



## wwPDB EM Validation Summary Report ⓘ

Feb 19, 2025 – 08:10 PM JST

PDB ID : 8ZY5  
EMDB ID : EMD-60556  
Title : Sarbecovirus RmYN02 Spike Trimer in a Locked Conformation  
Authors : Wang, J.; Xiong, X.  
Deposited on : 2024-06-16  
Resolution : 3.80 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](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	: <b>FAILED</b>
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	: <b>FAILED</b>
Ideal geometry (proteins)	: Engh & Huber (2001)
Ideal geometry (DNA, RNA)	: Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: 2.41.2

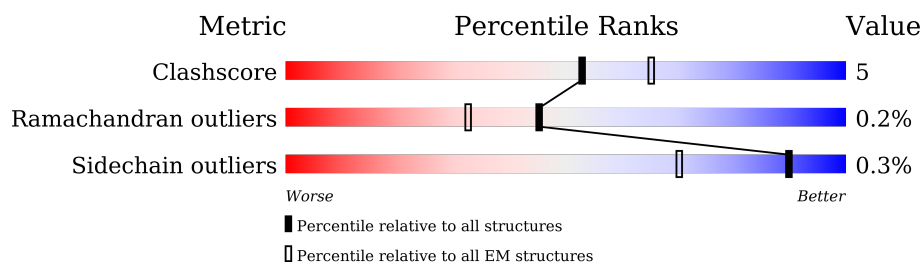
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
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  $\geq 3$ , 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	A	1241	71% 11% 19%
1	B	1241	70% 12% 19%
1	C	1241	70% 11% 19%
2	D	2	100%
2	E	2	50% 50%
2	F	2	50% 50%
2	G	2	100%
2	H	2	50% 50%
2	I	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	J	2	 50%50%
2	K	2	 50%50%
2	L	2	 50%50%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 24450 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.

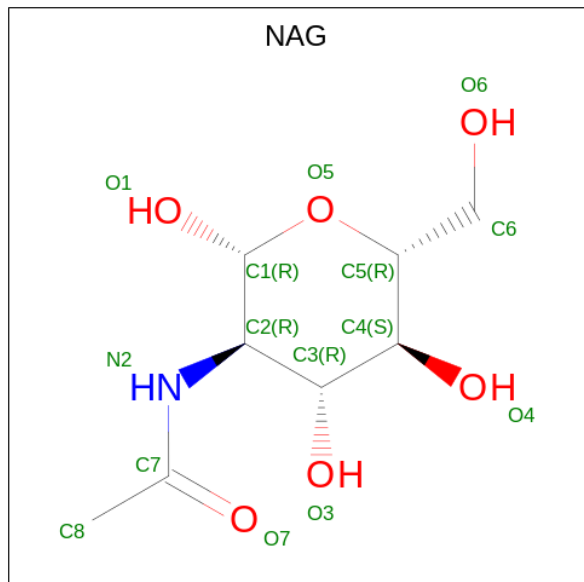
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1010	Total	C	N	O	S	0	0
			7856	5018	1306	1497	35		
1	B	1010	Total	C	N	O	S	0	0
			7856	5018	1306	1497	35		
1	C	1010	Total	C	N	O	S	0	0
			7856	5018	1306	1497	35		

- Molecule 2 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
2	D	2	Total	C	N	O	0	0
			28	16	2	10		
2	E	2	Total	C	N	O	0	0
			28	16	2	10		
2	F	2	Total	C	N	O	0	0
			28	16	2	10		
2	G	2	Total	C	N	O	0	0
			28	16	2	10		
2	H	2	Total	C	N	O	0	0
			28	16	2	10		
2	I	2	Total	C	N	O	0	0
			28	16	2	10		
2	J	2	Total	C	N	O	0	0
			28	16	2	10		
2	K	2	Total	C	N	O	0	0
			28	16	2	10		
2	L	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ) (labeled as "Ligand of Interest" by depositor).



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

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

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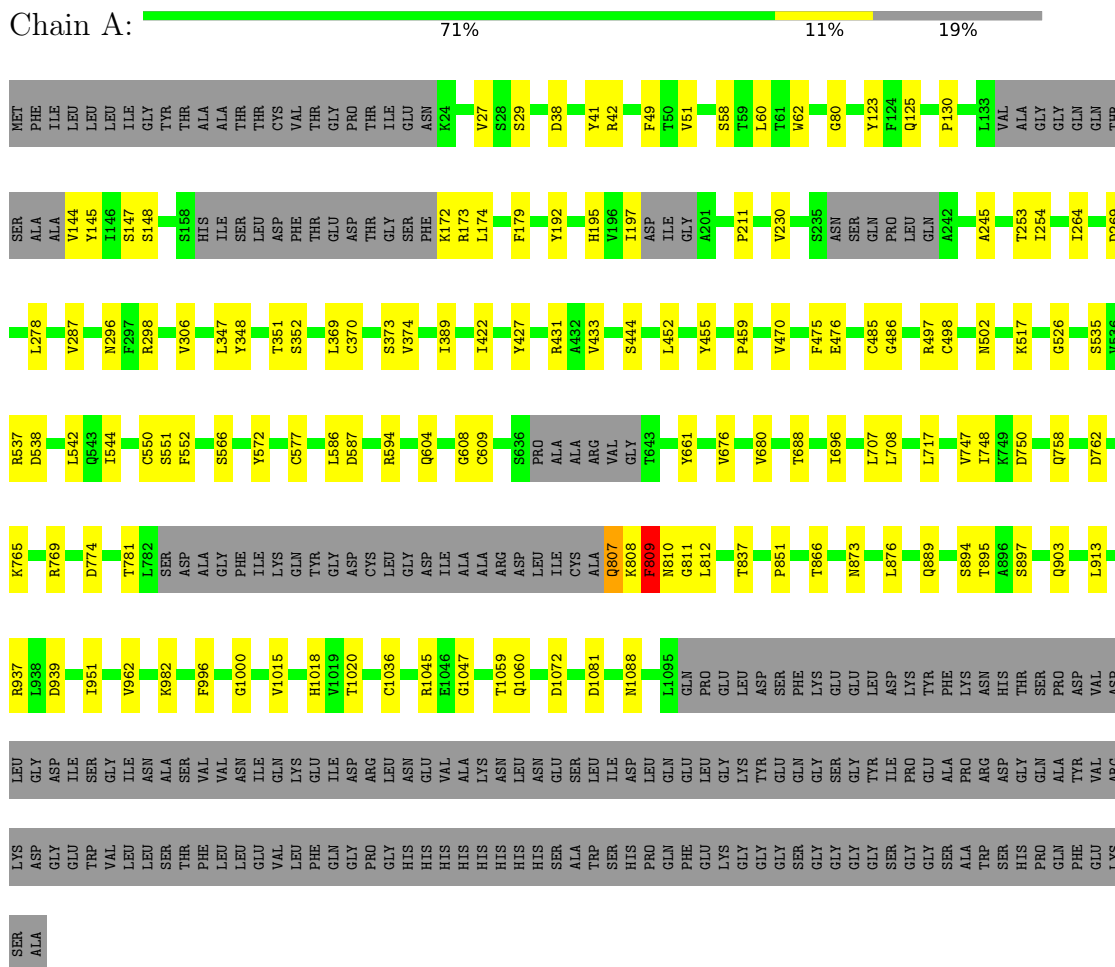
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Mol	Chain	Residues	Atoms				AltConf
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
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			14	8	1	5	
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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

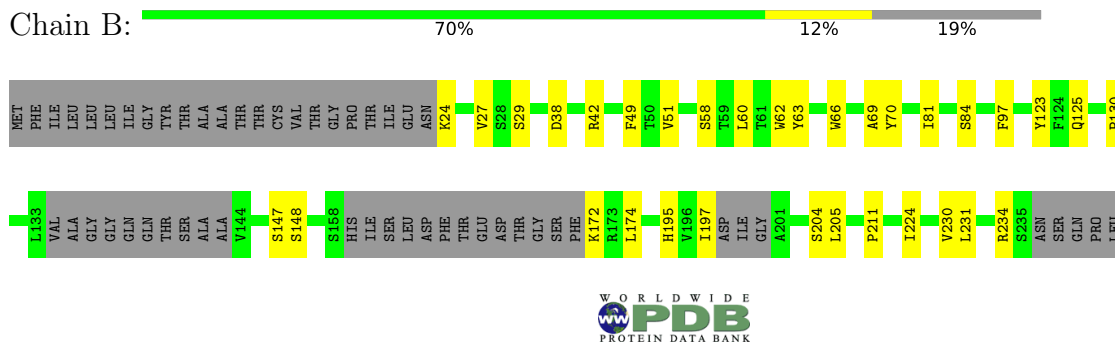
### 3 Residue-property plots [i](#)

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

- Molecule 1: Spike glycoprotein



- Molecule 1: Spike glycoprotein





PHE	GLU	GLU	GLY	GLY	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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● Molecule 1: Spike glycoprotein

Chain C:

70%																												11%											19%																		
MET	PHE	ILE	LEU	LEU	THR	LEU	ILE	GLY	TYR	THR	ALA	THR	THR	CYS	VAL	THR	GLY	PRO	THR	THR	ILE	GLU	ASN	K24	D38	R42	F49	T50	V51	R55	S58	T59	L60	W66	A69	M75	I81	S84	W95	Y123	F124	Q125	P130	L133	VAL												
GLY	GLY	GLN	GLN	THR	SER	ALA	ALA	V144	S147	S148	S158	HIS	ILE	SER	LEU	ASP	PHE	K172	I197	I197	ILE	GLY	A201	P211	F227	V230	R234	S235	ASN	SER	GLN	PRO	LEU	GLN	A242	A245	V246	T253	I254	R298	T284	D269															
L278	V287	N296	F297	R298	V306	F321	L347	T351	V361	L369	C370	S384	I389	V396	A398	Y402	I422	Y427	R431	A432	V433	S444	L452	Y455	P459	V470	V471	N479	C485	G486	R497	N502																									
K517	G526	S535	V536	R537	D538	L542	Q543	I544	S551	F552	Y572	C577	D578	T579	L586	D587	R594	Q604	G608	C609	S636	PRO	ALA	ARG	VAL	GLY	T643	Y661	P669	V676	V680	C692	T696	S700	N704	L707	Y710																				
G711	S712	Q716	N718	R719	Q738	V747	I748	K749	D750	R769	D774	K779	V780	T781	L782	SER	ASP	ALA	PHE	GLY	ILE	LYS	GLN	TYR	GLY	ASP	CYS	GLY	ARG	ALA	ASP	LEU	ILE	Q807	N810	L815	P816	L831	T837	T841	F842																
G843	I844	P851	T866	N873	L876	S894	T895	A896	S897	Q903	R937	L938	D939	I951	K982	W983	S984	F996	G1000	V1015	H1018	V1019	T1020	Q1025	C1036	R1045	E1046	G1047	T1059	Q1060	D1072	N1088	L1095	GLN	PRO	GLY	GLY	LYS	GLY	TYR	SER																
PHE	LYS	GLU	GLY	LEU	ASP	LYS	PHE	ALA	TRP	ARG	ASN	HIS	THR	SER	PRO	VAL	VAL	ASP	LEU	GLY	ASP	GLY	GLU	TRP	SER	ILE	ILE	ALA	ASN	LEU	GLY	GLU	ALA	SER	TRP	SER	HIS	PRO	GLN	PHE	GLY	LYS	GLY	GLY													
GLN	GLY	SER	GLY	TYR	ILE	PRO	GLY	ALA	ALA	TRP	ARG	ASN	GLY	GLN	VAL	ARG	LYS	ASP	GLY	GLY	GLU	TRP	VAL	LEU	LEU	VAL	GLY	HIS	HIS	HIS	VAL	ALA	SER	ALA	LEU	SER	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLY	LYS	GLY	GLY										
SER	GLY	GLY	GLY	SER	GLY	SER	ALA	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLY	LYS	SER	ALA	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU	VAL	GLY	HIS	HIS	HIS	VAL	ALA	SER	ALA	LEU	SER	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLY	LYS	GLY	GLY									

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

Chain D:  100%

MAG1  
MAG2

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

Chain E:  50% 50%

MAG1  
MAG2

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

Chain F:  50% 50%

MAG1  
MAG2

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

Chain G:  100%

MAG1  
MAG2

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

Chain H:  50% 50%

MAG1  
MAG2

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

Chain I:  50% 50%

MAG1  
MAG2

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

Chain J:  50% 50%



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

Chain K:  50% 50%



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

Chain L:  50% 50%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27757	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
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

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	0.29	0/8027	0.58	0/10926
1	B	0.29	0/8027	0.58	0/10926
1	C	0.30	0/8027	0.58	0/10926
All	All	0.30	0/24081	0.58	0/32778

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](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7856	0	7702	83	0
1	B	7856	0	7702	92	0
1	C	7856	0	7702	85	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
2	J	28	0	25	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	28	0	25	0	0
2	L	28	0	25	0	0
3	A	210	0	195	1	0
3	B	210	0	195	1	0
3	C	210	0	195	1	0
All	All	24450	0	23916	248	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 248 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:B:572:TYR:O	1:B:608:GLY:HA3	1.77	0.84
1:C:572:TYR:O	1:C:608:GLY:HA3	1.77	0.84
1:A:572:TYR:O	1:A:608:GLY:HA3	1.80	0.82
1:B:1047:GLY:HA3	1:B:1059:THR:O	1.86	0.76
1:A:1047:GLY:HA3	1:A:1059:THR:O	1.86	0.74

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	996/1241 (80%)	929 (93%)	64 (6%)	3 (0%)	37	69
1	B	996/1241 (80%)	928 (93%)	68 (7%)	0	100	100
1	C	996/1241 (80%)	927 (93%)	67 (7%)	2 (0%)	44	74
All	All	2988/3723 (80%)	2784 (93%)	199 (7%)	5 (0%)	45	74

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	810	ASN
1	C	711	GLY
1	A	809	PHE
1	C	396	VAL
1	A	811	GLY

### 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	881/1066 (83%)	879 (100%)	2 (0%)	92	94
1	B	881/1066 (83%)	879 (100%)	2 (0%)	92	94
1	C	881/1066 (83%)	878 (100%)	3 (0%)	91	92
All	All	2643/3198 (83%)	2636 (100%)	7 (0%)	90	92

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	809	PHE
1	C	75	MET
1	C	397	ILE
1	C	396	VAL
1	B	807	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [i](#)

18 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	D	1	1,2	14,14,15	0.35	0	17,19,21	0.86	1 (5%)
2	NAG	D	2	2	14,14,15	0.81	1 (7%)	17,19,21	0.68	1 (5%)
2	NAG	E	1	1,2	14,14,15	0.25	0	17,19,21	0.49	0
2	NAG	E	2	2	14,14,15	0.50	0	17,19,21	0.99	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.22	0	17,19,21	0.58	0
2	NAG	F	2	2	14,14,15	0.28	0	17,19,21	0.71	1 (5%)
2	NAG	G	1	1,2	14,14,15	0.38	0	17,19,21	0.88	1 (5%)
2	NAG	G	2	2	14,14,15	0.81	1 (7%)	17,19,21	0.70	1 (5%)
2	NAG	H	1	1,2	14,14,15	0.26	0	17,19,21	0.49	0
2	NAG	H	2	2	14,14,15	0.49	0	17,19,21	0.99	1 (5%)
2	NAG	I	1	1,2	14,14,15	0.22	0	17,19,21	0.64	0
2	NAG	I	2	2	14,14,15	0.27	0	17,19,21	0.71	1 (5%)
2	NAG	J	1	1,2	14,14,15	0.28	0	17,19,21	0.66	0
2	NAG	J	2	2	14,14,15	1.60	2 (14%)	17,19,21	1.41	1 (5%)
2	NAG	K	1	1,2	14,14,15	0.26	0	17,19,21	0.51	0
2	NAG	K	2	2	14,14,15	0.51	0	17,19,21	1.00	1 (5%)
2	NAG	L	1	1,2	14,14,15	0.26	0	17,19,21	0.65	0
2	NAG	L	2	2	14,14,15	0.27	0	17,19,21	0.71	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	2	2	-	1/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	4/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	1/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	4/6/23/26	0/1/1/1
2	NAG	J	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	J	2	2	-	2/6/23/26	0/1/1/1
2	NAG	K	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	1/6/23/26	0/1/1/1
2	NAG	L	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	L	2	2	-	4/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	2	NAG	O5-C1	5.37	1.52	1.43
2	J	2	NAG	C1-C2	2.56	1.56	1.52
2	G	2	NAG	C1-C2	2.44	1.56	1.52
2	D	2	NAG	C1-C2	2.40	1.55	1.52

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	2	NAG	C1-O5-C5	5.59	119.77	112.19
2	K	2	NAG	C2-N2-C7	3.09	127.30	122.90
2	E	2	NAG	C2-N2-C7	3.06	127.26	122.90
2	H	2	NAG	C2-N2-C7	3.05	127.24	122.90
2	G	1	NAG	C1-O5-C5	2.76	115.93	112.19

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	2	NAG	O5-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6

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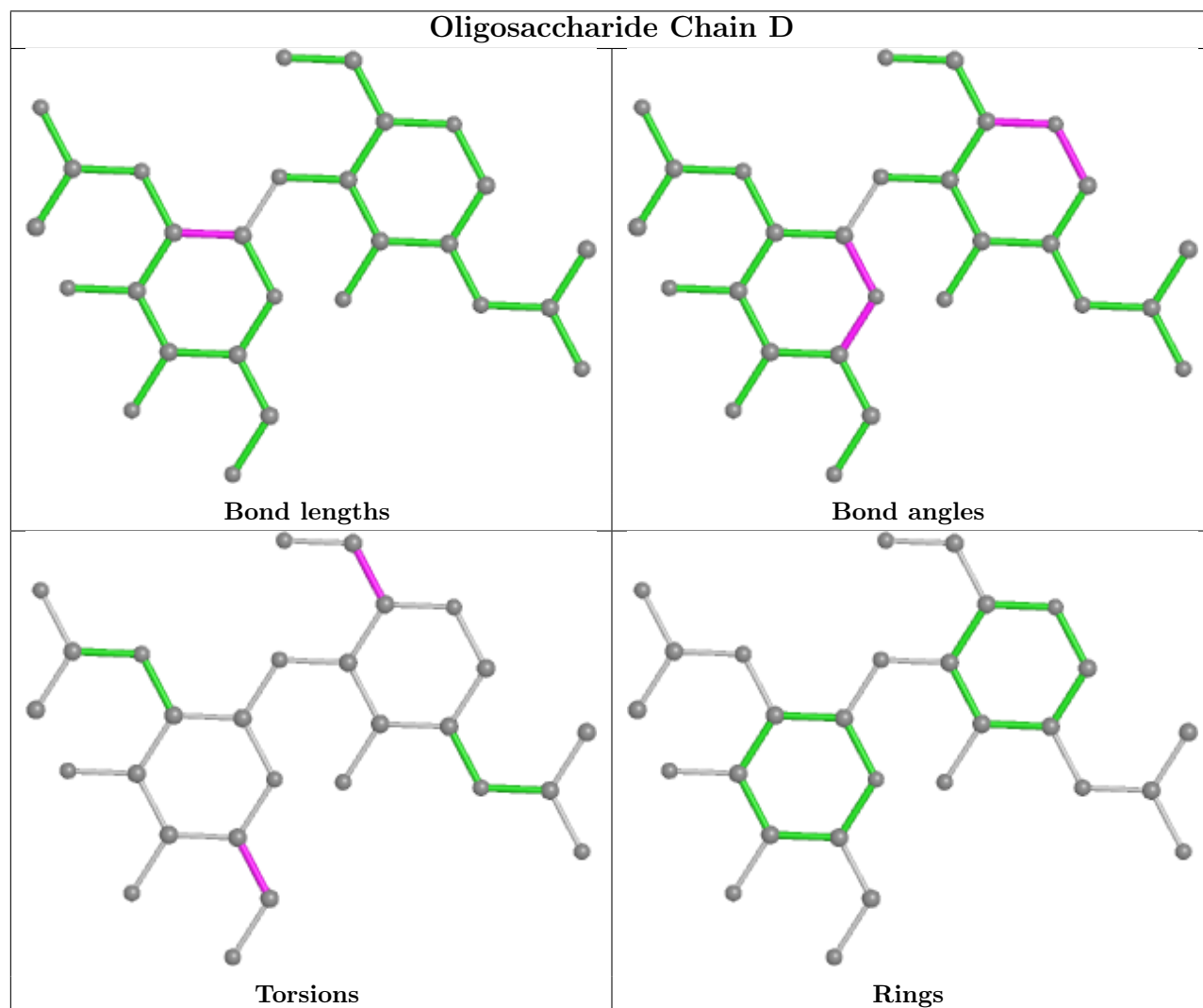
Mol	Chain	Res	Type	Atoms
2	I	1	NAG	O5-C5-C6-O6
2	L	2	NAG	O5-C5-C6-O6
2	K	1	NAG	O5-C5-C6-O6

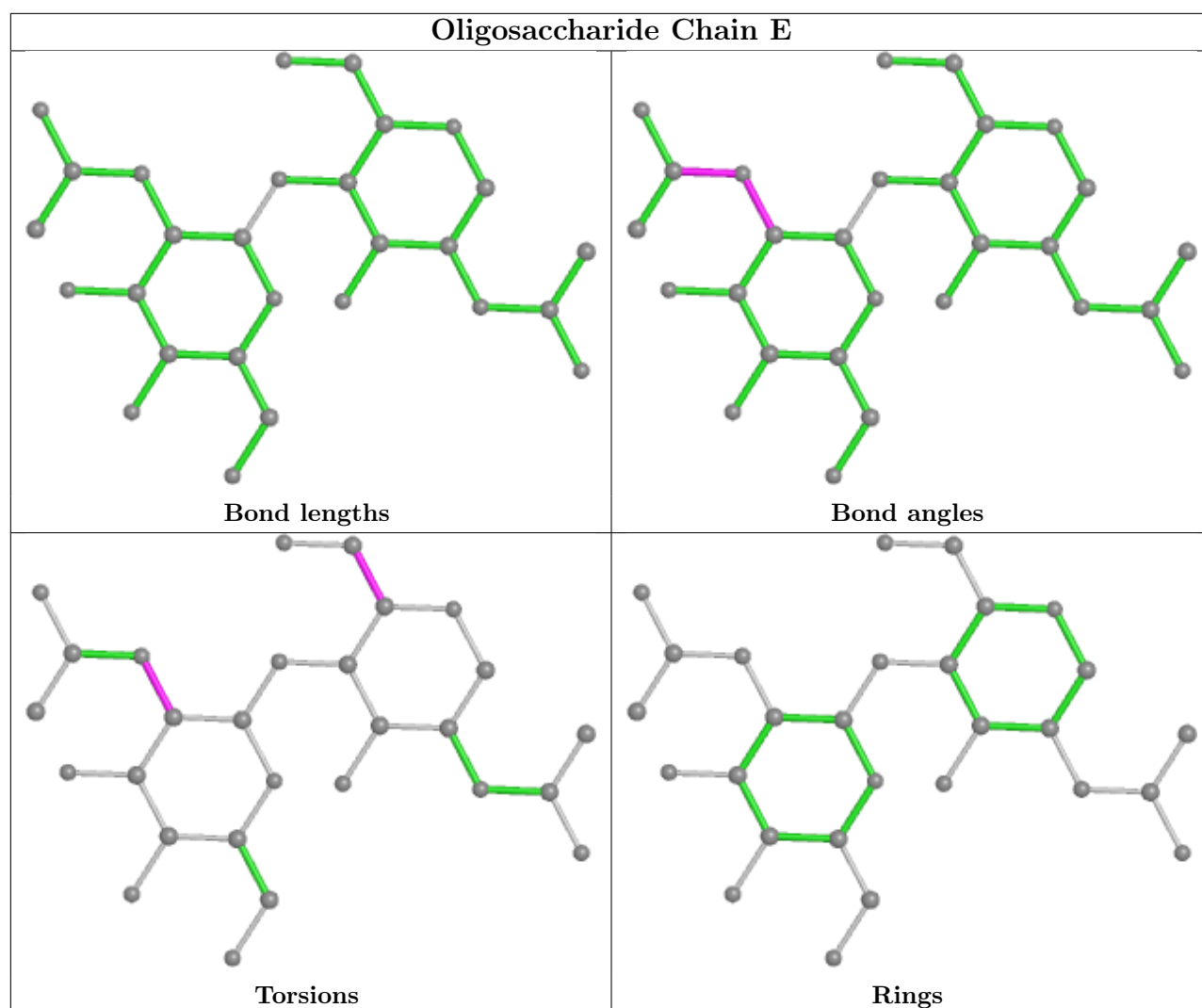
There are no ring outliers.

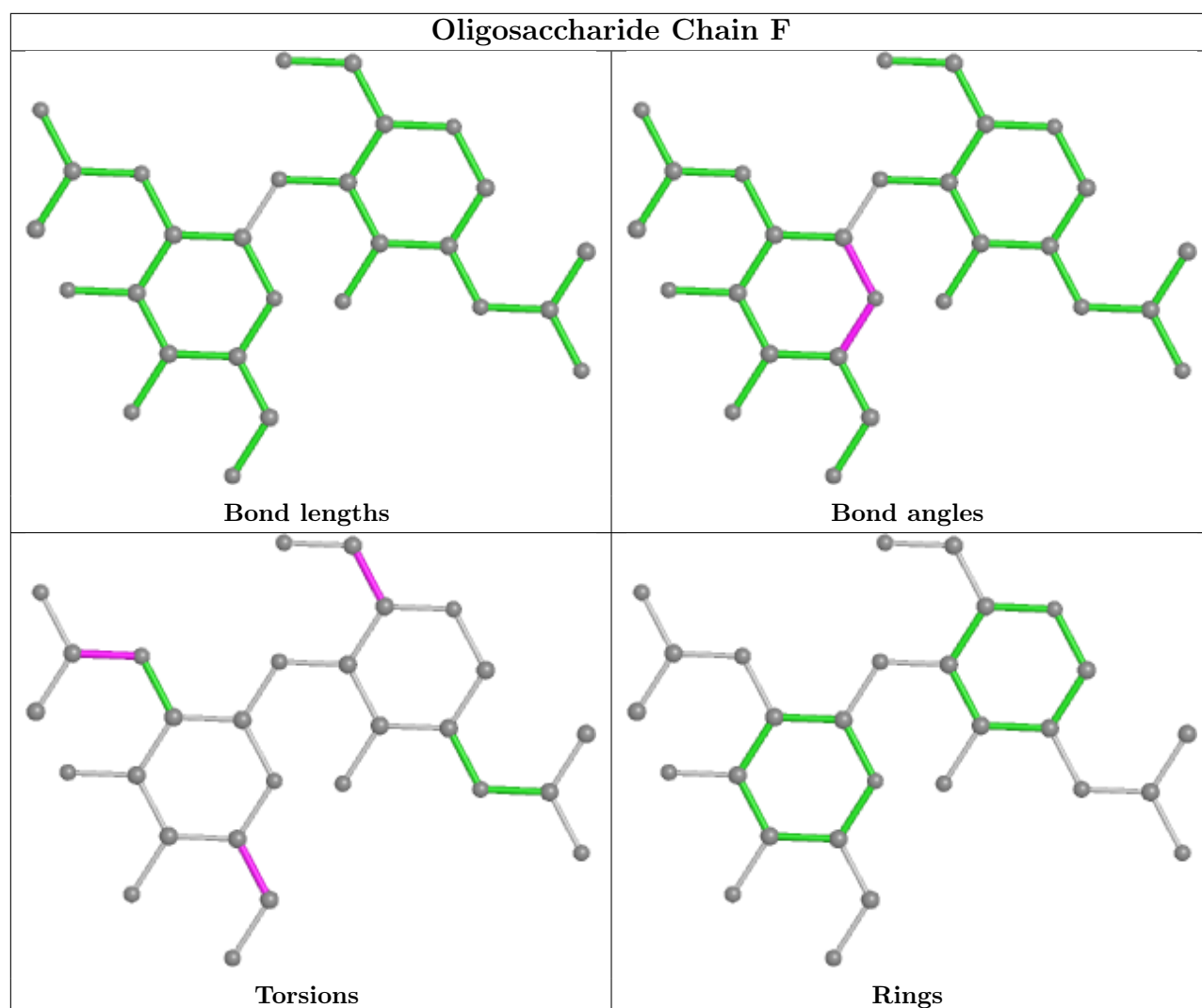
2 monomers are involved in 2 short contacts:

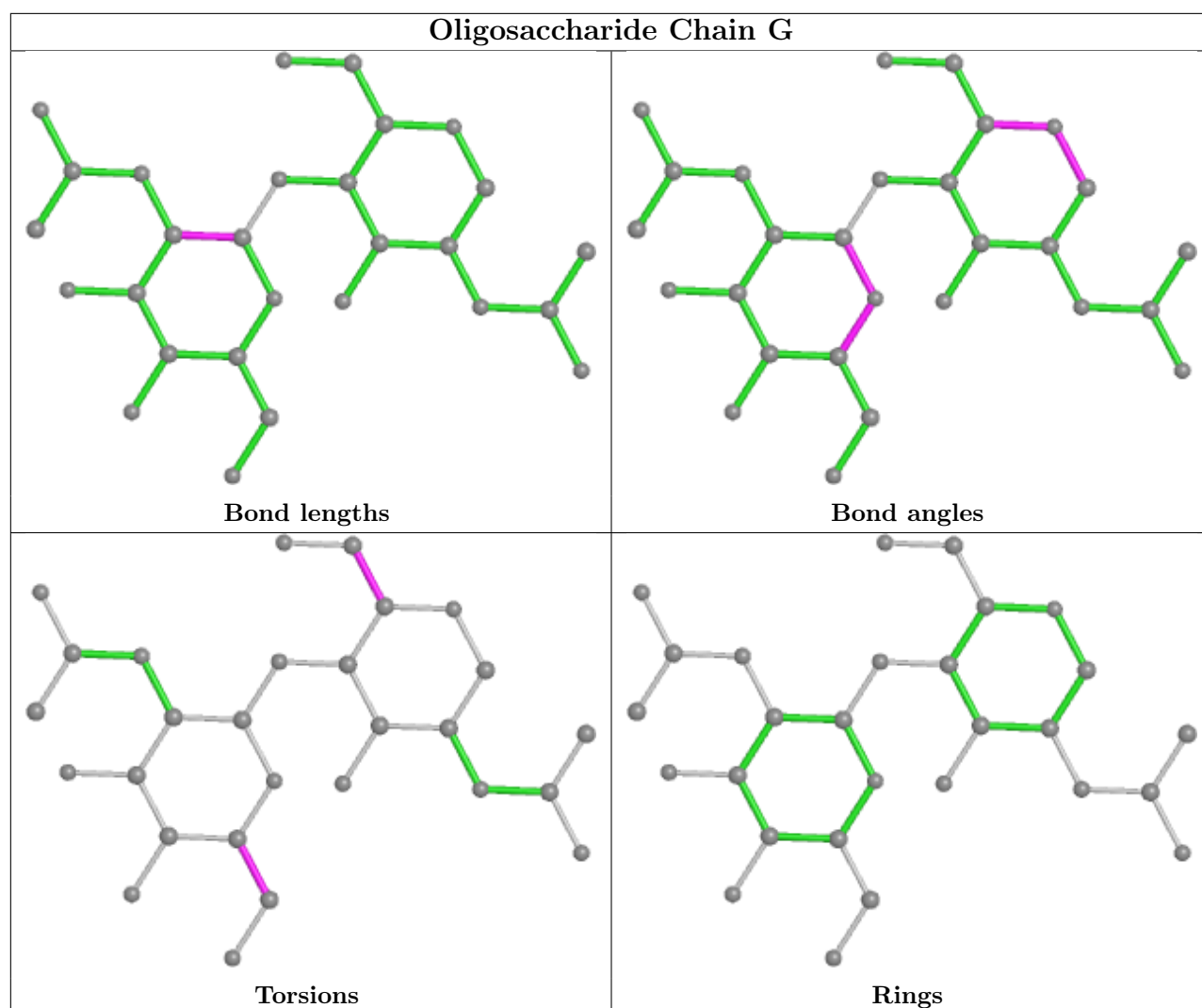
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	1	NAG	2	0
2	J	2	NAG	2	0

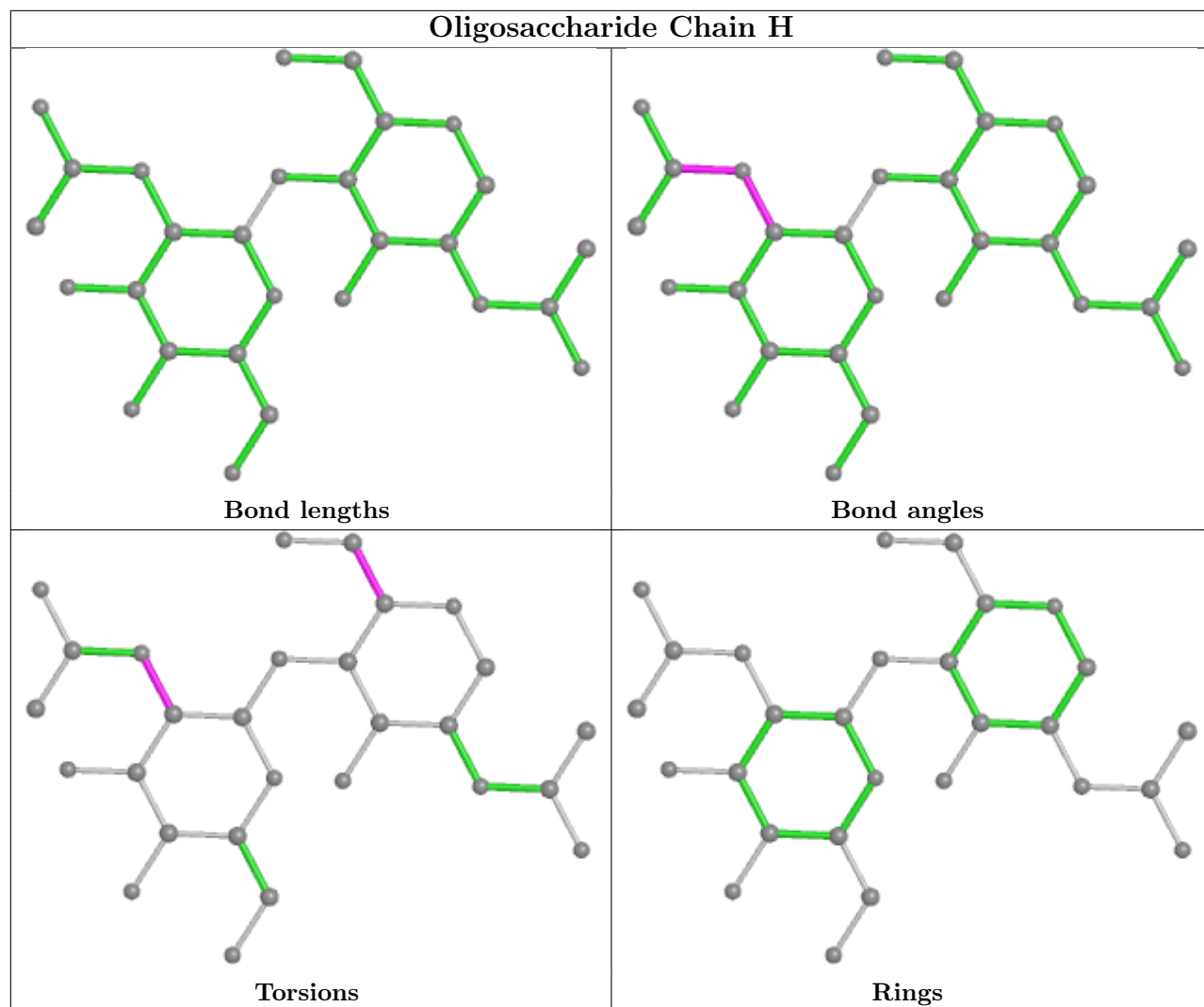
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

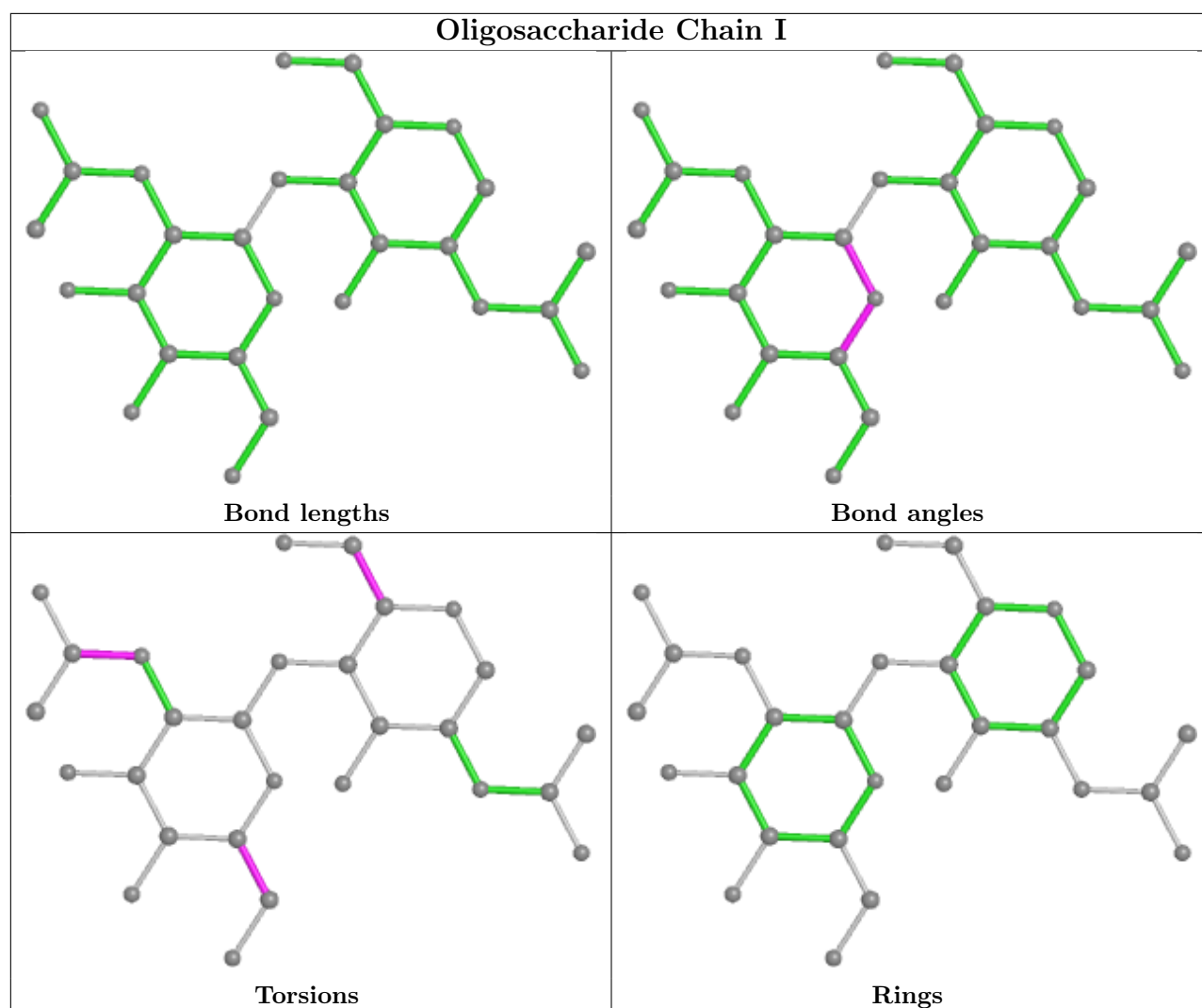


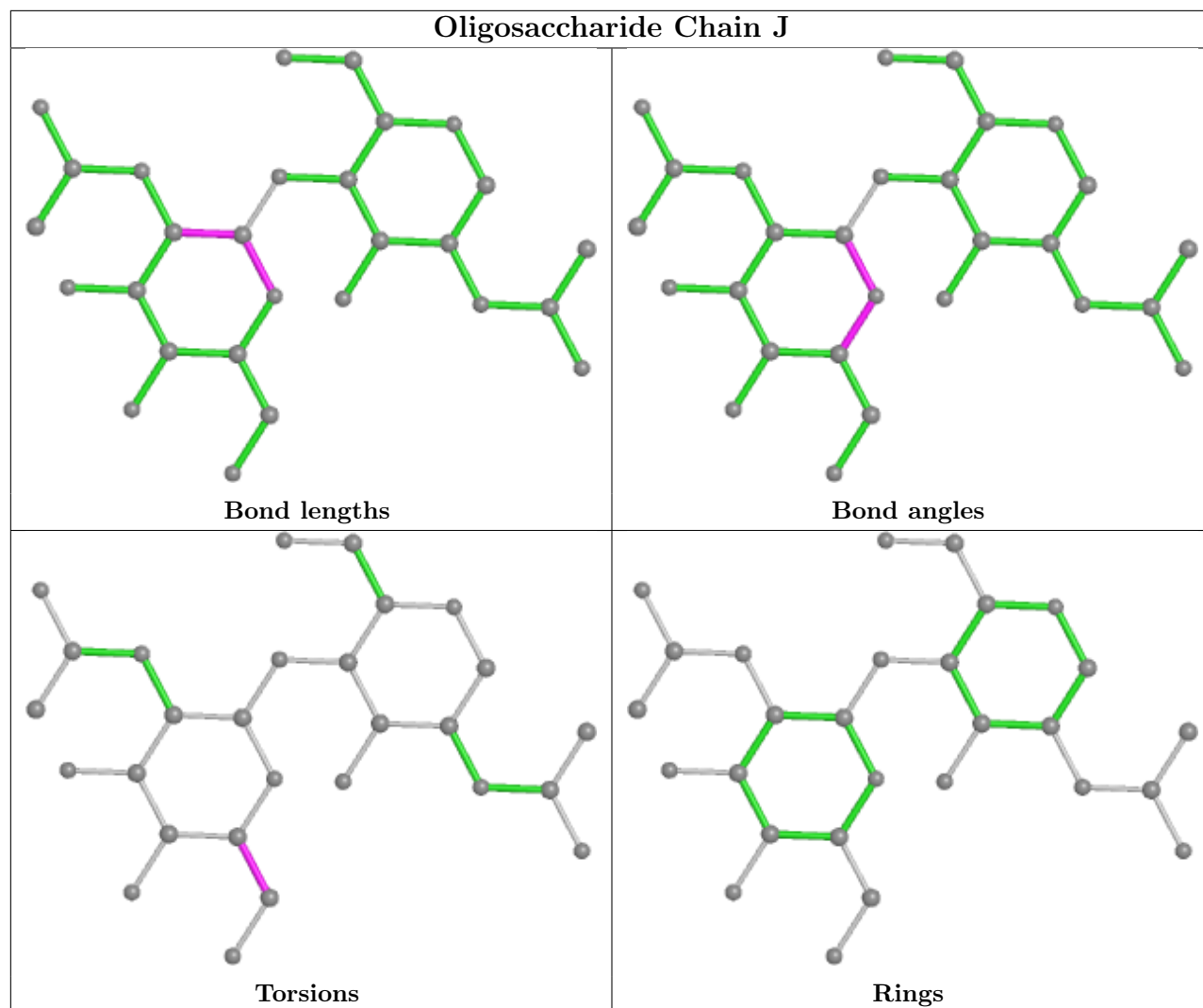




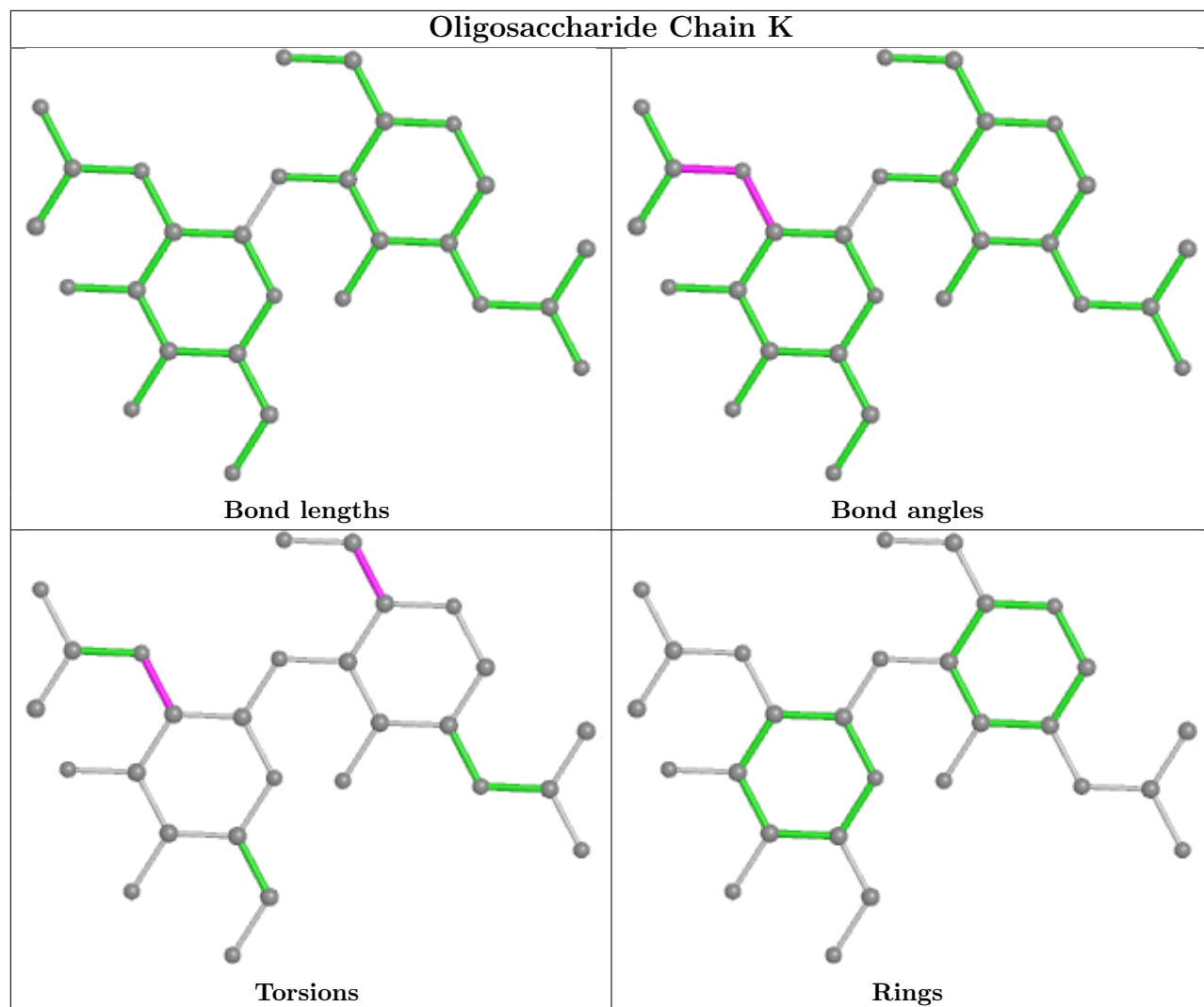


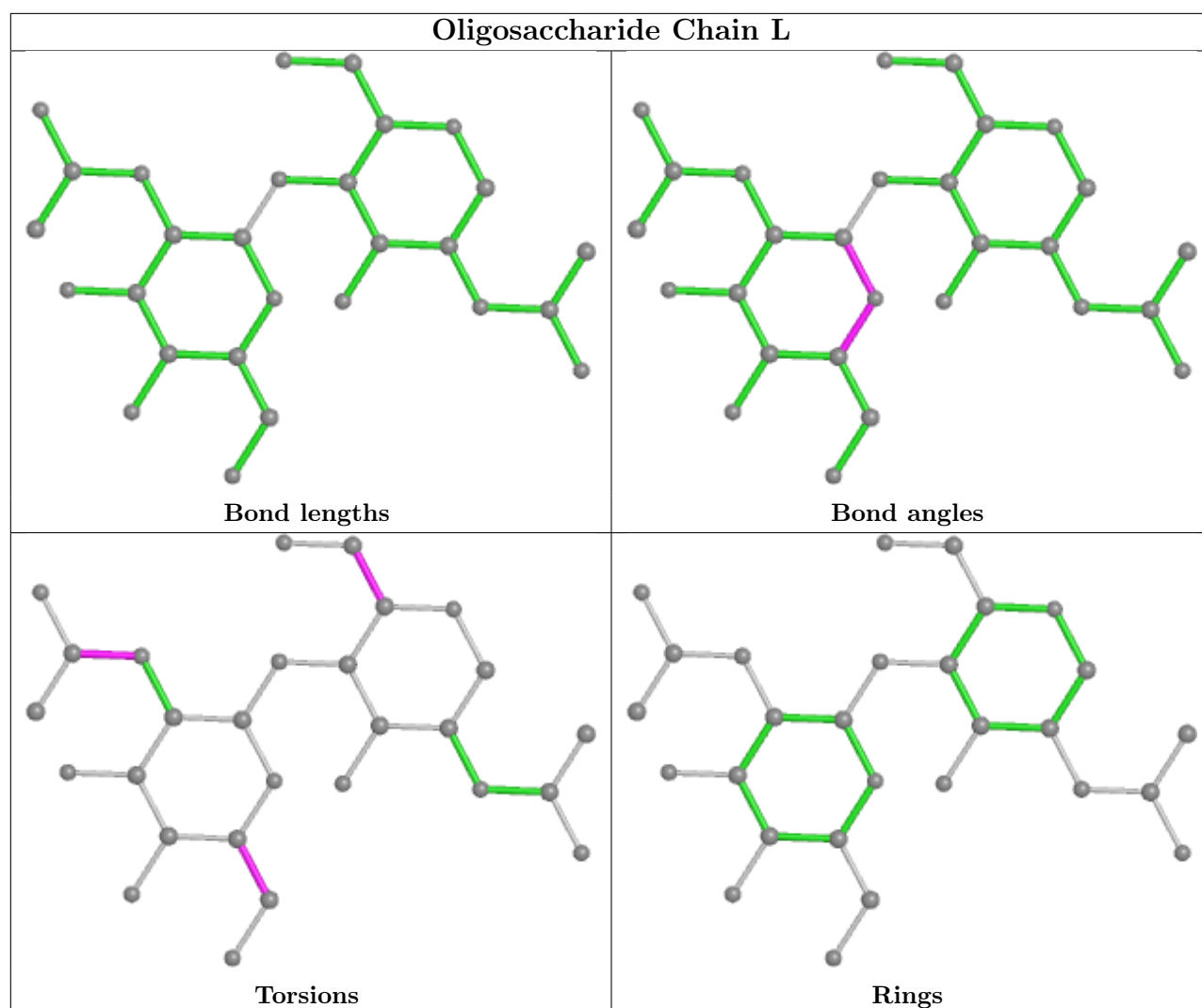












## 5.6 Ligand geometry [i](#)

45 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	$\# Z  > 2$
3	NAG	B	1301	1	14,14,15	0.32	0	17,19,21	0.47	0
3	NAG	C	1305	1	14,14,15	0.37	0	17,19,21	0.51	0
3	NAG	A	1302	1	14,14,15	0.86	1 (7%)	17,19,21	0.66	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	C	1308	1	14,14,15	0.34	0	17,19,21	0.43	0
3	NAG	C	1315	1	14,14,15	0.33	0	17,19,21	0.55	0
3	NAG	B	1309	1	14,14,15	0.38	0	17,19,21	0.97	1 (5%)
3	NAG	B	1315	1	14,14,15	0.31	0	17,19,21	0.55	0
3	NAG	A	1301	1	14,14,15	0.32	0	17,19,21	0.48	0
3	NAG	A	1309	1	14,14,15	0.38	0	17,19,21	0.97	1 (5%)
3	NAG	A	1312	1	14,14,15	0.44	0	17,19,21	0.55	0
3	NAG	C	1309	1	14,14,15	0.38	0	17,19,21	0.97	1 (5%)
3	NAG	A	1303	-	14,14,15	0.33	0	17,19,21	0.47	0
3	NAG	C	1311	1	14,14,15	0.78	1 (7%)	17,19,21	1.15	2 (11%)
3	NAG	A	1308	1	14,14,15	0.32	0	17,19,21	0.40	0
3	NAG	A	1315	1	14,14,15	0.33	0	17,19,21	0.56	0
3	NAG	B	1311	1	14,14,15	0.51	0	17,19,21	1.01	1 (5%)
3	NAG	C	1310	1	14,14,15	0.53	0	17,19,21	0.41	0
3	NAG	B	1308	1	14,14,15	0.31	0	17,19,21	0.41	0
3	NAG	C	1301	1	14,14,15	0.33	0	17,19,21	0.48	0
3	NAG	C	1307	1	14,14,15	0.34	0	17,19,21	0.50	0
3	NAG	C	1304	1	14,14,15	0.40	0	17,19,21	0.52	0
3	NAG	B	1314	1	14,14,15	0.46	0	17,19,21	0.52	0
3	NAG	C	1306	1	14,14,15	0.48	0	17,19,21	0.57	0
3	NAG	B	1305	1	14,14,15	0.38	0	17,19,21	0.53	0
3	NAG	A	1314	1	14,14,15	0.46	0	17,19,21	0.48	0
3	NAG	C	1313	1	14,14,15	0.31	0	17,19,21	0.50	0
3	NAG	B	1306	1	14,14,15	0.46	0	17,19,21	0.57	0
3	NAG	A	1305	1	14,14,15	0.37	0	17,19,21	0.52	0
3	NAG	C	1302	1	14,14,15	0.86	1 (7%)	17,19,21	0.65	1 (5%)
3	NAG	C	1312	1	14,14,15	0.44	0	17,19,21	0.55	0
3	NAG	B	1307	1	14,14,15	0.34	0	17,19,21	0.49	0
3	NAG	B	1313	1	14,14,15	0.29	0	17,19,21	0.46	0
3	NAG	B	1303	-	14,14,15	0.32	0	17,19,21	0.48	0
3	NAG	A	1311	1	14,14,15	0.47	0	17,19,21	1.00	1 (5%)
3	NAG	B	1310	1	14,14,15	0.49	0	17,19,21	0.58	0
3	NAG	A	1307	1	14,14,15	0.33	0	17,19,21	0.48	0
3	NAG	C	1303	-	14,14,15	0.32	0	17,19,21	0.48	0
3	NAG	A	1310	1	14,14,15	0.47	0	17,19,21	0.58	0
3	NAG	A	1304	1	14,14,15	0.42	0	17,19,21	0.54	0
3	NAG	B	1302	1	14,14,15	0.86	1 (7%)	17,19,21	0.65	1 (5%)
3	NAG	A	1306	1	14,14,15	0.46	0	17,19,21	0.57	0
3	NAG	B	1312	1	14,14,15	0.52	0	17,19,21	0.57	0
3	NAG	B	1304	1	14,14,15	0.44	0	17,19,21	0.54	0
3	NAG	A	1313	1	14,14,15	0.27	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	NAG	C	1314	1	14,14,15	0.46	0	17,19,21	0.51	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
3	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1305	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1308	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1315	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1309	1	-	3/6/23/26	0/1/1/1
3	NAG	B	1315	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1309	1	-	3/6/23/26	0/1/1/1
3	NAG	A	1312	1	-	4/6/23/26	0/1/1/1
3	NAG	C	1309	1	-	3/6/23/26	0/1/1/1
3	NAG	A	1303	-	-	0/6/23/26	0/1/1/1
3	NAG	C	1311	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1315	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1311	1	-	3/6/23/26	0/1/1/1
3	NAG	C	1310	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1308	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1307	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1304	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1314	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1305	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1314	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1313	1	-	4/6/23/26	0/1/1/1
3	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1312	1	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	1307	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1313	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1303	-	-	0/6/23/26	0/1/1/1
3	NAG	A	1311	1	-	3/6/23/26	0/1/1/1
3	NAG	B	1310	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1307	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1303	-	-	0/6/23/26	0/1/1/1
3	NAG	A	1310	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1302	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1306	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1312	1	-	3/6/23/26	0/1/1/1
3	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1313	1	-	4/6/23/26	0/1/1/1
3	NAG	C	1314	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1302	NAG	O5-C1	2.85	1.48	1.43
3	B	1302	NAG	O5-C1	2.83	1.48	1.43
3	A	1302	NAG	O5-C1	2.82	1.48	1.43
3	C	1311	NAG	C1-C2	2.41	1.55	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1309	NAG	C2-N2-C7	3.16	127.41	122.90
3	A	1309	NAG	C2-N2-C7	3.15	127.39	122.90
3	C	1309	NAG	C2-N2-C7	3.13	127.35	122.90
3	B	1311	NAG	C2-N2-C7	3.05	127.25	122.90
3	A	1311	NAG	C2-N2-C7	3.05	127.24	122.90

There are no chirality outliers.

5 of 85 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1315	NAG	O5-C5-C6-O6
3	B	1310	NAG	O5-C5-C6-O6

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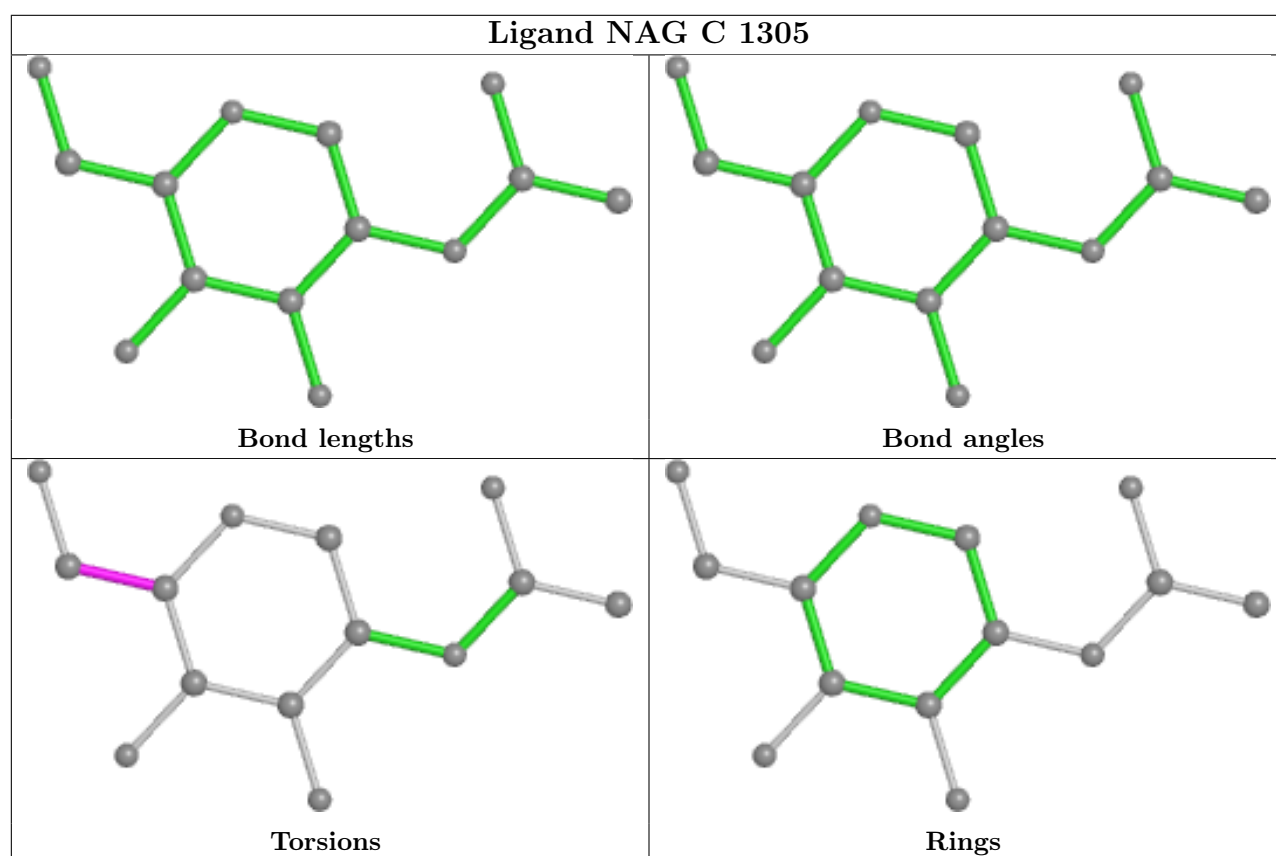
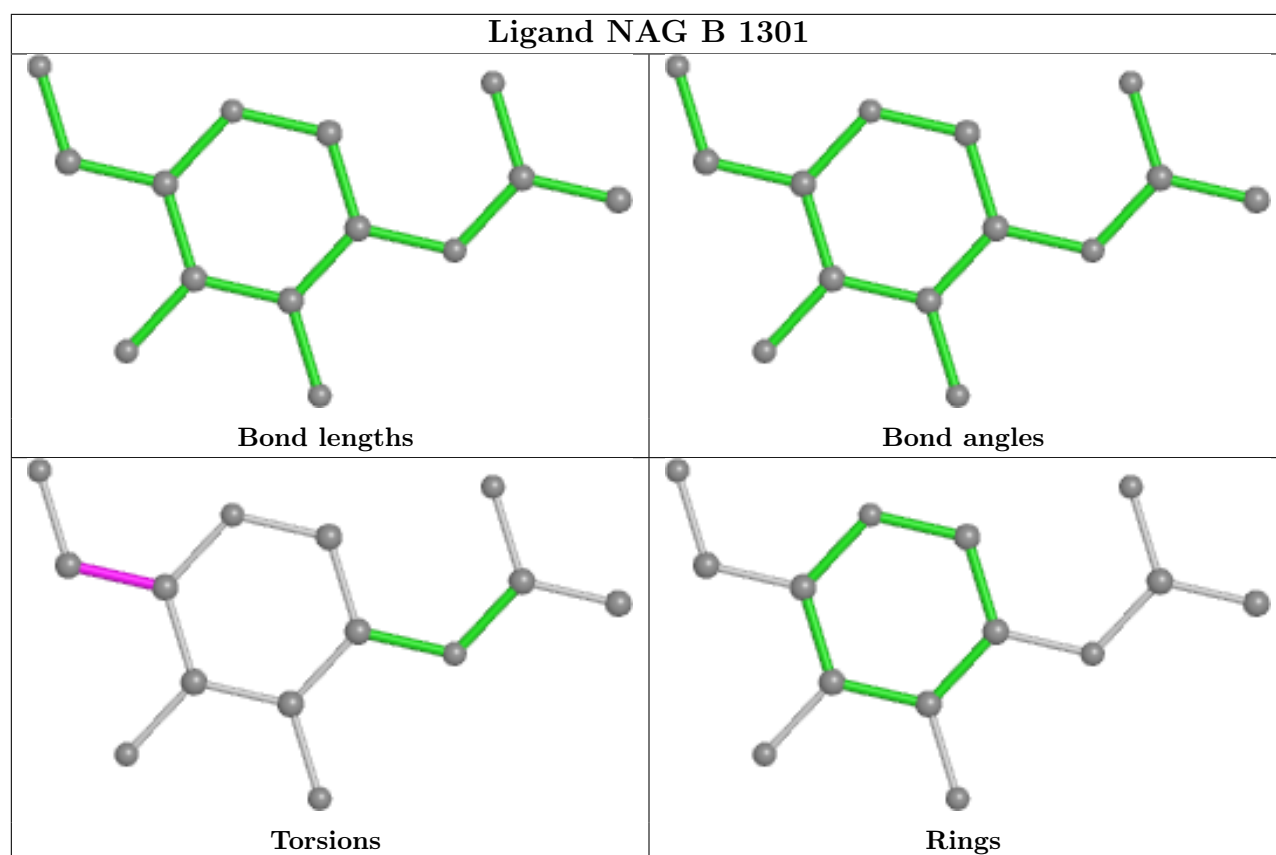
Mol	Chain	Res	Type	Atoms
3	C	1309	NAG	O5-C5-C6-O6
3	A	1311	NAG	O5-C5-C6-O6
3	B	1311	NAG	O5-C5-C6-O6

There are no ring outliers.

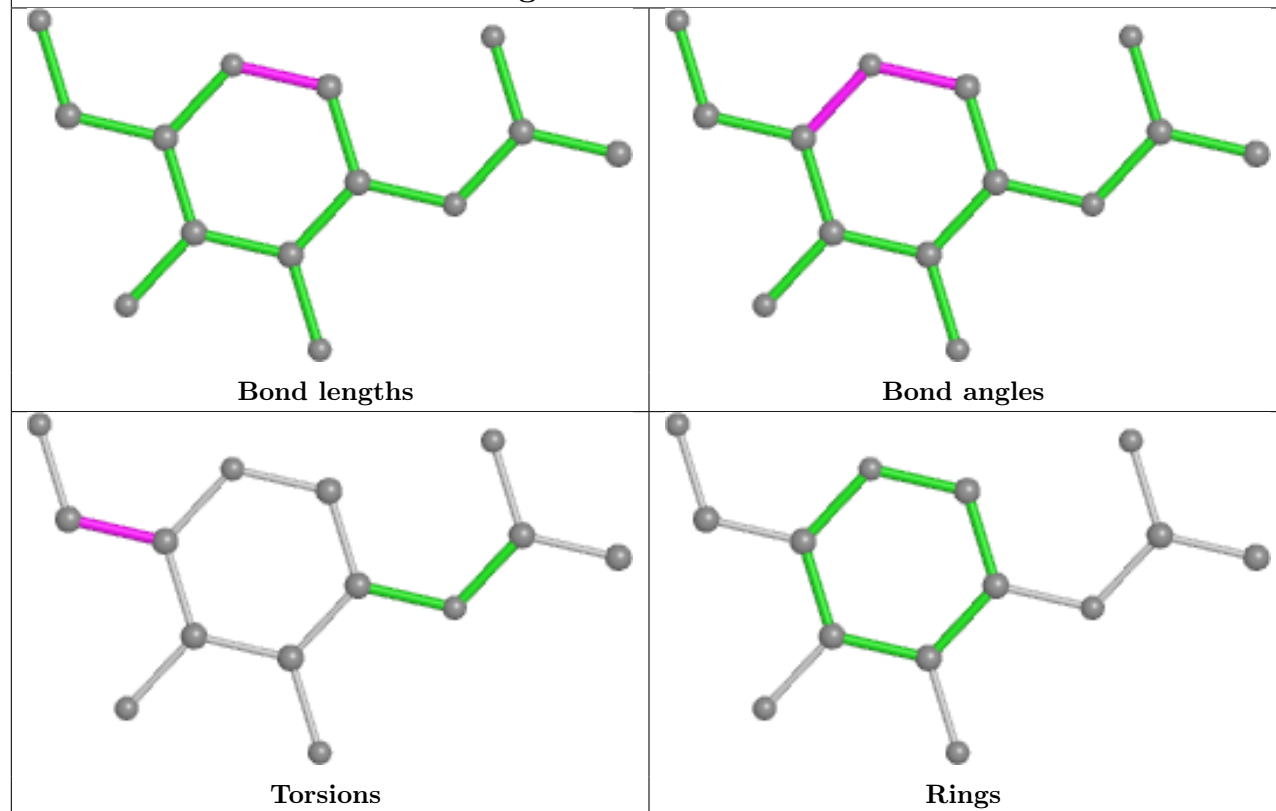
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1312	NAG	1	0
3	C	1312	NAG	1	0
3	B	1312	NAG	1	0

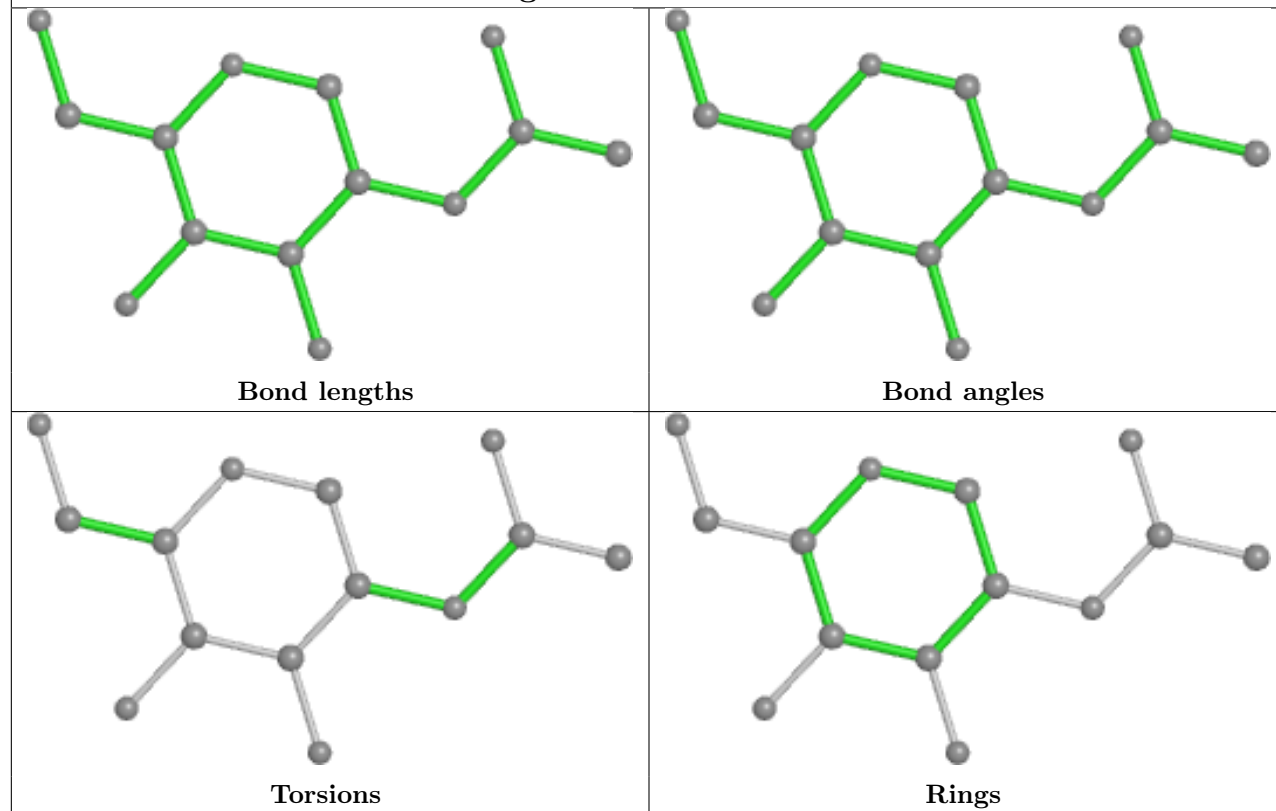
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



## Ligand NAG A 1302

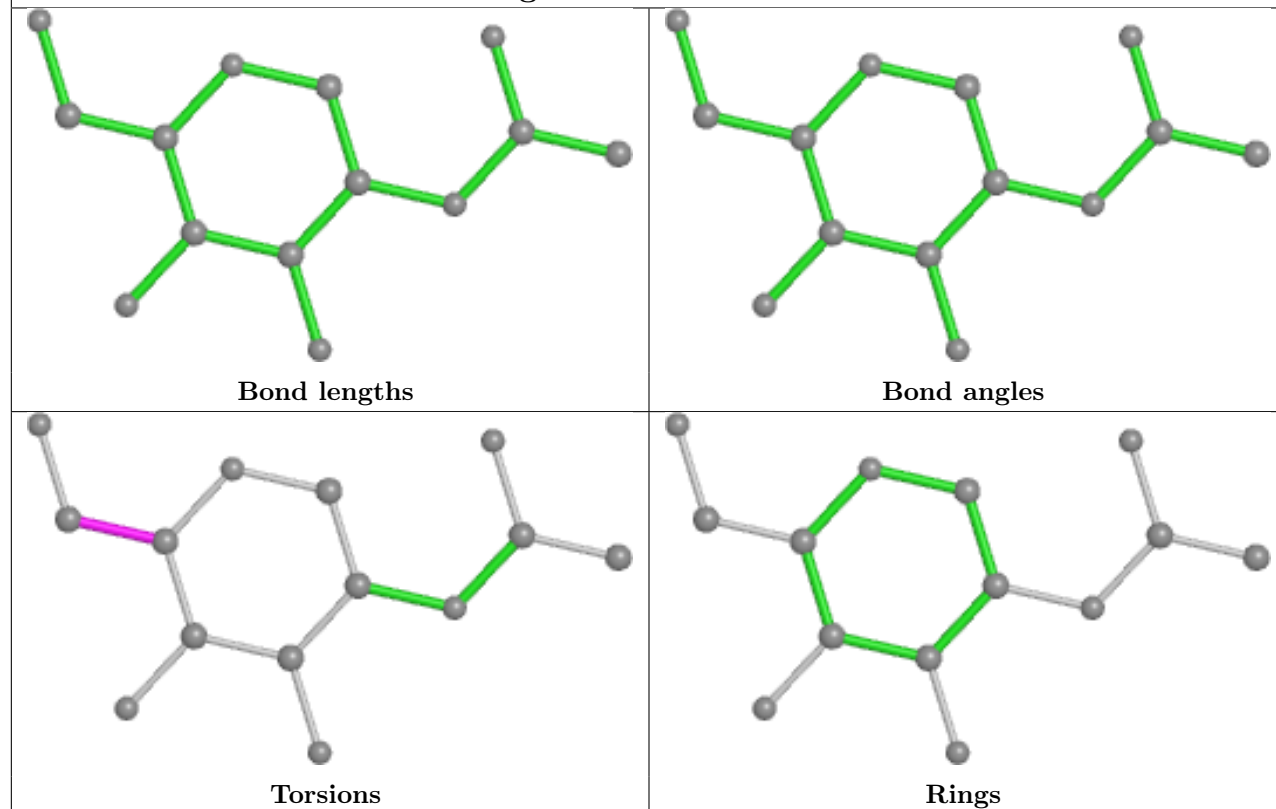


## Ligand NAG C 1308

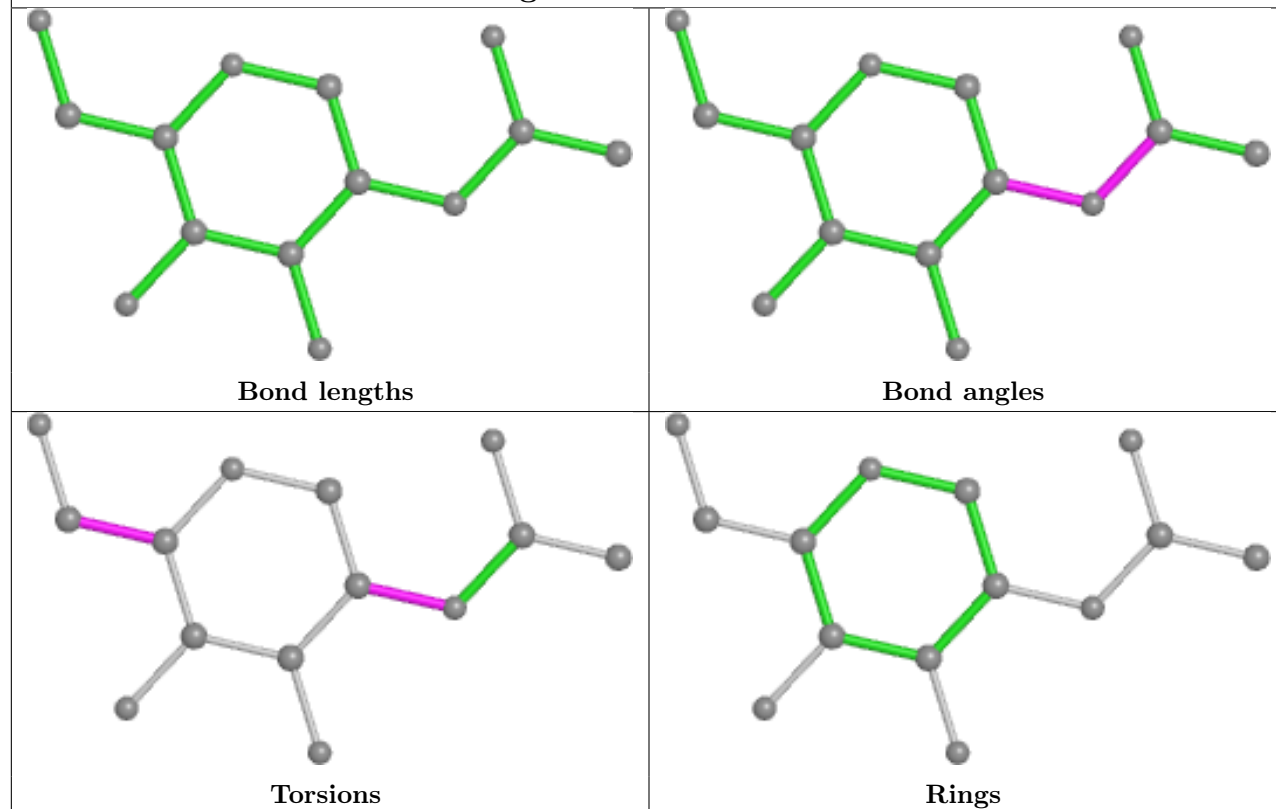


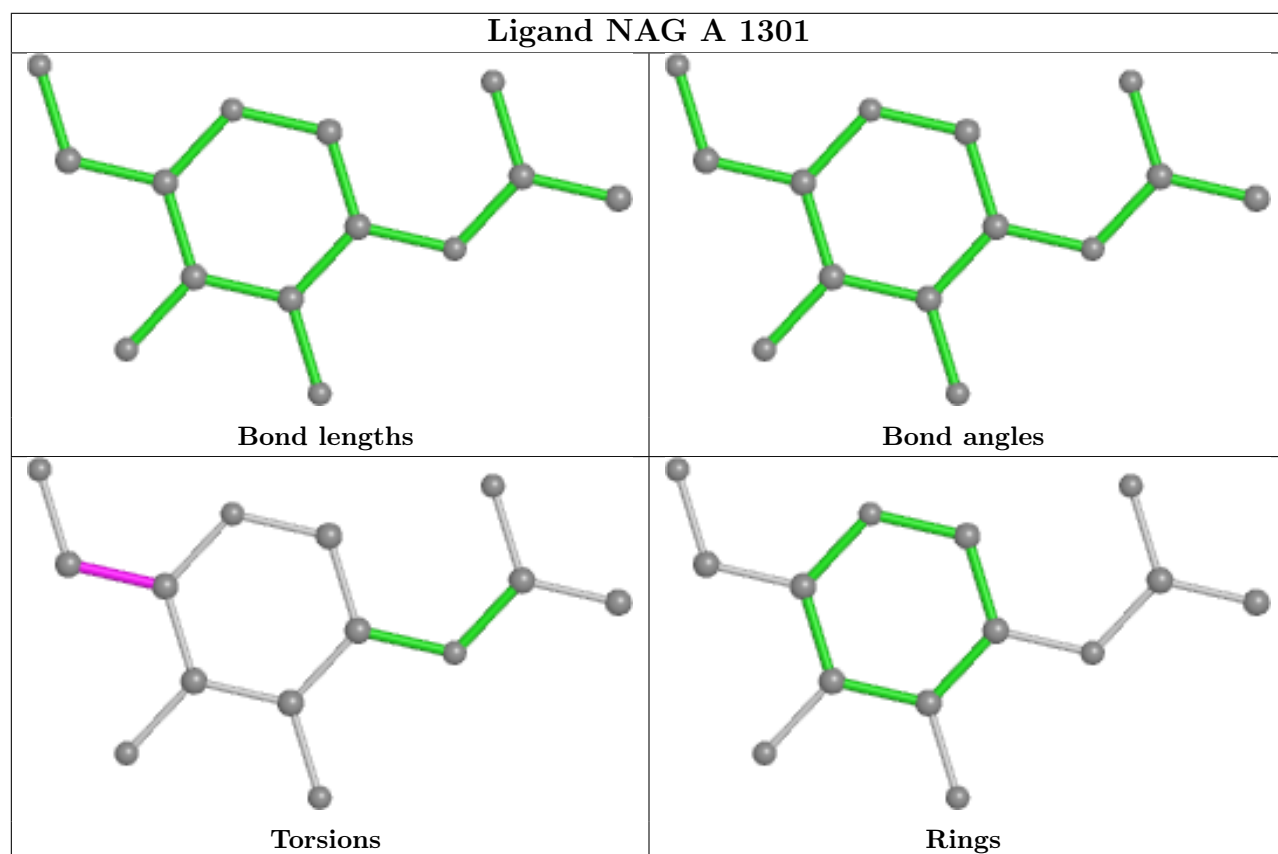
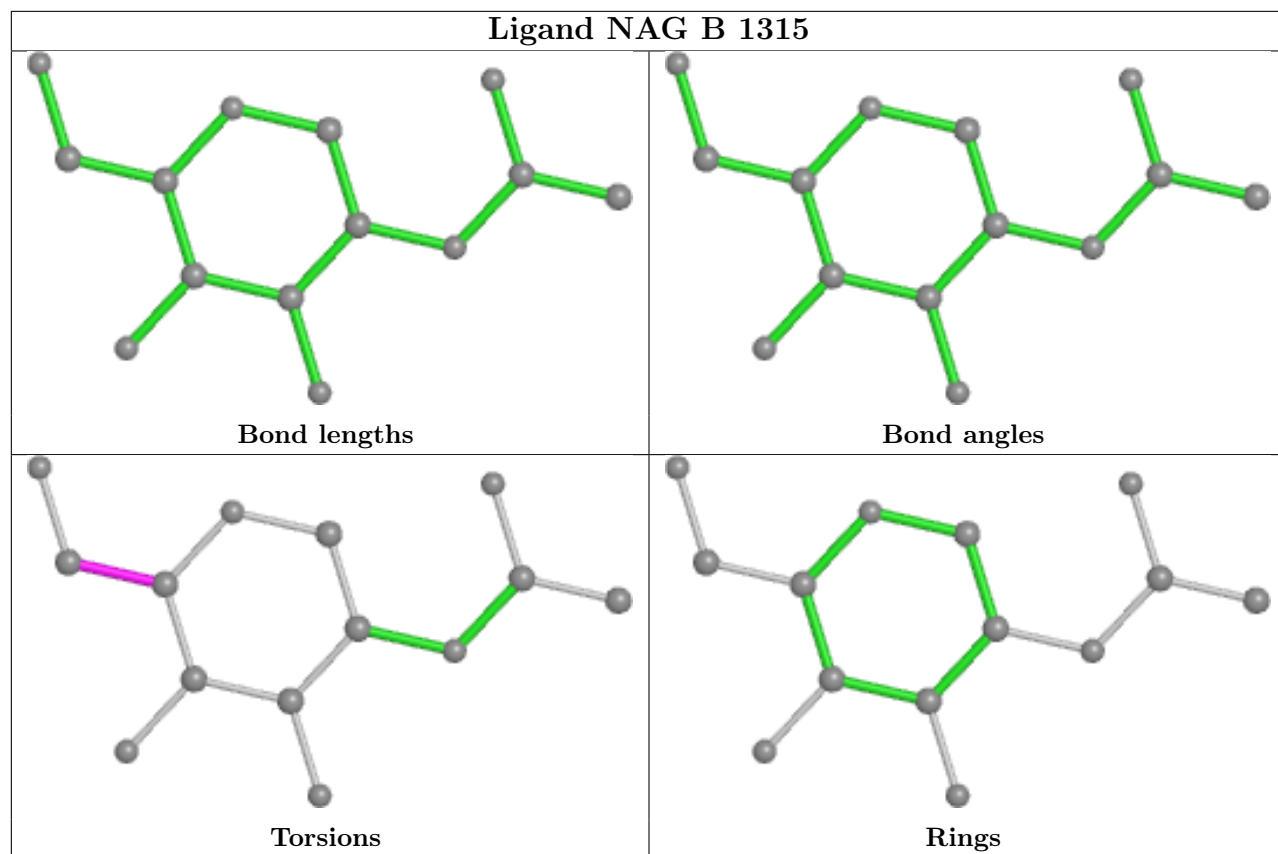


## Ligand NAG C 1315

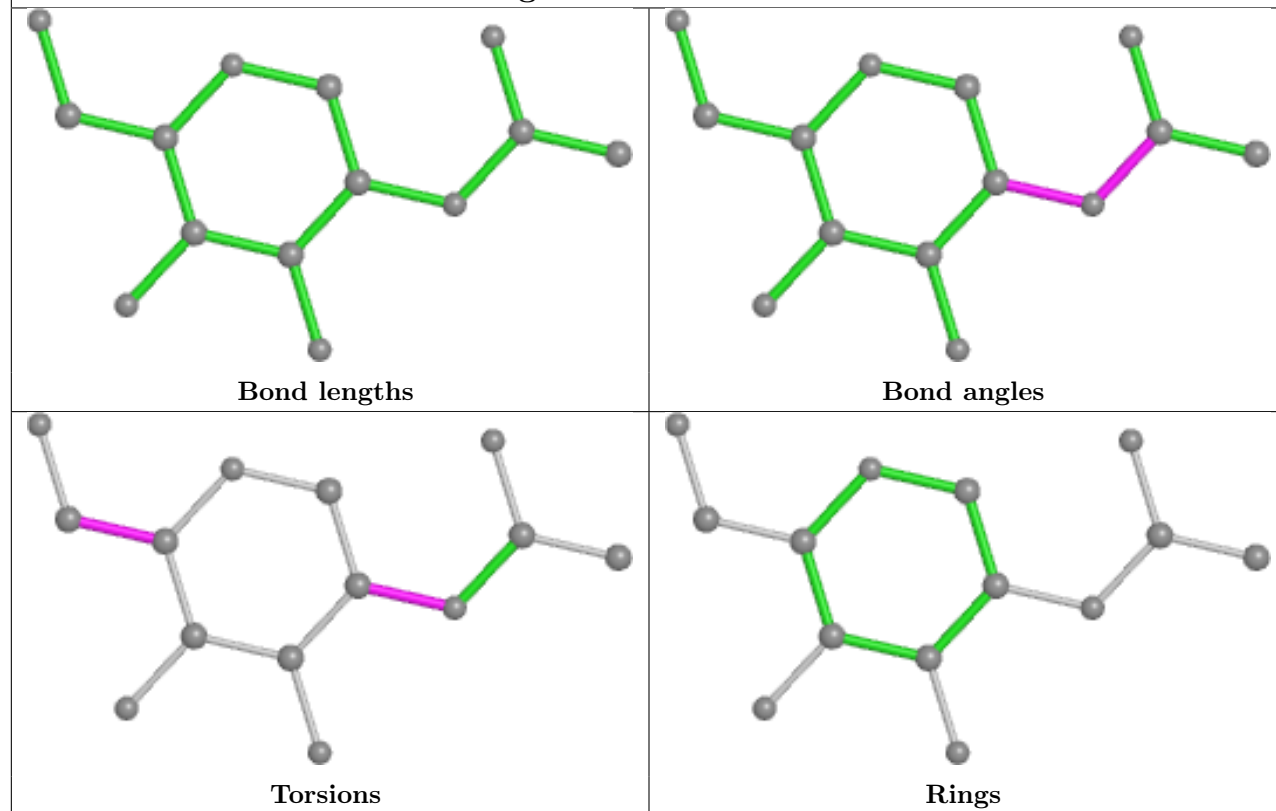


## Ligand NAG B 1309

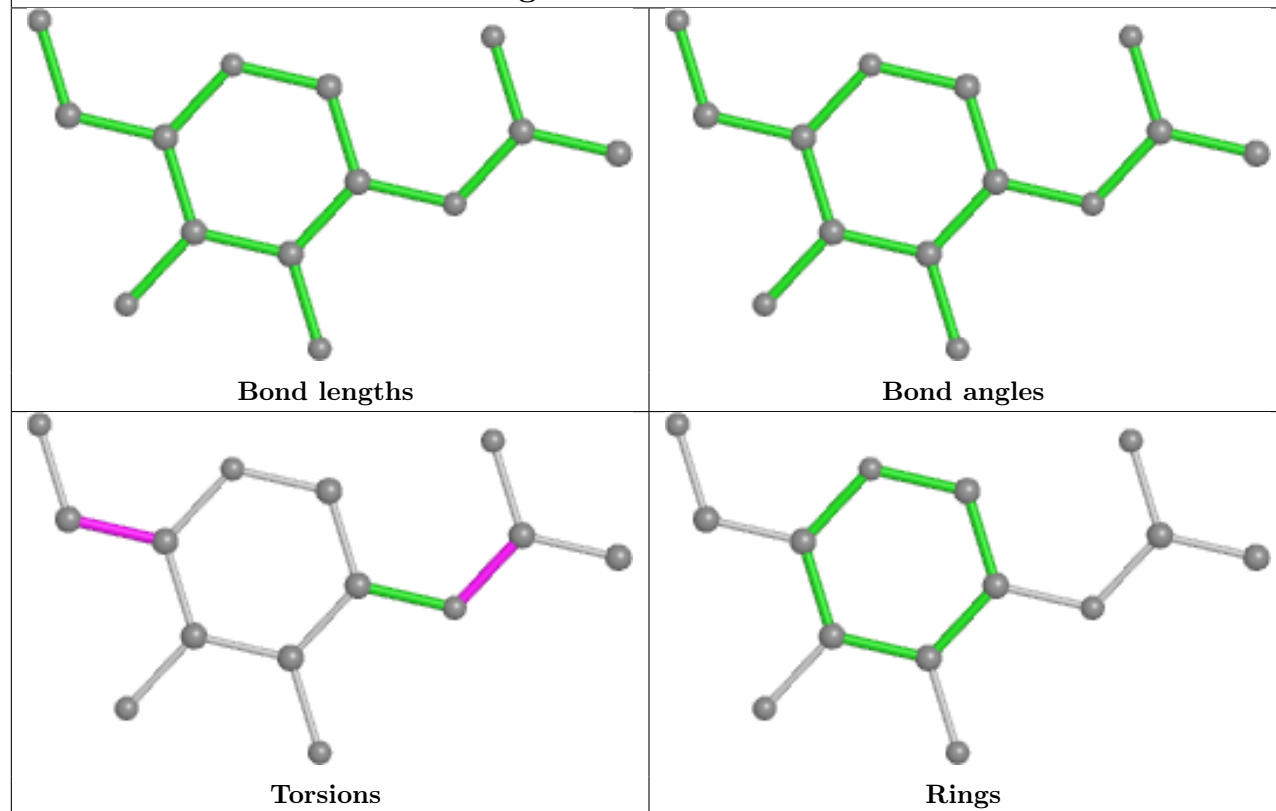




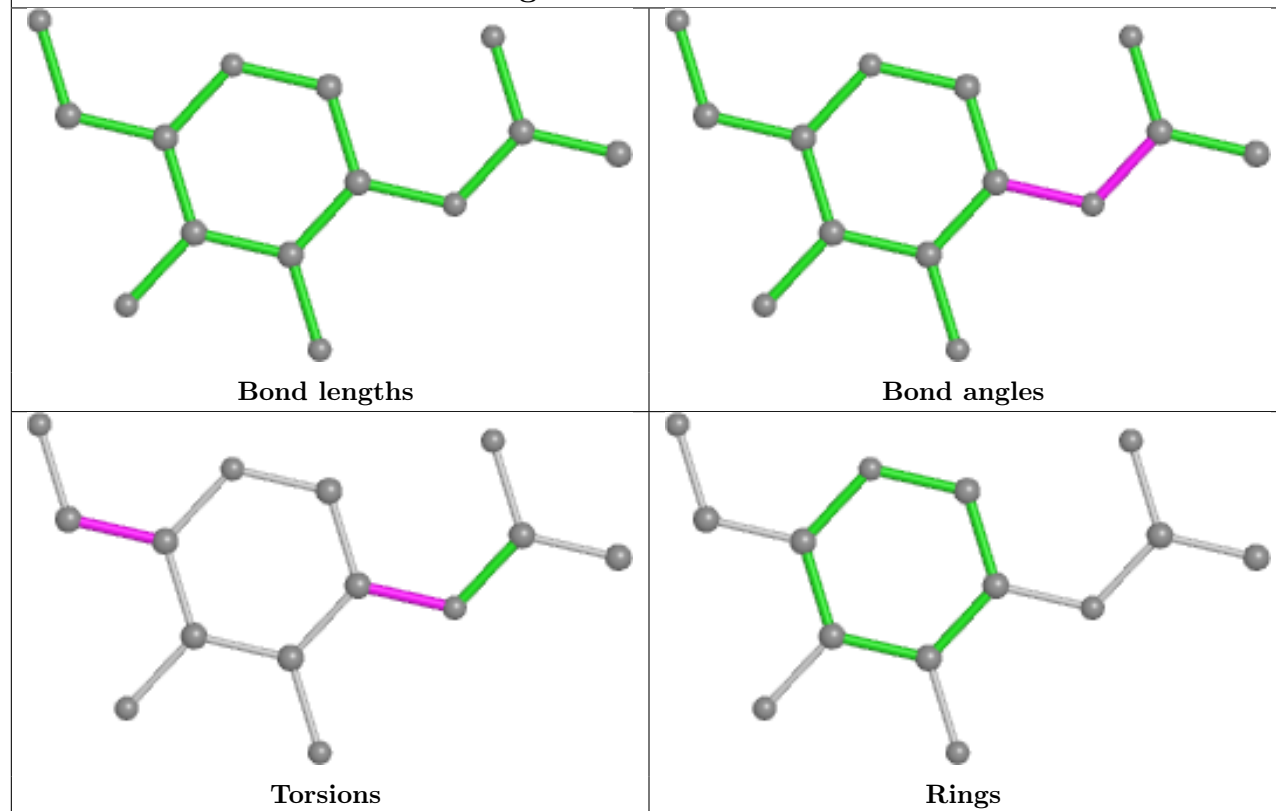
## Ligand NAG A 1309



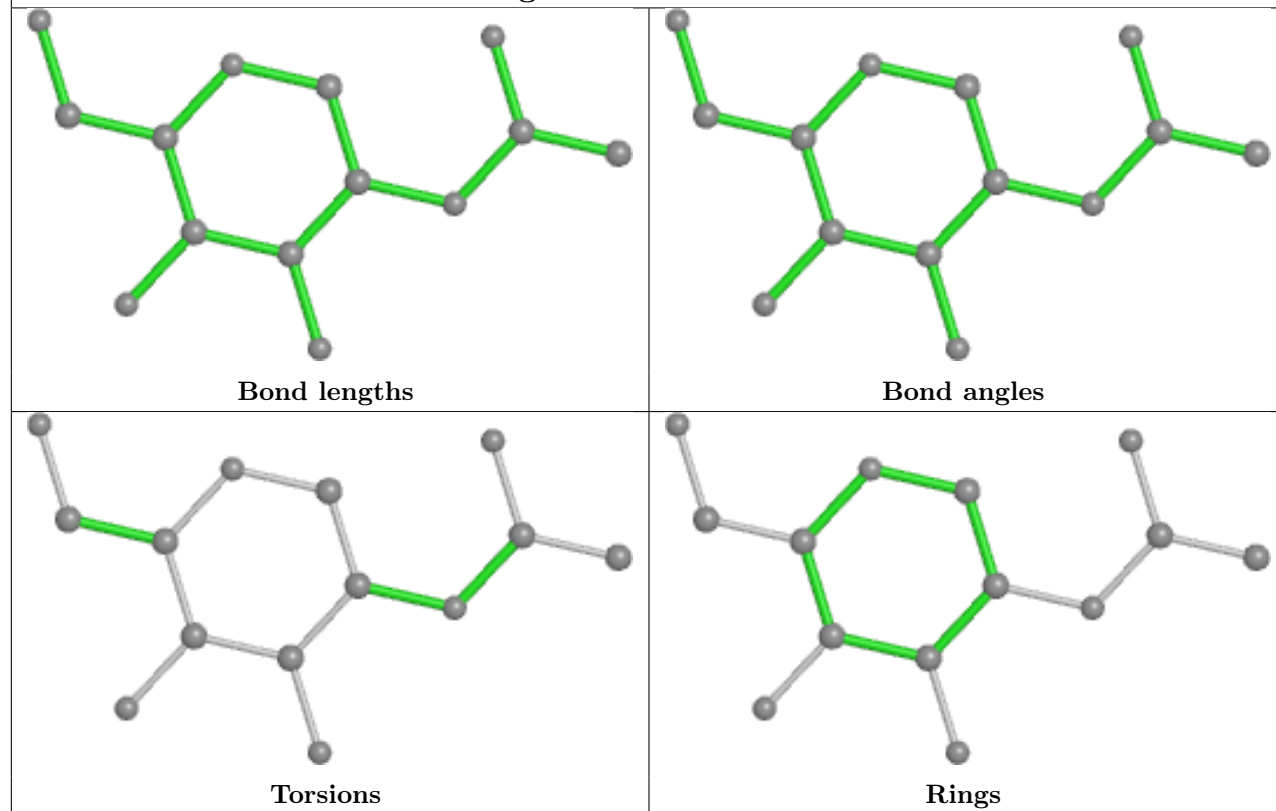
## Ligand NAG A 1312



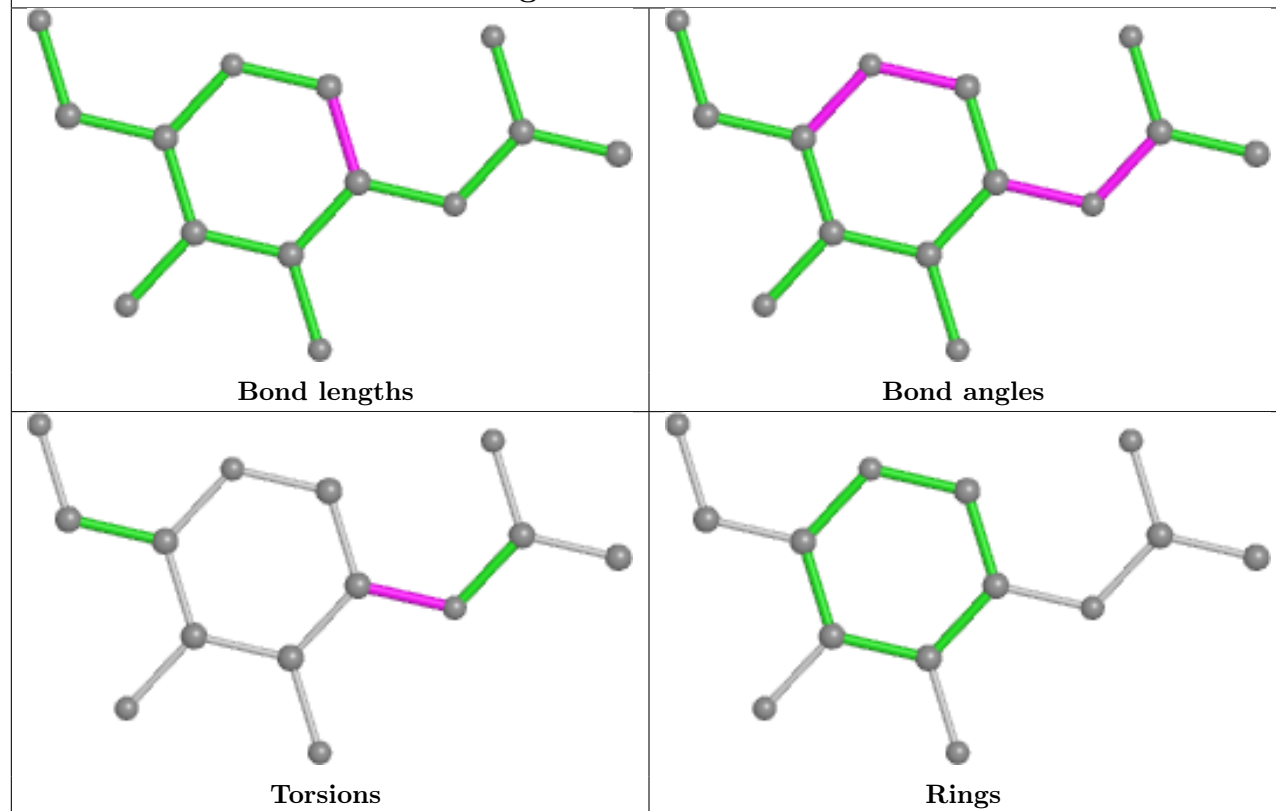
## Ligand NAG C 1309



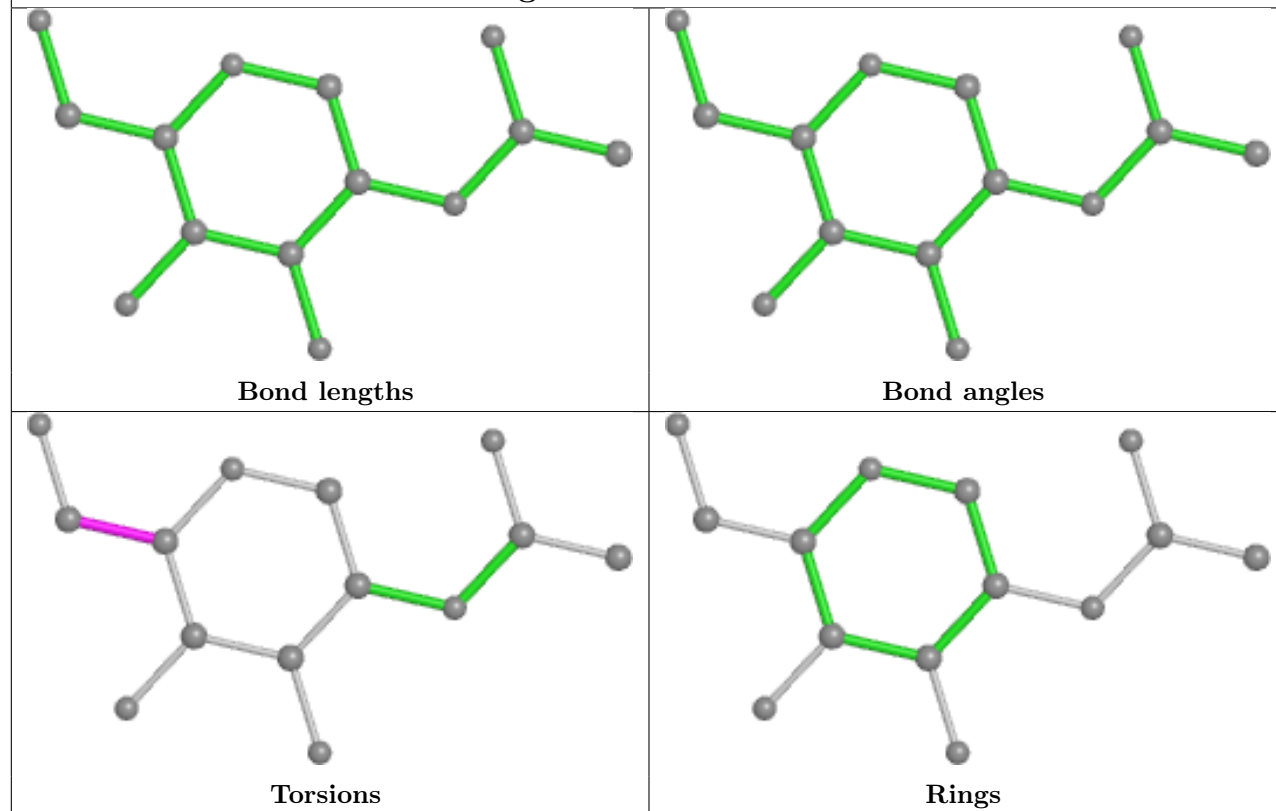
## Ligand NAG A 1303



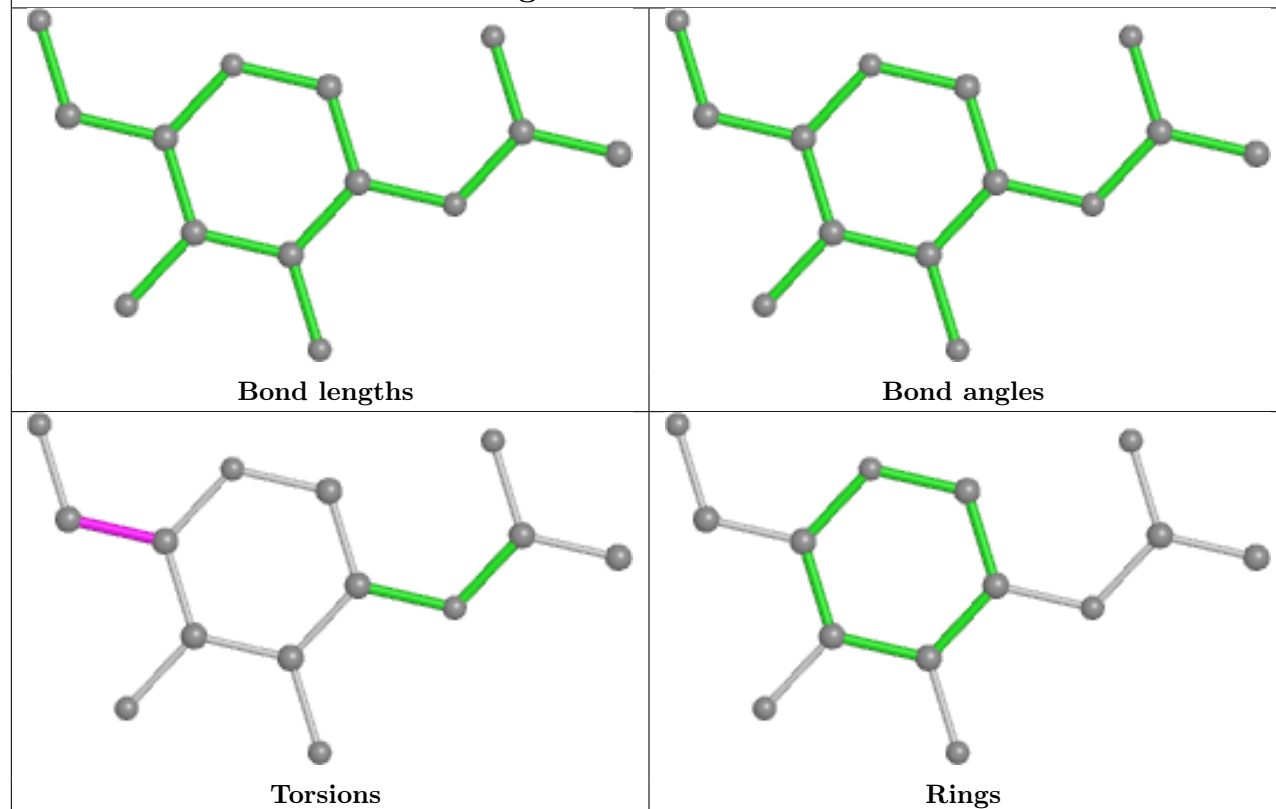
## Ligand NAG C 1311



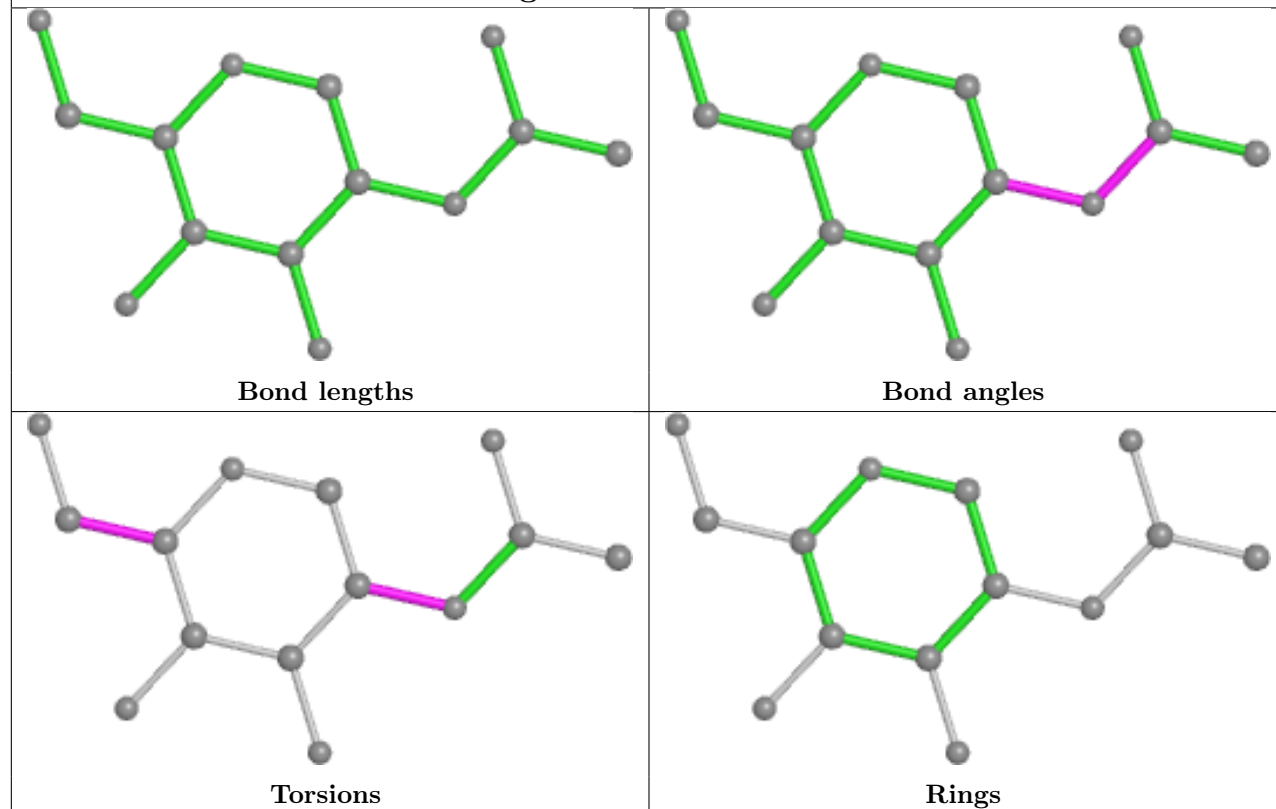
## Ligand NAG A 1308



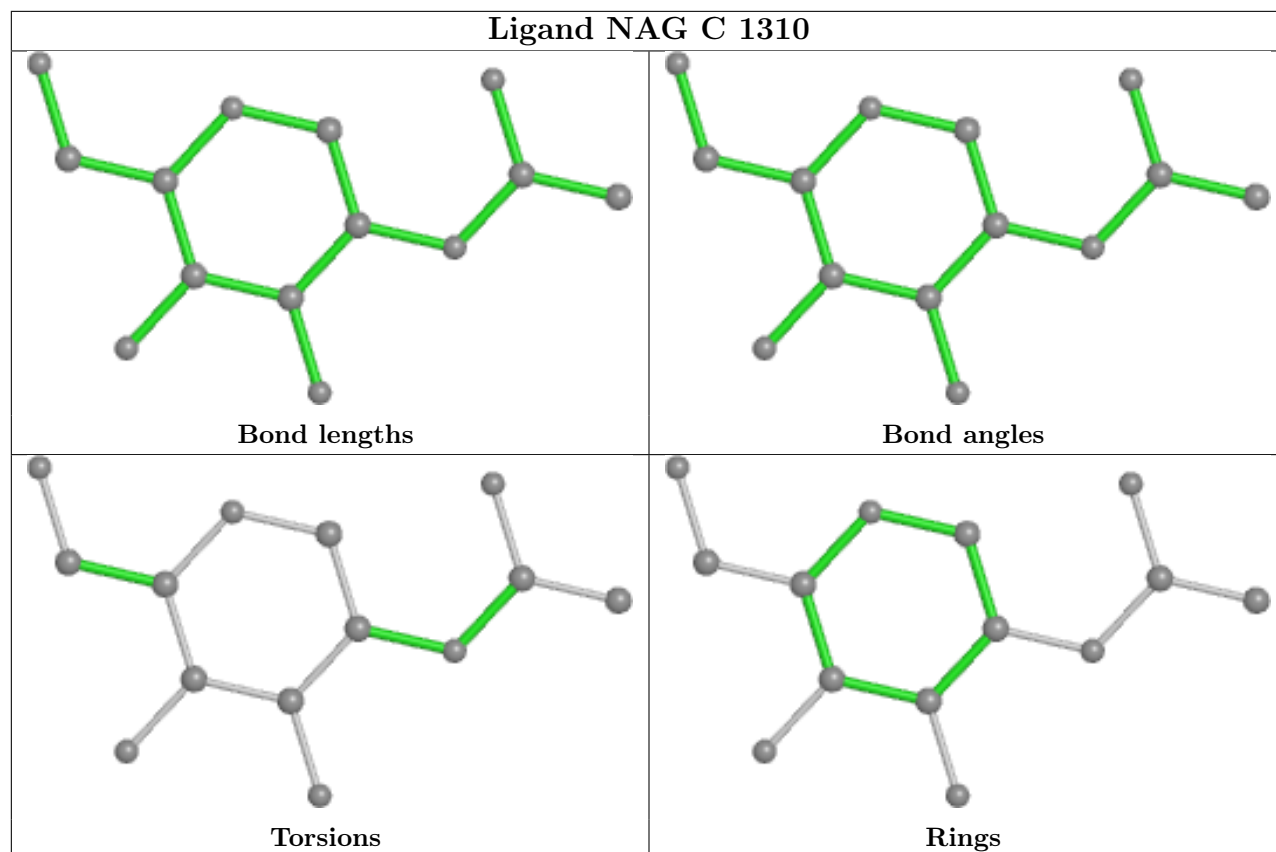
## Ligand NAG A 1315



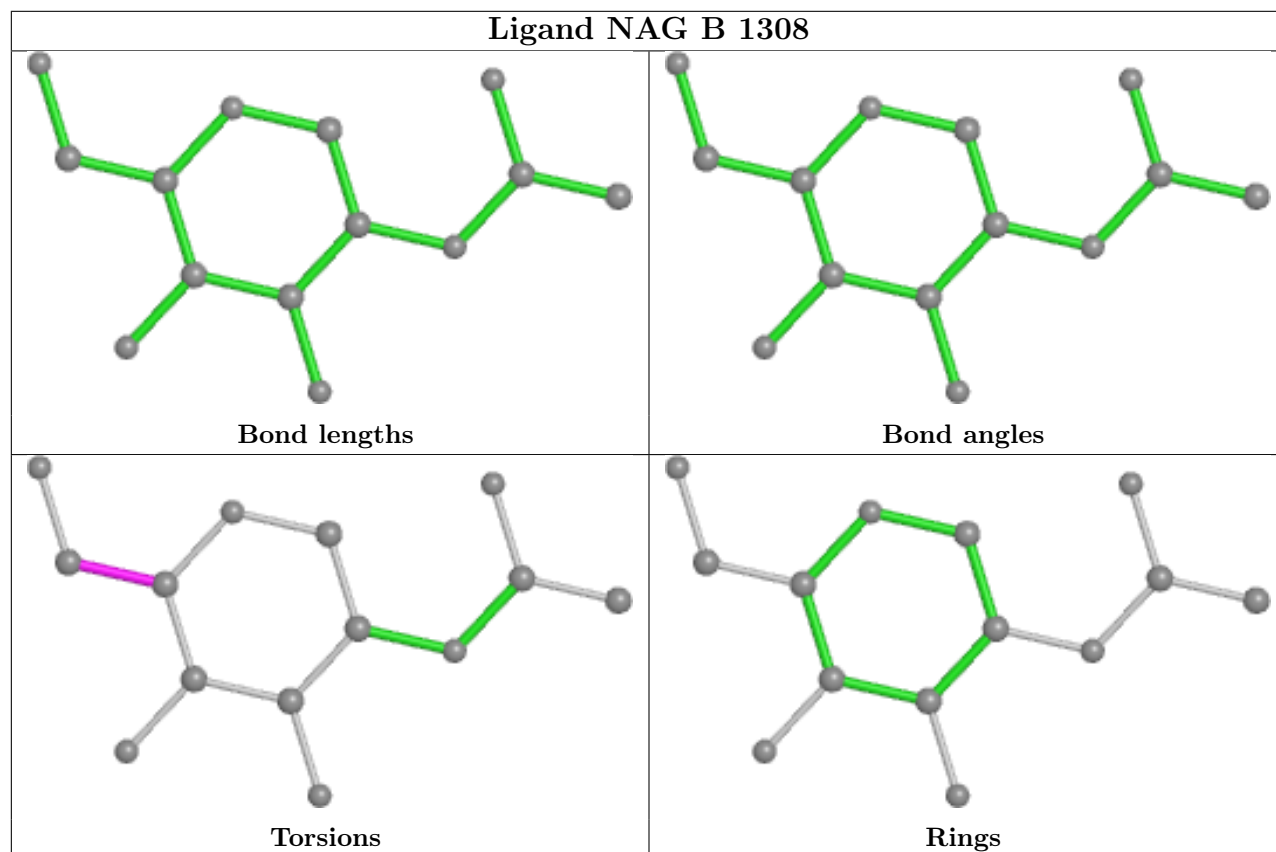
## Ligand NAG B 1311



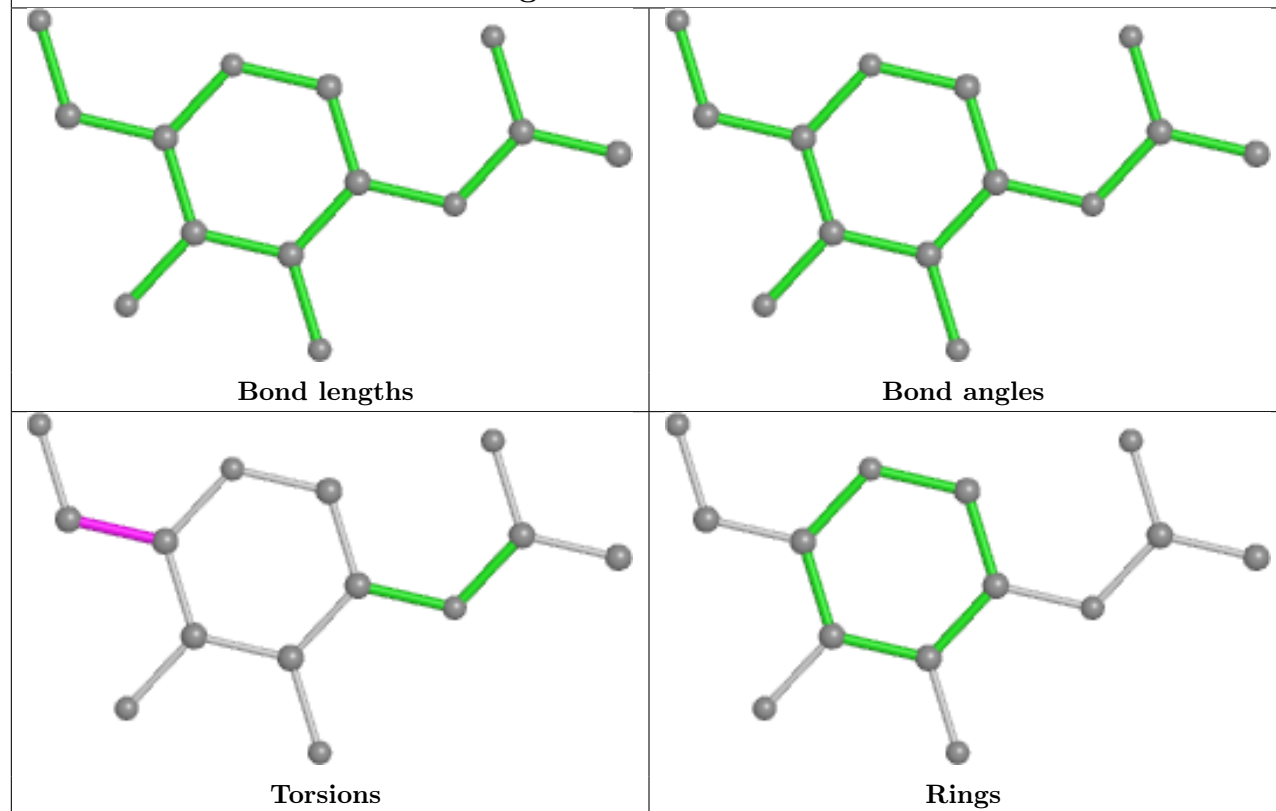
## Ligand NAG C 1310



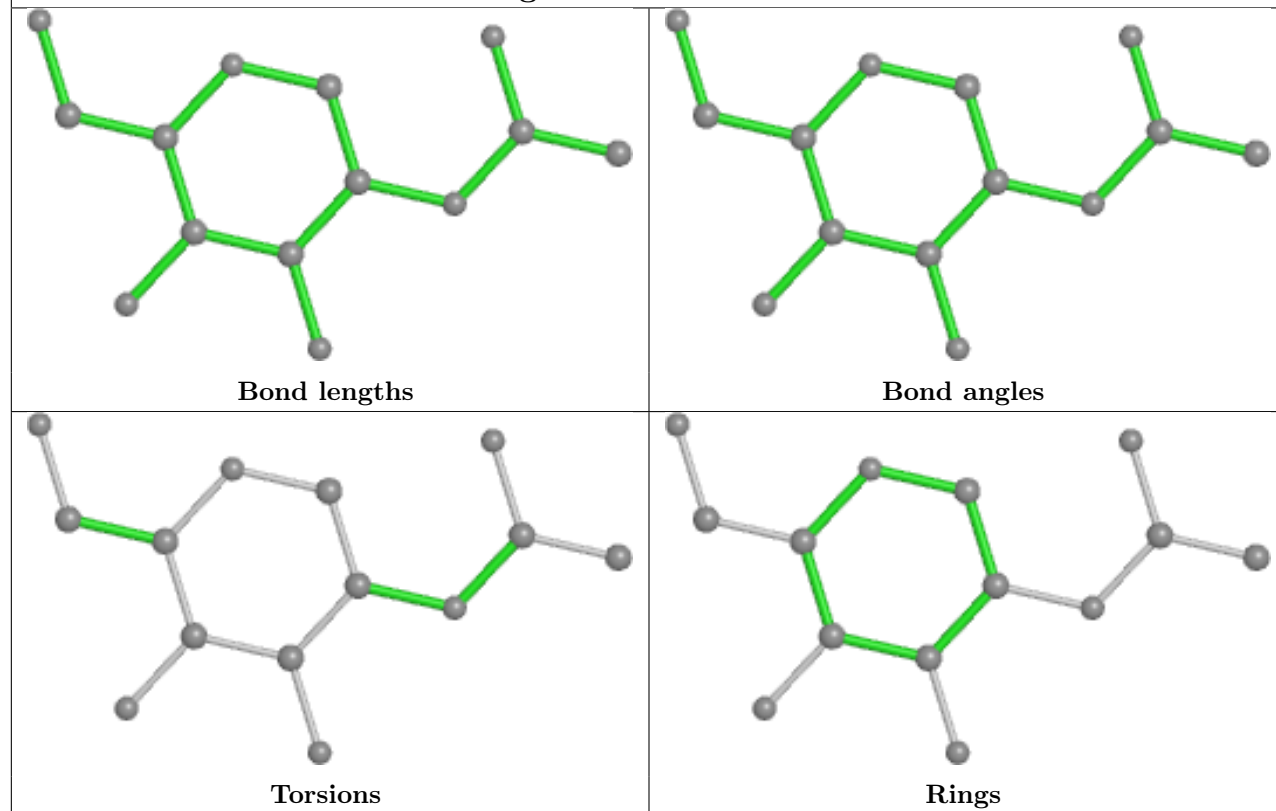
## Ligand NAG B 1308



## Ligand NAG C 1301

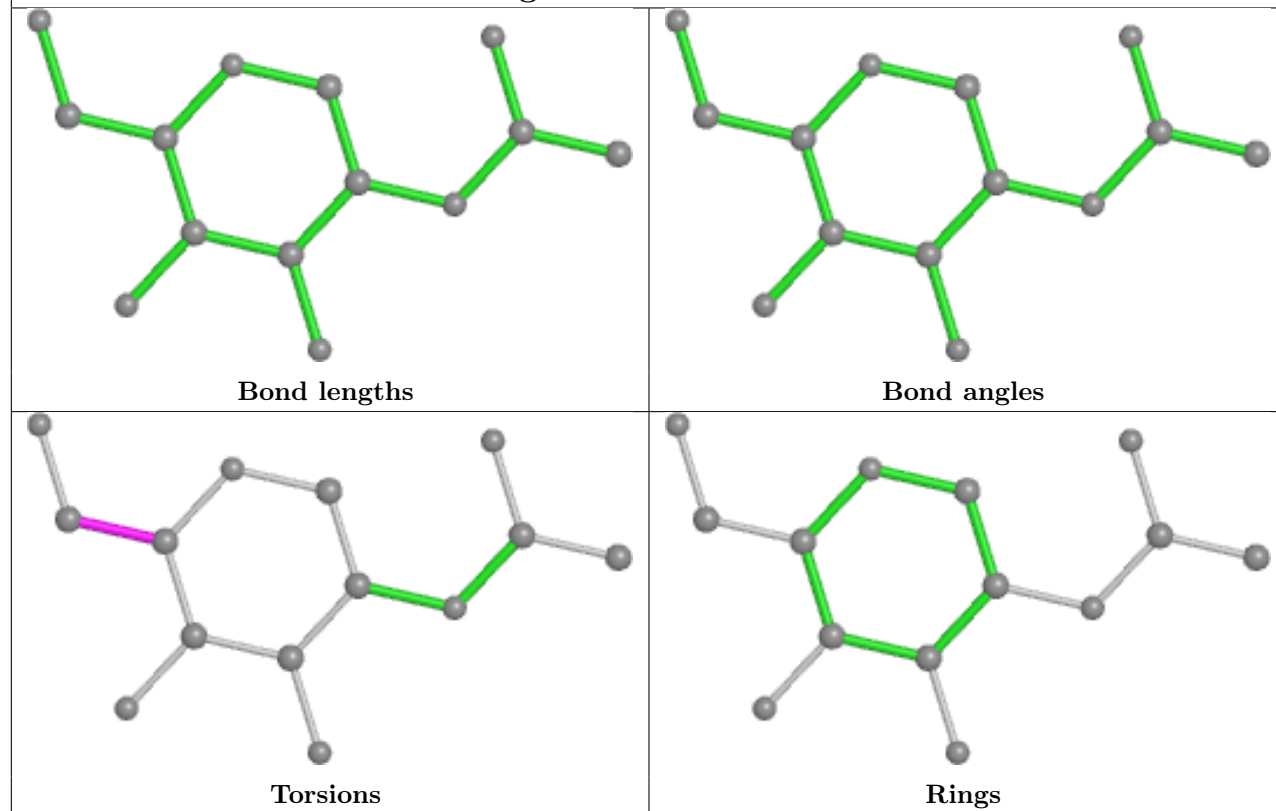


## Ligand NAG C 1307

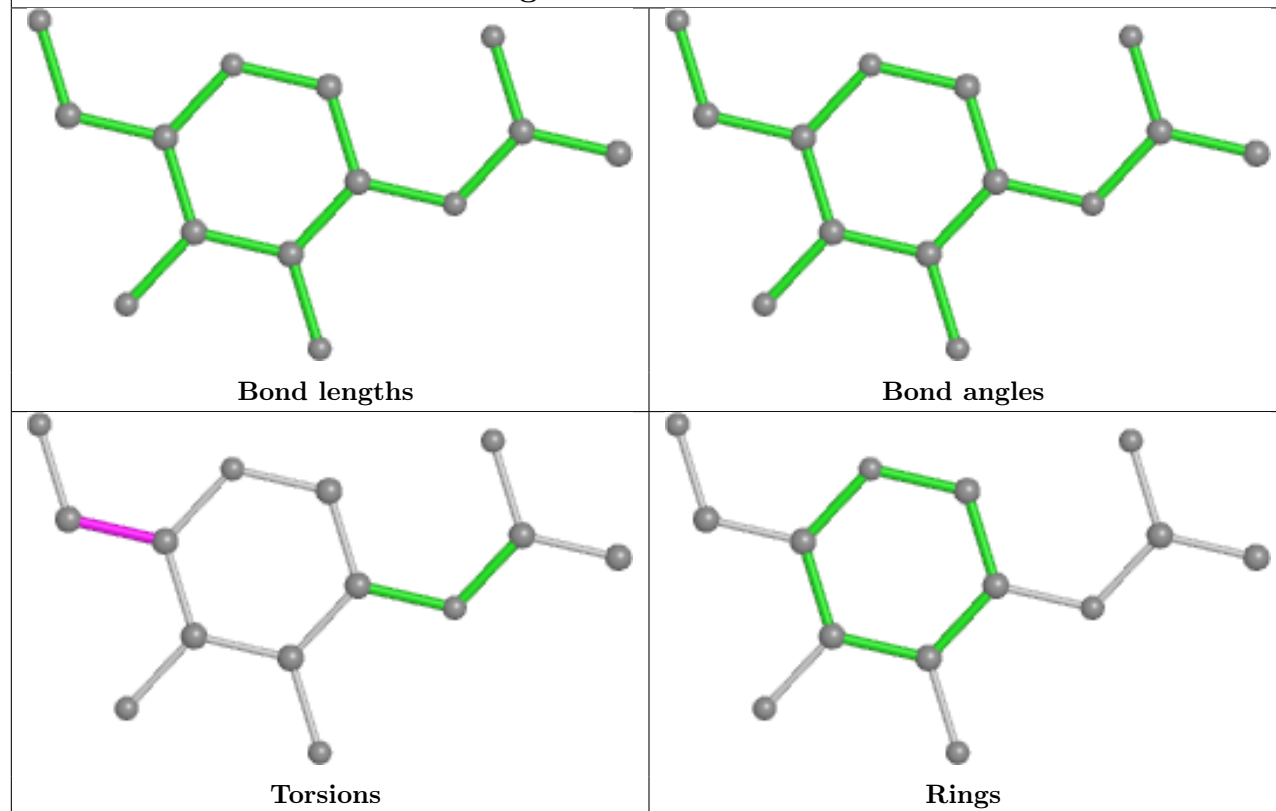


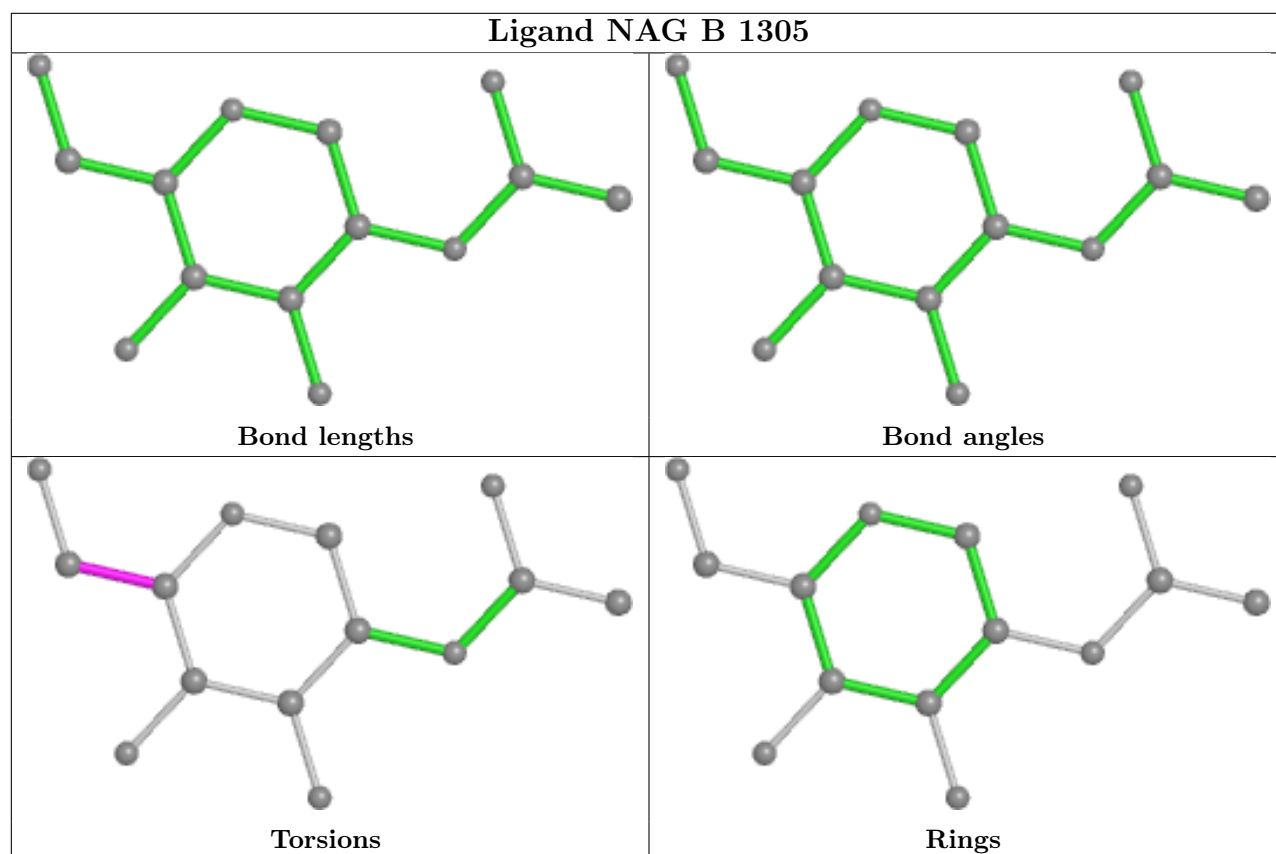
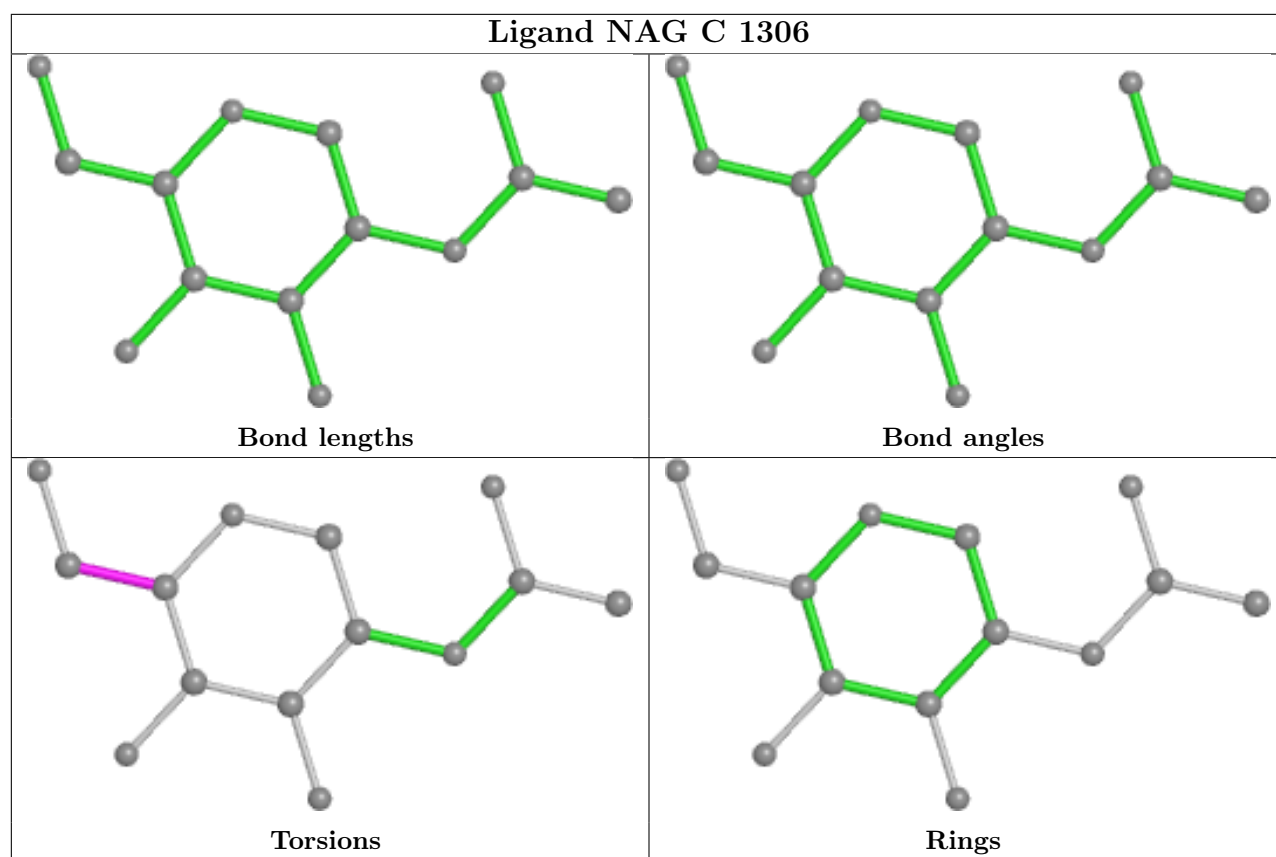


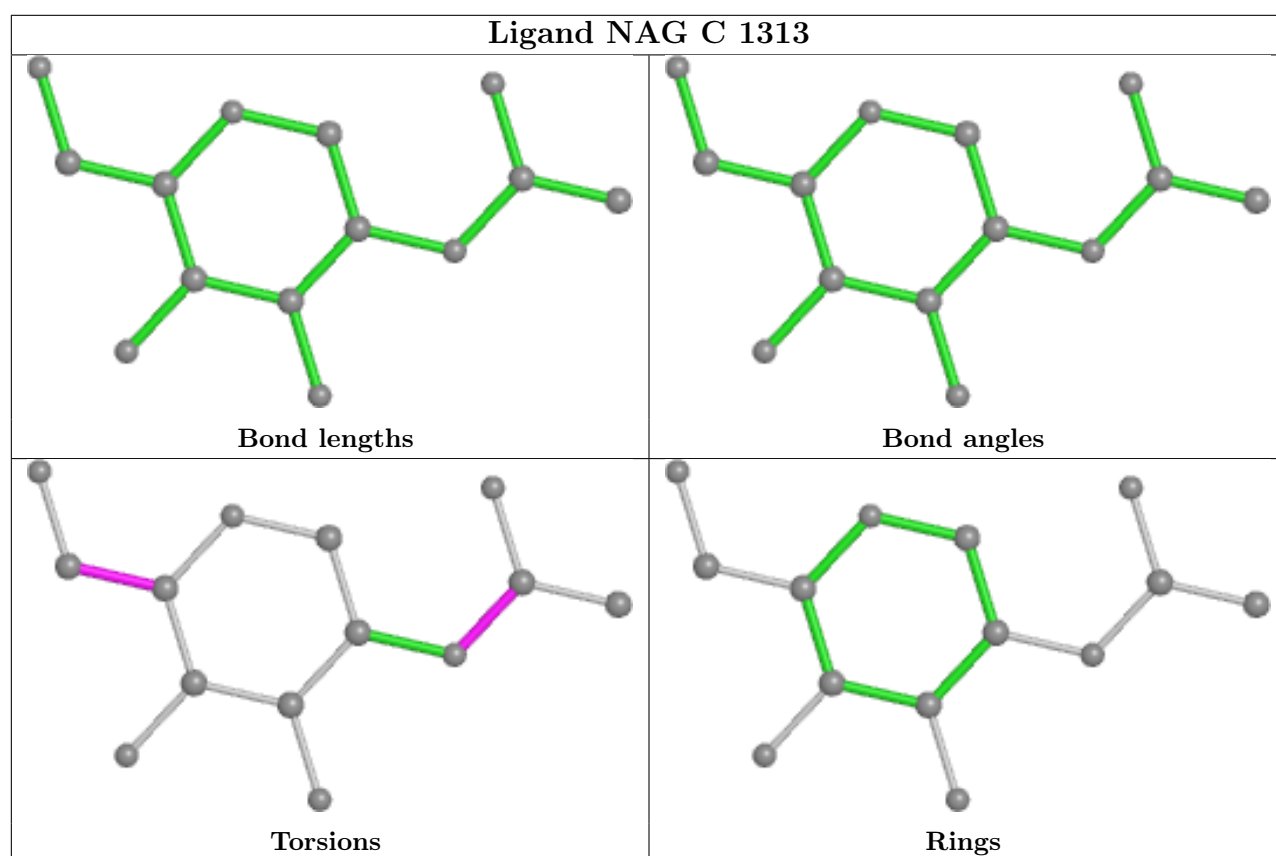
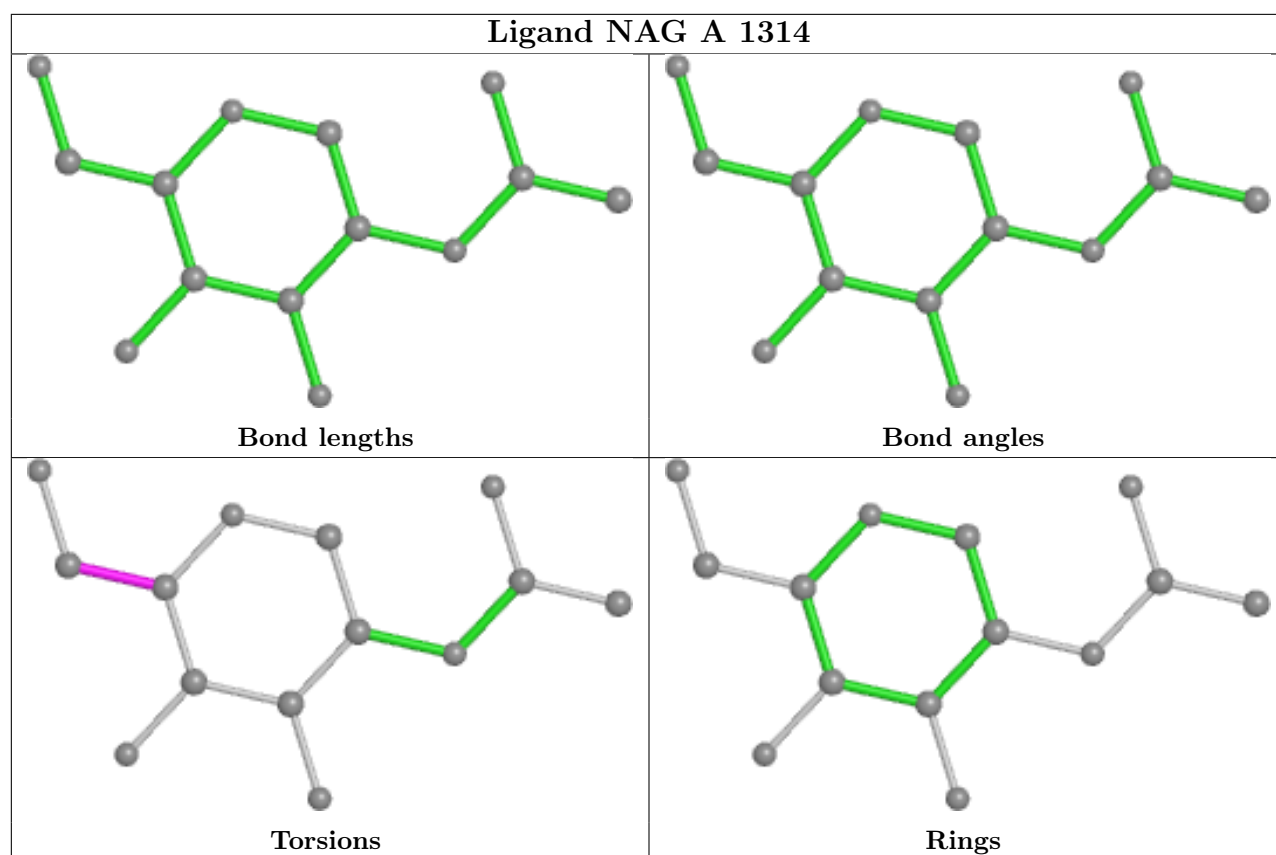
## Ligand NAG C 1304



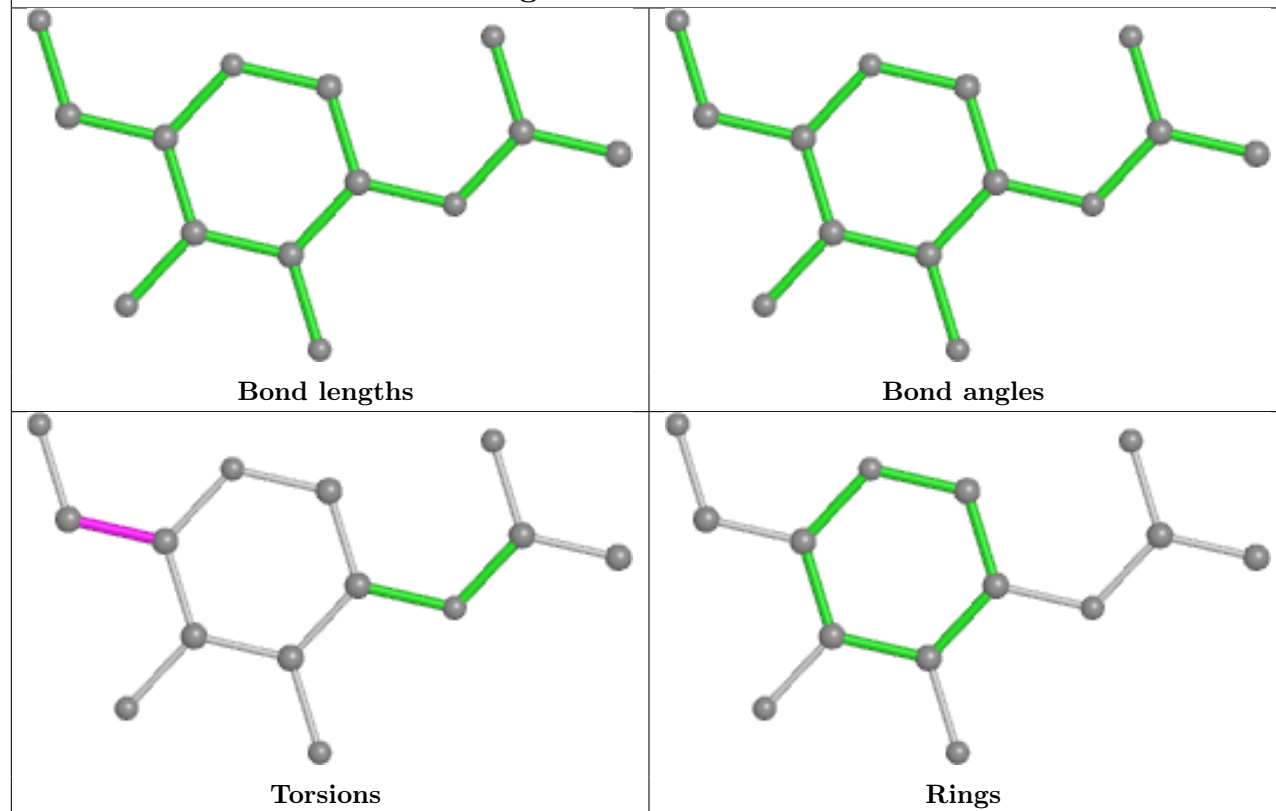
## Ligand NAG B 1314



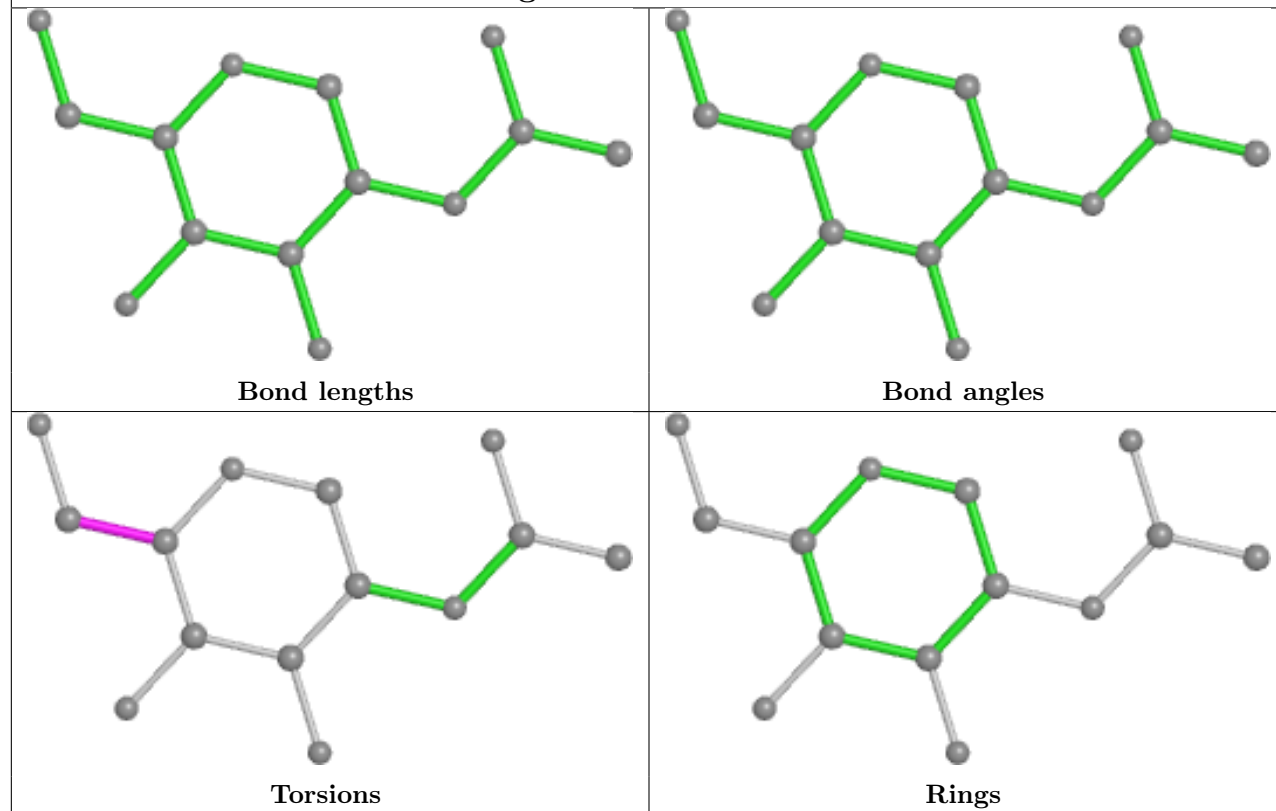




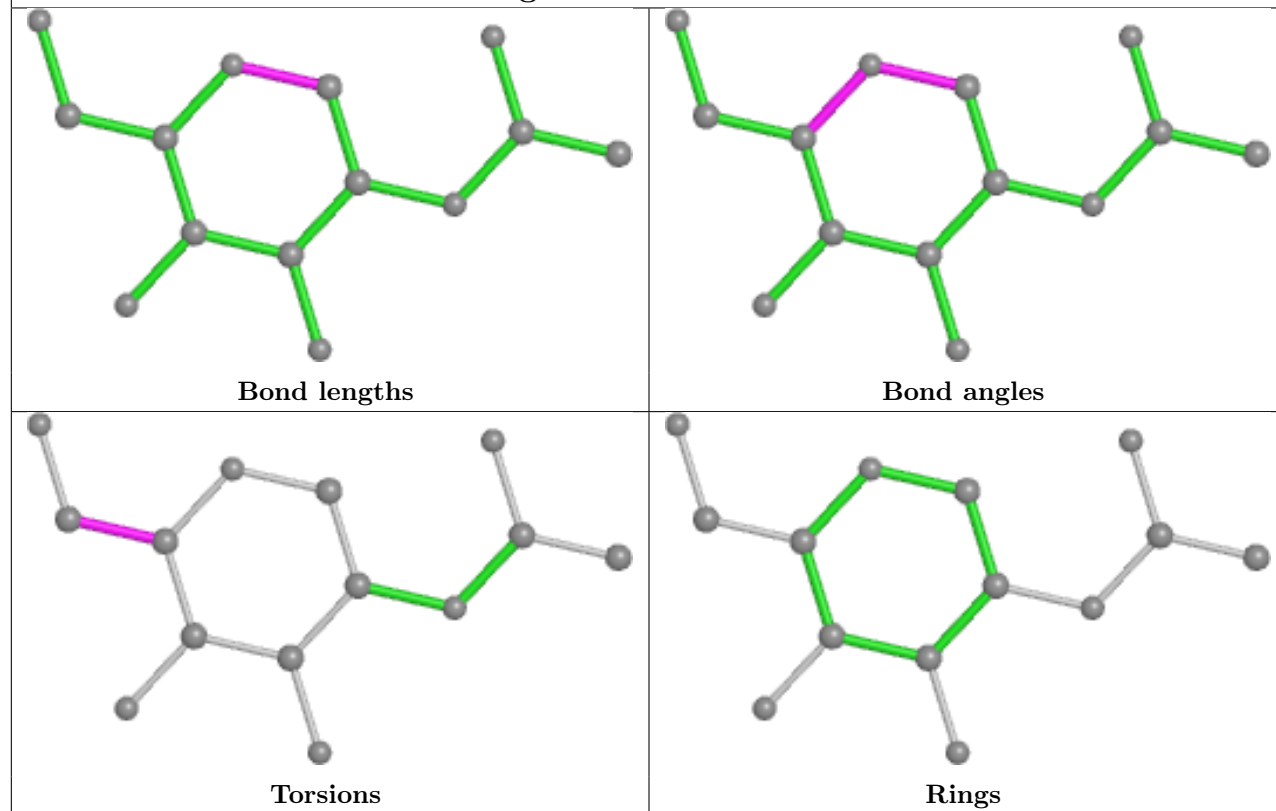
## Ligand NAG B 1306



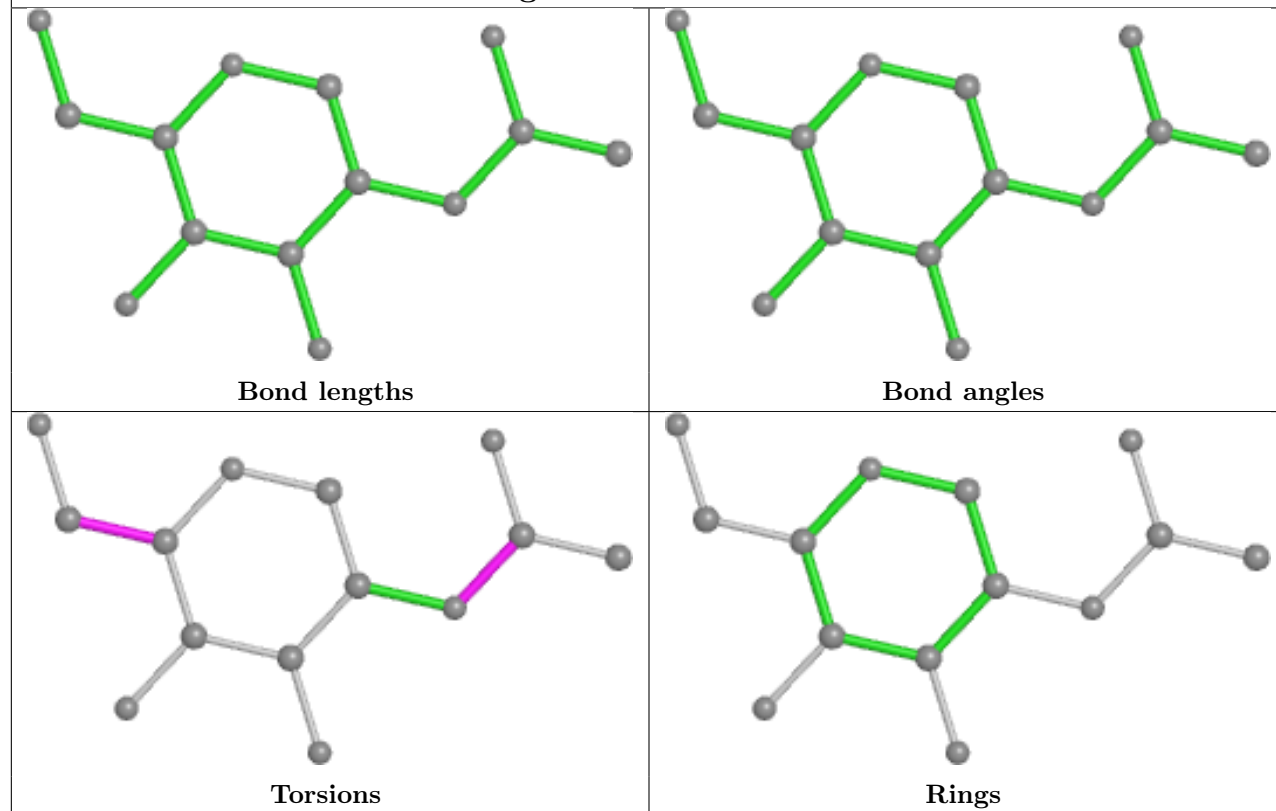
## Ligand NAG A 1305

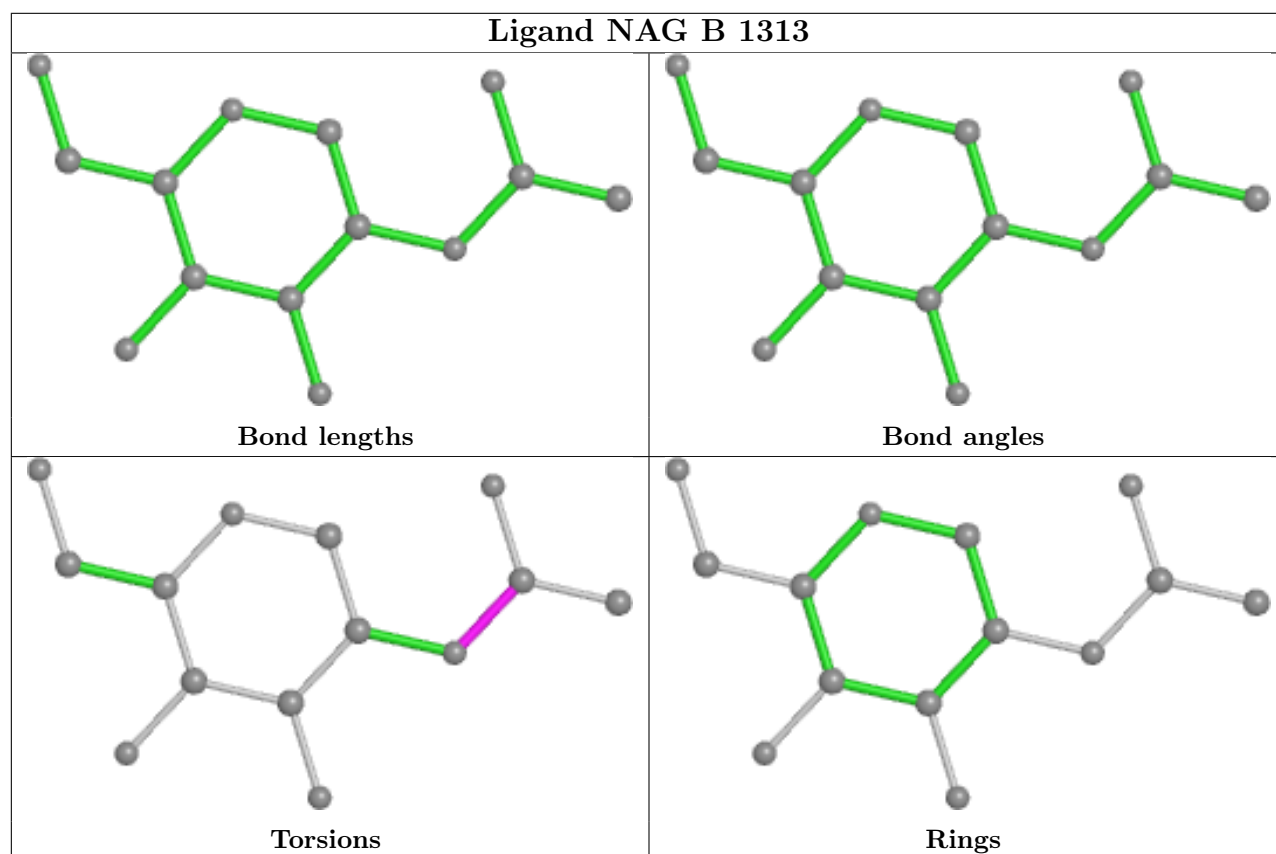
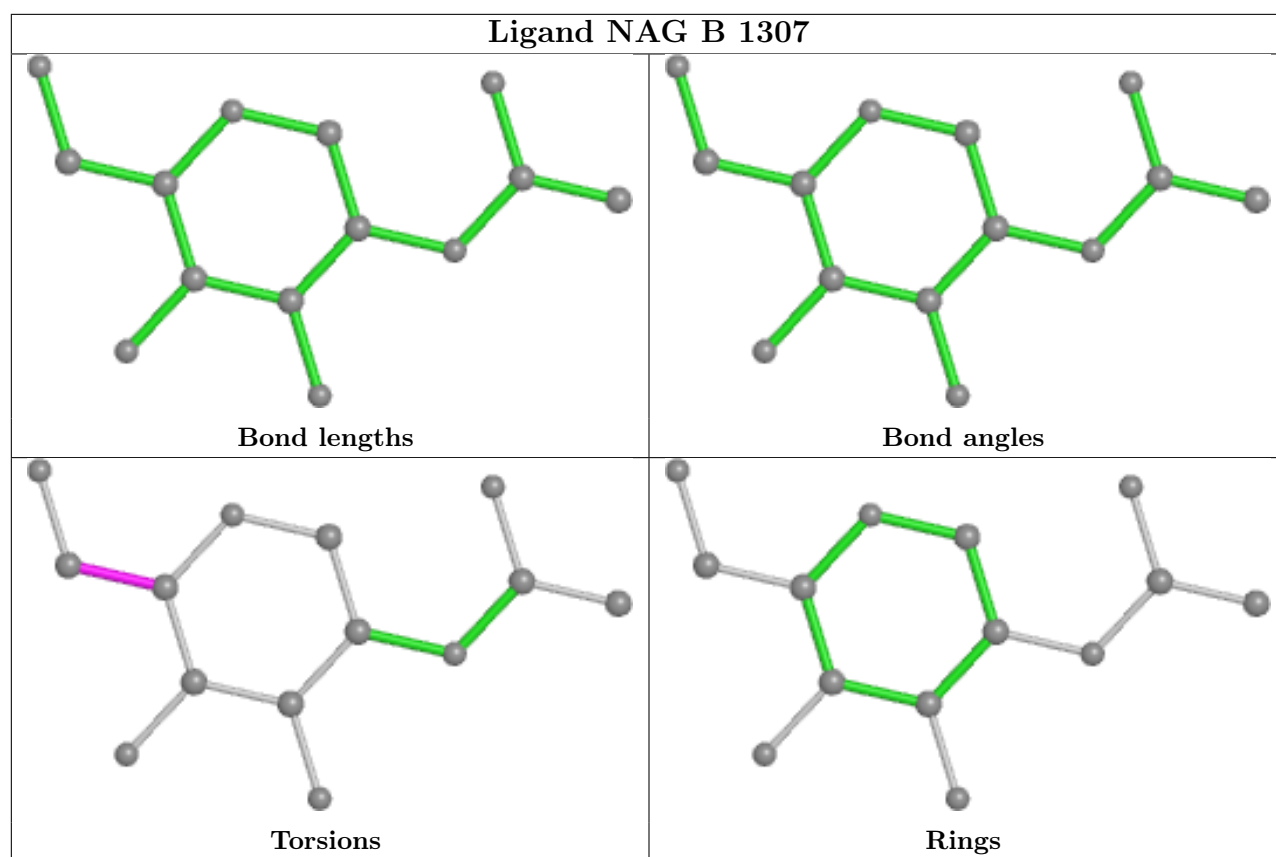


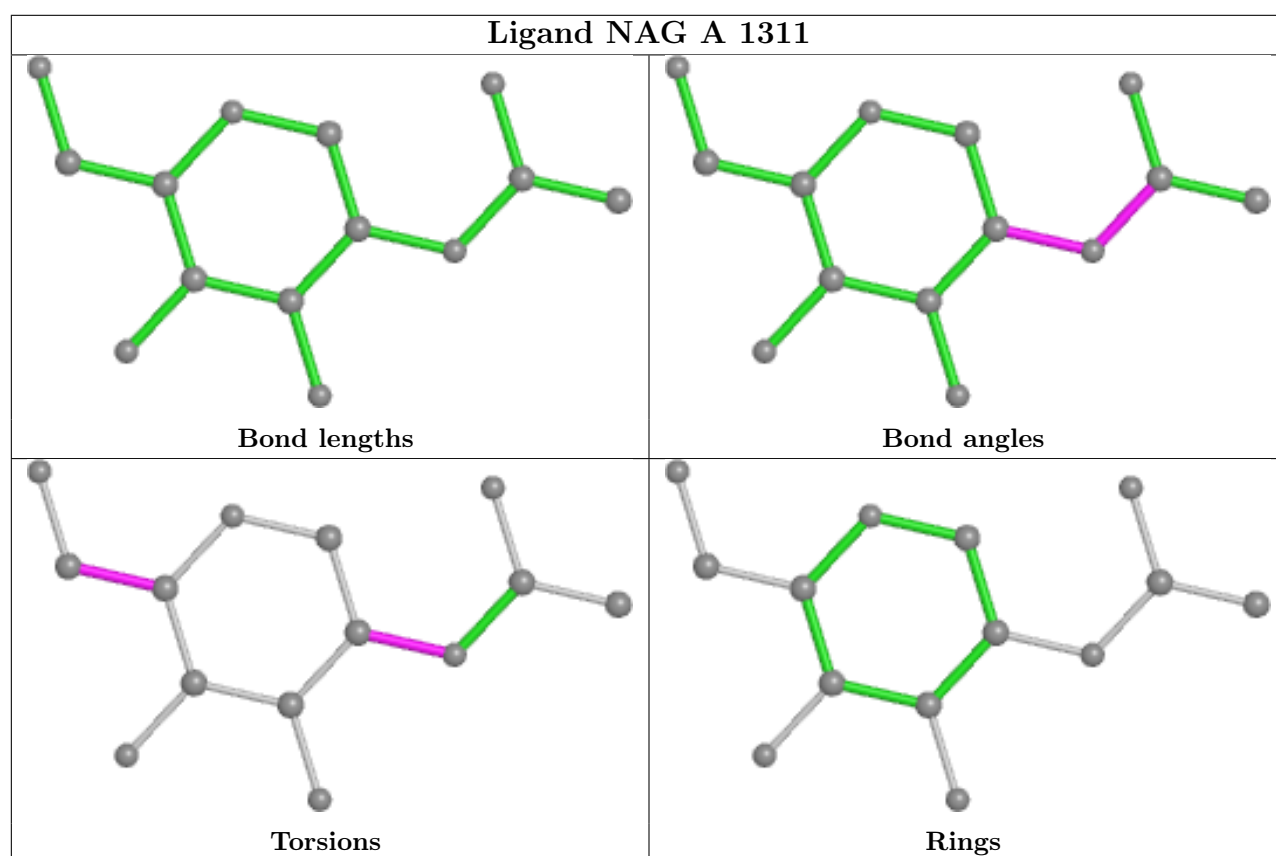
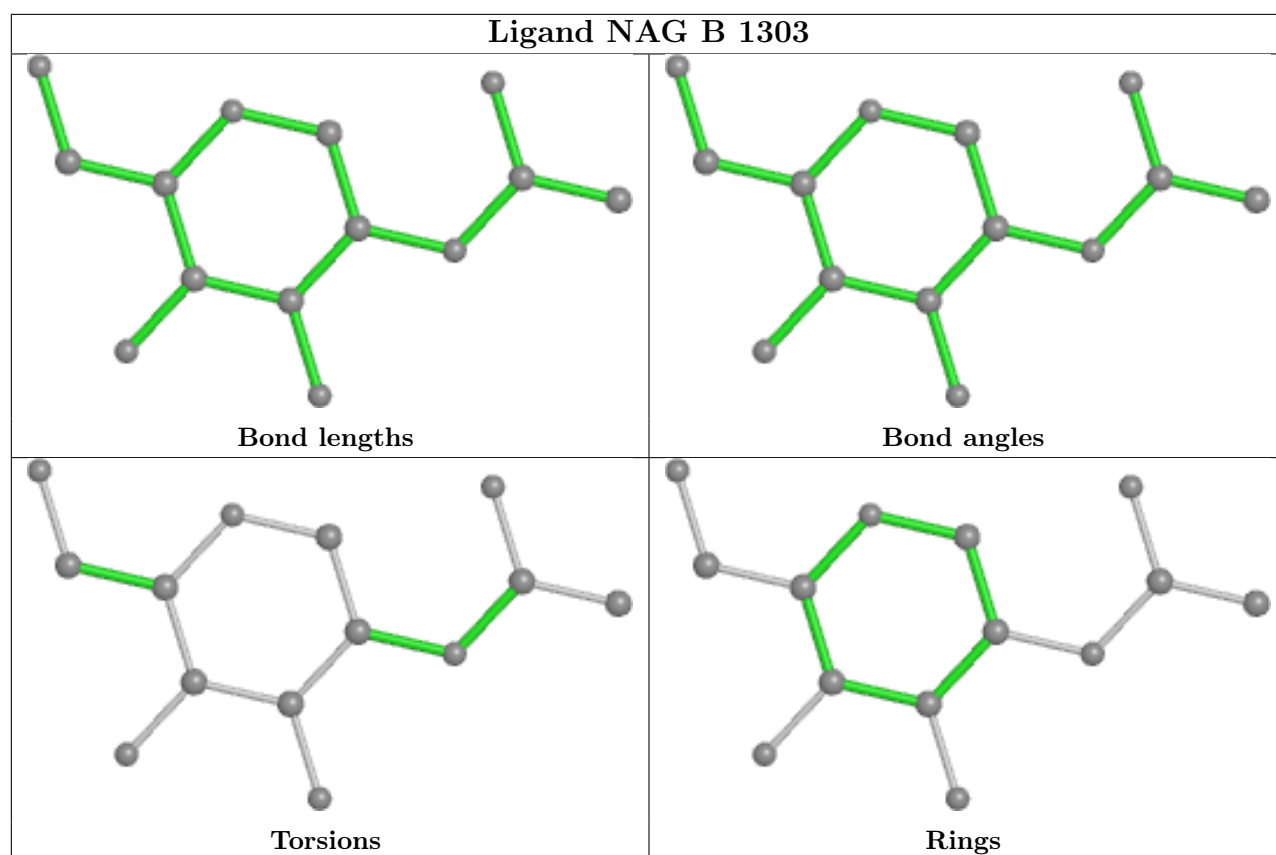
## Ligand NAG C 1302

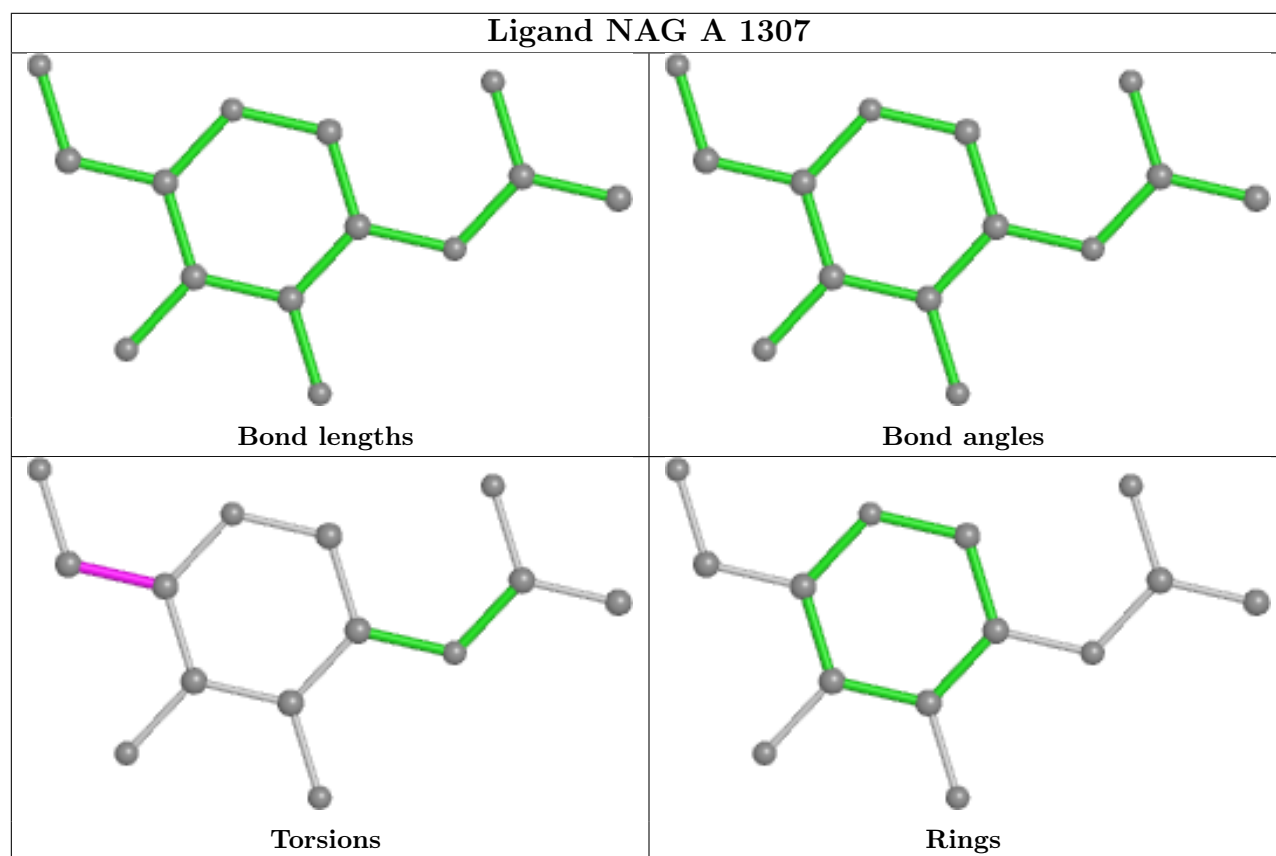
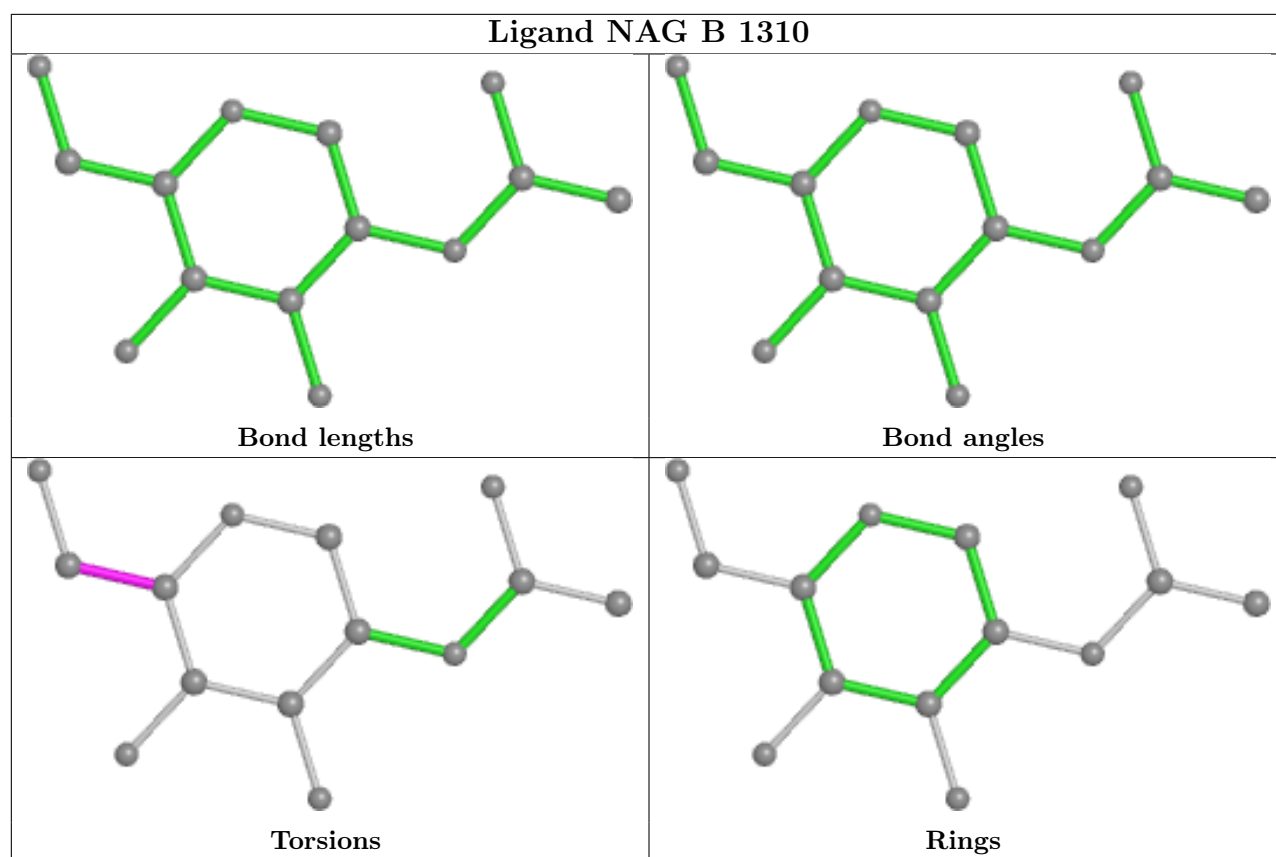


## Ligand NAG C 1312



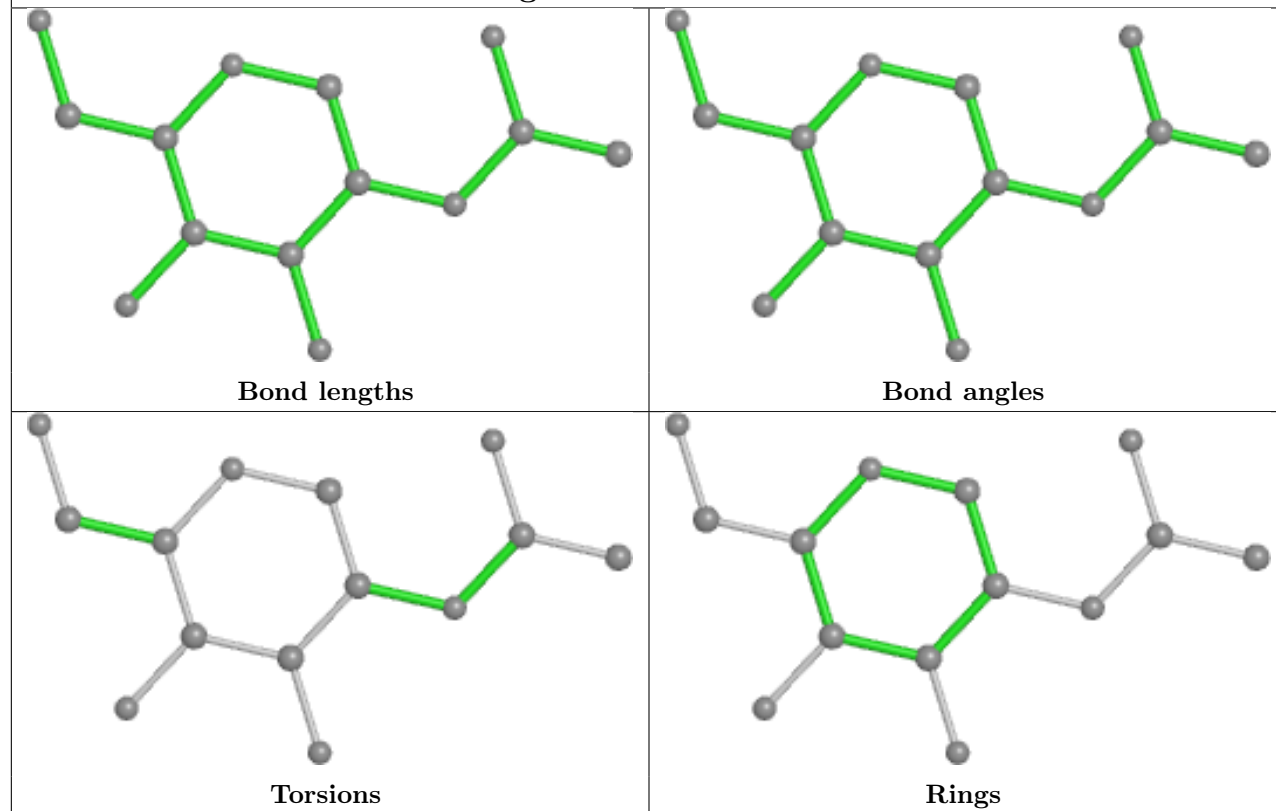




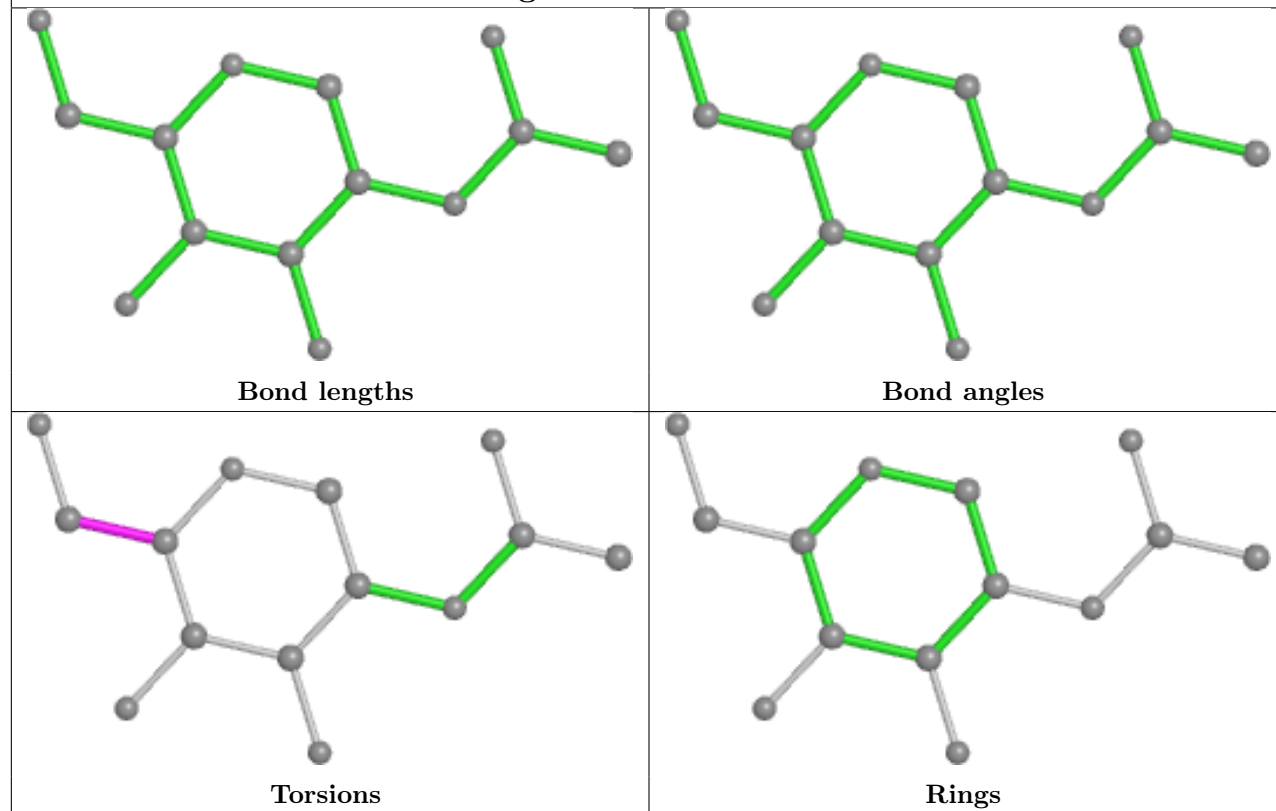


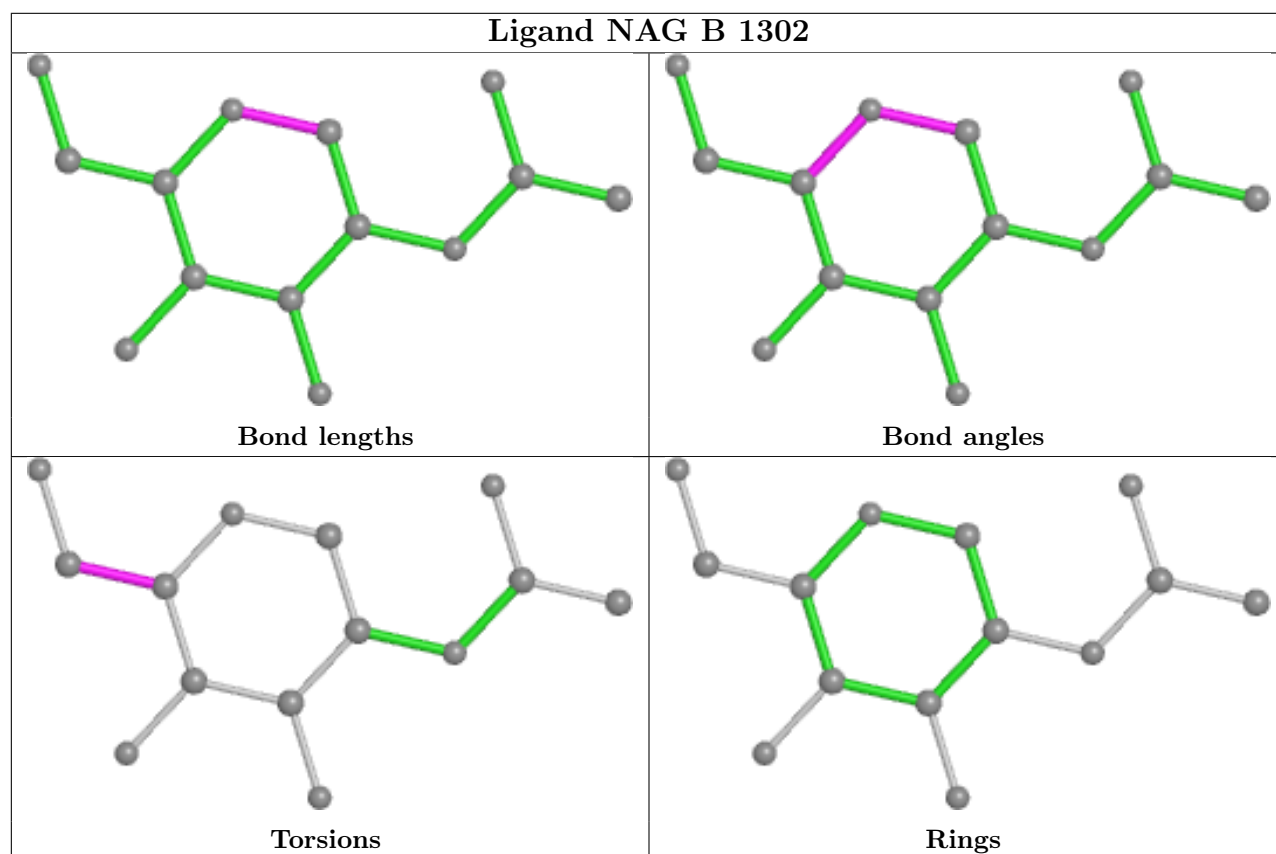
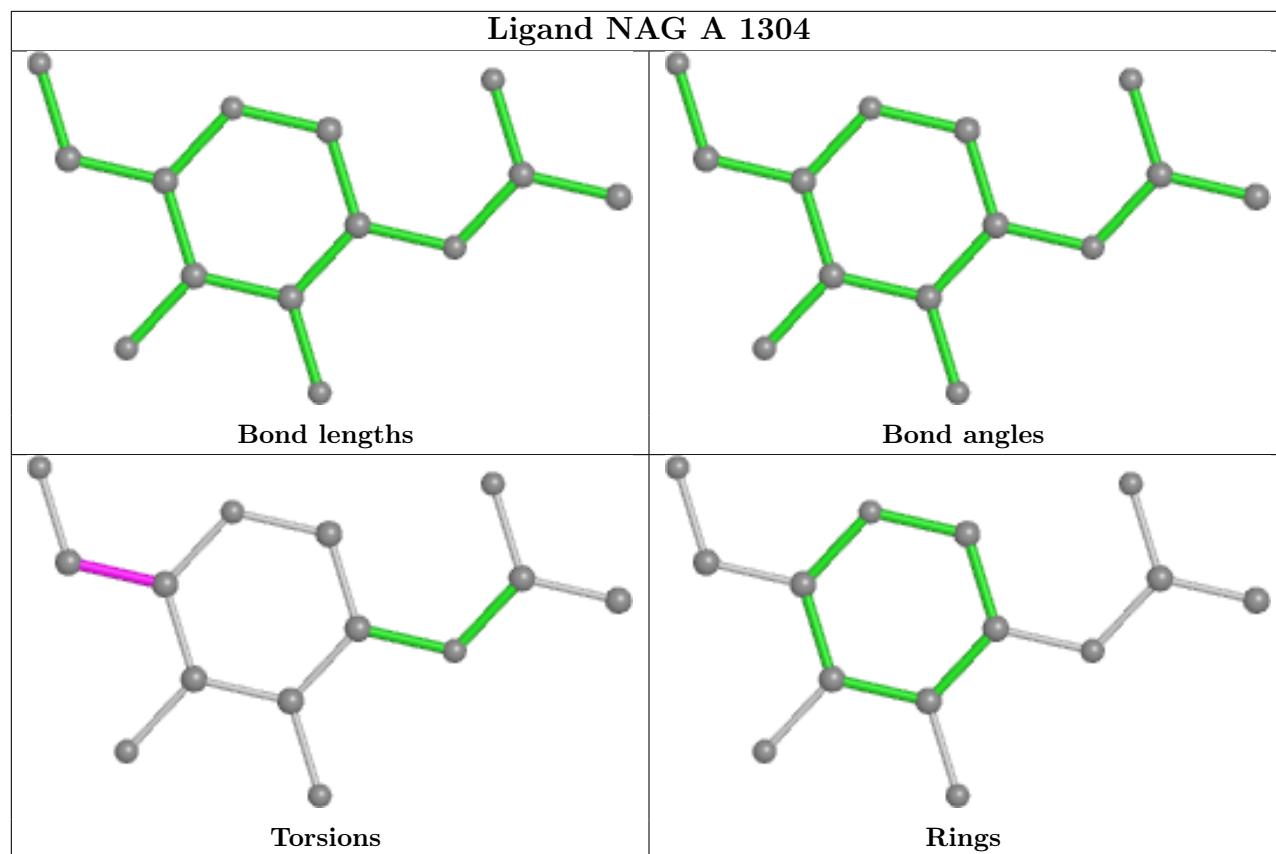


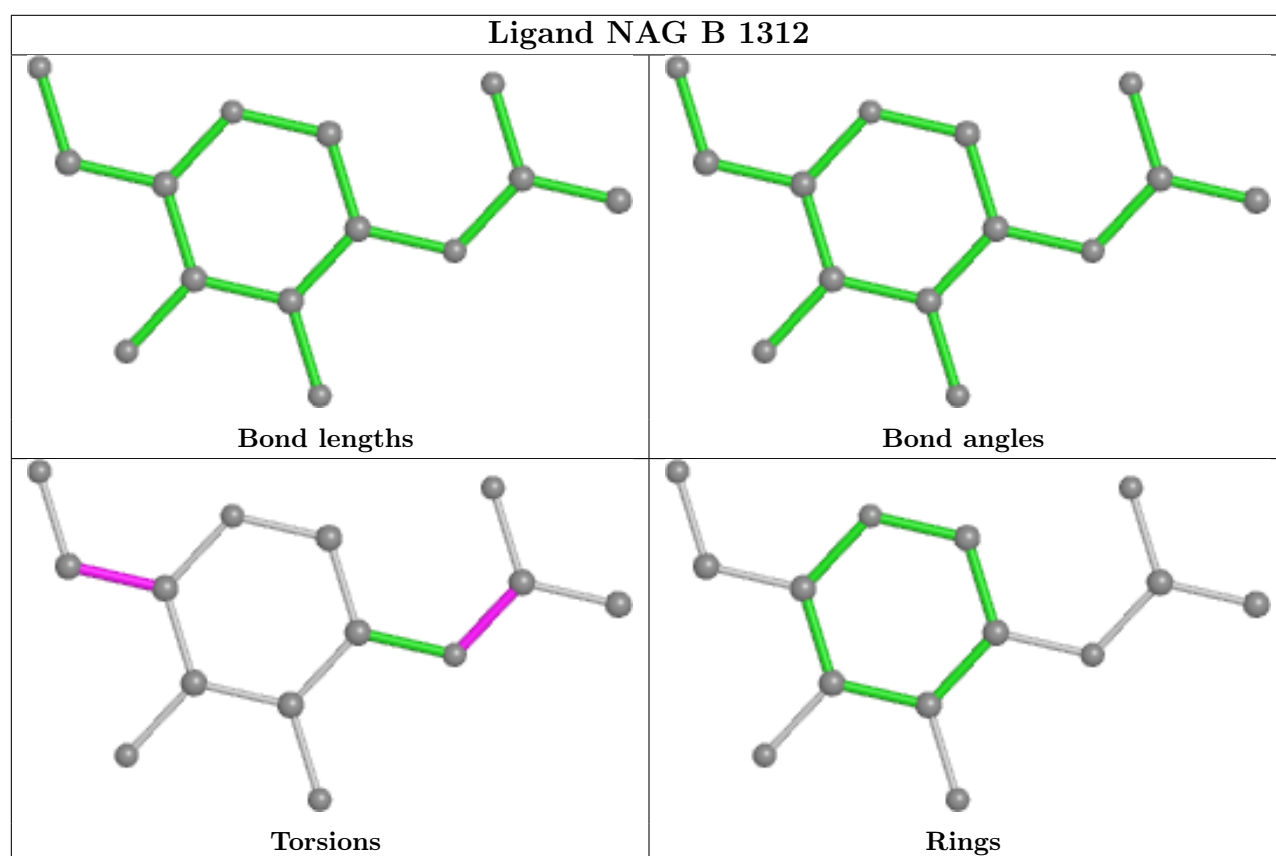
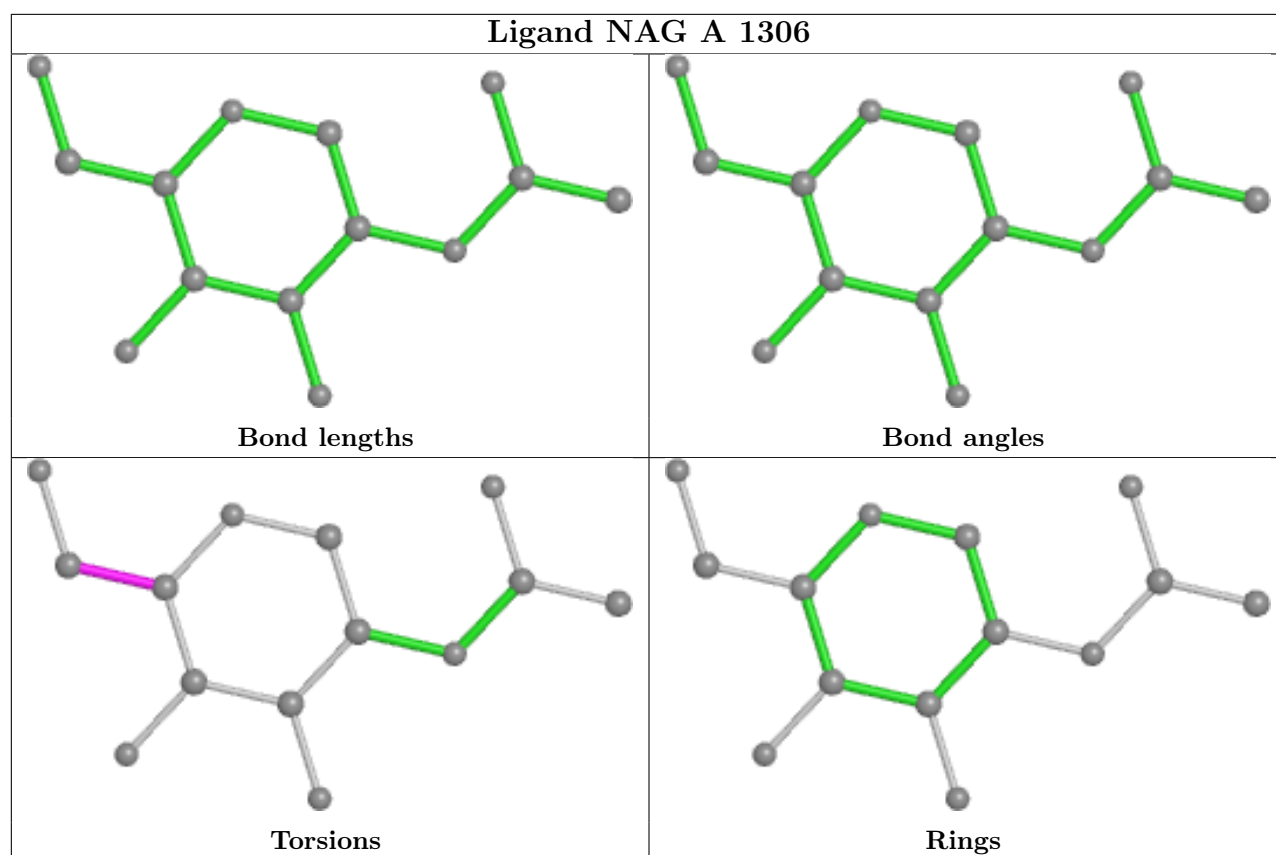
## Ligand NAG C 1303

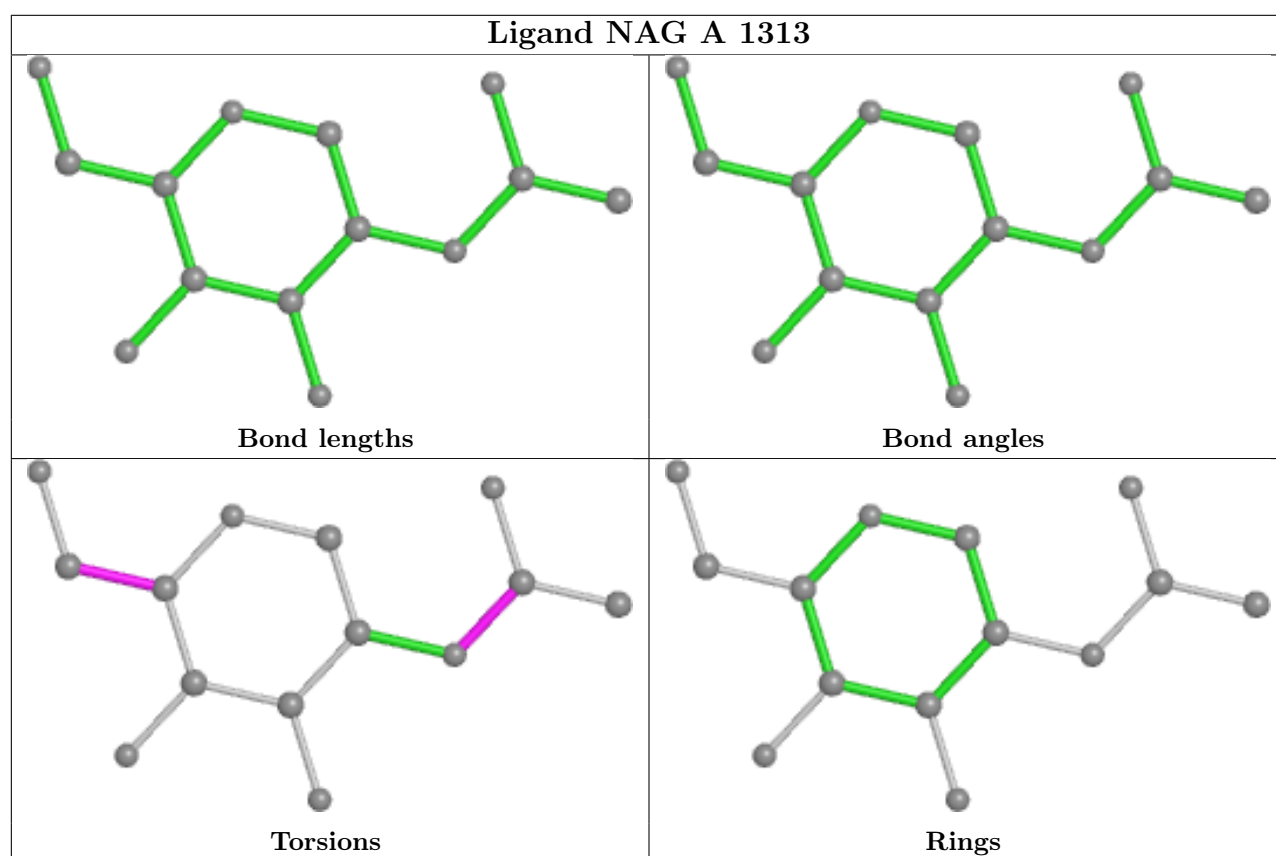
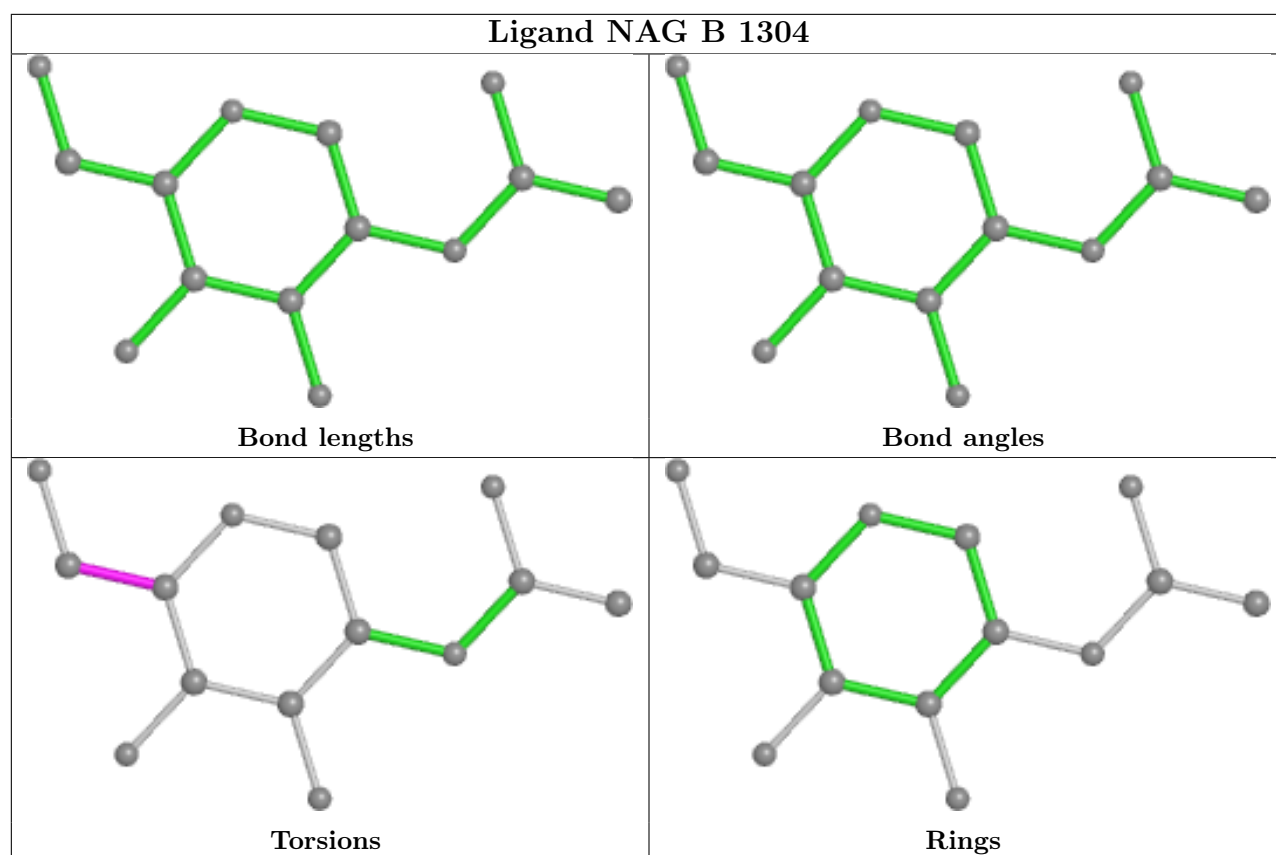


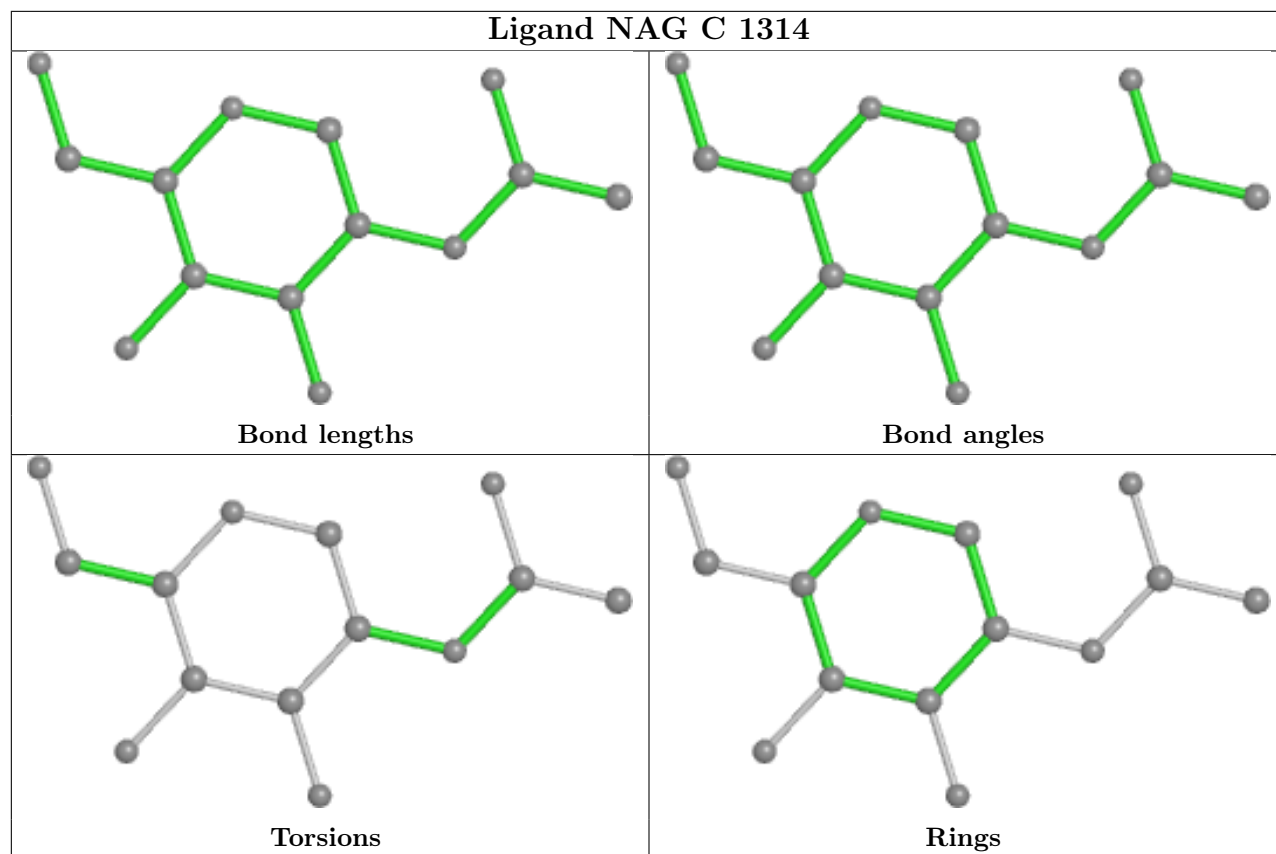
## Ligand NAG A 1310











## 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.