



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 4, 2023 – 11:19 PM EDT

PDB ID : 6VWP
Title : Crystal structure of E. coli guanosine kinase in complex with ppGpp
Authors : Wang, B.; Grant, R.A.; Laub, M.T.
Deposited on : 2020-02-20
Resolution : 3.45 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 Å.

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

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

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 51473 atoms, of which 24272 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Inosine-guanosine kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	435	6389	2148	2984	588	653	16	0	0	0
1	B	428	6368	2123	3006	579	643	17	0	0	0
1	C	429	6365	2120	3009	580	640	16	0	0	0
1	D	435	6415	2148	3010	588	653	16	0	0	0
1	E	422	6316	2089	3006	571	634	16	0	0	0
1	F	412	6248	2039	3022	555	616	16	0	0	0
1	G	421	6321	2095	3005	573	632	16	0	0	0
1	H	408	6128	2023	2934	547	608	16	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

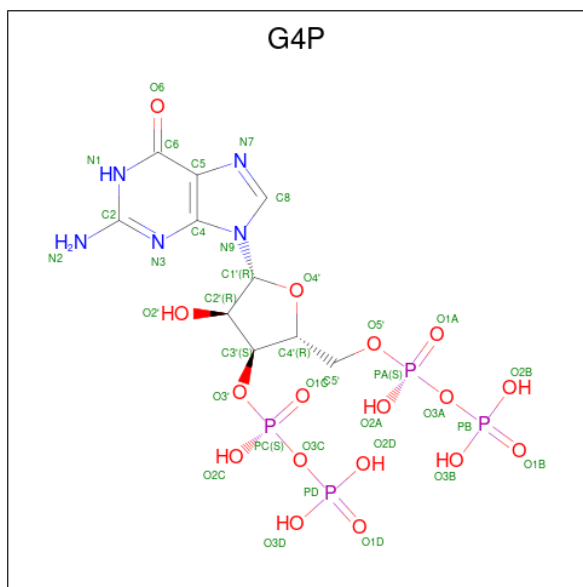
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P0AEW6
A	-1	SER	-	expression tag	UNP P0AEW6
A	0	HIS	-	expression tag	UNP P0AEW6
B	-2	GLY	-	expression tag	UNP P0AEW6
B	-1	SER	-	expression tag	UNP P0AEW6
B	0	HIS	-	expression tag	UNP P0AEW6
C	-2	GLY	-	expression tag	UNP P0AEW6
C	-1	SER	-	expression tag	UNP P0AEW6
C	0	HIS	-	expression tag	UNP P0AEW6
D	-2	GLY	-	expression tag	UNP P0AEW6
D	-1	SER	-	expression tag	UNP P0AEW6
D	0	HIS	-	expression tag	UNP P0AEW6
E	-2	GLY	-	expression tag	UNP P0AEW6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	expression tag	UNP P0AEW6
E	0	HIS	-	expression tag	UNP P0AEW6
F	-2	GLY	-	expression tag	UNP P0AEW6
F	-1	SER	-	expression tag	UNP P0AEW6
F	0	HIS	-	expression tag	UNP P0AEW6
G	-2	GLY	-	expression tag	UNP P0AEW6
G	-1	SER	-	expression tag	UNP P0AEW6
G	0	HIS	-	expression tag	UNP P0AEW6
H	-2	GLY	-	expression tag	UNP P0AEW6
H	-1	SER	-	expression tag	UNP P0AEW6
H	0	HIS	-	expression tag	UNP P0AEW6

- Molecule 2 is GUANOSINE-5',3'-TETRAPHOSPHATE (three-letter code: G4P) (formula: $C_{10}H_{17}N_5O_{17}P_4$) (labeled as "Ligand of Interest" by depositor).



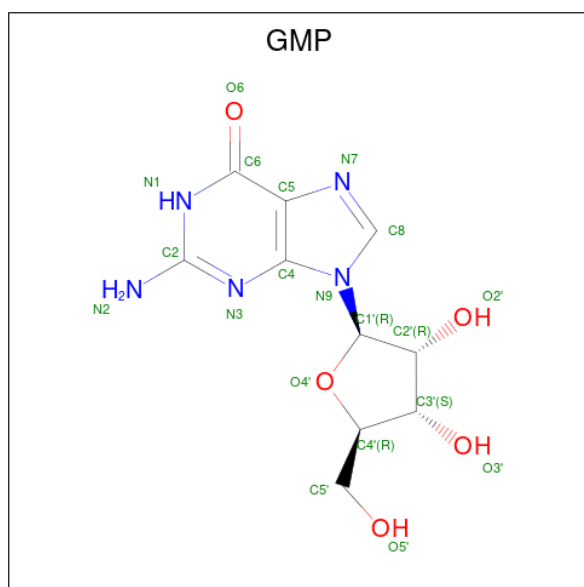
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
2	A	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		
2	B	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		
2	C	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		
2	D	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		
2	E	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	F	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		
2	G	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		
2	H	1	Total	C	H	N	O	P	0	0
			47	10	11	5	17	4		

- Molecule 3 is GUANOSINE (three-letter code: GMP) (formula: C₁₀H₁₃N₅O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	A	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	B	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	B	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	C	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	C	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	D	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	D	1	Total	C	H	N	O	0	0
			33	10	13	5	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	E	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	E	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	F	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	F	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	G	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	G	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	H	1	Total	C	H	N	O	0	0
			33	10	13	5	5		
3	H	1	Total	C	H	N	O	0	0
			33	10	13	5	5		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		
4	B	2	Total	K	0	0
			2	2		
4	C	2	Total	K	0	0
			2	2		
4	D	1	Total	K	0	0
			1	1		
4	E	2	Total	K	0	0
			2	2		
4	F	1	Total	K	0	0
			1	1		
4	G	1	Total	K	0	0
			1	1		
4	H	2	Total	K	0	0
			2	2		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total 1	Mg 1	0	0
5	D	1	Total 1	Mg 1	0	0
5	E	1	Total 1	Mg 1	0	0
5	F	1	Total 1	Mg 1	0	0
5	G	1	Total 1	Mg 1	0	0
5	H	1	Total 1	Mg 1	0	0

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

3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	245.95Å 245.95Å 221.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.16 – 3.45	Depositor
% Data completeness (in resolution range)	99.3 (49.16-3.45)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 3.40Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.200 , 0.242	Depositor
Wilson B-factor (Å ²)	133.5	Xtrriage
Anisotropy	0.162	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtrriage
Total number of atoms	51473	wwPDB-VP
Average B, all atoms (Å ²)	158.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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 monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 43 ligands modelled in this entry, 19 are monoatomic - leaving 24 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GMP	H	502	-	18,22,22	1.02	2 (11%)	19,33,33	0.80	0
3	GMP	H	503	-	18,22,22	1.06	2 (11%)	19,33,33	0.70	0
3	GMP	E	502	-	18,22,22	1.03	2 (11%)	19,33,33	0.74	0
2	G4P	E	501	-	30,38,38	0.94	1 (3%)	42,61,61	1.45	6 (14%)
2	G4P	D	501	-	30,38,38	0.93	1 (3%)	42,61,61	1.42	6 (14%)
2	G4P	B	501	-	30,38,38	0.94	2 (6%)	42,61,61	1.62	7 (16%)
2	G4P	C	501	-	30,38,38	0.97	2 (6%)	42,61,61	1.36	6 (14%)
3	GMP	A	503	-	18,22,22	0.99	2 (11%)	19,33,33	0.74	1 (5%)
3	GMP	C	503	-	18,22,22	1.02	2 (11%)	19,33,33	0.70	1 (5%)
2	G4P	G	501	-	30,38,38	0.88	1 (3%)	42,61,61	1.54	6 (14%)
3	GMP	D	503	-	18,22,22	1.04	2 (11%)	19,33,33	0.72	1 (5%)
3	GMP	D	502	-	18,22,22	1.02	2 (11%)	19,33,33	0.78	0
3	GMP	E	503	-	18,22,22	1.04	2 (11%)	19,33,33	0.71	1 (5%)
2	G4P	F	501	-	30,38,38	0.86	1 (3%)	42,61,61	1.28	5 (11%)
3	GMP	B	502	-	18,22,22	1.01	2 (11%)	19,33,33	0.82	1 (5%)
3	GMP	F	503	-	18,22,22	1.04	2 (11%)	19,33,33	0.71	1 (5%)
3	GMP	F	502	-	18,22,22	1.02	2 (11%)	19,33,33	0.77	1 (5%)
2	G4P	A	501	-	30,38,38	0.94	1 (3%)	42,61,61	1.63	8 (19%)
3	GMP	B	503	-	18,22,22	1.05	2 (11%)	19,33,33	0.69	0
3	GMP	C	502	-	18,22,22	1.04	3 (16%)	19,33,33	0.74	1 (5%)
3	GMP	G	502	-	18,22,22	1.01	2 (11%)	19,33,33	0.78	1 (5%)
3	GMP	G	503	-	18,22,22	1.03	2 (11%)	19,33,33	0.73	1 (5%)
3	GMP	A	502	-	18,22,22	1.01	2 (11%)	19,33,33	0.79	1 (5%)
2	G4P	H	501	-	30,38,38	0.86	1 (3%)	42,61,61	1.28	4 (9%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GMP	H	502	-	-	0/2/22/22	0/3/3/3
3	GMP	H	503	-	-	0/2/22/22	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GMP	E	502	-	-	0/2/22/22	0/3/3/3
2	G4P	E	501	-	-	3/23/43/43	0/3/3/3
2	G4P	D	501	-	-	1/23/43/43	0/3/3/3
2	G4P	B	501	-	-	0/23/43/43	0/3/3/3
2	G4P	C	501	-	-	5/23/43/43	0/3/3/3
3	GMP	A	503	-	-	2/2/22/22	0/3/3/3
3	GMP	C	503	-	-	2/2/22/22	0/3/3/3
2	G4P	G	501	-	-	4/23/43/43	0/3/3/3
3	GMP	D	503	-	-	2/2/22/22	0/3/3/3
3	GMP	D	502	-	-	0/2/22/22	0/3/3/3
3	GMP	E	503	-	-	0/2/22/22	0/3/3/3
2	G4P	F	501	-	-	4/23/43/43	0/3/3/3
3	GMP	B	502	-	-	0/2/22/22	0/3/3/3
3	GMP	F	503	-	-	2/2/22/22	0/3/3/3
3	GMP	F	502	-	-	0/2/22/22	0/3/3/3
2	G4P	A	501	-	-	3/23/43/43	0/3/3/3
3	GMP	B	503	-	-	2/2/22/22	0/3/3/3
3	GMP	C	502	-	-	0/2/22/22	0/3/3/3
3	GMP	G	502	-	-	0/2/22/22	0/3/3/3
3	GMP	G	503	-	-	2/2/22/22	0/3/3/3
3	GMP	A	502	-	-	0/2/22/22	0/3/3/3
2	G4P	H	501	-	-	4/23/43/43	0/3/3/3

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	G4P	C6-N1	-2.90	1.33	1.37
2	E	501	G4P	C6-N1	-2.90	1.33	1.37
3	C	502	GMP	C5-C6	-2.69	1.41	1.47
3	A	502	GMP	C5-C6	-2.66	1.42	1.47
3	E	502	GMP	C5-C6	-2.65	1.42	1.47
3	D	502	GMP	C5-C6	-2.62	1.42	1.47
3	E	503	GMP	C5-C6	-2.61	1.42	1.47
3	H	503	GMP	C5-C6	-2.61	1.42	1.47
3	B	502	GMP	C5-C6	-2.61	1.42	1.47
3	H	502	GMP	C5-C6	-2.60	1.42	1.47
2	A	501	G4P	C6-N1	-2.58	1.34	1.37
3	F	502	GMP	C5-C6	-2.57	1.42	1.47
3	D	503	GMP	C5-C6	-2.56	1.42	1.47
3	B	503	GMP	C5-C6	-2.56	1.42	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	503	GMP	C5-C6	-2.56	1.42	1.47
3	F	503	GMP	C5-C6	-2.55	1.42	1.47
3	G	502	GMP	C5-C6	-2.55	1.42	1.47
2	B	501	G4P	C6-N1	-2.54	1.34	1.37
3	C	503	GMP	C5-C6	-2.52	1.42	1.47
3	A	503	GMP	C5-C6	-2.52	1.42	1.47
2	D	501	G4P	C6-N1	-2.48	1.34	1.37
2	H	501	G4P	C6-N1	-2.46	1.34	1.37
2	C	501	G4P	O4'-C1'	2.44	1.44	1.41
2	G	501	G4P	C6-N1	-2.28	1.34	1.37
2	F	501	G4P	C6-N1	-2.22	1.34	1.37
3	G	502	GMP	C8-N7	-2.11	1.31	1.35
2	B	501	G4P	O4'-C1'	2.10	1.44	1.41
3	D	503	GMP	C8-N7	-2.10	1.31	1.35
3	H	502	GMP	C8-N7	-2.07	1.31	1.35
3	F	502	GMP	C8-N7	-2.07	1.31	1.35
3	E	502	GMP	C8-N7	-2.07	1.31	1.35
3	C	503	GMP	C8-N7	-2.05	1.31	1.35
3	B	503	GMP	C8-N7	-2.05	1.31	1.35
3	D	502	GMP	C8-N7	-2.03	1.31	1.35
3	A	502	GMP	C8-N7	-2.03	1.31	1.35
3	H	503	GMP	C8-N7	-2.03	1.31	1.35
3	G	503	GMP	C8-N7	-2.03	1.31	1.35
3	F	503	GMP	C8-N7	-2.02	1.31	1.35
3	A	503	GMP	C8-N7	-2.01	1.31	1.35
3	B	502	GMP	C5-C4	-2.01	1.38	1.43
3	C	502	GMP	C5-C4	-2.01	1.38	1.43
3	E	503	GMP	C8-N7	-2.00	1.31	1.35
3	C	502	GMP	C8-N7	-2.00	1.31	1.35

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	G4P	PC-O3C-PD	-5.81	112.88	132.83
2	A	501	G4P	PC-O3C-PD	-5.44	114.17	132.83
2	G	501	G4P	O3C-PC-O3'	-5.11	92.19	102.48
2	D	501	G4P	PC-O3C-PD	-4.30	118.08	132.83
2	E	501	G4P	PC-O3C-PD	-3.43	121.07	132.83
2	B	501	G4P	O3C-PC-O3'	-3.26	95.92	102.48
2	B	501	G4P	PA-O3A-PB	-3.19	121.89	132.83
2	H	501	G4P	PC-O3C-PD	-3.11	122.17	132.83
2	C	501	G4P	PC-O3C-PD	-3.11	122.17	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	501	G4P	C8-N7-C5	3.10	108.89	102.99
2	E	501	G4P	PA-O3A-PB	-3.10	122.20	132.83
2	C	501	G4P	C8-N7-C5	2.98	108.68	102.99
2	G	501	G4P	PC-O3'-C3'	2.97	130.23	119.41
2	F	501	G4P	PC-O3C-PD	-2.95	122.71	132.83
2	B	501	G4P	C8-N7-C5	2.87	108.47	102.99
2	F	501	G4P	C8-N7-C5	2.78	108.28	102.99
2	D	501	G4P	C8-N7-C5	2.77	108.28	102.99
2	G	501	G4P	C8-N7-C5	2.76	108.25	102.99
2	A	501	G4P	C8-N7-C5	2.71	108.15	102.99
2	H	501	G4P	C8-N7-C5	2.70	108.13	102.99
2	D	501	G4P	PA-O3A-PB	-2.69	123.60	132.83
2	A	501	G4P	PA-O3A-PB	-2.64	123.76	132.83
2	E	501	G4P	C5-C6-N1	2.58	118.52	113.95
2	A	501	G4P	O3C-PC-O3'	-2.48	97.49	102.48
2	G	501	G4P	O3'-C3'-C2'	-2.44	102.83	111.68
2	G	501	G4P	PA-O3A-PB	-2.42	124.52	132.83
2	G	501	G4P	C5-C6-N1	2.41	118.20	113.95
2	A	501	G4P	O3D-PD-O2D	2.33	116.55	107.64
2	C	501	G4P	C5'-C4'-C3'	-2.32	106.70	114.40
2	D	501	G4P	O3D-PD-O2D	2.32	116.49	107.64
2	E	501	G4P	C3'-C2'-C1'	2.31	105.00	99.89
2	F	501	G4P	C5-C6-N1	2.30	118.02	113.95
2	D	501	G4P	C3'-C2'-C1'	2.29	104.97	99.89
2	C	501	G4P	O3B-PB-O2B	2.28	116.36	107.64
2	F	501	G4P	PA-O3A-PB	-2.26	125.06	132.83
2	F	501	G4P	C3'-C2'-C1'	2.26	104.90	99.89
2	E	501	G4P	O6-C6-N1	-2.23	118.02	120.65
2	A	501	G4P	O2'-C2'-C3'	-2.22	104.85	111.17
2	B	501	G4P	C3'-C2'-C1'	2.20	104.76	99.89
2	H	501	G4P	PC-O3'-C3'	2.19	127.38	119.41
2	H	501	G4P	PA-O3A-PB	-2.19	125.32	132.83
2	D	501	G4P	C5-C6-N1	2.18	117.79	113.95
2	C	501	G4P	PA-O3A-PB	-2.17	125.38	132.83
2	A	501	G4P	O3'-C3'-C2'	-2.16	103.85	111.68
2	B	501	G4P	C5-C6-N1	2.13	117.72	113.95
3	B	502	GMP	O6-C6-C5	2.09	128.44	124.37
2	B	501	G4P	O3D-PD-O2D	2.06	115.51	107.64
3	G	503	GMP	O6-C6-C5	2.06	128.40	124.37
3	G	502	GMP	O6-C6-C5	2.06	128.39	124.37
3	A	502	GMP	O6-C6-C5	2.05	128.37	124.37
2	C	501	G4P	C5-C6-N1	2.04	117.55	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	G4P	C5-C6-N1	2.03	117.54	113.95
3	A	503	GMP	O6-C6-C5	2.03	128.34	124.37
3	F	502	GMP	O6-C6-C5	2.02	128.32	124.37
3	C	502	GMP	O6-C6-C5	2.01	128.31	124.37
3	E	503	GMP	O6-C6-C5	2.01	128.30	124.37
3	D	503	GMP	O6-C6-C5	2.01	128.29	124.37
3	C	503	GMP	O6-C6-C5	2.01	128.29	124.37
3	F	503	GMP	O6-C6-C5	2.00	128.28	124.37

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	G4P	PA-O3A-PB-O3B
2	C	501	G4P	PA-O3A-PB-O2B
2	C	501	G4P	PA-O3A-PB-O3B
2	E	501	G4P	PA-O3A-PB-O2B
2	E	501	G4P	PA-O3A-PB-O3B
2	F	501	G4P	PA-O3A-PB-O2B
2	F	501	G4P	PA-O3A-PB-O3B
2	G	501	G4P	PA-O3A-PB-O2B
2	G	501	G4P	PA-O3A-PB-O3B
2	H	501	G4P	PA-O3A-PB-O2B
2	H	501	G4P	PA-O3A-PB-O3B
2	H	501	G4P	C4'-C3'-O3'-PC
3	A	503	GMP	O4'-C4'-C5'-O5'
3	A	503	GMP	C3'-C4'-C5'-O5'
3	B	503	GMP	O4'-C4'-C5'-O5'
3	B	503	GMP	C3'-C4'-C5'-O5'
3	D	503	GMP	O4'-C4'-C5'-O5'
3	D	503	GMP	C3'-C4'-C5'-O5'
3	F	503	GMP	O4'-C4'-C5'-O5'
3	F	503	GMP	C3'-C4'-C5'-O5'
3	G	503	GMP	O4'-C4'-C5'-O5'
3	G	503	GMP	C3'-C4'-C5'-O5'
2	D	501	G4P	C3'-O3'-PC-O3C
3	C	503	GMP	O4'-C4'-C5'-O5'
2	A	501	G4P	PA-O3A-PB-O2B
2	H	501	G4P	PB-O3A-PA-O1A
3	C	503	GMP	C3'-C4'-C5'-O5'
2	C	501	G4P	C3'-O3'-PC-O3C
2	A	501	G4P	PA-O3A-PB-O1B

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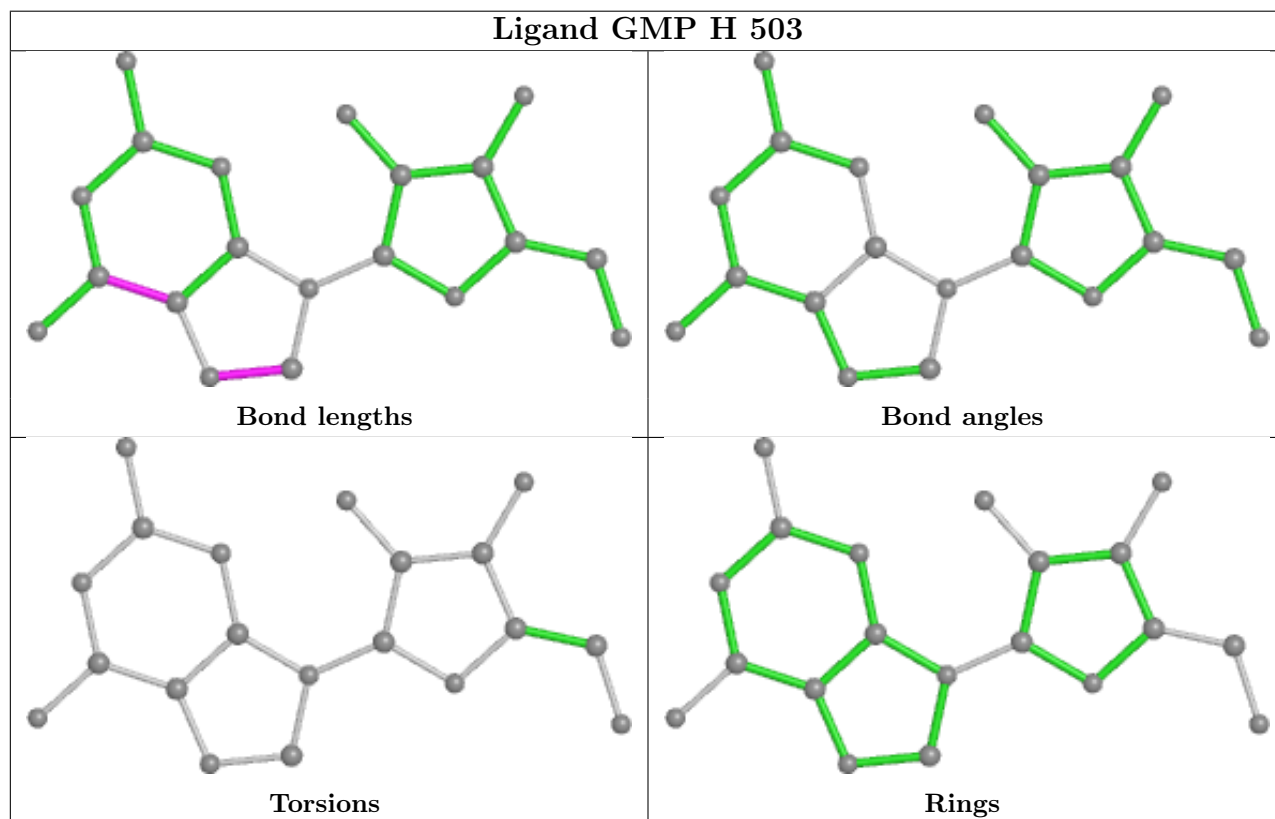
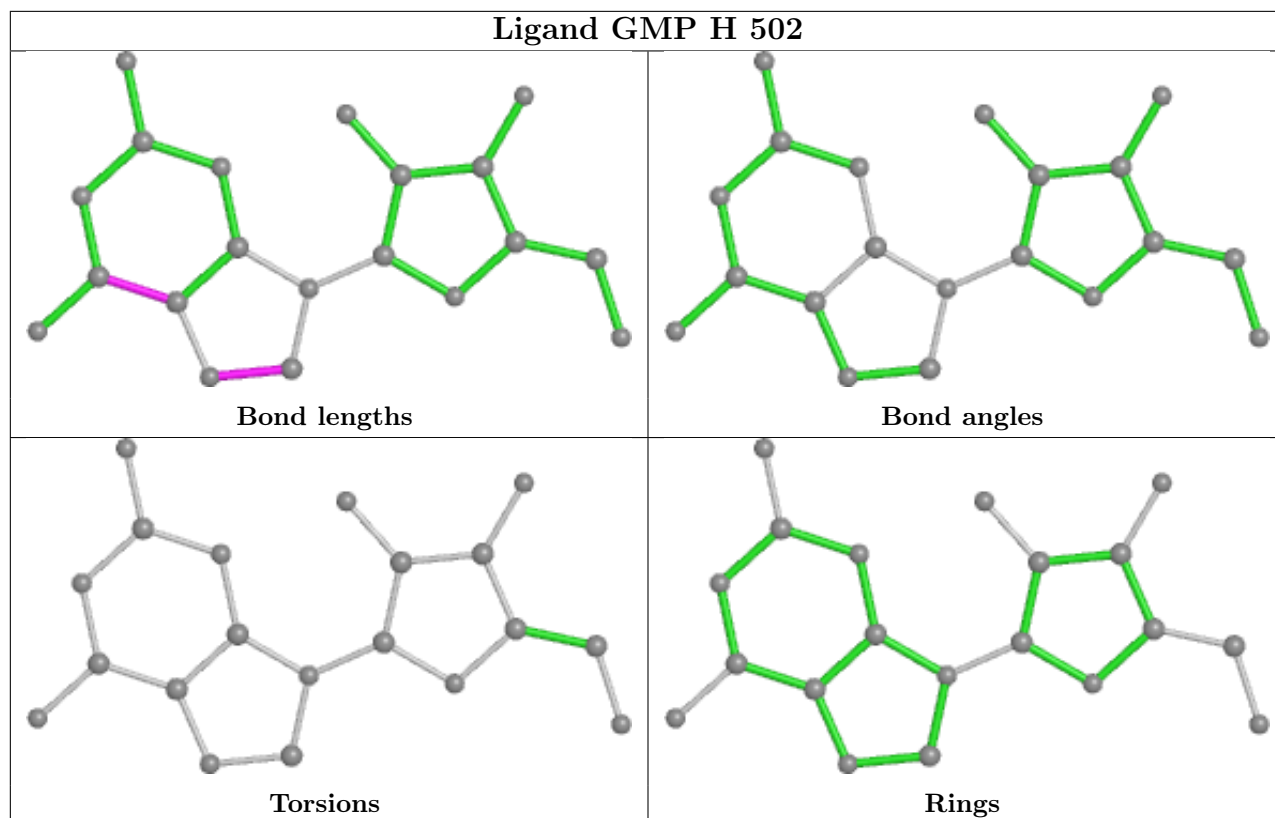
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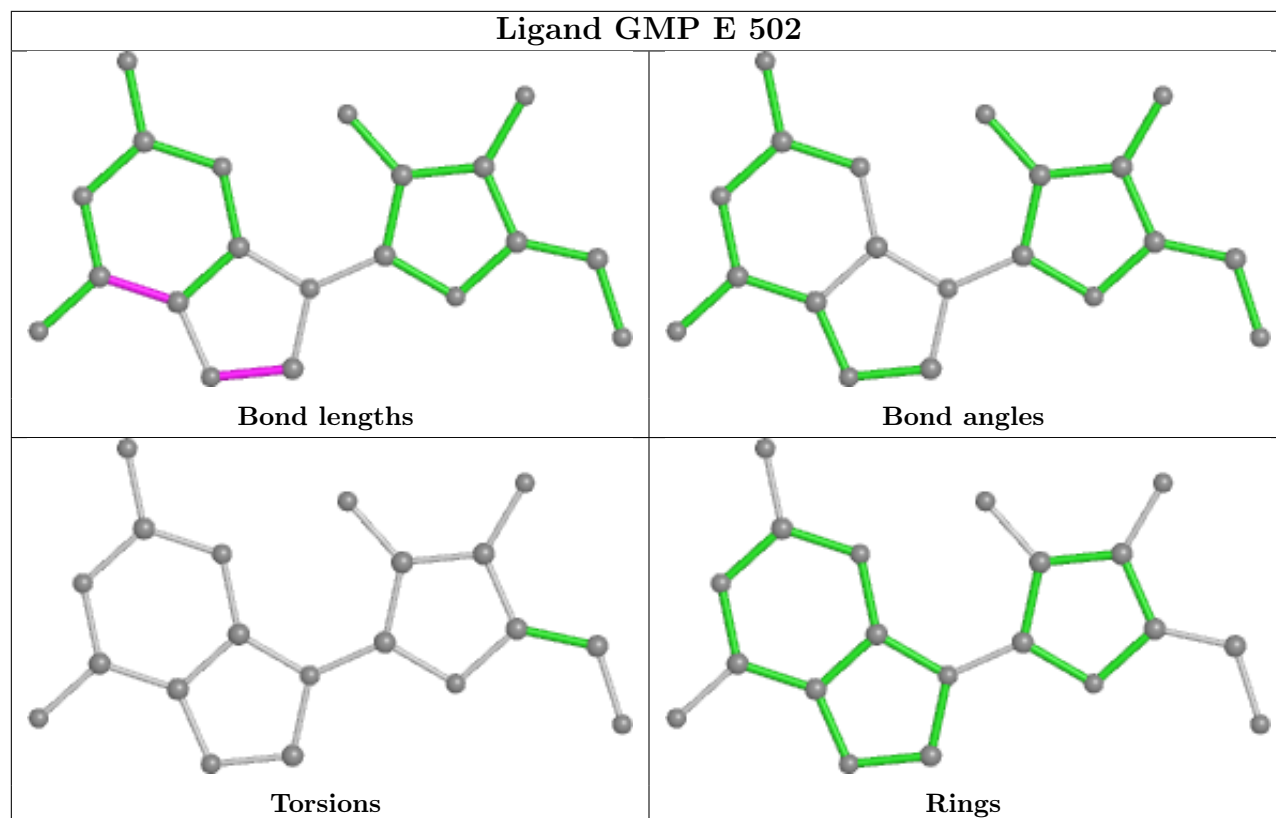
Mol	Chain	Res	Type	Atoms
2	F	501	G4P	PA-O3A-PB-O1B
2	C	501	G4P	PD-O3C-PC-O2C
2	E	501	G4P	PB-O3A-PA-O1A
2	F	501	G4P	PB-O3A-PA-O1A
2	G	501	G4P	PB-O3A-PA-O1A
2	C	501	G4P	PA-O3A-PB-O1B
2	G	501	G4P	PA-O3A-PB-O1B

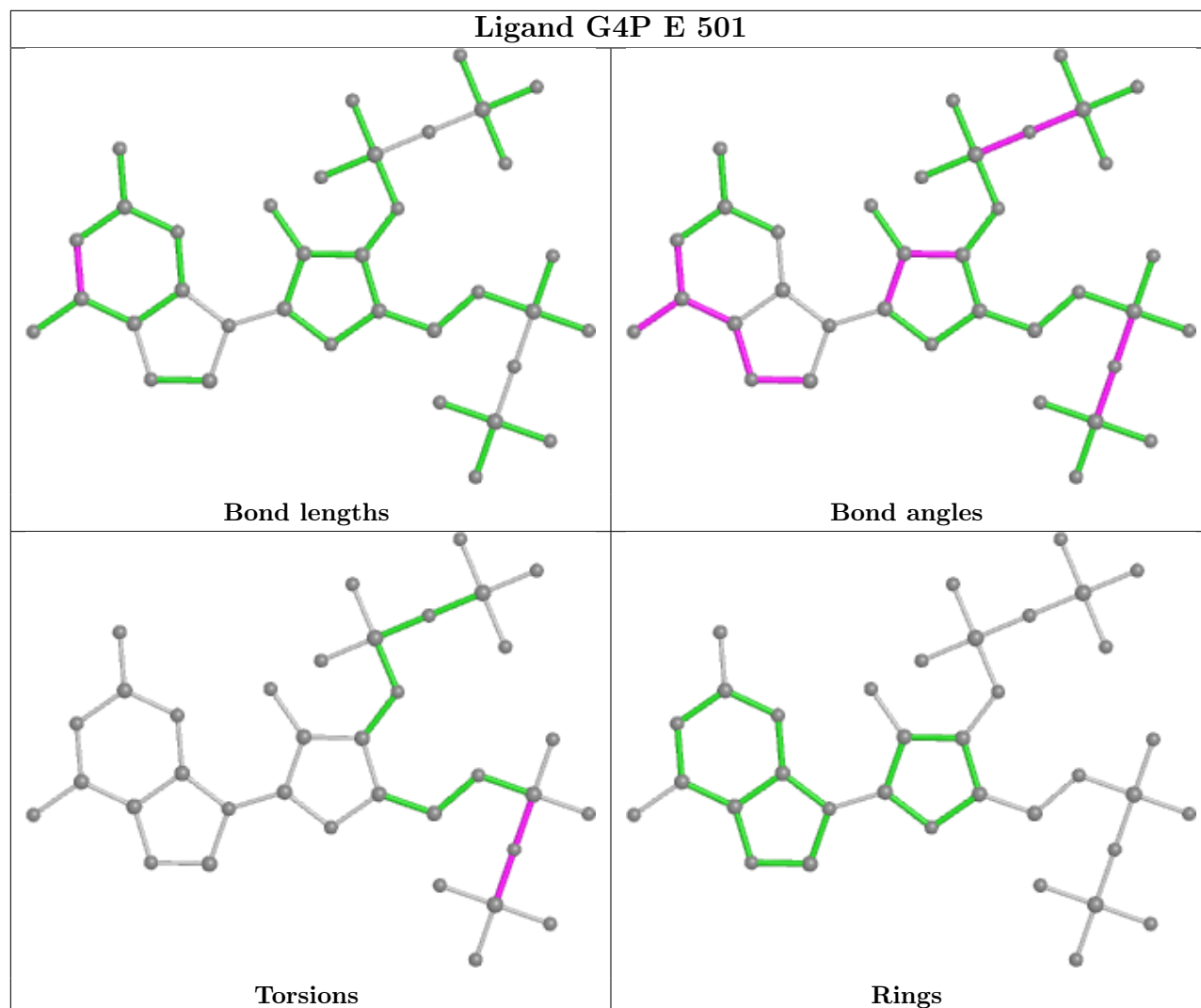
There are no ring outliers.

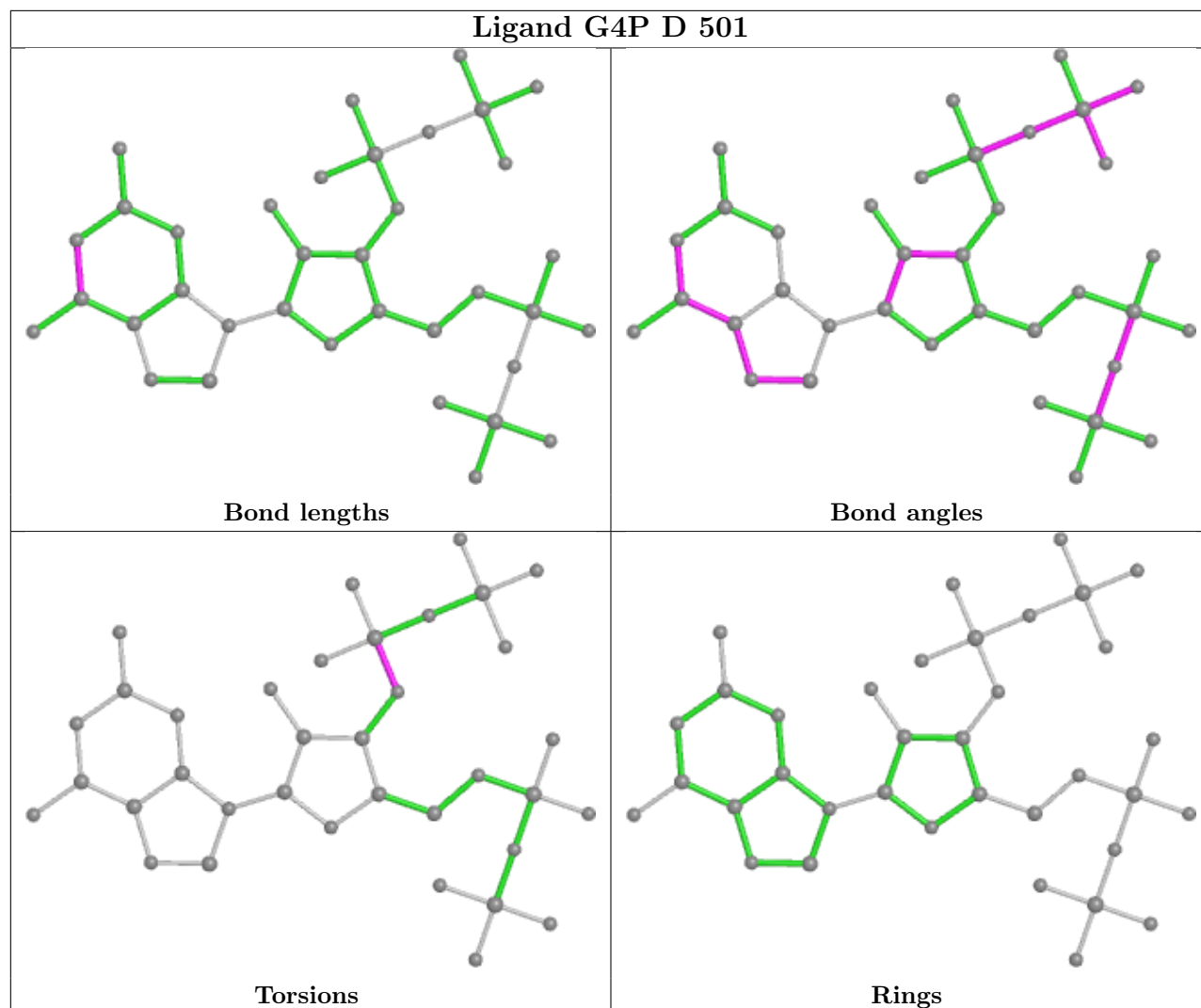
No monomer is involved in short contacts.

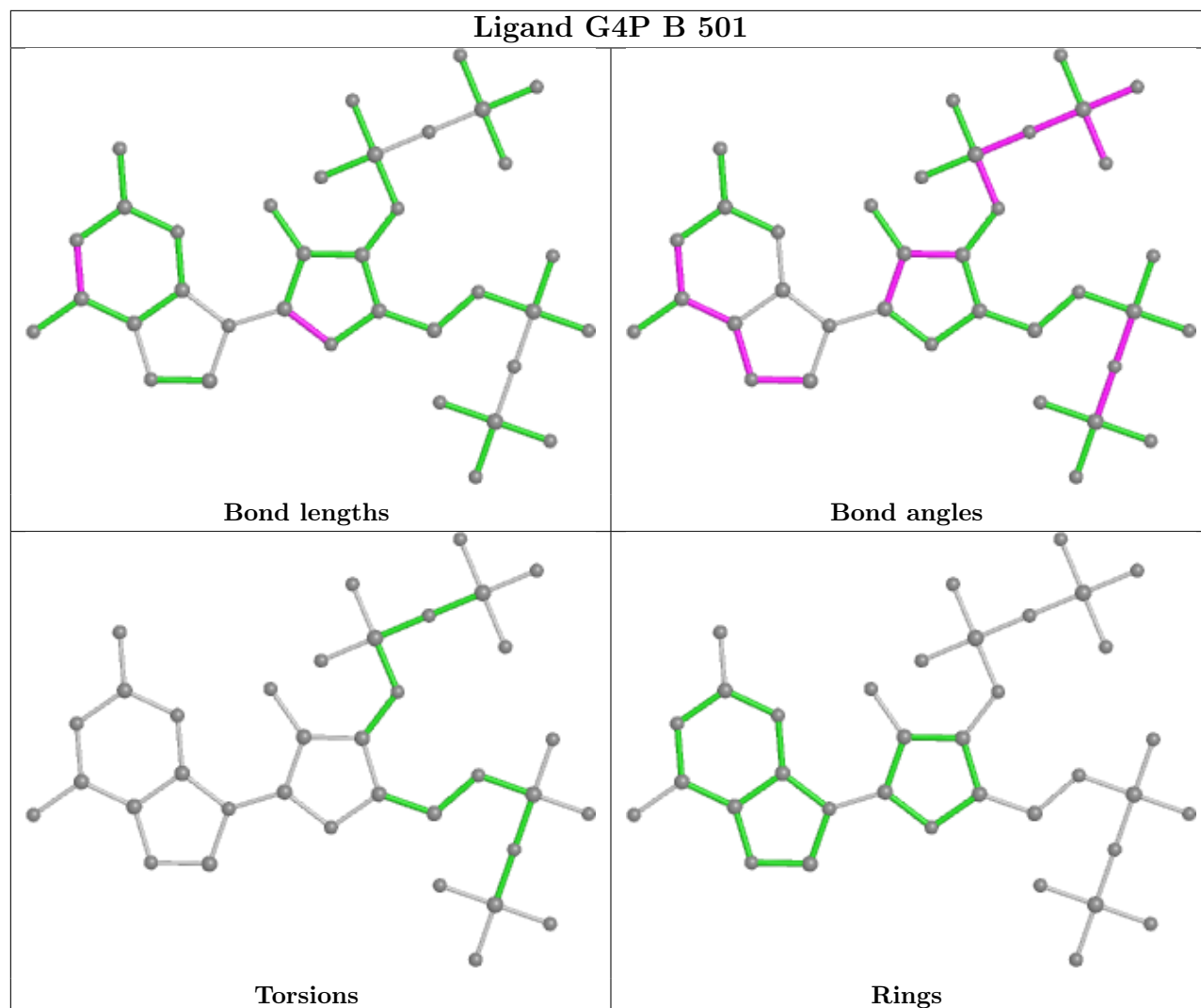
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

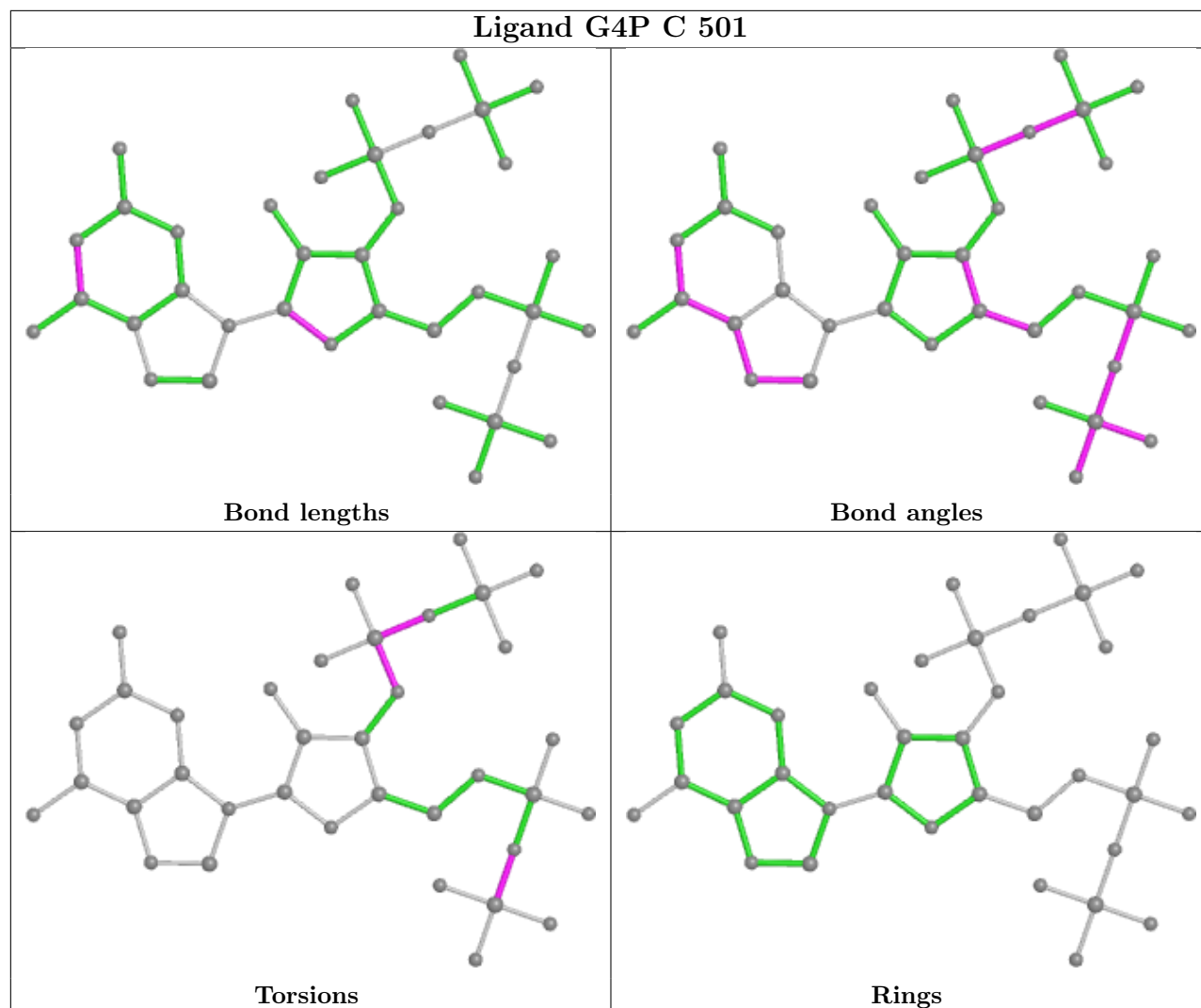


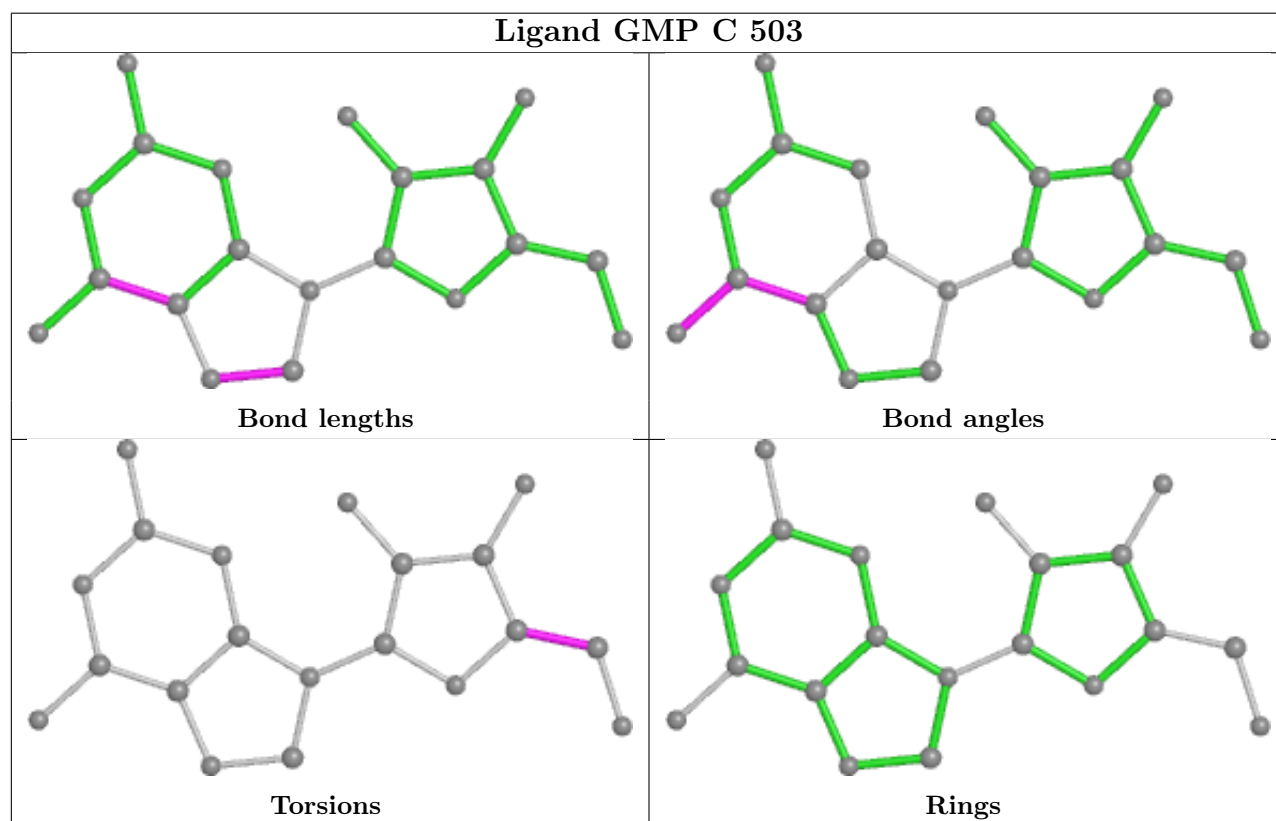
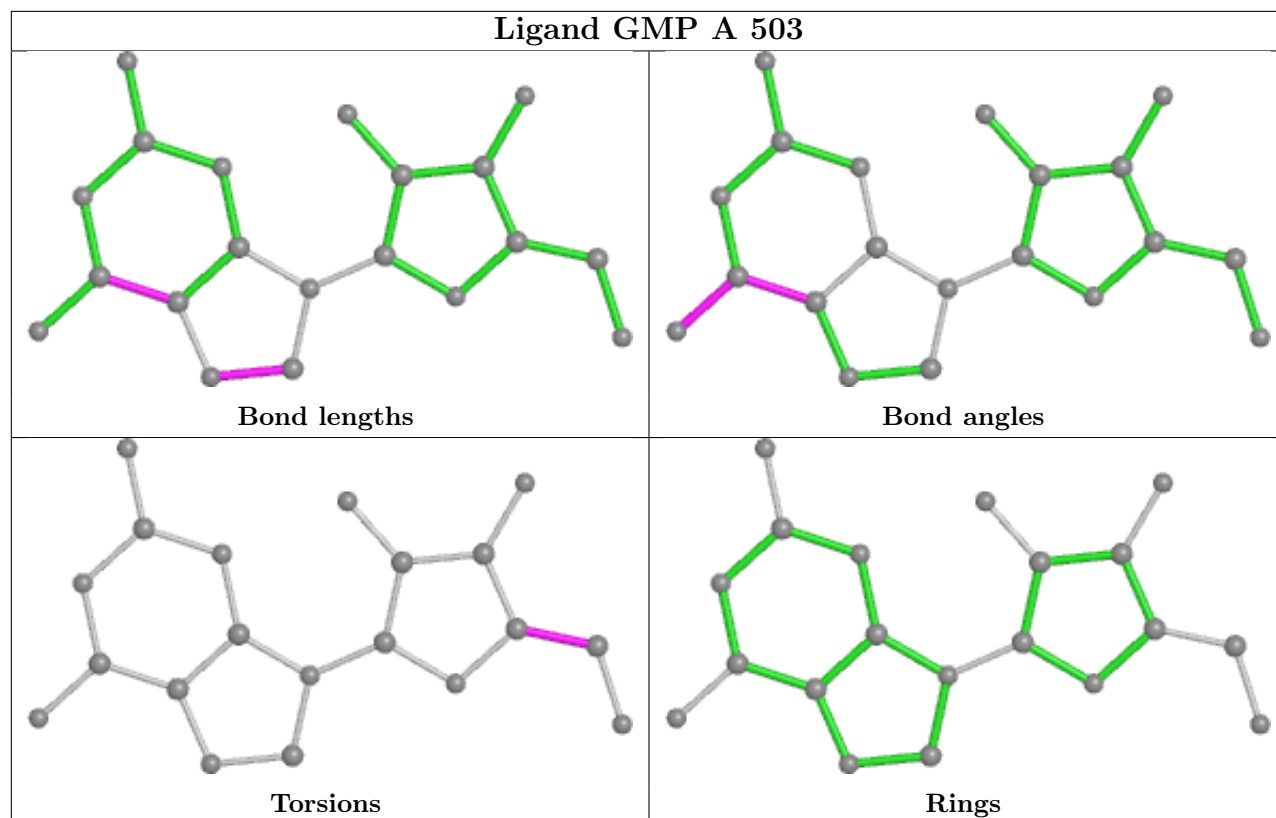


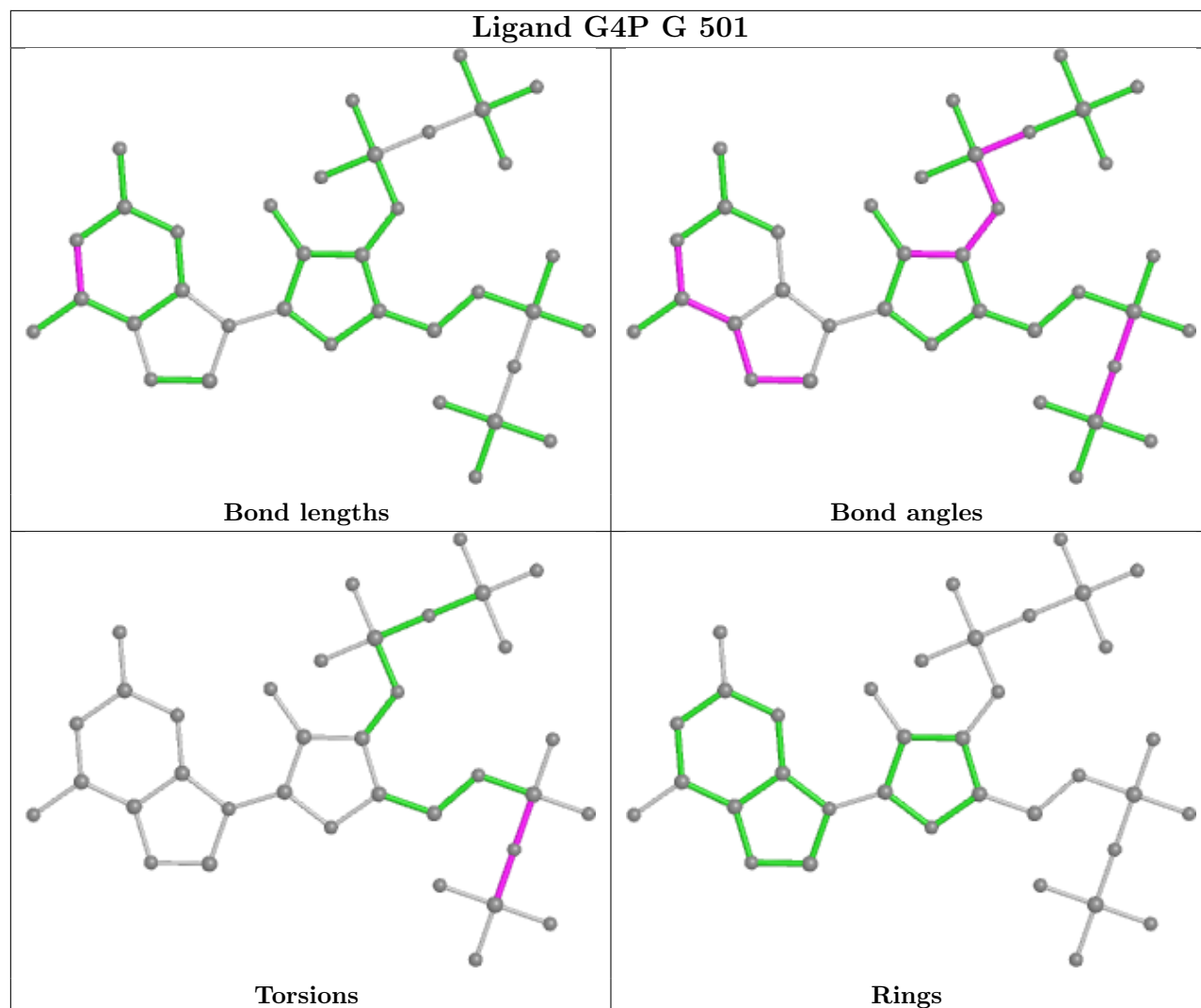


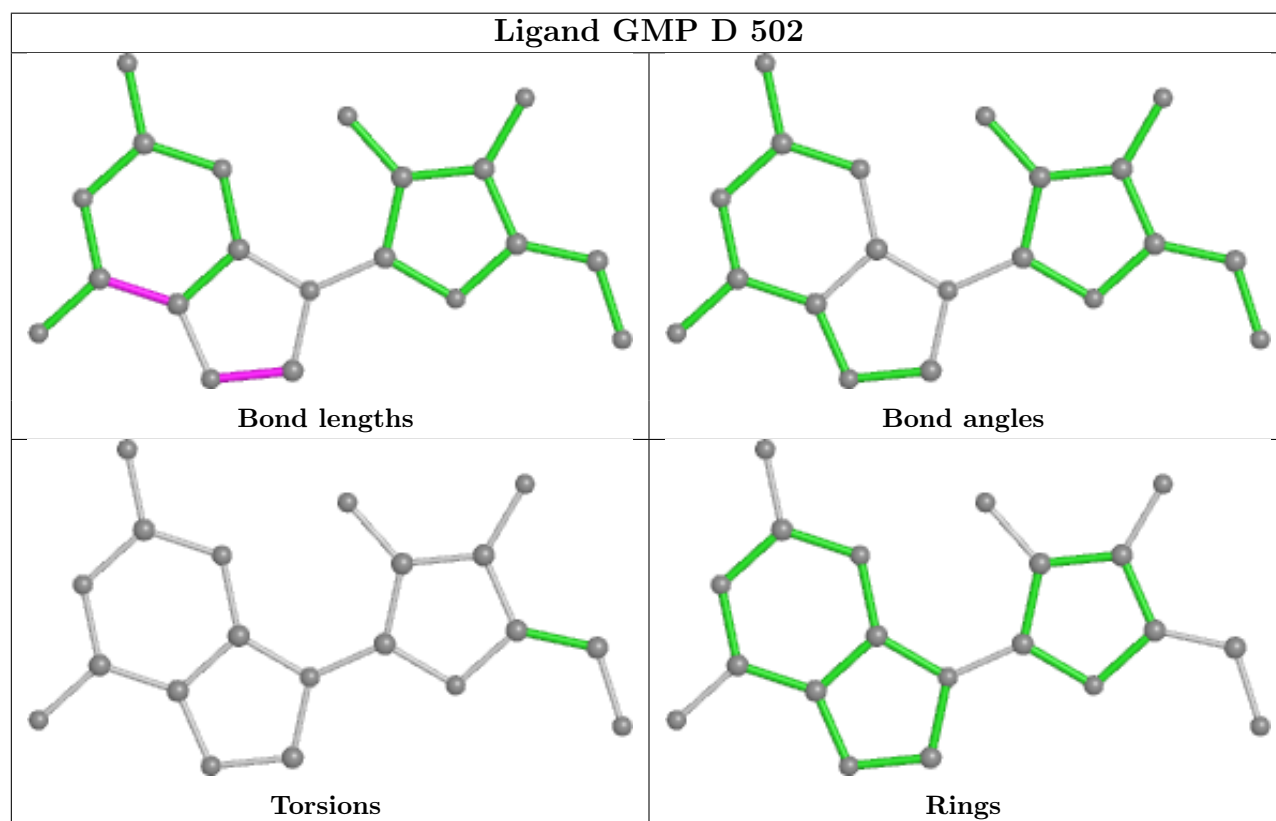
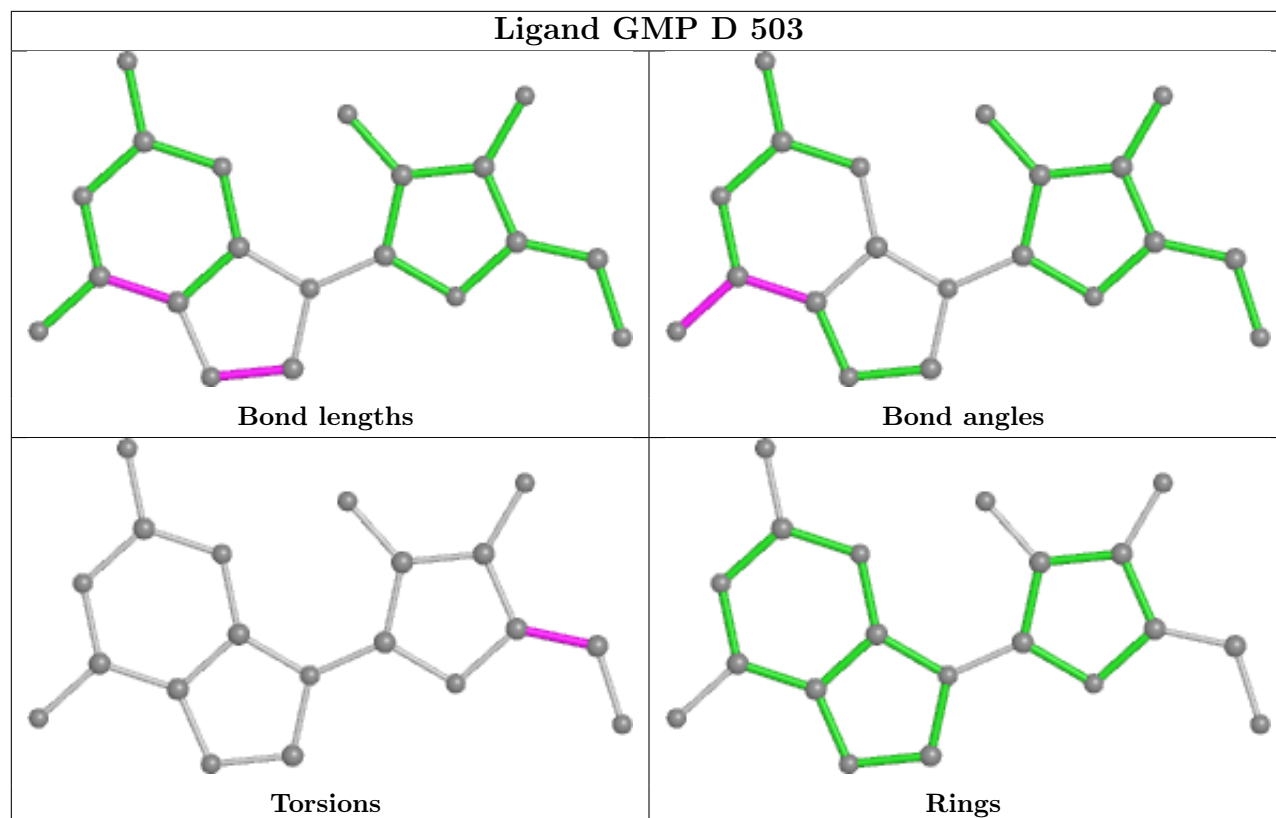


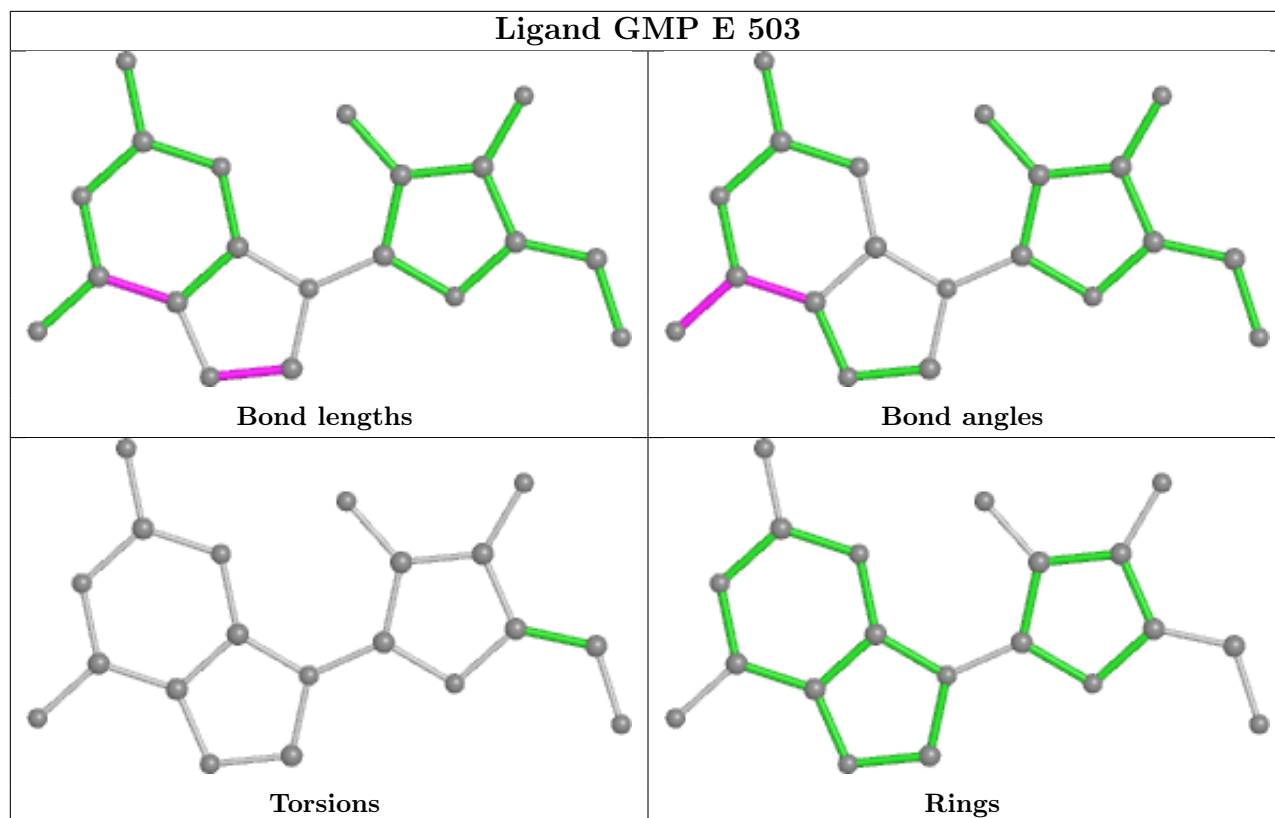


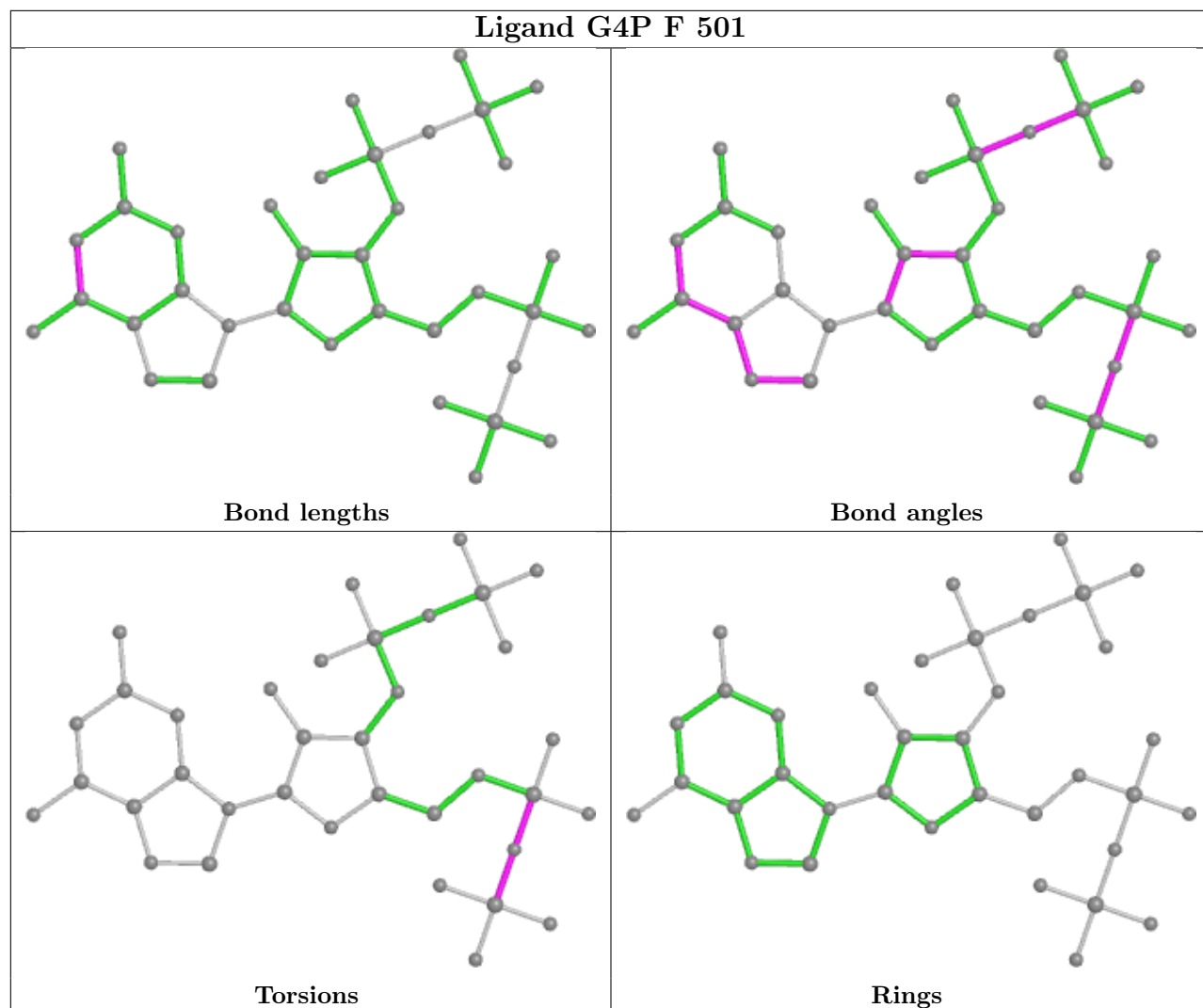


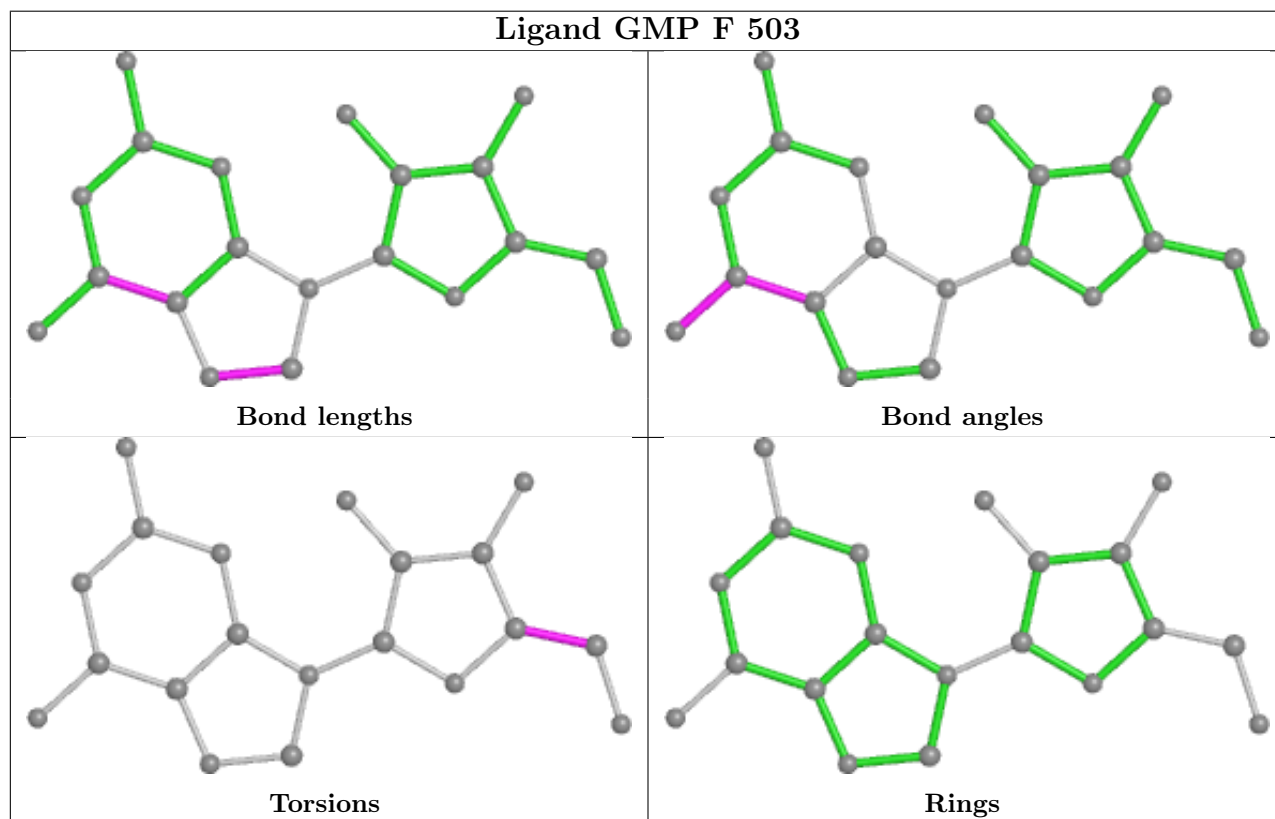
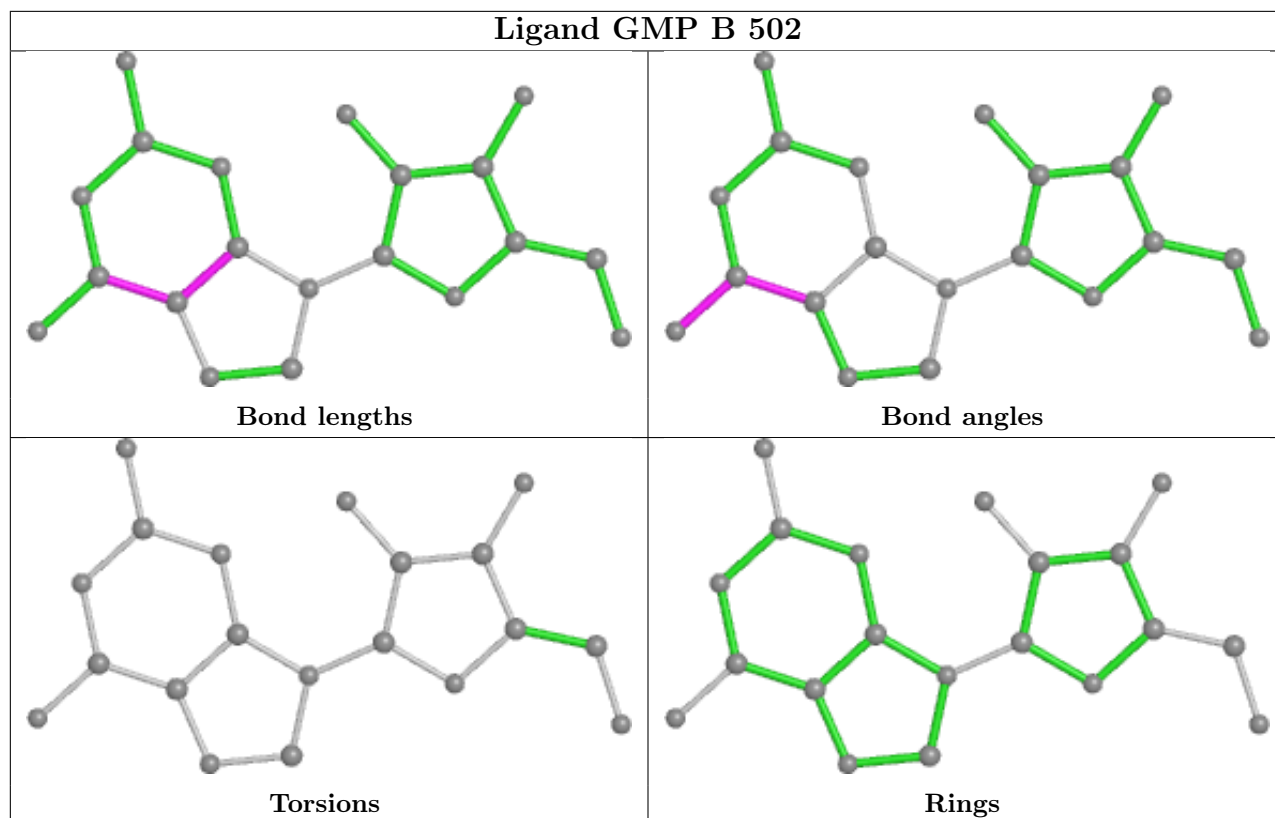


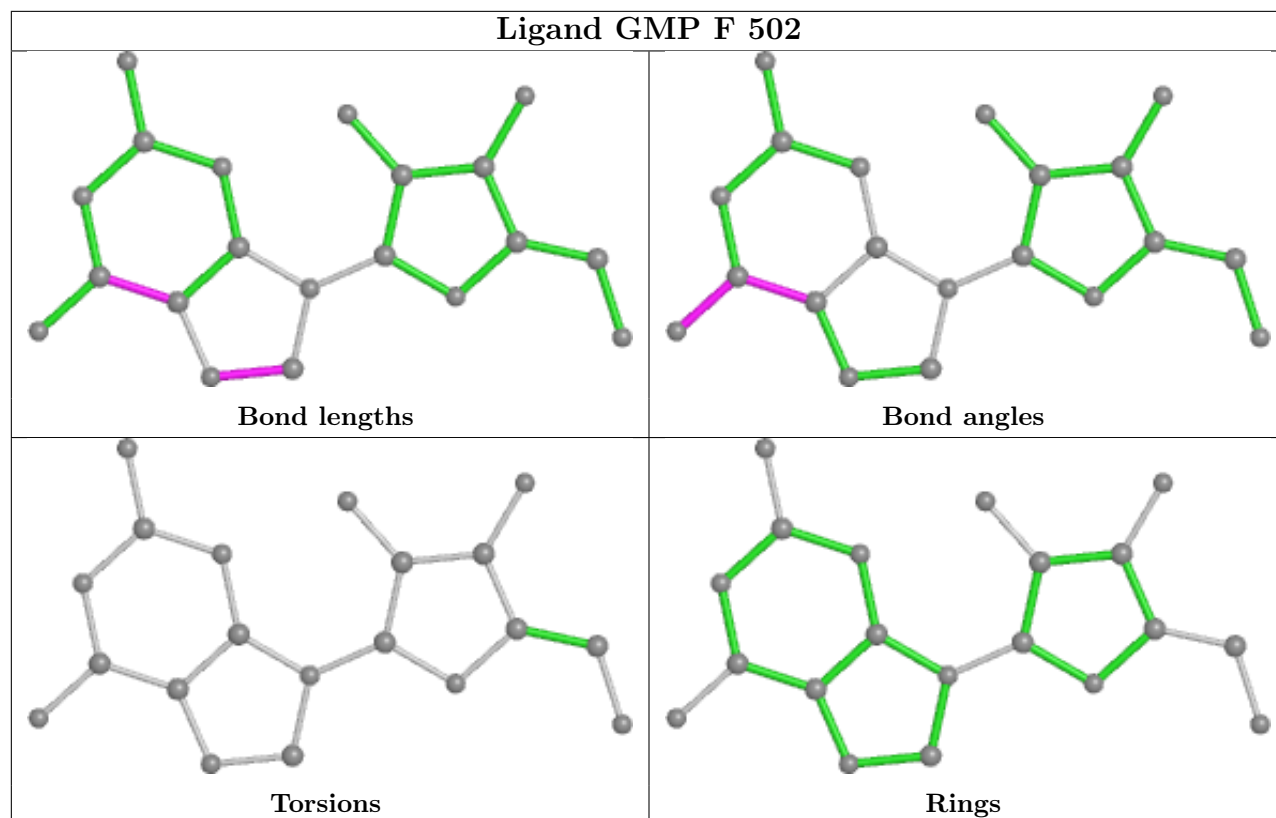


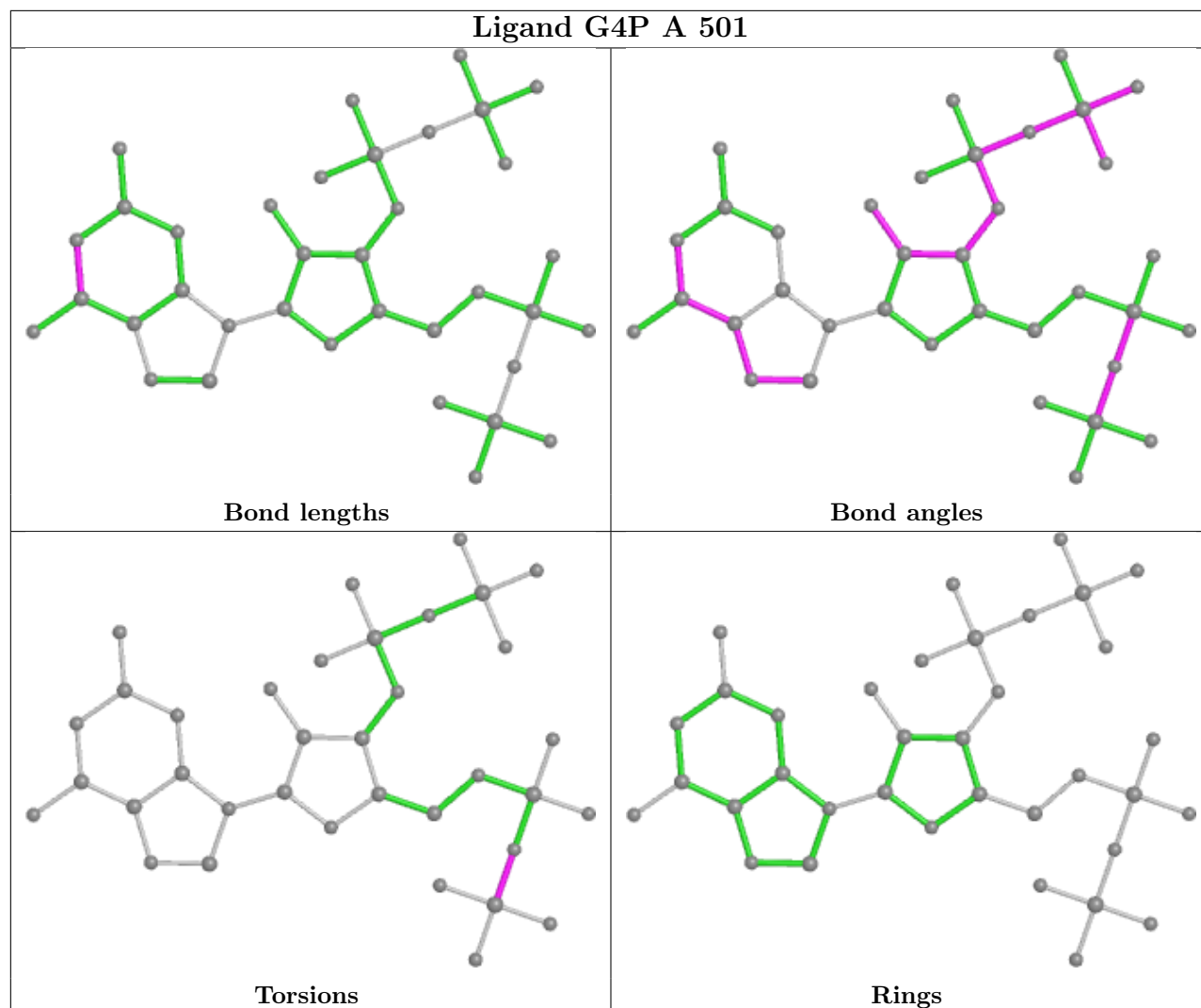


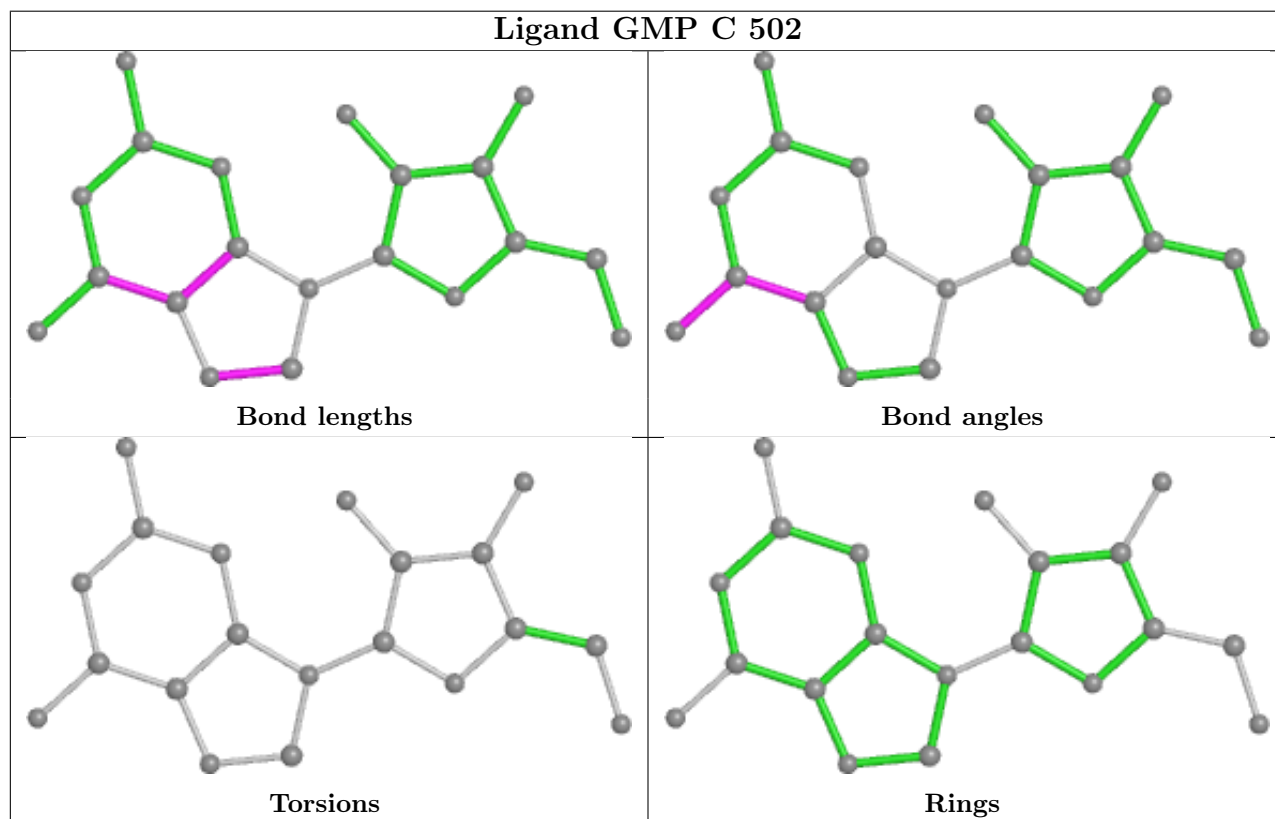
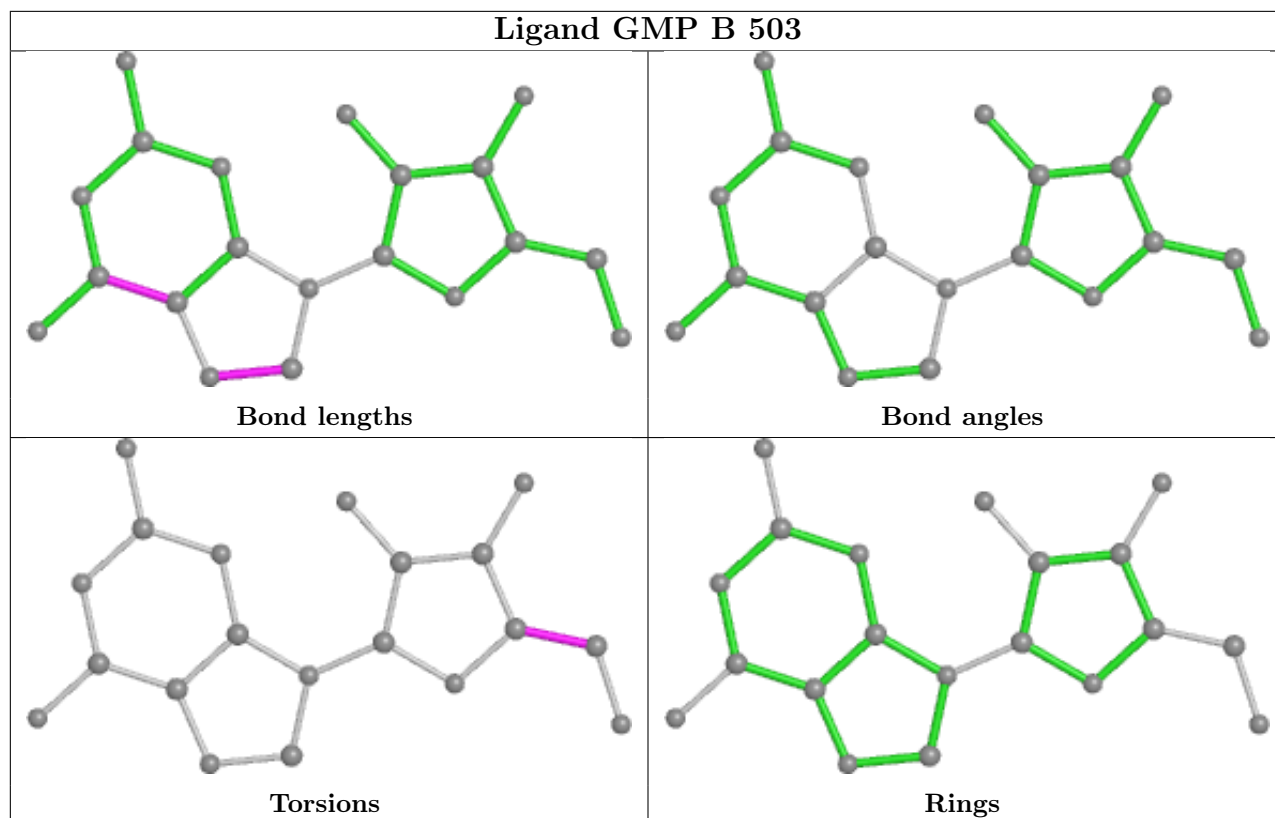


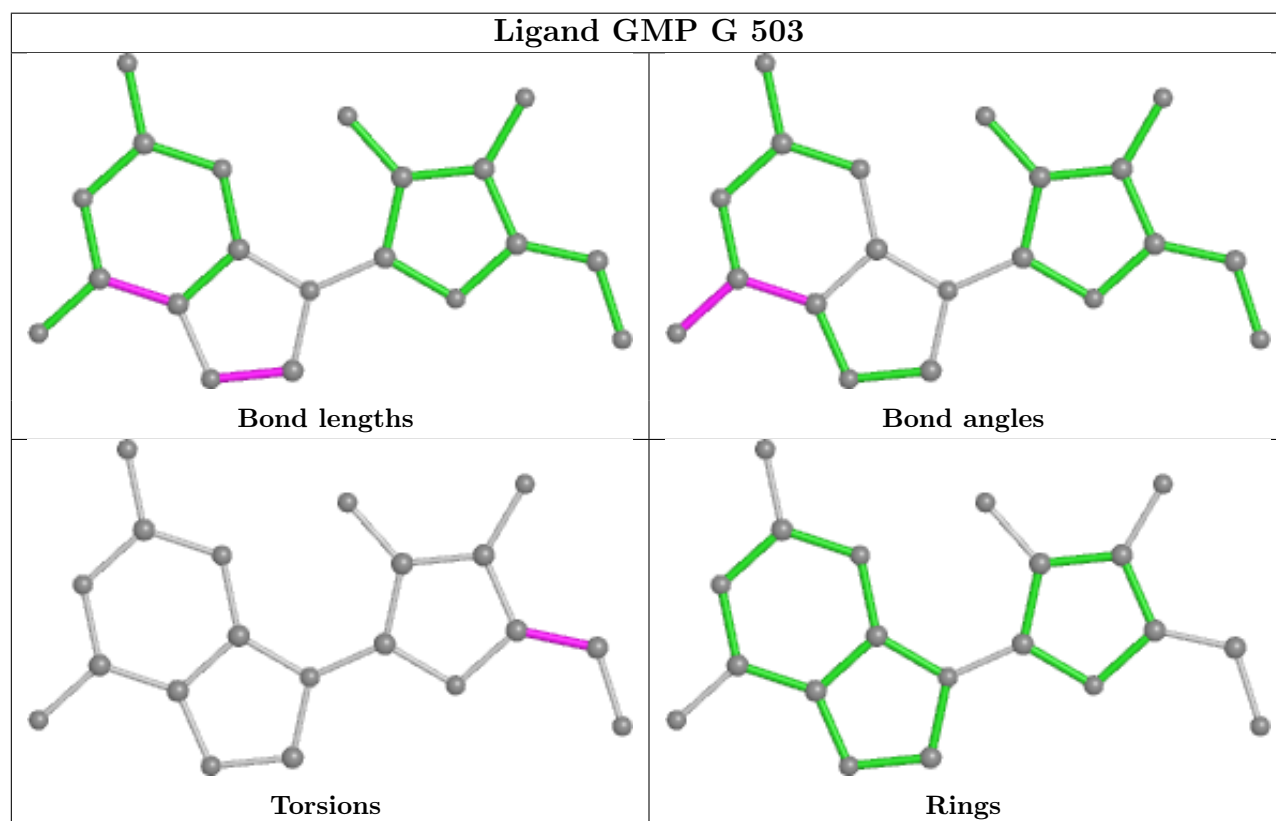
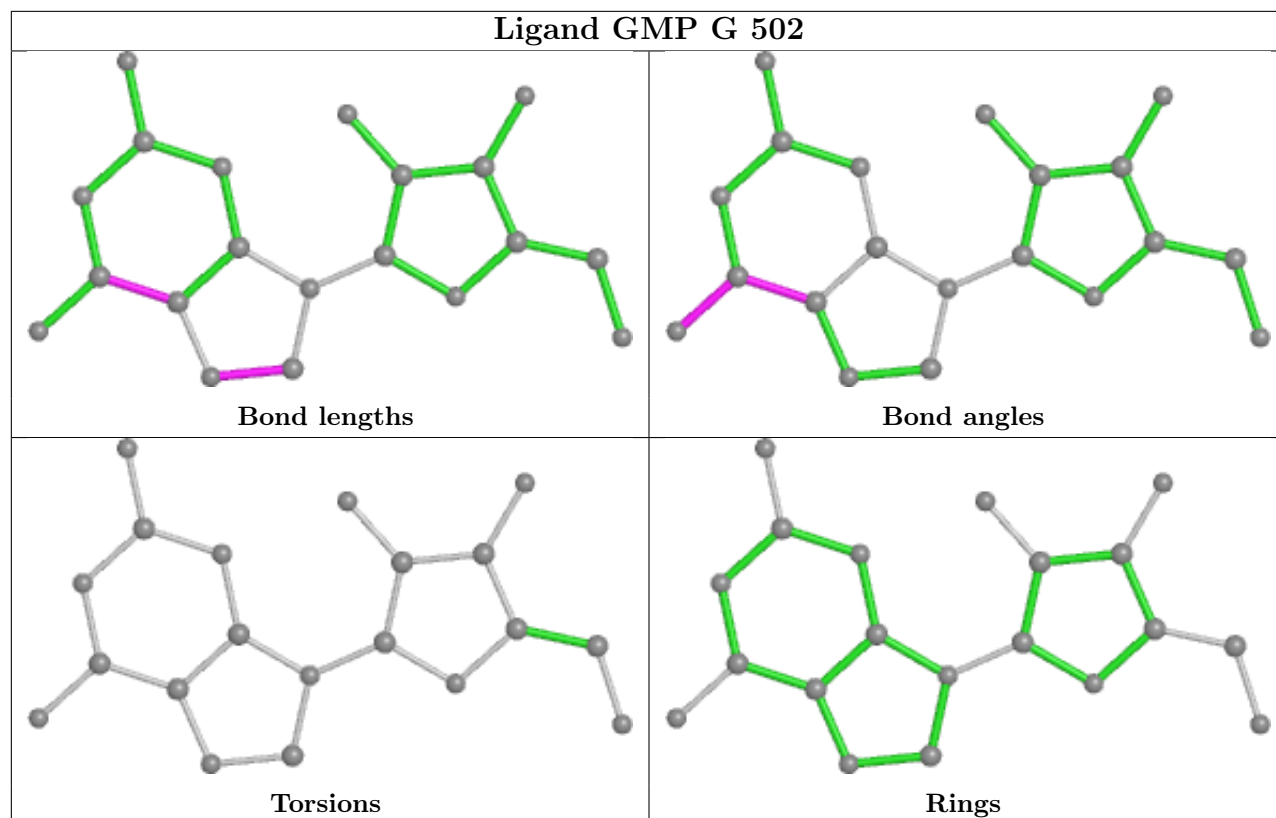


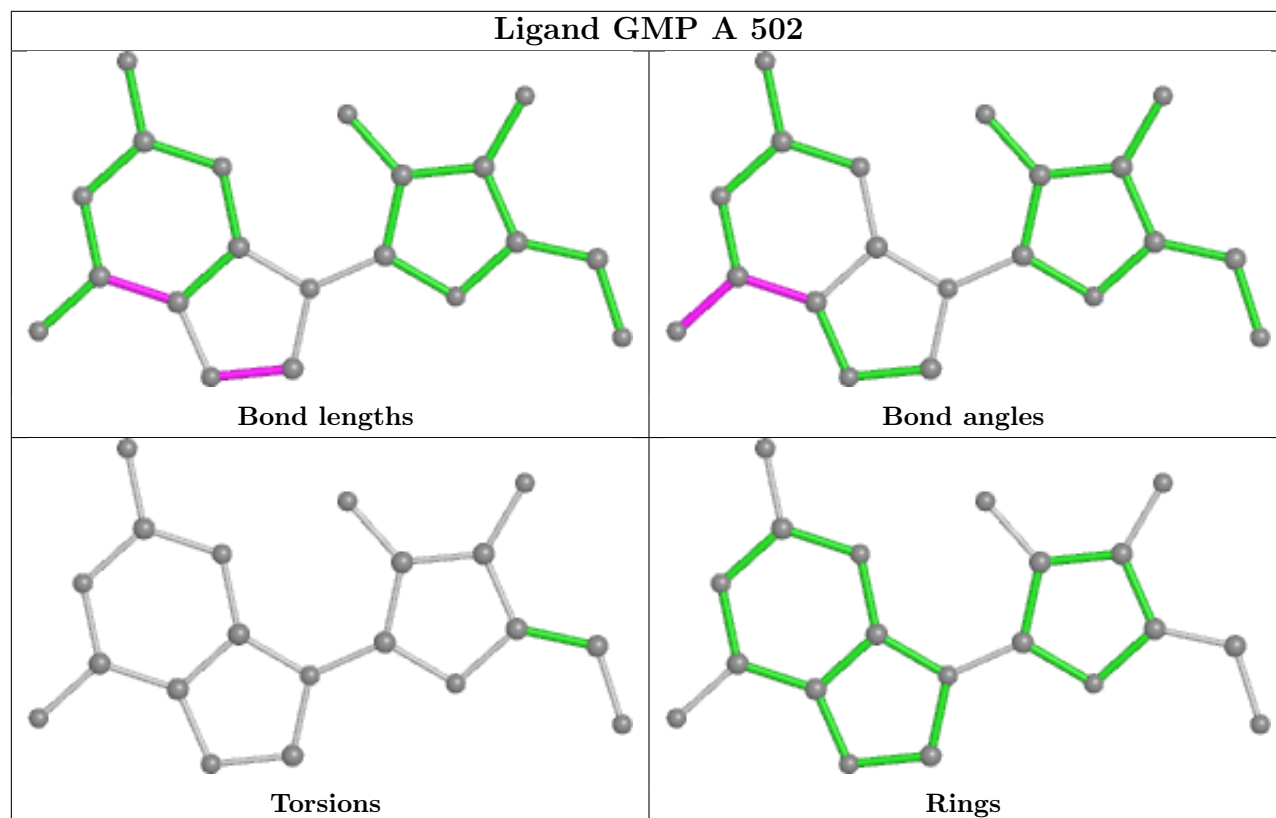


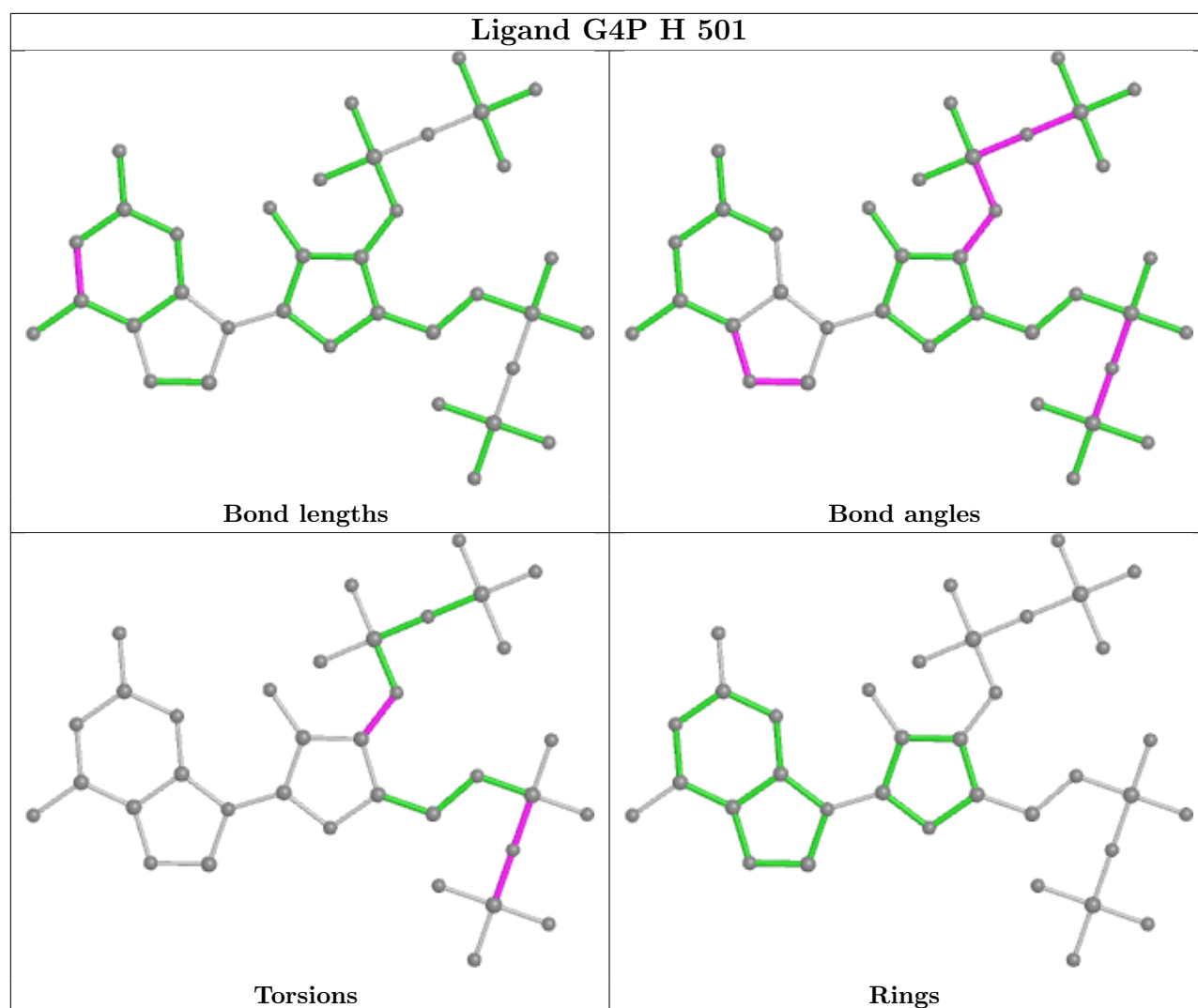












4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

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

5.2 Non-standard residues in protein, DNA, RNA chains

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

5.3 Carbohydrates

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

5.4 Ligands

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

5.5 Other polymers

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