



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 07:04 PM UTC

PDB ID : 9Y6S / pdb_00009y6s
EMDB ID : EMD-72629
Title : 96-nm repeat of the Leishmania tarentolae doublet microtubule
Authors : Doran, M.H.; Brown, A.
Deposited on : 2025-09-09
Resolution : 3.70 Å(reported)
Based on initial model : .

This is a wwPDB EM Validation Summary 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : **FAILED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
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 3.70 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

There are 168 unique types of molecules in this entry. The entry contains 3422719 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 Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AB	419	Total	C	N	O	S	0	0
			3283	2056	560	636	31		
1	AD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AN	419	Total	C	N	O	S	0	0
			3283	2056	560	636	31		
1	B	418	Total	C	N	O	S	0	0
			3270	2039	564	637	30		
1	BD	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	BF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CA	424	Total	C	N	O	S	0	0
			3319	2076	568	643	32		
1	CC	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CE	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	CG	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	CI	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CK	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CM	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DA	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DC	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DE	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DG	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DI	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DK	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DM	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	E	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EB	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	ED	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EF	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EH	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EJ	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	F	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FJ	429	Total	C	N	O	S	0	0
			3361	2100	578	652	31		
1	FL	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	G	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GD	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	GF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GJ	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	GL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	H	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HD	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HF	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HH	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HL	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	I	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	IB	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ID	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	IF	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	IH	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	IJ	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	IL	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JA	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JC	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JE	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JG	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JI	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JK	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	JM	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	KA	430	Total 3370	C 2106	N 579	O 653	S 32	0	0
1	KC	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	KE	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	KG	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	KI	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	KK	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	KM	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LA	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LC	429	Total 3362	C 2101	N 578	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	LE	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LG	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LI	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LK	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LM	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LO	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	M	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MB	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MD	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MF	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MH	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MJ	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	ML	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MN	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	N	420	Total 3290	C 2060	N 561	O 638	S 31	0	0
1	NB	420	Total 3290	C 2060	N 561	O 638	S 31	0	0
1	ND	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	NF	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	NH	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	NJ	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	NL	426	Total 3343	C 2089	N 575	O 648	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	O	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	OB	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	OD	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	OF	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	OH	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	OJ	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	OL	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	P	401	Total 3123	C 1946	N 540	O 609	S 28	0	0
1	PB	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PD	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PF	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PH	426	Total 3342	C 2089	N 575	O 647	S 31	0	0
1	PJ	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PL	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	QA	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QC	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QE	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	QG	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QI	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QK	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	RA	426	Total 3343	C 2089	N 575	O 648	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	RC	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	RE	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RG	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RI	426	Total	C	N	O	S	0	0
			3342	2088	575	648	31		
1	RK	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	S	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SB	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SD	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SF	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SH	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	SJ	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	T	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	TB	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	TD	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	TF	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	TH	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	TJ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	TL	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	U	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UB	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UD	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	UF	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	UH	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	UJ	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	UL	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	V	428	Total 3355	C 2096	N 577	O 651	S 31	0	0
1	VB	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	VD	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	VF	428	Total 3355	C 2096	N 577	O 651	S 31	0	0
1	VH	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	VJ	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	VL	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	W	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WB	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WD	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WF	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	WH	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WJ	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WL	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	AP	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	AR	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	AT	429	Total 3362	C 2101	N 578	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AV	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AX	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	AZ	419	Total	C	N	O	S	0	0
			3283	2056	560	636	31		
1	BP	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	BR	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BT	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BV	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	BX	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CO	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	CQ	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	CS	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	CU	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CW	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	CY	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DO	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DQ	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	DS	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DU	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DW	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	DY	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	EN	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	EP	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	ER	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	ET	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EV	430	Total	C	N	O	S	0	0
			3370	2106	579	653	32		
1	EX	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FP	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FR	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FT	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	FV	429	Total	C	N	O	S	0	0
			3361	2100	578	652	31		
1	FX	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	GN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GP	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	GR	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GT	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	GV	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	GX	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HP	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HR	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HT	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HV	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	HX	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IN	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IP	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IR	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IT	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IV	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	IX	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JO	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JQ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JS	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JU	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JW	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	JY	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	KO	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KQ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KS	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KU	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KW	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	KY	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	LQ	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	LS	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LU	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LW	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	LY	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MP	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MR	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MT	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MV	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MX	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	MZ	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PN	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PP	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PR	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PT	426	Total 3342	C 2089	N 575	O 647	S 31	0	0
1	PV	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	PX	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	QM	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QO	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QQ	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	QS	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	QU	427	Total 3348	C 2092	N 576	O 649	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	QW	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	RM	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RO	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	RQ	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RS	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	RU	426	Total	C	N	O	S	0	0
			3342	2088	575	648	31		
1	RW	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	SL	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SN	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SP	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	SR	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	ST	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	SV	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	TN	428	Total	C	N	O	S	0	0
			3355	2096	577	651	31		
1	TP	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	TR	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	TT	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	TV	429	Total	C	N	O	S	0	0
			3362	2101	578	652	31		
1	TX	427	Total	C	N	O	S	0	0
			3348	2092	576	649	31		
1	UN	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	UP	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	UR	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	UT	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	UV	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	UX	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	VN	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	VP	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	VR	428	Total 3355	C 2096	N 577	O 651	S 31	0	0
1	VT	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	VV	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	VX	429	Total 3362	C 2101	N 578	O 652	S 31	0	0
1	WN	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WP	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WR	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	WT	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WV	425	Total 3335	C 2085	N 574	O 645	S 31	0	0
1	WX	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	NN	420	Total 3290	C 2060	N 561	O 638	S 31	0	0
1	NP	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	NR	427	Total 3348	C 2092	N 576	O 649	S 31	0	0
1	NT	426	Total 3343	C 2089	N 575	O 648	S 31	0	0
1	NV	429	Total 3362	C 2101	N 578	O 652	S 31	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	NX	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	ON	425	Total	C	N	O	S	0	0
			3335	2085	574	645	31		
1	OP	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OR	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OT	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OV	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		
1	OX	426	Total	C	N	O	S	0	0
			3343	2089	575	648	31		

- Molecule 2 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	AC	433	Total	C	N	O	S	0	0
			3353	2117	570	643	23		
2	AE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AG	433	Total	C	N	O	S	0	0
			3352	2116	571	642	23		
2	AI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AK	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BA	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BE	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BG	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	BK	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	BM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	C	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CB	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CD	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CF	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	CH	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CJ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CL	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	D	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DB	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DF	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	DH	430	Total	C	N	O	S	0	0
			3328	2102	567	636	23		
2	DJ	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DL	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	EA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	EC	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	EE	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	EG	433	Total	C	N	O	S	0	0
			3351	2114	570	644	23		
2	EI	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	EK	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	FA	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	FC	434	Total	C	N	O	S	0	0
			3360	2119	571	647	23		
2	FE	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	FG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	FI	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	FK	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	GA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GC	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	GG	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HC	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	HG	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	HI	431	Total	C	N	O	S	0	0
			3336	2106	568	639	23		
2	HK	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	HM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IC	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	IE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	II	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	J	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	JB	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	JD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	JF	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	JH	432	Total	C	N	O	S	0	0
			3342	2110	569	640	23		
2	JJ	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	JL	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	JN	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	K	434	Total	C	N	O	S	0	0
			3358	2119	572	643	24		
2	KB	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	KF	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KH	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	KJ	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	KL	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KN	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LB	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	LD	429	Total	C	N	O	S	0	0
			3322	2097	566	637	22		
2	LF	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LH	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LJ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LL	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LN	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	MA	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	MC	437	Total	C	N	O	S	0	0
			3379	2133	575	647	24		
2	ME	436	Total	C	N	O	S	0	0
			3368	2124	573	647	24		
2	MG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MK	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MM	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	NA	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NC	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NK	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	NM	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	OA	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	OC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	OE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	OG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	OI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	OK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	OM	433	Total	C	N	O	S	0	0
			3352	2115	570	644	23		
2	PA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	PC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PG	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	PI	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PK	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	PM	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	Q	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	QB	429	Total	C	N	O	S	0	0
			3323	2100	566	634	23		
2	QD	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	QF	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	QH	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	QJ	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	QL	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	R	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	RB	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RD	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RF	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RH	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	RJ	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	RL	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SA	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	SC	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SE	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	SI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	SK	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	TA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TC	428	Total	C	N	O	S	0	0
			3314	2093	565	634	22		
2	TE	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	TI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TK	433	Total	C	N	O	S	0	0
			3353	2117	570	643	23		
2	UA	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	UC	429	Total	C	N	O	S	0	0
			3322	2097	566	637	22		
2	UE	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	UI	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	VA	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VE	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VI	432	Total	C	N	O	S	0	0
			3342	2109	569	641	23		
2	VK	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	VM	434	Total	C	N	O	S	0	0
			3360	2119	571	647	23		
2	WA	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WC	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WE	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WG	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WI	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WK	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WM	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AO	433	Total	C	N	O	S	0	0
			3353	2117	570	643	23		
2	AQ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	AS	433	Total	C	N	O	S	0	0
			3352	2116	571	642	23		
2	AU	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AW	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	AY	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BO	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BQ	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BS	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	BU	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	BW	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	BY	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	CN	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CP	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CR	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	CT	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CV	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	CX	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	DN	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DP	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	DR	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	DT	430	Total	C	N	O	S	0	0
			3328	2102	567	636	23		
2	DV	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	DX	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	EM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	EO	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	EQ	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	ES	433	Total	C	N	O	S	0	0
			3351	2114	570	644	23		
2	EU	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	EW	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	FM	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	FO	434	Total	C	N	O	S	0	0
			3360	2119	571	647	23		
2	FQ	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	FS	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	FU	429	Total	C	N	O	S	0	0
			3322	2098	566	635	23		
2	FW	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	GM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GO	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GQ	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	GS	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GU	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	GW	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HO	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	HQ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	HS	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	HU	431	Total	C	N	O	S	0	0
			3336	2106	568	639	23		
2	HW	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	HY	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IO	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	IQ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IS	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IU	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	IW	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	IY	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	JP	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	JR	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	JT	432	Total	C	N	O	S	0	0
			3342	2110	569	640	23		
2	JV	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	JX	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	JZ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KP	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	KR	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	KT	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	KV	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	KX	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	KZ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LP	429	Total	C	N	O	S	0	0
			3322	2097	566	637	22		
2	LR	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LT	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LV	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LX	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	LZ	432	Total	C	N	O	S	0	0
			3346	2112	569	642	23		
2	MO	437	Total	C	N	O	S	0	0
			3379	2133	575	647	24		
2	MQ	436	Total	C	N	O	S	0	0
			3368	2124	573	647	24		
2	MS	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MU	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MW	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	MY	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	PO	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PQ	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PS	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	PU	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	PW	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	PY	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	QN	429	Total	C	N	O	S	0	0
			3323	2100	566	634	23		
2	QP	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	QR	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	QT	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	QV	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	QX	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	RN	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RP	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RR	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	RT	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	RV	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	RX	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SM	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	SO	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SQ	431	Total	C	N	O	S	0	0
			3335	2106	568	638	23		
2	SS	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	SU	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	SW	432	Total	C	N	O	S	0	0
			3343	2110	569	641	23		
2	TM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TO	428	Total	C	N	O	S	0	0
			3314	2093	565	634	22		
2	TQ	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	TS	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	TU	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	TW	433	Total	C	N	O	S	0	0
			3353	2117	570	643	23		
2	UM	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UO	429	Total	C	N	O	S	0	0
			3322	2097	566	637	22		
2	UQ	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	US	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	UU	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	UW	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	VO	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VQ	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VS	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	VU	432	Total	C	N	O	S	0	0
			3342	2109	569	641	23		
2	VW	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	VY	434	Total	C	N	O	S	0	0
			3360	2119	571	647	23		
2	WO	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WQ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WS	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WU	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	WW	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	WY	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NO	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NQ	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	NS	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NU	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NW	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	NY	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	OO	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	OQ	431	Total	C	N	O	S	0	0
			3337	2107	568	639	23		
2	OS	439	Total	C	N	O	S	0	0
			3394	2141	577	652	24		
2	OU	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	OW	430	Total	C	N	O	S	0	0
			3329	2103	567	636	23		
2	OY	433	Total	C	N	O	S	0	0
			3352	2115	570	644	23		

- Molecule 3 is a protein called CFAP20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	X	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XA	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XB	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XC	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XD	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XE	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XF	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XG	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XH	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	XI	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XJ	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XK	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		
3	XL	183	Total	C	N	O	S	0	0
			1510	965	264	270	11		

- Molecule 4 is a protein called PACRGA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	XM	259	Total	C	N	O	S	0	0
			2045	1307	360	370	8		
4	XO	260	Total	C	N	O	S	0	0
			2053	1311	361	373	8		
4	XQ	260	Total	C	N	O	S	0	0
			2053	1311	361	373	8		
4	XR	260	Total	C	N	O	S	0	0
			2056	1313	364	371	8		
4	XT	260	Total	C	N	O	S	0	0
			2053	1311	361	373	8		
4	XV	260	Total	C	N	O	S	0	0
			2053	1311	361	373	8		
4	XW	260	Total	C	N	O	S	0	0
			2056	1313	364	371	8		

- Molecule 5 is a protein called PACRGB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	XN	269	Total	C	N	O	S	0	0
			2116	1359	366	384	7		
5	XP	269	Total	C	N	O	S	0	0
			2116	1359	366	384	7		
5	XS	269	Total	C	N	O	S	0	0
			2116	1359	366	384	7		
5	XU	269	Total	C	N	O	S	0	0
			2116	1359	366	384	7		

- Molecule 6 is a protein called CCDC81.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	0A	257	Total	C	N	O	S	0	0
			2004	1261	359	371	13		
6	0	257	Total	C	N	O	S	0	0
			2004	1261	359	371	13		
6	0B	257	Total	C	N	O	S	0	0
			2004	1261	359	371	13		

- Molecule 7 is a protein called CFAP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	0C	121	Total	C	N	O	S	0	0
			935	584	159	188	4		
7	0D	354	Total	C	N	O	S	0	0
			2723	1683	492	537	11		
7	0E	354	Total	C	N	O	S	0	0
			2723	1683	492	537	11		

- Molecule 8 is a protein called CFAP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	0F	176	Total	C	N	O	S	0	0
			1439	859	288	280	12		
8	0I	285	Total	C	N	O	S	0	0
			2369	1421	471	459	18		
8	0H	349	Total	C	N	O	S	0	0
			2955	1772	596	570	17		
8	0K	28	Total	C	N	O		0	0
			229	146	41	42			
8	9A	226	Total	C	N	O	S	0	0
			1906	1147	379	373	7		
8	0G	444	Total	C	N	O	S	0	0
			3711	2221	751	718	21		
8	0J	449	Total	C	N	O	S	0	0
			3757	2255	754	727	21		

- Molecule 9 is a protein called CFAP52.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	0L	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0M	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	0N	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0O	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0P	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	0Q	624	Total	C	N	O	S	0	0
			4757	2973	844	908	32		
9	9B	310	Total	C	N	O	S	0	0
			2357	1482	416	445	14		

- Molecule 10 is a protein called CFAP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	0R	309	Total	C	N	O	S	0	0
			2628	1579	535	501	13		
10	0T	221	Total	C	N	O	S	0	0
			1874	1148	360	359	7		
10	0S	460	Total	C	N	O	S	0	0
			3908	2370	779	743	16		

- Molecule 11 is a protein called CFAP67A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	0U	333	Total	C	N	O	S	0	0
			2570	1621	437	495	17		
11	0V	333	Total	C	N	O	S	0	0
			2570	1621	437	495	17		

- Molecule 12 is a protein called CFAP67B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	0W	339	Total	C	N	O	S	0	0
			2595	1647	427	501	20		
12	0X	339	Total	C	N	O	S	0	0
			2595	1647	427	501	20		

- Molecule 13 is a protein called CFAP106A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0Y	233	Total	C	N	O	S	0	0
			1836	1152	334	345	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	0Z	235	Total	C	N	O	S	0	0
			1849	1160	337	347	5		
13	0a	233	Total	C	N	O	S	0	0
			1836	1152	334	345	5		
13	0b	235	Total	C	N	O	S	0	0
			1849	1160	337	347	5		

- Molecule 14 is a protein called CFAP106B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	0c	237	Total	C	N	O	S	0	0
			1929	1221	337	362	9		
14	0d	265	Total	C	N	O	S	0	0
			2150	1359	378	404	9		
14	0e	265	Total	C	N	O	S	0	0
			2150	1359	378	404	9		

- Molecule 15 is a protein called CFAP107.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	0f	160	Total	C	N	O	S	0	0
			1257	783	222	241	11		
15	0g	160	Total	C	N	O	S	0	0
			1257	783	222	241	11		
15	0h	30	Total	C	N	O	S	0	0
			218	137	34	46	1		

- Molecule 16 is a protein called CFAP115.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	0i	180	Total	C	N	O	S	0	0
			1463	930	264	263	6		
16	0j	688	Total	C	N	O	S	0	0
			5411	3423	987	975	26		
16	0l	640	Total	C	N	O	S	0	0
			5045	3192	918	914	21		
16	0k	710	Total	C	N	O	S	0	0
			5599	3537	1026	1009	27		

- Molecule 17 is a protein called CFAP127.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	0m	142	Total	C	N	O	S	0	0
			1155	704	220	227	4		
17	0n	406	Total	C	N	O	S	0	0
			3388	2054	668	654	12		
17	0o	406	Total	C	N	O	S	0	0
			3388	2054	668	654	12		
17	9C	20	Total	C	N	O		0	0
			171	107	35	29			

- Molecule 18 is a protein called CFAP141.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	0p	108	Total	C	N	O	S	0	0
			906	557	177	169	3		
18	0q	108	Total	C	N	O	S	0	0
			906	557	177	169	3		

- Molecule 19 is a protein called CFAP143.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	0r	254	Total	C	N	O	S	0	0
			2033	1246	376	396	15		
19	0s	254	Total	C	N	O	S	0	0
			2033	1246	376	396	15		

- Molecule 20 is a protein called CFAP161.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	0t	262	Total	C	N	O	S	0	0
			2062	1298	358	388	18		
20	0u	227	Total	C	N	O	S	0	0
			1769	1117	306	330	16		
20	9D	227	Total	C	N	O	S	0	0
			1769	1117	306	330	16		

- Molecule 21 is a protein called CFAP210.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0w	449	Total	C	N	O	S	0	0
			3715	2242	741	724	8		
21	0v	73	Total	C	N	O		0	0
			582	351	115	116			

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Mol	Chain	Residues	Atoms					AltConf	Trace
21	0y	111	Total	C	N	O	S	0	0
			906	556	175	172	3		
21	0x	490	Total	C	N	O	S	0	0
			4059	2455	802	792	10		

- Molecule 22 is a protein called DMIP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0z	143	Total	C	N	O	S	0	0
			1160	716	220	219	5		
22	1w	180	Total	C	N	O	S	0	0
			1481	915	278	281	7		
22	1x	206	Total	C	N	O	S	0	0
			1680	1031	322	315	12		
22	2A	143	Total	C	N	O	S	0	0
			1157	715	220	217	5		
22	1y	180	Total	C	N	O	S	0	0
			1481	915	278	281	7		
22	1z	206	Total	C	N	O	S	0	0
			1680	1031	322	315	12		

- Molecule 23 is a protein called RIB43.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1A	270	Total	C	N	O	S	0	0
			2286	1390	449	436	11		
23	1D	54	Total	C	N	O	S	0	0
			464	285	91	85	3		
23	1E	362	Total	C	N	O	S	0	0
			3050	1855	590	590	15		
23	1C	195	Total	C	N	O	S	0	0
			1667	1015	321	322	9		
23	1G	74	Total	C	N	O	S	0	0
			635	387	120	124	4		
23	1F	362	Total	C	N	O	S	0	0
			3050	1855	590	590	15		
23	1B	348	Total	C	N	O	S	0	0
			2953	1796	574	568	15		

- Molecule 24 is a protein called RIB72A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1H	588	Total	C	N	O	S	0	0
			4698	2967	812	900	19		
24	1I	659	Total	C	N	O	S	0	0
			5276	3326	920	1003	27		
24	1J	670	Total	C	N	O	S	0	0
			5356	3372	940	1018	26		
24	1K	588	Total	C	N	O	S	0	0
			4697	2966	812	900	19		
24	1L	659	Total	C	N	O	S	0	0
			5276	3326	920	1003	27		
24	1M	670	Total	C	N	O	S	0	0
			5356	3372	940	1018	26		
24	1N	588	Total	C	N	O	S	0	0
			4697	2966	812	900	19		

- Molecule 25 is a protein called RIB72B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1O	710	Total	C	N	O	S	0	0
			5751	3614	1021	1096	20		
25	1P	710	Total	C	N	O	S	0	0
			5751	3614	1021	1096	20		

- Molecule 26 is a protein called RIB72C.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1Q	655	Total	C	N	O	S	0	0
			5263	3323	927	988	25		
26	1R	655	Total	C	N	O	S	0	0
			5263	3323	927	988	25		

- Molecule 27 is a protein called RIB72D.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1S	726	Total	C	N	O	S	0	0
			5834	3696	1029	1076	33		
27	1T	726	Total	C	N	O	S	0	0
			5834	3696	1029	1076	33		
27	9E	222	Total	C	N	O	S	0	0
			1787	1125	315	335	12		

- Molecule 28 is a protein called STOP family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1U	120	Total	C	N	O	S	0	0
			942	594	162	181	5		
28	1V	168	Total	C	N	O	S	0	0
			1313	823	230	250	10		
28	1X	120	Total	C	N	O	S	0	0
			942	594	162	181	5		
28	1a	57	Total	C	N	O	S	0	0
			446	279	80	84	3		
28	1b	168	Total	C	N	O	S	0	0
			1313	823	230	250	10		
28	1d	120	Total	C	N	O	S	0	0
			942	594	162	181	5		
28	1e	168	Total	C	N	O	S	0	0
			1313	823	230	250	10		
28	1g	120	Total	C	N	O	S	0	0
			942	594	162	181	5		
28	4V	62	Total	C	N	O	S	0	0
			486	305	86	91	4		
28	1W	48	Total	C	N	O	S	0	0
			371	229	68	69	5		
28	1Z	169	Total	C	N	O	S	0	0
			1325	829	237	252	7		
28	1c	168	Total	C	N	O	S	0	0
			1313	823	230	250	10		
28	9F	35	Total	C	N	O	S	0	0
			263	162	50	46	5		
28	1f	48	Total	C	N	O	S	0	0
			371	229	68	69	5		
28	1i	155	Total	C	N	O	S	0	0
			1218	767	214	230	7		
28	4X	188	Total	C	N	O	S	0	0
			1474	927	255	283	9		
28	4W	222	Total	C	N	O	S	0	0
			1742	1095	304	332	11		
28	1Y	241	Total	C	N	O	S	0	0
			1893	1188	334	360	11		
28	1h	229	Total	C	N	O	S	0	0
			1798	1132	313	342	11		

There are 342 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1U	52	LEU	ILE	conflict	UNP A0A504XB09
1U	83	GLU	ASP	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1U	86	GLN	LYS	conflict	UNP A0A504XB09
1U	128	ALA	THR	conflict	UNP A0A504XB09
1U	139	ARG	PRO	conflict	UNP A0A504XB09
1U	171	THR	ALA	conflict	UNP A0A504XB09
1U	186	ASN	SER	conflict	UNP A0A504XB09
1U	192	PRO	GLN	conflict	UNP A0A504XB09
1U	206	THR	VAL	conflict	UNP A0A504XB09
1U	207	LYS	GLN	conflict	UNP A0A504XB09
1U	209	ILE	VAL	conflict	UNP A0A504XB09
1U	220	ALA	THR	conflict	UNP A0A504XB09
1U	221	SER	VAL	conflict	UNP A0A504XB09
1U	223	SER	GLU	conflict	UNP A0A504XB09
1U	230	VAL	MET	conflict	UNP A0A504XB09
1U	239	THR	ALA	conflict	UNP A0A504XB09
1U	243	ILE	THR	conflict	UNP A0A504XB09
1U	252	ILE	LEU	conflict	UNP A0A504XB09
1V	52	LEU	ILE	conflict	UNP A0A504XB09
1V	83	GLU	ASP	conflict	UNP A0A504XB09
1V	86	GLN	LYS	conflict	UNP A0A504XB09
1V	128	ALA	THR	conflict	UNP A0A504XB09
1V	139	ARG	PRO	conflict	UNP A0A504XB09
1V	171	THR	ALA	conflict	UNP A0A504XB09
1V	186	ASN	SER	conflict	UNP A0A504XB09
1V	192	PRO	GLN	conflict	UNP A0A504XB09
1V	206	THR	VAL	conflict	UNP A0A504XB09
1V	207	LYS	GLN	conflict	UNP A0A504XB09
1V	209	ILE	VAL	conflict	UNP A0A504XB09
1V	220	ALA	THR	conflict	UNP A0A504XB09
1V	221	SER	VAL	conflict	UNP A0A504XB09
1V	223	SER	GLU	conflict	UNP A0A504XB09
1V	230	VAL	MET	conflict	UNP A0A504XB09
1V	239	THR	ALA	conflict	UNP A0A504XB09
1V	243	ILE	THR	conflict	UNP A0A504XB09
1V	252	ILE	LEU	conflict	UNP A0A504XB09
1X	52	LEU	ILE	conflict	UNP A0A504XB09
1X	83	GLU	ASP	conflict	UNP A0A504XB09
1X	86	GLN	LYS	conflict	UNP A0A504XB09
1X	128	ALA	THR	conflict	UNP A0A504XB09
1X	139	ARG	PRO	conflict	UNP A0A504XB09
1X	171	THR	ALA	conflict	UNP A0A504XB09
1X	186	ASN	SER	conflict	UNP A0A504XB09
1X	192	PRO	GLN	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1X	206	THR	VAL	conflict	UNP A0A504XB09
1X	207	LYS	GLN	conflict	UNP A0A504XB09
1X	209	ILE	VAL	conflict	UNP A0A504XB09
1X	220	ALA	THR	conflict	UNP A0A504XB09
1X	221	SER	VAL	conflict	UNP A0A504XB09
1X	223	SER	GLU	conflict	UNP A0A504XB09
1X	230	VAL	MET	conflict	UNP A0A504XB09
1X	239	THR	ALA	conflict	UNP A0A504XB09
1X	243	ILE	THR	conflict	UNP A0A504XB09
1X	252	ILE	LEU	conflict	UNP A0A504XB09
1a	52	LEU	ILE	conflict	UNP A0A504XB09
1a	83	GLU	ASP	conflict	UNP A0A504XB09
1a	86	GLN	LYS	conflict	UNP A0A504XB09
1a	128	ALA	THR	conflict	UNP A0A504XB09
1a	139	ARG	PRO	conflict	UNP A0A504XB09
1a	171	THR	ALA	conflict	UNP A0A504XB09
1a	186	ASN	SER	conflict	UNP A0A504XB09
1a	192	PRO	GLN	conflict	UNP A0A504XB09
1a	206	THR	VAL	conflict	UNP A0A504XB09
1a	207	LYS	GLN	conflict	UNP A0A504XB09
1a	209	ILE	VAL	conflict	UNP A0A504XB09
1a	220	ALA	THR	conflict	UNP A0A504XB09
1a	221	SER	VAL	conflict	UNP A0A504XB09
1a	223	SER	GLU	conflict	UNP A0A504XB09
1a	230	VAL	MET	conflict	UNP A0A504XB09
1a	239	THR	ALA	conflict	UNP A0A504XB09
1a	243	ILE	THR	conflict	UNP A0A504XB09
1a	252	ILE	LEU	conflict	UNP A0A504XB09
1b	52	LEU	ILE	conflict	UNP A0A504XB09
1b	83	GLU	ASP	conflict	UNP A0A504XB09
1b	86	GLN	LYS	conflict	UNP A0A504XB09
1b	128	ALA	THR	conflict	UNP A0A504XB09
1b	139	ARG	PRO	conflict	UNP A0A504XB09
1b	171	THR	ALA	conflict	UNP A0A504XB09
1b	186	ASN	SER	conflict	UNP A0A504XB09
1b	192	PRO	GLN	conflict	UNP A0A504XB09
1b	206	THR	VAL	conflict	UNP A0A504XB09
1b	207	LYS	GLN	conflict	UNP A0A504XB09
1b	209	ILE	VAL	conflict	UNP A0A504XB09
1b	220	ALA	THR	conflict	UNP A0A504XB09
1b	221	SER	VAL	conflict	UNP A0A504XB09
1b	223	SER	GLU	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1b	230	VAL	MET	conflict	UNP A0A504XB09
1b	239	THR	ALA	conflict	UNP A0A504XB09
1b	243	ILE	THR	conflict	UNP A0A504XB09
1b	252	ILE	LEU	conflict	UNP A0A504XB09
1d	52	LEU	ILE	conflict	UNP A0A504XB09
1d	83	GLU	ASP	conflict	UNP A0A504XB09
1d	86	GLN	LYS	conflict	UNP A0A504XB09
1d	128	ALA	THR	conflict	UNP A0A504XB09
1d	139	ARG	PRO	conflict	UNP A0A504XB09
1d	171	THR	ALA	conflict	UNP A0A504XB09
1d	186	ASN	SER	conflict	UNP A0A504XB09
1d	192	PRO	GLN	conflict	UNP A0A504XB09
1d	206	THR	VAL	conflict	UNP A0A504XB09
1d	207	LYS	GLN	conflict	UNP A0A504XB09
1d	209	ILE	VAL	conflict	UNP A0A504XB09
1d	220	ALA	THR	conflict	UNP A0A504XB09
1d	221	SER	VAL	conflict	UNP A0A504XB09
1d	223	SER	GLU	conflict	UNP A0A504XB09
1d	230	VAL	MET	conflict	UNP A0A504XB09
1d	239	THR	ALA	conflict	UNP A0A504XB09
1d	243	ILE	THR	conflict	UNP A0A504XB09
1d	252	ILE	LEU	conflict	UNP A0A504XB09
1e	52	LEU	ILE	conflict	UNP A0A504XB09
1e	83	GLU	ASP	conflict	UNP A0A504XB09
1e	86	GLN	LYS	conflict	UNP A0A504XB09
1e	128	ALA	THR	conflict	UNP A0A504XB09
1e	139	ARG	PRO	conflict	UNP A0A504XB09
1e	171	THR	ALA	conflict	UNP A0A504XB09
1e	186	ASN	SER	conflict	UNP A0A504XB09
1e	192	PRO	GLN	conflict	UNP A0A504XB09
1e	206	THR	VAL	conflict	UNP A0A504XB09
1e	207	LYS	GLN	conflict	UNP A0A504XB09
1e	209	ILE	VAL	conflict	UNP A0A504XB09
1e	220	ALA	THR	conflict	UNP A0A504XB09
1e	221	SER	VAL	conflict	UNP A0A504XB09
1e	223	SER	GLU	conflict	UNP A0A504XB09
1e	230	VAL	MET	conflict	UNP A0A504XB09
1e	239	THR	ALA	conflict	UNP A0A504XB09
1e	243	ILE	THR	conflict	UNP A0A504XB09
1e	252	ILE	LEU	conflict	UNP A0A504XB09
1g	52	LEU	ILE	conflict	UNP A0A504XB09
1g	83	GLU	ASP	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1g	86	GLN	LYS	conflict	UNP A0A504XB09
1g	128	ALA	THR	conflict	UNP A0A504XB09
1g	139	ARG	PRO	conflict	UNP A0A504XB09
1g	171	THR	ALA	conflict	UNP A0A504XB09
1g	186	ASN	SER	conflict	UNP A0A504XB09
1g	192	PRO	GLN	conflict	UNP A0A504XB09
1g	206	THR	VAL	conflict	UNP A0A504XB09
1g	207	LYS	GLN	conflict	UNP A0A504XB09
1g	209	ILE	VAL	conflict	UNP A0A504XB09
1g	220	ALA	THR	conflict	UNP A0A504XB09
1g	221	SER	VAL	conflict	UNP A0A504XB09
1g	223	SER	GLU	conflict	UNP A0A504XB09
1g	230	VAL	MET	conflict	UNP A0A504XB09
1g	239	THR	ALA	conflict	UNP A0A504XB09
1g	243	ILE	THR	conflict	UNP A0A504XB09
1g	252	ILE	LEU	conflict	UNP A0A504XB09
4V	52	LEU	ILE	conflict	UNP A0A504XB09
4V	83	GLU	ASP	conflict	UNP A0A504XB09
4V	86	GLN	LYS	conflict	UNP A0A504XB09
4V	128	ALA	THR	conflict	UNP A0A504XB09
4V	139	ARG	PRO	conflict	UNP A0A504XB09
4V	171	THR	ALA	conflict	UNP A0A504XB09
4V	186	ASN	SER	conflict	UNP A0A504XB09
4V	192	PRO	GLN	conflict	UNP A0A504XB09
4V	206	THR	VAL	conflict	UNP A0A504XB09
4V	207	LYS	GLN	conflict	UNP A0A504XB09
4V	209	ILE	VAL	conflict	UNP A0A504XB09
4V	220	ALA	THR	conflict	UNP A0A504XB09
4V	221	SER	VAL	conflict	UNP A0A504XB09
4V	223	SER	GLU	conflict	UNP A0A504XB09
4V	230	VAL	MET	conflict	UNP A0A504XB09
4V	239	THR	ALA	conflict	UNP A0A504XB09
4V	243	ILE	THR	conflict	UNP A0A504XB09
4V	252	ILE	LEU	conflict	UNP A0A504XB09
1W	52	LEU	ILE	conflict	UNP A0A504XB09
1W	83	GLU	ASP	conflict	UNP A0A504XB09
1W	86	GLN	LYS	conflict	UNP A0A504XB09
1W	128	ALA	THR	conflict	UNP A0A504XB09
1W	139	ARG	PRO	conflict	UNP A0A504XB09
1W	171	THR	ALA	conflict	UNP A0A504XB09
1W	186	ASN	SER	conflict	UNP A0A504XB09
1W	192	PRO	GLN	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1W	206	THR	VAL	conflict	UNP A0A504XB09
1W	207	LYS	GLN	conflict	UNP A0A504XB09
1W	209	ILE	VAL	conflict	UNP A0A504XB09
1W	220	ALA	THR	conflict	UNP A0A504XB09
1W	221	SER	VAL	conflict	UNP A0A504XB09
1W	223	SER	GLU	conflict	UNP A0A504XB09
1W	230	VAL	MET	conflict	UNP A0A504XB09
1W	239	THR	ALA	conflict	UNP A0A504XB09
1W	243	ILE	THR	conflict	UNP A0A504XB09
1W	252	ILE	LEU	conflict	UNP A0A504XB09
1Z	52	LEU	ILE	conflict	UNP A0A504XB09
1Z	83	GLU	ASP	conflict	UNP A0A504XB09
1Z	86	GLN	LYS	conflict	UNP A0A504XB09
1Z	128	ALA	THR	conflict	UNP A0A504XB09
1Z	139	ARG	PRO	conflict	UNP A0A504XB09
1Z	171	THR	ALA	conflict	UNP A0A504XB09
1Z	186	ASN	SER	conflict	UNP A0A504XB09
1Z	192	PRO	GLN	conflict	UNP A0A504XB09
1Z	206	THR	VAL	conflict	UNP A0A504XB09
1Z	207	LYS	GLN	conflict	UNP A0A504XB09
1Z	209	ILE	VAL	conflict	UNP A0A504XB09
1Z	220	ALA	THR	conflict	UNP A0A504XB09
1Z	221	SER	VAL	conflict	UNP A0A504XB09
1Z	223	SER	GLU	conflict	UNP A0A504XB09
1Z	230	VAL	MET	conflict	UNP A0A504XB09
1Z	239	THR	ALA	conflict	UNP A0A504XB09
1Z	243	ILE	THR	conflict	UNP A0A504XB09
1Z	252	ILE	LEU	conflict	UNP A0A504XB09
1c	52	LEU	ILE	conflict	UNP A0A504XB09
1c	83	GLU	ASP	conflict	UNP A0A504XB09
1c	86	GLN	LYS	conflict	UNP A0A504XB09
1c	128	ALA	THR	conflict	UNP A0A504XB09
1c	139	ARG	PRO	conflict	UNP A0A504XB09
1c	171	THR	ALA	conflict	UNP A0A504XB09
1c	186	ASN	SER	conflict	UNP A0A504XB09
1c	192	PRO	GLN	conflict	UNP A0A504XB09
1c	206	THR	VAL	conflict	UNP A0A504XB09
1c	207	LYS	GLN	conflict	UNP A0A504XB09
1c	209	ILE	VAL	conflict	UNP A0A504XB09
1c	220	ALA	THR	conflict	UNP A0A504XB09
1c	221	SER	VAL	conflict	UNP A0A504XB09
1c	223	SER	GLU	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1c	230	VAL	MET	conflict	UNP A0A504XB09
1c	239	THR	ALA	conflict	UNP A0A504XB09
1c	243	ILE	THR	conflict	UNP A0A504XB09
1c	252	ILE	LEU	conflict	UNP A0A504XB09
9F	52	LEU	ILE	conflict	UNP A0A504XB09
9F	83	GLU	ASP	conflict	UNP A0A504XB09
9F	86	GLN	LYS	conflict	UNP A0A504XB09
9F	128	ALA	THR	conflict	UNP A0A504XB09
9F	139	ARG	PRO	conflict	UNP A0A504XB09
9F	171	THR	ALA	conflict	UNP A0A504XB09
9F	186	ASN	SER	conflict	UNP A0A504XB09
9F	192	PRO	GLN	conflict	UNP A0A504XB09
9F	206	THR	VAL	conflict	UNP A0A504XB09
9F	207	LYS	GLN	conflict	UNP A0A504XB09
9F	209	ILE	VAL	conflict	UNP A0A504XB09
9F	220	ALA	THR	conflict	UNP A0A504XB09
9F	221	SER	VAL	conflict	UNP A0A504XB09
9F	223	SER	GLU	conflict	UNP A0A504XB09
9F	230	VAL	MET	conflict	UNP A0A504XB09
9F	239	THR	ALA	conflict	UNP A0A504XB09
9F	243	ILE	THR	conflict	UNP A0A504XB09
9F	252	ILE	LEU	conflict	UNP A0A504XB09
1f	52	LEU	ILE	conflict	UNP A0A504XB09
1f	83	GLU	ASP	conflict	UNP A0A504XB09
1f	86	GLN	LYS	conflict	UNP A0A504XB09
1f	128	ALA	THR	conflict	UNP A0A504XB09
1f	139	ARG	PRO	conflict	UNP A0A504XB09
1f	171	THR	ALA	conflict	UNP A0A504XB09
1f	186	ASN	SER	conflict	UNP A0A504XB09
1f	192	PRO	GLN	conflict	UNP A0A504XB09
1f	206	THR	VAL	conflict	UNP A0A504XB09
1f	207	LYS	GLN	conflict	UNP A0A504XB09
1f	209	ILE	VAL	conflict	UNP A0A504XB09
1f	220	ALA	THR	conflict	UNP A0A504XB09
1f	221	SER	VAL	conflict	UNP A0A504XB09
1f	223	SER	GLU	conflict	UNP A0A504XB09
1f	230	VAL	MET	conflict	UNP A0A504XB09
1f	239	THR	ALA	conflict	UNP A0A504XB09
1f	243	ILE	THR	conflict	UNP A0A504XB09
1f	252	ILE	LEU	conflict	UNP A0A504XB09
1i	52	LEU	ILE	conflict	UNP A0A504XB09
1i	83	GLU	ASP	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1i	86	GLN	LYS	conflict	UNP A0A504XB09
1i	128	ALA	THR	conflict	UNP A0A504XB09
1i	139	ARG	PRO	conflict	UNP A0A504XB09
1i	171	THR	ALA	conflict	UNP A0A504XB09
1i	186	ASN	SER	conflict	UNP A0A504XB09
1i	192	PRO	GLN	conflict	UNP A0A504XB09
1i	206	THR	VAL	conflict	UNP A0A504XB09
1i	207	LYS	GLN	conflict	UNP A0A504XB09
1i	209	ILE	VAL	conflict	UNP A0A504XB09
1i	220	ALA	THR	conflict	UNP A0A504XB09
1i	221	SER	VAL	conflict	UNP A0A504XB09
1i	223	SER	GLU	conflict	UNP A0A504XB09
1i	230	VAL	MET	conflict	UNP A0A504XB09
1i	239	THR	ALA	conflict	UNP A0A504XB09
1i	243	ILE	THR	conflict	UNP A0A504XB09
1i	252	ILE	LEU	conflict	UNP A0A504XB09
4X	52	LEU	ILE	conflict	UNP A0A504XB09
4X	83	GLU	ASP	conflict	UNP A0A504XB09
4X	86	GLN	LYS	conflict	UNP A0A504XB09
4X	128	ALA	THR	conflict	UNP A0A504XB09
4X	139	ARG	PRO	conflict	UNP A0A504XB09
4X	171	THR	ALA	conflict	UNP A0A504XB09
4X	186	ASN	SER	conflict	UNP A0A504XB09
4X	192	PRO	GLN	conflict	UNP A0A504XB09
4X	206	THR	VAL	conflict	UNP A0A504XB09
4X	207	LYS	GLN	conflict	UNP A0A504XB09
4X	209	ILE	VAL	conflict	UNP A0A504XB09
4X	220	ALA	THR	conflict	UNP A0A504XB09
4X	221	SER	VAL	conflict	UNP A0A504XB09
4X	223	SER	GLU	conflict	UNP A0A504XB09
4X	230	VAL	MET	conflict	UNP A0A504XB09
4X	239	THR	ALA	conflict	UNP A0A504XB09
4X	243	ILE	THR	conflict	UNP A0A504XB09
4X	252	ILE	LEU	conflict	UNP A0A504XB09
4W	52	LEU	ILE	conflict	UNP A0A504XB09
4W	83	GLU	ASP	conflict	UNP A0A504XB09
4W	86	GLN	LYS	conflict	UNP A0A504XB09
4W	128	ALA	THR	conflict	UNP A0A504XB09
4W	139	ARG	PRO	conflict	UNP A0A504XB09
4W	171	THR	ALA	conflict	UNP A0A504XB09
4W	186	ASN	SER	conflict	UNP A0A504XB09
4W	192	PRO	GLN	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
4W	206	THR	VAL	conflict	UNP A0A504XB09
4W	207	LYS	GLN	conflict	UNP A0A504XB09
4W	209	ILE	VAL	conflict	UNP A0A504XB09
4W	220	ALA	THR	conflict	UNP A0A504XB09
4W	221	SER	VAL	conflict	UNP A0A504XB09
4W	223	SER	GLU	conflict	UNP A0A504XB09
4W	230	VAL	MET	conflict	UNP A0A504XB09
4W	239	THR	ALA	conflict	UNP A0A504XB09
4W	243	ILE	THR	conflict	UNP A0A504XB09
4W	252	ILE	LEU	conflict	UNP A0A504XB09
1Y	52	LEU	ILE	conflict	UNP A0A504XB09
1Y	83	GLU	ASP	conflict	UNP A0A504XB09
1Y	86	GLN	LYS	conflict	UNP A0A504XB09
1Y	128	ALA	THR	conflict	UNP A0A504XB09
1Y	139	ARG	PRO	conflict	UNP A0A504XB09
1Y	171	THR	ALA	conflict	UNP A0A504XB09
1Y	186	ASN	SER	conflict	UNP A0A504XB09
1Y	192	PRO	GLN	conflict	UNP A0A504XB09
1Y	206	THR	VAL	conflict	UNP A0A504XB09
1Y	207	LYS	GLN	conflict	UNP A0A504XB09
1Y	209	ILE	VAL	conflict	UNP A0A504XB09
1Y	220	ALA	THR	conflict	UNP A0A504XB09
1Y	221	SER	VAL	conflict	UNP A0A504XB09
1Y	223	SER	GLU	conflict	UNP A0A504XB09
1Y	230	VAL	MET	conflict	UNP A0A504XB09
1Y	239	THR	ALA	conflict	UNP A0A504XB09
1Y	243	ILE	THR	conflict	UNP A0A504XB09
1Y	252	ILE	LEU	conflict	UNP A0A504XB09
1h	52	LEU	ILE	conflict	UNP A0A504XB09
1h	83	GLU	ASP	conflict	UNP A0A504XB09
1h	86	GLN	LYS	conflict	UNP A0A504XB09
1h	128	ALA	THR	conflict	UNP A0A504XB09
1h	139	ARG	PRO	conflict	UNP A0A504XB09
1h	171	THR	ALA	conflict	UNP A0A504XB09
1h	186	ASN	SER	conflict	UNP A0A504XB09
1h	192	PRO	GLN	conflict	UNP A0A504XB09
1h	206	THR	VAL	conflict	UNP A0A504XB09
1h	207	LYS	GLN	conflict	UNP A0A504XB09
1h	209	ILE	VAL	conflict	UNP A0A504XB09
1h	220	ALA	THR	conflict	UNP A0A504XB09
1h	221	SER	VAL	conflict	UNP A0A504XB09
1h	223	SER	GLU	conflict	UNP A0A504XB09

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Chain	Residue	Modelled	Actual	Comment	Reference
1h	230	VAL	MET	conflict	UNP A0A504XB09
1h	239	THR	ALA	conflict	UNP A0A504XB09
1h	243	ILE	THR	conflict	UNP A0A504XB09
1h	252	ILE	LEU	conflict	UNP A0A504XB09

- Molecule 29 is a protein called DMIP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	1j	113	Total	C	N	O	S	0	0
			909	584	153	168	4		
29	1k	103	Total	C	N	O	S	0	0
			801	502	140	157	2		
29	1l	113	Total	C	N	O	S	0	0
			909	584	153	168	4		
29	1m	103	Total	C	N	O	S	0	0
			801	502	140	157	2		
29	1n	113	Total	C	N	O	S	0	0
			909	584	153	168	4		
29	9G	53	Total	C	N	O	S	0	0
			420	268	72	78	2		

- Molecule 30 is a protein called DMIP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	1o	128	Total	C	N	O	S	0	0
			1035	645	193	192	5		
30	1p	128	Total	C	N	O	S	0	0
			1035	645	193	192	5		

- Molecule 31 is a protein called DMIP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1q	214	Total	C	N	O	S	0	0
			1679	1025	322	321	11		
31	1r	106	Total	C	N	O	S	0	0
			868	532	166	165	5		
31	1s	183	Total	C	N	O	S	0	0
			1446	884	273	277	12		
31	1t	214	Total	C	N	O	S	0	0
			1679	1025	322	321	11		
31	1u	106	Total	C	N	O	S	0	0
			868	532	166	165	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
31	1v	183	Total	C	N	O	S	0	0
			1446	884	273	277	12		
31	9H	75	Total	C	N	O	S	0	0
			618	372	125	116	5		

- Molecule 32 is a protein called DMIP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	2B	251	Total	C	N	O	S	0	0
			1977	1231	357	377	12		
32	2C	230	Total	C	N	O	S	0	0
			1814	1130	329	344	11		
32	2D	251	Total	C	N	O	S	0	0
			1977	1231	357	377	12		
32	2E	230	Total	C	N	O	S	0	0
			1814	1130	329	344	11		

- Molecule 33 is a protein called DMIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2F	284	Total	C	N	O	S	0	0
			2253	1411	411	418	13		
33	2G	283	Total	C	N	O	S	0	0
			2245	1407	409	416	13		
33	2H	288	Total	C	N	O	S	0	0
			2281	1428	416	424	13		
33	2I	243	Total	C	N	O	S	0	0
			1937	1208	355	363	11		
33	2J	283	Total	C	N	O	S	0	0
			2245	1407	409	416	13		
33	2K	288	Total	C	N	O	S	0	0
			2281	1428	416	424	13		
33	9I	243	Total	C	N	O	S	0	0
			1937	1208	355	363	11		

- Molecule 34 is a protein called DMIP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2L	172	Total	C	N	O	S	0	0
			1433	904	254	269	6		
34	2M	172	Total	C	N	O	S	0	0
			1433	904	254	269	6		

- Molecule 35 is a protein called DMIP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2N	135	Total	C	N	O	S	0	0
			1103	698	208	194	3		
35	2P	161	Total	C	N	O	S	0	0
			1324	827	251	240	6		
35	2O	274	Total	C	N	O	S	0	0
			2235	1404	420	402	9		

- Molecule 36 is a protein called DMIP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2Q	291	Total	C	N	O	S	0	0
			2320	1483	394	429	14		
36	2R	291	Total	C	N	O	S	0	0
			2320	1483	394	429	14		

- Molecule 37 is a protein called DMIP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2S	237	Total	C	N	O	S	0	0
			1798	1126	317	340	15		

- Molecule 38 is a protein called DMIP12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2U	229	Total	C	N	O	S	0	0
			1807	1111	329	355	12		
38	2V	109	Total	C	N	O	S	0	0
			870	530	167	169	4		
38	2W	109	Total	C	N	O	S	0	0
			870	530	167	169	4		

- Molecule 39 is a protein called DMIP13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2X	227	Total	C	N	O	S	0	0
			1774	1081	355	328	10		
39	2Y	227	Total	C	N	O	S	0	0
			1774	1081	355	328	10		

- Molecule 40 is a protein called DMIP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	2Z	283	Total	C	N	O	S	0	0
			2258	1427	412	414	5		
40	2a	283	Total	C	N	O	S	0	0
			2258	1427	412	414	5		

- Molecule 41 is a protein called DMIP15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	2b	121	Total	C	N	O	S	0	0
			1006	613	195	194	4		
41	2e	325	Total	C	N	O	S	0	0
			2735	1649	546	526	14		
41	2h	237	Total	C	N	O	S	0	0
			1978	1187	396	385	10		
41	2k	167	Total	C	N	O	S	0	0
			1369	834	266	262	7		
41	2n	42	Total	C	N	O		0	0
			361	219	72	70			
41	2o	287	Total	C	N	O	S	0	0
			2453	1473	490	478	12		
41	2d	245	Total	C	N	O	S	0	0
			2092	1254	418	408	12		
41	2f	325	Total	C	N	O	S	0	0
			2735	1649	546	526	14		
41	2g	52	Total	C	N	O	S	0	0
			454	275	89	88	2		
41	2j	149	Total	C	N	O	S	0	0
			1301	776	266	252	7		
41	2m	264	Total	C	N	O	S	0	0
			2228	1338	445	432	13		
41	2p	287	Total	C	N	O	S	0	0
			2453	1473	490	478	12		
41	2q	49	Total	C	N	O	S	0	0
			425	257	86	80	2		
41	2c	306	Total	C	N	O	S	0	0
			2599	1565	519	502	13		
41	2i	309	Total	C	N	O	S	0	0
			2615	1574	523	505	13		
41	2l	325	Total	C	N	O	S	0	0
			2735	1649	546	526	14		

- Molecule 42 is a protein called DMIP16.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	2r	315	Total	C	N	O	S	0	0
			2473	1564	439	460	10		
42	2s	315	Total	C	N	O	S	0	0
			2473	1564	439	460	10		

- Molecule 43 is a protein called DMIP17.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	2t	214	Total	C	N	O	S	0	0
			1713	1075	302	324	12		
43	2u	214	Total	C	N	O	S	0	0
			1713	1075	302	324	12		

- Molecule 44 is a protein called DMIP18.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2v	280	Total	C	N	O	S	0	0
			2264	1438	391	425	10		
44	2w	412	Total	C	N	O	S	0	0
			3291	2082	565	629	15		
44	2x	412	Total	C	N	O	S	0	0
			3291	2082	565	629	15		

- Molecule 45 is a protein called DMIP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2y	287	Total	C	N	O	S	0	0
			2316	1424	424	460	8		
45	3A	187	Total	C	N	O	S	0	0
			1435	890	257	287	1		
45	2z	409	Total	C	N	O	S	0	0
			3258	2010	596	644	8		

- Molecule 46 is a protein called DMIP20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3B	418	Total	C	N	O	S	0	0
			3308	2069	596	631	12		
46	3C	418	Total	C	N	O	S	0	0
			3308	2069	596	631	12		

- Molecule 47 is a protein called DMIP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3D	412	Total	C	N	O	S	0	0
			3212	1986	586	628	12		
47	3E	412	Total	C	N	O	S	0	0
			3212	1986	586	628	12		

- Molecule 48 is a protein called DMIP22.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	3I	80	Total	C	N	O	S	0	0
			640	400	114	122	4		
48	3F	155	Total	C	N	O	S	0	0
			1254	777	240	230	7		
48	3G	90	Total	C	N	O	S	0	0
			733	456	139	134	4		
48	3H	103	Total	C	N	O	S	0	0
			832	516	161	151	4		
48	3M	29	Total	C	N	O	S	0	0
			247	155	44	45	3		
48	3L	29	Total	C	N	O	S	0	0
			247	155	44	45	3		
48	9J	80	Total	C	N	O	S	0	0
			640	400	114	122	4		
48	3J	90	Total	C	N	O	S	0	0
			733	456	139	134	4		
48	3K	103	Total	C	N	O	S	0	0
			832	516	161	151	4		
48	3O	29	Total	C	N	O	S	0	0
			247	155	44	45	3		
48	3N	29	Total	C	N	O	S	0	0
			247	155	44	45	3		

- Molecule 49 is a protein called DMIP23.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3P	256	Total	C	N	O	S	0	0
			2002	1260	351	380	11		
49	3Q	490	Total	C	N	O	S	0	0
			3825	2406	666	735	18		
49	3R	490	Total	C	N	O	S	0	0
			3825	2406	666	735	18		

- Molecule 50 is a protein called DMIP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3S	25	Total	C	N	O	S	0	0
			182	109	36	33	4		
50	X1	39	Total	C	N	O	S	0	0
			304	183	58	63			
50	3T	64	Total	C	N	O	S	0	0
			486	292	94	96	4		

- Molecule 51 is a protein called DMIP25.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3U	140	Total	C	N	O	S	0	0
			1074	681	186	203	4		
51	3V	140	Total	C	N	O	S	0	0
			1074	681	186	203	4		

- Molecule 52 is a protein called DMIP26.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3X	202	Total	C	N	O	S	0	0
			1650	1025	305	309	11		
52	3W	153	Total	C	N	O	S	0	0
			1264	786	231	239	8		
52	3Y	49	Total	C	N	O	S	0	0
			386	239	74	70	3		

- Molecule 53 is a protein called DMIP27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3Z	181	Total	C	N	O	S	0	0
			1405	862	264	271	8		
53	3a	87	Total	C	N	O	S	0	0
			712	442	130	136	4		
53	4Y	181	Total	C	N	O	S	0	0
			1403	860	264	271	8		

- Molecule 54 is a protein called ArcMAP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3b	136	Total	C	N	O	S	0	0
			1126	695	204	223	4		
54	3c	136	Total	C	N	O	S	0	0
			1126	695	204	223	4		

- Molecule 55 is a protein called ArcMAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	3d	148	Total	C	N	O	S	0	0
			1240	765	229	240	6		
55	3e	148	Total	C	N	O	S	0	0
			1240	765	229	240	6		

- Molecule 56 is a protein called ArcMAP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	3f	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
56	3g	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
56	3h	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
56	3i	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
56	3j	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
56	3k	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		
56	3l	165	Total	C	N	O	S	0	0
			1408	857	263	280	8		

- Molecule 57 is a protein called ArcMAP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	3m	144	Total	C	N	O	S	0	0
			1216	745	236	231	4		
57	3n	144	Total	C	N	O	S	0	0
			1216	745	236	231	4		

- Molecule 58 is a protein called CFAP96.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	3o	55	Total	C	N	O	S	0	0
			459	293	79	85	2		
58	3p	161	Total	C	N	O	S	0	0
			1276	821	220	233	2		
58	4O	175	Total	C	N	O	S	0	0
			1399	899	245	253	2		
58	4a	154	Total	C	N	O	S	0	0
			1233	796	213	223	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	3q	148	Total	C	N	O	S	0	0
			1159	744	201	212	2		
58	4Q	69	Total	C	N	O	S	0	0
			529	346	84	98	1		
58	4c	69	Total	C	N	O	S	0	0
			529	346	84	98	1		
58	4P	215	Total	C	N	O	S	0	0
			1707	1103	290	311	3		
58	4b	194	Total	C	N	O	S	0	0
			1541	1000	258	281	2		

- Molecule 59 is a protein called CFAP97.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	3r	130	Total	C	N	O	S	0	0
			1098	668	221	205	4		
59	3s	130	Total	C	N	O	S	0	0
			1098	668	221	205	4		
59	3t	130	Total	C	N	O	S	0	0
			1098	668	221	205	4		
59	3u	130	Total	C	N	O	S	0	0
			1098	668	221	205	4		
59	3v	63	Total	C	N	O	S	0	0
			533	326	105	98	4		

- Molecule 60 is a protein called DMAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	3w	166	Total	C	N	O	S	0	0
			1362	872	235	249	6		
60	3y	126	Total	C	N	O	S	0	0
			985	625	178	181	1		
60	3x	267	Total	C	N	O	S	0	0
			2165	1380	381	397	7		

- Molecule 61 is a protein called DMAP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	4A	29	Total	C	N	O	S	0	0
			229	142	43	43	1		
61	4B	201	Total	C	N	O	S	0	0
			1584	1003	275	302	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
61	4C	201	Total	C	N	O	S	0	0
			1584	1003	275	302	4		

- Molecule 62 is a protein called distal DC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	5B	393	Total	C	N	O	S	0	0
			3140	1922	594	613	11		
62	5C	393	Total	C	N	O	S	0	0
			3140	1922	594	613	11		
62	5D	393	Total	C	N	O	S	0	0
			3140	1922	594	613	11		
62	5E	168	Total	C	N	O	S	0	0
			1348	828	258	257	5		
62	5A	225	Total	C	N	O	S	0	0
			1792	1094	336	356	6		

- Molecule 63 is a protein called ODAD1 central coiled coil region domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5G	444	Total	C	N	O	S	0	0
			3594	2191	674	710	19		
63	5H	444	Total	C	N	O	S	0	0
			3594	2191	674	710	19		
63	5I	444	Total	C	N	O	S	0	0
			3594	2191	674	710	19		
63	5J	185	Total	C	N	O	S	0	0
			1541	942	295	296	8		
63	5F	259	Total	C	N	O	S	0	0
			2053	1249	379	414	11		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5G	273	PHE	SER	conflict	UNP A0A640KPU2
5H	273	PHE	SER	conflict	UNP A0A640KPU2
5I	273	PHE	SER	conflict	UNP A0A640KPU2
5J	273	PHE	SER	conflict	UNP A0A640KPU2
5F	273	PHE	SER	conflict	UNP A0A640KPU2

- Molecule 64 is a protein called ODA dDC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	5K	384	Total	C	N	O	S	0	0
			3128	1989	546	572	21		
64	5L	384	Total	C	N	O	S	0	0
			3128	1989	546	572	21		
64	5M	384	Total	C	N	O	S	0	0
			3128	1989	546	572	21		
64	5N	384	Total	C	N	O	S	0	0
			3128	1989	546	572	21		

- Molecule 65 is a protein called DC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	5O	107	Total	C	N	O	S	0	0
			809	523	130	152	4		
65	5P	107	Total	C	N	O	S	0	0
			809	523	130	152	4		
65	5Q	107	Total	C	N	O	S	0	0
			809	523	130	152	4		
65	5R	107	Total	C	N	O	S	0	0
			809	523	130	152	4		

- Molecule 66 is a protein called DC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	5S	92	Total	C	N	O	S	0	0
			749	470	137	133	9		
66	5T	92	Total	C	N	O	S	0	0
			749	470	137	133	9		
66	5U	92	Total	C	N	O	S	0	0
			749	470	137	133	9		
66	5V	92	Total	C	N	O	S	0	0
			749	470	137	133	9		

- Molecule 67 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	5X	4565	Total	C	N	O	S	0	0
			36792	23377	6358	6859	198		
67	5W	3144	Total	C	N	O	S	0	0
			25199	16022	4339	4693	145		
67	5Y	4565	Total	C	N	O	S	0	0
			36794	23378	6359	6859	198		

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Mol	Chain	Residues	Atoms					AltConf	Trace
67	5Z	4565	Total	C	N	O	S	0	0
			36793	23378	6358	6859	198		
67	5a	1201	Total	C	N	O	S	0	0
			9781	6190	1721	1827	43		

- Molecule 68 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	5c	4178	Total	C	N	O	S	0	0
			33422	21212	5674	6353	183		
68	5b	2730	Total	C	N	O	S	0	0
			21827	13877	3716	4102	132		
68	5d	4178	Total	C	N	O	S	0	0
			33422	21212	5674	6353	183		
68	5e	4178	Total	C	N	O	S	0	0
			33422	21212	5674	6353	183		
68	5f	1240	Total	C	N	O	S	0	0
			9901	6257	1666	1934	44		

- Molecule 69 is a protein called Dynein intermediate-chain-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	5g	565	Total	C	N	O	S	0	0
			4413	2802	751	830	30		
69	5h	565	Total	C	N	O	S	0	0
			4413	2802	751	830	30		
69	5i	565	Total	C	N	O	S	0	0
			4413	2802	751	830	30		
69	5j	565	Total	C	N	O	S	0	0
			4413	2802	751	830	30		

- Molecule 70 is a protein called Dynein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	5k	596	Total	C	N	O	S	0	0
			4766	2990	832	918	26		
70	5l	596	Total	C	N	O	S	0	0
			4766	2990	832	918	26		
70	5m	596	Total	C	N	O	S	0	0
			4766	2990	832	918	26		
70	5n	596	Total	C	N	O	S	0	0
			4766	2990	832	918	26		

- Molecule 71 is a protein called Dynein axonemal light chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	5o	208	Total	C	N	O	S	0	0
			1661	1047	292	312	10		
71	5p	208	Total	C	N	O	S	0	0
			1661	1047	292	312	10		
71	5q	208	Total	C	N	O	S	0	0
			1661	1047	292	312	10		
71	5r	208	Total	C	N	O	S	0	0
			1661	1047	292	312	10		

- Molecule 72 is a protein called EF-hand domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	5s	202	Total	C	N	O	S	0	0
			1576	1004	271	292	9		
72	5t	202	Total	C	N	O	S	0	0
			1576	1004	271	292	9		
72	5u	202	Total	C	N	O	S	0	0
			1576	1004	271	292	9		
72	5v	202	Total	C	N	O	S	0	0
			1576	1004	271	292	9		

- Molecule 73 is a protein called Dynein light chain roadblock.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	5w	112	Total	C	N	O	S	0	0
			867	544	152	166	5		
73	5x	112	Total	C	N	O	S	0	0
			867	544	152	166	5		
73	5y	112	Total	C	N	O	S	0	0
			867	544	152	166	5		
73	5z	112	Total	C	N	O	S	0	0
			867	544	152	166	5		

- Molecule 74 is a protein called Dynein light chain roadblock.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	6A	97	Total	C	N	O	S	0	0
			771	481	137	148	5		
74	6B	97	Total	C	N	O	S	0	0
			771	481	137	148	5		
74	6C	97	Total	C	N	O	S	0	0
			771	481	137	148	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	6D	97	Total	C	N	O	S	0	0
			771	481	137	148	5		

- Molecule 75 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	6E	99	Total	C	N	O	S	0	0
			824	532	133	151	8		
75	6F	99	Total	C	N	O	S	0	0
			824	532	133	151	8		
75	6G	99	Total	C	N	O	S	0	0
			824	532	133	151	8		
75	6H	99	Total	C	N	O	S	0	0
			824	532	133	151	8		

- Molecule 76 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	6I	90	Total	C	N	O	S	0	0
			721	466	117	133	5		
76	6J	90	Total	C	N	O	S	0	0
			721	466	117	133	5		
76	6K	90	Total	C	N	O	S	0	0
			721	466	117	133	5		
76	6L	90	Total	C	N	O	S	0	0
			721	466	117	133	5		

- Molecule 77 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	6M	91	Total	C	N	O	S	0	0
			745	481	121	136	7		
77	6N	91	Total	C	N	O	S	0	0
			745	481	121	136	7		
77	6O	91	Total	C	N	O	S	0	0
			745	481	121	136	7		
77	6P	91	Total	C	N	O	S	0	0
			745	481	121	136	7		
77	7U	88	Total	C	N	O	S	0	0
			717	463	117	131	6		
77	7V	88	Total	C	N	O	S	0	0
			717	463	117	131	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
77	7W	83	Total 677	C 440	N 108	O 123	S 6	0	0
77	7X	83	Total 677	C 440	N 108	O 123	S 6	0	0
77	7S	87	Total 709	C 459	N 115	O 129	S 6	0	0
77	7T	77	Total 632	C 413	N 100	O 113	S 6	0	0
77	9k	88	Total 717	C 463	N 117	O 131	S 6	0	0
77	9l	88	Total 717	C 463	N 117	O 131	S 6	0	0
77	9m	83	Total 677	C 440	N 108	O 123	S 6	0	0
77	9n	83	Total 677	C 440	N 108	O 123	S 6	0	0
77	9i	87	Total 709	C 459	N 115	O 129	S 6	0	0
77	9j	77	Total 632	C 413	N 100	O 113	S 6	0	0
77	8s	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8t	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8c	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8d	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8e	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8f	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8g	83	Total 677	C 440	N 108	O 123	S 6	0	0
77	8h	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8i	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8j	91	Total 745	C 481	N 121	O 136	S 7	0	0
77	8k	91	Total 745	C 481	N 121	O 136	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
77	8l	91	Total	C	N	O	S	0	0
			745	481	121	136	7		
77	8m	91	Total	C	N	O	S	0	0
			745	481	121	136	7		
77	8n	91	Total	C	N	O	S	0	0
			745	481	121	136	7		

- Molecule 78 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	6Q	89	Total	C	N	O	S	0	0
			733	470	126	133	4		
78	6R	89	Total	C	N	O	S	0	0
			733	470	126	133	4		
78	6S	89	Total	C	N	O	S	0	0
			733	470	126	133	4		
78	6T	89	Total	C	N	O	S	0	0
			733	470	126	133	4		

- Molecule 79 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	6U	91	Total	C	N	O	S	0	0
			749	489	119	134	7		
79	6V	91	Total	C	N	O	S	0	0
			749	489	119	134	7		
79	6W	91	Total	C	N	O	S	0	0
			749	489	119	134	7		
79	6X	91	Total	C	N	O	S	0	0
			749	489	119	134	7		

- Molecule 80 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	6Y	96	Total	C	N	O	S	0	0
			767	483	134	146	4		
80	6Z	96	Total	C	N	O	S	0	0
			767	483	134	146	4		
80	6a	96	Total	C	N	O	S	0	0
			767	483	134	146	4		
80	6b	96	Total	C	N	O	S	0	0
			767	483	134	146	4		

- Molecule 81 is a protein called Outer arm dynein-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	6c	100	Total	C	N	O	S	0	0
			795	515	126	150	4		
81	6d	100	Total	C	N	O	S	0	0
			795	515	126	150	4		
81	6e	100	Total	C	N	O	S	0	0
			795	515	126	150	4		
81	6f	100	Total	C	N	O	S	0	0
			795	515	126	150	4		

- Molecule 82 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	6g	113	Total	C	N	O	S	0	0
			913	580	156	171	6		
82	6h	113	Total	C	N	O	S	0	0
			913	580	156	171	6		
82	6i	113	Total	C	N	O	S	0	0
			913	580	156	171	6		
82	6j	113	Total	C	N	O	S	0	0
			913	580	156	171	6		

- Molecule 83 is a protein called IDAa heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	6k	3972	Total	C	N	O	S	0	0
			31758	20128	5481	5984	165		

- Molecule 84 is a protein called Actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	6l	371	Total	C	N	O	S	0	0
			2911	1836	495	556	24		
84	7A	361	Total	C	N	O	S	0	0
			2835	1789	480	544	22		

- Molecule 85 is a protein called DLP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	6m	410	Total	C	N	O	S	0	0
			3265	2032	592	633	8		

- Molecule 86 is a protein called Dynein arm light chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	6n	207	Total	C	N	O	S	0	0
			1701	1060	306	330	5		
86	6r	211	Total	C	N	O	S	0	0
			1725	1070	311	338	6		

- Molecule 87 is a protein called Putative dynein heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	6o	3797	Total	C	N	O	S	0	0
			30354	19276	5261	5630	187		

- Molecule 88 is a protein called Actin-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	6p	407	Total	C	N	O	S	0	0
			3087	1937	529	608	13		

- Molecule 89 is a protein called 33 kDa inner dynein arm light chain, axonemal, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	6q	226	Total	C	N	O	S	0	0
			1812	1131	340	337	4		

- Molecule 90 is a protein called Anaphase-promoting complex subunit 5 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	6s	245	Total	C	N	O	S	0	0
			1886	1182	344	345	15		

- Molecule 91 is a protein called Actin-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	9R	302	Total	C	N	O	S	0	0
			2382	1509	413	448	12		

- Molecule 92 is a protein called Centrin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	9S	129	Total	C	N	O	S	0	0
			1052	652	181	213	6		

- Molecule 93 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	9Q	3918	Total	C	N	O	S	0	0
			30600	19344	5306	5780	170		

- Molecule 94 is a protein called ARM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	9T	381	Total	C	N	O	S	0	0
			2975	1859	557	548	11		

- Molecule 95 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	6t	4062	Total	C	N	O	S	0	0
			32279	20527	5507	6050	195		

- Molecule 96 is a protein called Actin-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	6u	392	Total	C	N	O	S	0	0
			3067	1935	536	580	16		

- Molecule 97 is a protein called DLP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	6v	312	Total	C	N	O	S	0	0
			2471	1523	461	475	12		

- Molecule 98 is a protein called Dynein arm light chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	6w	274	Total	C	N	O	S	0	0
			2183	1354	416	409	4		

- Molecule 99 is a protein called TAX-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	6x	326	Total	C	N	O	S	0	0
			2613	1656	458	486	13		

- Molecule 100 is a protein called Tetratricopeptide repeat protein 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	6y	383	Total	C	N	O	S	0	0
			3020	1880	539	583	18		

- Molecule 101 is a protein called Roadblock/LAMTOR2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	7Q	96	Total	C	N	O	S	0	0
			734	460	126	144	4		
101	9g	96	Total	C	N	O	S	0	0
			734	460	126	144	4		

- Molecule 102 is a protein called Dynein-associated protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	7R	109	Total	C	N	O	S	0	0
			867	546	153	164	4		
102	9h	109	Total	C	N	O	S	0	0
			867	546	153	164	4		

- Molecule 103 is a protein called IC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	7N	325	Total	C	N	O	S	0	0
			2566	1645	445	462	14		
103	9c	325	Total	C	N	O	S	0	0
			2566	1645	445	462	14		

- Molecule 104 is a protein called Dynein axonemal intermediate chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	7O	233	Total	C	N	O	S	0	0
			1828	1167	315	337	9		
104	9d	392	Total	C	N	O	S	0	0
			3092	1954	531	590	17		

- Molecule 105 is a protein called Dynein light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	9M	103	Total	C	N	O	S	0	0
			845	535	144	161	5		
105	9p	103	Total	C	N	O	S	0	0
			845	535	144	161	5		

- Molecule 106 is a protein called Dynein-light chain-protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	9L	103	Total	C	N	O	S	0	0
			791	498	134	153	6		
106	9o	103	Total	C	N	O	S	0	0
			791	498	134	153	6		

- Molecule 107 is a protein called Ankyrin/TPR repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	7F	296	Total	C	N	O	S	0	0
			2252	1376	409	452	15		
107	9e	296	Total	C	N	O	S	0	0
			2252	1376	409	452	15		

- Molecule 108 is a protein called IC97/Casc1 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	9K	565	Total	C	N	O	S	0	0
			4601	2917	798	866	20		
108	9f	565	Total	C	N	O	S	0	0
			4601	2917	798	866	20		

- Molecule 109 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	7G	3724	Total	C	N	O	S	0	0
			29867	18977	5125	5599	166		
109	9a	1431	Total	C	N	O	S	0	0
			11631	7372	2038	2172	49		

- Molecule 110 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
110	7I	3788	Total	C	N	O	S	0	0
			30637	19418	5331	5707	181		
110	9b	1106	Total	C	N	O	S	0	0
			9051	5738	1585	1677	51		

- Molecule 111 is a protein called DUF4200 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	9U	81	Total	C	N	O	S	0	0
			616	373	115	122	6		
111	9r	286	Total	C	N	O	S	0	0
			2334	1425	442	451	16		

- Molecule 112 is a protein called DUF4200 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	9V	83	Total	C	N	O	S	0	0
			692	428	134	126	4		
112	9s	298	Total	C	N	O	S	0	0
			2453	1506	457	478	12		

- Molecule 113 is a protein called Leucine-rich repeat-containing protein 51.

Mol	Chain	Residues	Atoms					AltConf	Trace
113	9q	442	Total	C	N	O	S	0	0
			3509	2209	633	652	15		

- Molecule 114 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	6z	3680	Total	C	N	O	S	0	0
			29150	18419	5041	5528	162		

- Molecule 115 is a protein called Centrin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	7B	152	Total	C	N	O	S	0	0
			1202	758	200	237	7		

- Molecule 116 is a protein called Dynein heavy chain, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	7C	3636	Total	C	N	O	S	0	0
			28996	18416	4982	5443	155		

- Molecule 117 is a protein called Actin-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	7D	419	Total	C	N	O	S	0	0
			3190	1998	563	609	20		

- Molecule 118 is a protein called Centrin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	7E	150	Total	C	N	O	S	0	0
			1210	750	209	247	4		

- Molecule 119 is a protein called Dynein regulatory complex protein 1 C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	8A	452	Total	C	N	O	S	0	0
			3770	2334	704	721	11		

- Molecule 120 is a protein called Cilia- and flagella-associated protein 91.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	8K	214	Total	C	N	O	S	0	0
			1728	1060	340	322	6		

- Molecule 121 is a protein called T-lymphocyte triggering factor, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
121	8E	431	Total	C	N	O	S	0	0
			3596	2204	671	704	17		

- Molecule 122 is a protein called T-lymphocyte triggering factor, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
122	8D	400	Total	C	N	O	S	0	0
			3394	2103	619	662	10		

- Molecule 123 is a protein called Dynein regulatory complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
123	8B	372	Total	C	N	O	S	0	0
			3062	1883	550	609	20		

- Molecule 124 is a protein called AAA+ ATPase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
124	8J	778	Total	C	N	O	S	0	0
			6100	3823	1111	1137	29		

- Molecule 125 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
125	8F	456	Total	C	N	O	S	0	0
			3580	2241	648	668	23		

- Molecule 126 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
126	8M	148	Total	C	N	O	S	0	0
			1163	713	186	254	10		
126	8L	148	Total	C	N	O	S	0	0
			1163	713	186	254	10		
126	9N	149	Total	C	N	O	S	0	0
			1173	719	188	256	10		
126	9O	149	Total	C	N	O	S	0	0
			1173	719	188	256	10		

- Molecule 127 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
127	8N	323	Total	C	N	O	S	0	0
			2458	1543	438	462	15		

- Molecule 128 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
128	8O	387	Total	C	N	O	S	0	0
			2870	1778	522	556	14		

- Molecule 129 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
129	8P	99	Total	C	N	O	S	0	0
			814	519	135	157	3		
129	4f	73	Total	C	N	O	S	0	0
			621	396	106	117	2		

- Molecule 130 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
130	8R	337	Total	C	N	O	S	0	0
			2445	1514	433	488	10		

- Molecule 131 is a protein called Transglutaminase-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
131	8G	606	Total	C	N	O	S	0	0
			4902	3115	848	917	22		

- Molecule 132 is a protein called Dynein regulatory complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
132	8C	546	Total	C	N	O	S	0	0
			4418	2757	806	840	15		

- Molecule 133 is a protein called Dynein regulatory complex protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
133	8H	120	Total	C	N	O	S	0	0
			935	565	177	189	4		

- Molecule 134 is a protein called Dynein regulatory complex protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
134	8I	174	Total	C	N	O	S	0	0
			1433	873	278	277	5		

- Molecule 135 is a protein called Cilia- and flagella-associated protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
135	7K	1298	Total	C	N	O	S	0	0
			10069	6250	1827	1919	73		

- Molecule 136 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
136	7L	1476	Total	C	N	O	S	0	0
			11521	7199	2068	2189	65		

- Molecule 137 is a protein called Tudor domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
137	7M	252	Total	C	N	O	S	0	0
			1985	1261	325	387	12		

- Molecule 138 is a protein called CFAP253.

Mol	Chain	Residues	Atoms					AltConf	Trace
138	8r	197	Total	C	N	O	S	0	0
			1627	1014	313	297	3		

- Molecule 139 is a protein called Radial spoke protein 3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
139	8u	44	Total	C	N	O	S	0	0
			354	211	74	66	3		
139	8v	40	Total	C	N	O	S	0	0
			330	200	66	60	4		
139	8o	59	Total	C	N	O	S	0	0
			483	299	79	104	1		
139	8p	99	Total	C	N	O	S	0	0
			803	499	136	163	5		

- Molecule 140 is a protein called Kinesin-MORN.

Mol	Chain	Residues	Atoms					AltConf	Trace
140	8a	620	Total	C	N	O	S	0	0
			5006	3129	913	936	28		

- Molecule 141 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
141	8b	366	Total	C	N	O	S	0	0
			2764	1713	496	535	20		

- Molecule 142 is a protein called Cilia- and flagella-associated protein 206.

Mol	Chain	Residues	Atoms					AltConf	Trace
142	8q	560	Total	C	N	O	S	0	0
			4277	2684	757	807	29		

- Molecule 143 is a protein called Cilia- and flagella-associated protein 251.

Mol	Chain	Residues	Atoms					AltConf	Trace
143	8w	1005	Total	C	N	O	S	0	0
			7768	4918	1350	1452	48		

- Molecule 144 is a protein called Coiled-coil domain-containing protein 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
144	4R	359	Total	C	N	O	S	0	0
			2942	1806	541	587	8		
144	4S	282	Total	C	N	O	S	0	0
			2339	1419	439	473	8		

- Molecule 145 is a protein called Coiled-coil domain-containing protein 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
145	4T	430	Total	C	N	O	S	0	0
			3493	2145	643	684	21		
145	4U	276	Total	C	N	O	S	0	0
			2260	1372	421	458	9		

- Molecule 146 is a protein called CCDC113/CCDC96 coiled-coil domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
146	9t	255	Total	C	N	O	S	0	0
			2109	1292	421	388	8		

- Molecule 147 is a protein called Cilia- and flagella-associated protein 263.

Mol	Chain	Residues	Atoms					AltConf	Trace
147	9u	283	Total	C	N	O	S	0	0
			2270	1377	438	444	11		

- Molecule 148 is a protein called Enkurin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
148	4D	105	Total	C	N	O	S	0	0
			836	517	167	150	2		

- Molecule 149 is a protein called C2HC/C3H-type domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
149	4E	27	Total	C	N	O	0	0
			216	134	44	38		

- Molecule 150 is a protein called Sperm-tail PG-rich repeat.

Mol	Chain	Residues	Atoms					AltConf	Trace
150	4F	254	Total	C	N	O	S	0	0
			1945	1226	351	361	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
150	4G	83	Total	C	N	O	S	0	0
			661	420	111	127	3		

- Molecule 151 is a protein called DMAP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
151	4H	45	Total	C	N	O	S	0	0
			359	223	67	68	1		

- Molecule 152 is a protein called DMAP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
152	4I	120	Total	C	N	O	S	0	0
			959	595	194	168	2		
152	4J	57	Total	C	N	O	S	0	0
			456	279	78	94	5		

- Molecule 153 is a protein called IJAP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
153	4K	50	Total	C	N	O	S	0	0
			400	245	82	68	5		

- Molecule 154 is a protein called LIM zinc-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
154	4L	128	Total	C	N	O	S	0	0
			998	614	187	184	13		

- Molecule 155 is a protein called IJAP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
155	4M	75	Total	C	N	O	S	0	0
			581	362	105	112	2		
155	4N	177	Total	C	N	O	S	0	0
			1437	893	277	263	4		

- Molecule 156 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
156	4d	491	Total	C	N	O	S	0	0
			3737	2317	683	711	26		

- Molecule 157 is a protein called Ribonuclease inhibitor-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
157	4e	507	Total	C	N	O	S	0	0
			3833	2362	721	729	21		

- Molecule 158 is a protein called Leucine-rich repeat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
158	4g	84	Total	C	N	O	S	0	0
			660	408	128	121	3		

- Molecule 159 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
159	9W	919	Total	C	N	O	S	0	0
			7288	4584	1287	1377	40		

- Molecule 160 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
160	9X	971	Total	C	N	O	S	0	0
			7686	4789	1396	1462	39		

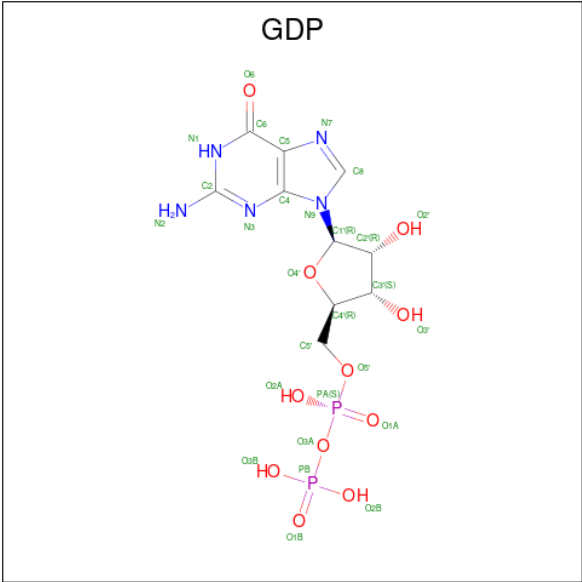
- Molecule 161 is a protein called Cilia- and flagella-associated protein 58 central coiled coil domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
161	9Y	539	Total	C	N	O	S	0	0
			4412	2692	835	860	25		

- Molecule 162 is a protein called Cilia- and flagella-associated protein 58 central coiled coil domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
162	9Z	534	Total	C	N	O	S	0	0
			4339	2668	838	820	13		

- Molecule 163 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
163	A	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BN	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	CA	1	Total 28	C 10	N 5	O 11	P 2	0
163	CC	1	Total 28	C 10	N 5	O 11	P 2	0
163	CE	1	Total 28	C 10	N 5	O 11	P 2	0
163	CG	1	Total 28	C 10	N 5	O 11	P 2	0
163	CI	1	Total 28	C 10	N 5	O 11	P 2	0
163	CK	1	Total 28	C 10	N 5	O 11	P 2	0
163	CM	1	Total 28	C 10	N 5	O 11	P 2	0
163	DA	1	Total 28	C 10	N 5	O 11	P 2	0
163	DC	1	Total 28	C 10	N 5	O 11	P 2	0
163	DE	1	Total 28	C 10	N 5	O 11	P 2	0
163	DG	1	Total 28	C 10	N 5	O 11	P 2	0
163	DI	1	Total 28	C 10	N 5	O 11	P 2	0
163	DK	1	Total 28	C 10	N 5	O 11	P 2	0
163	DM	1	Total 28	C 10	N 5	O 11	P 2	0
163	E	1	Total 28	C 10	N 5	O 11	P 2	0
163	EB	1	Total 28	C 10	N 5	O 11	P 2	0
163	ED	1	Total 28	C 10	N 5	O 11	P 2	0
163	EF	1	Total 28	C 10	N 5	O 11	P 2	0
163	EH	1	Total 28	C 10	N 5	O 11	P 2	0
163	EJ	1	Total 28	C 10	N 5	O 11	P 2	0
163	EL	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
163	F	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	G	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	H	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HL	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	I	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	ID	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JA	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JC	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JE	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JG	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JI	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JK	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JM	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KA	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KC	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KE	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KG	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KI	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KK	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KM	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	LA	1	Total 28	C 10	N 5	O 11	P 2	0
163	LC	1	Total 28	C 10	N 5	O 11	P 2	0
163	LE	1	Total 28	C 10	N 5	O 11	P 2	0
163	LG	1	Total 28	C 10	N 5	O 11	P 2	0
163	LI	1	Total 28	C 10	N 5	O 11	P 2	0
163	LK	1	Total 28	C 10	N 5	O 11	P 2	0
163	LM	1	Total 28	C 10	N 5	O 11	P 2	0
163	LO	1	Total 28	C 10	N 5	O 11	P 2	0
163	M	1	Total 28	C 10	N 5	O 11	P 2	0
163	MB	1	Total 28	C 10	N 5	O 11	P 2	0
163	MD	1	Total 28	C 10	N 5	O 11	P 2	0
163	MF	1	Total 28	C 10	N 5	O 11	P 2	0
163	MH	1	Total 28	C 10	N 5	O 11	P 2	0
163	MJ	1	Total 28	C 10	N 5	O 11	P 2	0
163	ML	1	Total 28	C 10	N 5	O 11	P 2	0
163	MN	1	Total 28	C 10	N 5	O 11	P 2	0
163	N	1	Total 28	C 10	N 5	O 11	P 2	0
163	NB	1	Total 28	C 10	N 5	O 11	P 2	0
163	ND	1	Total 28	C 10	N 5	O 11	P 2	0
163	NF	1	Total 28	C 10	N 5	O 11	P 2	0
163	NH	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
163	NJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	NL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	O	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	P	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	PB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	PD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	PF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	PH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	PJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	PL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QA	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QC	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QE	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QG	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QI	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	QK	1	Total 28	C 10	N 5	O 11	P 2	0
163	RA	1	Total 28	C 10	N 5	O 11	P 2	0
163	RC	1	Total 28	C 10	N 5	O 11	P 2	0
163	RE	1	Total 28	C 10	N 5	O 11	P 2	0
163	RG	1	Total 28	C 10	N 5	O 11	P 2	0
163	RI	1	Total 28	C 10	N 5	O 11	P 2	0
163	RK	1	Total 28	C 10	N 5	O 11	P 2	0
163	S	1	Total 28	C 10	N 5	O 11	P 2	0
163	SB	1	Total 28	C 10	N 5	O 11	P 2	0
163	SD	1	Total 28	C 10	N 5	O 11	P 2	0
163	SF	1	Total 28	C 10	N 5	O 11	P 2	0
163	SH	1	Total 28	C 10	N 5	O 11	P 2	0
163	SJ	1	Total 28	C 10	N 5	O 11	P 2	0
163	T	1	Total 28	C 10	N 5	O 11	P 2	0
163	TB	1	Total 28	C 10	N 5	O 11	P 2	0
163	TD	1	Total 28	C 10	N 5	O 11	P 2	0
163	TF	1	Total 28	C 10	N 5	O 11	P 2	0
163	TH	1	Total 28	C 10	N 5	O 11	P 2	0
163	TJ	1	Total 28	C 10	N 5	O 11	P 2	0
163	TL	1	Total 28	C 10	N 5	O 11	P 2	0
163	U	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
163	UB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	V	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	W	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WB	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WD	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WF	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WH	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AP	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	AR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	AZ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	BX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	CO	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	CQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	CS	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	CU	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	CW	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	CY	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	DO	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	DQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	DS	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	DU	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	DW	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	DY	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	EN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	EP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	ER	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	ET	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	EV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	EX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	FX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	GX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HP	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	HR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	HX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	IX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JO	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JS	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JU	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JW	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	JY	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KO	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KS	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KU	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	KW	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	KY	1	Total 28	C 10	N 5	O 11	P 2	0
163	LQ	1	Total 28	C 10	N 5	O 11	P 2	0
163	LS	1	Total 28	C 10	N 5	O 11	P 2	0
163	LU	1	Total 28	C 10	N 5	O 11	P 2	0
163	LW	1	Total 28	C 10	N 5	O 11	P 2	0
163	LY	1	Total 28	C 10	N 5	O 11	P 2	0
163	MP	1	Total 28	C 10	N 5	O 11	P 2	0
163	MR	1	Total 28	C 10	N 5	O 11	P 2	0
163	MT	1	Total 28	C 10	N 5	O 11	P 2	0
163	MV	1	Total 28	C 10	N 5	O 11	P 2	0
163	MX	1	Total 28	C 10	N 5	O 11	P 2	0
163	MZ	1	Total 28	C 10	N 5	O 11	P 2	0
163	PN	1	Total 28	C 10	N 5	O 11	P 2	0
163	PP	1	Total 28	C 10	N 5	O 11	P 2	0
163	PR	1	Total 28	C 10	N 5	O 11	P 2	0
163	PT	1	Total 28	C 10	N 5	O 11	P 2	0
163	PV	1	Total 28	C 10	N 5	O 11	P 2	0
163	PX	1	Total 28	C 10	N 5	O 11	P 2	0
163	QM	1	Total 28	C 10	N 5	O 11	P 2	0
163	QO	1	Total 28	C 10	N 5	O 11	P 2	0
163	QQ	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
163	QS	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QU	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	QW	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	RM	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	RO	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	RQ	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	RS	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	RU	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	RW	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	SL	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	SN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	SP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	SR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	ST	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	SV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	TN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	TP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	TR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	TT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	TV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	TX	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	UN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	UX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	VX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	WX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	NN	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	NP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	NR	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
163	NT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	NV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	NX	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	ON	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OP	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OR	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OT	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OV	1	Total	C	N	O	P	0
			28	10	5	11	2	
163	OX	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 164 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
164	A	1	Total	Mg	0
			1	1	
164	AC	1	Total	Mg	0
			1	1	
164	AE	1	Total	Mg	0
			1	1	
164	AG	1	Total	Mg	0
			1	1	
164	AI	1	Total	Mg	0
			1	1	
164	AK	1	Total	Mg	0
			1	1	
164	AM	1	Total	Mg	0
			1	1	
164	BA	1	Total	Mg	0
			1	1	
164	BE	1	Total	Mg	0
			1	1	
164	BG	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
164	BI	1	Total 1	Mg 1	0
164	BK	1	Total 1	Mg 1	0
164	BM	1	Total 1	Mg 1	0
164	C	1	Total 1	Mg 1	0
164	CB	1	Total 1	Mg 1	0
164	CD	1	Total 1	Mg 1	0
164	CF	1	Total 1	Mg 1	0
164	CH	1	Total 1	Mg 1	0
164	CJ	1	Total 1	Mg 1	0
164	CK	1	Total 1	Mg 1	0
164	D	1	Total 1	Mg 1	0
164	DB	1	Total 1	Mg 1	0
164	DD	1	Total 1	Mg 1	0
164	DF	1	Total 1	Mg 1	0
164	DH	1	Total 1	Mg 1	0
164	DJ	1	Total 1	Mg 1	0
164	DK	1	Total 1	Mg 1	0
164	EA	1	Total 1	Mg 1	0
164	EC	1	Total 1	Mg 1	0
164	EE	1	Total 1	Mg 1	0
164	EG	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	EI	1	Total 1	Mg 1	0
164	EK	1	Total 1	Mg 1	0
164	FA	1	Total 1	Mg 1	0
164	FC	1	Total 1	Mg 1	0
164	FE	1	Total 1	Mg 1	0
164	FG	1	Total 1	Mg 1	0
164	FI	1	Total 1	Mg 1	0
164	FJ	1	Total 1	Mg 1	0
164	GA	1	Total 1	Mg 1	0
164	GC	1	Total 1	Mg 1	0
164	GE	1	Total 1	Mg 1	0
164	GG	1	Total 1	Mg 1	0
164	GI	1	Total 1	Mg 1	0
164	GK	1	Total 1	Mg 1	0
164	HA	1	Total 1	Mg 1	0
164	HB	1	Total 1	Mg 1	0
164	HD	1	Total 1	Mg 1	0
164	HG	1	Total 1	Mg 1	0
164	HH	1	Total 1	Mg 1	0
164	HK	1	Total 1	Mg 1	0
164	HL	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	I	1	Total 1	Mg 1	0
164	IC	1	Total 1	Mg 1	0
164	IE	1	Total 1	Mg 1	0
164	IG	1	Total 1	Mg 1	0
164	II	1	Total 1	Mg 1	0
164	IK	1	Total 1	Mg 1	0
164	IL	1	Total 1	Mg 1	0
164	J	1	Total 1	Mg 1	0
164	JB	1	Total 1	Mg 1	0
164	JD	1	Total 1	Mg 1	0
164	JF	1	Total 1	Mg 1	0
164	JH	1	Total 1	Mg 1	0
164	JJ	1	Total 1	Mg 1	0
164	JL	1	Total 1	Mg 1	0
164	JM	1	Total 1	Mg 1	0
164	K	1	Total 1	Mg 1	0
164	KB	1	Total 1	Mg 1	0
164	KD	1	Total 1	Mg 1	0
164	KF	1	Total 1	Mg 1	0
164	KH	1	Total 1	Mg 1	0
164	KJ	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
164	KL	1	1	1	0
164	KN	1	1	1	0
164	L	1	1	1	0
164	LB	1	1	1	0
164	LD	1	1	1	0
164	LF	1	1	1	0
164	LG	1	1	1	0
164	LJ	1	1	1	0
164	LL	1	1	1	0
164	LN	1	1	1	0
164	MA	1	1	1	0
164	MC	1	1	1	0
164	ME	1	1	1	0
164	MG	1	1	1	0
164	MI	1	1	1	0
164	MK	1	1	1	0
164	MM	1	1	1	0
164	NA	1	1	1	0
164	NC	1	1	1	0
164	NE	1	1	1	0
164	NG	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
164	NI	1	1	1	0
164	NJ	1	1	1	0
164	NM	1	1	1	0
164	OA	1	1	1	0
164	OC	1	1	1	0
164	OD	1	1	1	0
164	OG	1	1	1	0
164	OI	1	1	1	0
164	OK	1	1	1	0
164	OM	1	1	1	0
164	PA	1	1	1	0
164	PC	1	1	1	0
164	PE	1	1	1	0
164	PF	1	1	1	0
164	PI	1	1	1	0
164	PK	1	1	1	0
164	PL	1	1	1	0
164	Q	1	1	1	0
164	QB	1	1	1	0
164	QD	1	1	1	0
164	QF	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
164	QH	1	Total 1	Mg 1	0
164	QJ	1	Total 1	Mg 1	0
164	QL	1	Total 1	Mg 1	0
164	R	1	Total 1	Mg 1	0
164	RB	1	Total 1	Mg 1	0
164	RD	1	Total 1	Mg 1	0
164	RF	1	Total 1	Mg 1	0
164	RH	1	Total 1	Mg 1	0
164	RJ	1	Total 1	Mg 1	0
164	RL	1	Total 1	Mg 1	0
164	SA	1	Total 1	Mg 1	0
164	SB	1	Total 1	Mg 1	0
164	SE	1	Total 1	Mg 1	0
164	SG	1	Total 1	Mg 1	0
164	SI	1	Total 1	Mg 1	0
164	SJ	1	Total 1	Mg 1	0
164	T	1	Total 1	Mg 1	0
164	TC	1	Total 1	Mg 1	0
164	TE	1	Total 1	Mg 1	0
164	TG	1	Total 1	Mg 1	0
164	TI	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	TK	1	Total 1	Mg 1	0
164	TL	1	Total 1	Mg 1	0
164	UA	1	Total 1	Mg 1	0
164	UC	1	Total 1	Mg 1	0
164	UE	1	Total 1	Mg 1	0
164	UG	1	Total 1	Mg 1	0
164	UI	1	Total 1	Mg 1	0
164	UK	1	Total 1	Mg 1	0
164	VA	1	Total 1	Mg 1	0
164	VC	1	Total 1	Mg 1	0
164	VE	1	Total 1	Mg 1	0
164	VG	1	Total 1	Mg 1	0
164	VI	1	Total 1	Mg 1	0
164	VK	1	Total 1	Mg 1	0
164	VM	1	Total 1	Mg 1	0
164	WA	1	Total 1	Mg 1	0
164	WC	1	Total 1	Mg 1	0
164	WE	1	Total 1	Mg 1	0
164	WF	1	Total 1	Mg 1	0
164	WI	1	Total 1	Mg 1	0
164	WK	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	WM	1	Total 1	Mg 1	0
164	AO	1	Total 1	Mg 1	0
164	AQ	1	Total 1	Mg 1	0
164	AS	1	Total 1	Mg 1	0
164	AU	1	Total 1	Mg 1	0
164	AW	1	Total 1	Mg 1	0
164	AY	1	Total 1	Mg 1	0
164	BO	1	Total 1	Mg 1	0
164	BQ	1	Total 1	Mg 1	0
164	BS	1	Total 1	Mg 1	0
164	BU	1	Total 1	Mg 1	0
164	BW	1	Total 1	Mg 1	0
164	BY	1	Total 1	Mg 1	0
164	CN	1	Total 1	Mg 1	0
164	CP	1	Total 1	Mg 1	0
164	CR	1	Total 1	Mg 1	0
164	CT	1	Total 1	Mg 1	0
164	CV	1	Total 1	Mg 1	0
164	CX	1	Total 1	Mg 1	0
164	DN	1	Total 1	Mg 1	0
164	DP	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	DR	1	Total 1	Mg 1	0
164	DT	1	Total 1	Mg 1	0
164	DV	1	Total 1	Mg 1	0
164	DW	1	Total 1	Mg 1	0
164	EM	1	Total 1	Mg 1	0
164	EO	1	Total 1	Mg 1	0
164	EQ	1	Total 1	Mg 1	0
164	ES	1	Total 1	Mg 1	0
164	EU	1	Total 1	Mg 1	0
164	EW	1	Total 1	Mg 1	0
164	FM	1	Total 1	Mg 1	0
164	FO	1	Total 1	Mg 1	0
164	FQ	1	Total 1	Mg 1	0
164	FR	1	Total 1	Mg 1	0
164	FT	1	Total 1	Mg 1	0
164	FV	1	Total 1	Mg 1	0
164	GM	1	Total 1	Mg 1	0
164	GO	1	Total 1	Mg 1	0
164	GQ	1	Total 1	Mg 1	0
164	GS	1	Total 1	Mg 1	0
164	GT	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	GV	1	Total 1	Mg 1	0
164	HN	1	Total 1	Mg 1	0
164	HP	1	Total 1	Mg 1	0
164	HS	1	Total 1	Mg 1	0
164	HT	1	Total 1	Mg 1	0
164	HW	1	Total 1	Mg 1	0
164	HX	1	Total 1	Mg 1	0
164	IO	1	Total 1	Mg 1	0
164	IQ	1	Total 1	Mg 1	0
164	IS	1	Total 1	Mg 1	0
164	IT	1	Total 1	Mg 1	0
164	IW	1	Total 1	Mg 1	0
164	IX	1	Total 1	Mg 1	0
164	JP	1	Total 1	Mg 1	0
164	JR	1	Total 1	Mg 1	0
164	JT	1	Total 1	Mg 1	0
164	JV	1	Total 1	Mg 1	0
164	JX	1	Total 1	Mg 1	0
164	JY	1	Total 1	Mg 1	0
164	KP	1	Total 1	Mg 1	0
164	KR	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	KT	1	Total 1	Mg 1	0
164	KV	1	Total 1	Mg 1	0
164	KX	1	Total 1	Mg 1	0
164	KZ	1	Total 1	Mg 1	0
164	LP	1	Total 1	Mg 1	0
164	LR	1	Total 1	Mg 1	0
164	LT	1	Total 1	Mg 1	0
164	LV	1	Total 1	Mg 1	0
164	LX	1	Total 1	Mg 1	0
164	LZ	1	Total 1	Mg 1	0
164	MO	1	Total 1	Mg 1	0
164	MQ	1	Total 1	Mg 1	0
164	MS	1	Total 1	Mg 1	0
164	MU	1	Total 1	Mg 1	0
164	MW	1	Total 1	Mg 1	0
164	MY	1	Total 1	Mg 1	0
164	PO	1	Total 1	Mg 1	0
164	PQ	1	Total 1	Mg 1	0
164	PR	1	Total 1	Mg 1	0
164	PU	1	Total 1	Mg 1	0
164	PW	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	PX	1	Total 1	Mg 1	0
164	QN	1	Total 1	Mg 1	0
164	QP	1	Total 1	Mg 1	0
164	QR	1	Total 1	Mg 1	0
164	QT	1	Total 1	Mg 1	0
164	QV	1	Total 1	Mg 1	0
164	QX	1	Total 1	Mg 1	0
164	RN	1	Total 1	Mg 1	0
164	RP	1	Total 1	Mg 1	0
164	RR	1	Total 1	Mg 1	0
164	RT	1	Total 1	Mg 1	0
164	RV	1	Total 1	Mg 1	0
164	RX	1	Total 1	Mg 1	0
164	SM	1	Total 1	Mg 1	0
164	SN	1	Total 1	Mg 1	0
164	SQ	1	Total 1	Mg 1	0
164	SS	1	Total 1	Mg 1	0
164	SU	1	Total 1	Mg 1	0
164	SV	1	Total 1	Mg 1	0
164	TO	1	Total 1	Mg 1	0
164	TQ	1	Total 1	Mg 1	0

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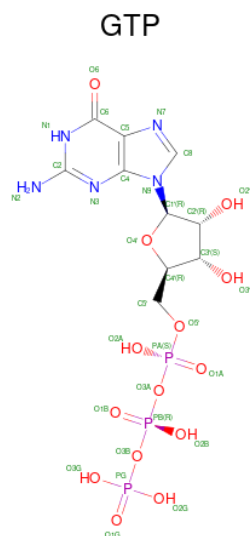
Mol	Chain	Residues	Atoms		AltConf
164	TS	1	Total 1	Mg 1	0
164	TU	1	Total 1	Mg 1	0
164	TW	1	Total 1	Mg 1	0
164	UM	1	Total 1	Mg 1	0
164	UO	1	Total 1	Mg 1	0
164	UQ	1	Total 1	Mg 1	0
164	US	1	Total 1	Mg 1	0
164	UU	1	Total 1	Mg 1	0
164	UW	1	Total 1	Mg 1	0
164	VO	1	Total 1	Mg 1	0
164	VQ	1	Total 1	Mg 1	0
164	VS	1	Total 1	Mg 1	0
164	VU	1	Total 1	Mg 1	0
164	VW	1	Total 1	Mg 1	0
164	VY	1	Total 1	Mg 1	0
164	WO	1	Total 1	Mg 1	0
164	WQ	1	Total 1	Mg 1	0
164	WR	1	Total 1	Mg 1	0
164	WU	1	Total 1	Mg 1	0
164	WW	1	Total 1	Mg 1	0
164	WY	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
164	NO	1	Total 1	Mg 1	0
164	NQ	1	Total 1	Mg 1	0
164	NS	1	Total 1	Mg 1	0
164	NU	1	Total 1	Mg 1	0
164	NV	1	Total 1	Mg 1	0
164	NY	1	Total 1	Mg 1	0
164	OO	1	Total 1	Mg 1	0
164	OP	1	Total 1	Mg 1	0
164	OS	1	Total 1	Mg 1	0
164	OU	1	Total 1	Mg 1	0
164	OW	1	Total 1	Mg 1	0
164	OY	1	Total 1	Mg 1	0
164	6l	1	Total 1	Mg 1	0
164	6p	1	Total 1	Mg 1	0
164	9R	1	Total 1	Mg 1	0
164	7A	1	Total 1	Mg 1	0
164	7D	1	Total 1	Mg 1	0

- Molecule 165 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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Mol	Chain	Residues	Atoms					AltConf
165	CB	1	Total 32	C 10	N 5	O 14	P 3	0
165	CC	1	Total 32	C 10	N 5	O 14	P 3	0
165	CE	1	Total 32	C 10	N 5	O 14	P 3	0
165	CH	1	Total 32	C 10	N 5	O 14	P 3	0
165	CJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	CK	1	Total 32	C 10	N 5	O 14	P 3	0
165	D	1	Total 32	C 10	N 5	O 14	P 3	0
165	DB	1	Total 32	C 10	N 5	O 14	P 3	0
165	DD	1	Total 32	C 10	N 5	O 14	P 3	0
165	DE	1	Total 32	C 10	N 5	O 14	P 3	0
165	DH	1	Total 32	C 10	N 5	O 14	P 3	0
165	DJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	DL	1	Total 32	C 10	N 5	O 14	P 3	0
165	EA	1	Total 32	C 10	N 5	O 14	P 3	0
165	EC	1	Total 32	C 10	N 5	O 14	P 3	0
165	ED	1	Total 32	C 10	N 5	O 14	P 3	0
165	EG	1	Total 32	C 10	N 5	O 14	P 3	0
165	EI	1	Total 32	C 10	N 5	O 14	P 3	0
165	EJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	FA	1	Total 32	C 10	N 5	O 14	P 3	0
165	FC	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	FE	1	Total 32	C 10	N 5	O 14	P 3	0
165	FG	1	Total 32	C 10	N 5	O 14	P 3	0
165	FI	1	Total 32	C 10	N 5	O 14	P 3	0
165	FJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	G	1	Total 32	C 10	N 5	O 14	P 3	0
165	GC	1	Total 32	C 10	N 5	O 14	P 3	0
165	GE	1	Total 32	C 10	N 5	O 14	P 3	0
165	GG	1	Total 32	C 10	N 5	O 14	P 3	0
165	GI	1	Total 32	C 10	N 5	O 14	P 3	0
165	GK	1	Total 32	C 10	N 5	O 14	P 3	0
165	GL	1	Total 32	C 10	N 5	O 14	P 3	0
165	HA	1	Total 32	C 10	N 5	O 14	P 3	0
165	HB	1	Total 32	C 10	N 5	O 14	P 3	0
165	HE	1	Total 32	C 10	N 5	O 14	P 3	0
165	HG	1	Total 32	C 10	N 5	O 14	P 3	0
165	HI	1	Total 32	C 10	N 5	O 14	P 3	0
165	HK	1	Total 32	C 10	N 5	O 14	P 3	0
165	HM	1	Total 32	C 10	N 5	O 14	P 3	0
165	IA	1	Total 32	C 10	N 5	O 14	P 3	0
165	IC	1	Total 32	C 10	N 5	O 14	P 3	0
165	IE	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	IG	1	Total 32	C 10	N 5	O 14	P 3	0
165	II	1	Total 32	C 10	N 5	O 14	P 3	0
165	IK	1	Total 32	C 10	N 5	O 14	P 3	0
165	IM	1	Total 32	C 10	N 5	O 14	P 3	0
165	J	1	Total 32	C 10	N 5	O 14	P 3	0
165	JB	1	Total 32	C 10	N 5	O 14	P 3	0
165	JD	1	Total 32	C 10	N 5	O 14	P 3	0
165	JF	1	Total 32	C 10	N 5	O 14	P 3	0
165	JH	1	Total 32	C 10	N 5	O 14	P 3	0
165	JJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	JK	1	Total 32	C 10	N 5	O 14	P 3	0
165	JN	1	Total 32	C 10	N 5	O 14	P 3	0
165	K	1	Total 32	C 10	N 5	O 14	P 3	0
165	KB	1	Total 32	C 10	N 5	O 14	P 3	0
165	KD	1	Total 32	C 10	N 5	O 14	P 3	0
165	KF	1	Total 32	C 10	N 5	O 14	P 3	0
165	KH	1	Total 32	C 10	N 5	O 14	P 3	0
165	KJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	KL	1	Total 32	C 10	N 5	O 14	P 3	0
165	KN	1	Total 32	C 10	N 5	O 14	P 3	0
165	L	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	LB	1	Total 32	C 10	N 5	O 14	P 3	0
165	LD	1	Total 32	C 10	N 5	O 14	P 3	0
165	LF	1	Total 32	C 10	N 5	O 14	P 3	0
165	LH	1	Total 32	C 10	N 5	O 14	P 3	0
165	LJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	LL	1	Total 32	C 10	N 5	O 14	P 3	0
165	LN	1	Total 32	C 10	N 5	O 14	P 3	0
165	MA	1	Total 32	C 10	N 5	O 14	P 3	0
165	MC	1	Total 32	C 10	N 5	O 14	P 3	0
165	ME	1	Total 32	C 10	N 5	O 14	P 3	0
165	MG	1	Total 32	C 10	N 5	O 14	P 3	0
165	MI	1	Total 32	C 10	N 5	O 14	P 3	0
165	MJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	MM	1	Total 32	C 10	N 5	O 14	P 3	0
165	NA	1	Total 32	C 10	N 5	O 14	P 3	0
165	NC	1	Total 32	C 10	N 5	O 14	P 3	0
165	NE	1	Total 32	C 10	N 5	O 14	P 3	0
165	NF	1	Total 32	C 10	N 5	O 14	P 3	0
165	NI	1	Total 32	C 10	N 5	O 14	P 3	0
165	NK	1	Total 32	C 10	N 5	O 14	P 3	0
165	NM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	OA	1	Total 32	C 10	N 5	O 14	P 3	0
165	OC	1	Total 32	C 10	N 5	O 14	P 3	0
165	OD	1	Total 32	C 10	N 5	O 14	P 3	0
165	OG	1	Total 32	C 10	N 5	O 14	P 3	0
165	OI	1	Total 32	C 10	N 5	O 14	P 3	0
165	OK	1	Total 32	C 10	N 5	O 14	P 3	0
165	OM	1	Total 32	C 10	N 5	O 14	P 3	0
165	PA	1	Total 32	C 10	N 5	O 14	P 3	0
165	PC	1	Total 32	C 10	N 5	O 14	P 3	0
165	PE	1	Total 32	C 10	N 5	O 14	P 3	0
165	PG	1	Total 32	C 10	N 5	O 14	P 3	0
165	PI	1	Total 32	C 10	N 5	O 14	P 3	0
165	PK	1	Total 32	C 10	N 5	O 14	P 3	0
165	PM	1	Total 32	C 10	N 5	O 14	P 3	0
165	Q	1	Total 32	C 10	N 5	O 14	P 3	0
165	QB	1	Total 32	C 10	N 5	O 14	P 3	0
165	QC	1	Total 32	C 10	N 5	O 14	P 3	0
165	QF	1	Total 32	C 10	N 5	O 14	P 3	0
165	QH	1	Total 32	C 10	N 5	O 14	P 3	0
165	QI	1	Total 32	C 10	N 5	O 14	P 3	0
165	QL	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	R	1	Total 32	C 10	N 5	O 14	P 3	0
165	RB	1	Total 32	C 10	N 5	O 14	P 3	0
165	RC	1	Total 32	C 10	N 5	O 14	P 3	0
165	RF	1	Total 32	C 10	N 5	O 14	P 3	0
165	RH	1	Total 32	C 10	N 5	O 14	P 3	0
165	RJ	1	Total 32	C 10	N 5	O 14	P 3	0
165	RL	1	Total 32	C 10	N 5	O 14	P 3	0
165	SA	1	Total 32	C 10	N 5	O 14	P 3	0
165	SC	1	Total 32	C 10	N 5	O 14	P 3	0
165	SE	1	Total 32	C 10	N 5	O 14	P 3	0
165	SG	1	Total 32	C 10	N 5	O 14	P 3	0
165	SI	1	Total 32	C 10	N 5	O 14	P 3	0
165	SK	1	Total 32	C 10	N 5	O 14	P 3	0
165	T	1	Total 32	C 10	N 5	O 14	P 3	0
165	TC	1	Total 32	C 10	N 5	O 14	P 3	0
165	TE	1	Total 32	C 10	N 5	O 14	P 3	0
165	TG	1	Total 32	C 10	N 5	O 14	P 3	0
165	TI	1	Total 32	C 10	N 5	O 14	P 3	0
165	TK	1	Total 32	C 10	N 5	O 14	P 3	0
165	UA	1	Total 32	C 10	N 5	O 14	P 3	0
165	UC	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	UE	1	Total 32	C 10	N 5	O 14	P 3	0
165	UG	1	Total 32	C 10	N 5	O 14	P 3	0
165	UI	1	Total 32	C 10	N 5	O 14	P 3	0
165	UK	1	Total 32	C 10	N 5	O 14	P 3	0
165	VA	1	Total 32	C 10	N 5	O 14	P 3	0
165	VC	1	Total 32	C 10	N 5	O 14	P 3	0
165	VE	1	Total 32	C 10	N 5	O 14	P 3	0
165	VG	1	Total 32	C 10	N 5	O 14	P 3	0
165	VH	1	Total 32	C 10	N 5	O 14	P 3	0
165	VK	1	Total 32	C 10	N 5	O 14	P 3	0
165	VM	1	Total 32	C 10	N 5	O 14	P 3	0
165	WA	1	Total 32	C 10	N 5	O 14	P 3	0
165	WC	1	Total 32	C 10	N 5	O 14	P 3	0
165	WE	1	Total 32	C 10	N 5	O 14	P 3	0
165	WG	1	Total 32	C 10	N 5	O 14	P 3	0
165	WI	1	Total 32	C 10	N 5	O 14	P 3	0
165	WK	1	Total 32	C 10	N 5	O 14	P 3	0
165	WM	1	Total 32	C 10	N 5	O 14	P 3	0
165	AO	1	Total 32	C 10	N 5	O 14	P 3	0
165	AP	1	Total 32	C 10	N 5	O 14	P 3	0
165	AS	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	AU	1	Total 32	C 10	N 5	O 14	P 3	0
165	AW	1	Total 32	C 10	N 5	O 14	P 3	0
165	AY	1	Total 32	C 10	N 5	O 14	P 3	0
165	BO	1	Total 32	C 10	N 5	O 14	P 3	0
165	BQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	BS	1	Total 32	C 10	N 5	O 14	P 3	0
165	BU	1	Total 32	C 10	N 5	O 14	P 3	0
165	BW	1	Total 32	C 10	N 5	O 14	P 3	0
165	BY	1	Total 32	C 10	N 5	O 14	P 3	0
165	CN	1	Total 32	C 10	N 5	O 14	P 3	0
165	CO	1	Total 32	C 10	N 5	O 14	P 3	0
165	CQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	CT	1	Total 32	C 10	N 5	O 14	P 3	0
165	CV	1	Total 32	C 10	N 5	O 14	P 3	0
165	CW	1	Total 32	C 10	N 5	O 14	P 3	0
165	DN	1	Total 32	C 10	N 5	O 14	P 3	0
165	DP	1	Total 32	C 10	N 5	O 14	P 3	0
165	DQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	DT	1	Total 32	C 10	N 5	O 14	P 3	0
165	DV	1	Total 32	C 10	N 5	O 14	P 3	0
165	DX	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	EM	1	Total 32	C 10	N 5	O 14	P 3	0
165	EO	1	Total 32	C 10	N 5	O 14	P 3	0
165	EP	1	Total 32	C 10	N 5	O 14	P 3	0
165	ES	1	Total 32	C 10	N 5	O 14	P 3	0
165	EU	1	Total 32	C 10	N 5	O 14	P 3	0
165	EV	1	Total 32	C 10	N 5	O 14	P 3	0
165	FM	1	Total 32	C 10	N 5	O 14	P 3	0
165	FO	1	Total 32	C 10	N 5	O 14	P 3	0
165	FQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	FS	1	Total 32	C 10	N 5	O 14	P 3	0
165	FT	1	Total 32	C 10	N 5	O 14	P 3	0
165	FV	1	Total 32	C 10	N 5	O 14	P 3	0
165	GO	1	Total 32	C 10	N 5	O 14	P 3	0
165	GQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	GS	1	Total 32	C 10	N 5	O 14	P 3	0
165	GU	1	Total 32	C 10	N 5	O 14	P 3	0
165	GW	1	Total 32	C 10	N 5	O 14	P 3	0
165	HN	1	Total 32	C 10	N 5	O 14	P 3	0
165	HQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	HS	1	Total 32	C 10	N 5	O 14	P 3	0
165	HU	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	HW	1	Total 32	C 10	N 5	O 14	P 3	0
165	HY	1	Total 32	C 10	N 5	O 14	P 3	0
165	IO	1	Total 32	C 10	N 5	O 14	P 3	0
165	IQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	IS	1	Total 32	C 10	N 5	O 14	P 3	0
165	IU	1	Total 32	C 10	N 5	O 14	P 3	0
165	IW	1	Total 32	C 10	N 5	O 14	P 3	0
165	IY	1	Total 32	C 10	N 5	O 14	P 3	0
165	JP	1	Total 32	C 10	N 5	O 14	P 3	0
165	JR	1	Total 32	C 10	N 5	O 14	P 3	0
165	JT	1	Total 32	C 10	N 5	O 14	P 3	0
165	JV	1	Total 32	C 10	N 5	O 14	P 3	0
165	JW	1	Total 32	C 10	N 5	O 14	P 3	0
165	JZ	1	Total 32	C 10	N 5	O 14	P 3	0
165	KP	1	Total 32	C 10	N 5	O 14	P 3	0
165	KR	1	Total 32	C 10	N 5	O 14	P 3	0
165	KT	1	Total 32	C 10	N 5	O 14	P 3	0
165	KV	1	Total 32	C 10	N 5	O 14	P 3	0
165	KX	1	Total 32	C 10	N 5	O 14	P 3	0
165	KZ	1	Total 32	C 10	N 5	O 14	P 3	0
165	LP	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	LR	1	Total 32	C 10	N 5	O 14	P 3	0
165	LT	1	Total 32	C 10	N 5	O 14	P 3	0
165	LV	1	Total 32	C 10	N 5	O 14	P 3	0
165	LX	1	Total 32	C 10	N 5	O 14	P 3	0
165	LZ	1	Total 32	C 10	N 5	O 14	P 3	0
165	MO	1	Total 32	C 10	N 5	O 14	P 3	0
165	MQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	MS	1	Total 32	C 10	N 5	O 14	P 3	0
165	MU	1	Total 32	C 10	N 5	O 14	P 3	0
165	MV	1	Total 32	C 10	N 5	O 14	P 3	0
165	MY	1	Total 32	C 10	N 5	O 14	P 3	0
165	PO	1	Total 32	C 10	N 5	O 14	P 3	0
165	PQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	PS	1	Total 32	C 10	N 5	O 14	P 3	0
165	PU	1	Total 32	C 10	N 5	O 14	P 3	0
165	PW	1	Total 32	C 10	N 5	O 14	P 3	0
165	PY	1	Total 32	C 10	N 5	O 14	P 3	0
165	QN	1	Total 32	C 10	N 5	O 14	P 3	0
165	QO	1	Total 32	C 10	N 5	O 14	P 3	0
165	QR	1	Total 32	C 10	N 5	O 14	P 3	0
165	QT	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	QU	1	Total 32	C 10	N 5	O 14	P 3	0
165	QX	1	Total 32	C 10	N 5	O 14	P 3	0
165	RN	1	Total 32	C 10	N 5	O 14	P 3	0
165	RO	1	Total 32	C 10	N 5	O 14	P 3	0
165	RR	1	Total 32	C 10	N 5	O 14	P 3	0
165	RT	1	Total 32	C 10	N 5	O 14	P 3	0
165	RV	1	Total 32	C 10	N 5	O 14	P 3	0
165	RX	1	Total 32	C 10	N 5	O 14	P 3	0
165	SM	1	Total 32	C 10	N 5	O 14	P 3	0
165	SO	1	Total 32	C 10	N 5	O 14	P 3	0
165	SQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	SS	1	Total 32	C 10	N 5	O 14	P 3	0
165	SU	1	Total 32	C 10	N 5	O 14	P 3	0
165	SW	1	Total 32	C 10	N 5	O 14	P 3	0
165	TM	1	Total 32	C 10	N 5	O 14	P 3	0
165	TO	1	Total 32	C 10	N 5	O 14	P 3	0
165	TQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	TS	1	Total 32	C 10	N 5	O 14	P 3	0
165	TU	1	Total 32	C 10	N 5	O 14	P 3	0
165	TW	1	Total 32	C 10	N 5	O 14	P 3	0
165	UM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	UO	1	Total 32	C 10	N 5	O 14	P 3	0
165	UQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	US	1	Total 32	C 10	N 5	O 14	P 3	0
165	UU	1	Total 32	C 10	N 5	O 14	P 3	0
165	UW	1	Total 32	C 10	N 5	O 14	P 3	0
165	VO	1	Total 32	C 10	N 5	O 14	P 3	0
165	VQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	VS	1	Total 32	C 10	N 5	O 14	P 3	0
165	VT	1	Total 32	C 10	N 5	O 14	P 3	0
165	VW	1	Total 32	C 10	N 5	O 14	P 3	0
165	VY	1	Total 32	C 10	N 5	O 14	P 3	0
165	WO	1	Total 32	C 10	N 5	O 14	P 3	0
165	WQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	WS	1	Total 32	C 10	N 5	O 14	P 3	0
165	WU	1	Total 32	C 10	N 5	O 14	P 3	0
165	WW	1	Total 32	C 10	N 5	O 14	P 3	0
165	WY	1	Total 32	C 10	N 5	O 14	P 3	0
165	NO	1	Total 32	C 10	N 5	O 14	P 3	0
165	NQ	1	Total 32	C 10	N 5	O 14	P 3	0
165	NR	1	Total 32	C 10	N 5	O 14	P 3	0
165	NU	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
165	NW	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	NY	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	OO	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	OP	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	OS	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	OU	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	OW	1	Total	C	N	O	P	0
			32	10	5	14	3	
165	OY	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 166 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
166	KB	1	Total	Zn	0
			1	1	
166	KD	1	Total	Zn	0
			1	1	
166	KN	1	Total	Zn	0
			1	1	
166	LD	1	Total	Zn	0
			1	1	
166	LF	1	Total	Zn	0
			1	1	
166	LN	1	Total	Zn	0
			1	1	
166	KP	1	Total	Zn	0
			1	1	
166	LP	1	Total	Zn	0
			1	1	
166	LR	1	Total	Zn	0
			1	1	
166	LZ	1	Total	Zn	0
			1	1	
166	0A	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
166	0	1	Total 1	Zn 1	0
166	0z	1	Total 1	Zn 1	0
166	1V	2	Total 2	Zn 2	0
166	1b	2	Total 2	Zn 2	0
166	1e	2	Total 2	Zn 2	0
166	1q	1	Total 1	Zn 1	0
166	1s	1	Total 1	Zn 1	0
166	1w	1	Total 1	Zn 1	0
166	1x	1	Total 1	Zn 1	0
166	3S	1	Total 1	Zn 1	0
166	0B	1	Total 1	Zn 1	0
166	2A	1	Total 1	Zn 1	0
166	1W	2	Total 2	Zn 2	0
166	1Z	1	Total 1	Zn 1	0
166	1c	2	Total 2	Zn 2	0
166	9F	2	Total 2	Zn 2	0
166	1f	2	Total 2	Zn 2	0
166	1i	2	Total 2	Zn 2	0
166	1t	1	Total 1	Zn 1	0
166	1v	1	Total 1	Zn 1	0
166	1z	1	Total 1	Zn 1	0

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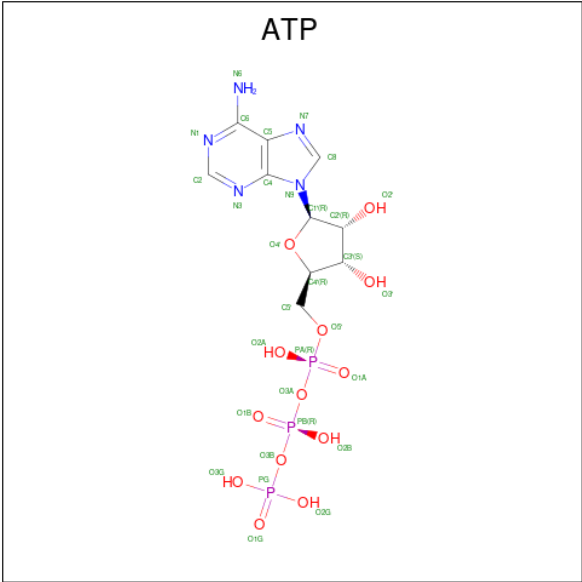
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Mol	Chain	Residues	Atoms		AltConf
166	3T	1	Total 1	Zn 1	0
166	4X	2	Total 2	Zn 2	0
166	1Y	1	Total 1	Zn 1	0
166	5S	1	Total 1	Zn 1	0
166	5T	1	Total 1	Zn 1	0
166	5U	1	Total 1	Zn 1	0
166	5V	1	Total 1	Zn 1	0
166	4L	2	Total 2	Zn 2	0

- Molecule 167 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
167	1S	1	Total 1	Ca 1	0
167	2v	1	Total 1	Ca 1	0
167	2w	1	Total 1	Ca 1	0
167	1T	1	Total 1	Ca 1	0
167	2x	1	Total 1	Ca 1	0

- Molecule 168 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
168	2v	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	2w	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	2x	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	6l	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	6p	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	9R	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	6u	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	7A	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	7D	1	Total	C	N	O	P	0
			31	10	5	13	3	
168	8a	1	Total	C	N	O	P	0
			31	10	5	13	3	

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	281984	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k 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](#)

Of 956 ligands modelled in this entry, 355 are monoatomic - leaving 601 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
165	GTP	VK	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	AF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	6 (13%)
165	GTP	FG	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	SW	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	MJ	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	VR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	TF	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	6 (13%)
163	GDP	DS	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	CB	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	GB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	6 (13%)
163	GDP	HB	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	QI	501	164	33,34,34	0.95	2 (6%)	50,54,54	1.58	10 (20%)
165	GTP	SC	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	IW	501	164	33,34,34	1.23	5 (15%)	50,54,54	1.63	10 (20%)
163	GDP	JE	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	MZ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	DQ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	AU	501	164	33,34,34	0.85	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	VP	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	IB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	GI	501	164	33,34,34	0.93	2 (6%)	50,54,54	1.60	10 (20%)
163	GDP	AX	500	-	29,30,30	1.15	4 (13%)	45,47,47	1.71	7 (15%)
163	GDP	ON	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	MU	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.54	8 (16%)
165	GTP	AB	501	164	33,34,34	0.93	0	50,54,54	1.51	8 (16%)
163	GDP	NV	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	HE	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.55	9 (18%)
165	GTP	TI	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	CO	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	MQ	501	164	33,34,34	0.99	2 (6%)	50,54,54	1.58	9 (18%)
168	ATP	2w	501	-	32,33,33	0.33	0	48,52,52	0.29	0
163	GDP	NX	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	TE	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	LY	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	LT	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
163	GDP	UB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
168	ATP	7D	601	164	32,33,33	0.42	0	48,52,52	0.30	0
163	GDP	JW	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	FA	501	164	33,34,34	0.91	0	50,54,54	1.54	8 (16%)
165	GTP	QB	501	164	33,34,34	0.96	2 (6%)	50,54,54	1.59	8 (16%)
165	GTP	CC	501	164	33,34,34	0.97	0	50,54,54	1.58	9 (18%)
163	GDP	DA	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	6 (13%)
165	GTP	DB	501	164	33,34,34	0.91	0	50,54,54	1.62	10 (20%)
165	GTP	GC	501	164	33,34,34	0.89	0	50,54,54	1.60	10 (20%)
168	ATP	8a	801	-	32,33,33	0.49	1 (3%)	48,52,52	0.30	0
163	GDP	OD	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	VV	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	8 (17%)
165	GTP	R	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	WY	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	TG	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	MD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	VH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	BL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	BN	500	-	29,30,30	1.16	4 (13%)	45,47,47	1.73	7 (15%)
165	GTP	D	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.62	10 (20%)
165	GTP	NI	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	GJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	PX	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	DP	501	164	33,34,34	0.91	0	50,54,54	1.63	12 (24%)
165	GTP	VG	501	164	33,34,34	1.00	2 (6%)	50,54,54	1.58	9 (18%)
163	GDP	GR	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	6 (13%)
165	GTP	MJ	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	C	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	RC	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	GE	501	164	33,34,34	0.91	0	50,54,54	1.61	9 (18%)
163	GDP	HR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	AM	501	164	33,34,34	0.90	0	50,54,54	1.56	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	G	501	164	33,34,34	0.89	0	50,54,54	1.54	9 (18%)
165	GTP	LZ	502	164	33,34,34	0.97	1 (3%)	50,54,54	1.55	9 (18%)
165	GTP	OM	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	O	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	QX	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	VX	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	6 (13%)
165	GTP	II	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.60	9 (18%)
163	GDP	OJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	LB	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.56	9 (18%)
163	GDP	PT	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	6 (13%)
163	GDP	CI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
165	GTP	UO	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	PA	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	IH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	SS	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.59	10 (20%)
163	GDP	QW	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.74	6 (13%)
163	GDP	NH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	DX	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.62	10 (20%)
163	GDP	AD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	8 (17%)
163	GDP	NP	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	8 (17%)
165	GTP	EG	501	164	33,34,34	0.92	0	50,54,54	1.63	10 (20%)
165	GTP	HK	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.60	9 (18%)
165	GTP	CO	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	AS	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.54	8 (16%)
163	GDP	SN	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	BV	500	-	29,30,30	1.16	4 (13%)	45,47,47	1.70	5 (11%)
165	GTP	SQ	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.59	10 (20%)
165	GTP	OY	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	WR	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	LC	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	6 (13%)
165	GTP	HA	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.54	9 (18%)
165	GTP	FM	501	164	33,34,34	0.89	0	50,54,54	1.53	8 (16%)
163	GDP	SJ	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	EV	501	164	33,34,34	0.94	0	50,54,54	1.55	9 (18%)
163	GDP	IV	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
163	GDP	TX	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	CG	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	AY	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.52	8 (16%)
163	GDP	NB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	IX	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	TN	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	HT	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	WJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	FP	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	LI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	BT	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.80	7 (15%)
163	GDP	GD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	7 (15%)
165	GTP	HU	501	164	33,34,34	0.88	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	HY	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.55	9 (18%)
165	GTP	BW	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.54	8 (16%)
163	GDP	ET	500	-	29,30,30	1.15	4 (13%)	45,47,47	1.68	5 (11%)
163	GDP	BJ	500	-	29,30,30	1.16	4 (13%)	45,47,47	1.75	7 (15%)
163	GDP	KO	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	HV	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	OC	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	LE	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	RA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
165	GTP	NK	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
163	GDP	TP	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
165	GTP	NW	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)
163	GDP	EJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	PS	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	PN	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	WI	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	WE	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.59	10 (20%)
165	GTP	BO	501	164	33,34,34	0.95	0	50,54,54	1.56	9 (18%)
163	GDP	HL	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	MR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	CJ	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	FN	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.75	8 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
163	GDP	GH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	6 (13%)
163	GDP	MX	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	FE	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.54	9 (18%)
163	GDP	I	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	QN	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.59	8 (16%)
163	GDP	KY	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
165	GTP	FT	503	164	33,34,34	0.87	2 (6%)	50,54,54	1.65	11 (22%)
165	GTP	EU	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.61	9 (18%)
165	GTP	HI	501	164	33,34,34	0.88	1 (3%)	50,54,54	1.55	9 (18%)
165	GTP	OO	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	DJ	501	164	33,34,34	0.93	0	50,54,54	1.52	8 (16%)
165	GTP	HS	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	NC	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	SO	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	IK	501	164	33,34,34	1.23	5 (15%)	50,54,54	1.62	10 (20%)
165	GTP	JV	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	VN	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	HF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	RS	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	JK	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	FD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	6 (13%)
165	GTP	K	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.58	9 (18%)
163	GDP	H	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	MY	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	JJ	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	AJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	CE	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	SH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	BH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	FX	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	AP	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	LO	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	6 (13%)
165	GTP	CH	501	164	33,34,34	0.91	2 (6%)	50,54,54	1.65	9 (18%)
165	GTP	WA	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	DV	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.57	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	QF	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	VM	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	UW	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	JM	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	AO	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.54	9 (18%)
163	GDP	QK	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.73	6 (13%)
163	GDP	E	500	-	29,30,30	1.24	4 (13%)	45,47,47	1.80	7 (15%)
163	GDP	ST	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	CE	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.56	9 (18%)
163	GDP	PD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	OR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	SA	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	AG	501	164	33,34,34	0.89	0	50,54,54	1.53	8 (16%)
163	GDP	OF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	BQ	501	164	33,34,34	0.86	1 (3%)	50,54,54	1.56	8 (16%)
168	ATP	7A	402	-	32,33,33	0.45	0	48,52,52	0.29	0
163	GDP	RQ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.79	8 (17%)
163	GDP	T	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	RN	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	EL	500	-	29,30,30	1.20	3 (10%)	45,47,47	1.74	5 (11%)
163	GDP	LM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	VC	501	164	33,34,34	1.00	2 (6%)	50,54,54	1.56	9 (18%)
163	GDP	MB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	6 (13%)
163	GDP	S	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	CV	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.61	9 (18%)
163	GDP	SP	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)
165	GTP	BA	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	QS	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	RL	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
165	GTP	UI	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	PI	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	UJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	GL	501	164	33,34,34	0.95	0	50,54,54	1.58	9 (18%)
165	GTP	OG	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)
165	GTP	SG	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.59	10 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	PO	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	TW	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.54	9 (18%)
163	GDP	IN	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	WF	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	KS	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	M	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	VT	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	L	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
165	GTP	MV	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	LW	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	DK	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	ID	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	WW	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	AT	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	LX	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.54	8 (16%)
163	GDP	ER	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	VL	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.74	6 (13%)
165	GTP	QL	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	NQ	501	164	33,34,34	1.00	2 (6%)	50,54,54	1.57	9 (18%)
163	GDP	WL	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	CN	501	164	33,34,34	0.97	0	50,54,54	1.55	8 (16%)
165	GTP	DQ	501	164	33,34,34	0.95	2 (6%)	50,54,54	1.60	9 (18%)
163	GDP	PL	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	OK	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.61	9 (18%)
163	GDP	LK	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	OW	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.60	9 (18%)
165	GTP	IO	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.61	9 (18%)
165	GTP	TM	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.58	10 (20%)
165	GTP	IE	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.62	9 (18%)
163	GDP	DU	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	GG	501	164	33,34,34	0.86	1 (3%)	50,54,54	1.62	10 (20%)
163	GDP	CS	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	5 (11%)
165	GTP	TS	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	US	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	SL	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	LL	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.54	8 (16%)
163	GDP	MV	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	HN	503	164	33,34,34	0.97	2 (6%)	50,54,54	1.59	9 (18%)
168	ATP	6l	400	164	32,33,33	0.36	0	48,52,52	0.38	0
165	GTP	LV	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)
163	GDP	DM	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	JC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	KA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	HP	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	PE	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.59	8 (16%)
163	GDP	LS	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	6 (13%)
163	GDP	JQ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	KH	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
163	GDP	FF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	UK	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	QA	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	GW	501	164	33,34,34	0.93	0	50,54,54	1.59	9 (18%)
165	GTP	HW	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.60	9 (18%)
163	GDP	CC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	6 (13%)
165	GTP	RO	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.55	8 (16%)
165	GTP	JW	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	CY	500	-	29,30,30	1.20	3 (10%)	45,47,47	1.81	7 (15%)
163	GDP	JK	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	HM	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.55	9 (18%)
163	GDP	N	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	CW	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.86	7 (15%)
165	GTP	UA	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	9 (18%)
165	GTP	VH	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
163	GDP	A	501	-	29,30,30	1.19	3 (10%)	45,47,47	1.80	7 (15%)
163	GDP	EX	500	-	29,30,30	1.24	4 (13%)	45,47,47	1.71	6 (13%)
165	GTP	OP	503	164	33,34,34	0.95	2 (6%)	50,54,54	1.58	10 (20%)
163	GDP	FL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	JY	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	IS	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	RV	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.58	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	DH	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	RX	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	EV	500	-	29,30,30	1.14	4 (13%)	45,47,47	1.75	7 (15%)
168	ATP	6p	500	164	32,33,33	0.48	0	48,52,52	0.30	0
163	GDP	KK	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	QH	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.63	10 (20%)
163	GDP	TD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	SR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	KZ	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	PG	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	LA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	RO	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	JZ	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	DE	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	5 (11%)
165	GTP	UQ	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.55	9 (18%)
163	GDP	RG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	OB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	JO	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	NJ	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	GT	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	HQ	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.55	9 (18%)
163	GDP	UF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	DI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	PM	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	MG	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	RC	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.55	8 (16%)
163	GDP	QM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	IF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	IU	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.60	9 (18%)
165	GTP	LJ	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)
163	GDP	CU	500	-	29,30,30	1.15	4 (13%)	45,47,47	1.72	7 (15%)
163	GDP	WN	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	KC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	BF	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.72	6 (13%)
163	GDP	TV	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	RF	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
163	GDP	ED	500	-	29,30,30	1.17	4 (13%)	45,47,47	1.76	6 (13%)
163	GDP	WD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	UN	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	FC	501	164	33,34,34	0.89	0	50,54,54	1.55	8 (16%)
163	GDP	GN	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	WX	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	HH	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	QC	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	QU	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
165	GTP	T	503	164	33,34,34	0.97	2 (6%)	50,54,54	1.58	10 (20%)
163	GDP	GP	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	PB	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	ES	501	164	33,34,34	0.93	0	50,54,54	1.63	10 (20%)
165	GTP	EJ	501	164	33,34,34	0.99	2 (6%)	50,54,54	1.61	10 (20%)
165	GTP	BK	501	164	33,34,34	0.93	0	50,54,54	1.55	8 (16%)
165	GTP	MA	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	DC	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.72	6 (13%)
163	GDP	RI	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	MI	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.54	8 (16%)
165	GTP	DN	501	164	33,34,34	0.92	0	50,54,54	1.60	8 (16%)
163	GDP	U	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	NO	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	HB	503	164	33,34,34	0.97	2 (6%)	50,54,54	1.59	10 (20%)
165	GTP	NA	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
165	GTP	QO	501	164	33,34,34	0.96	2 (6%)	50,54,54	1.59	9 (18%)
165	GTP	PK	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
165	GTP	SE	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.59	10 (20%)
163	GDP	KQ	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	FV	503	-	33,34,34	0.90	1 (3%)	50,54,54	1.62	8 (16%)
165	GTP	LF	502	164	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)
163	GDP	TJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	6 (13%)
163	GDP	BR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	MC	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	WC	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.55	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	MS	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	IR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	DD	501	164	33,34,34	0.92	0	50,54,54	1.63	10 (20%)
165	GTP	IG	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	FR	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	SU	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	NM	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	CT	501	164	33,34,34	0.93	2 (6%)	50,54,54	1.64	10 (20%)
163	GDP	BP	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	EO	501	164	33,34,34	0.92	0	50,54,54	1.55	9 (18%)
163	GDP	KI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	JG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	LH	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
165	GTP	VA	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	HD	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	BM	501	164	33,34,34	0.95	0	50,54,54	1.55	8 (16%)
165	GTP	HG	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	AK	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	VS	501	164	33,34,34	1.00	3 (9%)	50,54,54	1.57	9 (18%)
165	GTP	OD	503	164	33,34,34	0.96	2 (6%)	50,54,54	1.59	10 (20%)
163	GDP	SD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	6 (13%)
165	GTP	TU	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	TB	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	TT	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	NU	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	EH	500	-	29,30,30	1.17	4 (13%)	45,47,47	1.75	8 (17%)
163	GDP	VF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	QO	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	LP	502	164	33,34,34	0.95	1 (3%)	50,54,54	1.54	8 (16%)
163	GDP	FB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	SB	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	OL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	IT	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	ED	501	164	33,34,34	0.94	0	50,54,54	1.58	9 (18%)
163	GDP	AH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
163	GDP	UX	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	6 (13%)
165	GTP	WK	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	SM	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	TQ	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	NT	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	WU	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	PJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	OH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	SK	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	J	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	8 (16%)
165	GTP	QU	501	164	33,34,34	0.95	2 (6%)	50,54,54	1.59	10 (20%)
165	GTP	DL	501	-	33,34,34	0.90	0	50,54,54	1.59	9 (18%)
165	GTP	RR	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
163	GDP	AZ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	QI	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	VY	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	HJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	OV	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	MO	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	KP	502	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	WM	501	164	33,34,34	0.98	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	KL	501	164	33,34,34	0.96	2 (6%)	50,54,54	1.58	9 (18%)
165	GTP	ME	501	164	33,34,34	0.99	2 (6%)	50,54,54	1.58	9 (18%)
168	ATP	2x	501	-	32,33,33	0.33	0	48,52,52	0.28	0
165	GTP	IM	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	RB	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.56	8 (16%)
163	GDP	EN	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	FI	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.59	10 (20%)
165	GTP	UG	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	F	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
168	ATP	2v	501	-	32,33,33	0.30	0	48,52,52	0.31	0
165	GTP	OS	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	LD	502	164	33,34,34	0.96	1 (3%)	50,54,54	1.55	8 (16%)
165	GTP	QT	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.63	11 (22%)
165	GTP	TO	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.58	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	TC	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	HN	501	-	29,30,30	1.15	2 (6%)	45,47,47	1.75	7 (15%)
165	GTP	NR	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.60	9 (18%)
165	GTP	KF	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.56	9 (18%)
165	GTP	VE	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	NF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	VT	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.59	9 (18%)
163	GDP	UR	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	MF	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	KU	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	MP	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	TK	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.53	8 (16%)
163	GDP	QQ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	FQ	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	NL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	WT	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	RH	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	RM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
165	GTP	KB	502	164	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)
165	GTP	BS	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	IJ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	IC	501	164	33,34,34	0.98	2 (6%)	50,54,54	1.61	9 (18%)
165	GTP	WO	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.55	9 (18%)
163	GDP	EP	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	BD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	8 (17%)
165	GTP	KX	501	164	33,34,34	0.96	2 (6%)	50,54,54	1.59	9 (18%)
165	GTP	GO	501	164	33,34,34	0.89	0	50,54,54	1.59	9 (18%)
163	GDP	VB	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	V	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	WP	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
163	GDP	FJ	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	AP	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	LN	502	164	33,34,34	0.96	1 (3%)	50,54,54	1.55	9 (18%)
165	GTP	WS	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	GK	501	164	33,34,34	0.95	0	50,54,54	1.58	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
163	GDP	NR	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	ML	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	LG	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	6 (13%)
163	GDP	MH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	DW	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	EM	501	164	33,34,34	0.94	0	50,54,54	1.56	8 (16%)
165	GTP	GS	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.61	8 (16%)
165	GTP	KT	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.61	9 (18%)
163	GDP	OP	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	UE	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	JI	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	ND	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	8 (17%)
163	GDP	RU	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	HX	501	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	DT	501	164	33,34,34	0.87	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	NE	501	164	33,34,34	1.00	2 (6%)	50,54,54	1.56	9 (18%)
165	GTP	UC	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	MT	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	PP	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	TL	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	UD	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	VQ	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	KN	502	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	PH	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	6 (13%)
163	GDP	AR	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	6 (13%)
163	GDP	FV	501	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	WQ	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.59	9 (18%)
163	GDP	CM	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.81	9 (20%)
163	GDP	W	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	WG	501	164	33,34,34	0.88	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	NF	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.60	9 (18%)
165	GTP	KJ	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.58	8 (16%)
165	GTP	VO	501	164	33,34,34	0.99	2 (6%)	50,54,54	1.55	8 (16%)
165	GTP	BY	501	164	33,34,34	0.94	0	50,54,54	1.53	8 (16%)
165	GTP	KR	501	164	33,34,34	0.99	2 (6%)	50,54,54	1.56	9 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	PU	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	CK	501	-	29,30,30	1.17	3 (10%)	45,47,47	1.80	7 (15%)
163	GDP	DY	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	6 (13%)
163	GDP	EB	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.71	6 (13%)
163	GDP	WB	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	AL	500	-	29,30,30	1.16	4 (13%)	45,47,47	1.77	8 (17%)
163	GDP	FH	500	-	29,30,30	1.15	4 (13%)	45,47,47	1.72	7 (15%)
163	GDP	NN	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	SI	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	G	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	KD	502	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	RJ	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	CA	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	EP	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.58	9 (18%)
165	GTP	PC	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.56	8 (16%)
163	GDP	UT	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	IQ	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.62	9 (18%)
165	GTP	UU	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.60	9 (18%)
163	GDP	UL	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	LU	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	AI	501	164	33,34,34	0.87	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	PR	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	6 (13%)
163	GDP	MN	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	BX	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.72	6 (13%)
165	GTP	JF	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.60	9 (18%)
163	GDP	DG	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	6 (13%)
165	GTP	KV	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	GL	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	CQ	501	164	33,34,34	0.96	2 (6%)	50,54,54	1.57	9 (18%)
165	GTP	PQ	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.59	8 (16%)
165	GTP	JR	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.60	9 (18%)
165	GTP	JD	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	EF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	P	500	-	29,30,30	1.18	3 (10%)	45,47,47	1.82	7 (15%)
165	GTP	AA	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.55	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	EA	501	164	33,34,34	0.96	1 (3%)	50,54,54	1.62	8 (16%)
163	GDP	LQ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	EC	501	164	33,34,34	0.92	0	50,54,54	1.55	9 (18%)
163	GDP	OT	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.74	7 (15%)
163	GDP	OX	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	RE	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.80	8 (17%)
163	GDP	QE	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	IL	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.78	7 (15%)
165	GTP	PY	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	GX	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	GU	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	KM	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	JA	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	OA	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.55	8 (16%)
165	GTP	JB	501	164	33,34,34	0.93	1 (3%)	50,54,54	1.57	8 (16%)
163	GDP	JU	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	GV	501	-	29,30,30	1.13	3 (10%)	45,47,47	1.77	6 (13%)
165	GTP	VW	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	GQ	501	164	33,34,34	0.88	2 (6%)	50,54,54	1.70	10 (20%)
163	GDP	SF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	UM	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.55	9 (18%)
163	GDP	PV	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)
165	GTP	CW	501	164	33,34,34	0.95	0	50,54,54	1.53	8 (16%)
165	GTP	IA	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	8 (16%)
163	GDP	WH	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	QG	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	IP	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	6 (13%)
163	GDP	UV	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	BU	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.61	10 (20%)
165	GTP	CK	503	164	33,34,34	0.92	1 (3%)	50,54,54	1.57	8 (16%)
165	GTP	IY	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.57	8 (16%)
168	ATP	6u	700	-	32,33,33	0.36	0	48,52,52	0.28	0
163	GDP	VD	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	VJ	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	8 (17%)
163	GDP	WV	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
163	GDP	CQ	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	LR	502	164	33,34,34	0.91	1 (3%)	50,54,54	1.59	8 (16%)
163	GDP	UP	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.73	7 (15%)
165	GTP	JN	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	Q	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.57	9 (18%)
165	GTP	JH	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	9 (18%)
165	GTP	OU	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
163	GDP	AN	500	-	29,30,30	1.14	4 (13%)	45,47,47	1.71	7 (15%)
165	GTP	EI	501	164	33,34,34	0.90	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	FO	501	164	33,34,34	0.90	0	50,54,54	1.55	9 (18%)
165	GTP	PW	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	RT	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.58	9 (18%)
165	GTP	AW	501	164	33,34,34	0.95	1 (3%)	50,54,54	1.56	8 (16%)
165	GTP	NY	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.56	9 (18%)
165	GTP	BE	501	164	33,34,34	0.91	0	50,54,54	1.58	10 (20%)
163	GDP	KW	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
165	GTP	AD	501	164	33,34,34	0.88	1 (3%)	50,54,54	1.60	10 (20%)
163	GDP	UH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	BI	501	164	33,34,34	0.97	3 (9%)	50,54,54	1.62	9 (18%)
163	GDP	JS	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	SV	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	AB	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
165	GTP	DE	501	164	33,34,34	0.92	2 (6%)	50,54,54	1.62	9 (18%)
165	GTP	JP	501	164	33,34,34	0.94	1 (3%)	50,54,54	1.55	8 (16%)
163	GDP	TH	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	KE	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
163	GDP	KG	500	-	29,30,30	1.17	3 (10%)	45,47,47	1.76	7 (15%)
163	GDP	DO	500	-	29,30,30	1.16	4 (13%)	45,47,47	1.74	5 (11%)
168	ATP	9R	500	164	32,33,33	0.36	0	48,52,52	0.30	0
165	GTP	JT	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.58	9 (18%)
163	GDP	AV	500	-	29,30,30	1.15	4 (13%)	45,47,47	1.73	7 (15%)
163	GDP	TR	500	-	29,30,30	1.13	3 (10%)	45,47,47	1.76	6 (13%)
163	GDP	RW	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
163	GDP	PF	501	-	29,30,30	1.15	3 (10%)	45,47,47	1.73	7 (15%)
163	GDP	GF	500	-	29,30,30	1.14	3 (10%)	45,47,47	1.75	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
165	GTP	FS	501	164	33,34,34	0.88	0	50,54,54	1.62	8 (16%)
165	GTP	QR	501	164	33,34,34	0.89	1 (3%)	50,54,54	1.59	9 (18%)
165	GTP	QC	501	164	33,34,34	0.97	2 (6%)	50,54,54	1.58	9 (18%)
165	GTP	BG	501	164	33,34,34	0.91	1 (3%)	50,54,54	1.58	9 (18%)
165	GTP	FJ	503	164	33,34,34	0.93	1 (3%)	50,54,54	1.60	8 (16%)
163	GDP	RK	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.77	7 (15%)
165	GTP	OI	501	164	33,34,34	0.92	1 (3%)	50,54,54	1.56	9 (18%)
163	GDP	FT	501	-	29,30,30	1.16	4 (13%)	45,47,47	1.68	7 (15%)
165	GTP	MM	501	164	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)

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
165	GTP	VK	501	164	-	5/22/38/38	0/3/3/3
163	GDP	AF	500	-	-	1/16/32/32	0/3/3/3
165	GTP	FG	501	164	-	8/22/38/38	0/3/3/3
165	GTP	SW	501	164	-	0/22/38/38	0/3/3/3
163	GDP	MJ	500	-	-	3/16/32/32	0/3/3/3
163	GDP	VR	500	-	-	1/16/32/32	0/3/3/3
163	GDP	TF	500	-	-	1/16/32/32	0/3/3/3
163	GDP	DS	500	-	-	2/16/32/32	0/3/3/3
165	GTP	CB	501	164	-	3/22/38/38	0/3/3/3
163	GDP	GB	500	-	-	2/16/32/32	0/3/3/3
163	GDP	HB	501	-	-	3/16/32/32	0/3/3/3
165	GTP	QI	501	164	-	4/22/38/38	0/3/3/3
165	GTP	SC	501	164	-	6/22/38/38	0/3/3/3
165	GTP	IW	501	164	-	3/22/38/38	0/3/3/3
163	GDP	JE	500	-	-	1/16/32/32	0/3/3/3
163	GDP	MZ	500	-	-	2/16/32/32	0/3/3/3
163	GDP	DQ	500	-	-	3/16/32/32	0/3/3/3
165	GTP	AU	501	164	-	3/22/38/38	0/3/3/3
163	GDP	VP	500	-	-	1/16/32/32	0/3/3/3
163	GDP	IB	500	-	-	3/16/32/32	0/3/3/3
165	GTP	GI	501	164	-	1/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	AX	500	-	-	2/16/32/32	0/3/3/3
163	GDP	ON	500	-	-	5/16/32/32	0/3/3/3
165	GTP	MU	501	164	-	5/22/38/38	0/3/3/3
165	GTP	AB	501	164	-	5/22/38/38	0/3/3/3
163	GDP	NV	501	-	-	1/16/32/32	0/3/3/3
165	GTP	HE	501	164	-	4/22/38/38	0/3/3/3
165	GTP	TI	501	164	-	4/22/38/38	0/3/3/3
163	GDP	CO	500	-	-	0/16/32/32	0/3/3/3
165	GTP	MQ	501	164	-	5/22/38/38	0/3/3/3
168	ATP	2w	501	-	-	7/22/38/38	0/3/3/3
163	GDP	NX	500	-	-	1/16/32/32	0/3/3/3
165	GTP	TE	501	164	-	6/22/38/38	0/3/3/3
163	GDP	LY	500	-	-	1/16/32/32	0/3/3/3
165	GTP	LT	501	164	-	3/22/38/38	0/3/3/3
163	GDP	UB	500	-	-	3/16/32/32	0/3/3/3
168	ATP	7D	601	164	-	10/22/38/38	0/3/3/3
163	GDP	JW	500	-	-	3/16/32/32	0/3/3/3
165	GTP	FA	501	164	-	4/22/38/38	0/3/3/3
165	GTP	QB	501	164	-	2/22/38/38	0/3/3/3
165	GTP	CC	501	164	-	4/22/38/38	0/3/3/3
163	GDP	DA	500	-	-	4/16/32/32	0/3/3/3
165	GTP	DB	501	164	-	3/22/38/38	0/3/3/3
165	GTP	GC	501	164	-	5/22/38/38	0/3/3/3
168	ATP	8a	801	-	-	1/22/38/38	0/3/3/3
163	GDP	OD	501	-	-	2/16/32/32	0/3/3/3
163	GDP	VV	500	-	-	2/16/32/32	0/3/3/3
165	GTP	R	501	164	-	6/22/38/38	0/3/3/3
165	GTP	WY	501	164	-	3/22/38/38	0/3/3/3
165	GTP	TG	501	164	-	1/22/38/38	0/3/3/3
163	GDP	MD	500	-	-	1/16/32/32	0/3/3/3
163	GDP	VH	500	-	-	1/16/32/32	0/3/3/3
163	GDP	BL	500	-	-	4/16/32/32	0/3/3/3
163	GDP	BN	500	-	-	3/16/32/32	0/3/3/3
165	GTP	D	501	-	-	9/22/38/38	0/3/3/3
165	GTP	NI	501	164	-	1/22/38/38	0/3/3/3
163	GDP	GJ	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	PX	501	-	-	1/16/32/32	0/3/3/3
165	GTP	DP	501	164	-	3/22/38/38	0/3/3/3
165	GTP	VG	501	164	-	4/22/38/38	0/3/3/3
163	GDP	GR	500	-	-	0/16/32/32	0/3/3/3
165	GTP	MJ	501	164	-	5/22/38/38	0/3/3/3
165	GTP	C	501	164	-	6/22/38/38	0/3/3/3
163	GDP	RC	500	-	-	1/16/32/32	0/3/3/3
165	GTP	GE	501	164	-	5/22/38/38	0/3/3/3
163	GDP	HR	500	-	-	2/16/32/32	0/3/3/3
165	GTP	AM	501	164	-	5/22/38/38	0/3/3/3
165	GTP	G	501	164	-	7/22/38/38	0/3/3/3
165	GTP	LZ	502	164	-	3/22/38/38	0/3/3/3
165	GTP	OM	501	164	-	5/22/38/38	0/3/3/3
163	GDP	O	500	-	-	2/16/32/32	0/3/3/3
165	GTP	QX	501	-	-	3/22/38/38	0/3/3/3
163	GDP	VX	500	-	-	1/16/32/32	0/3/3/3
165	GTP	II	501	164	-	3/22/38/38	0/3/3/3
163	GDP	OJ	500	-	-	3/16/32/32	0/3/3/3
165	GTP	LB	501	164	-	3/22/38/38	0/3/3/3
163	GDP	PT	500	-	-	1/16/32/32	0/3/3/3
163	GDP	CI	500	-	-	4/16/32/32	0/3/3/3
165	GTP	UO	501	164	-	3/22/38/38	0/3/3/3
165	GTP	PA	501	164	-	0/22/38/38	0/3/3/3
163	GDP	IH	500	-	-	2/16/32/32	0/3/3/3
165	GTP	SS	501	164	-	8/22/38/38	0/3/3/3
163	GDP	QW	500	-	-	5/16/32/32	0/3/3/3
163	GDP	NH	500	-	-	2/16/32/32	0/3/3/3
165	GTP	DX	501	-	-	9/22/38/38	0/3/3/3
163	GDP	AD	500	-	-	3/16/32/32	0/3/3/3
163	GDP	NP	500	-	-	0/16/32/32	0/3/3/3
165	GTP	EG	501	164	-	7/22/38/38	0/3/3/3
165	GTP	HK	501	164	-	4/22/38/38	0/3/3/3
165	GTP	CO	501	164	-	4/22/38/38	0/3/3/3
165	GTP	AS	501	164	-	8/22/38/38	0/3/3/3
163	GDP	SN	501	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	BV	500	-	-	2/16/32/32	0/3/3/3
165	GTP	SQ	501	164	-	5/22/38/38	0/3/3/3
165	GTP	OY	501	164	-	5/22/38/38	0/3/3/3
163	GDP	WR	501	-	-	1/16/32/32	0/3/3/3
163	GDP	LC	500	-	-	2/16/32/32	0/3/3/3
165	GTP	HA	501	164	-	3/22/38/38	0/3/3/3
165	GTP	FM	501	164	-	2/22/38/38	0/3/3/3
163	GDP	SJ	501	-	-	2/16/32/32	0/3/3/3
165	GTP	EV	501	164	-	4/22/38/38	0/3/3/3
163	GDP	IV	500	-	-	2/16/32/32	0/3/3/3
163	GDP	TX	500	-	-	0/16/32/32	0/3/3/3
163	GDP	CG	500	-	-	1/16/32/32	0/3/3/3
165	GTP	AY	501	164	-	5/22/38/38	0/3/3/3
163	GDP	NB	500	-	-	3/16/32/32	0/3/3/3
163	GDP	IX	501	-	-	0/16/32/32	0/3/3/3
163	GDP	TN	500	-	-	3/16/32/32	0/3/3/3
163	GDP	HT	501	-	-	1/16/32/32	0/3/3/3
163	GDP	WJ	500	-	-	1/16/32/32	0/3/3/3
163	GDP	FP	500	-	-	1/16/32/32	0/3/3/3
163	GDP	LI	500	-	-	3/16/32/32	0/3/3/3
163	GDP	BT	500	-	-	3/16/32/32	0/3/3/3
163	GDP	GD	500	-	-	4/16/32/32	0/3/3/3
165	GTP	HU	501	164	-	2/22/38/38	0/3/3/3
165	GTP	HY	501	164	-	3/22/38/38	0/3/3/3
165	GTP	BW	501	164	-	3/22/38/38	0/3/3/3
163	GDP	ET	500	-	-	1/16/32/32	0/3/3/3
163	GDP	BJ	500	-	-	3/16/32/32	0/3/3/3
163	GDP	KO	500	-	-	1/16/32/32	0/3/3/3
163	GDP	HV	500	-	-	2/16/32/32	0/3/3/3
165	GTP	OC	501	164	-	1/22/38/38	0/3/3/3
163	GDP	LE	500	-	-	2/16/32/32	0/3/3/3
163	GDP	RA	500	-	-	1/16/32/32	0/3/3/3
165	GTP	NK	501	-	-	3/22/38/38	0/3/3/3
163	GDP	TP	500	-	-	1/16/32/32	0/3/3/3
165	GTP	NW	501	-	-	3/22/38/38	0/3/3/3
163	GDP	EJ	500	-	-	1/16/32/32	0/3/3/3
165	GTP	PS	501	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	PN	500	-	-	1/16/32/32	0/3/3/3
165	GTP	WI	501	164	-	3/22/38/38	0/3/3/3
165	GTP	WE	501	164	-	8/22/38/38	0/3/3/3
165	GTP	BO	501	164	-	4/22/38/38	0/3/3/3
163	GDP	HL	501	-	-	1/16/32/32	0/3/3/3
163	GDP	MR	500	-	-	3/16/32/32	0/3/3/3
165	GTP	CJ	501	164	-	3/22/38/38	0/3/3/3
163	GDP	FN	500	-	-	0/16/32/32	0/3/3/3
163	GDP	GH	500	-	-	3/16/32/32	0/3/3/3
163	GDP	MX	500	-	-	1/16/32/32	0/3/3/3
165	GTP	FE	501	164	-	6/22/38/38	0/3/3/3
163	GDP	I	501	-	-	0/16/32/32	0/3/3/3
165	GTP	QN	501	164	-	2/22/38/38	0/3/3/3
163	GDP	KY	500	-	-	2/16/32/32	0/3/3/3
165	GTP	FT	503	164	-	5/22/38/38	0/3/3/3
165	GTP	EU	501	164	-	4/22/38/38	0/3/3/3
165	GTP	HI	501	164	-	2/22/38/38	0/3/3/3
165	GTP	OO	501	164	-	1/22/38/38	0/3/3/3
165	GTP	DJ	501	164	-	4/22/38/38	0/3/3/3
165	GTP	HS	501	164	-	3/22/38/38	0/3/3/3
165	GTP	NC	501	164	-	3/22/38/38	0/3/3/3
165	GTP	SO	501	164	-	6/22/38/38	0/3/3/3
165	GTP	IK	501	164	-	3/22/38/38	0/3/3/3
165	GTP	JV	501	164	-	3/22/38/38	0/3/3/3
163	GDP	VN	500	-	-	1/16/32/32	0/3/3/3
163	GDP	HF	500	-	-	2/16/32/32	0/3/3/3
163	GDP	RS	500	-	-	1/16/32/32	0/3/3/3
165	GTP	JK	501	164	-	3/22/38/38	0/3/3/3
163	GDP	FD	500	-	-	3/16/32/32	0/3/3/3
165	GTP	K	501	164	-	2/22/38/38	0/3/3/3
163	GDP	H	500	-	-	1/16/32/32	0/3/3/3
165	GTP	MY	501	164	-	2/22/38/38	0/3/3/3
165	GTP	JJ	501	164	-	3/22/38/38	0/3/3/3
163	GDP	AJ	500	-	-	2/16/32/32	0/3/3/3
163	GDP	CE	500	-	-	3/16/32/32	0/3/3/3
163	GDP	SH	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	BH	500	-	-	3/16/32/32	0/3/3/3
163	GDP	FX	500	-	-	4/16/32/32	0/3/3/3
163	GDP	AP	500	-	-	1/16/32/32	0/3/3/3
163	GDP	LO	500	-	-	3/16/32/32	0/3/3/3
165	GTP	CH	501	164	-	5/22/38/38	0/3/3/3
165	GTP	WA	501	164	-	2/22/38/38	0/3/3/3
165	GTP	DV	501	164	-	3/22/38/38	0/3/3/3
165	GTP	QF	501	164	-	2/22/38/38	0/3/3/3
165	GTP	VM	501	164	-	5/22/38/38	0/3/3/3
165	GTP	UW	501	164	-	5/22/38/38	0/3/3/3
163	GDP	JM	501	-	-	0/16/32/32	0/3/3/3
165	GTP	AO	501	164	-	4/22/38/38	0/3/3/3
163	GDP	QK	500	-	-	5/16/32/32	0/3/3/3
163	GDP	E	500	-	-	3/16/32/32	0/3/3/3
163	GDP	ST	500	-	-	2/16/32/32	0/3/3/3
165	GTP	CE	501	164	-	6/22/38/38	0/3/3/3
163	GDP	PD	500	-	-	4/16/32/32	0/3/3/3
163	GDP	OR	500	-	-	1/16/32/32	0/3/3/3
165	GTP	SA	501	164	-	3/22/38/38	0/3/3/3
165	GTP	AG	501	164	-	6/22/38/38	0/3/3/3
163	GDP	OF	500	-	-	1/16/32/32	0/3/3/3
165	GTP	BQ	501	164	-	8/22/38/38	0/3/3/3
168	ATP	7A	402	-	-	6/22/38/38	0/3/3/3
163	GDP	RQ	500	-	-	0/16/32/32	0/3/3/3
163	GDP	T	501	-	-	1/16/32/32	0/3/3/3
165	GTP	RN	501	164	-	3/22/38/38	0/3/3/3
163	GDP	EL	500	-	-	3/16/32/32	0/3/3/3
163	GDP	LM	500	-	-	1/16/32/32	0/3/3/3
165	GTP	VC	501	164	-	6/22/38/38	0/3/3/3
163	GDP	MB	500	-	-	2/16/32/32	0/3/3/3
163	GDP	S	500	-	-	2/16/32/32	0/3/3/3
165	GTP	CV	501	164	-	3/22/38/38	0/3/3/3
163	GDP	SP	500	-	-	3/16/32/32	0/3/3/3
165	GTP	BA	501	164	-	3/22/38/38	0/3/3/3
163	GDP	QS	500	-	-	1/16/32/32	0/3/3/3
165	GTP	RL	501	164	-	9/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	UI	501	164	-	3/22/38/38	0/3/3/3
165	GTP	PI	501	164	-	4/22/38/38	0/3/3/3
163	GDP	UJ	500	-	-	1/16/32/32	0/3/3/3
165	GTP	GL	501	164	-	9/22/38/38	0/3/3/3
165	GTP	OG	501	164	-	3/22/38/38	0/3/3/3
165	GTP	SG	501	164	-	8/22/38/38	0/3/3/3
165	GTP	PO	501	164	-	3/22/38/38	0/3/3/3
165	GTP	TW	501	164	-	5/22/38/38	0/3/3/3
163	GDP	IN	500	-	-	3/16/32/32	0/3/3/3
163	GDP	WF	501	-	-	1/16/32/32	0/3/3/3
163	GDP	KS	500	-	-	2/16/32/32	0/3/3/3
163	GDP	M	500	-	-	3/16/32/32	0/3/3/3
163	GDP	VT	500	-	-	1/16/32/32	0/3/3/3
165	GTP	L	501	164	-	4/22/38/38	0/3/3/3
165	GTP	MV	501	164	-	5/22/38/38	0/3/3/3
163	GDP	LW	500	-	-	1/16/32/32	0/3/3/3
163	GDP	DK	501	-	-	2/16/32/32	0/3/3/3
163	GDP	ID	500	-	-	1/16/32/32	0/3/3/3
165	GTP	WW	501	164	-	5/22/38/38	0/3/3/3
163	GDP	AT	500	-	-	4/16/32/32	0/3/3/3
165	GTP	LX	501	164	-	4/22/38/38	0/3/3/3
163	GDP	ER	500	-	-	2/16/32/32	0/3/3/3
163	GDP	VL	500	-	-	1/16/32/32	0/3/3/3
165	GTP	QL	501	-	-	3/22/38/38	0/3/3/3
165	GTP	NQ	501	164	-	4/22/38/38	0/3/3/3
163	GDP	WL	500	-	-	1/16/32/32	0/3/3/3
165	GTP	CN	501	164	-	3/22/38/38	0/3/3/3
165	GTP	DQ	501	164	-	6/22/38/38	0/3/3/3
163	GDP	PL	501	-	-	1/16/32/32	0/3/3/3
165	GTP	OK	501	-	-	6/22/38/38	0/3/3/3
163	GDP	LK	500	-	-	1/16/32/32	0/3/3/3
165	GTP	OW	501	-	-	6/22/38/38	0/3/3/3
165	GTP	IO	501	164	-	4/22/38/38	0/3/3/3
165	GTP	TM	501	164	-	7/22/38/38	0/3/3/3
165	GTP	IE	501	164	-	2/22/38/38	0/3/3/3
163	GDP	DU	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	GG	501	164	-	4/22/38/38	0/3/3/3
163	GDP	CS	500	-	-	2/16/32/32	0/3/3/3
165	GTP	TS	501	164	-	1/22/38/38	0/3/3/3
165	GTP	US	501	164	-	5/22/38/38	0/3/3/3
163	GDP	SL	500	-	-	2/16/32/32	0/3/3/3
165	GTP	LL	501	164	-	4/22/38/38	0/3/3/3
163	GDP	MV	500	-	-	3/16/32/32	0/3/3/3
165	GTP	HN	503	164	-	7/22/38/38	0/3/3/3
168	ATP	6I	400	164	-	7/22/38/38	0/3/3/3
165	GTP	LV	501	164	-	5/22/38/38	0/3/3/3
163	GDP	DM	500	-	-	2/16/32/32	0/3/3/3
163	GDP	JC	500	-	-	2/16/32/32	0/3/3/3
163	GDP	KA	500	-	-	3/16/32/32	0/3/3/3
163	GDP	HP	501	-	-	3/16/32/32	0/3/3/3
165	GTP	PE	501	164	-	0/22/38/38	0/3/3/3
163	GDP	LS	500	-	-	2/16/32/32	0/3/3/3
163	GDP	JQ	500	-	-	1/16/32/32	0/3/3/3
165	GTP	KH	501	164	-	5/22/38/38	0/3/3/3
163	GDP	FF	500	-	-	4/16/32/32	0/3/3/3
165	GTP	UK	501	164	-	5/22/38/38	0/3/3/3
163	GDP	QA	500	-	-	1/16/32/32	0/3/3/3
165	GTP	GW	501	164	-	3/22/38/38	0/3/3/3
165	GTP	HW	501	164	-	4/22/38/38	0/3/3/3
163	GDP	CC	500	-	-	3/16/32/32	0/3/3/3
165	GTP	RO	501	164	-	7/22/38/38	0/3/3/3
165	GTP	JW	501	164	-	3/22/38/38	0/3/3/3
163	GDP	CY	500	-	-	5/16/32/32	0/3/3/3
163	GDP	JK	500	-	-	3/16/32/32	0/3/3/3
165	GTP	HM	501	164	-	3/22/38/38	0/3/3/3
163	GDP	N	500	-	-	1/16/32/32	0/3/3/3
163	GDP	CW	500	-	-	5/16/32/32	0/3/3/3
165	GTP	UA	501	164	-	5/22/38/38	0/3/3/3
165	GTP	VH	501	164	-	4/22/38/38	0/3/3/3
163	GDP	A	501	-	-	2/16/32/32	0/3/3/3
163	GDP	EX	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	OP	503	164	-	4/22/38/38	0/3/3/3
163	GDP	FL	500	-	-	4/16/32/32	0/3/3/3
163	GDP	JY	501	-	-	0/16/32/32	0/3/3/3
165	GTP	IS	501	164	-	7/22/38/38	0/3/3/3
165	GTP	RV	501	-	-	1/22/38/38	0/3/3/3
165	GTP	DH	501	164	-	1/22/38/38	0/3/3/3
165	GTP	RX	501	164	-	9/22/38/38	0/3/3/3
163	GDP	EV	500	-	-	4/16/32/32	0/3/3/3
168	ATP	6p	500	164	-	9/22/38/38	0/3/3/3
163	GDP	KK	500	-	-	1/16/32/32	0/3/3/3
165	GTP	QH	501	164	-	10/22/38/38	0/3/3/3
163	GDP	TD	500	-	-	1/16/32/32	0/3/3/3
163	GDP	SR	500	-	-	1/16/32/32	0/3/3/3
165	GTP	KZ	501	164	-	3/22/38/38	0/3/3/3
165	GTP	PG	501	-	-	5/22/38/38	0/3/3/3
163	GDP	LA	500	-	-	2/16/32/32	0/3/3/3
163	GDP	RO	500	-	-	1/16/32/32	0/3/3/3
165	GTP	JZ	501	164	-	3/22/38/38	0/3/3/3
163	GDP	DE	500	-	-	4/16/32/32	0/3/3/3
165	GTP	UQ	501	164	-	9/22/38/38	0/3/3/3
163	GDP	RG	500	-	-	1/16/32/32	0/3/3/3
163	GDP	OB	500	-	-	5/16/32/32	0/3/3/3
163	GDP	JO	500	-	-	2/16/32/32	0/3/3/3
163	GDP	NJ	501	-	-	1/16/32/32	0/3/3/3
163	GDP	GT	501	-	-	2/16/32/32	0/3/3/3
165	GTP	HQ	501	164	-	4/22/38/38	0/3/3/3
163	GDP	UF	500	-	-	1/16/32/32	0/3/3/3
163	GDP	DI	500	-	-	2/16/32/32	0/3/3/3
165	GTP	PM	501	164	-	3/22/38/38	0/3/3/3
165	GTP	MG	501	164	-	5/22/38/38	0/3/3/3
165	GTP	RC	501	164	-	7/22/38/38	0/3/3/3
163	GDP	QM	500	-	-	2/16/32/32	0/3/3/3
163	GDP	IF	500	-	-	3/16/32/32	0/3/3/3
165	GTP	IU	501	164	-	3/22/38/38	0/3/3/3
165	GTP	LJ	501	164	-	4/22/38/38	0/3/3/3
163	GDP	CU	500	-	-	0/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	WN	500	-	-	1/16/32/32	0/3/3/3
163	GDP	KC	500	-	-	1/16/32/32	0/3/3/3
163	GDP	BF	500	-	-	1/16/32/32	0/3/3/3
163	GDP	TV	500	-	-	2/16/32/32	0/3/3/3
165	GTP	RF	501	164	-	1/22/38/38	0/3/3/3
163	GDP	ED	500	-	-	4/16/32/32	0/3/3/3
163	GDP	WD	500	-	-	2/16/32/32	0/3/3/3
163	GDP	UN	500	-	-	3/16/32/32	0/3/3/3
165	GTP	FC	501	164	-	4/22/38/38	0/3/3/3
163	GDP	GN	500	-	-	1/16/32/32	0/3/3/3
163	GDP	WX	500	-	-	1/16/32/32	0/3/3/3
163	GDP	HH	501	-	-	1/16/32/32	0/3/3/3
163	GDP	QC	500	-	-	2/16/32/32	0/3/3/3
163	GDP	QU	500	-	-	2/16/32/32	0/3/3/3
165	GTP	T	503	164	-	7/22/38/38	0/3/3/3
163	GDP	GP	500	-	-	4/16/32/32	0/3/3/3
163	GDP	PB	500	-	-	1/16/32/32	0/3/3/3
165	GTP	ES	501	164	-	7/22/38/38	0/3/3/3
165	GTP	EJ	501	164	-	5/22/38/38	0/3/3/3
165	GTP	BK	501	164	-	3/22/38/38	0/3/3/3
165	GTP	MA	501	164	-	0/22/38/38	0/3/3/3
163	GDP	DC	500	-	-	4/16/32/32	0/3/3/3
163	GDP	RI	500	-	-	0/16/32/32	0/3/3/3
165	GTP	MI	501	164	-	5/22/38/38	0/3/3/3
165	GTP	DN	501	164	-	3/22/38/38	0/3/3/3
163	GDP	U	500	-	-	2/16/32/32	0/3/3/3
165	GTP	NO	501	164	-	3/22/38/38	0/3/3/3
165	GTP	HB	503	164	-	7/22/38/38	0/3/3/3
165	GTP	NA	501	-	-	7/22/38/38	0/3/3/3
165	GTP	QO	501	164	-	5/22/38/38	0/3/3/3
165	GTP	PK	501	164	-	3/22/38/38	0/3/3/3
165	GTP	SE	501	164	-	5/22/38/38	0/3/3/3
163	GDP	KQ	500	-	-	1/16/32/32	0/3/3/3
165	GTP	FV	503	-	-	3/22/38/38	0/3/3/3
165	GTP	LF	502	164	-	2/22/38/38	0/3/3/3
163	GDP	TJ	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	BR	500	-	-	3/16/32/32	0/3/3/3
165	GTP	MC	501	164	-	4/22/38/38	0/3/3/3
165	GTP	WC	501	164	-	2/22/38/38	0/3/3/3
165	GTP	MS	501	164	-	5/22/38/38	0/3/3/3
163	GDP	IR	500	-	-	3/16/32/32	0/3/3/3
165	GTP	DD	501	164	-	3/22/38/38	0/3/3/3
165	GTP	IG	501	164	-	7/22/38/38	0/3/3/3
163	GDP	FR	501	-	-	3/16/32/32	0/3/3/3
165	GTP	SU	501	164	-	3/22/38/38	0/3/3/3
165	GTP	NM	501	164	-	4/22/38/38	0/3/3/3
165	GTP	CT	501	164	-	6/22/38/38	0/3/3/3
163	GDP	BP	500	-	-	2/16/32/32	0/3/3/3
165	GTP	EO	501	164	-	4/22/38/38	0/3/3/3
163	GDP	KI	500	-	-	3/16/32/32	0/3/3/3
163	GDP	JG	500	-	-	2/16/32/32	0/3/3/3
165	GTP	LH	501	164	-	3/22/38/38	0/3/3/3
165	GTP	VA	501	164	-	4/22/38/38	0/3/3/3
163	GDP	HD	501	-	-	3/16/32/32	0/3/3/3
165	GTP	BM	501	164	-	3/22/38/38	0/3/3/3
165	GTP	HG	501	164	-	3/22/38/38	0/3/3/3
165	GTP	AK	501	164	-	3/22/38/38	0/3/3/3
165	GTP	VS	501	164	-	4/22/38/38	0/3/3/3
165	GTP	OD	503	164	-	4/22/38/38	0/3/3/3
163	GDP	SD	500	-	-	3/16/32/32	0/3/3/3
165	GTP	TU	501	164	-	4/22/38/38	0/3/3/3
163	GDP	TB	500	-	-	3/16/32/32	0/3/3/3
163	GDP	TT	500	-	-	1/16/32/32	0/3/3/3
165	GTP	NU	501	164	-	1/22/38/38	0/3/3/3
163	GDP	EH	500	-	-	1/16/32/32	0/3/3/3
163	GDP	VF	500	-	-	1/16/32/32	0/3/3/3
163	GDP	QO	500	-	-	2/16/32/32	0/3/3/3
165	GTP	LP	502	164	-	6/22/38/38	0/3/3/3
163	GDP	FB	500	-	-	0/16/32/32	0/3/3/3
163	GDP	SB	501	-	-	3/16/32/32	0/3/3/3
163	GDP	OL	500	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
163	GDP	IT	501	-	-	2/16/32/32	0/3/3/3
165	GTP	ED	501	164	-	4/22/38/38	0/3/3/3
163	GDP	AH	500	-	-	3/16/32/32	0/3/3/3
163	GDP	UX	500	-	-	1/16/32/32	0/3/3/3
165	GTP	WK	501	164	-	5/22/38/38	0/3/3/3
165	GTP	SM	501	164	-	3/22/38/38	0/3/3/3
165	GTP	TQ	501	164	-	6/22/38/38	0/3/3/3
163	GDP	NT	500	-	-	2/16/32/32	0/3/3/3
165	GTP	WU	501	164	-	3/22/38/38	0/3/3/3
163	GDP	PJ	500	-	-	3/16/32/32	0/3/3/3
163	GDP	OH	500	-	-	3/16/32/32	0/3/3/3
165	GTP	SK	501	164	-	0/22/38/38	0/3/3/3
165	GTP	J	501	164	-	8/22/38/38	0/3/3/3
165	GTP	QU	501	164	-	4/22/38/38	0/3/3/3
165	GTP	DL	501	-	-	10/22/38/38	0/3/3/3
165	GTP	RR	501	164	-	1/22/38/38	0/3/3/3
163	GDP	AZ	500	-	-	2/16/32/32	0/3/3/3
163	GDP	QI	500	-	-	2/16/32/32	0/3/3/3
165	GTP	VY	501	164	-	5/22/38/38	0/3/3/3
163	GDP	HJ	500	-	-	2/16/32/32	0/3/3/3
163	GDP	OV	500	-	-	3/16/32/32	0/3/3/3
165	GTP	MO	501	164	-	4/22/38/38	0/3/3/3
165	GTP	KP	502	164	-	3/22/38/38	0/3/3/3
165	GTP	WM	501	164	-	3/22/38/38	0/3/3/3
165	GTP	KL	501	164	-	2/22/38/38	0/3/3/3
165	GTP	ME	501	164	-	5/22/38/38	0/3/3/3
168	ATP	2x	501	-	-	7/22/38/38	0/3/3/3
165	GTP	IM	501	164	-	4/22/38/38	0/3/3/3
165	GTP	RB	501	164	-	3/22/38/38	0/3/3/3
163	GDP	EN	500	-	-	3/16/32/32	0/3/3/3
165	GTP	FI	501	164	-	5/22/38/38	0/3/3/3
165	GTP	UG	501	164	-	5/22/38/38	0/3/3/3
163	GDP	F	500	-	-	3/16/32/32	0/3/3/3
168	ATP	2v	501	-	-	5/22/38/38	0/3/3/3
165	GTP	OS	501	164	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	LD	502	164	-	6/22/38/38	0/3/3/3
165	GTP	QT	501	164	-	10/22/38/38	0/3/3/3
165	GTP	TO	501	164	-	5/22/38/38	0/3/3/3
165	GTP	TC	501	164	-	5/22/38/38	0/3/3/3
163	GDP	HN	501	-	-	3/16/32/32	0/3/3/3
165	GTP	NR	501	-	-	6/22/38/38	0/3/3/3
165	GTP	KF	501	164	-	6/22/38/38	0/3/3/3
165	GTP	VE	501	164	-	1/22/38/38	0/3/3/3
163	GDP	NF	500	-	-	3/16/32/32	0/3/3/3
165	GTP	VT	501	164	-	4/22/38/38	0/3/3/3
163	GDP	UR	500	-	-	1/16/32/32	0/3/3/3
163	GDP	MF	500	-	-	3/16/32/32	0/3/3/3
163	GDP	KU	500	-	-	3/16/32/32	0/3/3/3
163	GDP	MP	500	-	-	1/16/32/32	0/3/3/3
165	GTP	TK	501	164	-	5/22/38/38	0/3/3/3
163	GDP	QQ	500	-	-	2/16/32/32	0/3/3/3
165	GTP	FQ	501	164	-	6/22/38/38	0/3/3/3
163	GDP	NL	500	-	-	1/16/32/32	0/3/3/3
163	GDP	WT	500	-	-	2/16/32/32	0/3/3/3
165	GTP	RH	501	164	-	2/22/38/38	0/3/3/3
163	GDP	RM	500	-	-	1/16/32/32	0/3/3/3
165	GTP	KB	502	164	-	4/22/38/38	0/3/3/3
165	GTP	BS	501	164	-	1/22/38/38	0/3/3/3
163	GDP	IJ	500	-	-	2/16/32/32	0/3/3/3
165	GTP	IC	501	164	-	4/22/38/38	0/3/3/3
165	GTP	WO	501	164	-	2/22/38/38	0/3/3/3
163	GDP	EP	500	-	-	1/16/32/32	0/3/3/3
163	GDP	BD	500	-	-	2/16/32/32	0/3/3/3
165	GTP	KX	501	164	-	2/22/38/38	0/3/3/3
165	GTP	GO	501	164	-	4/22/38/38	0/3/3/3
163	GDP	VB	500	-	-	1/16/32/32	0/3/3/3
163	GDP	V	500	-	-	1/16/32/32	0/3/3/3
163	GDP	WP	500	-	-	2/16/32/32	0/3/3/3
163	GDP	FJ	501	-	-	2/16/32/32	0/3/3/3
165	GTP	AP	501	164	-	4/22/38/38	0/3/3/3
165	GTP	LN	502	164	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	WS	501	164	-	1/22/38/38	0/3/3/3
165	GTP	GK	501	164	-	3/22/38/38	0/3/3/3
163	GDP	NR	500	-	-	3/16/32/32	0/3/3/3
163	GDP	ML	500	-	-	1/16/32/32	0/3/3/3
163	GDP	LG	501	-	-	2/16/32/32	0/3/3/3
163	GDP	MH	500	-	-	1/16/32/32	0/3/3/3
163	GDP	DW	501	-	-	1/16/32/32	0/3/3/3
165	GTP	EM	501	164	-	4/22/38/38	0/3/3/3
165	GTP	GS	501	164	-	4/22/38/38	0/3/3/3
165	GTP	KT	501	164	-	5/22/38/38	0/3/3/3
163	GDP	OP	501	-	-	2/16/32/32	0/3/3/3
165	GTP	UE	501	164	-	9/22/38/38	0/3/3/3
163	GDP	JI	500	-	-	1/16/32/32	0/3/3/3
163	GDP	ND	500	-	-	0/16/32/32	0/3/3/3
163	GDP	RU	500	-	-	0/16/32/32	0/3/3/3
163	GDP	HX	501	-	-	1/16/32/32	0/3/3/3
165	GTP	DT	501	164	-	3/22/38/38	0/3/3/3
165	GTP	NE	501	164	-	4/22/38/38	0/3/3/3
165	GTP	UC	501	164	-	3/22/38/38	0/3/3/3
163	GDP	MT	500	-	-	1/16/32/32	0/3/3/3
163	GDP	PP	500	-	-	4/16/32/32	0/3/3/3
163	GDP	TL	501	-	-	0/16/32/32	0/3/3/3
163	GDP	UD	500	-	-	3/16/32/32	0/3/3/3
165	GTP	VQ	501	164	-	1/22/38/38	0/3/3/3
165	GTP	KN	502	164	-	3/22/38/38	0/3/3/3
163	GDP	PH	500	-	-	1/16/32/32	0/3/3/3
163	GDP	AR	500	-	-	1/16/32/32	0/3/3/3
163	GDP	FV	501	-	-	1/16/32/32	0/3/3/3
165	GTP	WQ	501	164	-	8/22/38/38	0/3/3/3
163	GDP	CM	500	-	-	3/16/32/32	0/3/3/3
163	GDP	W	500	-	-	1/16/32/32	0/3/3/3
165	GTP	WG	501	164	-	1/22/38/38	0/3/3/3
165	GTP	NF	501	-	-	6/22/38/38	0/3/3/3
165	GTP	KJ	501	164	-	3/22/38/38	0/3/3/3
165	GTP	VO	501	164	-	6/22/38/38	0/3/3/3
165	GTP	BY	501	164	-	4/22/38/38	0/3/3/3
165	GTP	KR	501	164	-	6/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	PU	501	164	-	4/22/38/38	0/3/3/3
163	GDP	CK	501	-	-	6/16/32/32	0/3/3/3
163	GDP	DY	500	-	-	1/16/32/32	0/3/3/3
163	GDP	EB	500	-	-	4/16/32/32	0/3/3/3
163	GDP	WB	500	-	-	1/16/32/32	0/3/3/3
163	GDP	AL	500	-	-	3/16/32/32	0/3/3/3
163	GDP	FH	500	-	-	0/16/32/32	0/3/3/3
163	GDP	NN	500	-	-	3/16/32/32	0/3/3/3
165	GTP	SI	501	164	-	3/22/38/38	0/3/3/3
163	GDP	G	500	-	-	2/16/32/32	0/3/3/3
165	GTP	KD	502	164	-	3/22/38/38	0/3/3/3
165	GTP	RJ	501	-	-	1/22/38/38	0/3/3/3
163	GDP	CA	500	-	-	3/16/32/32	0/3/3/3
165	GTP	EP	501	164	-	5/22/38/38	0/3/3/3
165	GTP	PC	501	164	-	3/22/38/38	0/3/3/3
163	GDP	UT	500	-	-	1/16/32/32	0/3/3/3
165	GTP	IQ	501	164	-	2/22/38/38	0/3/3/3
165	GTP	UU	501	164	-	3/22/38/38	0/3/3/3
163	GDP	UL	500	-	-	1/16/32/32	0/3/3/3
163	GDP	LU	500	-	-	3/16/32/32	0/3/3/3
165	GTP	AI	501	164	-	3/22/38/38	0/3/3/3
163	GDP	PR	501	-	-	3/16/32/32	0/3/3/3
163	GDP	MN	500	-	-	2/16/32/32	0/3/3/3
163	GDP	BX	500	-	-	3/16/32/32	0/3/3/3
165	GTP	JF	501	164	-	3/22/38/38	0/3/3/3
163	GDP	DG	500	-	-	2/16/32/32	0/3/3/3
165	GTP	KV	501	164	-	3/22/38/38	0/3/3/3
163	GDP	GL	500	-	-	3/16/32/32	0/3/3/3
165	GTP	CQ	501	164	-	6/22/38/38	0/3/3/3
165	GTP	PQ	501	164	-	0/22/38/38	0/3/3/3
165	GTP	JR	501	164	-	3/22/38/38	0/3/3/3
165	GTP	JD	501	164	-	5/22/38/38	0/3/3/3
163	GDP	EF	500	-	-	3/16/32/32	0/3/3/3
163	GDP	P	500	-	-	2/16/32/32	0/3/3/3
165	GTP	AA	501	164	-	6/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	EA	501	164	-	2/22/38/38	0/3/3/3
163	GDP	LQ	500	-	-	2/16/32/32	0/3/3/3
165	GTP	EC	501	164	-	3/22/38/38	0/3/3/3
163	GDP	OT	500	-	-	3/16/32/32	0/3/3/3
163	GDP	OX	500	-	-	2/16/32/32	0/3/3/3
163	GDP	RE	500	-	-	0/16/32/32	0/3/3/3
163	GDP	QE	500	-	-	2/16/32/32	0/3/3/3
163	GDP	IL	501	-	-	0/16/32/32	0/3/3/3
165	GTP	PY	501	164	-	3/22/38/38	0/3/3/3
163	GDP	GX	500	-	-	4/16/32/32	0/3/3/3
165	GTP	GU	501	164	-	4/22/38/38	0/3/3/3
163	GDP	KM	500	-	-	2/16/32/32	0/3/3/3
163	GDP	JA	500	-	-	1/16/32/32	0/3/3/3
165	GTP	OA	501	164	-	4/22/38/38	0/3/3/3
165	GTP	JB	501	164	-	2/22/38/38	0/3/3/3
163	GDP	JU	500	-	-	1/16/32/32	0/3/3/3
163	GDP	GV	501	-	-	4/16/32/32	0/3/3/3
165	GTP	VW	501	164	-	5/22/38/38	0/3/3/3
165	GTP	GQ	501	164	-	4/22/38/38	0/3/3/3
163	GDP	SF	500	-	-	1/16/32/32	0/3/3/3
165	GTP	UM	501	164	-	5/22/38/38	0/3/3/3
163	GDP	PV	500	-	-	3/16/32/32	0/3/3/3
165	GTP	CW	501	164	-	4/22/38/38	0/3/3/3
165	GTP	IA	501	164	-	6/22/38/38	0/3/3/3
163	GDP	WH	500	-	-	2/16/32/32	0/3/3/3
163	GDP	QG	500	-	-	1/16/32/32	0/3/3/3
163	GDP	IP	500	-	-	1/16/32/32	0/3/3/3
163	GDP	UV	500	-	-	1/16/32/32	0/3/3/3
165	GTP	BU	501	164	-	4/22/38/38	0/3/3/3
165	GTP	CK	503	164	-	3/22/38/38	0/3/3/3
165	GTP	IY	501	164	-	4/22/38/38	0/3/3/3
168	ATP	6u	700	-	-	7/22/38/38	0/3/3/3
163	GDP	VD	500	-	-	1/16/32/32	0/3/3/3
163	GDP	VJ	500	-	-	2/16/32/32	0/3/3/3
163	GDP	WV	500	-	-	1/16/32/32	0/3/3/3
163	GDP	CQ	500	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	LR	502	164	-	2/22/38/38	0/3/3/3
163	GDP	UP	500	-	-	3/16/32/32	0/3/3/3
165	GTP	JN	501	164	-	3/22/38/38	0/3/3/3
165	GTP	Q	501	164	-	3/22/38/38	0/3/3/3
165	GTP	JH	501	164	-	5/22/38/38	0/3/3/3
165	GTP	OU	501	164	-	6/22/38/38	0/3/3/3
163	GDP	AN	500	-	-	2/16/32/32	0/3/3/3
165	GTP	EI	501	164	-	5/22/38/38	0/3/3/3
165	GTP	FO	501	164	-	3/22/38/38	0/3/3/3
165	GTP	PW	501	164	-	3/22/38/38	0/3/3/3
165	GTP	RT	501	164	-	2/22/38/38	0/3/3/3
165	GTP	AW	501	164	-	3/22/38/38	0/3/3/3
165	GTP	NY	501	164	-	4/22/38/38	0/3/3/3
165	GTP	BE	501	164	-	7/22/38/38	0/3/3/3
163	GDP	KW	500	-	-	1/16/32/32	0/3/3/3
165	GTP	AD	501	164	-	4/22/38/38	0/3/3/3
163	GDP	UH	500	-	-	1/16/32/32	0/3/3/3
165	GTP	BI	501	164	-	5/22/38/38	0/3/3/3
163	GDP	JS	500	-	-	2/16/32/32	0/3/3/3
163	GDP	SV	501	-	-	2/16/32/32	0/3/3/3
163	GDP	AB	500	-	-	3/16/32/32	0/3/3/3
165	GTP	DE	501	164	-	6/22/38/38	0/3/3/3
165	GTP	JP	501	164	-	5/22/38/38	0/3/3/3
163	GDP	TH	500	-	-	1/16/32/32	0/3/3/3
163	GDP	KE	500	-	-	1/16/32/32	0/3/3/3
163	GDP	KG	500	-	-	2/16/32/32	0/3/3/3
163	GDP	DO	500	-	-	1/16/32/32	0/3/3/3
168	ATP	9R	500	164	-	6/22/38/38	0/3/3/3
165	GTP	JT	501	164	-	5/22/38/38	0/3/3/3
163	GDP	AV	500	-	-	3/16/32/32	0/3/3/3
163	GDP	TR	500	-	-	1/16/32/32	0/3/3/3
163	GDP	RW	500	-	-	2/16/32/32	0/3/3/3
163	GDP	PF	501	-	-	3/16/32/32	0/3/3/3
163	GDP	GF	500	-	-	4/16/32/32	0/3/3/3
165	GTP	FS	501	164	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
165	GTP	QR	501	164	-	2/22/38/38	0/3/3/3
165	GTP	QC	501	164	-	5/22/38/38	0/3/3/3
165	GTP	BG	501	164	-	1/22/38/38	0/3/3/3
165	GTP	FJ	503	164	-	5/22/38/38	0/3/3/3
163	GDP	RK	500	-	-	2/16/32/32	0/3/3/3
165	GTP	OI	501	164	-	6/22/38/38	0/3/3/3
163	GDP	FT	501	-	-	1/16/32/32	0/3/3/3
165	GTP	MM	501	164	-	2/22/38/38	0/3/3/3

The worst 5 of 1224 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
165	IK	501	GTP	PB-O3A	3.47	1.63	1.59
165	IW	501	GTP	PB-O3A	3.41	1.63	1.59
163	CK	501	GDP	C5-C4	3.21	1.47	1.38
163	KY	500	GDP	C5-C4	3.13	1.47	1.38
163	O	500	GDP	C5-C4	3.12	1.47	1.38

The worst 5 of 4620 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
163	CW	500	GDP	C5-C4-N3	-6.47	118.10	128.39
163	P	500	GDP	C5-C4-N3	-6.38	118.23	128.39
163	CK	501	GDP	C5-C4-N3	-6.27	118.41	128.39
163	QK	500	GDP	C5-C4-N3	-6.25	118.45	128.39
163	QW	500	GDP	C5-C4-N3	-6.25	118.45	128.39

There are no chirality outliers.

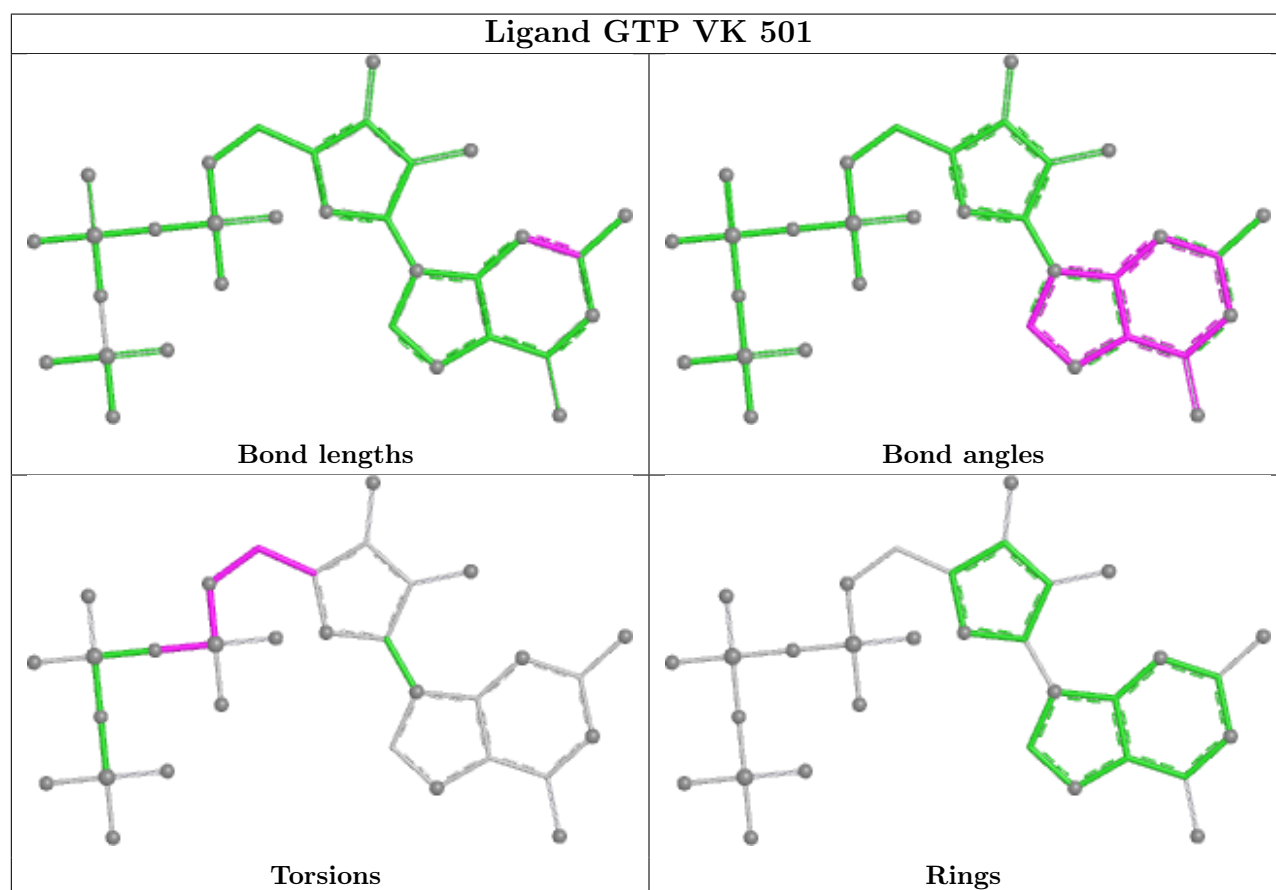
5 of 1851 torsion outliers are listed below:

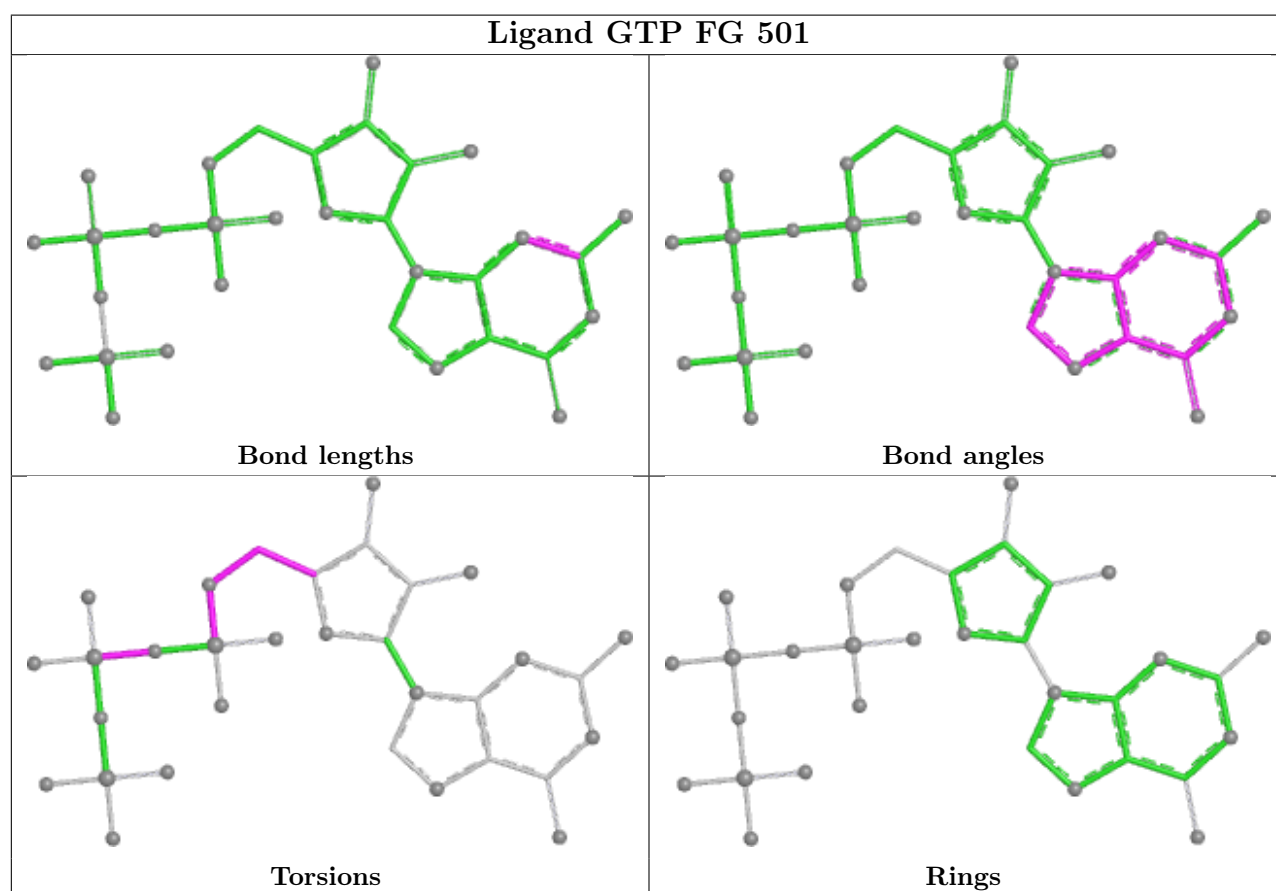
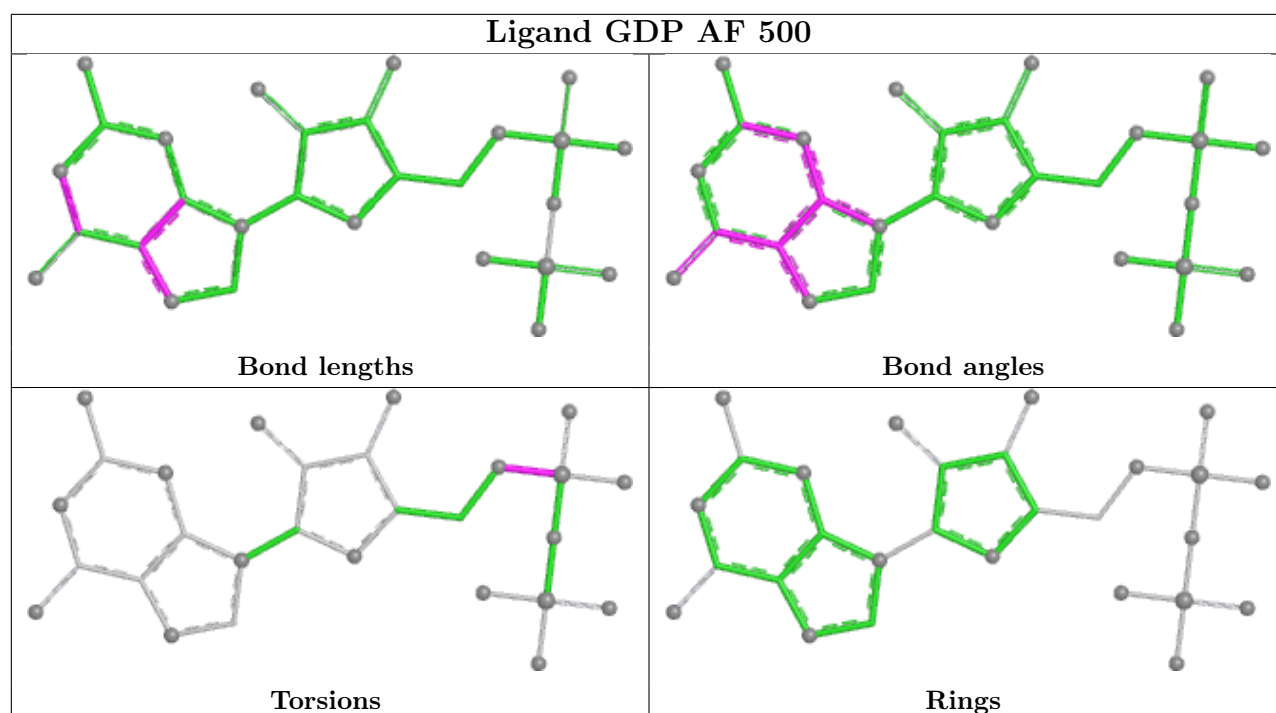
Mol	Chain	Res	Type	Atoms
163	AB	500	GDP	C5'-O5'-PA-O3A
163	AB	500	GDP	C5'-O5'-PA-O1A
163	AD	500	GDP	C5'-O5'-PA-O3A
163	AD	500	GDP	C5'-O5'-PA-O1A
163	AF	500	GDP	C5'-O5'-PA-O1A

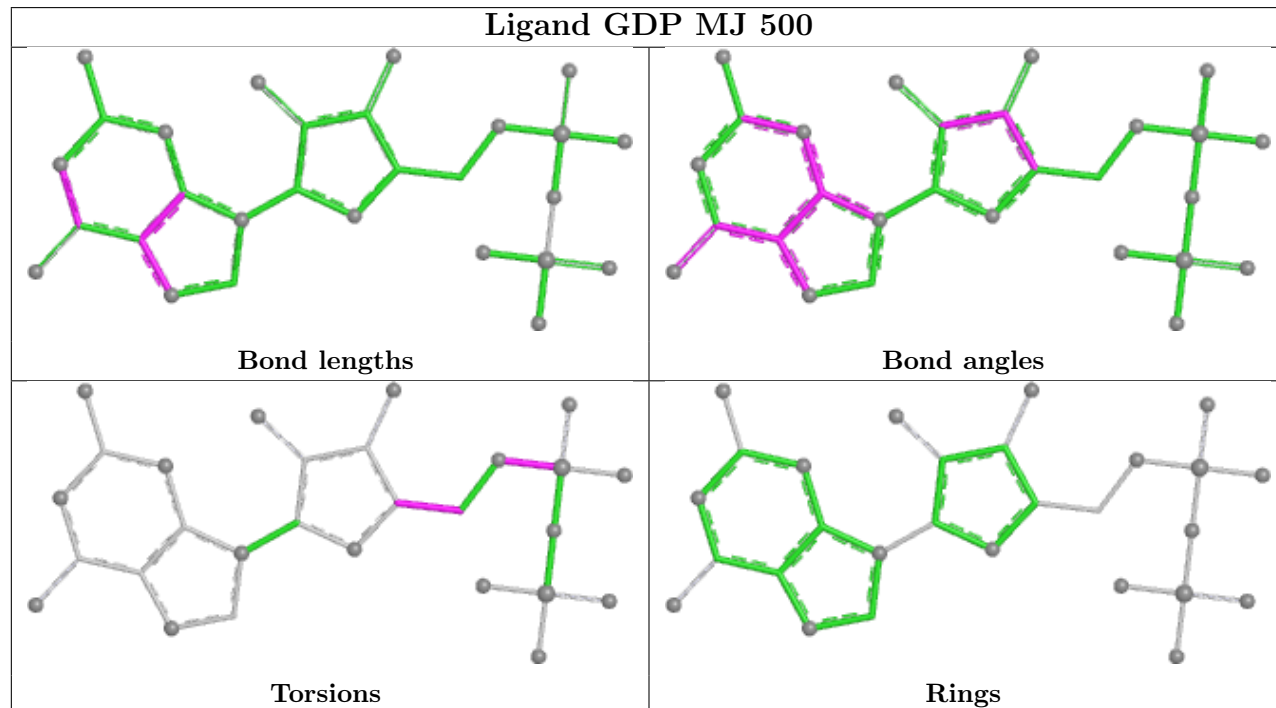
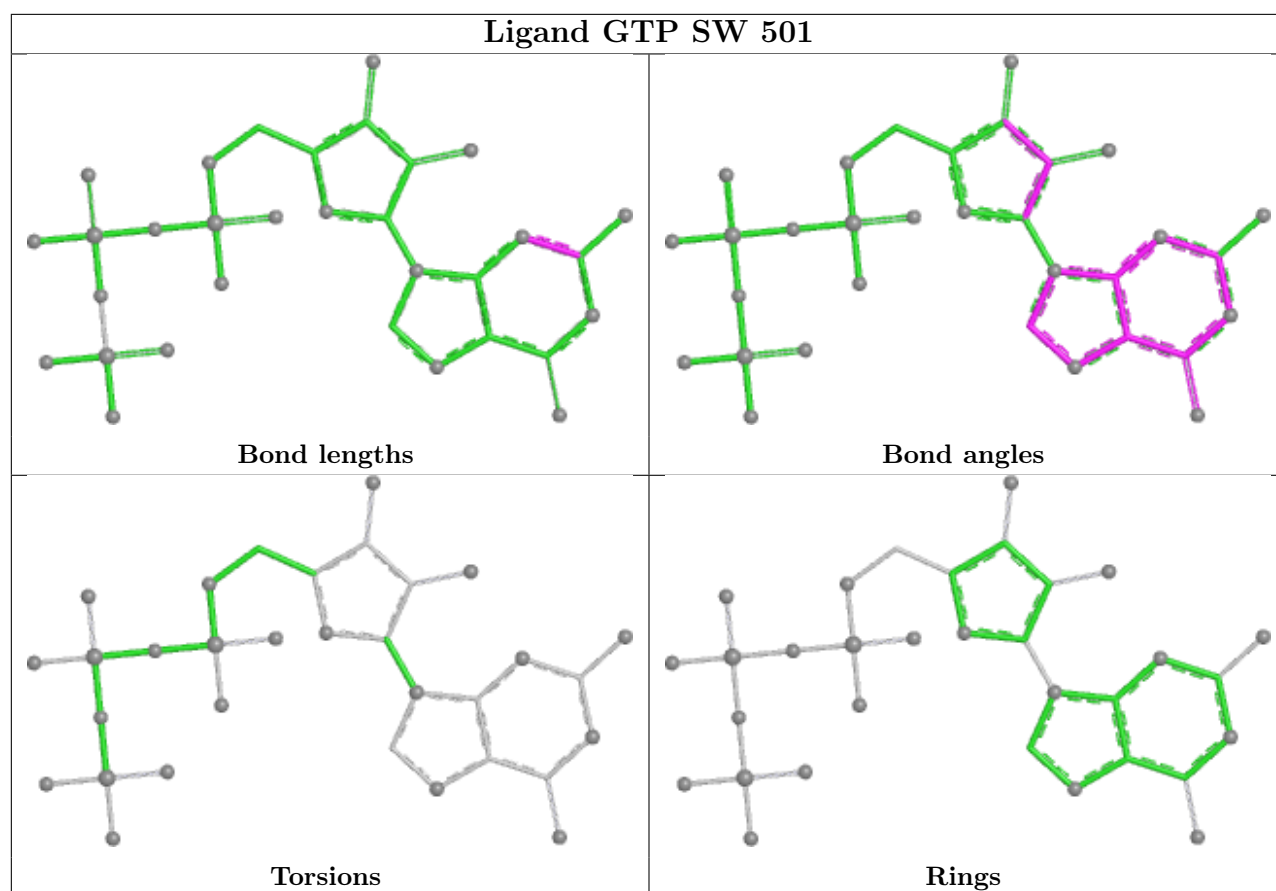
There are no ring outliers.

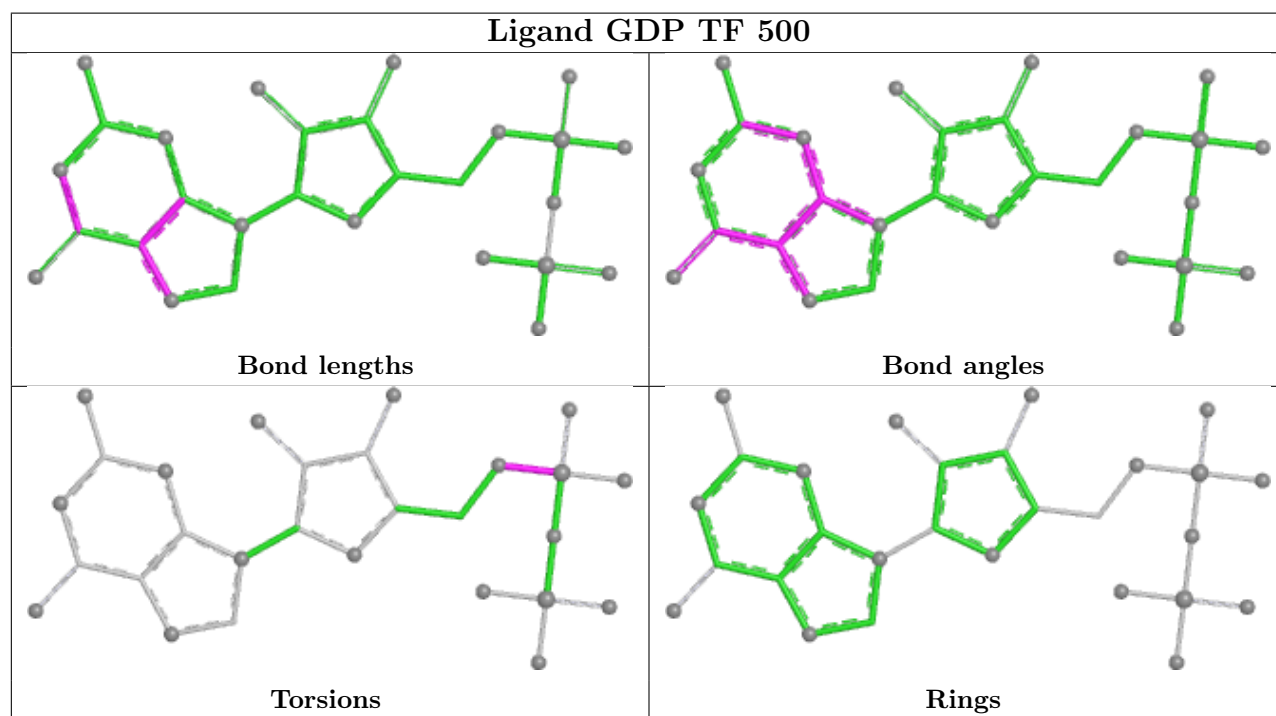
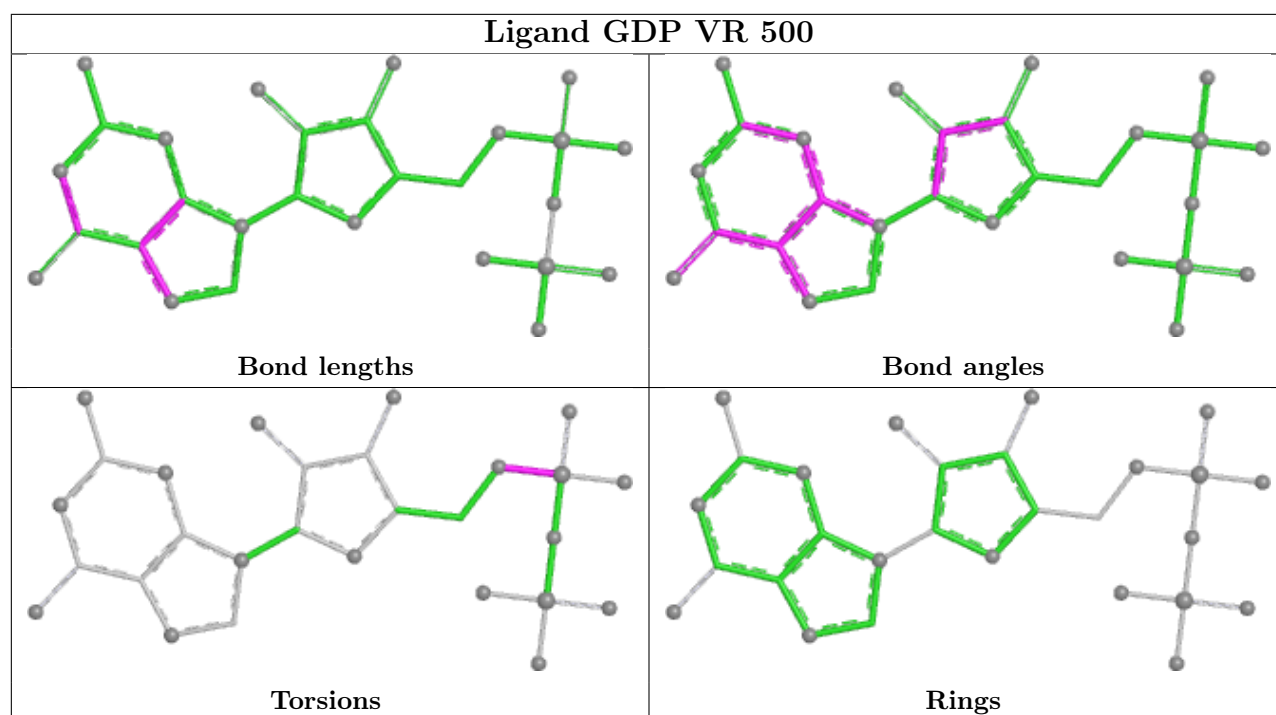
No monomer is involved in short contacts.

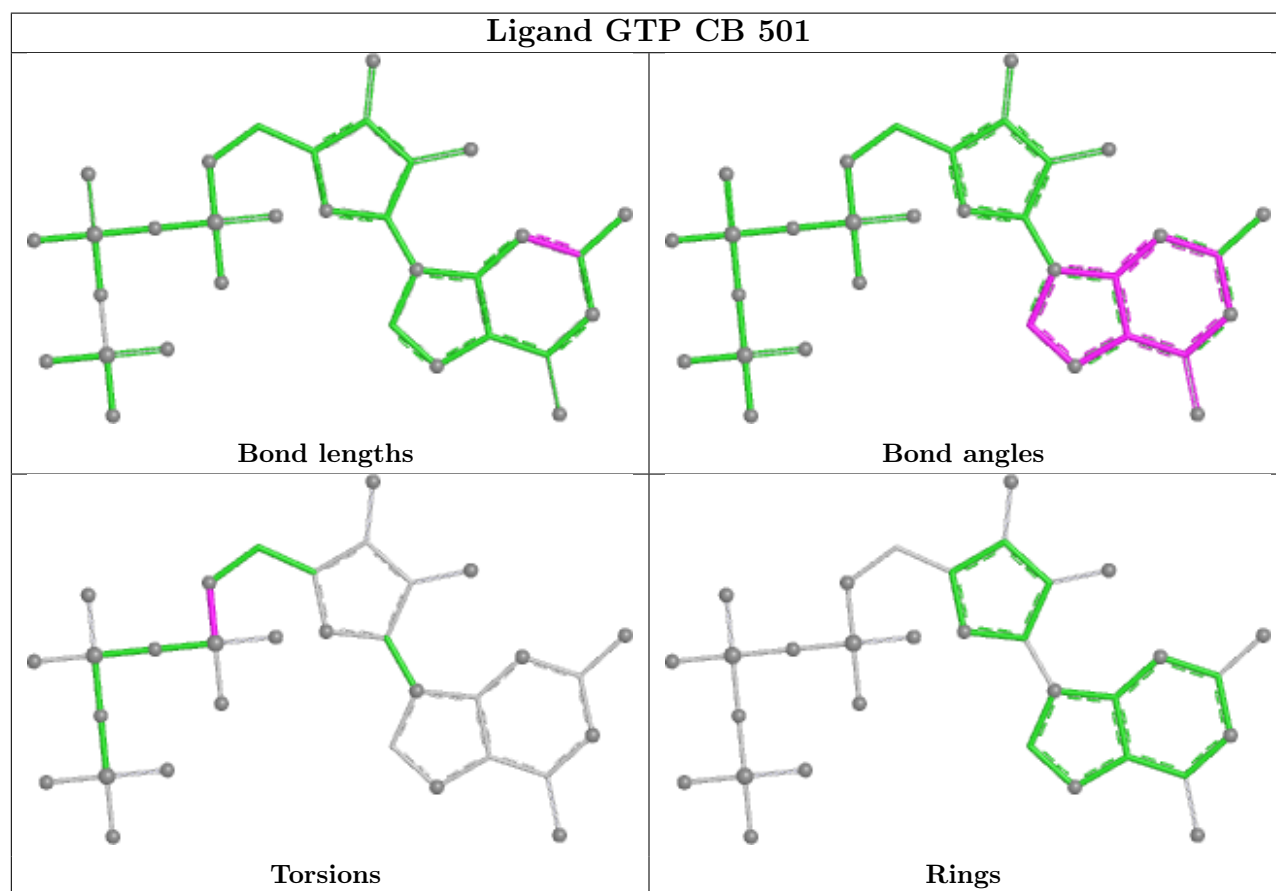
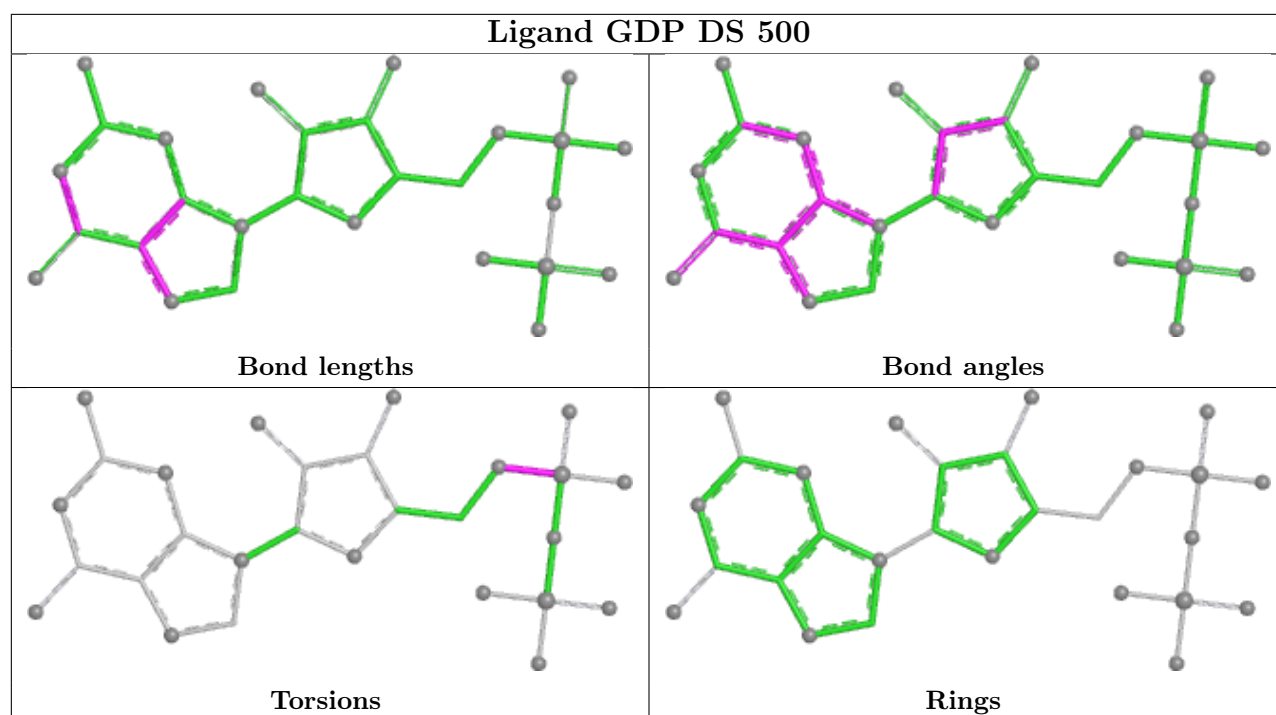
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

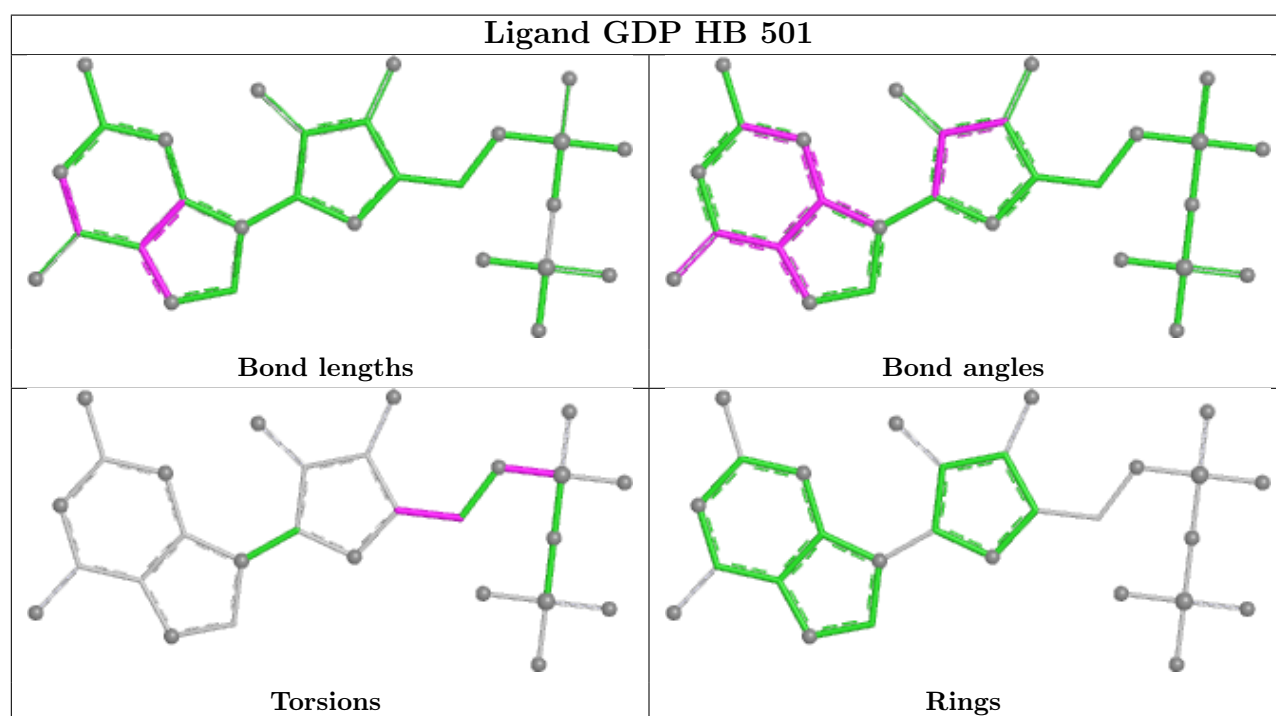
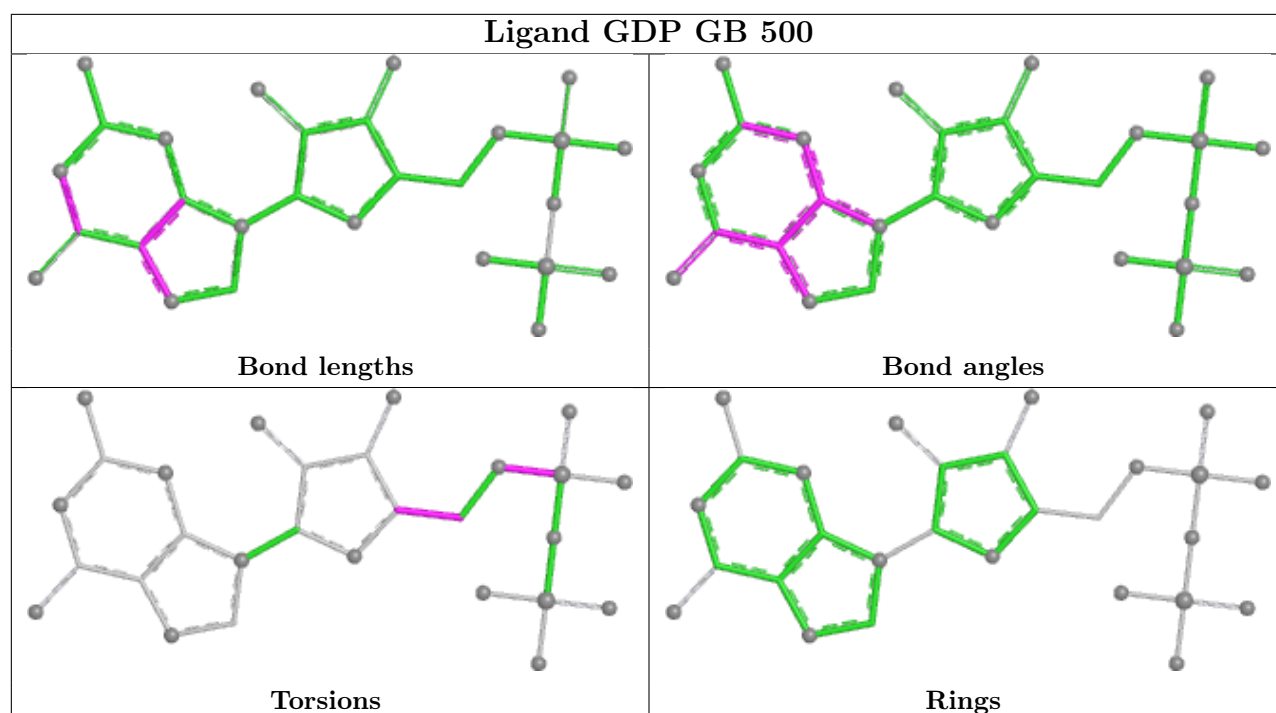


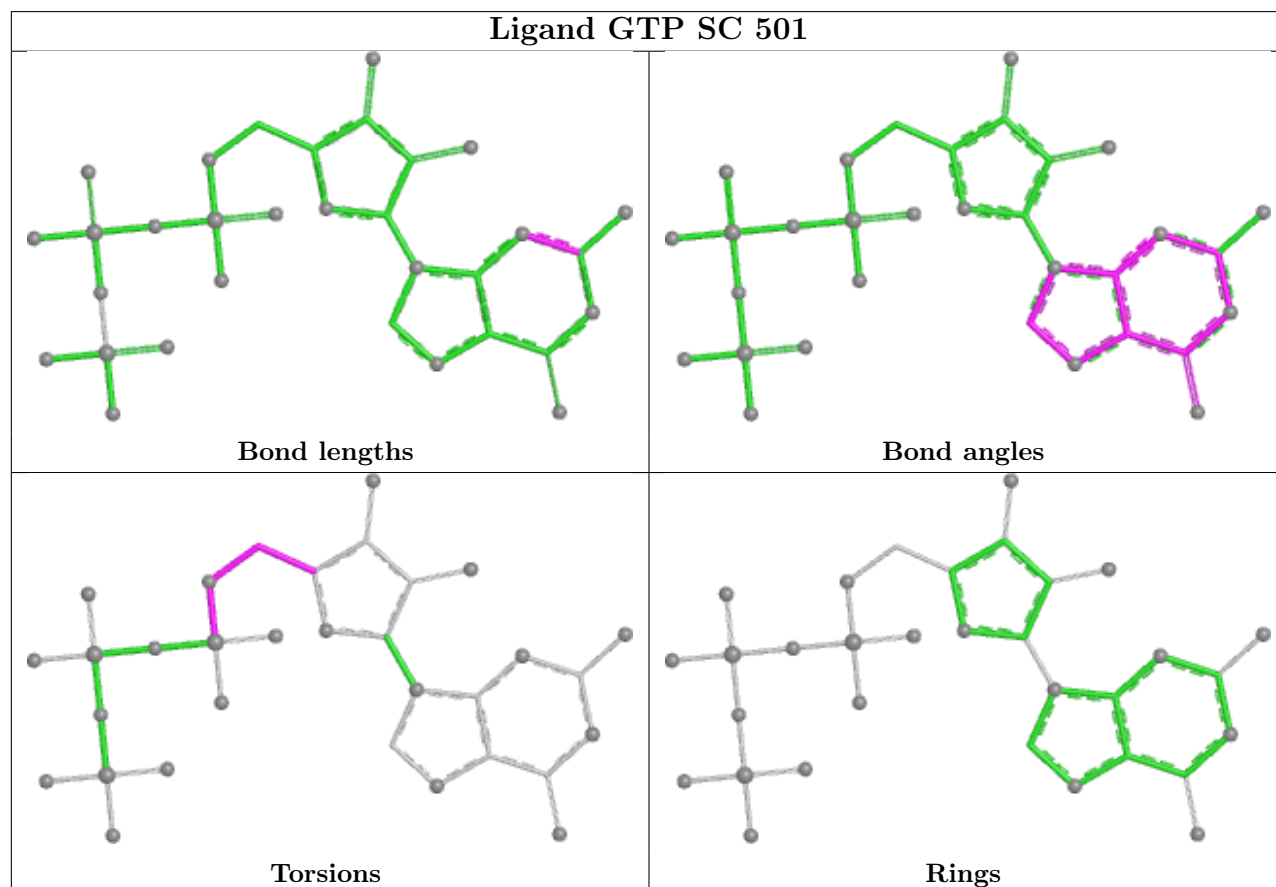
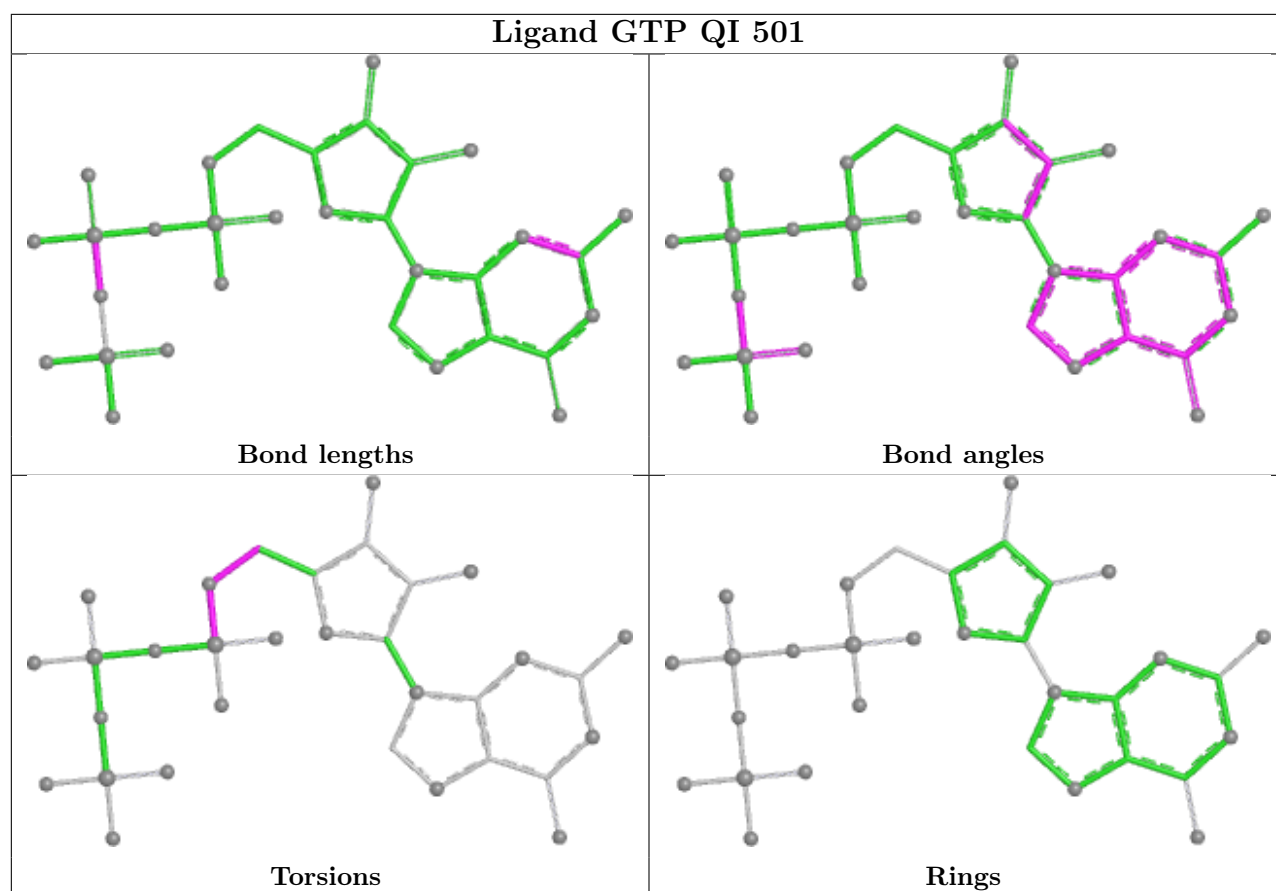


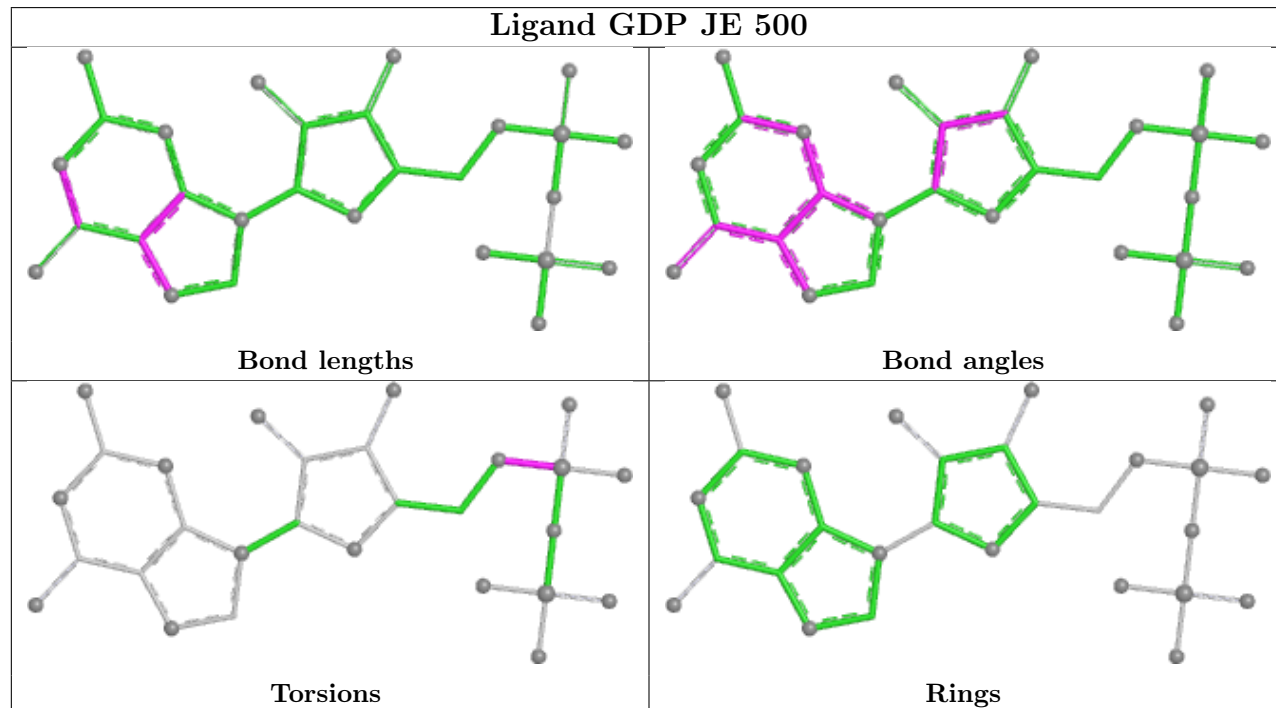
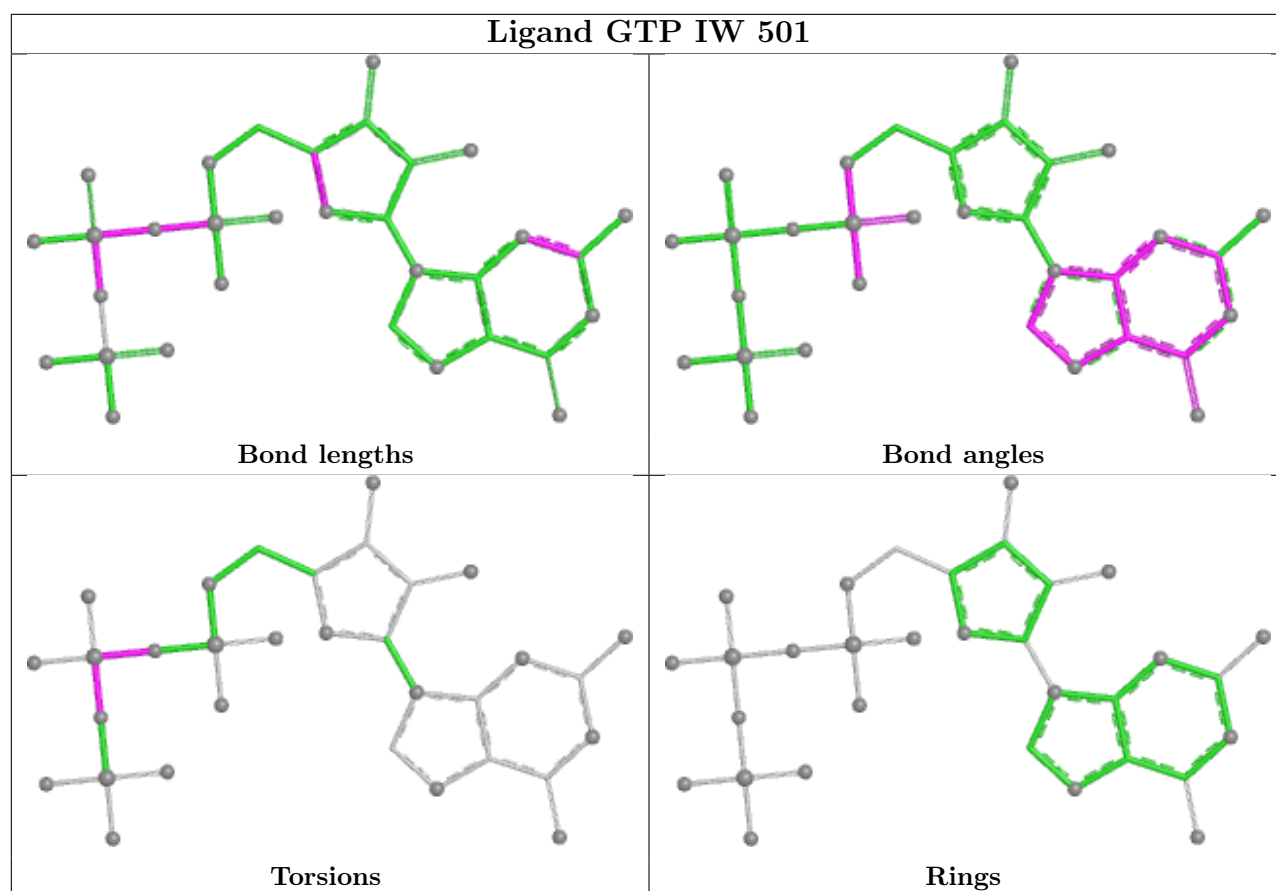


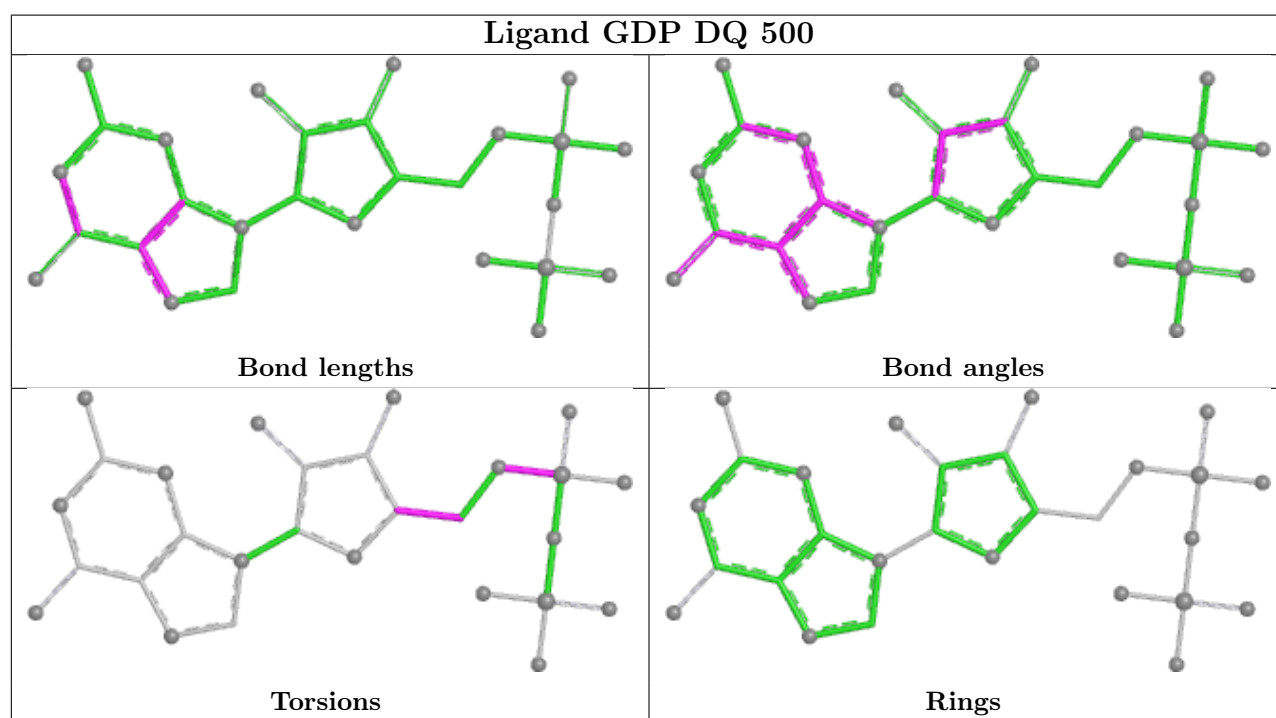
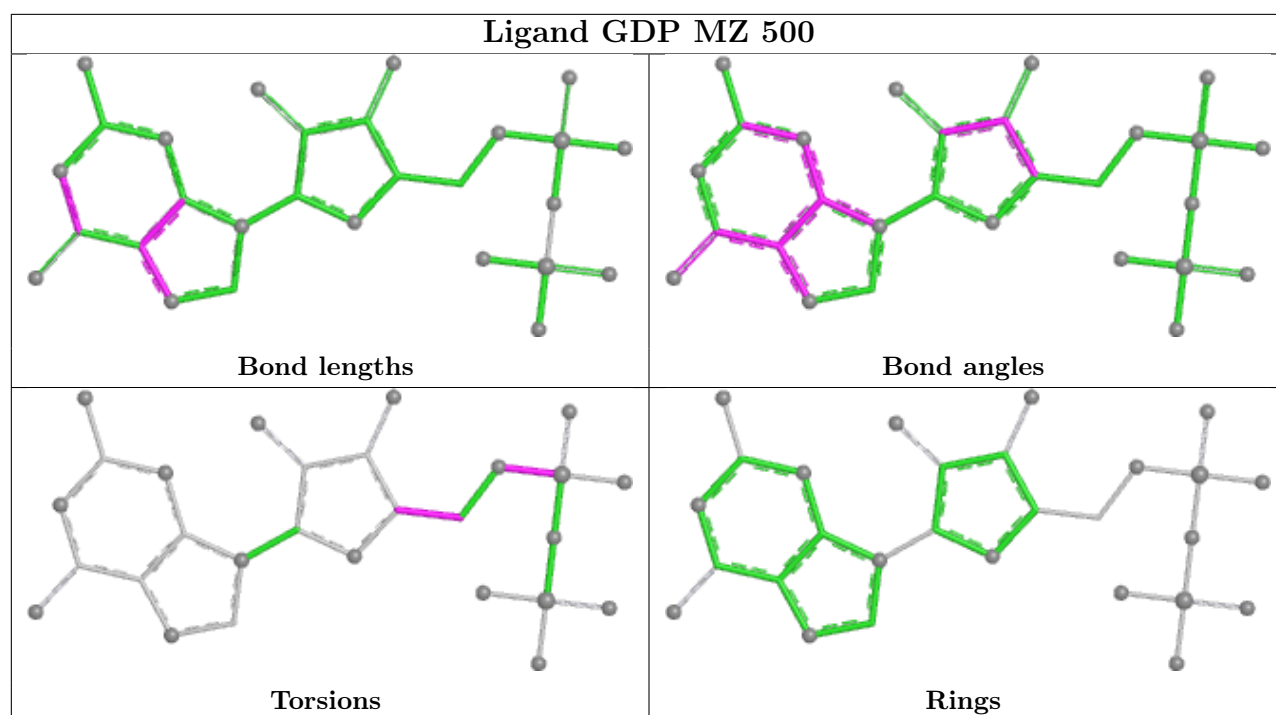


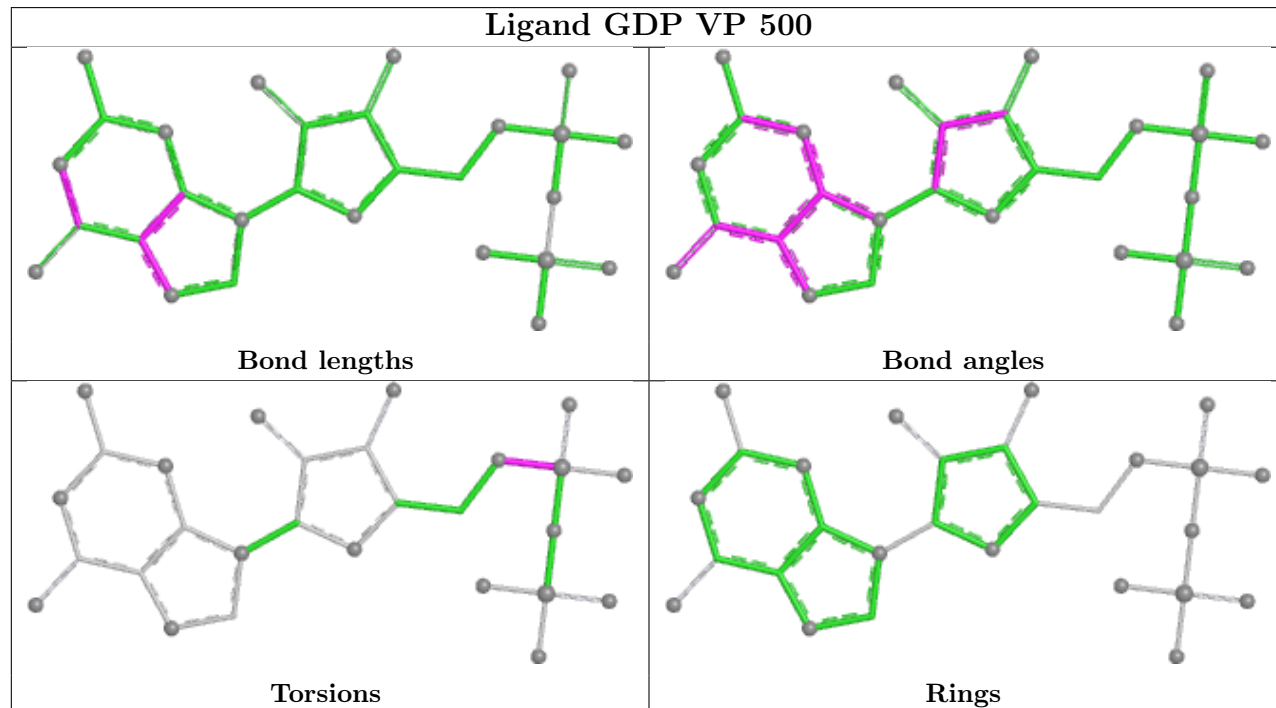
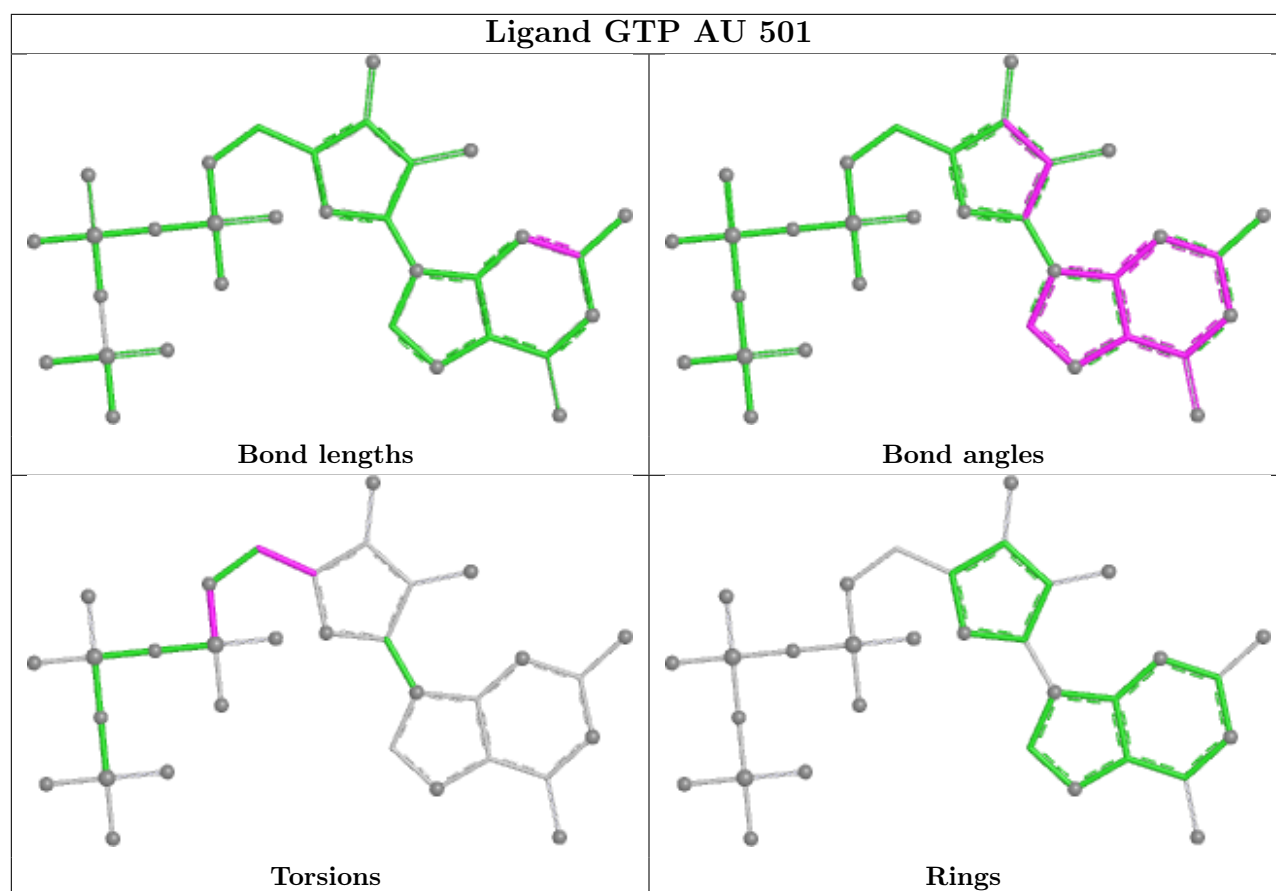


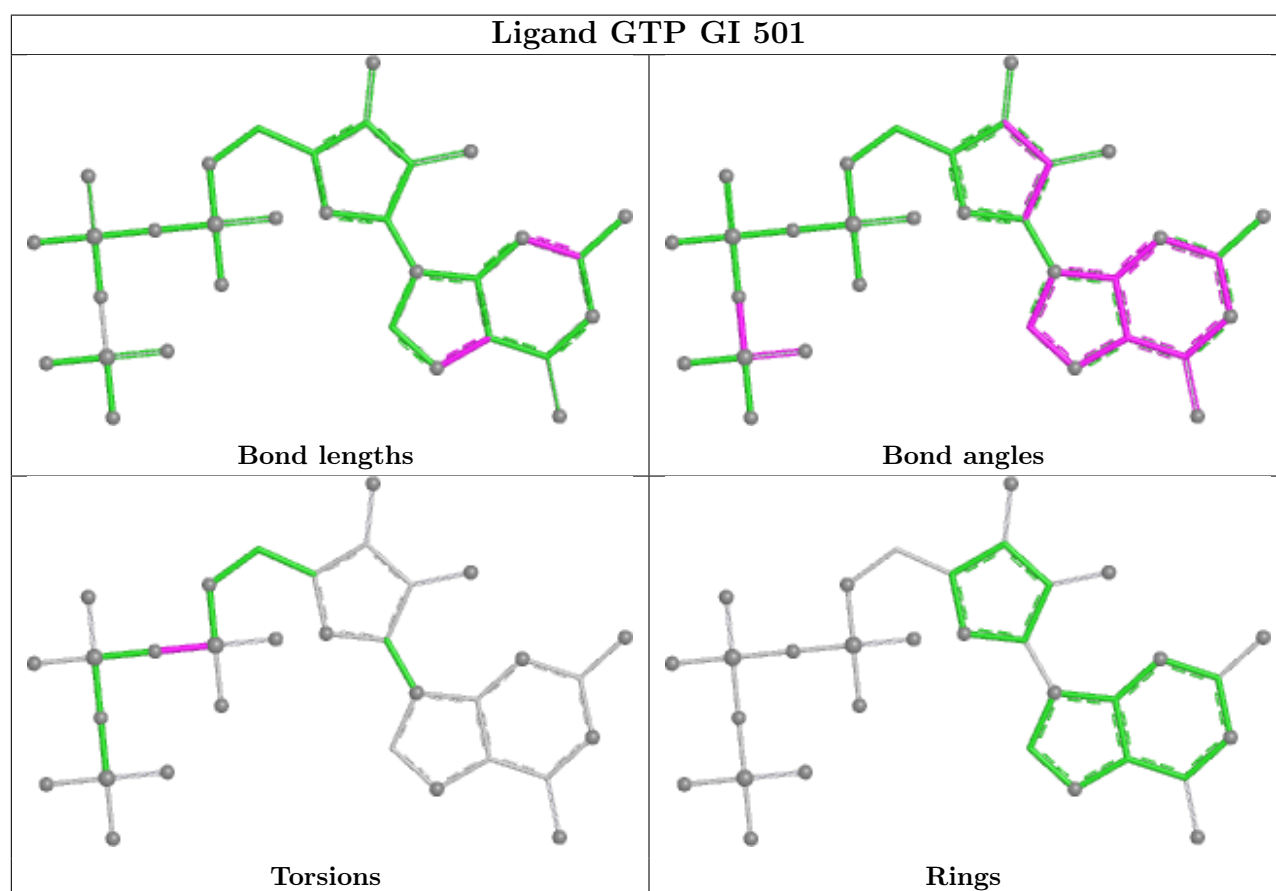
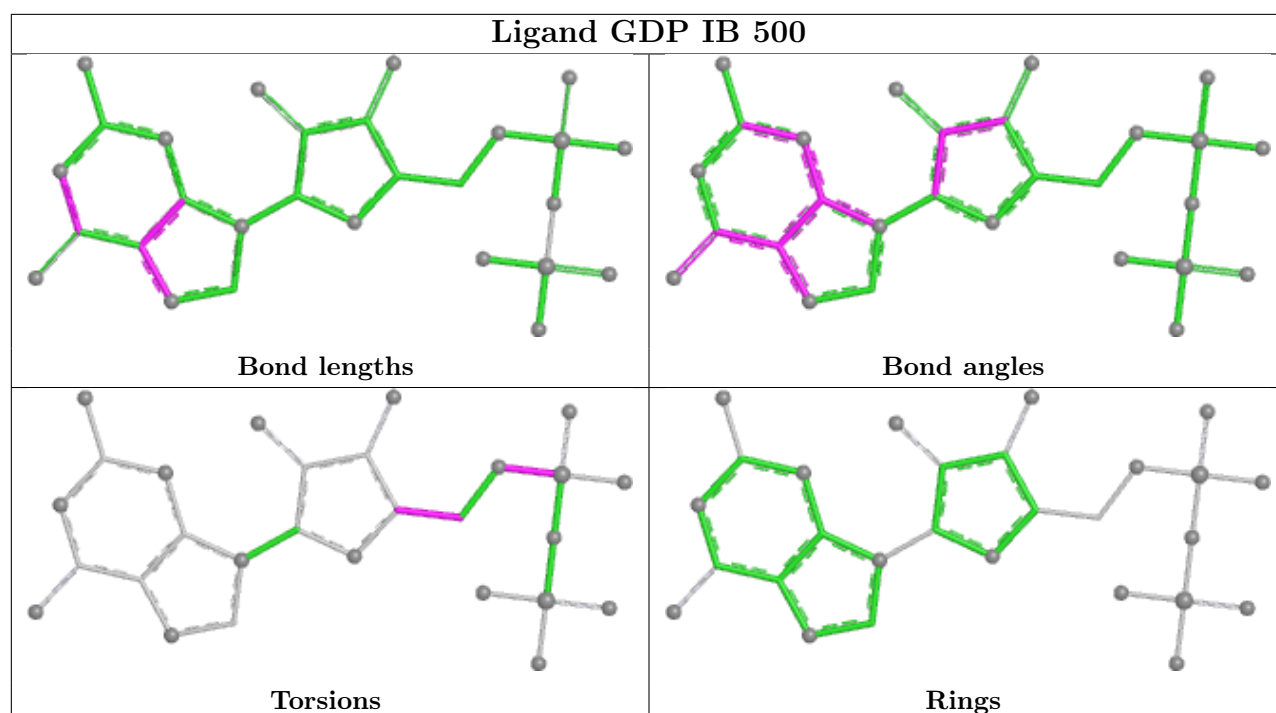


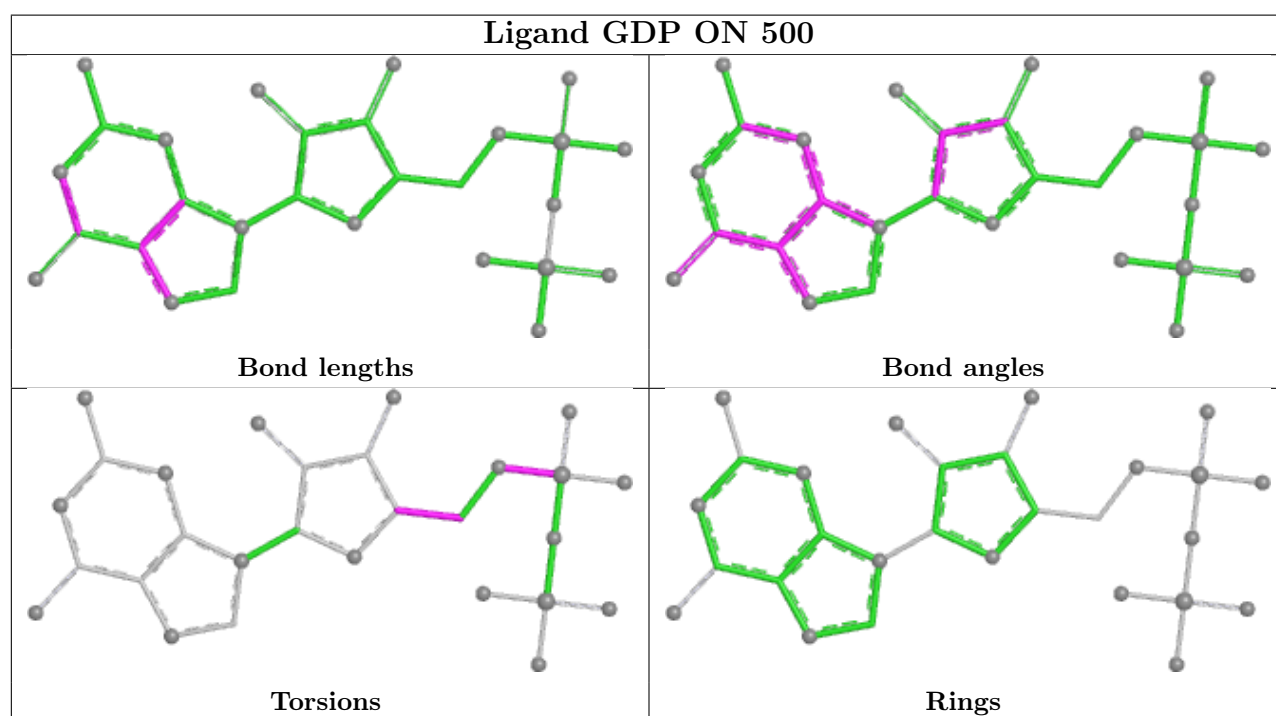
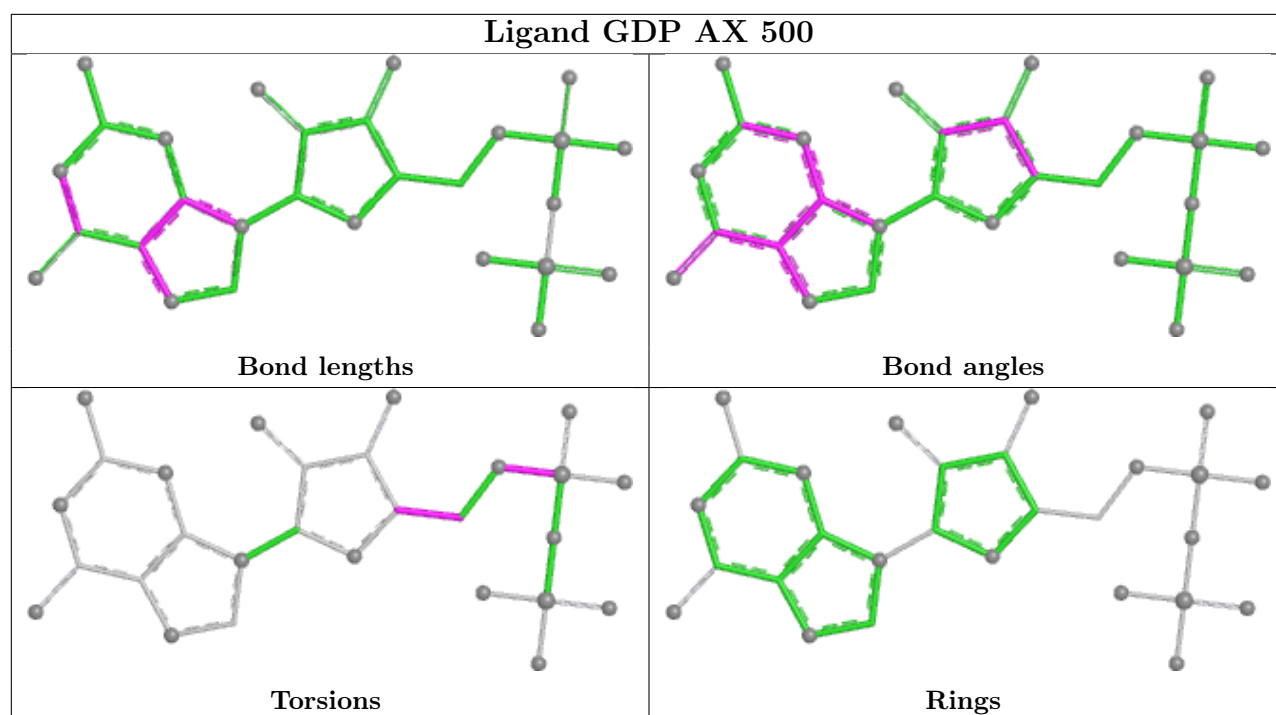




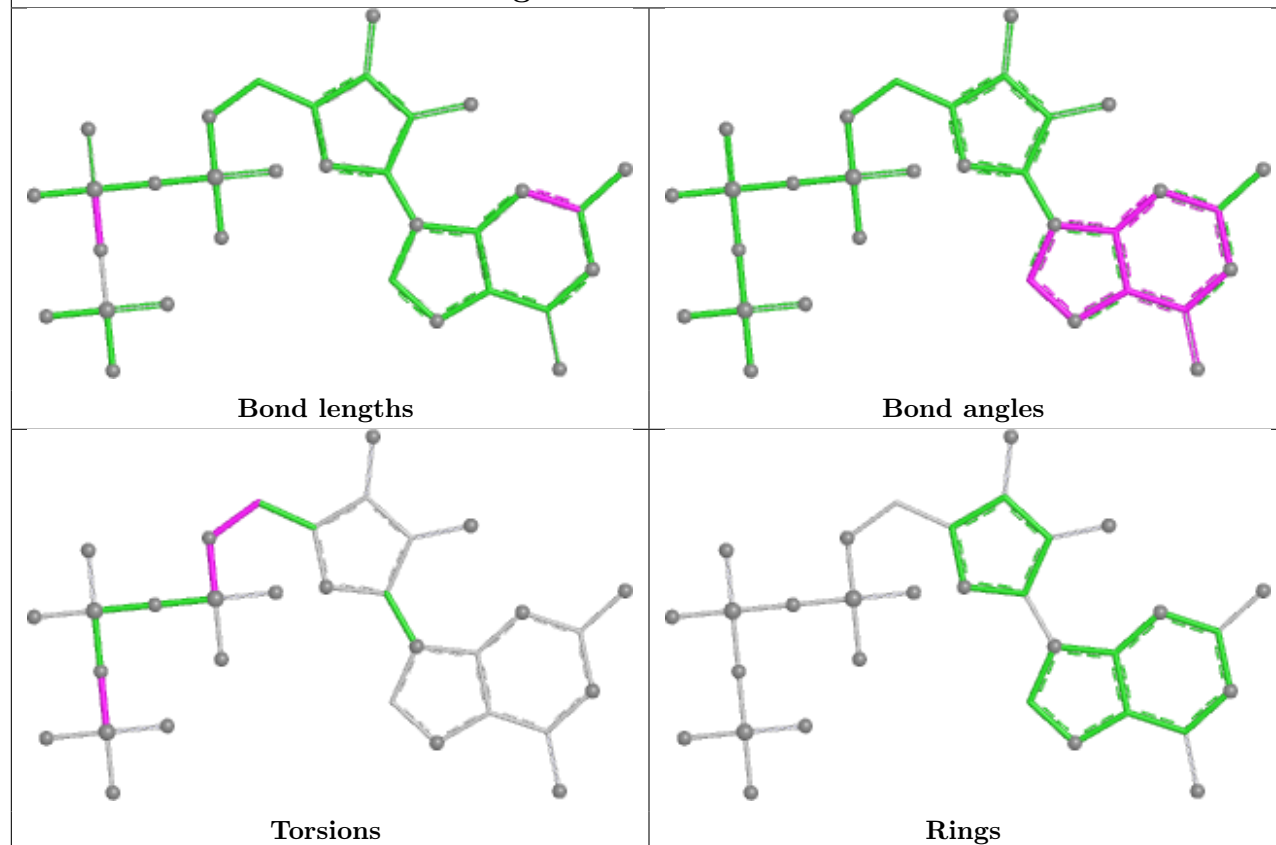




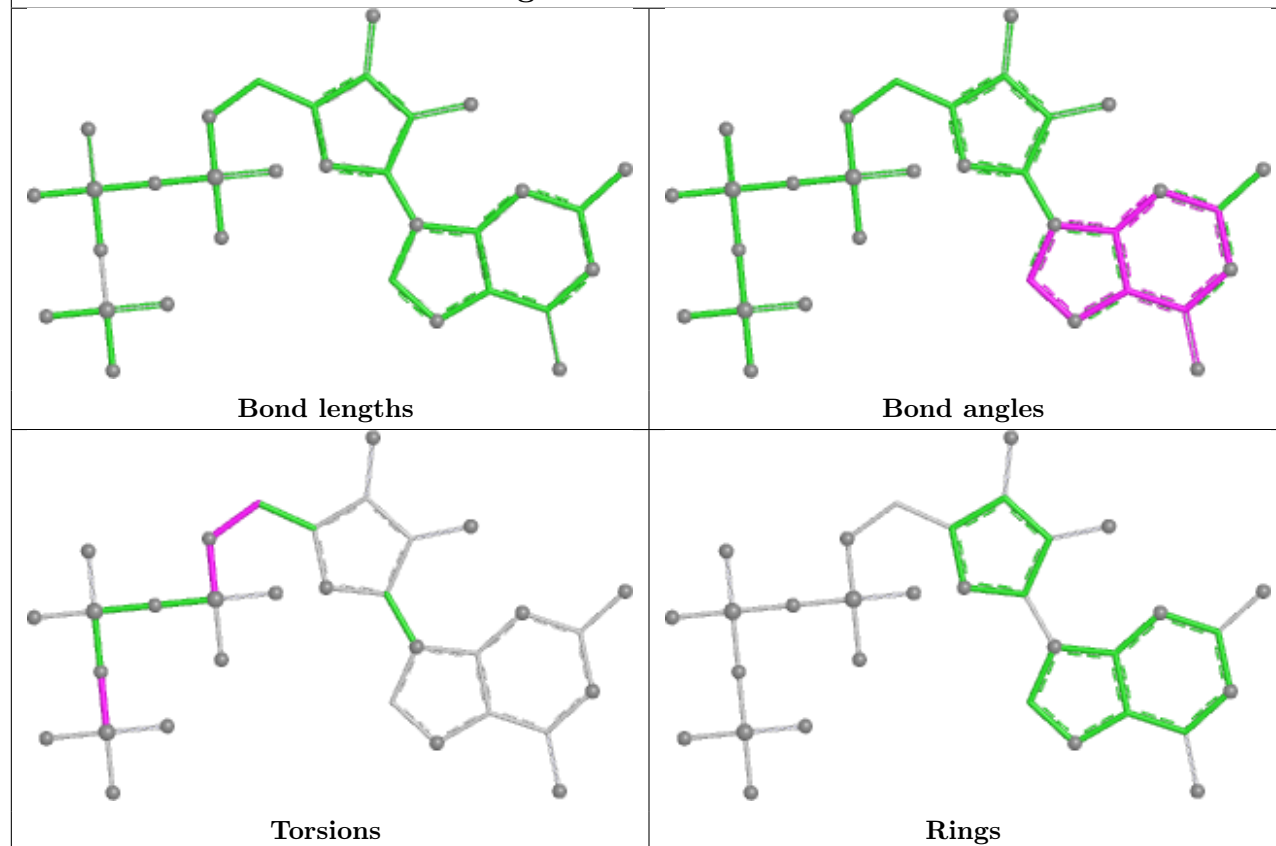


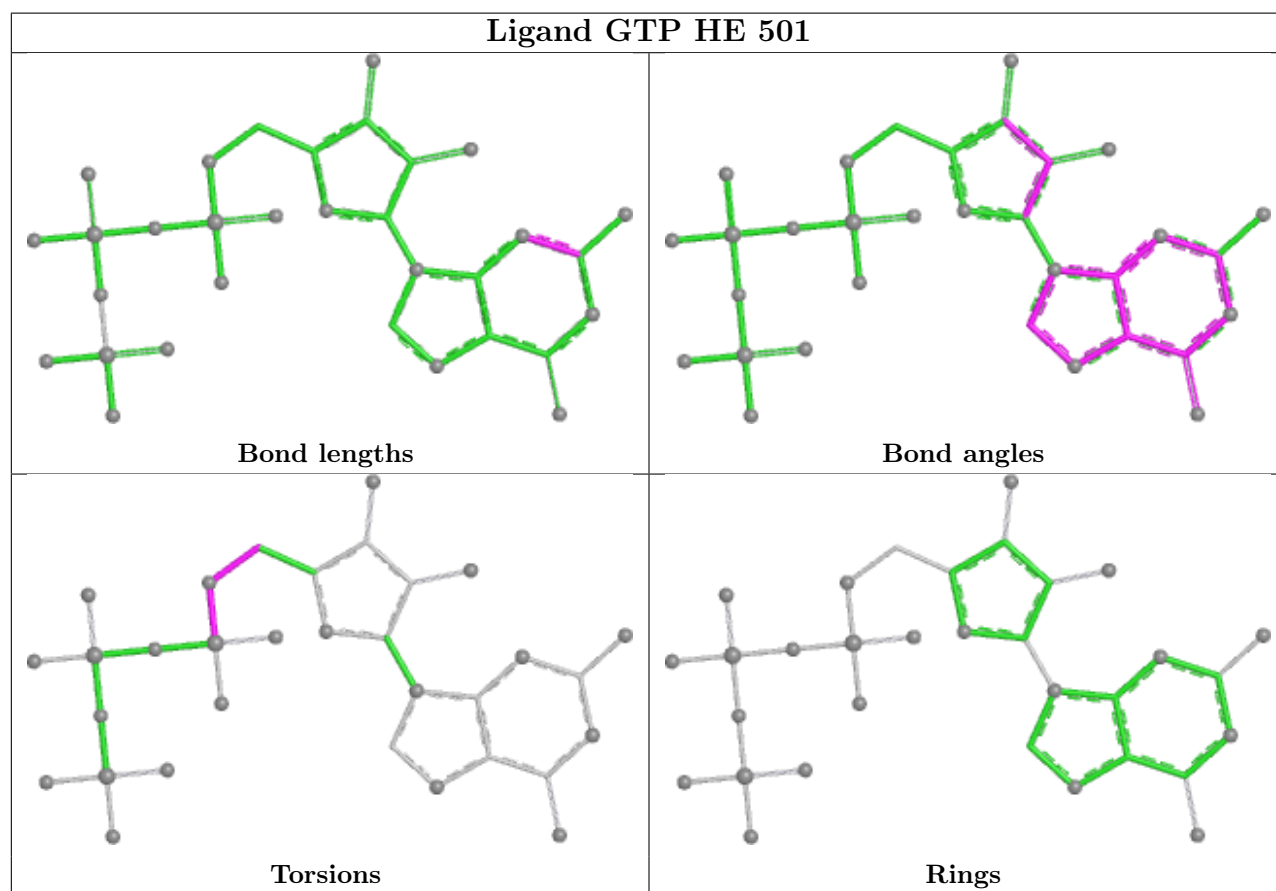
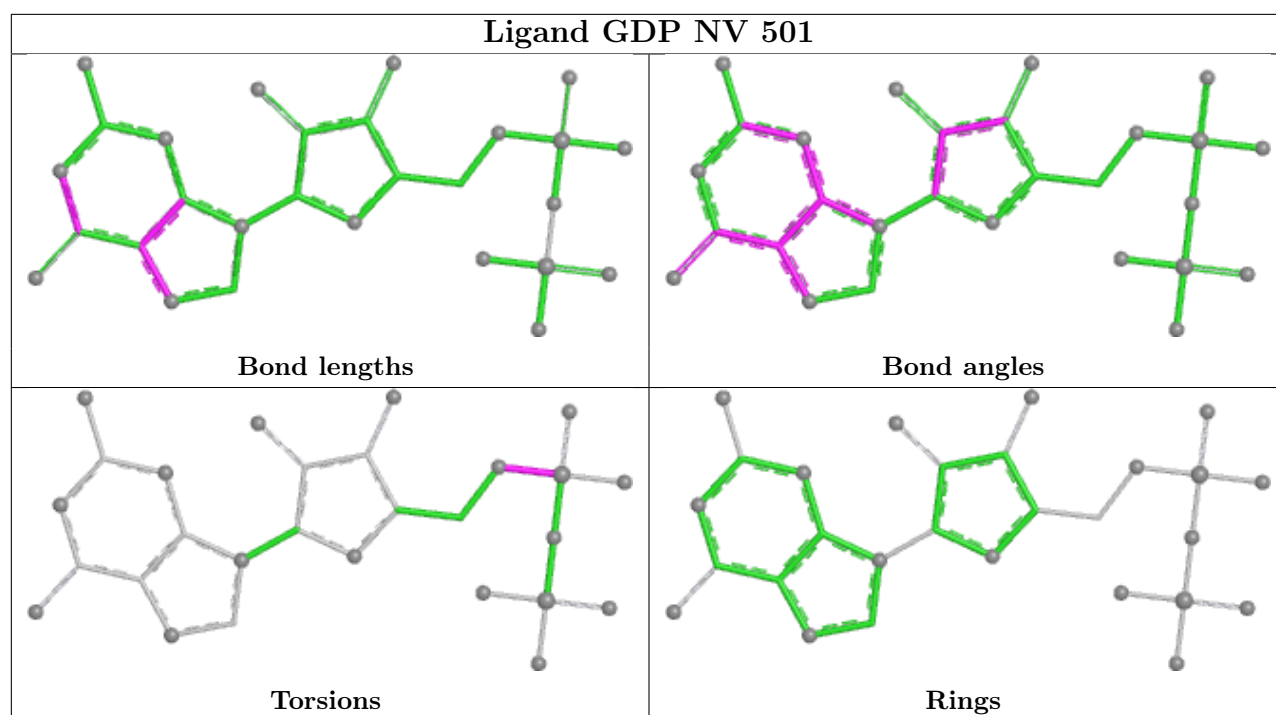


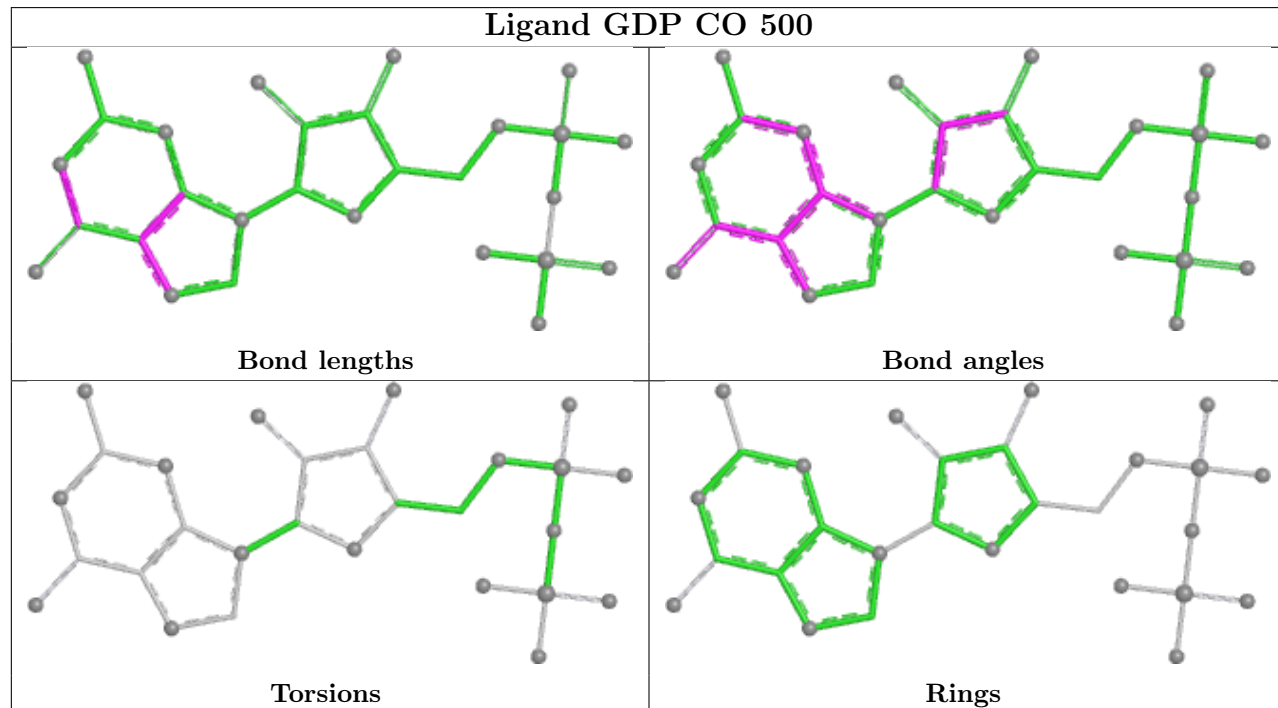
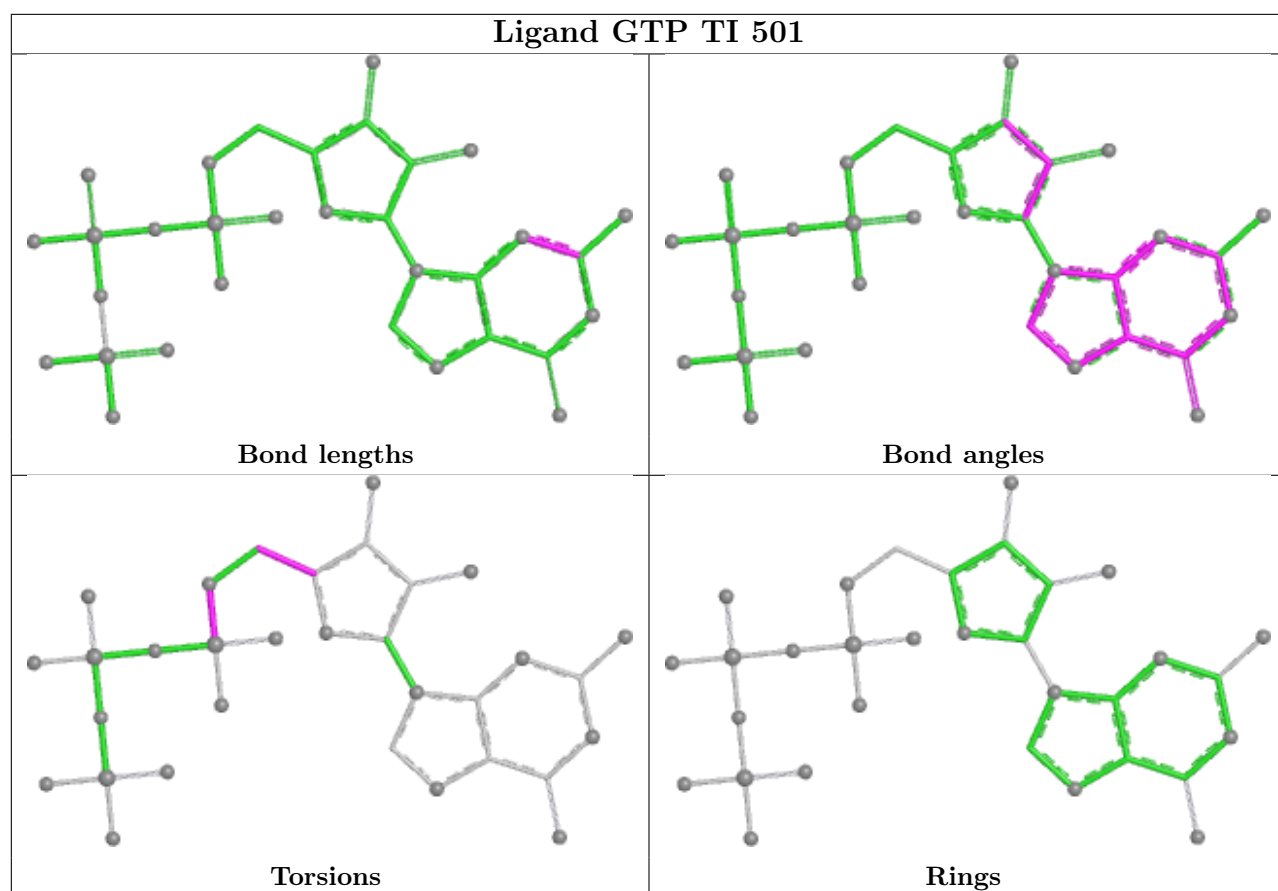
Ligand GTP MU 501

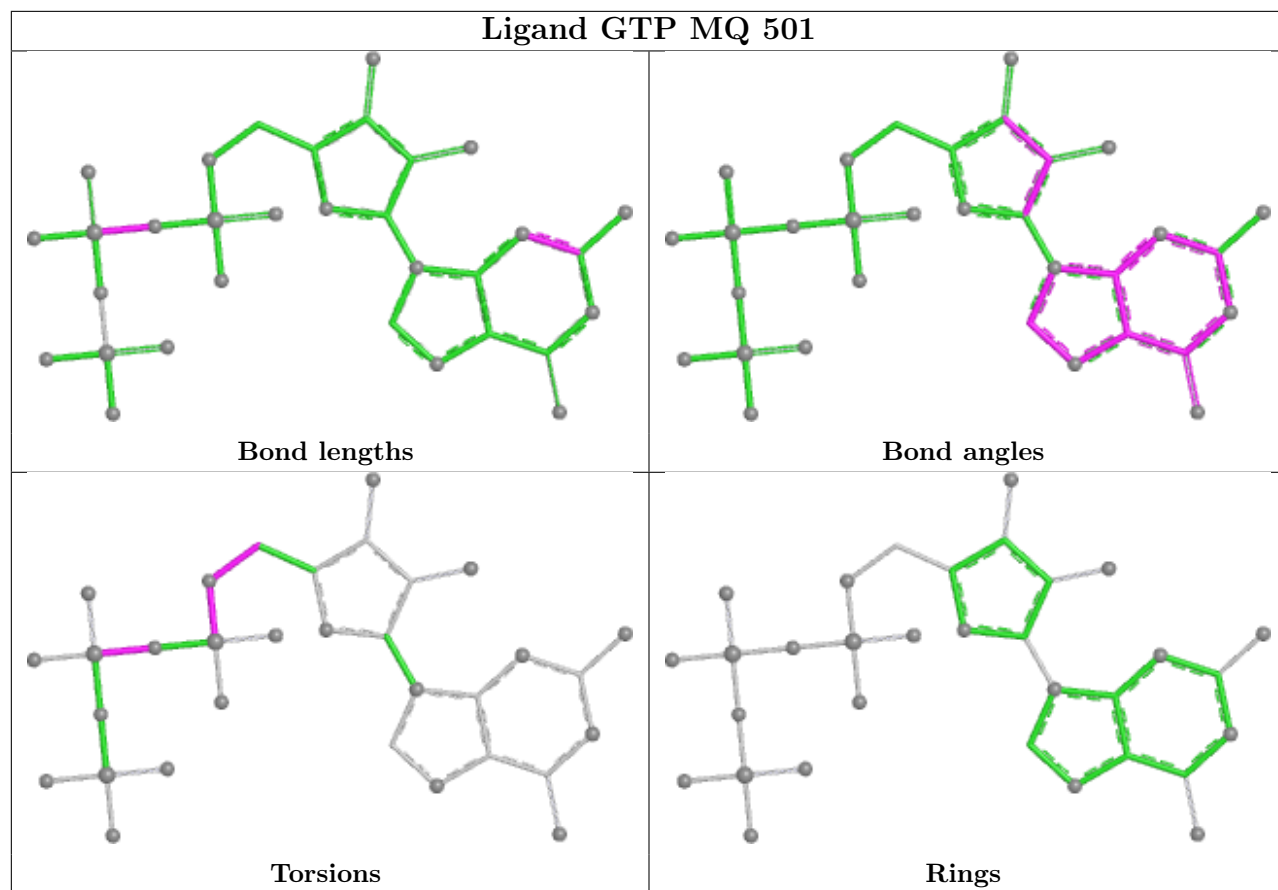


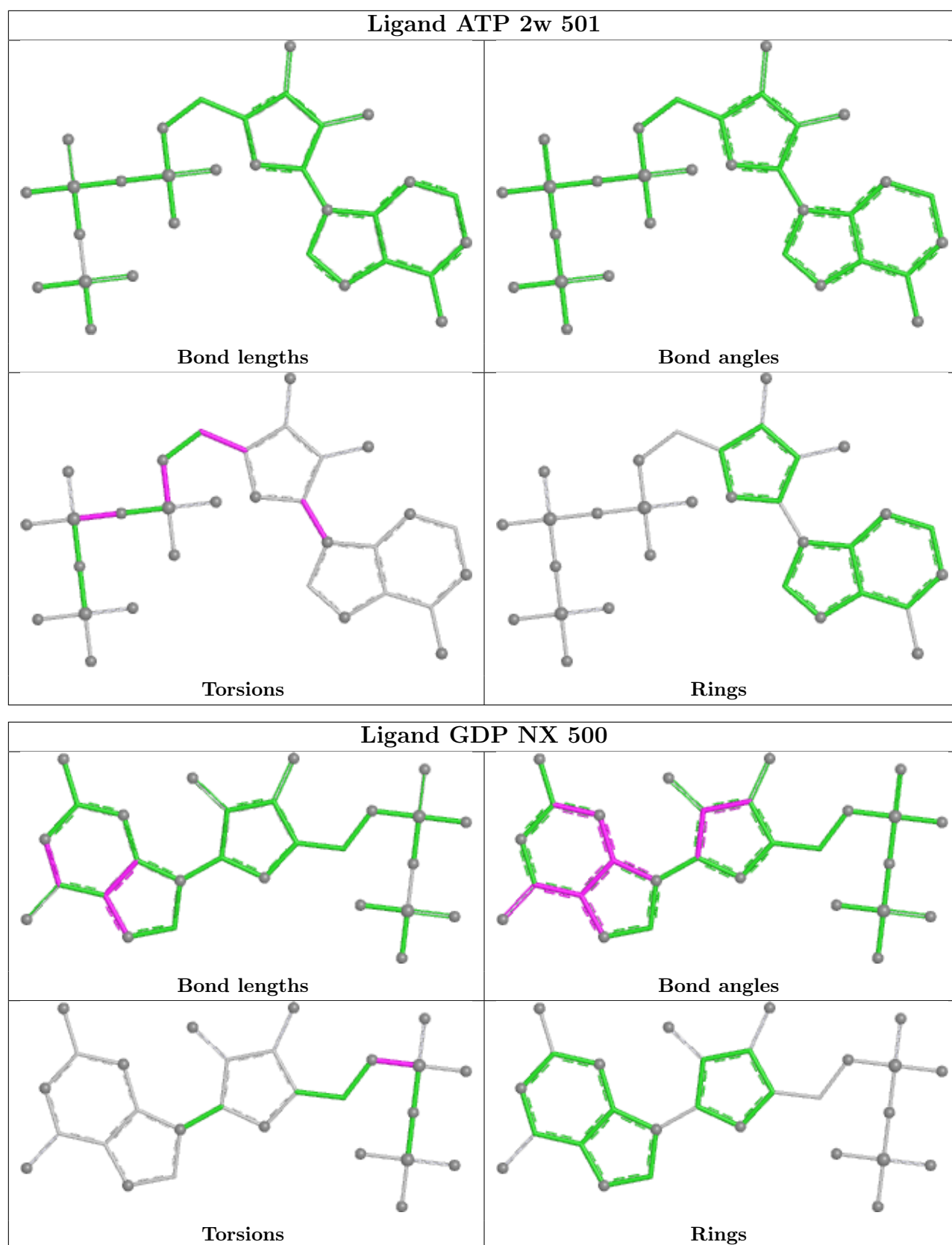
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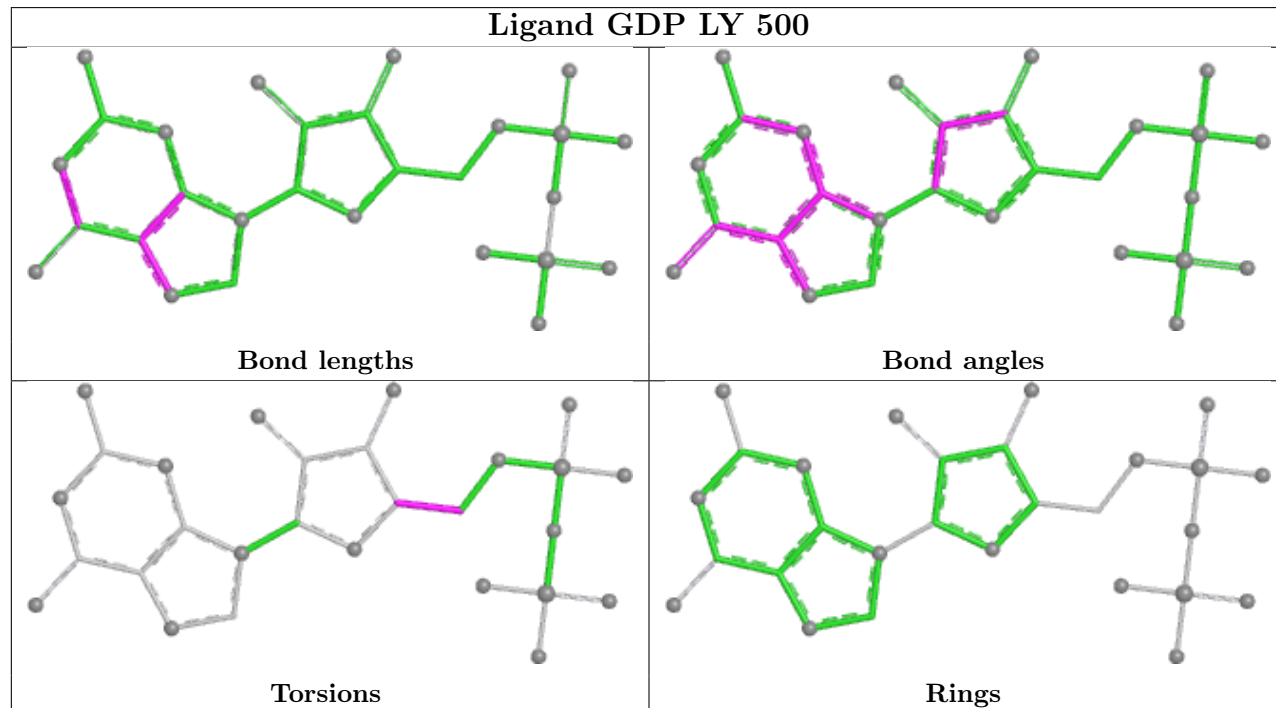
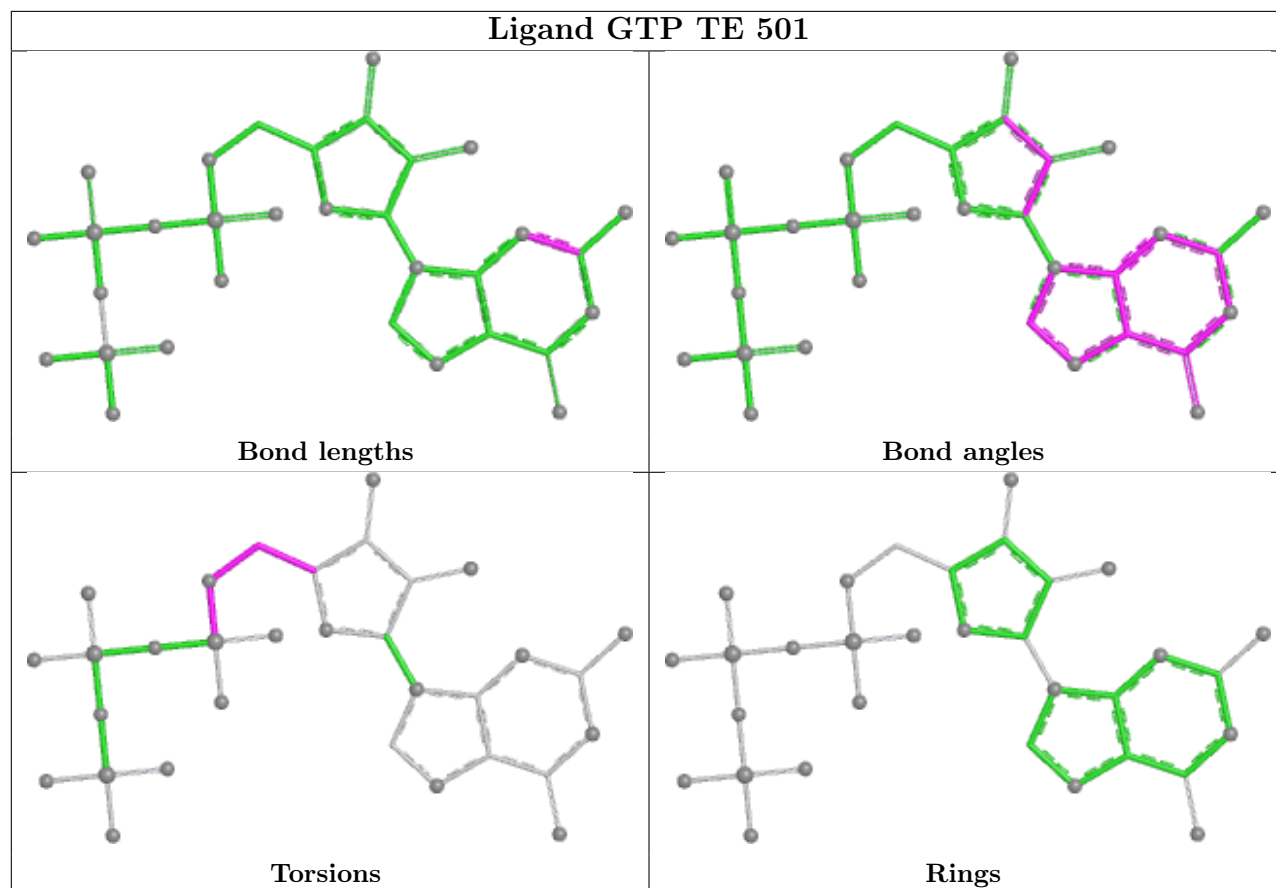


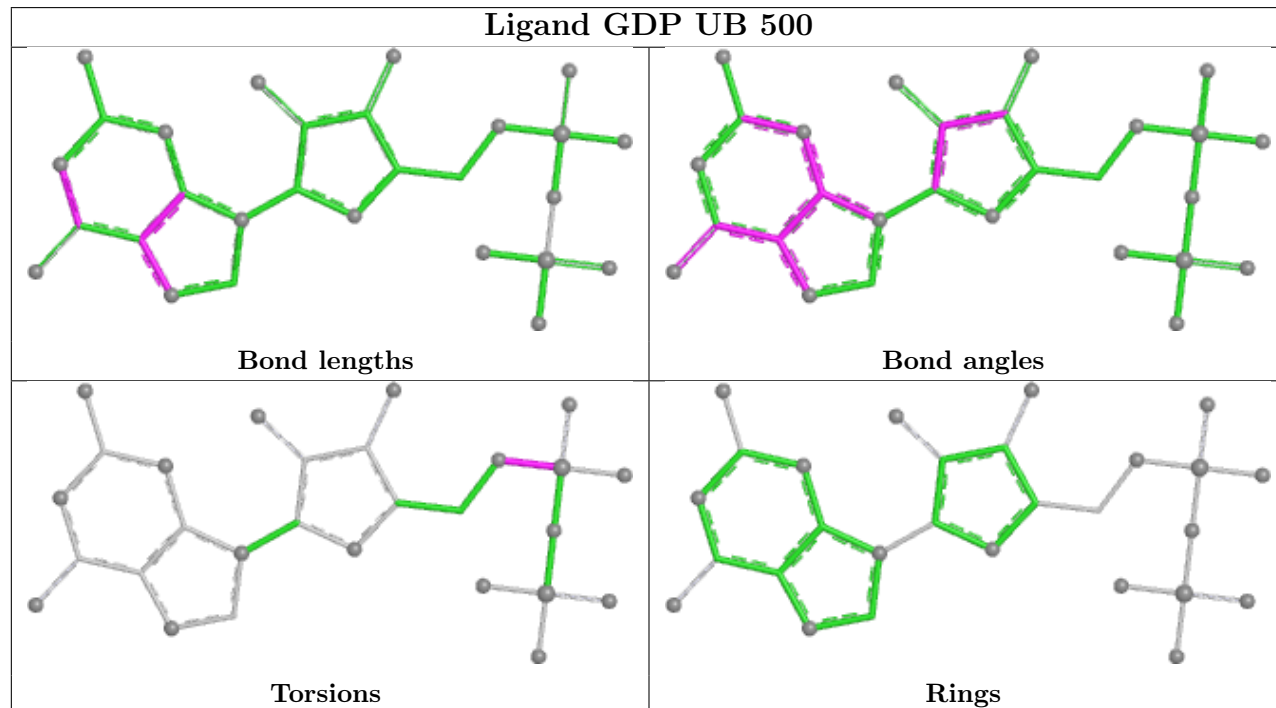
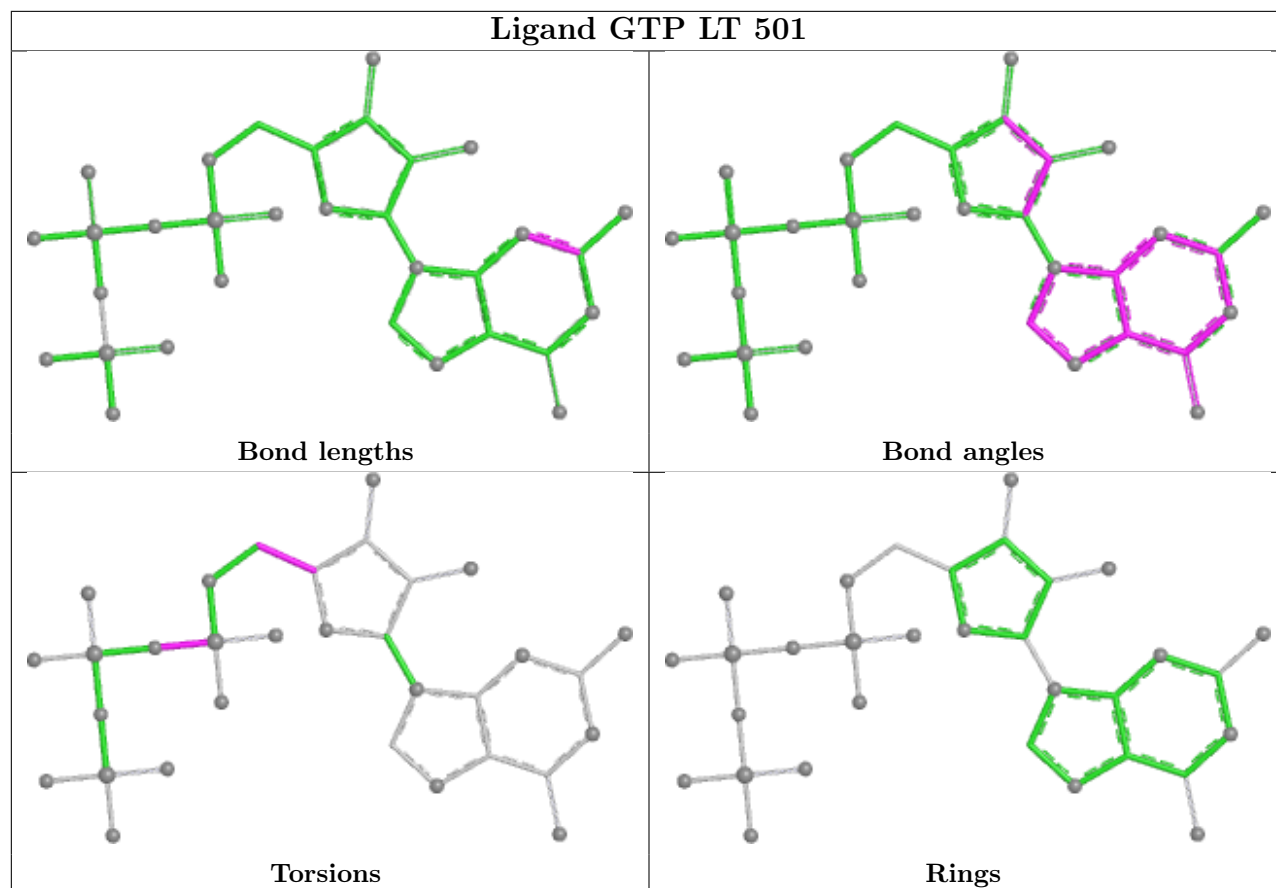


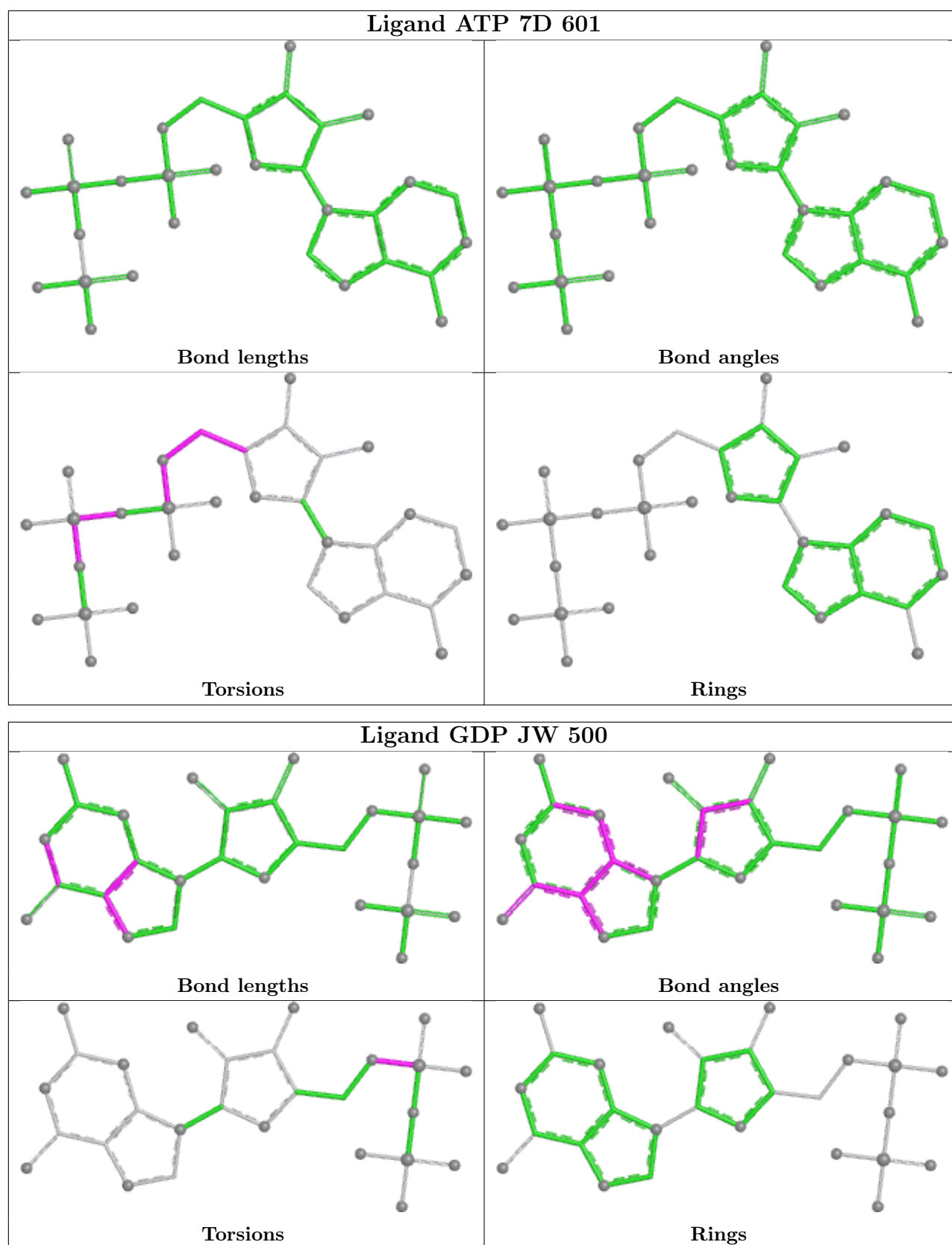




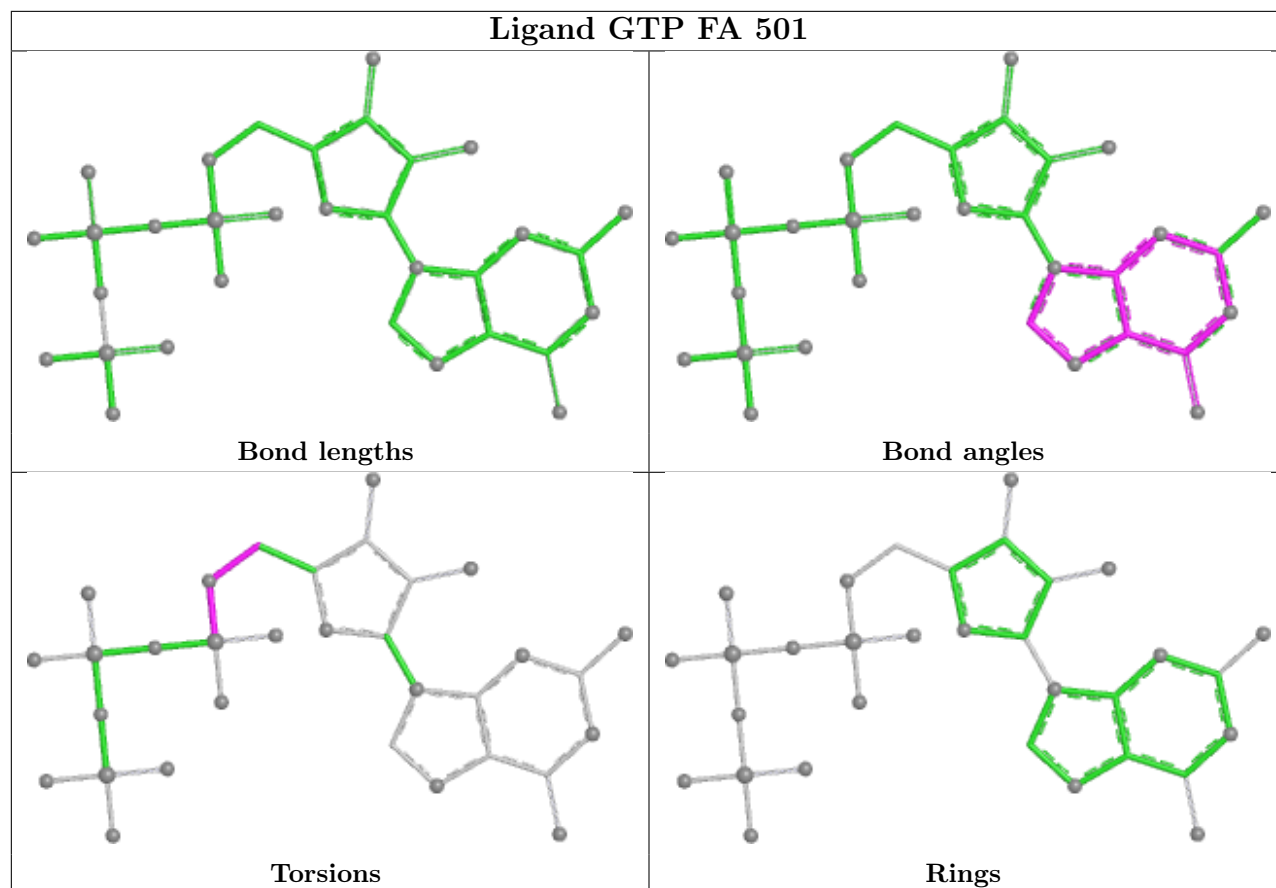




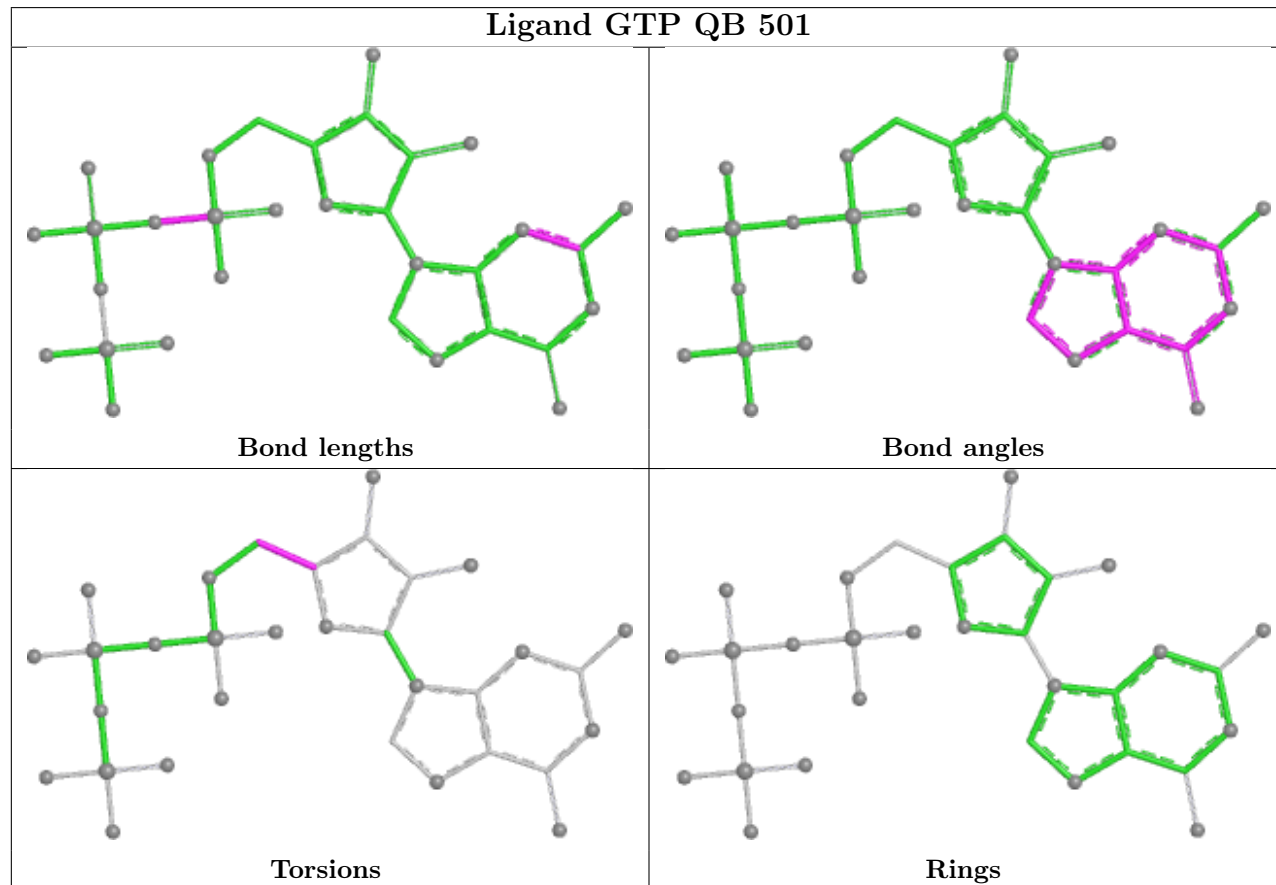


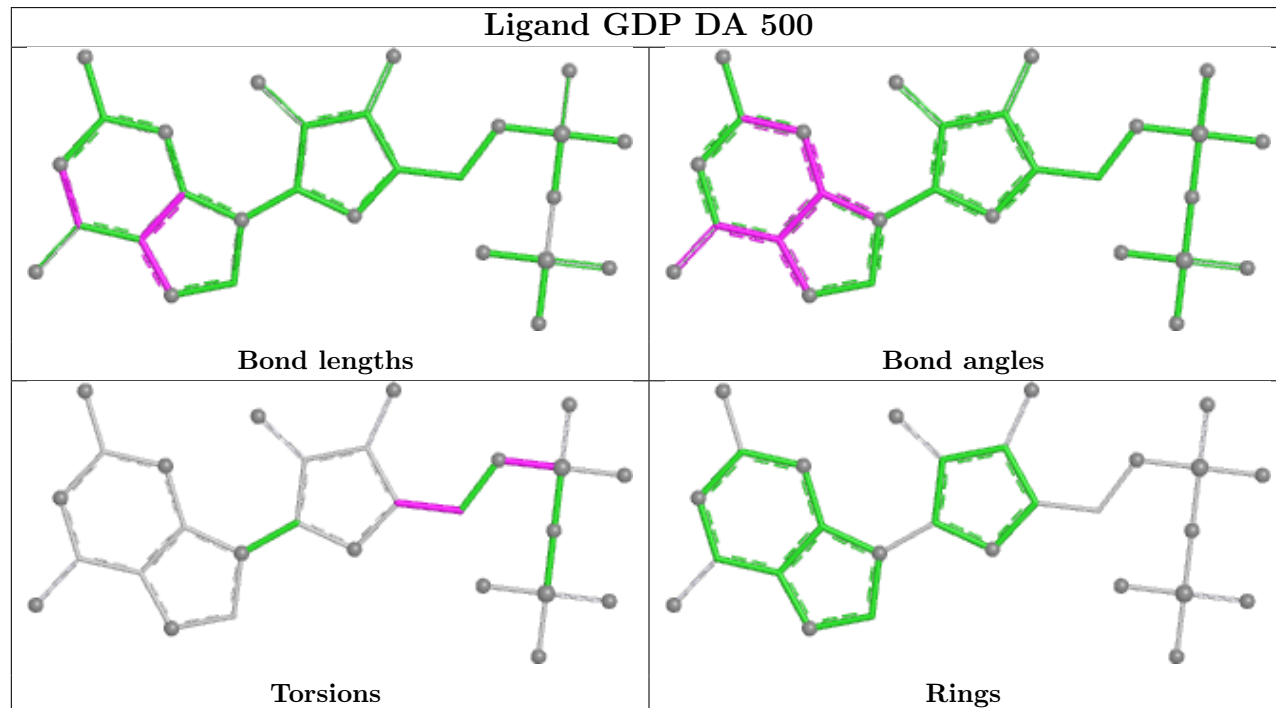
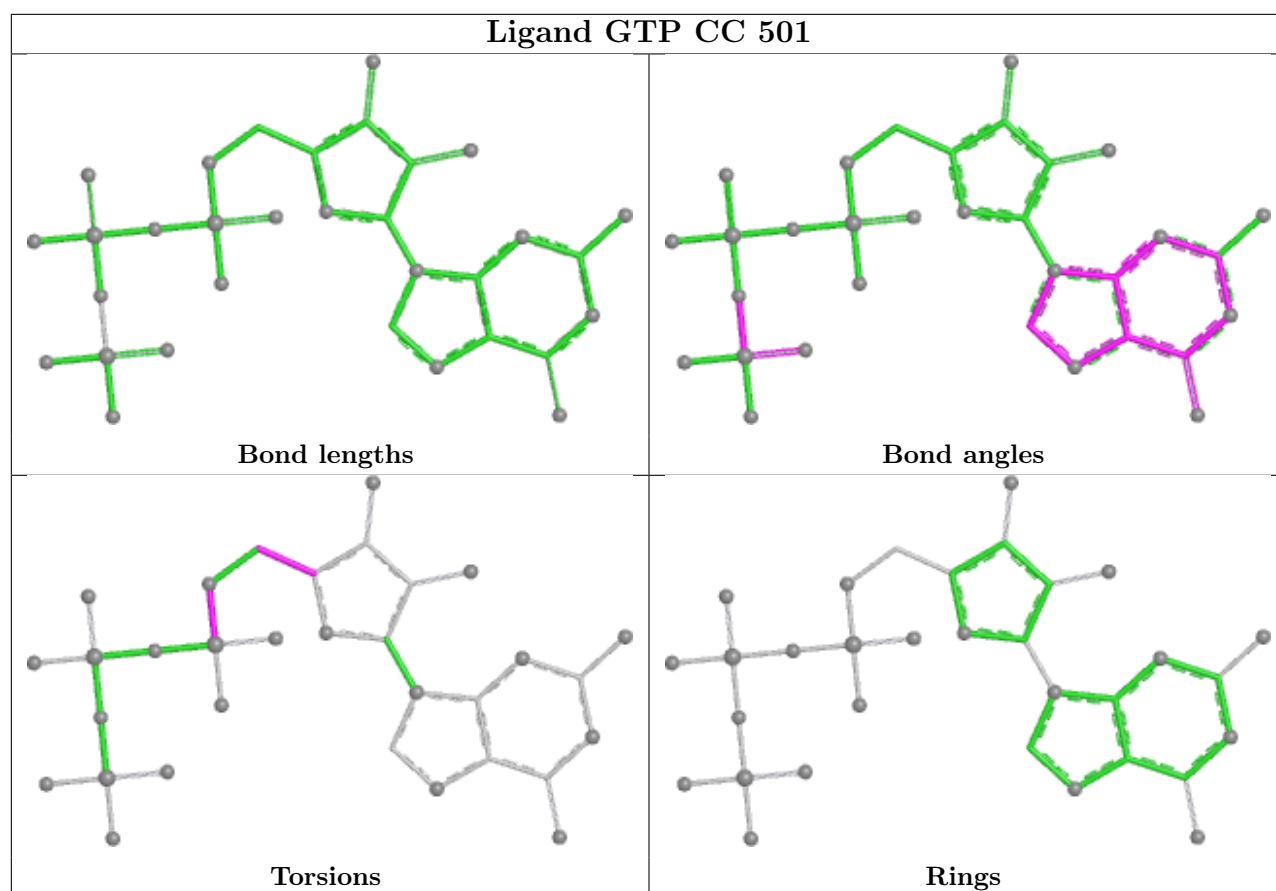


Ligand GTP FA 501

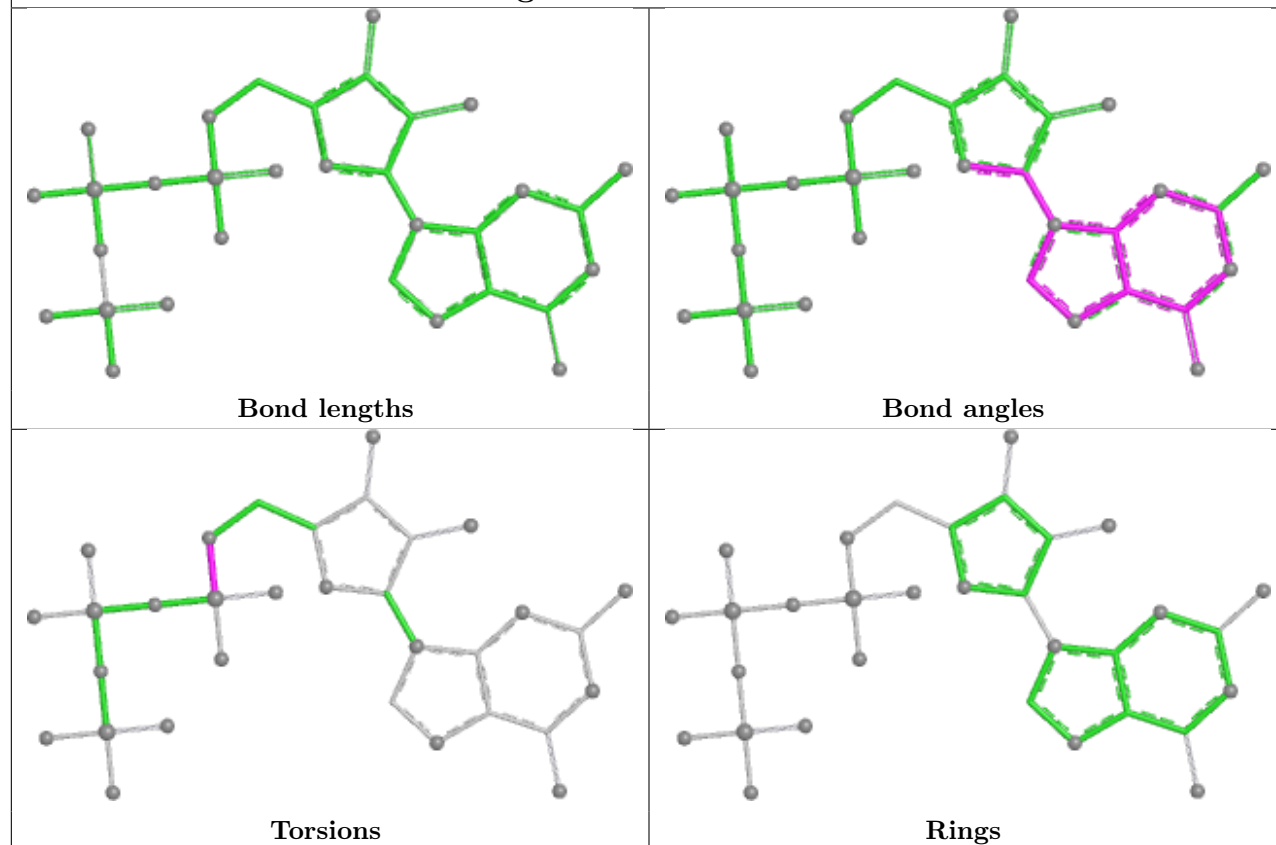


Ligand GTP QB 501

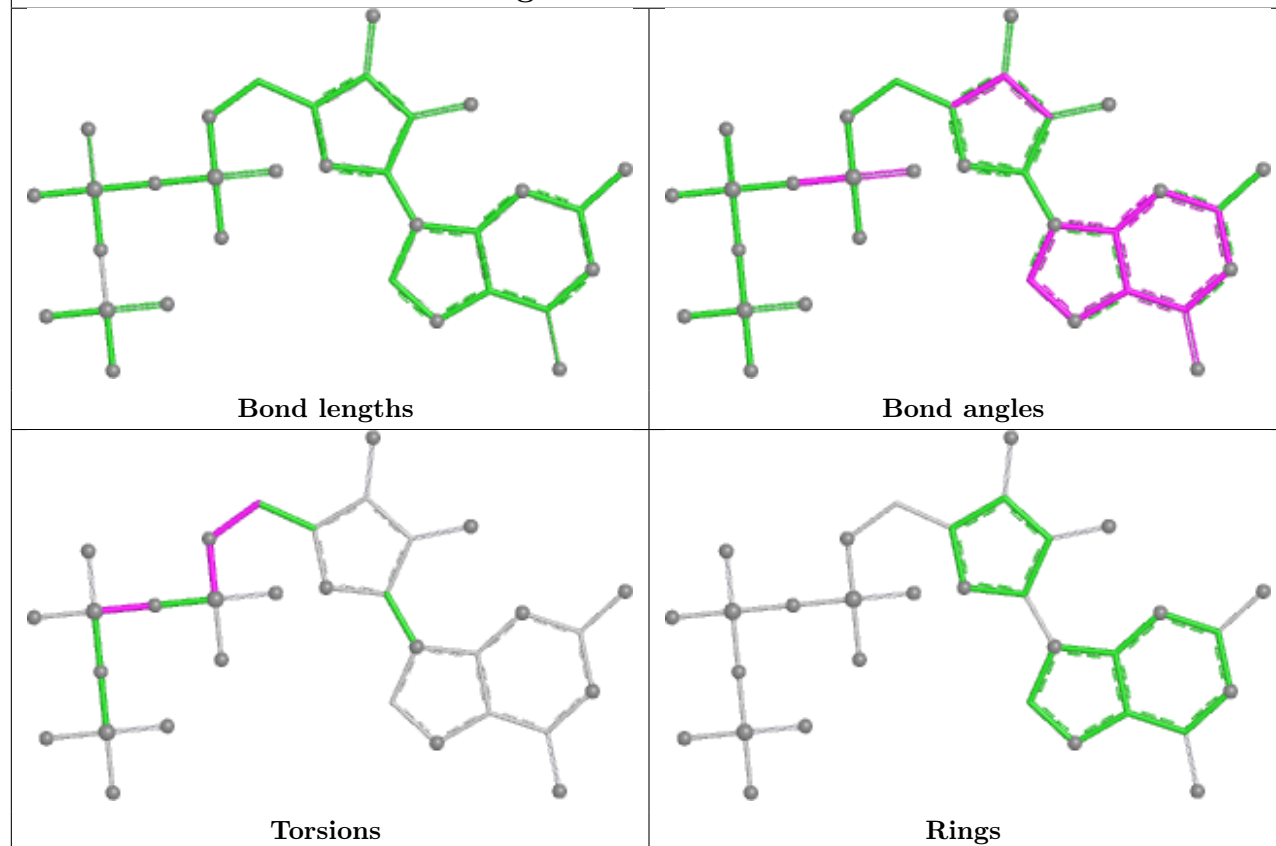


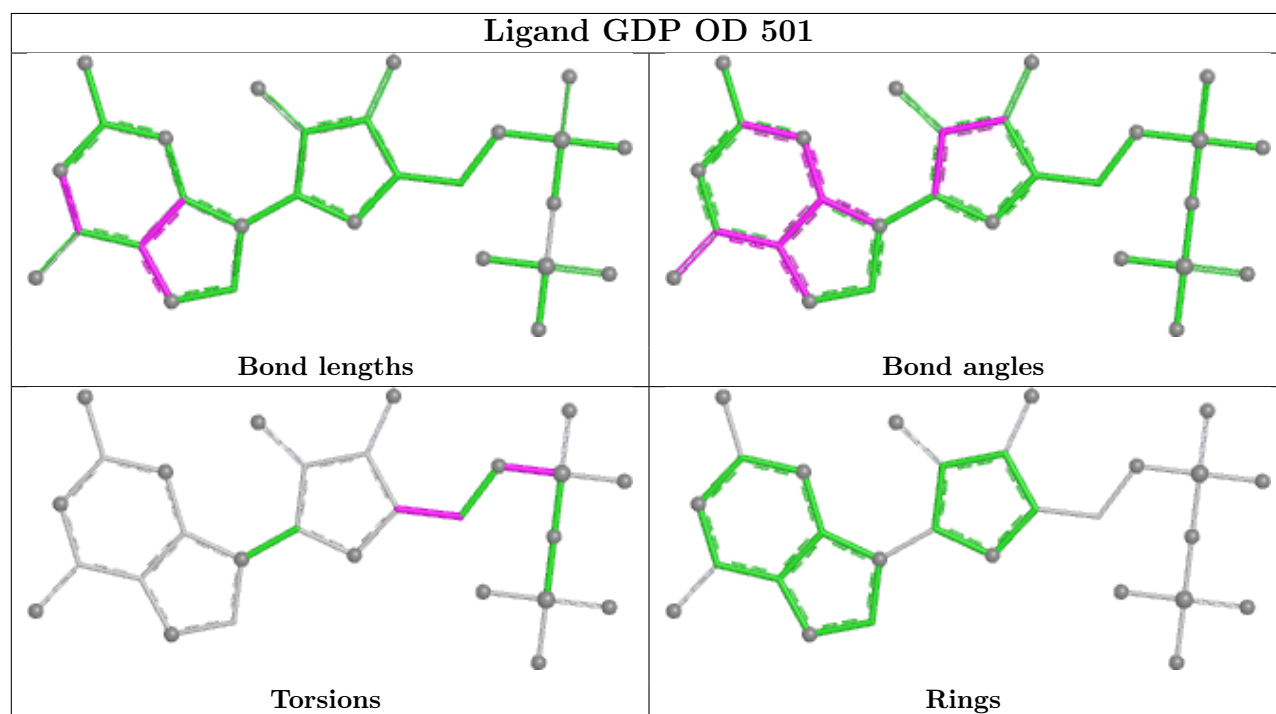
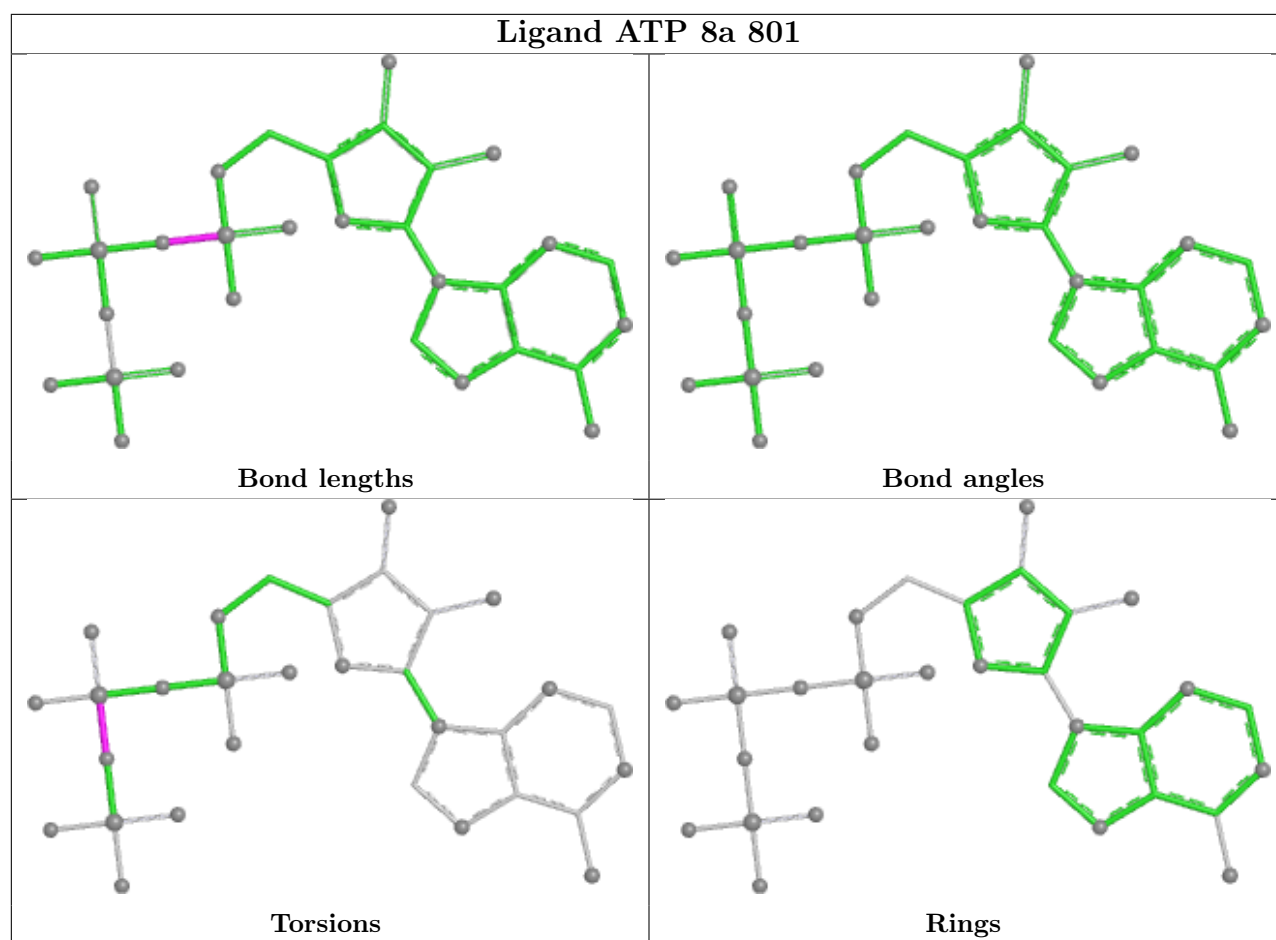


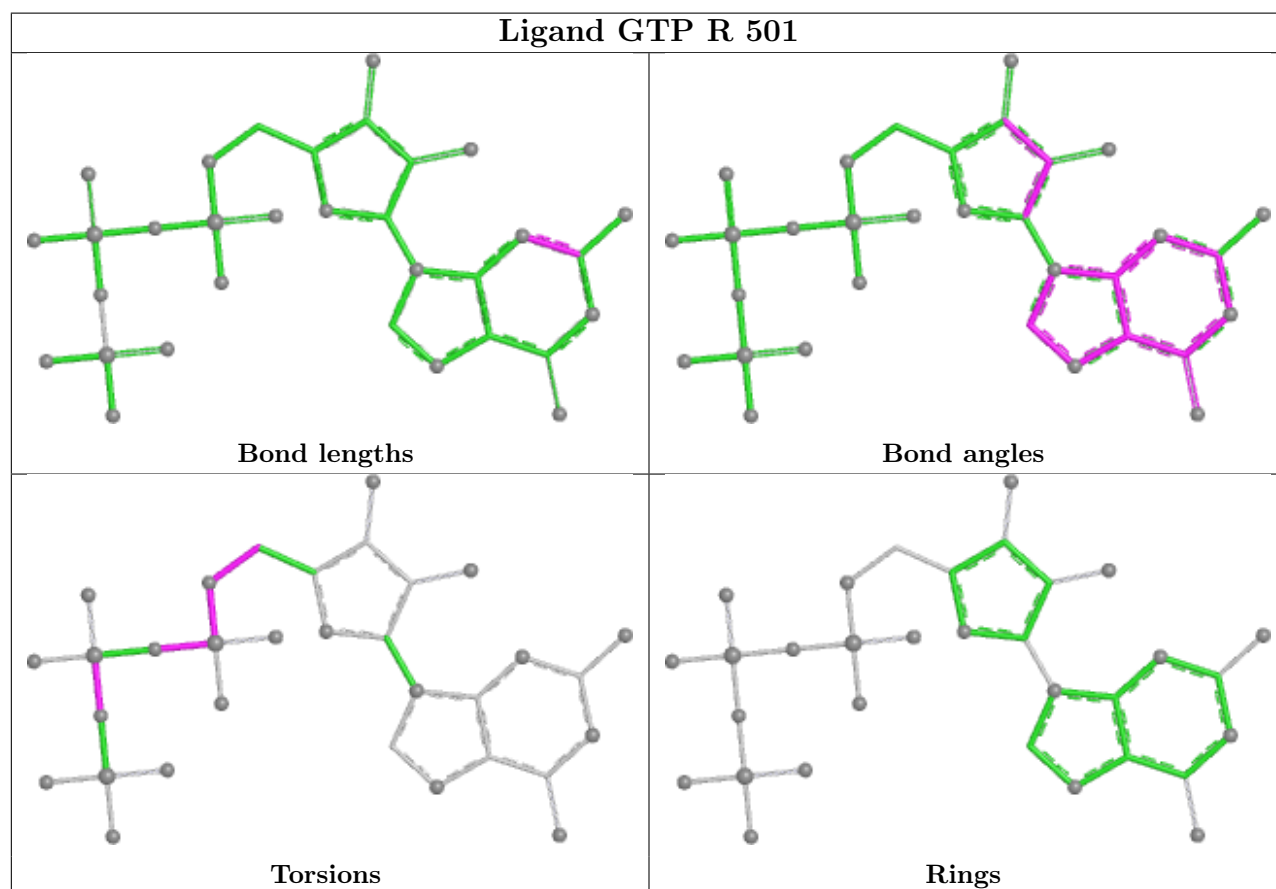
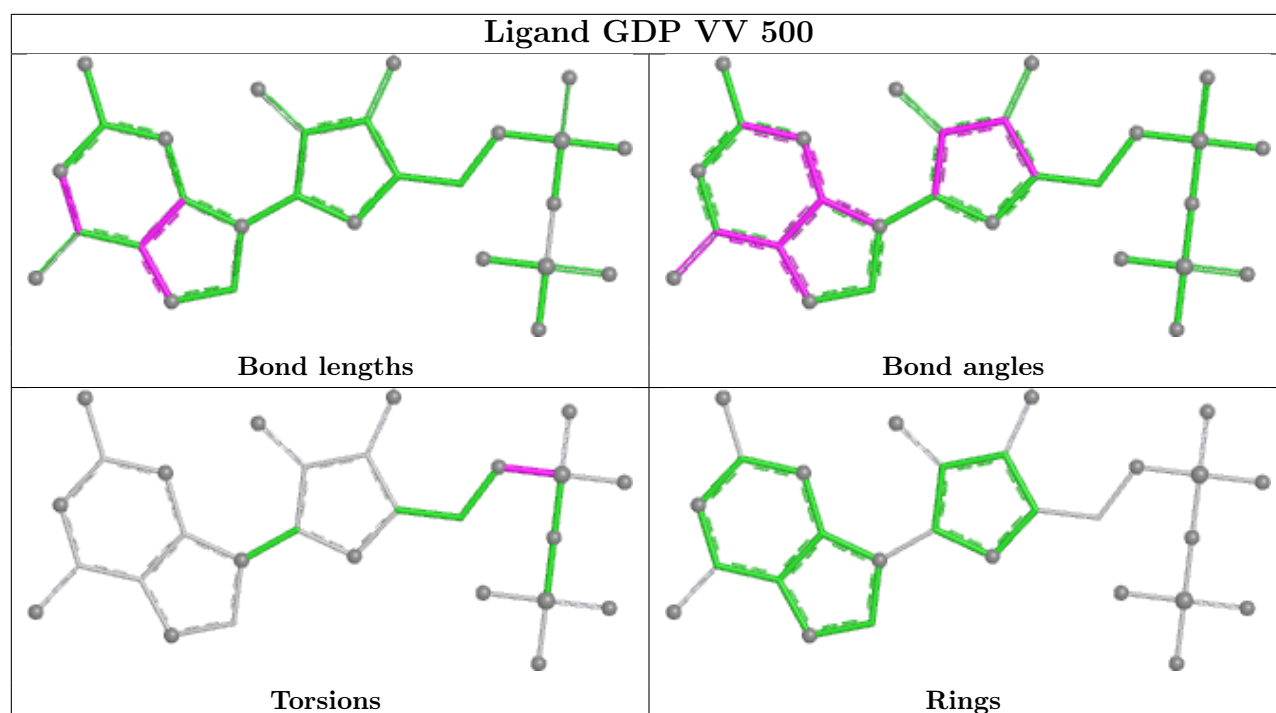
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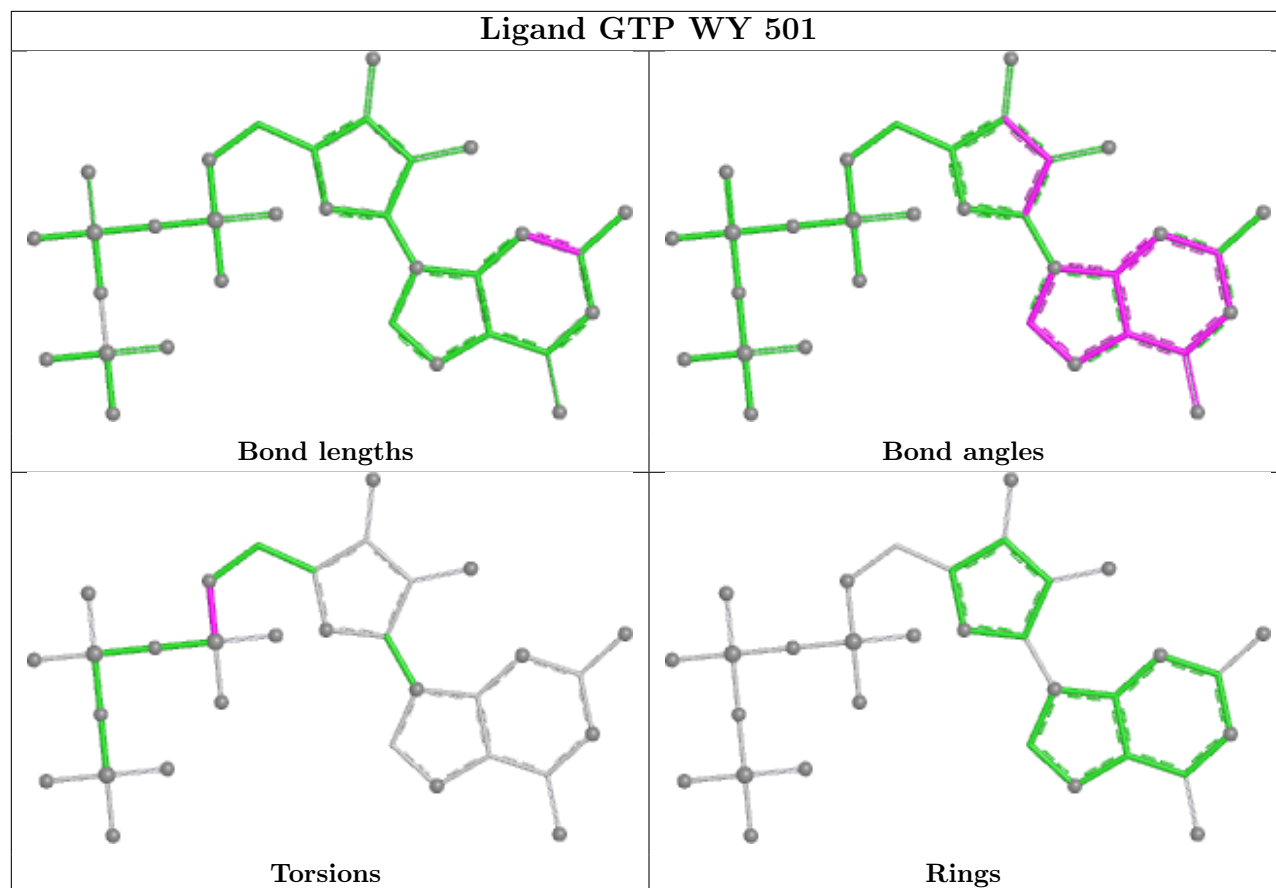
Ligand GTP GC 501



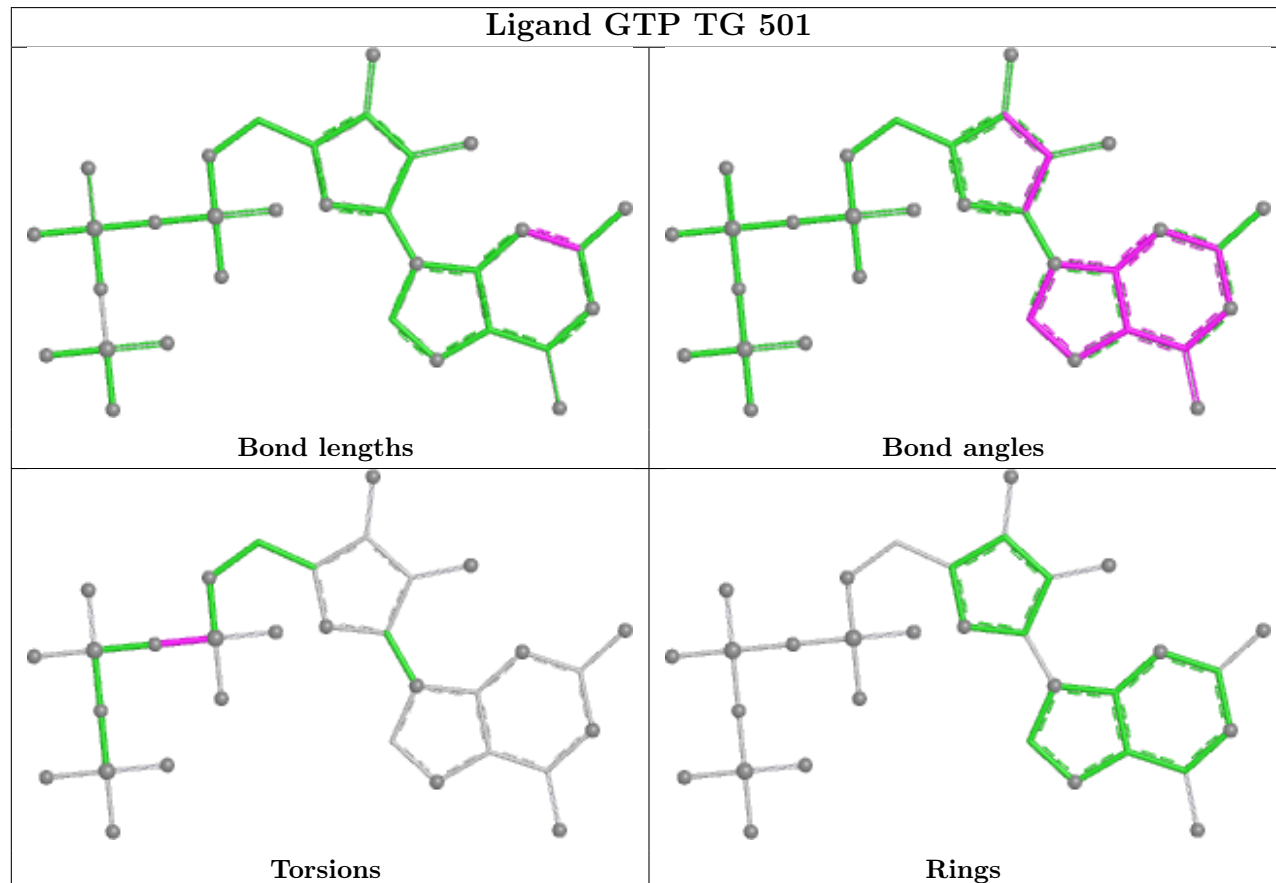


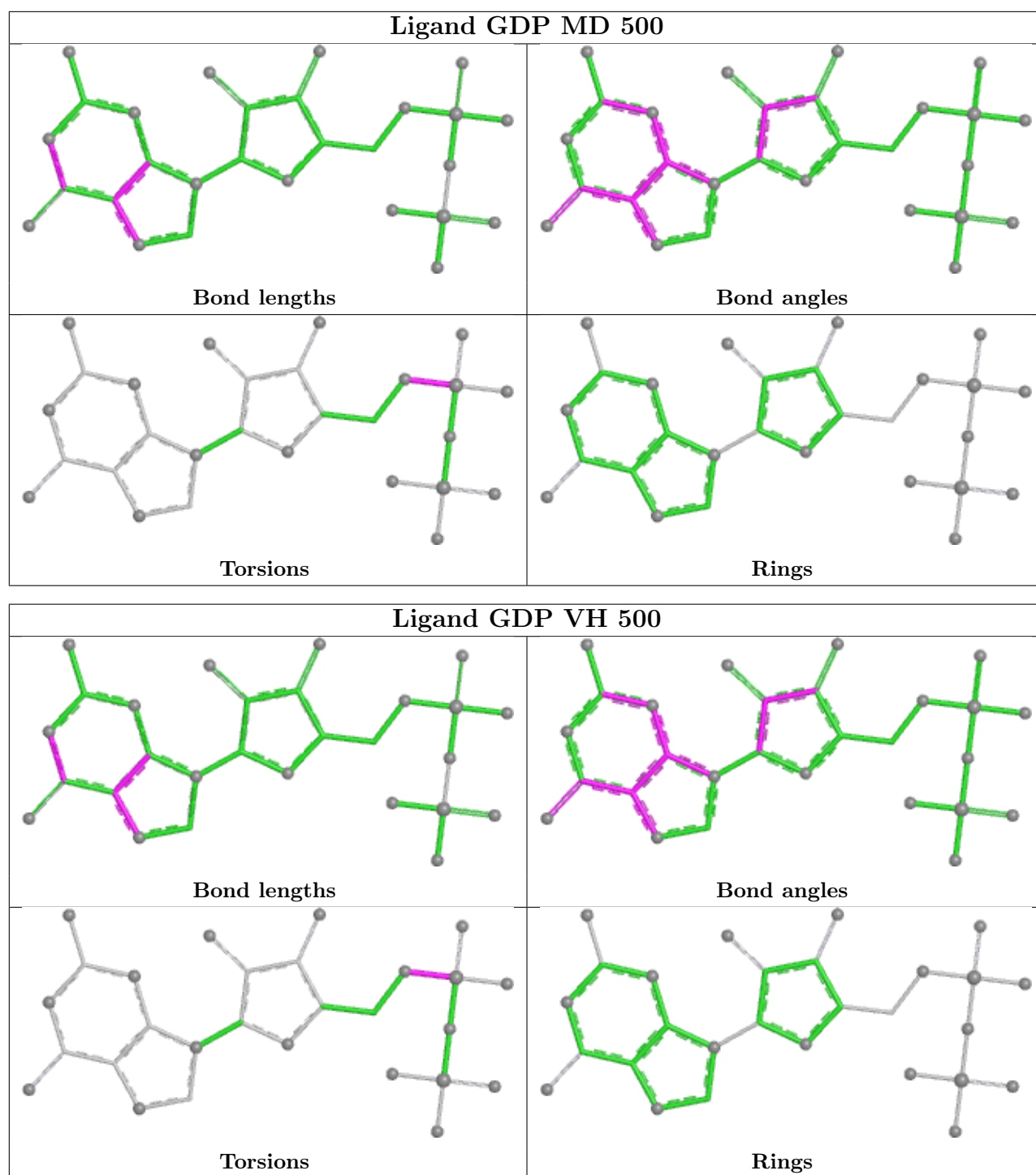


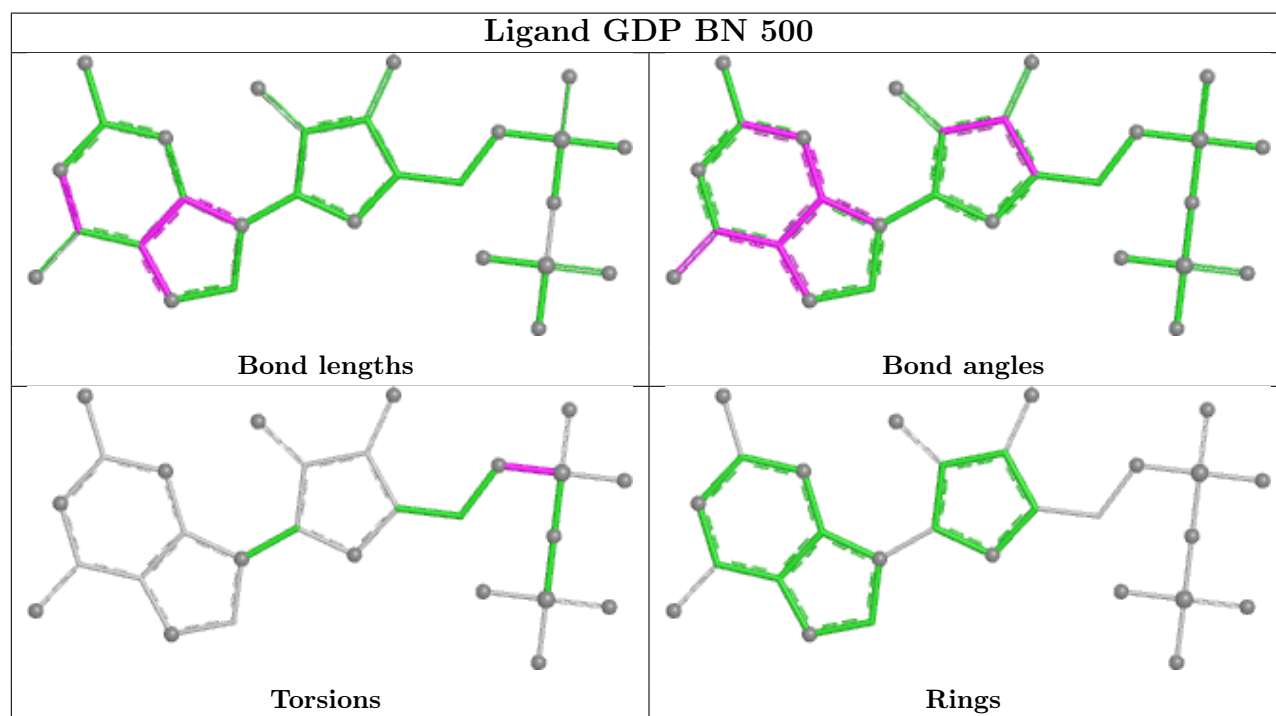
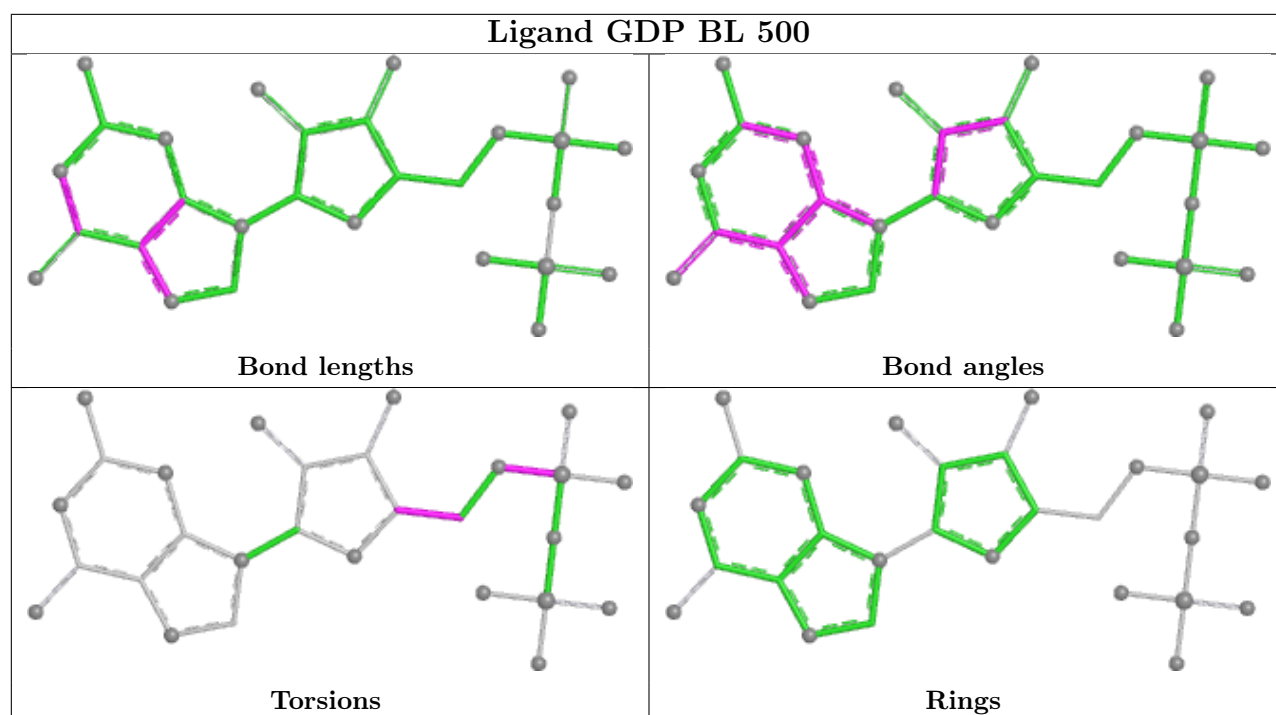
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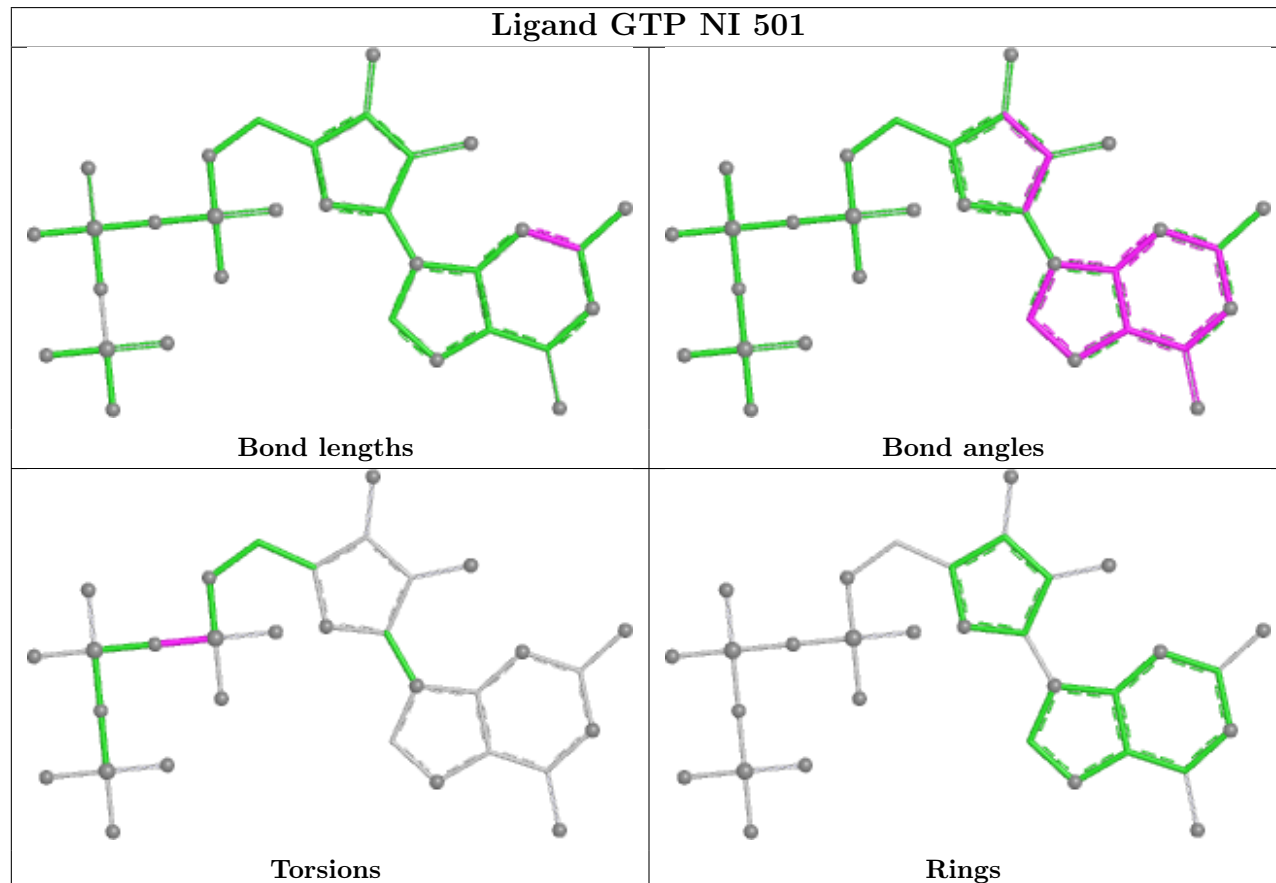
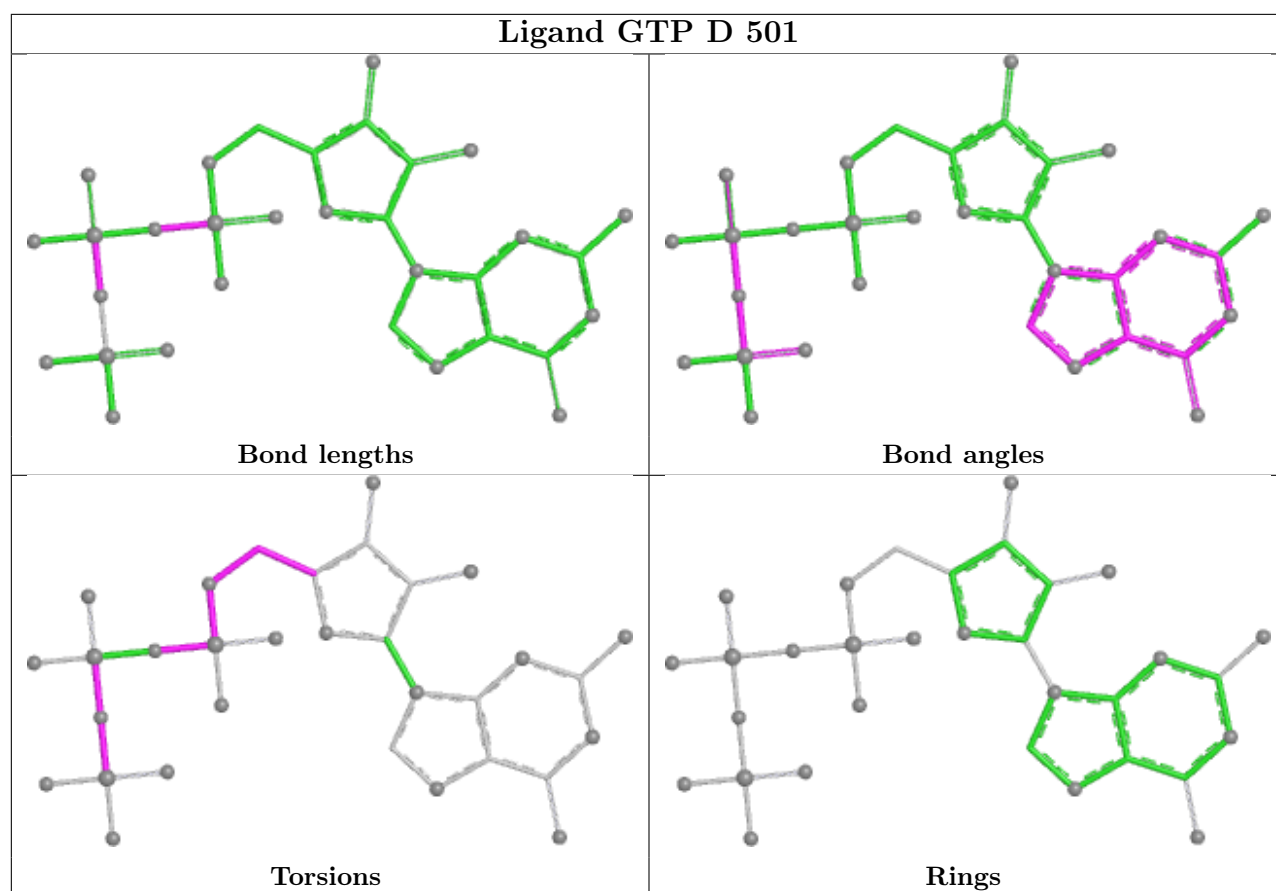


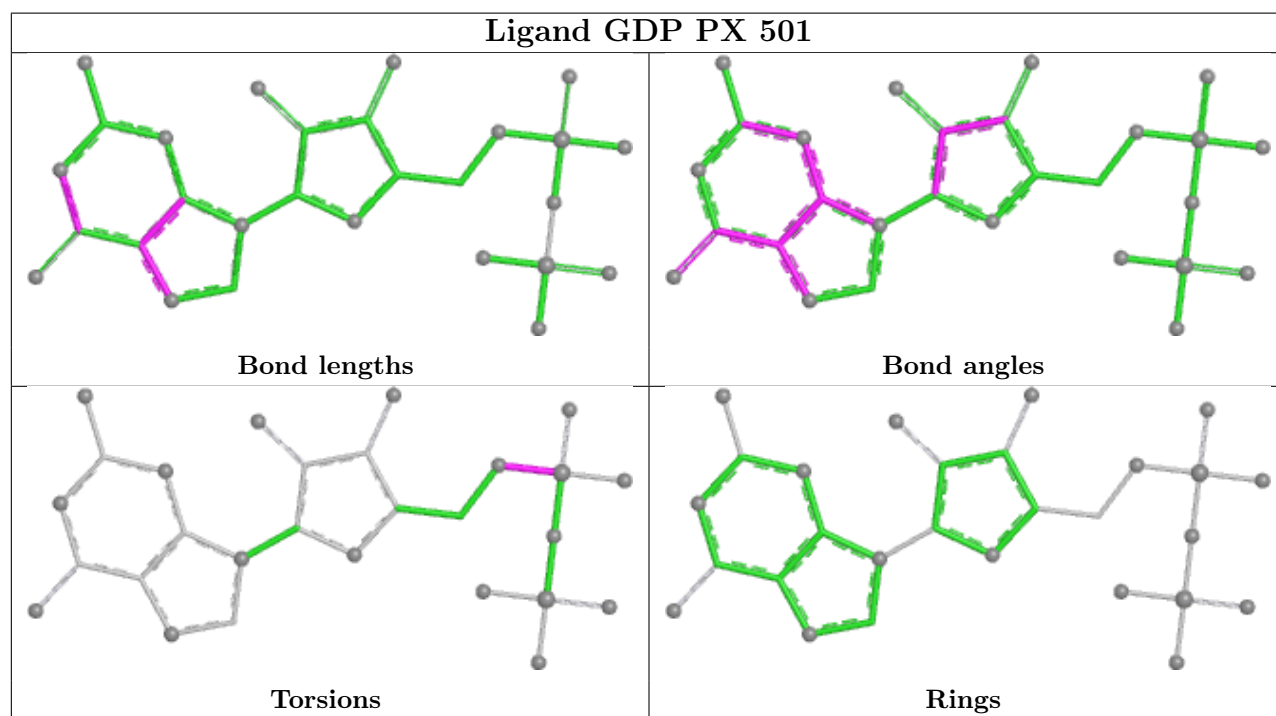
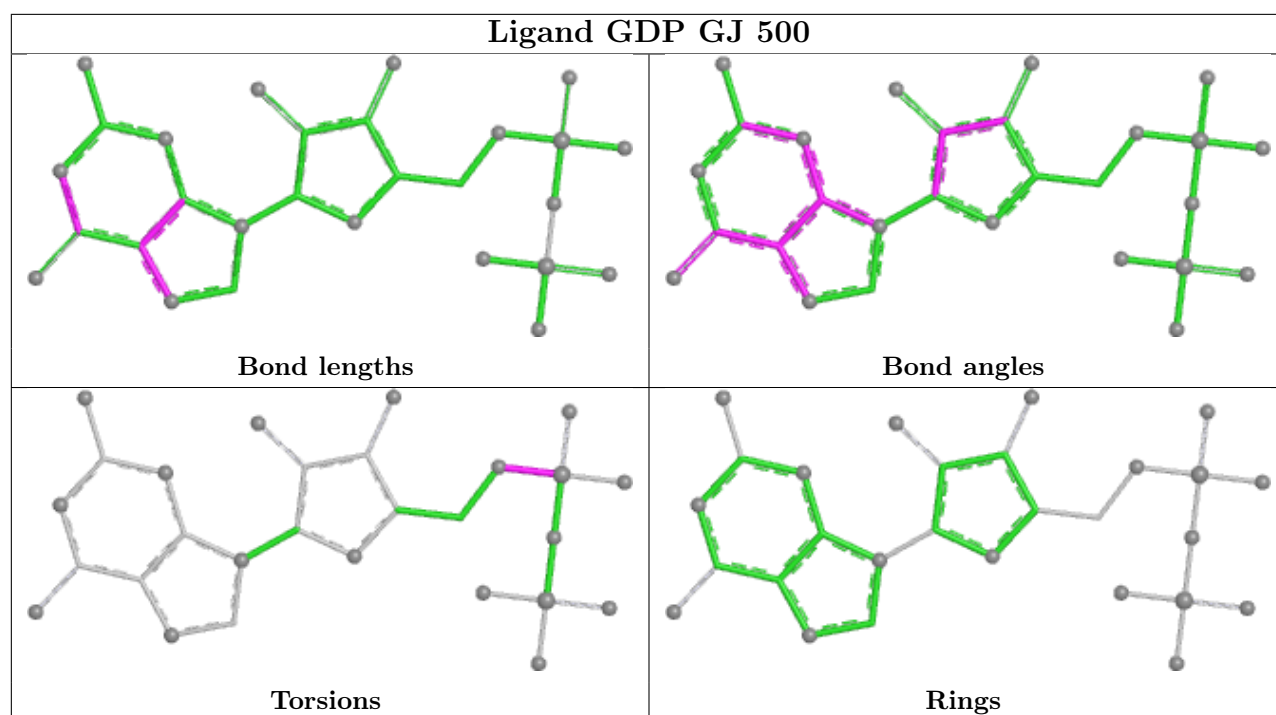
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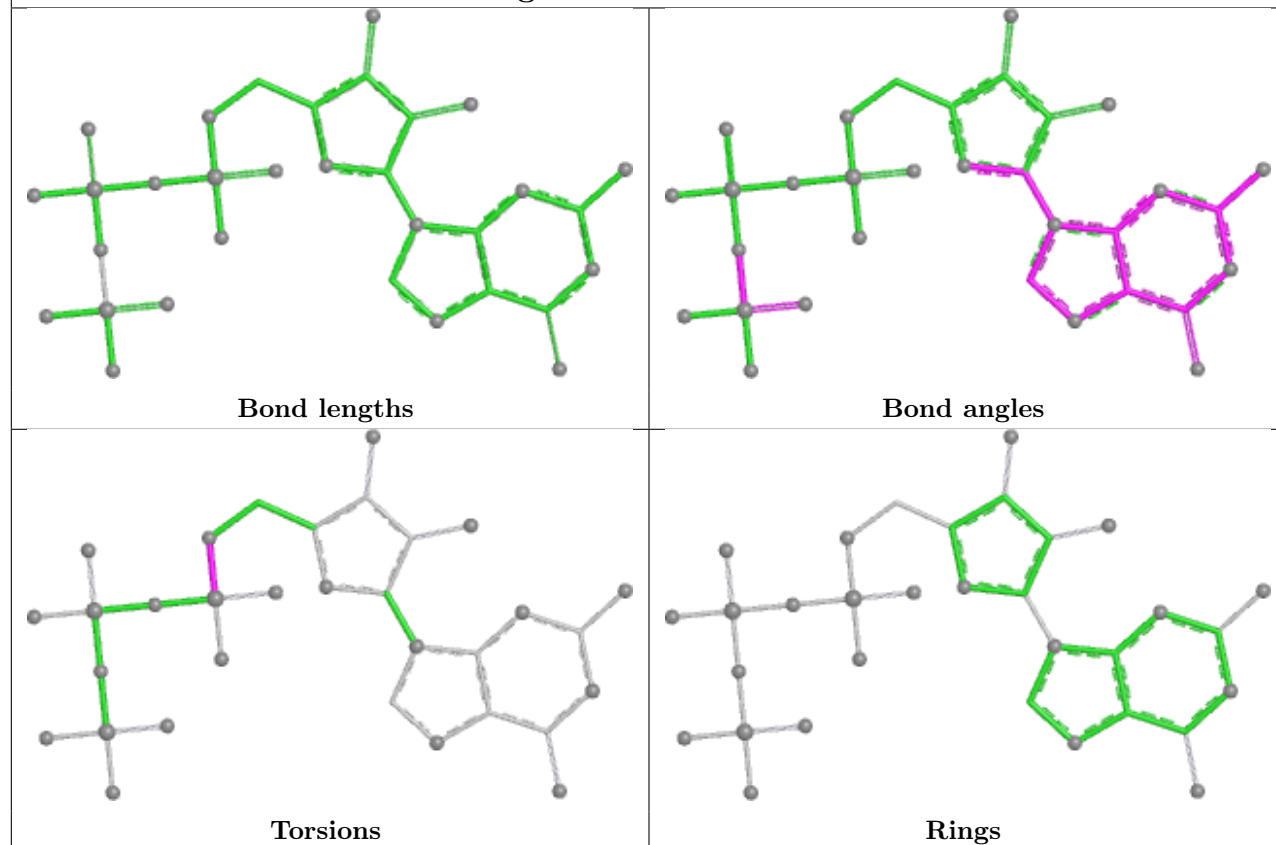




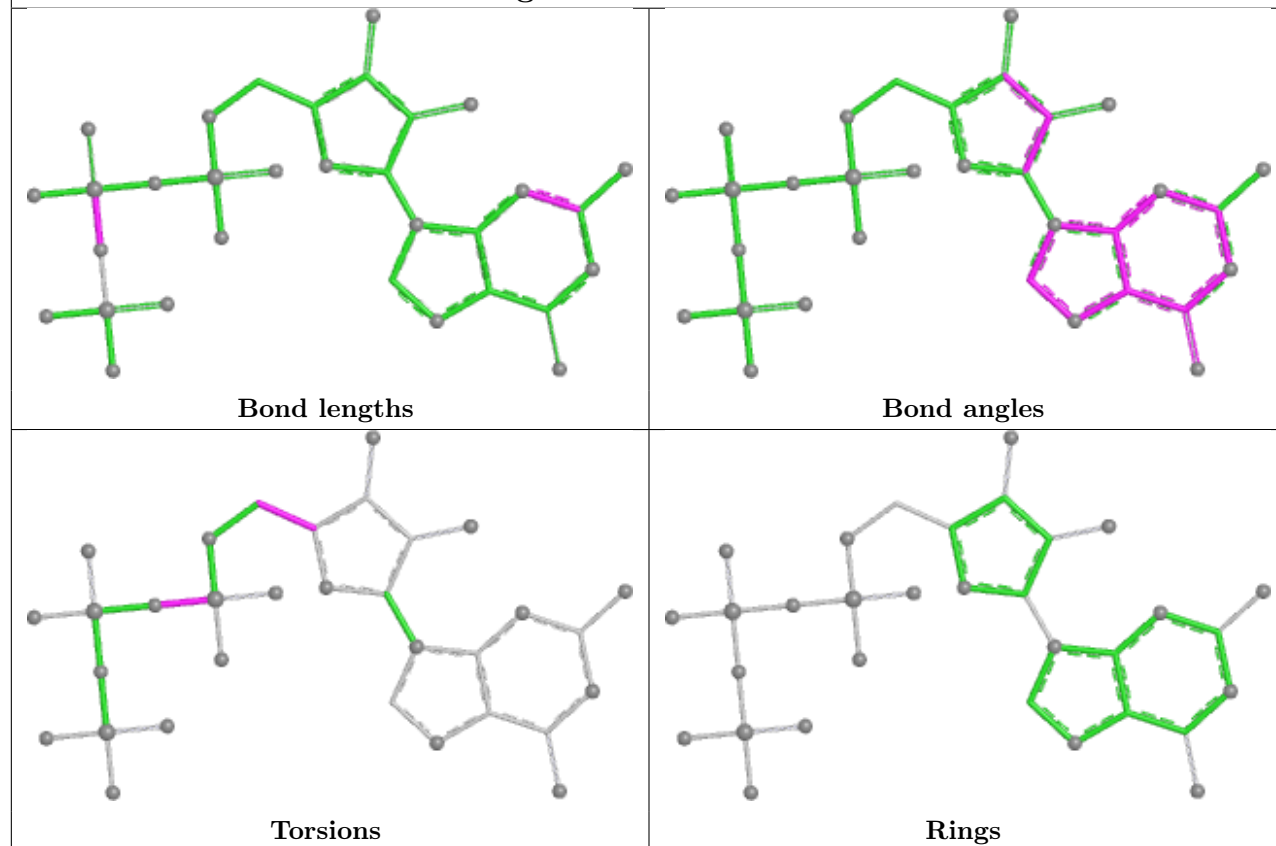


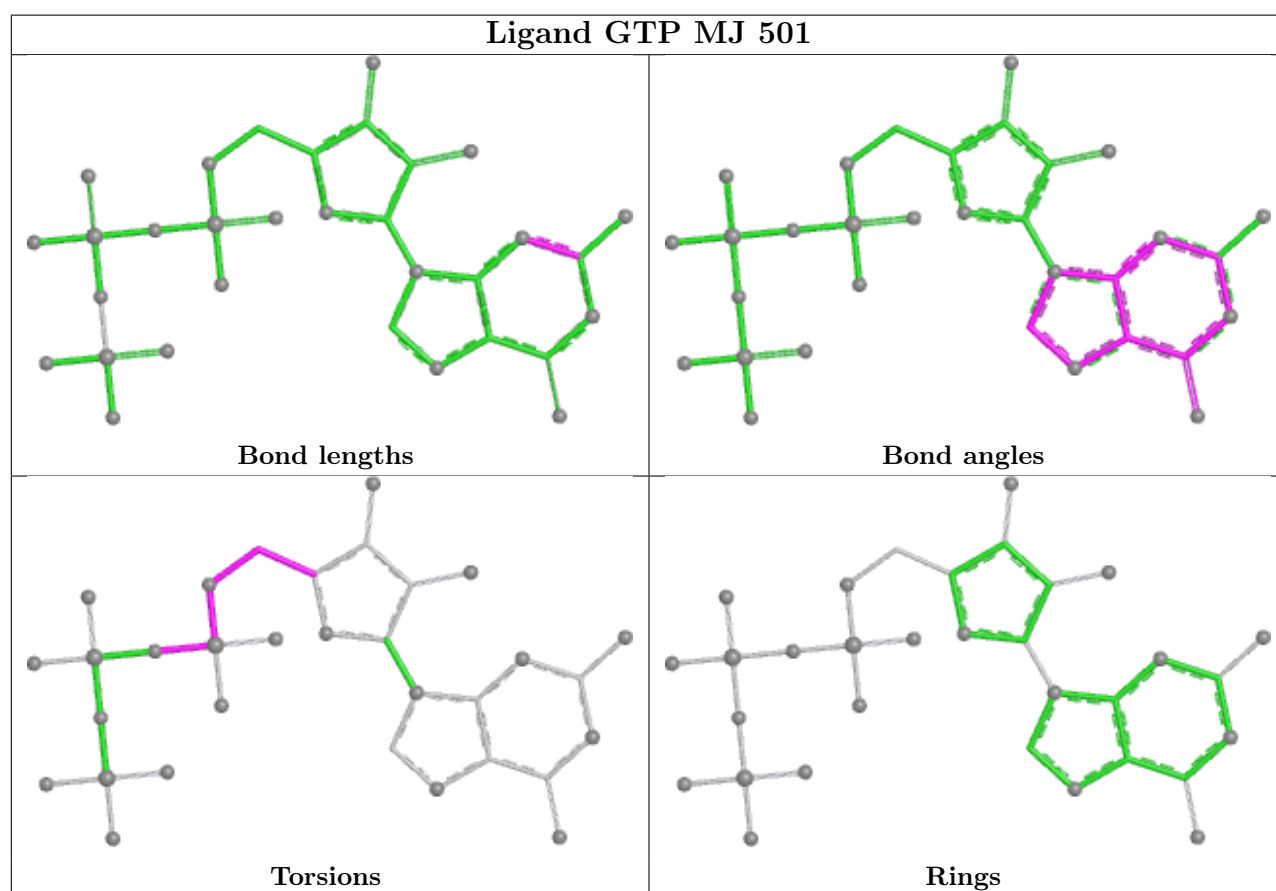
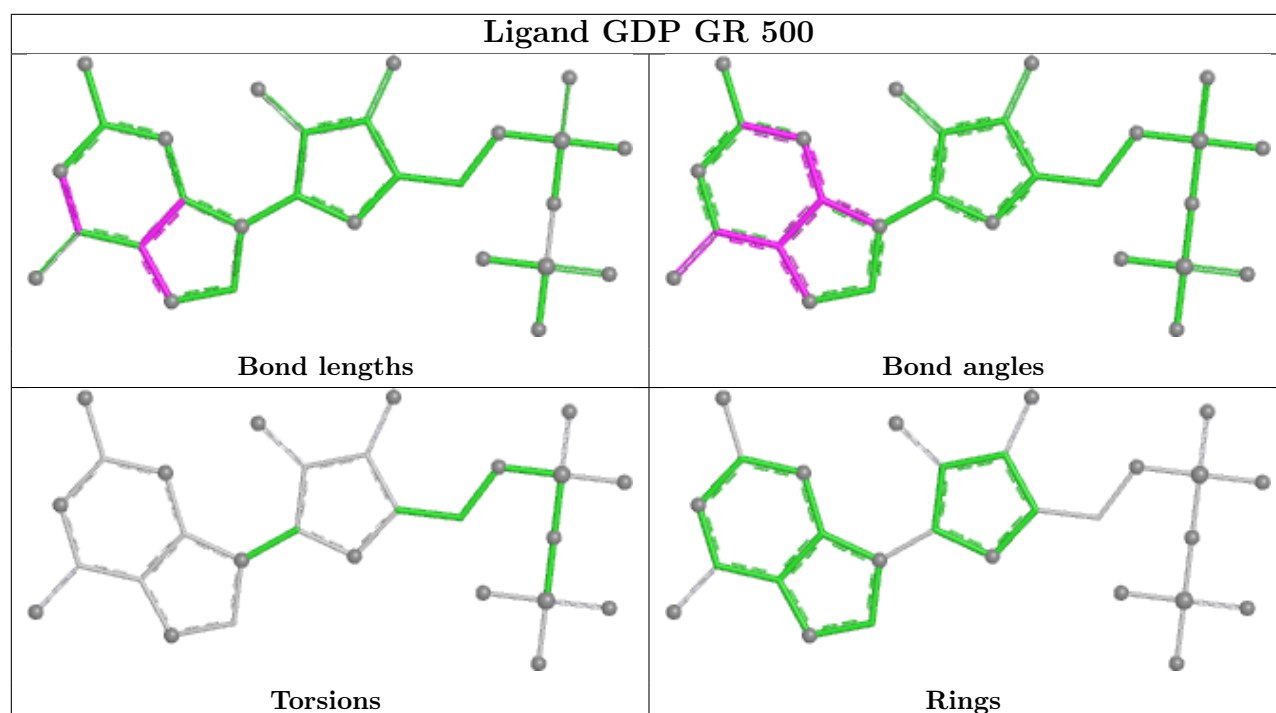


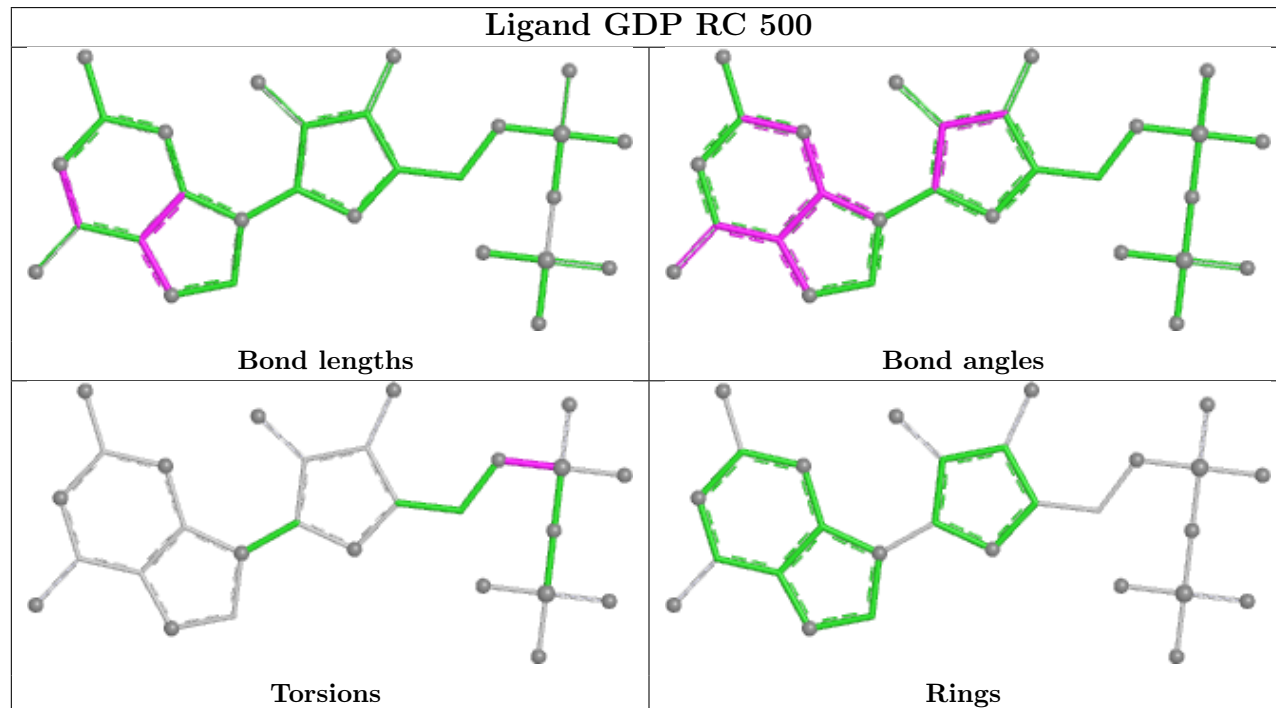
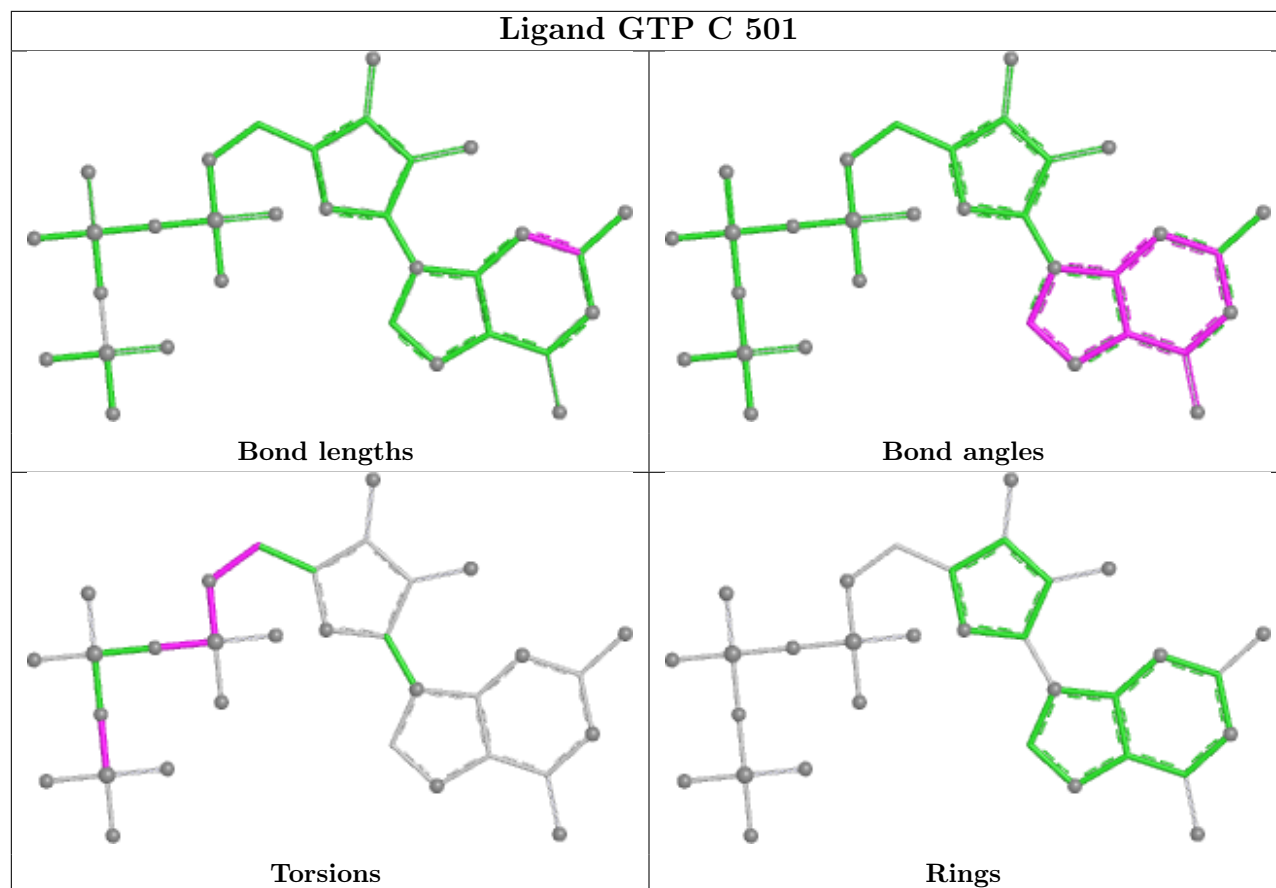
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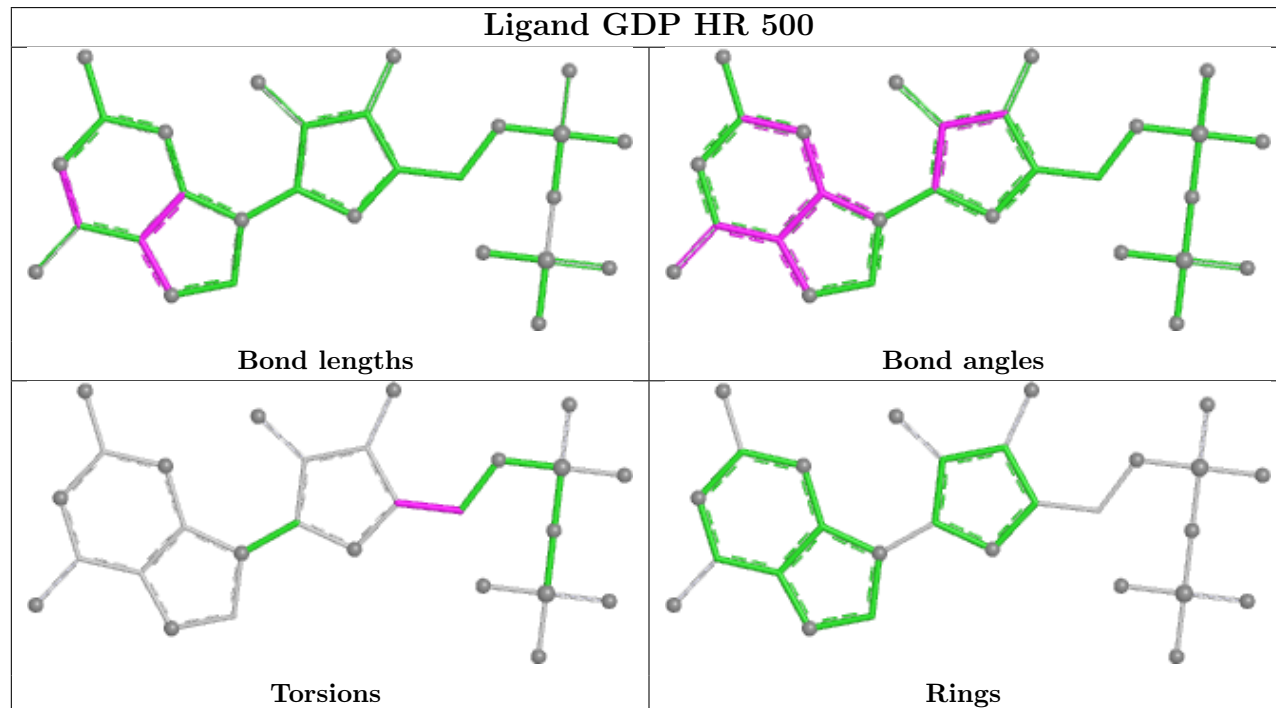
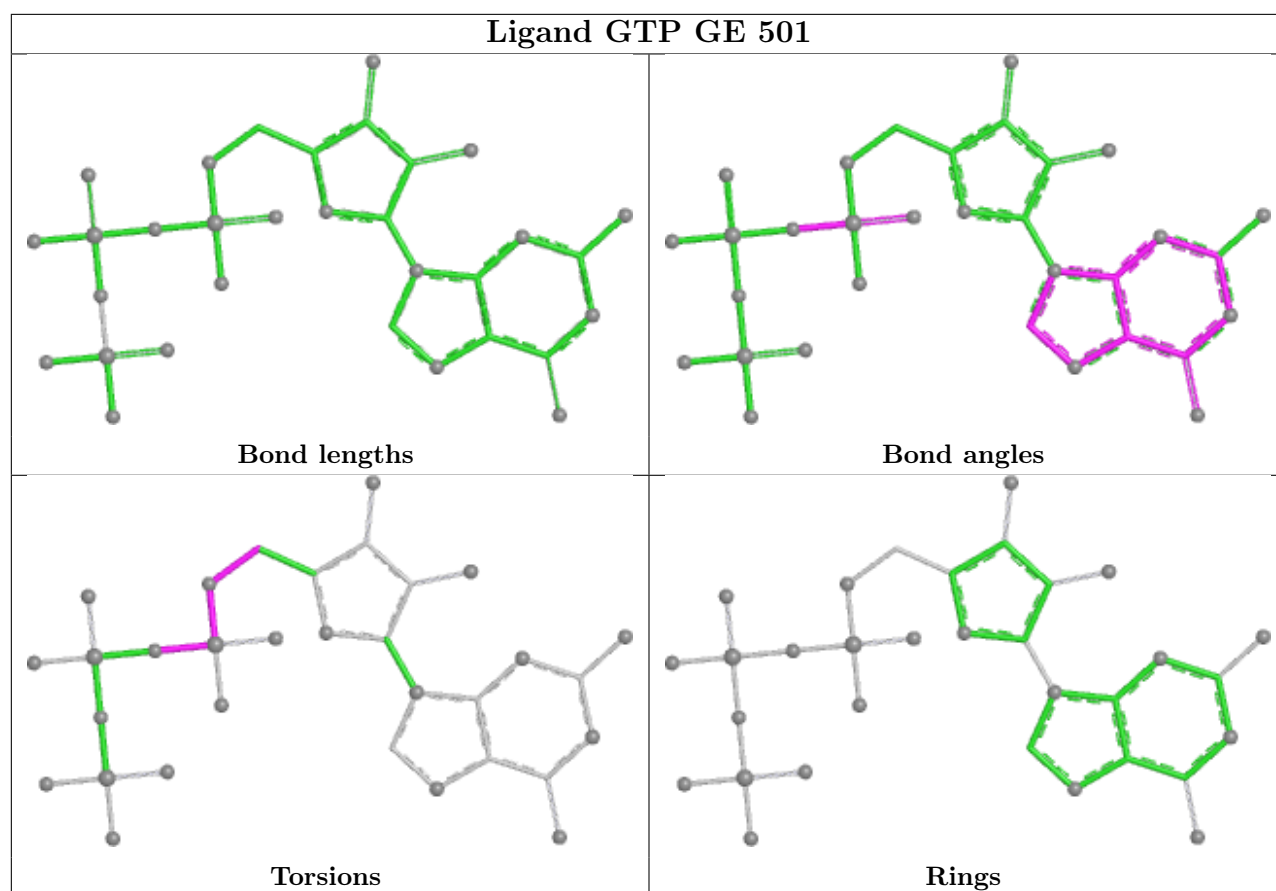


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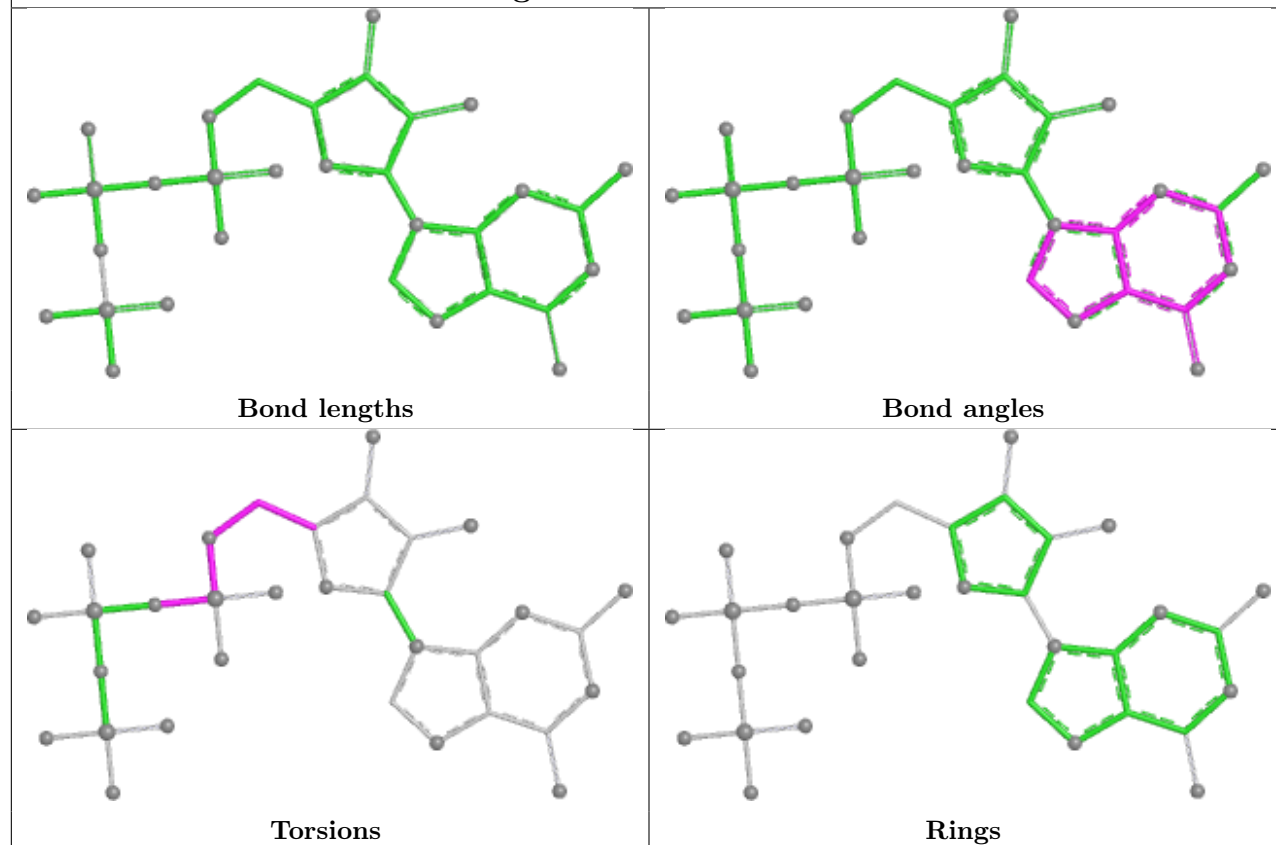




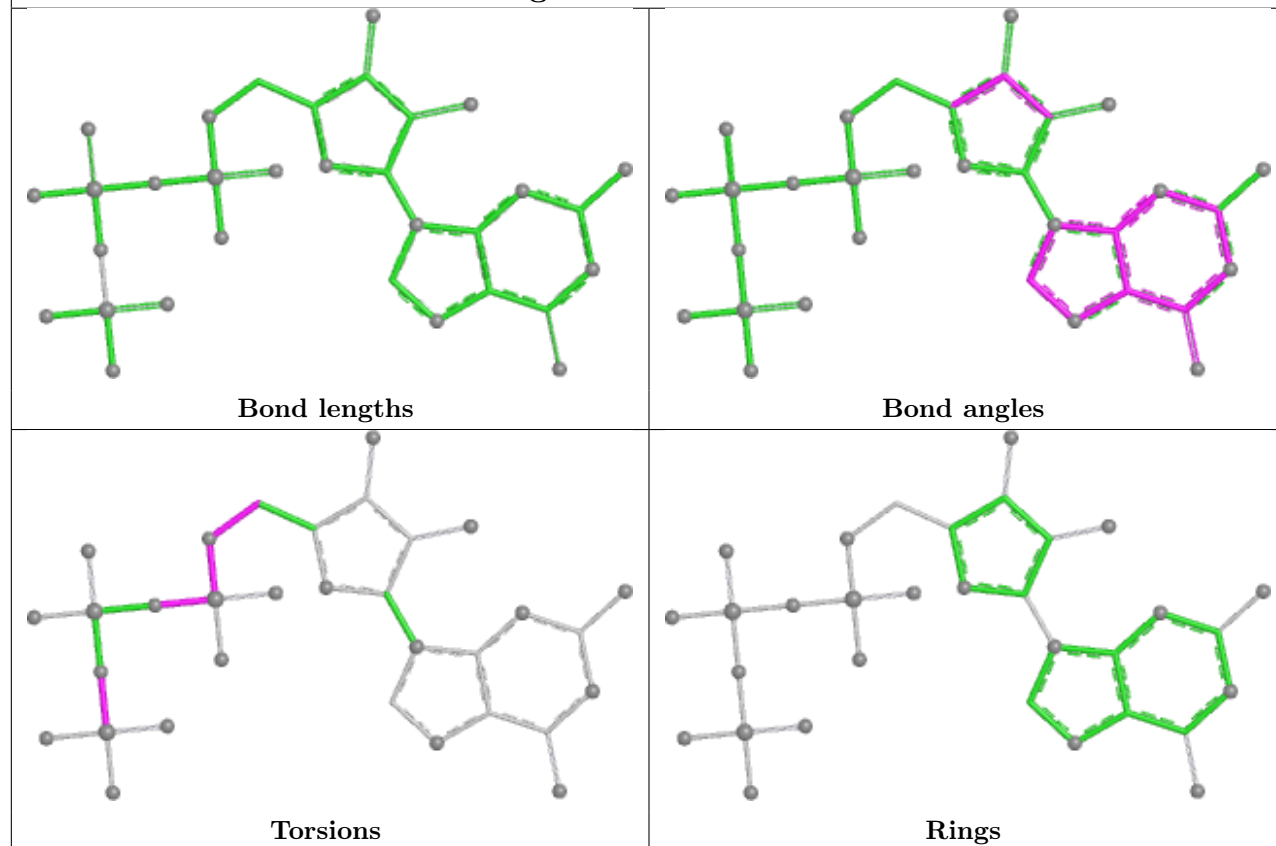




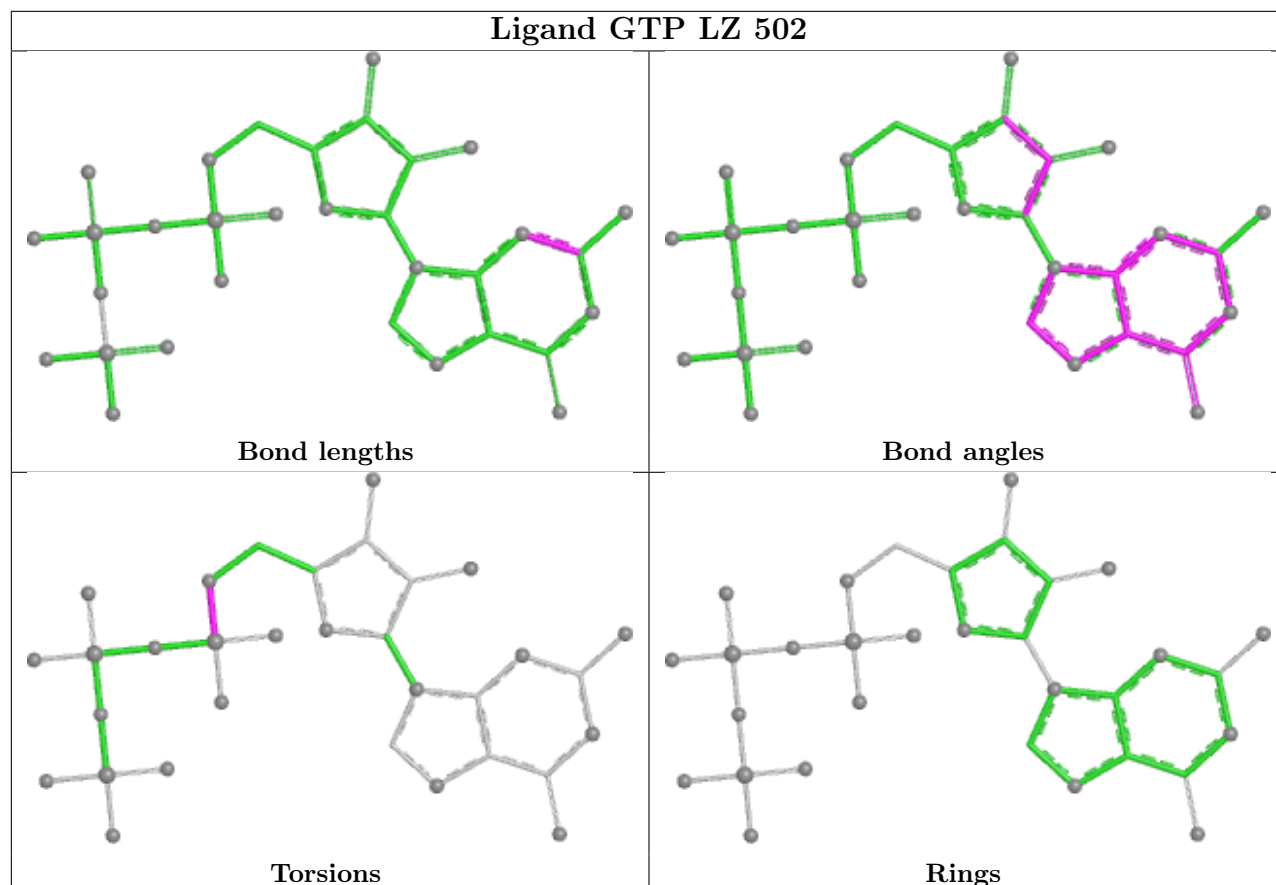
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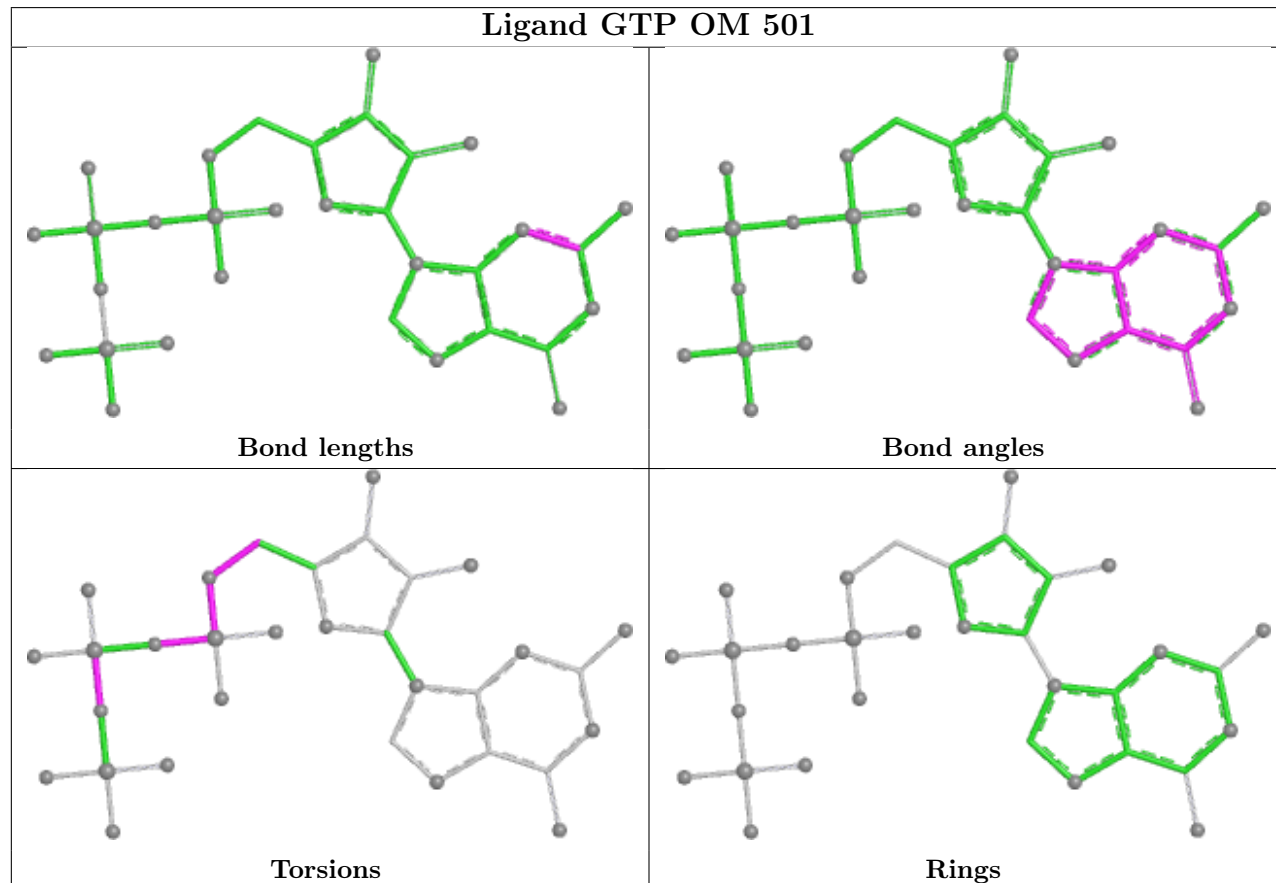
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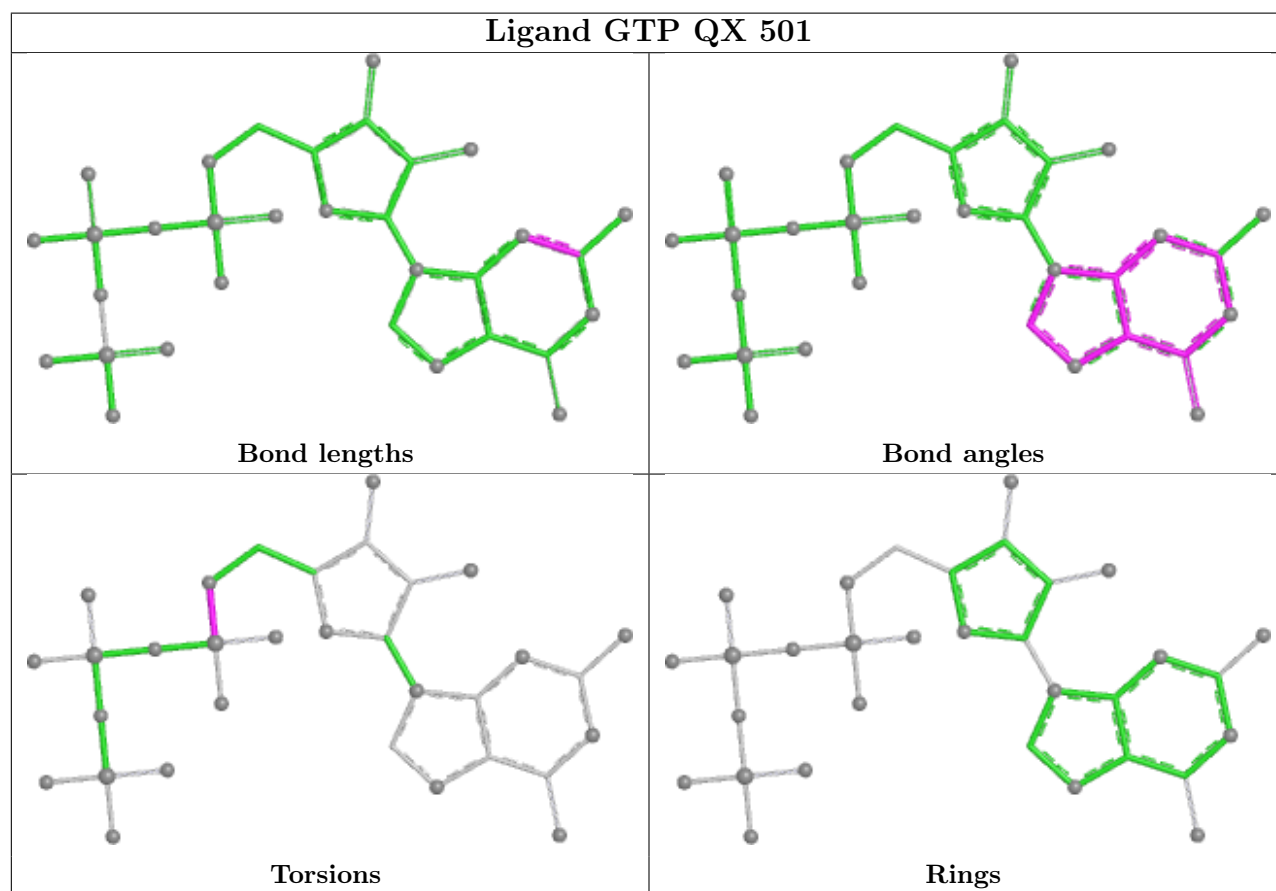
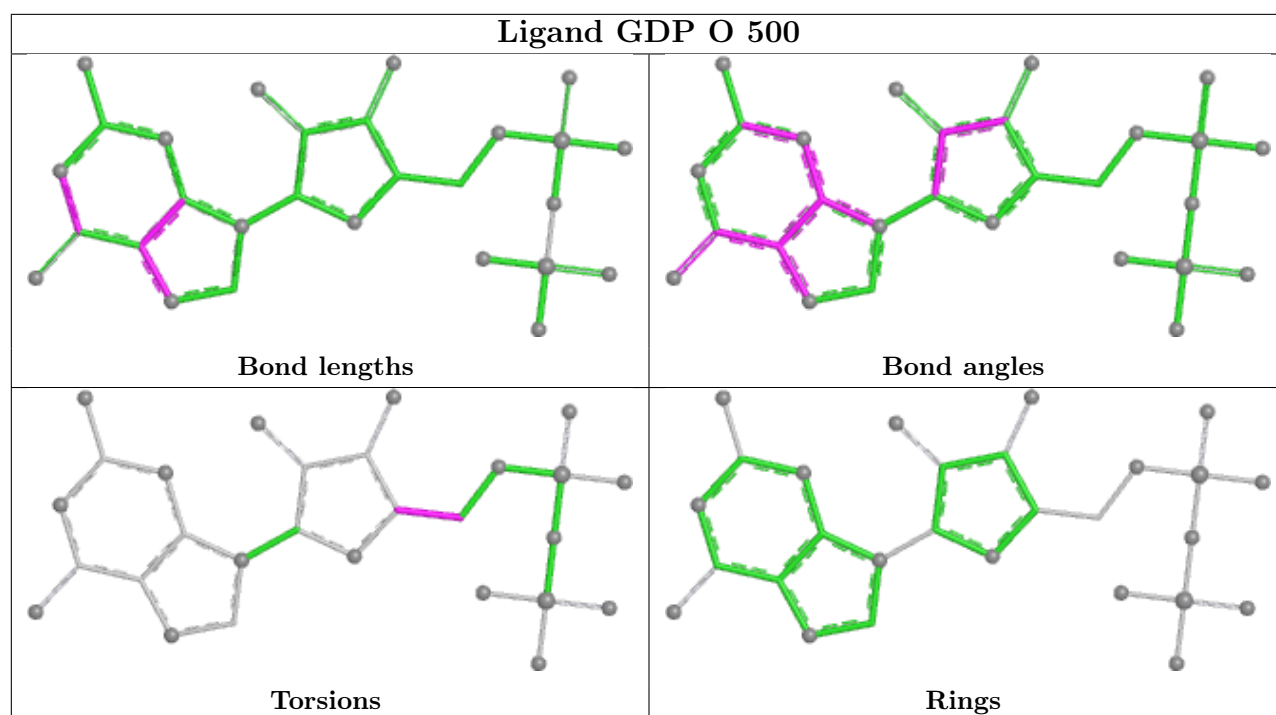


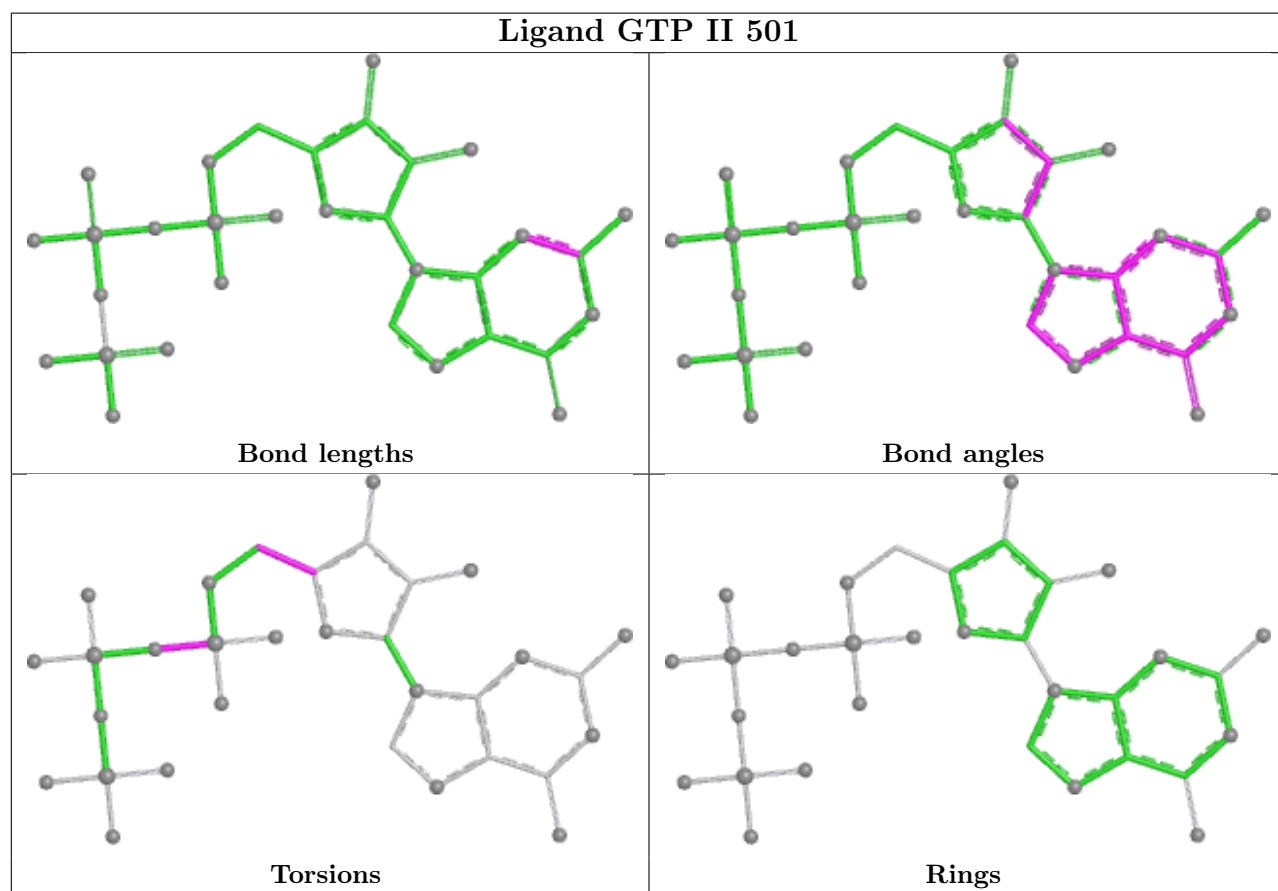
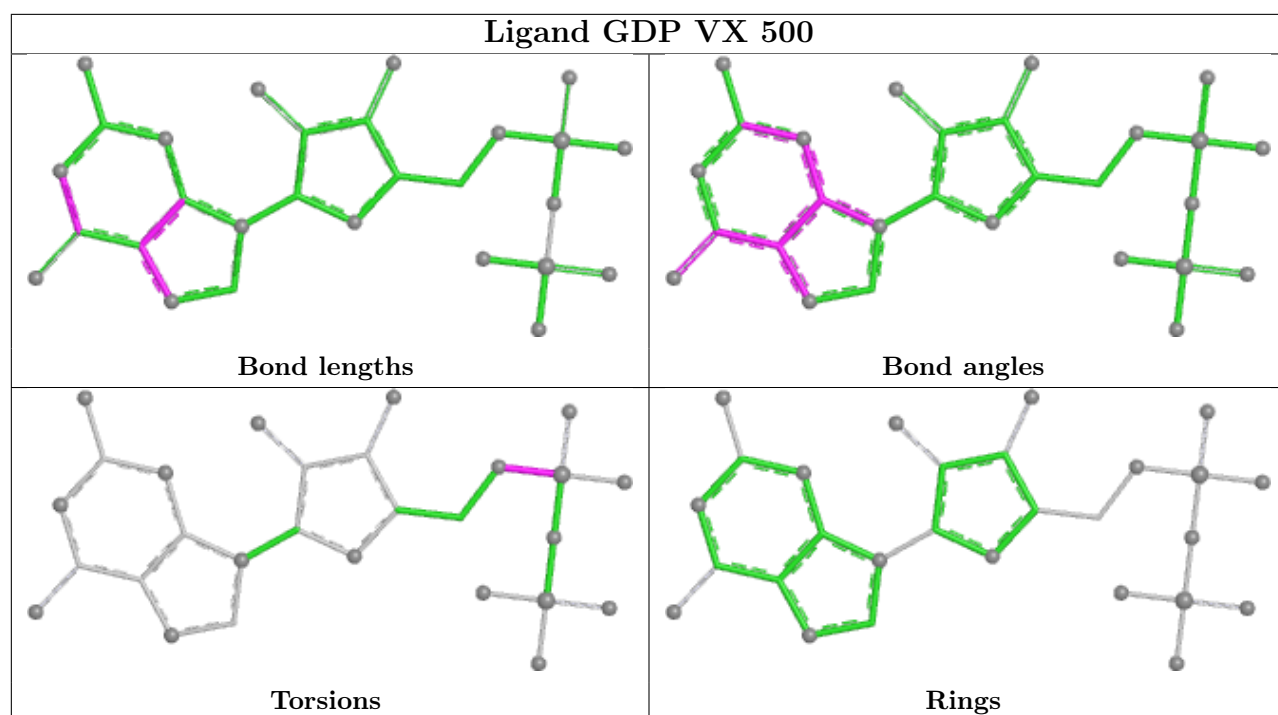
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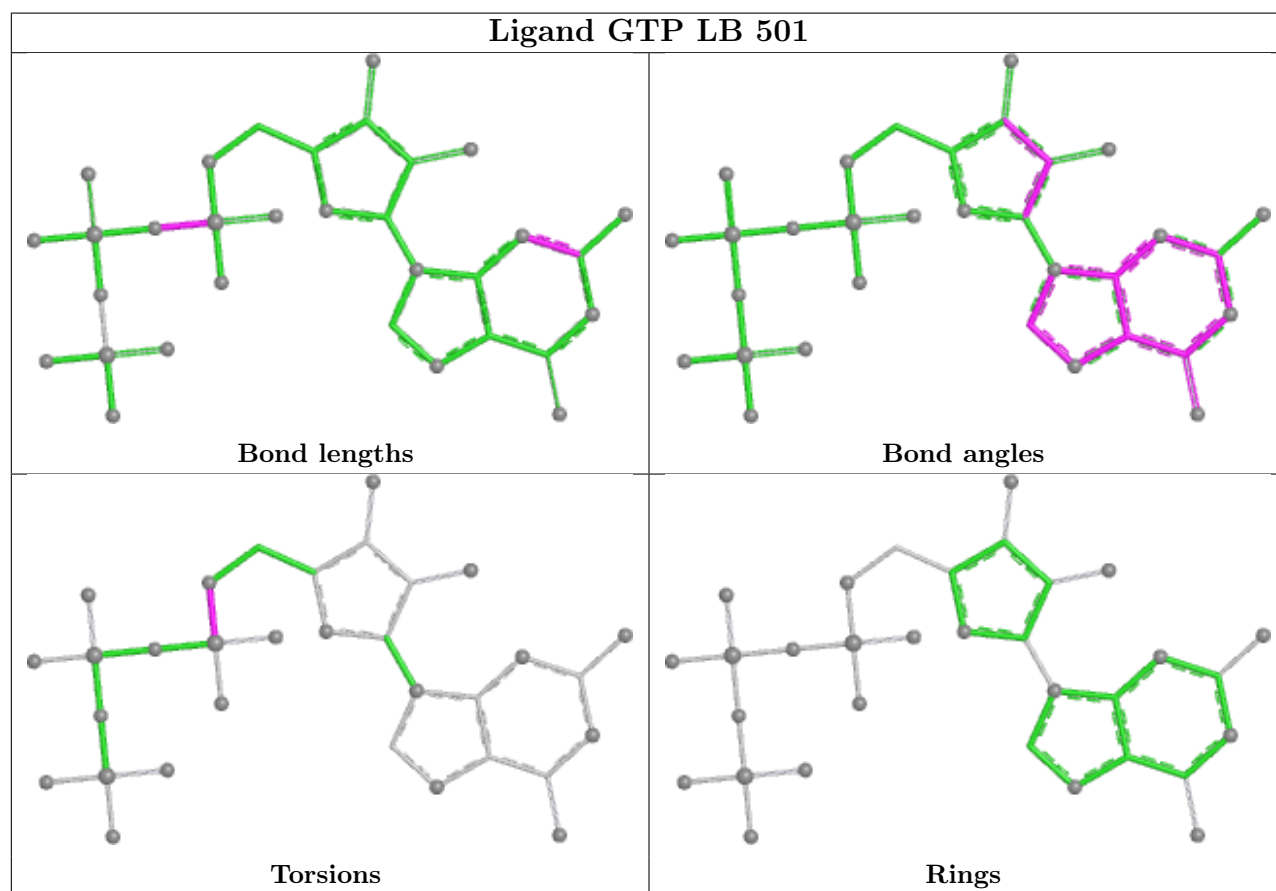
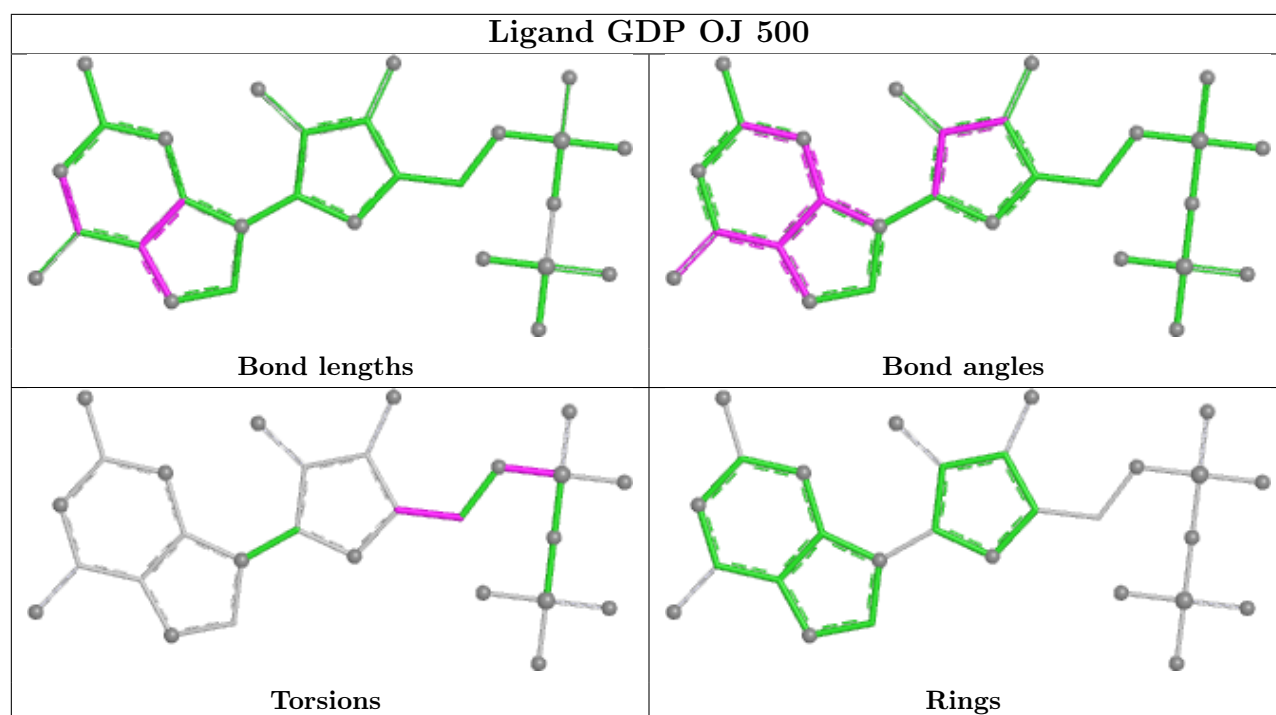


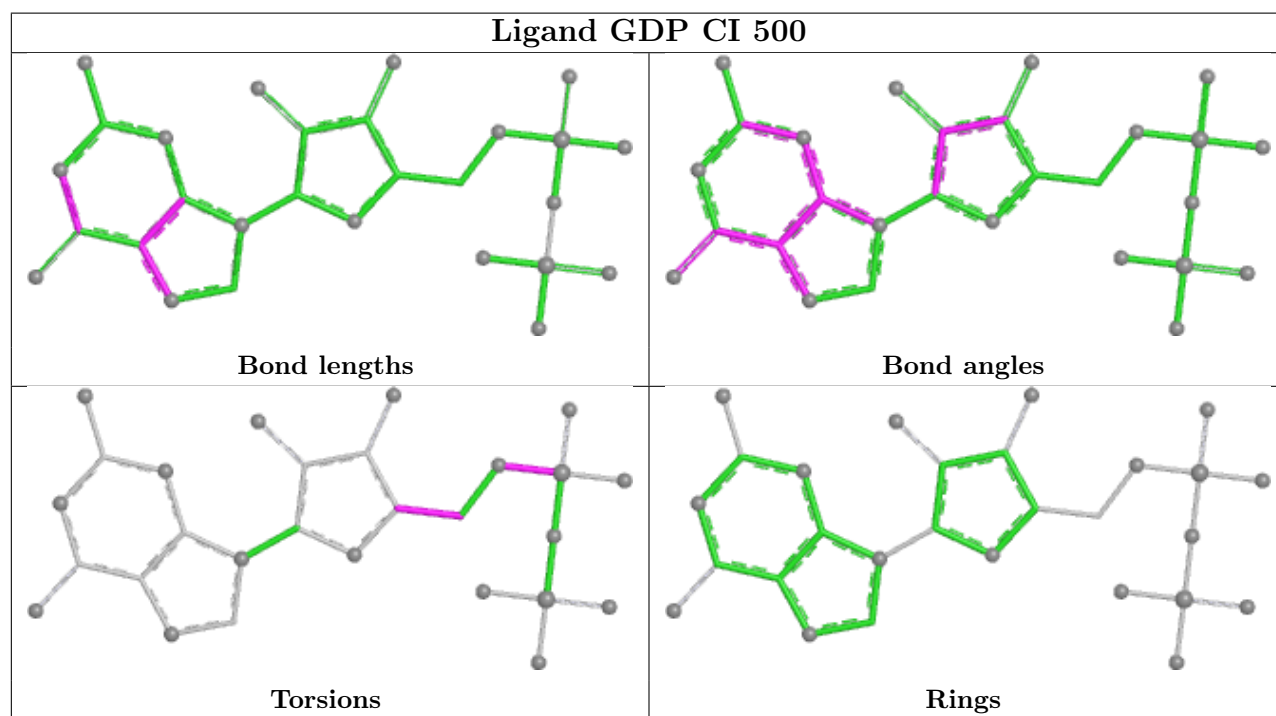
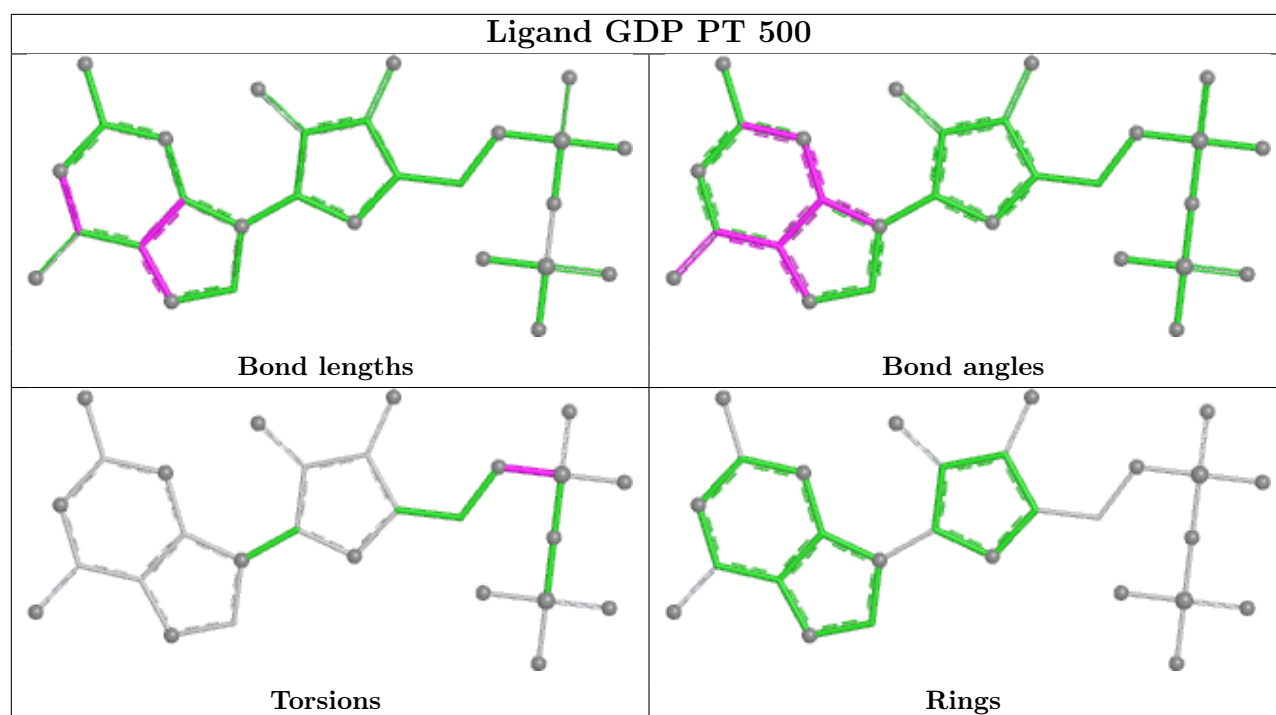
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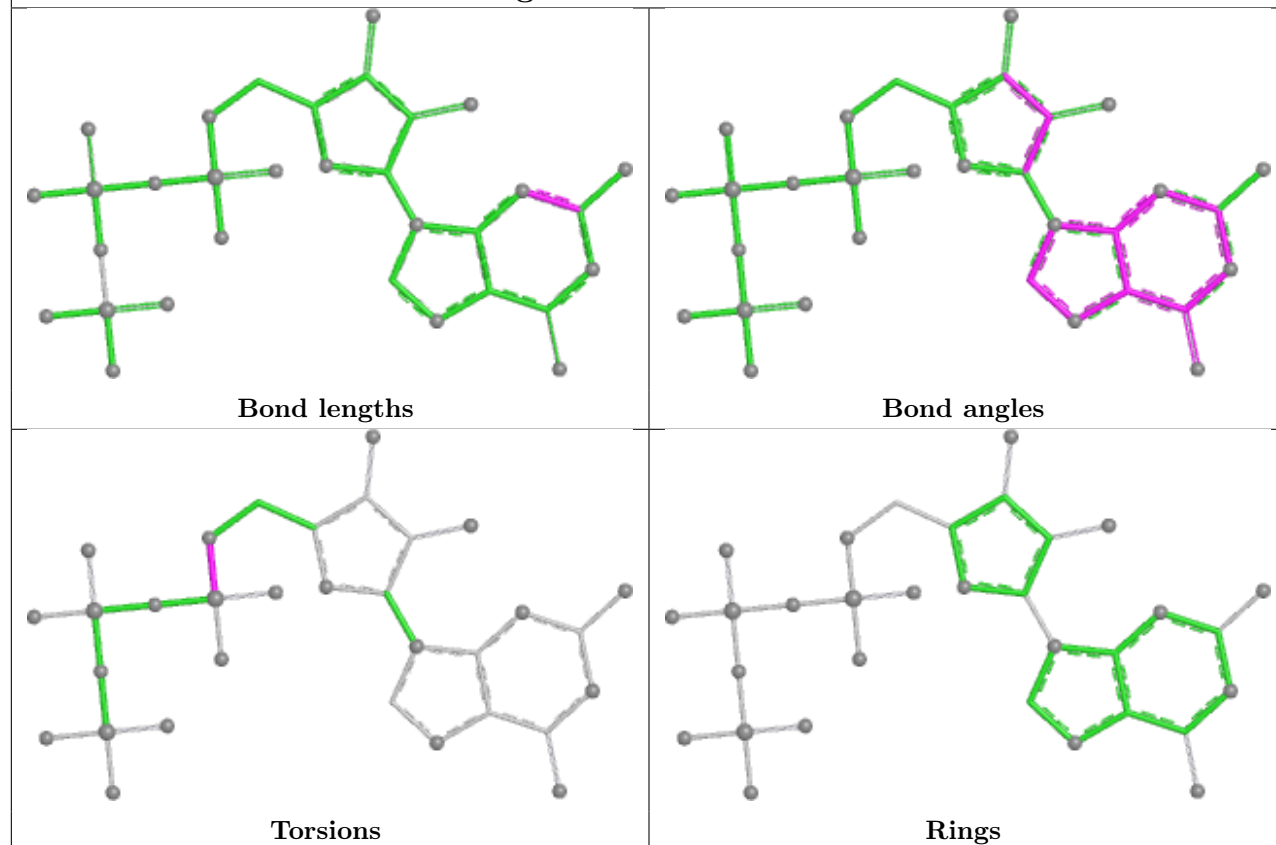




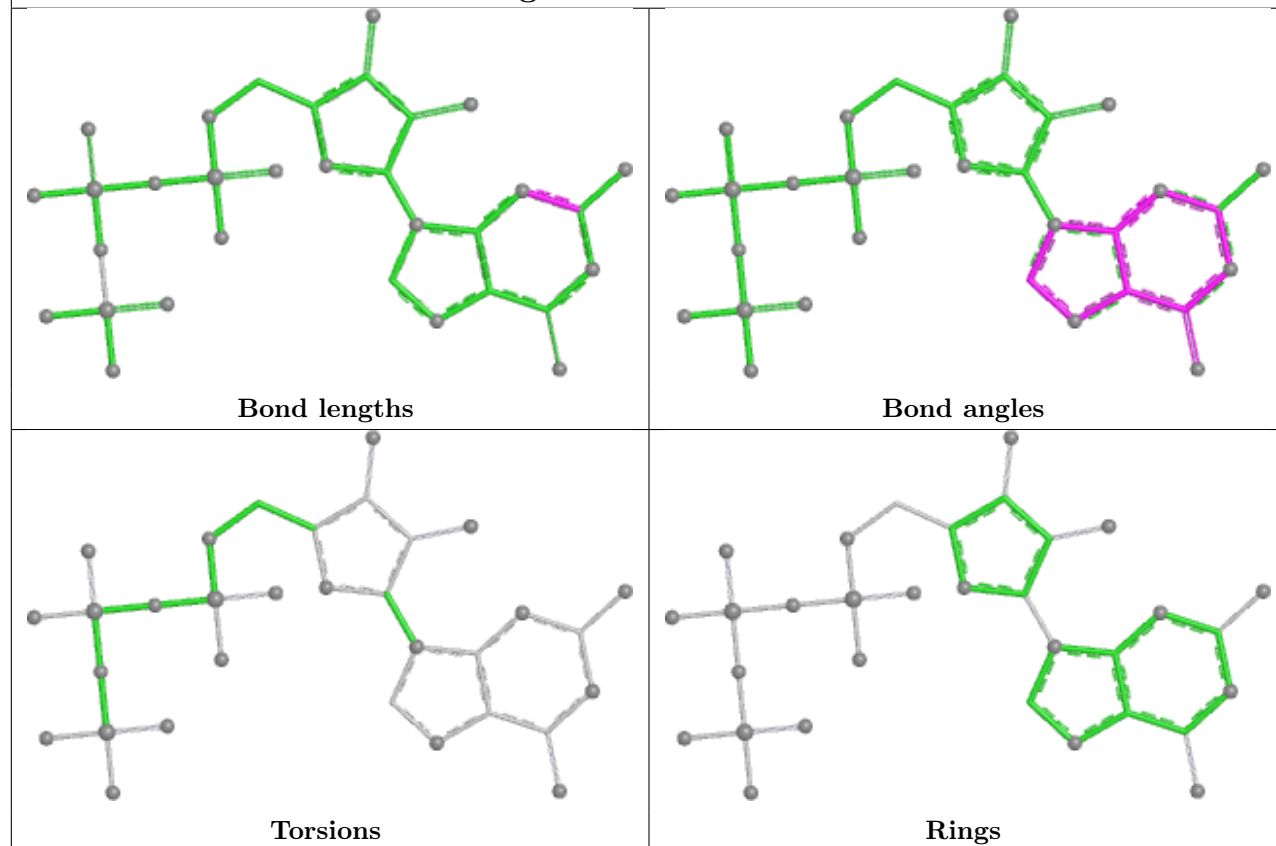


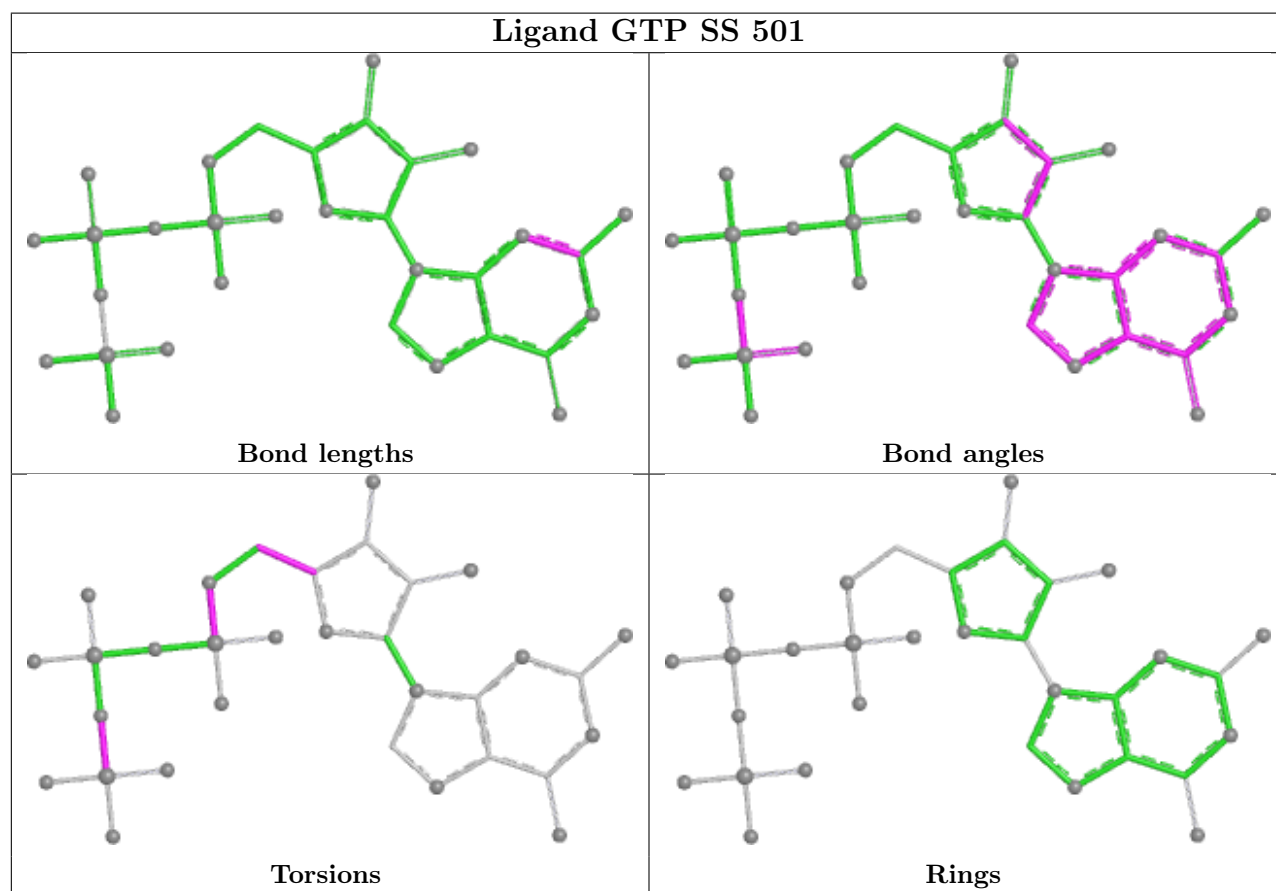
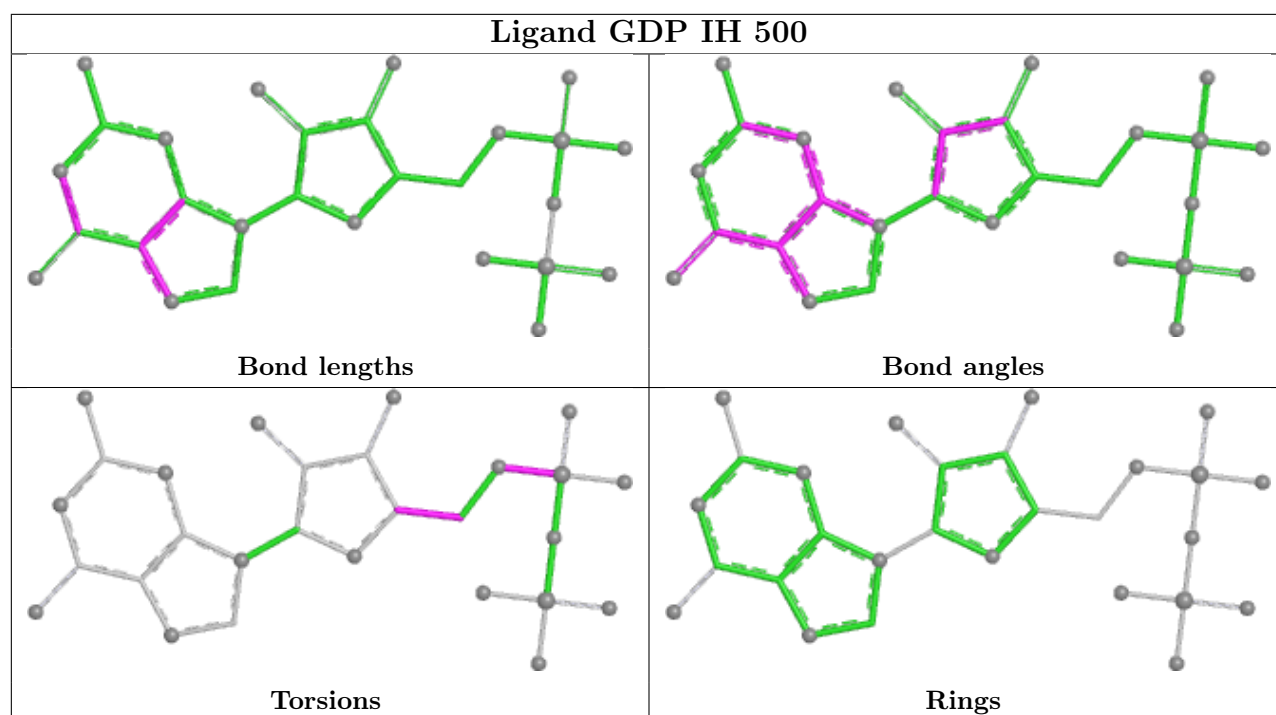


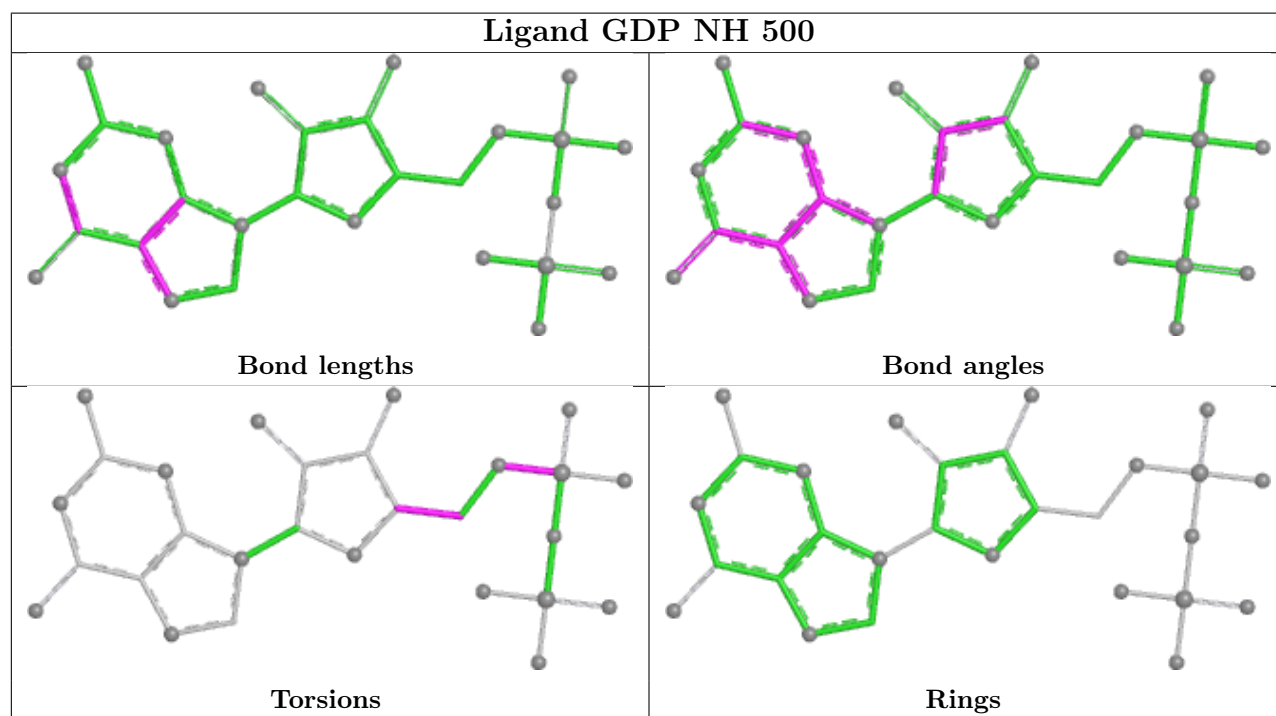
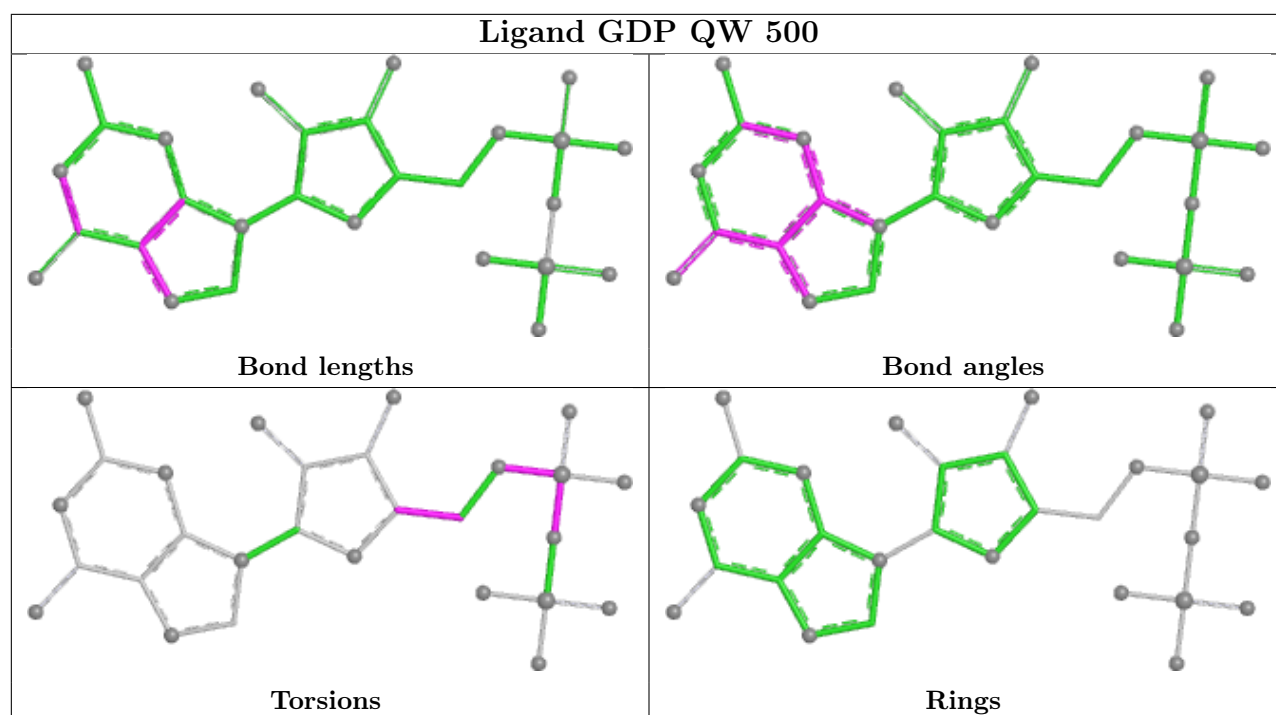
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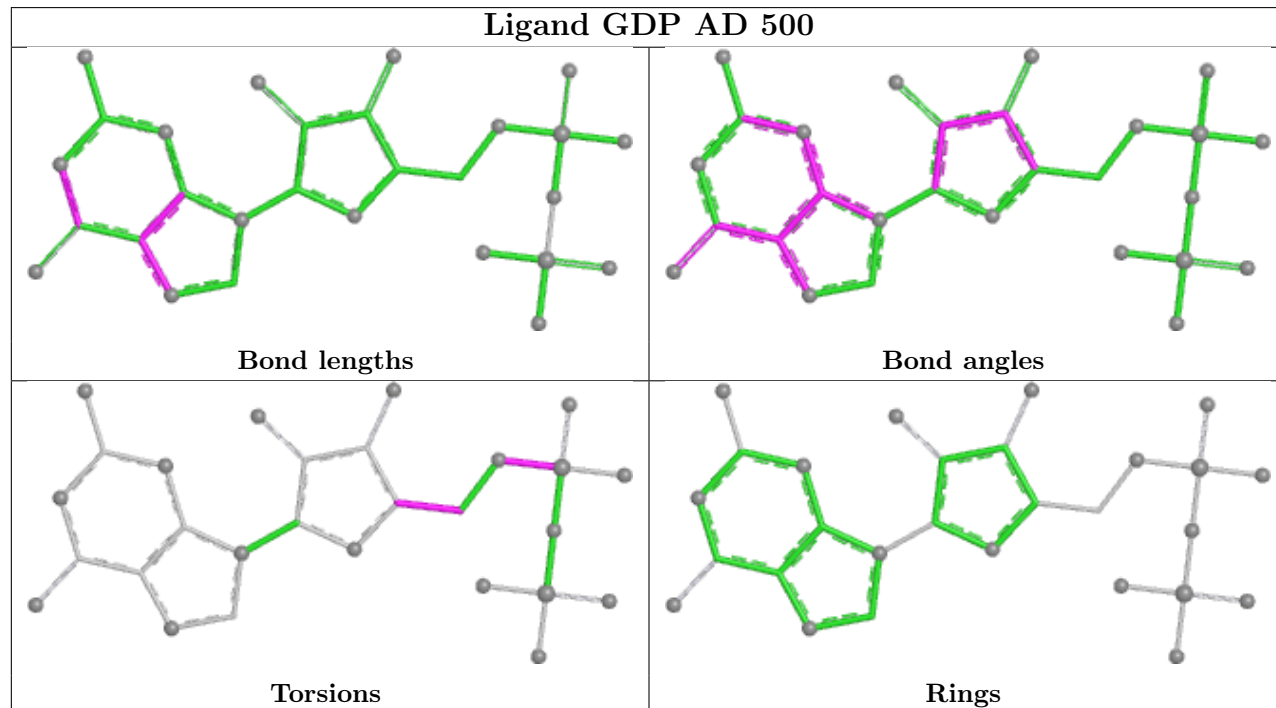
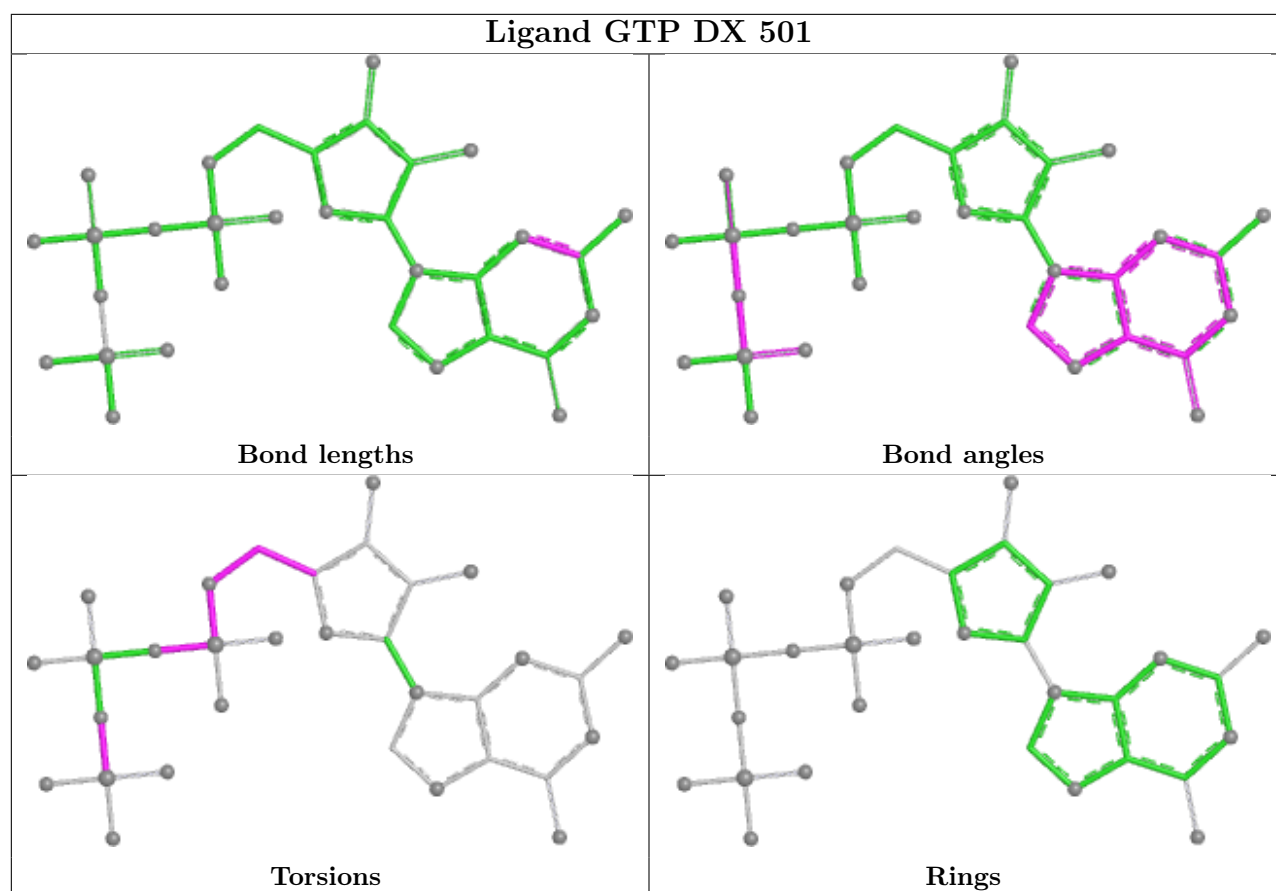


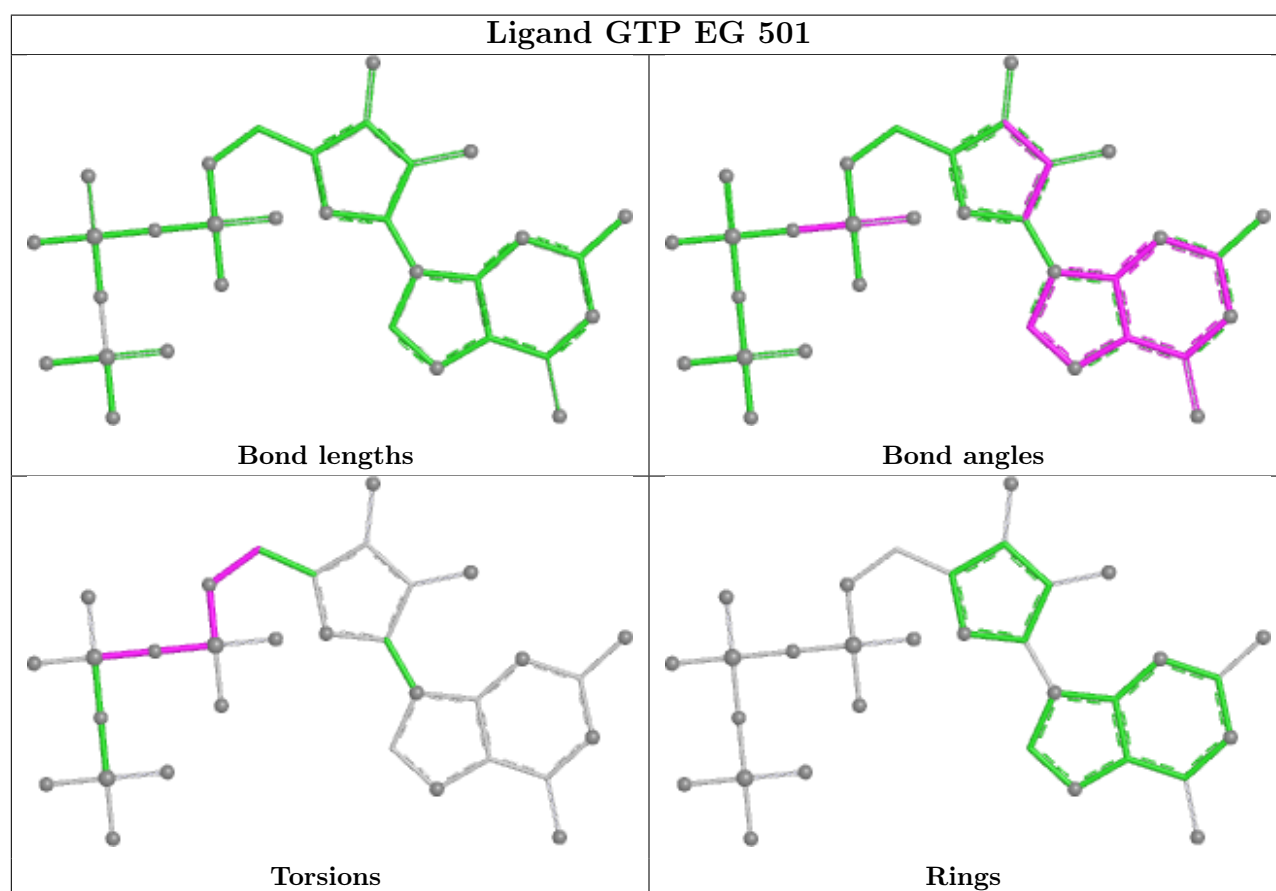
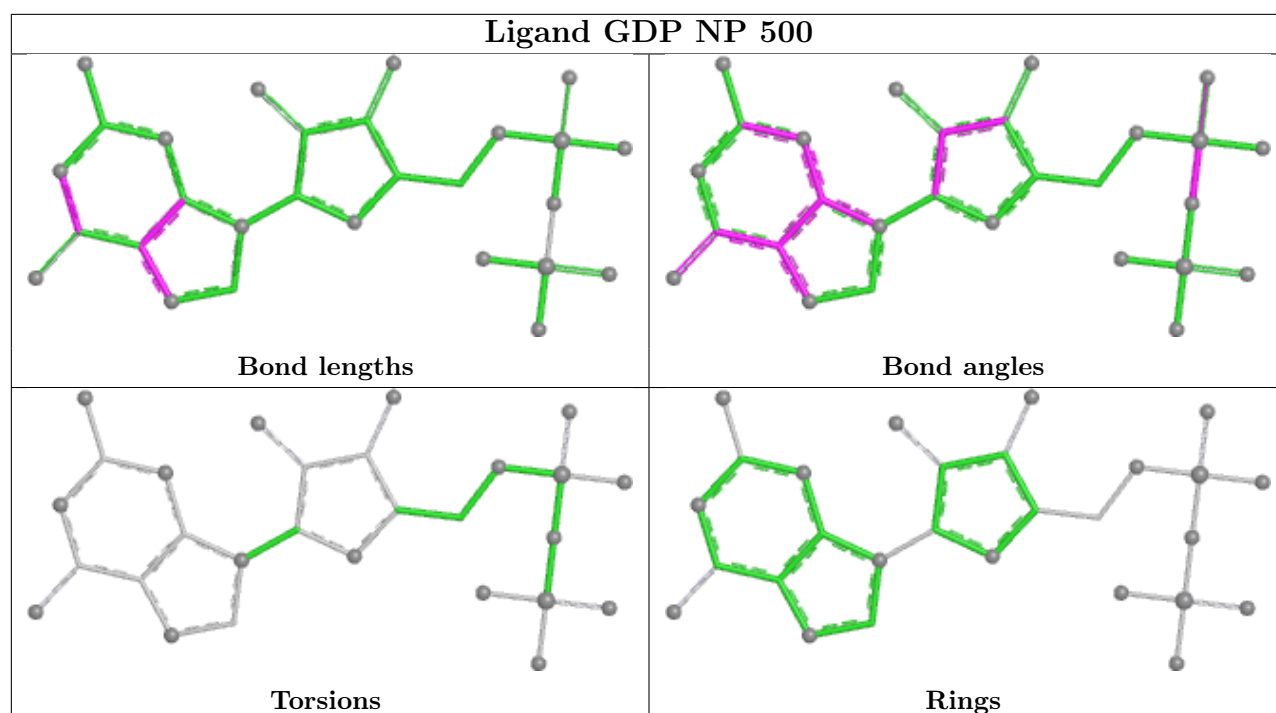
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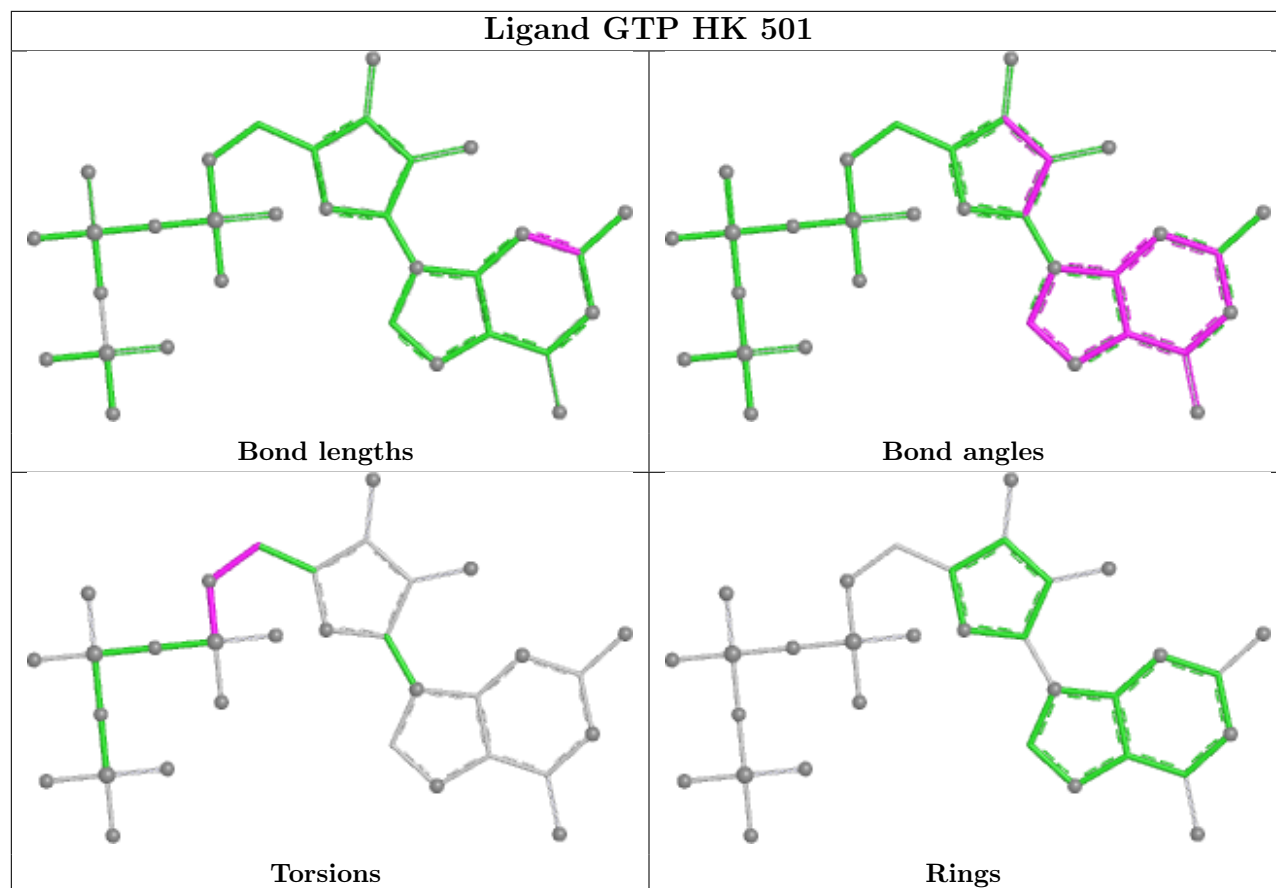




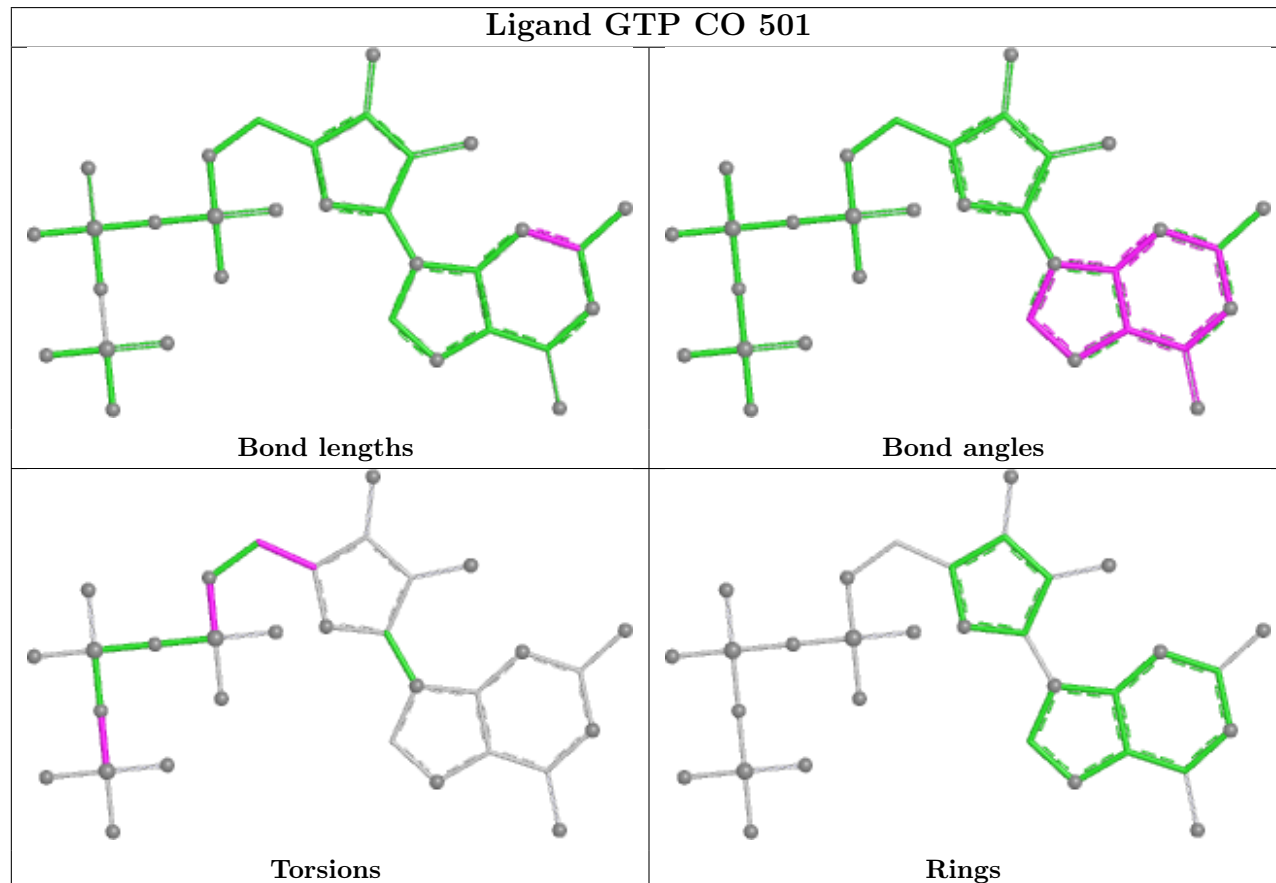


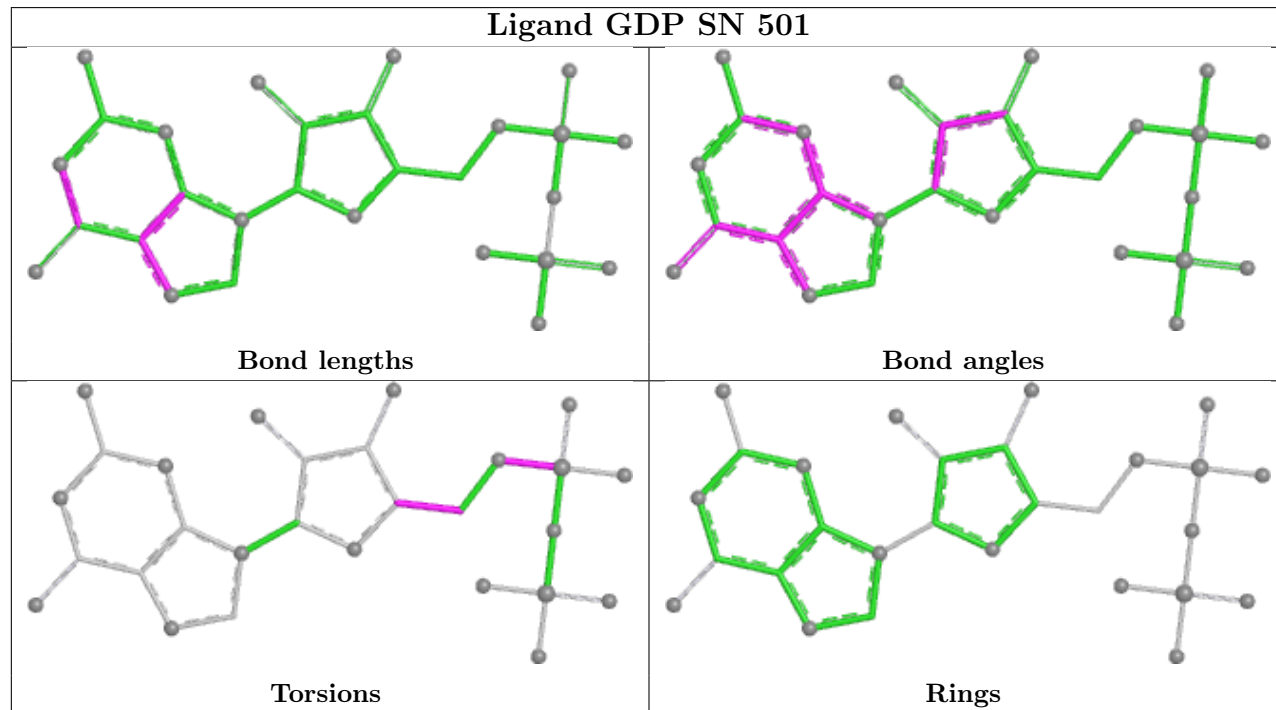
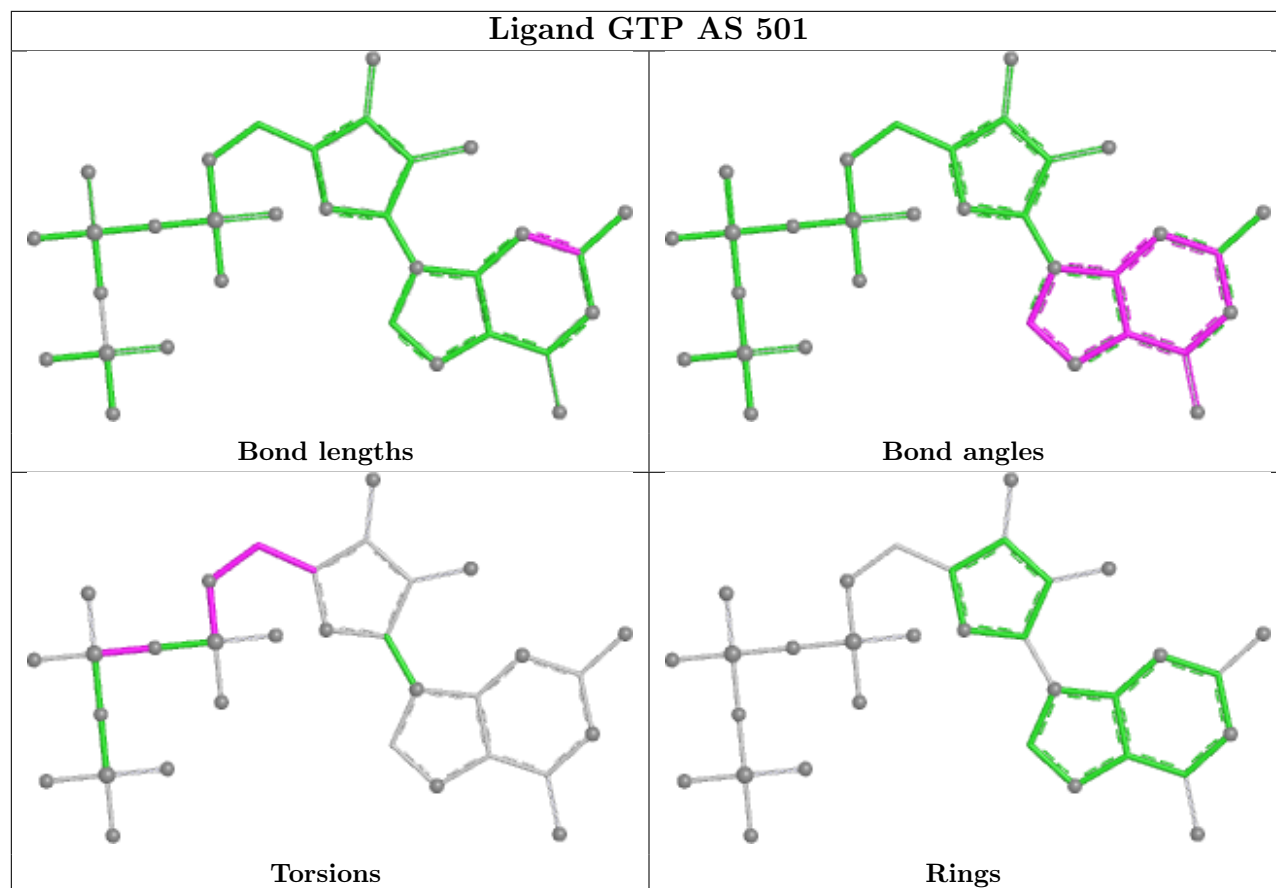


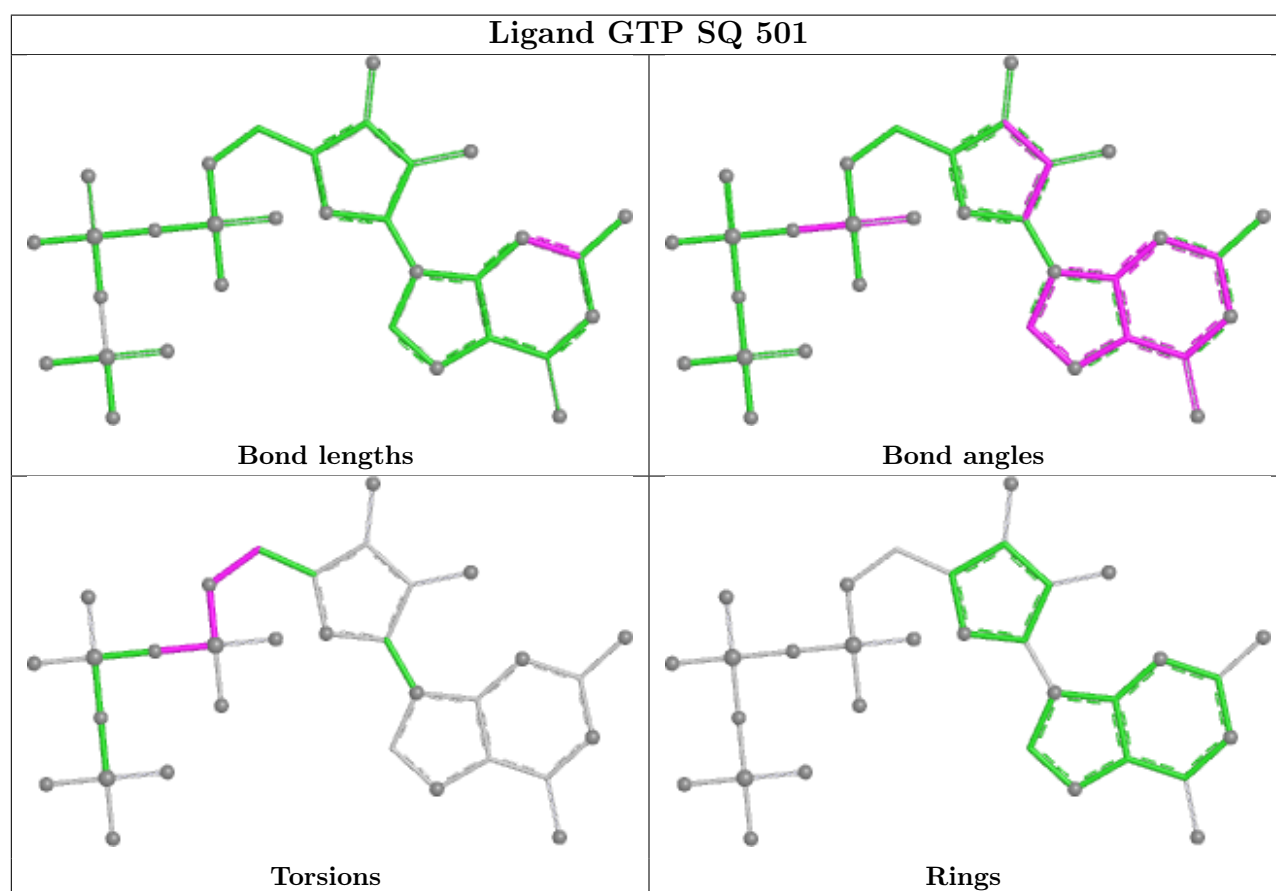
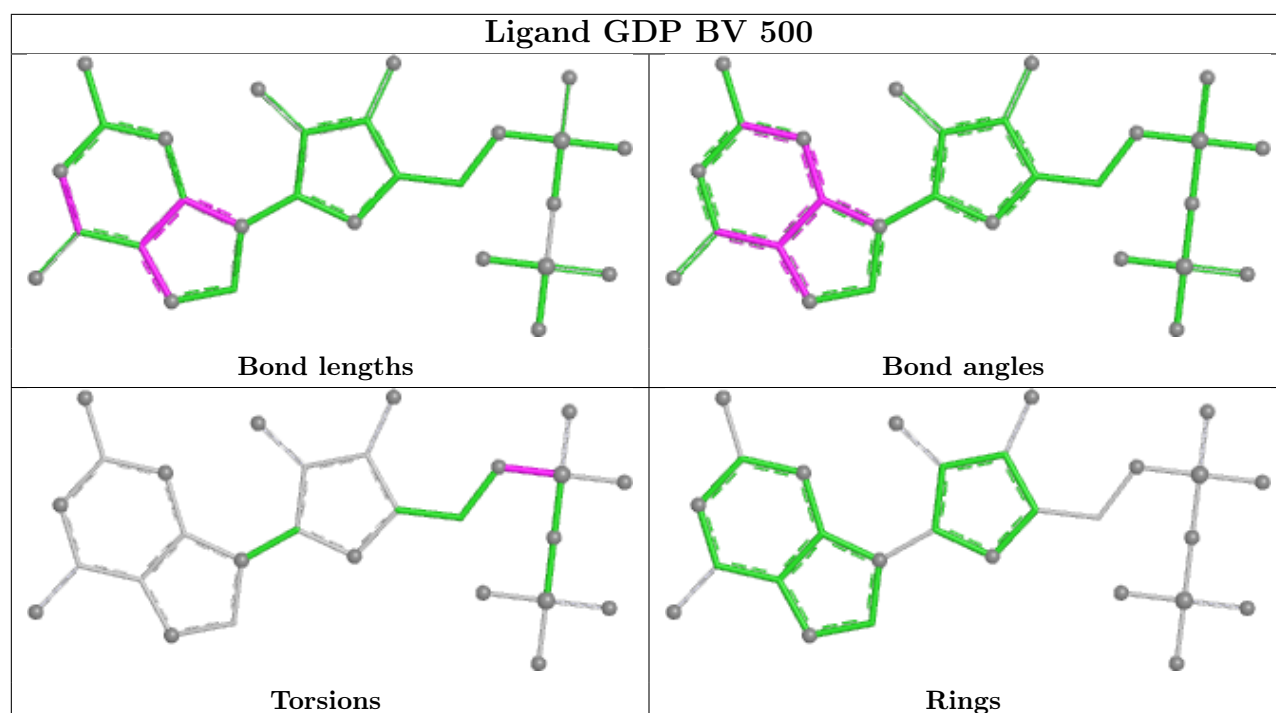
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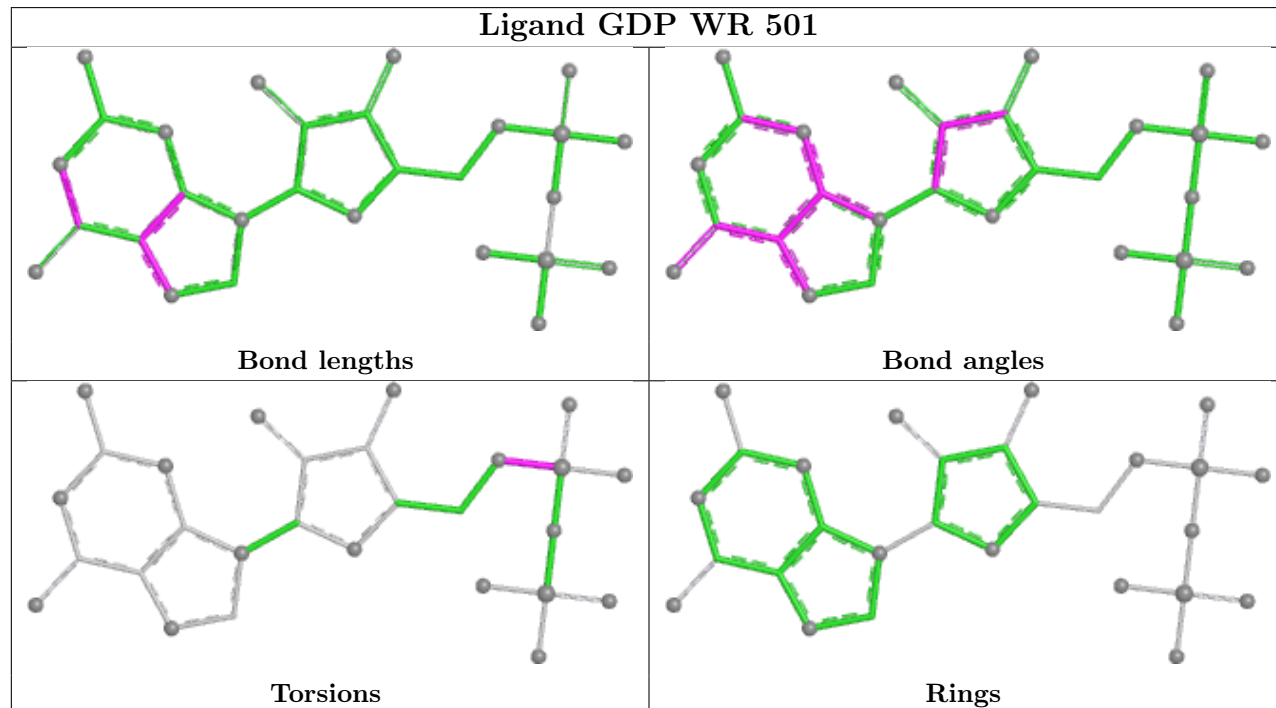
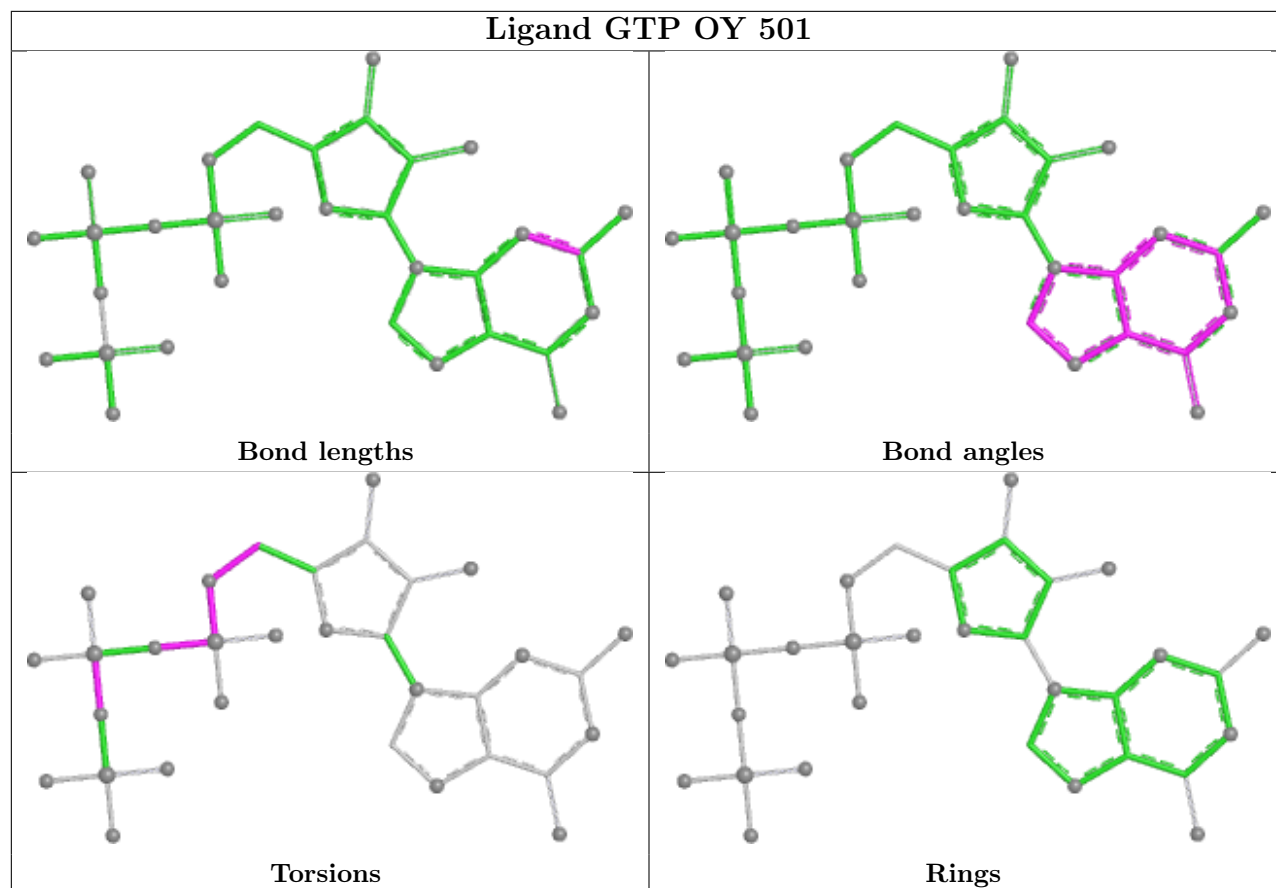


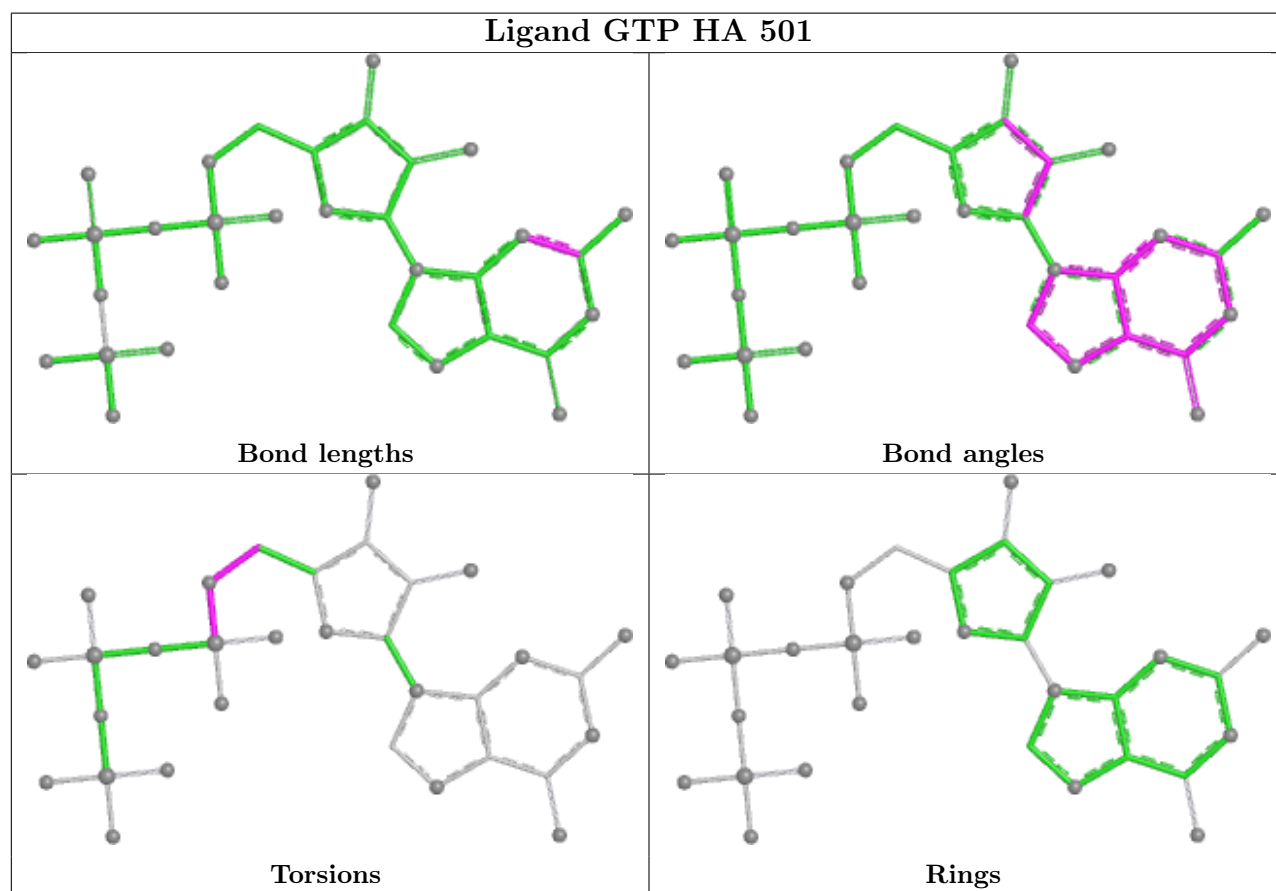
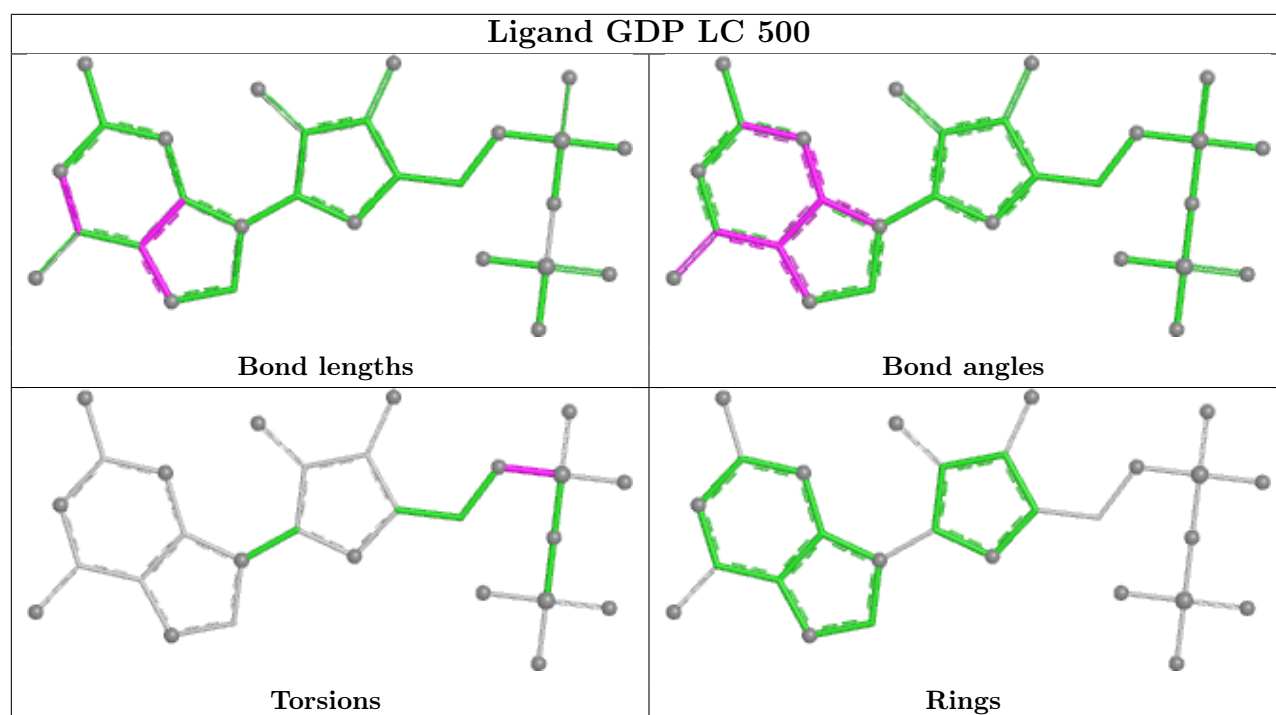
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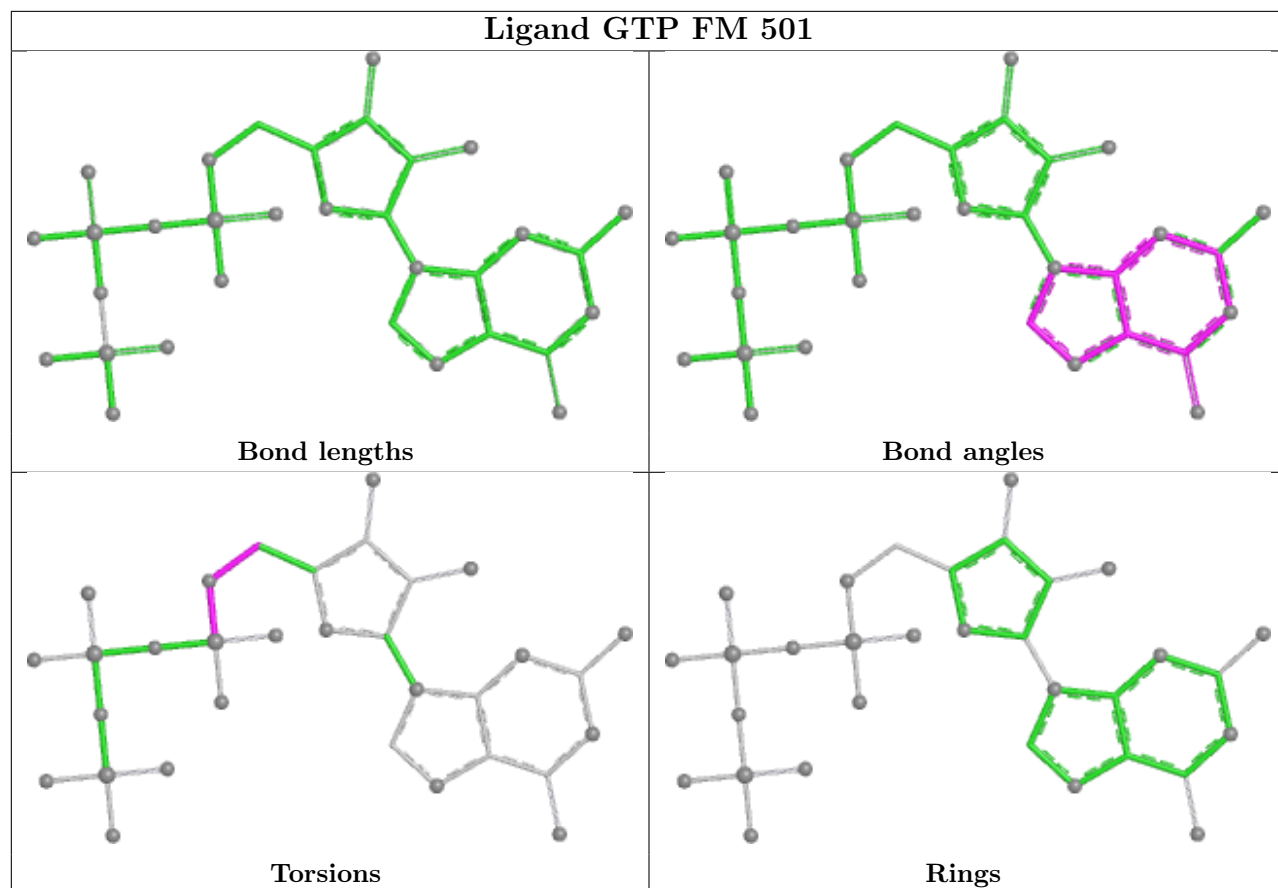




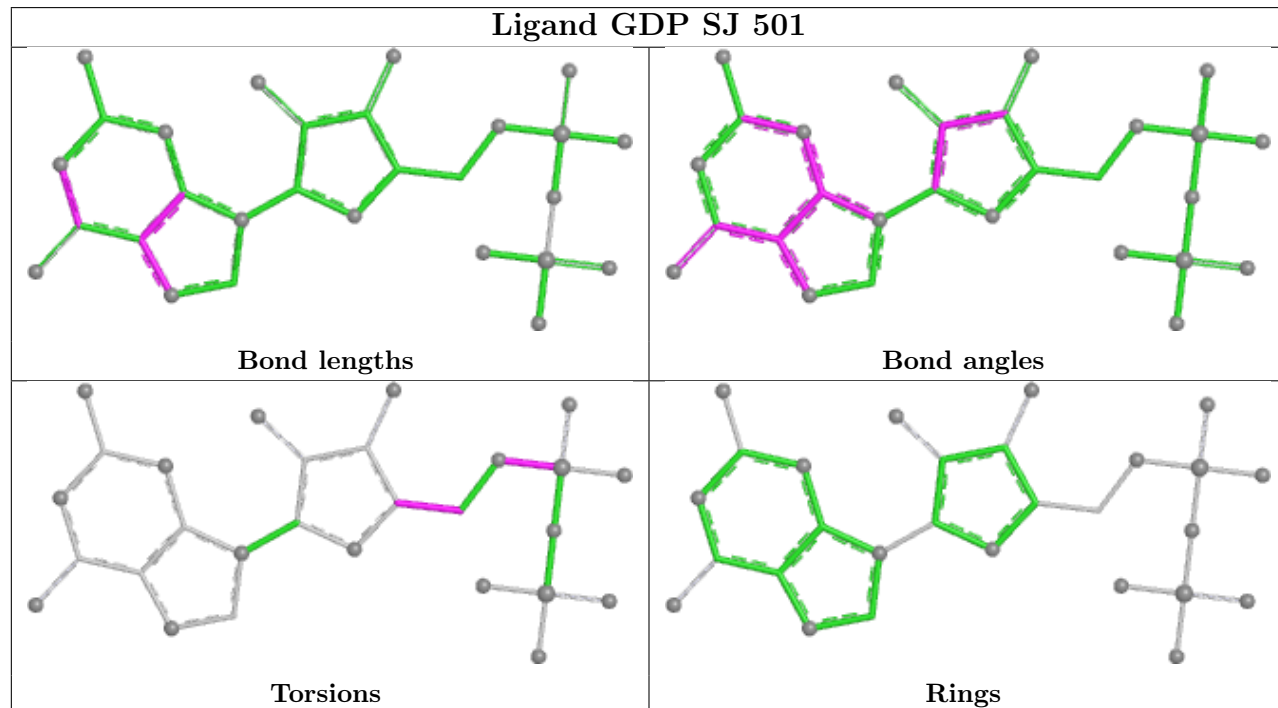


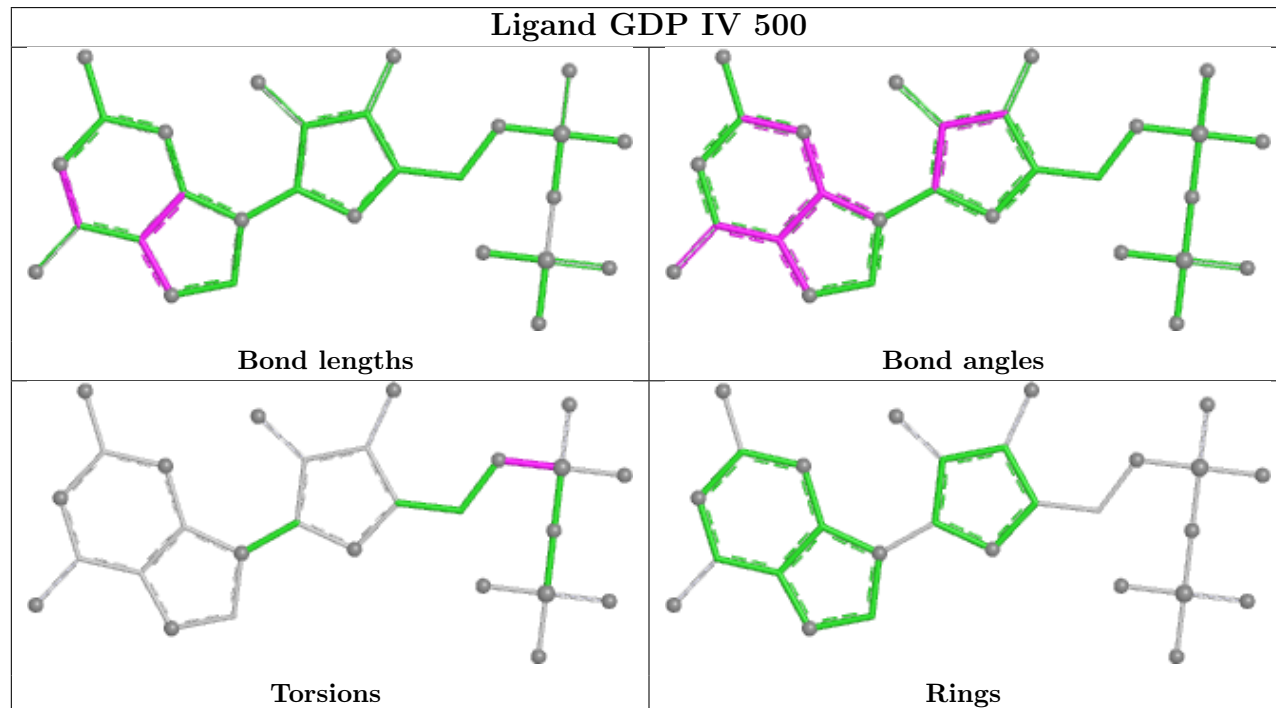
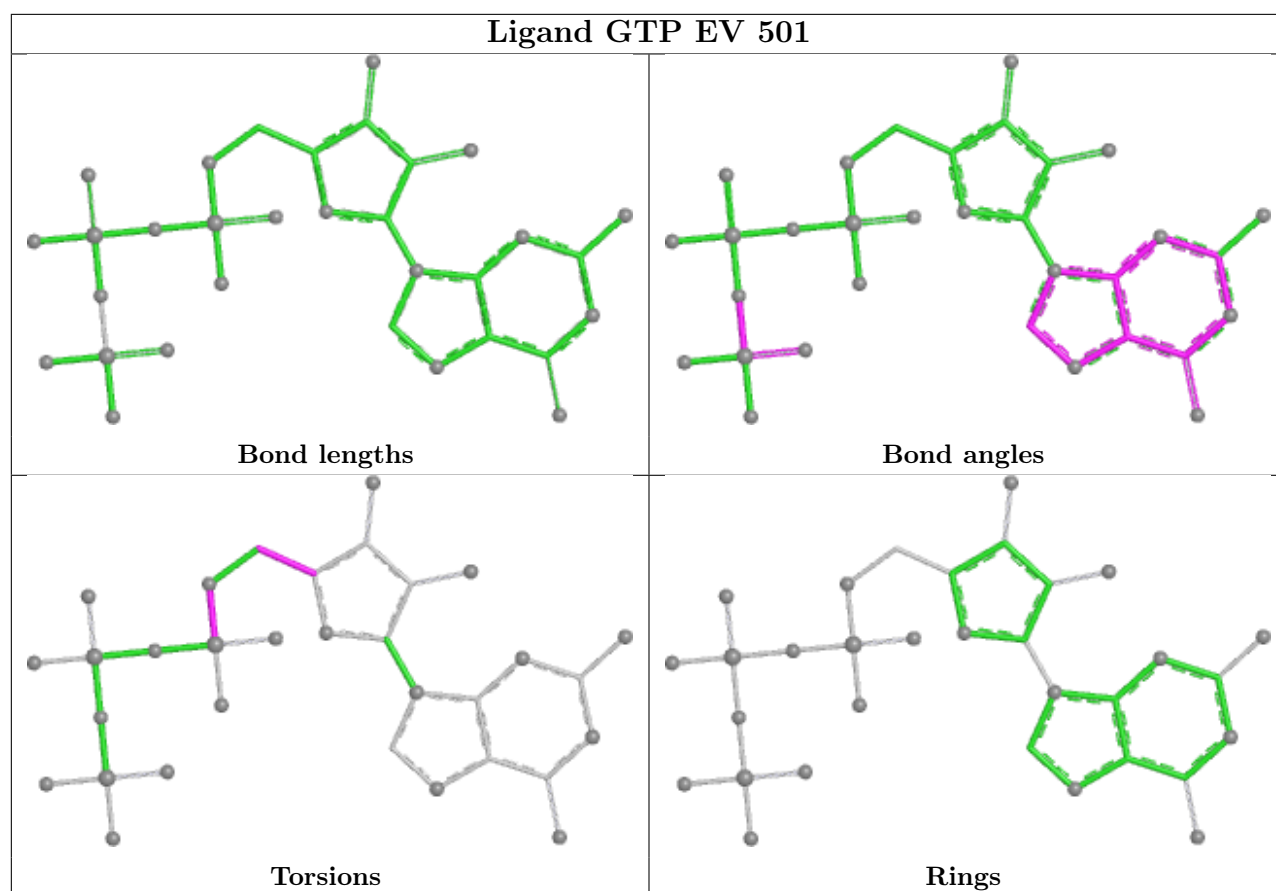


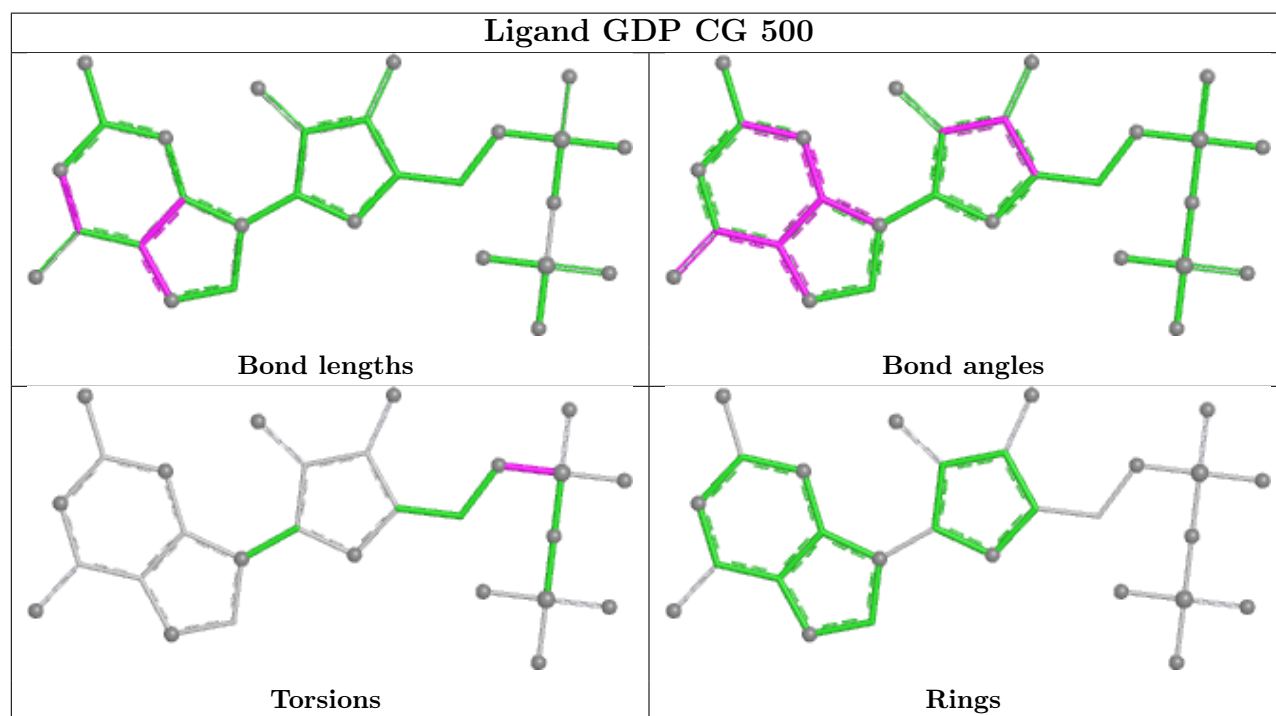
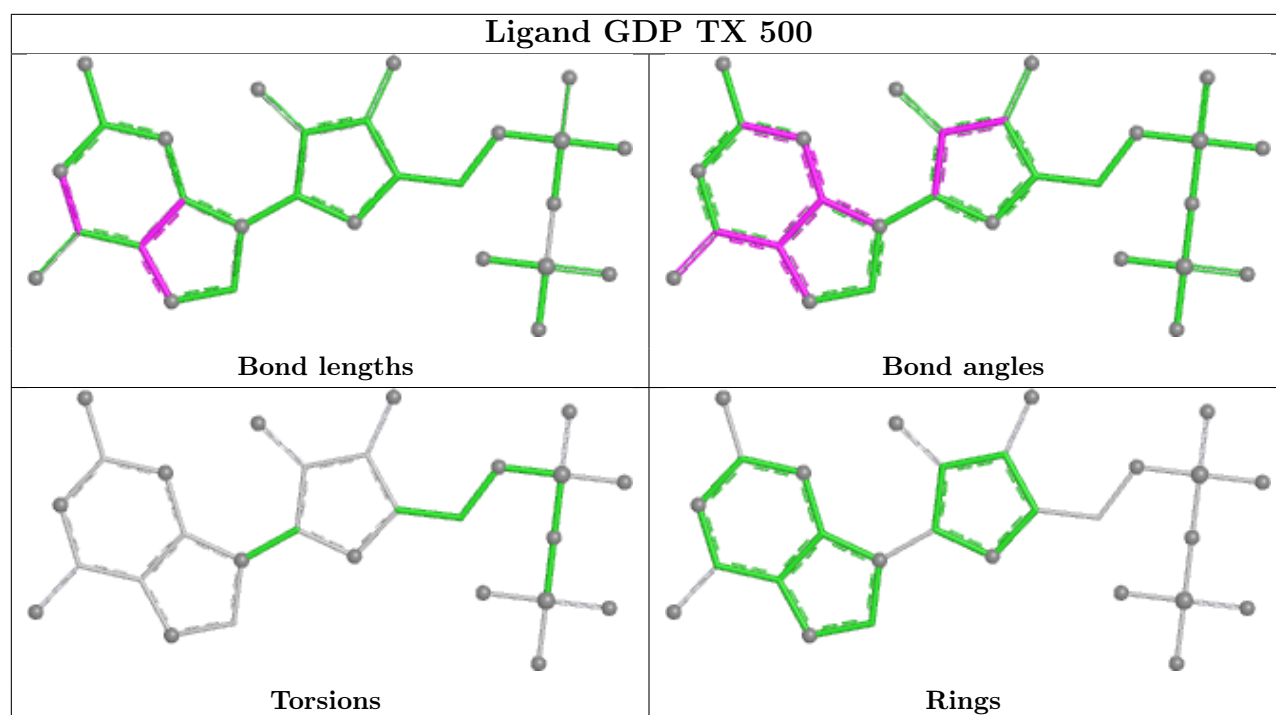
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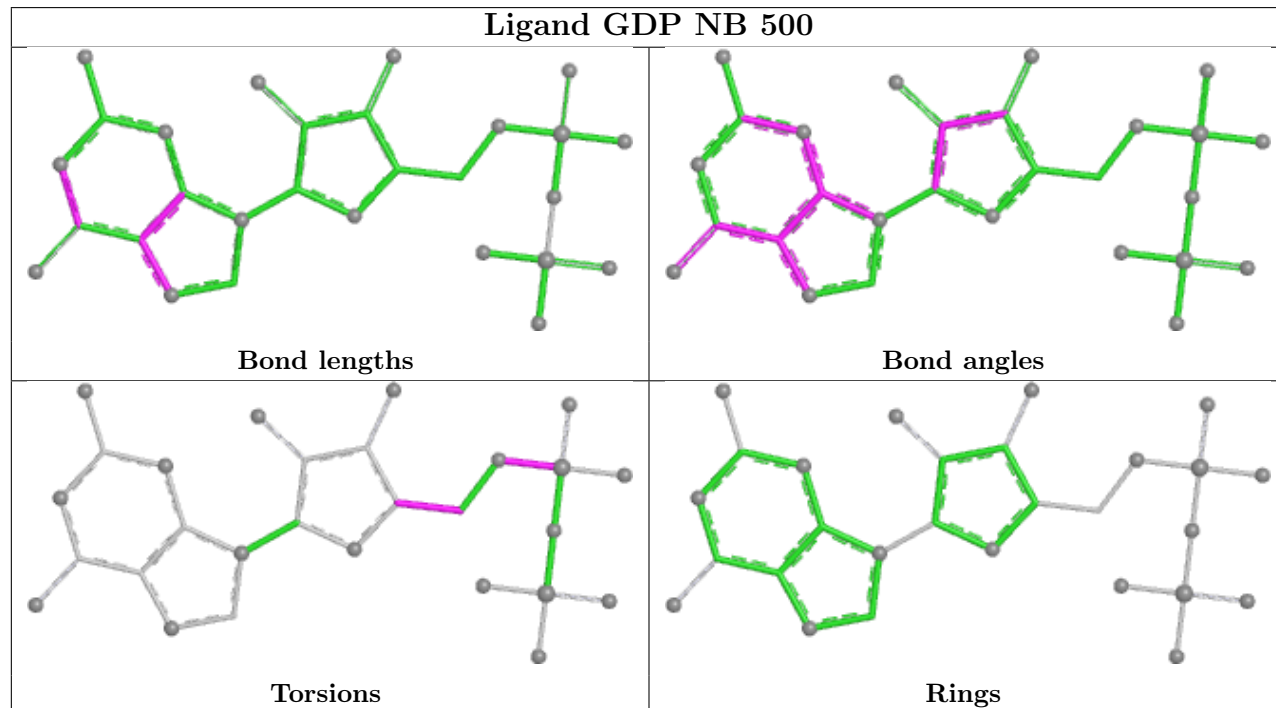
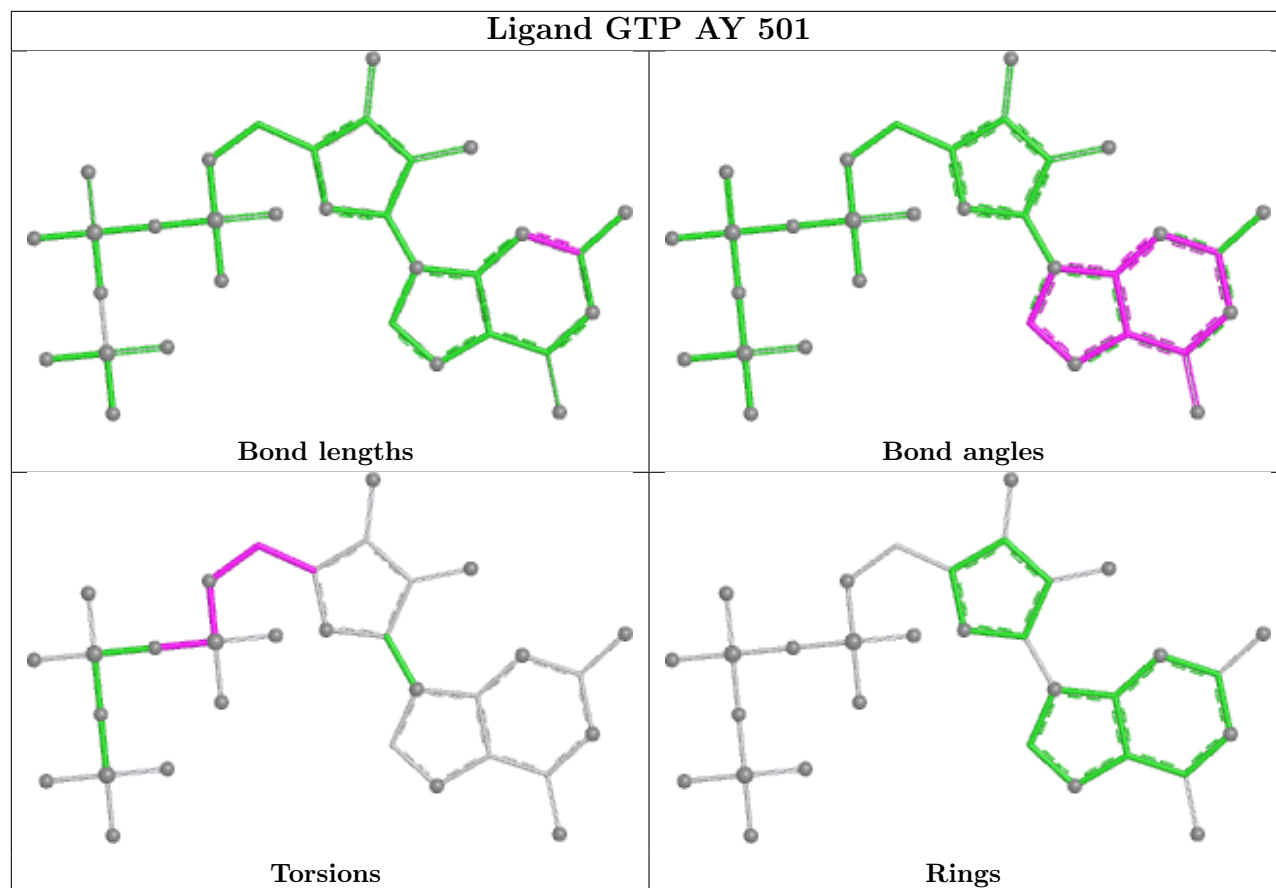


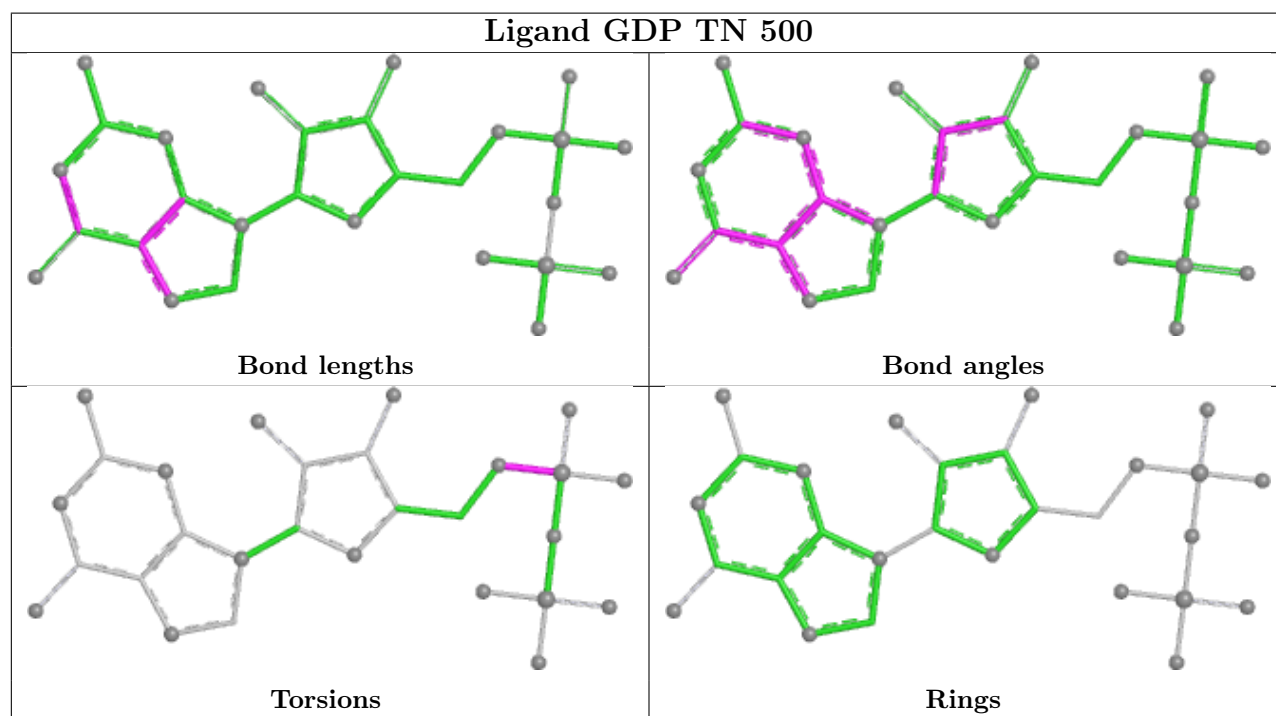
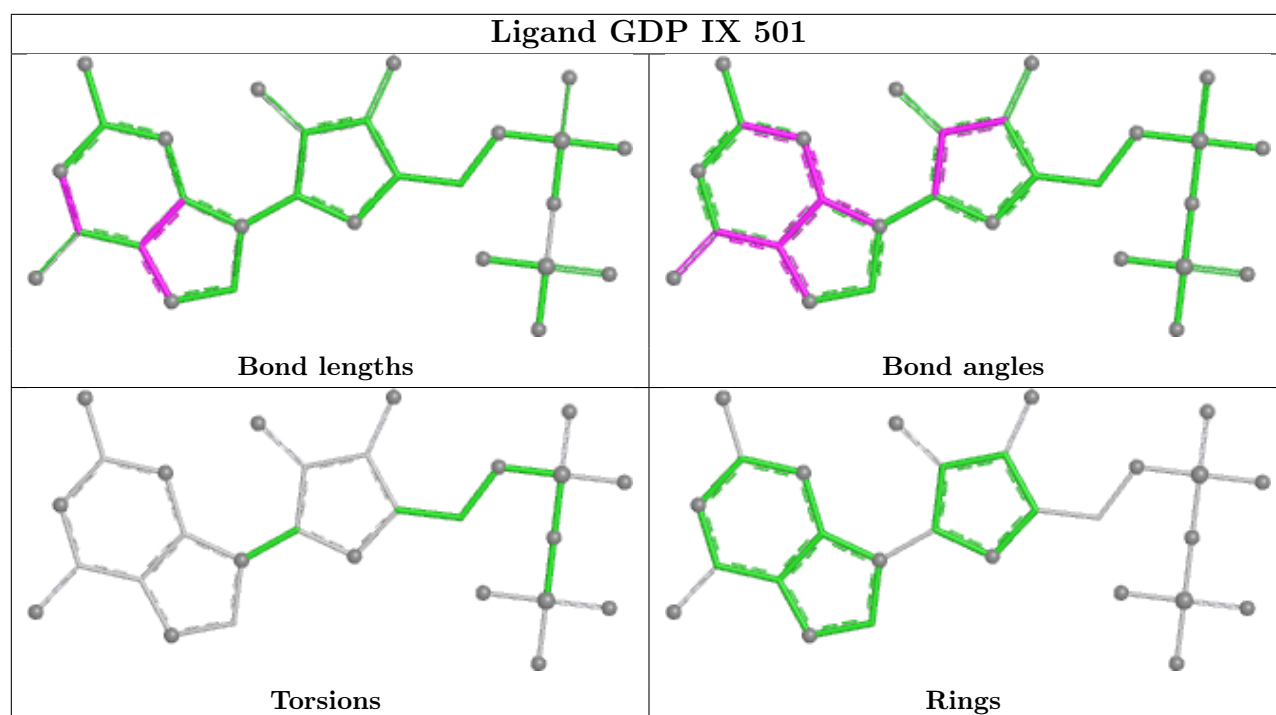
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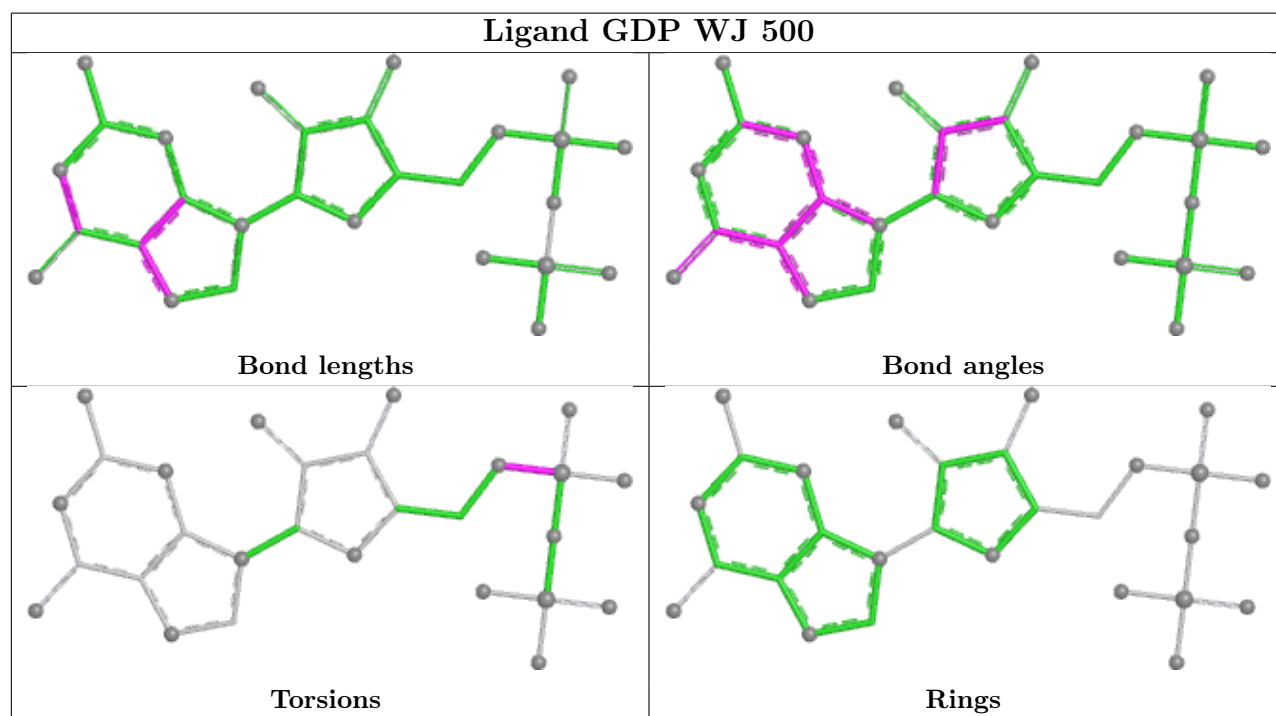
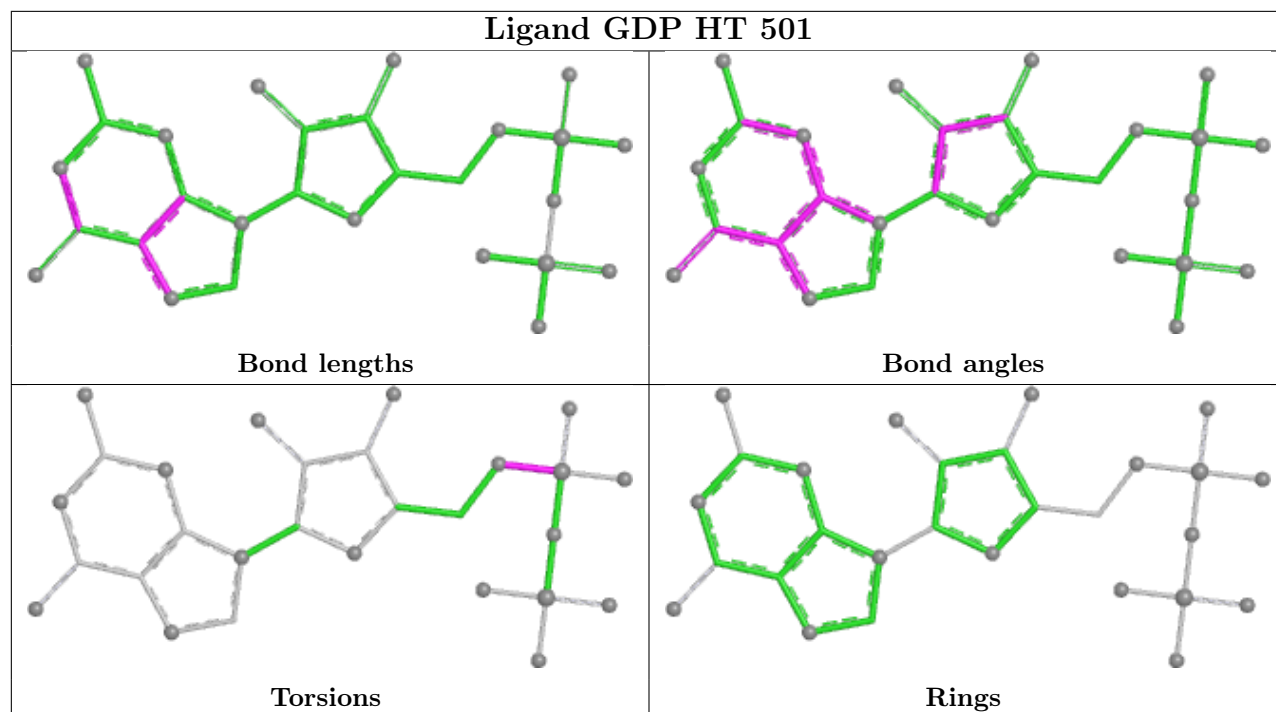


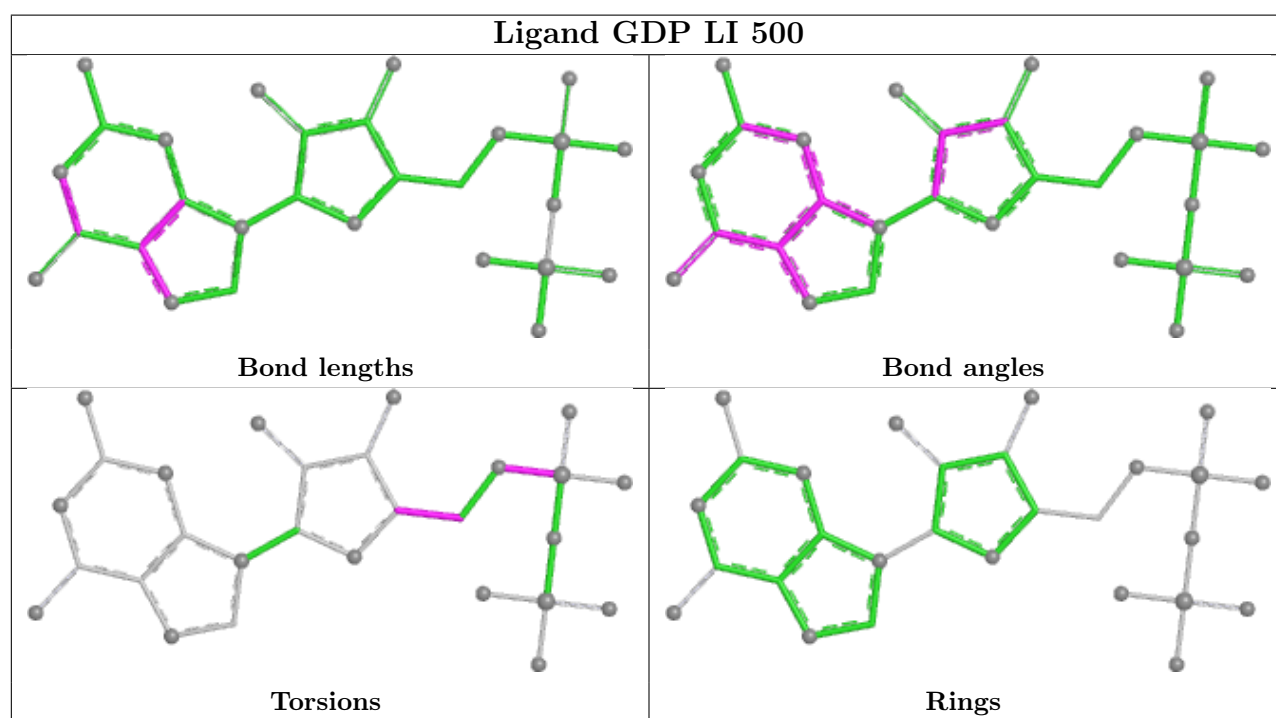
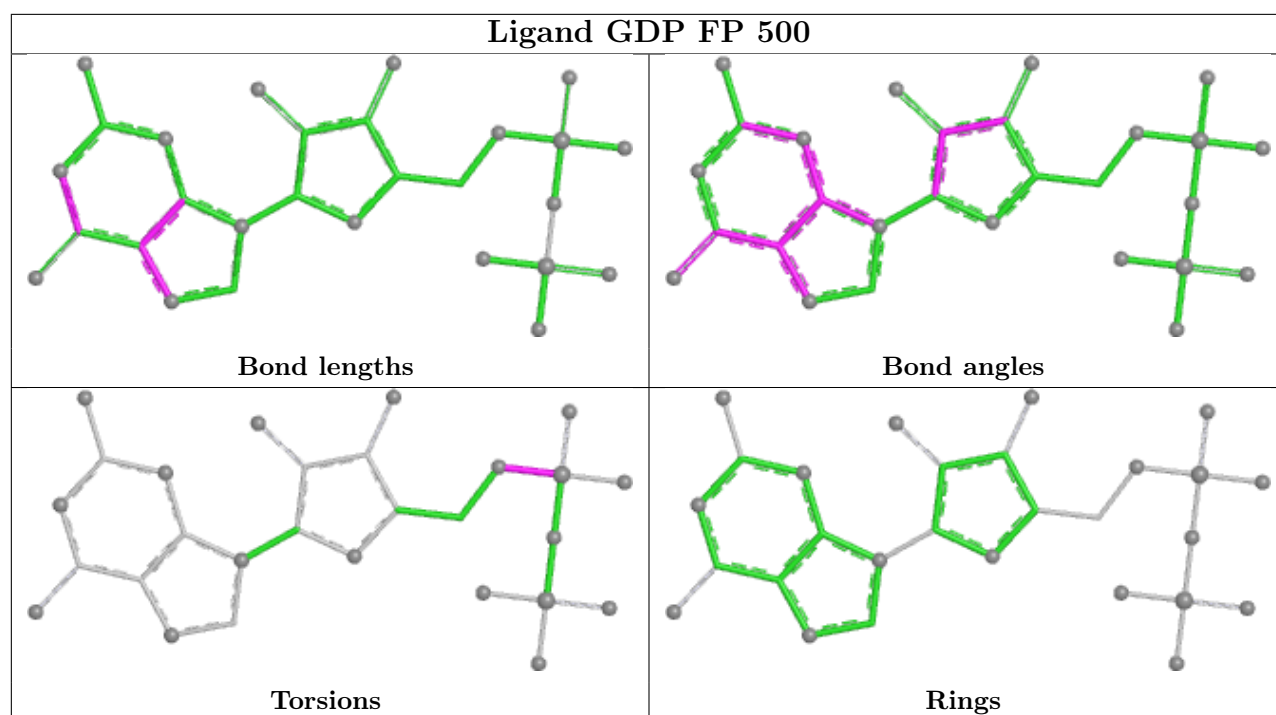


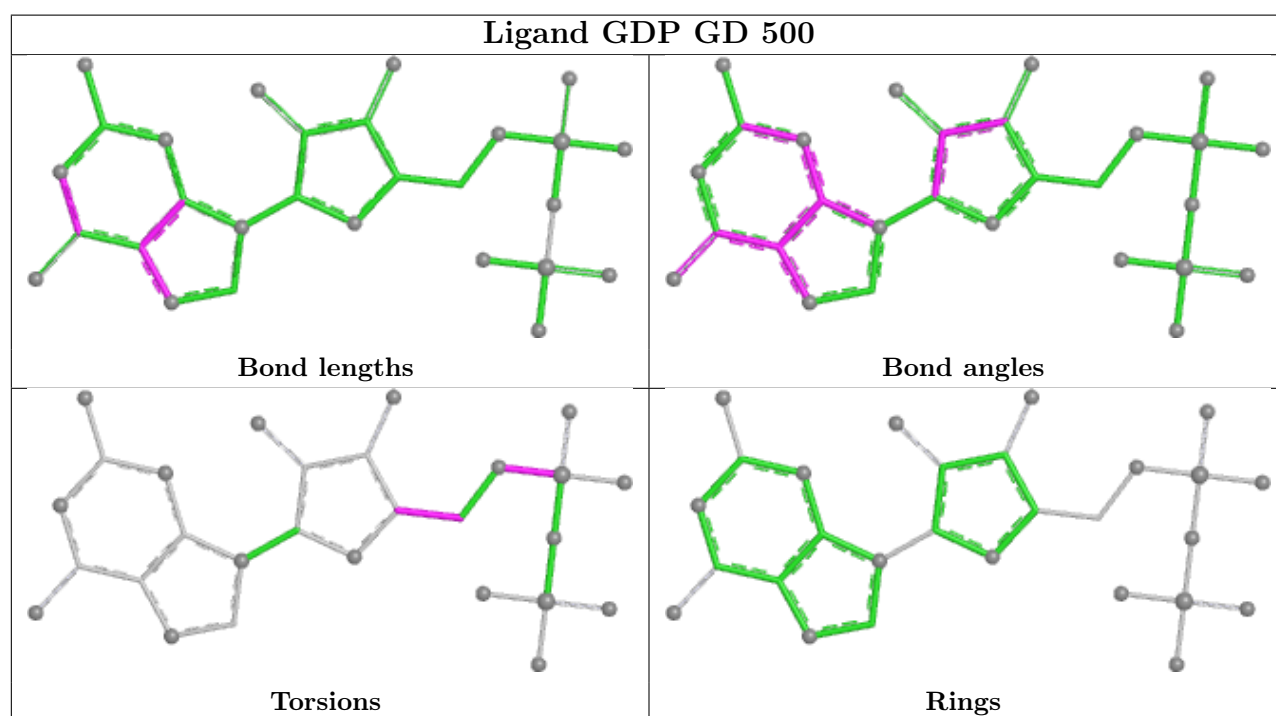
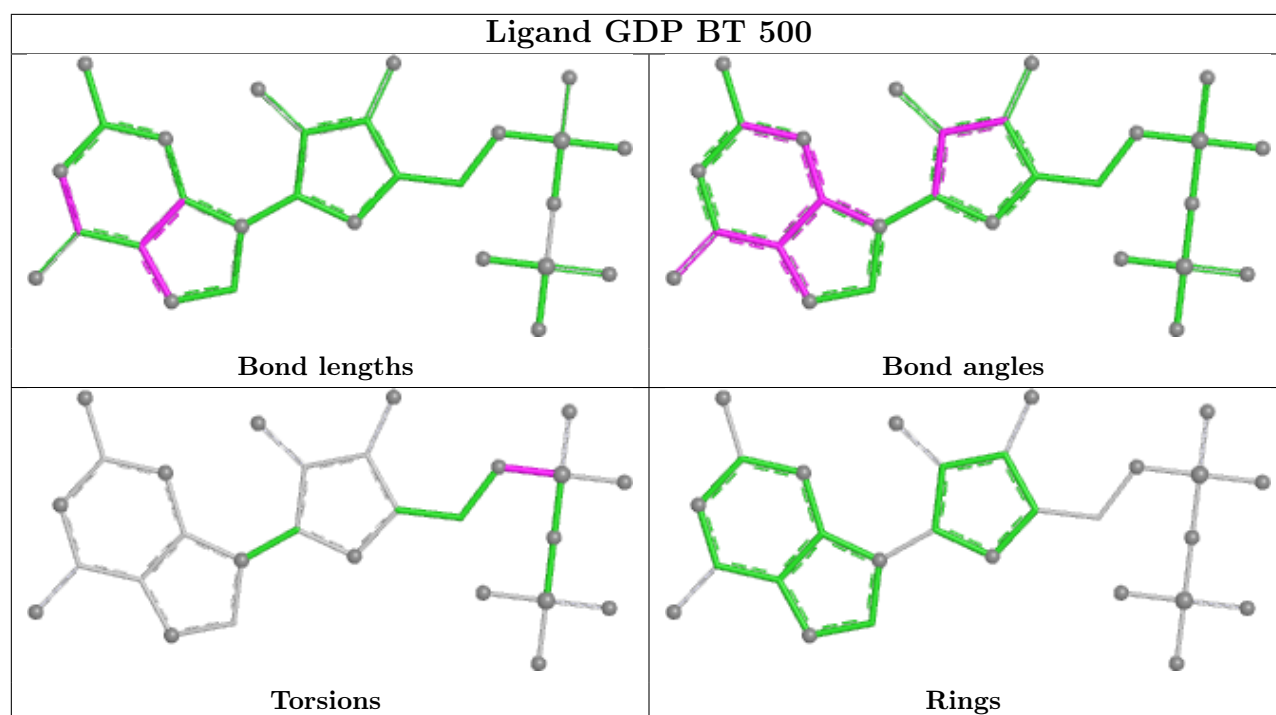




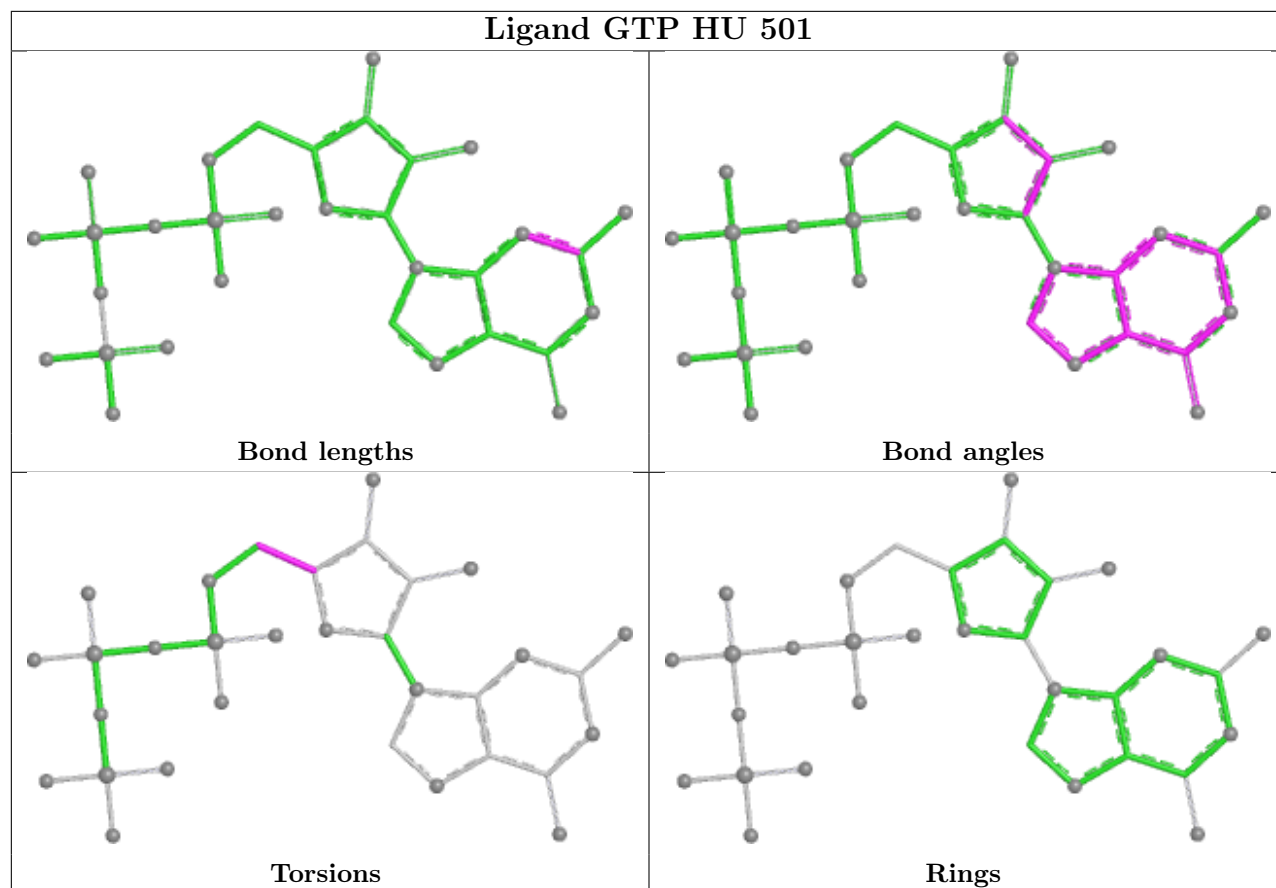




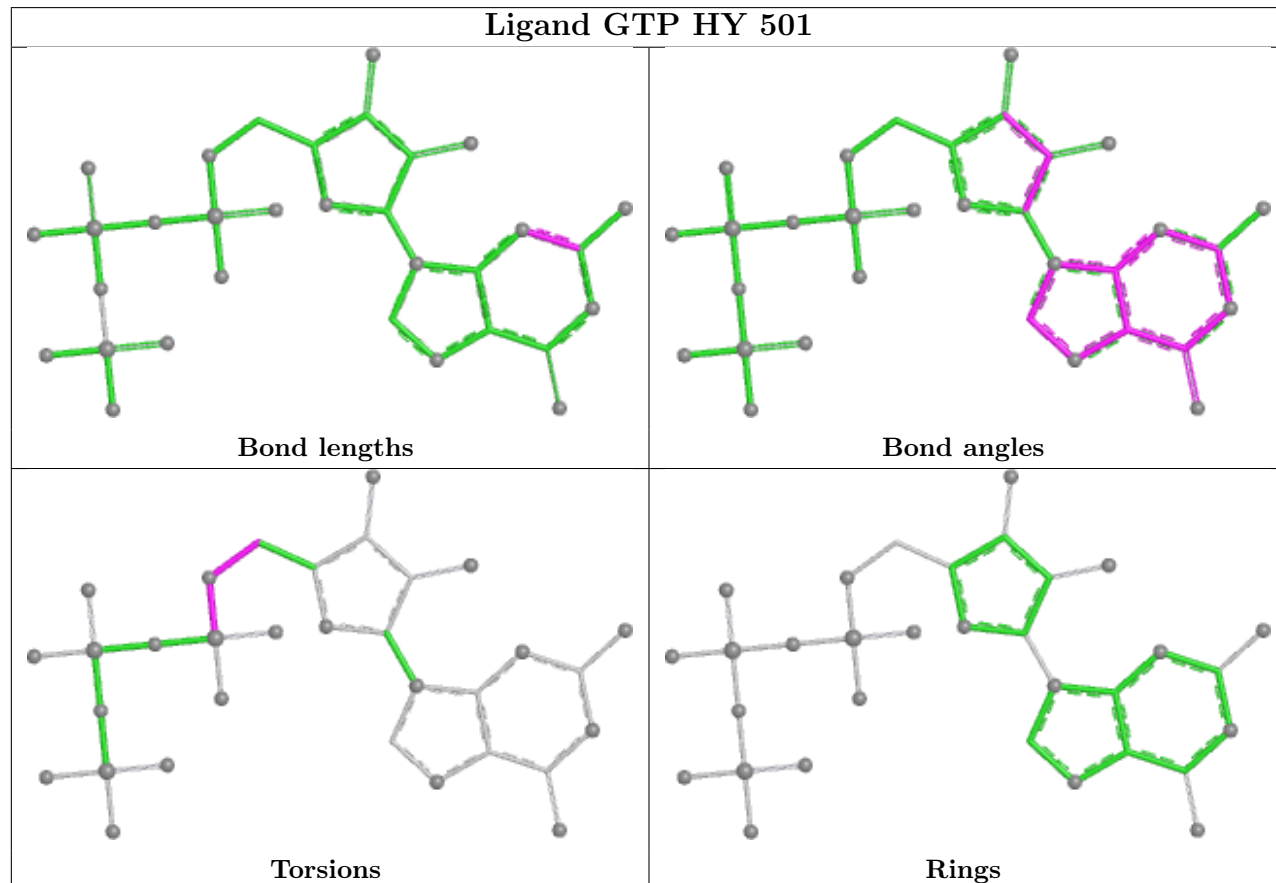




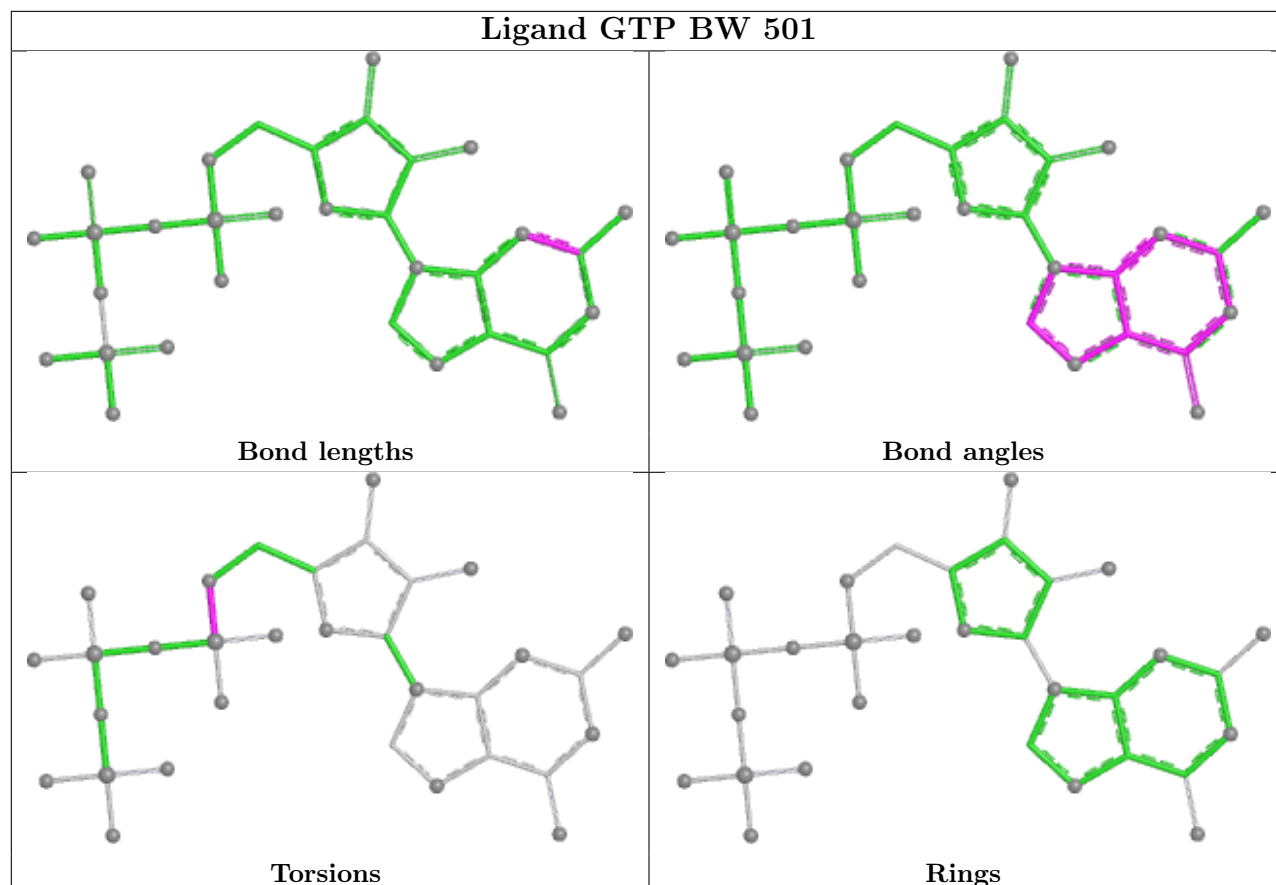
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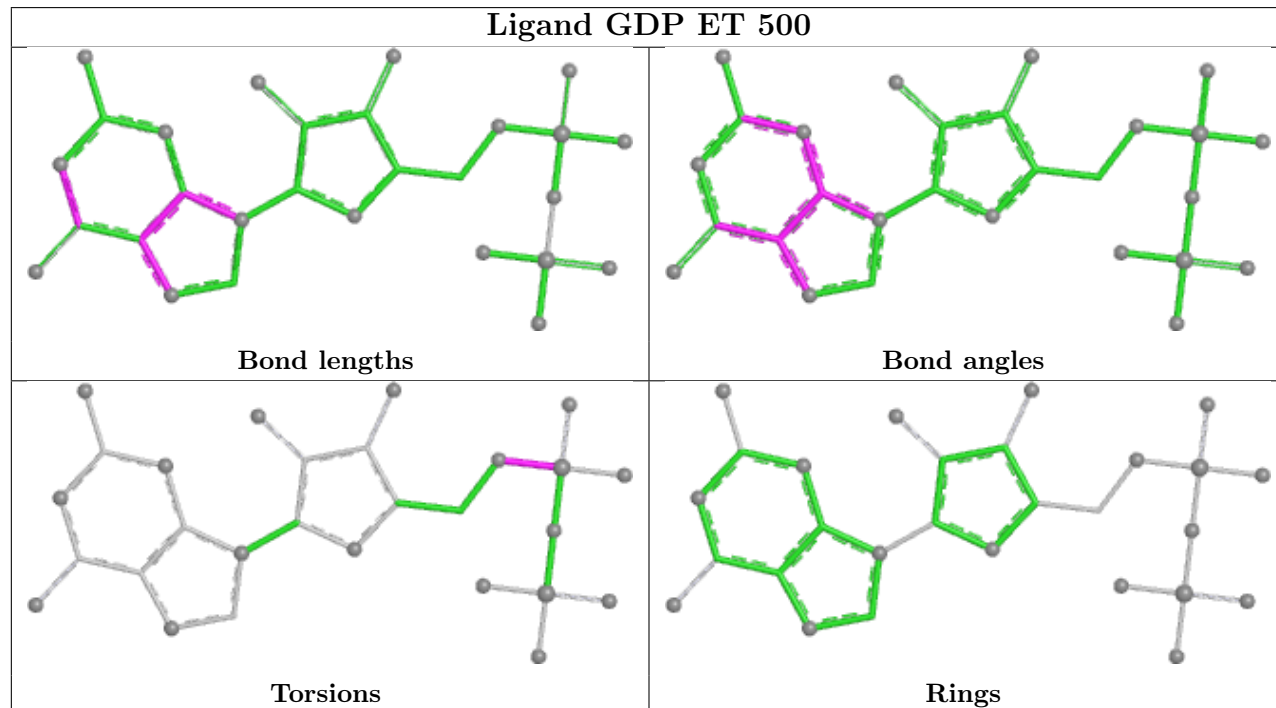
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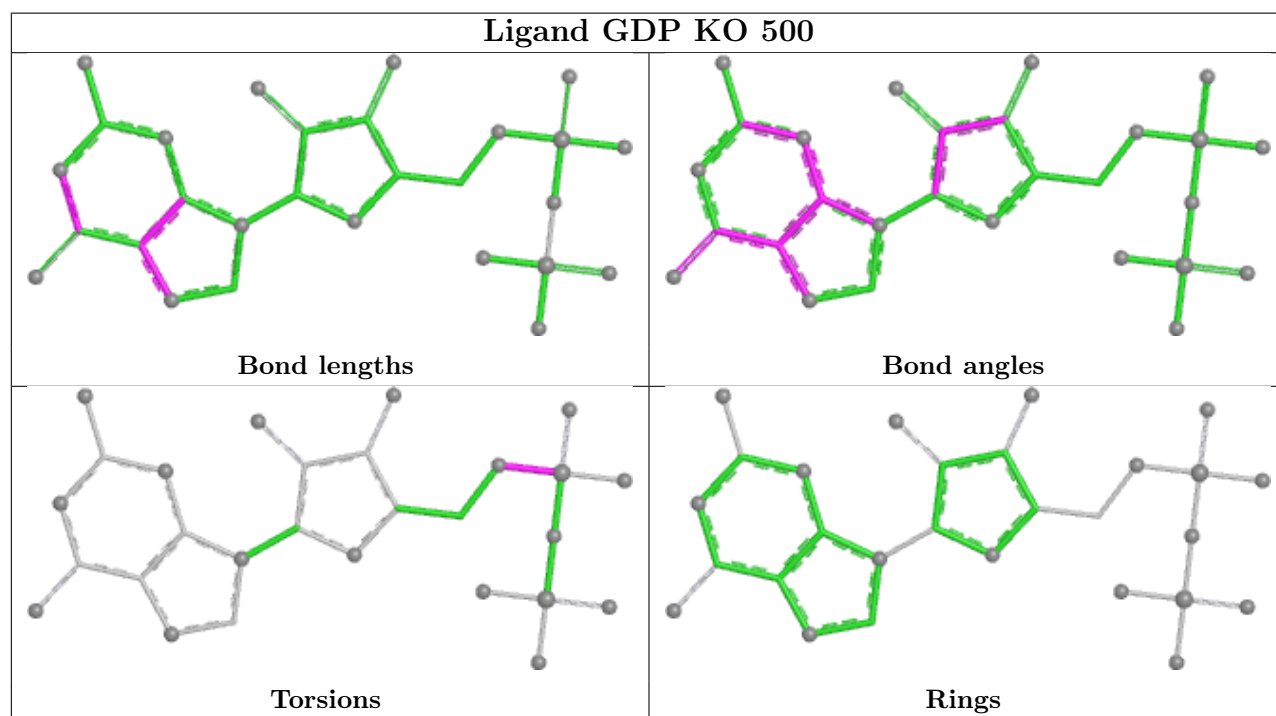
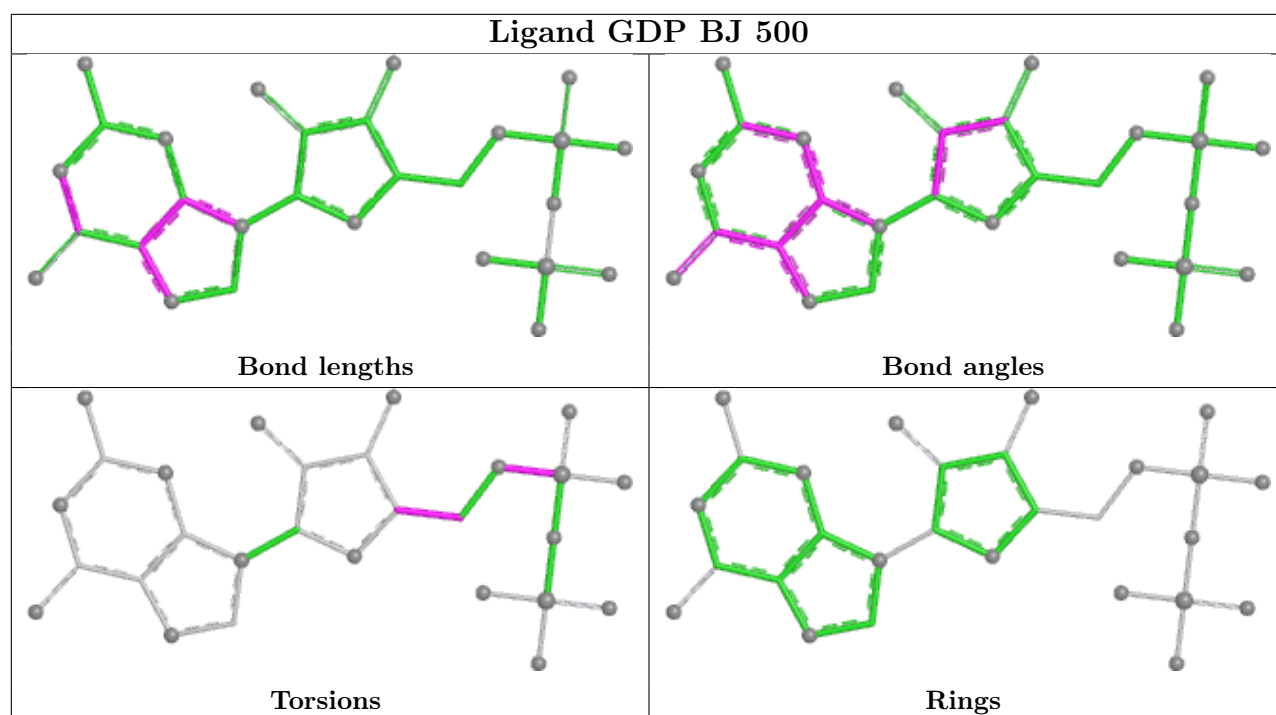


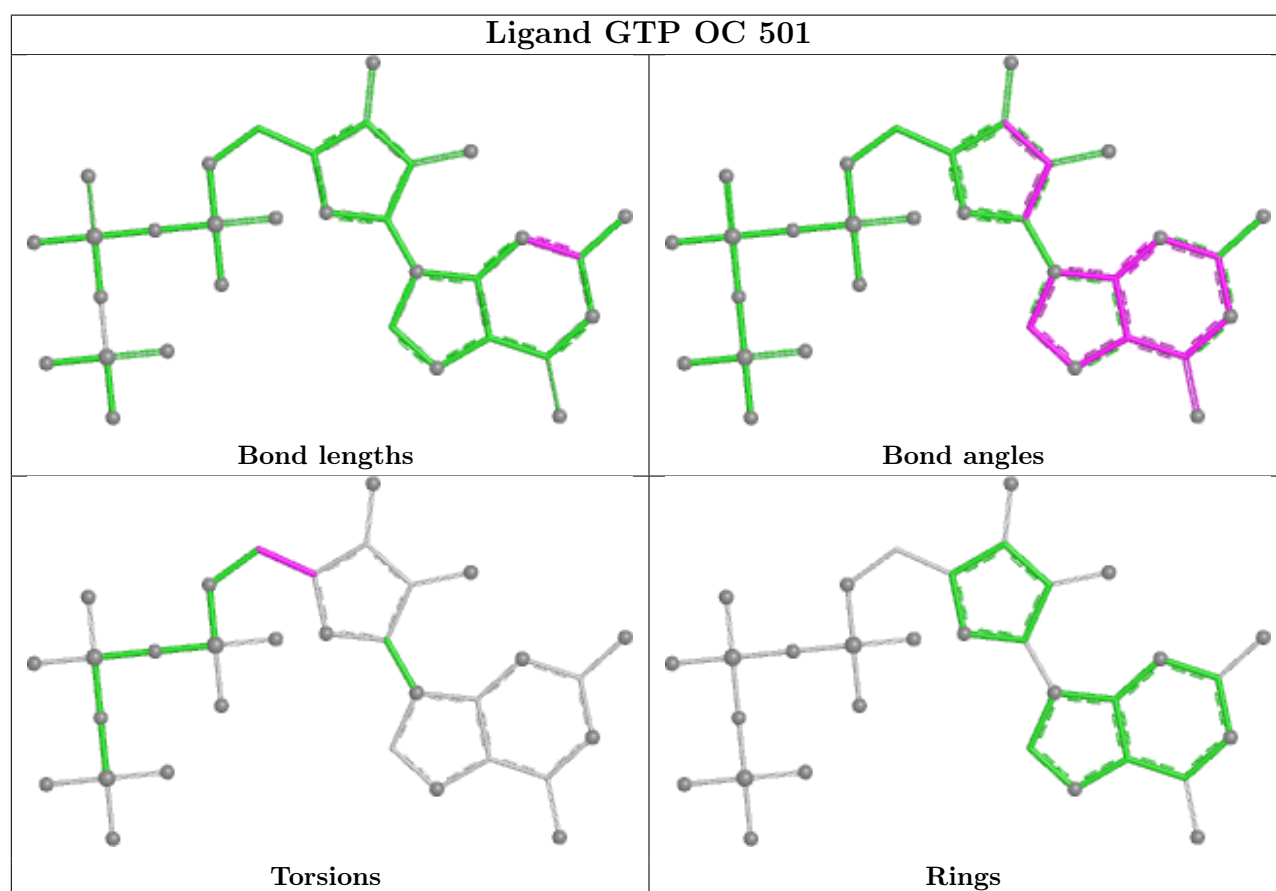
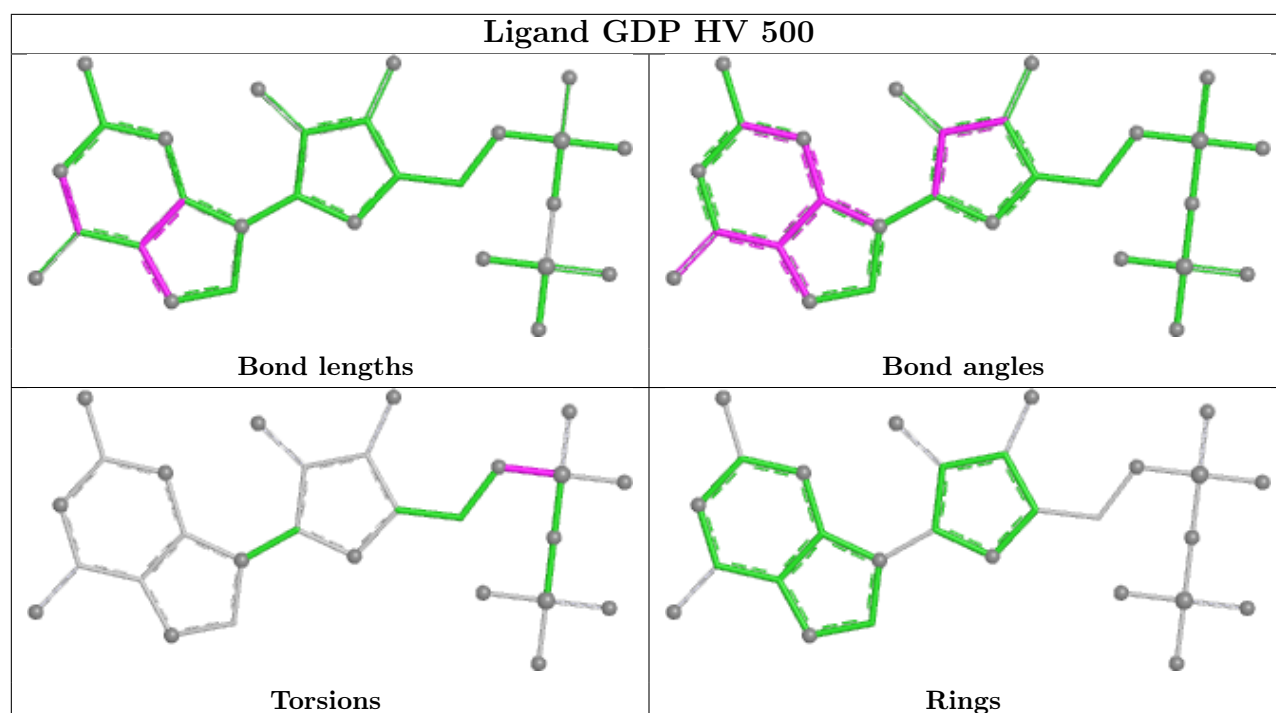
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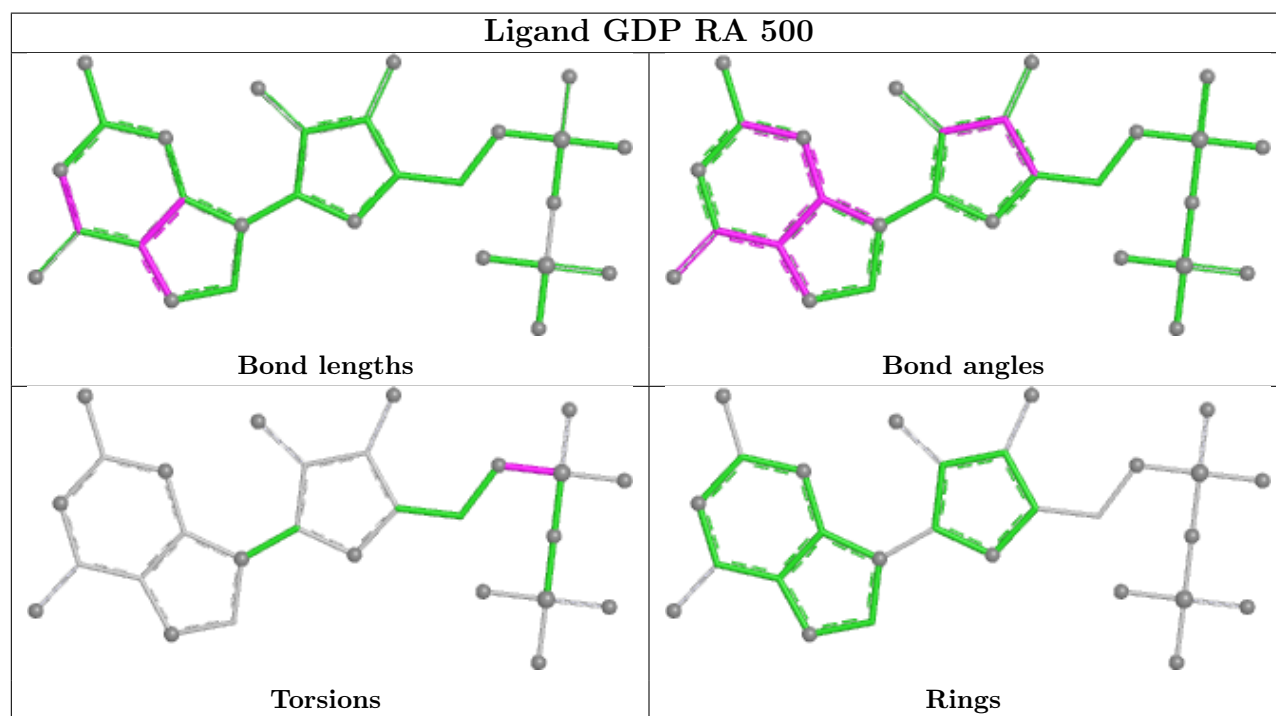
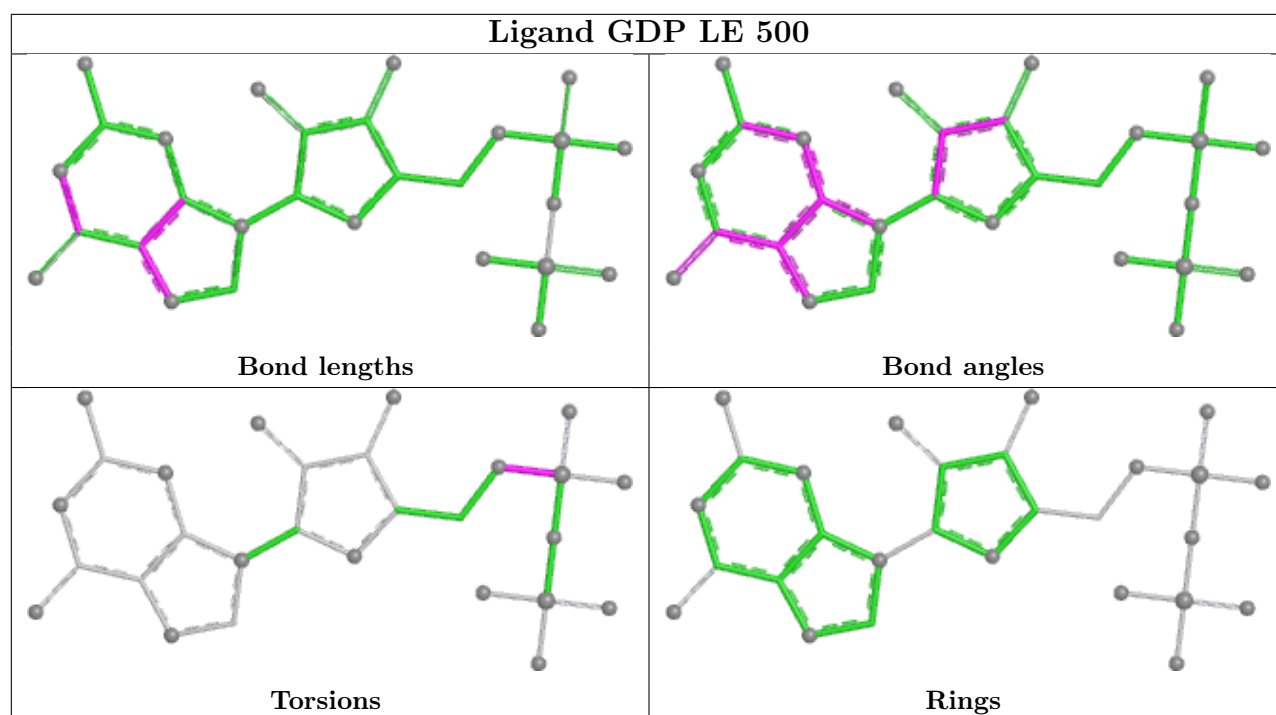


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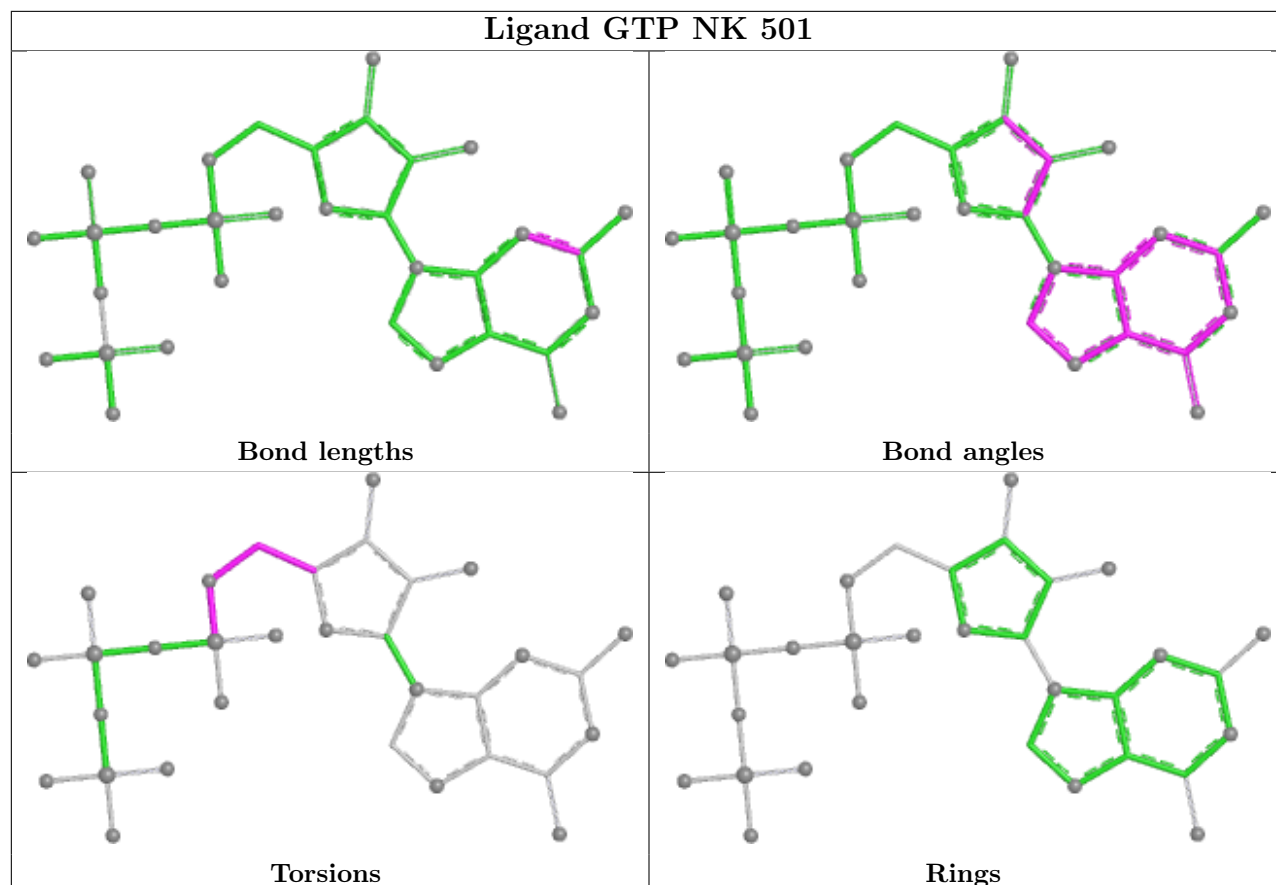




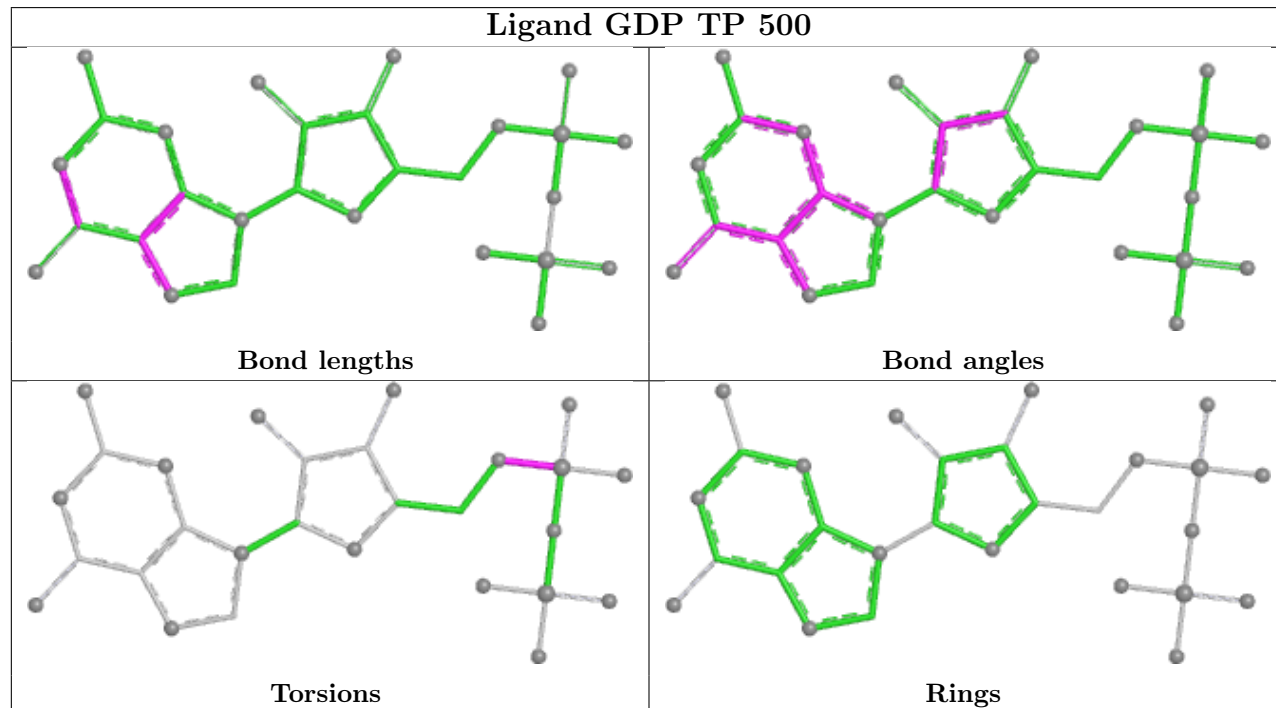


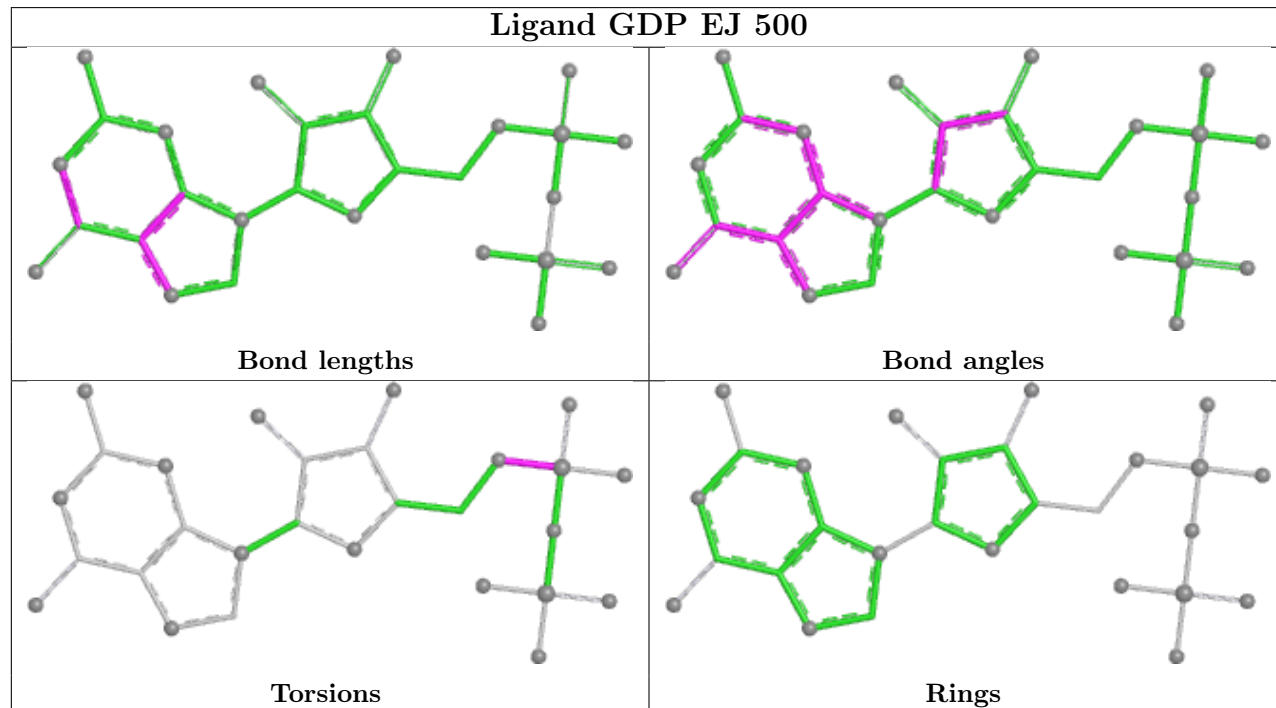
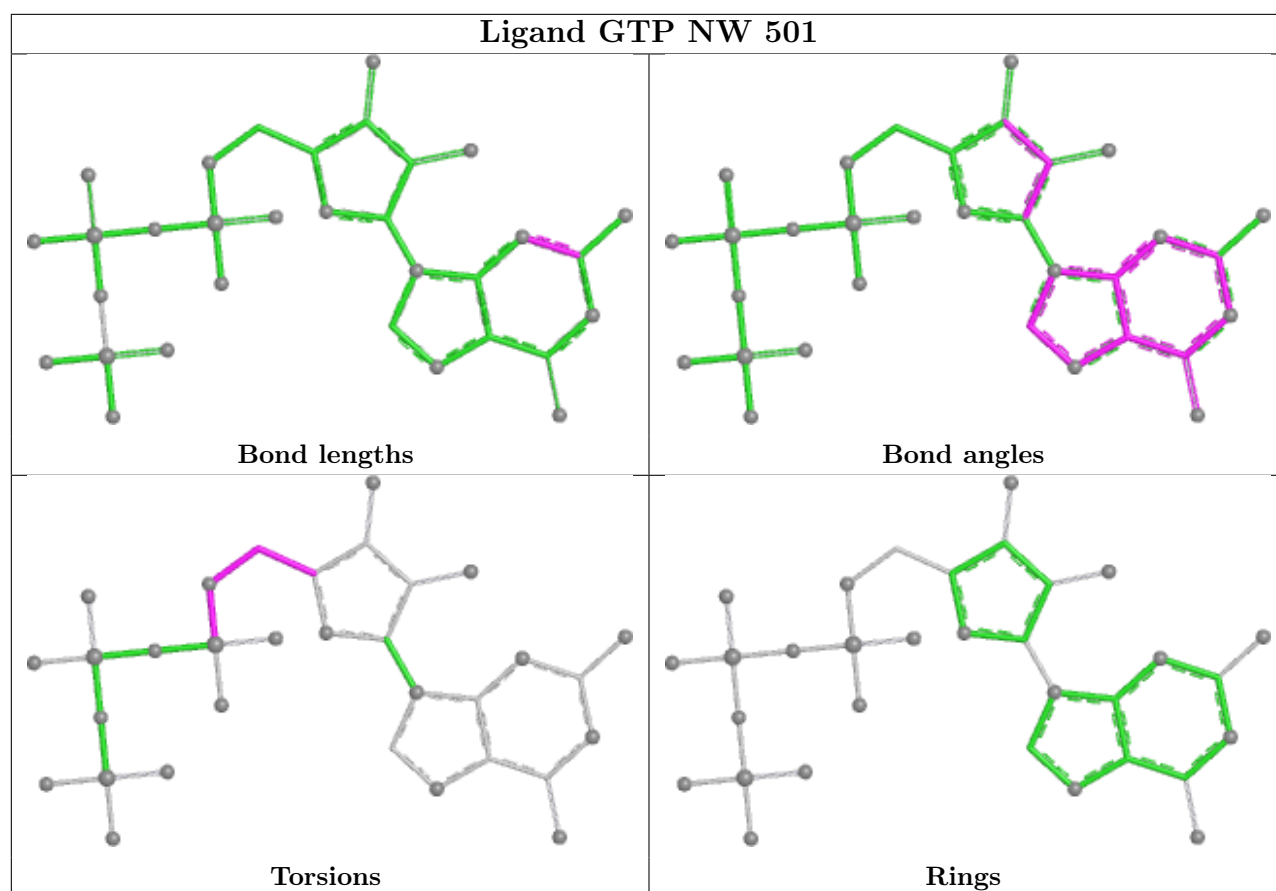


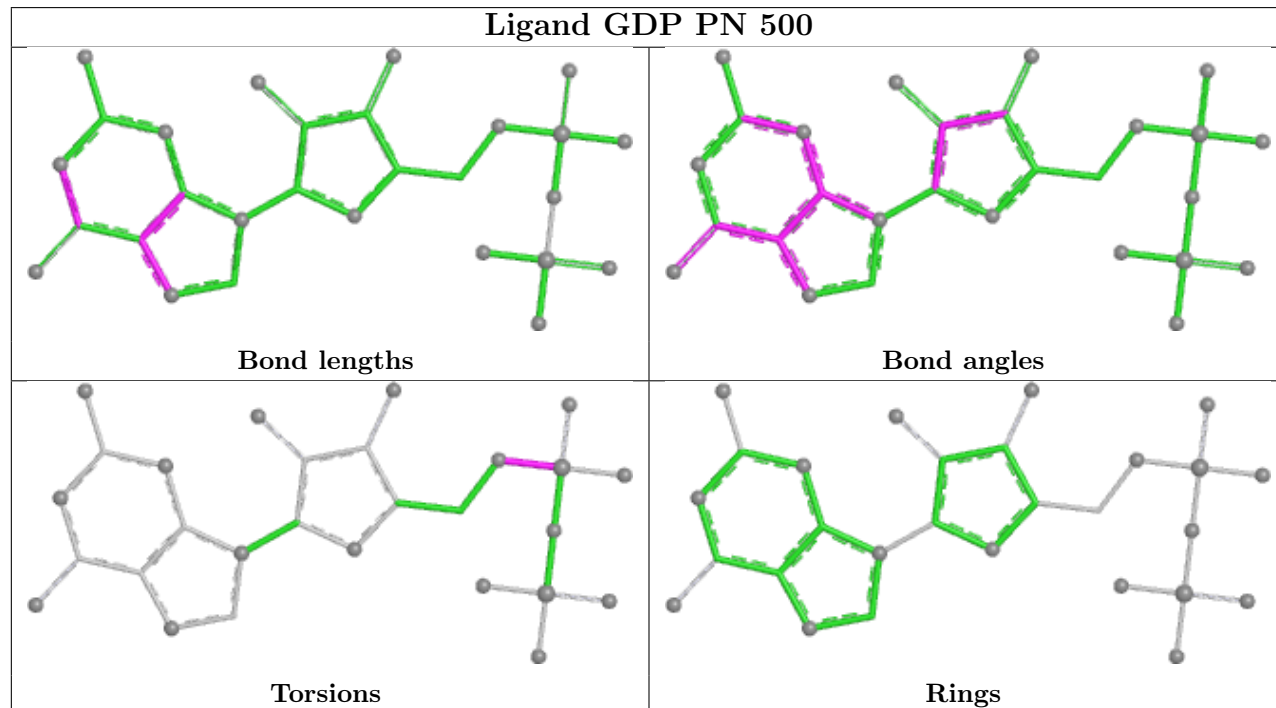
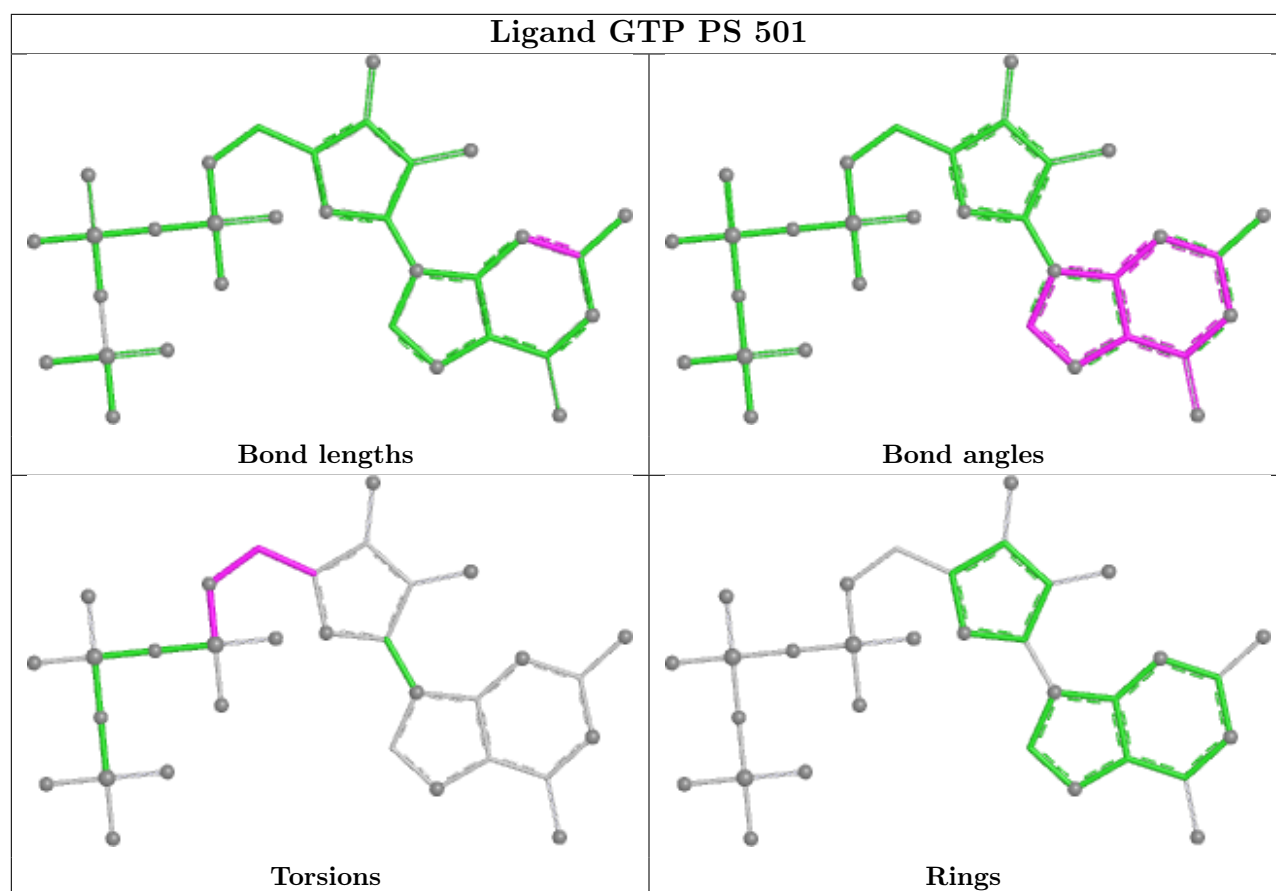
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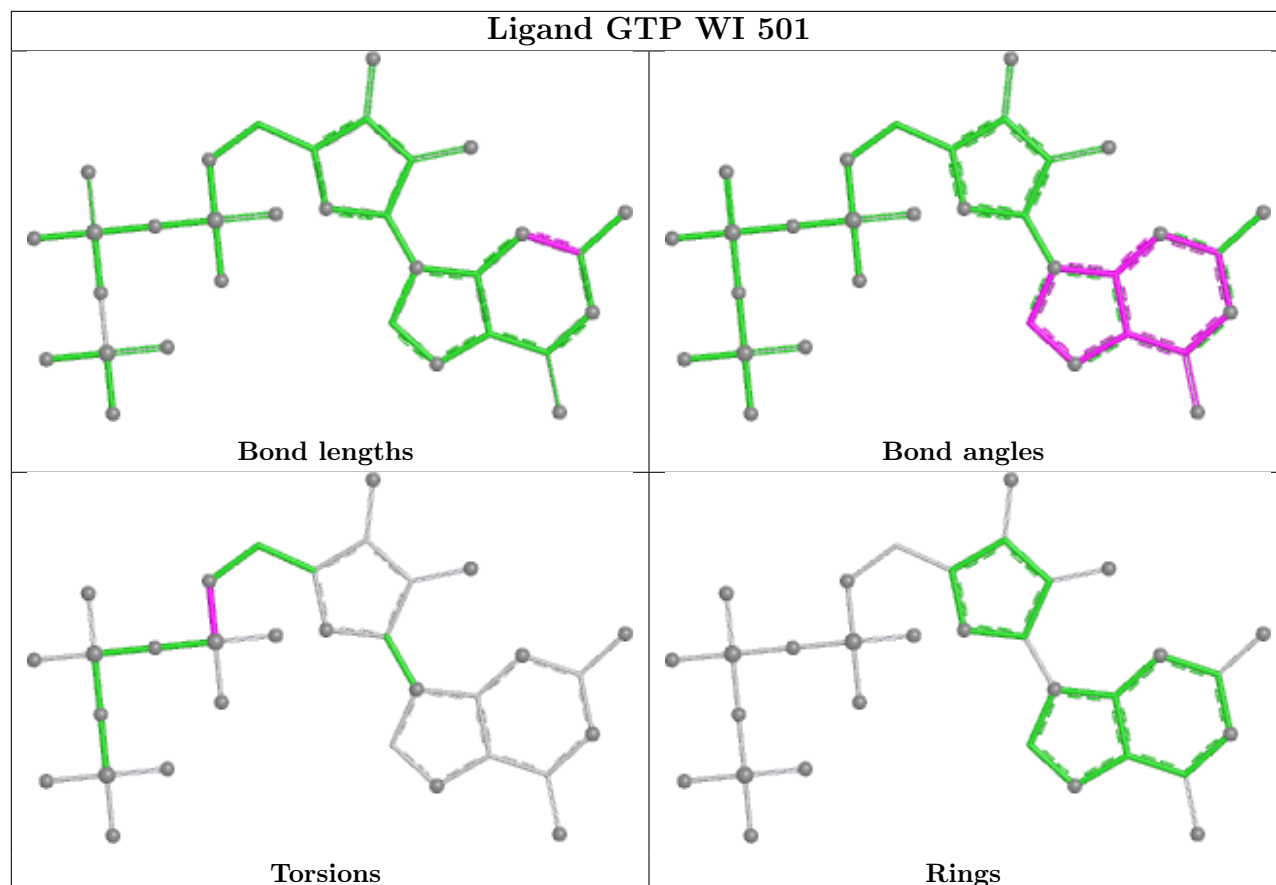
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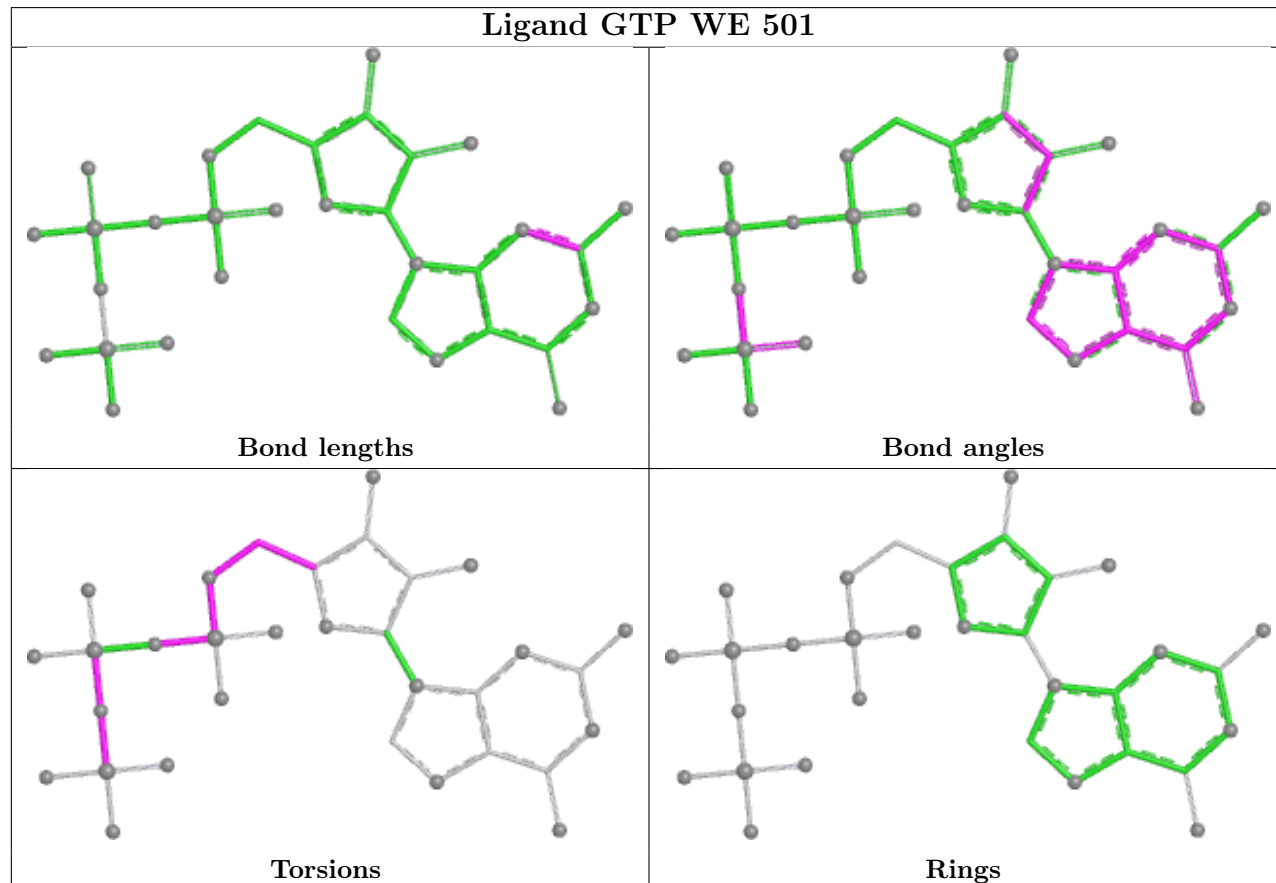




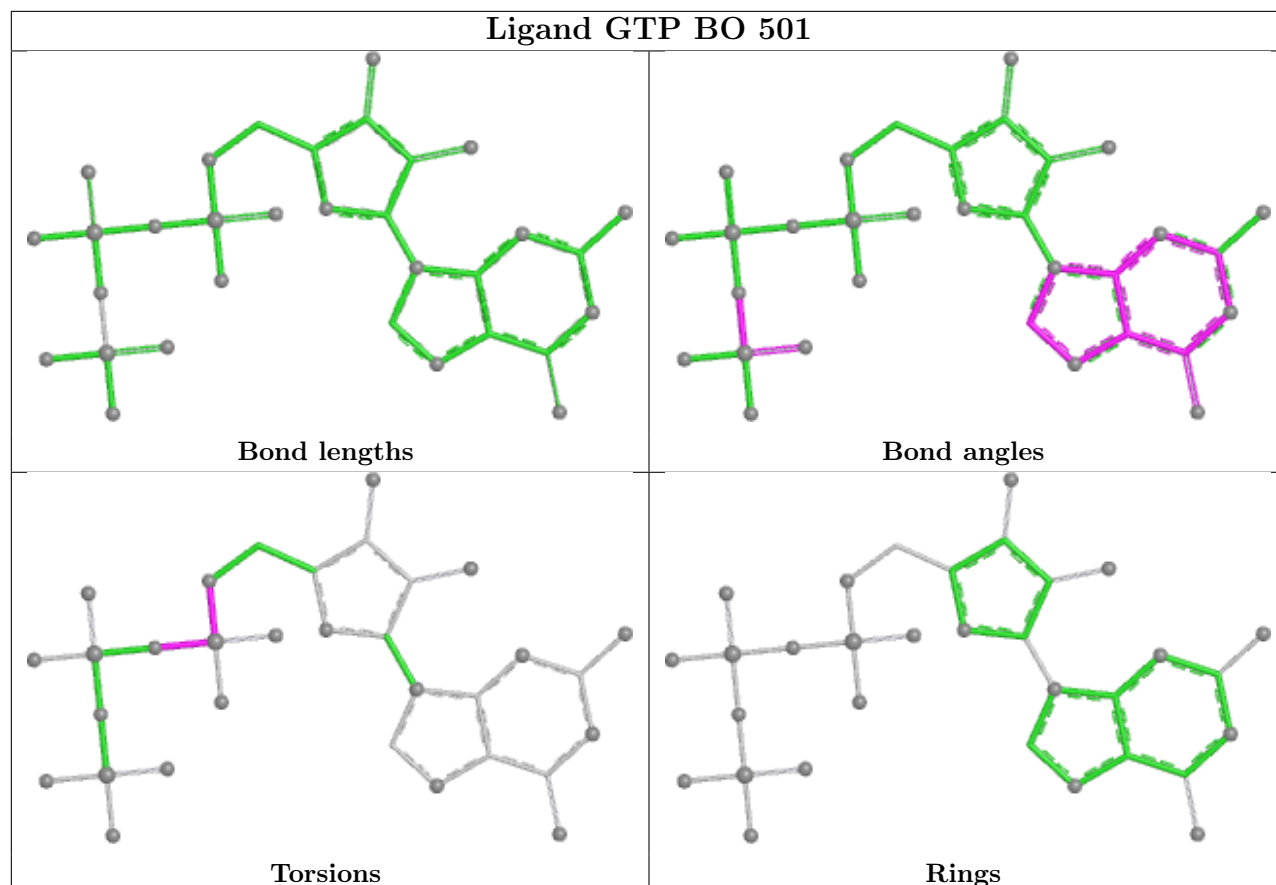
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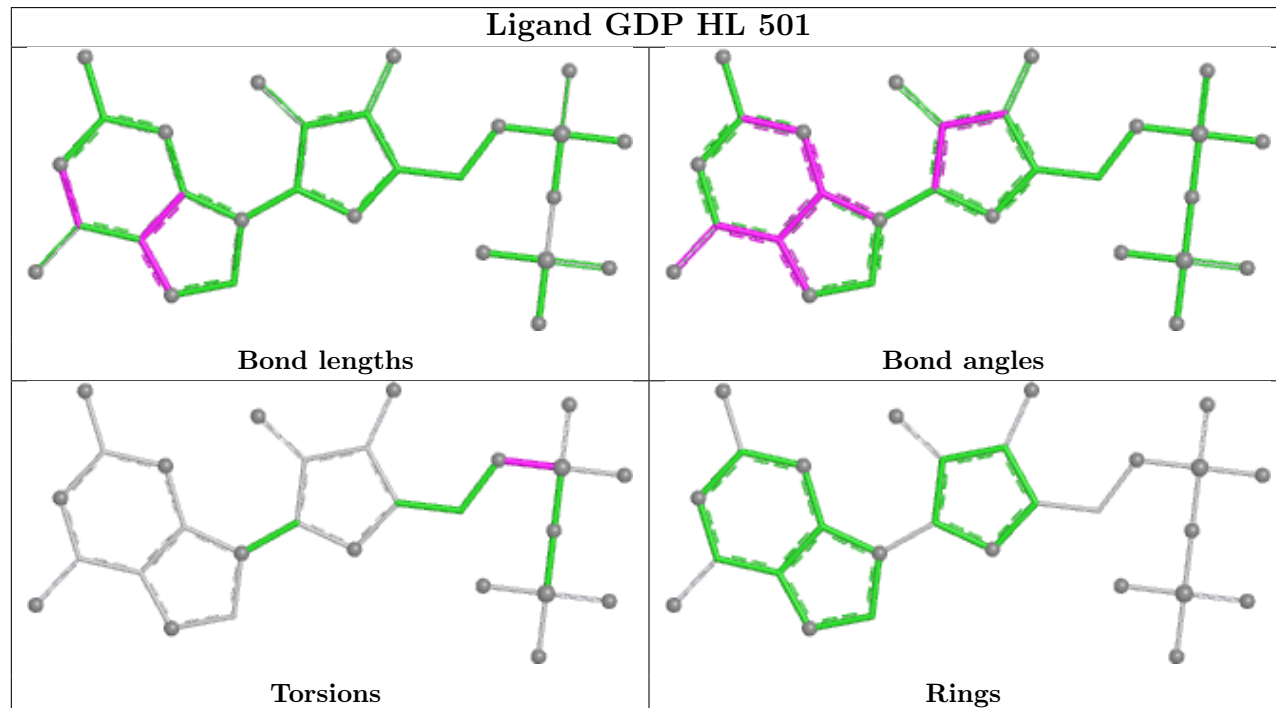
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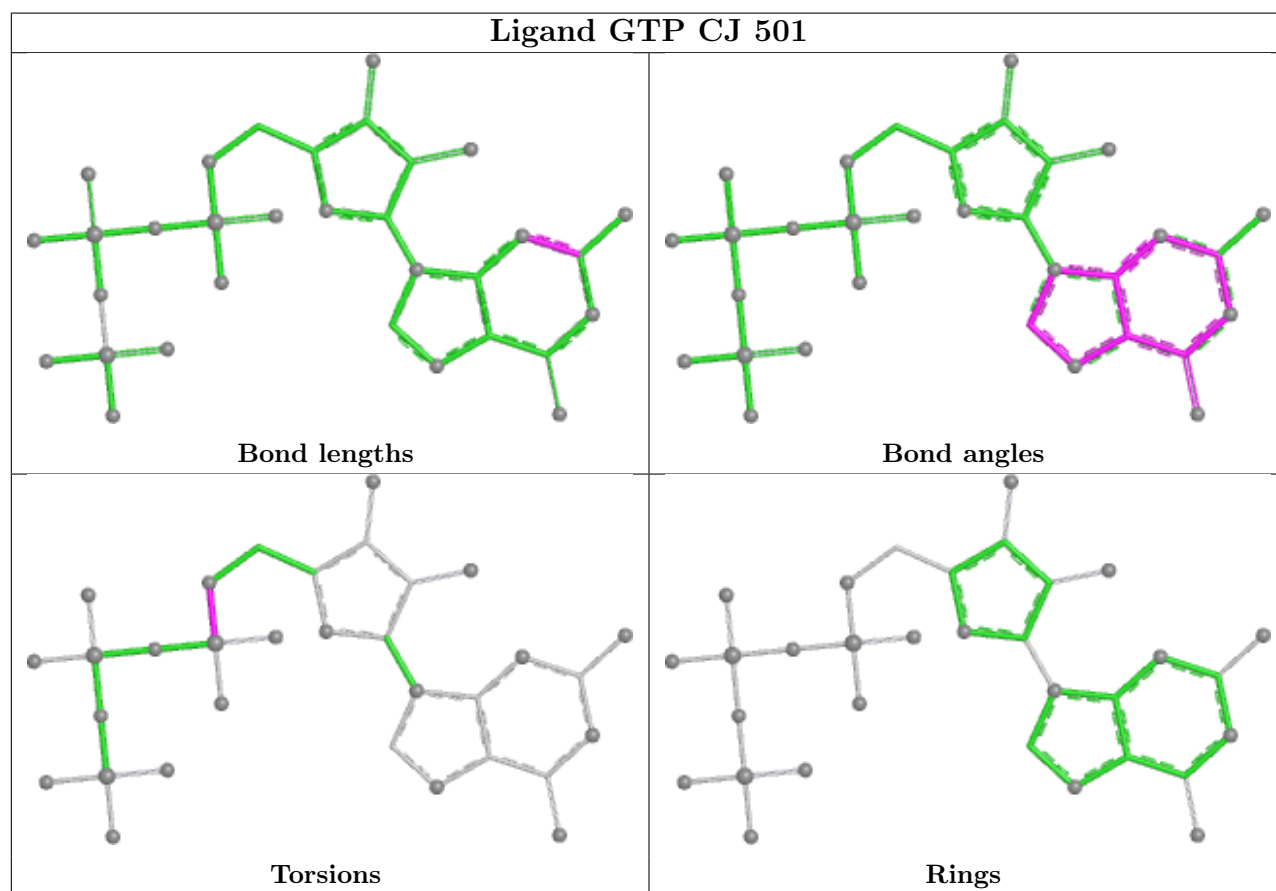
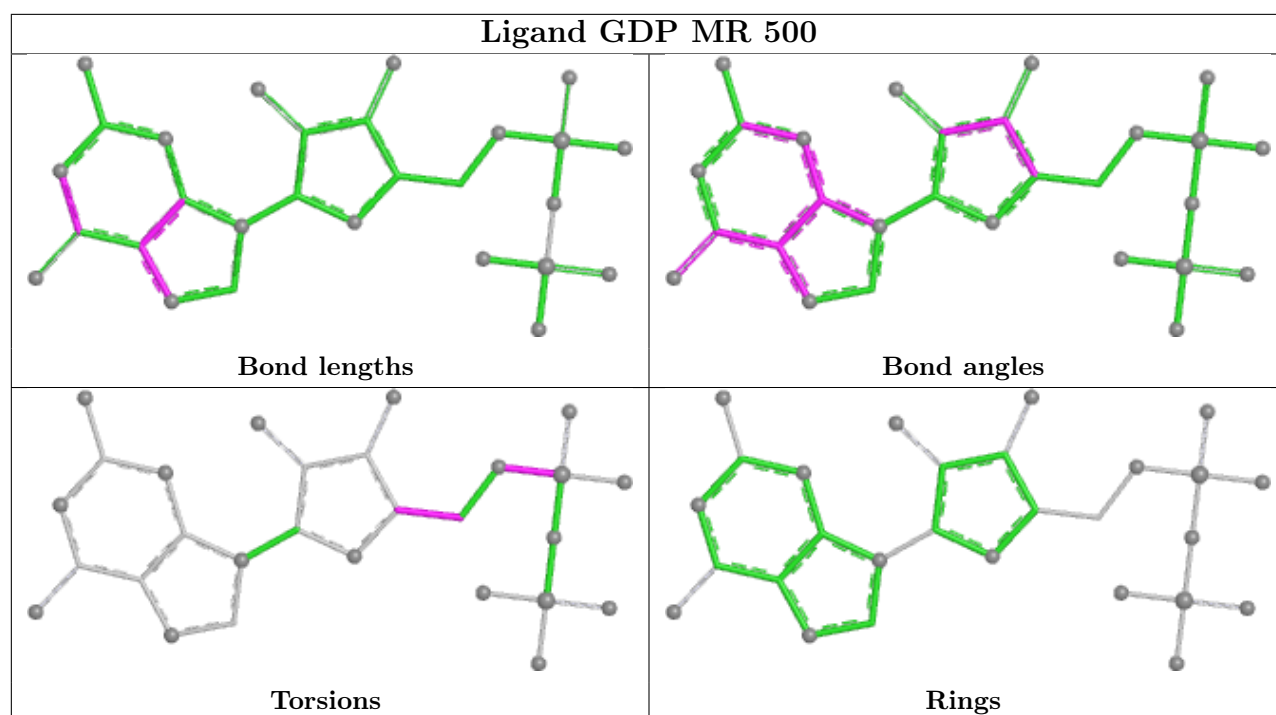


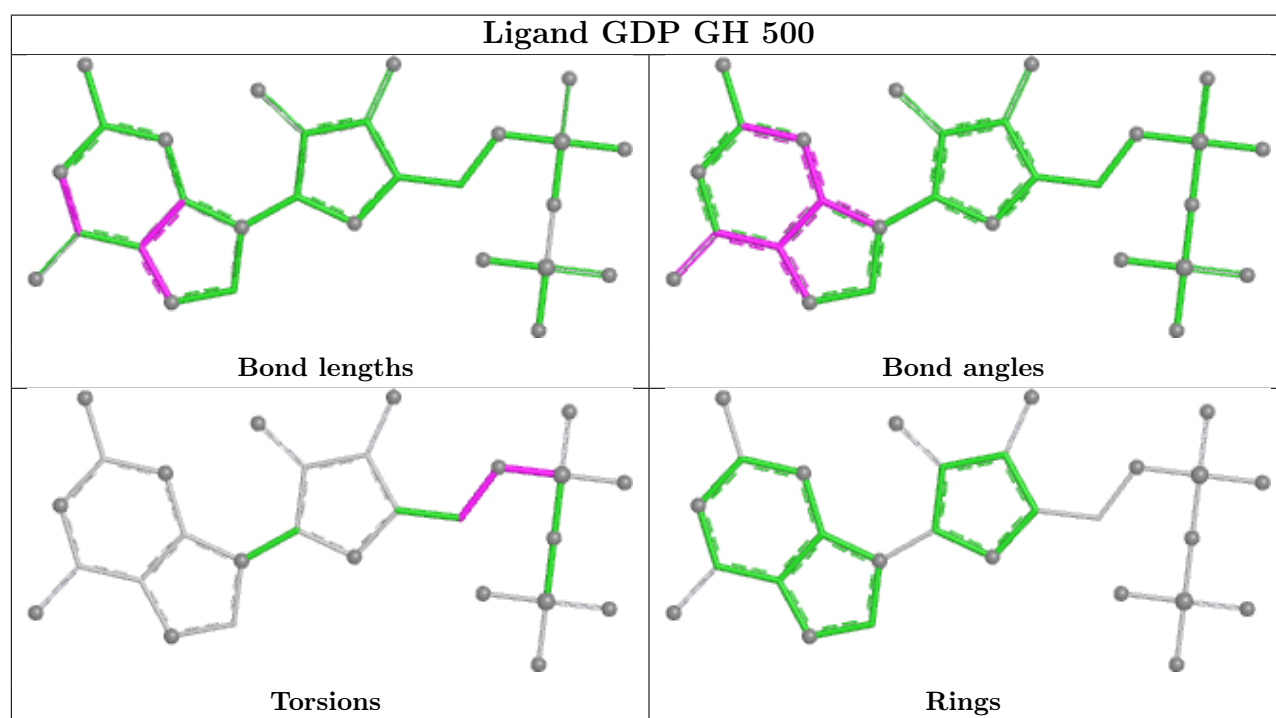
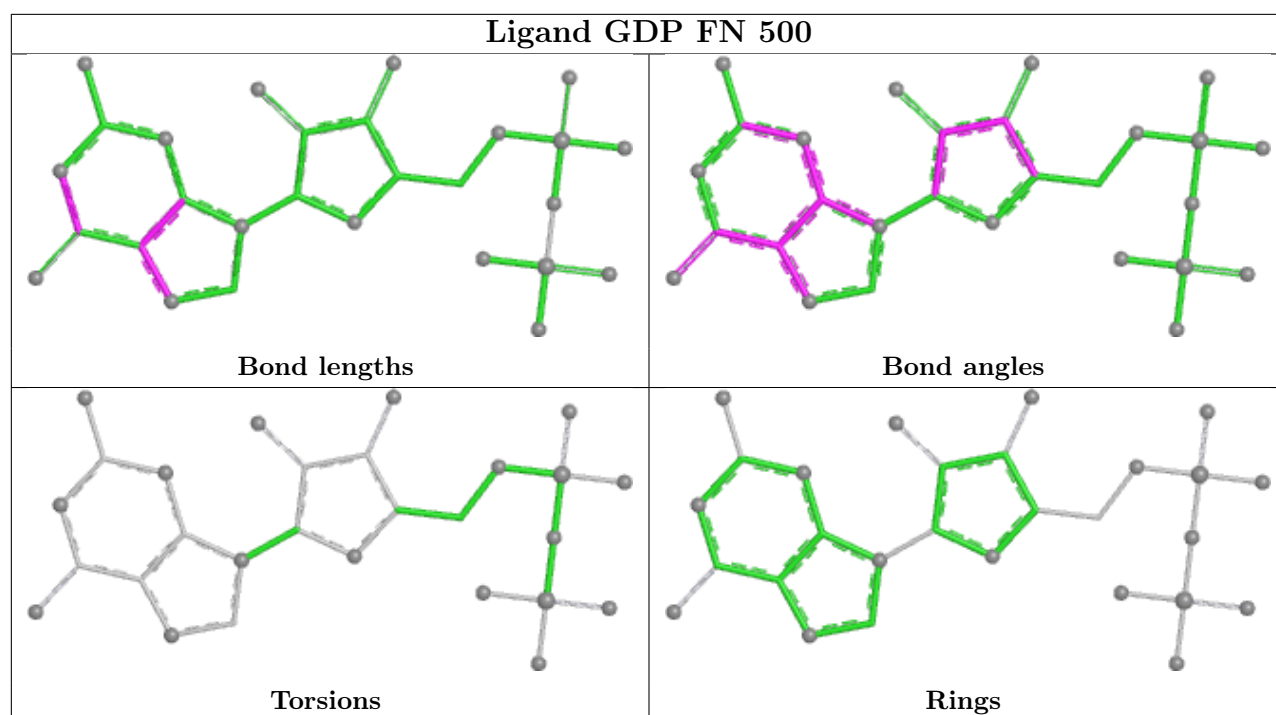
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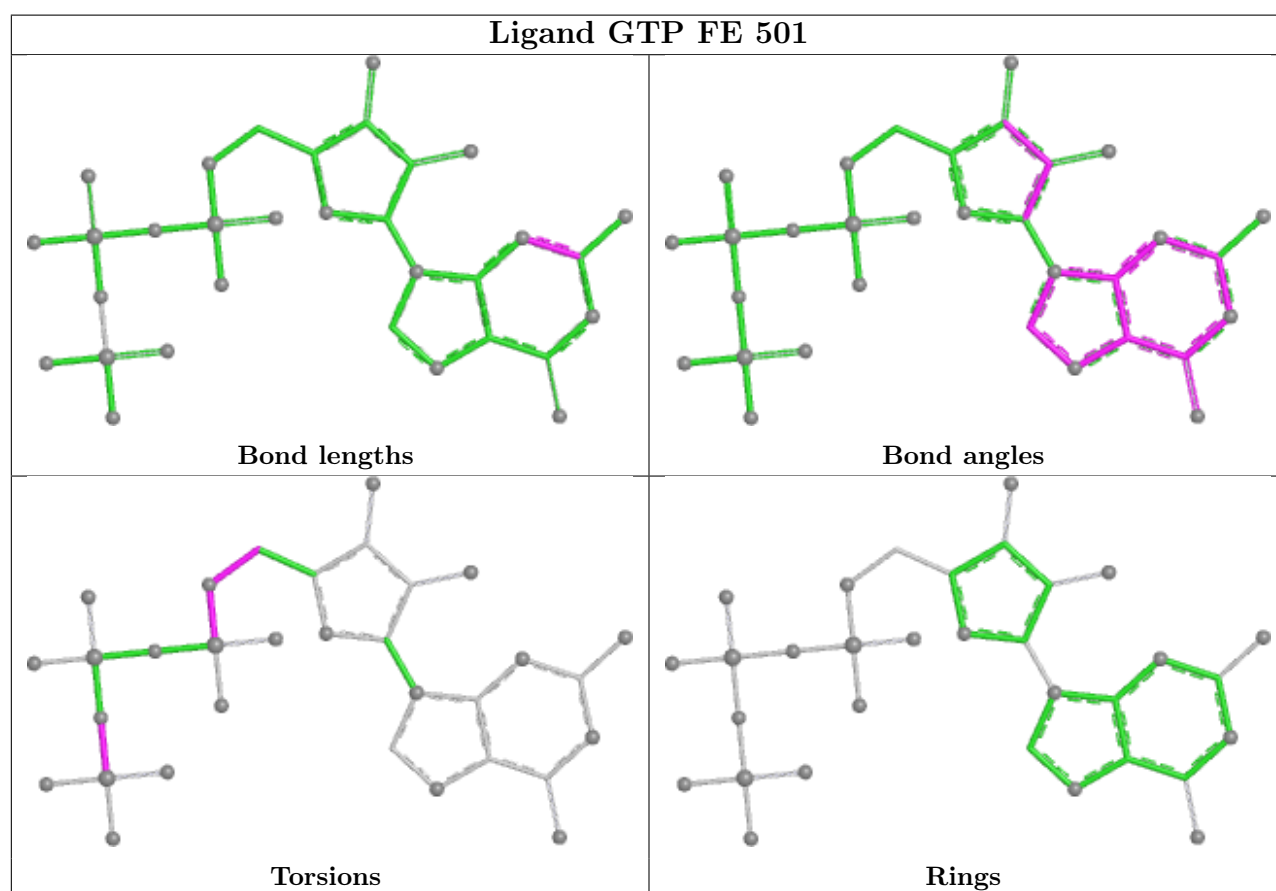
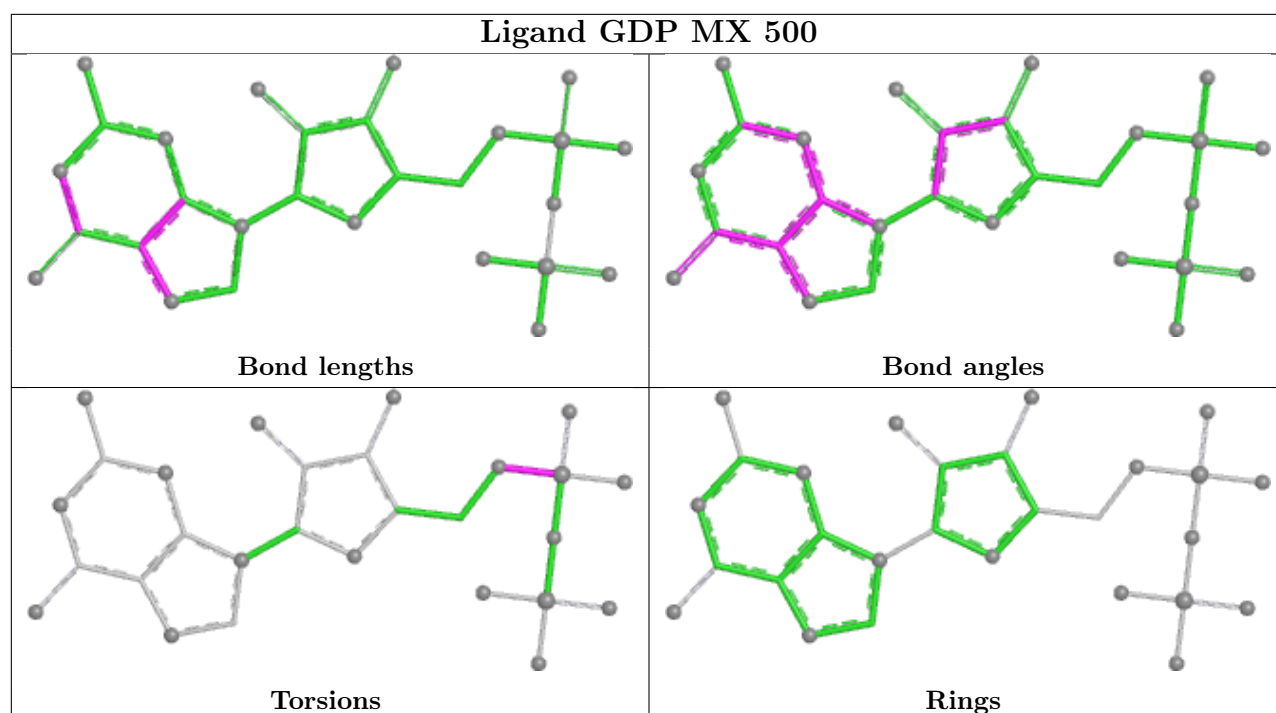


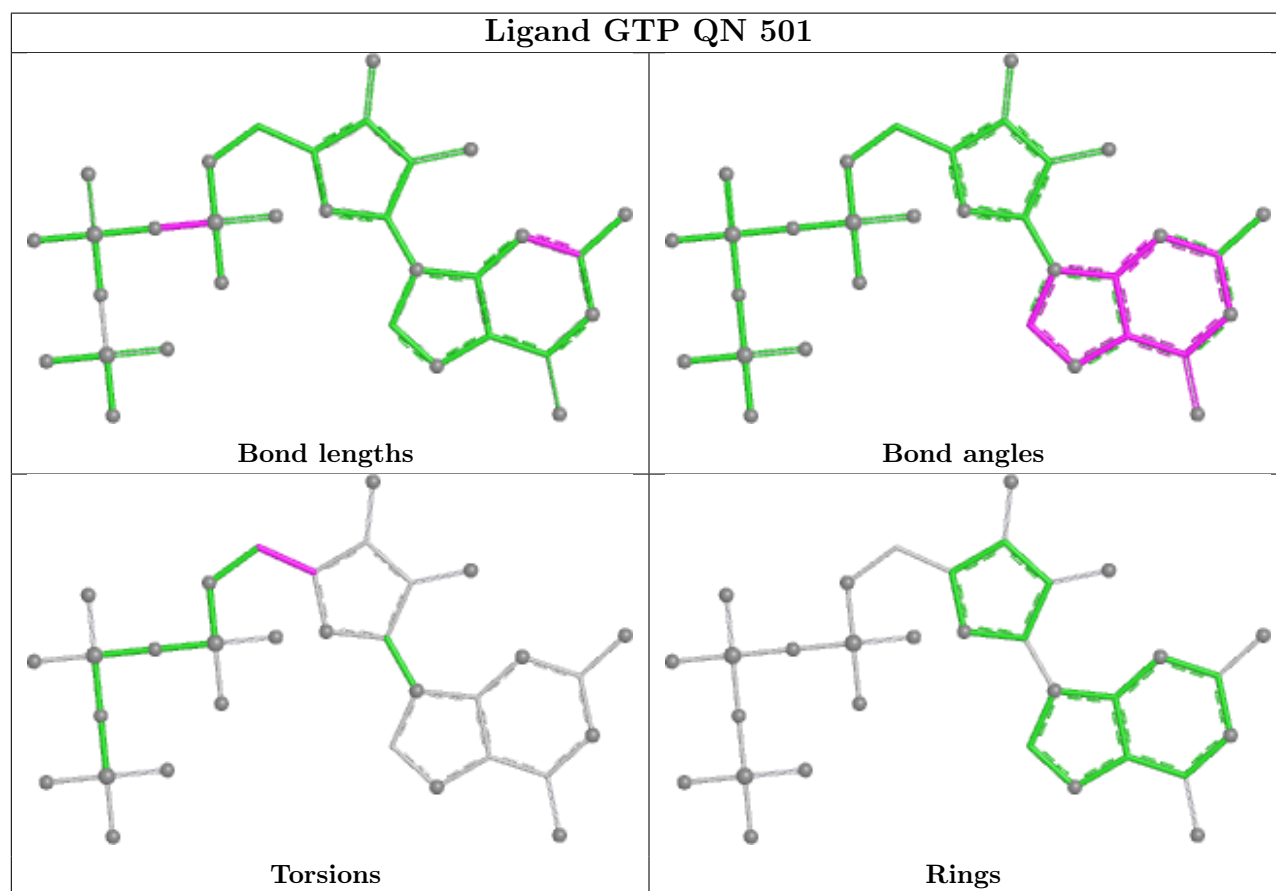
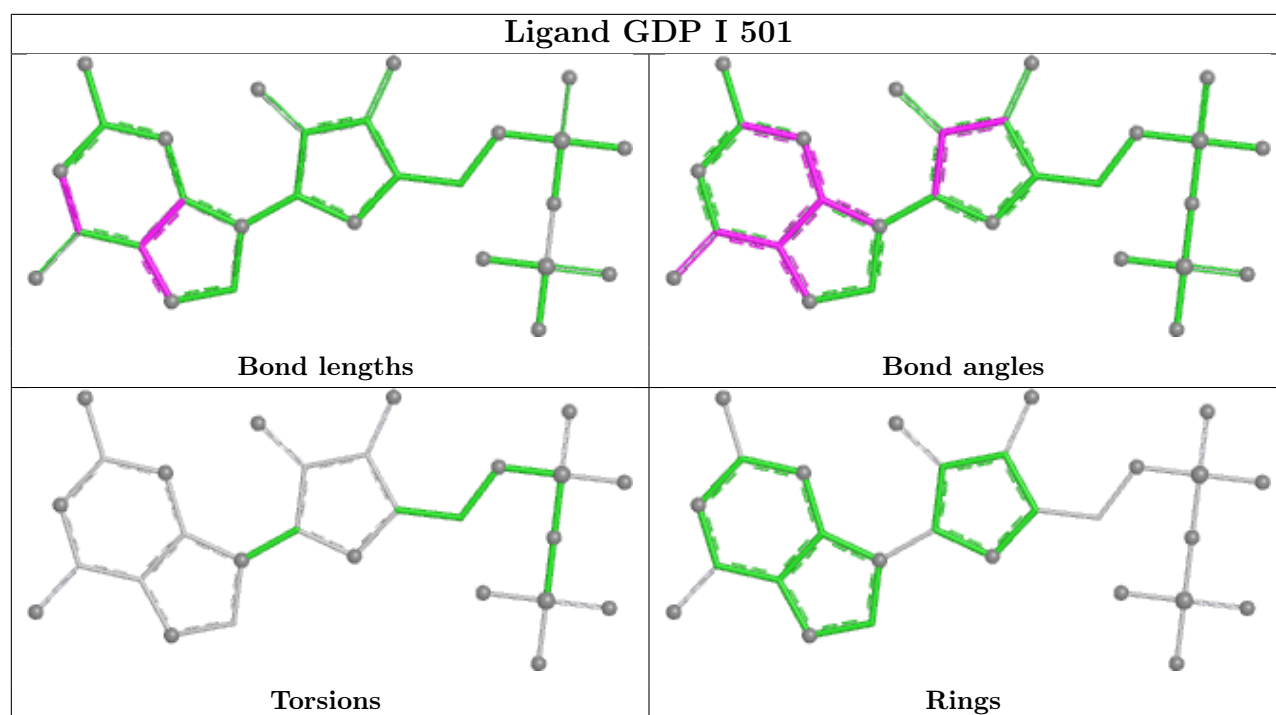
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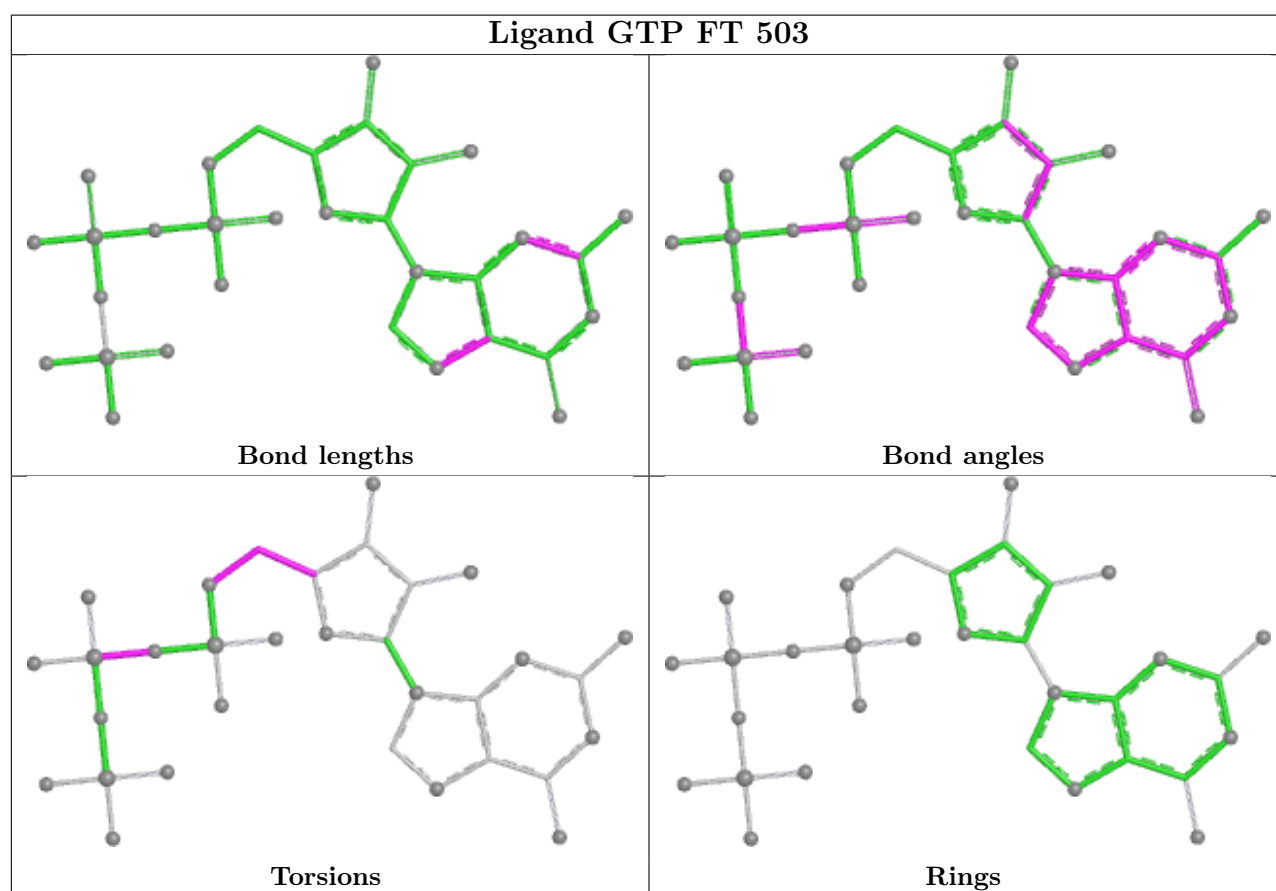
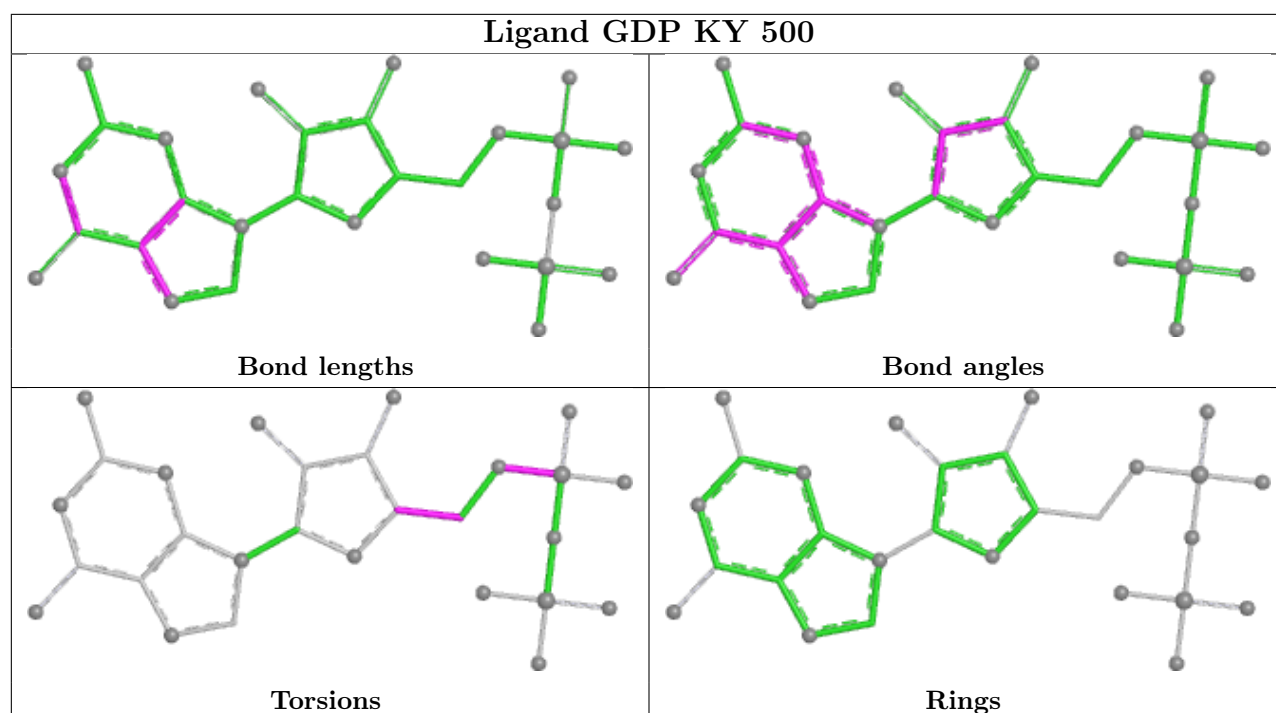




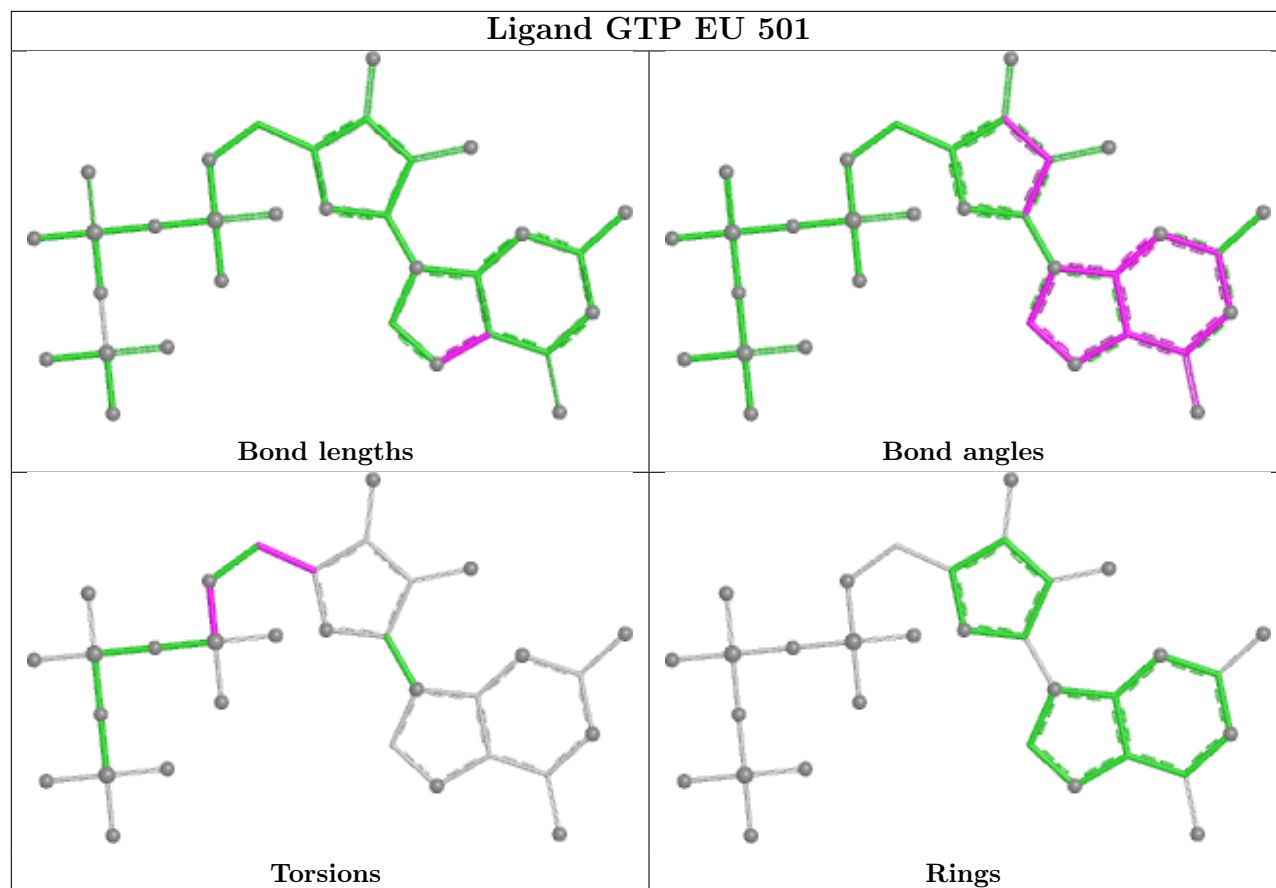




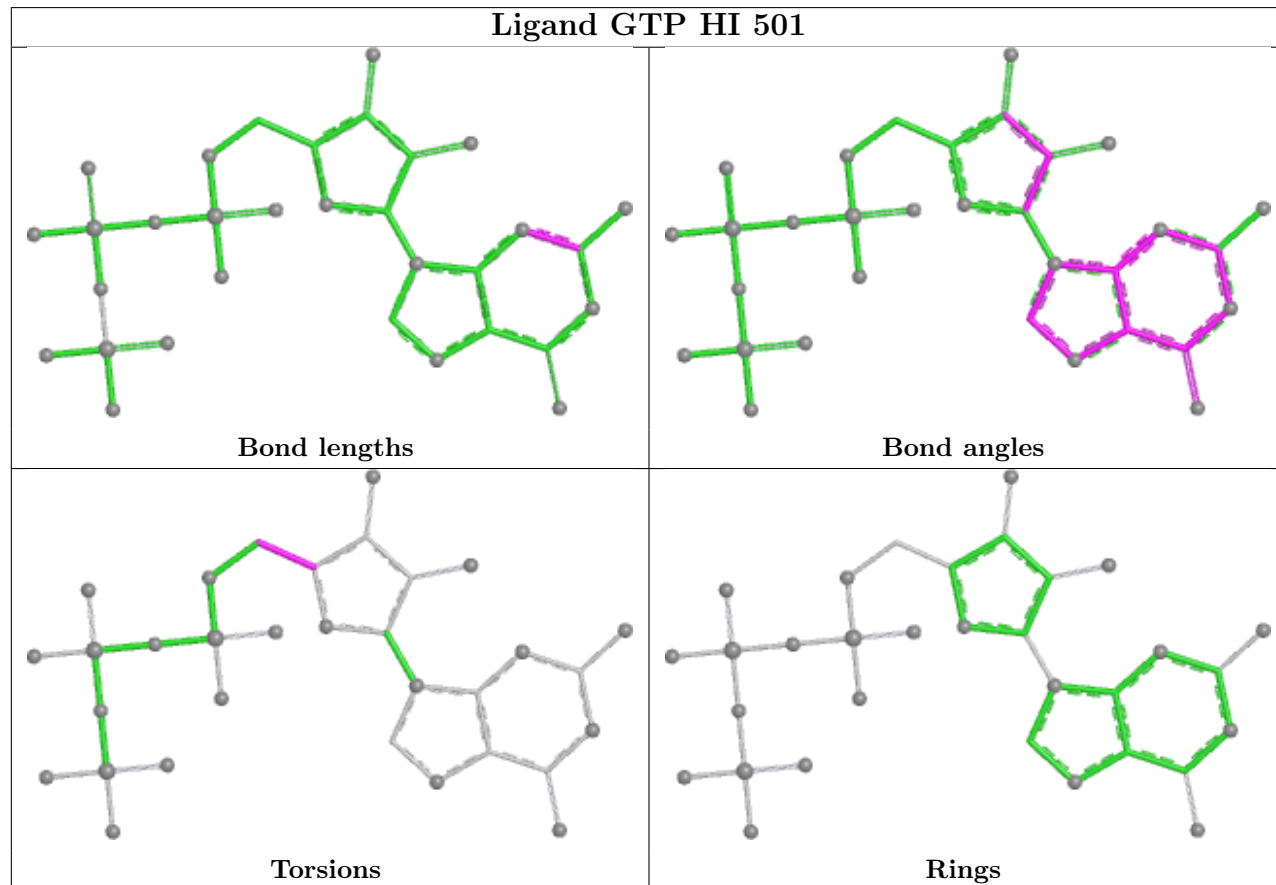




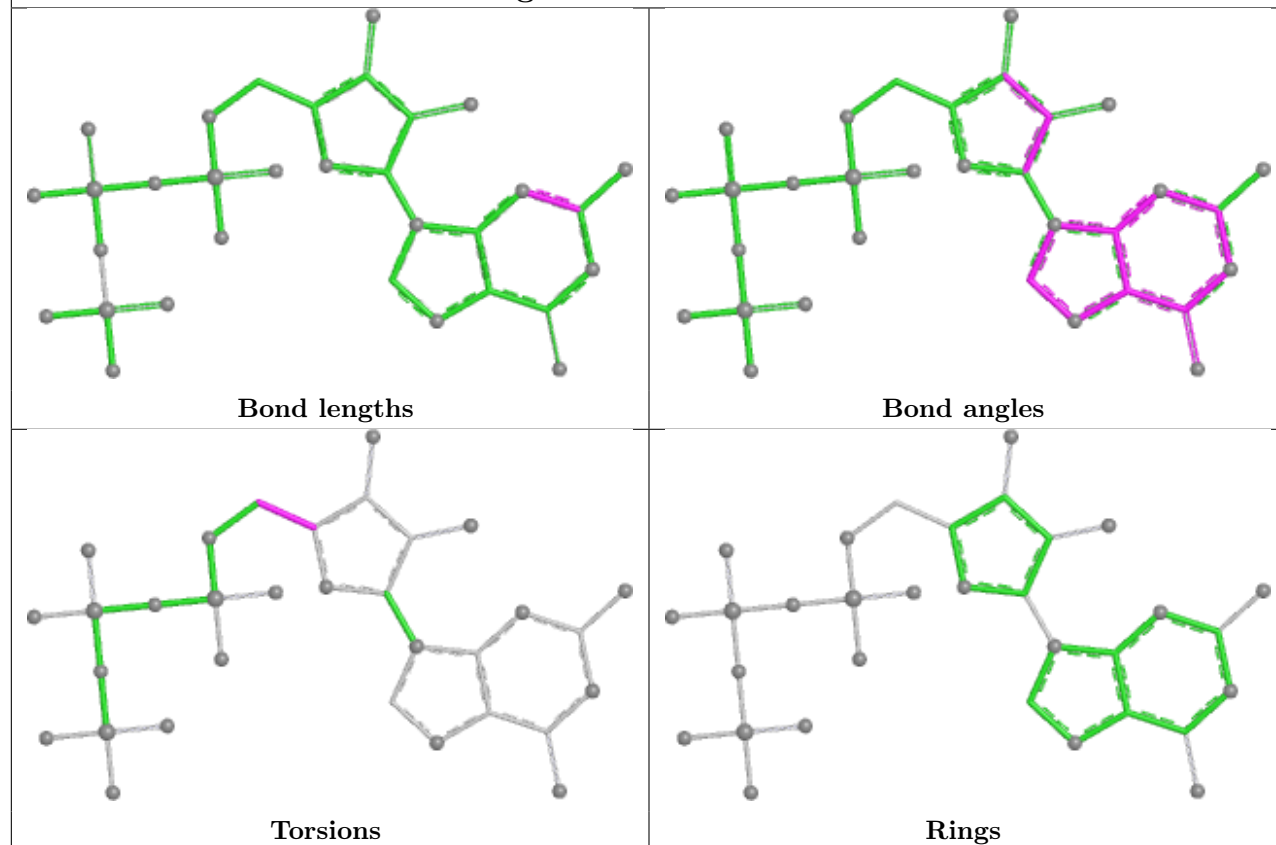
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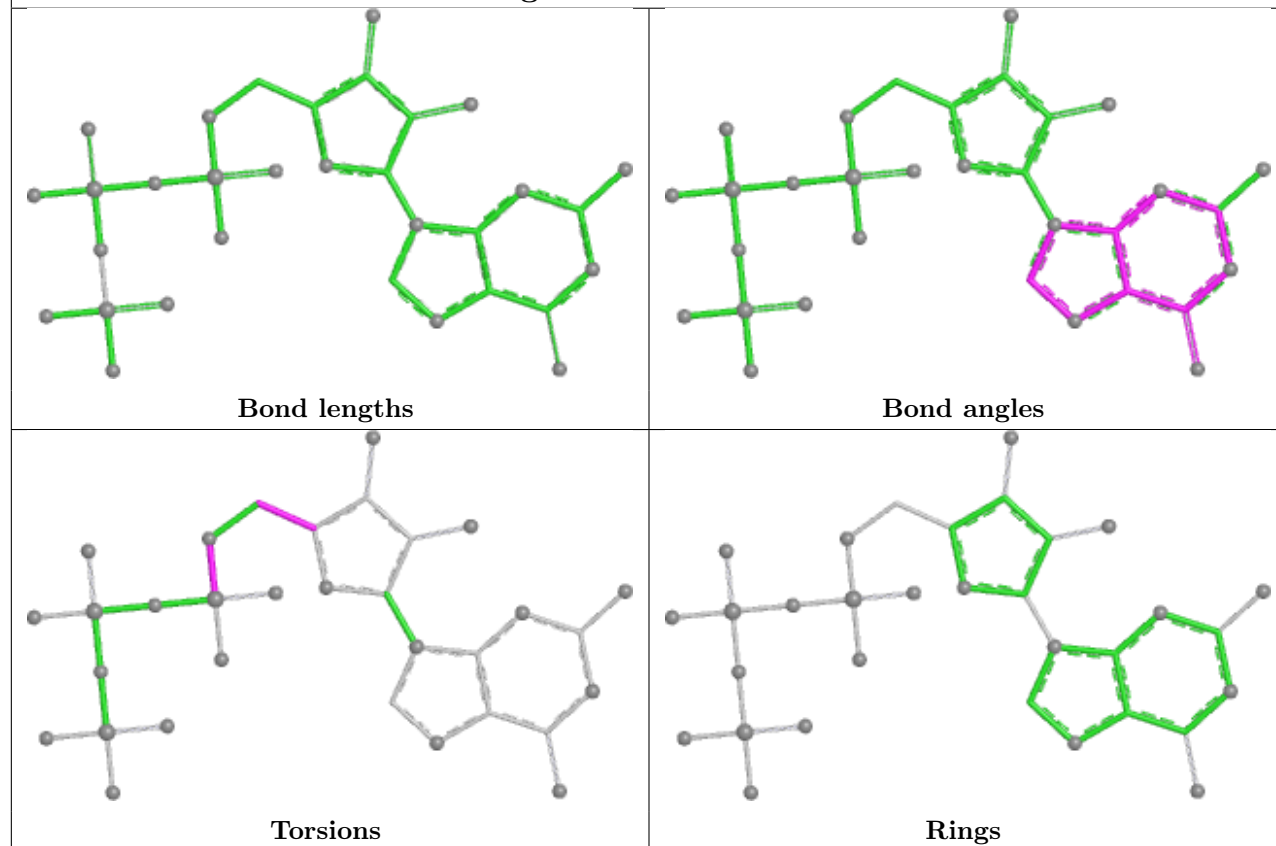
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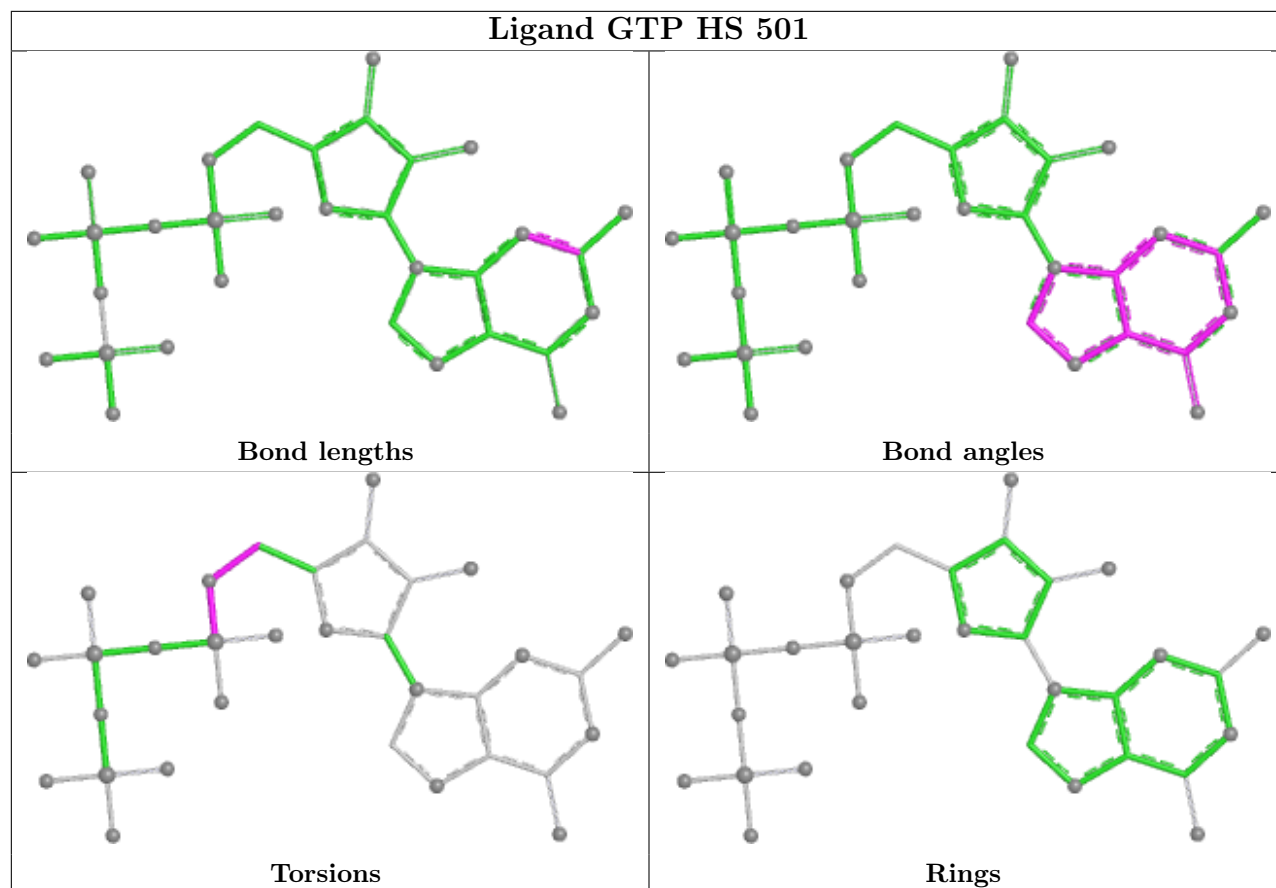
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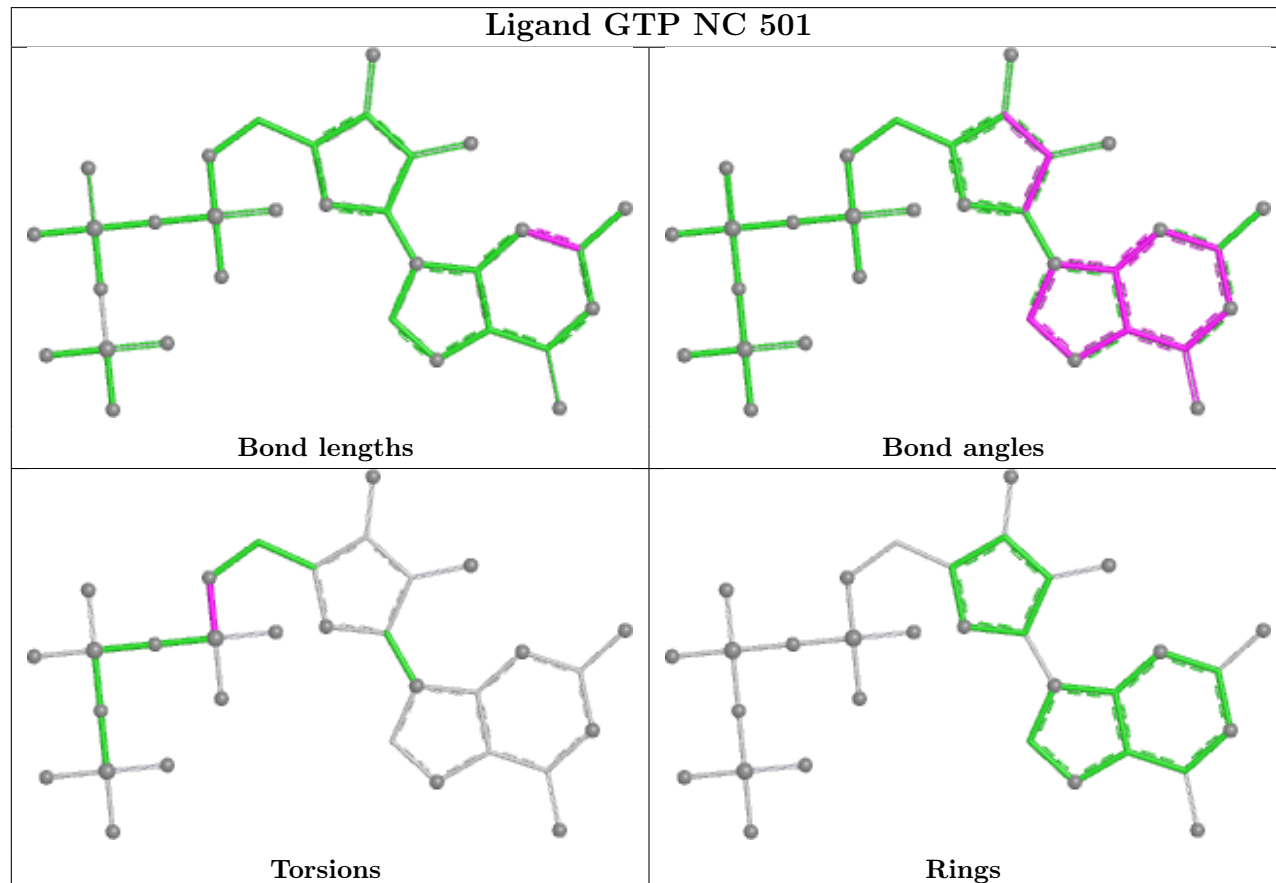
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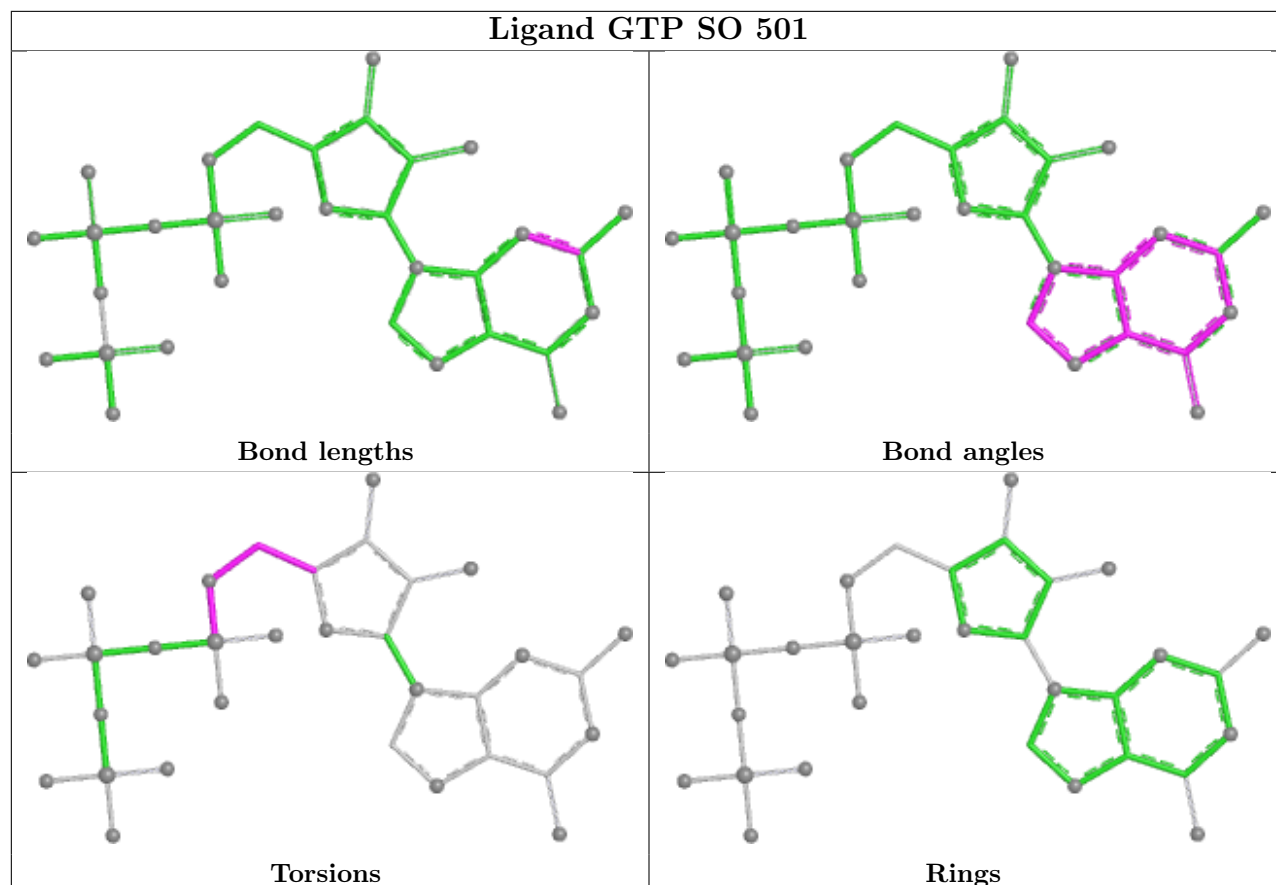
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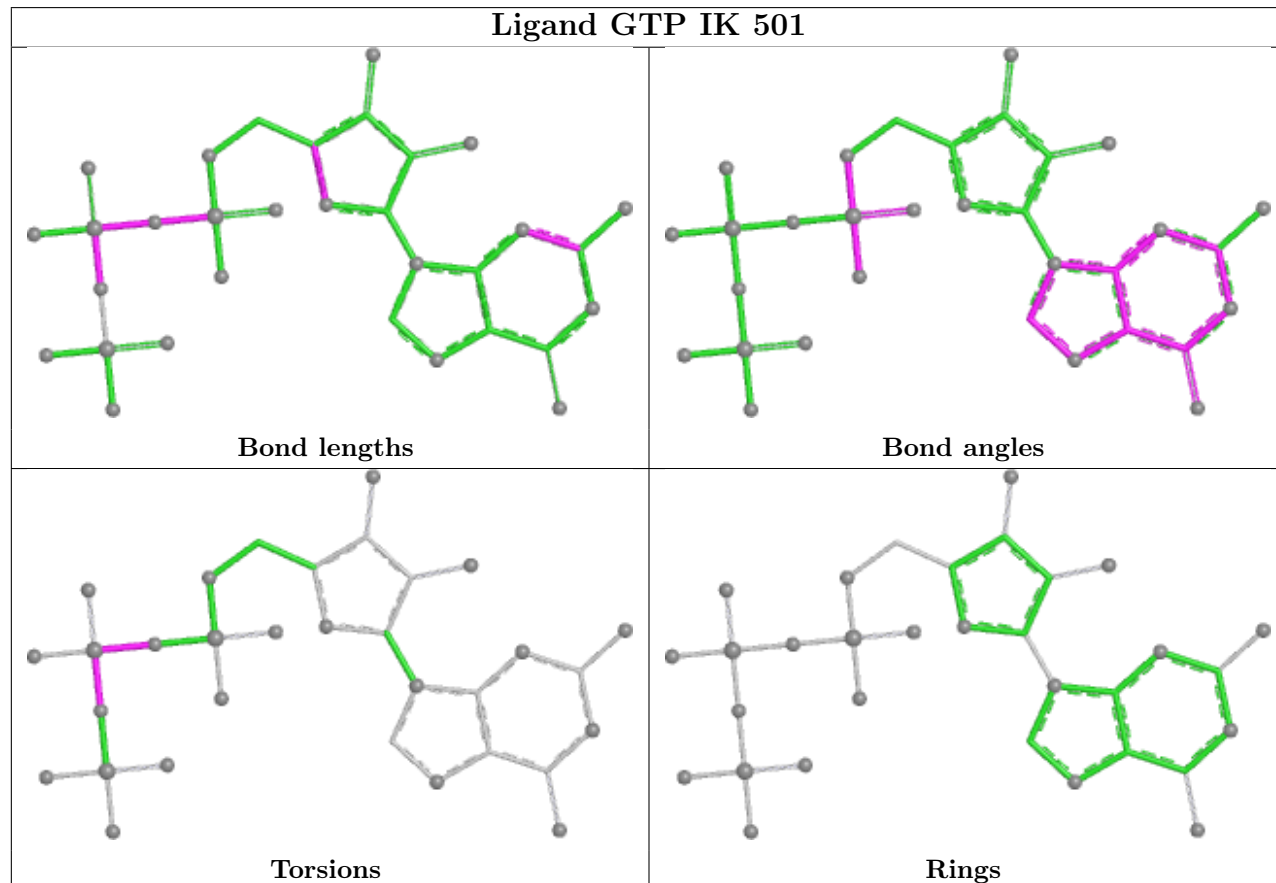
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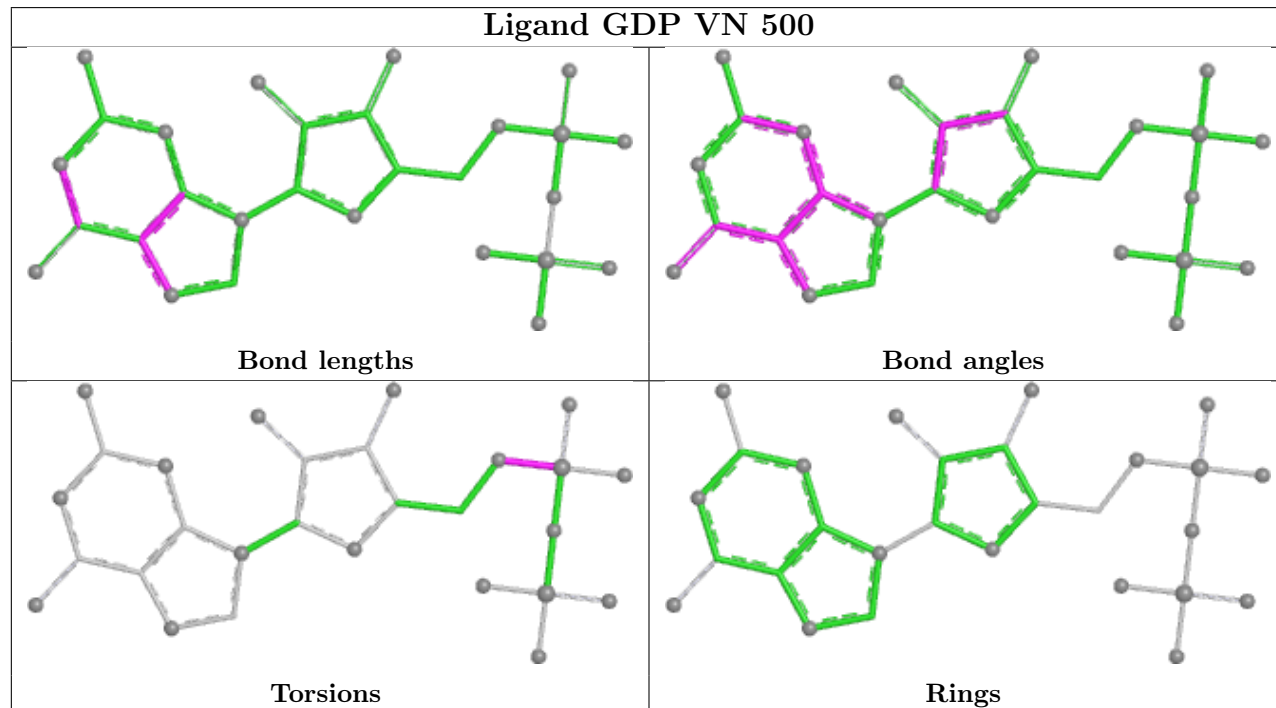
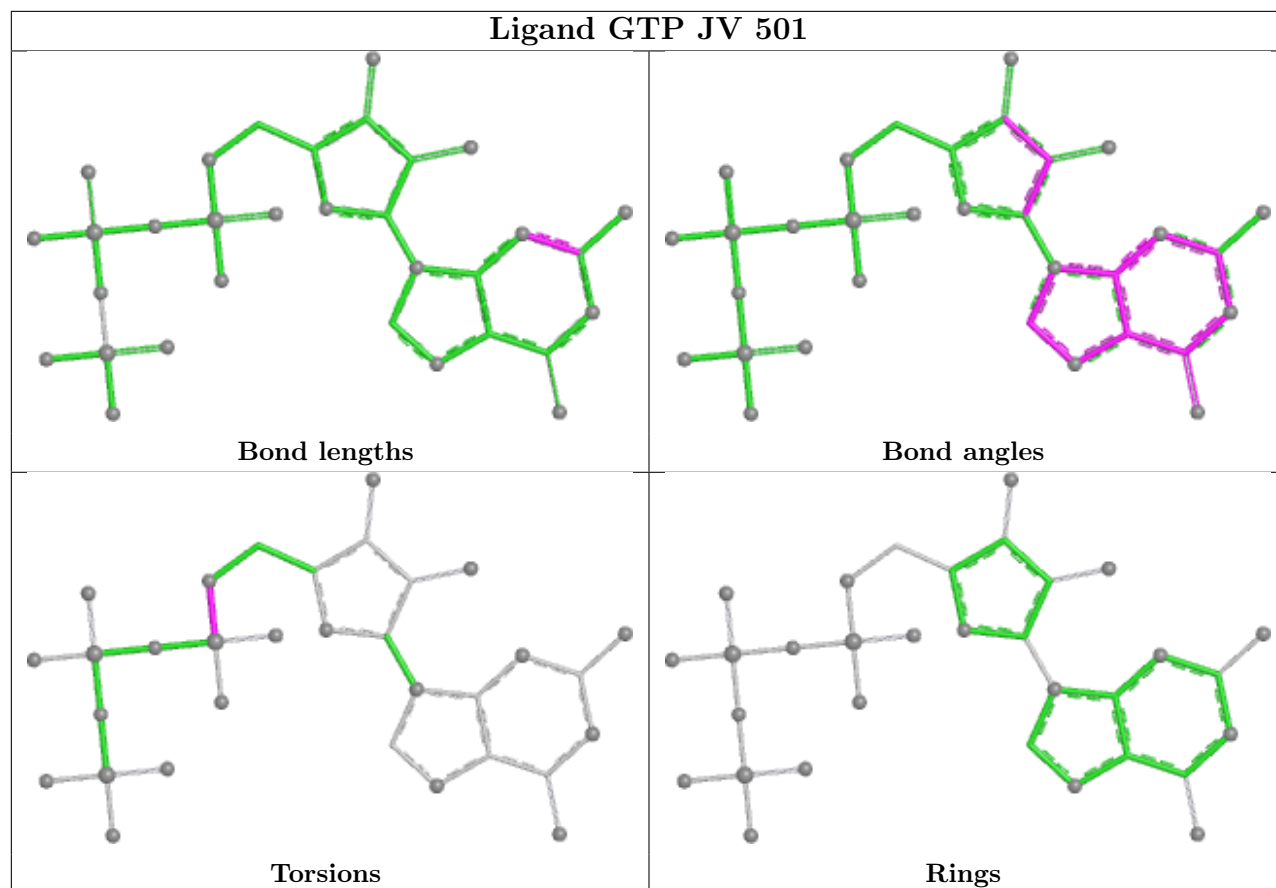


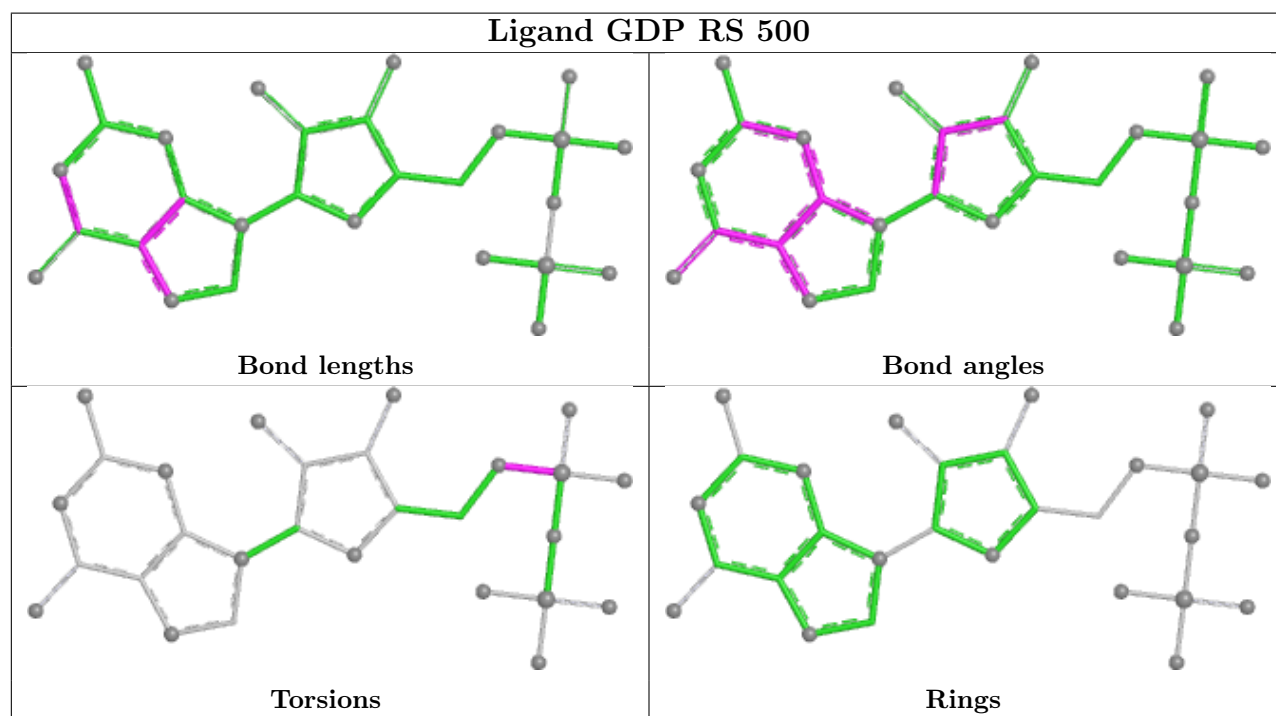
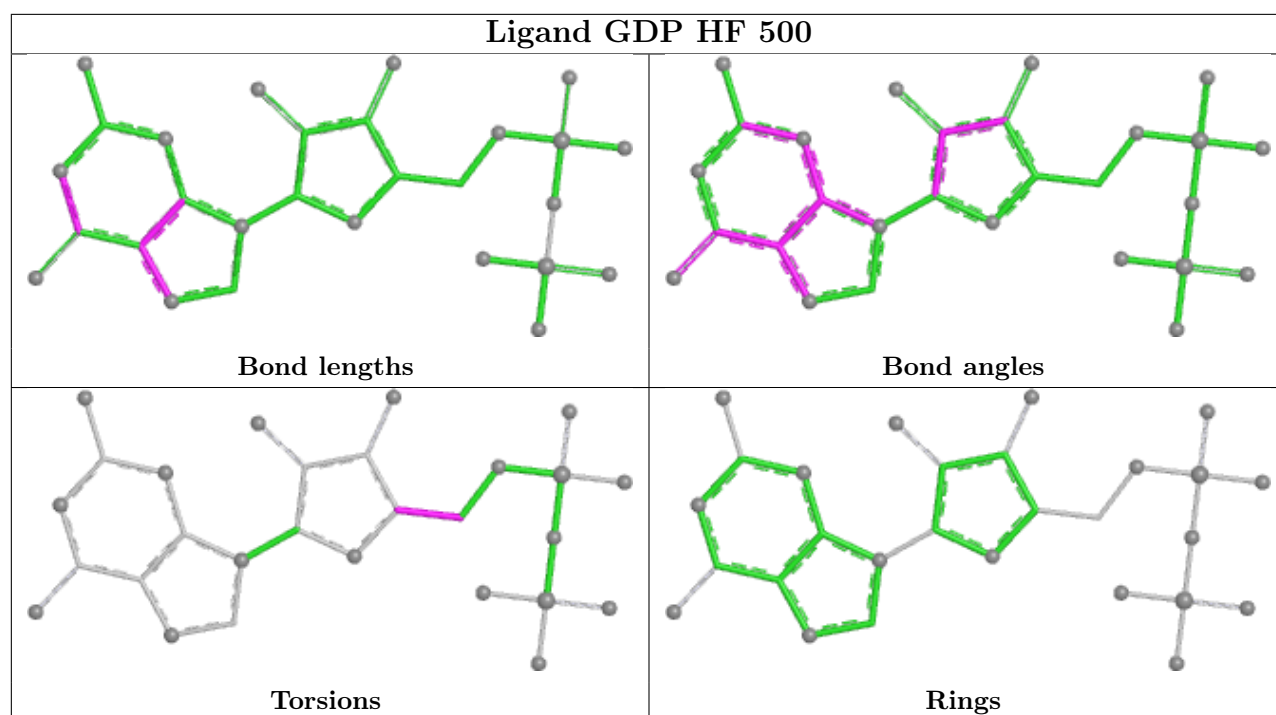
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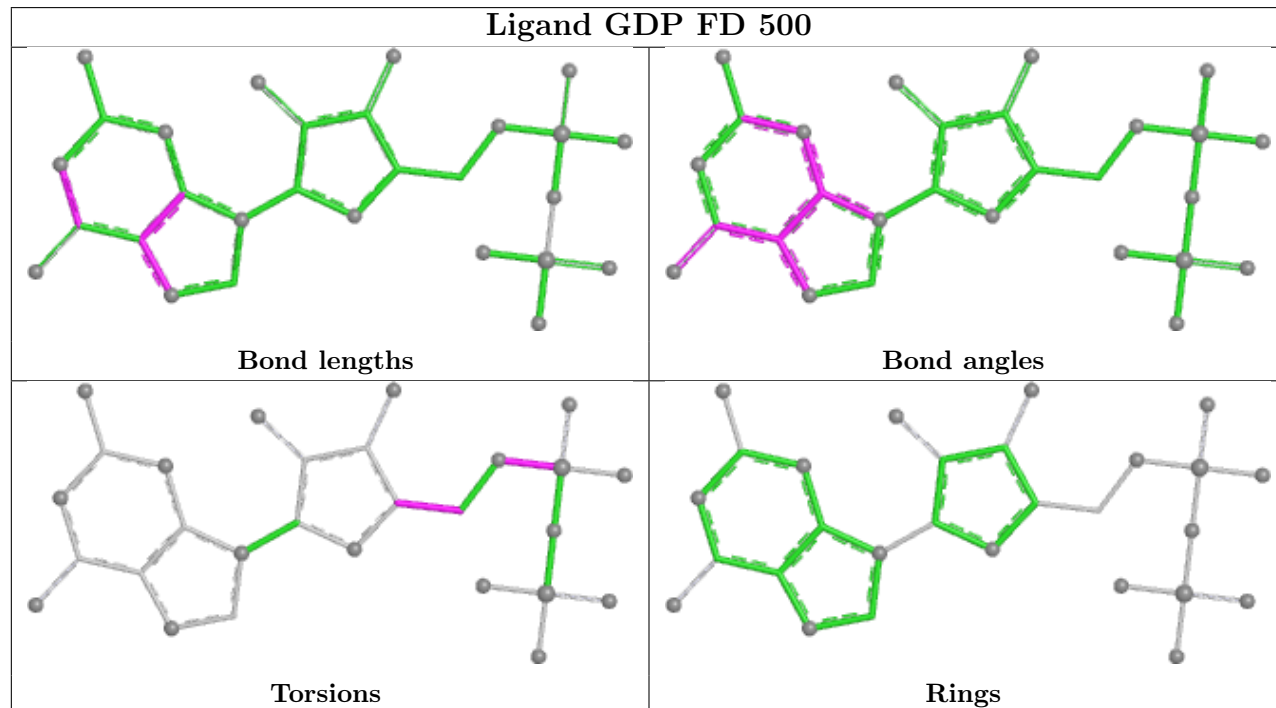
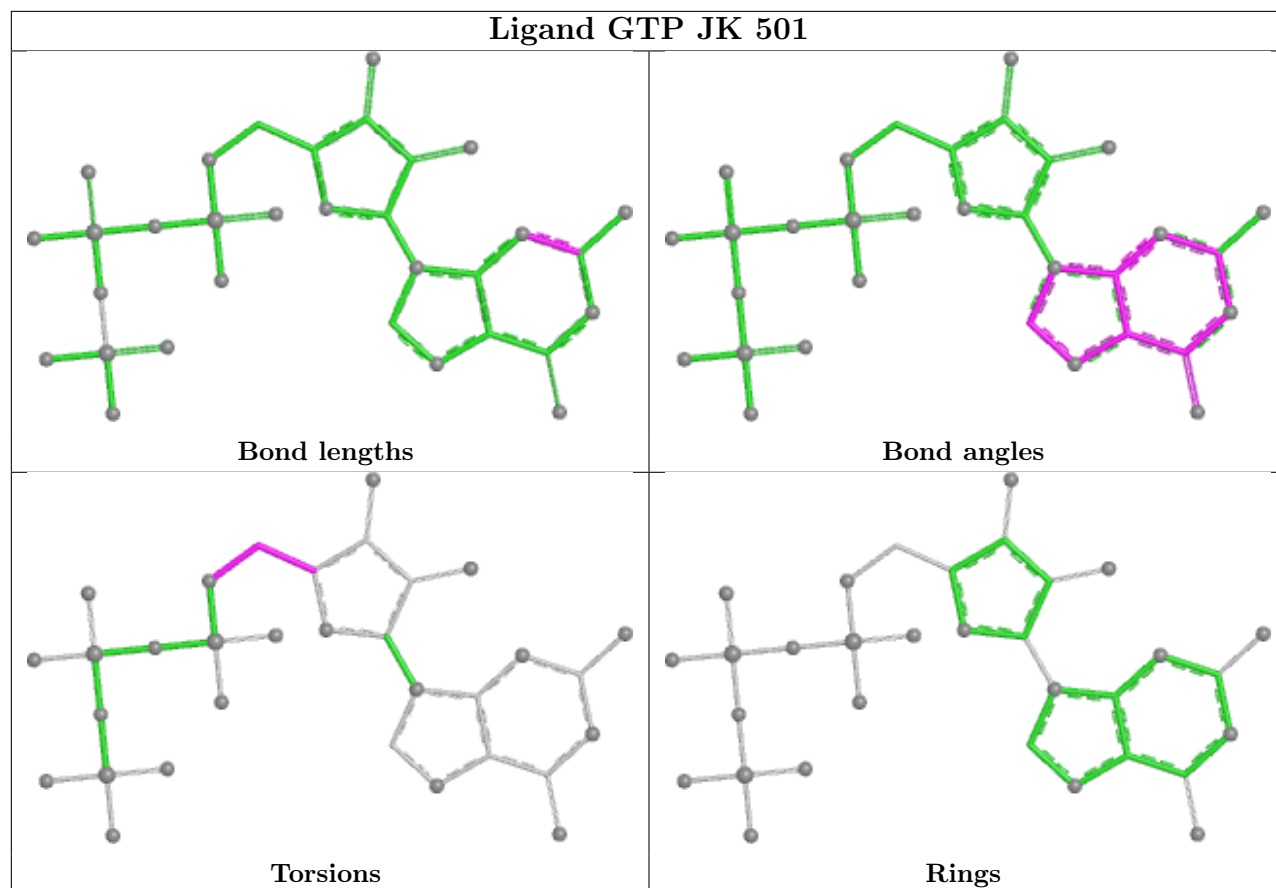


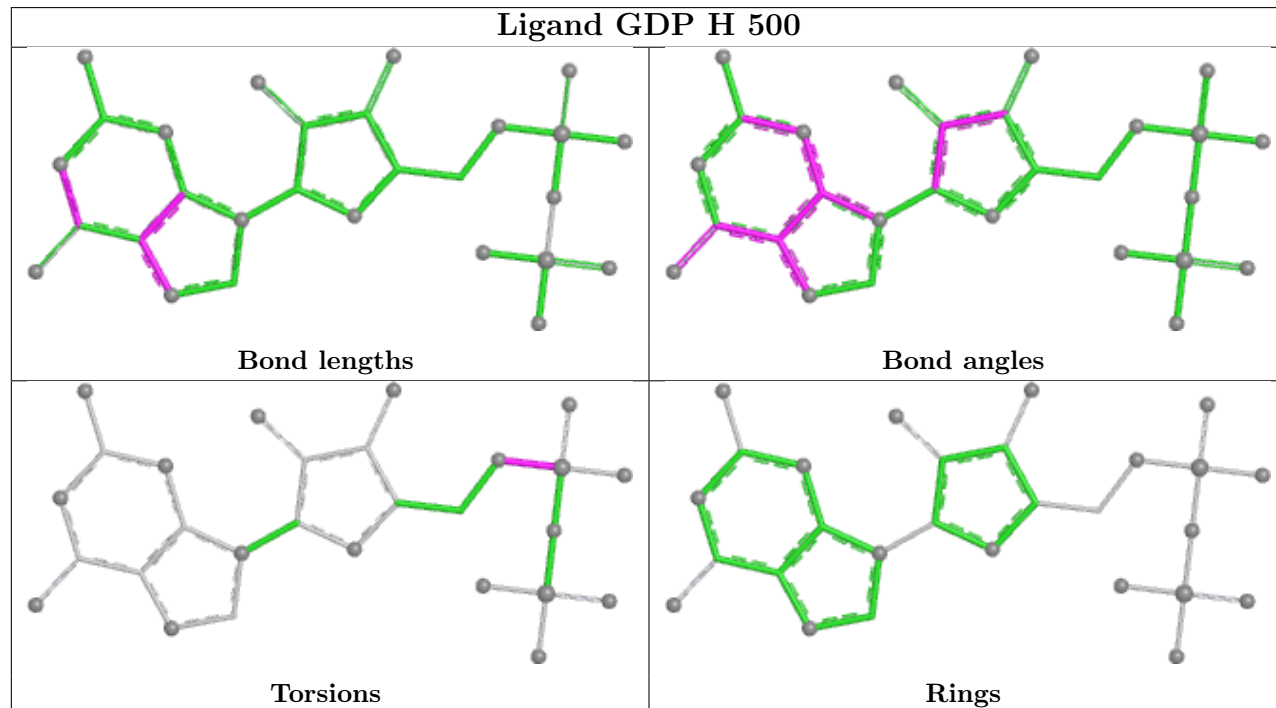
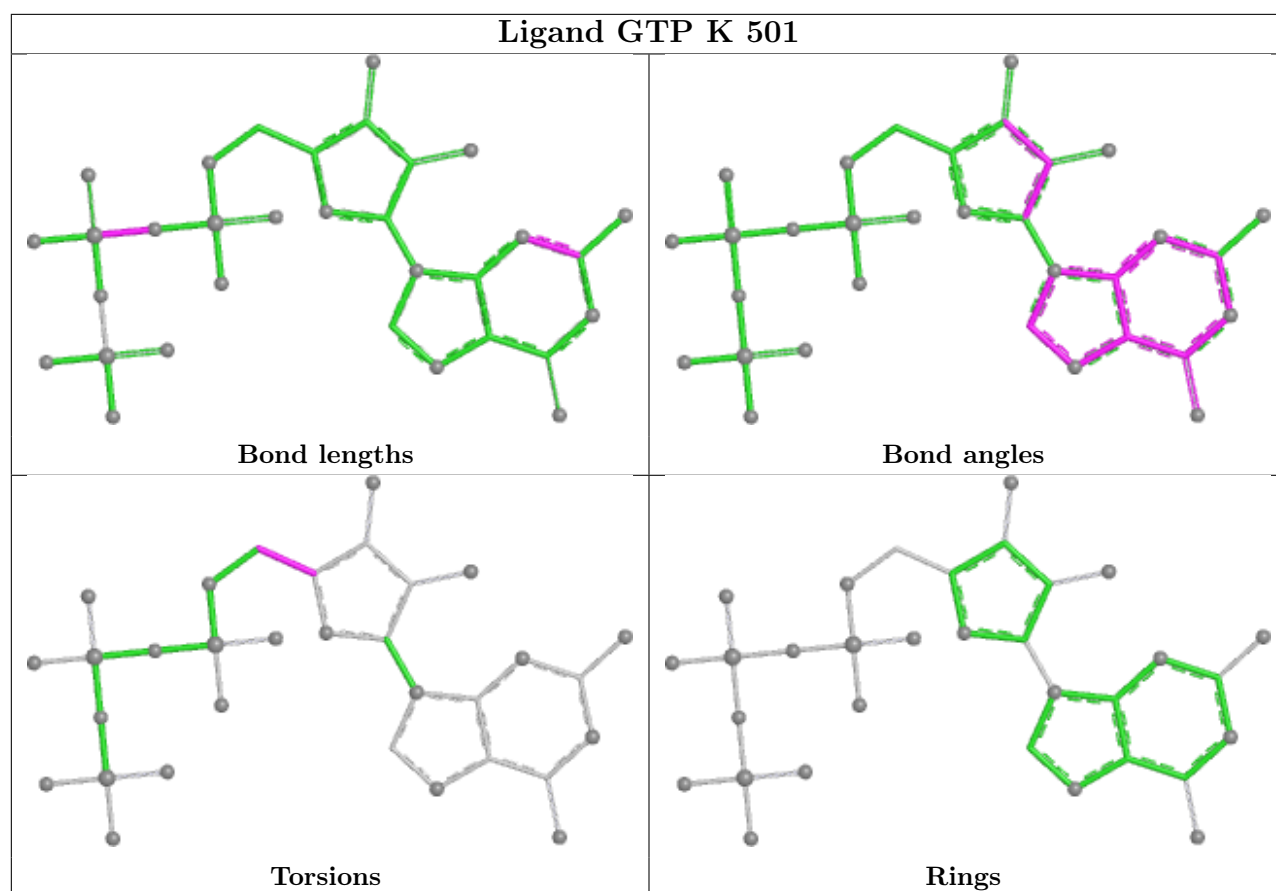
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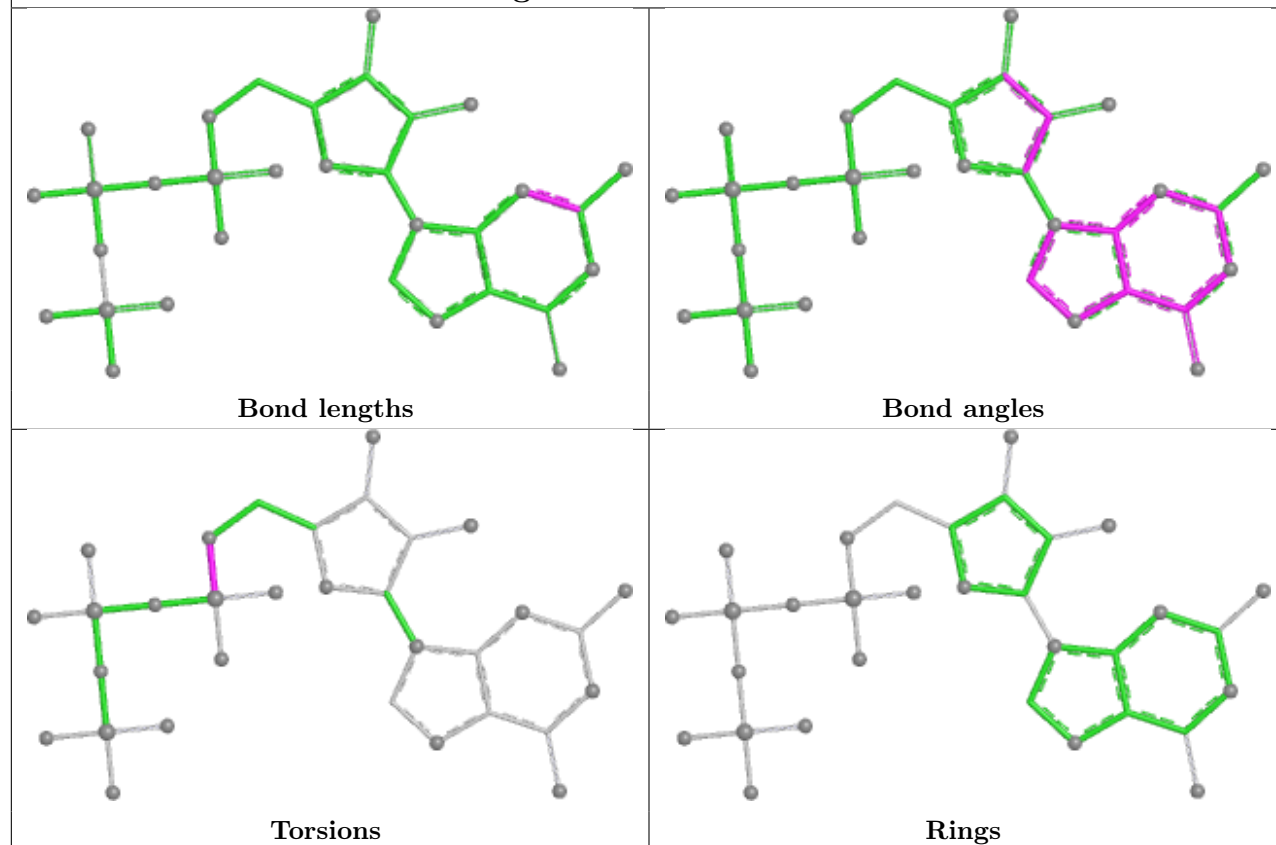




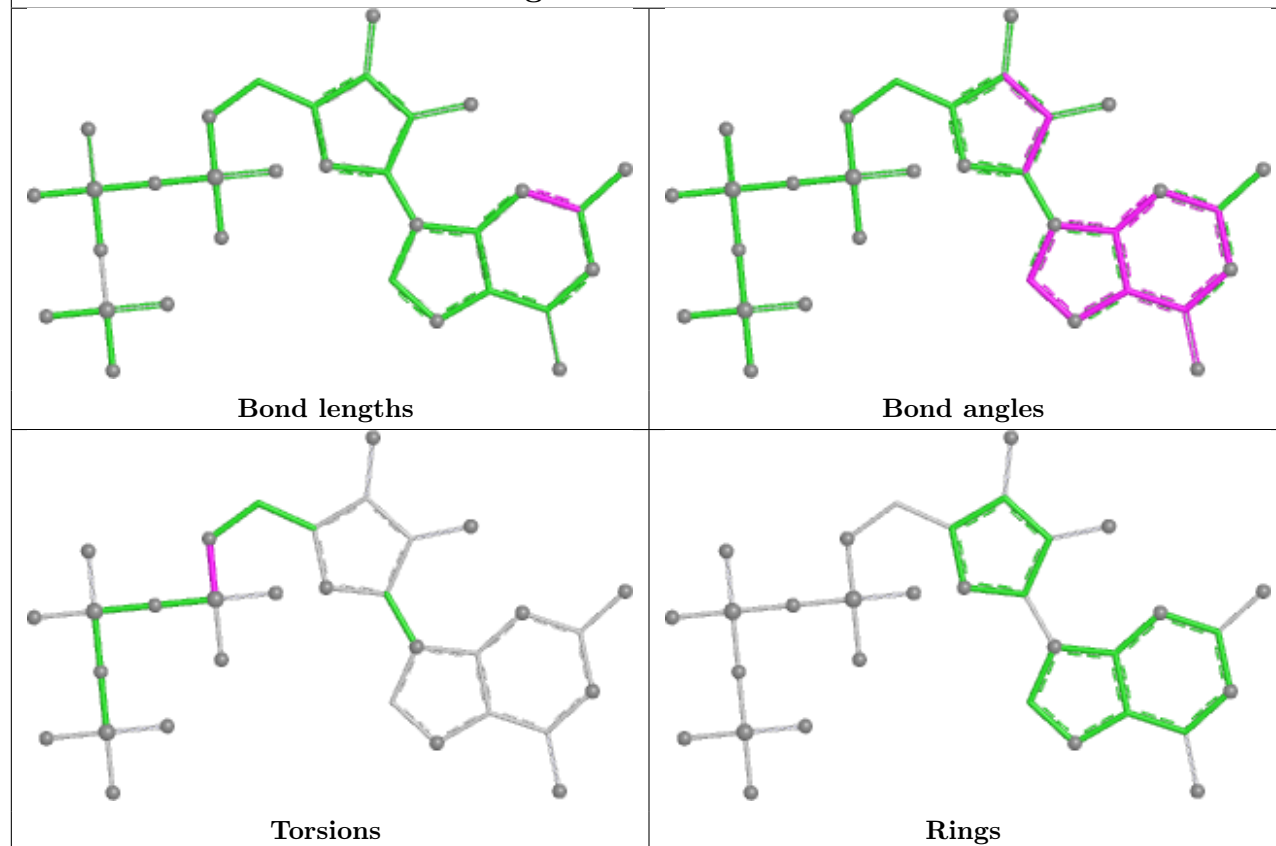


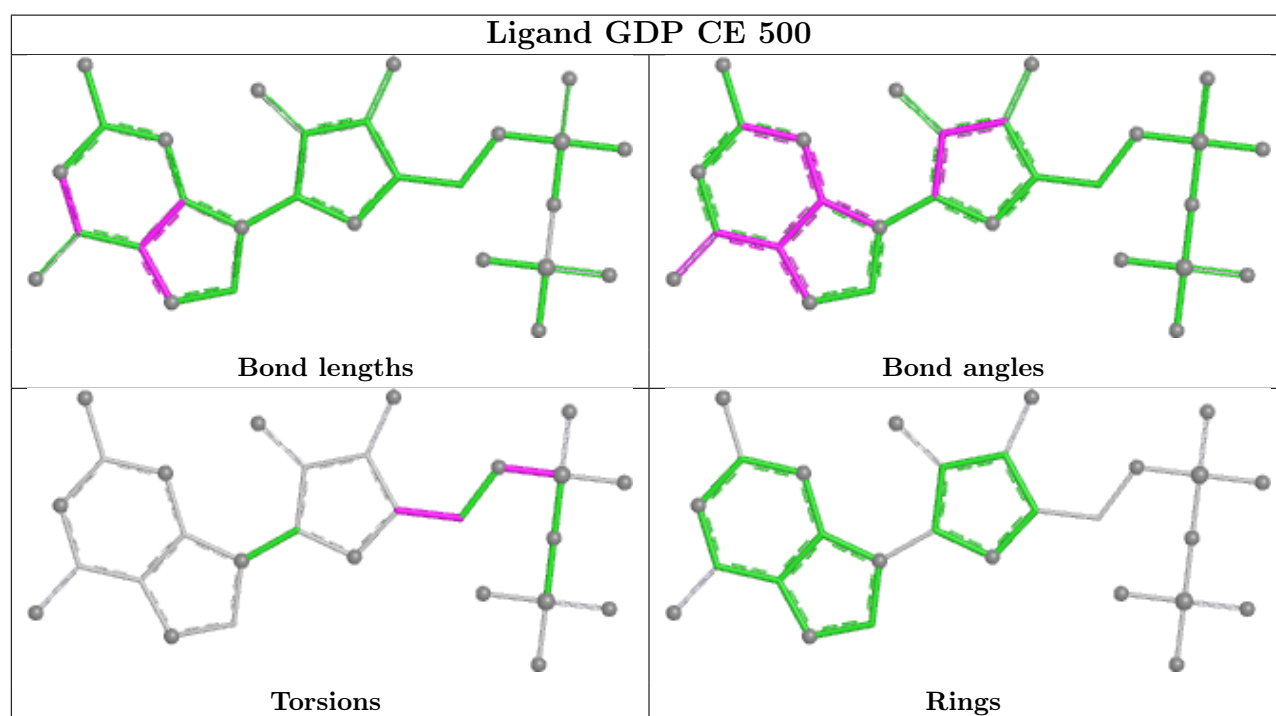
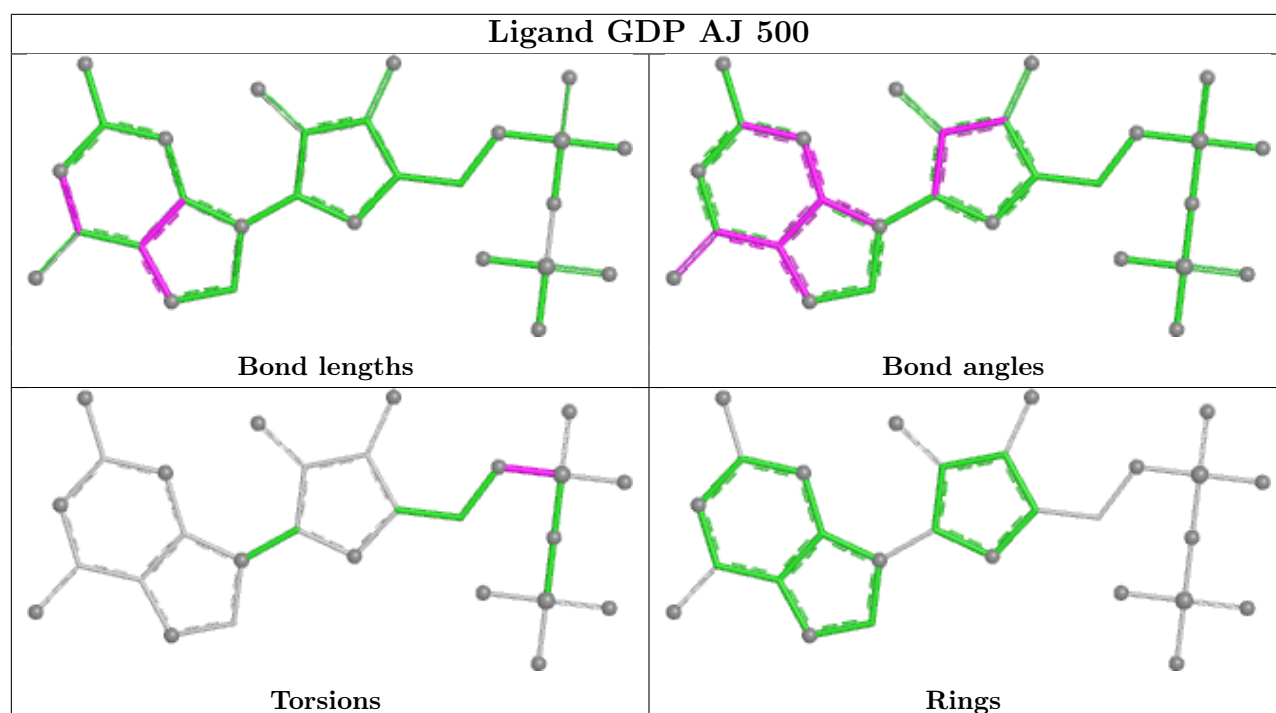


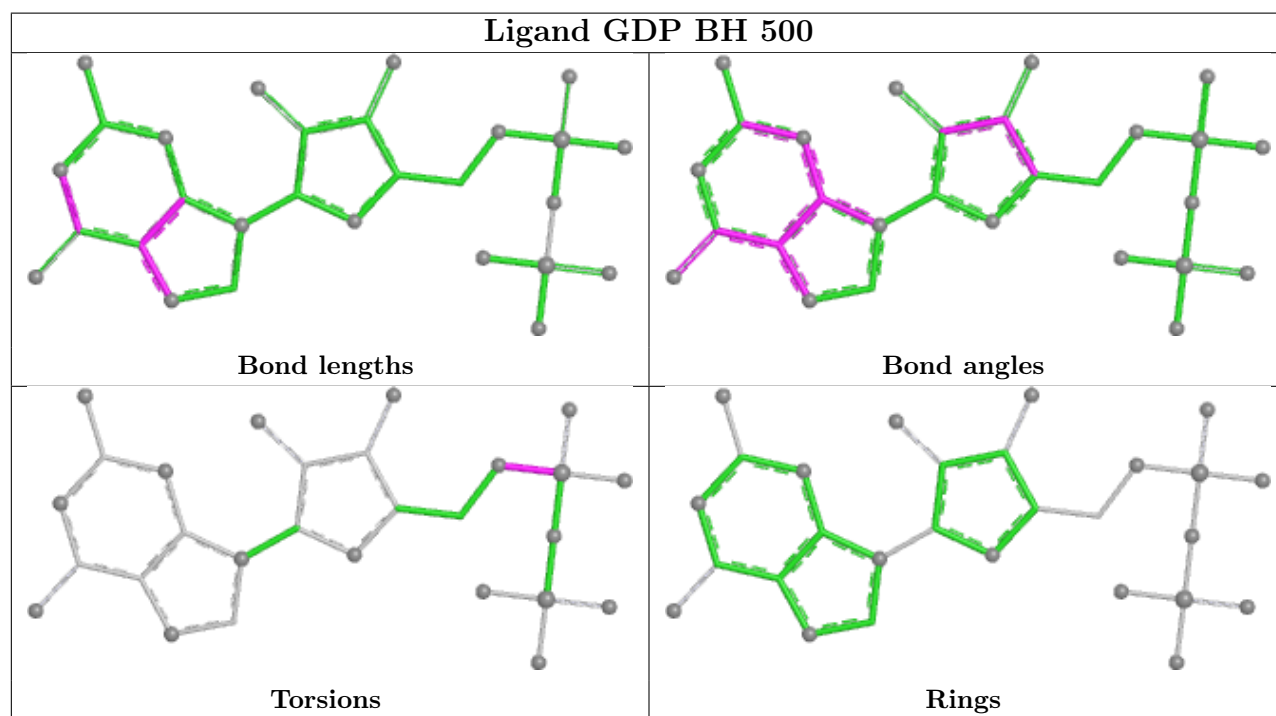
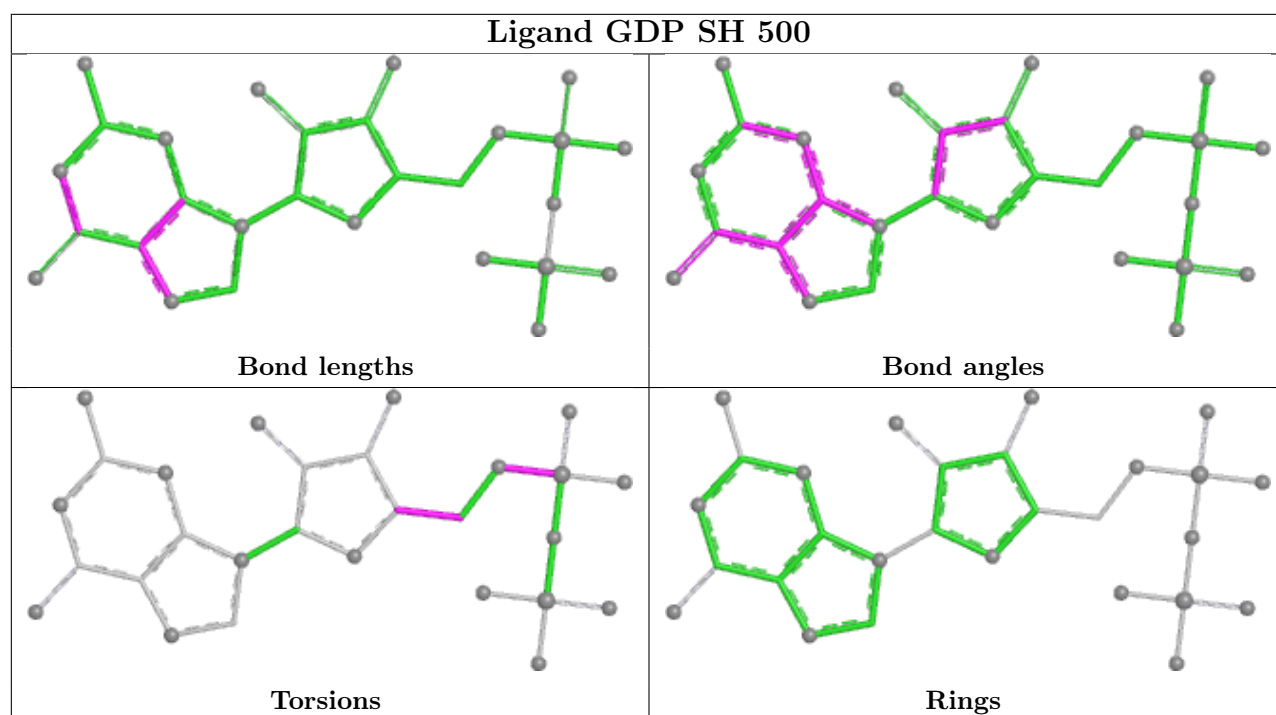
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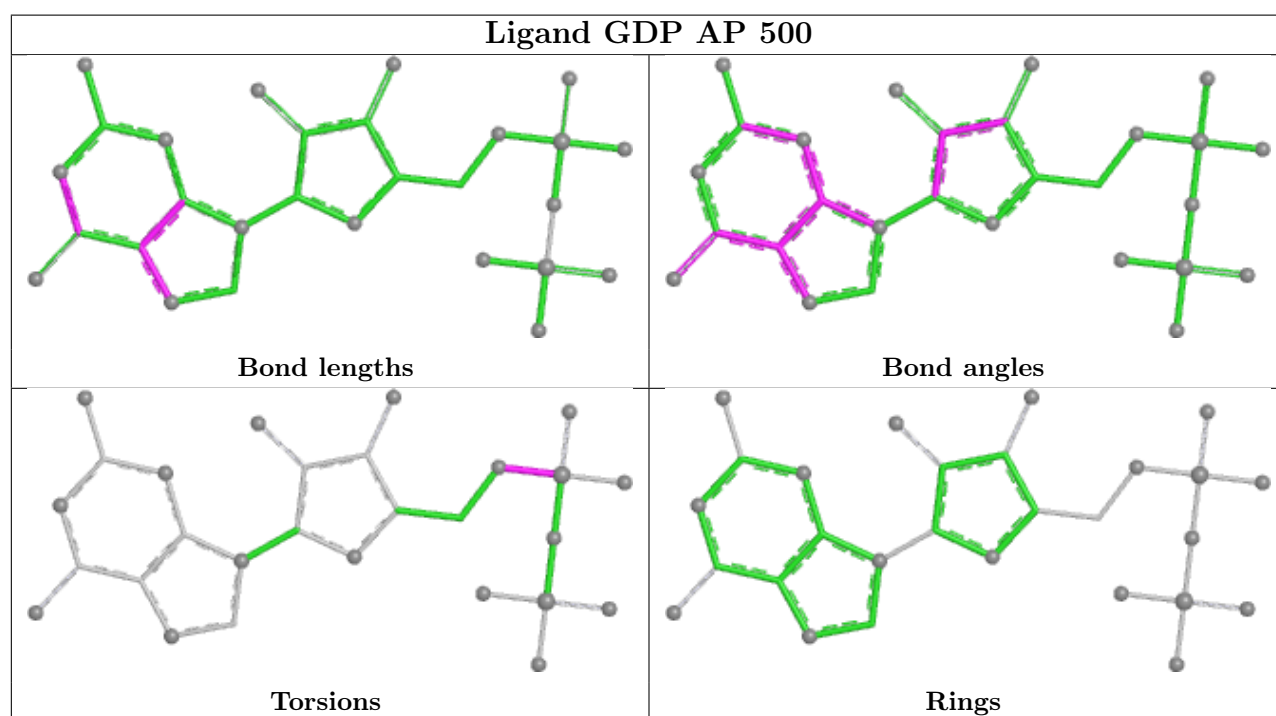
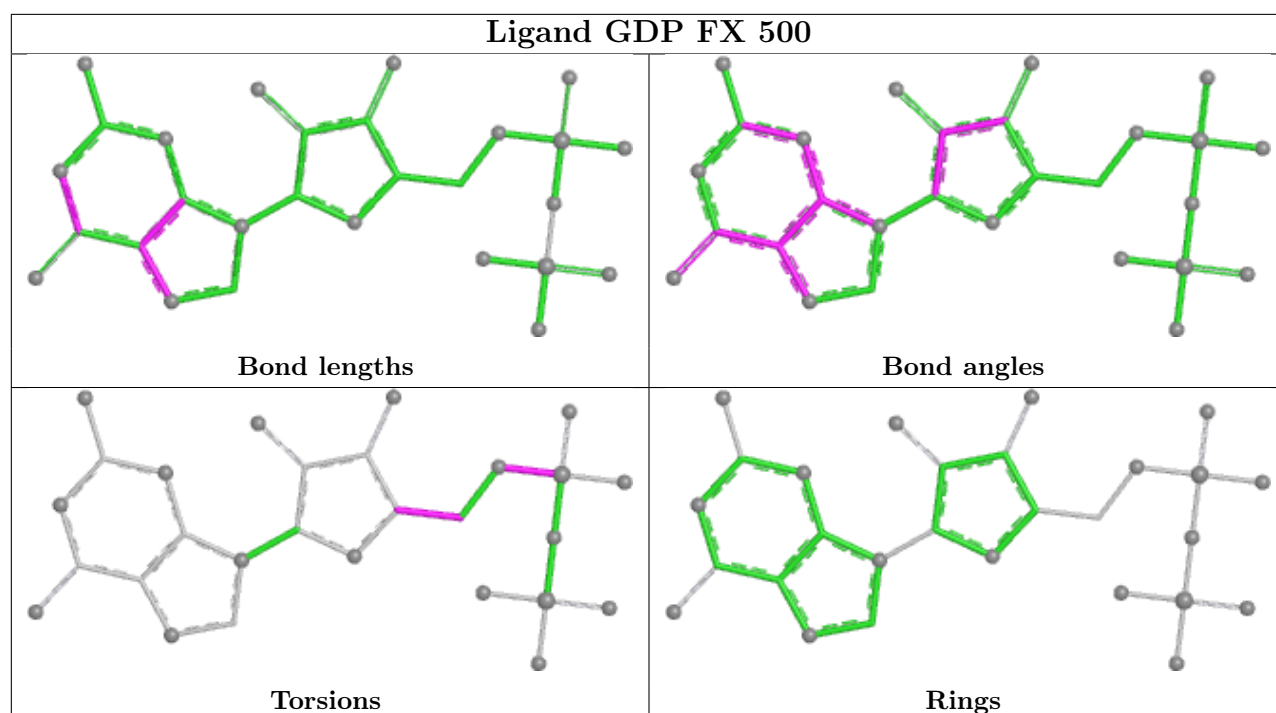


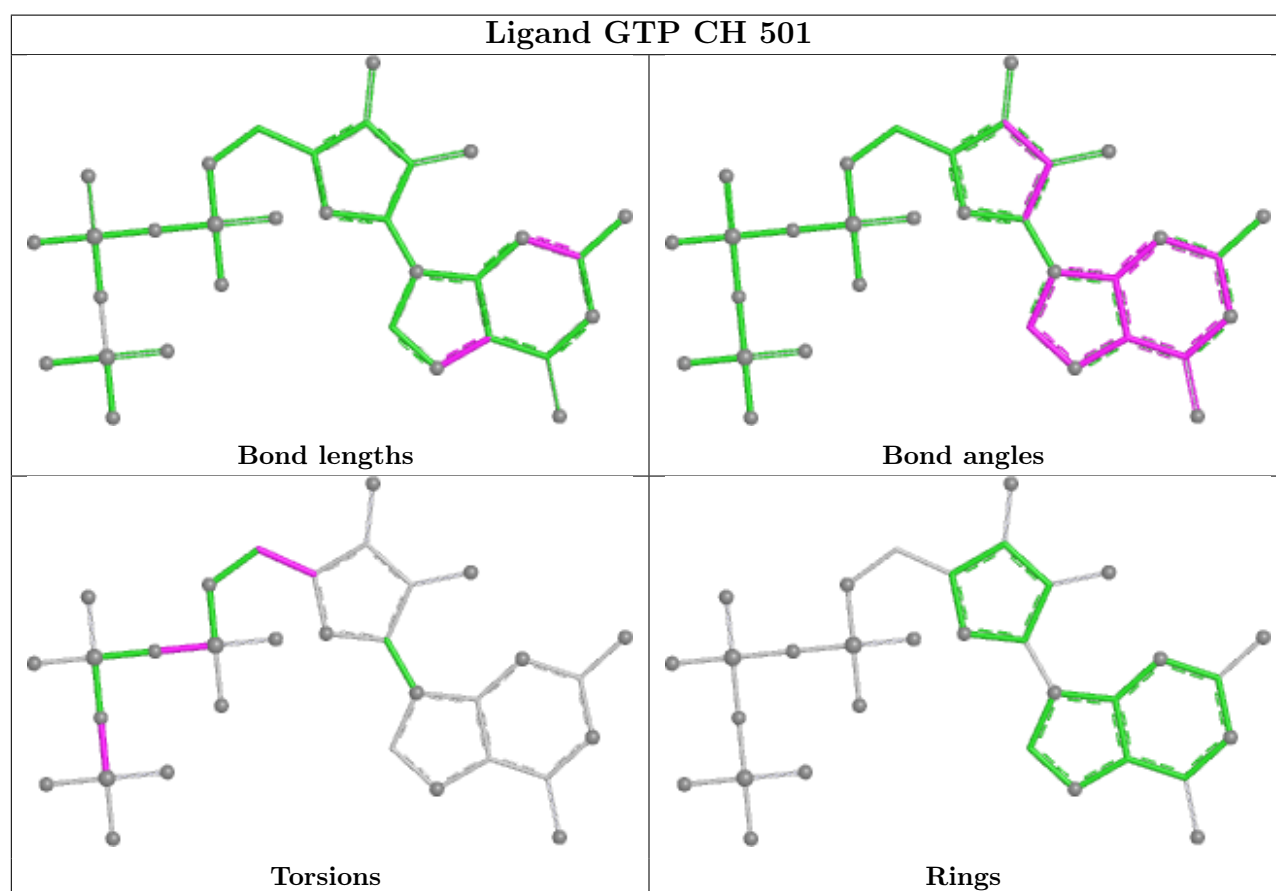
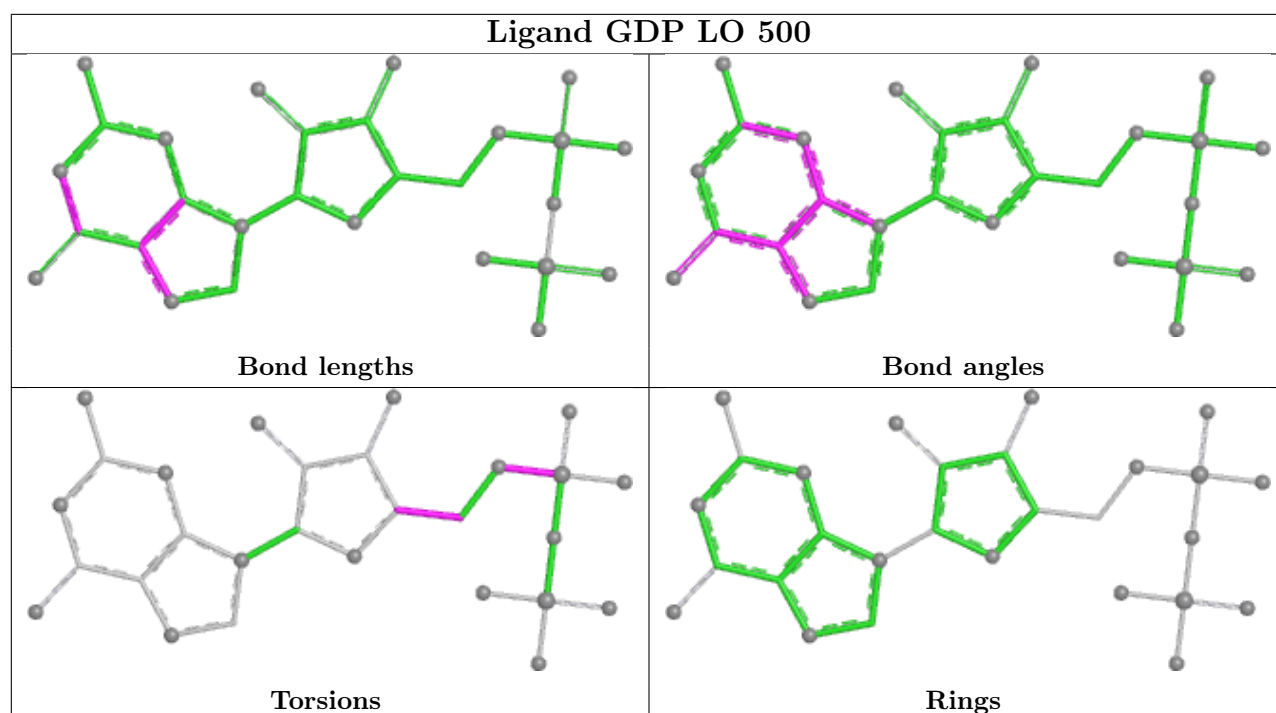
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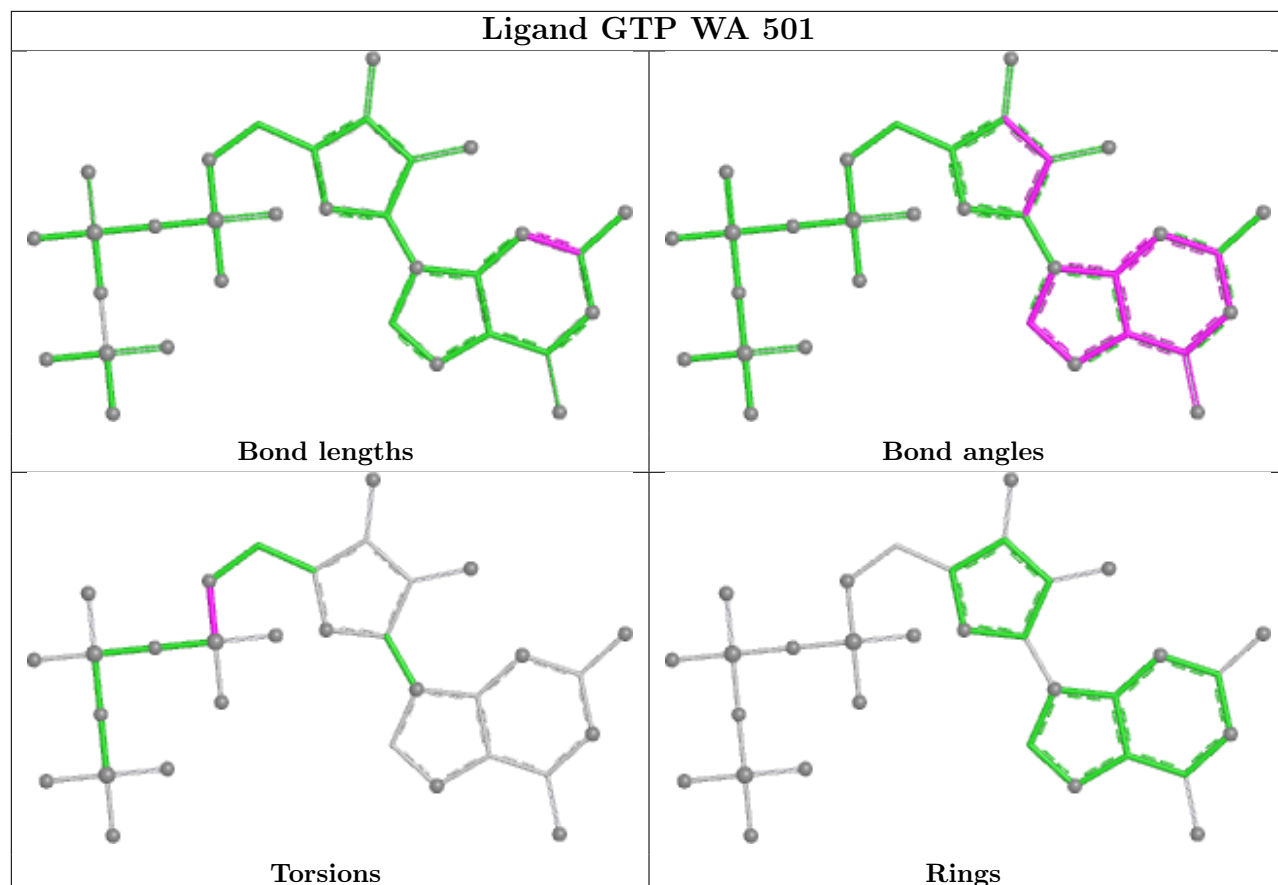




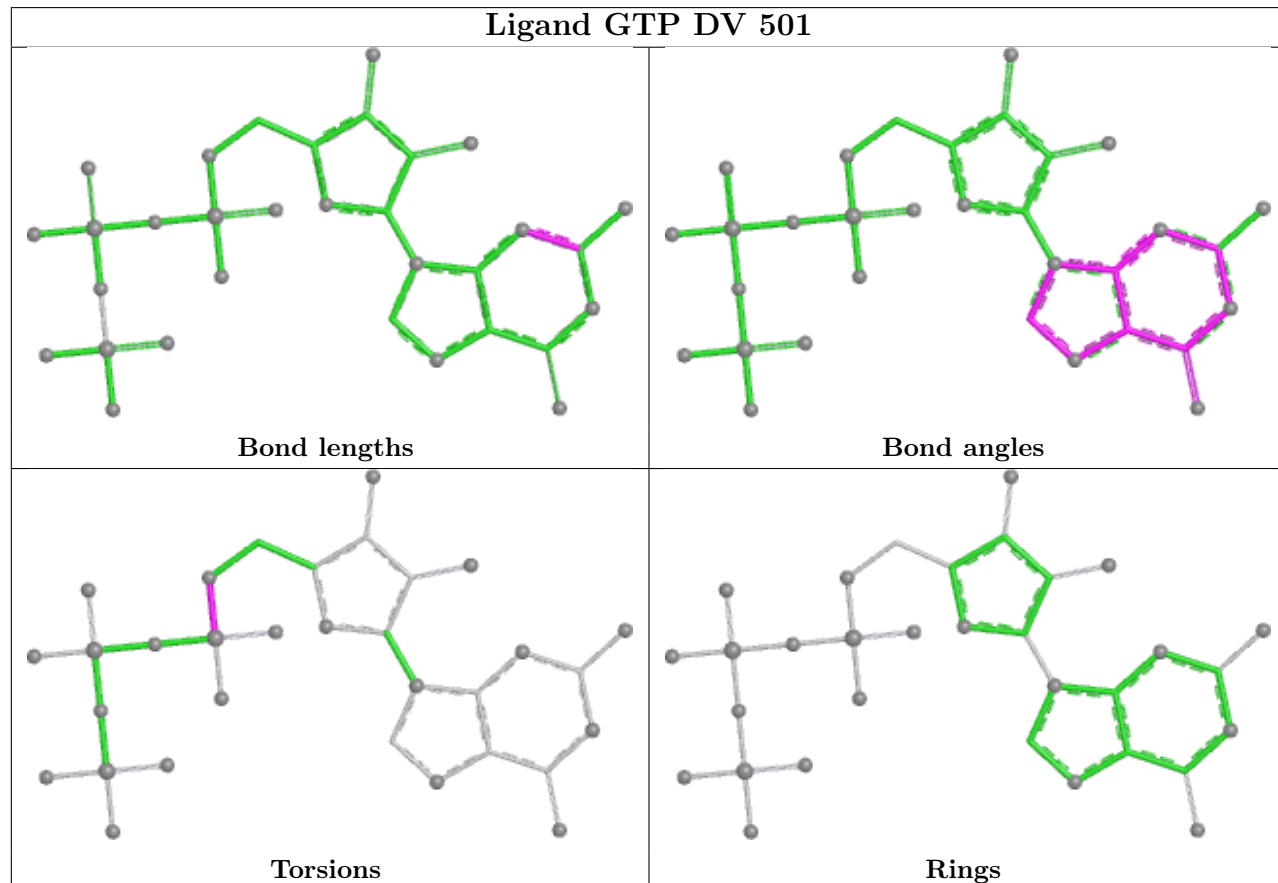




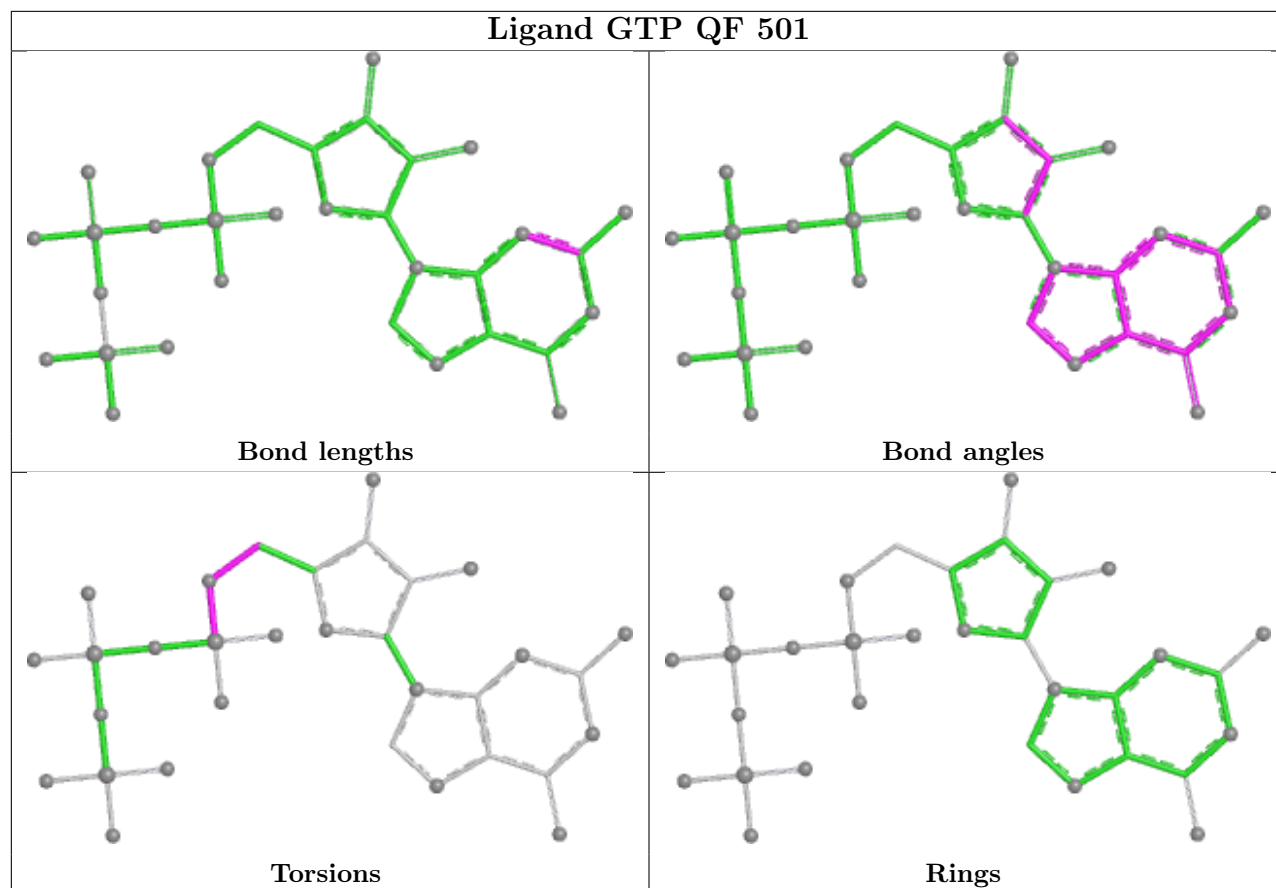
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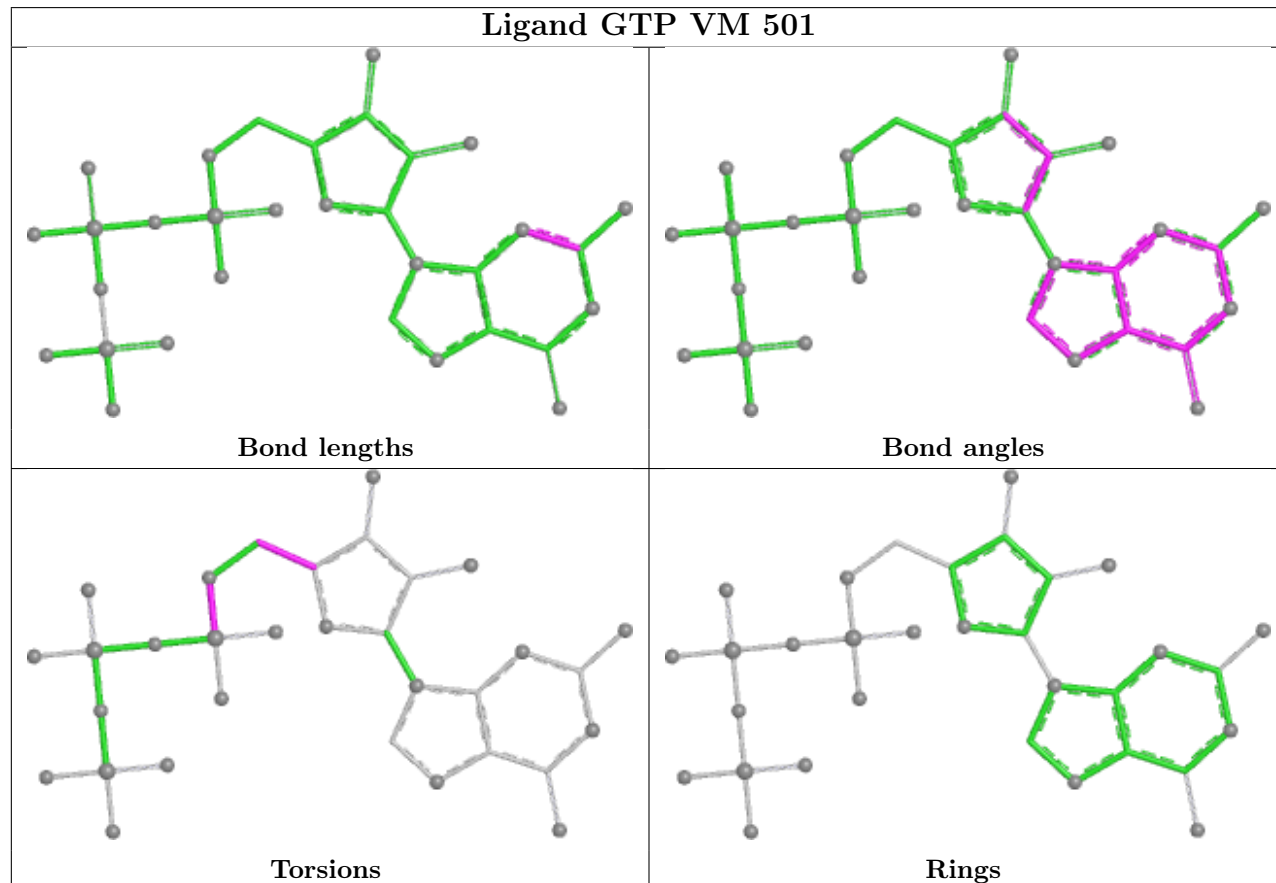
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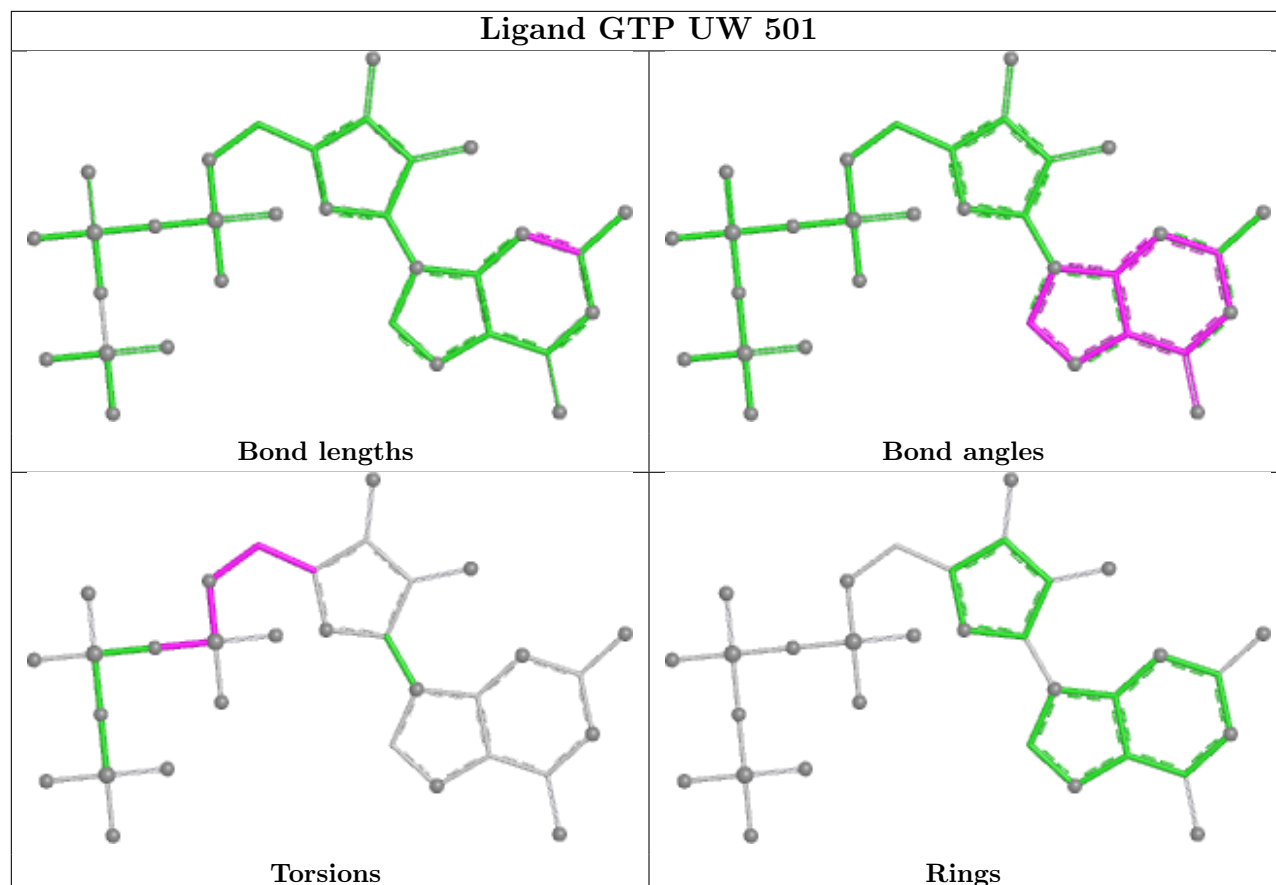
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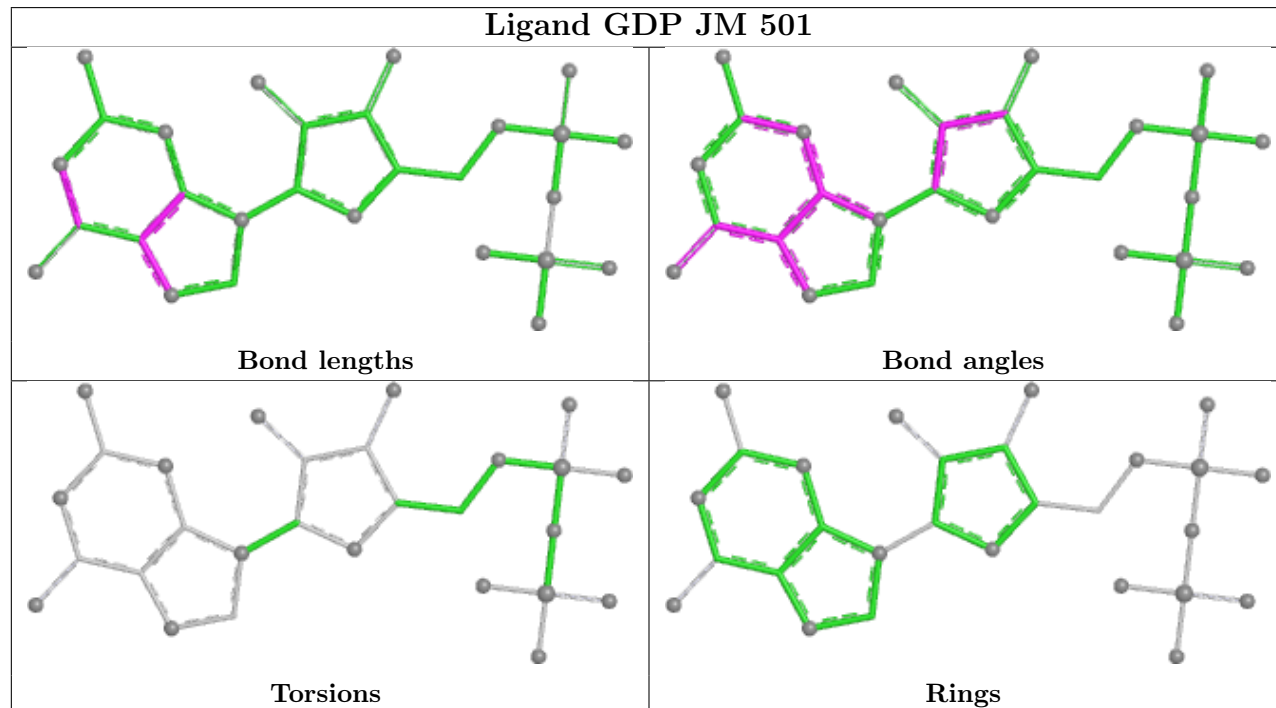
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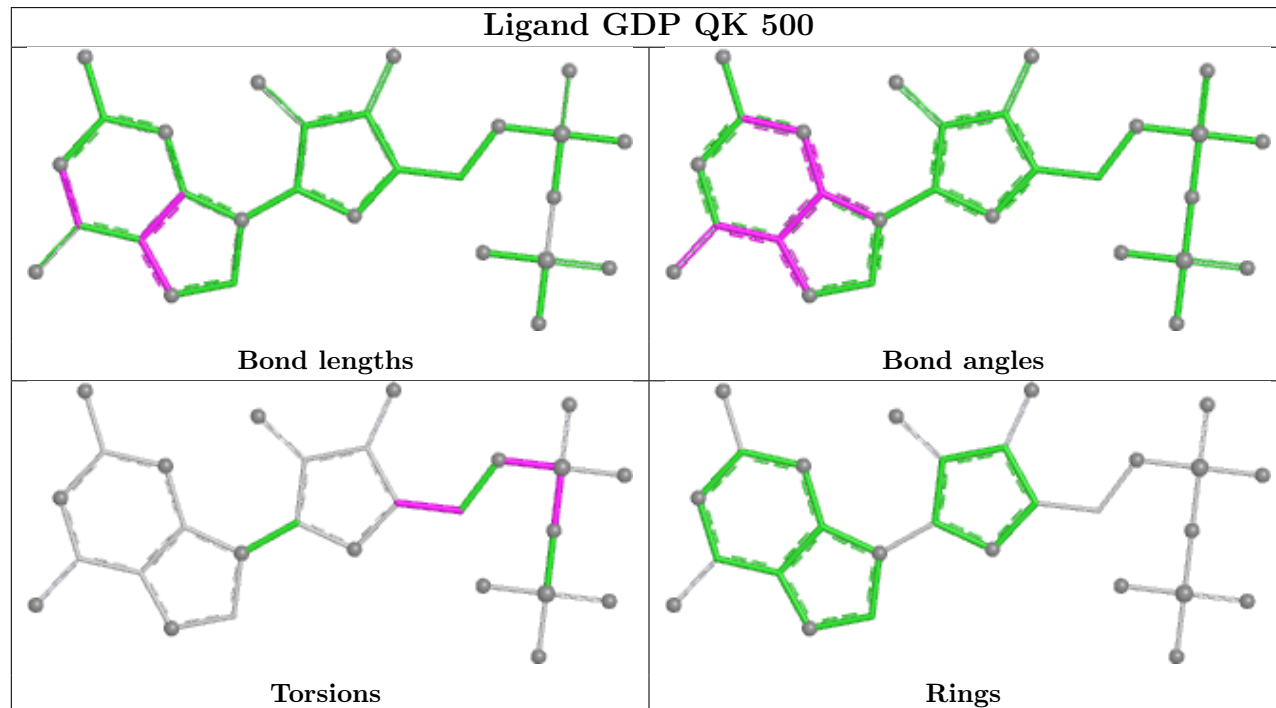
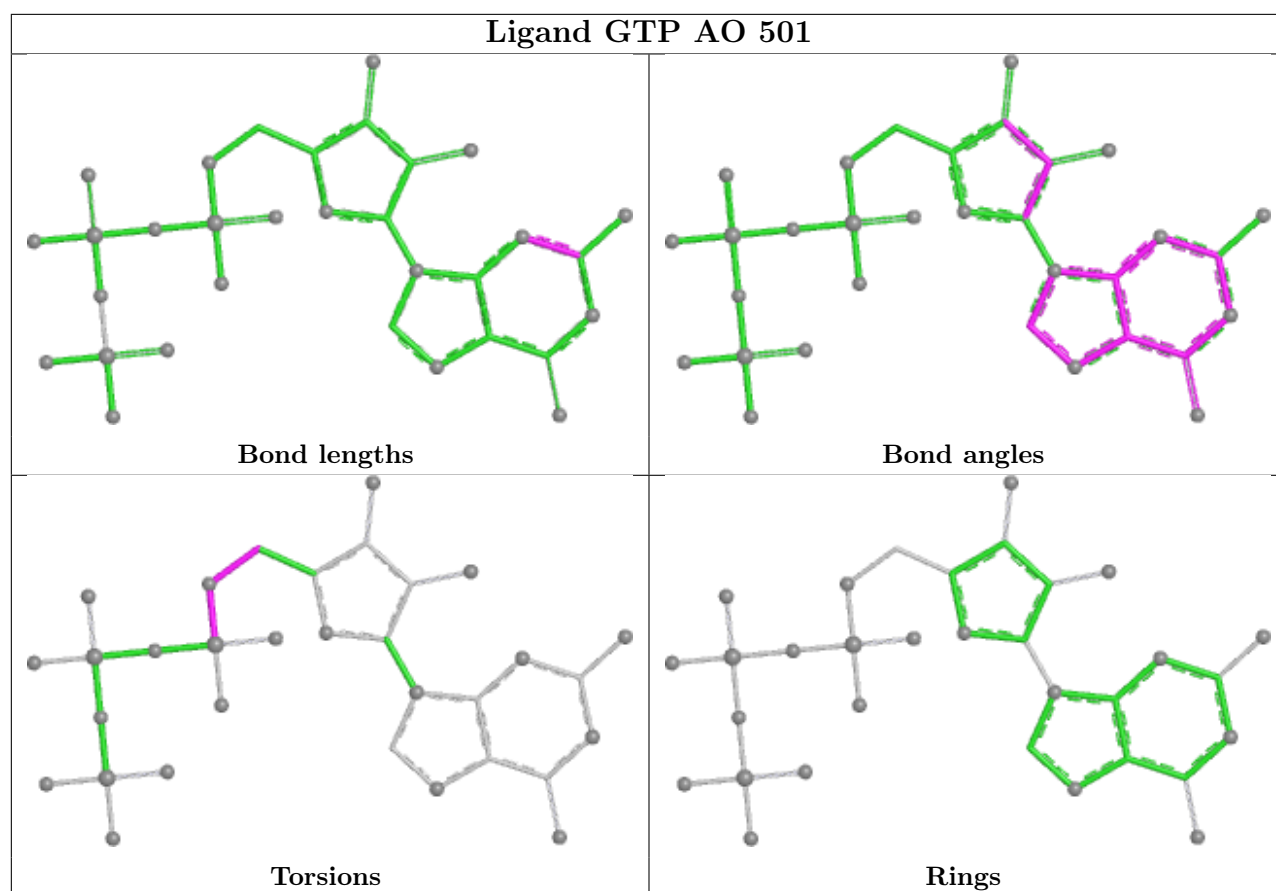


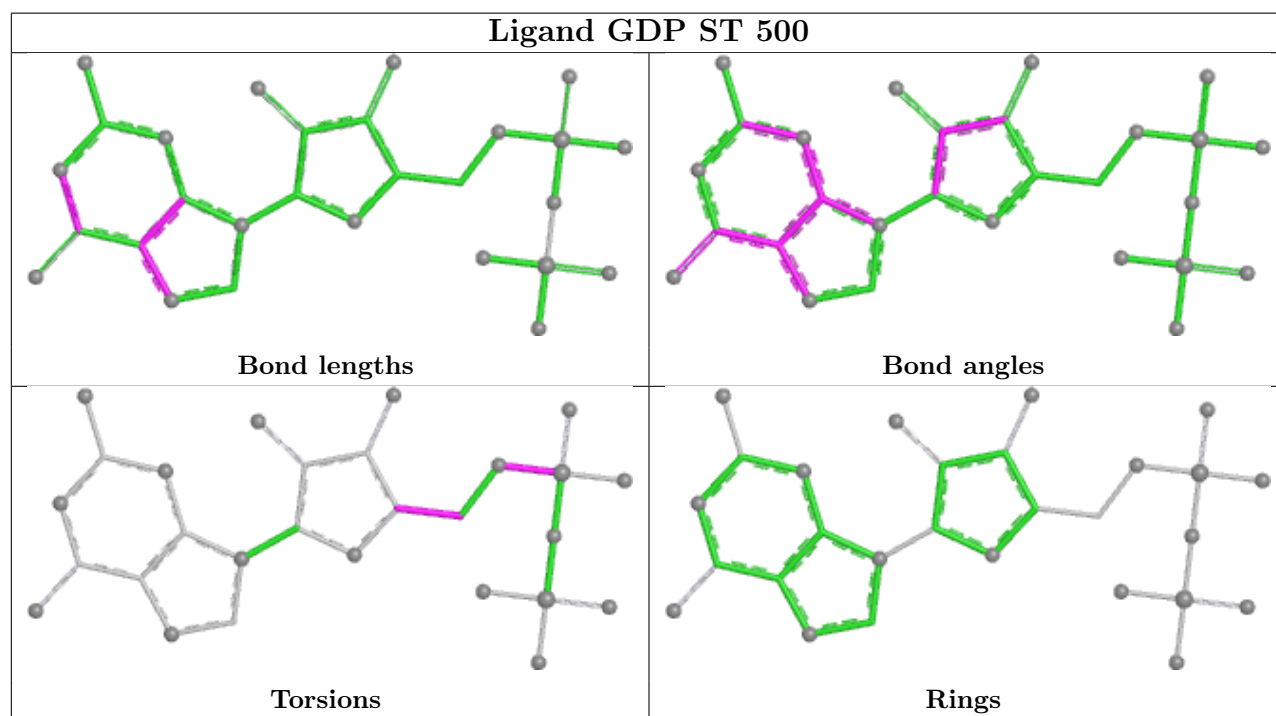
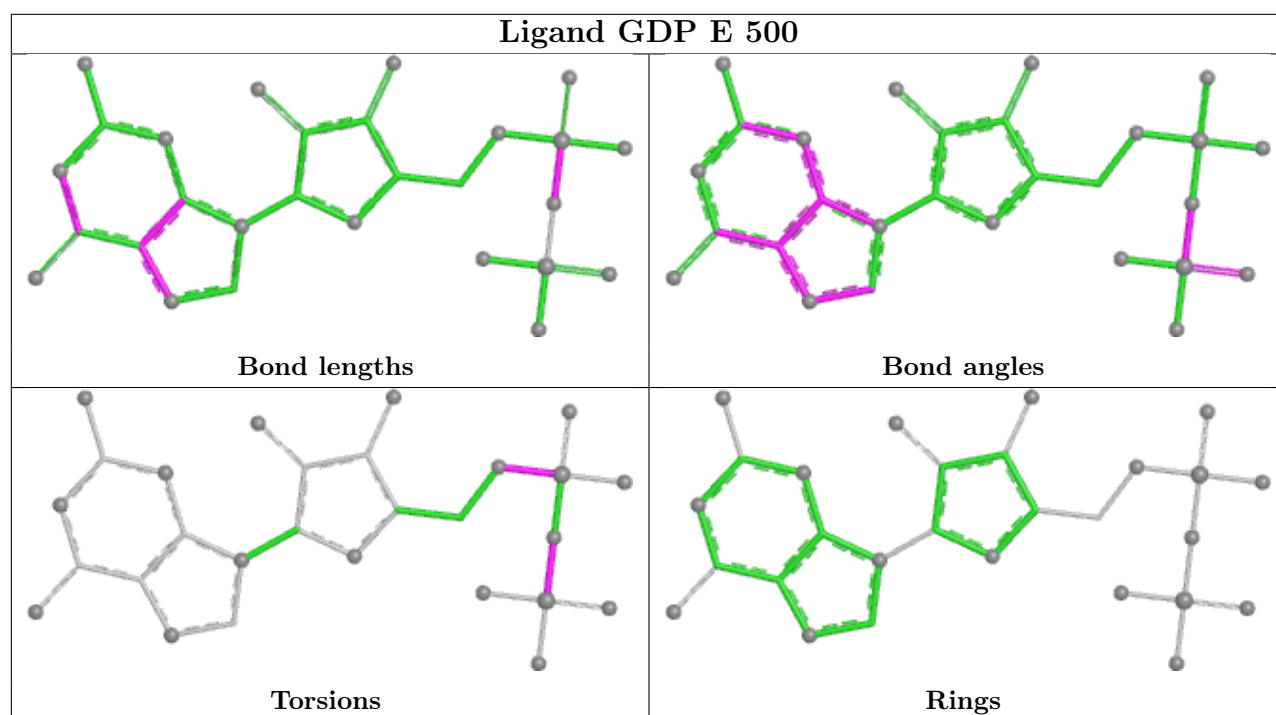
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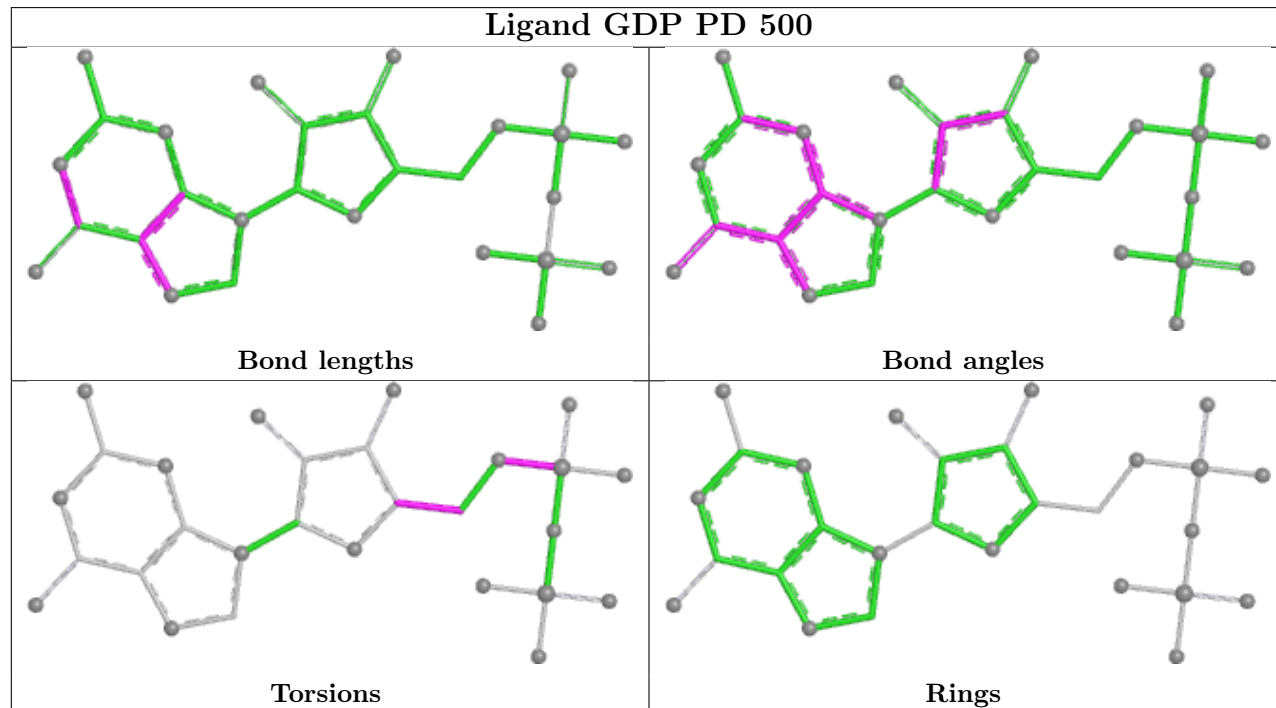
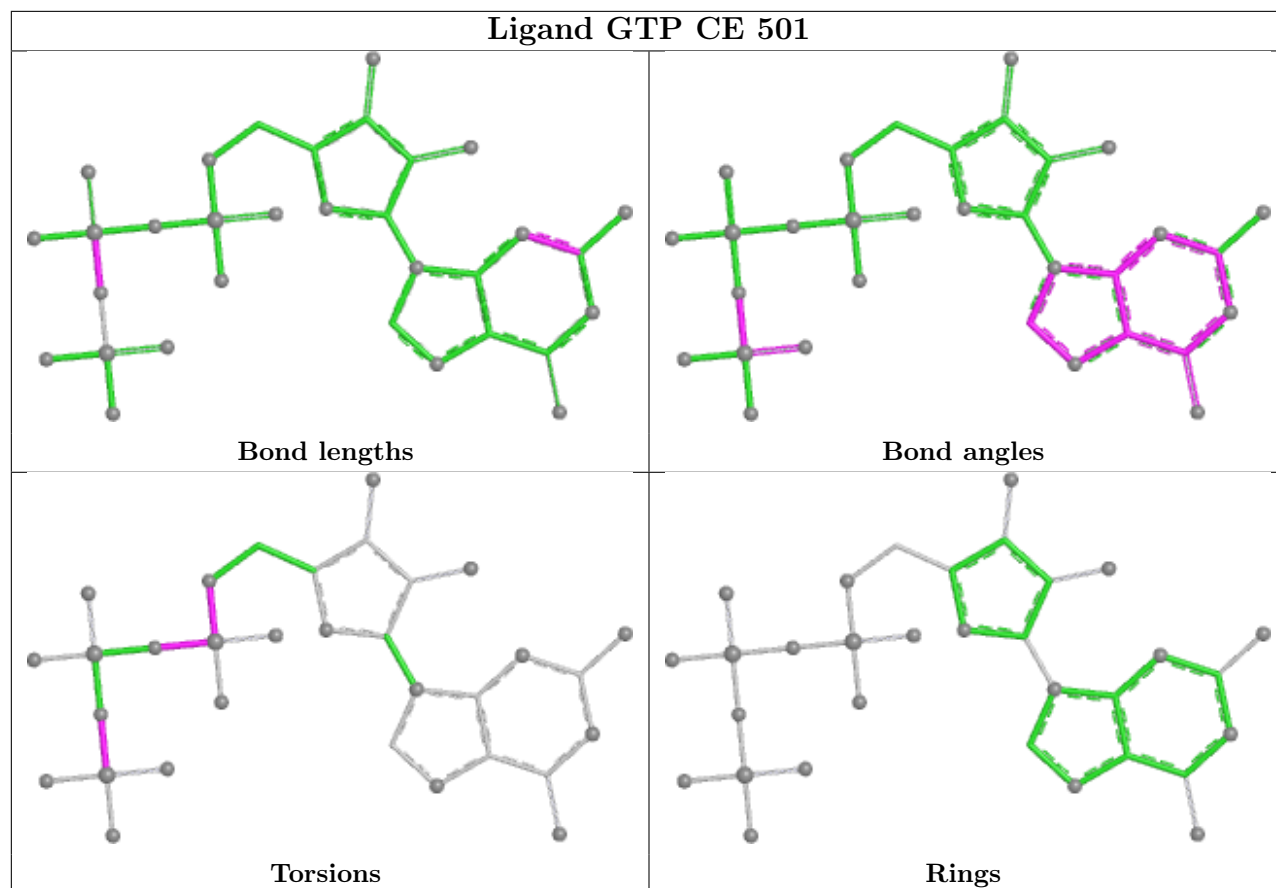


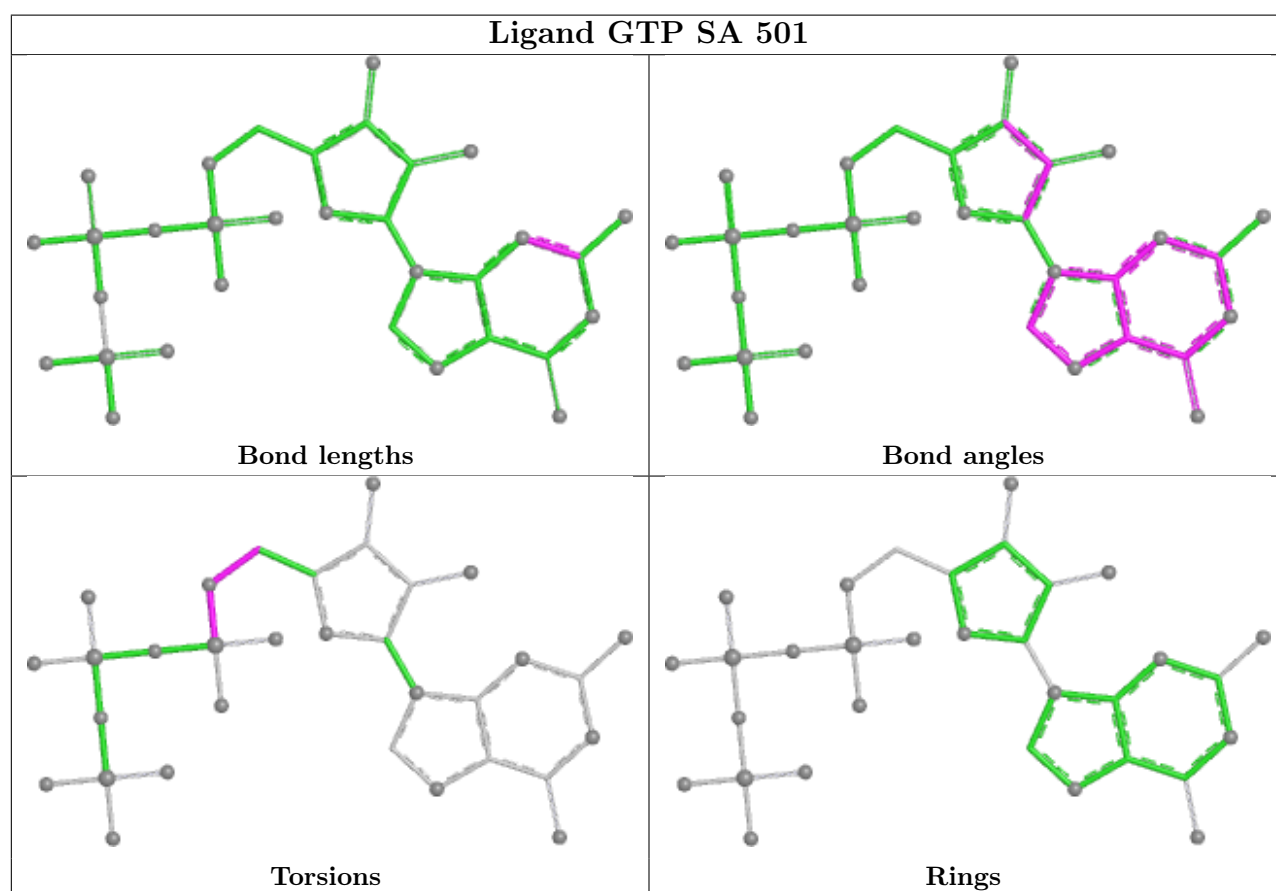
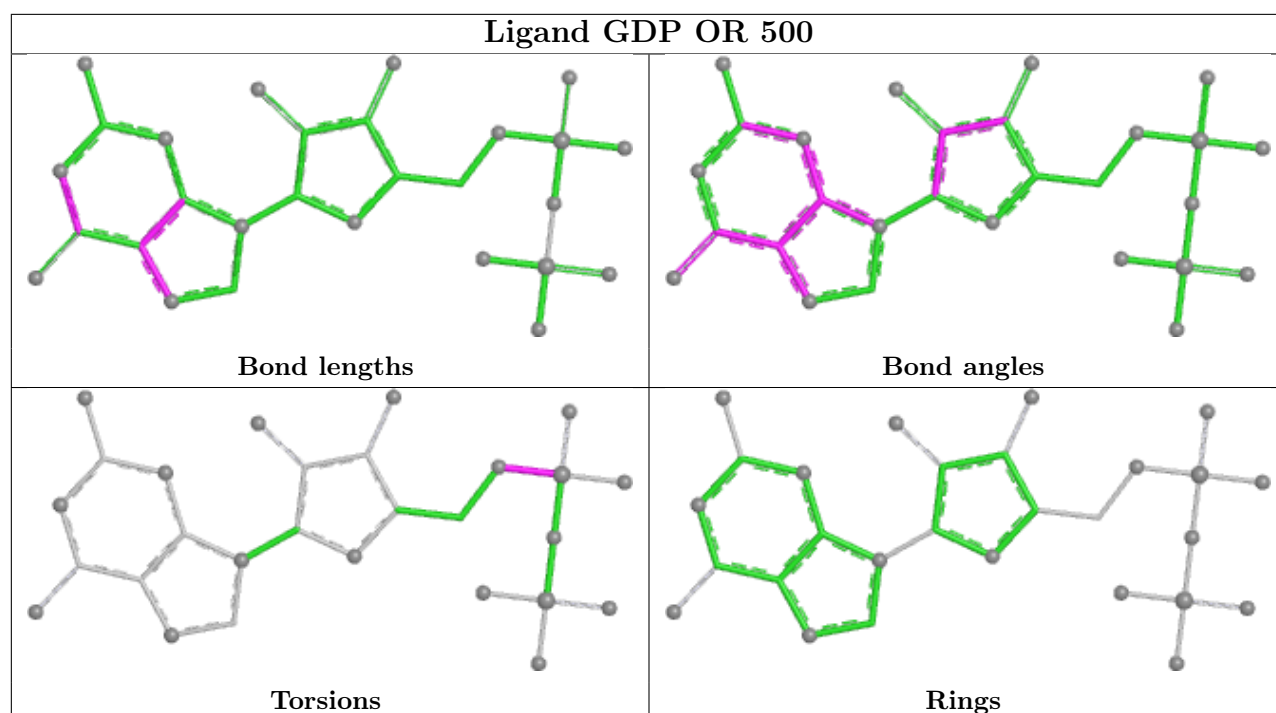
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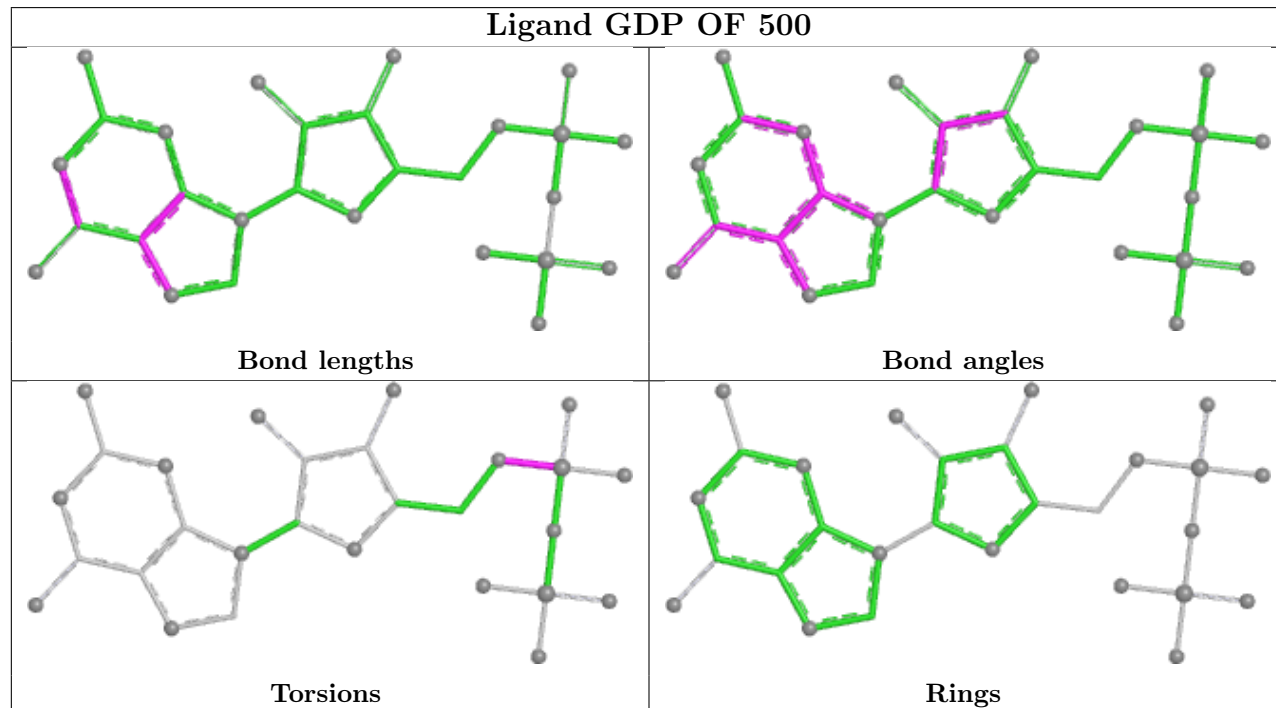
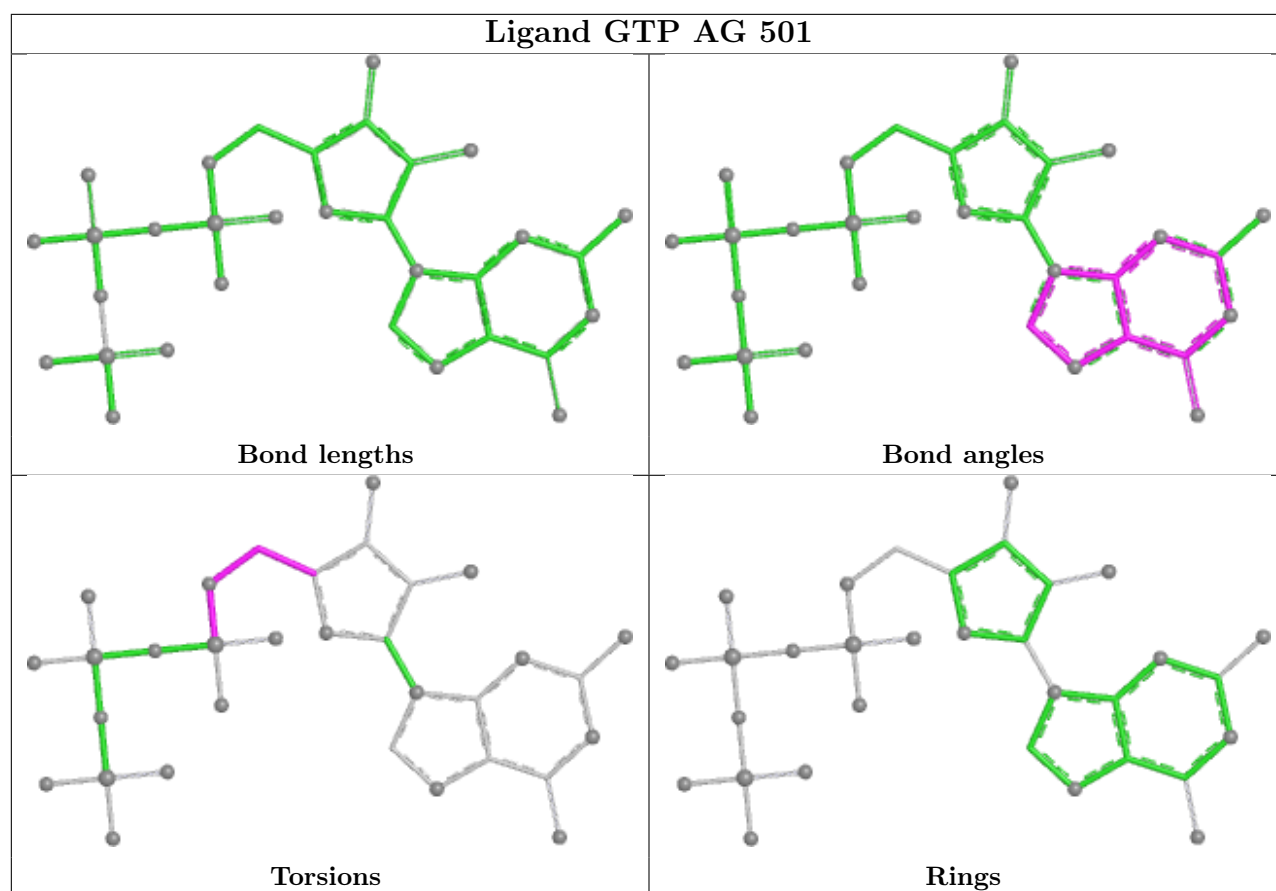


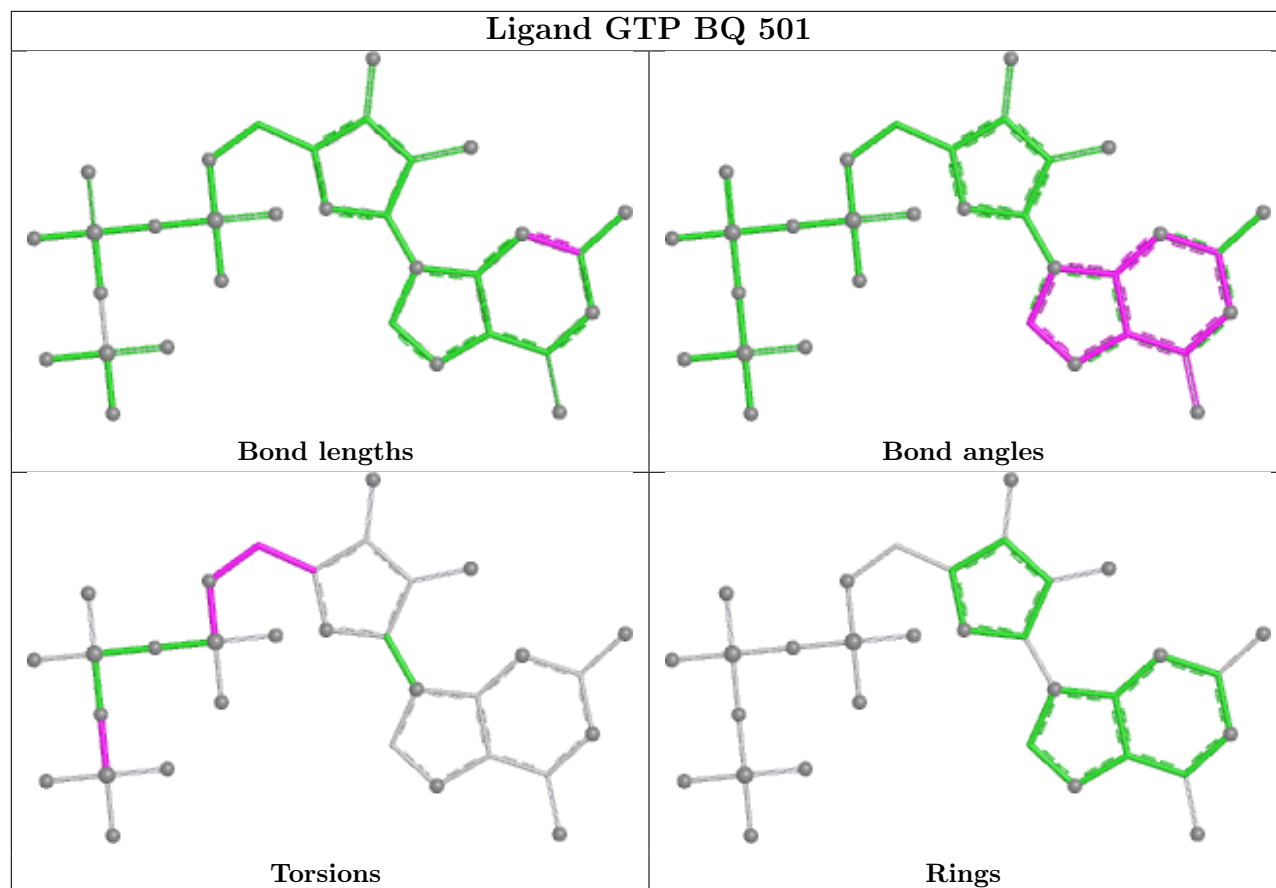


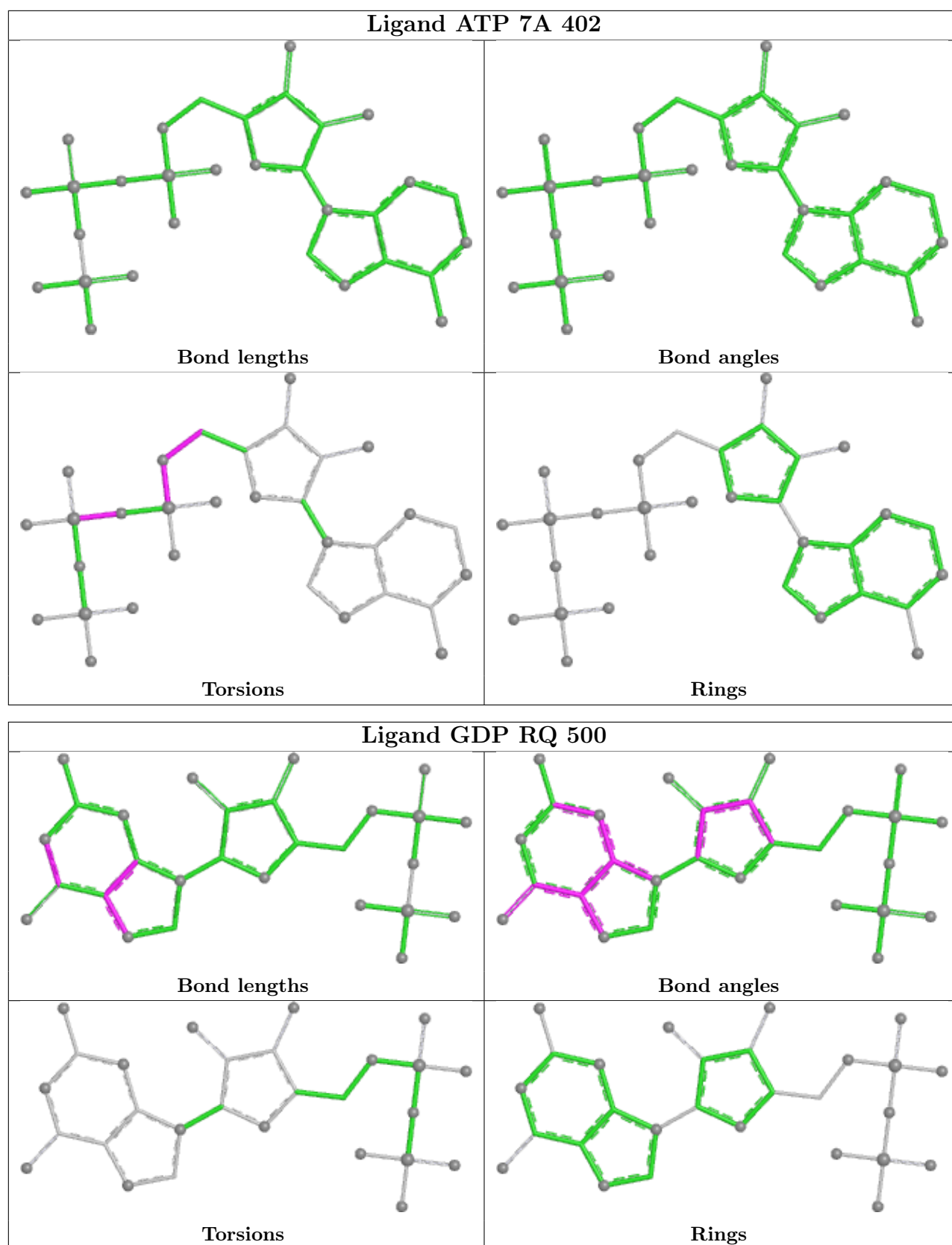


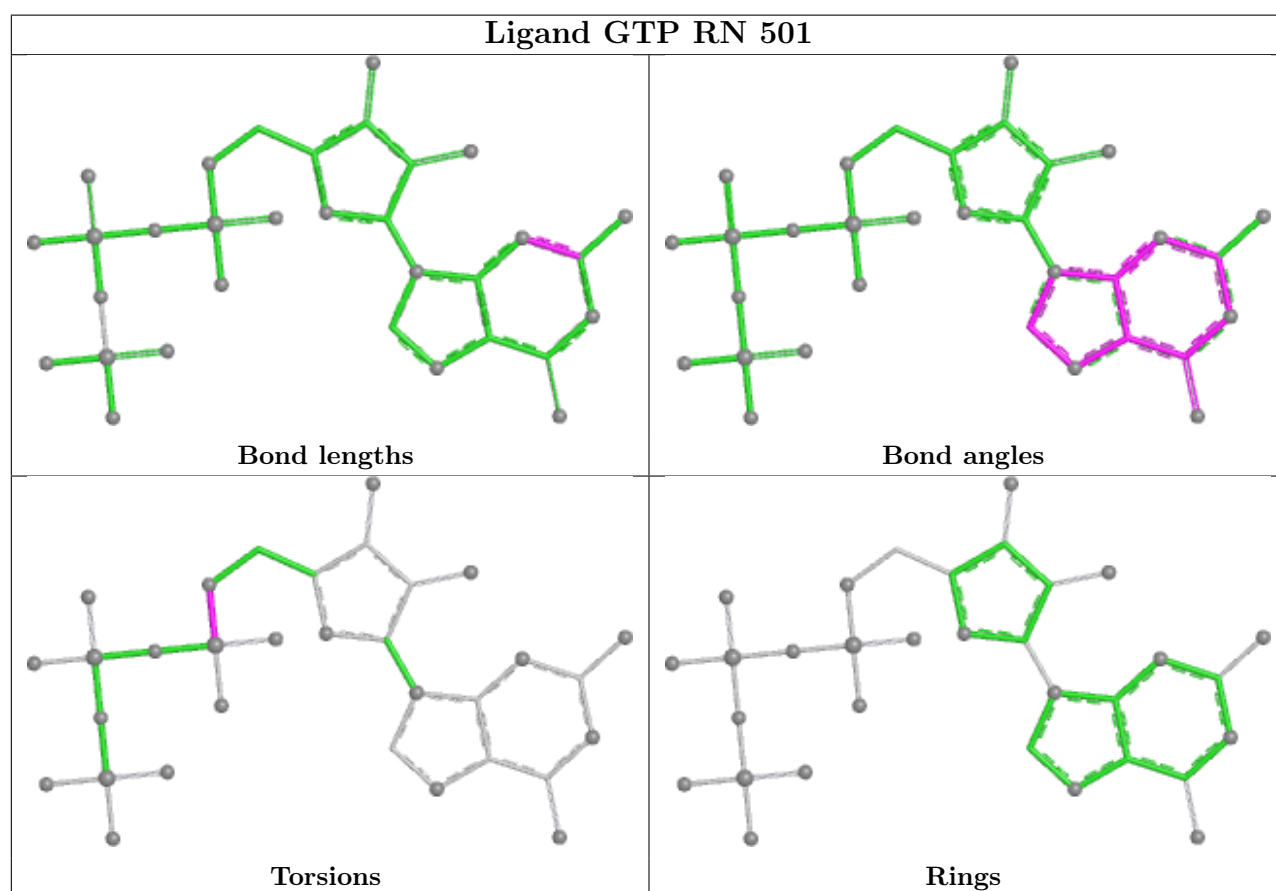
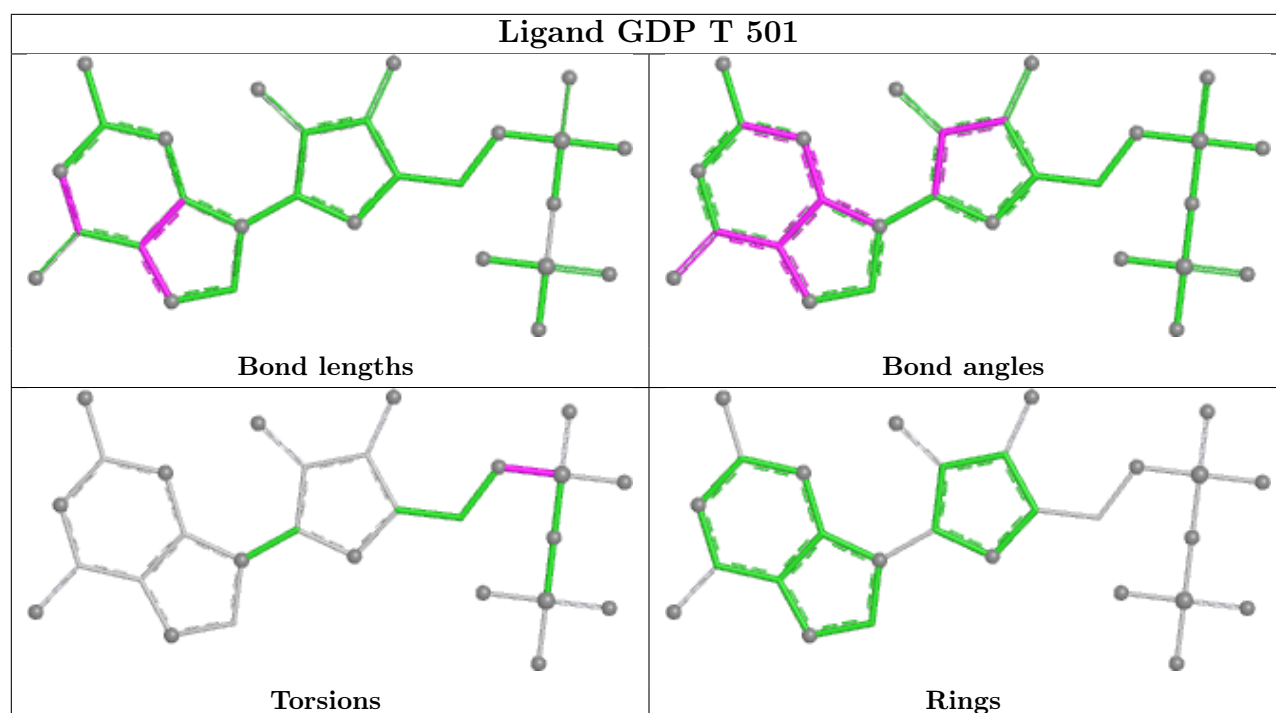


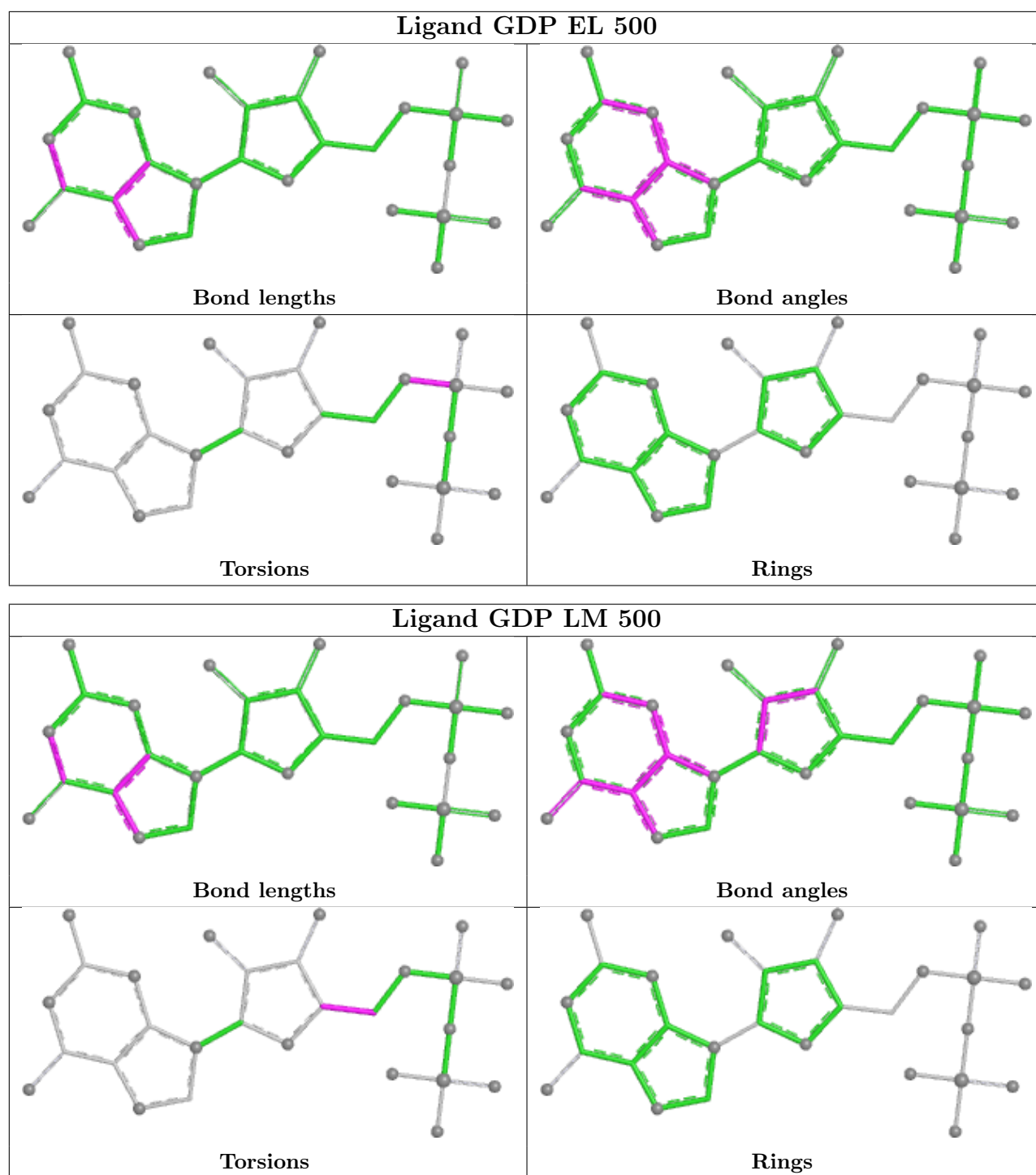


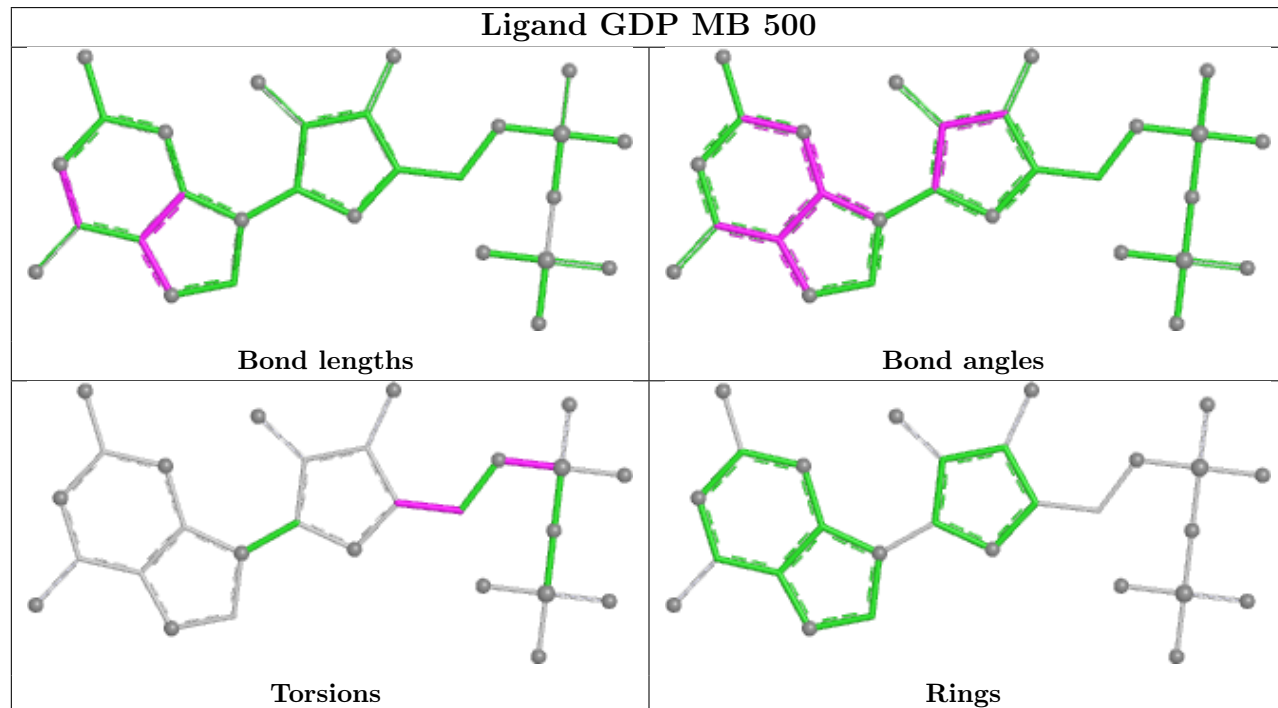
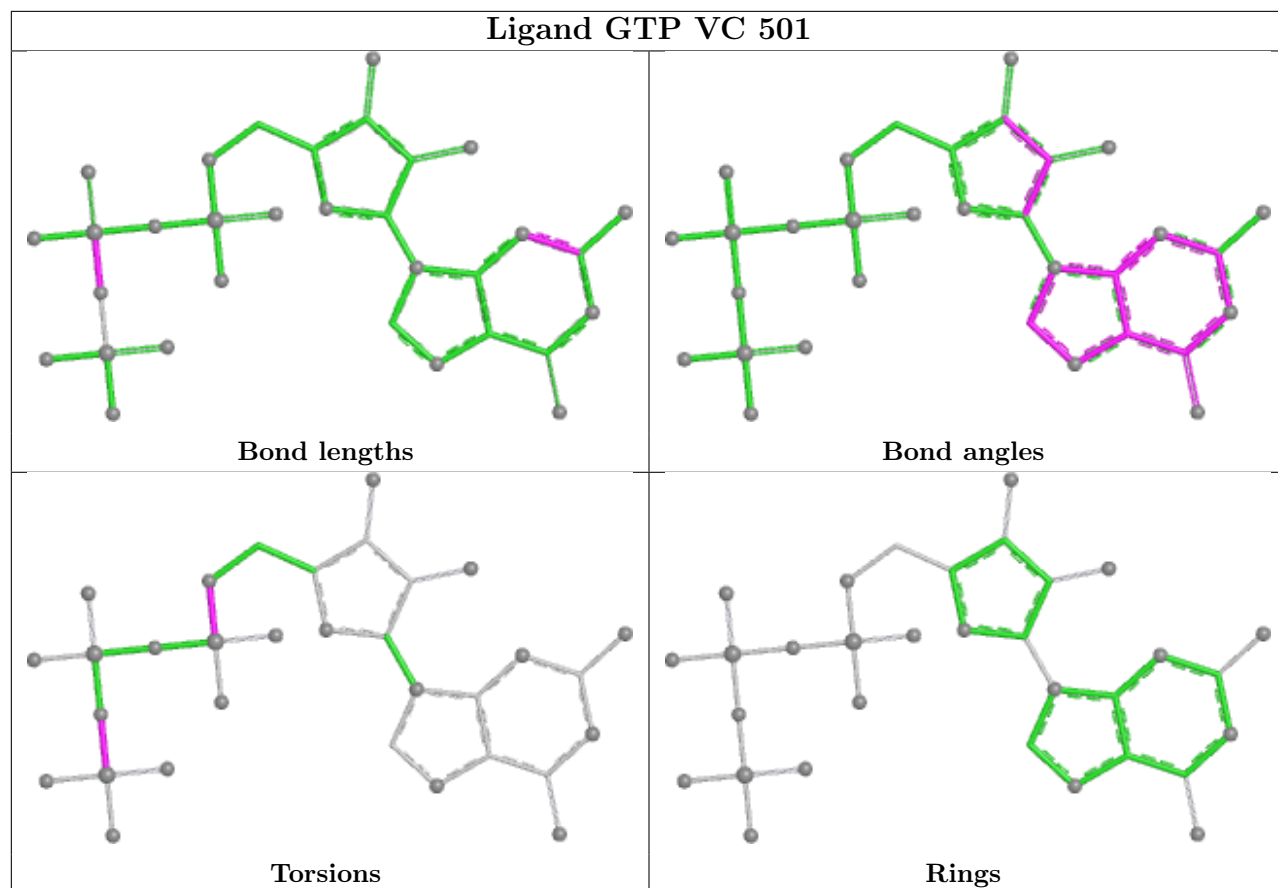


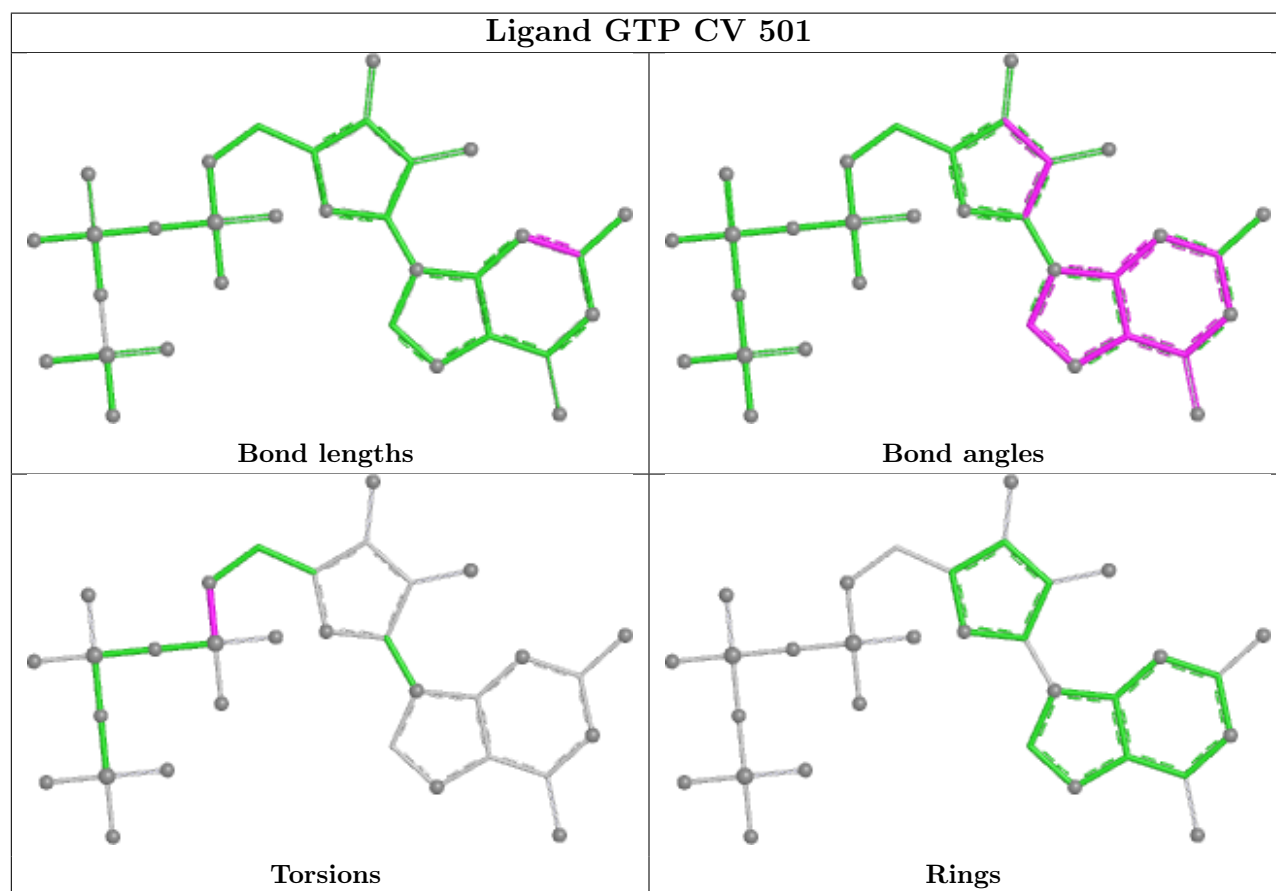
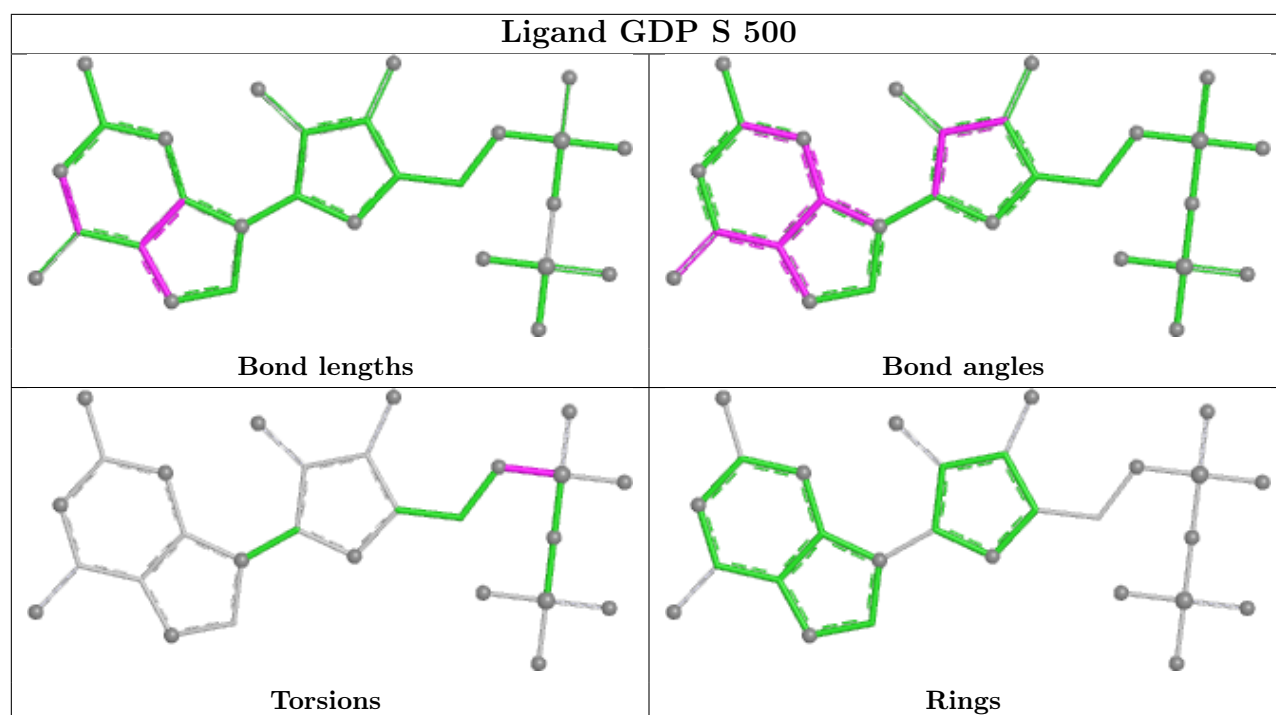


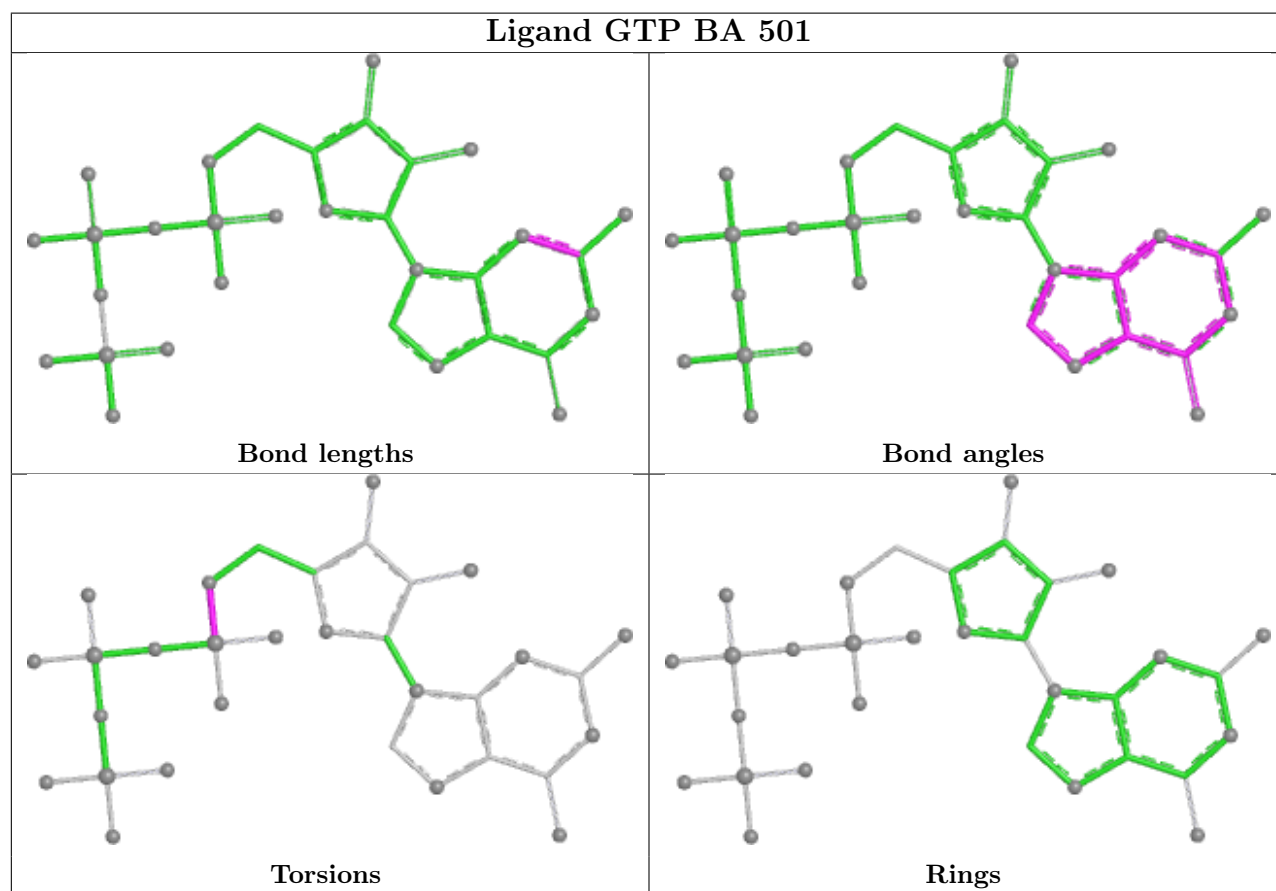
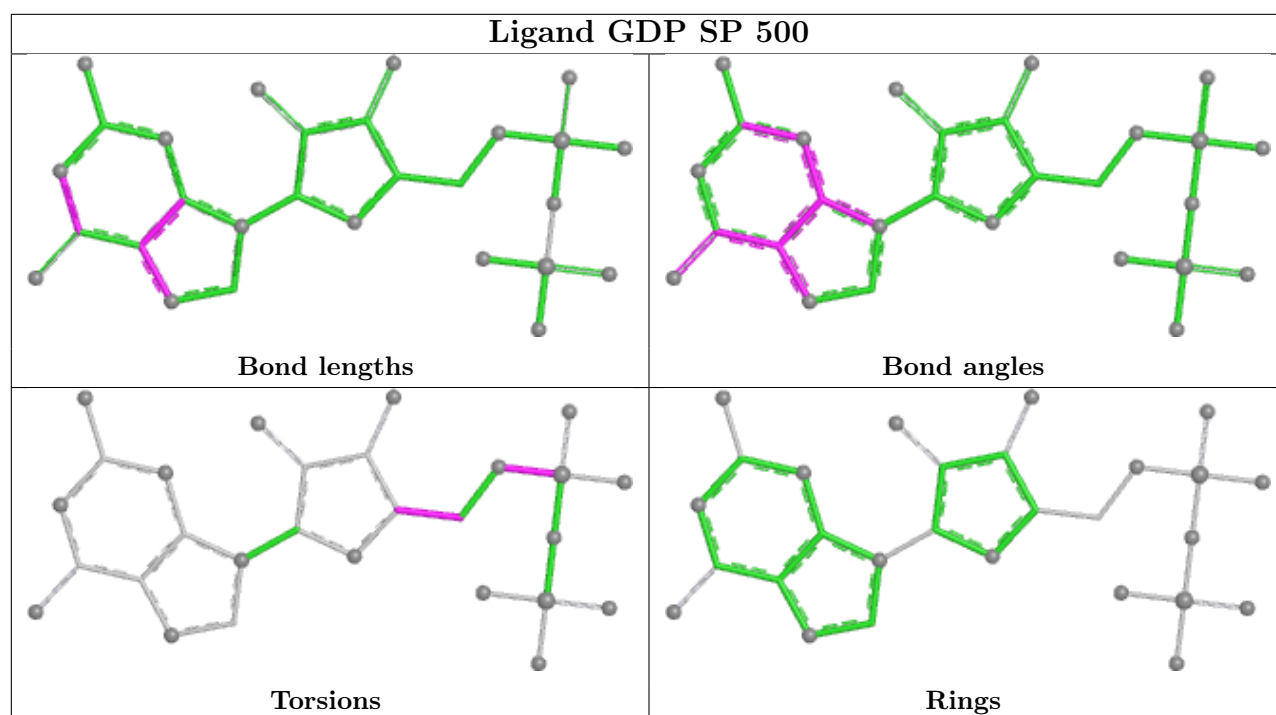


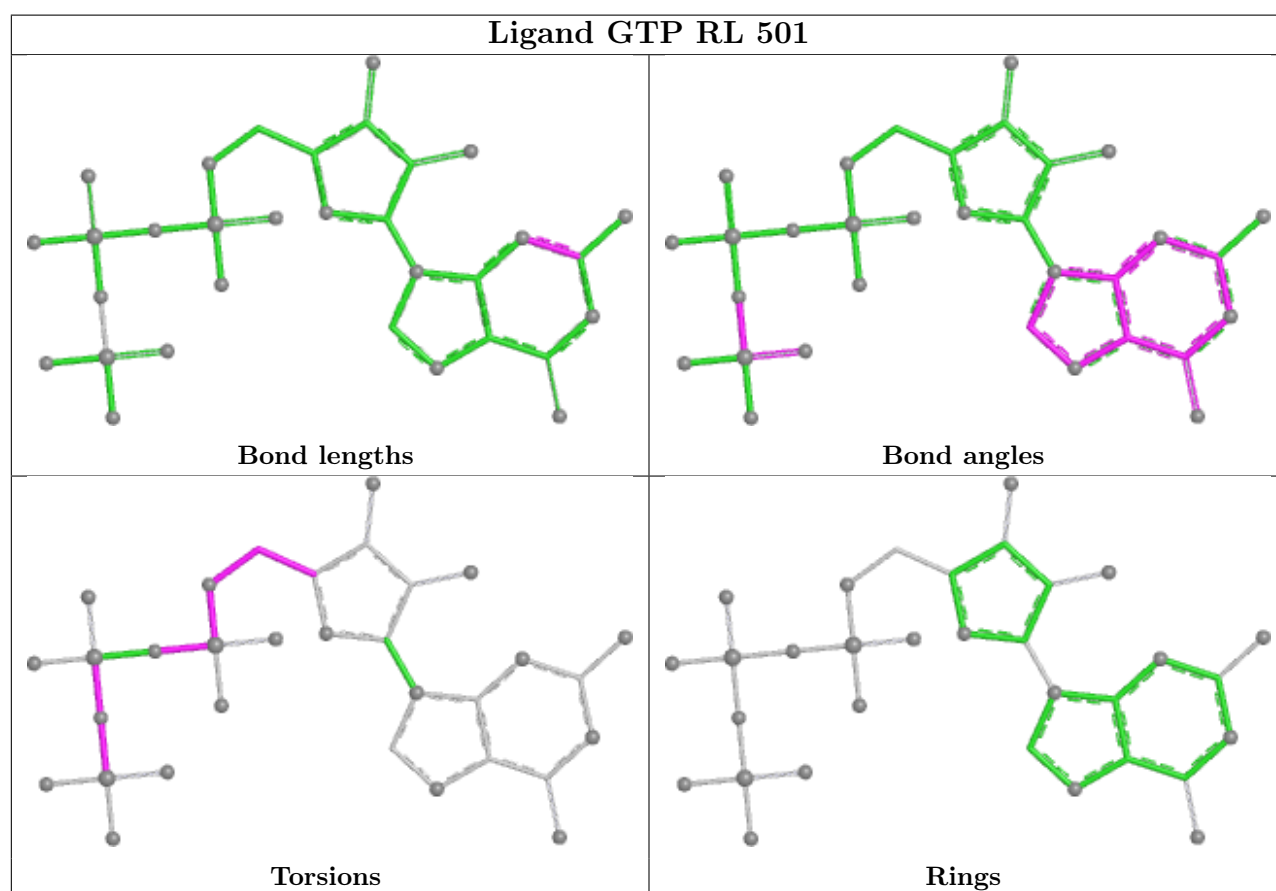
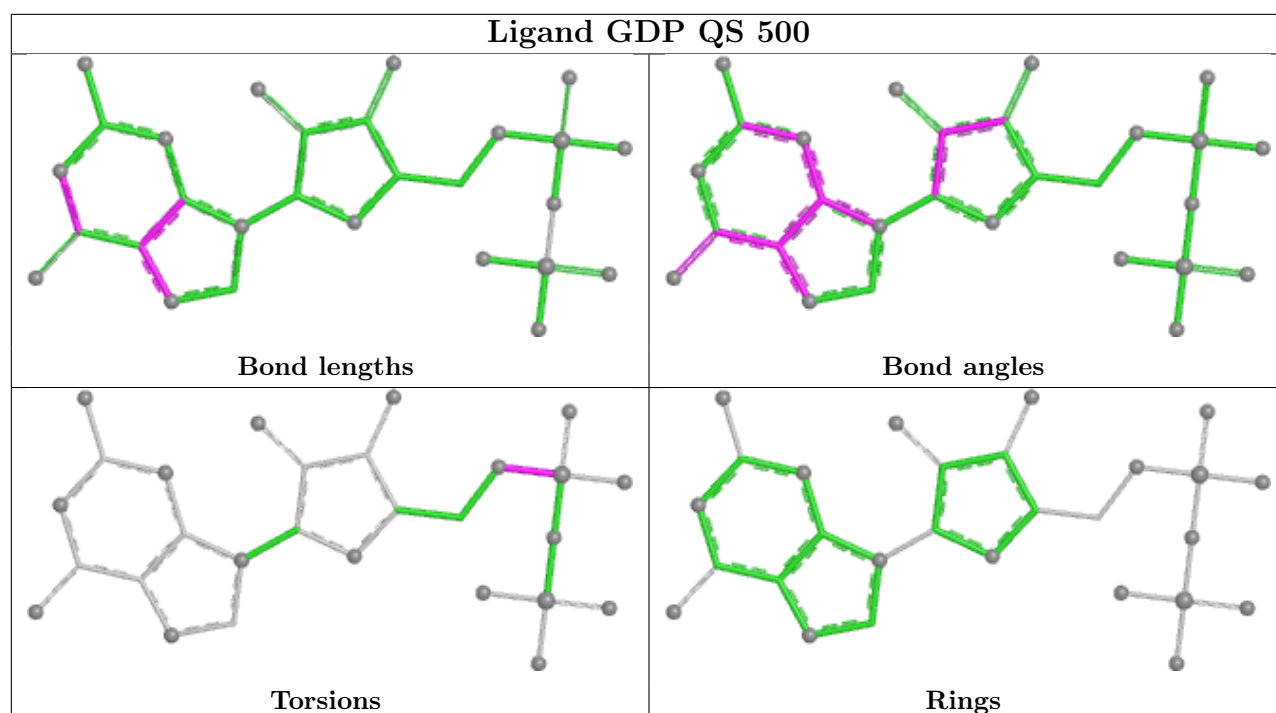




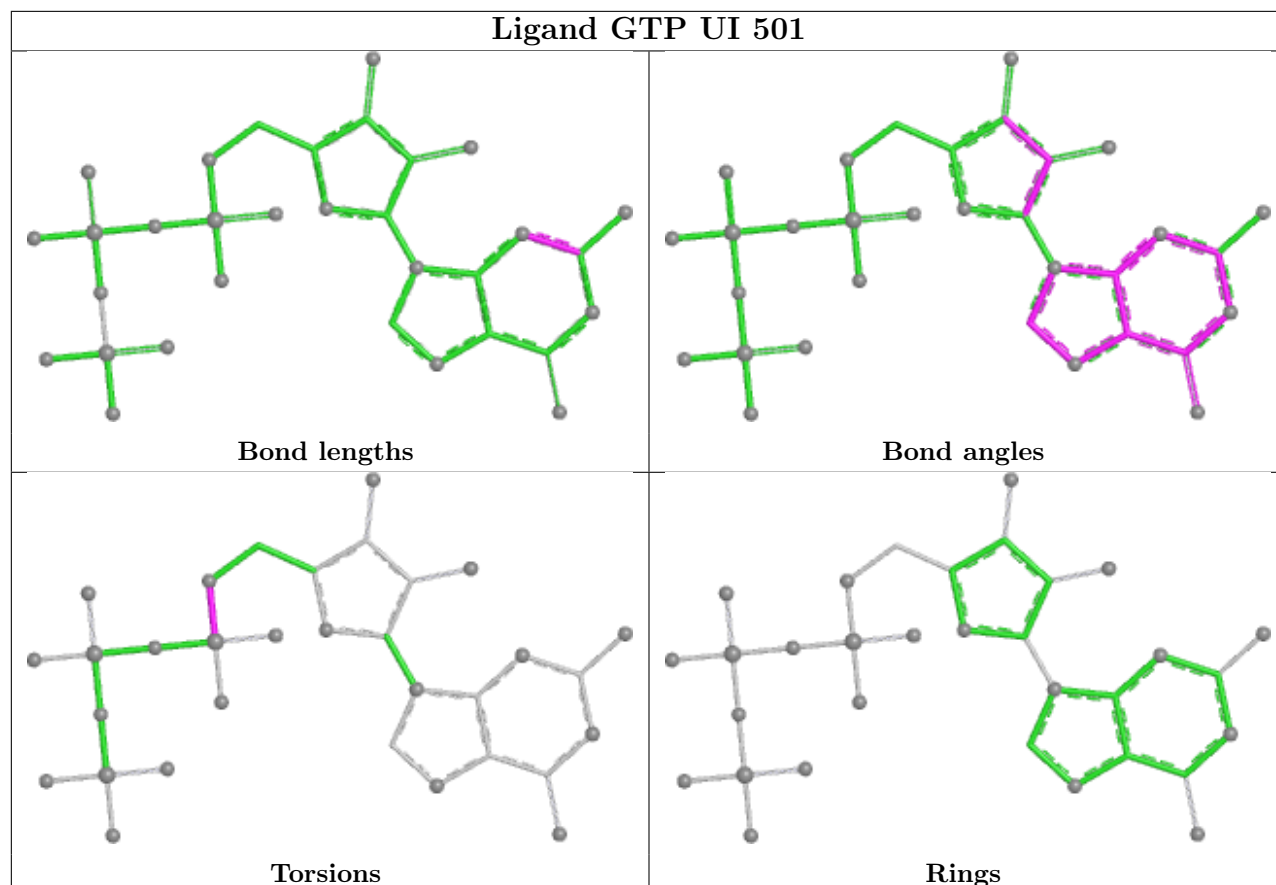




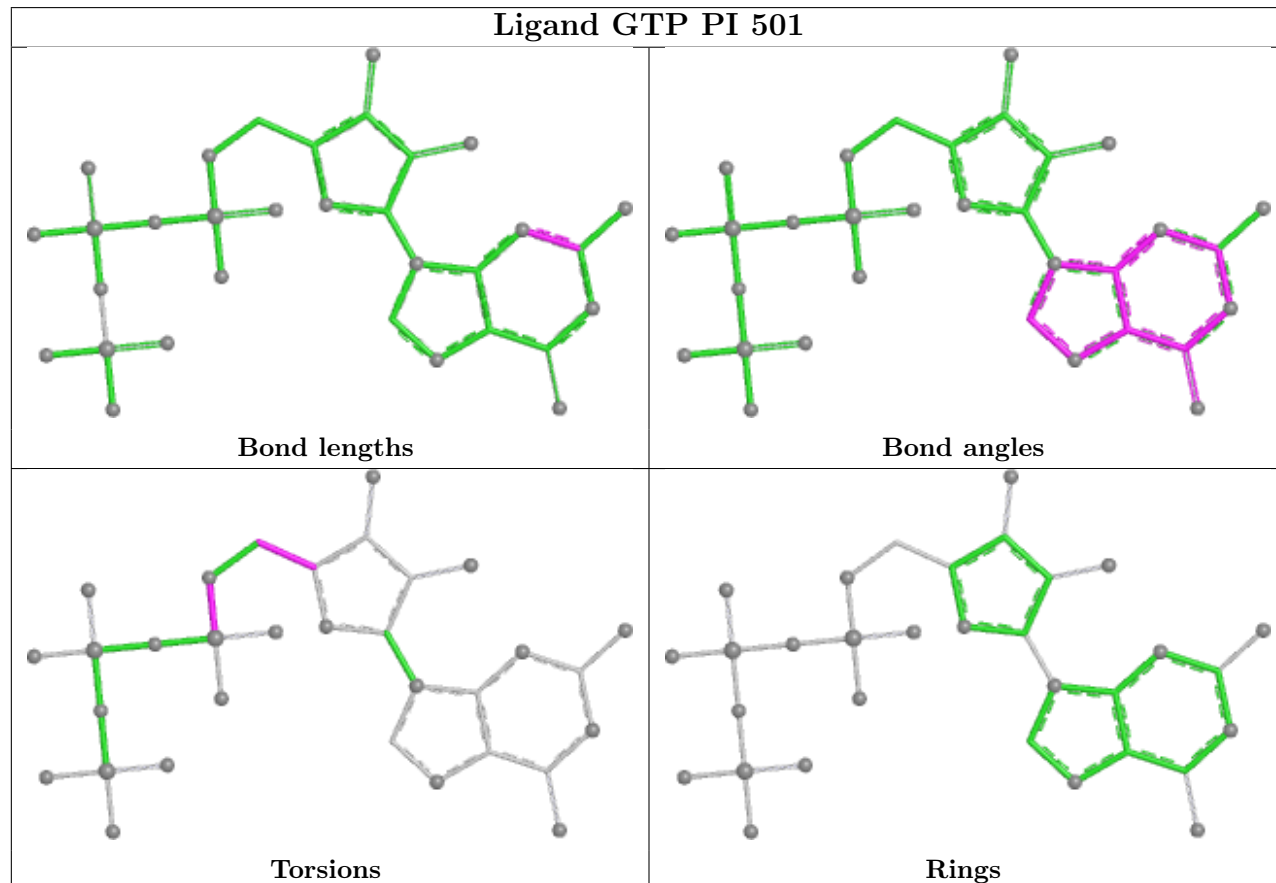


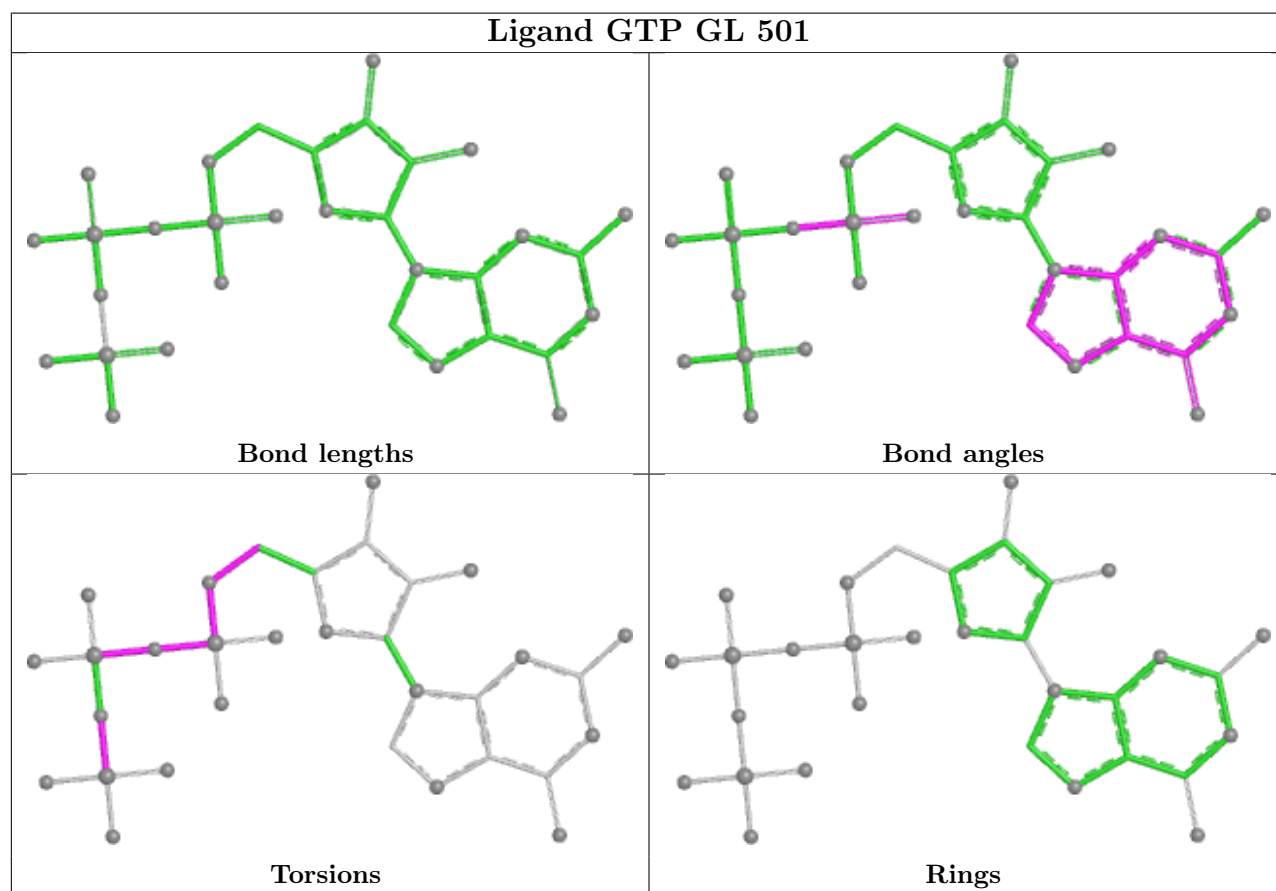
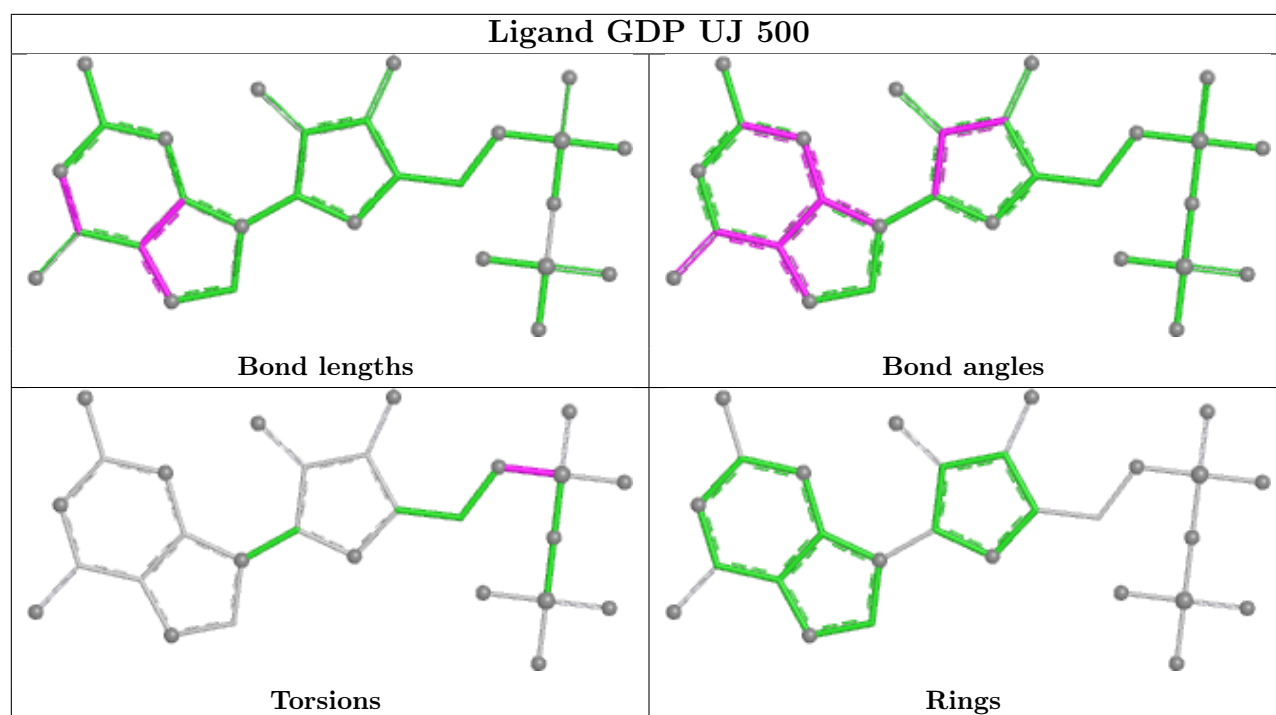


Ligand GTP UI 501

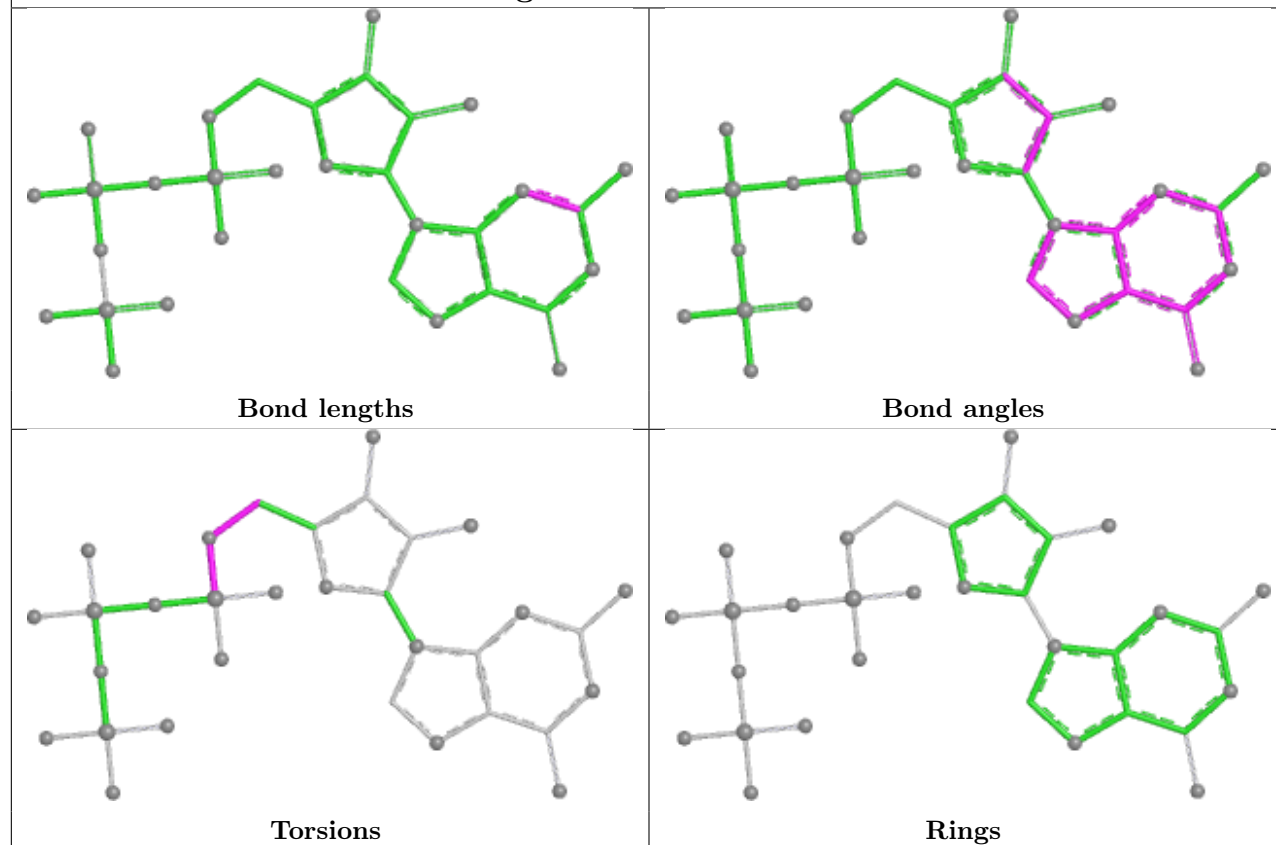


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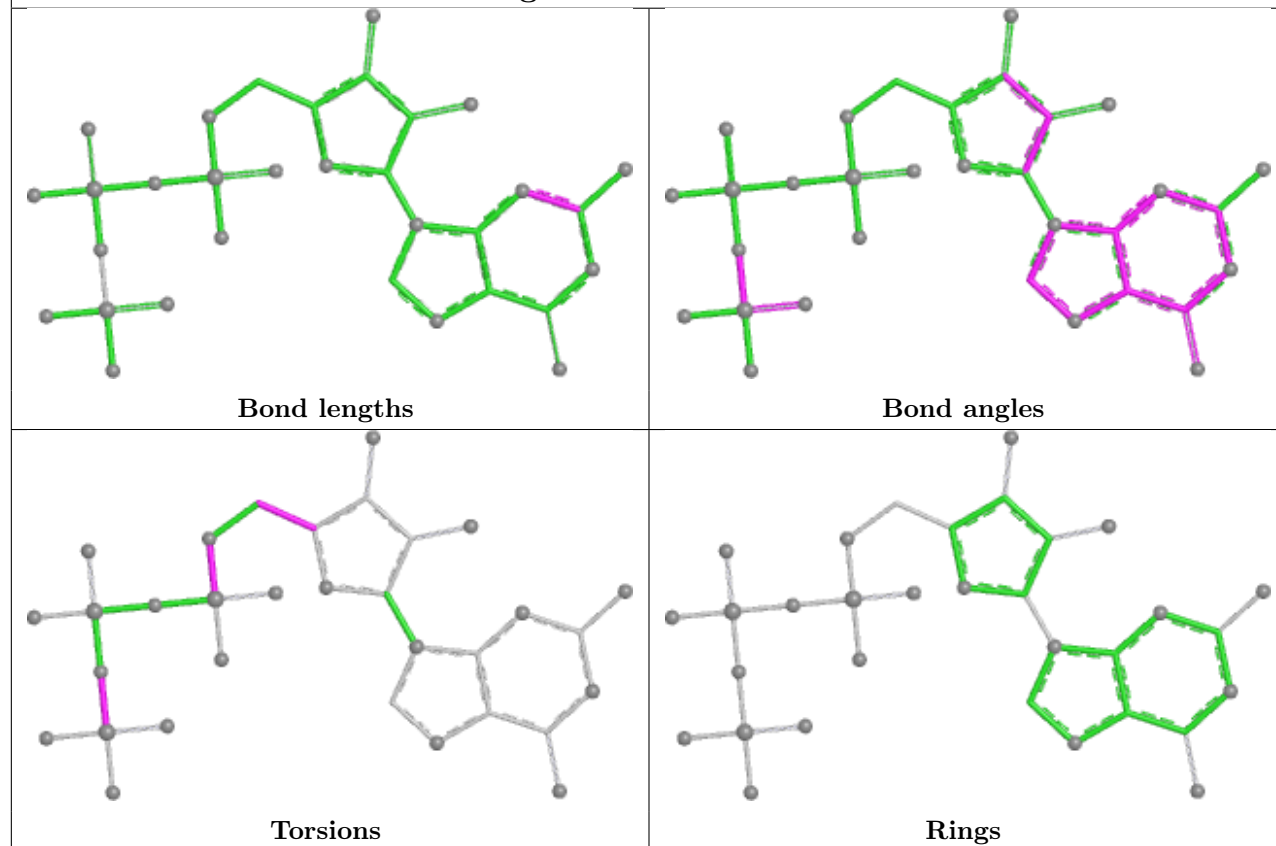




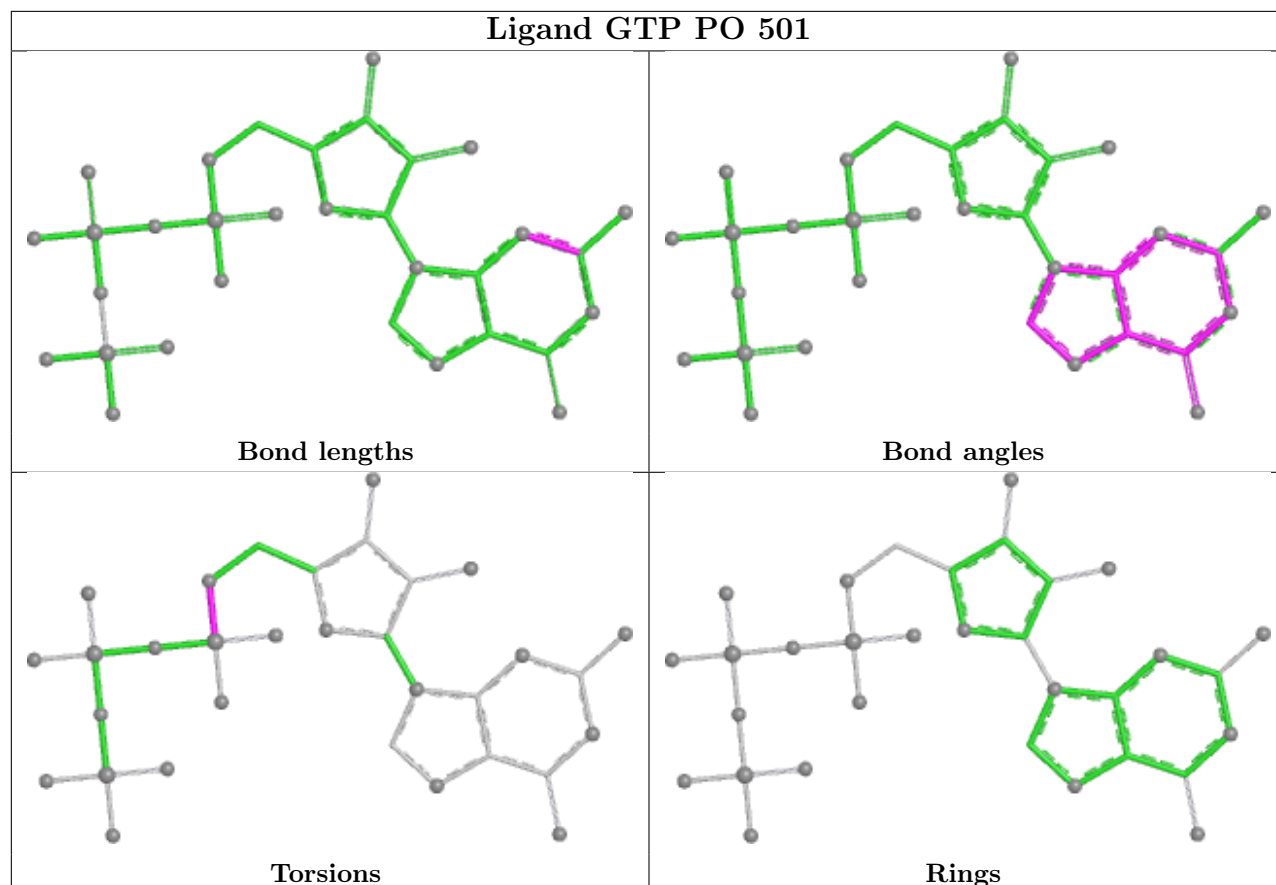
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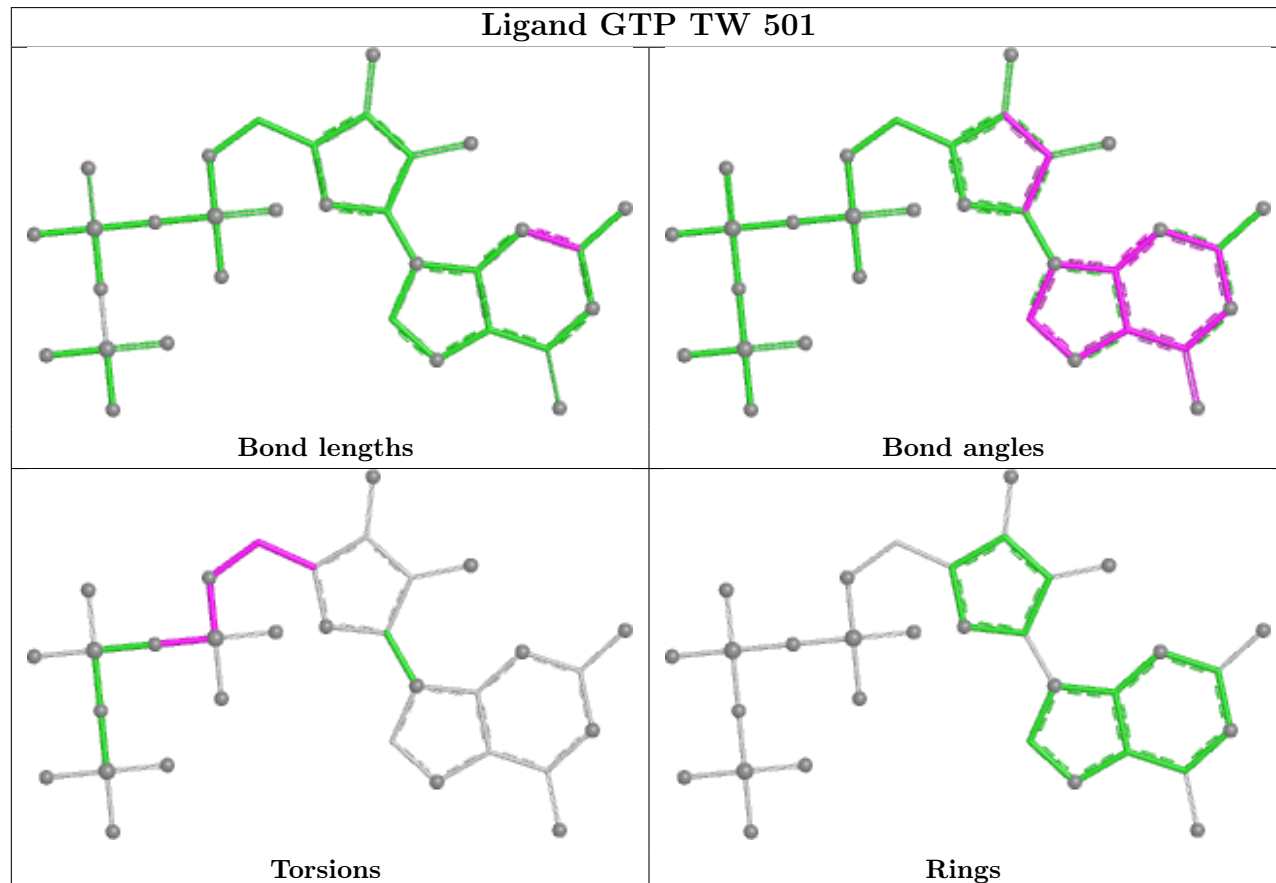
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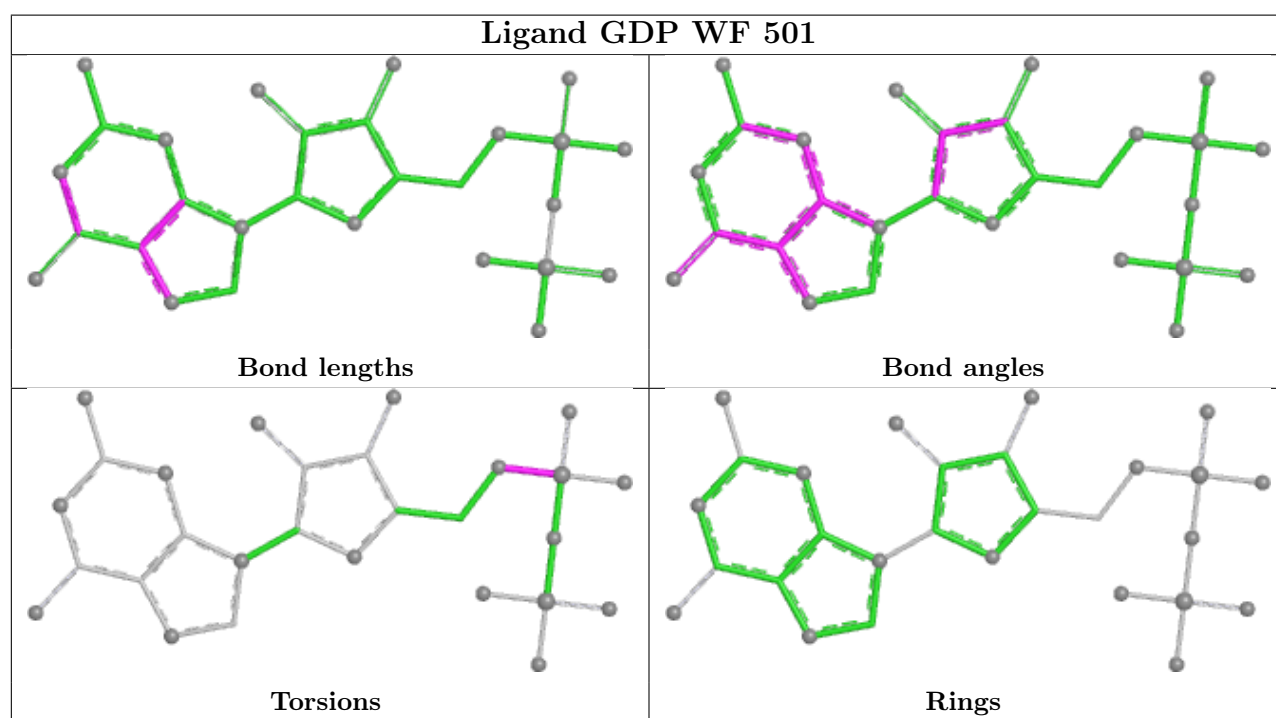
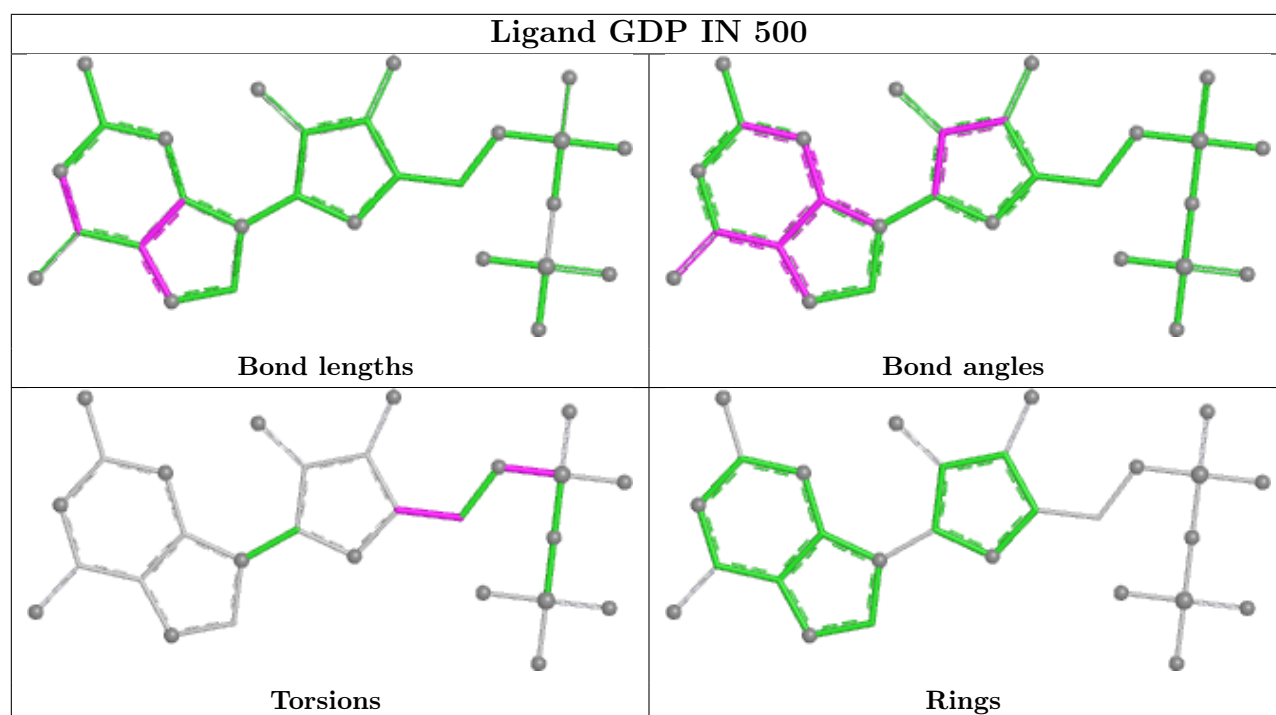


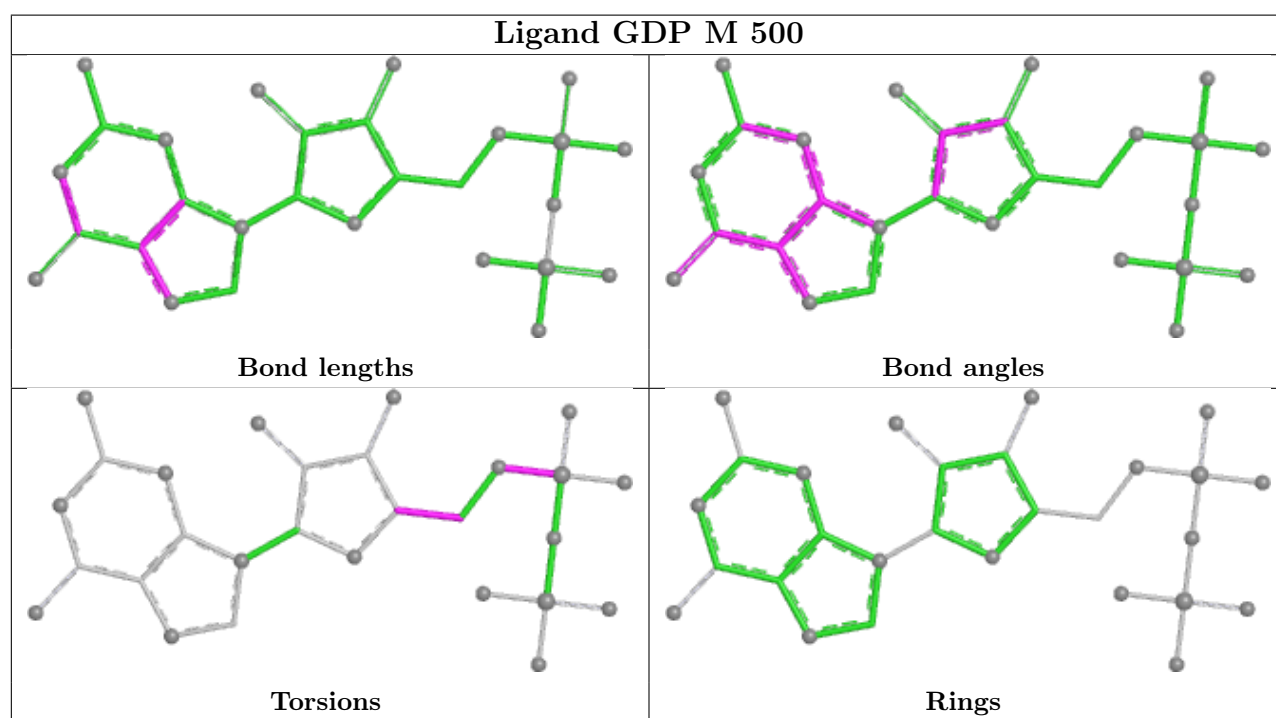
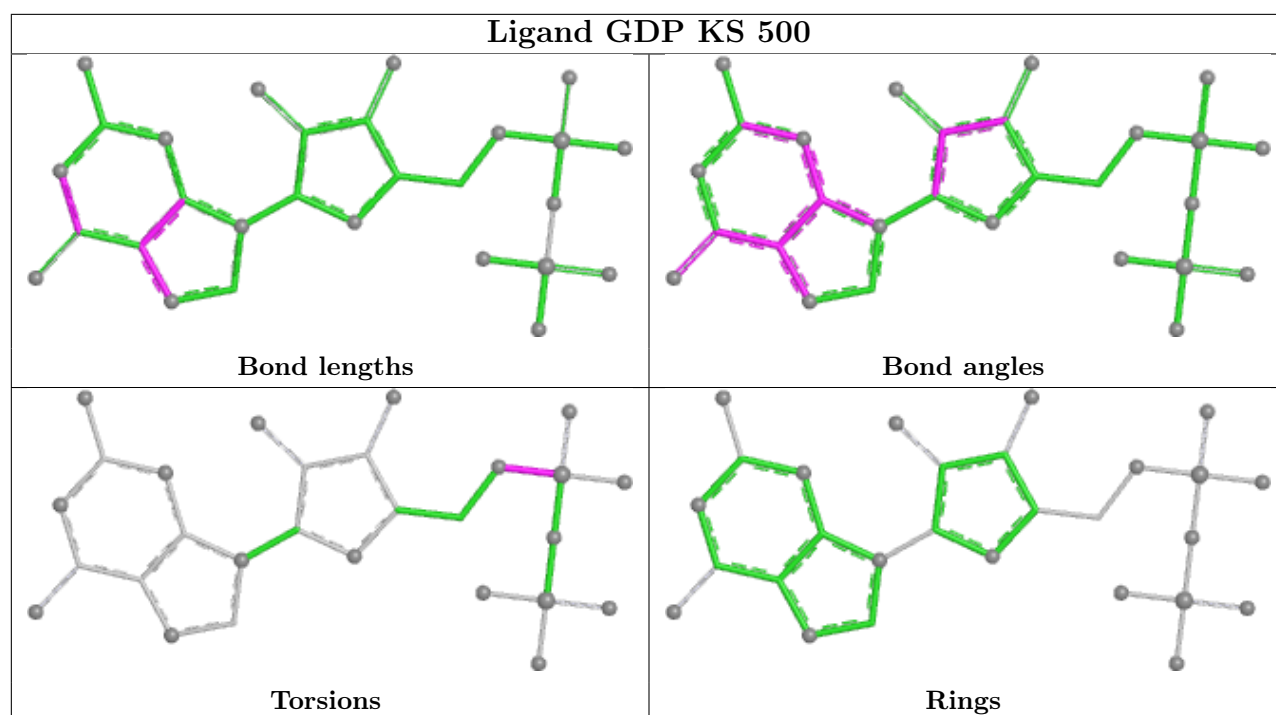
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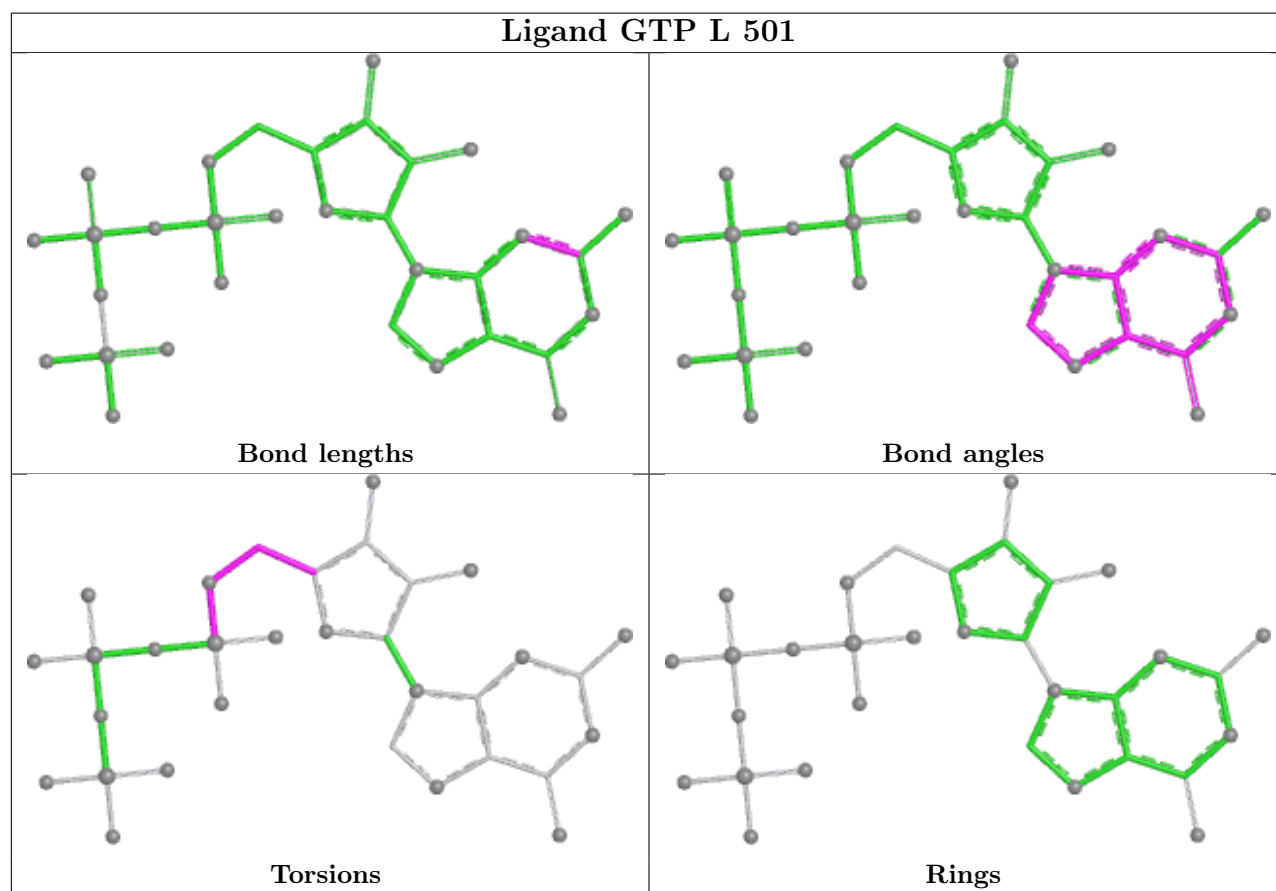
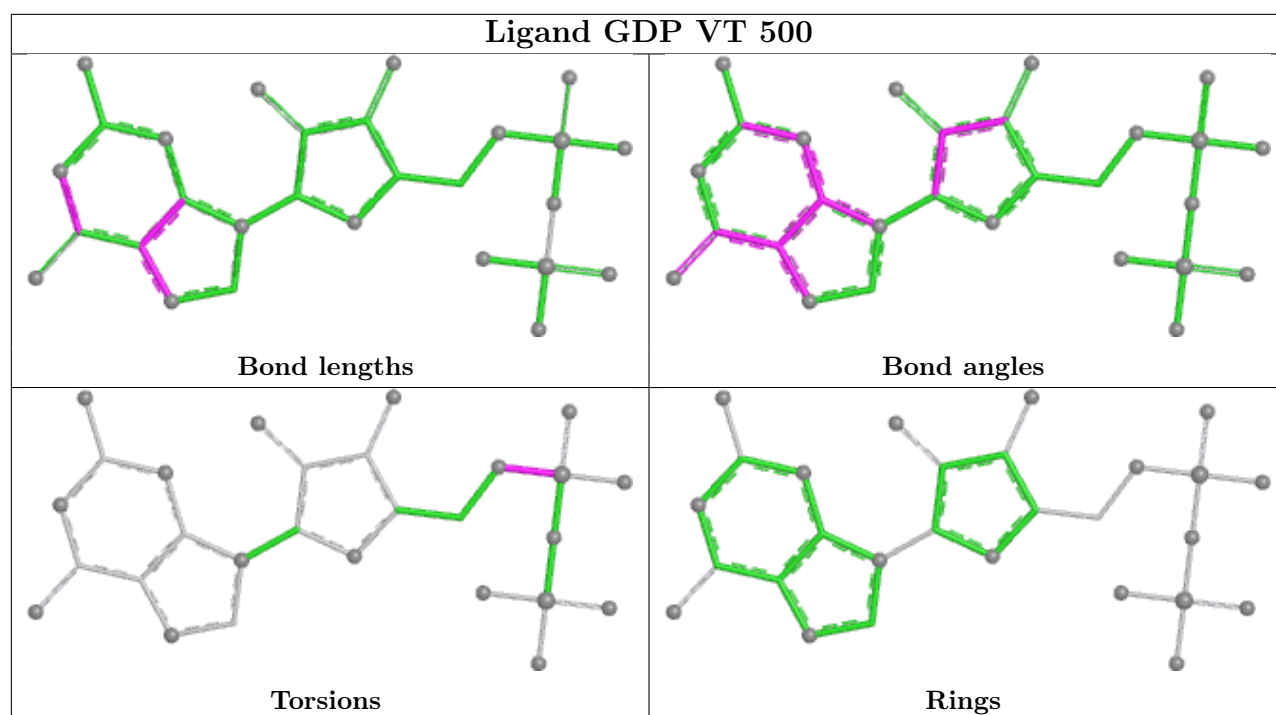


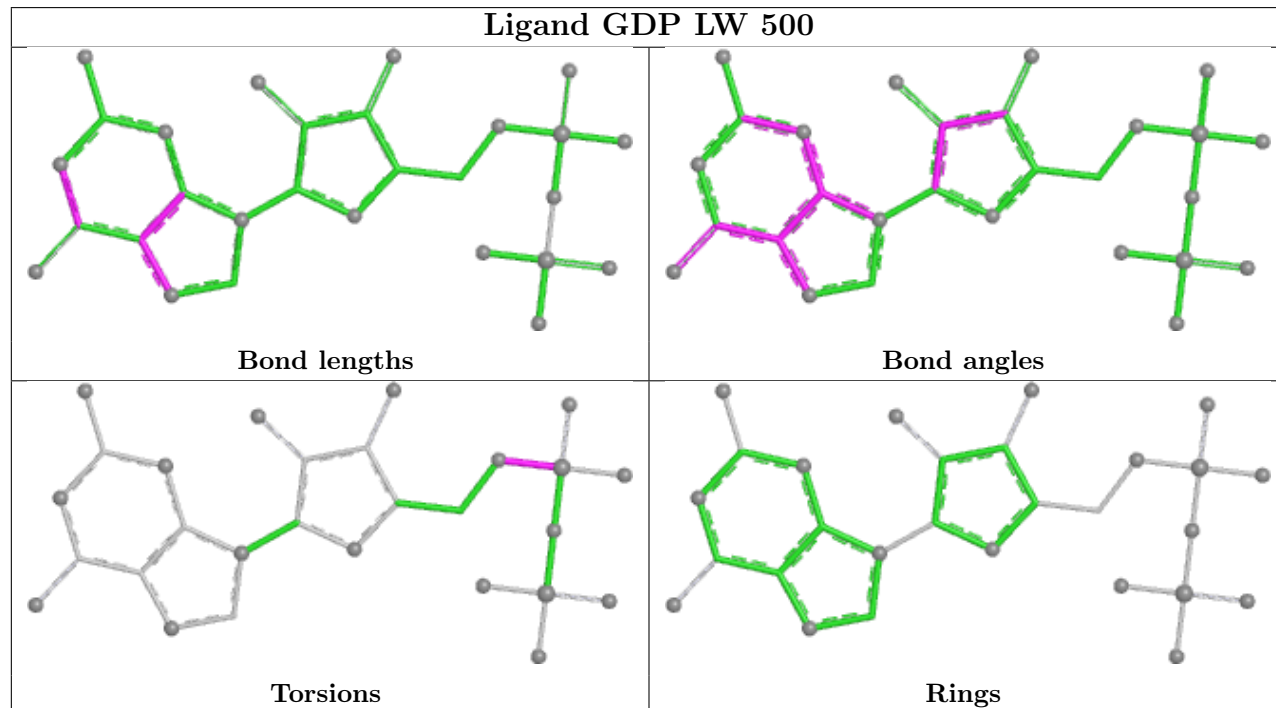
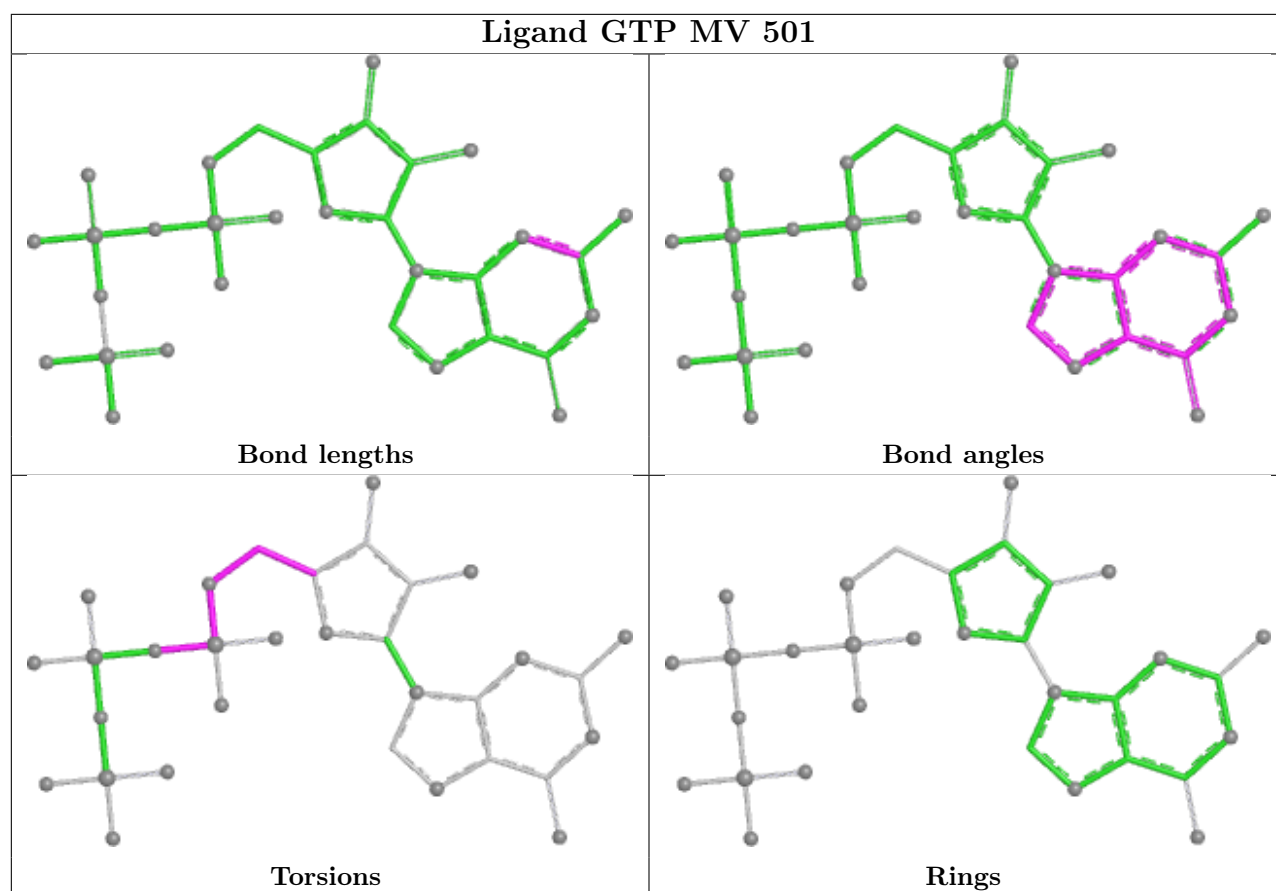
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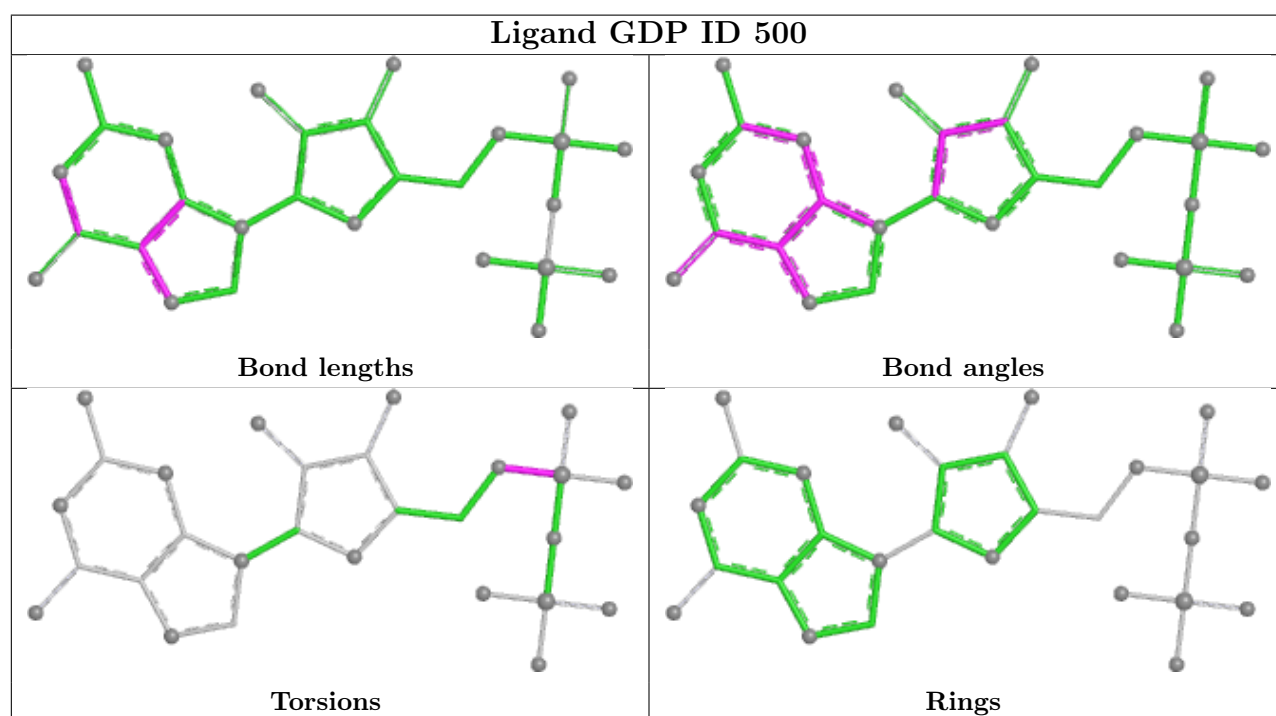
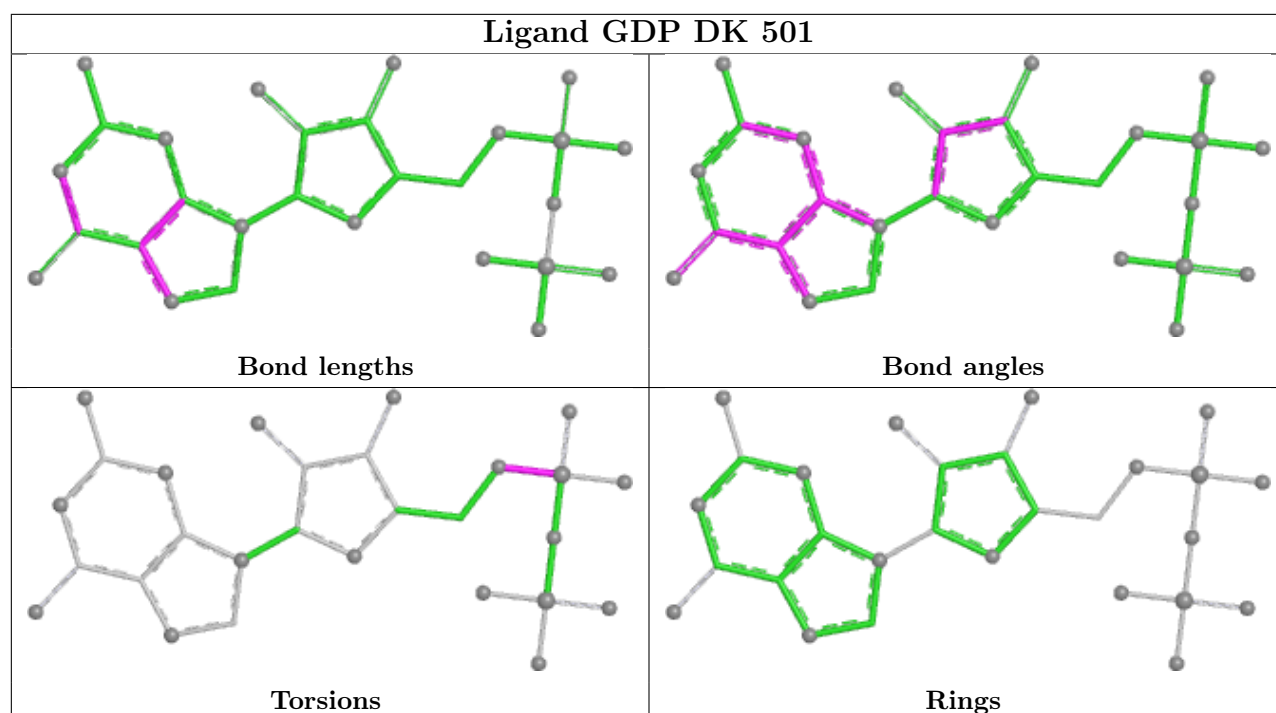


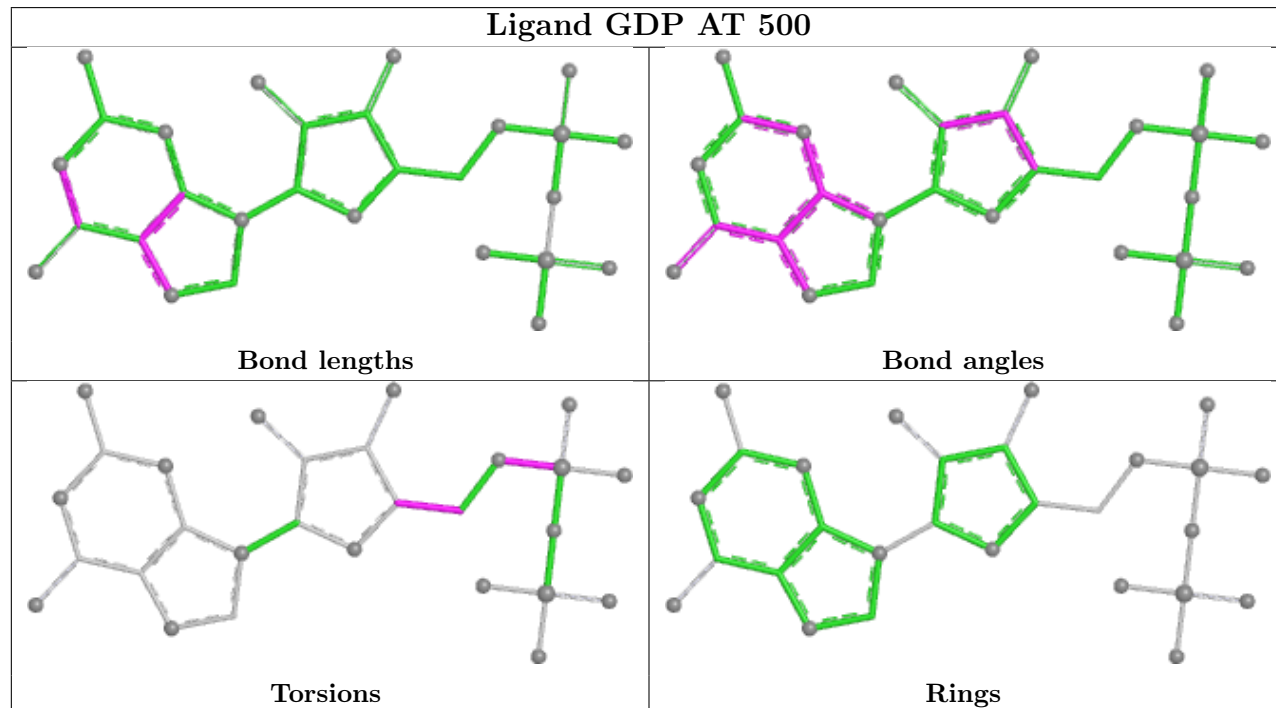
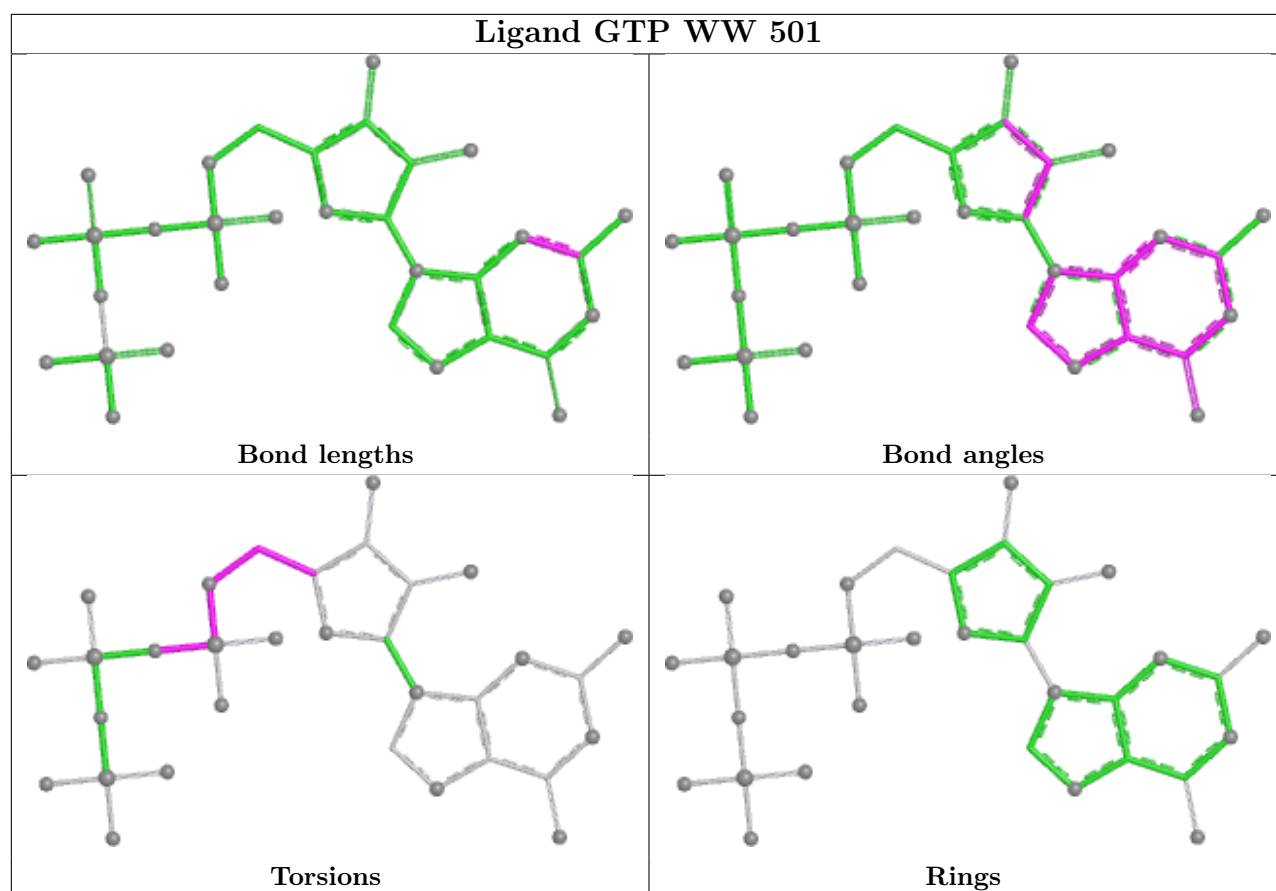


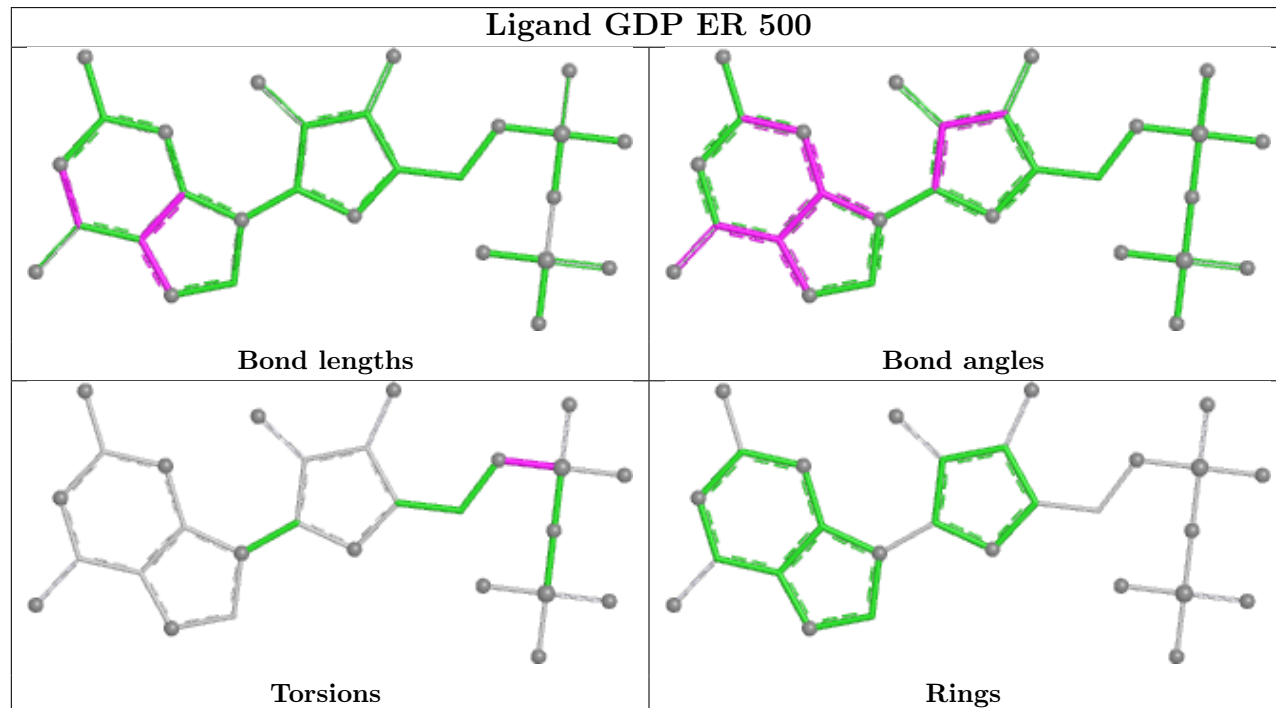
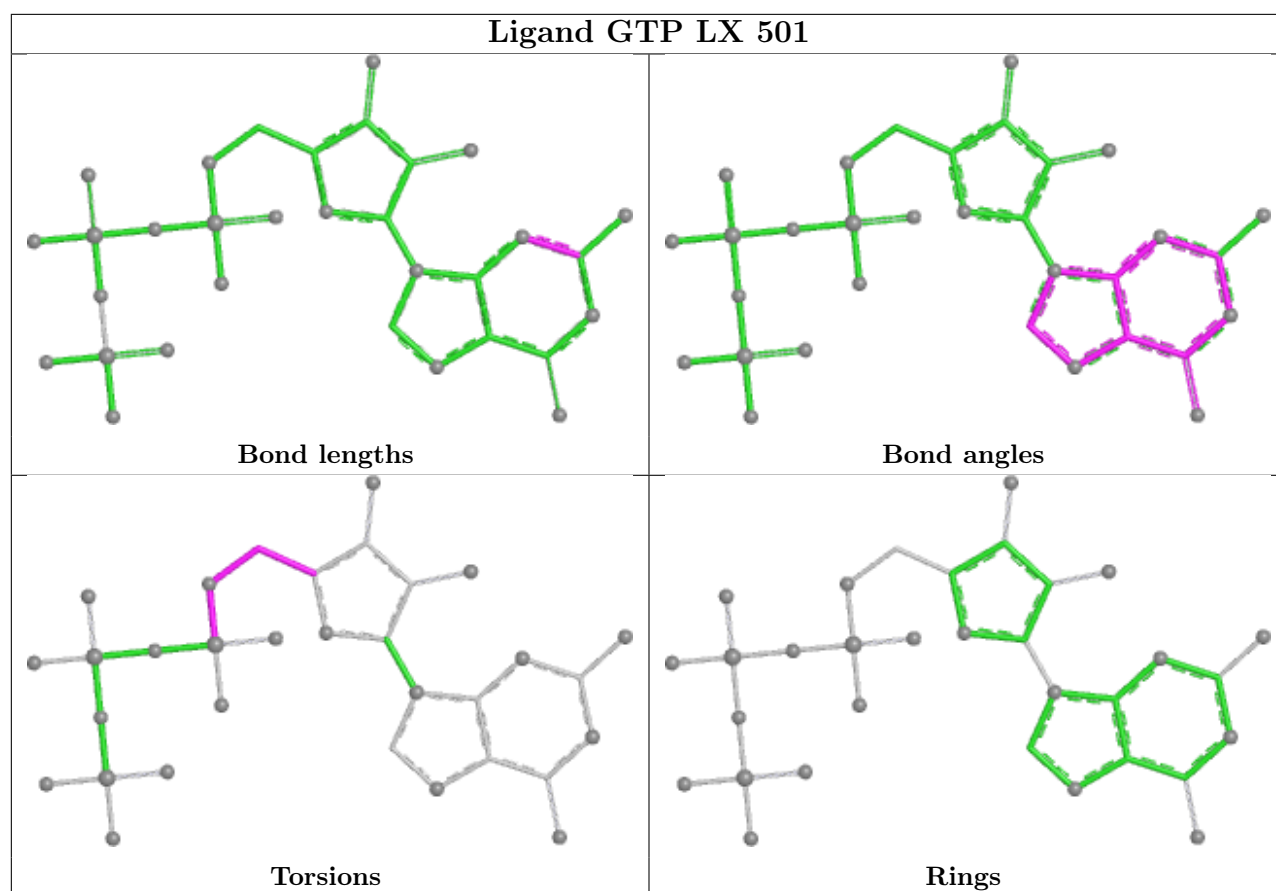


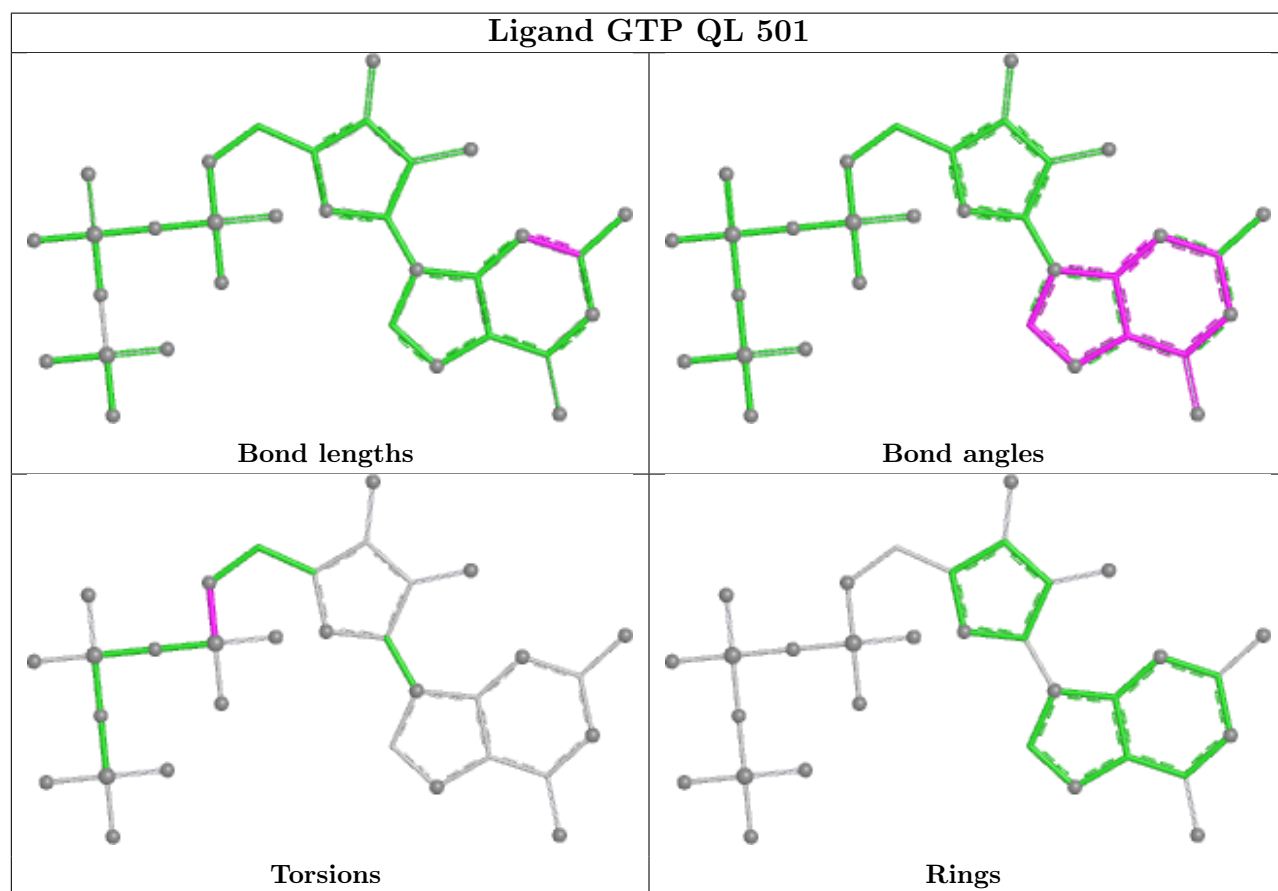
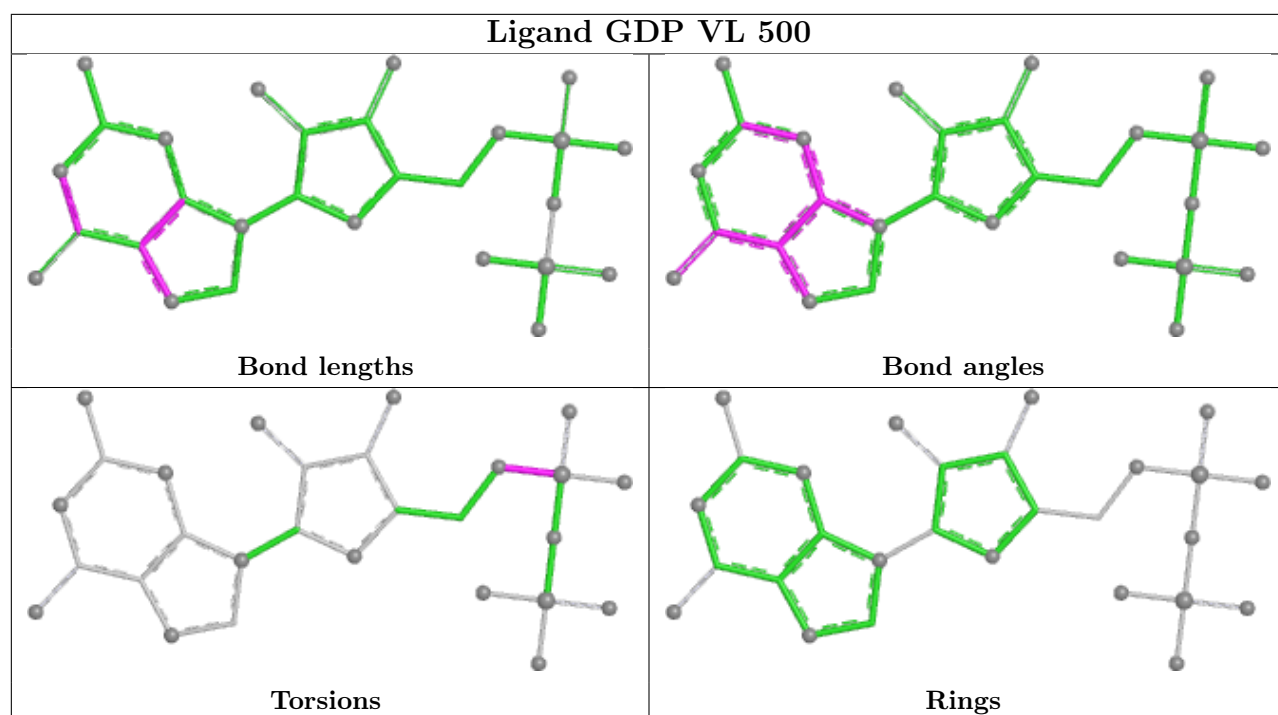




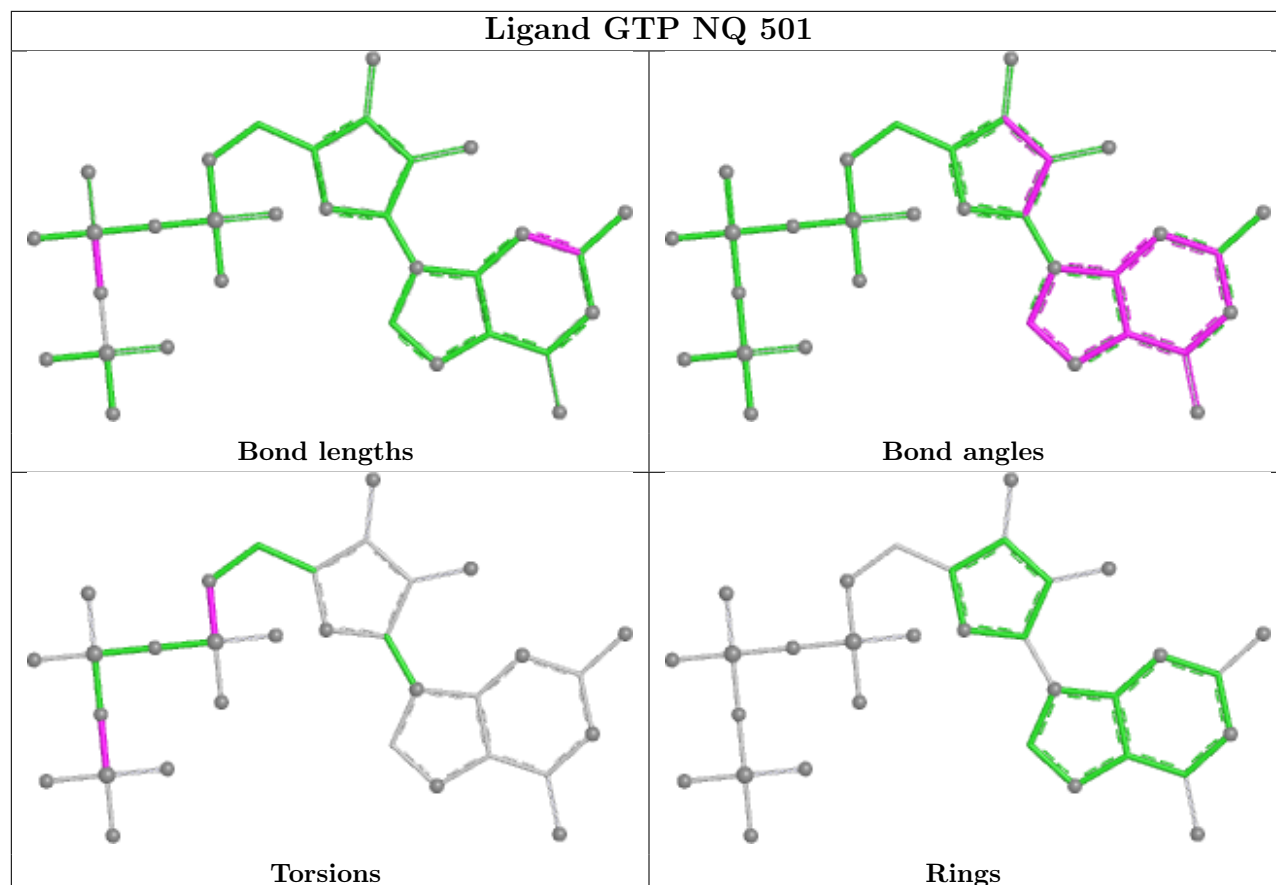




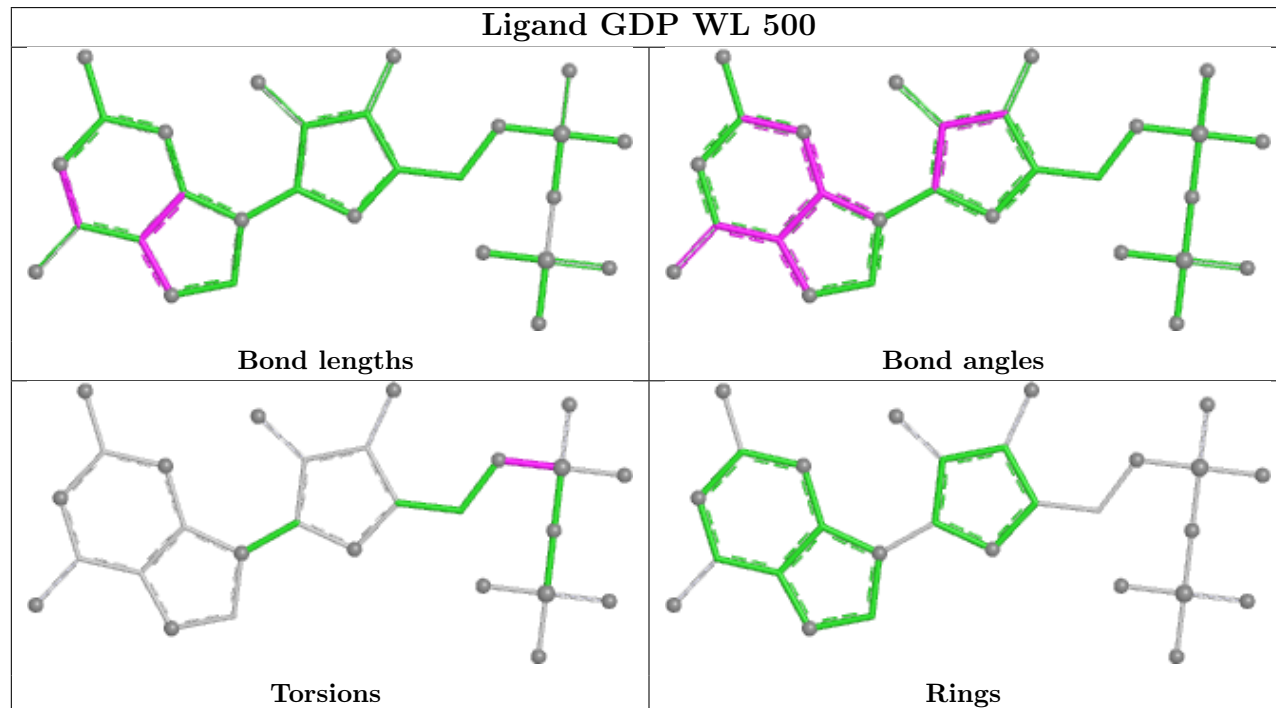




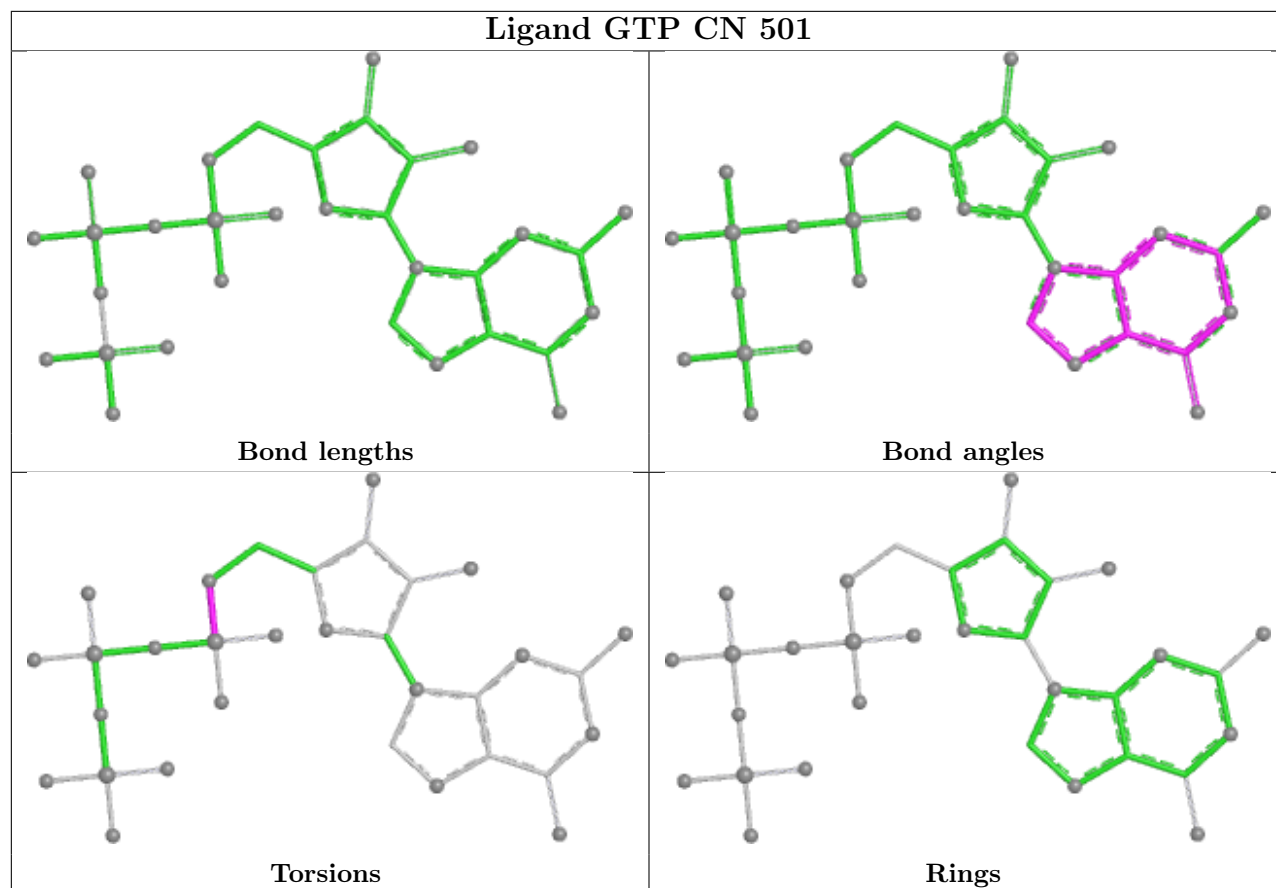
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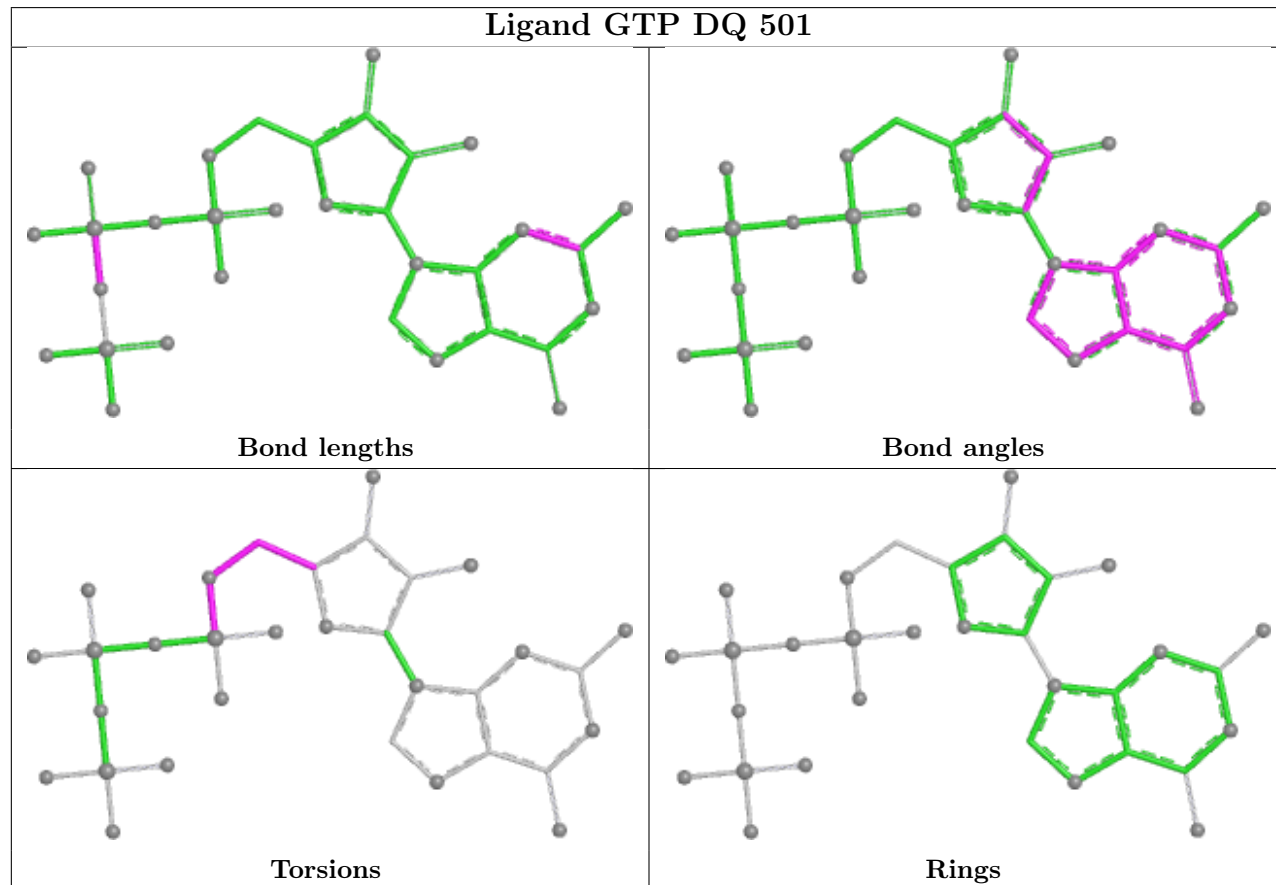
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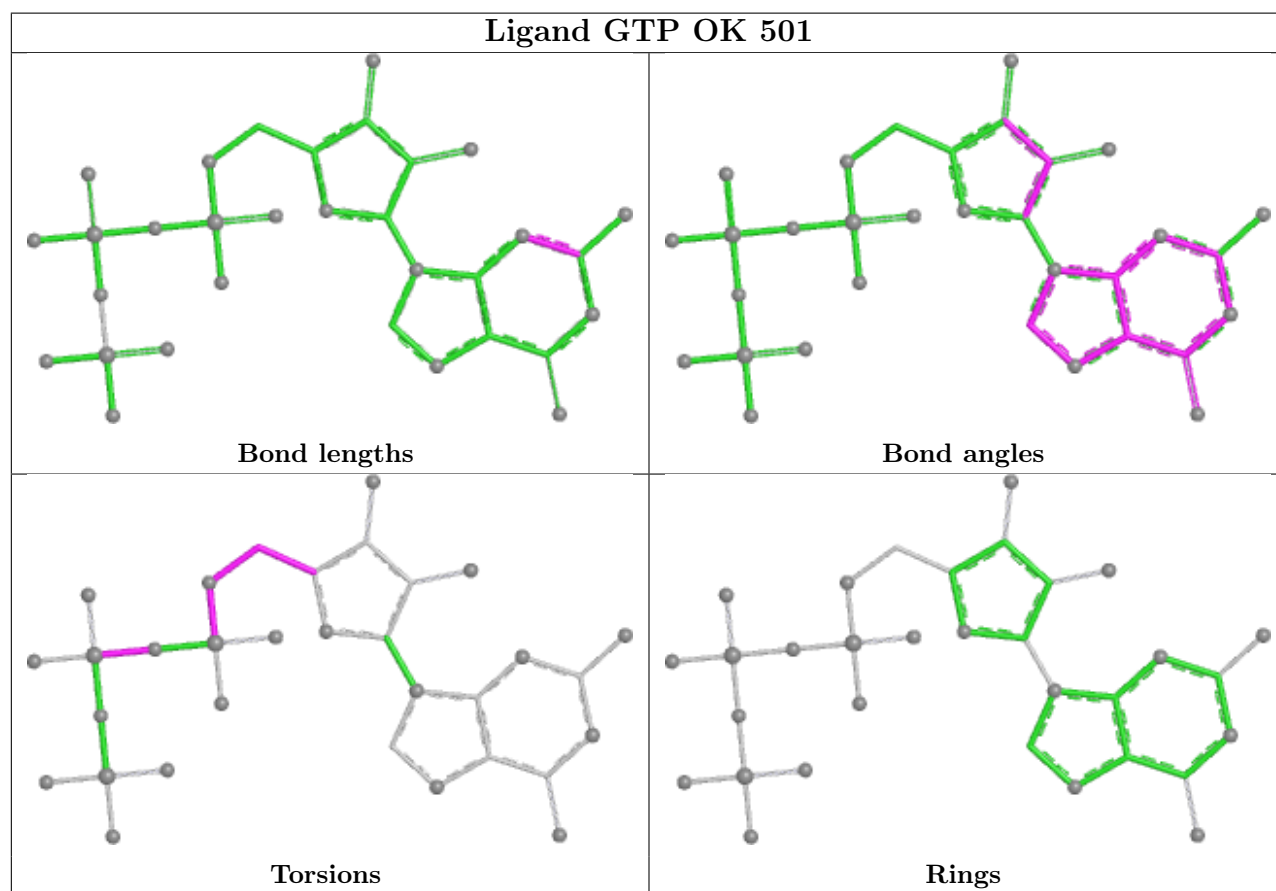
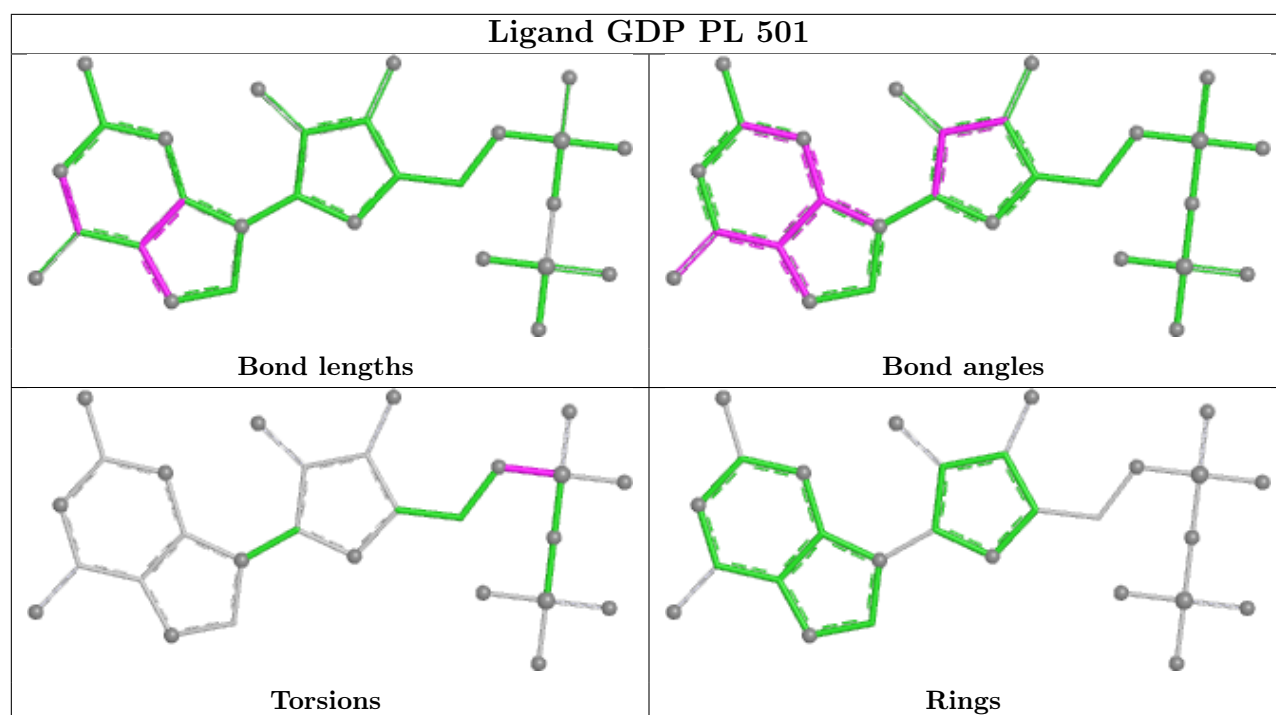


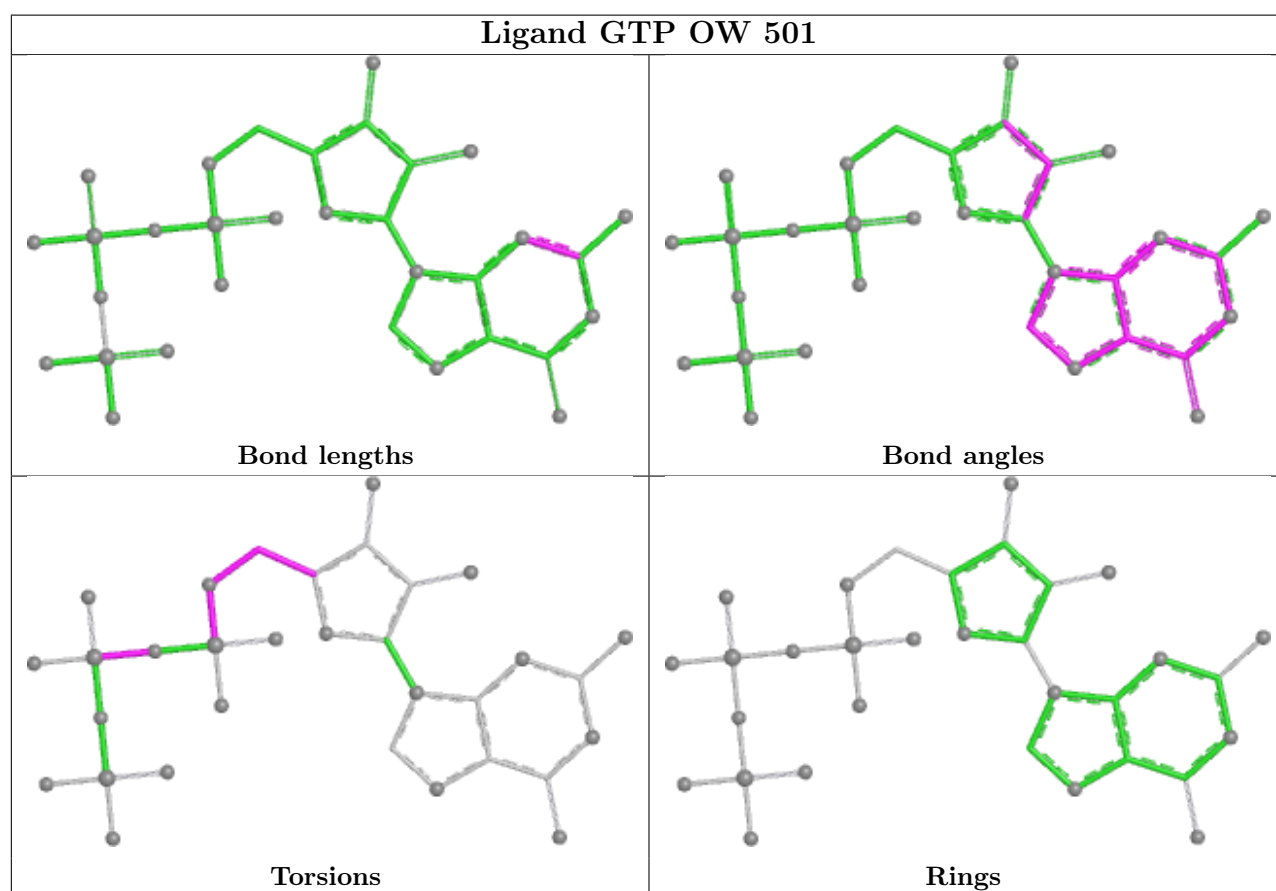
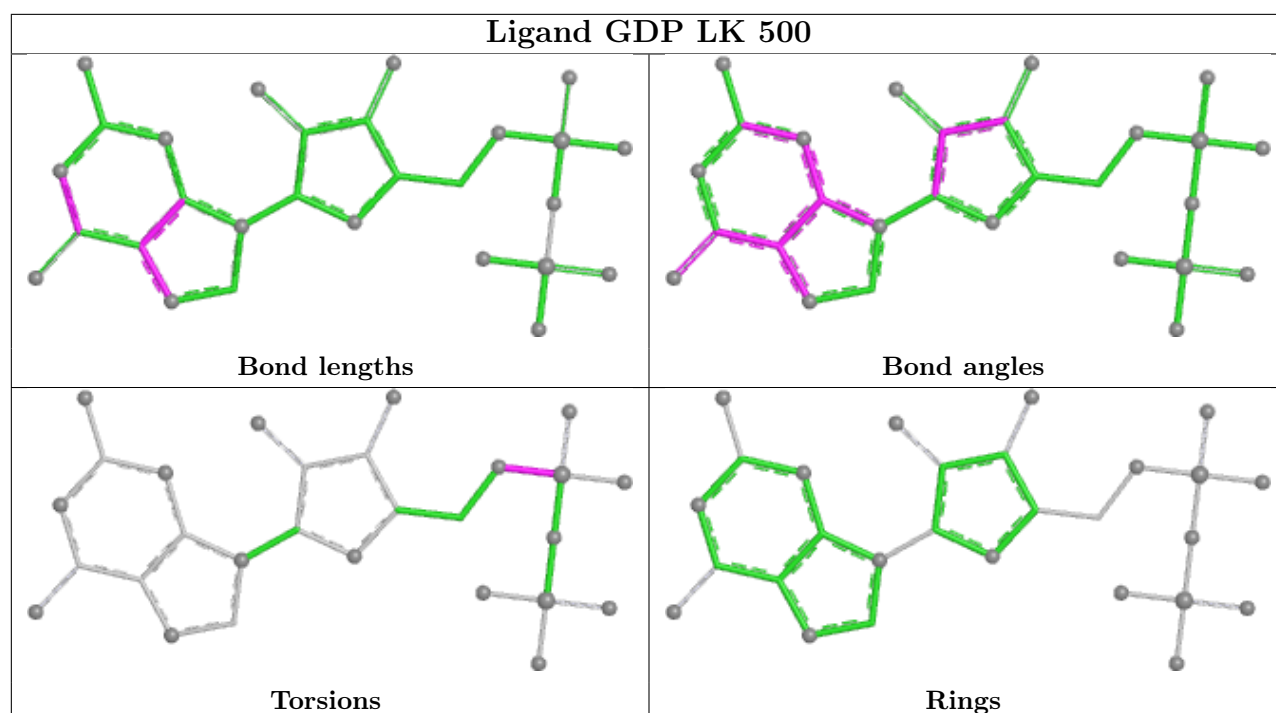
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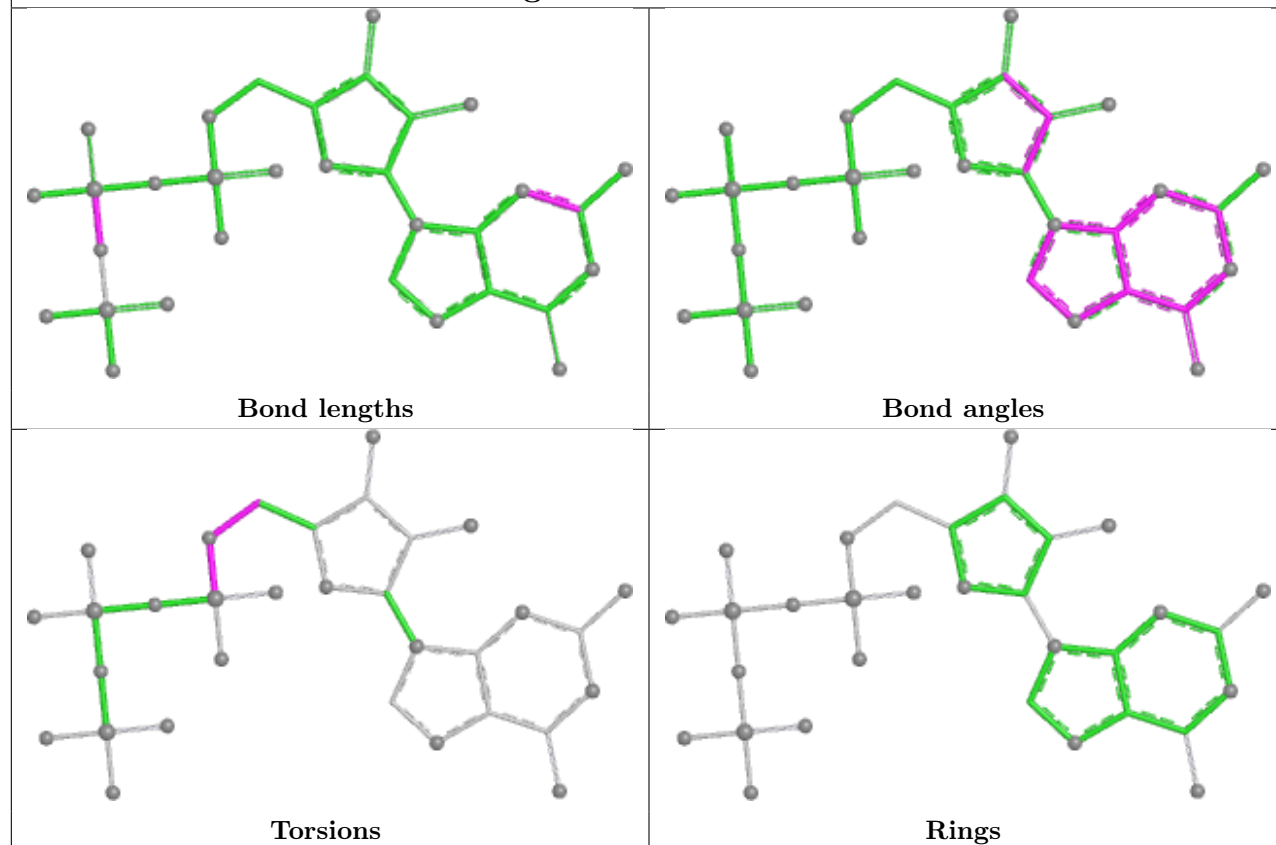
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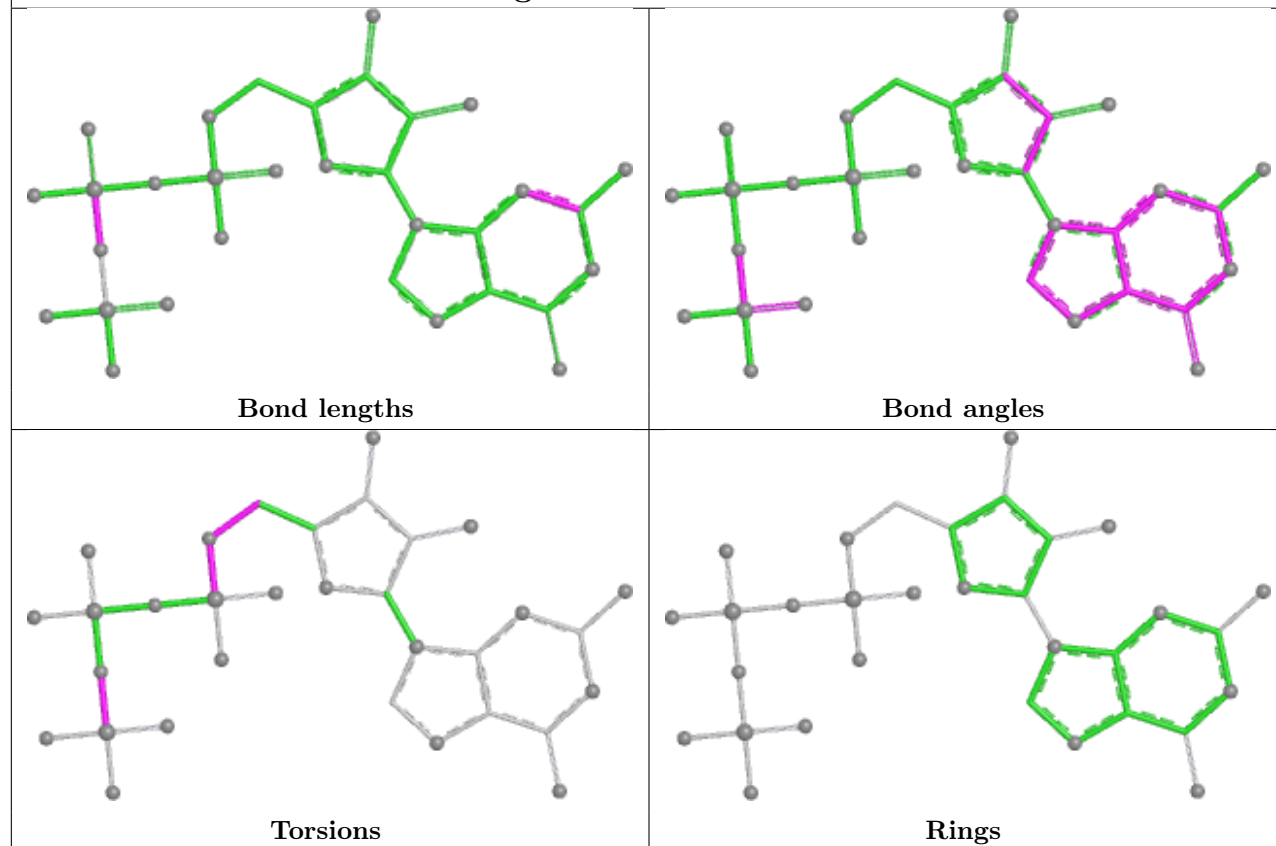


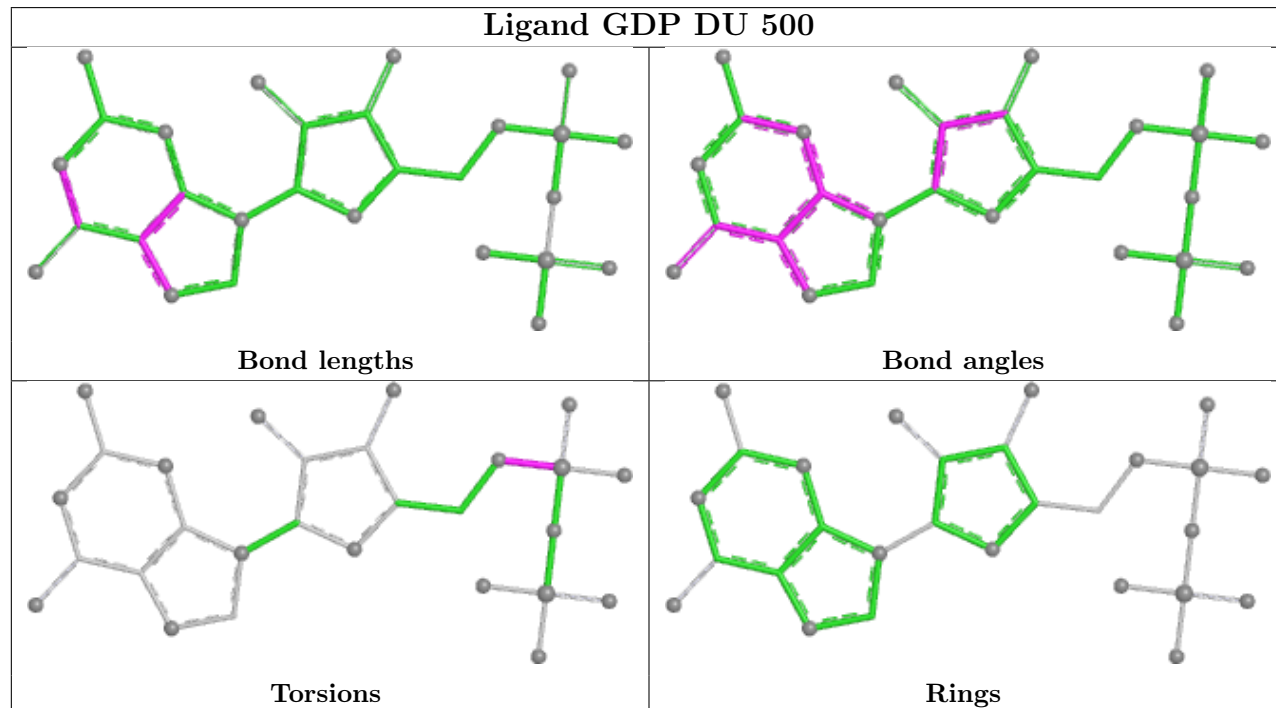
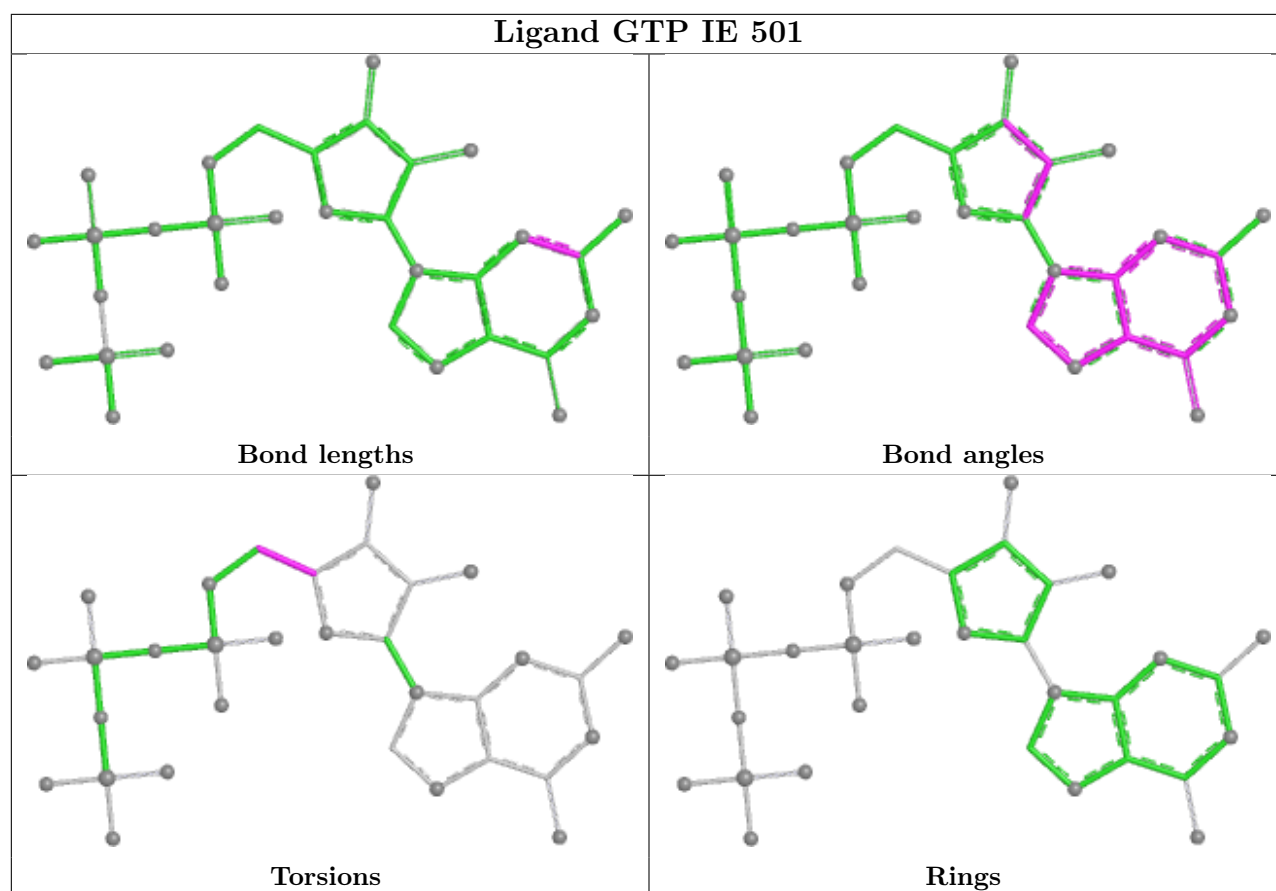


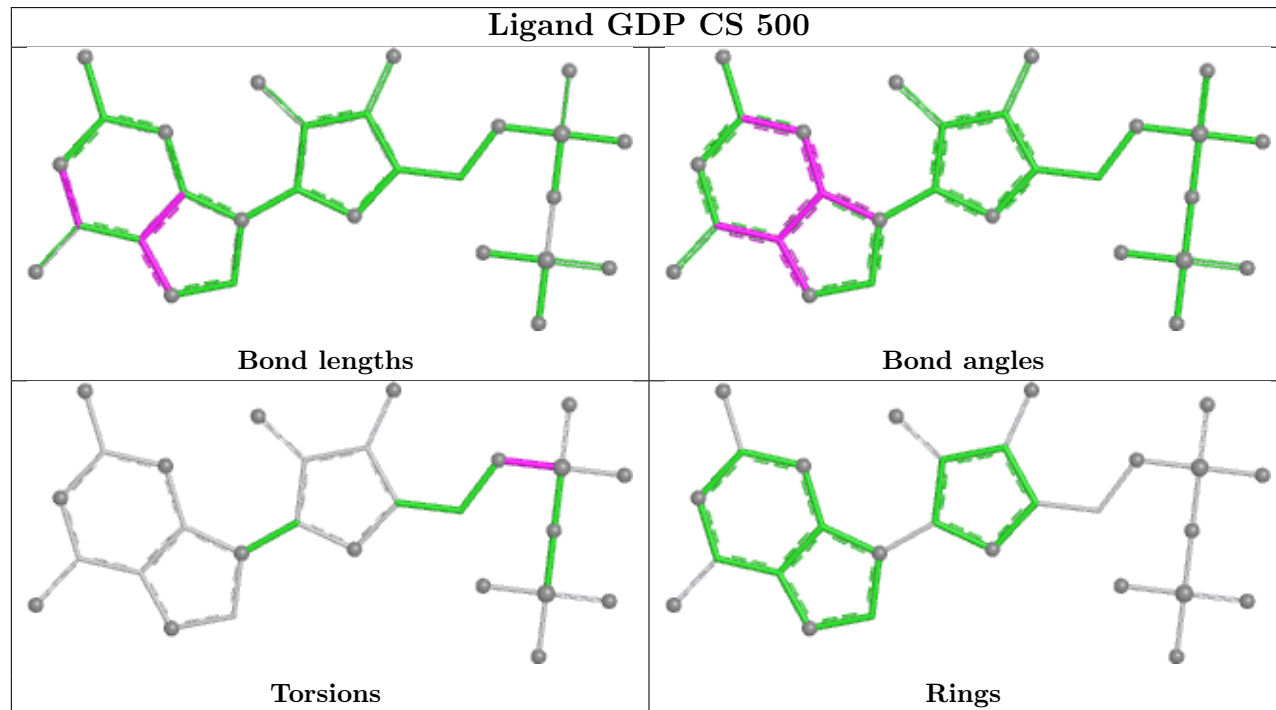
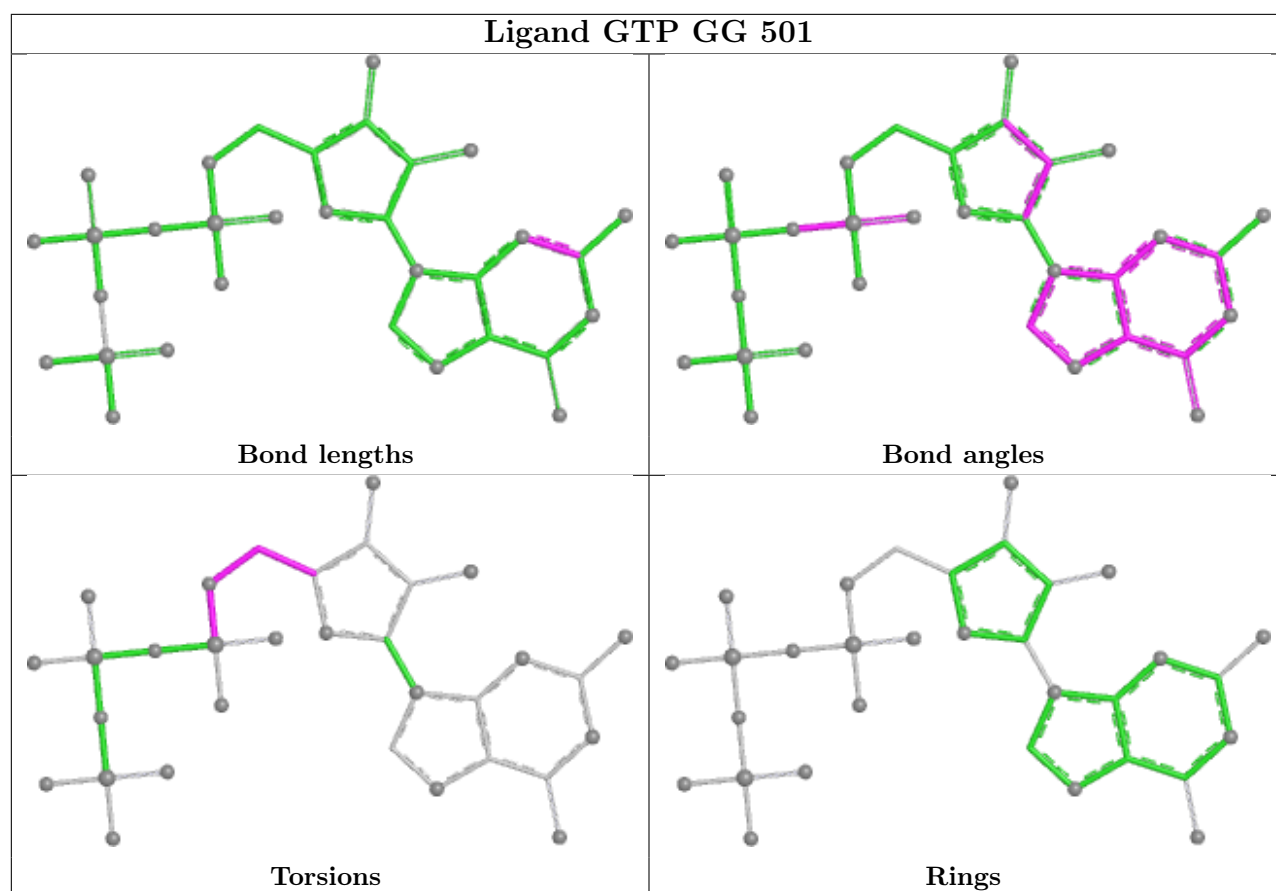
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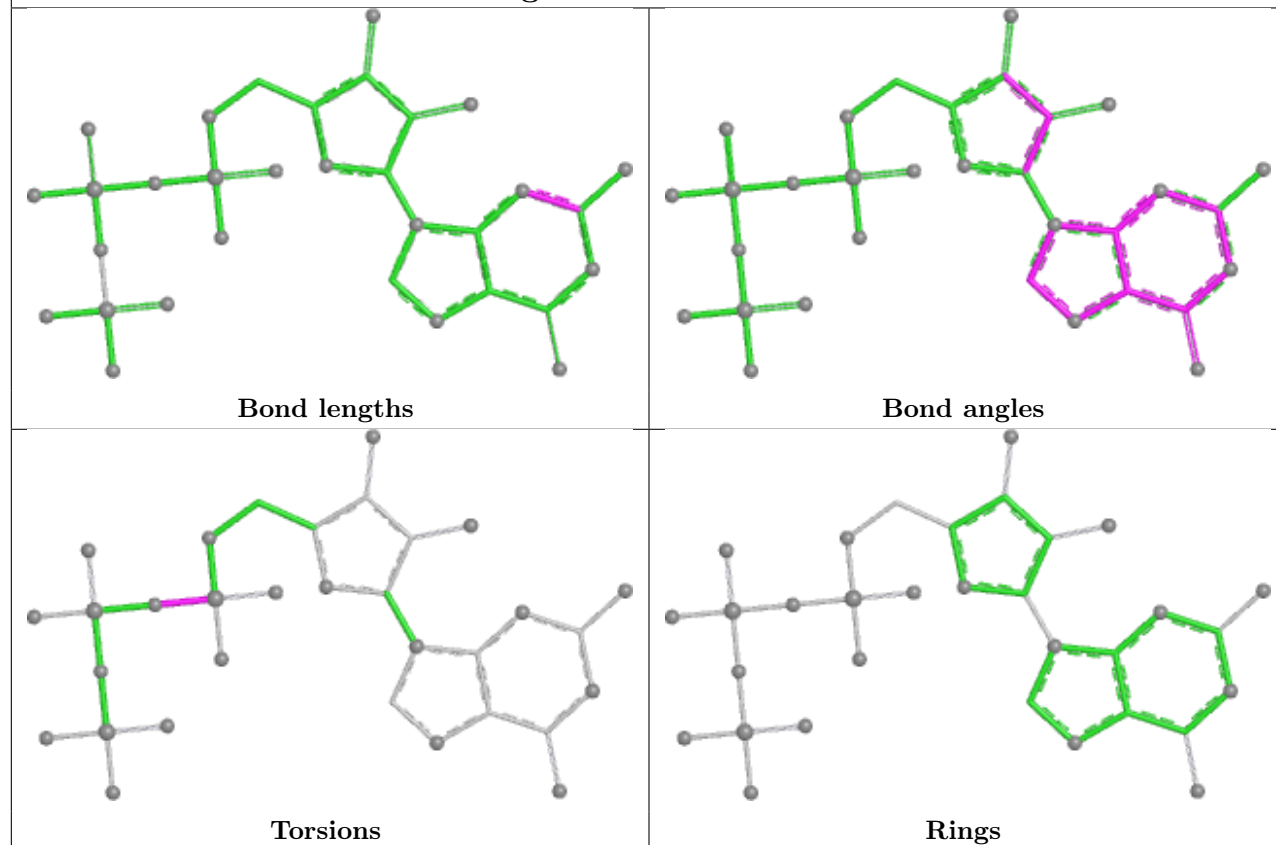
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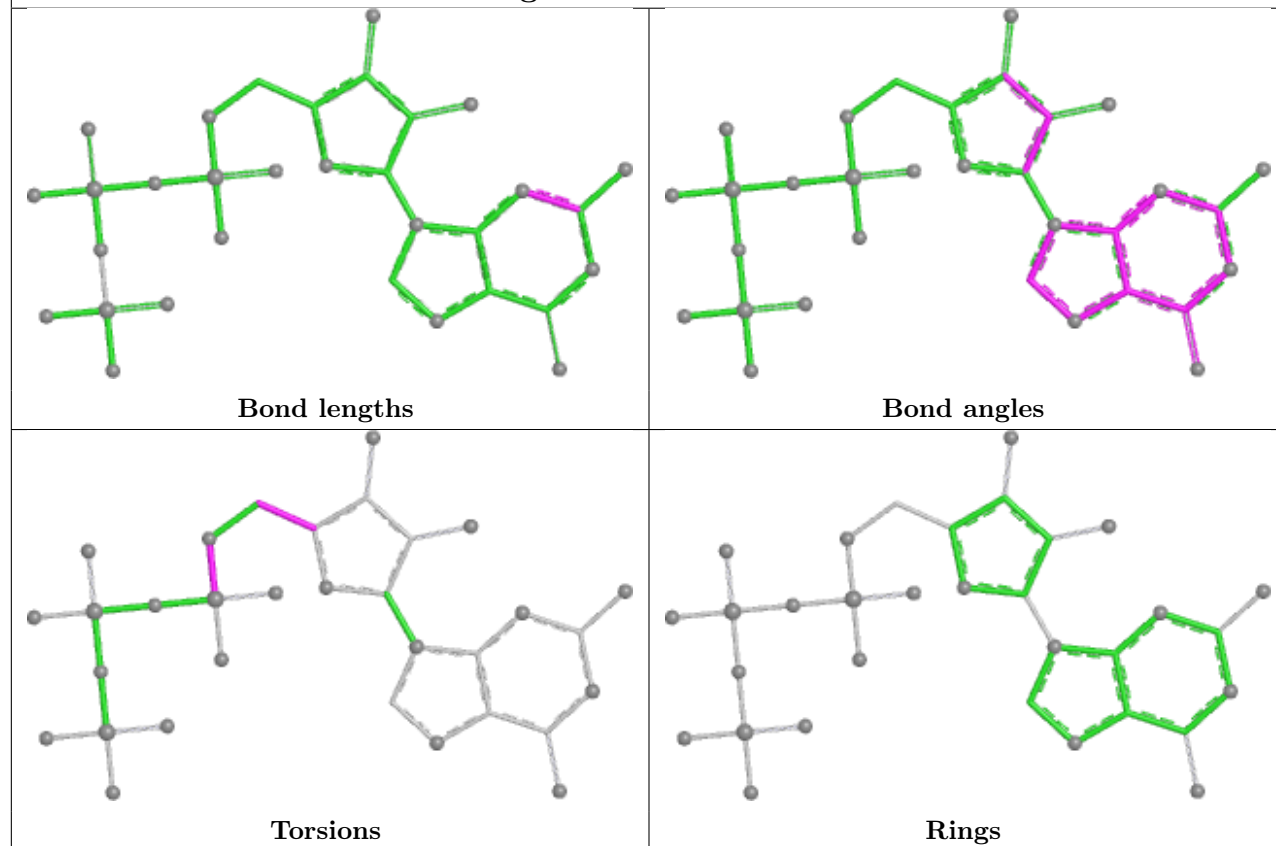


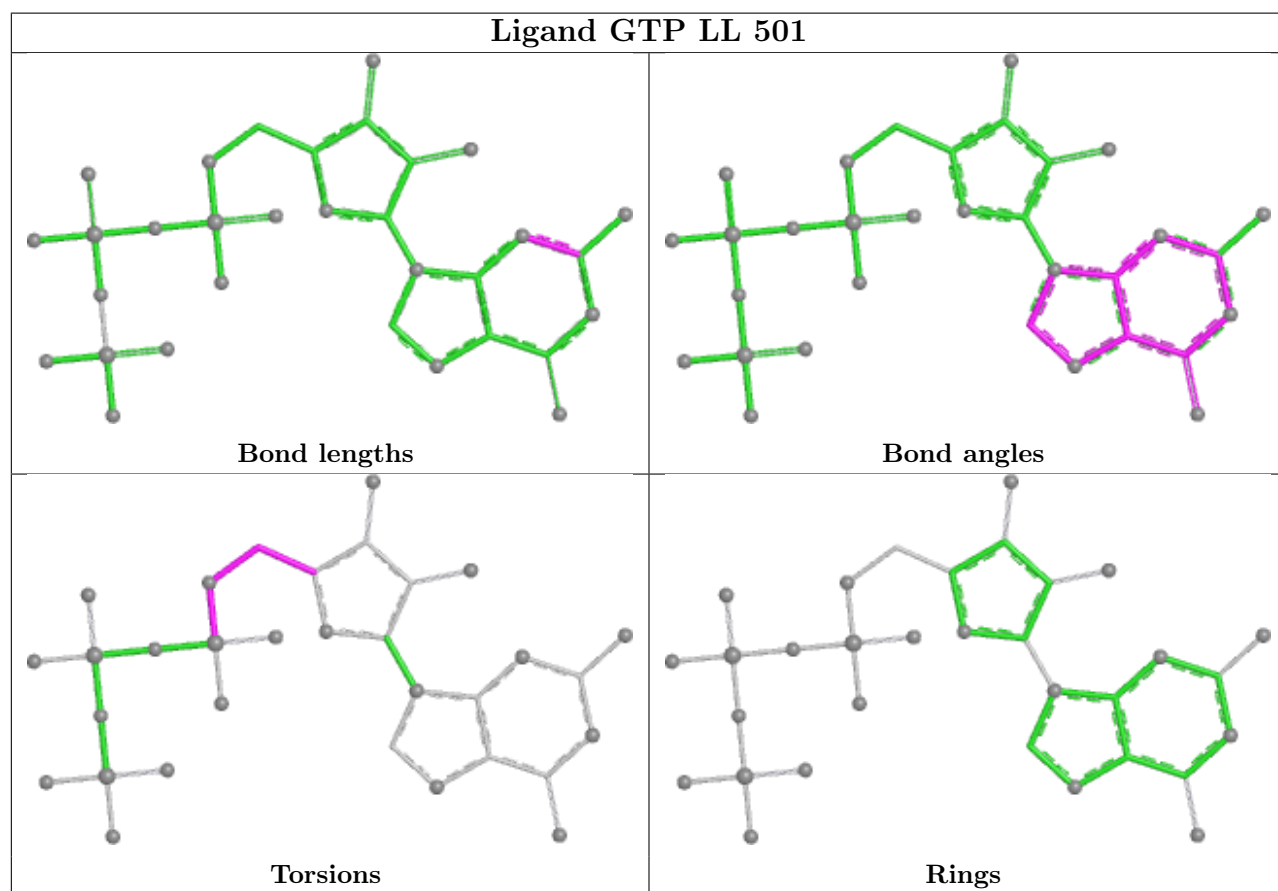
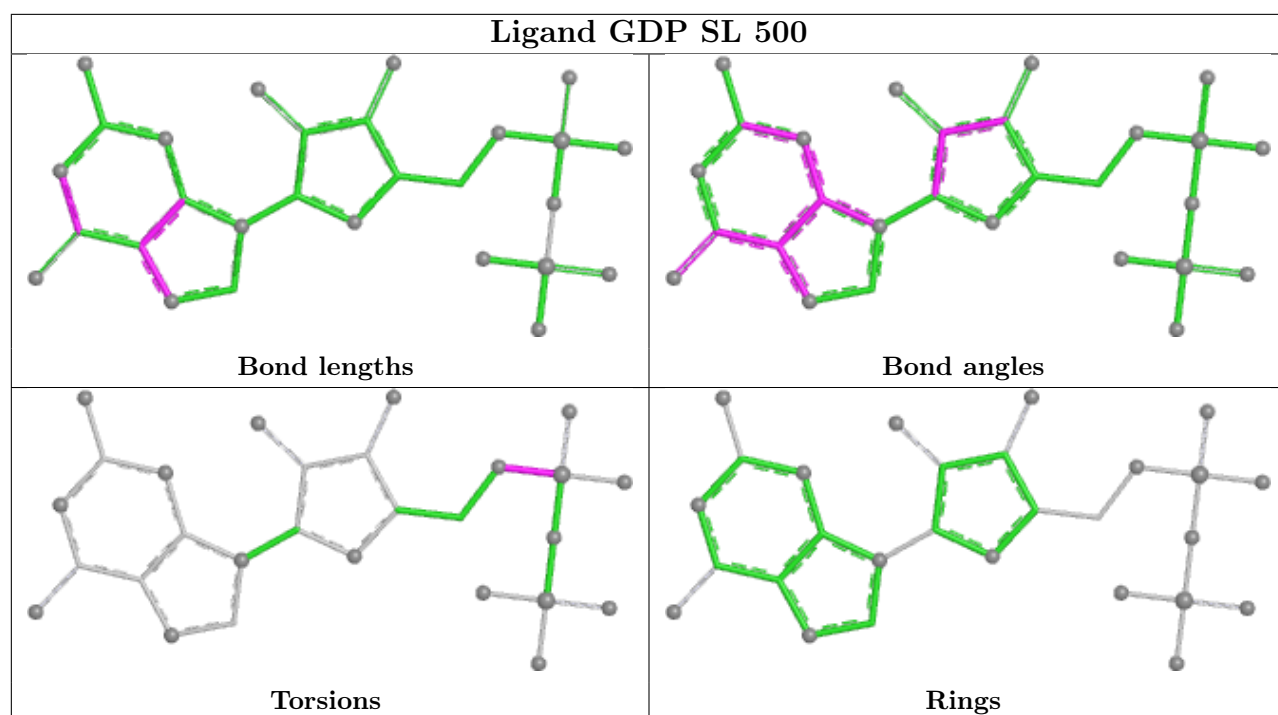


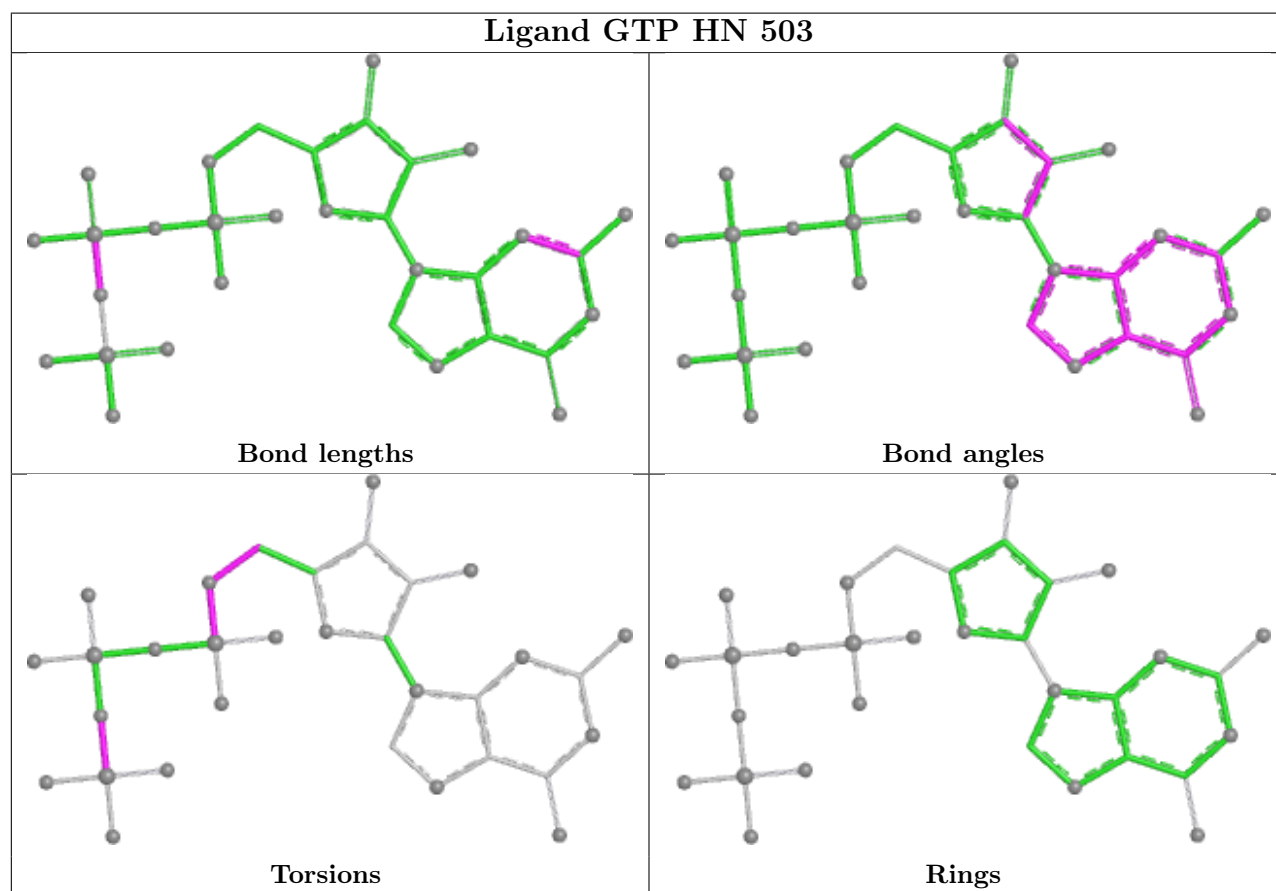
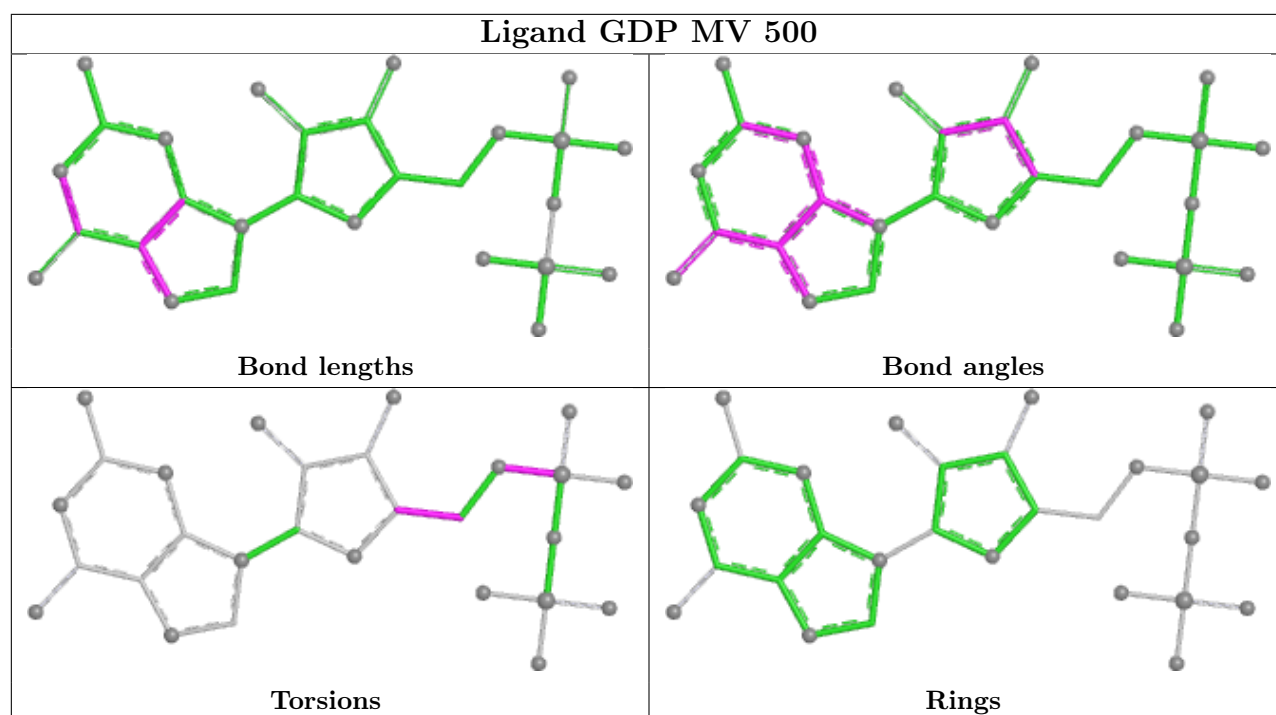
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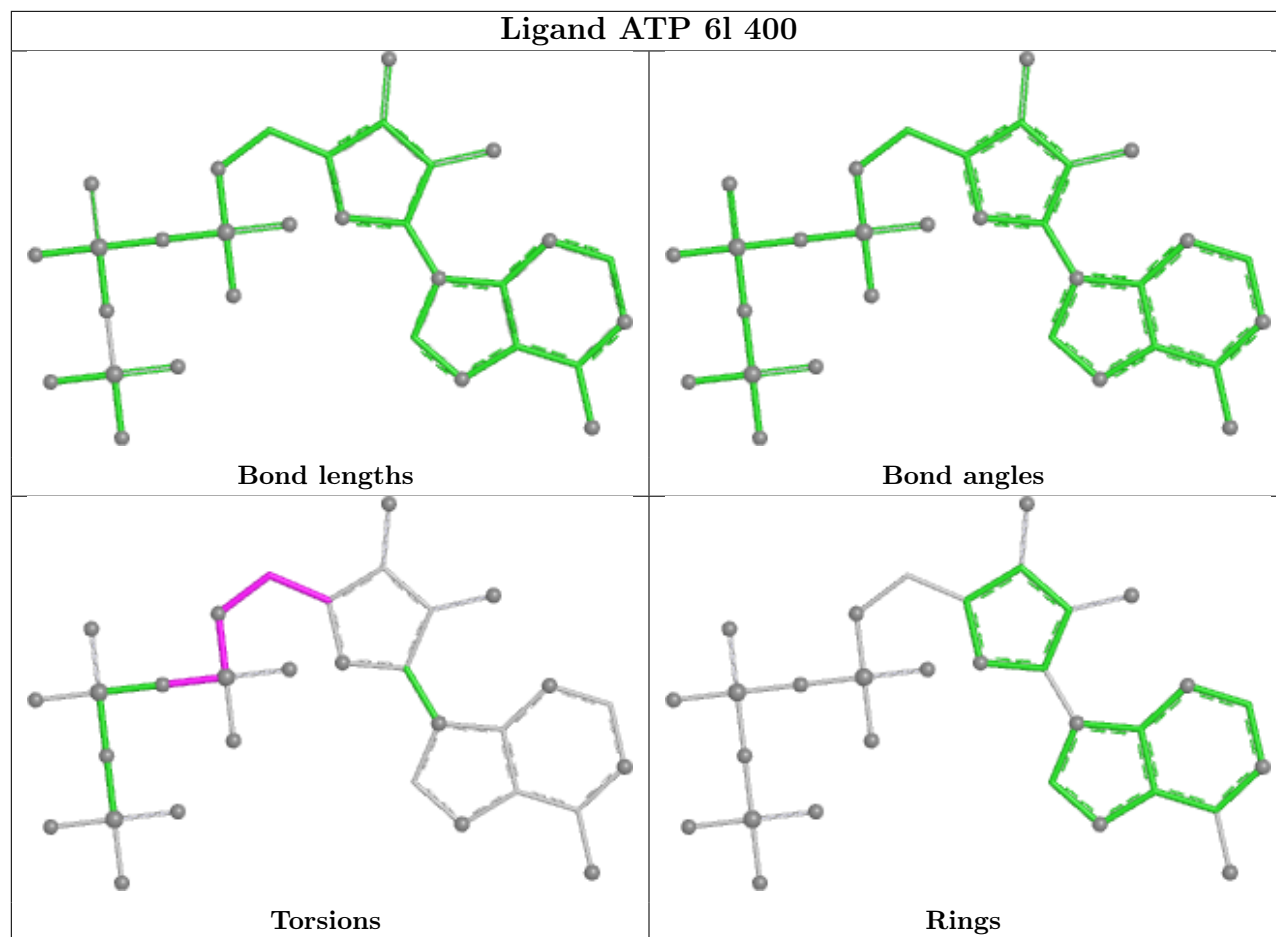


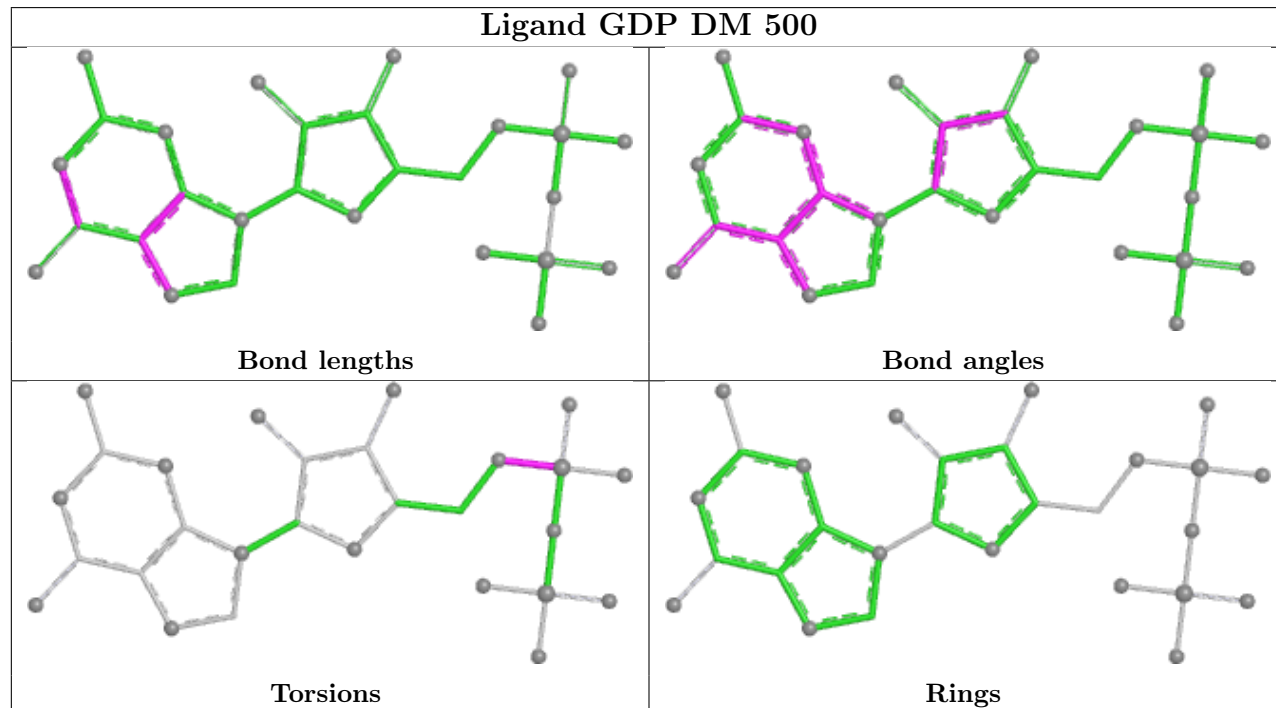
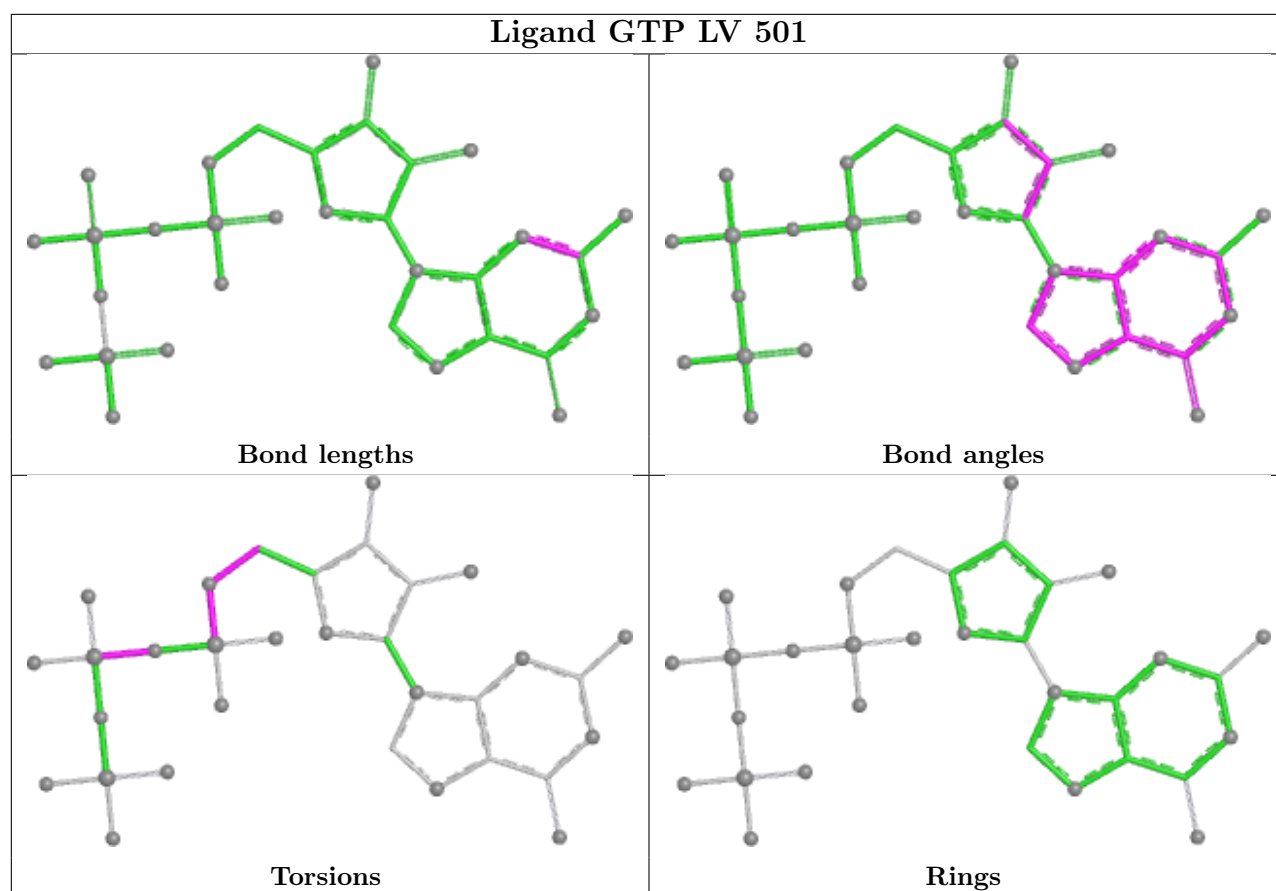
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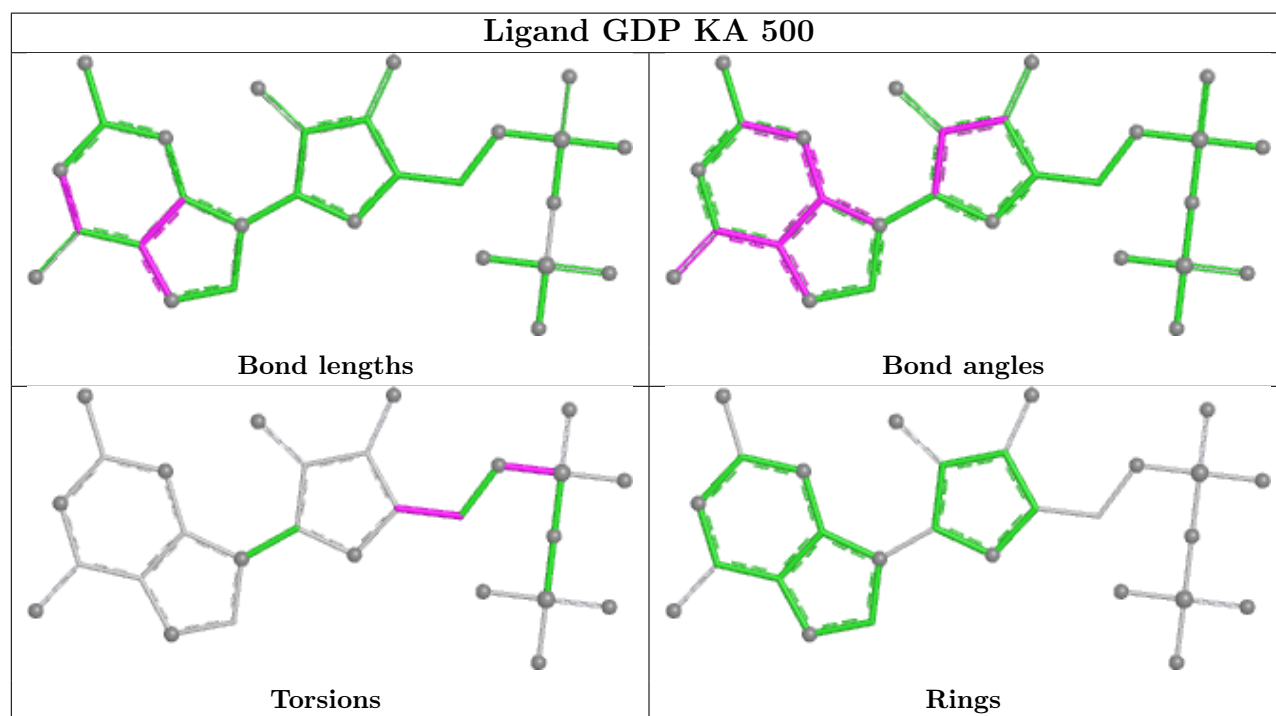
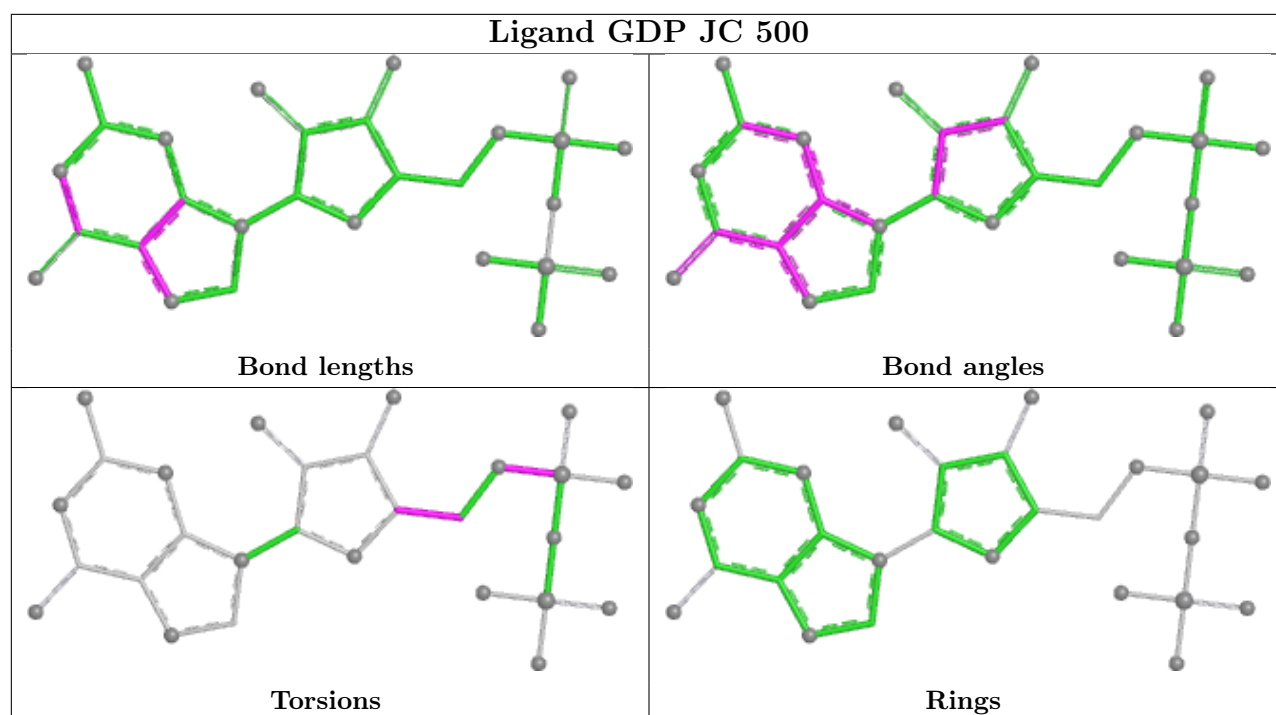


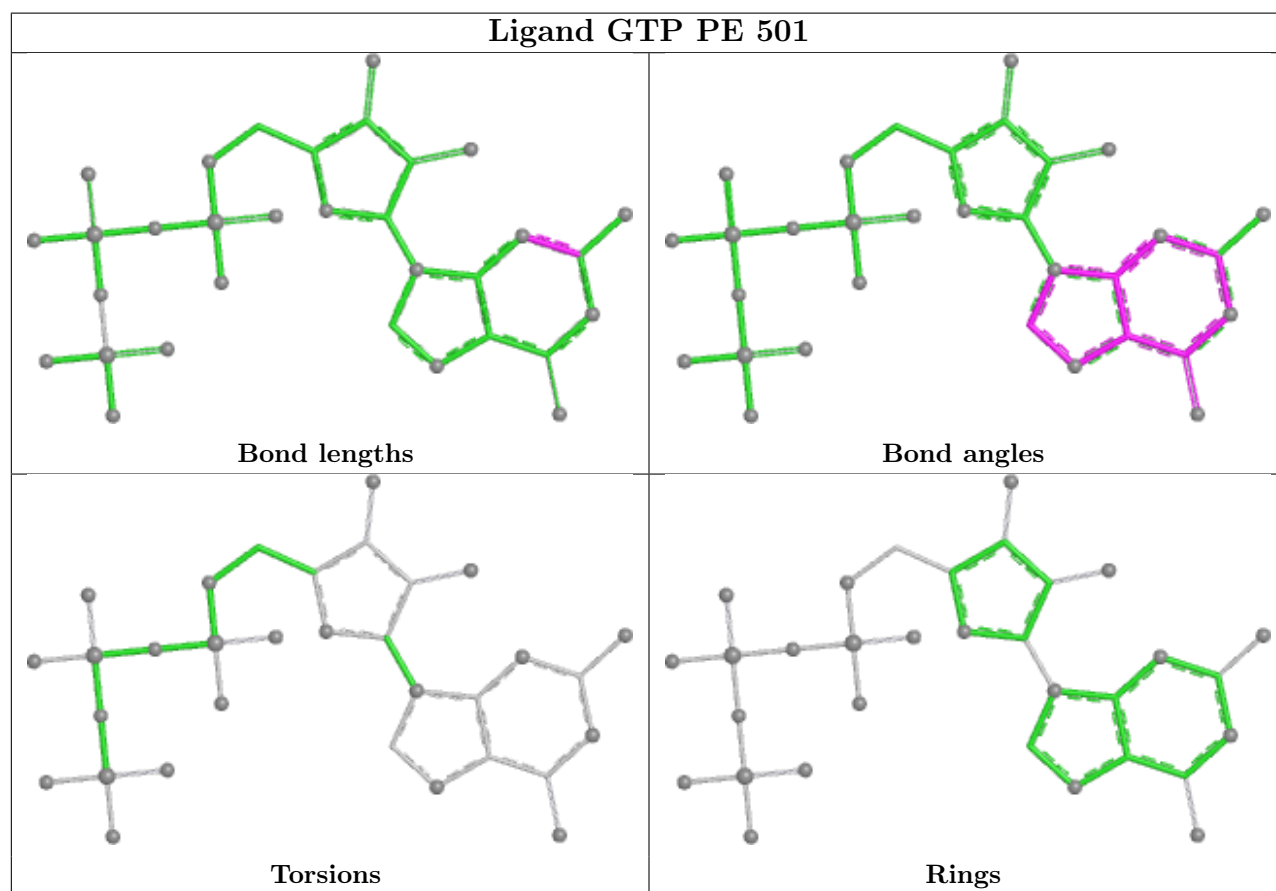
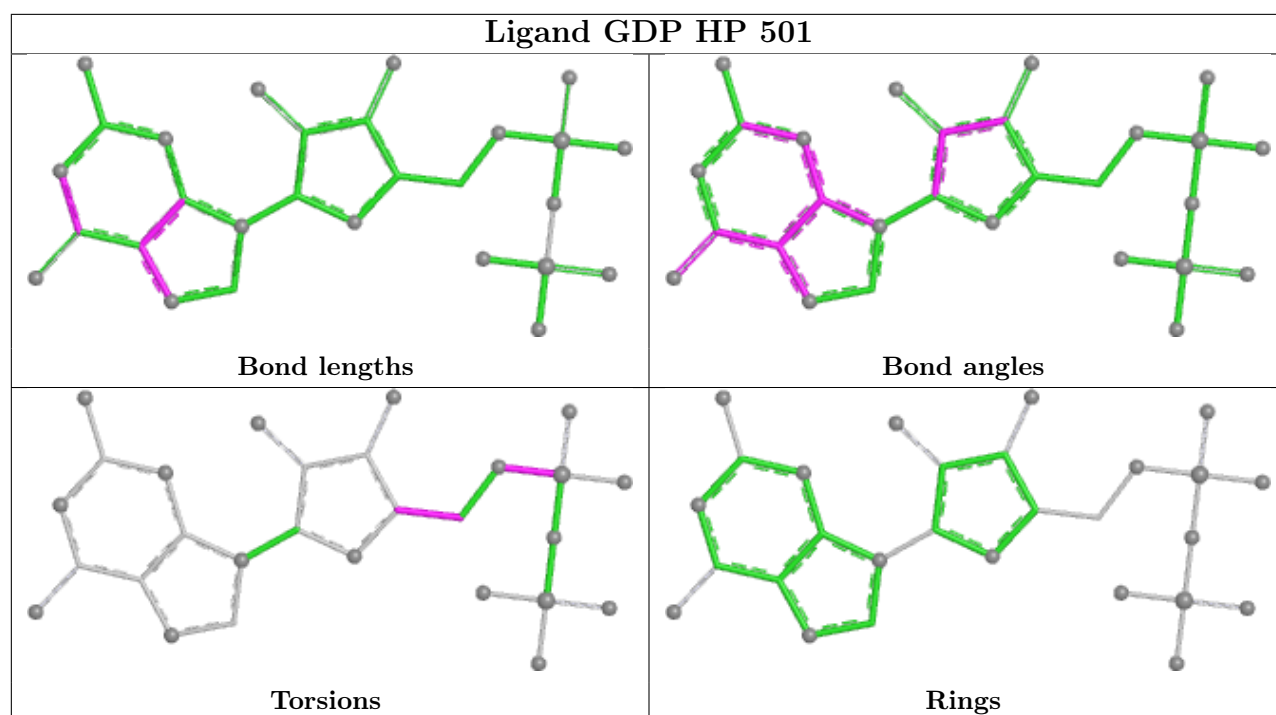


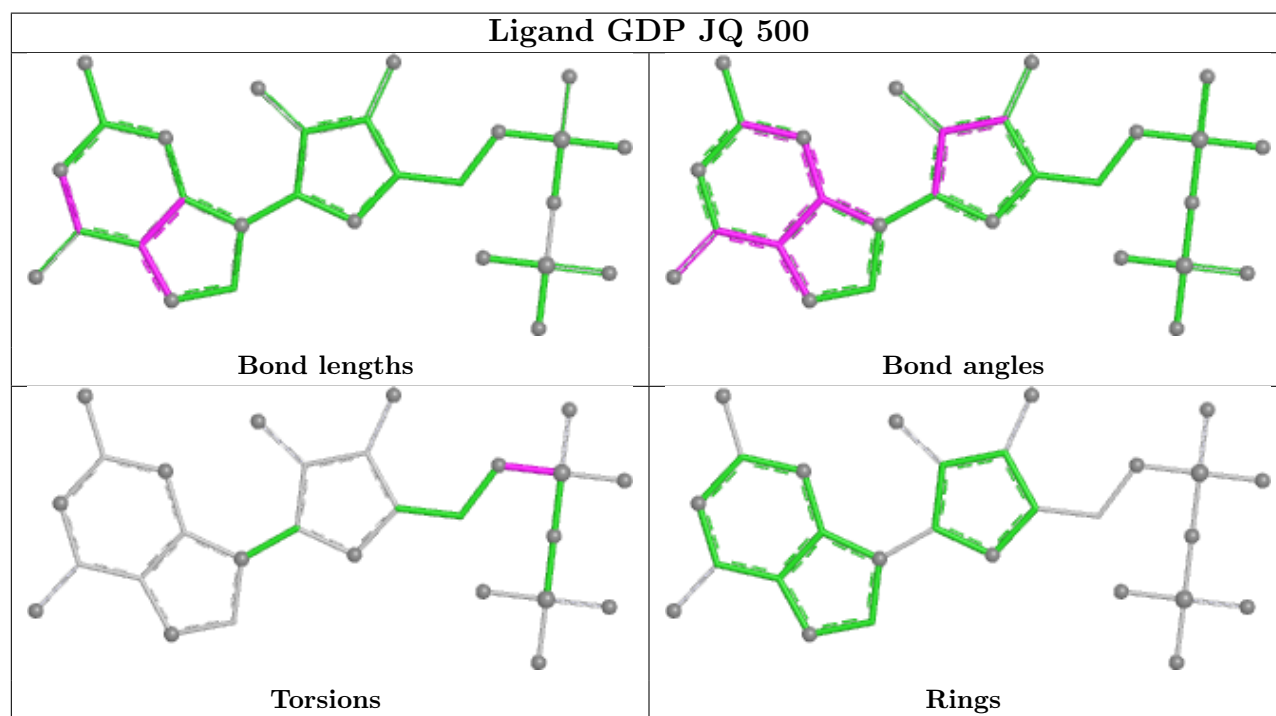
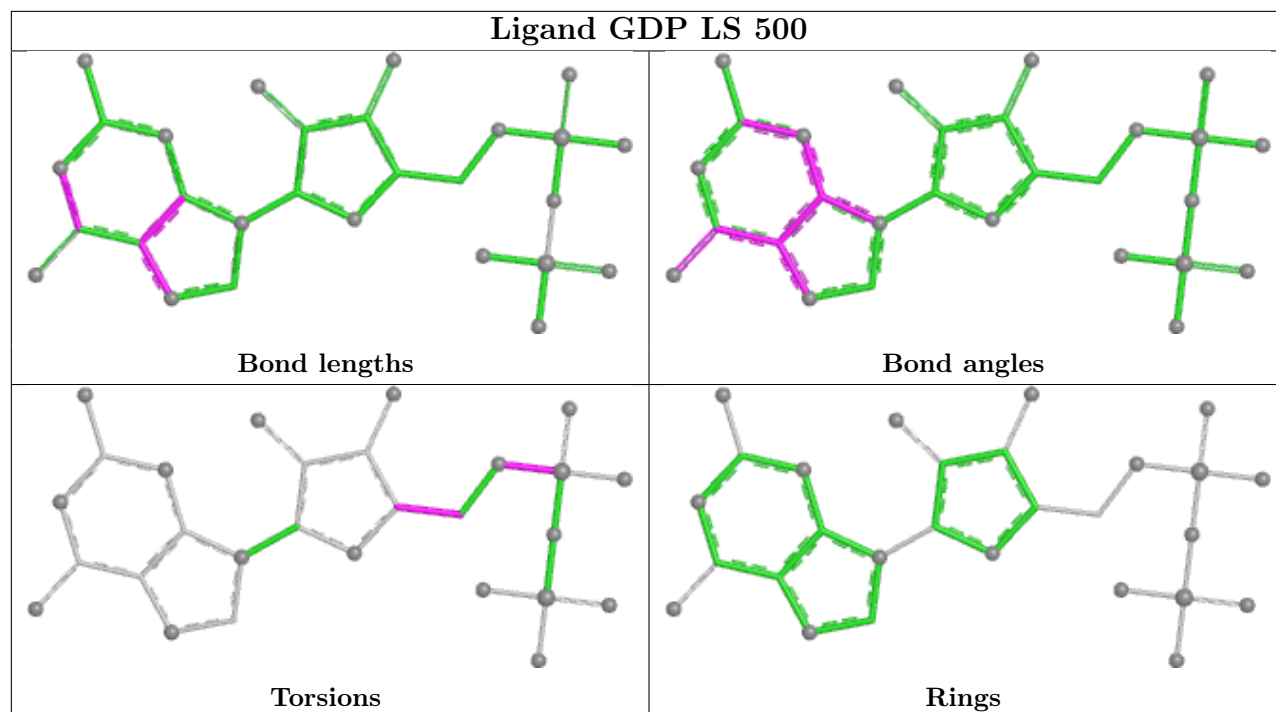




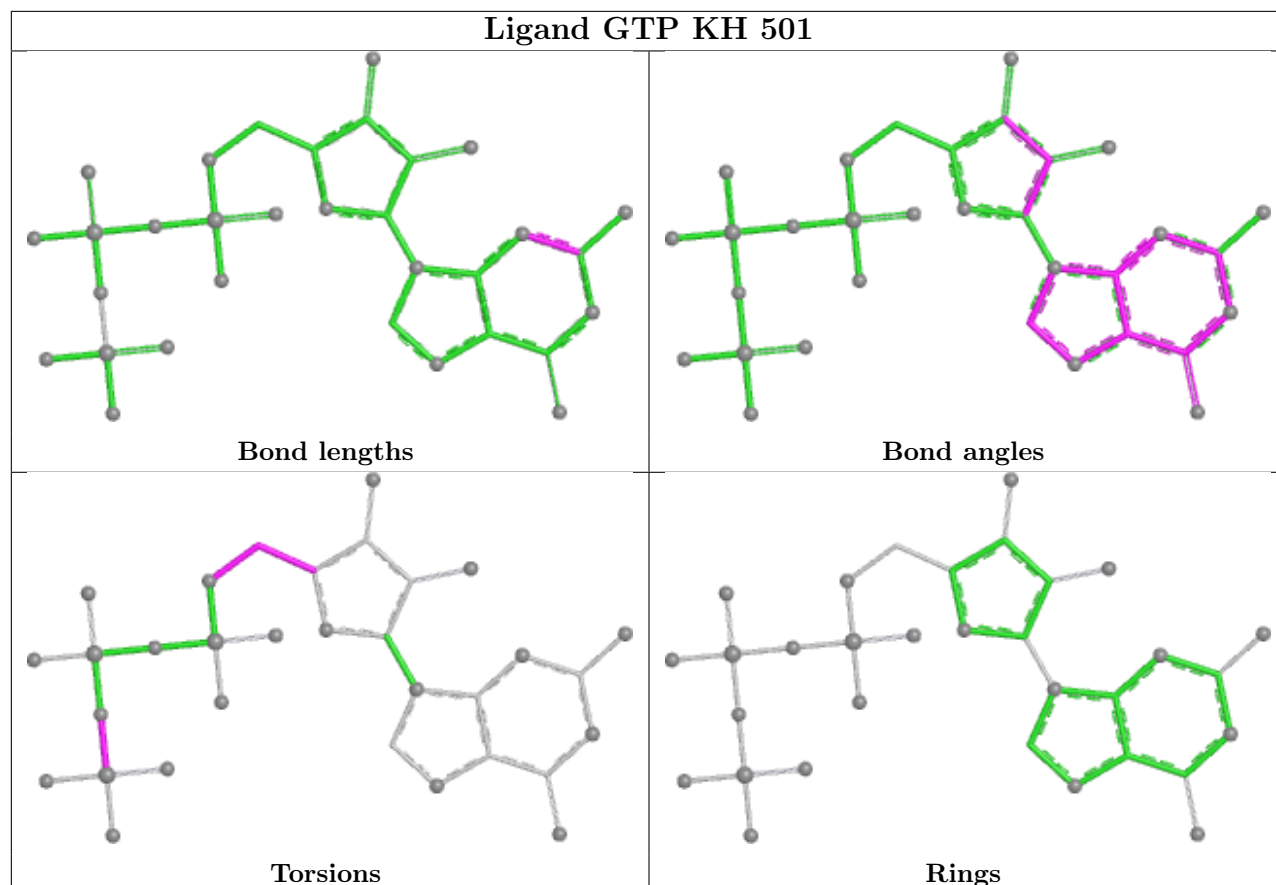




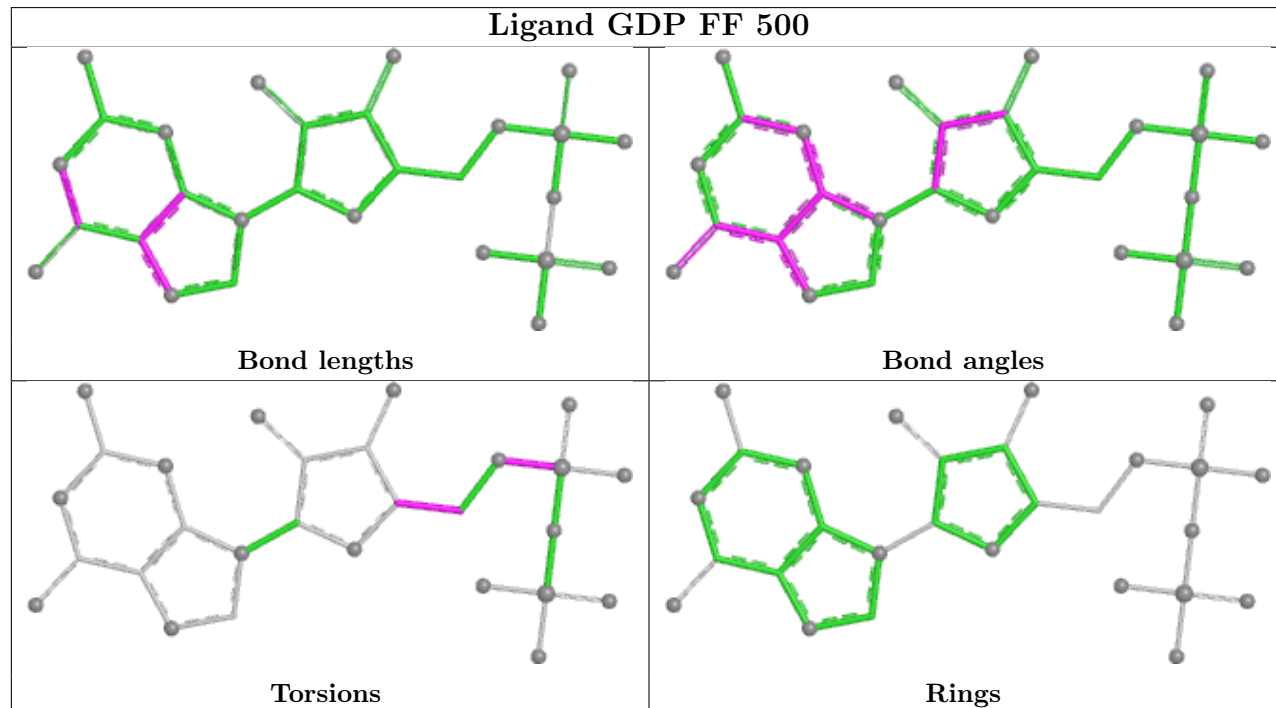




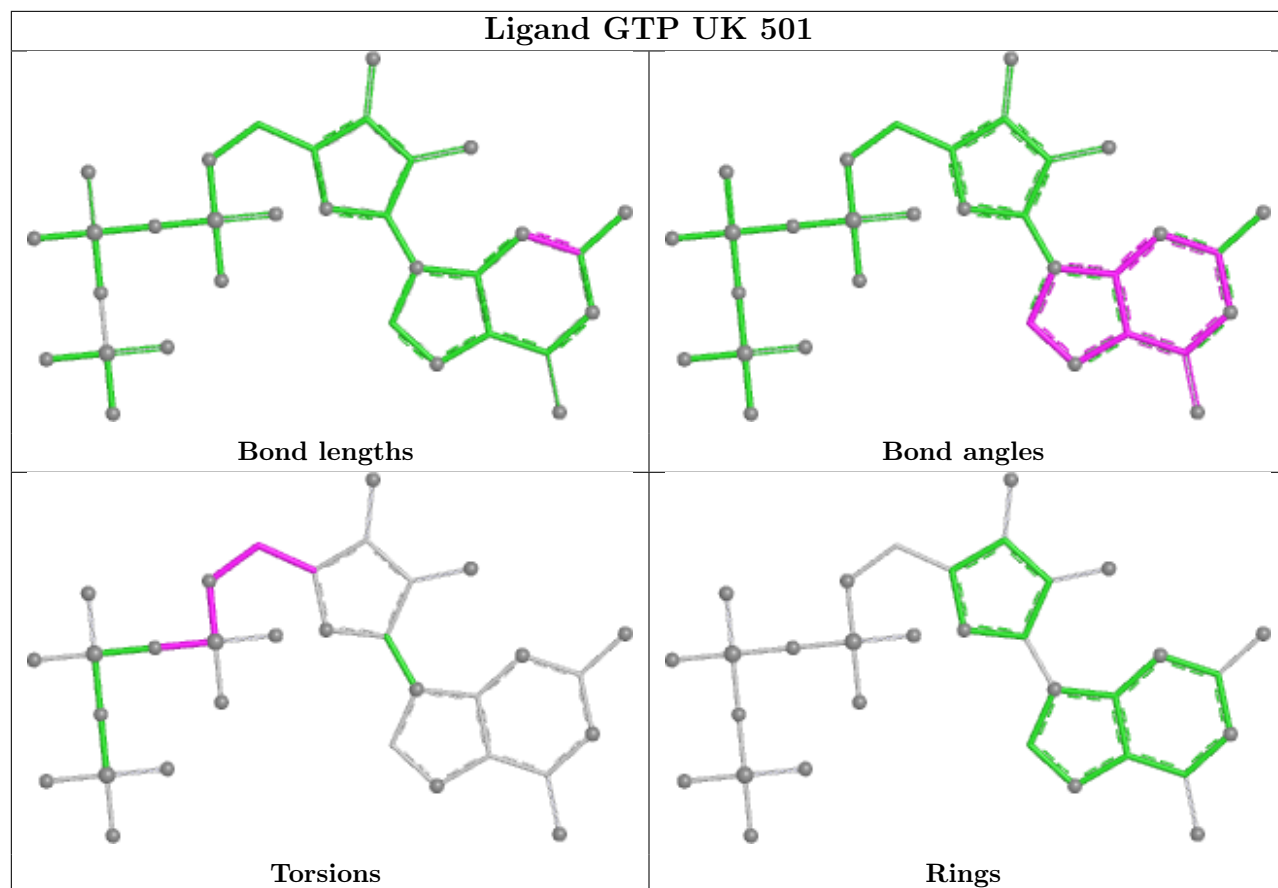
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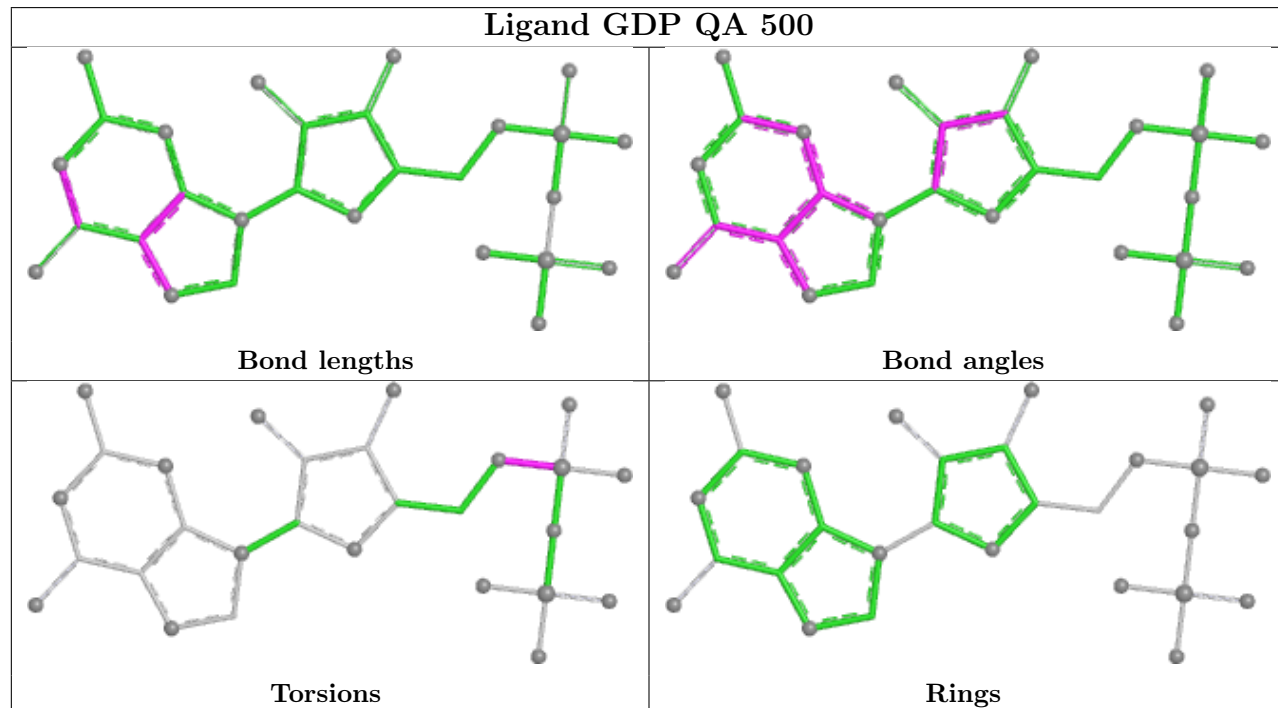
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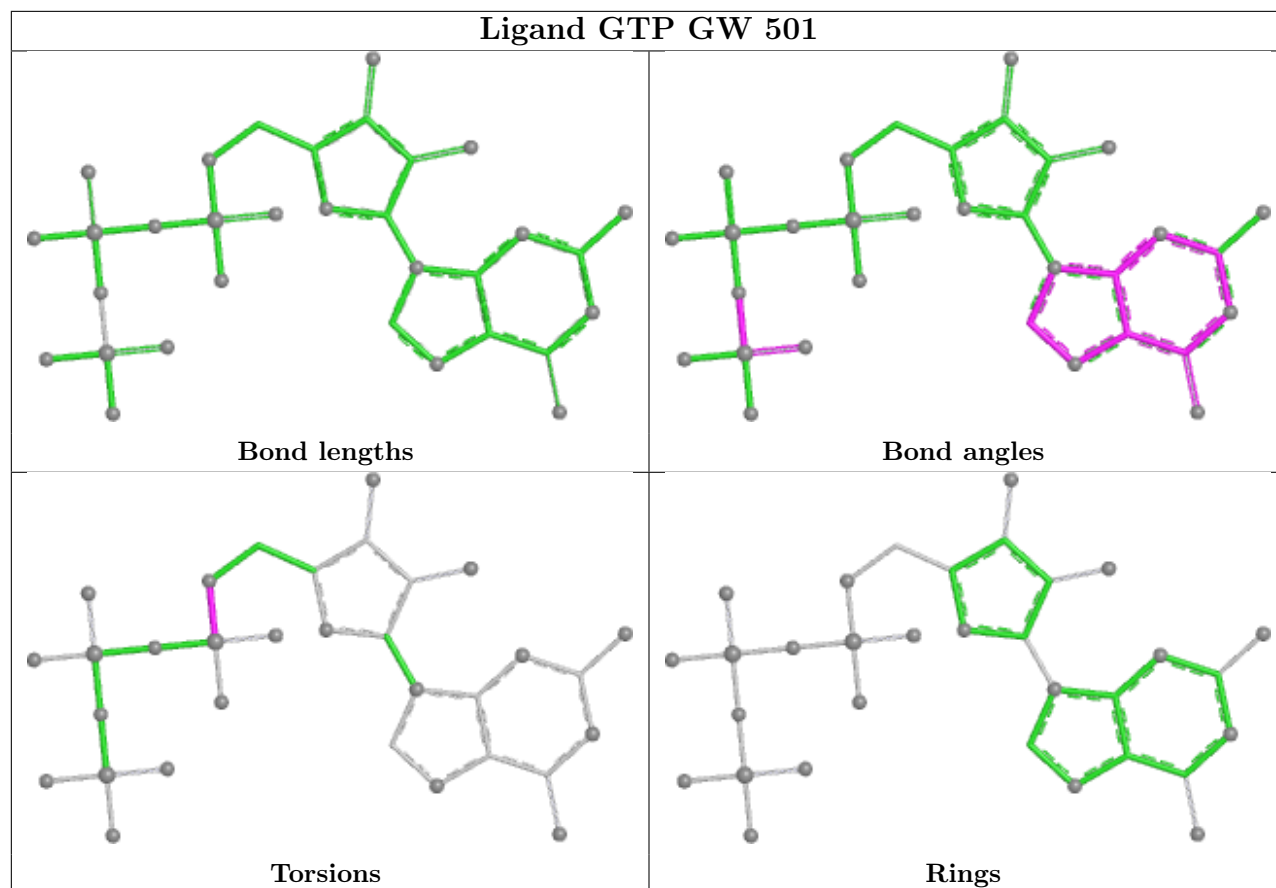
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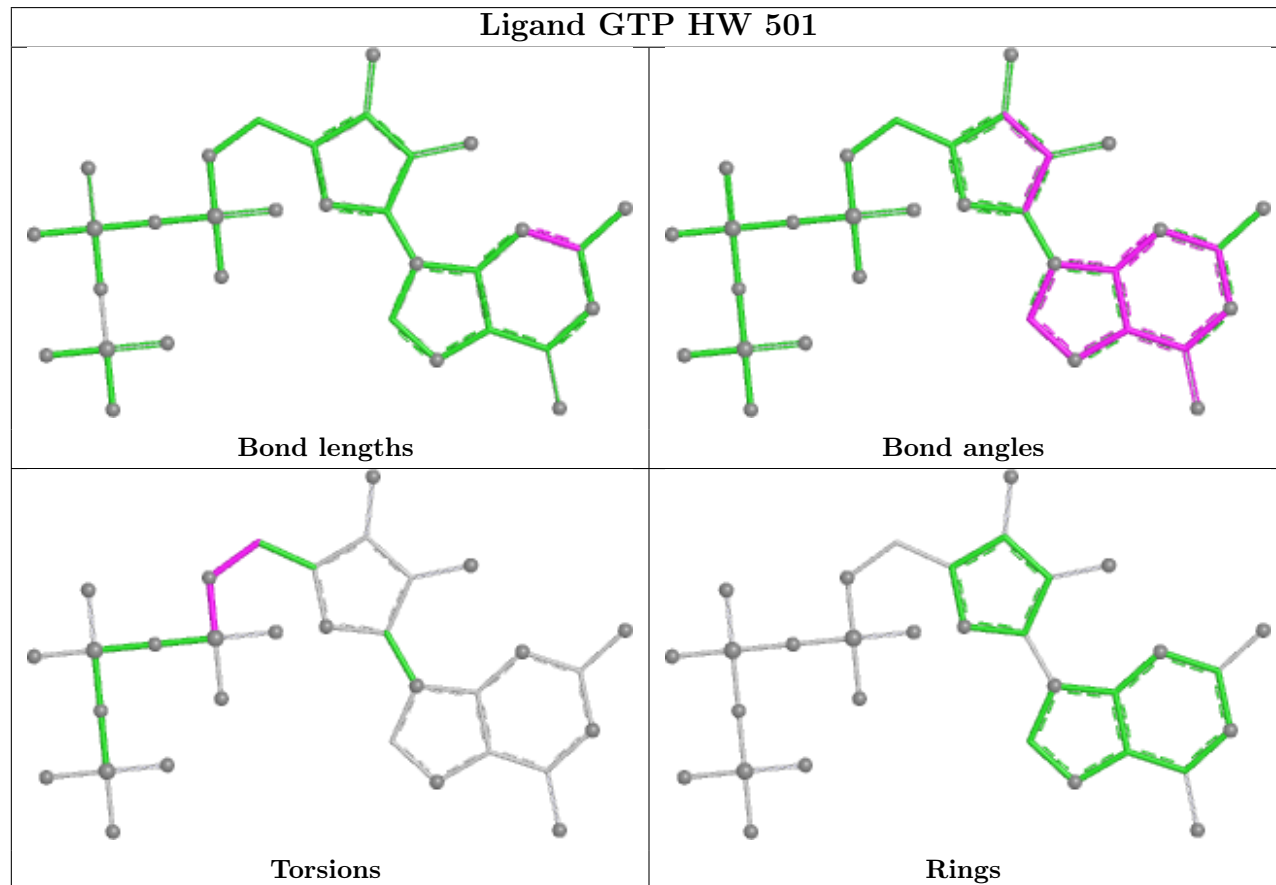
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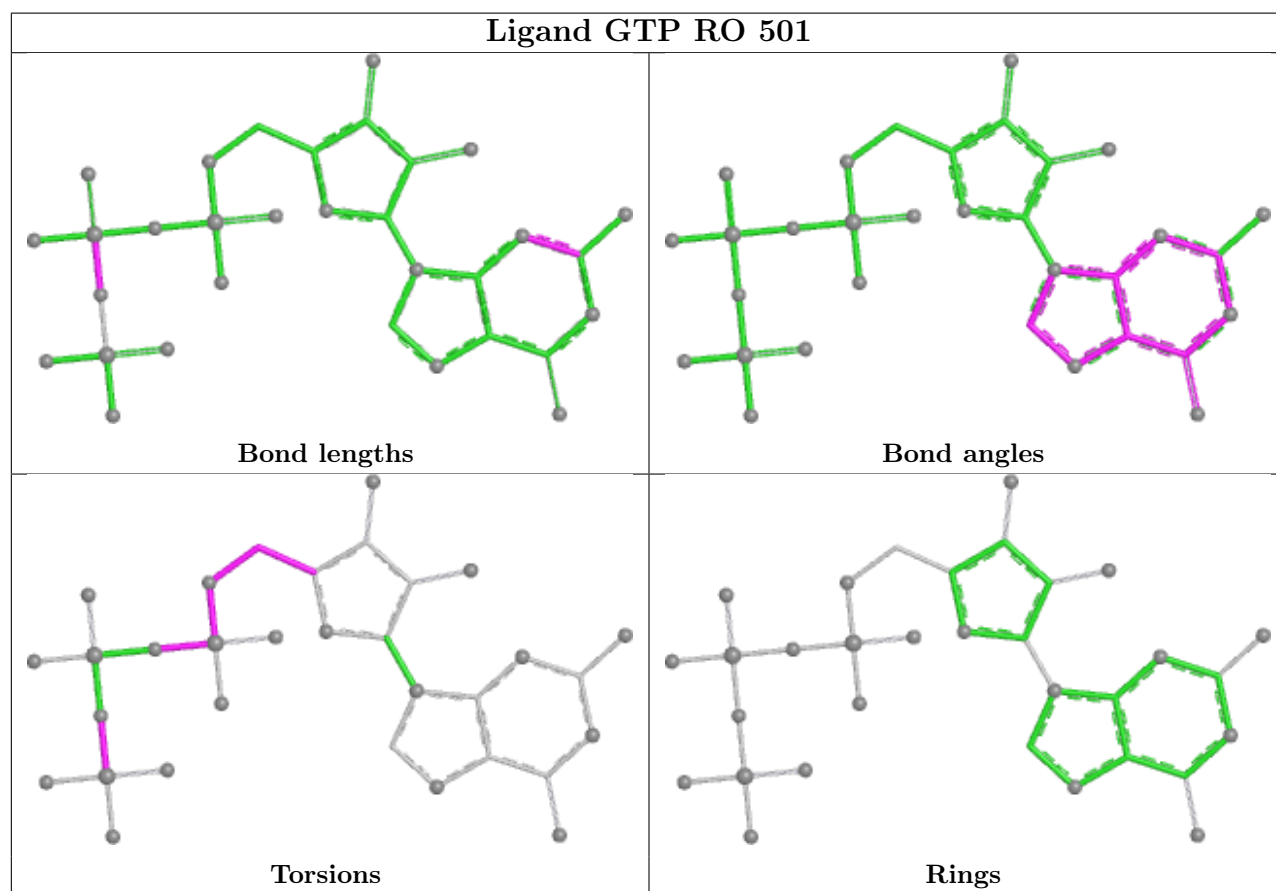
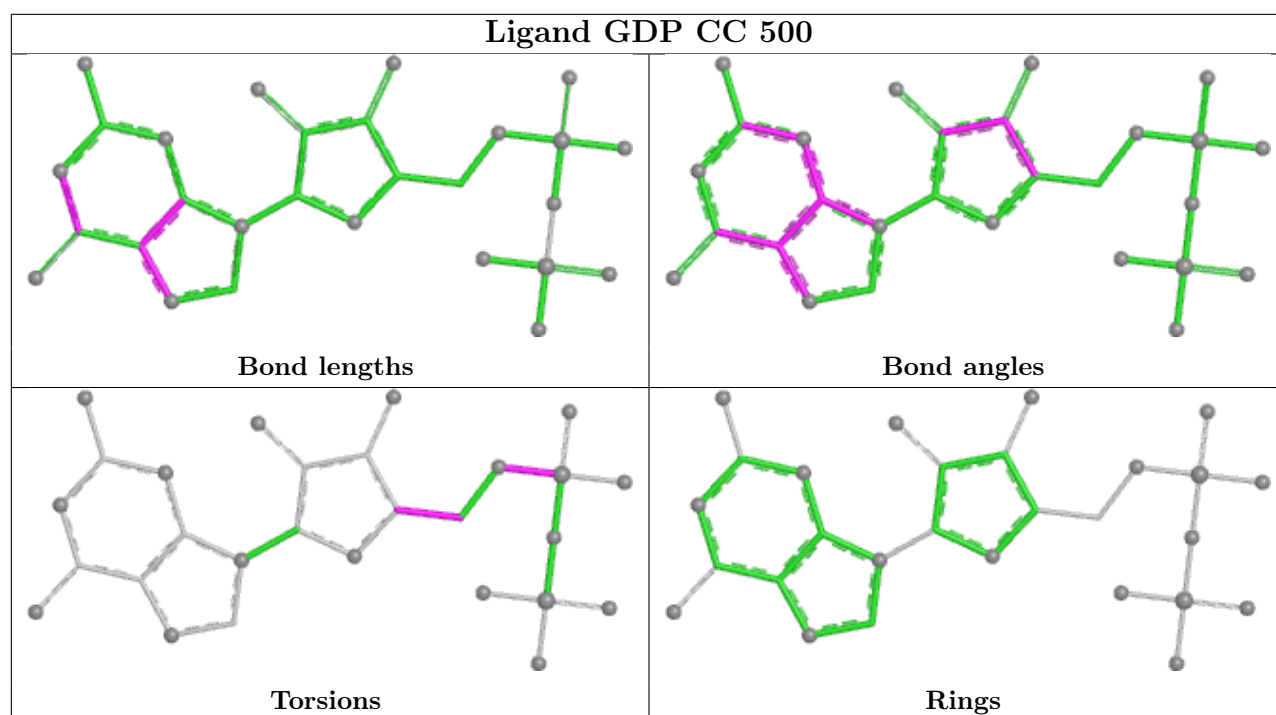


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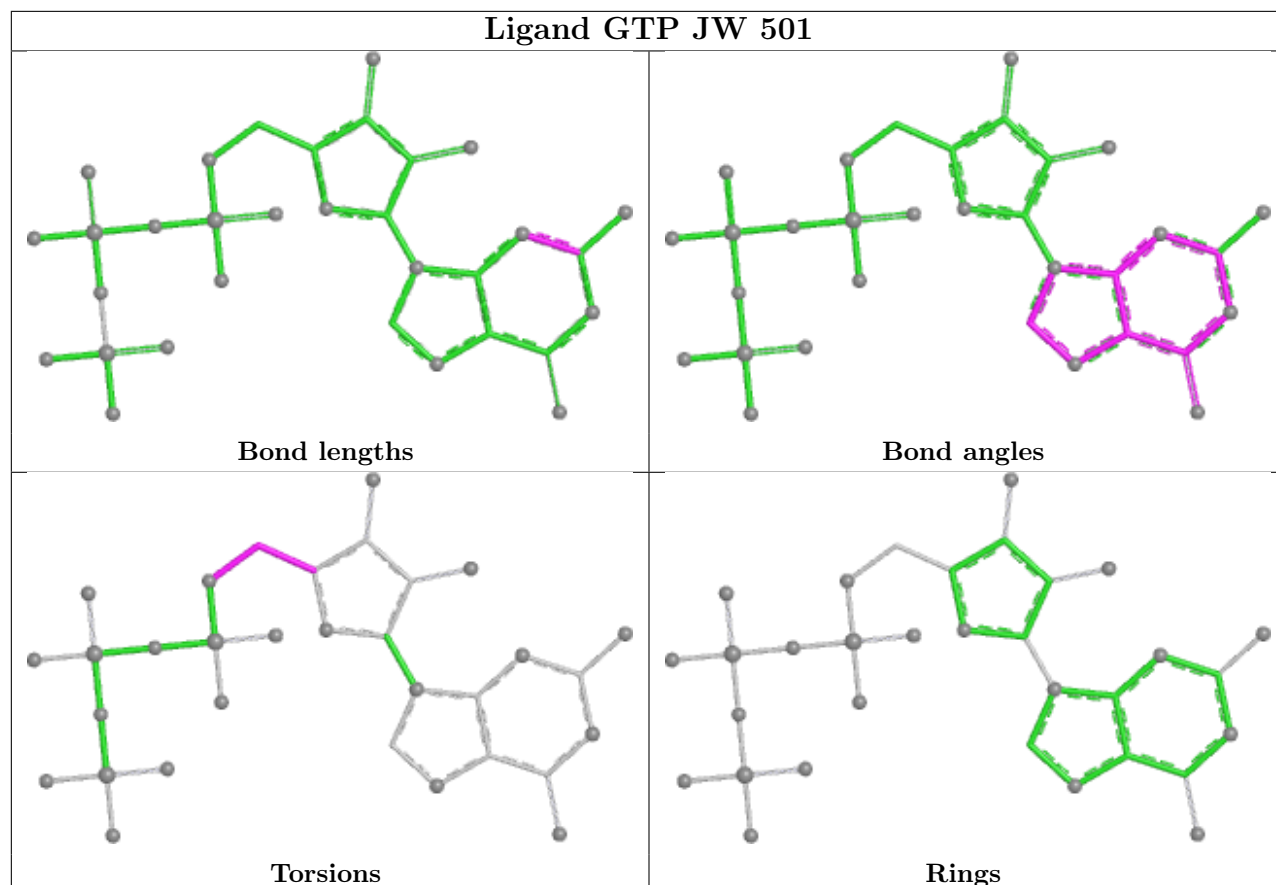


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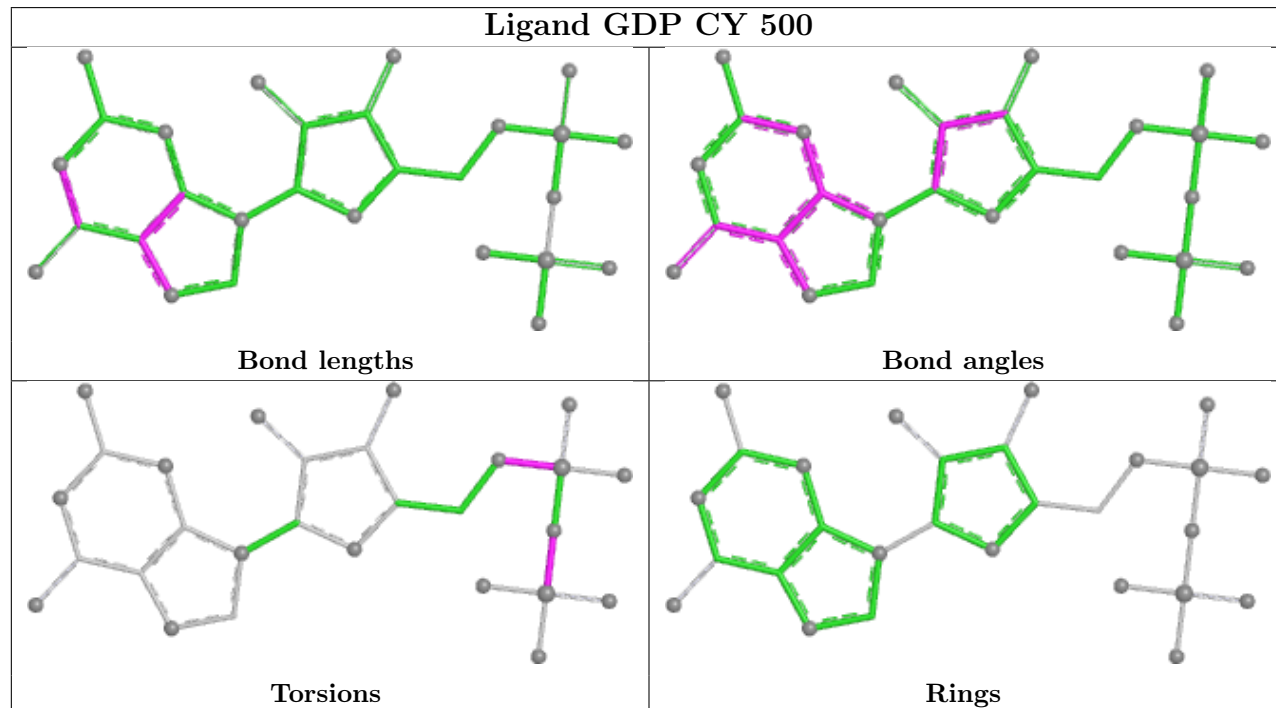


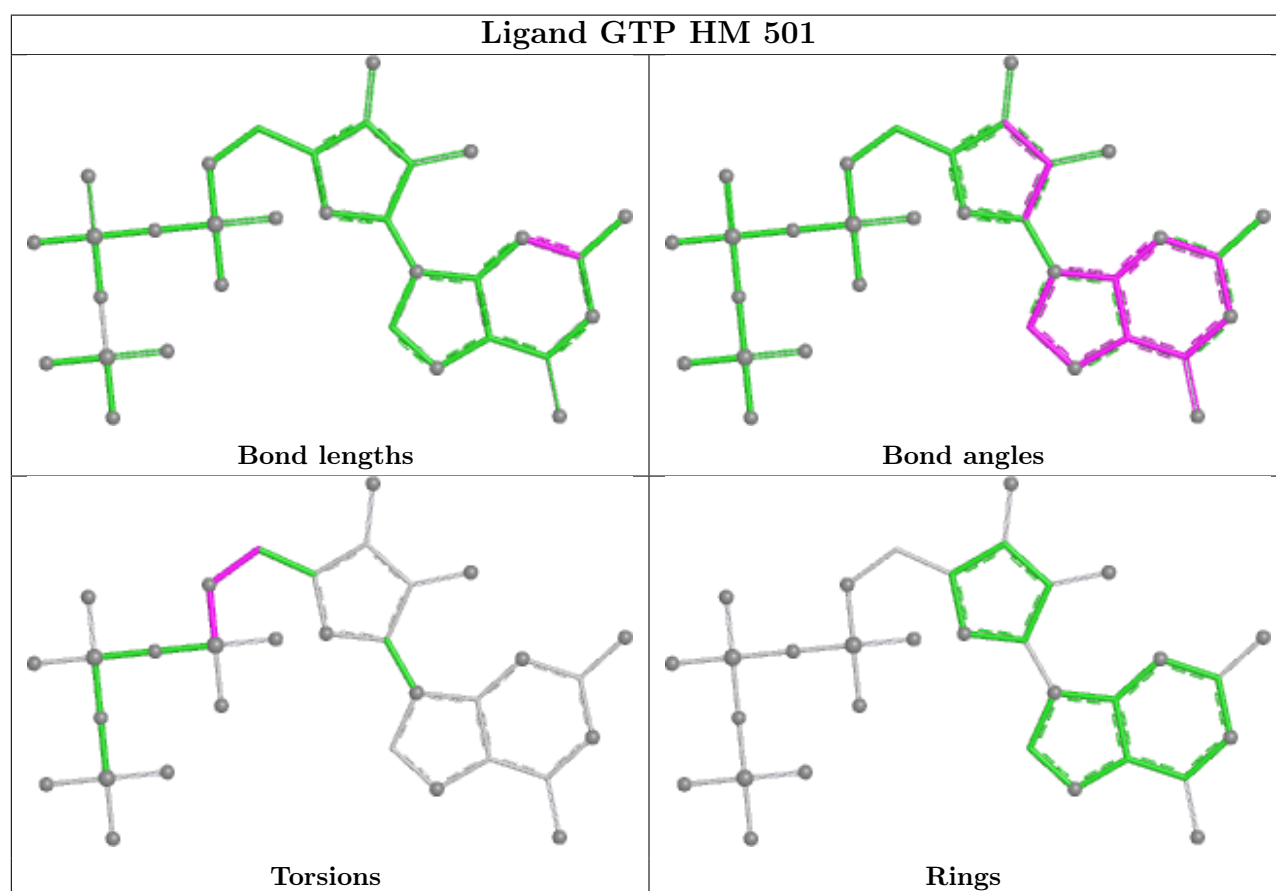
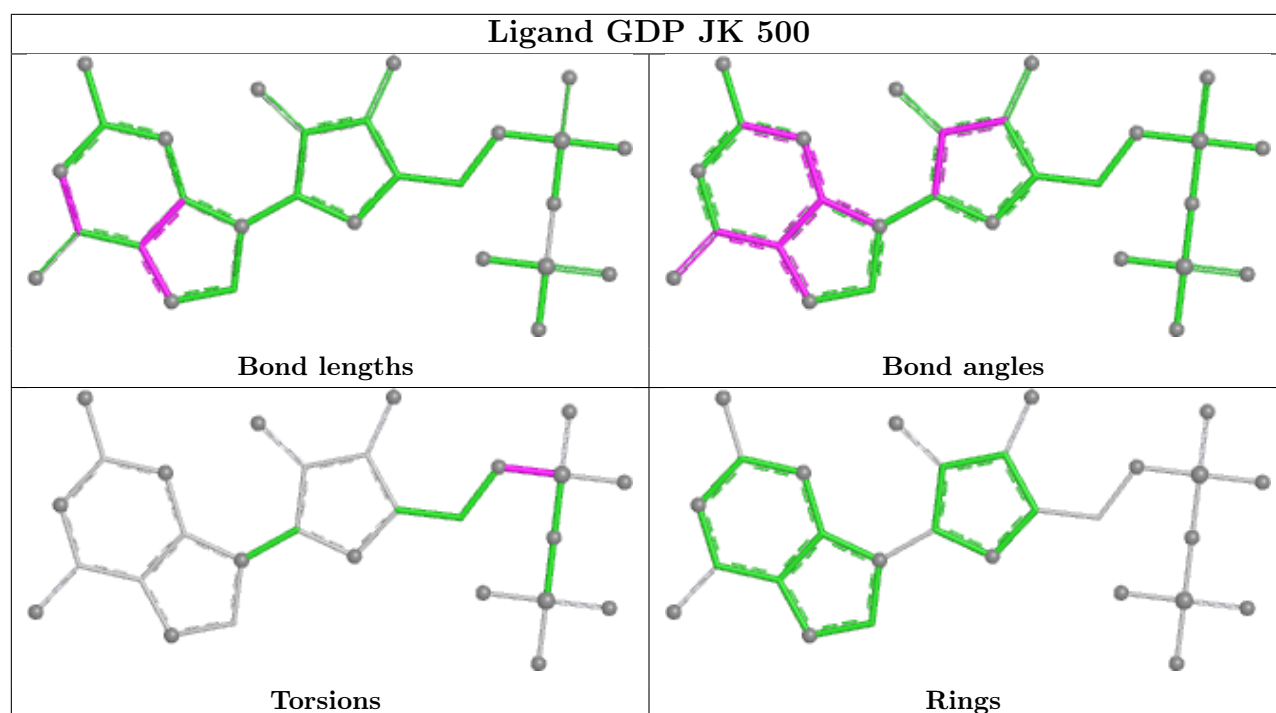


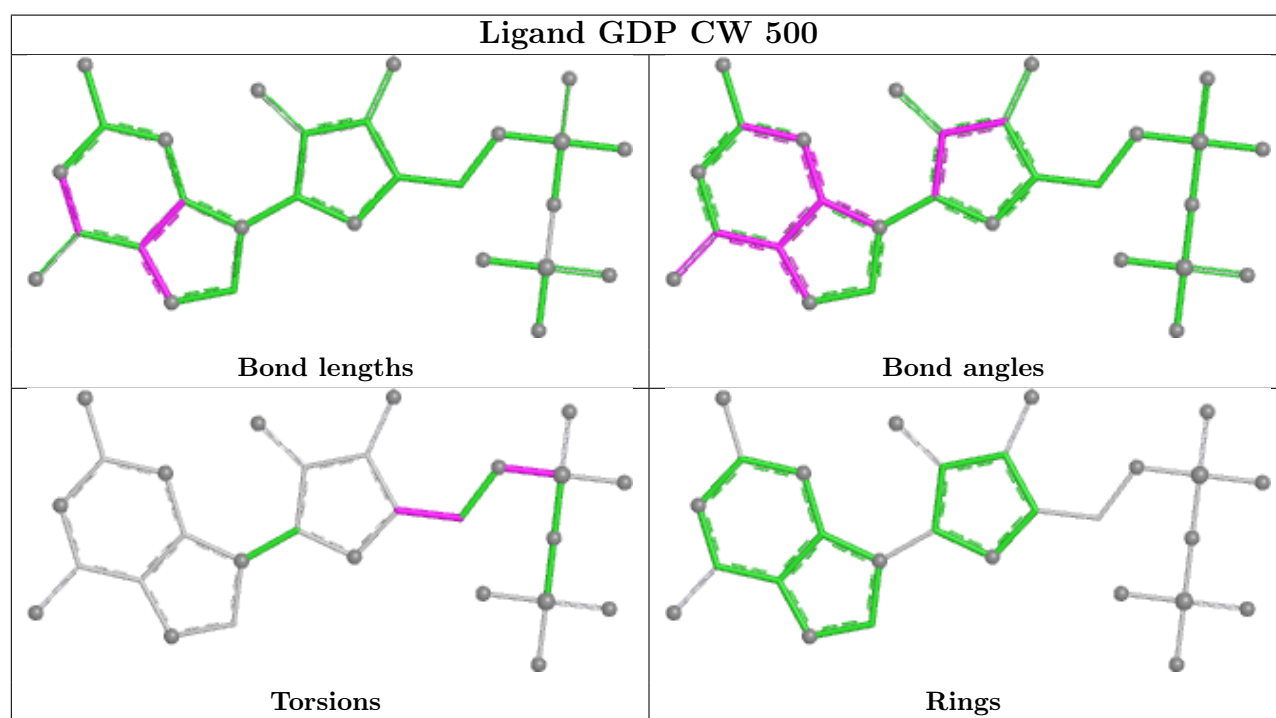
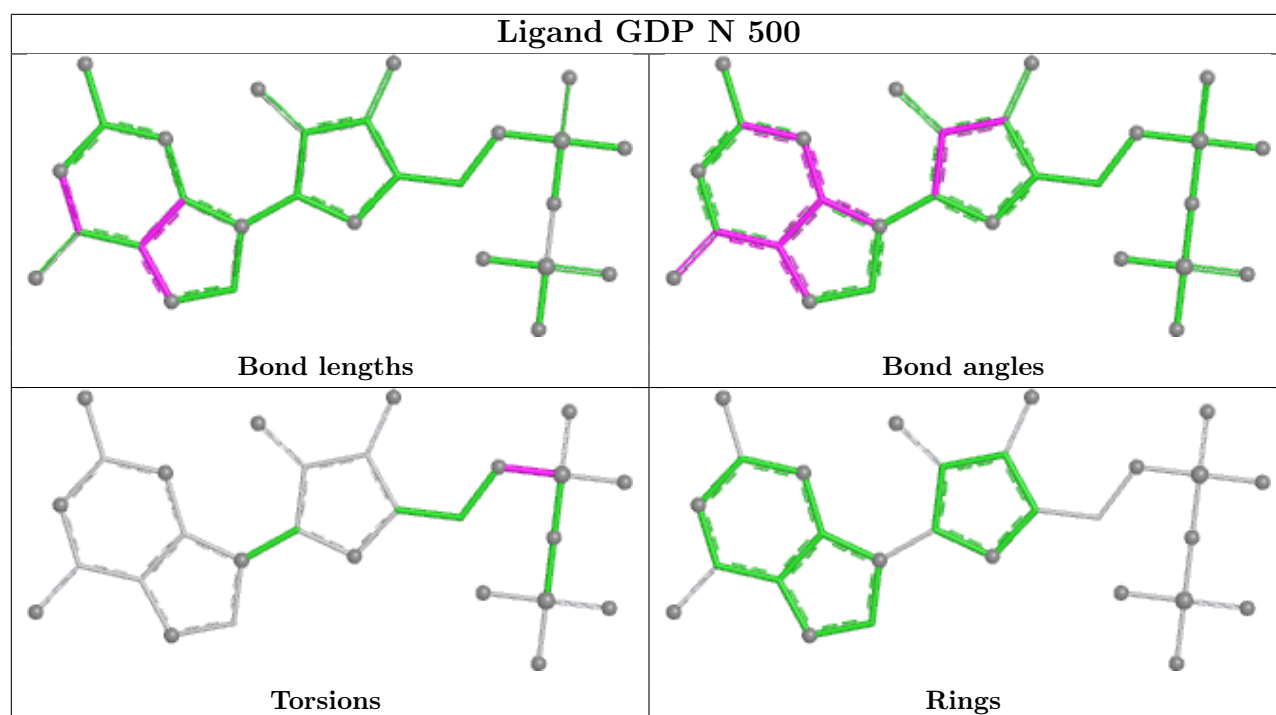
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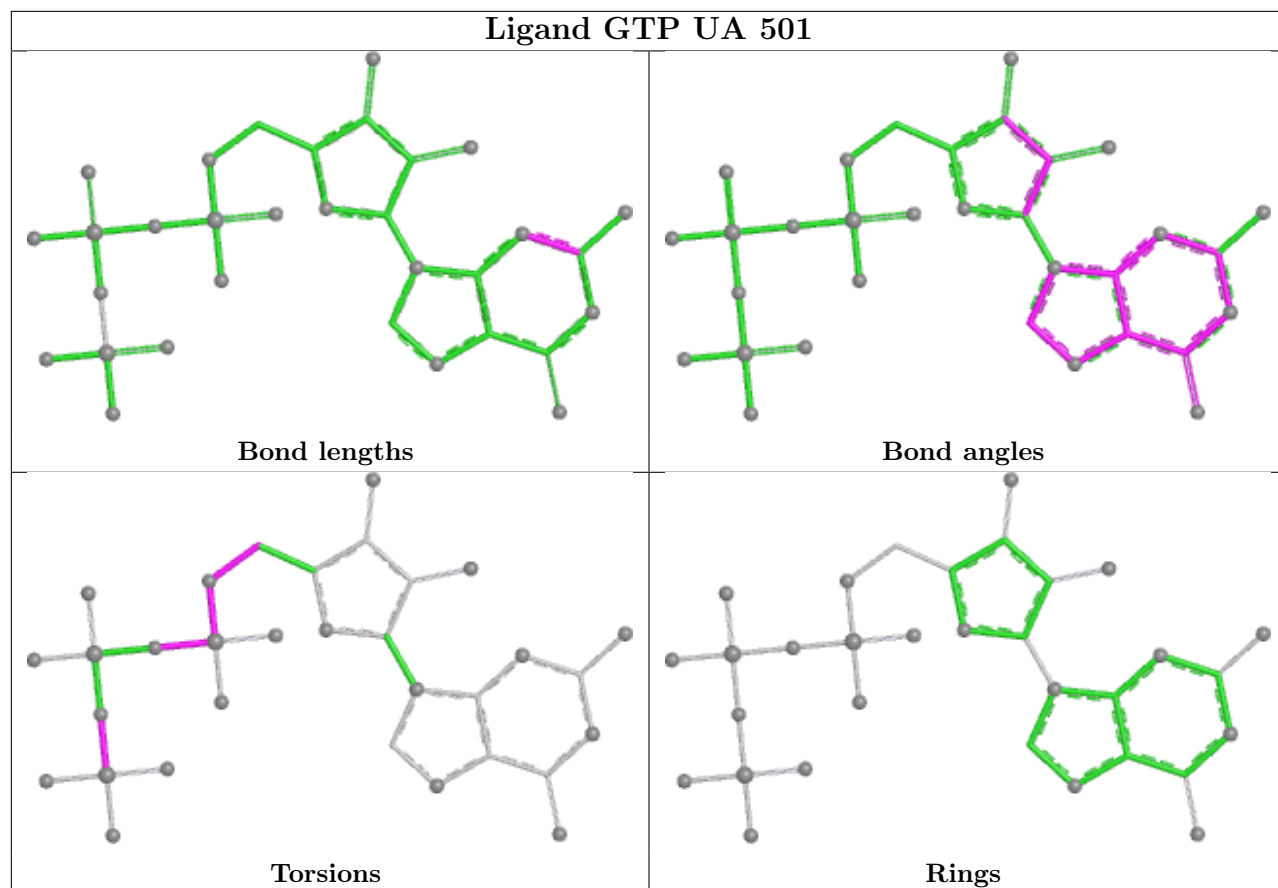
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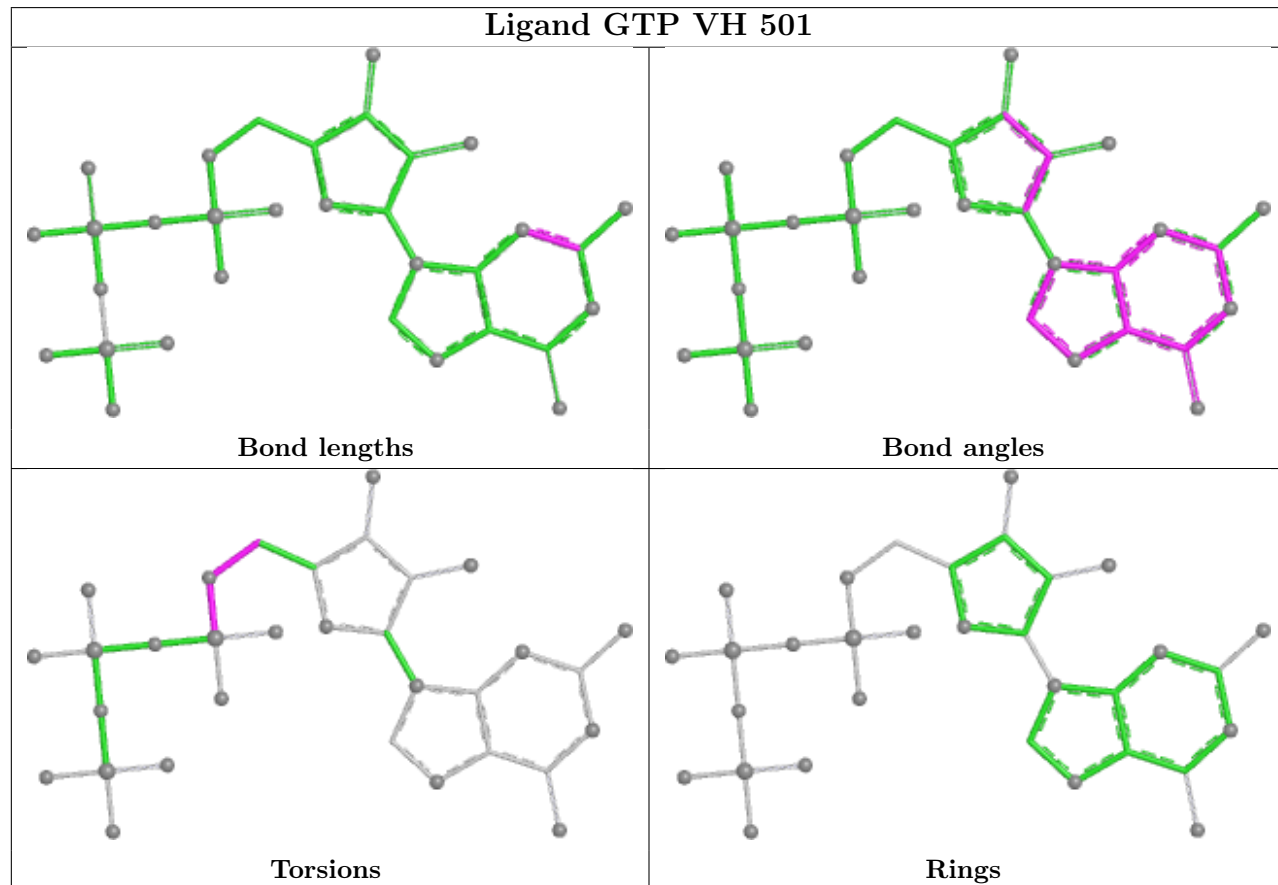


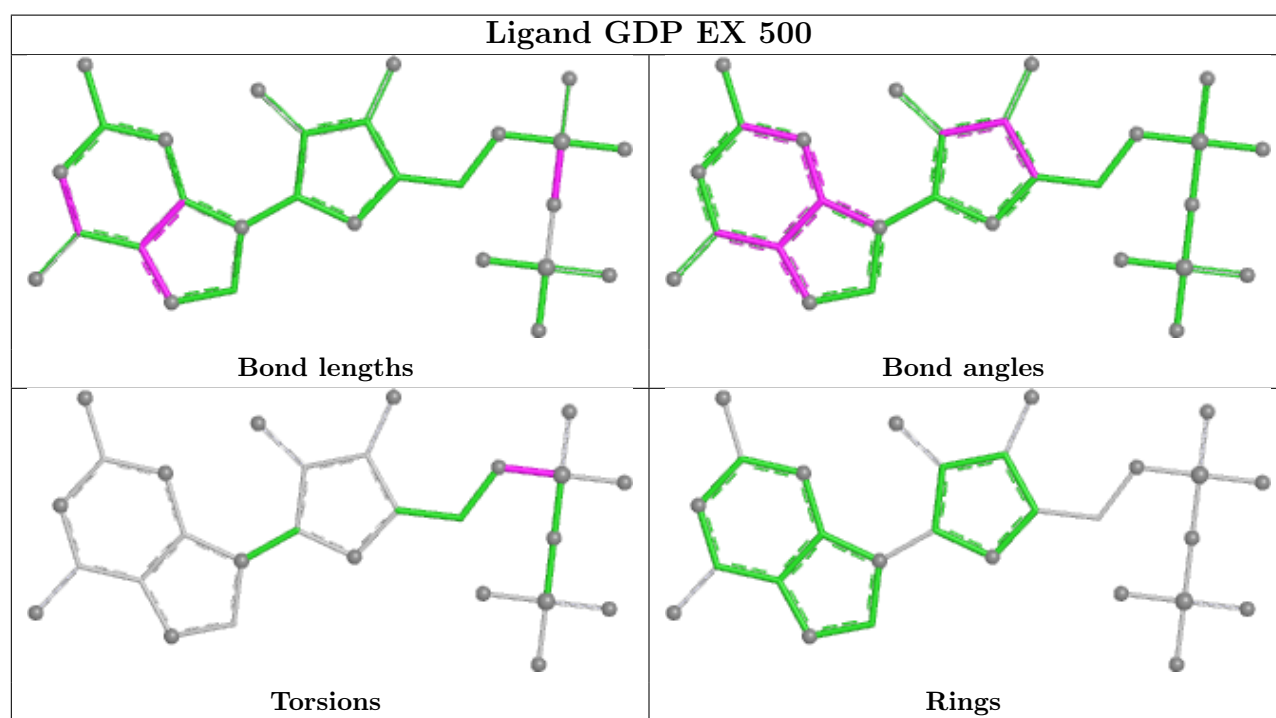
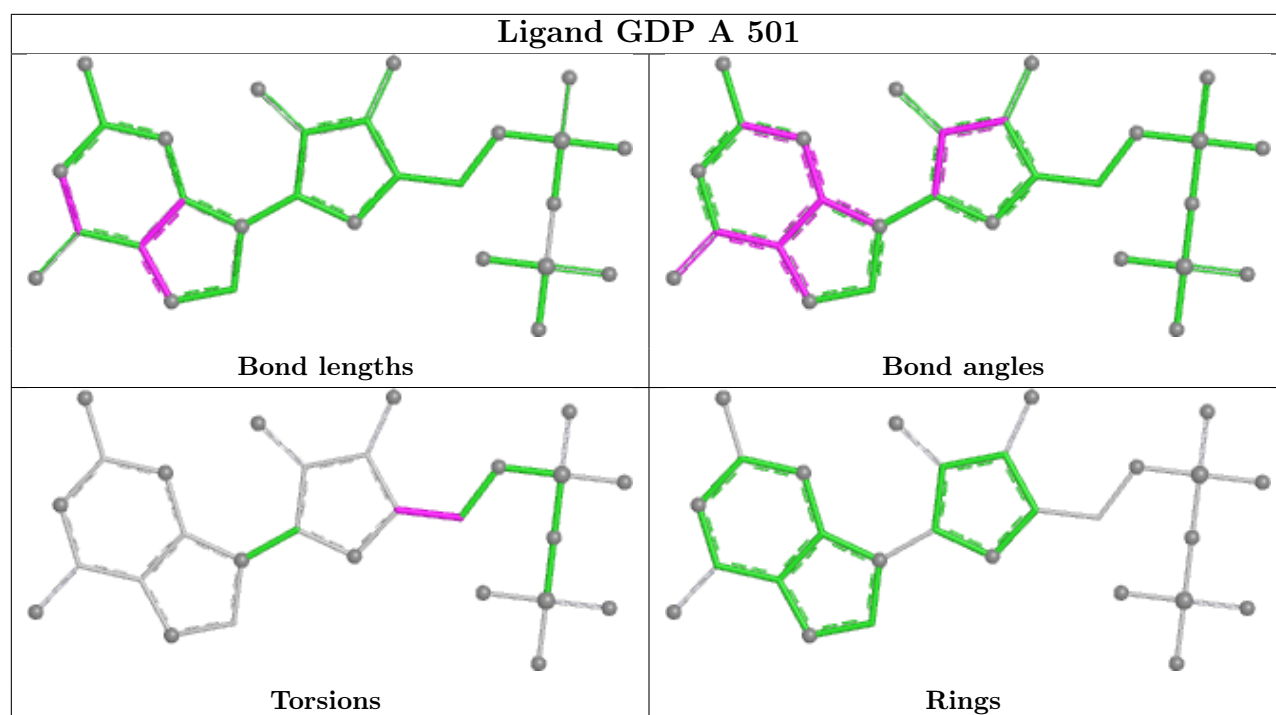


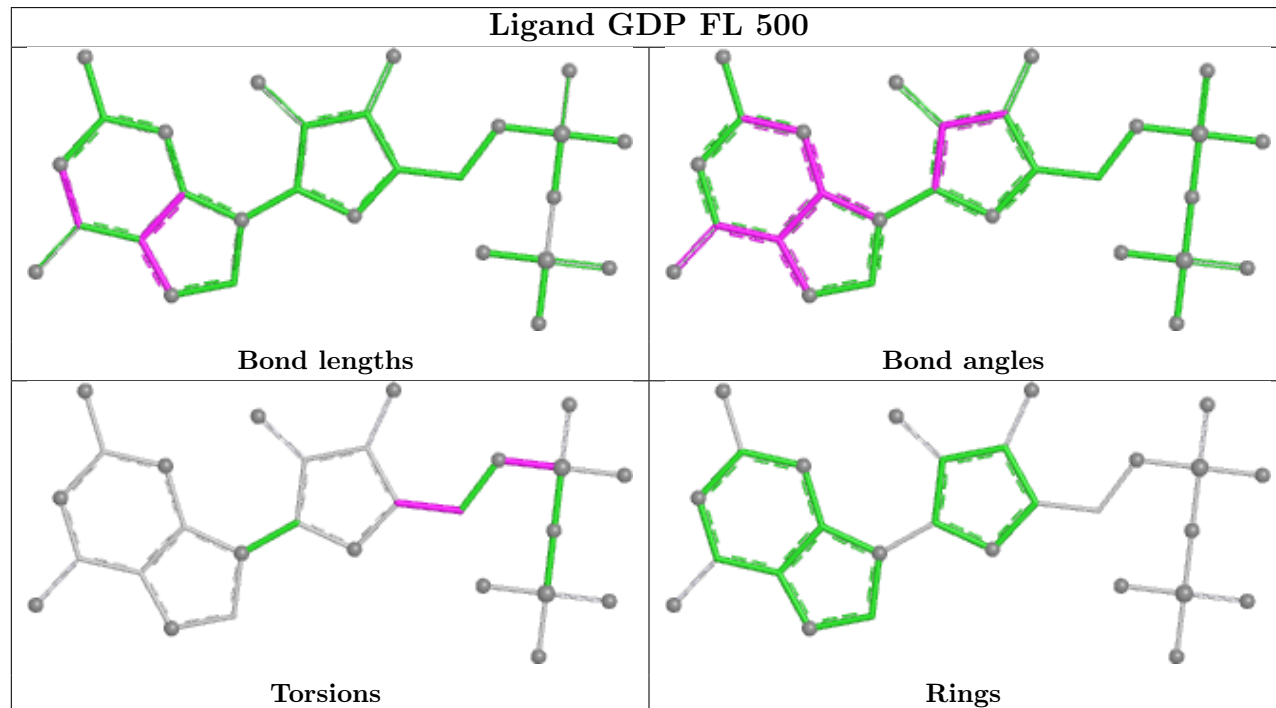
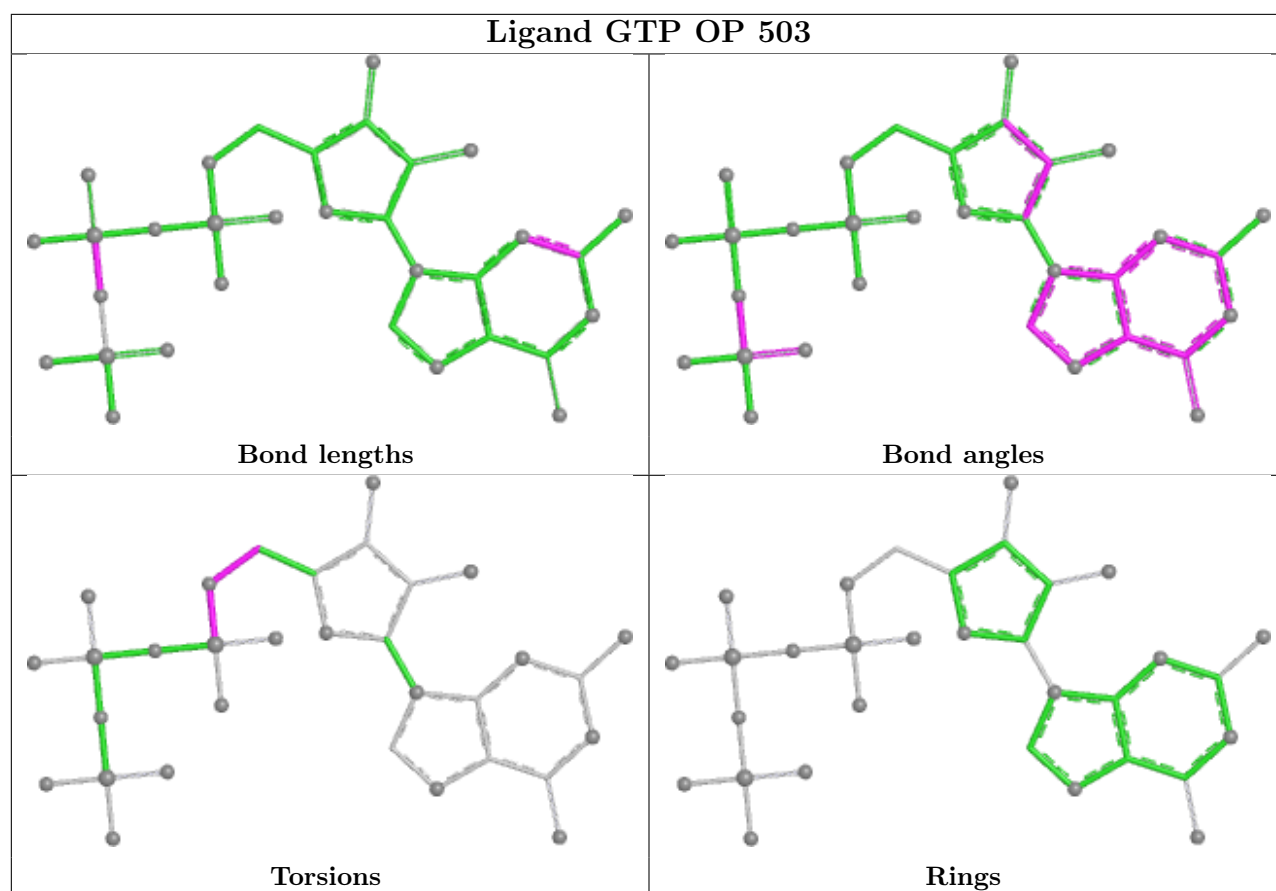
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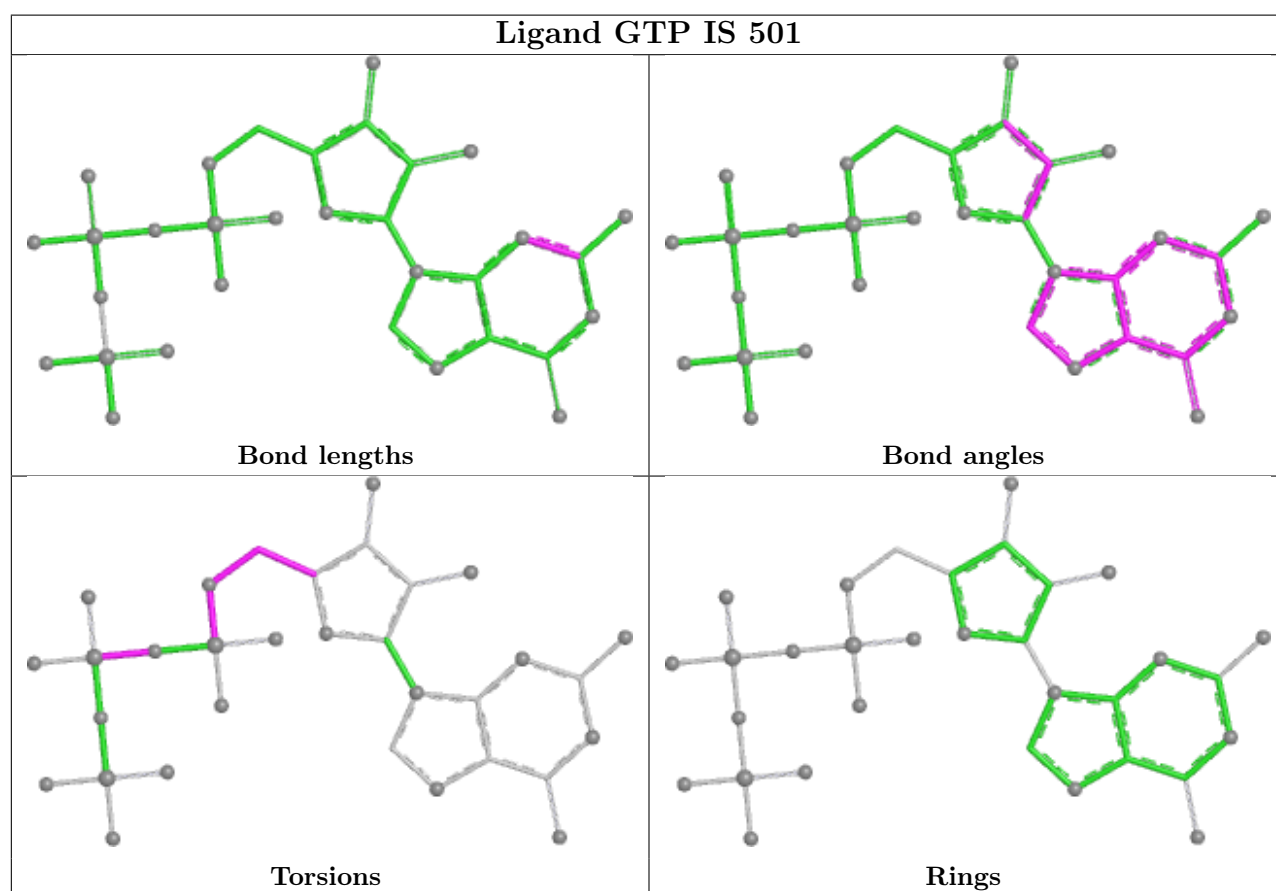
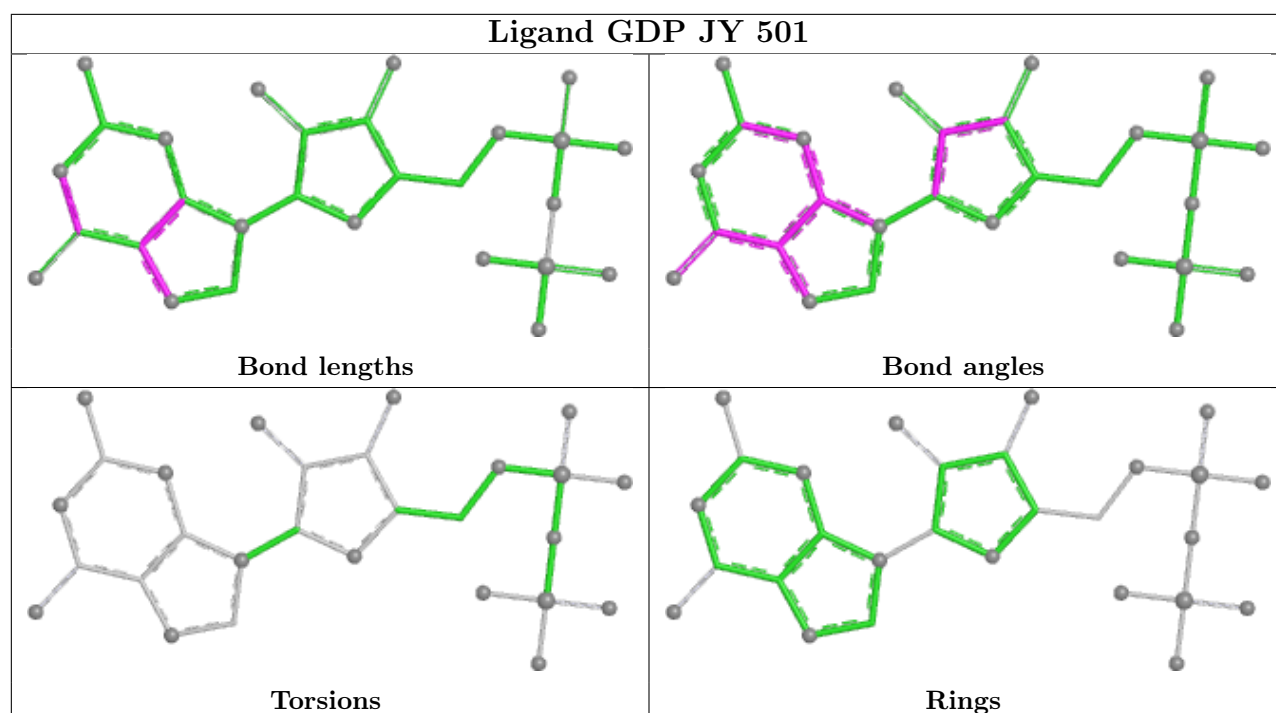


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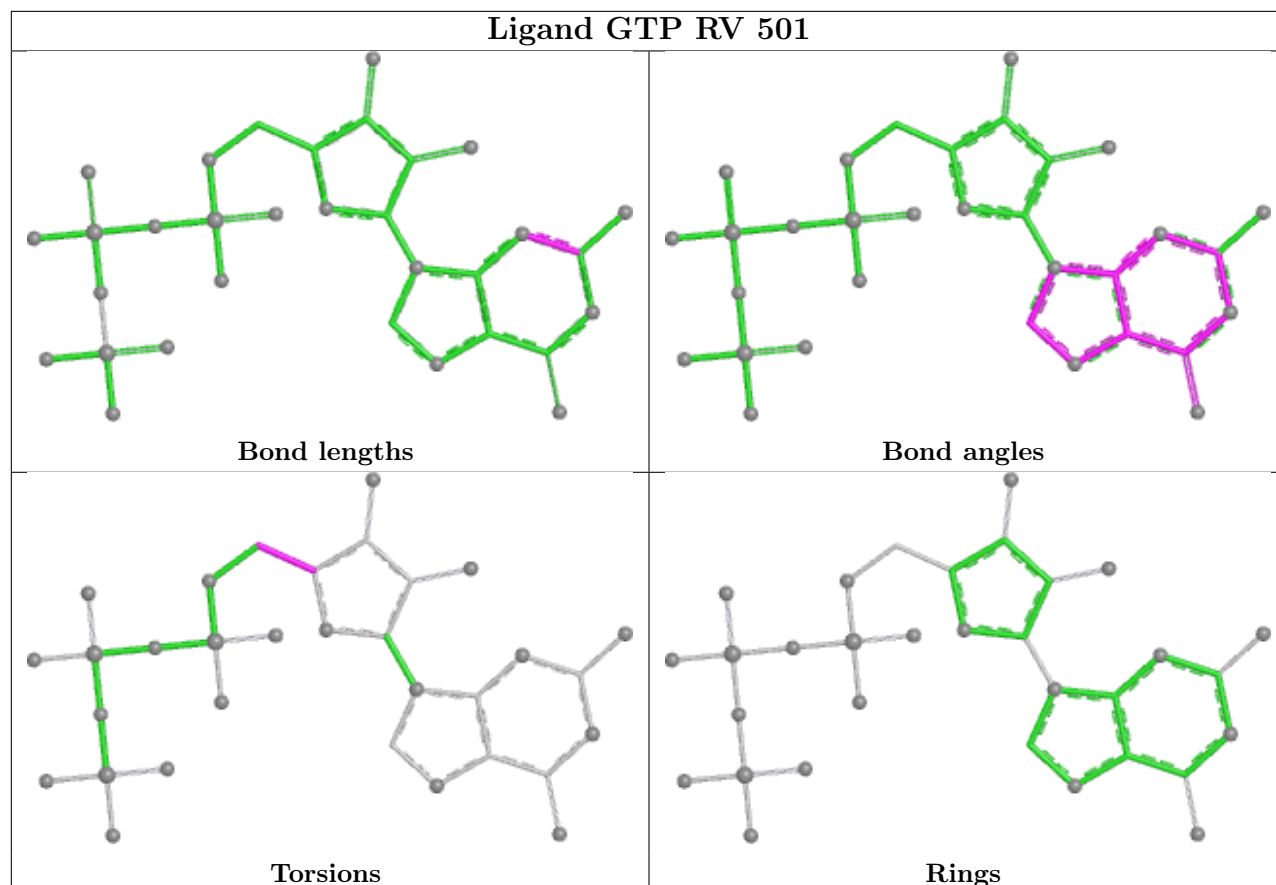




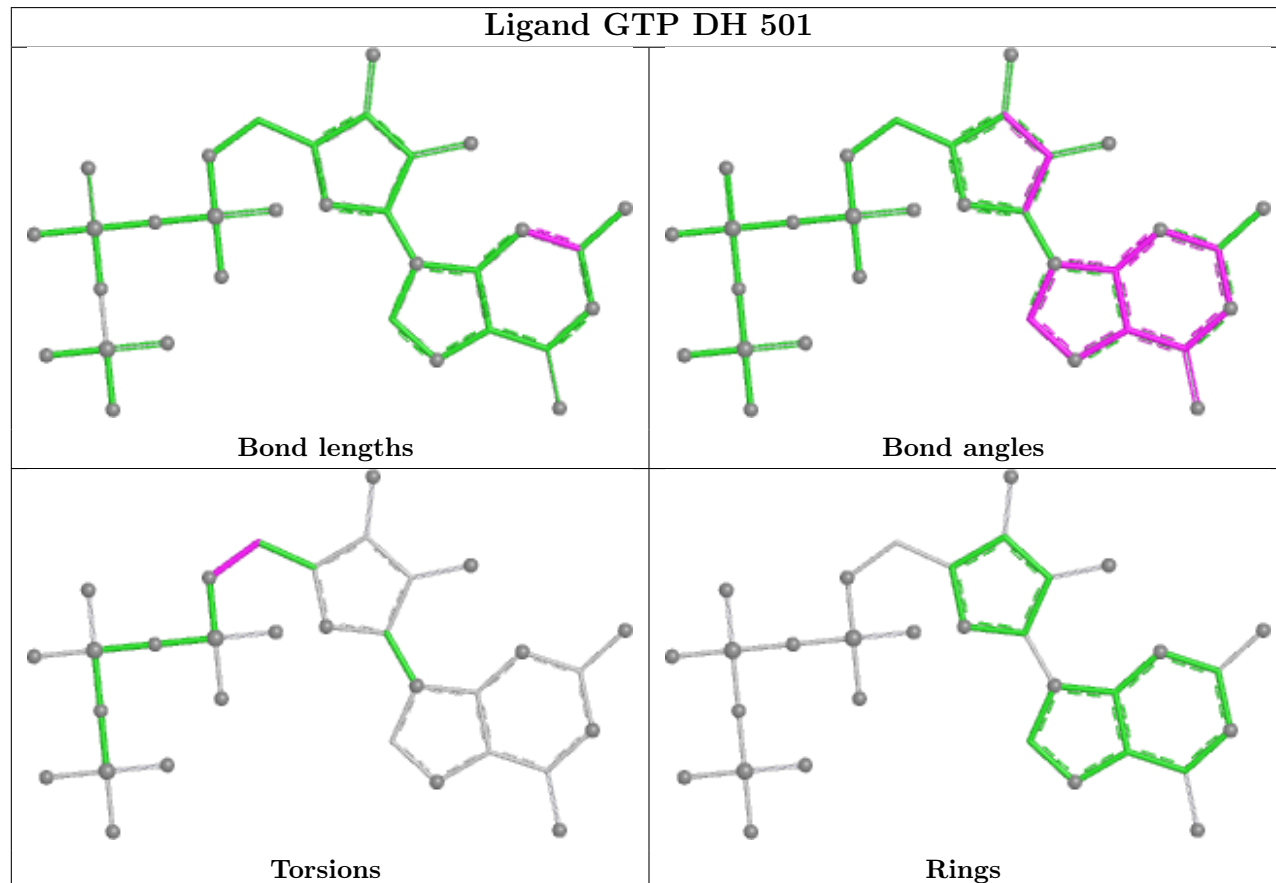


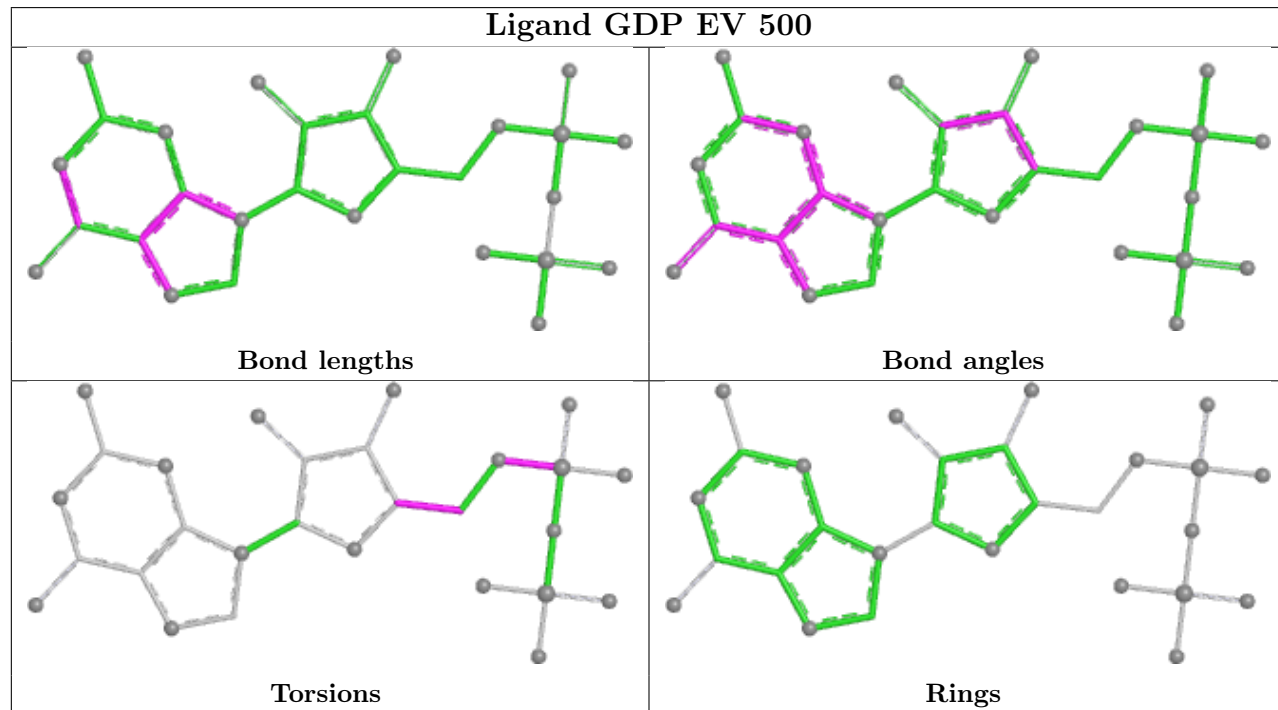
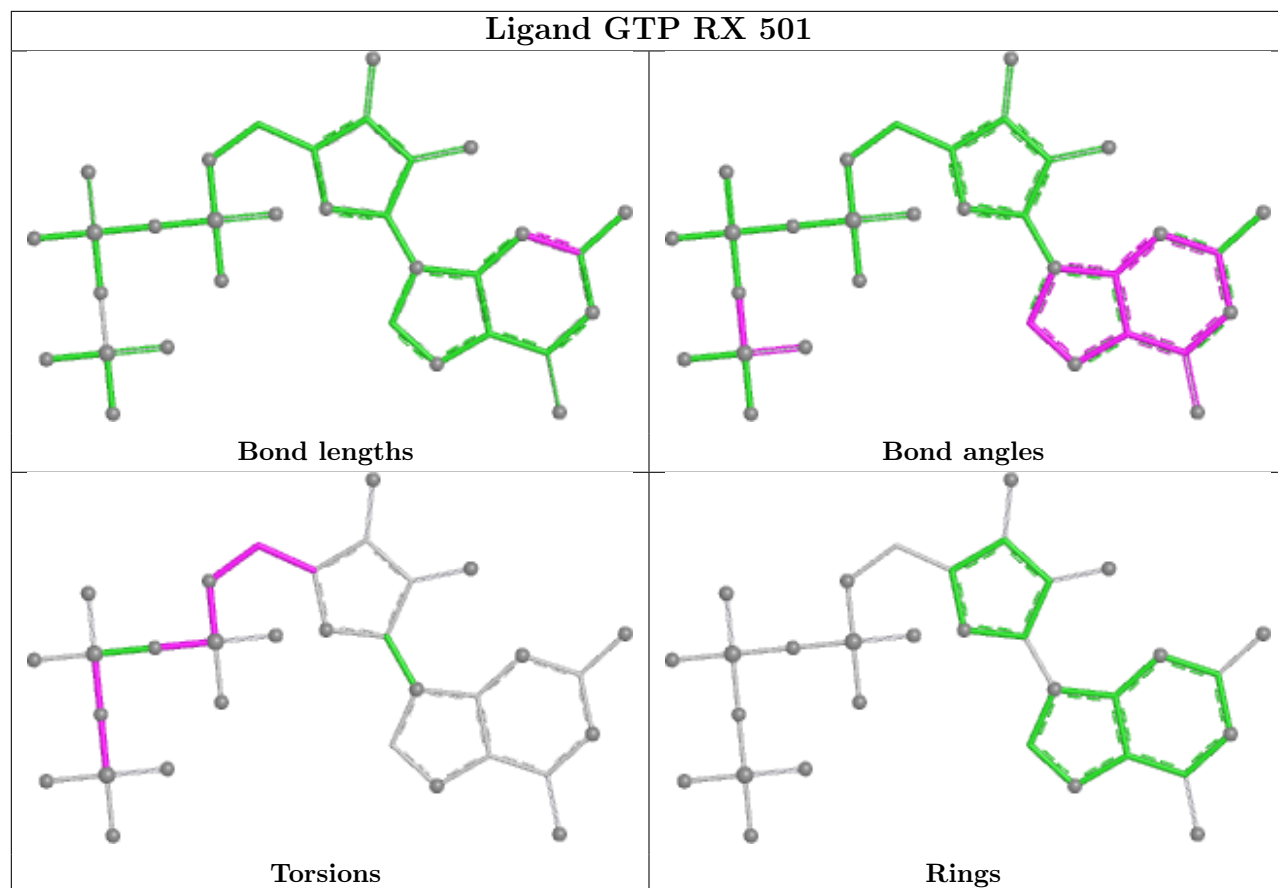


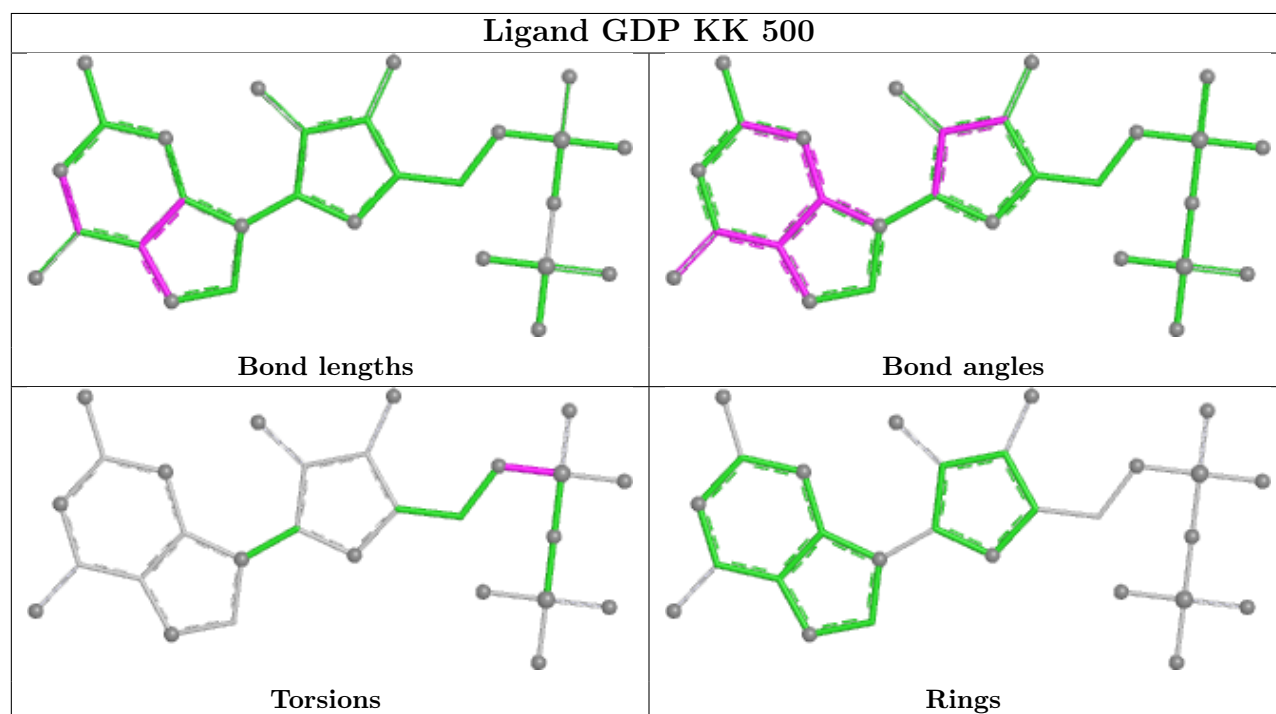
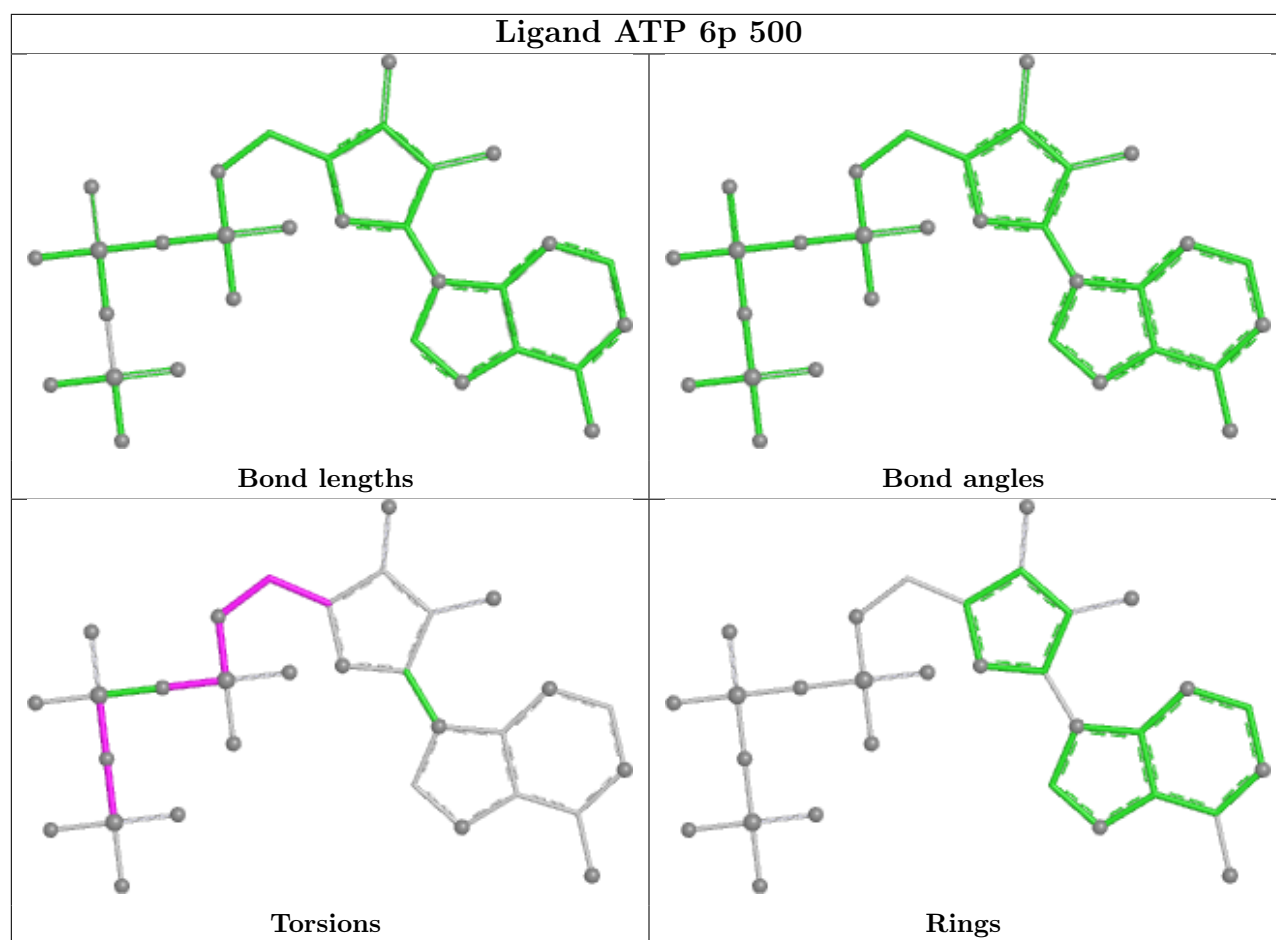
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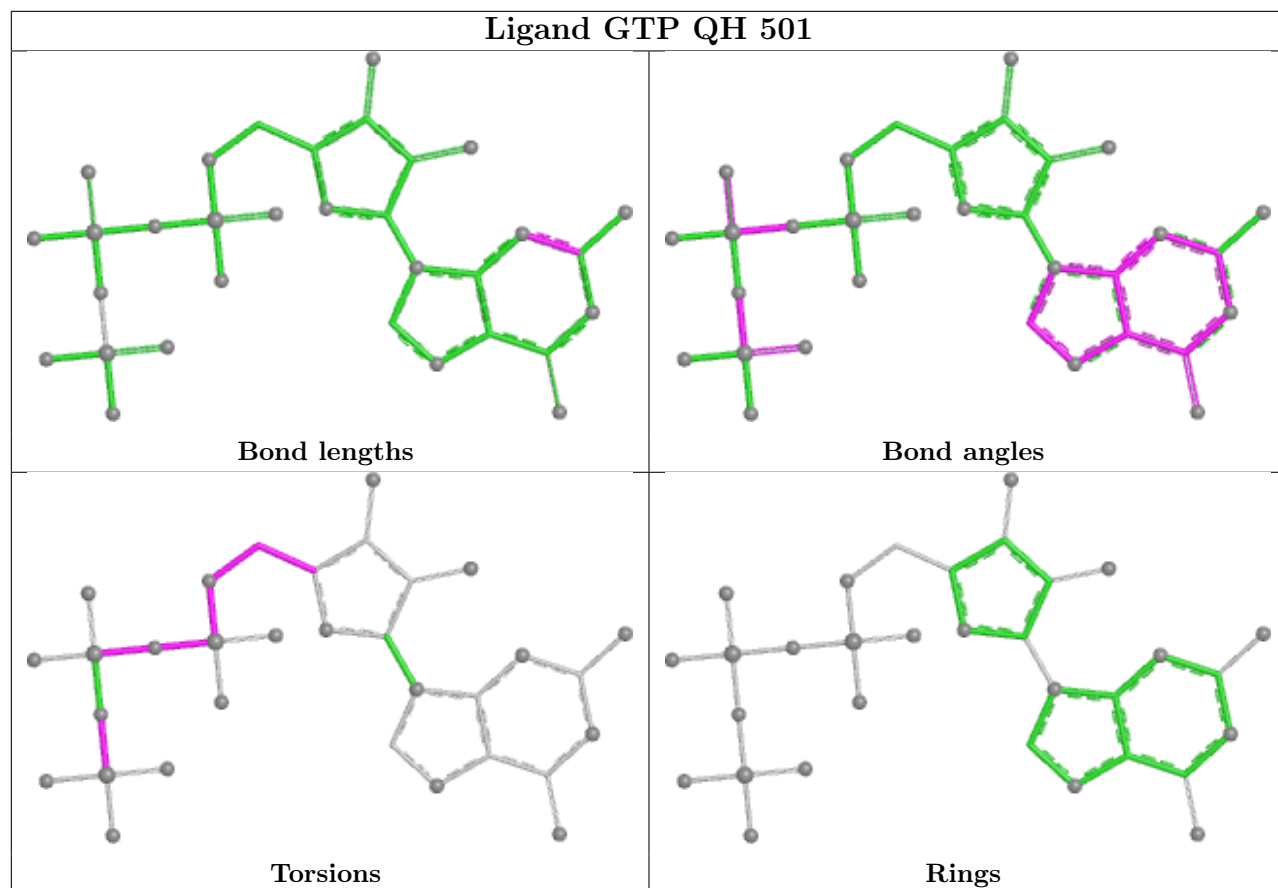
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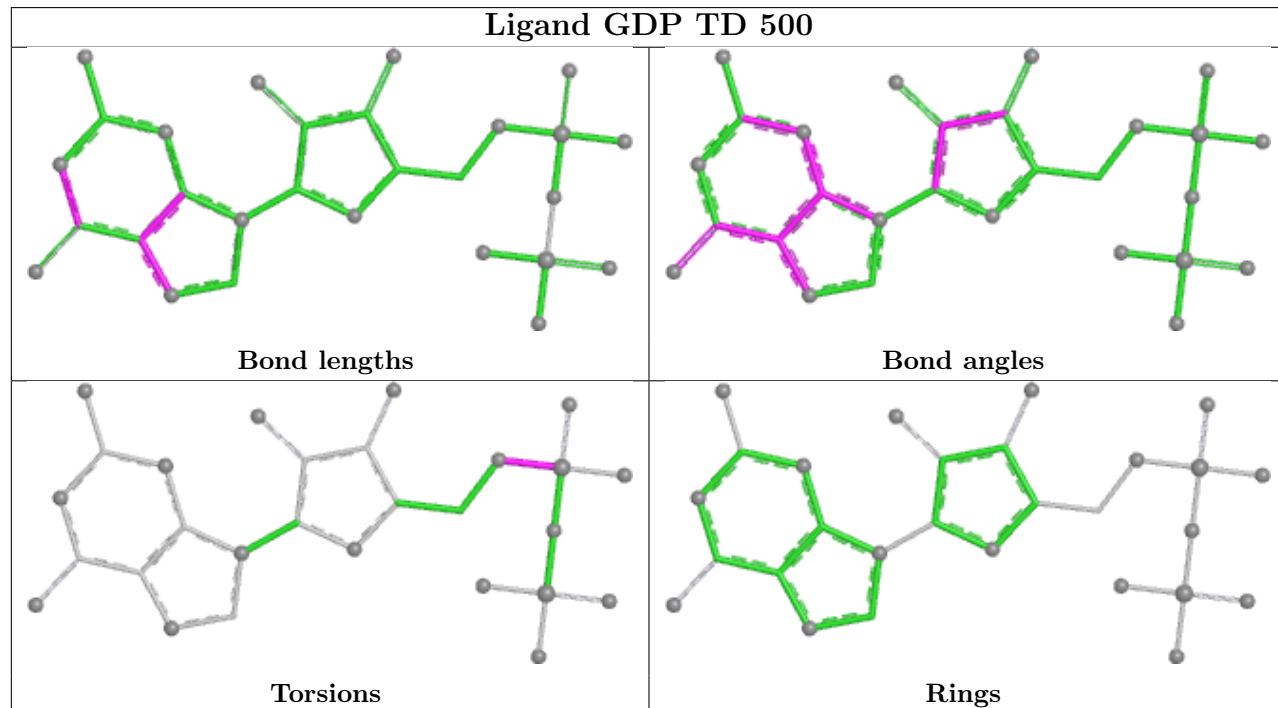


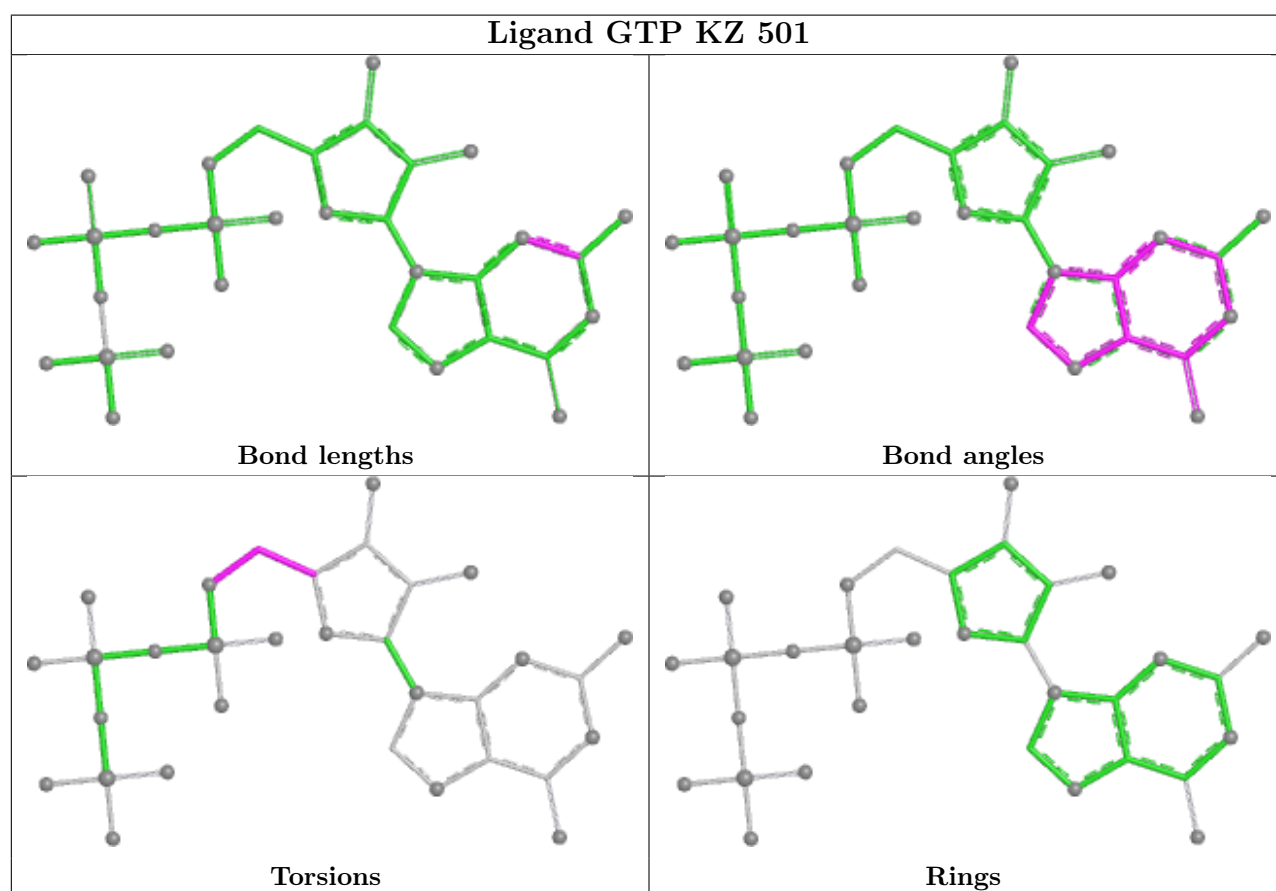
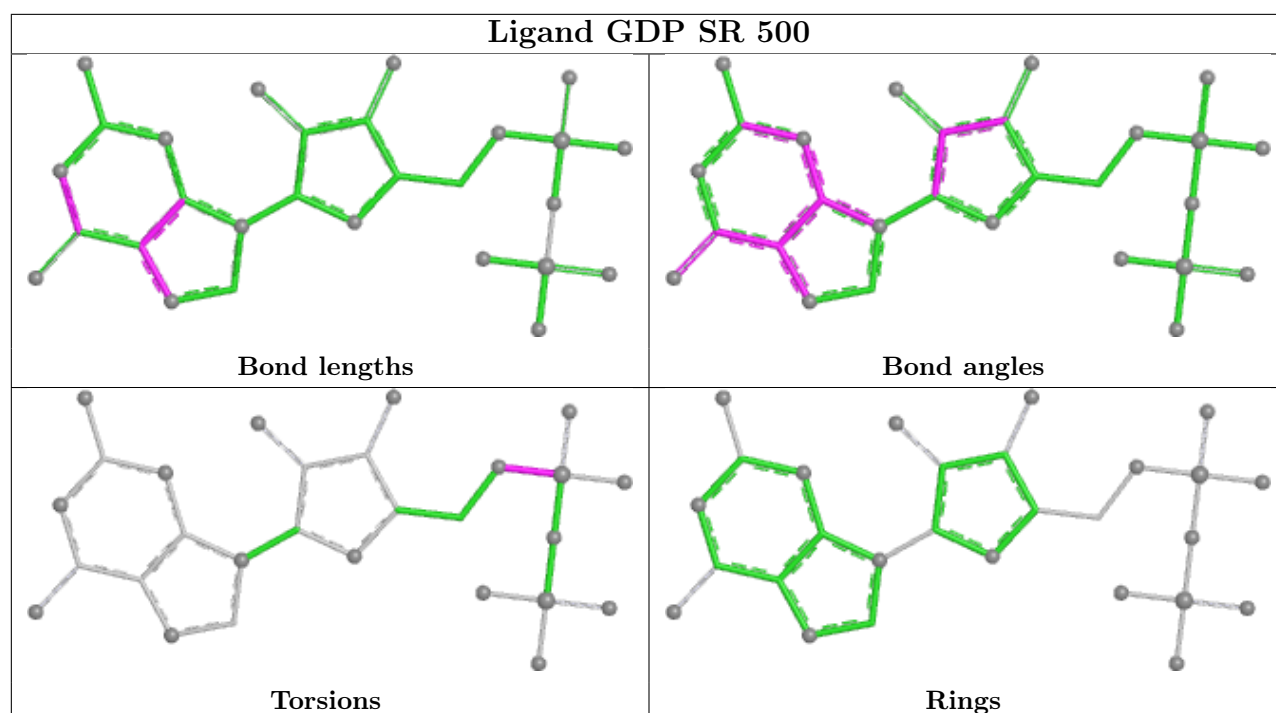


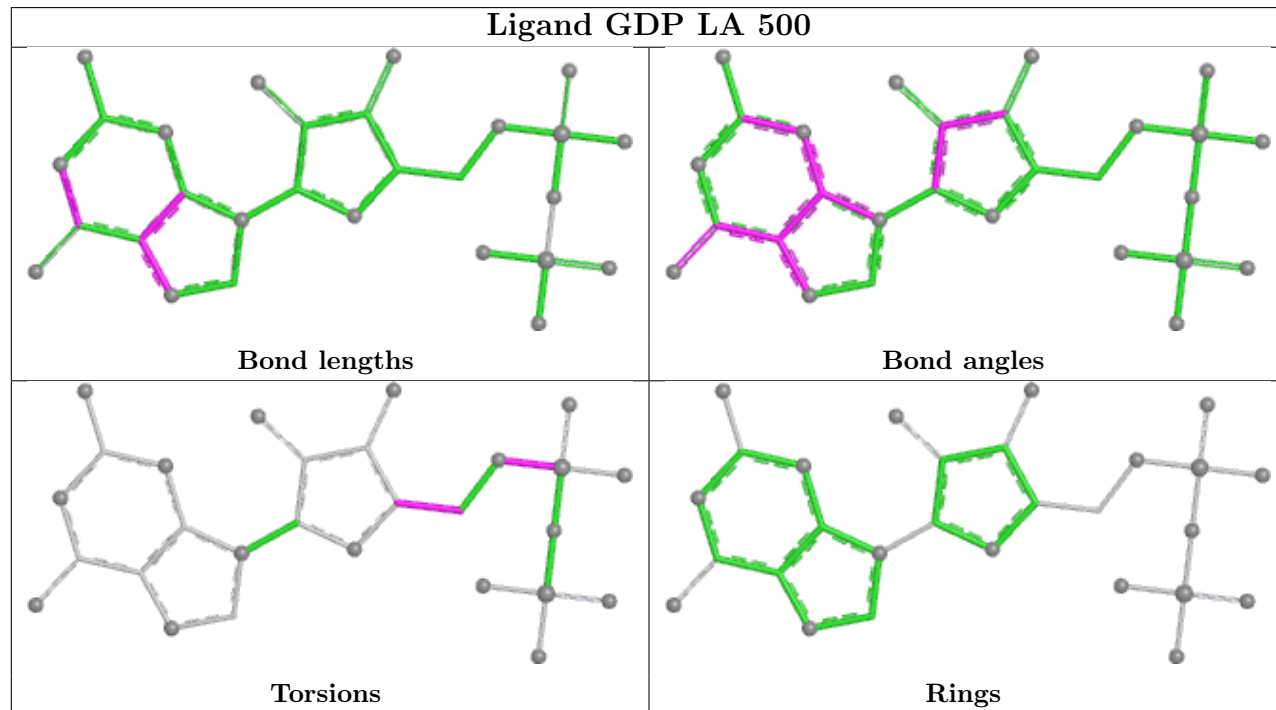
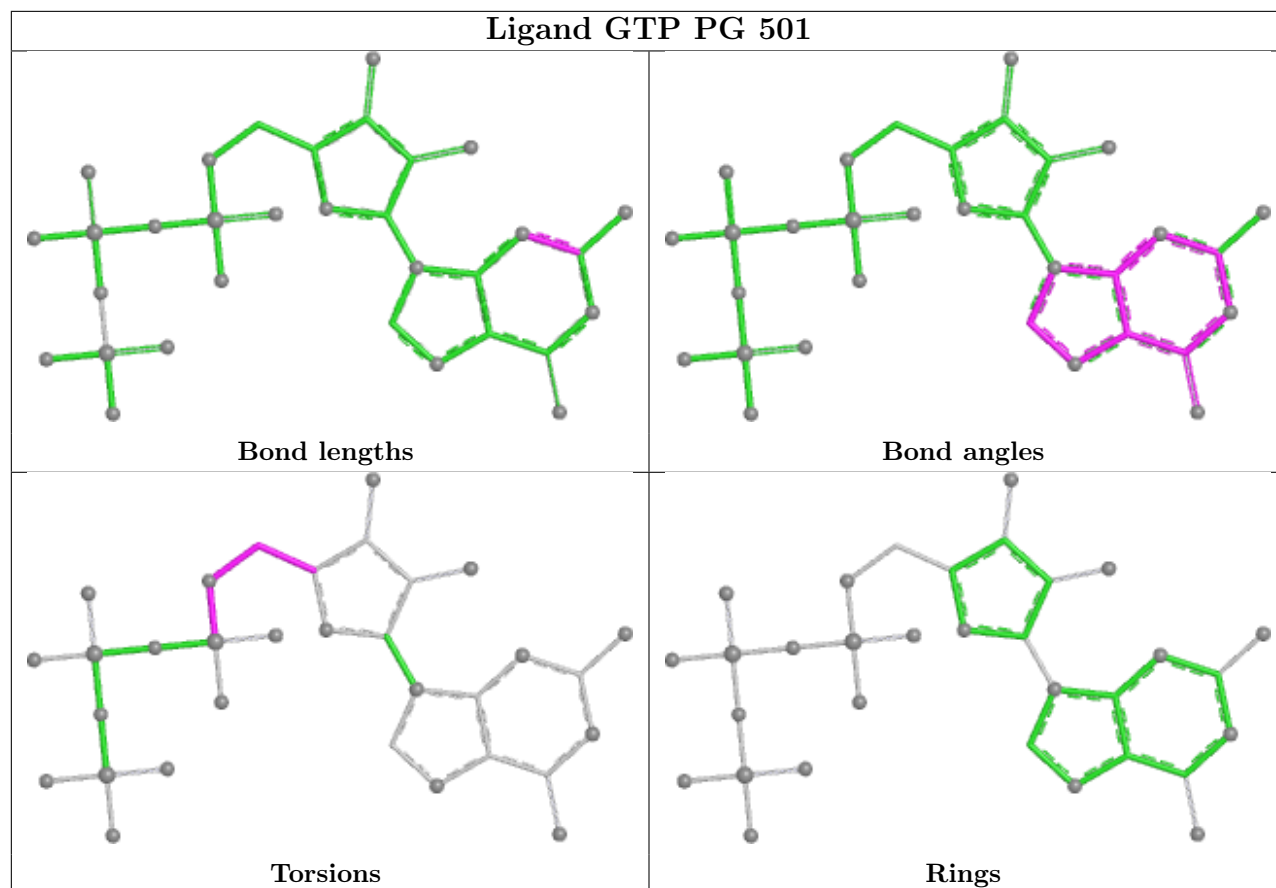
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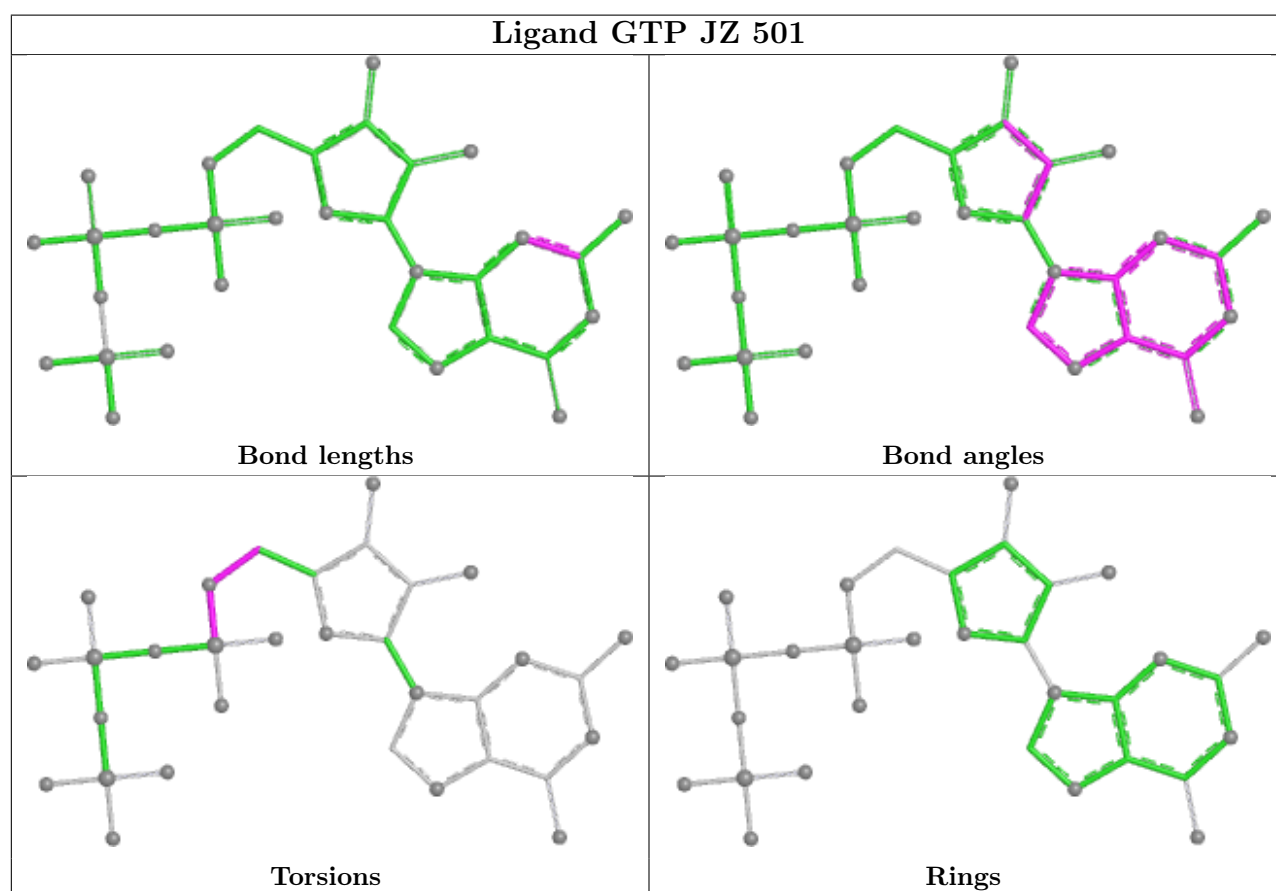
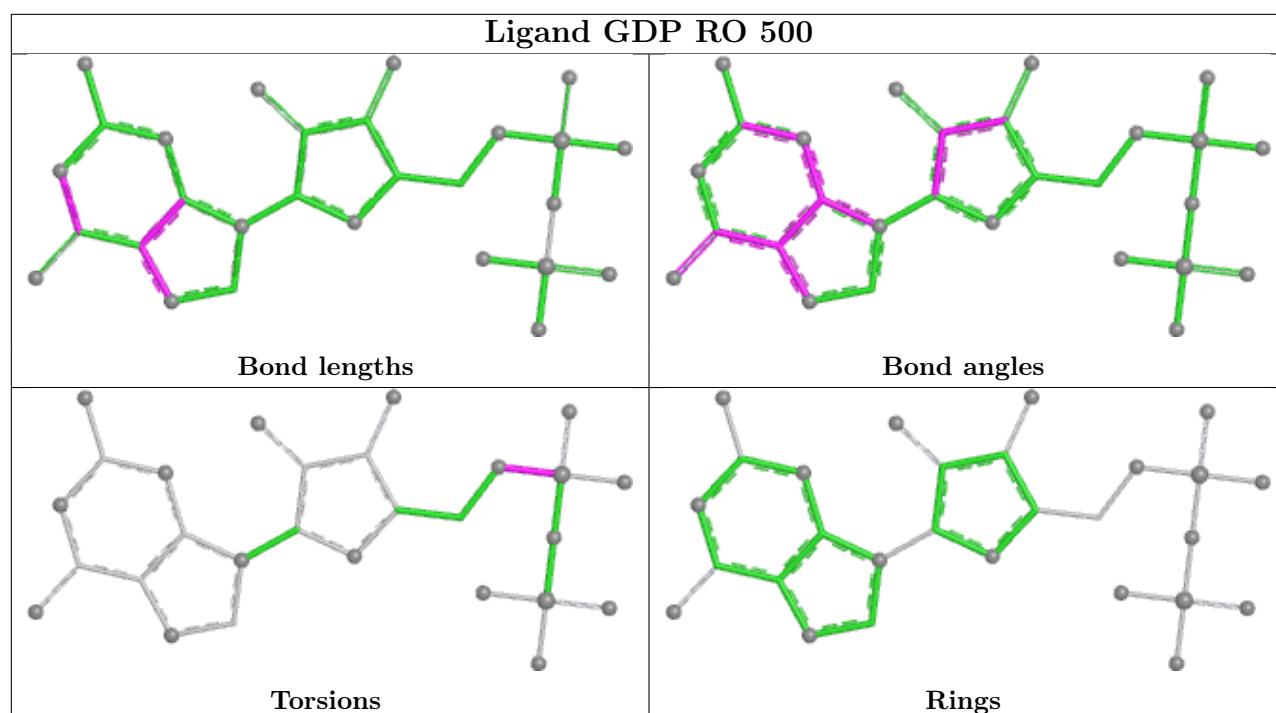


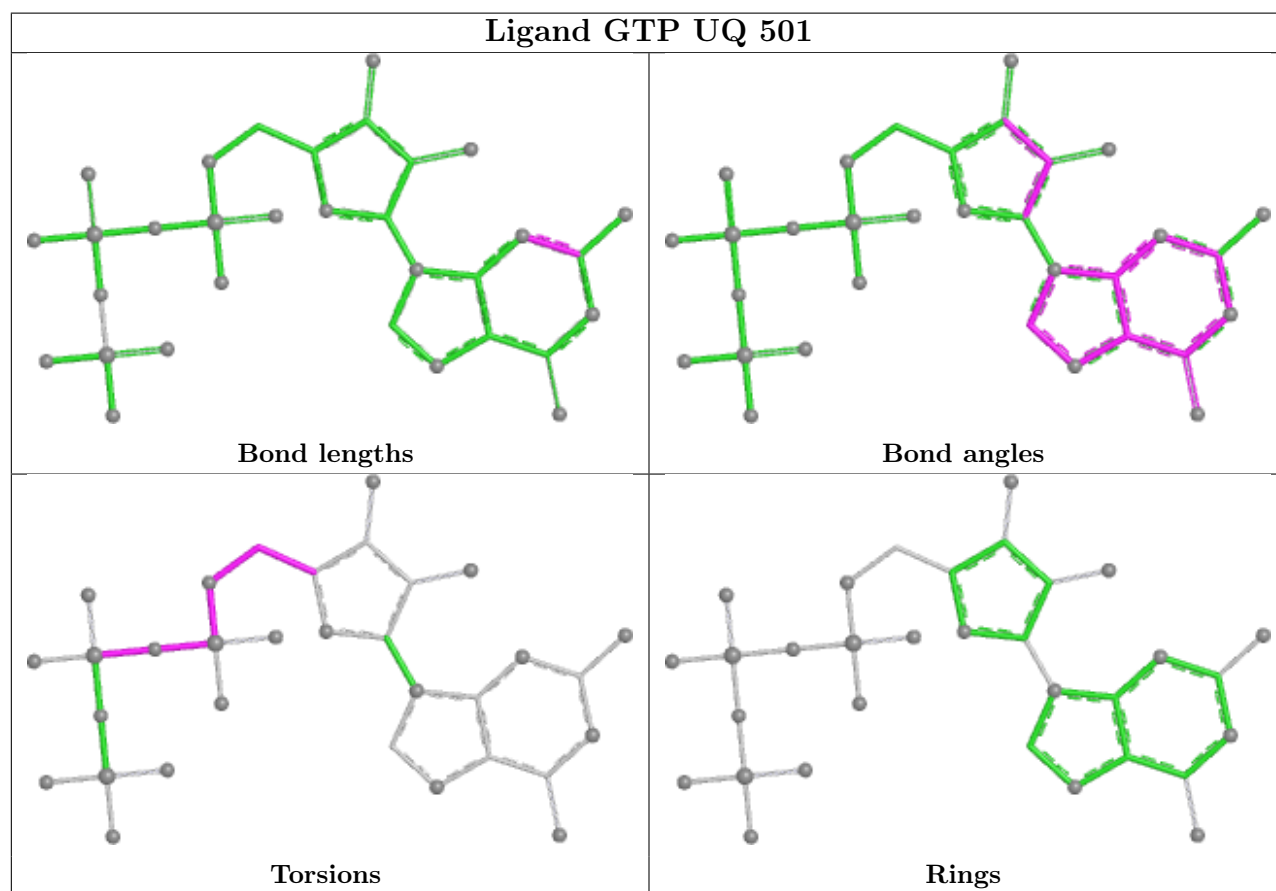
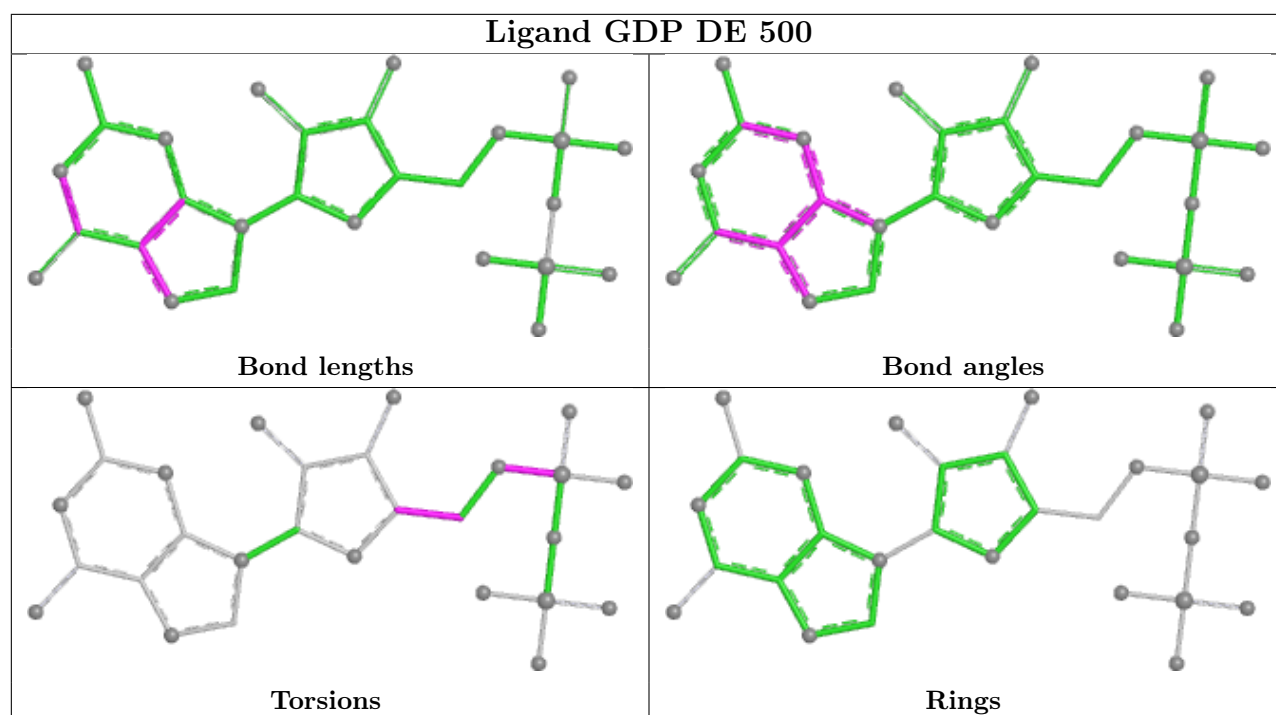
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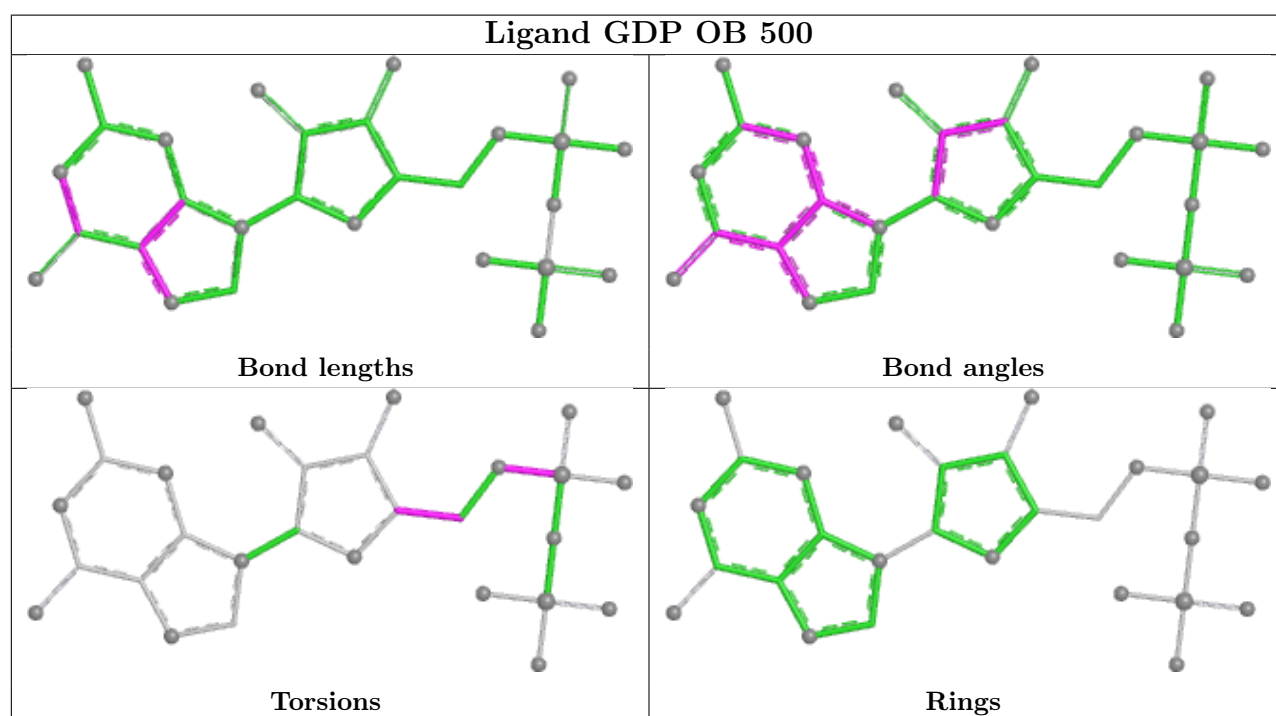
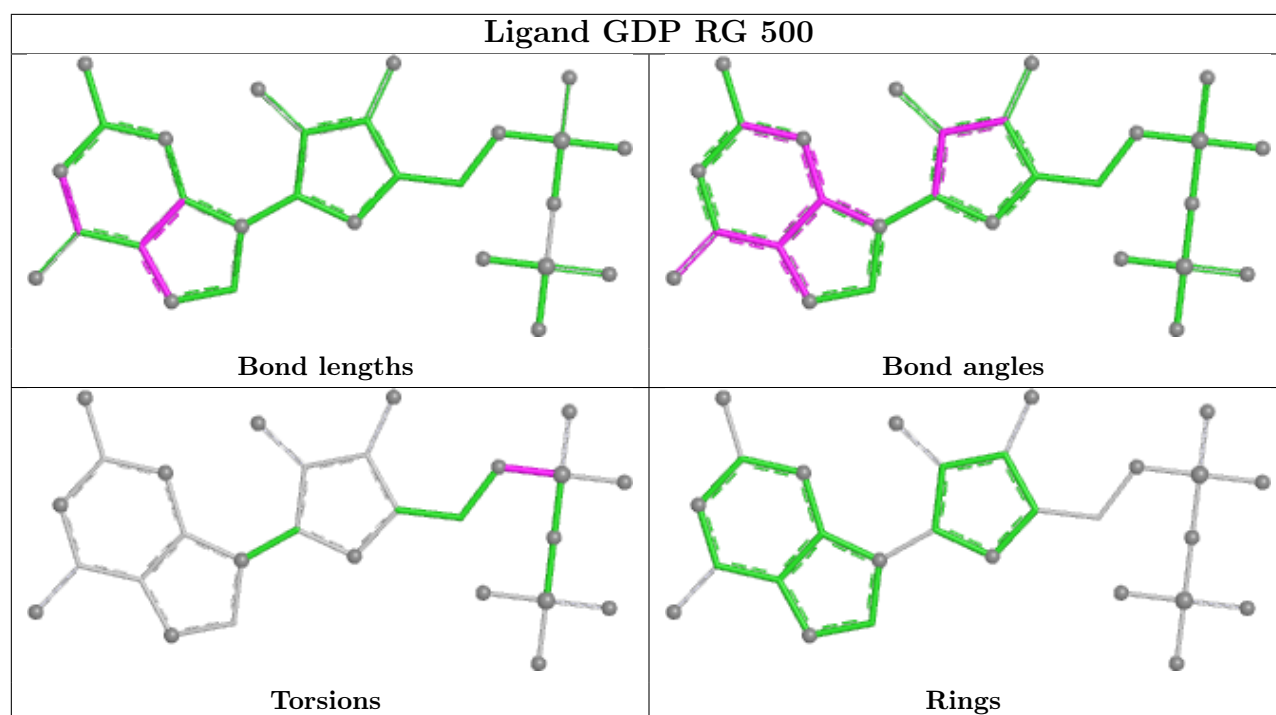


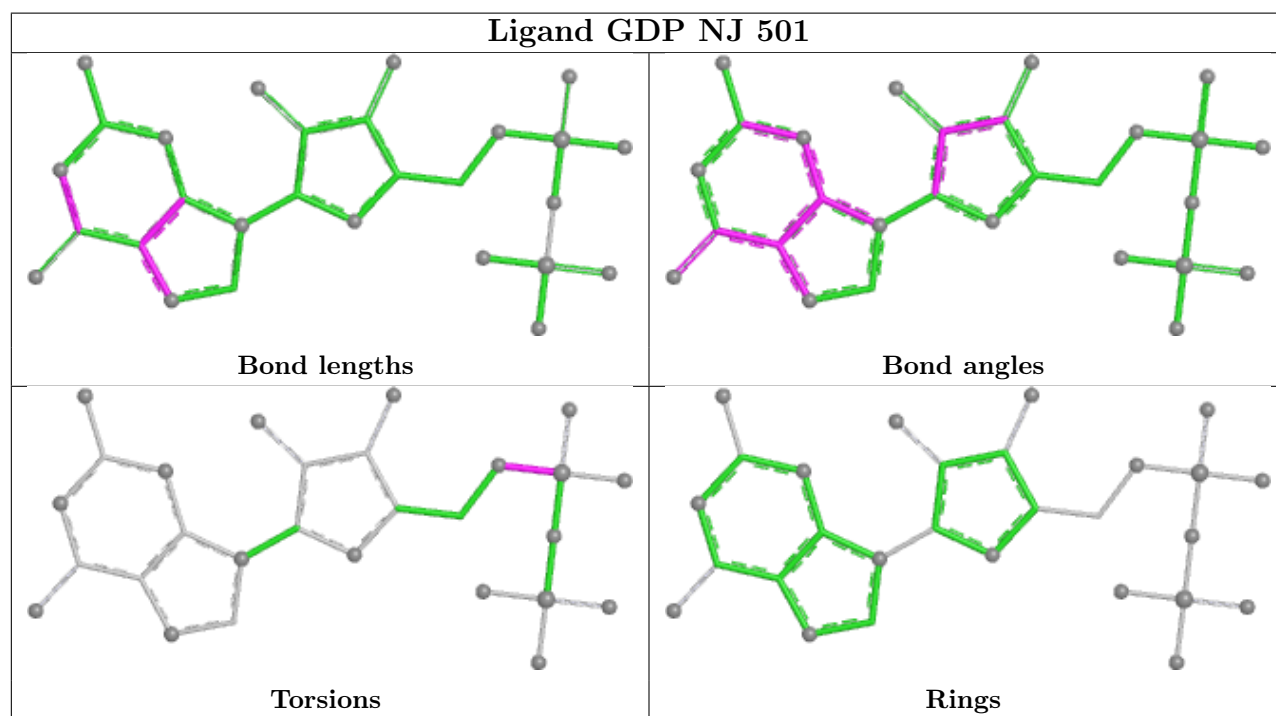
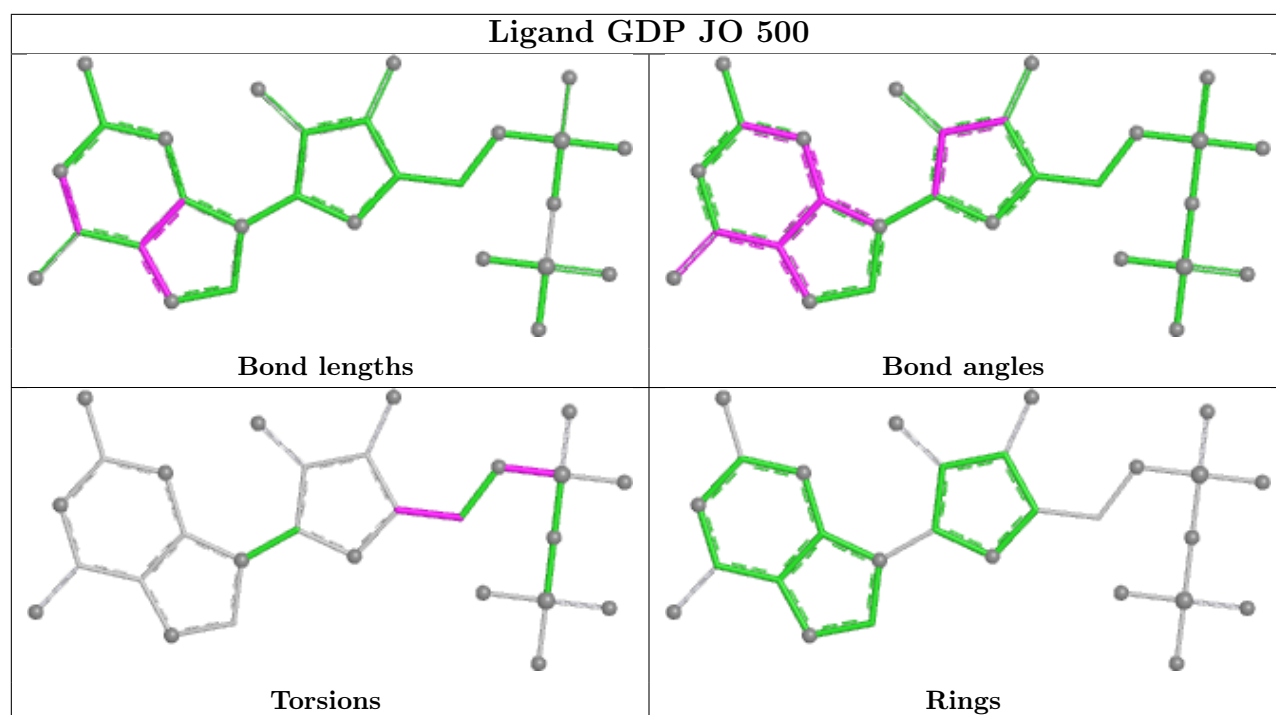


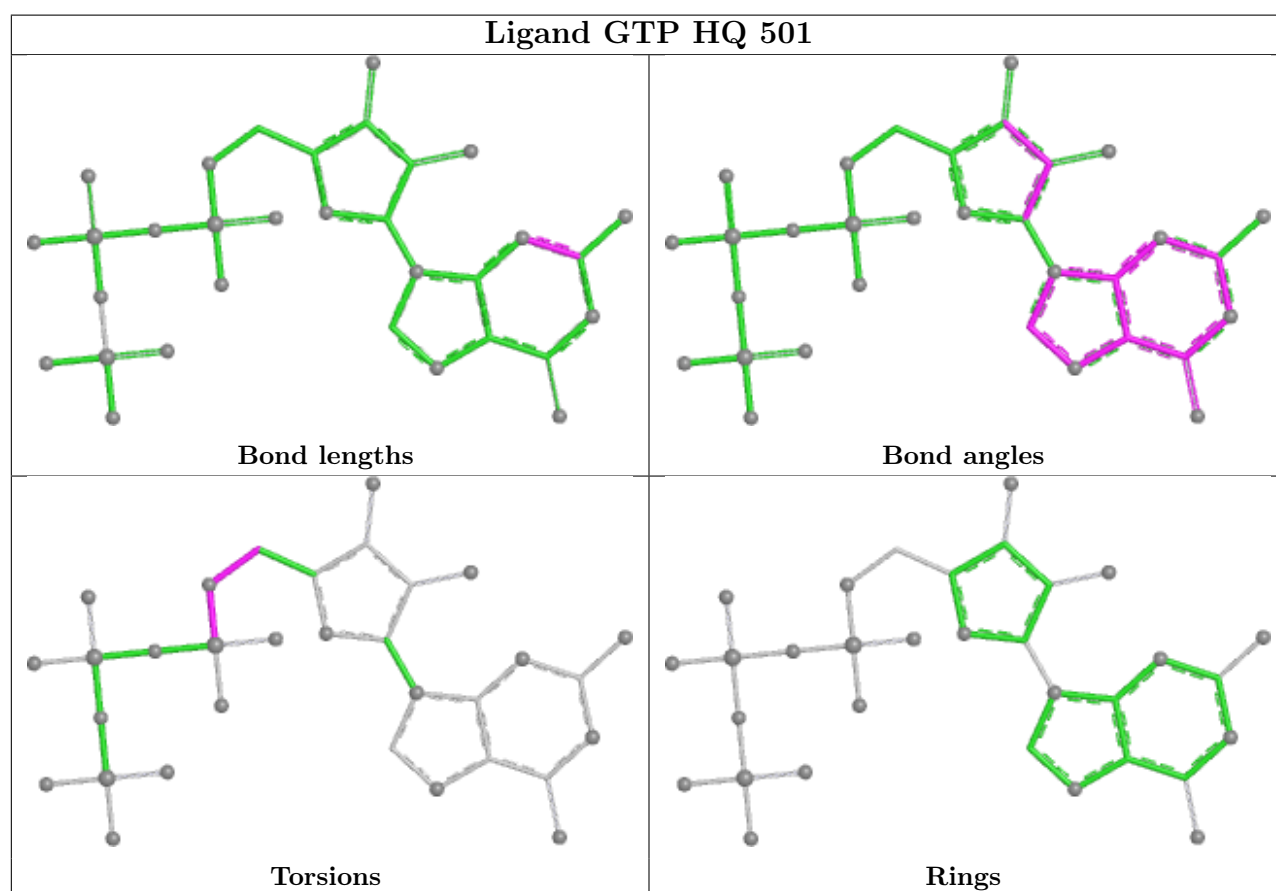
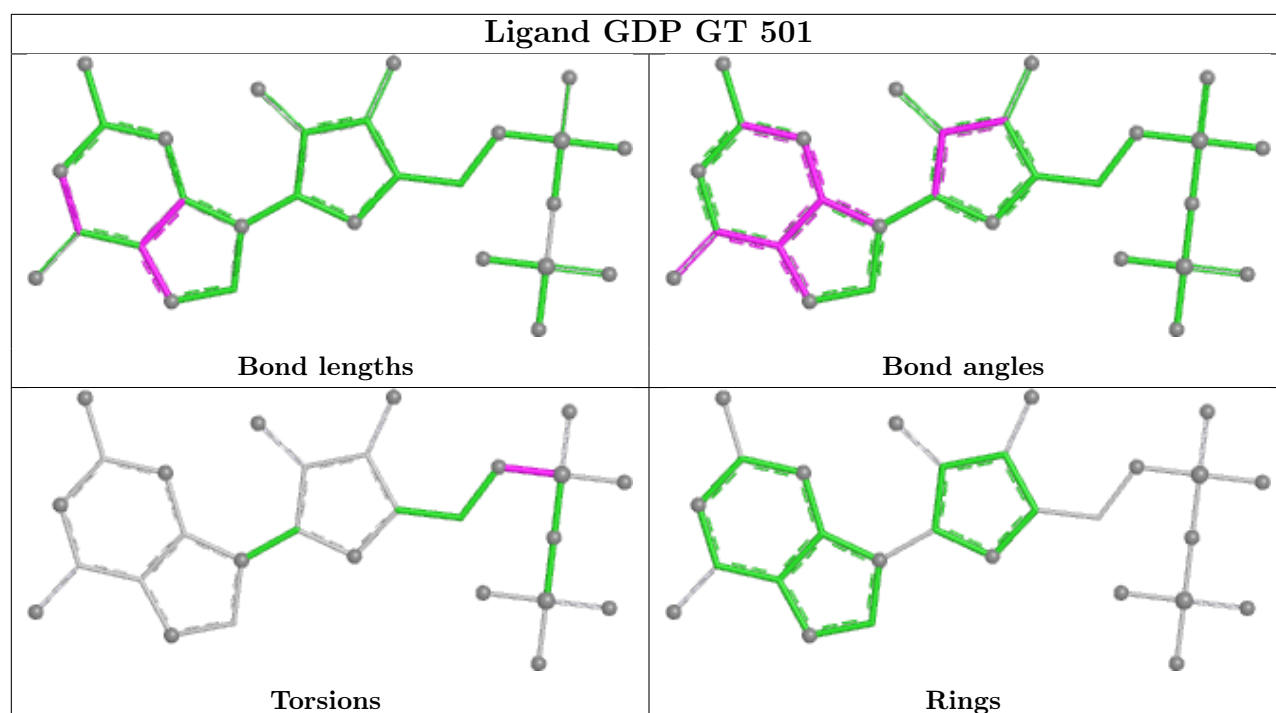


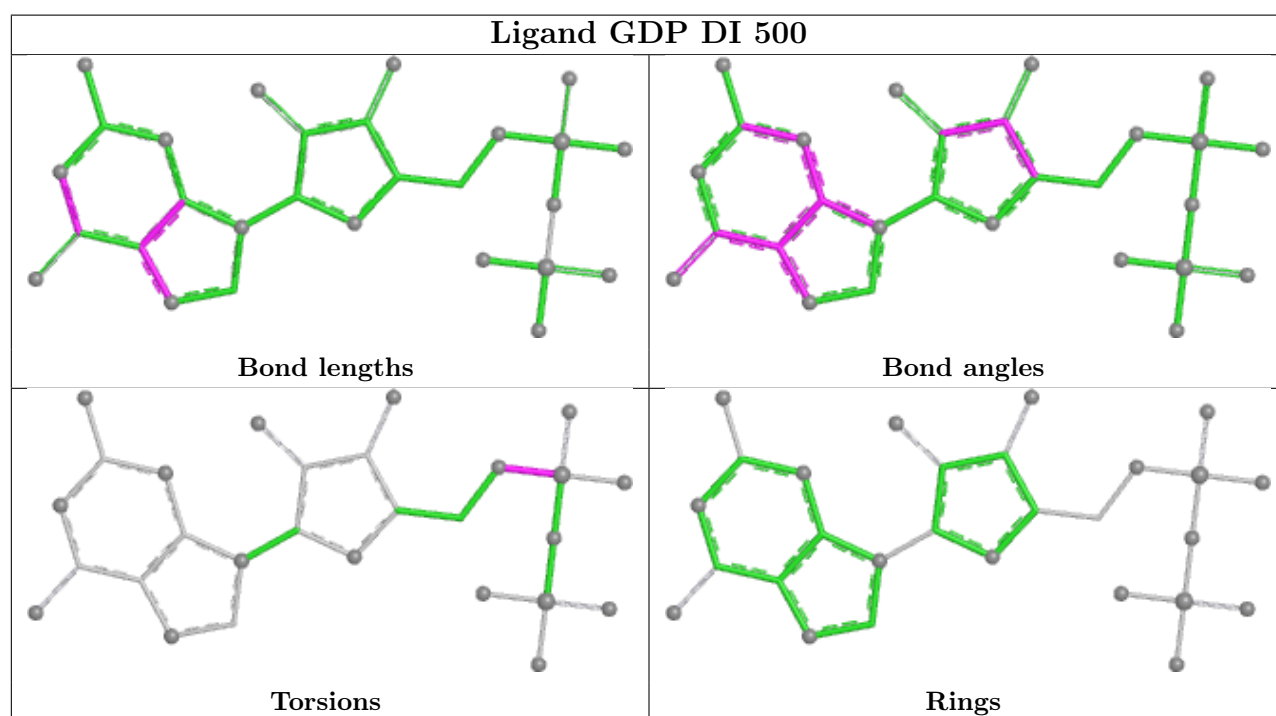
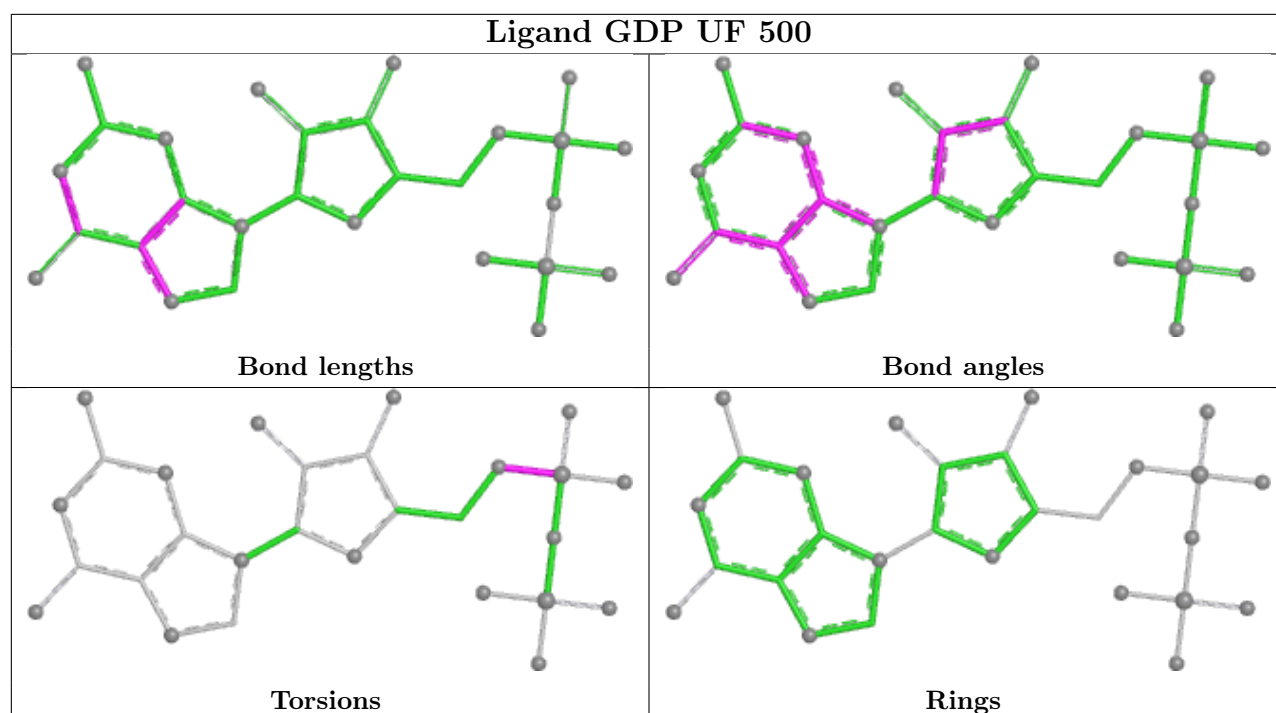




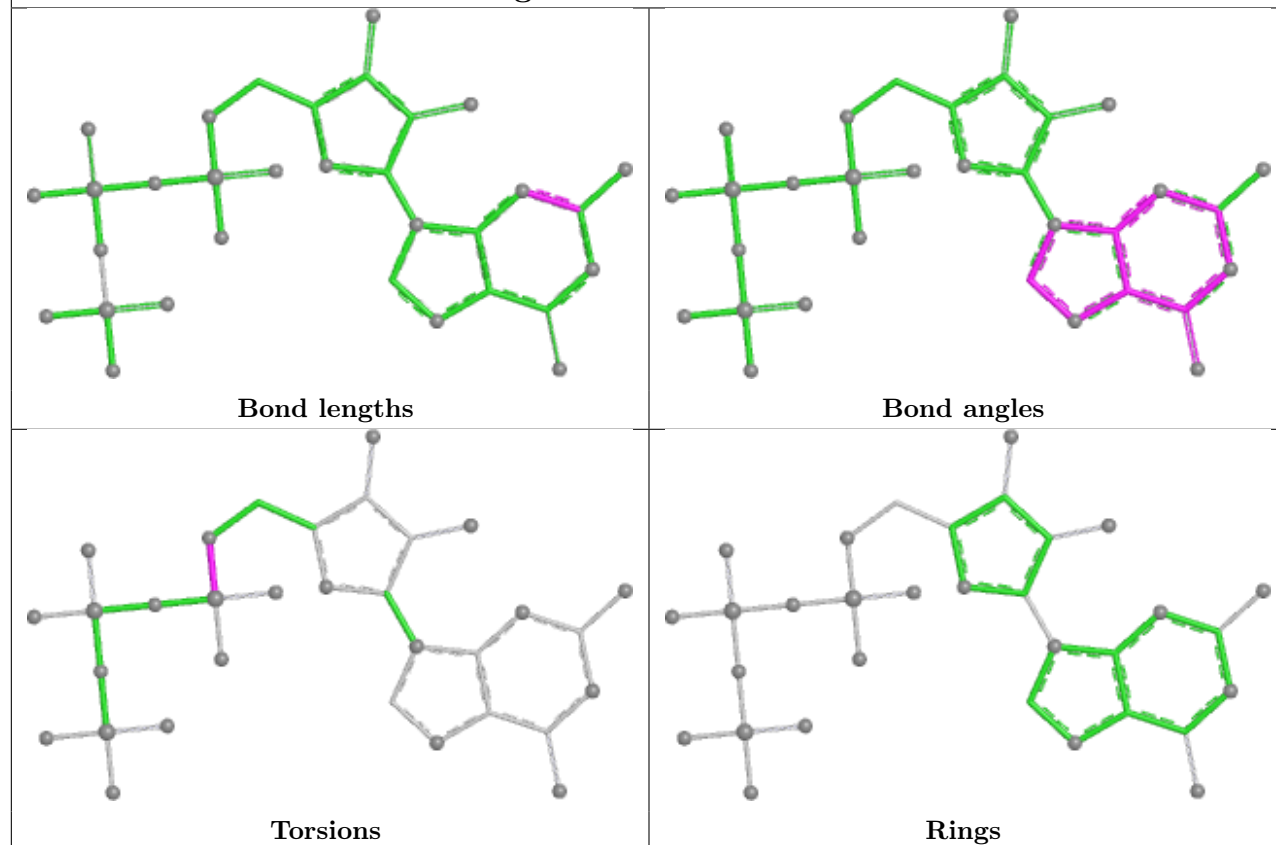




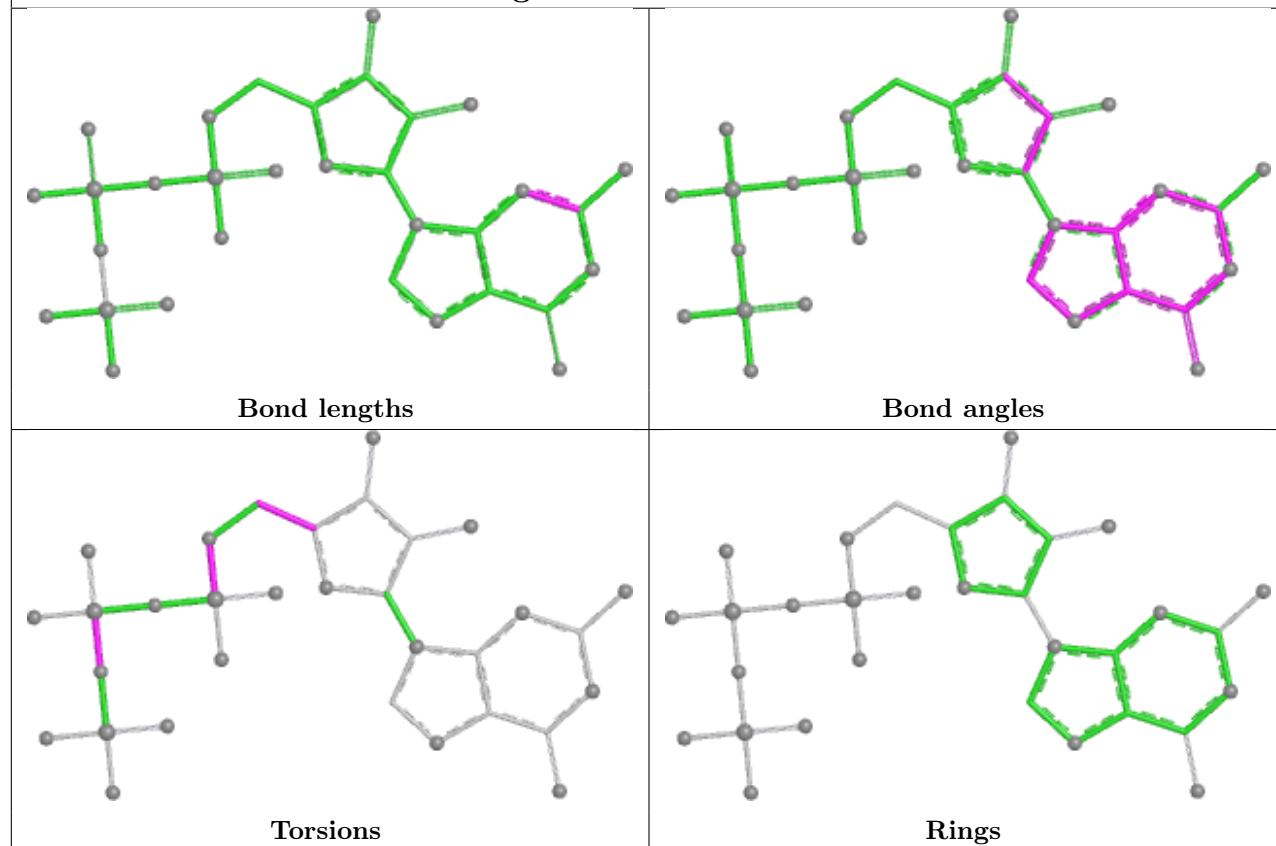




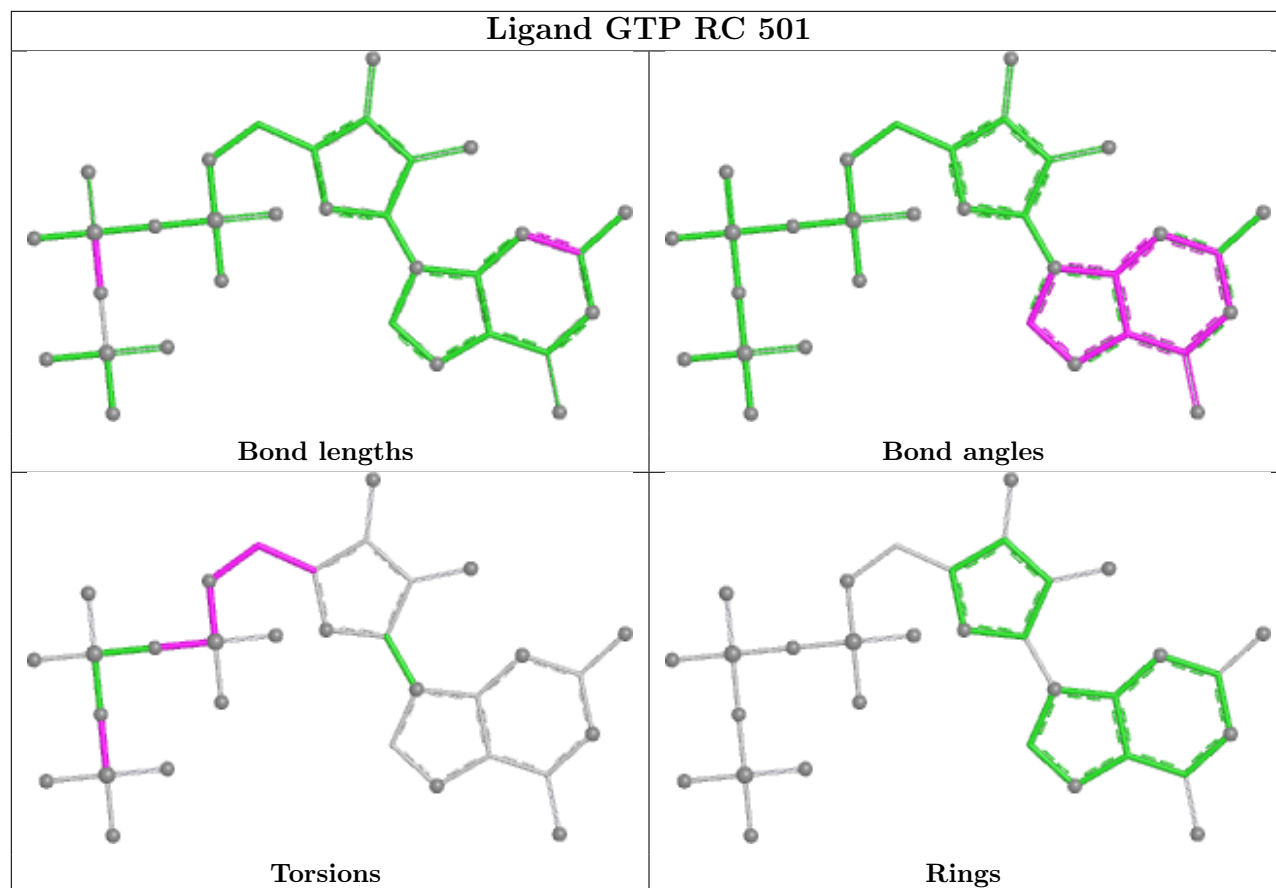
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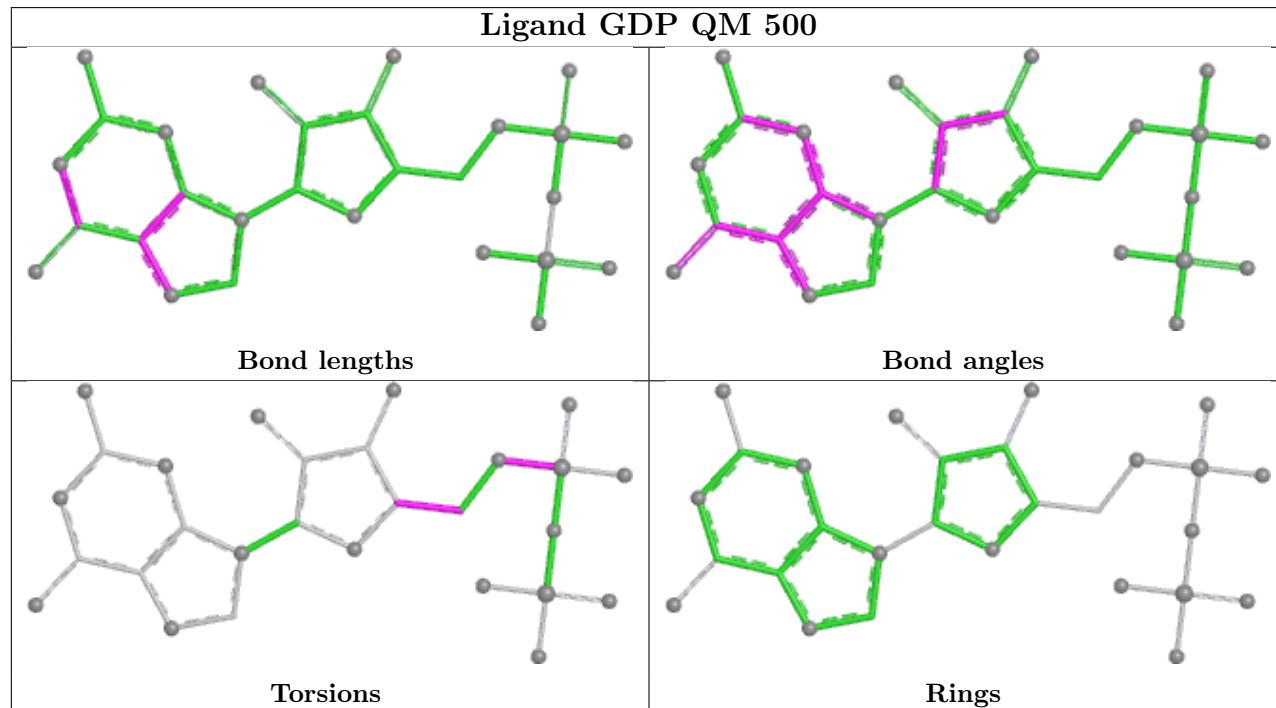
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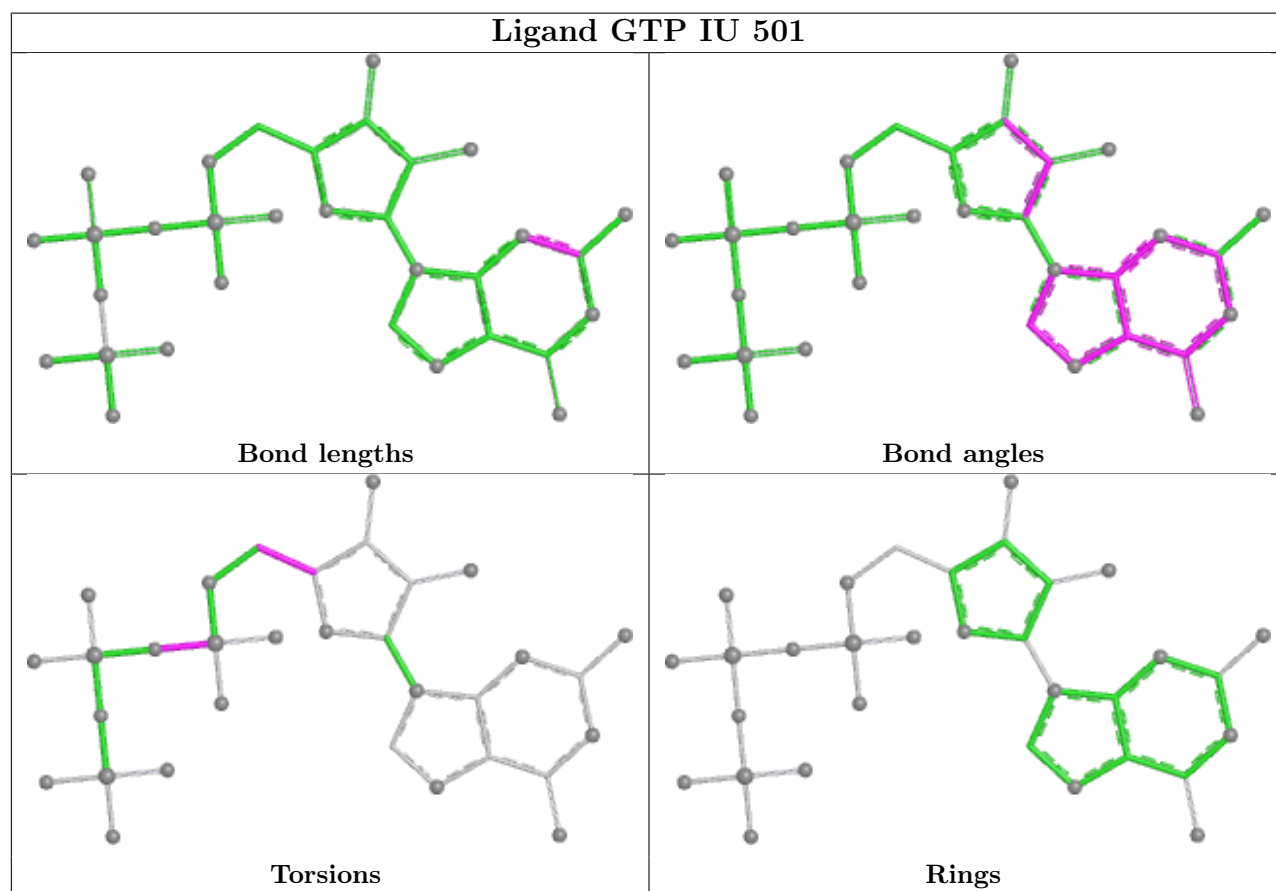
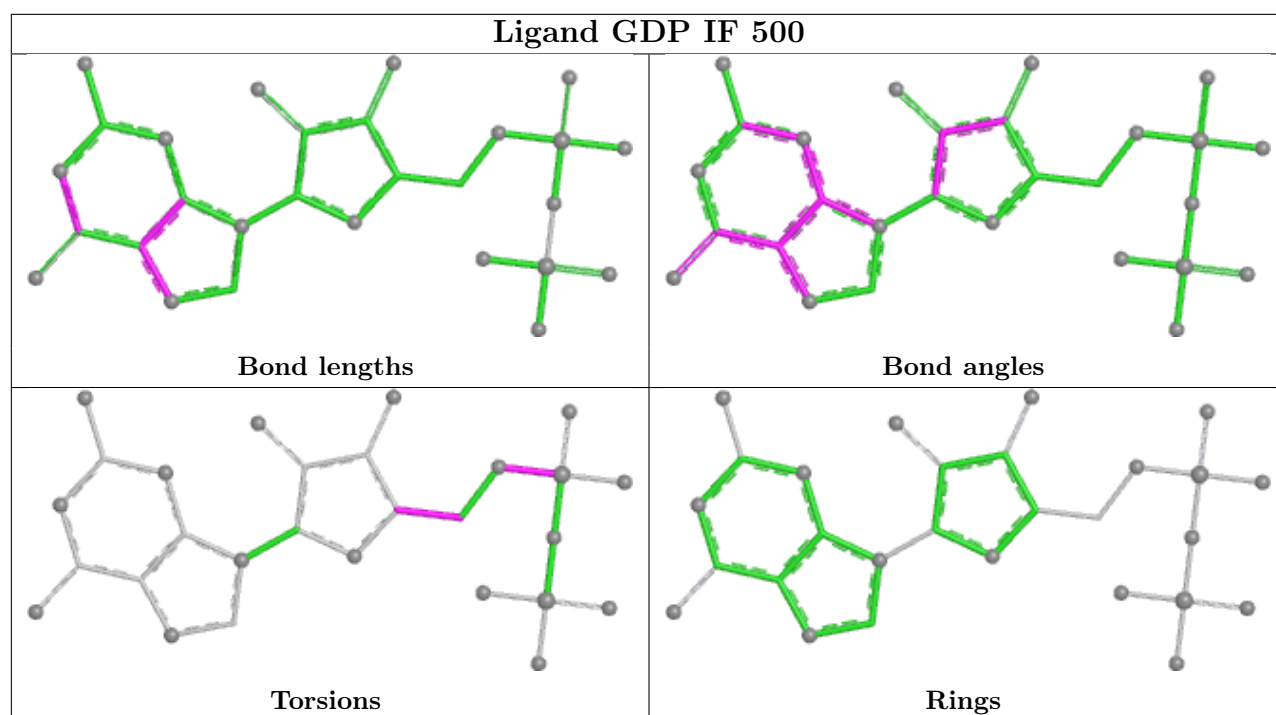


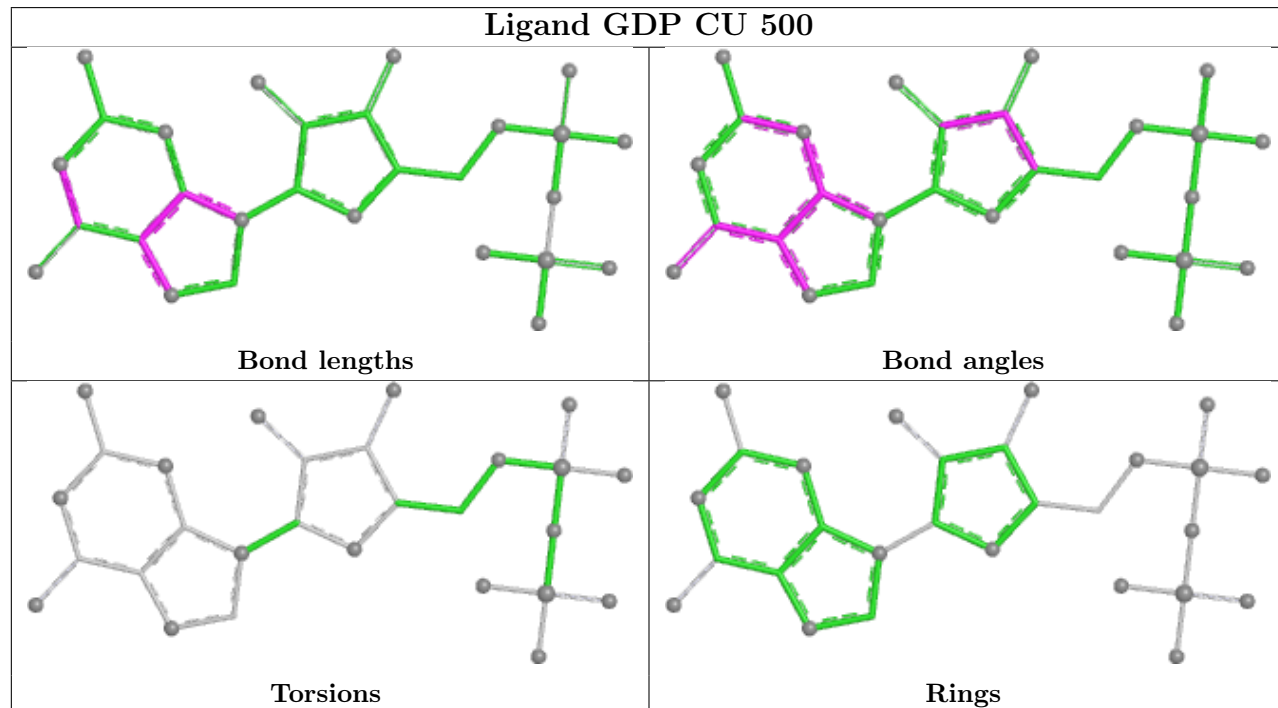
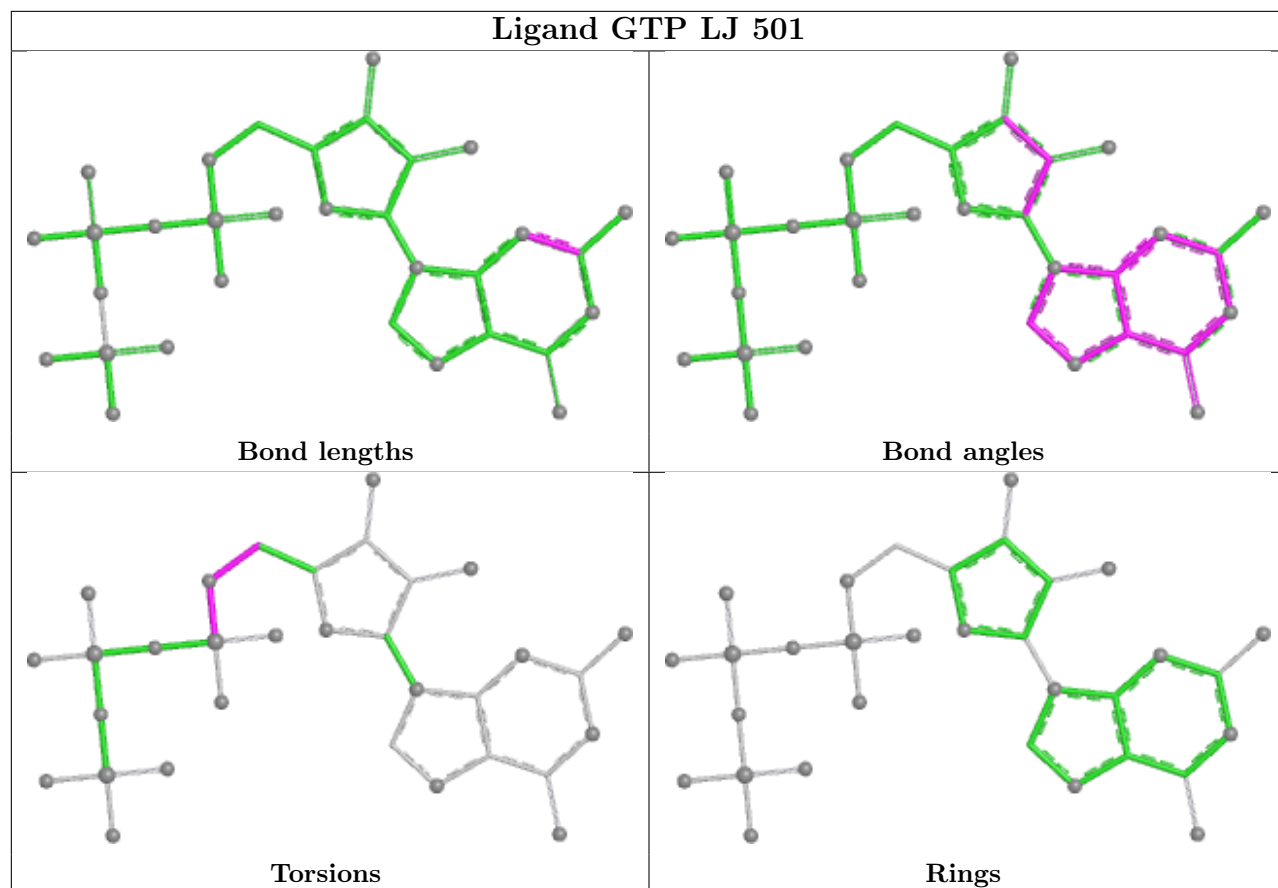
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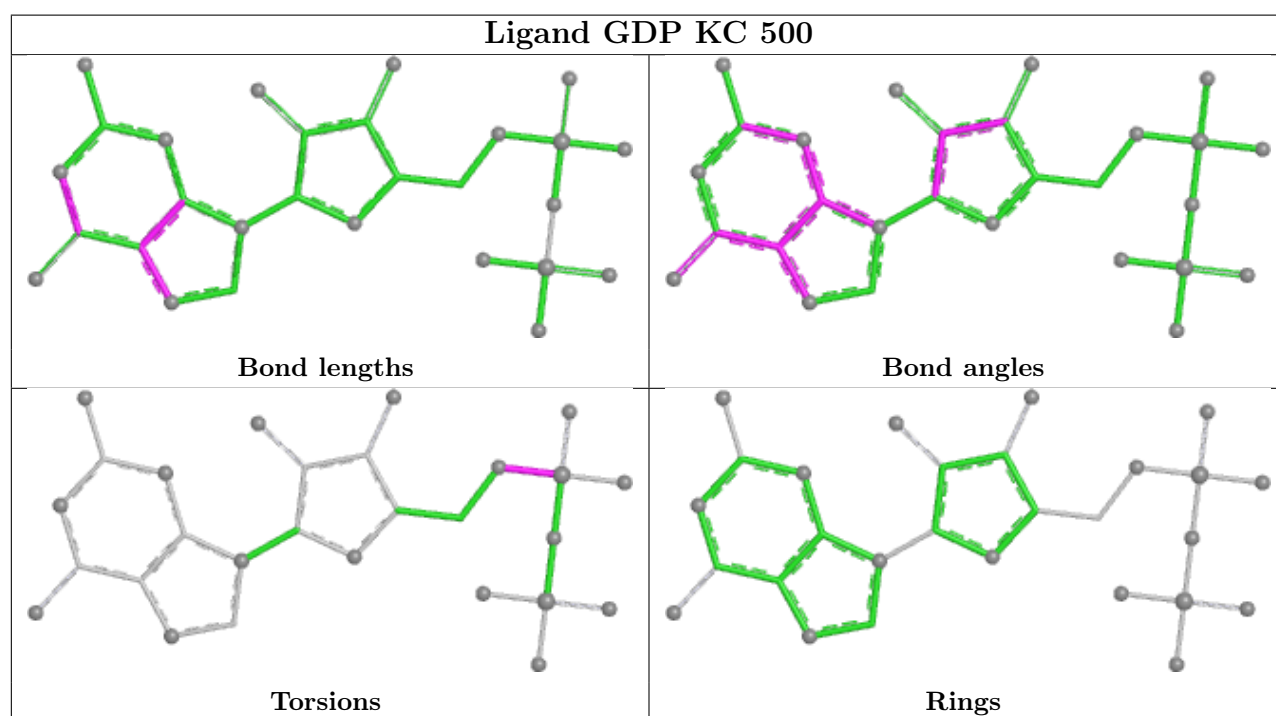
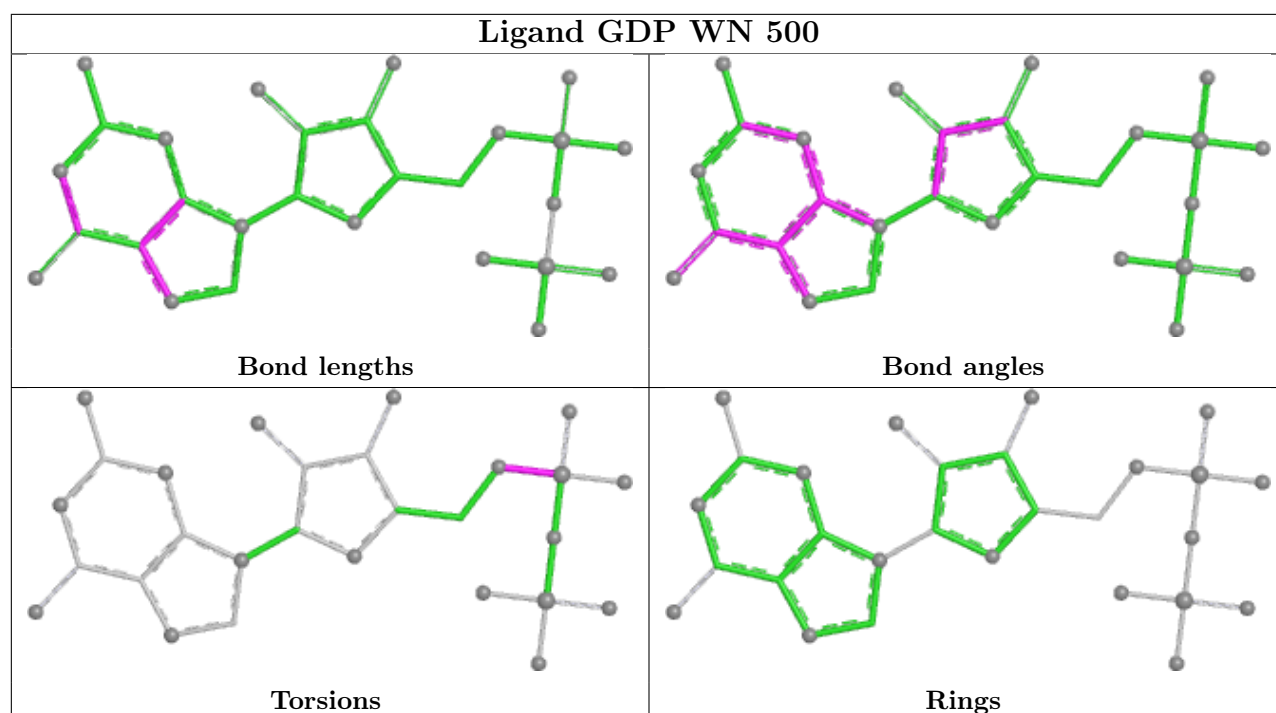


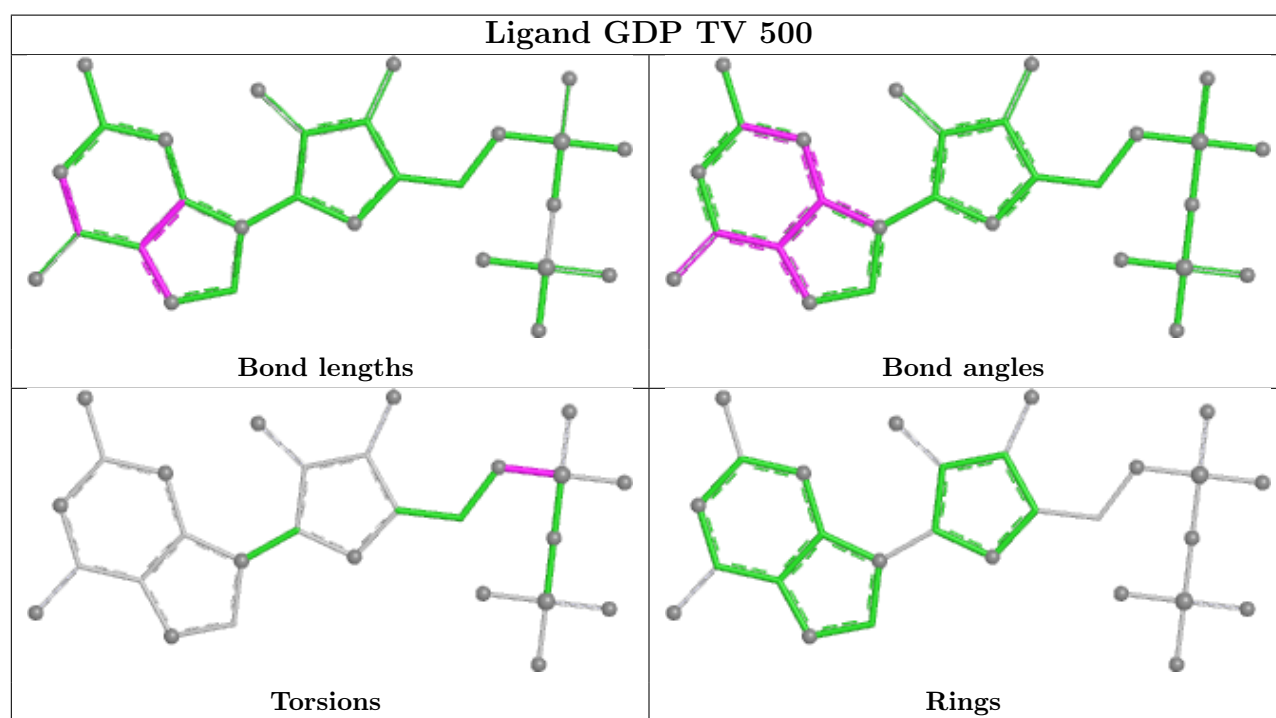
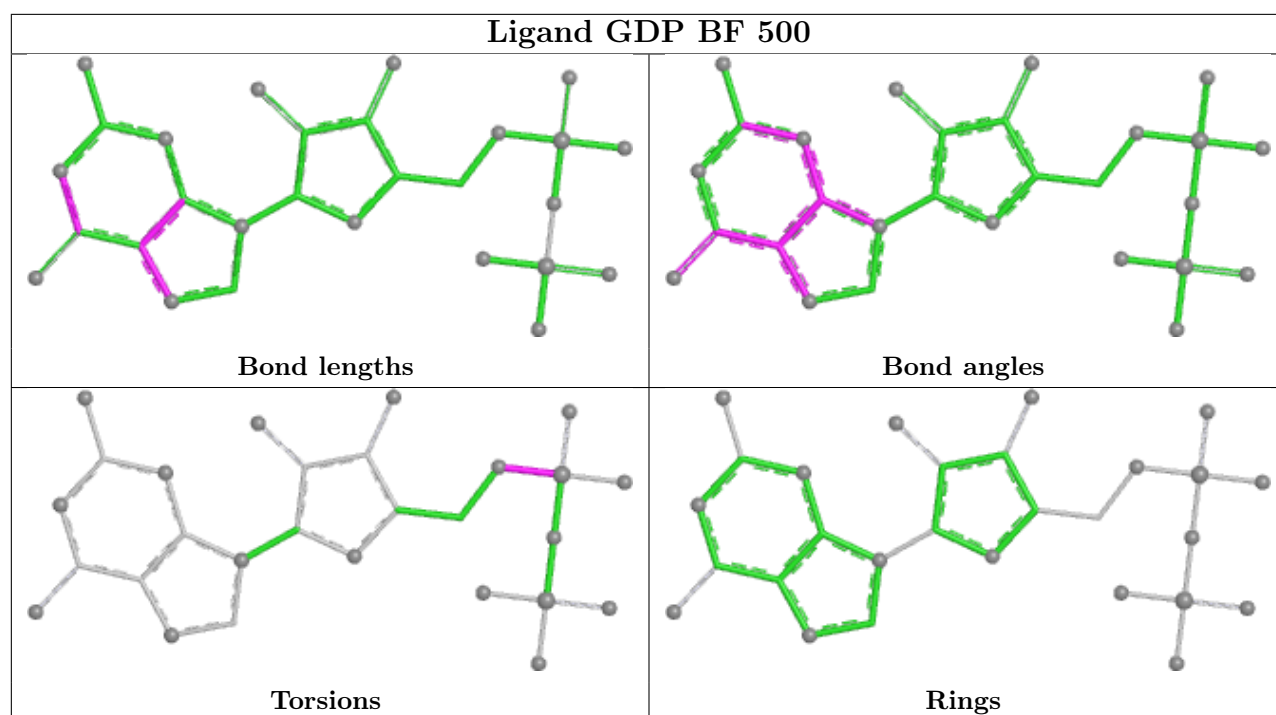
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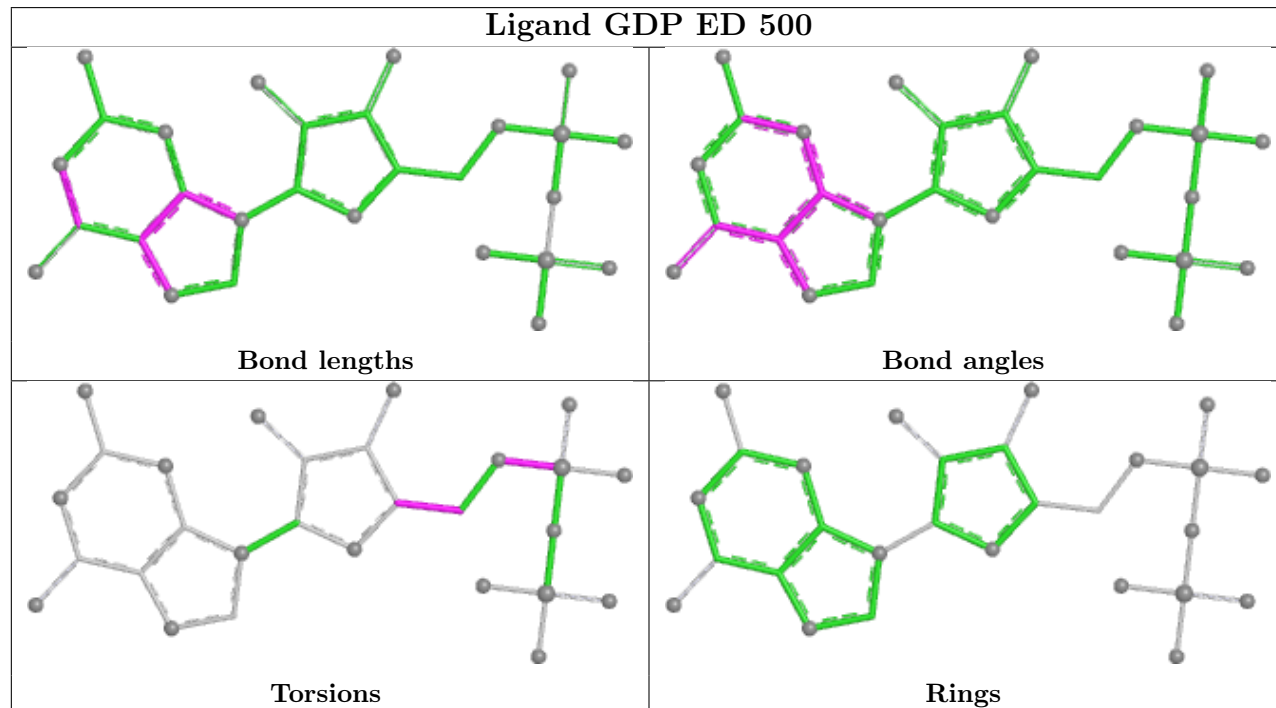
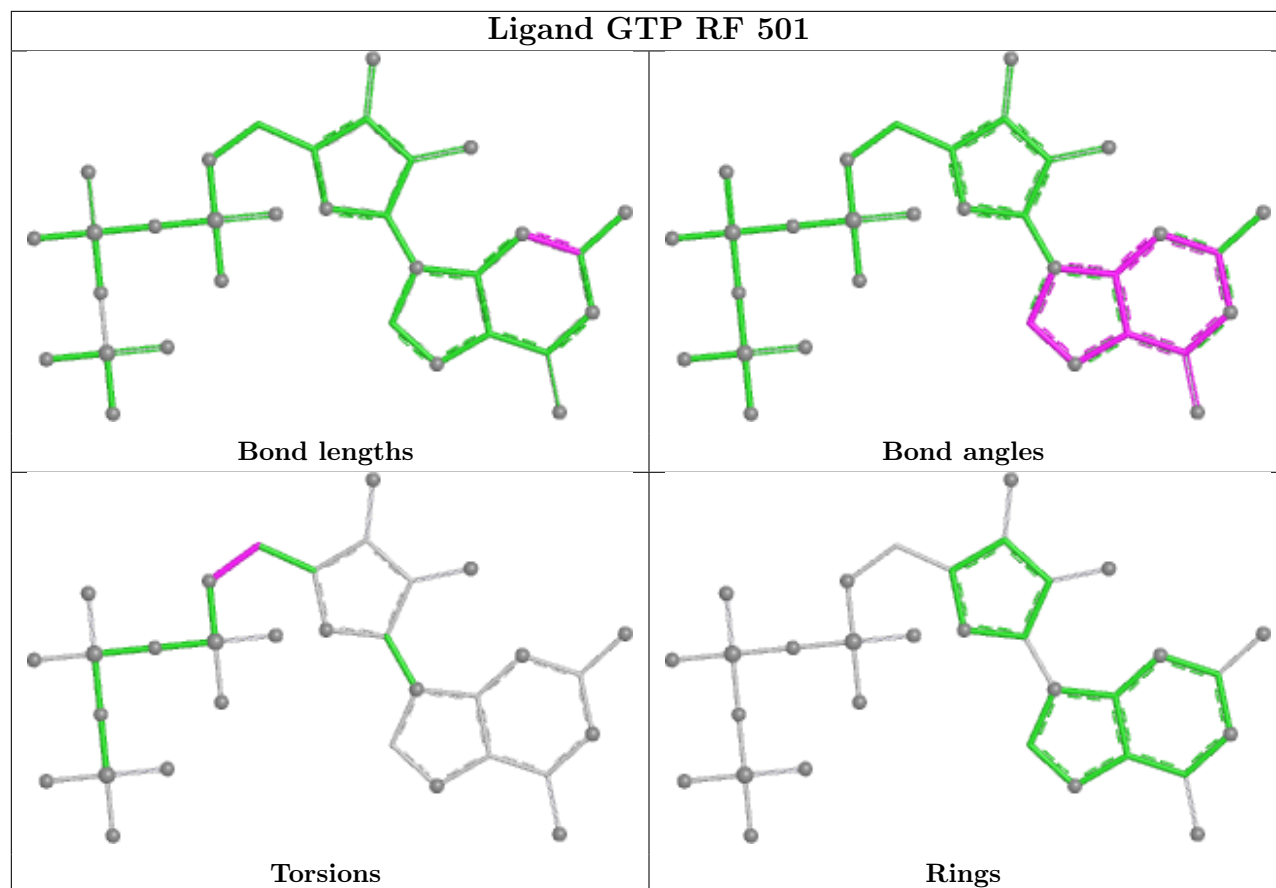


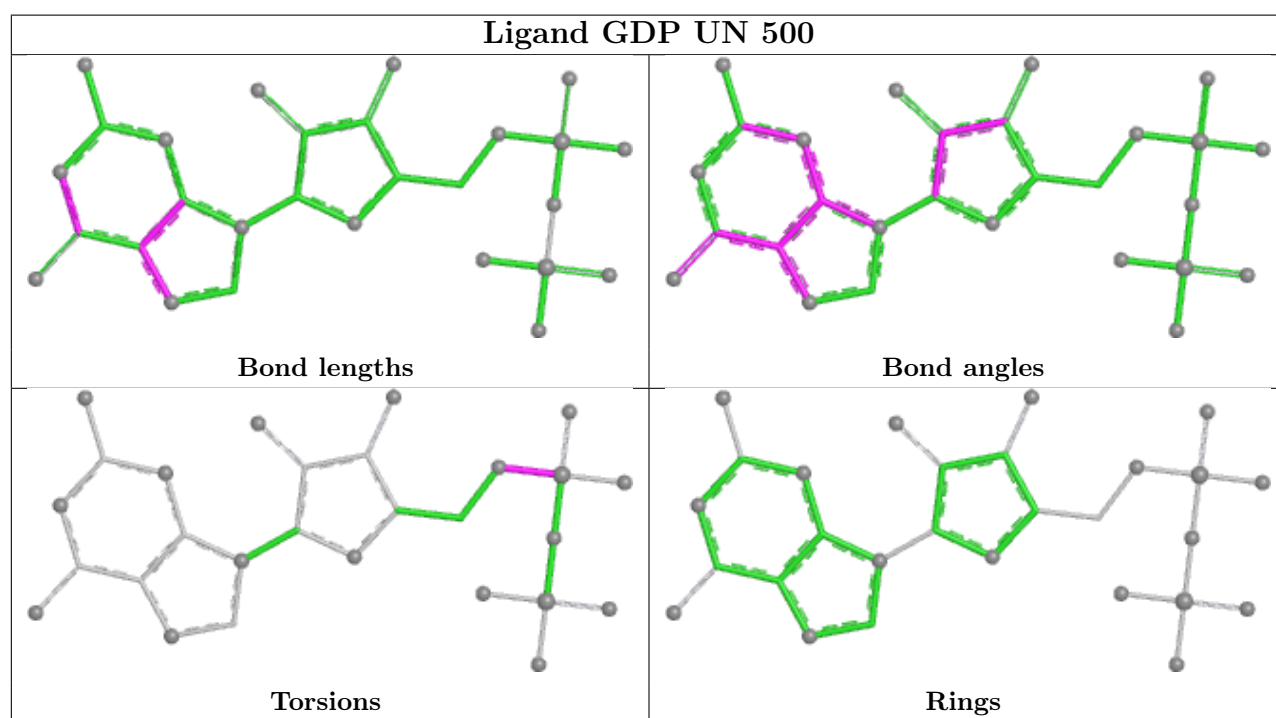
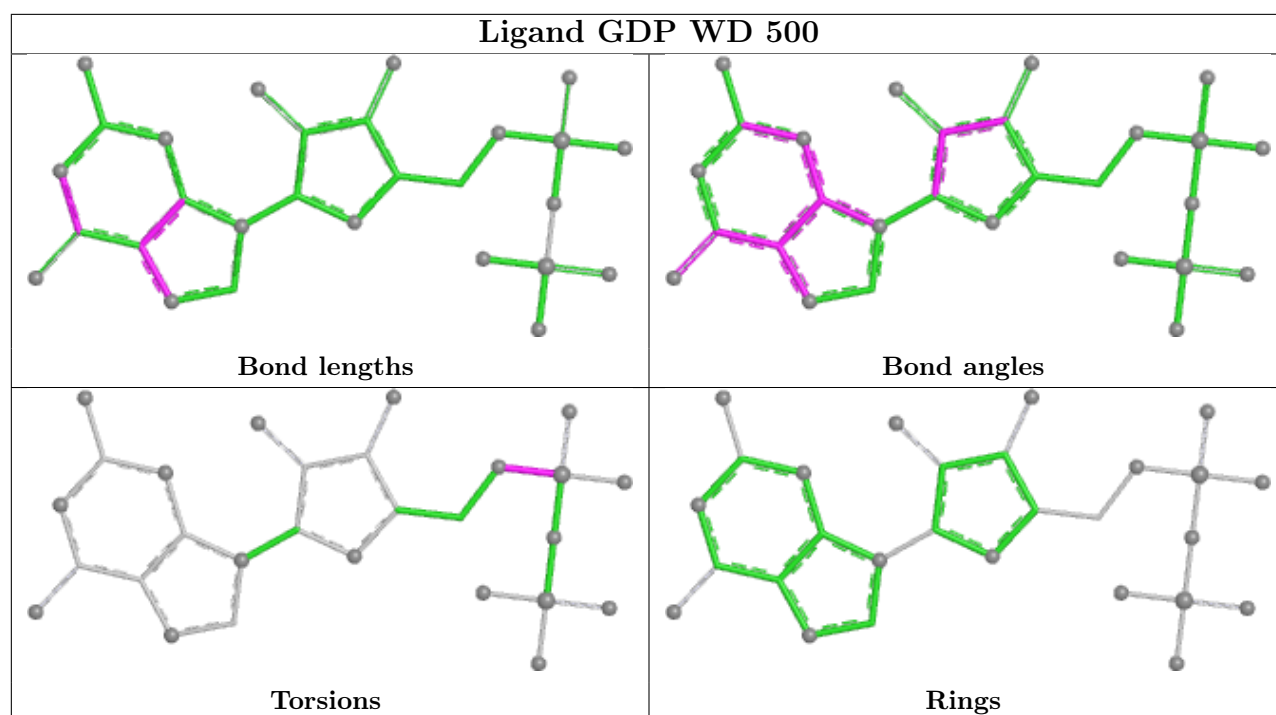


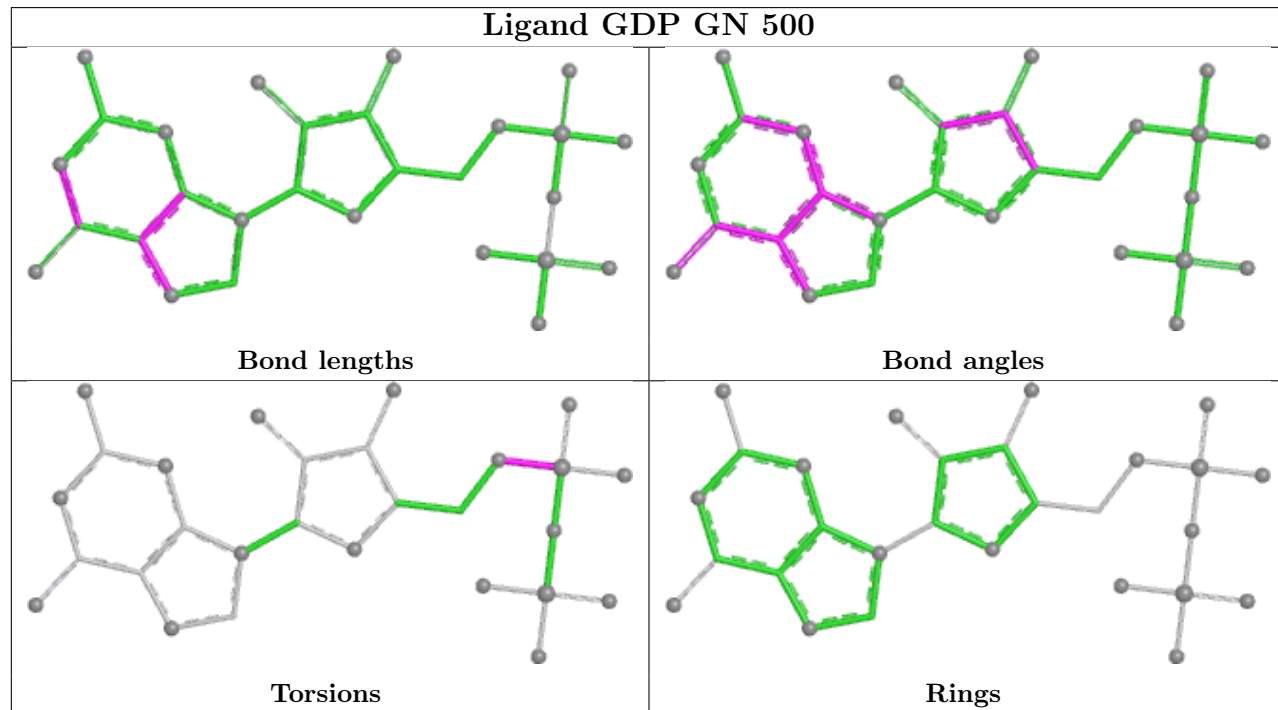
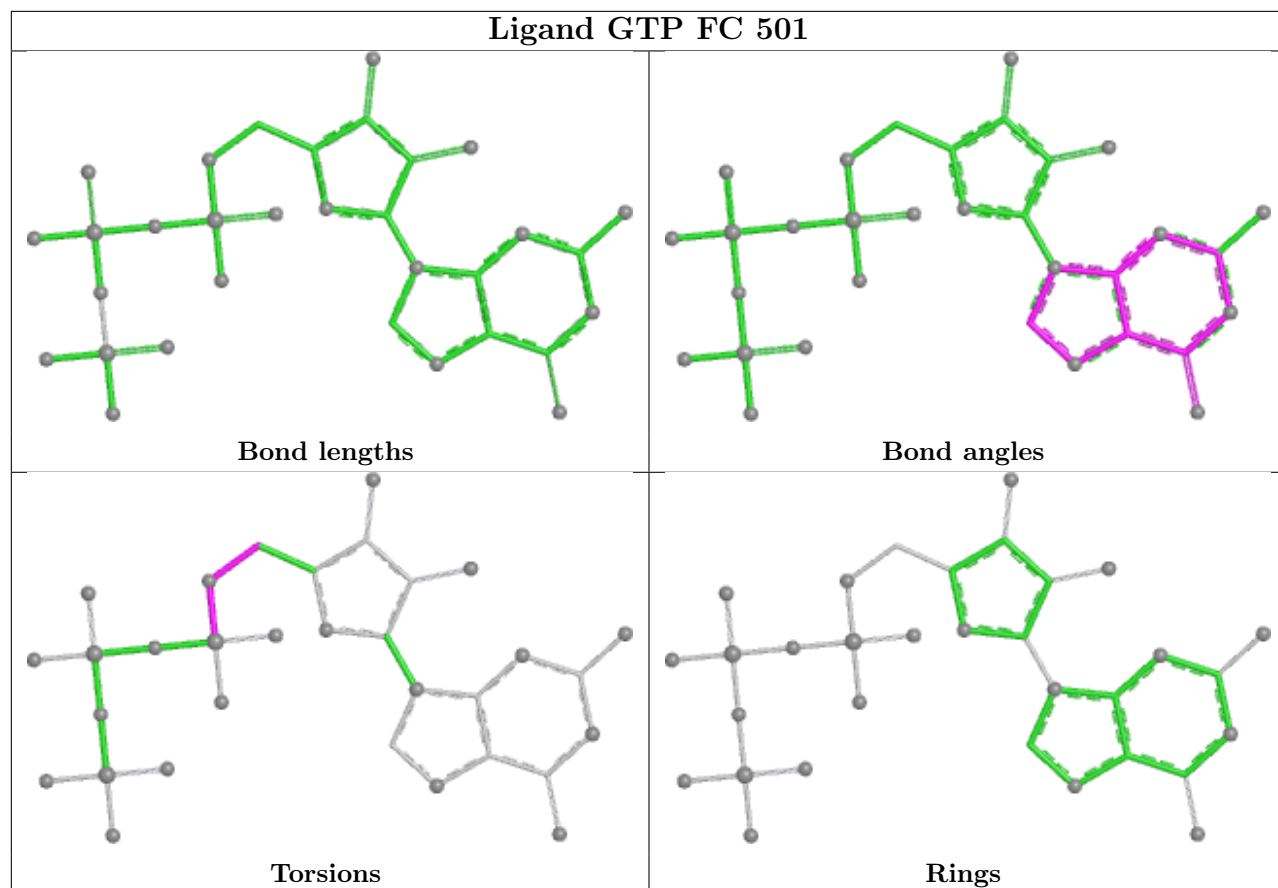


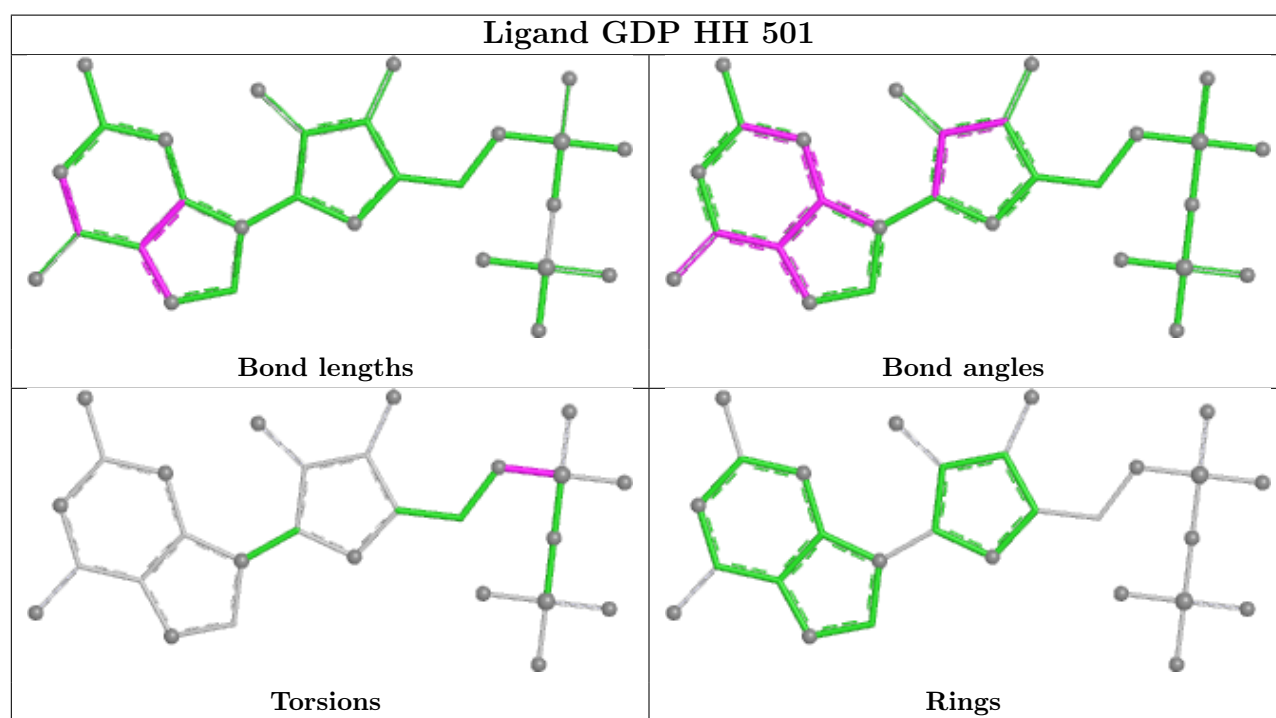
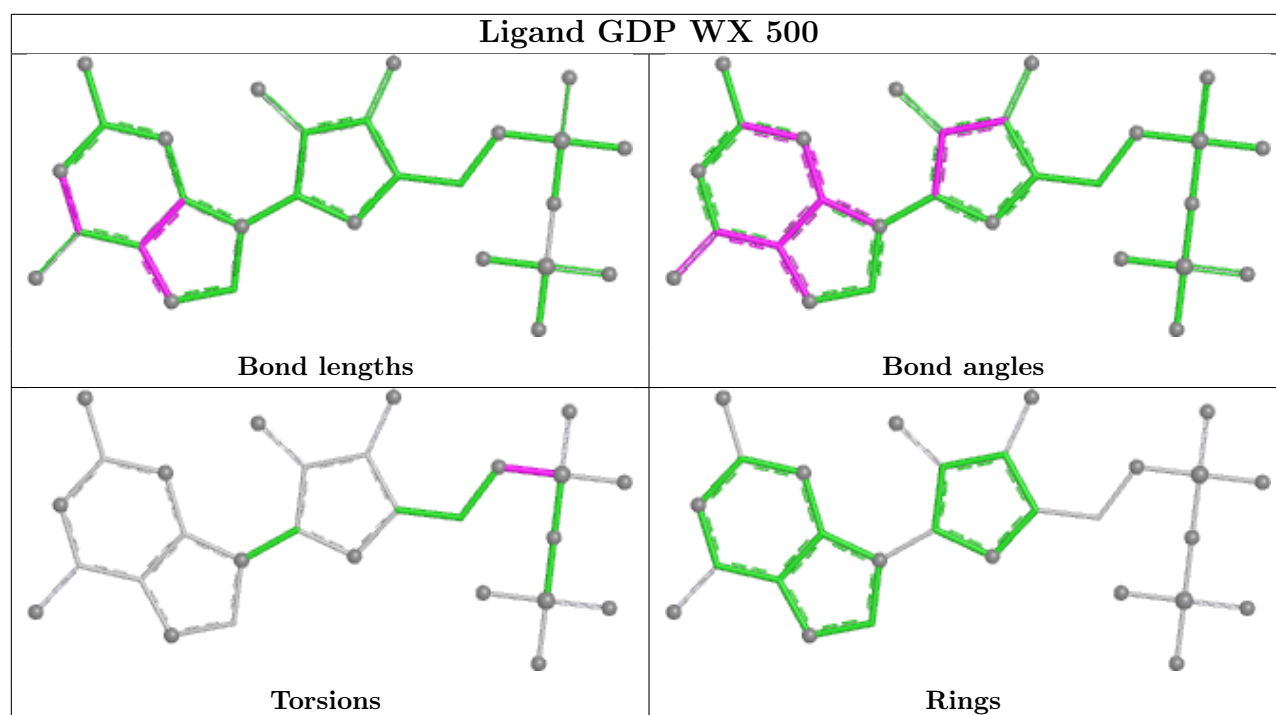


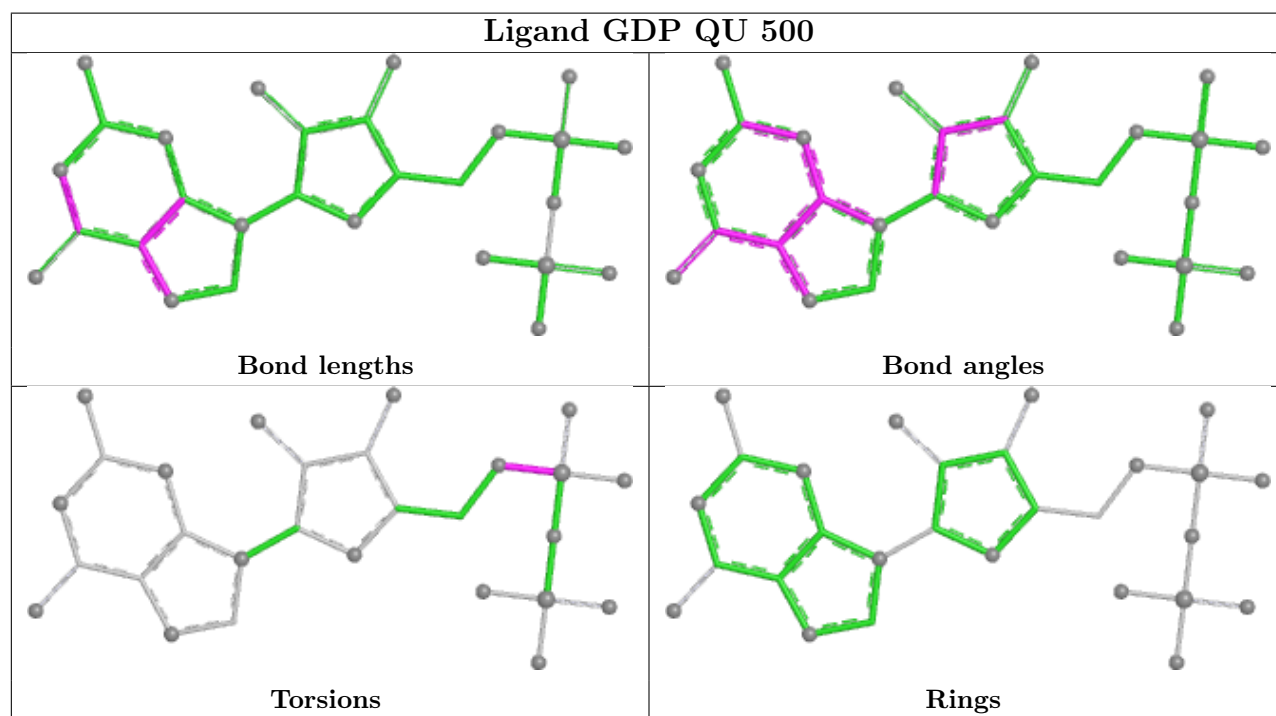
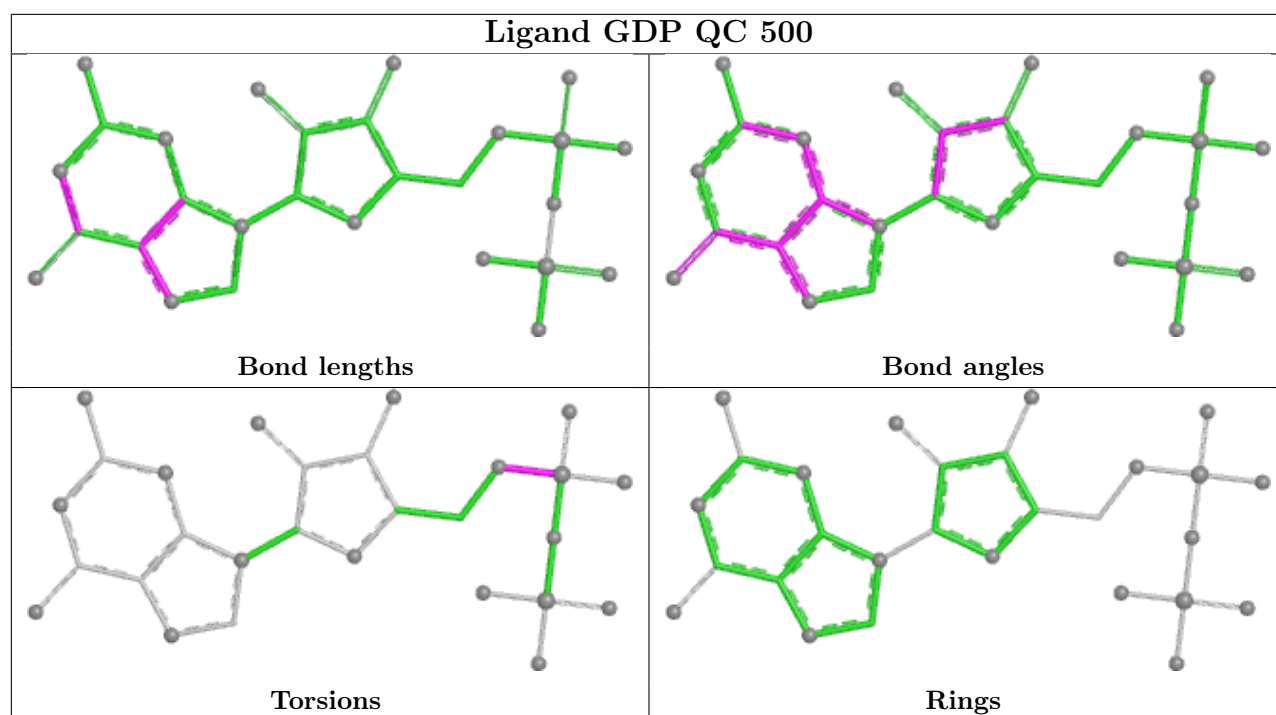


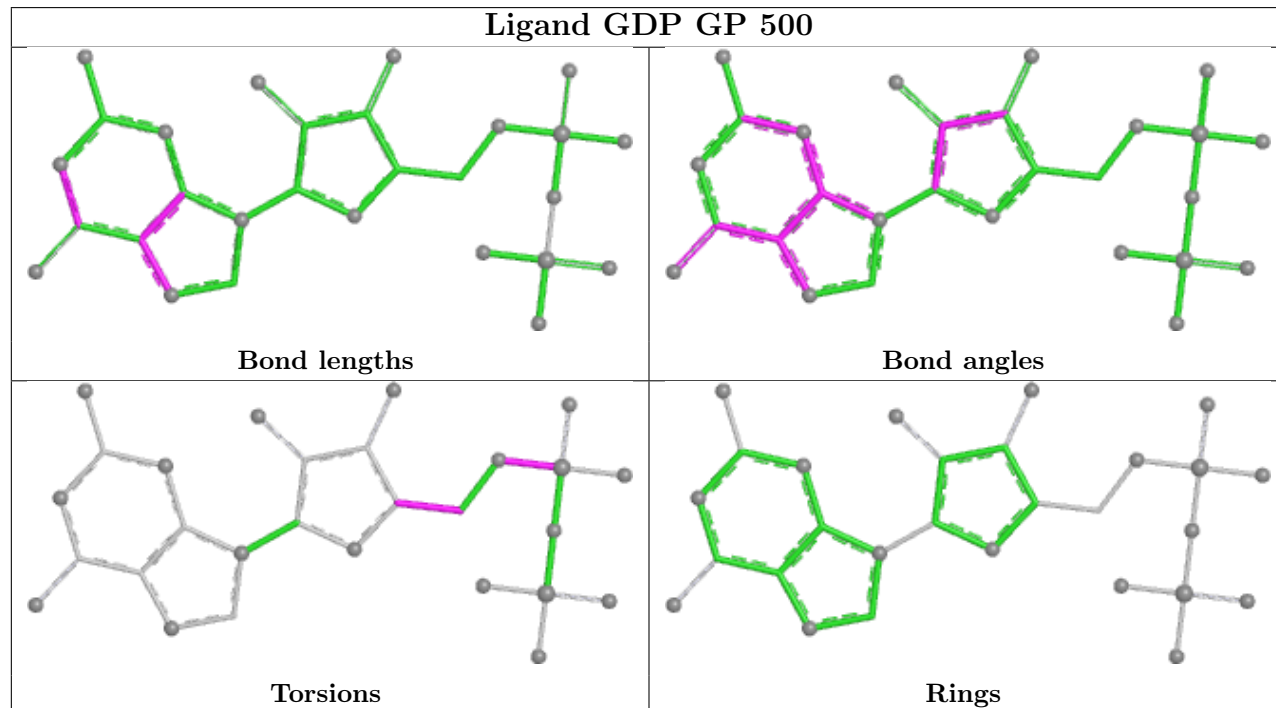
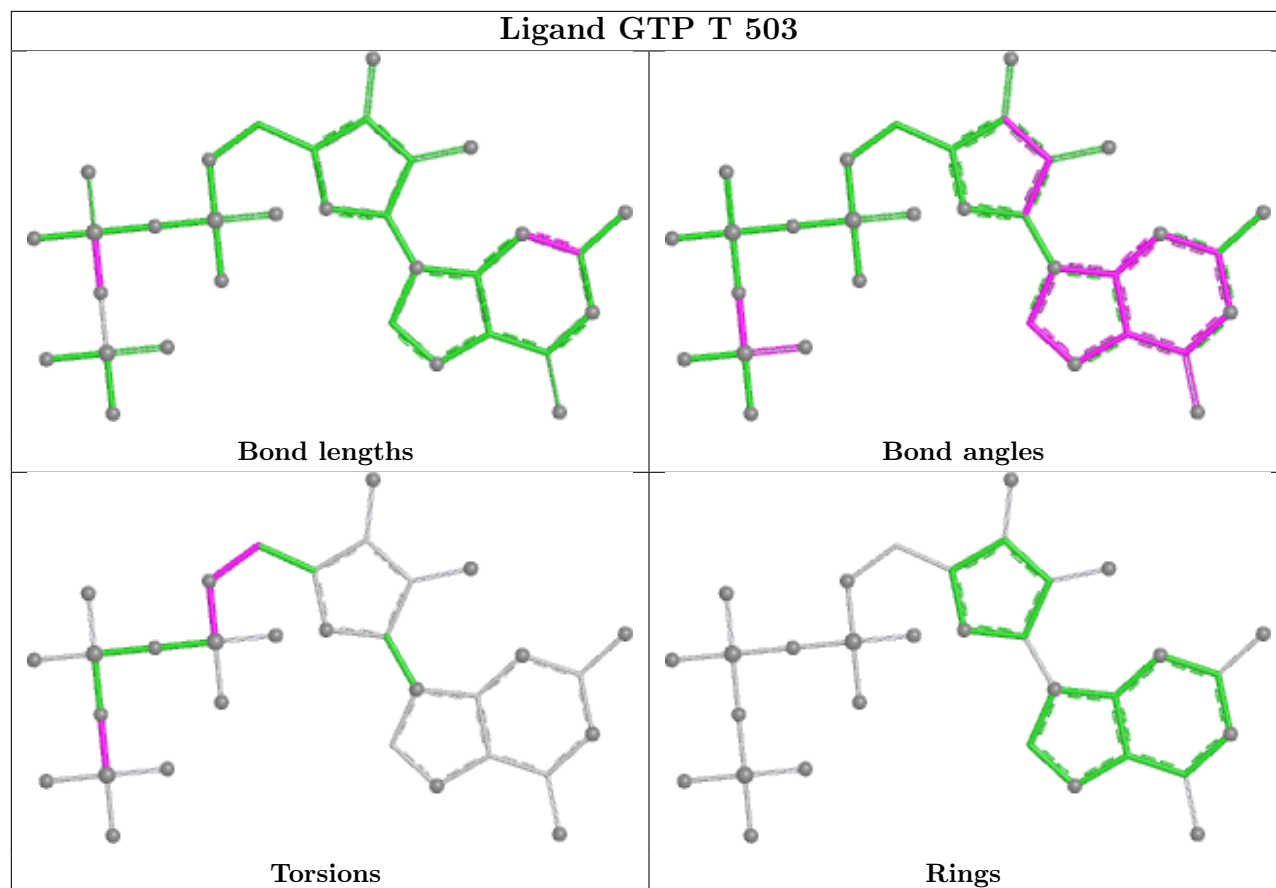


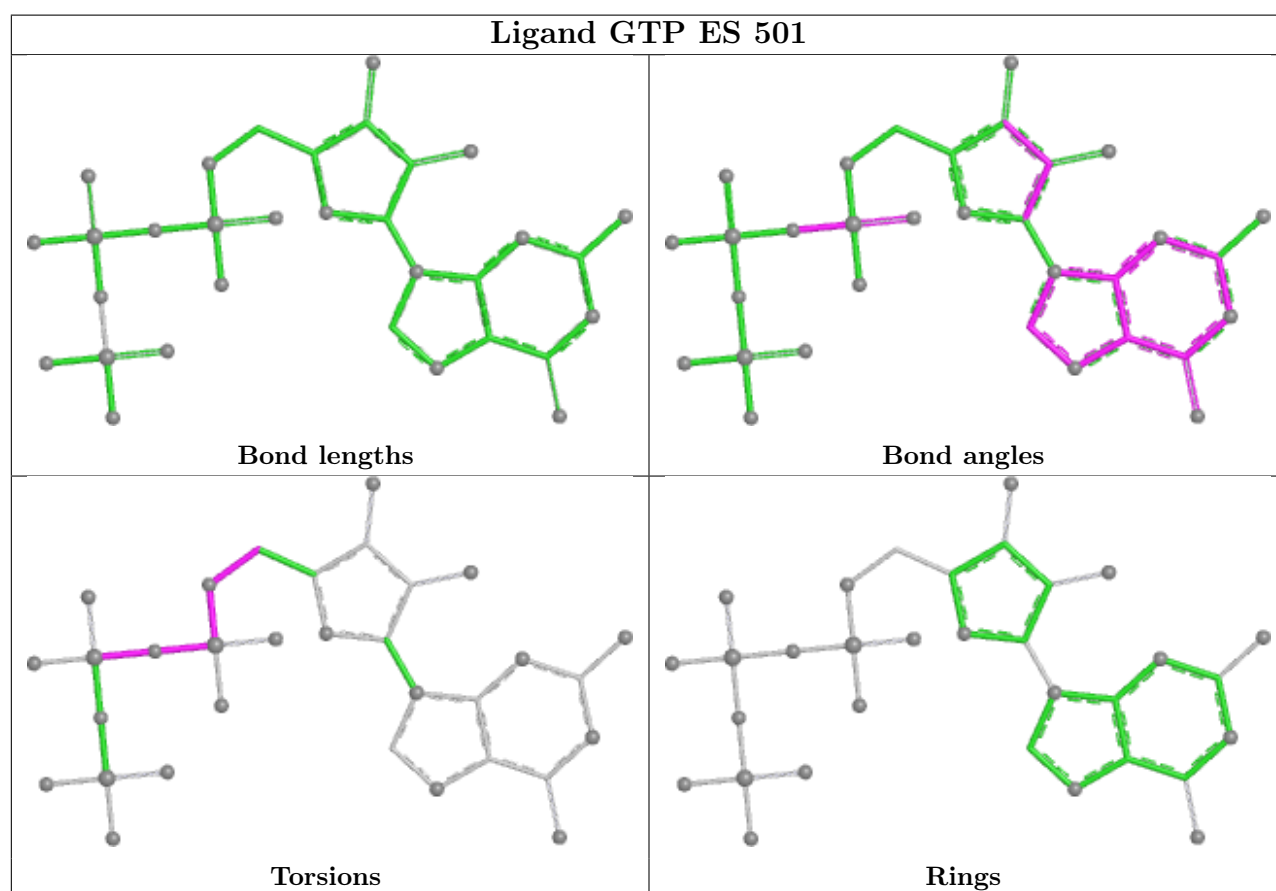
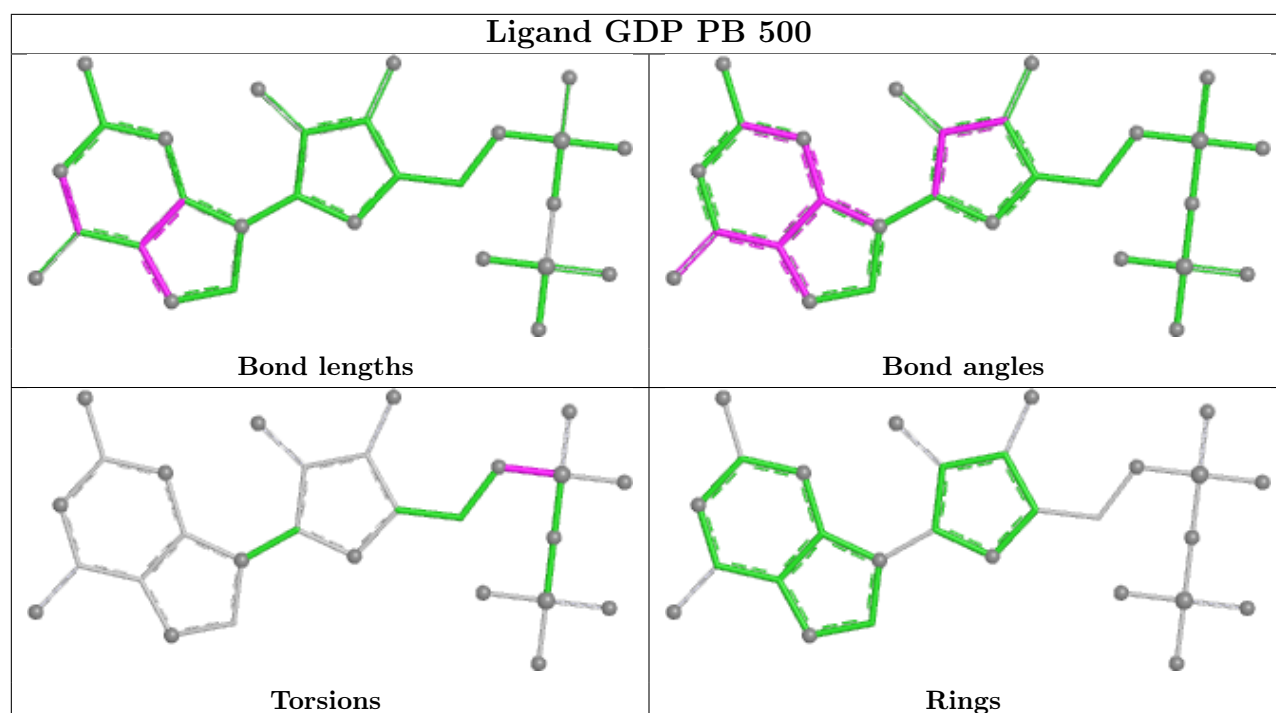




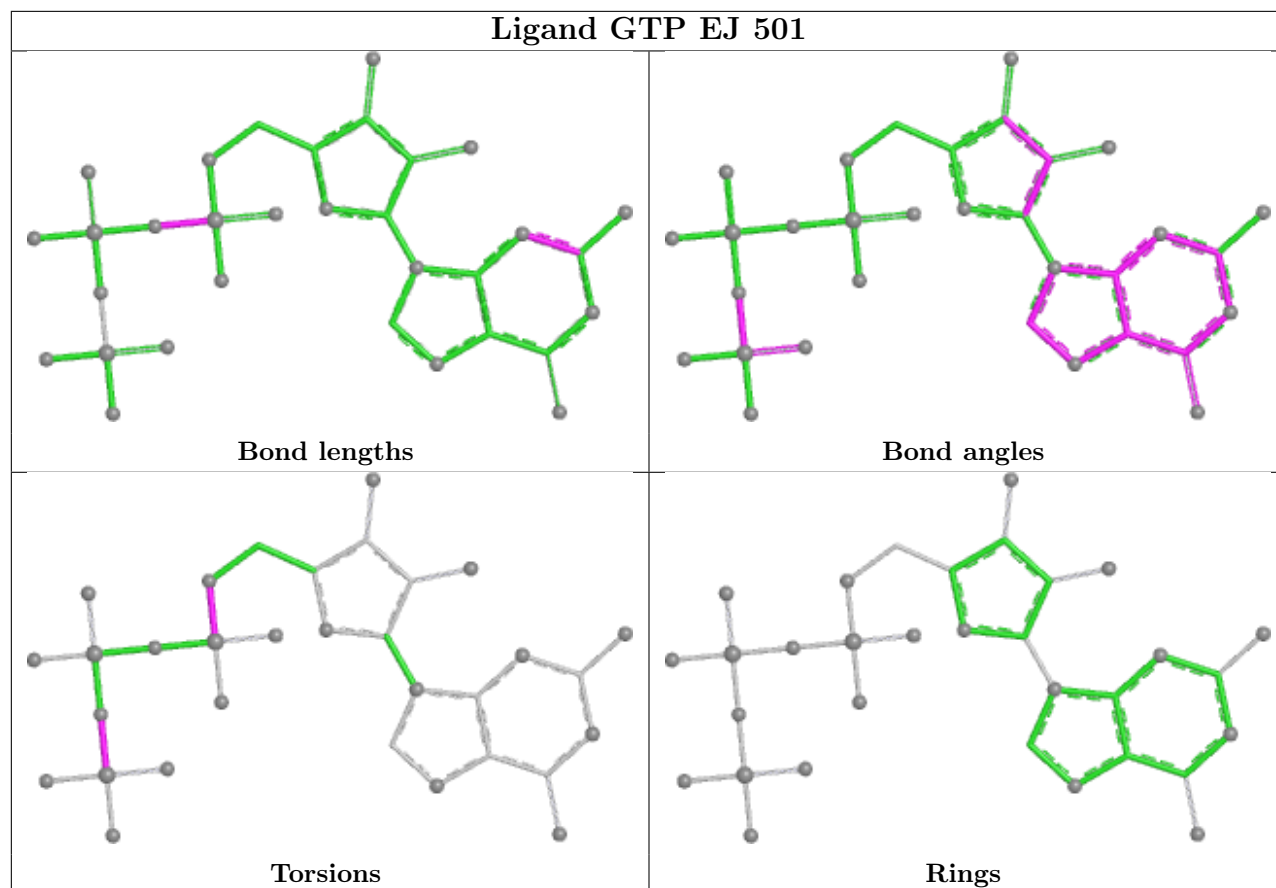




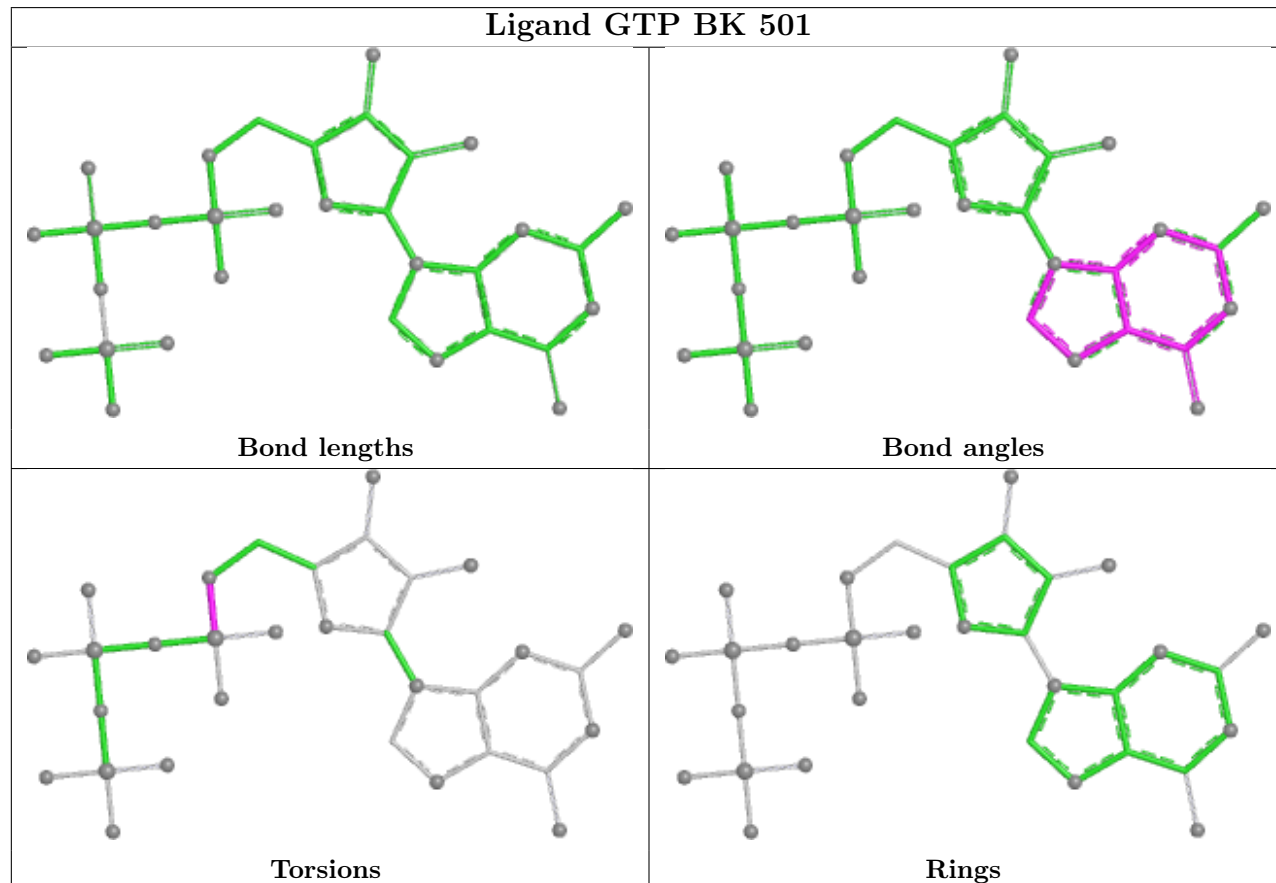


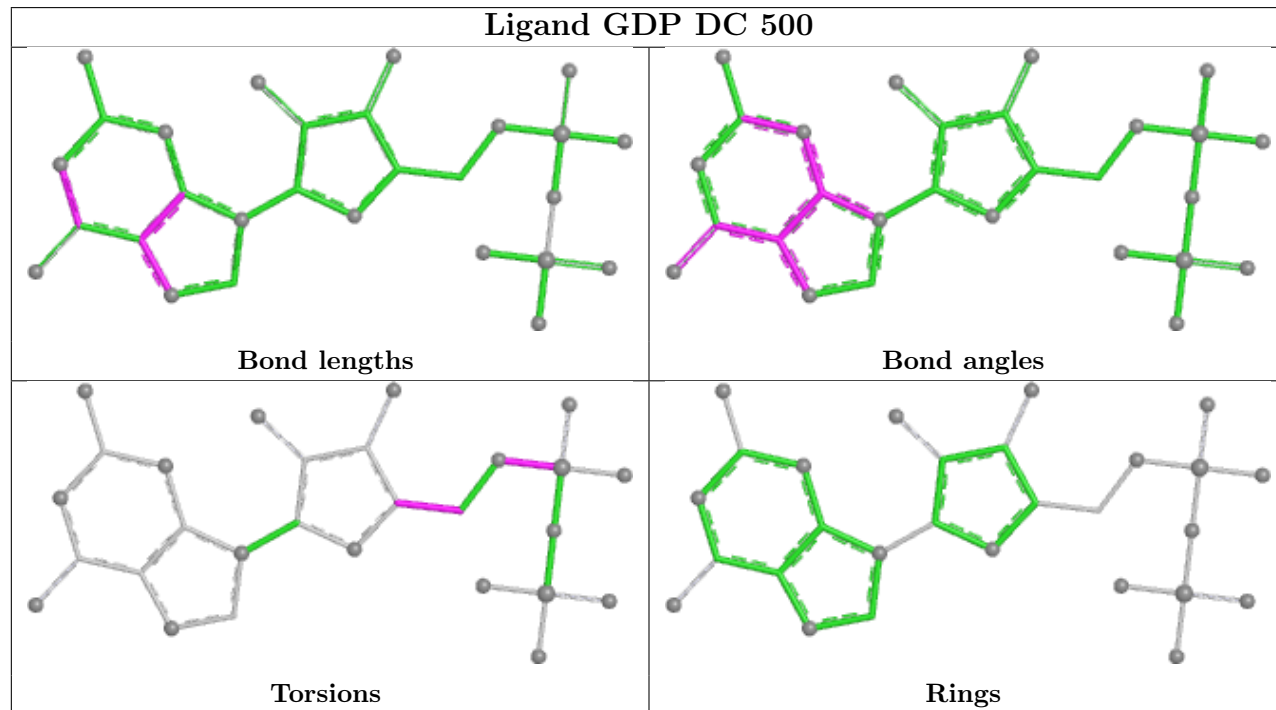
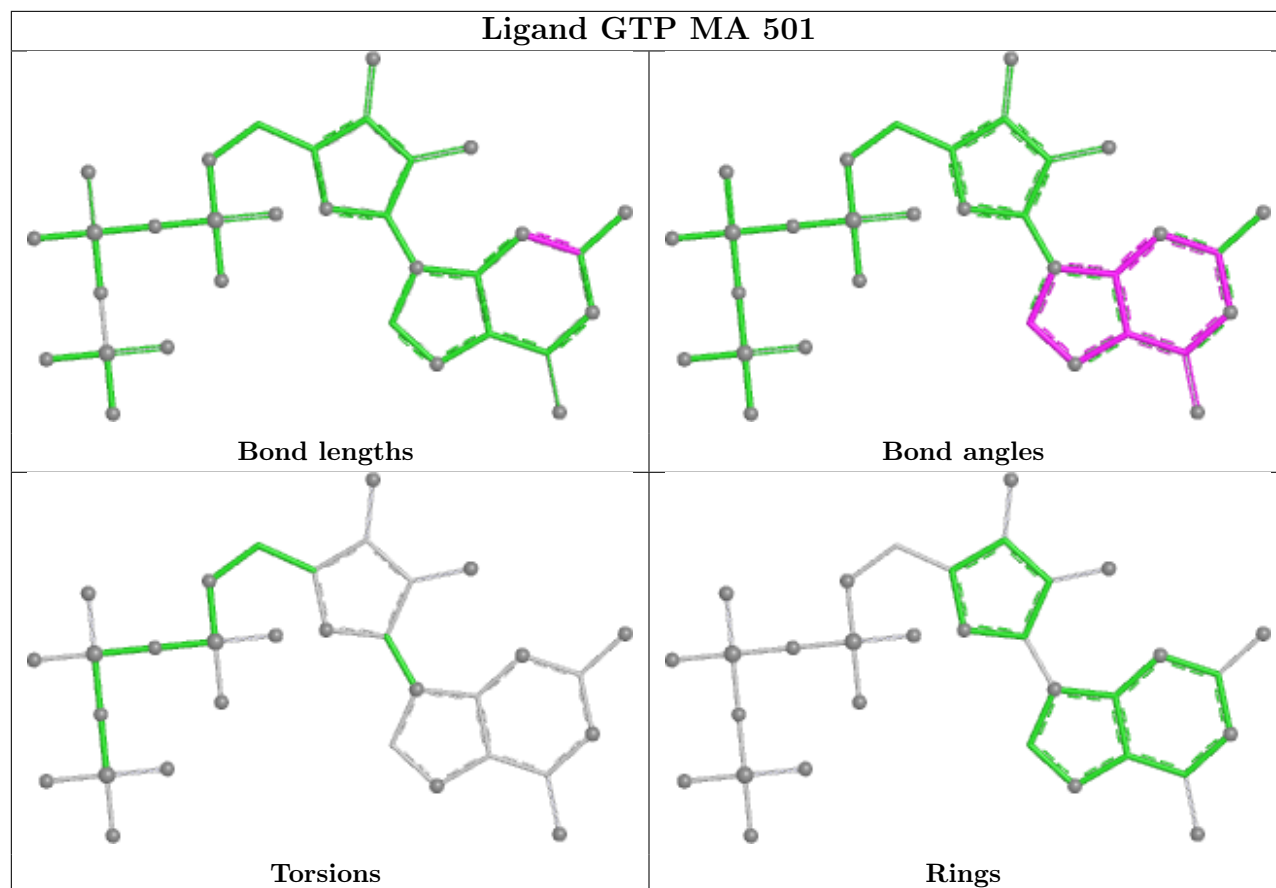


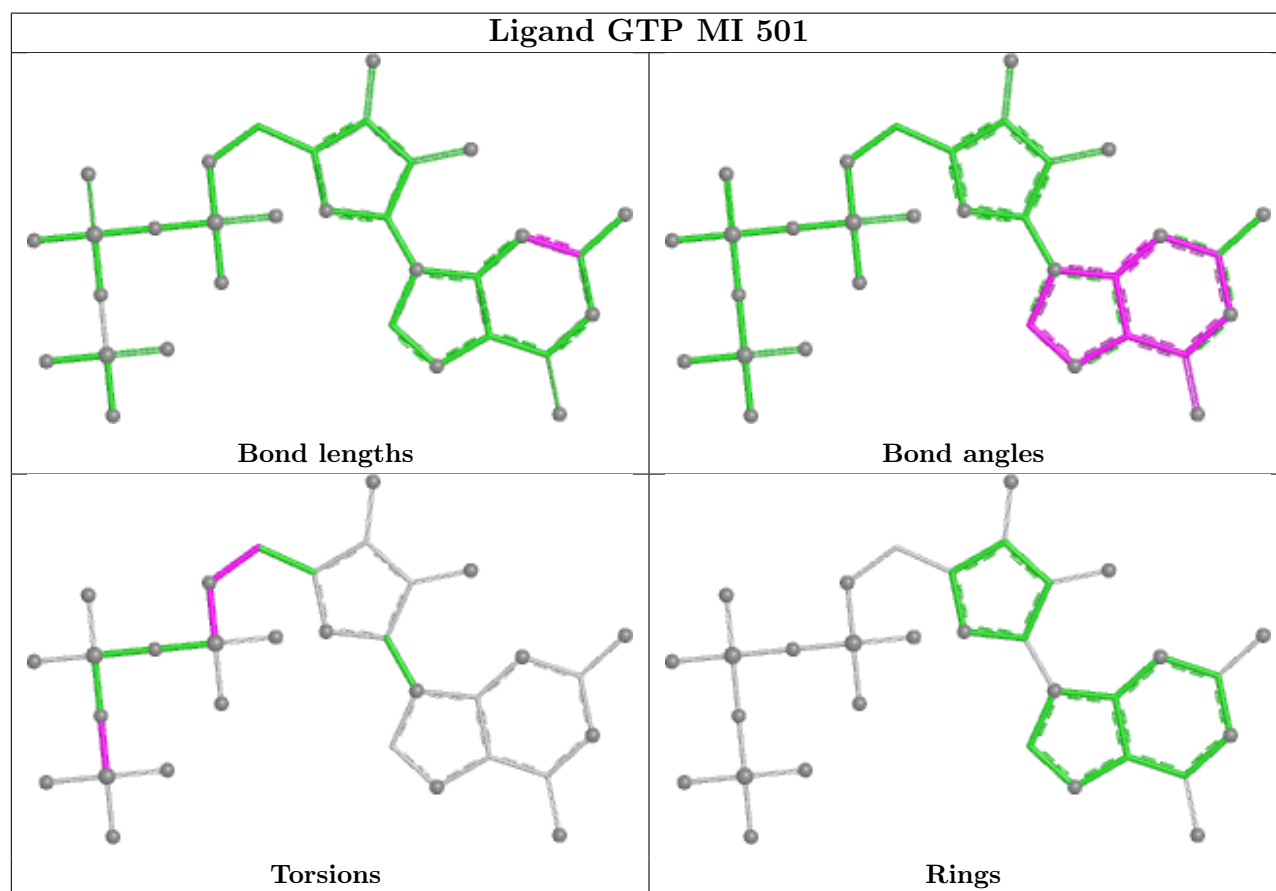
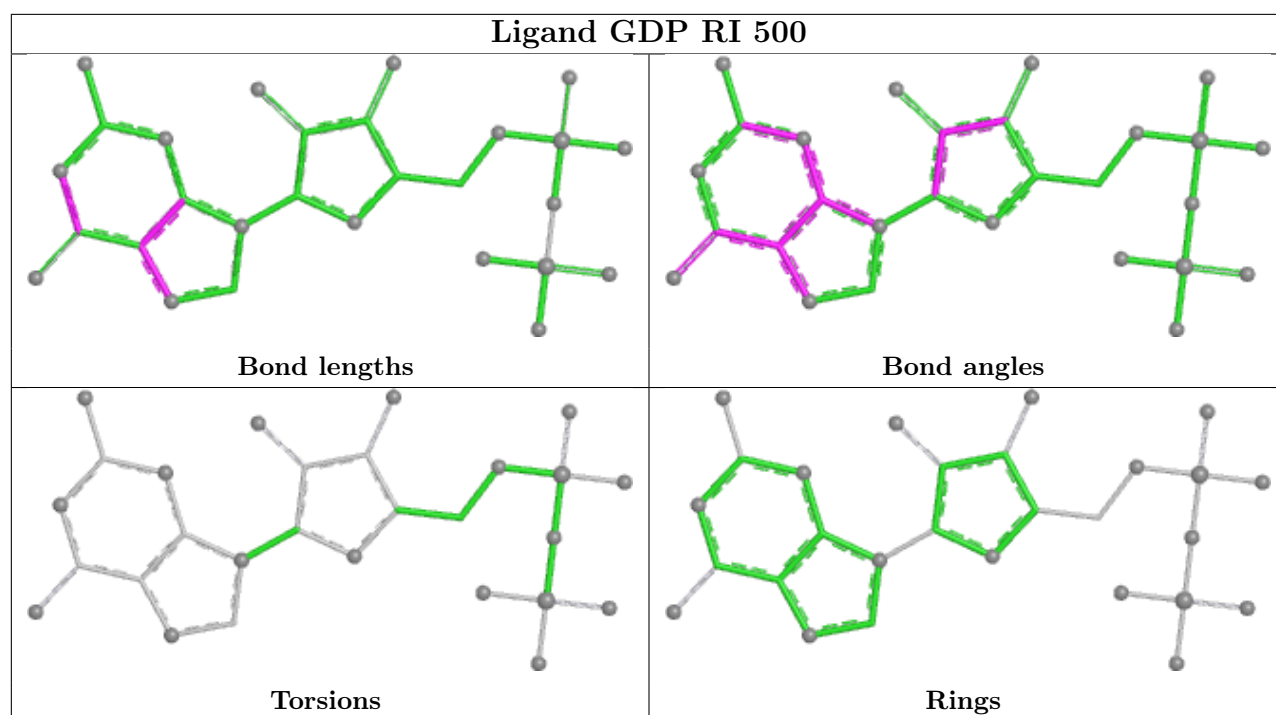
Ligand GTP EJ 501



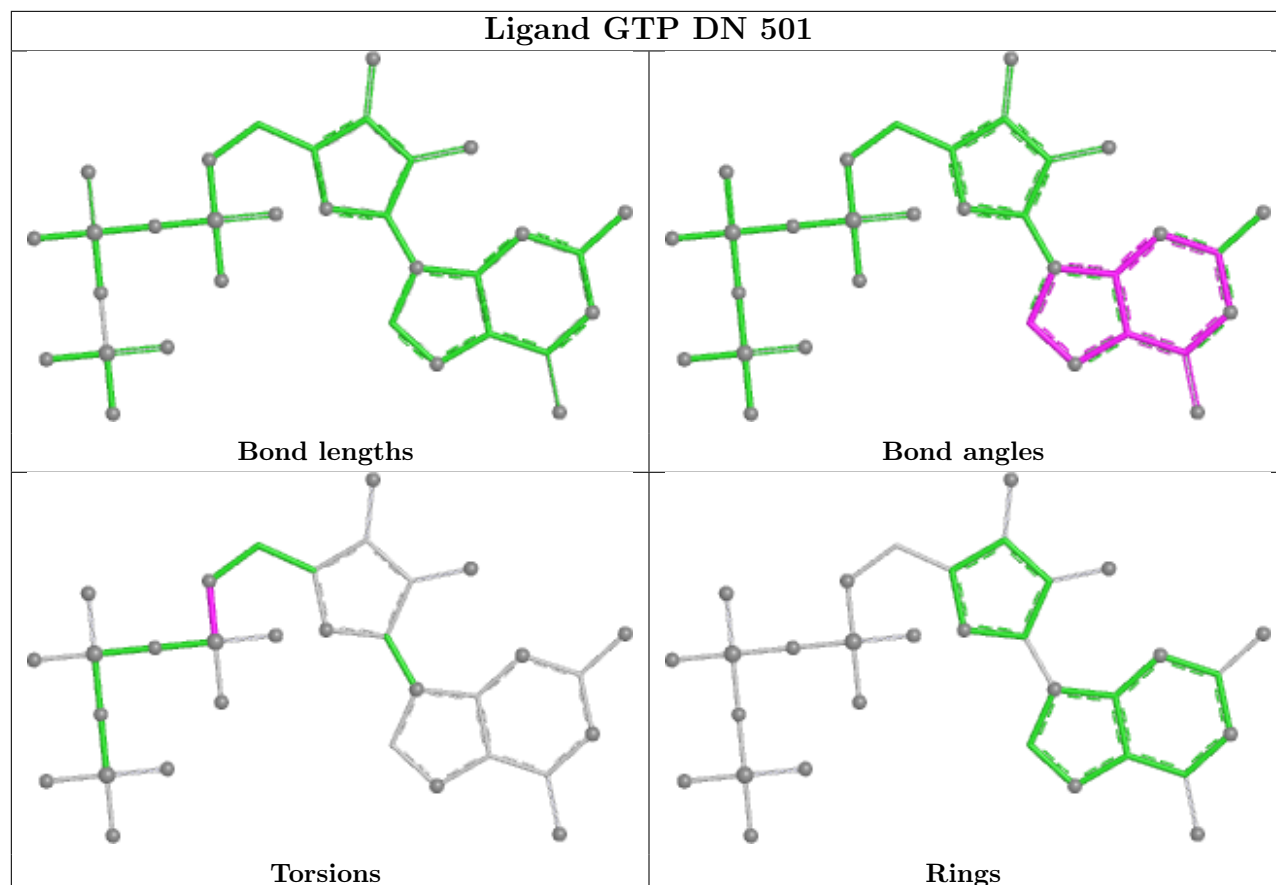
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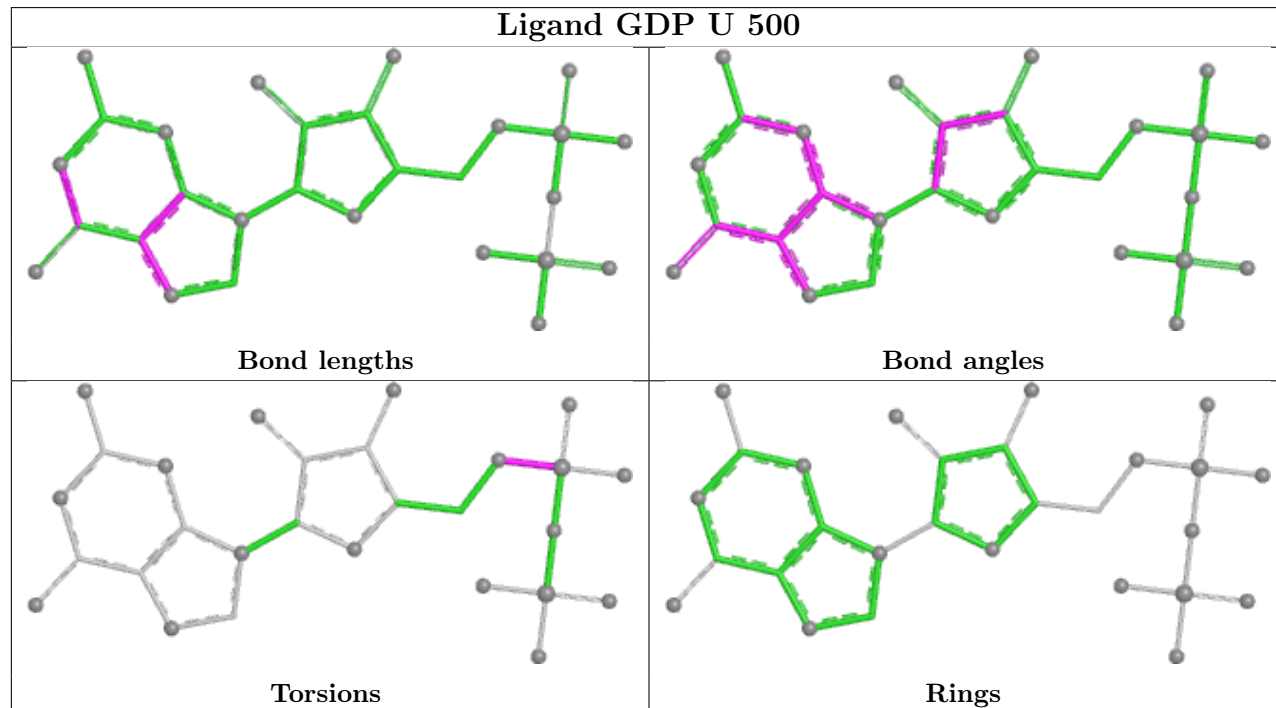




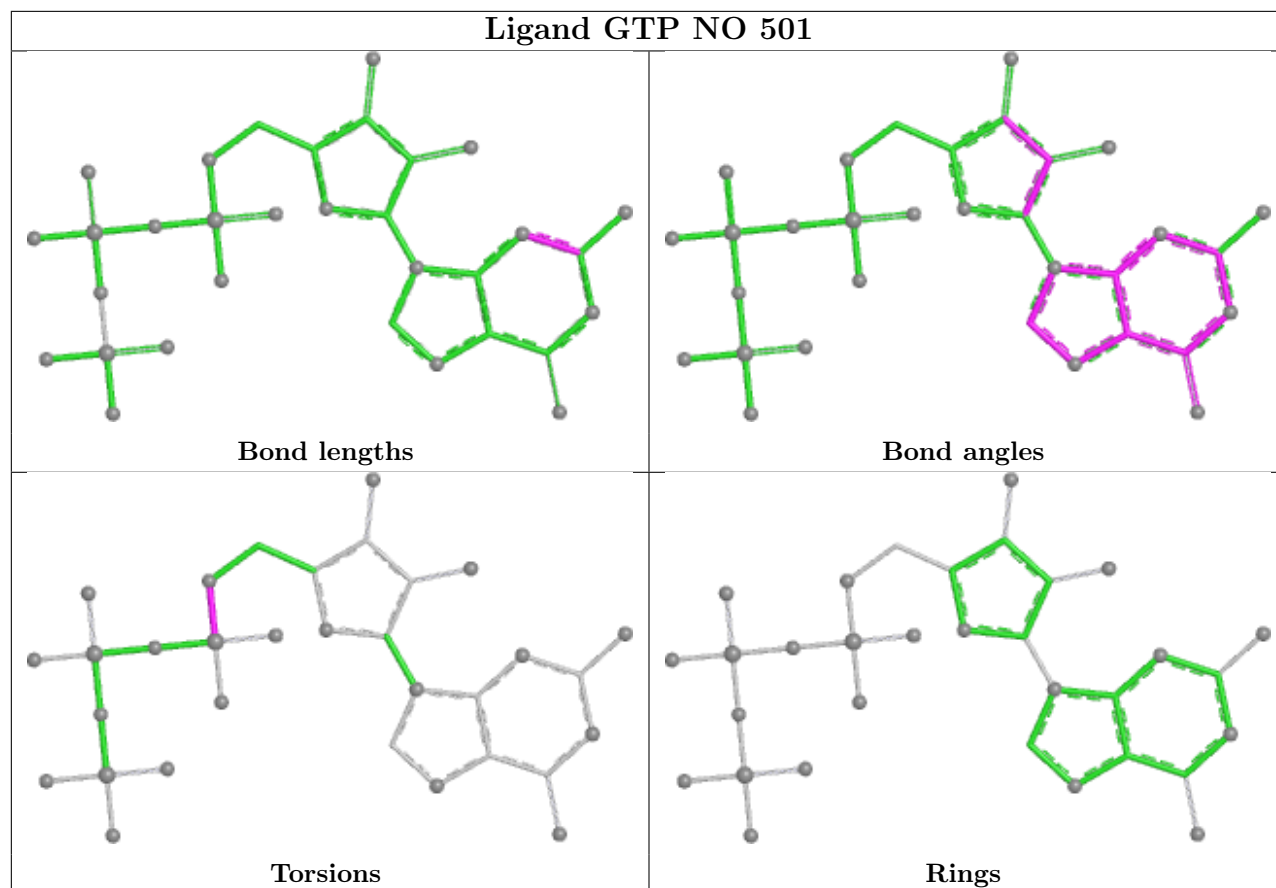
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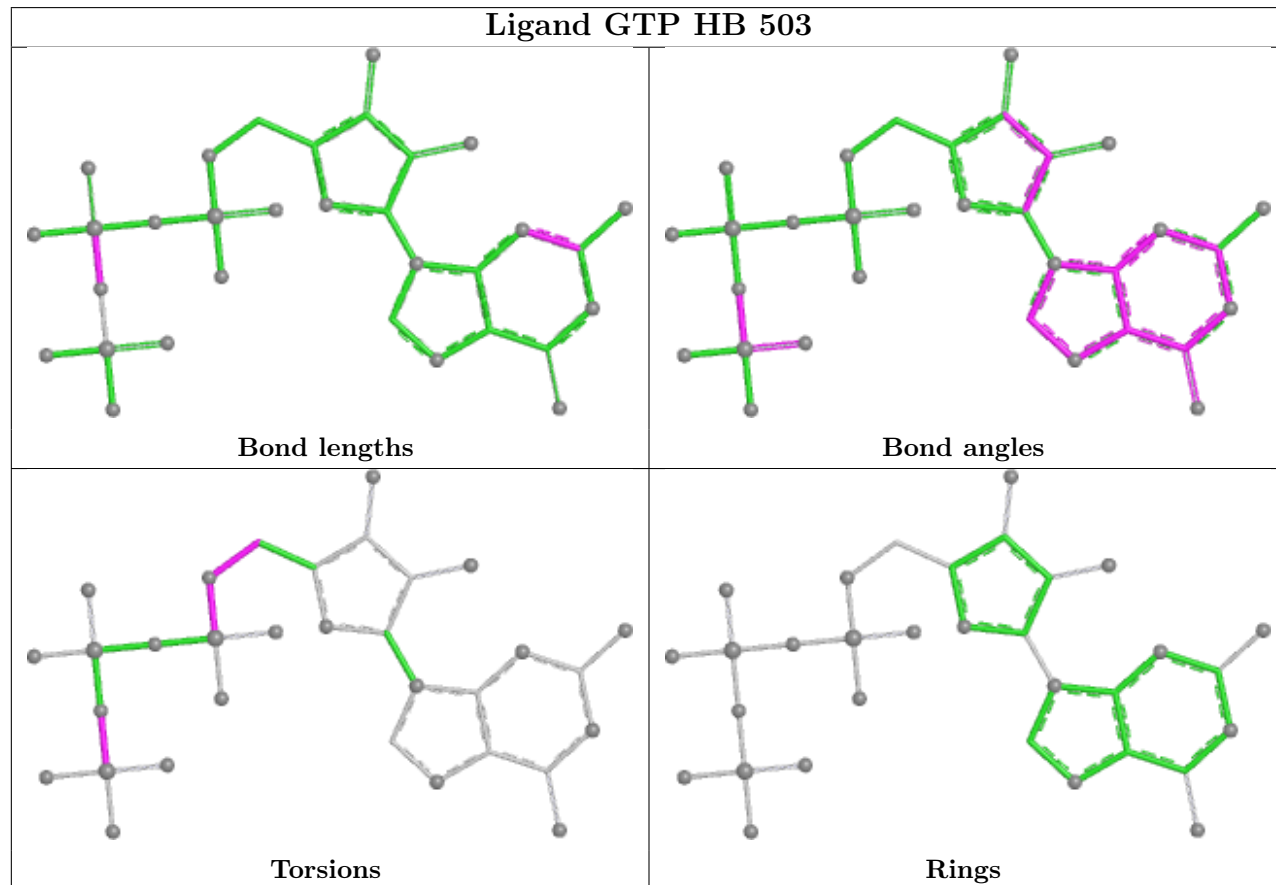
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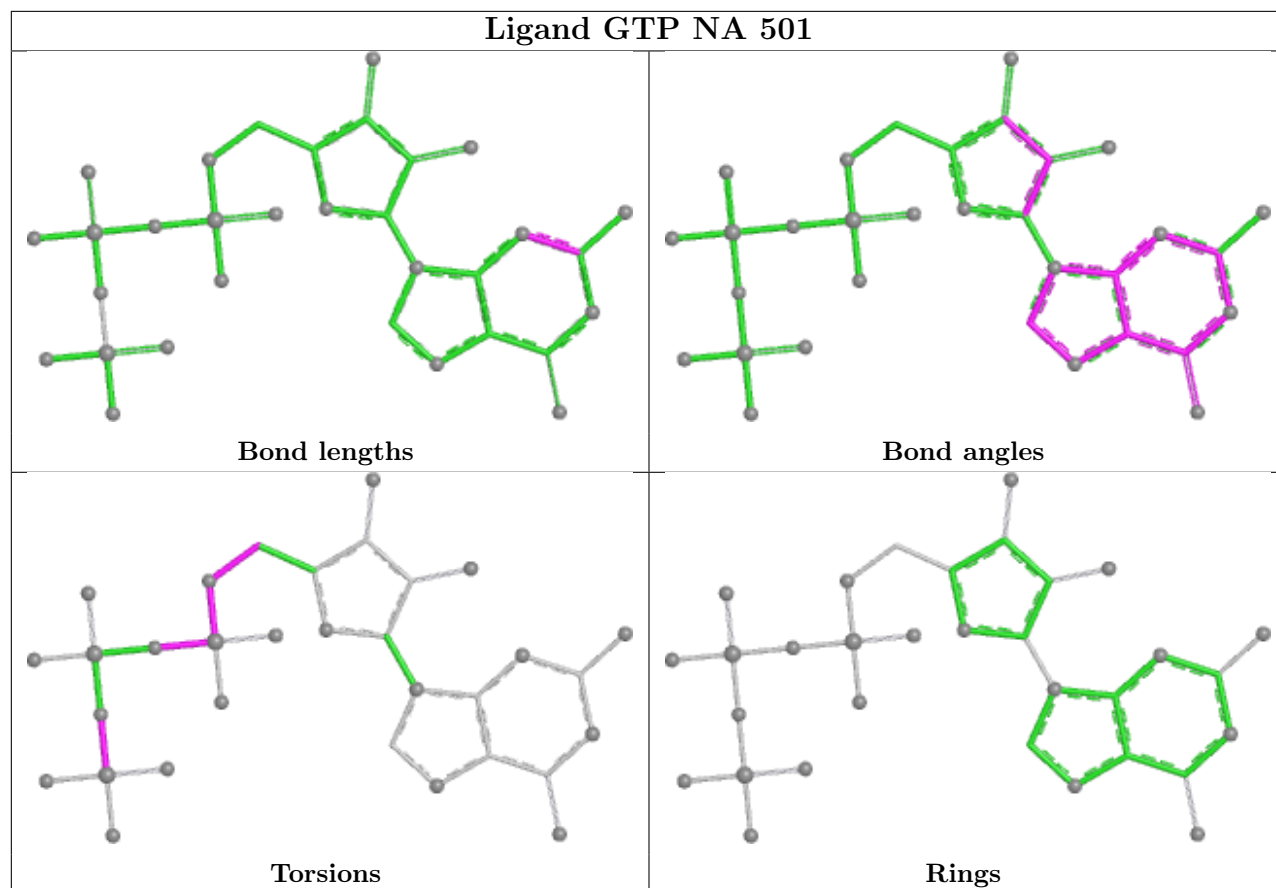
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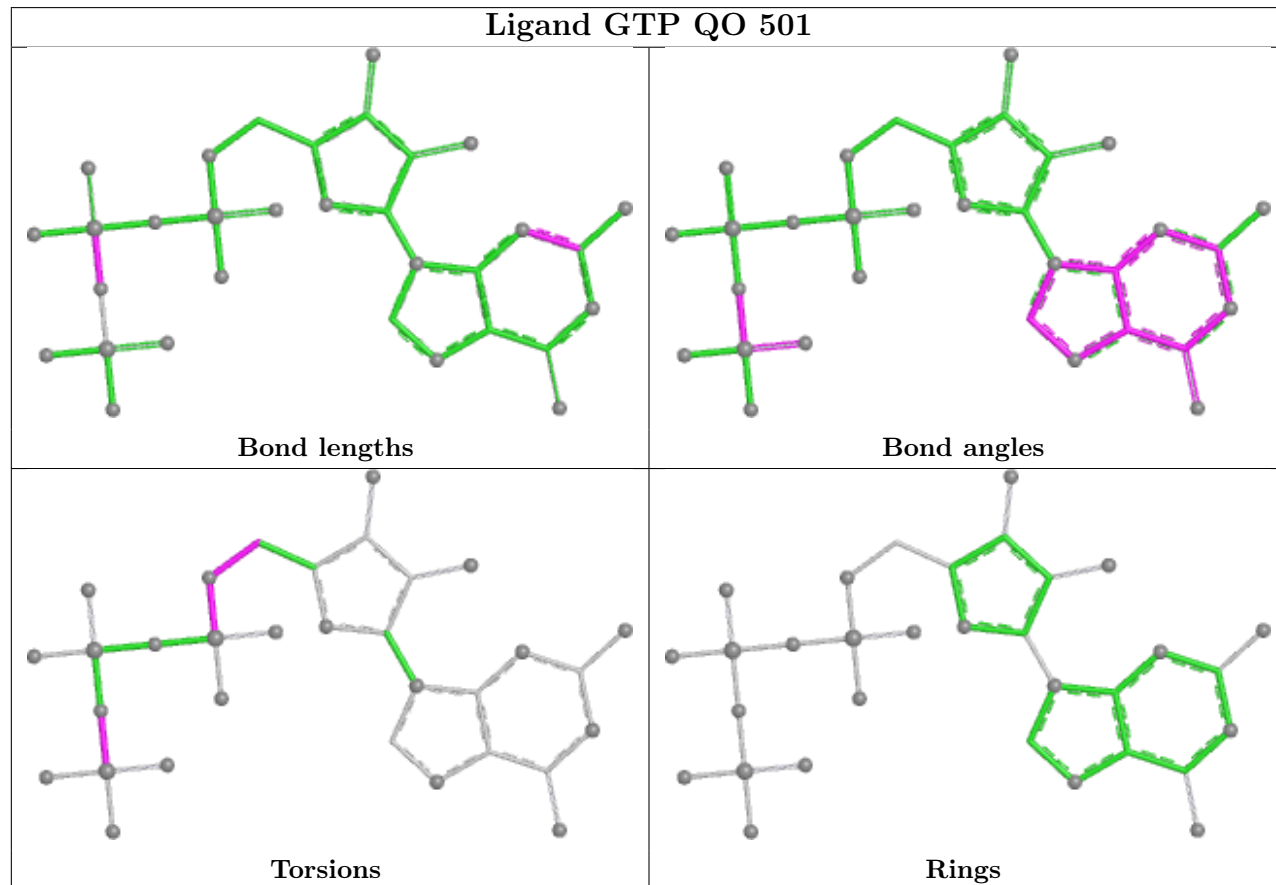
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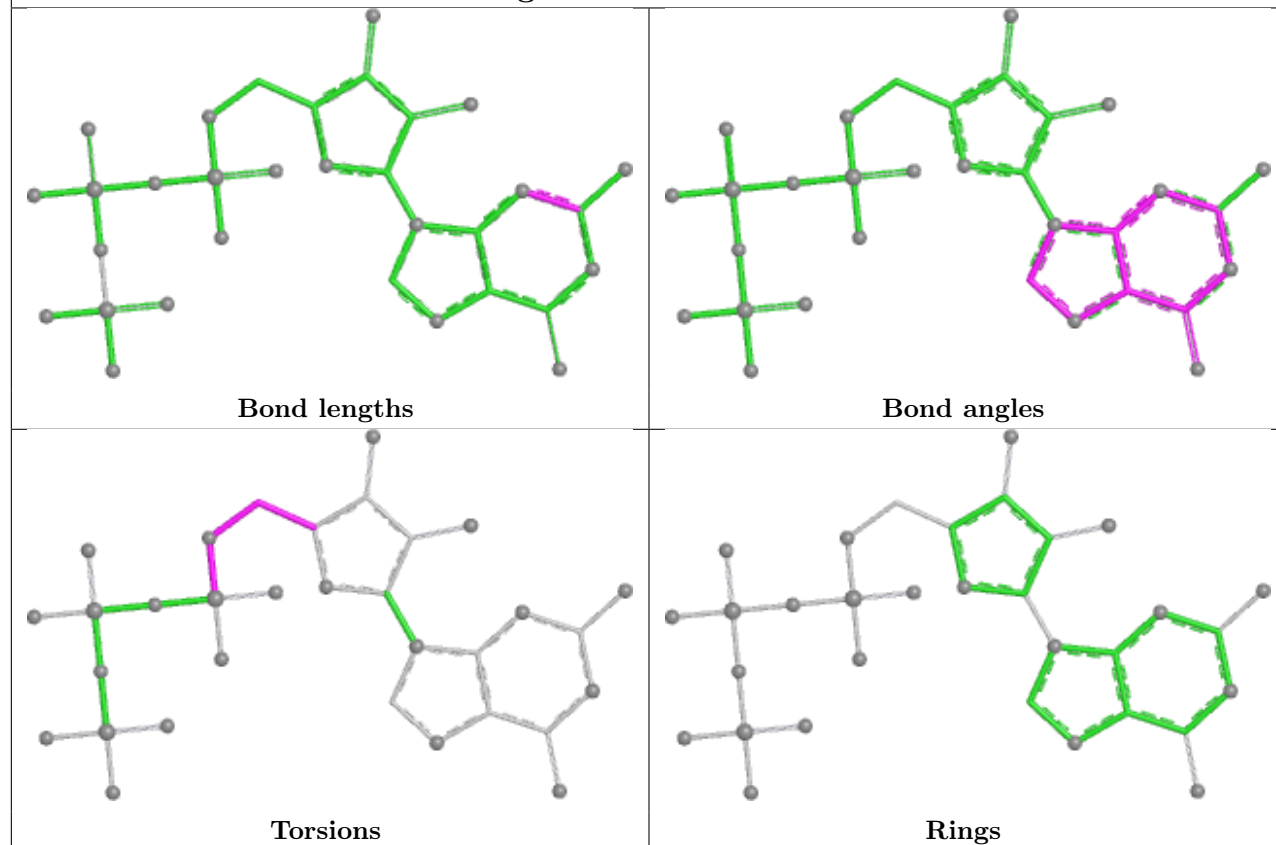
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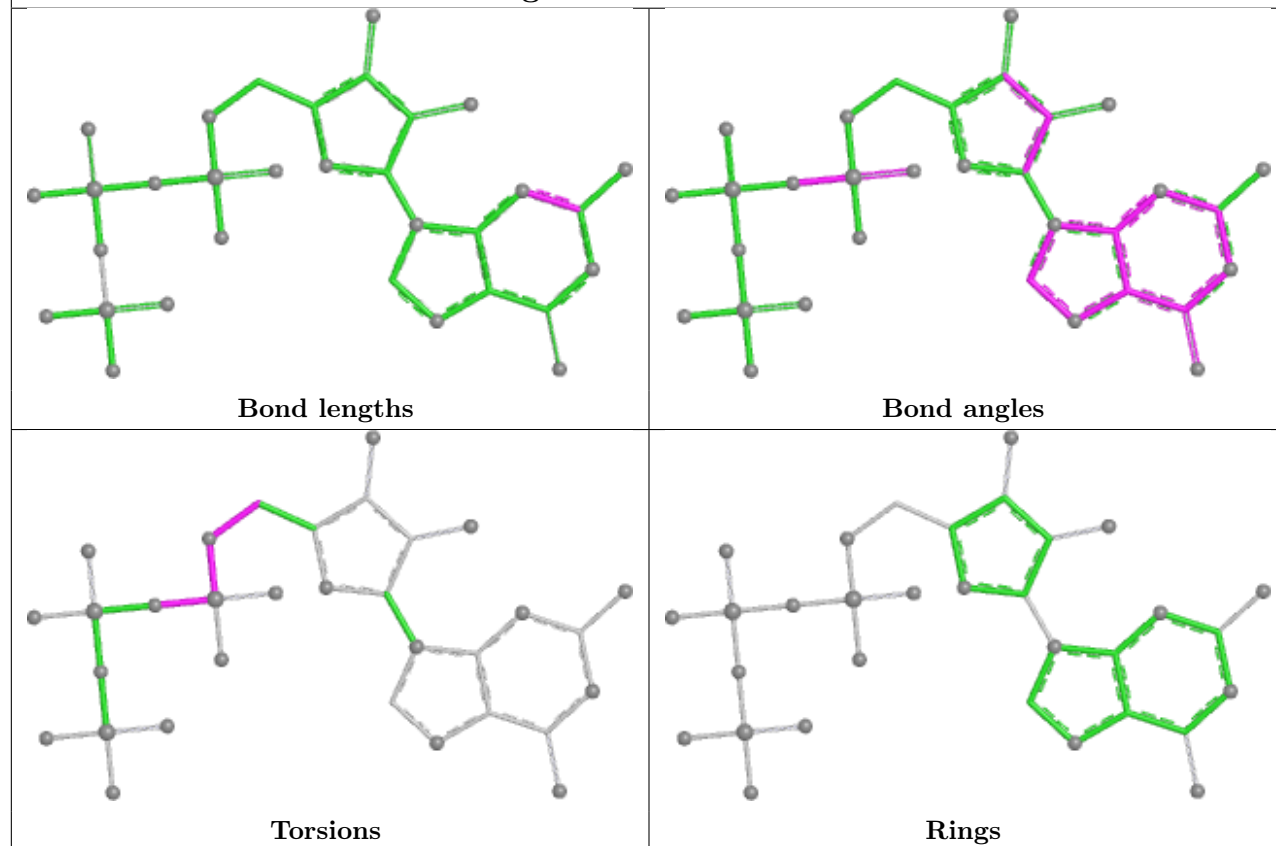
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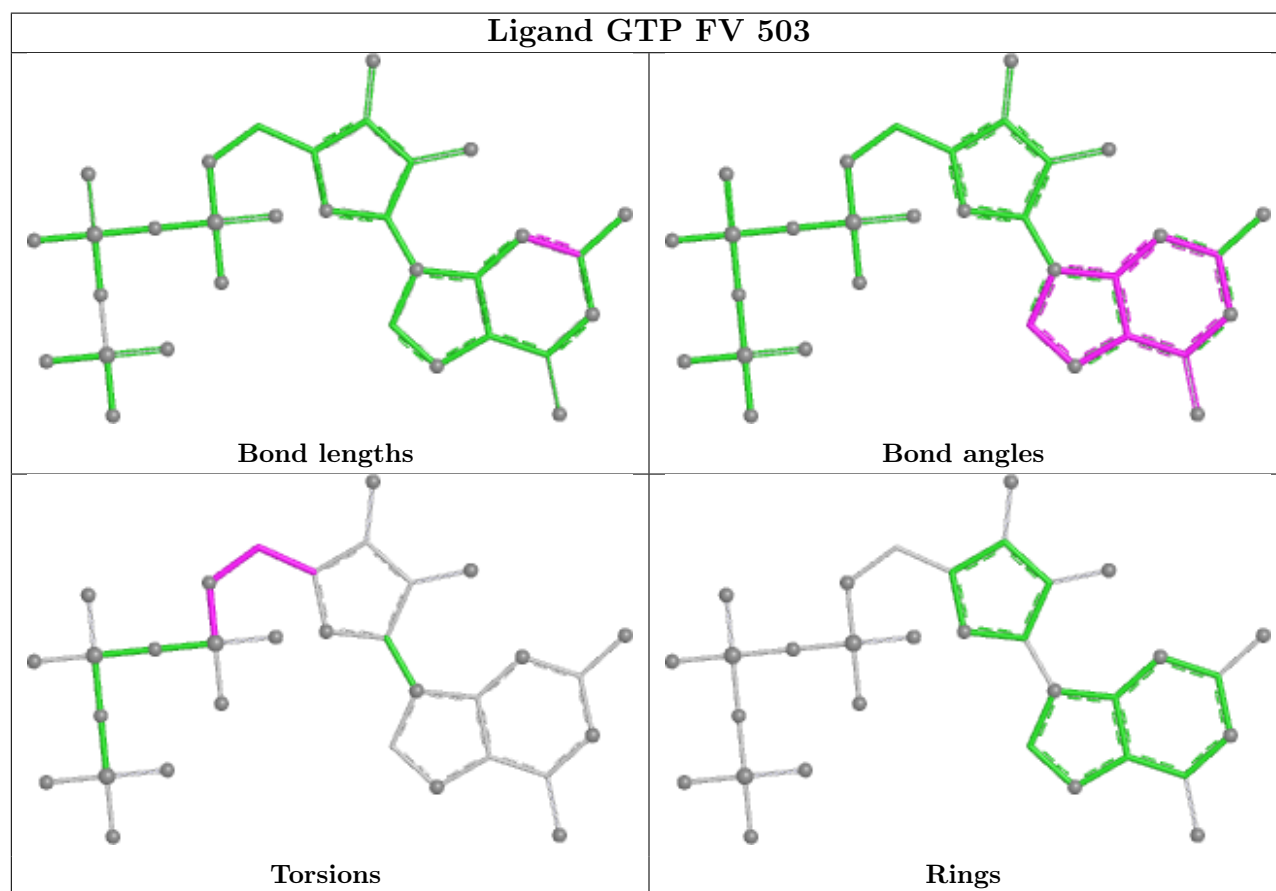
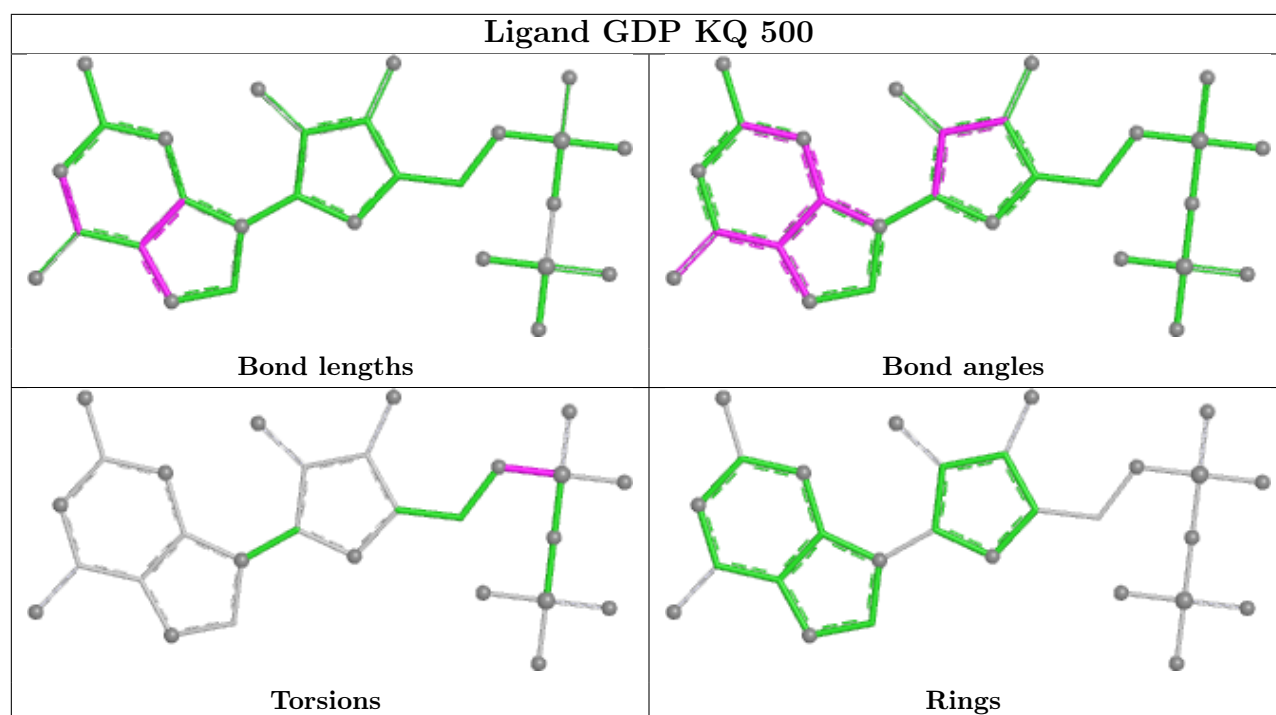


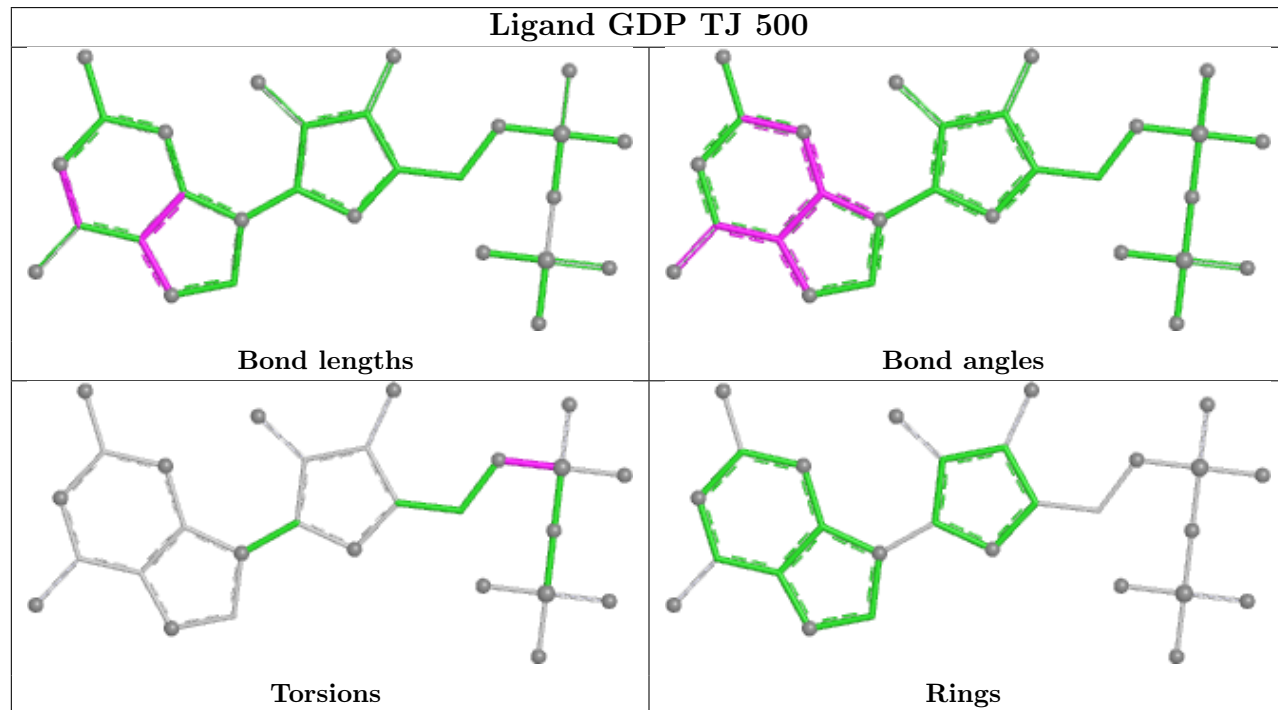
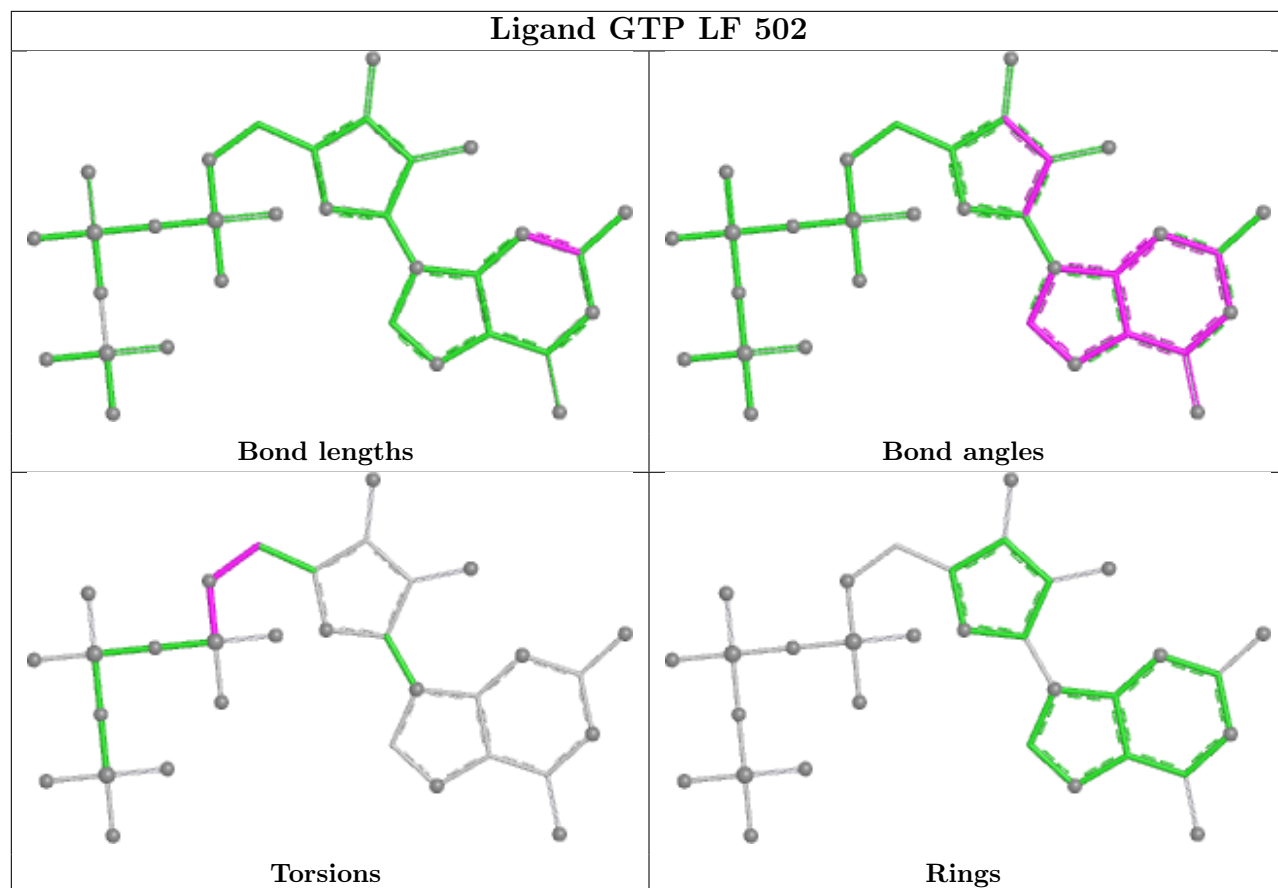
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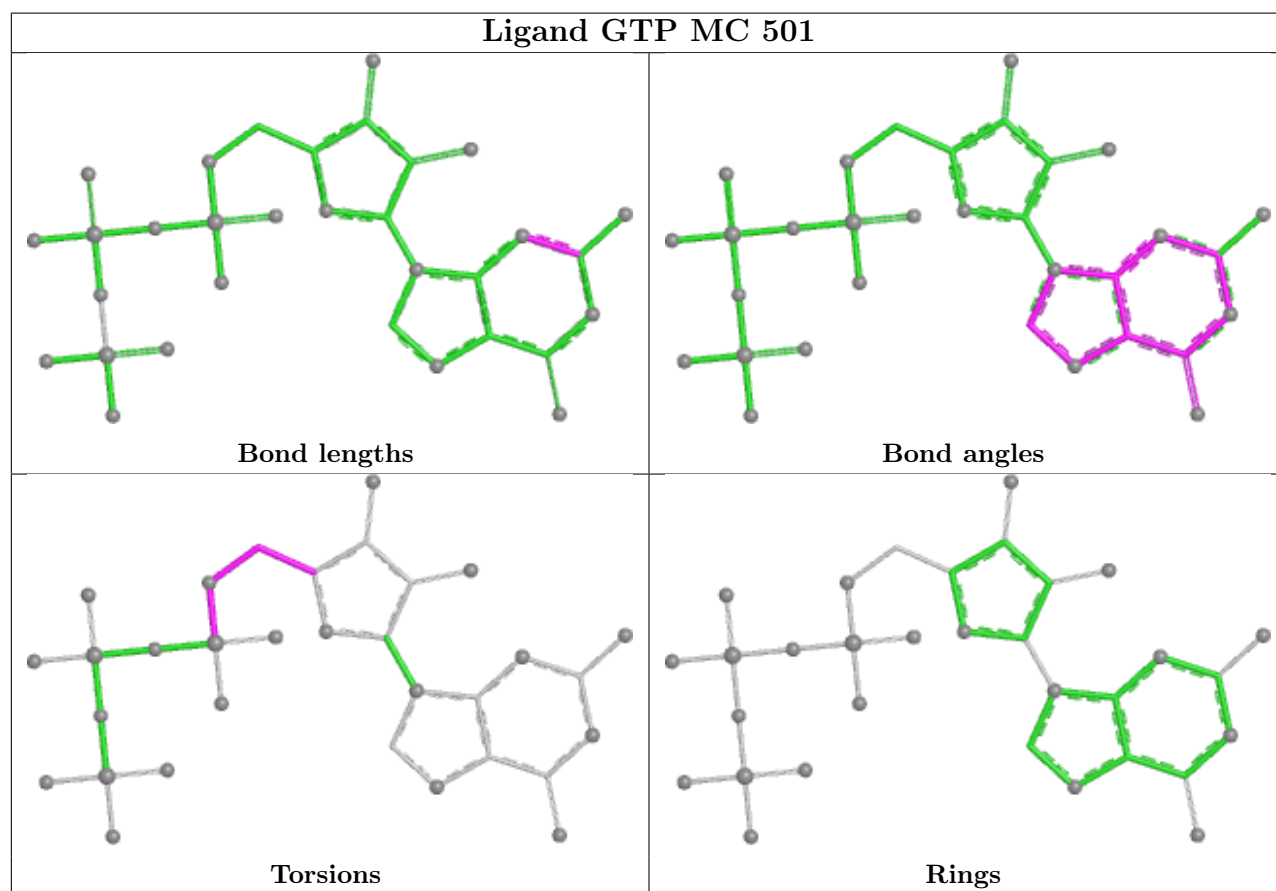
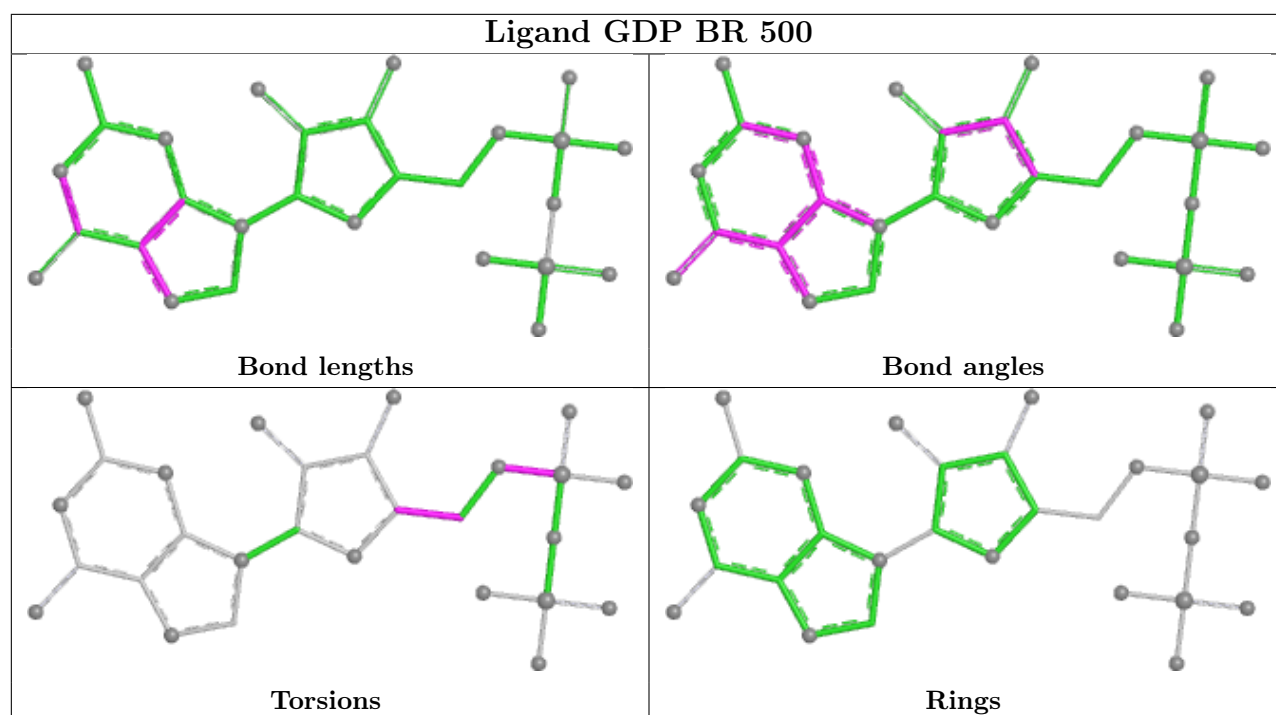


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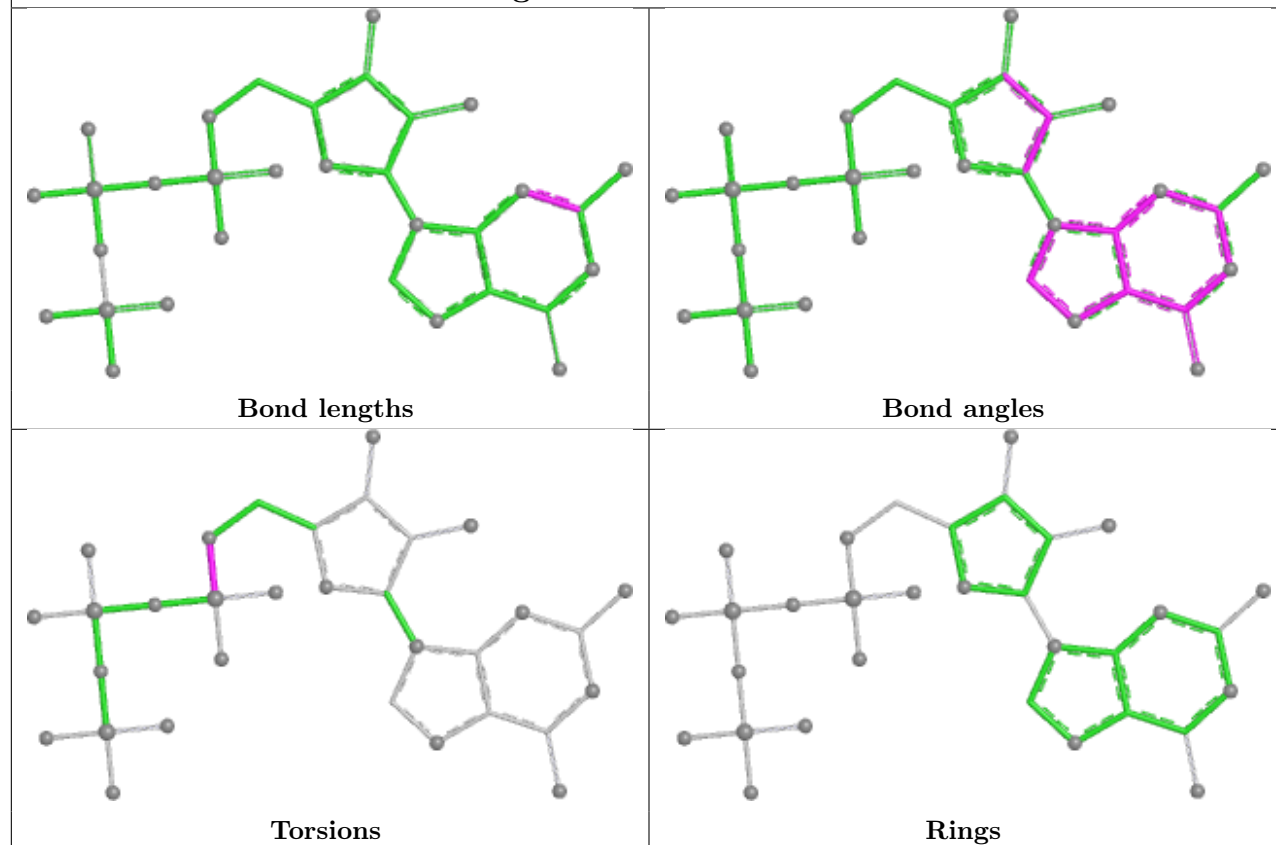




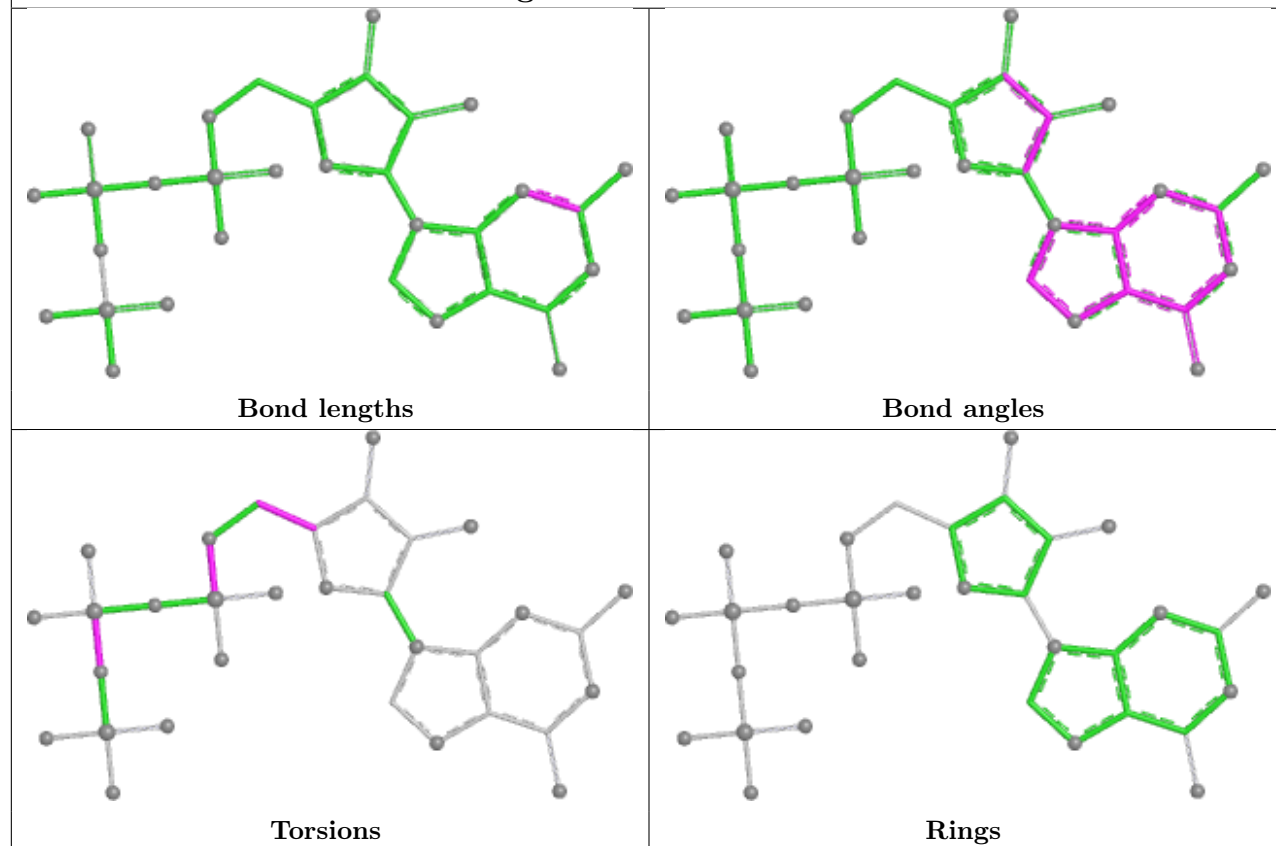


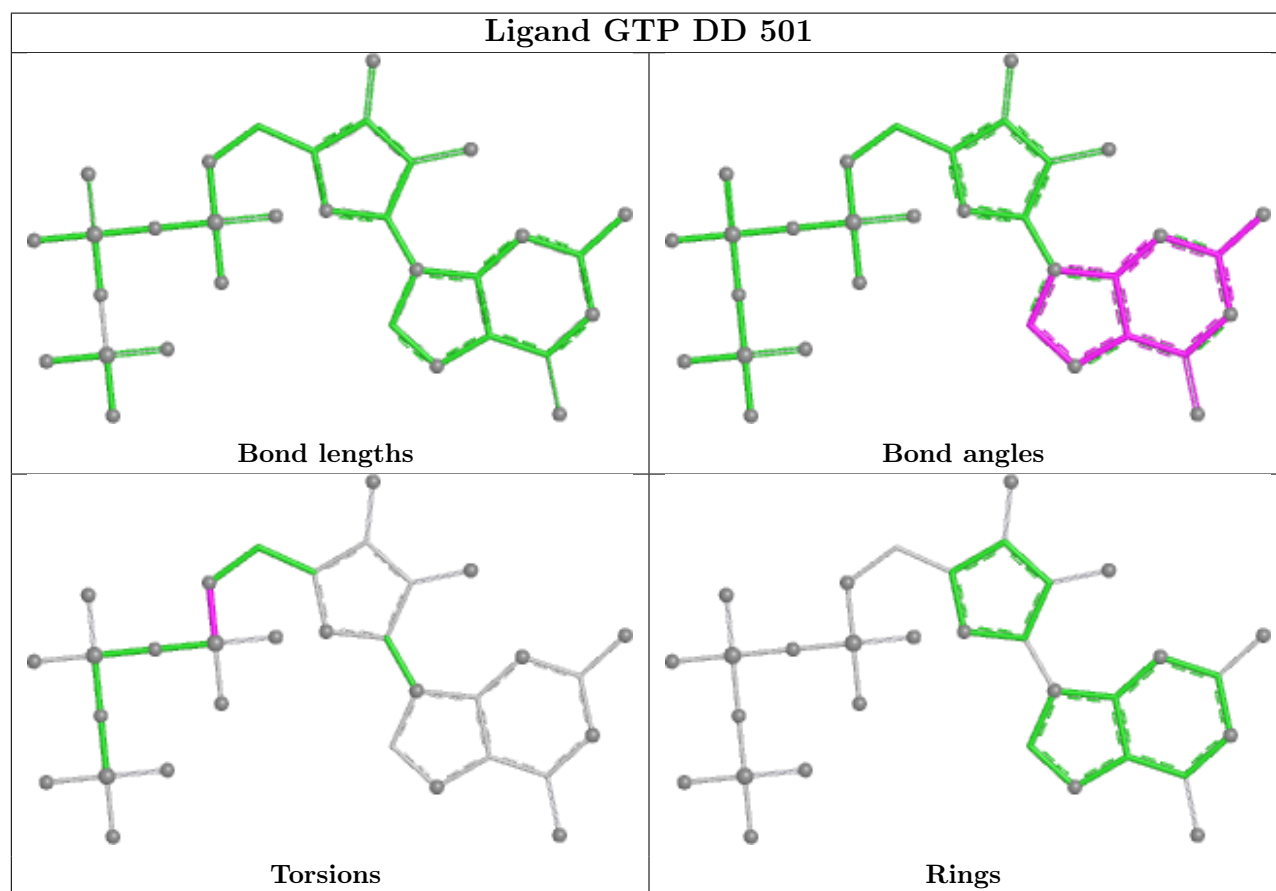
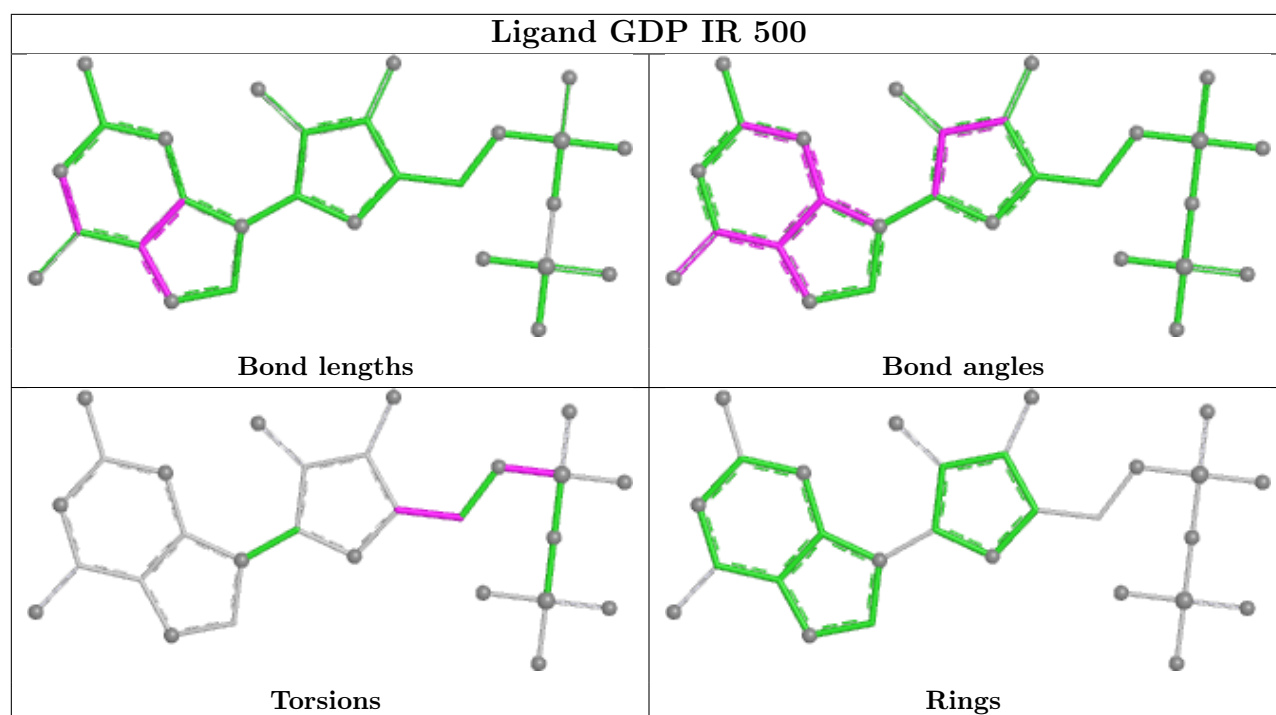


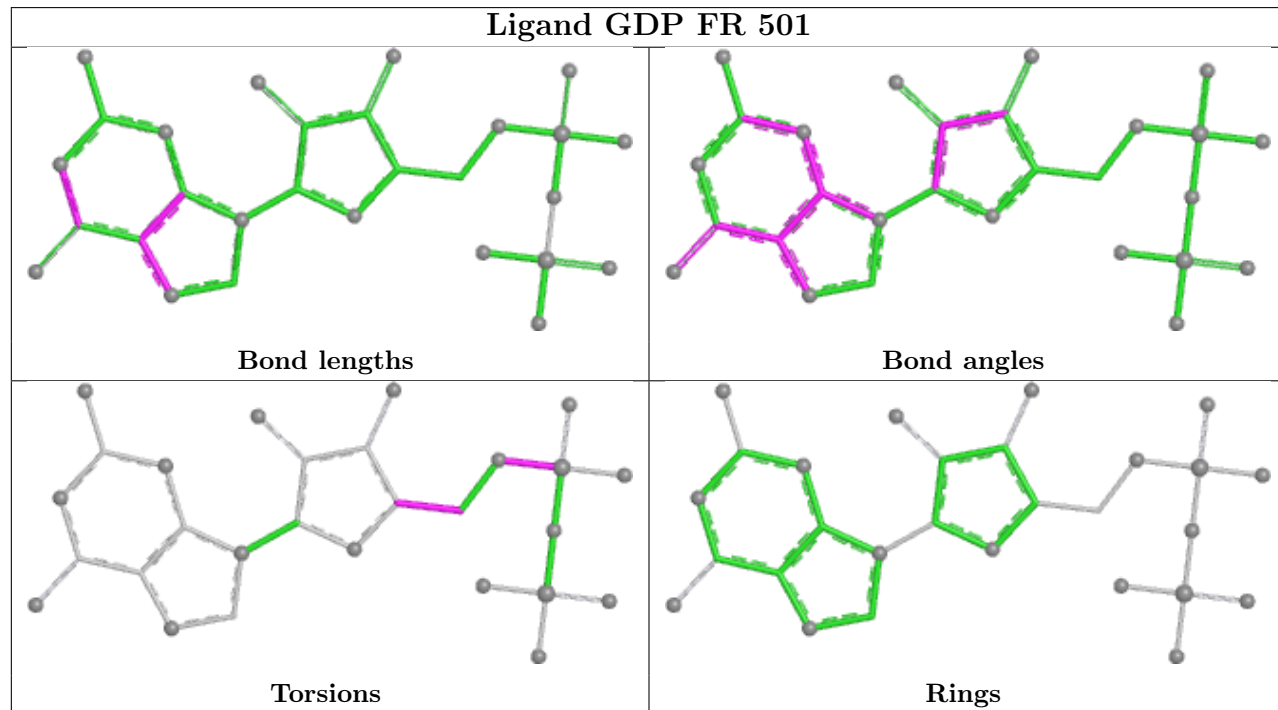
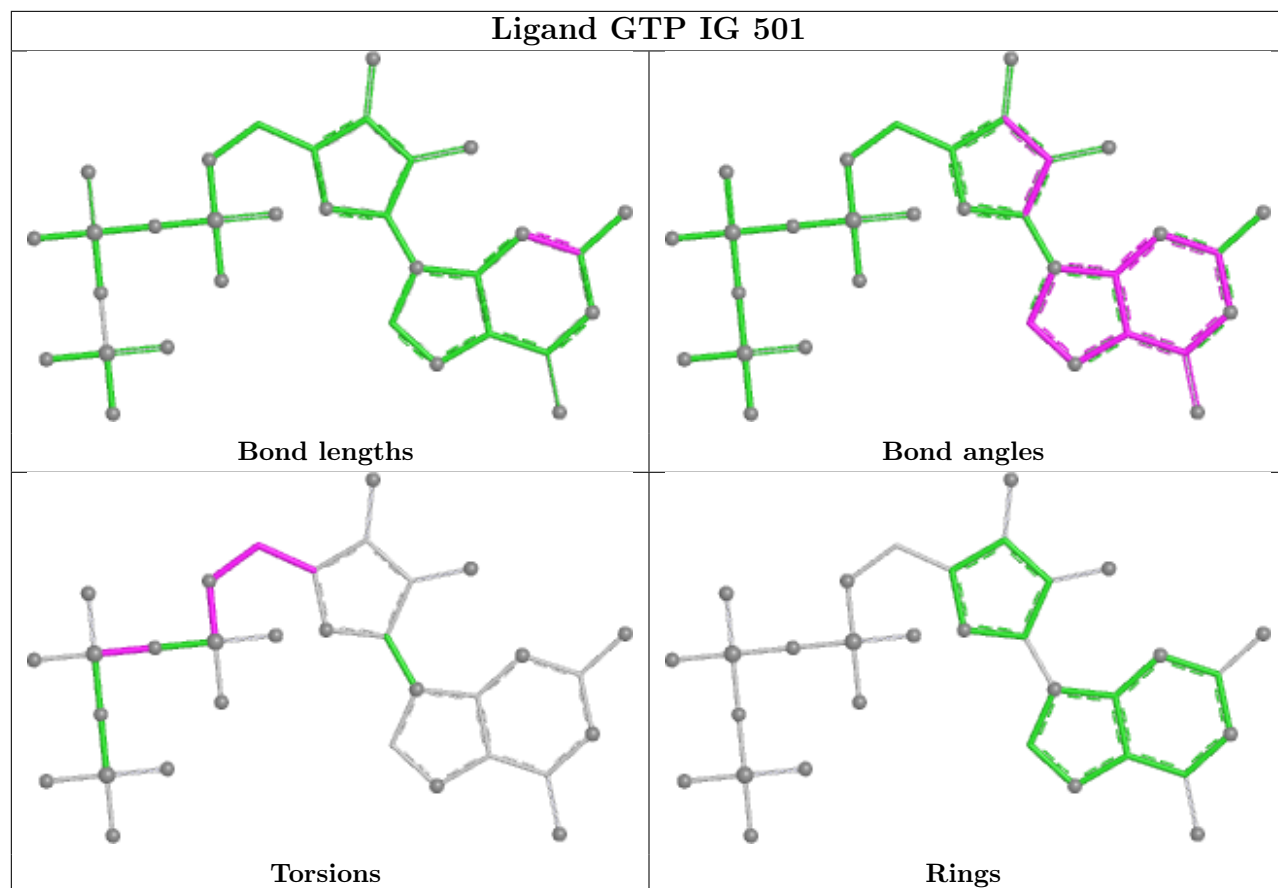
Ligand GTP WC 501



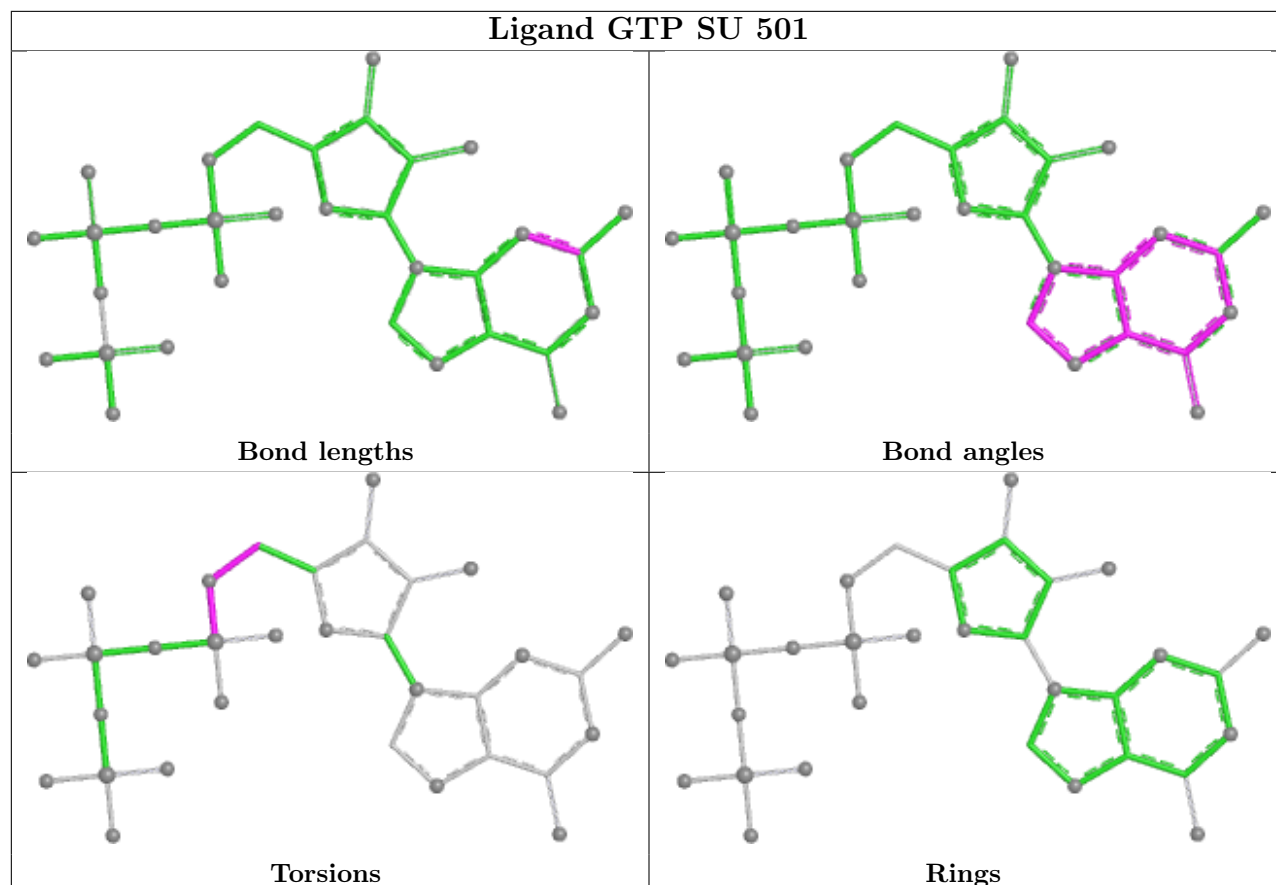
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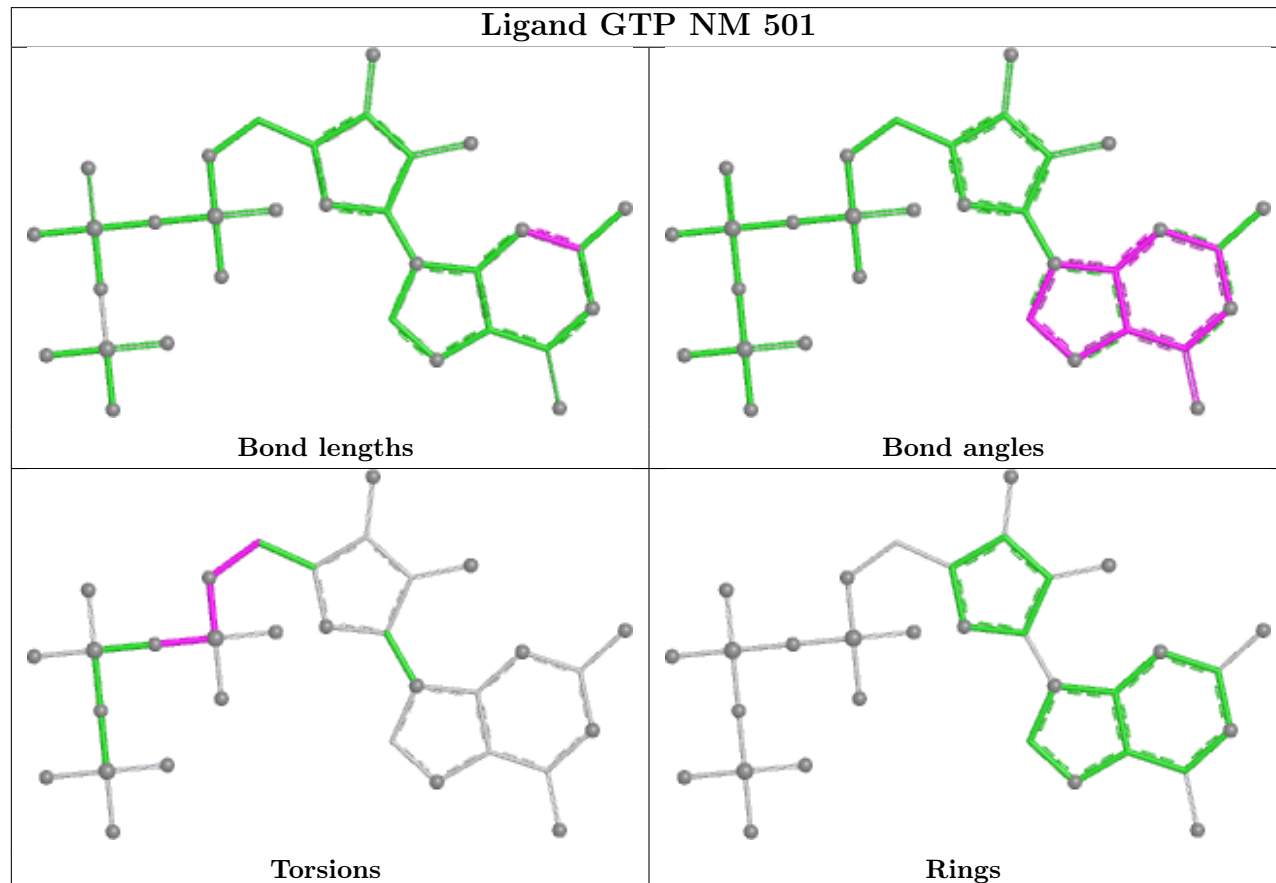


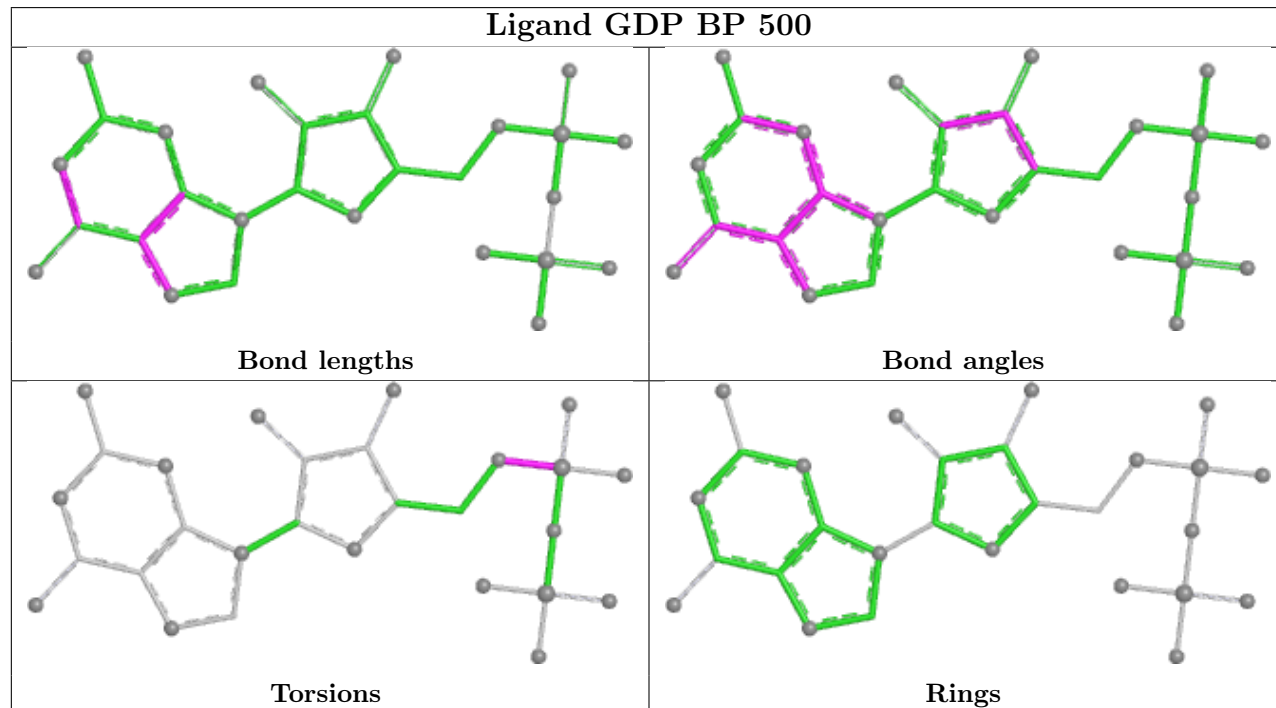
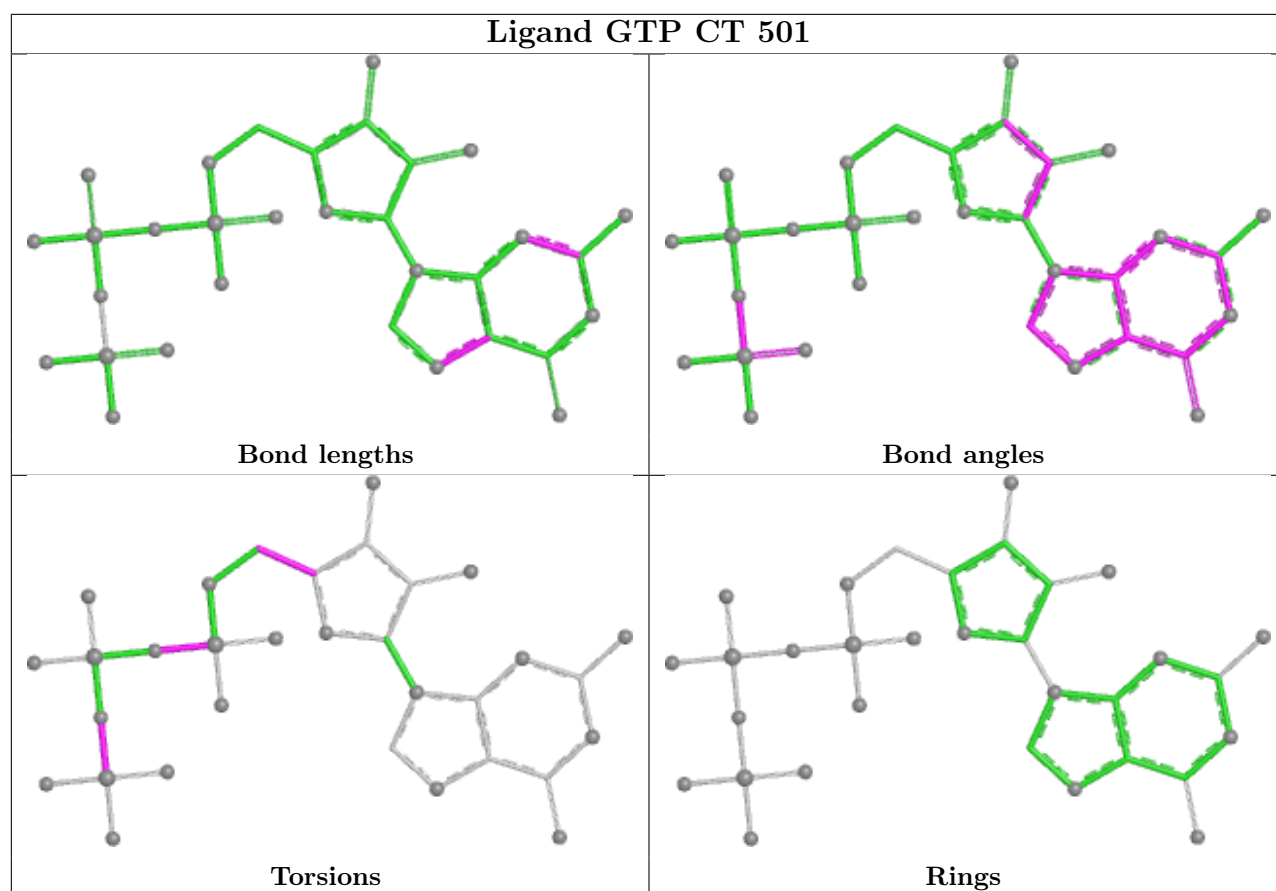


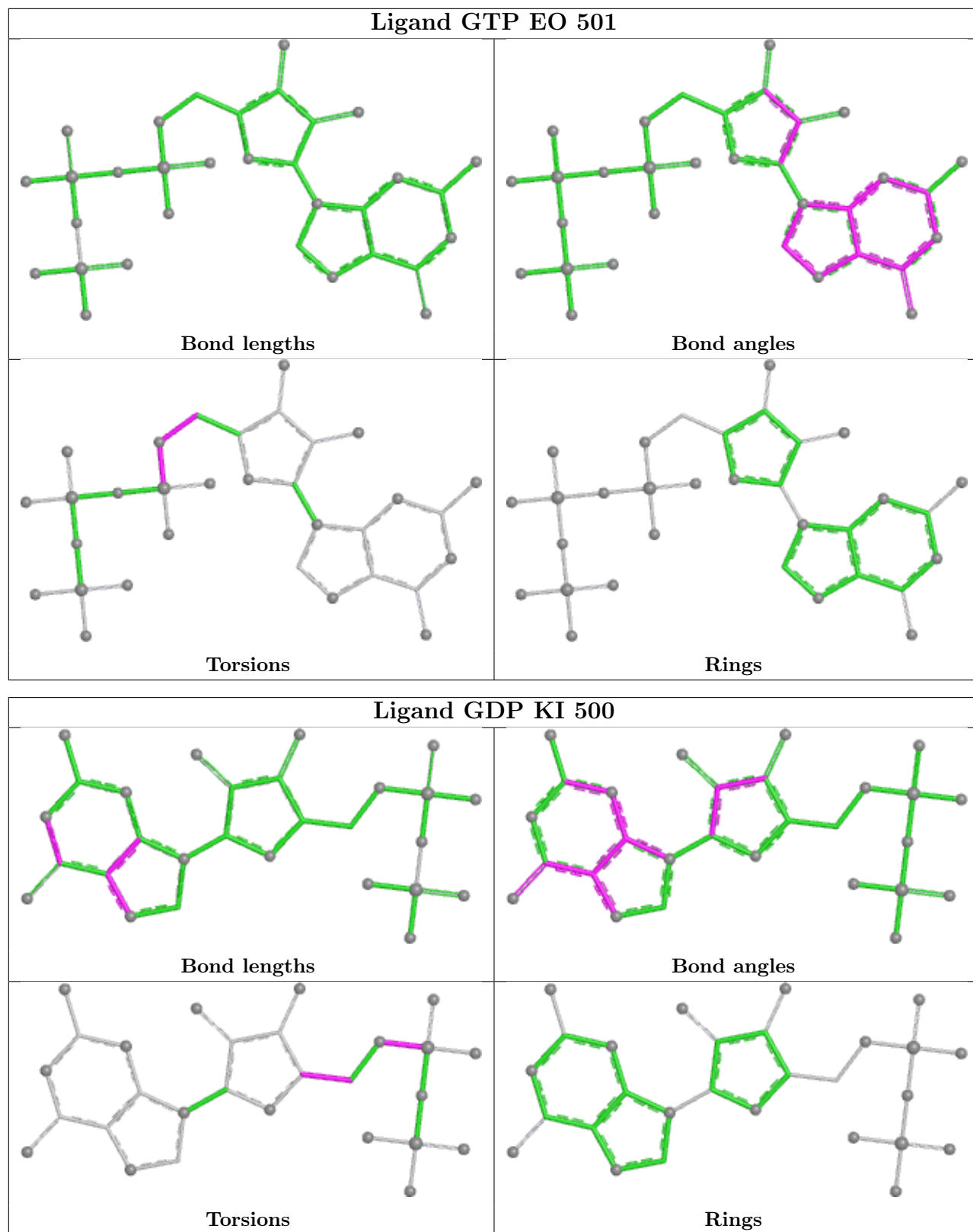
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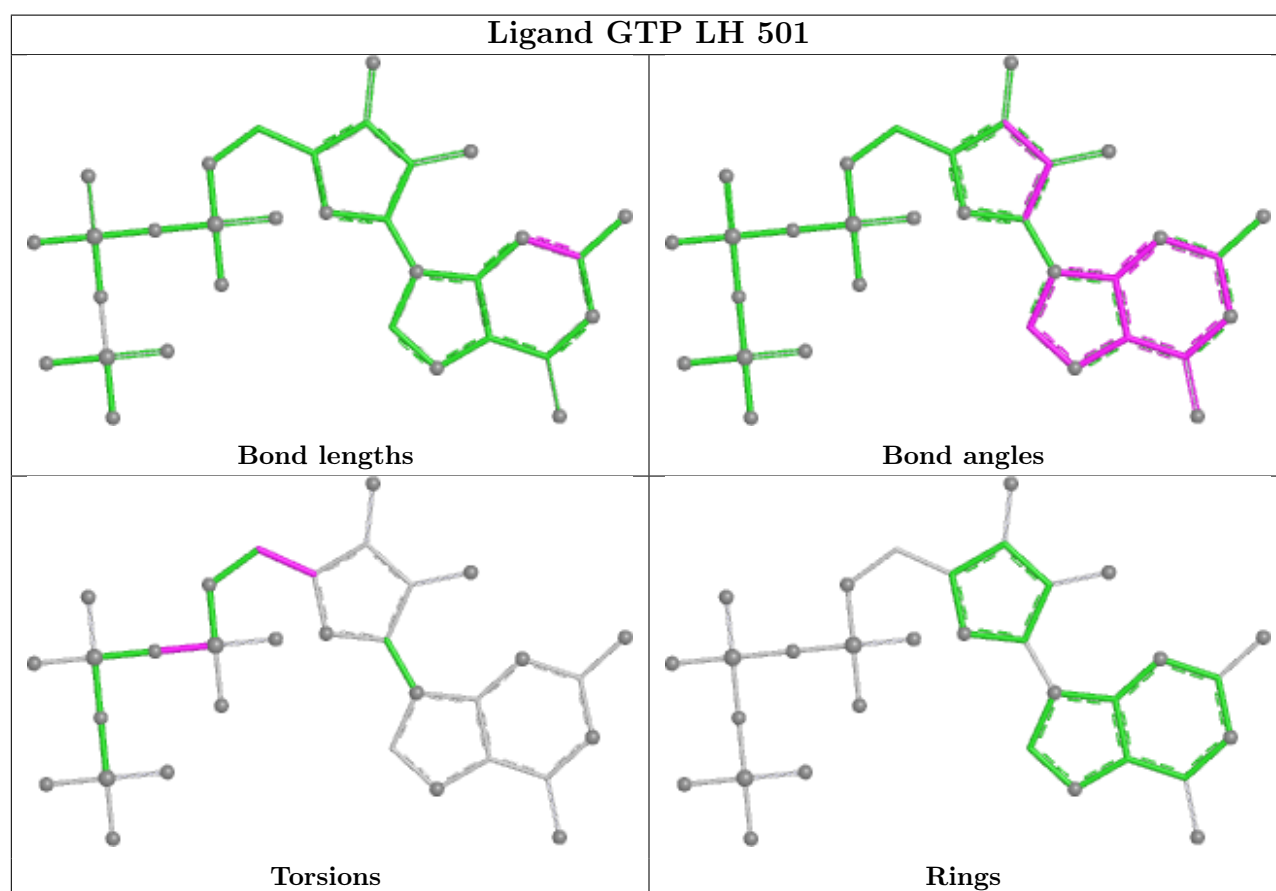
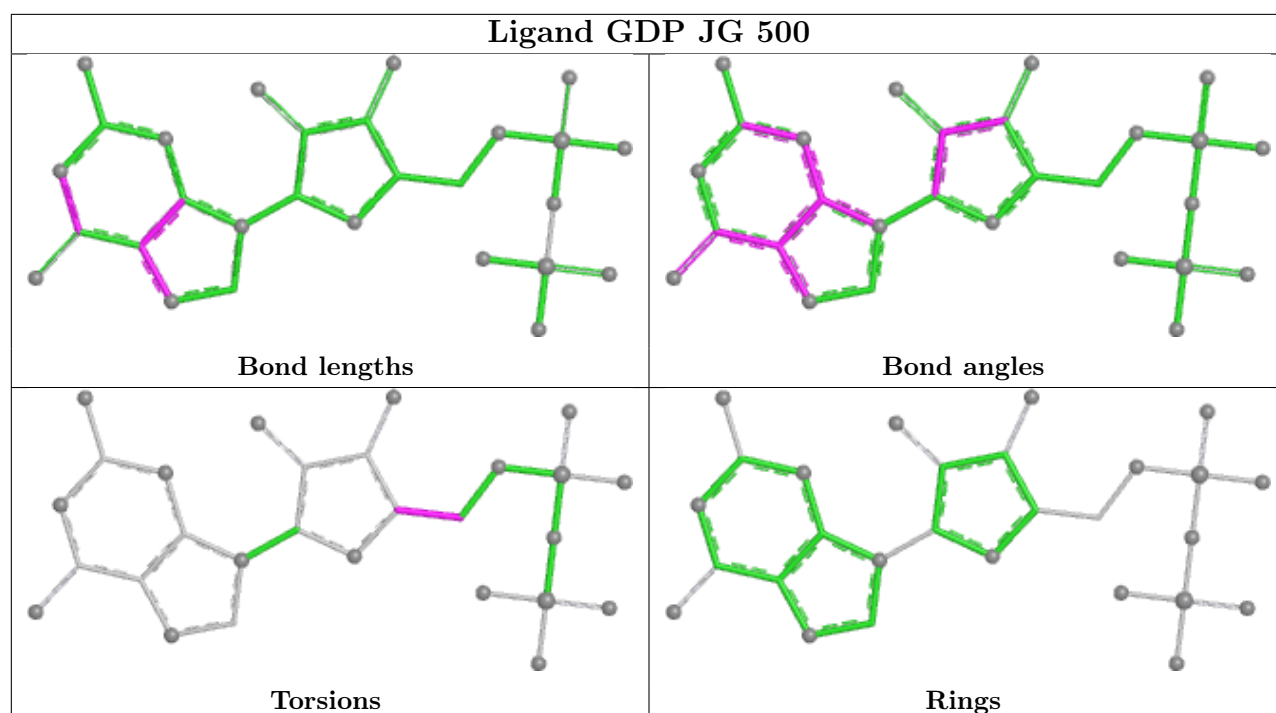


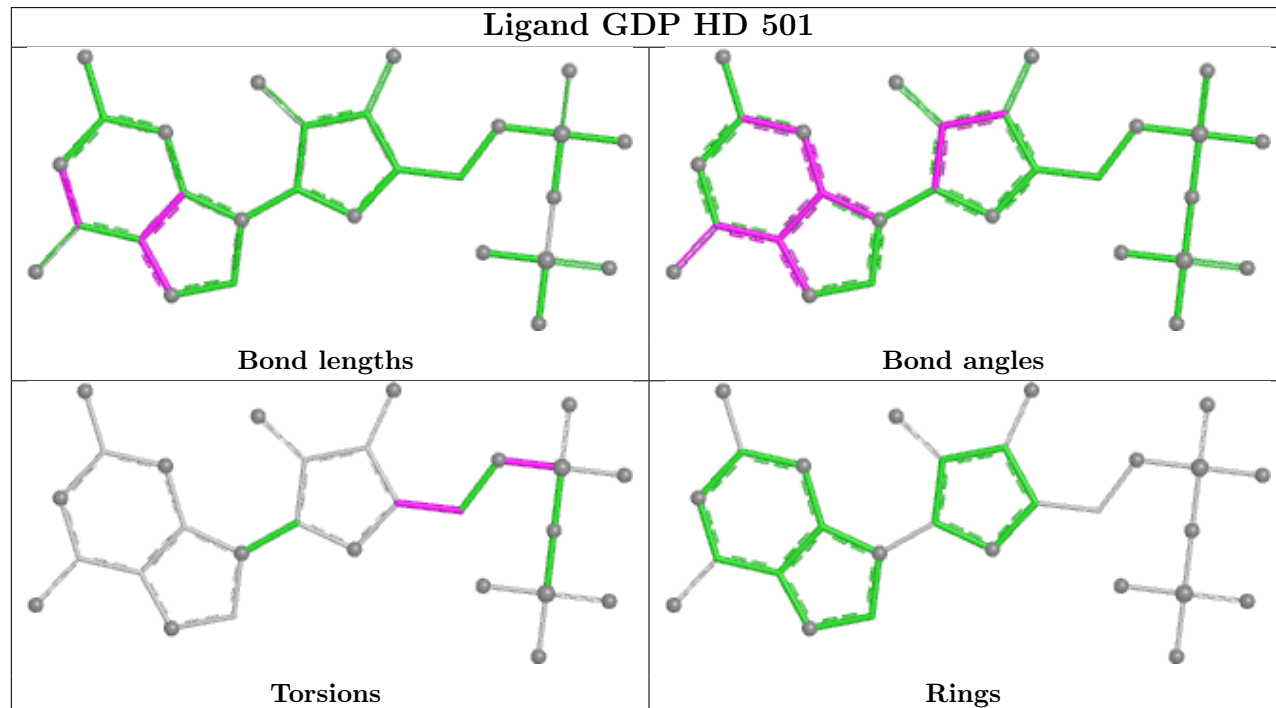
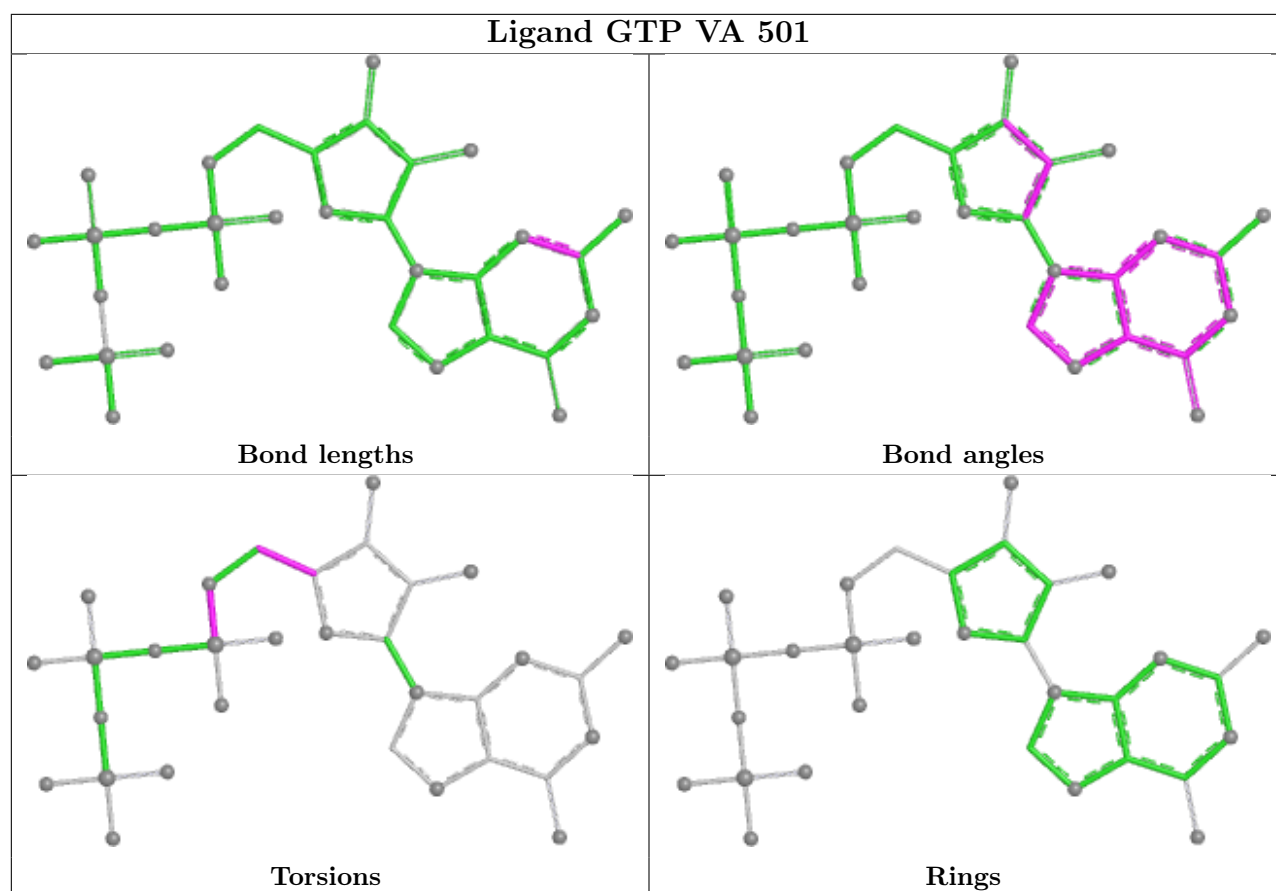
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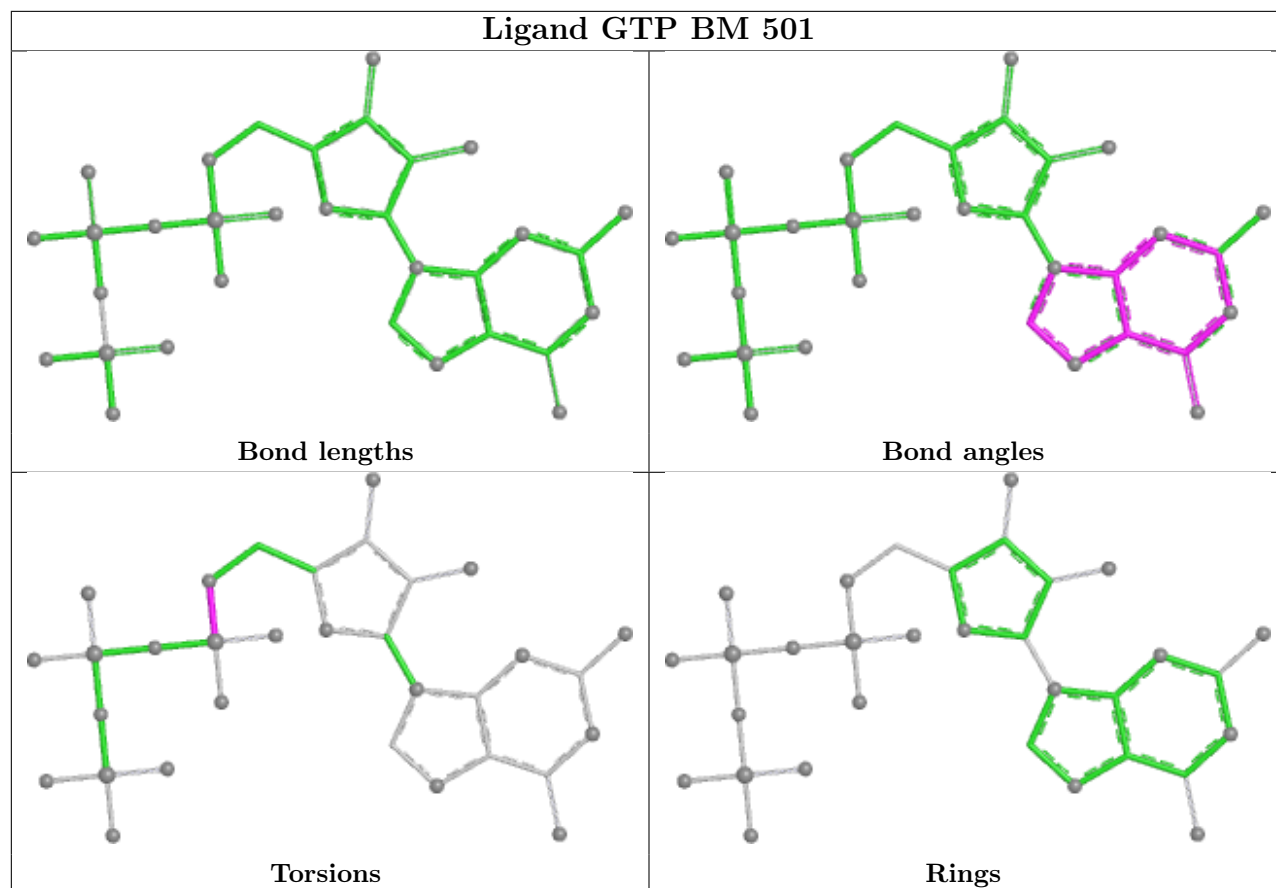




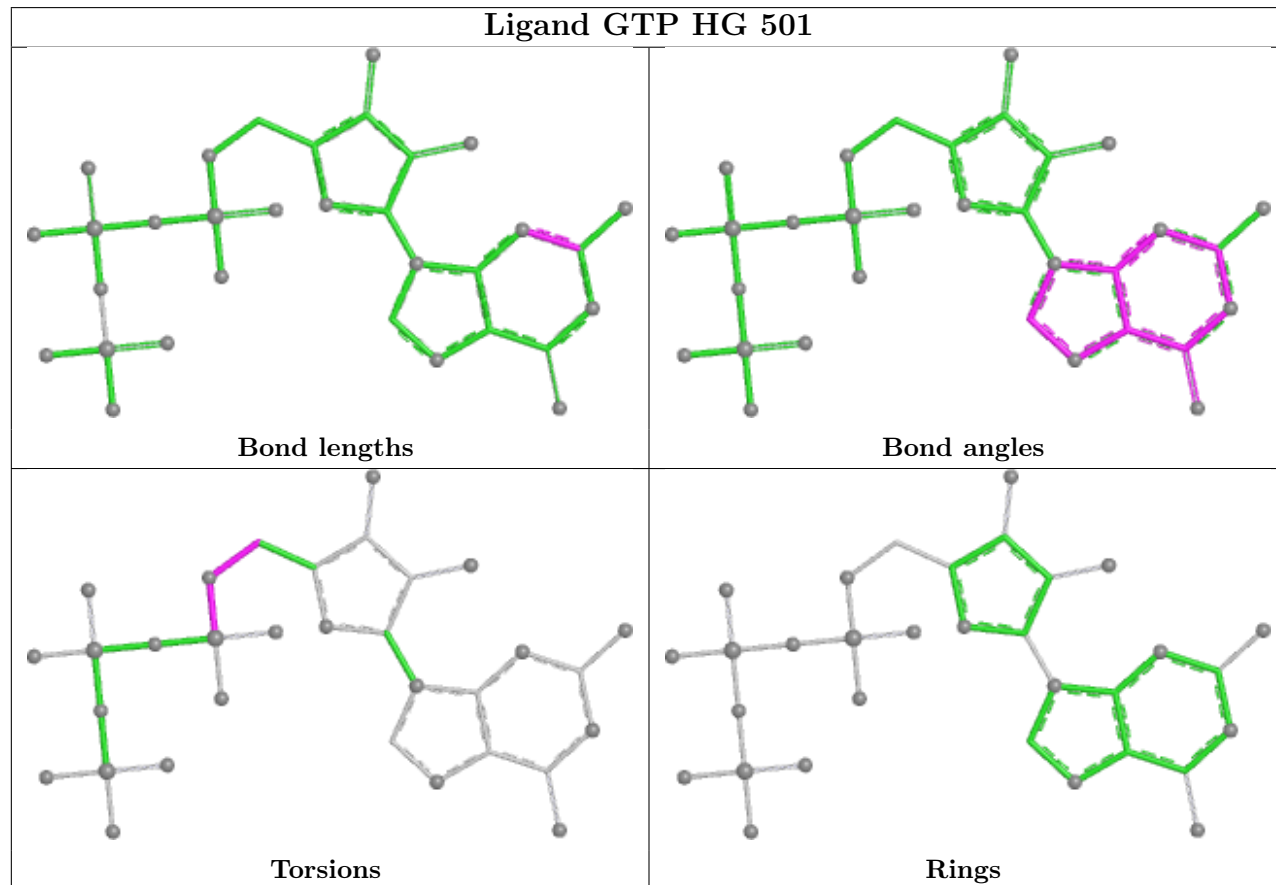




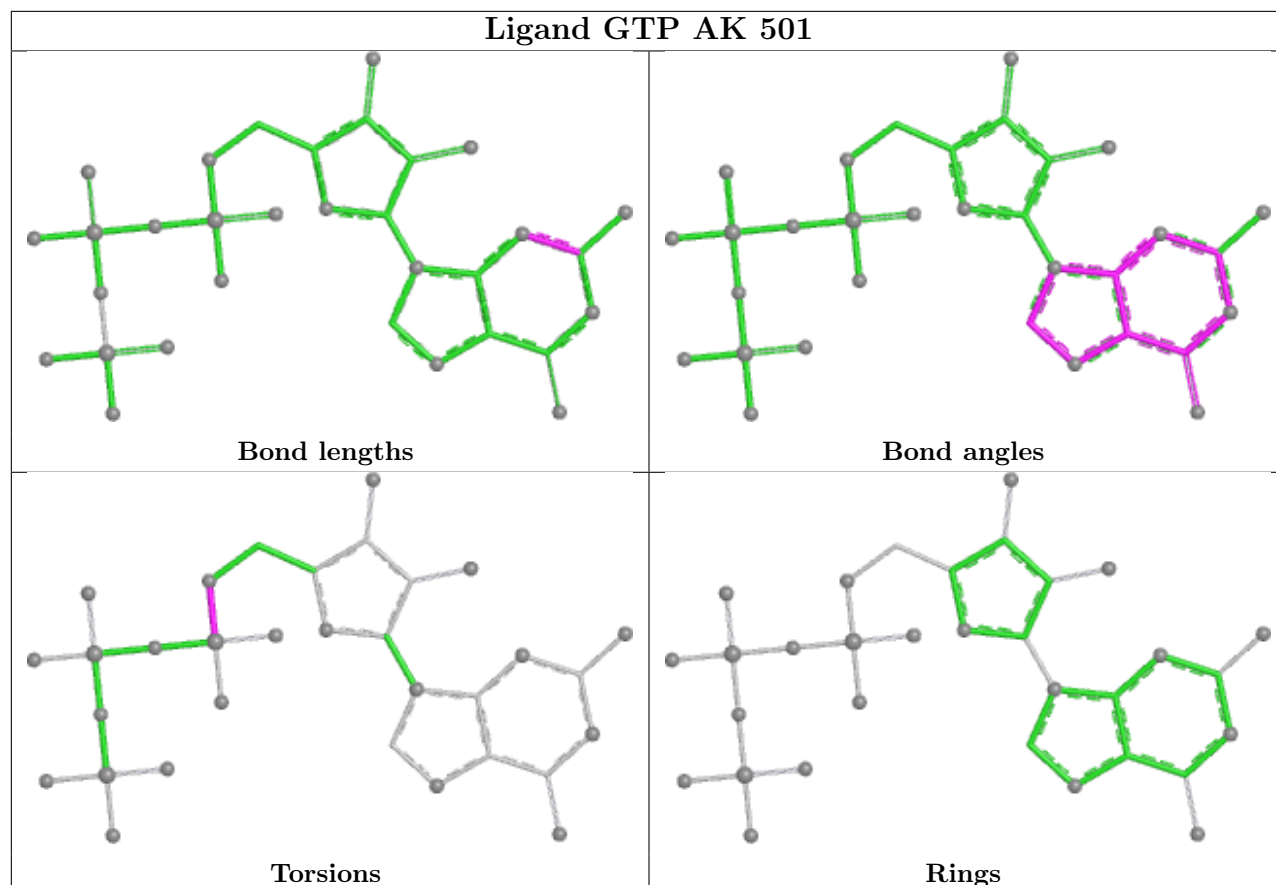
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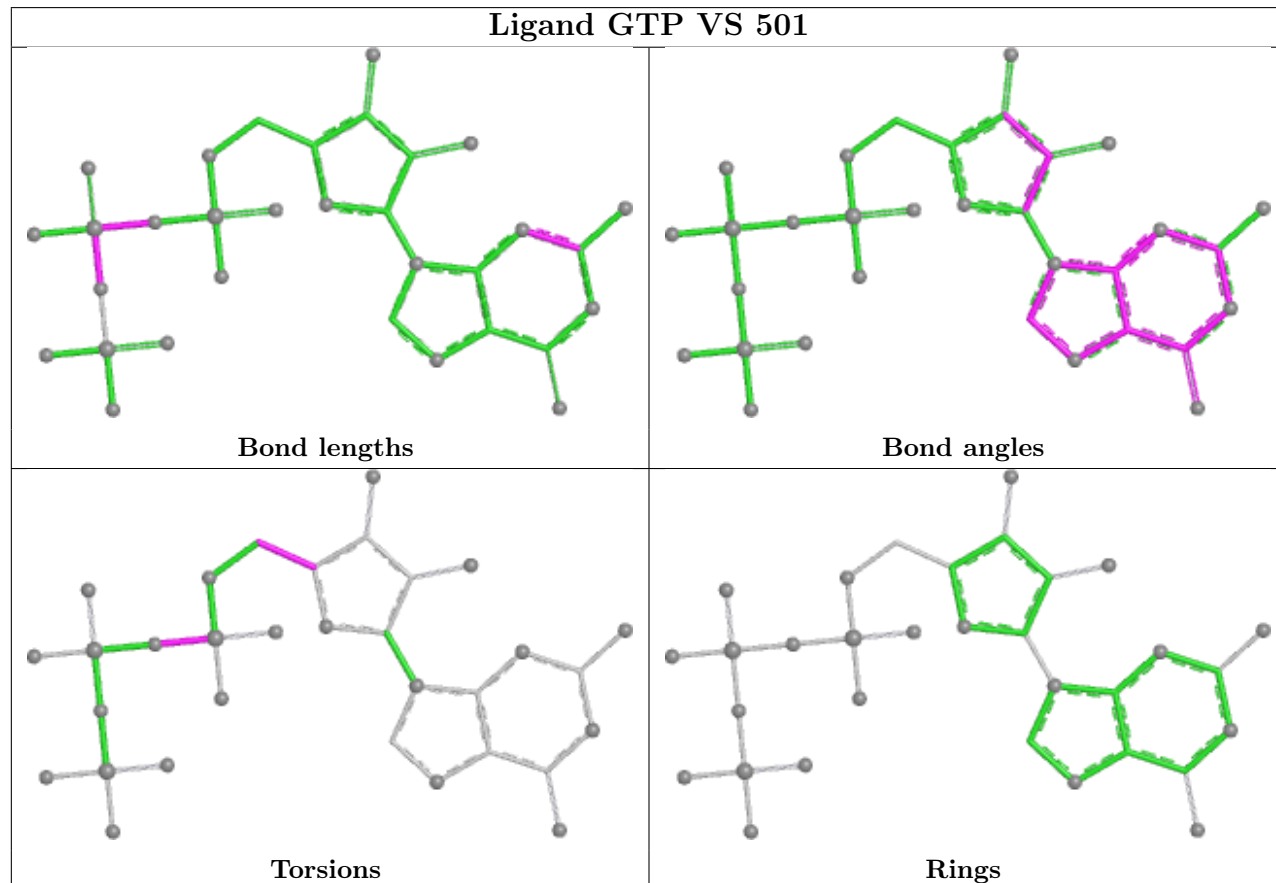
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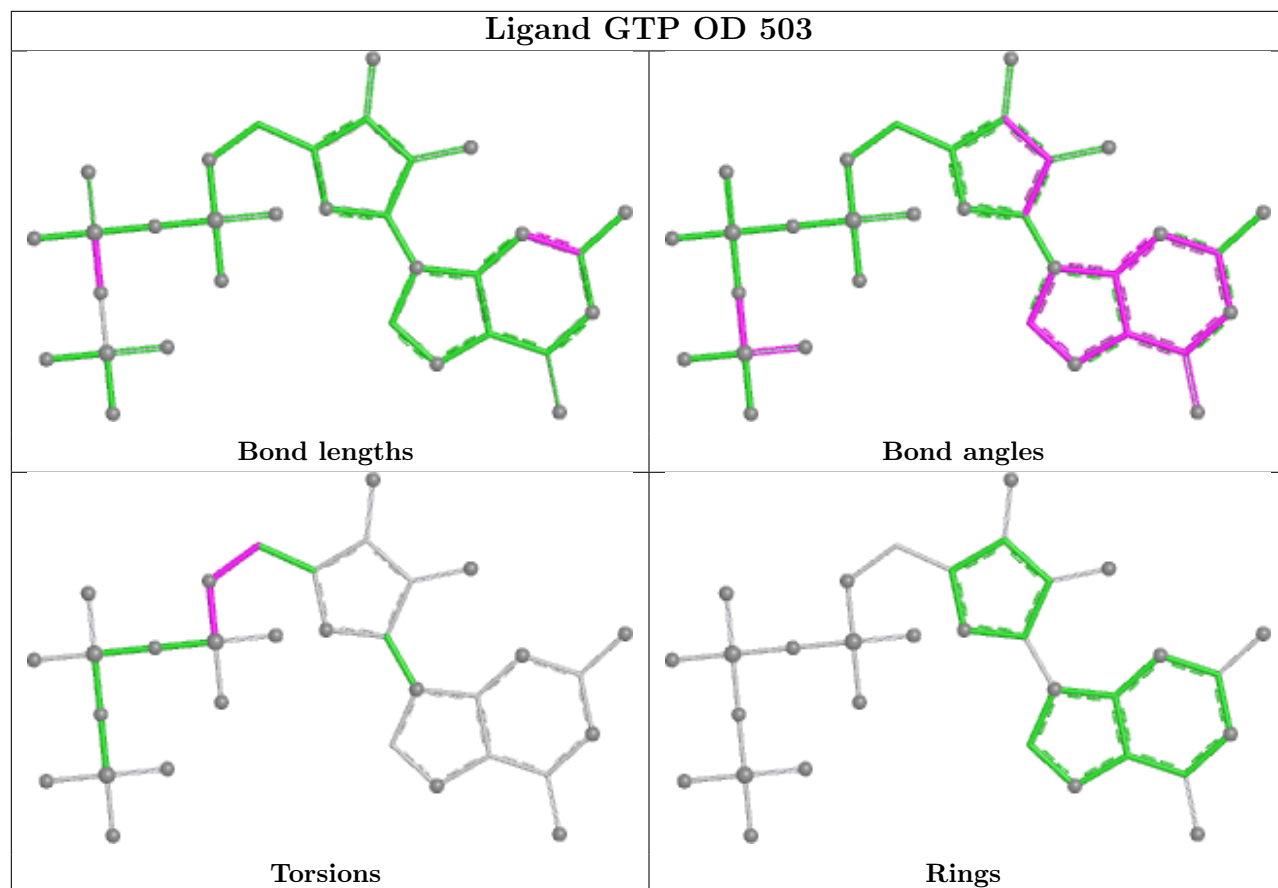
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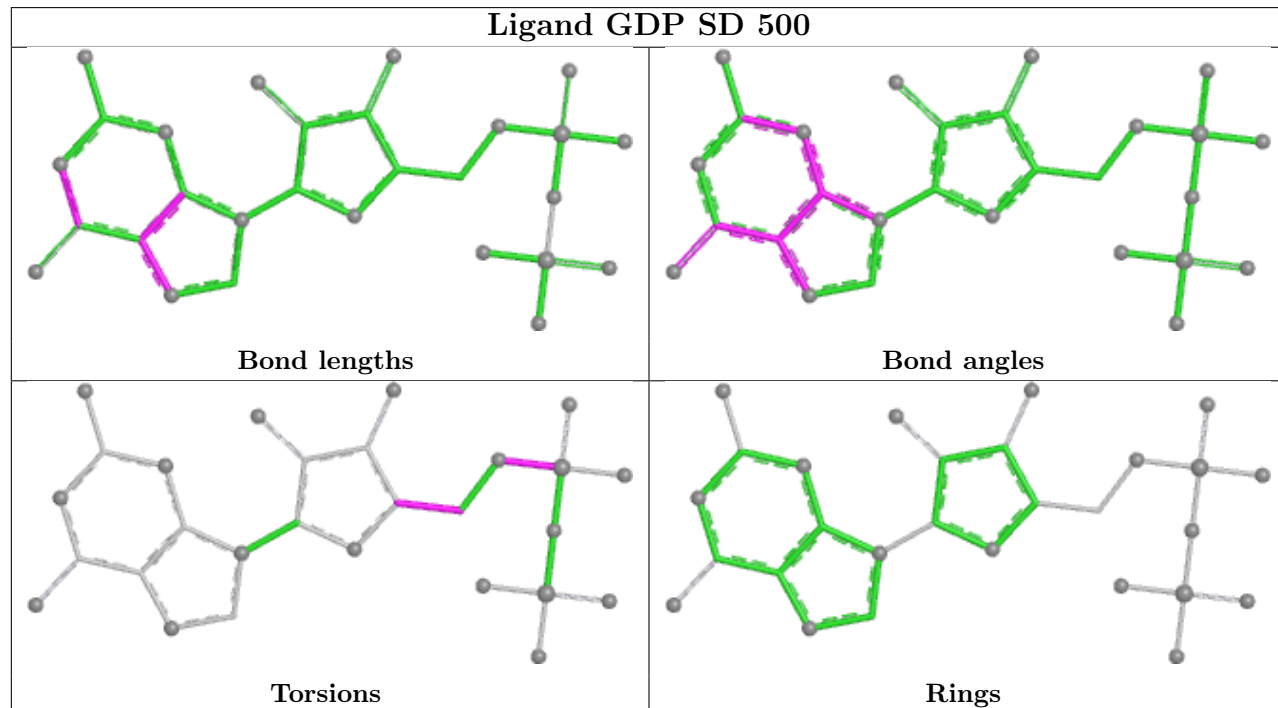
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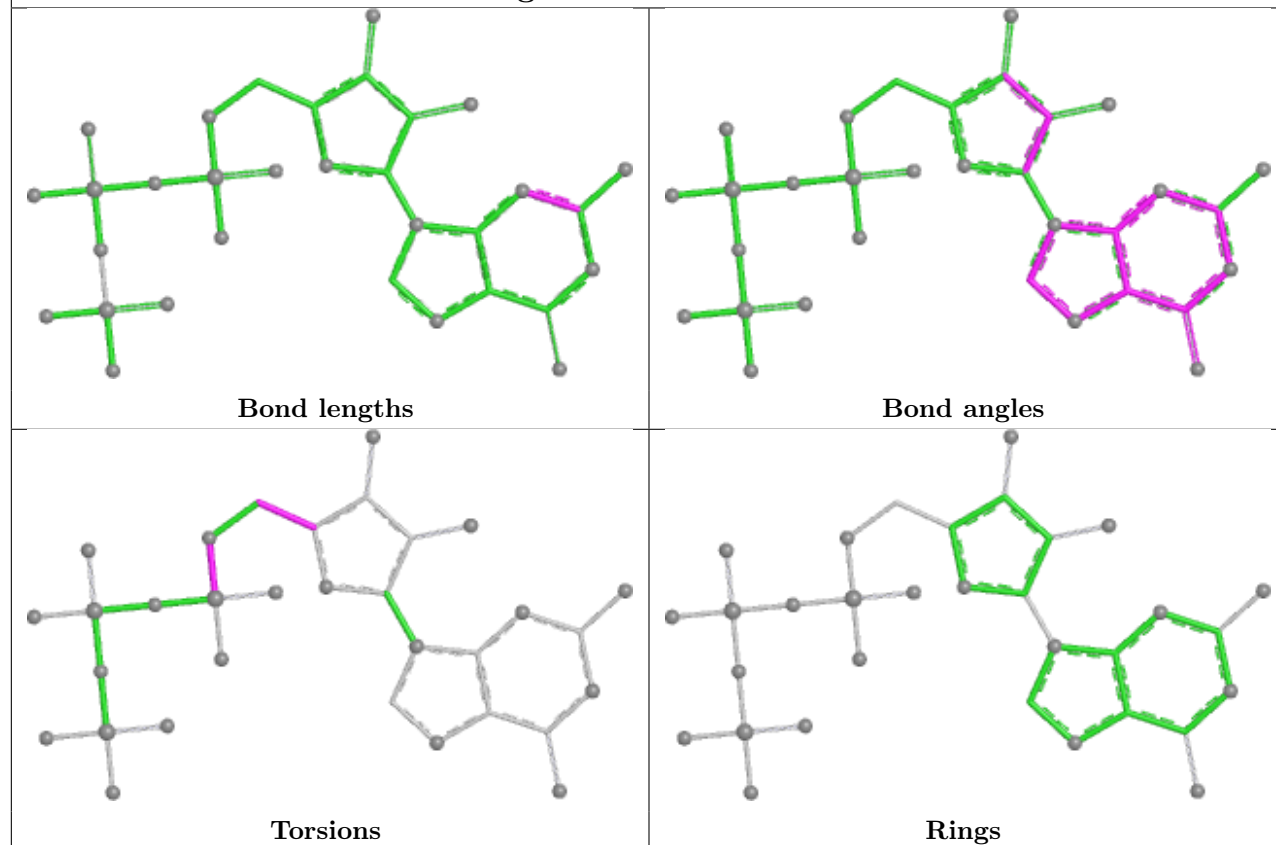
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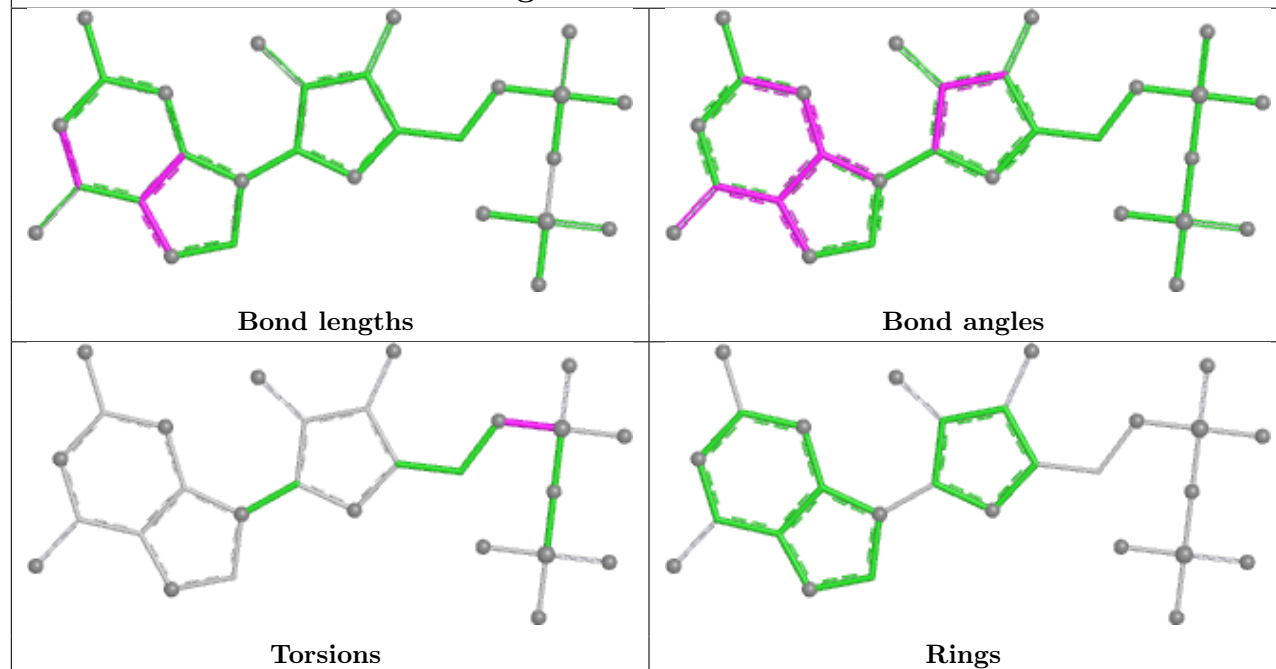
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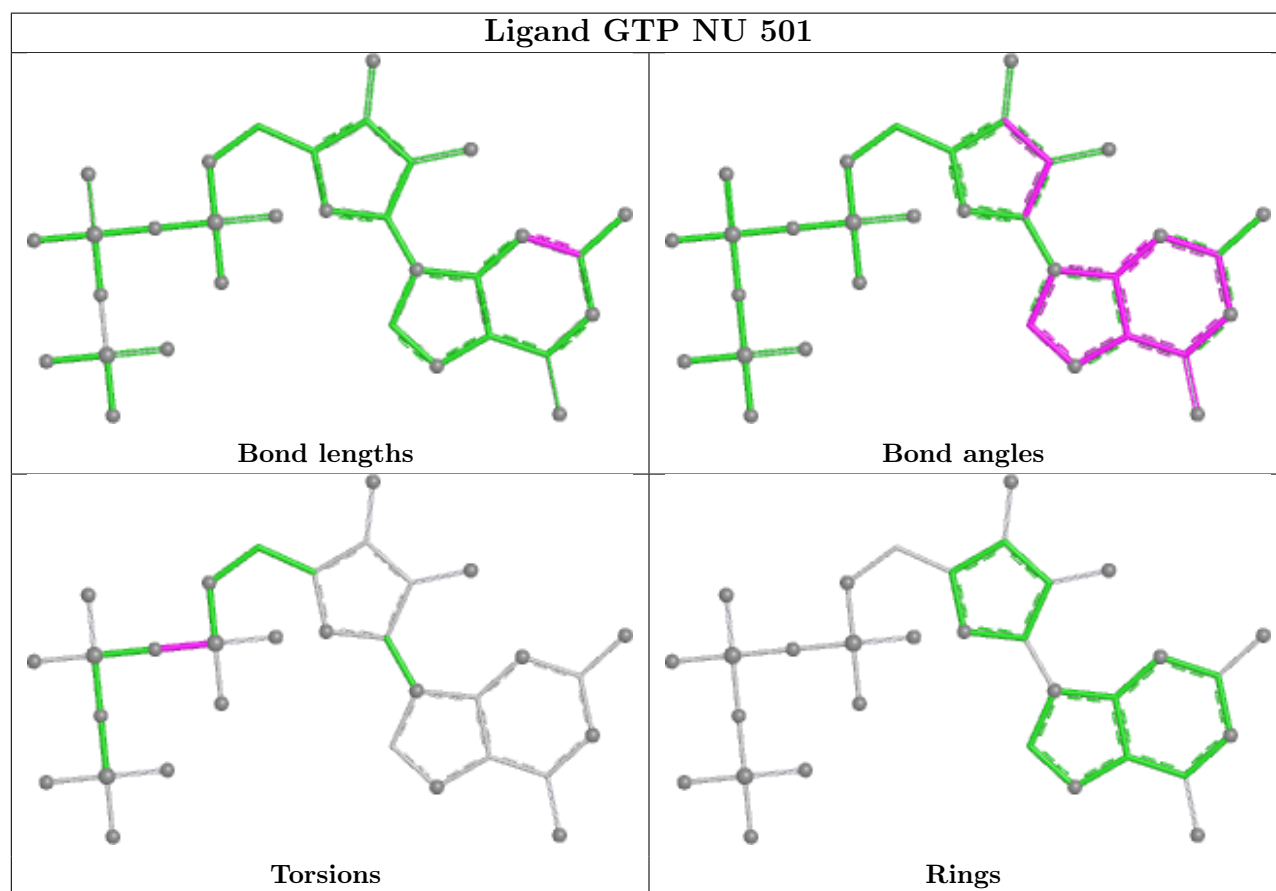
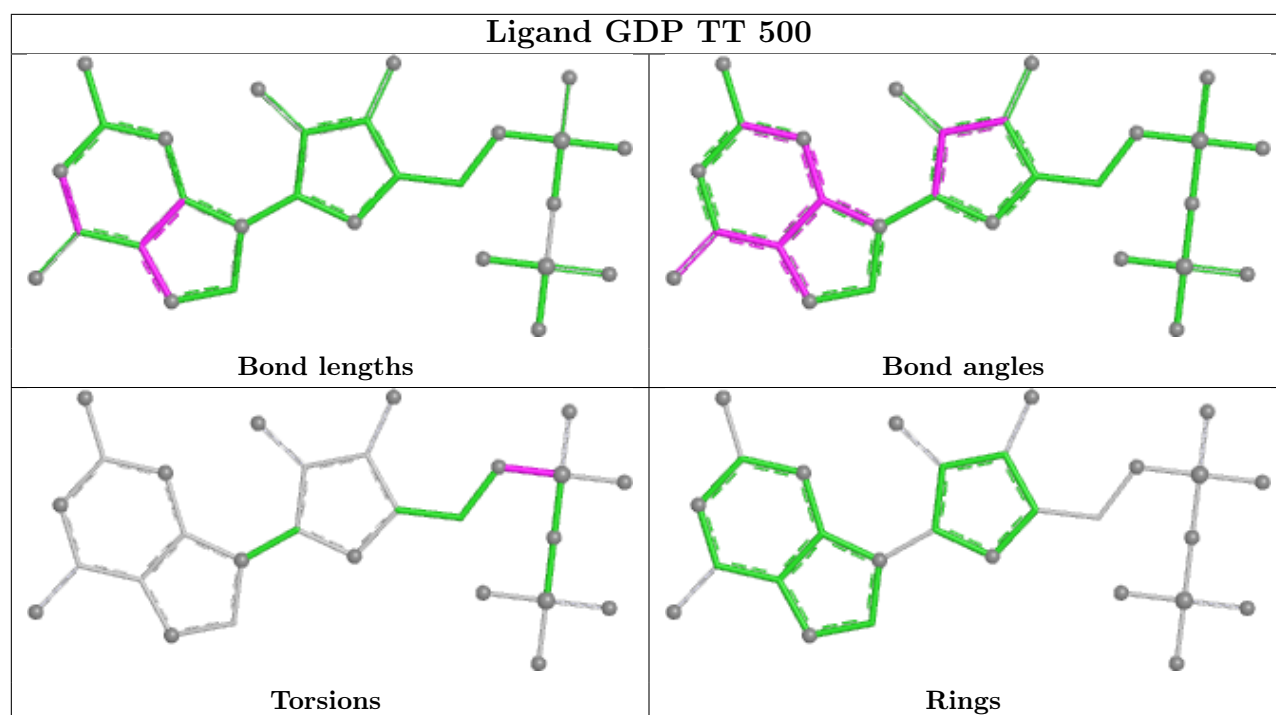


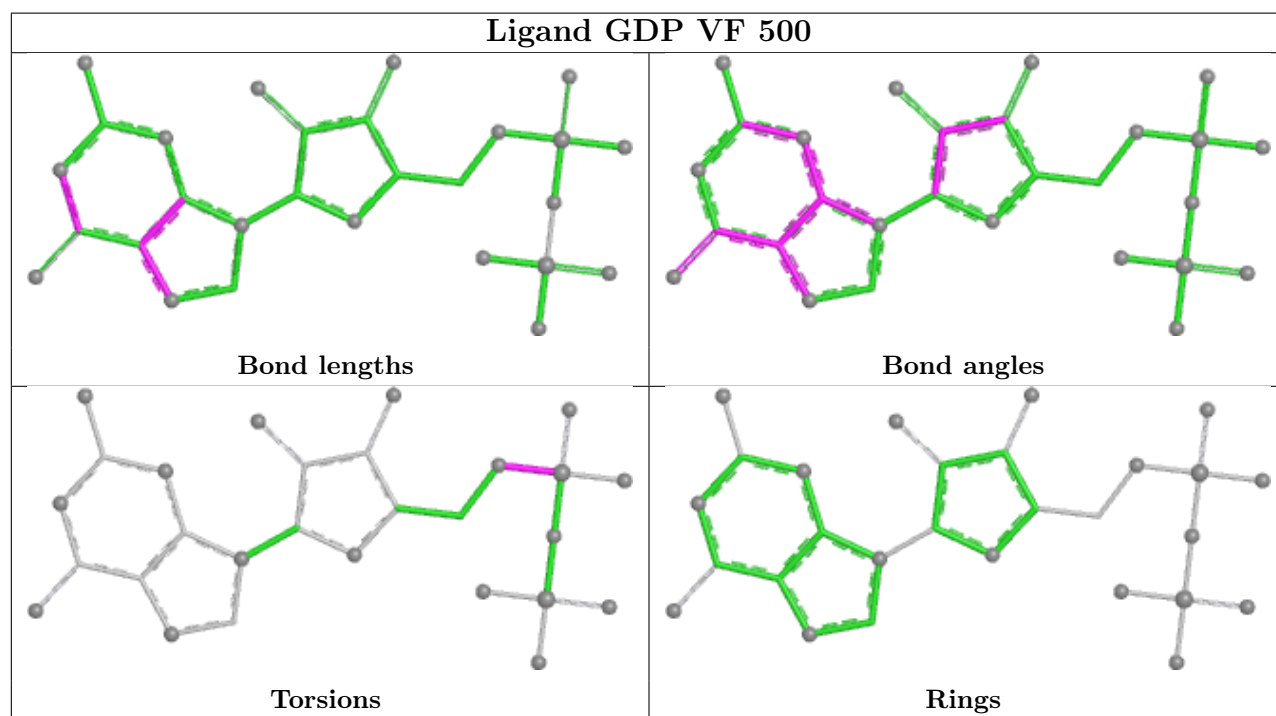
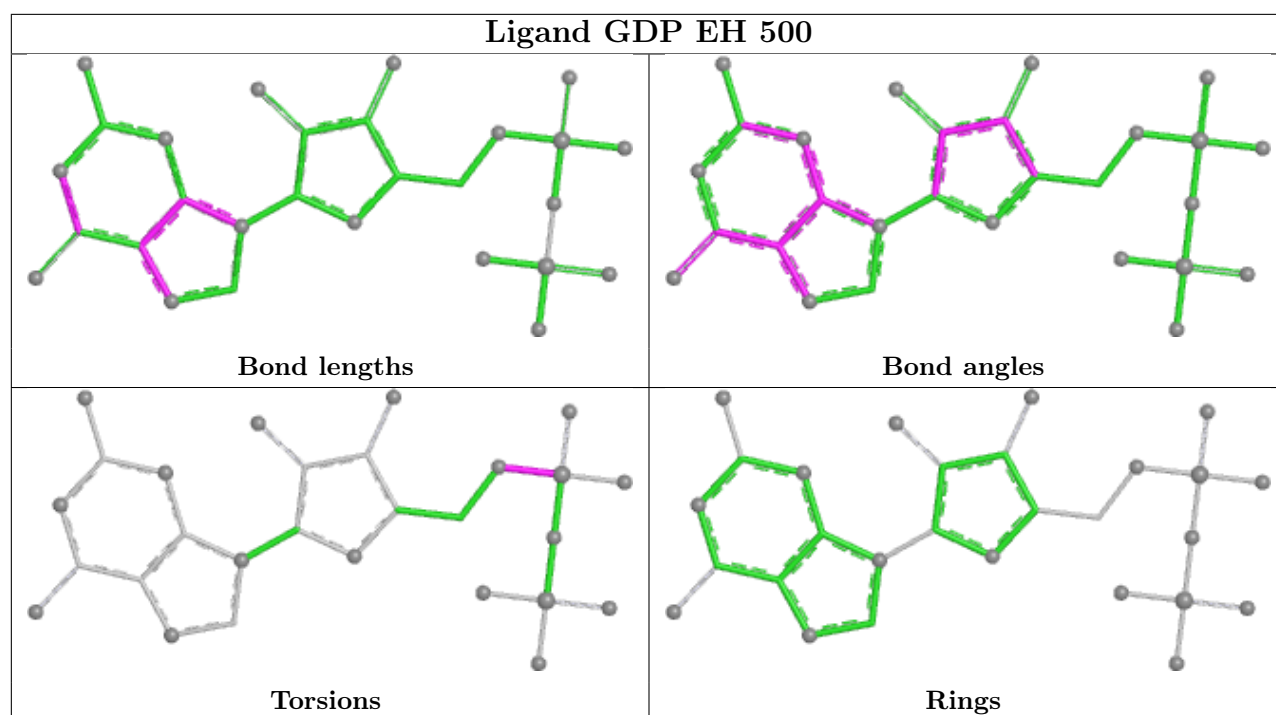
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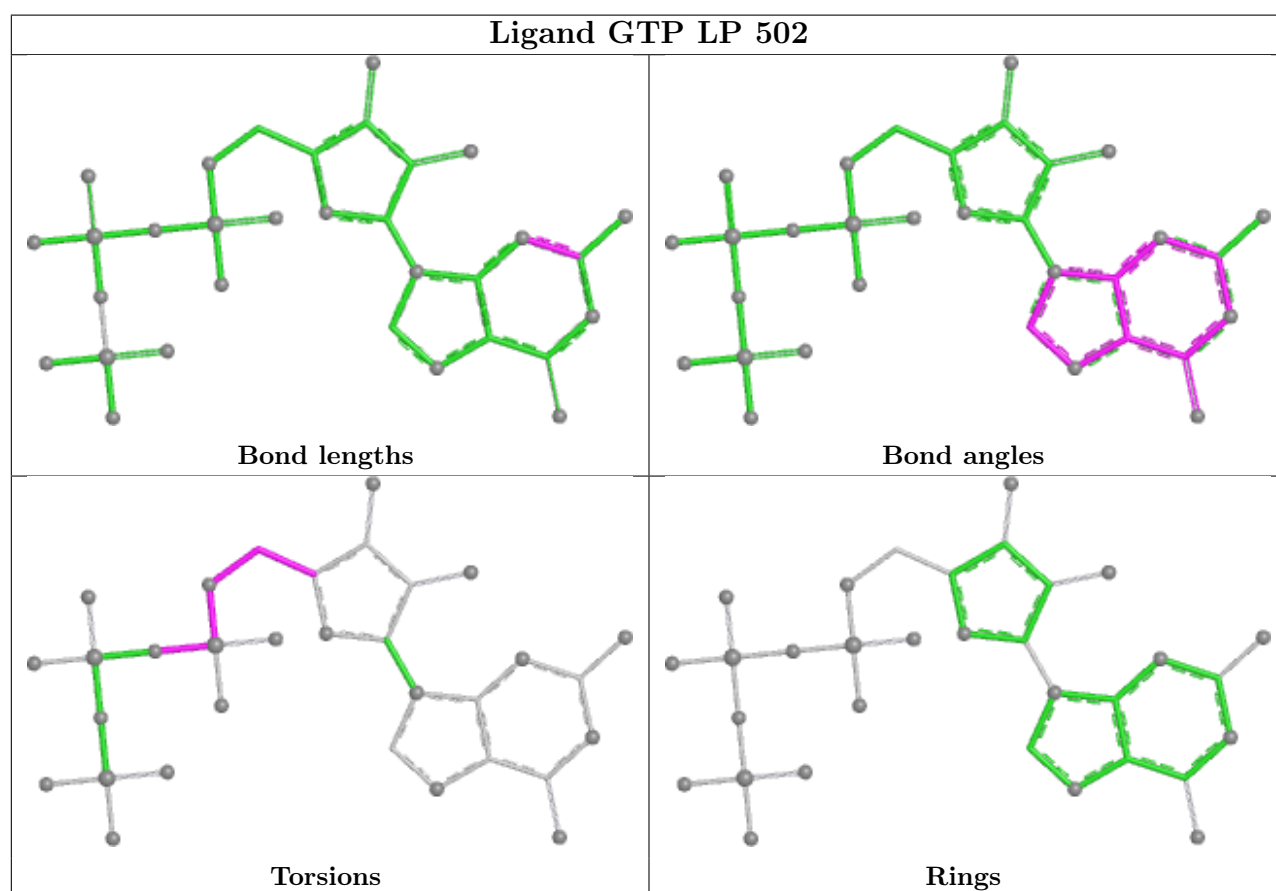
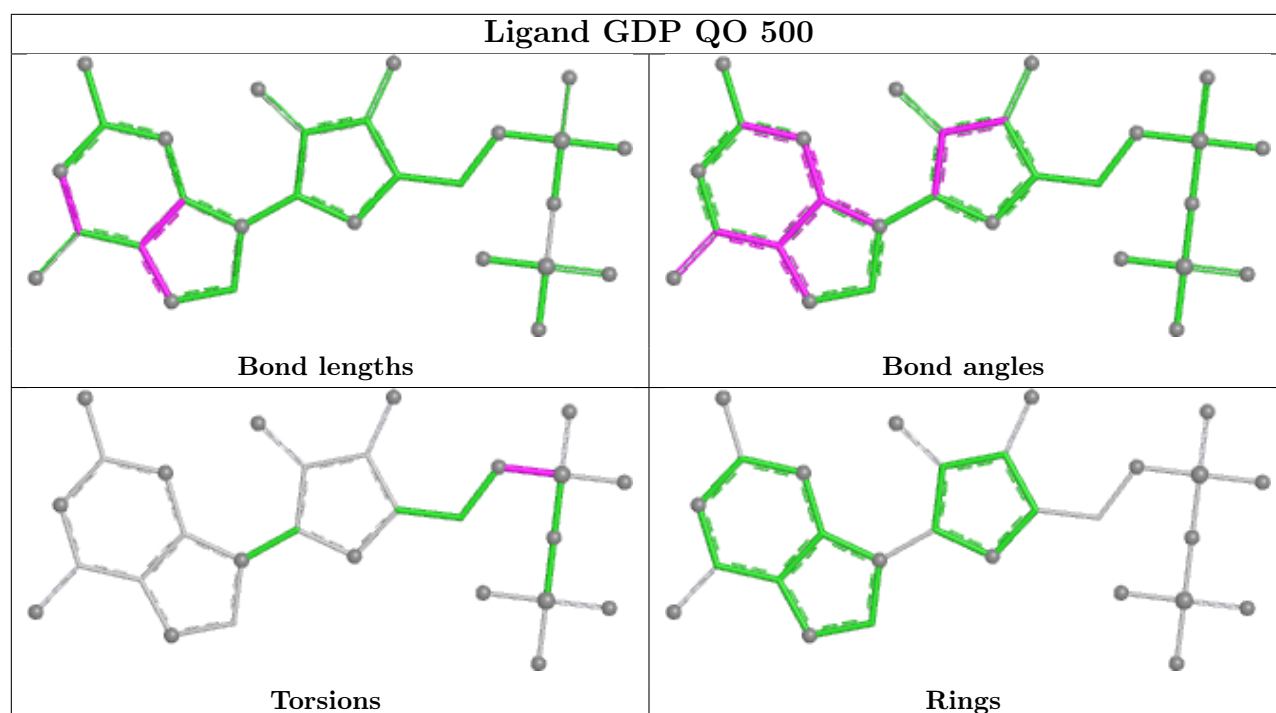


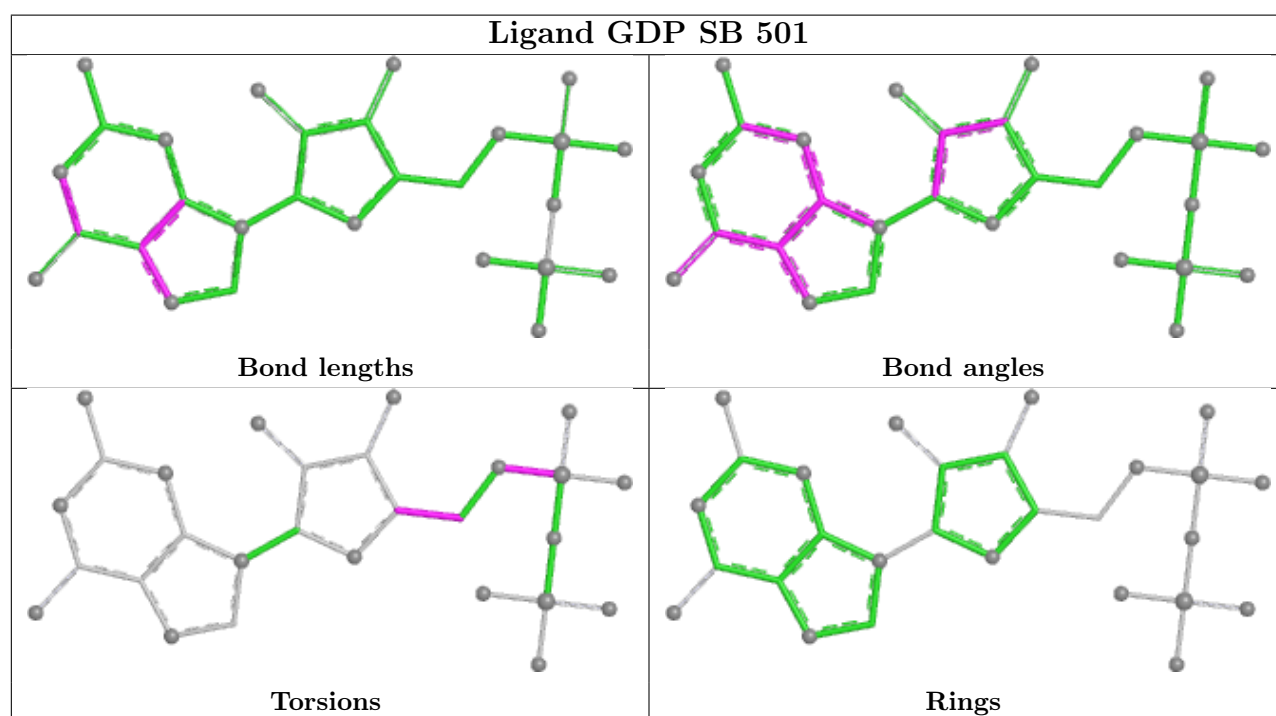
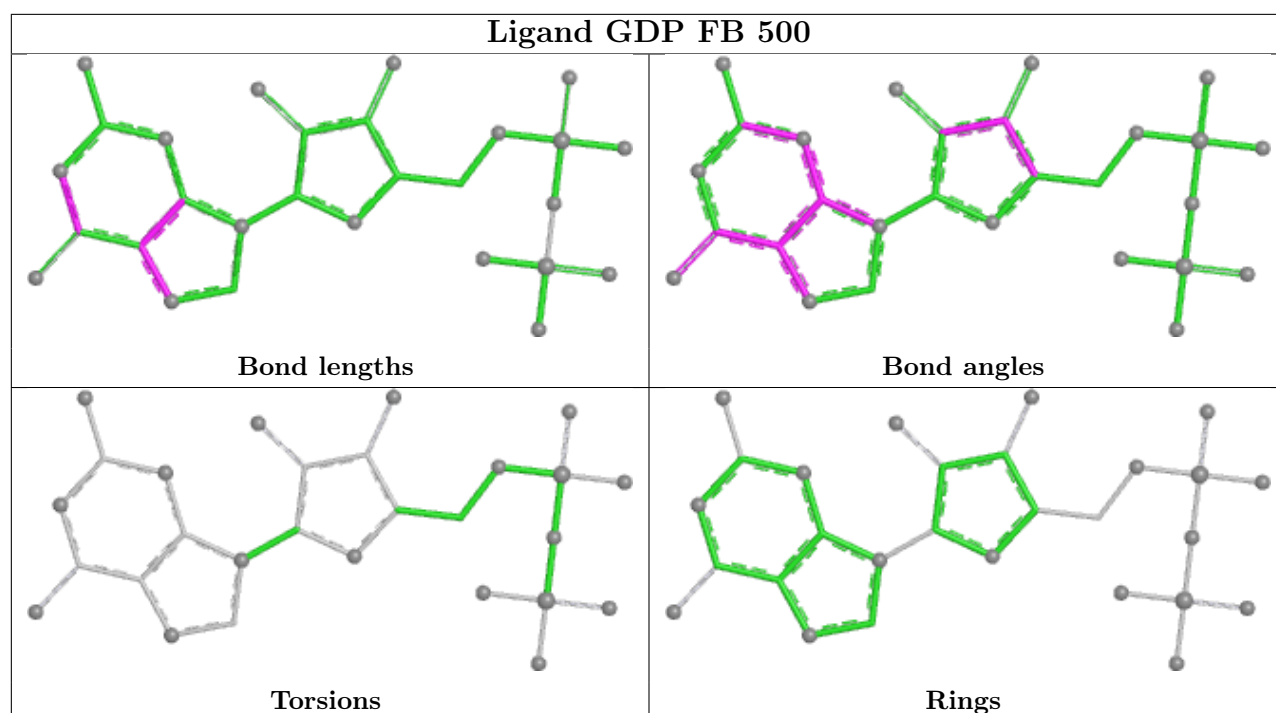
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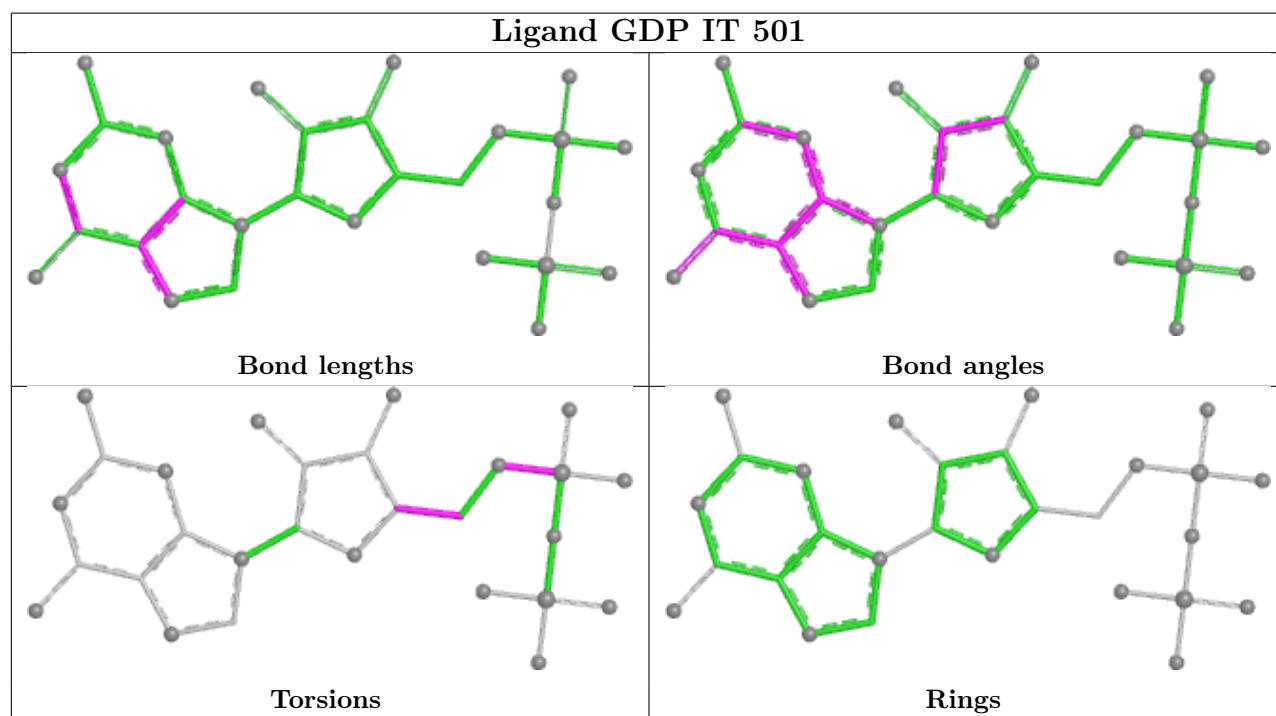
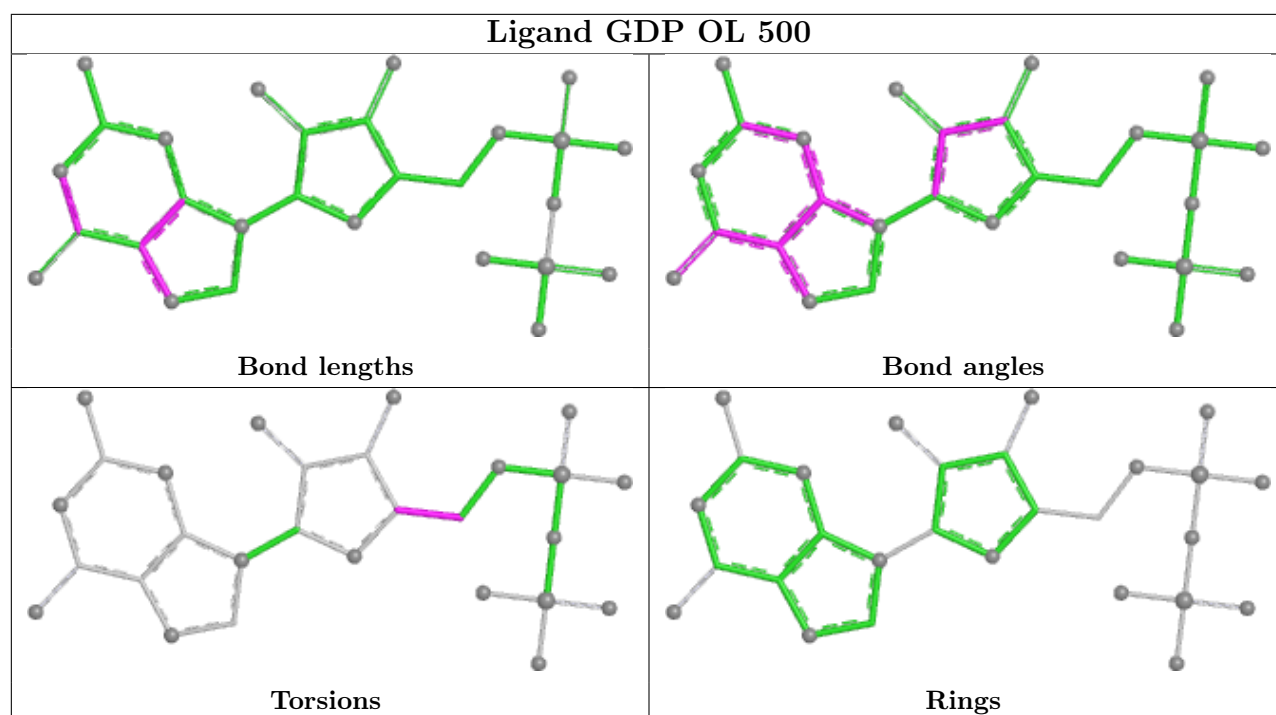


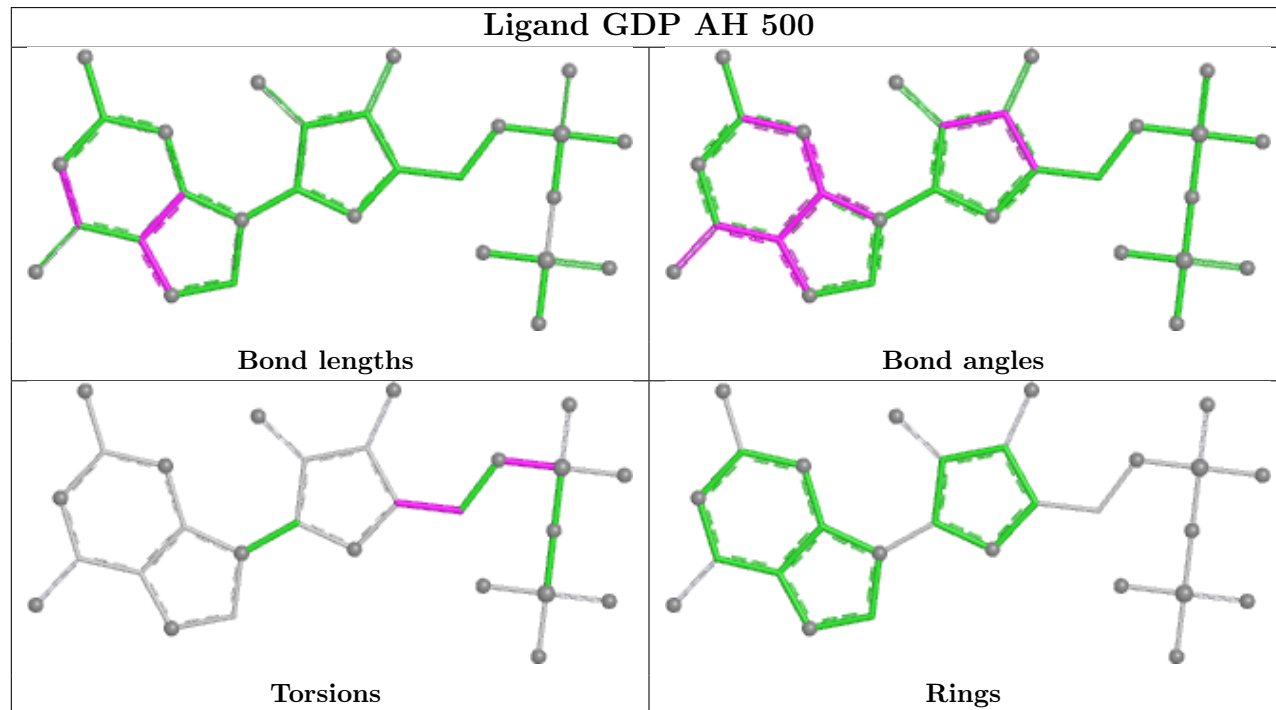
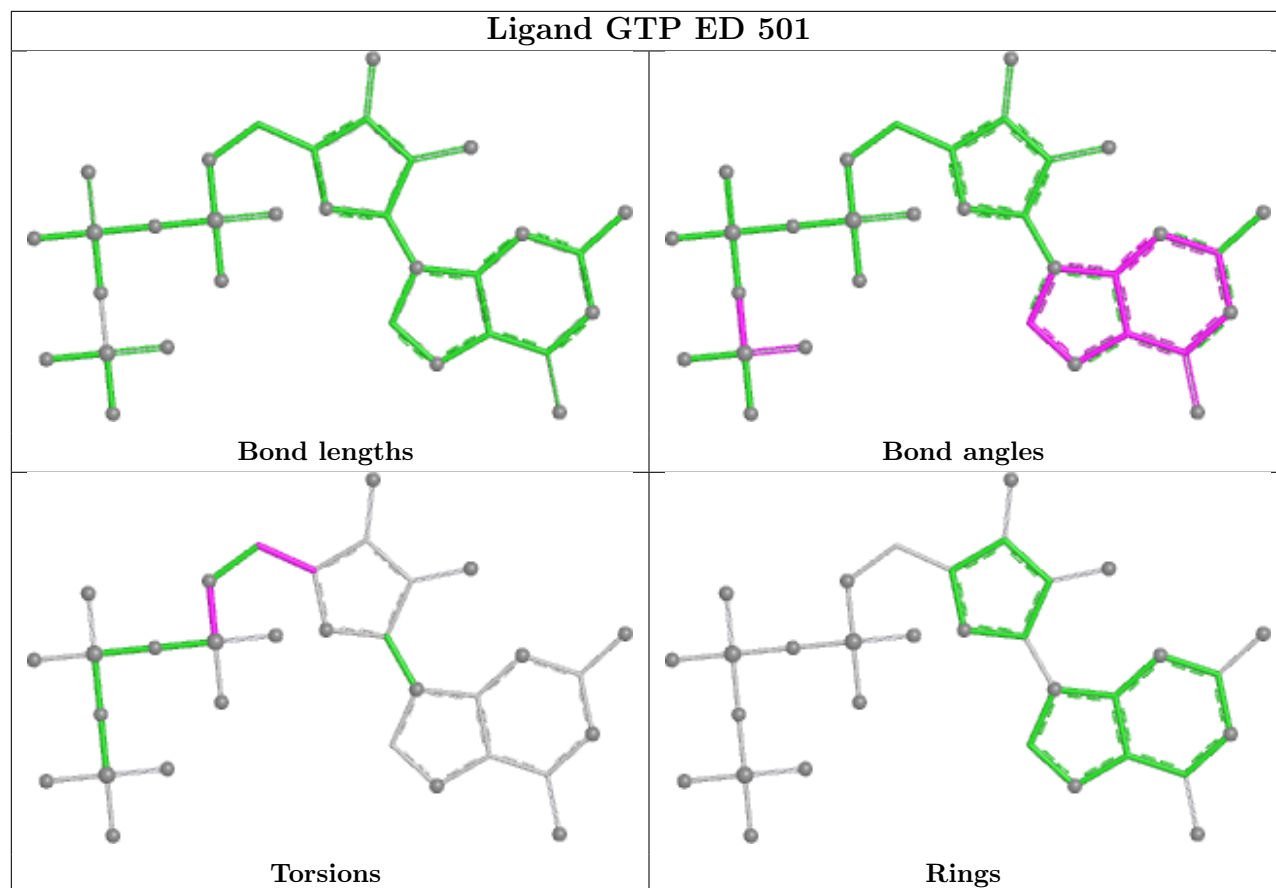


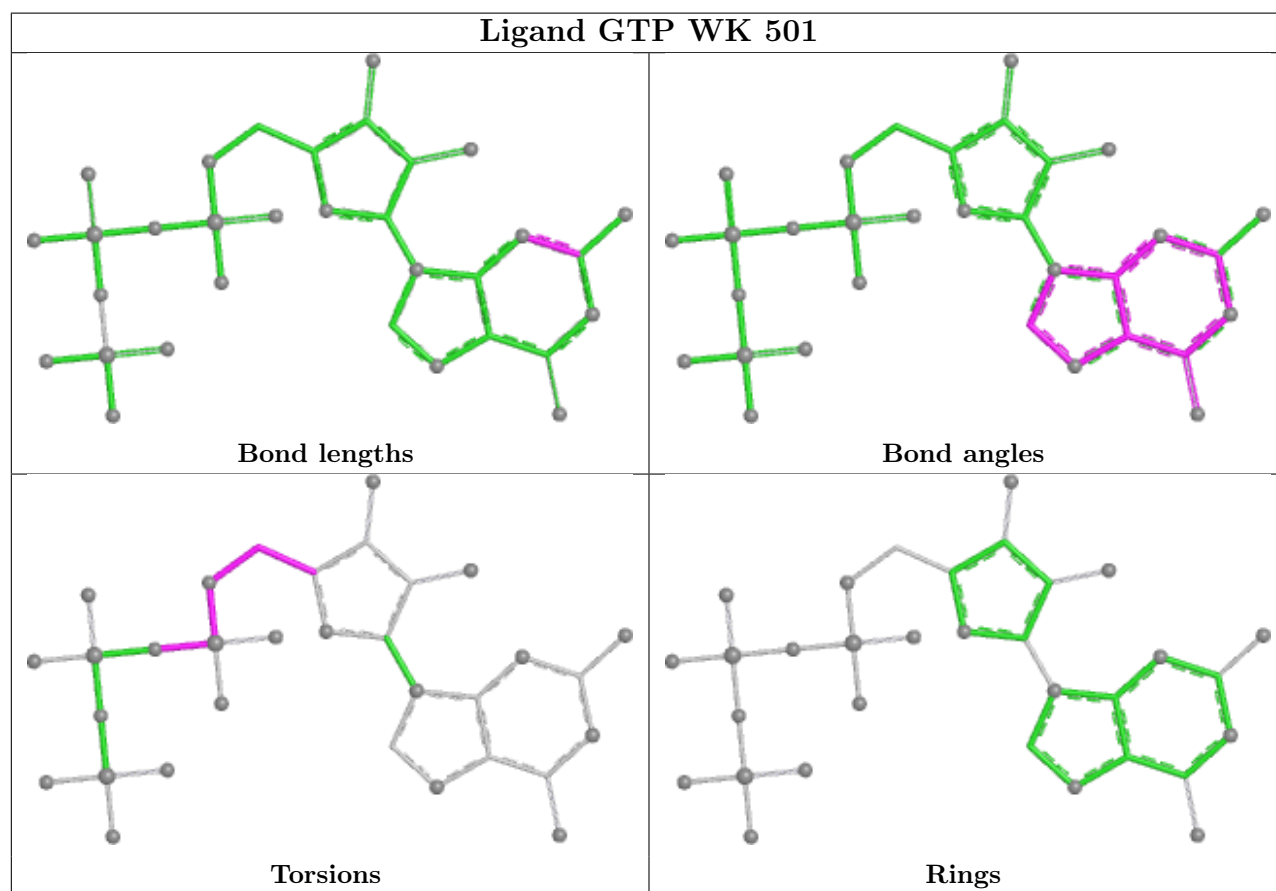
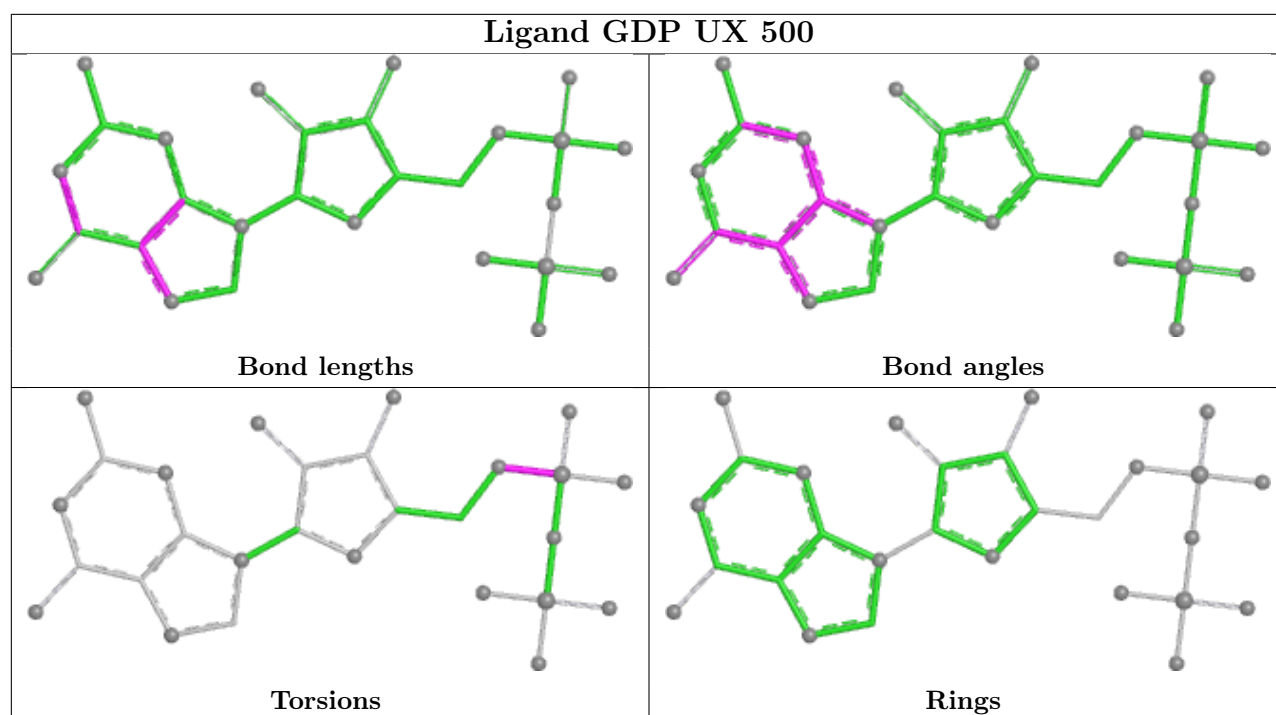




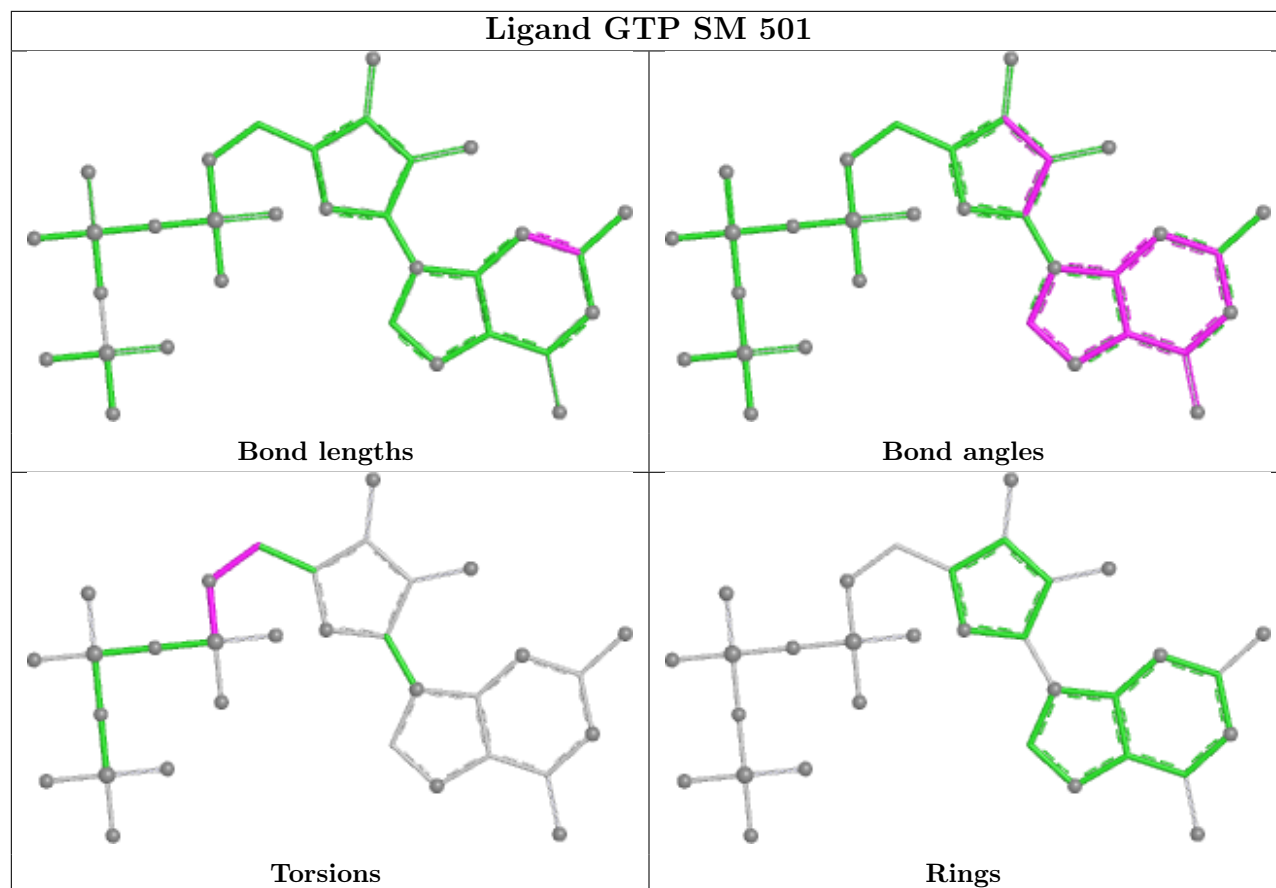




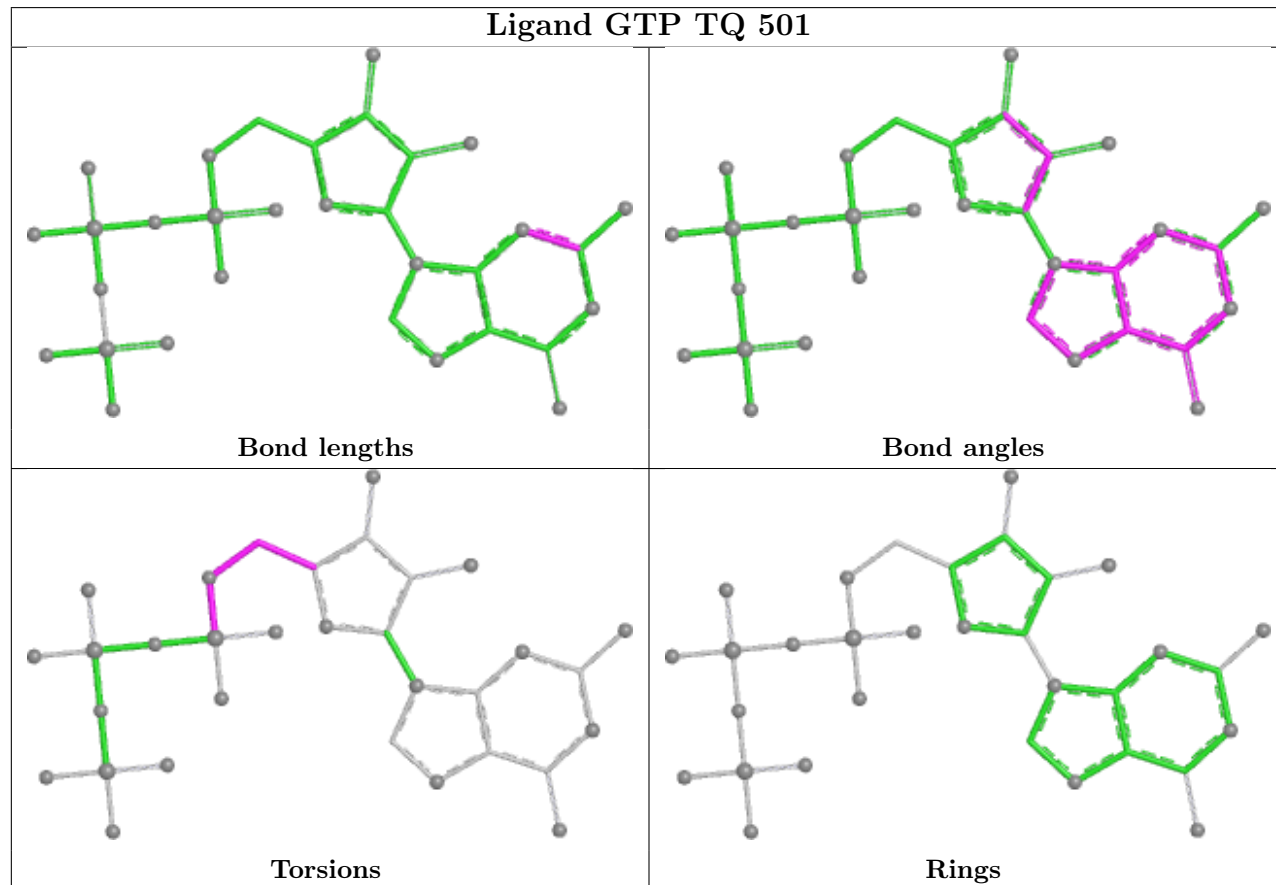


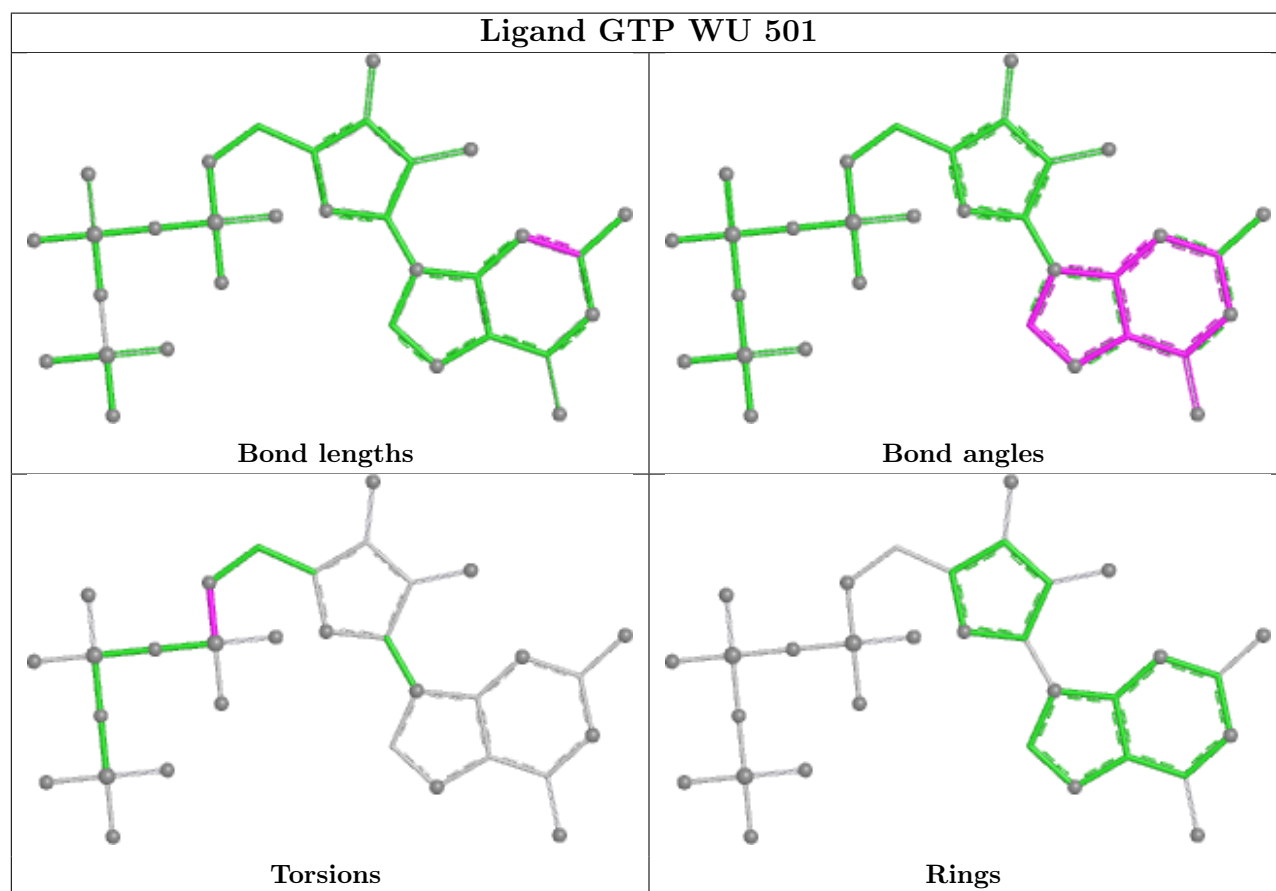
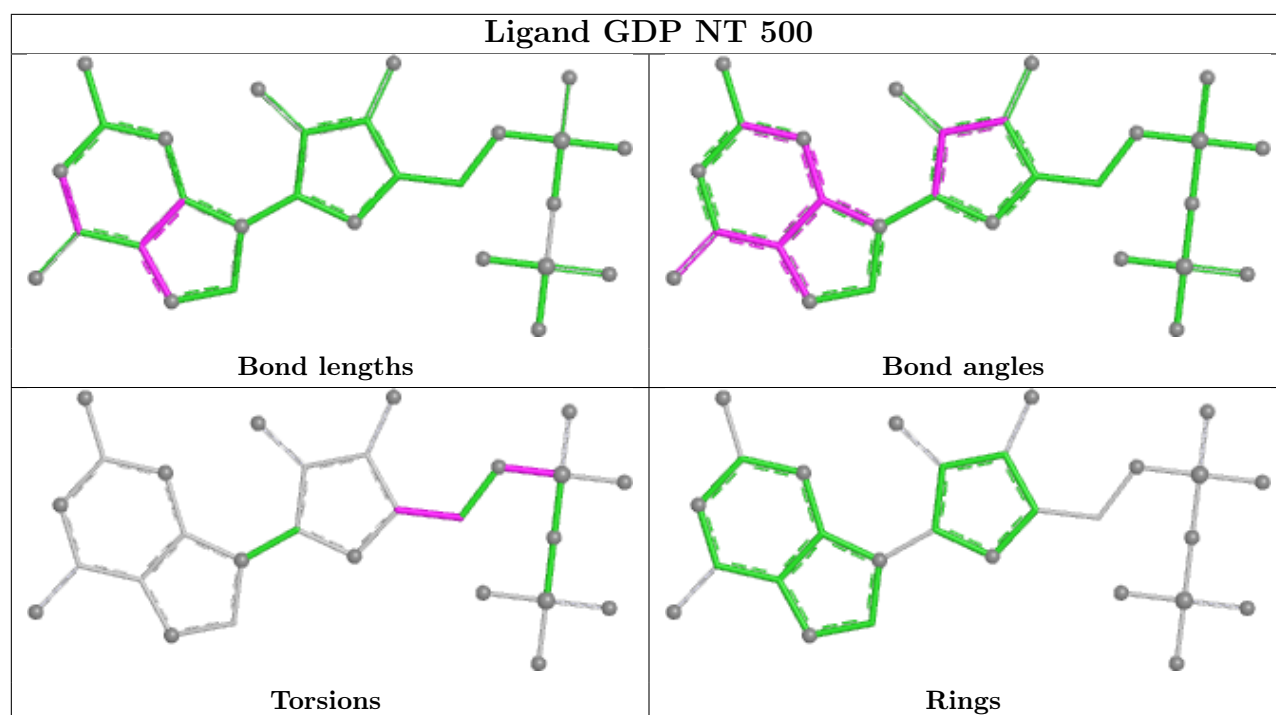


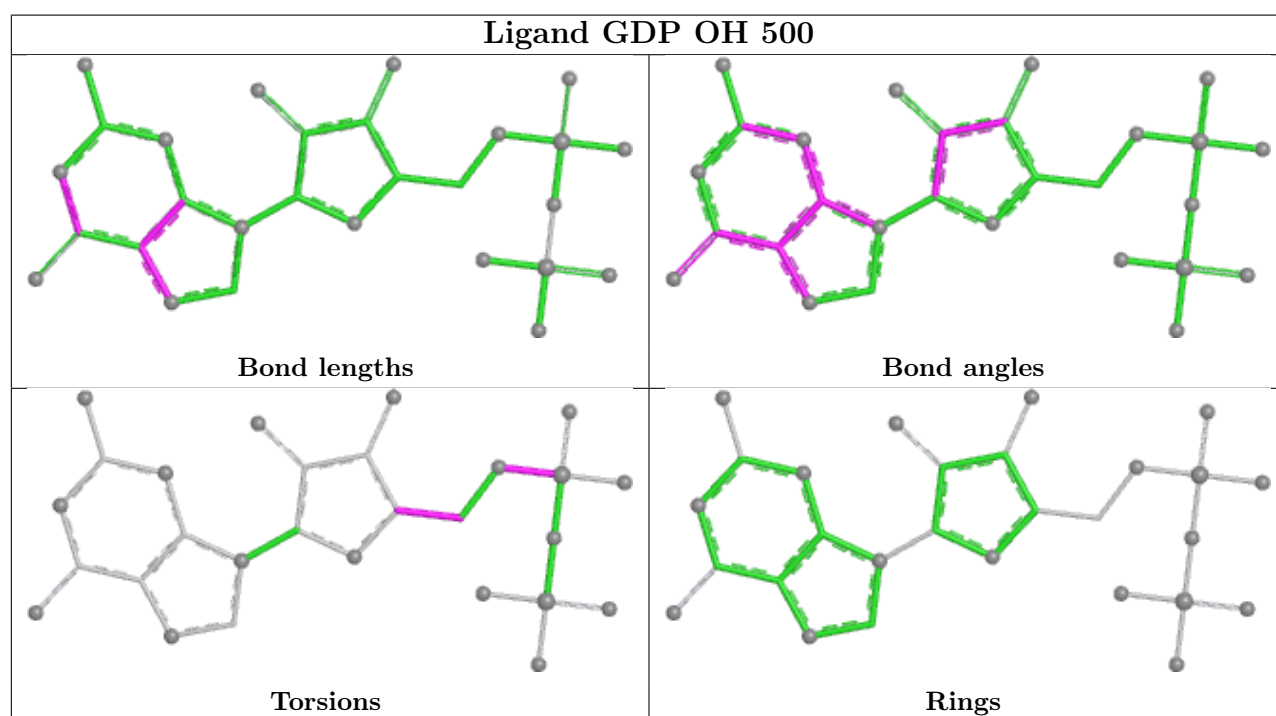
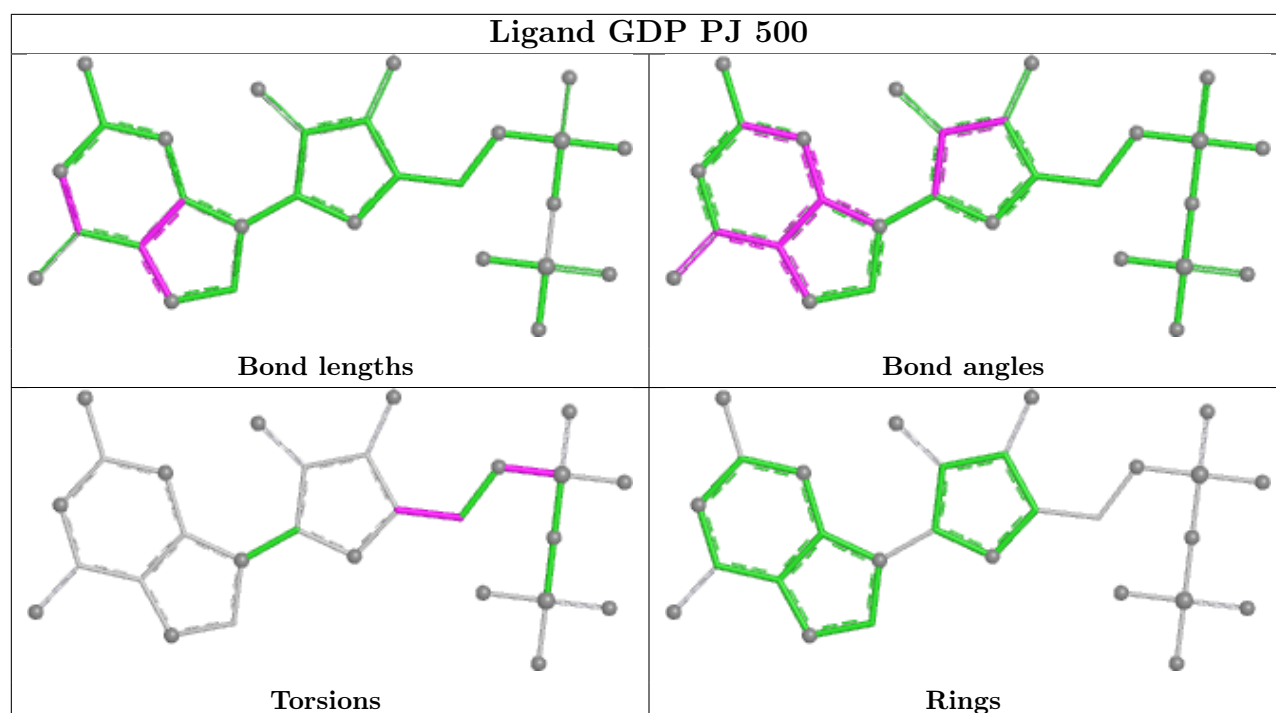
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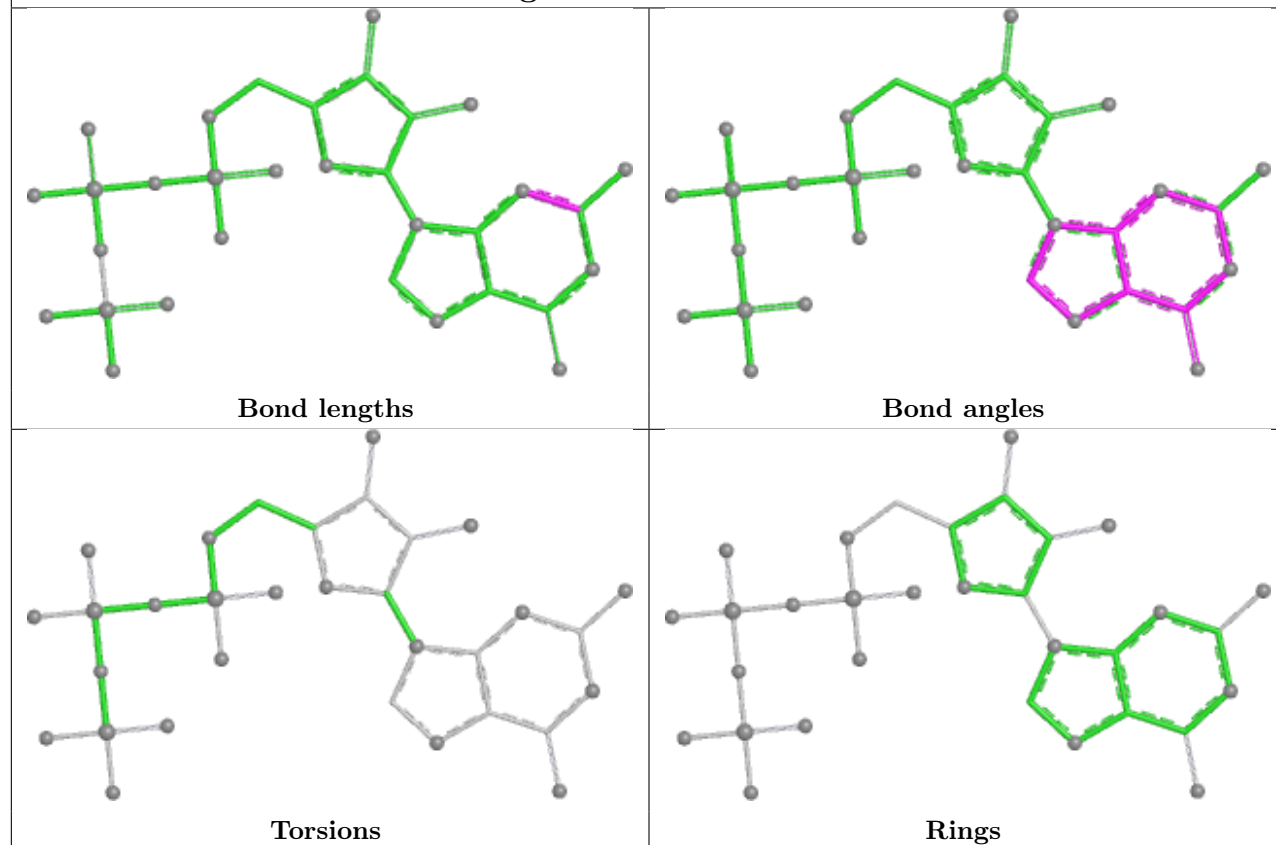
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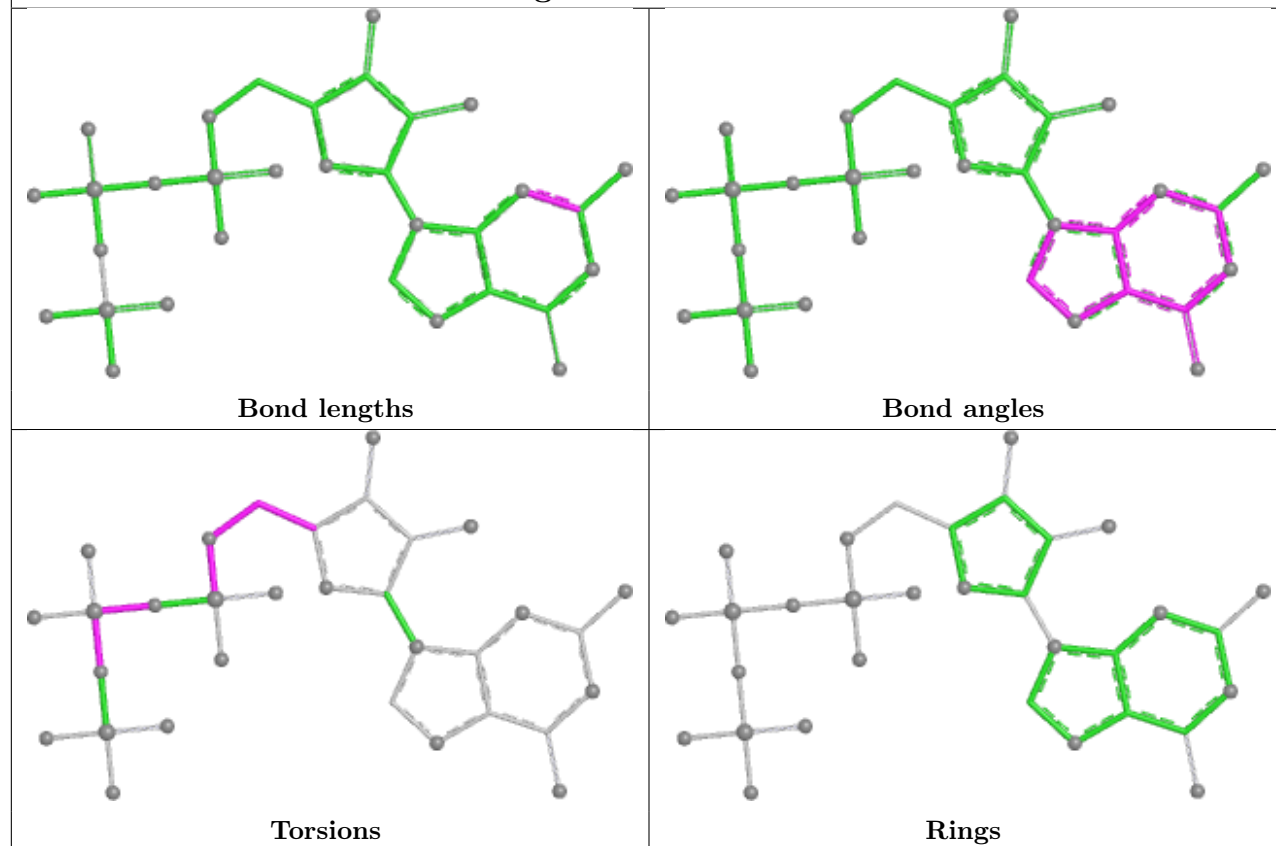




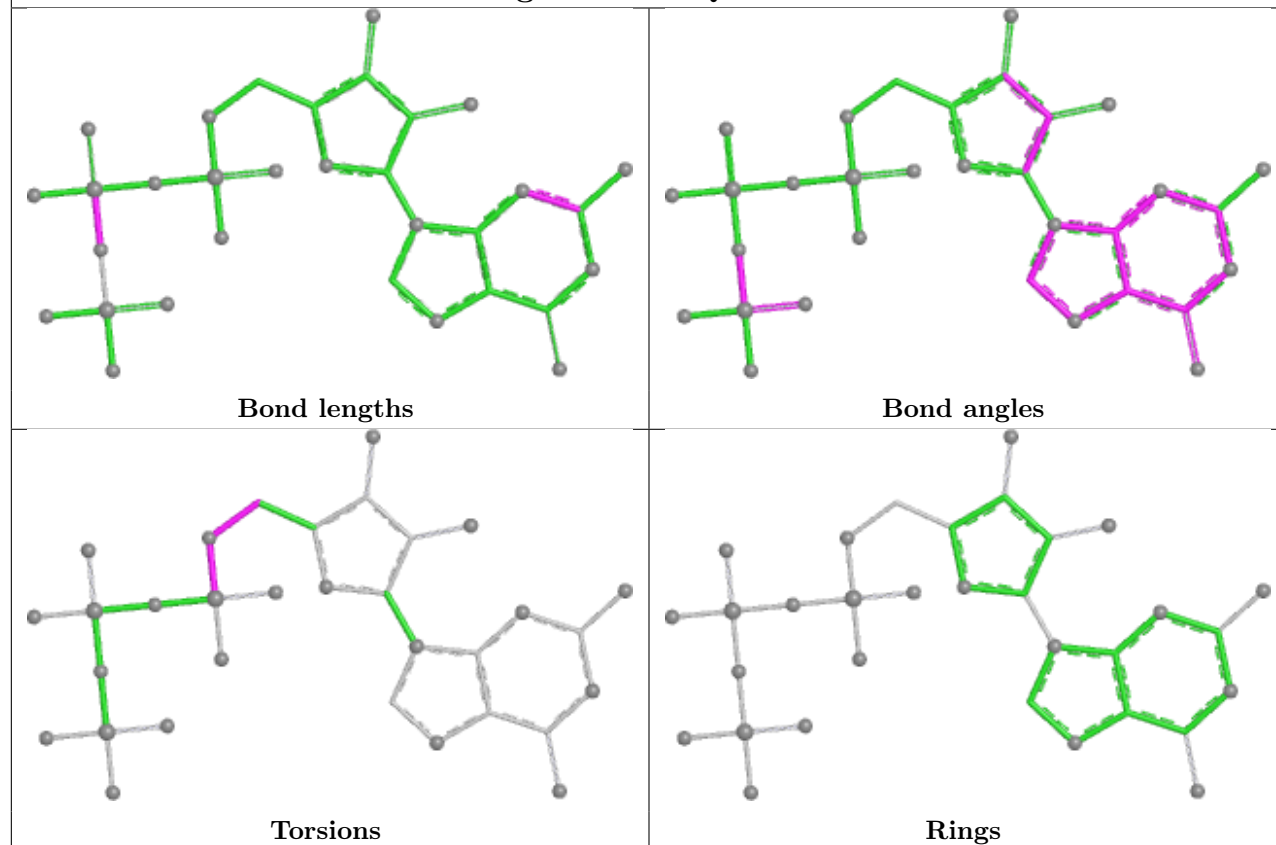
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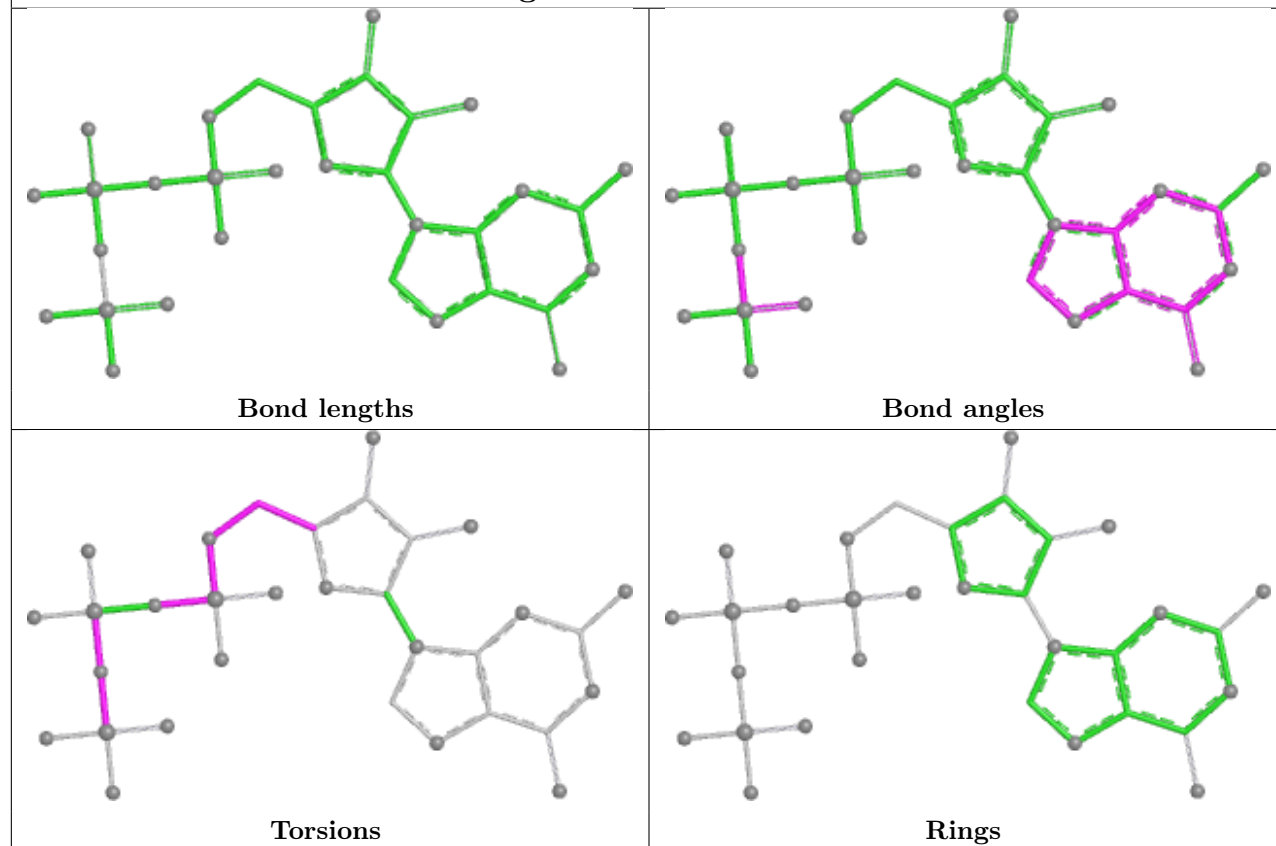
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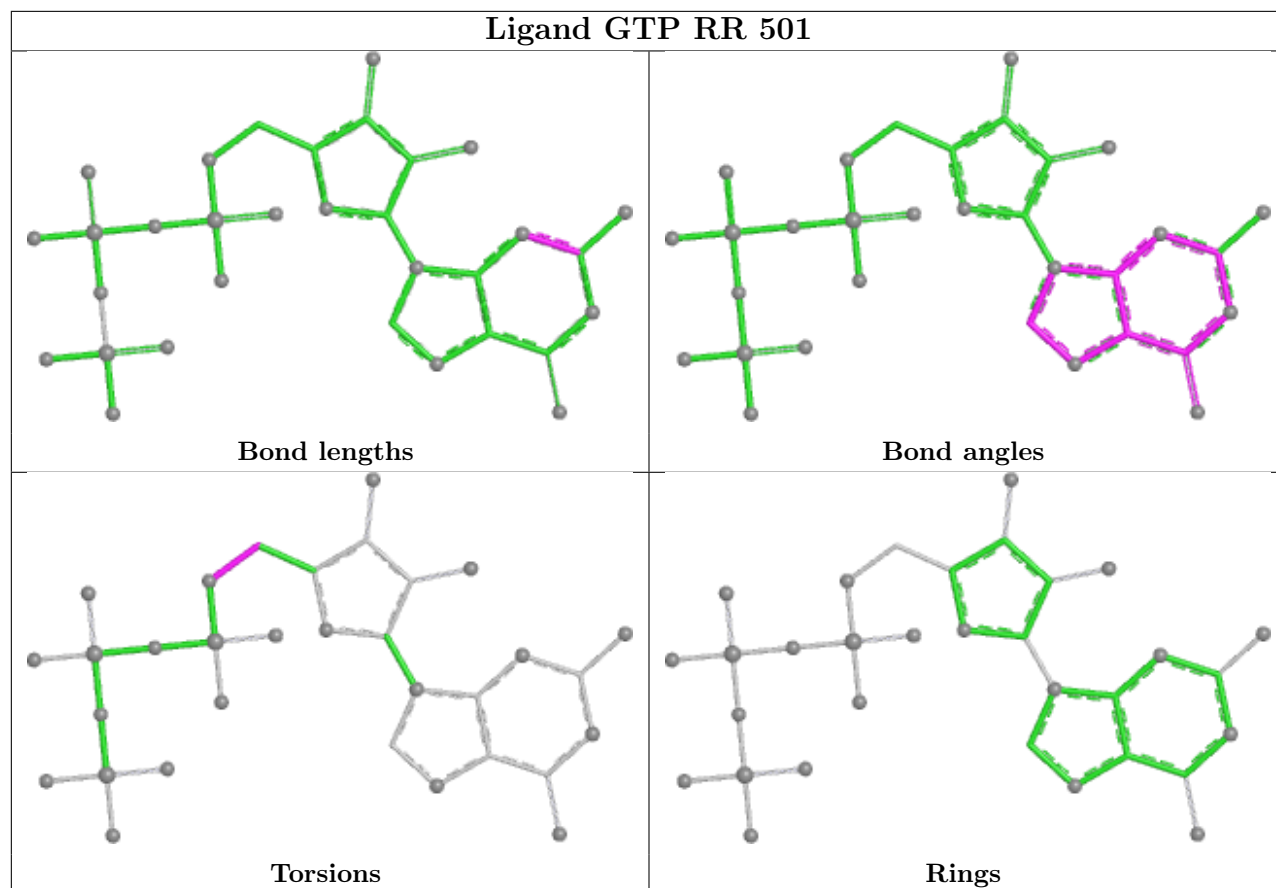
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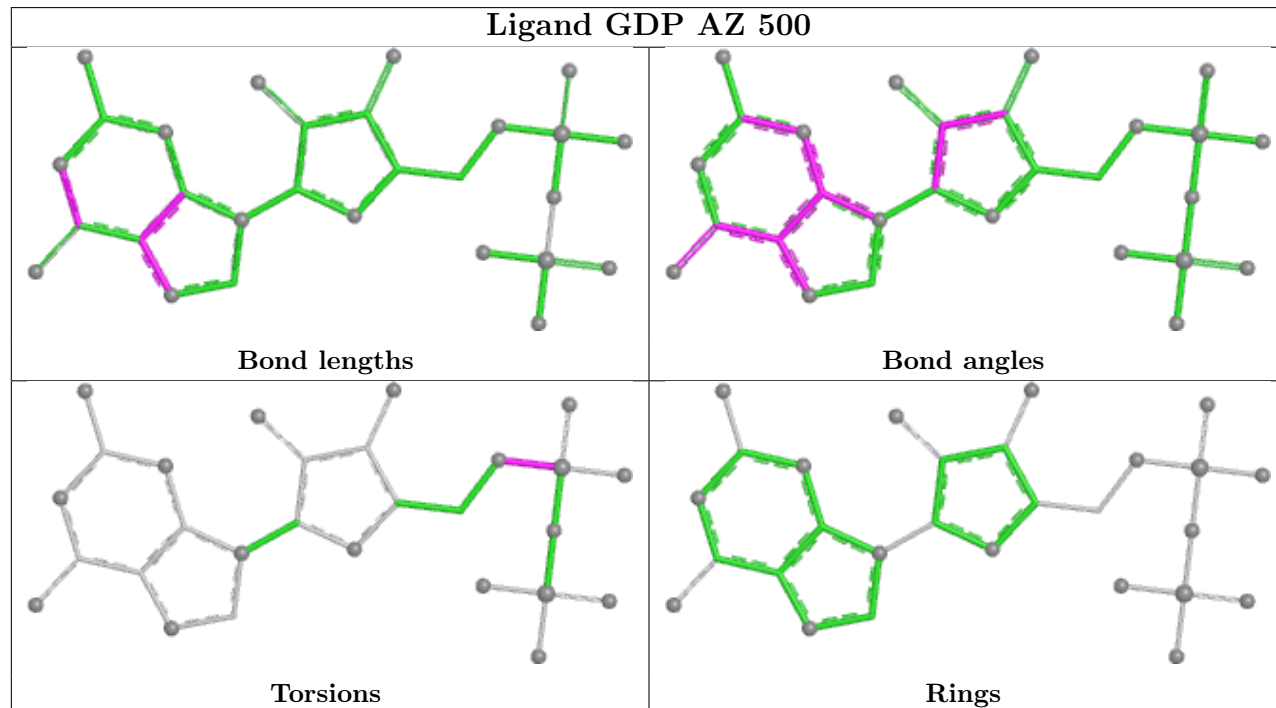
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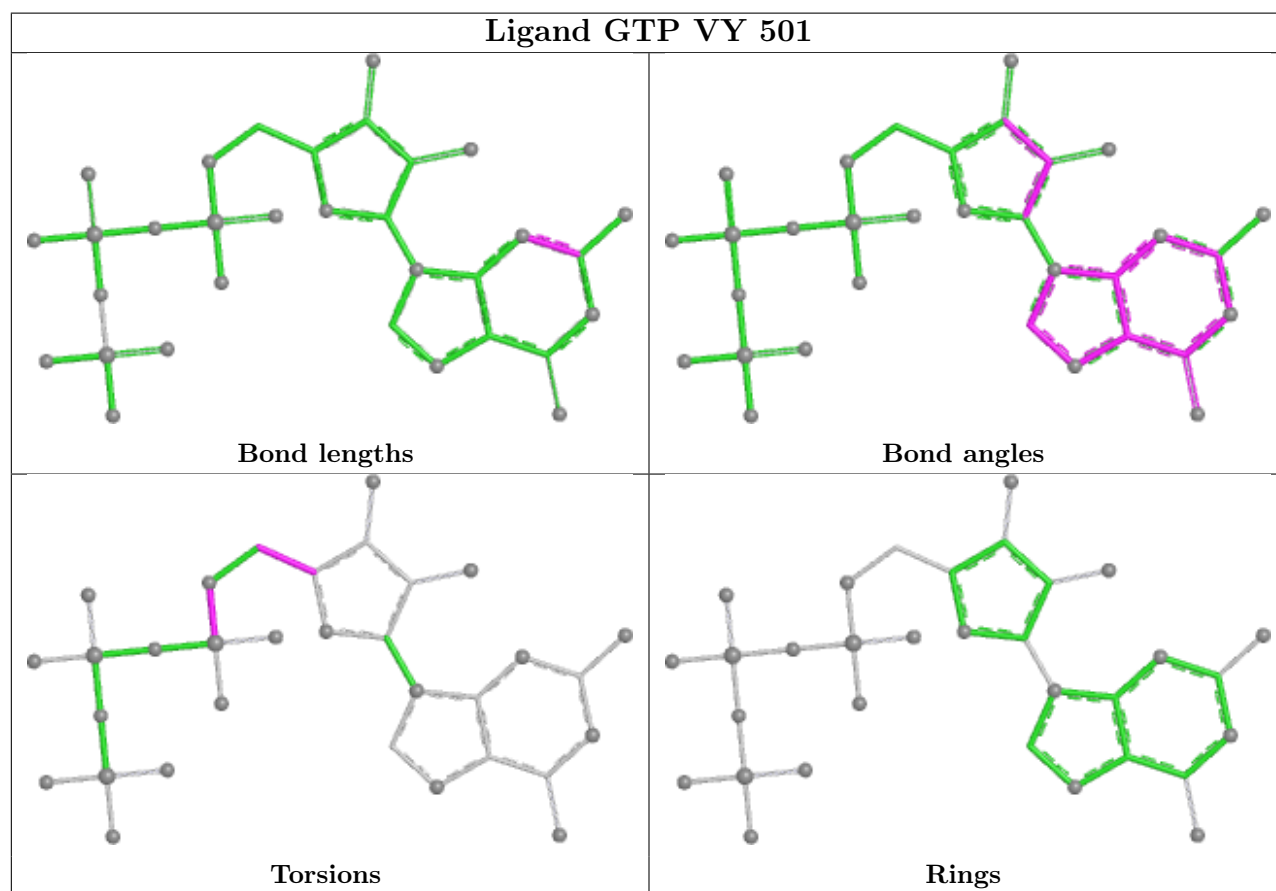
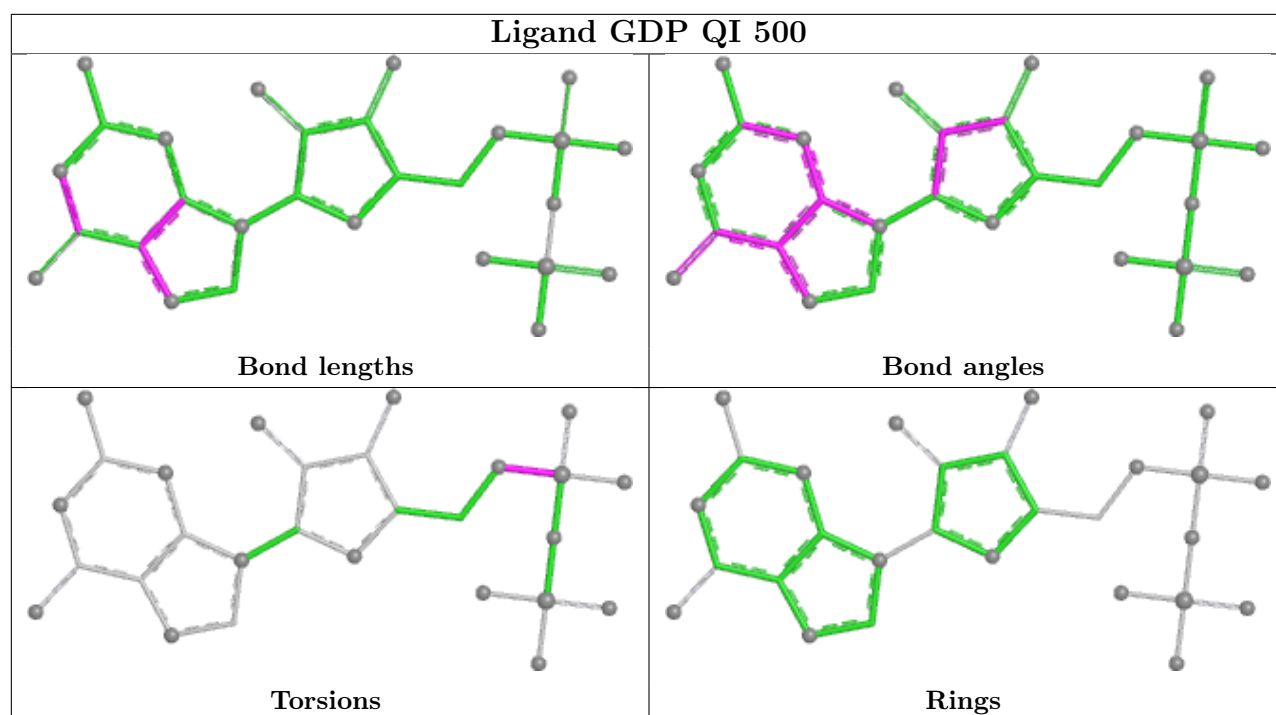


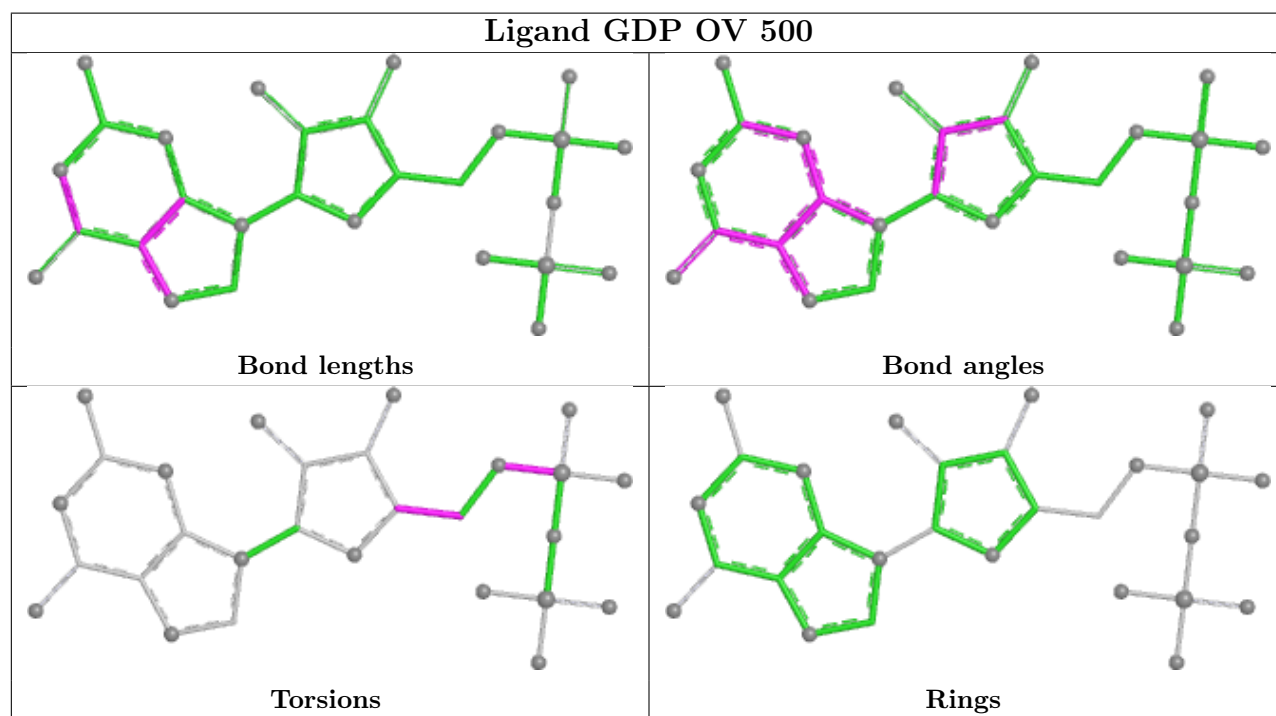
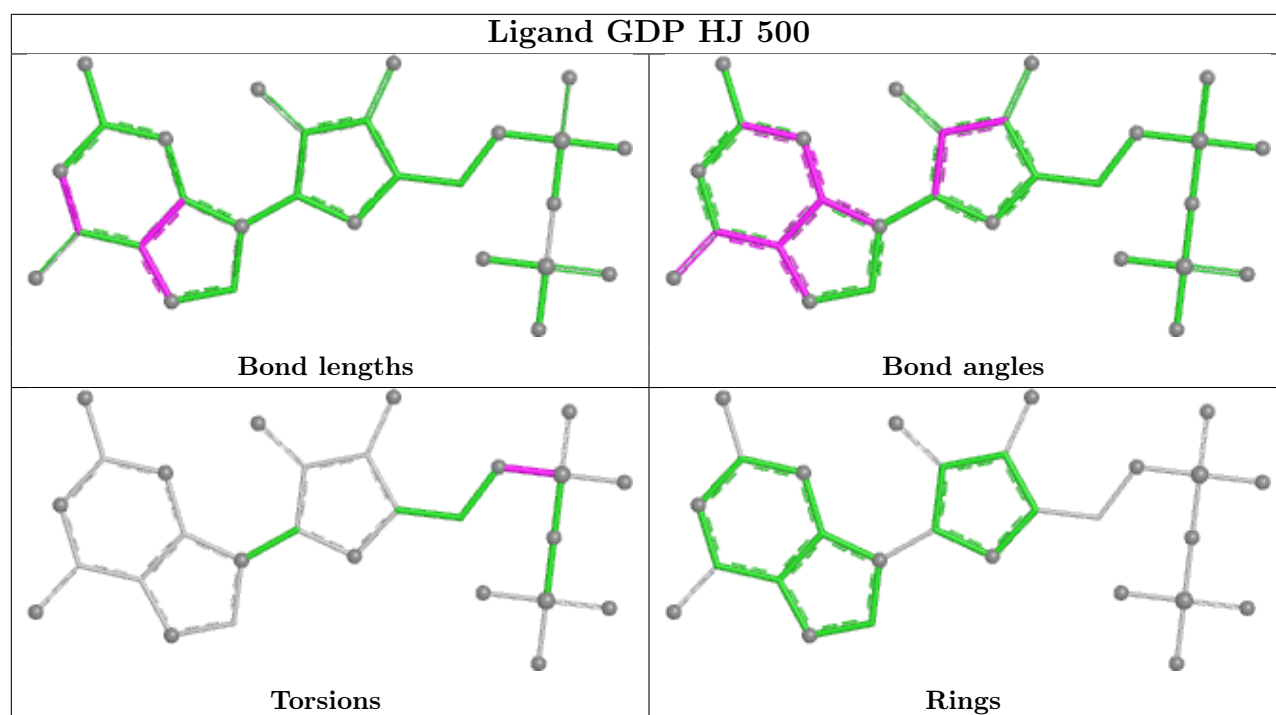
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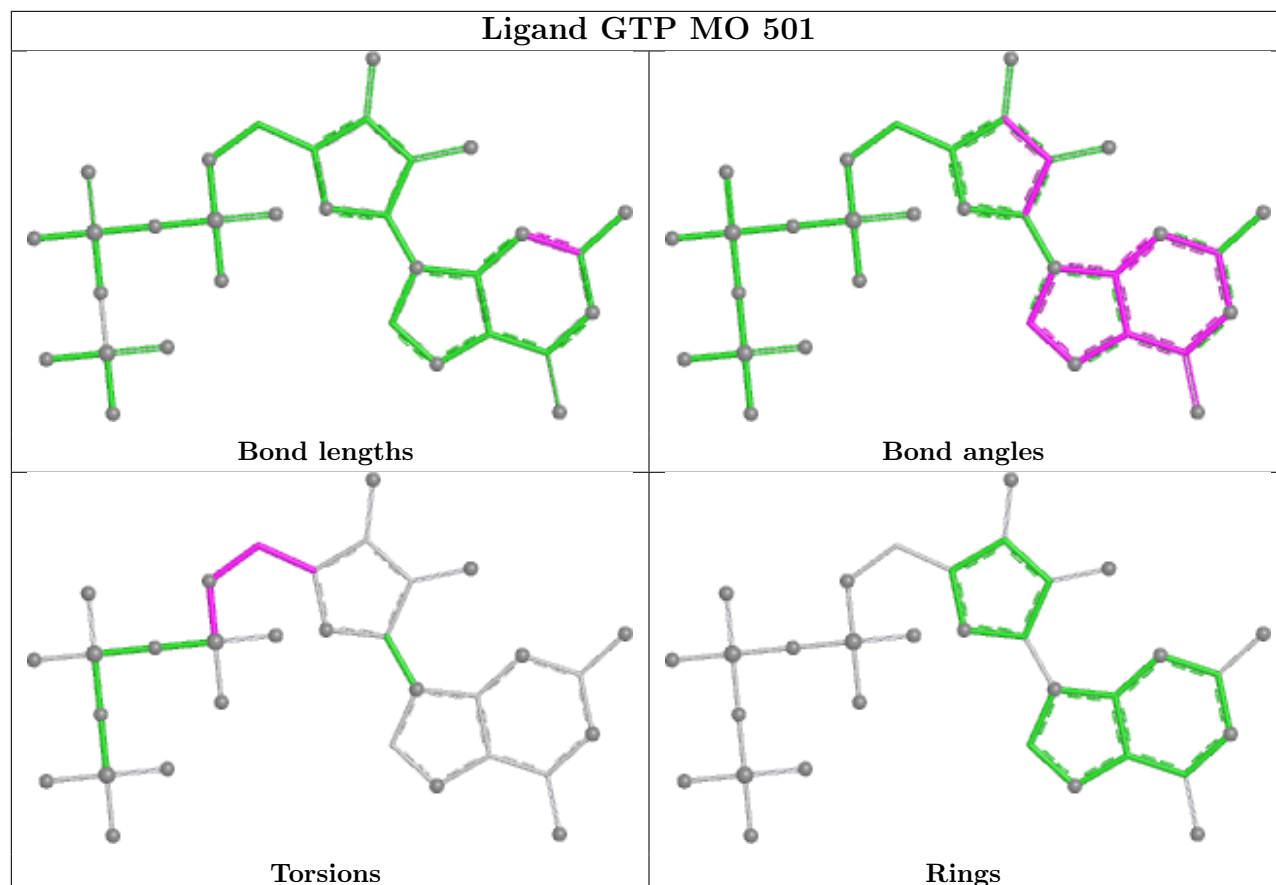
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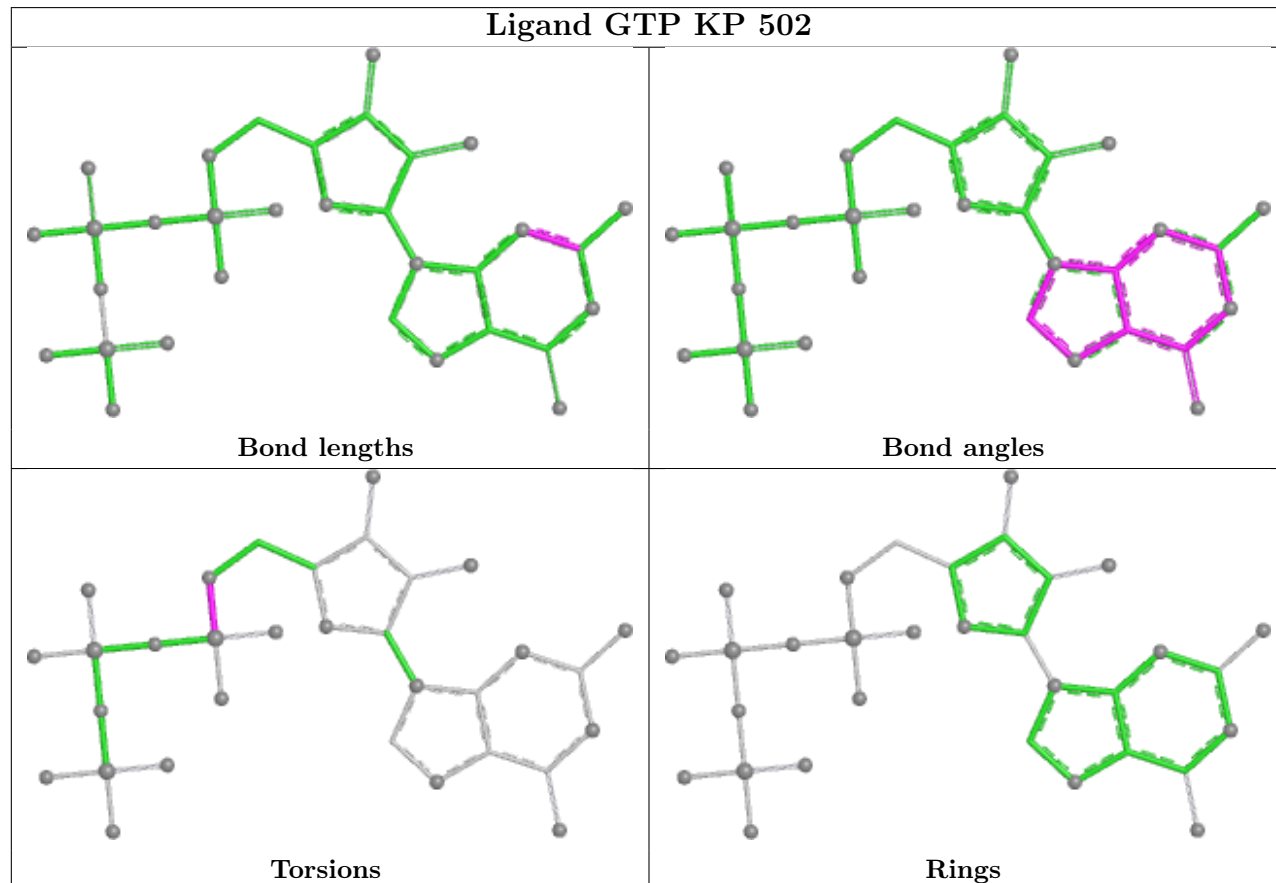




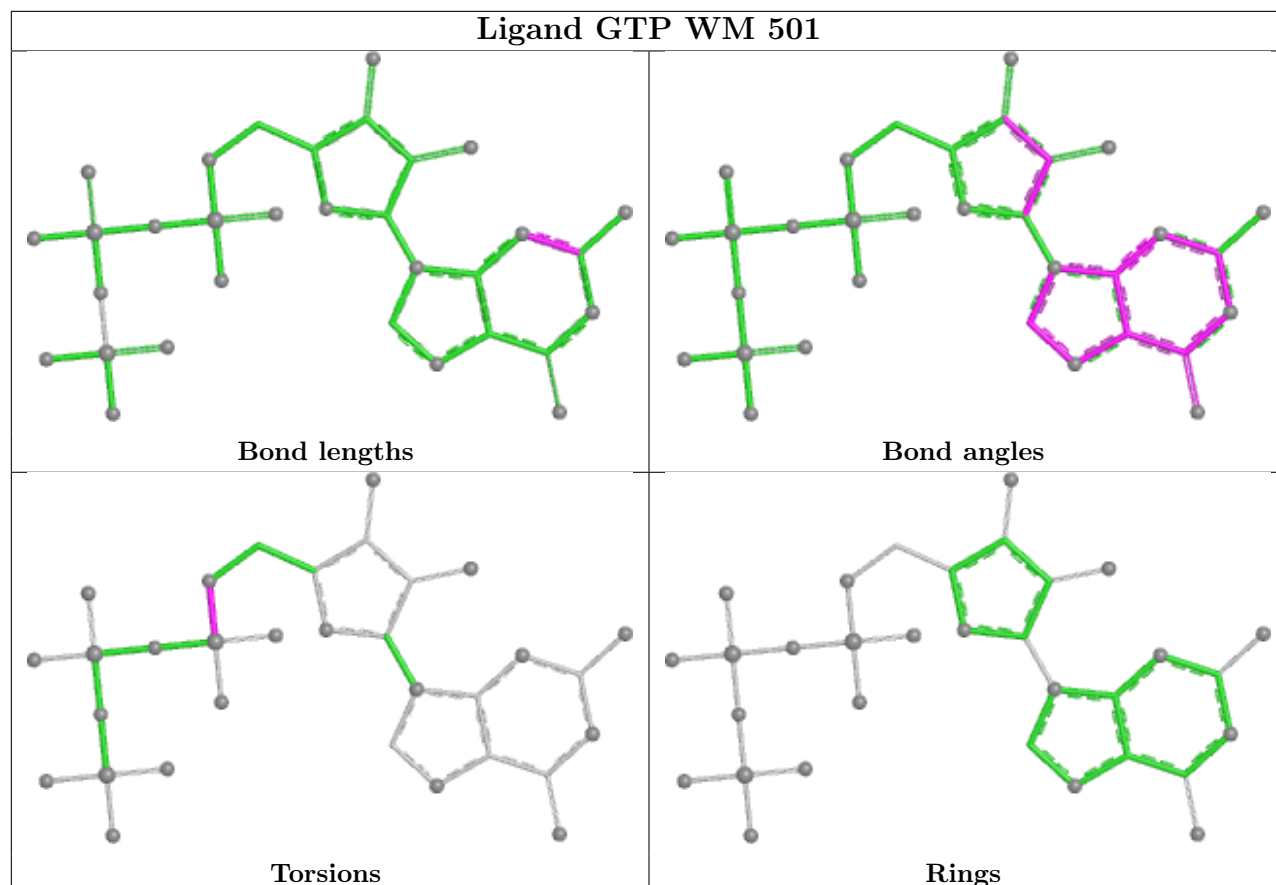
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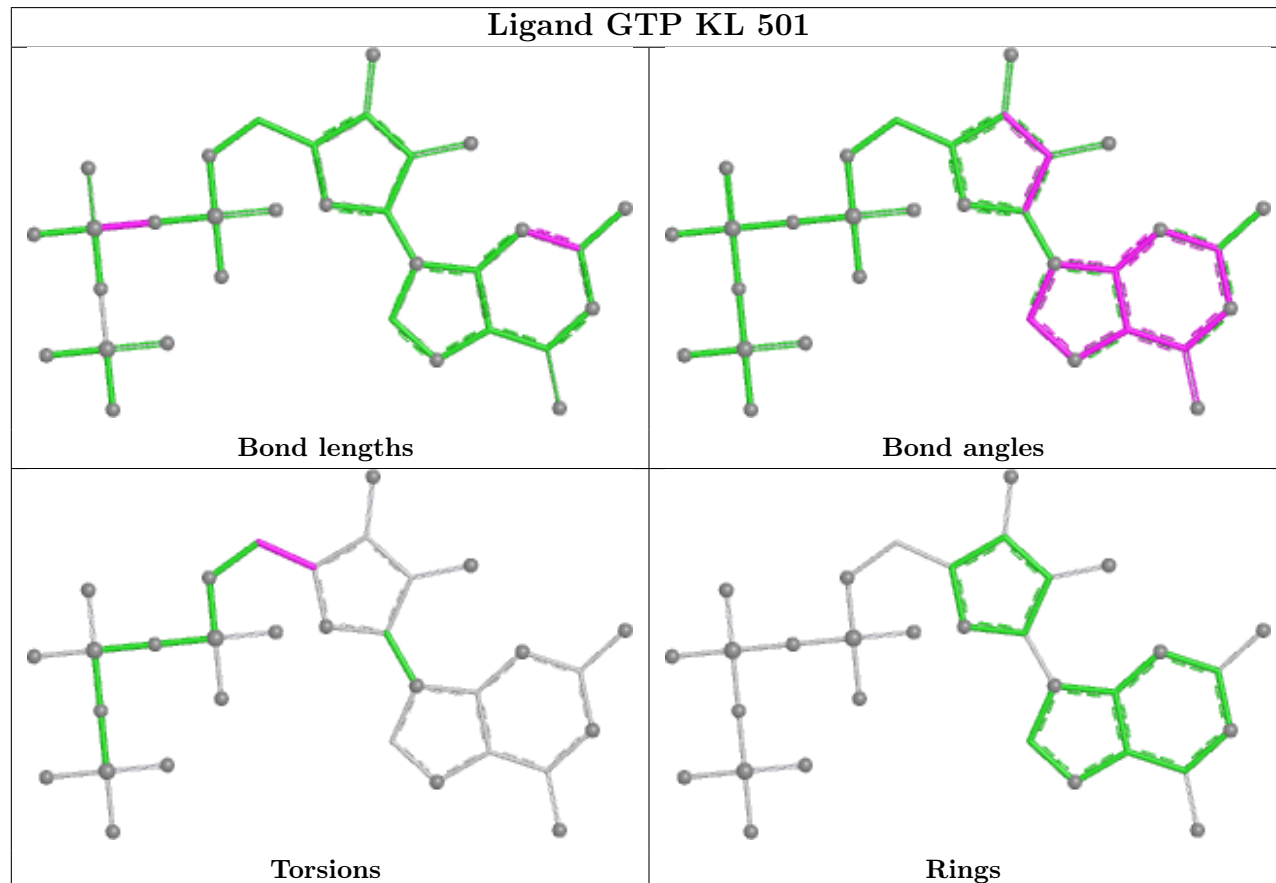
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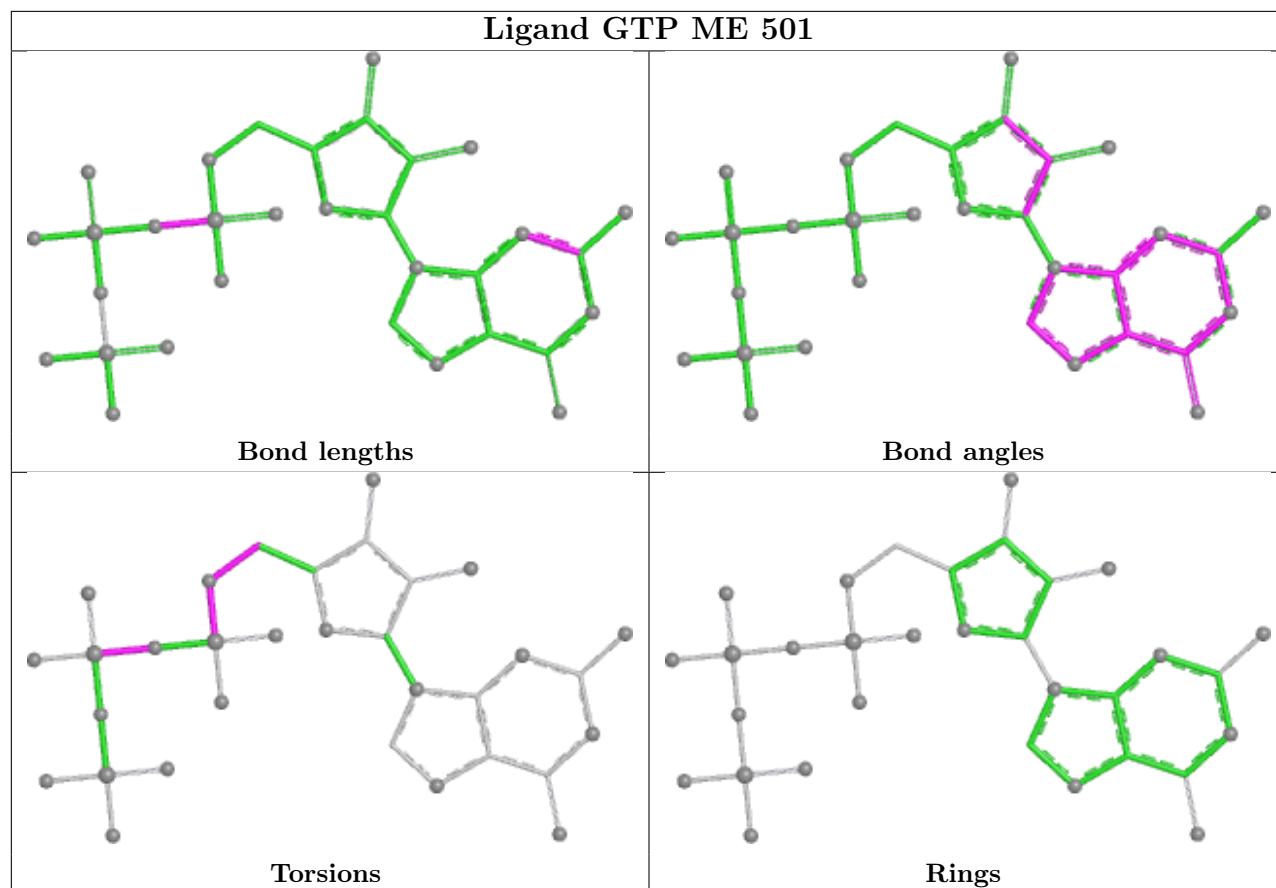


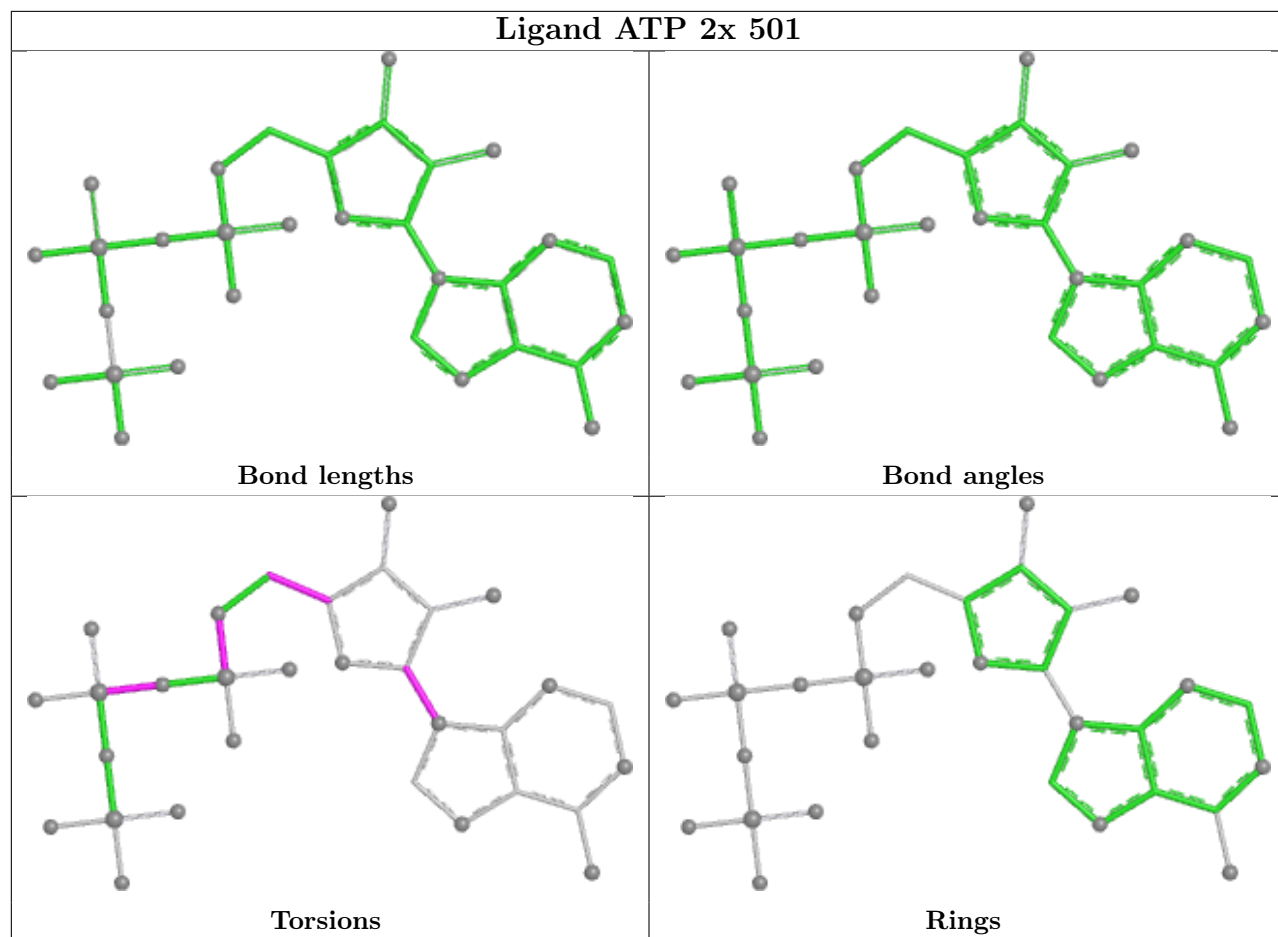
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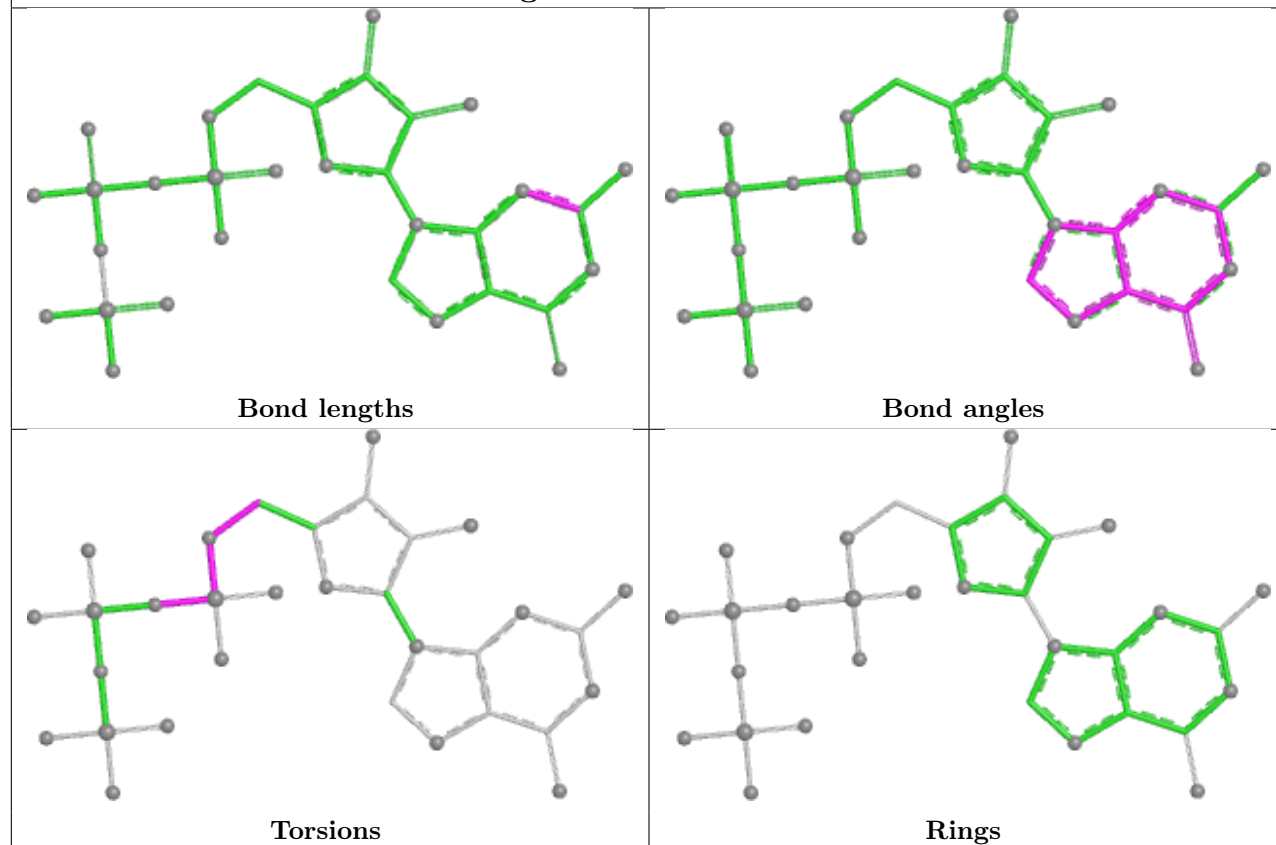
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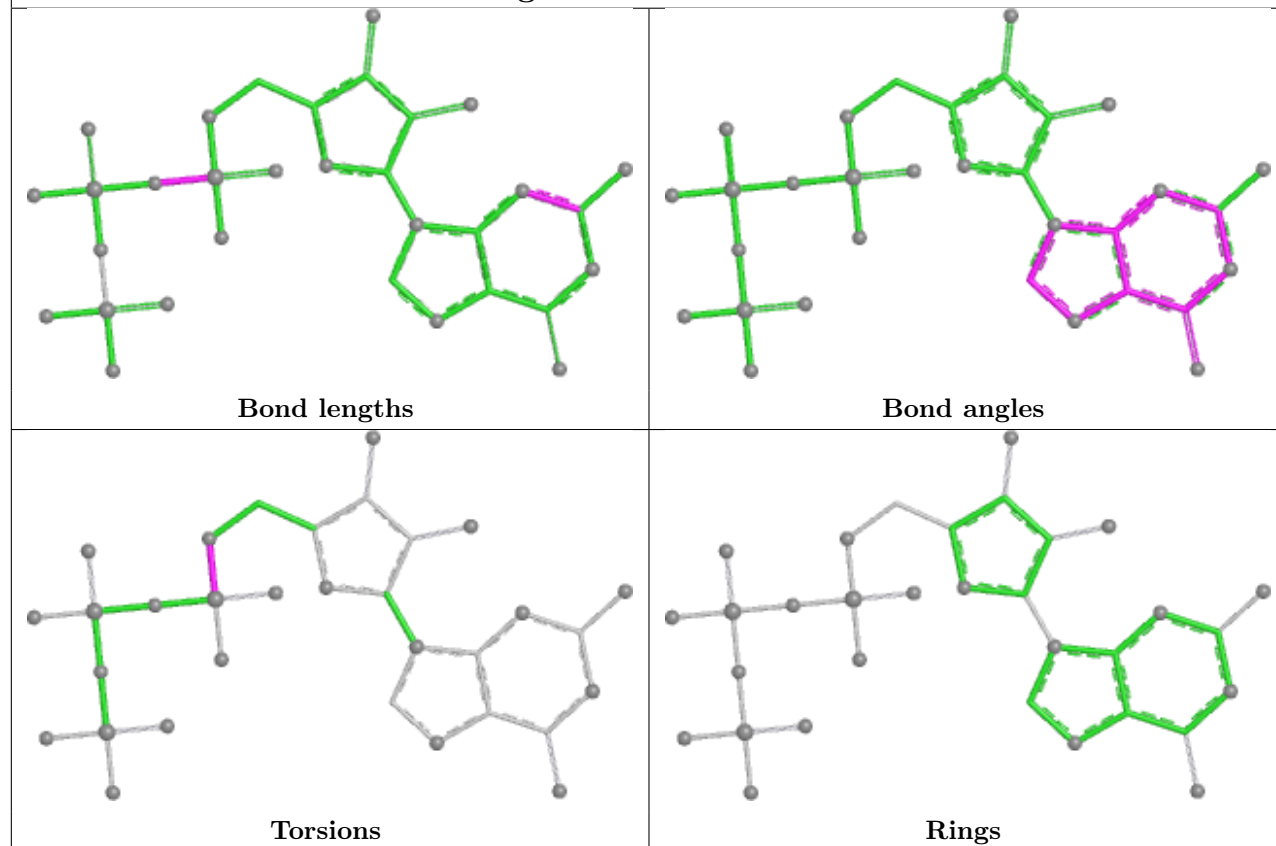


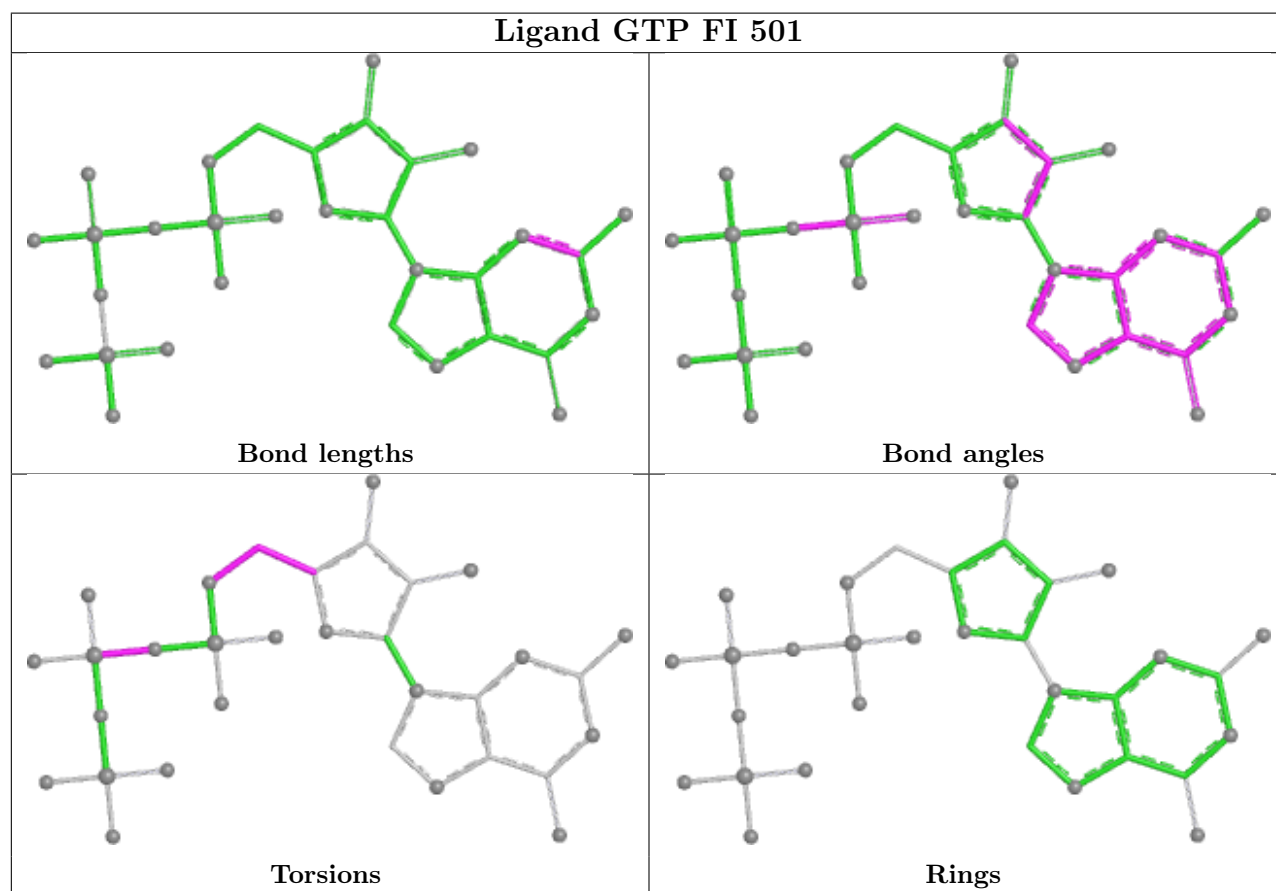
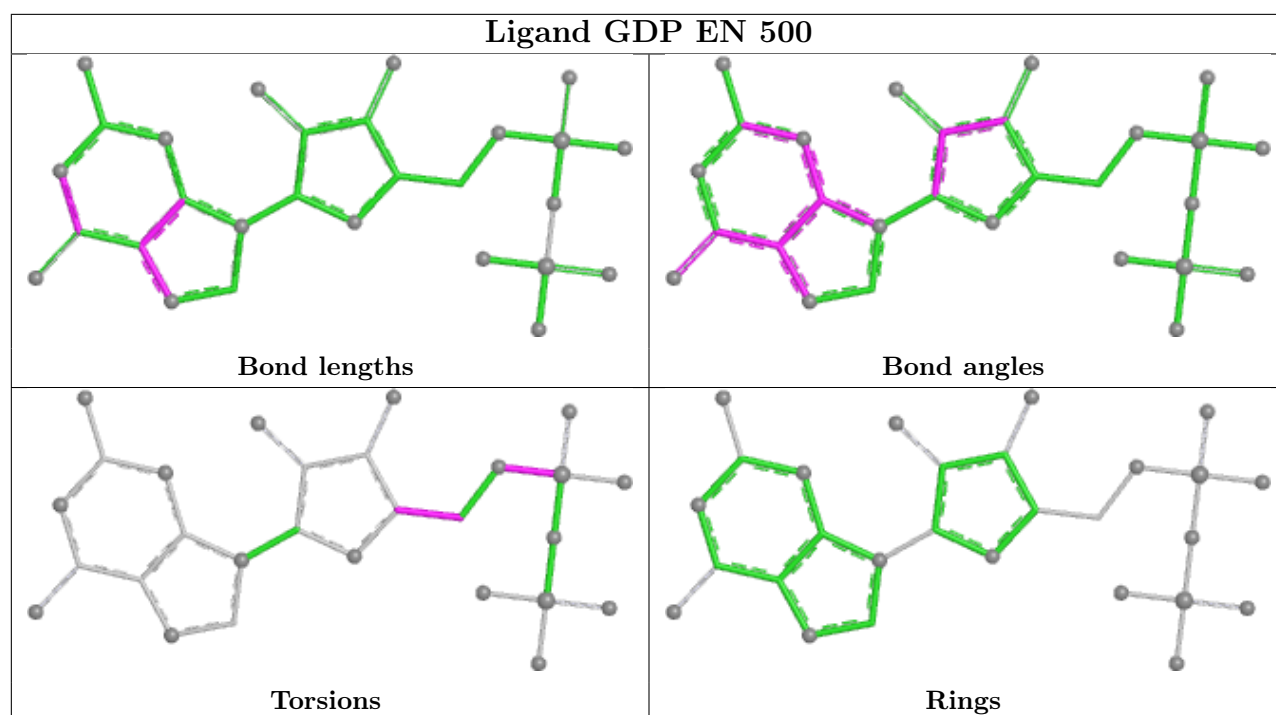


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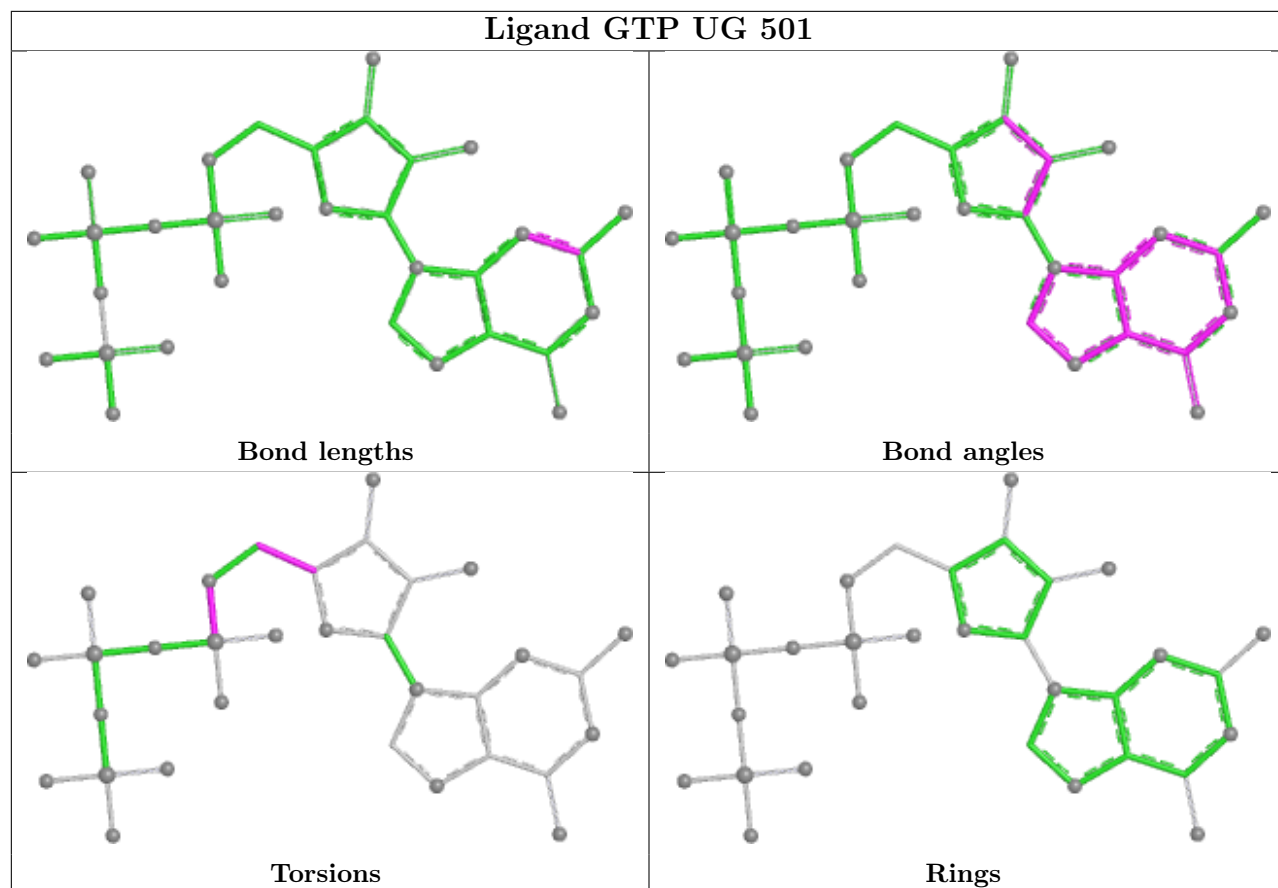


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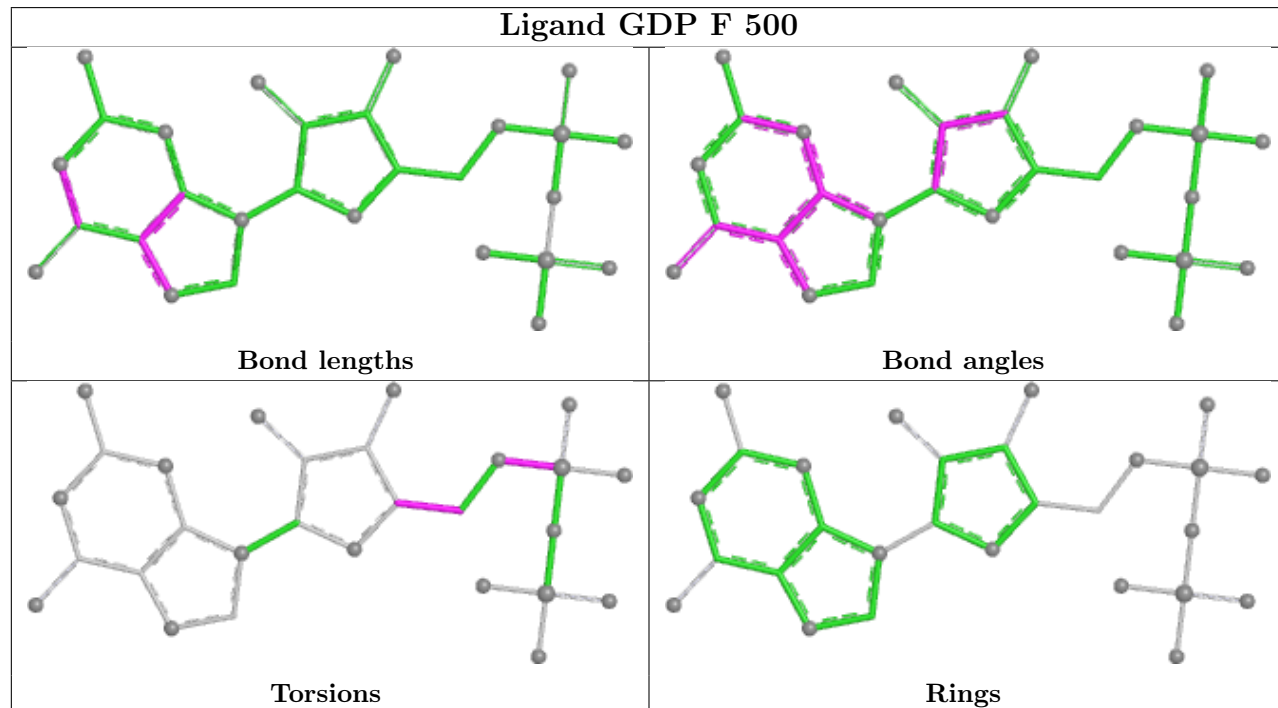


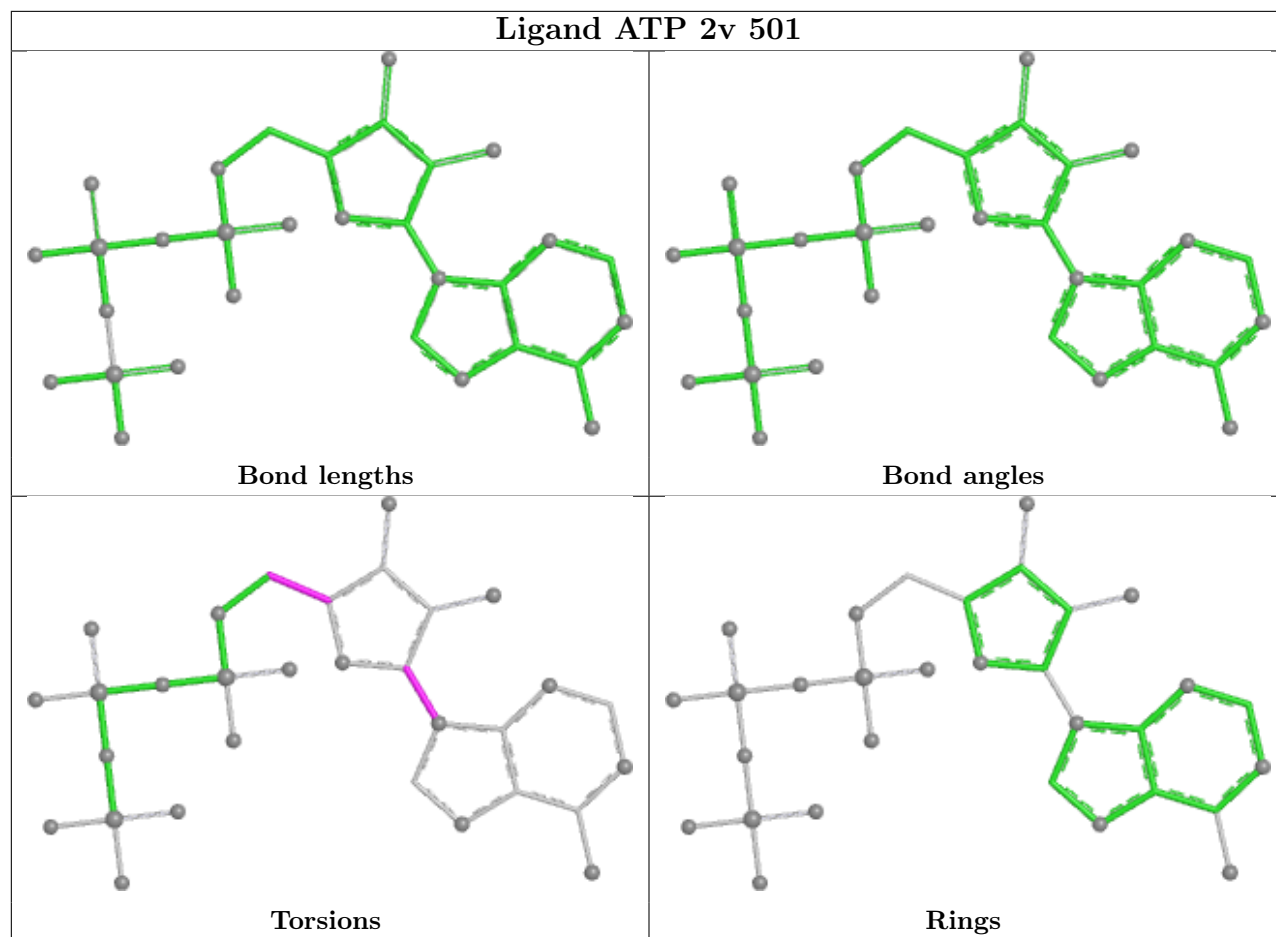


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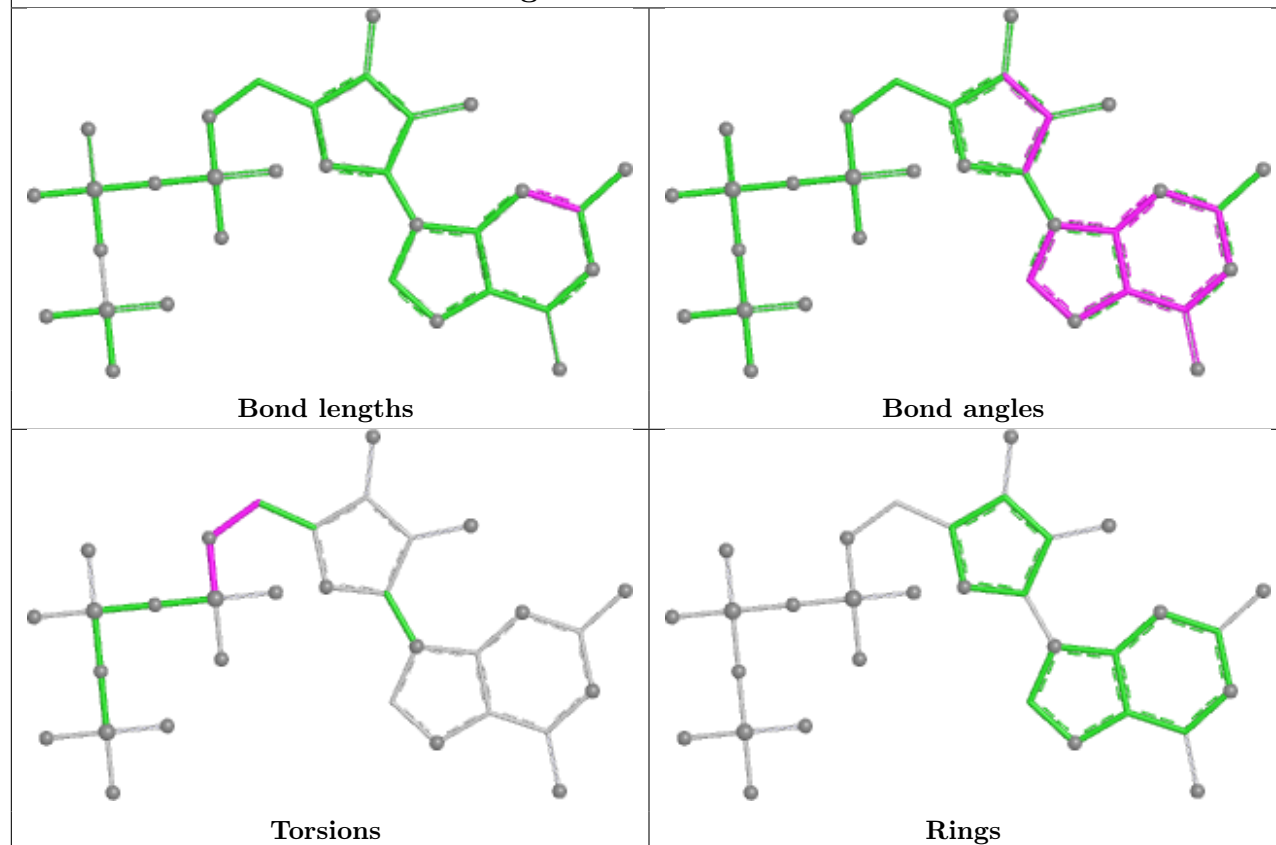


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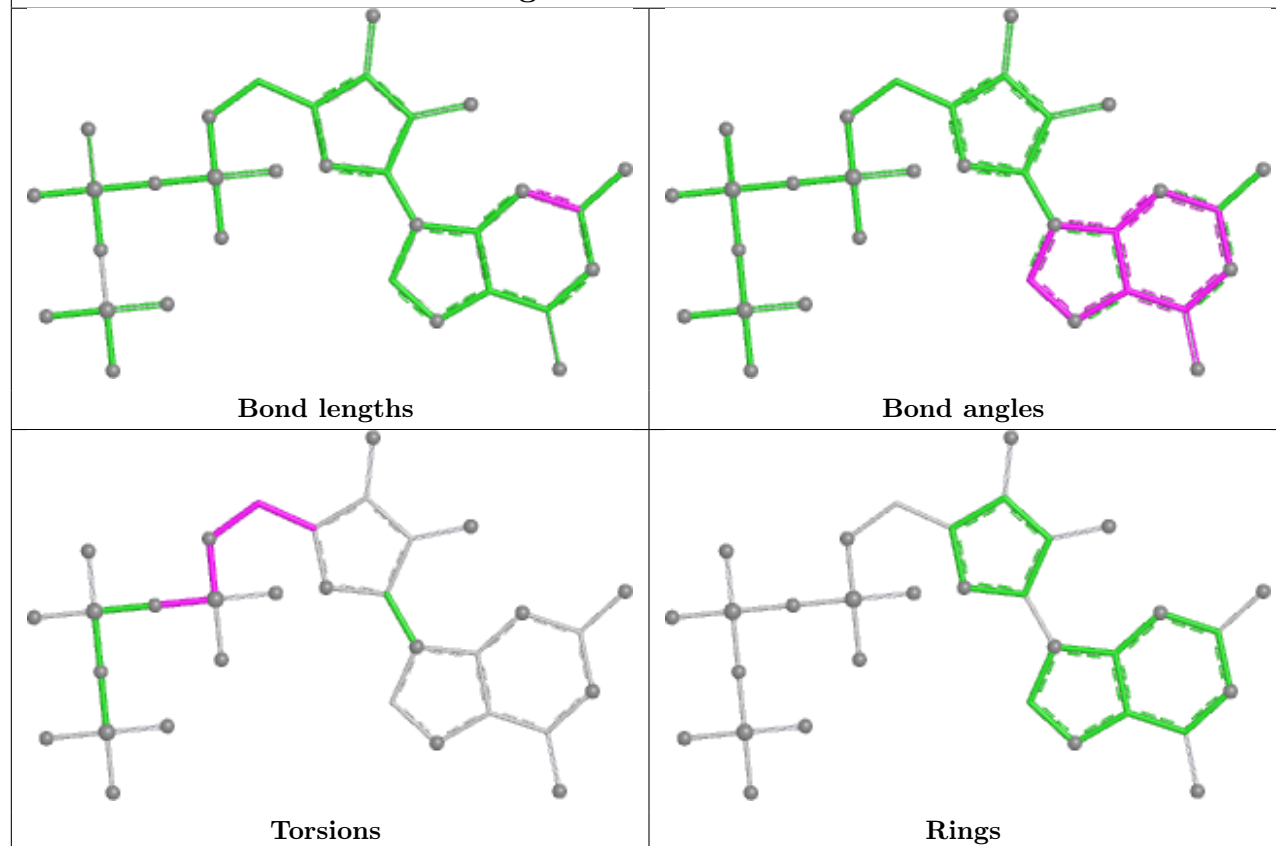




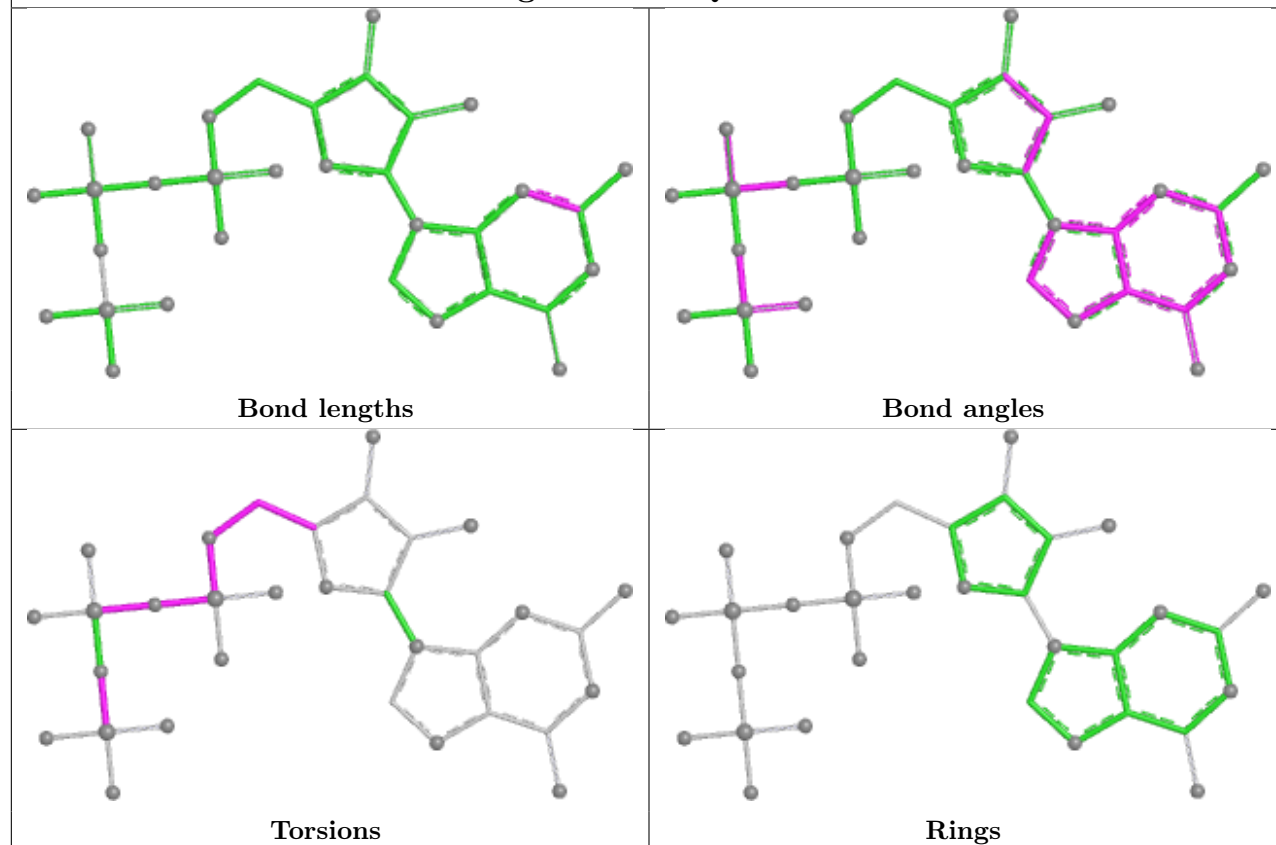
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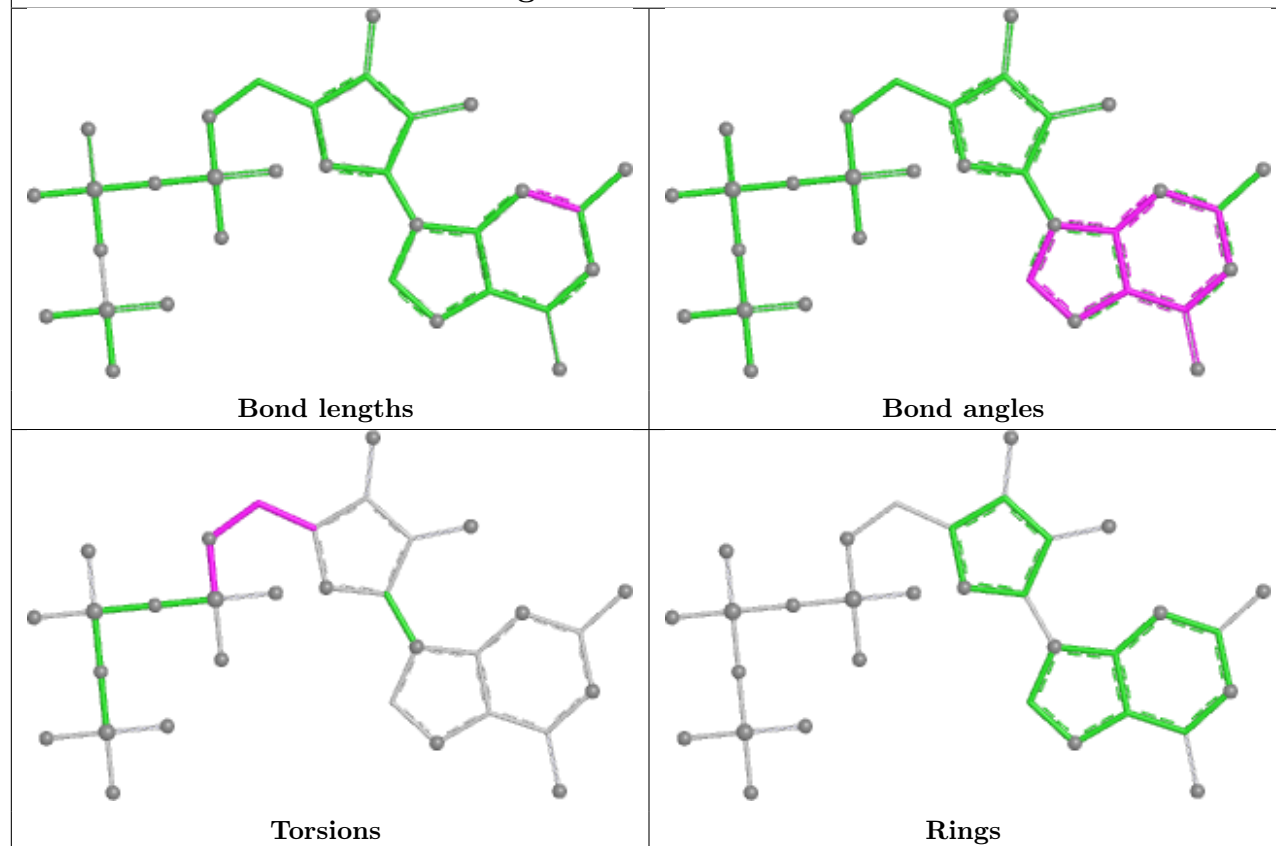
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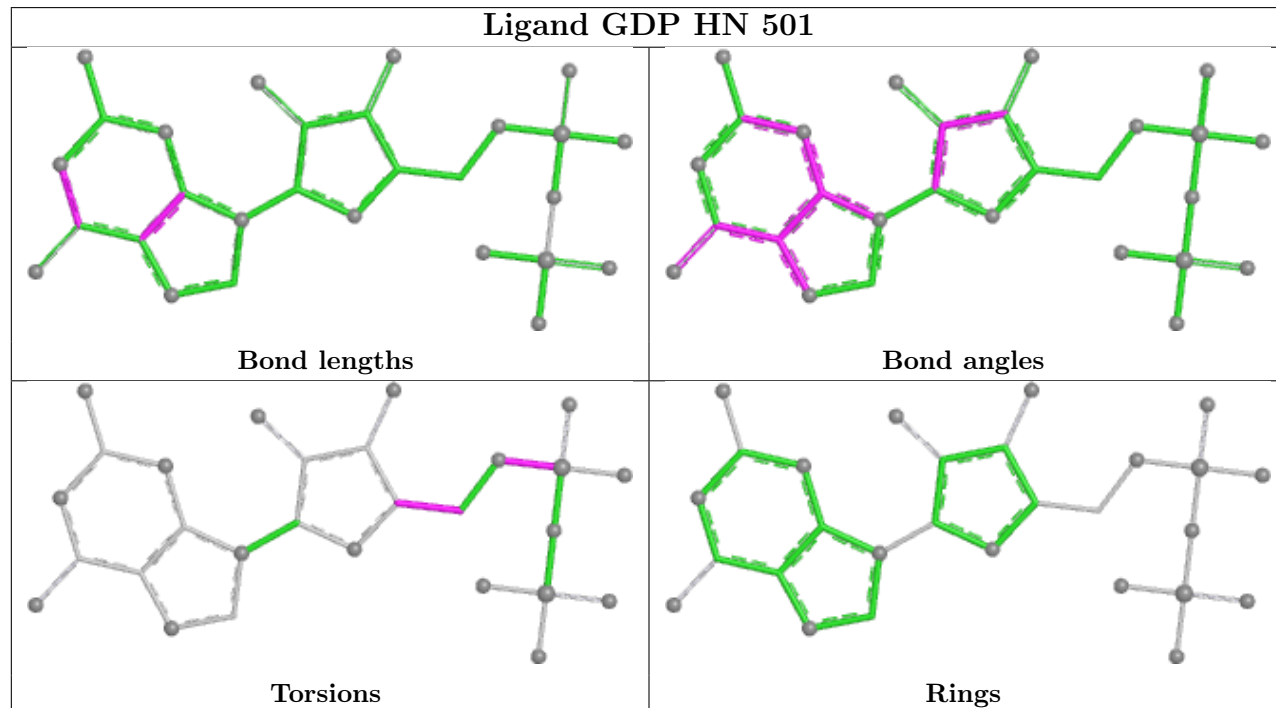
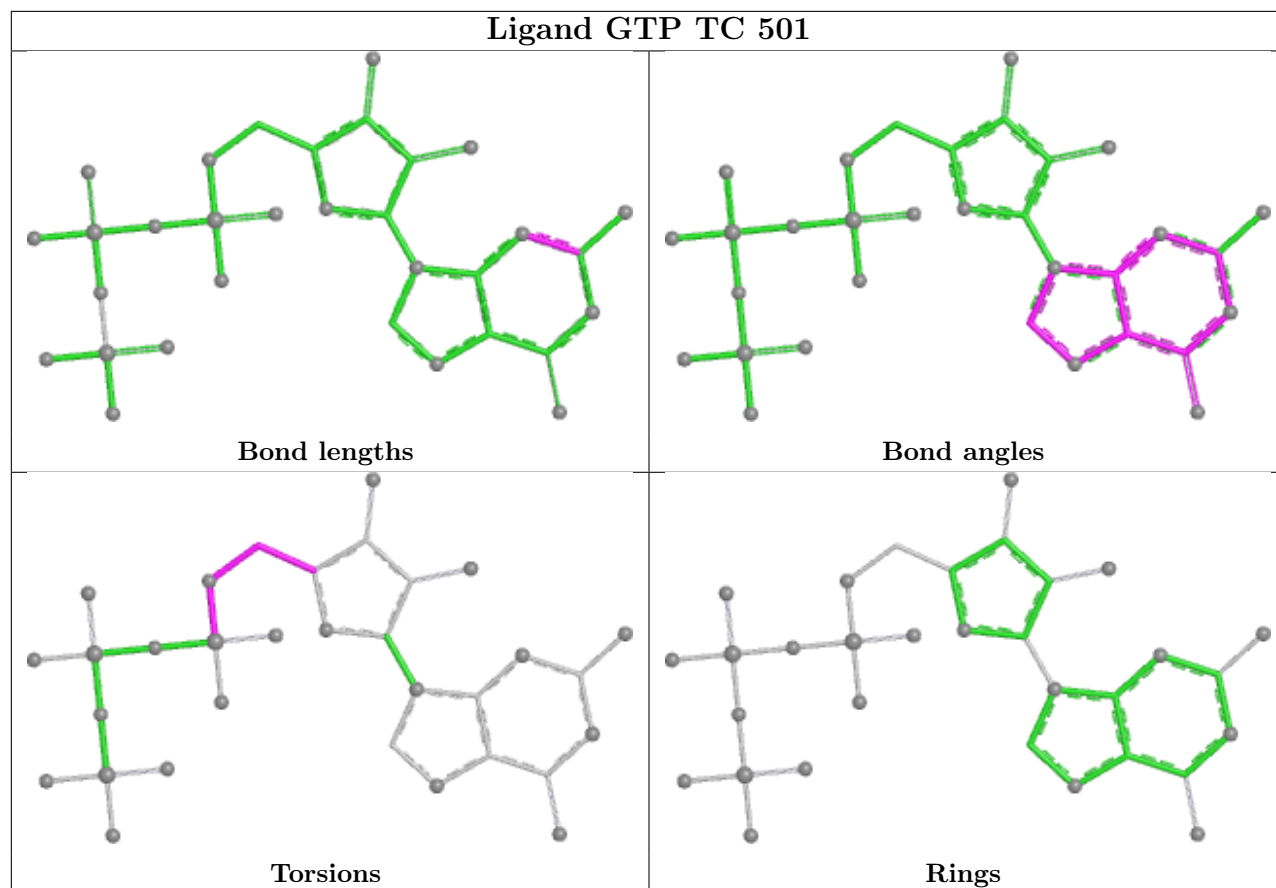


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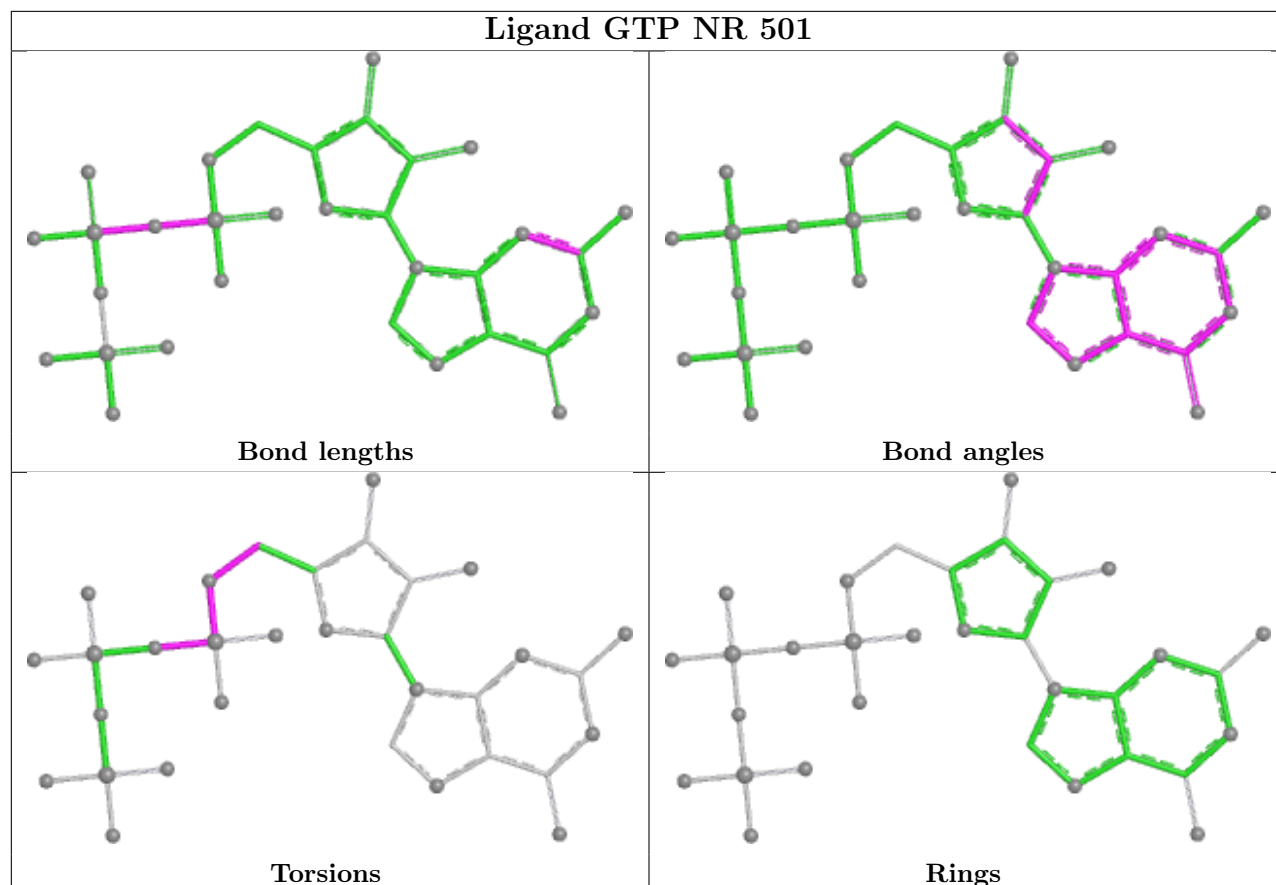


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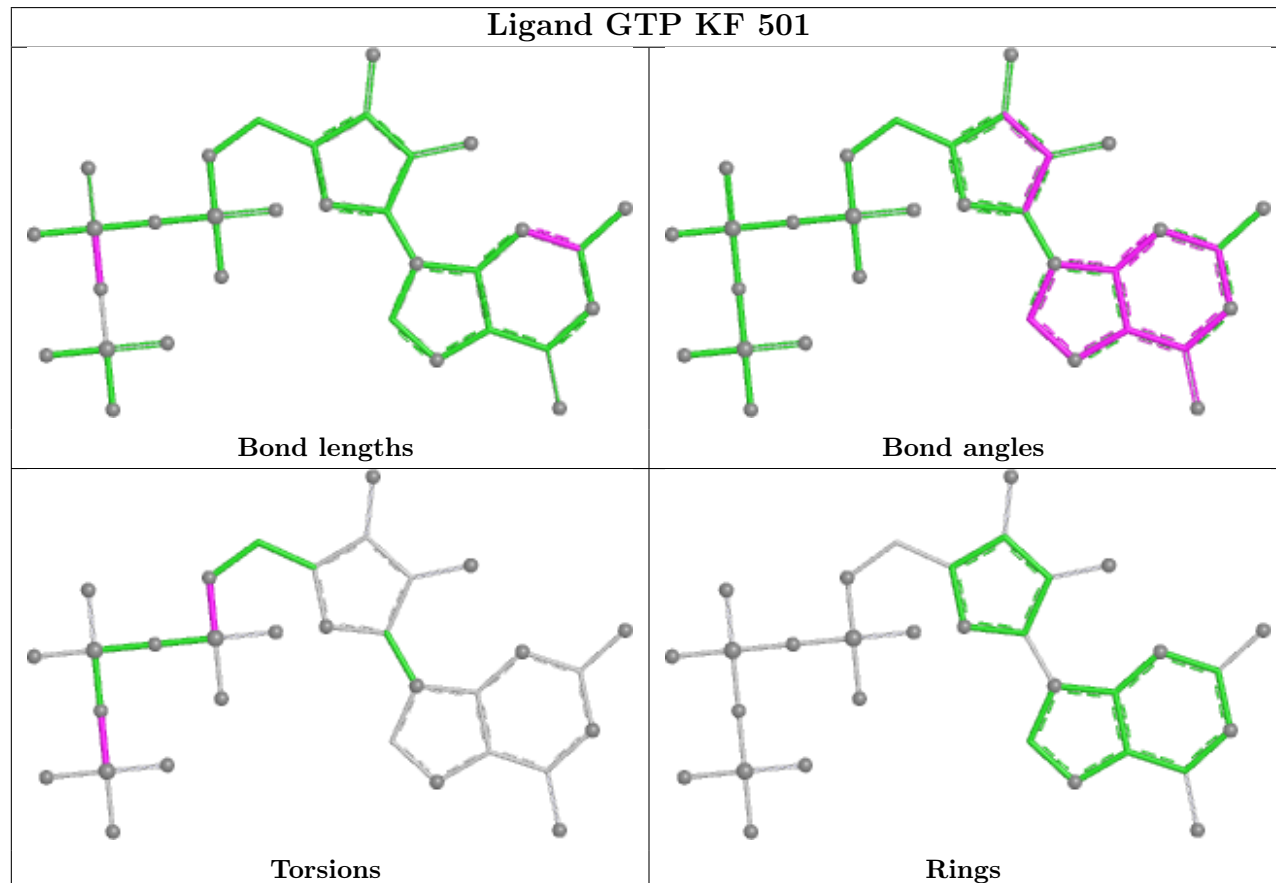


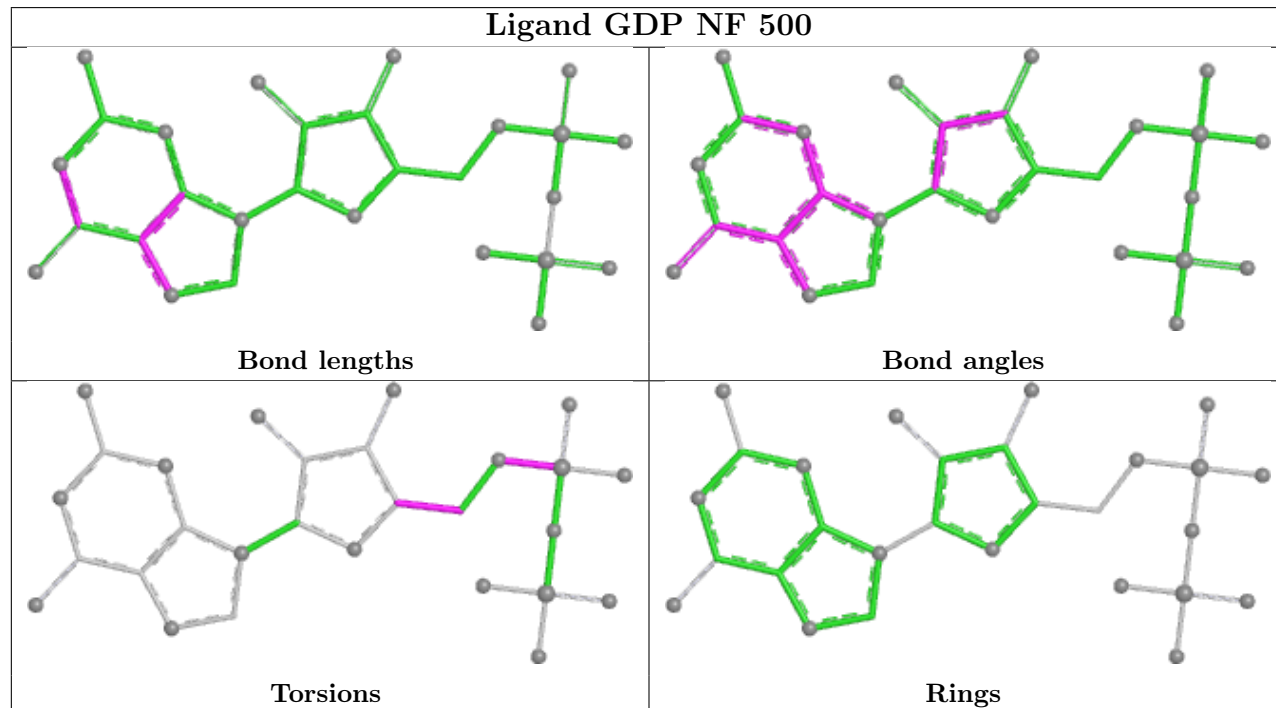
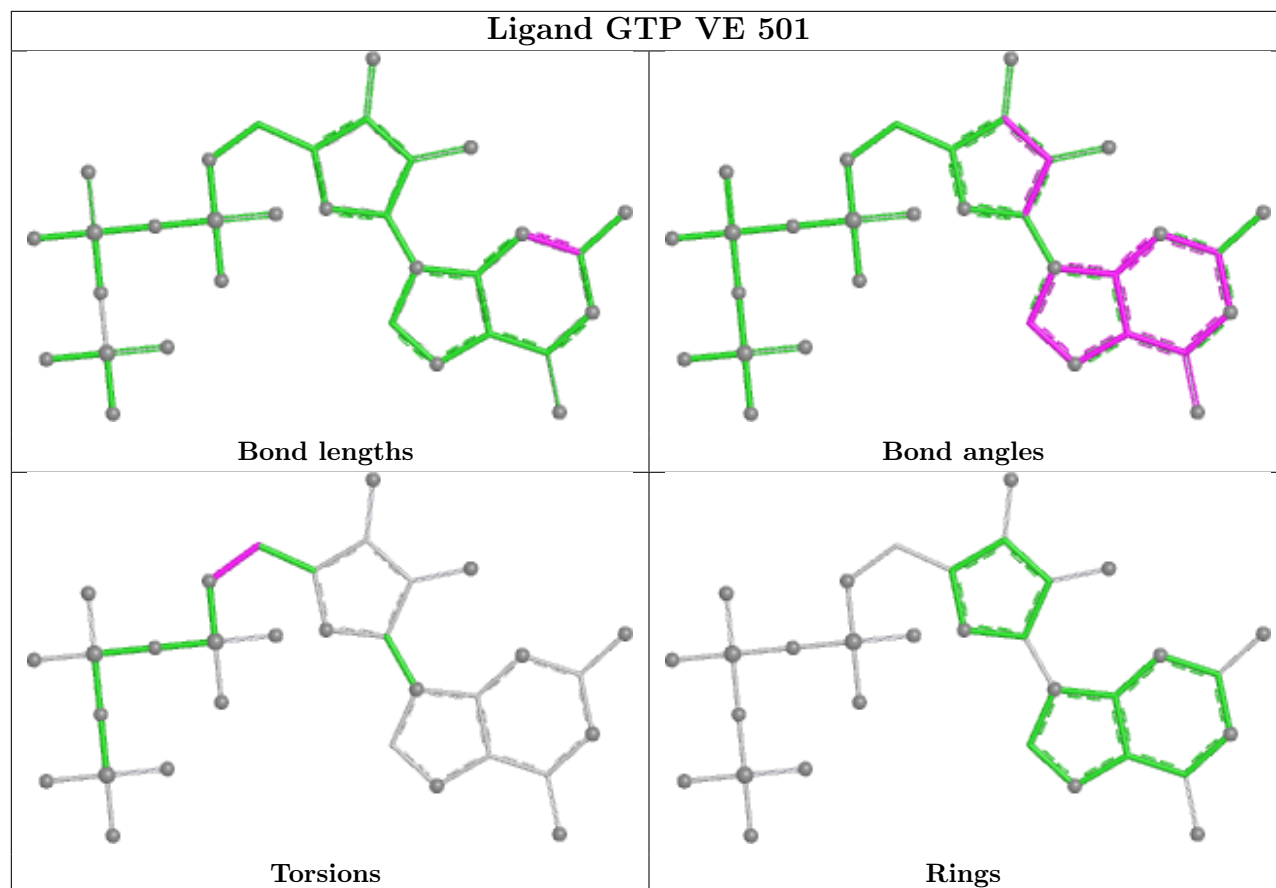


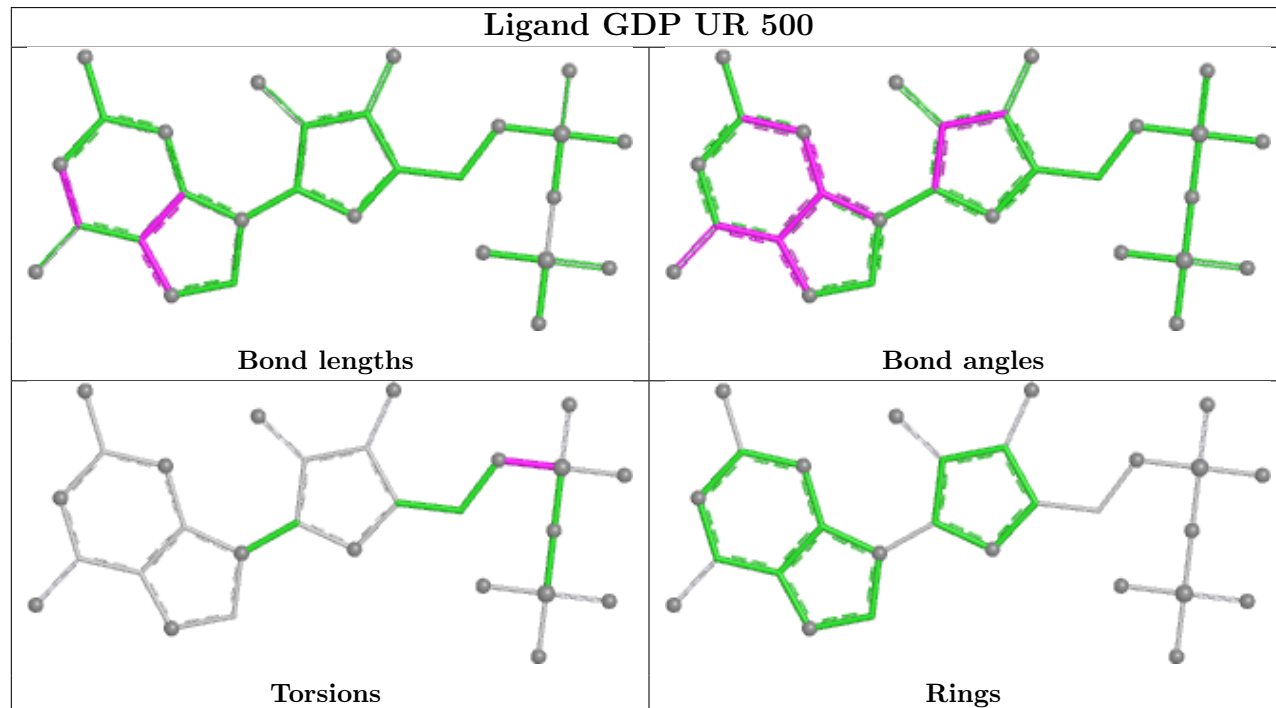
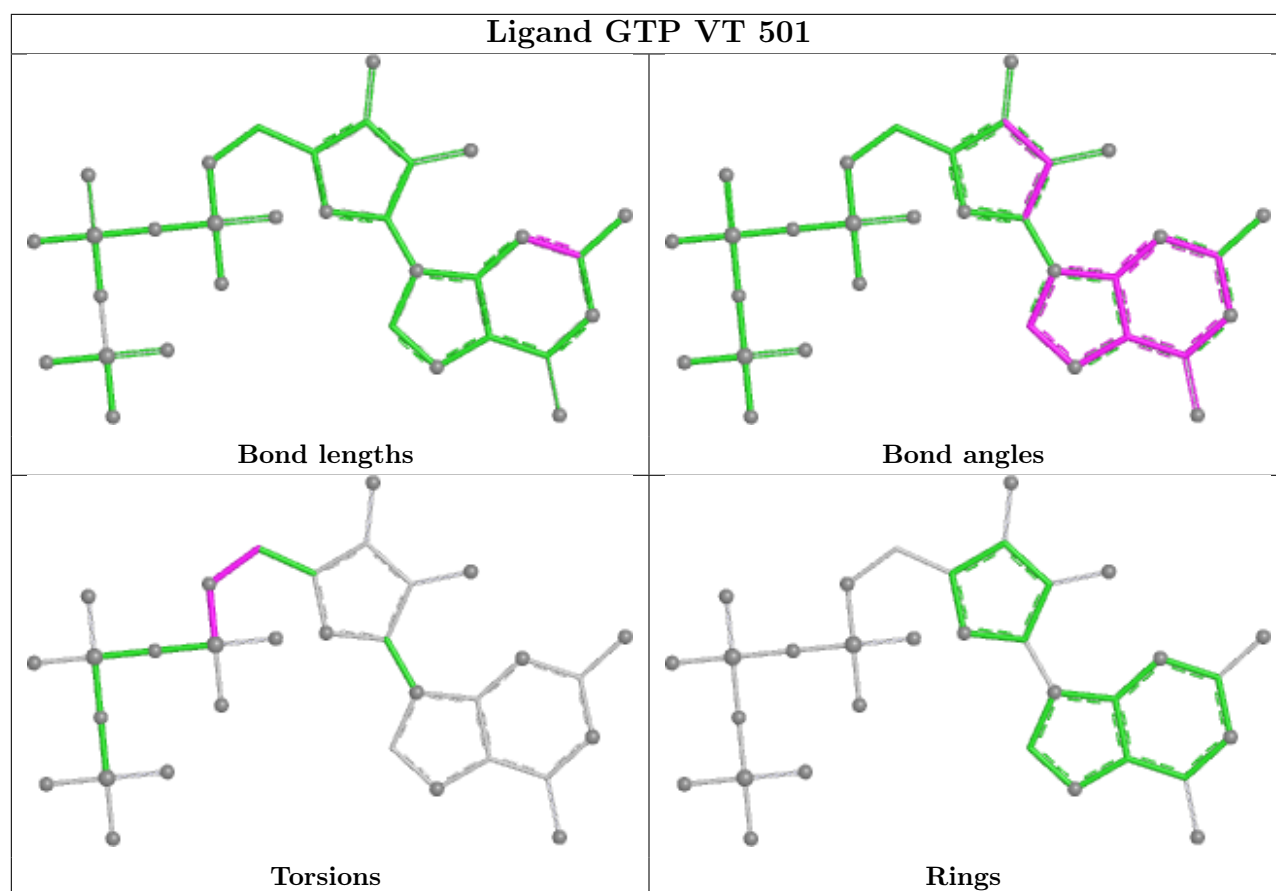
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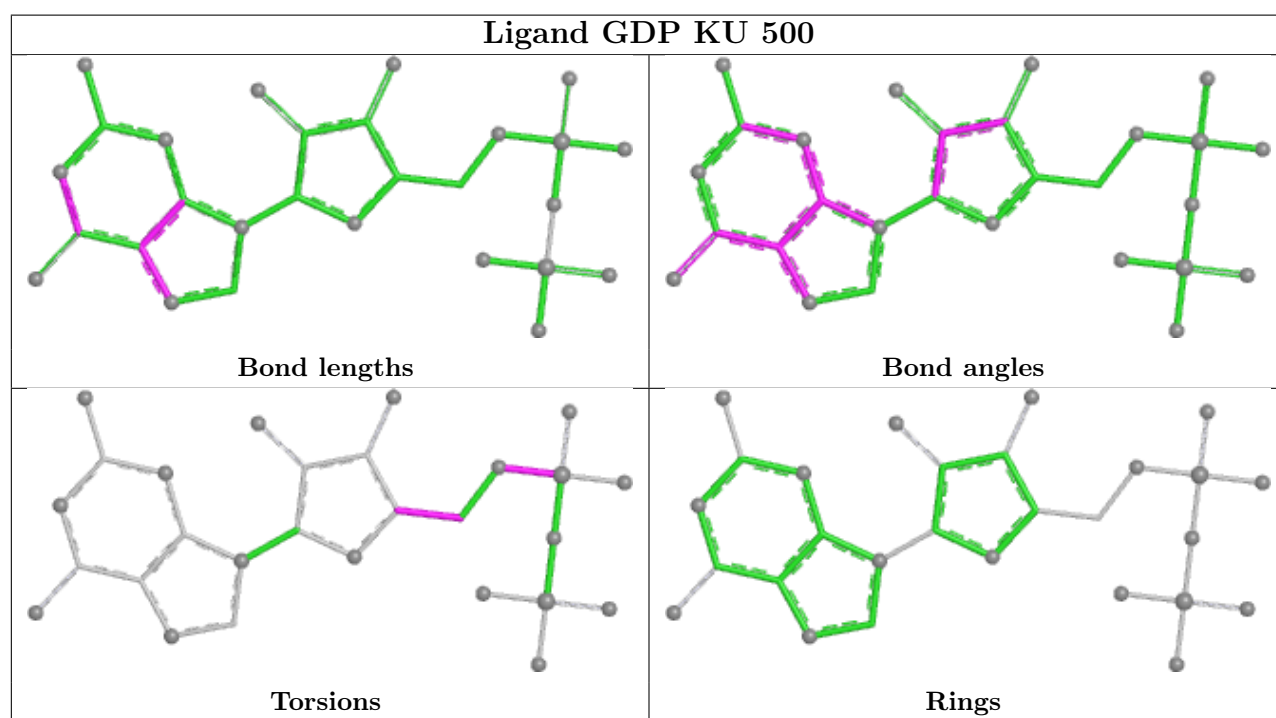
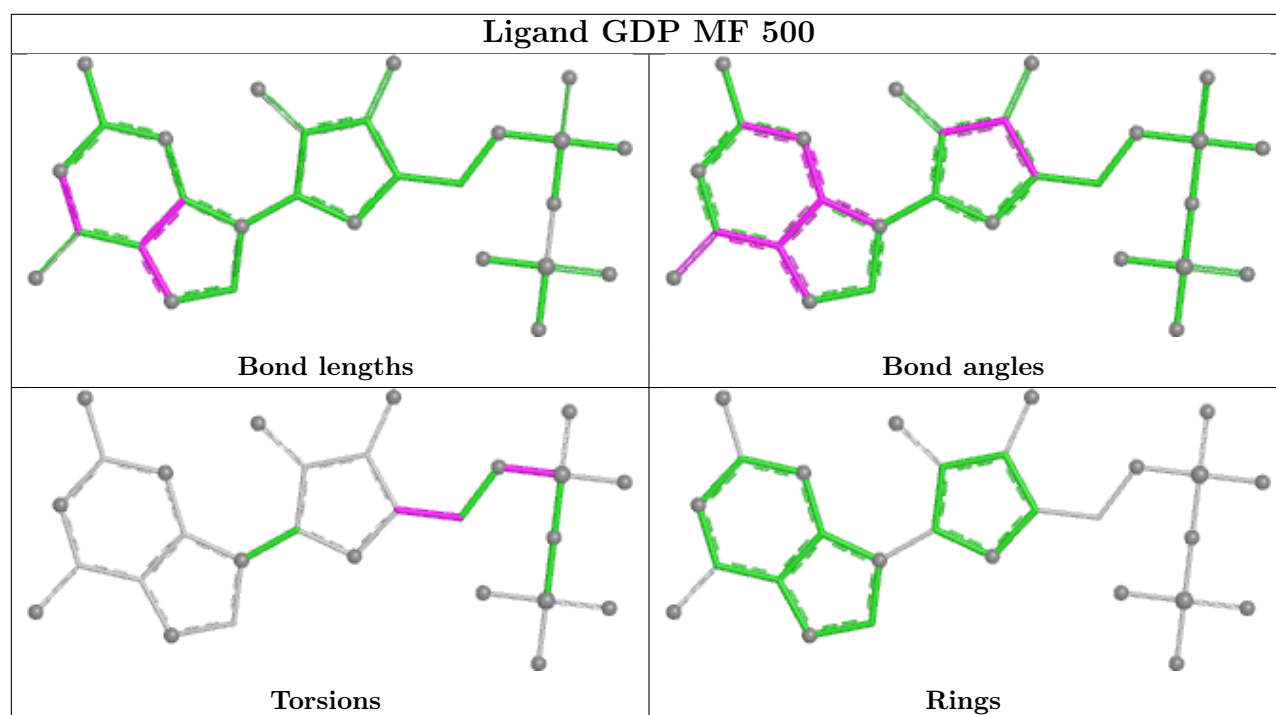


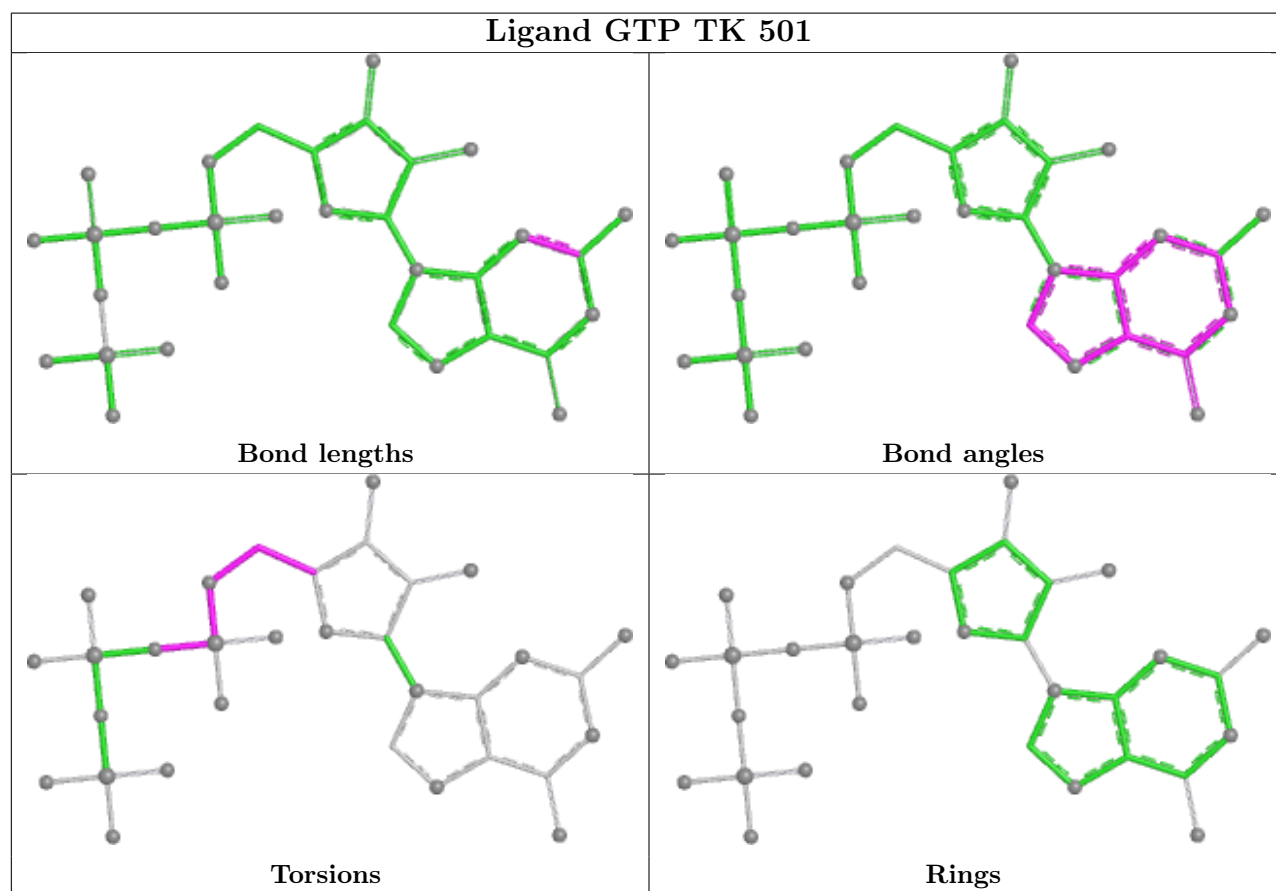
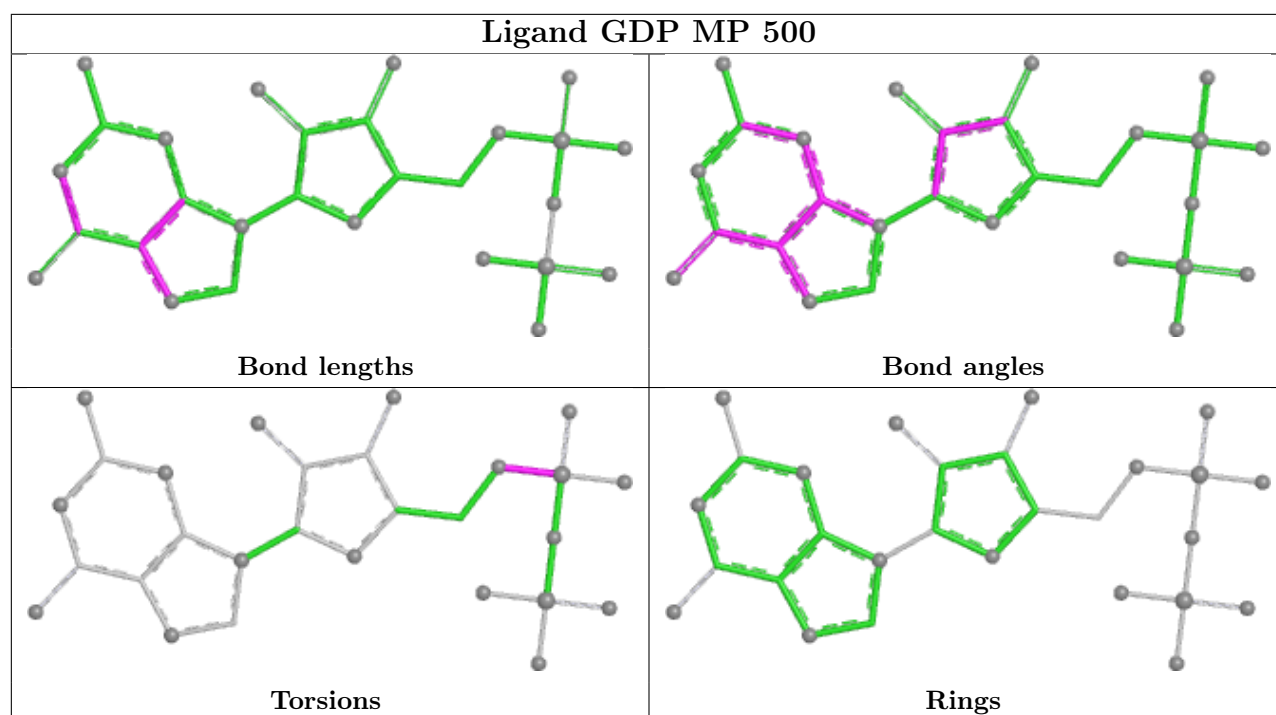
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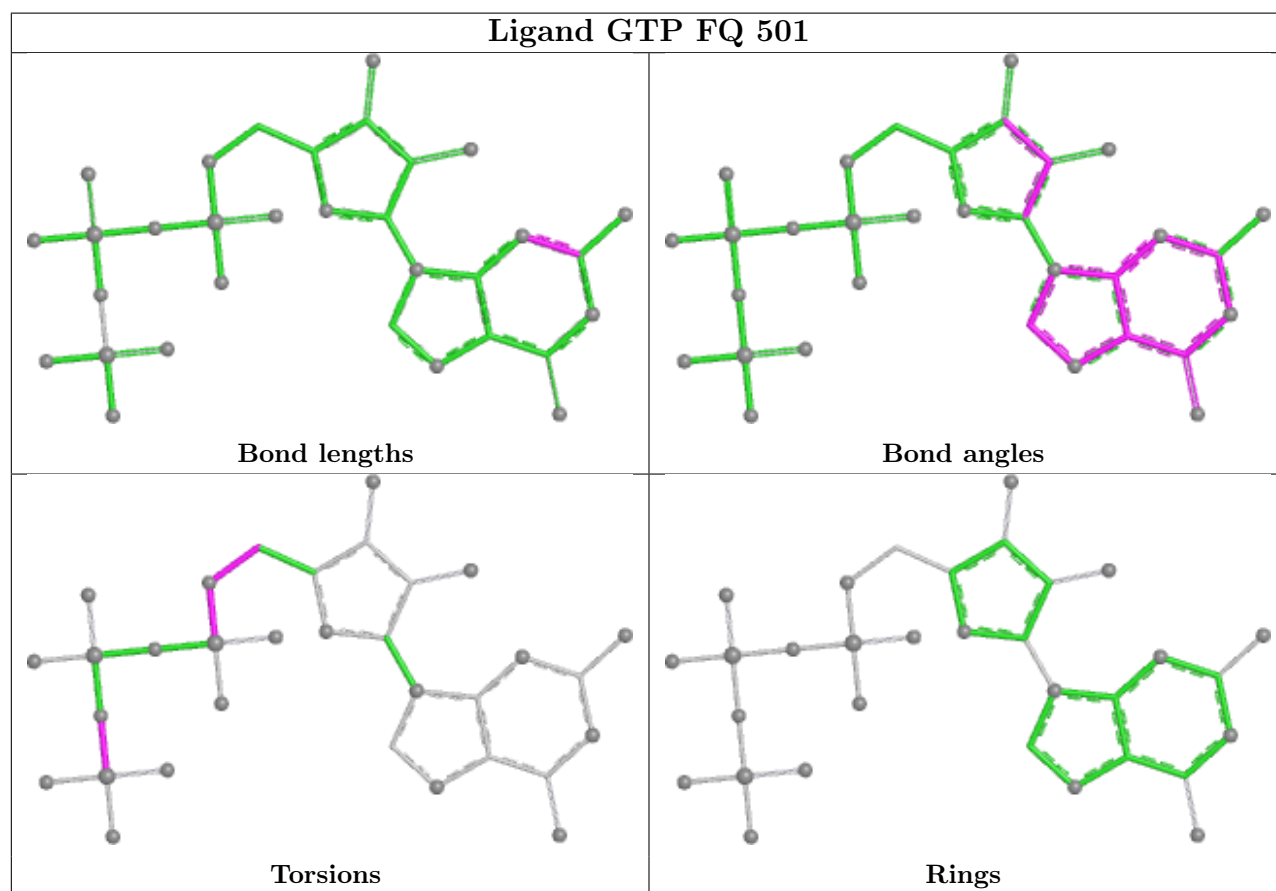
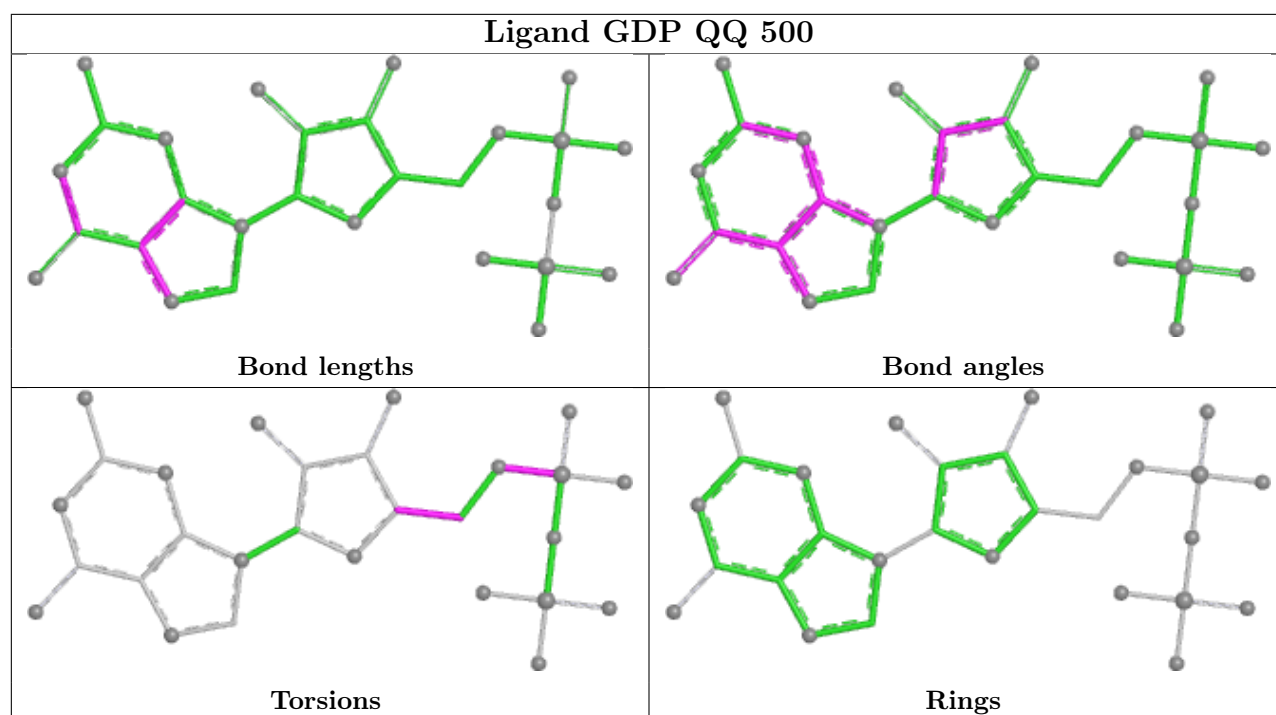


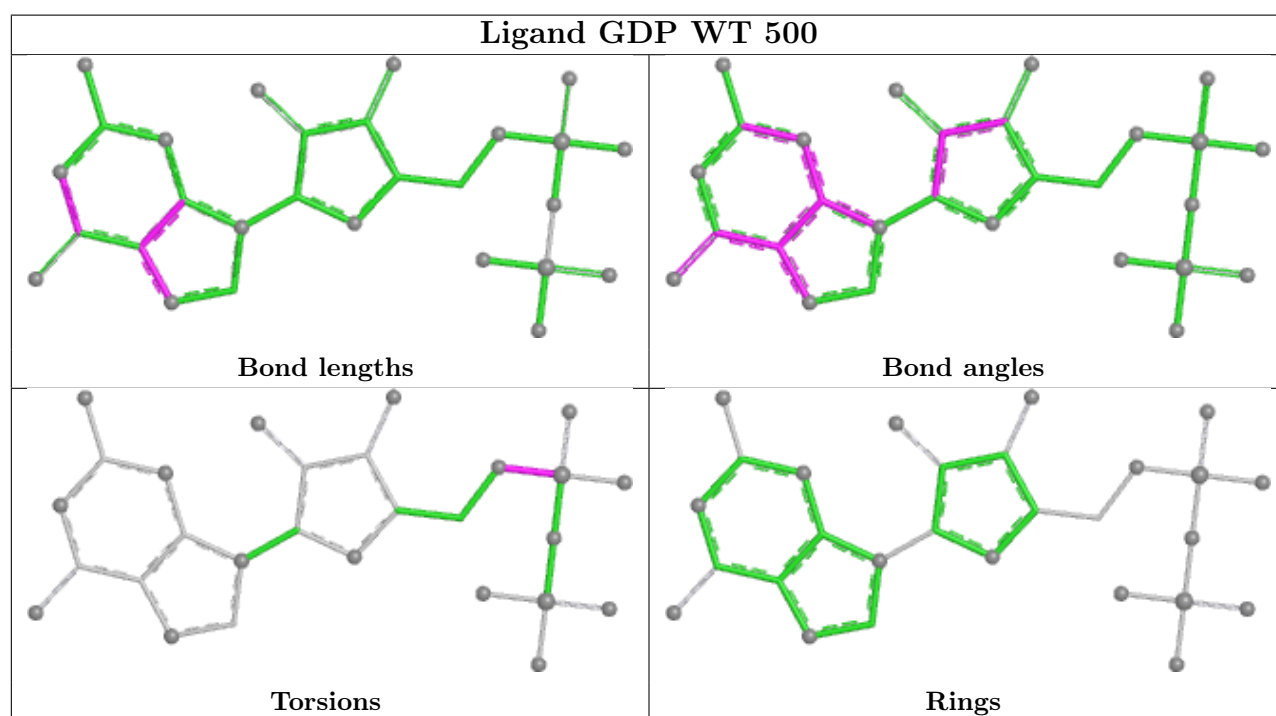
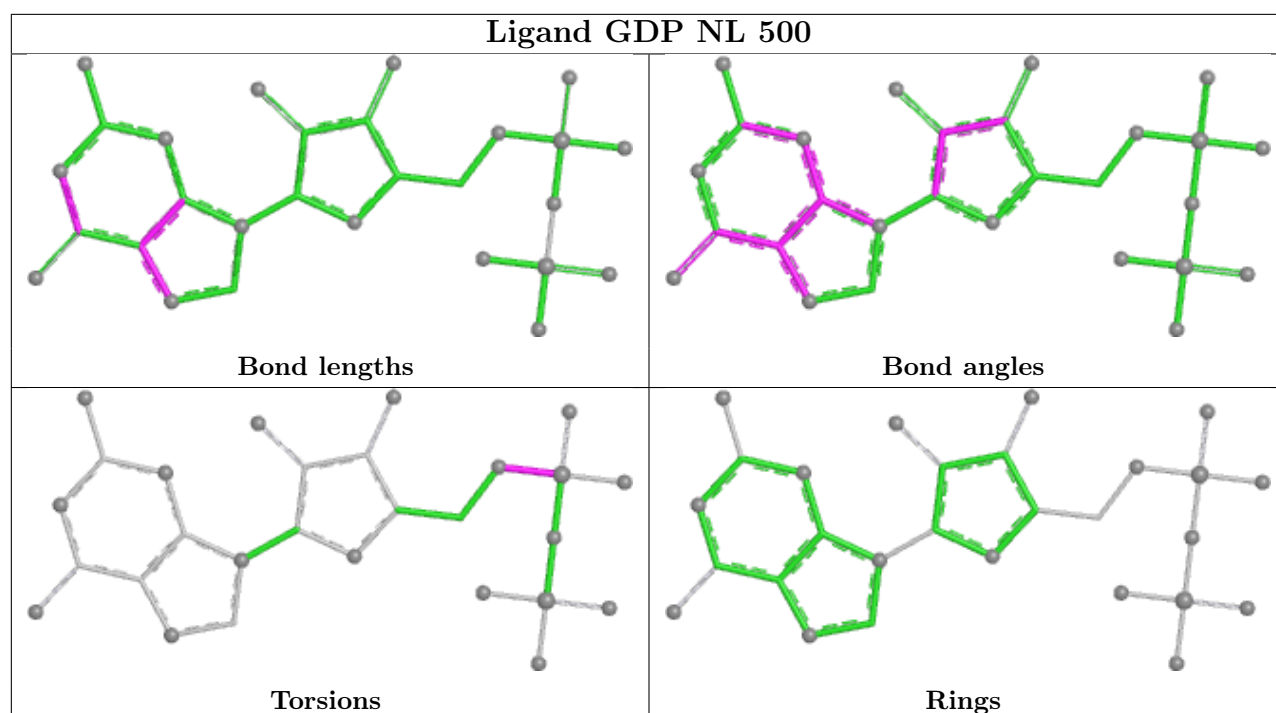




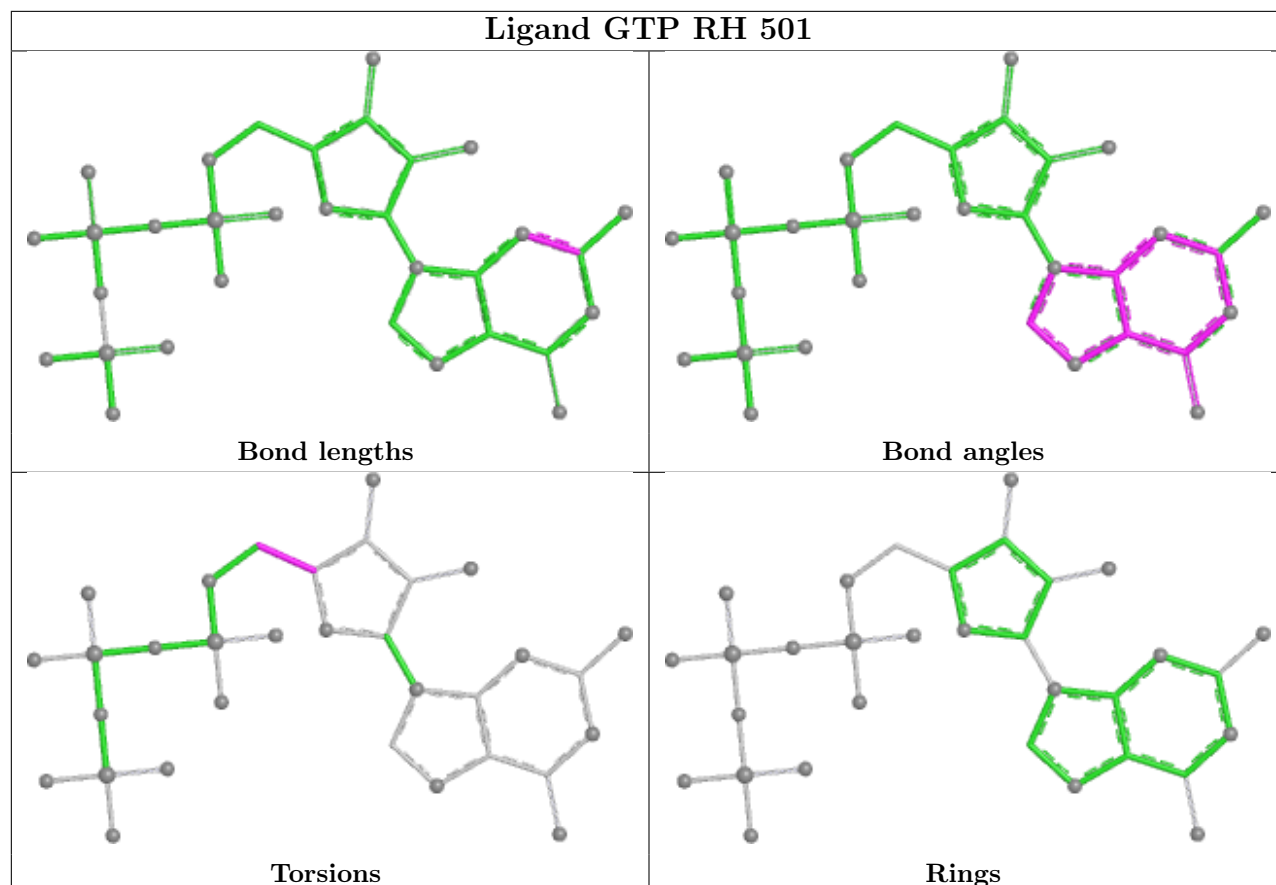




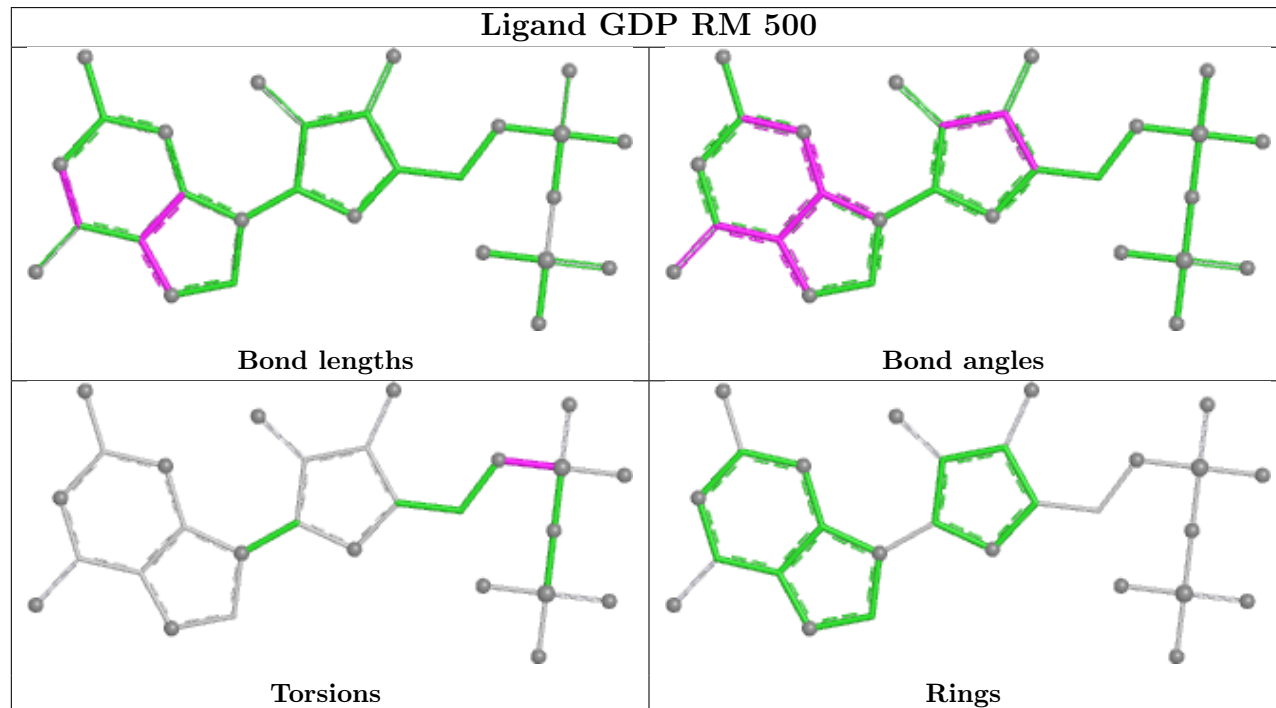




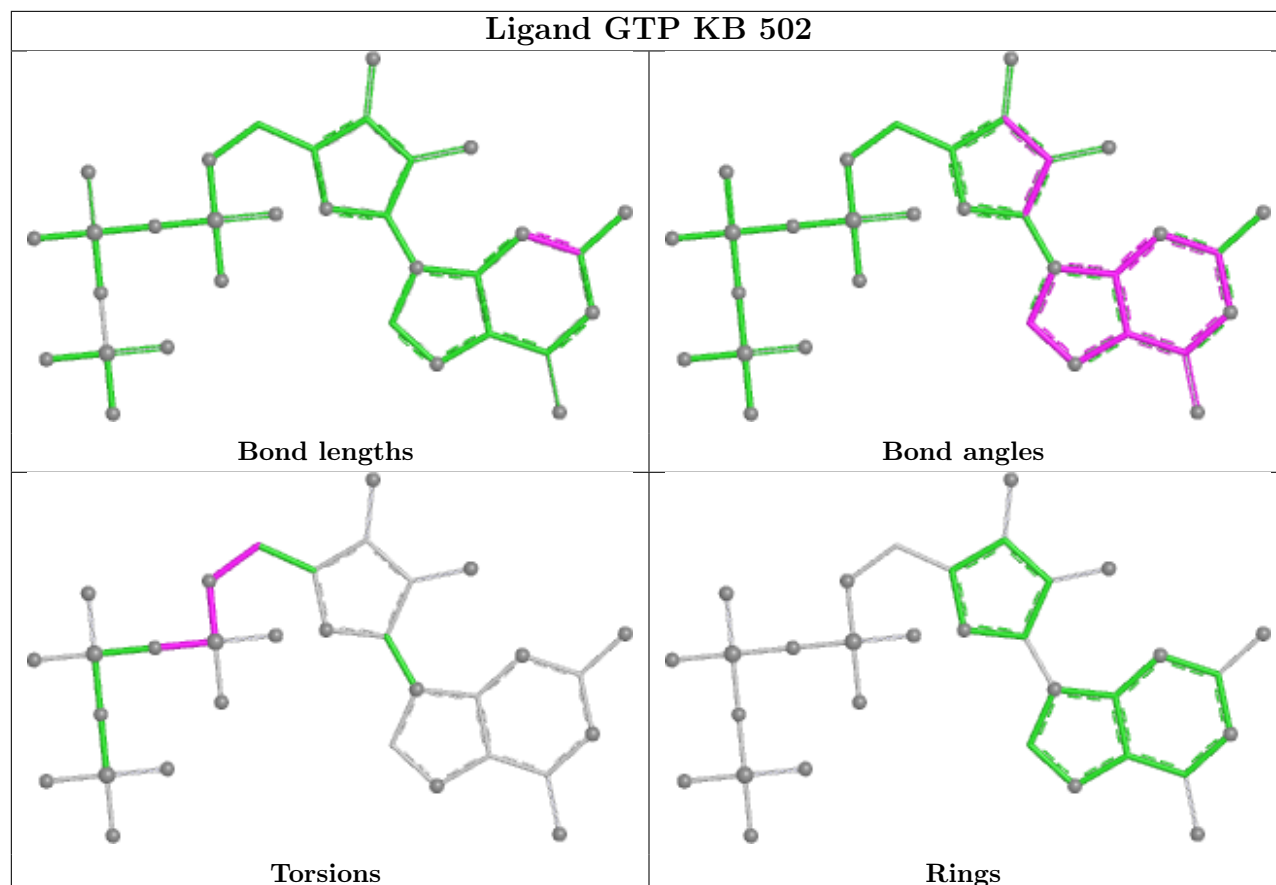
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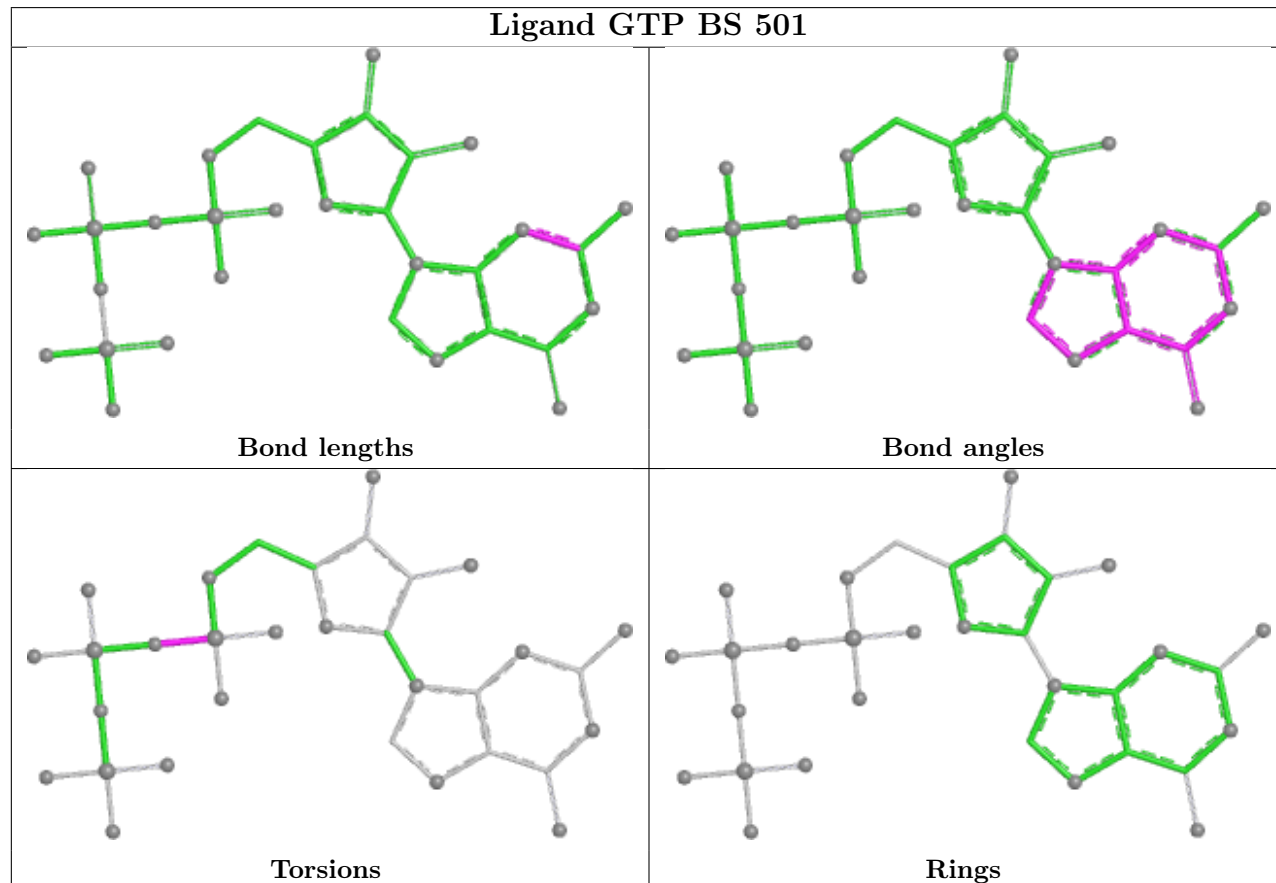
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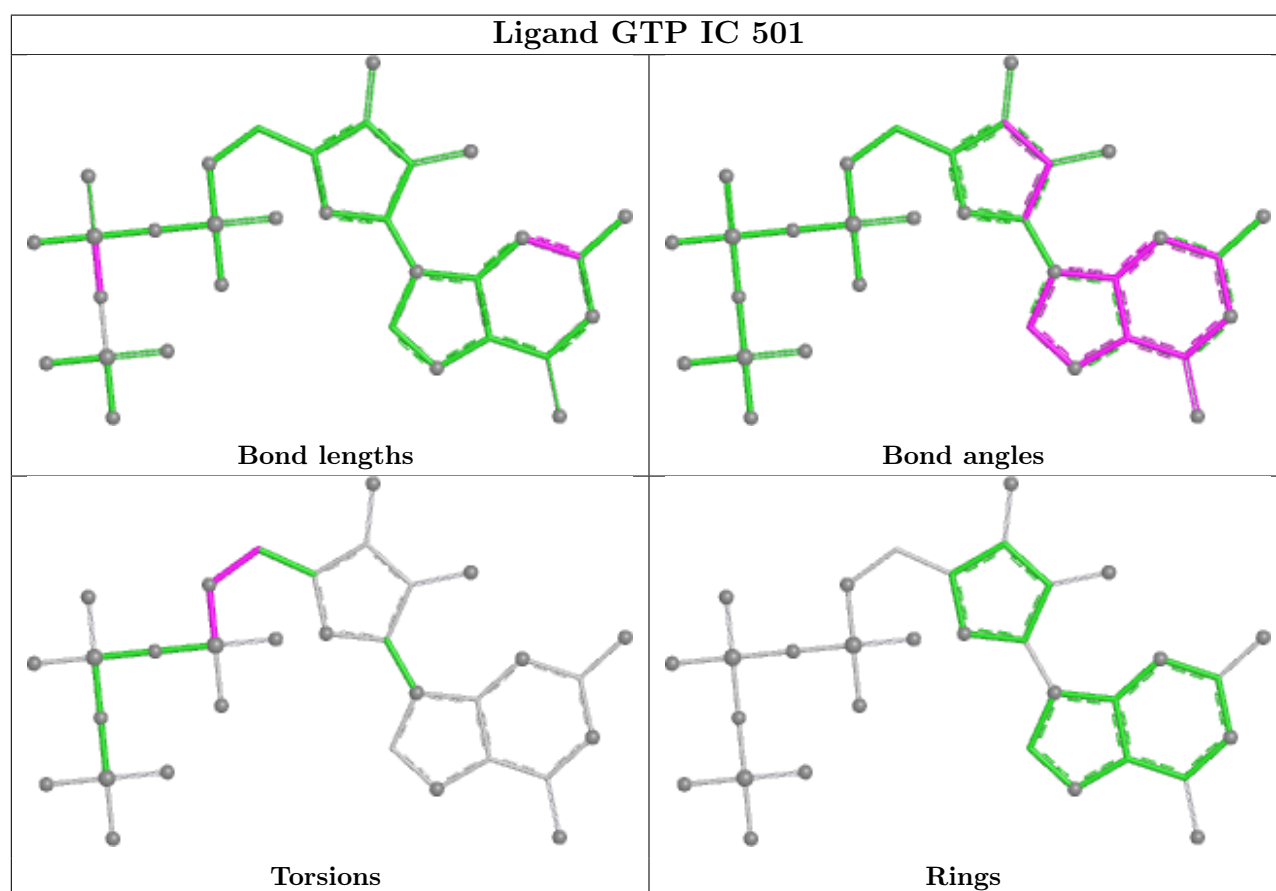
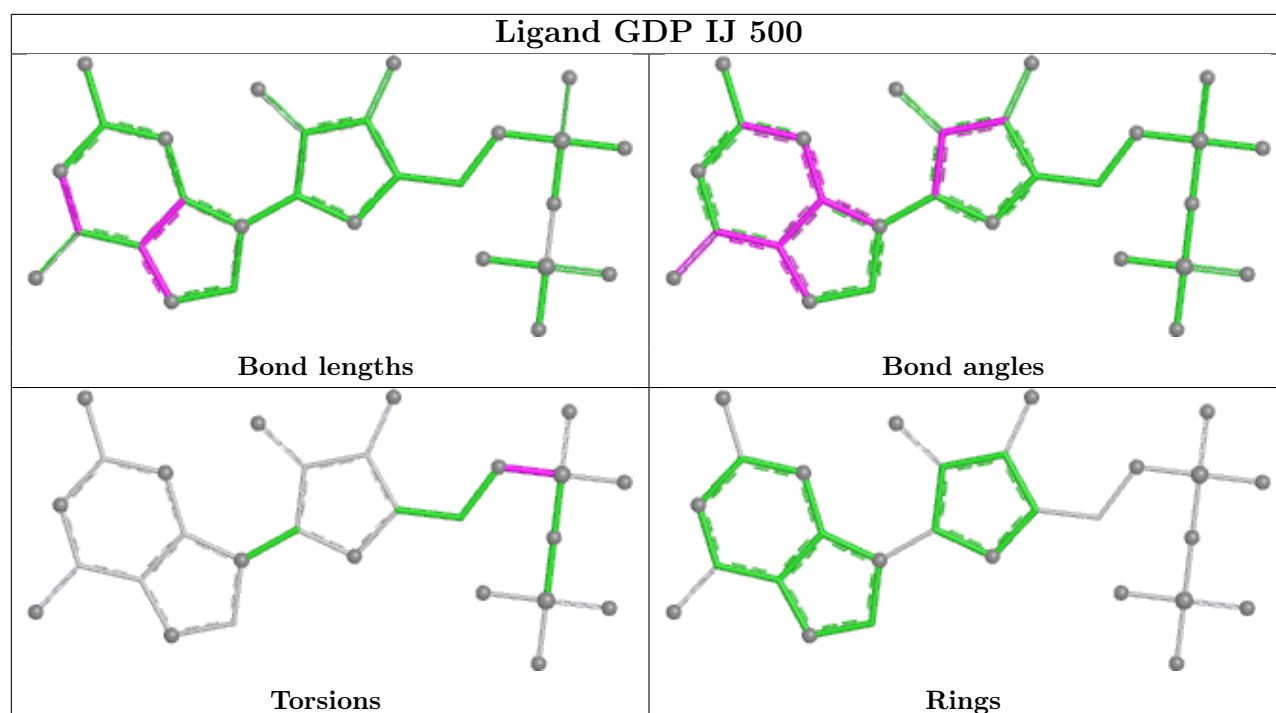


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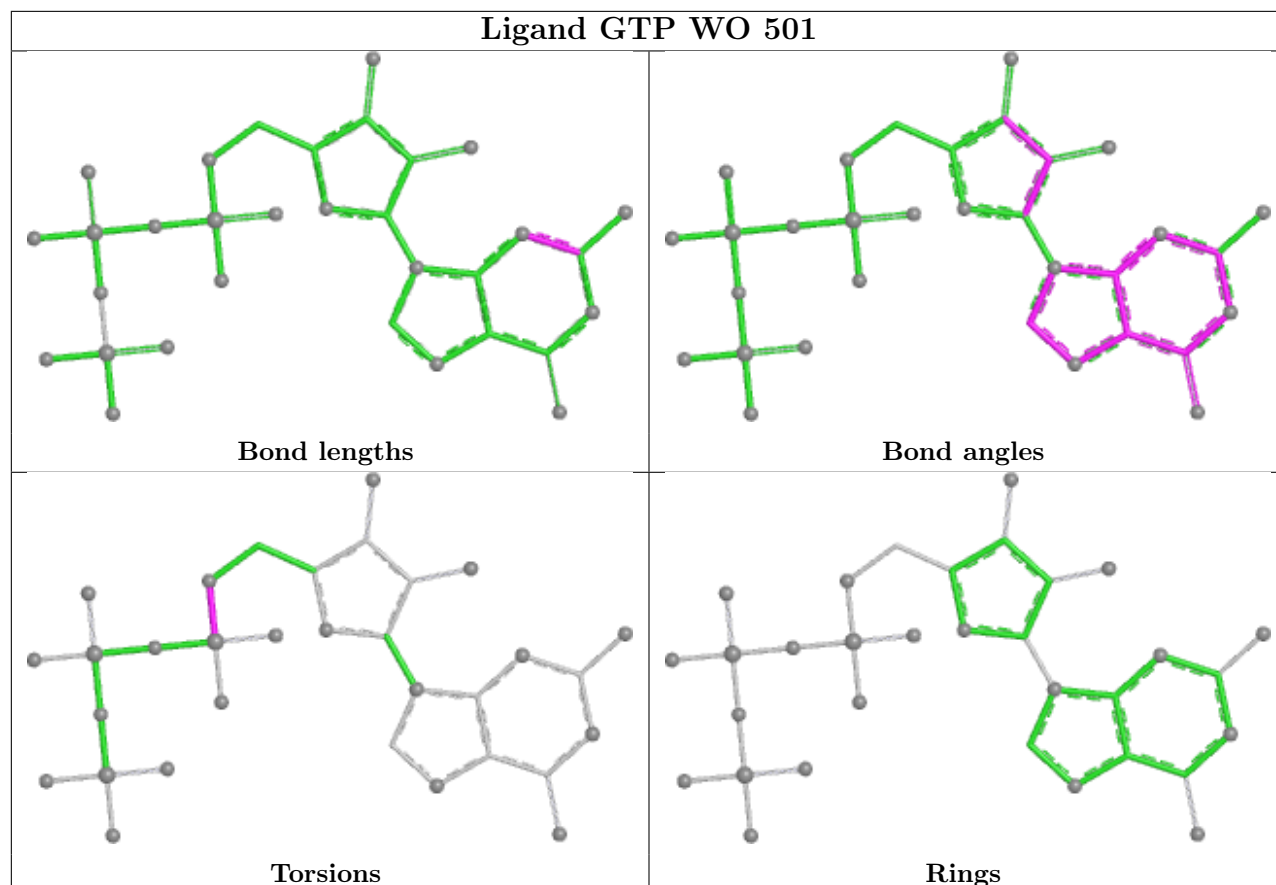


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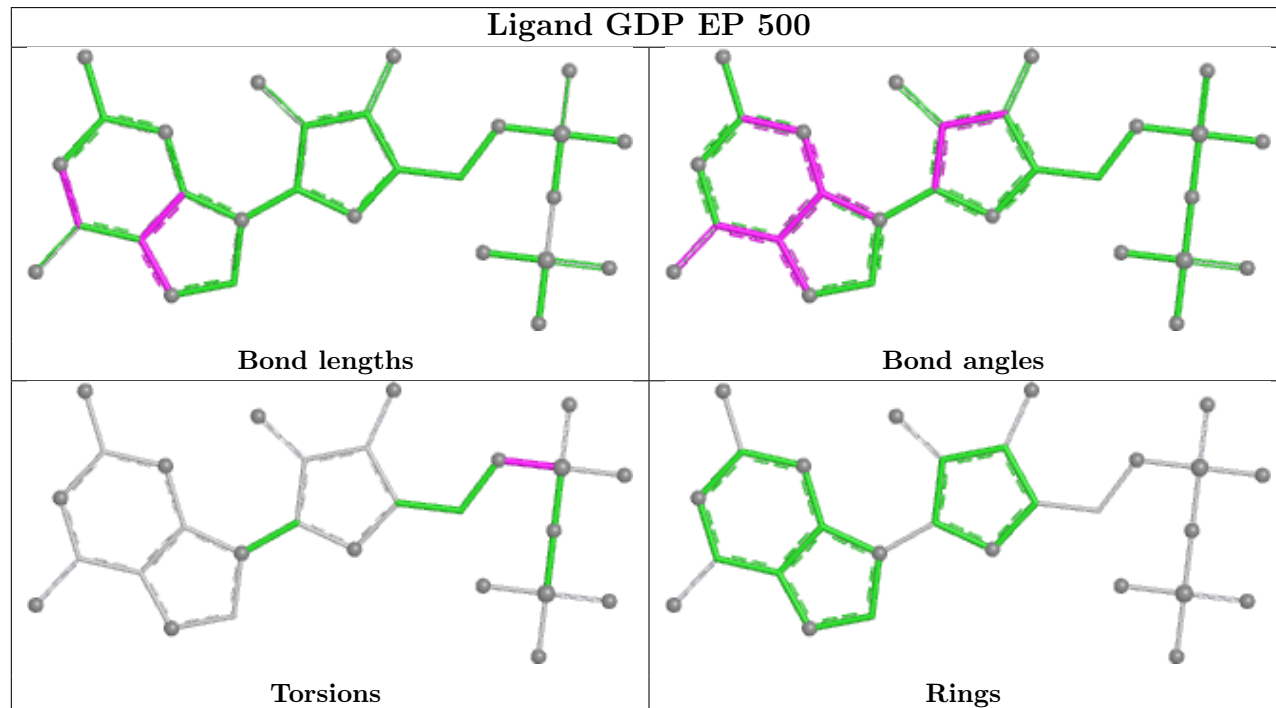


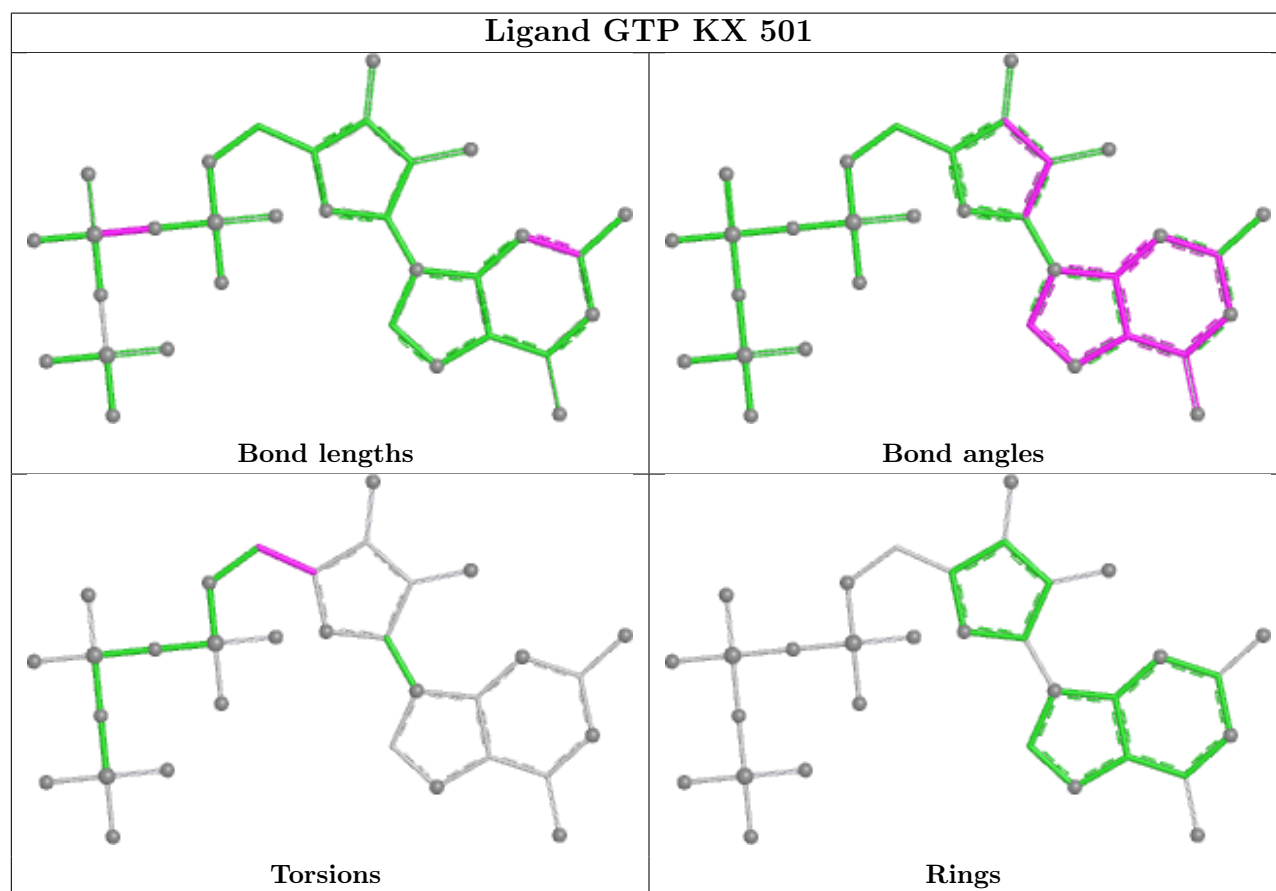
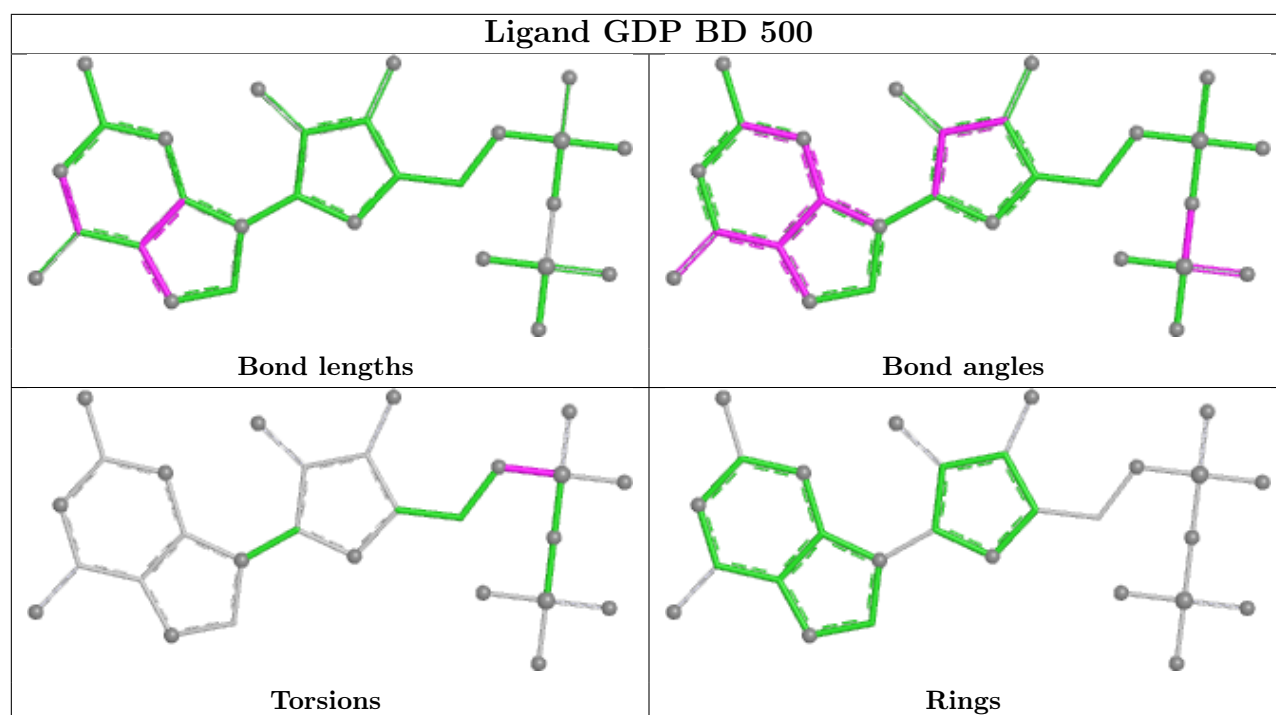


Ligand GTP WO 501

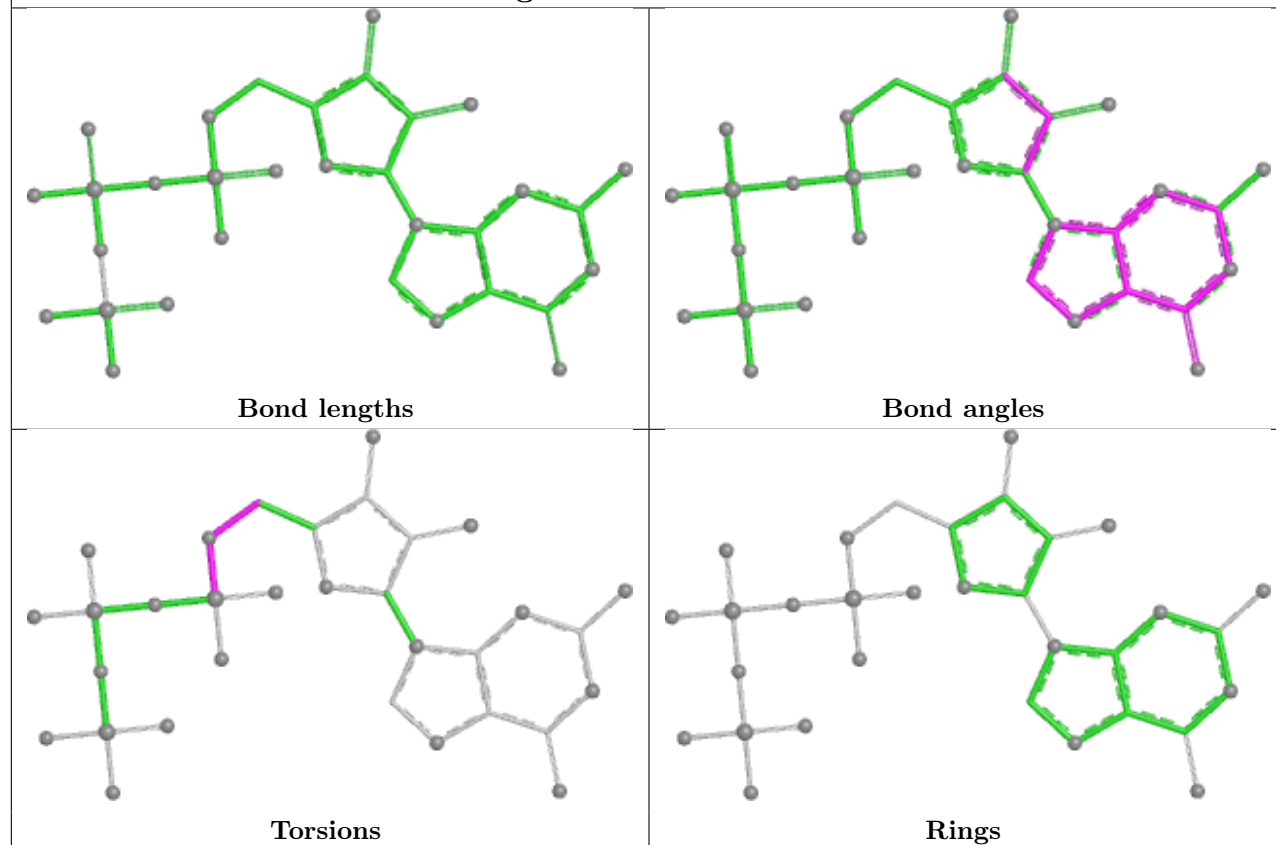


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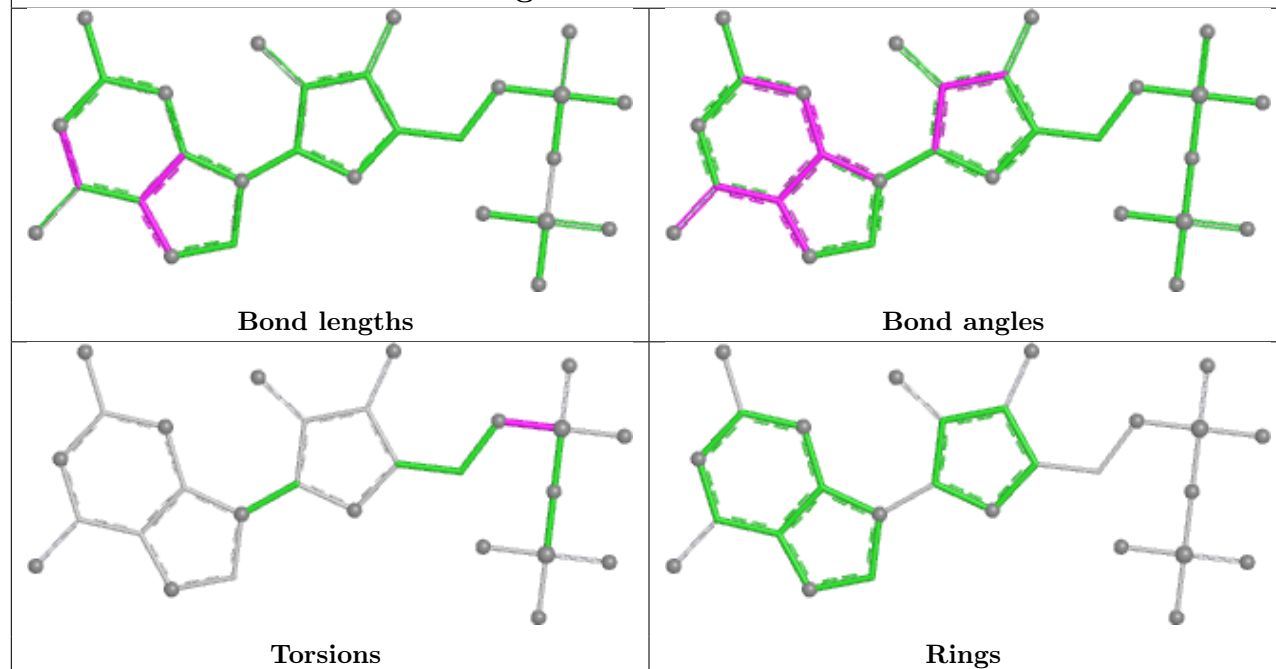


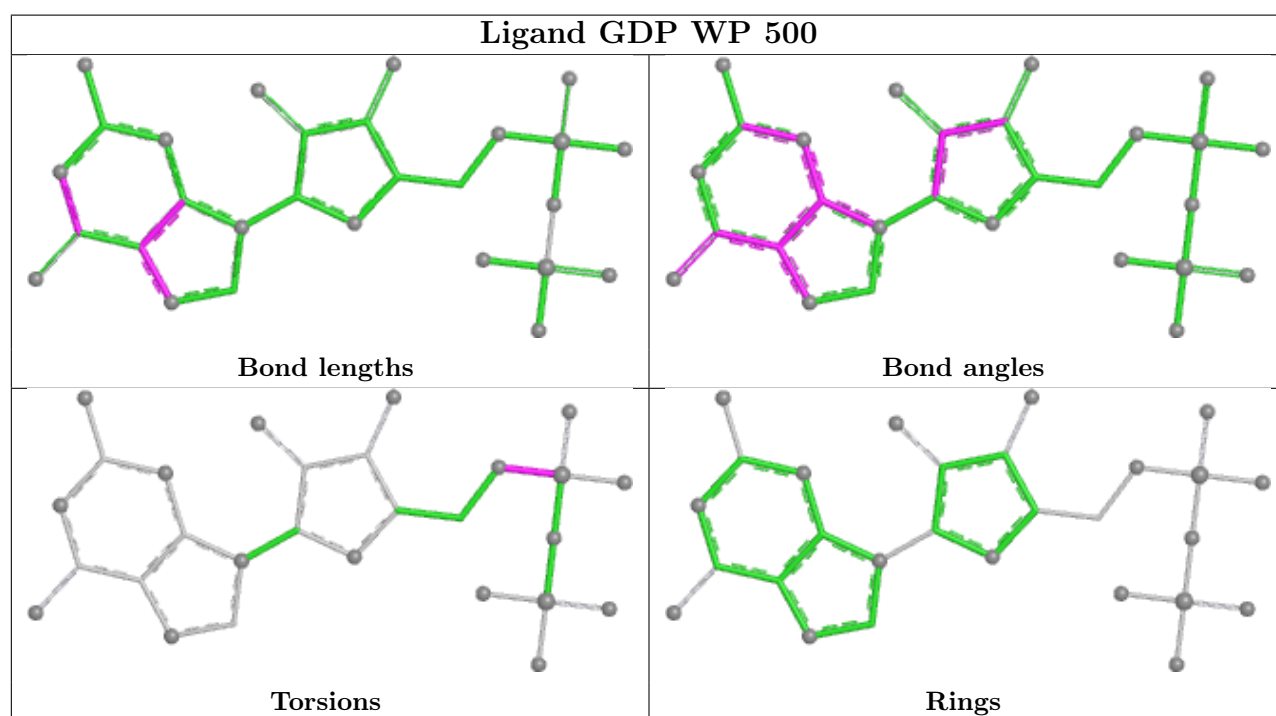
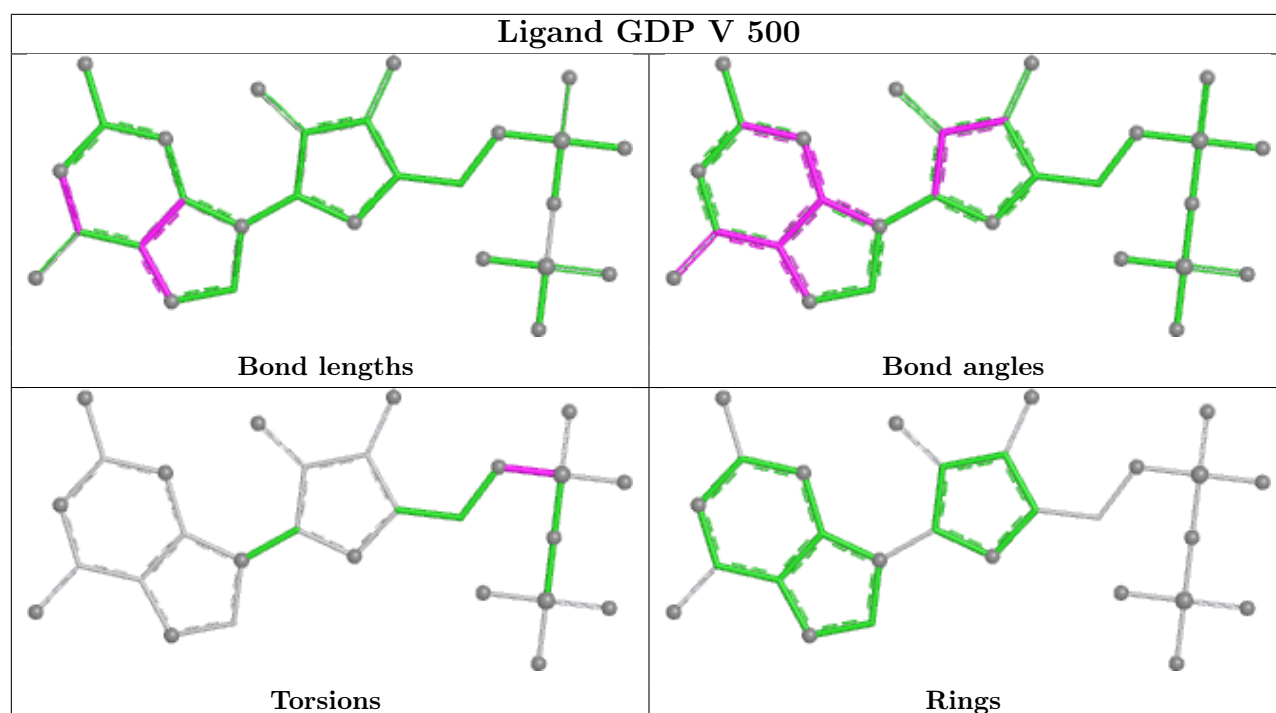


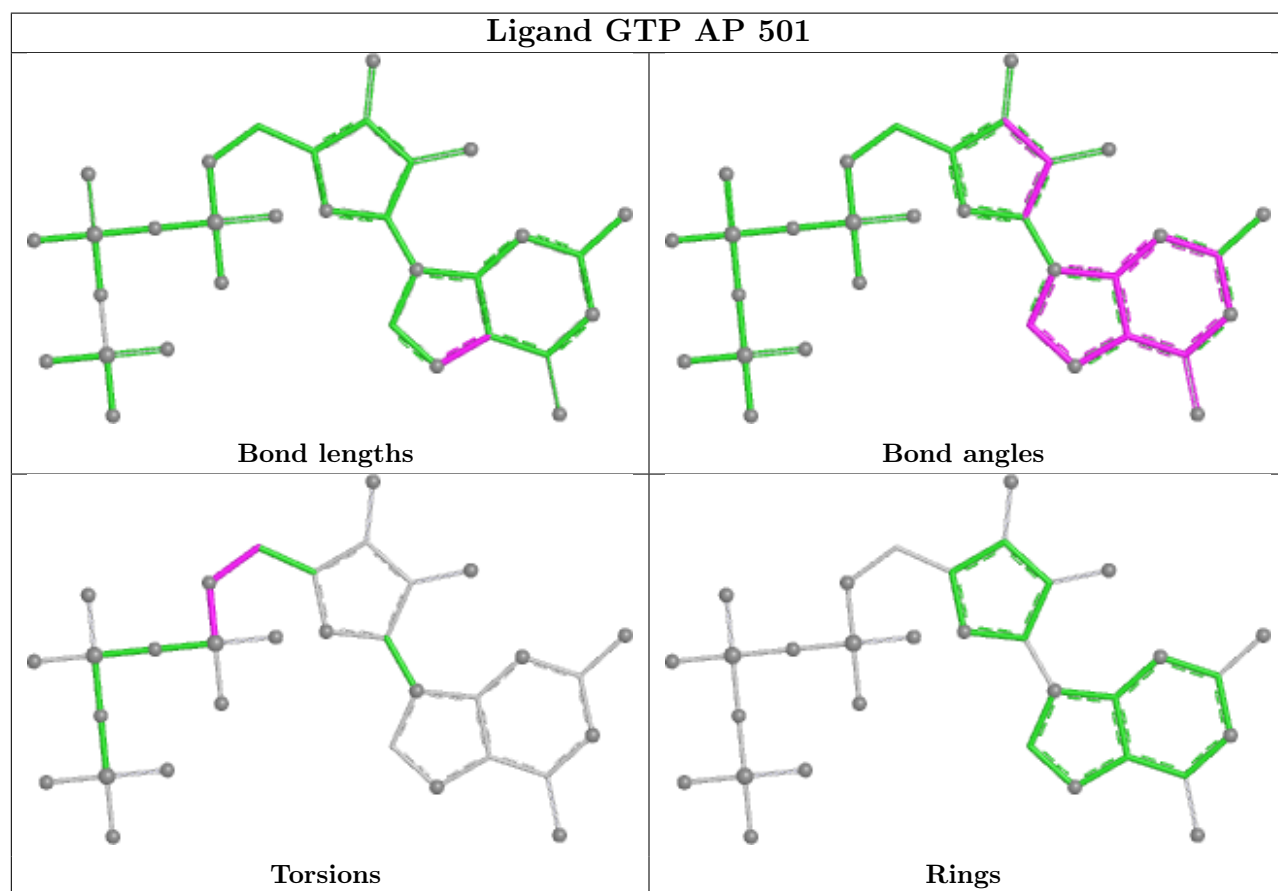
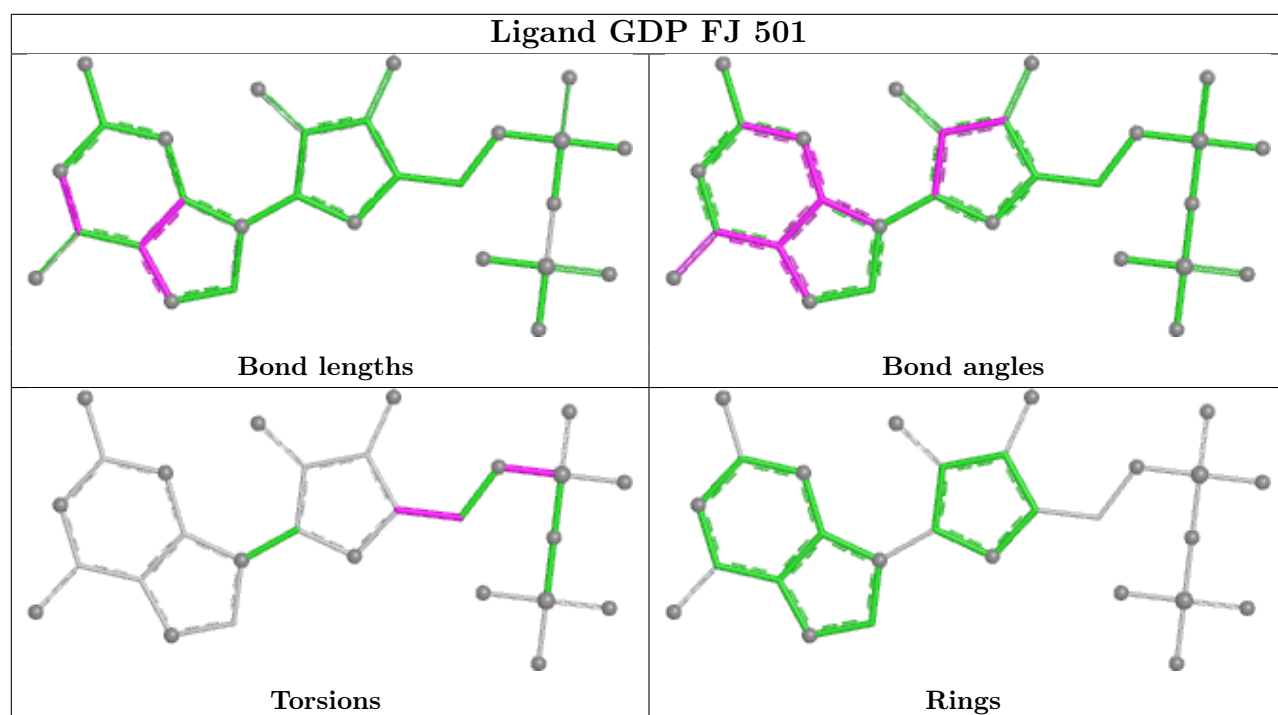
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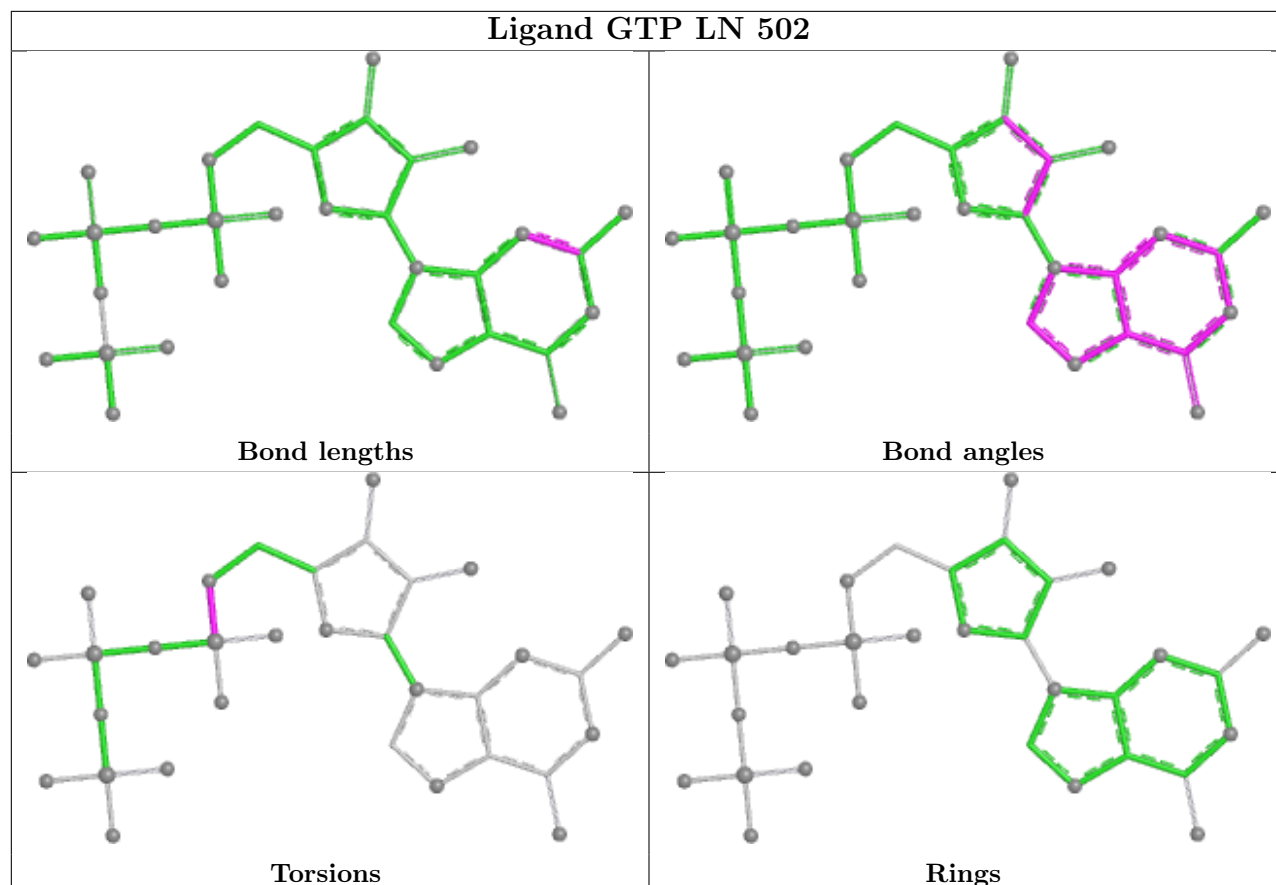
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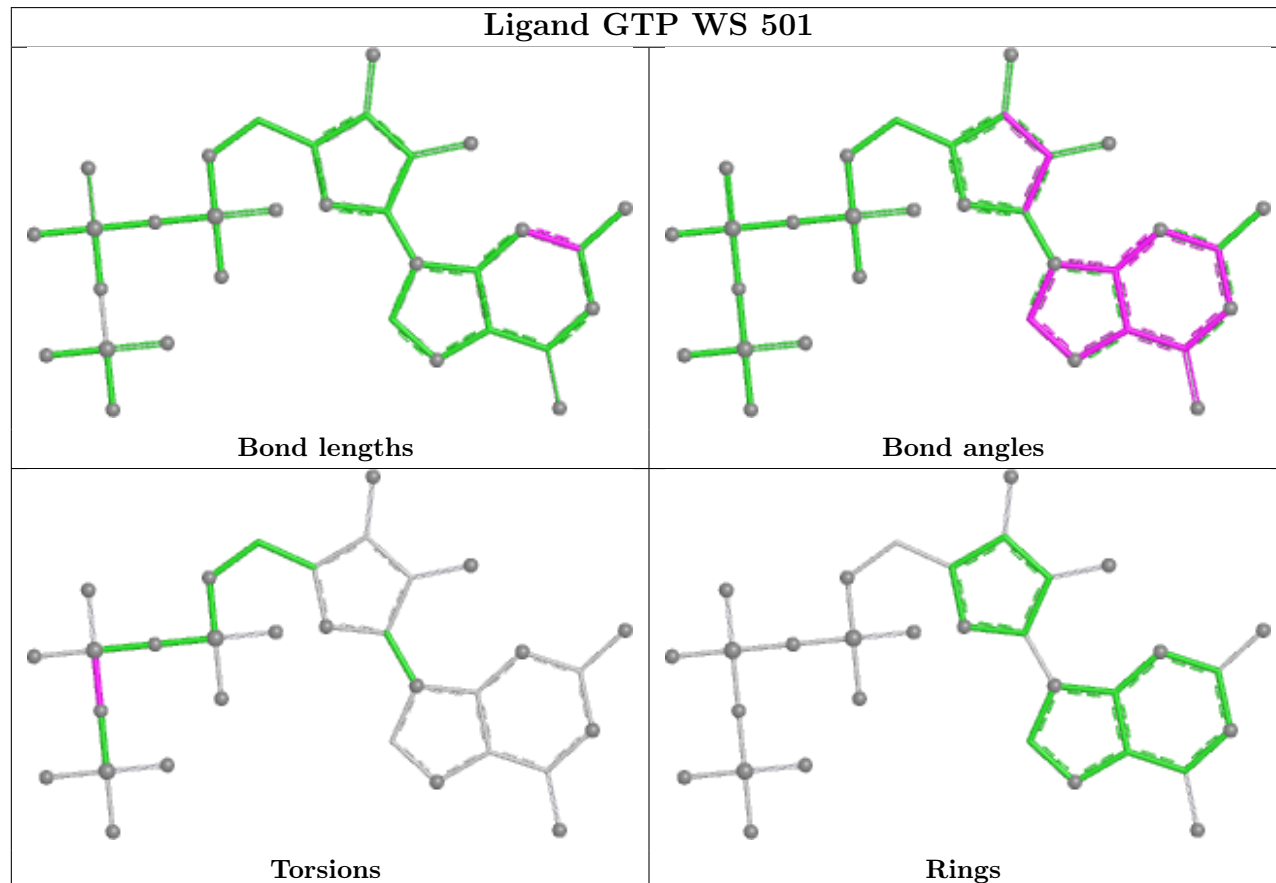




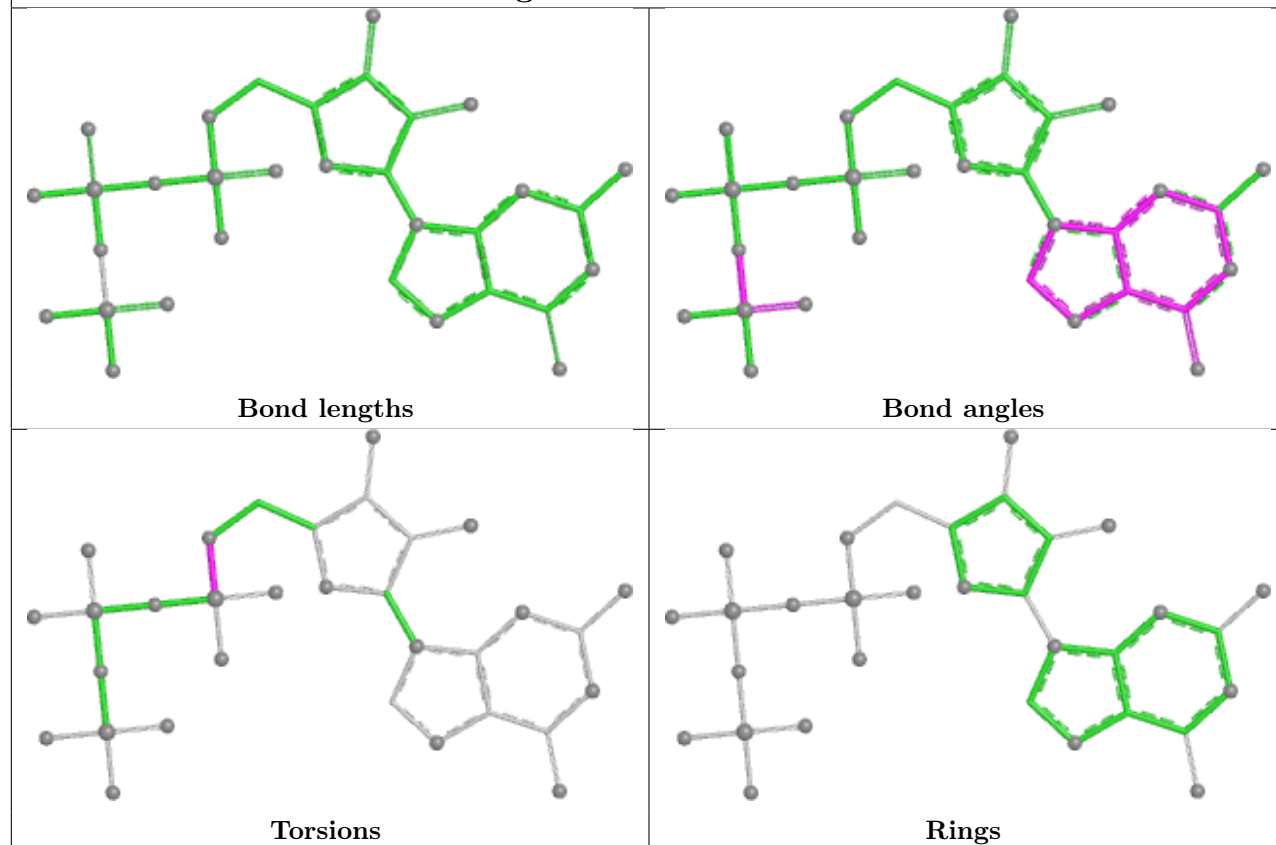
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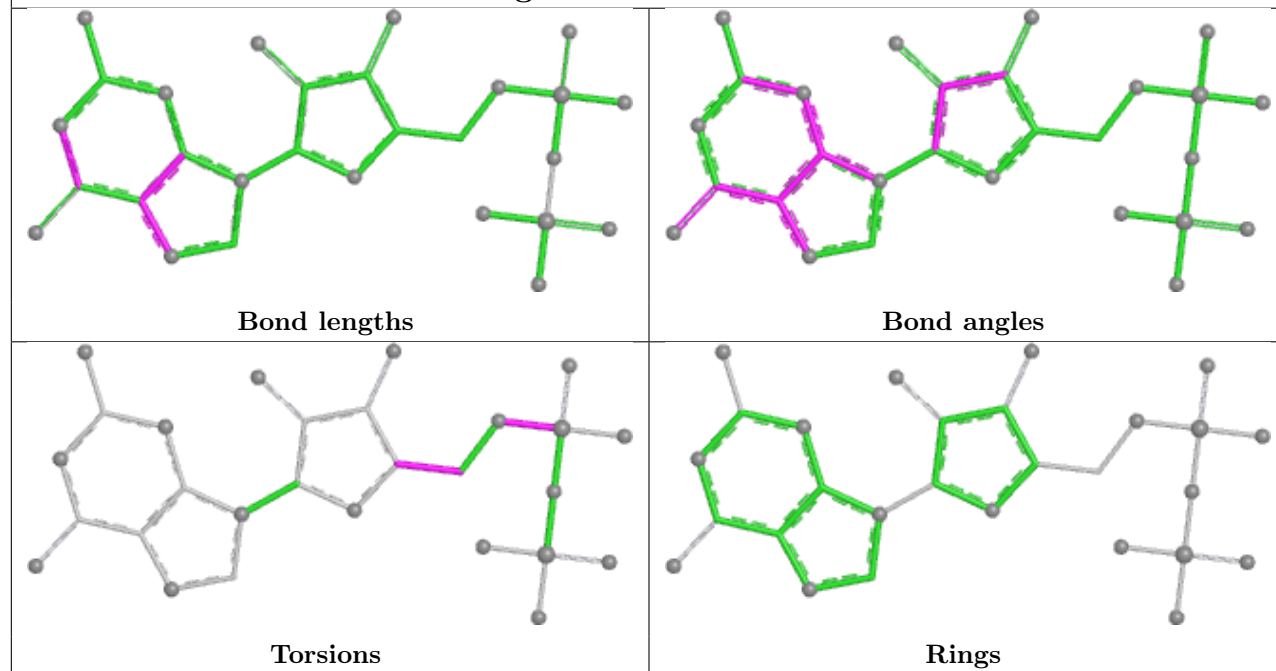
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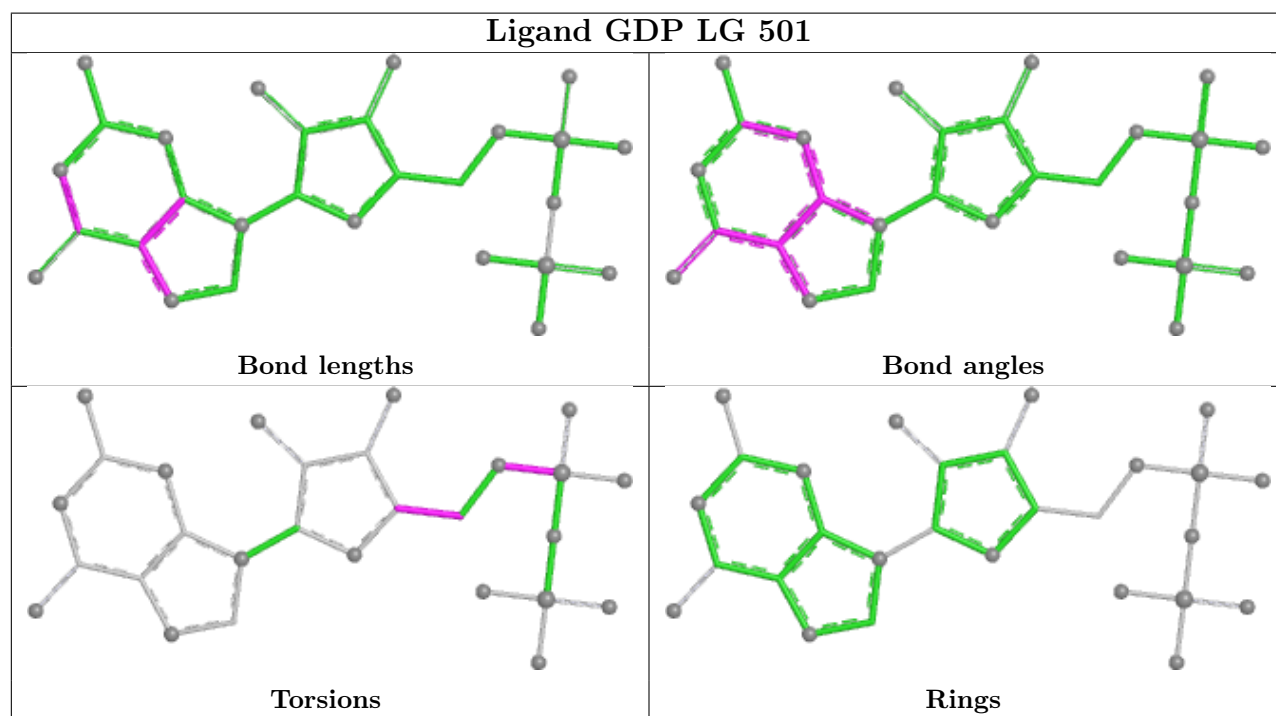
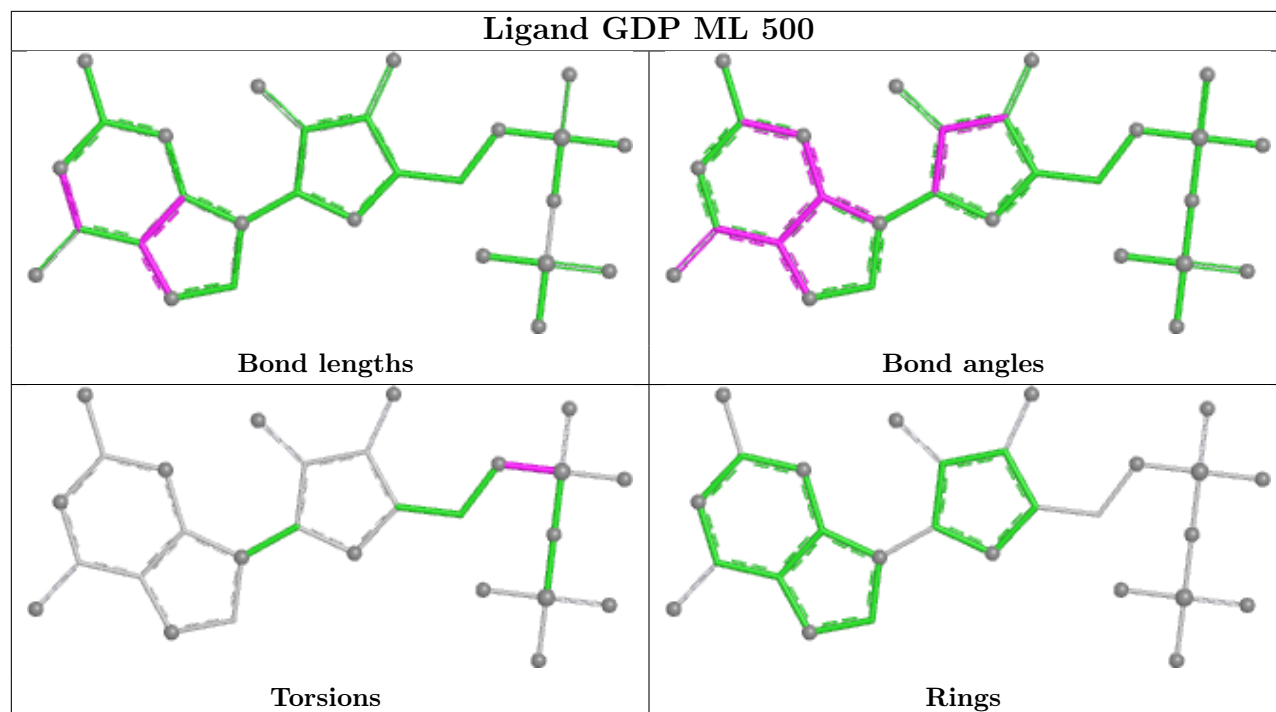


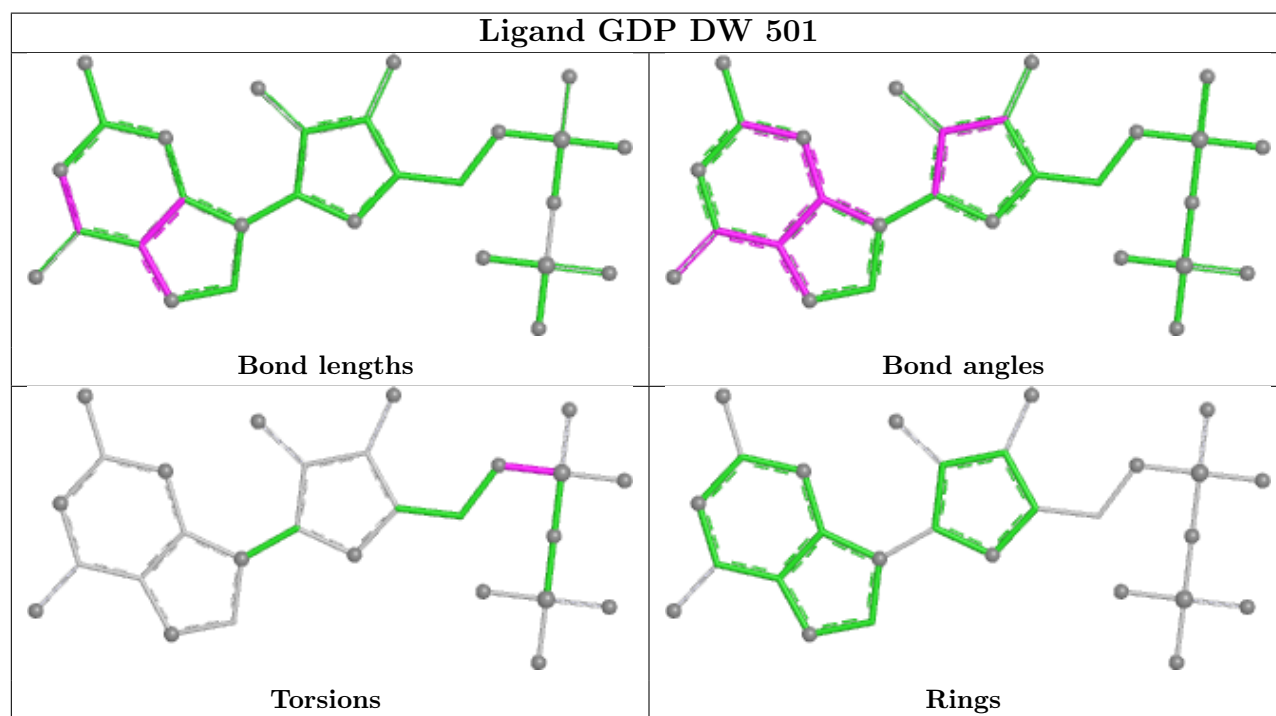
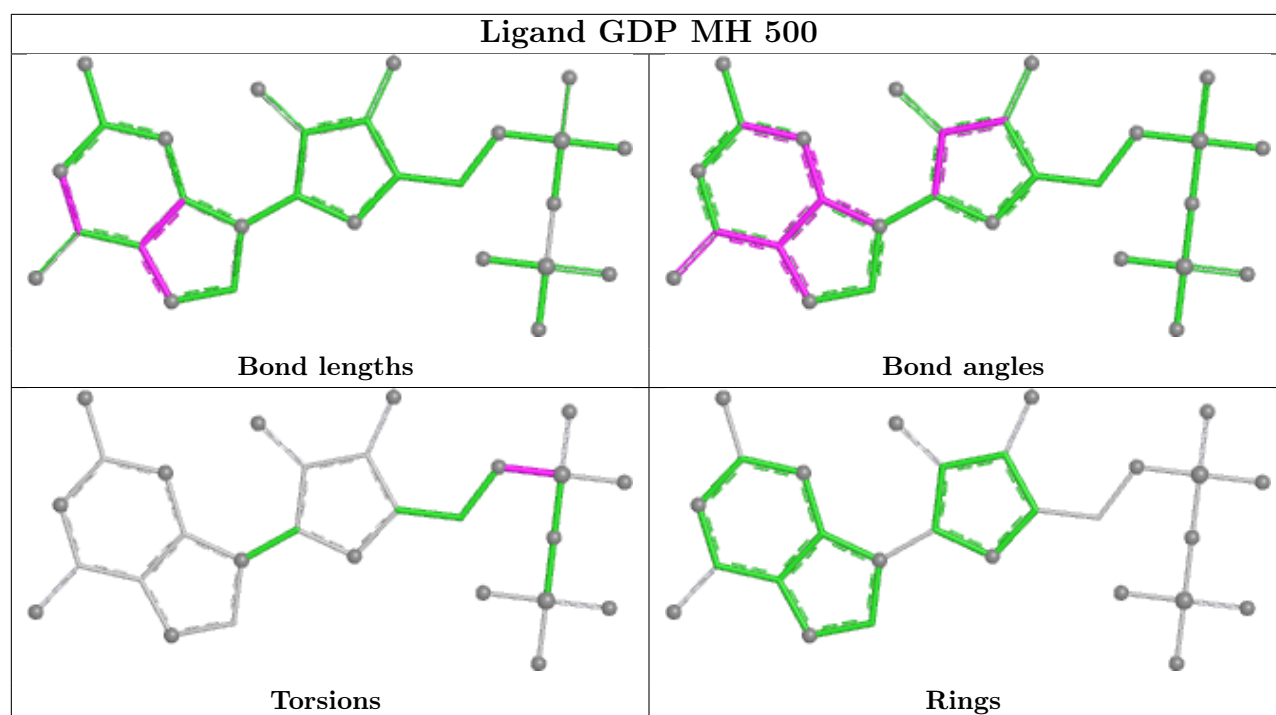
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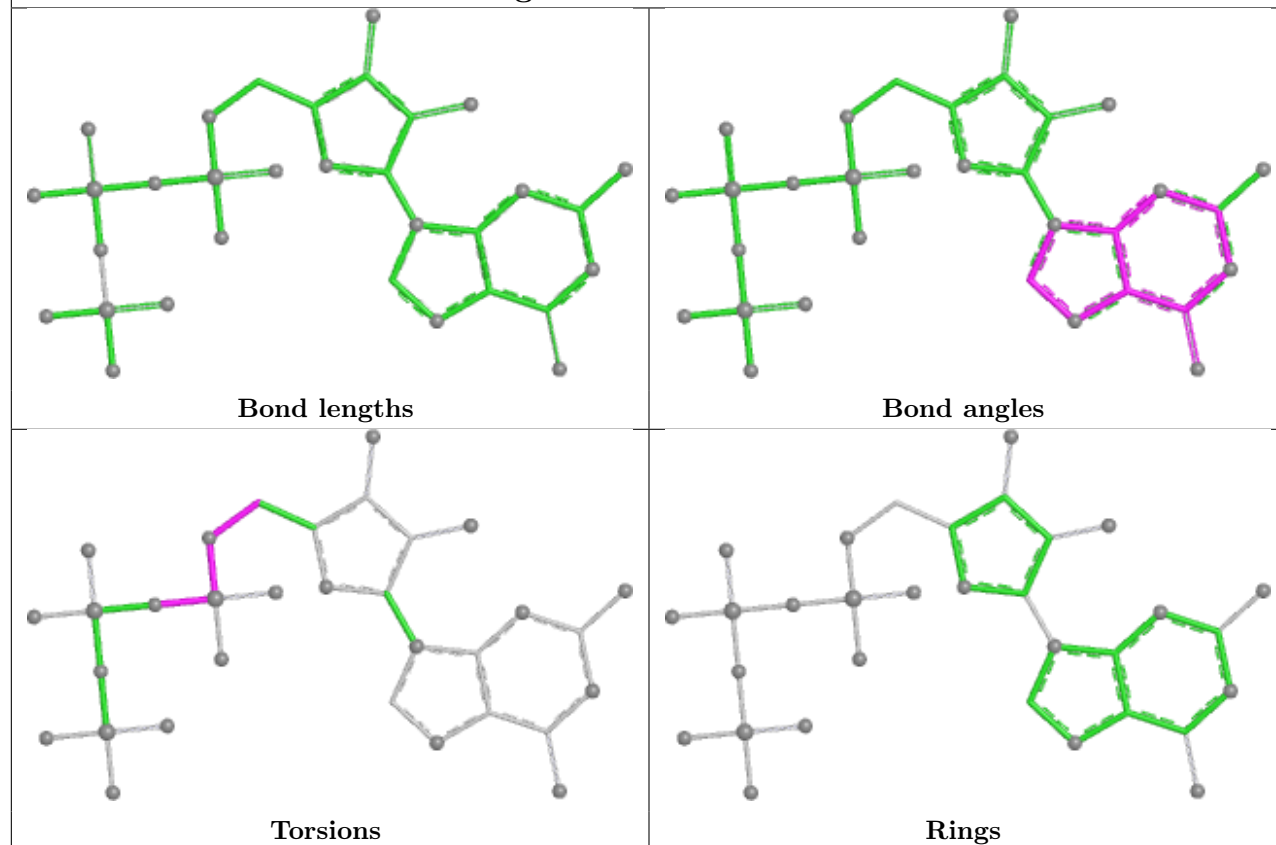
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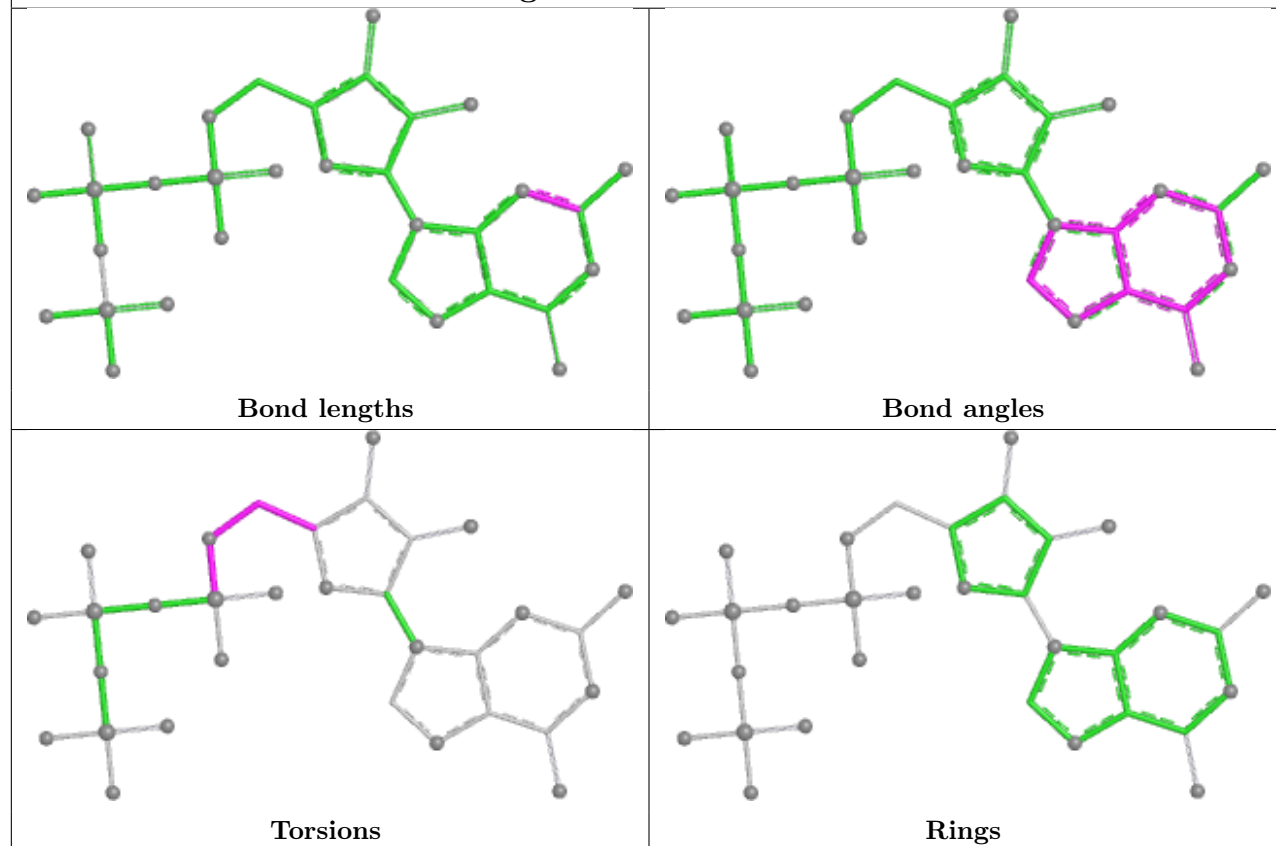


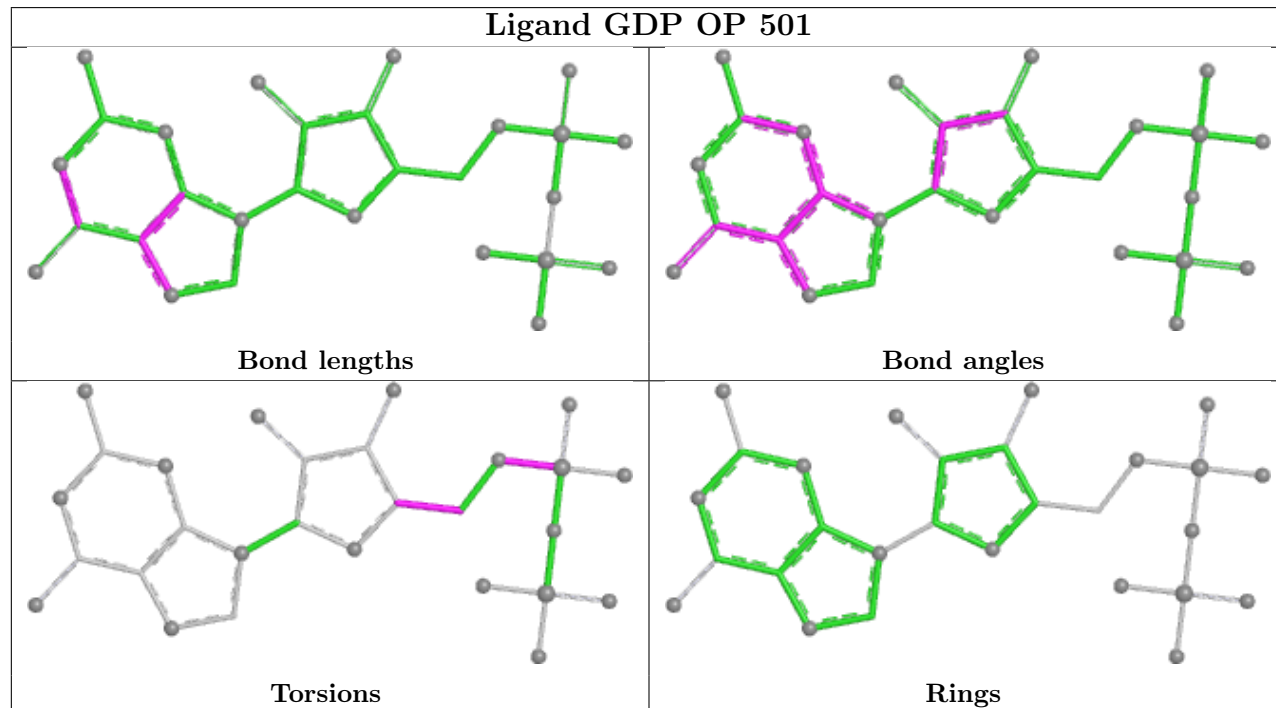
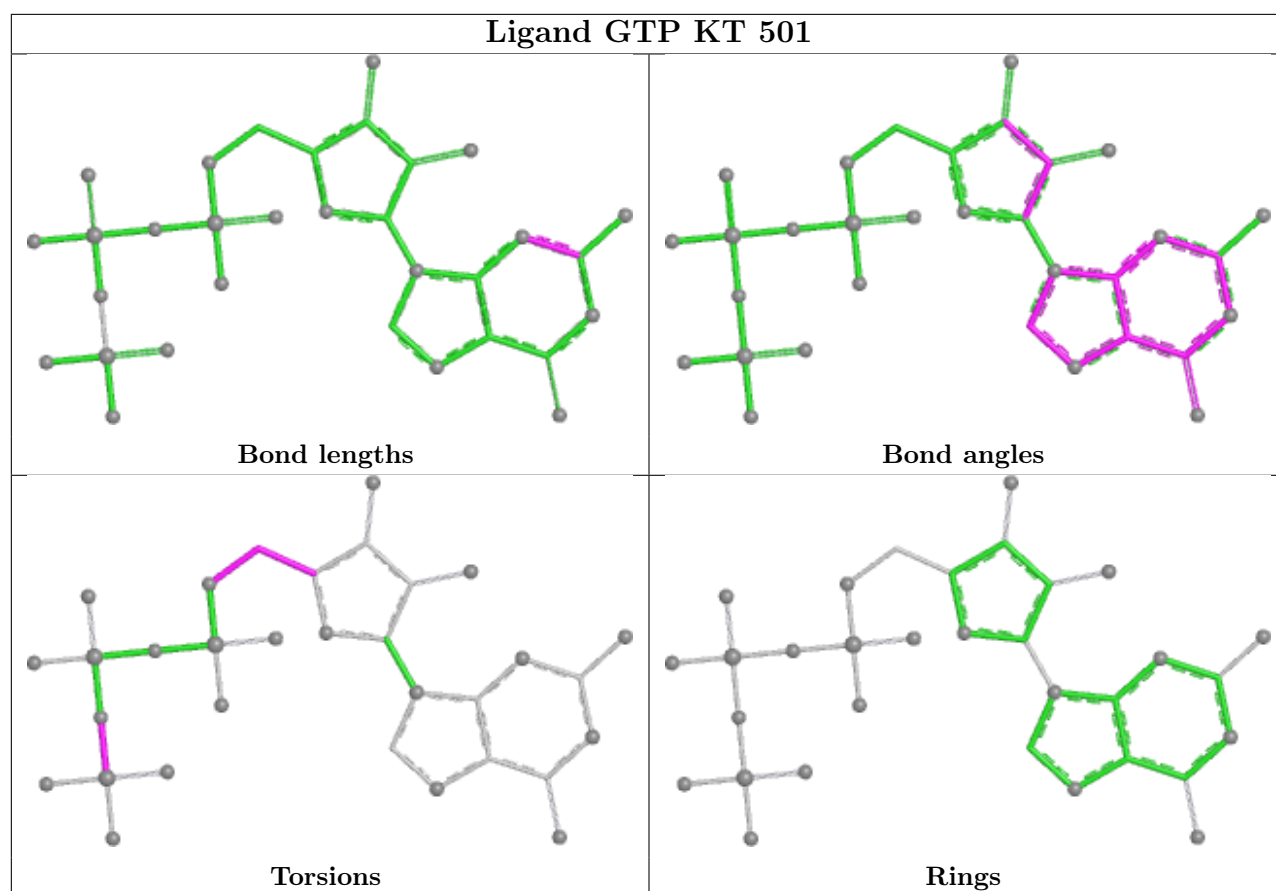


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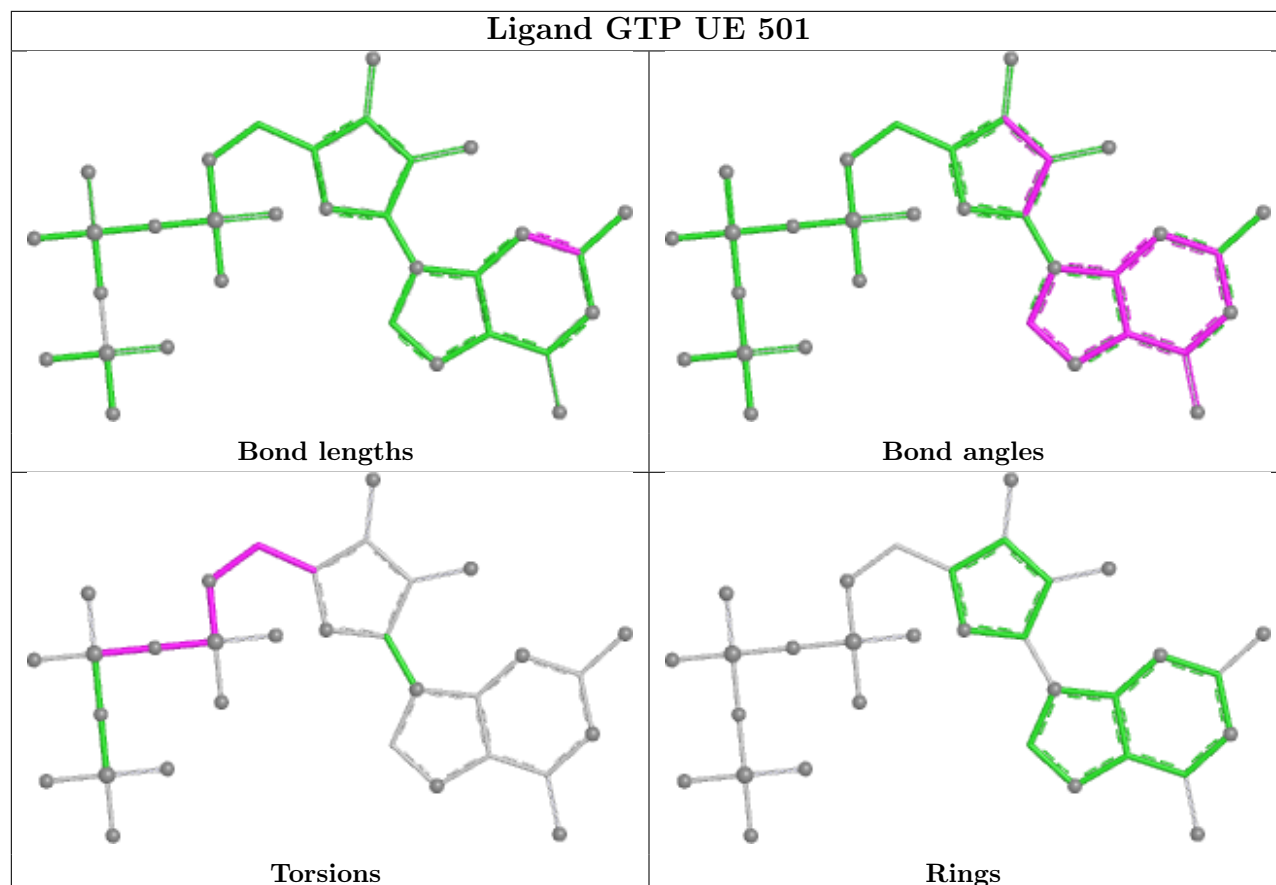


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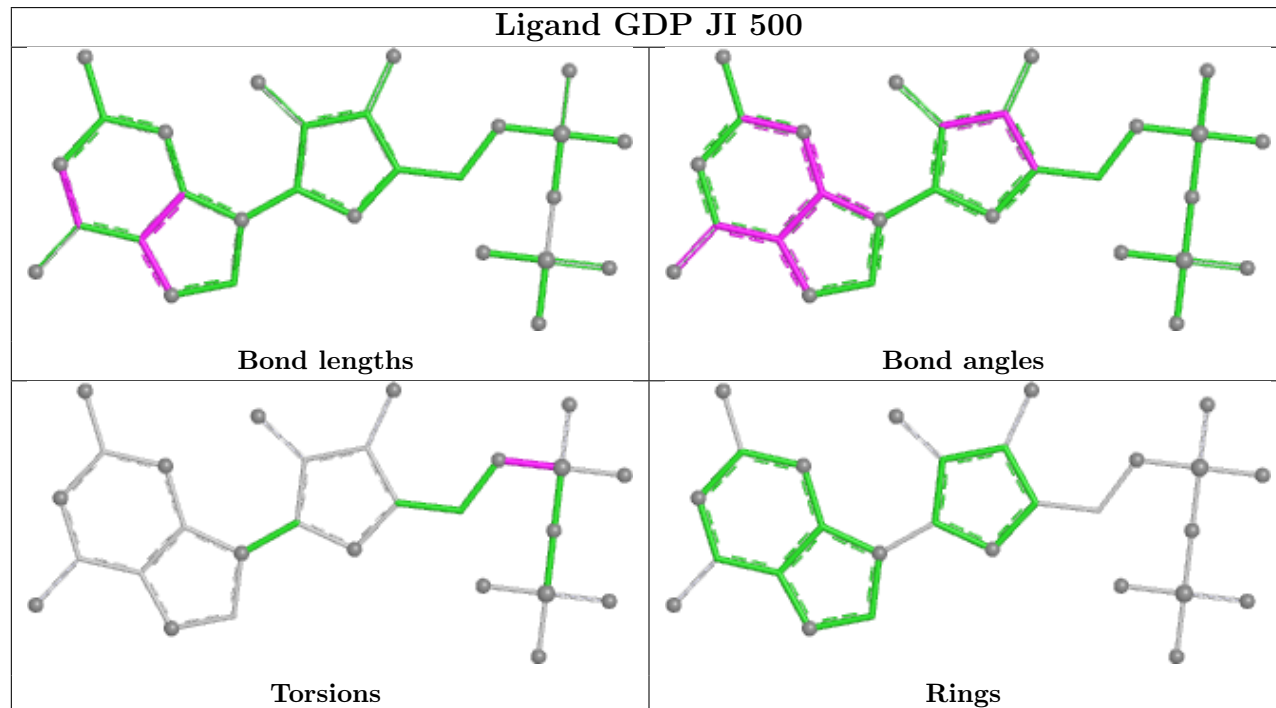


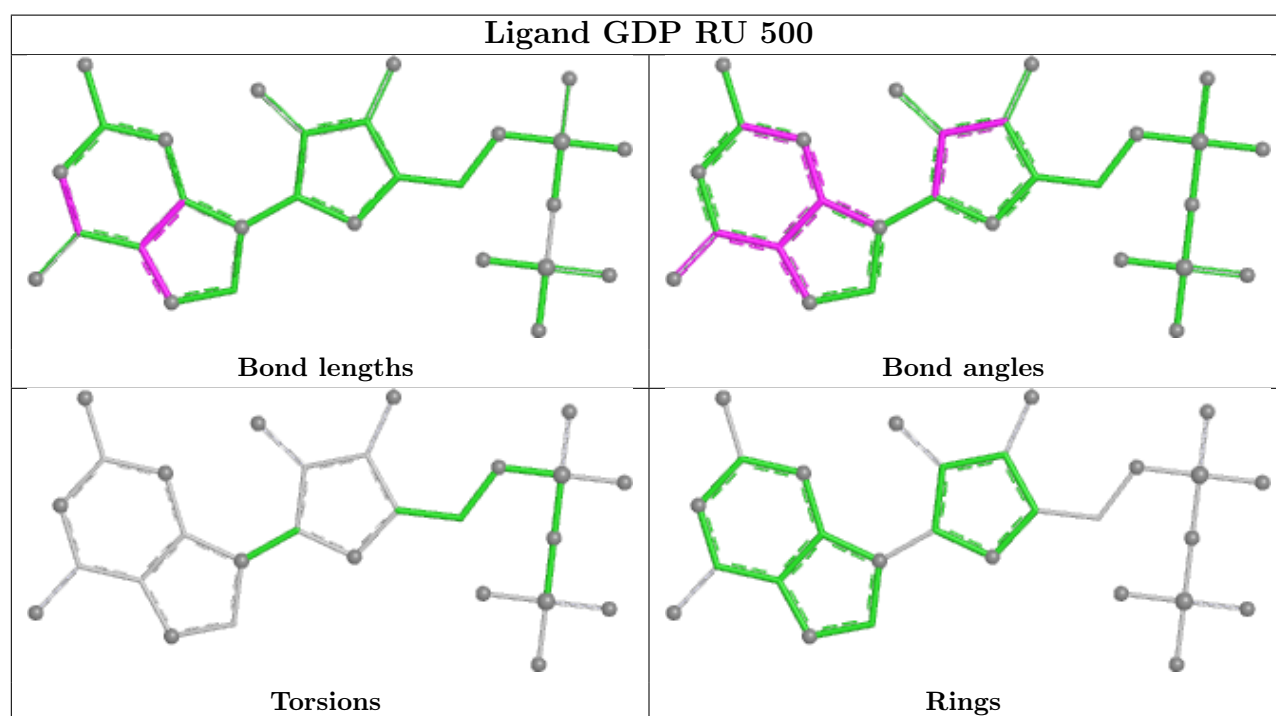
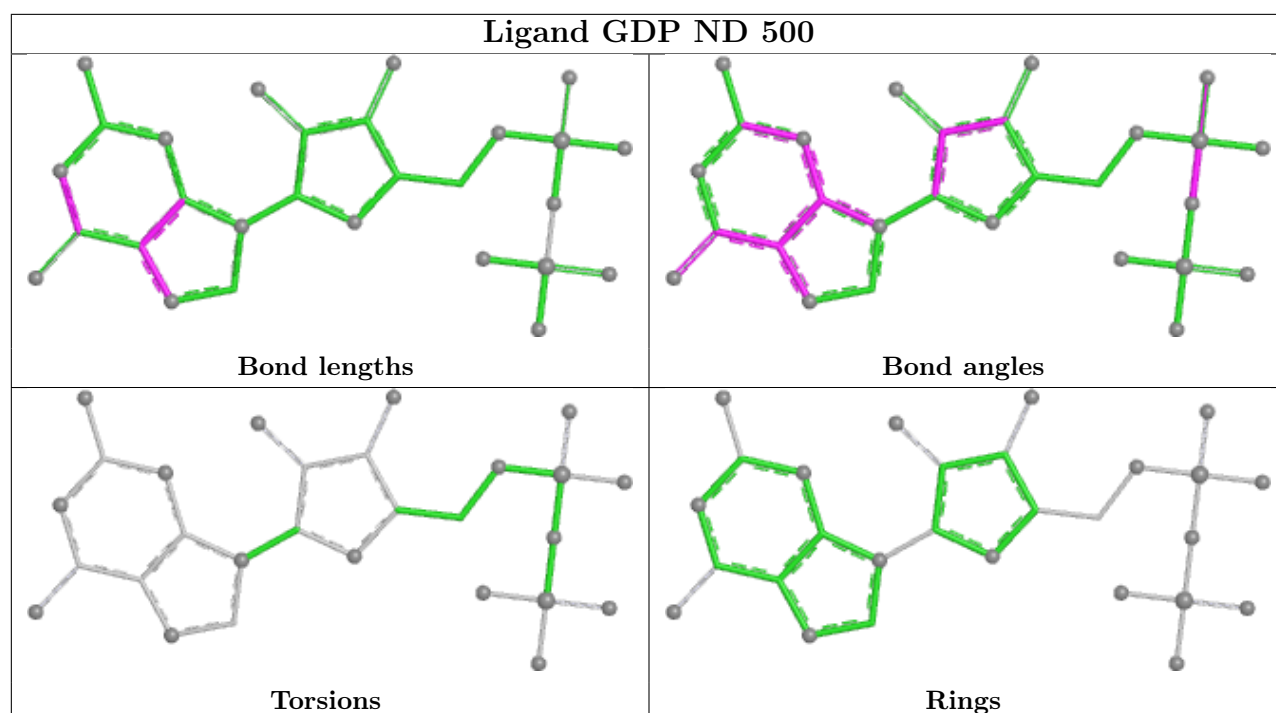


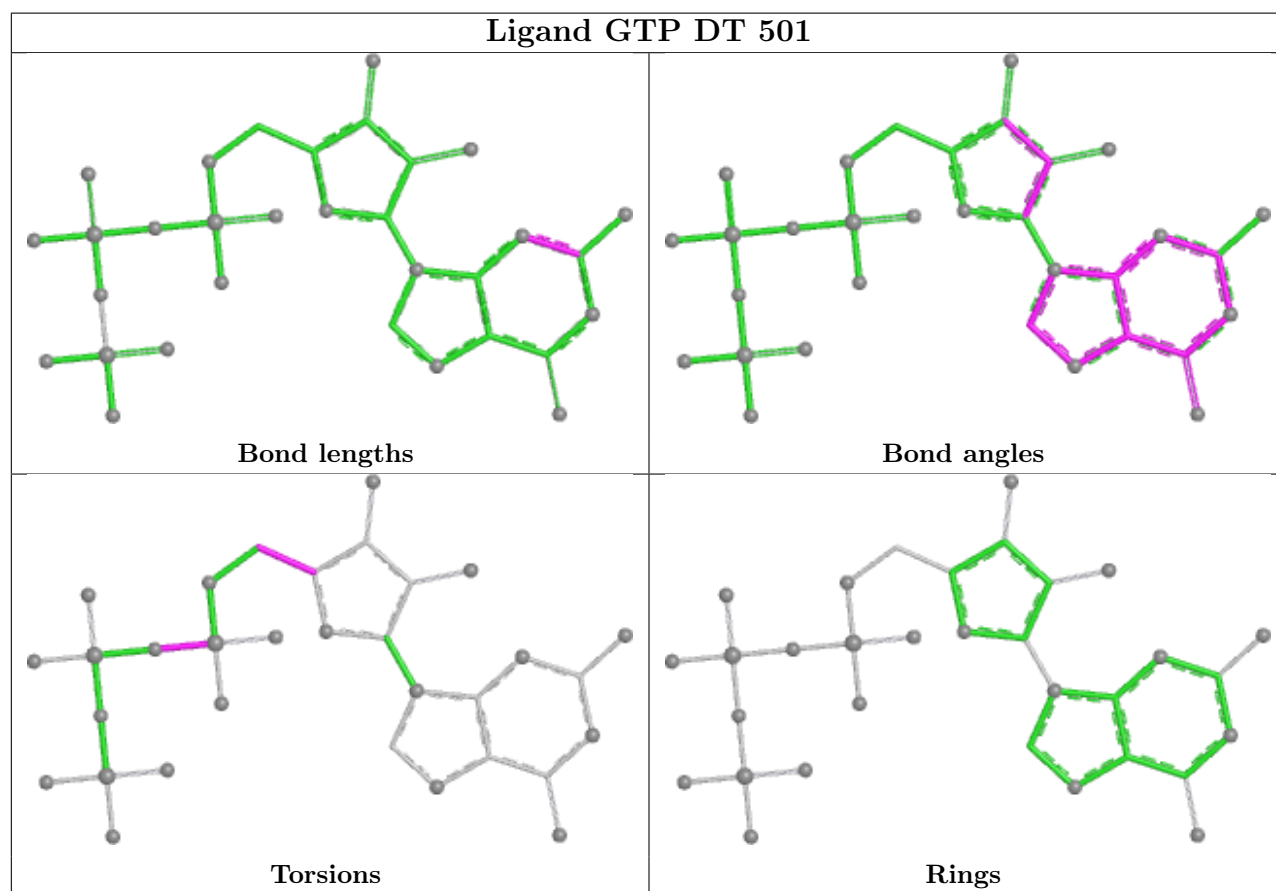
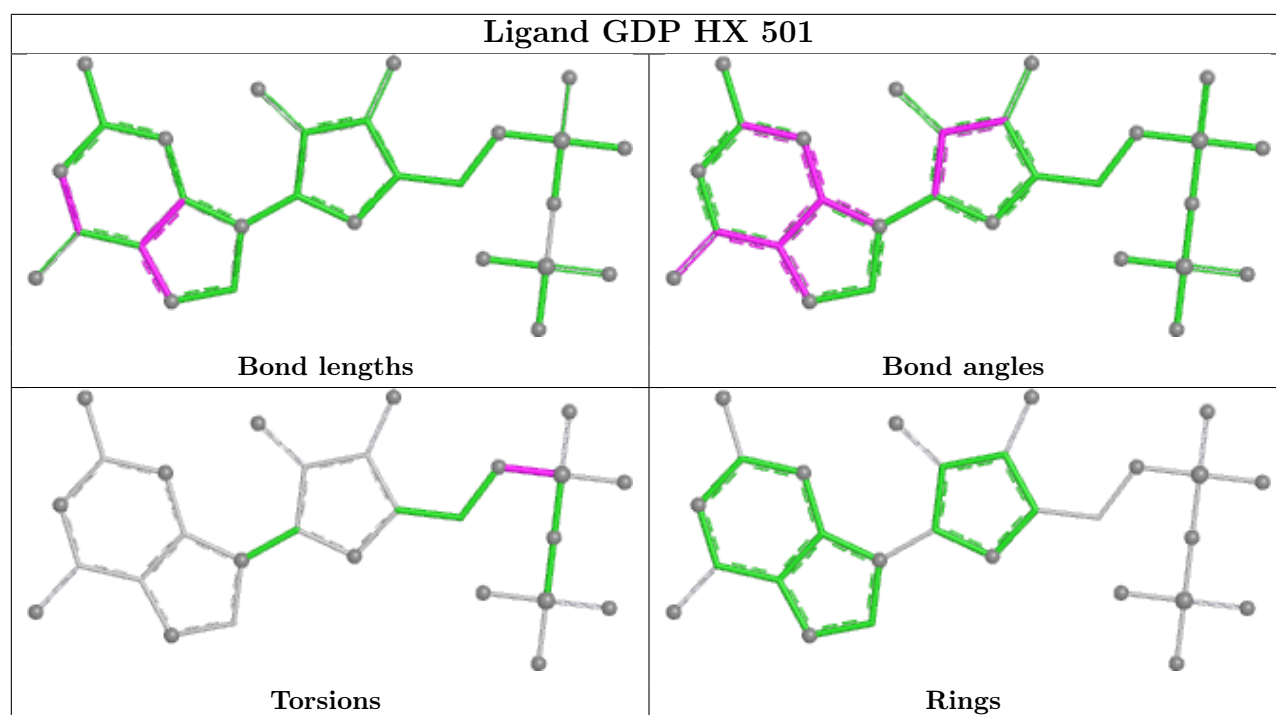
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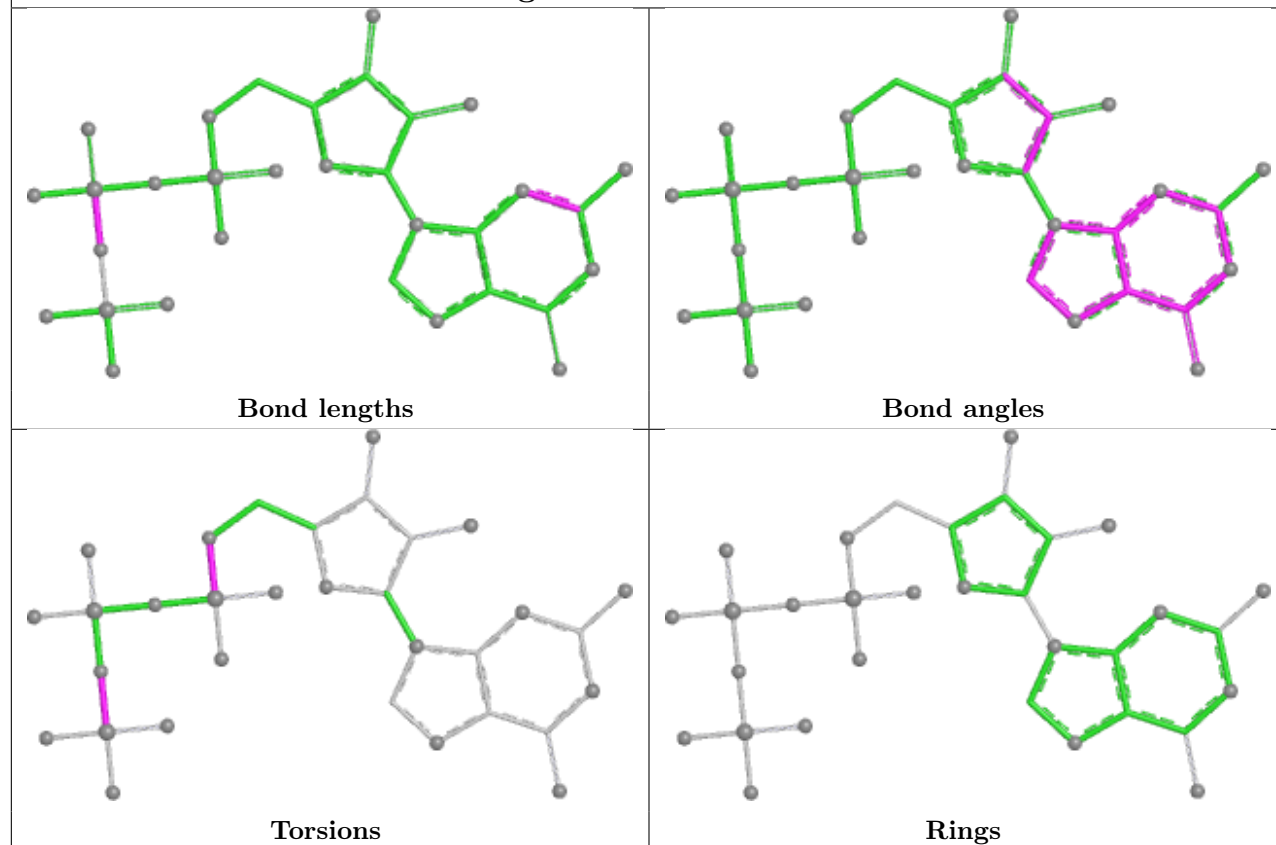
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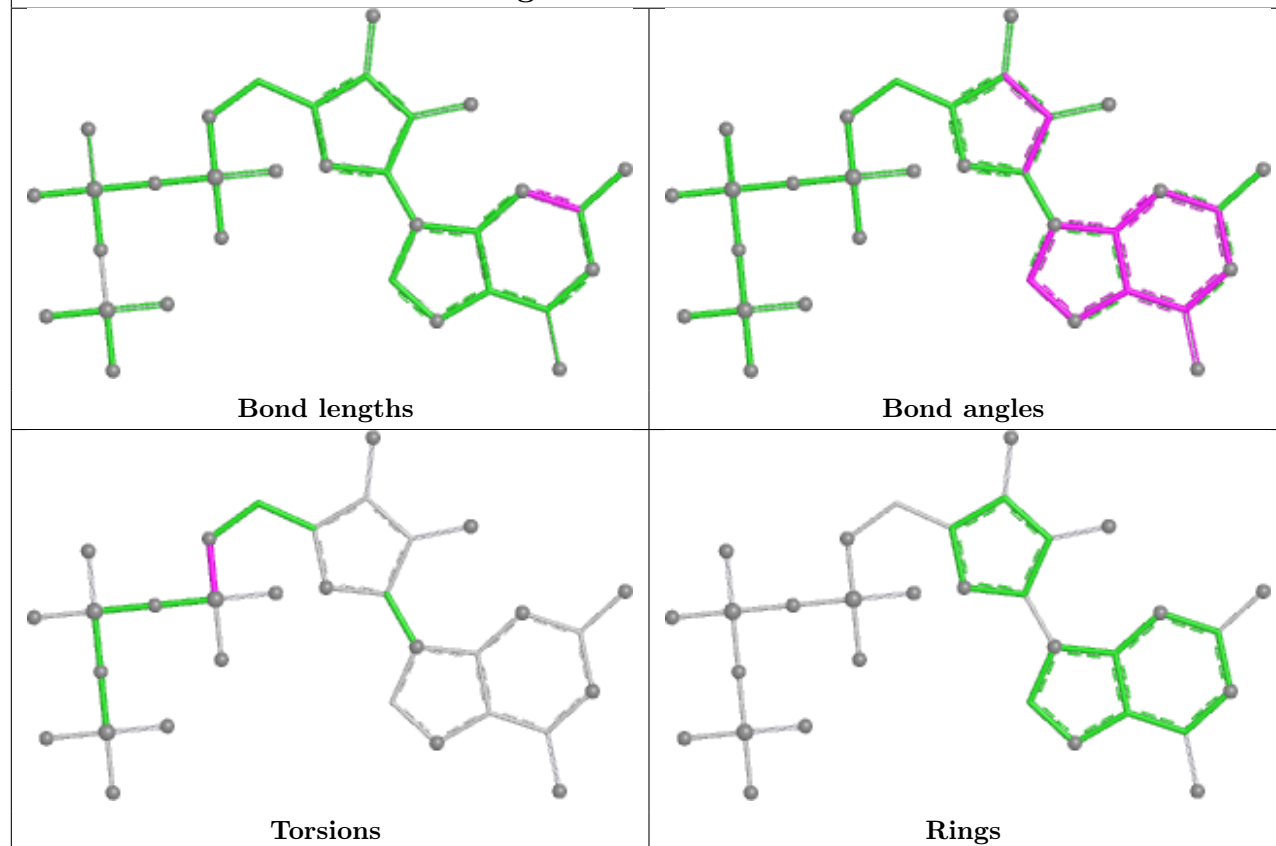


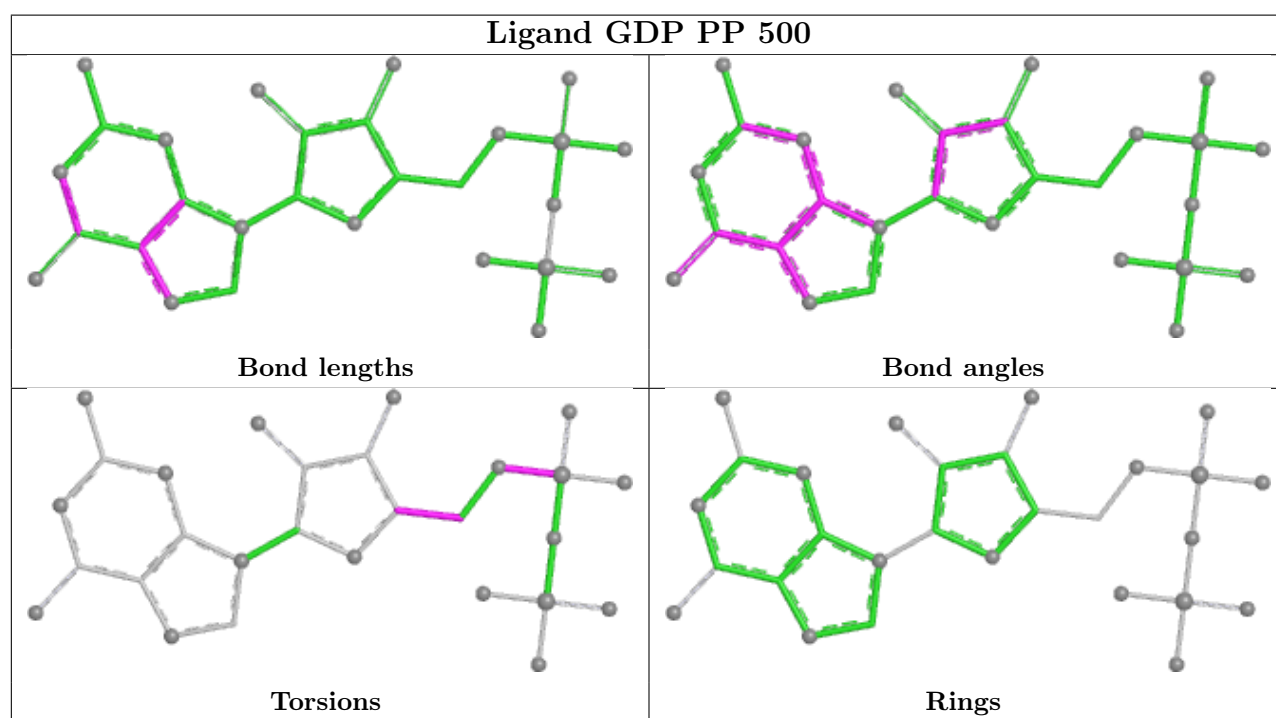
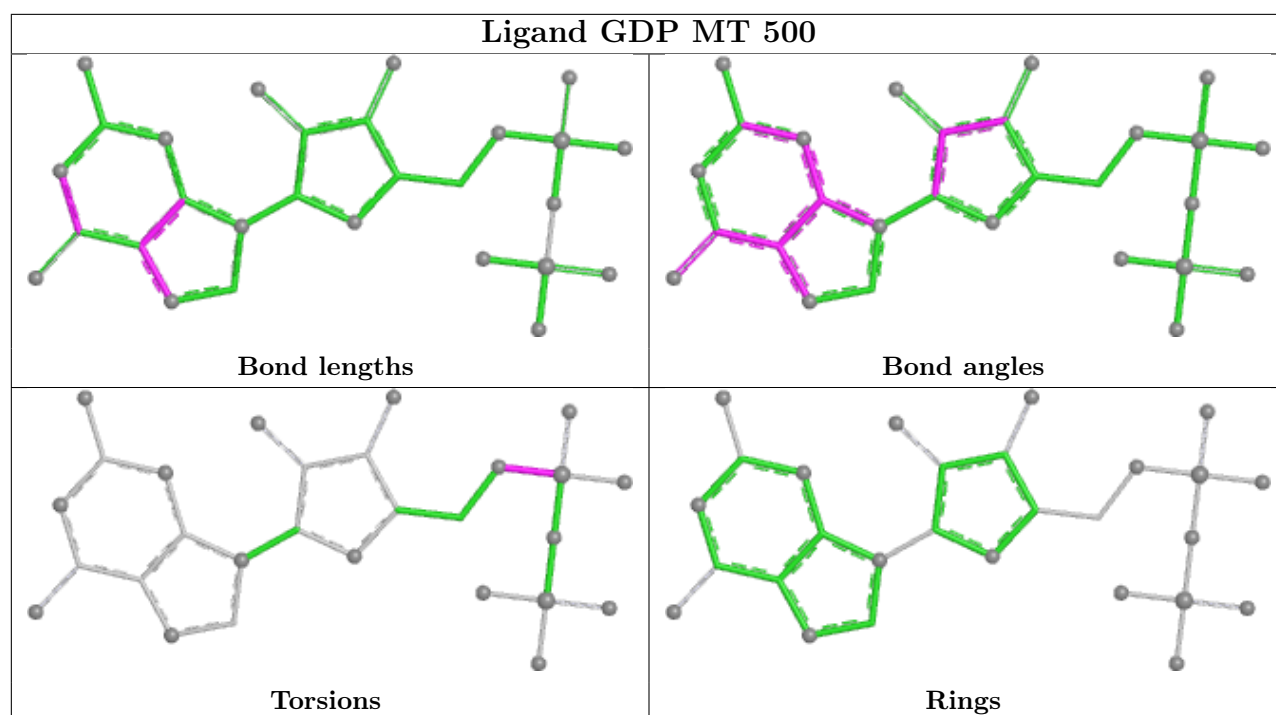


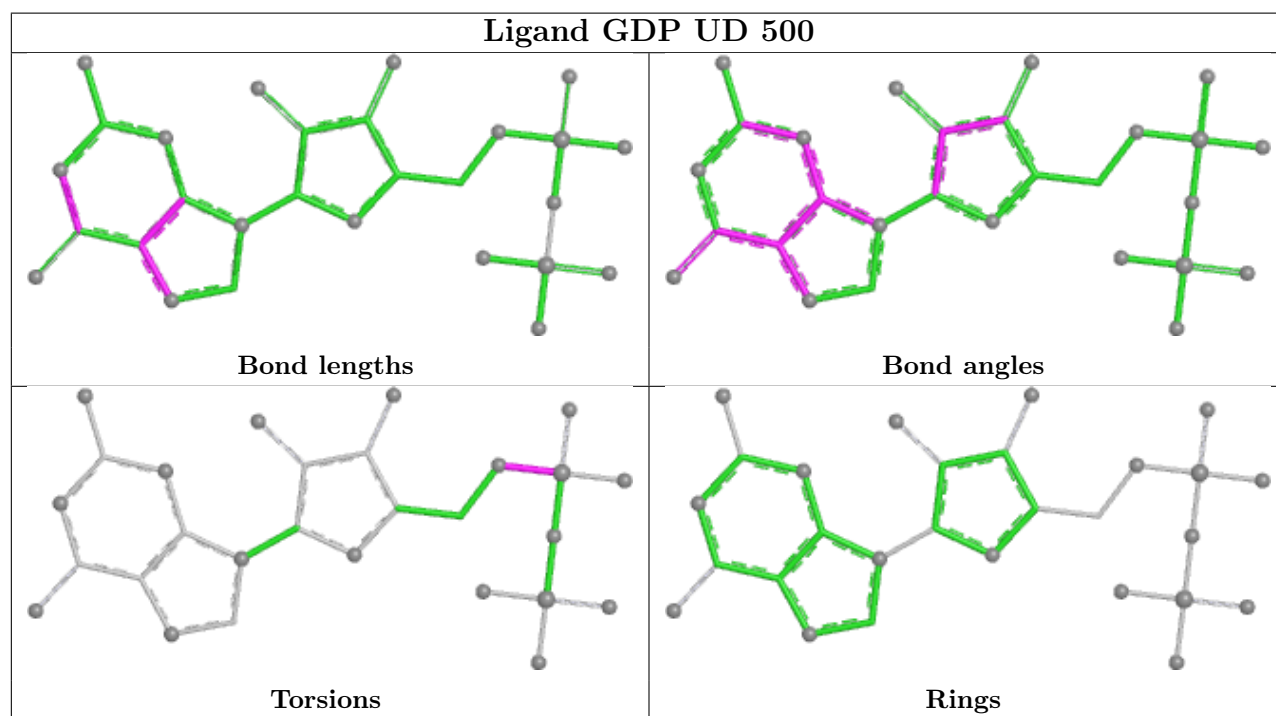
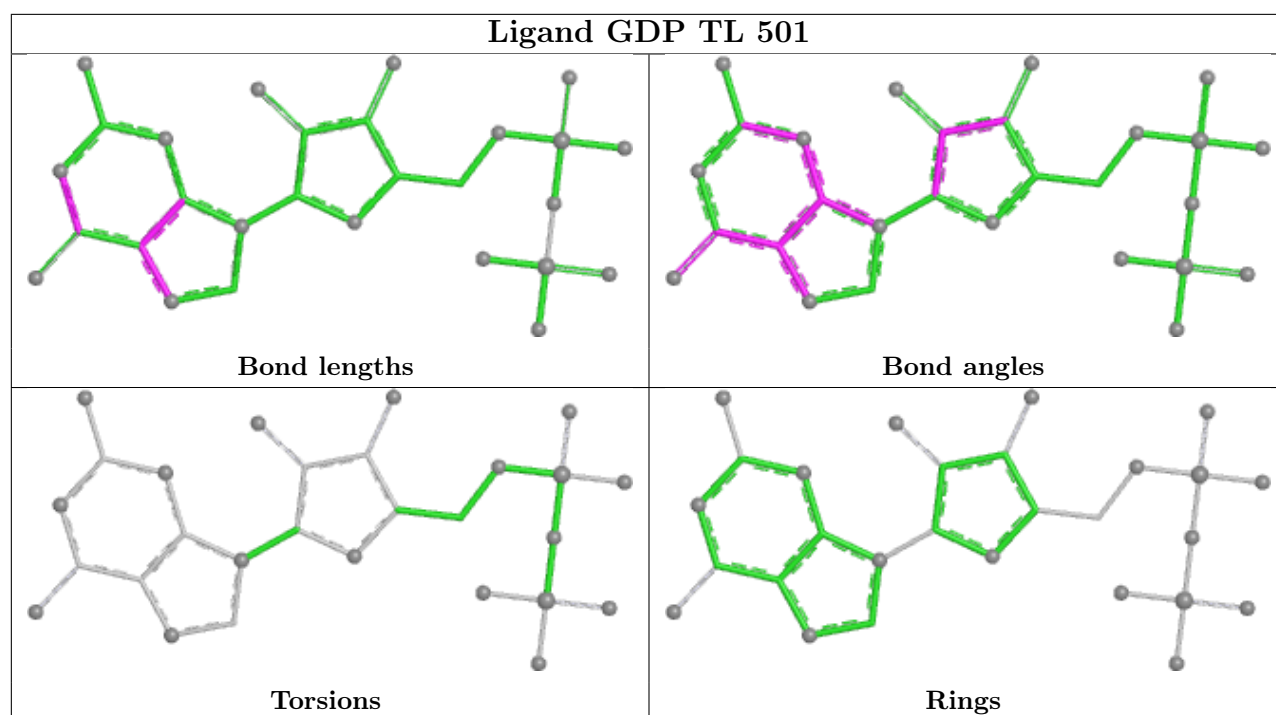
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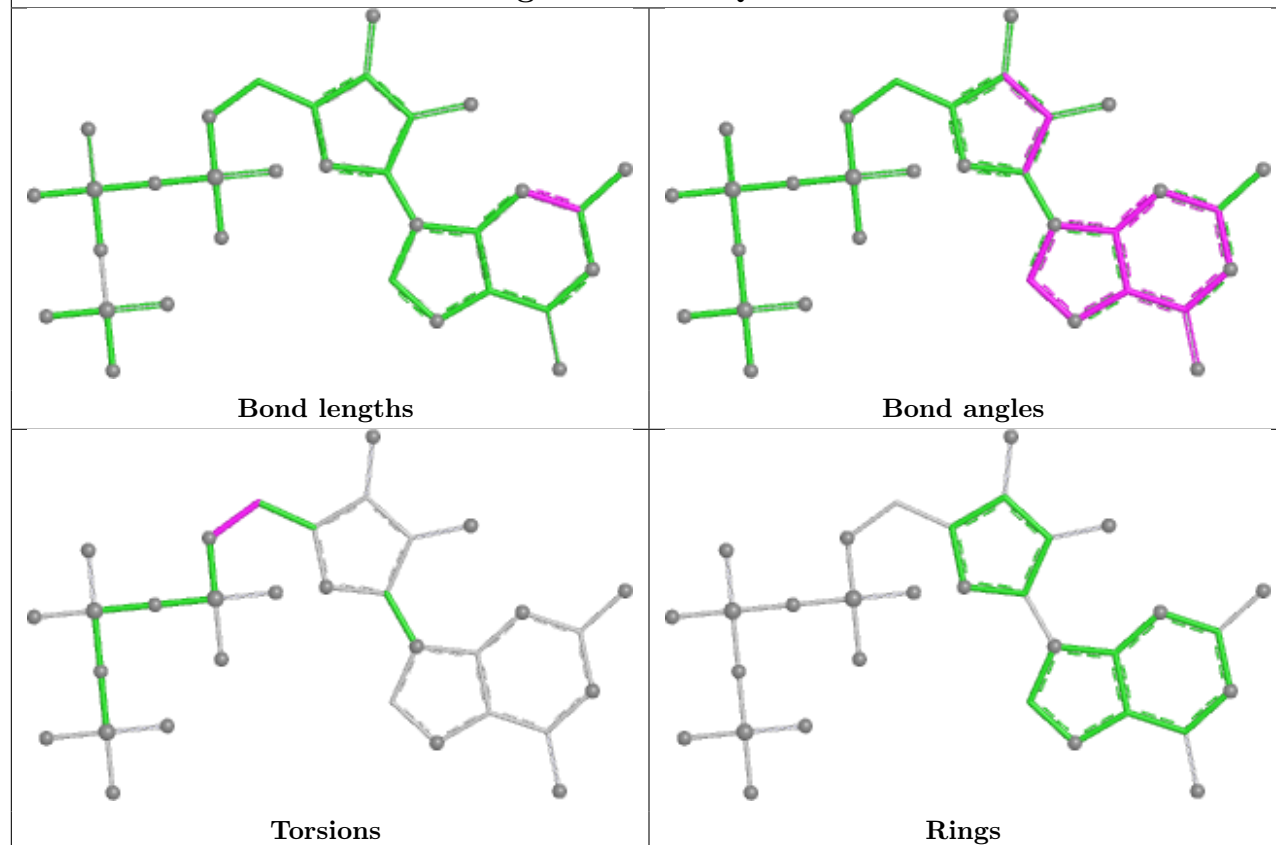
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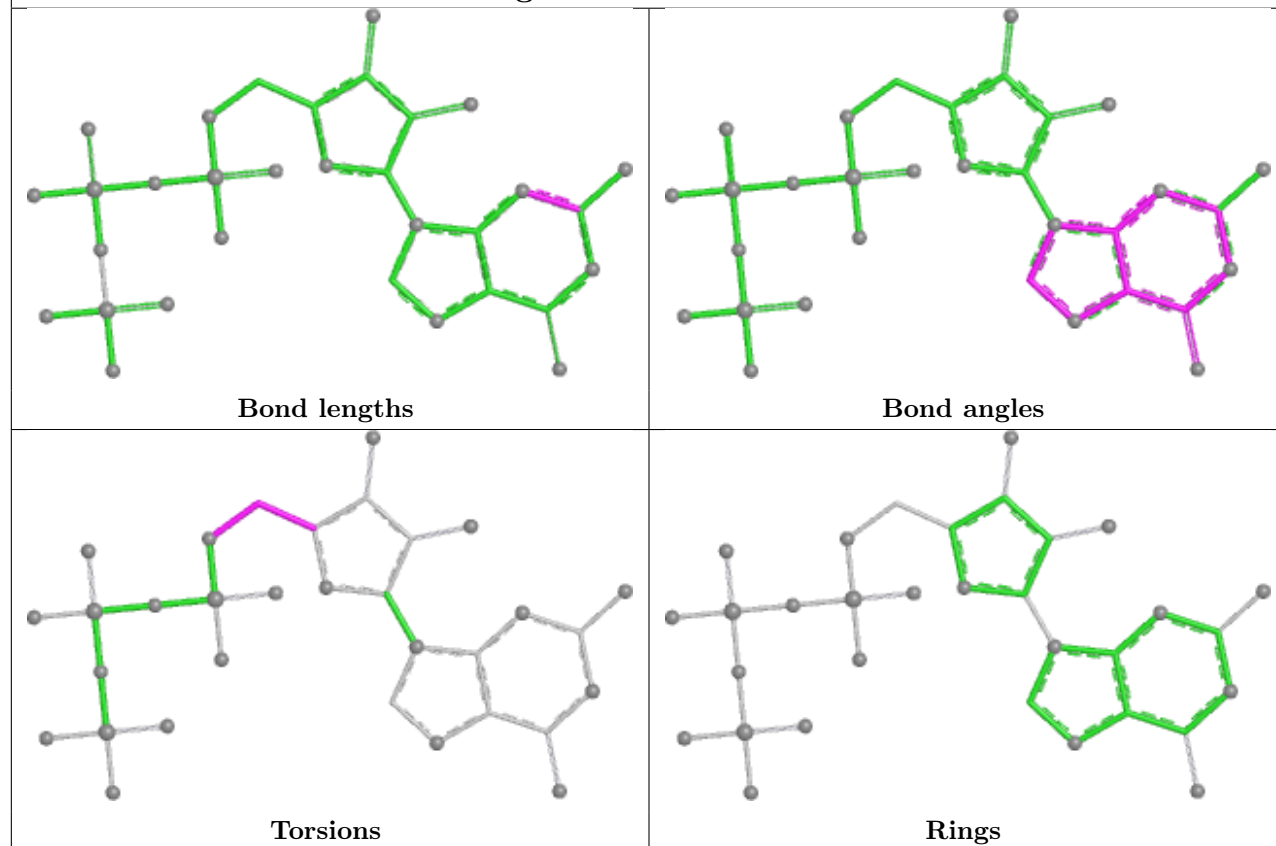


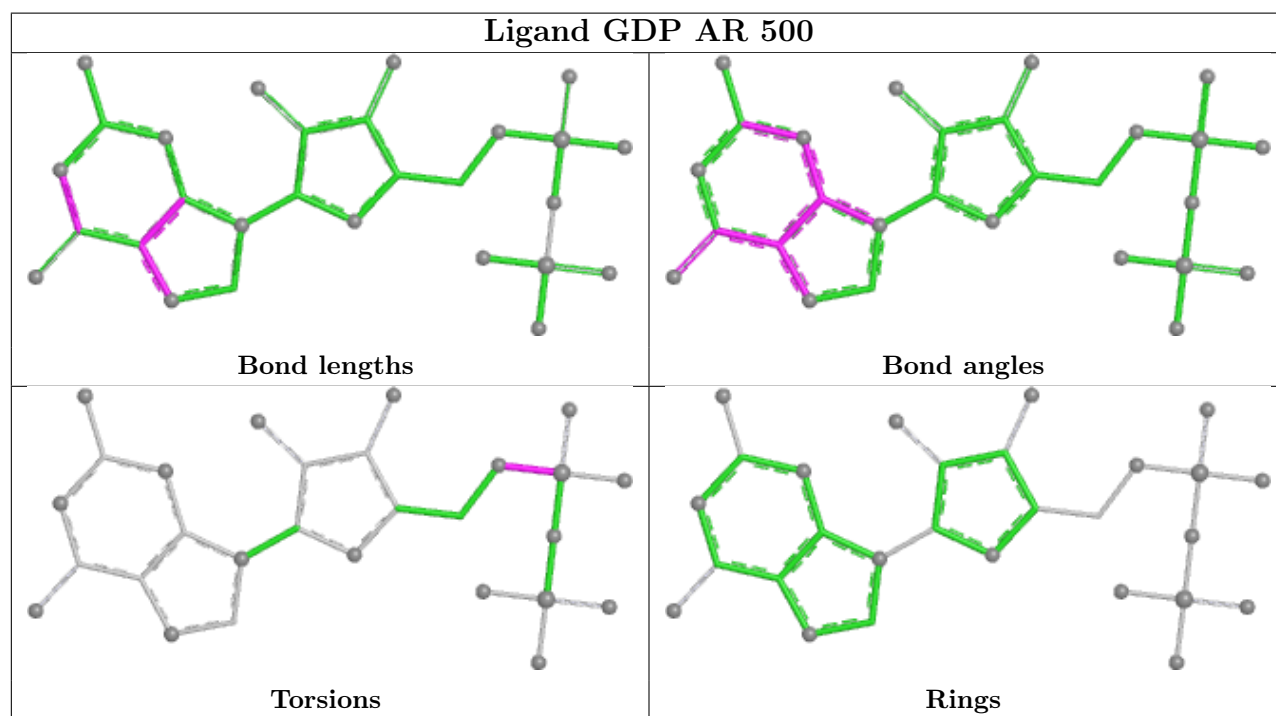
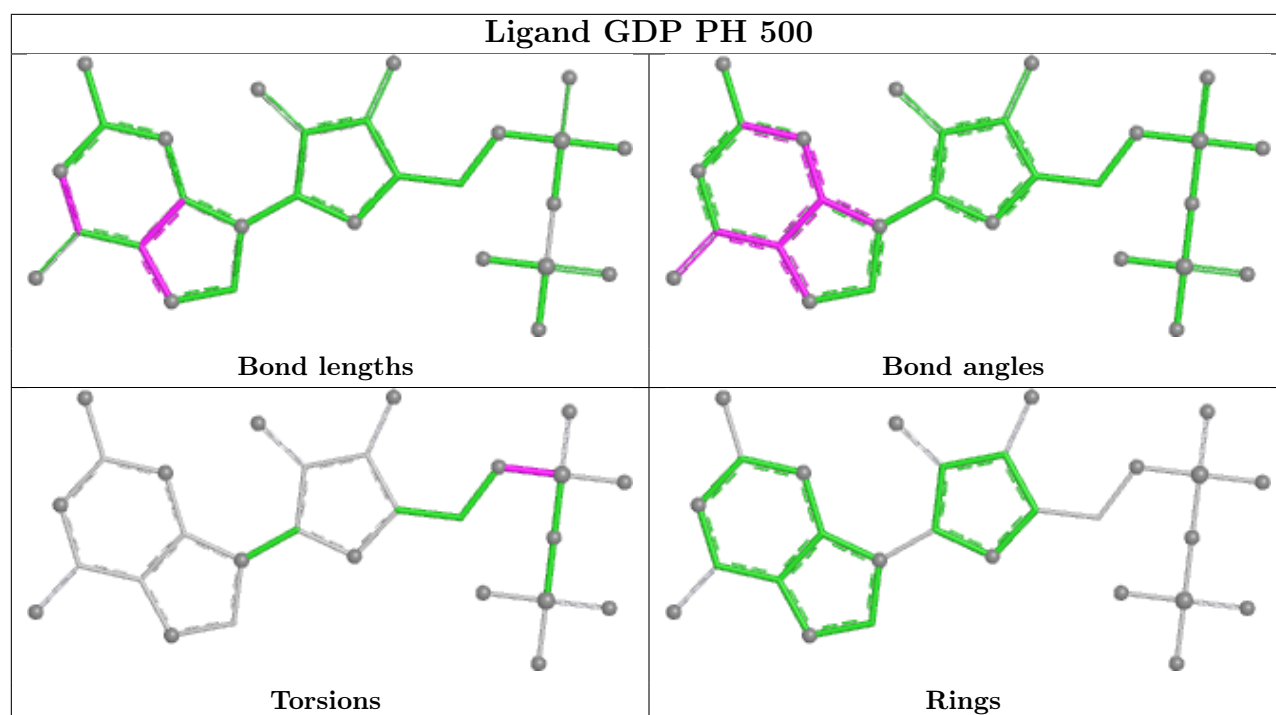


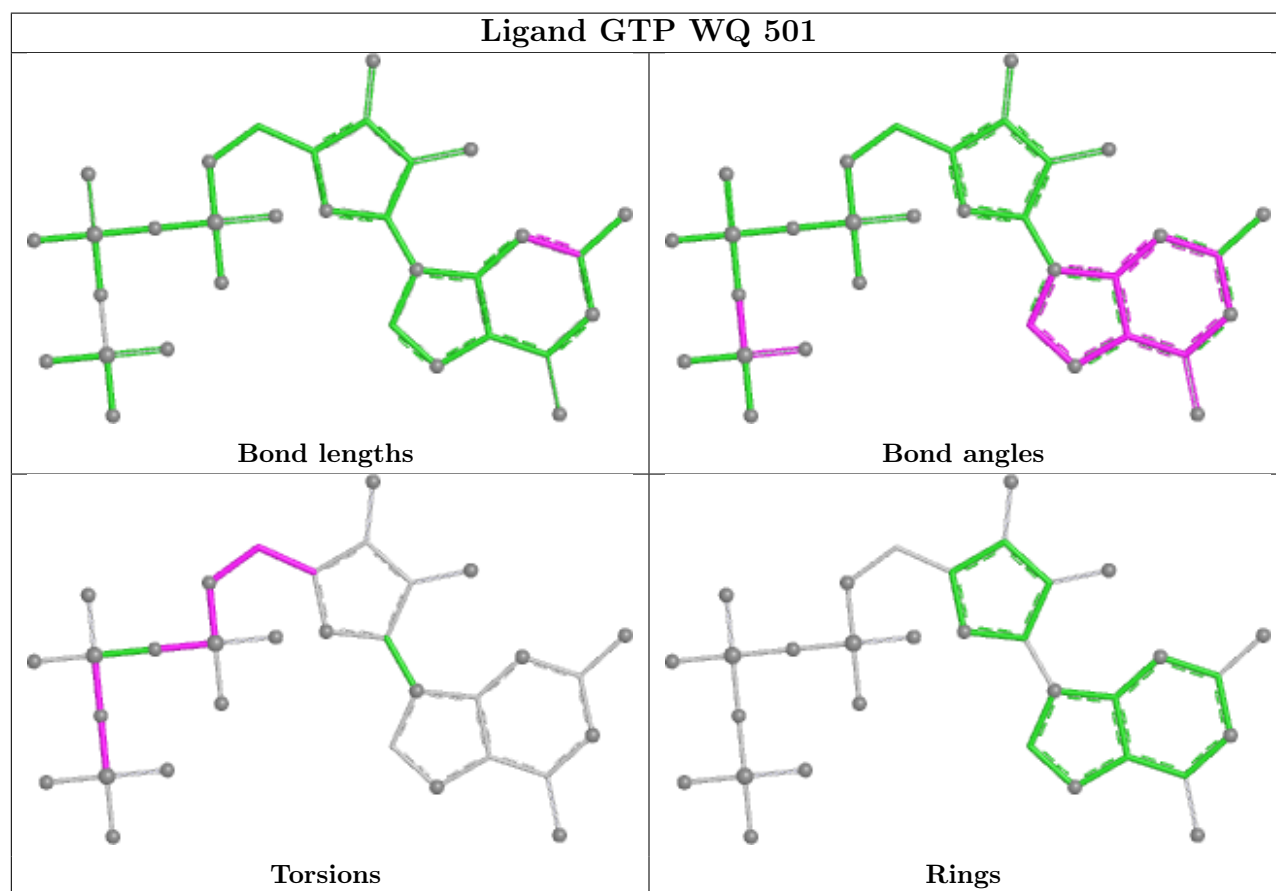
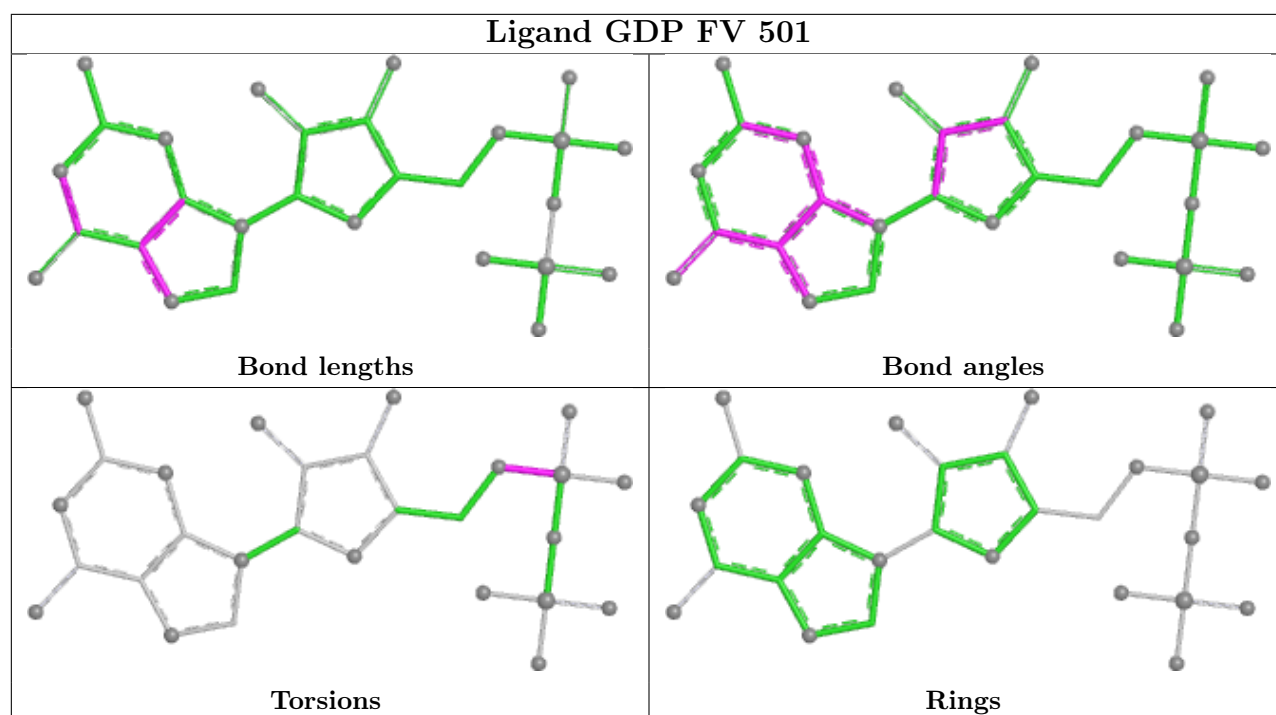
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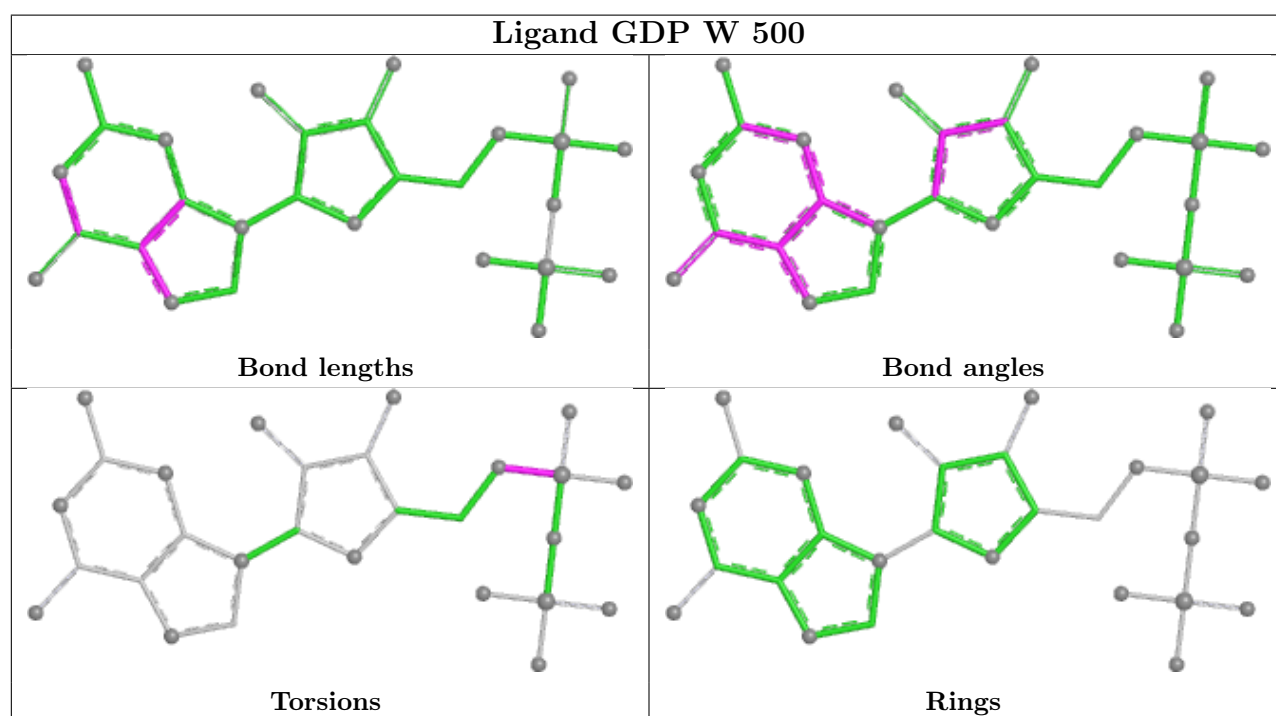
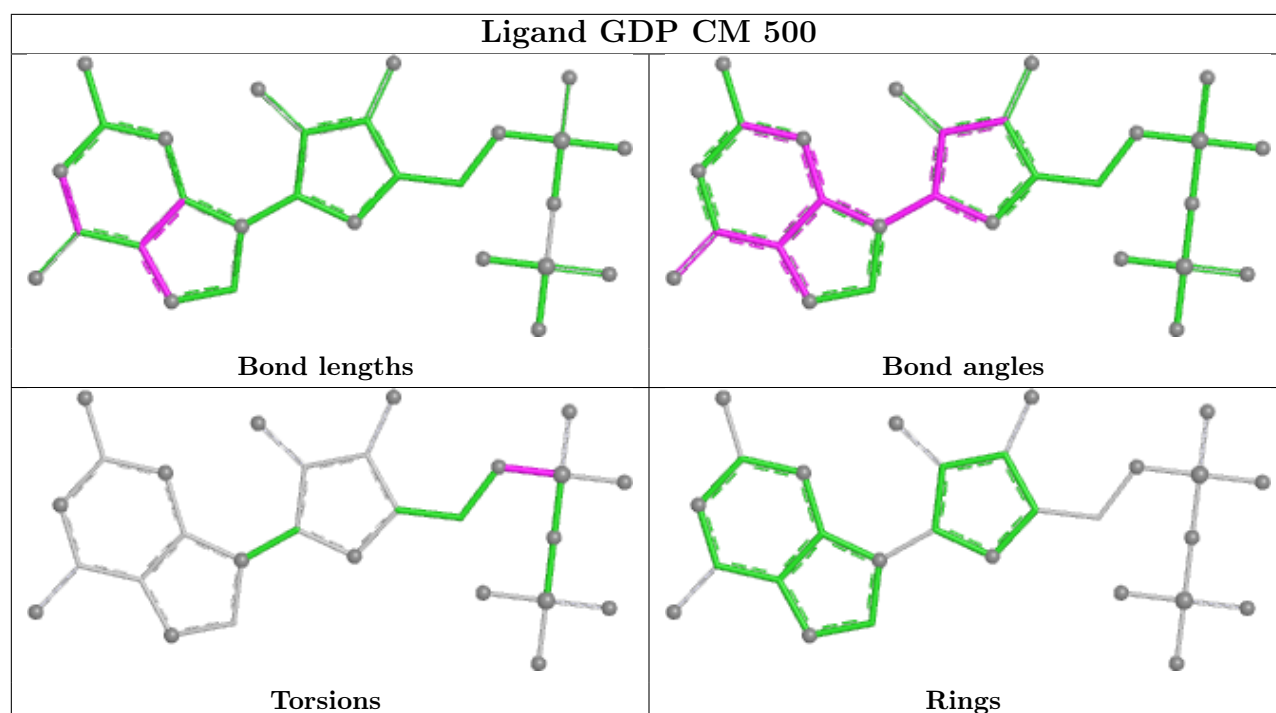


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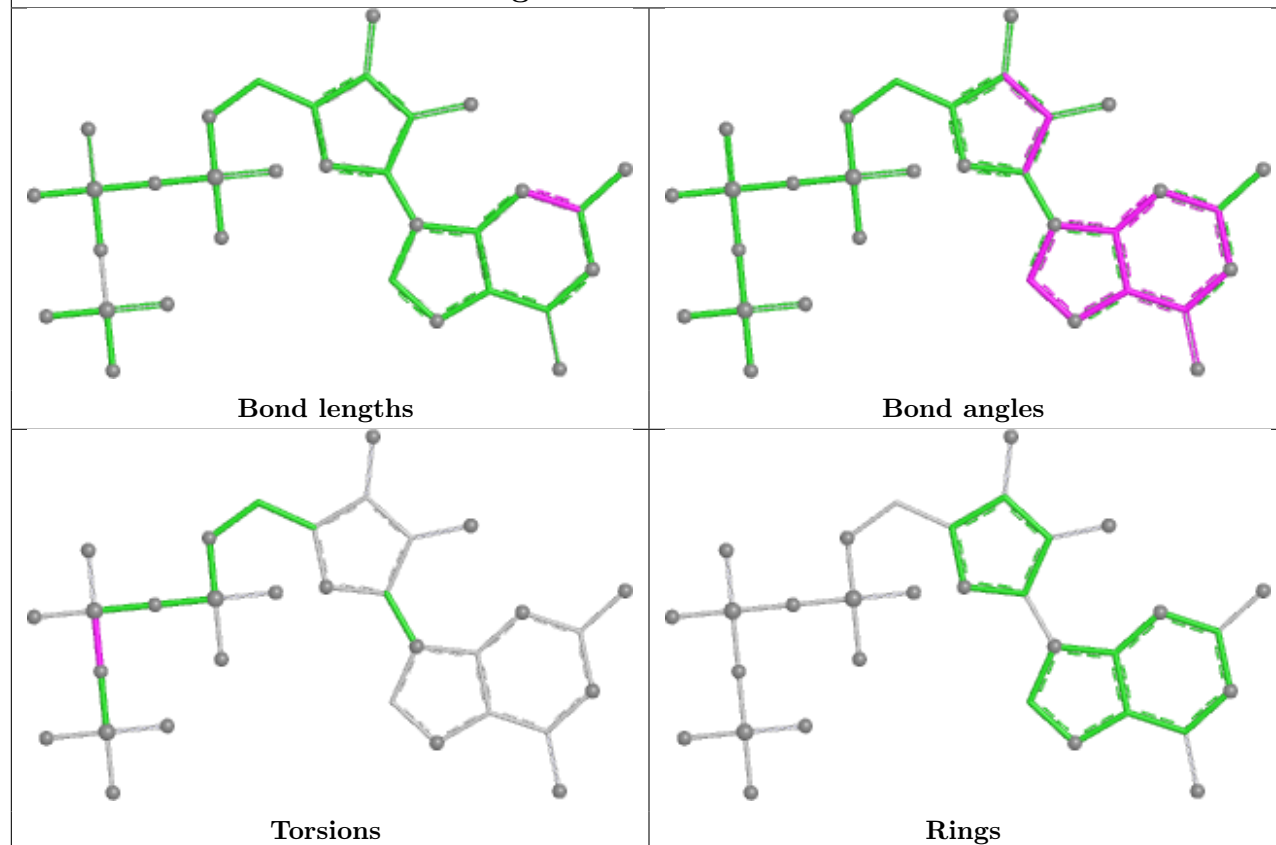




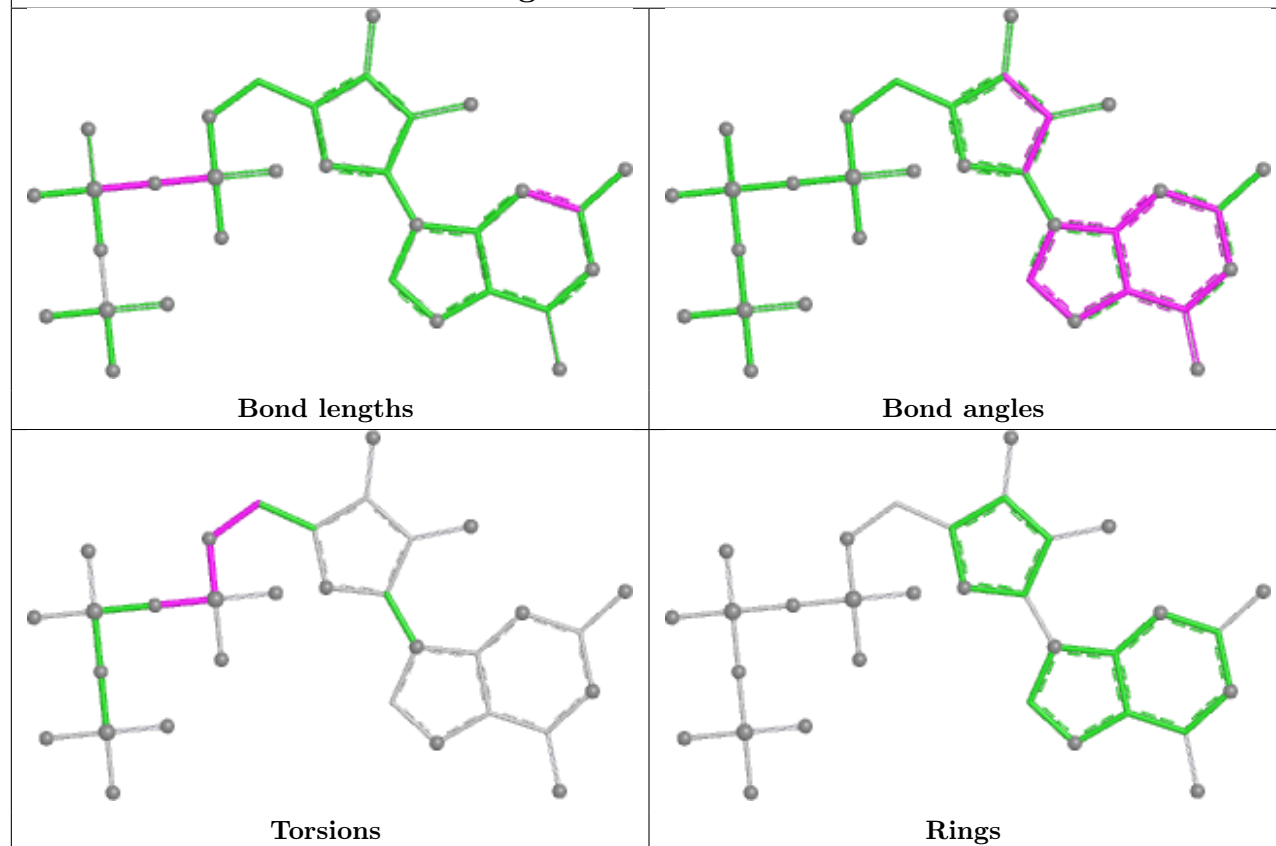




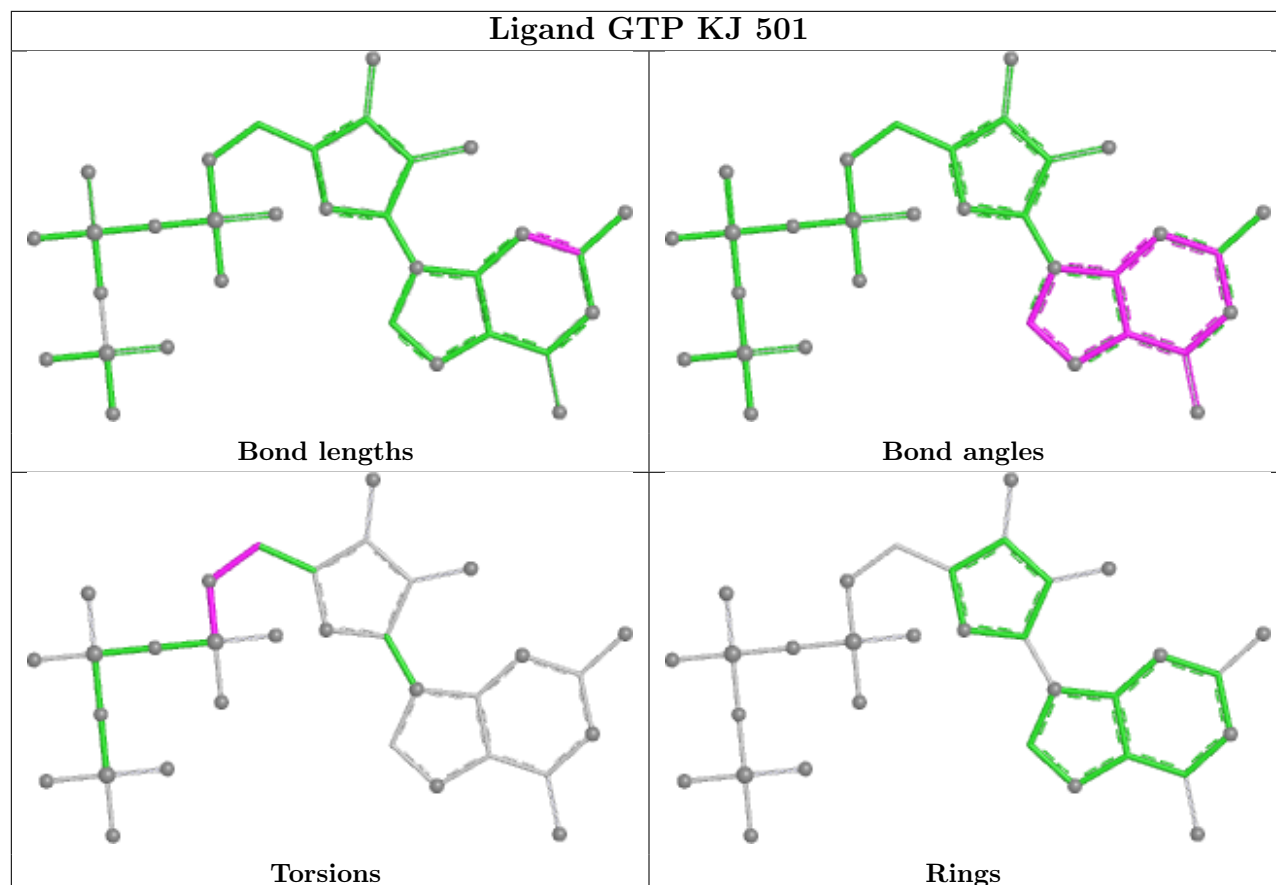
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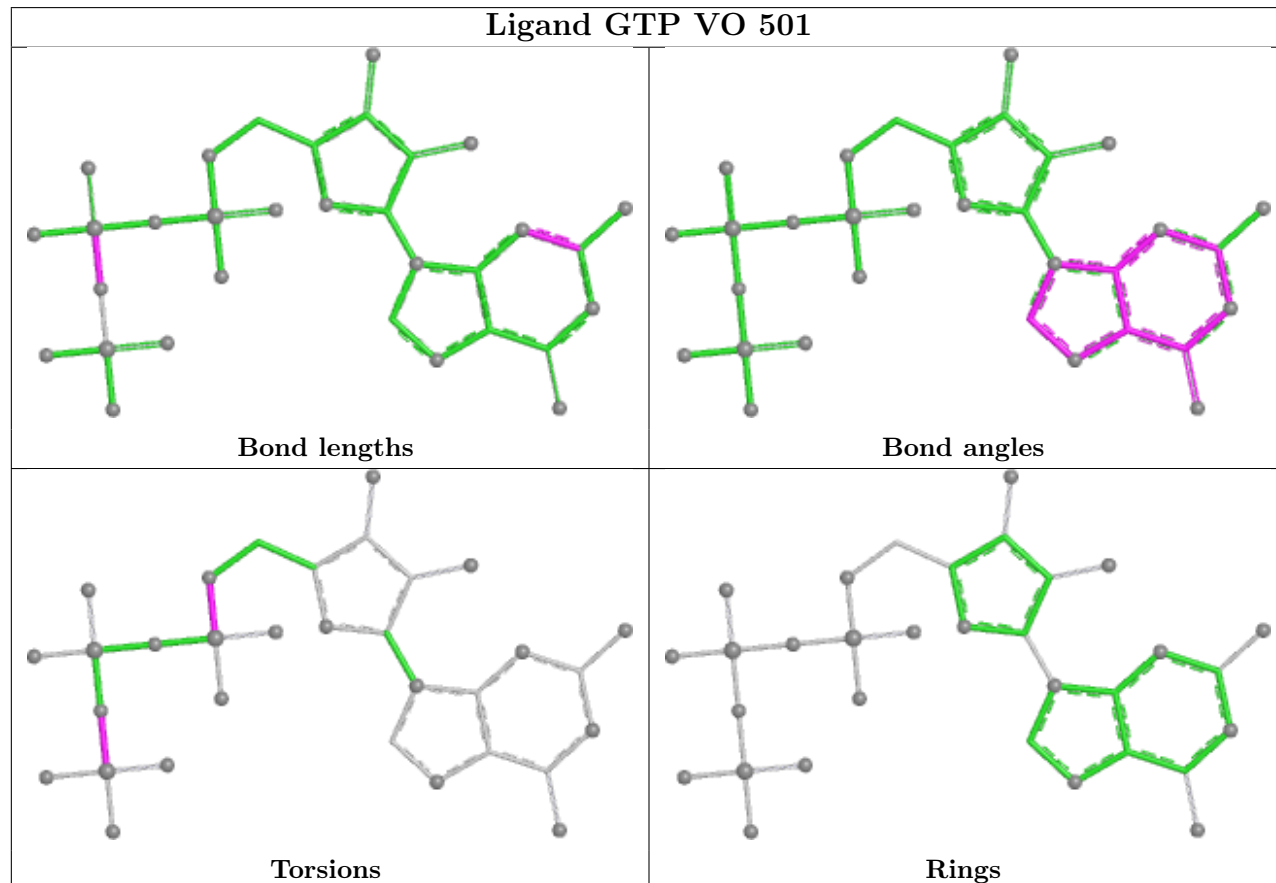
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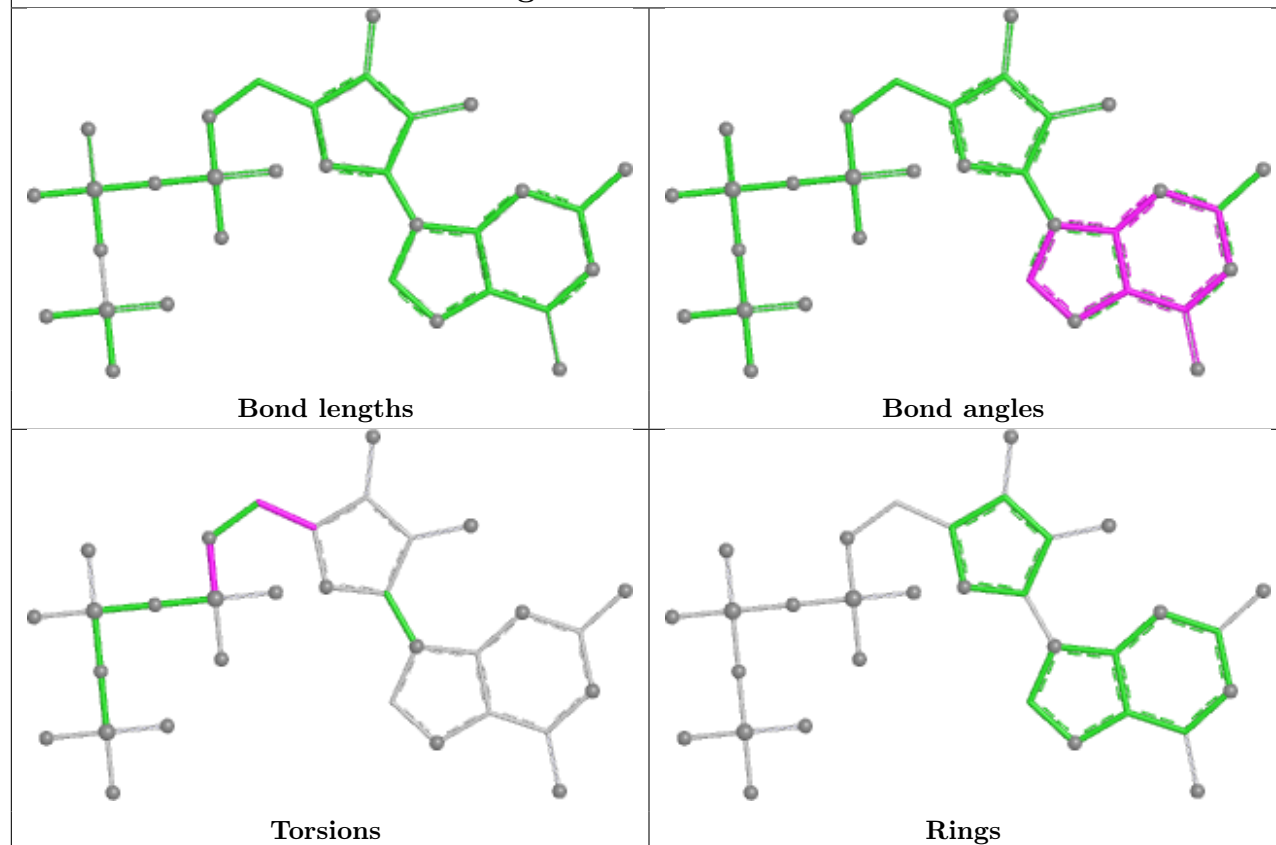
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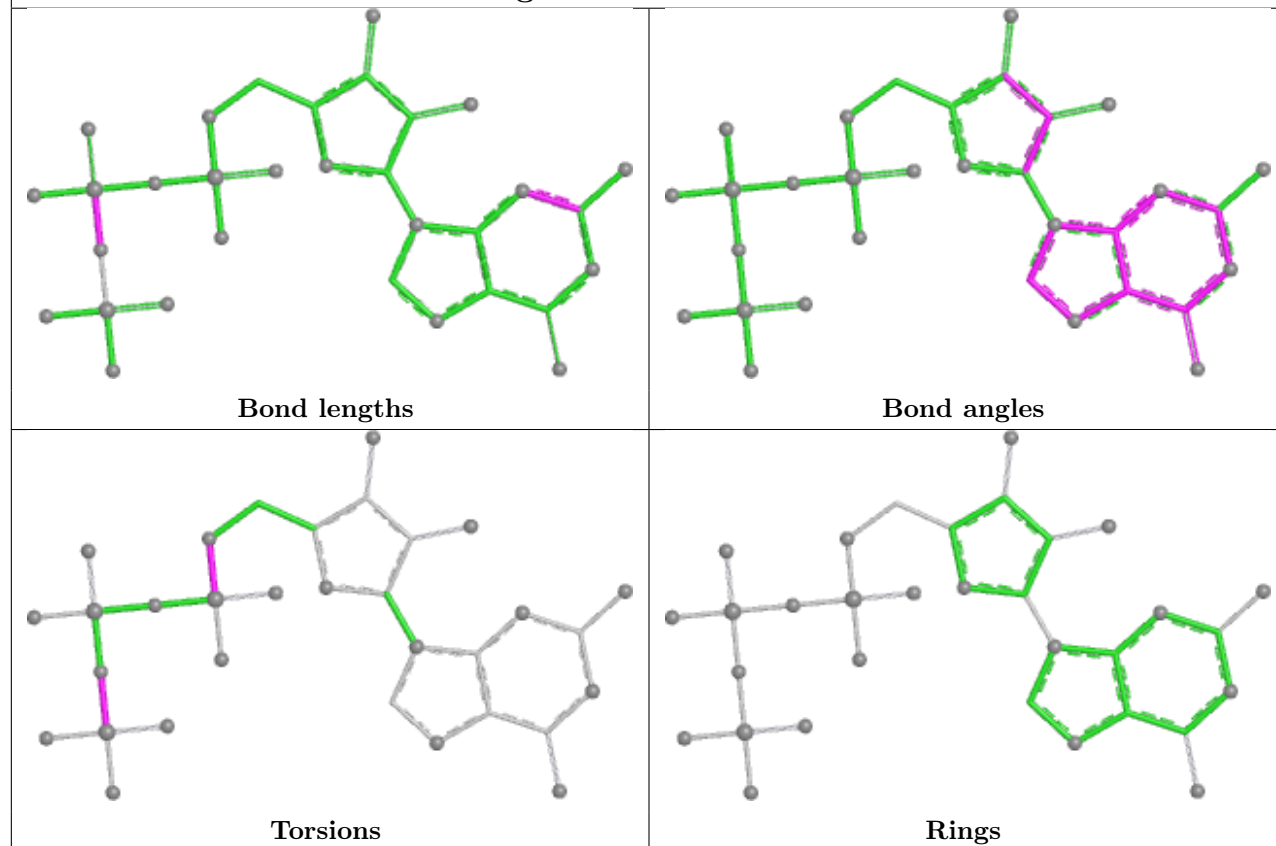
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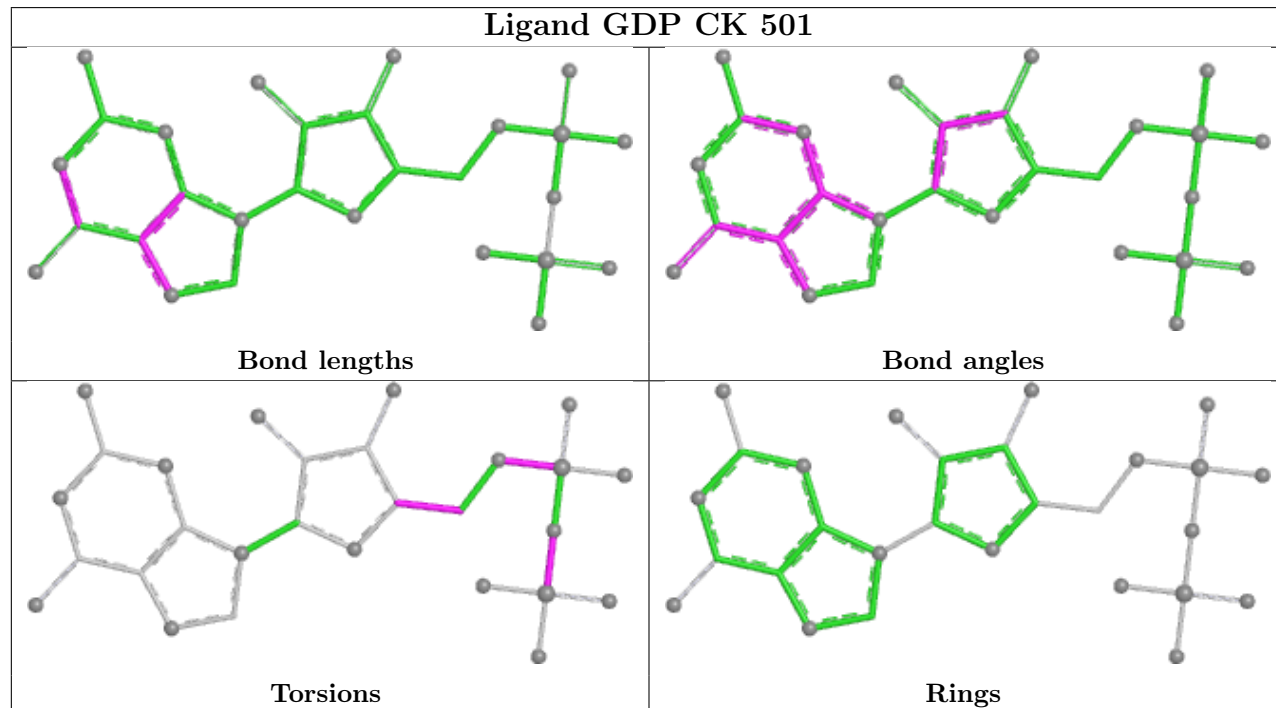
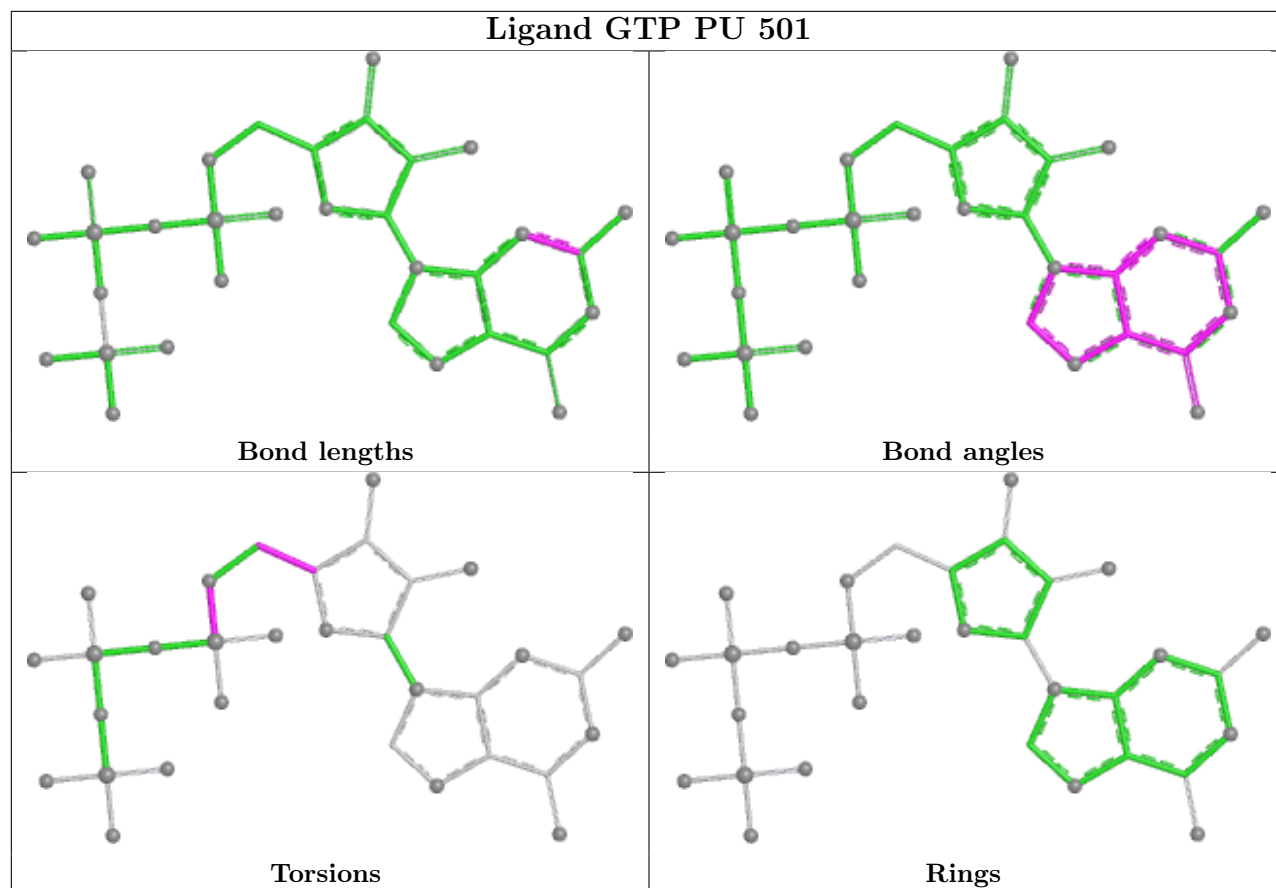


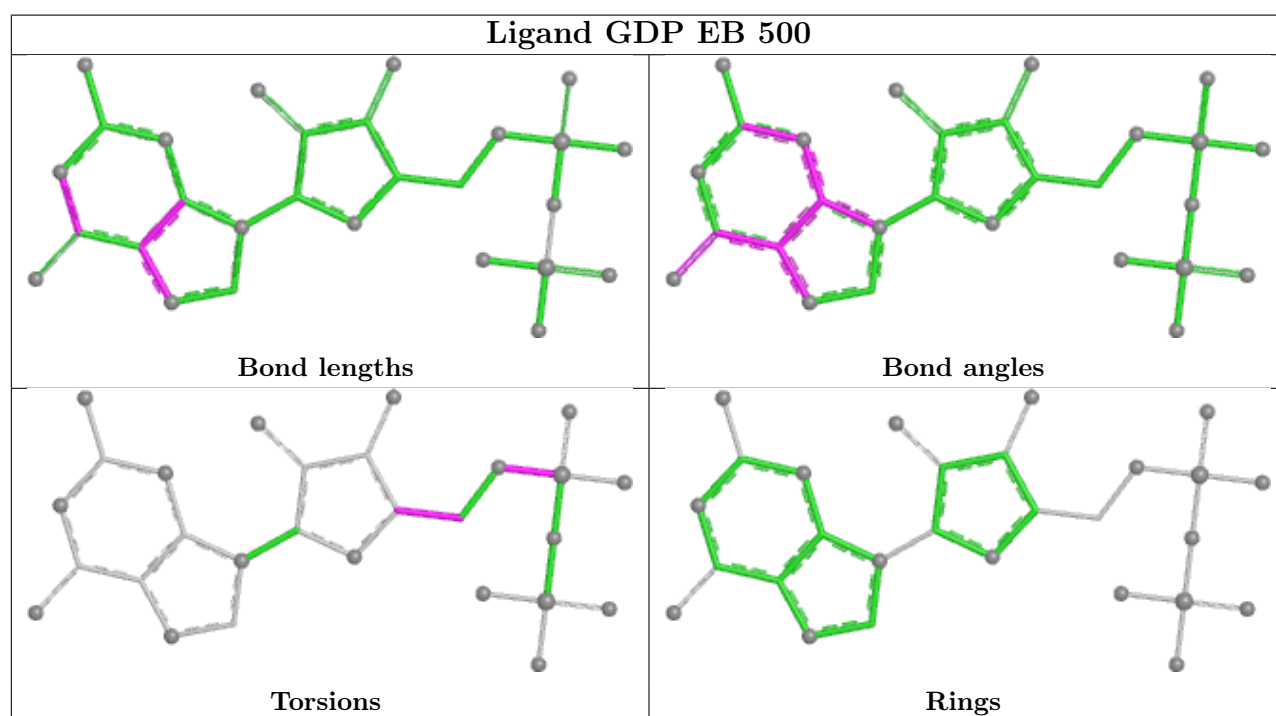
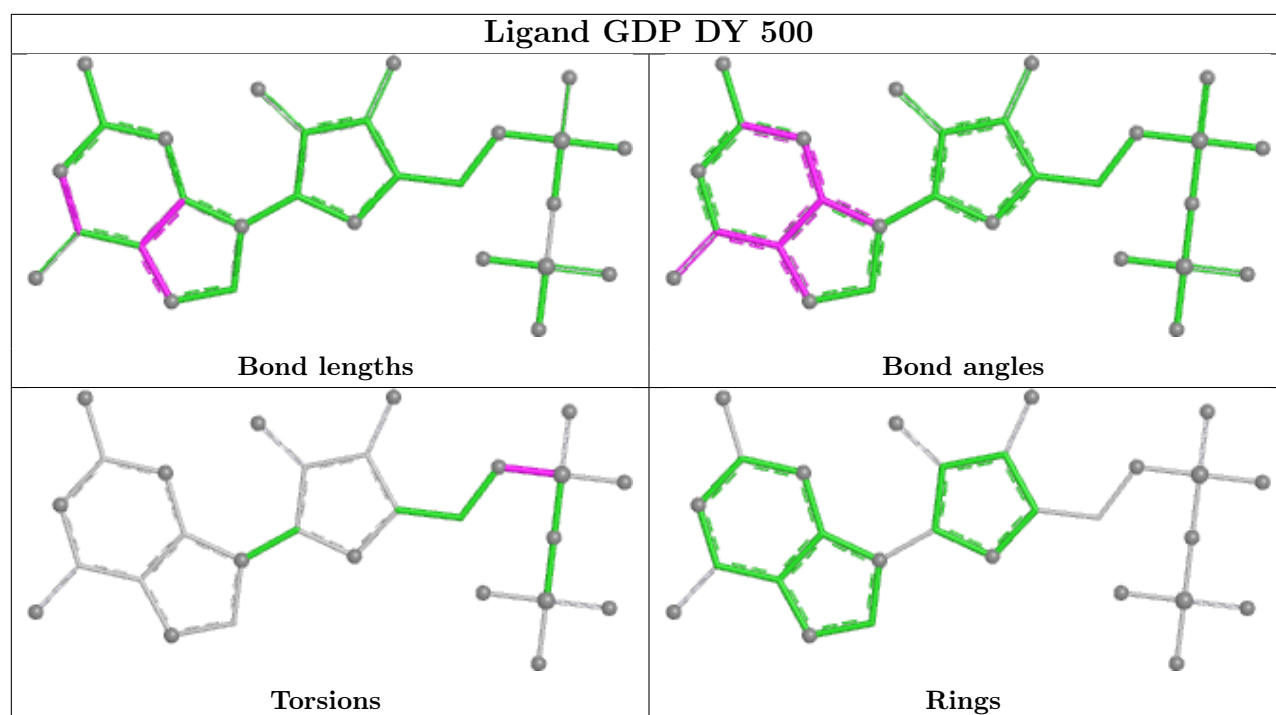
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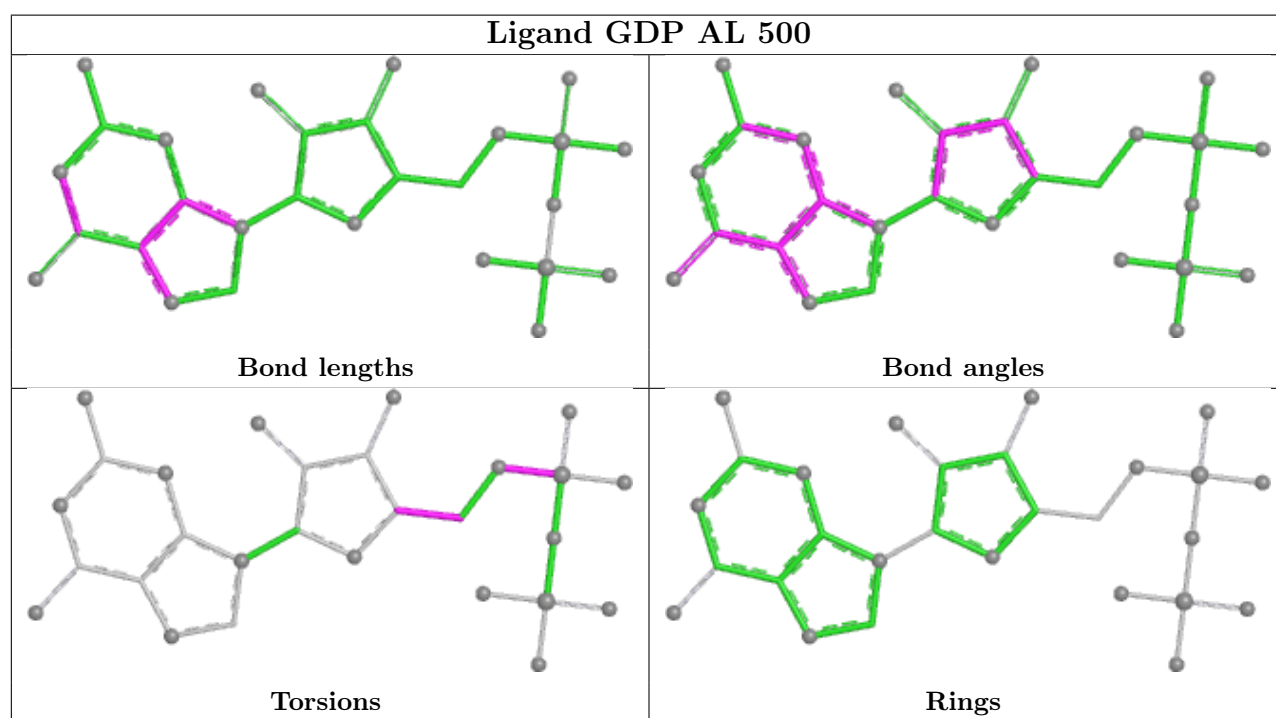
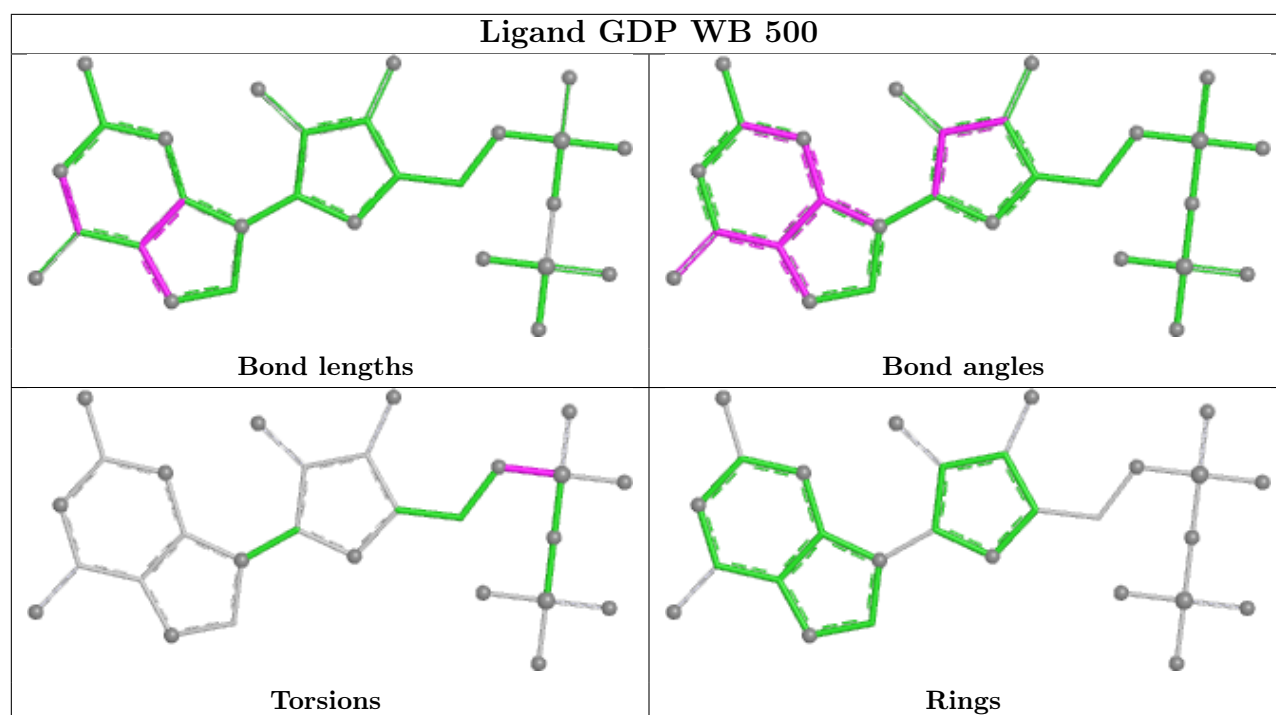


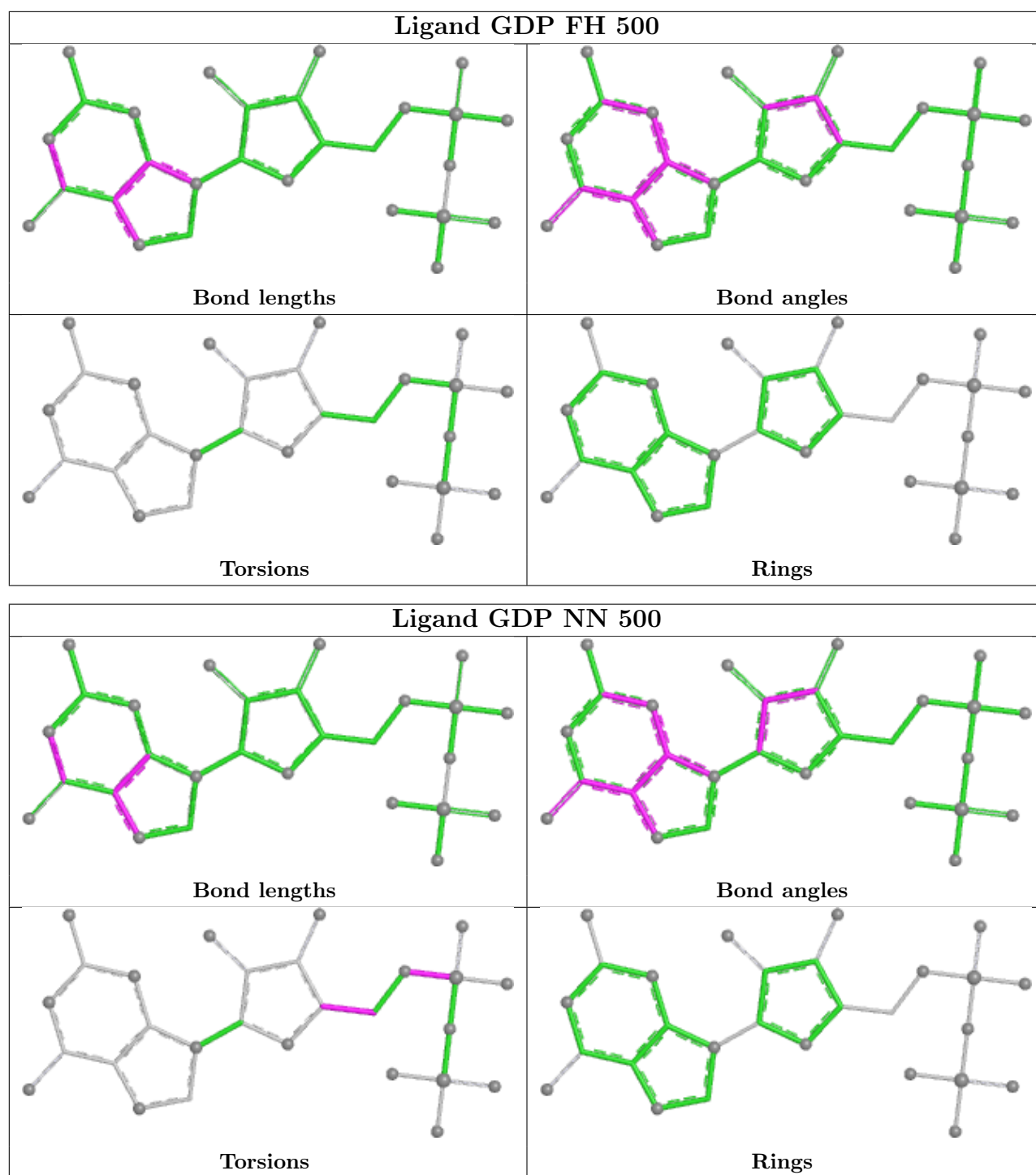
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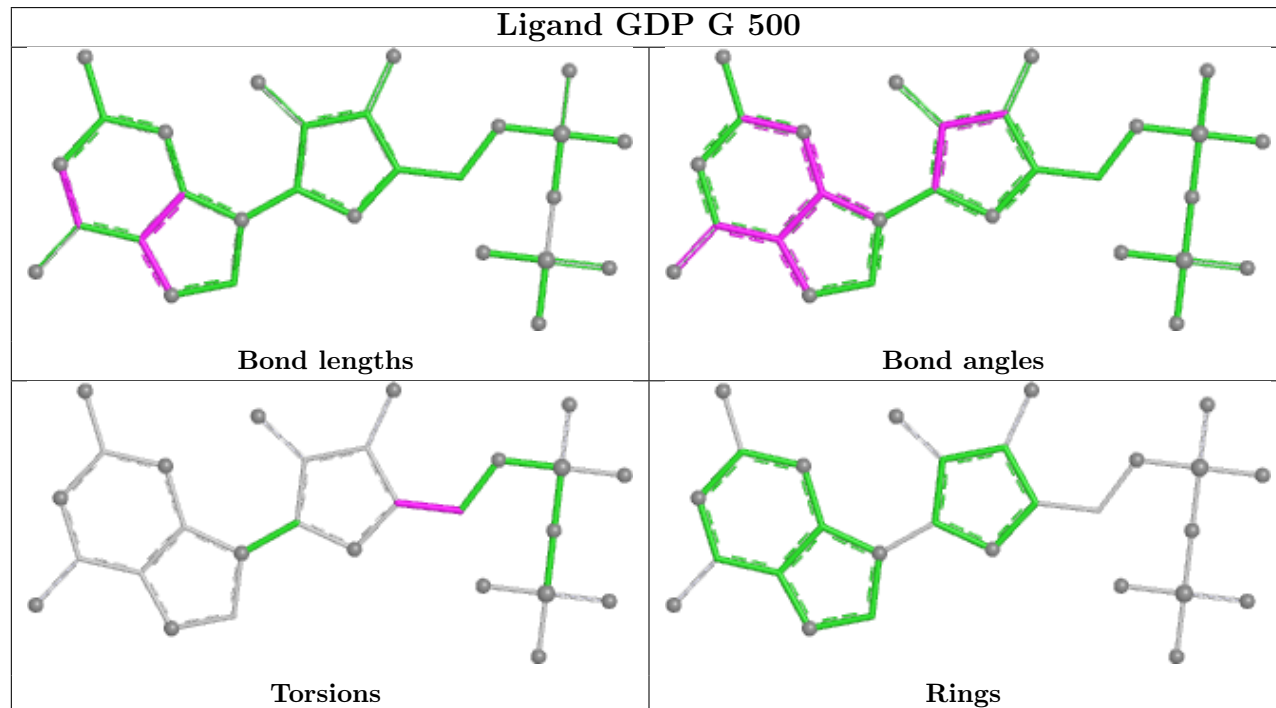
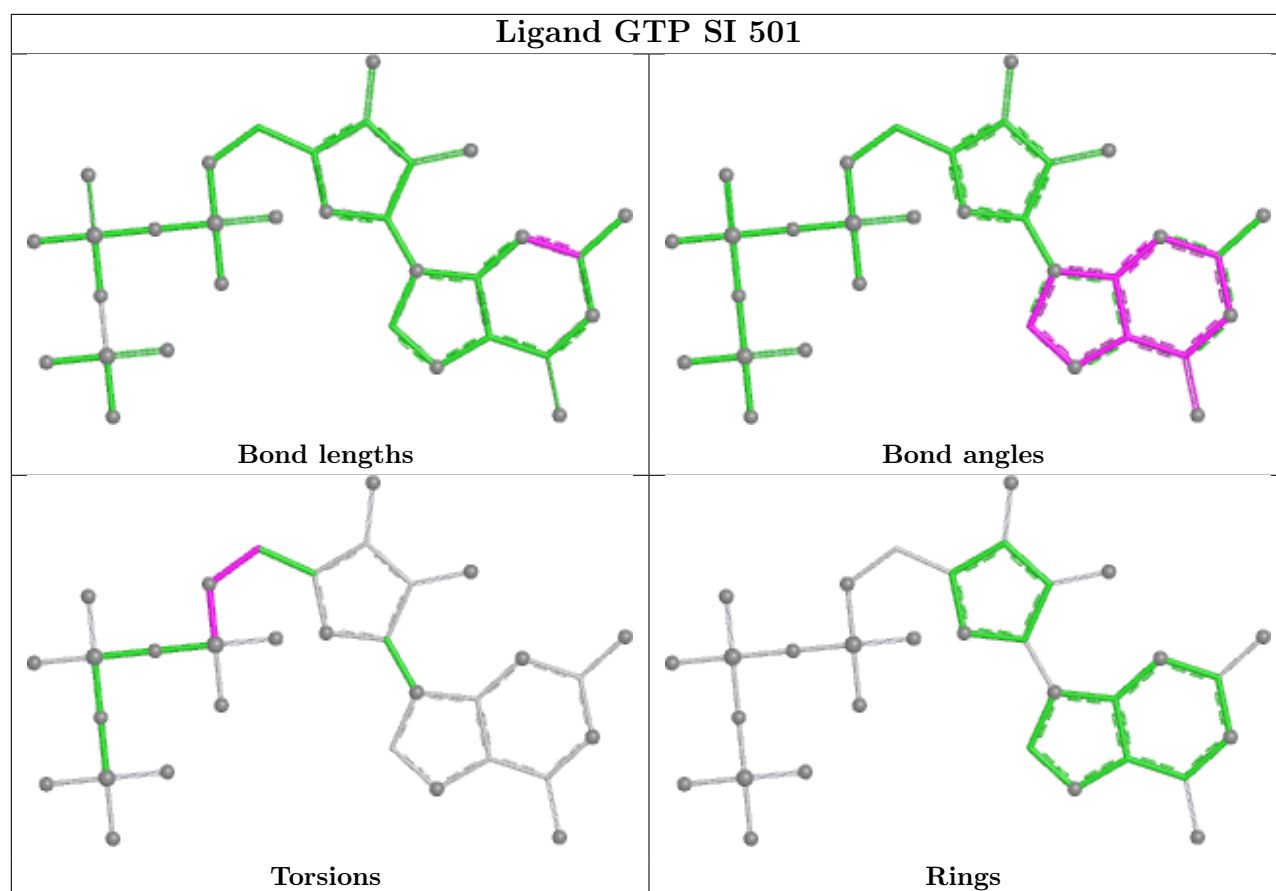




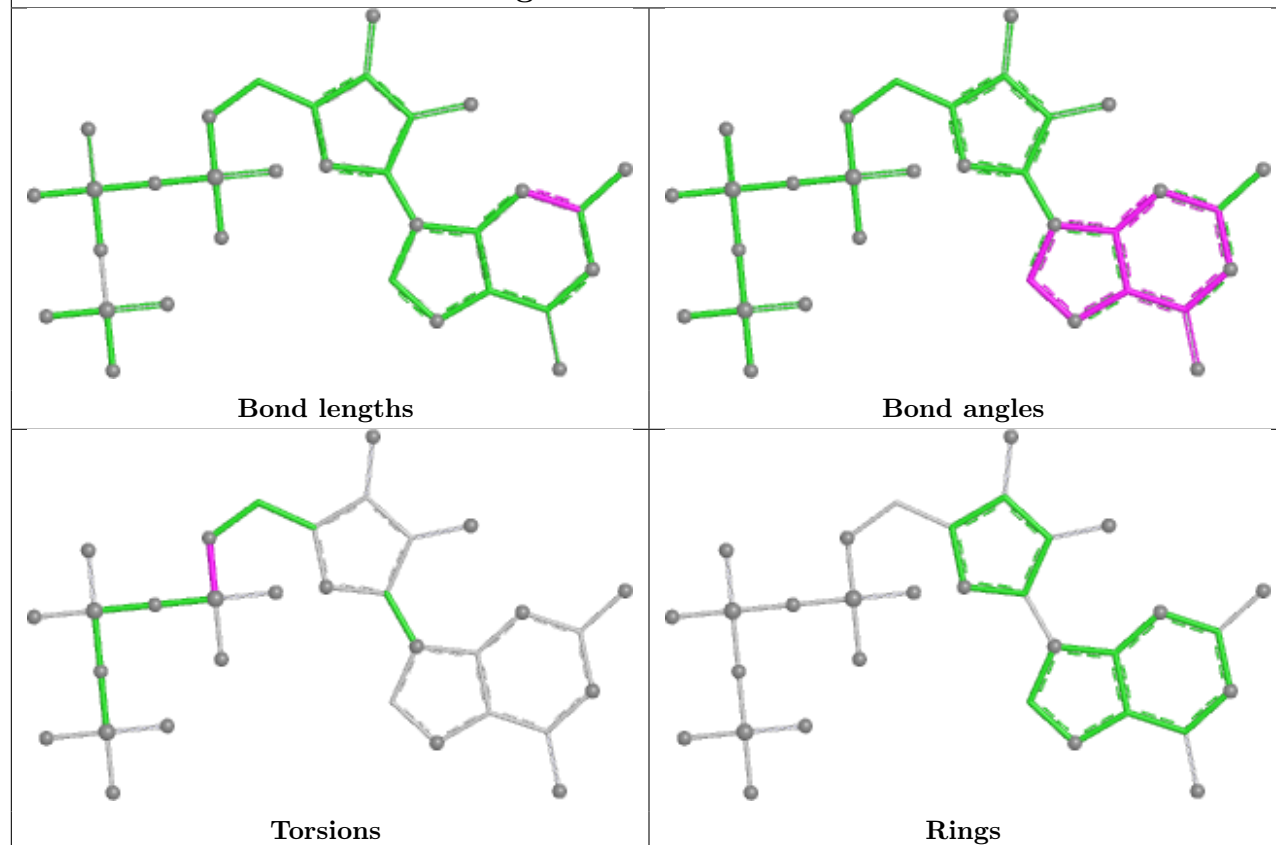




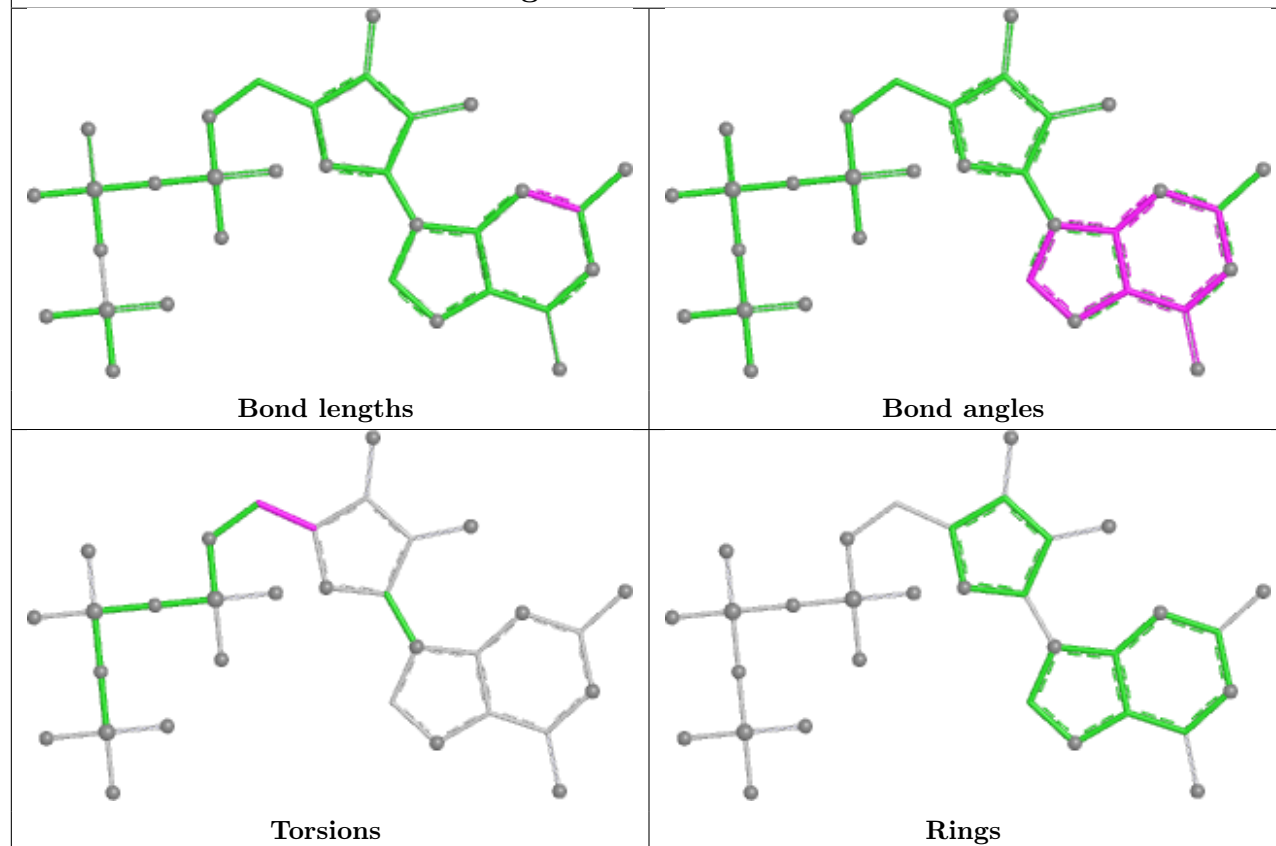


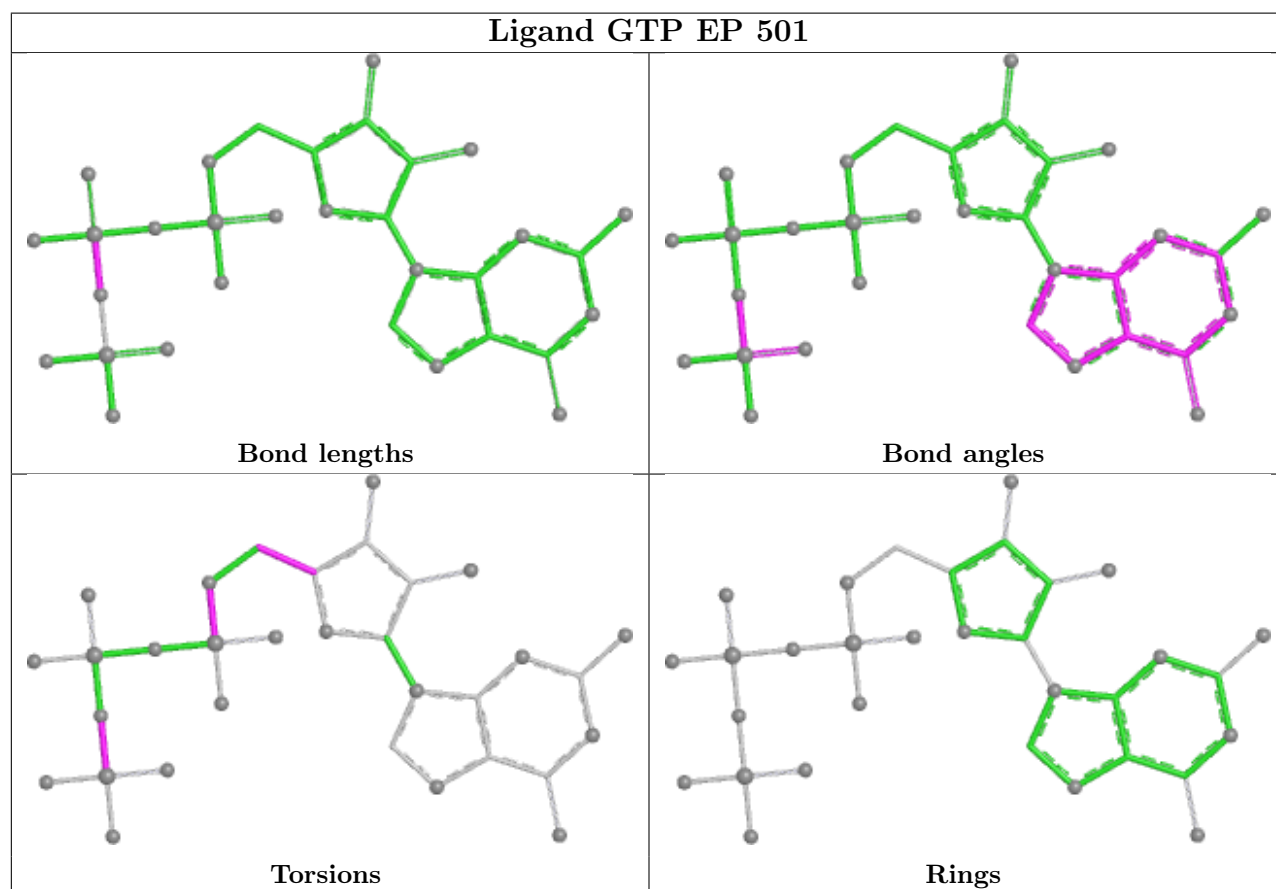
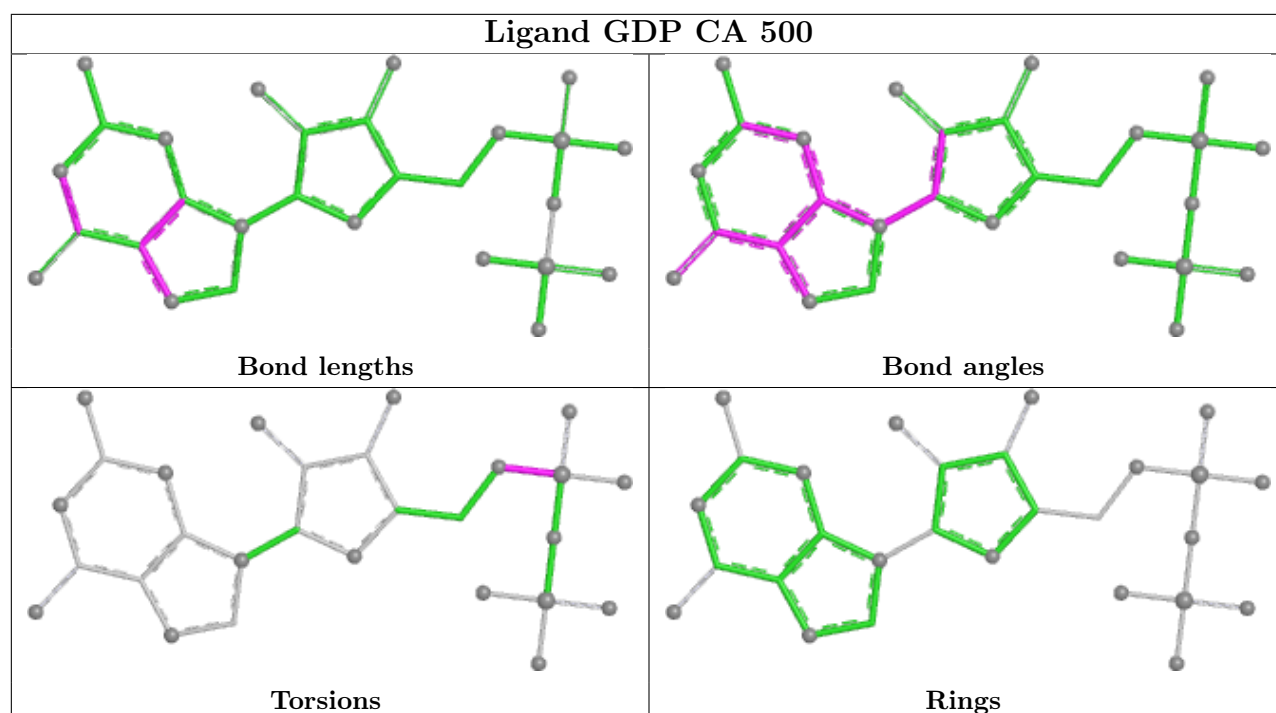


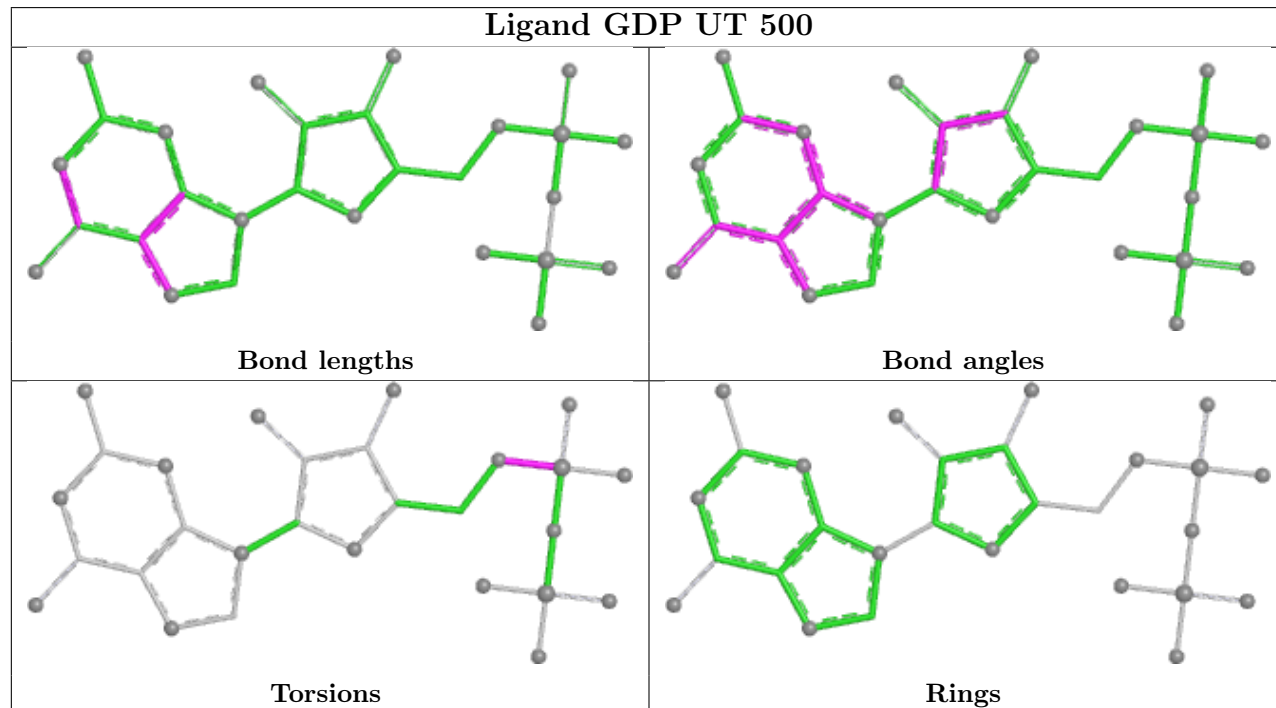
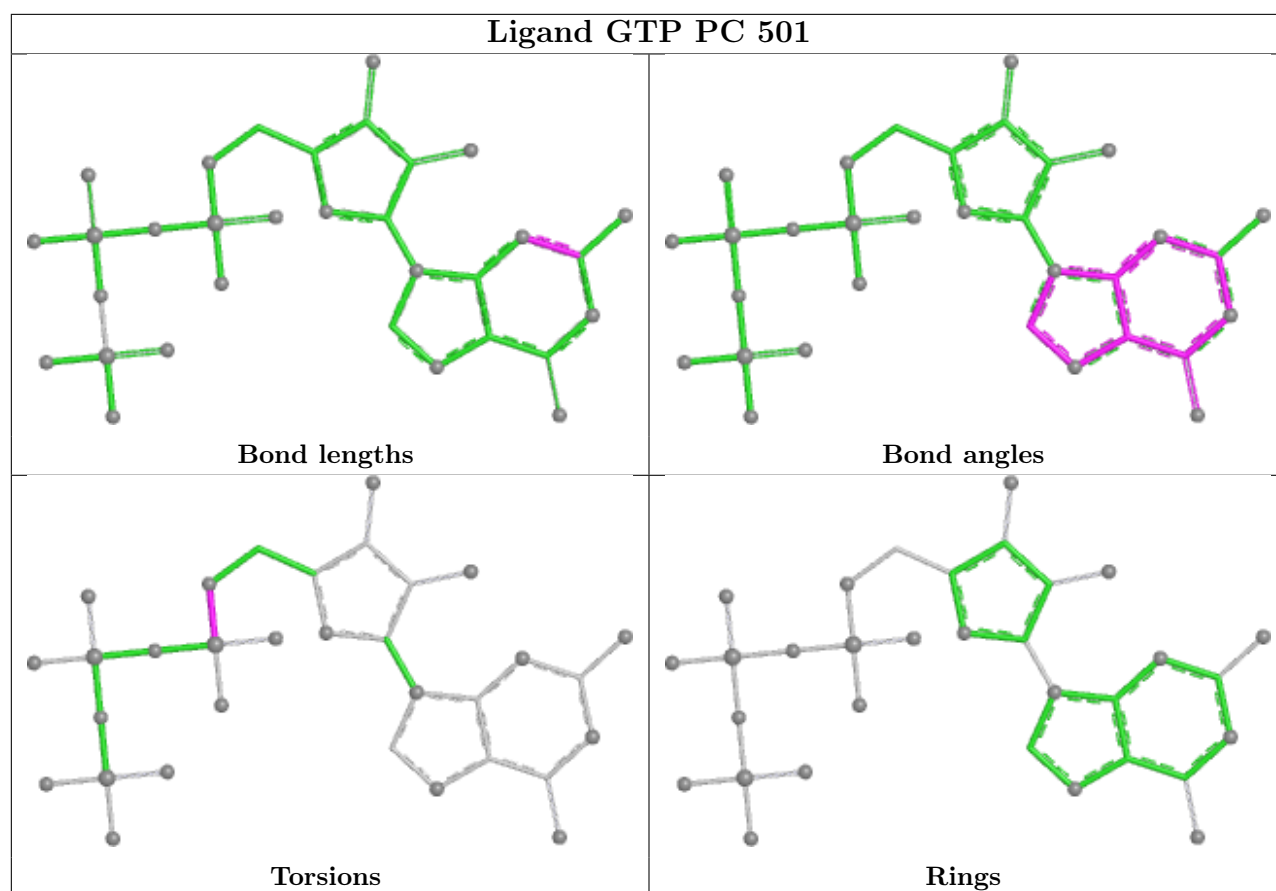
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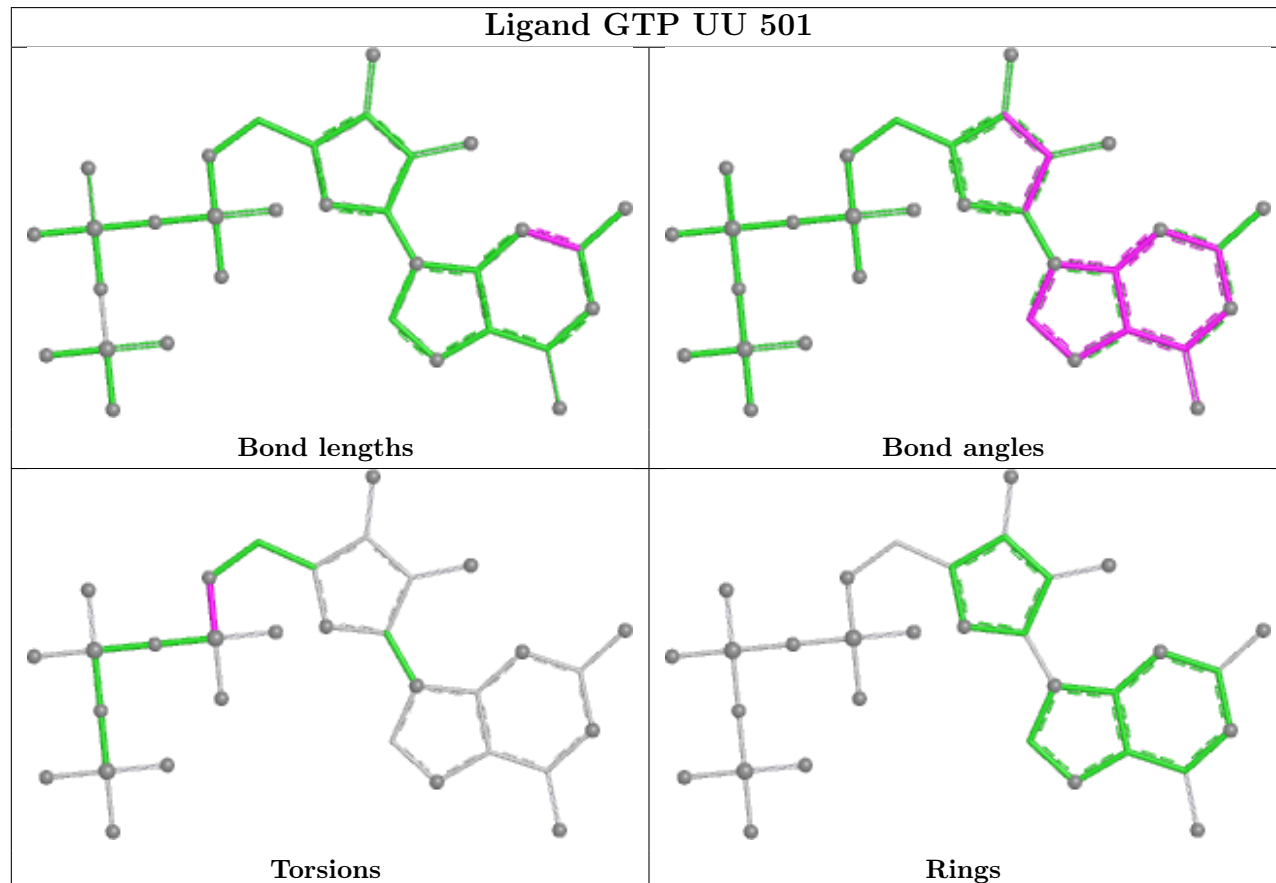
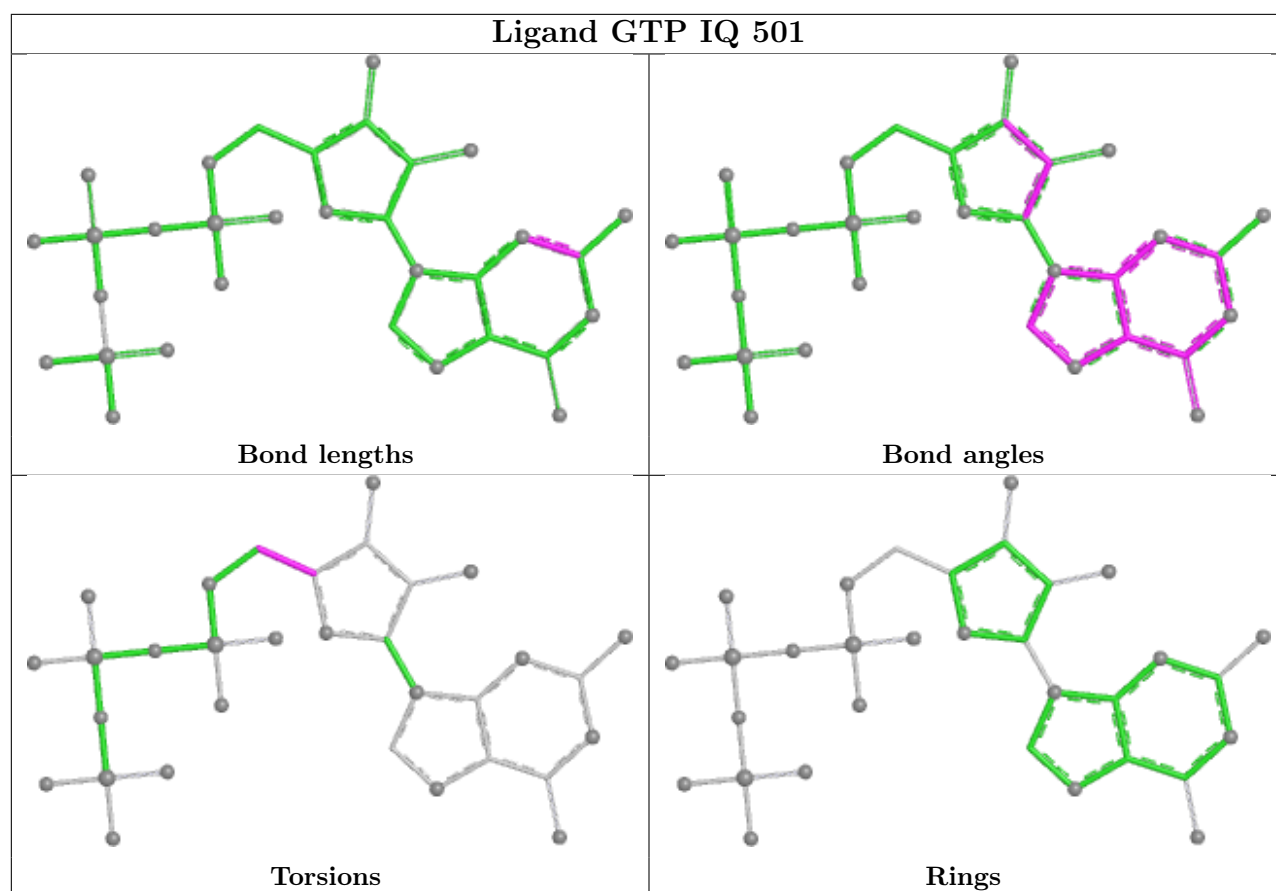


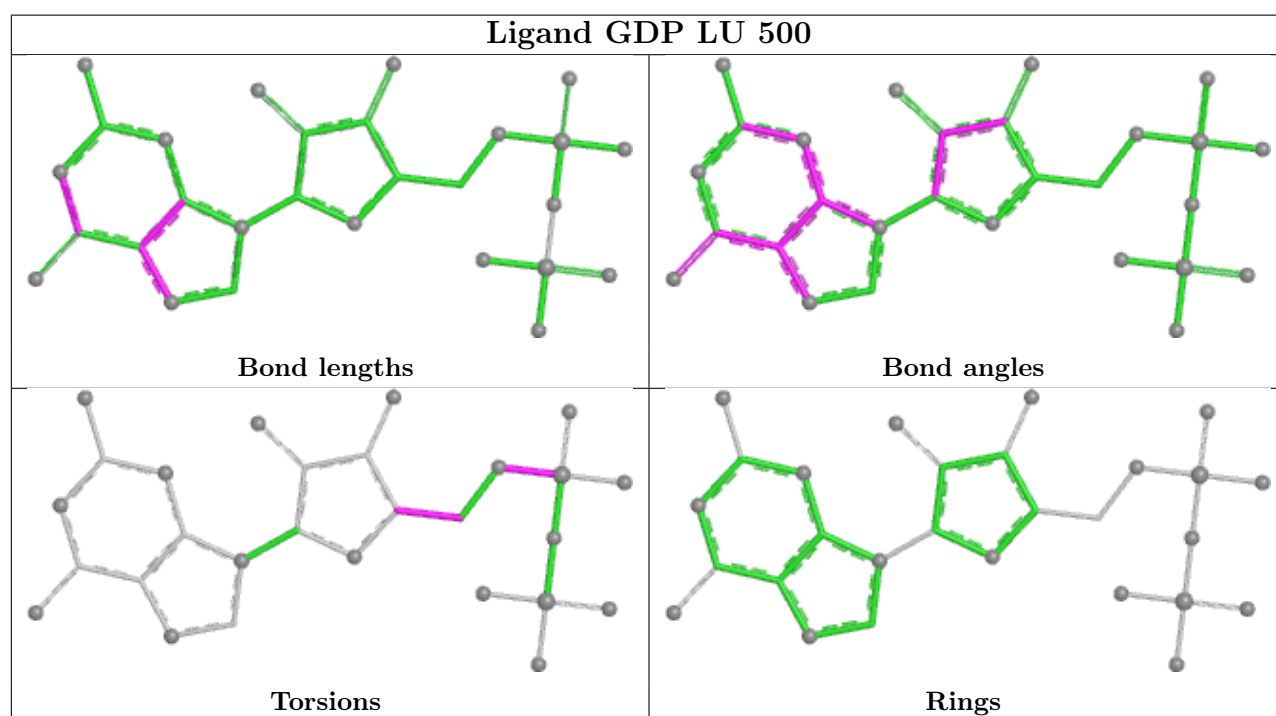
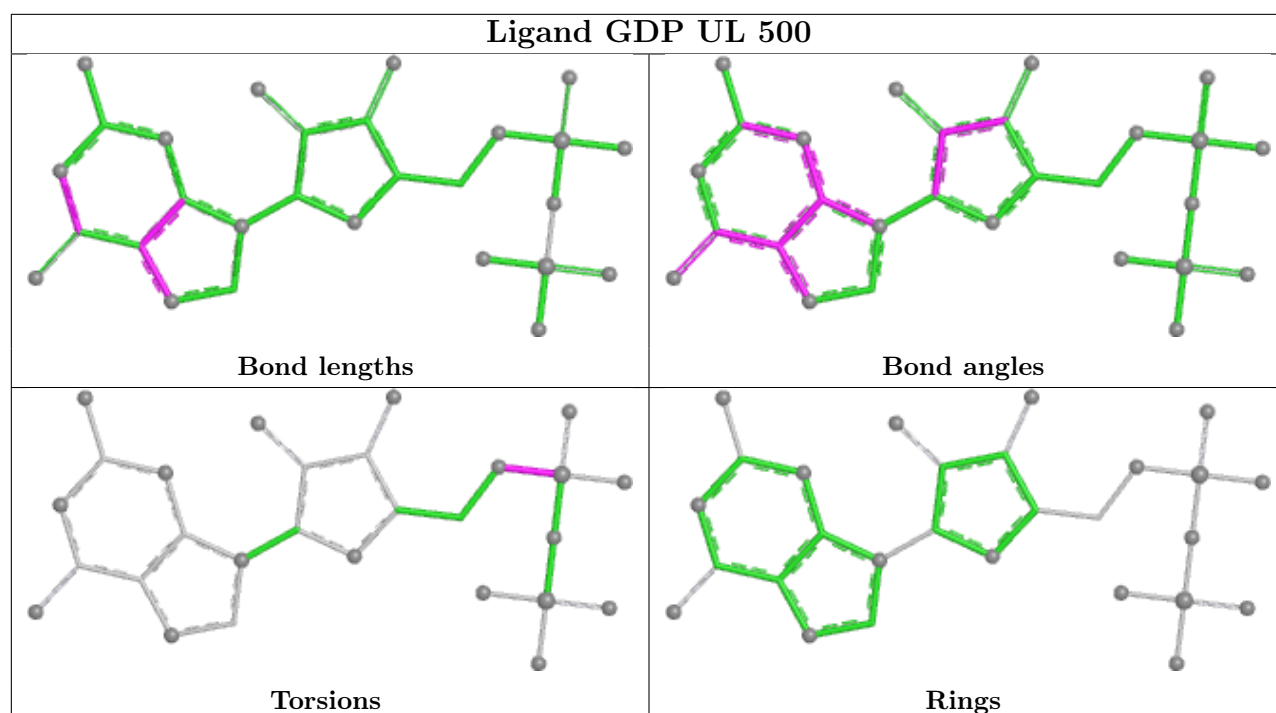
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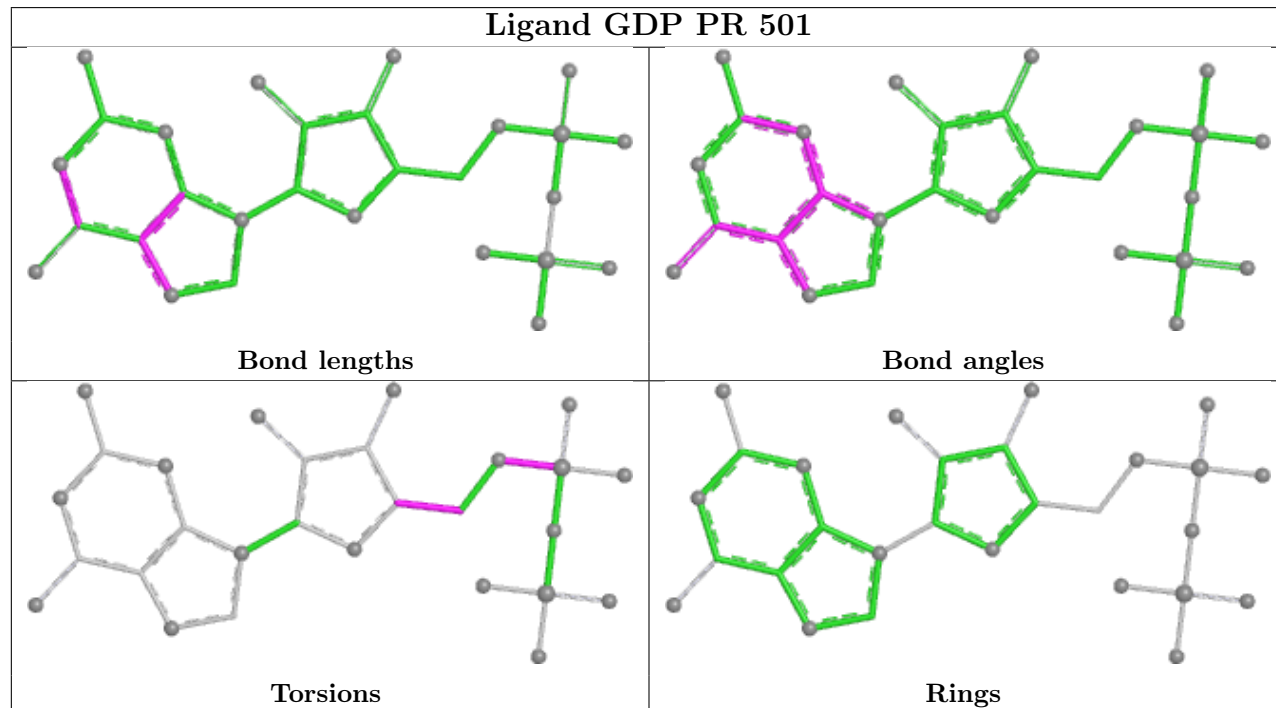
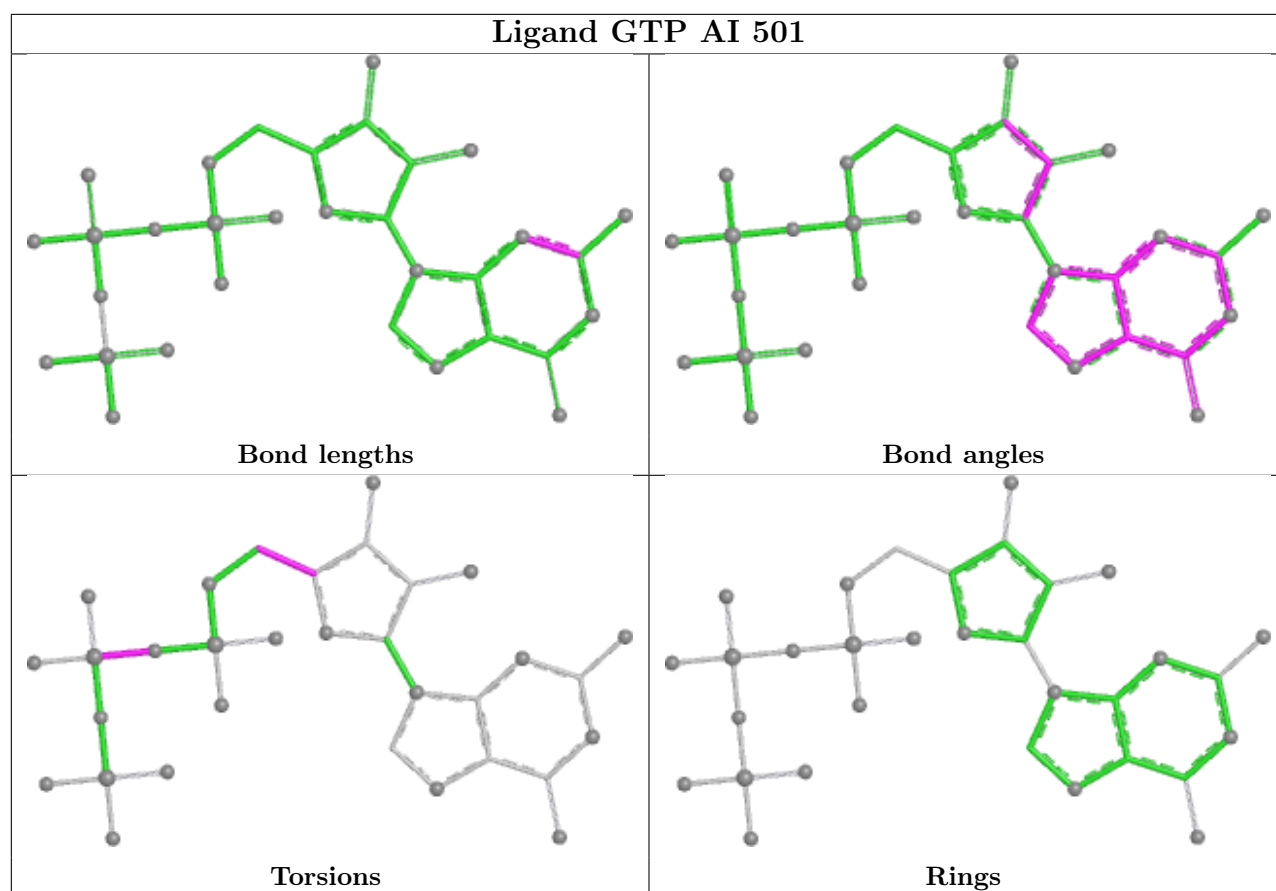


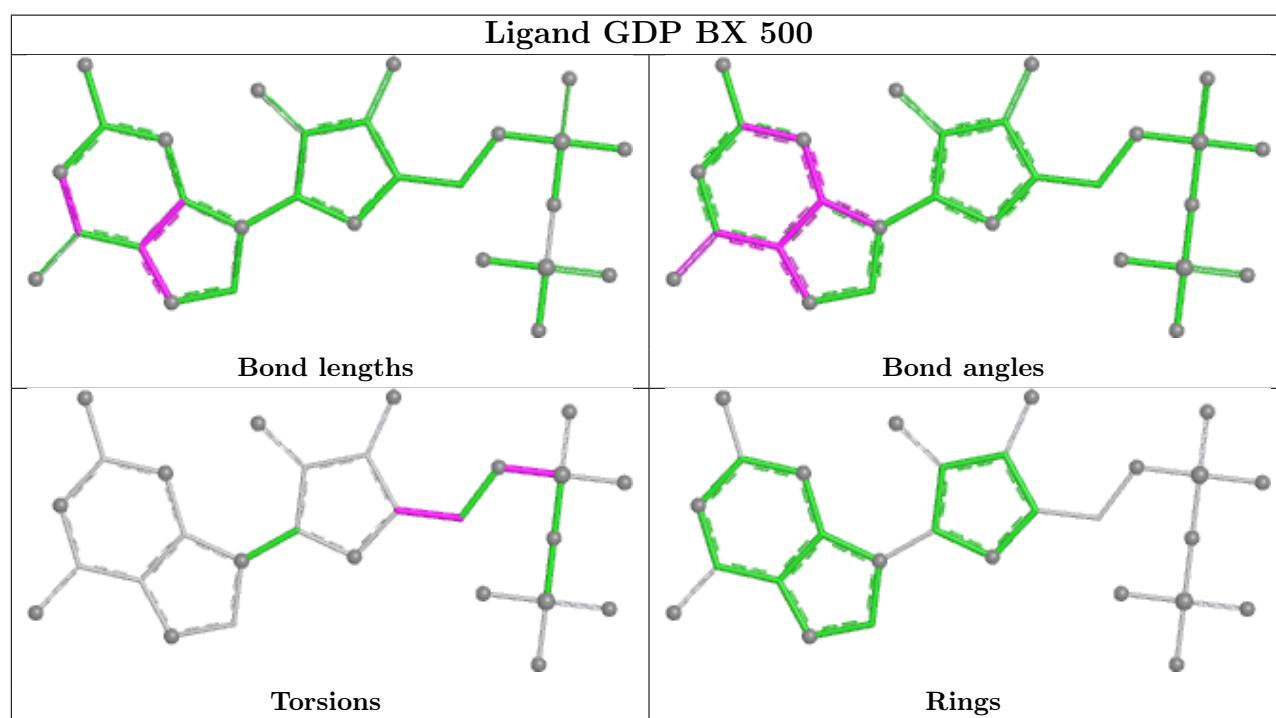
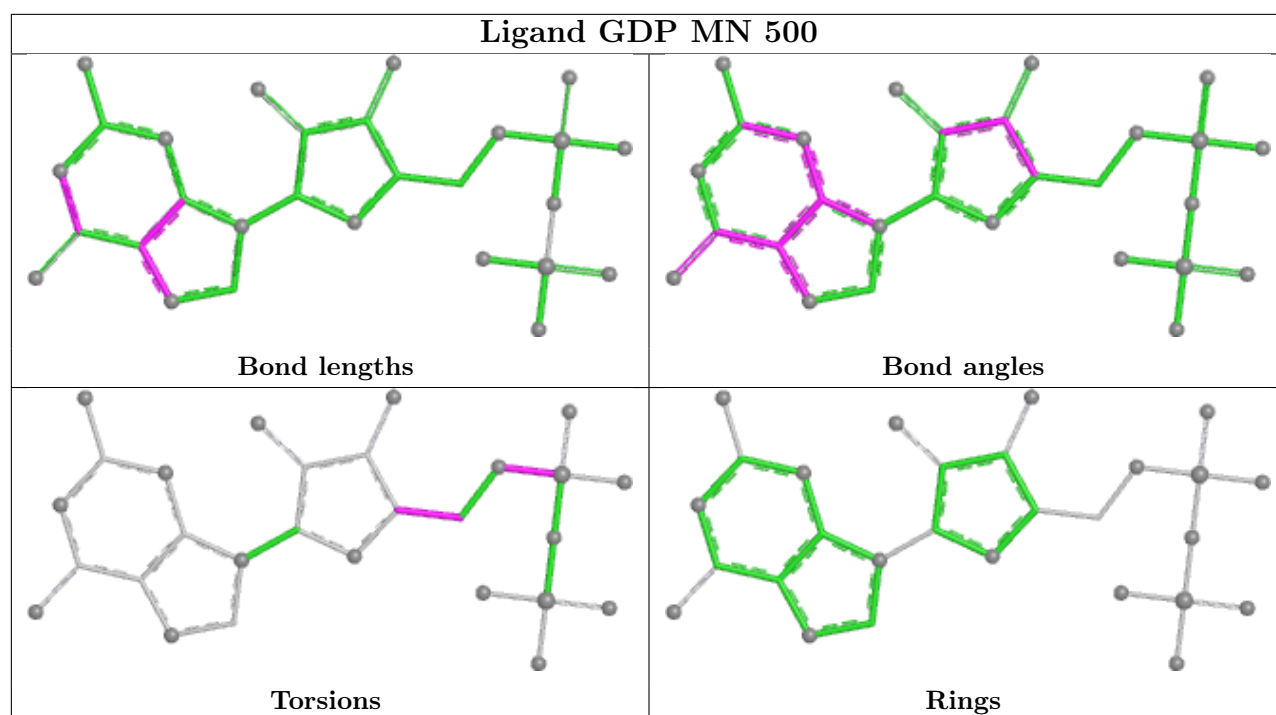


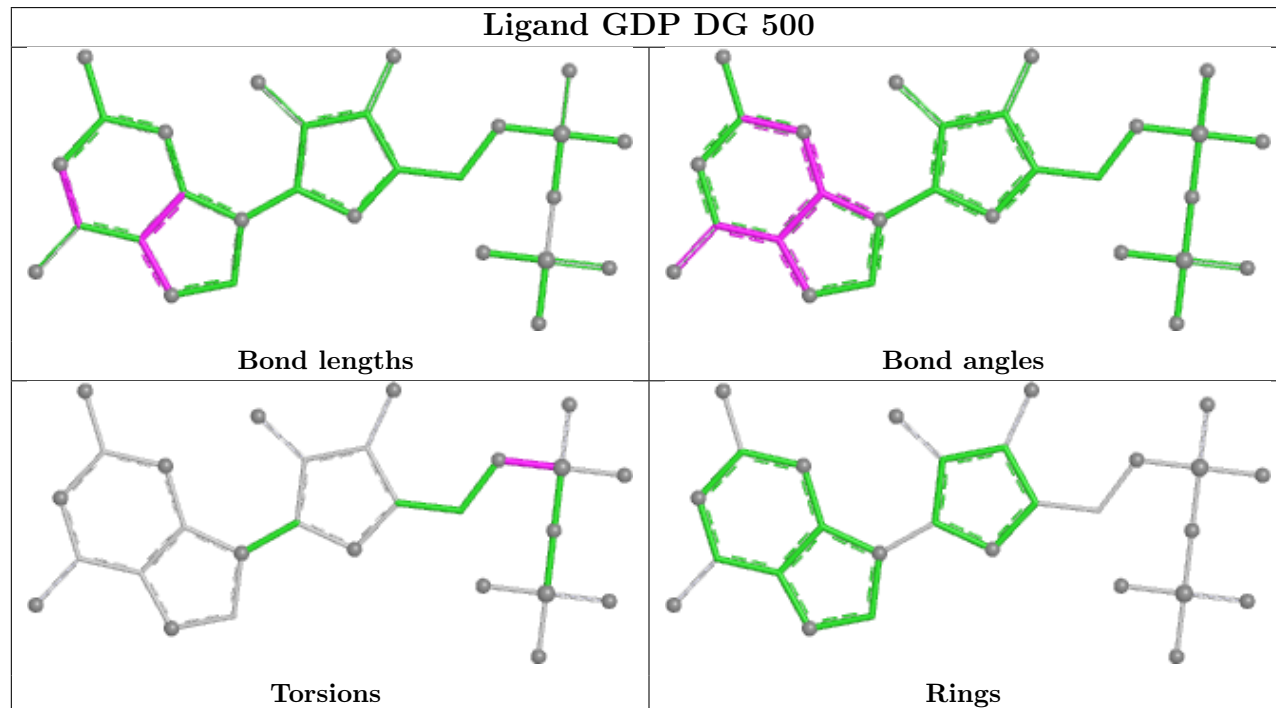
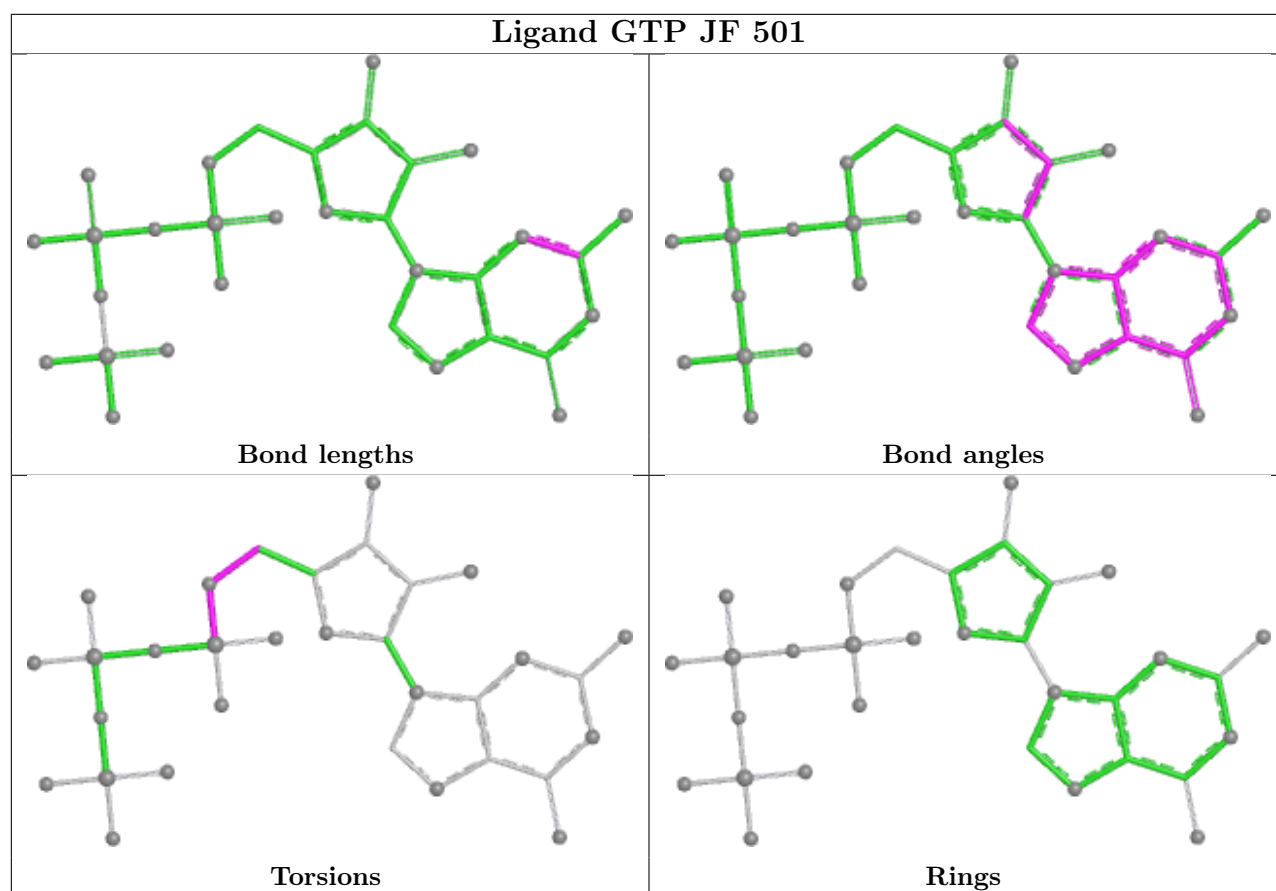




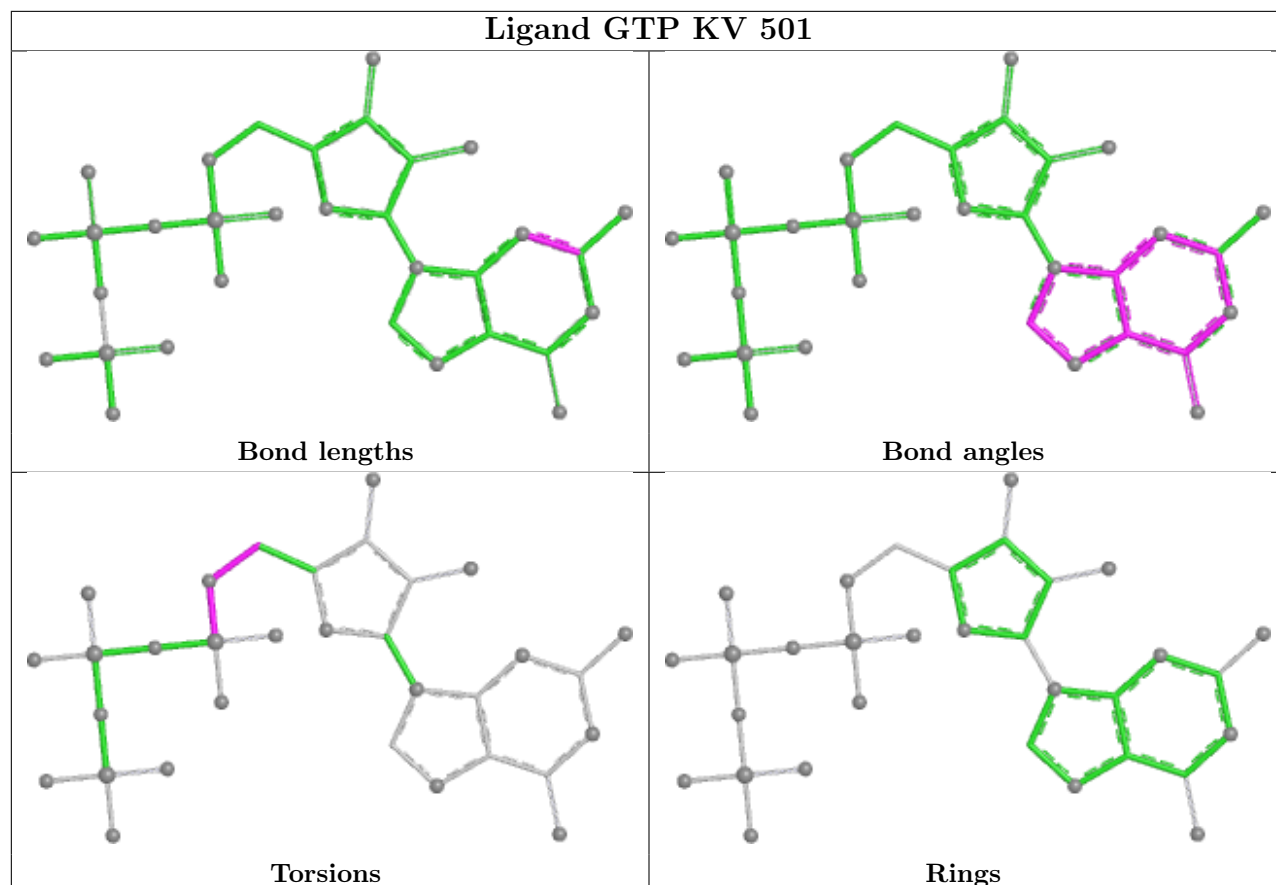




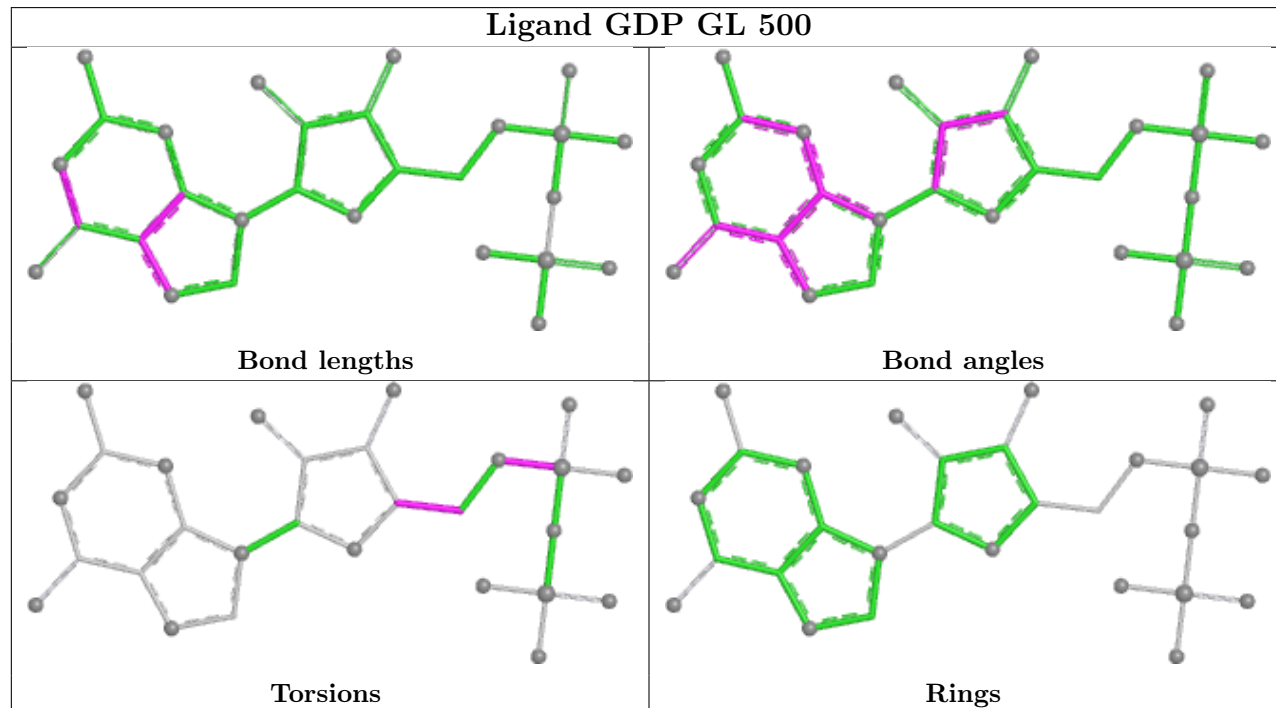




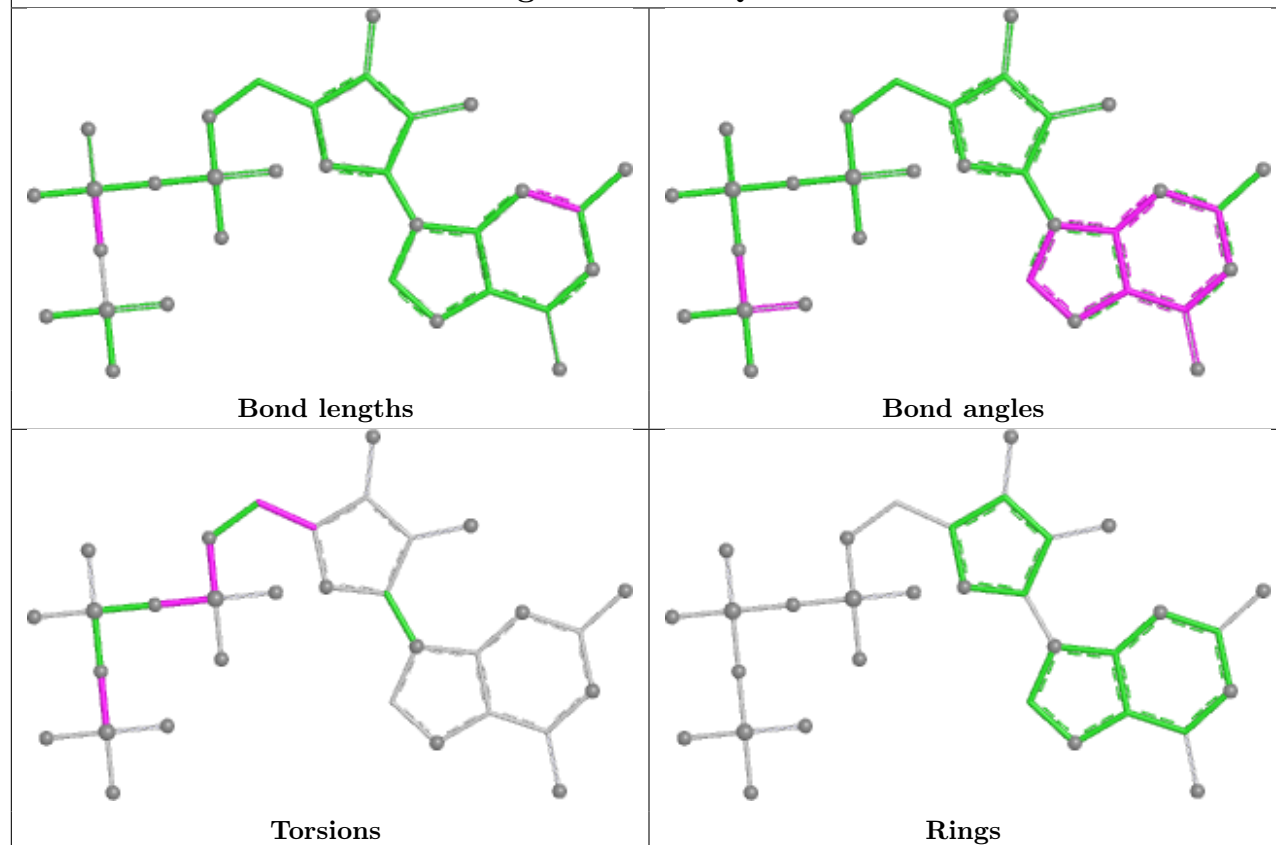
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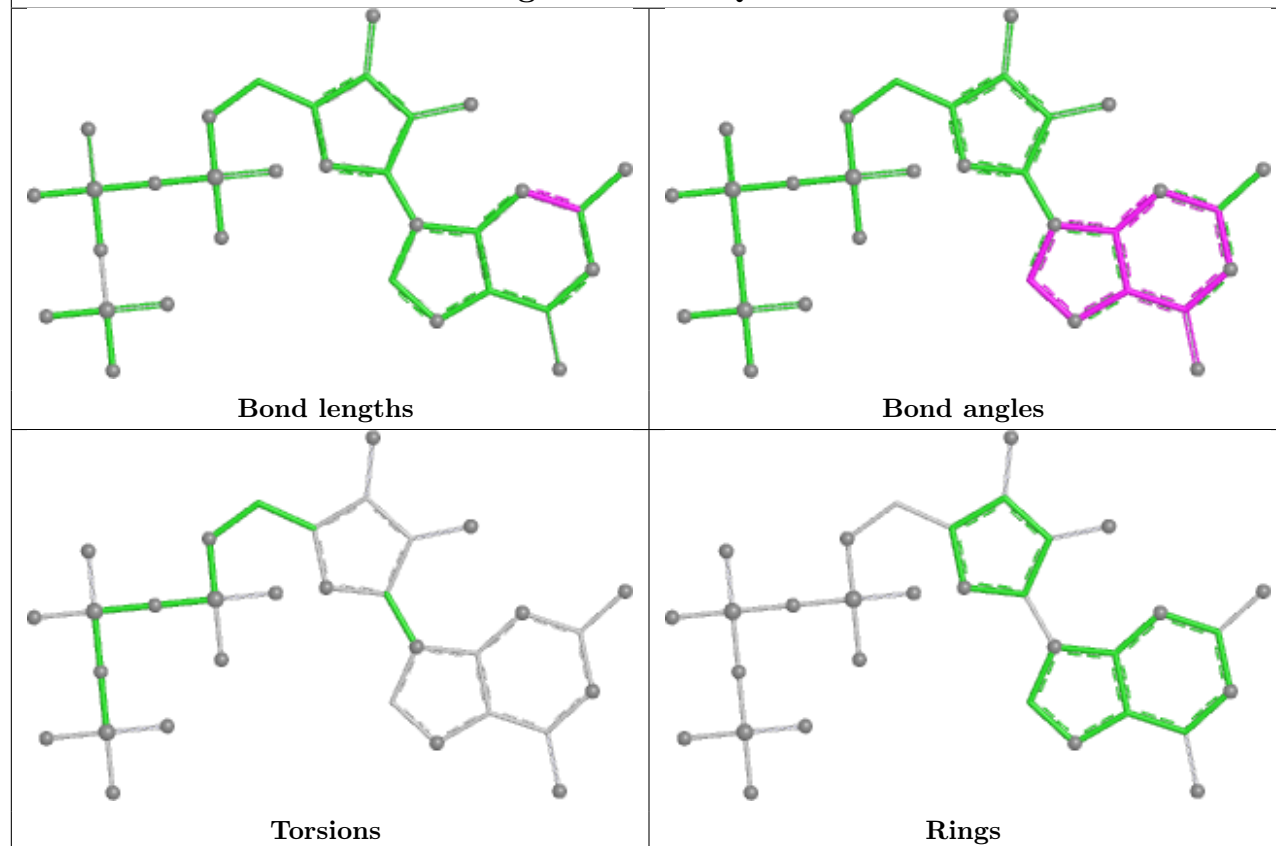
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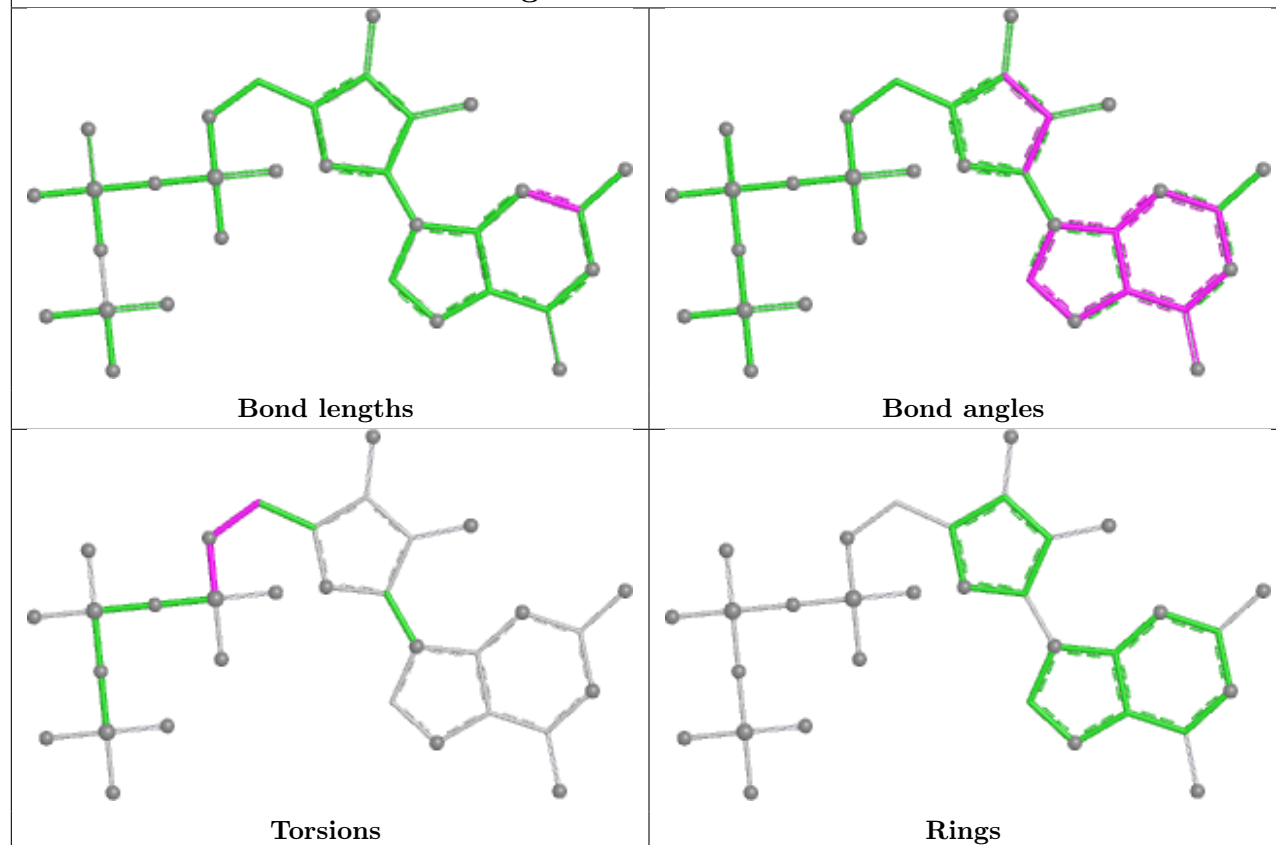
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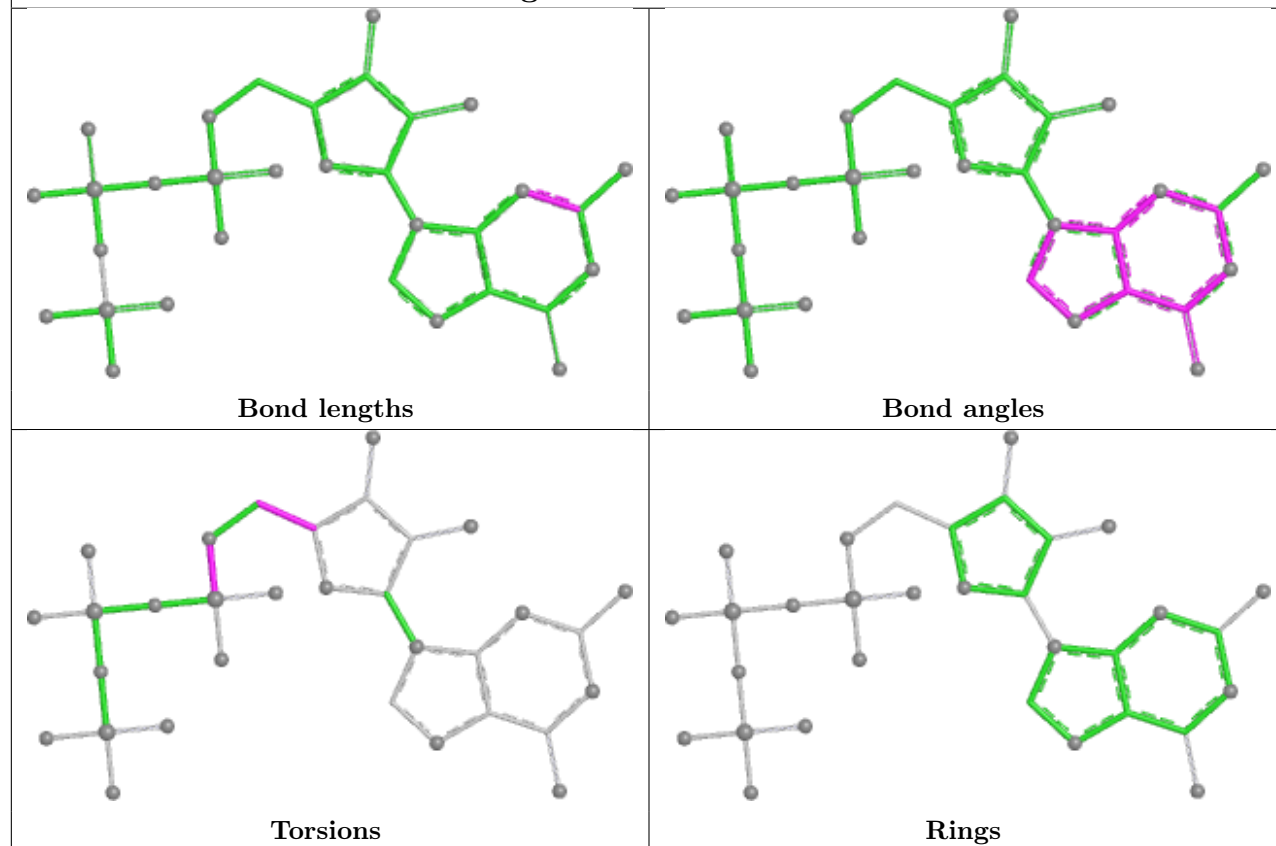
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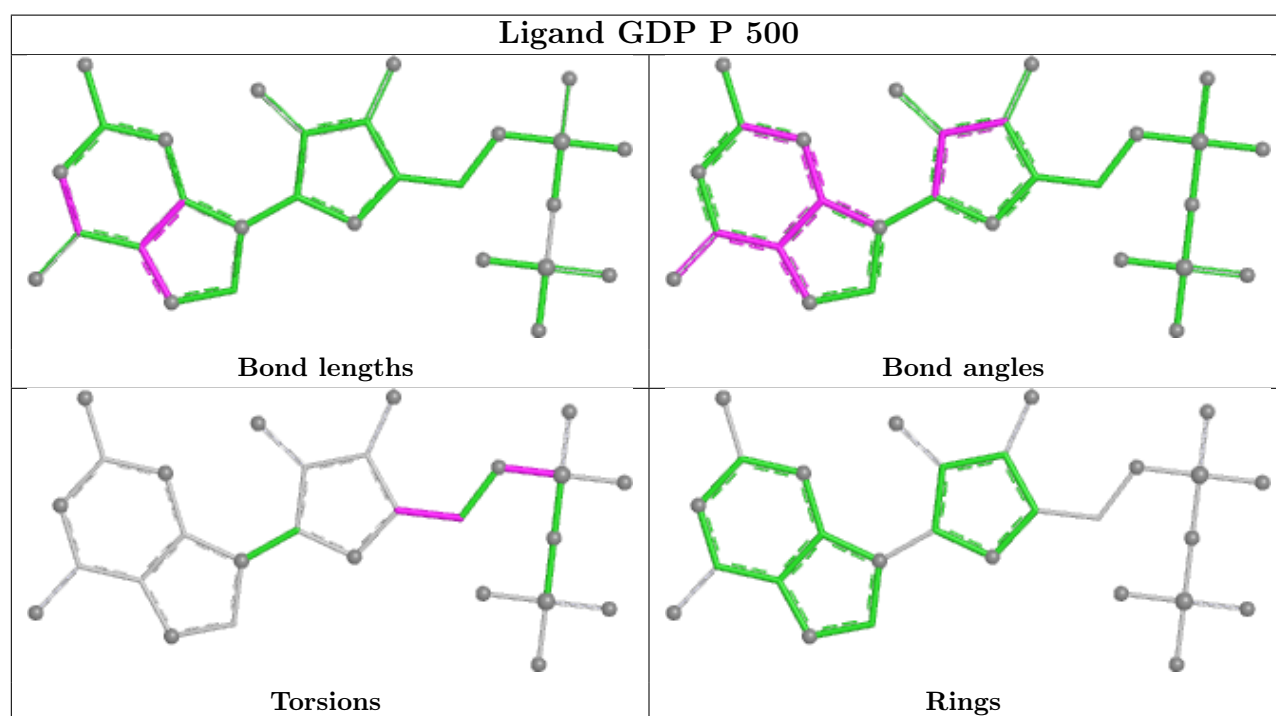
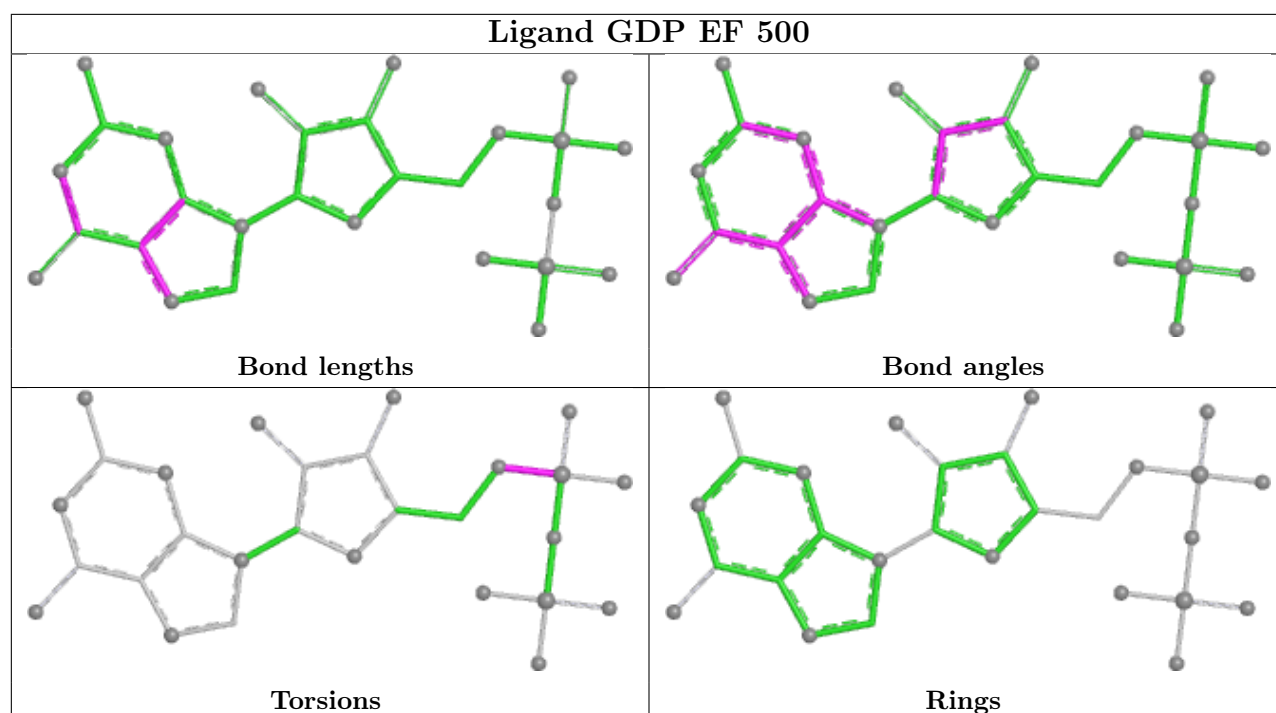


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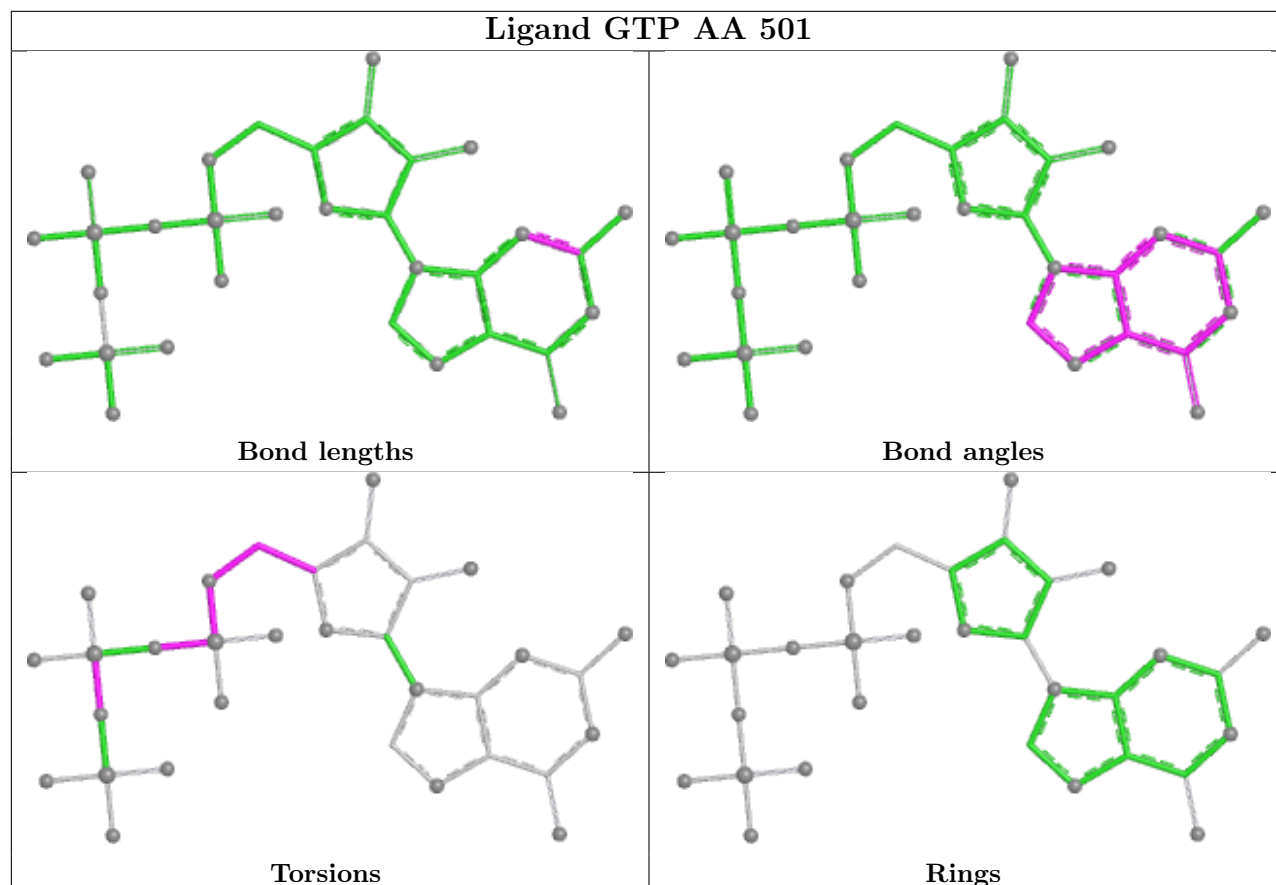


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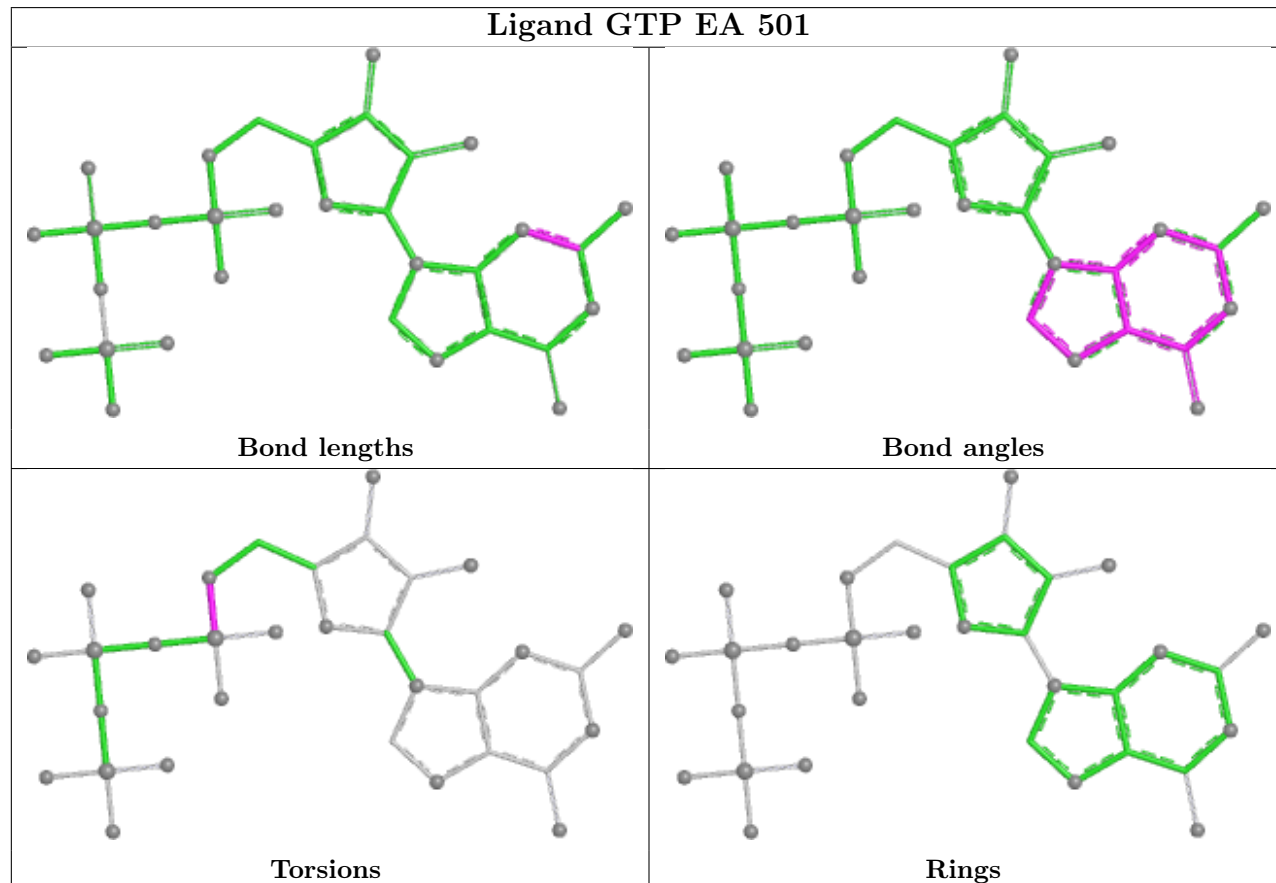


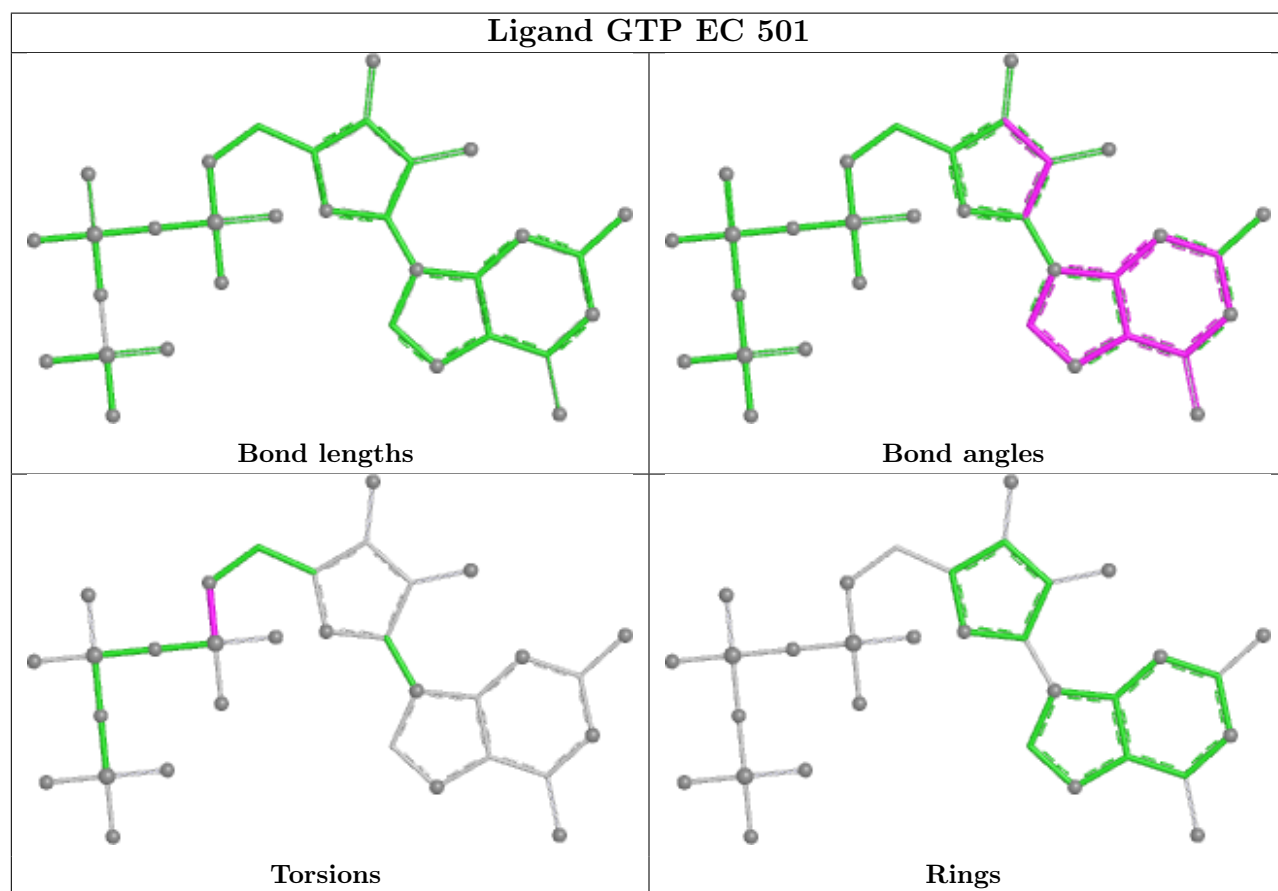
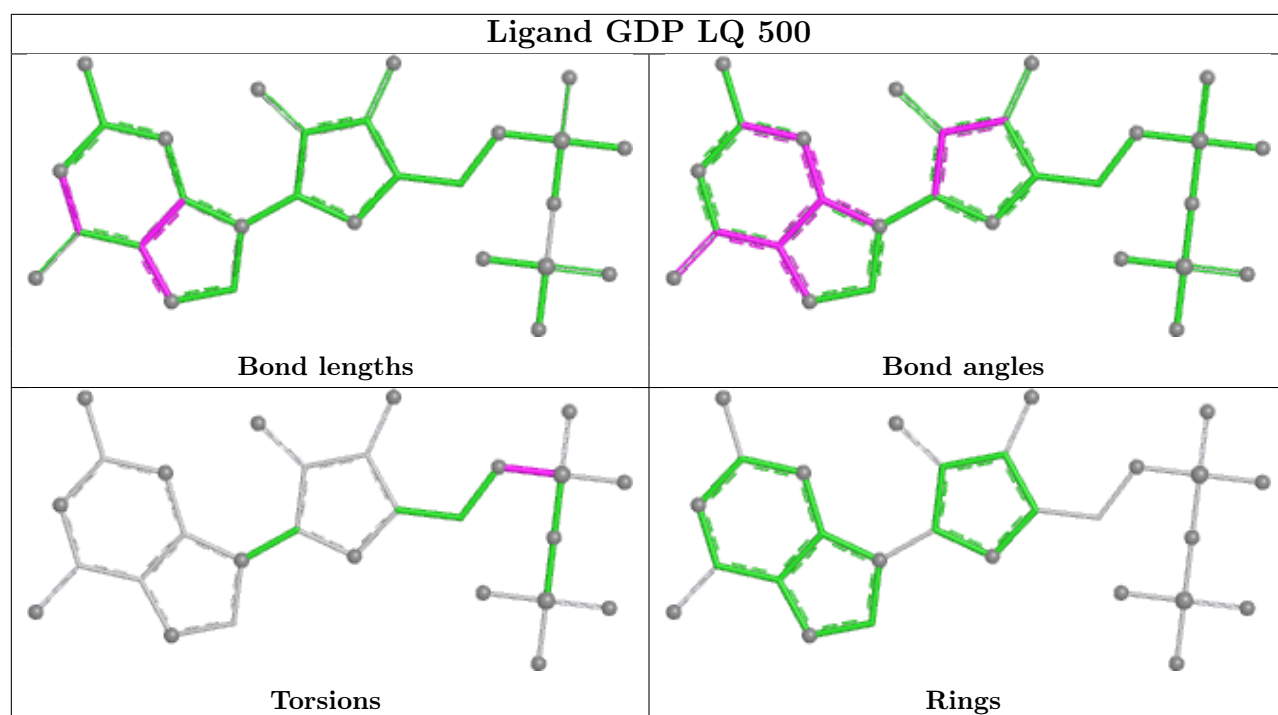


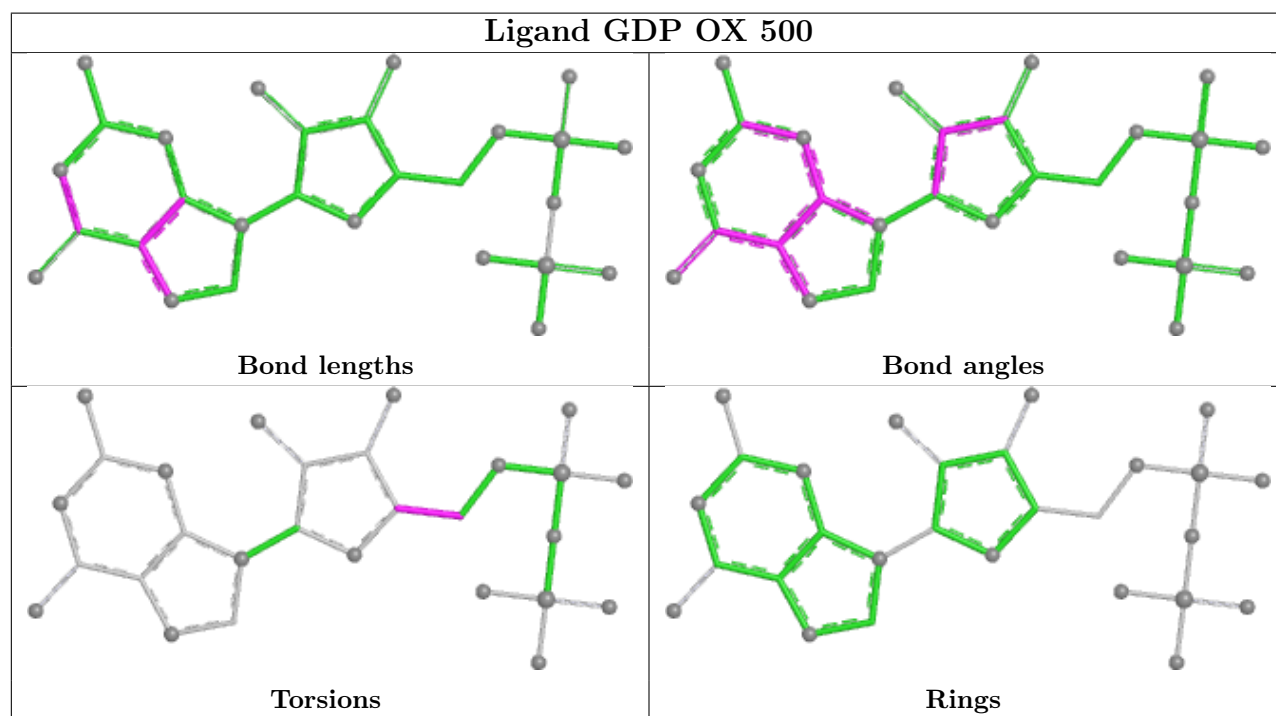
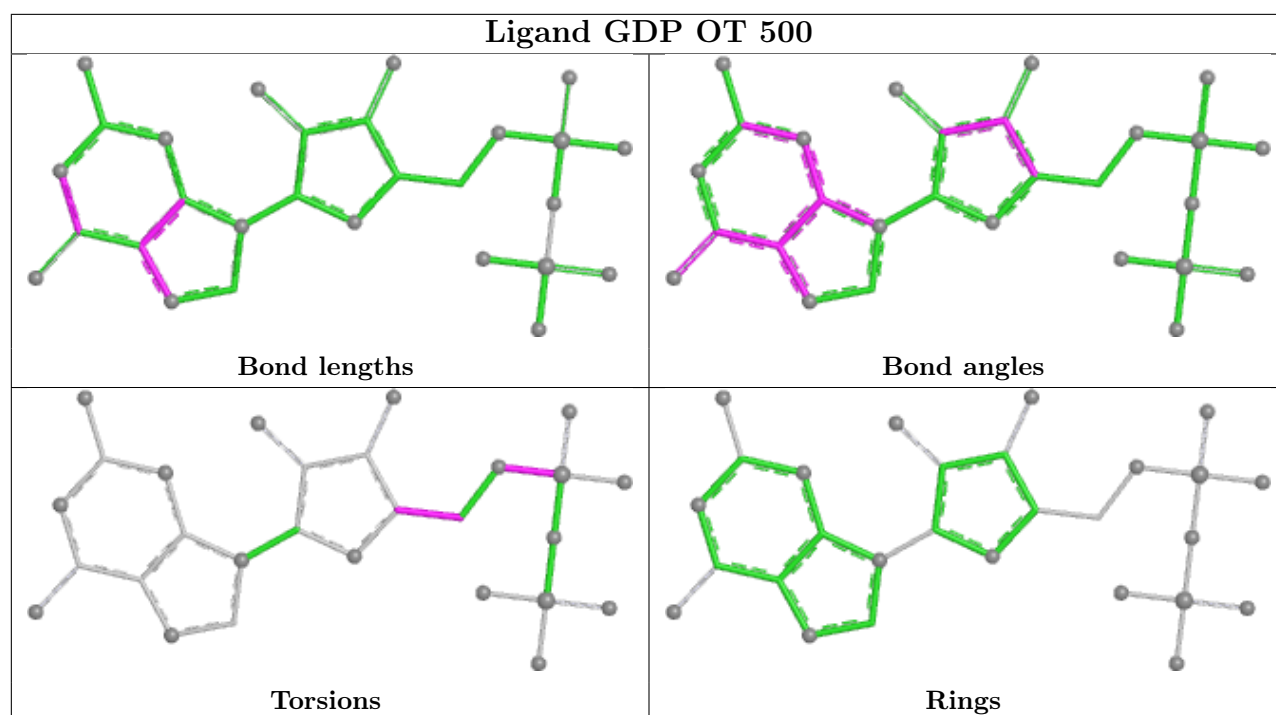
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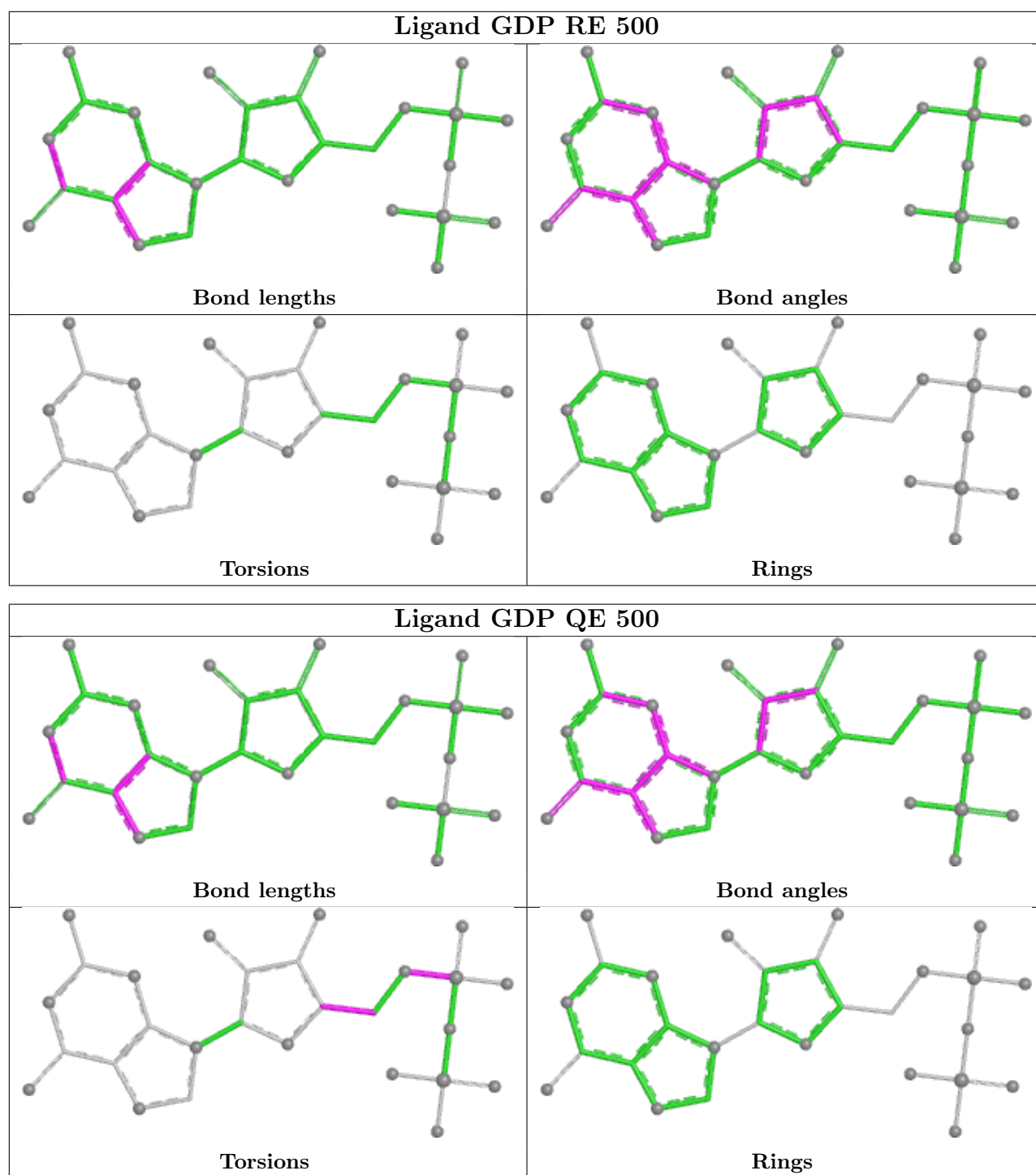


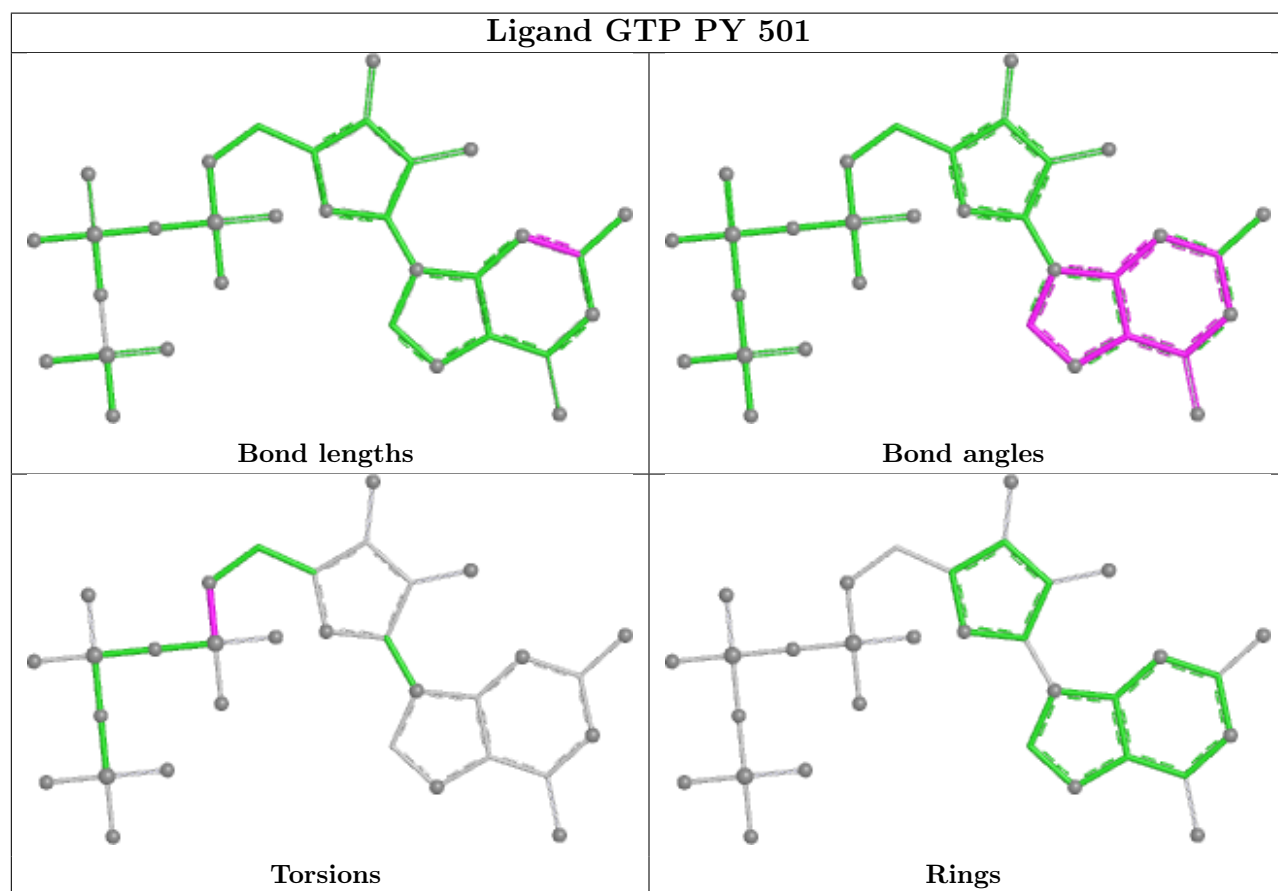
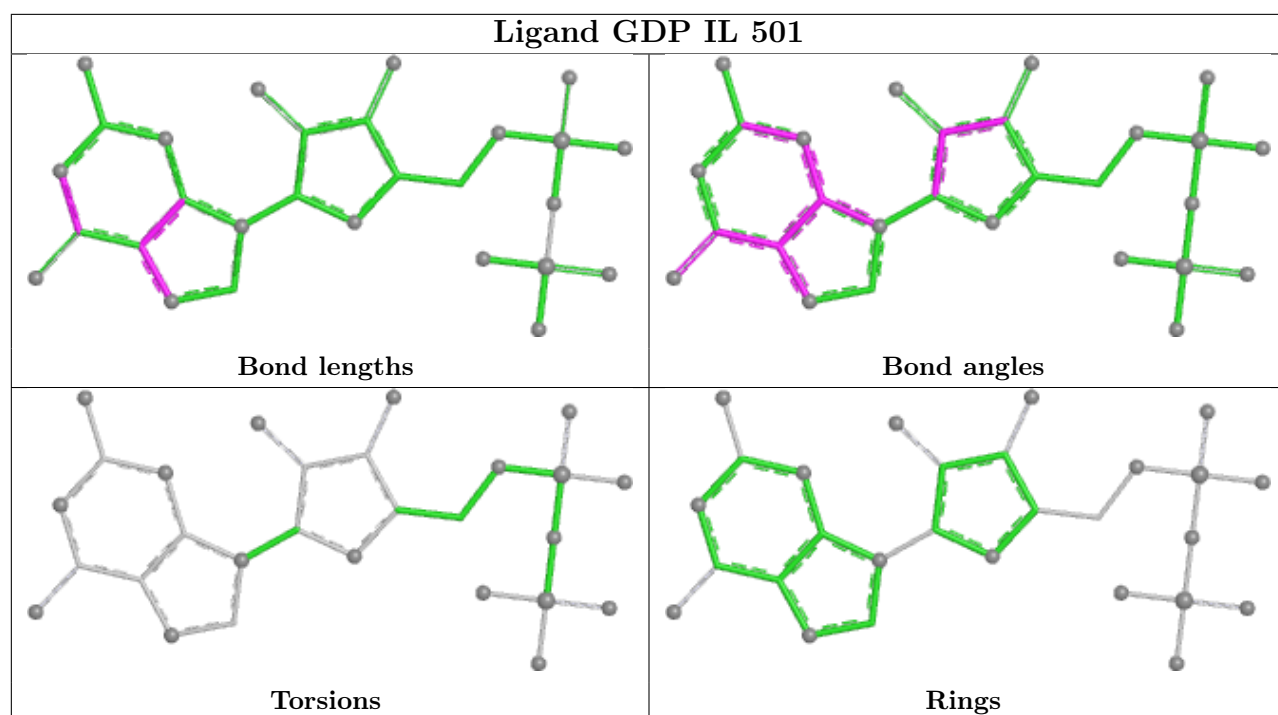
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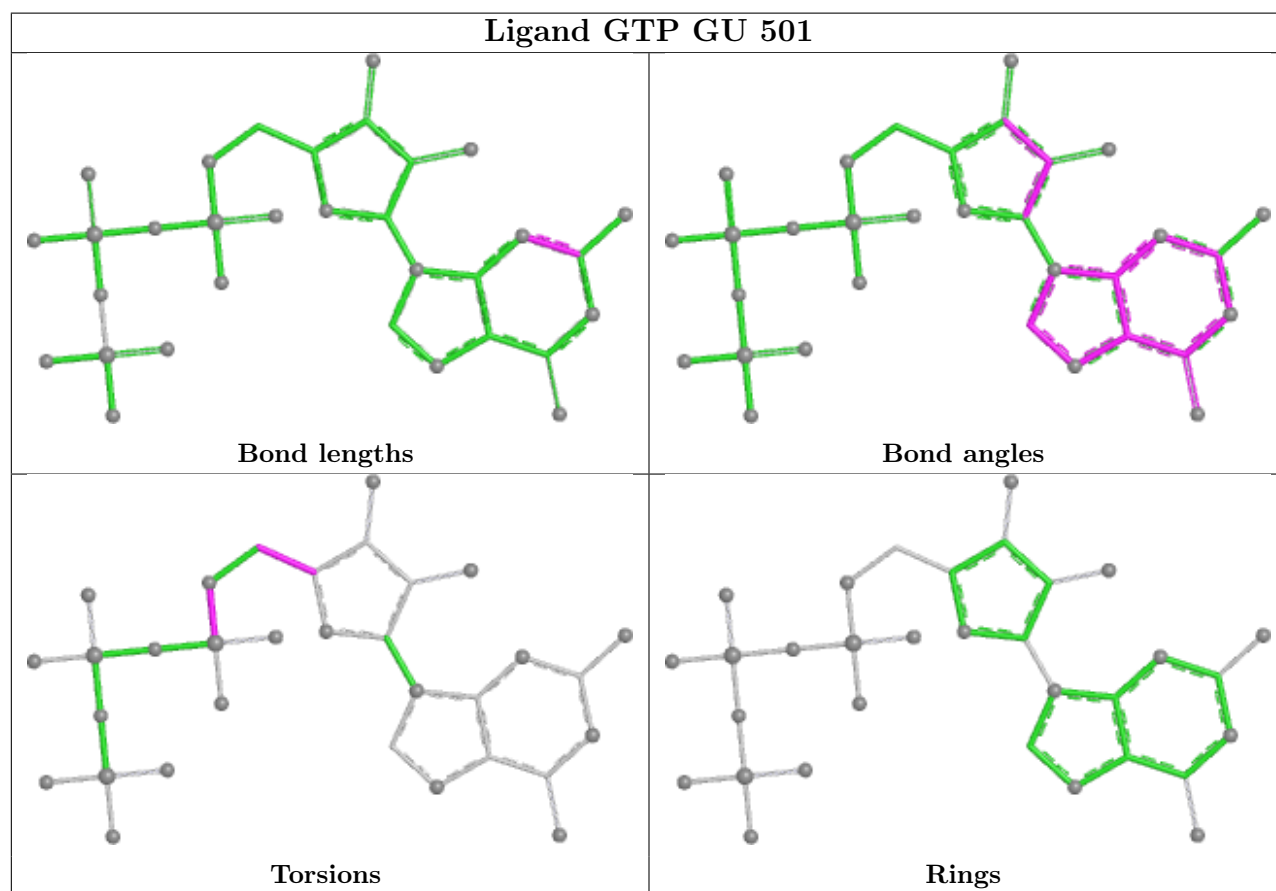
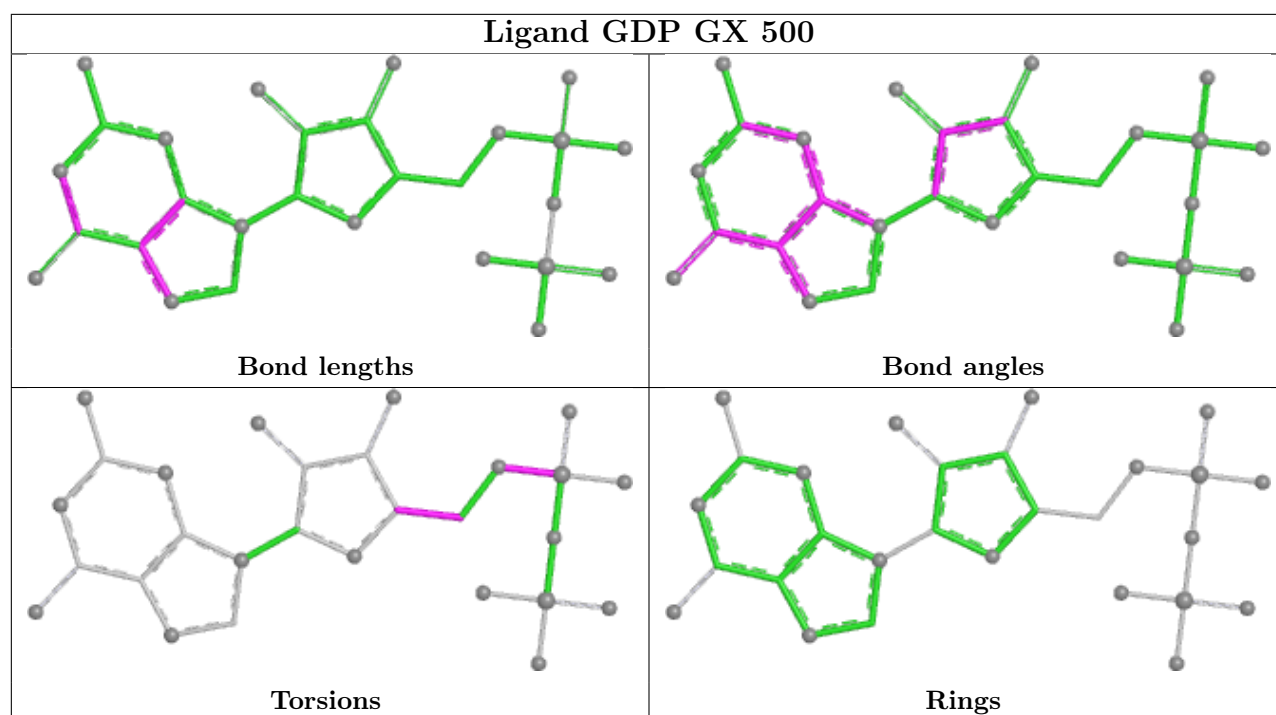


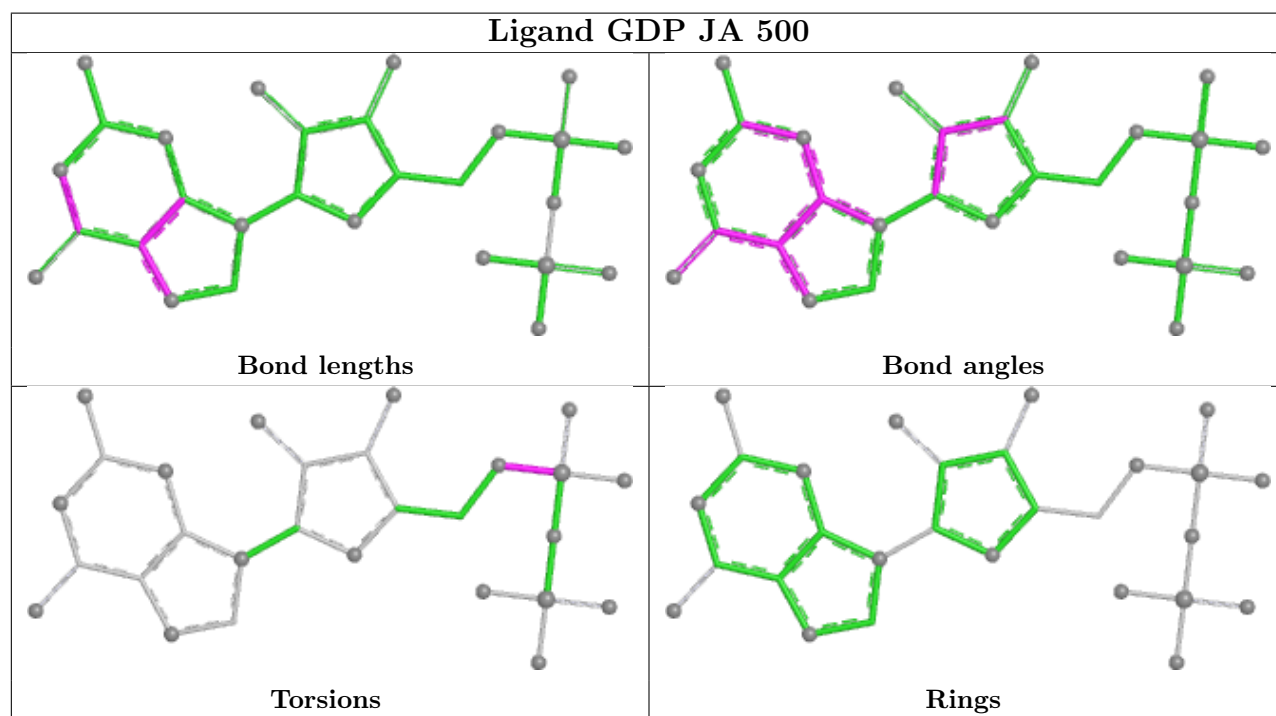
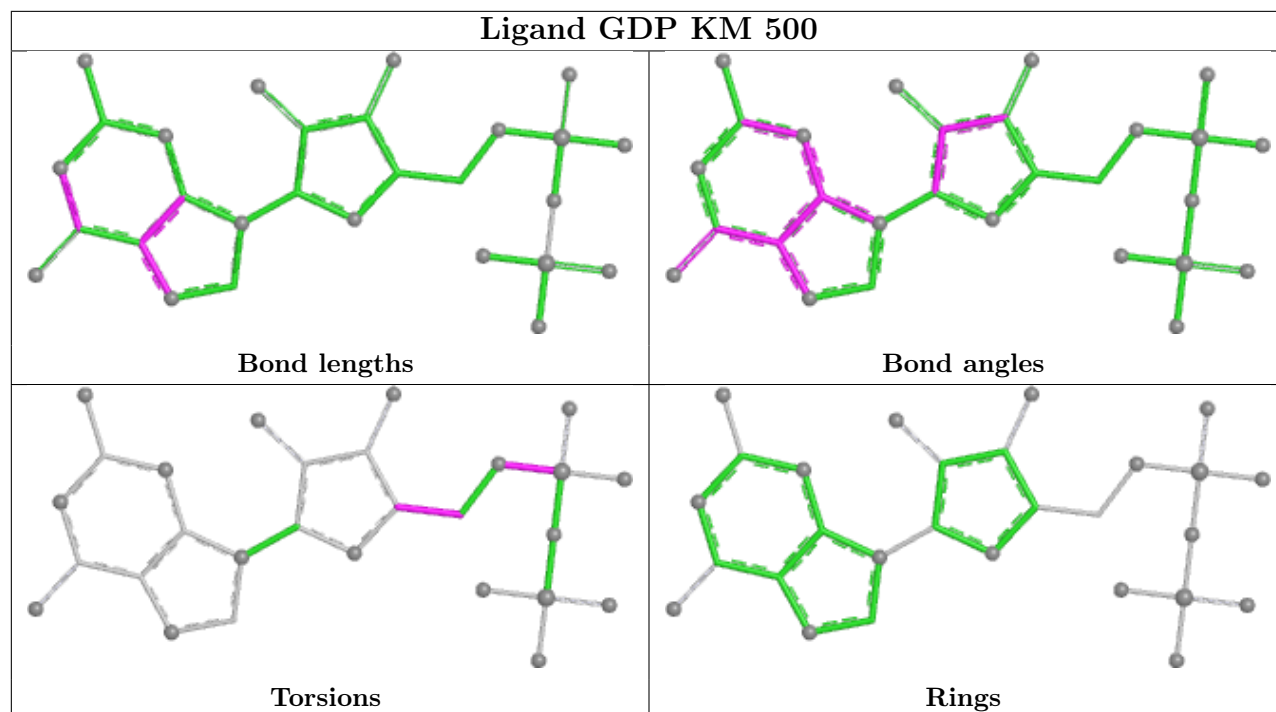




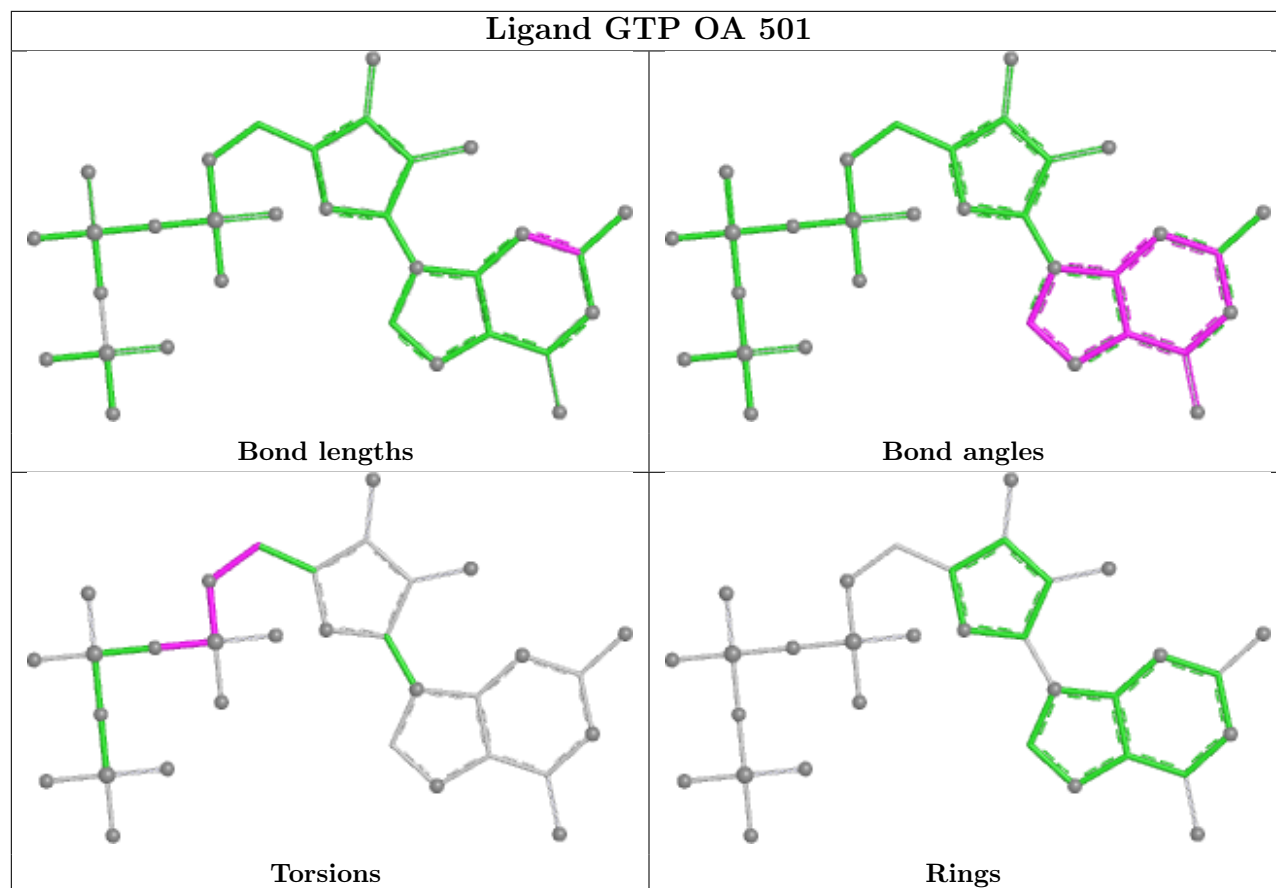




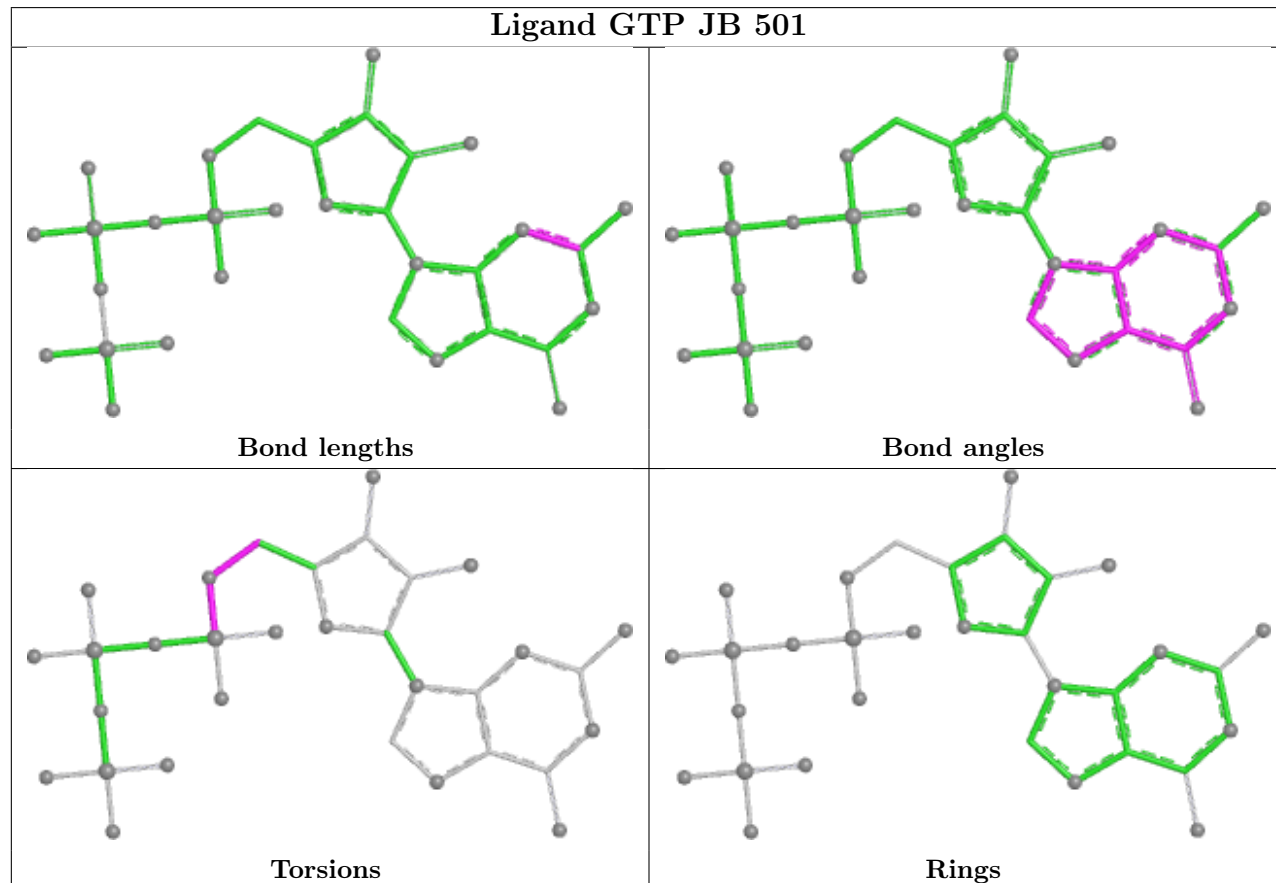


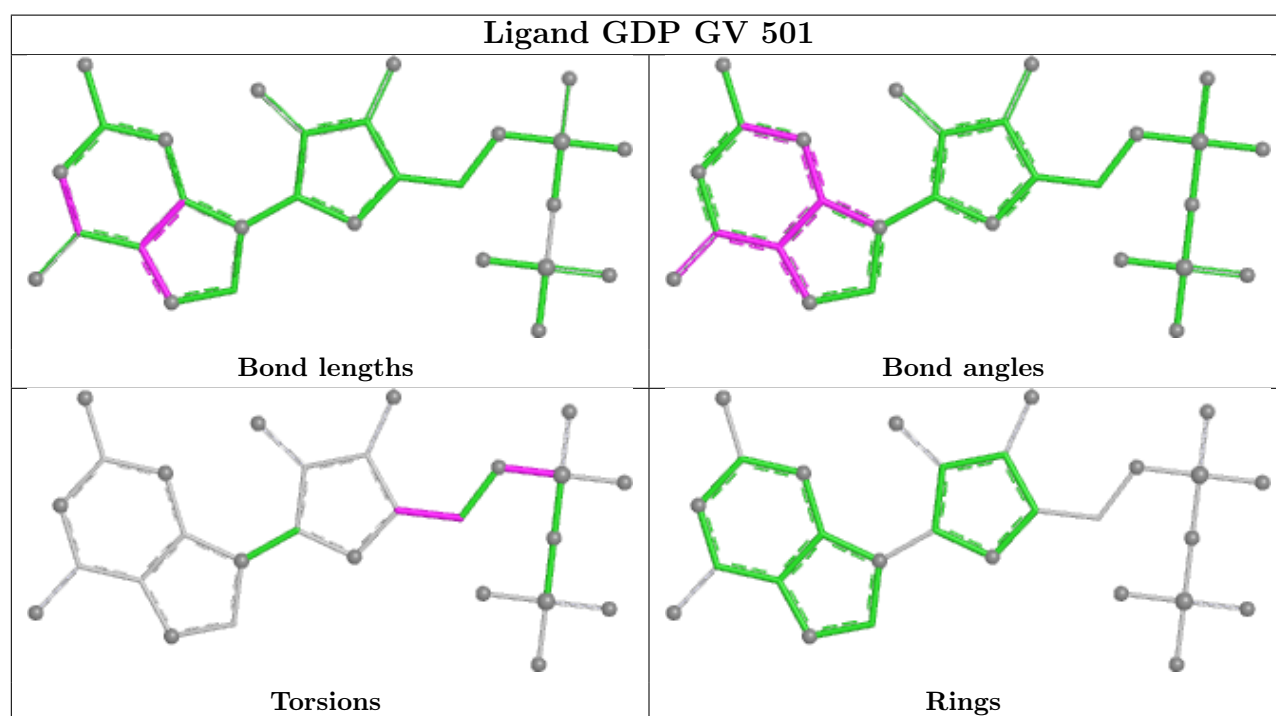
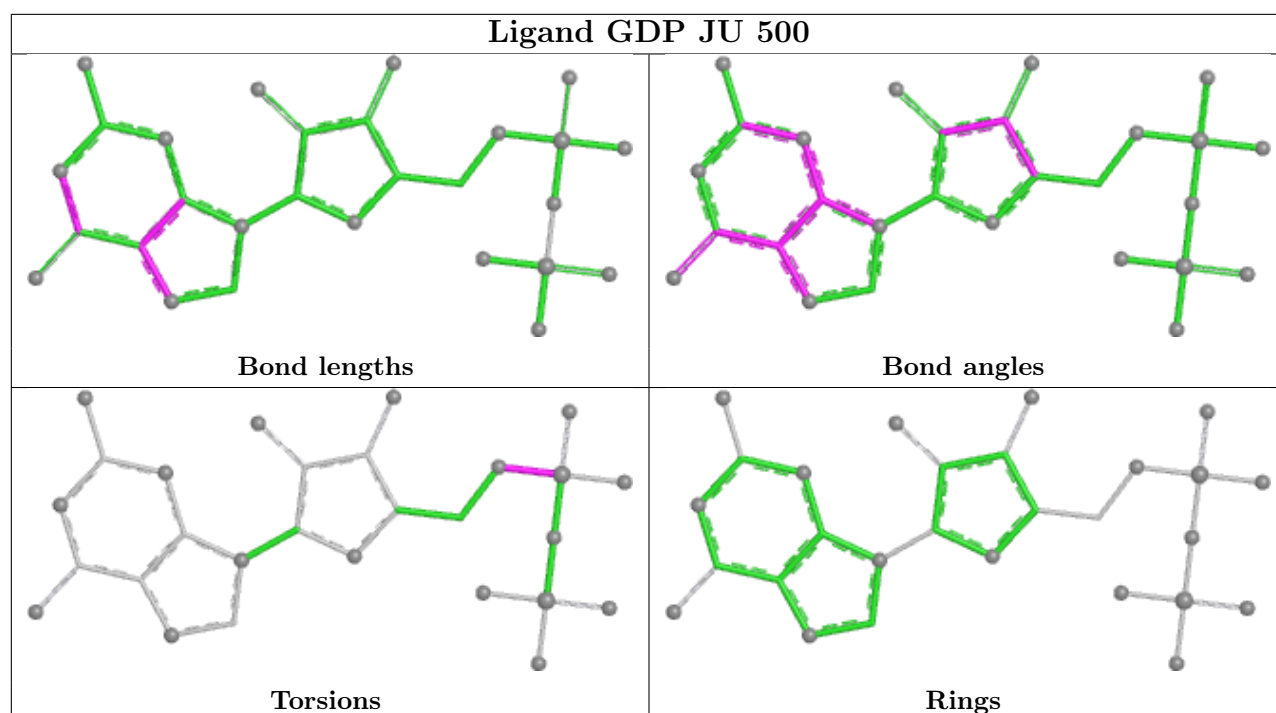


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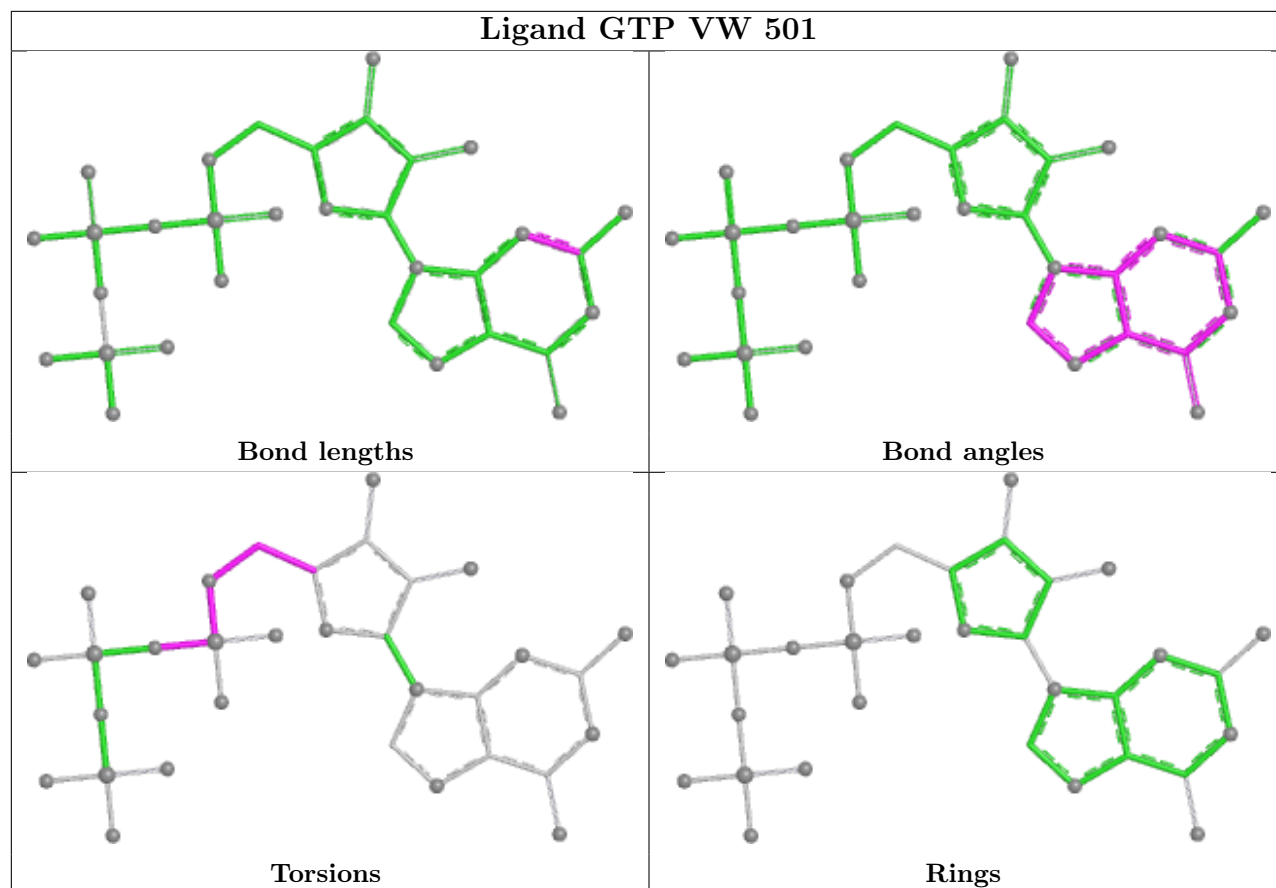


Ligand GTP JB 501

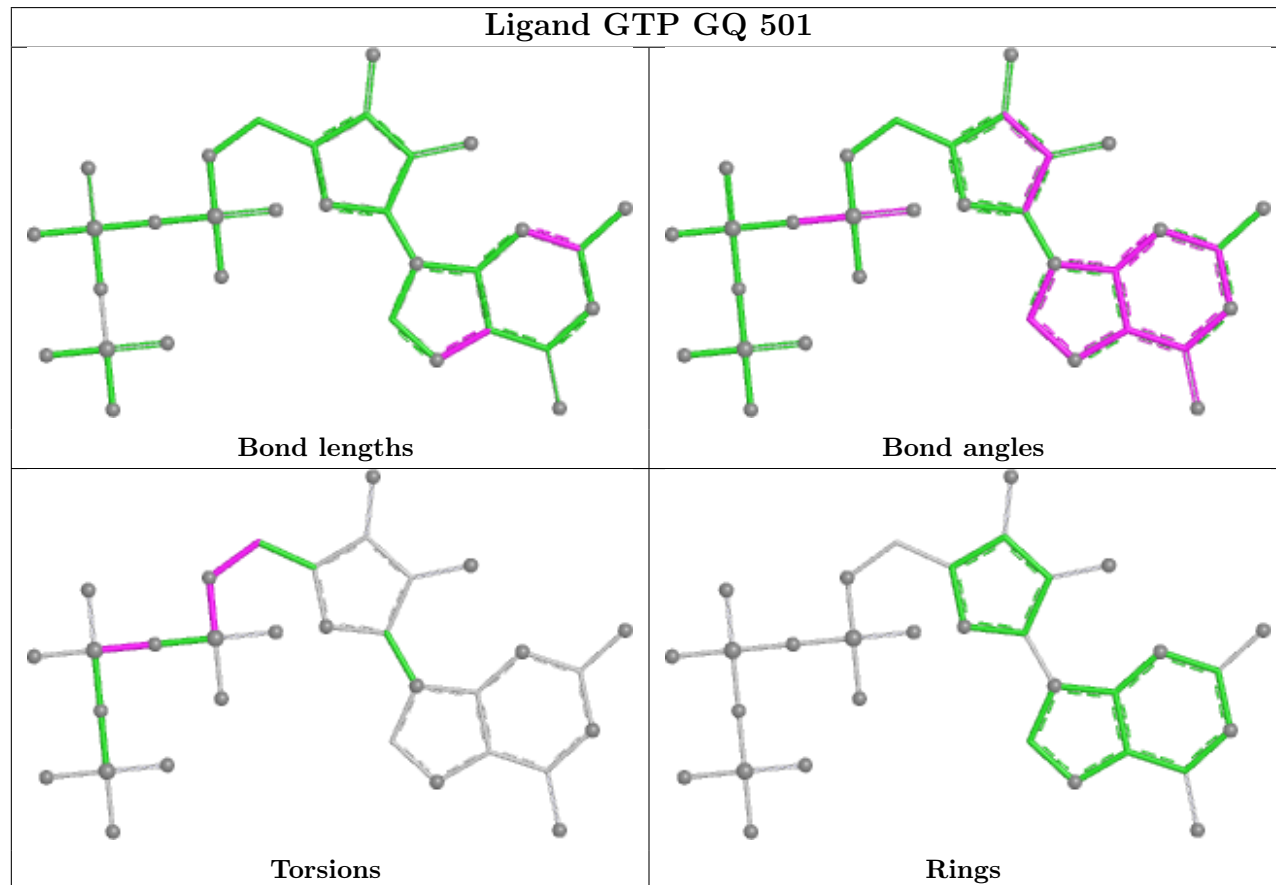


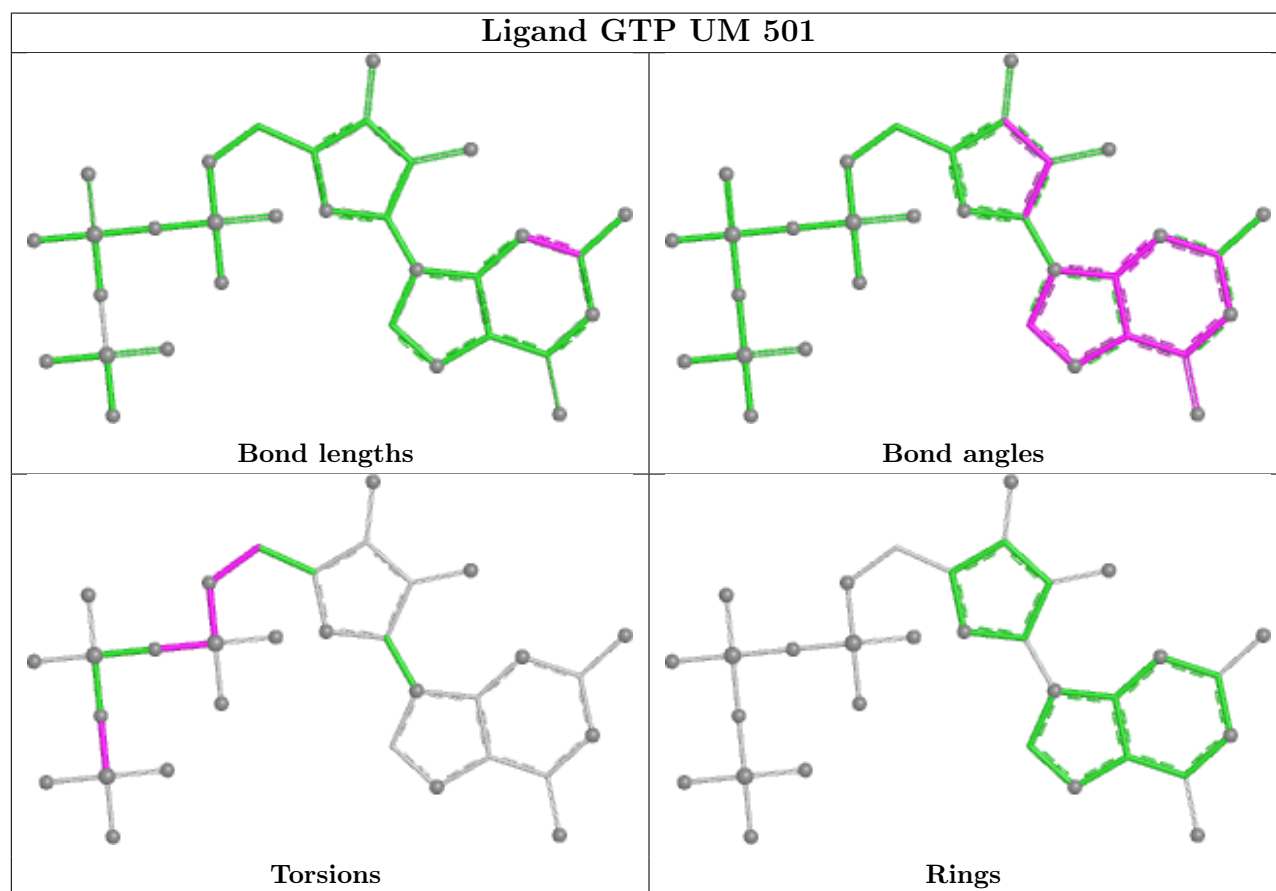
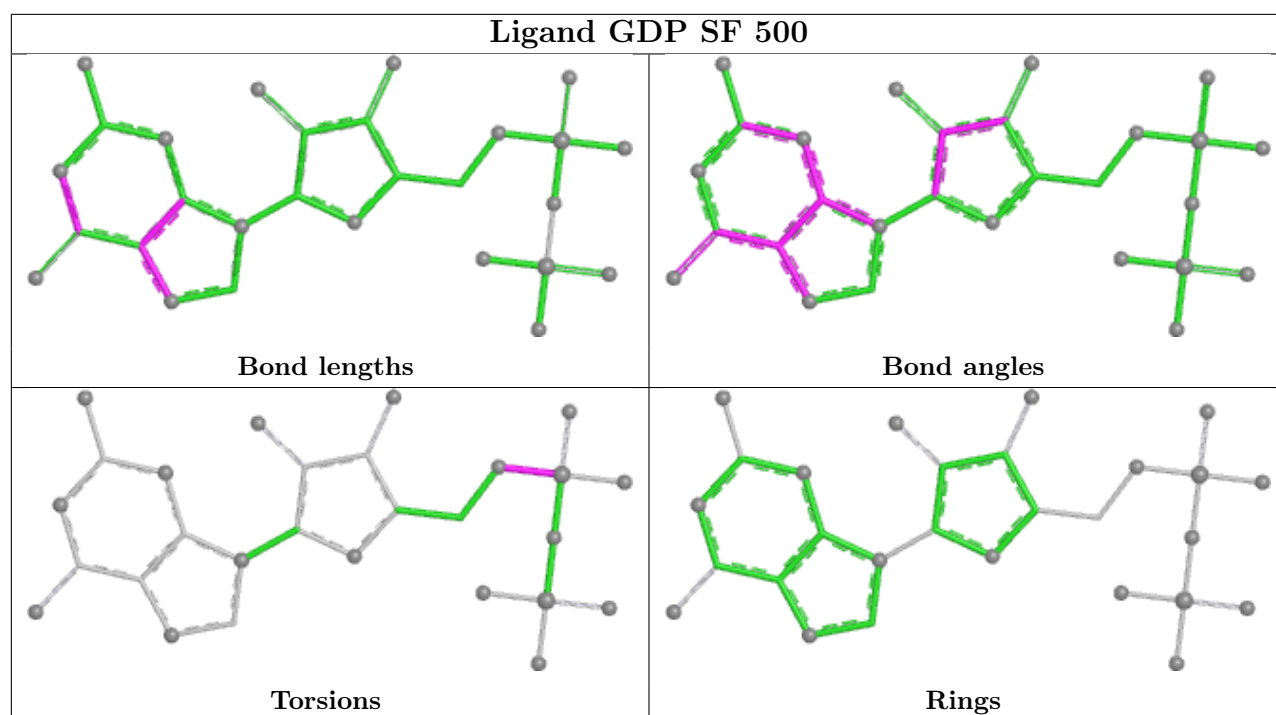


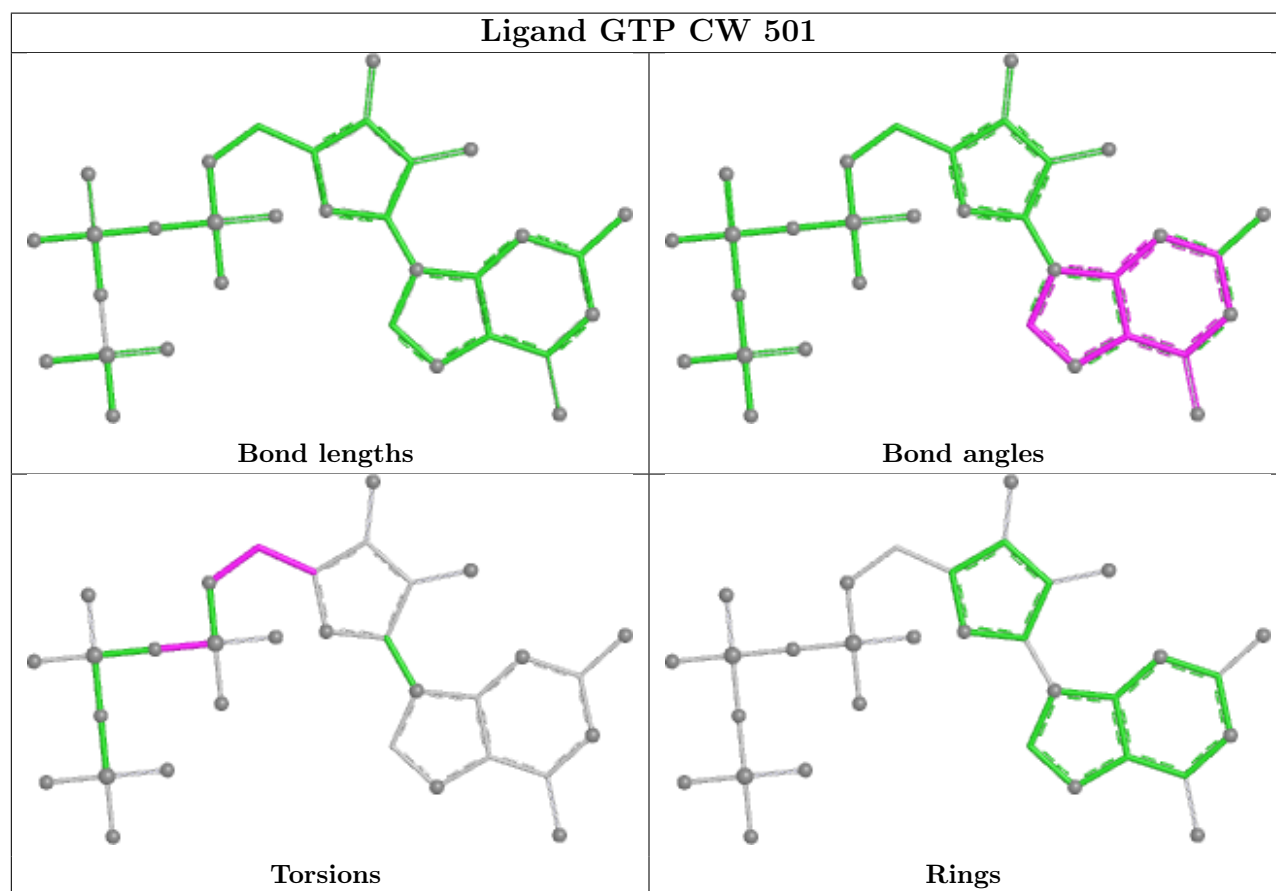
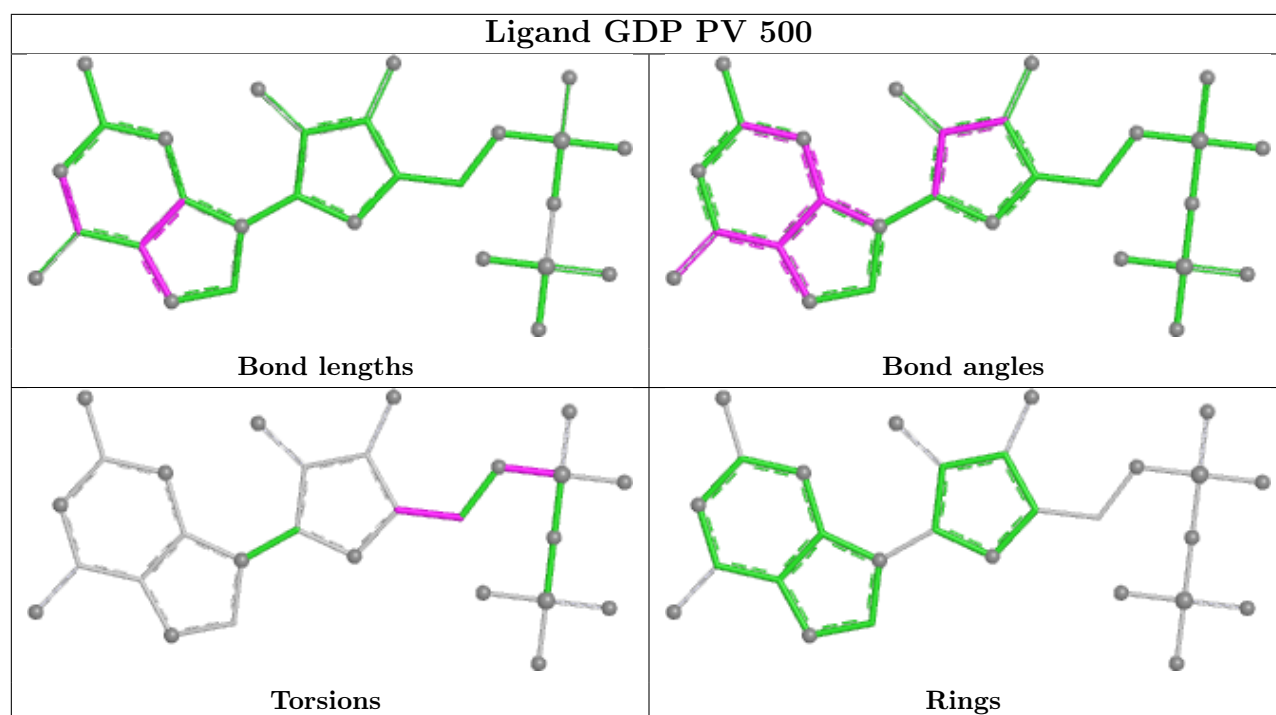
Ligand GTP VW 501

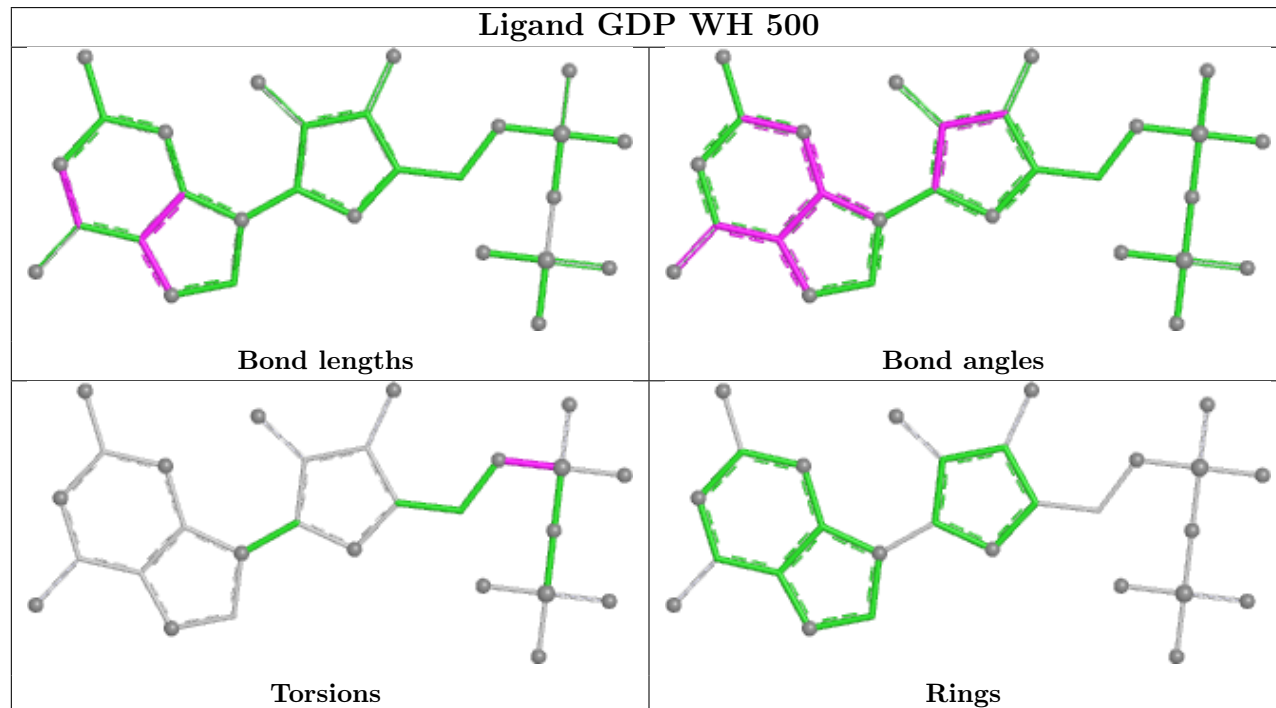
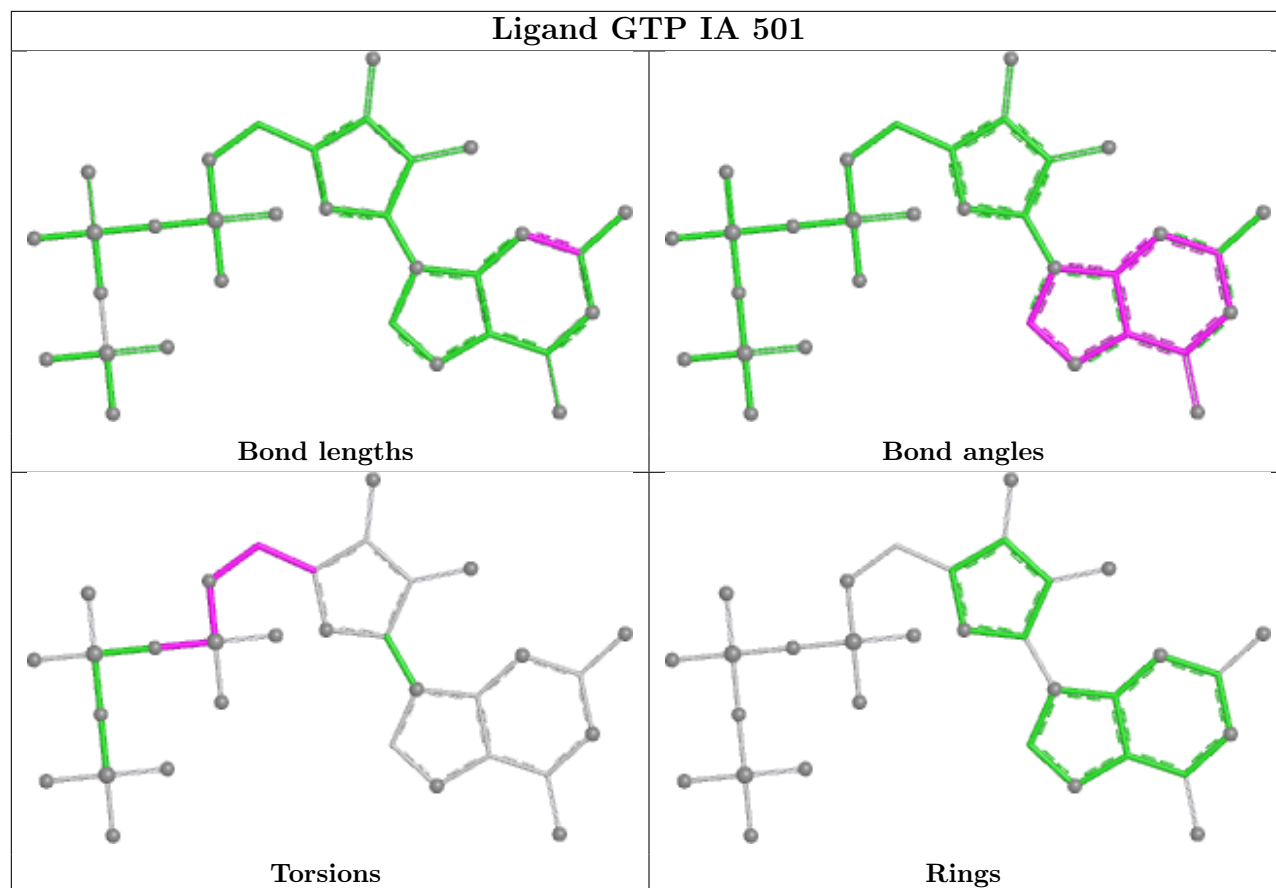


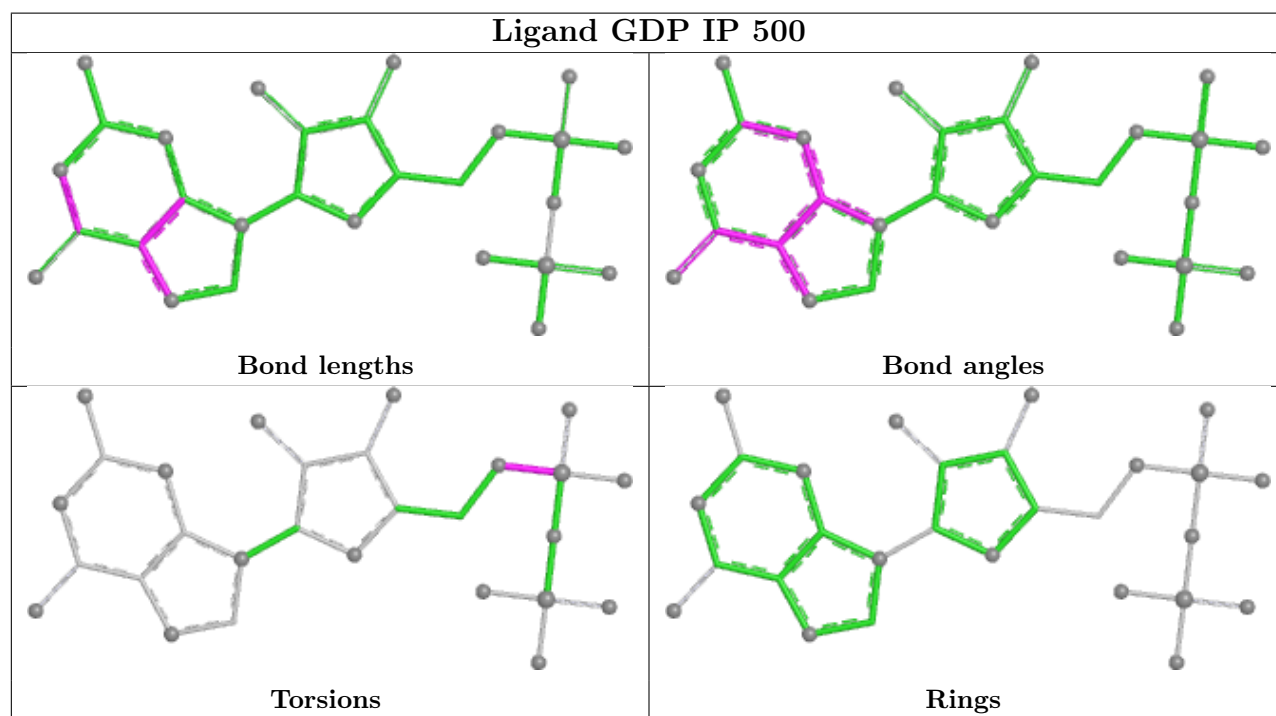
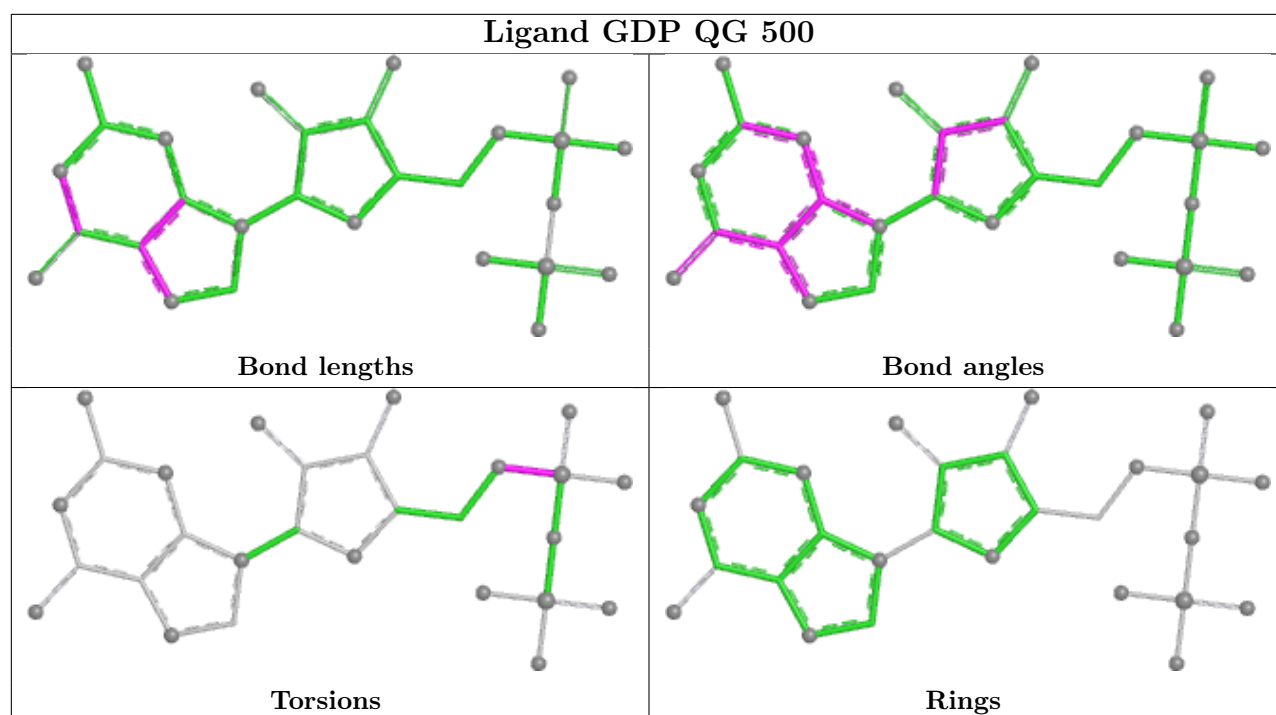
Ligand GTP GQ 501

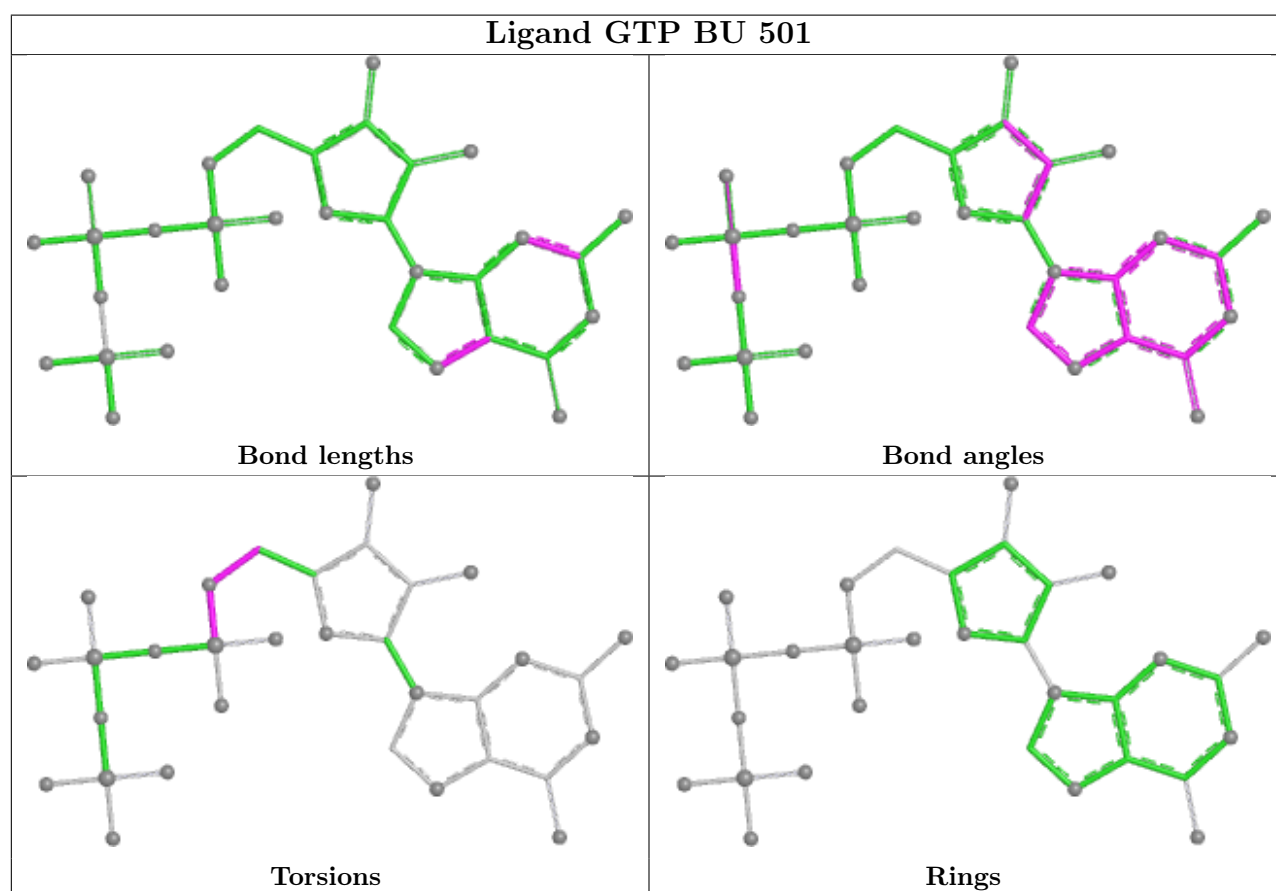
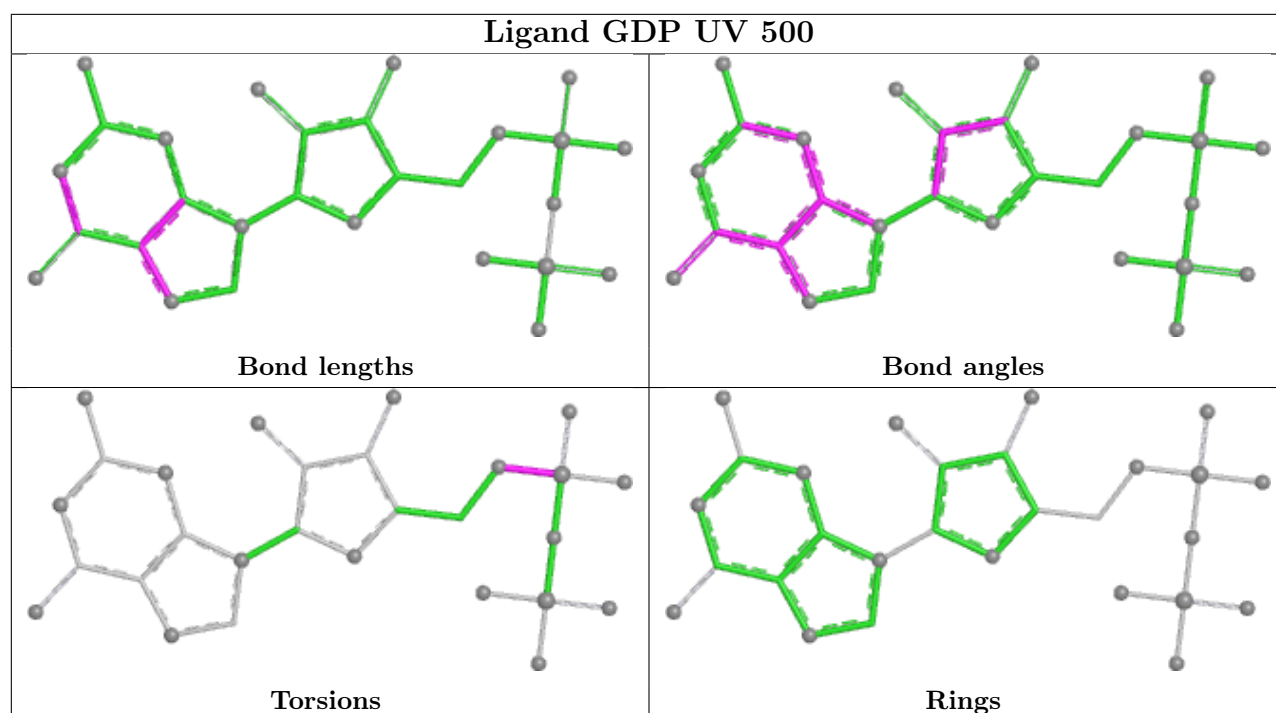




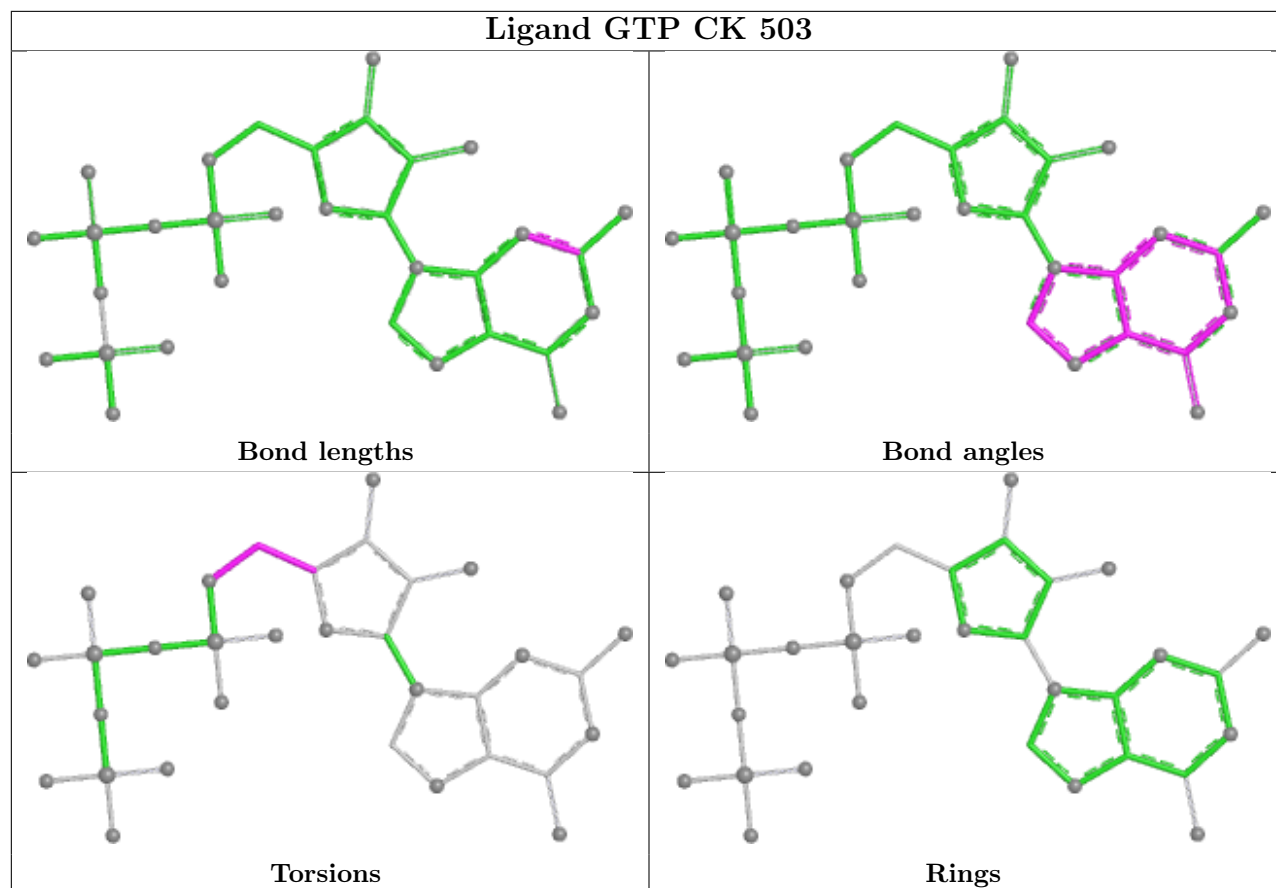




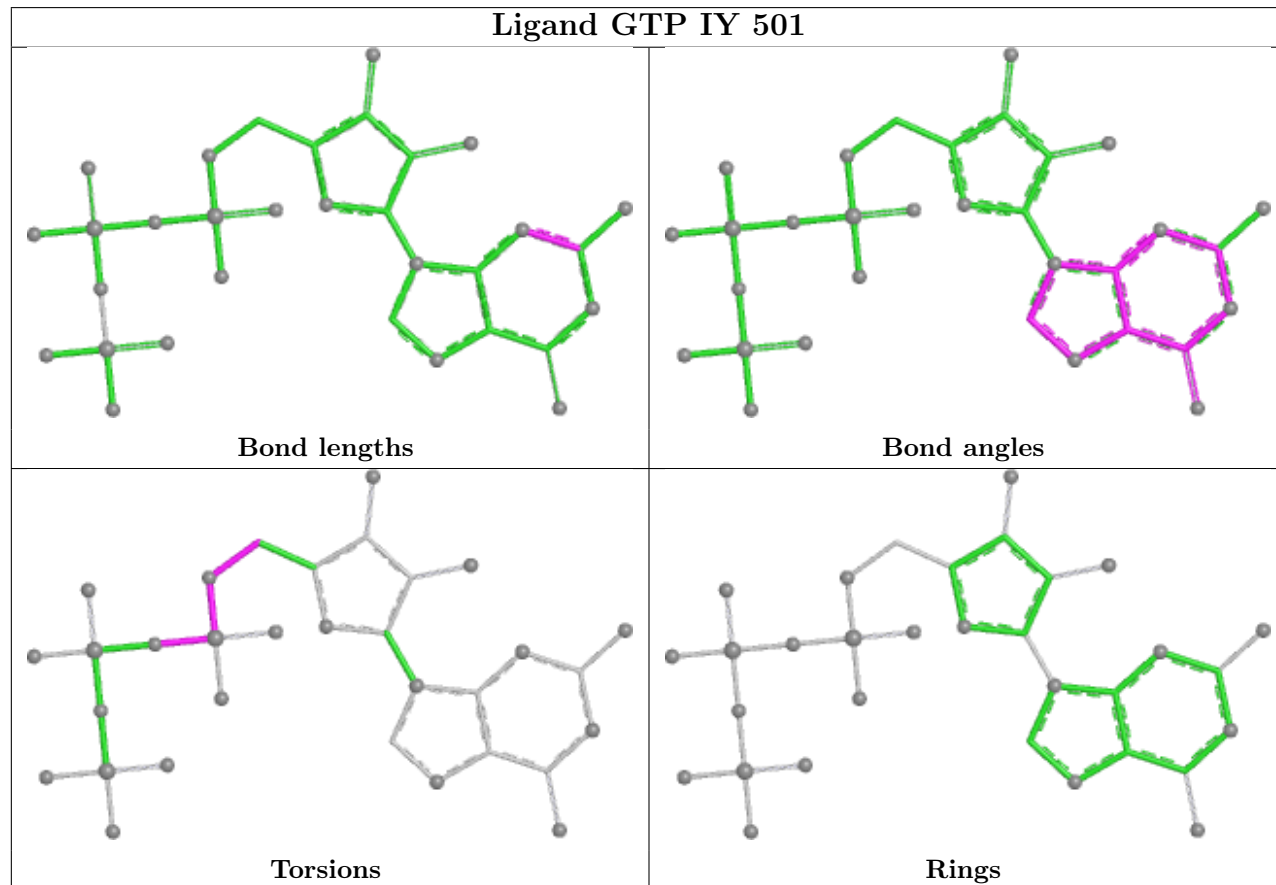


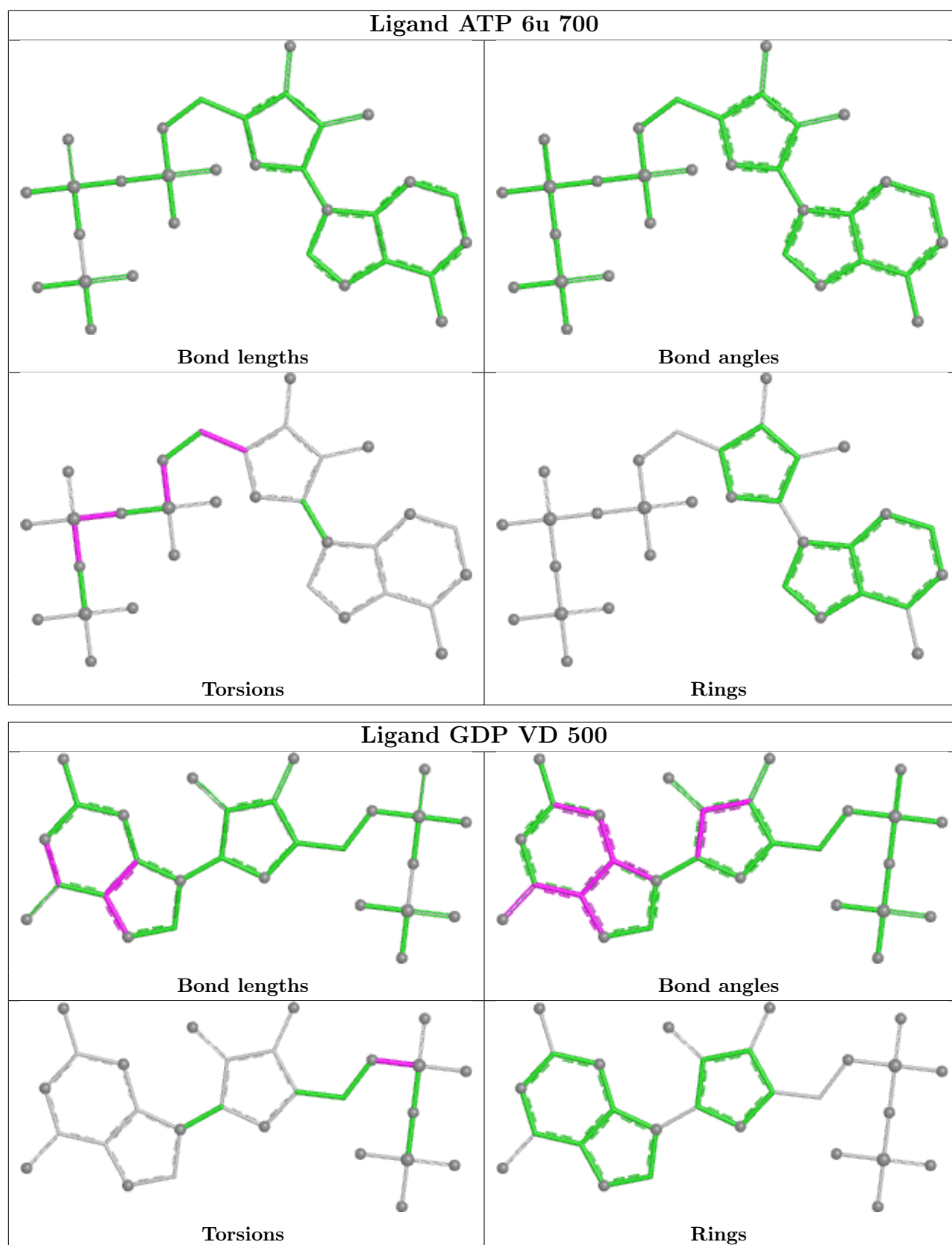


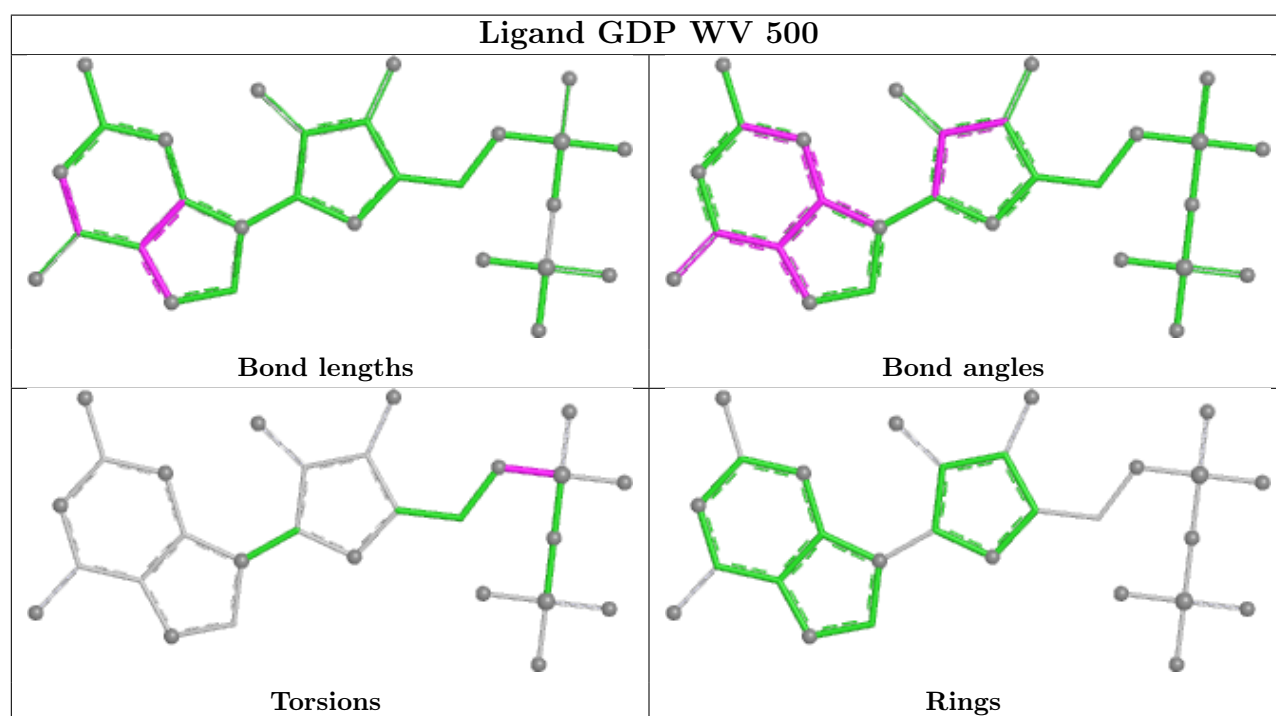
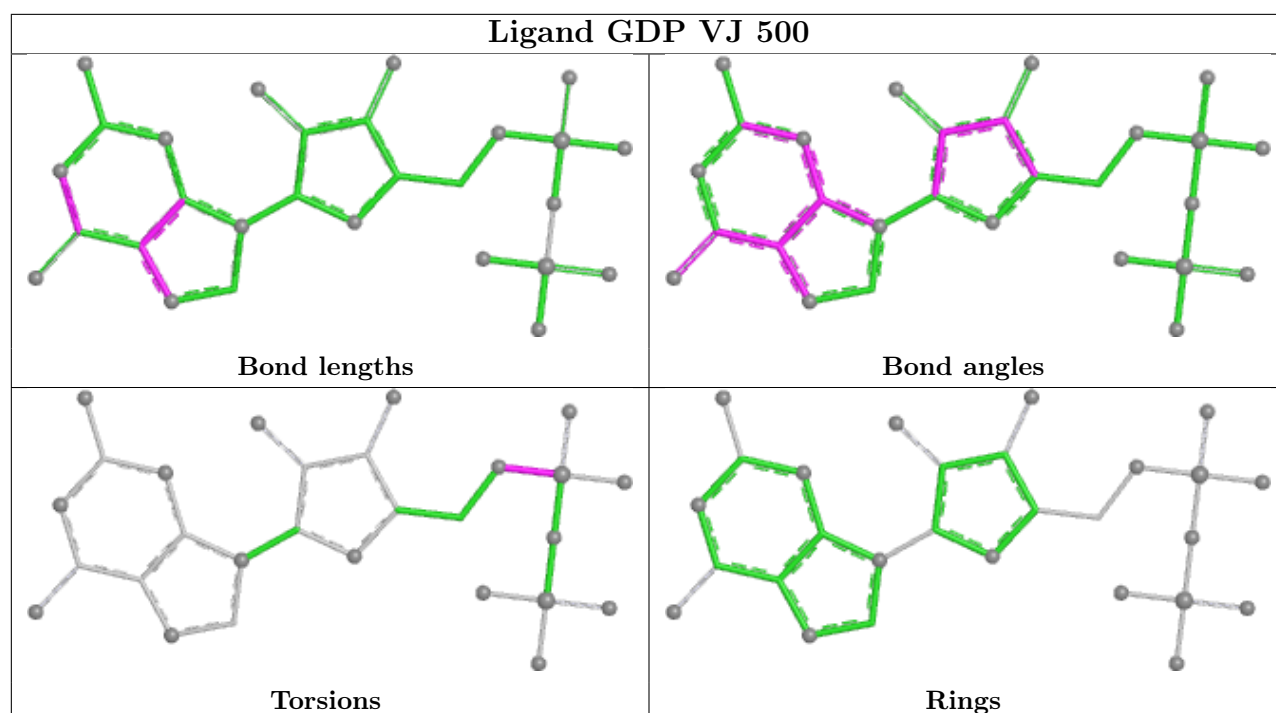
Ligand GTP CK 503

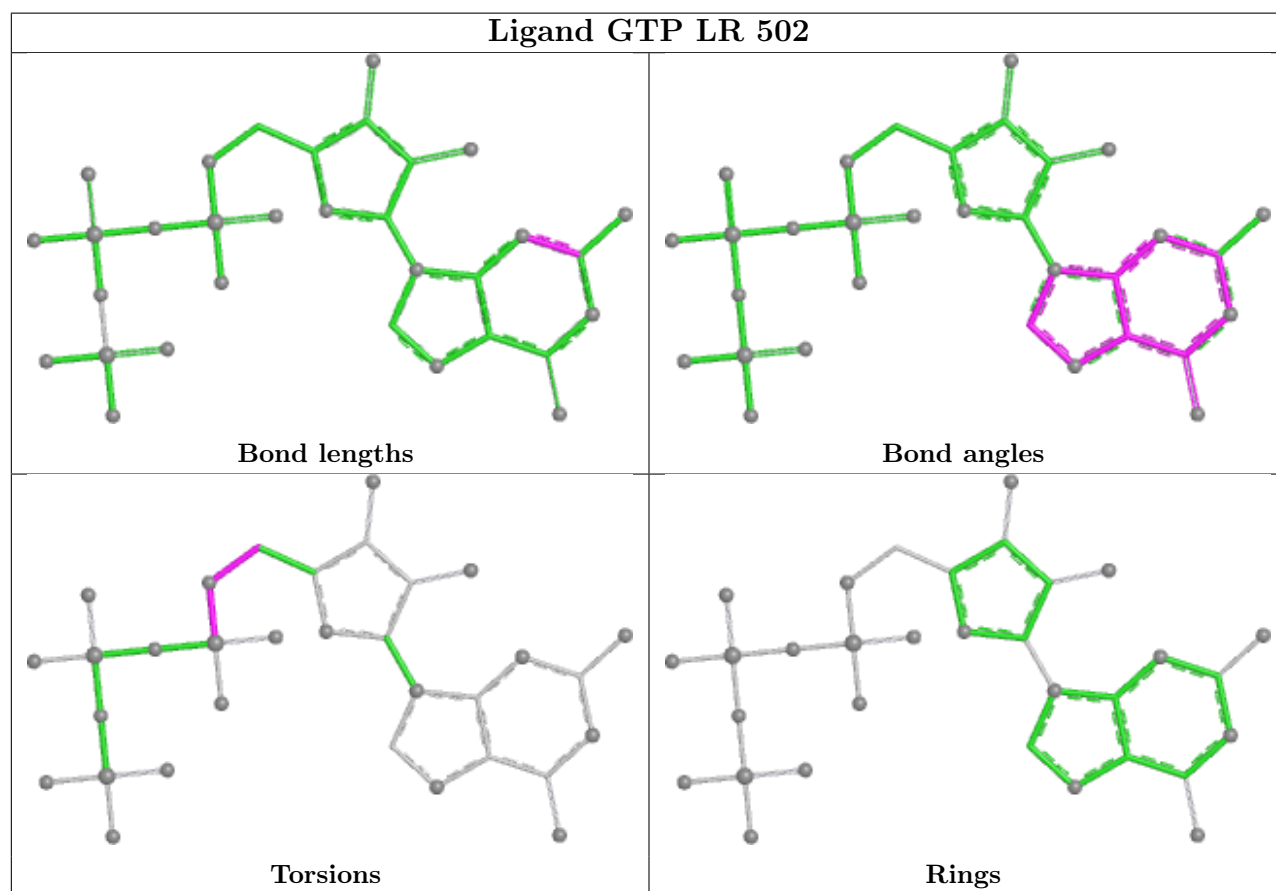
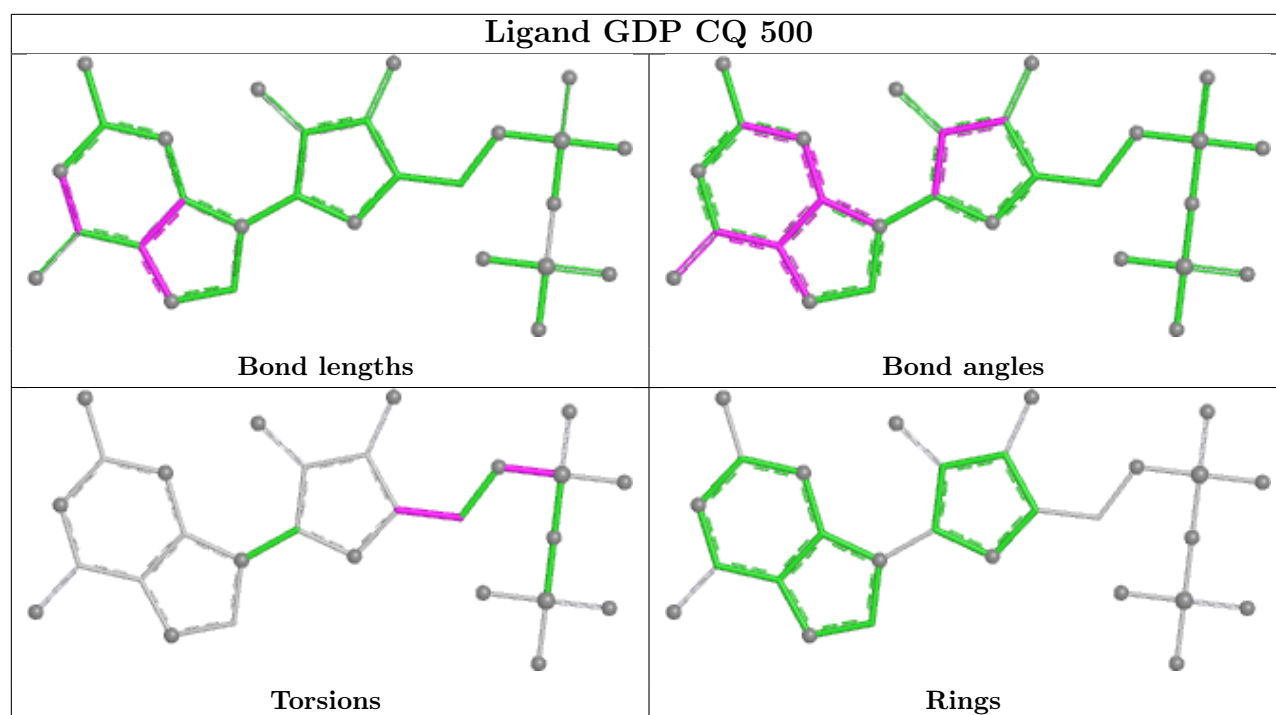


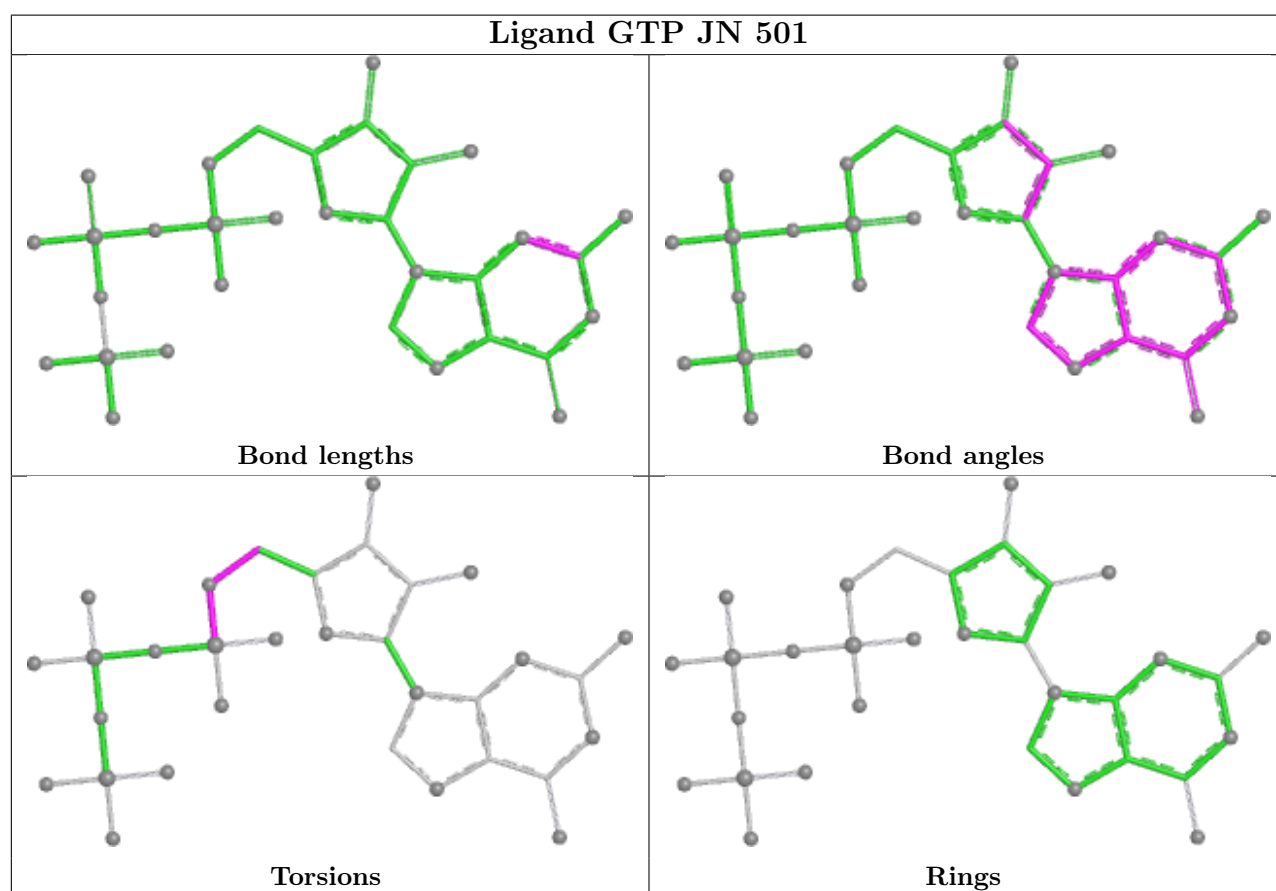
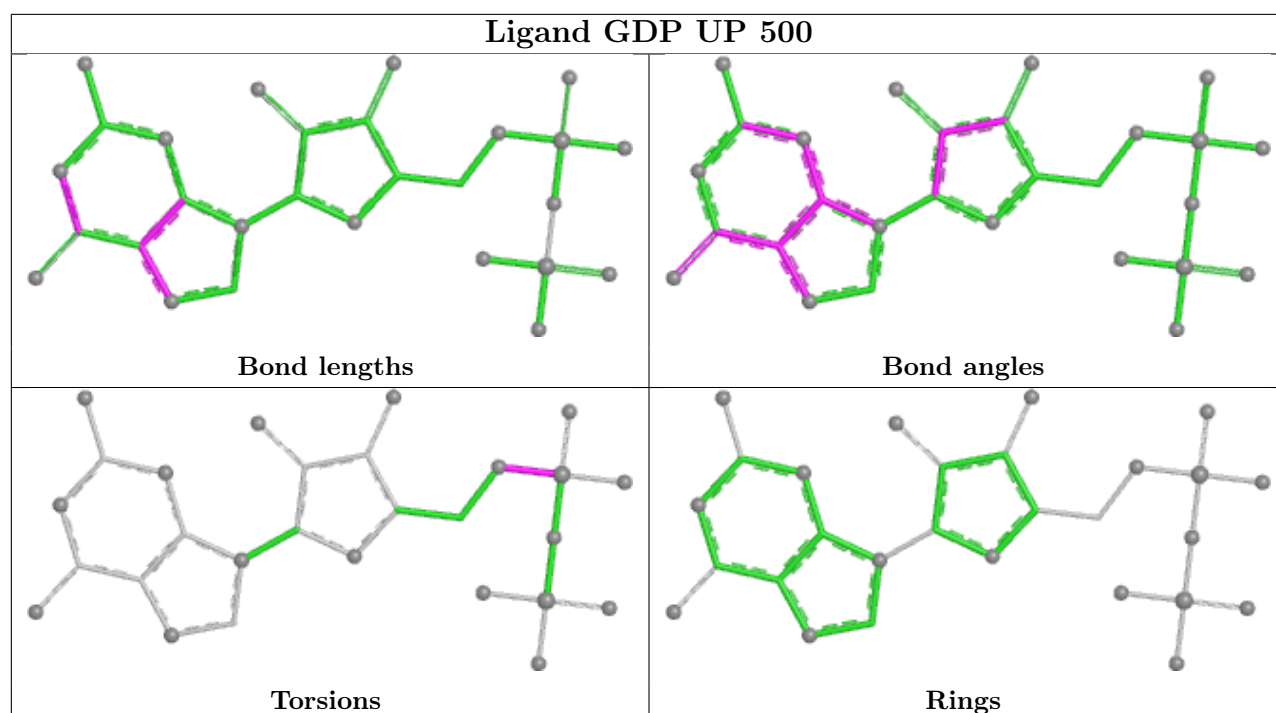
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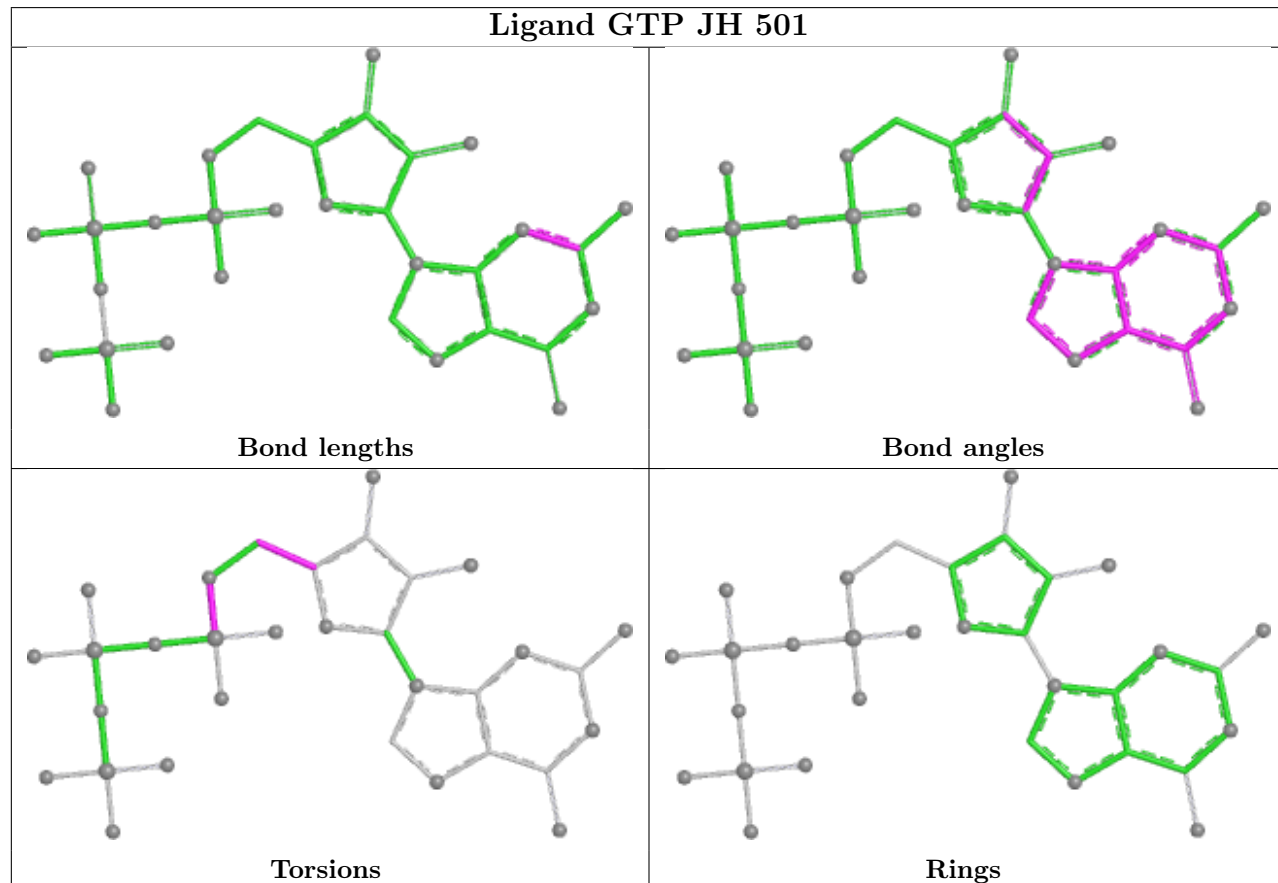
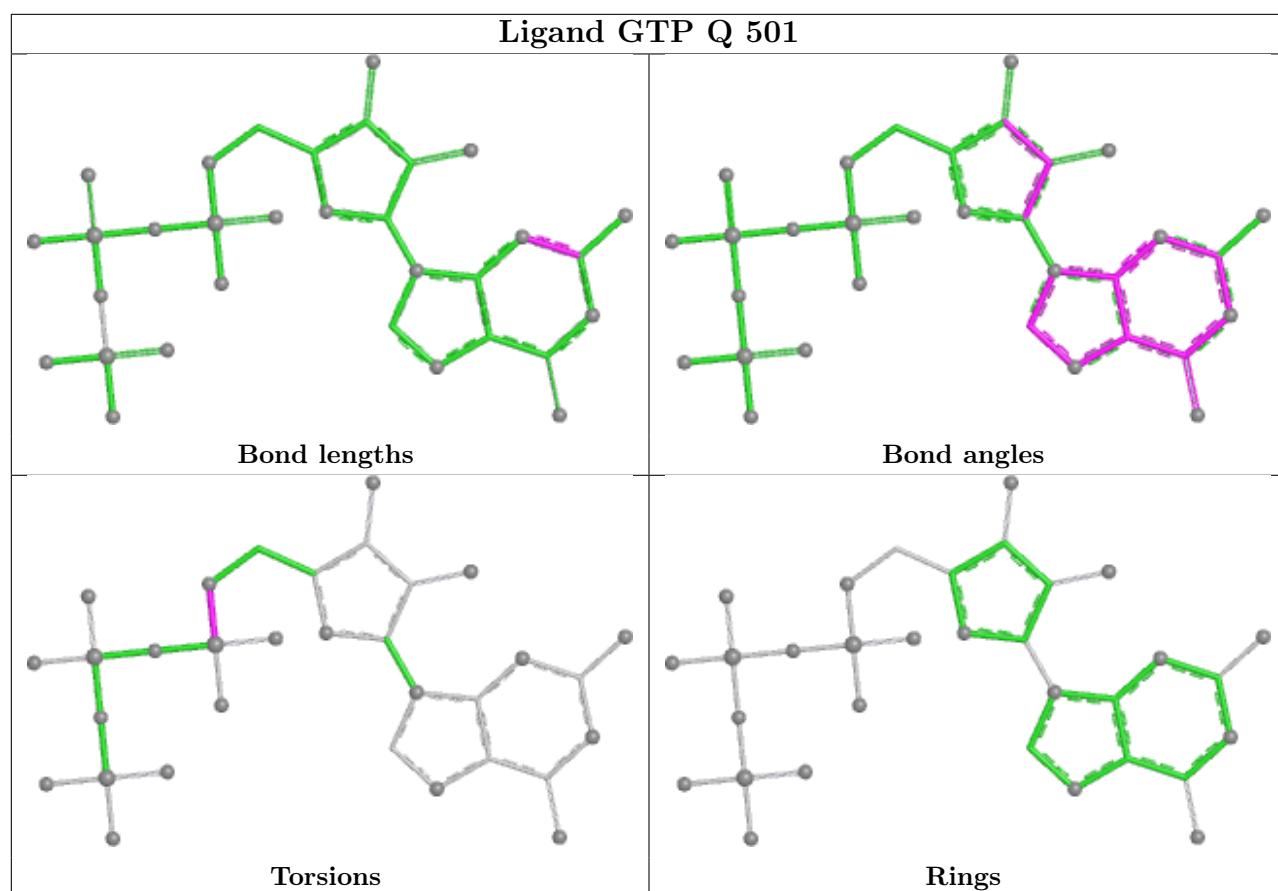




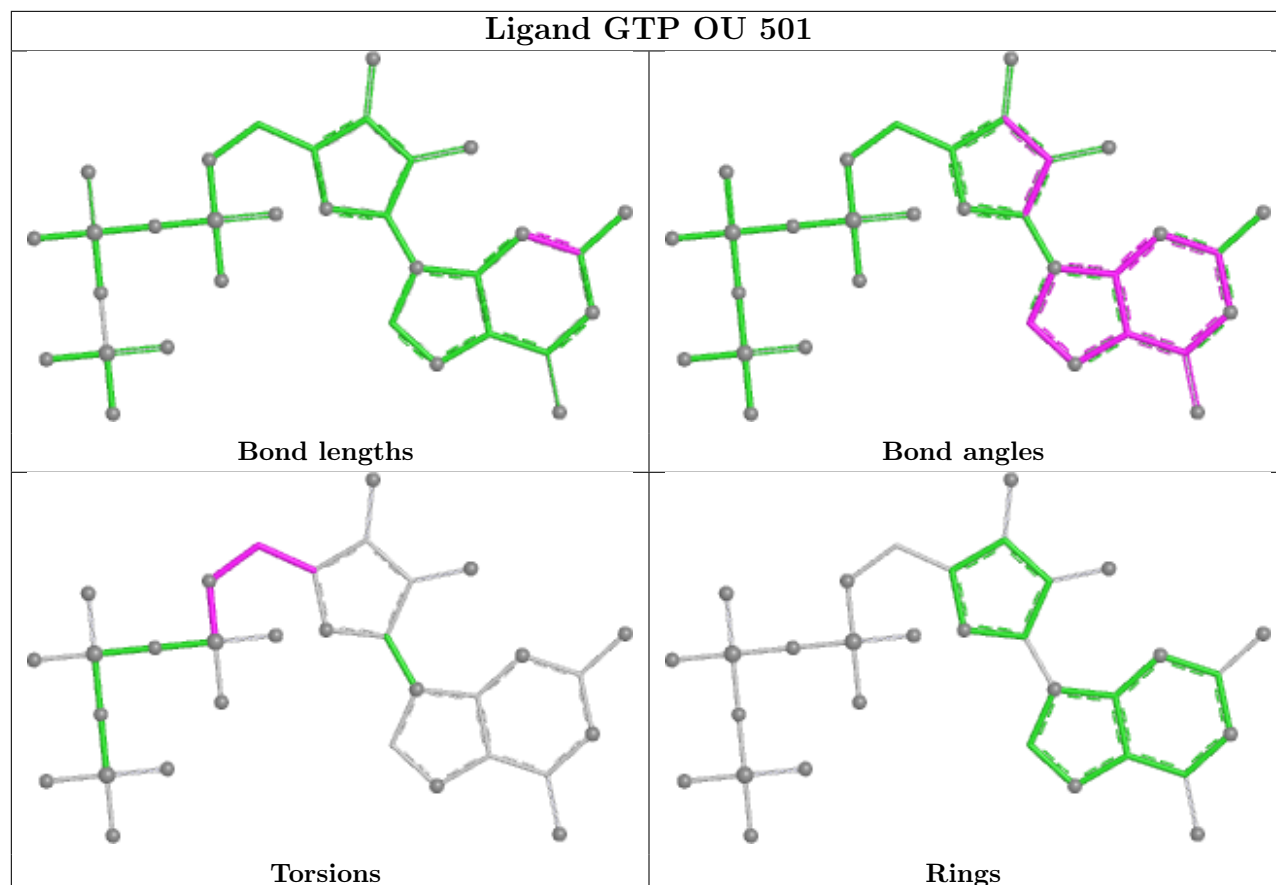




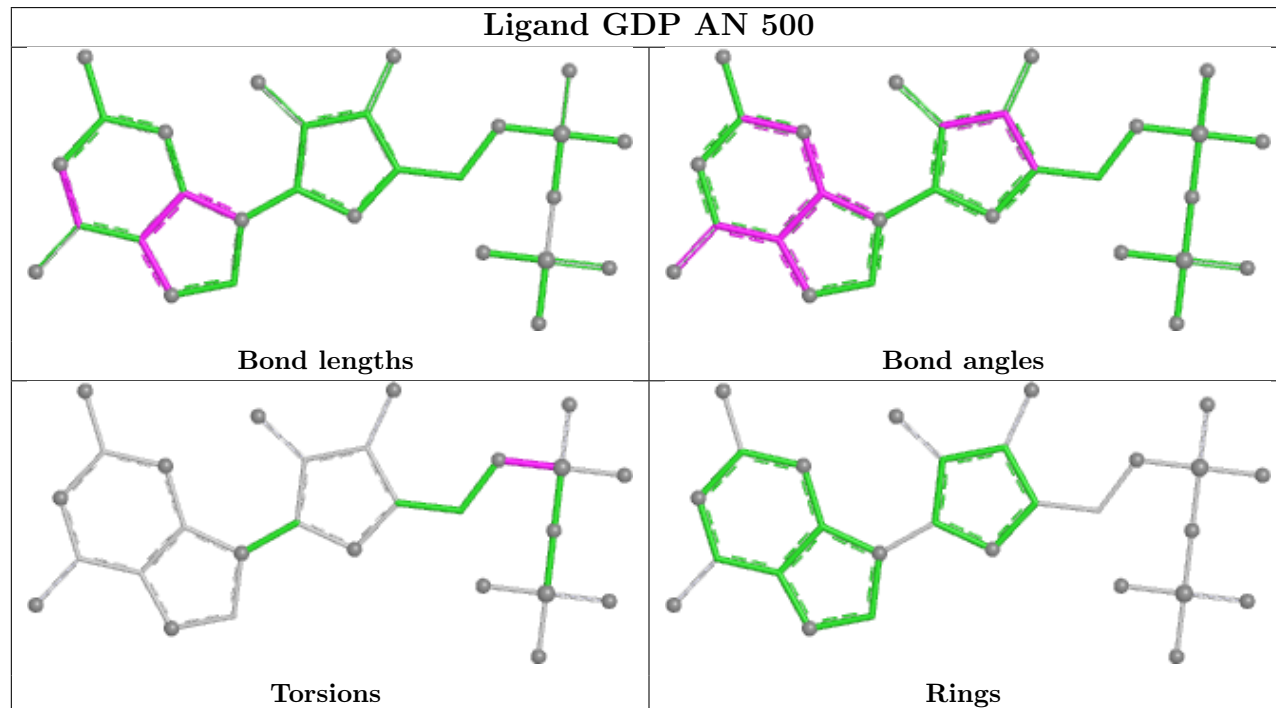


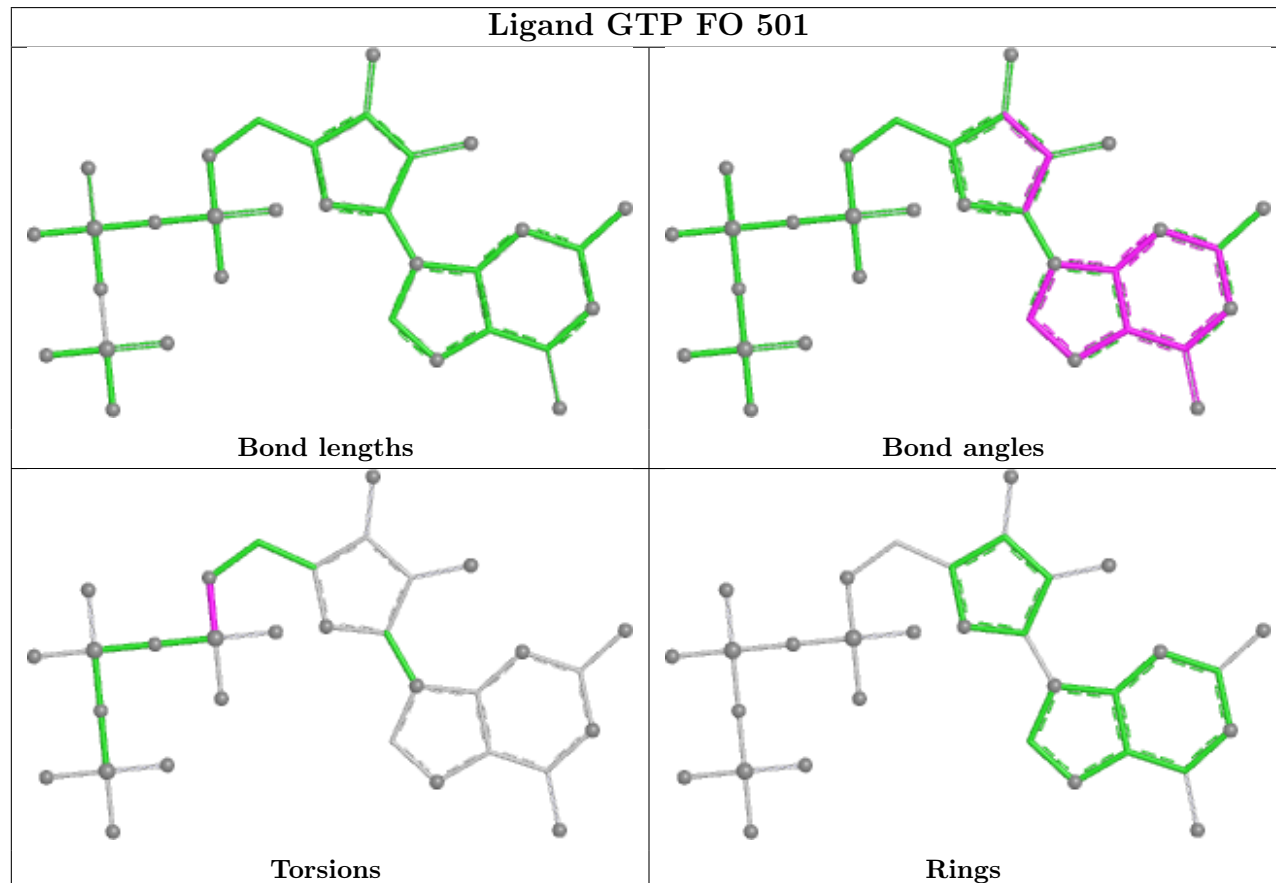
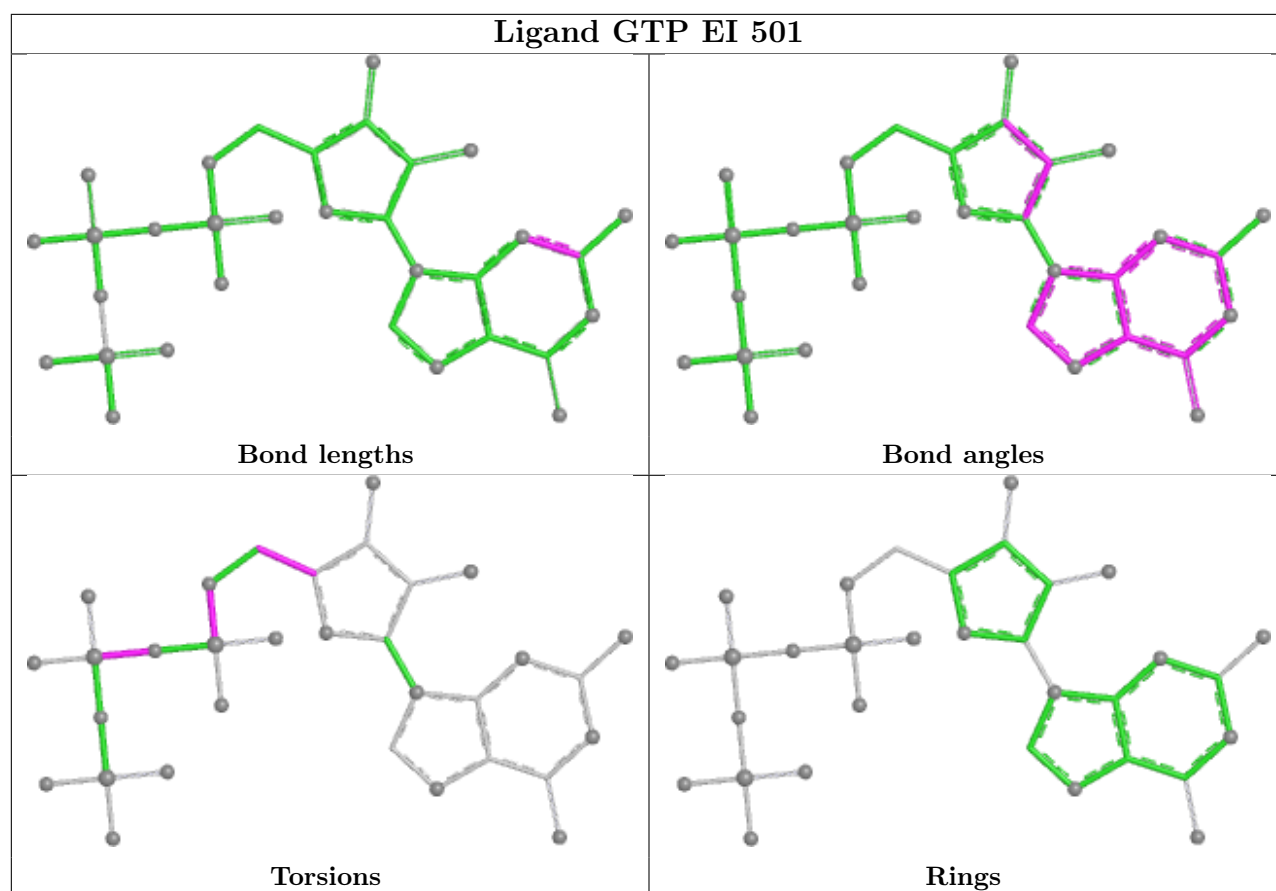


Ligand GTP OU 501

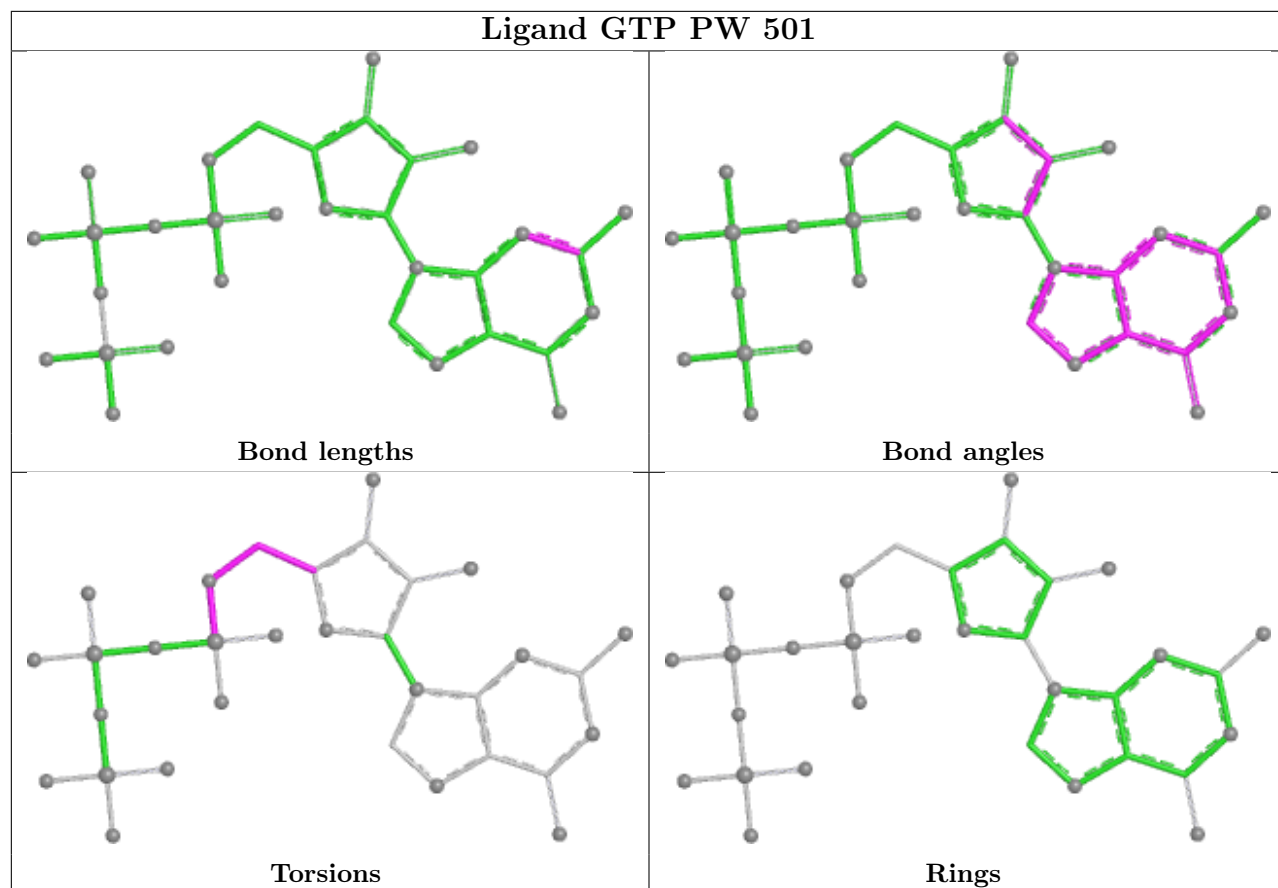


Ligand GDP AN 500

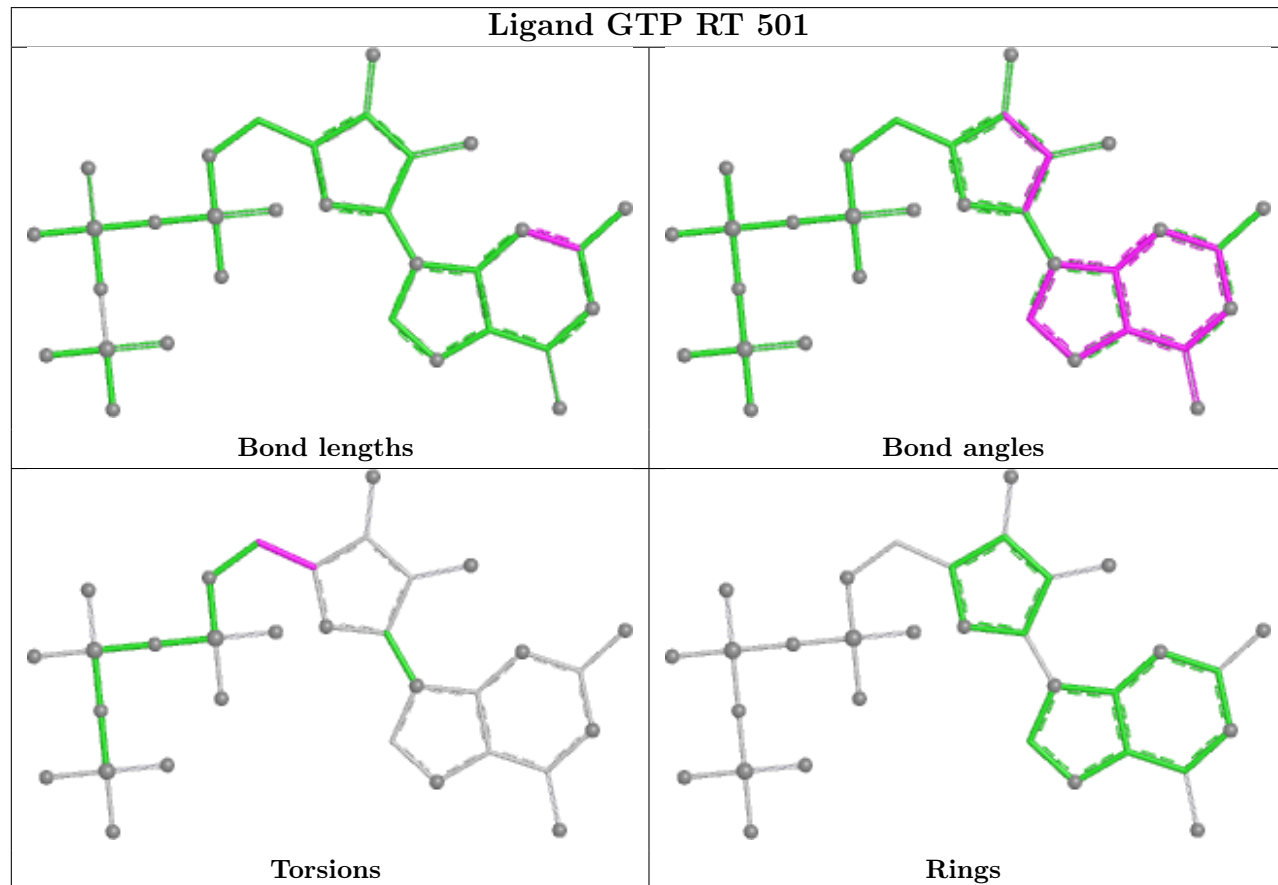




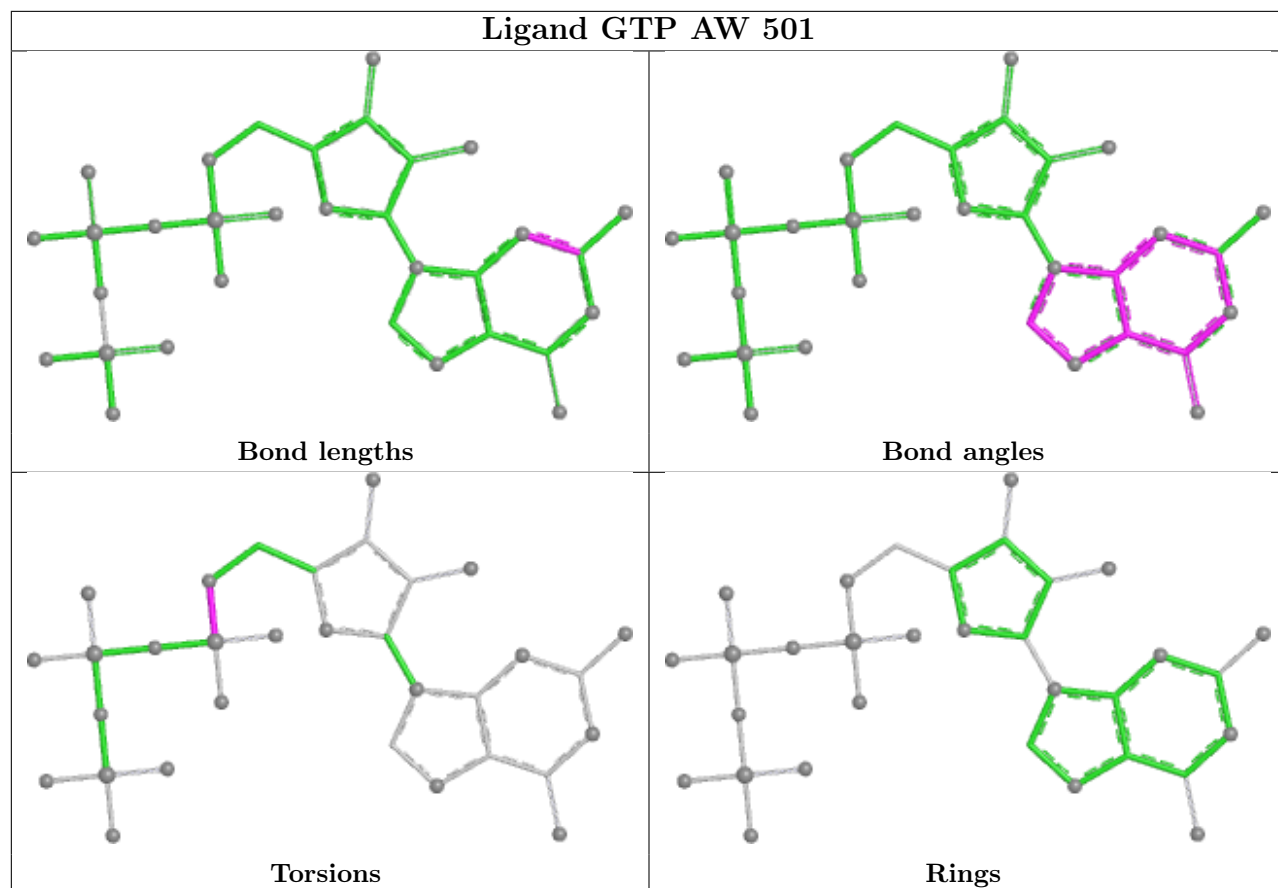
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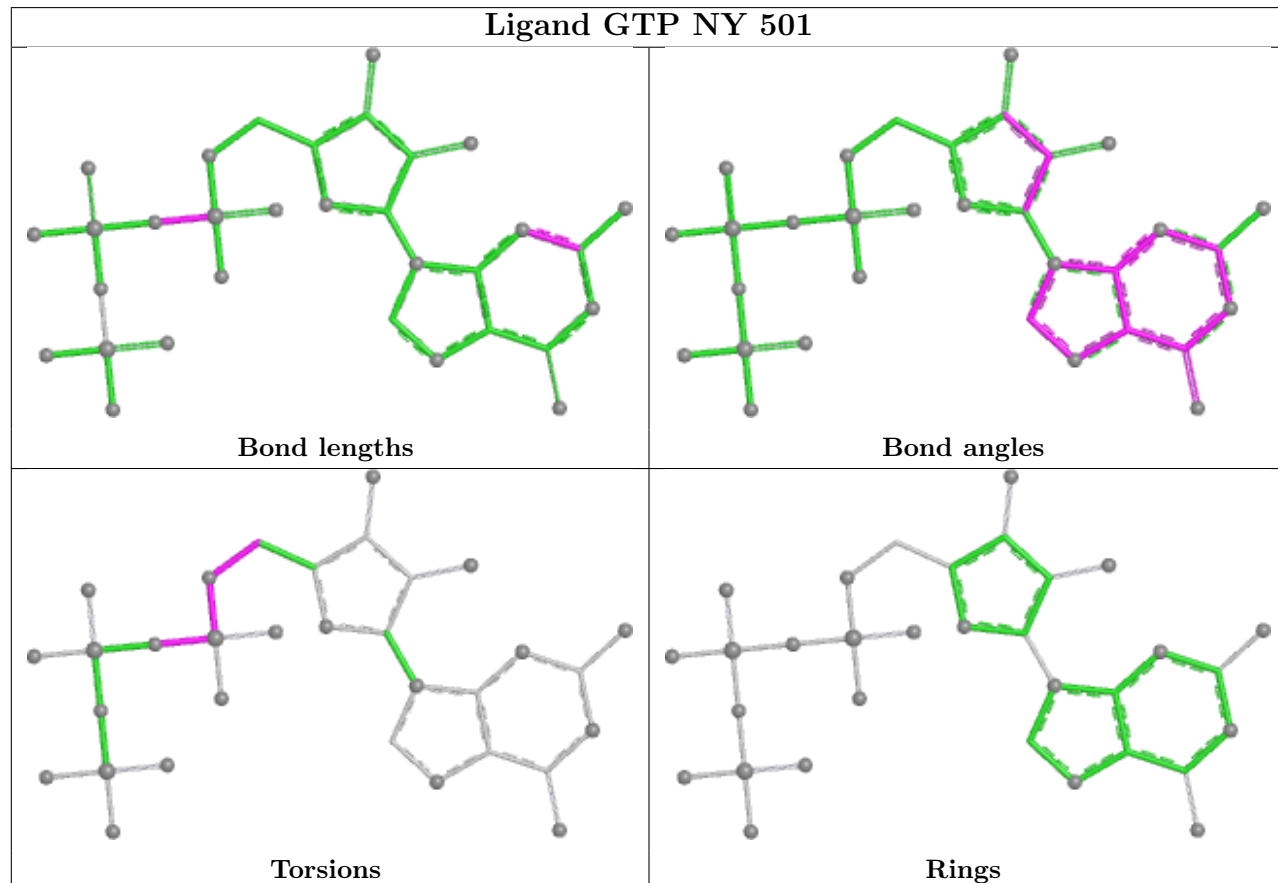
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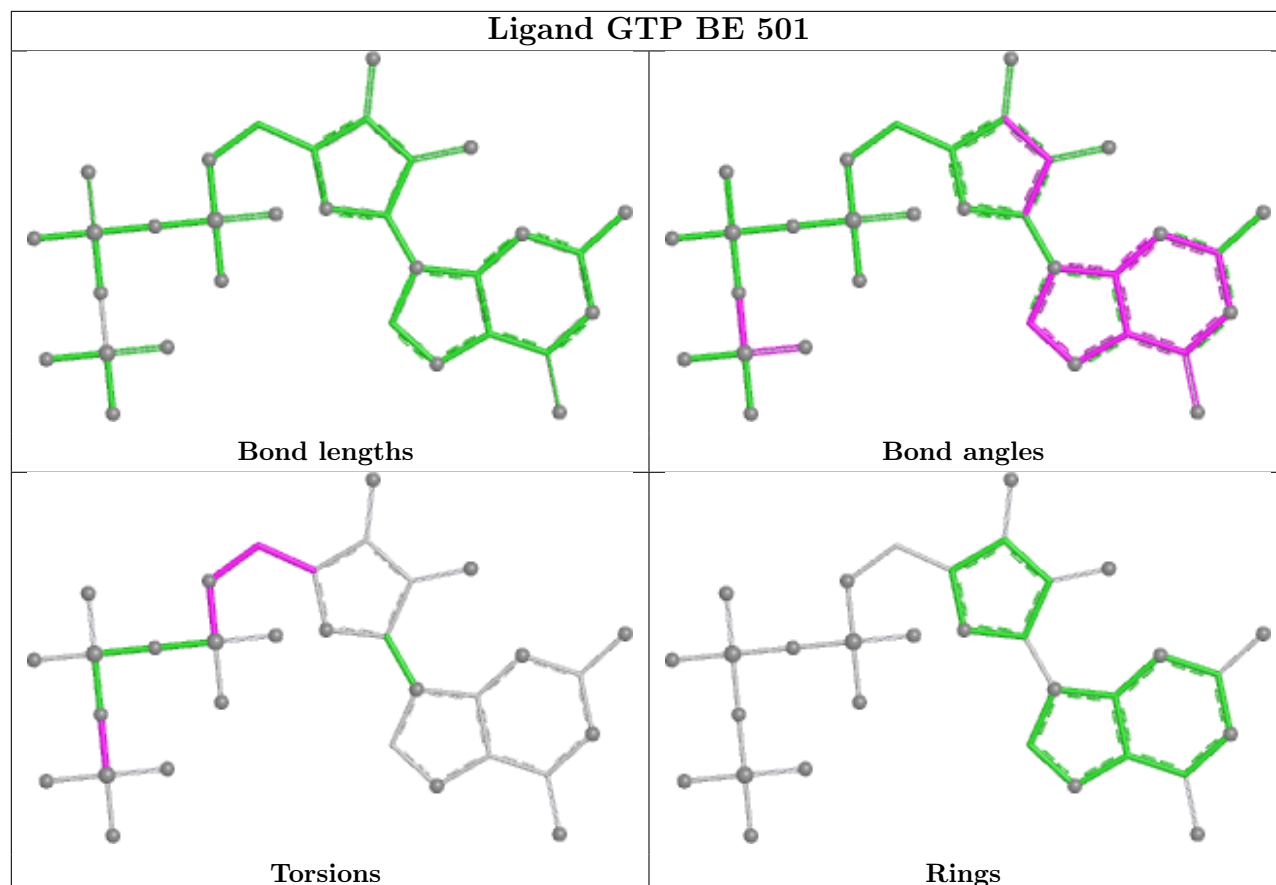
Ligand GTP AW 501



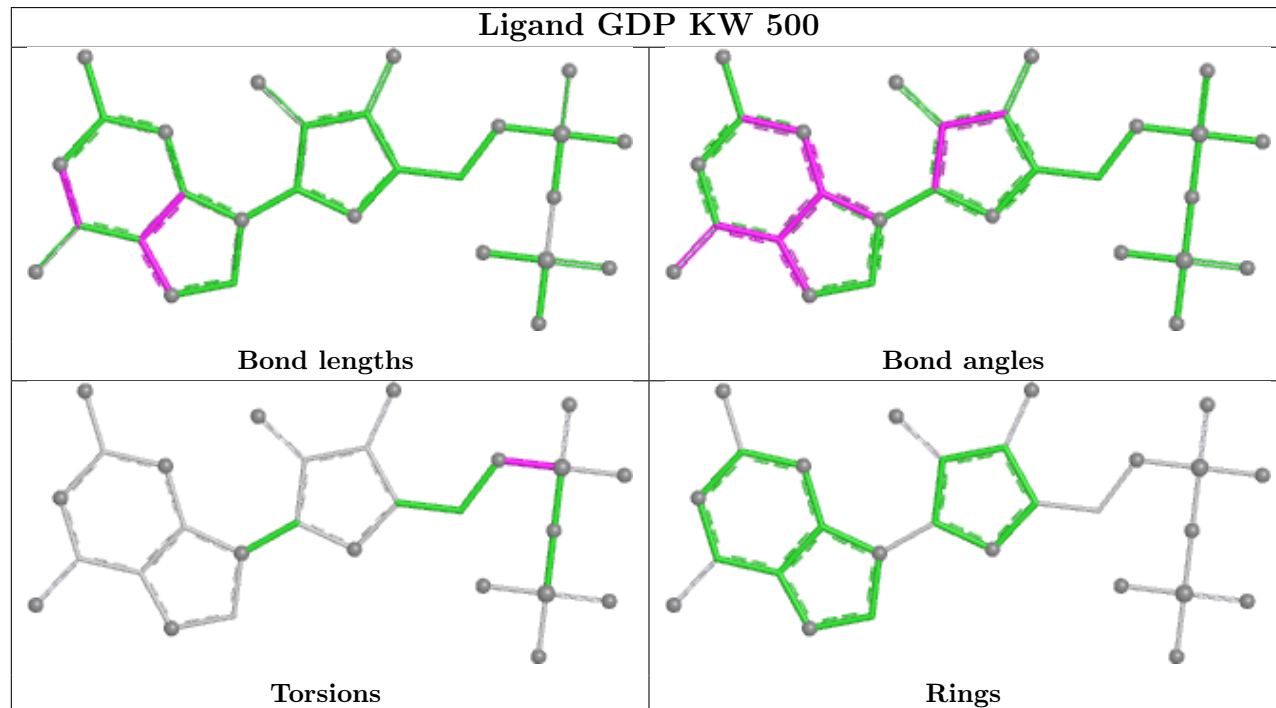
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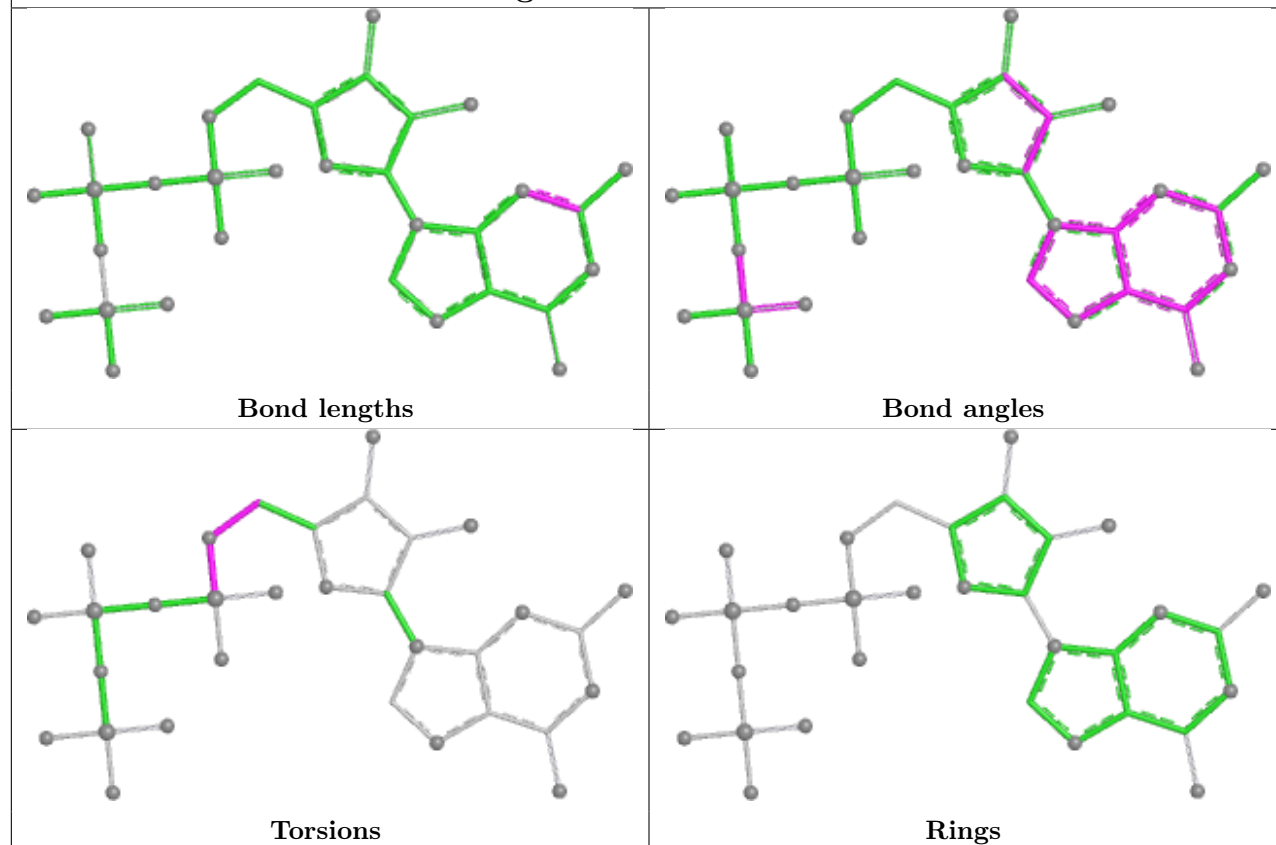
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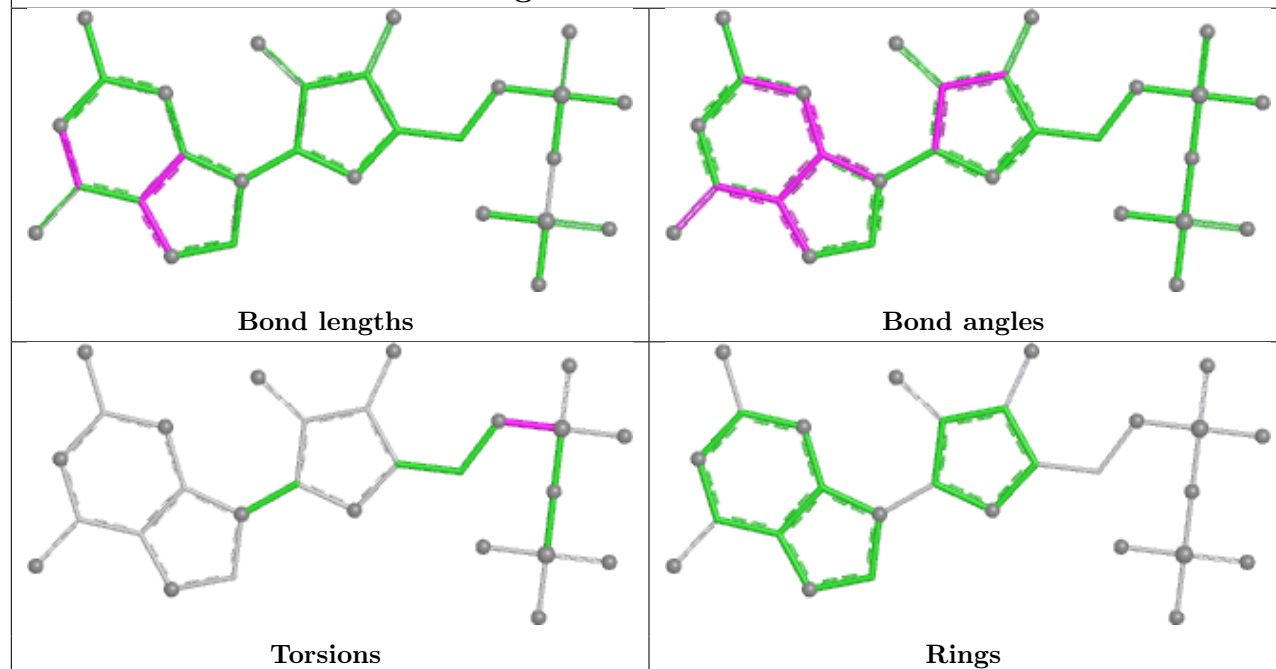
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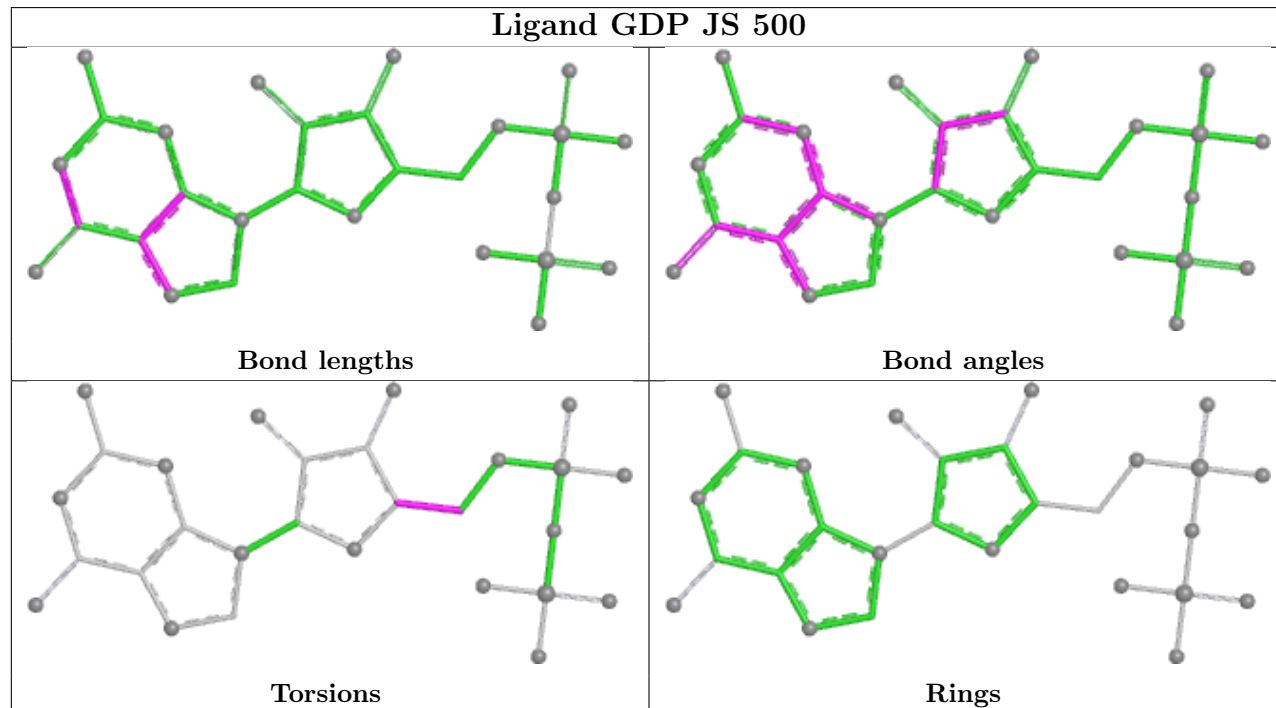
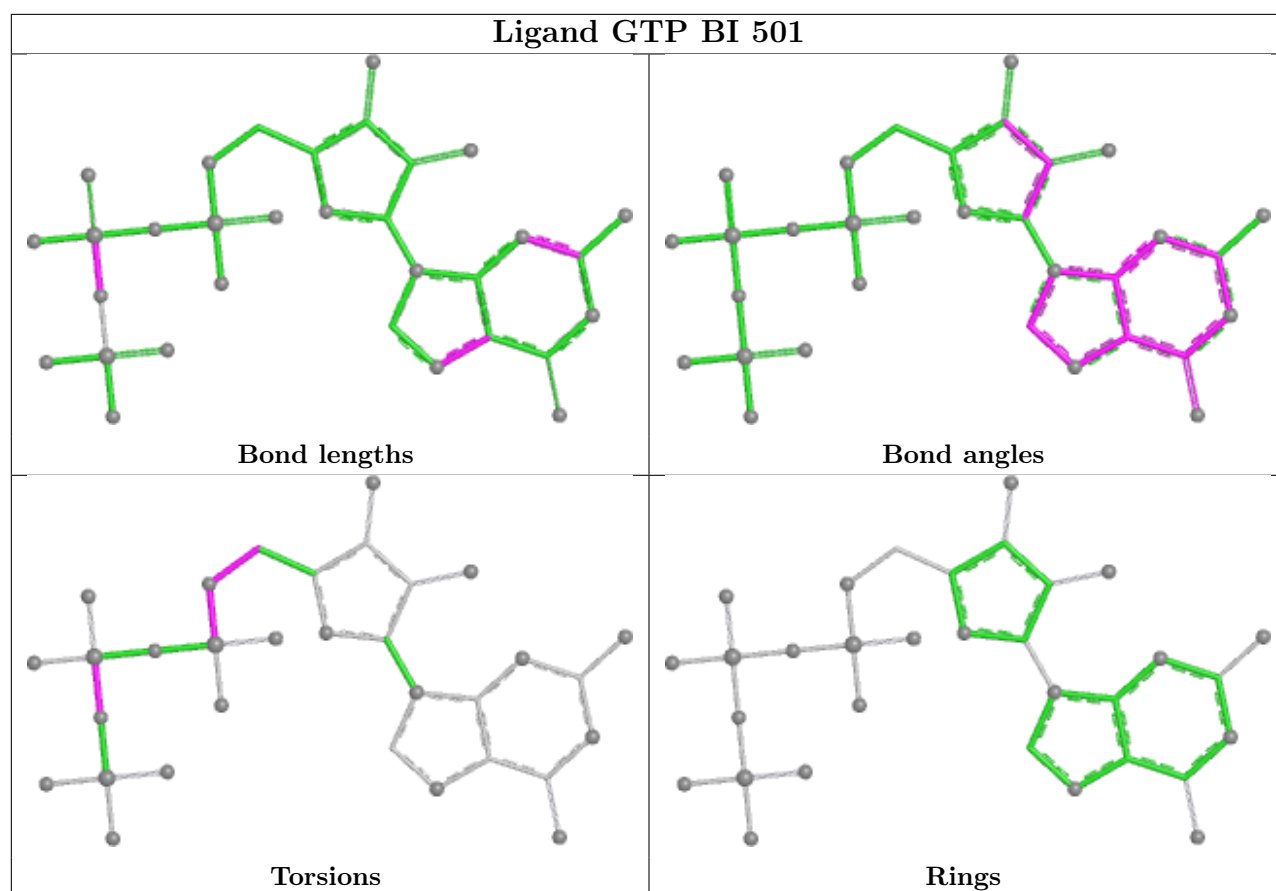


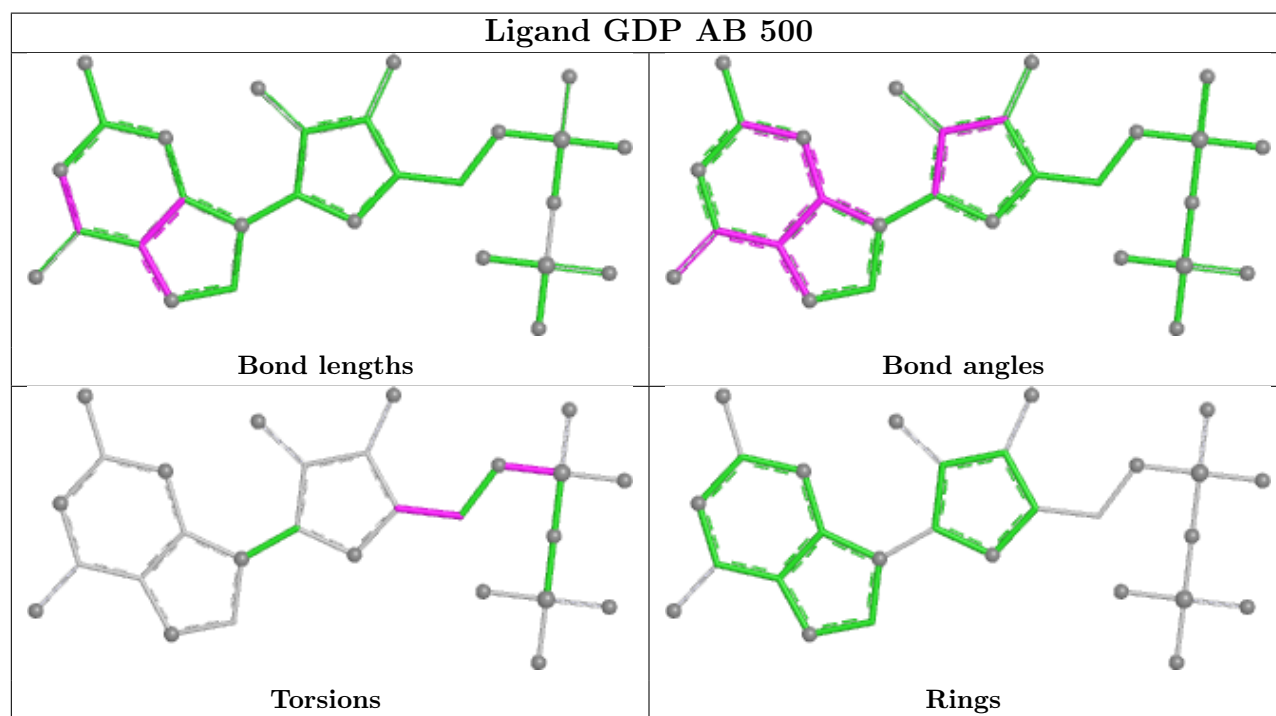
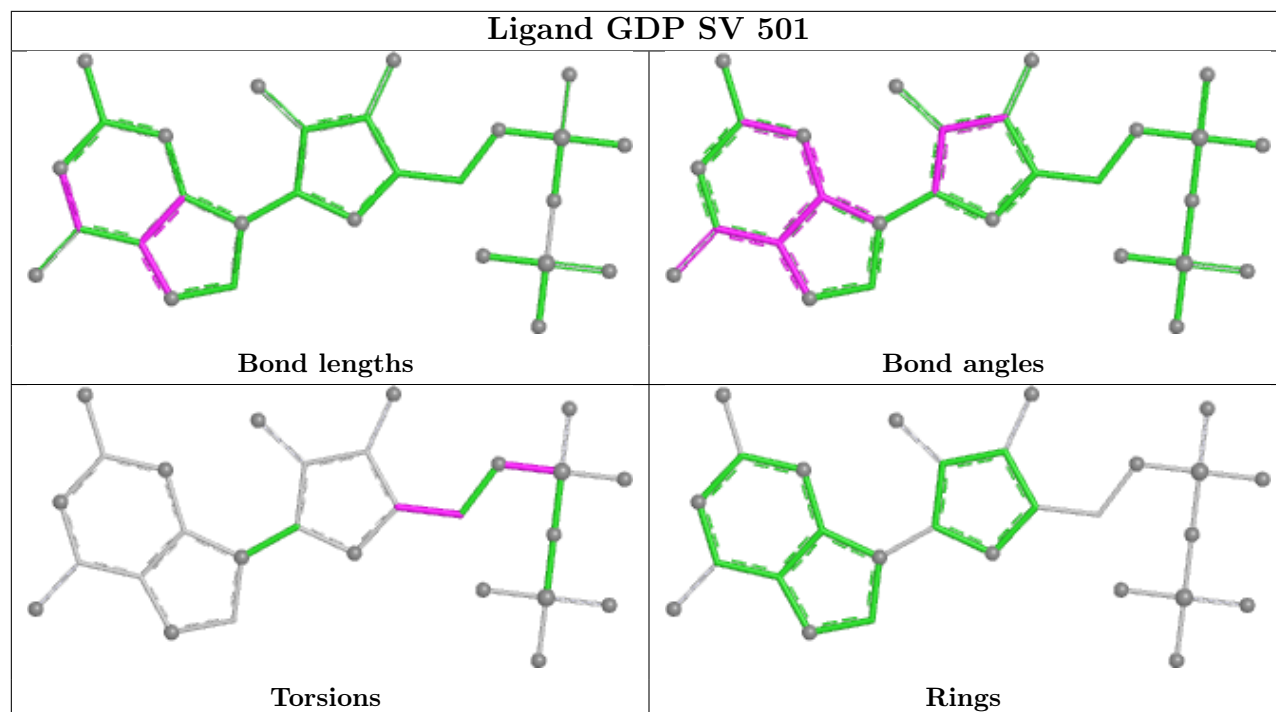
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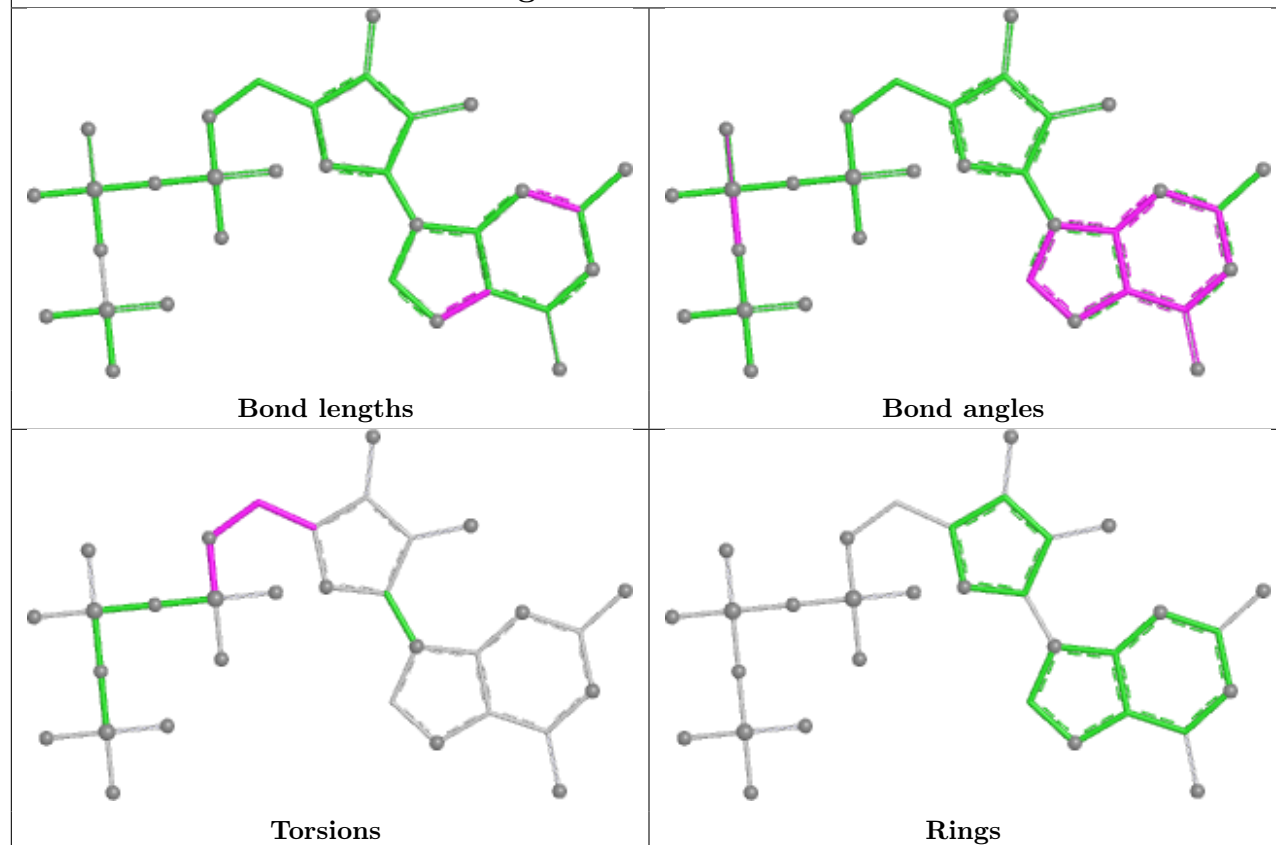
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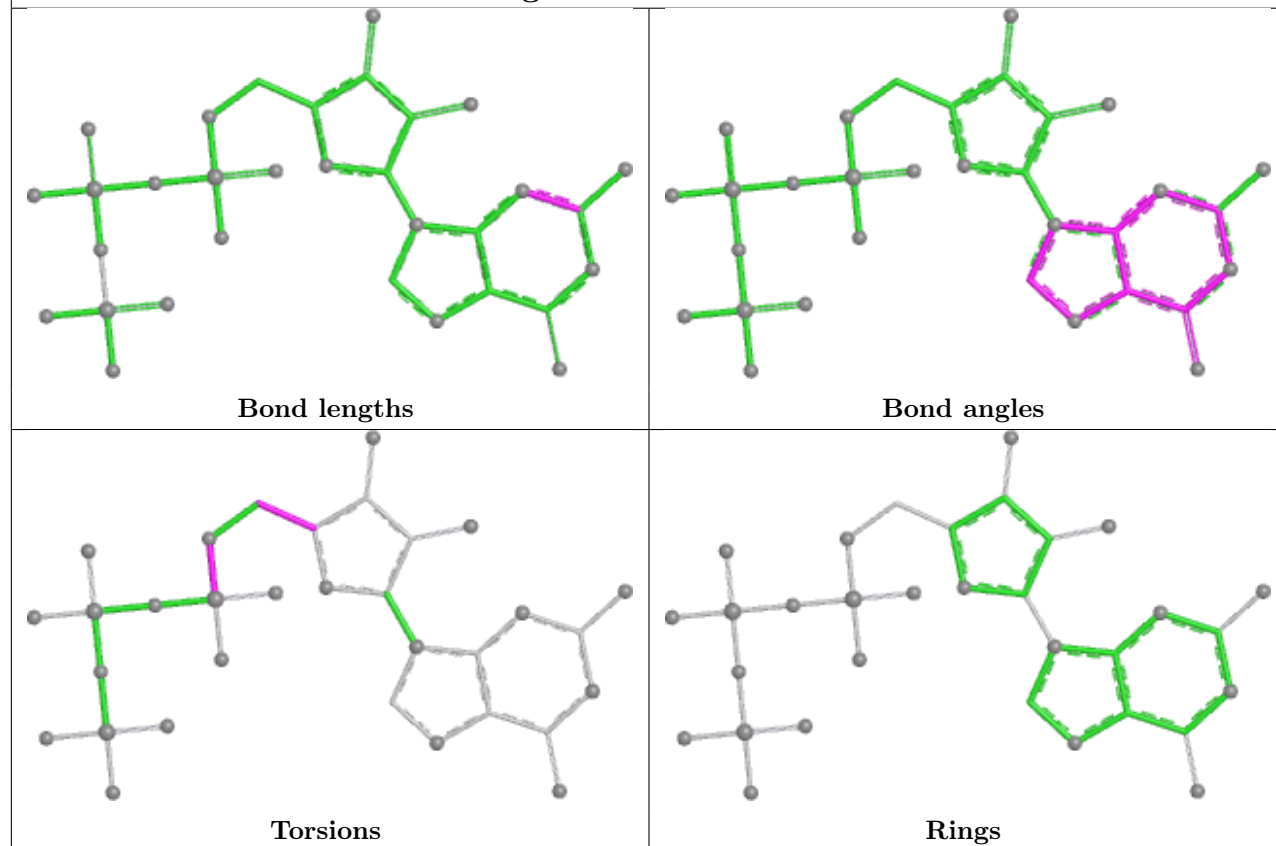


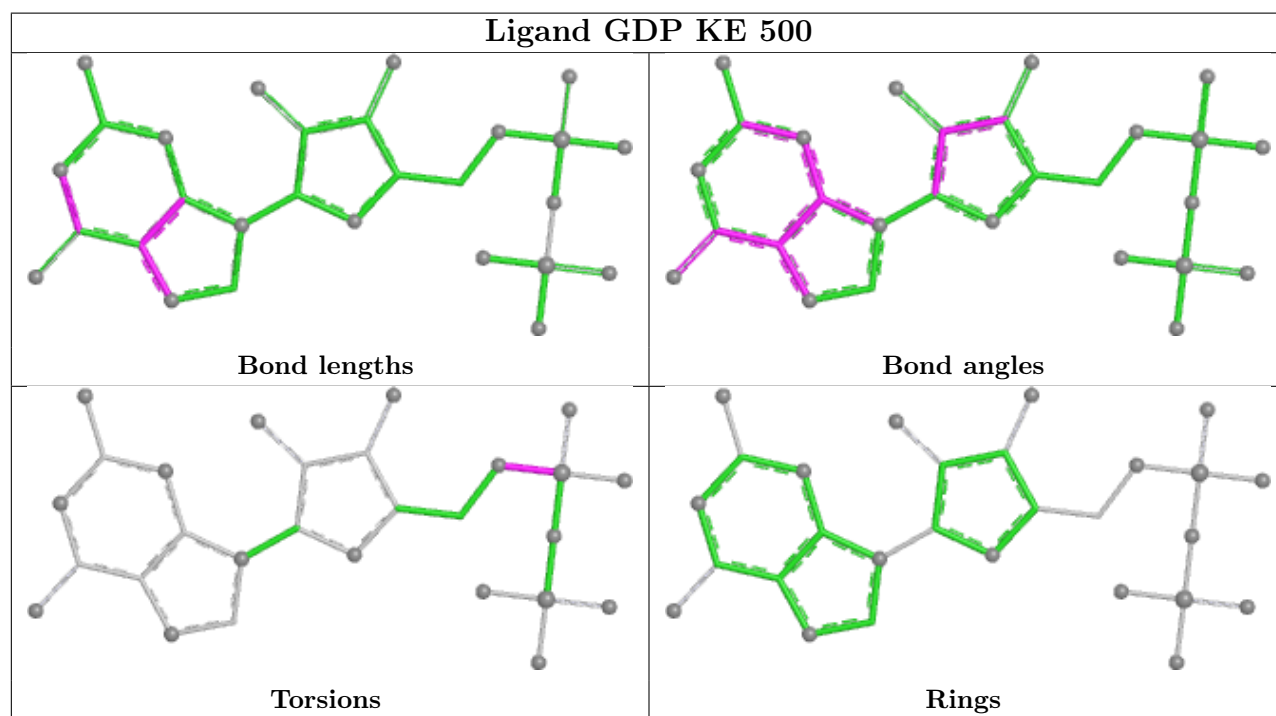
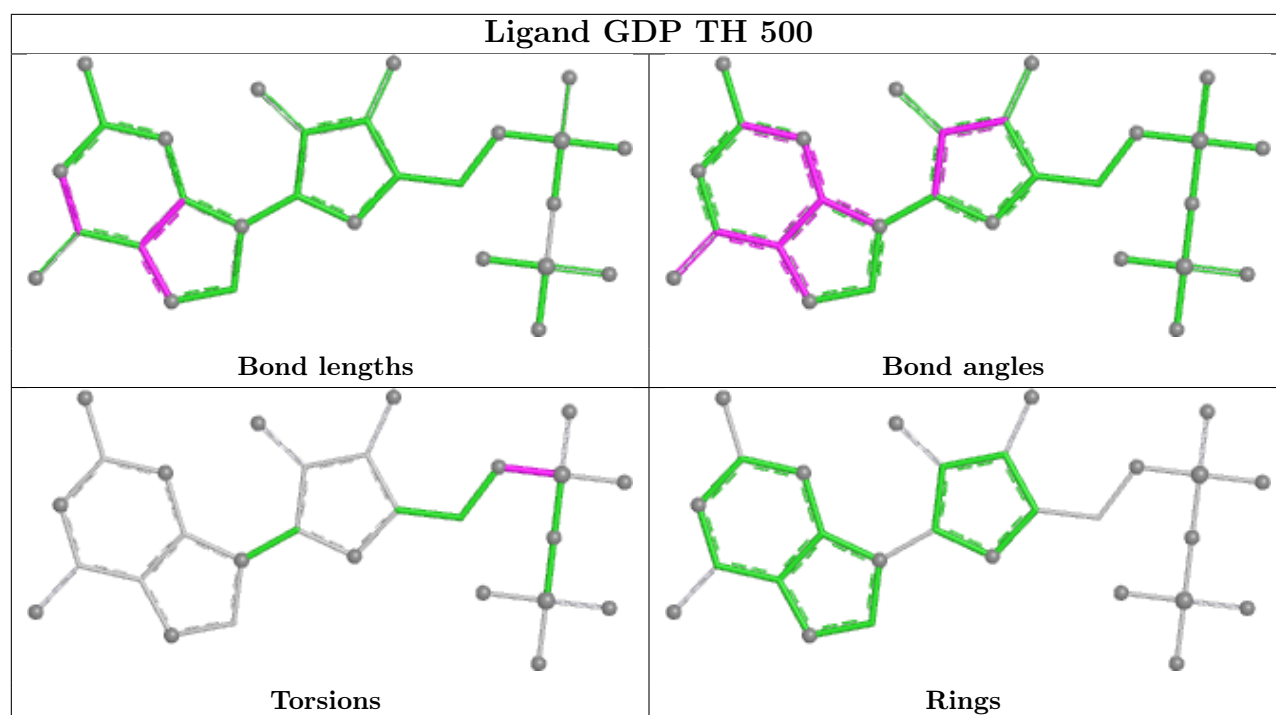


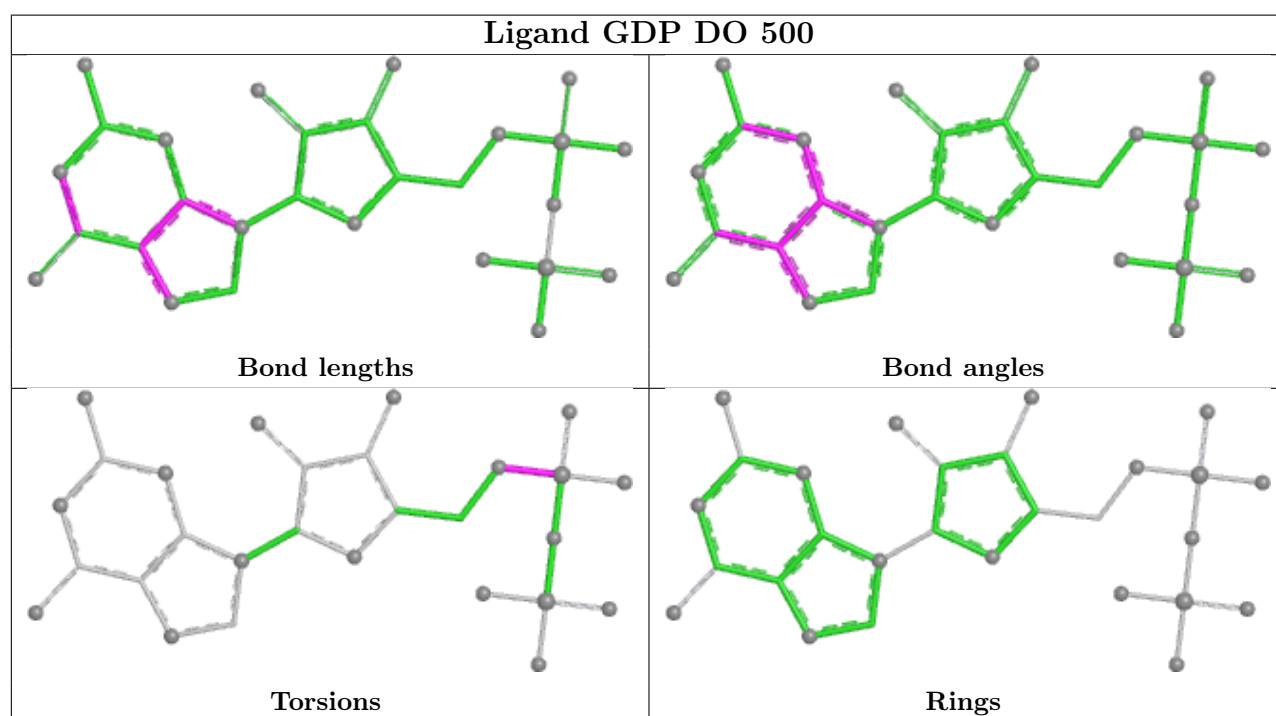
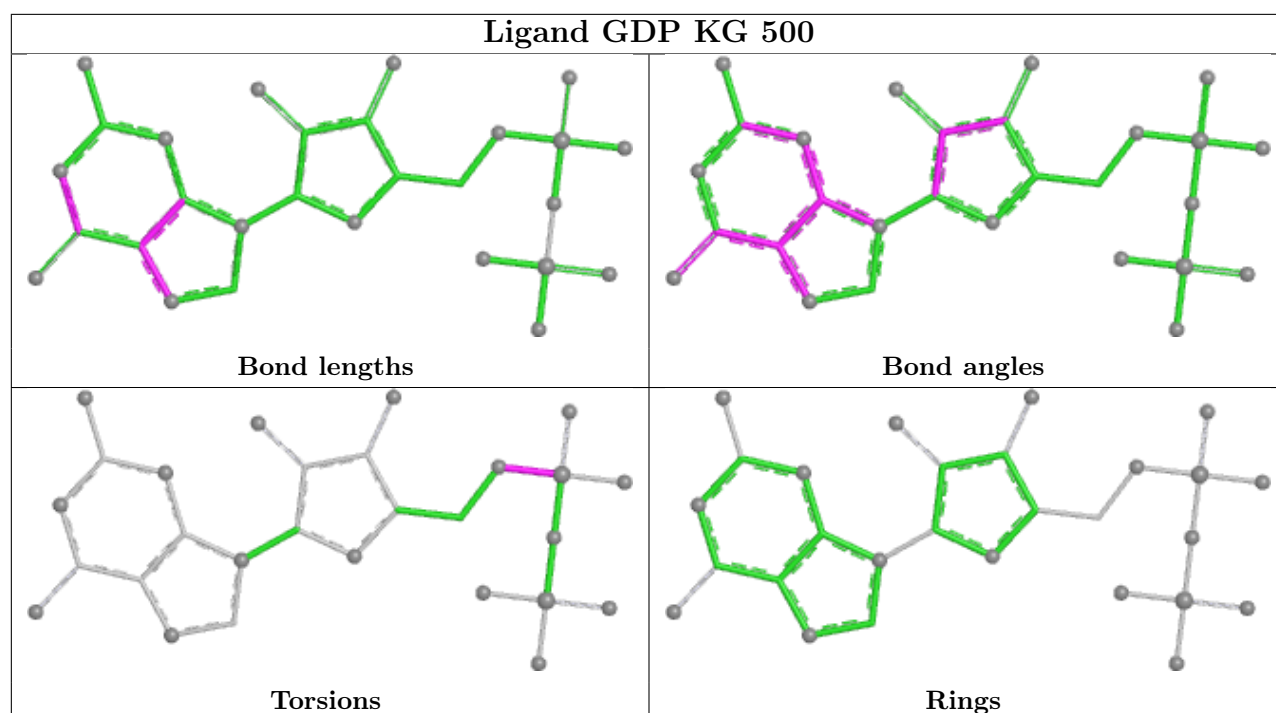
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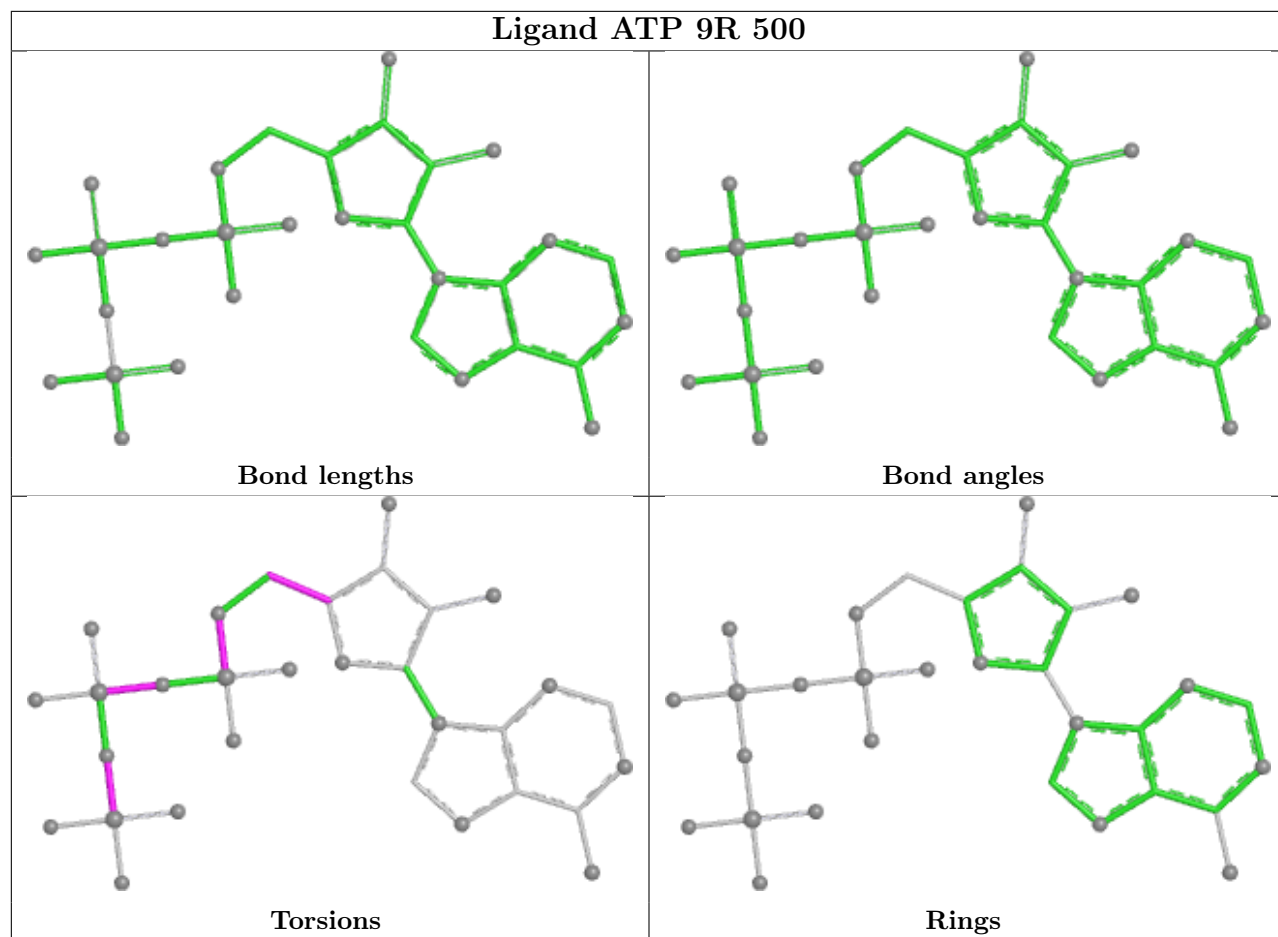


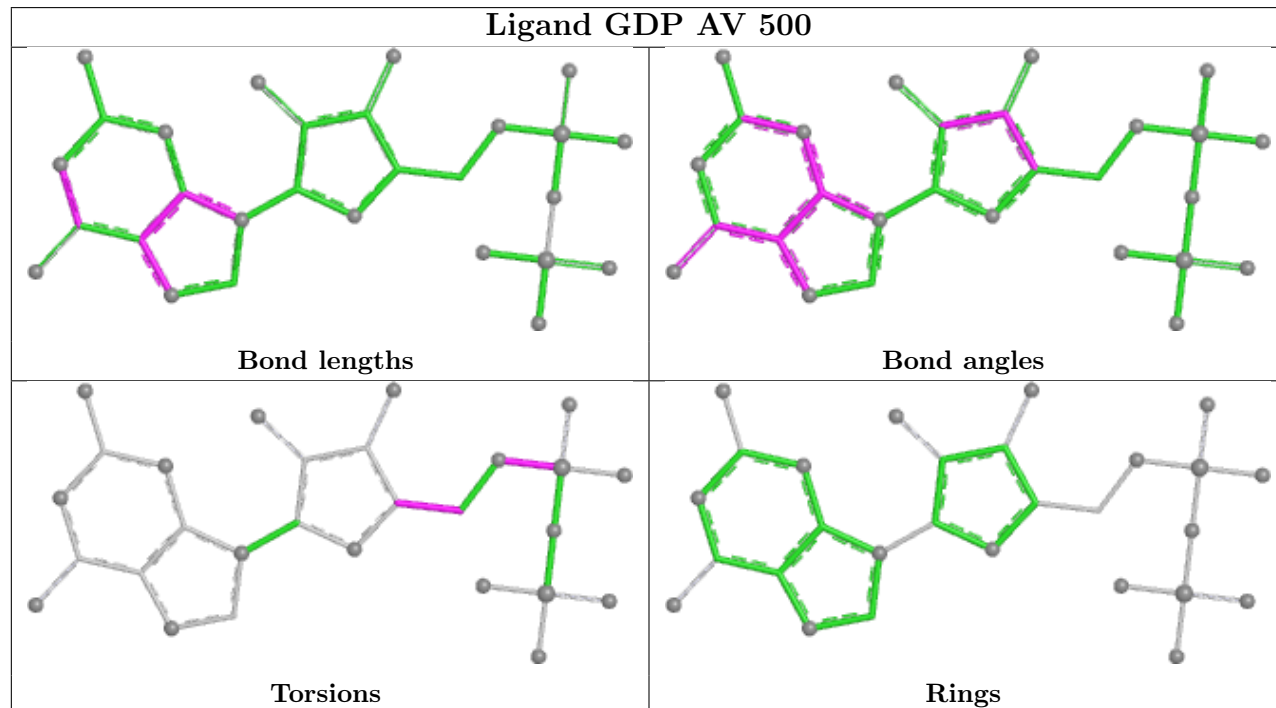
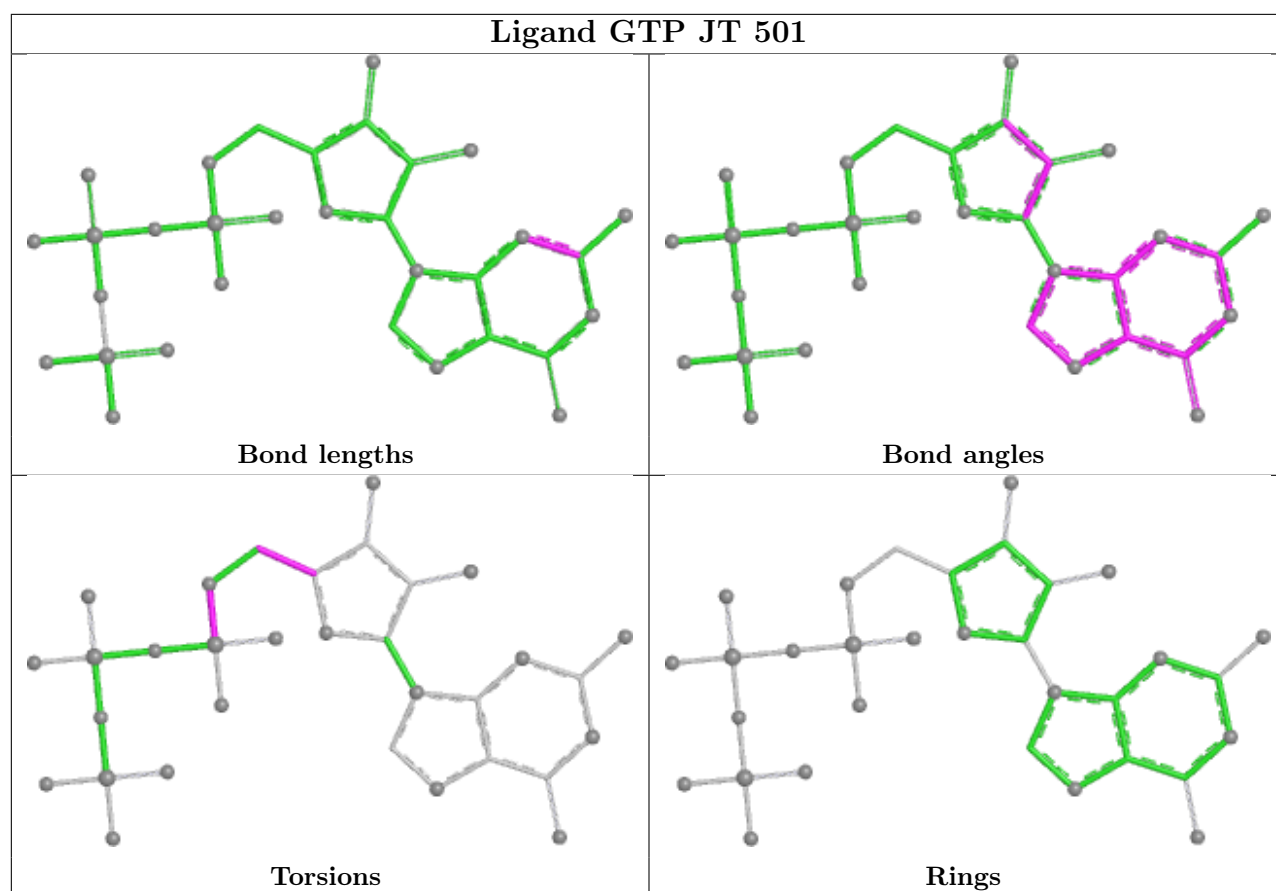
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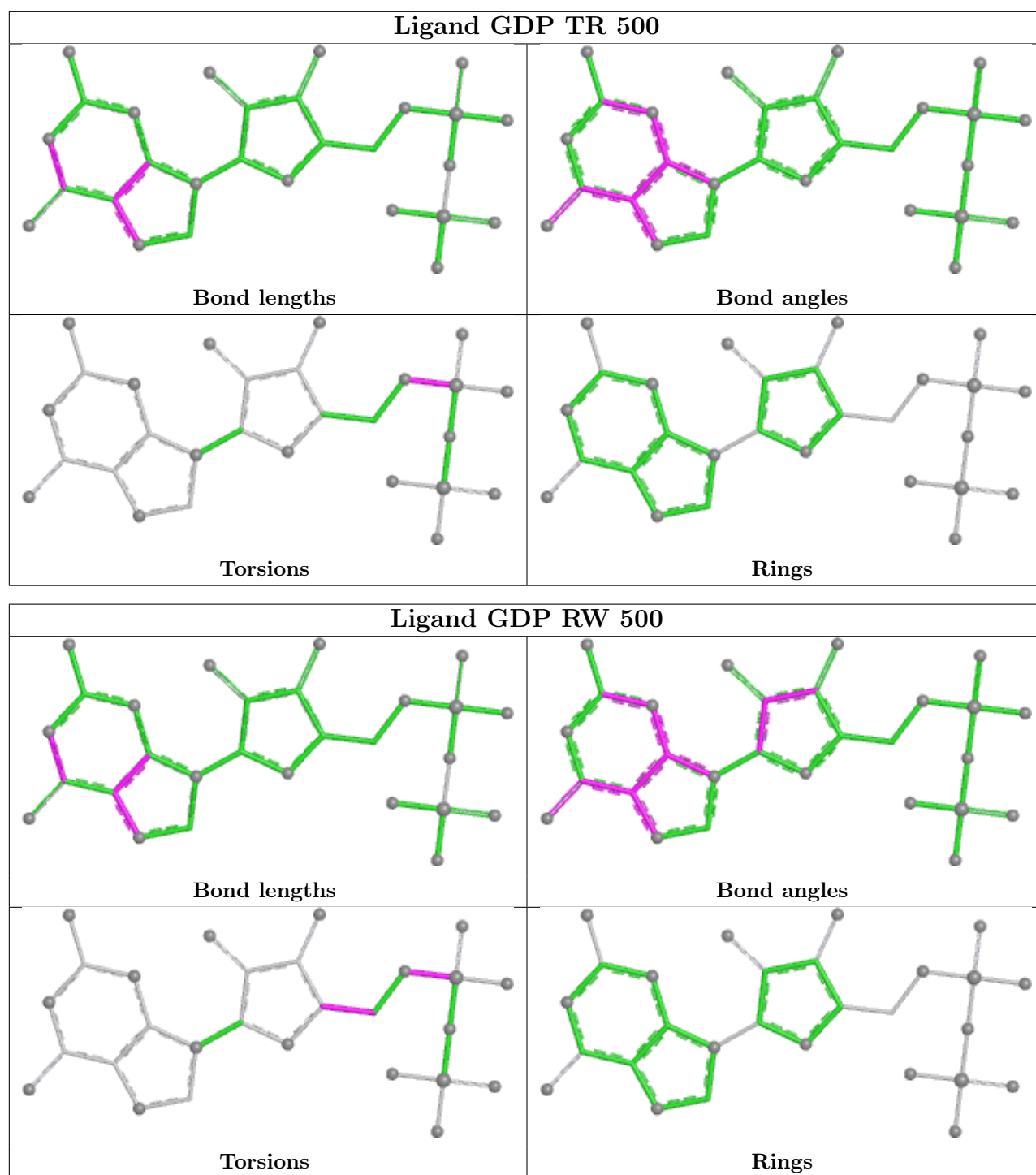


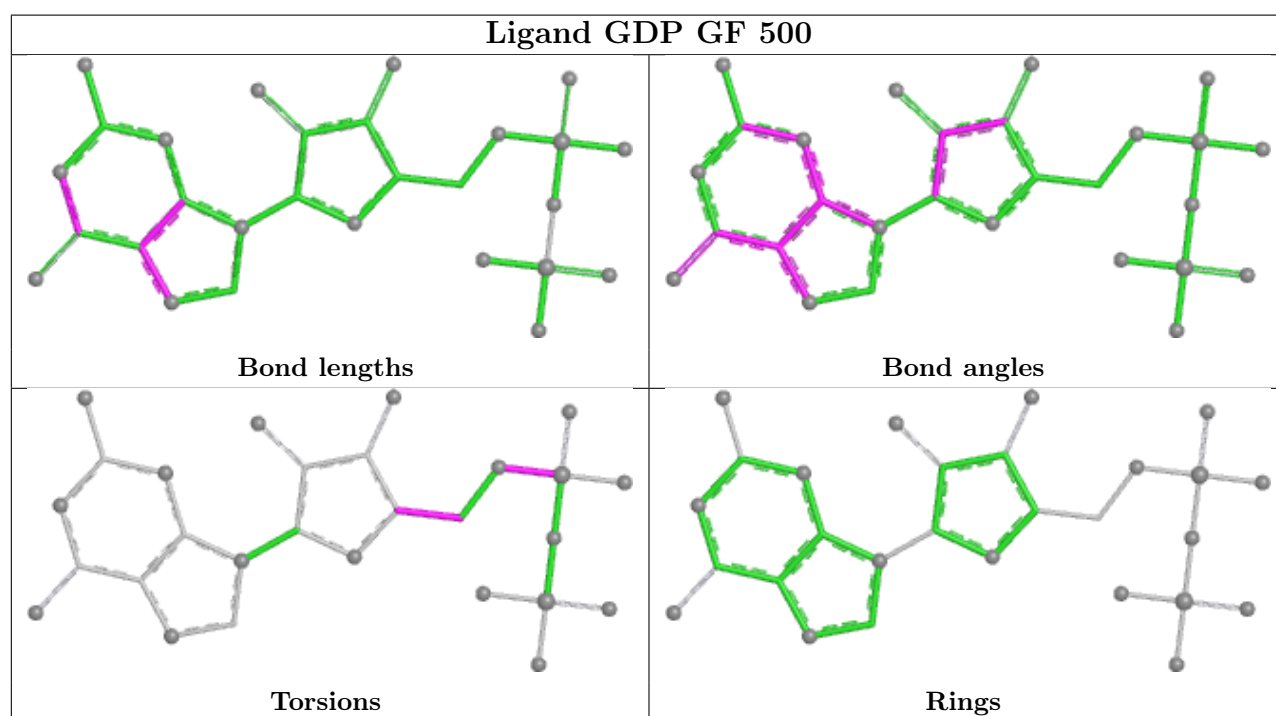
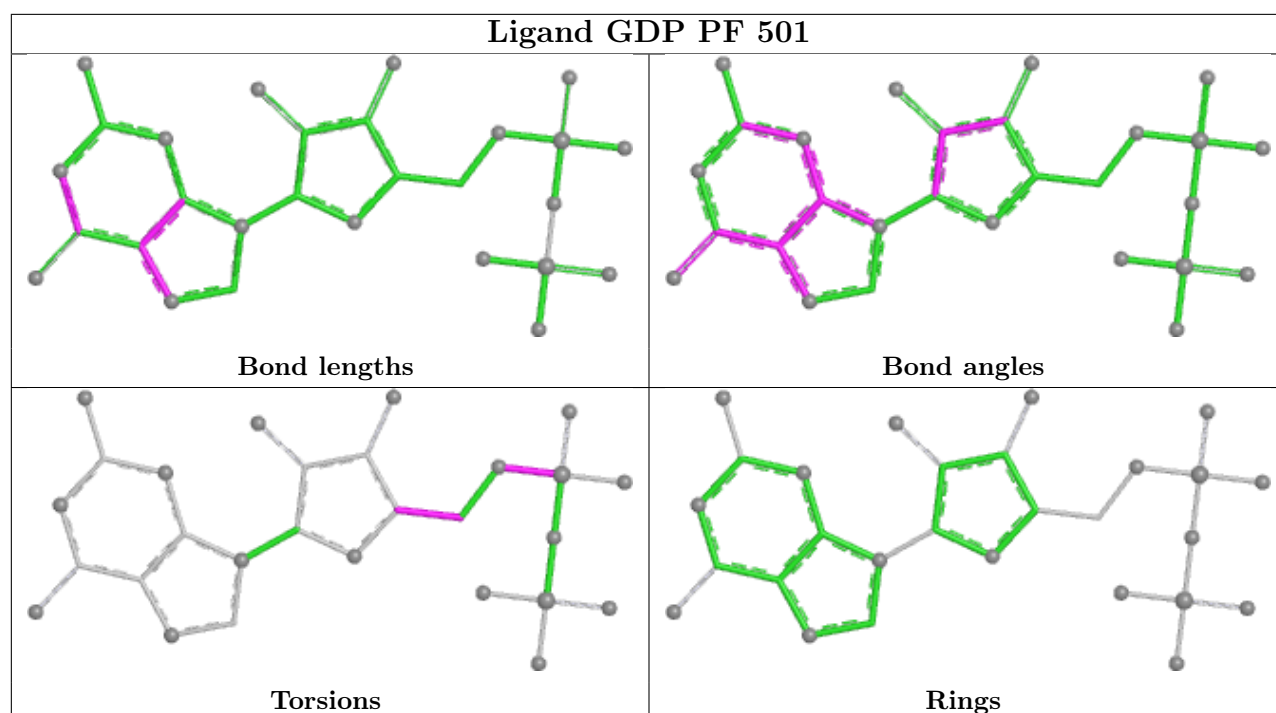




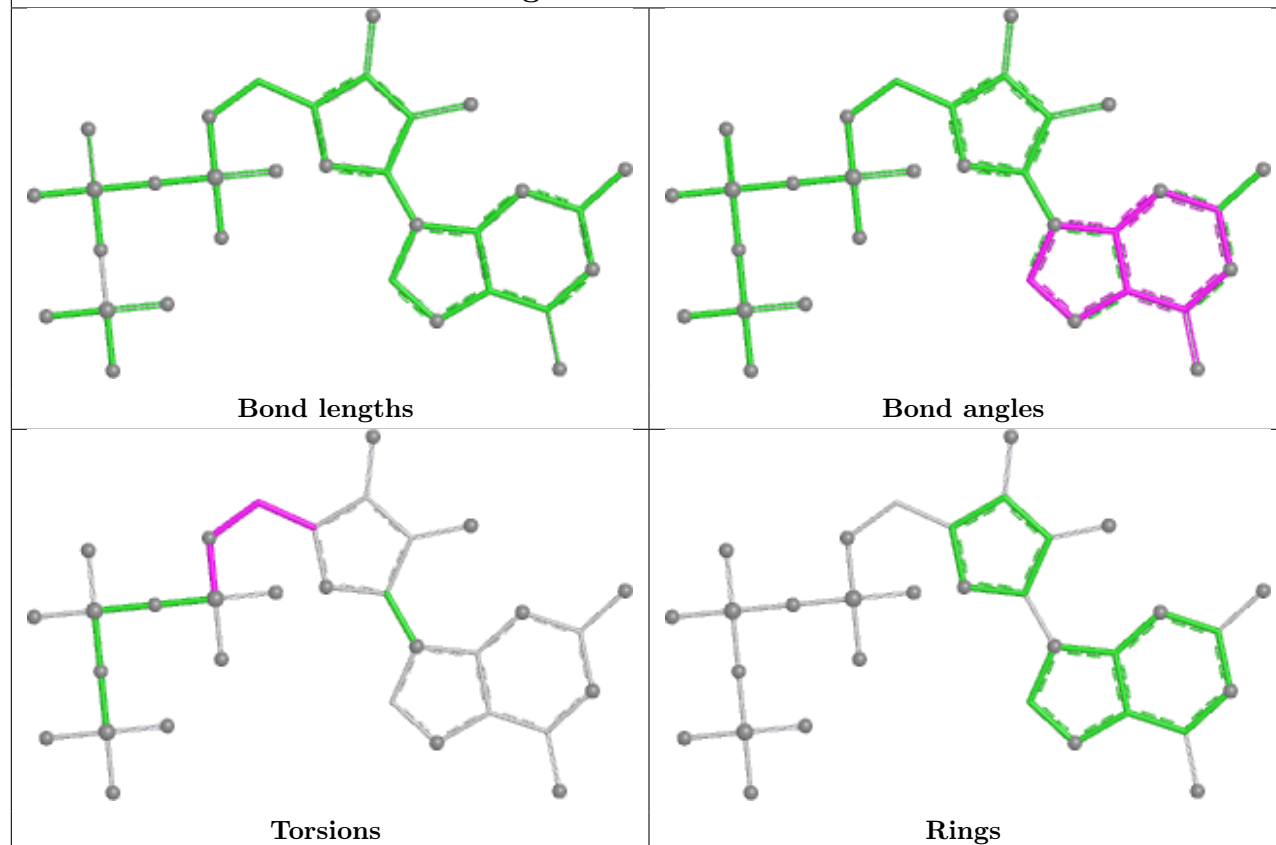




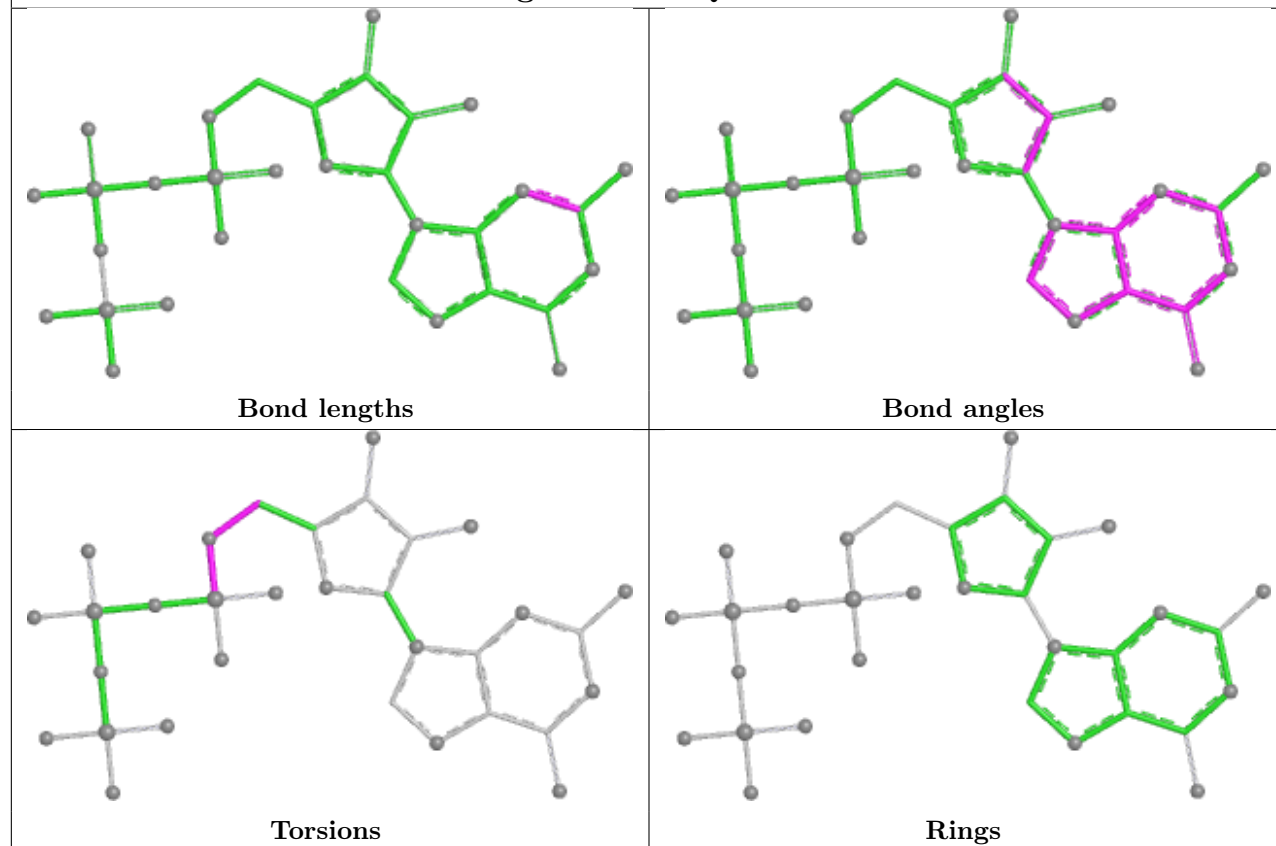




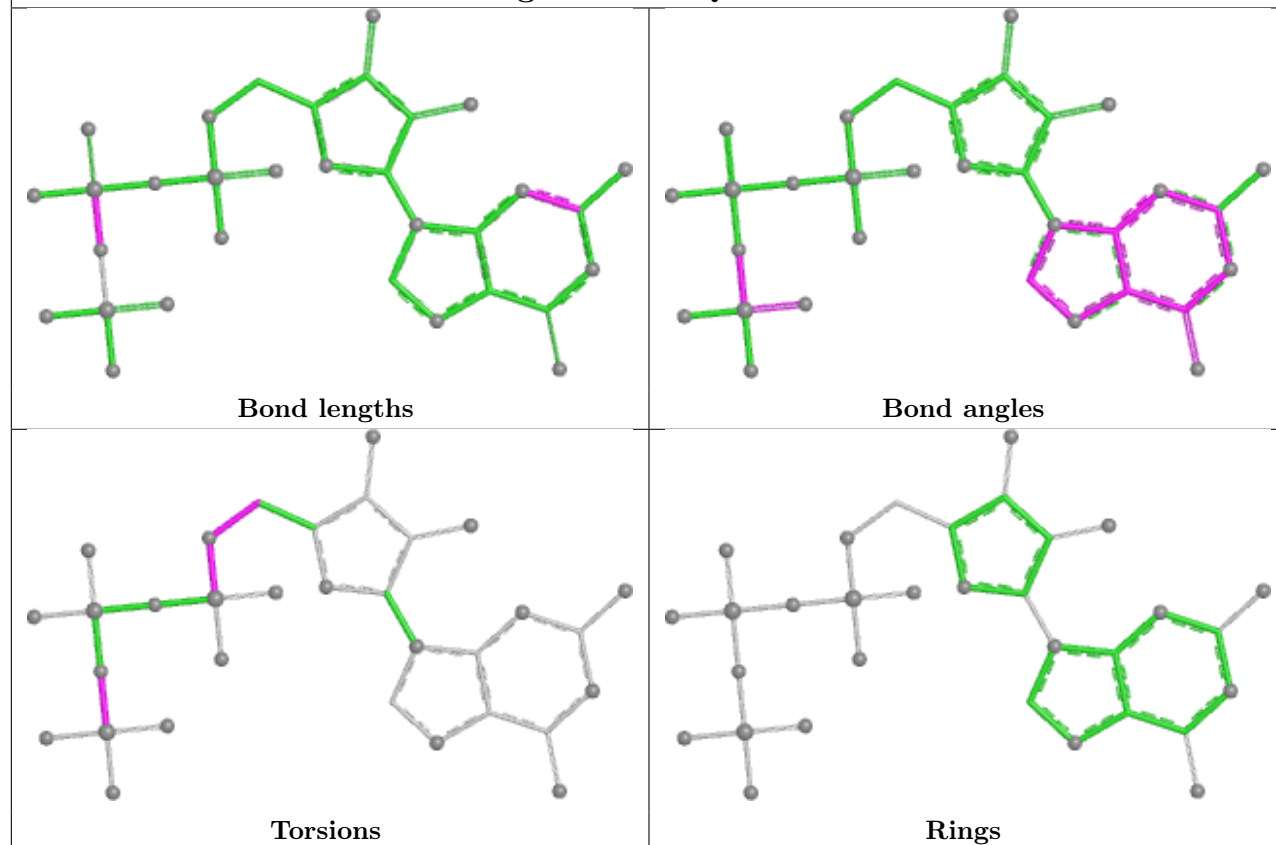
Ligand GTP FS 501



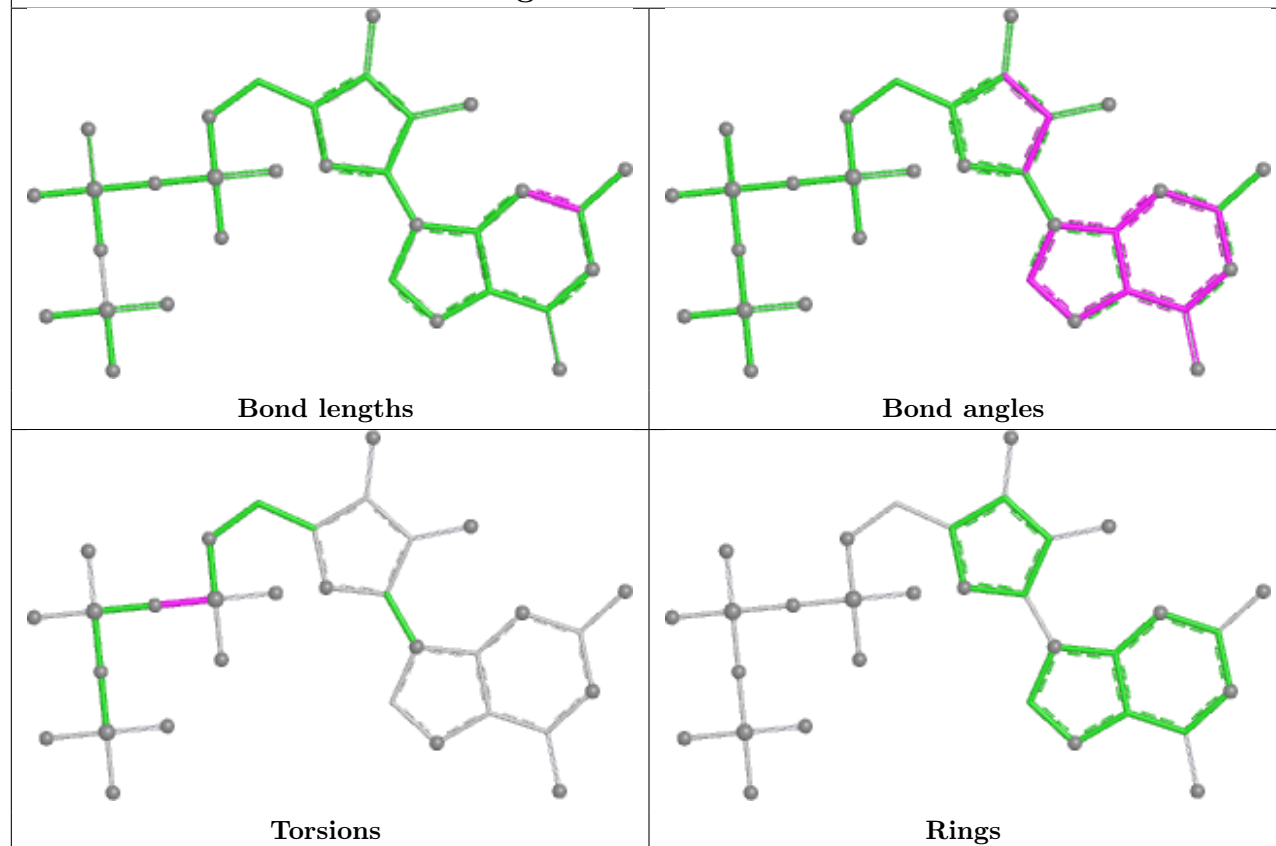
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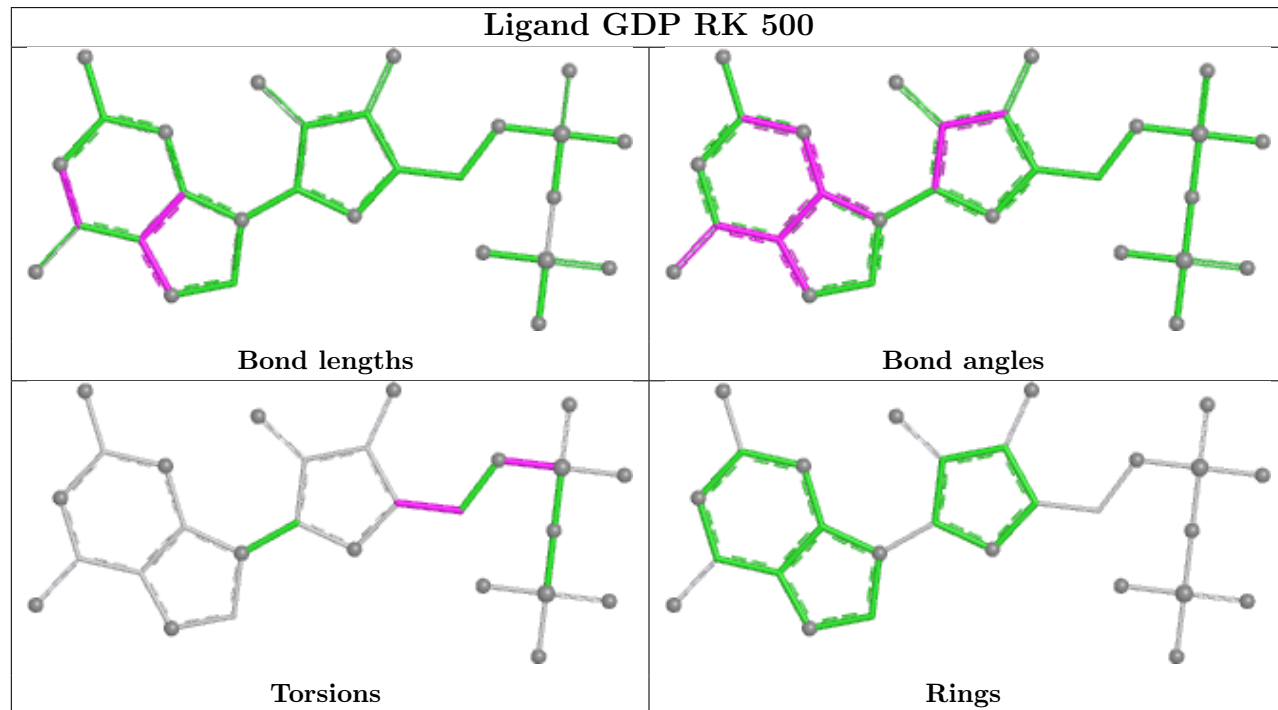
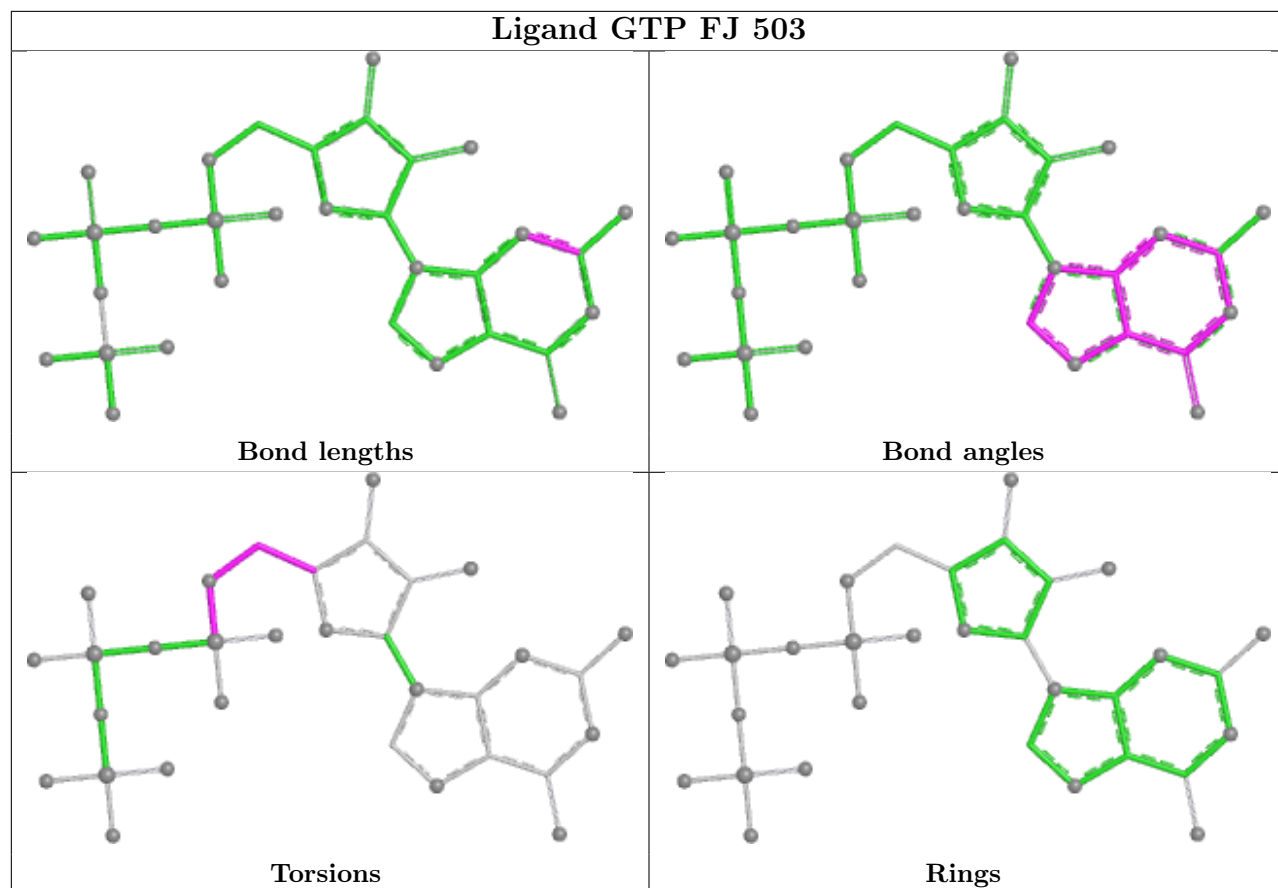


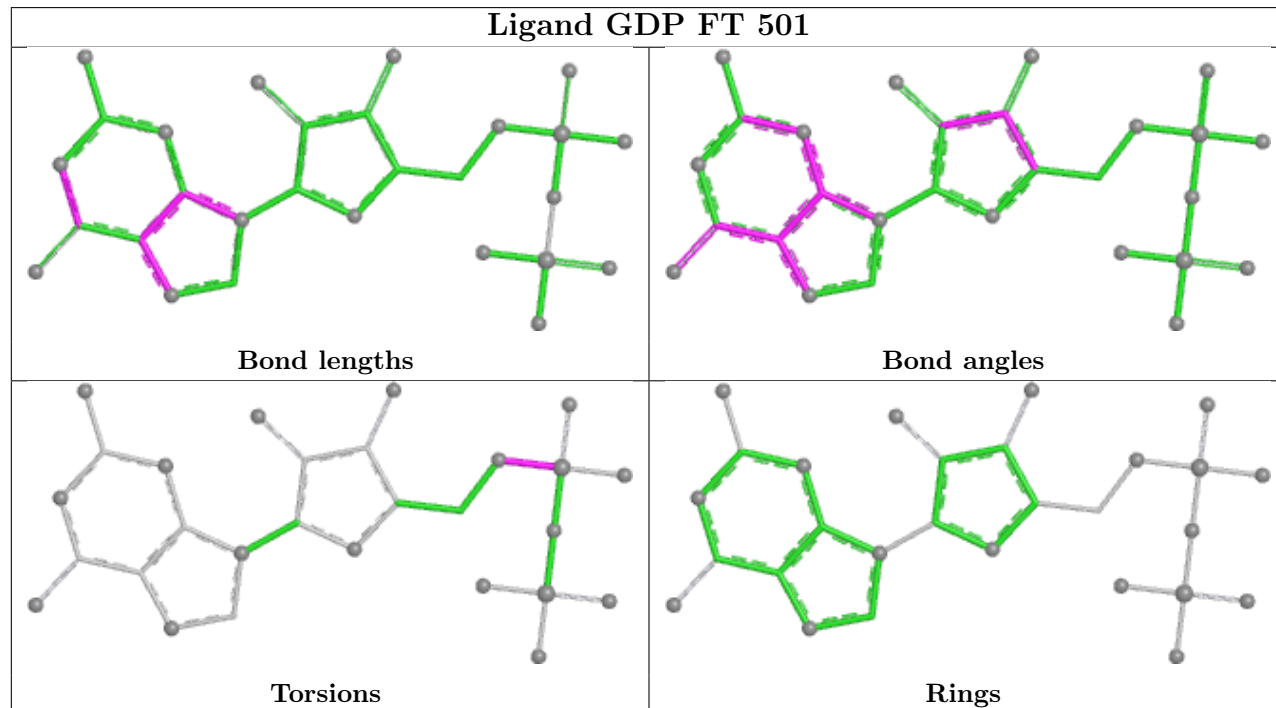
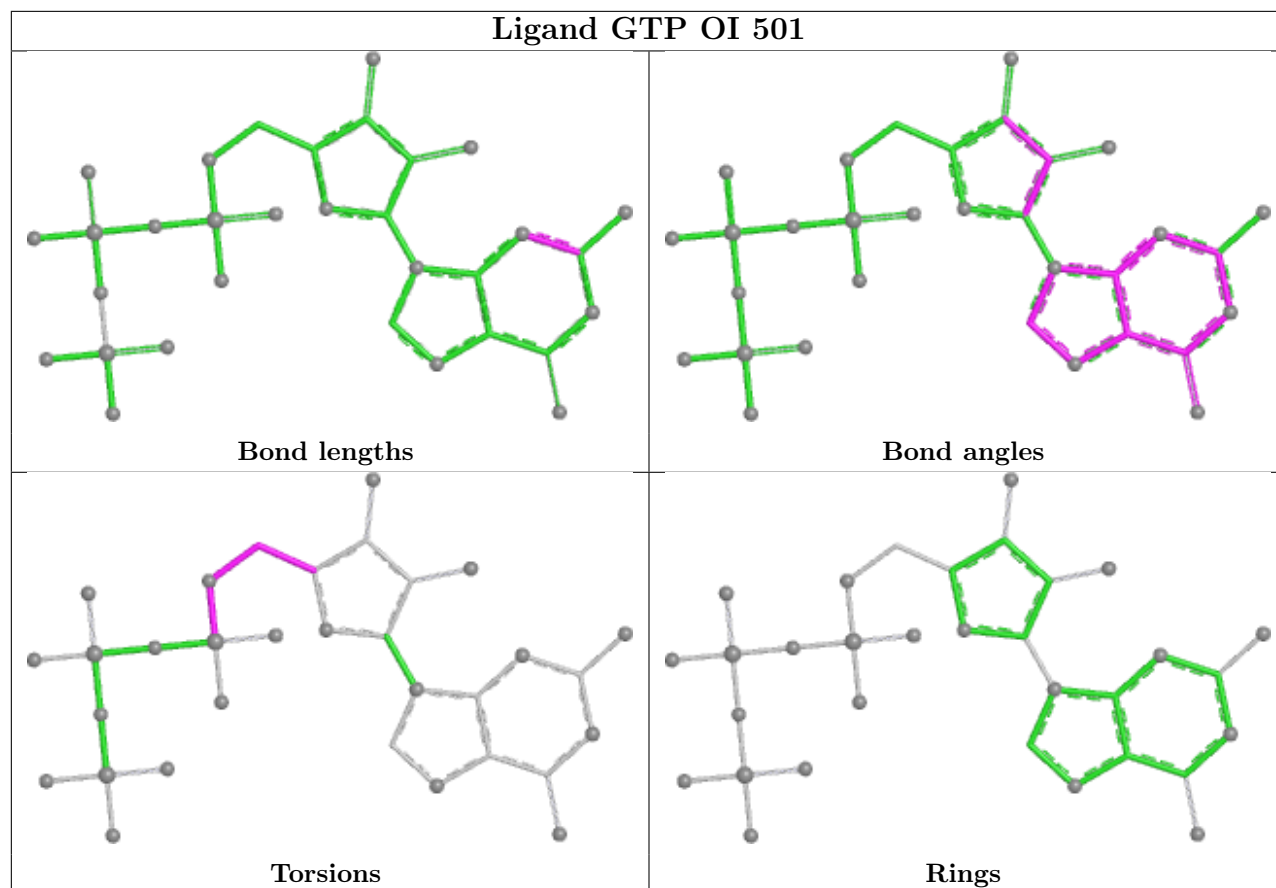
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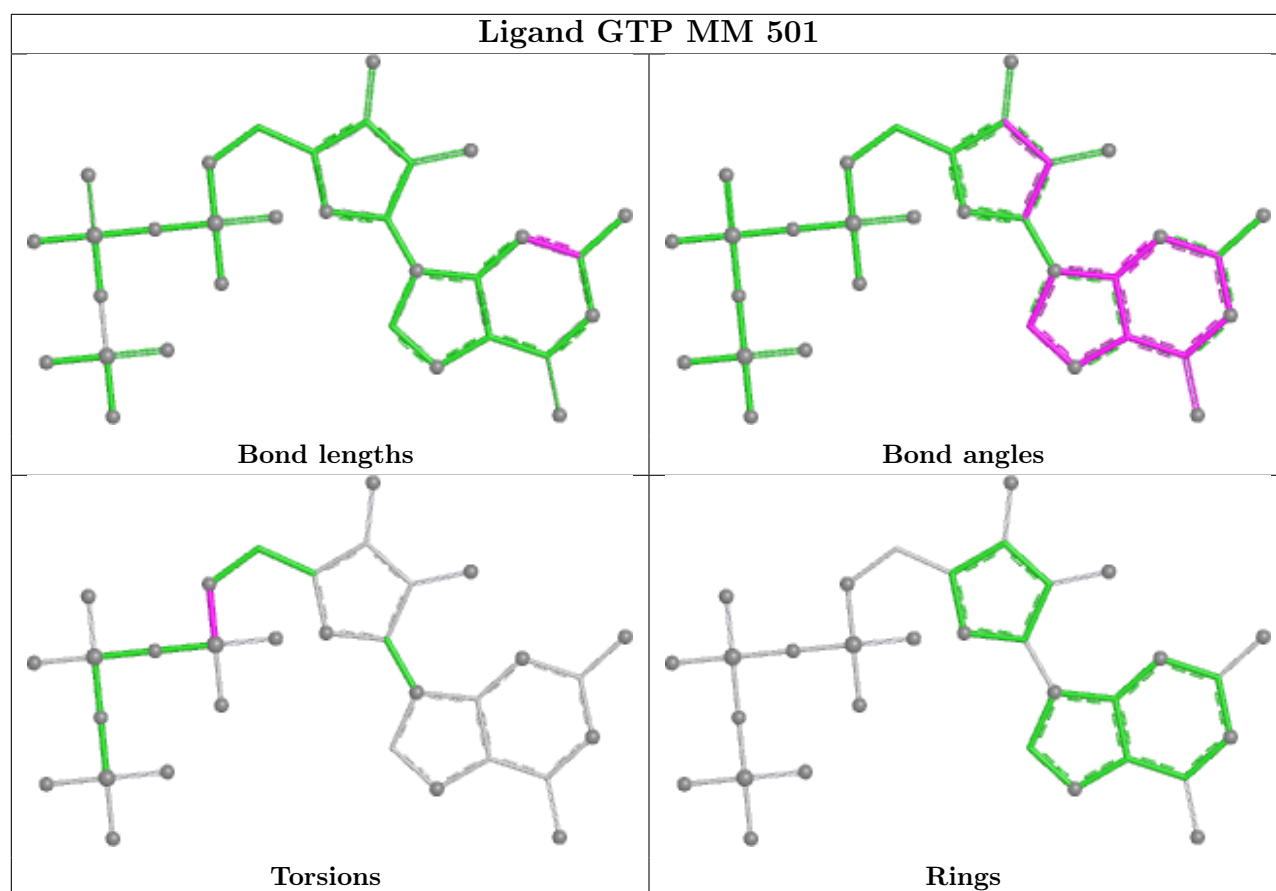


Ligand GTP BG 501









4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
67	5Z	4
67	5Y	4
67	5X	4
67	5a	3
68	5f	2
95	6t	1
68	5c	1
68	5d	1
109	9a	1
68	5e	1
67	5W	1

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Mol	Chain	Number of breaks
83	6k	1
16	0i	1
126	9N	1
2	GU	1
2	CB	1

The worst 5 of 28 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5a	233:ASP	C	234:ASP	N	8.58
1	5Z	233:ASP	C	234:ASP	N	8.37
1	5Y	233:ASP	C	234:ASP	N	7.90
1	5X	233:ASP	C	234:ASP	N	7.70
1	5Z	496:PHE	C	497:LEU	N	7.54

5 Map visualisation

This section contains visualisations of the EMDB entry EMD-72629. 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.

5.1 Orthogonal projections

This section was not generated.

5.2 Central slices

This section was not generated.

5.3 Largest variance slices

This section was not generated.

5.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

5.5 Orthogonal surface views

This section was not generated.

5.6 Mask visualisation

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

6 Map analysis ⓘ

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

6.1 Map-value distribution ⓘ

This section was not generated.

6.2 Volume estimate versus contour level ⓘ

This section was not generated.

6.3 Rotationally averaged power spectrum ⓘ

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

7 Fourier-Shell correlation

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

8 Map-model fit

This section was not generated.