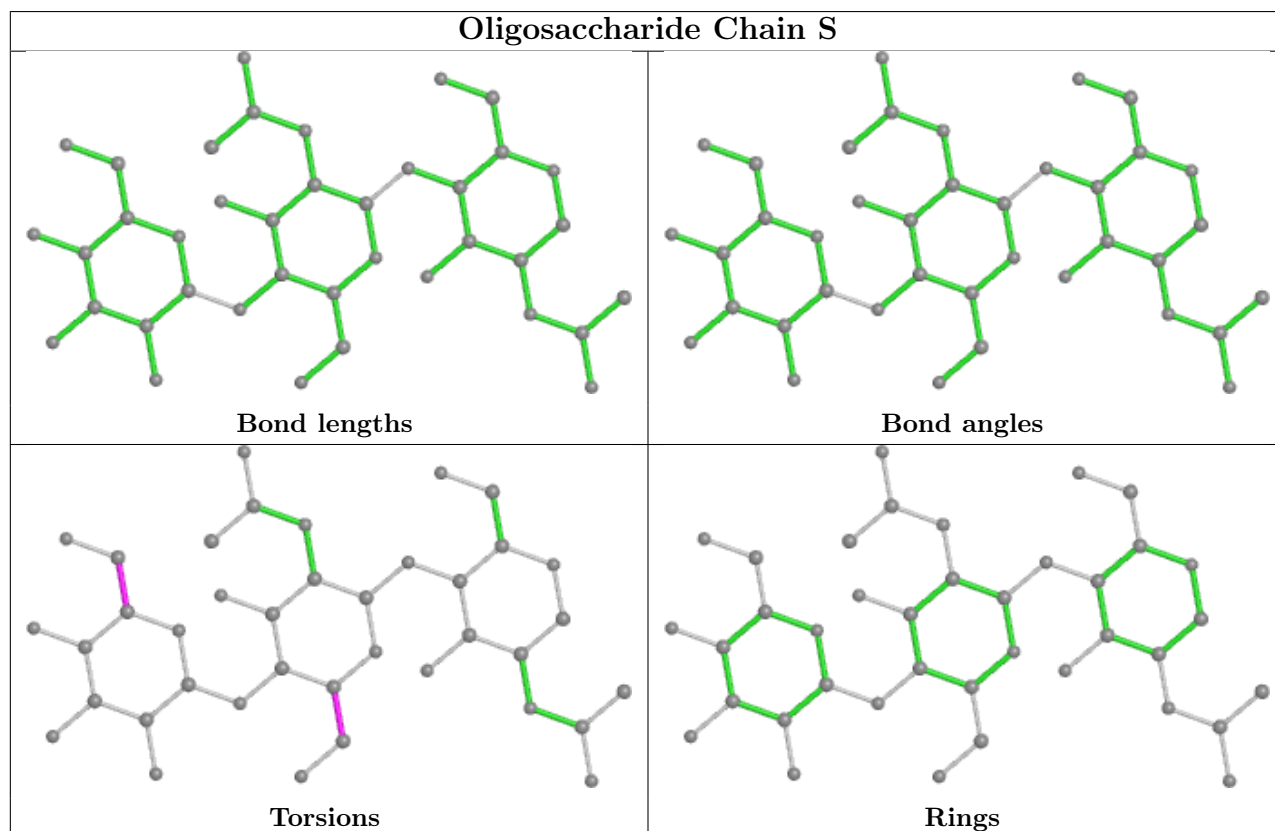
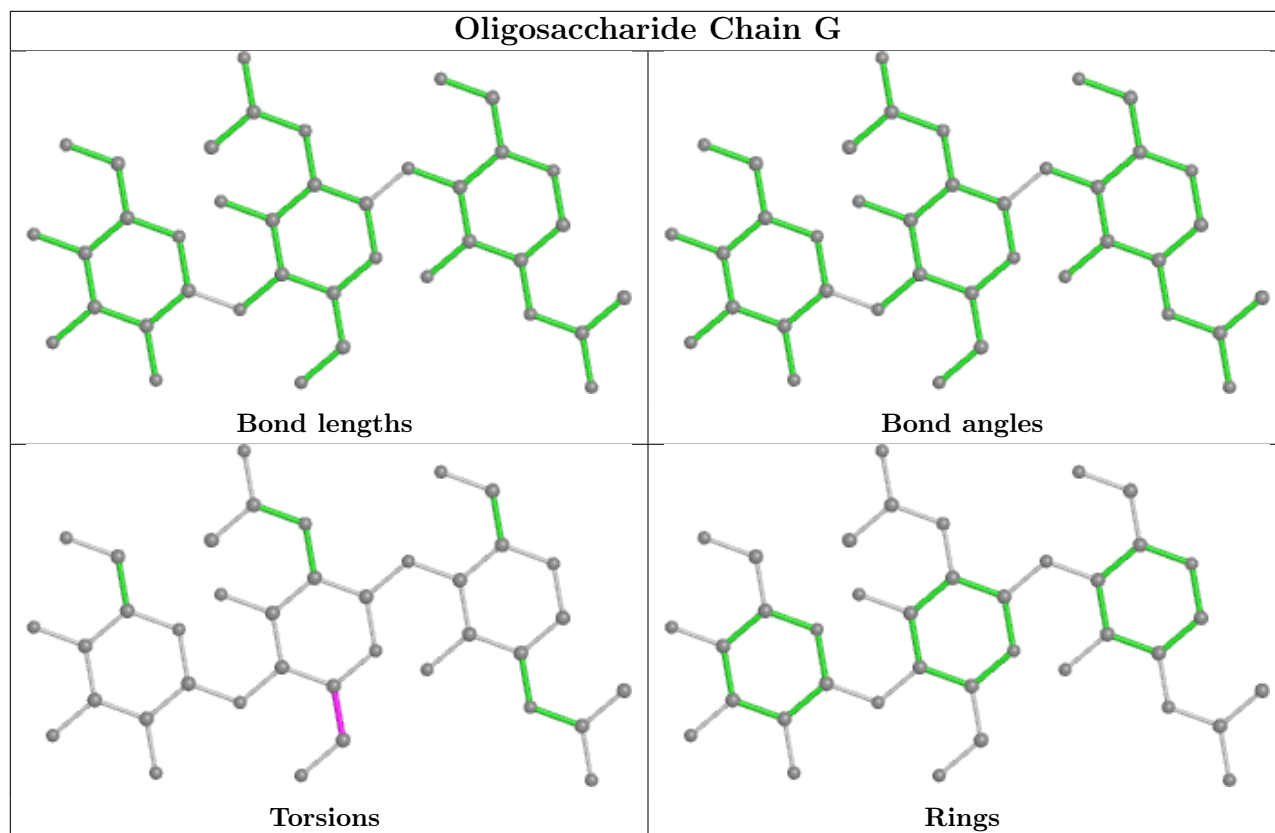




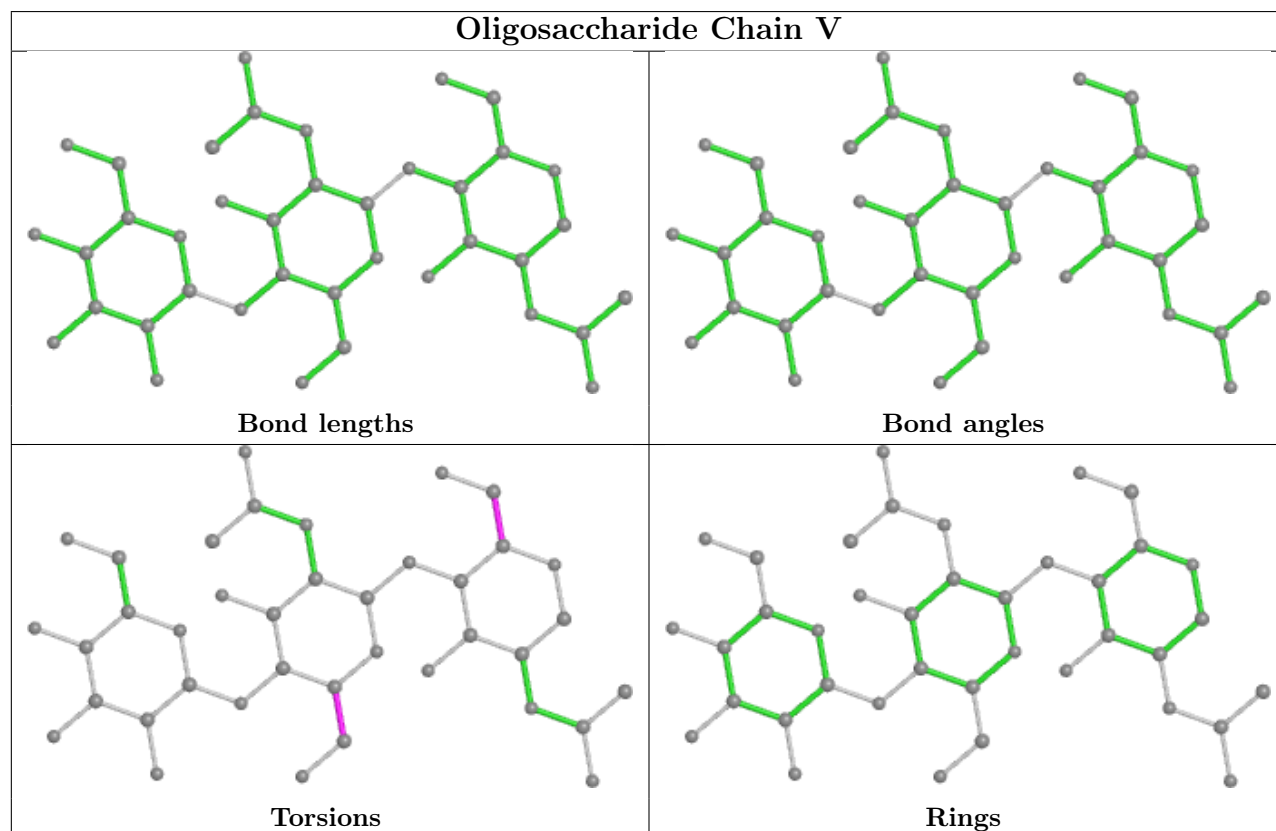
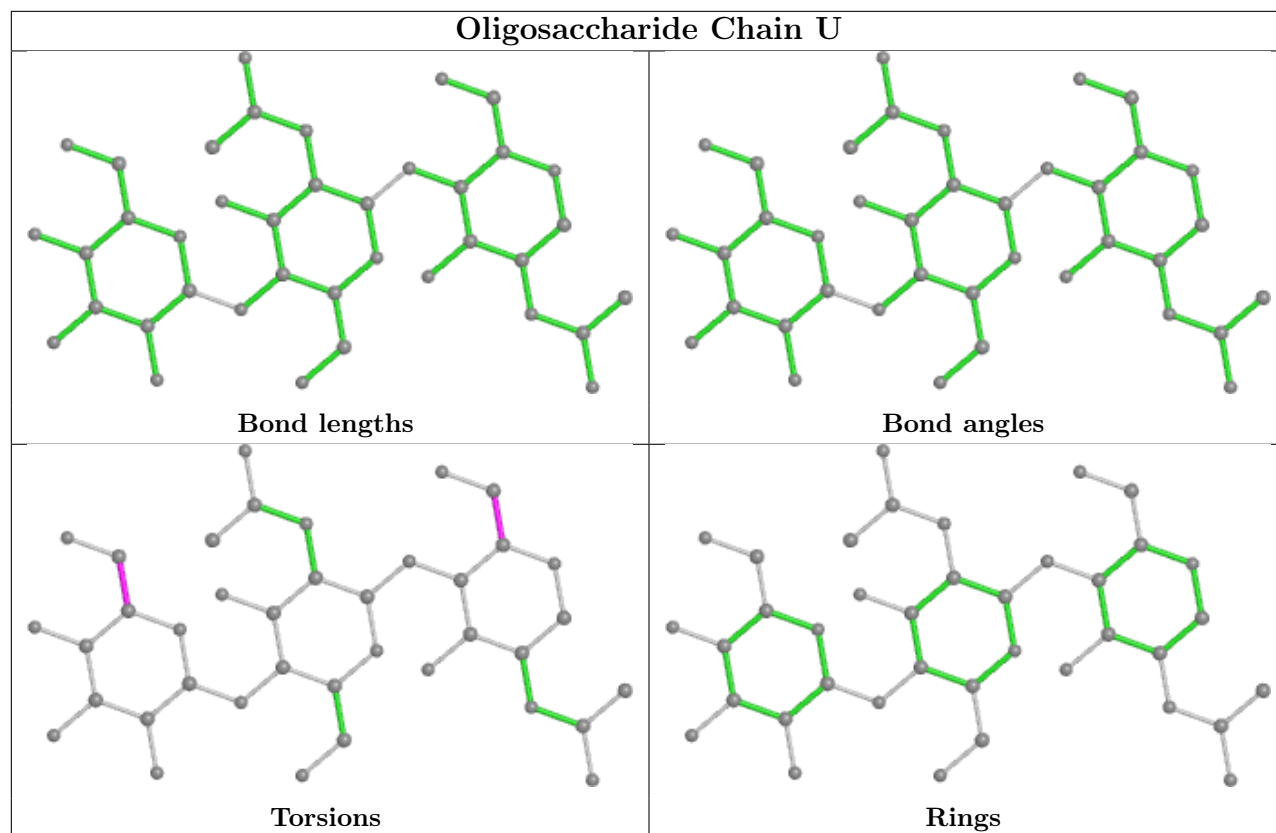


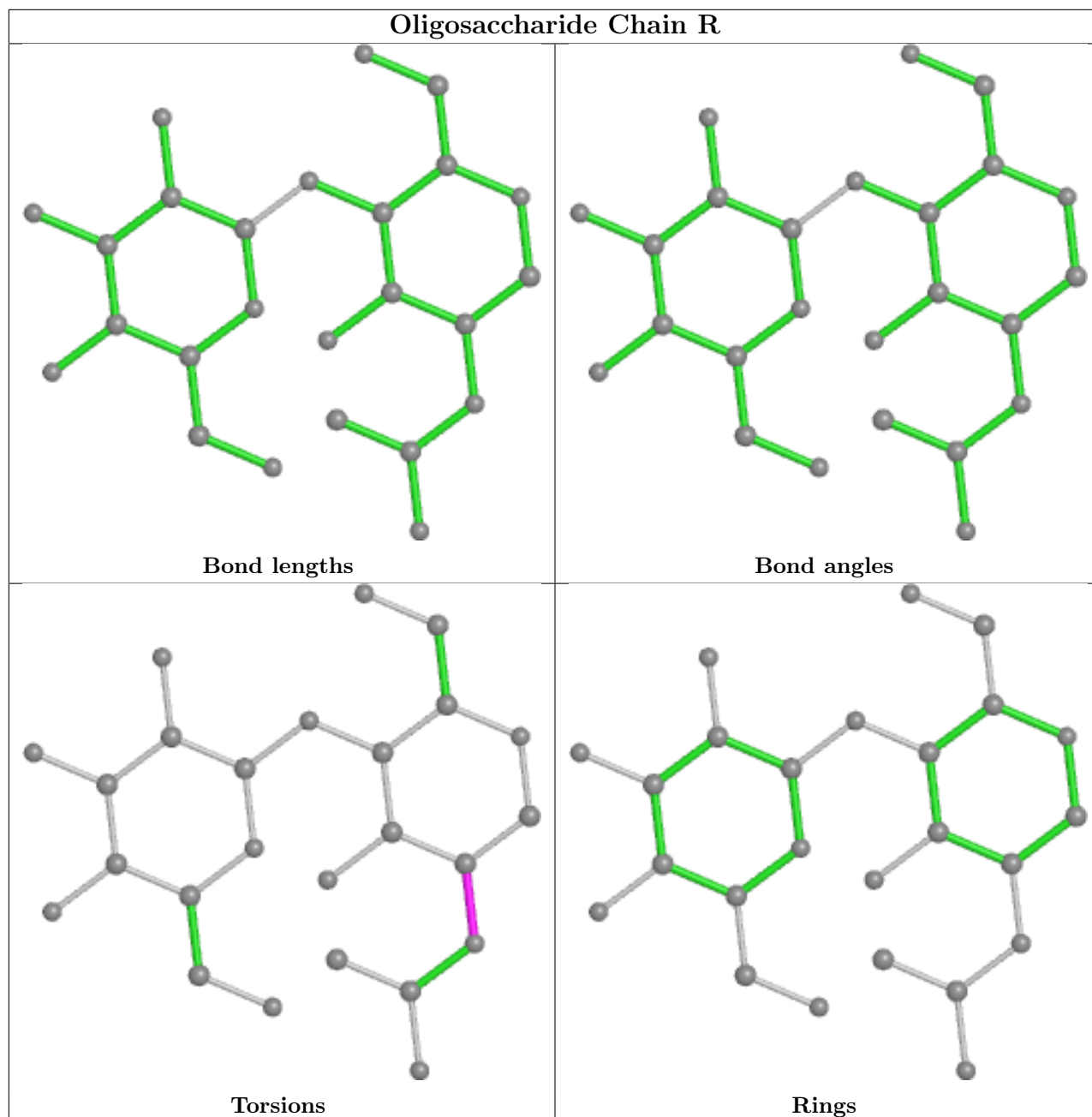












## 5.6 Ligand geometry [i](#)

29 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
6	NAG	E	1301	1	14,14,15	0.21	0	17,19,21	0.50	0
6	NAG	B	1301	1	14,14,15	0.22	0	17,19,21	0.42	0
6	NAG	B	1310	1	14,14,15	0.26	0	17,19,21	0.53	0
6	NAG	C	1309	1	14,14,15	0.20	0	17,19,21	0.45	0
6	NAG	E	1305	1	14,14,15	0.26	0	17,19,21	0.39	0
6	NAG	C	1303	1	14,14,15	0.21	0	17,19,21	0.45	0
6	NAG	B	1302	1	14,14,15	0.15	0	17,19,21	0.54	0
6	NAG	E	1308	1	14,14,15	0.30	0	17,19,21	1.14	2 (11%)
6	NAG	B	1305	1	14,14,15	0.20	0	17,19,21	0.45	0
6	NAG	C	1302	1	14,14,15	0.19	0	17,19,21	0.50	0
6	NAG	E	1307	1	14,14,15	0.30	0	17,19,21	1.10	3 (17%)
6	NAG	C	1305	1	14,14,15	0.25	0	17,19,21	0.36	0
6	NAG	B	1309	1	14,14,15	0.25	0	17,19,21	0.43	0
6	NAG	E	1306	1	14,14,15	0.39	0	17,19,21	1.13	3 (17%)
6	NAG	C	1310	1	14,14,15	0.25	0	17,19,21	0.46	0
6	NAG	C	1308	1	14,14,15	0.20	0	17,19,21	0.42	0
6	NAG	E	1302	1	14,14,15	0.21	0	17,19,21	0.55	0
6	NAG	B	1303	1	14,14,15	0.30	0	17,19,21	0.46	0
6	NAG	B	1304	1	14,14,15	0.24	0	17,19,21	0.41	0
6	NAG	E	1303	1	14,14,15	0.23	0	17,19,21	0.48	0
6	NAG	B	1307	1	14,14,15	0.43	0	17,19,21	0.76	0
6	NAG	C	1307	1	14,14,15	0.29	0	17,19,21	0.51	0
6	NAG	C	1306	1	14,14,15	0.27	0	17,19,21	0.36	0
6	NAG	B	1308	1	14,14,15	0.31	0	17,19,21	0.59	0
6	NAG	C	1304	1	14,14,15	0.20	0	17,19,21	0.43	0
6	NAG	E	1309	1	14,14,15	0.25	0	17,19,21	0.55	0
6	NAG	C	1301	1	14,14,15	0.19	0	17,19,21	0.47	0
6	NAG	B	1306	1	14,14,15	0.42	0	17,19,21	0.54	0
6	NAG	E	1304	1	14,14,15	0.23	0	17,19,21	0.39	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
6	NAG	E	1301	1	-	4/6/23/26	0/1/1/1
6	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1310	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1309	1	-	2/6/23/26	0/1/1/1
6	NAG	E	1305	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	C	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1302	1	-	3/6/23/26	0/1/1/1
6	NAG	E	1308	1	-	4/6/23/26	0/1/1/1
6	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1302	1	-	3/6/23/26	0/1/1/1
6	NAG	E	1307	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1305	1	-	3/6/23/26	0/1/1/1
6	NAG	B	1309	1	-	3/6/23/26	0/1/1/1
6	NAG	E	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1310	1	-	1/6/23/26	0/1/1/1
6	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
6	NAG	E	1302	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1307	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1308	1	-	4/6/23/26	0/1/1/1
6	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1309	1	-	3/6/23/26	0/1/1/1
6	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1306	1	-	4/6/23/26	0/1/1/1
6	NAG	E	1304	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1307	NAG	C1-O5-C5	-2.75	108.47	112.19
6	E	1306	NAG	C1-O5-C5	-2.31	109.06	112.19
6	E	1308	NAG	O5-C1-C2	-2.29	107.68	111.29
6	E	1308	NAG	C1-O5-C5	-2.26	109.13	112.19
6	E	1307	NAG	O5-C5-C6	2.15	110.58	107.20

There are no chirality outliers.

5 of 59 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	1308	NAG	C8-C7-N2-C2
6	B	1308	NAG	O7-C7-N2-C2
6	C	1306	NAG	C4-C5-C6-O6
6	B	1310	NAG	O5-C5-C6-O6
6	E	1301	NAG	C4-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1309	NAG	1	0
6	B	1303	NAG	1	0
6	C	1306	NAG	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24077. 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

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal surface views

This section was not generated.

### 6.5 Mask visualisation

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

## 7 Map analysis

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

### 7.1 Map-value distribution

This section was not generated.

### 7.2 Volume estimate versus contour level

This section was not generated.

### 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

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



## 9 Map-model fit

This section was not generated.