



## wwPDB EM Validation Summary Report ⓘ

Feb 19, 2025 – 08:10 PM JST

PDB ID : 8ZY0  
EMDB ID : EMD-60551  
Title : Sarbecovirus BtKY72 Spike Trimer in a Locked Conformation  
Authors : Wang, J.; Xiong, X.  
Deposited on : 2024-06-16  
Resolution : 3.00 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

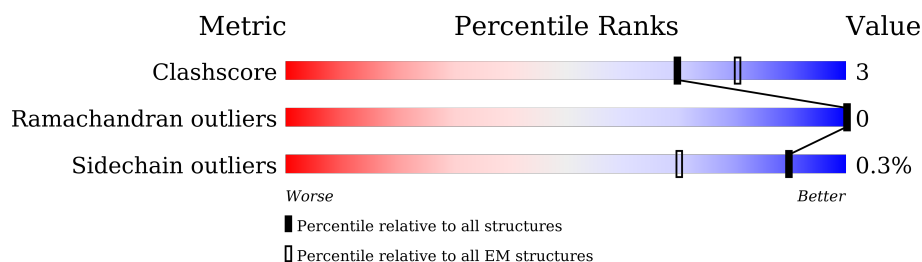
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 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	1193	82% 9% 8%
1	B	1193	83% 8% 8%
1	C	1193	82% 9% 8%
2	D	2	100%
2	F	2	100%
2	H	2	100%
3	E	5	40% 60%
4	G	4	75% 25%
4	I	4	75% 25%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 26611 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.

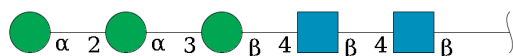
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1092	Total	C	N	O	S	0	0
			8509	5419	1413	1633	44		
1	B	1092	Total	C	N	O	S	0	0
			8509	5419	1413	1633	44		
1	C	1092	Total	C	N	O	S	0	0
			8505	5416	1412	1633	44		

- 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	F	2	Total	C	N	O	0	0
			28	16	2	10		
2	H	2	Total	C	N	O	0	0
			28	16	2	10		

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



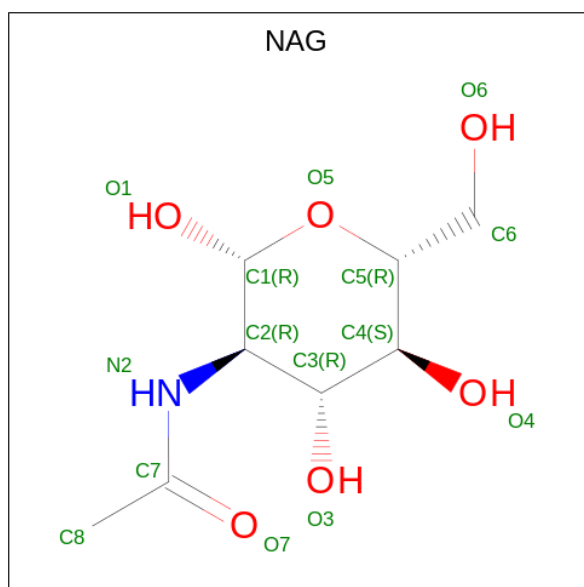
Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	5	Total	C	N	O	0	0
			61	34	2	25		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	4	Total	C	N	O	0	0
			50	28	2	20		
4	I	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 5 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
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	

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

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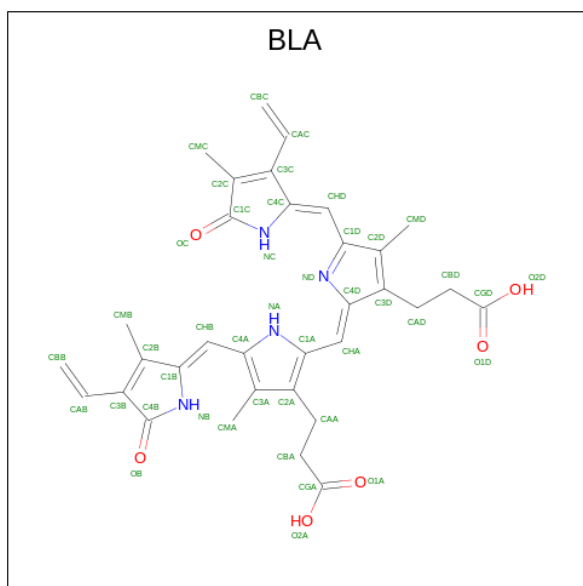
Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5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

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

- Molecule 6 is BILIVERDINE IX ALPHA (three-letter code: BLA) (formula:  $C_{33}H_{34}N_4O_6$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			43	33	4	6	
6	B	1	Total	C	N	O	0
			43	33	4	6	
6	C	1	Total	C	N	O	0
			43	33	4	6	








nose

Chain E:  40% 60%



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

Chain G:  75% 25%



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

Chain I:  75% 25%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98797	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	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: MAN, BLA, BMA, 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	0.27	0/8706	0.53	0/11843
1	B	0.28	0/8706	0.52	0/11843
1	C	0.26	0/8702	0.52	0/11839
All	All	0.27	0/26114	0.52	0/35525

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	8509	0	8238	64	0
1	B	8509	0	8238	54	0
1	C	8505	0	8227	60	0
2	D	28	0	25	0	0
2	F	28	0	25	0	0
2	H	28	0	25	0	0
3	E	61	0	52	0	0
4	G	50	0	43	0	0
4	I	50	0	43	0	0
5	A	238	0	221	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	238	0	221	0	0
5	C	238	0	221	0	0
6	A	43	0	32	4	0
6	B	43	0	32	0	0
6	C	43	0	32	3	0
All	All	26611	0	25675	179	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 3.

The worst 5 of 179 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:382:CYS:HA	1:B:514:CYS:HB3	1.48	0.95
6:A:1218:BLA:HHA	6:A:1218:BLA:HBD2	1.70	0.73
6:A:1218:BLA:HHD	6:A:1218:BLA:HBC1	1.71	0.73
1:C:382:CYS:SG	1:C:513:VAL:O	2.50	0.70
1:B:104:ILE:HG22	1:B:238:MET:HG2	1.72	0.70

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	1086/1193 (91%)	1035 (95%)	51 (5%)	0	100	100
1	B	1086/1193 (91%)	1038 (96%)	48 (4%)	0	100	100
1	C	1086/1193 (91%)	1035 (95%)	51 (5%)	0	100	100
All	All	3258/3579 (91%)	3108 (95%)	150 (5%)	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	A	952/1042 (91%)	950 (100%)	2 (0%)	92	97
1	B	952/1042 (91%)	948 (100%)	4 (0%)	89	95
1	C	951/1042 (91%)	949 (100%)	2 (0%)	92	97
All	All	2855/3126 (91%)	2847 (100%)	8 (0%)	90	96

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1091	GLN
1	C	771	LYS
1	B	771	LYS
1	B	640	CYS
1	B	795	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	886	GLN
1	C	907	GLN
1	C	1091	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 ⓘ

19 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	0.63	0	17,19,21	1.97	2 (11%)
2	NAG	D	2	2	14,14,15	0.37	0	17,19,21	0.81	1 (5%)
3	NAG	E	1	3,1	14,14,15	0.26	0	17,19,21	0.53	0
3	NAG	E	2	3	14,14,15	0.33	0	17,19,21	0.56	0
3	BMA	E	3	3	11,11,12	1.25	2 (18%)	15,15,17	1.30	2 (13%)
3	MAN	E	4	3	11,11,12	1.72	3 (27%)	15,15,17	2.27	2 (13%)
3	MAN	E	5	3	11,11,12	0.70	0	15,15,17	1.05	2 (13%)
2	NAG	F	1	2,1	14,14,15	0.62	0	17,19,21	1.97	2 (11%)
2	NAG	F	2	2	14,14,15	0.36	0	17,19,21	0.82	1 (5%)
4	NAG	G	1	1,4	14,14,15	0.25	0	17,19,21	0.52	0
4	NAG	G	2	4	14,14,15	0.22	0	17,19,21	0.48	0
4	BMA	G	3	4	11,11,12	0.72	0	15,15,17	0.86	0
4	MAN	G	4	4	11,11,12	0.98	1 (9%)	15,15,17	1.09	2 (13%)
2	NAG	H	1	2,1	14,14,15	0.65	0	17,19,21	1.96	2 (11%)
2	NAG	H	2	2	14,14,15	0.37	0	17,19,21	0.81	1 (5%)
4	NAG	I	1	1,4	14,14,15	0.23	0	17,19,21	0.53	0
4	NAG	I	2	4	14,14,15	0.23	0	17,19,21	0.48	0
4	BMA	I	3	4	11,11,12	0.71	0	15,15,17	0.88	0
4	MAN	I	4	4	11,11,12	0.97	1 (9%)	15,15,17	1.13	2 (13%)

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	-	5/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	2/2/19/22	0/1/1/1
2	NAG	F	1	2,1	-	5/6/23/26	0/1/1/1
2	NAG	F	2	2	-	3/6/23/26	0/1/1/1
4	NAG	G	1	1,4	-	2/6/23/26	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
4	MAN	G	4	4	-	0/2/19/22	1/1/1/1
2	NAG	H	1	2,1	-	5/6/23/26	0/1/1/1
2	NAG	H	2	2	-	3/6/23/26	0/1/1/1
4	NAG	I	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	MAN	I	4	4	-	0/2/19/22	1/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	4	MAN	O5-C1	3.60	1.49	1.43
3	E	4	MAN	O5-C5	3.10	1.49	1.43
3	E	4	MAN	C1-C2	2.71	1.58	1.52
3	E	3	BMA	C2-C3	2.58	1.56	1.52
3	E	3	BMA	C1-C2	2.17	1.57	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4	MAN	C1-O5-C5	7.70	122.63	112.19
2	F	1	NAG	C2-N2-C7	6.94	132.78	122.90
2	D	1	NAG	C2-N2-C7	6.90	132.73	122.90
2	H	1	NAG	C2-N2-C7	6.88	132.70	122.90
2	F	1	NAG	C1-C2-N2	3.26	116.05	110.49

There are no chirality outliers.

5 of 40 torsion outliers are listed below:



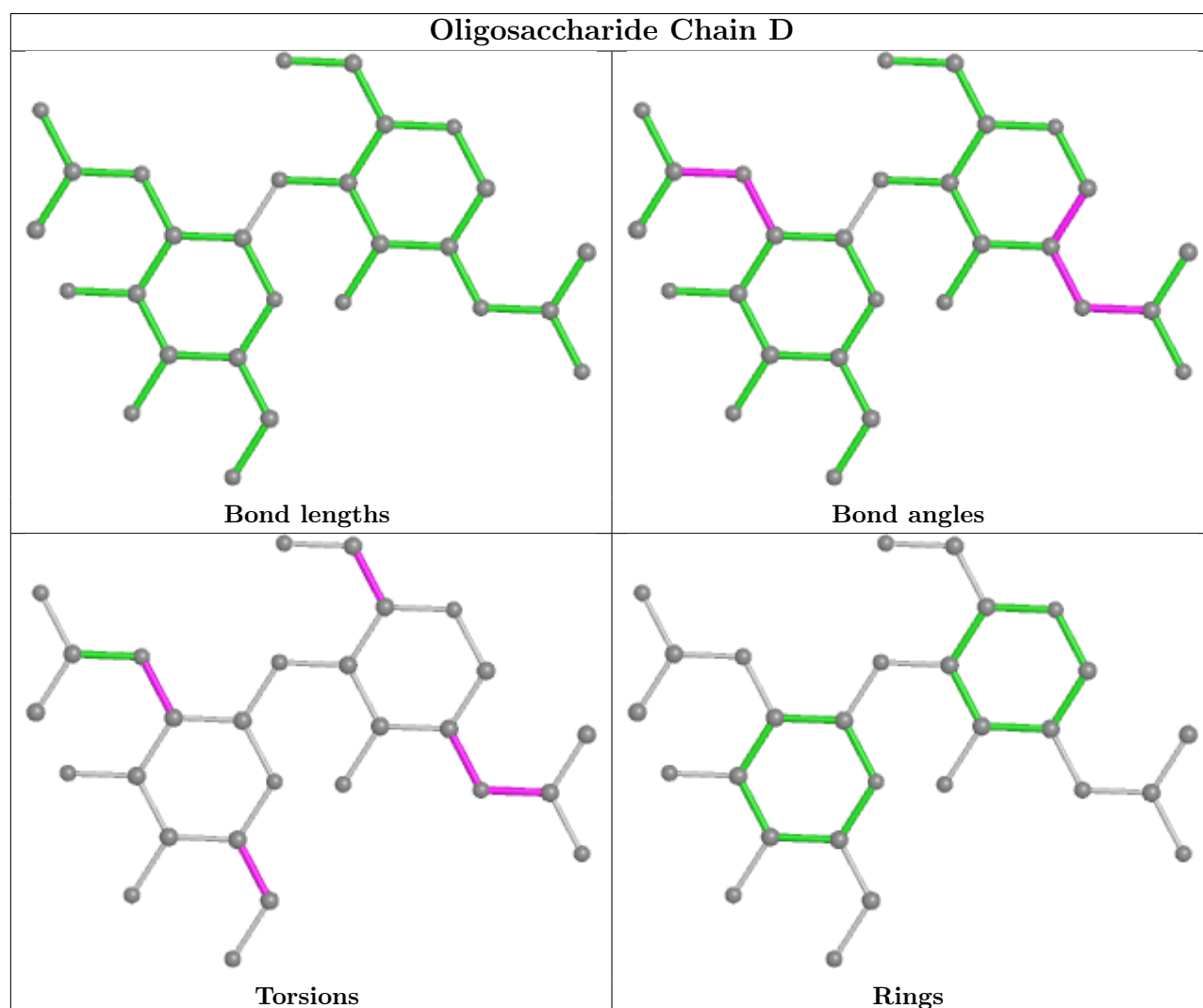
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	O5-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
4	G	1	NAG	O5-C5-C6-O6

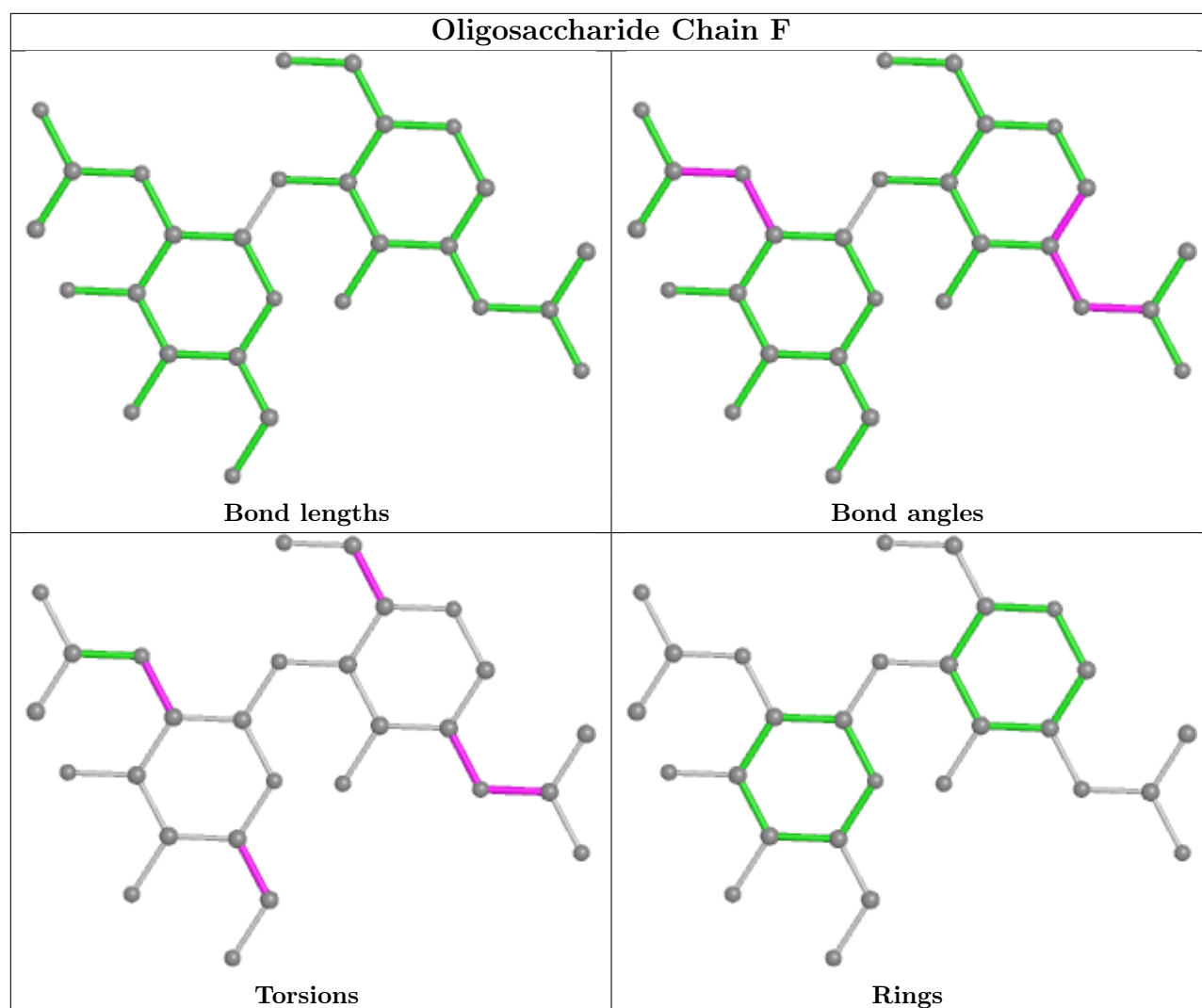
All (2) ring outliers are listed below:

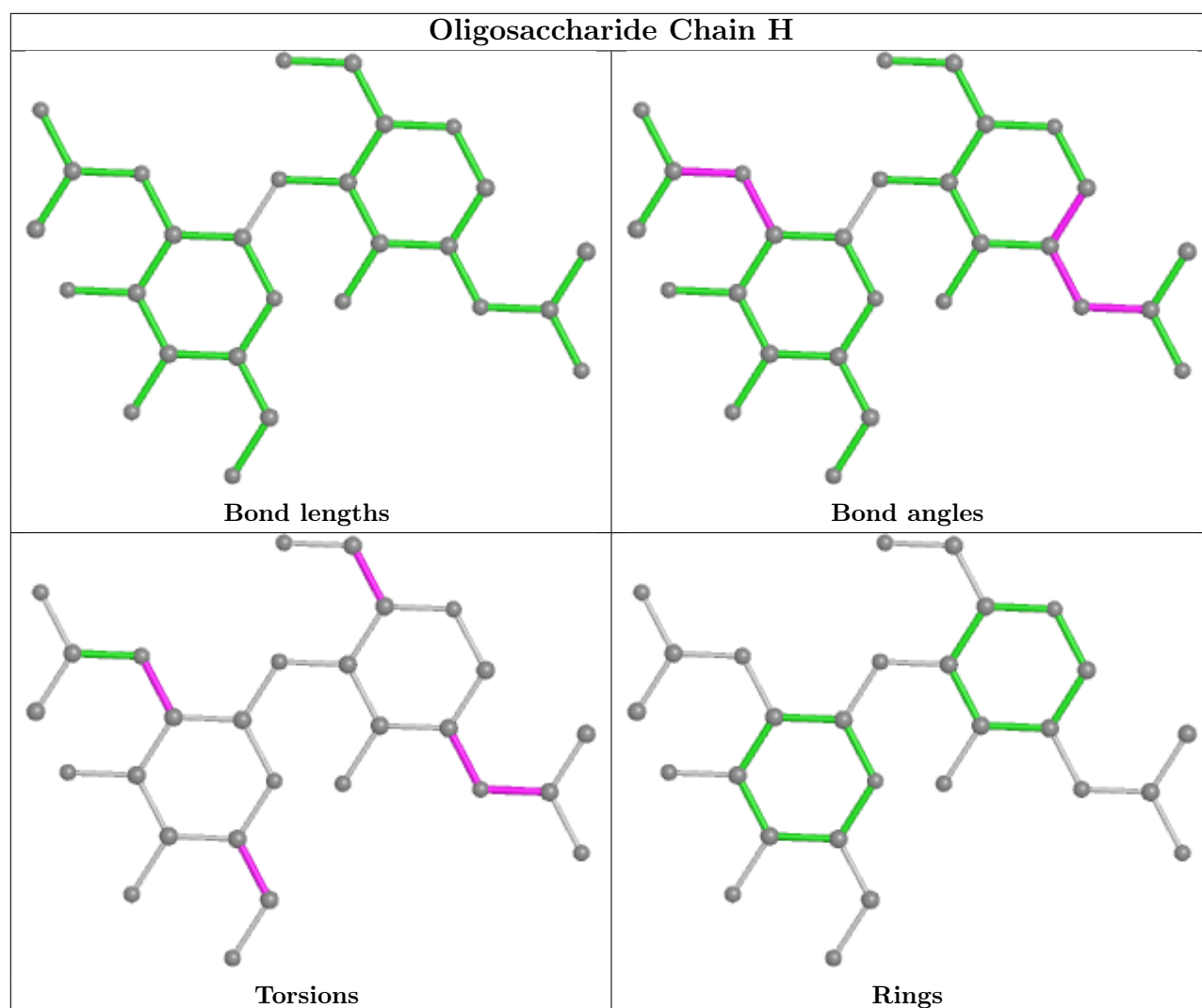
Mol	Chain	Res	Type	Atoms
4	G	4	MAN	C1-C2-C3-C4-C5-O5
4	I	4	MAN	C1-C2-C3-C4-C5-O5

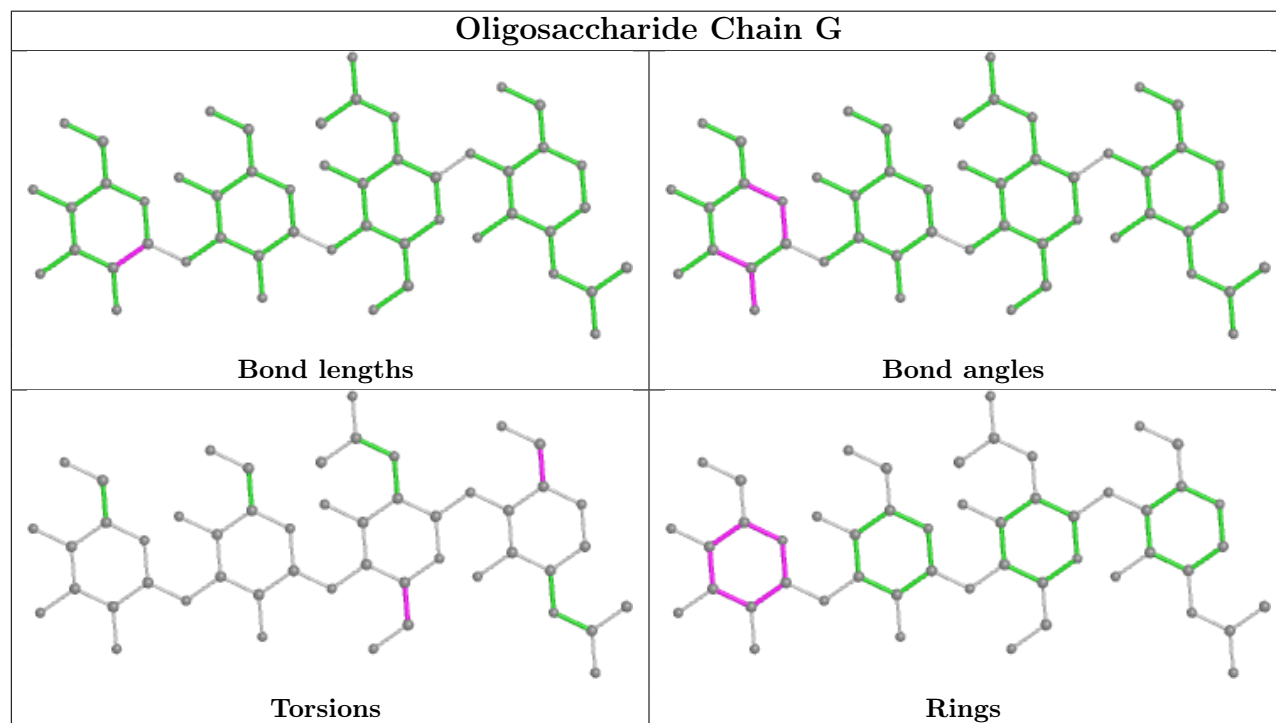
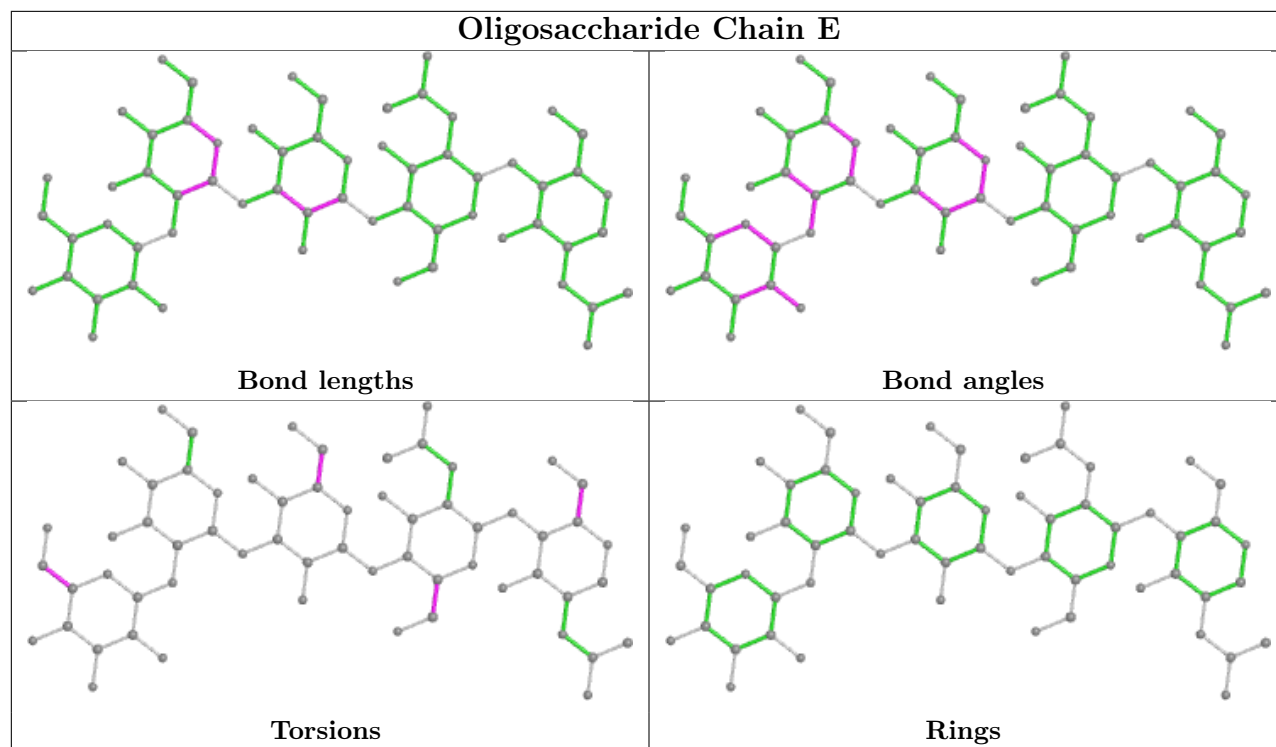
No monomer is involved in short contacts.

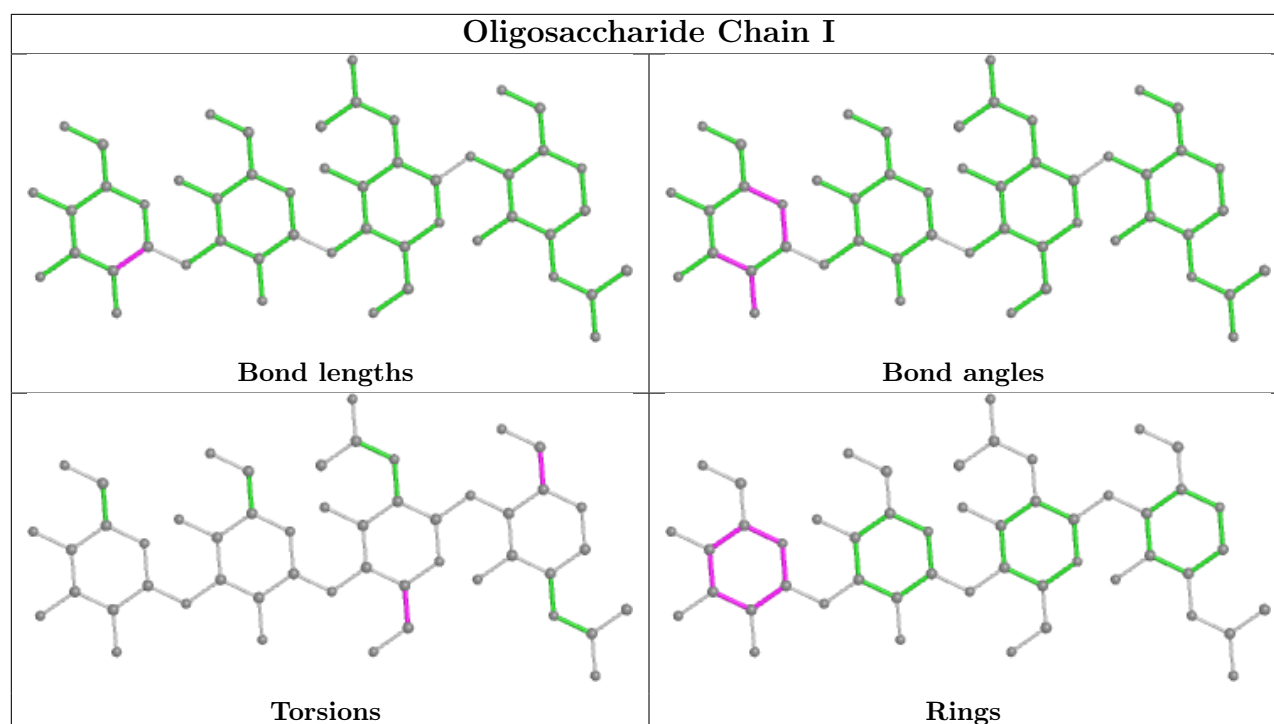
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











## 5.6 Ligand geometry [i](#)

54 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	$\# Z  > 2$
5	NAG	A	1201	1	14,14,15	0.25	0	17,19,21	0.48	0
5	NAG	A	1203	1	14,14,15	0.71	1 (7%)	17,19,21	1.98	2 (11%)
5	NAG	C	1216	1	14,14,15	0.26	0	17,19,21	0.47	0
5	NAG	A	1217	1	14,14,15	0.27	0	17,19,21	0.48	0
5	NAG	C	1209	1	14,14,15	0.32	0	17,19,21	0.48	0
5	NAG	B	1205	1	14,14,15	0.27	0	17,19,21	0.47	0
5	NAG	C	1214	1	14,14,15	0.27	0	17,19,21	0.47	0
5	NAG	B	1218	1	14,14,15	0.26	0	17,19,21	0.37	0
5	NAG	A	1210	1	14,14,15	0.32	0	17,19,21	0.50	0
5	NAG	A	1208	1	14,14,15	0.42	0	17,19,21	0.53	0
5	NAG	A	1204	1	14,14,15	0.23	0	17,19,21	0.42	0
5	NAG	B	1201	1	14,14,15	0.26	0	17,19,21	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	A	1202	1	14,14,15	0.32	0	17,19,21	0.45	0
5	NAG	C	1207	1	14,14,15	0.40	0	17,19,21	0.52	0
5	NAG	A	1212	1	14,14,15	0.35	0	17,19,21	0.81	1 (5%)
5	NAG	B	1208	1	14,14,15	0.32	0	17,19,21	0.80	1 (5%)
5	NAG	A	1216	1	14,14,15	0.27	0	17,19,21	0.47	0
5	NAG	B	1215	1	14,14,15	0.29	0	17,19,21	0.45	0
5	NAG	A	1211	1	14,14,15	0.24	0	17,19,21	0.43	0
5	NAG	B	1202	1	14,14,15	0.34	0	17,19,21	0.45	0
5	NAG	B	1209	1	14,14,15	0.30	0	17,19,21	0.47	0
5	NAG	B	1211	1	14,14,15	0.35	0	17,19,21	0.82	1 (5%)
5	NAG	A	1213	1	14,14,15	0.26	0	17,19,21	0.46	0
5	NAG	C	1206	1	14,14,15	0.35	0	17,19,21	0.84	1 (5%)
5	NAG	B	1210	1	14,14,15	0.25	0	17,19,21	0.44	0
5	NAG	A	1215	1	14,14,15	0.28	0	17,19,21	0.47	0
5	NAG	C	1201	1	14,14,15	0.27	0	17,19,21	0.48	0
5	NAG	A	1209	1	14,14,15	0.32	0	17,19,21	0.80	1 (5%)
5	NAG	B	1216	1	14,14,15	0.26	0	17,19,21	0.46	0
5	NAG	A	1214	1	14,14,15	0.41	0	17,19,21	0.85	1 (5%)
5	NAG	C	1205	1	14,14,15	0.32	0	17,19,21	0.43	0
6	BLA	B	1217	-	42,46,46	1.28	4 (9%)	53,67,67	1.19	5 (9%)
5	NAG	C	1202	1	14,14,15	0.34	0	17,19,21	0.44	0
5	NAG	A	1206	1	14,14,15	0.34	0	17,19,21	0.45	0
5	NAG	C	1215	1	14,14,15	0.26	0	17,19,21	0.48	0
5	NAG	B	1204	1	14,14,15	0.24	0	17,19,21	0.42	0
5	NAG	B	1212	1	14,14,15	0.27	0	17,19,21	0.47	0
5	NAG	B	1203	1	14,14,15	0.71	1 (7%)	17,19,21	1.97	2 (11%)
5	NAG	C	1218	1	14,14,15	0.38	0	17,19,21	0.83	1 (5%)
5	NAG	B	1213	1	14,14,15	0.41	0	17,19,21	0.85	1 (5%)
5	NAG	C	1203	1	14,14,15	0.25	0	17,19,21	0.43	0
5	NAG	B	1207	1	14,14,15	0.41	0	17,19,21	0.52	0
5	NAG	A	1205	1	14,14,15	0.27	0	17,19,21	0.47	0
5	NAG	C	1208	1	14,14,15	0.31	0	17,19,21	0.80	1 (5%)
6	BLA	C	1217	-	42,46,46	1.31	4 (9%)	53,67,67	1.16	4 (7%)
6	BLA	A	1218	-	42,46,46	1.28	4 (9%)	53,67,67	1.22	4 (7%)
5	NAG	B	1214	1	14,14,15	0.27	0	17,19,21	0.47	0
5	NAG	C	1204	1	14,14,15	0.28	0	17,19,21	0.47	0
5	NAG	B	1206	1	14,14,15	0.36	0	17,19,21	0.83	1 (5%)
5	NAG	A	1207	1	14,14,15	0.36	0	17,19,21	0.81	1 (5%)
5	NAG	C	1212	1	14,14,15	0.27	0	17,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	C	1211	1	14,14,15	0.36	0	17,19,21	0.82	1 (5%)
5	NAG	C	1213	1	14,14,15	0.41	0	17,19,21	0.85	1 (5%)
5	NAG	C	1210	1	14,14,15	0.25	0	17,19,21	0.45	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1201	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1203	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1216	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1217	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1209	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1205	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1214	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1218	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1210	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1208	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1204	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1201	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1202	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1207	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1212	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1208	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1216	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1215	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1211	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1202	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1209	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1211	1	-	3/6/23/26	0/1/1/1
5	NAG	A	1213	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1206	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1210	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1215	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1201	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1209	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1216	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1214	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1205	1	-	1/6/23/26	0/1/1/1
6	BLA	B	1217	-	-	7/26/74/74	0/4/4/4
5	NAG	C	1202	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1206	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1215	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1204	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1212	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1203	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1218	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1213	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1203	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1207	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1205	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1208	1	-	2/6/23/26	0/1/1/1
6	BLA	C	1217	-	-	11/26/74/74	0/4/4/4
6	BLA	A	1218	-	-	9/26/74/74	0/4/4/4
5	NAG	B	1214	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1204	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1206	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1207	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1212	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1211	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1213	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1210	1	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1217	BLA	CHA-C4D	4.64	1.39	1.35
6	A	1218	BLA	CHA-C4D	4.38	1.38	1.35
6	B	1217	BLA	CHA-C4D	4.33	1.38	1.35
6	A	1218	BLA	CAB-C3B	-2.72	1.40	1.47
6	C	1217	BLA	CAB-C3B	-2.72	1.40	1.47

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1203	NAG	C2-N2-C7	6.90	132.73	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1203	NAG	C2-N2-C7	6.86	132.67	122.90
6	A	1218	BLA	CHA-C4D-ND	-3.89	123.43	128.83
6	C	1217	BLA	CHA-C4D-ND	-3.62	123.80	128.83
6	B	1217	BLA	CHA-C4D-ND	-3.54	123.91	128.83

There are no chirality outliers.

5 of 104 torsion outliers are listed below:

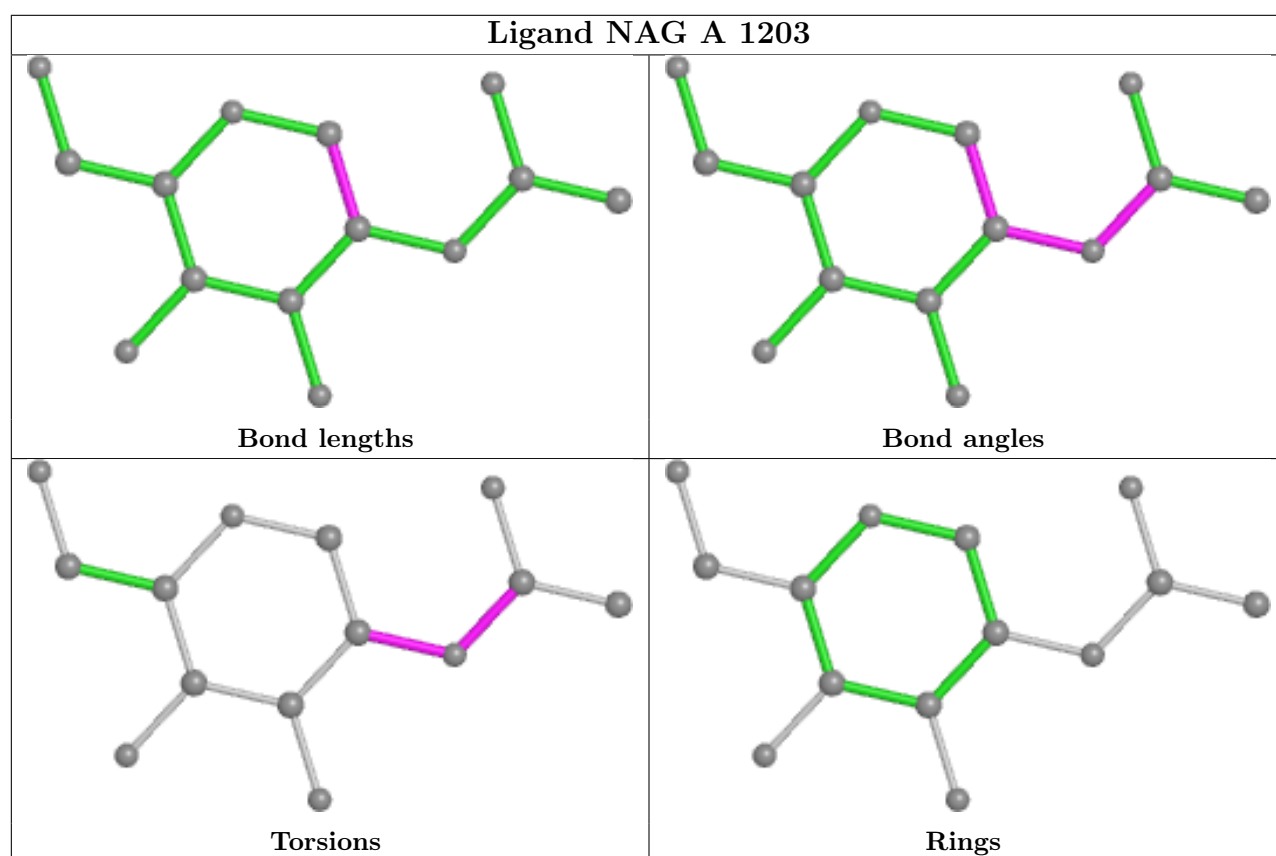
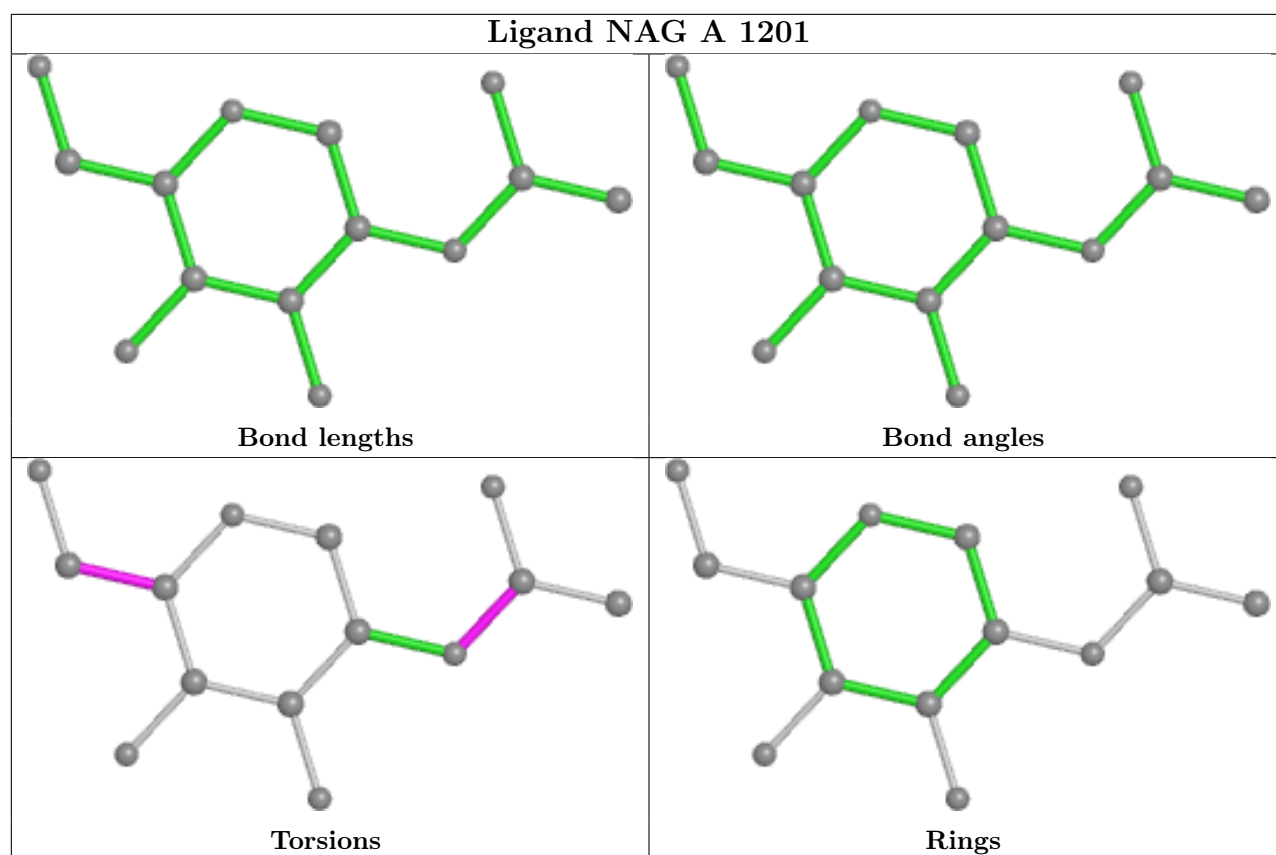
Mol	Chain	Res	Type	Atoms
5	B	1213	NAG	C4-C5-C6-O6
5	B	1213	NAG	O5-C5-C6-O6
6	A	1218	BLA	C4D-C3D-CAD-CBD
6	C	1217	BLA	C4D-C3D-CAD-CBD
5	A	1201	NAG	C4-C5-C6-O6

There are no ring outliers.

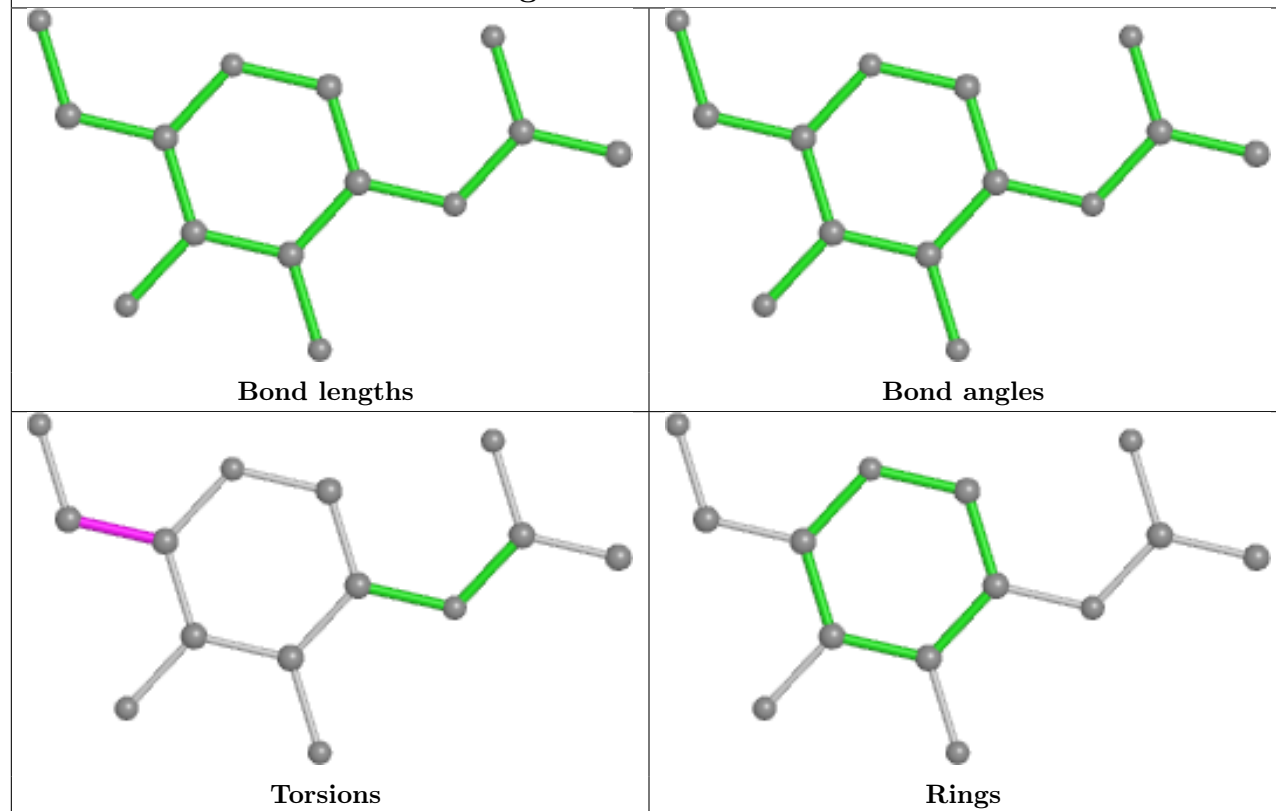
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1217	BLA	3	0
6	A	1218	BLA	4	0

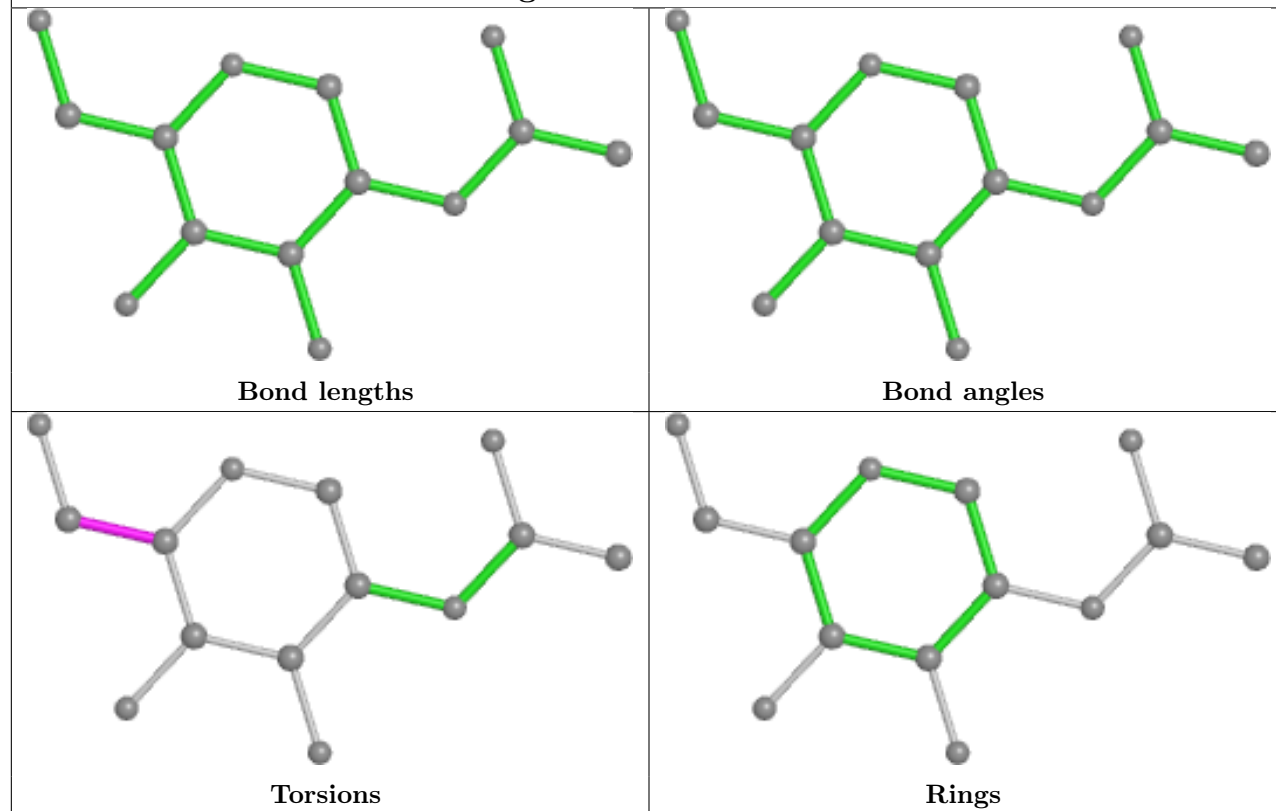
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

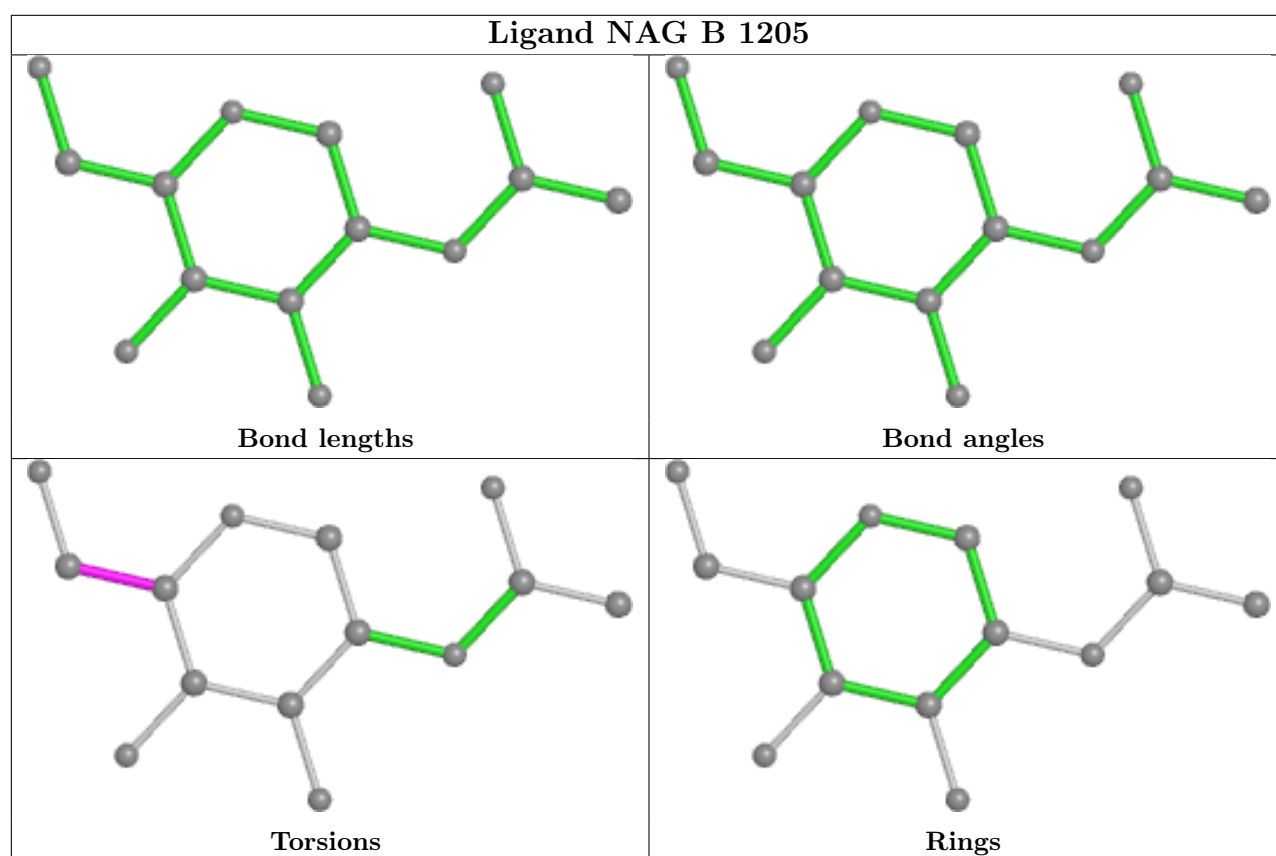
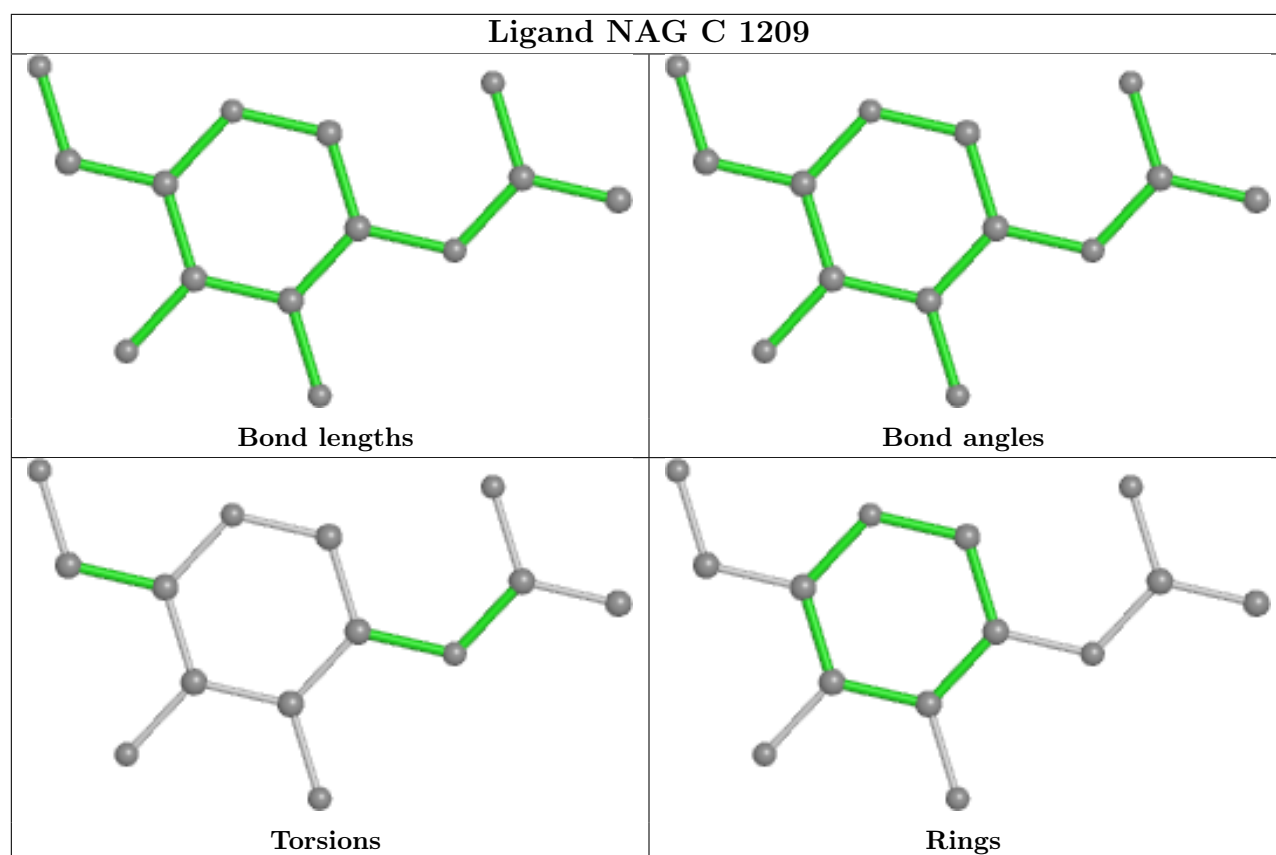


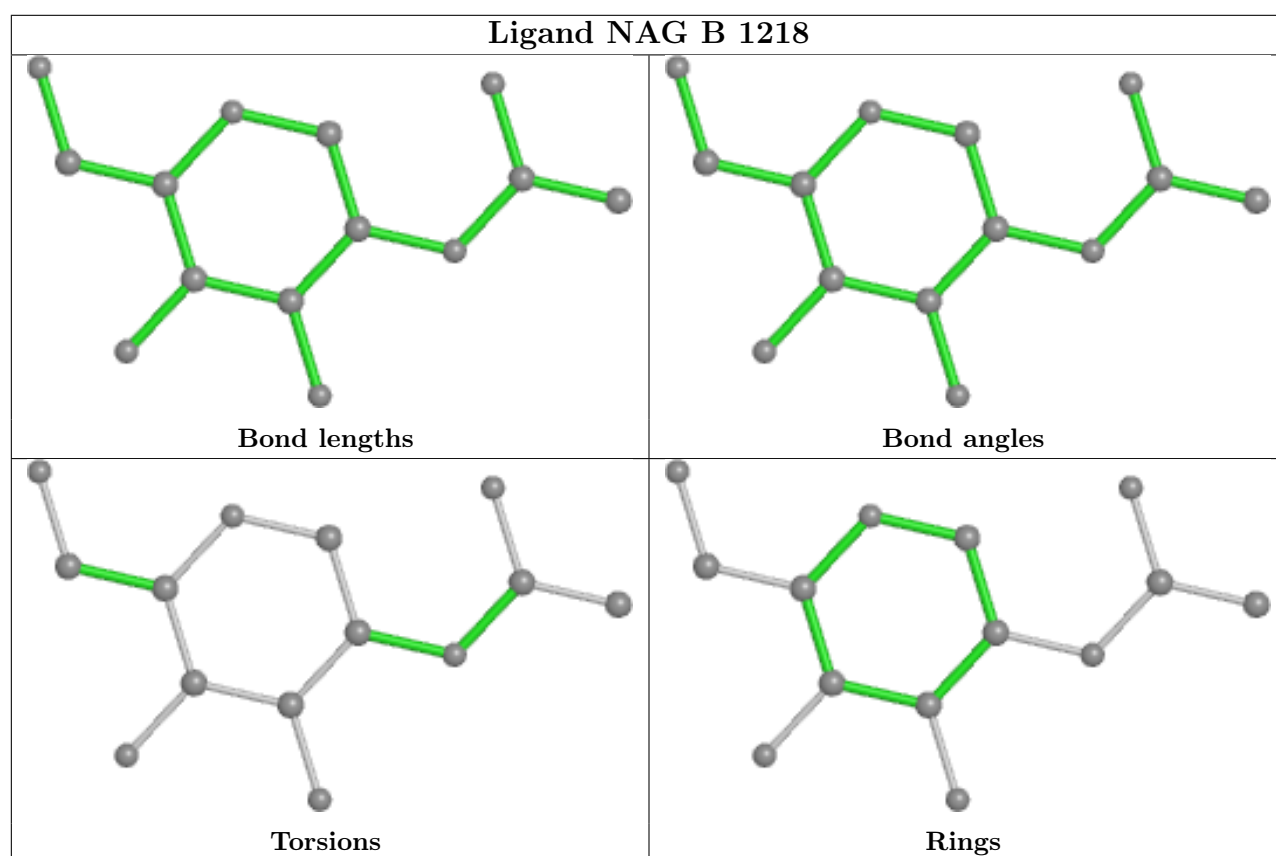
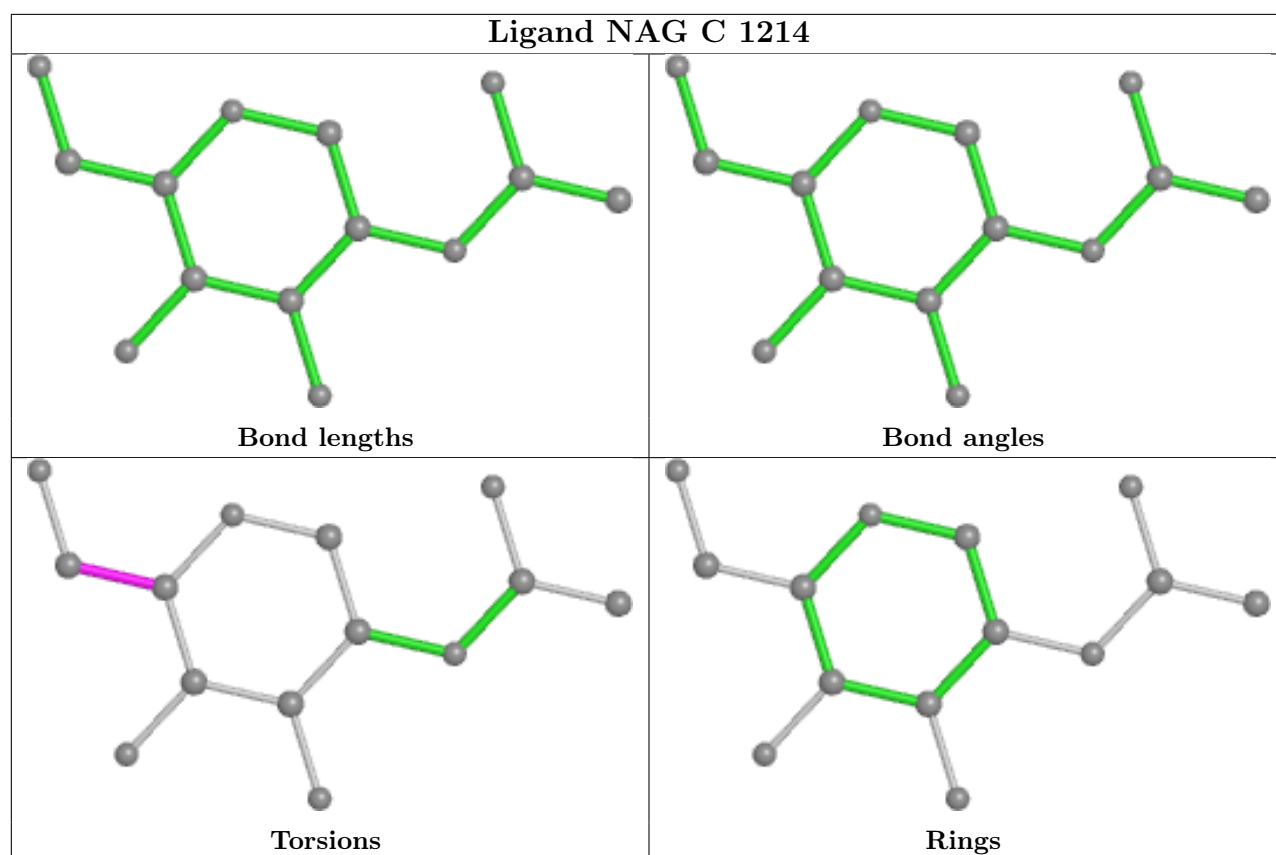
## Ligand NAG C 1216

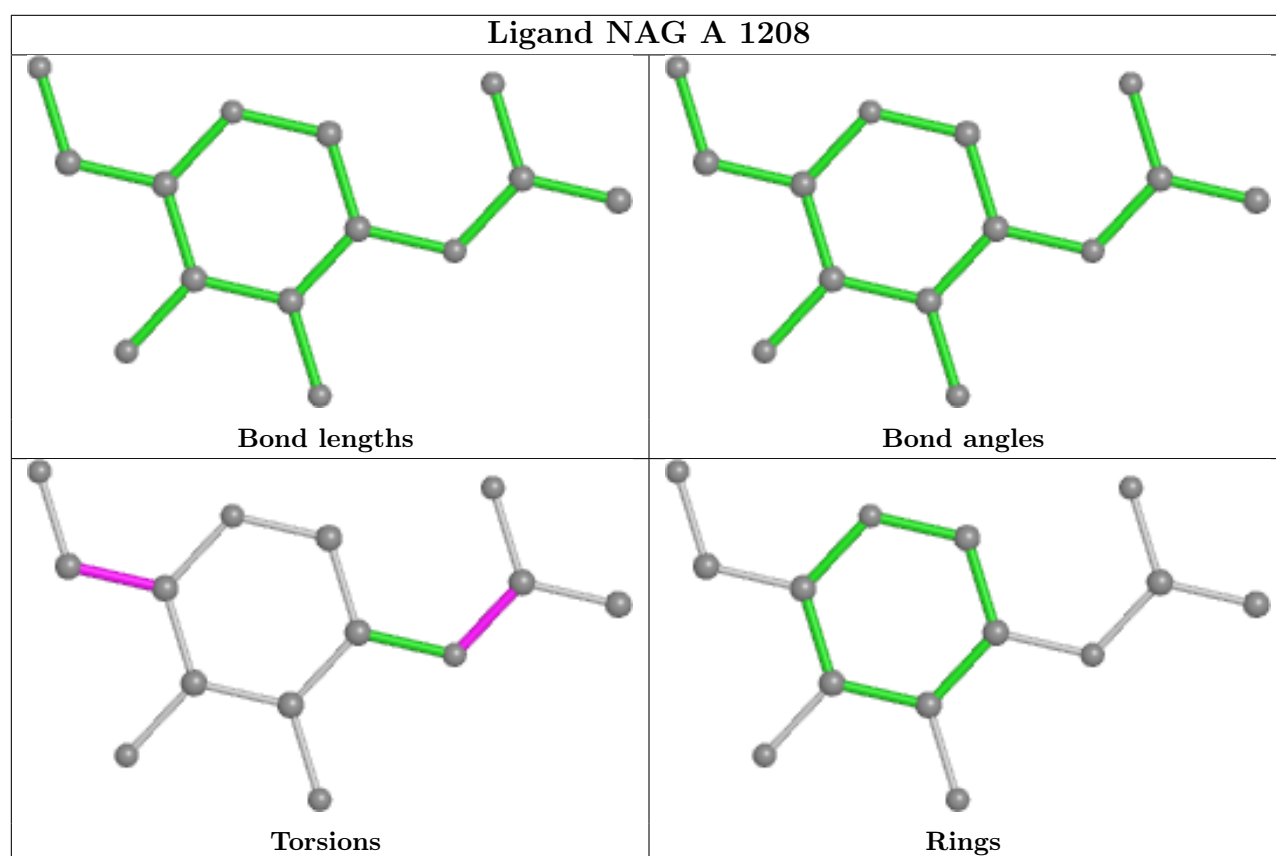
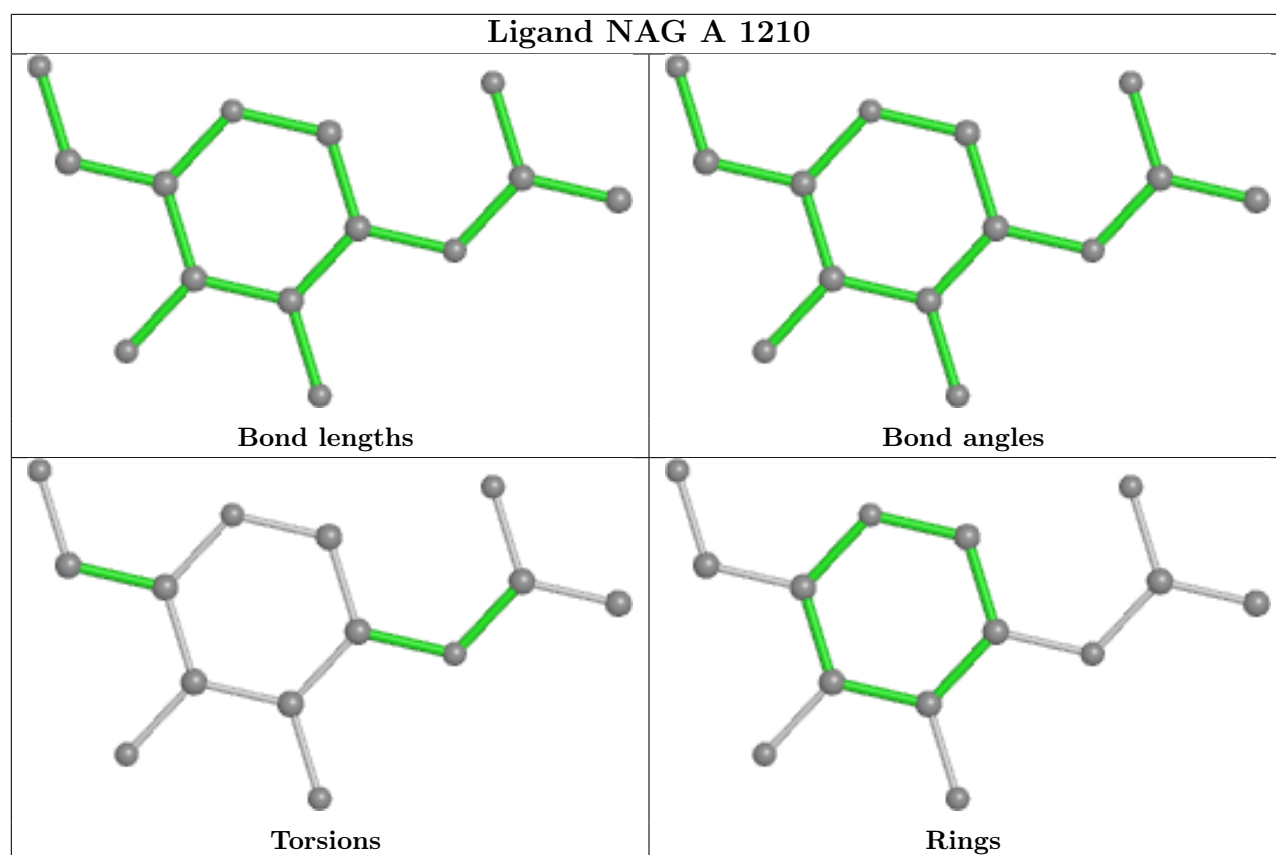


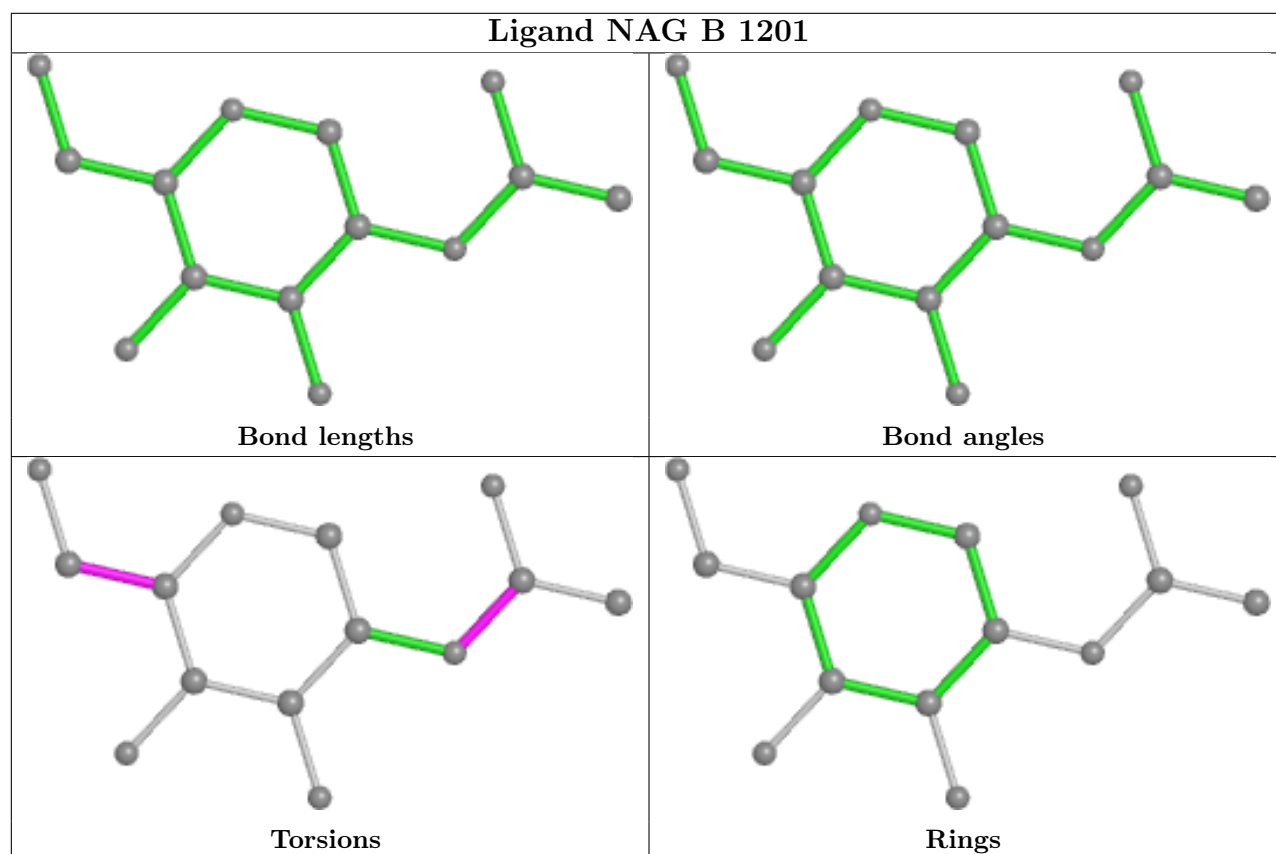
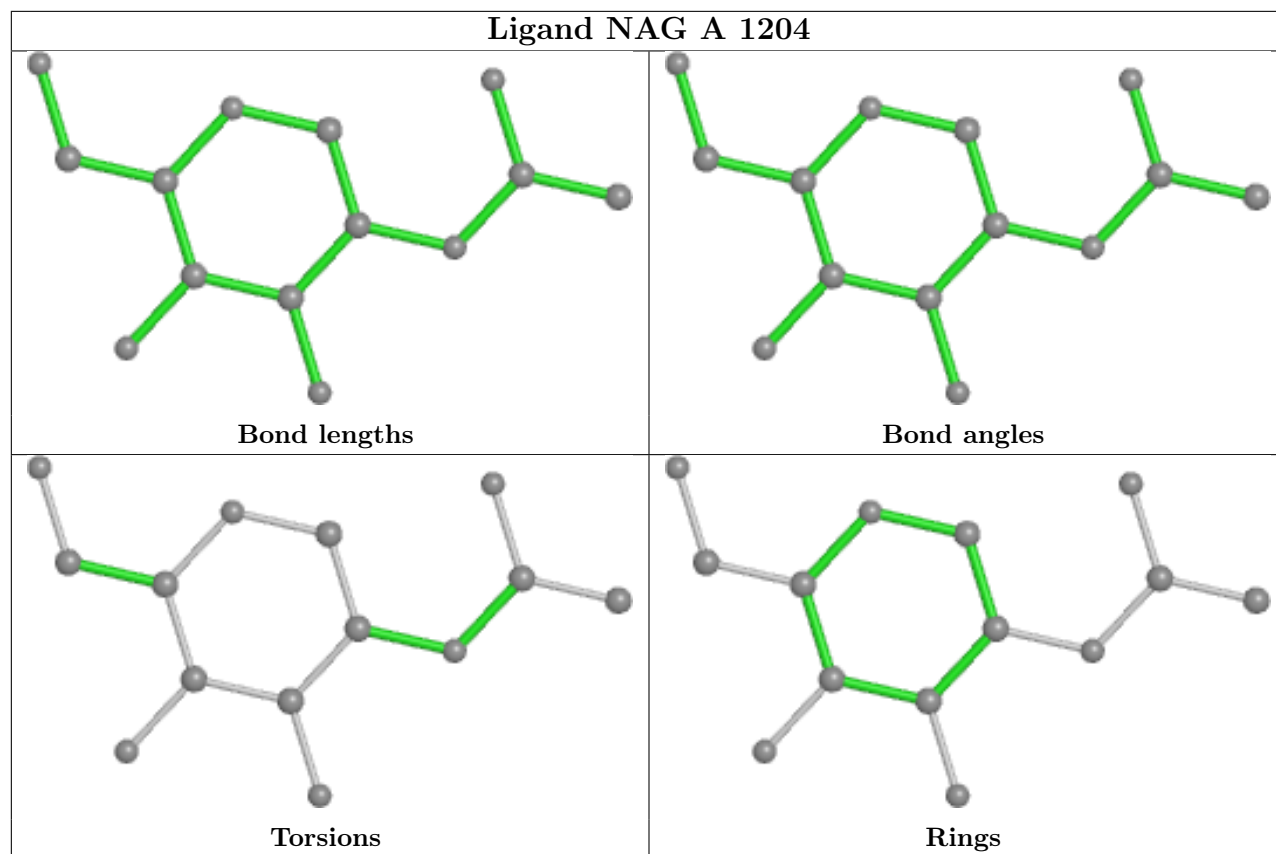
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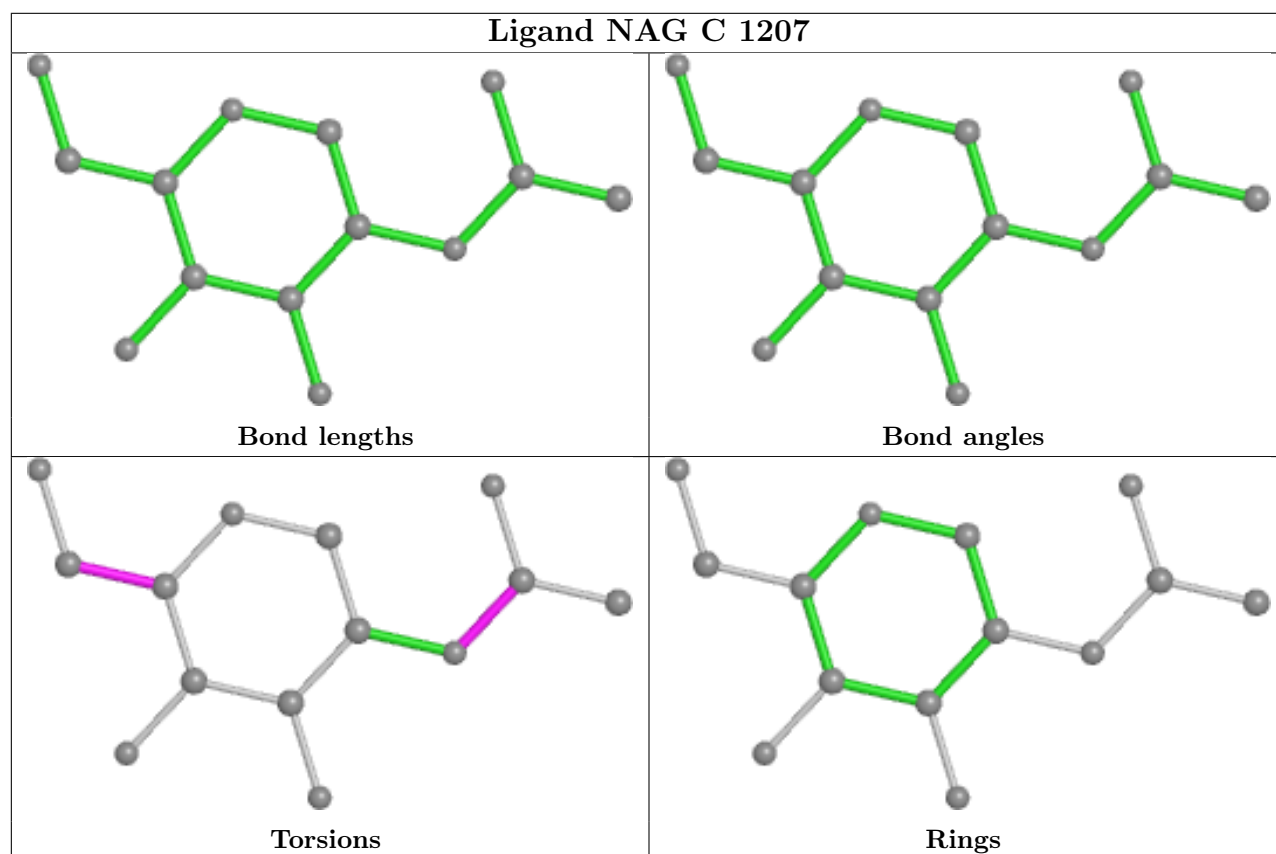
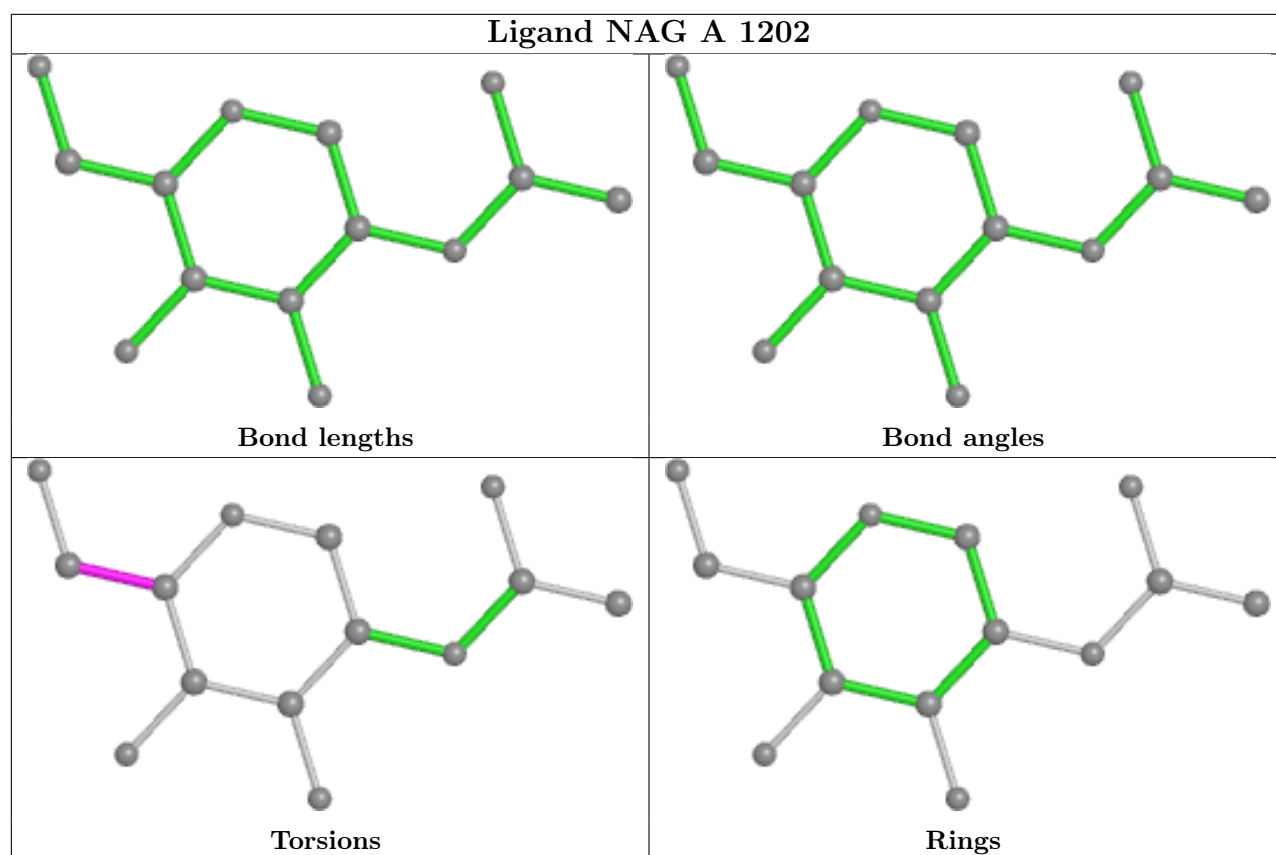




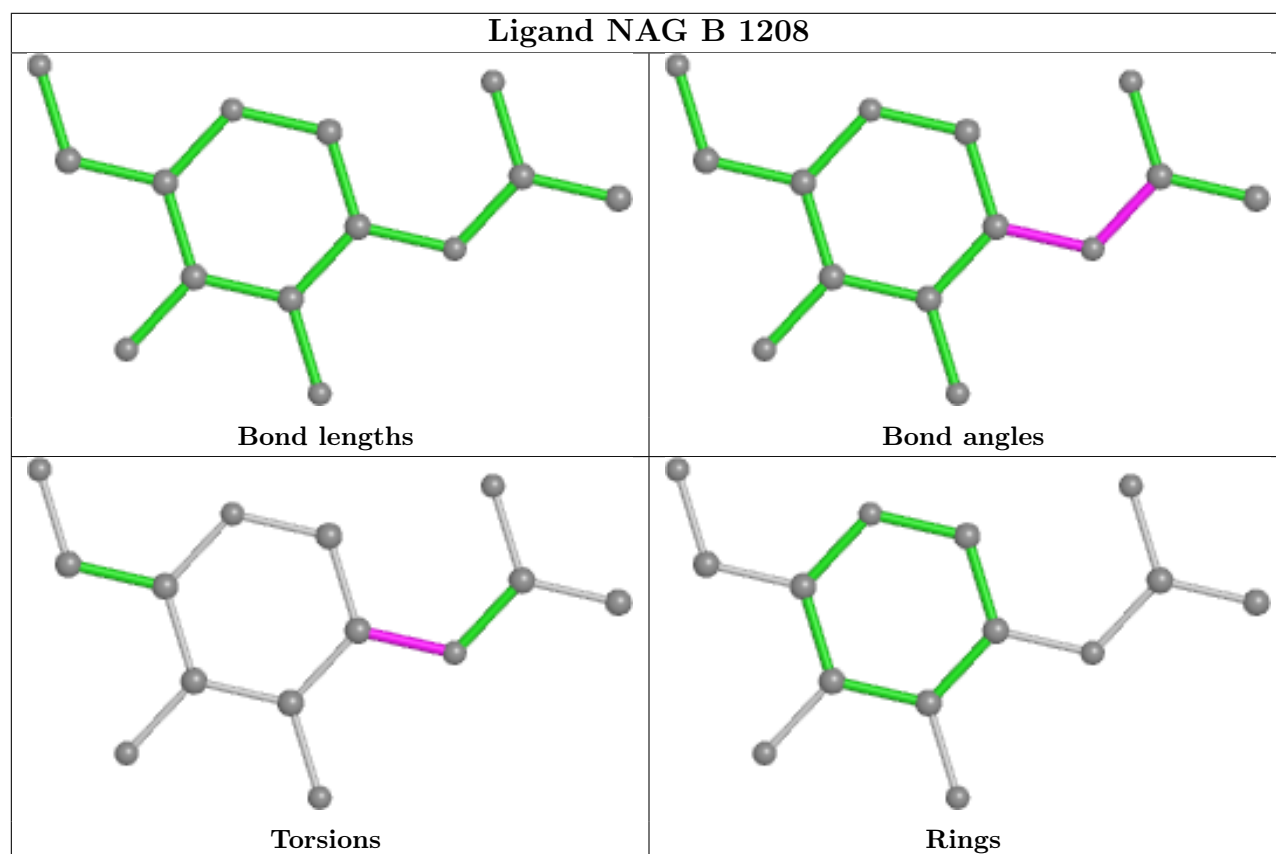
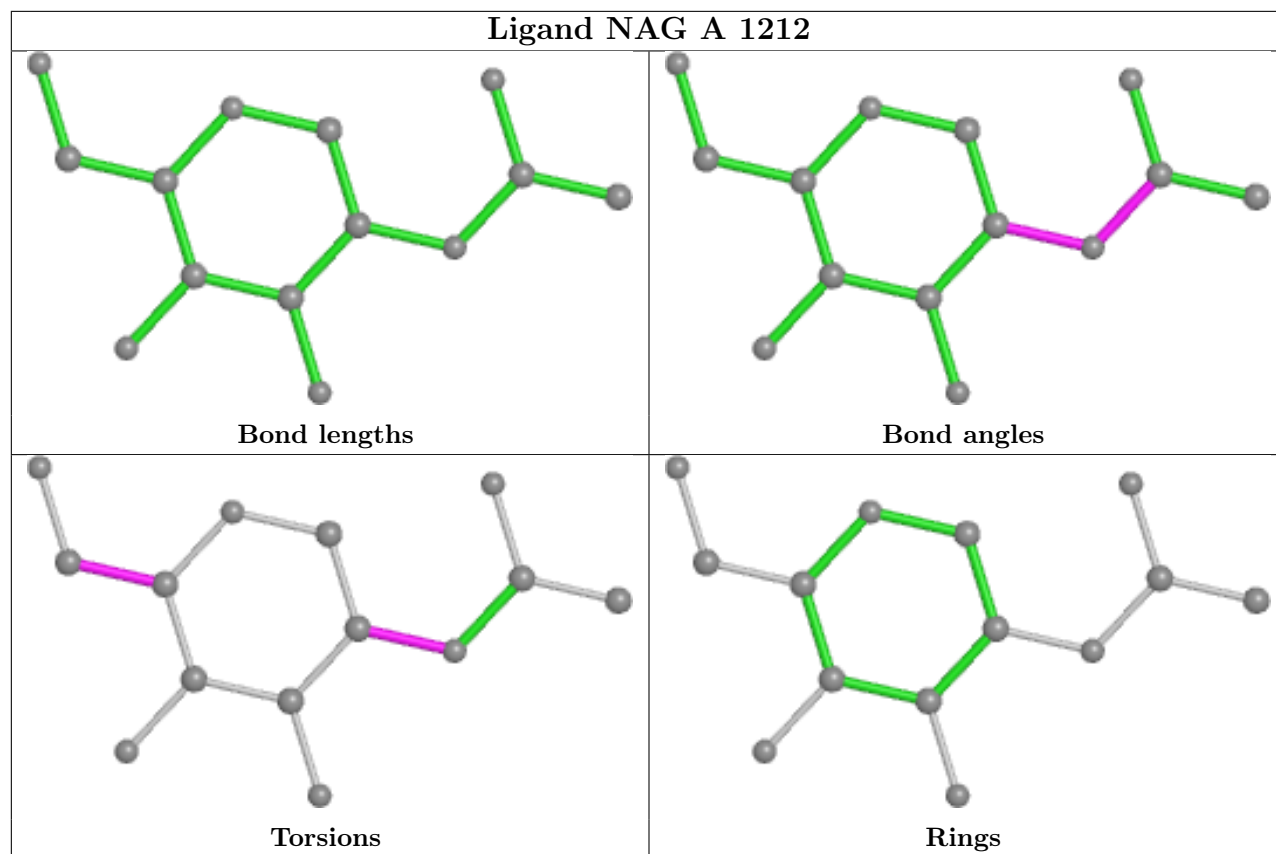




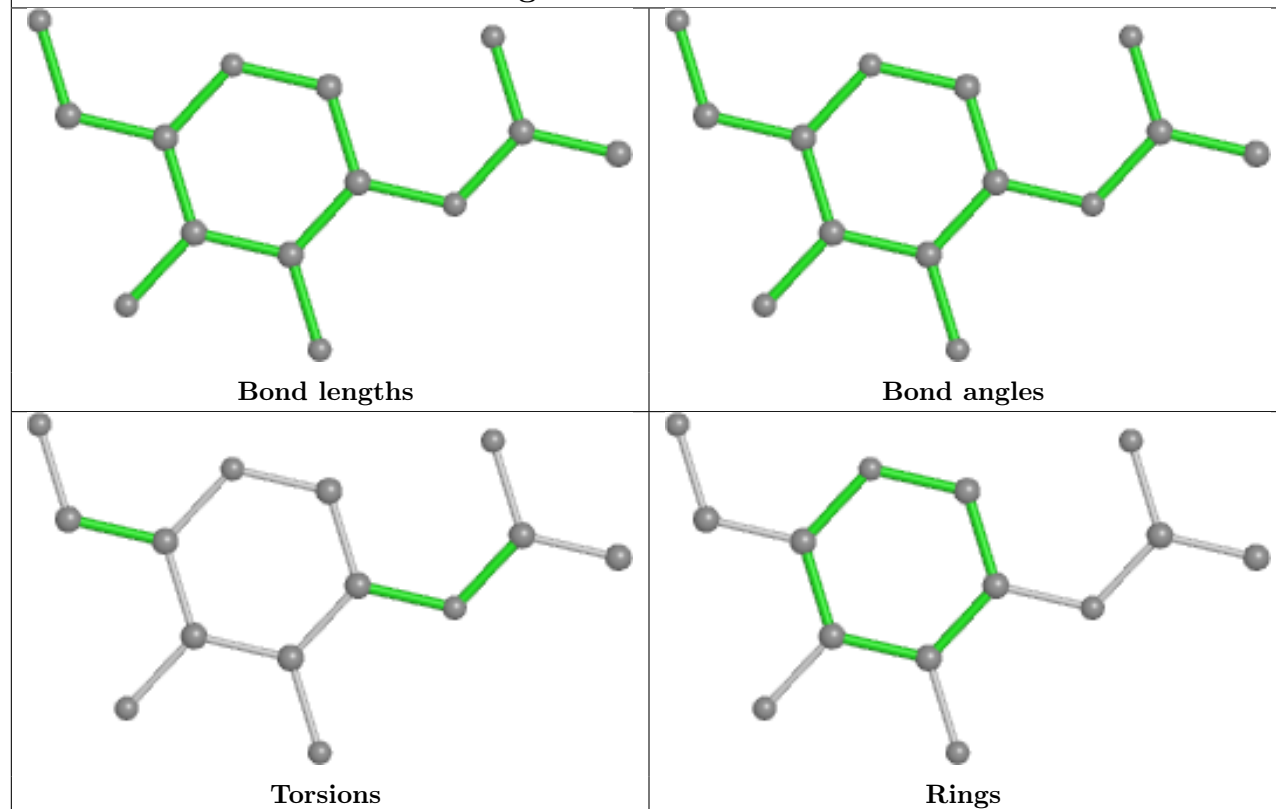




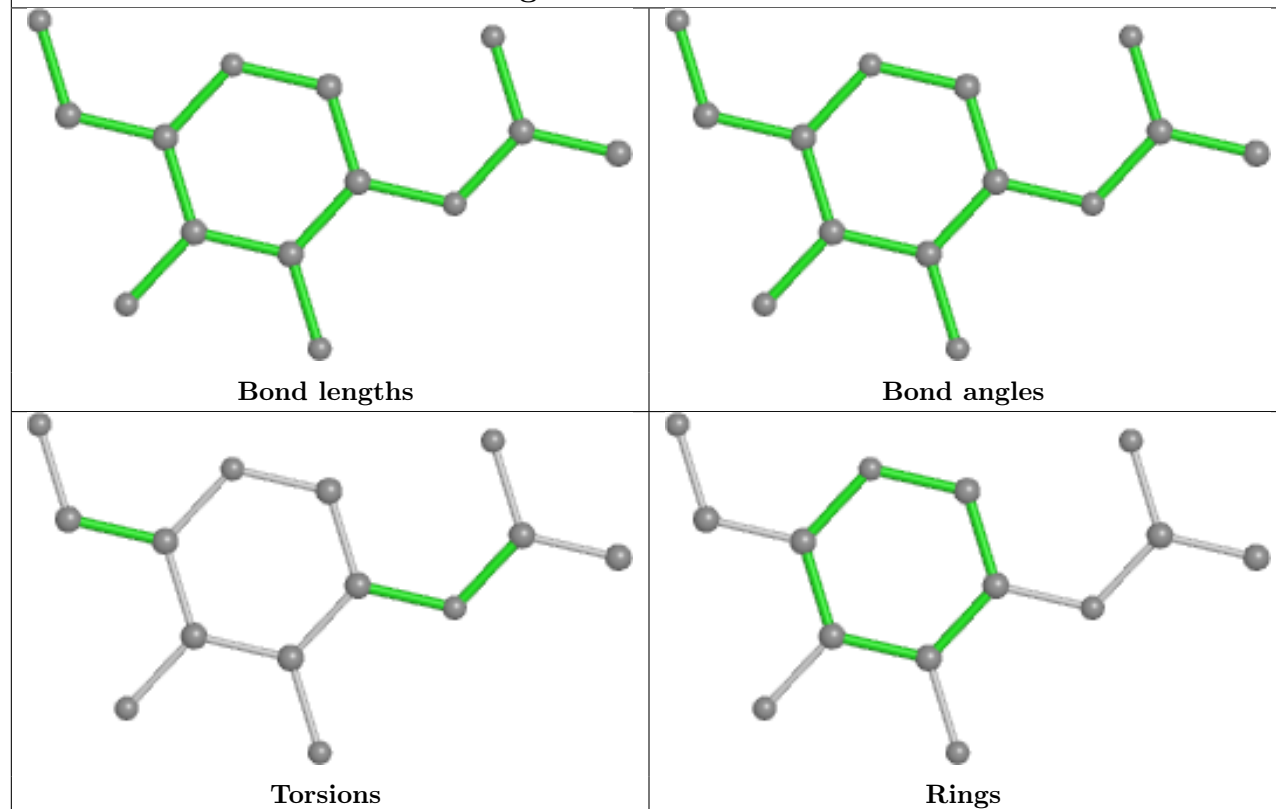




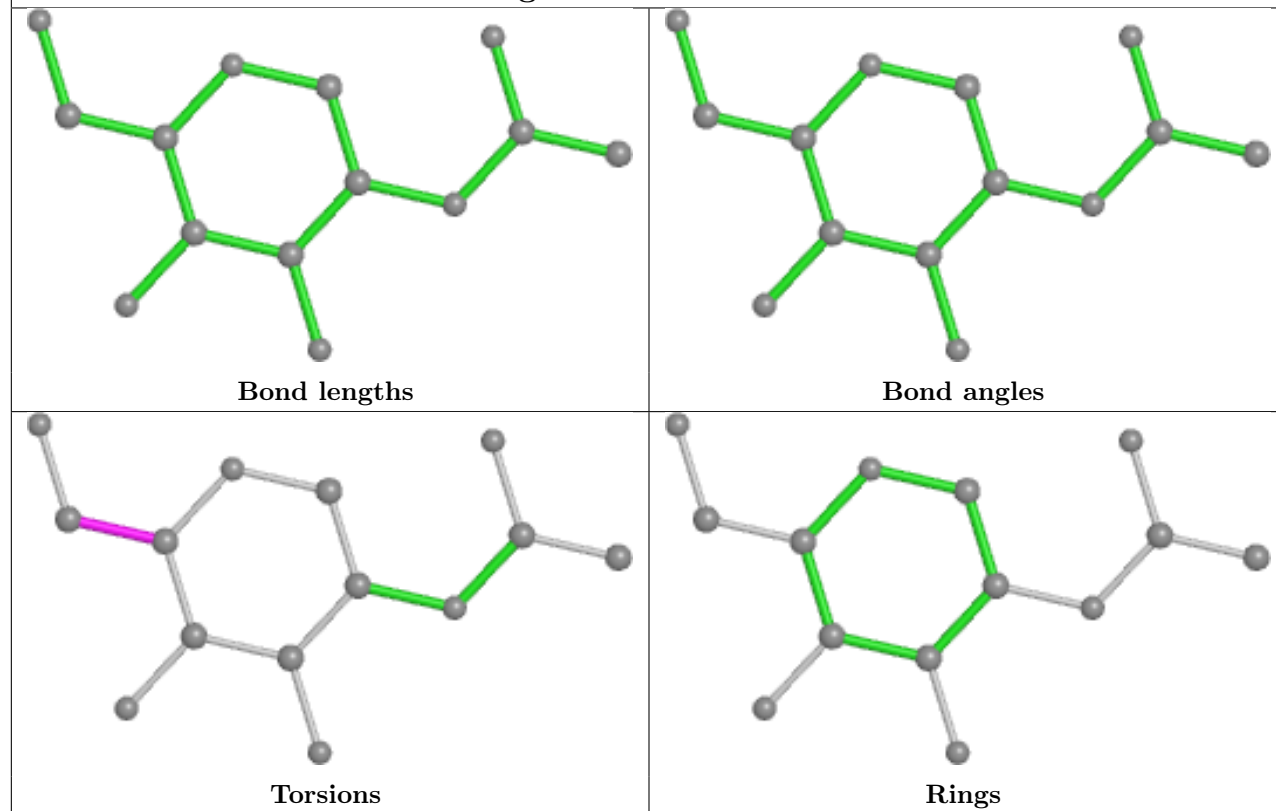
## Ligand NAG A 1216



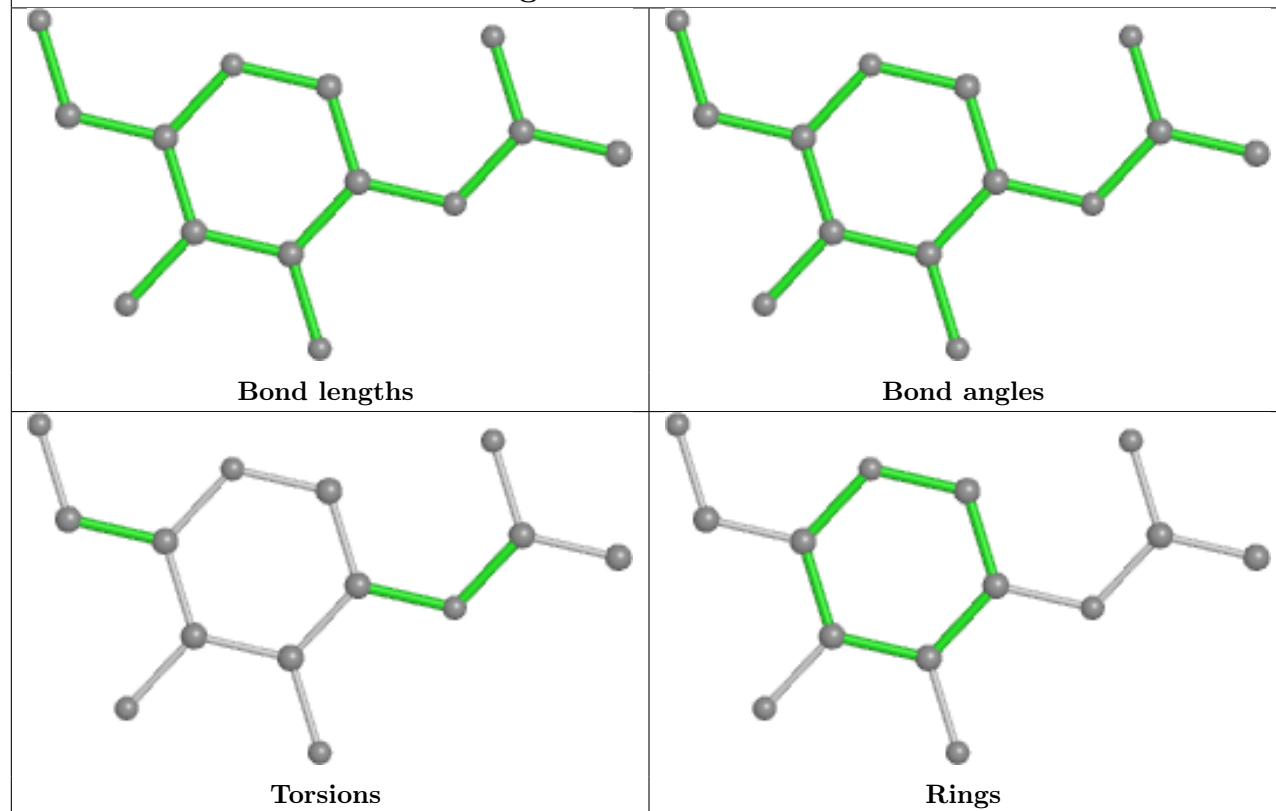
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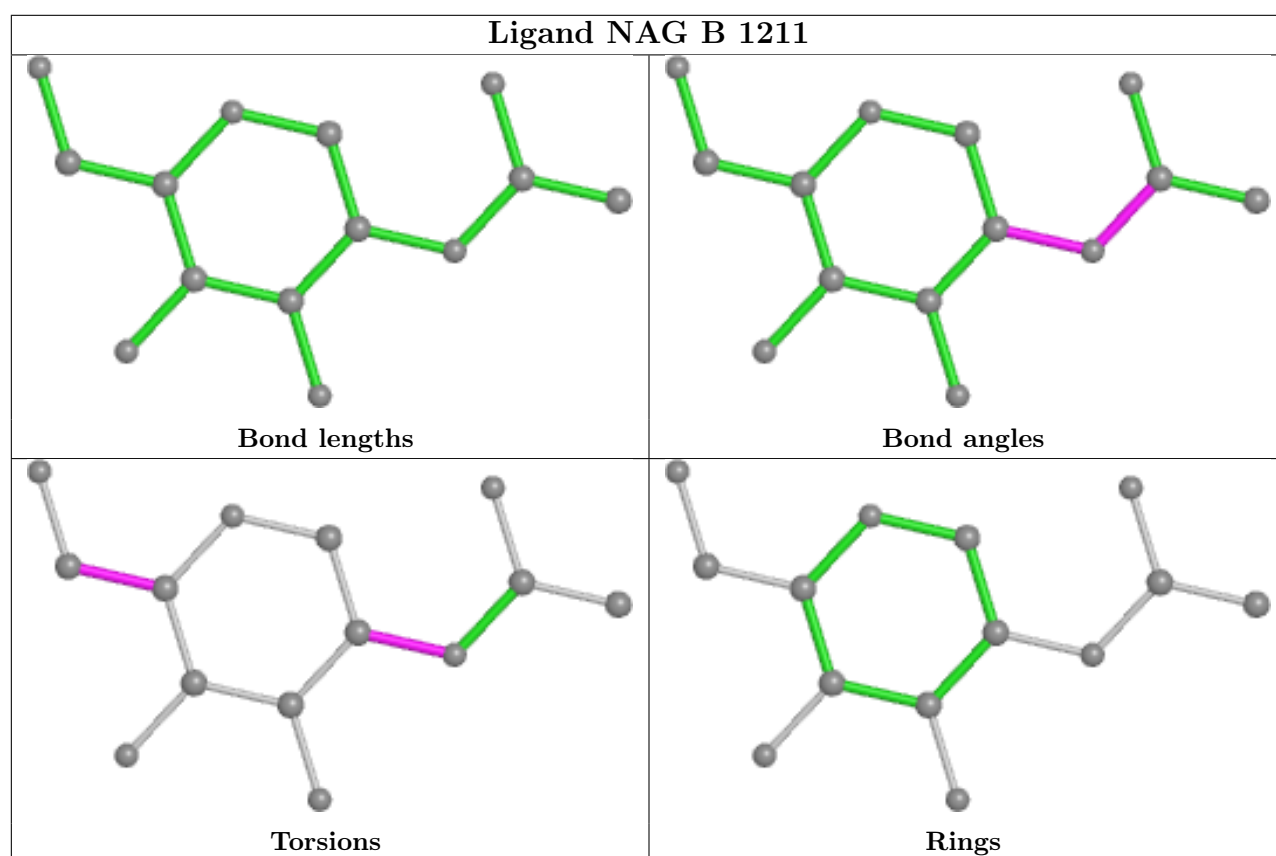
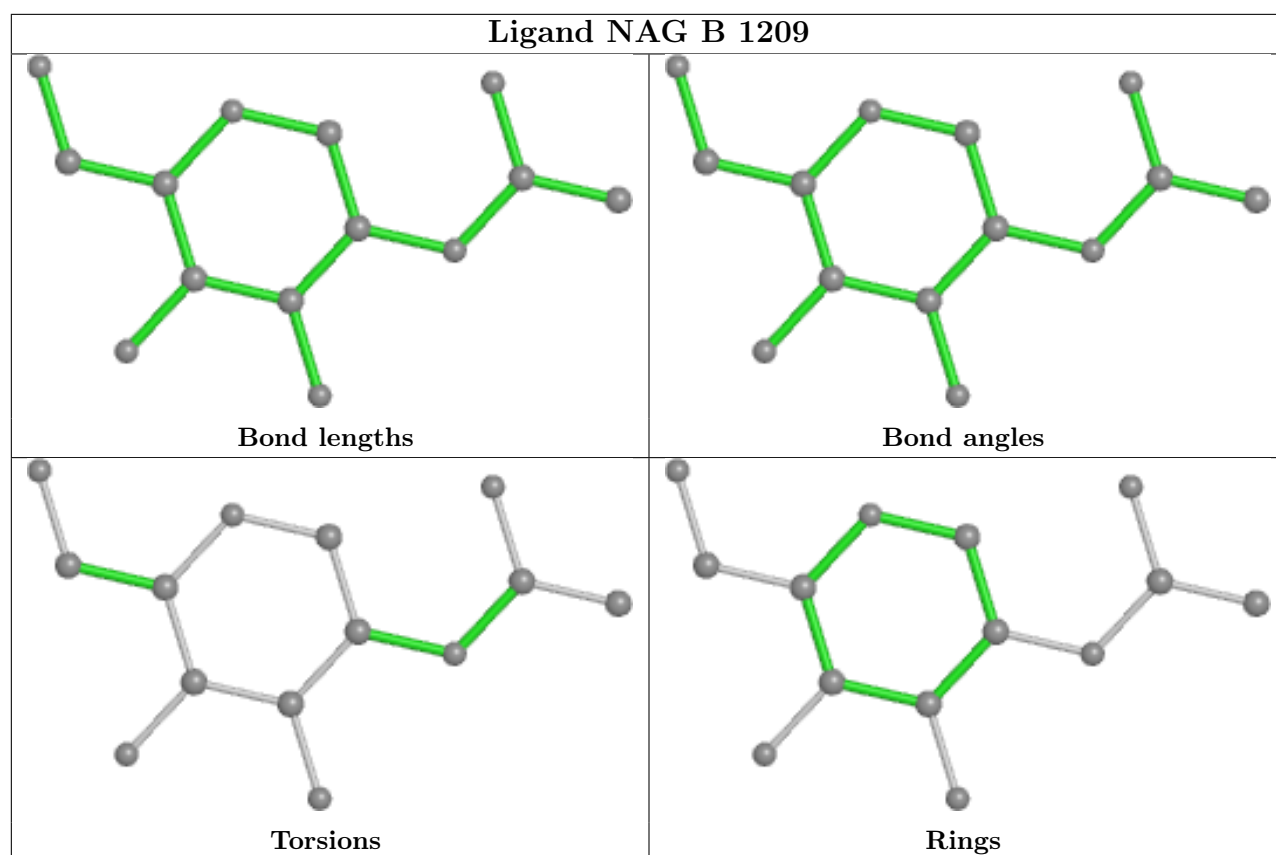


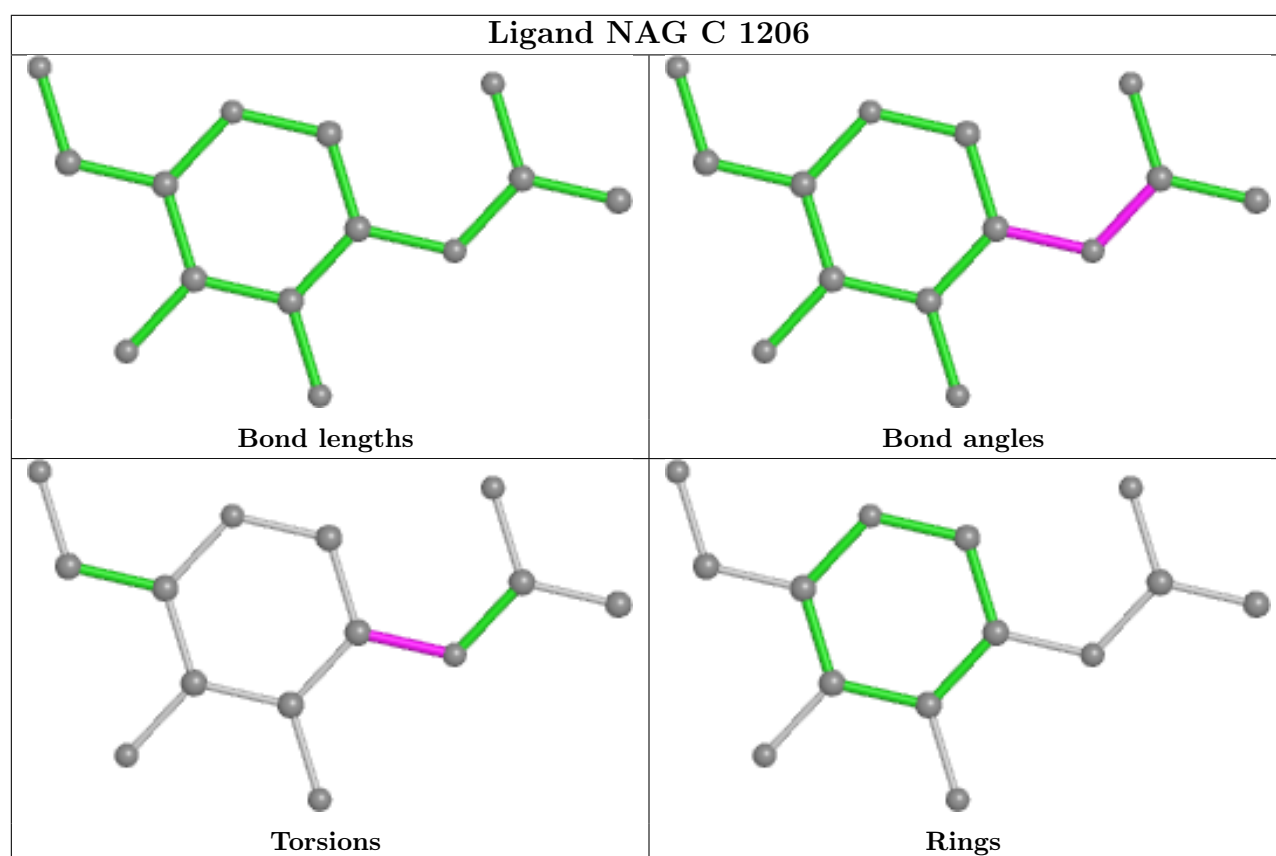
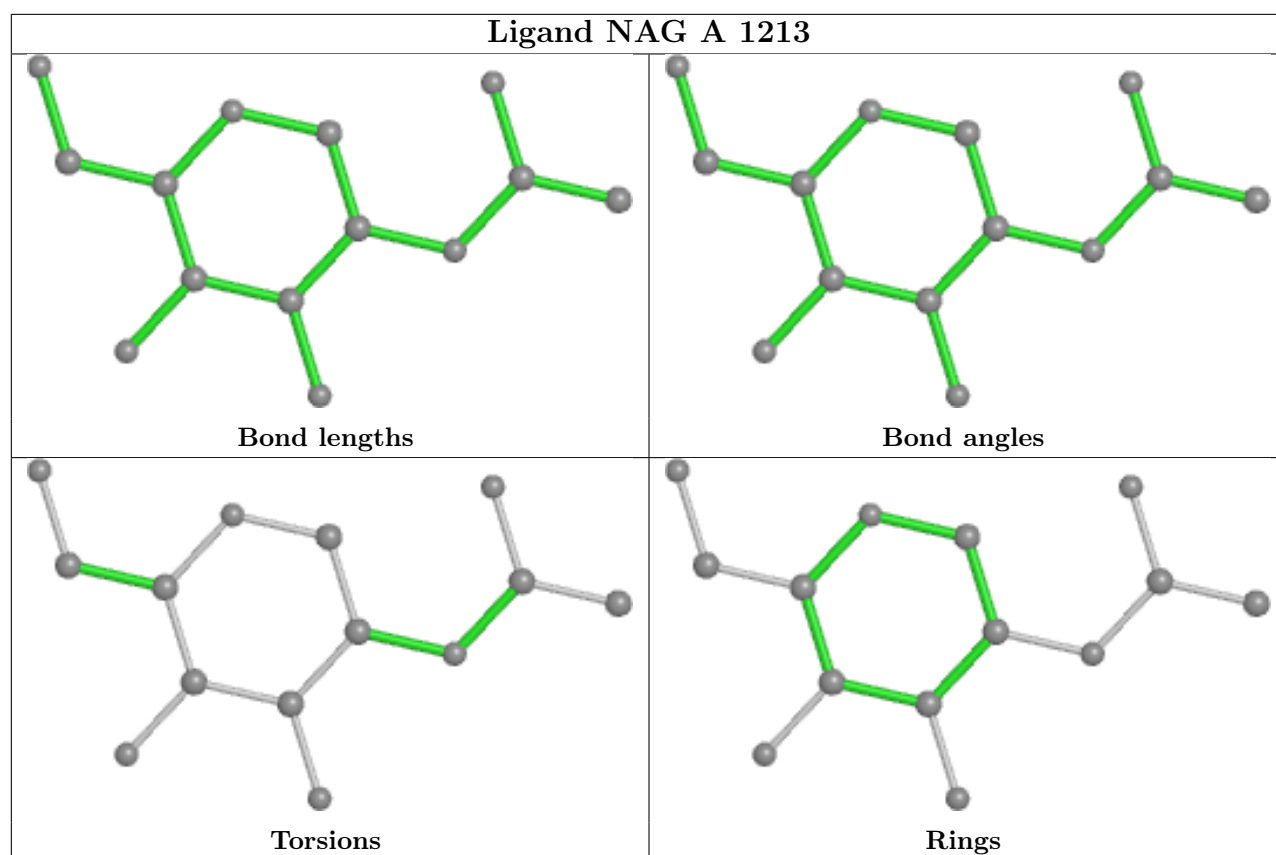
## Ligand NAG A 1211



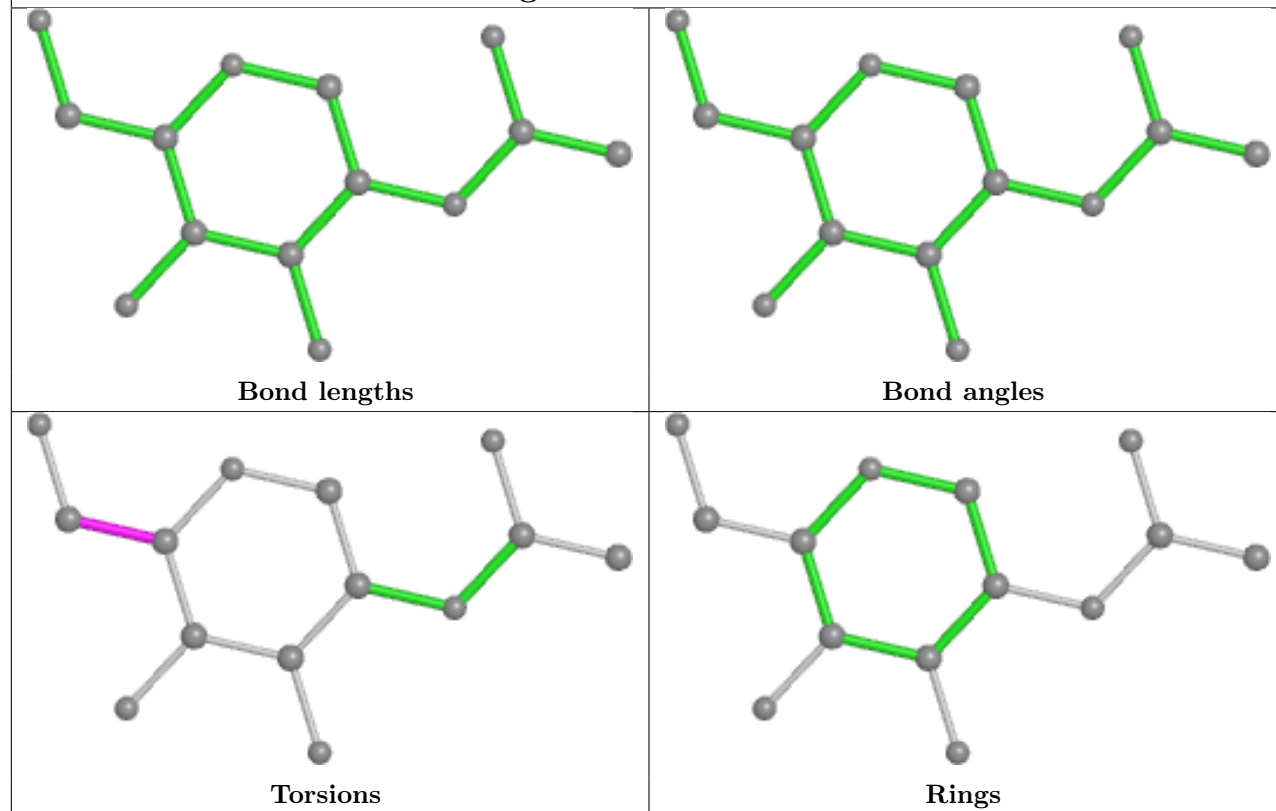
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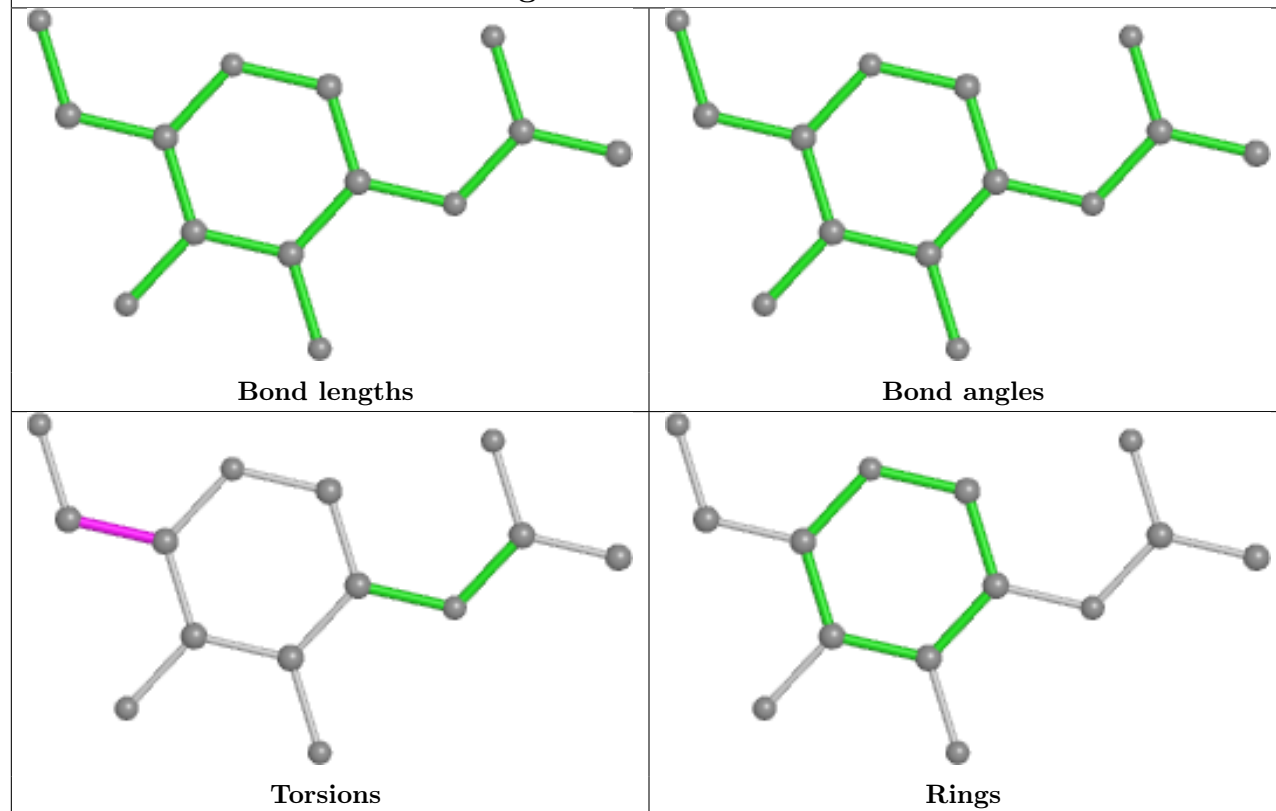


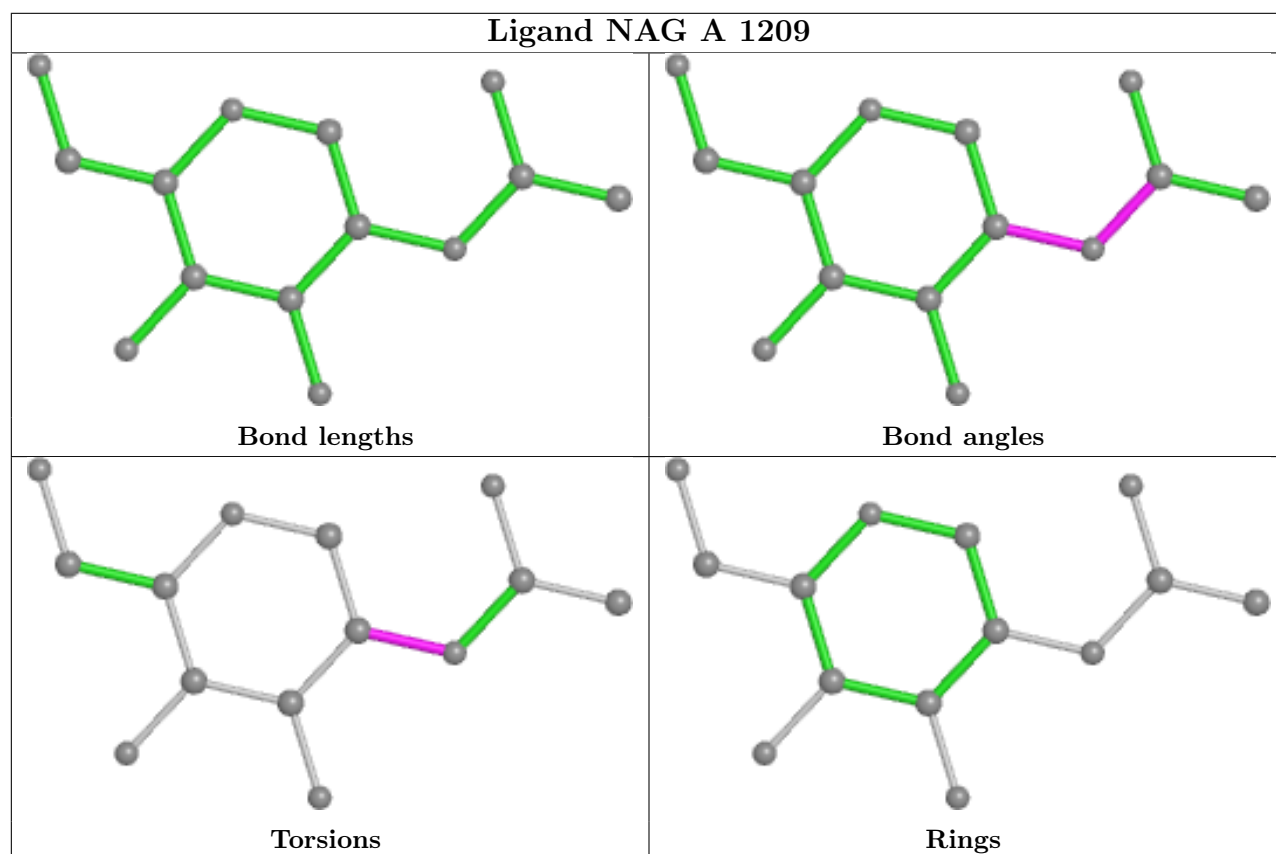
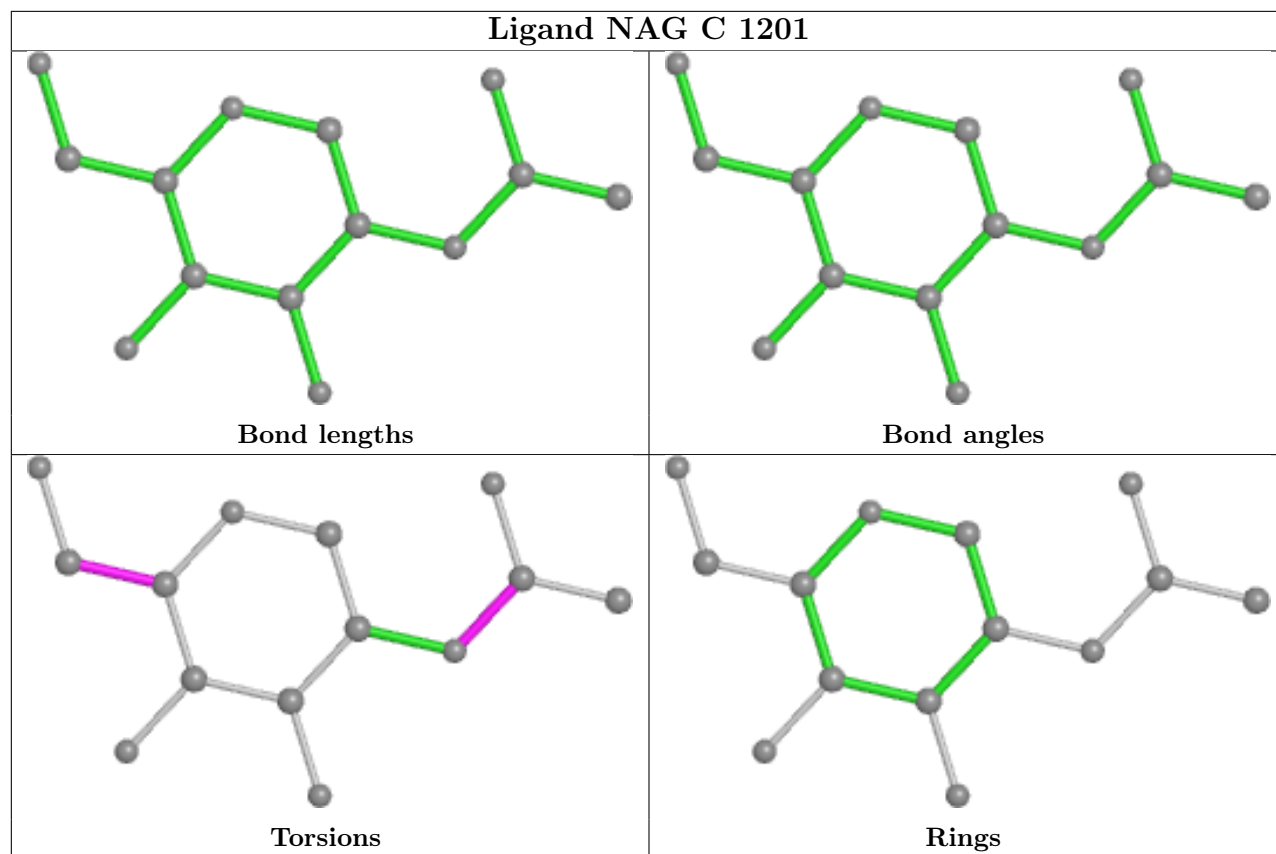


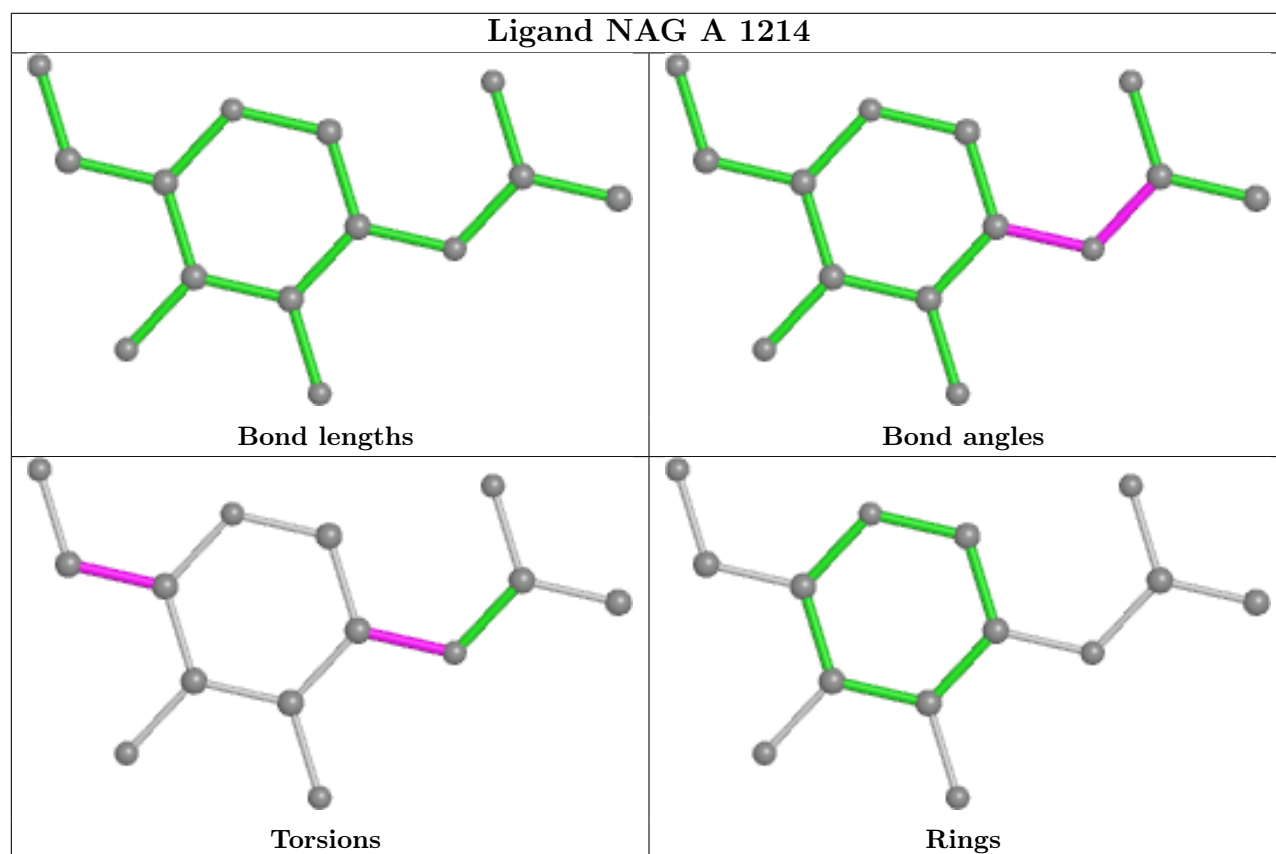
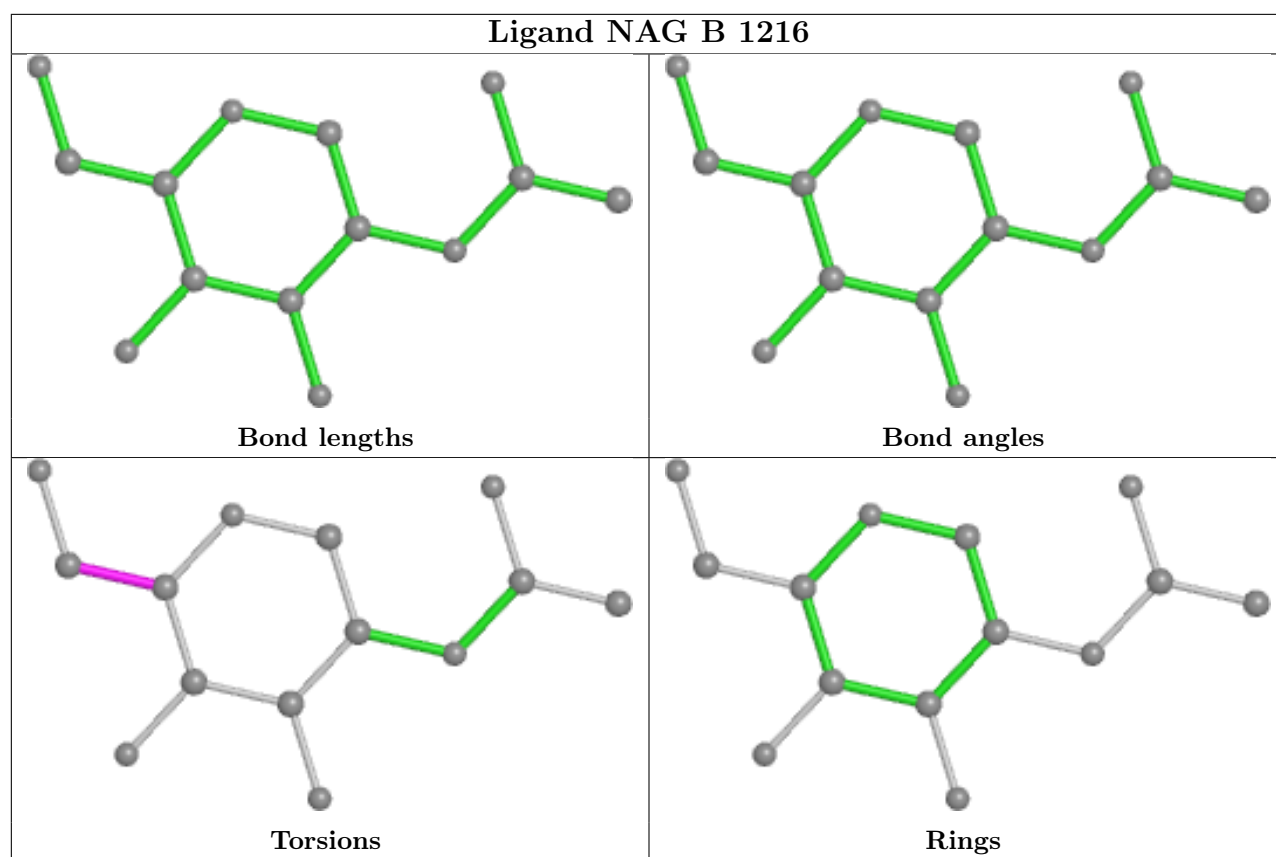
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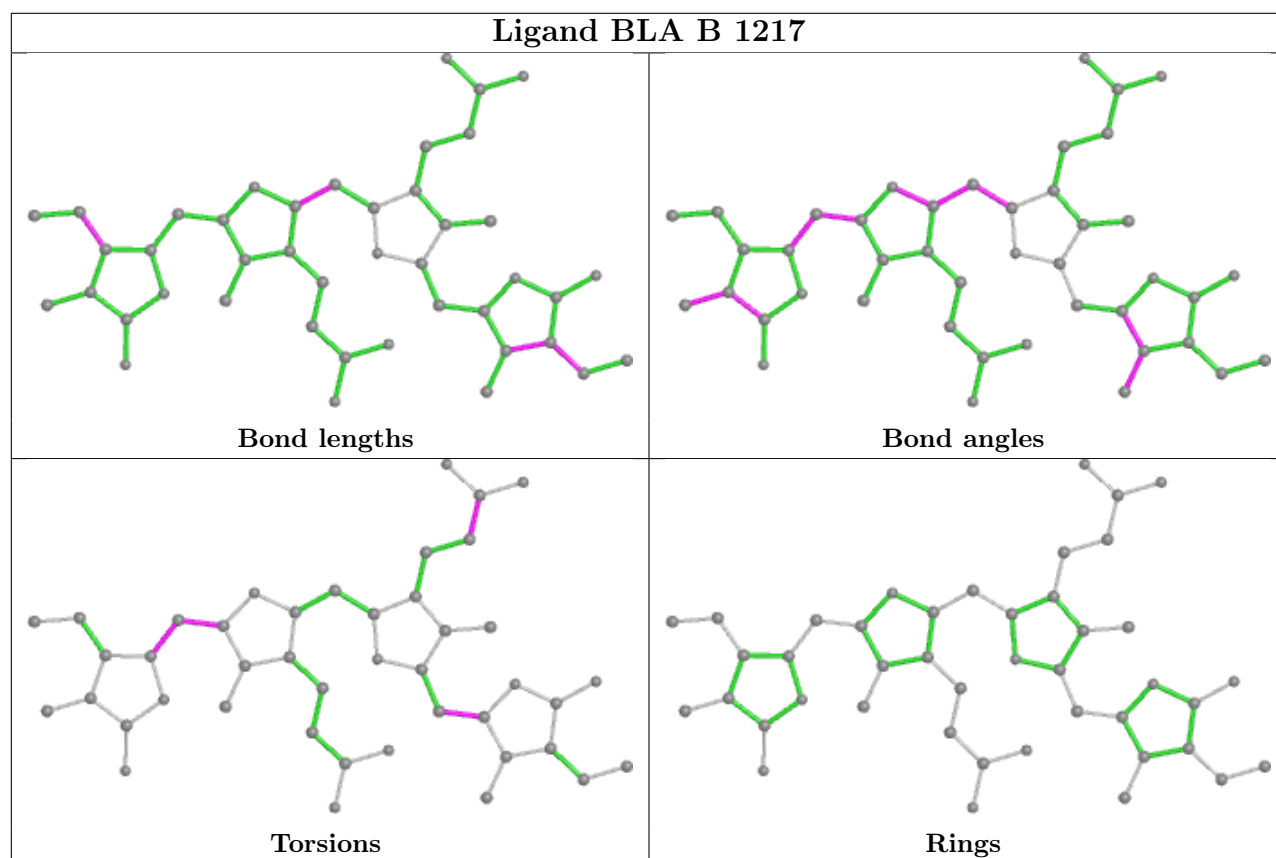
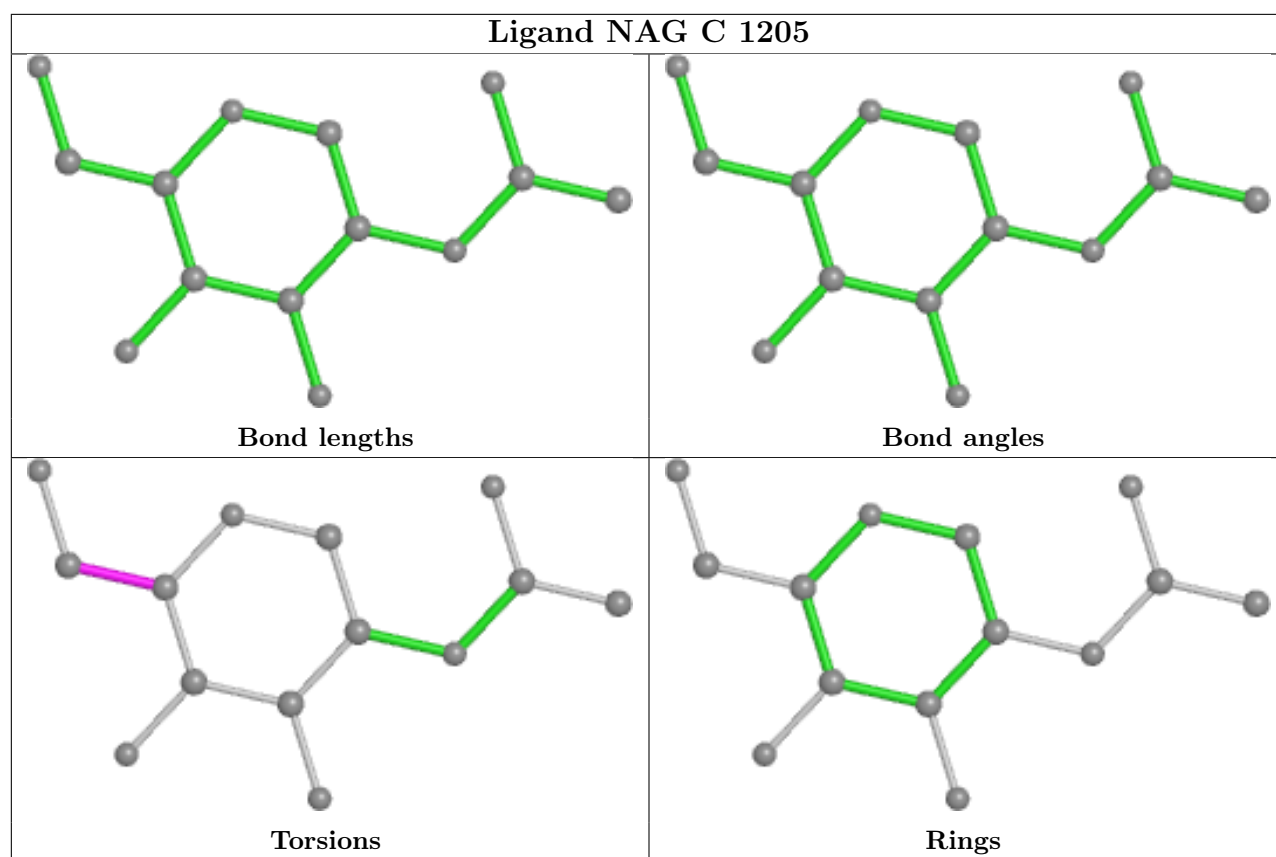
## Ligand NAG A 1215



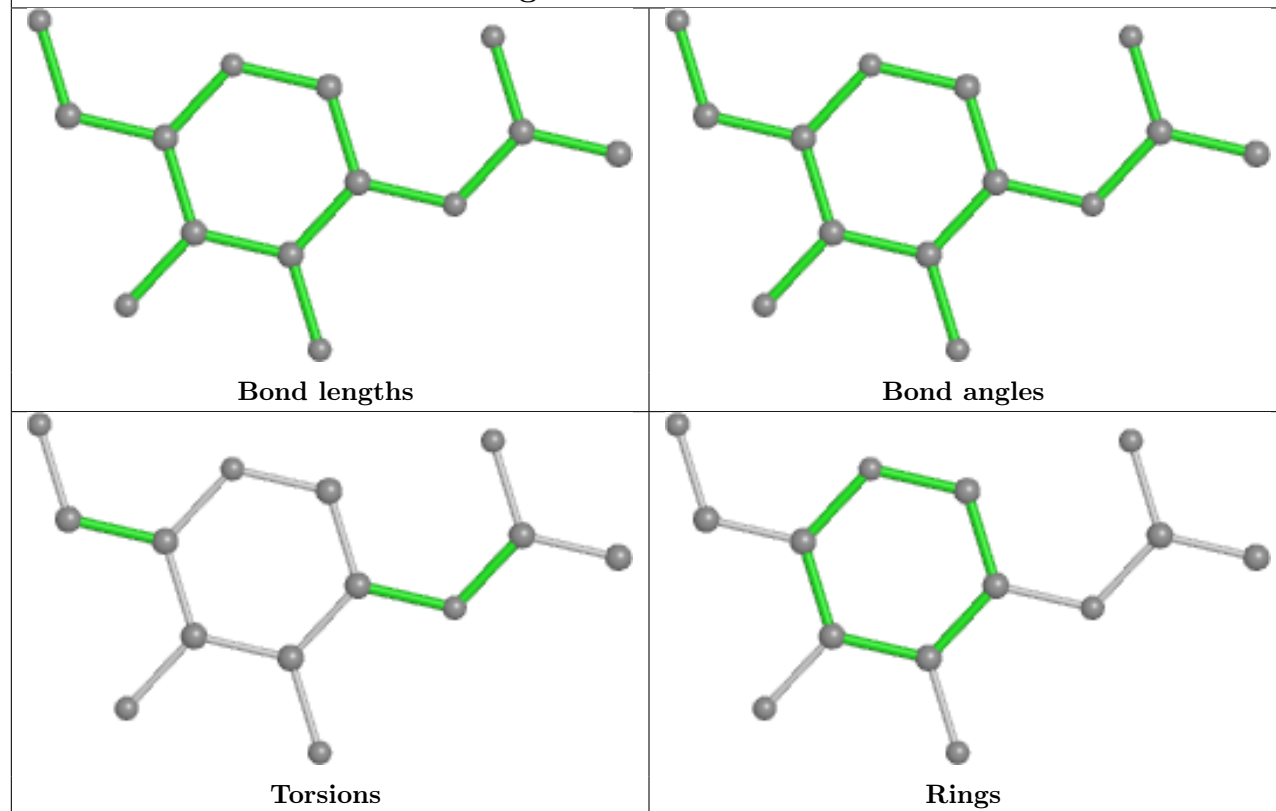




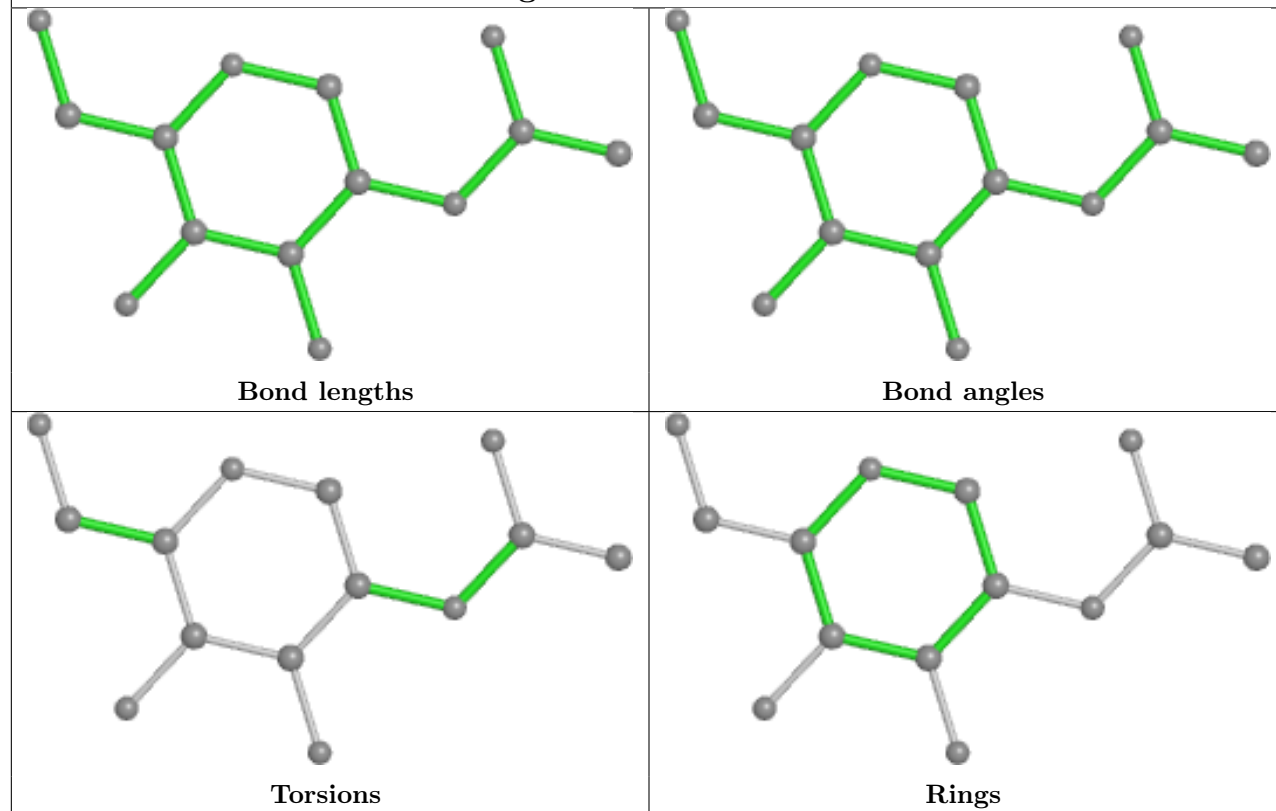




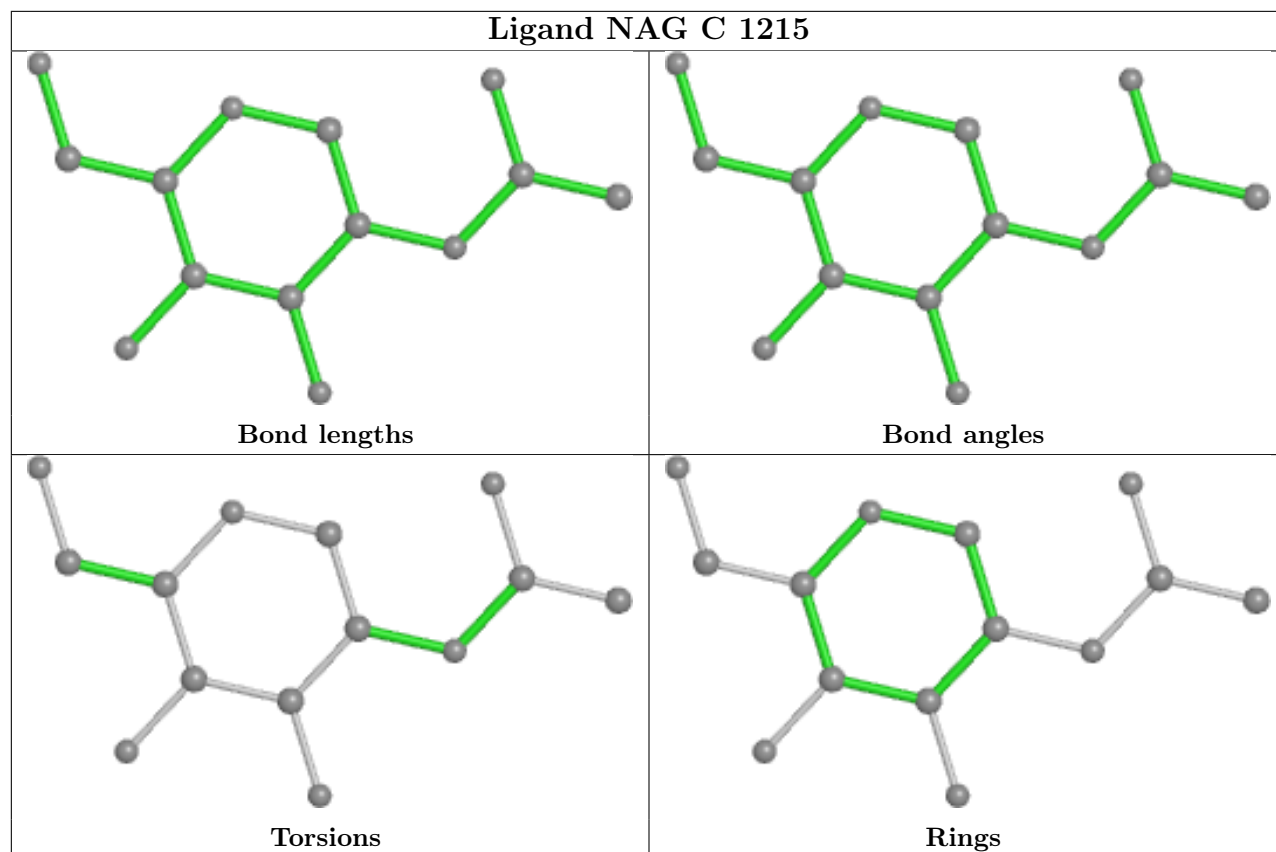
## Ligand NAG C 1202



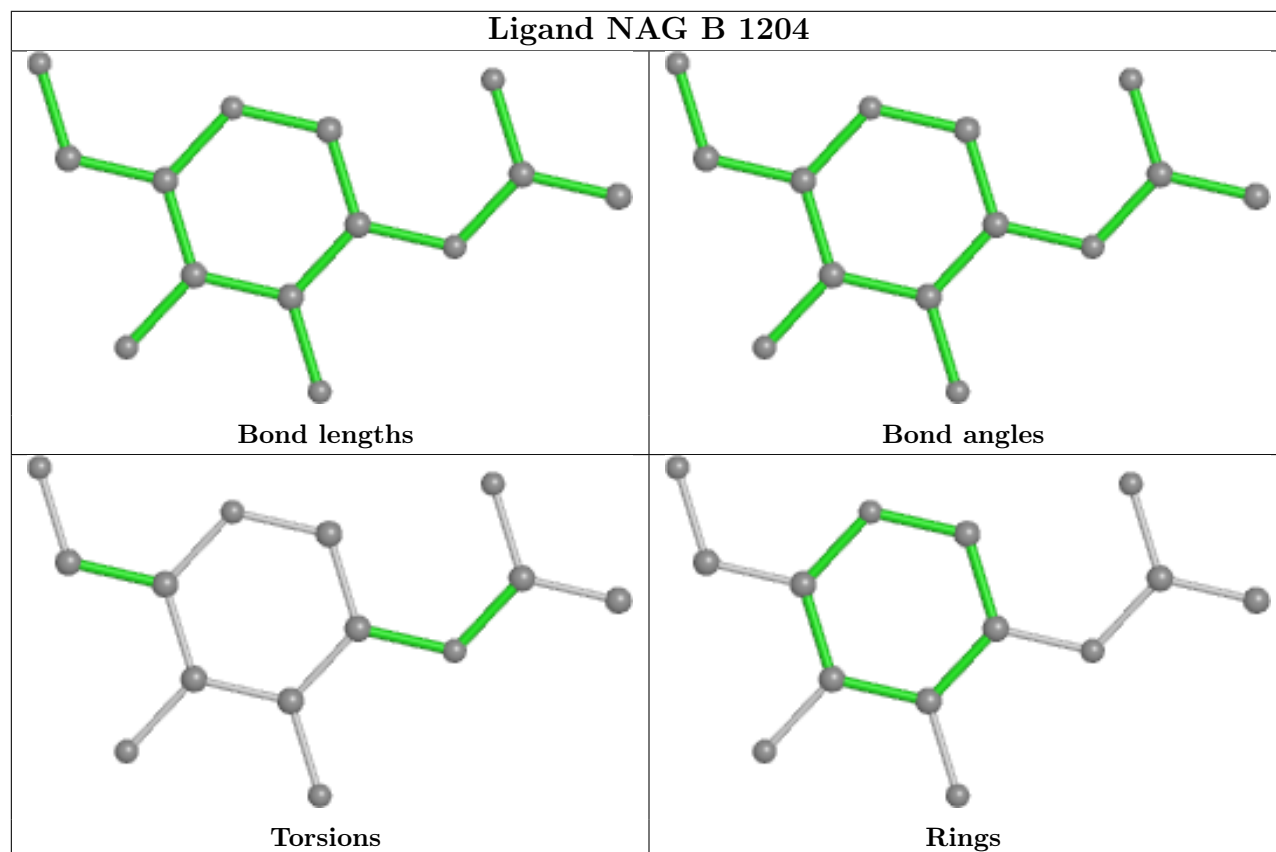
## Ligand NAG A 1206

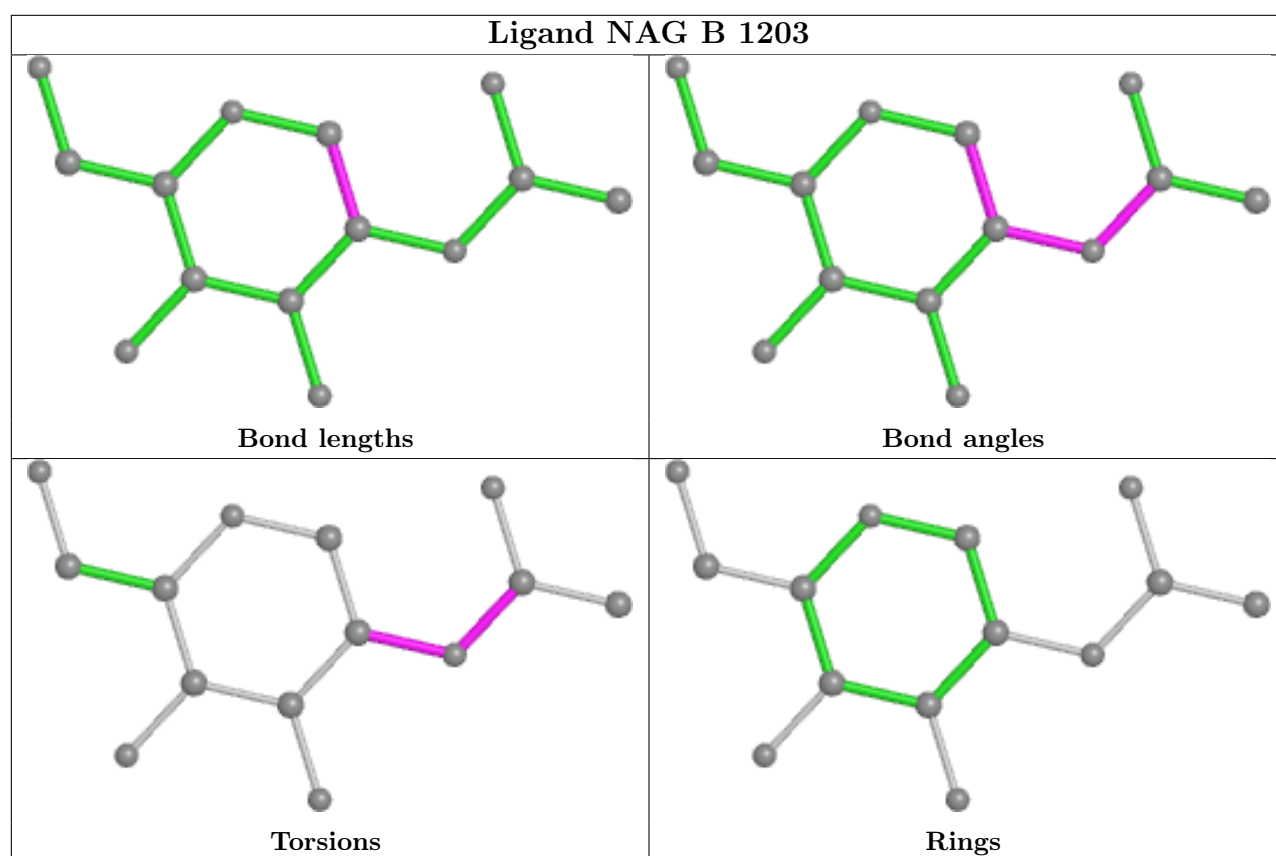
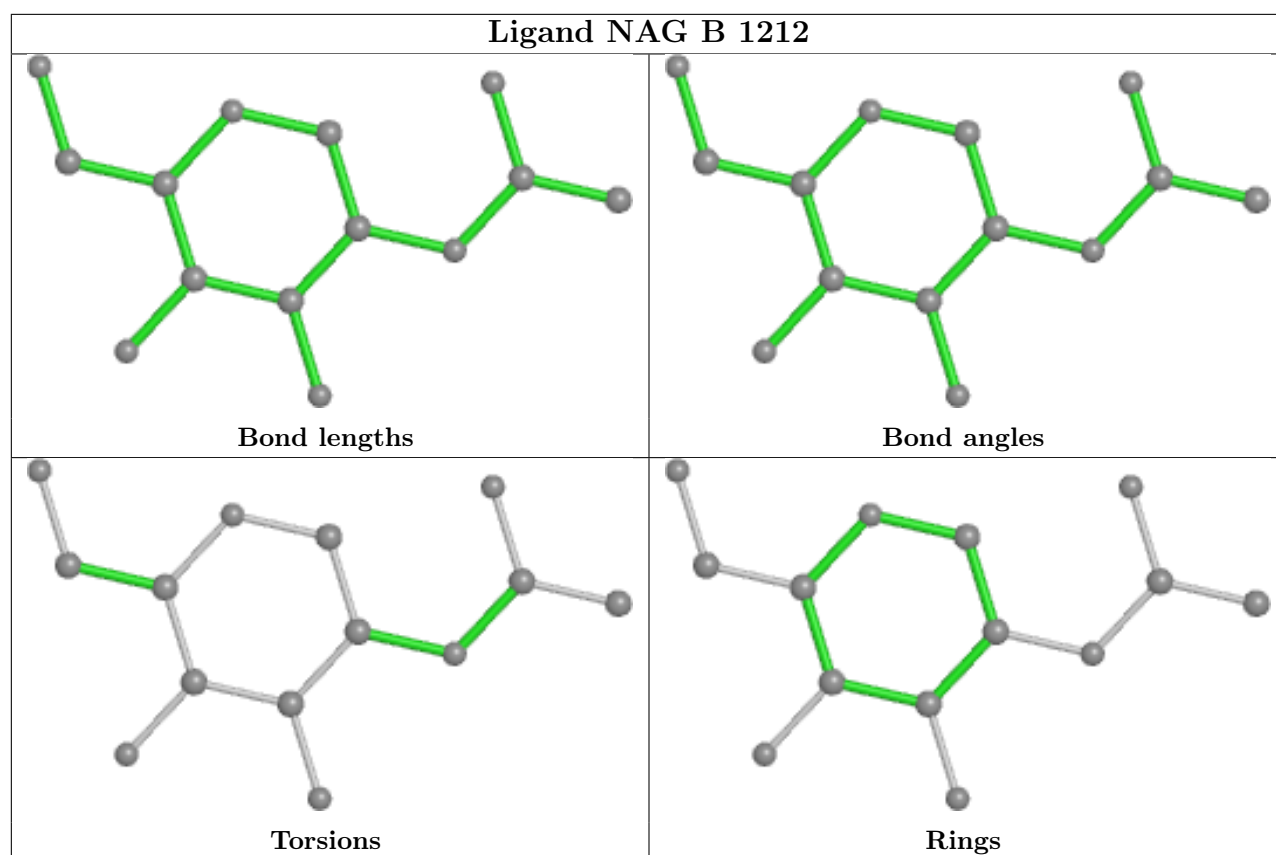


## Ligand NAG C 1215

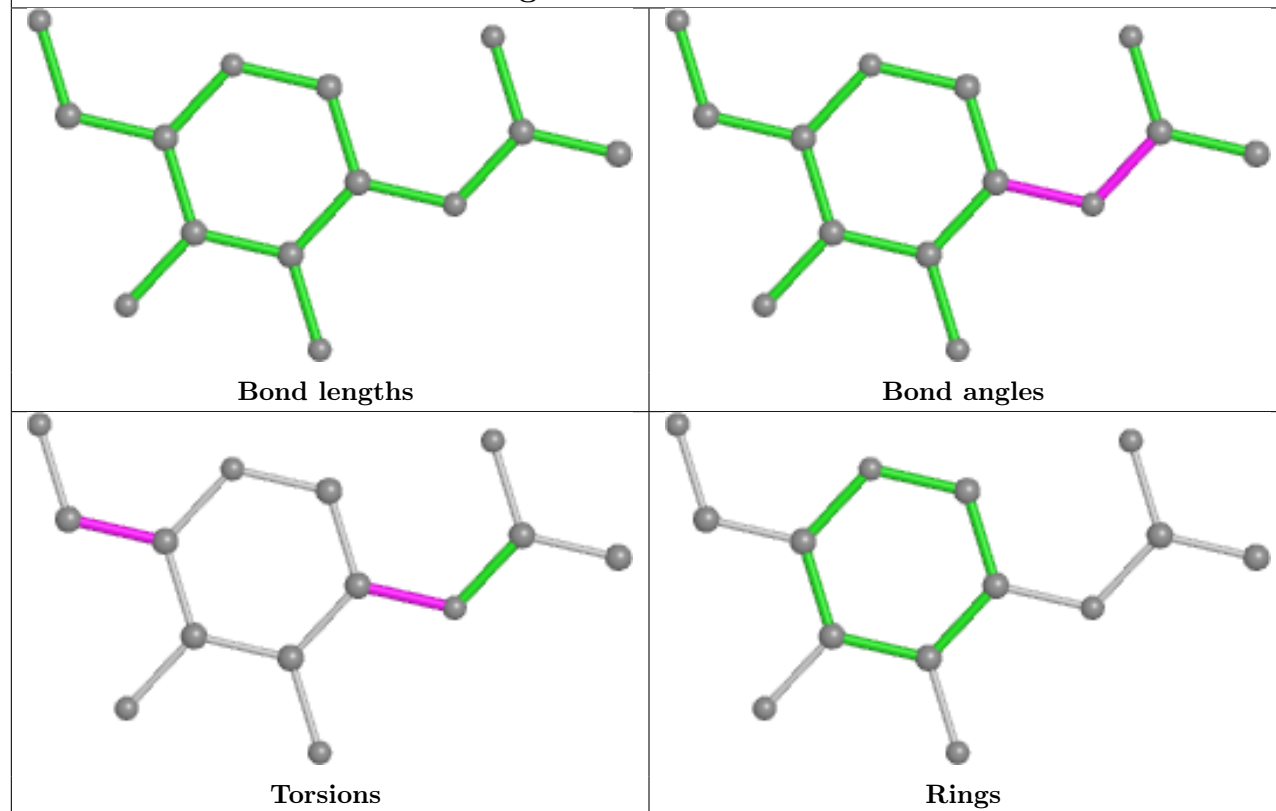


## Ligand NAG B 1204

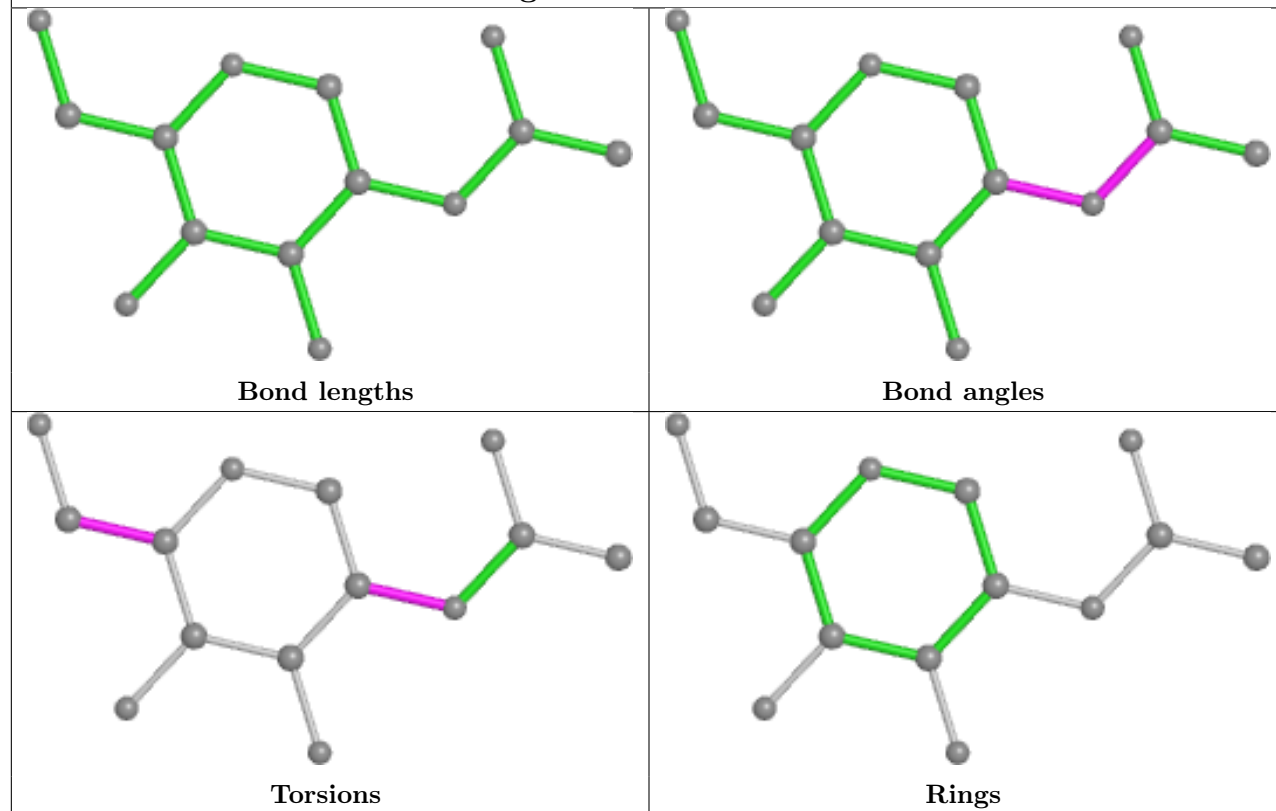


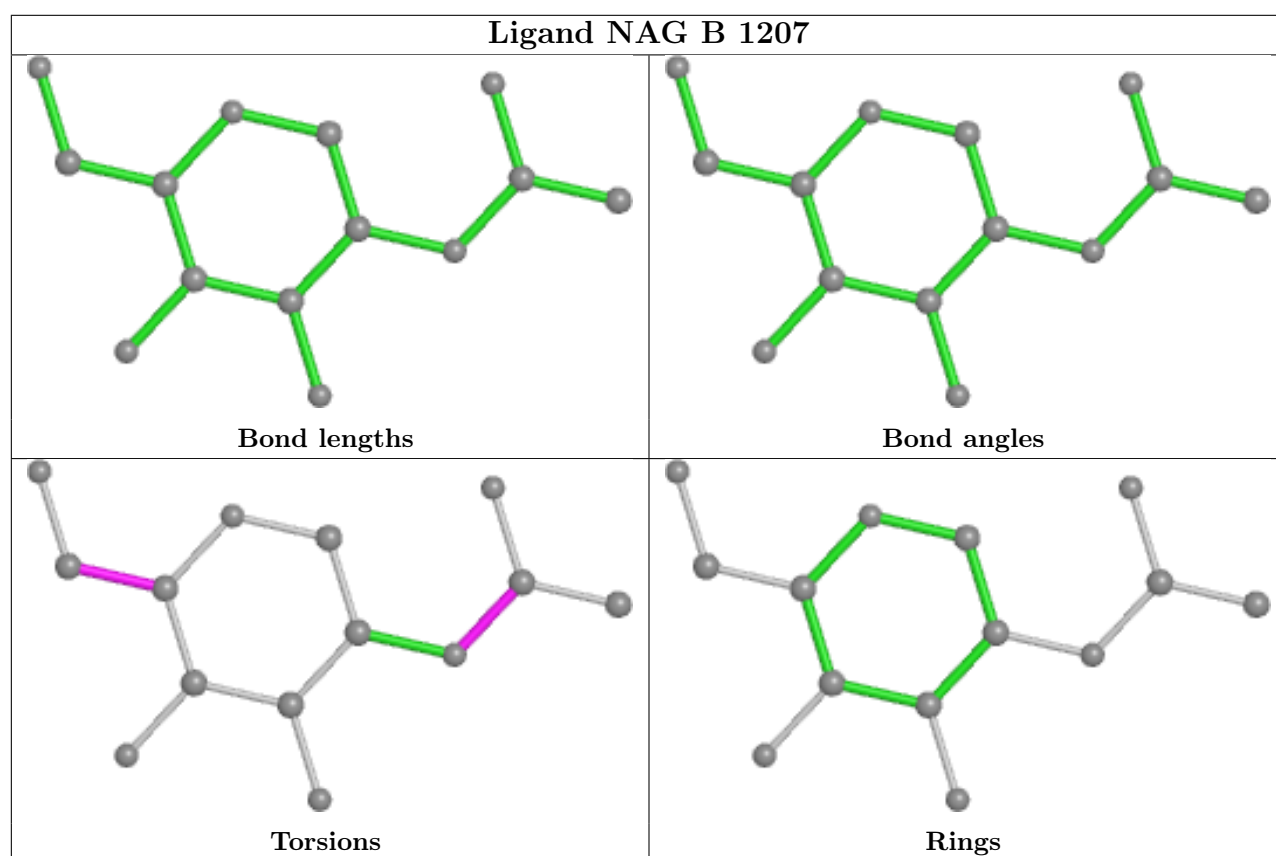
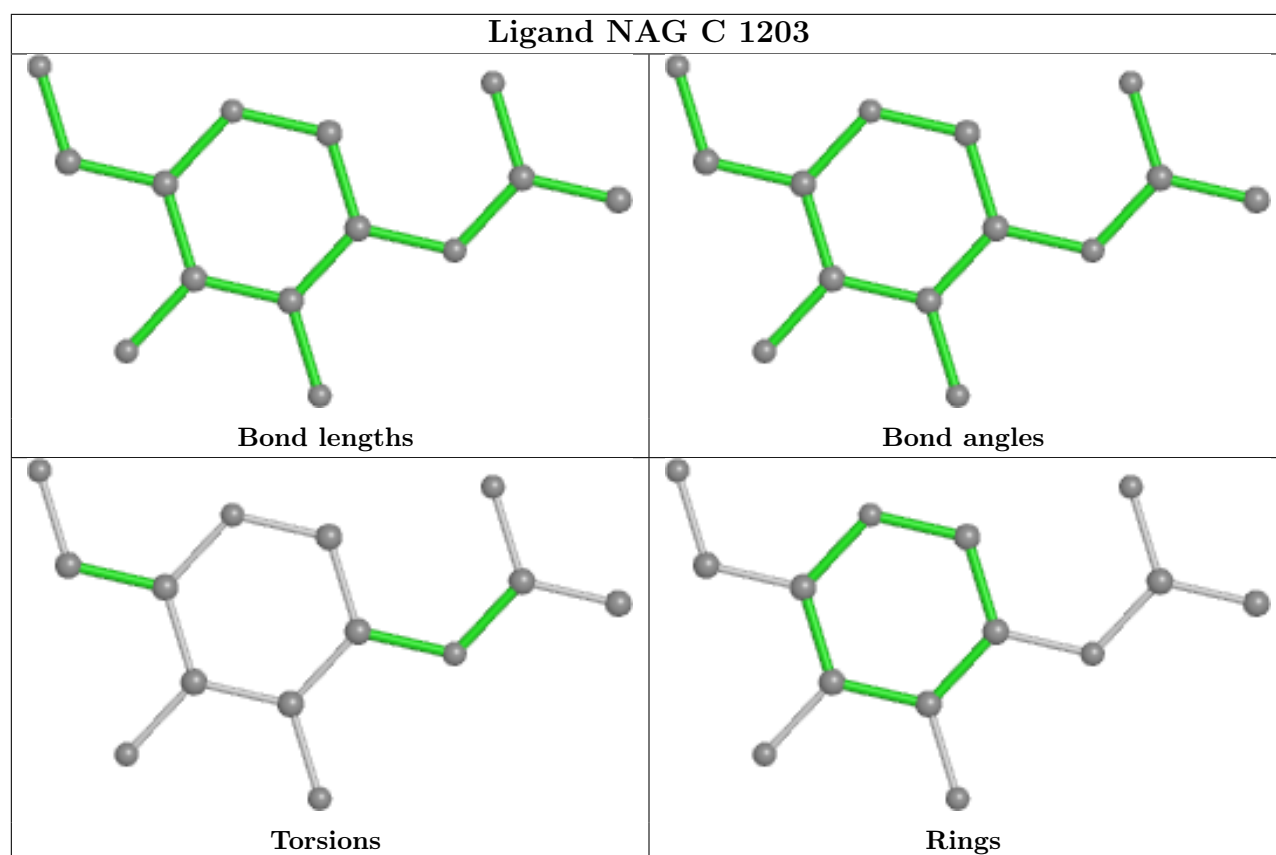


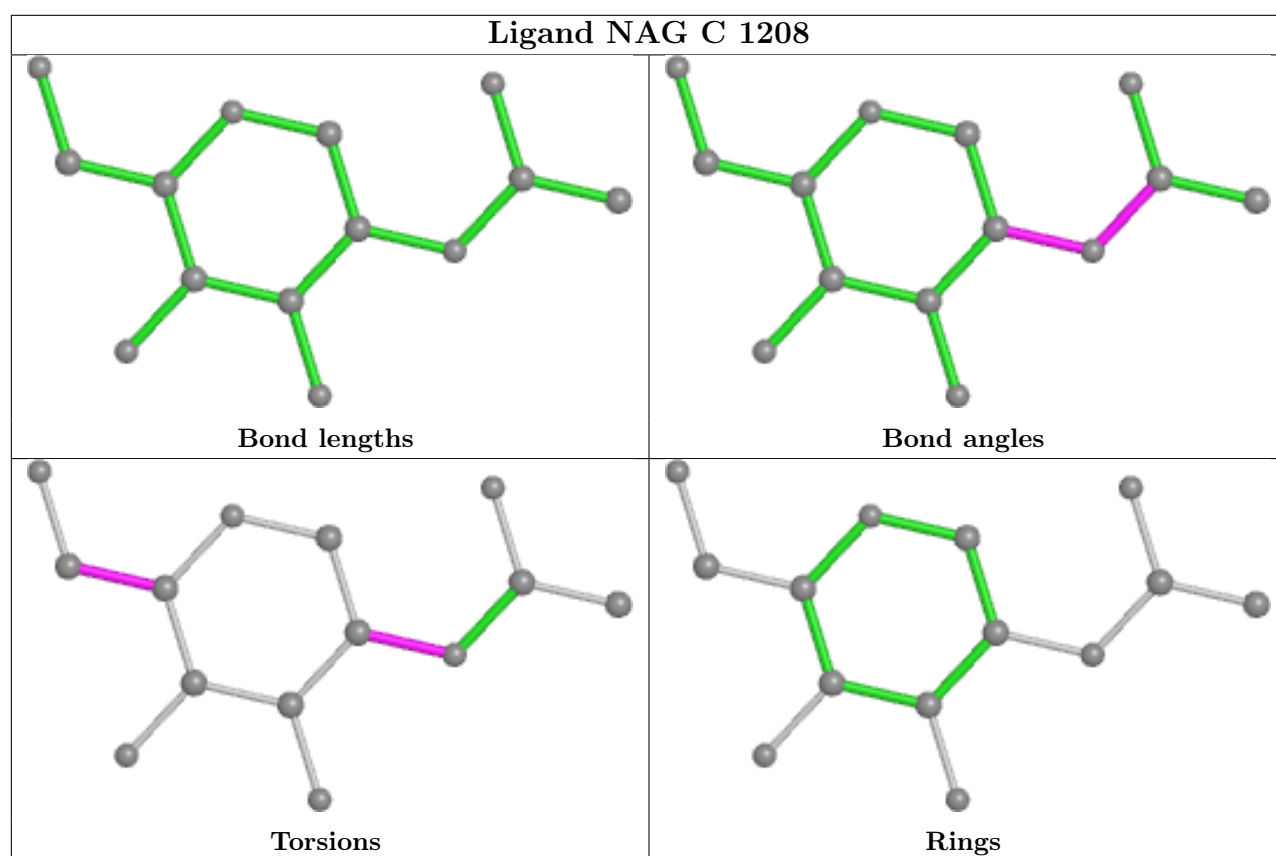
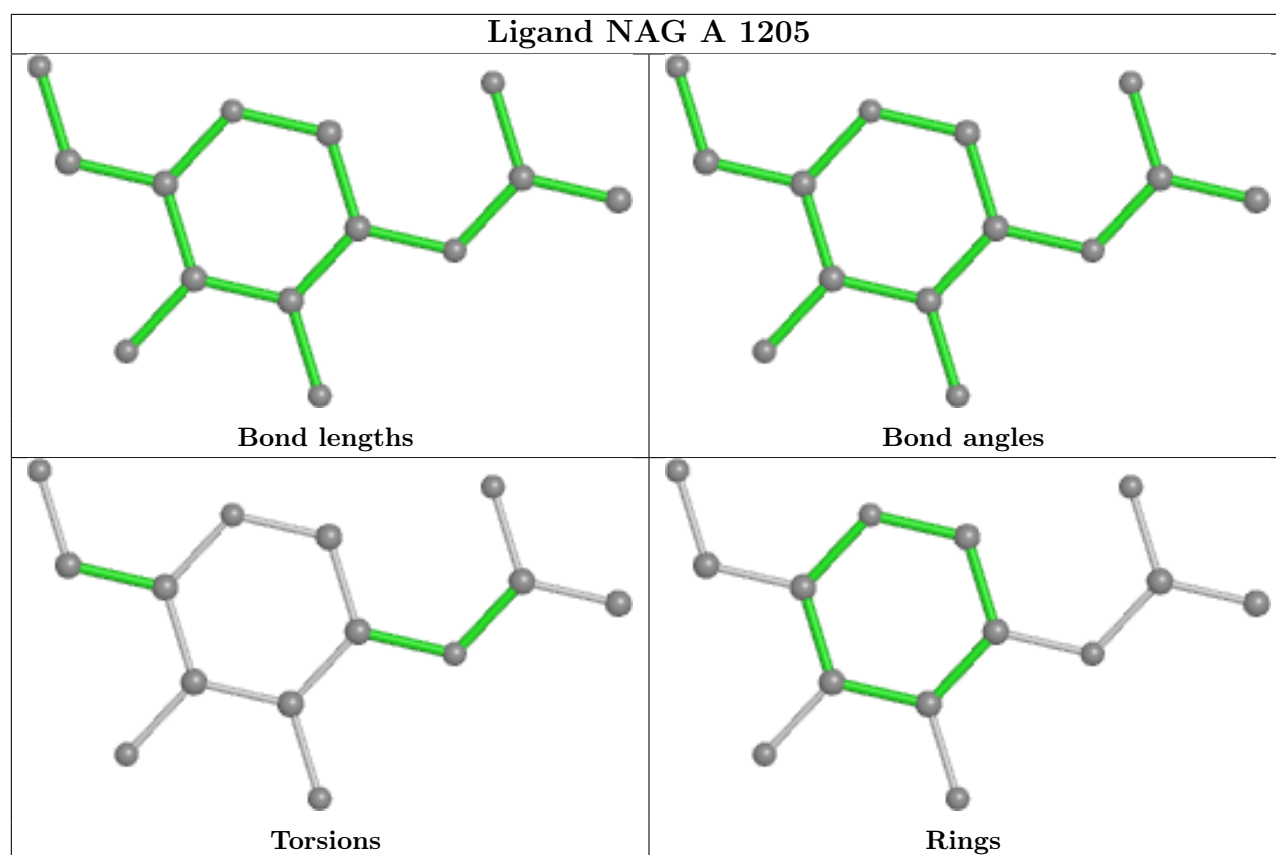
## Ligand NAG C 1218

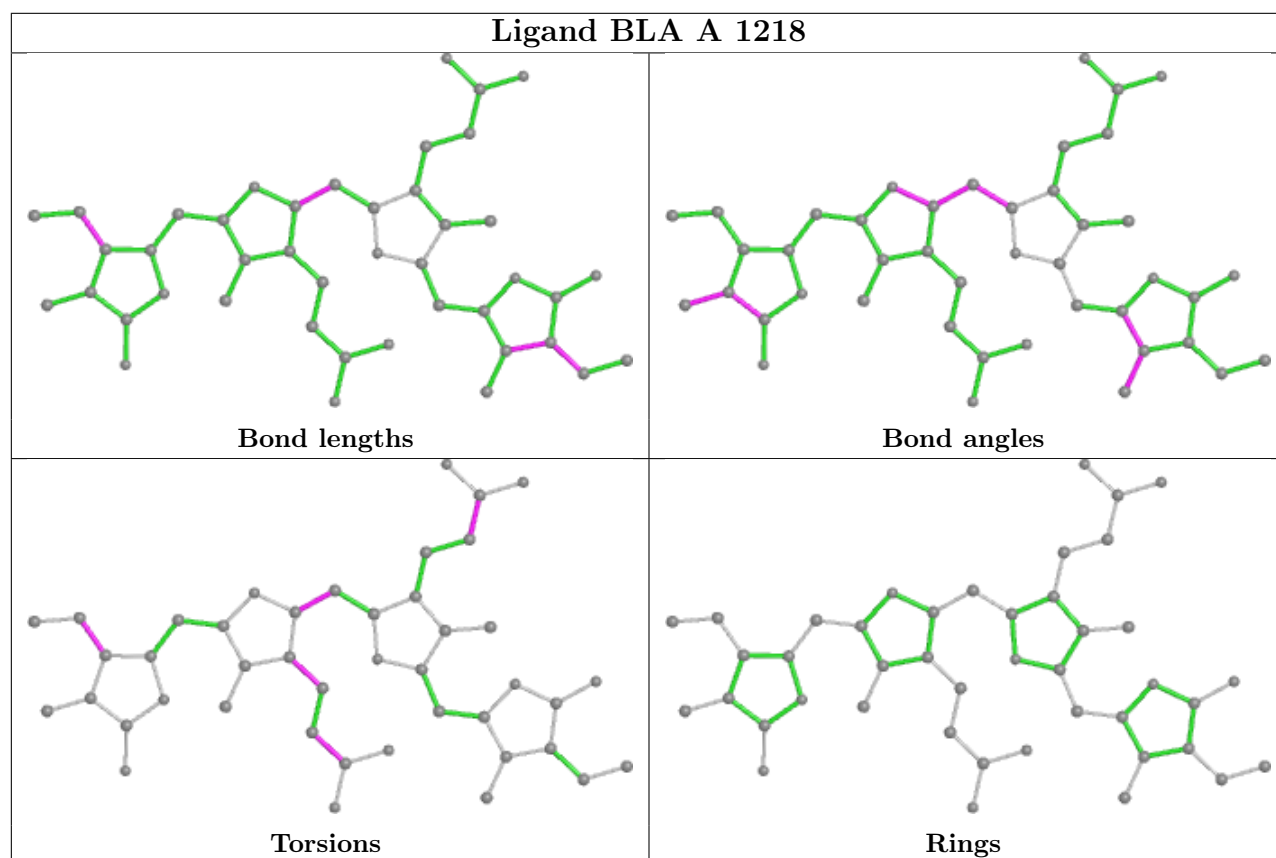
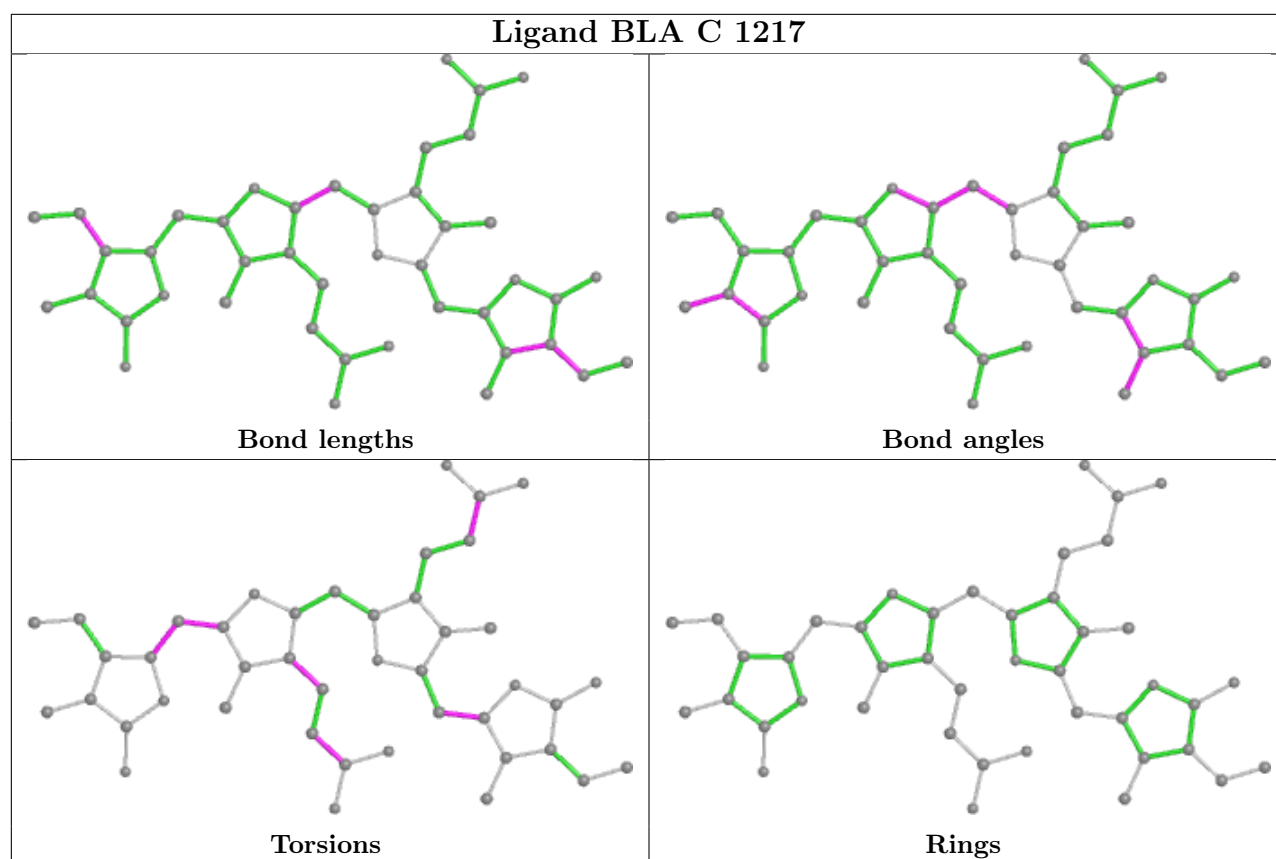


## Ligand NAG B 1213



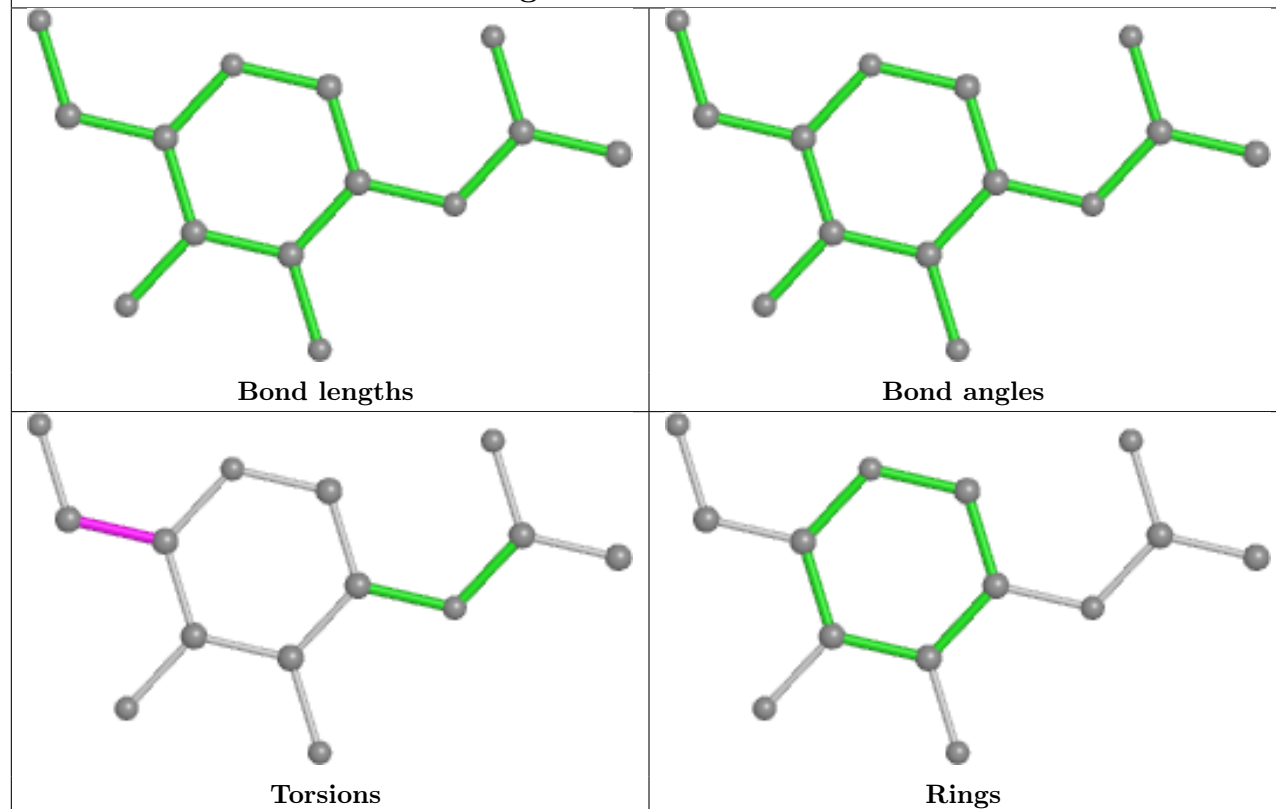




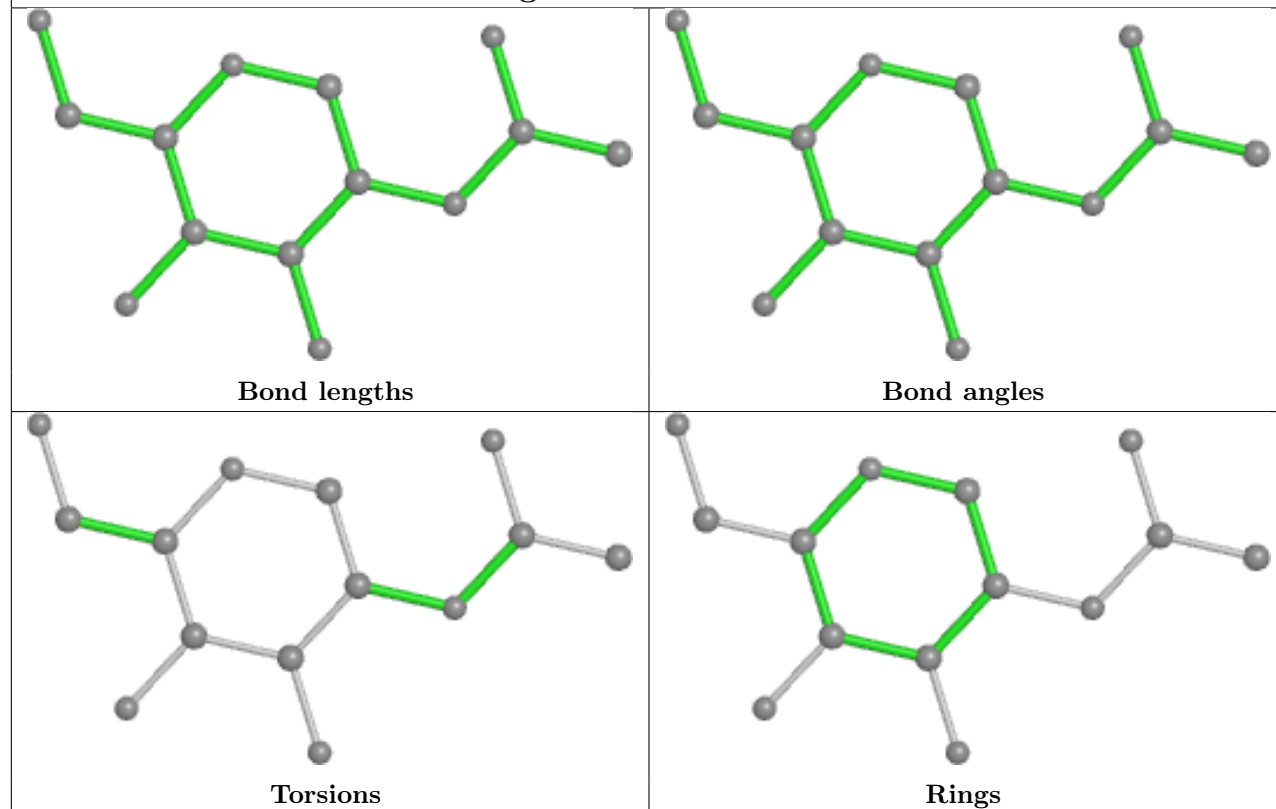


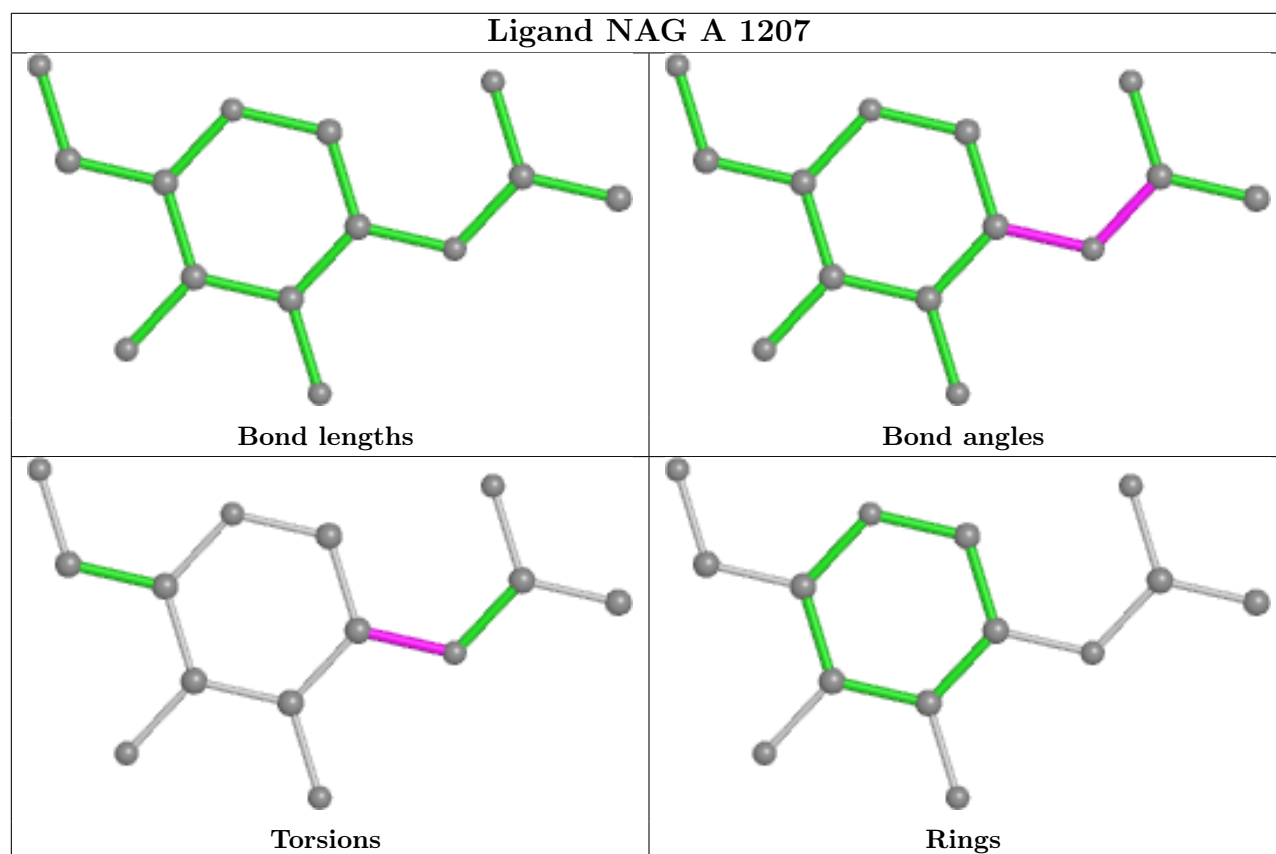
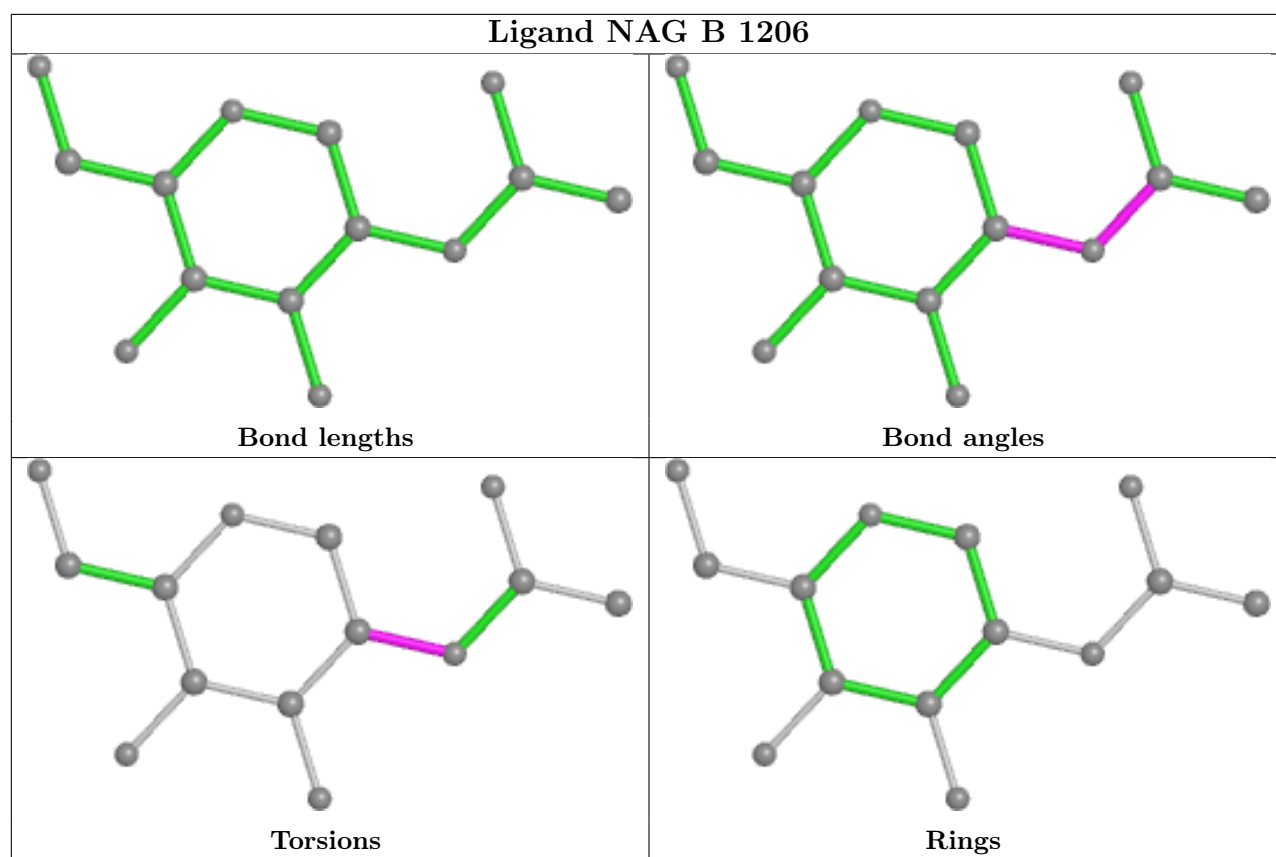


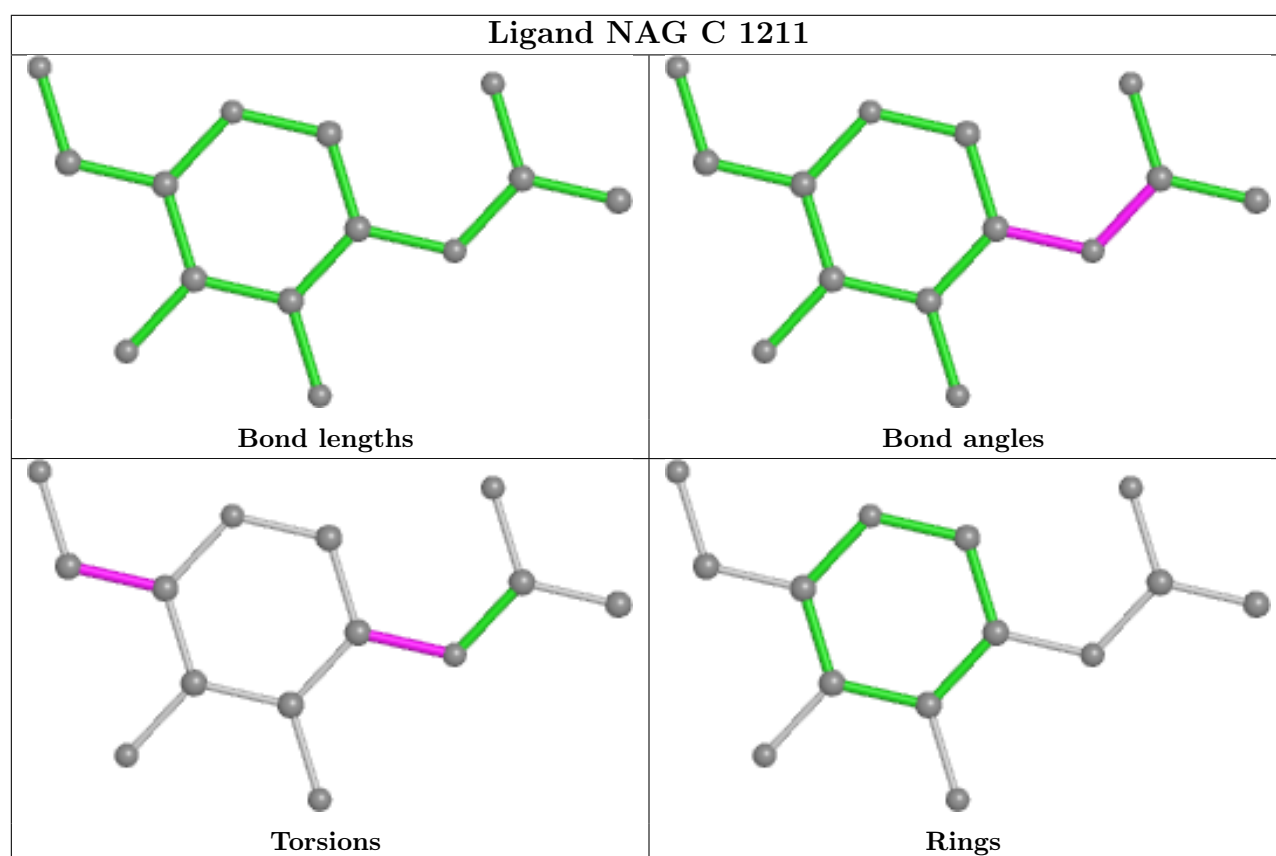
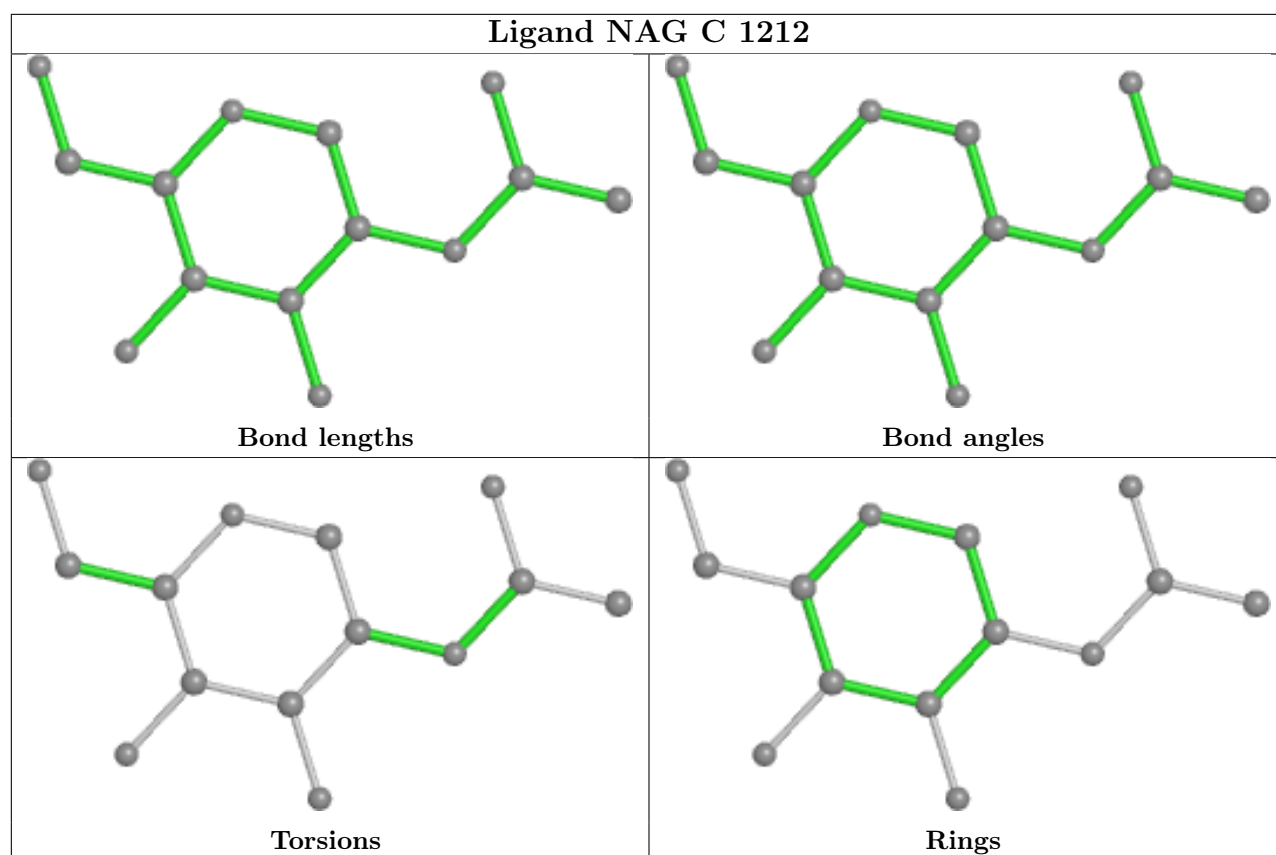
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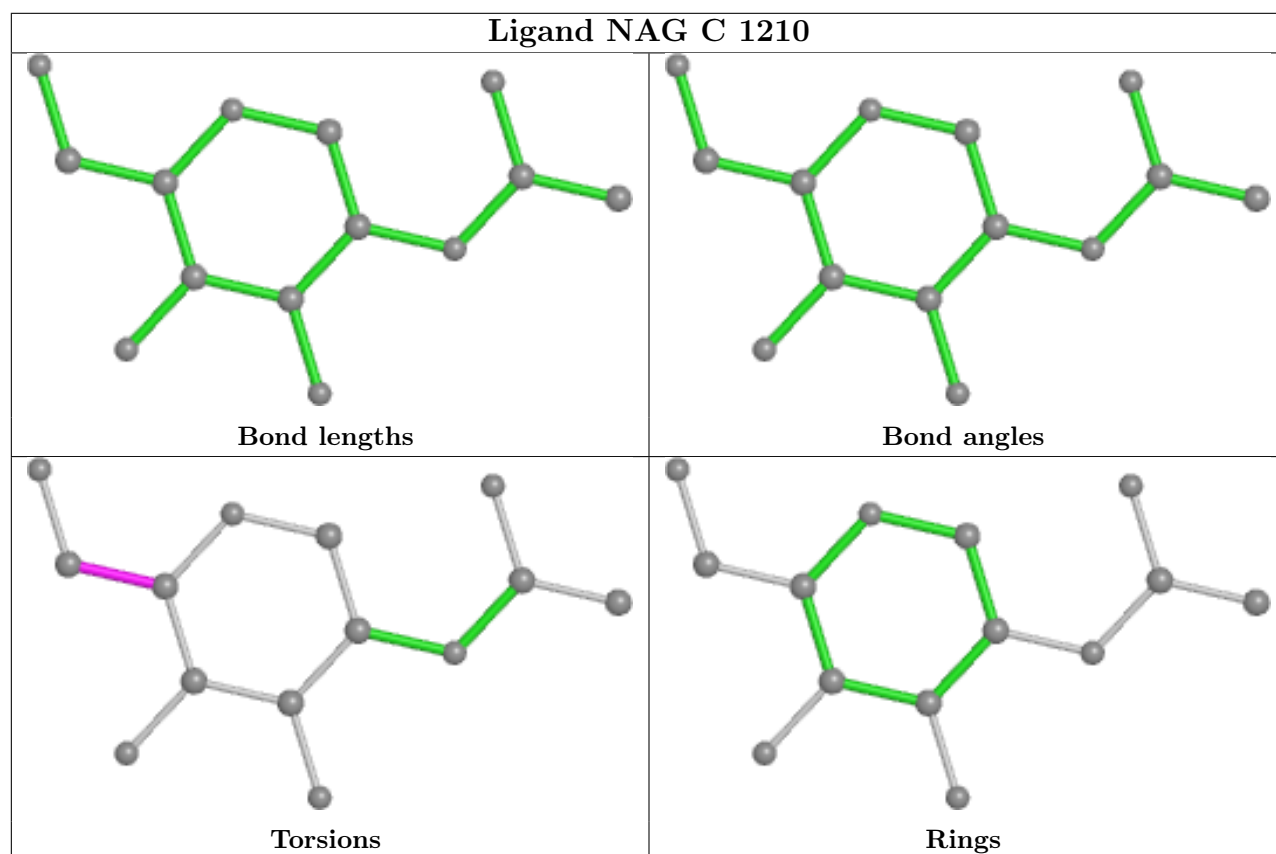
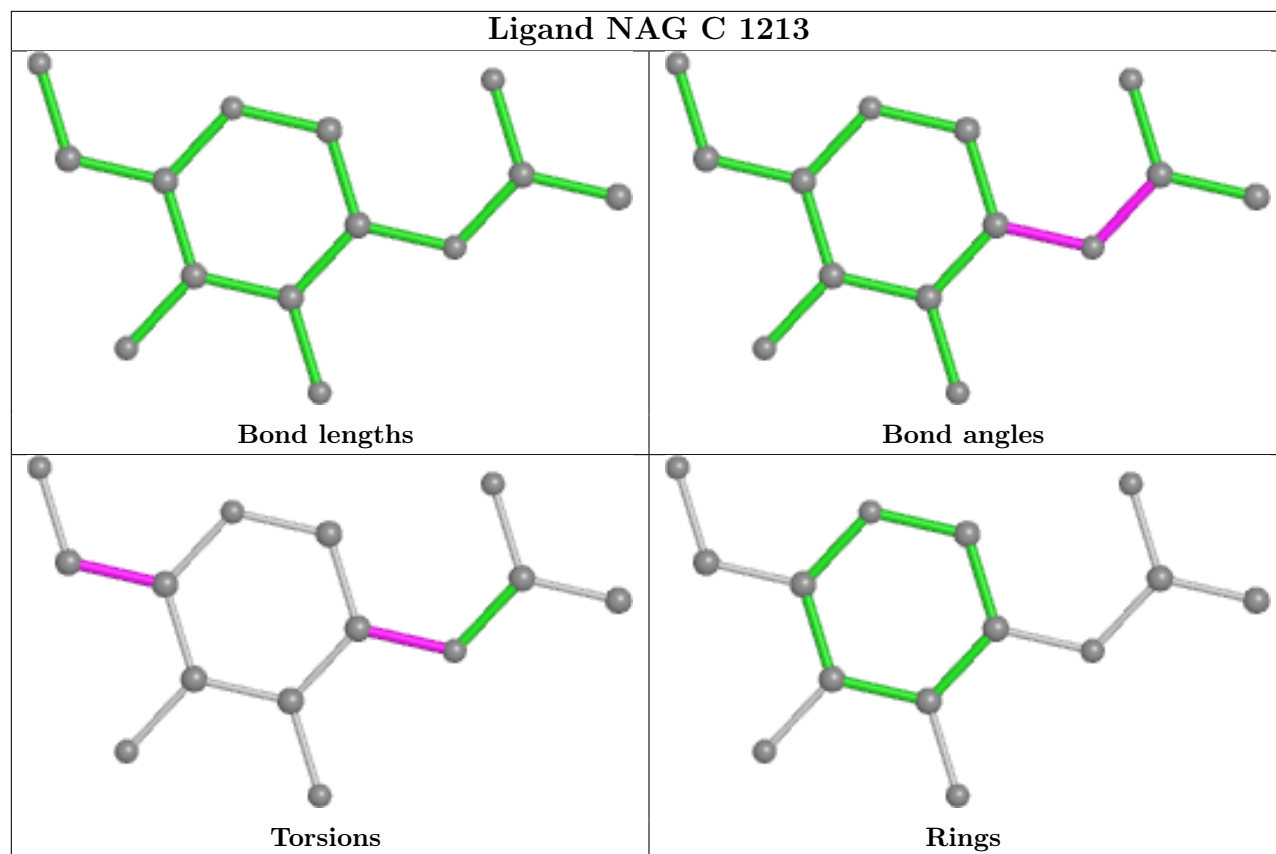


## Ligand NAG C 1204









## 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.