



Full wwPDB EM Validation Report ⓘ

Nov 21, 2022 – 03:38 AM EST

PDB ID : 7MUA
EMDB ID : EMD-24003
Title : Structure of the adeno-associated virus 9 capsid at pH pH 5.5 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 : 2.68 Å (reported)
Based on initial model : 3UX1

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

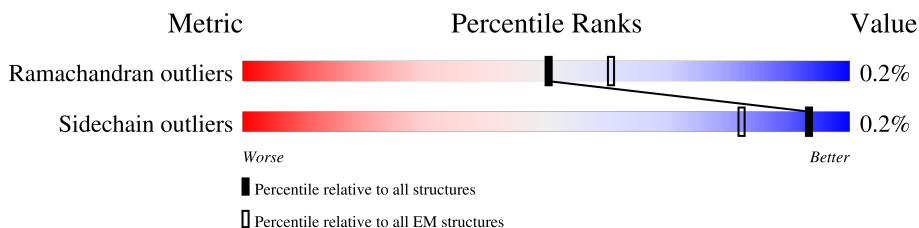
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	1	518	99% .
1	2	518	99% .
1	3	518	99% .
1	4	518	99% .
1	5	518	99% .
1	6	518	99% .
1	7	518	99% .
1	8	518	99% .
1	A	518	99% .
1	B	518	99% .

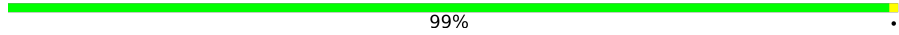
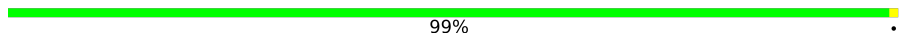
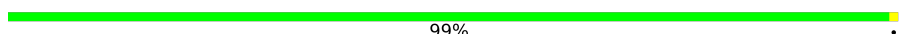
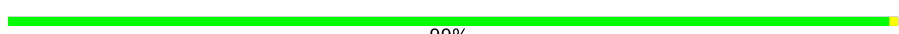


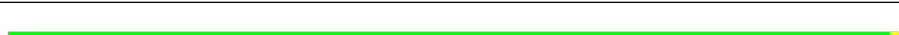
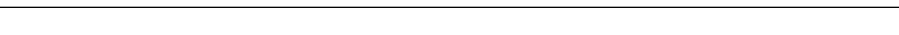
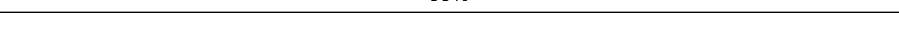
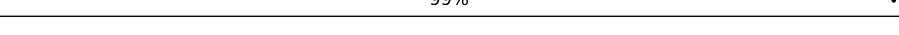
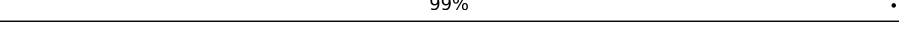
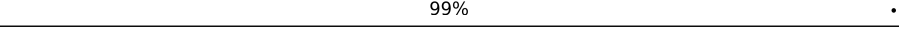
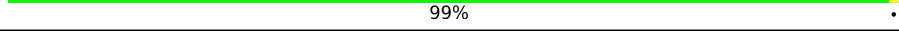
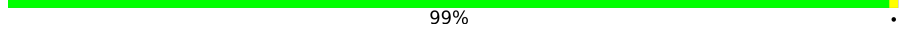
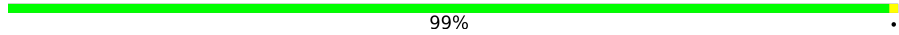
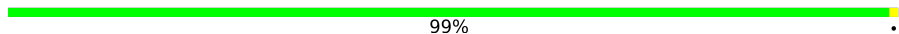
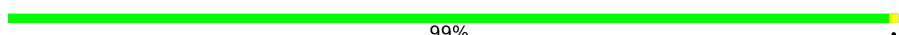
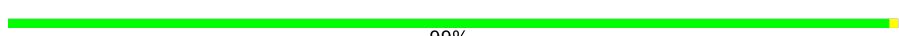





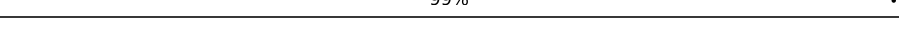
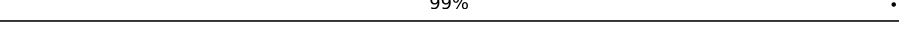
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	C	518	99%
1	D	518	99%
1	E	518	99%
1	F	518	99%
1	G	518	99%
1	H	518	99%
1	I	518	99%
1	J	518	99%
1	K	518	99%
1	L	518	99%
1	M	518	99%
1	N	518	99%
1	O	518	99%
1	P	518	99%
1	Q	518	99%
1	R	518	99%
1	S	518	99%
1	T	518	99%
1	U	518	99%
1	V	518	99%
1	W	518	99%
1	X	518	99%
1	Y	518	99%
1	Z	518	99%
1	a	518	99%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	b	518	 99%
1	c	518	 99%
1	d	518	 99%
1	e	518	 99%
1	f	518	 99%
1	g	518	 99%
1	h	518	 99%
1	i	518	 99%
1	j	518	 99%
1	k	518	 99%
1	l	518	 99%
1	m	518	 99%
1	n	518	 99%
1	o	518	 99%
1	p	518	 99%
1	q	518	 99%
1	r	518	 99%
1	s	518	 99%
1	t	518	 99%
1	u	518	 99%
1	v	518	 99%
1	w	518	 99%
1	x	518	 99%
1	y	518	 99%
1	z	518	 99%

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

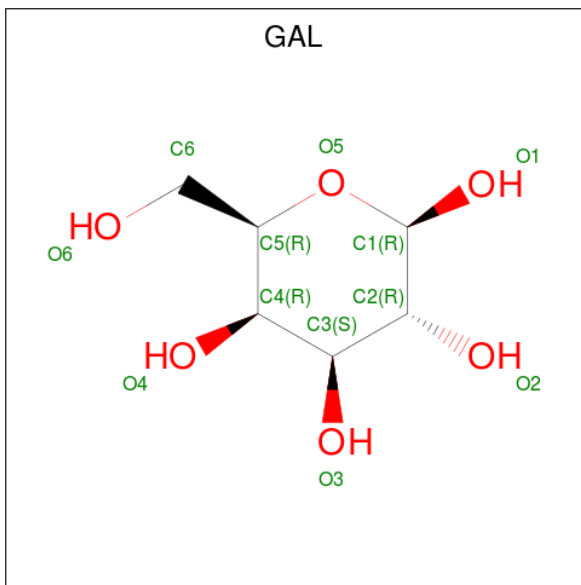
Mol	Chain	Residues	Atoms					AltConf	Trace
1	g	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	h	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	i	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	j	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	k	518	Total 4131	C 2608	N 718	O 791	S 14	0	0
1	l	518	Total 4131	C 2608	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

Continued on next page...

Continued from previous page...

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 (three-letter code: 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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

3 Residue-property plots

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: Capsid protein VP1

Chain A:  99%



- Molecule 1: Capsid protein VP1

Chain B:  99%



- Molecule 1: Capsid protein VP1

Chain C:  99%



- Molecule 1: Capsid protein VP1

Chain D:  99%



- Molecule 1: Capsid protein VP1

Chain E:  99%



- Molecule 1: Capsid protein VP1

Chain F:  99%



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1





- Molecule 1: Capsid protein VP1

Chain N:  99%



- Molecule 1: Capsid protein VP1

Chain O:  99%



- Molecule 1: Capsid protein VP1

Chain P:  99%



- Molecule 1: Capsid protein VP1

Chain Q:  99%



- Molecule 1: Capsid protein VP1

Chain R:  99%



- Molecule 1: Capsid protein VP1

Chain S:  99%



- Molecule 1: Capsid protein VP1

Chain T:  99%



- Molecule 1: Capsid protein VP1

Chain U:  99%



- Molecule 1: Capsid protein VP1

Chain V:  99%



- Molecule 1: Capsid protein VP1

Chain W:  99%



- Molecule 1: Capsid protein VP1

Chain X:  99%



- Molecule 1: Capsid protein VP1

Chain Y:  99%



- Molecule 1: Capsid protein VP1

Chain Z:  99%



- Molecule 1: Capsid protein VP1

Chain 1:  99%



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1





● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1





• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1





- Molecule 1: Capsid protein VP1

Chain q:  99%



- Molecule 1: Capsid protein VP1

Chain r:  99%



- Molecule 1: Capsid protein VP1

Chain s:  99%



- Molecule 1: Capsid protein VP1

Chain t:  99%



- Molecule 1: Capsid protein VP1

Chain u:  99%



- Molecule 1: Capsid protein VP1

Chain v:  99%



- Molecule 1: Capsid protein VP1

Chain w:  99%



- Molecule 1: Capsid protein VP1

Chain x:  99%

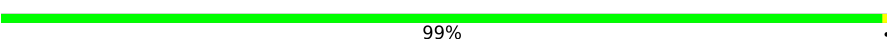


- Molecule 1: Capsid protein VP1

Chain y:  99%



- Molecule 1: Capsid protein VP1

Chain z:  99%



- Molecule 1: Capsid protein VP1

Chain 7:  99%



- Molecule 1: Capsid protein VP1

Chain 8:  99%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	110690	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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GAL

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	1	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	2	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	3	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	4	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	5	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	6	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	7	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	8	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	A	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	B	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	C	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	D	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	E	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	F	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	G	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	H	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	I	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	J	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	K	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	L	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	M	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	N	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	O	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	P	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	Q	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	R	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	S	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	T	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	U	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	V	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	W	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	X	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Y	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	Z	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	a	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	b	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	c	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	d	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	e	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	f	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	g	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	h	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	i	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	j	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	k	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	l	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	m	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	n	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	o	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	p	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	q	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	r	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	s	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	t	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	u	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	v	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	w	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	x	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	y	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
1	z	0.55	1/4256 (0.0%)	0.57	1/5800 (0.0%)
All	All	0.55	60/255360 (0.0%)	0.57	60/348000 (0.0%)

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	239	VAL	CB-CG2	-5.17	1.42	1.52
1	O	239	VAL	CB-CG2	-5.16	1.42	1.52
1	Z	239	VAL	CB-CG2	-5.16	1.42	1.52
1	f	239	VAL	CB-CG2	-5.16	1.42	1.52
1	8	239	VAL	CB-CG2	-5.16	1.42	1.52
1	E	239	VAL	CB-CG2	-5.15	1.42	1.52
1	G	239	VAL	CB-CG2	-5.15	1.42	1.52
1	M	239	VAL	CB-CG2	-5.15	1.42	1.52
1	X	239	VAL	CB-CG2	-5.15	1.42	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	b	239	VAL	CB-CG2	-5.15	1.42	1.52
1	i	239	VAL	CB-CG2	-5.15	1.42	1.52
1	n	239	VAL	CB-CG2	-5.15	1.42	1.52
1	q	239	VAL	CB-CG2	-5.15	1.42	1.52
1	D	239	VAL	CB-CG2	-5.14	1.42	1.52
1	N	239	VAL	CB-CG2	-5.14	1.42	1.52
1	W	239	VAL	CB-CG2	-5.14	1.42	1.52
1	c	239	VAL	CB-CG2	-5.14	1.42	1.52
1	e	239	VAL	CB-CG2	-5.14	1.42	1.52
1	z	239	VAL	CB-CG2	-5.14	1.42	1.52
1	C	239	VAL	CB-CG2	-5.14	1.42	1.52
1	I	239	VAL	CB-CG2	-5.14	1.42	1.52
1	K	239	VAL	CB-CG2	-5.14	1.42	1.52
1	Q	239	VAL	CB-CG2	-5.14	1.42	1.52
1	T	239	VAL	CB-CG2	-5.14	1.42	1.52
1	V	239	VAL	CB-CG2	-5.14	1.42	1.52
1	a	239	VAL	CB-CG2	-5.14	1.42	1.52
1	g	239	VAL	CB-CG2	-5.14	1.42	1.52
1	j	239	VAL	CB-CG2	-5.14	1.42	1.52
1	o	239	VAL	CB-CG2	-5.14	1.42	1.52
1	r	239	VAL	CB-CG2	-5.14	1.42	1.52
1	x	239	VAL	CB-CG2	-5.14	1.42	1.52
1	A	239	VAL	CB-CG2	-5.13	1.42	1.52
1	F	239	VAL	CB-CG2	-5.13	1.42	1.52
1	1	239	VAL	CB-CG2	-5.13	1.42	1.52
1	2	239	VAL	CB-CG2	-5.13	1.42	1.52
1	3	239	VAL	CB-CG2	-5.13	1.42	1.52
1	5	239	VAL	CB-CG2	-5.13	1.42	1.52
1	6	239	VAL	CB-CG2	-5.13	1.42	1.52
1	h	239	VAL	CB-CG2	-5.13	1.42	1.52
1	p	239	VAL	CB-CG2	-5.13	1.42	1.52
1	s	239	VAL	CB-CG2	-5.13	1.42	1.52
1	w	239	VAL	CB-CG2	-5.13	1.42	1.52
1	B	239	VAL	CB-CG2	-5.12	1.42	1.52
1	R	239	VAL	CB-CG2	-5.12	1.42	1.52
1	k	239	VAL	CB-CG2	-5.12	1.42	1.52
1	u	239	VAL	CB-CG2	-5.12	1.42	1.52
1	H	239	VAL	CB-CG2	-5.11	1.42	1.52
1	d	239	VAL	CB-CG2	-5.11	1.42	1.52
1	y	239	VAL	CB-CG2	-5.11	1.42	1.52
1	J	239	VAL	CB-CG2	-5.10	1.42	1.52
1	L	239	VAL	CB-CG2	-5.10	1.42	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S	239	VAL	CB-CG2	-5.10	1.42	1.52
1	U	239	VAL	CB-CG2	-5.10	1.42	1.52
1	l	239	VAL	CB-CG2	-5.10	1.42	1.52
1	m	239	VAL	CB-CG2	-5.10	1.42	1.52
1	t	239	VAL	CB-CG2	-5.10	1.42	1.52
1	v	239	VAL	CB-CG2	-5.10	1.42	1.52
1	4	239	VAL	CB-CG2	-5.09	1.42	1.52
1	Y	239	VAL	CB-CG2	-5.08	1.42	1.52
1	7	239	VAL	CB-CG2	-5.08	1.42	1.52

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	f	517	LEU	CA-CB-CG	6.68	130.67	115.30
1	D	517	LEU	CA-CB-CG	6.68	130.67	115.30
1	Z	517	LEU	CA-CB-CG	6.68	130.67	115.30
1	e	517	LEU	CA-CB-CG	6.68	130.67	115.30
1	8	517	LEU	CA-CB-CG	6.68	130.67	115.30
1	O	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	b	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	B	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	N	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	R	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	W	517	LEU	CA-CB-CG	6.67	130.64	115.30
1	k	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	u	517	LEU	CA-CB-CG	6.67	130.65	115.30
1	z	517	LEU	CA-CB-CG	6.67	130.64	115.30
1	K	517	LEU	CA-CB-CG	6.67	130.63	115.30
1	T	517	LEU	CA-CB-CG	6.67	130.63	115.30
1	x	517	LEU	CA-CB-CG	6.67	130.63	115.30
1	J	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	L	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	S	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	U	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	a	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	l	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	m	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	t	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	v	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	A	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	F	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	M	517	LEU	CA-CB-CG	6.66	130.62	115.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	1	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	4	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	h	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	p	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	s	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	w	517	LEU	CA-CB-CG	6.66	130.62	115.30
1	H	517	LEU	CA-CB-CG	6.66	130.61	115.30
1	Y	517	LEU	CA-CB-CG	6.66	130.61	115.30
1	y	517	LEU	CA-CB-CG	6.66	130.61	115.30
1	7	517	LEU	CA-CB-CG	6.66	130.61	115.30
1	I	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	Q	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	o	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	r	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	E	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	G	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	g	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	n	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	q	517	LEU	CA-CB-CG	6.65	130.60	115.30
1	C	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	V	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	i	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	j	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	2	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	3	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	5	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	6	517	LEU	CA-CB-CG	6.65	130.59	115.30
1	P	517	LEU	CA-CB-CG	6.64	130.58	115.30
1	d	517	LEU	CA-CB-CG	6.64	130.58	115.30
1	c	517	LEU	CA-CB-CG	6.64	130.58	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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	1	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	2	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	3	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	4	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	5	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	6	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	7	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	8	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	A	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	B	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	C	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	D	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	E	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	F	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	G	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	H	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	I	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	J	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	K	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	L	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	M	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	N	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	O	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	P	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	Q	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	S	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	T	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	U	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	V	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	W	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	X	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	Y	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	Z	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	a	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	b	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	c	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	d	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	e	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	f	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	g	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	h	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	i	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	j	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	k	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	l	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	m	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	n	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	o	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	p	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	q	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	r	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	s	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	t	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	u	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	v	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	x	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	y	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
1	z	516/518 (100%)	505 (98%)	10 (2%)	1 (0%)	47	71
All	All	30960/31080 (100%)	30300 (98%)	600 (2%)	60 (0%)	50	71

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	520	PRO
1	B	520	PRO
1	C	520	PRO
1	D	520	PRO
1	E	520	PRO
1	F	520	PRO
1	G	520	PRO
1	H	520	PRO
1	I	520	PRO
1	J	520	PRO
1	K	520	PRO
1	L	520	PRO
1	M	520	PRO
1	N	520	PRO
1	O	520	PRO
1	P	520	PRO
1	Q	520	PRO
1	R	520	PRO
1	S	520	PRO
1	T	520	PRO
1	U	520	PRO
1	V	520	PRO
1	X	520	PRO
1	Y	520	PRO
1	Z	520	PRO
1	1	520	PRO
1	2	520	PRO
1	3	520	PRO
1	4	520	PRO
1	5	520	PRO
1	6	520	PRO
1	a	520	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	b	520	PRO
1	c	520	PRO
1	d	520	PRO
1	e	520	PRO
1	f	520	PRO
1	g	520	PRO
1	h	520	PRO
1	i	520	PRO
1	j	520	PRO
1	k	520	PRO
1	l	520	PRO
1	m	520	PRO
1	n	520	PRO
1	o	520	PRO
1	p	520	PRO
1	q	520	PRO
1	r	520	PRO
1	s	520	PRO
1	t	520	PRO
1	u	520	PRO
1	v	520	PRO
1	w	520	PRO
1	x	520	PRO
1	y	520	PRO
1	z	520	PRO
1	7	520	PRO
1	8	520	PRO
1	W	520	PRO

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	1	453/453 (100%)	452 (100%)	1 (0%)	93 98
1	2	453/453 (100%)	452 (100%)	1 (0%)	93 98
1	3	453/453 (100%)	452 (100%)	1 (0%)	93 98

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	5	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	6	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	7	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	8	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	A	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	B	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	C	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	D	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	E	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	F	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	G	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	H	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	I	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	J	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	K	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	L	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	M	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	N	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	O	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	P	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	Q	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	R	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	S	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	T	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	U	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	V	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	W	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	X	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	Y	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	Z	453/453 (100%)	452 (100%)	1 (0%)	93	98

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	b	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	c	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	d	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	e	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	f	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	g	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	h	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	i	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	j	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	k	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	l	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	m	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	n	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	o	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	p	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	q	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	r	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	s	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	t	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	u	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	v	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	w	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	x	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	y	453/453 (100%)	452 (100%)	1 (0%)	93	98
1	z	453/453 (100%)	452 (100%)	1 (0%)	93	98
All	All	27180/27180 (100%)	27120 (100%)	60 (0%)	93	98

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	556	ASP
1	B	556	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	556	ASP
1	D	556	ASP
1	E	556	ASP
1	F	556	ASP
1	G	556	ASP
1	H	556	ASP
1	I	556	ASP
1	J	556	ASP
1	K	556	ASP
1	L	556	ASP
1	M	556	ASP
1	N	556	ASP
1	O	556	ASP
1	P	556	ASP
1	Q	556	ASP
1	R	556	ASP
1	S	556	ASP
1	T	556	ASP
1	U	556	ASP
1	V	556	ASP
1	W	556	ASP
1	X	556	ASP
1	Y	556	ASP
1	Z	556	ASP
1	1	556	ASP
1	2	556	ASP
1	3	556	ASP
1	4	556	ASP
1	5	556	ASP
1	6	556	ASP
1	a	556	ASP
1	b	556	ASP
1	c	556	ASP
1	d	556	ASP
1	e	556	ASP
1	f	556	ASP
1	g	556	ASP
1	h	556	ASP
1	i	556	ASP
1	j	556	ASP
1	k	556	ASP
1	l	556	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	m	556	ASP
1	n	556	ASP
1	o	556	ASP
1	p	556	ASP
1	q	556	ASP
1	r	556	ASP
1	s	556	ASP
1	t	556	ASP
1	u	556	ASP
1	v	556	ASP
1	w	556	ASP
1	x	556	ASP
1	y	556	ASP
1	z	556	ASP
1	7	556	ASP
1	8	556	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (690) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	233	GLN
1	A	304	ASN
1	A	428	HIS
1	A	495	GLN
1	A	497	ASN
1	A	527	HIS
1	A	585	GLN
1	A	624	HIS
1	A	646	GLN
1	A	651	ASN
1	A	673	GLN
1	A	710	ASN
1	B	233	GLN
1	B	304	ASN
1	B	428	HIS
1	B	495	GLN
1	B	497	ASN
1	B	527	HIS
1	B	585	GLN
1	B	624	HIS
1	B	646	GLN
1	B	651	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	673	GLN
1	B	710	ASN
1	C	233	GLN
1	C	304	ASN
1	C	428	HIS
1	C	497	ASN
1	C	527	HIS
1	C	585	GLN
1	C	624	HIS
1	C	646	GLN
1	C	673	GLN
1	C	710	ASN
1	D	233	GLN
1	D	304	ASN
1	D	428	HIS
1	D	495	GLN
1	D	497	ASN
1	D	527	HIS
1	D	585	GLN
1	D	624	HIS
1	D	646	GLN
1	D	673	GLN
1	D	710	ASN
1	E	233	GLN
1	E	304	ASN
1	E	428	HIS
1	E	495	GLN
1	E	497	ASN
1	E	527	HIS
1	E	585	GLN
1	E	624	HIS
1	E	646	GLN
1	E	673	GLN
1	E	710	ASN
1	F	233	GLN
1	F	304	ASN
1	F	428	HIS
1	F	495	GLN
1	F	497	ASN
1	F	527	HIS
1	F	585	GLN
1	F	624	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	646	GLN
1	F	651	ASN
1	F	673	GLN
1	F	710	ASN
1	G	233	GLN
1	G	304	ASN
1	G	428	HIS
1	G	495	GLN
1	G	497	ASN
1	G	527	HIS
1	G	585	GLN
1	G	624	HIS
1	G	646	GLN
1	G	651	ASN
1	G	673	GLN
1	G	710	ASN
1	H	233	GLN
1	H	304	ASN
1	H	428	HIS
1	H	495	GLN
1	H	497	ASN
1	H	527	HIS
1	H	585	GLN
1	H	624	HIS
1	H	646	GLN
1	H	651	ASN
1	H	673	GLN
1	H	710	ASN
1	I	233	GLN
1	I	304	ASN
1	I	428	HIS
1	I	495	GLN
1	I	497	ASN
1	I	527	HIS
1	I	585	GLN
1	I	624	HIS
1	I	646	GLN
1	I	651	ASN
1	I	673	GLN
1	I	710	ASN
1	J	233	GLN
1	J	304	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	428	HIS
1	J	497	ASN
1	J	527	HIS
1	J	584	HIS
1	J	585	GLN
1	J	624	HIS
1	J	646	GLN
1	J	673	GLN
1	J	710	ASN
1	K	233	GLN
1	K	304	ASN
1	K	428	HIS
1	K	495	GLN
1	K	497	ASN
1	K	527	HIS
1	K	585	GLN
1	K	624	HIS
1	K	646	GLN
1	K	673	GLN
1	K	710	ASN
1	L	233	GLN
1	L	304	ASN
1	L	428	HIS
1	L	497	ASN
1	L	527	HIS
1	L	585	GLN
1	L	624	HIS
1	L	646	GLN
1	L	673	GLN
1	L	710	ASN
1	M	233	GLN
1	M	304	ASN
1	M	428	HIS
1	M	495	GLN
1	M	497	ASN
1	M	527	HIS
1	M	585	GLN
1	M	624	HIS
1	M	646	GLN
1	M	651	ASN
1	M	673	GLN
1	M	710	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	N	233	GLN
1	N	304	ASN
1	N	428	HIS
1	N	495	GLN
1	N	497	ASN
1	N	527	HIS
1	N	585	GLN
1	N	624	HIS
1	N	646	GLN
1	N	673	GLN
1	N	710	ASN
1	O	233	GLN
1	O	304	ASN
1	O	428	HIS
1	O	495	GLN
1	O	497	ASN
1	O	527	HIS
1	O	585	GLN
1	O	624	HIS
1	O	646	GLN
1	O	651	ASN
1	O	673	GLN
1	O	710	ASN
1	P	233	GLN
1	P	304	ASN
1	P	428	HIS
1	P	497	ASN
1	P	527	HIS
1	P	585	GLN
1	P	624	HIS
1	P	646	GLN
1	P	651	ASN
1	P	673	GLN
1	P	710	ASN
1	Q	233	GLN
1	Q	304	ASN
1	Q	428	HIS
1	Q	497	ASN
1	Q	527	HIS
1	Q	585	GLN
1	Q	624	HIS
1	Q	646	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Q	651	ASN
1	Q	673	GLN
1	Q	710	ASN
1	R	233	GLN
1	R	304	ASN
1	R	428	HIS
1	R	495	GLN
1	R	497	ASN
1	R	527	HIS
1	R	585	GLN
1	R	624	HIS
1	R	646	GLN
1	R	651	ASN
1	R	673	GLN
1	R	710	ASN
1	S	233	GLN
1	S	304	ASN
1	S	428	HIS
1	S	495	GLN
1	S	497	ASN
1	S	527	HIS
1	S	585	GLN
1	S	624	HIS
1	S	646	GLN
1	S	651	ASN
1	S	673	GLN
1	S	710	ASN
1	T	233	GLN
1	T	304	ASN
1	T	428	HIS
1	T	495	GLN
1	T	497	ASN
1	T	527	HIS
1	T	585	GLN
1	T	624	HIS
1	T	646	GLN
1	T	651	ASN
1	T	673	GLN
1	T	710	ASN
1	U	233	GLN
1	U	304	ASN
1	U	428	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	U	495	GLN
1	U	497	ASN
1	U	527	HIS
1	U	585	GLN
1	U	624	HIS
1	U	646	GLN
1	U	651	ASN
1	U	673	GLN
1	U	710	ASN
1	V	233	GLN
1	V	304	ASN
1	V	428	HIS
1	V	495	GLN
1	V	497	ASN
1	V	527	HIS
1	V	584	HIS
1	V	585	GLN
1	V	624	HIS
1	V	646	GLN
1	V	651	ASN
1	V	673	GLN
1	V	710	ASN
1	W	233	GLN
1	W	304	ASN
1	W	428	HIS
1	W	495	GLN
1	W	497	ASN
1	W	527	HIS
1	W	585	GLN
1	W	624	HIS
1	W	646	GLN
1	W	651	ASN
1	W	673	GLN
1	W	710	ASN
1	X	233	GLN
1	X	304	ASN
1	X	428	HIS
1	X	495	GLN
1	X	497	ASN
1	X	527	HIS
1	X	585	GLN
1	X	624	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	X	646	GLN
1	X	673	GLN
1	X	710	ASN
1	Y	233	GLN
1	Y	304	ASN
1	Y	428	HIS
1	Y	497	ASN
1	Y	527	HIS
1	Y	585	GLN
1	Y	624	HIS
1	Y	646	GLN
1	Y	673	GLN
1	Y	710	ASN
1	Z	233	GLN
1	Z	304	ASN
1	Z	428	HIS
1	Z	495	GLN
1	Z	497	ASN
1	Z	527	HIS
1	Z	585	GLN
1	Z	624	HIS
1	Z	646	GLN
1	Z	651	ASN
1	Z	673	GLN
1	Z	710	ASN
1	1	233	GLN
1	1	304	ASN
1	1	428	HIS
1	1	495	GLN
1	1	497	ASN
1	1	527	HIS
1	1	585	GLN
1	1	624	HIS
1	1	646	GLN
1	1	673	GLN
1	1	710	ASN
1	2	233	GLN
1	2	304	ASN
1	2	428	HIS
1	2	495	GLN
1	2	497	ASN
1	2	527	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	2	585	GLN
1	2	624	HIS
1	2	646	GLN
1	2	651	ASN
1	2	673	GLN
1	2	710	ASN
1	3	233	GLN
1	3	304	ASN
1	3	428	HIS
1	3	495	GLN
1	3	497	ASN
1	3	527	HIS
1	3	585	GLN
1	3	624	HIS
1	3	646	GLN
1	3	651	ASN
1	3	673	GLN
1	3	710	ASN
1	4	233	GLN
1	4	304	ASN
1	4	428	HIS
1	4	497	ASN
1	4	527	HIS
1	4	585	GLN
1	4	624	HIS
1	4	646	GLN
1	4	651	ASN
1	4	673	GLN
1	4	710	ASN
1	5	233	GLN
1	5	304	ASN
1	5	428	HIS
1	5	495	GLN
1	5	497	ASN
1	5	527	HIS
1	5	585	GLN
1	5	624	HIS
1	5	646	GLN
1	5	673	GLN
1	5	710	ASN
1	6	233	GLN
1	6	304	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	6	428	HIS
1	6	495	GLN
1	6	497	ASN
1	6	527	HIS
1	6	585	GLN
1	6	624	HIS
1	6	646	GLN
1	6	651	ASN
1	6	673	GLN
1	6	710	ASN
1	a	233	GLN
1	a	304	ASN
1	a	428	HIS
1	a	495	GLN
1	a	497	ASN
1	a	527	HIS
1	a	585	GLN
1	a	624	HIS
1	a	646	GLN
1	a	673	GLN
1	a	710	ASN
1	b	233	GLN
1	b	304	ASN
1	b	428	HIS
1	b	495	GLN
1	b	497	ASN
1	b	527	HIS
1	b	585	GLN
1	b	624	HIS
1	b	646	GLN
1	b	651	ASN
1	b	673	GLN
1	b	710	ASN
1	c	233	GLN
1	c	304	ASN
1	c	428	HIS
1	c	495	GLN
1	c	497	ASN
1	c	527	HIS
1	c	585	GLN
1	c	624	HIS
1	c	646	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	c	673	GLN
1	c	710	ASN
1	d	233	GLN
1	d	304	ASN
1	d	428	HIS
1	d	497	ASN
1	d	527	HIS
1	d	585	GLN
1	d	624	HIS
1	d	646	GLN
1	d	651	ASN
1	d	673	GLN
1	d	710	ASN
1	e	233	GLN
1	e	304	ASN
1	e	428	HIS
1	e	497	ASN
1	e	527	HIS
1	e	585	GLN
1	e	624	HIS
1	e	646	GLN
1	e	673	GLN
1	e	710	ASN
1	f	233	GLN
1	f	304	ASN
1	f	428	HIS
1	f	495	GLN
1	f	497	ASN
1	f	527	HIS
1	f	585	GLN
1	f	624	HIS
1	f	646	GLN
1	f	651	ASN
1	f	673	GLN
1	f	710	ASN
1	g	233	GLN
1	g	304	ASN
1	g	428	HIS
1	g	495	GLN
1	g	497	ASN
1	g	527	HIS
1	g	585	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	g	624	HIS
1	g	646	GLN
1	g	651	ASN
1	g	673	GLN
1	g	710	ASN
1	h	233	GLN
1	h	304	ASN
1	h	428	HIS
1	h	497	ASN
1	h	527	HIS
1	h	585	GLN
1	h	624	HIS
1	h	646	GLN
1	h	651	ASN
1	h	673	GLN
1	h	710	ASN
1	i	233	GLN
1	i	304	ASN
1	i	428	HIS
1	i	495	GLN
1	i	497	ASN
1	i	527	HIS
1	i	585	GLN
1	i	624	HIS
1	i	646	GLN
1	i	673	GLN
1	i	710	ASN
1	j	233	GLN
1	j	304	ASN
1	j	428	HIS
1	j	495	GLN
1	j	497	ASN
1	j	527	HIS
1	j	584	HIS
1	j	585	GLN
1	j	624	HIS
1	j	646	GLN
1	j	673	GLN
1	j	710	ASN
1	k	233	GLN
1	k	304	ASN
1	k	428	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	k	495	GLN
1	k	497	ASN
1	k	527	HIS
1	k	585	GLN
1	k	624	HIS
1	k	646	GLN
1	k	651	ASN
1	k	673	GLN
1	k	710	ASN
1	l	233	GLN
1	l	304	ASN
1	l	428	HIS
1	l	495	GLN
1	l	497	ASN
1	l	527	HIS
1	l	585	GLN
1	l	624	HIS
1	l	646	GLN
1	l	651	ASN
1	l	673	GLN
1	l	710	ASN
1	m	233	GLN
1	m	304	ASN
1	m	428	HIS
1	m	495	GLN
1	m	497	ASN
1	m	527	HIS
1	m	585	GLN
1	m	624	HIS
1	m	646	GLN
1	m	651	ASN
1	m	673	GLN
1	m	710	ASN
1	n	233	GLN
1	n	304	ASN
1	n	428	HIS
1	n	495	GLN
1	n	497	ASN
1	n	527	HIS
1	n	585	GLN
1	n	624	HIS
1	n	646	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	n	673	GLN
1	n	710	ASN
1	o	233	GLN
1	o	304	ASN
1	o	428	HIS
1	o	495	GLN
1	o	497	ASN
1	o	527	HIS
1	o	584	HIS
1	o	585	GLN
1	o	624	HIS
1	o	646	GLN
1	o	651	ASN
1	o	673	GLN
1	o	710	ASN
1	p	233	GLN
1	p	304	ASN
1	p	428	HIS
1	p	495	GLN
1	p	497	ASN
1	p	527	HIS
1	p	585	GLN
1	p	624	HIS
1	p	646	GLN
1	p	651	ASN
1	p	673	GLN
1	p	710	ASN
1	q	233	GLN
1	q	304	ASN
1	q	428	HIS
1	q	495	GLN
1	q	497	ASN
1	q	527	HIS
1	q	585	GLN
1	q	624	HIS
1	q	646	GLN
1	q	651	ASN
1	q	673	GLN
1	q	710	ASN
1	r	233	GLN
1	r	304	ASN
1	r	428	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	r	497	ASN
1	r	527	HIS
1	r	585	GLN
1	r	624	HIS
1	r	646	GLN
1	r	651	ASN
1	r	673	GLN
1	r	710	ASN
1	s	233	GLN
1	s	304	ASN
1	s	428	HIS
1	s	495	GLN
1	s	497	ASN
1	s	527	HIS
1	s	585	GLN
1	s	624	HIS
1	s	646	GLN
1	s	651	ASN
1	s	673	GLN
1	s	710	ASN
1	t	233	GLN
1	t	304	ASN
1	t	428	HIS
1	t	497	ASN
1	t	527	HIS
1	t	585	GLN
1	t	624	HIS
1	t	646	GLN
1	t	651	ASN
1	t	673	GLN
1	t	710	ASN
1	u	233	GLN
1	u	304	ASN
1	u	428	HIS
1	u	495	GLN
1	u	497	ASN
1	u	527	HIS
1	u	585	GLN
1	u	624	HIS
1	u	646	GLN
1	u	673	GLN
1	u	710	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	v	233	GLN
1	v	304	ASN
1	v	428	HIS
1	v	497	ASN
1	v	527	HIS
1	v	584	HIS
1	v	585	GLN
1	v	624	HIS
1	v	646	GLN
1	v	673	GLN
1	v	710	ASN
1	w	233	GLN
1	w	304	ASN
1	w	428	HIS
1	w	495	GLN
1	w	497	ASN
1	w	527	HIS
1	w	585	GLN
1	w	624	HIS
1	w	646	GLN
1	w	673	GLN
1	w	710	ASN
1	x	233	GLN
1	x	304	ASN
1	x	428	HIS
1	x	495	GLN
1	x	497	ASN
1	x	527	HIS
1	x	585	GLN
1	x	624	HIS
1	x	646	GLN
1	x	673	GLN
1	x	710	ASN
1	y	233	GLN
1	y	304	ASN
1	y	428	HIS
1	y	495	GLN
1	y	497	ASN
1	y	527	HIS
1	y	585	GLN
1	y	624	HIS
1	y	646	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	y	651	ASN
1	y	673	GLN
1	y	710	ASN
1	z	233	GLN
1	z	304	ASN
1	z	428	HIS
1	z	495	GLN
1	z	497	ASN
1	z	527	HIS
1	z	585	GLN
1	z	624	HIS
1	z	646	GLN
1	z	651	ASN
1	z	673	GLN
1	z	710	ASN
1	7	233	GLN
1	7	304	ASN
1	7	428	HIS
1	7	497	ASN
1	7	527	HIS
1	7	585	GLN
1	7	624	HIS
1	7	646	GLN
1	7	651	ASN
1	7	673	GLN
1	7	710	ASN
1	8	233	GLN
1	8	304	ASN
1	8	428	HIS
1	8	495	GLN
1	8	497	ASN
1	8	527	HIS
1	8	585	GLN
1	8	624	HIS
1	8	646	GLN
1	8	651	ASN
1	8	673	GLN
1	8	710	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 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	7	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	S	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	V	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	o	801	-	12,12,12	0.50	0	17,17,17	0.87	0
2	GAL	W	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	x	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	g	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	m	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	L	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	a	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	q	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	G	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	r	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	T	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	M	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	H	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	e	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	6	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	l	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	p	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	Q	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	z	801	-	12,12,12	0.49	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	E	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	I	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	s	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	b	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	Y	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	h	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	w	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	3	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	X	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	l	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	k	801	-	12,12,12	0.50	0	17,17,17	0.87	0
2	GAL	J	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	c	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	f	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	D	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	d	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	F	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	R	801	-	12,12,12	0.50	0	17,17,17	0.87	0
2	GAL	N	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	K	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	n	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	u	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	B	801	-	12,12,12	0.50	0	17,17,17	0.87	0
2	GAL	i	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	O	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	2	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	C	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	5	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	v	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	t	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	A	801	-	12,12,12	0.50	0	17,17,17	0.86	0
2	GAL	P	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	4	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	Z	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	8	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	U	801	-	12,12,12	0.49	0	17,17,17	0.86	0
2	GAL	j	801	-	12,12,12	0.49	0	17,17,17	0.87	0
2	GAL	y	801	-	12,12,12	0.49	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	7	801	-	-	1/2/22/22	0/1/1/1
2	GAL	S	801	-	-	1/2/22/22	0/1/1/1
2	GAL	V	801	-	-	1/2/22/22	0/1/1/1
2	GAL	o	801	-	-	1/2/22/22	0/1/1/1
2	GAL	W	801	-	-	1/2/22/22	0/1/1/1
2	GAL	x	801	-	-	1/2/22/22	0/1/1/1
2	GAL	g	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
2	GAL	a	801	-	-	1/2/22/22	0/1/1/1
2	GAL	q	801	-	-	1/2/22/22	0/1/1/1
2	GAL	G	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
2	GAL	M	801	-	-	1/2/22/22	0/1/1/1
2	GAL	H	801	-	-	1/2/22/22	0/1/1/1
2	GAL	e	801	-	-	1/2/22/22	0/1/1/1
2	GAL	6	801	-	-	1/2/22/22	0/1/1/1
2	GAL	l	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	z	801	-	-	1/2/22/22	0/1/1/1
2	GAL	E	801	-	-	1/2/22/22	0/1/1/1
2	GAL	I	801	-	-	1/2/22/22	0/1/1/1
2	GAL	s	801	-	-	1/2/22/22	0/1/1/1
2	GAL	b	801	-	-	1/2/22/22	0/1/1/1
2	GAL	Y	801	-	-	1/2/22/22	0/1/1/1
2	GAL	h	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	X	801	-	-	1/2/22/22	0/1/1/1
2	GAL	1	801	-	-	1/2/22/22	0/1/1/1
2	GAL	k	801	-	-	1/2/22/22	0/1/1/1
2	GAL	J	801	-	-	1/2/22/22	0/1/1/1
2	GAL	c	801	-	-	1/2/22/22	0/1/1/1
2	GAL	f	801	-	-	1/2/22/22	0/1/1/1
2	GAL	D	801	-	-	1/2/22/22	0/1/1/1
2	GAL	d	801	-	-	1/2/22/22	0/1/1/1
2	GAL	F	801	-	-	1/2/22/22	0/1/1/1
2	GAL	R	801	-	-	1/2/22/22	0/1/1/1
2	GAL	N	801	-	-	1/2/22/22	0/1/1/1
2	GAL	K	801	-	-	1/2/22/22	0/1/1/1
2	GAL	n	801	-	-	1/2/22/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	i	801	-	-	1/2/22/22	0/1/1/1
2	GAL	O	801	-	-	1/2/22/22	0/1/1/1
2	GAL	2	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	v	801	-	-	1/2/22/22	0/1/1/1
2	GAL	t	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	4	801	-	-	1/2/22/22	0/1/1/1
2	GAL	Z	801	-	-	1/2/22/22	0/1/1/1
2	GAL	8	801	-	-	1/2/22/22	0/1/1/1
2	GAL	U	801	-	-	1/2/22/22	0/1/1/1
2	GAL	j	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.

All (60) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	GAL	O5-C5-C6-O6
2	B	801	GAL	O5-C5-C6-O6
2	D	801	GAL	O5-C5-C6-O6
2	E	801	GAL	O5-C5-C6-O6
2	F	801	GAL	O5-C5-C6-O6
2	G	801	GAL	O5-C5-C6-O6
2	H	801	GAL	O5-C5-C6-O6
2	I	801	GAL	O5-C5-C6-O6
2	J	801	GAL	O5-C5-C6-O6
2	K	801	GAL	O5-C5-C6-O6
2	L	801	GAL	O5-C5-C6-O6
2	M	801	GAL	O5-C5-C6-O6
2	N	801	GAL	O5-C5-C6-O6
2	P	801	GAL	O5-C5-C6-O6
2	Q	801	GAL	O5-C5-C6-O6
2	R	801	GAL	O5-C5-C6-O6
2	S	801	GAL	O5-C5-C6-O6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	T	801	GAL	O5-C5-C6-O6
2	U	801	GAL	O5-C5-C6-O6
2	X	801	GAL	O5-C5-C6-O6
2	Y	801	GAL	O5-C5-C6-O6
2	Z	801	GAL	O5-C5-C6-O6
2	1	801	GAL	O5-C5-C6-O6
2	2	801	GAL	O5-C5-C6-O6
2	3	801	GAL	O5-C5-C6-O6
2	4	801	GAL	O5-C5-C6-O6
2	5	801	GAL	O5-C5-C6-O6
2	6	801	GAL	O5-C5-C6-O6
2	b	801	GAL	O5-C5-C6-O6
2	c	801	GAL	O5-C5-C6-O6
2	d	801	GAL	O5-C5-C6-O6
2	e	801	GAL	O5-C5-C6-O6
2	f	801	GAL	O5-C5-C6-O6
2	g	801	GAL	O5-C5-C6-O6
2	h	801	GAL	O5-C5-C6-O6
2	i	801	GAL	O5-C5-C6-O6
2	k	801	GAL	O5-C5-C6-O6
2	l	801	GAL	O5-C5-C6-O6
2	m	801	GAL	O5-C5-C6-O6
2	n	801	GAL	O5-C5-C6-O6
2	o	801	GAL	O5-C5-C6-O6
2	p	801	GAL	O5-C5-C6-O6
2	q	801	GAL	O5-C5-C6-O6
2	r	801	GAL	O5-C5-C6-O6
2	s	801	GAL	O5-C5-C6-O6
2	t	801	GAL	O5-C5-C6-O6
2	u	801	GAL	O5-C5-C6-O6
2	v	801	GAL	O5-C5-C6-O6
2	w	801	GAL	O5-C5-C6-O6
2	x	801	GAL	O5-C5-C6-O6
2	y	801	GAL	O5-C5-C6-O6
2	7	801	GAL	O5-C5-C6-O6
2	8	801	GAL	O5-C5-C6-O6
2	C	801	GAL	O5-C5-C6-O6
2	O	801	GAL	O5-C5-C6-O6
2	V	801	GAL	O5-C5-C6-O6
2	W	801	GAL	O5-C5-C6-O6
2	a	801	GAL	O5-C5-C6-O6
2	j	801	GAL	O5-C5-C6-O6

Continued on next page...

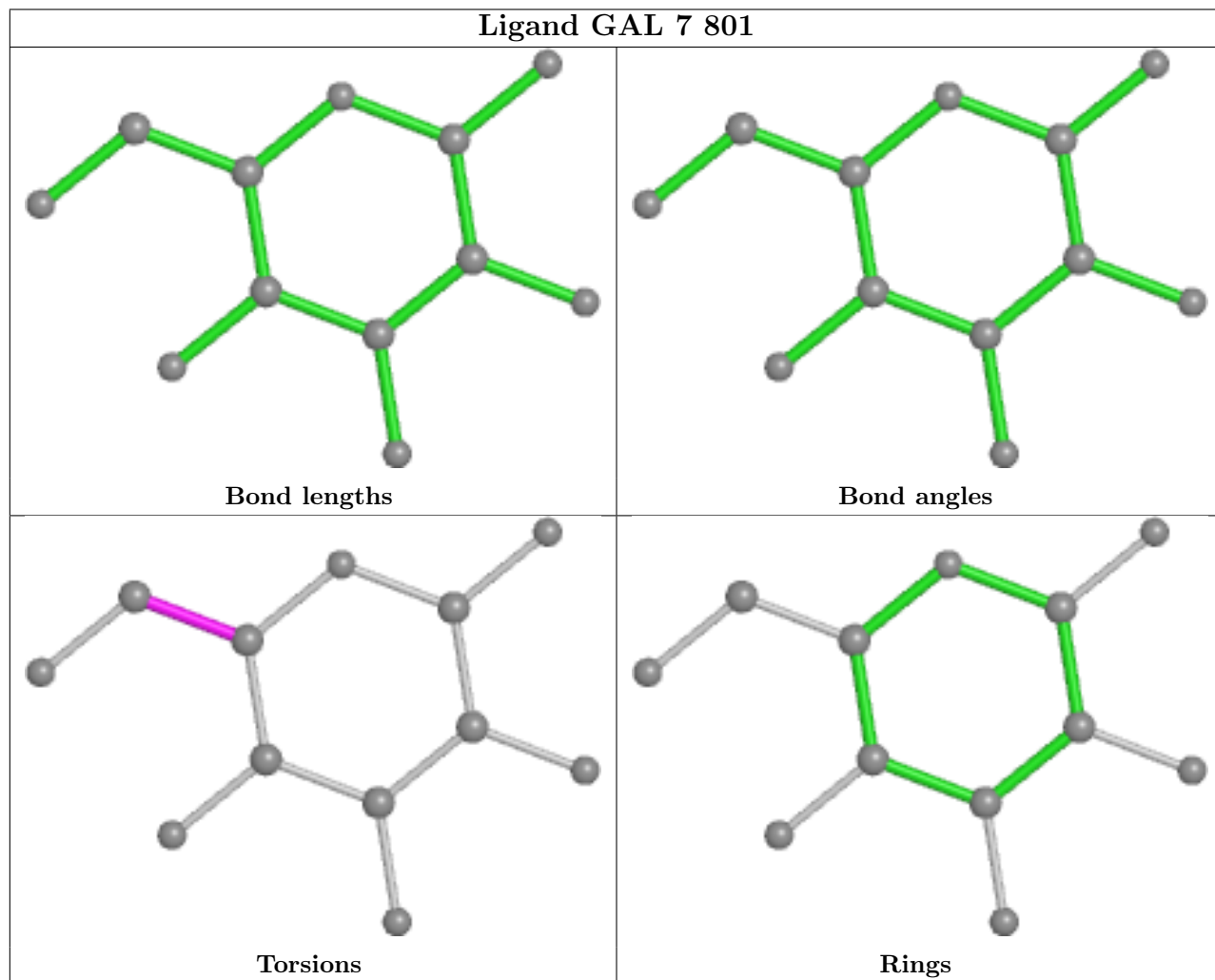
Continued from previous page...

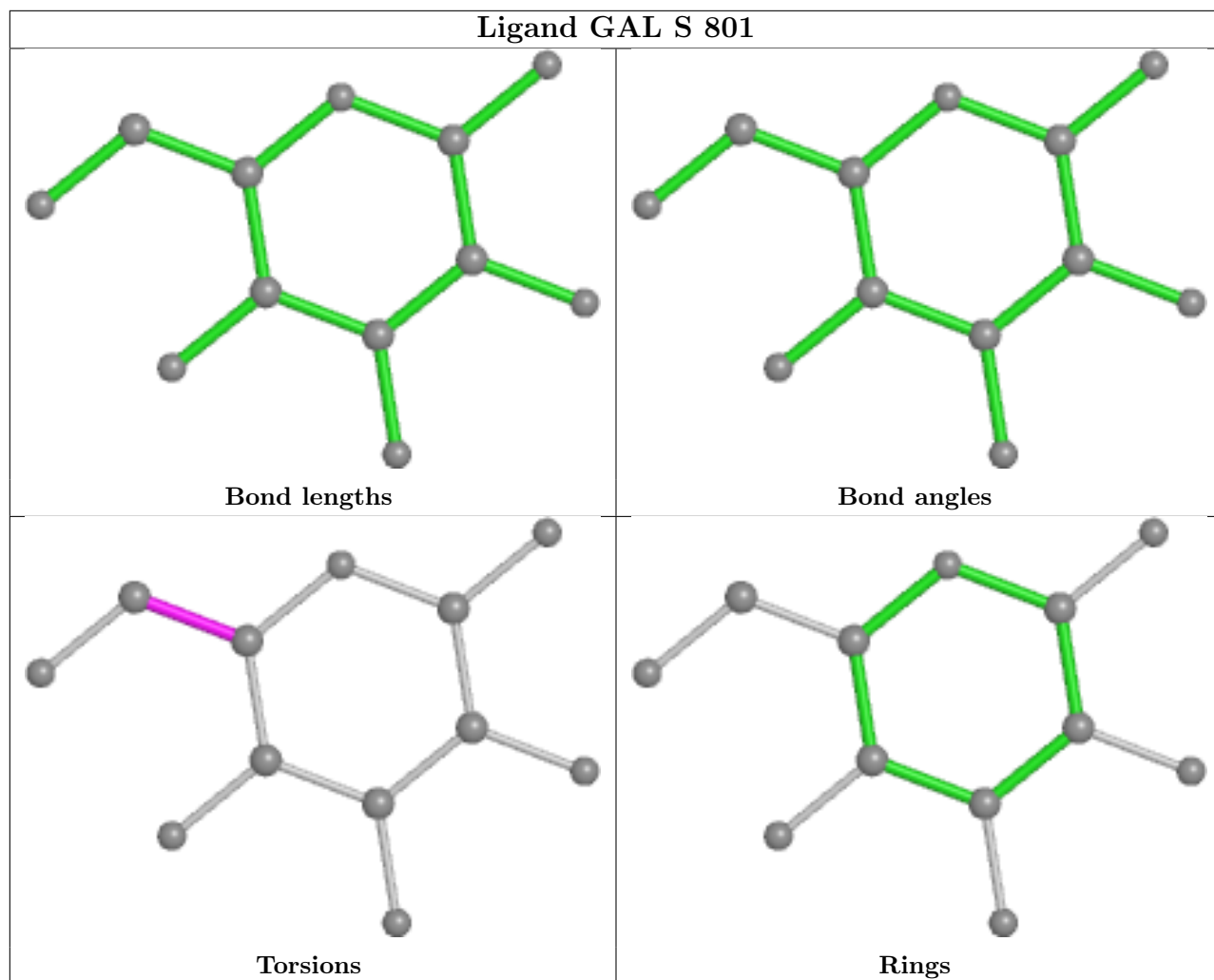
Mol	Chain	Res	Type	Atoms
2	z	801	GAL	O5-C5-C6-O6

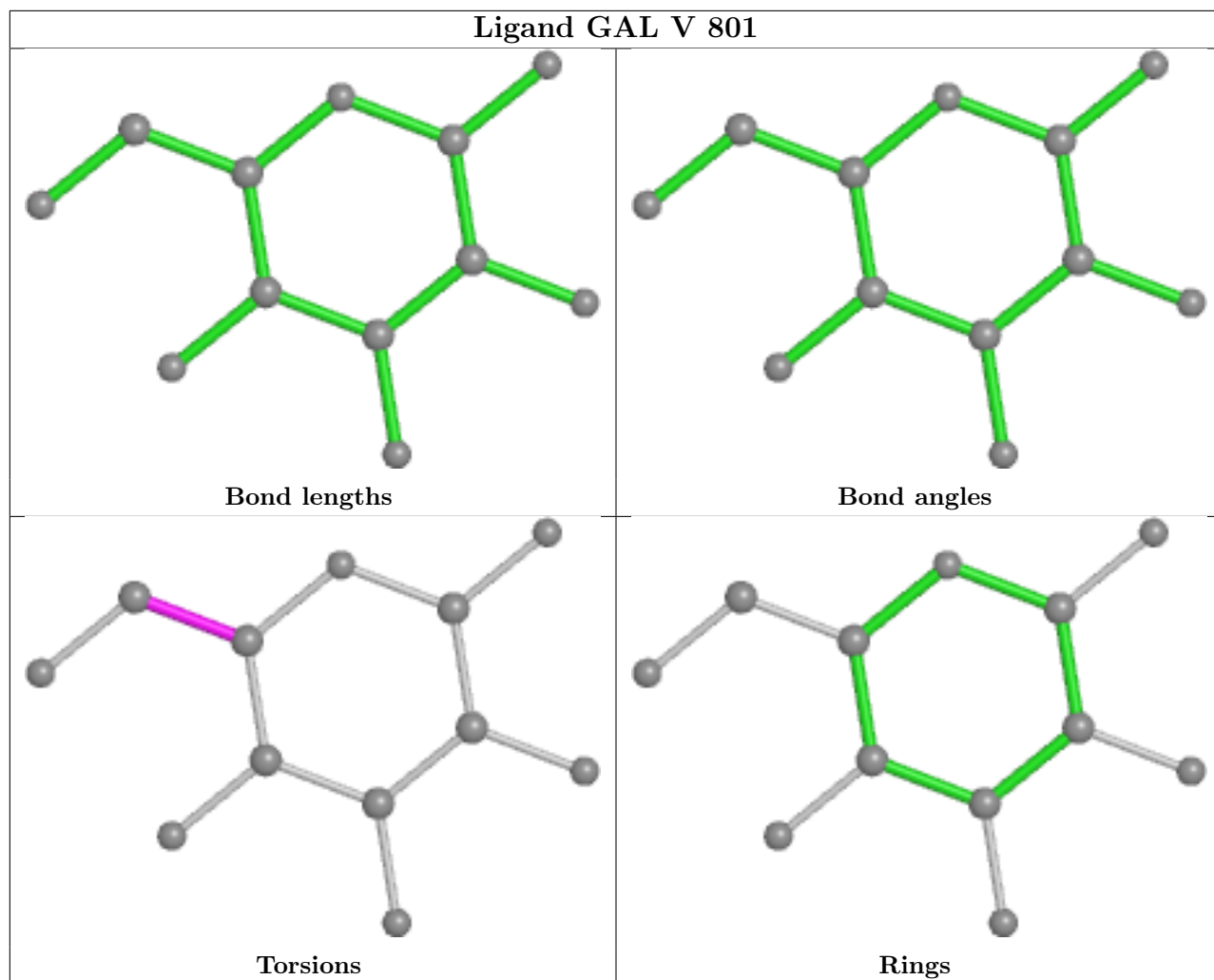
There are no ring outliers.

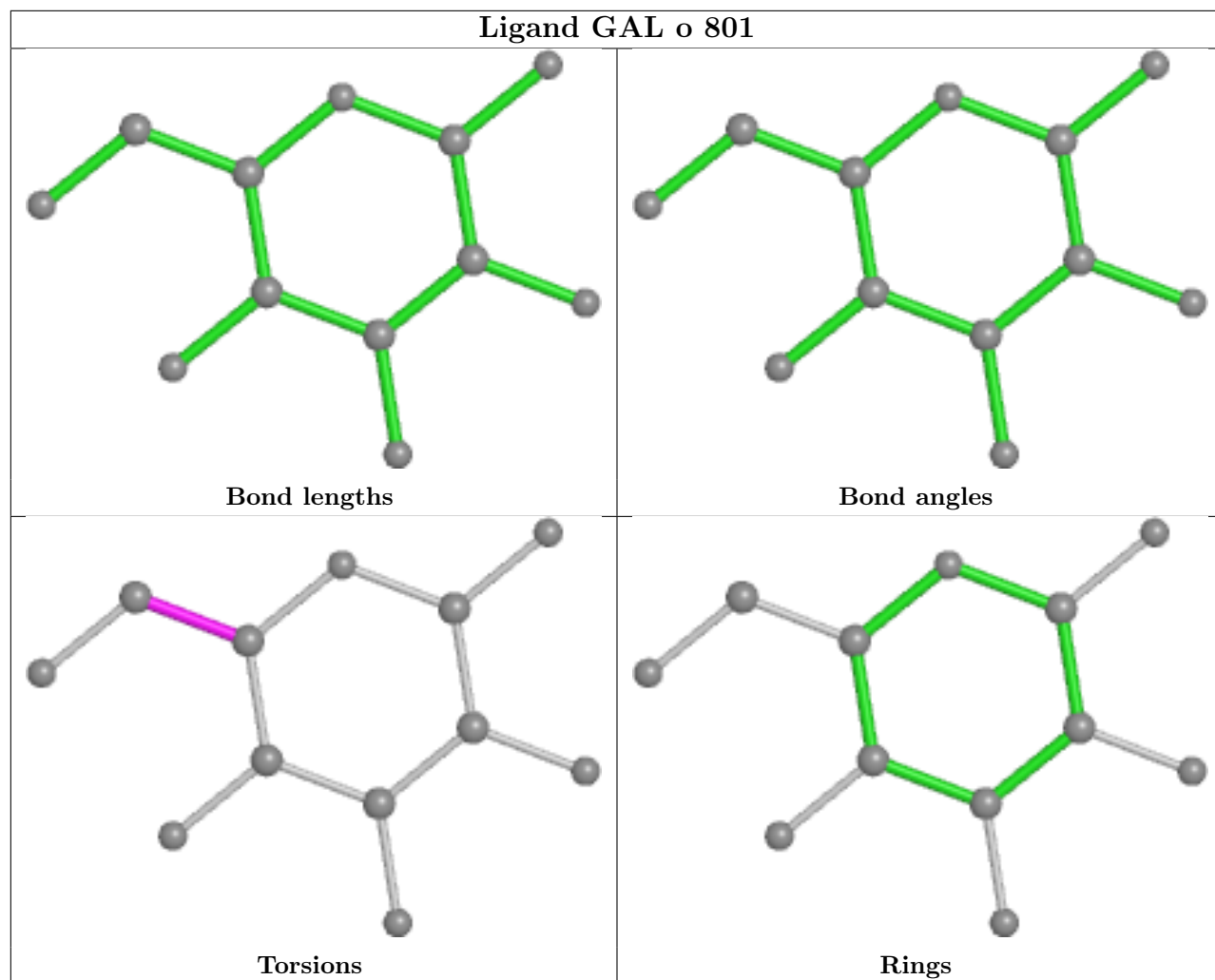
No monomer is involved in short contacts.

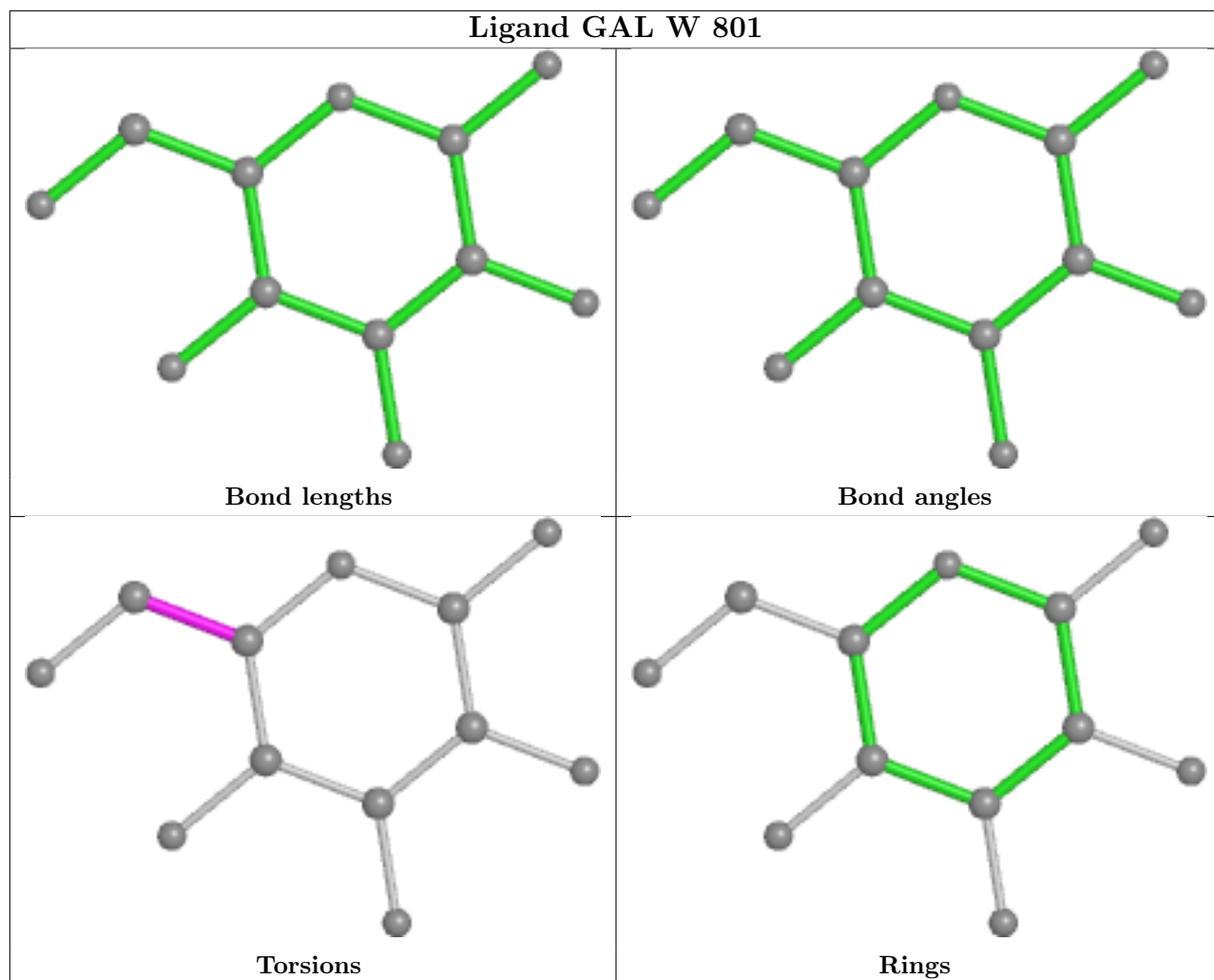
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

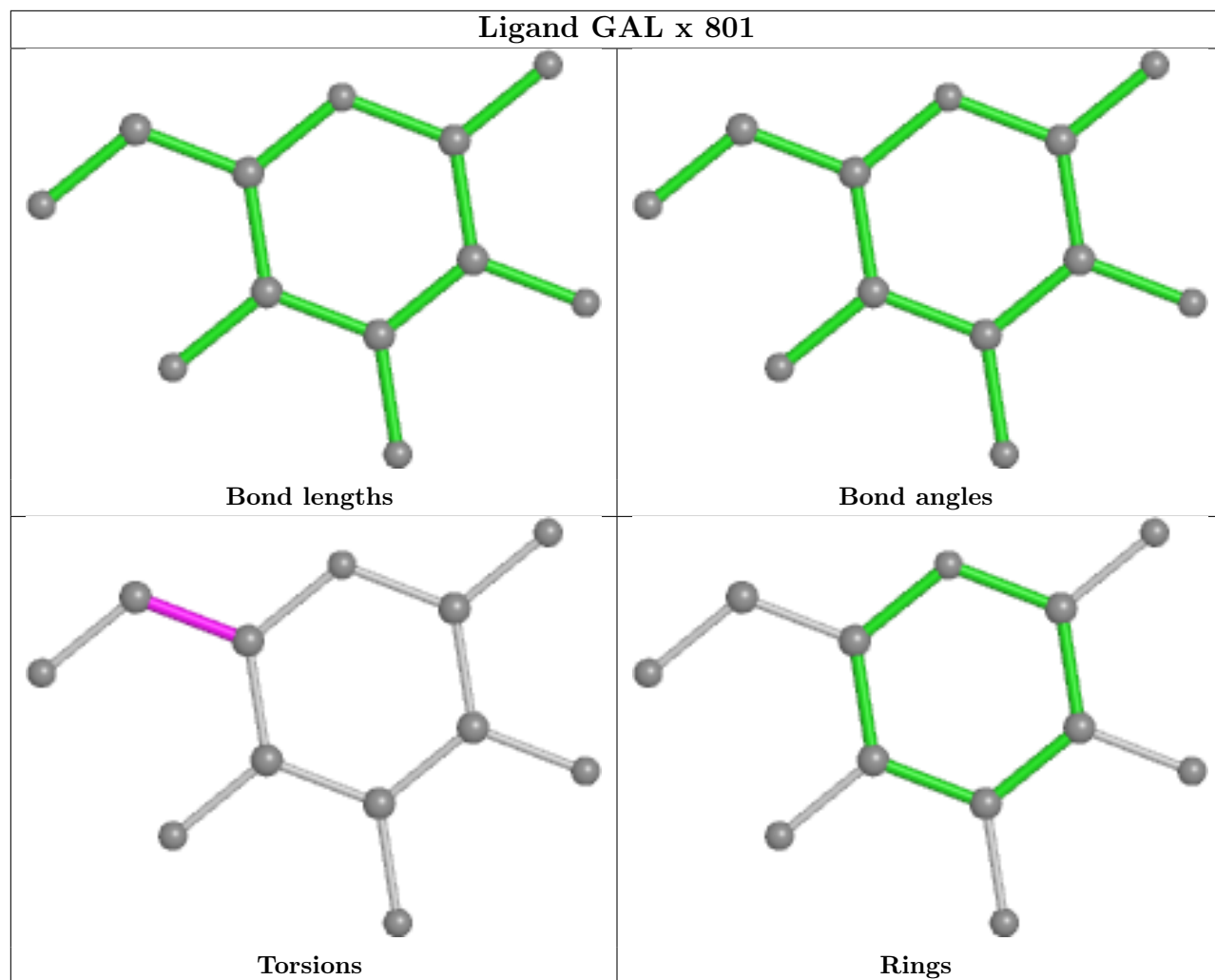


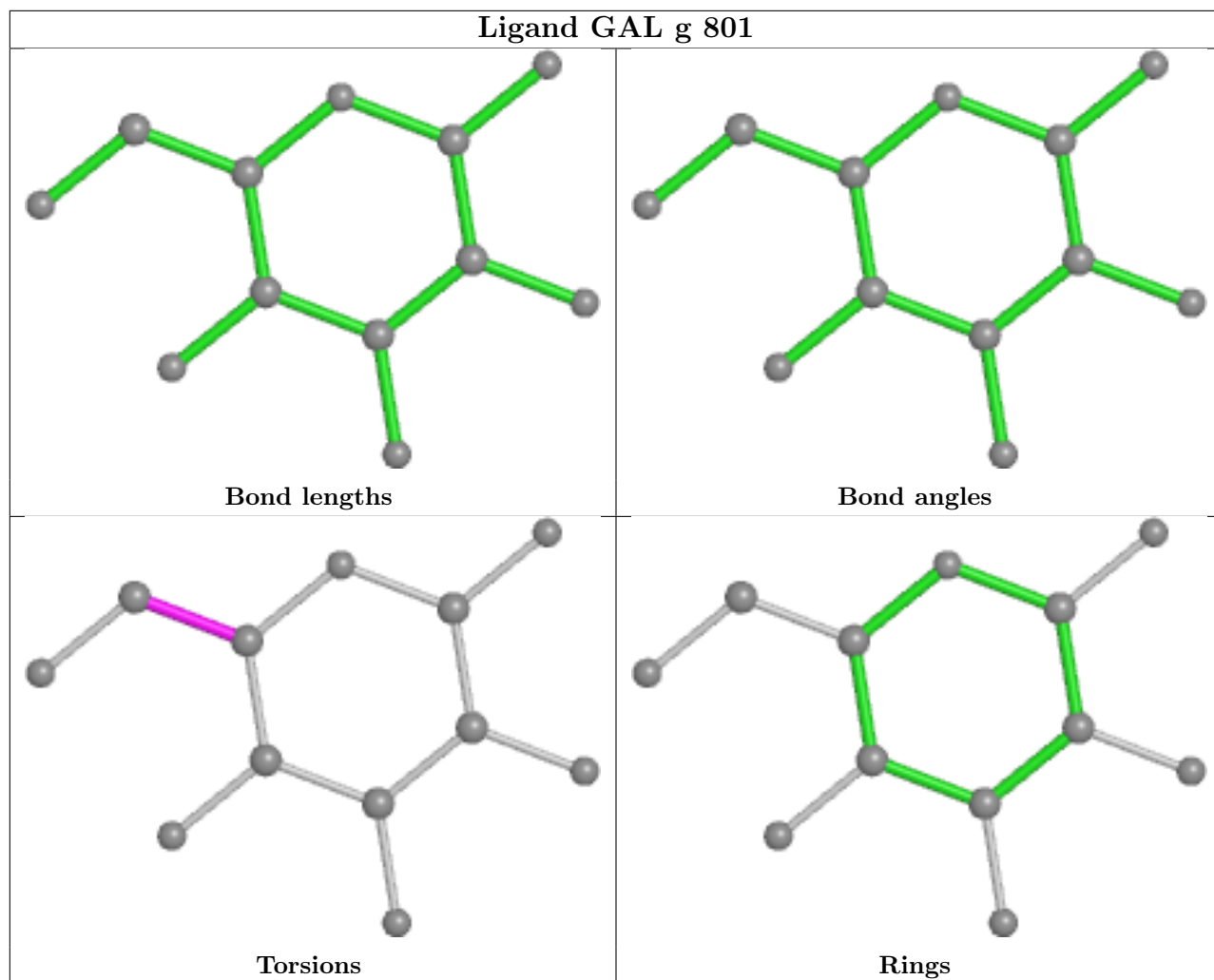


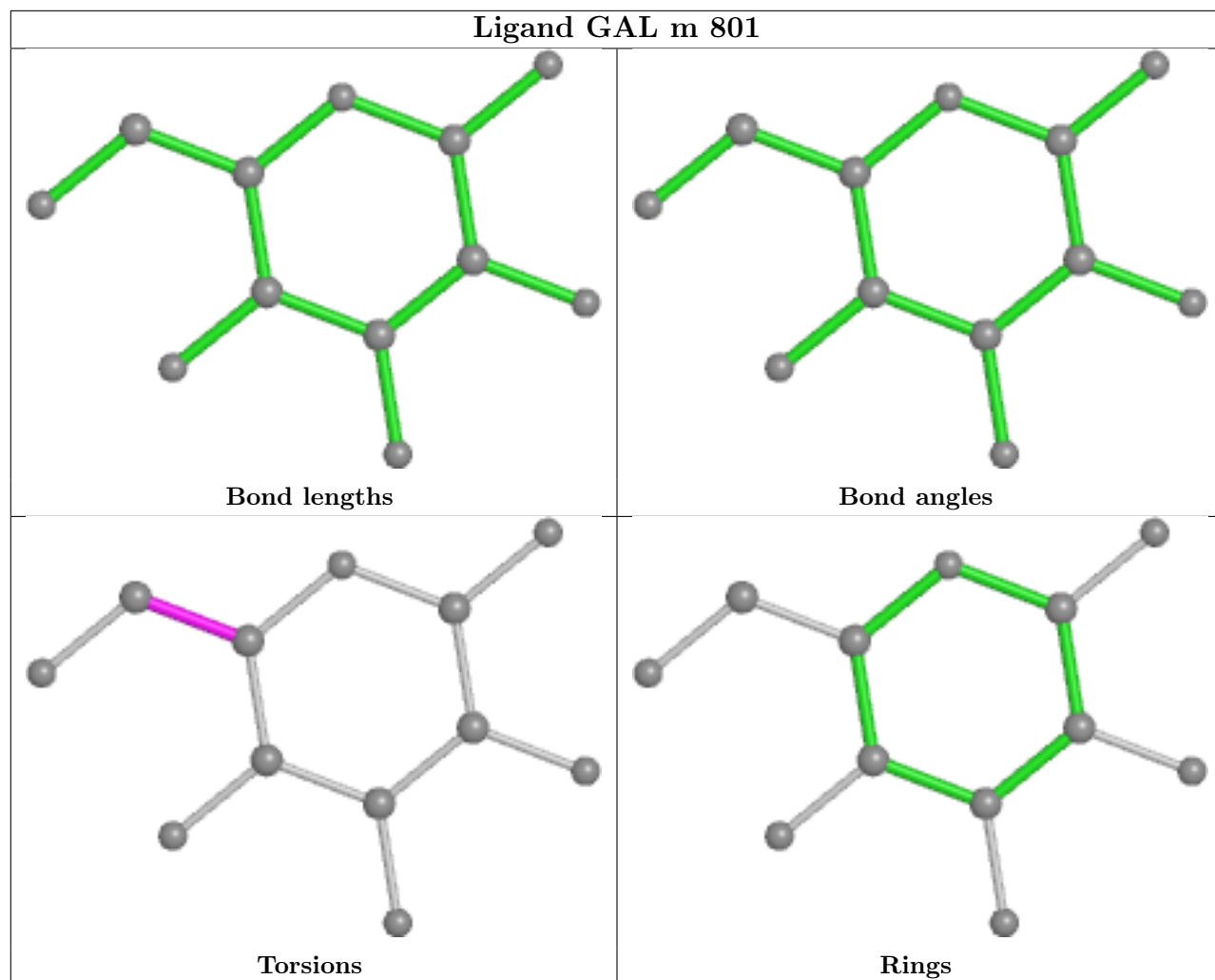


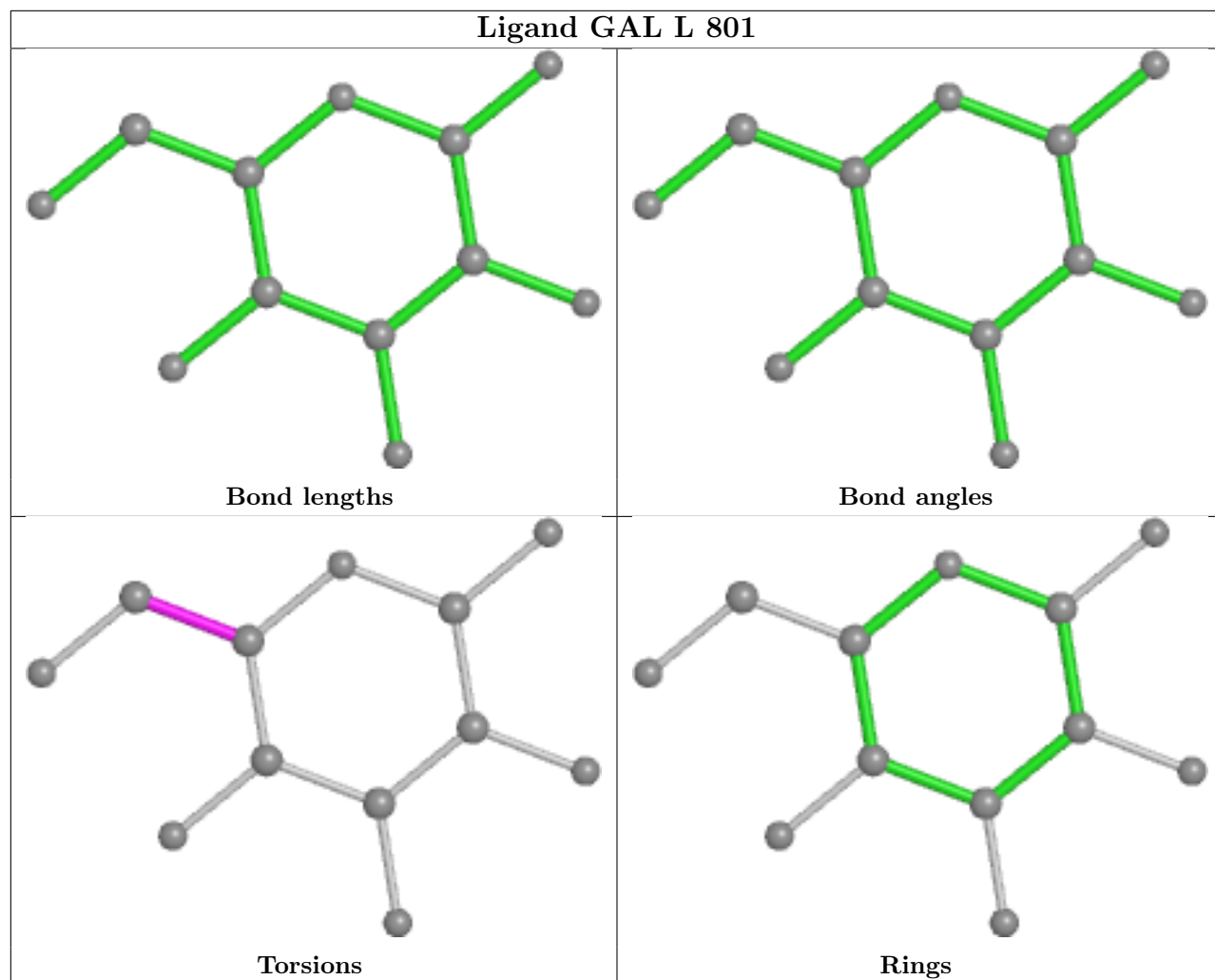


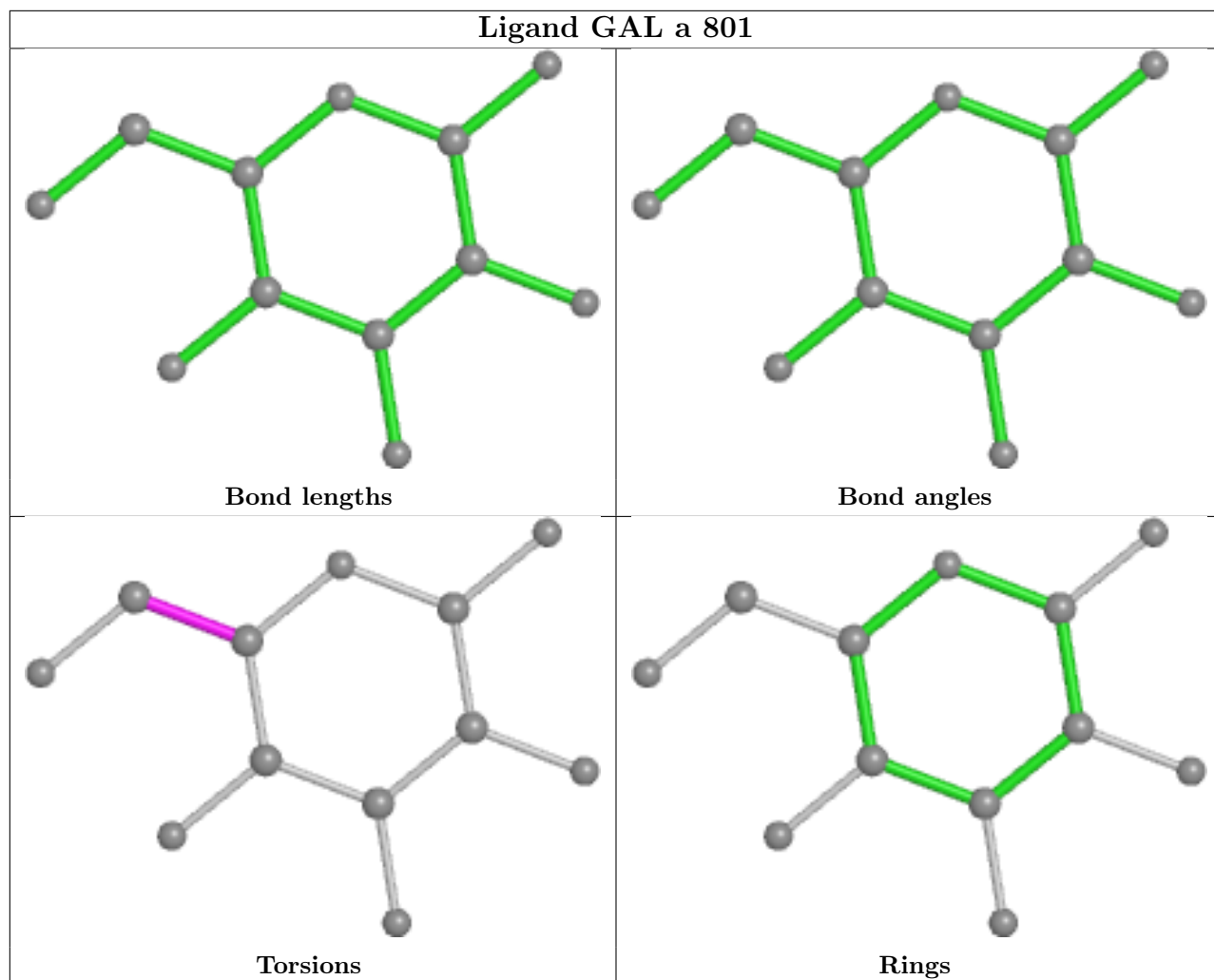


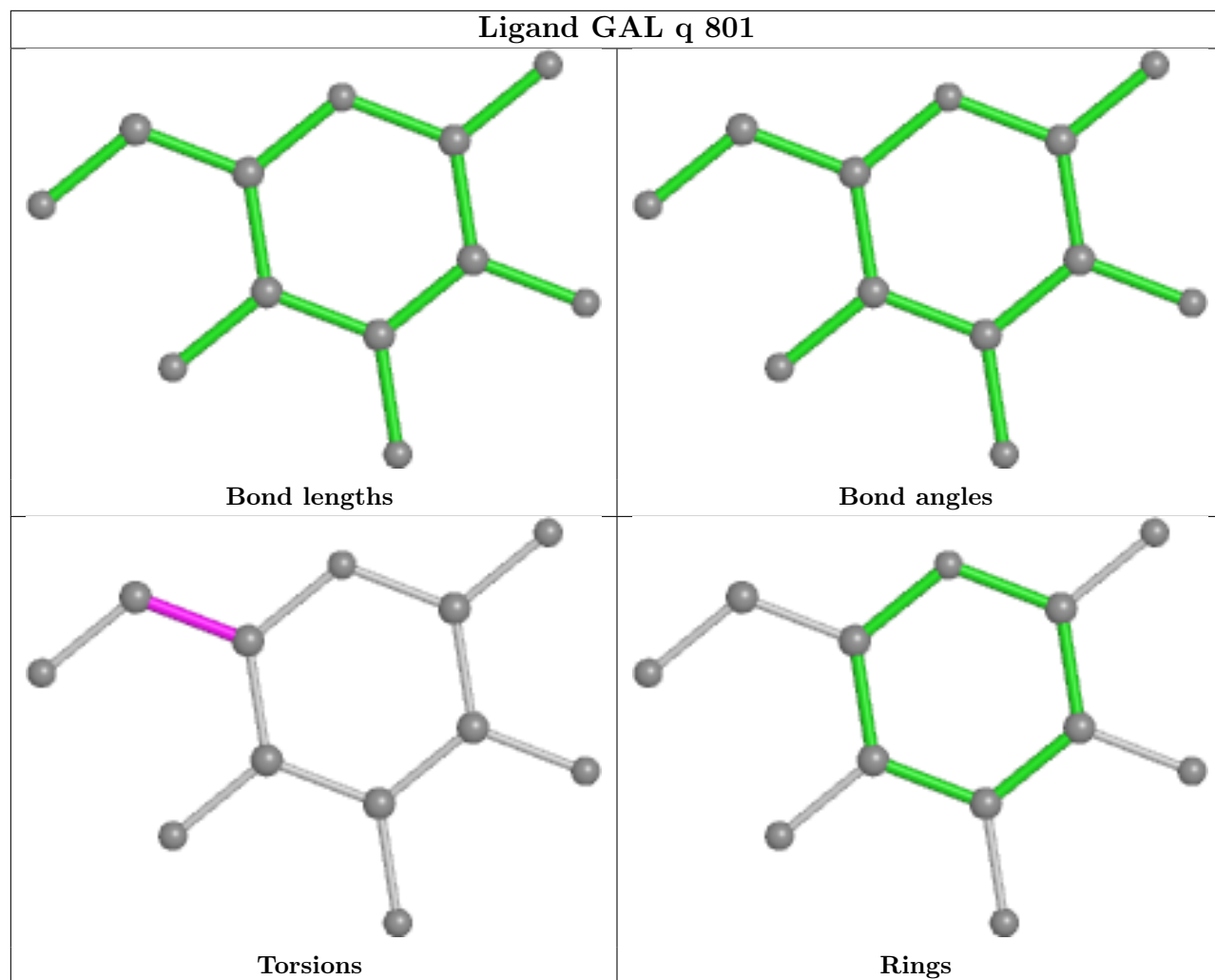


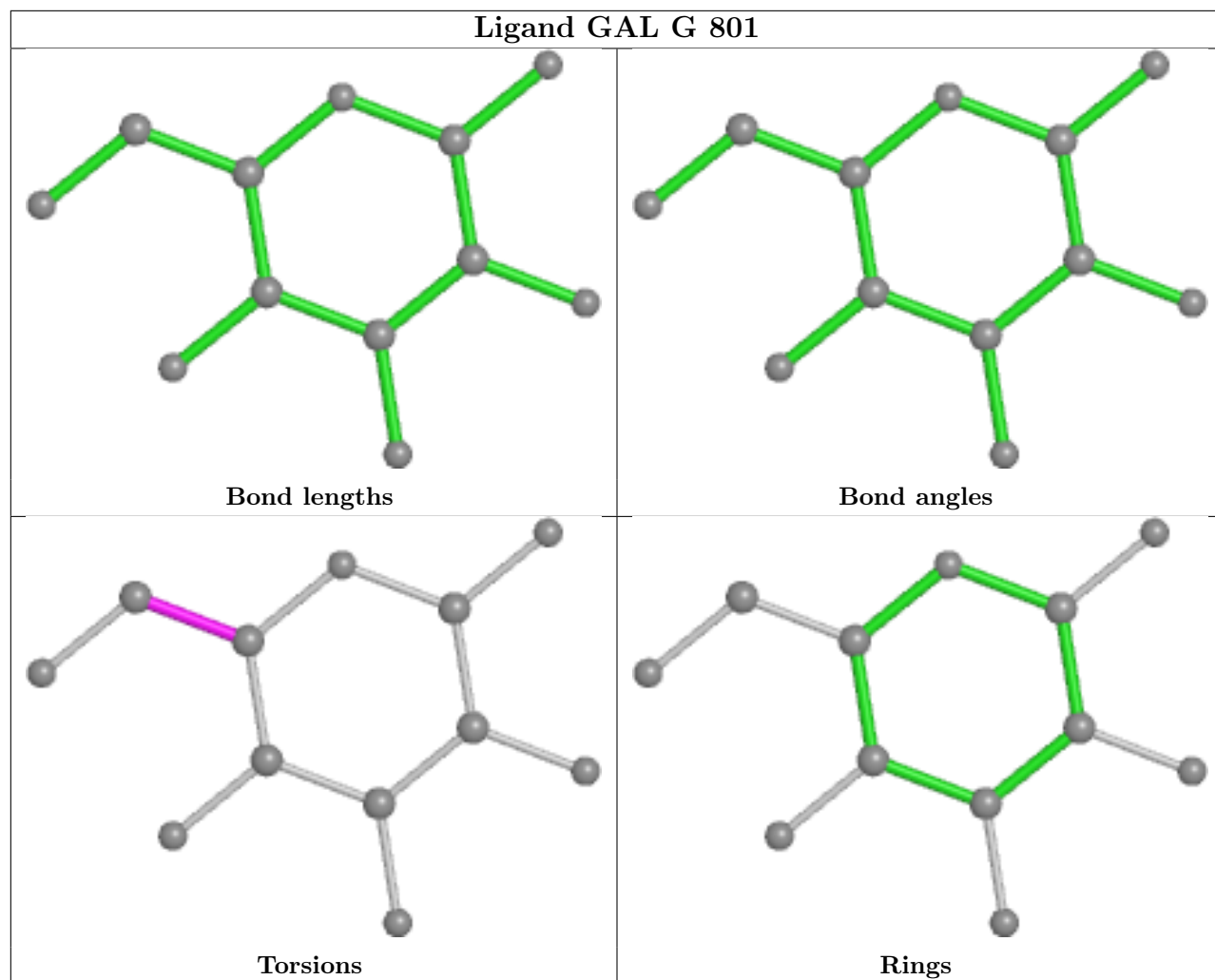


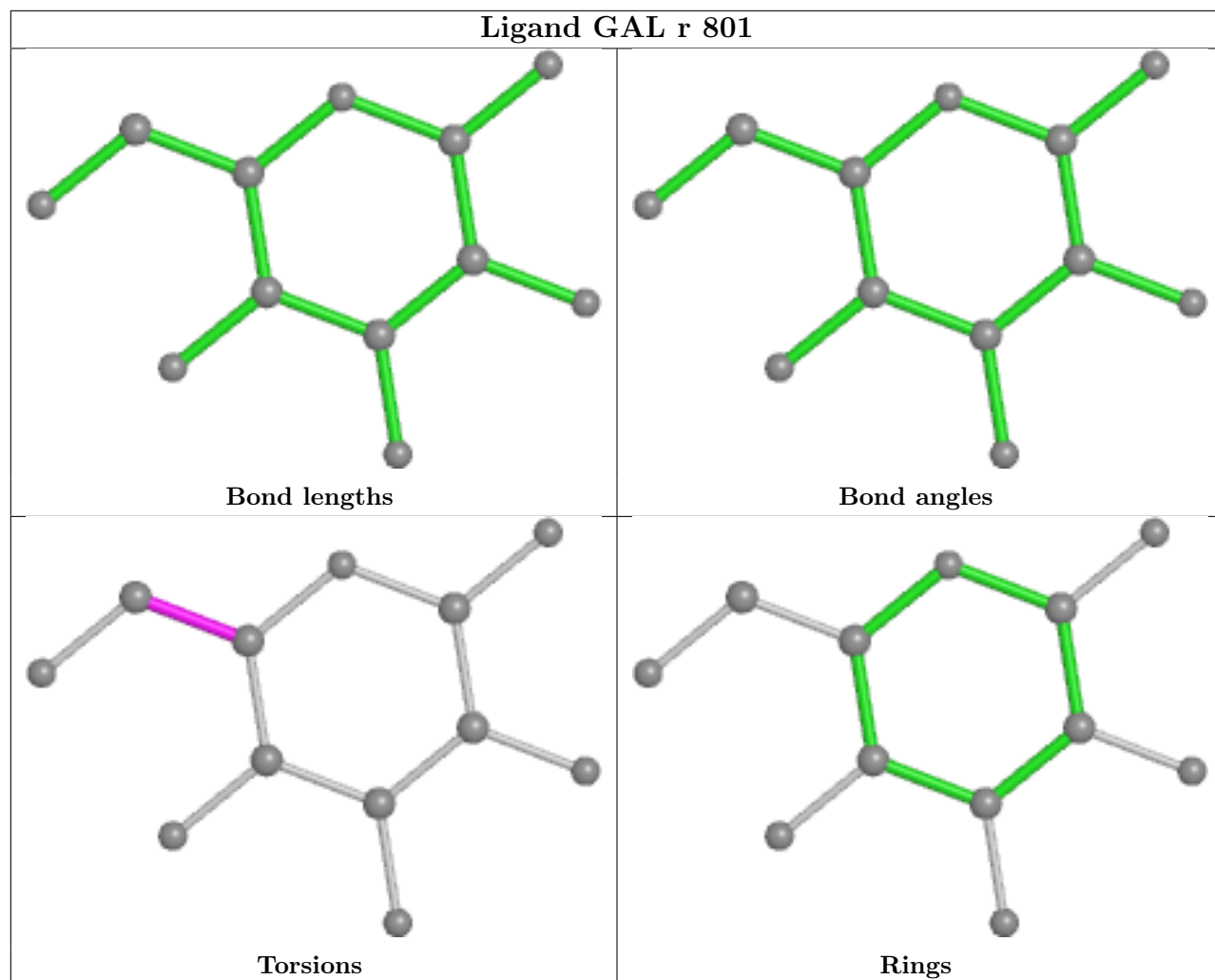


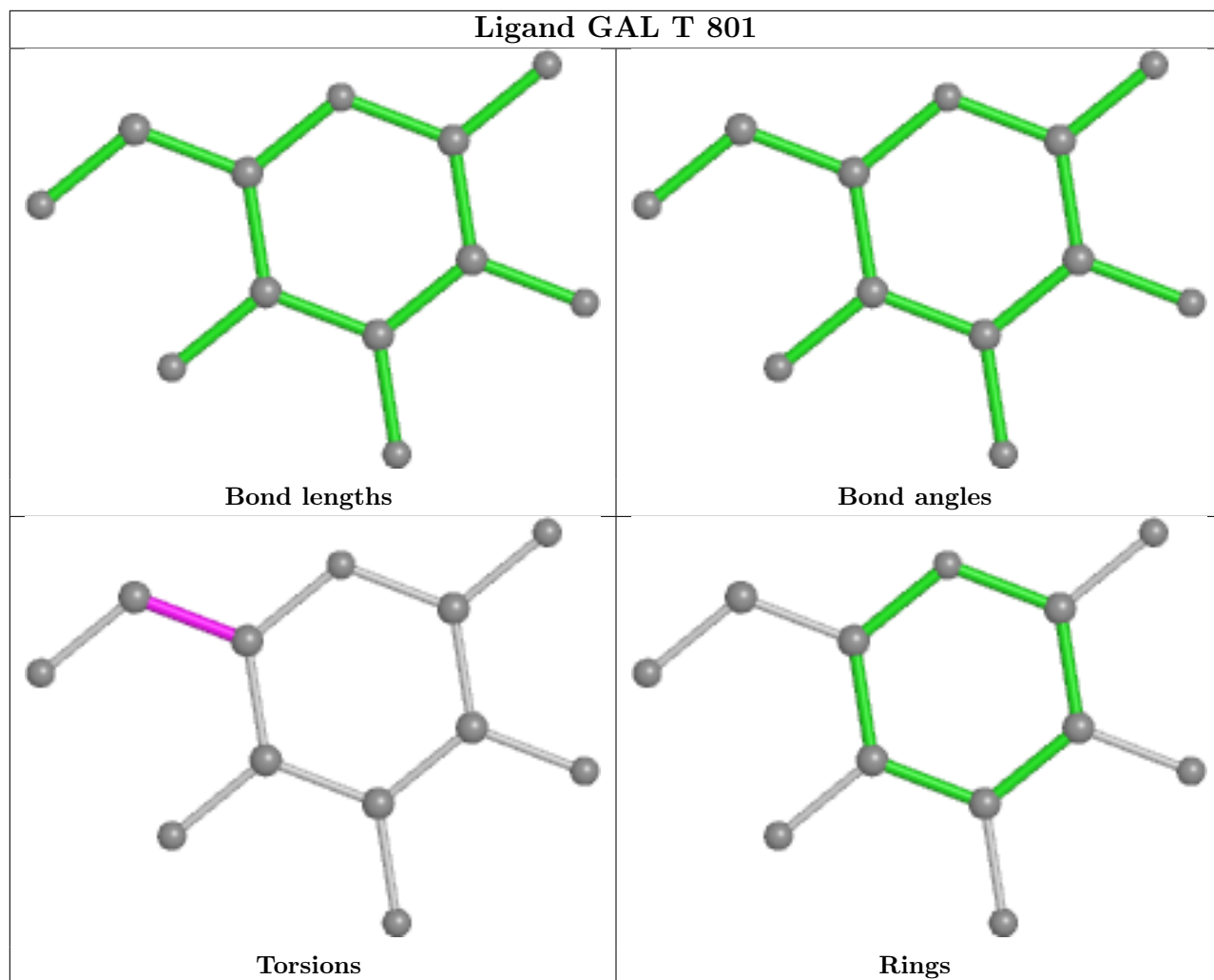


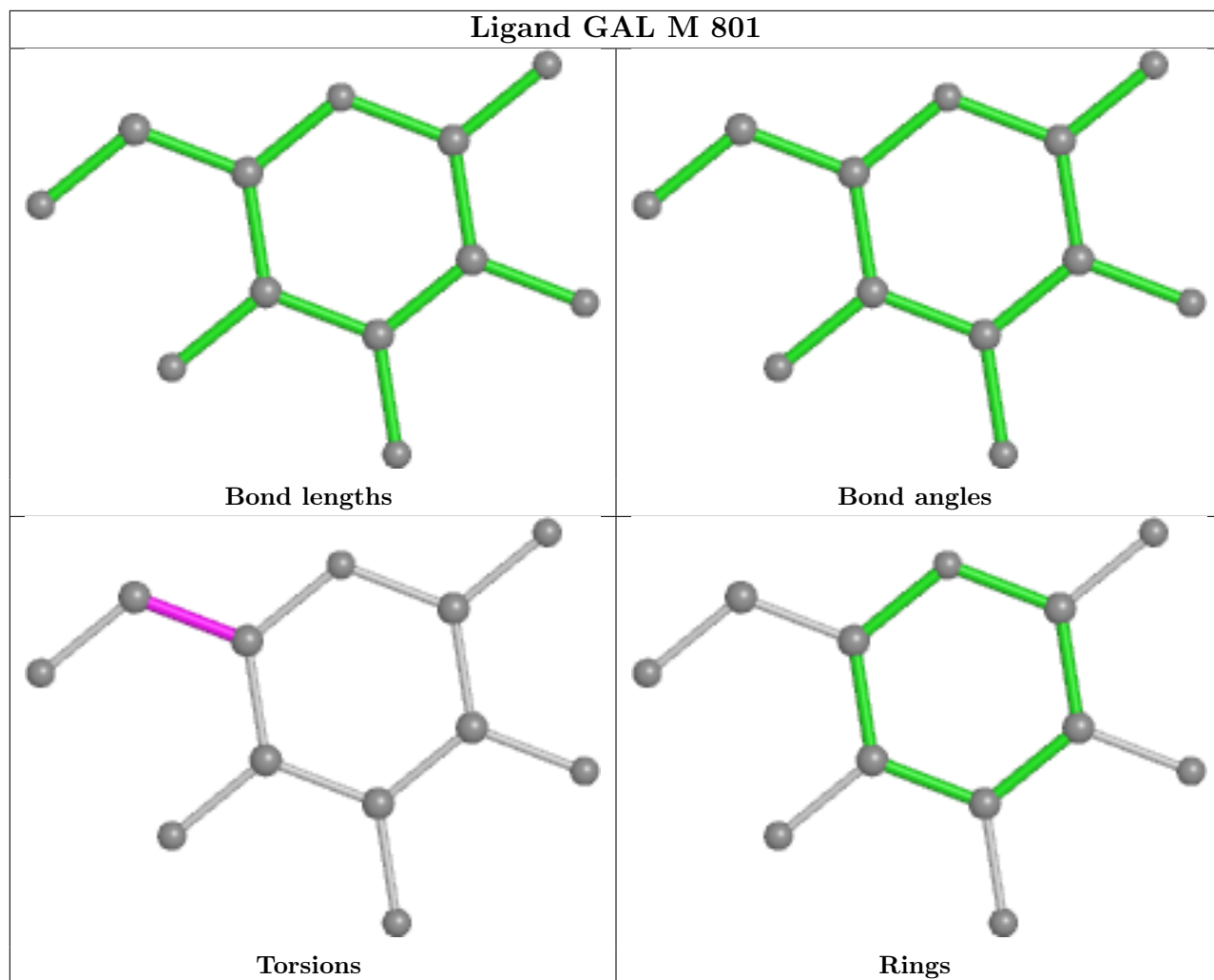


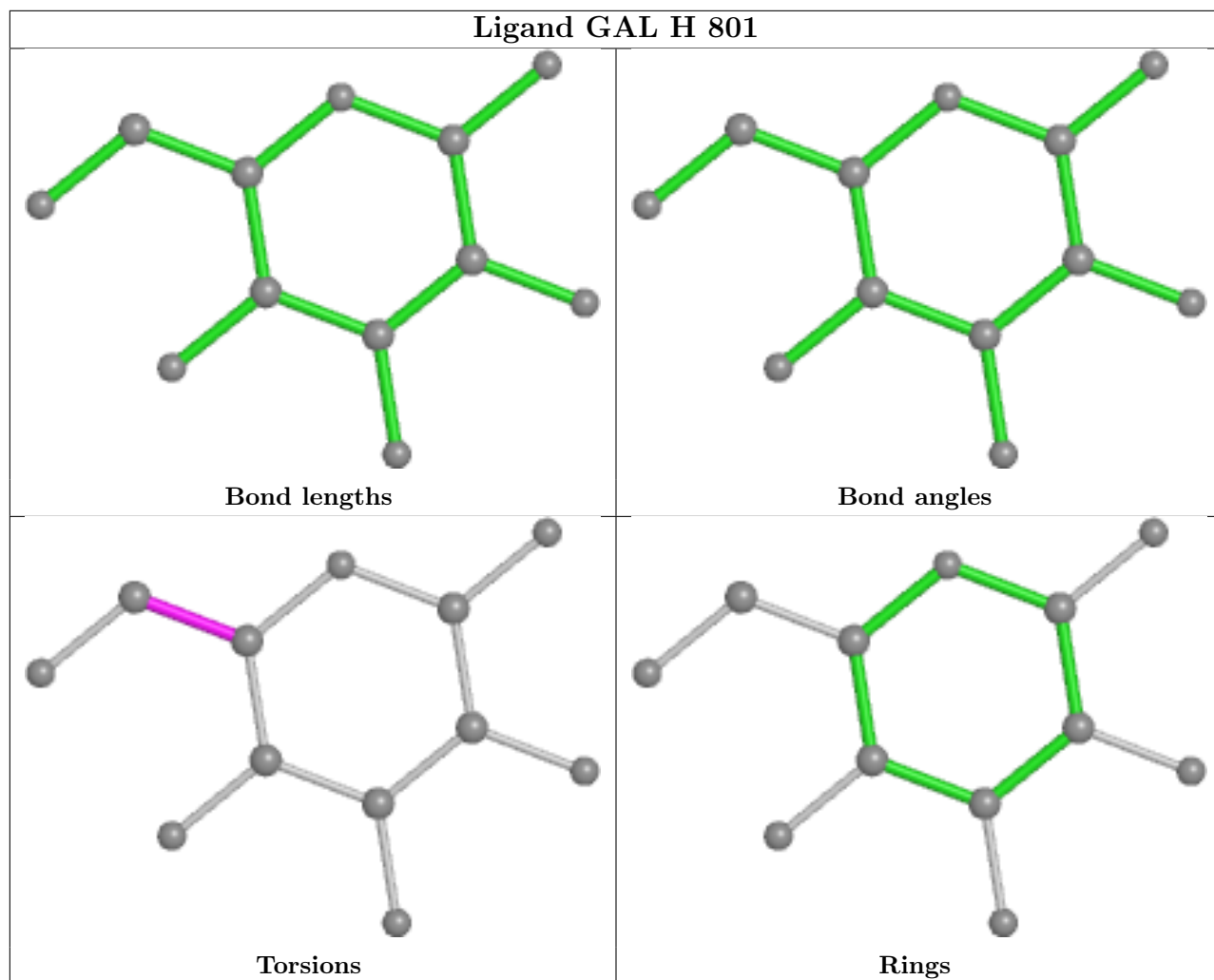


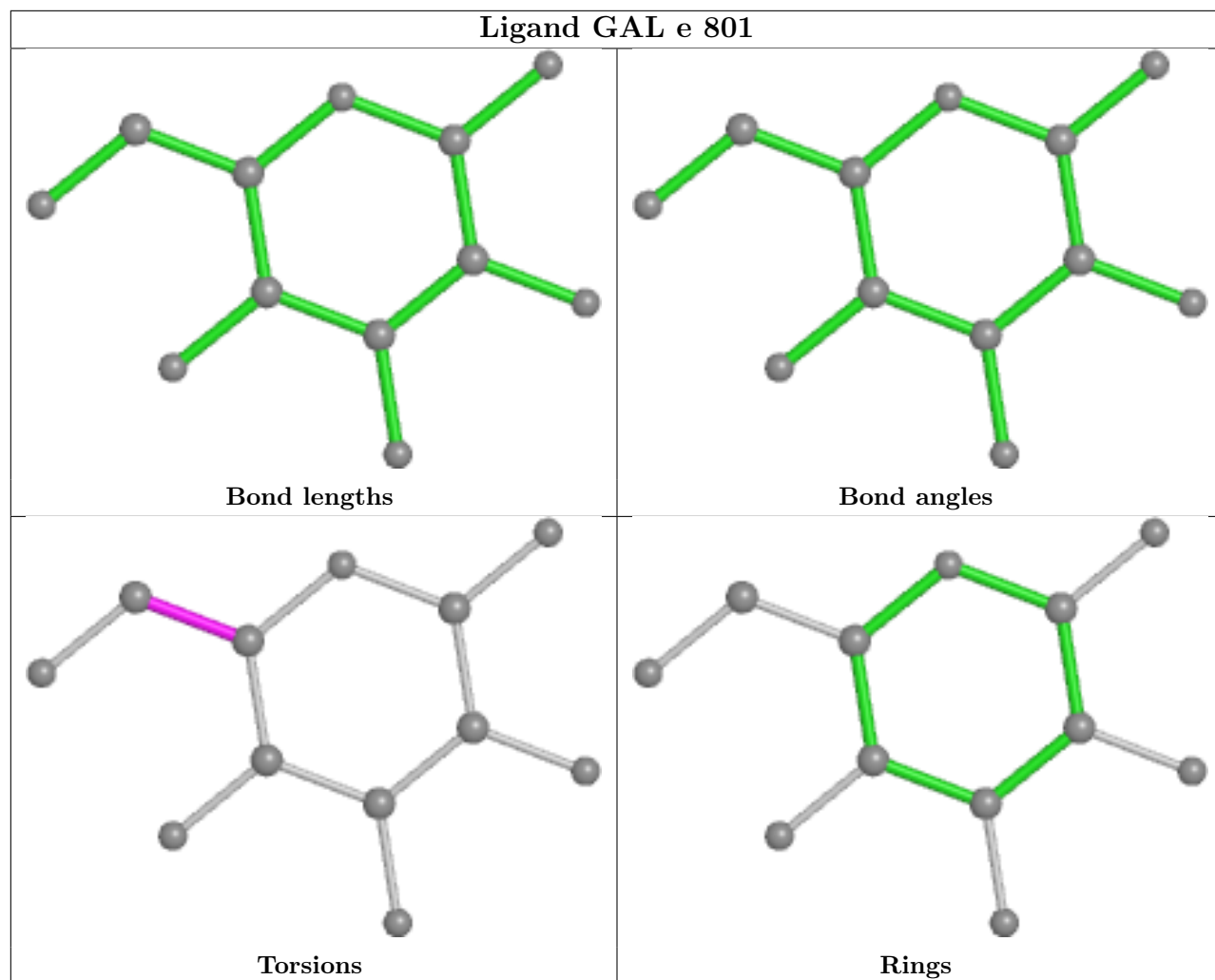


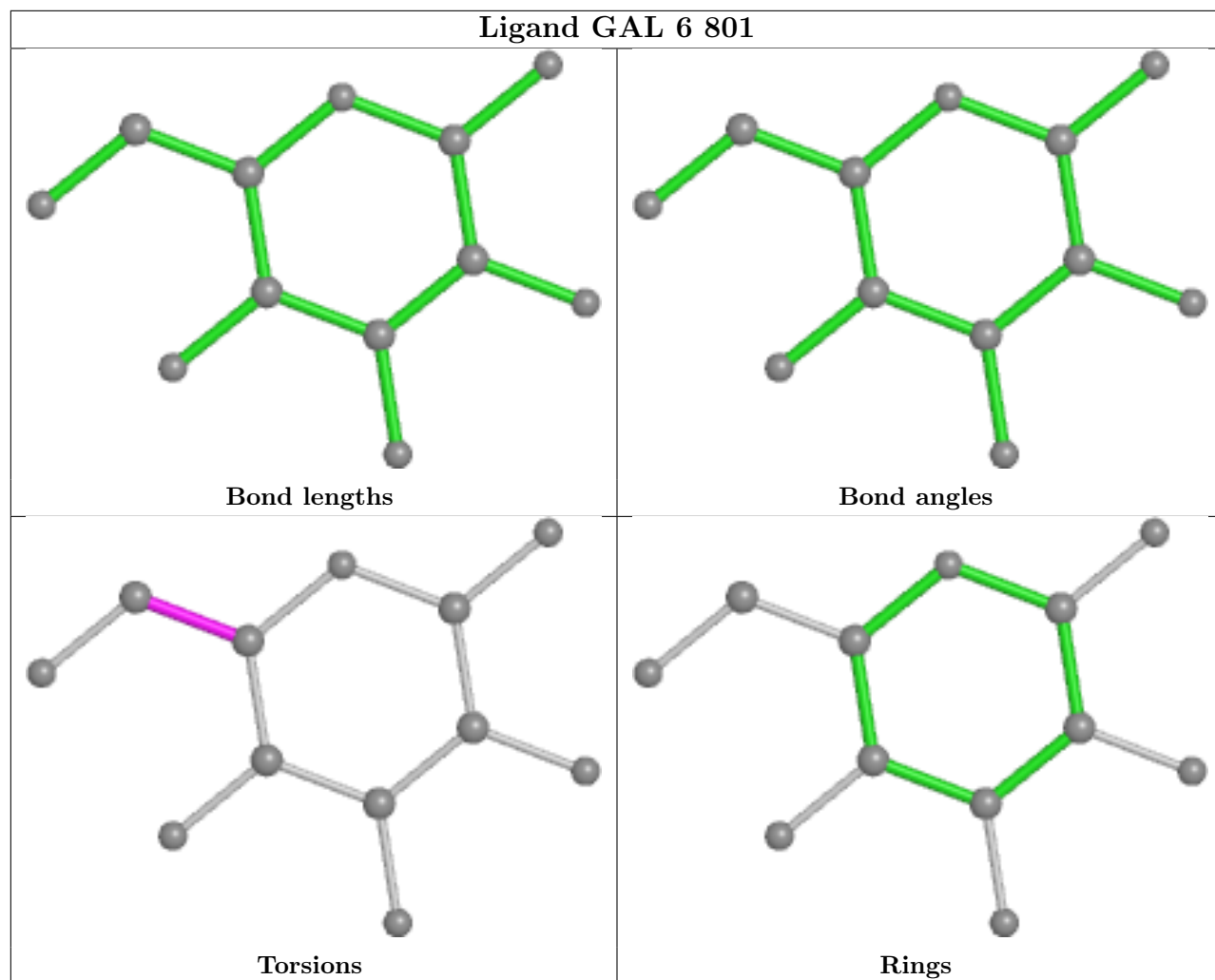


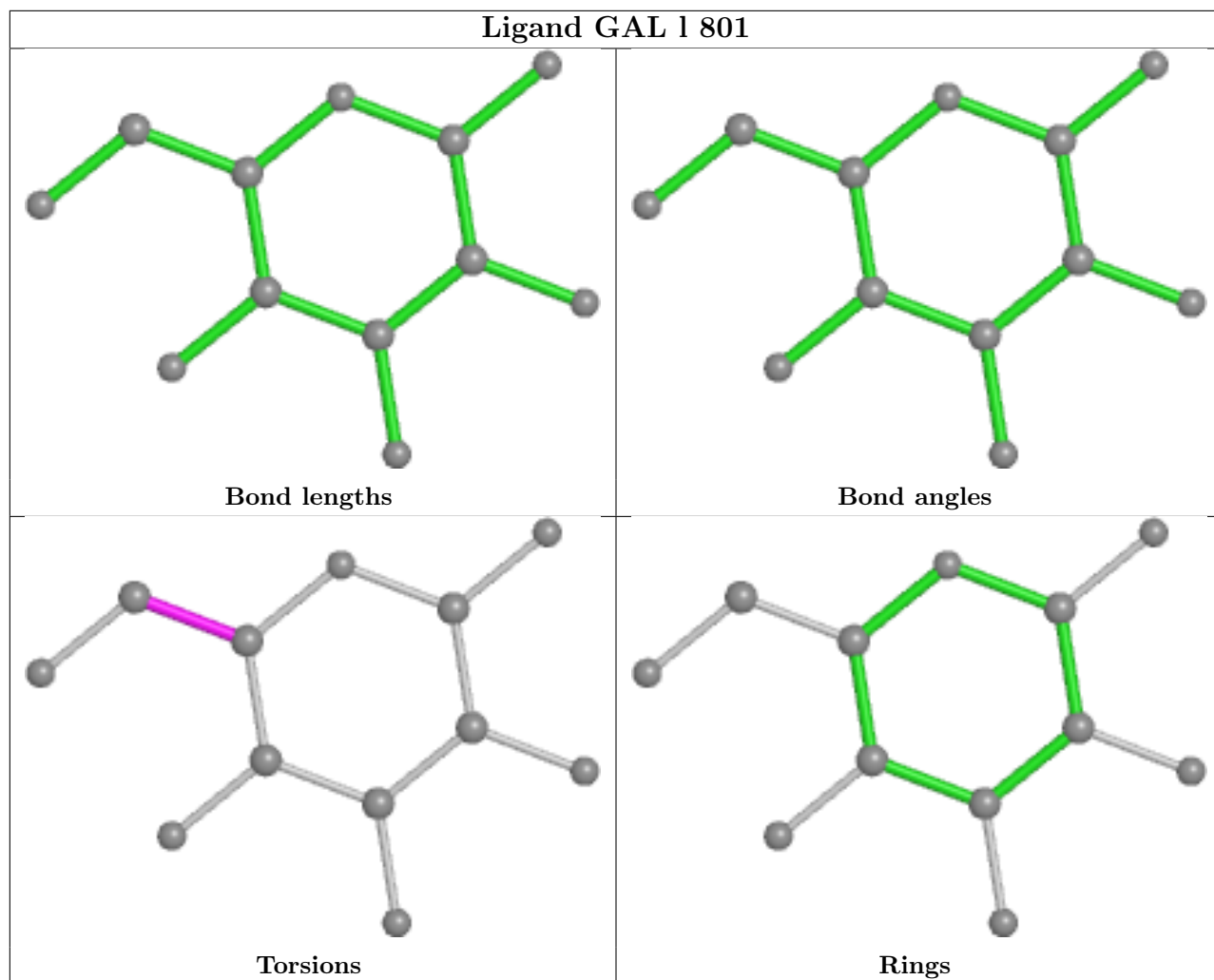


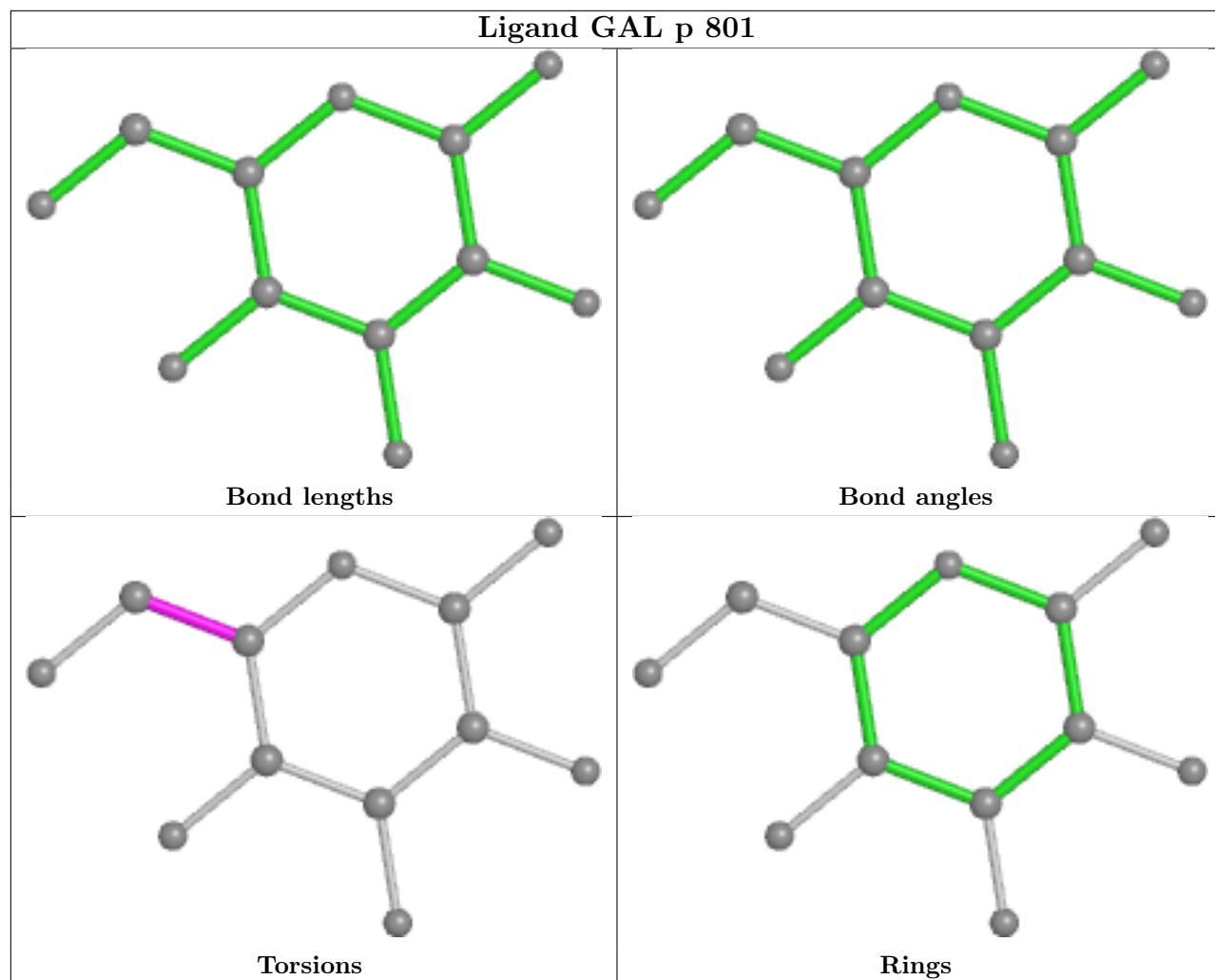


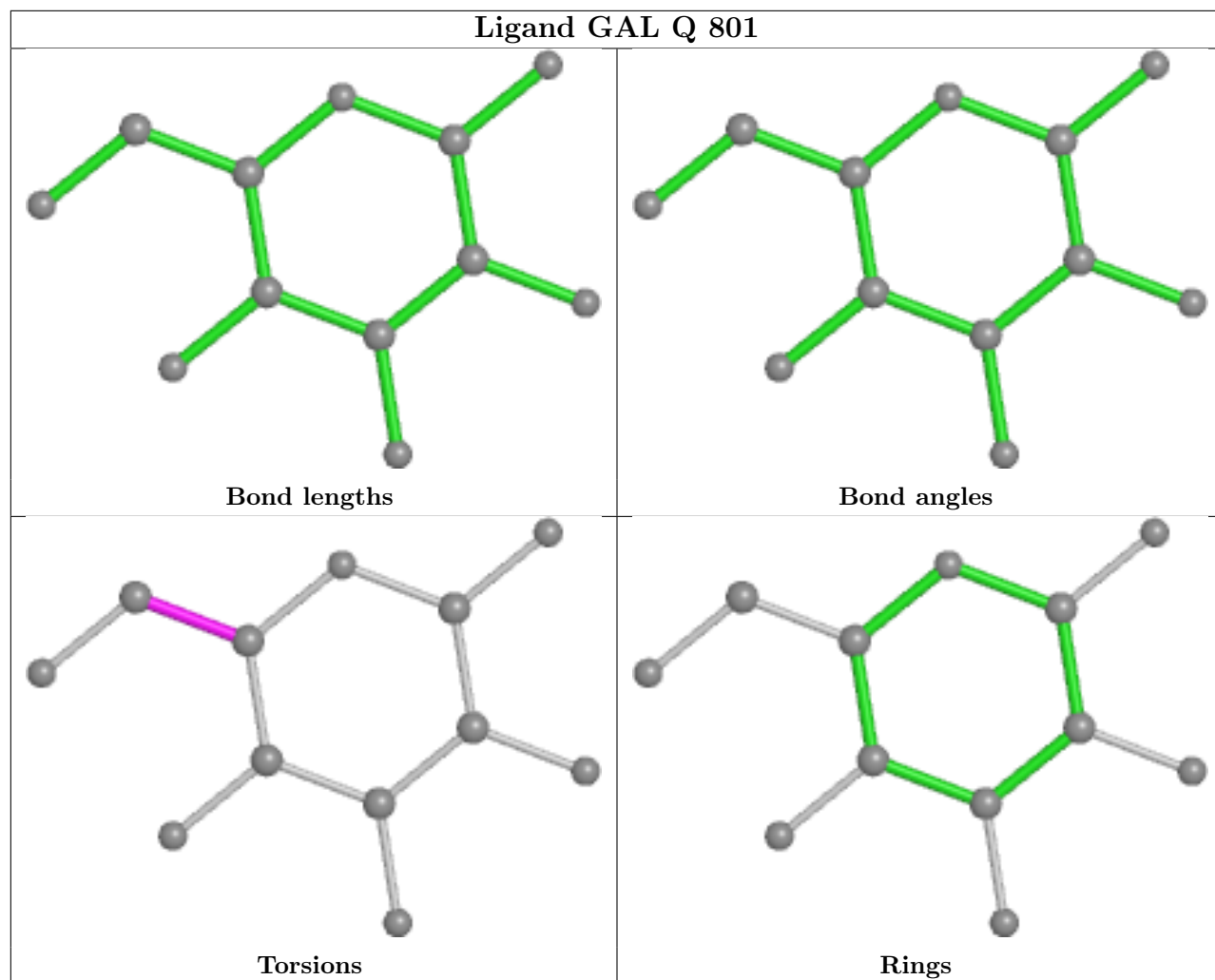


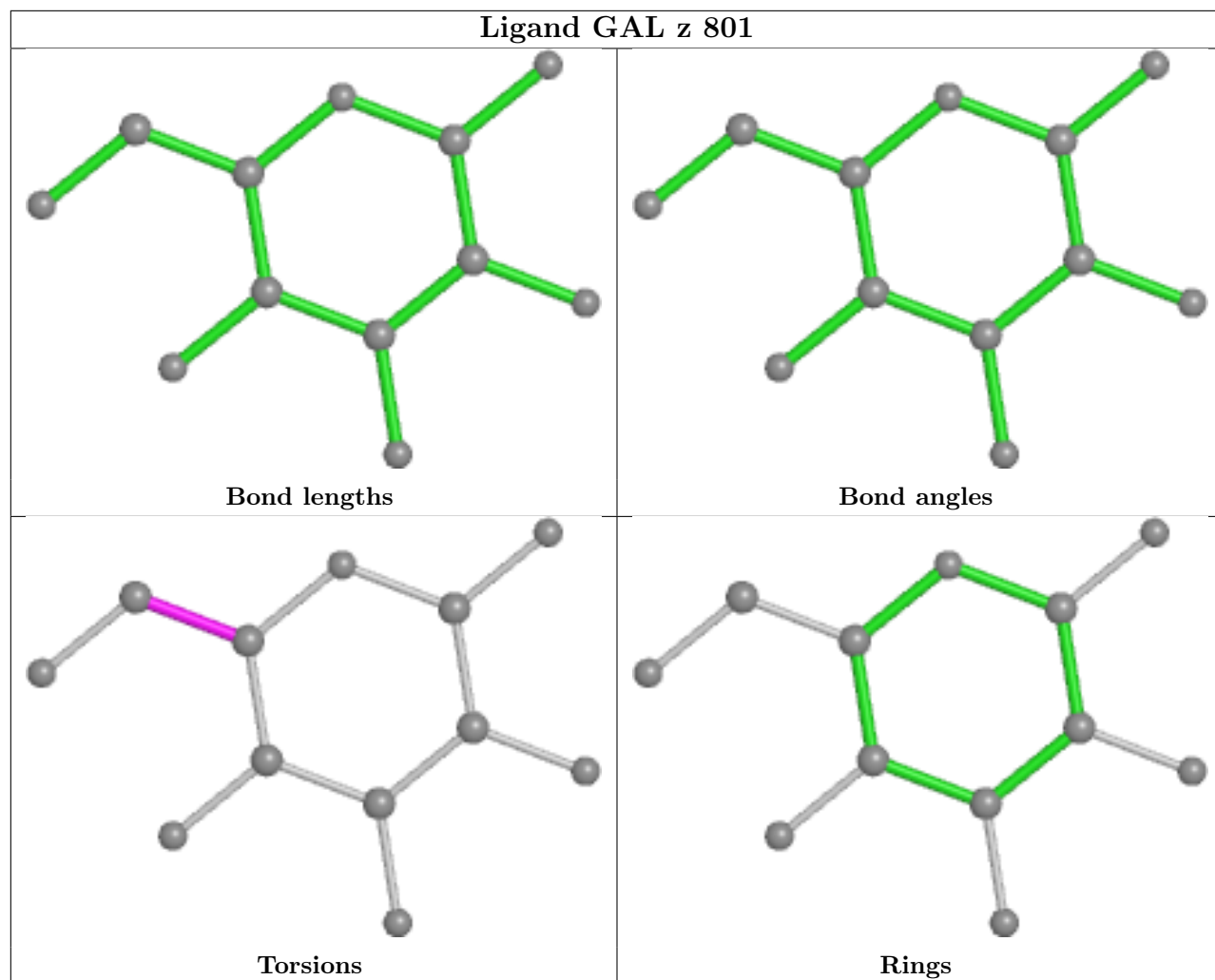


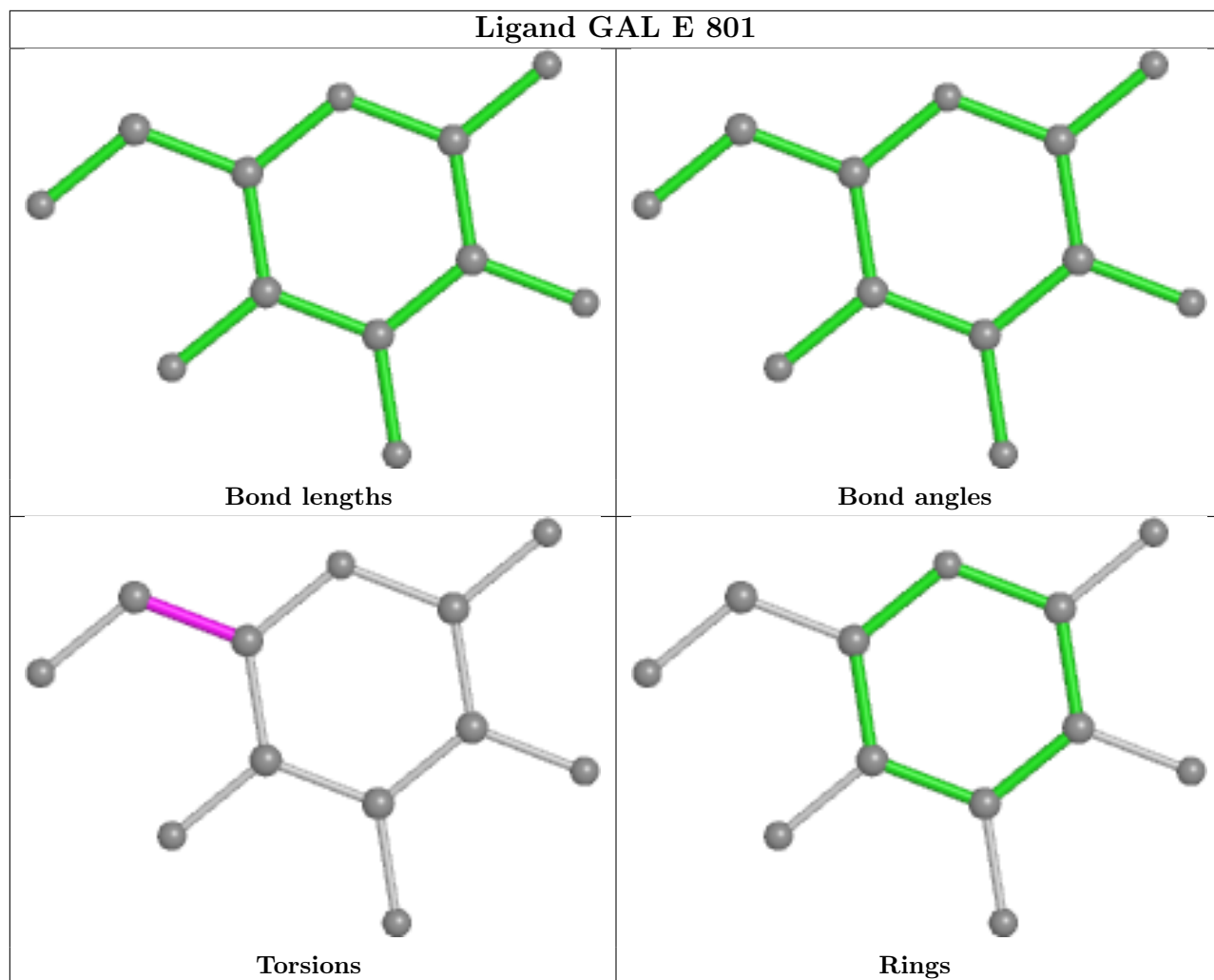


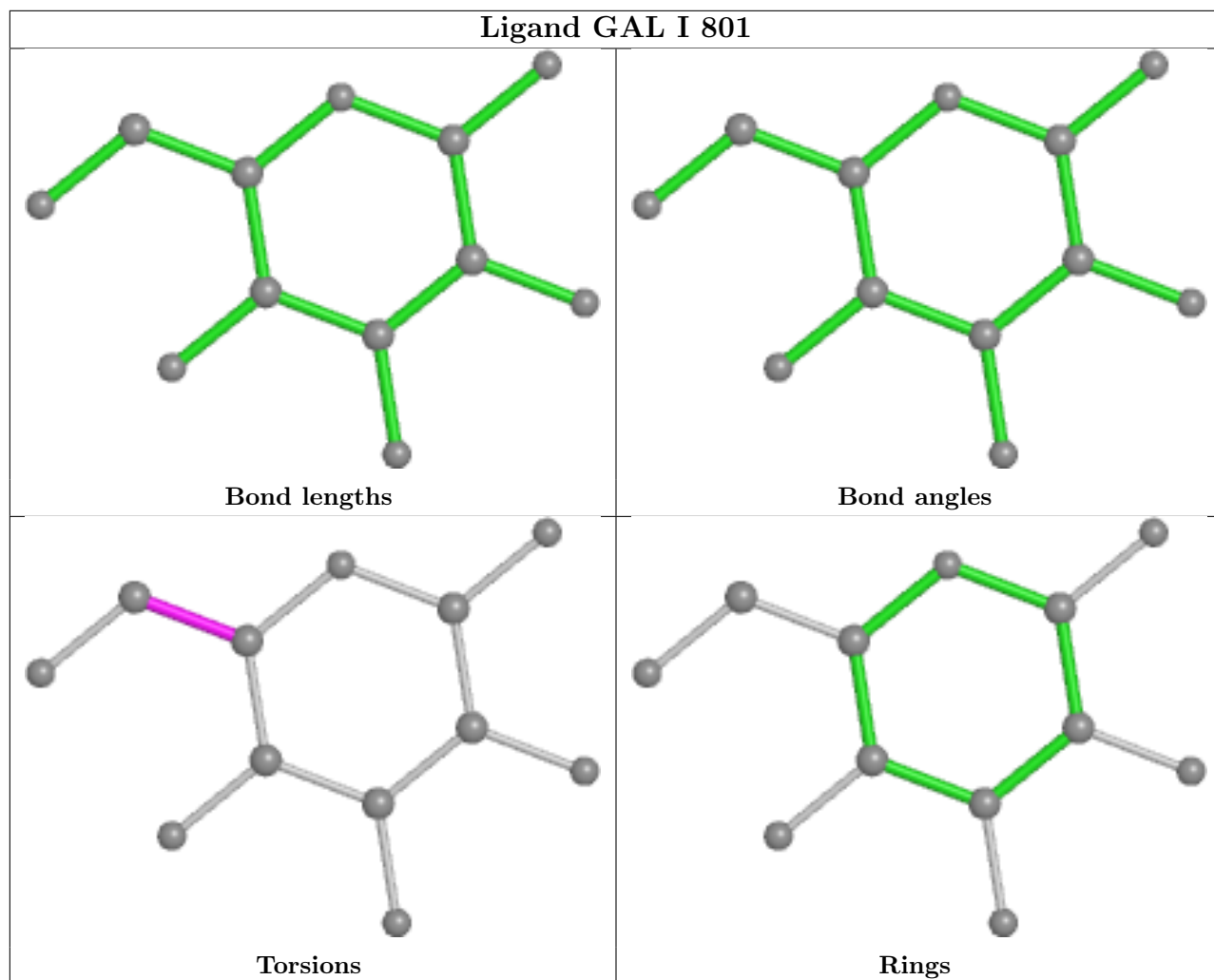


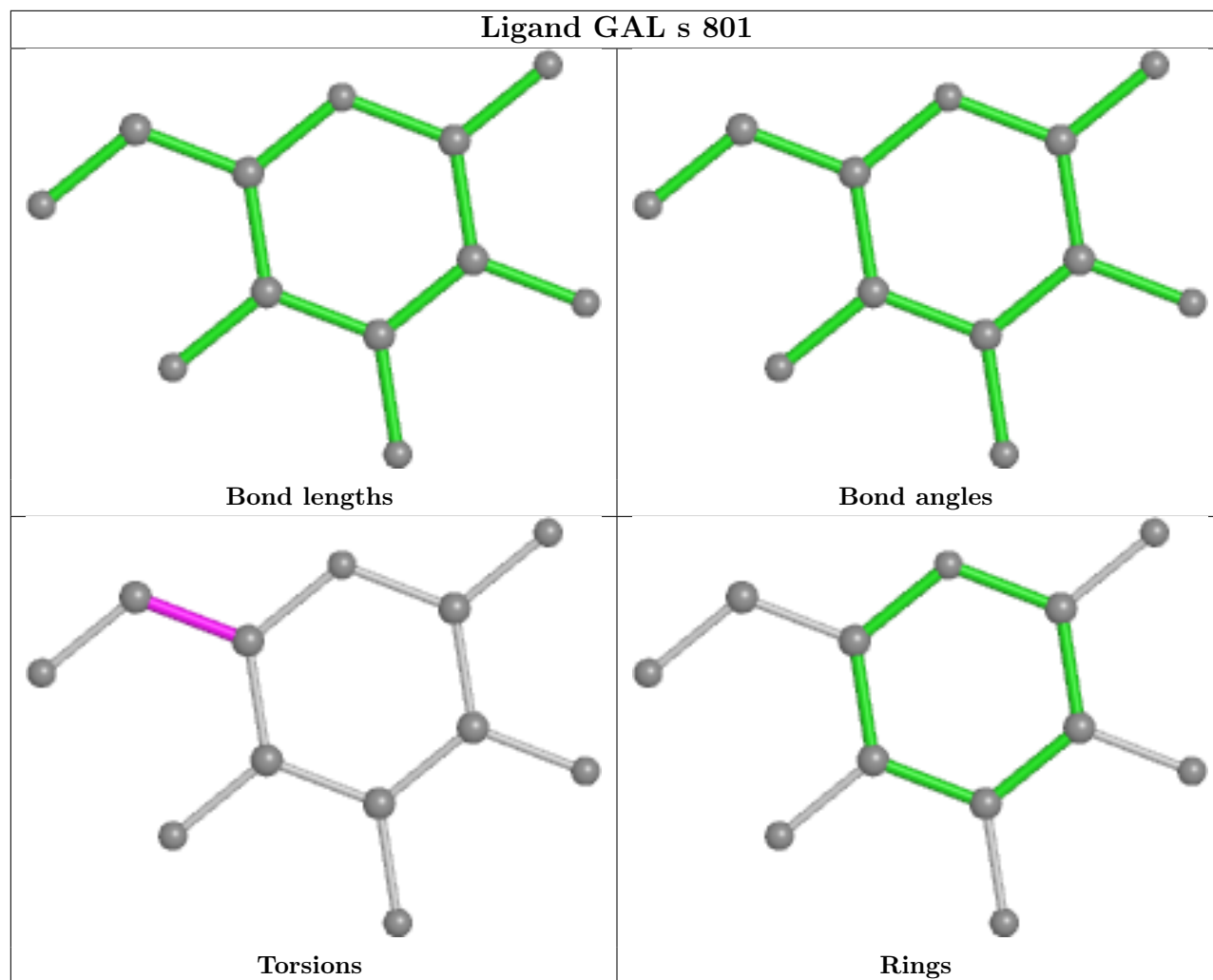


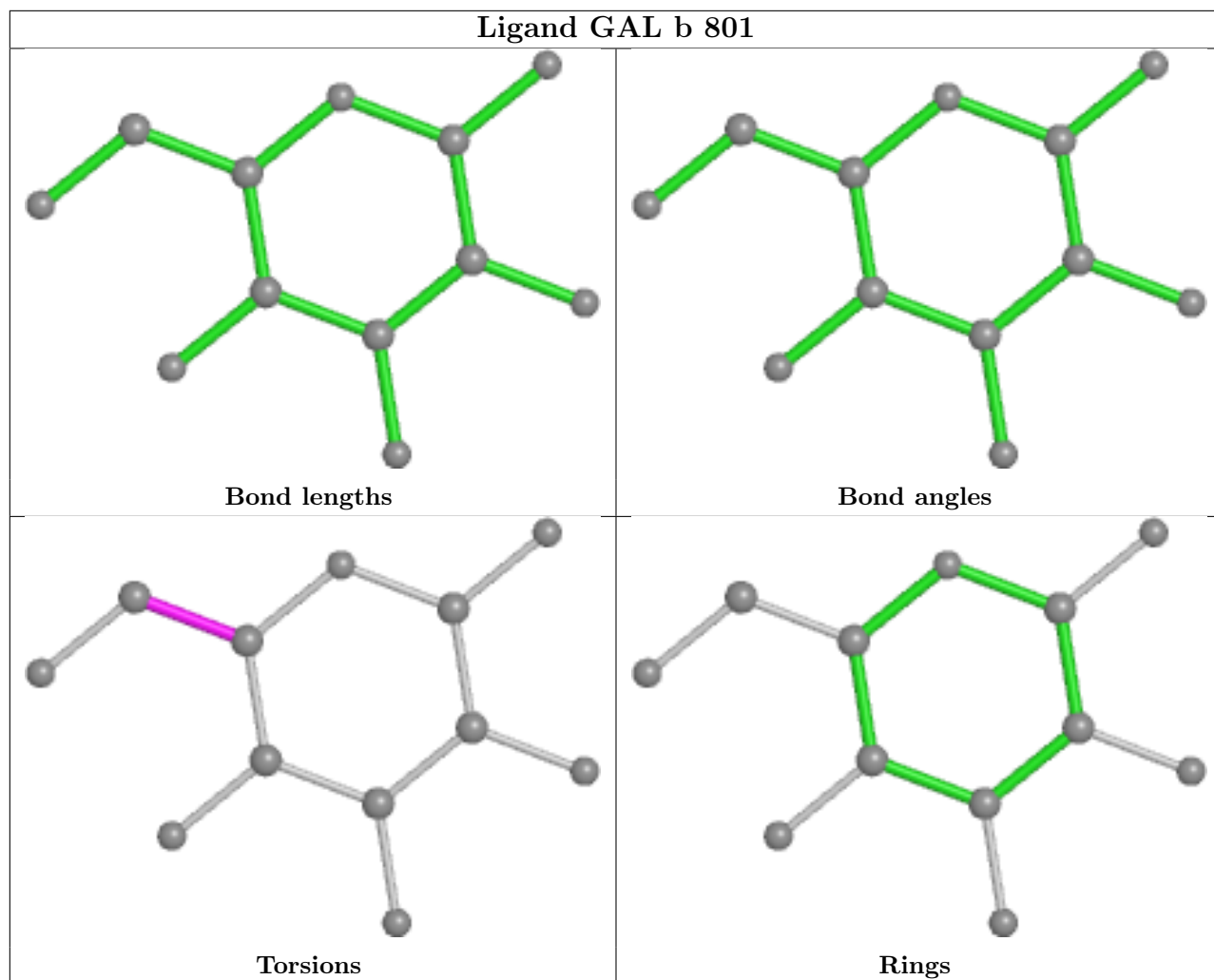


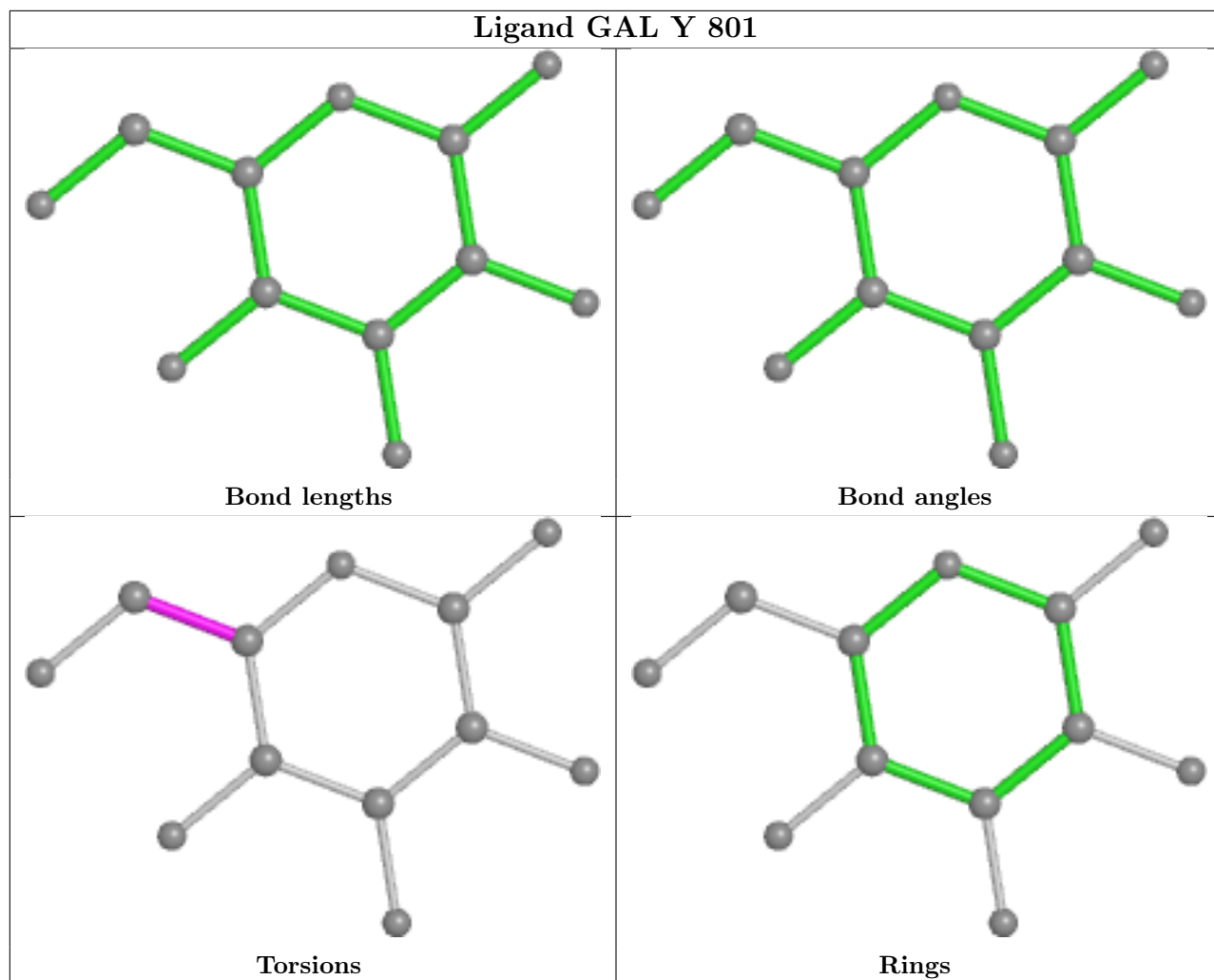


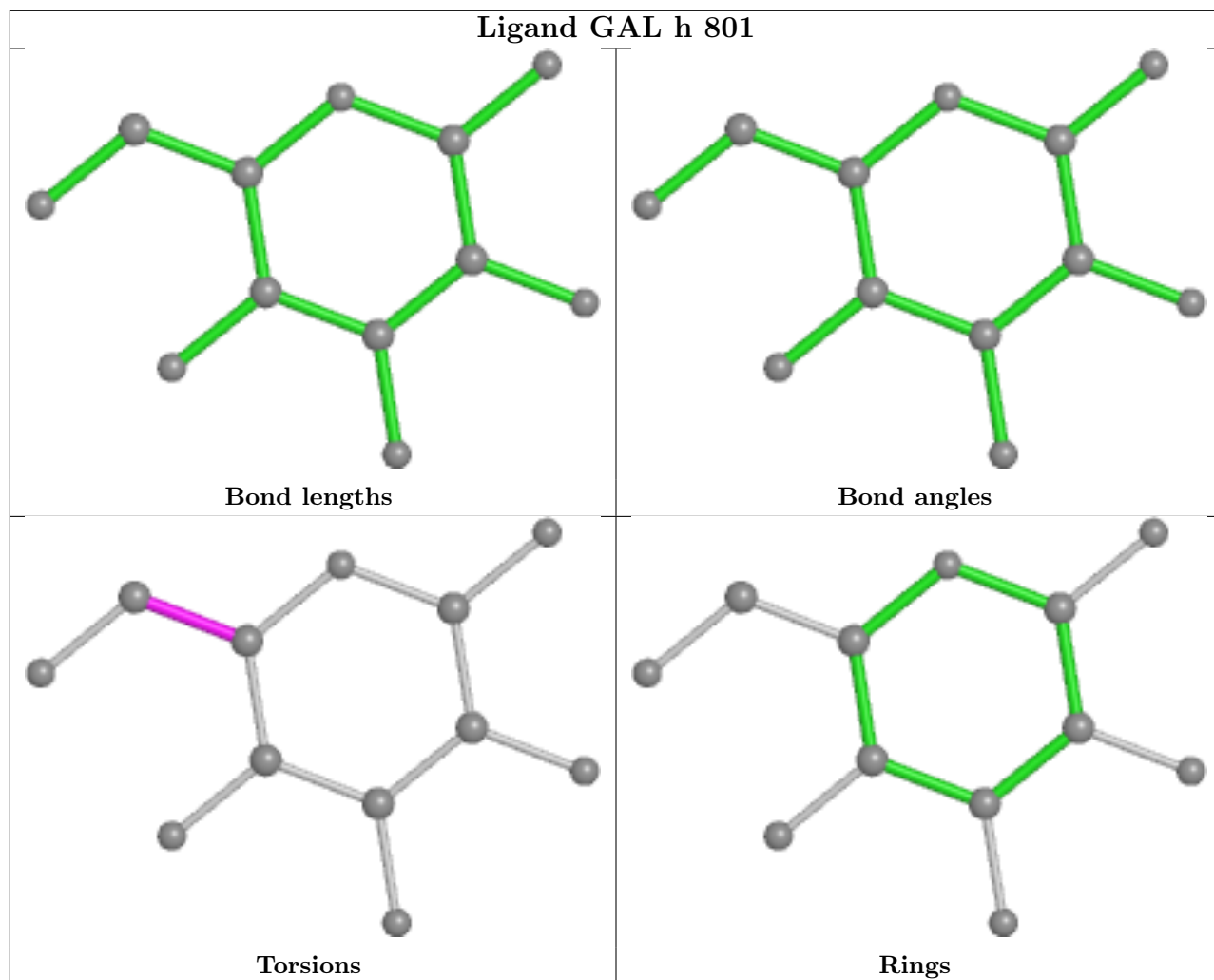


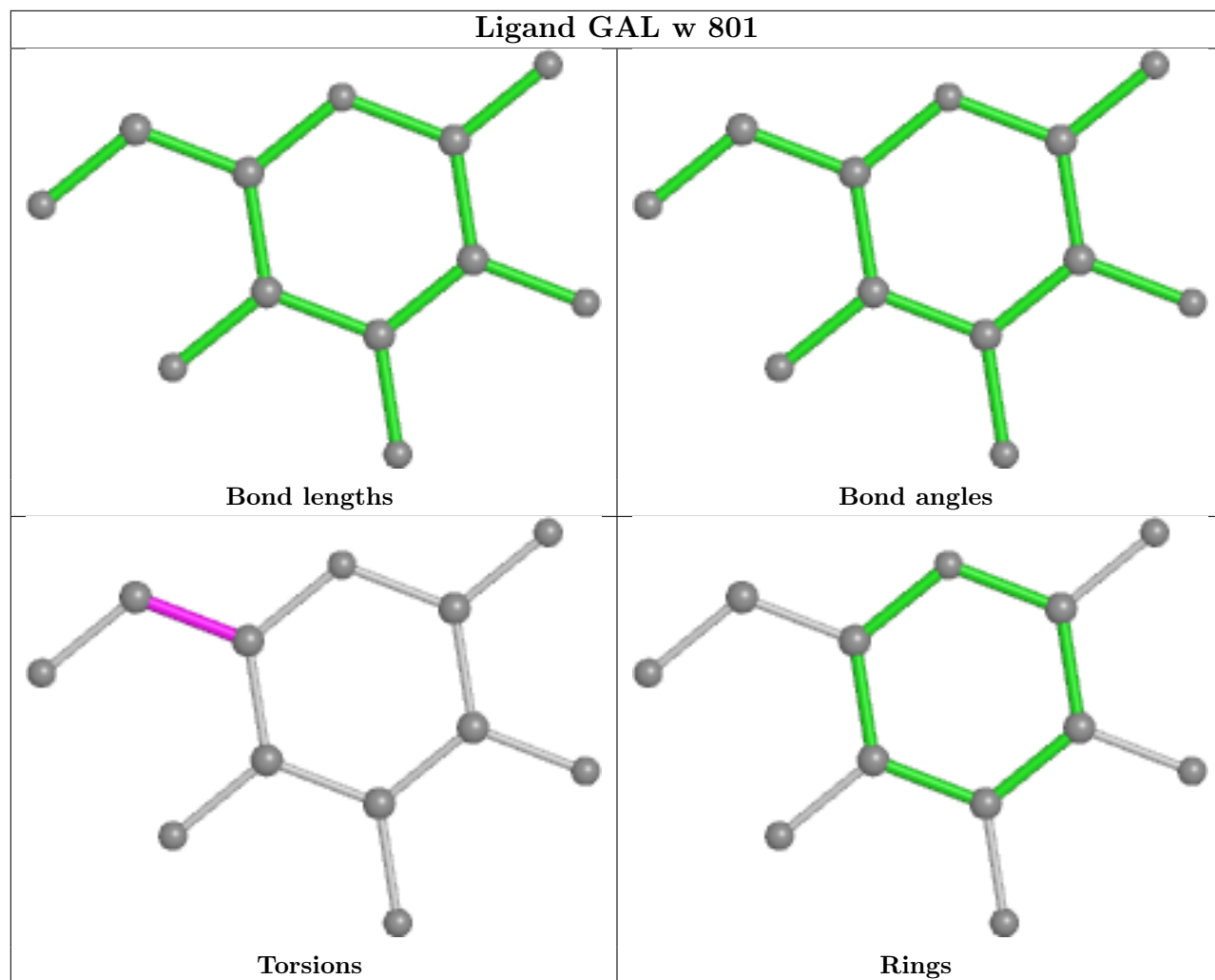


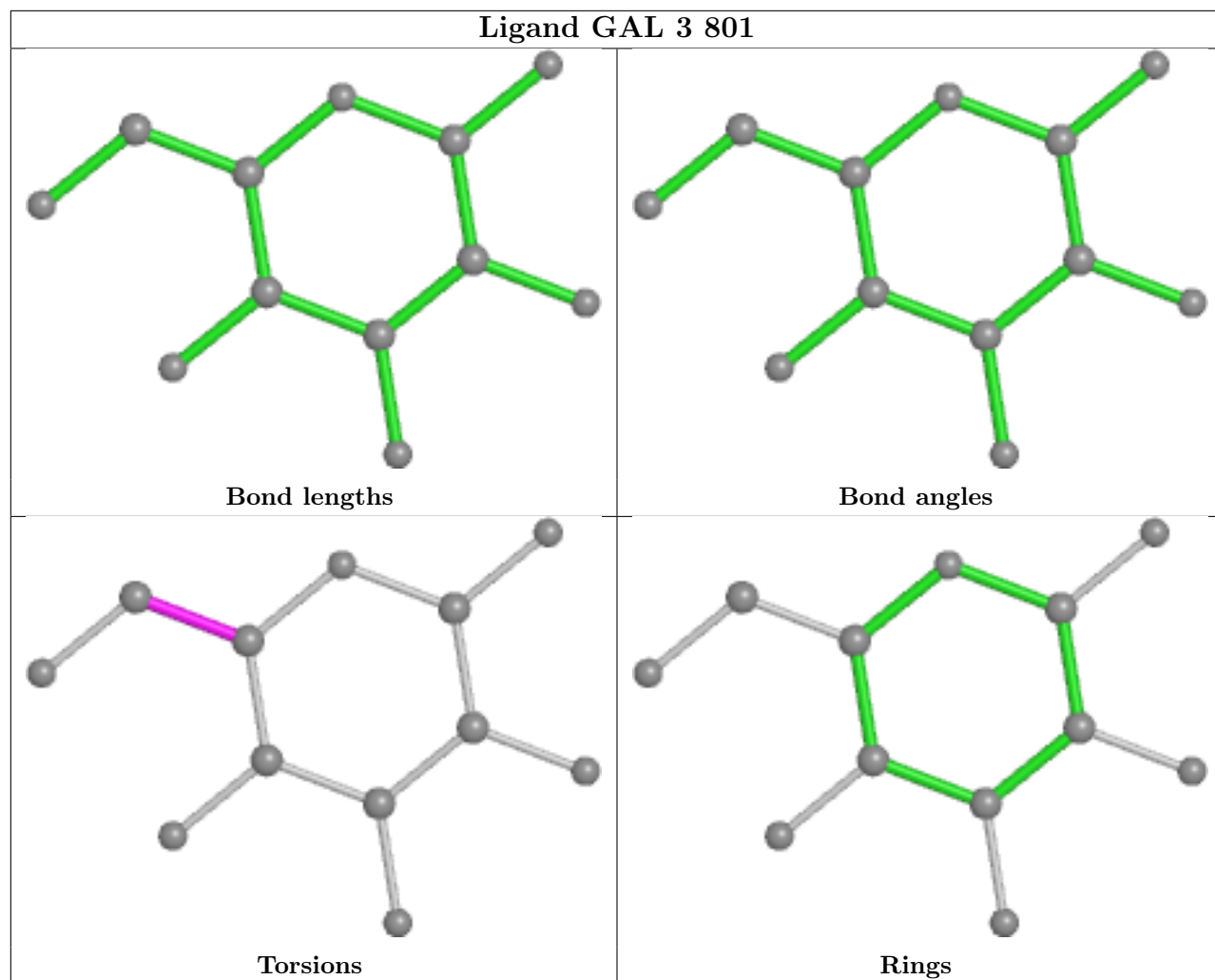


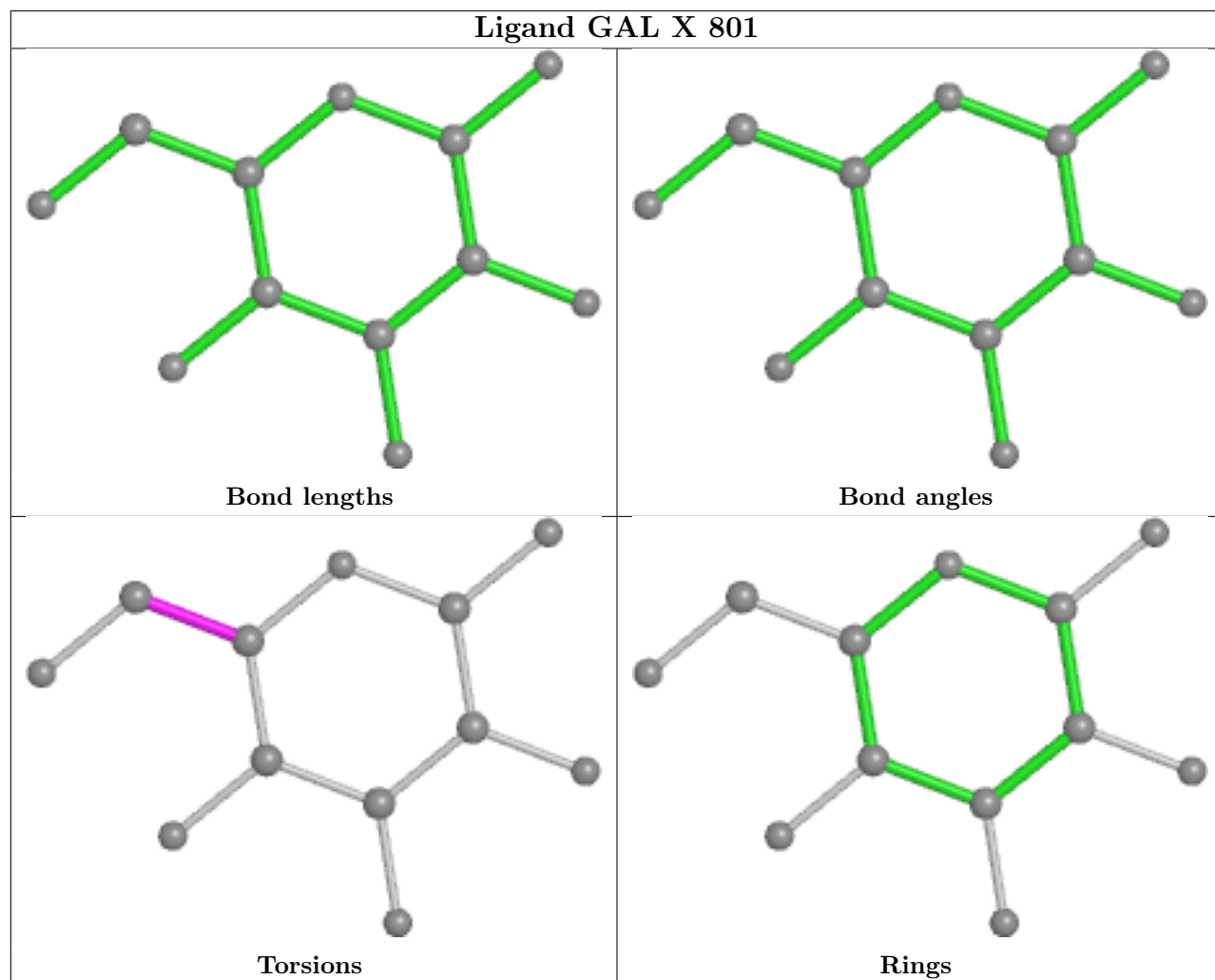


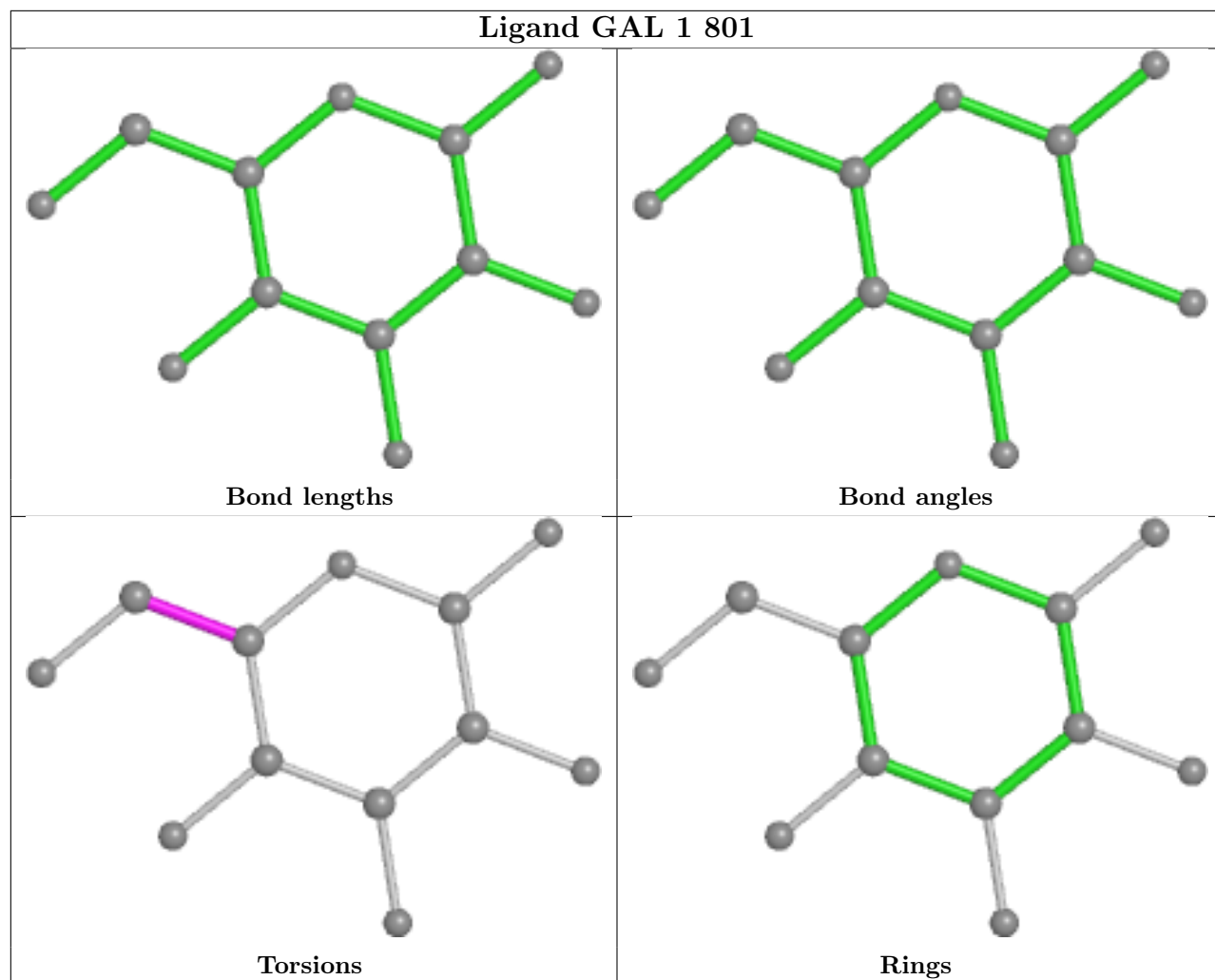


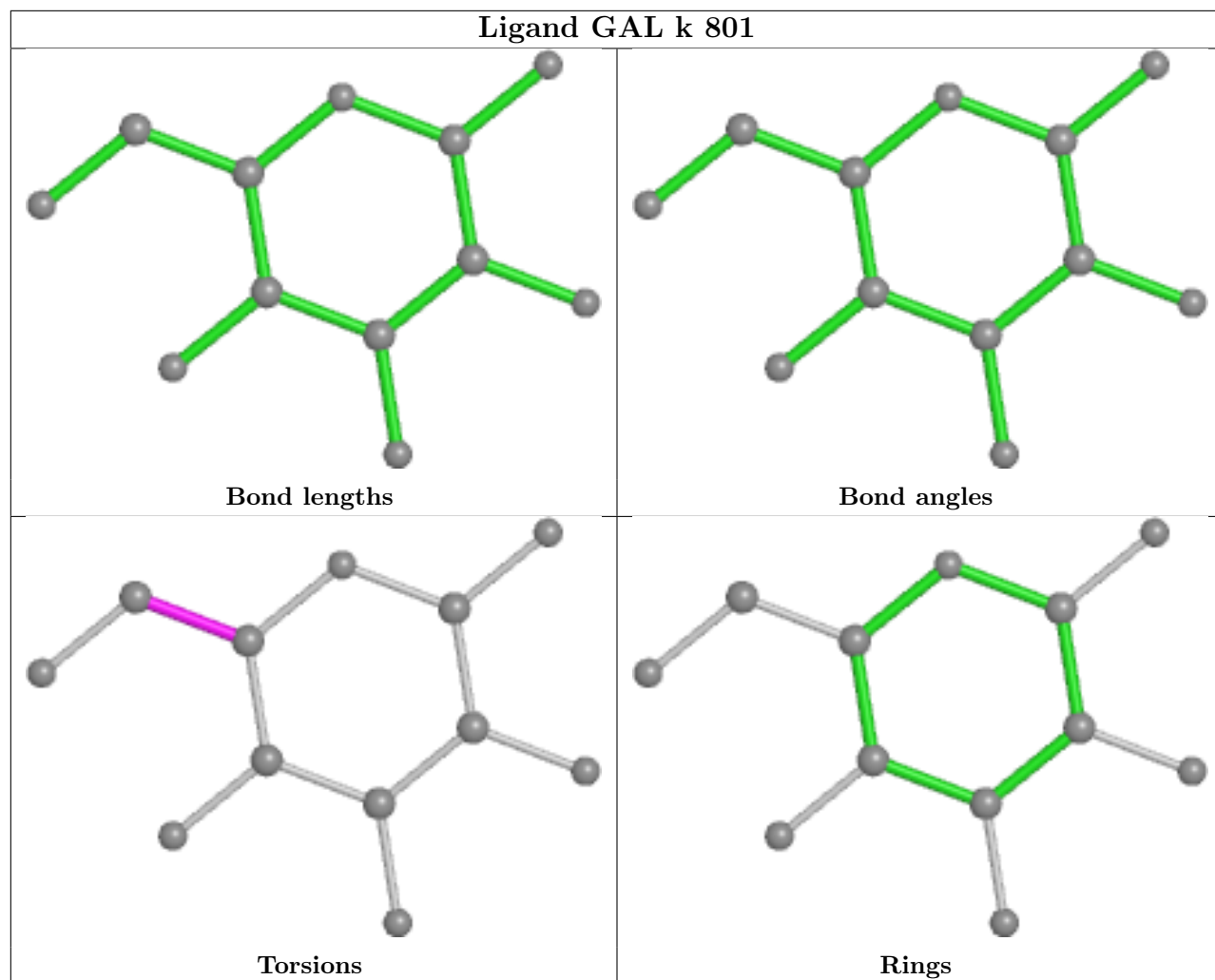


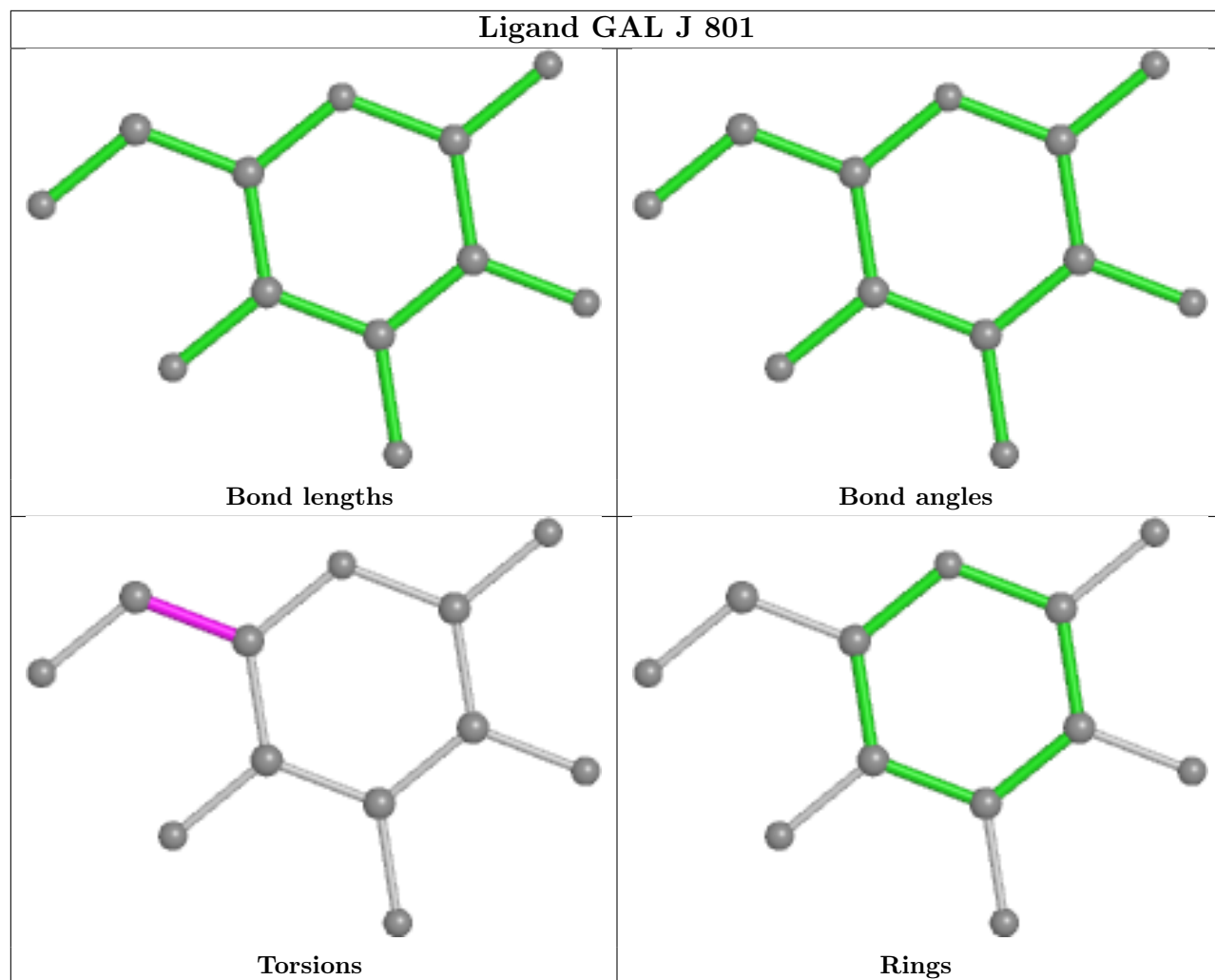


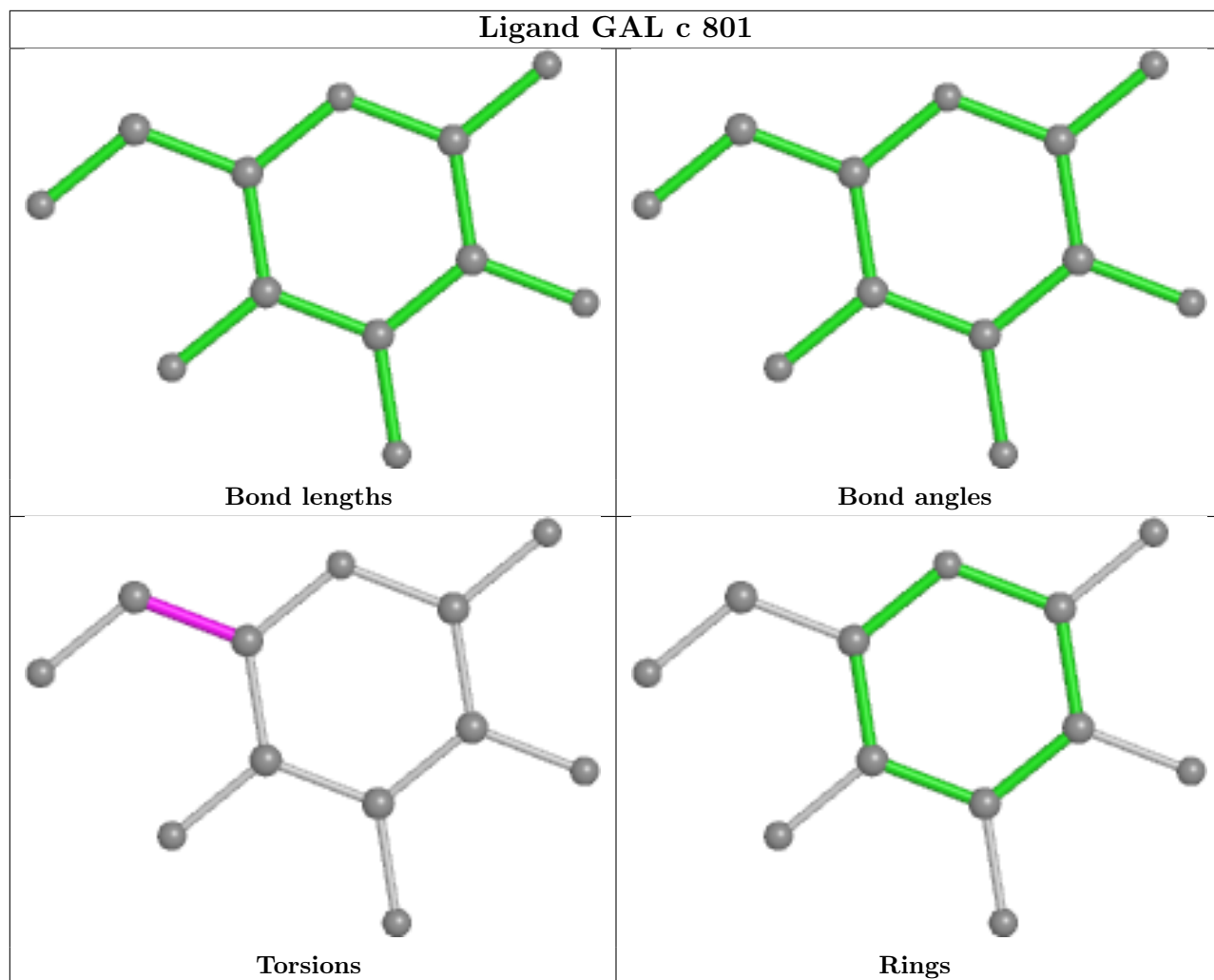


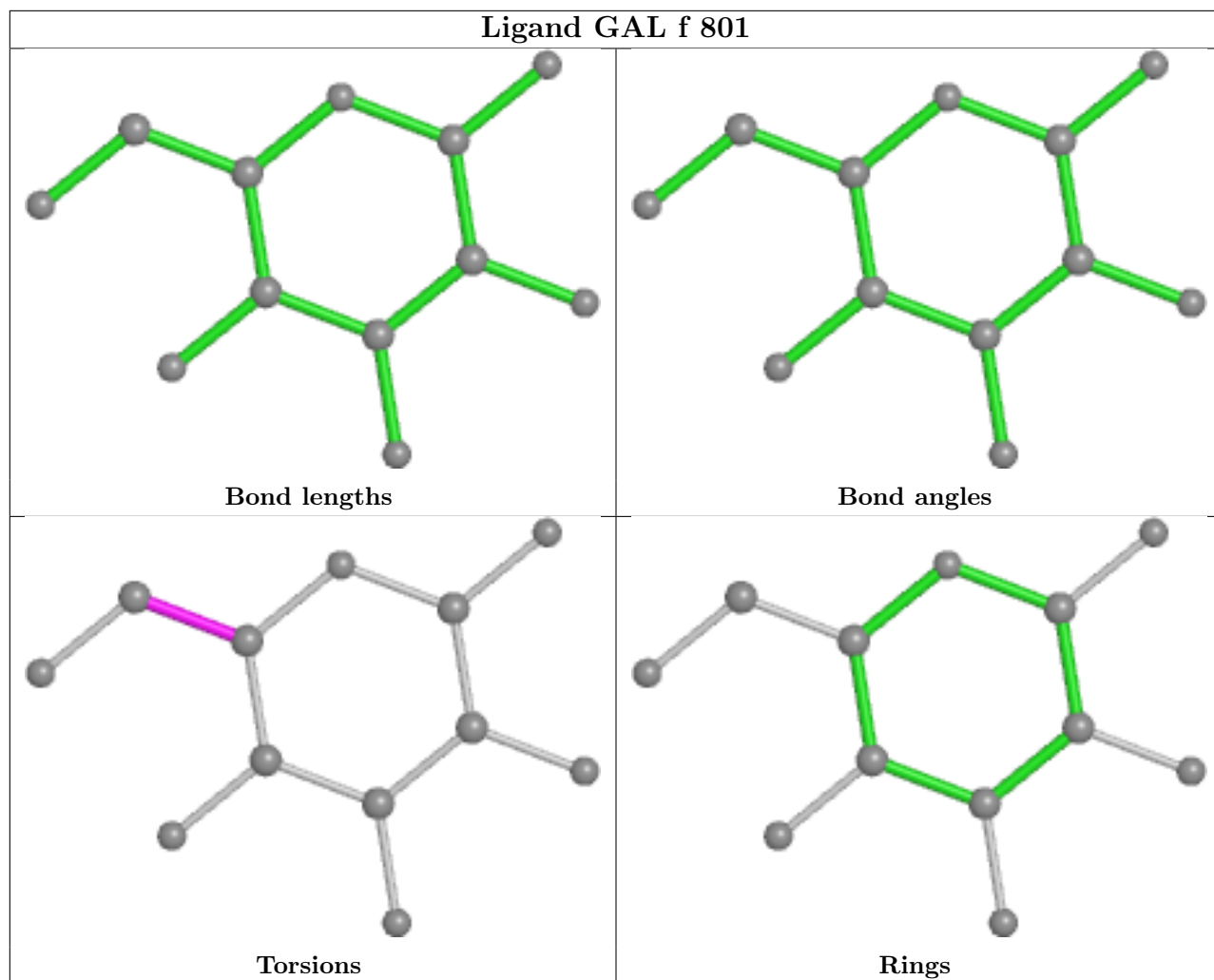


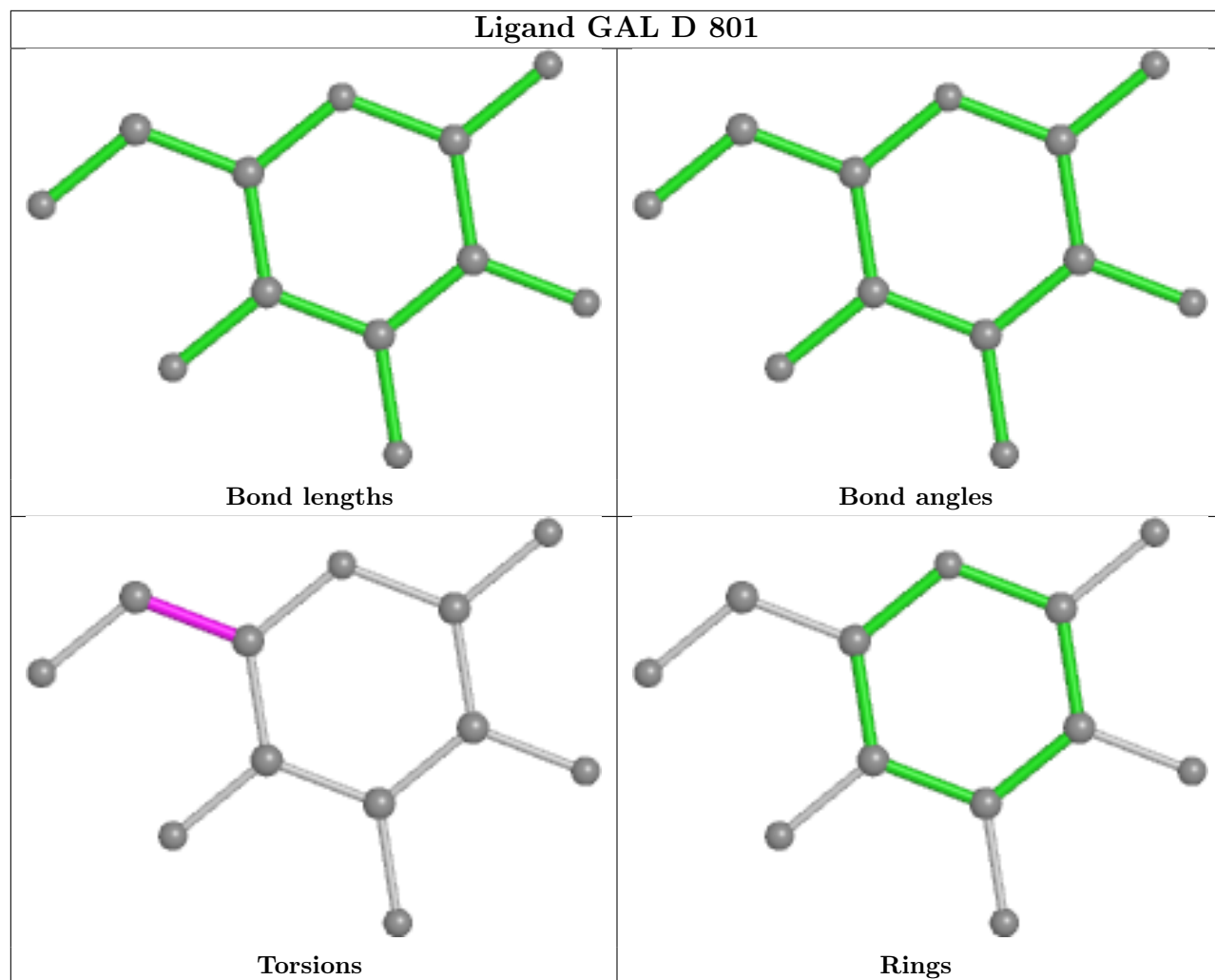


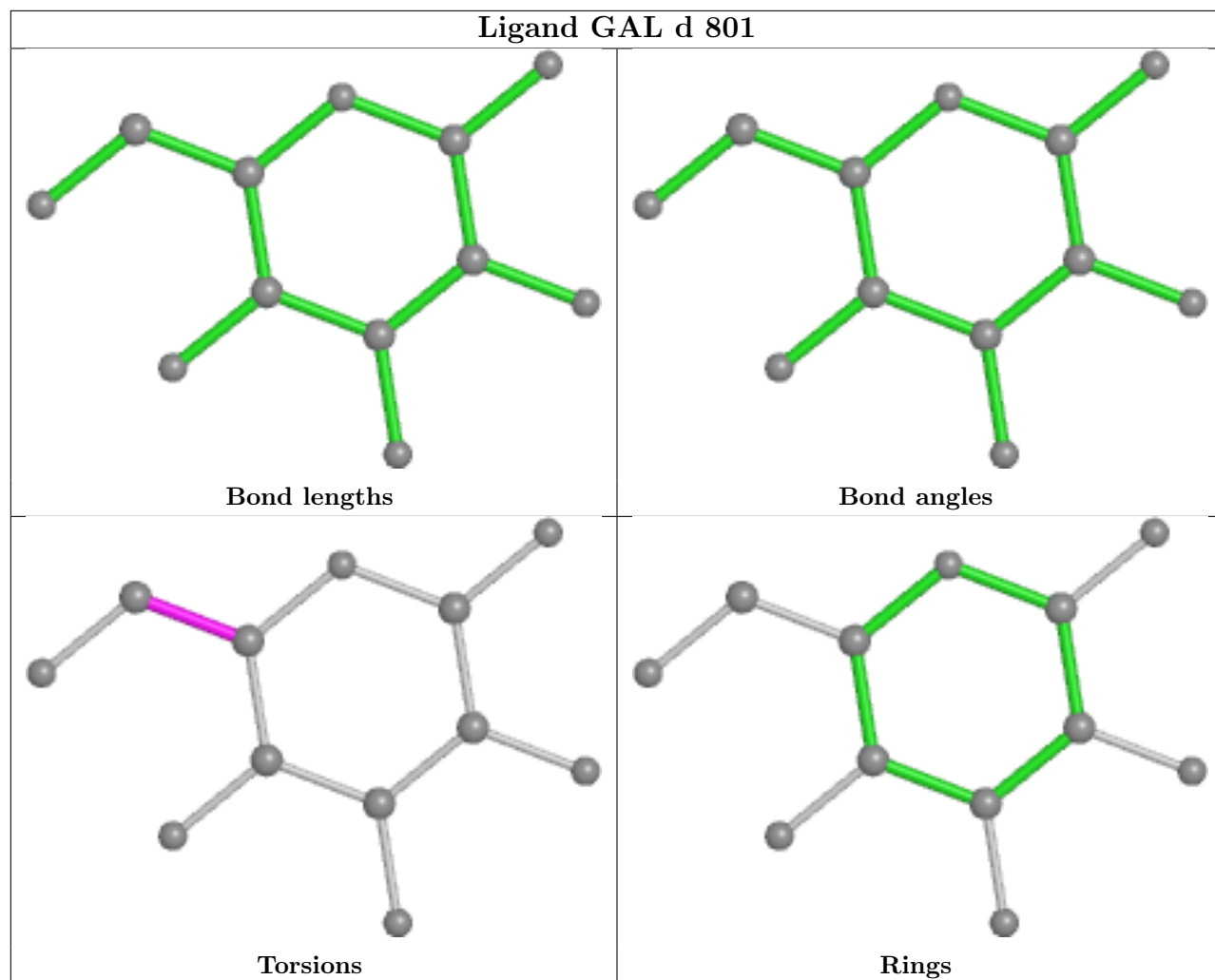


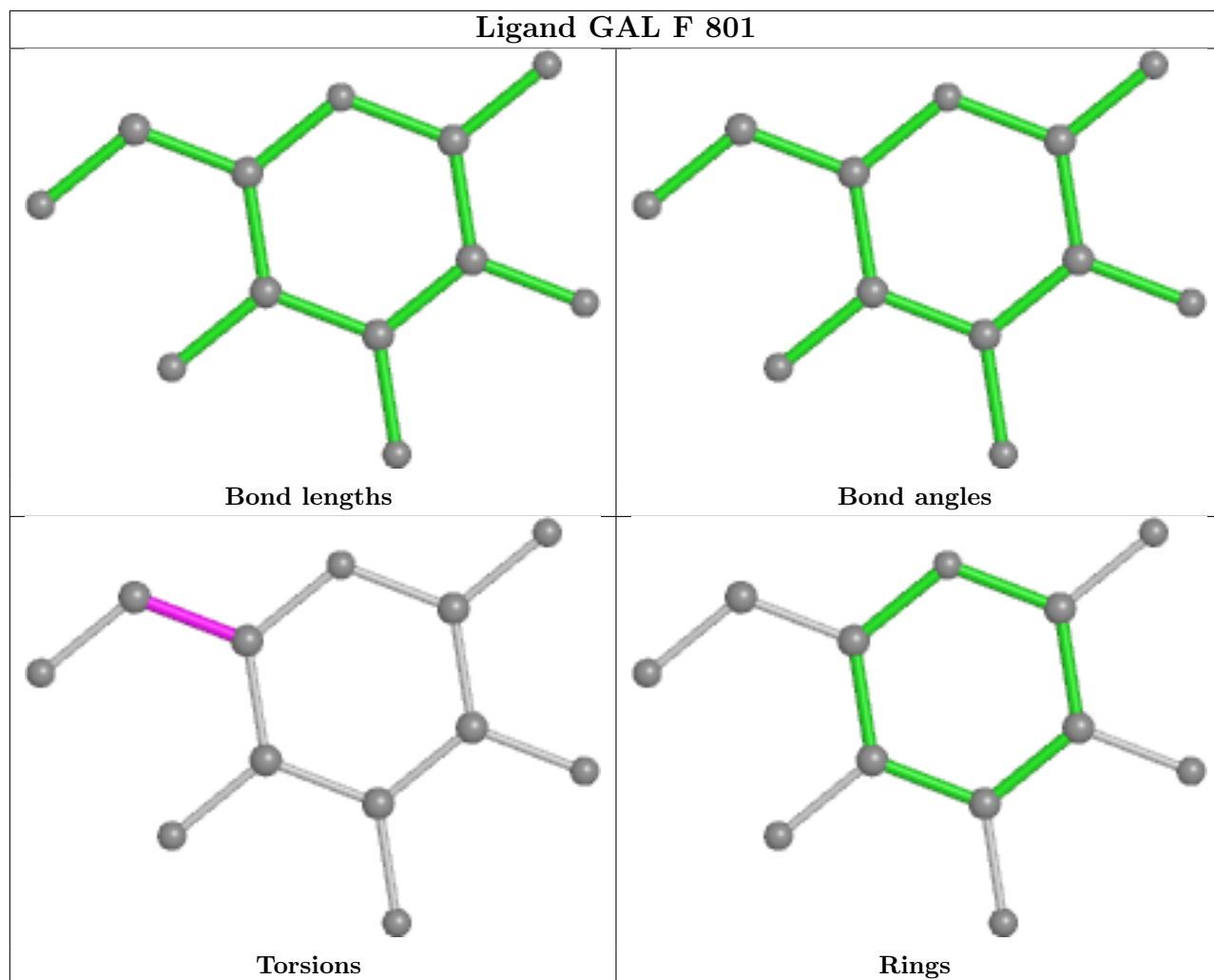


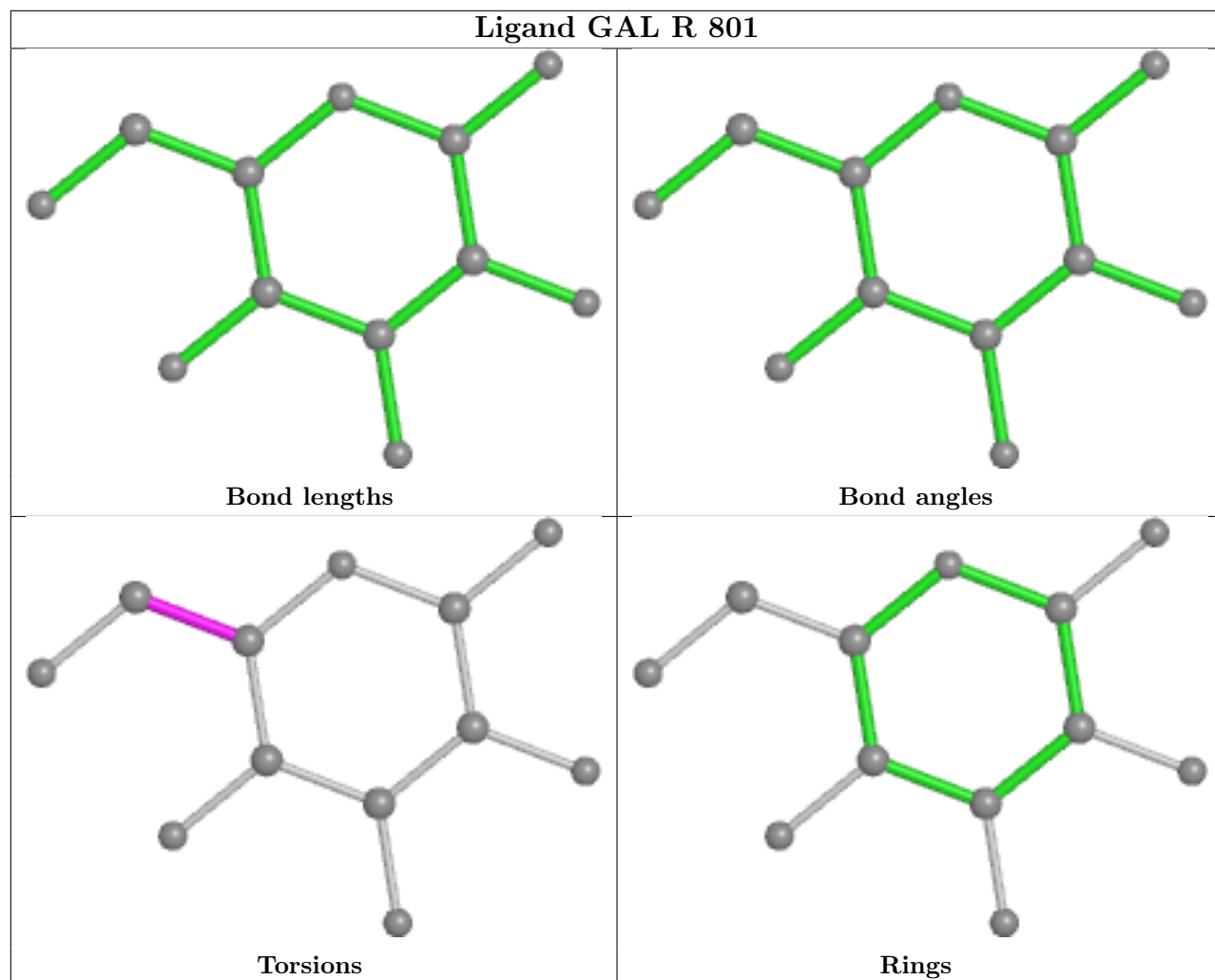


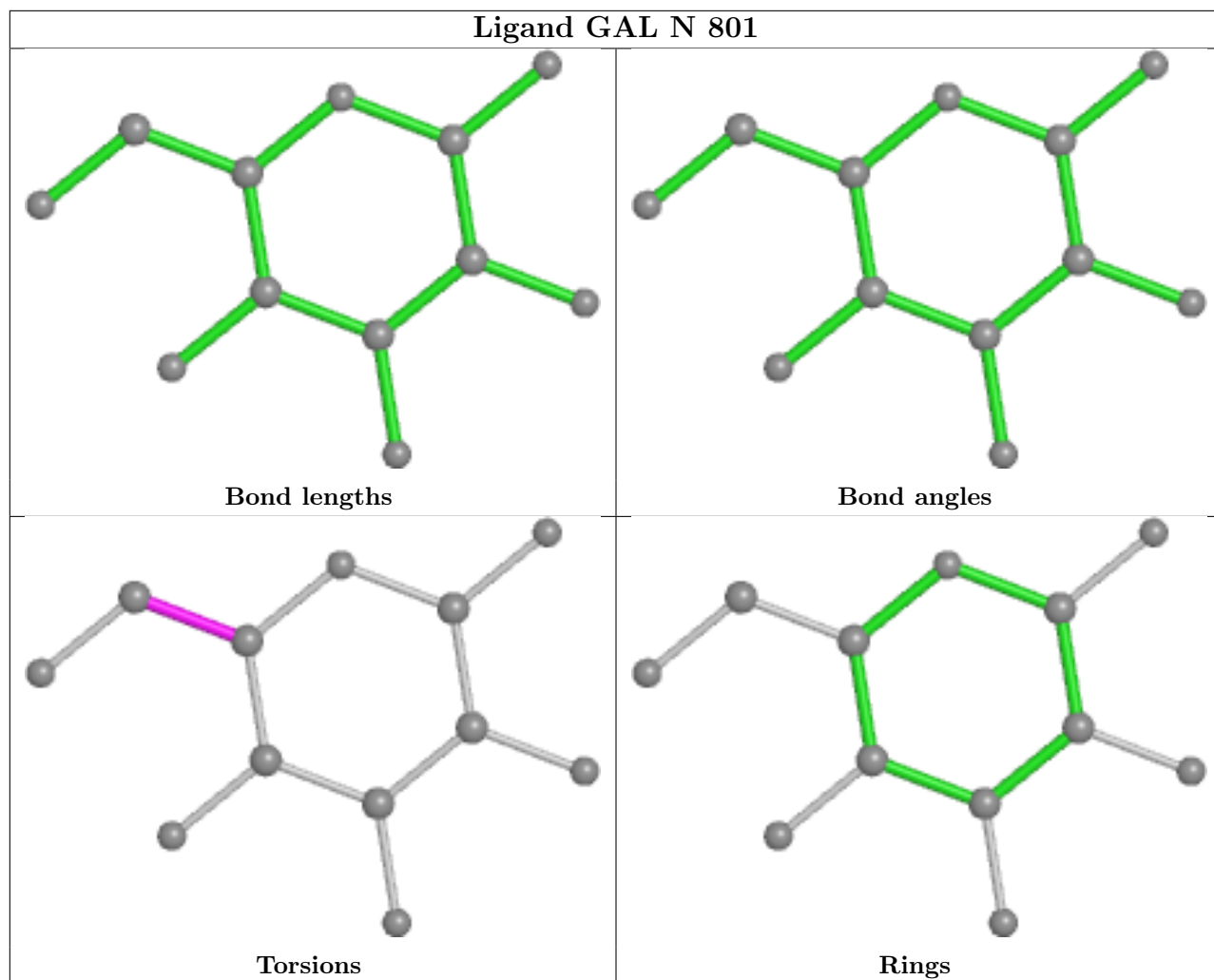


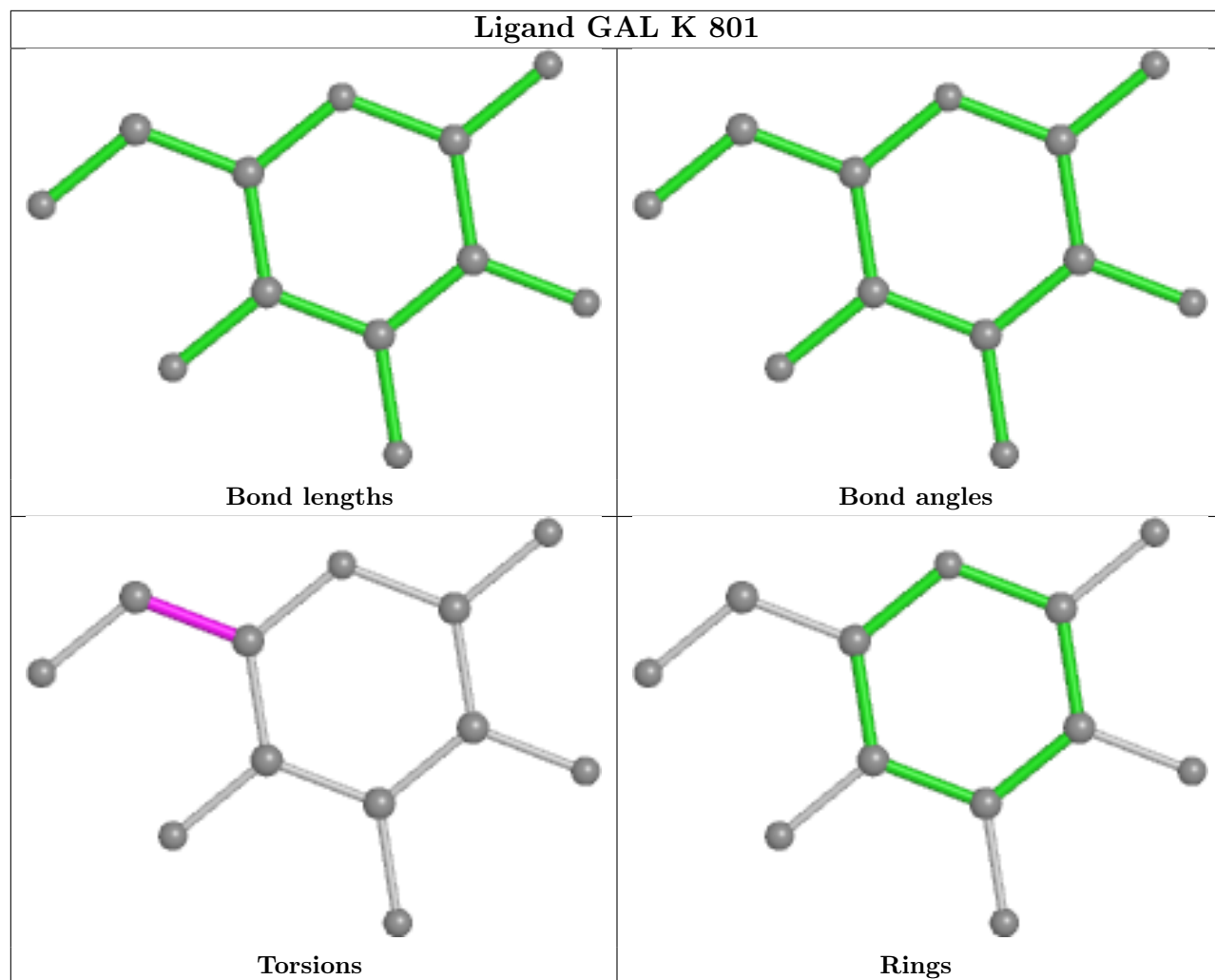


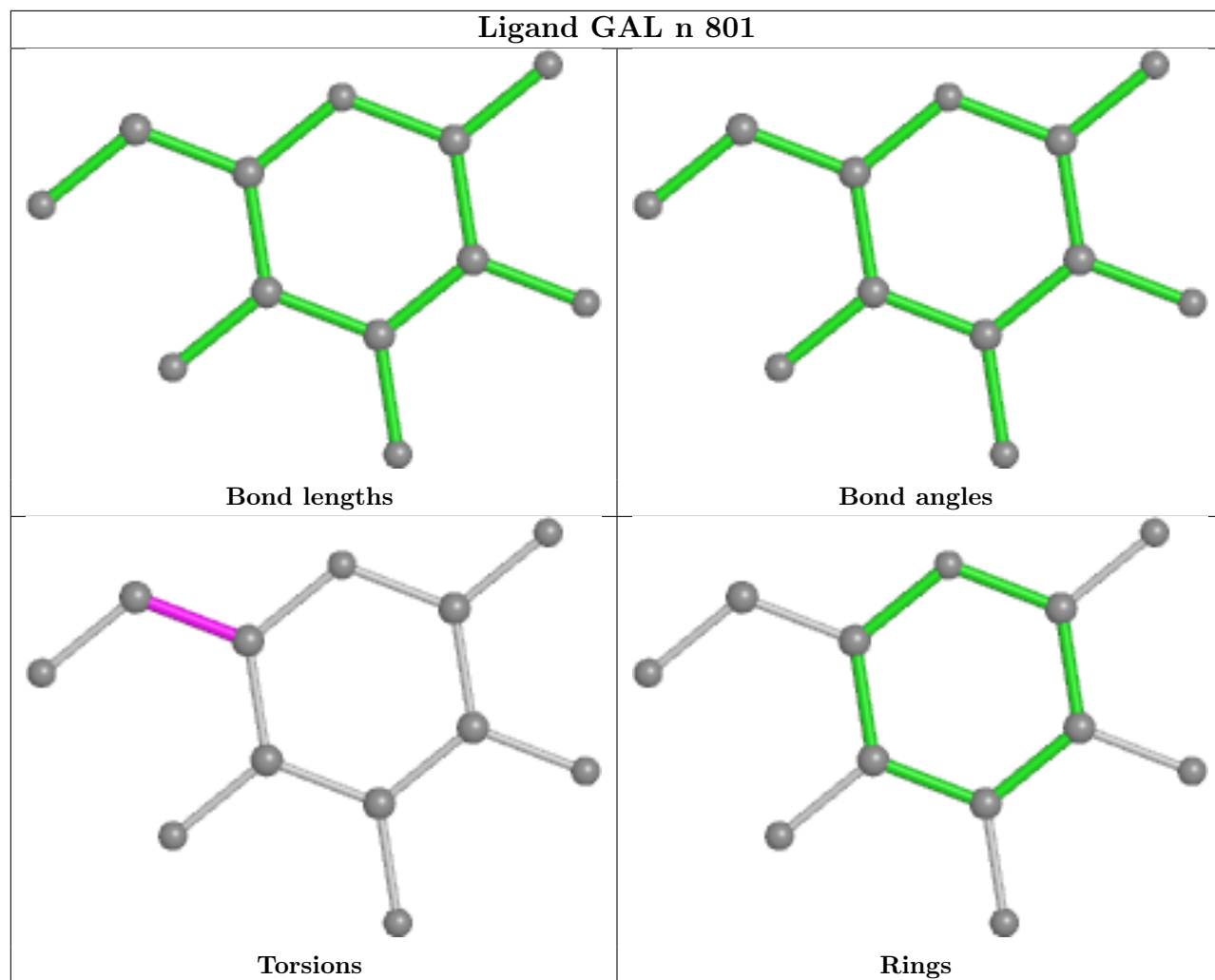


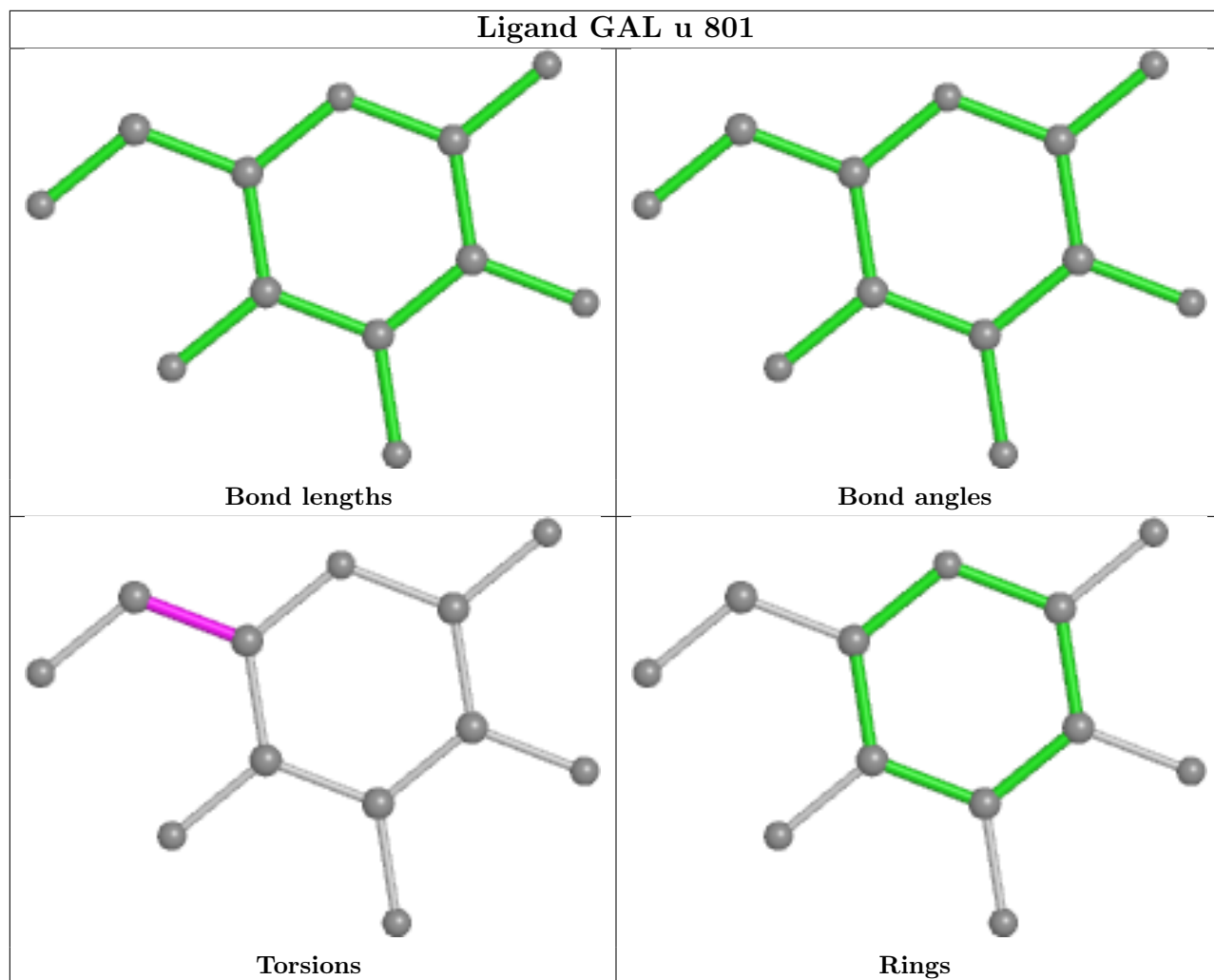


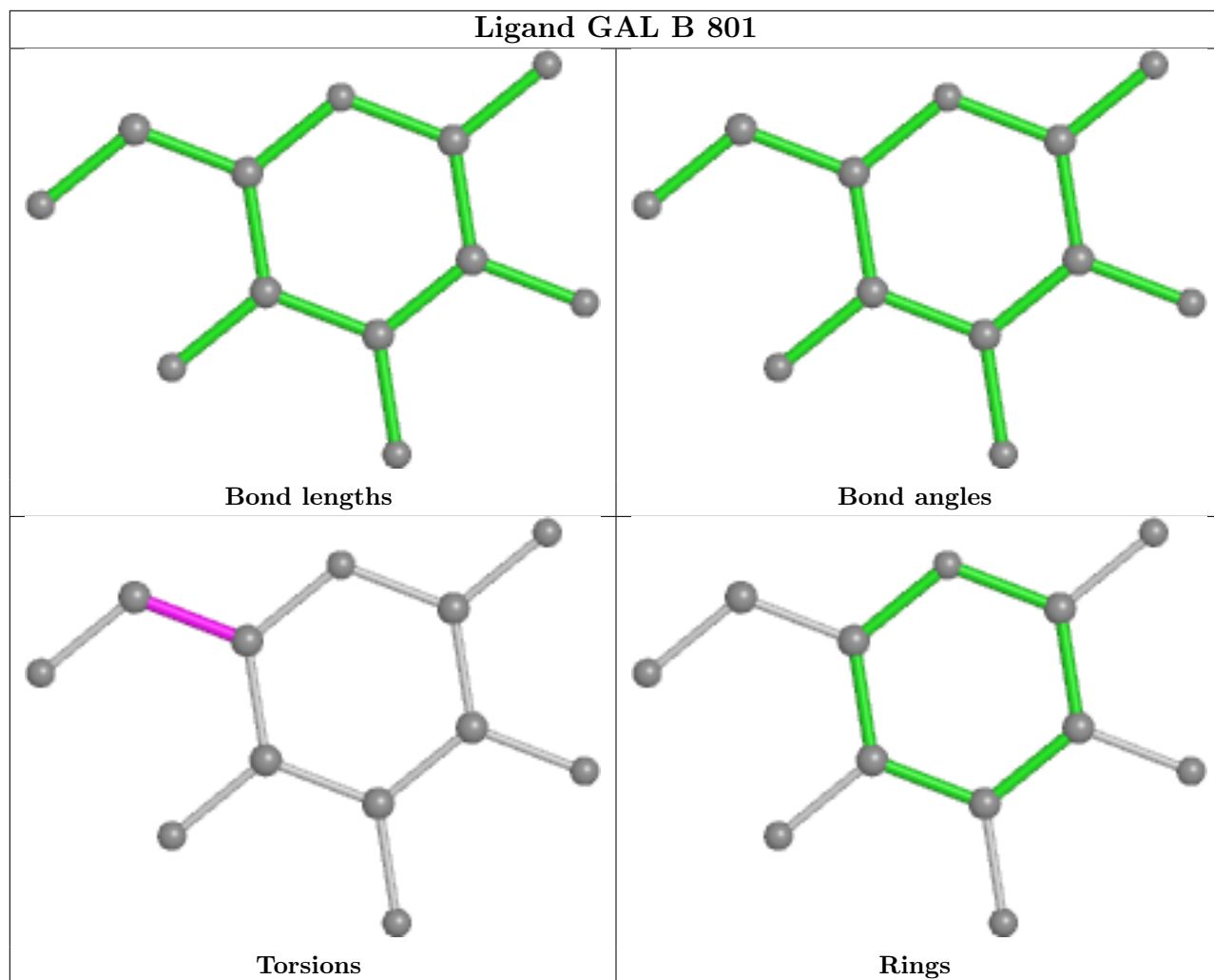


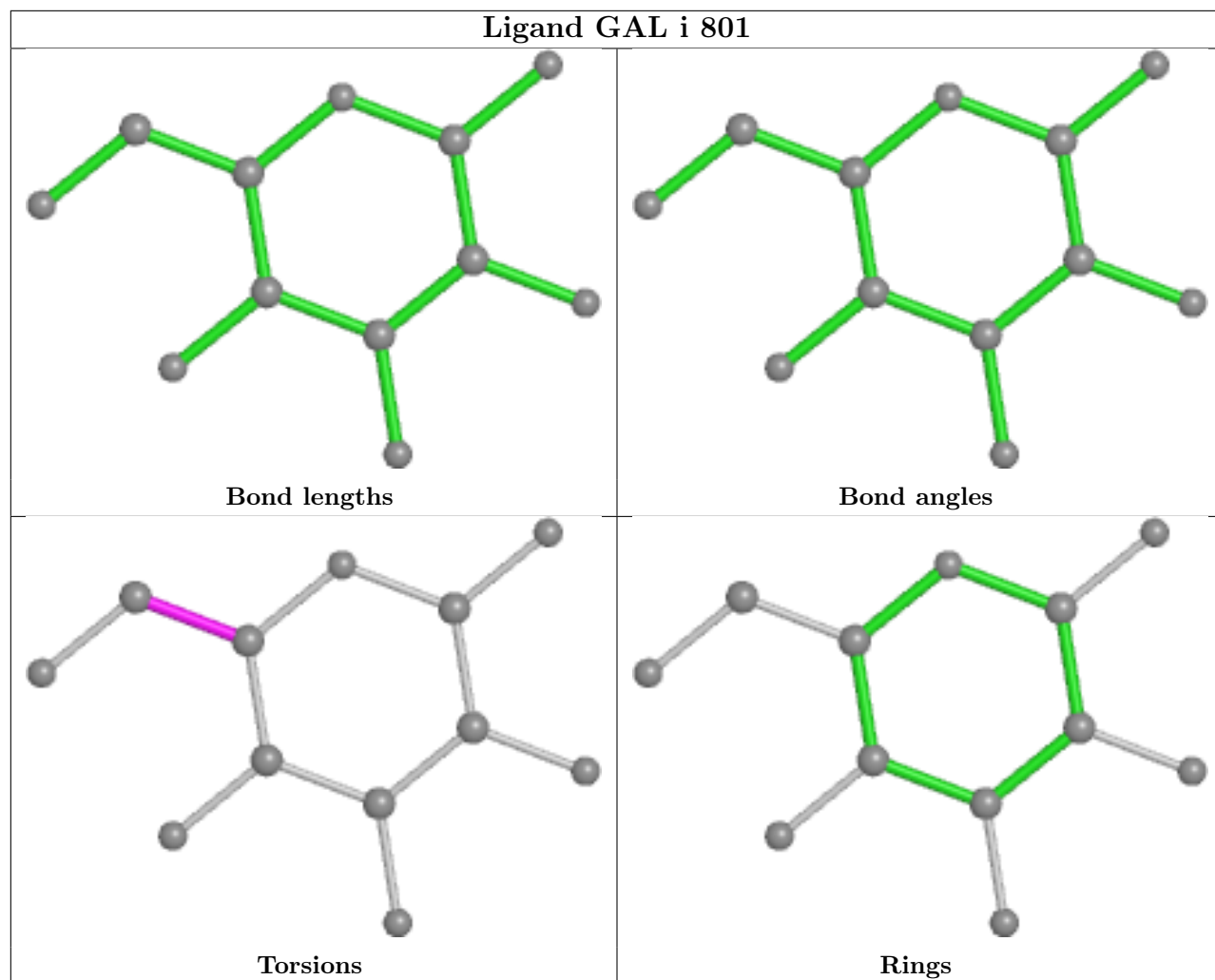


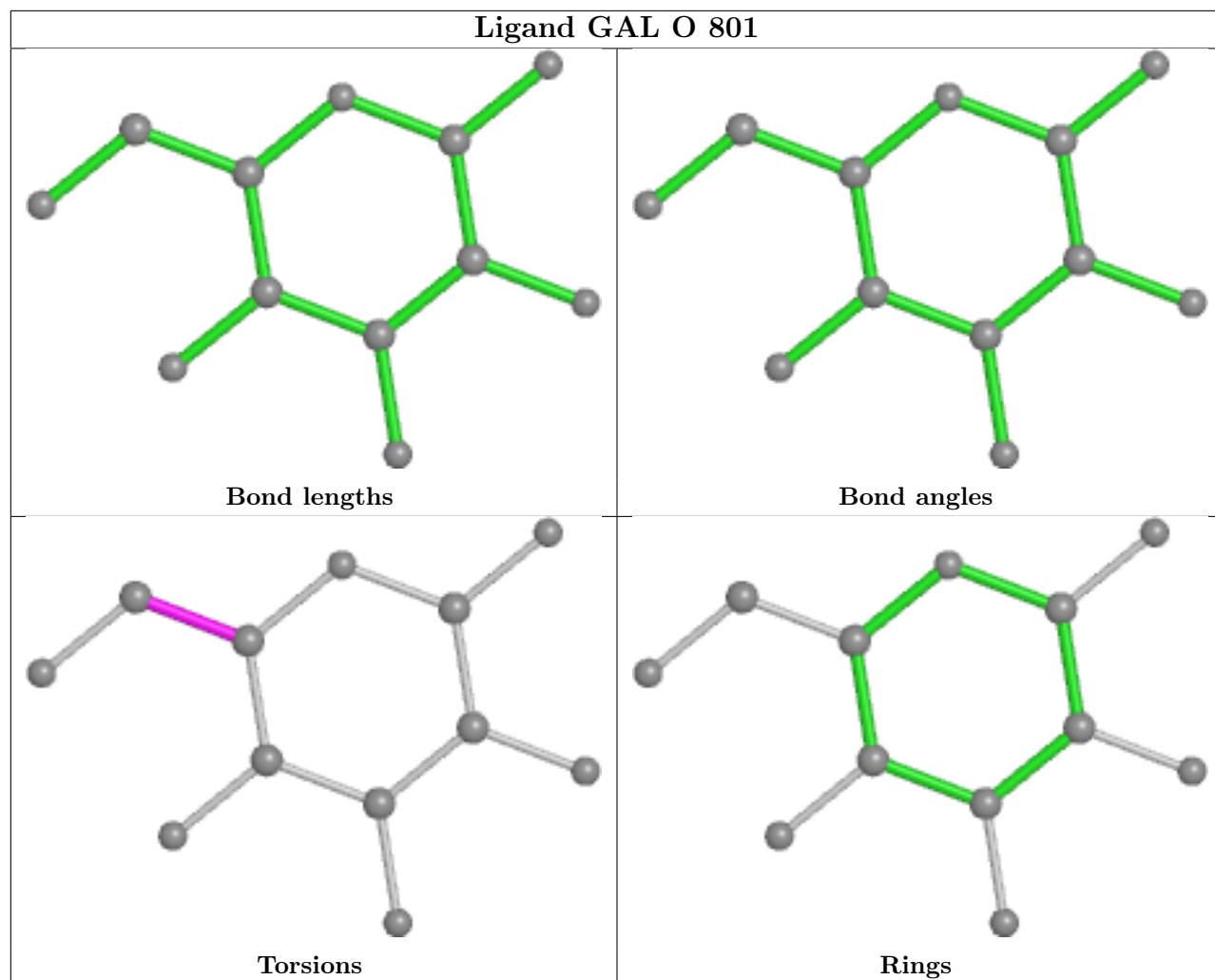


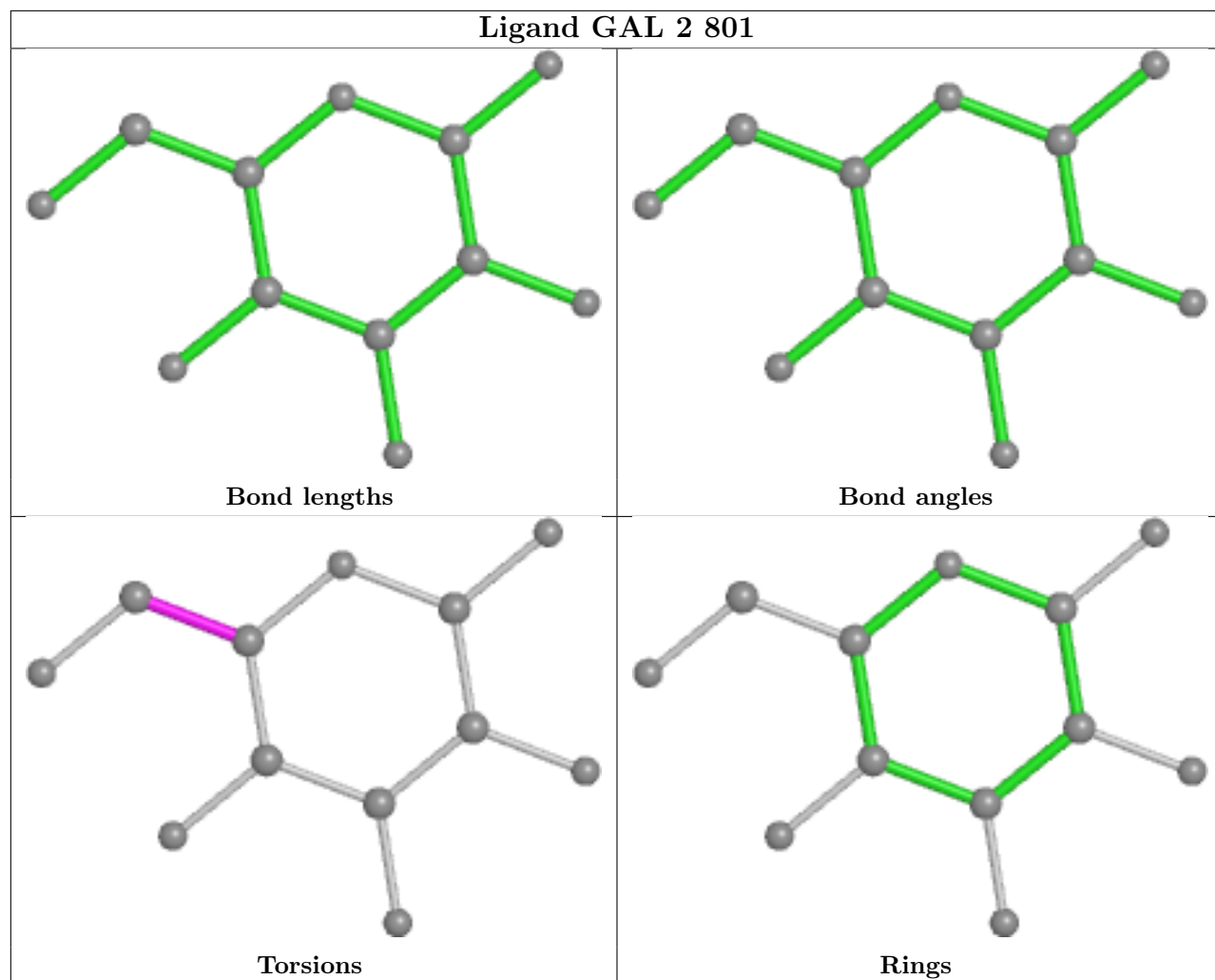


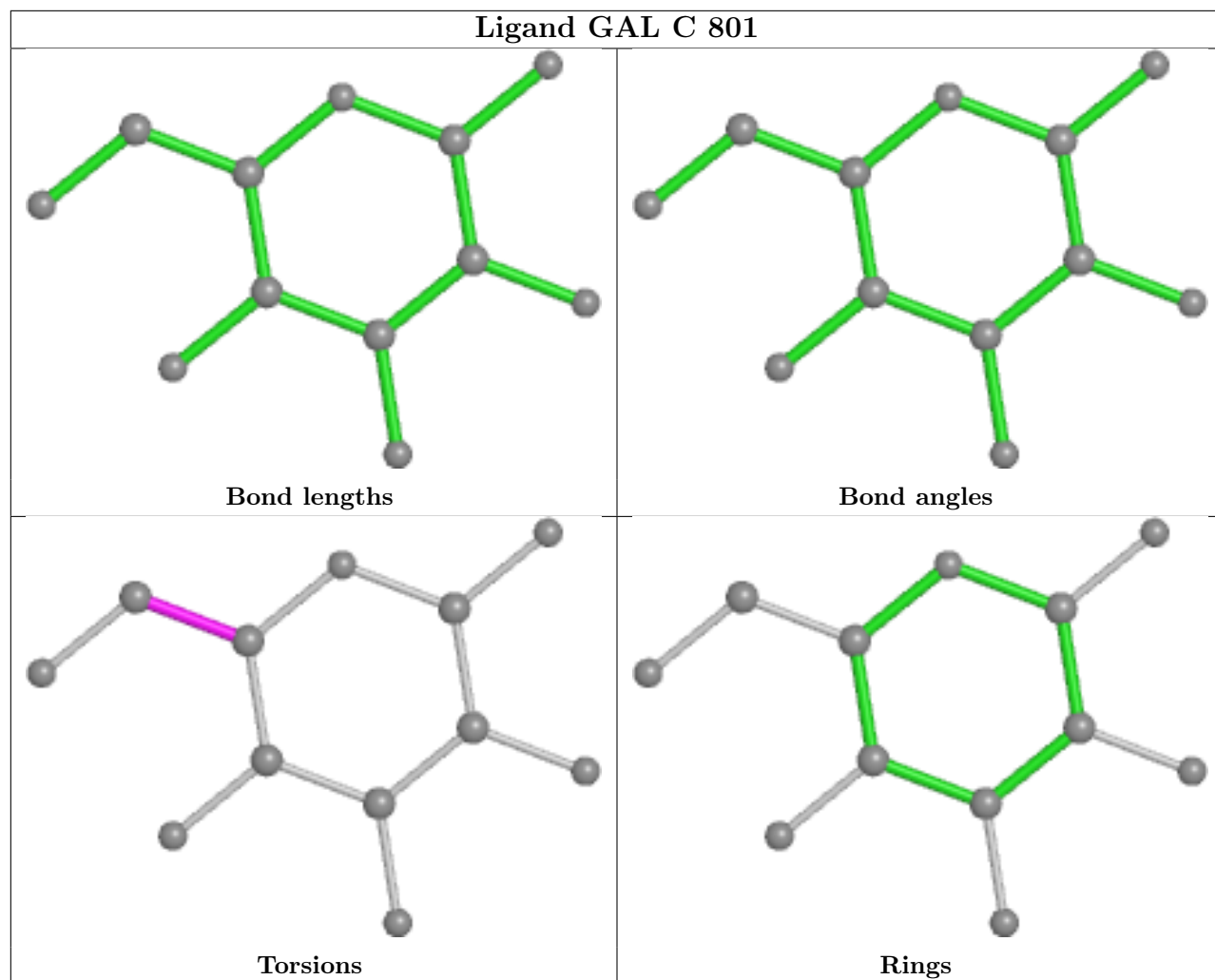


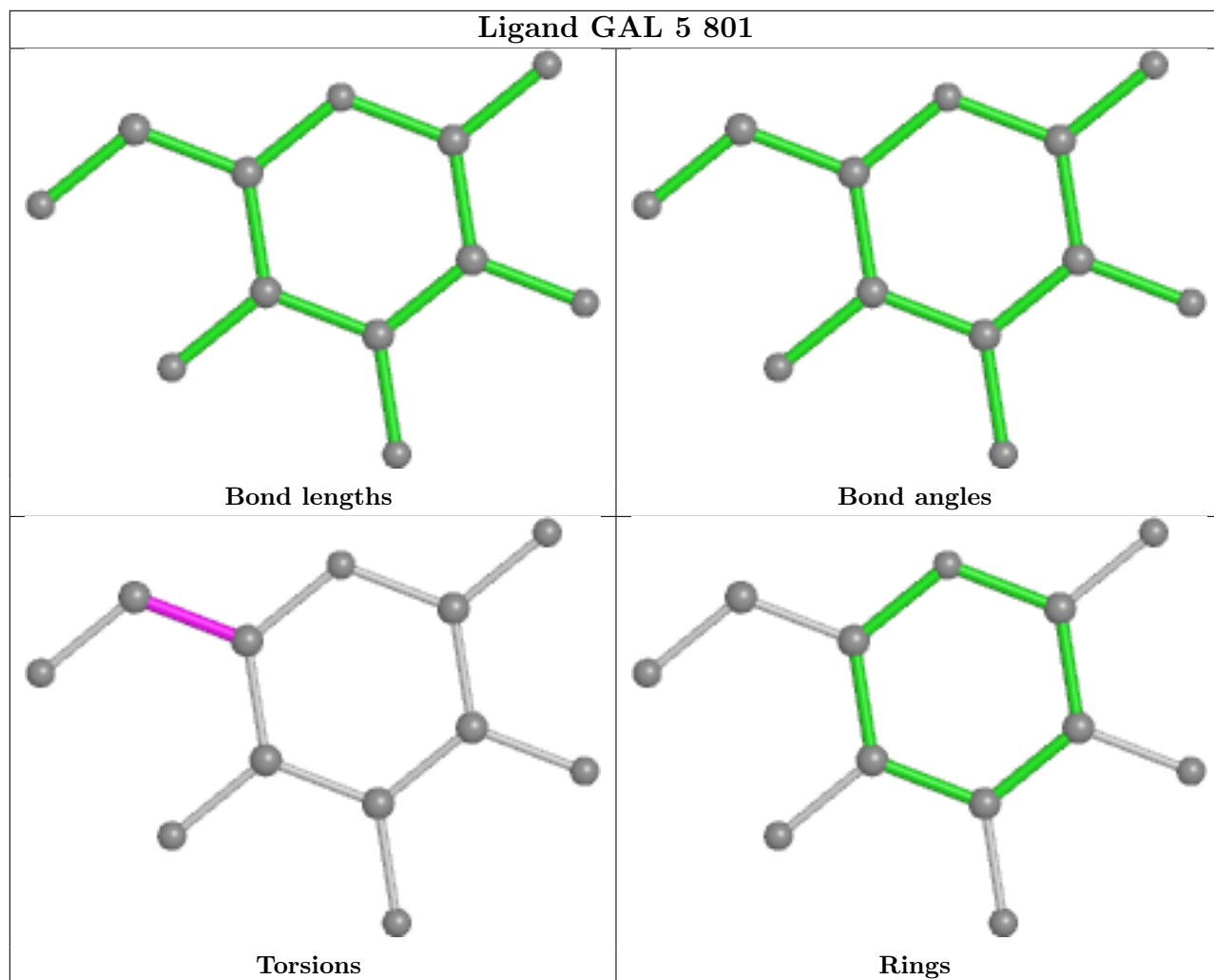


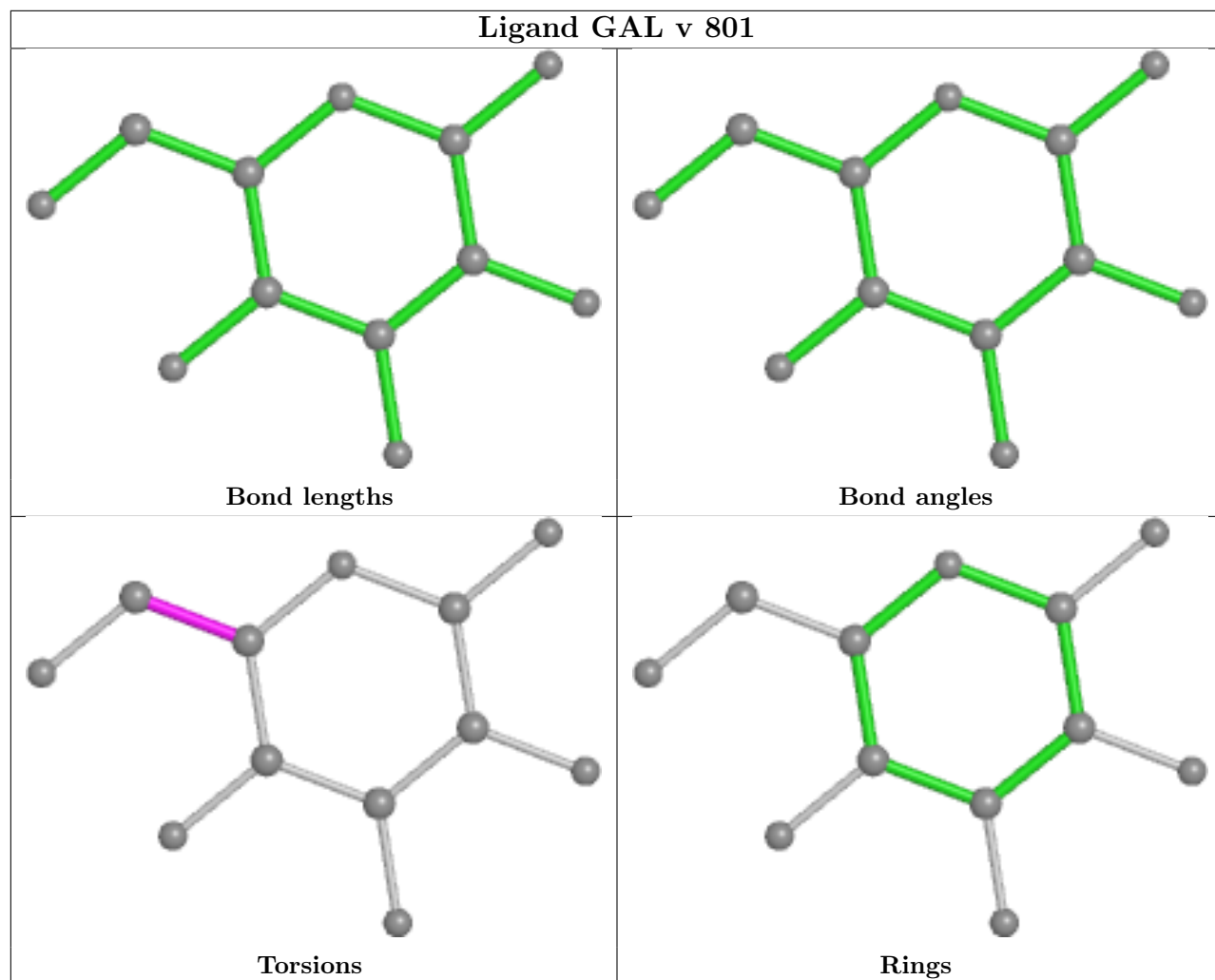


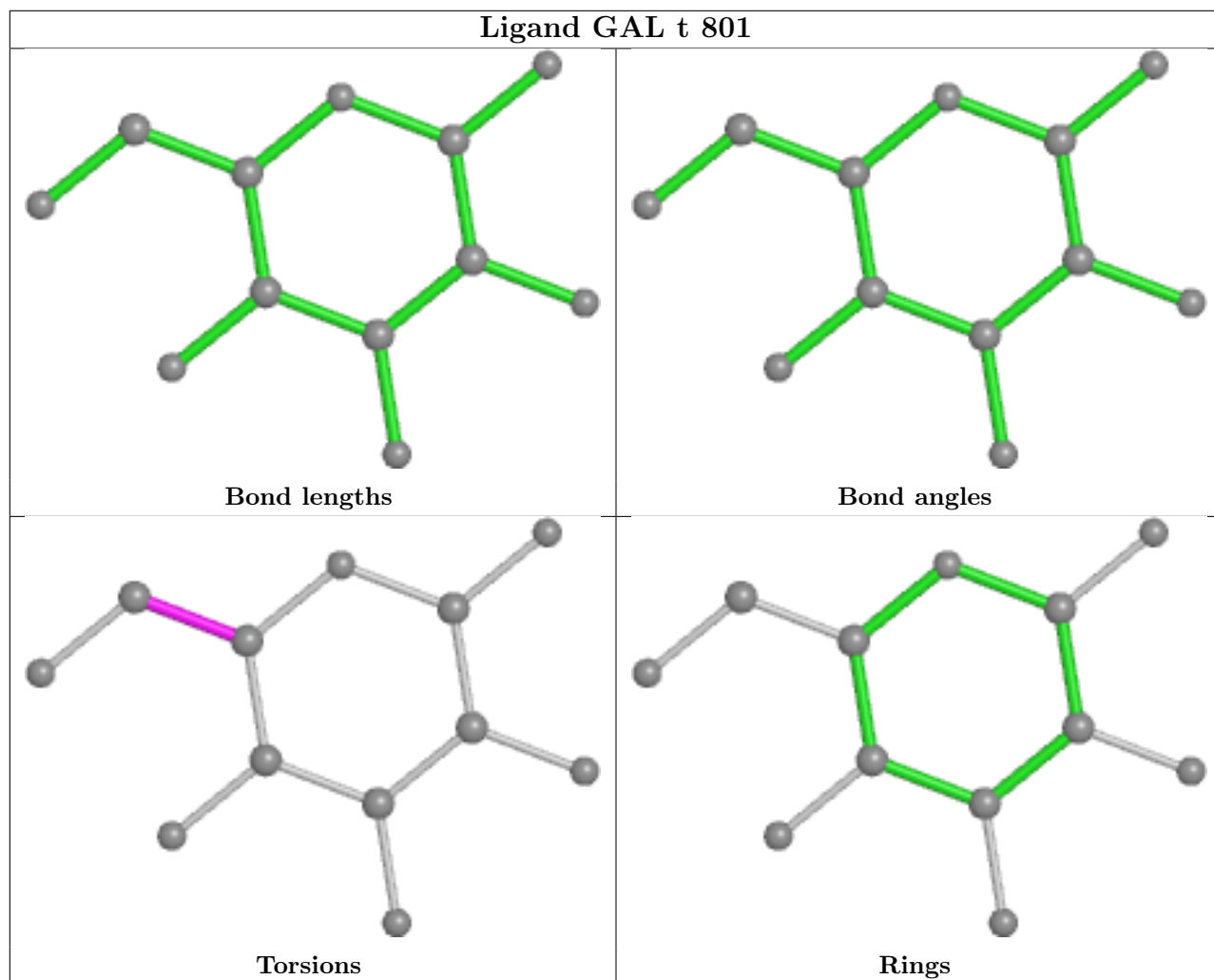


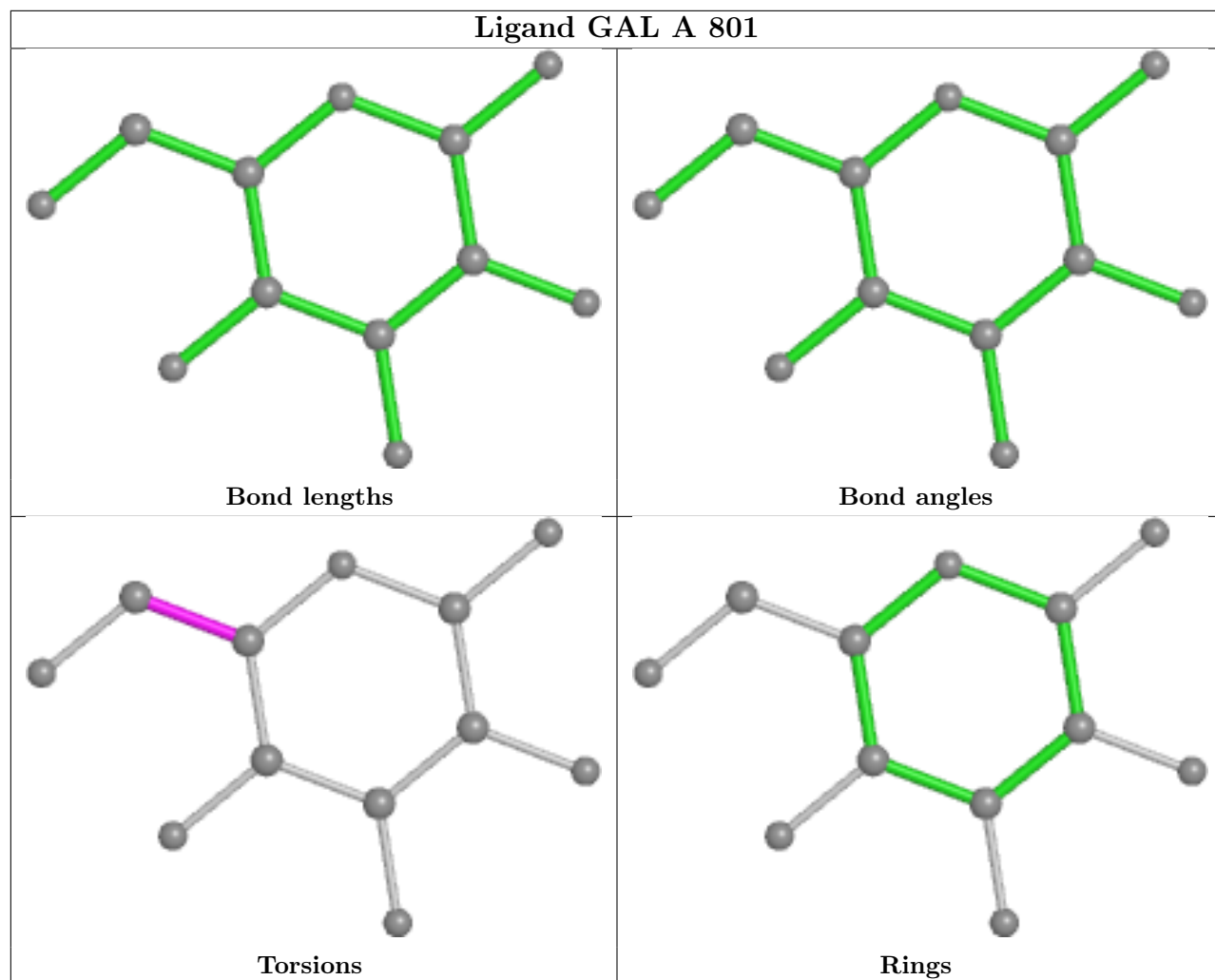


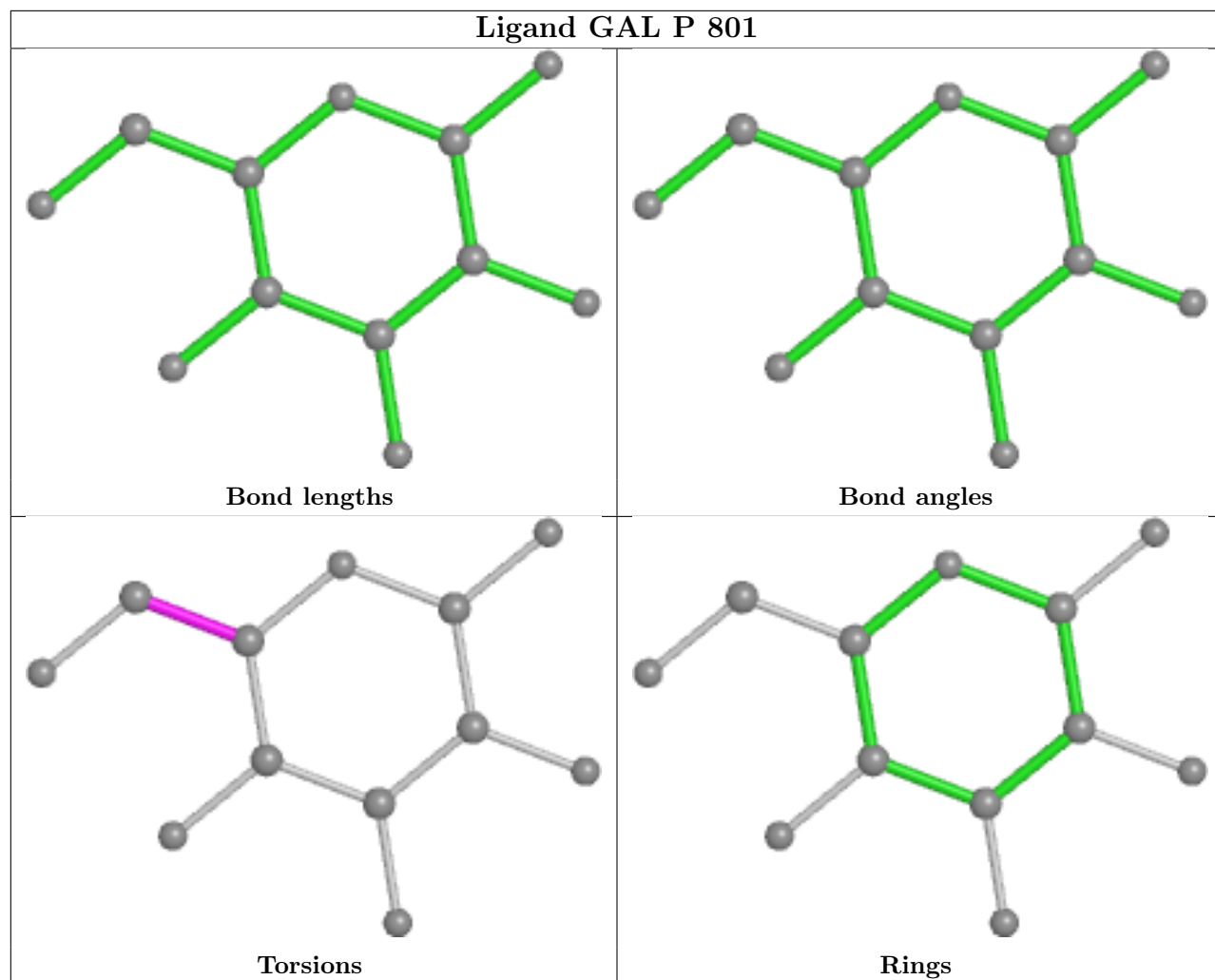


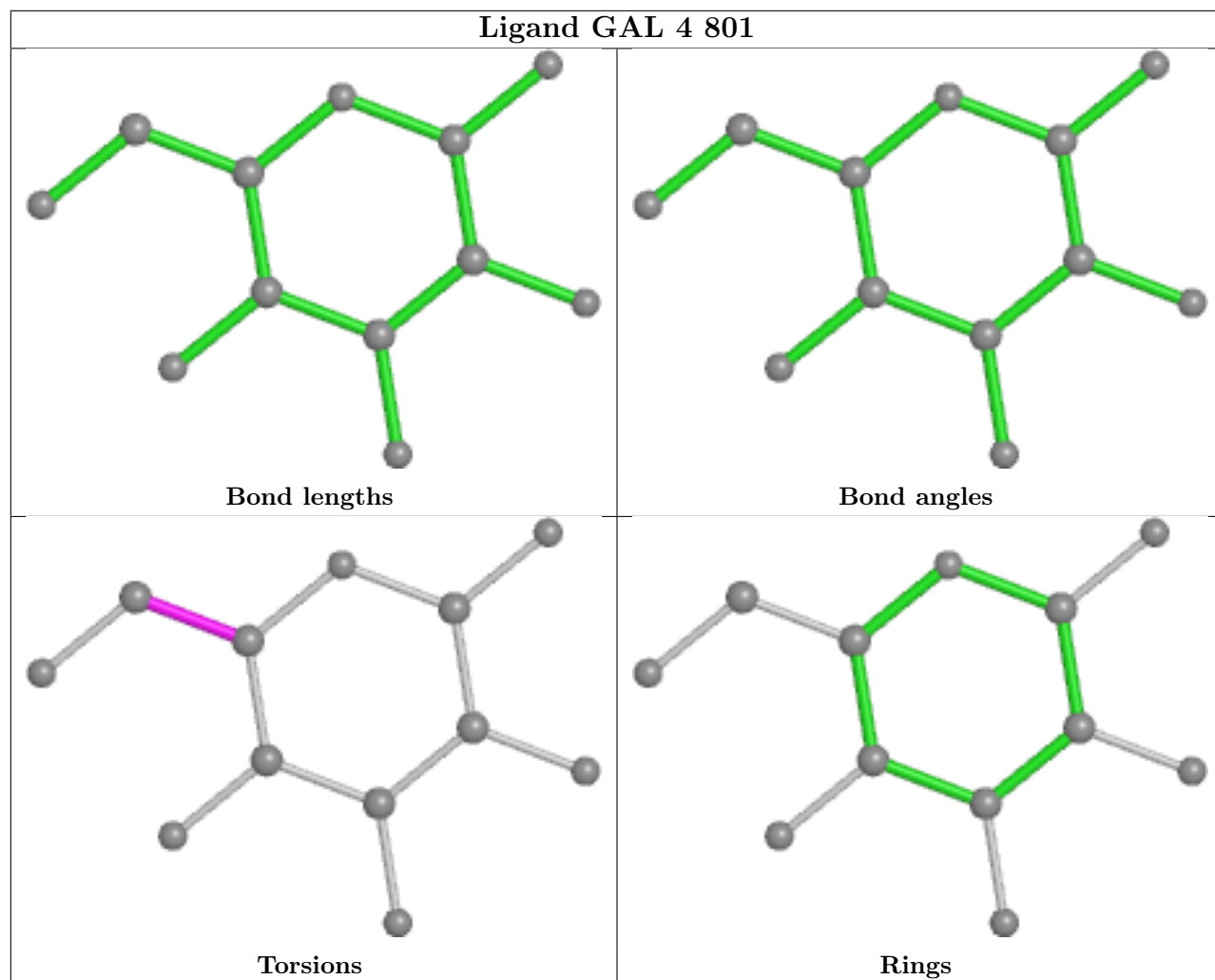


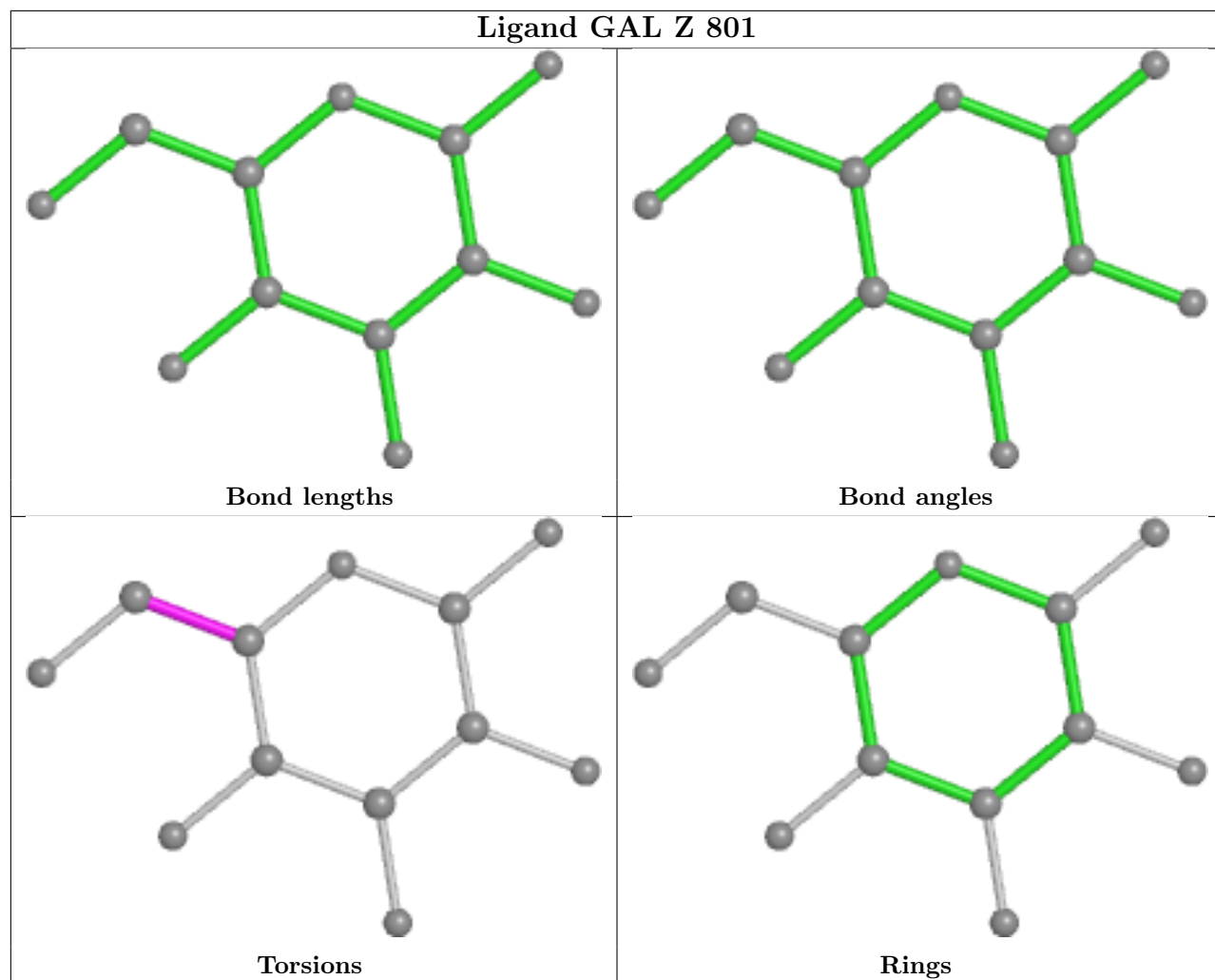


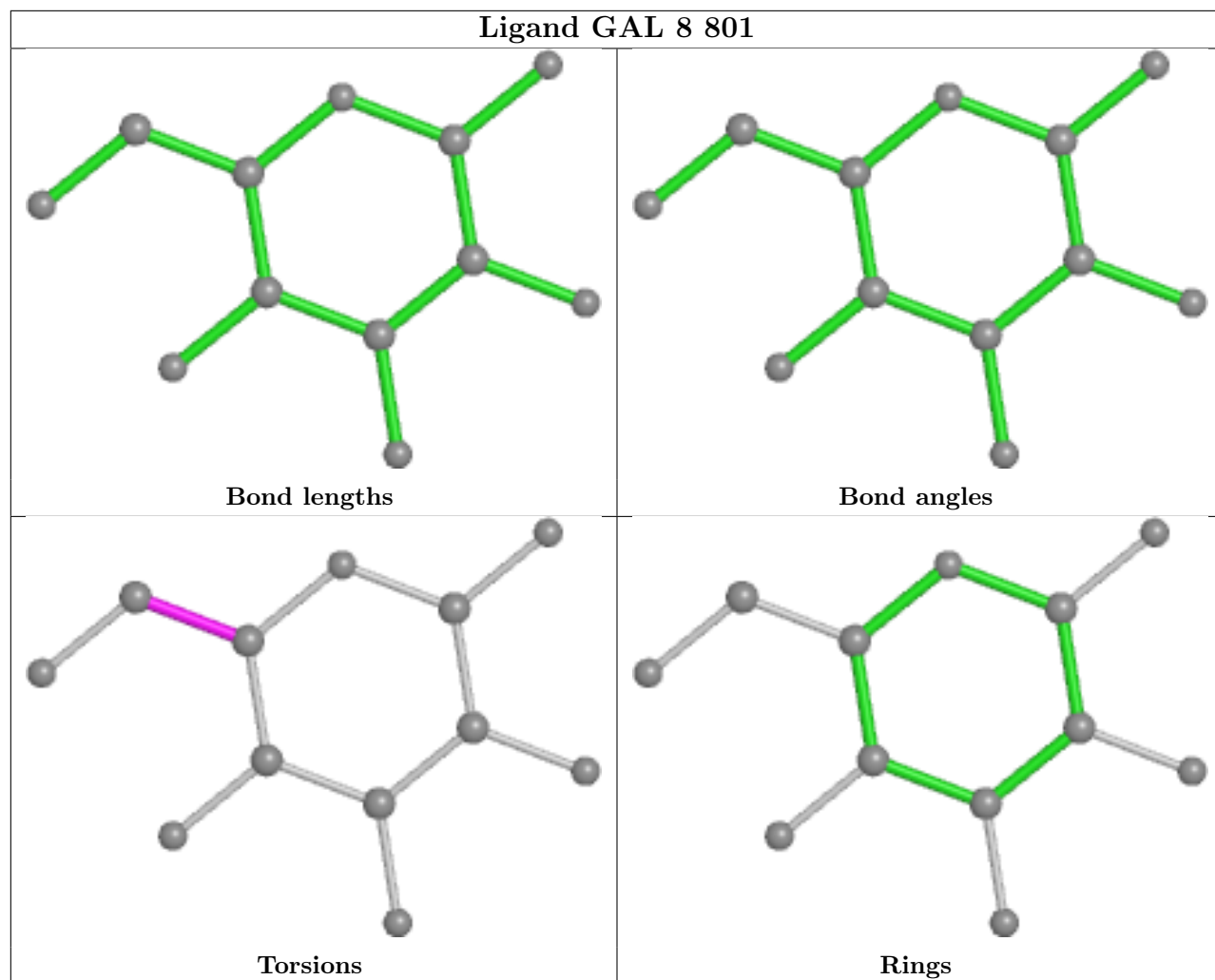


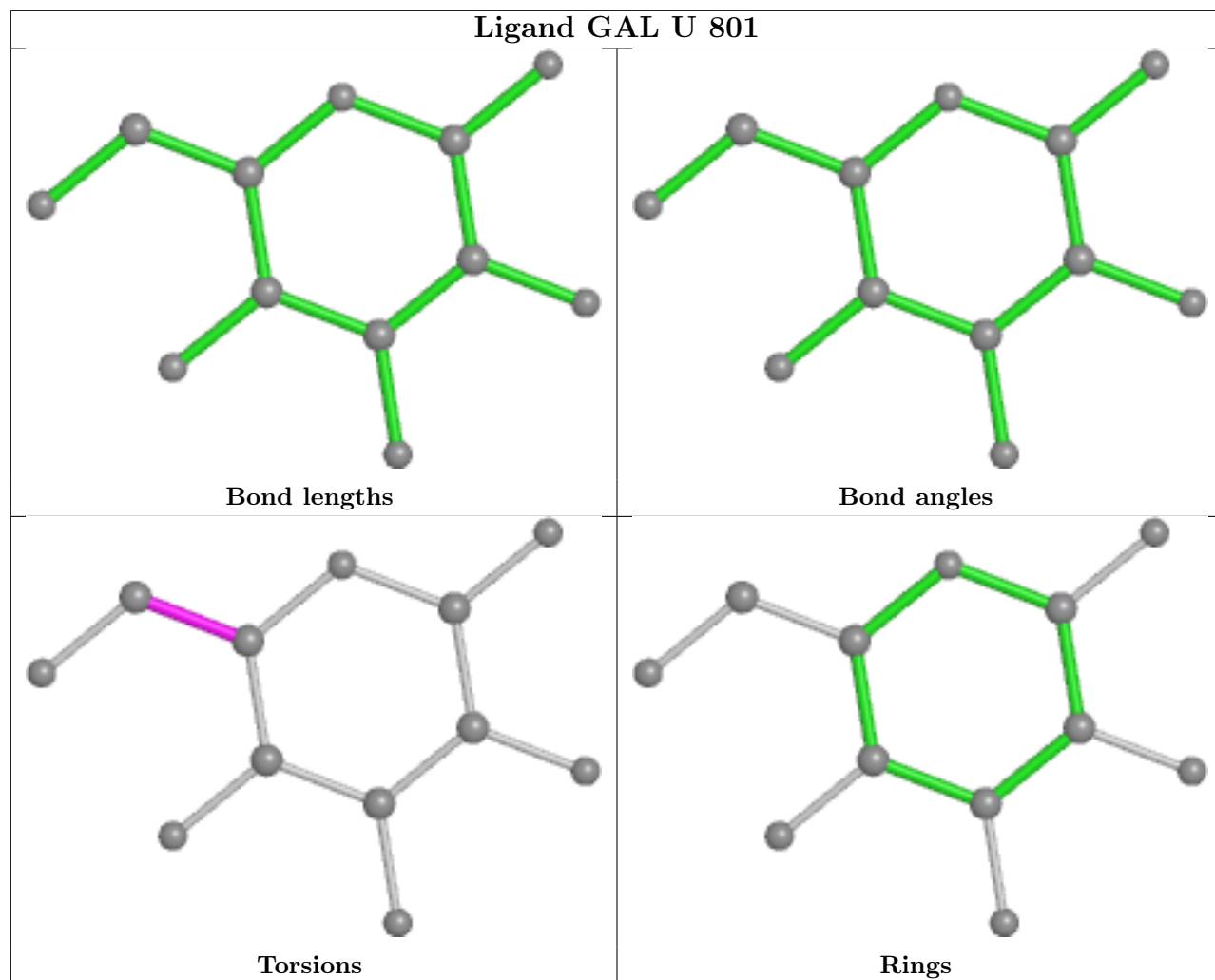


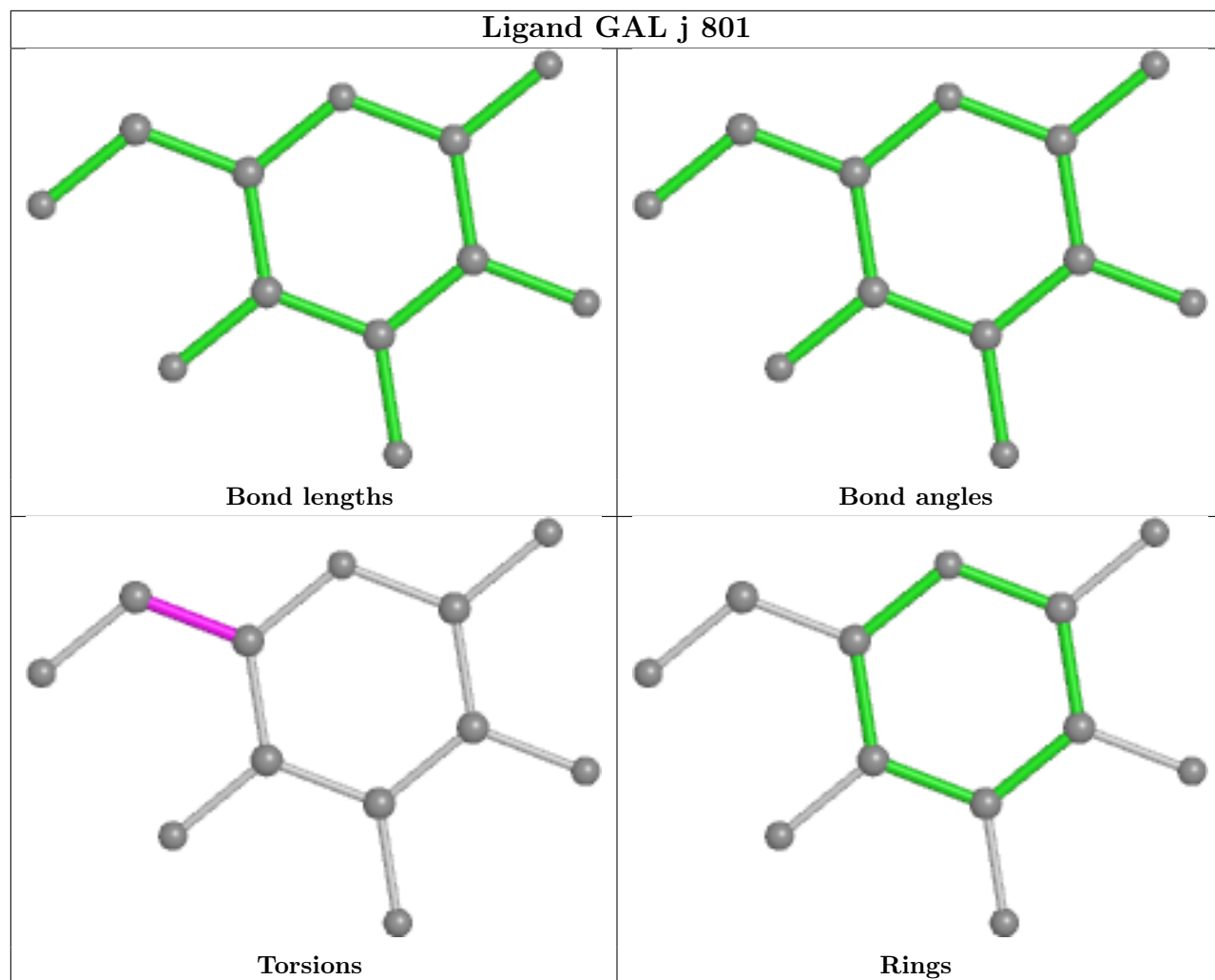


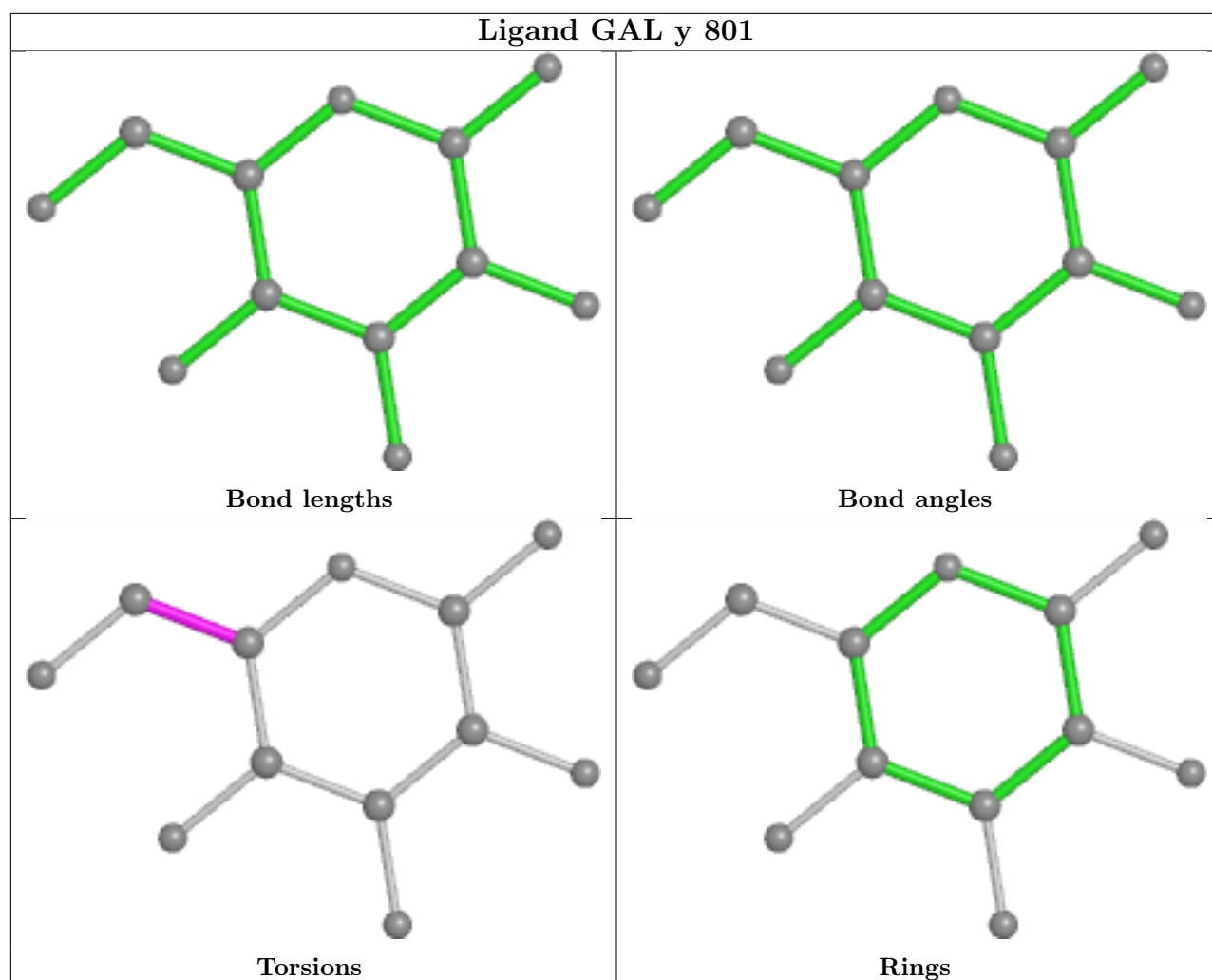












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24003. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

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

7 Map analysis

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

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.