



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:51 AM UTC

PDB ID : 7MTZ / pdb_00007mtz
EMDB ID : EMD-24000
Title : Structure of the adeno-associated virus 9 capsid at pH pH 7.4 in complex with terminal galactose
Authors : Penzes, J.J.; Chipman, P.; Bhattacharya, N.; Zeher, A.; Huang, R.; McKenna, R.; Agbandje-McKenna, M.
Deposited on : 2021-05-14
Resolution : 2.43 Å (reported)
Based on initial model : 3UX1

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : **FAILED**
Mogul : 2022.3.0, CSD as543be (2022)
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.43 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 248580 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	518	4131	2608	718	791	14	0	0
1	B	518	4131	2608	718	791	14	0	0
1	C	518	4131	2608	718	791	14	0	0
1	D	518	4131	2608	718	791	14	0	0
1	E	518	4131	2608	718	791	14	0	0
1	F	518	4131	2608	718	791	14	0	0
1	G	518	4131	2608	718	791	14	0	0
1	H	518	4131	2608	718	791	14	0	0
1	I	518	4131	2608	718	791	14	0	0
1	J	518	4131	2608	718	791	14	0	0
1	K	518	4131	2608	718	791	14	0	0
1	L	518	4131	2608	718	791	14	0	0
1	M	518	4131	2608	718	791	14	0	0
1	N	518	4131	2608	718	791	14	0	0
1	O	518	4131	2608	718	791	14	0	0
1	P	518	4131	2608	718	791	14	0	0
1	Q	518	4131	2608	718	791	14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	S	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	T	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	U	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	V	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	W	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	X	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	Y	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	Z	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	1	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	2	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	3	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	4	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	5	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	6	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	a	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	b	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	c	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	d	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	e	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	f	518	Total 4131	C 2608	N 718	O 791	S 14	0	0

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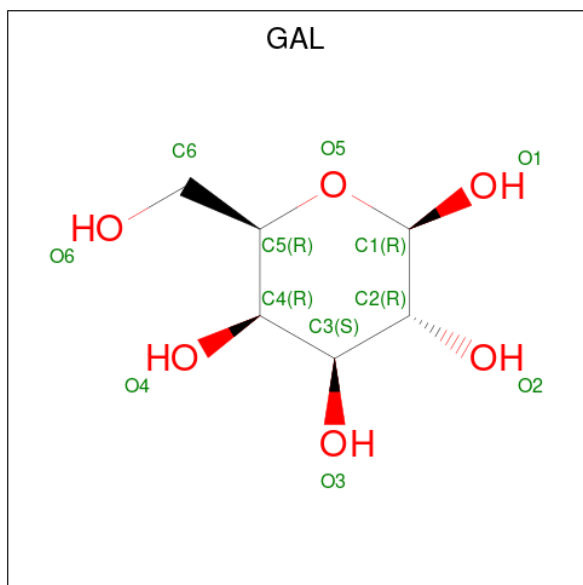
Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	h	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	i	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	j	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	k	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	l	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	m	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	n	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	o	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	p	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	q	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	r	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	s	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	t	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	u	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	v	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	w	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	x	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	y	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	z	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	7	518	Total 4131	C 2608	N 718	O 791	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	8	518	4131	2608	718	791	14	0	0

- Molecule 2 is beta-D-galactopyranose (CCD ID: GAL) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	A	1	12	6	6	0
2	B	1	12	6	6	0
2	C	1	12	6	6	0
2	D	1	12	6	6	0
2	E	1	12	6	6	0
2	F	1	12	6	6	0
2	G	1	12	6	6	0
2	H	1	12	6	6	0
2	I	1	12	6	6	0
2	J	1	12	6	6	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	K	1	12	6	6	0
2	L	1	12	6	6	0
2	M	1	12	6	6	0
2	N	1	12	6	6	0
2	O	1	12	6	6	0
2	P	1	12	6	6	0
2	Q	1	12	6	6	0
2	R	1	12	6	6	0
2	S	1	12	6	6	0
2	T	1	12	6	6	0
2	U	1	12	6	6	0
2	V	1	12	6	6	0
2	W	1	12	6	6	0
2	X	1	12	6	6	0
2	Y	1	12	6	6	0
2	Z	1	12	6	6	0
2	1	1	12	6	6	0
2	2	1	12	6	6	0
2	3	1	12	6	6	0
2	4	1	12	6	6	0
2	5	1	12	6	6	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	6	1	Total 12	C 6	O 6	0
2	a	1	Total 12	C 6	O 6	0
2	b	1	Total 12	C 6	O 6	0
2	c	1	Total 12	C 6	O 6	0
2	d	1	Total 12	C 6	O 6	0
2	e	1	Total 12	C 6	O 6	0
2	f	1	Total 12	C 6	O 6	0
2	g	1	Total 12	C 6	O 6	0
2	h	1	Total 12	C 6	O 6	0
2	i	1	Total 12	C 6	O 6	0
2	j	1	Total 12	C 6	O 6	0
2	k	1	Total 12	C 6	O 6	0
2	l	1	Total 12	C 6	O 6	0
2	m	1	Total 12	C 6	O 6	0
2	n	1	Total 12	C 6	O 6	0
2	o	1	Total 12	C 6	O 6	0
2	p	1	Total 12	C 6	O 6	0
2	q	1	Total 12	C 6	O 6	0
2	r	1	Total 12	C 6	O 6	0
2	s	1	Total 12	C 6	O 6	0
2	t	1	Total 12	C 6	O 6	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	u	1	12	6	6	0
2	v	1	12	6	6	0
2	w	1	12	6	6	0
2	x	1	12	6	6	0
2	y	1	12	6	6	0
2	z	1	12	6	6	0
2	7	1	12	6	6	0
2	8	1	12	6	6	0

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56370	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

60 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
2	GAL	j	801	-	12,12,12	0.53	0	17,17,17	0.87	0
2	GAL	I	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	C	801	-	12,12,12	0.53	0	17,17,17	0.87	0
2	GAL	5	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	B	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	h	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	F	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	A	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	W	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	n	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	R	801	-	12,12,12	0.53	0	17,17,17	0.87	0
2	GAL	g	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	K	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	m	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	L	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	8	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	k	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	o	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	J	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	w	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	3	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	2	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	Q	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	V	801	-	12,12,12	0.53	0	17,17,17	0.87	0
2	GAL	l	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	a	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	p	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	X	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	6	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	d	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	P	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	q	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	i	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	Y	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	e	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	G	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	H	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	x	801	-	12,12,12	0.53	0	17,17,17	0.87	0
2	GAL	D	801	-	12,12,12	0.52	0	17,17,17	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GAL	M	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	N	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	1	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	T	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	4	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	u	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	v	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	c	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	s	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	O	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	f	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	E	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	7	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	U	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	b	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	z	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	r	801	-	12,12,12	0.52	0	17,17,17	0.87	0
2	GAL	t	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	S	801	-	12,12,12	0.52	0	17,17,17	0.86	0
2	GAL	Z	801	-	12,12,12	0.53	0	17,17,17	0.86	0
2	GAL	y	801	-	12,12,12	0.52	0	17,17,17	0.86	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GAL	j	801	-	-	1/2/22/22	0/1/1/1
2	GAL	I	801	-	-	1/2/22/22	0/1/1/1
2	GAL	C	801	-	-	1/2/22/22	0/1/1/1
2	GAL	5	801	-	-	1/2/22/22	0/1/1/1
2	GAL	B	801	-	-	1/2/22/22	0/1/1/1
2	GAL	h	801	-	-	1/2/22/22	0/1/1/1
2	GAL	F	801	-	-	1/2/22/22	0/1/1/1
2	GAL	A	801	-	-	1/2/22/22	0/1/1/1
2	GAL	W	801	-	-	1/2/22/22	0/1/1/1
2	GAL	n	801	-	-	1/2/22/22	0/1/1/1
2	GAL	R	801	-	-	1/2/22/22	0/1/1/1
2	GAL	g	801	-	-	1/2/22/22	0/1/1/1
2	GAL	K	801	-	-	1/2/22/22	0/1/1/1
2	GAL	m	801	-	-	1/2/22/22	0/1/1/1
2	GAL	L	801	-	-	1/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GAL	8	801	-	-	1/2/22/22	0/1/1/1
2	GAL	k	801	-	-	1/2/22/22	0/1/1/1
2	GAL	o	801	-	-	1/2/22/22	0/1/1/1
2	GAL	J	801	-	-	1/2/22/22	0/1/1/1
2	GAL	w	801	-	-	1/2/22/22	0/1/1/1
2	GAL	3	801	-	-	1/2/22/22	0/1/1/1
2	GAL	2	801	-	-	1/2/22/22	0/1/1/1
2	GAL	Q	801	-	-	1/2/22/22	0/1/1/1
2	GAL	V	801	-	-	1/2/22/22	0/1/1/1
2	GAL	l	801	-	-	1/2/22/22	0/1/1/1
2	GAL	a	801	-	-	1/2/22/22	0/1/1/1
2	GAL	p	801	-	-	1/2/22/22	0/1/1/1
2	GAL	X	801	-	-	1/2/22/22	0/1/1/1
2	GAL	6	801	-	-	1/2/22/22	0/1/1/1
2	GAL	d	801	-	-	1/2/22/22	0/1/1/1
2	GAL	P	801	-	-	1/2/22/22	0/1/1/1
2	GAL	q	801	-	-	1/2/22/22	0/1/1/1
2	GAL	i	801	-	-	1/2/22/22	0/1/1/1
2	GAL	Y	801	-	-	1/2/22/22	0/1/1/1
2	GAL	e	801	-	-	1/2/22/22	0/1/1/1
2	GAL	G	801	-	-	1/2/22/22	0/1/1/1
2	GAL	H	801	-	-	1/2/22/22	0/1/1/1
2	GAL	x	801	-	-	1/2/22/22	0/1/1/1
2	GAL	D	801	-	-	1/2/22/22	0/1/1/1
2	GAL	M	801	-	-	1/2/22/22	0/1/1/1
2	GAL	N	801	-	-	1/2/22/22	0/1/1/1
2	GAL	1	801	-	-	1/2/22/22	0/1/1/1
2	GAL	T	801	-	-	1/2/22/22	0/1/1/1
2	GAL	4	801	-	-	1/2/22/22	0/1/1/1
2	GAL	u	801	-	-	1/2/22/22	0/1/1/1
2	GAL	v	801	-	-	1/2/22/22	0/1/1/1
2	GAL	c	801	-	-	1/2/22/22	0/1/1/1
2	GAL	s	801	-	-	1/2/22/22	0/1/1/1
2	GAL	O	801	-	-	1/2/22/22	0/1/1/1
2	GAL	f	801	-	-	1/2/22/22	0/1/1/1
2	GAL	E	801	-	-	1/2/22/22	0/1/1/1
2	GAL	7	801	-	-	1/2/22/22	0/1/1/1
2	GAL	U	801	-	-	1/2/22/22	0/1/1/1
2	GAL	b	801	-	-	1/2/22/22	0/1/1/1
2	GAL	z	801	-	-	1/2/22/22	0/1/1/1
2	GAL	r	801	-	-	1/2/22/22	0/1/1/1
2	GAL	t	801	-	-	1/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GAL	S	801	-	-	1/2/22/22	0/1/1/1
2	GAL	Z	801	-	-	1/2/22/22	0/1/1/1
2	GAL	y	801	-	-	1/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

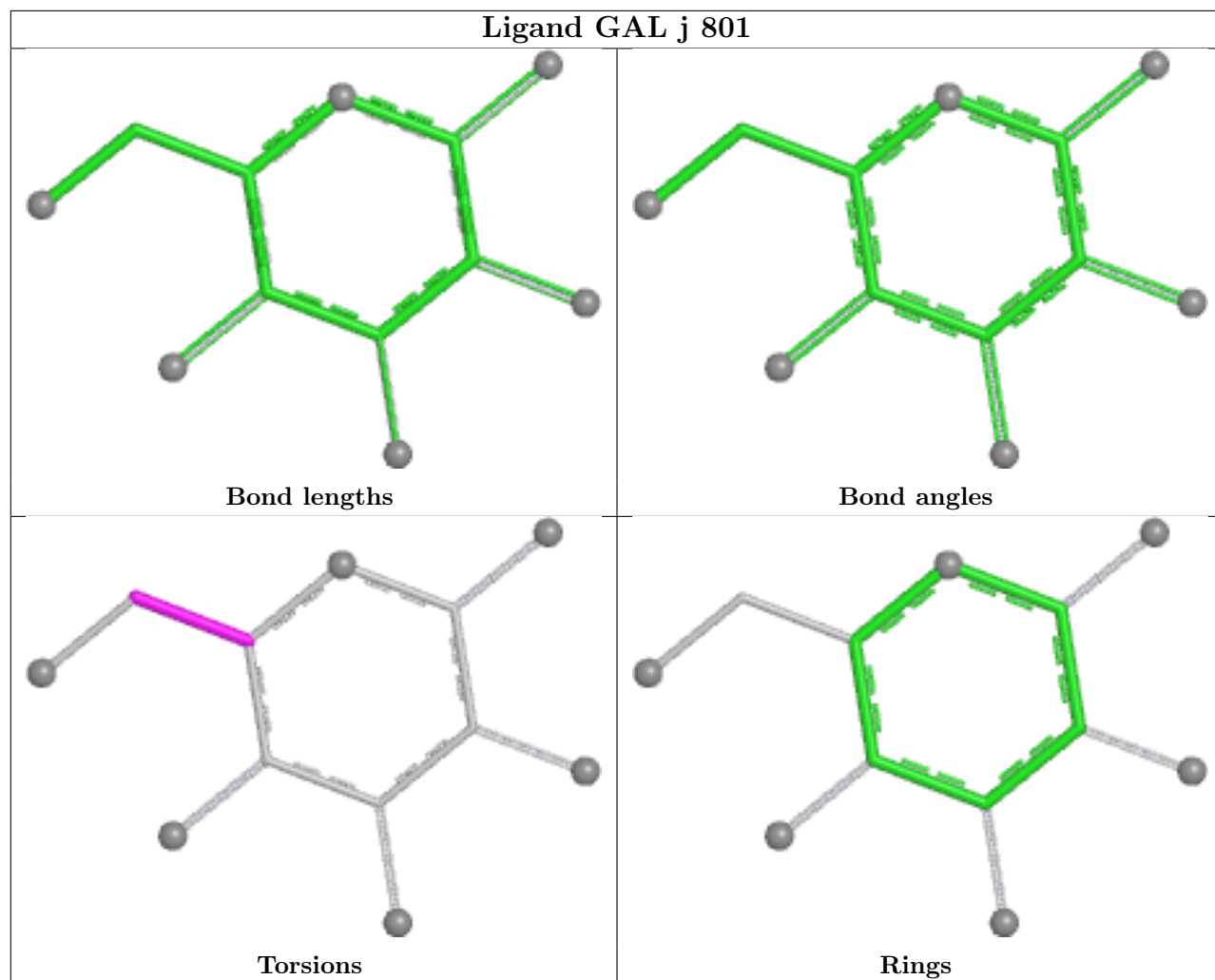
5 of 60 torsion outliers are listed below:

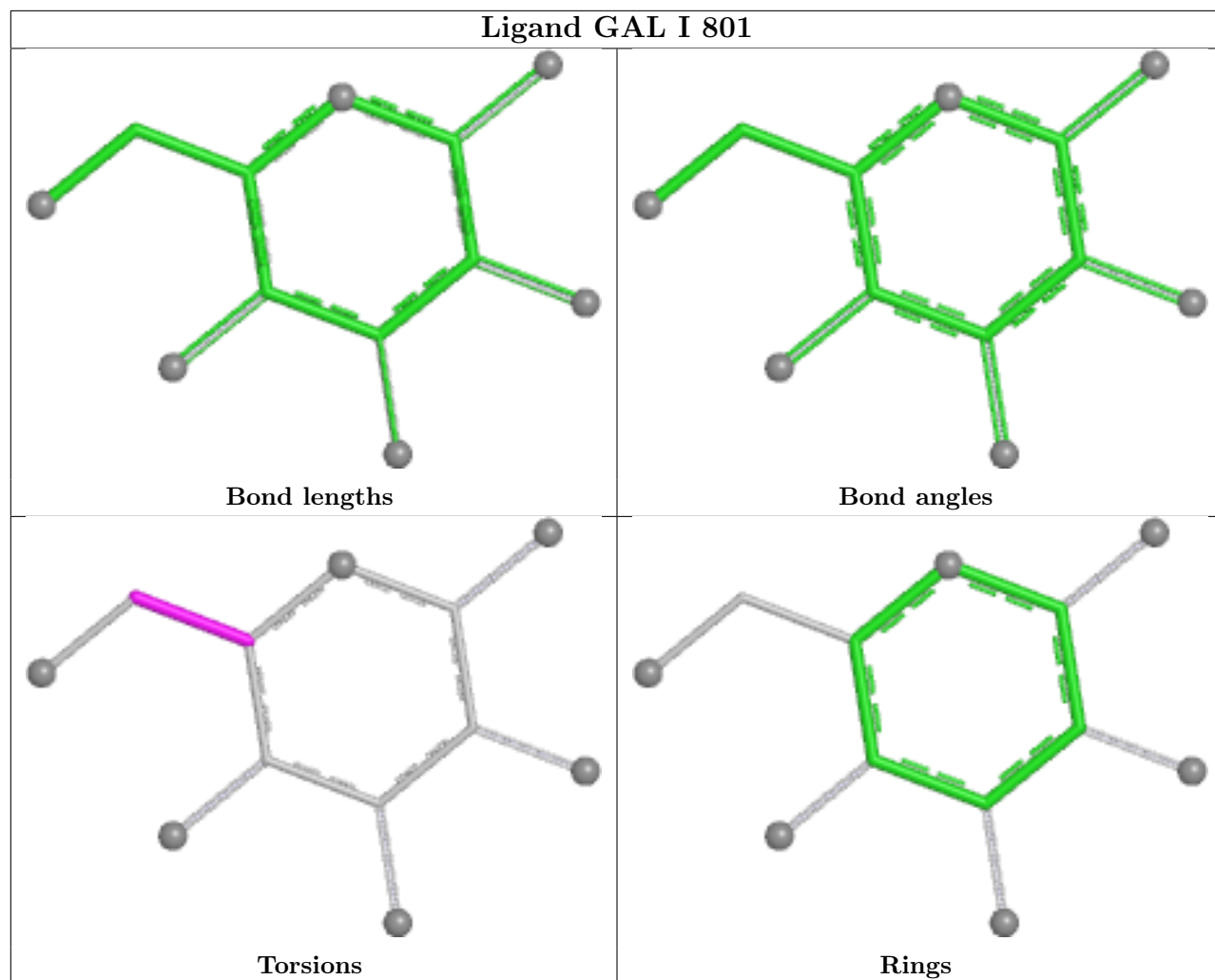
Mol	Chain	Res	Type	Atoms
2	O	801	GAL	O5-C5-C6-O6
2	d	801	GAL	O5-C5-C6-O6
2	f	801	GAL	O5-C5-C6-O6
2	x	801	GAL	O5-C5-C6-O6
2	8	801	GAL	O5-C5-C6-O6

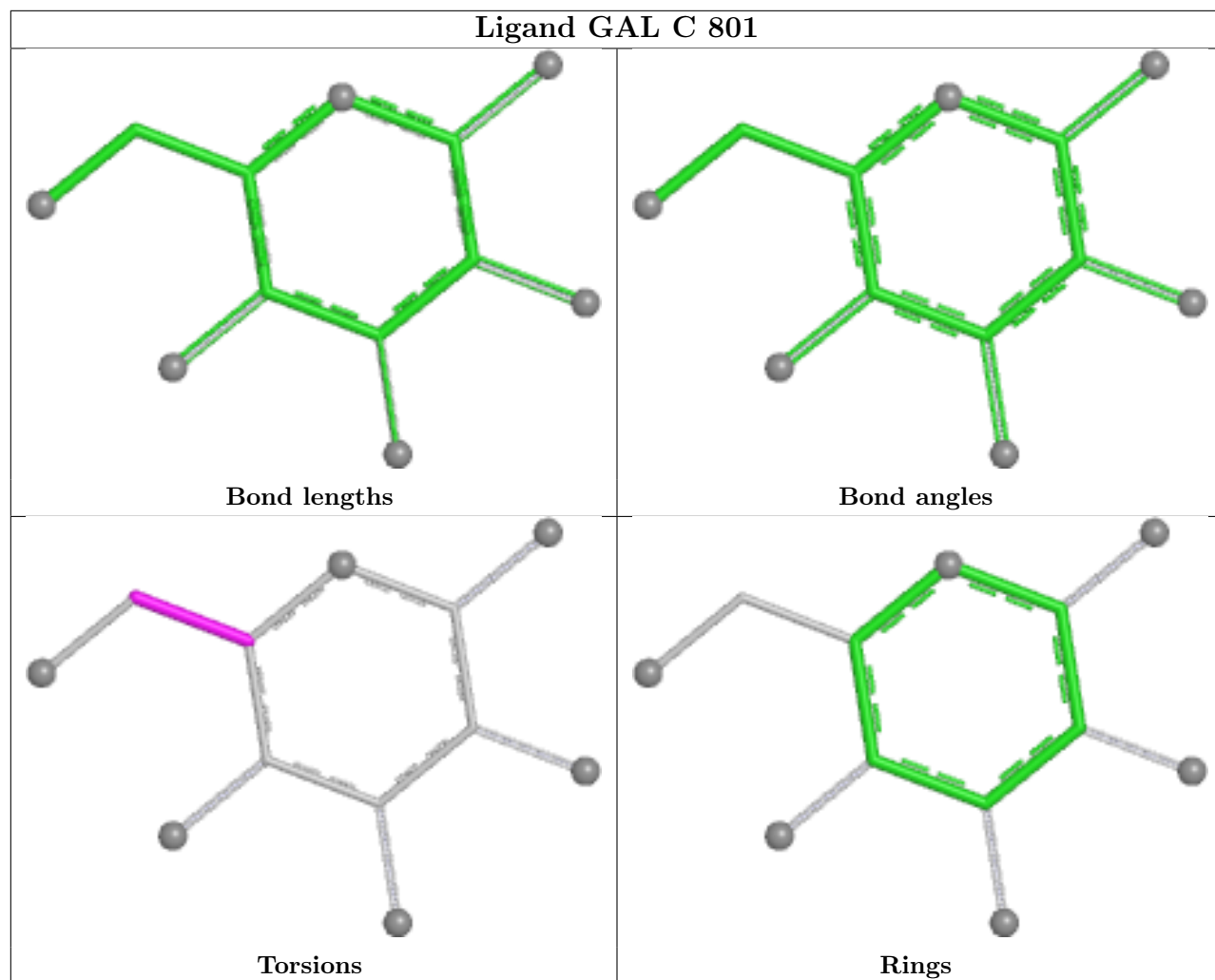
There are no ring outliers.

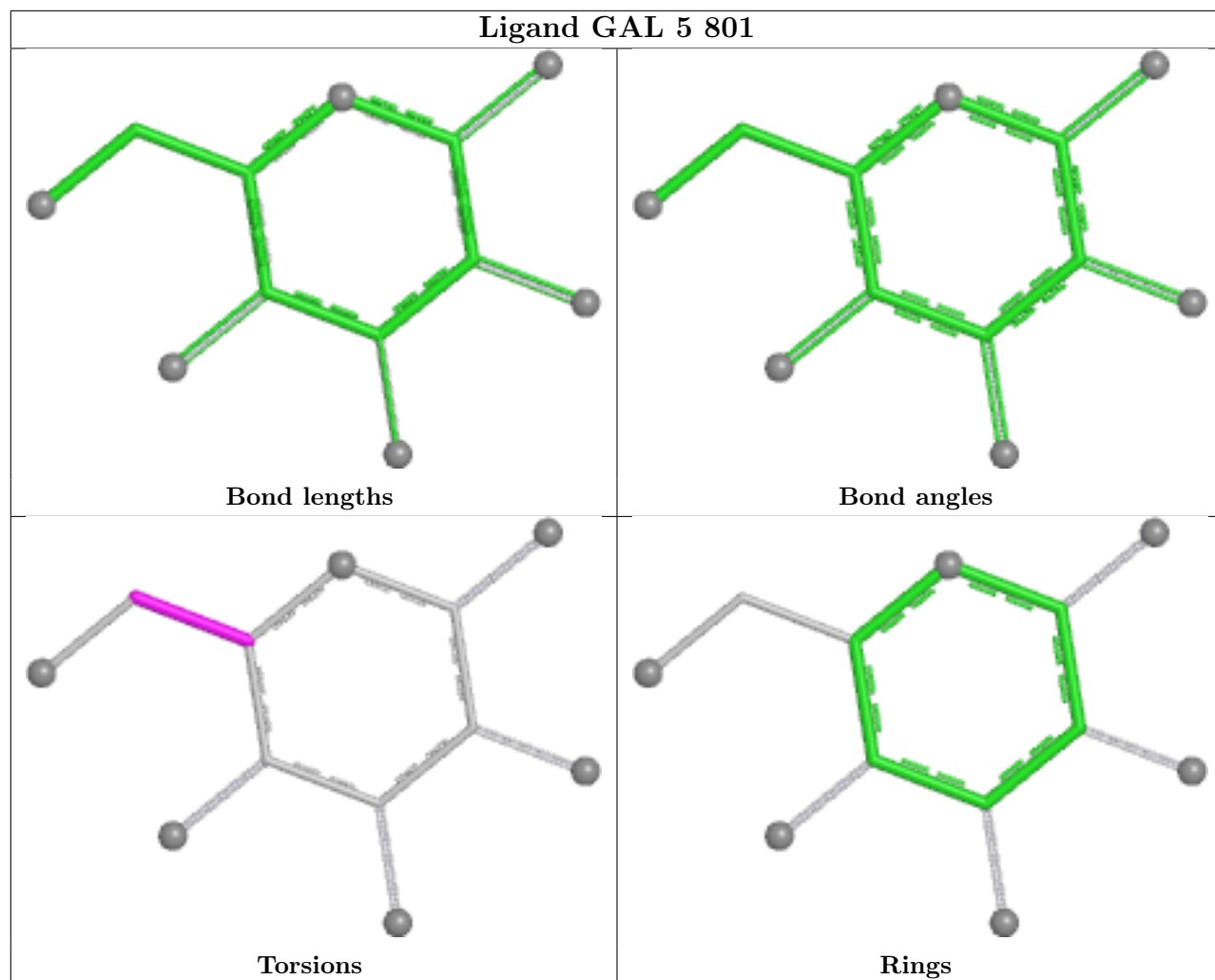
No monomer is involved in short contacts.

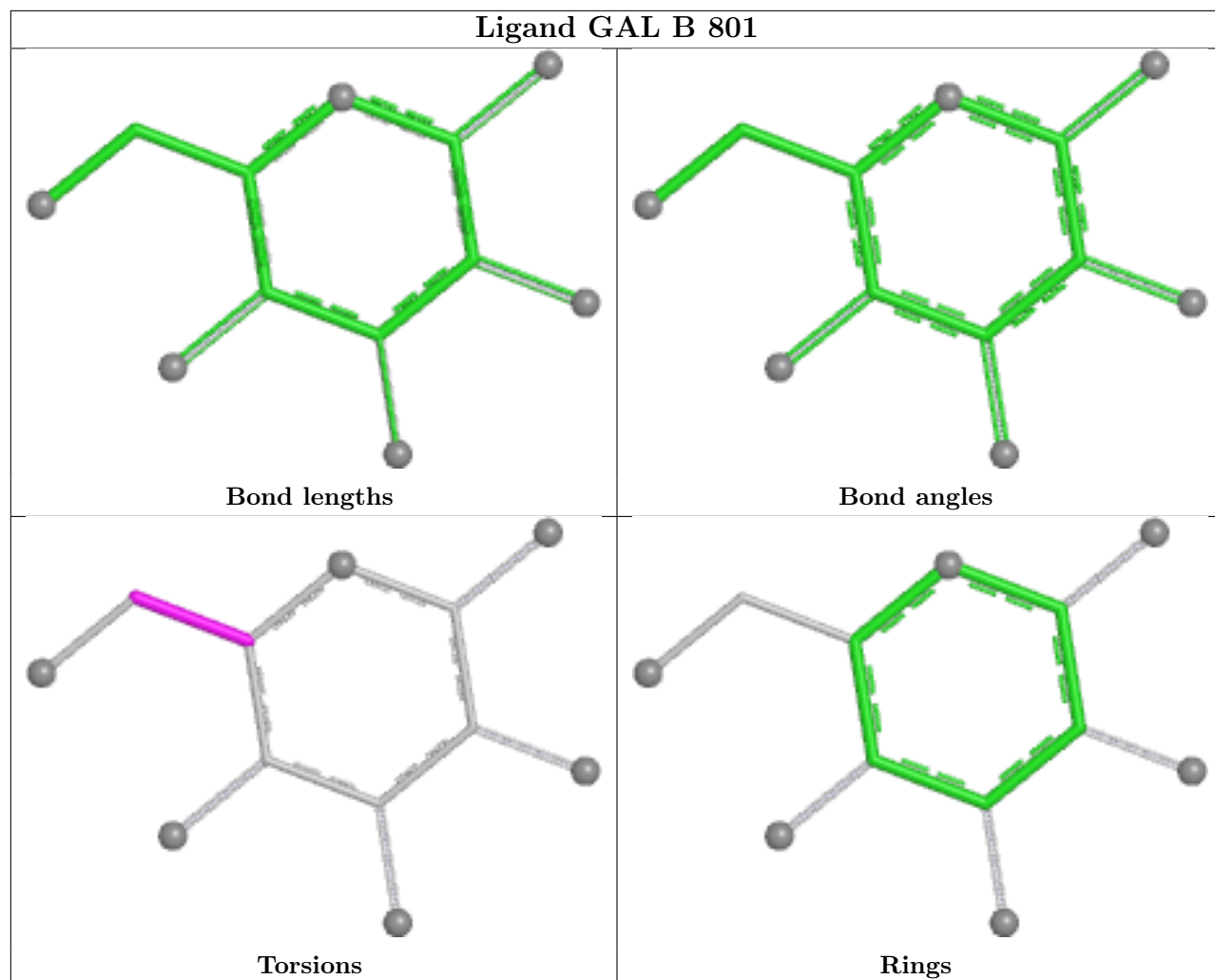
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

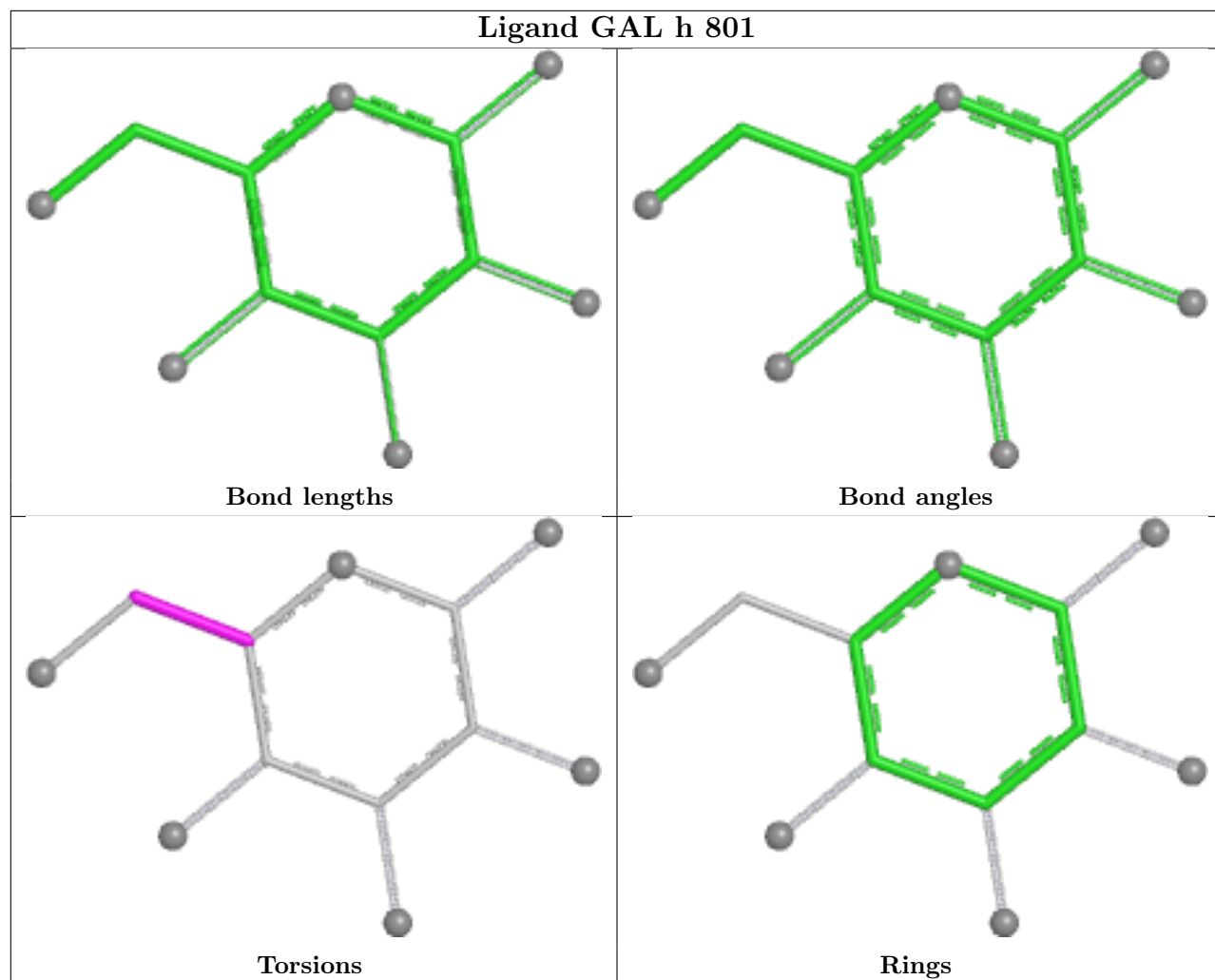


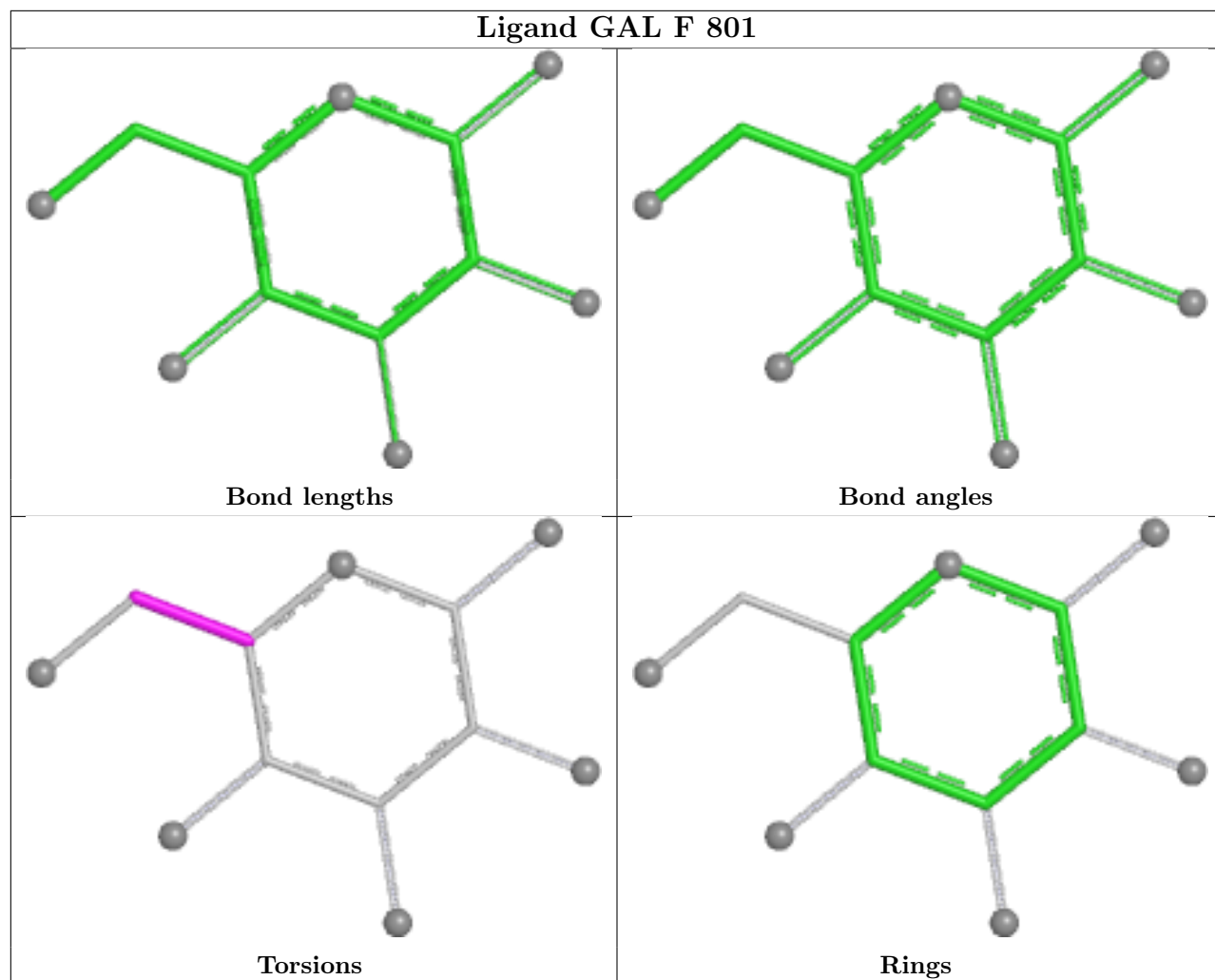


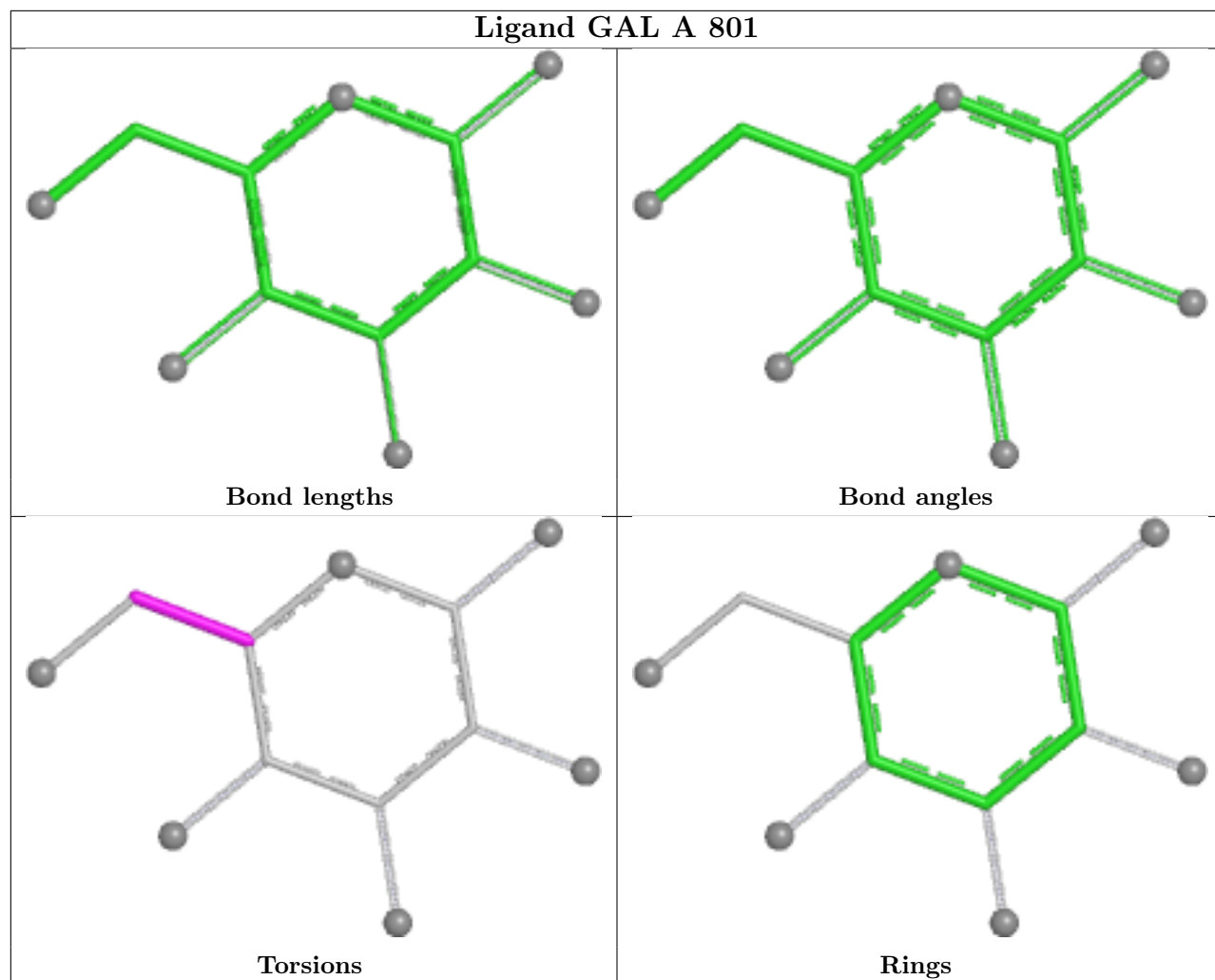


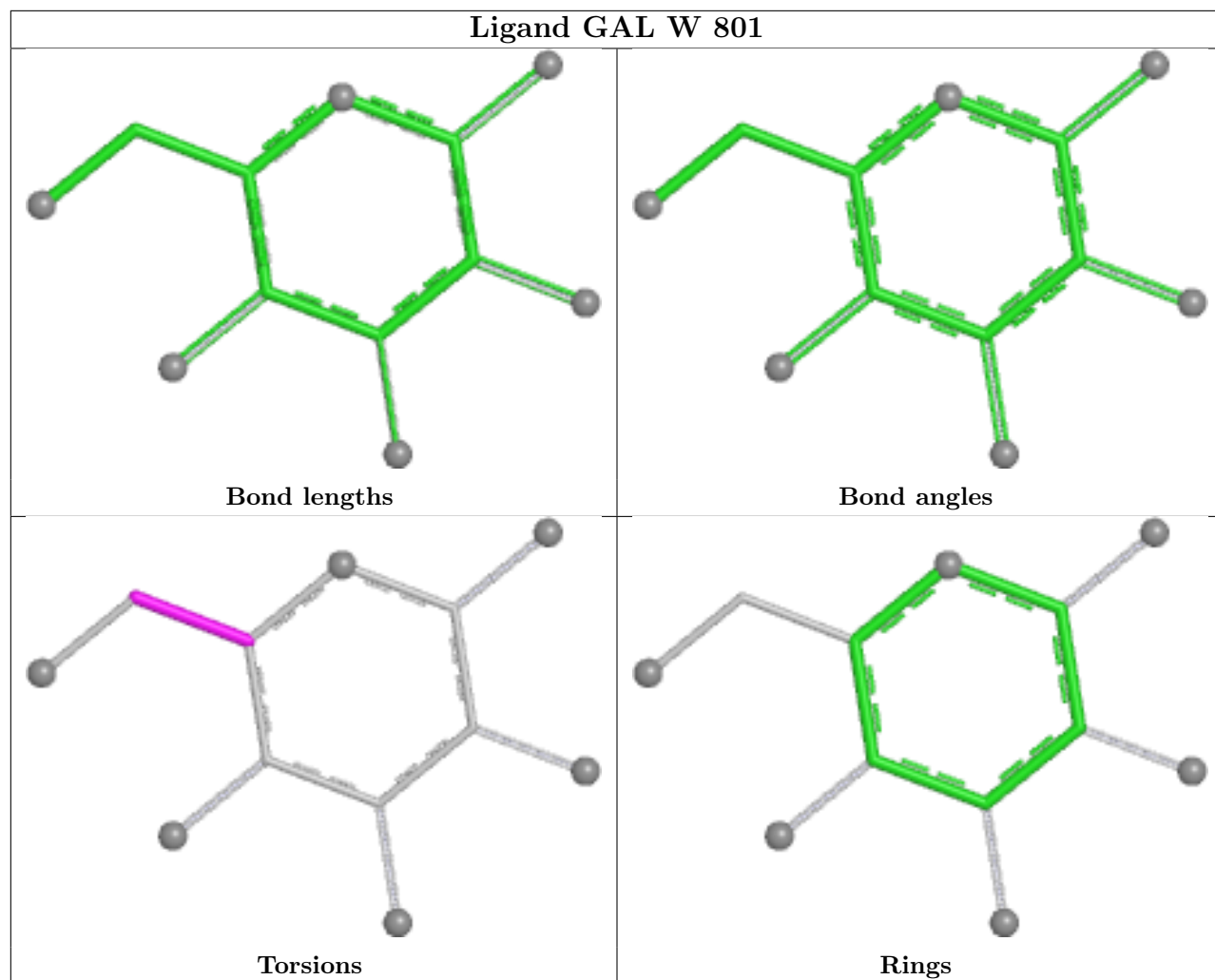


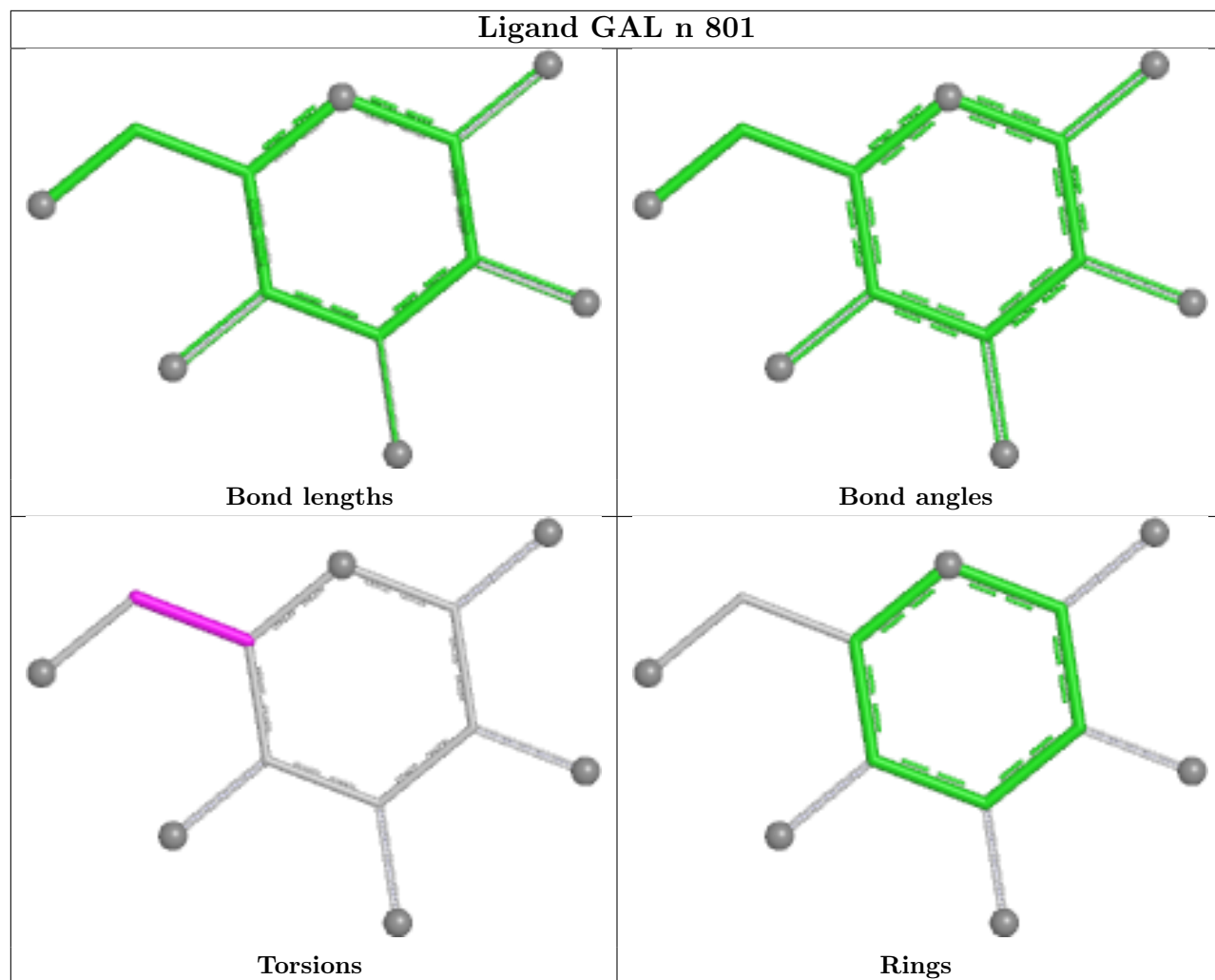


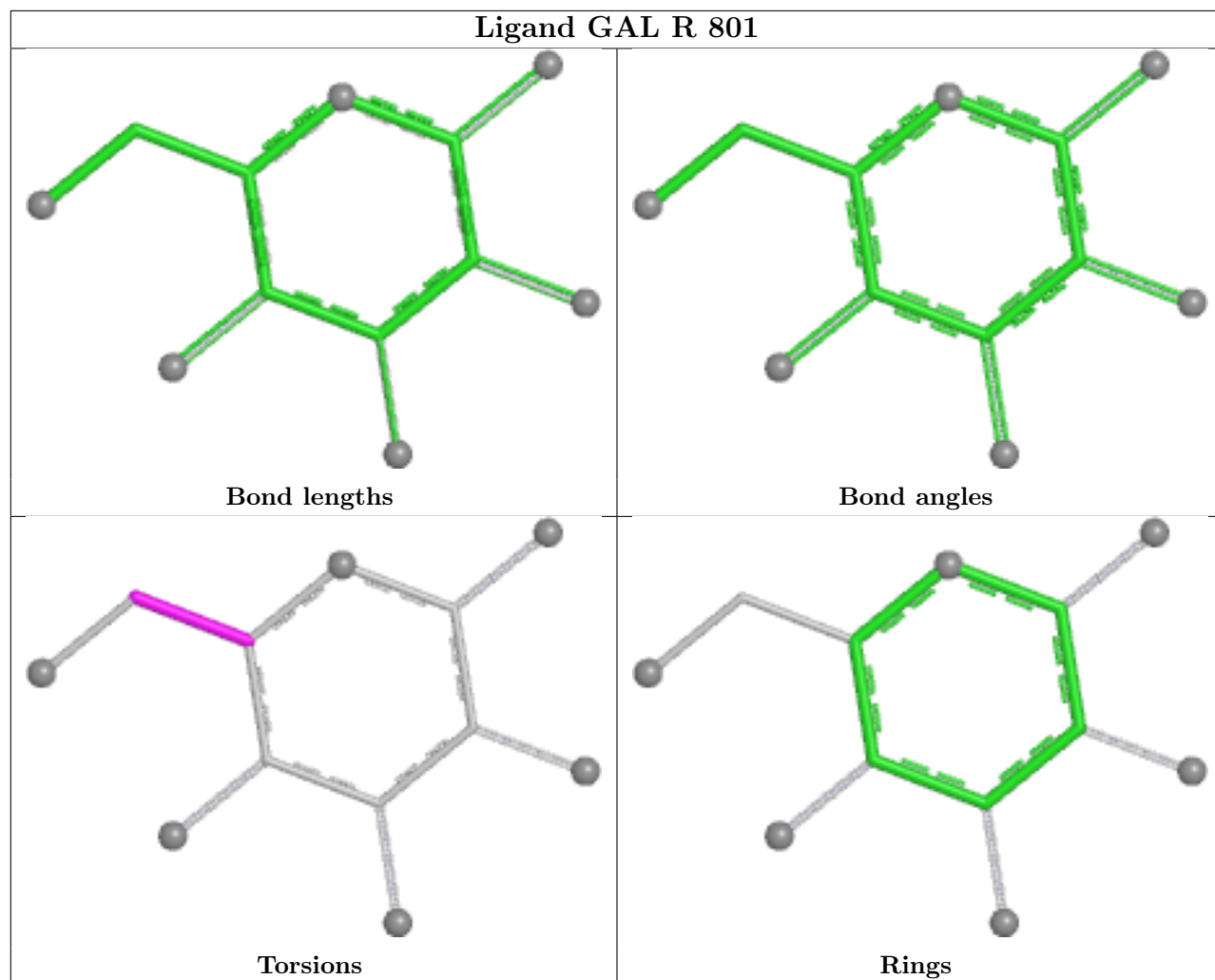


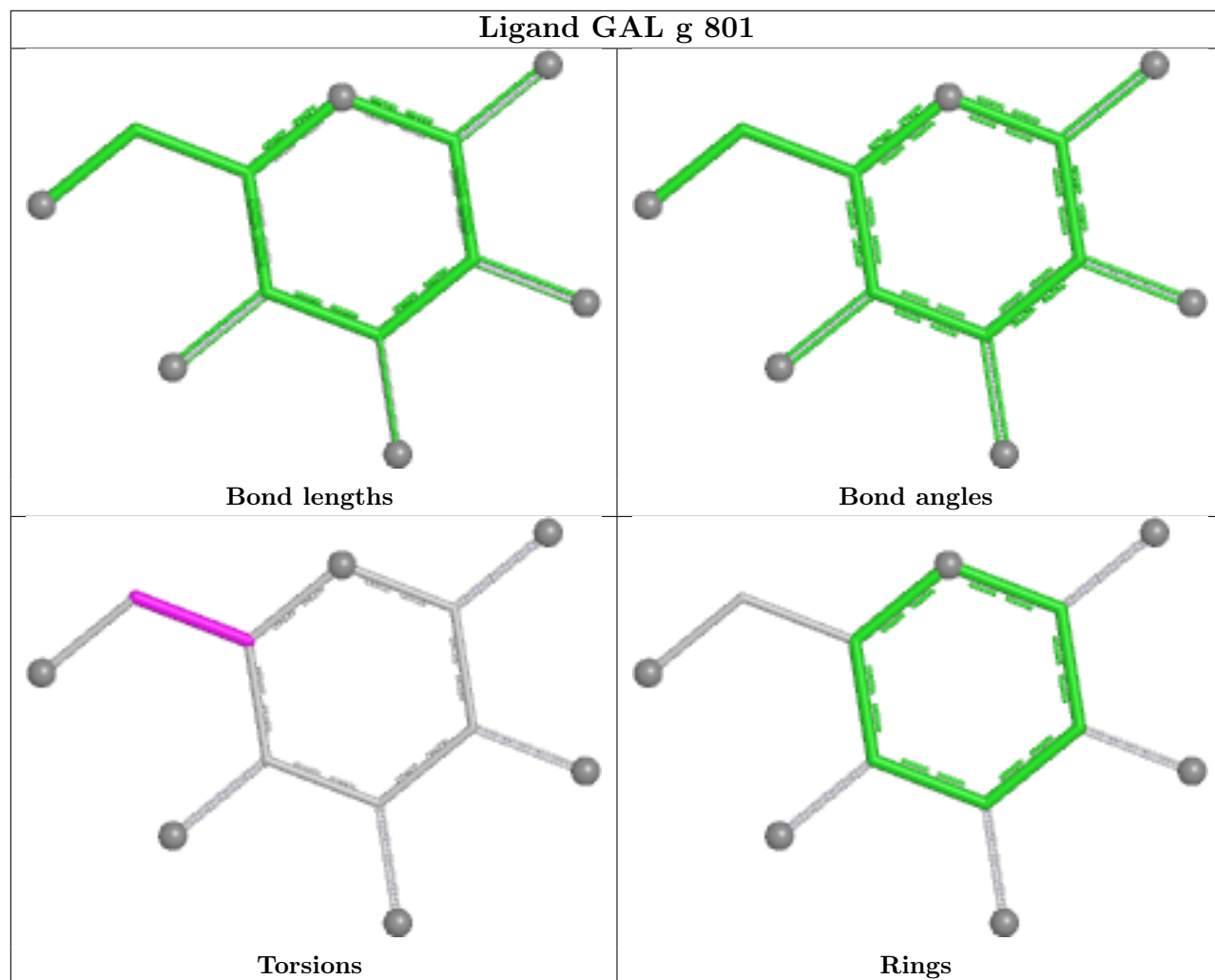


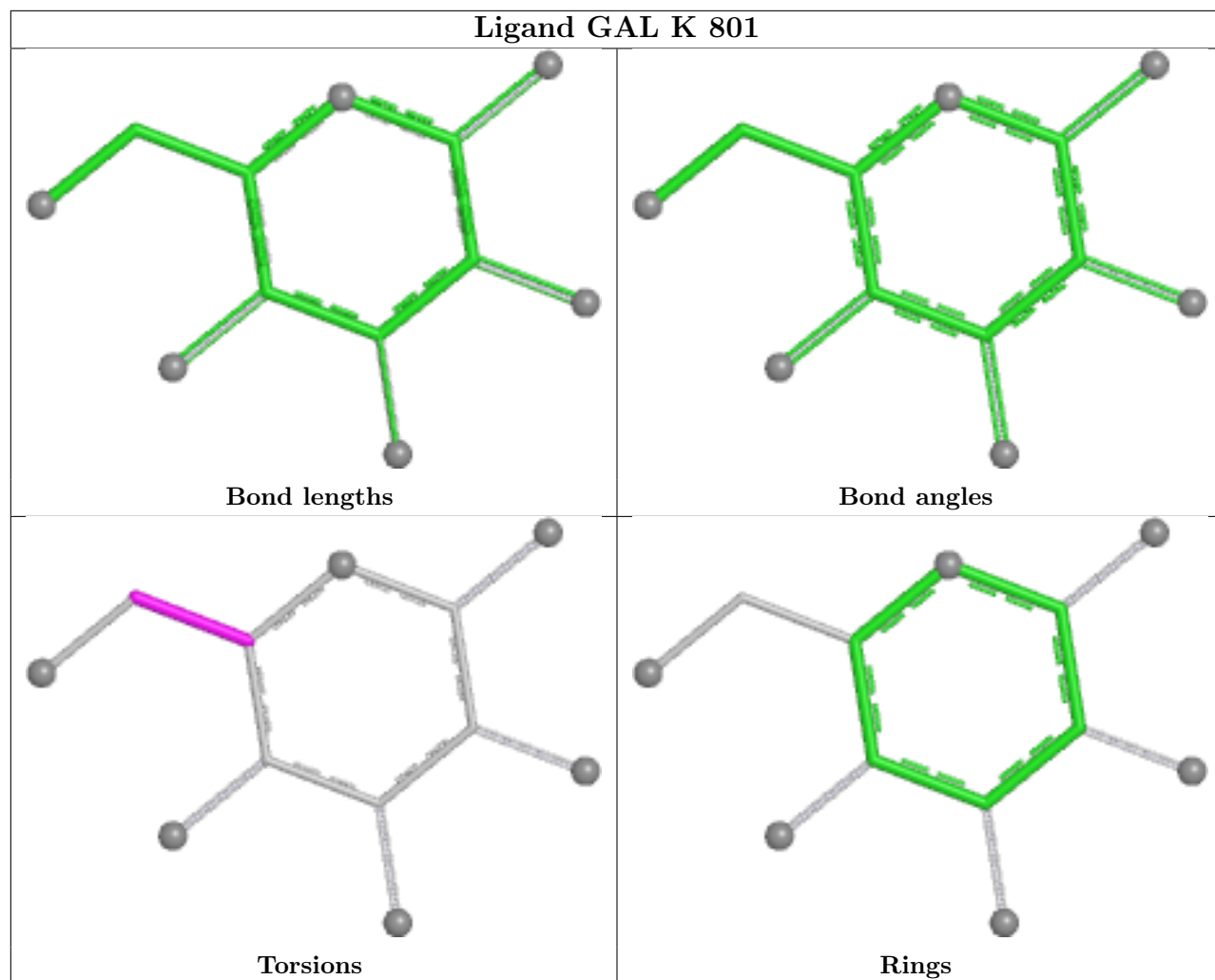


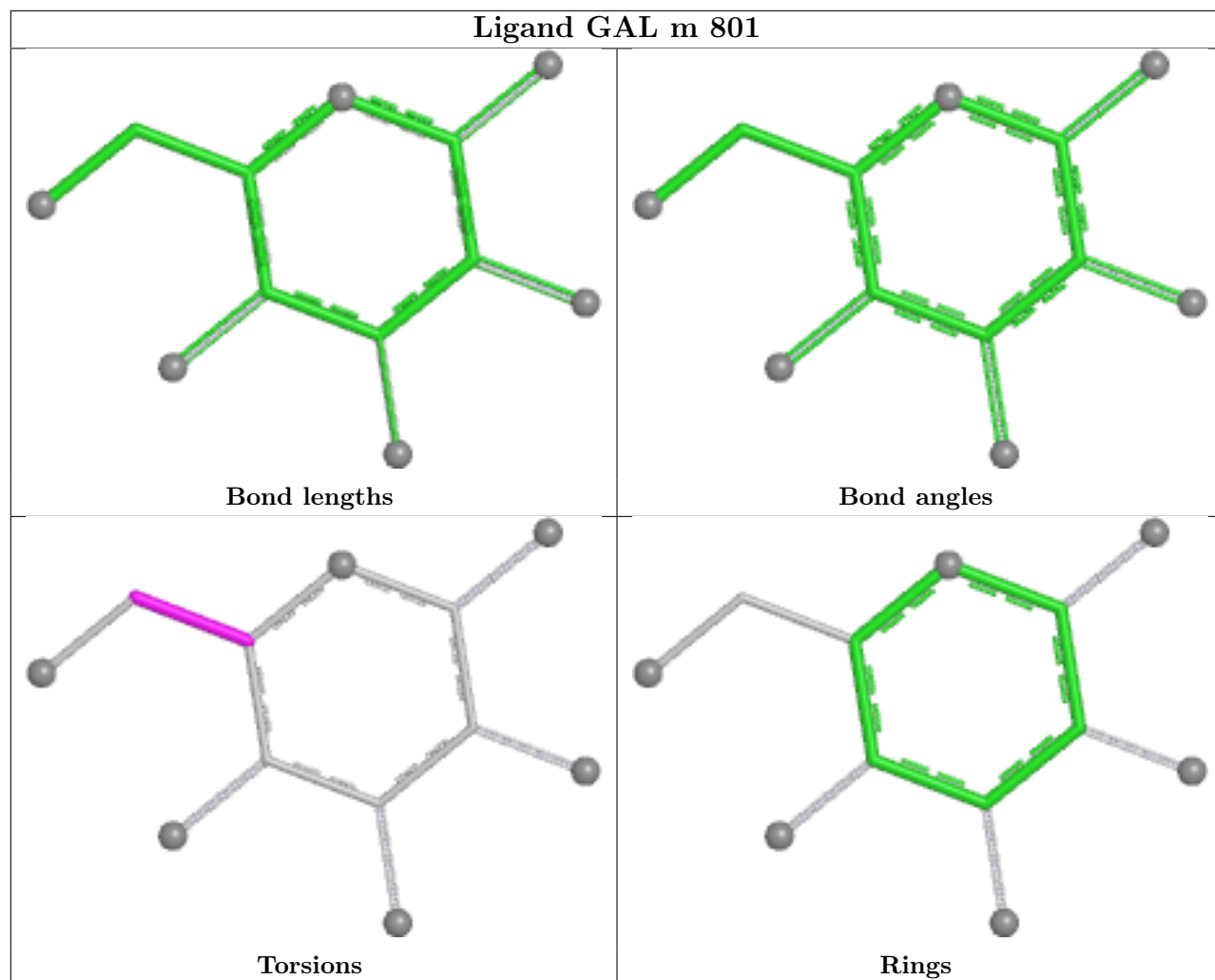


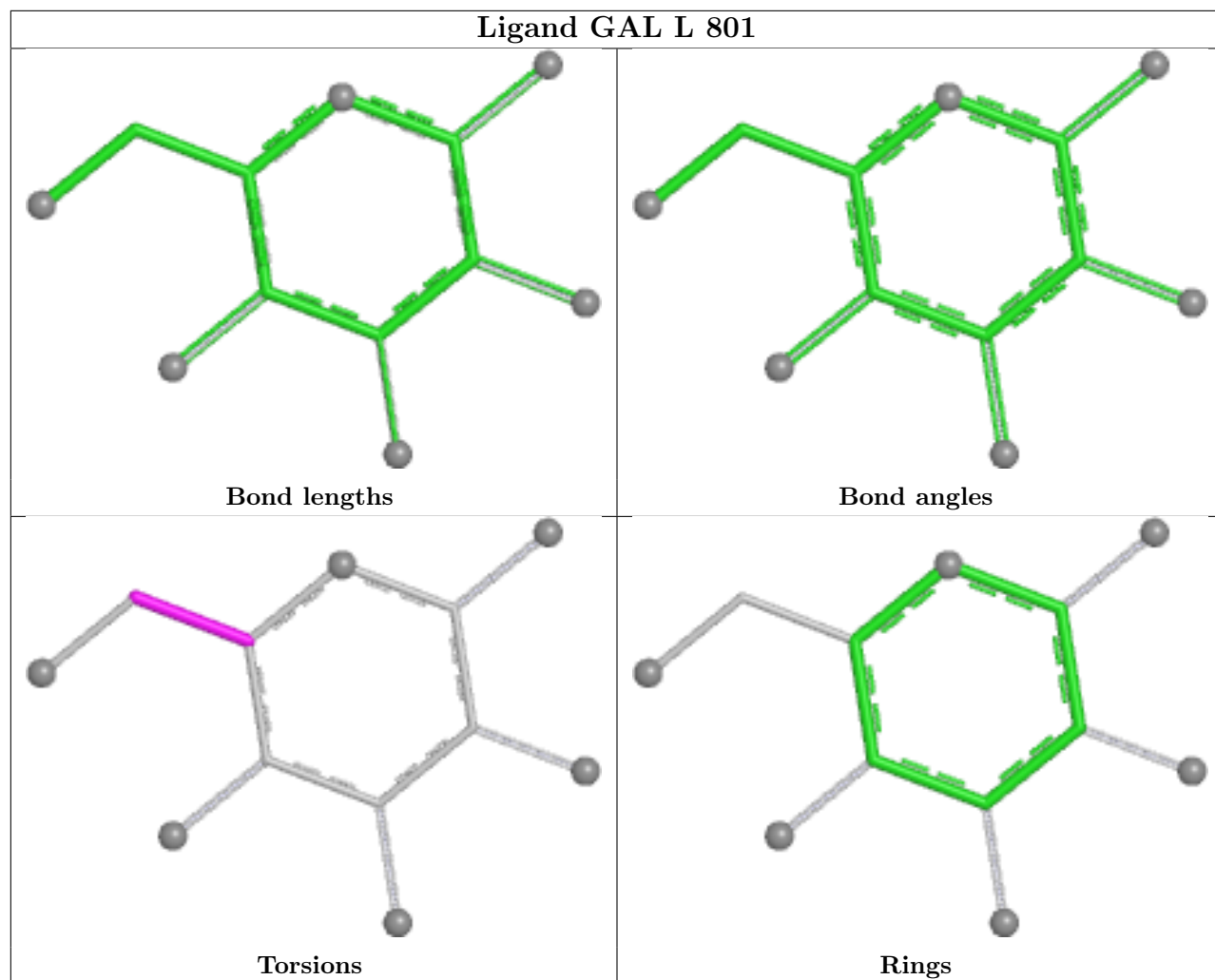


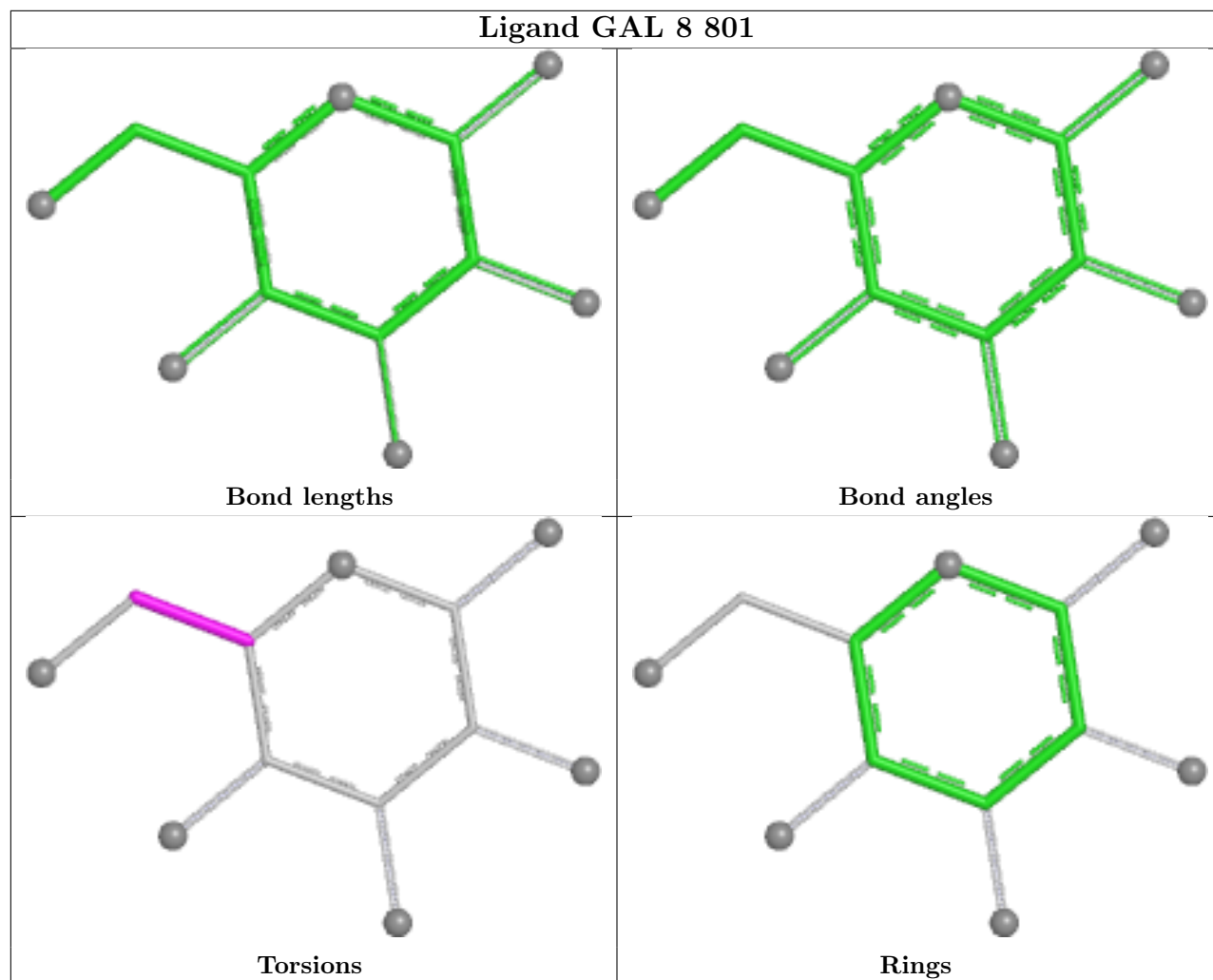


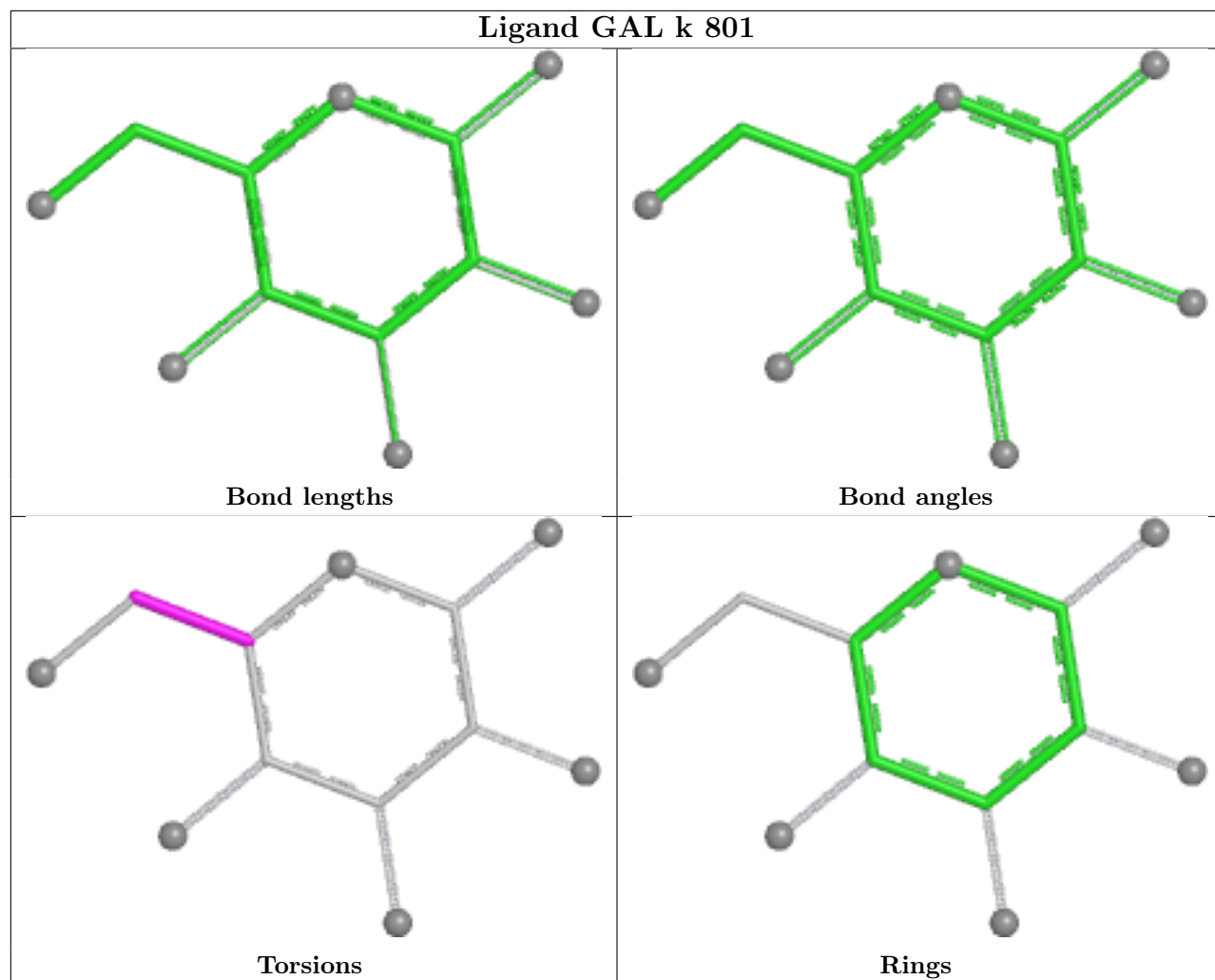


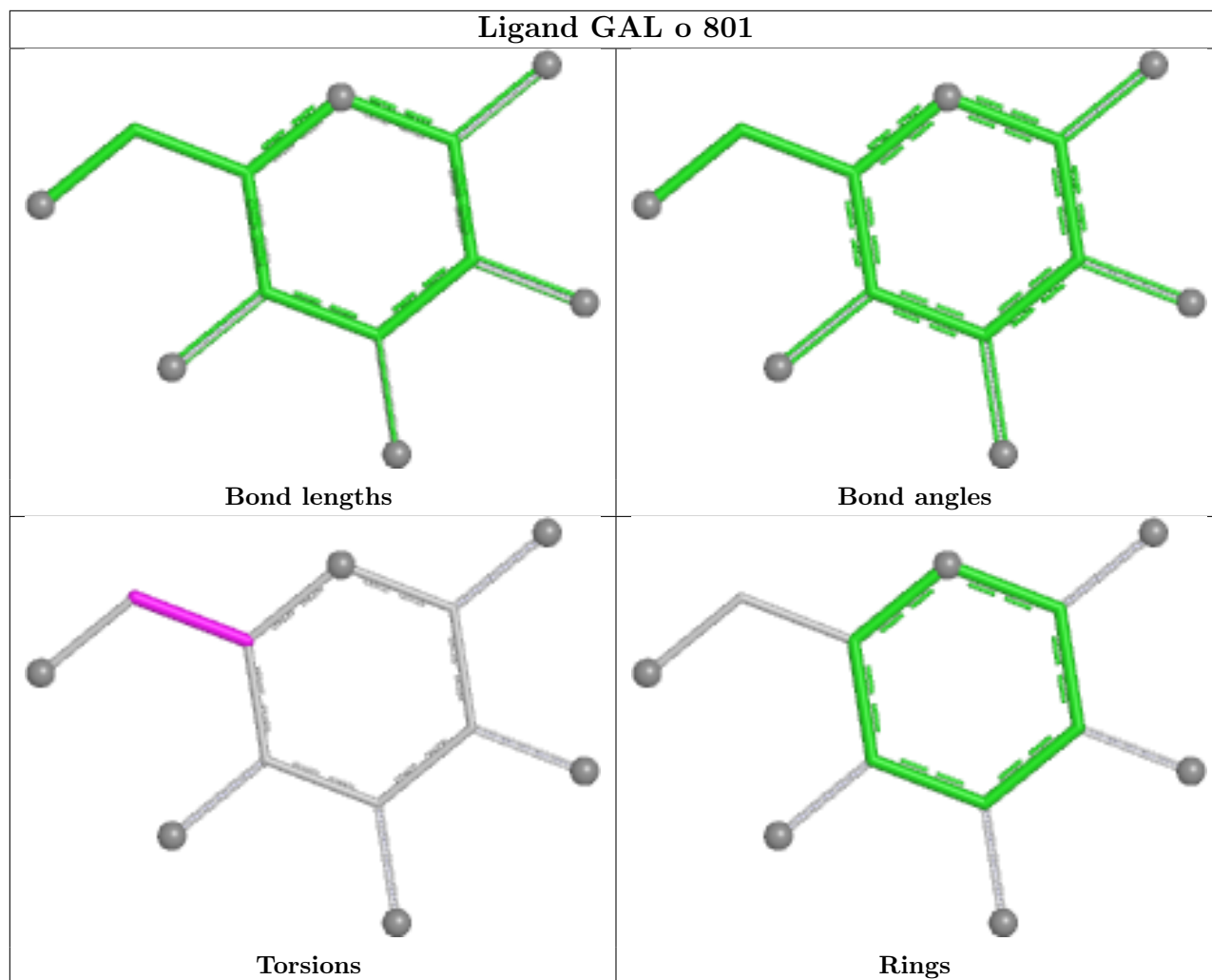


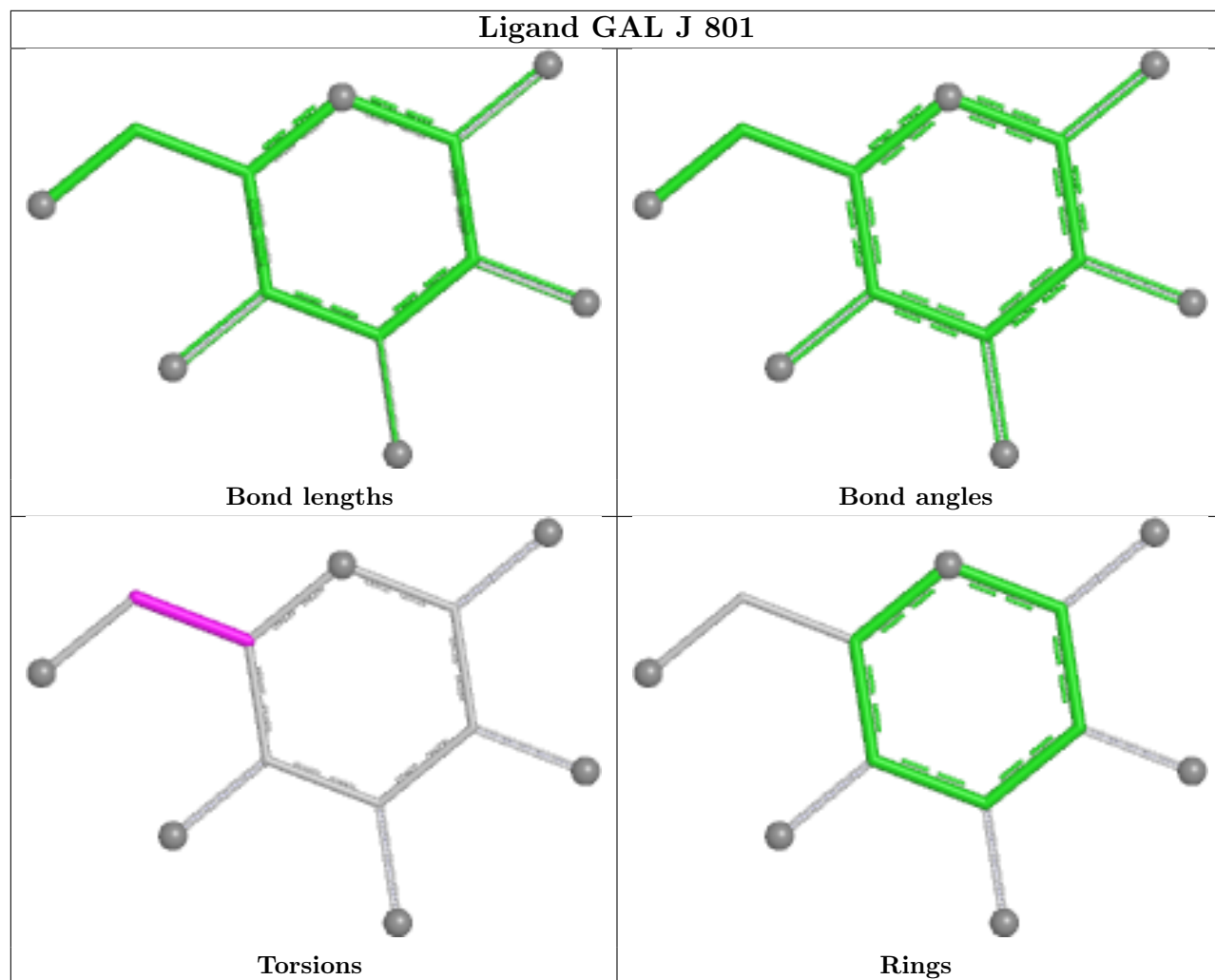


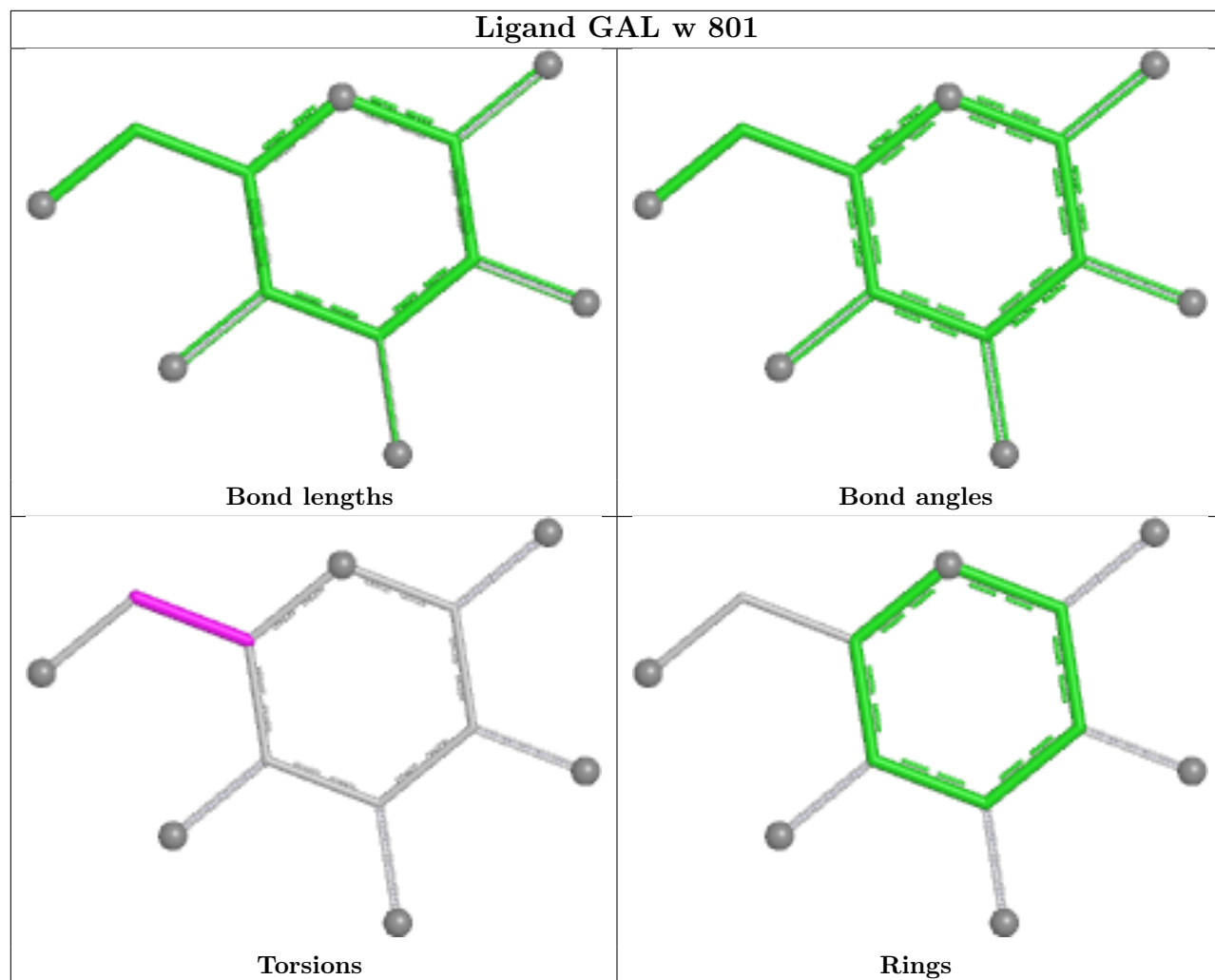


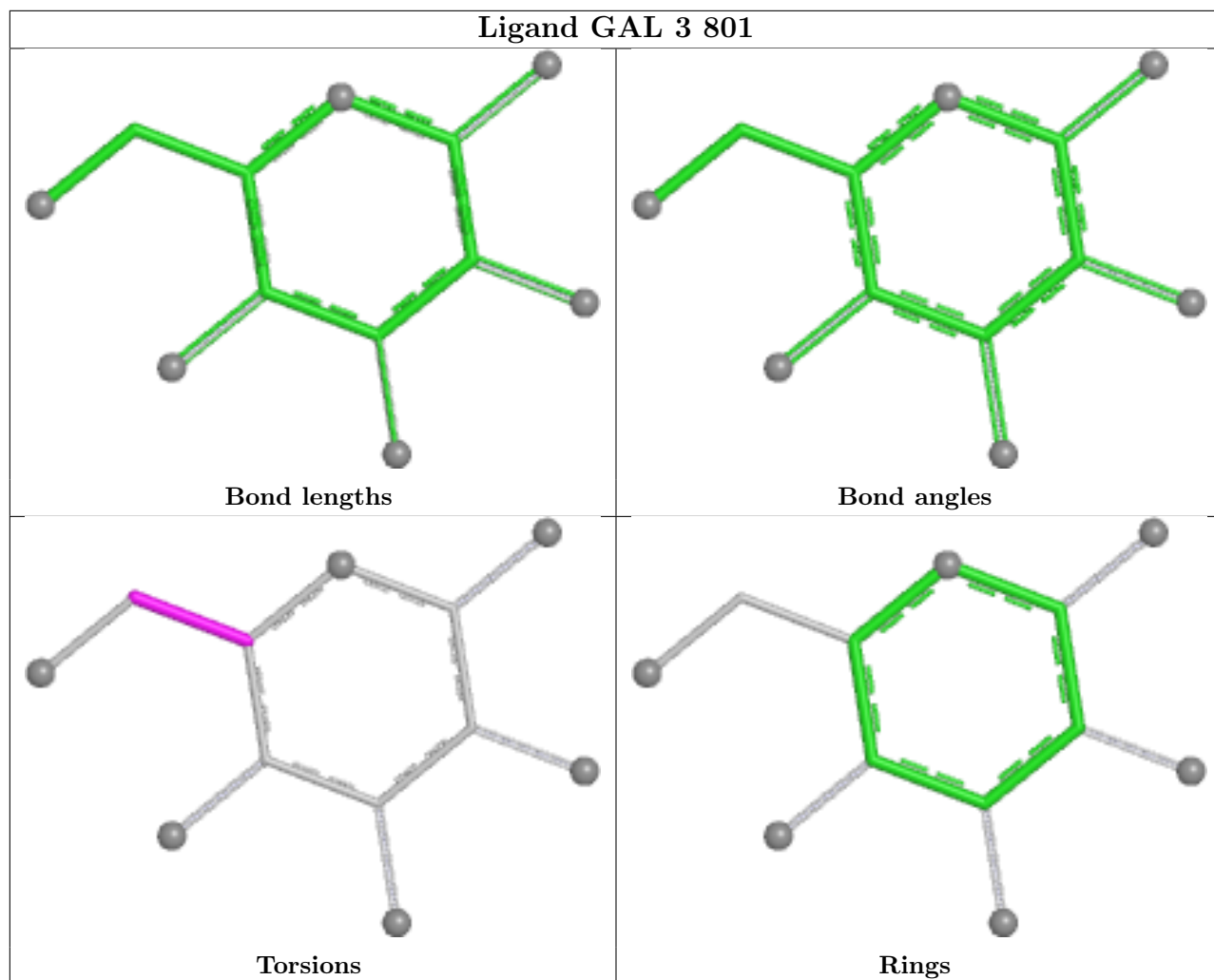


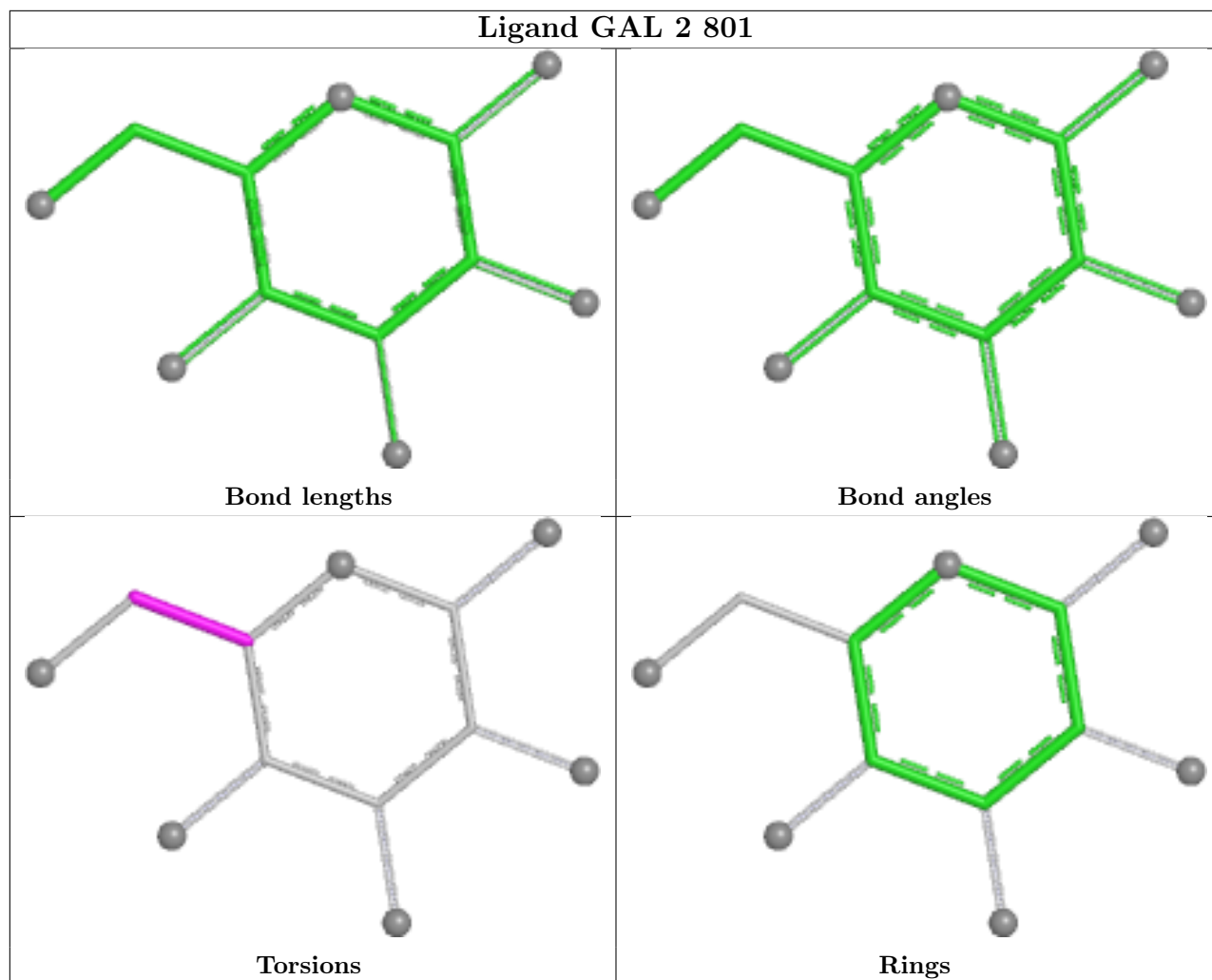


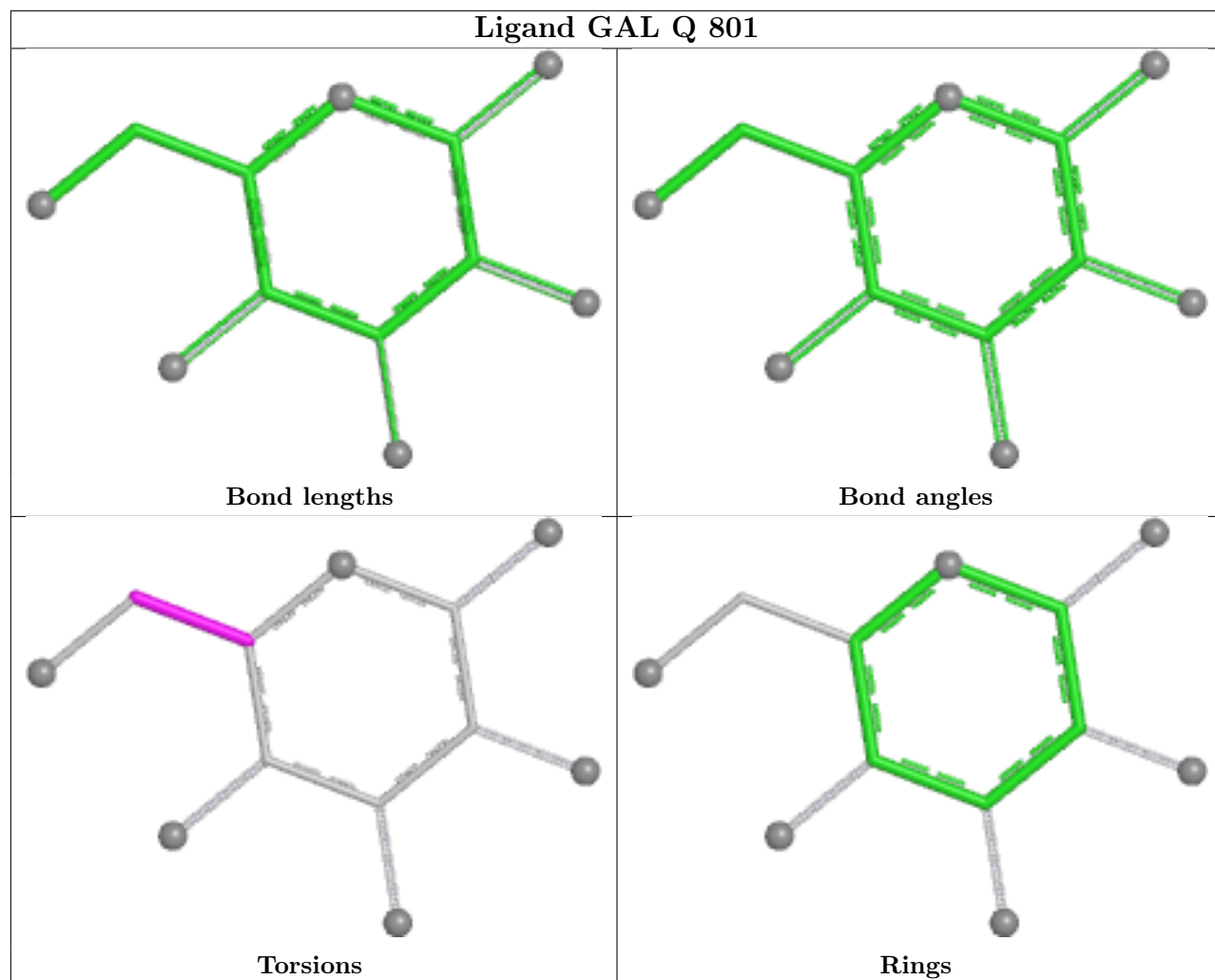


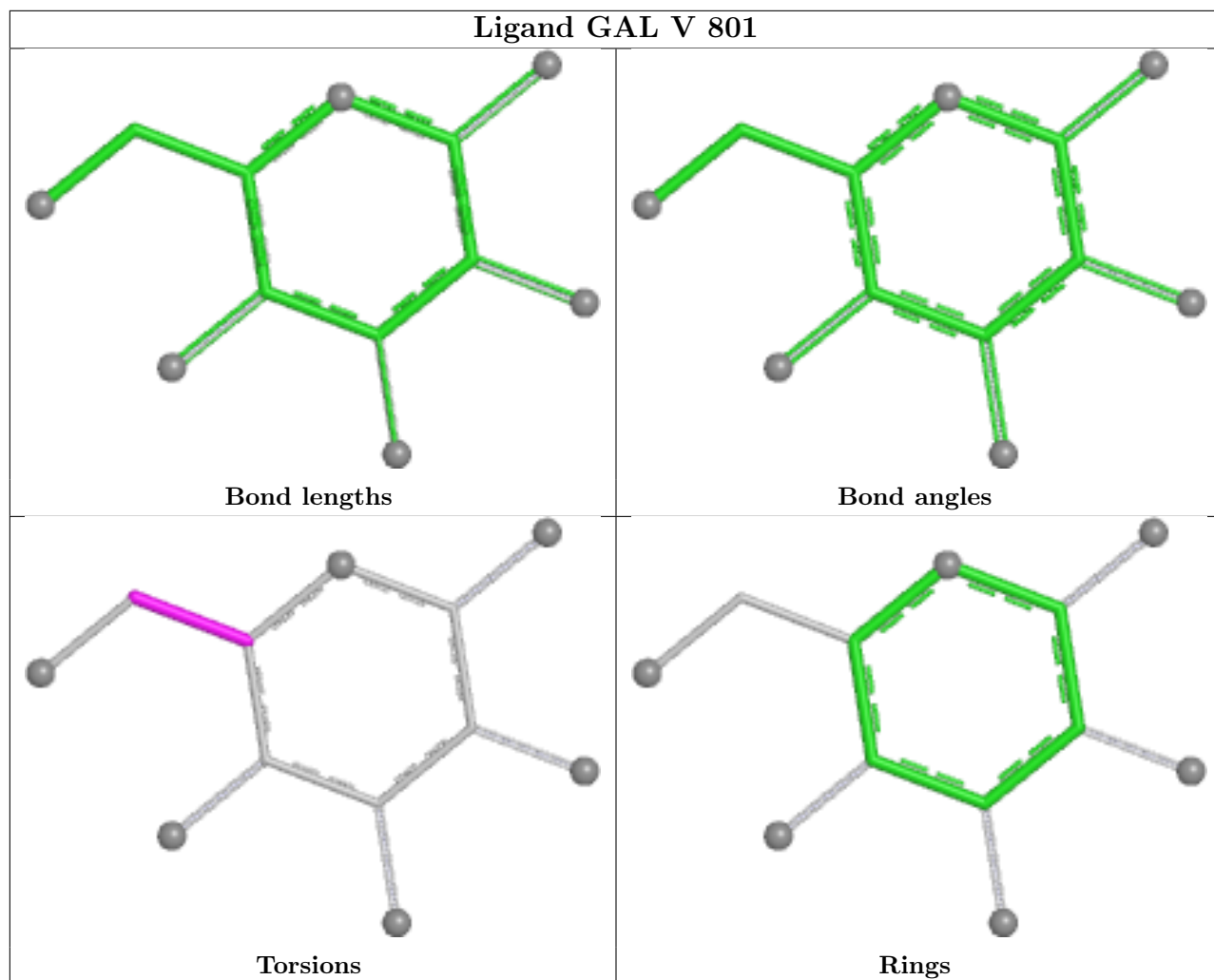


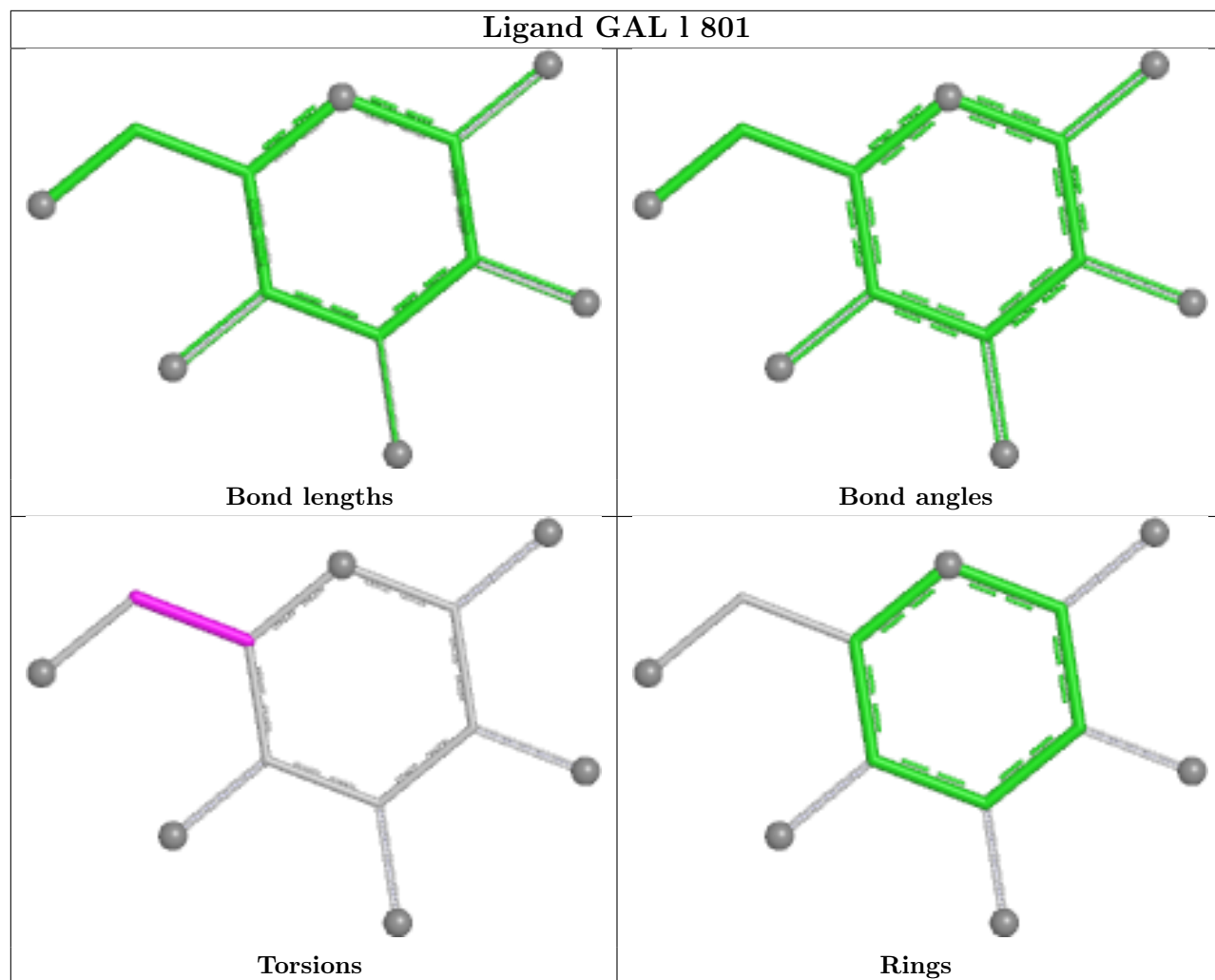


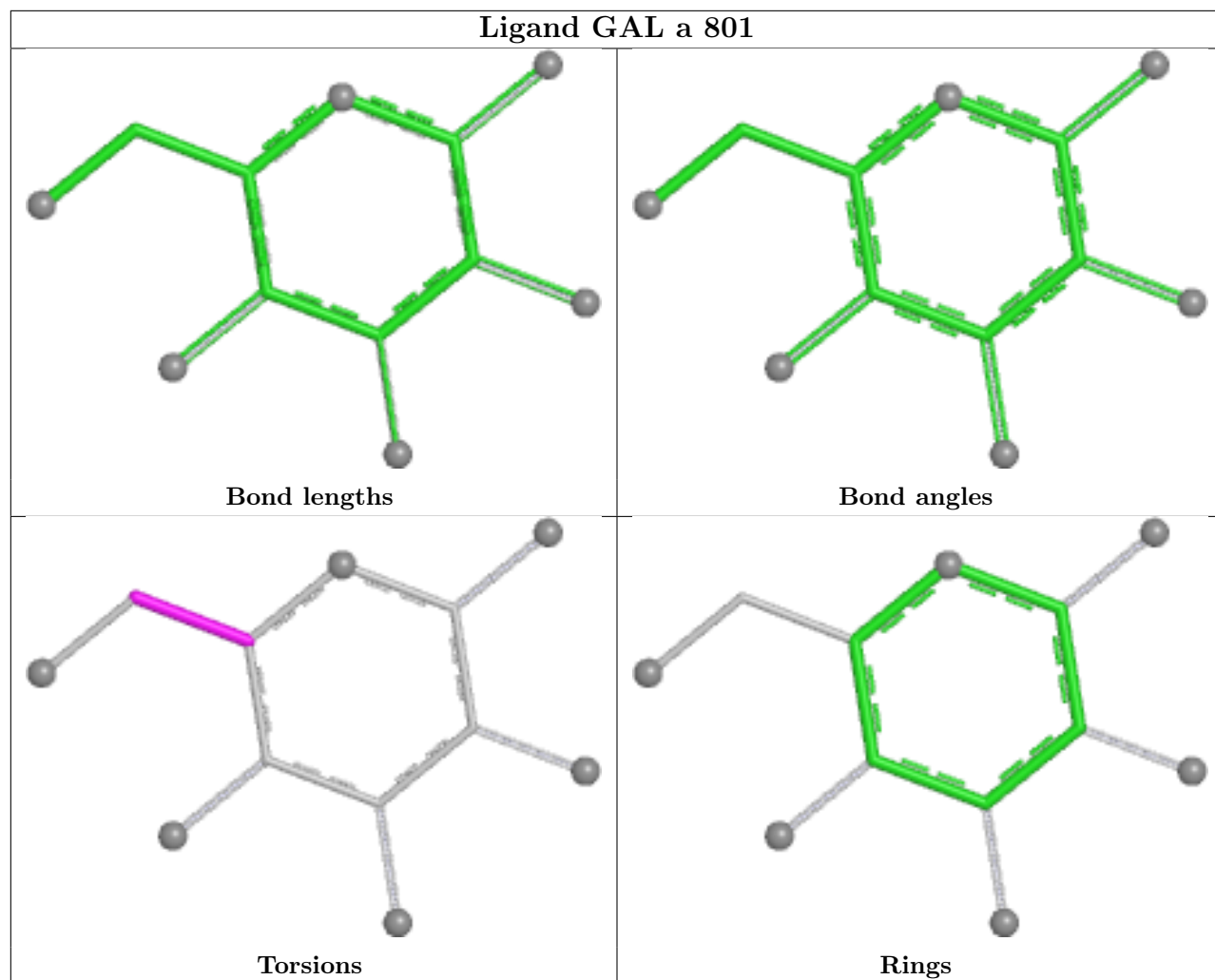


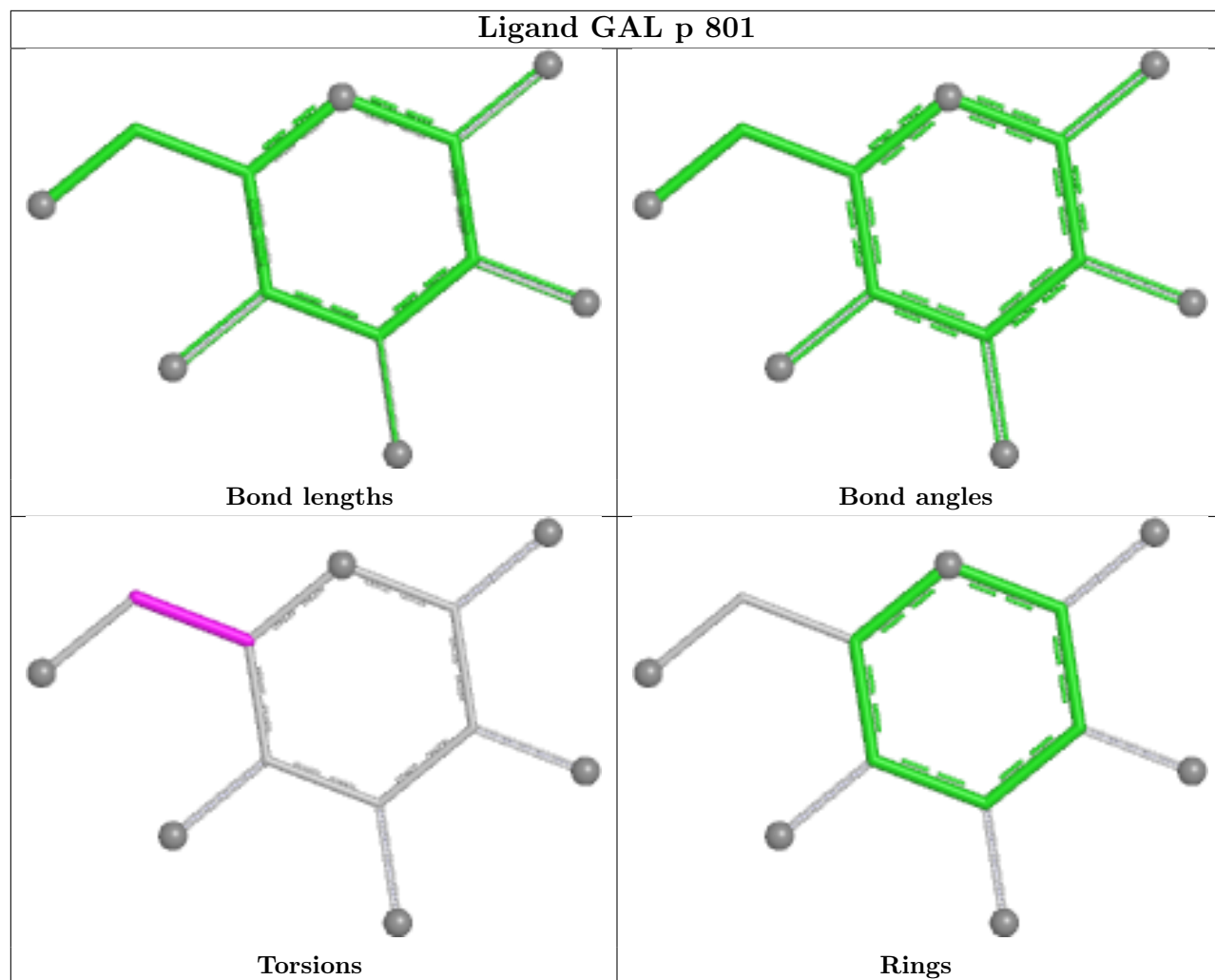


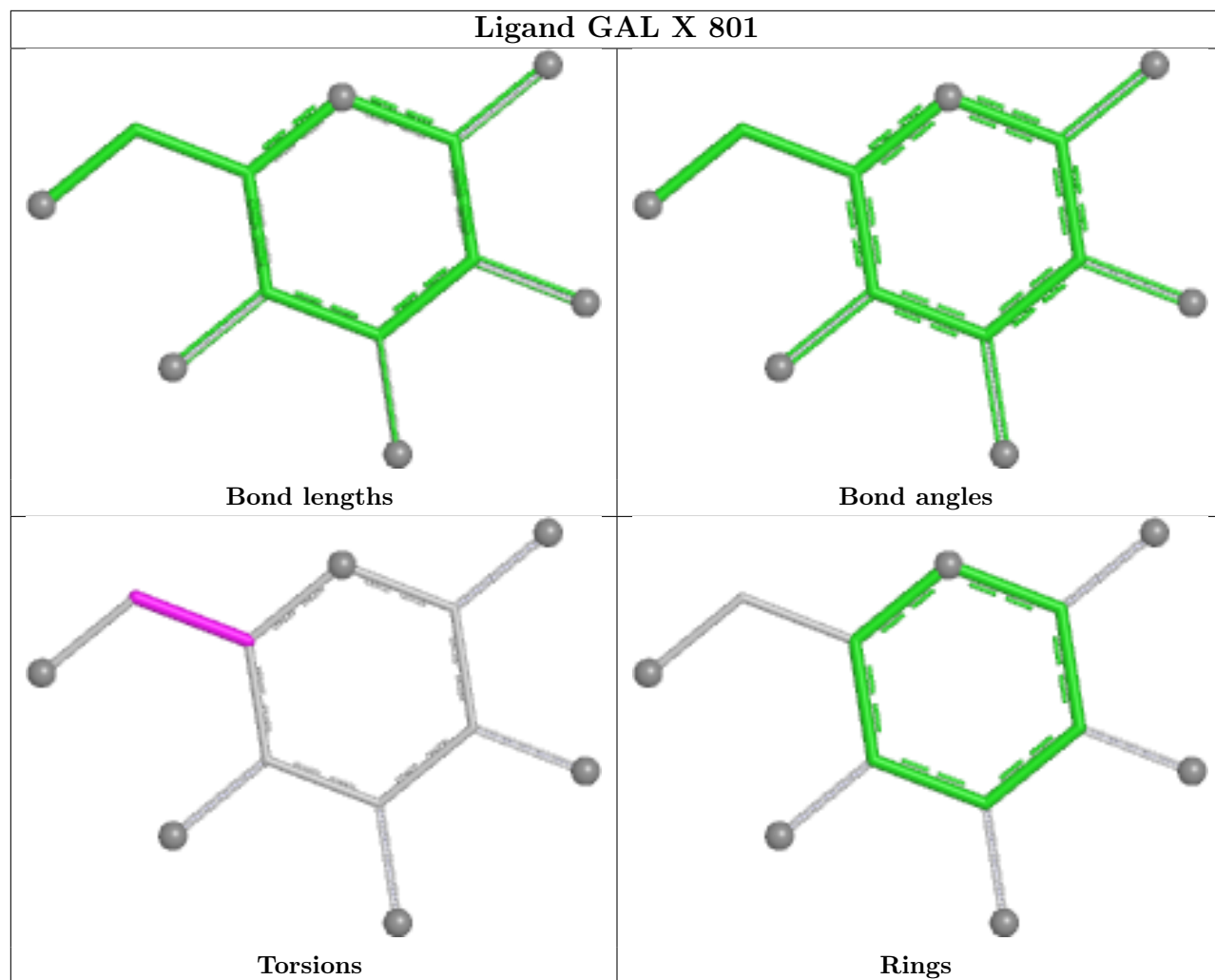


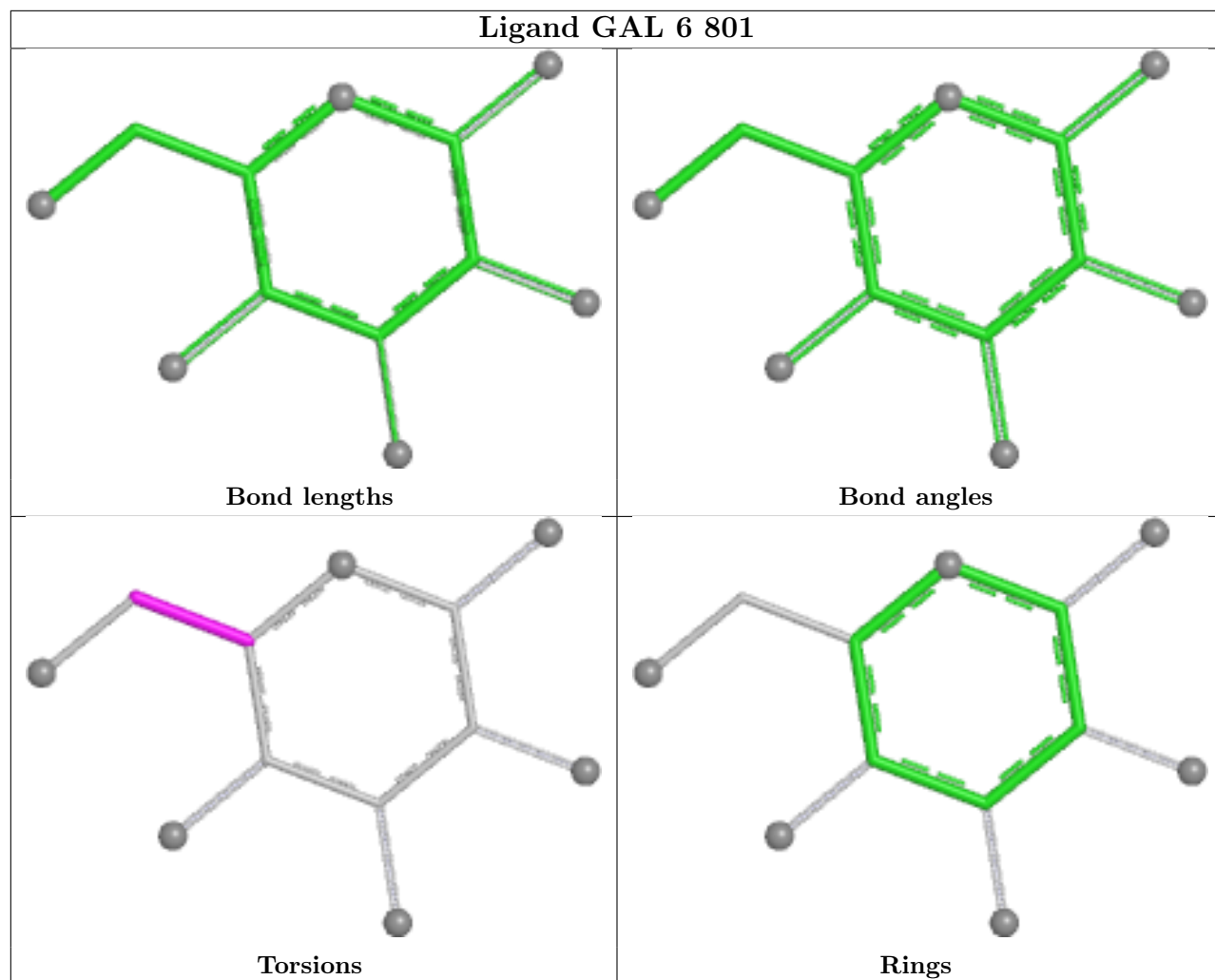


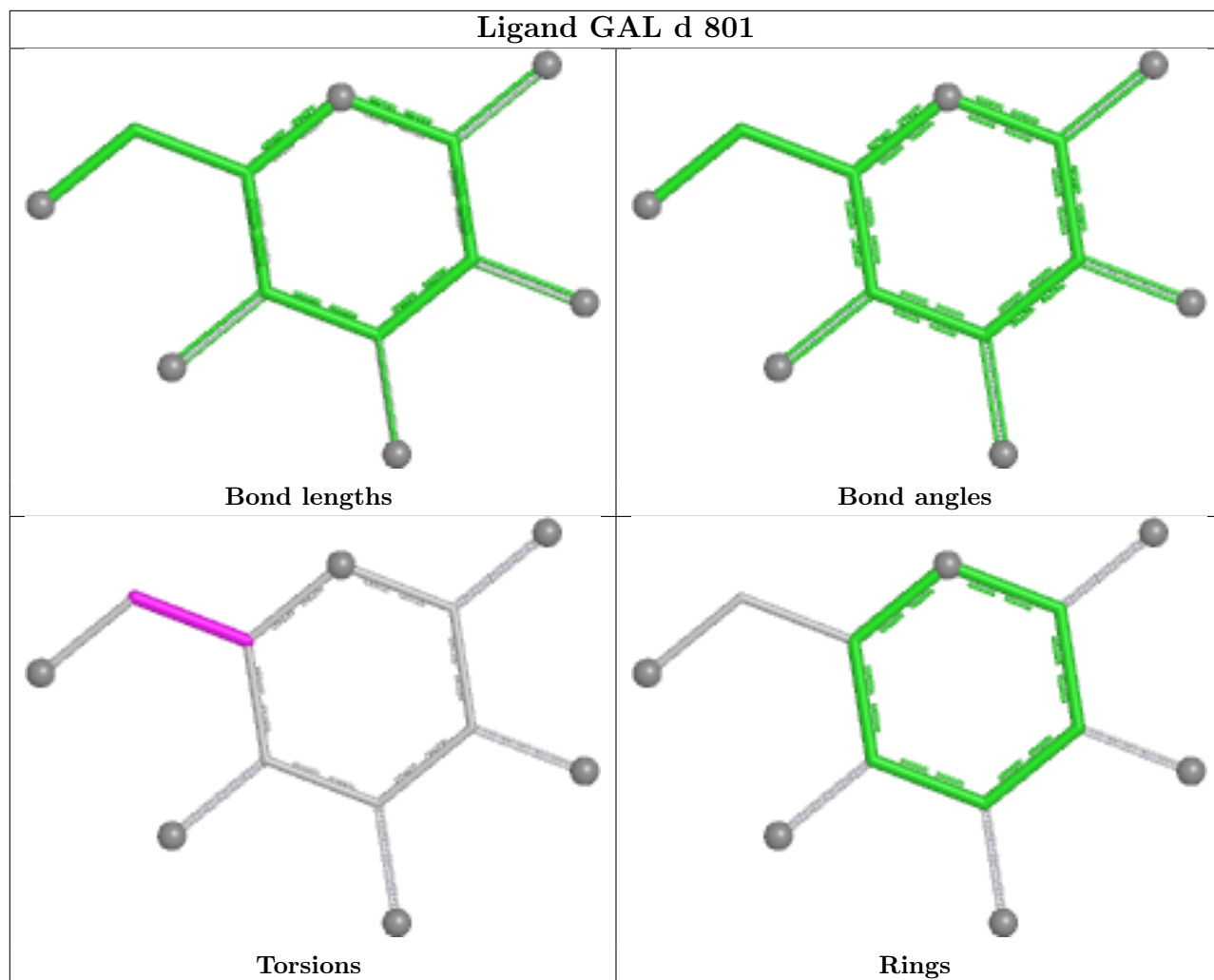


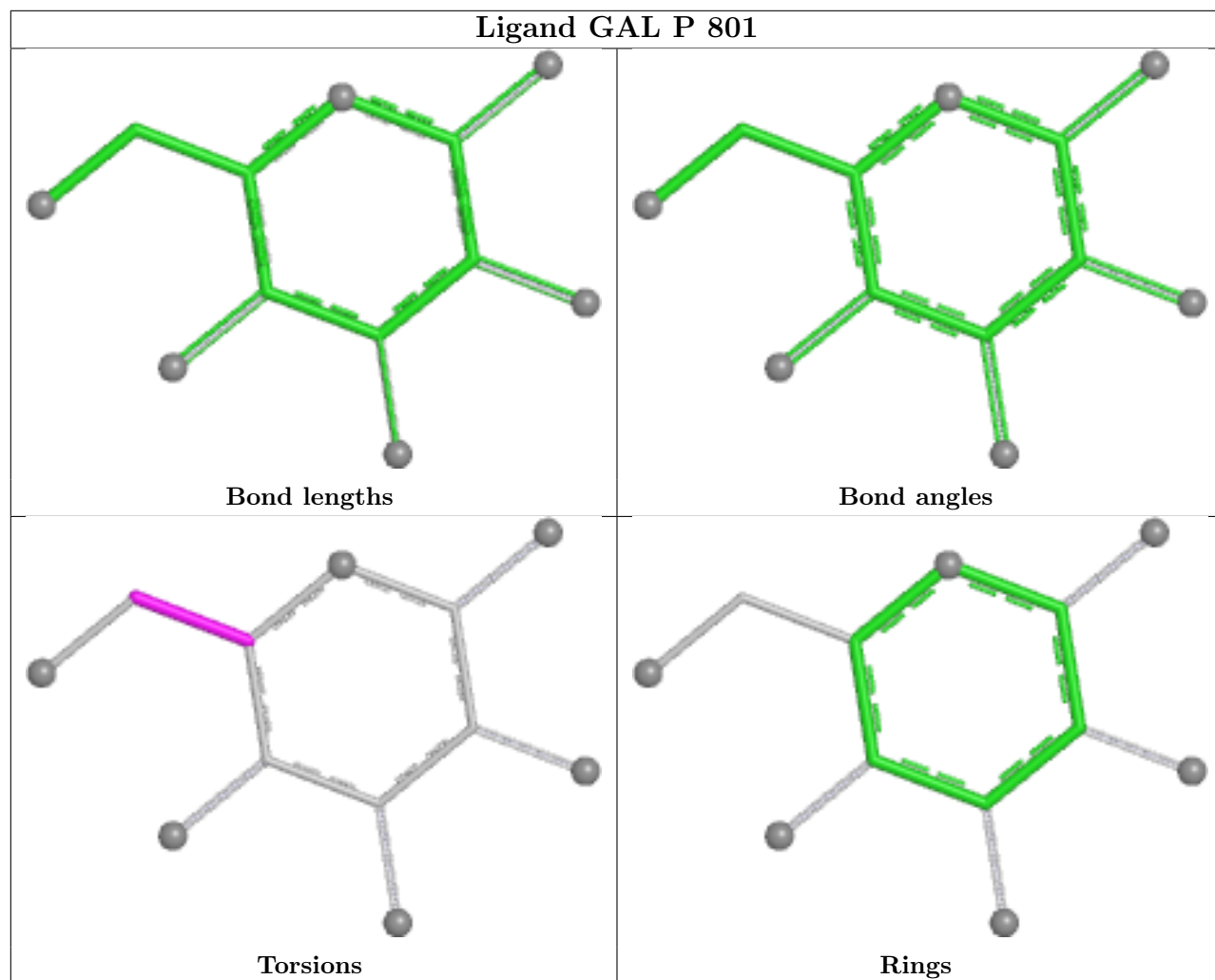


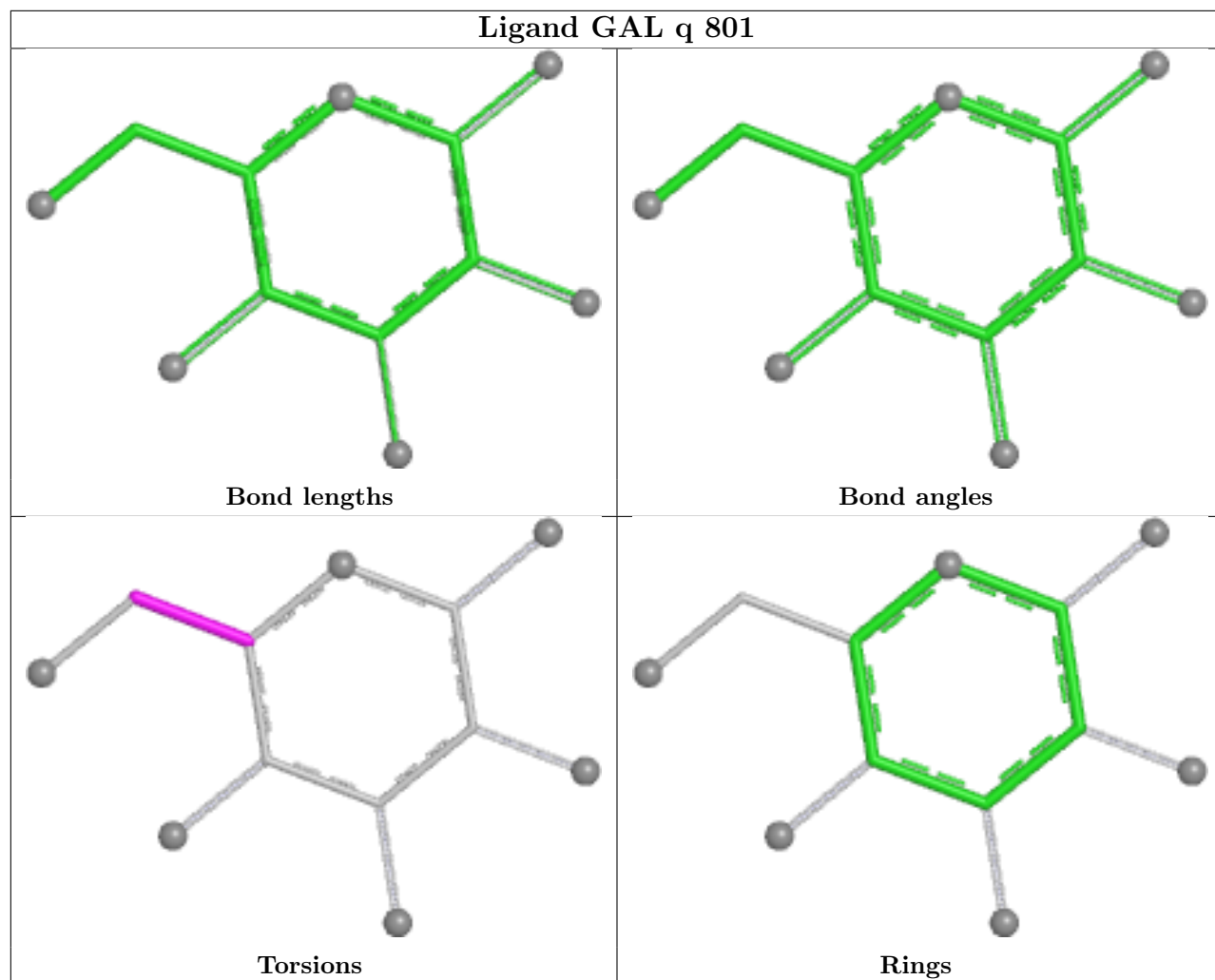


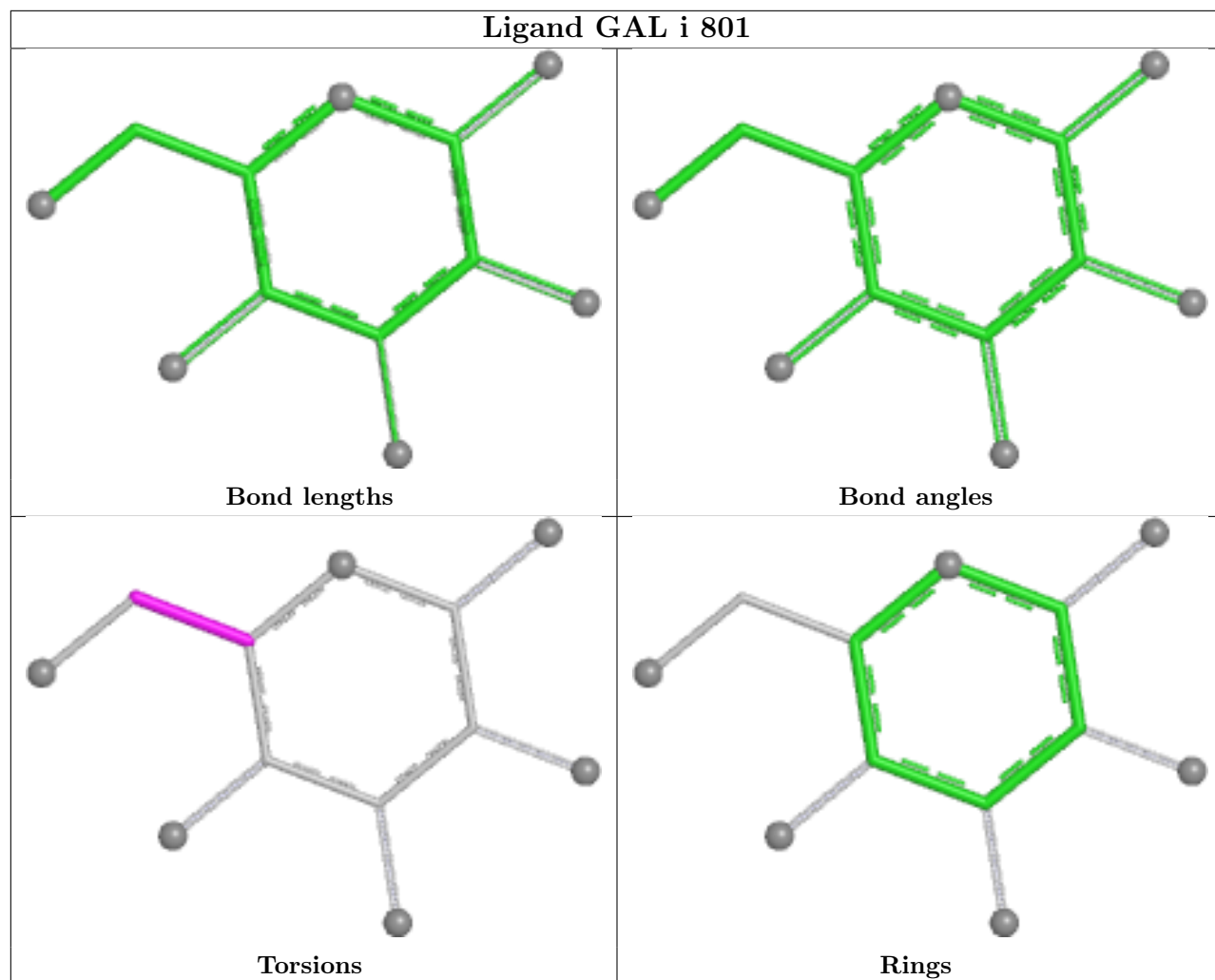


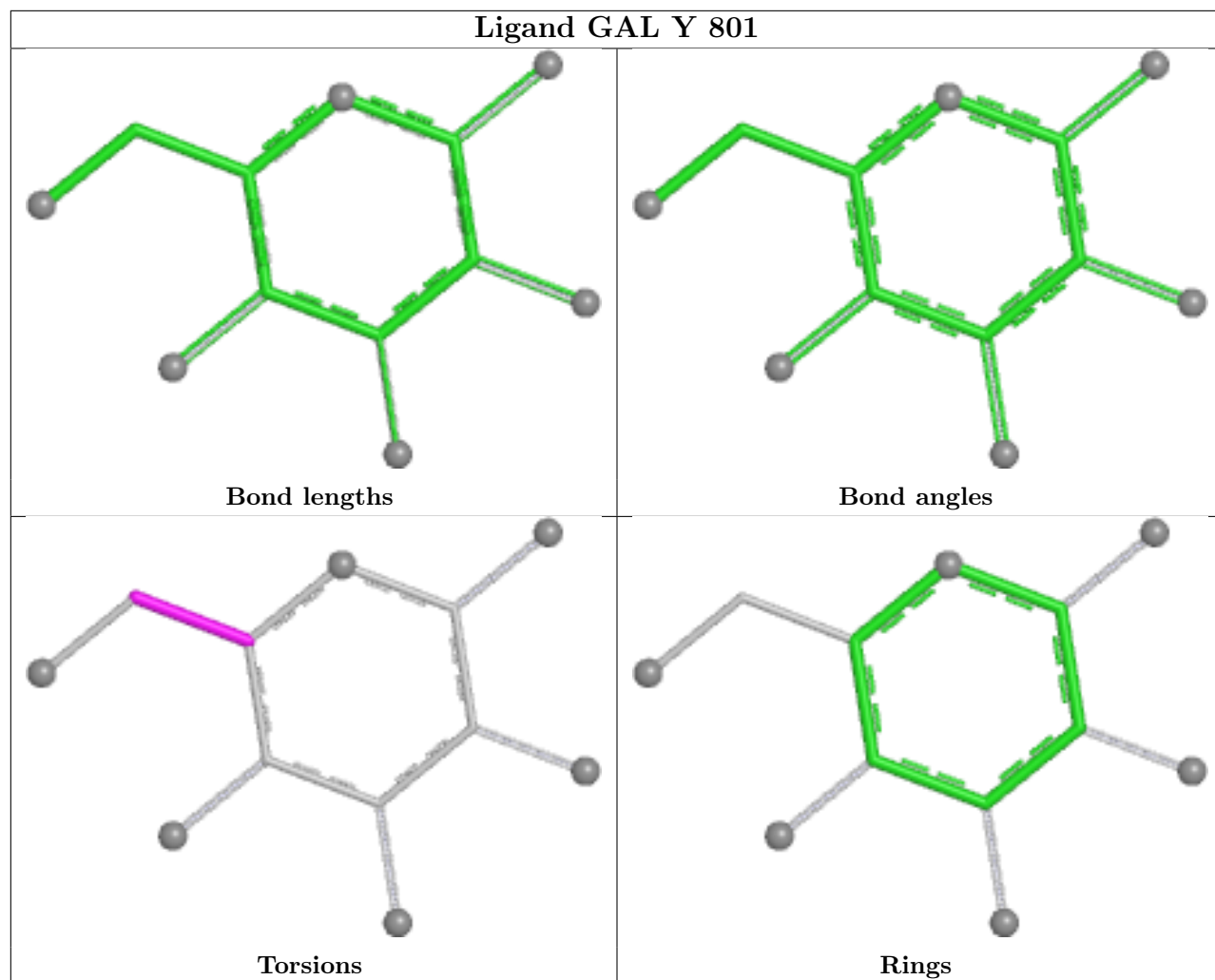


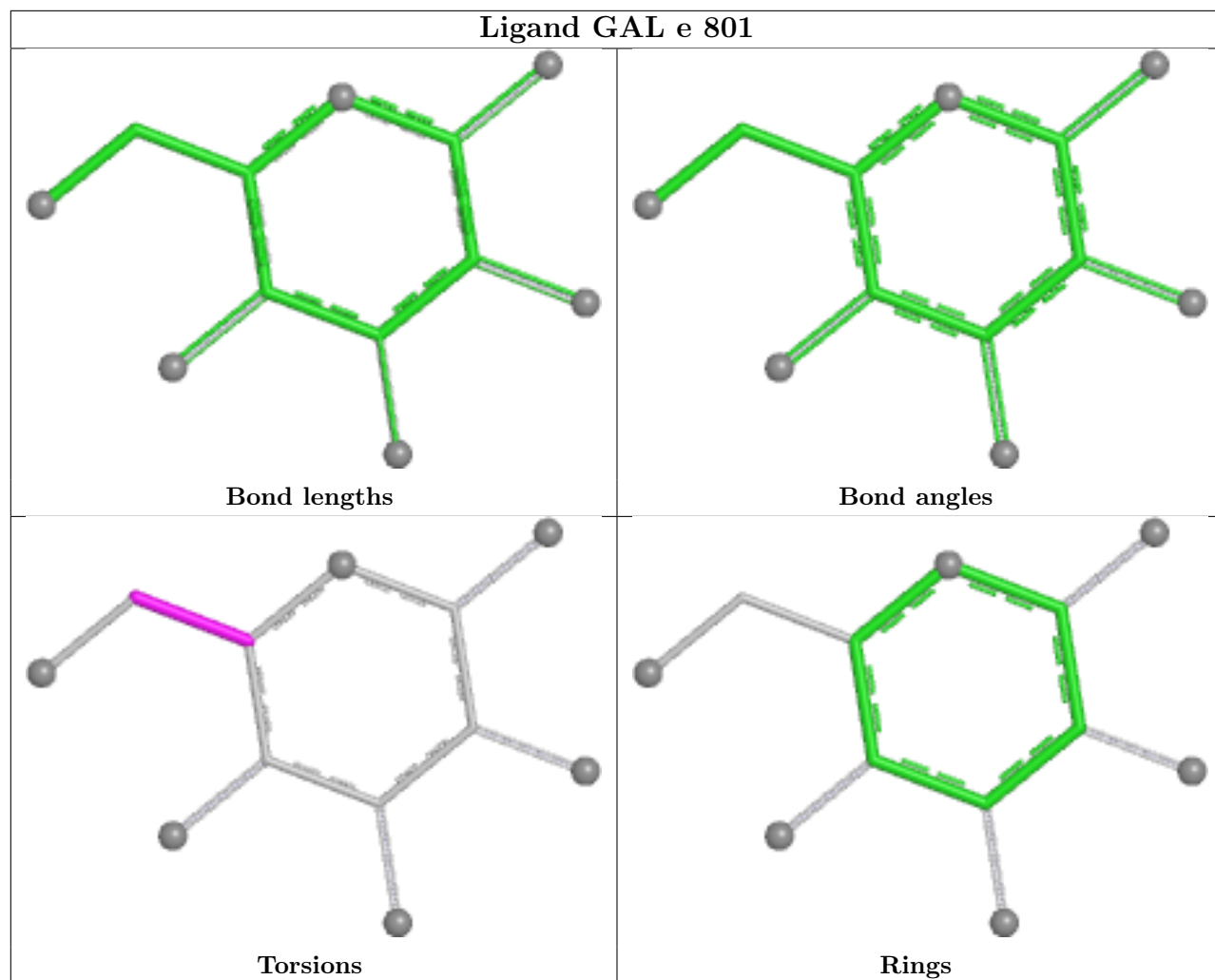


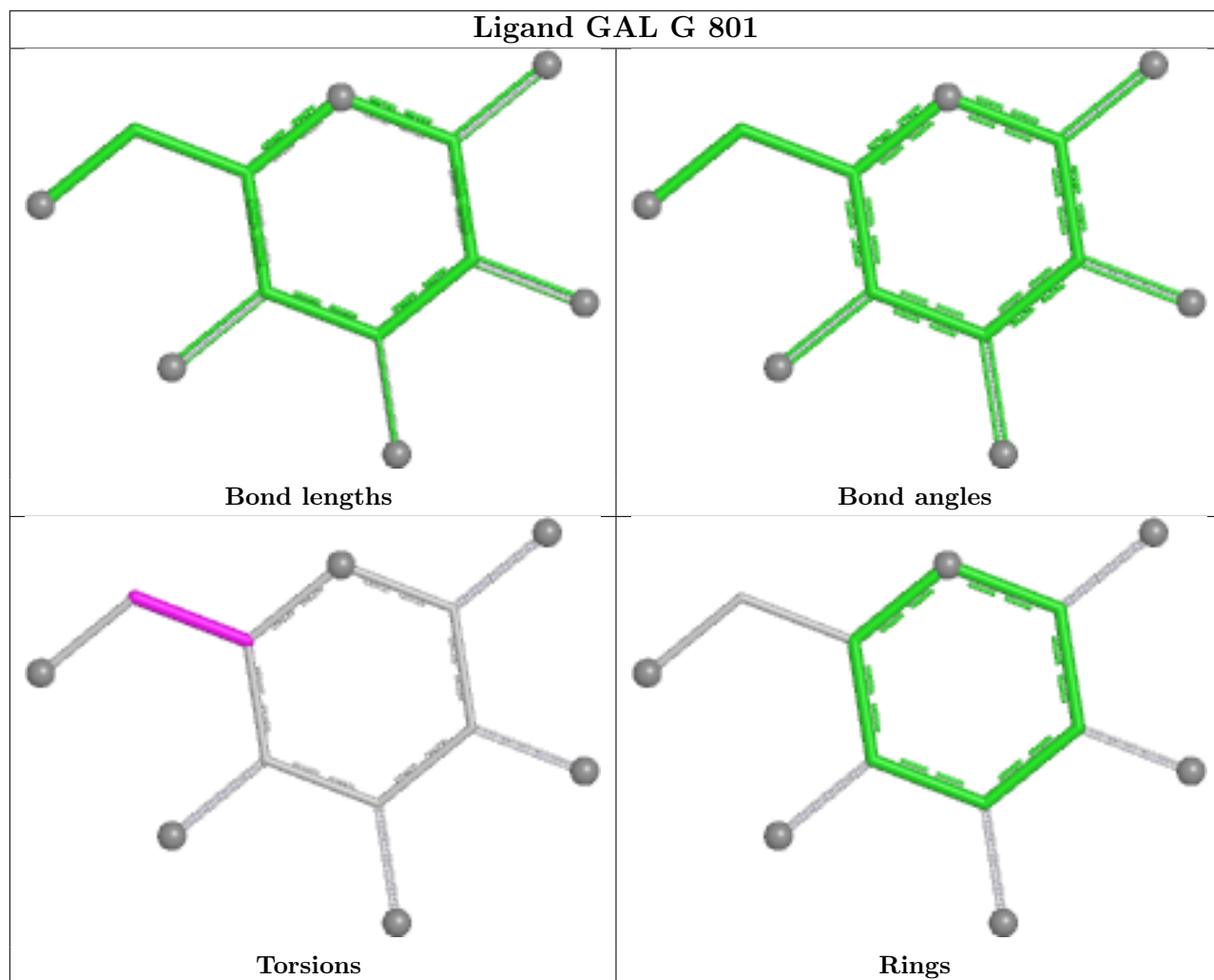


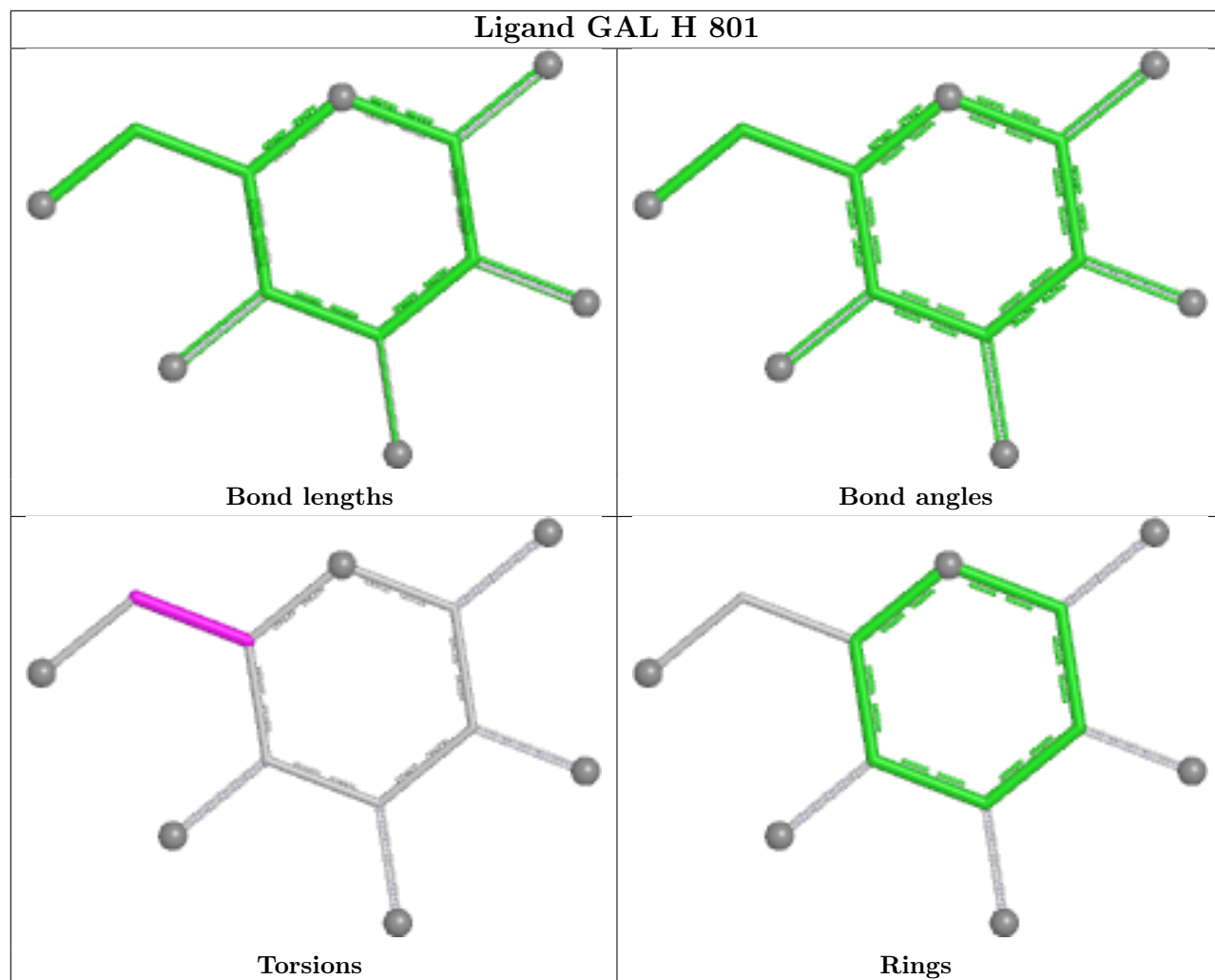


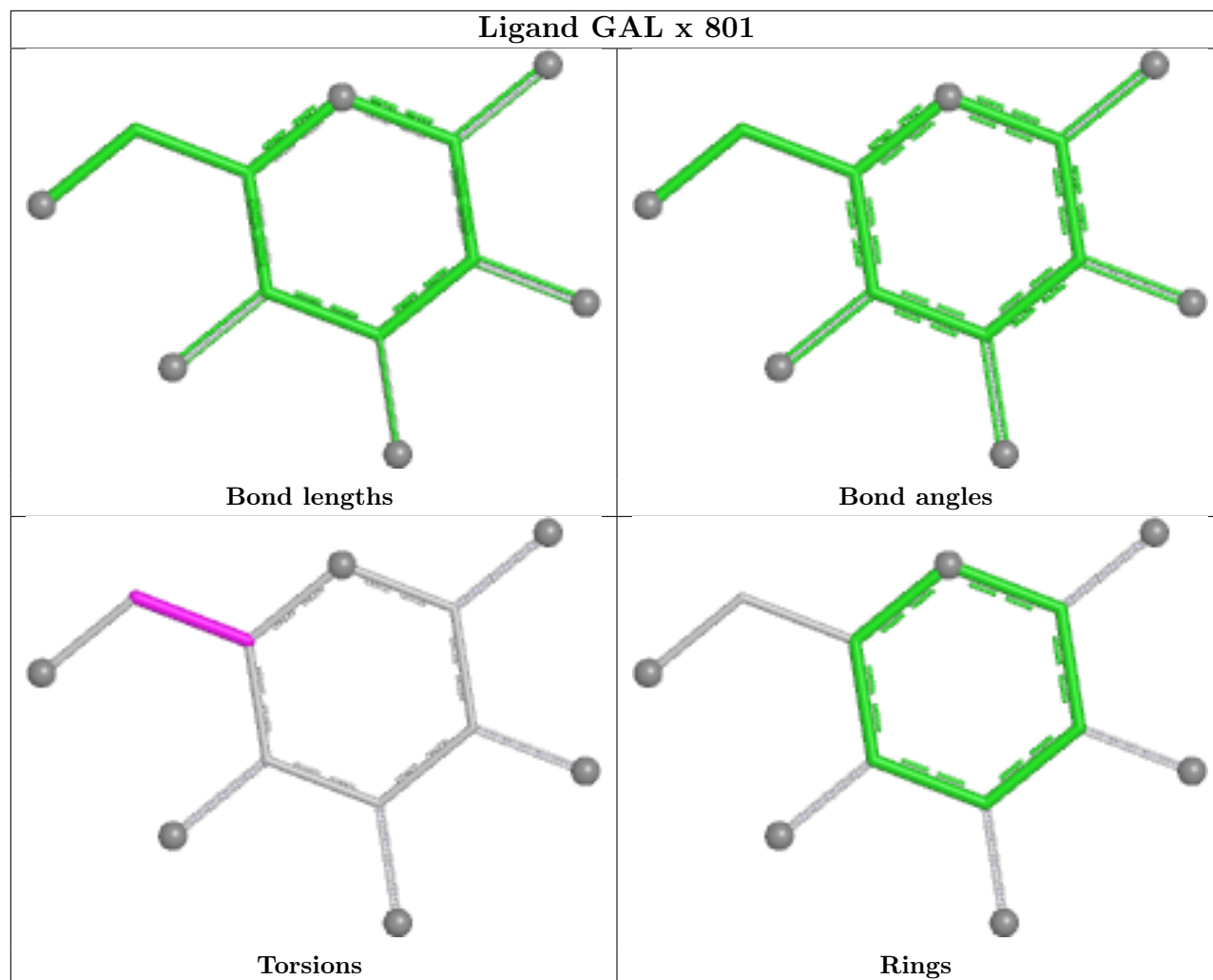


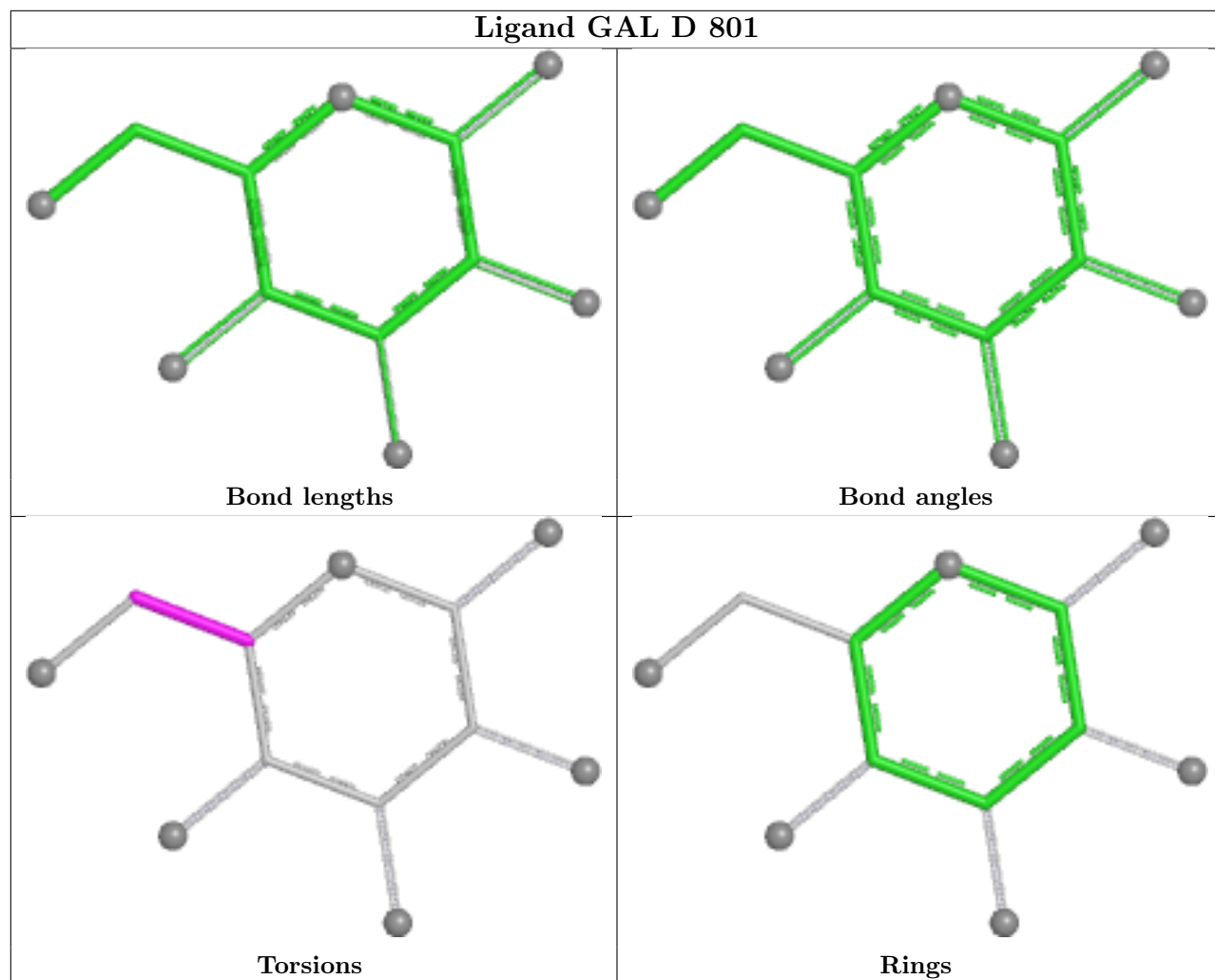


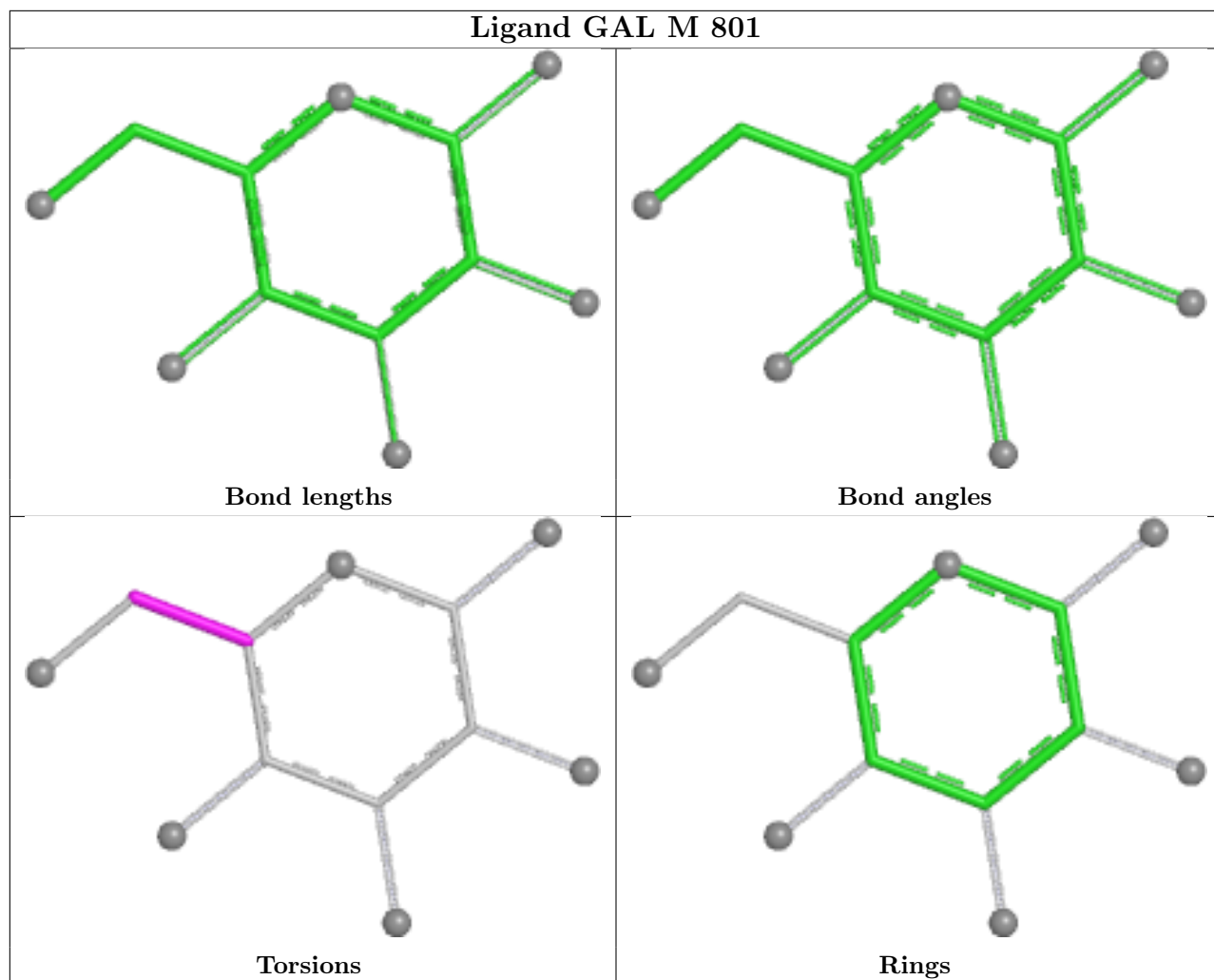


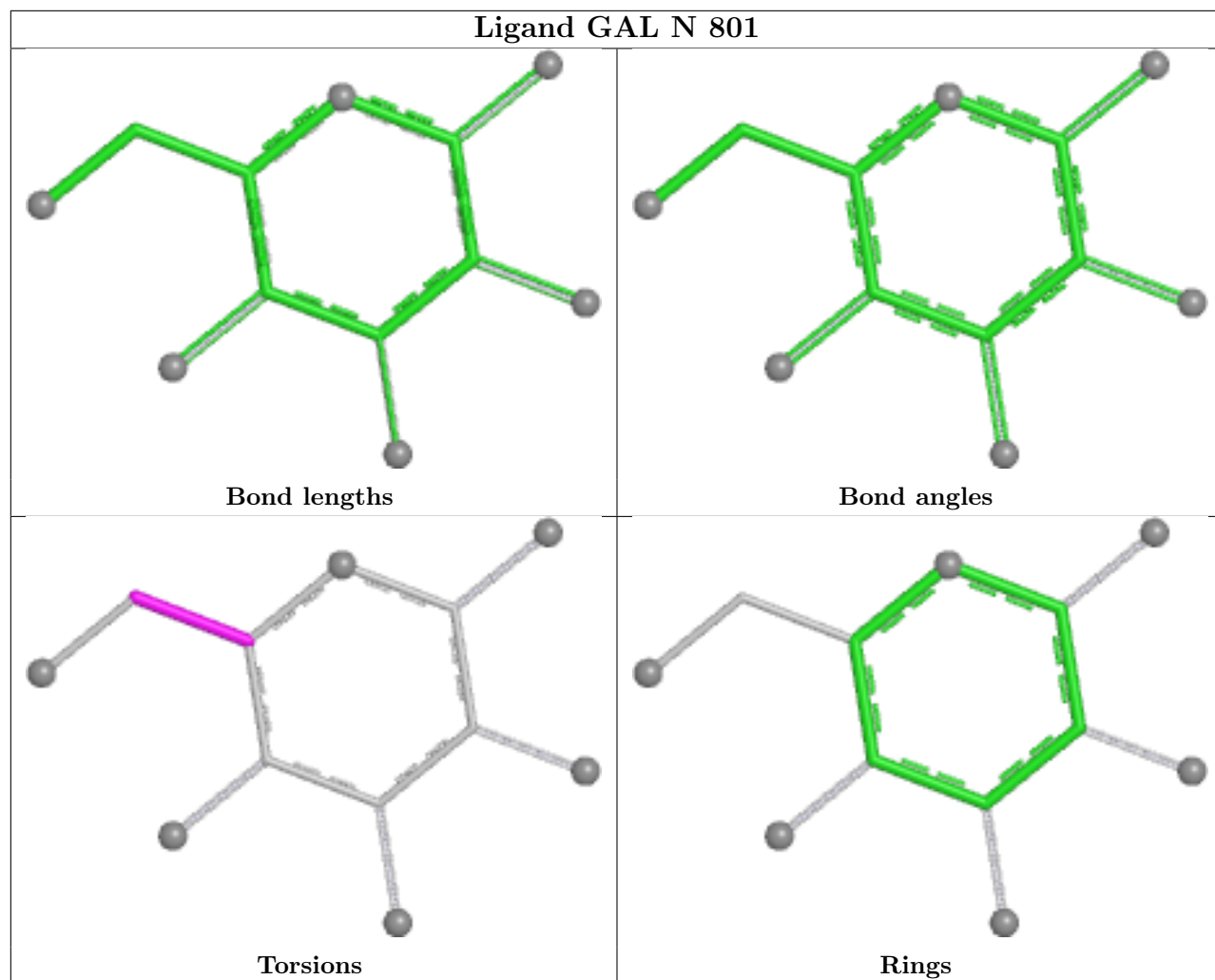


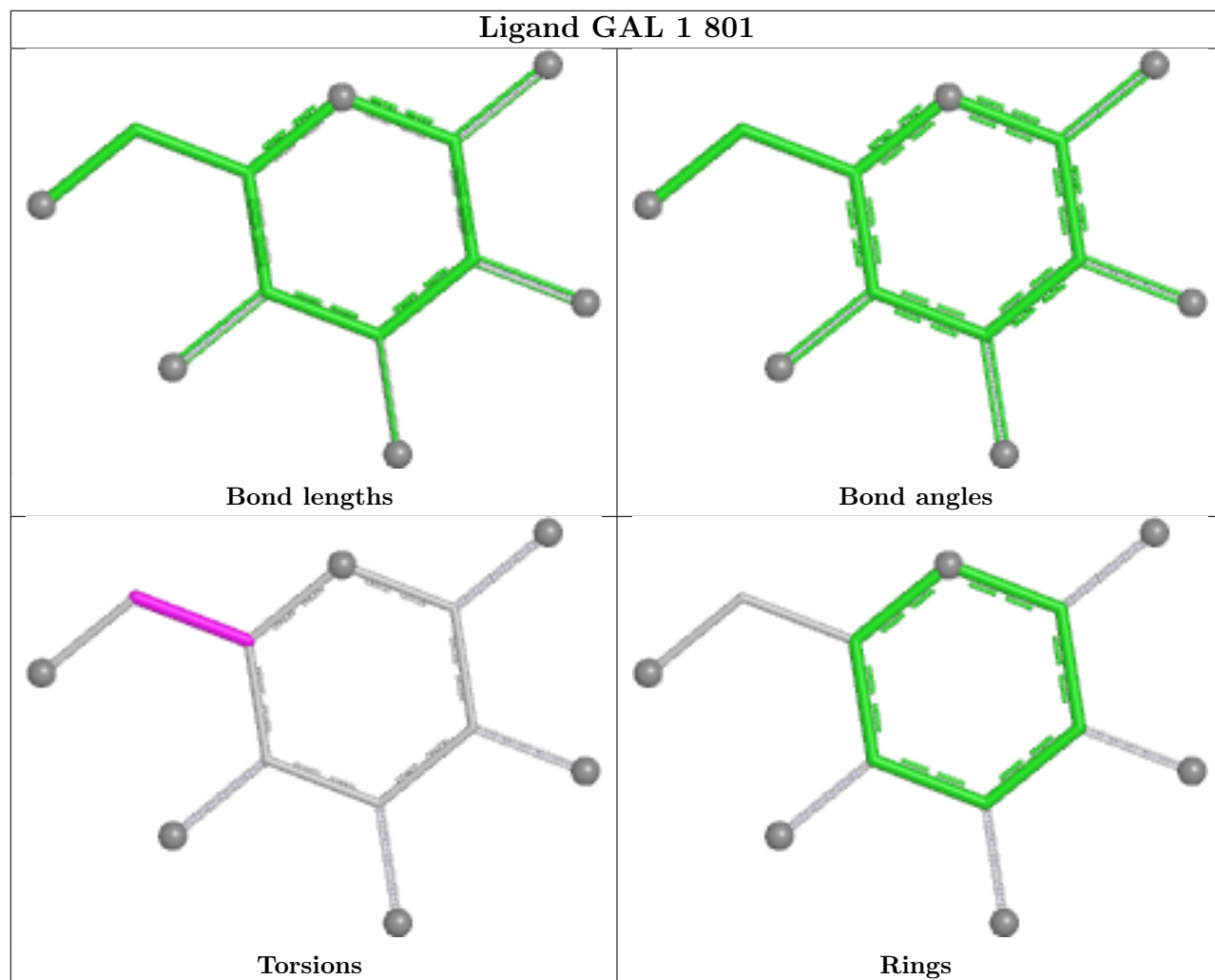


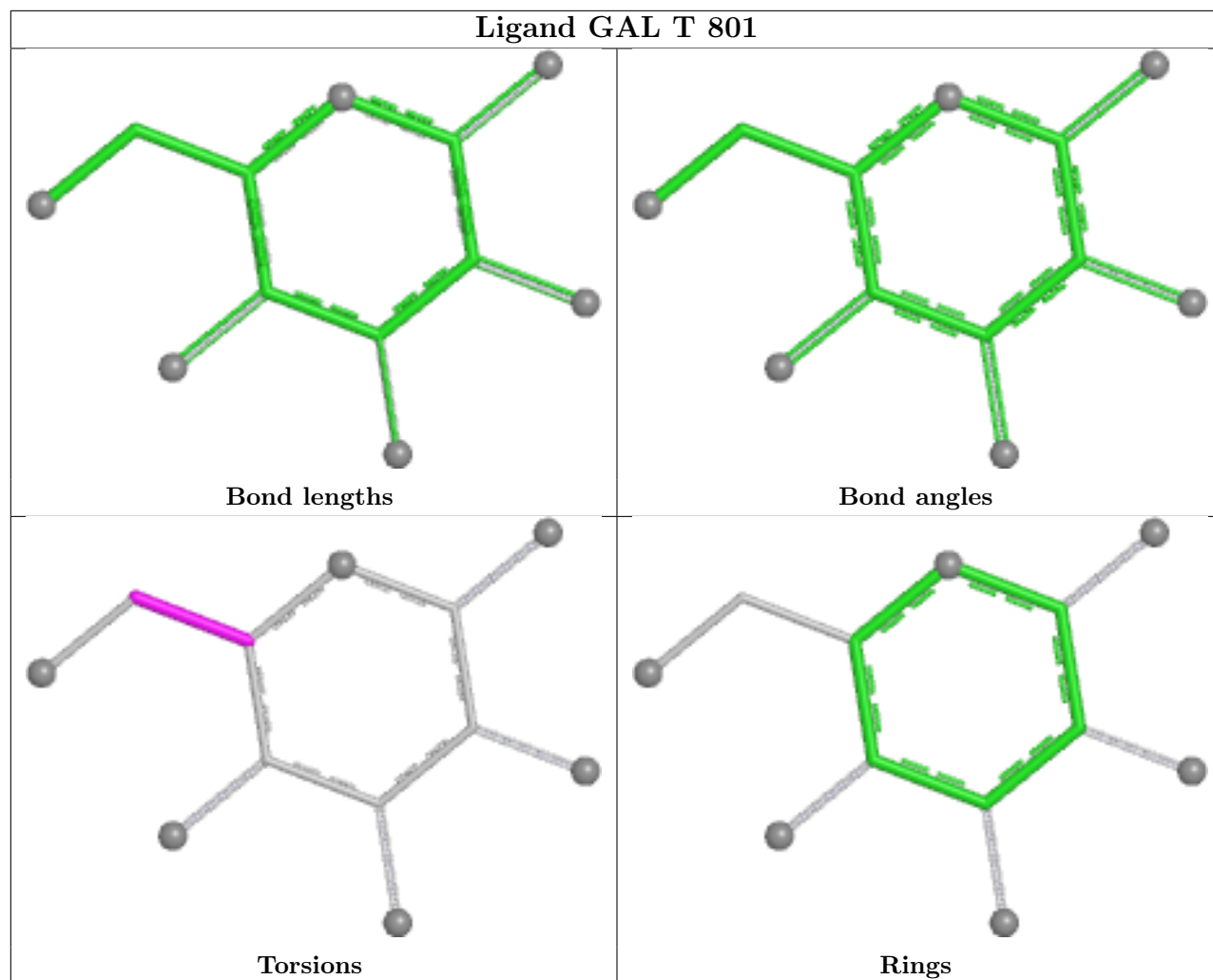


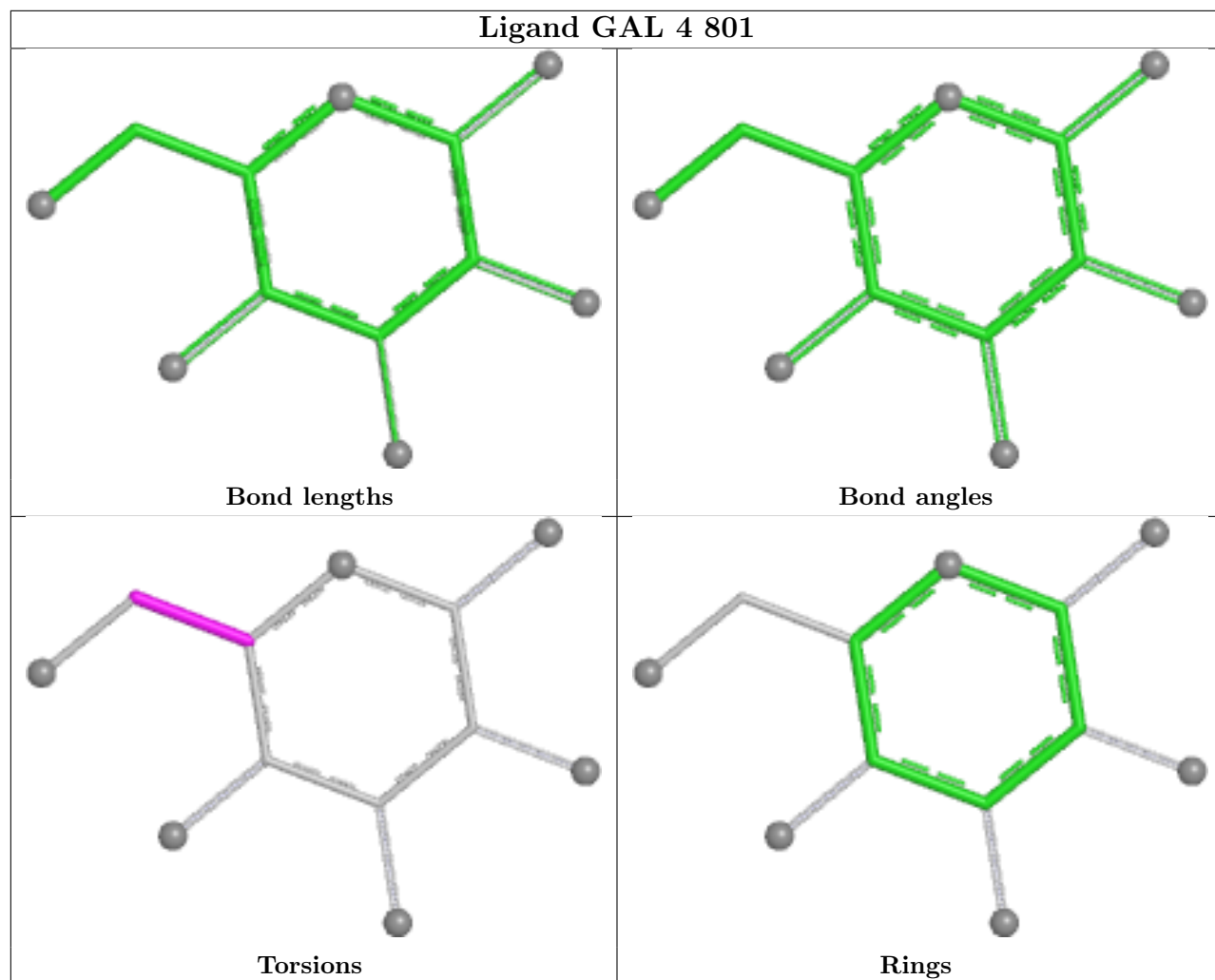


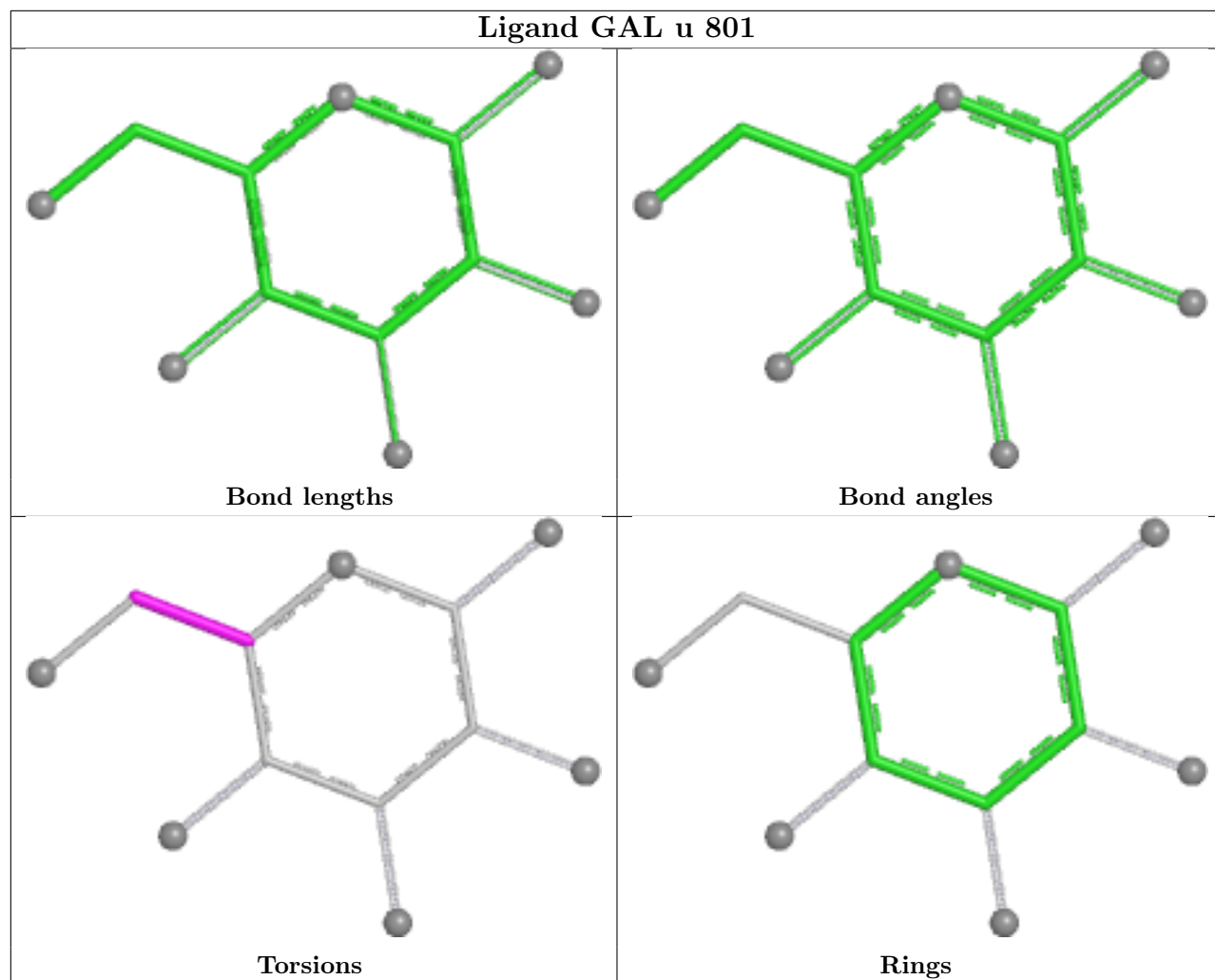


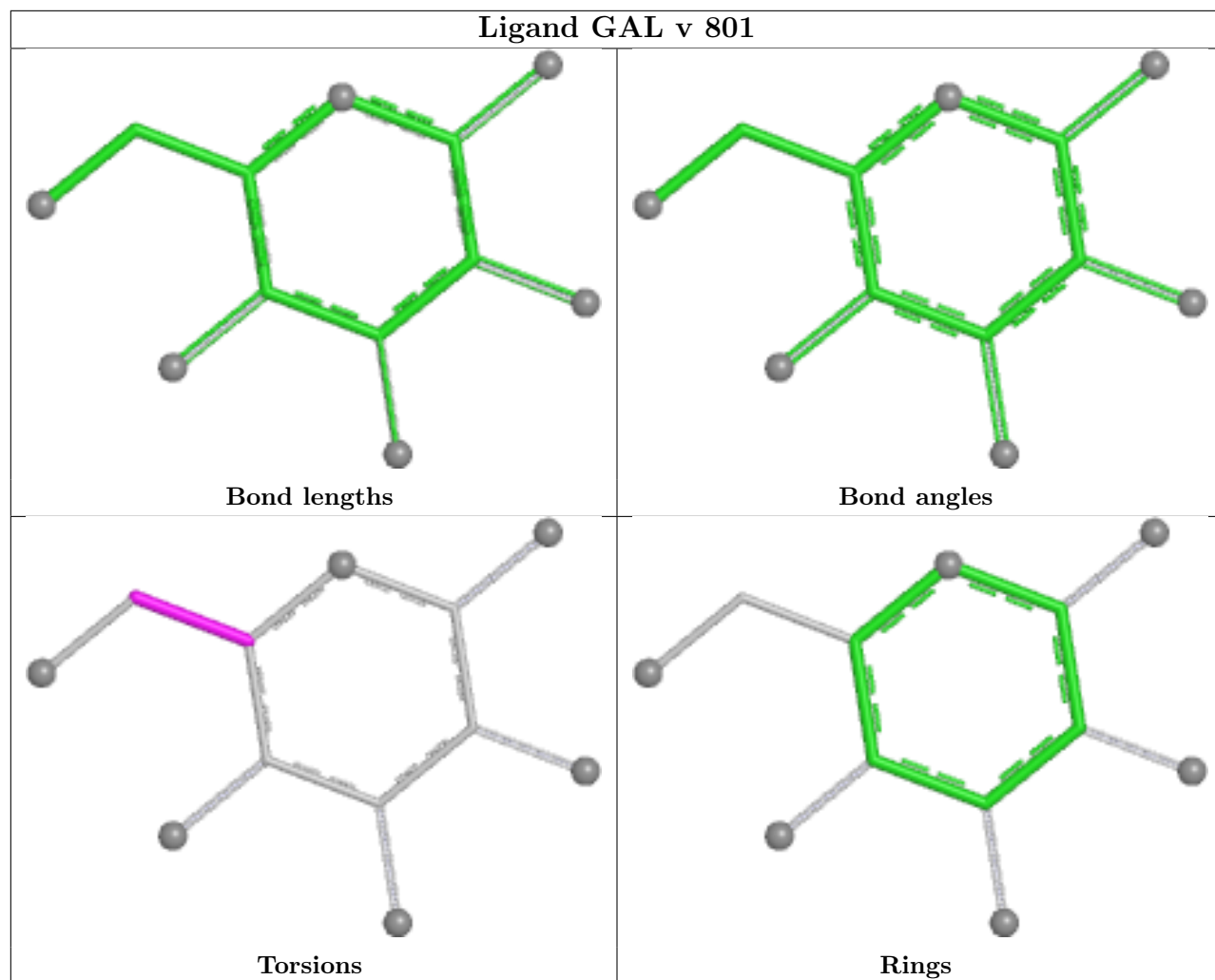


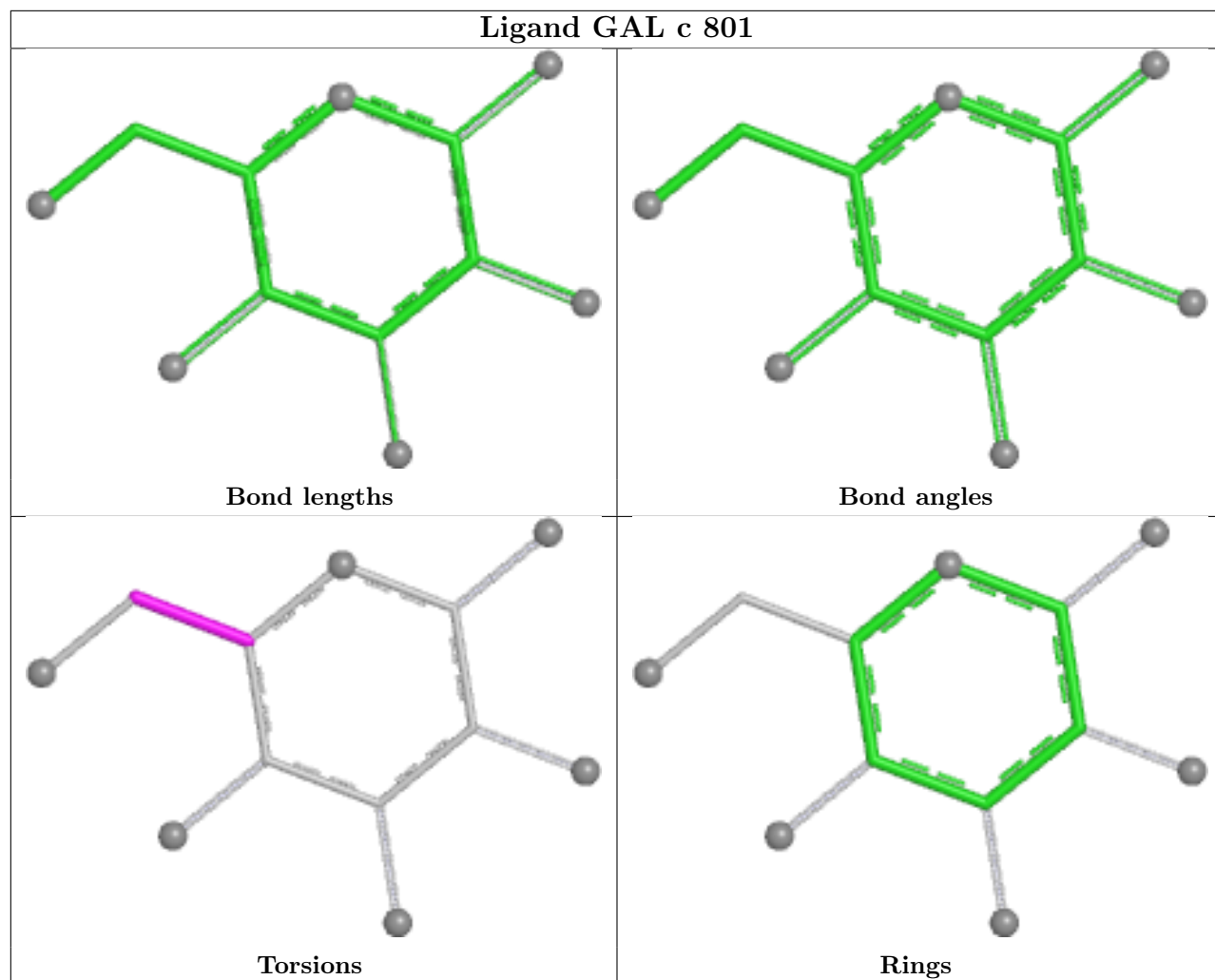


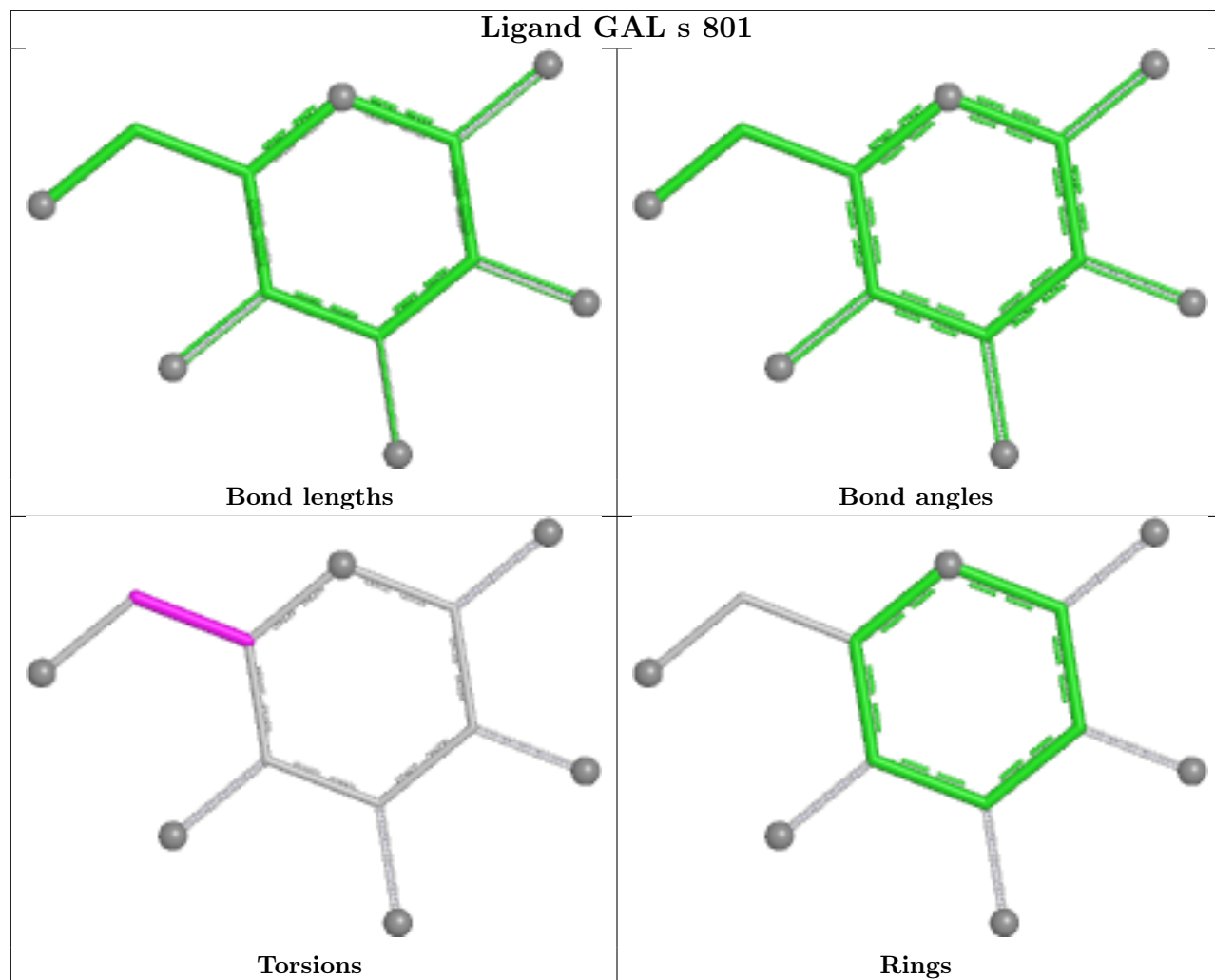


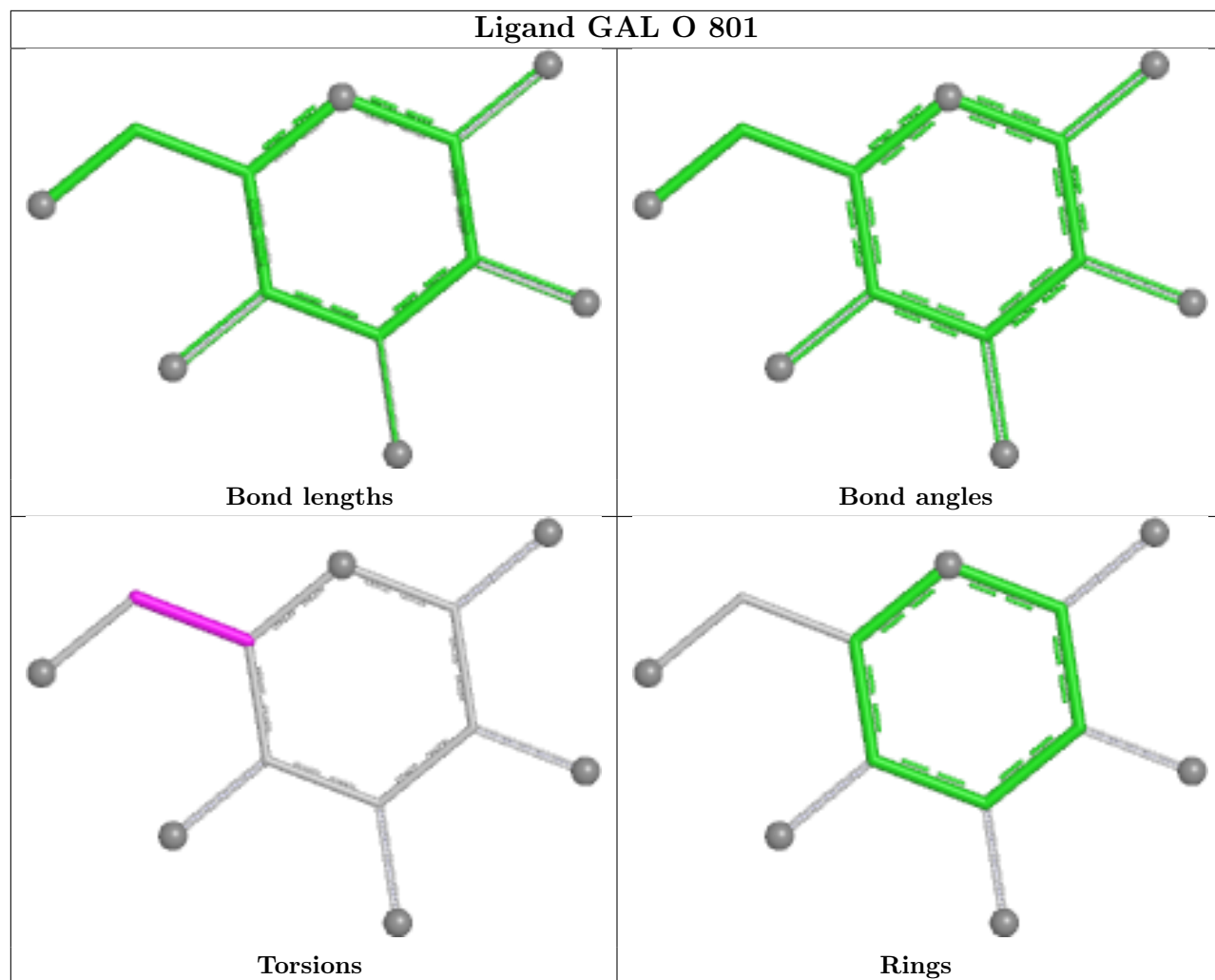


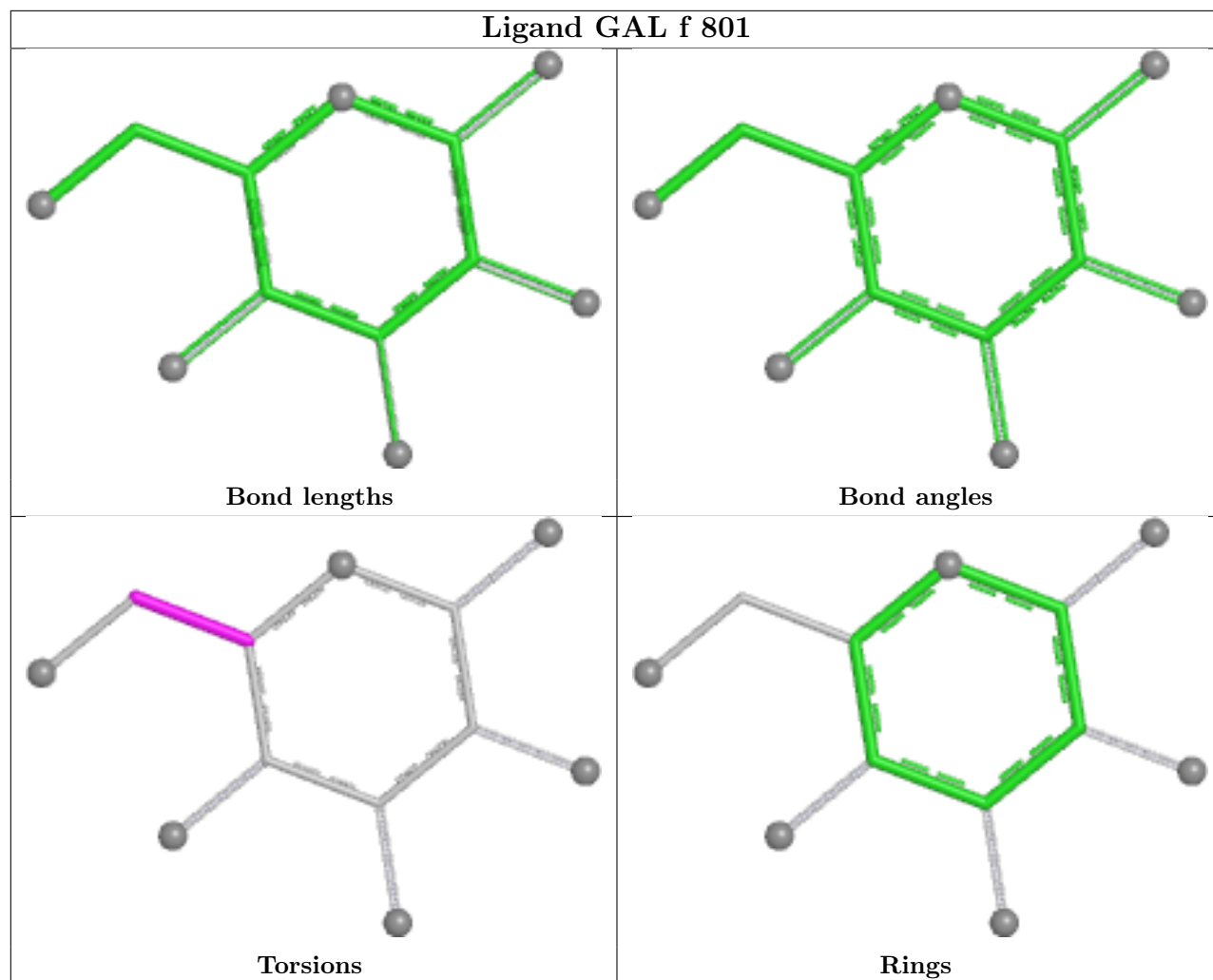


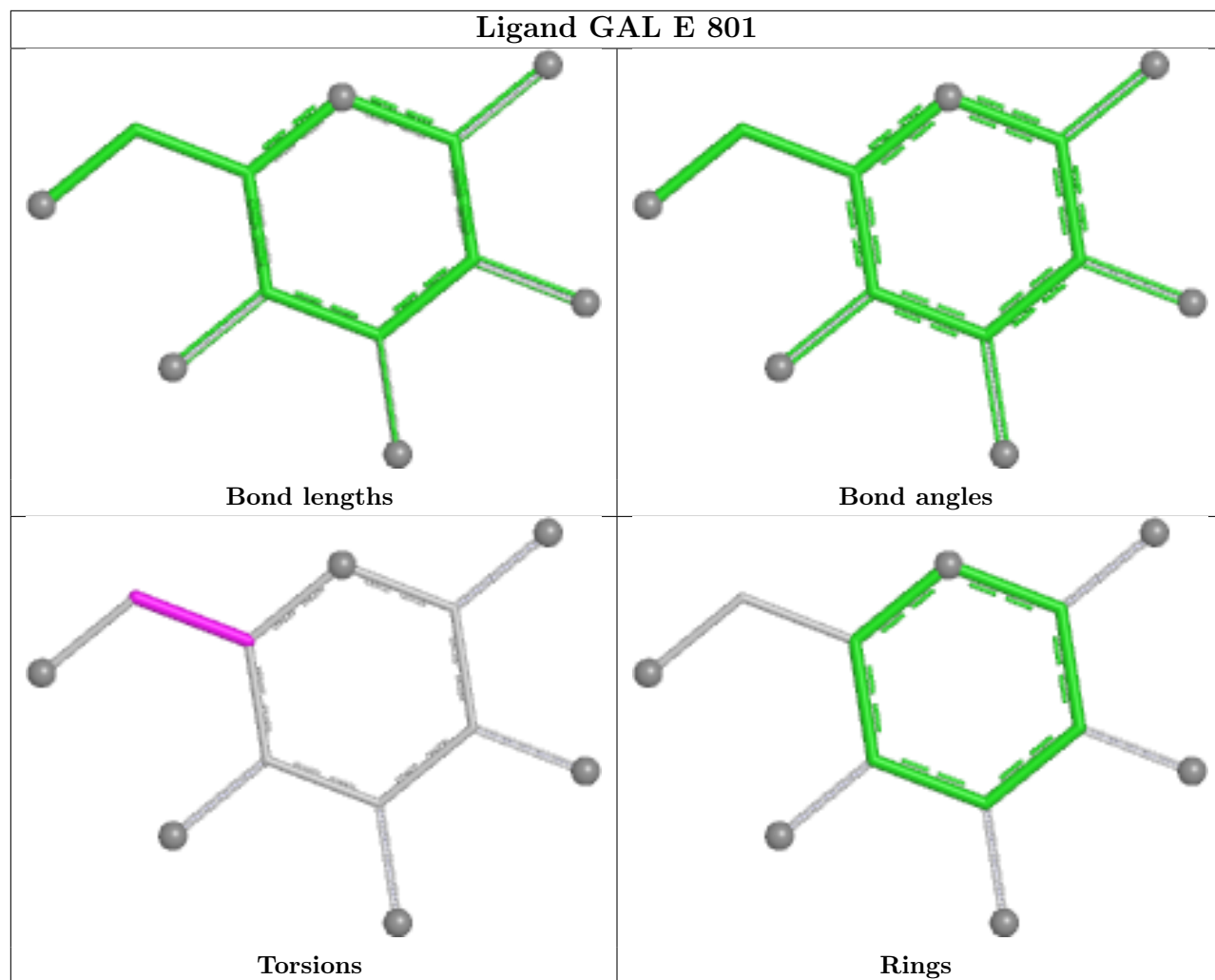


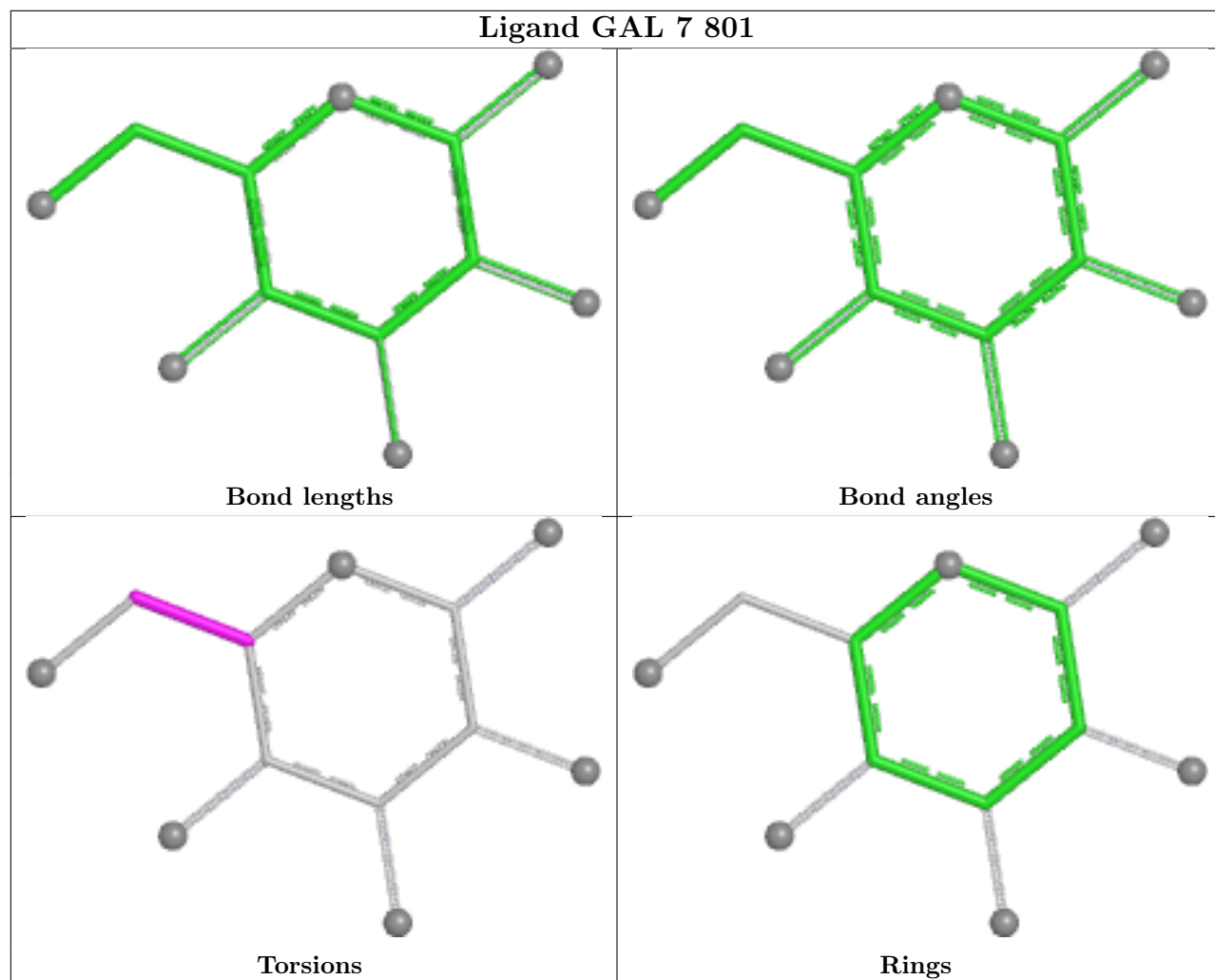


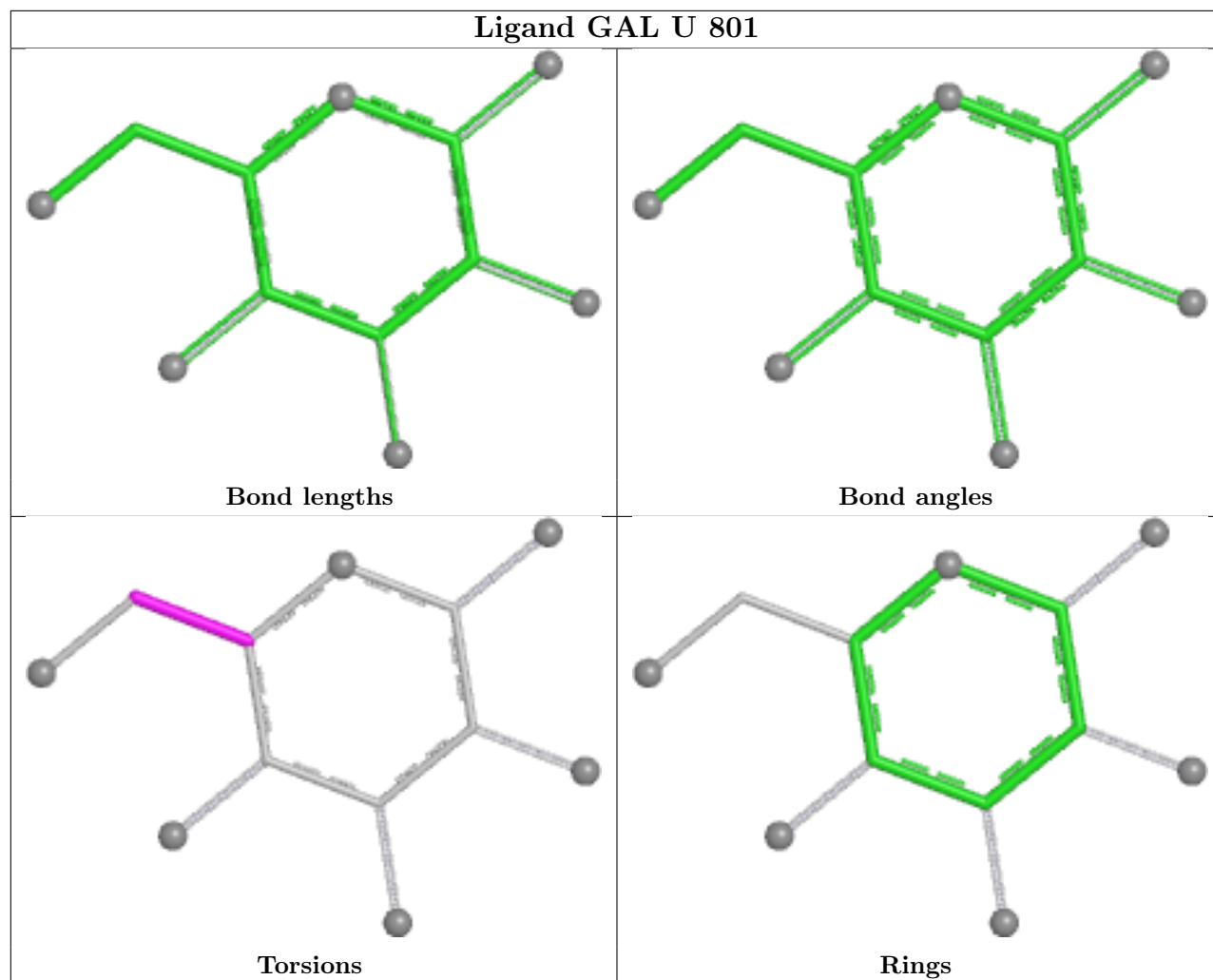


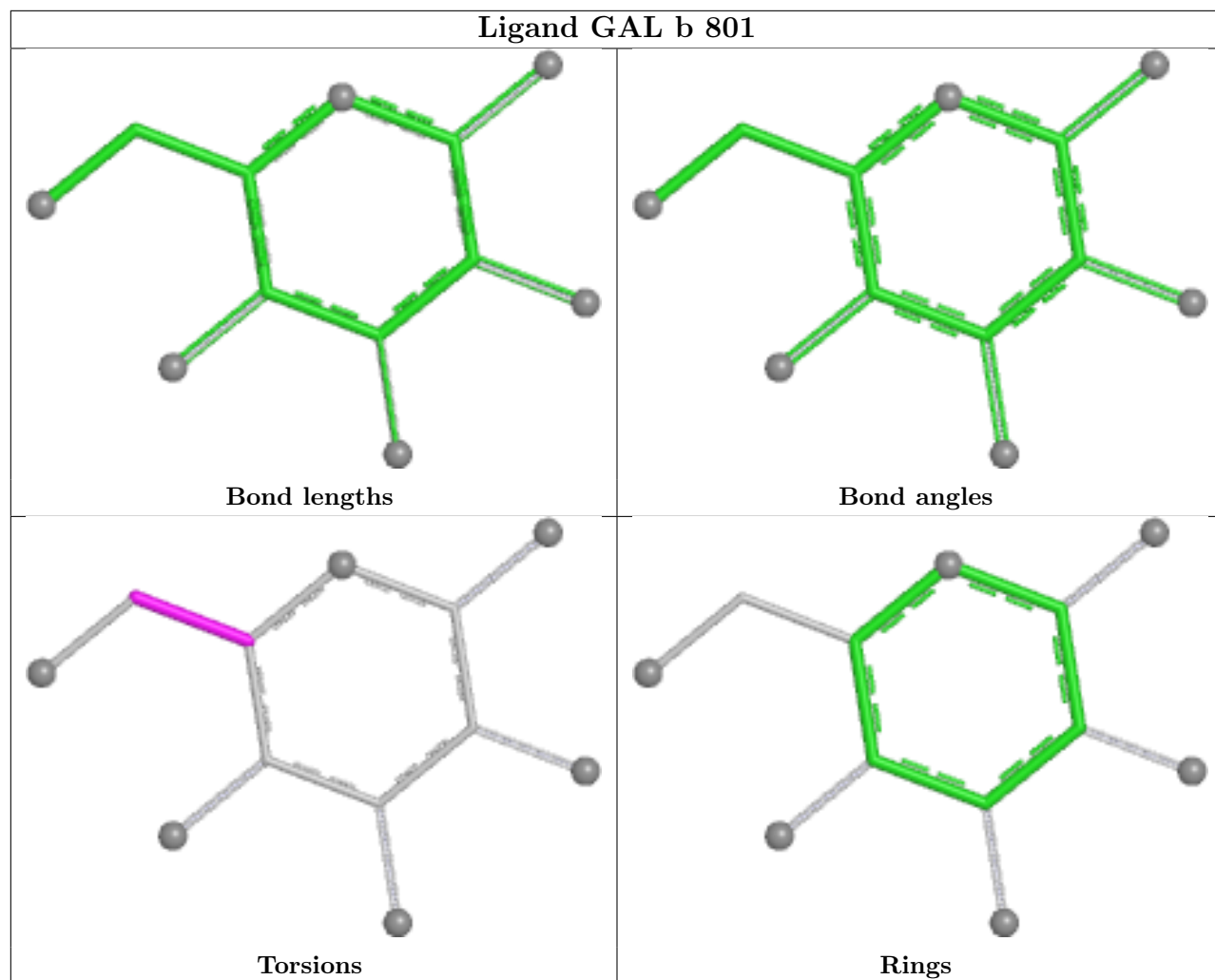


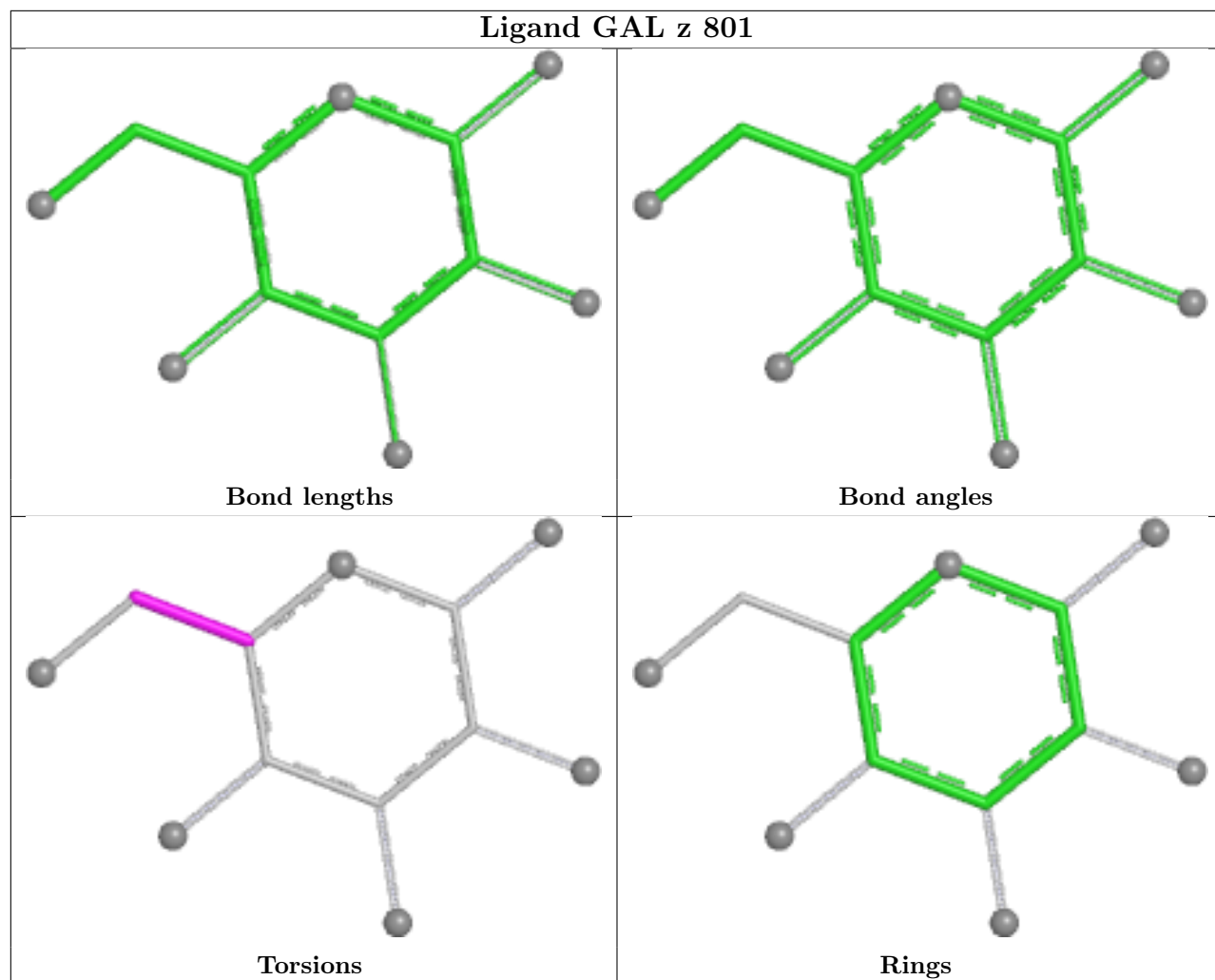


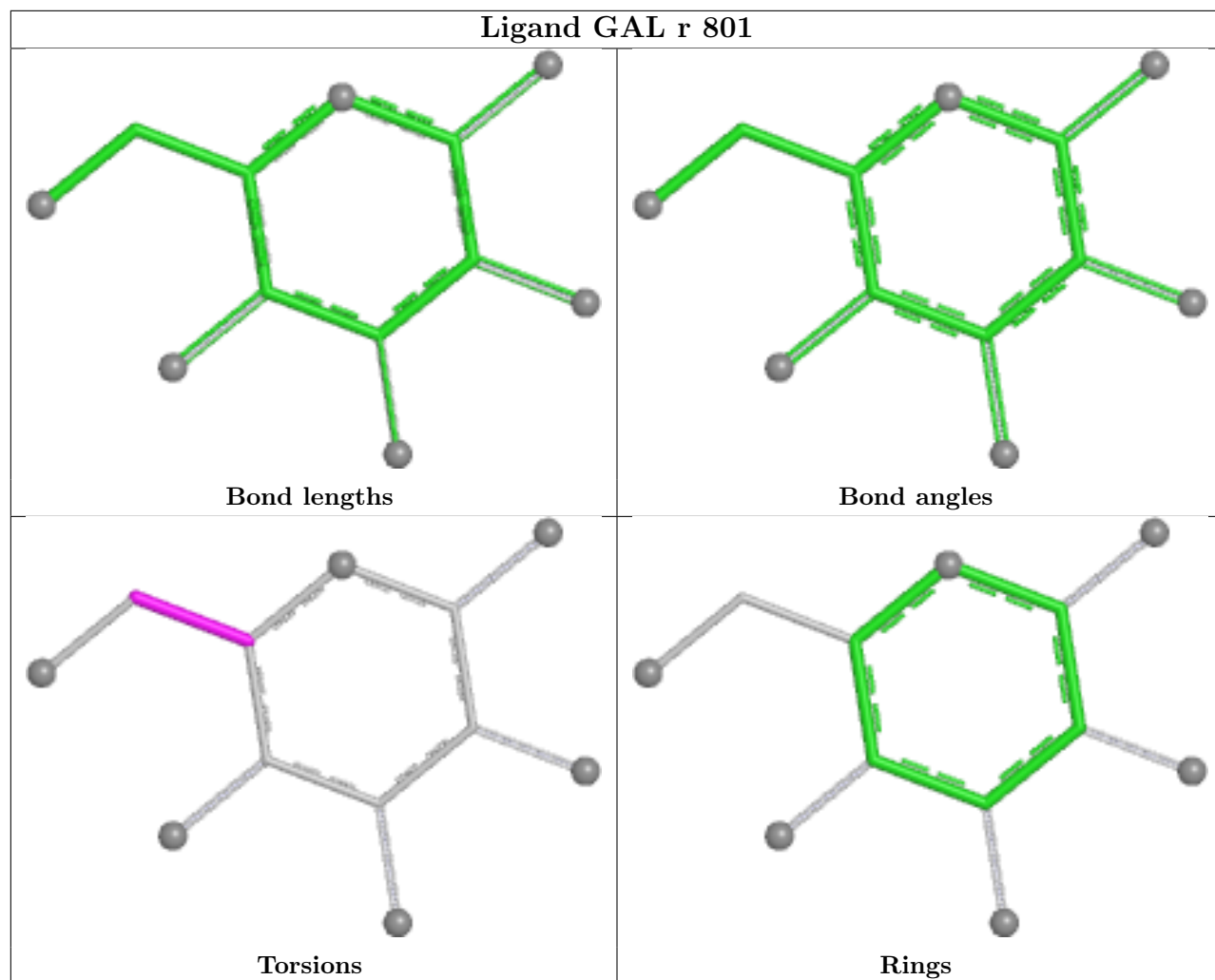


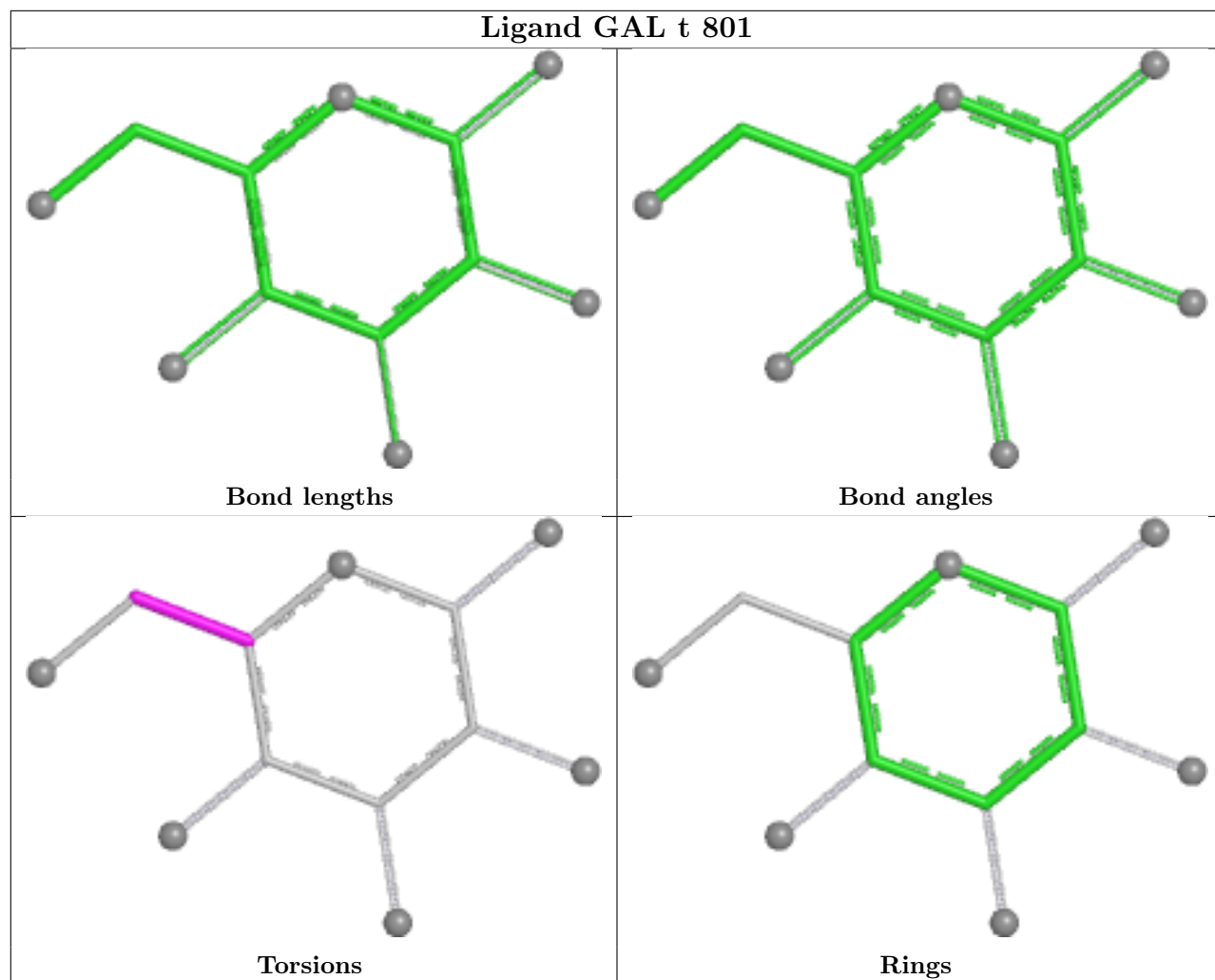


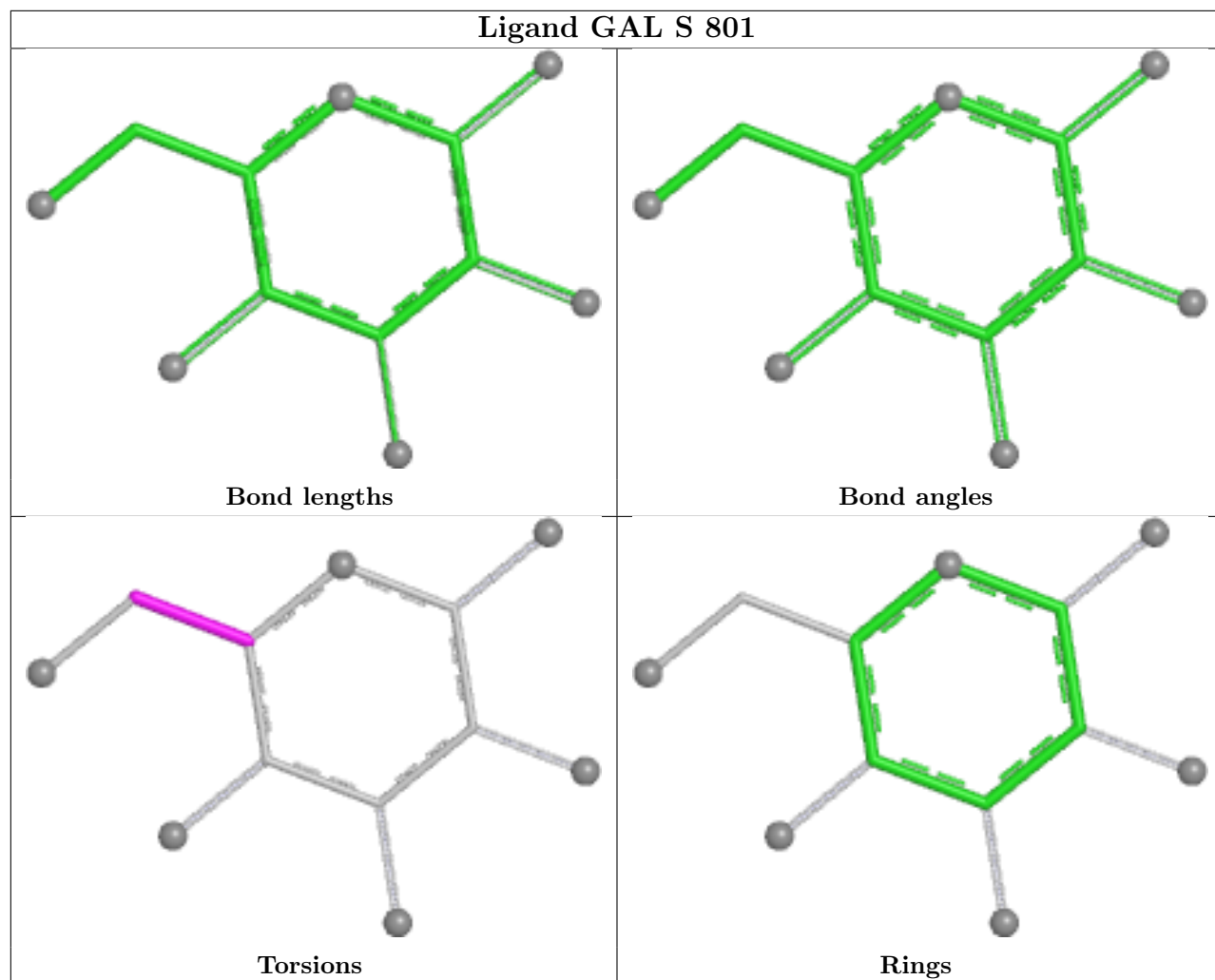


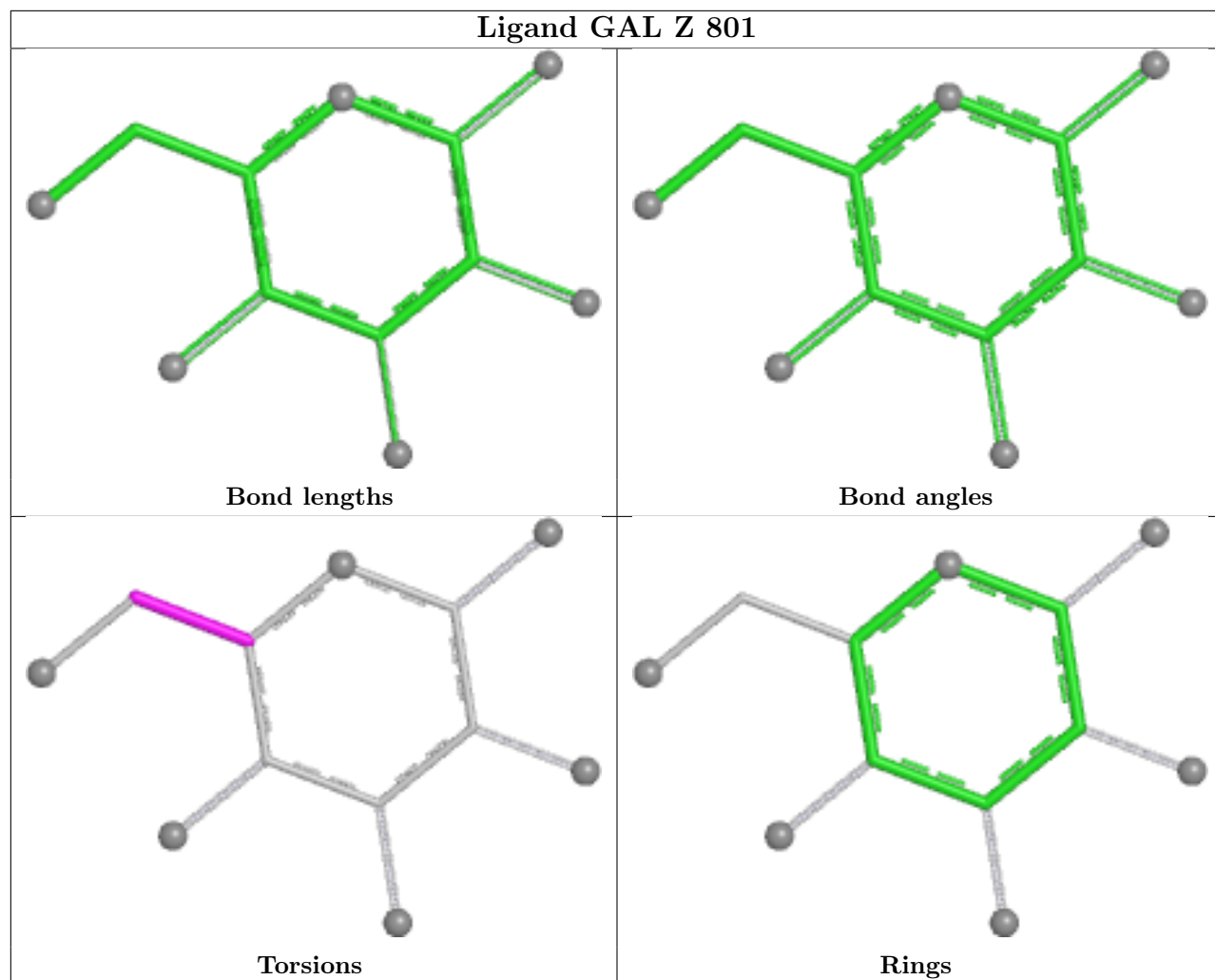


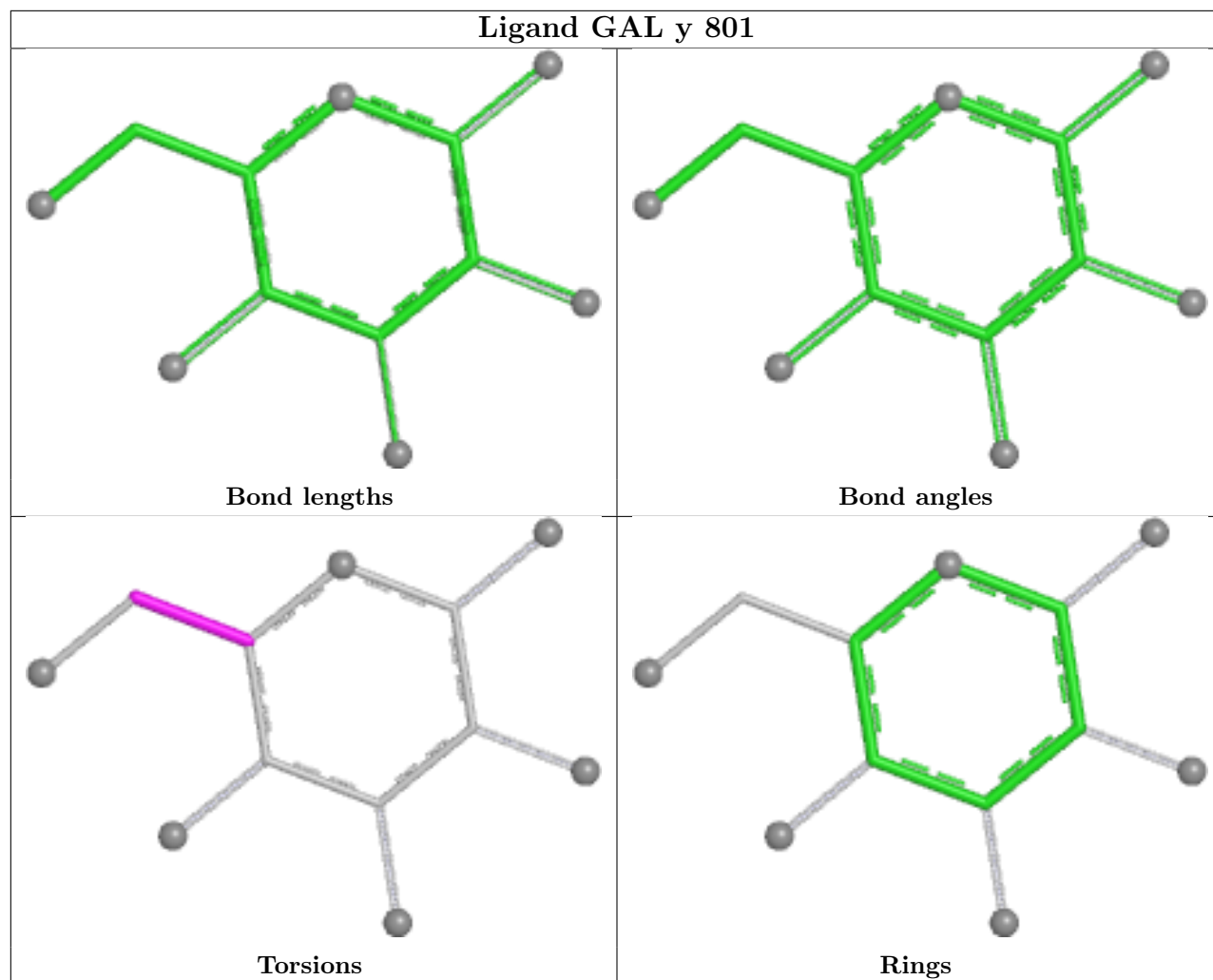












4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.