



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 01:54 AM UTC

PDB ID : 7RRO / pdb_00007rro
EMDB ID : EMD-24664
Title : Structure of the 48-nm repeat doublet microtubule from bovine tracheal cilia
Authors : Gui, M.; Anderson, J.R.; Botsch, J.J.; Meleppattu, S.; Singh, S.K.; Zhang, Q.; Brown, A.
Deposited on : 2021-08-10
Resolution : 3.40 Å(reported)

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

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

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 3.40 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 39 unique types of molecules in this entry. The entry contains 1276281 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 Protein C9orf135 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	40	Total	C	N	O	S	0	0
			330	205	63	61	1		
1	7	121	Total	C	N	O	S	0	0
			806	494	146	164	2		

- Molecule 2 is a protein called EF-hand domain family member B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	152	Total	C	N	O	S	0	0
			921	570	172	178	1		
2	2	292	Total	C	N	O		0	0
			1526	915	312	299			

- Molecule 3 is a protein called Methyl-CpG binding domain protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	306	Total	C	N	O	S	0	0
			2295	1393	444	448	10		
3	4	217	Total	C	N	O	S	0	0
			1855	1127	350	364	14		

- Molecule 4 is a protein called Nucleoside diphosphate kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	372	Total	C	N	O	S	0	0
			2533	1589	451	481	12		
4	6	372	Total	C	N	O	S	0	0
			2947	1880	499	546	22		

- Molecule 5 is a protein called Uncharacterized protein C1orf158 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	8	191	Total	C	N	O	S	0	0
			1607	1037	288	281	1		
5	9	35	Total	C	N	O		0	0
			287	181	51	55			

- Molecule 6 is a protein called Meiosis-specific nuclear structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	170	Total	C	N	O	S	0	0
			1427	869	270	281	7		
6	B	354	Total	C	N	O	S	0	0
			3044	1882	553	592	17		

- Molecule 7 is a protein called Tektin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A0	221	Total	C	N	O	S	0	0
			1797	1120	329	341	7		
7	A1	396	Total	C	N	O	S	0	0
			3258	2026	592	631	9		
7	A2	393	Total	C	N	O	S	0	0
			3238	2016	589	624	9		
7	A3	334	Total	C	N	O	S	0	0
			2759	1716	498	537	8		
7	A4	34	Total	C	N	O		0	0
			290	179	61	50			

- Molecule 8 is a protein called Tubulin alpha-1D chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AA	438	Total	C	N	O	S	0	0
			3422	2165	582	653	22		
8	AC	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	AE	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	AG	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	AI	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	AK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	AM	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	BA	430	Total	C	N	O	S	0	0
			3372	2136	573	641	22		
8	BC	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	BE	433	Total	C	N	O	S	0	0
			3396	2151	576	646	23		
8	BG	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	BI	430	Total	C	N	O	S	0	0
			3374	2138	573	640	23		
8	BK	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	BM	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	CA	438	Total	C	N	O	S	0	0
			3422	2165	582	653	22		
8	CC	438	Total	C	N	O	S	0	0
			3424	2167	582	652	23		
8	CE	438	Total	C	N	O	S	0	0
			3424	2167	582	652	23		
8	CG	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	CI	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	CK	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	CM	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	DA	401	Total	C	N	O	S	0	0
			3140	1992	535	594	19		
8	DC	429	Total	C	N	O	S	0	0
			3366	2134	572	637	23		
8	DE	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	DG	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	DI	429	Total	C	N	O	S	0	0
			3364	2133	572	636	23		
8	DK	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	DM	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	EC	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	EE	441	Total	C	N	O	S	0	0
			3446	2180	585	658	23		
8	EG	437	Total	C	N	O	S	0	0
			3416	2163	581	649	23		
8	EI	436	Total	C	N	O	S	0	0
			3408	2158	580	648	22		
8	EK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	EM	428	Total	C	N	O	S	0	0
			3358	2130	571	634	23		
8	FC	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	FE	425	Total	C	N	O	S	0	0
			3339	2118	568	631	22		
8	FG	426	Total	C	N	O	S	0	0
			3346	2123	569	632	22		
8	FI	427	Total	C	N	O	S	0	0
			3347	2121	570	633	23		
8	FK	424	Total	C	N	O	S	0	0
			3326	2109	566	629	22		
8	FM	429	Total	C	N	O	S	0	0
			3365	2132	572	638	23		
8	GC	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	GE	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	GG	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	GI	429	Total	C	N	O	S	0	0
			3365	2135	572	635	23		
8	GK	429	Total	C	N	O	S	0	0
			3364	2133	572	636	23		
8	GM	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	HC	427	Total	C	N	O	S	0	0
			3350	2126	570	631	23		
8	HE	430	Total	C	N	O	S	0	0
			3374	2138	573	640	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	HG	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	HI	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	HK	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	HM	429	Total	C	N	O	S	0	0
			3365	2132	572	638	23		
8	HO	386	Total	C	N	O	S	0	0
			3037	1926	518	572	21		
8	IC	429	Total	C	N	O	S	0	0
			3365	2135	572	635	23		
8	IE	432	Total	C	N	O	S	0	0
			3388	2147	575	643	23		
8	IG	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	II	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		
8	IK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	IM	431	Total	C	N	O	S	0	0
			3378	2140	574	641	23		
8	IO	427	Total	C	N	O	S	0	0
			3350	2125	570	633	22		
8	JC	432	Total	C	N	O	S	0	0
			3384	2143	575	643	23		
8	JE	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	JG	428	Total	C	N	O	S	0	0
			3358	2130	571	634	23		
8	JI	429	Total	C	N	O	S	0	0
			3366	2134	572	637	23		
8	JK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	JM	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	KC	432	Total	C	N	O	S	0	0
			3384	2143	575	643	23		
8	KE	431	Total	C	N	O	S	0	0
			3380	2141	574	642	23		
8	KG	430	Total	C	N	O	S	0	0
			3370	2136	573	638	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	KI	428	Total	C	N	O	S	0	0
			3358	2130	571	634	23		
8	KK	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	KM	432	Total	C	N	O	S	0	0
			3376	2138	575	641	22		
8	KO	408	Total	C	N	O	S	0	0
			3217	2040	546	608	23		
8	LC	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	LE	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	LG	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	LI	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	LK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	LM	431	Total	C	N	O	S	0	0
			3378	2140	574	641	23		
8	MC	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	ME	429	Total	C	N	O	S	0	0
			3366	2134	572	637	23		
8	MG	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	MI	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	MK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	MM	431	Total	C	N	O	S	0	0
			3376	2138	574	642	22		
8	NA	430	Total	C	N	O	S	0	0
			3372	2136	573	641	22		
8	NC	429	Total	C	N	O	S	0	0
			3365	2135	572	635	23		
8	NE	430	Total	C	N	O	S	0	0
			3374	2140	573	638	23		
8	NG	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		
8	NI	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	NK	430	Total	C	N	O	S	0	0
			3374	2138	573	640	23		
8	OA	428	Total	C	N	O	S	0	0
			3358	2129	571	636	22		
8	OC	429	Total	C	N	O	S	0	0
			3366	2134	572	637	23		
8	OE	433	Total	C	N	O	S	0	0
			3396	2151	576	646	23		
8	OG	433	Total	C	N	O	S	0	0
			3391	2148	576	644	23		
8	OI	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		
8	OK	431	Total	C	N	O	S	0	0
			3380	2141	574	642	23		
8	PA	430	Total	C	N	O	S	0	0
			3372	2136	573	641	22		
8	PC	432	Total	C	N	O	S	0	0
			3386	2144	575	644	23		
8	PE	431	Total	C	N	O	S	0	0
			3380	2143	574	640	23		
8	PG	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	PI	427	Total	C	N	O	S	0	0
			3349	2123	570	634	22		
8	PK	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	PM	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	QA	431	Total	C	N	O	S	0	0
			3376	2138	574	642	22		
8	QC	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	QE	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	QG	431	Total	C	N	O	S	0	0
			3380	2141	574	642	23		
8	QI	429	Total	C	N	O	S	0	0
			3366	2134	572	637	23		
8	QK	431	Total	C	N	O	S	0	0
			3380	2141	574	642	23		
8	QM	431	Total	C	N	O	S	0	0
			3378	2140	574	641	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	RA	429	Total	C	N	O	S	0	0
			3364	2132	572	638	22		
8	RC	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		
8	RE	428	Total	C	N	O	S	0	0
			3358	2130	571	634	23		
8	RG	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	RI	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	RK	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	RM	428	Total	C	N	O	S	0	0
			3356	2128	571	635	22		
8	SA	430	Total	C	N	O	S	0	0
			3372	2136	573	641	22		
8	SC	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	SE	431	Total	C	N	O	S	0	0
			3381	2142	574	642	23		
8	SG	431	Total	C	N	O	S	0	0
			3379	2142	574	640	23		
8	SI	427	Total	C	N	O	S	0	0
			3358	2129	569	637	23		
8	SK	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		
8	SM	431	Total	C	N	O	S	0	0
			3378	2140	574	641	23		
8	TC	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	TE	432	Total	C	N	O	S	0	0
			3388	2147	575	643	23		
8	TG	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	TI	430	Total	C	N	O	S	0	0
			3371	2138	573	637	23		
8	TK	432	Total	C	N	O	S	0	0
			3387	2146	575	643	23		
8	TM	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	UC	433	Total	C	N	O	S	0	0
			3393	2149	576	645	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	UE	432	Total	C	N	O	S	0	0
			3388	2147	575	643	23		
8	UG	433	Total	C	N	O	S	0	0
			3393	2149	576	645	23		
8	UI	433	Total	C	N	O	S	0	0
			3393	2149	576	645	23		
8	UK	433	Total	C	N	O	S	0	0
			3391	2148	576	644	23		
8	UM	431	Total	C	N	O	S	0	0
			3378	2140	574	641	23		
8	VC	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	VE	433	Total	C	N	O	S	0	0
			3396	2151	576	646	23		
8	VG	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	VI	433	Total	C	N	O	S	0	0
			3393	2149	576	645	23		
8	VK	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	VM	430	Total	C	N	O	S	0	0
			3372	2137	573	639	23		
8	WC	440	Total	C	N	O	S	0	0
			3437	2175	584	655	23		
8	WE	431	Total	C	N	O	S	0	0
			3380	2141	574	642	23		
8	WG	439	Total	C	N	O	S	0	0
			3430	2170	583	654	23		
8	WI	431	Total	C	N	O	S	0	0
			3380	2141	574	642	23		
8	WK	438	Total	C	N	O	S	0	0
			3424	2167	582	652	23		
8	WM	431	Total	C	N	O	S	0	0
			3378	2140	574	641	23		

- Molecule 9 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AB	436	Total	C	N	O	S	0	0
			3424	2150	584	664	26		
9	AD	436	Total	C	N	O	S	0	0
			3424	2150	584	664	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	436	Total	C	N	O	S	0	0
			3424	2150	584	664	26		
9	AH	436	Total	C	N	O	S	0	0
			3424	2150	584	664	26		
9	AJ	436	Total	C	N	O	S	0	0
			3424	2150	584	664	26		
9	AL	435	Total	C	N	O	S	0	0
			3416	2145	583	663	25		
9	BB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	BD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	BF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	BH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	BJ	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	BL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	CB	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	CD	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	CF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	CH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	CJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	CL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	DB	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	DD	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	DF	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	DH	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	DJ	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	DL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	DN	387	Total	C	N	O	S	0	0
			3035	1911	519	582	23		
9	EB	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	ED	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	EF	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	EH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	EJ	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	EL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	EN	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	FB	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	FD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	FF	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	FH	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	FJ	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	FL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	FN	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	GB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	GD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	GF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	GH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	GJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	GL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	GN	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	HB	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	HD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	HF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	HH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	HJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	HL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	HN	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	IB	370	Total	C	N	O	S	0	0
			2905	1824	501	557	23		
9	ID	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	IF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	IH	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	IJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	IL	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	IN	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	JB	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	JD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	JF	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	JH	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	JJ	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	JL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	JN	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	KB	403	Total 3165	C 1989	N 539	O 613	S 24	0	0
9	KD	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	KF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	KH	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	KJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	KL	429	Total 3368	C 2116	N 577	O 649	S 26	0	0
9	KN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LD	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	LF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	LL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	LN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	MB	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	MD	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	MF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	MH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	MJ	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	ML	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	MN	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	N0	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	NB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	ND	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	NF	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	NH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	NJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	NL	425	Total	C	N	O	S	0	0
			3339	2100	572	641	26		
9	O0	412	Total	C	N	O	S	0	0
			3224	2024	553	623	24		
9	OB	425	Total	C	N	O	S	0	0
			3339	2100	572	641	26		
9	OD	424	Total	C	N	O	S	0	0
			3327	2091	571	639	26		
9	OF	425	Total	C	N	O	S	0	0
			3339	2100	572	641	26		
9	OH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	OJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	OL	424	Total	C	N	O	S	0	0
			3327	2091	571	639	26		
9	PB	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	PD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	PF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	PH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	PJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	PL	425	Total	C	N	O	S	0	0
			3340	2100	573	642	25		
9	QB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	QD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	QF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	QH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	QJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	QL	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	RB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	RD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	RF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	RH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	RJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	RL	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	SB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	SD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		
9	SF	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	SH	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	SJ	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	SL	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	TB	428	Total	C	N	O	S	0	0
			3361	2112	576	647	26		
9	TD	427	Total	C	N	O	S	0	0
			3356	2109	575	646	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	TF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	TH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	TJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	TL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	UD	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	UF	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	UH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	UJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	UL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	UN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	VB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	VD	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	VF	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	VH	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	VJ	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	VL	426	Total 3348	C 2105	N 574	O 643	S 26	0	0
9	VN	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	WB	428	Total 3361	C 2112	N 576	O 647	S 26	0	0
9	WD	427	Total 3356	C 2109	N 575	O 646	S 26	0	0
9	WF	426	Total 3348	C 2105	N 574	O 643	S 26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	WH	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	WJ	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	WL	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		
9	WN	426	Total	C	N	O	S	0	0
			3348	2105	574	643	26		

- Molecule 10 is a protein called Tektin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B0	189	Total	C	N	O	S	0	0
			1538	941	290	301	6		
10	B1	416	Total	C	N	O	S	0	0
			3391	2090	627	660	14		
10	B2	416	Total	C	N	O	S	0	0
			3391	2090	627	660	14		
10	B3	383	Total	C	N	O	S	0	0
			3113	1920	568	610	15		
10	B4	49	Total	C	N	O	S	0	0
			406	248	79	77	2		
10	B5	51	Total	C	N	O	S	0	0
			419	257	81	79	2		
10	B6	358	Total	C	N	O	S	0	0
			2911	1793	534	570	14		
10	B7	414	Total	C	N	O	S	0	0
			3372	2080	621	657	14		
10	B8	403	Total	C	N	O	S	0	0
			3284	2025	607	638	14		
10	B9	187	Total	C	N	O	S	0	0
			1523	933	287	297	6		

- Molecule 11 is a protein called Uncharacterized protein C1orf189 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	91	Total	C	N	O	S	0	0
			785	495	151	133	6		

- Molecule 12 is a protein called Tektin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C0	30	Total	C	N	O		0	0
			261	157	50	54			
12	C1	334	Total	C	N	O	S	0	0
			2710	1667	493	537	13		
12	C2	394	Total	C	N	O	S	0	0
			3208	1974	588	631	15		
12	C3	394	Total	C	N	O	S	0	0
			3208	1974	588	631	15		
12	C4	215	Total	C	N	O	S	0	0
			1745	1083	314	335	13		
12	C5	113	Total	C	N	O	S	0	0
			908	559	165	181	3		
12	C6	385	Total	C	N	O	S	0	0
			3131	1925	573	618	15		
12	C7	413	Total	C	N	O	S	0	0
			3359	2066	615	661	17		
12	C8	407	Total	C	N	O	S	0	0
			3310	2039	602	653	16		
12	C9	112	Total	C	N	O	S	0	0
			926	559	177	187	3		
12	F0	139	Total	C	N	O	S	0	0
			1156	714	214	226	2		
12	F1	421	Total	C	N	O	S	0	0
			3433	2121	624	672	16		
12	F2	421	Total	C	N	O	S	0	0
			3433	2121	624	672	16		
12	F3	378	Total	C	N	O	S	0	0
			3064	1884	561	604	15		
12	F4	99	Total	C	N	O	S	0	0
			809	500	147	159	3		

- Molecule 13 is a protein called Sperm associated antigen 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	147	Total	C	N	O	S	0	0
			944	587	174	182	1		

- Molecule 14 is a protein called Tektin-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D0	291	Total	C	N	O	S	0	0
			2377	1468	435	462	12		
14	D1	425	Total	C	N	O	S	0	0
			3483	2143	653	672	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	D2	425	Total	C	N	O	S	0	0
			3483	2143	653	672	15		
14	D3	316	Total	C	N	O	S	0	0
			2593	1603	483	495	12		
14	D5	9	Total	C	N	O	S	0	0
			77	46	18	12	1		
14	D6	319	Total	C	N	O	S	0	0
			2619	1617	489	501	12		
14	D7	414	Total	C	N	O	S	0	0
			3390	2085	634	656	15		
14	D8	413	Total	C	N	O	S	0	0
			3381	2080	632	654	15		
14	D9	277	Total	C	N	O	S	0	0
			2259	1395	410	443	11		

- Molecule 15 is a protein called Cilia and flagella associated protein 161.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	255	Total	C	N	O	S	0	0
			2055	1302	369	373	11		
15	F	255	Total	C	N	O	S	0	0
			2055	1302	369	373	11		

- Molecule 16 is a protein called TEKTI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E0	68	Total	C	N	O	S	0	0
			581	371	113	96	1		
16	E1	127	Total	C	N	O	S	0	0
			1062	675	200	185	2		
16	E2	144	Total	C	N	O	S	0	0
			1202	766	220	214	2		
16	E3	144	Total	C	N	O	S	0	0
			1202	766	220	214	2		

- Molecule 17 is a protein called Pierce2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	G	96	Total	C	N	O	S	0	0
			775	496	130	142	7		

- Molecule 18 is a protein called Protein FAM166B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	H	84	Total	C	N	O	S	0	0
			647	421	111	110	5		
18	I	152	Total	C	N	O	S	0	0
			1188	780	201	201	6		
18	J	152	Total	C	N	O	S	0	0
			1188	780	201	201	6		
18	K	152	Total	C	N	O	S	0	0
			1188	780	201	201	6		
18	L	152	Total	C	N	O	S	0	0
			1188	780	201	201	6		
18	M	152	Total	C	N	O	S	0	0
			1188	780	201	201	6		
18	N	155	Total	C	N	O	S	0	0
			1218	797	209	206	6		

- Molecule 19 is a protein called Coiled-coil domain containing 114.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H1	192	Total	C	N	O	S	0	0
			1571	959	306	300	6		
19	H2	250	Total	C	N	O	S	0	0
			2069	1261	414	386	8		
19	H3	105	Total	C	N	O	S	0	0
			880	530	182	164	4		

- Molecule 20 is a protein called Outer dynein arm-docking complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	H4	193	Total	C	N	O	S	0	0
			1625	1009	304	308	4		
20	H5	249	Total	C	N	O	S	0	0
			2097	1303	390	399	5		
20	H6	125	Total	C	N	O	S	0	0
			1060	666	198	195	1		

- Molecule 21 is a protein called Armadillo repeat containing 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	H7	580	Total	C	N	O	0	0
			2867	1707	580	580		
21	H8	579	Total	C	N	O	0	0
			2862	1704	579	579		

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Mol	Chain	Residues	Atoms				AltConf	Trace
21	H9	358	Total	C	N	O	0	0
			1768	1052	358	358		

- Molecule 22 is a protein called TTC25 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I1	192	Total	C	N	O	S	0	0
			1300	812	232	249	7		
22	I2	192	Total	C	N	O	S	0	0
			1300	812	232	249	7		

- Molecule 23 is a protein called EF-hand calcium-binding domain-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	I3	186	Total	C	N	O	0	0
			921	549	186	186		
23	I4	187	Total	C	N	O	0	0
			925	551	187	187		

- Molecule 24 is a protein called RIB43A-like with coiled-coils protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	31	Total	C	N	O		0	0
			270	170	58	42			
24	P	373	Total	C	N	O	S	0	0
			3104	1890	607	592	15		
24	Q	39	Total	C	N	O	S	0	0
			317	193	58	63	3		
24	R	249	Total	C	N	O	S	0	0
			2041	1239	395	397	10		
24	S	170	Total	C	N	O	S	0	0
			1412	857	277	271	7		

- Molecule 25 is a protein called EF-hand domain containing 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	452	Total	C	N	O	S	0	0
			3726	2406	627	678	15		
25	U	452	Total	C	N	O	S	0	0
			3726	2406	627	678	15		
25	V	452	Total	C	N	O	S	0	0
			3726	2406	627	678	15		

- Molecule 26 is a protein called EFHC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	553	Total	C	N	O	S	0	0
			4558	2931	763	841	23		
26	X	636	Total	C	N	O	S	0	0
			5234	3358	881	968	27		
26	Y	636	Total	C	N	O	S	0	0
			5234	3358	881	968	27		
26	Z	449	Total	C	N	O	S	0	0
			3691	2365	618	687	21		

- Molecule 27 is a protein called Cilia- and flagella-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	XA	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
27	XB	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
27	XC	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
27	XD	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
27	XE	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
27	XF	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		
27	XG	184	Total	C	N	O	S	0	0
			1532	984	268	273	7		

- Molecule 28 is a protein called PACRG protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	YB	219	Total	C	N	O	S	0	0
			1767	1144	298	316	9		
28	YC	219	Total	C	N	O	S	0	0
			1767	1144	298	316	9		
28	YD	219	Total	C	N	O	S	0	0
			1767	1144	298	316	9		
28	YE	219	Total	C	N	O	S	0	0
			1767	1144	298	316	9		
28	YF	219	Total	C	N	O	S	0	0
			1767	1144	298	316	9		
28	YG	219	Total	C	N	O	S	0	0
			1767	1144	298	316	9		

- Molecule 29 is a protein called Cilia and flagella associated protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	169	Total	C	N	O	S	0	0
			1426	879	270	269	8		
29	b	332	Total	C	N	O	S	0	0
			2854	1723	570	549	12		
29	c	277	Total	C	N	O	S	0	0
			2361	1445	446	455	15		
29	d	215	Total	C	N	O	S	0	0
			1830	1110	368	346	6		

- Molecule 30 is a protein called Cilia and flagella associated protein 52.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	610	Total	C	N	O	S	0	0
			4722	2990	823	877	32		
30	f	610	Total	C	N	O	S	0	0
			4722	2990	823	877	32		
30	g	610	Total	C	N	O	S	0	0
			4722	2990	823	877	32		

- Molecule 31 is a protein called Enkurin, TRPC channel interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	148	Total	C	N	O	S	0	0
			1220	772	213	231	4		
31	i	235	Total	C	N	O	S	0	0
			1939	1242	336	354	7		
31	j	235	Total	C	N	O	S	0	0
			1939	1242	336	354	7		
31	k	235	Total	C	N	O	S	0	0
			1939	1242	336	354	7		

- Molecule 32 is a protein called Protein Flattop.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	l	114	Total	C	N	O	S	0	0
			894	569	162	161	2		
32	m	116	Total	C	N	O	S	0	0
			910	580	165	163	2		
32	n	118	Total	C	N	O	S	0	0
			928	590	169	167	2		

- Molecule 33 is a protein called Coiled-coil domain containing 173.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	378	Total	C	N	O	S	0	0
			2068	1246	415	405	2		
33	p	100	Total	C	N	O	S	0	0
			835	524	144	164	3		

- Molecule 34 is a protein called Chromosome 3 C1orf194 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	q	79	Total	C	N	O		0	0
			631	395	116	120			
34	r	79	Total	C	N	O		0	0
			631	395	116	120			
34	s	79	Total	C	N	O		0	0
			631	395	116	120			

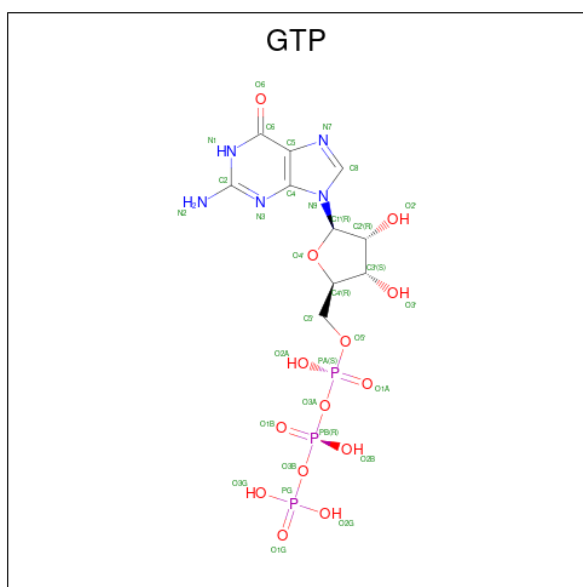
- Molecule 35 is a protein called EFCAB6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	178	Total	C	N	O		0	0
			882	526	178	178			

- Molecule 36 is a protein called Pierce1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	y	63	Total	C	N	O	S	0	0
			515	329	88	94	4		
36	z	115	Total	C	N	O	S	0	0
			950	602	168	175	5		

- Molecule 37 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
37	AA	1	Total 32	C 10	N 5	O 14	P 3	0
37	AC	1	Total 32	C 10	N 5	O 14	P 3	0
37	AE	1	Total 32	C 10	N 5	O 14	P 3	0
37	AG	1	Total 32	C 10	N 5	O 14	P 3	0
37	AI	1	Total 32	C 10	N 5	O 14	P 3	0
37	AK	1	Total 32	C 10	N 5	O 14	P 3	0
37	AM	1	Total 32	C 10	N 5	O 14	P 3	0
37	BA	1	Total 32	C 10	N 5	O 14	P 3	0
37	BC	1	Total 32	C 10	N 5	O 14	P 3	0
37	BE	1	Total 32	C 10	N 5	O 14	P 3	0
37	BG	1	Total 32	C 10	N 5	O 14	P 3	0
37	BI	1	Total 32	C 10	N 5	O 14	P 3	0
37	BK	1	Total 32	C 10	N 5	O 14	P 3	0
37	BM	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	CA	1	Total 32	C 10	N 5	O 14	P 3	0
37	CC	1	Total 32	C 10	N 5	O 14	P 3	0
37	CE	1	Total 32	C 10	N 5	O 14	P 3	0
37	CG	1	Total 32	C 10	N 5	O 14	P 3	0
37	CI	1	Total 32	C 10	N 5	O 14	P 3	0
37	CK	1	Total 32	C 10	N 5	O 14	P 3	0
37	CM	1	Total 32	C 10	N 5	O 14	P 3	0
37	DA	1	Total 32	C 10	N 5	O 14	P 3	0
37	DC	1	Total 32	C 10	N 5	O 14	P 3	0
37	DE	1	Total 32	C 10	N 5	O 14	P 3	0
37	DG	1	Total 32	C 10	N 5	O 14	P 3	0
37	DI	1	Total 32	C 10	N 5	O 14	P 3	0
37	DK	1	Total 32	C 10	N 5	O 14	P 3	0
37	DM	1	Total 32	C 10	N 5	O 14	P 3	0
37	EC	1	Total 32	C 10	N 5	O 14	P 3	0
37	EE	1	Total 32	C 10	N 5	O 14	P 3	0
37	EG	1	Total 32	C 10	N 5	O 14	P 3	0
37	EI	1	Total 32	C 10	N 5	O 14	P 3	0
37	EK	1	Total 32	C 10	N 5	O 14	P 3	0
37	EM	1	Total 32	C 10	N 5	O 14	P 3	0
37	FC	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	FE	1	Total 32	C 10	N 5	O 14	P 3	0
37	FG	1	Total 32	C 10	N 5	O 14	P 3	0
37	FI	1	Total 32	C 10	N 5	O 14	P 3	0
37	FK	1	Total 32	C 10	N 5	O 14	P 3	0
37	FM	1	Total 32	C 10	N 5	O 14	P 3	0
37	GC	1	Total 32	C 10	N 5	O 14	P 3	0
37	GE	1	Total 32	C 10	N 5	O 14	P 3	0
37	GG	1	Total 32	C 10	N 5	O 14	P 3	0
37	GI	1	Total 32	C 10	N 5	O 14	P 3	0
37	GK	1	Total 32	C 10	N 5	O 14	P 3	0
37	GM	1	Total 32	C 10	N 5	O 14	P 3	0
37	HC	1	Total 32	C 10	N 5	O 14	P 3	0
37	HE	1	Total 32	C 10	N 5	O 14	P 3	0
37	HG	1	Total 32	C 10	N 5	O 14	P 3	0
37	HI	1	Total 32	C 10	N 5	O 14	P 3	0
37	HK	1	Total 32	C 10	N 5	O 14	P 3	0
37	HM	1	Total 32	C 10	N 5	O 14	P 3	0
37	HO	1	Total 32	C 10	N 5	O 14	P 3	0
37	IC	1	Total 32	C 10	N 5	O 14	P 3	0
37	IE	1	Total 32	C 10	N 5	O 14	P 3	0
37	IG	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	II	1	Total 32	C 10	N 5	O 14	P 3	0
37	IK	1	Total 32	C 10	N 5	O 14	P 3	0
37	IM	1	Total 32	C 10	N 5	O 14	P 3	0
37	IO	1	Total 32	C 10	N 5	O 14	P 3	0
37	JC	1	Total 32	C 10	N 5	O 14	P 3	0
37	JE	1	Total 32	C 10	N 5	O 14	P 3	0
37	JG	1	Total 32	C 10	N 5	O 14	P 3	0
37	JI	1	Total 32	C 10	N 5	O 14	P 3	0
37	JK	1	Total 32	C 10	N 5	O 14	P 3	0
37	JM	1	Total 32	C 10	N 5	O 14	P 3	0
37	KC	1	Total 32	C 10	N 5	O 14	P 3	0
37	KE	1	Total 32	C 10	N 5	O 14	P 3	0
37	KG	1	Total 32	C 10	N 5	O 14	P 3	0
37	KI	1	Total 32	C 10	N 5	O 14	P 3	0
37	KK	1	Total 32	C 10	N 5	O 14	P 3	0
37	KM	1	Total 32	C 10	N 5	O 14	P 3	0
37	KO	1	Total 32	C 10	N 5	O 14	P 3	0
37	LC	1	Total 32	C 10	N 5	O 14	P 3	0
37	LE	1	Total 32	C 10	N 5	O 14	P 3	0
37	LG	1	Total 32	C 10	N 5	O 14	P 3	0
37	LI	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	LK	1	Total 32	C 10	N 5	O 14	P 3	0
37	LM	1	Total 32	C 10	N 5	O 14	P 3	0
37	MC	1	Total 32	C 10	N 5	O 14	P 3	0
37	ME	1	Total 32	C 10	N 5	O 14	P 3	0
37	MG	1	Total 32	C 10	N 5	O 14	P 3	0
37	MI	1	Total 32	C 10	N 5	O 14	P 3	0
37	MK	1	Total 32	C 10	N 5	O 14	P 3	0
37	MM	1	Total 32	C 10	N 5	O 14	P 3	0
37	NA	1	Total 32	C 10	N 5	O 14	P 3	0
37	NC	1	Total 32	C 10	N 5	O 14	P 3	0
37	NE	1	Total 32	C 10	N 5	O 14	P 3	0
37	NG	1	Total 32	C 10	N 5	O 14	P 3	0
37	NI	1	Total 32	C 10	N 5	O 14	P 3	0
37	NK	1	Total 32	C 10	N 5	O 14	P 3	0
37	OA	1	Total 32	C 10	N 5	O 14	P 3	0
37	OC	1	Total 32	C 10	N 5	O 14	P 3	0
37	OE	1	Total 32	C 10	N 5	O 14	P 3	0
37	OG	1	Total 32	C 10	N 5	O 14	P 3	0
37	OI	1	Total 32	C 10	N 5	O 14	P 3	0
37	OK	1	Total 32	C 10	N 5	O 14	P 3	0
37	PA	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	PC	1	Total 32	C 10	N 5	O 14	P 3	0
37	PE	1	Total 32	C 10	N 5	O 14	P 3	0
37	PG	1	Total 32	C 10	N 5	O 14	P 3	0
37	PI	1	Total 32	C 10	N 5	O 14	P 3	0
37	PK	1	Total 32	C 10	N 5	O 14	P 3	0
37	PM	1	Total 32	C 10	N 5	O 14	P 3	0
37	QA	1	Total 32	C 10	N 5	O 14	P 3	0
37	QC	1	Total 32	C 10	N 5	O 14	P 3	0
37	QE	1	Total 32	C 10	N 5	O 14	P 3	0
37	QG	1	Total 32	C 10	N 5	O 14	P 3	0
37	QI	1	Total 32	C 10	N 5	O 14	P 3	0
37	QK	1	Total 32	C 10	N 5	O 14	P 3	0
37	QM	1	Total 32	C 10	N 5	O 14	P 3	0
37	RA	1	Total 32	C 10	N 5	O 14	P 3	0
37	RC	1	Total 32	C 10	N 5	O 14	P 3	0
37	RE	1	Total 32	C 10	N 5	O 14	P 3	0
37	RG	1	Total 32	C 10	N 5	O 14	P 3	0
37	RI	1	Total 32	C 10	N 5	O 14	P 3	0
37	RK	1	Total 32	C 10	N 5	O 14	P 3	0
37	RM	1	Total 32	C 10	N 5	O 14	P 3	0
37	SA	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	SC	1	Total 32	C 10	N 5	O 14	P 3	0
37	SE	1	Total 32	C 10	N 5	O 14	P 3	0
37	SG	1	Total 32	C 10	N 5	O 14	P 3	0
37	SI	1	Total 32	C 10	N 5	O 14	P 3	0
37	SK	1	Total 32	C 10	N 5	O 14	P 3	0
37	SM	1	Total 32	C 10	N 5	O 14	P 3	0
37	TC	1	Total 32	C 10	N 5	O 14	P 3	0
37	TE	1	Total 32	C 10	N 5	O 14	P 3	0
37	TG	1	Total 32	C 10	N 5	O 14	P 3	0
37	TI	1	Total 32	C 10	N 5	O 14	P 3	0
37	TK	1	Total 32	C 10	N 5	O 14	P 3	0
37	TM	1	Total 32	C 10	N 5	O 14	P 3	0
37	UC	1	Total 32	C 10	N 5	O 14	P 3	0
37	UE	1	Total 32	C 10	N 5	O 14	P 3	0
37	UG	1	Total 32	C 10	N 5	O 14	P 3	0
37	UI	1	Total 32	C 10	N 5	O 14	P 3	0
37	UK	1	Total 32	C 10	N 5	O 14	P 3	0
37	UM	1	Total 32	C 10	N 5	O 14	P 3	0
37	VC	1	Total 32	C 10	N 5	O 14	P 3	0
37	VE	1	Total 32	C 10	N 5	O 14	P 3	0
37	VG	1	Total 32	C 10	N 5	O 14	P 3	0

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Mol	Chain	Residues	Atoms					AltConf
37	VI	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	VK	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	VM	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	WC	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	WE	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	WG	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	WI	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	WK	1	Total	C	N	O	P	0
			32	10	5	14	3	
37	WM	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 38 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
38	AA	1	Total	Mg	0
			1	1	
38	AC	1	Total	Mg	0
			1	1	
38	AE	1	Total	Mg	0
			1	1	
38	AG	1	Total	Mg	0
			1	1	
38	AI	1	Total	Mg	0
			1	1	
38	AK	1	Total	Mg	0
			1	1	
38	AM	1	Total	Mg	0
			1	1	
38	BA	1	Total	Mg	0
			1	1	
38	BC	1	Total	Mg	0
			1	1	
38	BE	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
38	BG	1	Total 1	Mg 1	0
38	BI	1	Total 1	Mg 1	0
38	BK	1	Total 1	Mg 1	0
38	BM	1	Total 1	Mg 1	0
38	CA	1	Total 1	Mg 1	0
38	CC	1	Total 1	Mg 1	0
38	CE	1	Total 1	Mg 1	0
38	CG	1	Total 1	Mg 1	0
38	CI	1	Total 1	Mg 1	0
38	CK	1	Total 1	Mg 1	0
38	CM	1	Total 1	Mg 1	0
38	DA	1	Total 1	Mg 1	0
38	DC	1	Total 1	Mg 1	0
38	DE	1	Total 1	Mg 1	0
38	DG	1	Total 1	Mg 1	0
38	DI	1	Total 1	Mg 1	0
38	DK	1	Total 1	Mg 1	0
38	DM	1	Total 1	Mg 1	0
38	EC	1	Total 1	Mg 1	0
38	EE	1	Total 1	Mg 1	0
38	EG	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
38	EI	1	Total 1	Mg 1	0
38	EK	1	Total 1	Mg 1	0
38	EM	1	Total 1	Mg 1	0
38	FC	1	Total 1	Mg 1	0
38	FE	1	Total 1	Mg 1	0
38	FG	1	Total 1	Mg 1	0
38	FI	1	Total 1	Mg 1	0
38	FK	1	Total 1	Mg 1	0
38	FM	1	Total 1	Mg 1	0
38	GC	1	Total 1	Mg 1	0
38	GE	1	Total 1	Mg 1	0
38	GG	1	Total 1	Mg 1	0
38	GI	1	Total 1	Mg 1	0
38	GK	1	Total 1	Mg 1	0
38	GM	1	Total 1	Mg 1	0
38	HC	1	Total 1	Mg 1	0
38	HE	1	Total 1	Mg 1	0
38	HG	1	Total 1	Mg 1	0
38	HI	1	Total 1	Mg 1	0
38	HK	1	Total 1	Mg 1	0
38	HM	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
38	HO	1	Total 1	Mg 1	0
38	IC	1	Total 1	Mg 1	0
38	IE	1	Total 1	Mg 1	0
38	IG	1	Total 1	Mg 1	0
38	II	1	Total 1	Mg 1	0
38	IK	1	Total 1	Mg 1	0
38	IM	1	Total 1	Mg 1	0
38	IO	1	Total 1	Mg 1	0
38	JC	1	Total 1	Mg 1	0
38	JE	1	Total 1	Mg 1	0
38	JG	1	Total 1	Mg 1	0
38	JI	1	Total 1	Mg 1	0
38	JK	1	Total 1	Mg 1	0
38	JM	1	Total 1	Mg 1	0
38	KC	1	Total 1	Mg 1	0
38	KE	1	Total 1	Mg 1	0
38	KG	1	Total 1	Mg 1	0
38	KI	1	Total 1	Mg 1	0
38	KK	1	Total 1	Mg 1	0
38	KM	1	Total 1	Mg 1	0
38	KO	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
38	LC	1	Total 1	Mg 1	0
38	LE	1	Total 1	Mg 1	0
38	LG	1	Total 1	Mg 1	0
38	LI	1	Total 1	Mg 1	0
38	LK	1	Total 1	Mg 1	0
38	LM	1	Total 1	Mg 1	0
38	MC	1	Total 1	Mg 1	0
38	ME	1	Total 1	Mg 1	0
38	MG	1	Total 1	Mg 1	0
38	MI	1	Total 1	Mg 1	0
38	MK	1	Total 1	Mg 1	0
38	MM	1	Total 1	Mg 1	0
38	NA	1	Total 1	Mg 1	0
38	NC	1	Total 1	Mg 1	0
38	NE	1	Total 1	Mg 1	0
38	NG	1	Total 1	Mg 1	0
38	NI	1	Total 1	Mg 1	0
38	NK	1	Total 1	Mg 1	0
38	OA	1	Total 1	Mg 1	0
38	OC	1	Total 1	Mg 1	0
38	OE	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
38	OG	1	Total 1	Mg 1	0
38	OI	1	Total 1	Mg 1	0
38	OK	1	Total 1	Mg 1	0
38	PA	1	Total 1	Mg 1	0
38	PC	1	Total 1	Mg 1	0
38	PE	1	Total 1	Mg 1	0
38	PG	1	Total 1	Mg 1	0
38	PI	1	Total 1	Mg 1	0
38	PK	1	Total 1	Mg 1	0
38	PM	1	Total 1	Mg 1	0
38	QA	1	Total 1	Mg 1	0
38	QC	1	Total 1	Mg 1	0
38	QE	1	Total 1	Mg 1	0
38	QG	1	Total 1	Mg 1	0
38	QI	1	Total 1	Mg 1	0
38	QK	1	Total 1	Mg 1	0
38	QM	1	Total 1	Mg 1	0
38	RA	1	Total 1	Mg 1	0
38	RC	1	Total 1	Mg 1	0
38	RE	1	Total 1	Mg 1	0
38	RG	1	Total 1	Mg 1	0

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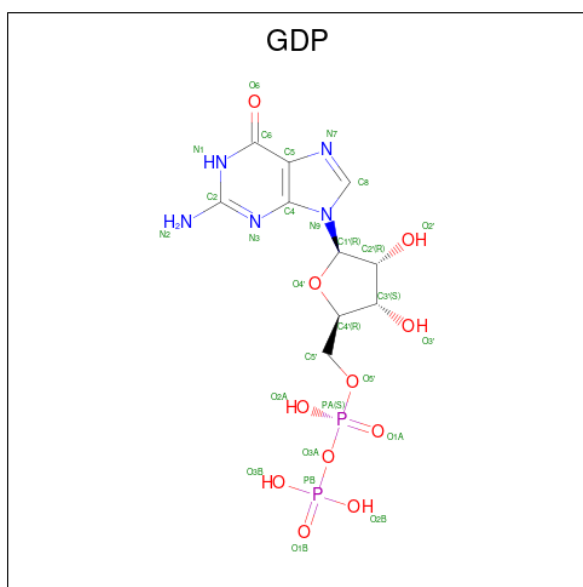
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
38	RI	1	1	1	0
38	RK	1	1	1	0
38	RM	1	1	1	0
38	SA	1	1	1	0
38	SC	1	1	1	0
38	SE	1	1	1	0
38	SG	1	1	1	0
38	SI	1	1	1	0
38	SK	1	1	1	0
38	SM	1	1	1	0
38	TC	1	1	1	0
38	TE	1	1	1	0
38	TG	1	1	1	0
38	TI	1	1	1	0
38	TK	1	1	1	0
38	TM	1	1	1	0
38	UC	1	1	1	0
38	UE	1	1	1	0
38	UG	1	1	1	0
38	UI	1	1	1	0
38	UK	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
38	UM	1	Total 1	Mg 1	0
38	VC	1	Total 1	Mg 1	0
38	VE	1	Total 1	Mg 1	0
38	VG	1	Total 1	Mg 1	0
38	VI	1	Total 1	Mg 1	0
38	VK	1	Total 1	Mg 1	0
38	VM	1	Total 1	Mg 1	0
38	WC	1	Total 1	Mg 1	0
38	WE	1	Total 1	Mg 1	0
38	WG	1	Total 1	Mg 1	0
38	WI	1	Total 1	Mg 1	0
38	WK	1	Total 1	Mg 1	0
38	WM	1	Total 1	Mg 1	0

- Molecule 39 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
39	AB	1	Total 28	C 10	N 5	O 11	P 2	0
39	AD	1	Total 28	C 10	N 5	O 11	P 2	0
39	AF	1	Total 28	C 10	N 5	O 11	P 2	0
39	AH	1	Total 28	C 10	N 5	O 11	P 2	0
39	AJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	AL	1	Total 28	C 10	N 5	O 11	P 2	0
39	BB	1	Total 28	C 10	N 5	O 11	P 2	0
39	BD	1	Total 28	C 10	N 5	O 11	P 2	0
39	BF	1	Total 28	C 10	N 5	O 11	P 2	0
39	BH	1	Total 28	C 10	N 5	O 11	P 2	0
39	BJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	BL	1	Total 28	C 10	N 5	O 11	P 2	0
39	CB	1	Total 28	C 10	N 5	O 11	P 2	0
39	CD	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
39	CF	1	Total 28	C 10	N 5	O 11	P 2	0
39	CH	1	Total 28	C 10	N 5	O 11	P 2	0
39	CJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	CL	1	Total 28	C 10	N 5	O 11	P 2	0
39	DB	1	Total 28	C 10	N 5	O 11	P 2	0
39	DD	1	Total 28	C 10	N 5	O 11	P 2	0
39	DF	1	Total 28	C 10	N 5	O 11	P 2	0
39	DH	1	Total 28	C 10	N 5	O 11	P 2	0
39	DJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	DL	1	Total 28	C 10	N 5	O 11	P 2	0
39	DN	1	Total 28	C 10	N 5	O 11	P 2	0
39	EB	1	Total 28	C 10	N 5	O 11	P 2	0
39	ED	1	Total 28	C 10	N 5	O 11	P 2	0
39	EF	1	Total 28	C 10	N 5	O 11	P 2	0
39	EH	1	Total 28	C 10	N 5	O 11	P 2	0
39	EJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	EL	1	Total 28	C 10	N 5	O 11	P 2	0
39	EN	1	Total 28	C 10	N 5	O 11	P 2	0
39	FB	1	Total 28	C 10	N 5	O 11	P 2	0
39	FD	1	Total 28	C 10	N 5	O 11	P 2	0
39	FF	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
39	FH	1	Total 28	C 10	N 5	O 11	P 2	0
39	FJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	FL	1	Total 28	C 10	N 5	O 11	P 2	0
39	FN	1	Total 28	C 10	N 5	O 11	P 2	0
39	GB	1	Total 28	C 10	N 5	O 11	P 2	0
39	GD	1	Total 28	C 10	N 5	O 11	P 2	0
39	GF	1	Total 28	C 10	N 5	O 11	P 2	0
39	GH	1	Total 28	C 10	N 5	O 11	P 2	0
39	GJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	GL	1	Total 28	C 10	N 5	O 11	P 2	0
39	GN	1	Total 28	C 10	N 5	O 11	P 2	0
39	HB	1	Total 28	C 10	N 5	O 11	P 2	0
39	HD	1	Total 28	C 10	N 5	O 11	P 2	0
39	HF	1	Total 28	C 10	N 5	O 11	P 2	0
39	HH	1	Total 28	C 10	N 5	O 11	P 2	0
39	HJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	HL	1	Total 28	C 10	N 5	O 11	P 2	0
39	HN	1	Total 28	C 10	N 5	O 11	P 2	0
39	IB	1	Total 28	C 10	N 5	O 11	P 2	0
39	ID	1	Total 28	C 10	N 5	O 11	P 2	0
39	IF	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
39	IH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	IJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	IL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	IN	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JD	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JF	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	JN	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KD	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KF	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	KN	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	LB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	LD	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	LF	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
39	LH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	LJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	LL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	LN	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	MB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	MD	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	MF	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	MH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	MJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	ML	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	MN	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	N0	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	NB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	ND	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	NF	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	NH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	NJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	NL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	O0	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	OB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	OD	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
39	OF	1	Total 28	C 10	N 5	O 11	P 2	0
39	OH	1	Total 28	C 10	N 5	O 11	P 2	0
39	OJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	OL	1	Total 28	C 10	N 5	O 11	P 2	0
39	PB	1	Total 28	C 10	N 5	O 11	P 2	0
39	PD	1	Total 28	C 10	N 5	O 11	P 2	0
39	PF	1	Total 28	C 10	N 5	O 11	P 2	0
39	PH	1	Total 28	C 10	N 5	O 11	P 2	0
39	PJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	PL	1	Total 28	C 10	N 5	O 11	P 2	0
39	QB	1	Total 28	C 10	N 5	O 11	P 2	0
39	QD	1	Total 28	C 10	N 5	O 11	P 2	0
39	QF	1	Total 28	C 10	N 5	O 11	P 2	0
39	QH	1	Total 28	C 10	N 5	O 11	P 2	0
39	QJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	QL	1	Total 28	C 10	N 5	O 11	P 2	0
39	RB	1	Total 28	C 10	N 5	O 11	P 2	0
39	RD	1	Total 28	C 10	N 5	O 11	P 2	0
39	RF	1	Total 28	C 10	N 5	O 11	P 2	0
39	RH	1	Total 28	C 10	N 5	O 11	P 2	0
39	RJ	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
39	RL	1	Total 28	C 10	N 5	O 11	P 2	0
39	SB	1	Total 28	C 10	N 5	O 11	P 2	0
39	SD	1	Total 28	C 10	N 5	O 11	P 2	0
39	SF	1	Total 28	C 10	N 5	O 11	P 2	0
39	SH	1	Total 28	C 10	N 5	O 11	P 2	0
39	SJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	SL	1	Total 28	C 10	N 5	O 11	P 2	0
39	TB	1	Total 28	C 10	N 5	O 11	P 2	0
39	TD	1	Total 28	C 10	N 5	O 11	P 2	0
39	TF	1	Total 28	C 10	N 5	O 11	P 2	0
39	TH	1	Total 28	C 10	N 5	O 11	P 2	0
39	TJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	TL	1	Total 28	C 10	N 5	O 11	P 2	0
39	UB	1	Total 28	C 10	N 5	O 11	P 2	0
39	UD	1	Total 28	C 10	N 5	O 11	P 2	0
39	UF	1	Total 28	C 10	N 5	O 11	P 2	0
39	UH	1	Total 28	C 10	N 5	O 11	P 2	0
39	UJ	1	Total 28	C 10	N 5	O 11	P 2	0
39	UL	1	Total 28	C 10	N 5	O 11	P 2	0
39	UN	1	Total 28	C 10	N 5	O 11	P 2	0
39	VB	1	Total 28	C 10	N 5	O 11	P 2	0

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Mol	Chain	Residues	Atoms					AltConf
39	VD	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	VF	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	VH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	VJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	VL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	VN	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WB	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WD	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WF	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WH	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WJ	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WL	1	Total	C	N	O	P	0
			28	10	5	11	2	
39	WN	1	Total	C	N	O	P	0
			28	10	5	11	2	

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	80503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (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 451 ligands modelled in this entry, 149 are monoatomic - leaving 302 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
39	GDP	SJ	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.74	8 (17%)
39	GDP	WN	502	-	29,30,30	1.21	2 (6%)	45,47,47	1.93	8 (17%)
37	GTP	PM	501	-	33,34,34	1.04	3 (9%)	50,54,54	1.49	7 (14%)
39	GDP	LD	502	-	29,30,30	1.26	3 (10%)	45,47,47	1.81	8 (17%)
39	GDP	IB	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.94	8 (17%)
39	GDP	CJ	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.91	10 (22%)
37	GTP	LG	501	-	33,34,34	0.99	1 (3%)	50,54,54	1.75	9 (18%)
37	GTP	TK	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.58	10 (20%)
39	GDP	VL	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.91	9 (20%)
37	GTP	GG	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.60	9 (18%)
37	GTP	HI	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.62	10 (20%)
39	GDP	LH	502	-	29,30,30	1.24	3 (10%)	45,47,47	1.83	8 (17%)
37	GTP	QG	501	-	33,34,34	0.94	0	50,54,54	1.53	8 (16%)
39	GDP	DJ	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.86	7 (15%)
37	GTP	EG	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.55	9 (18%)
39	GDP	NJ	502	-	29,30,30	1.19	4 (13%)	45,47,47	1.73	7 (15%)
39	GDP	PJ	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.90	8 (17%)
37	GTP	TI	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.58	9 (18%)
39	GDP	IF	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.82	7 (15%)
37	GTP	FE	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.72	11 (22%)
37	GTP	MM	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.59	9 (18%)
37	GTP	BC	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.59	8 (16%)
39	GDP	WF	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.80	6 (13%)
39	GDP	ED	502	-	29,30,30	1.19	4 (13%)	45,47,47	1.81	8 (17%)
37	GTP	AI	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.68	9 (18%)
37	GTP	SI	501	-	33,34,34	0.92	0	50,54,54	1.61	8 (16%)
37	GTP	UI	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.64	8 (16%)
37	GTP	GK	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.66	9 (18%)
37	GTP	JI	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.76	6 (12%)
37	GTP	NA	501	-	33,34,34	0.91	0	50,54,54	1.50	9 (18%)
39	GDP	JD	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.92	8 (17%)
39	GDP	EH	502	-	29,30,30	1.19	4 (13%)	45,47,47	1.69	5 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	GDP	GN	502	-	29,30,30	1.16	4 (13%)	45,47,47	1.84	8 (17%)
39	GDP	DF	502	-	29,30,30	1.20	3 (10%)	45,47,47	1.84	8 (17%)
39	GDP	QL	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.95	9 (20%)
37	GTP	RK	501	-	33,34,34	1.05	4 (12%)	50,54,54	1.69	9 (18%)
39	GDP	UJ	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.83	8 (17%)
39	GDP	BJ	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.74	7 (15%)
37	GTP	SK	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.63	8 (16%)
37	GTP	LM	501	-	33,34,34	1.07	2 (6%)	50,54,54	1.67	9 (18%)
37	GTP	WC	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.64	10 (20%)
37	GTP	TM	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.64	12 (24%)
37	GTP	UG	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.59	8 (16%)
37	GTP	VG	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.70	9 (18%)
37	GTP	NI	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.57	9 (18%)
37	GTP	OG	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.60	10 (20%)
39	GDP	ND	502	-	29,30,30	1.15	4 (13%)	45,47,47	1.75	7 (15%)
39	GDP	SD	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.80	9 (20%)
37	GTP	SE	501	-	33,34,34	0.93	3 (9%)	50,54,54	1.62	8 (16%)
37	GTP	HO	501	-	33,34,34	0.88	2 (6%)	50,54,54	1.60	8 (16%)
37	GTP	DI	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.68	12 (24%)
39	GDP	ID	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.83	7 (15%)
39	GDP	RL	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.82	7 (15%)
39	GDP	N0	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.78	7 (15%)
37	GTP	MG	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.46	7 (14%)
39	GDP	WD	502	-	29,30,30	1.16	4 (13%)	45,47,47	1.93	9 (20%)
39	GDP	IN	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.94	11 (24%)
37	GTP	LE	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.72	9 (18%)
37	GTP	SM	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.68	10 (20%)
39	GDP	EN	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.68	6 (13%)
37	GTP	KO	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.62	10 (20%)
37	GTP	IO	501	-	33,34,34	0.90	1 (3%)	50,54,54	1.76	10 (20%)
39	GDP	MH	502	-	29,30,30	1.17	4 (13%)	45,47,47	1.71	7 (15%)
37	GTP	LI	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.76	10 (20%)
37	GTP	WK	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.66	10 (20%)
39	GDP	HD	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.81	7 (15%)
37	GTP	CM	501	-	33,34,34	0.91	2 (6%)	50,54,54	1.78	11 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
37	GTP	AA	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.71	12 (24%)
37	GTP	FC	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.65	6 (12%)
37	GTP	DC	501	-	33,34,34	1.04	2 (6%)	50,54,54	1.57	9 (18%)
37	GTP	KI	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.68	9 (18%)
37	GTP	CK	501	-	33,34,34	0.88	1 (3%)	50,54,54	1.61	10 (20%)
39	GDP	NB	502	-	29,30,30	1.17	4 (13%)	45,47,47	1.78	7 (15%)
39	GDP	QJ	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.81	8 (17%)
39	GDP	EJ	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.77	7 (15%)
37	GTP	KK	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.73	10 (20%)
39	GDP	DL	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.87	6 (13%)
39	GDP	RH	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.86	8 (17%)
37	GTP	JE	501	-	33,34,34	1.03	1 (3%)	50,54,54	1.66	8 (16%)
39	GDP	VD	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.86	10 (22%)
37	GTP	QI	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.67	11 (22%)
37	GTP	DK	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.70	10 (20%)
37	GTP	NK	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.65	10 (20%)
37	GTP	KG	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.60	10 (20%)
37	GTP	PC	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.69	9 (18%)
39	GDP	TF	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.82	6 (13%)
37	GTP	HK	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
39	GDP	TL	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	6 (13%)
39	GDP	IH	502	-	29,30,30	1.20	3 (10%)	45,47,47	1.87	8 (17%)
39	GDP	LL	502	-	29,30,30	1.27	3 (10%)	45,47,47	1.83	8 (17%)
39	GDP	VH	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.84	8 (17%)
37	GTP	LK	501	-	33,34,34	0.99	1 (3%)	50,54,54	1.80	11 (22%)
39	GDP	BB	502	-	29,30,30	1.11	3 (10%)	45,47,47	1.99	10 (22%)
39	GDP	JB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.83	7 (15%)
39	GDP	PL	502	-	29,30,30	1.22	4 (13%)	45,47,47	1.71	6 (13%)
39	GDP	QD	502	-	29,30,30	1.14	2 (6%)	45,47,47	1.85	7 (15%)
37	GTP	HM	501	-	33,34,34	0.88	0	50,54,54	1.67	9 (18%)
37	GTP	OI	501	-	33,34,34	0.91	2 (6%)	50,54,54	1.61	9 (18%)
39	GDP	PF	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.90	9 (20%)
39	GDP	UD	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	5 (11%)
39	GDP	WB	502	-	29,30,30	1.13	4 (13%)	45,47,47	1.89	8 (17%)
39	GDP	LB	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.88	10 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
37	GTP	BE	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.54	8 (16%)
37	GTP	RC	501	-	33,34,34	1.06	2 (6%)	50,54,54	1.65	9 (18%)
39	GDP	TJ	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.79	6 (13%)
39	GDP	WJ	502	-	29,30,30	1.18	4 (13%)	45,47,47	1.83	6 (13%)
37	GTP	UK	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.61	11 (22%)
39	GDP	SF	502	-	29,30,30	1.17	4 (13%)	45,47,47	1.76	8 (17%)
39	GDP	TD	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.76	6 (13%)
37	GTP	DM	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.65	11 (22%)
39	GDP	FF	502	-	29,30,30	1.20	3 (10%)	45,47,47	1.76	9 (20%)
39	GDP	EB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.92	7 (15%)
37	GTP	WG	501	-	33,34,34	0.87	1 (3%)	50,54,54	1.62	10 (20%)
39	GDP	UH	502	-	29,30,30	1.13	3 (10%)	45,47,47	1.77	7 (15%)
39	GDP	HL	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.81	7 (15%)
39	GDP	QH	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.83	7 (15%)
39	GDP	UF	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.80	7 (15%)
39	GDP	GD	502	-	29,30,30	1.17	4 (13%)	45,47,47	1.74	6 (13%)
37	GTP	TG	501	-	33,34,34	0.94	0	50,54,54	1.52	11 (22%)
37	GTP	PG	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.64	11 (22%)
39	GDP	MD	502	-	29,30,30	1.24	4 (13%)	45,47,47	1.73	6 (13%)
39	GDP	KB	502	-	29,30,30	1.20	3 (10%)	45,47,47	1.70	6 (13%)
37	GTP	AG	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.66	9 (18%)
37	GTP	CI	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.71	9 (18%)
37	GTP	OE	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.61	9 (18%)
39	GDP	VB	502	-	29,30,30	1.12	2 (6%)	45,47,47	1.87	8 (17%)
37	GTP	GE	501	-	33,34,34	0.88	1 (3%)	50,54,54	1.63	8 (16%)
37	GTP	SG	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.57	8 (16%)
39	GDP	BL	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.76	8 (17%)
39	GDP	GB	502	-	29,30,30	1.16	4 (13%)	45,47,47	1.80	7 (15%)
39	GDP	DN	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.85	5 (11%)
39	GDP	DB	502	-	29,30,30	1.26	3 (10%)	45,47,47	1.93	9 (20%)
39	GDP	BH	502	-	29,30,30	1.19	4 (13%)	45,47,47	1.73	6 (13%)
39	GDP	GH	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.82	7 (15%)
37	GTP	TC	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.64	9 (18%)
39	GDP	BD	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.83	7 (15%)
37	GTP	FM	501	-	33,34,34	0.98	2 (6%)	50,54,54	1.67	12 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	GDP	WL	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.86	8 (17%)
39	GDP	GF	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.75	7 (15%)
37	GTP	EM	501	-	33,34,34	1.17	5 (15%)	50,54,54	1.72	9 (18%)
39	GDP	JJ	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.82	6 (13%)
37	GTP	EC	501	-	33,34,34	1.01	1 (3%)	50,54,54	1.70	7 (14%)
37	GTP	EK	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.44	6 (12%)
37	GTP	MK	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.59	10 (20%)
39	GDP	JF	502	-	29,30,30	1.25	3 (10%)	45,47,47	1.89	5 (11%)
39	GDP	FH	502	-	29,30,30	1.20	3 (10%)	45,47,47	1.78	10 (22%)
39	GDP	CH	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.91	8 (17%)
39	GDP	OF	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.76	8 (17%)
39	GDP	LJ	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.85	8 (17%)
39	GDP	RJ	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.77	8 (17%)
39	GDP	AL	502	-	29,30,30	1.20	4 (13%)	45,47,47	1.83	8 (17%)
39	GDP	FD	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.75	6 (13%)
39	GDP	VF	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.85	6 (13%)
39	GDP	AD	502	-	29,30,30	1.14	4 (13%)	45,47,47	1.78	7 (15%)
37	GTP	UM	501	-	33,34,34	0.89	2 (6%)	50,54,54	1.70	9 (18%)
39	GDP	HF	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
37	GTP	QE	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.73	9 (18%)
37	GTP	CE	501	-	33,34,34	0.90	2 (6%)	50,54,54	1.72	11 (22%)
37	GTP	FI	501	-	33,34,34	0.91	1 (3%)	50,54,54	2.08	14 (28%)
37	GTP	NG	501	-	33,34,34	0.99	1 (3%)	50,54,54	1.50	10 (20%)
39	GDP	WH	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.80	8 (17%)
37	GTP	JM	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.68	10 (20%)
37	GTP	VM	501	-	33,34,34	0.97	2 (6%)	50,54,54	1.77	9 (18%)
37	GTP	RA	501	-	33,34,34	0.94	0	50,54,54	1.63	8 (16%)
39	GDP	MB	502	-	29,30,30	1.12	4 (13%)	45,47,47	1.98	10 (22%)
37	GTP	RG	501	-	33,34,34	1.02	3 (9%)	50,54,54	1.66	8 (16%)
37	GTP	EI	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.68	9 (18%)
37	GTP	QM	501	-	33,34,34	1.11	5 (15%)	50,54,54	1.72	11 (22%)
39	GDP	OB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
37	GTP	RI	501	-	33,34,34	0.92	0	50,54,54	1.83	12 (24%)
37	GTP	SA	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.59	9 (18%)
37	GTP	FG	501	-	33,34,34	1.01	2 (6%)	50,54,54	1.82	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
37	GTP	JC	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.64	10 (20%)
37	GTP	NC	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.57	9 (18%)
37	GTP	KM	501	-	33,34,34	1.09	3 (9%)	50,54,54	1.64	8 (16%)
39	GDP	KF	502	-	29,30,30	1.21	4 (13%)	45,47,47	1.72	7 (15%)
37	GTP	RM	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.63	9 (18%)
39	GDP	SH	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.71	6 (13%)
39	GDP	JL	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.81	7 (15%)
39	GDP	RF	502	-	29,30,30	1.23	3 (10%)	45,47,47	1.75	6 (13%)
37	GTP	II	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.59	11 (22%)
39	GDP	HB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.87	8 (17%)
39	GDP	HN	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.84	8 (17%)
39	GDP	RD	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.79	6 (13%)
39	GDP	JN	502	-	29,30,30	1.24	3 (10%)	45,47,47	1.92	8 (17%)
39	GDP	LF	502	-	29,30,30	1.22	4 (13%)	45,47,47	1.76	8 (17%)
39	GDP	KD	502	-	29,30,30	1.23	4 (13%)	45,47,47	1.78	7 (15%)
39	GDP	UB	502	-	29,30,30	1.19	4 (13%)	45,47,47	1.77	6 (13%)
39	GDP	LN	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.80	8 (17%)
37	GTP	IM	501	-	33,34,34	1.18	5 (15%)	50,54,54	1.90	10 (20%)
39	GDP	O0	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.76	7 (15%)
37	GTP	BA	501	-	33,34,34	0.96	1 (3%)	50,54,54	1.62	9 (18%)
37	GTP	BI	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.58	10 (20%)
39	GDP	FJ	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.98	11 (24%)
39	GDP	GL	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.73	7 (15%)
39	GDP	OH	502	-	29,30,30	1.17	3 (10%)	45,47,47	1.79	8 (17%)
39	GDP	SB	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.73	8 (17%)
39	GDP	AF	502	-	29,30,30	1.23	3 (10%)	45,47,47	1.85	8 (17%)
37	GTP	MI	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.58	11 (22%)
39	GDP	CF	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.91	8 (17%)
37	GTP	JG	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.58	9 (18%)
39	GDP	TB	502	-	29,30,30	1.12	2 (6%)	45,47,47	1.79	8 (17%)
37	GTP	BK	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.56	8 (16%)
39	GDP	BF	502	-	29,30,30	1.18	4 (13%)	45,47,47	1.76	8 (17%)
39	GDP	ML	502	-	29,30,30	1.29	4 (13%)	45,47,47	1.72	7 (15%)
37	GTP	QC	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.67	10 (20%)
39	GDP	PB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.93	9 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
37	GTP	PE	501	-	33,34,34	1.00	1 (3%)	50,54,54	1.82	9 (18%)
39	GDP	AH	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.87	8 (17%)
39	GDP	KL	502	-	29,30,30	1.18	4 (13%)	45,47,47	1.78	7 (15%)
37	GTP	PI	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.67	9 (18%)
39	GDP	KJ	502	-	29,30,30	1.24	4 (13%)	45,47,47	1.80	8 (17%)
37	GTP	JK	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.71	9 (18%)
37	GTP	UE	501	-	33,34,34	0.88	0	50,54,54	1.62	10 (20%)
37	GTP	MC	501	-	33,34,34	1.06	2 (6%)	50,54,54	1.60	7 (14%)
37	GTP	VK	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.70	10 (20%)
37	GTP	PA	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.73	12 (24%)
37	GTP	VC	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.69	9 (18%)
39	GDP	KN	502	-	29,30,30	1.21	4 (13%)	45,47,47	1.74	7 (15%)
39	GDP	UL	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.80	7 (15%)
37	GTP	KC	501	-	33,34,34	1.09	3 (9%)	50,54,54	1.69	10 (20%)
37	GTP	VI	501	-	33,34,34	0.88	2 (6%)	50,54,54	1.71	10 (20%)
39	GDP	HH	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.80	6 (13%)
39	GDP	RB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	6 (13%)
39	GDP	CL	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.84	7 (15%)
37	GTP	DA	501	-	33,34,34	1.00	3 (9%)	50,54,54	1.71	11 (22%)
37	GTP	HE	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.67	8 (16%)
37	GTP	ME	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.69	10 (20%)
39	GDP	FB	502	-	29,30,30	1.16	2 (6%)	45,47,47	1.76	7 (15%)
37	GTP	CG	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.81	11 (22%)
39	GDP	HJ	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.76	6 (13%)
39	GDP	MN	502	-	29,30,30	1.23	3 (10%)	45,47,47	1.75	7 (15%)
39	GDP	DD	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.86	7 (15%)
39	GDP	DH	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.80	7 (15%)
37	GTP	AC	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.67	9 (18%)
37	GTP	OK	501	-	33,34,34	1.06	3 (9%)	50,54,54	1.79	12 (24%)
39	GDP	UN	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.79	7 (15%)
39	GDP	VJ	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.84	6 (13%)
39	GDP	PH	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.86	9 (20%)
39	GDP	IL	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.92	9 (20%)
39	GDP	PD	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.74	6 (13%)
37	GTP	UC	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.56	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	GDP	TH	502	-	29,30,30	1.20	2 (6%)	45,47,47	1.84	7 (15%)
39	GDP	FL	502	-	29,30,30	1.19	3 (10%)	45,47,47	1.77	7 (15%)
39	GDP	FN	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.70	5 (11%)
39	GDP	IJ	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.88	8 (17%)
37	GTP	DG	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.63	8 (16%)
37	GTP	HG	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.69	8 (16%)
39	GDP	NF	502	-	29,30,30	1.11	4 (13%)	45,47,47	1.76	7 (15%)
39	GDP	MF	502	-	29,30,30	1.21	3 (10%)	45,47,47	1.71	7 (15%)
39	GDP	NL	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.84	7 (15%)
37	GTP	VE	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.74	9 (18%)
39	GDP	CB	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	8 (17%)
37	GTP	IE	501	-	33,34,34	0.96	2 (6%)	50,54,54	1.64	11 (22%)
37	GTP	KE	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.60	8 (16%)
39	GDP	VN	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.89	9 (20%)
37	GTP	GI	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.84	10 (20%)
37	GTP	WI	501	-	33,34,34	0.93	1 (3%)	50,54,54	1.62	9 (18%)
39	GDP	AB	502	-	29,30,30	1.24	4 (13%)	45,47,47	1.76	6 (13%)
39	GDP	SL	502	-	29,30,30	1.18	3 (10%)	45,47,47	1.67	5 (11%)
37	GTP	OA	501	-	33,34,34	0.95	2 (6%)	50,54,54	1.61	9 (18%)
37	GTP	GC	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.60	9 (18%)
37	GTP	IC	501	-	33,34,34	0.88	2 (6%)	50,54,54	1.60	11 (22%)
39	GDP	EF	502	-	29,30,30	1.25	3 (10%)	45,47,47	1.76	6 (13%)
39	GDP	GJ	502	-	29,30,30	1.18	4 (13%)	45,47,47	1.75	6 (13%)
39	GDP	KH	502	-	29,30,30	1.24	4 (13%)	45,47,47	1.86	9 (20%)
37	GTP	LC	501	-	33,34,34	1.04	2 (6%)	50,54,54	1.60	8 (16%)
37	GTP	RE	501	-	33,34,34	0.87	0	50,54,54	1.65	8 (16%)
39	GDP	MJ	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.83	7 (15%)
39	GDP	OD	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.77	7 (15%)
39	GDP	AJ	502	-	29,30,30	1.23	4 (13%)	45,47,47	1.85	9 (20%)
39	GDP	QB	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.85	6 (13%)
37	GTP	AK	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.70	8 (16%)
37	GTP	AM	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.59	8 (16%)
37	GTP	WM	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.58	9 (18%)
39	GDP	JH	502	-	29,30,30	1.22	3 (10%)	45,47,47	1.76	6 (13%)
37	GTP	IG	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.60	12 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
37	GTP	OC	501	-	33,34,34	0.99	2 (6%)	50,54,54	1.69	9 (18%)
37	GTP	CA	501	-	33,34,34	0.93	2 (6%)	50,54,54	1.80	9 (18%)
37	GTP	QK	501	-	33,34,34	1.07	5 (15%)	50,54,54	1.69	9 (18%)
39	GDP	OL	502	-	29,30,30	1.16	3 (10%)	45,47,47	1.83	9 (20%)
37	GTP	HC	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.63	8 (16%)
39	GDP	QF	502	-	29,30,30	1.14	3 (10%)	45,47,47	1.80	6 (13%)
37	GTP	CC	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.75	10 (20%)
39	GDP	EL	502	-	29,30,30	1.31	4 (13%)	45,47,47	1.85	8 (17%)
39	GDP	OJ	502	-	29,30,30	1.16	4 (13%)	45,47,47	1.75	8 (17%)
37	GTP	EE	501	-	33,34,34	0.96	0	50,54,54	1.57	8 (16%)
37	GTP	QA	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.74	9 (18%)
39	GDP	CD	502	-	29,30,30	1.12	4 (13%)	45,47,47	1.85	7 (15%)
37	GTP	IK	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.69	10 (20%)
37	GTP	PK	501	-	33,34,34	1.08	3 (9%)	50,54,54	1.82	11 (22%)
37	GTP	NE	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.64	9 (18%)
37	GTP	BG	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.63	9 (18%)
37	GTP	DE	501	-	33,34,34	0.90	2 (6%)	50,54,54	1.69	12 (24%)
37	GTP	AE	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.62	8 (16%)
37	GTP	BM	501	-	33,34,34	0.94	2 (6%)	50,54,54	1.51	8 (16%)
37	GTP	WE	501	-	33,34,34	0.92	1 (3%)	50,54,54	1.64	9 (18%)
37	GTP	GM	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.57	8 (16%)
37	GTP	SC	501	-	33,34,34	0.95	1 (3%)	50,54,54	1.53	9 (18%)
39	GDP	NH	502	-	29,30,30	1.15	3 (10%)	45,47,47	1.82	7 (15%)
37	GTP	TE	501	-	33,34,34	1.02	2 (6%)	50,54,54	1.52	9 (18%)
37	GTP	FK	501	-	33,34,34	1.03	3 (9%)	50,54,54	1.66	12 (24%)

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
39	GDP	SJ	502	-	-	2/16/32/32	0/3/3/3
39	GDP	WN	502	-	-	7/16/32/32	0/3/3/3
37	GTP	PM	501	-	-	3/22/38/38	0/3/3/3
39	GDP	LD	502	-	-	7/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GDP	IB	502	-	-	6/16/32/32	0/3/3/3
39	GDP	CJ	502	-	-	6/16/32/32	0/3/3/3
37	GTP	LG	501	-	-	4/22/38/38	0/3/3/3
37	GTP	TK	501	-	-	5/22/38/38	0/3/3/3
39	GDP	VL	502	-	-	4/16/32/32	0/3/3/3
37	GTP	GG	501	-	-	7/22/38/38	0/3/3/3
37	GTP	HI	501	-	-	4/22/38/38	0/3/3/3
39	GDP	LH	502	-	-	5/16/32/32	0/3/3/3
37	GTP	QG	501	-	-	4/22/38/38	0/3/3/3
39	GDP	DJ	502	-	-	2/16/32/32	0/3/3/3
37	GTP	EG	501	-	-	8/22/38/38	0/3/3/3
39	GDP	NJ	502	-	-	2/16/32/32	0/3/3/3
39	GDP	PJ	502	-	-	4/16/32/32	0/3/3/3
37	GTP	TI	501	-	-	6/22/38/38	0/3/3/3
39	GDP	IF	502	-	-	0/16/32/32	0/3/3/3
37	GTP	FE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	MM	501	-	-	7/22/38/38	0/3/3/3
37	GTP	BC	501	-	-	7/22/38/38	0/3/3/3
39	GDP	WF	502	-	-	2/16/32/32	0/3/3/3
39	GDP	ED	502	-	-	4/16/32/32	0/3/3/3
37	GTP	AI	501	-	-	1/22/38/38	0/3/3/3
37	GTP	SI	501	-	-	3/22/38/38	0/3/3/3
37	GTP	UI	501	-	-	7/22/38/38	0/3/3/3
37	GTP	GK	501	-	-	3/22/38/38	0/3/3/3
37	GTP	JI	501	-	-	5/22/38/38	0/3/3/3
37	GTP	NA	501	-	-	8/22/38/38	0/3/3/3
39	GDP	JD	502	-	-	1/16/32/32	0/3/3/3
39	GDP	EH	502	-	-	6/16/32/32	0/3/3/3
39	GDP	GN	502	-	-	4/16/32/32	0/3/3/3
39	GDP	DF	502	-	-	5/16/32/32	0/3/3/3
39	GDP	QL	502	-	-	1/16/32/32	0/3/3/3
37	GTP	RK	501	-	-	3/22/38/38	0/3/3/3
39	GDP	UJ	502	-	-	5/16/32/32	0/3/3/3
39	GDP	BJ	502	-	-	7/16/32/32	0/3/3/3
37	GTP	SK	501	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	GTP	LM	501	-	-	4/22/38/38	0/3/3/3
37	GTP	WC	501	-	-	2/22/38/38	0/3/3/3
37	GTP	TM	501	-	-	6/22/38/38	0/3/3/3
37	GTP	UG	501	-	-	6/22/38/38	0/3/3/3
37	GTP	VG	501	-	-	3/22/38/38	0/3/3/3
37	GTP	NI	501	-	-	8/22/38/38	0/3/3/3
37	GTP	OG	501	-	-	0/22/38/38	0/3/3/3
39	GDP	ND	502	-	-	4/16/32/32	0/3/3/3
39	GDP	SD	502	-	-	1/16/32/32	0/3/3/3
37	GTP	SE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	HO	501	-	-	6/22/38/38	0/3/3/3
37	GTP	DI	501	-	-	6/22/38/38	0/3/3/3
39	GDP	ID	502	-	-	6/16/32/32	0/3/3/3
39	GDP	RL	502	-	-	2/16/32/32	0/3/3/3
39	GDP	N0	502	-	-	5/16/32/32	0/3/3/3
37	GTP	MG	501	-	-	4/22/38/38	0/3/3/3
39	GDP	WD	502	-	-	4/16/32/32	0/3/3/3
39	GDP	IN	502	-	-	4/16/32/32	0/3/3/3
37	GTP	LE	501	-	-	7/22/38/38	0/3/3/3
37	GTP	SM	501	-	-	7/22/38/38	0/3/3/3
39	GDP	EN	502	-	-	4/16/32/32	0/3/3/3
37	GTP	KO	501	-	-	5/22/38/38	0/3/3/3
37	GTP	IO	501	-	-	3/22/38/38	0/3/3/3
39	GDP	MH	502	-	-	3/16/32/32	0/3/3/3
37	GTP	LI	501	-	-	7/22/38/38	0/3/3/3
37	GTP	WK	501	-	-	8/22/38/38	0/3/3/3
39	GDP	HD	502	-	-	2/16/32/32	0/3/3/3
37	GTP	CM	501	-	-	7/22/38/38	0/3/3/3
37	GTP	AA	501	-	-	5/22/38/38	0/3/3/3
37	GTP	FC	501	-	-	8/22/38/38	0/3/3/3
37	GTP	DC	501	-	-	7/22/38/38	0/3/3/3
37	GTP	KI	501	-	-	8/22/38/38	0/3/3/3
37	GTP	CK	501	-	-	5/22/38/38	0/3/3/3
39	GDP	NB	502	-	-	3/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GDP	QJ	502	-	-	3/16/32/32	0/3/3/3
39	GDP	EJ	502	-	-	4/16/32/32	0/3/3/3
37	GTP	KK	501	-	-	8/22/38/38	0/3/3/3
39	GDP	DL	502	-	-	3/16/32/32	0/3/3/3
39	GDP	RH	502	-	-	1/16/32/32	0/3/3/3
37	GTP	JE	501	-	-	2/22/38/38	0/3/3/3
39	GDP	VD	502	-	-	2/16/32/32	0/3/3/3
37	GTP	QI	501	-	-	2/22/38/38	0/3/3/3
37	GTP	DK	501	-	-	3/22/38/38	0/3/3/3
37	GTP	NK	501	-	-	1/22/38/38	0/3/3/3
37	GTP	KG	501	-	-	5/22/38/38	0/3/3/3
37	GTP	PC	501	-	-	1/22/38/38	0/3/3/3
39	GDP	TF	502	-	-	1/16/32/32	0/3/3/3
37	GTP	HK	501	-	-	6/22/38/38	0/3/3/3
39	GDP	TL	502	-	-	3/16/32/32	0/3/3/3
39	GDP	IH	502	-	-	6/16/32/32	0/3/3/3
39	GDP	LL	502	-	-	3/16/32/32	0/3/3/3
39	GDP	VH	502	-	-	4/16/32/32	0/3/3/3
37	GTP	LK	501	-	-	9/22/38/38	0/3/3/3
39	GDP	BB	502	-	-	5/16/32/32	0/3/3/3
39	GDP	JB	502	-	-	1/16/32/32	0/3/3/3
39	GDP	PL	502	-	-	7/16/32/32	0/3/3/3
39	GDP	QD	502	-	-	3/16/32/32	0/3/3/3
37	GTP	HM	501	-	-	2/22/38/38	0/3/3/3
37	GTP	OI	501	-	-	6/22/38/38	0/3/3/3
39	GDP	PF	502	-	-	3/16/32/32	0/3/3/3
39	GDP	UD	502	-	-	2/16/32/32	0/3/3/3
39	GDP	WB	502	-	-	1/16/32/32	0/3/3/3
39	GDP	LB	502	-	-	1/16/32/32	0/3/3/3
37	GTP	BE	501	-	-	4/22/38/38	0/3/3/3
37	GTP	RC	501	-	-	7/22/38/38	0/3/3/3
39	GDP	TJ	502	-	-	2/16/32/32	0/3/3/3
39	GDP	WJ	502	-	-	4/16/32/32	0/3/3/3
37	GTP	UK	501	-	-	2/22/38/38	0/3/3/3
39	GDP	SF	502	-	-	0/16/32/32	0/3/3/3
39	GDP	TD	502	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	GTP	DM	501	-	-	1/22/38/38	0/3/3/3
39	GDP	FF	502	-	-	1/16/32/32	0/3/3/3
39	GDP	EB	502	-	-	3/16/32/32	0/3/3/3
37	GTP	WG	501	-	-	5/22/38/38	0/3/3/3
39	GDP	UH	502	-	-	4/16/32/32	0/3/3/3
39	GDP	HL	502	-	-	1/16/32/32	0/3/3/3
39	GDP	QH	502	-	-	0/16/32/32	0/3/3/3
39	GDP	UF	502	-	-	5/16/32/32	0/3/3/3
39	GDP	GD	502	-	-	1/16/32/32	0/3/3/3
37	GTP	TG	501	-	-	7/22/38/38	0/3/3/3
37	GTP	PG	501	-	-	4/22/38/38	0/3/3/3
39	GDP	MD	502	-	-	4/16/32/32	0/3/3/3
39	GDP	KB	502	-	-	3/16/32/32	0/3/3/3
37	GTP	AG	501	-	-	5/22/38/38	0/3/3/3
37	GTP	CI	501	-	-	7/22/38/38	0/3/3/3
37	GTP	OE	501	-	-	8/22/38/38	0/3/3/3
39	GDP	VB	502	-	-	5/16/32/32	0/3/3/3
37	GTP	GE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	SG	501	-	-	9/22/38/38	0/3/3/3
39	GDP	BL	502	-	-	1/16/32/32	0/3/3/3
39	GDP	GB	502	-	-	2/16/32/32	0/3/3/3
39	GDP	DN	502	-	-	3/16/32/32	0/3/3/3
39	GDP	DB	502	-	-	0/16/32/32	0/3/3/3
39	GDP	BH	502	-	-	4/16/32/32	0/3/3/3
39	GDP	GH	502	-	-	4/16/32/32	0/3/3/3
37	GTP	TC	501	-	-	9/22/38/38	0/3/3/3
39	GDP	BD	502	-	-	5/16/32/32	0/3/3/3
37	GTP	FM	501	-	-	5/22/38/38	0/3/3/3
39	GDP	WL	502	-	-	5/16/32/32	0/3/3/3
39	GDP	GF	502	-	-	6/16/32/32	0/3/3/3
37	GTP	EM	501	-	-	7/22/38/38	0/3/3/3
39	GDP	JJ	502	-	-	0/16/32/32	0/3/3/3
37	GTP	EC	501	-	-	6/22/38/38	0/3/3/3
37	GTP	EK	501	-	-	6/22/38/38	0/3/3/3
37	GTP	MK	501	-	-	6/22/38/38	0/3/3/3
39	GDP	JF	502	-	-	0/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GDP	FH	502	-	-	4/16/32/32	0/3/3/3
39	GDP	CH	502	-	-	4/16/32/32	0/3/3/3
39	GDP	OF	502	-	-	3/16/32/32	0/3/3/3
39	GDP	LJ	502	-	-	5/16/32/32	0/3/3/3
39	GDP	RJ	502	-	-	2/16/32/32	0/3/3/3
39	GDP	AL	502	-	-	1/16/32/32	0/3/3/3
39	GDP	FD	502	-	-	6/16/32/32	0/3/3/3
39	GDP	VF	502	-	-	2/16/32/32	0/3/3/3
39	GDP	AD	502	-	-	3/16/32/32	0/3/3/3
37	GTP	UM	501	-	-	4/22/38/38	0/3/3/3
39	GDP	HF	502	-	-	1/16/32/32	0/3/3/3
37	GTP	QE	501	-	-	3/22/38/38	0/3/3/3
37	GTP	CE	501	-	-	4/22/38/38	0/3/3/3
37	GTP	FI	501	-	-	6/22/38/38	0/3/3/3
37	GTP	NG	501	-	-	4/22/38/38	0/3/3/3
39	GDP	WH	502	-	-	2/16/32/32	0/3/3/3
37	GTP	JM	501	-	-	3/22/38/38	0/3/3/3
37	GTP	VM	501	-	-	3/22/38/38	0/3/3/3
37	GTP	RA	501	-	-	8/22/38/38	0/3/3/3
39	GDP	MB	502	-	-	0/16/32/32	0/3/3/3
37	GTP	RG	501	-	-	4/22/38/38	0/3/3/3
37	GTP	EI	501	-	-	6/22/38/38	0/3/3/3
37	GTP	QM	501	-	-	3/22/38/38	0/3/3/3
39	GDP	OB	502	-	-	4/16/32/32	0/3/3/3
37	GTP	RI	501	-	-	4/22/38/38	0/3/3/3
37	GTP	SA	501	-	-	3/22/38/38	0/3/3/3
37	GTP	FG	501	-	-	6/22/38/38	0/3/3/3
37	GTP	JC	501	-	-	0/22/38/38	0/3/3/3
37	GTP	NC	501	-	-	6/22/38/38	0/3/3/3
37	GTP	KM	501	-	-	5/22/38/38	0/3/3/3
39	GDP	KF	502	-	-	4/16/32/32	0/3/3/3
37	GTP	RM	501	-	-	4/22/38/38	0/3/3/3
39	GDP	SH	502	-	-	0/16/32/32	0/3/3/3
39	GDP	JL	502	-	-	2/16/32/32	0/3/3/3
39	GDP	RF	502	-	-	1/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	GTP	II	501	-	-	5/22/38/38	0/3/3/3
39	GDP	HB	502	-	-	3/16/32/32	0/3/3/3
39	GDP	HN	502	-	-	1/16/32/32	0/3/3/3
39	GDP	RD	502	-	-	2/16/32/32	0/3/3/3
39	GDP	JN	502	-	-	3/16/32/32	0/3/3/3
39	GDP	LF	502	-	-	2/16/32/32	0/3/3/3
39	GDP	KD	502	-	-	5/16/32/32	0/3/3/3
39	GDP	UB	502	-	-	5/16/32/32	0/3/3/3
39	GDP	LN	502	-	-	3/16/32/32	0/3/3/3
37	GTP	IM	501	-	-	6/22/38/38	0/3/3/3
39	GDP	O0	502	-	-	1/16/32/32	0/3/3/3
37	GTP	BA	501	-	-	6/22/38/38	0/3/3/3
37	GTP	BI	501	-	-	4/22/38/38	0/3/3/3
39	GDP	FJ	502	-	-	3/16/32/32	0/3/3/3
39	GDP	GL	502	-	-	1/16/32/32	0/3/3/3
39	GDP	OH	502	-	-	2/16/32/32	0/3/3/3
39	GDP	SB	502	-	-	1/16/32/32	0/3/3/3
39	GDP	AF	502	-	-	6/16/32/32	0/3/3/3
37	GTP	MI	501	-	-	8/22/38/38	0/3/3/3
39	GDP	CF	502	-	-	6/16/32/32	0/3/3/3
37	GTP	JG	501	-	-	7/22/38/38	0/3/3/3
39	GDP	TB	502	-	-	6/16/32/32	0/3/3/3
37	GTP	BK	501	-	-	6/22/38/38	0/3/3/3
39	GDP	BF	502	-	-	5/16/32/32	0/3/3/3
39	GDP	ML	502	-	-	3/16/32/32	0/3/3/3
37	GTP	QC	501	-	-	3/22/38/38	0/3/3/3
39	GDP	PB	502	-	-	5/16/32/32	0/3/3/3
37	GTP	PE	501	-	-	6/22/38/38	0/3/3/3
39	GDP	AH	502	-	-	1/16/32/32	0/3/3/3
39	GDP	KL	502	-	-	1/16/32/32	0/3/3/3
37	GTP	PI	501	-	-	5/22/38/38	0/3/3/3
39	GDP	KJ	502	-	-	3/16/32/32	0/3/3/3
37	GTP	JK	501	-	-	4/22/38/38	0/3/3/3
37	GTP	UE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	MC	501	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	GTP	VK	501	-	-	5/22/38/38	0/3/3/3
37	GTP	PA	501	-	-	8/22/38/38	0/3/3/3
37	GTP	VC	501	-	-	6/22/38/38	0/3/3/3
39	GDP	KN	502	-	-	3/16/32/32	0/3/3/3
39	GDP	UL	502	-	-	3/16/32/32	0/3/3/3
37	GTP	KC	501	-	-	11/22/38/38	0/3/3/3
37	GTP	VI	501	-	-	4/22/38/38	0/3/3/3
39	GDP	HH	502	-	-	6/16/32/32	0/3/3/3
39	GDP	RB	502	-	-	4/16/32/32	0/3/3/3
39	GDP	CL	502	-	-	5/16/32/32	0/3/3/3
37	GTP	DA	501	-	-	4/22/38/38	0/3/3/3
37	GTP	HE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	ME	501	-	-	4/22/38/38	0/3/3/3
39	GDP	FB	502	-	-	3/16/32/32	0/3/3/3
37	GTP	CG	501	-	-	4/22/38/38	0/3/3/3
39	GDP	HJ	502	-	-	3/16/32/32	0/3/3/3
39	GDP	MN	502	-	-	3/16/32/32	0/3/3/3
39	GDP	DD	502	-	-	7/16/32/32	0/3/3/3
39	GDP	DH	502	-	-	2/16/32/32	0/3/3/3
37	GTP	AC	501	-	-	4/22/38/38	0/3/3/3
37	GTP	OK	501	-	-	7/22/38/38	0/3/3/3
39	GDP	UN	502	-	-	2/16/32/32	0/3/3/3
39	GDP	VJ	502	-	-	3/16/32/32	0/3/3/3
39	GDP	PH	502	-	-	0/16/32/32	0/3/3/3
39	GDP	IL	502	-	-	0/16/32/32	0/3/3/3
39	GDP	PD	502	-	-	4/16/32/32	0/3/3/3
37	GTP	UC	501	-	-	5/22/38/38	0/3/3/3
39	GDP	TH	502	-	-	2/16/32/32	0/3/3/3
39	GDP	FL	502	-	-	5/16/32/32	0/3/3/3
39	GDP	FN	502	-	-	2/16/32/32	0/3/3/3
39	GDP	IJ	502	-	-	3/16/32/32	0/3/3/3
37	GTP	DG	501	-	-	5/22/38/38	0/3/3/3
37	GTP	HG	501	-	-	4/22/38/38	0/3/3/3
39	GDP	NF	502	-	-	4/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GDP	MF	502	-	-	2/16/32/32	0/3/3/3
39	GDP	NL	502	-	-	3/16/32/32	0/3/3/3
37	GTP	VE	501	-	-	5/22/38/38	0/3/3/3
39	GDP	CB	502	-	-	2/16/32/32	0/3/3/3
37	GTP	IE	501	-	-	2/22/38/38	0/3/3/3
37	GTP	KE	501	-	-	5/22/38/38	0/3/3/3
39	GDP	VN	502	-	-	0/16/32/32	0/3/3/3
37	GTP	GI	501	-	-	6/22/38/38	0/3/3/3
37	GTP	WI	501	-	-	6/22/38/38	0/3/3/3
39	GDP	AB	502	-	-	4/16/32/32	0/3/3/3
39	GDP	SL	502	-	-	2/16/32/32	0/3/3/3
37	GTP	OA	501	-	-	5/22/38/38	0/3/3/3
37	GTP	GC	501	-	-	6/22/38/38	0/3/3/3
37	GTP	IC	501	-	-	7/22/38/38	0/3/3/3
39	GDP	EF	502	-	-	4/16/32/32	0/3/3/3
39	GDP	GJ	502	-	-	2/16/32/32	0/3/3/3
39	GDP	KH	502	-	-	4/16/32/32	0/3/3/3
37	GTP	LC	501	-	-	1/22/38/38	0/3/3/3
37	GTP	RE	501	-	-	3/22/38/38	0/3/3/3
39	GDP	MJ	502	-	-	2/16/32/32	0/3/3/3
39	GDP	OD	502	-	-	1/16/32/32	0/3/3/3
39	GDP	AJ	502	-	-	3/16/32/32	0/3/3/3
39	GDP	QB	502	-	-	5/16/32/32	0/3/3/3
37	GTP	AK	501	-	-	2/22/38/38	0/3/3/3
37	GTP	AM	501	-	-	4/22/38/38	0/3/3/3
37	GTP	WM	501	-	-	6/22/38/38	0/3/3/3
39	GDP	JH	502	-	-	2/16/32/32	0/3/3/3
37	GTP	IG	501	-	-	3/22/38/38	0/3/3/3
37	GTP	OC	501	-	-	6/22/38/38	0/3/3/3
37	GTP	CA	501	-	-	3/22/38/38	0/3/3/3
37	GTP	QK	501	-	-	7/22/38/38	0/3/3/3
39	GDP	OL	502	-	-	3/16/32/32	0/3/3/3
37	GTP	HC	501	-	-	6/22/38/38	0/3/3/3
39	GDP	QF	502	-	-	0/16/32/32	0/3/3/3
37	GTP	CC	501	-	-	4/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	GDP	EL	502	-	-	4/16/32/32	0/3/3/3
39	GDP	OJ	502	-	-	2/16/32/32	0/3/3/3
37	GTP	EE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	QA	501	-	-	6/22/38/38	0/3/3/3
39	GDP	CD	502	-	-	1/16/32/32	0/3/3/3
37	GTP	IK	501	-	-	5/22/38/38	0/3/3/3
37	GTP	PK	501	-	-	7/22/38/38	0/3/3/3
37	GTP	NE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	BG	501	-	-	6/22/38/38	0/3/3/3
37	GTP	DE	501	-	-	10/22/38/38	0/3/3/3
37	GTP	AE	501	-	-	4/22/38/38	0/3/3/3
37	GTP	BM	501	-	-	3/22/38/38	0/3/3/3
37	GTP	WE	501	-	-	6/22/38/38	0/3/3/3
37	GTP	GM	501	-	-	6/22/38/38	0/3/3/3
37	GTP	SC	501	-	-	3/22/38/38	0/3/3/3
39	GDP	NH	502	-	-	4/16/32/32	0/3/3/3
37	GTP	TE	501	-	-	4/22/38/38	0/3/3/3
37	GTP	FK	501	-	-	9/22/38/38	0/3/3/3

The worst 5 of 742 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	QL	502	GDP	C5-C4	3.39	1.48	1.38
39	EF	502	GDP	C6-N1	-3.39	1.32	1.38
39	IL	502	GDP	C6-N1	-3.36	1.32	1.38
39	ML	502	GDP	C6-N1	-3.35	1.32	1.38
39	QB	502	GDP	C5-C4	3.32	1.47	1.38

The worst 5 of 2518 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	QL	502	GDP	C5-C4-N3	-7.27	116.83	128.39
39	IL	502	GDP	C5-C4-N3	-7.22	116.89	128.39
39	FJ	502	GDP	C5-C4-N3	-7.06	117.15	128.39
39	IB	502	GDP	C5-C4-N3	-7.01	117.24	128.39
39	DB	502	GDP	C5-C4-N3	-7.00	117.24	128.39

There are no chirality outliers.

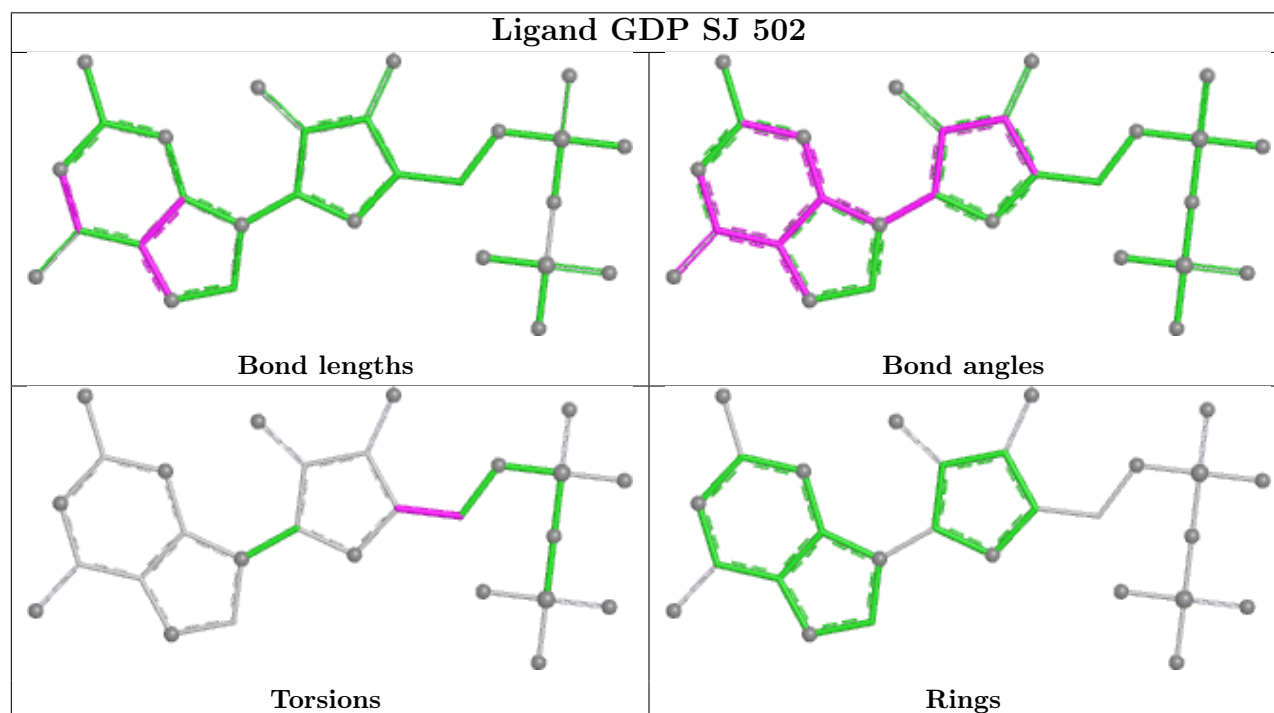
5 of 1227 torsion outliers are listed below:

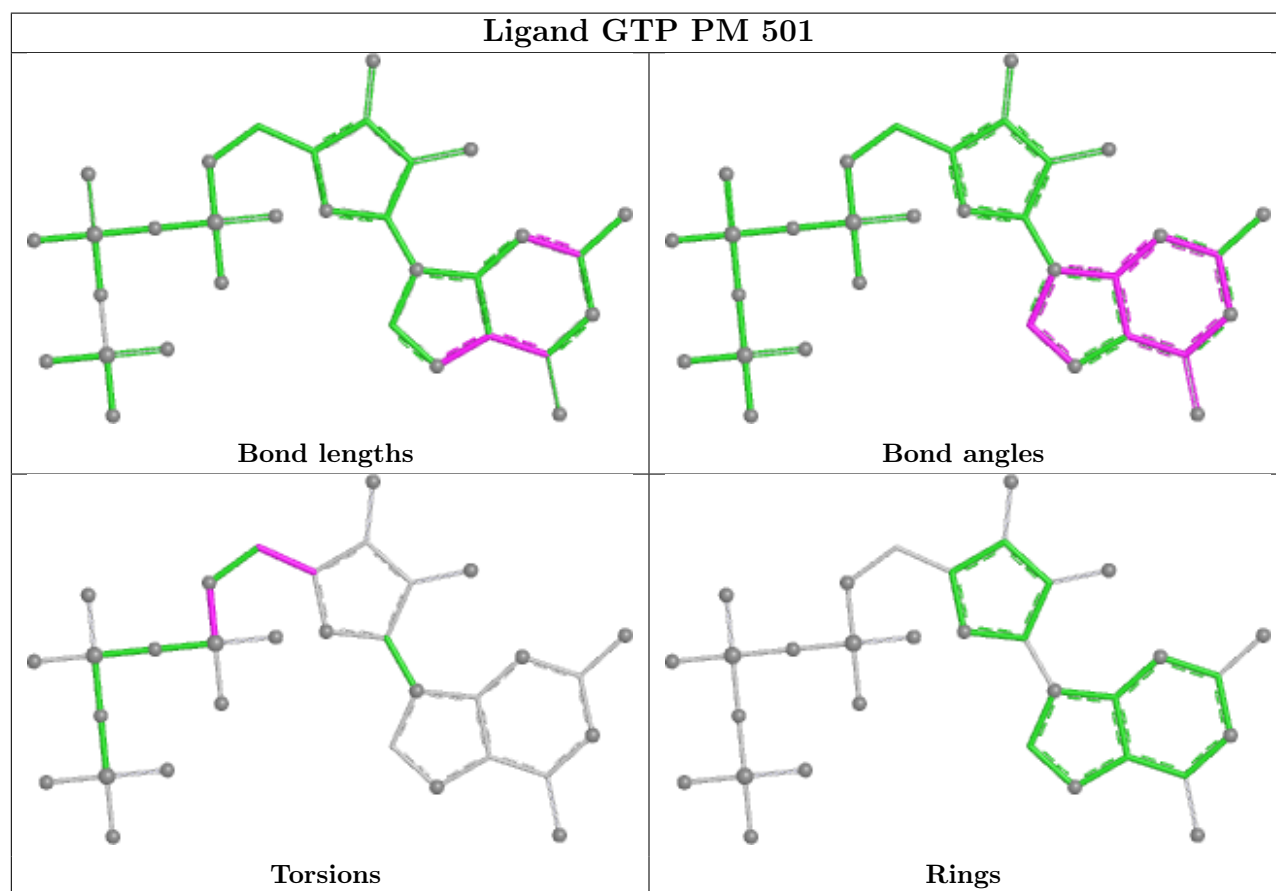
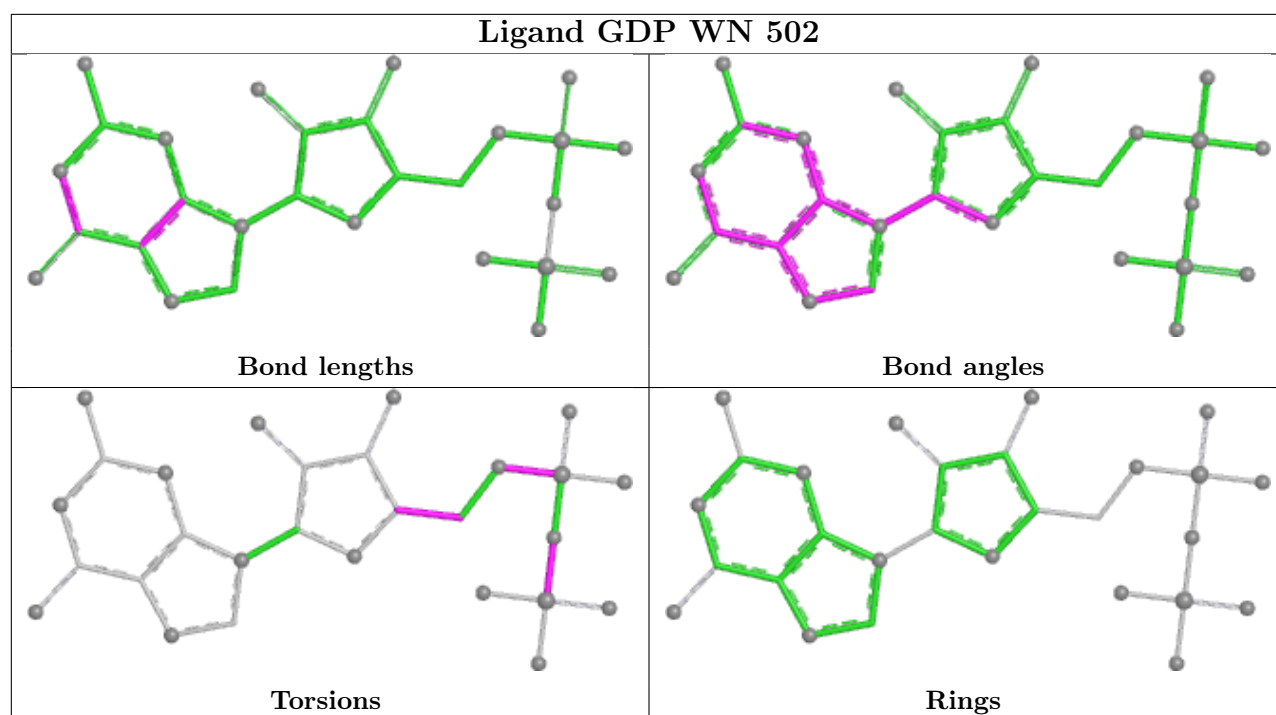
Mol	Chain	Res	Type	Atoms
37	AA	501	GTP	C5'-O5'-PA-O3A
37	AA	501	GTP	C5'-O5'-PA-O1A
37	AA	501	GTP	C5'-O5'-PA-O2A
37	AC	501	GTP	C5'-O5'-PA-O3A
37	AC	501	GTP	C5'-O5'-PA-O2A

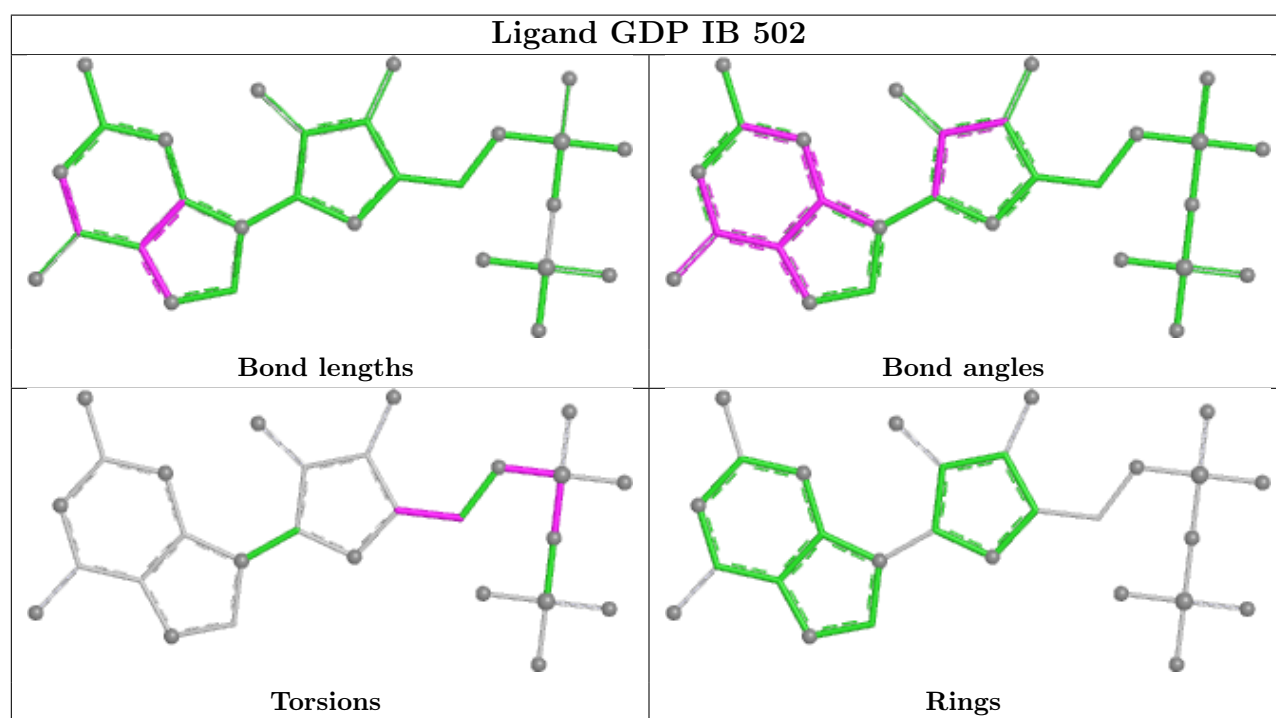
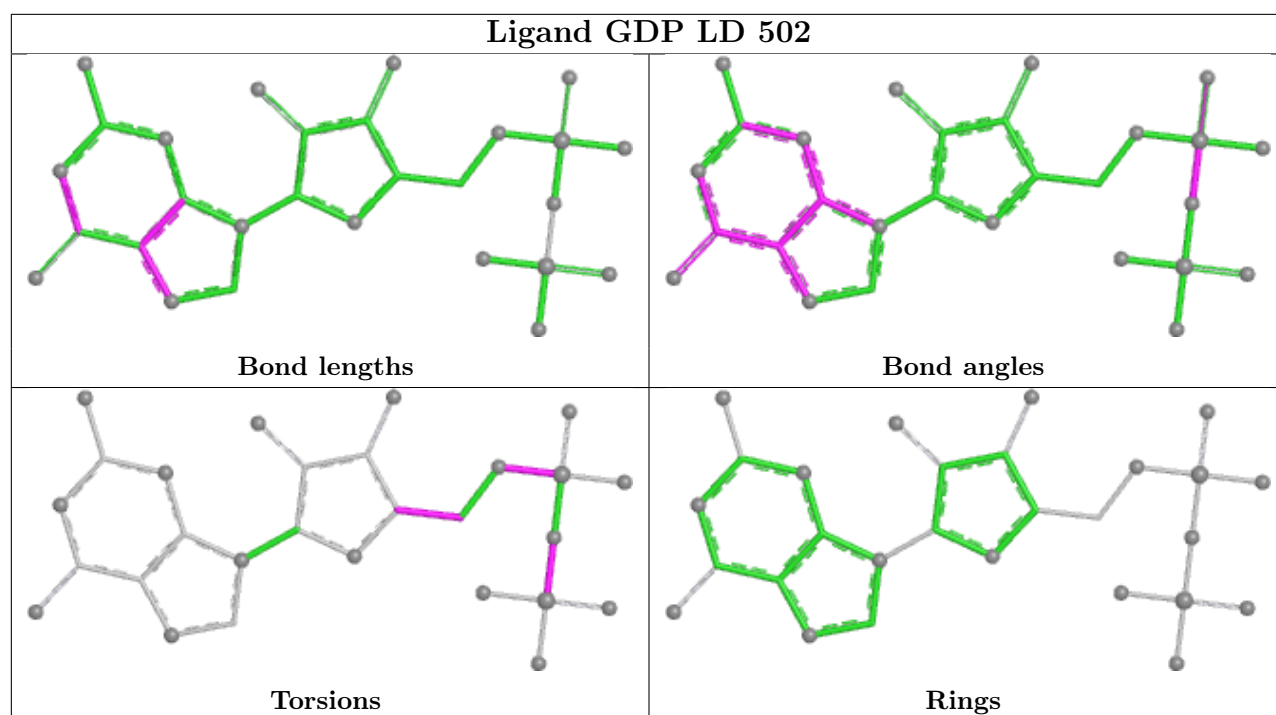
There are no ring outliers.

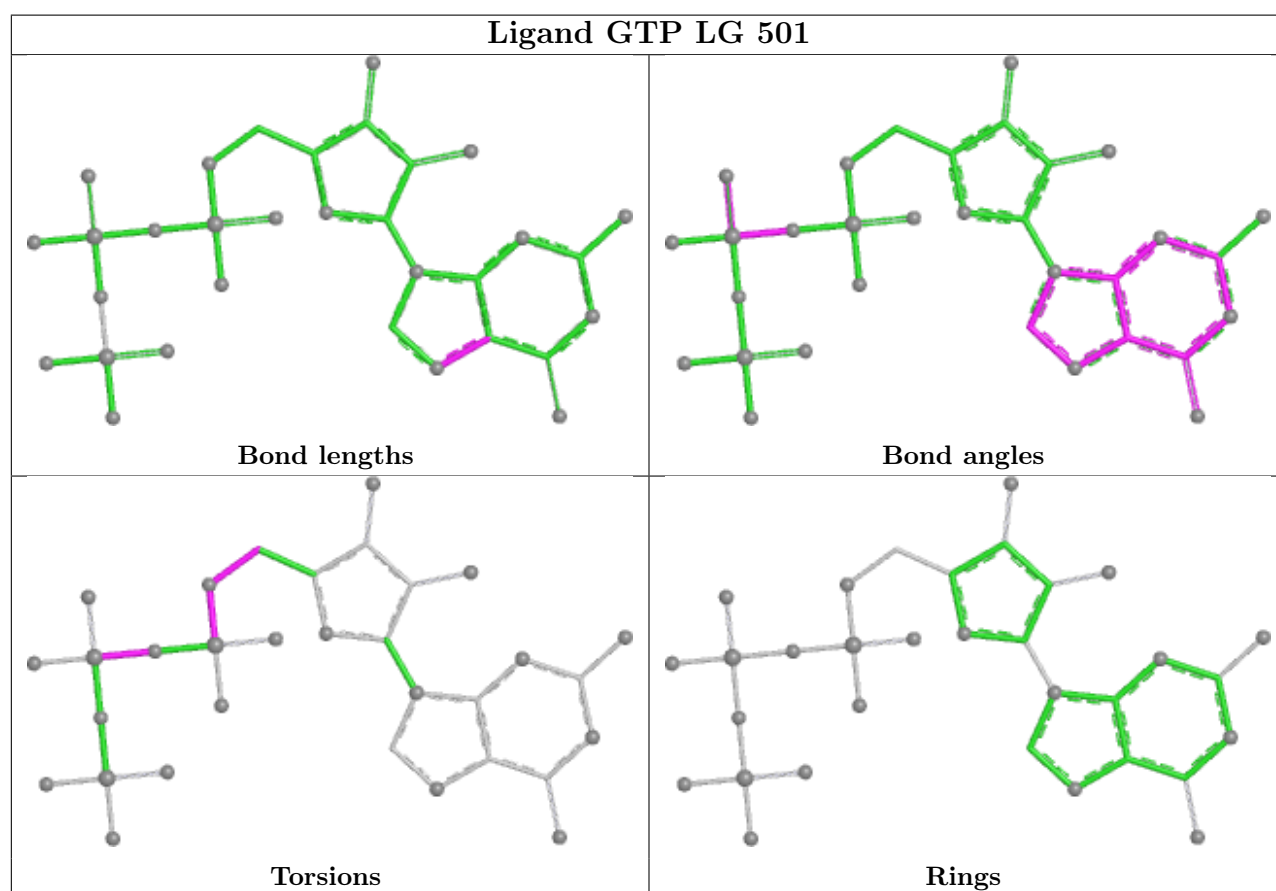
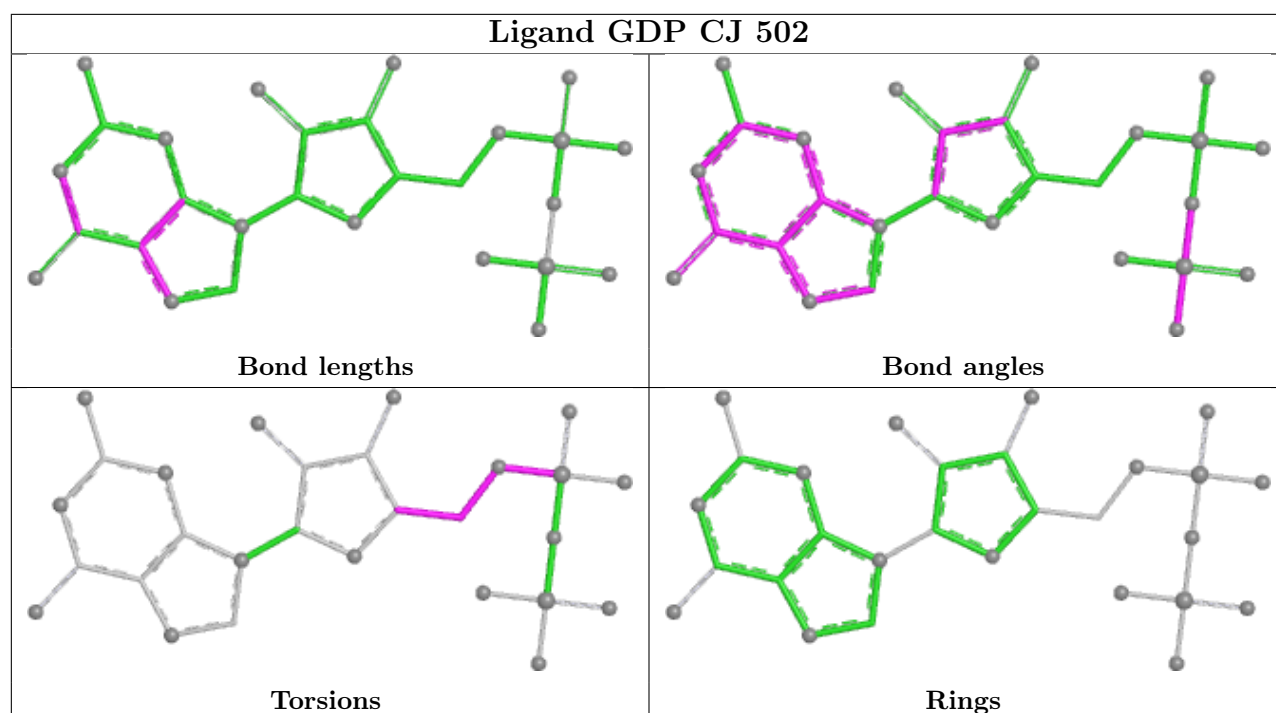
No monomer is involved in short contacts.

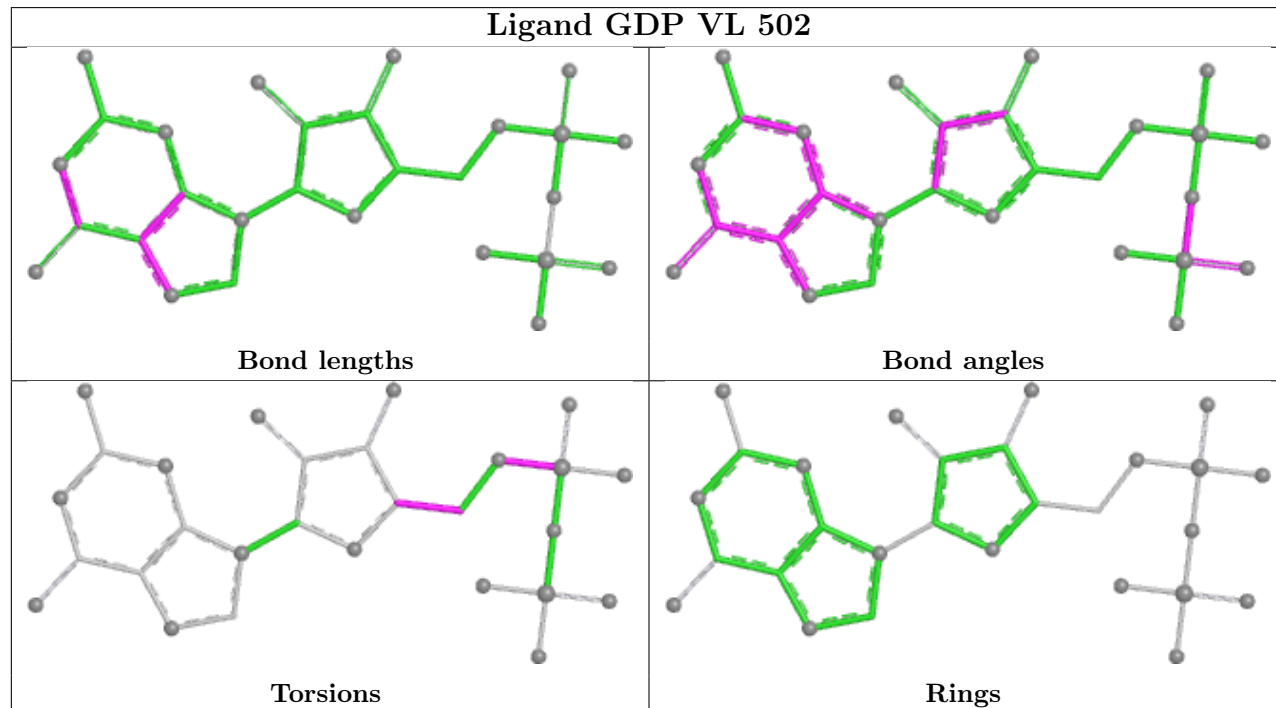
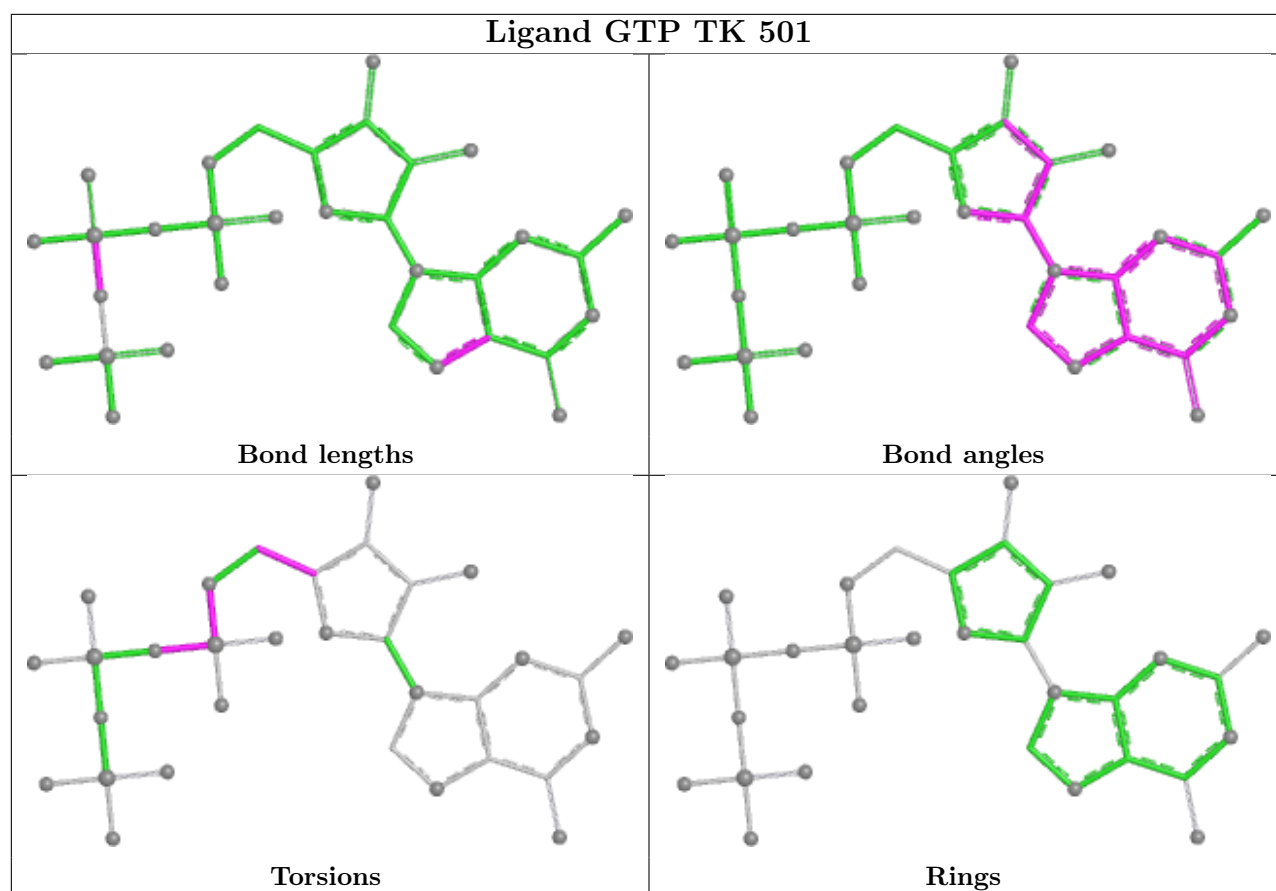
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



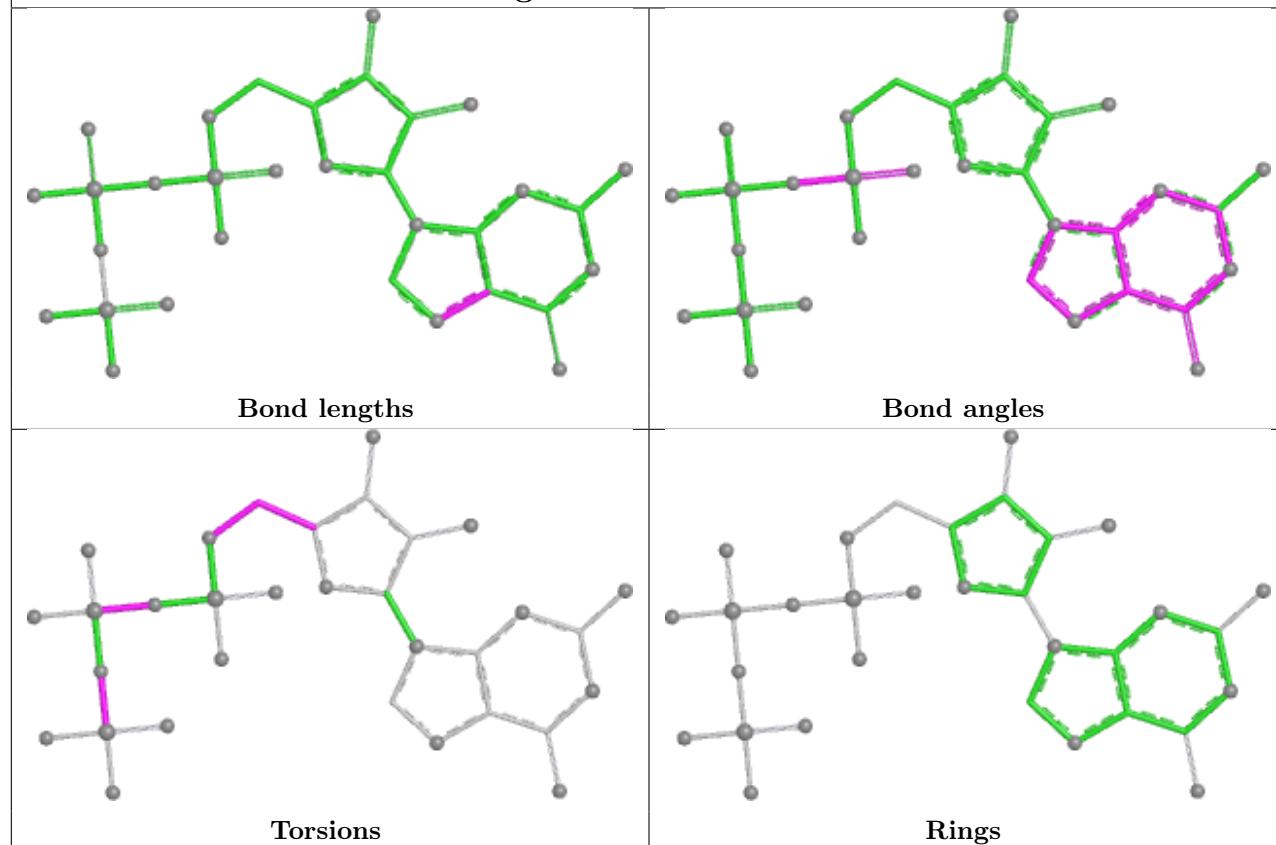




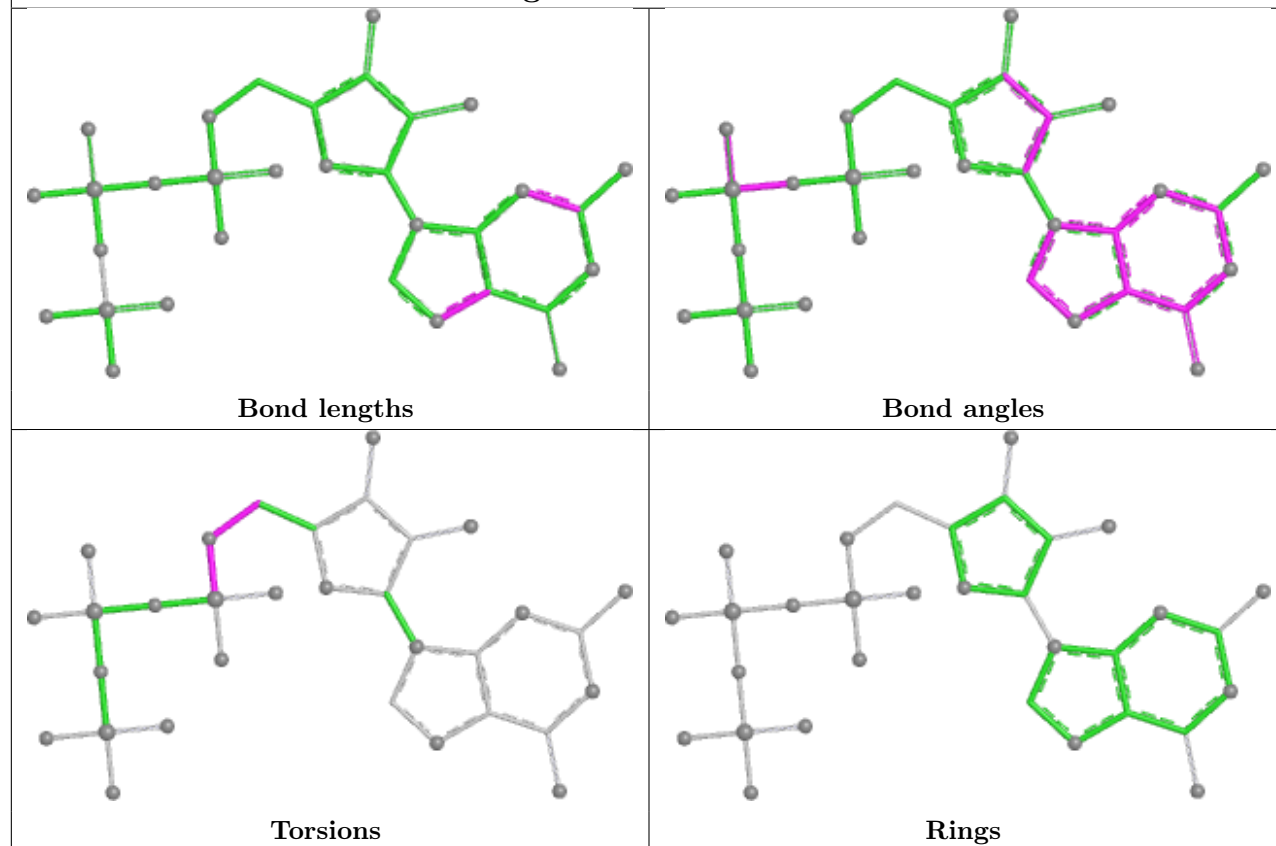


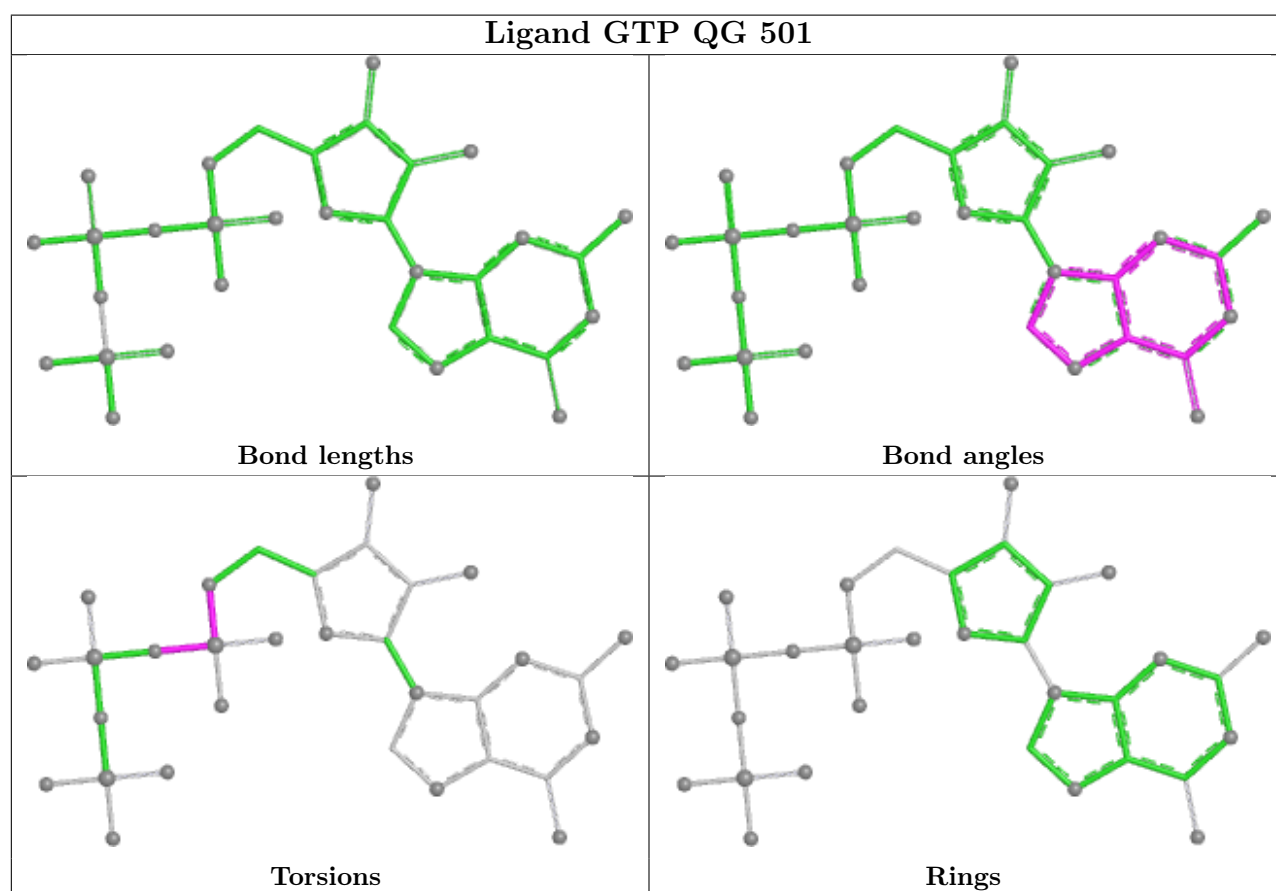
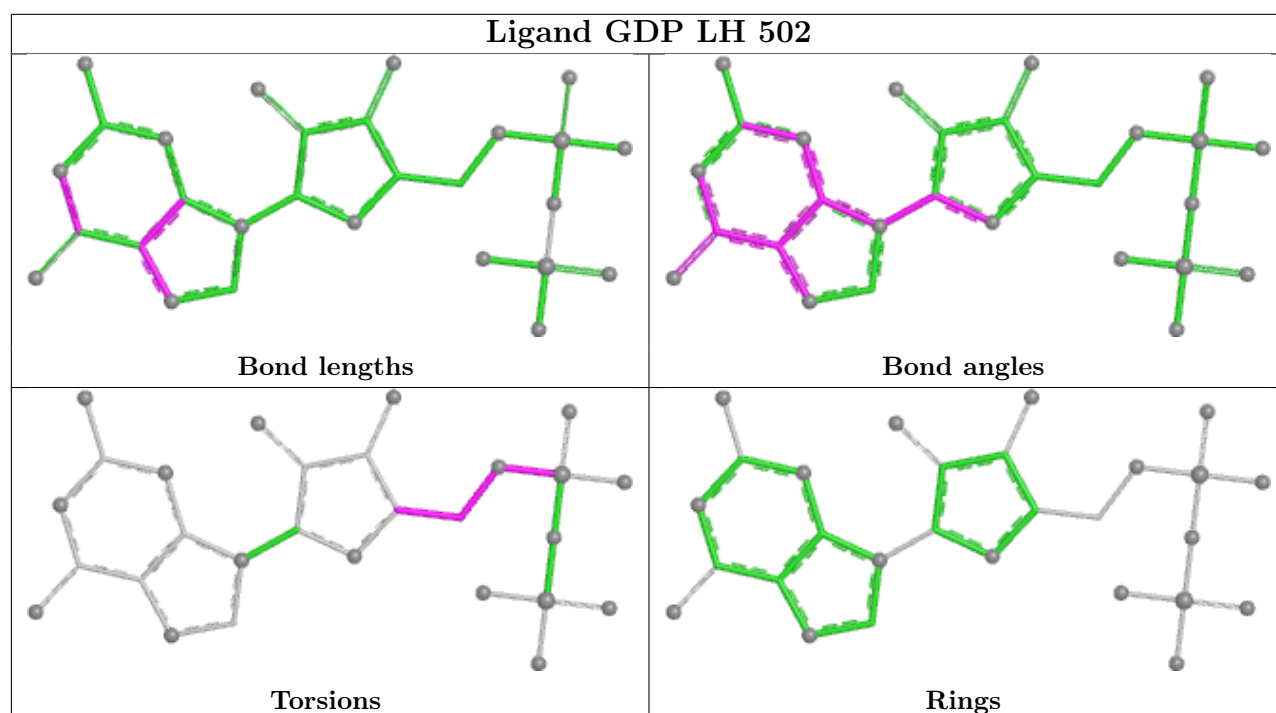


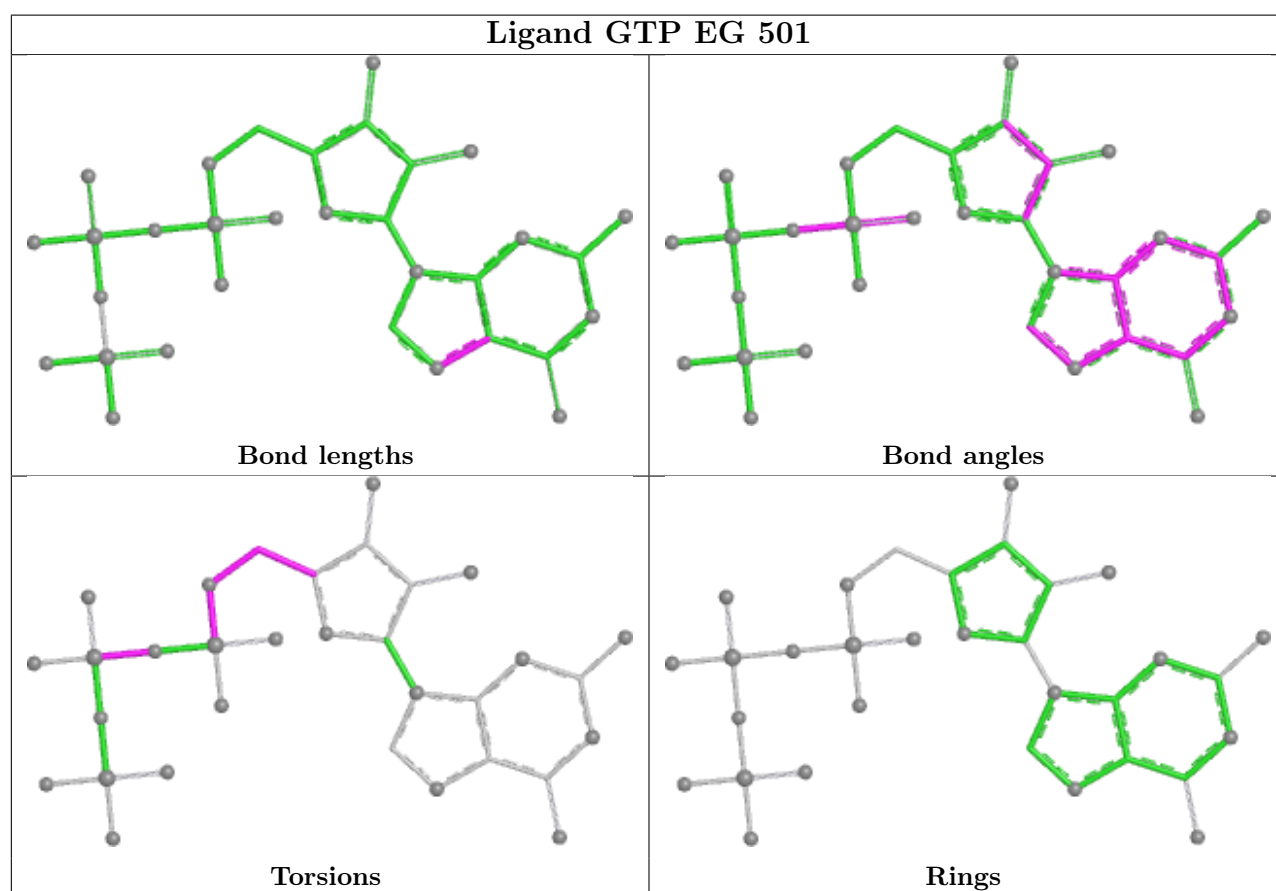
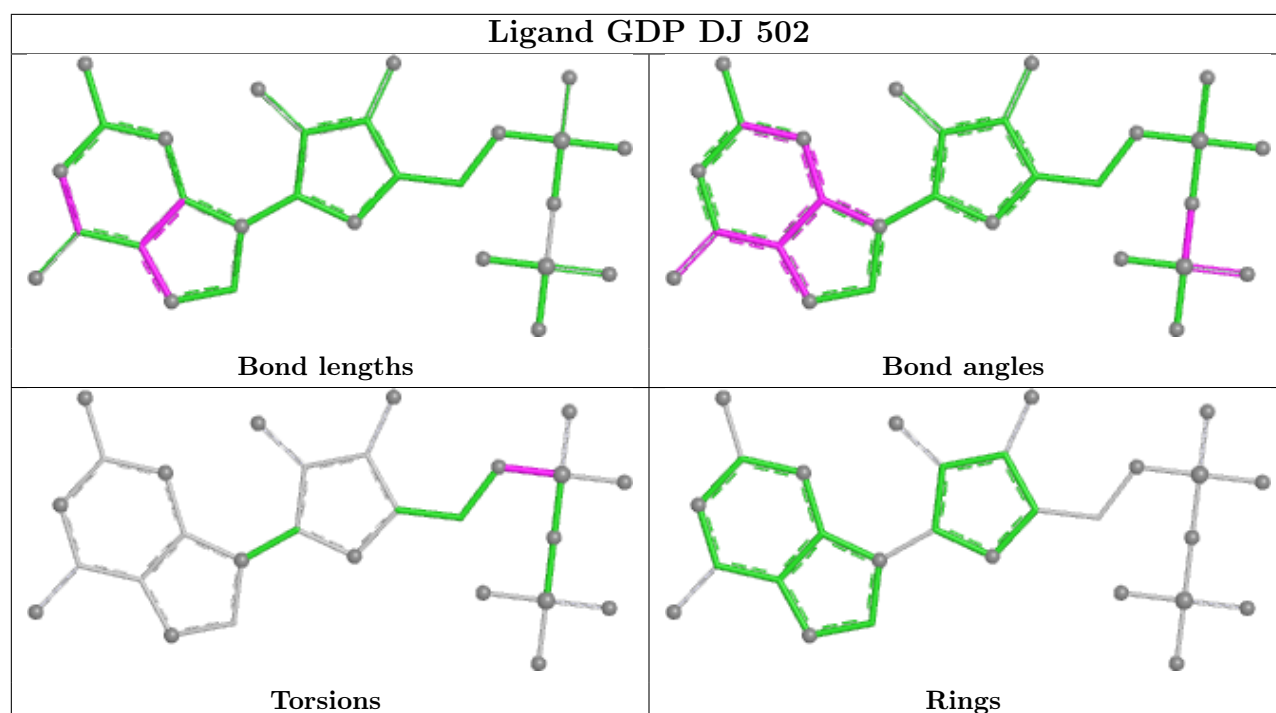
Ligand GTP GG 501

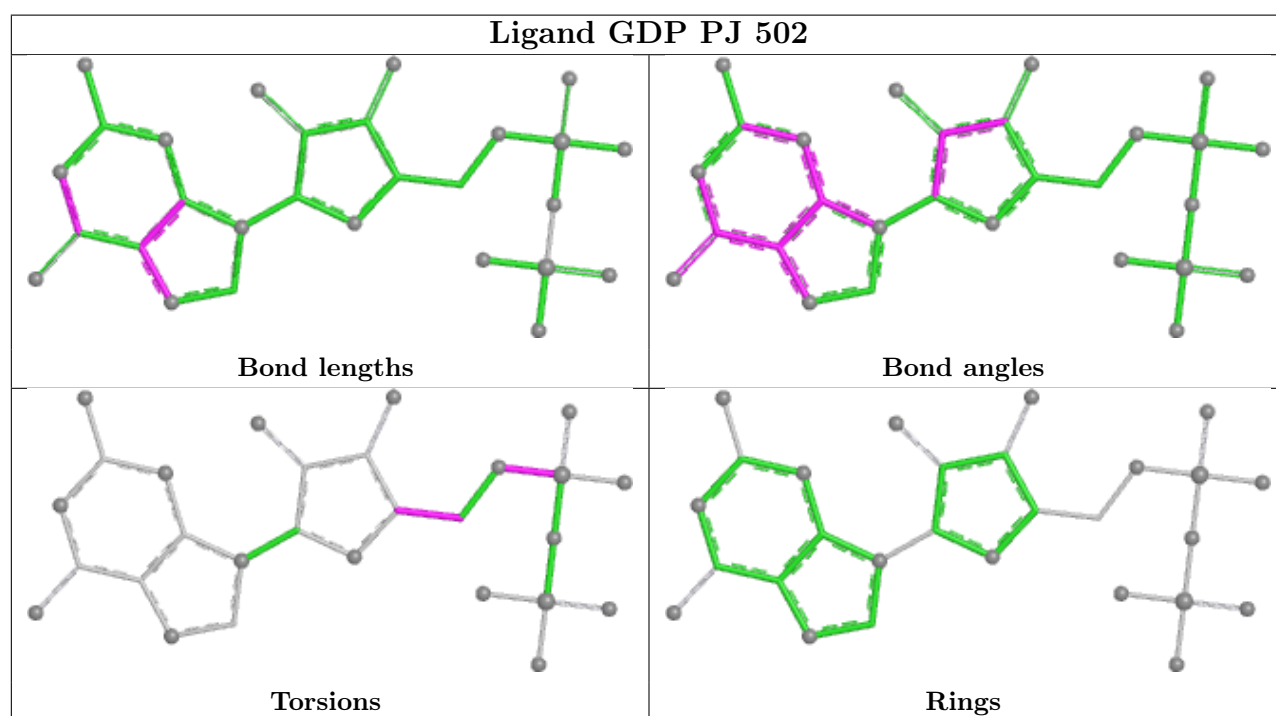
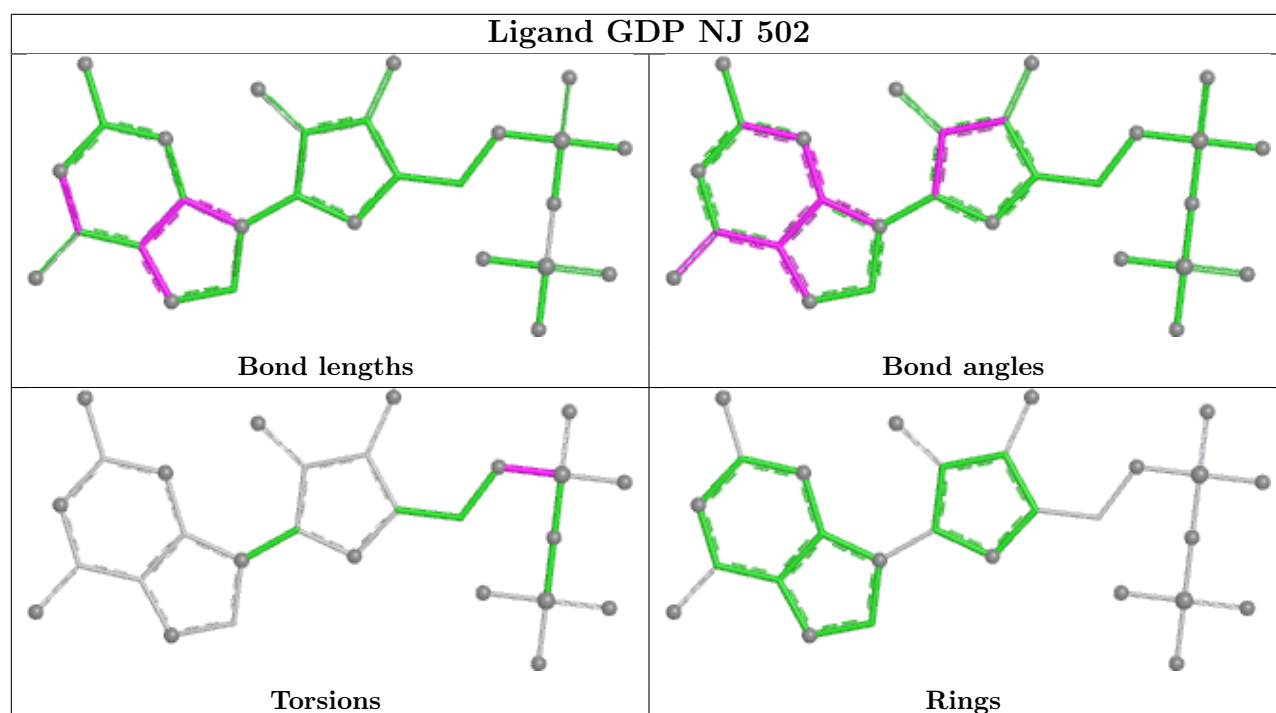


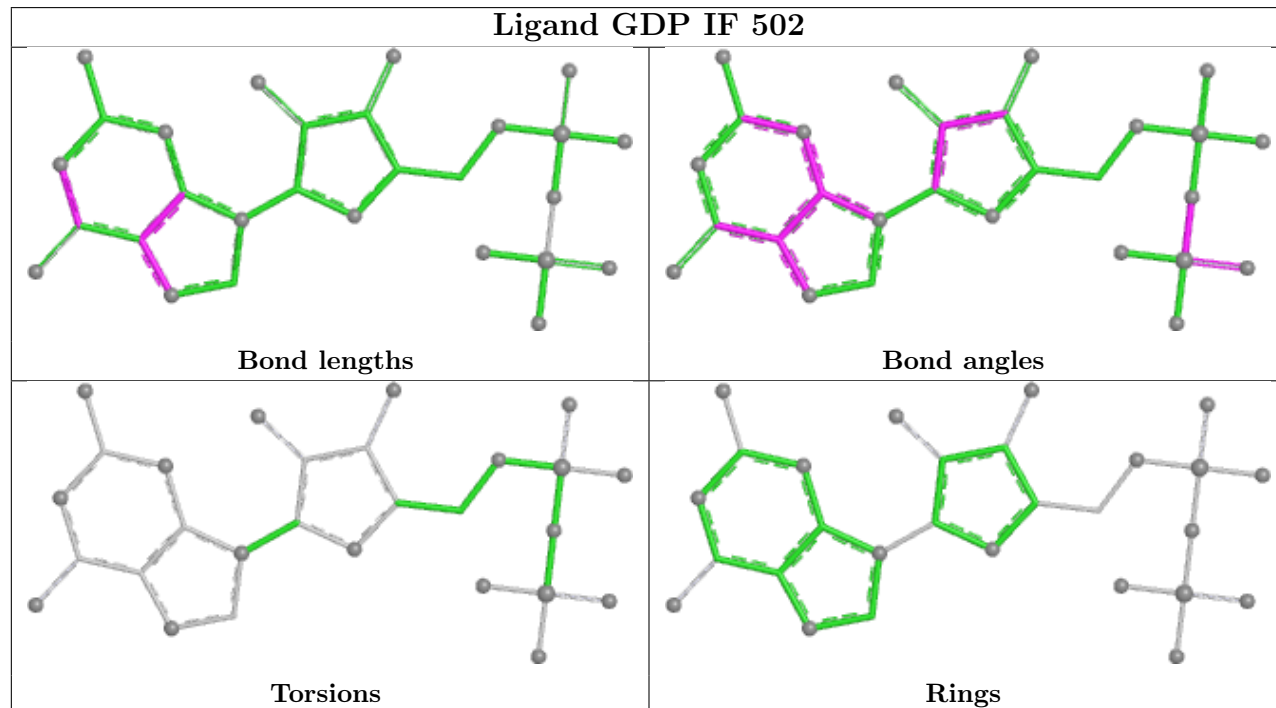
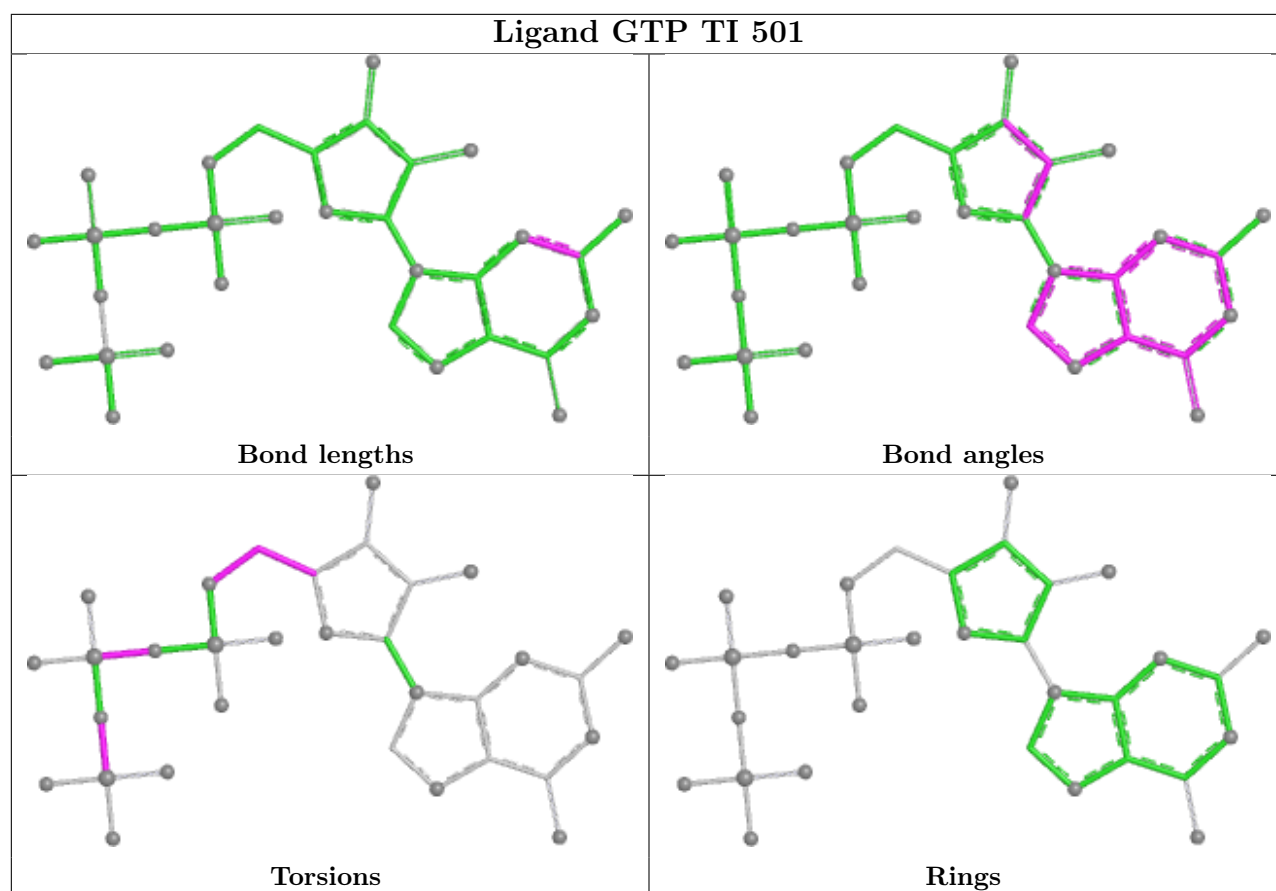
Ligand GTP HI 501



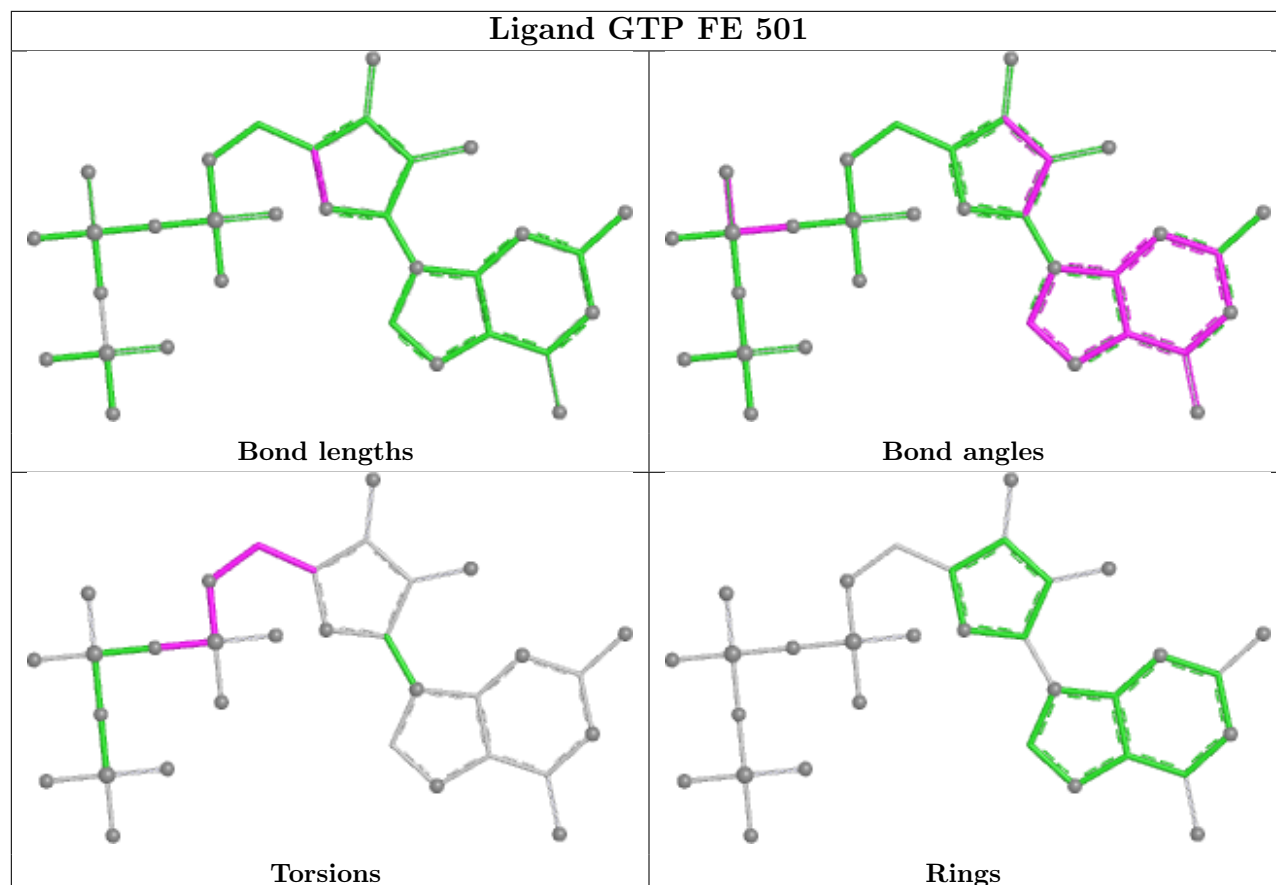




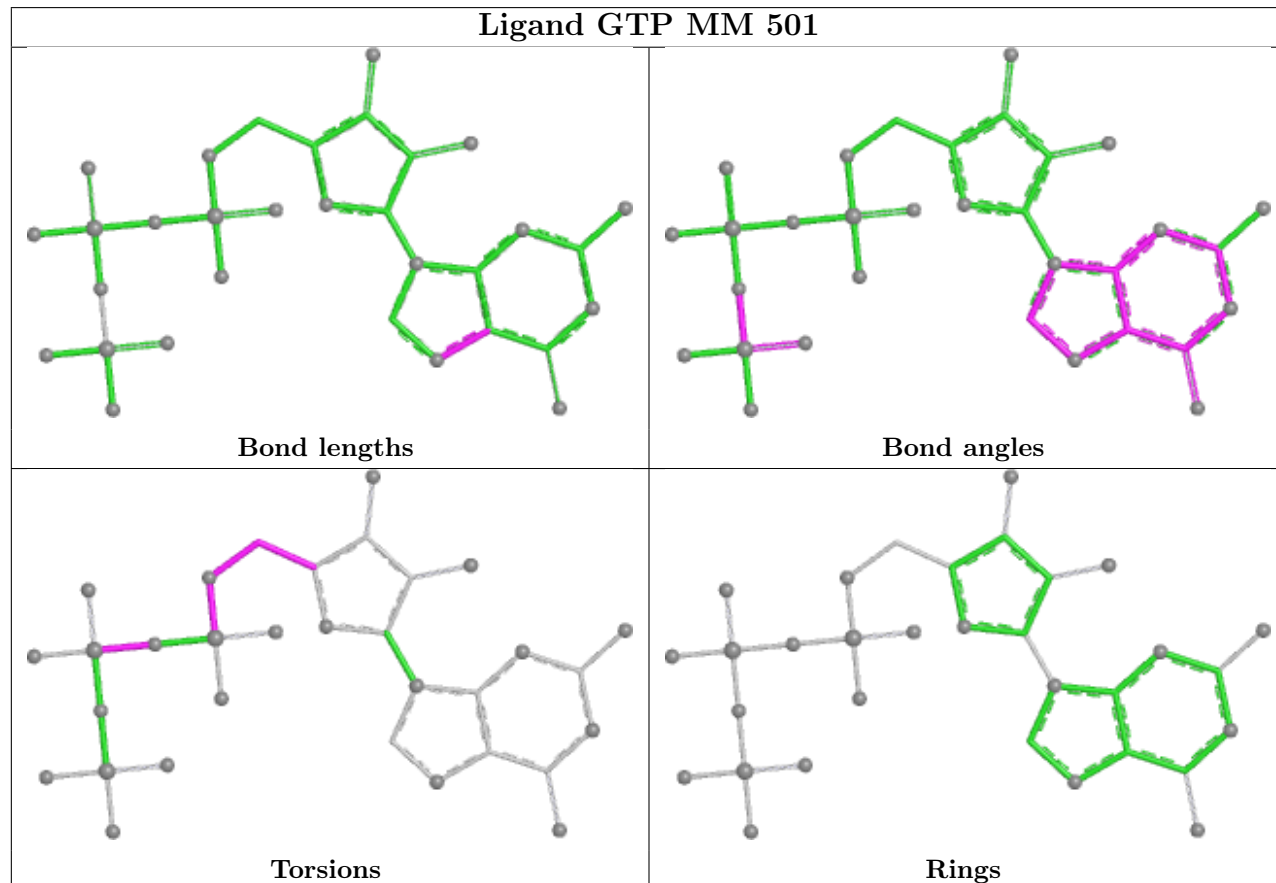


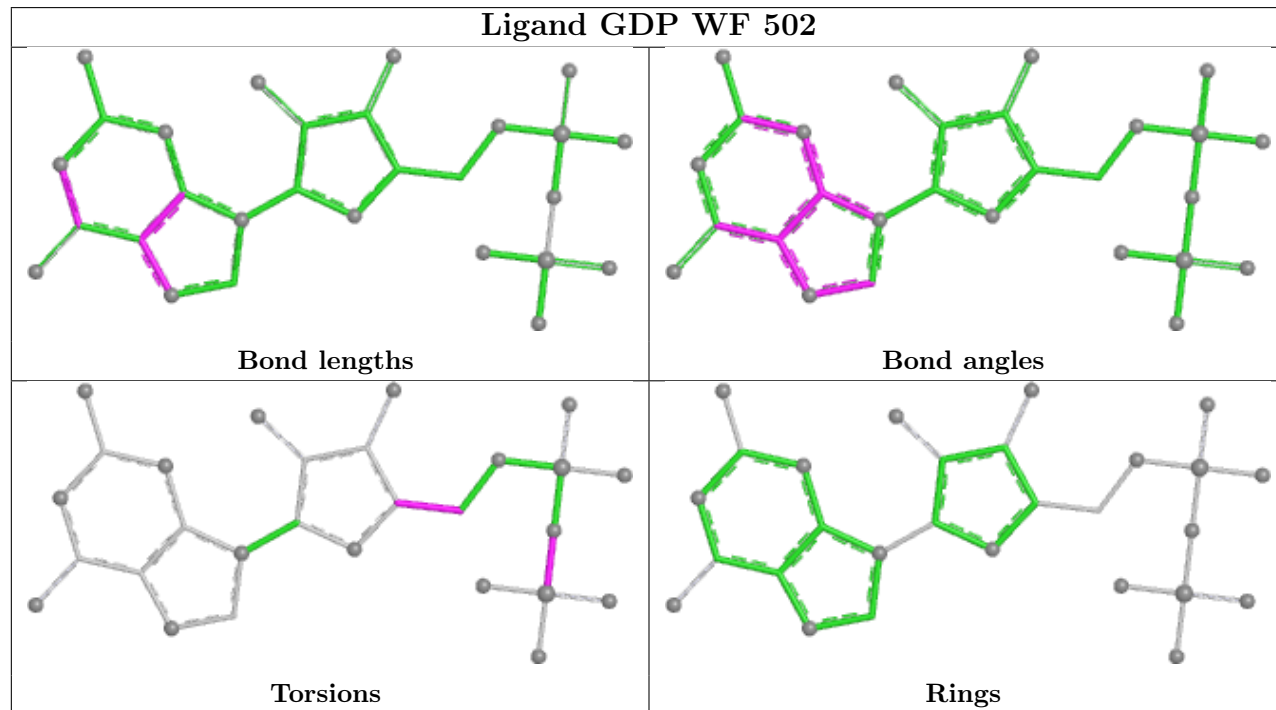
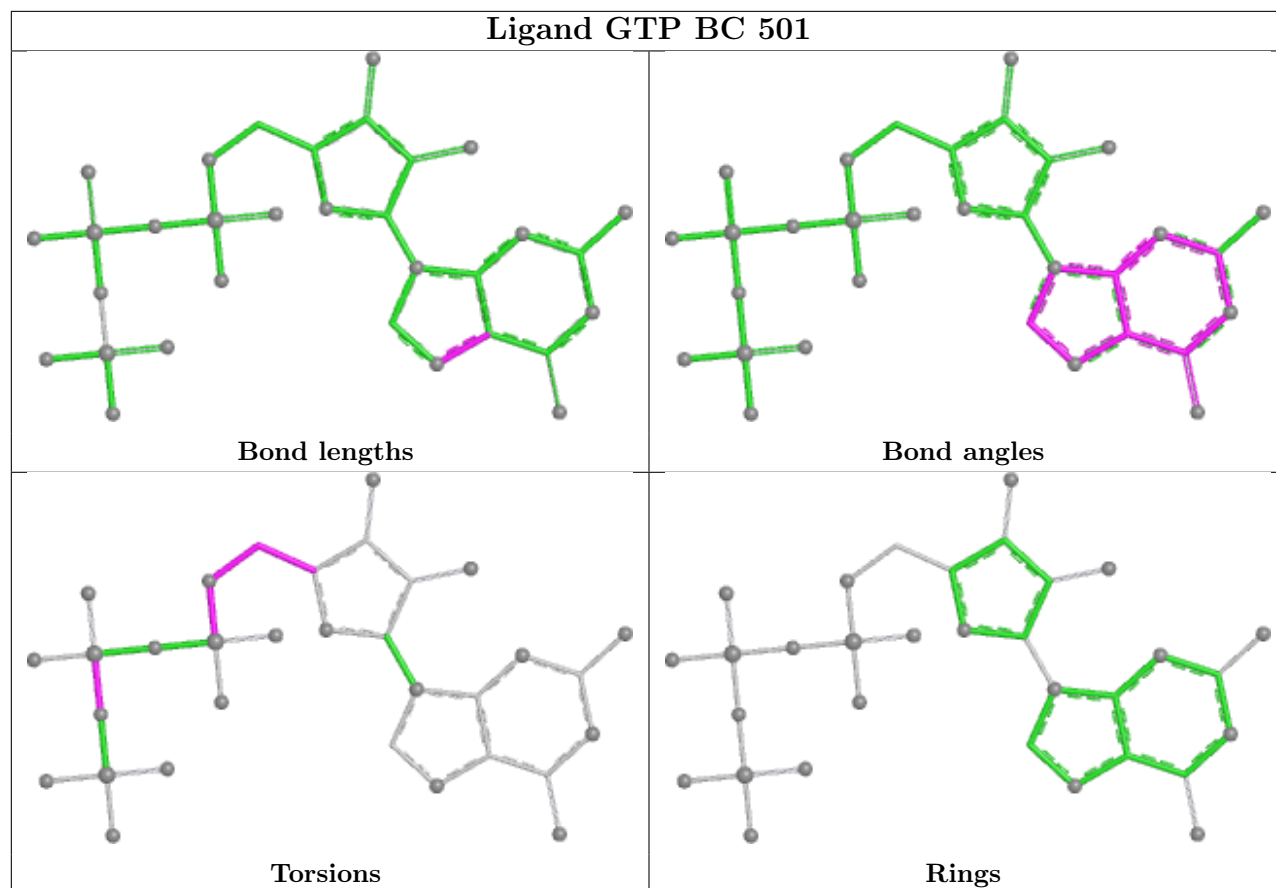


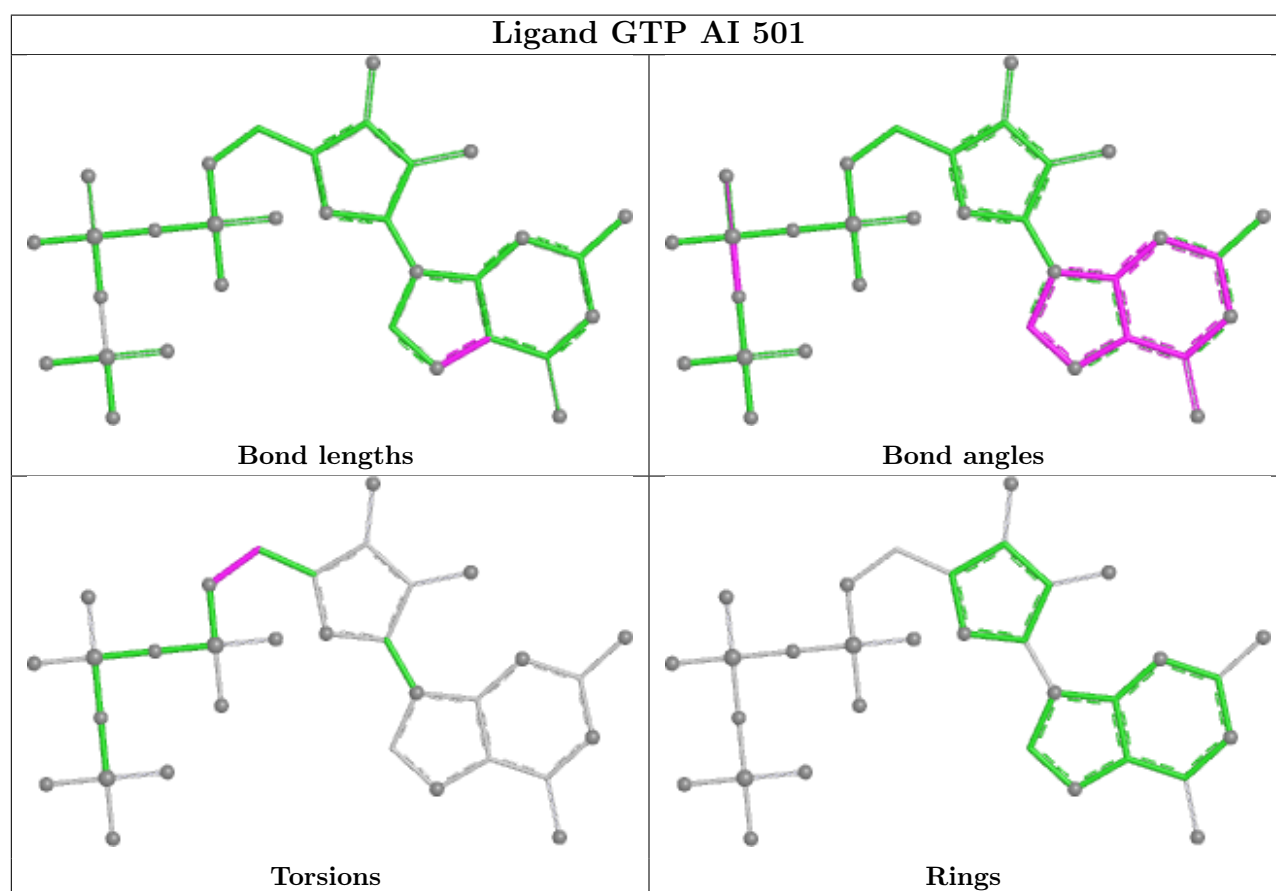
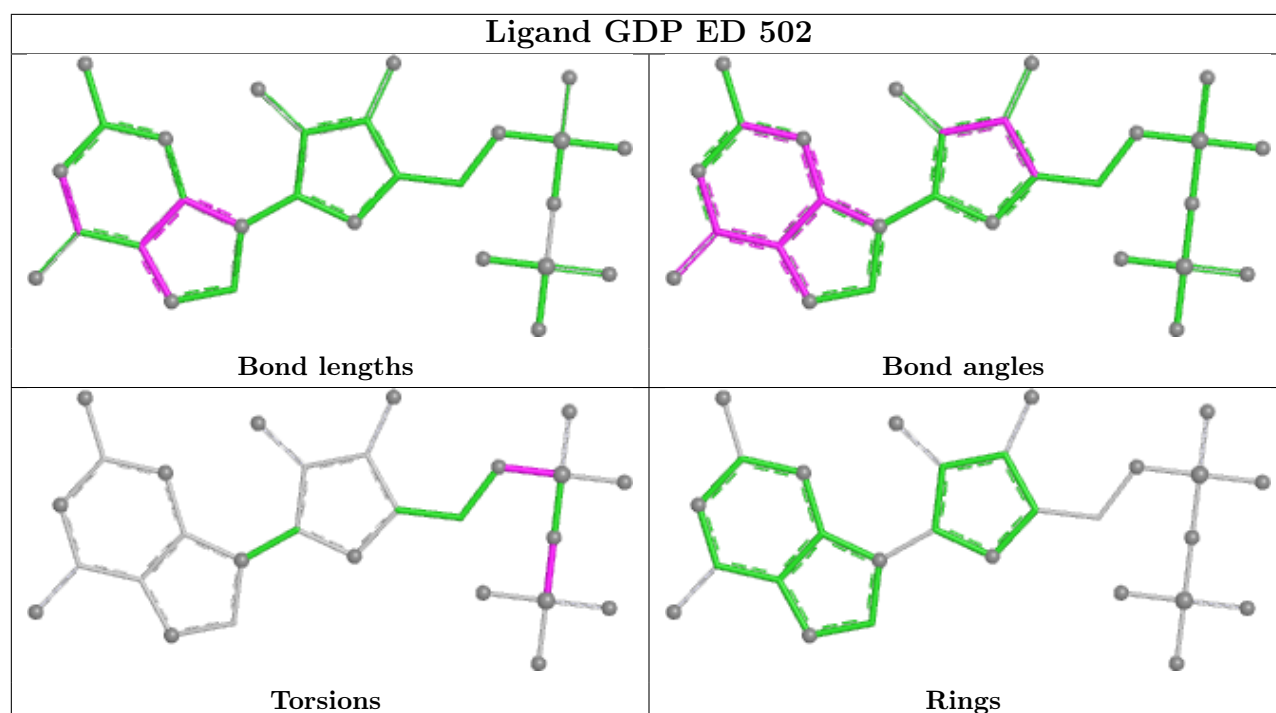
Ligand GTP FE 501

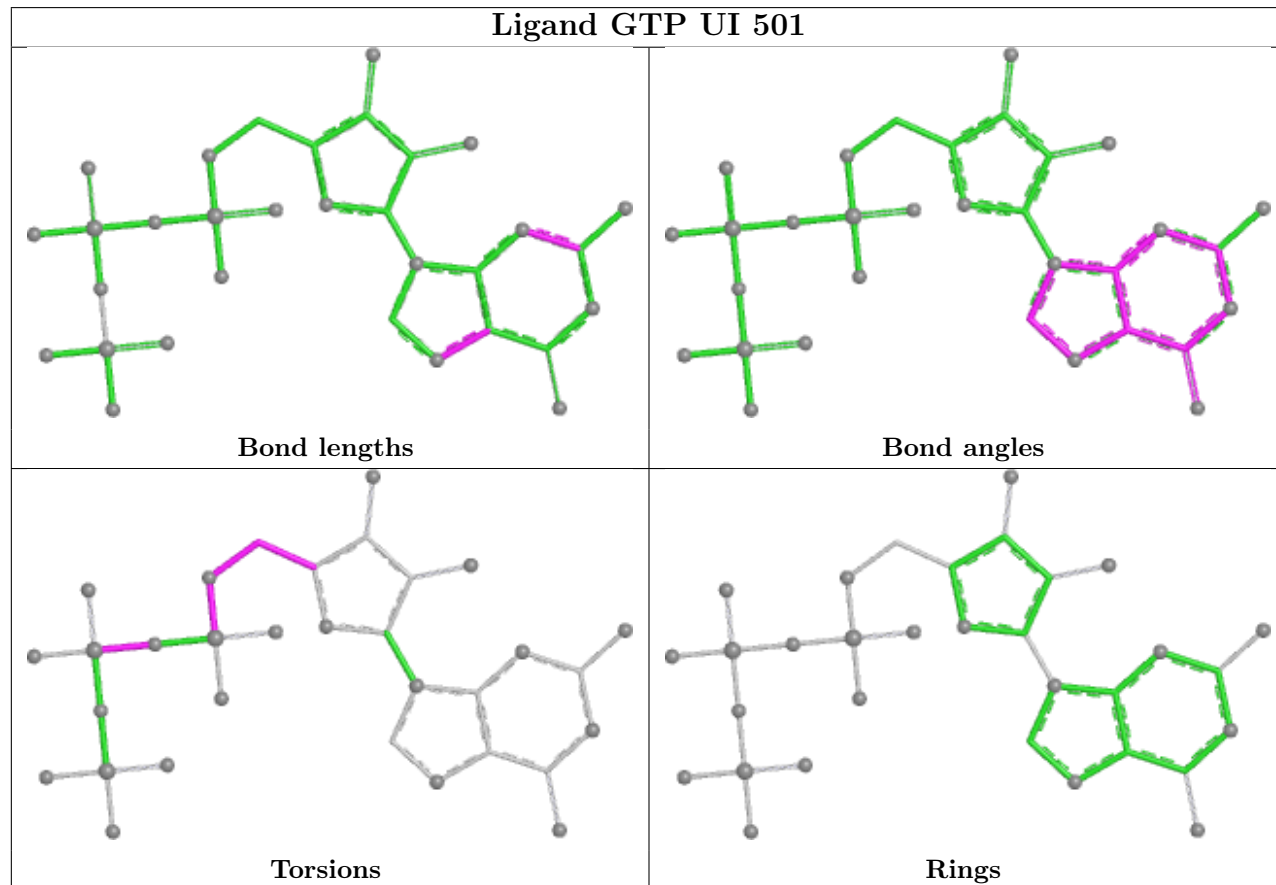
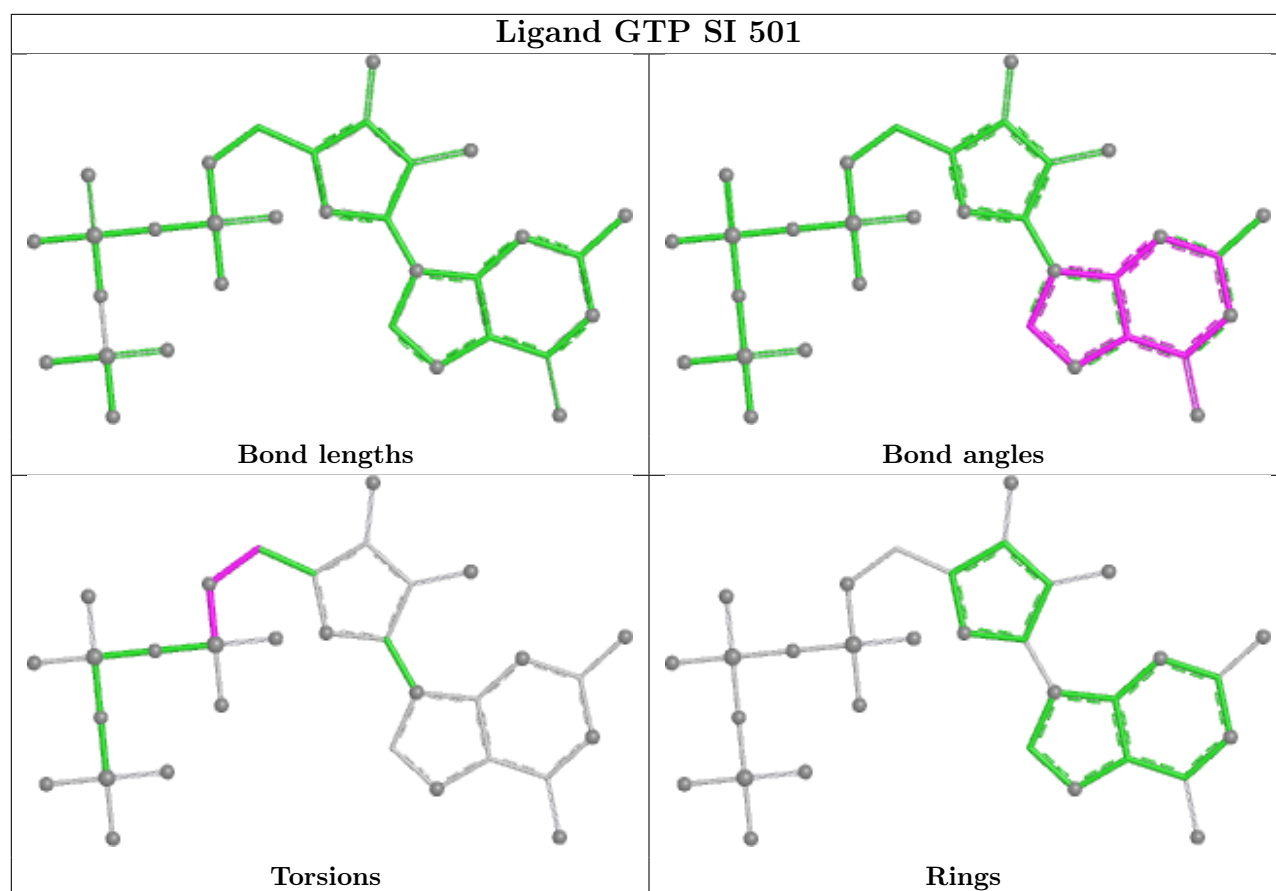


Ligand GTP MM 501

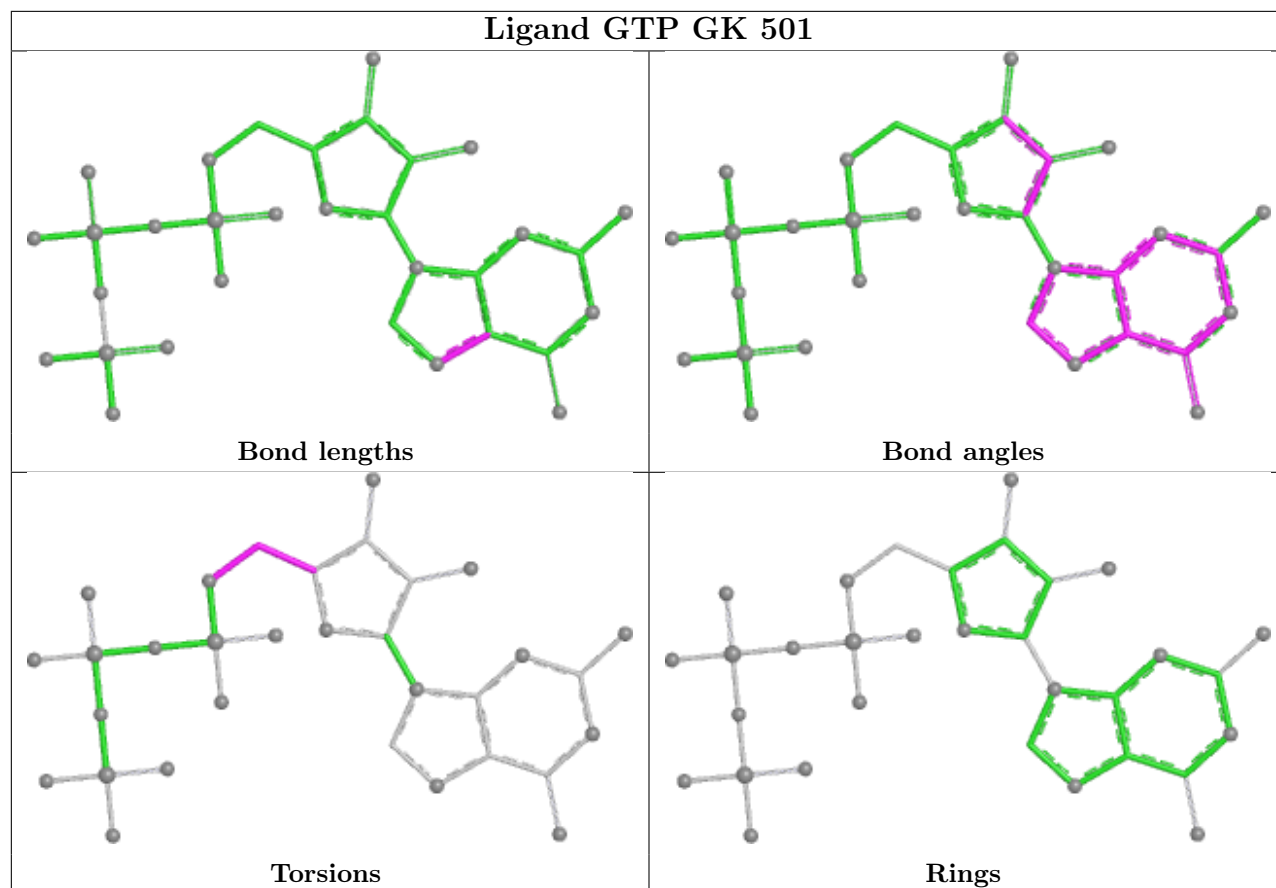




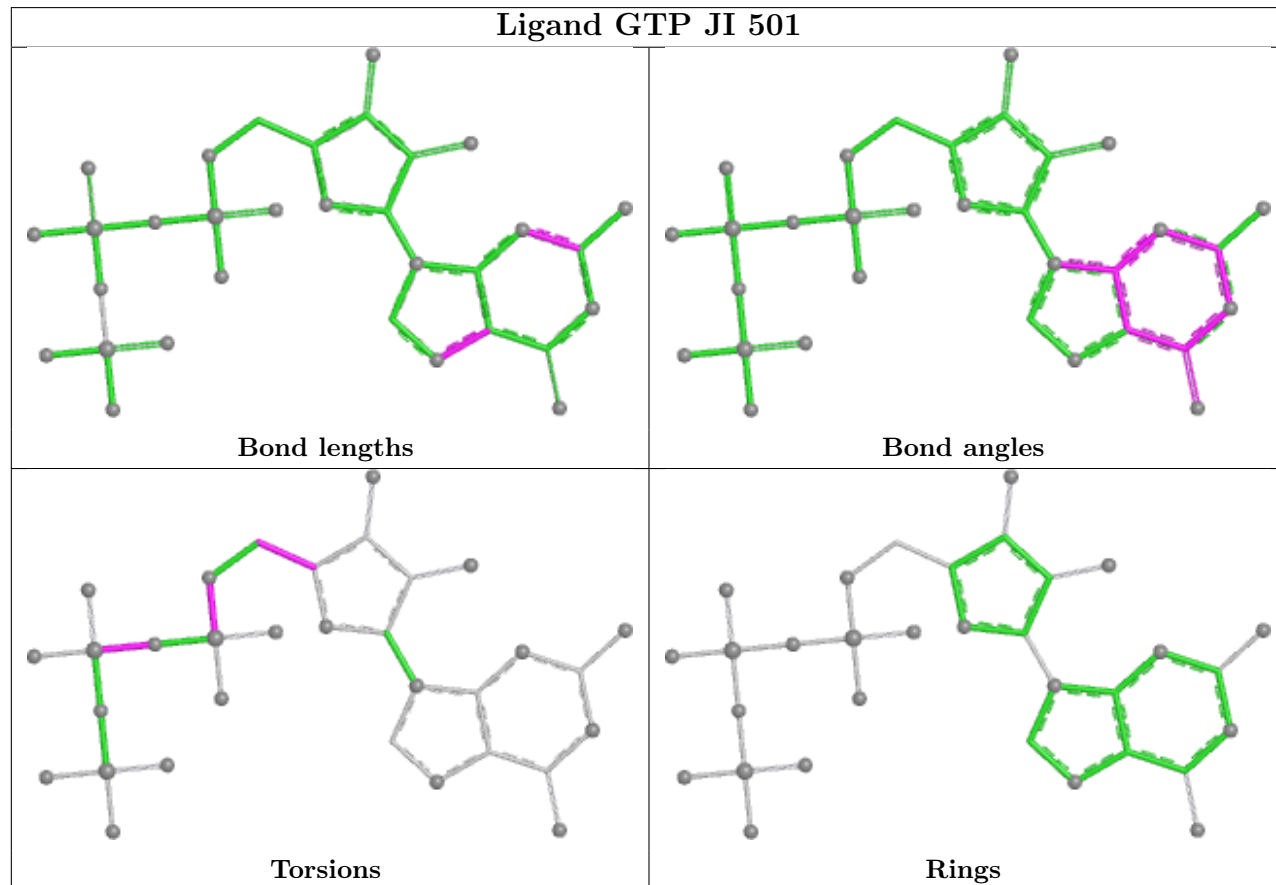


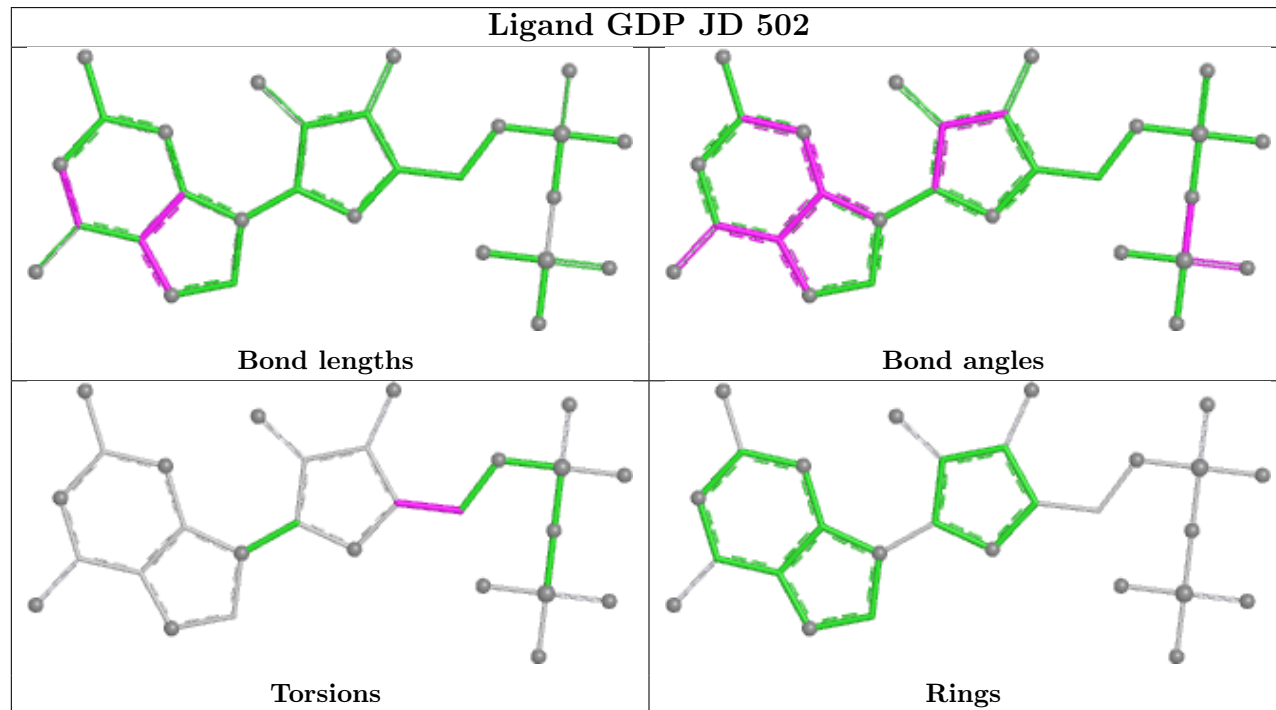
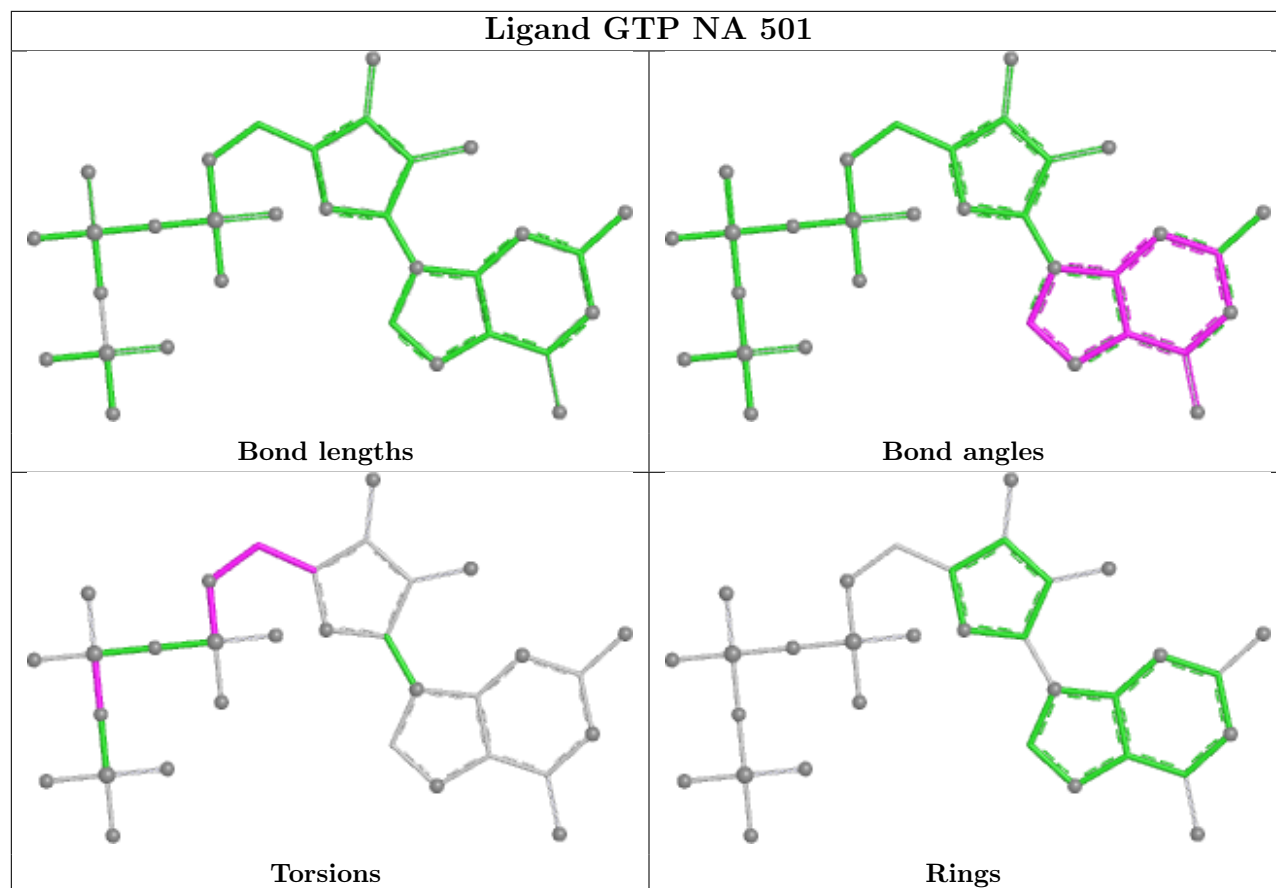


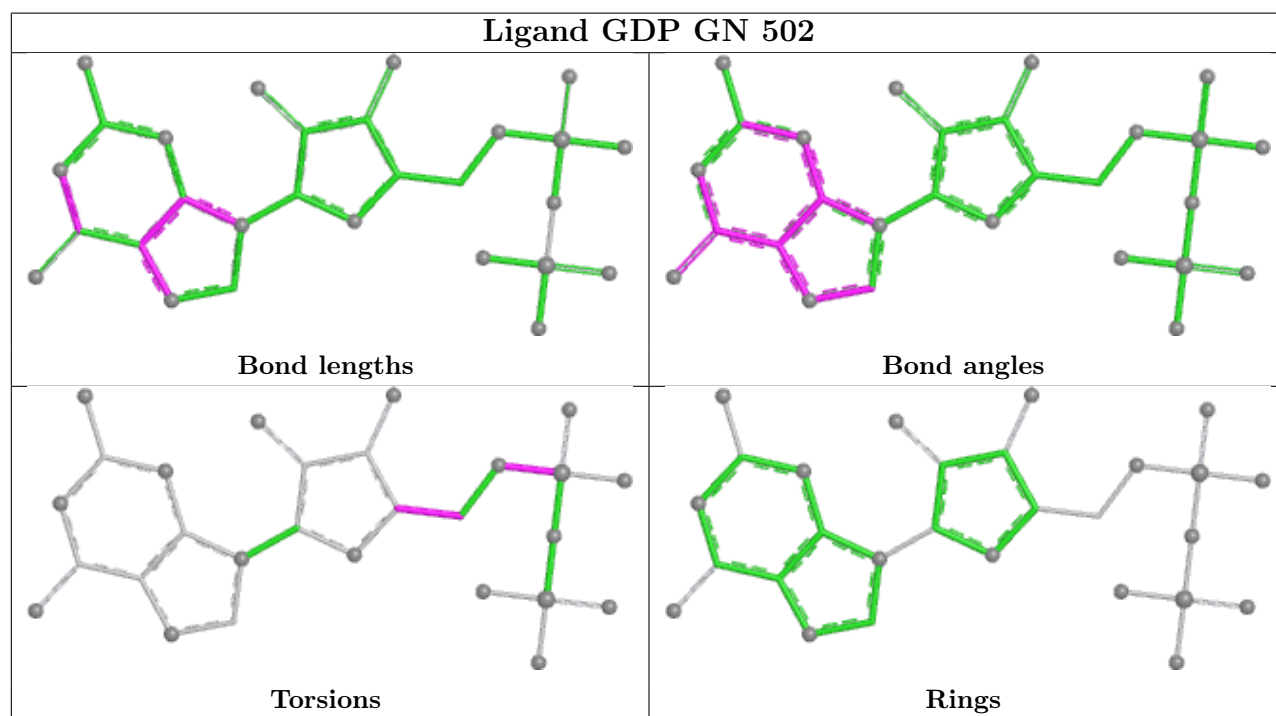
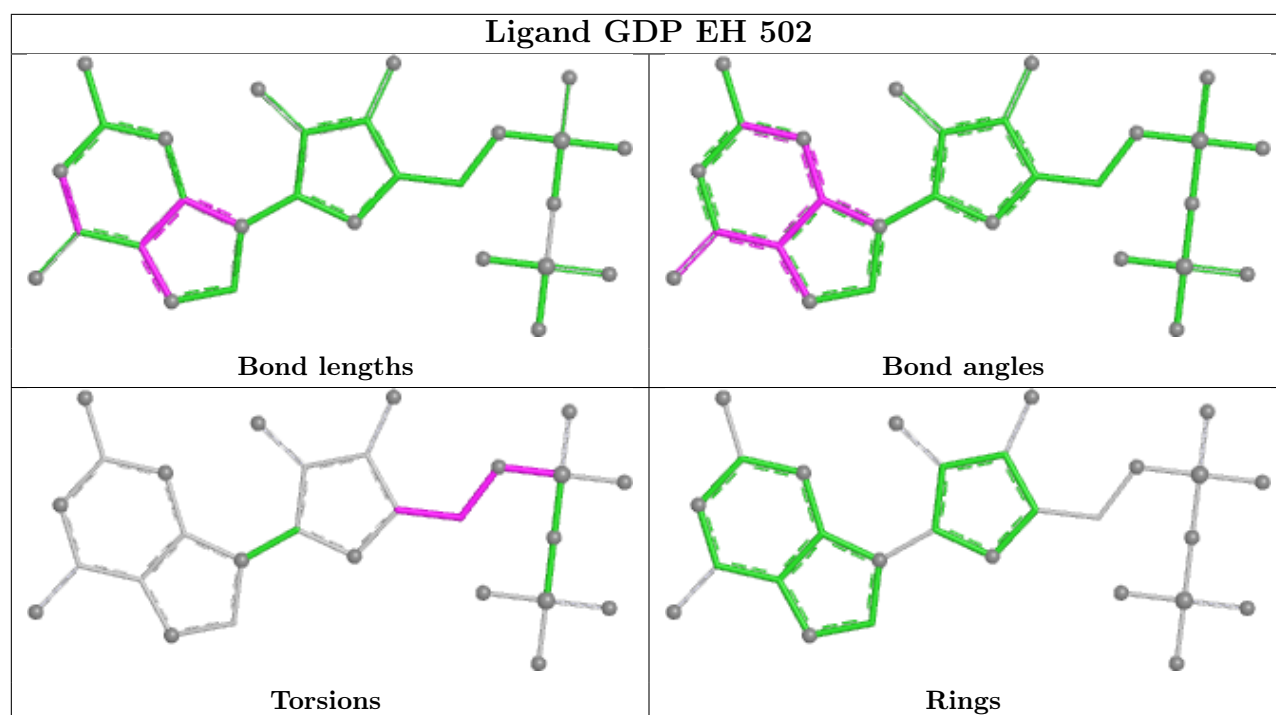
Ligand GTP GK 501

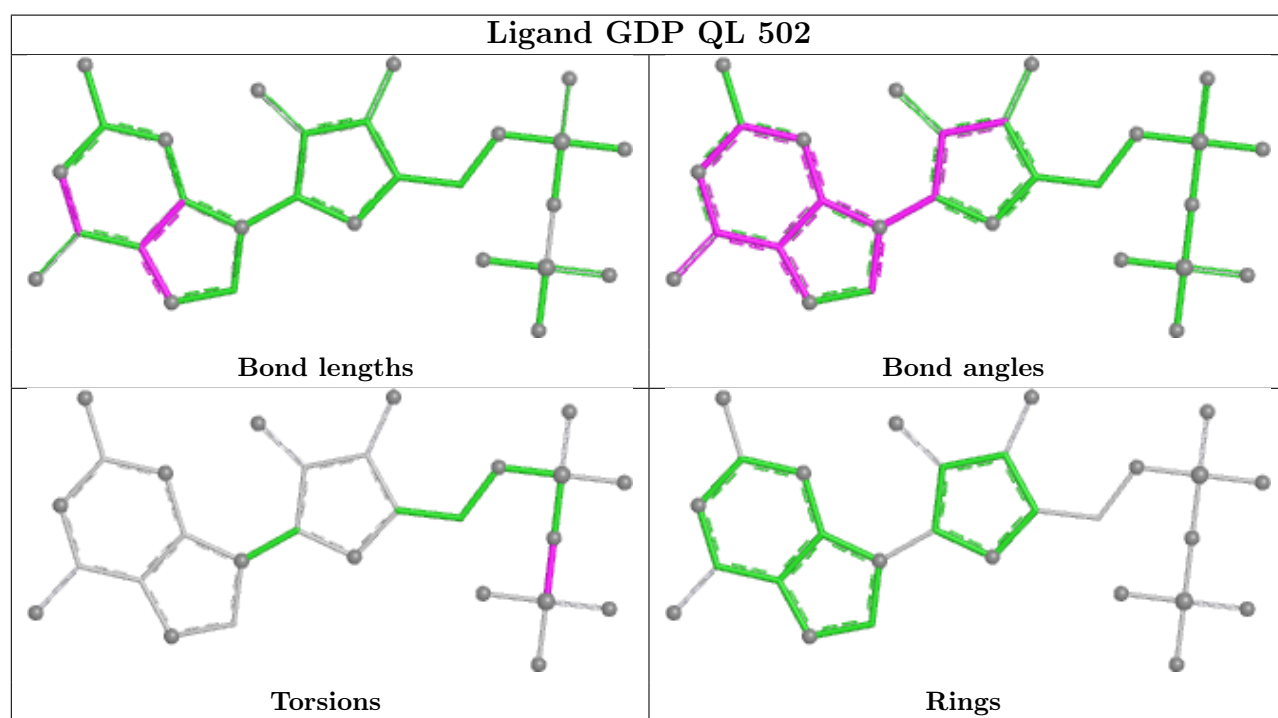
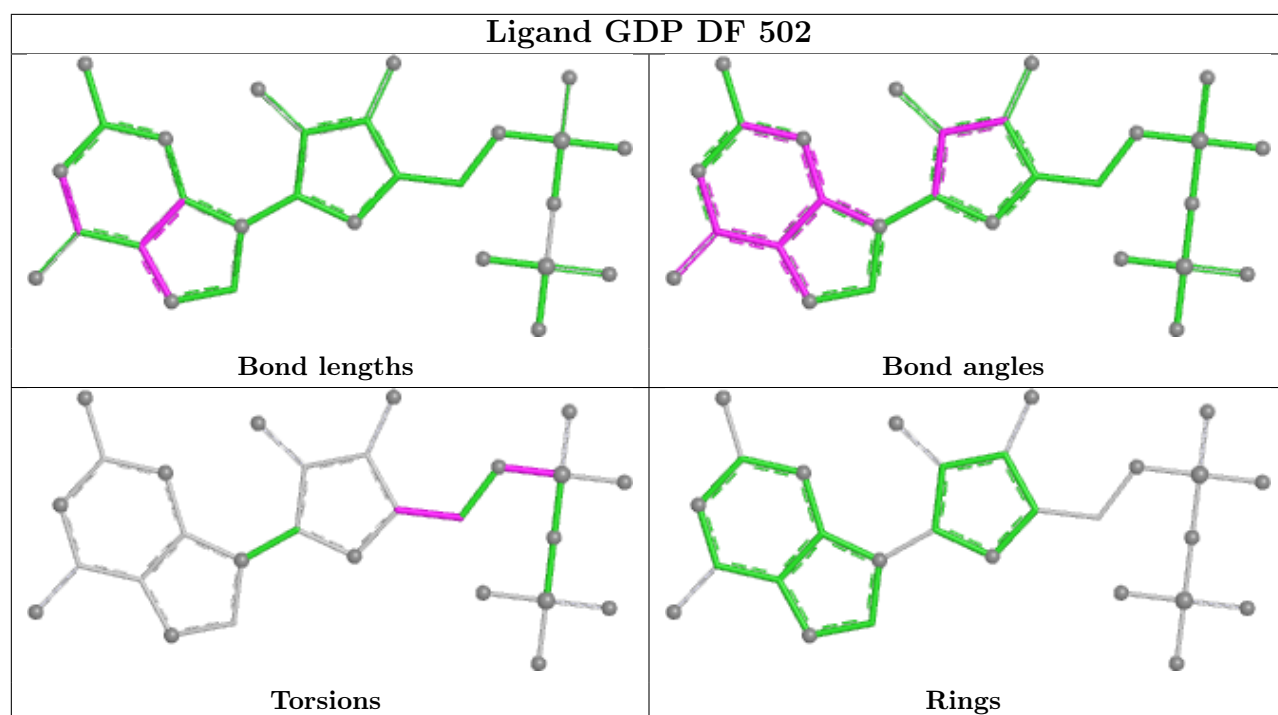


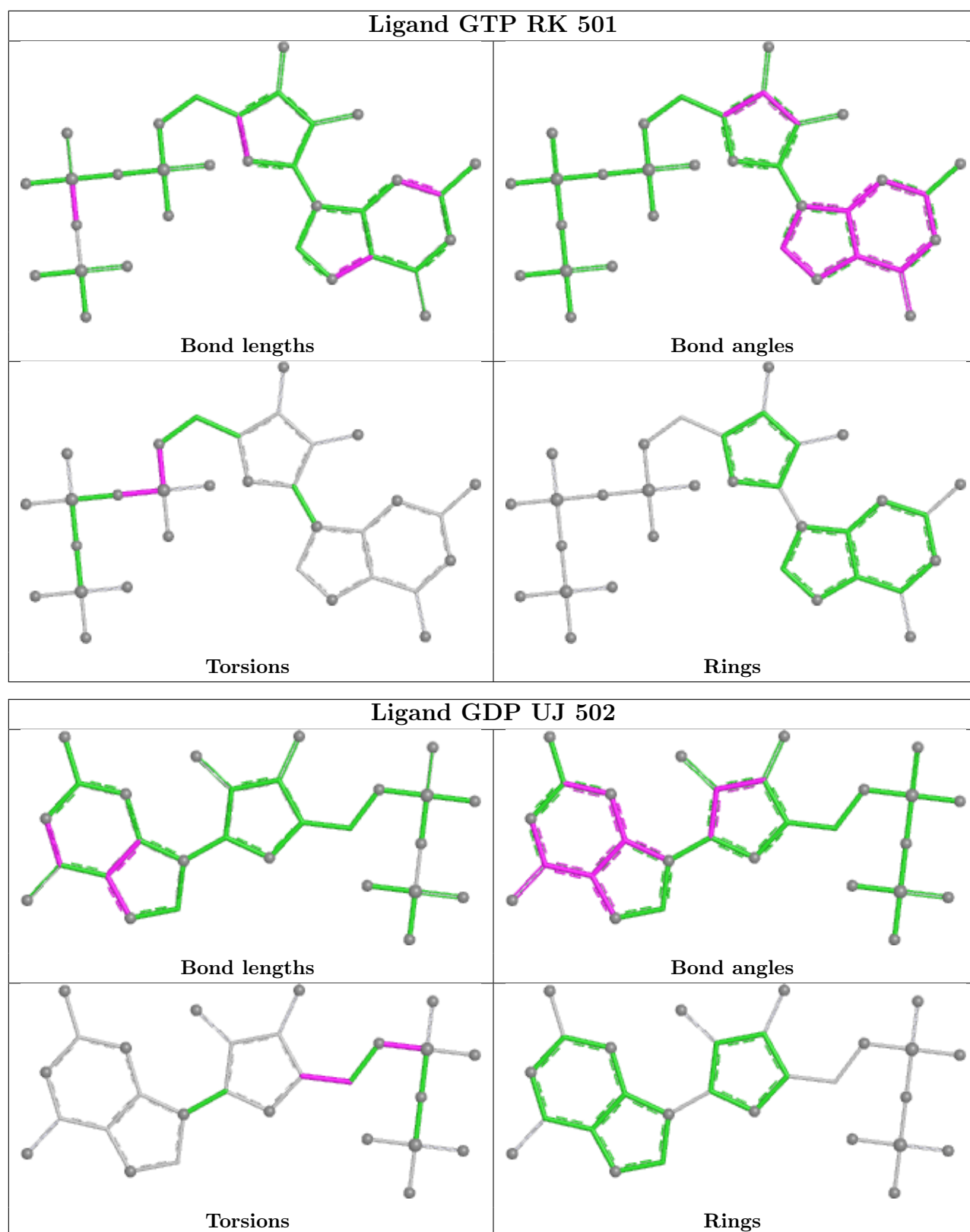
Ligand GTP JI 501

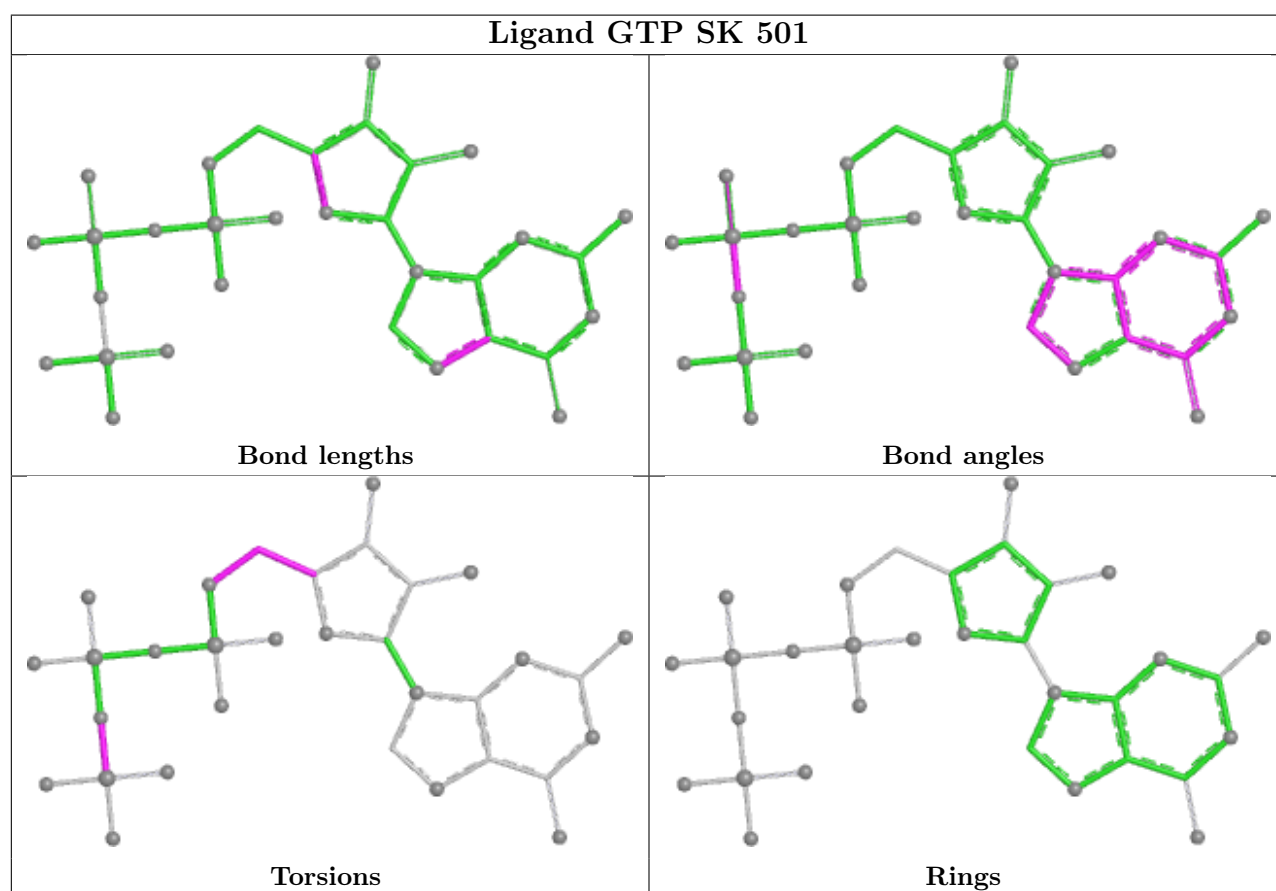
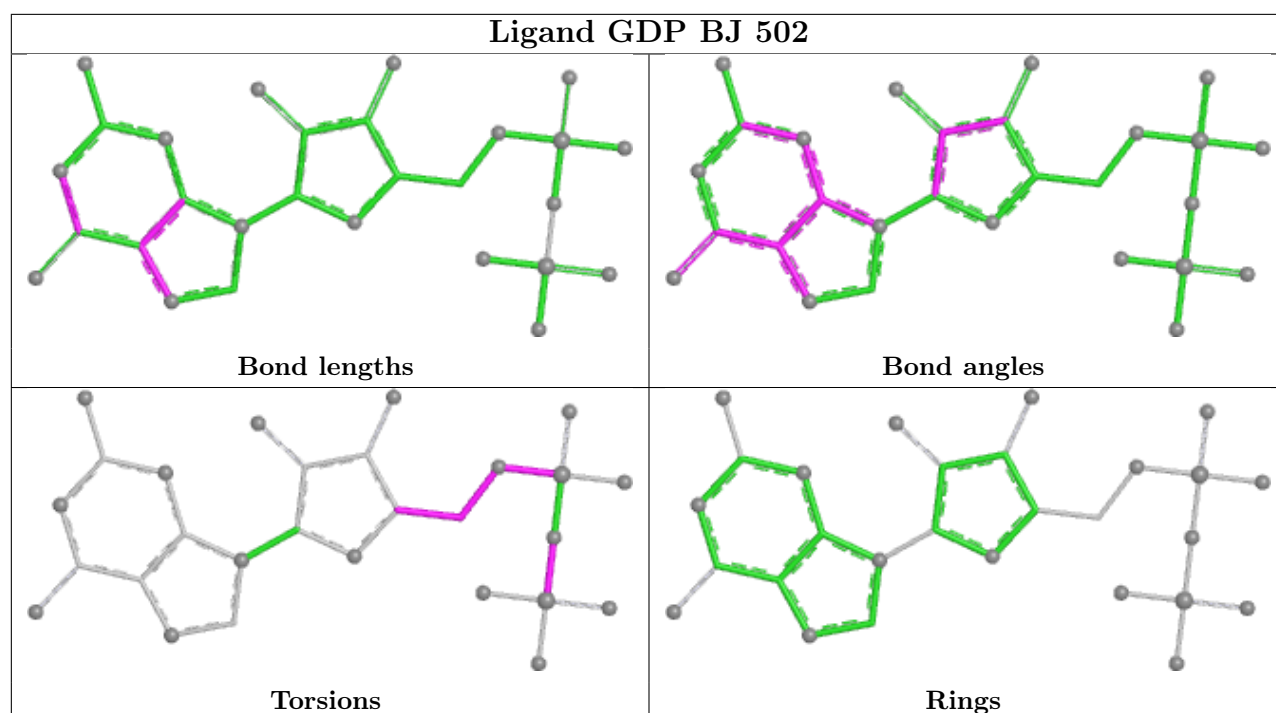




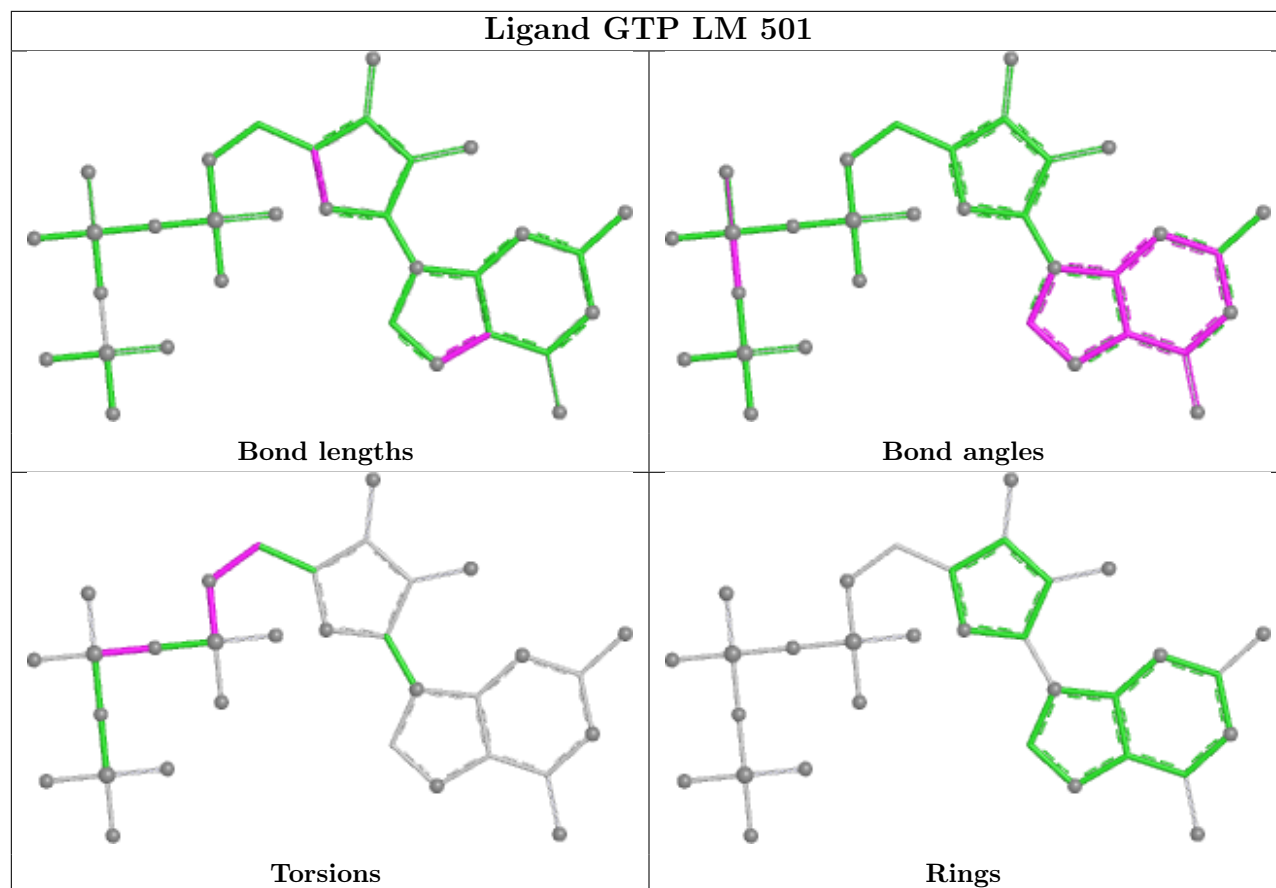




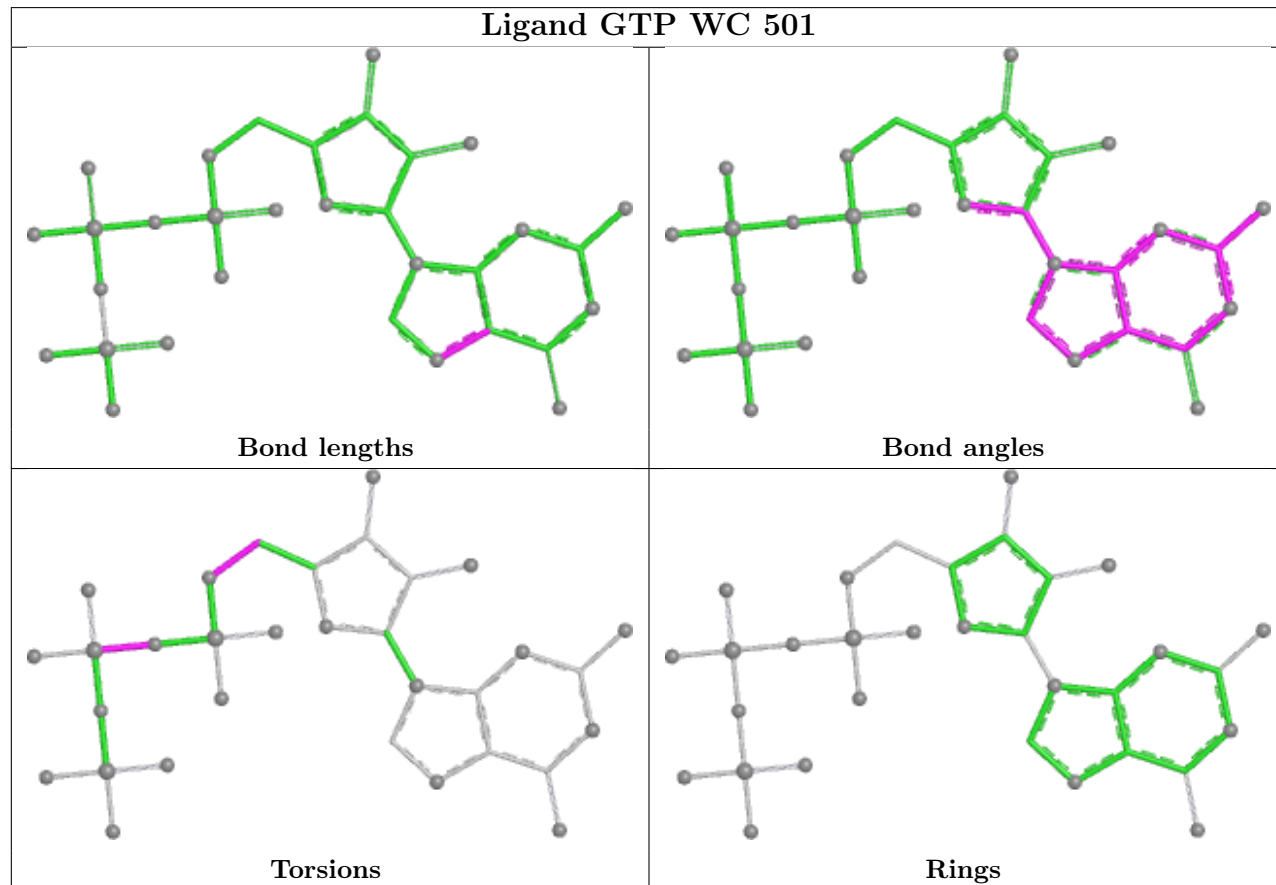




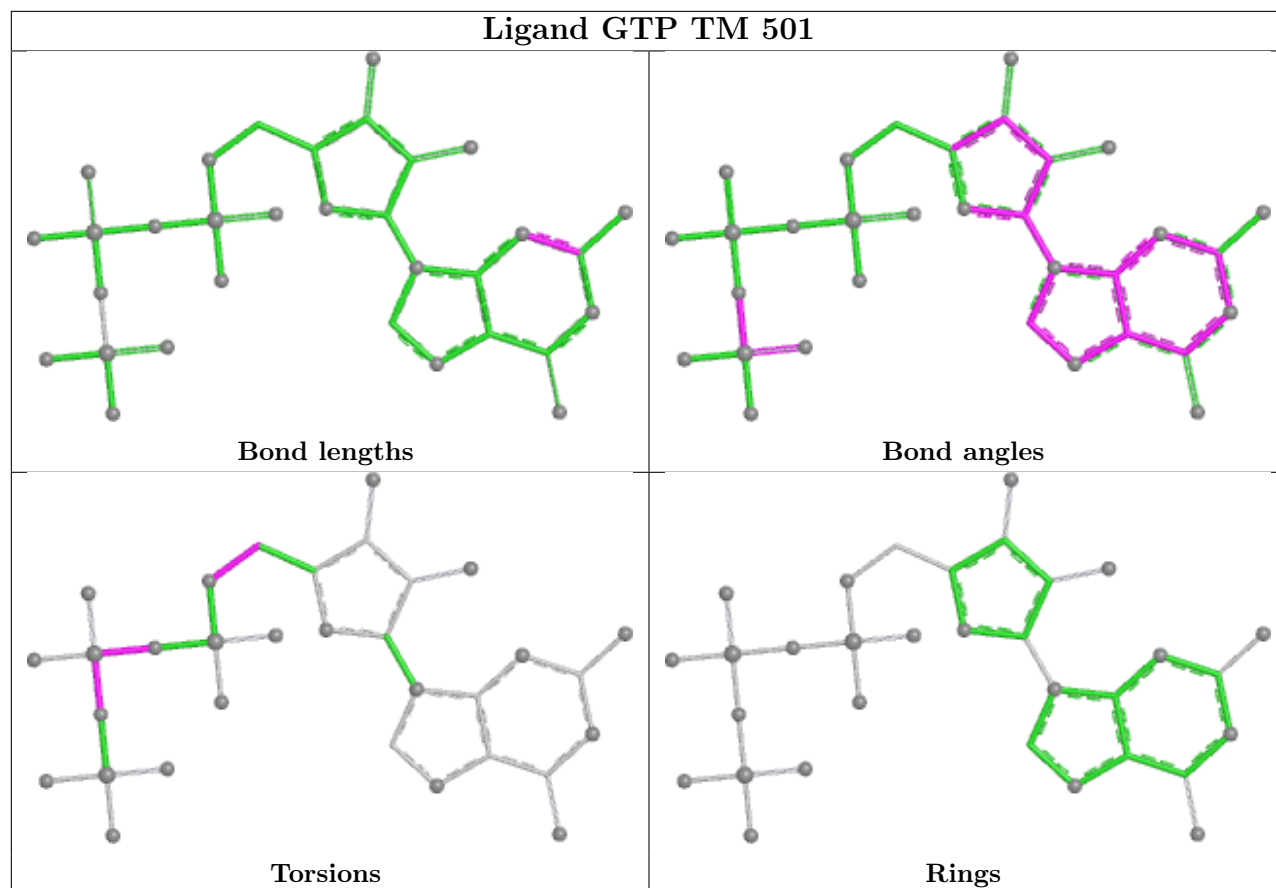
Ligand GTP LM 501



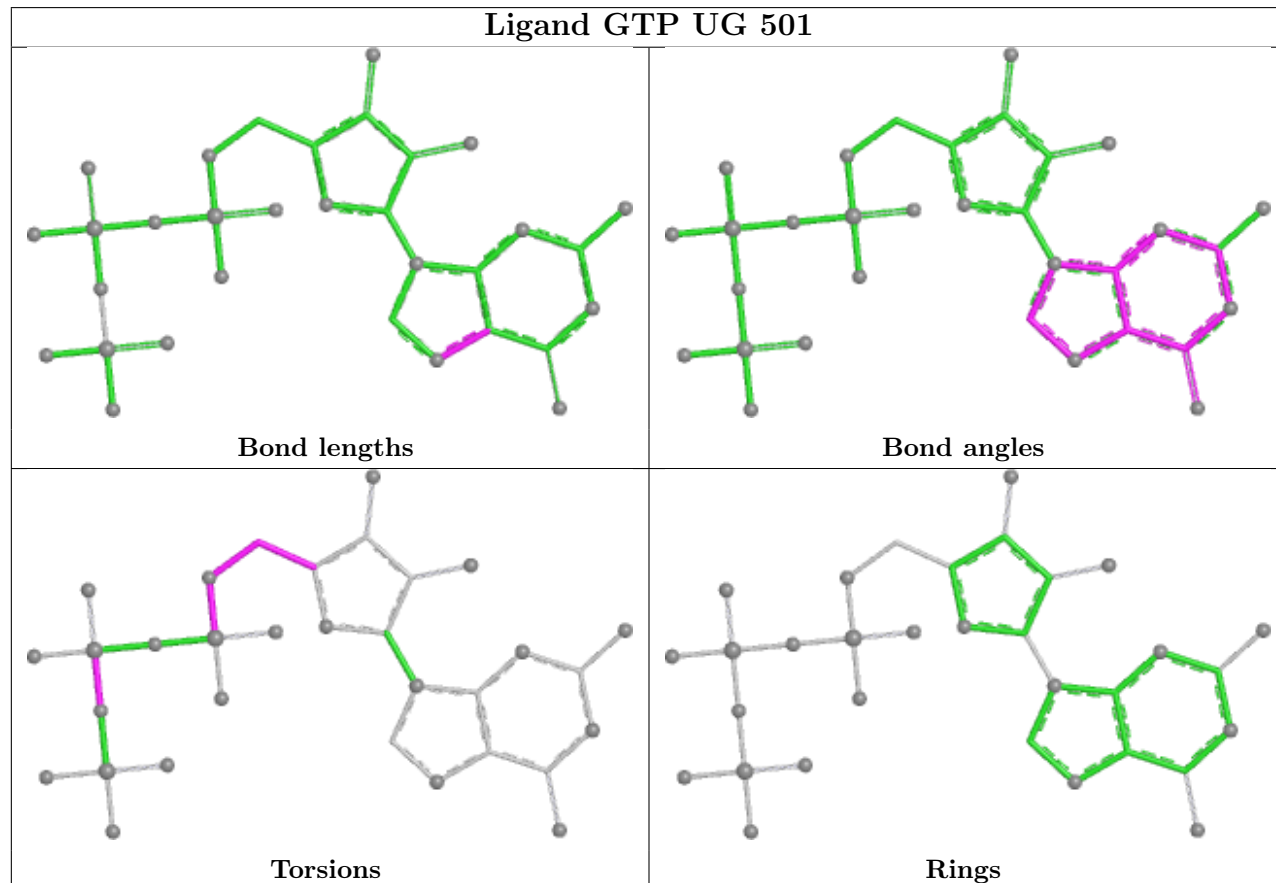
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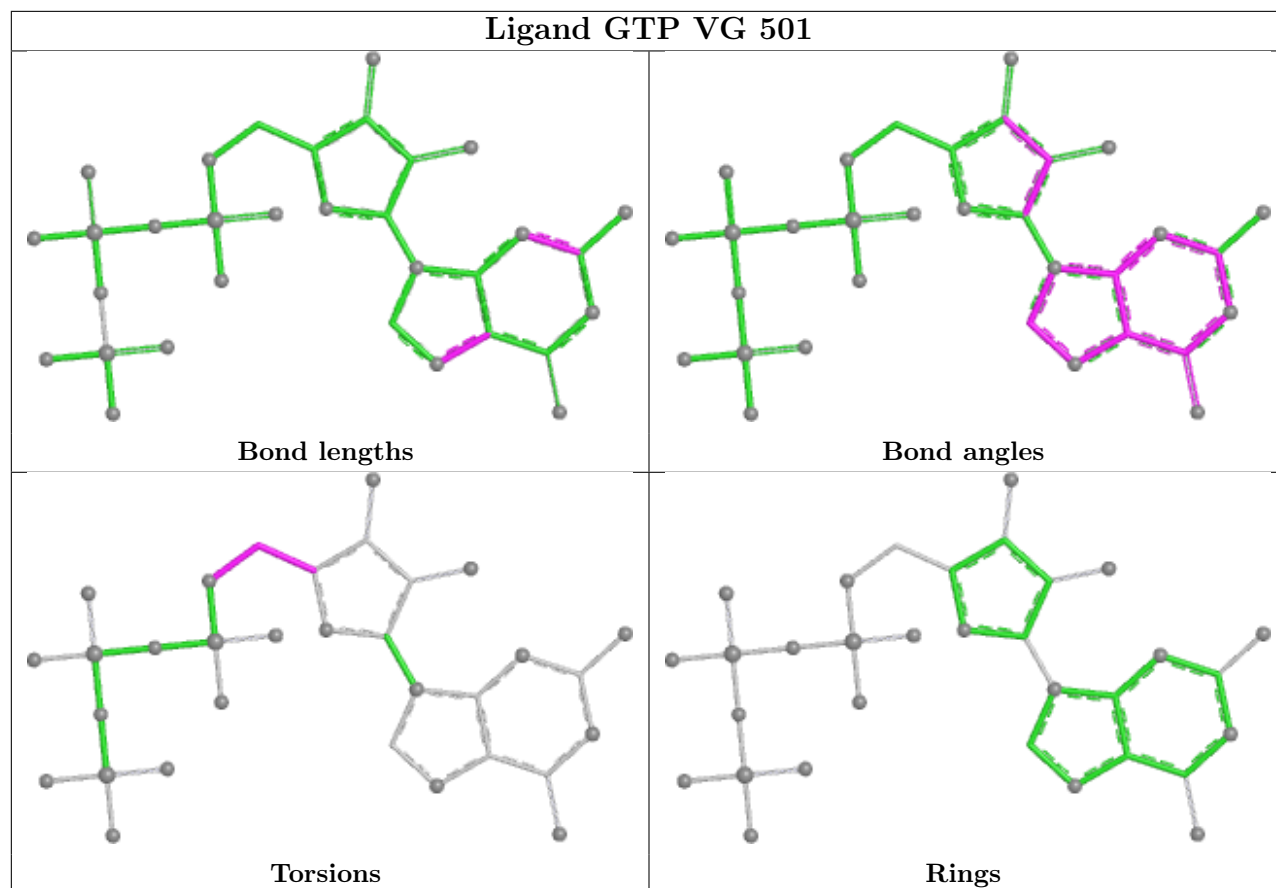
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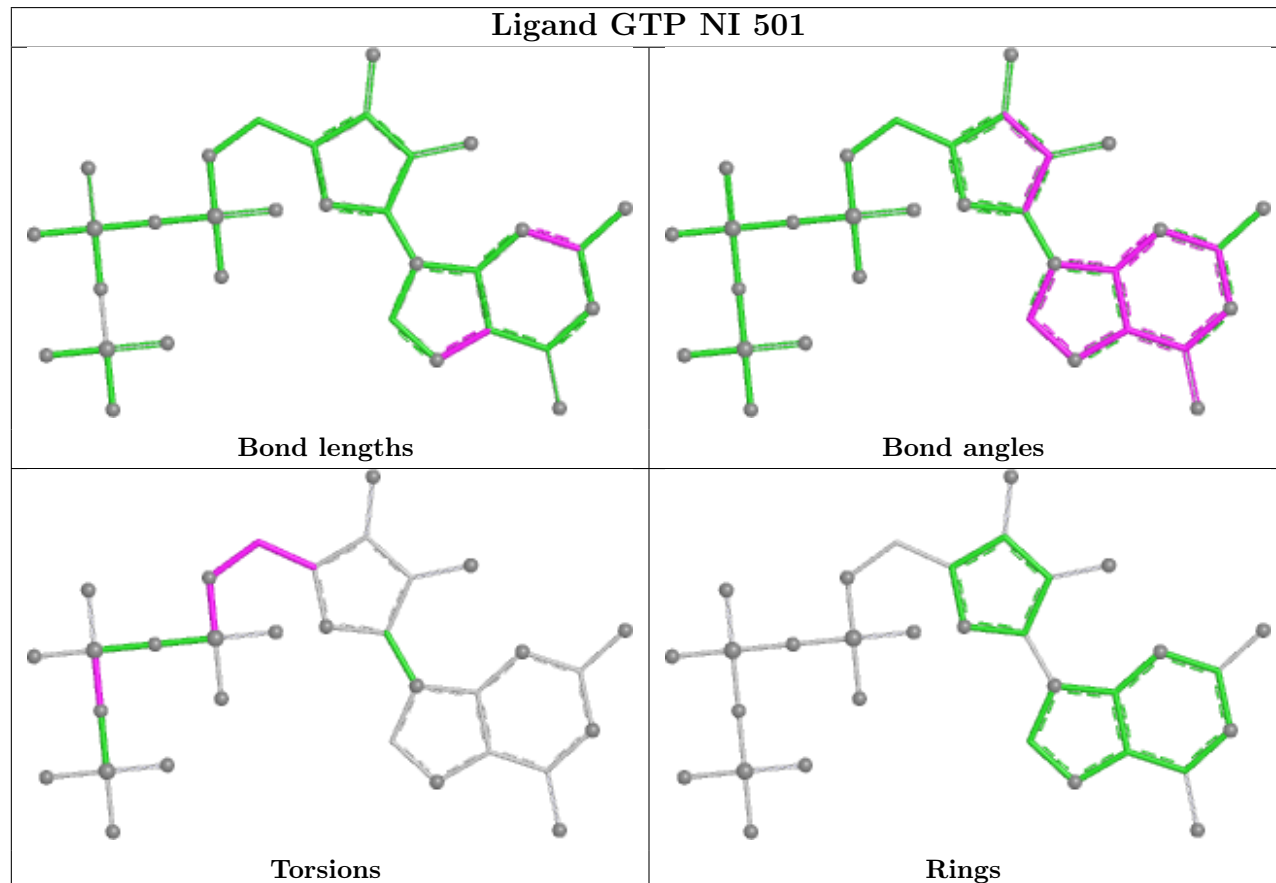
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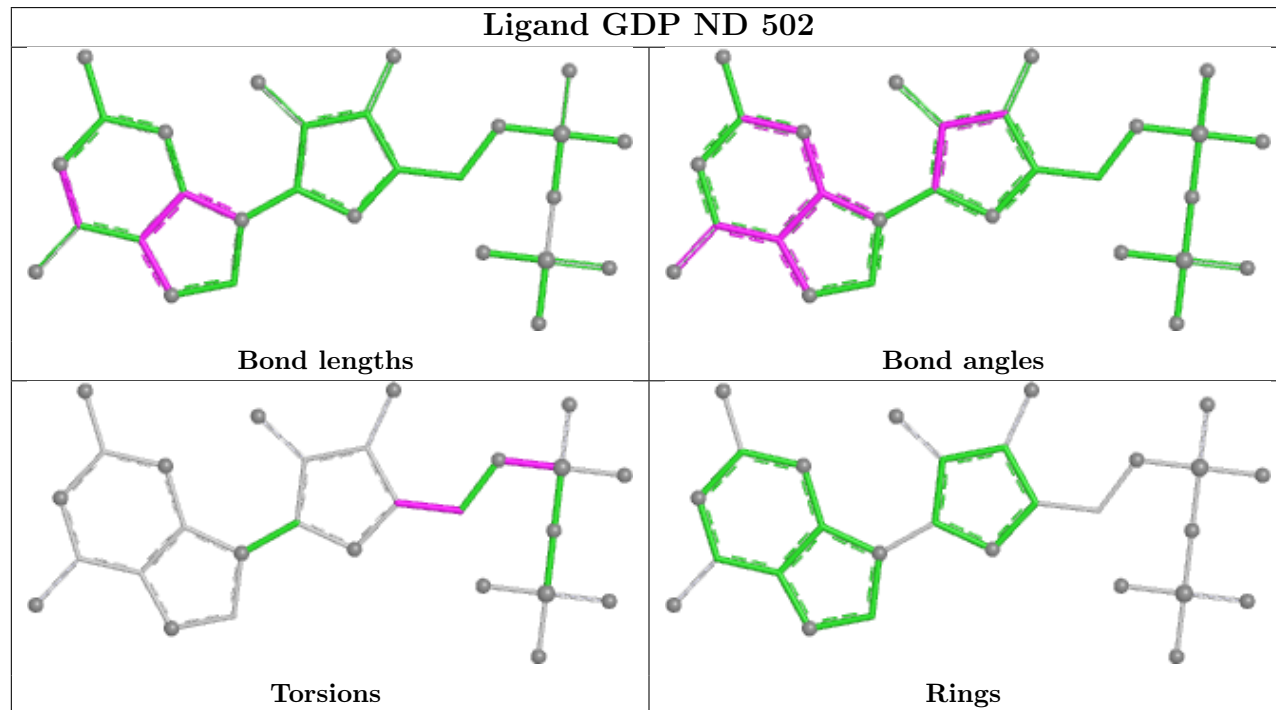
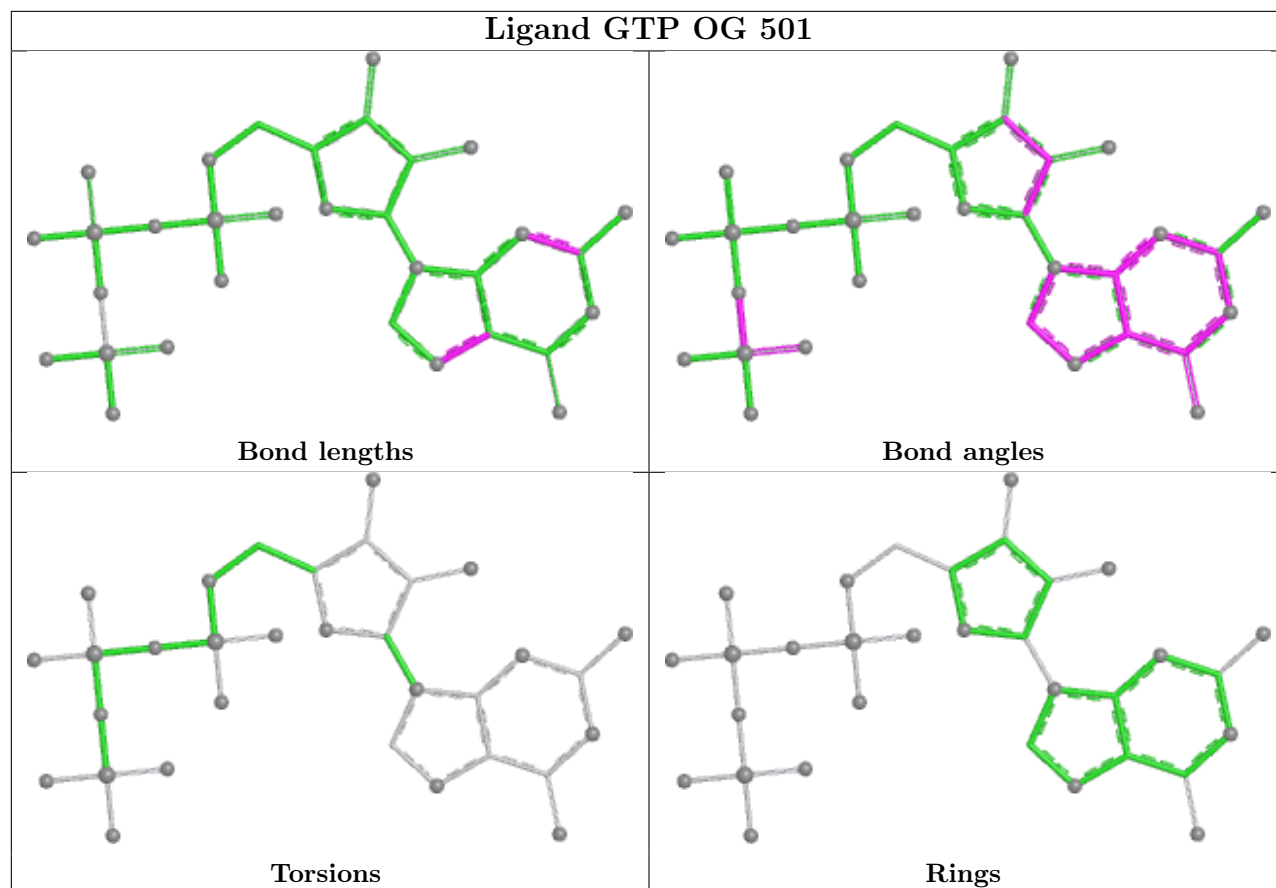


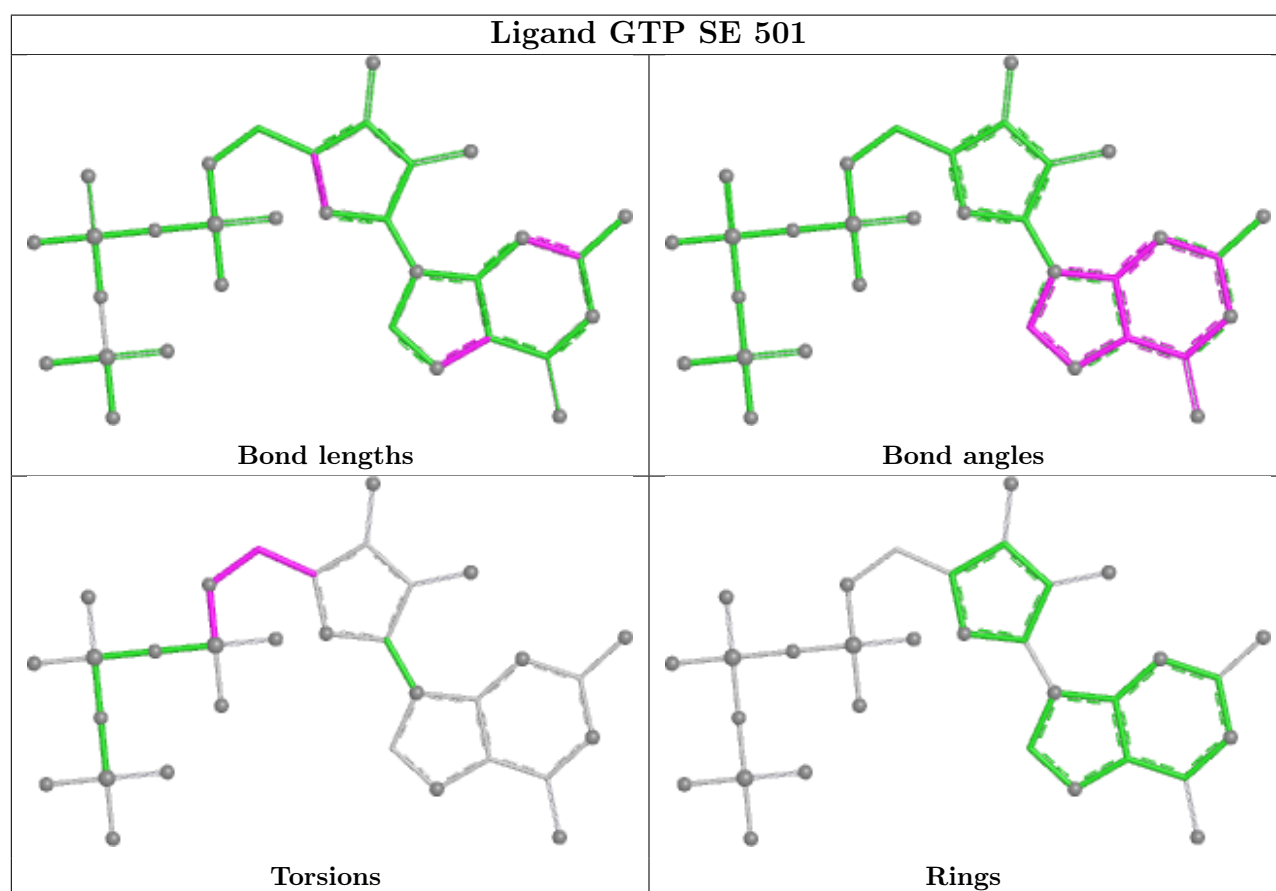
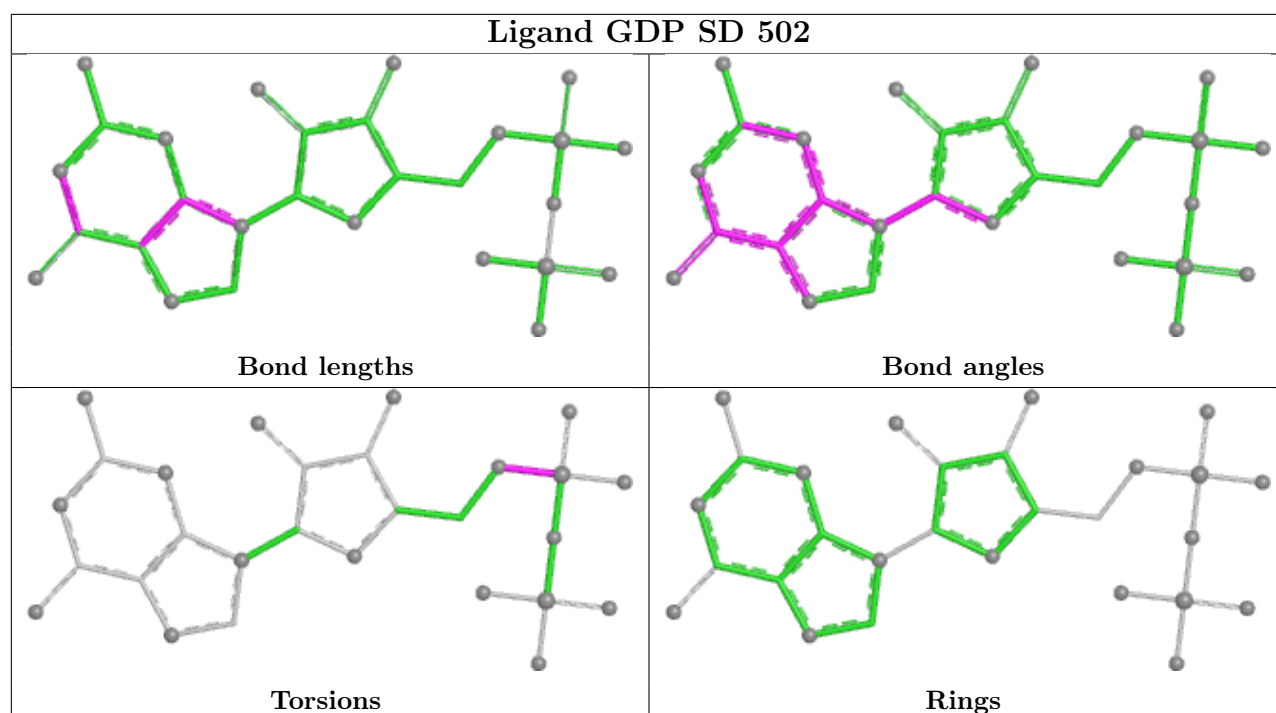
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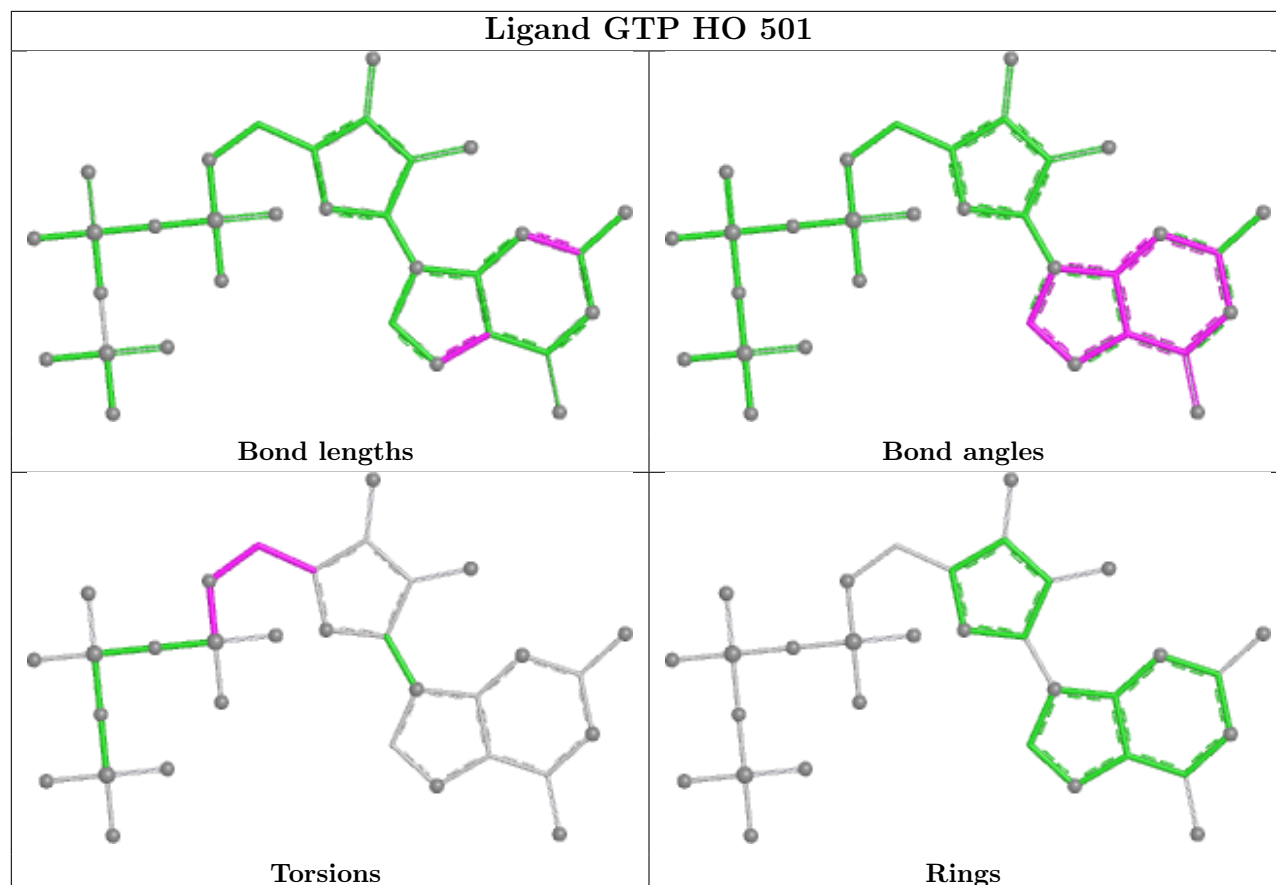
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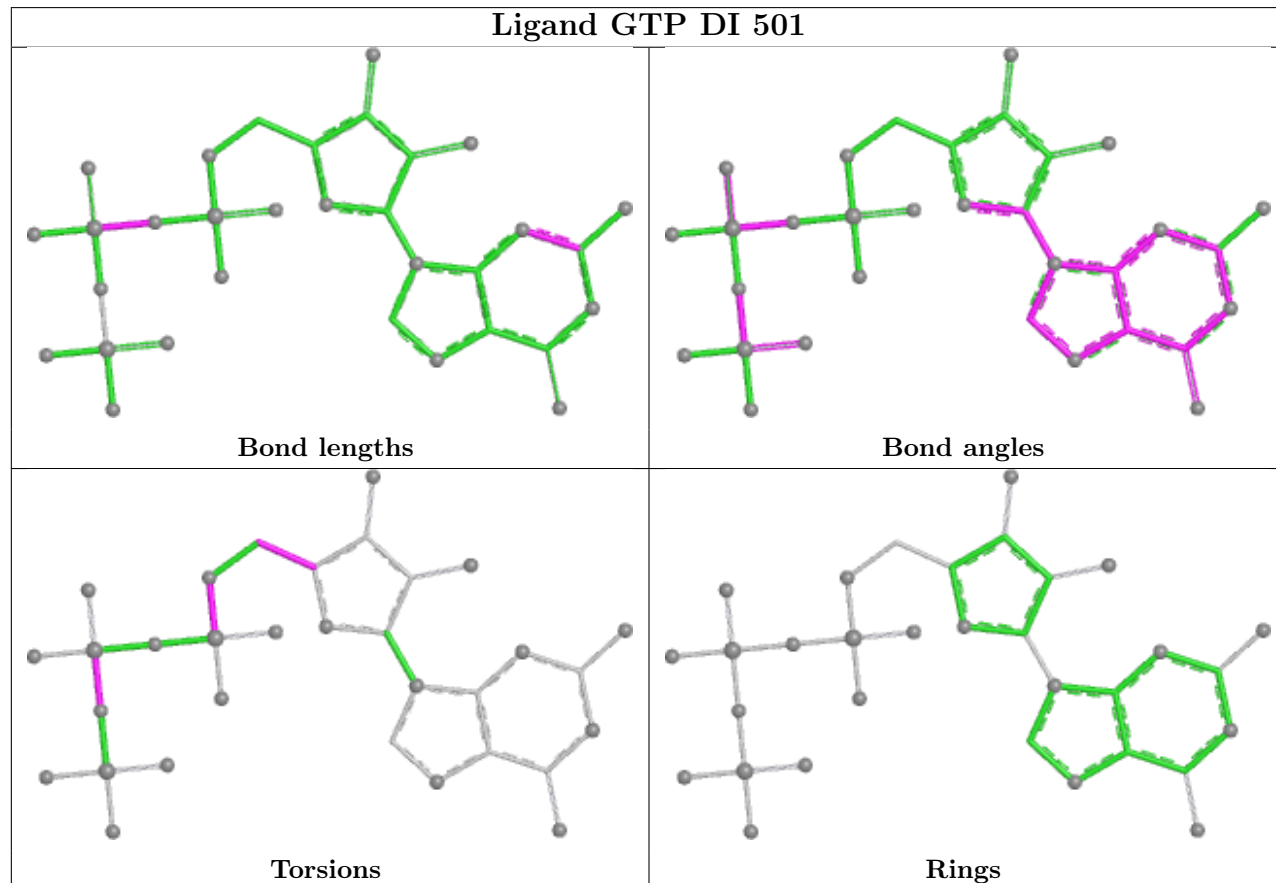


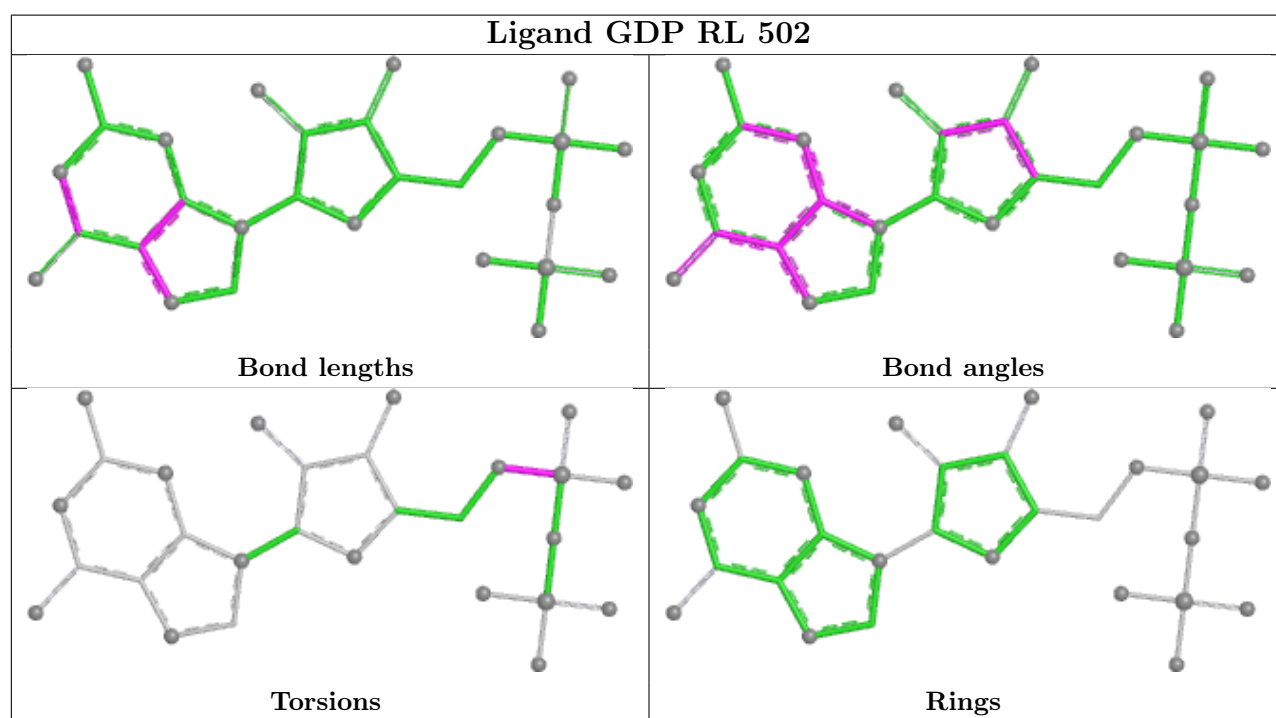
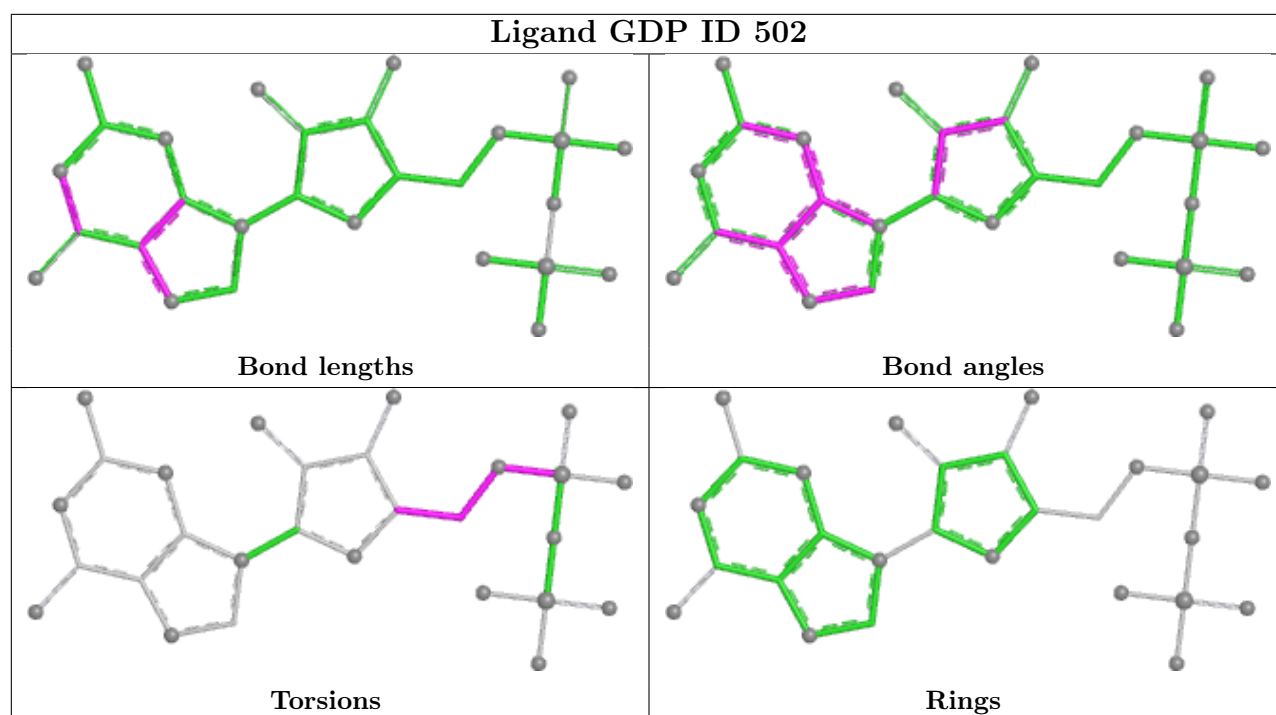


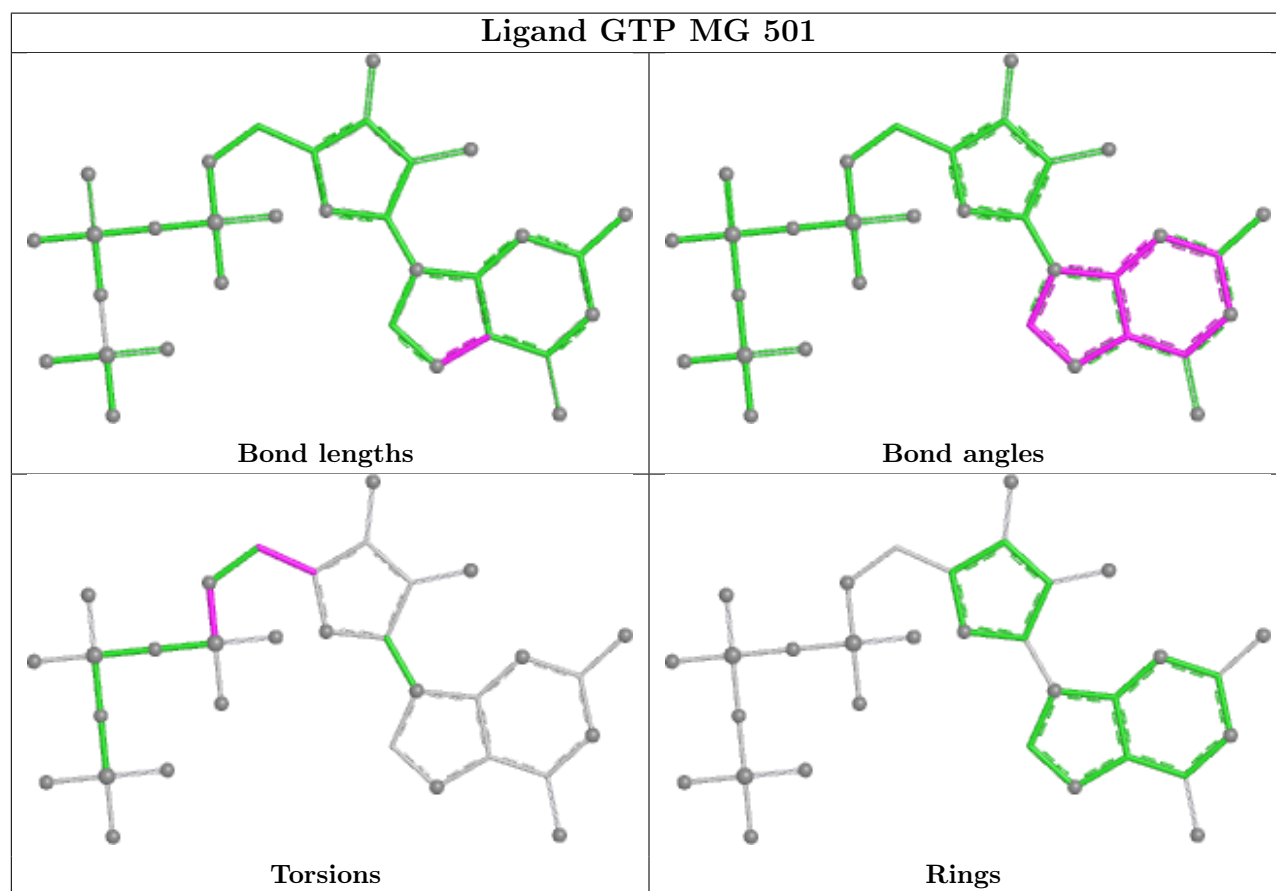
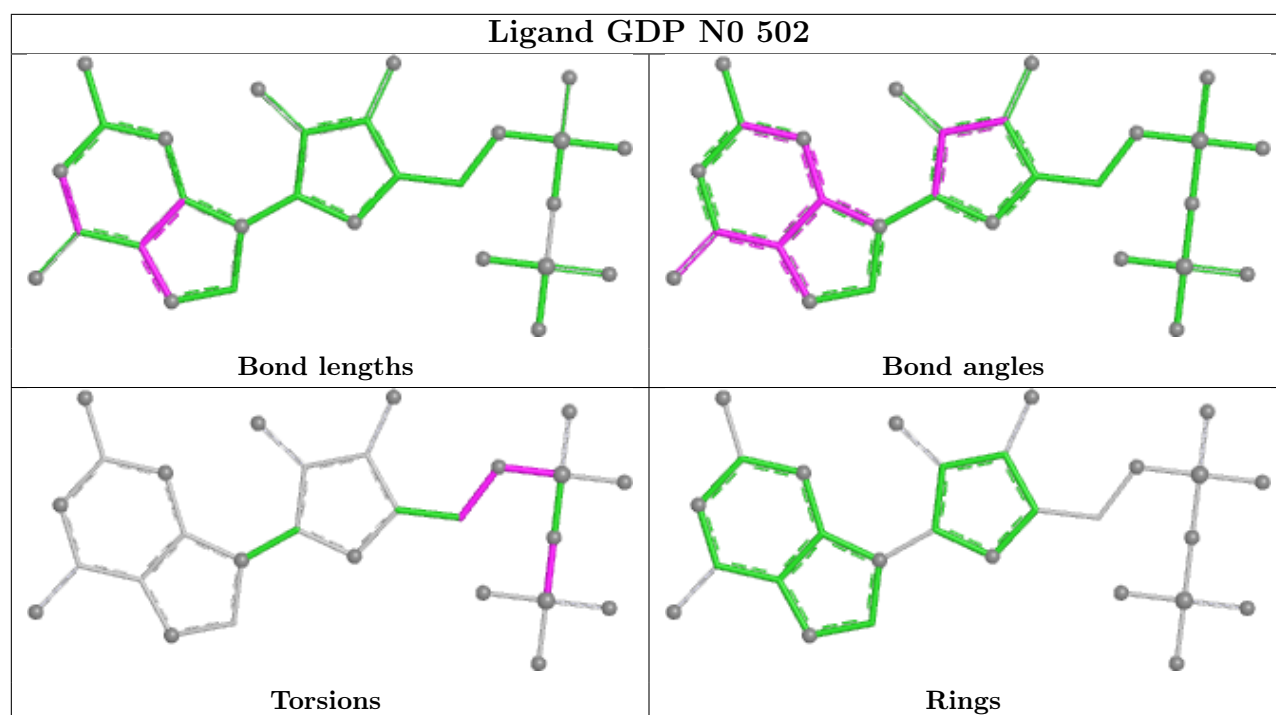
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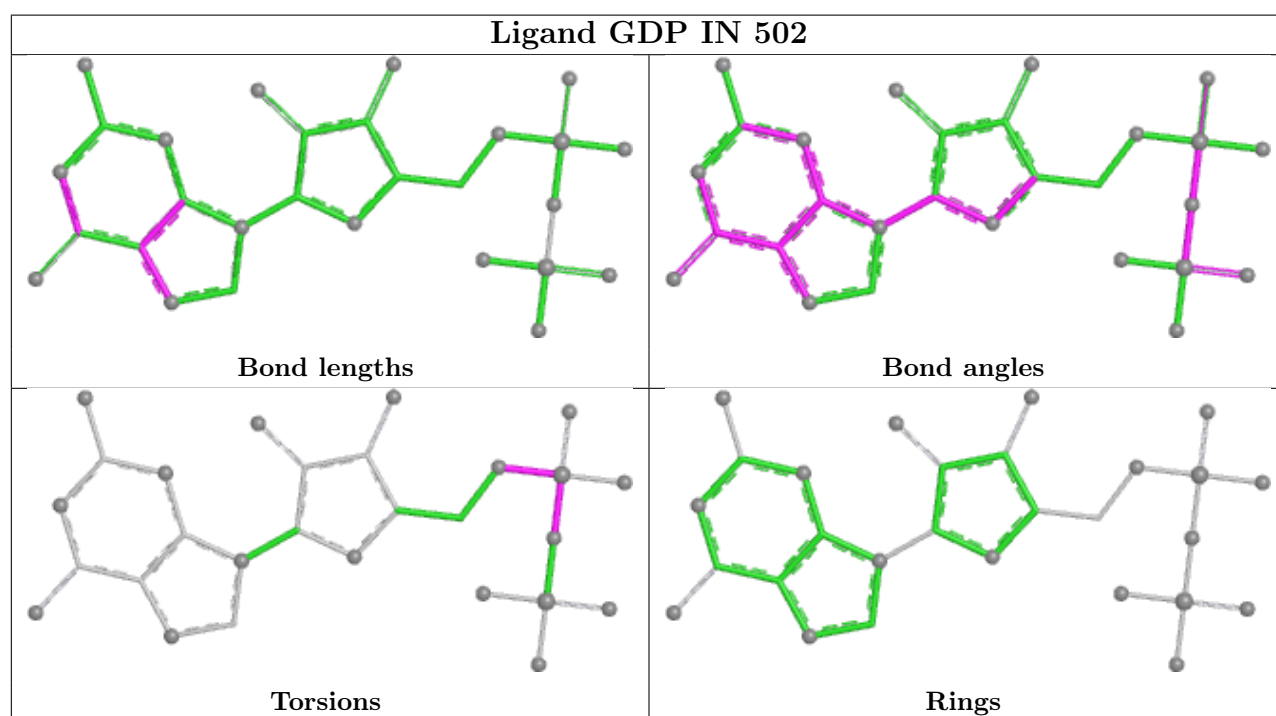
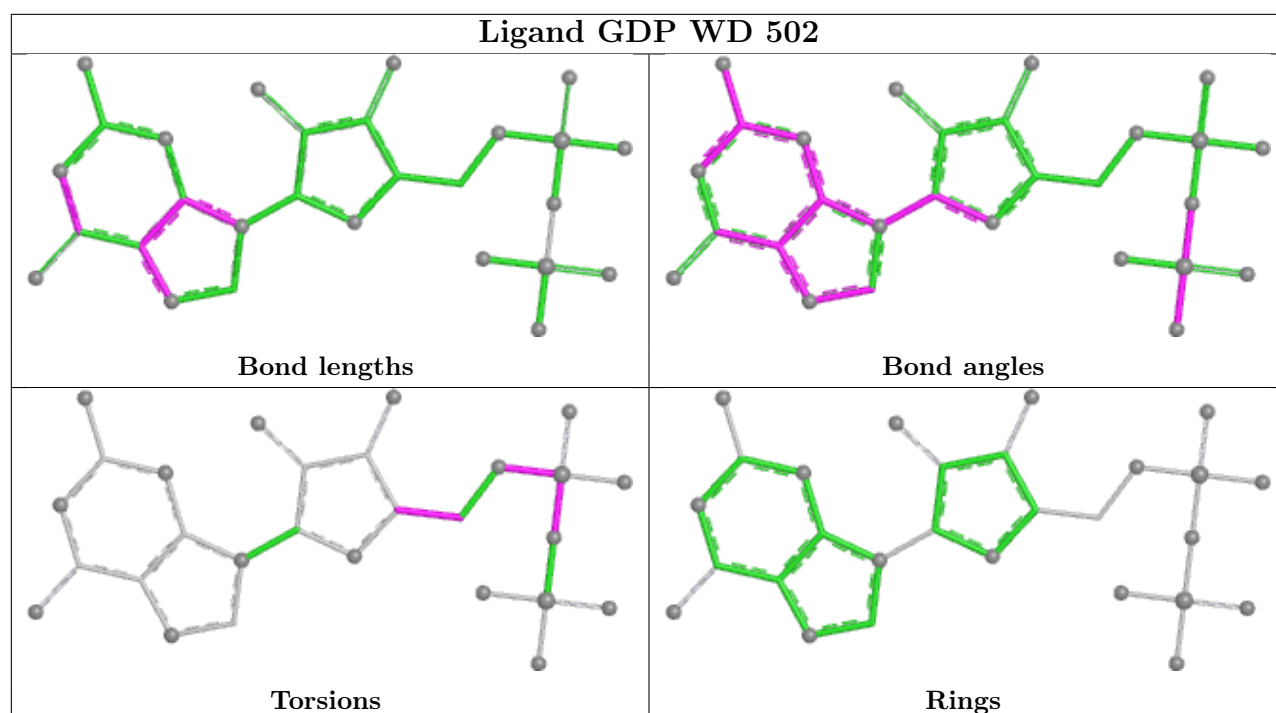


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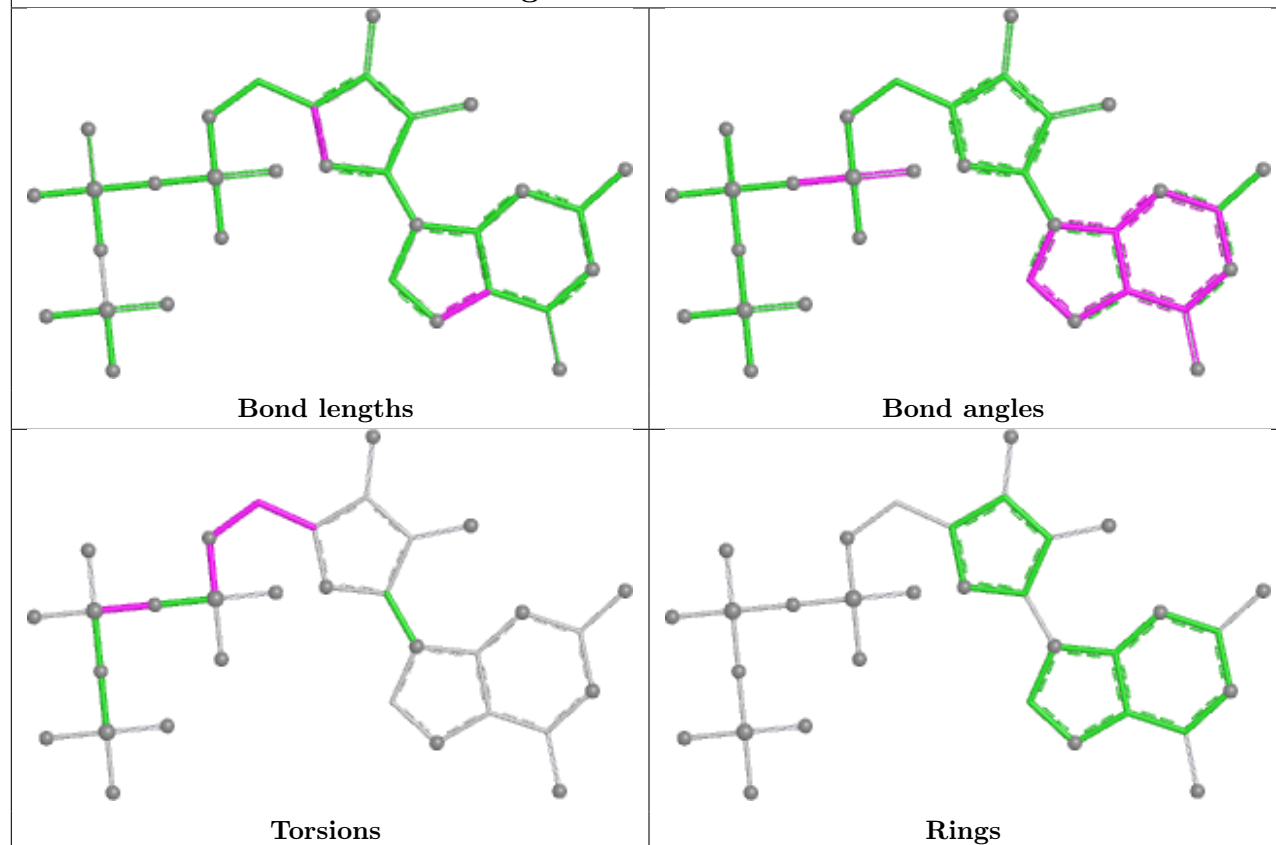




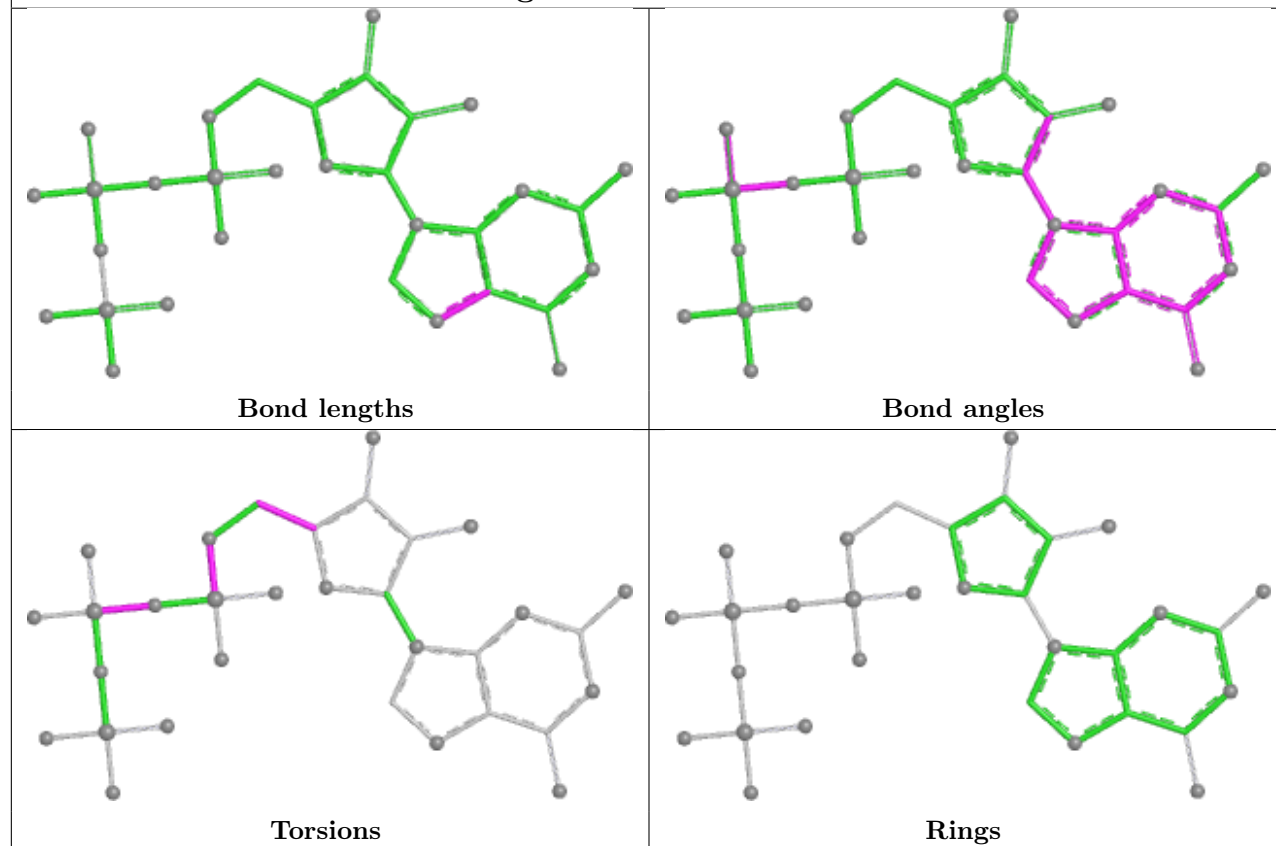


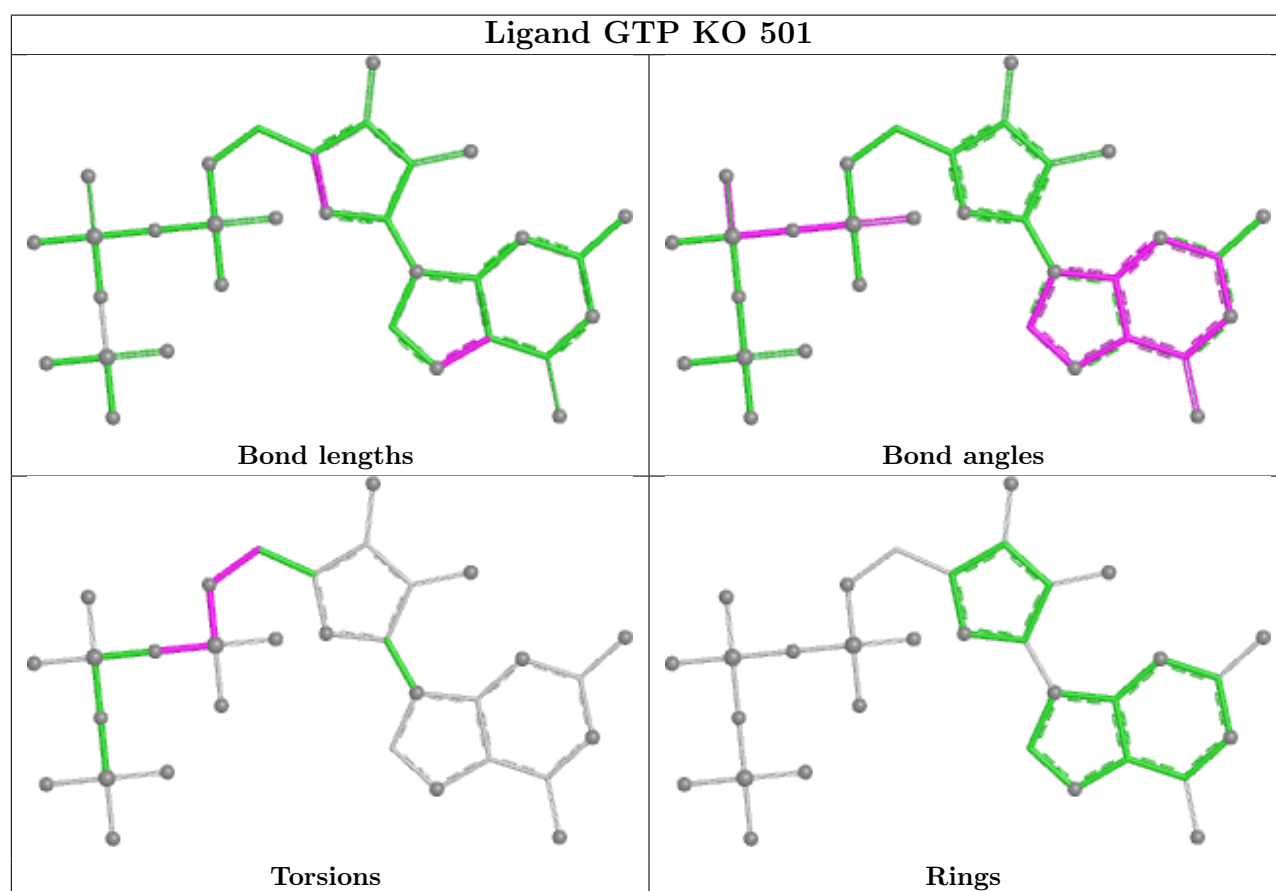
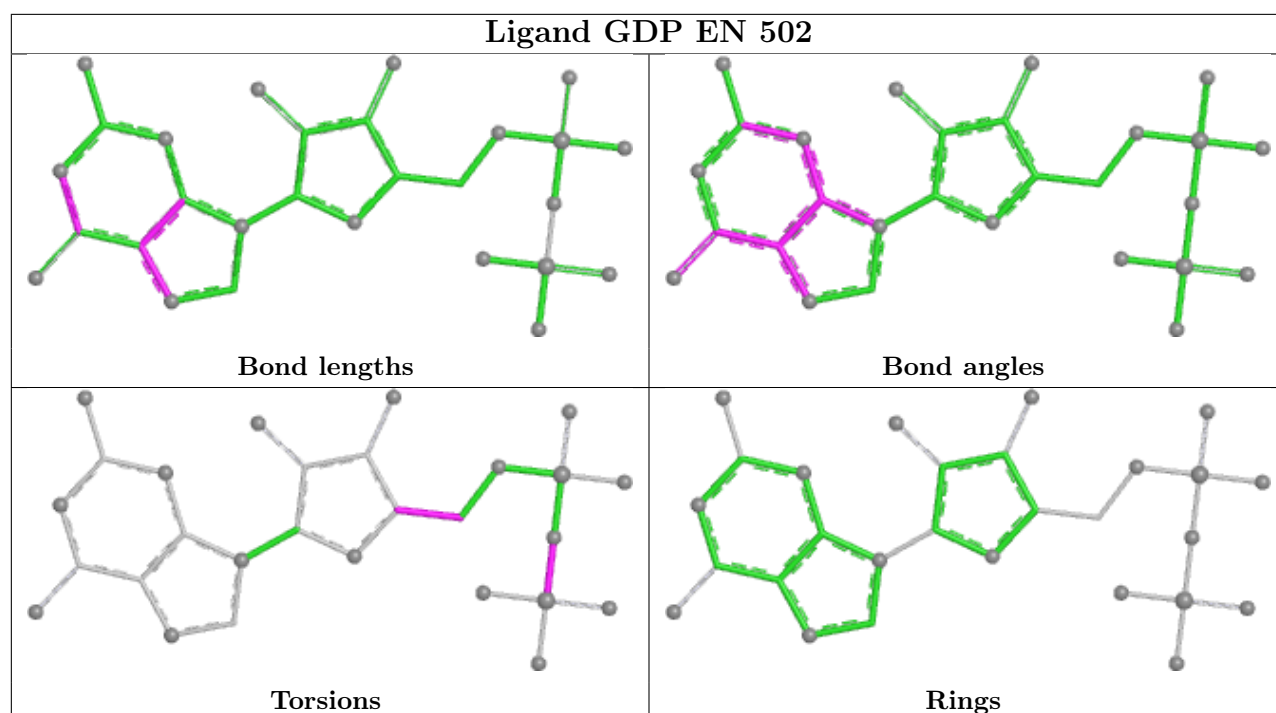


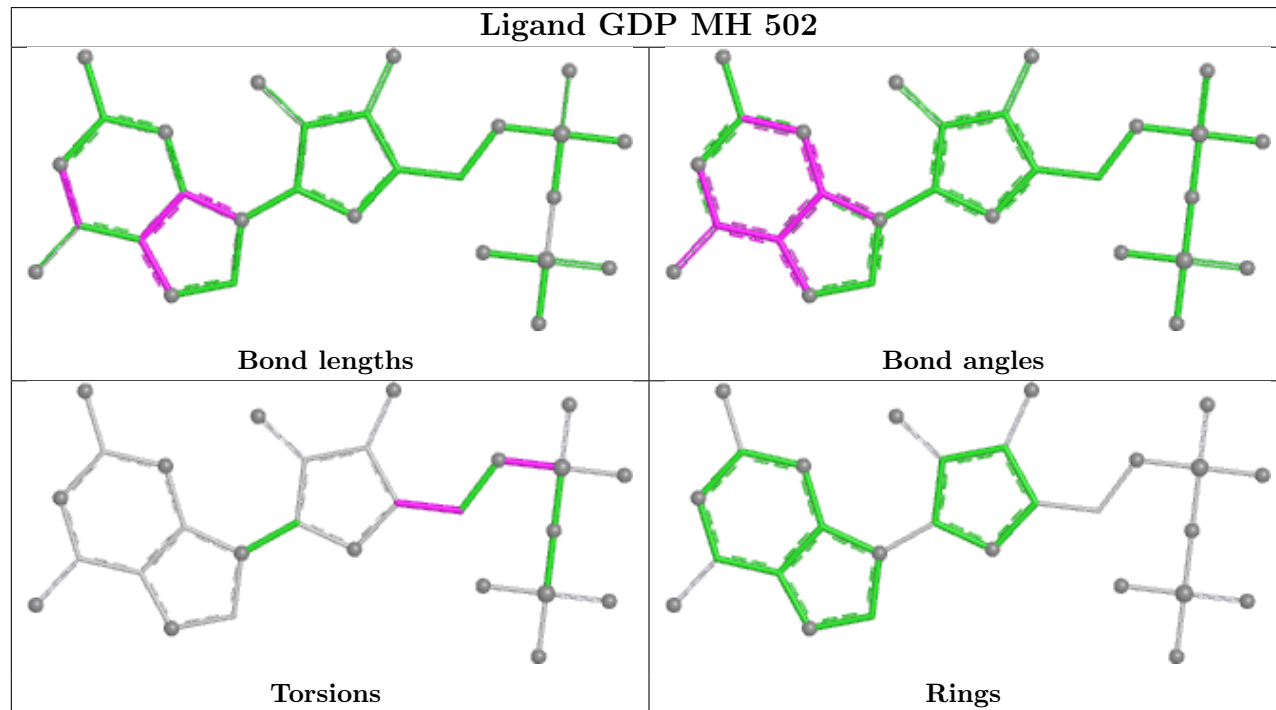
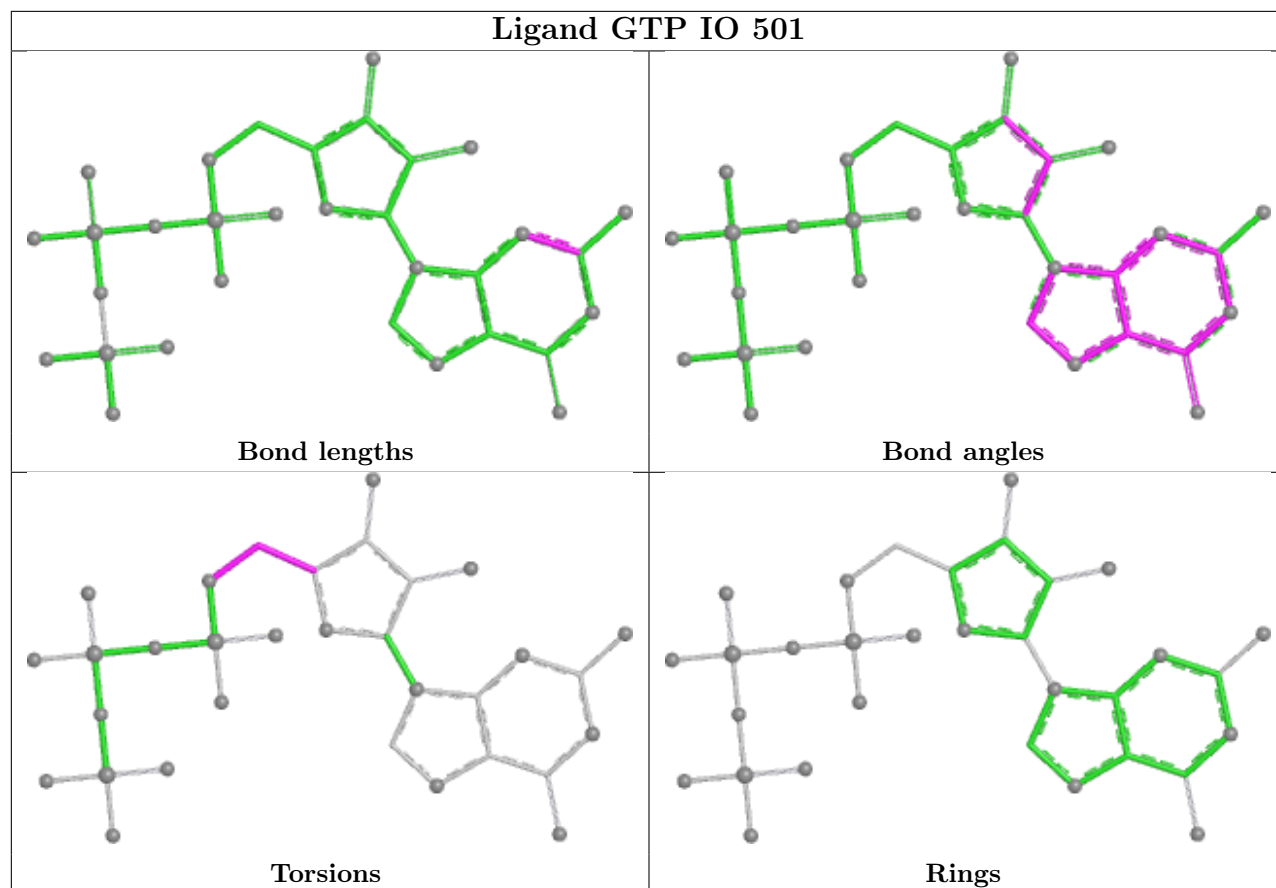
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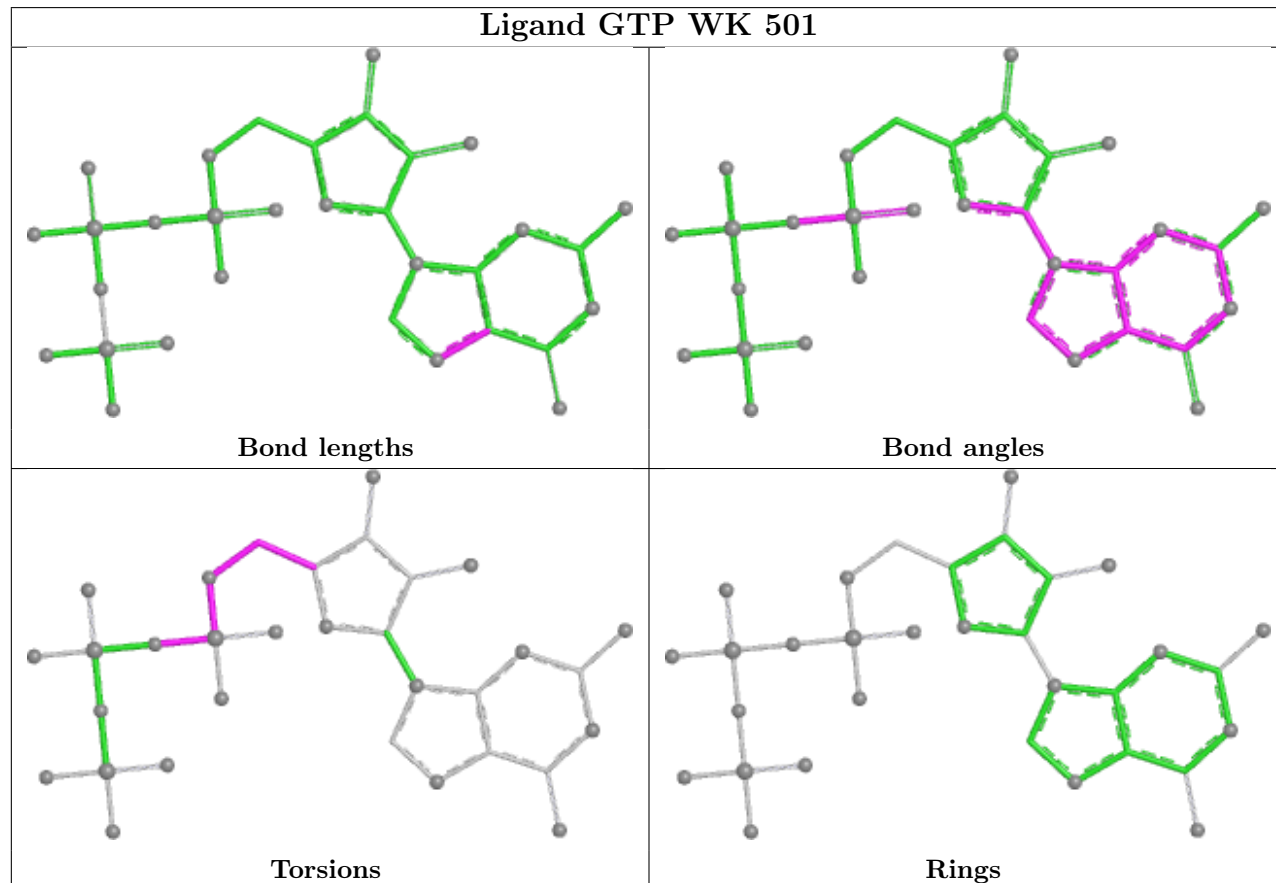
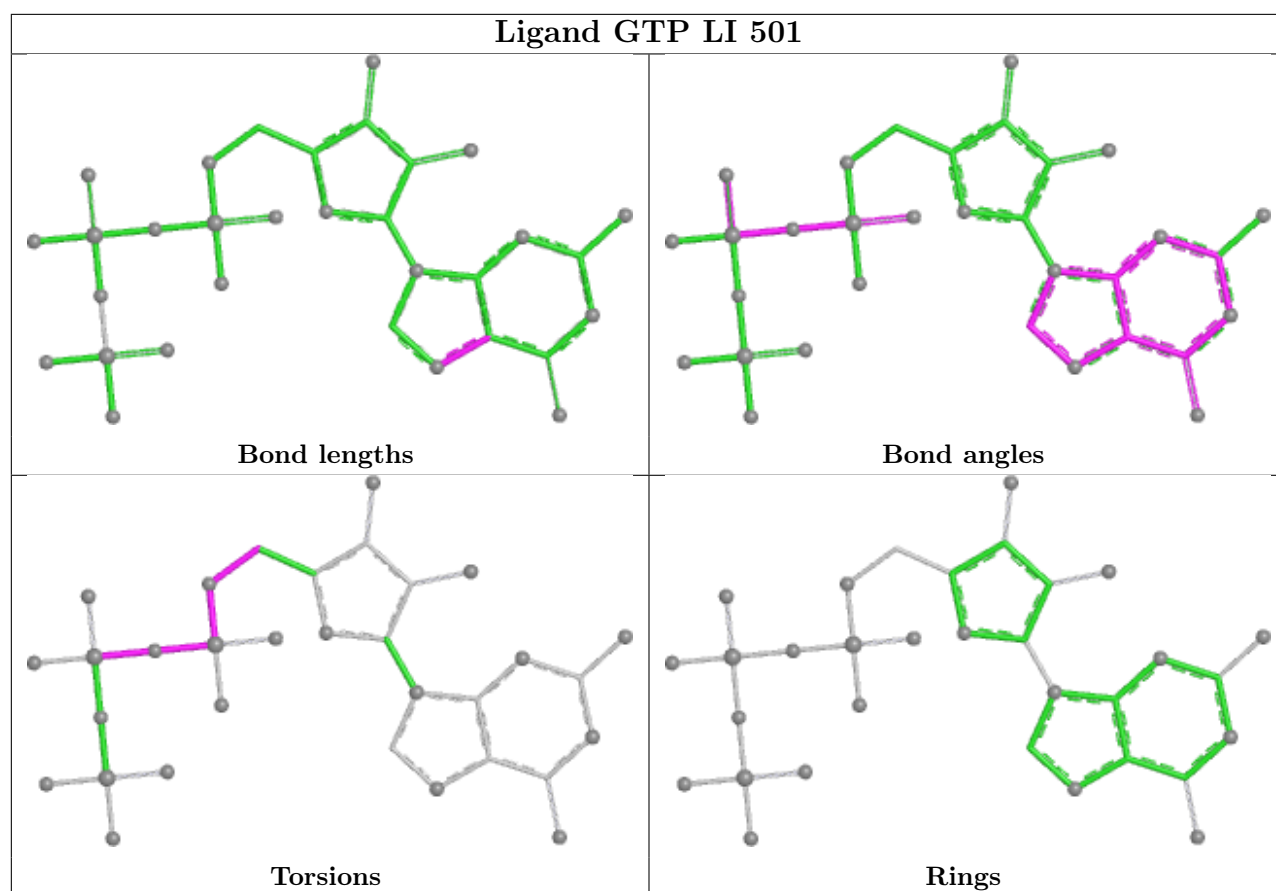


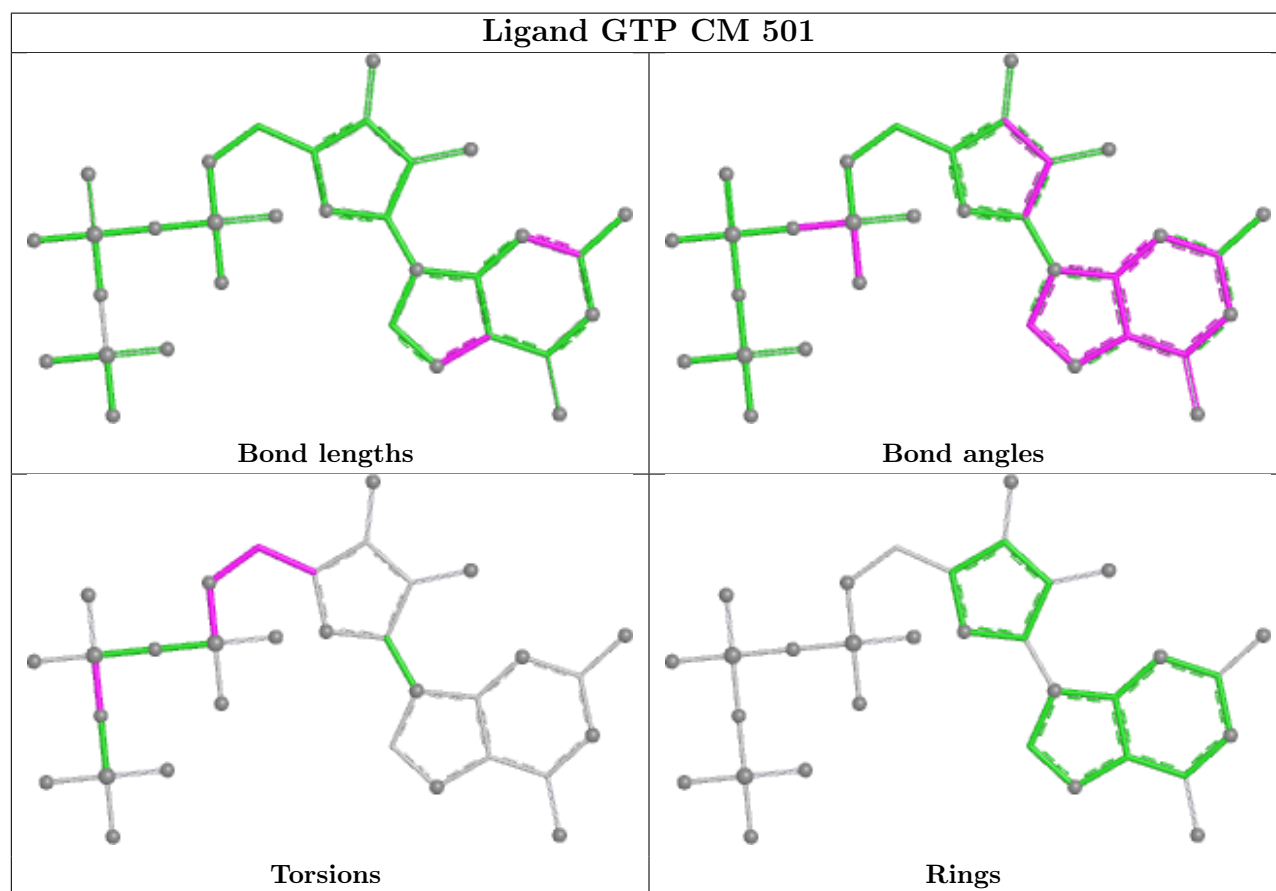
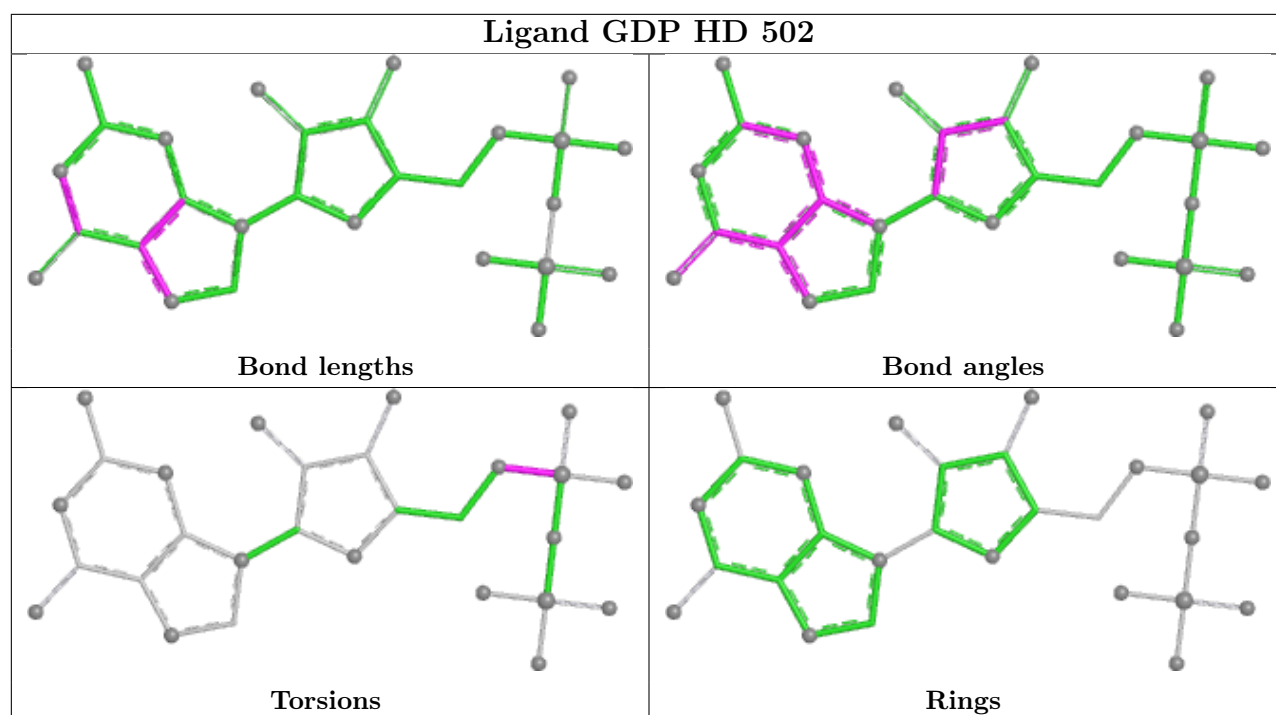
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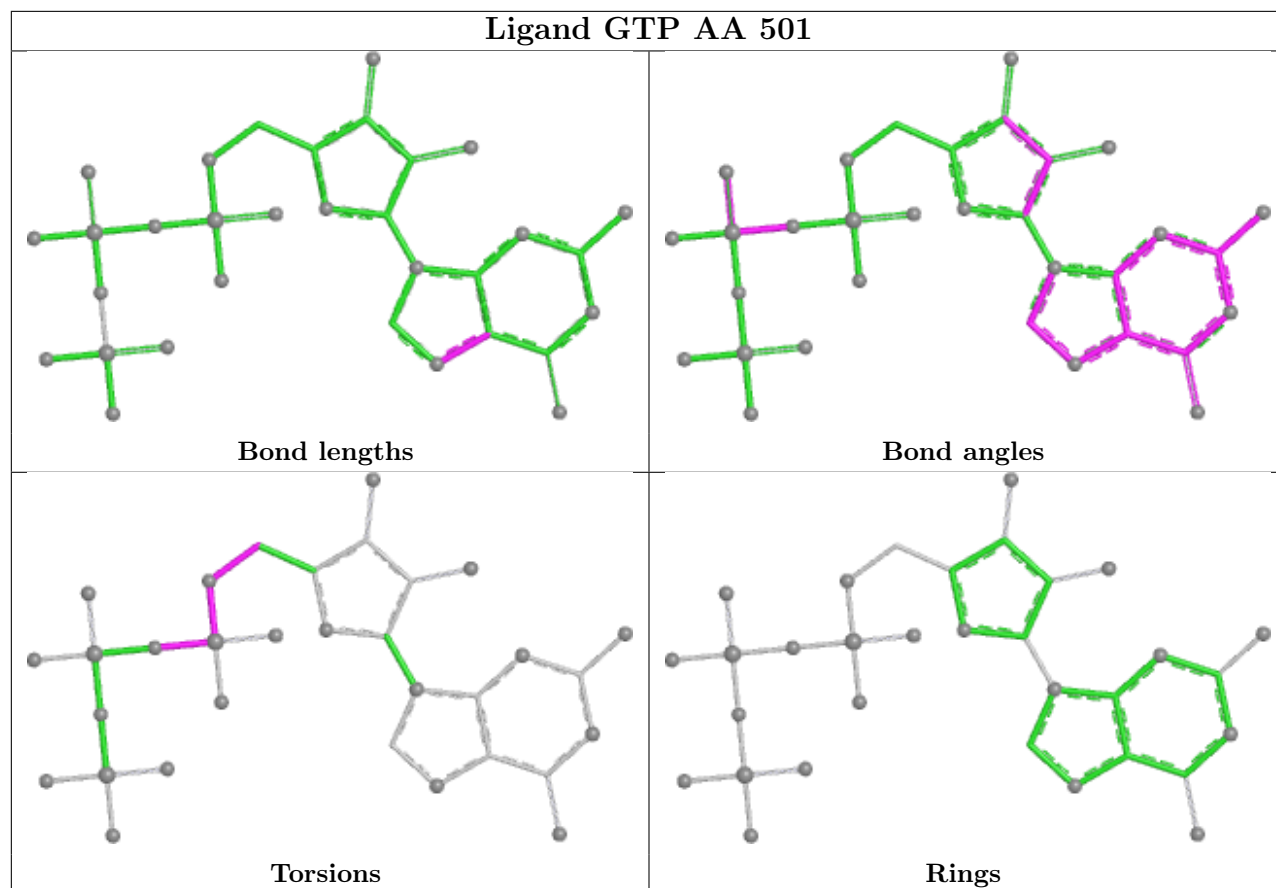




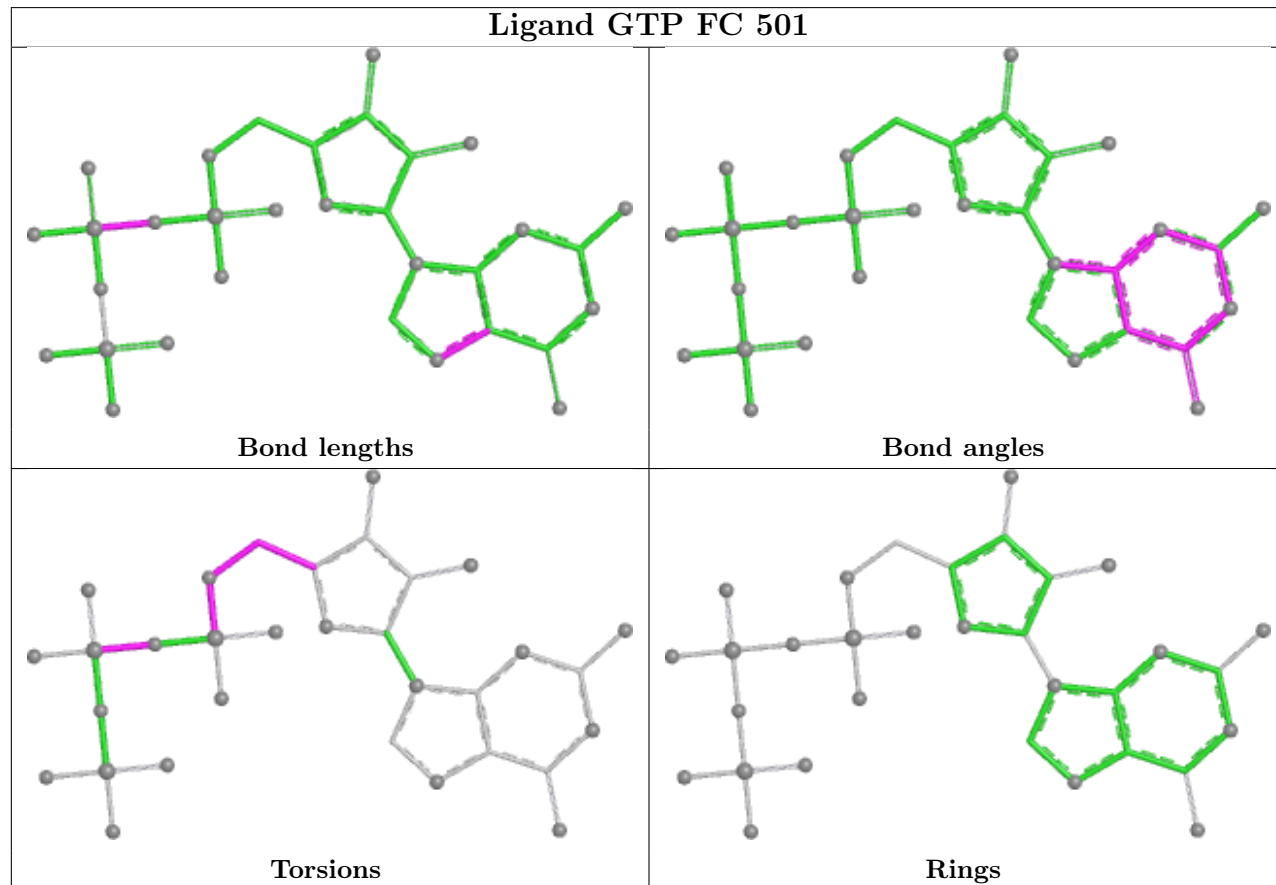




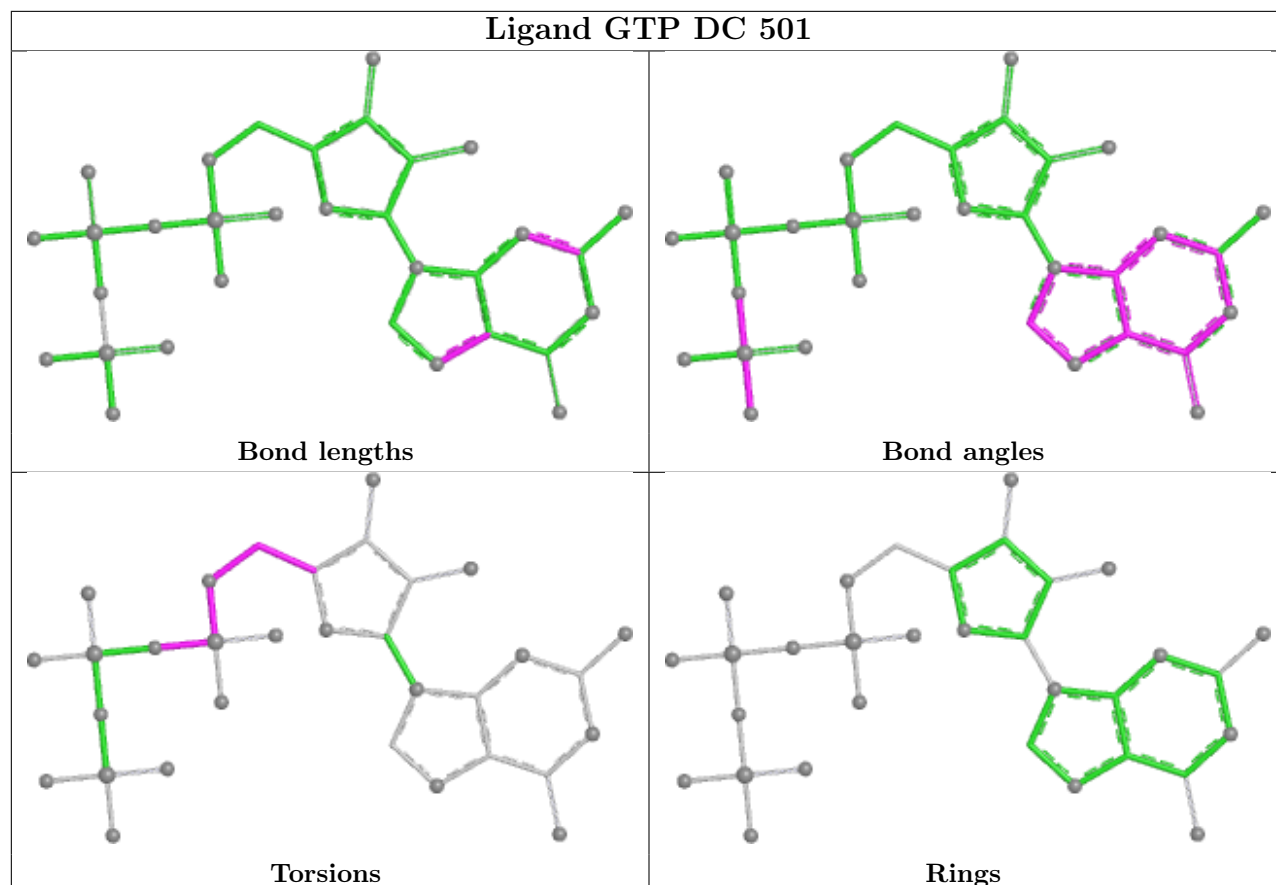
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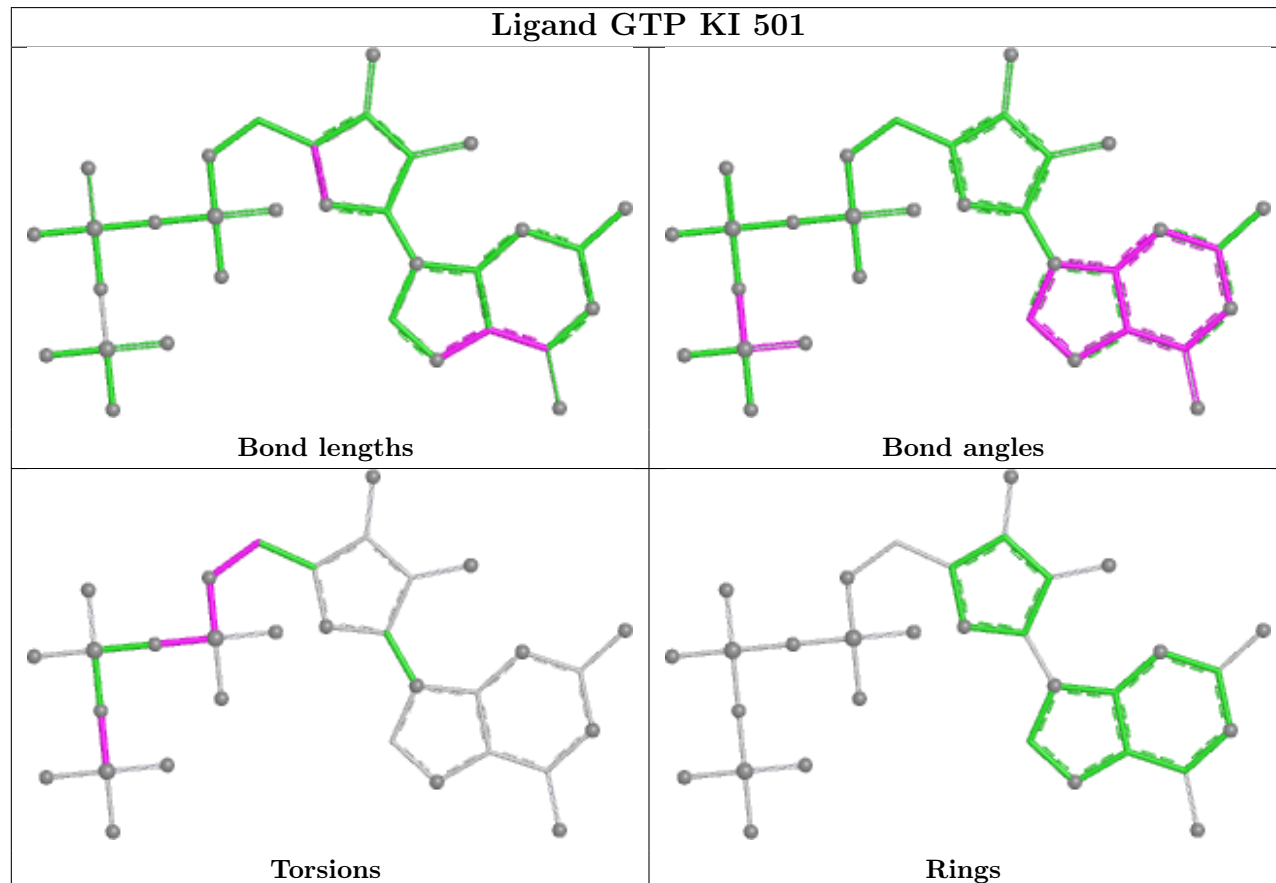
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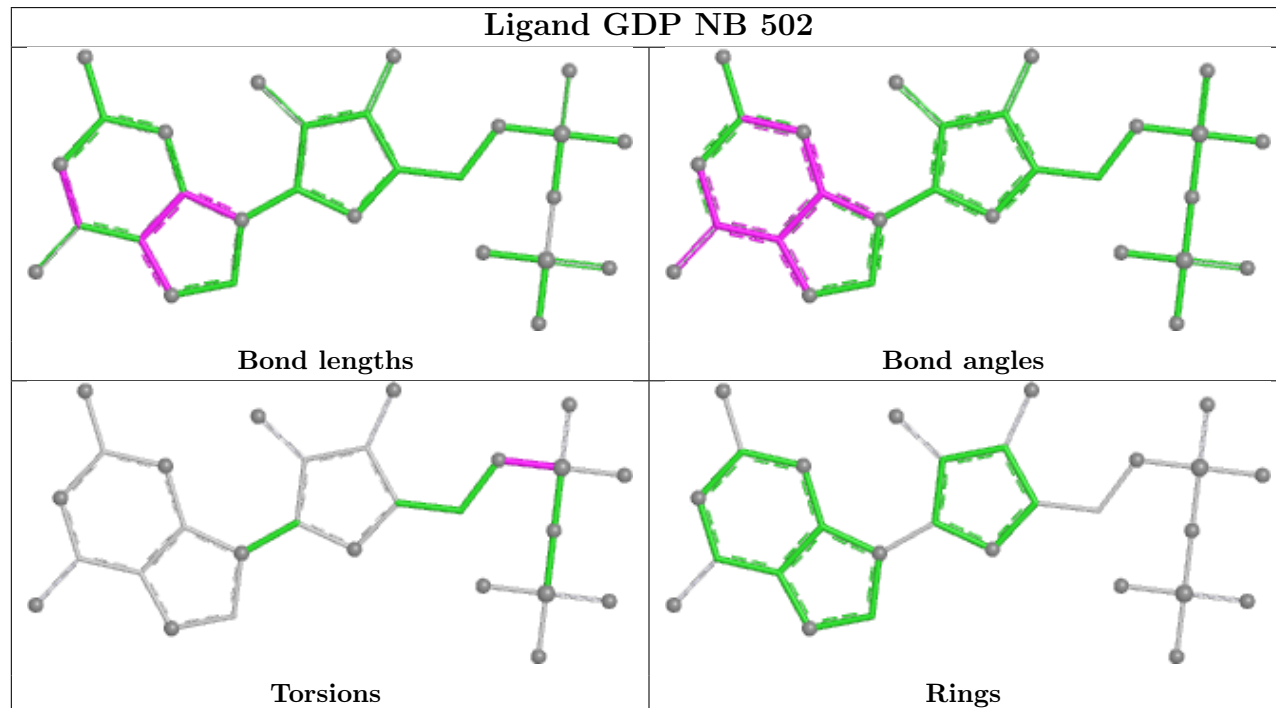
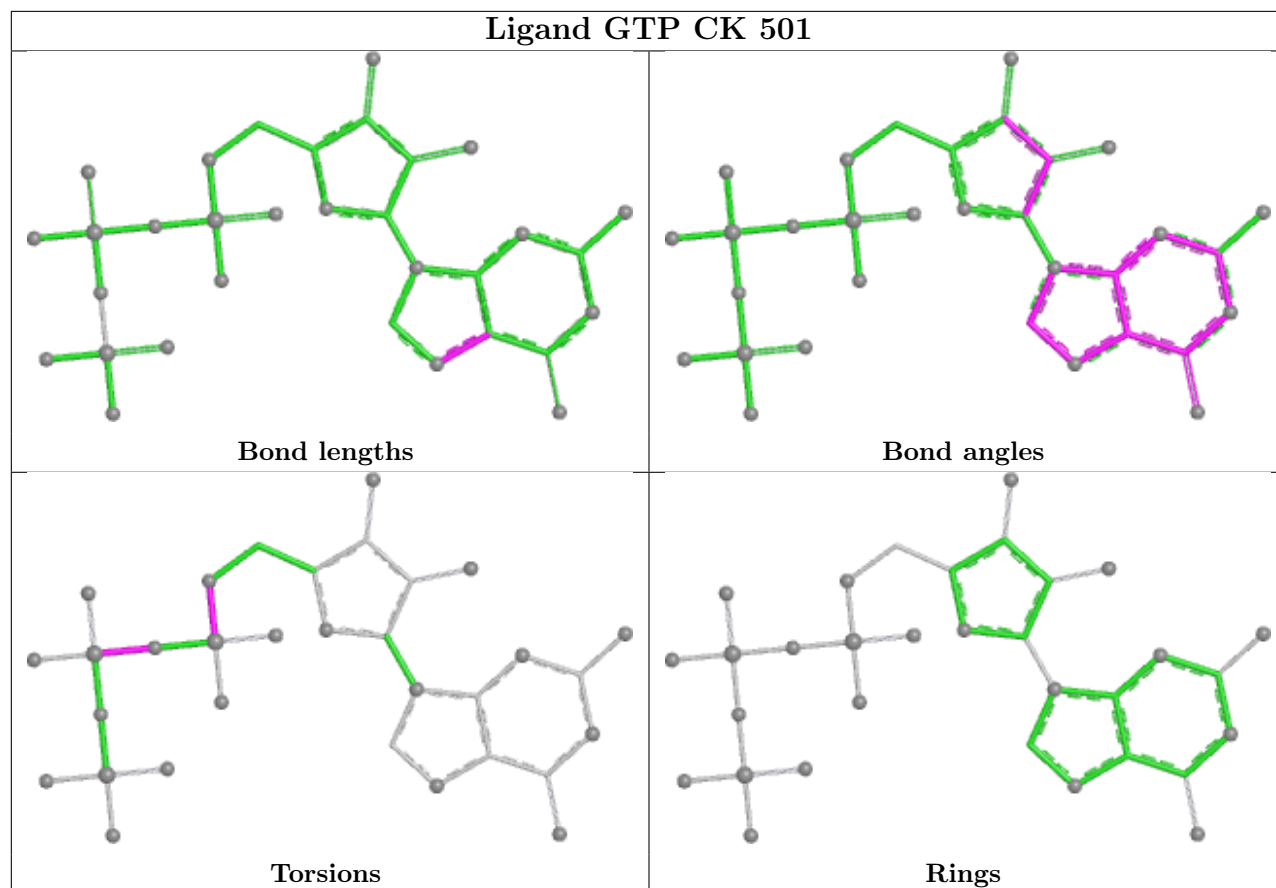


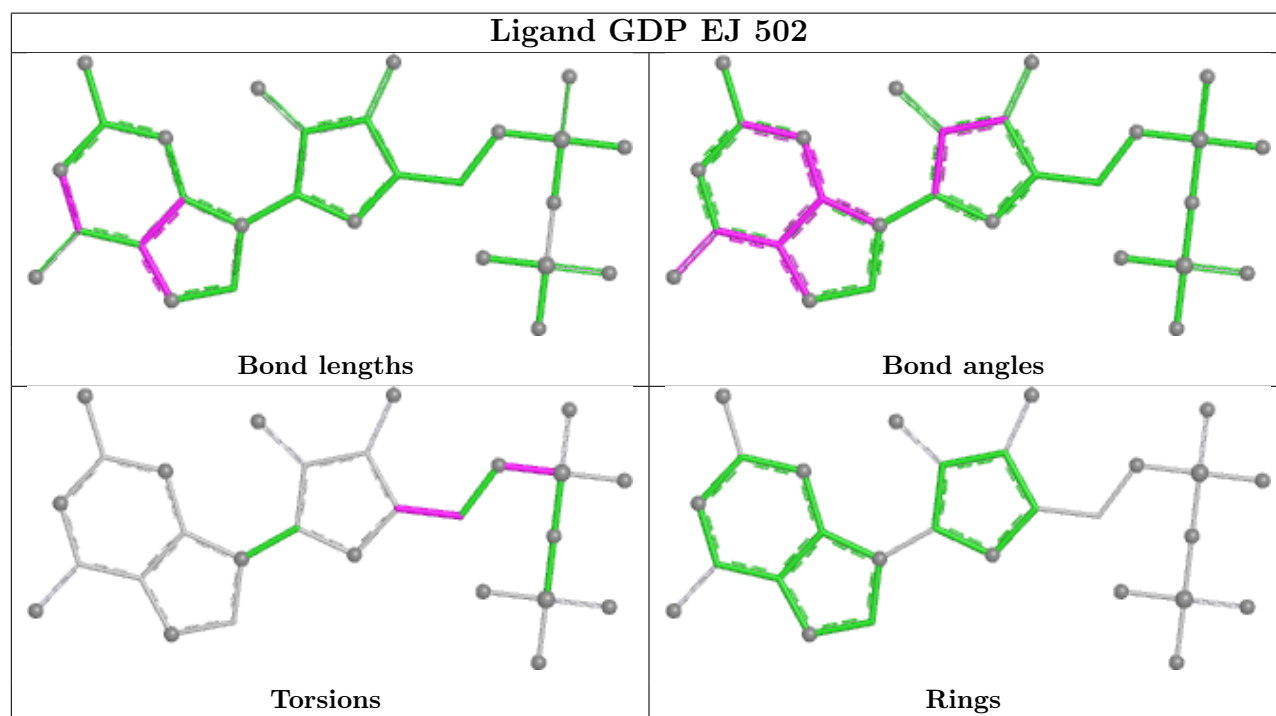
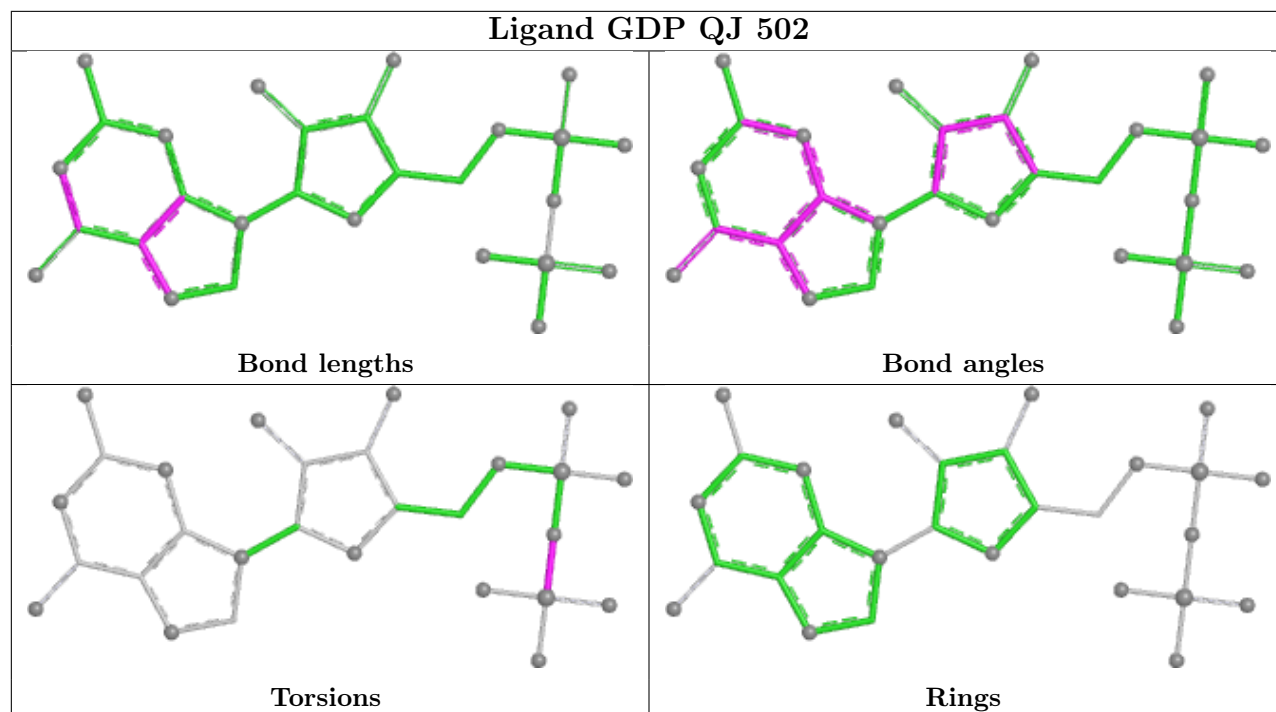
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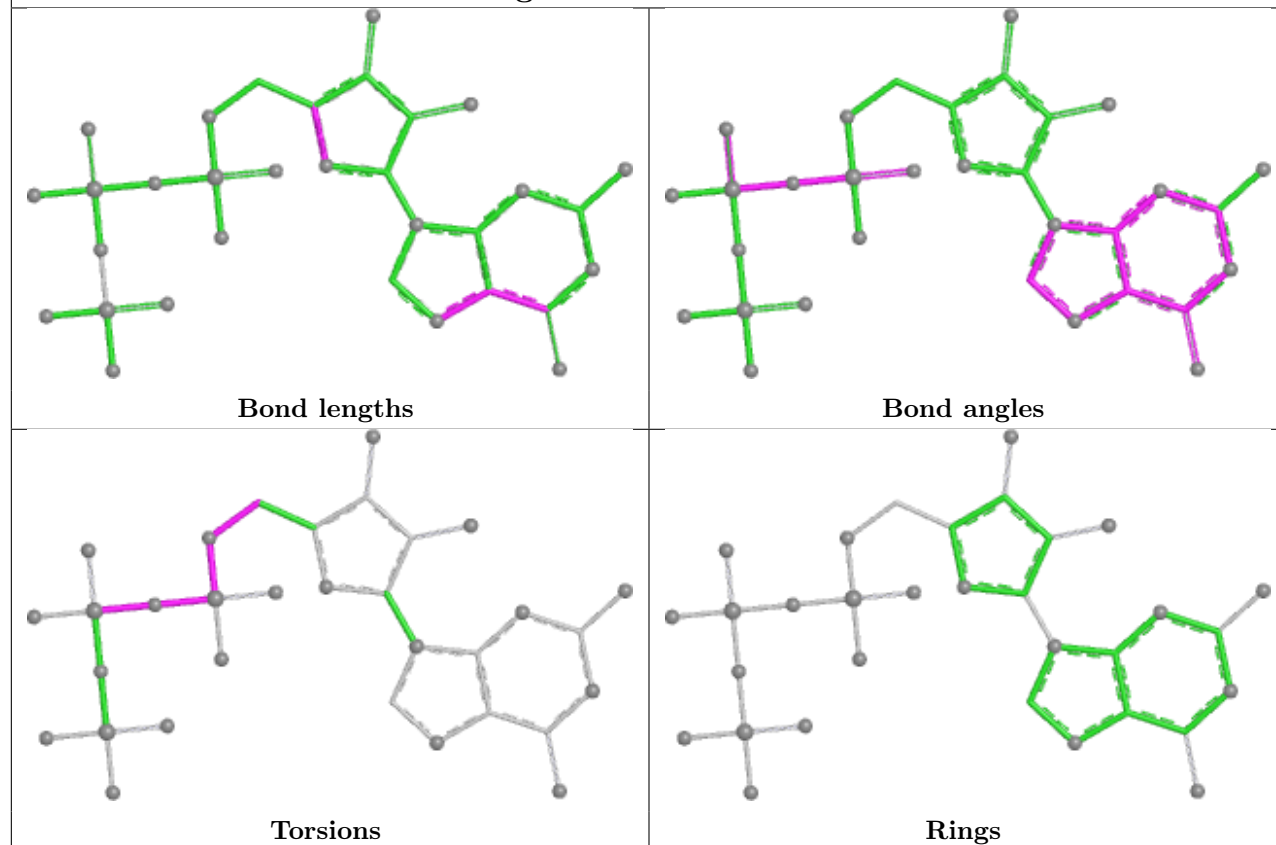
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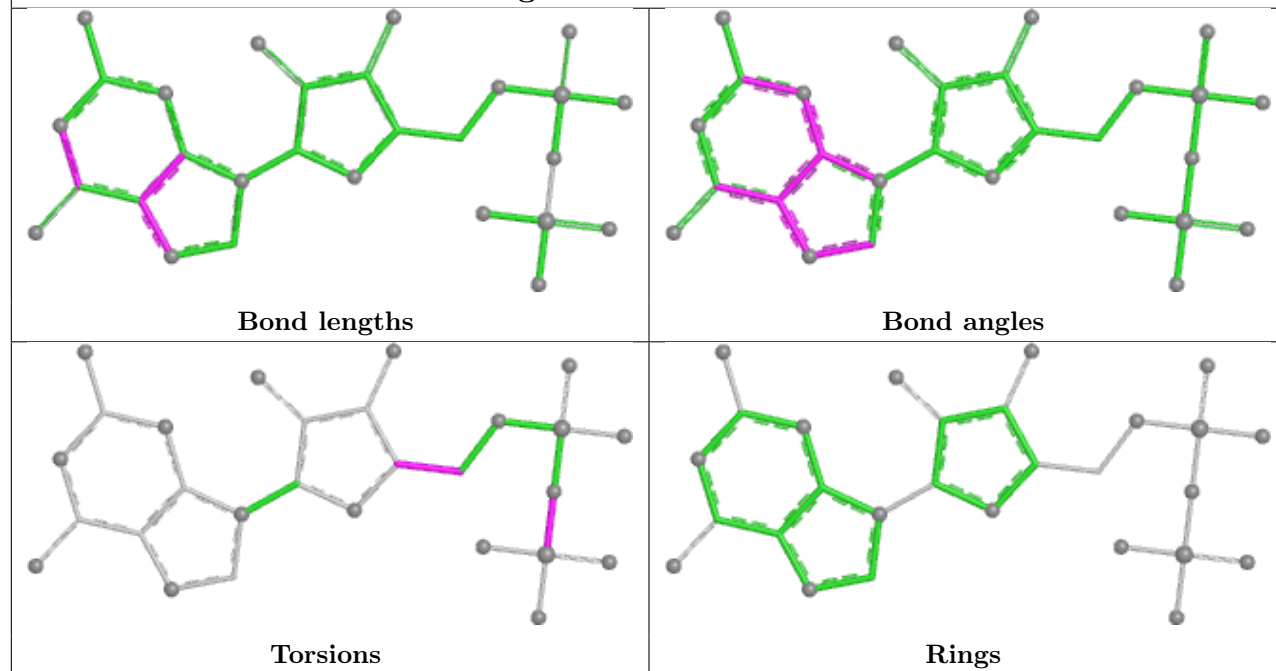


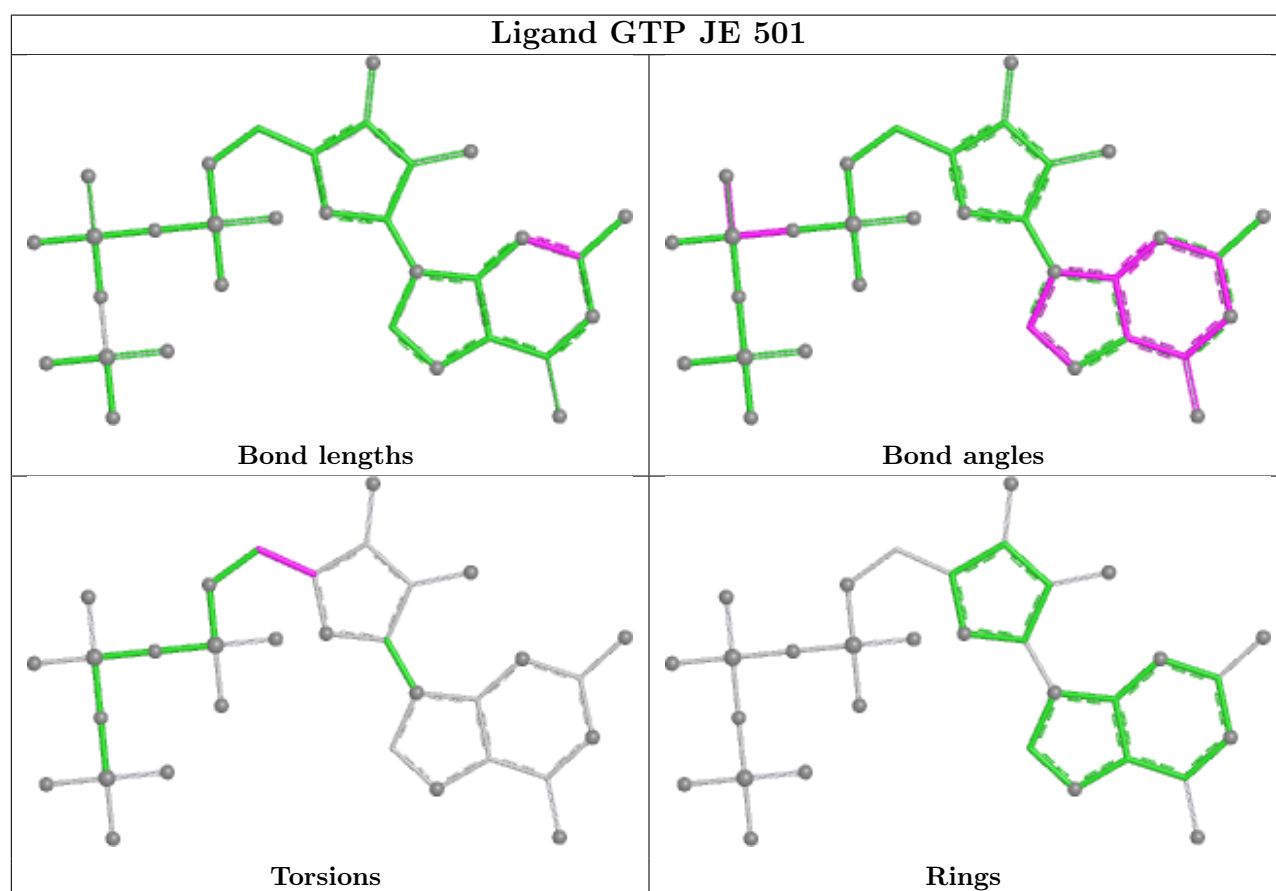
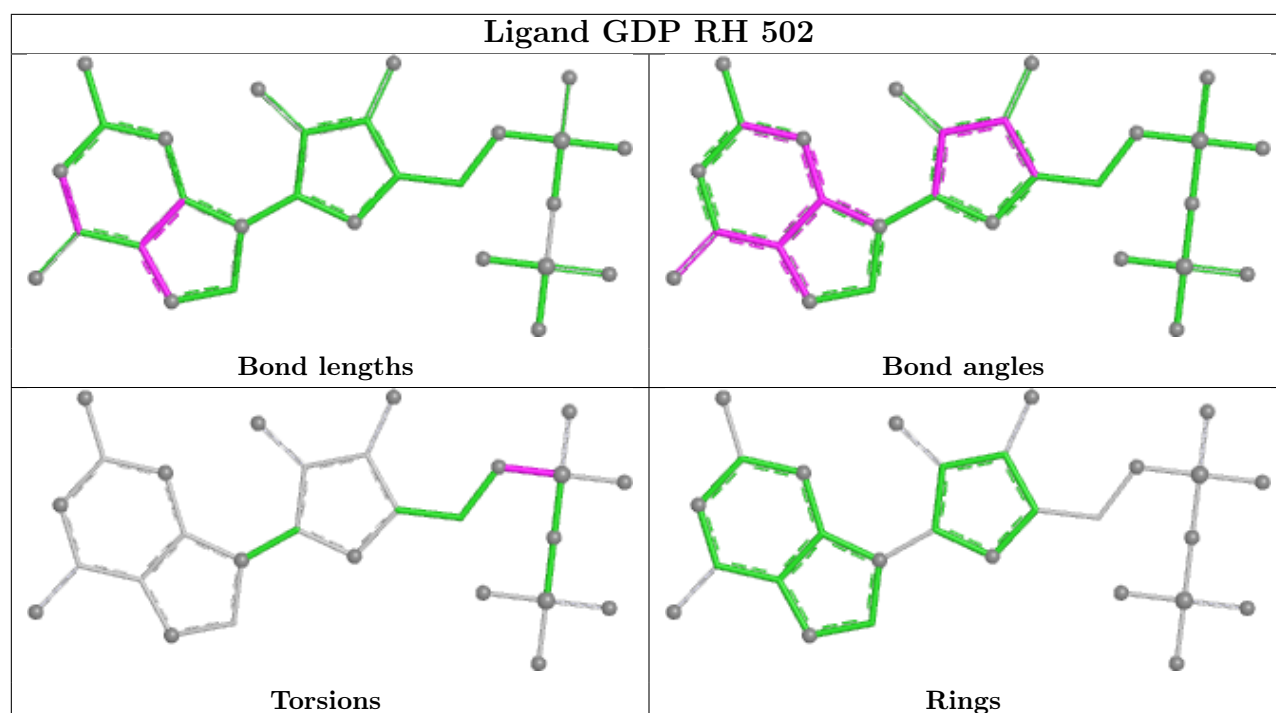


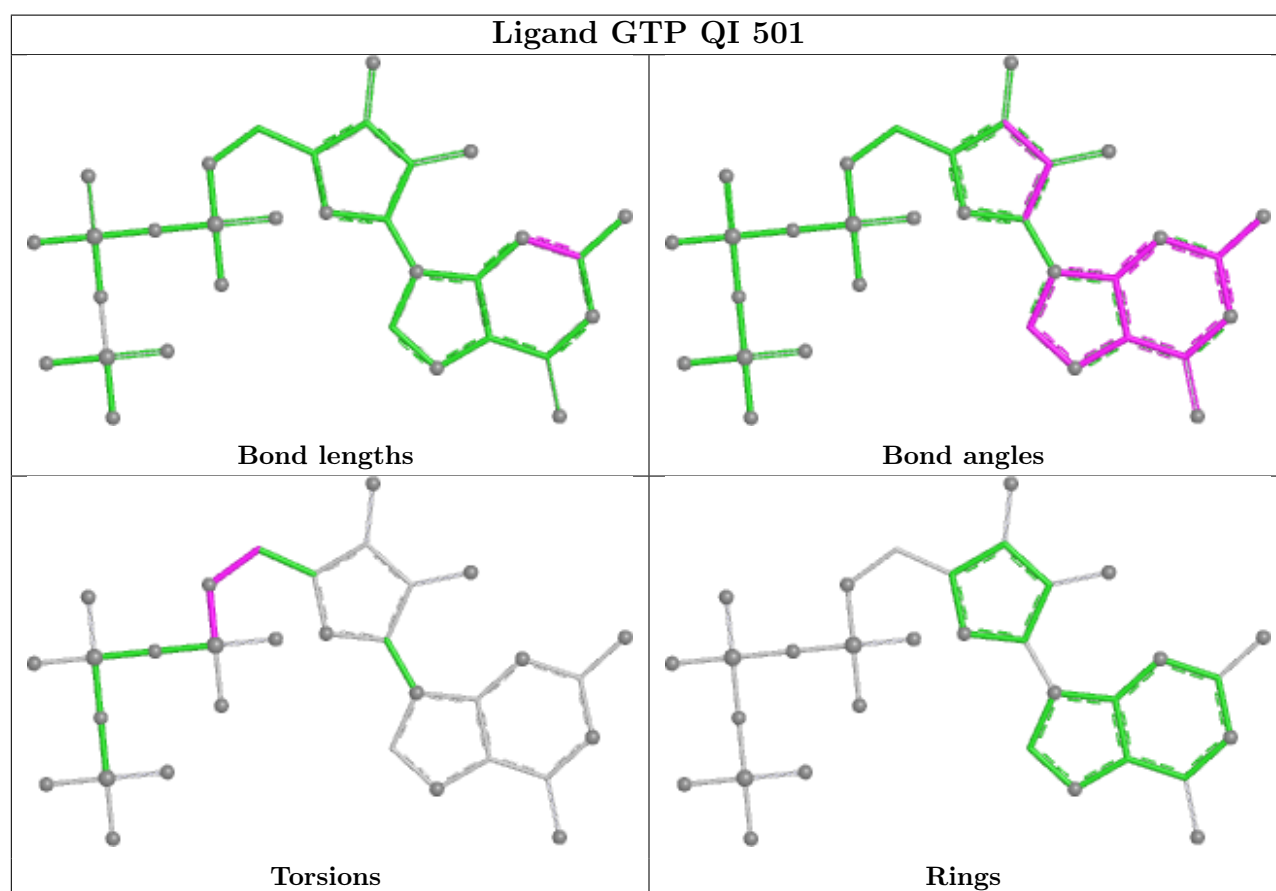
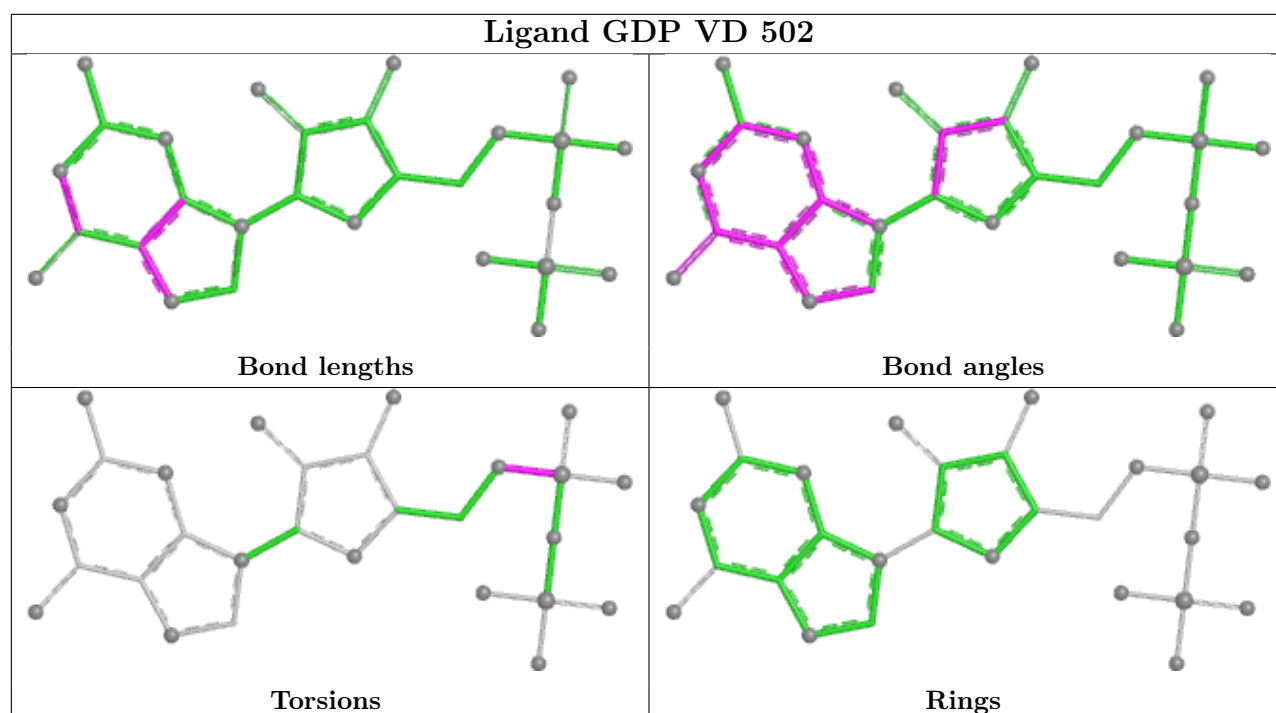
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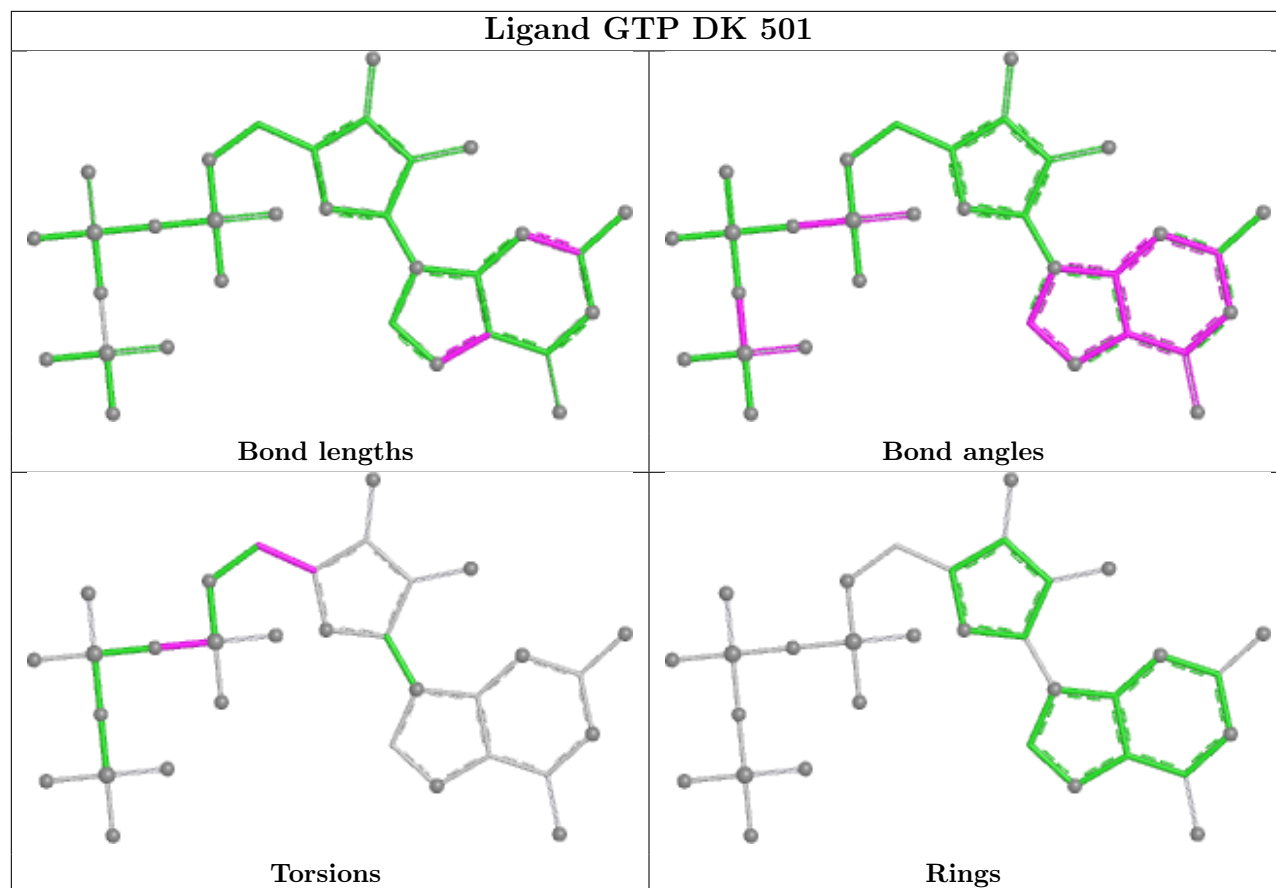
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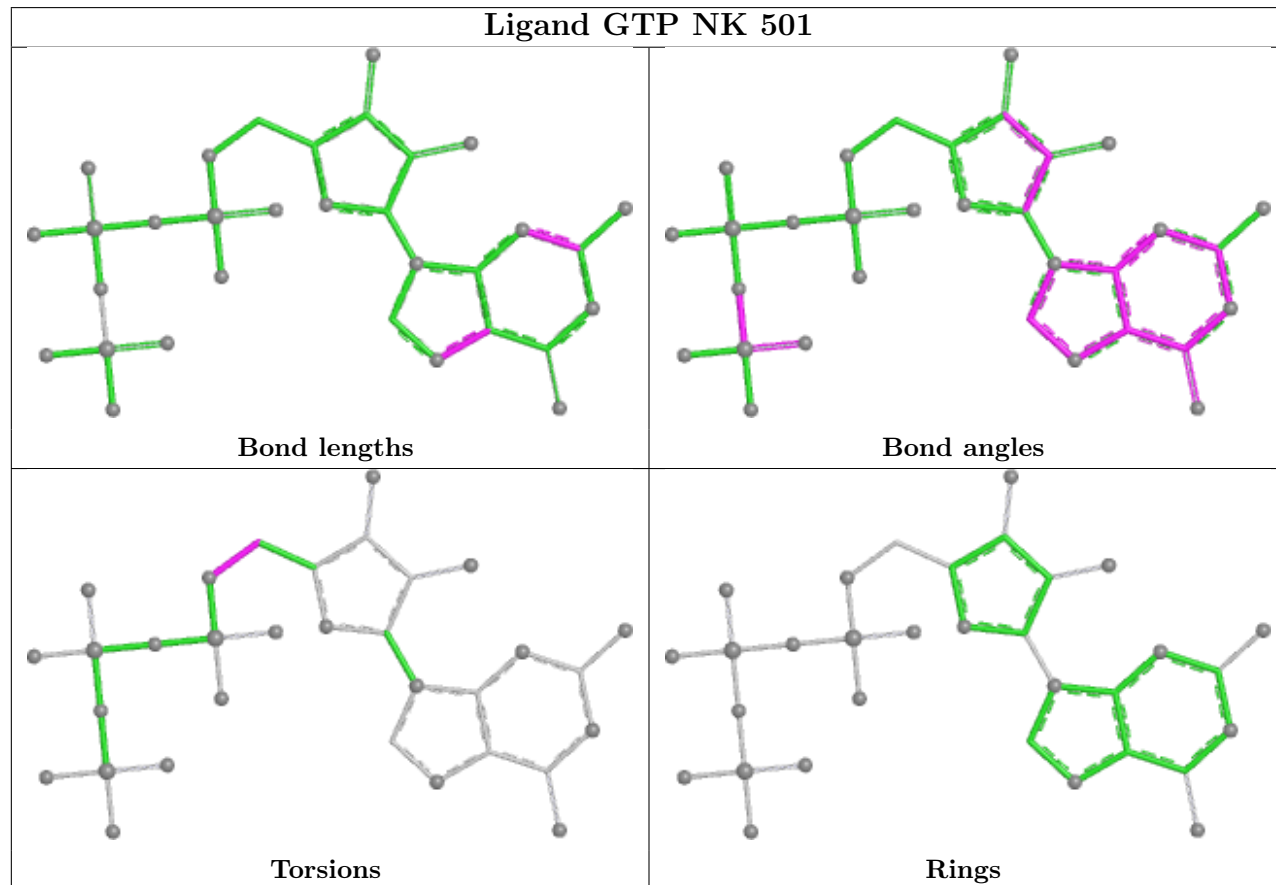




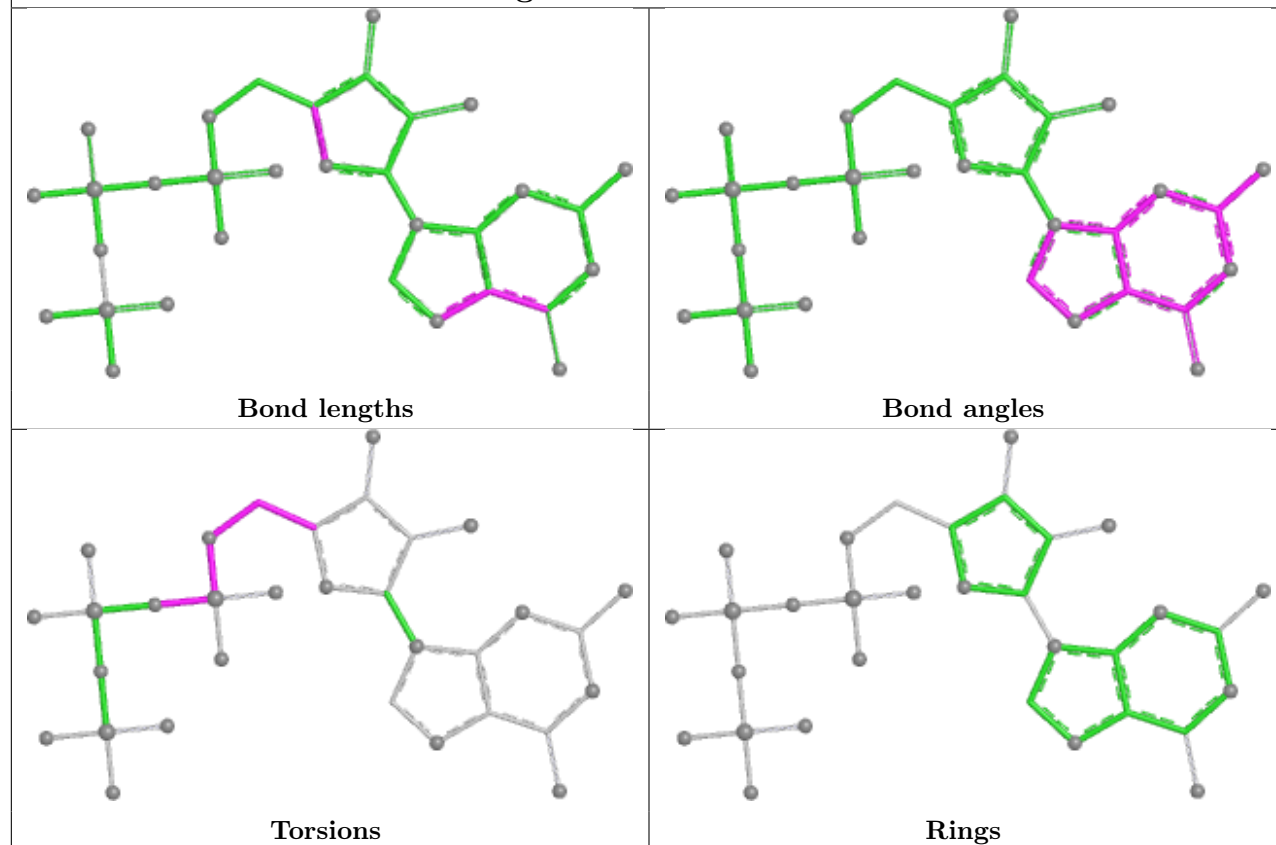
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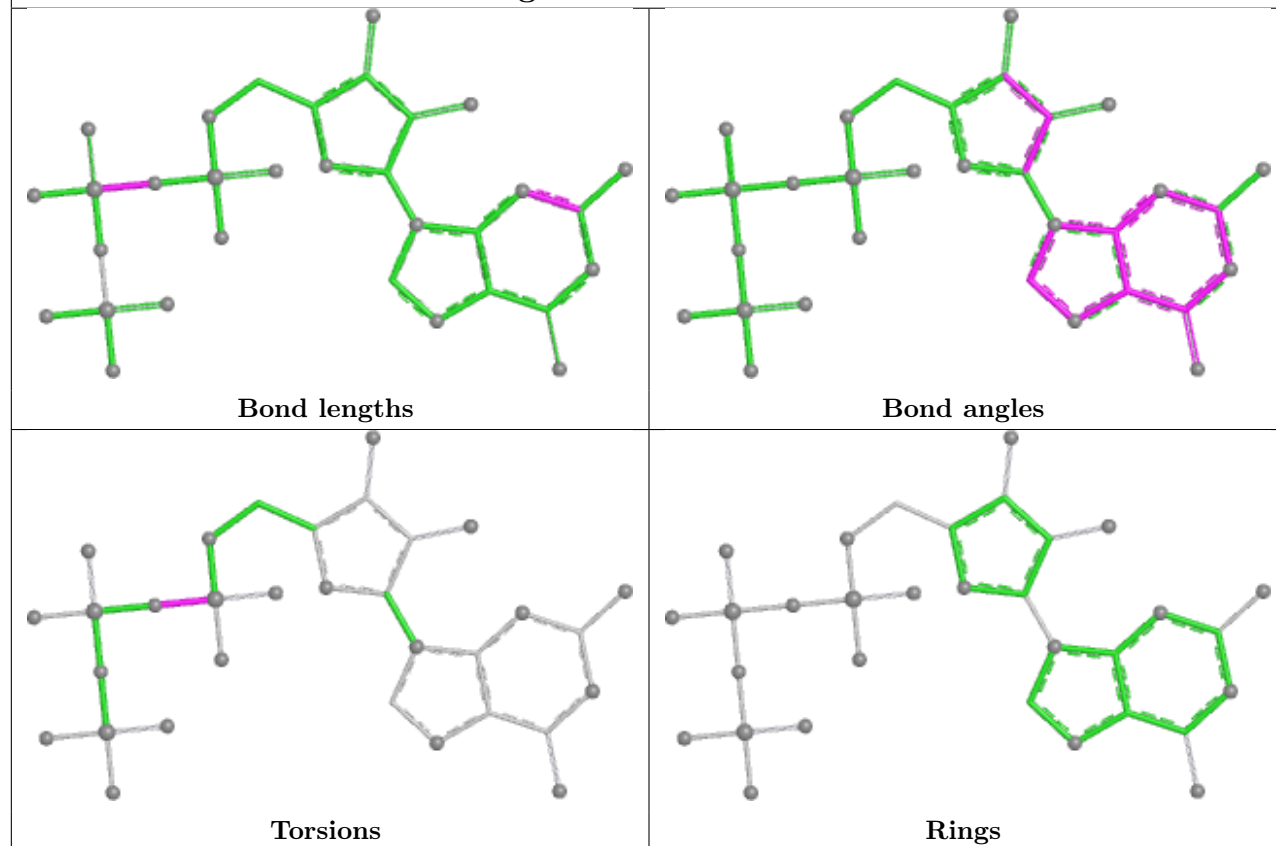
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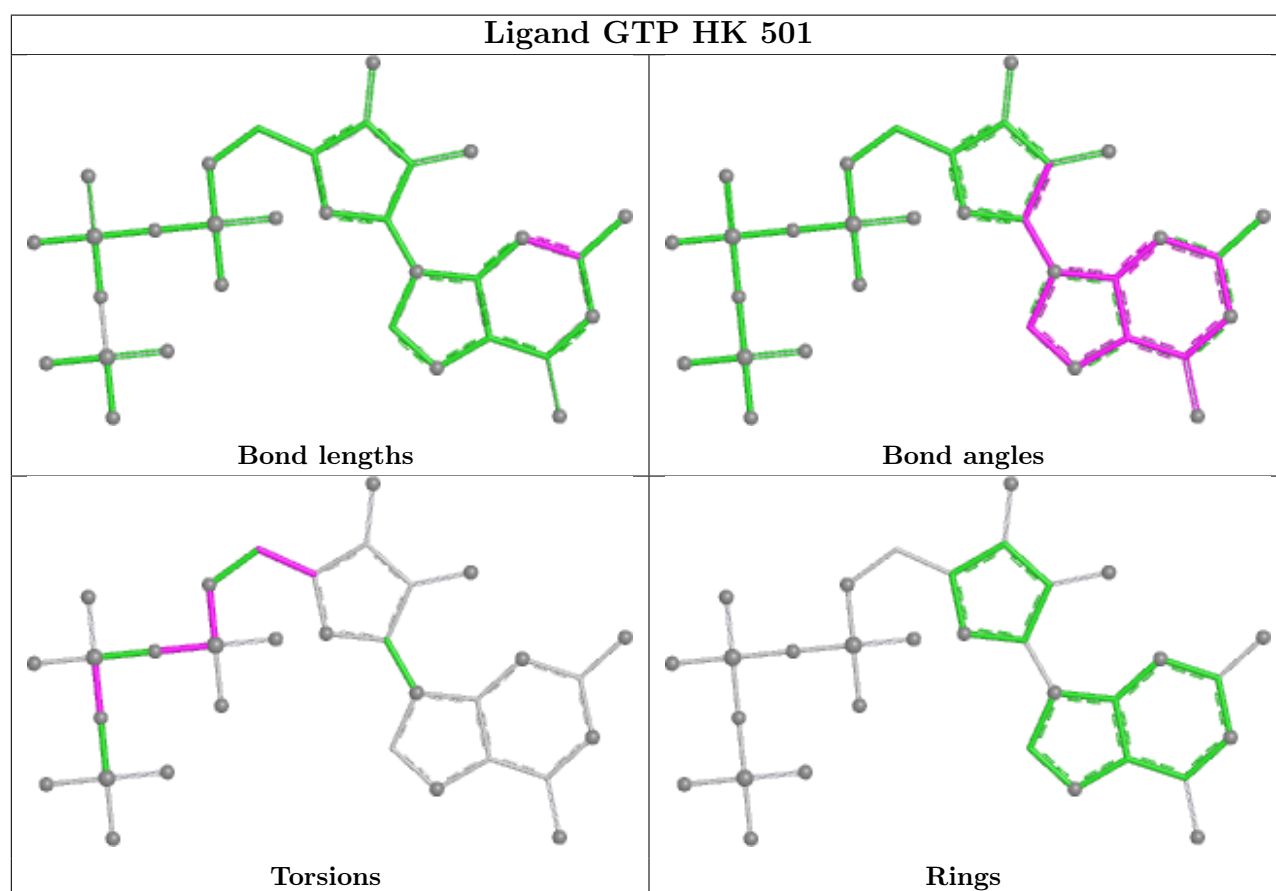
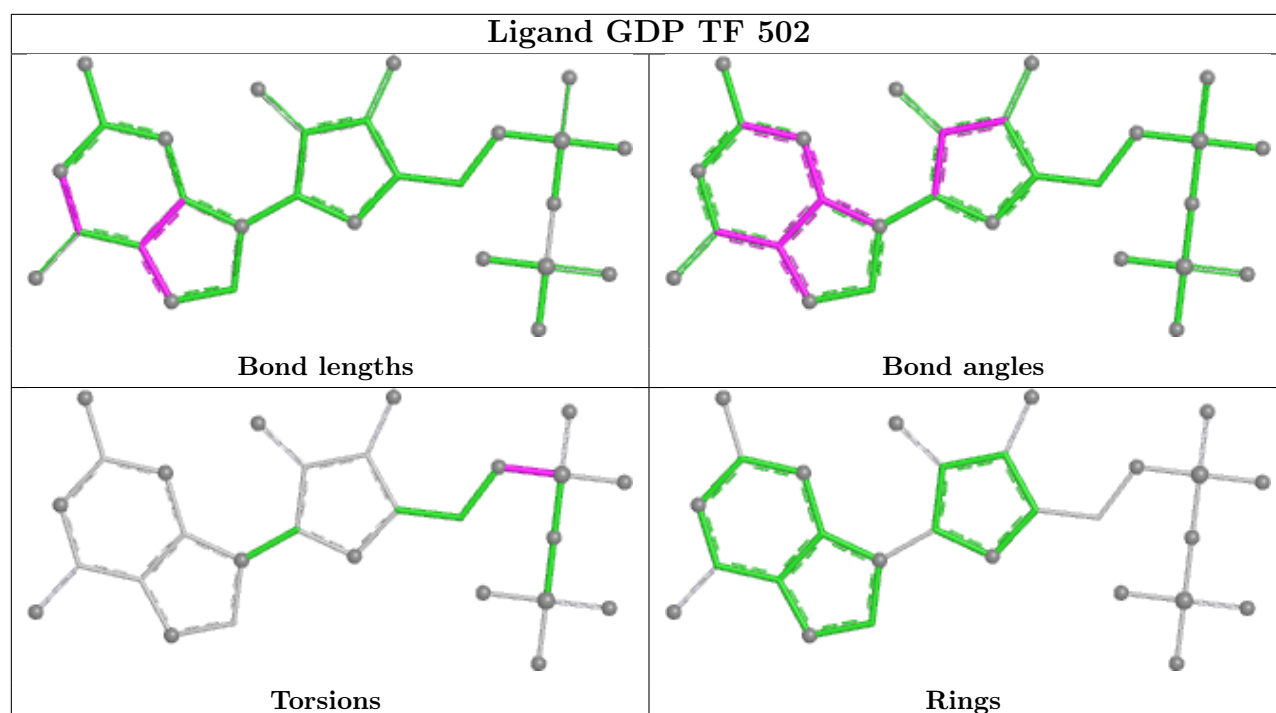


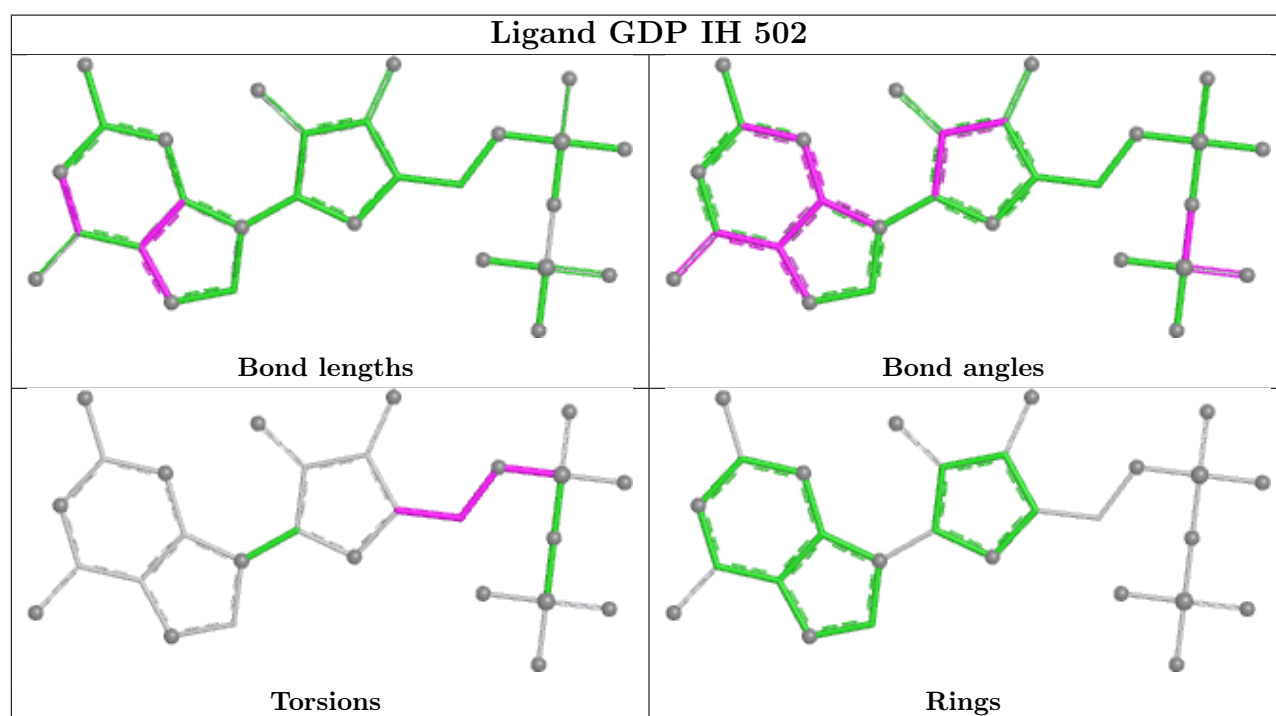
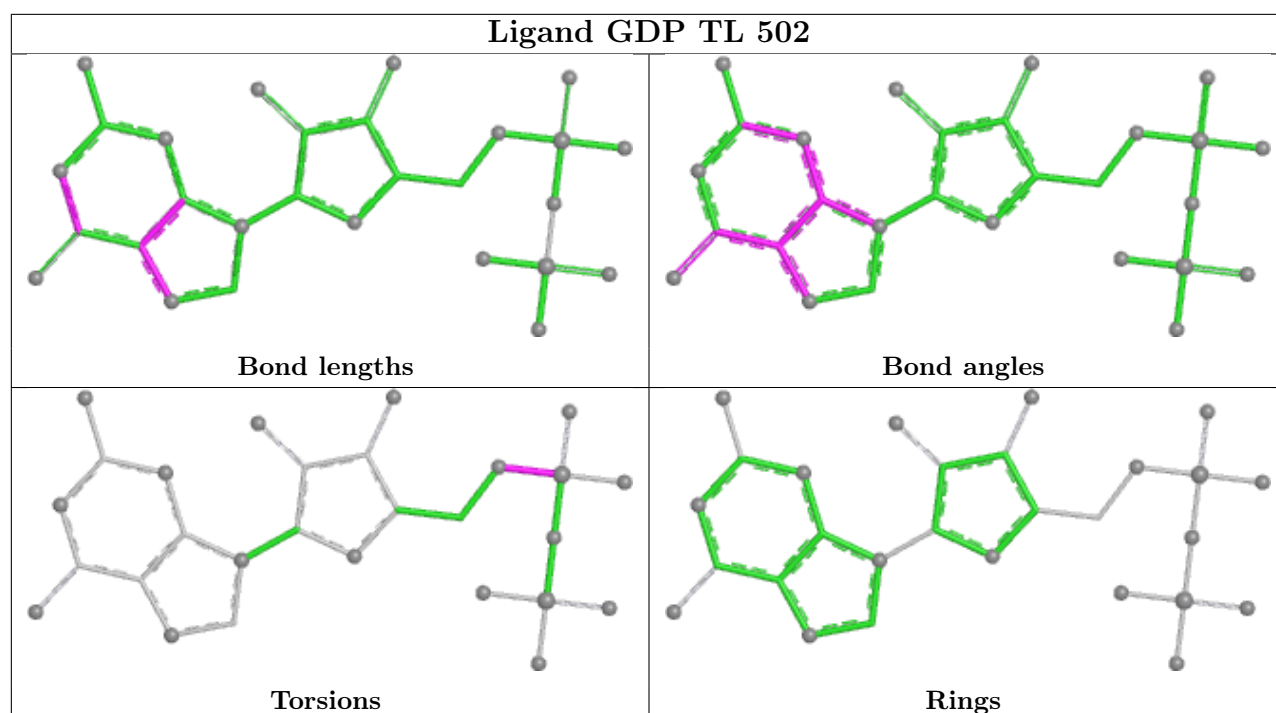
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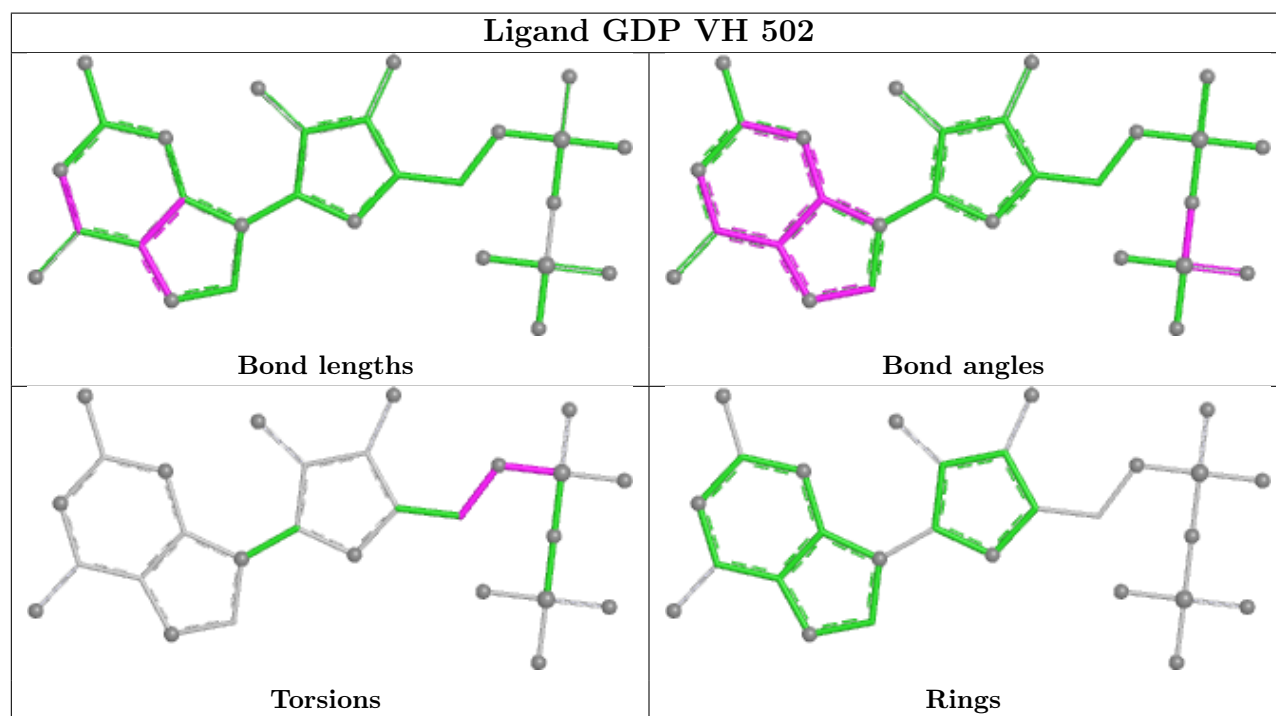
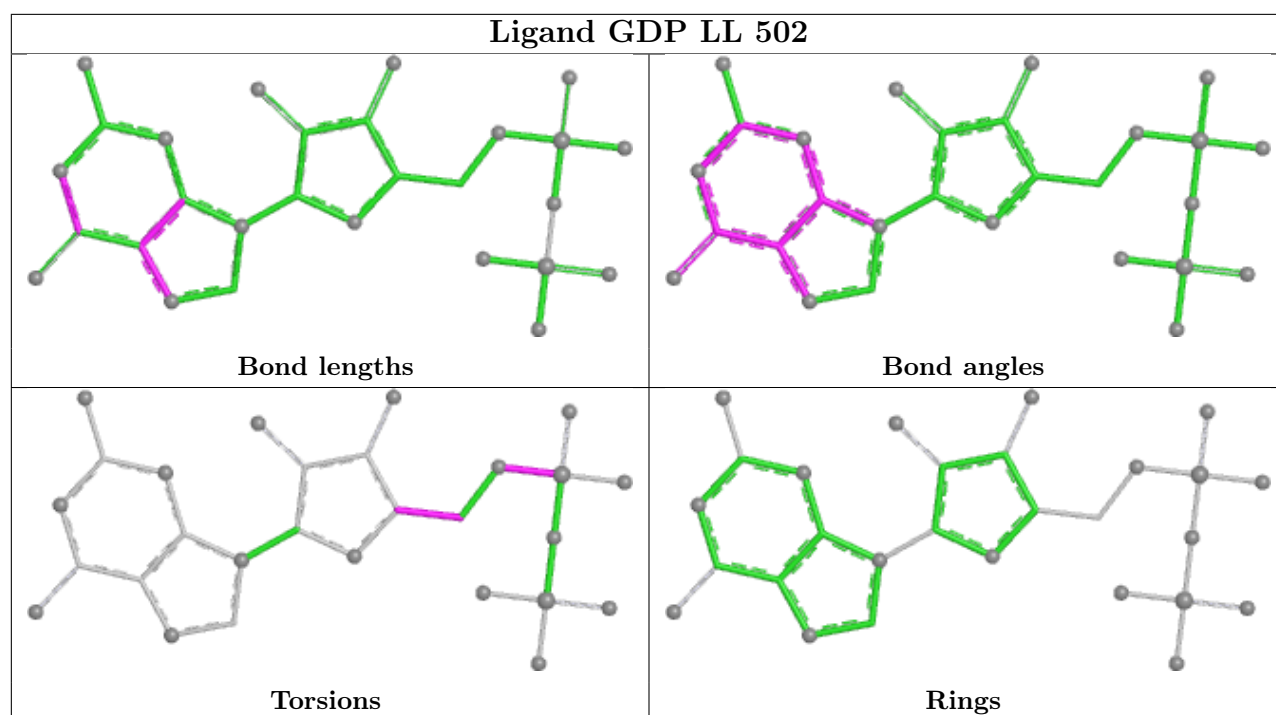


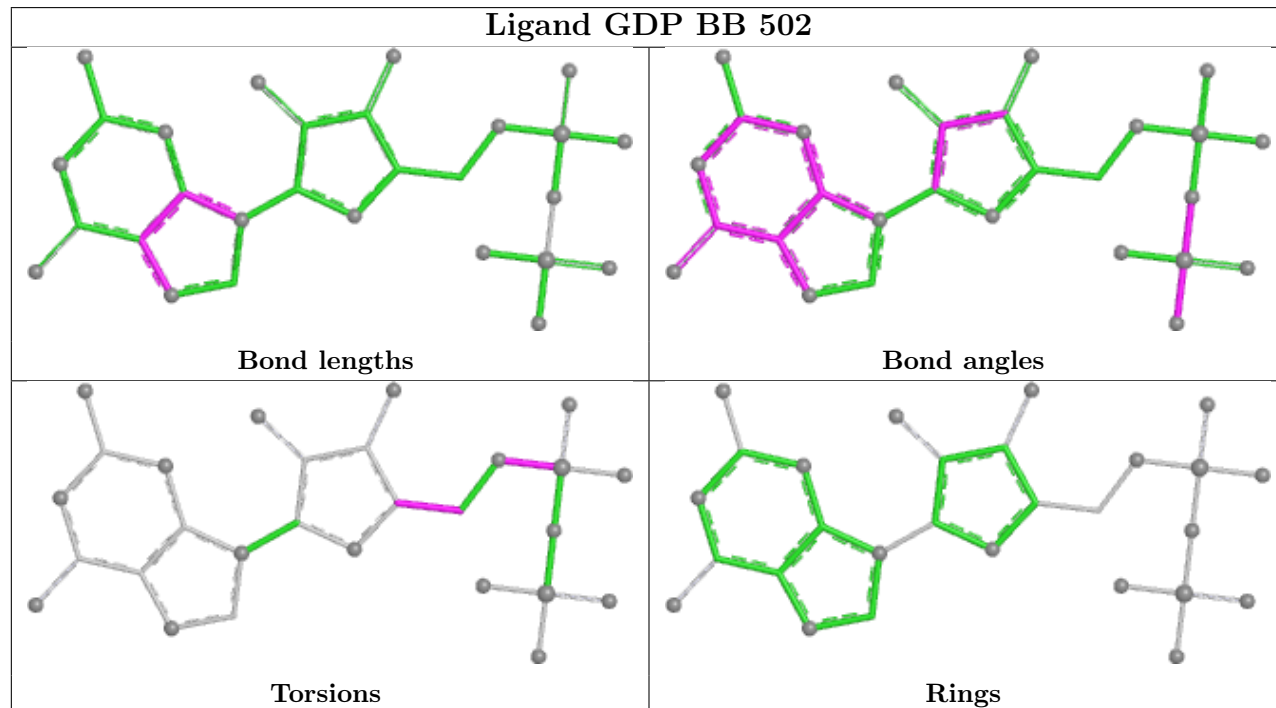
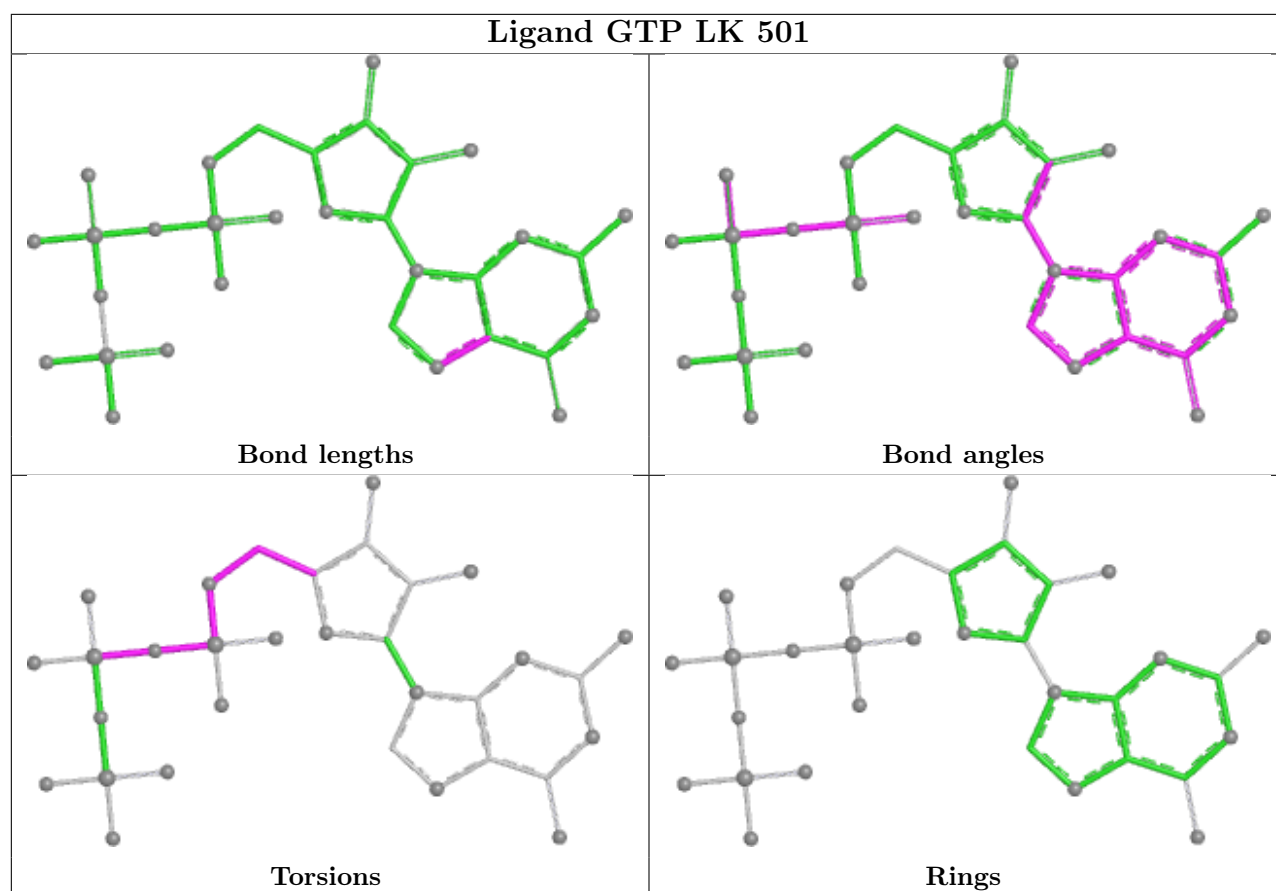
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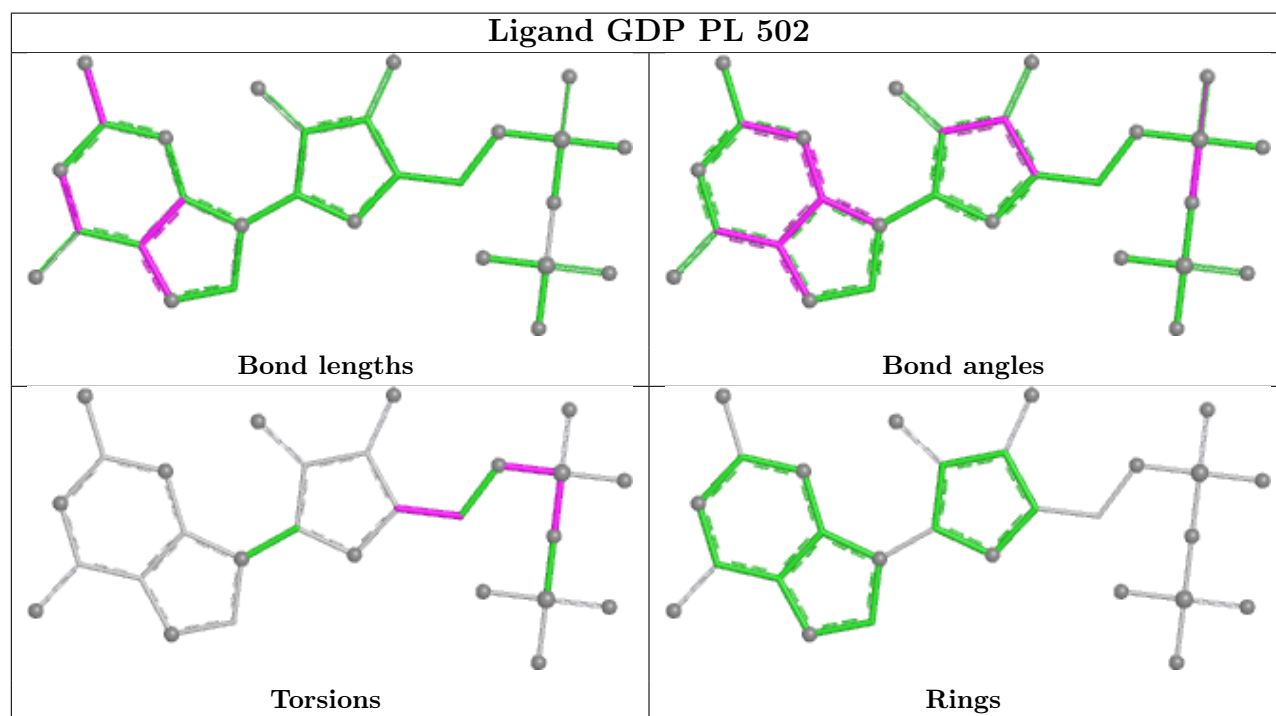
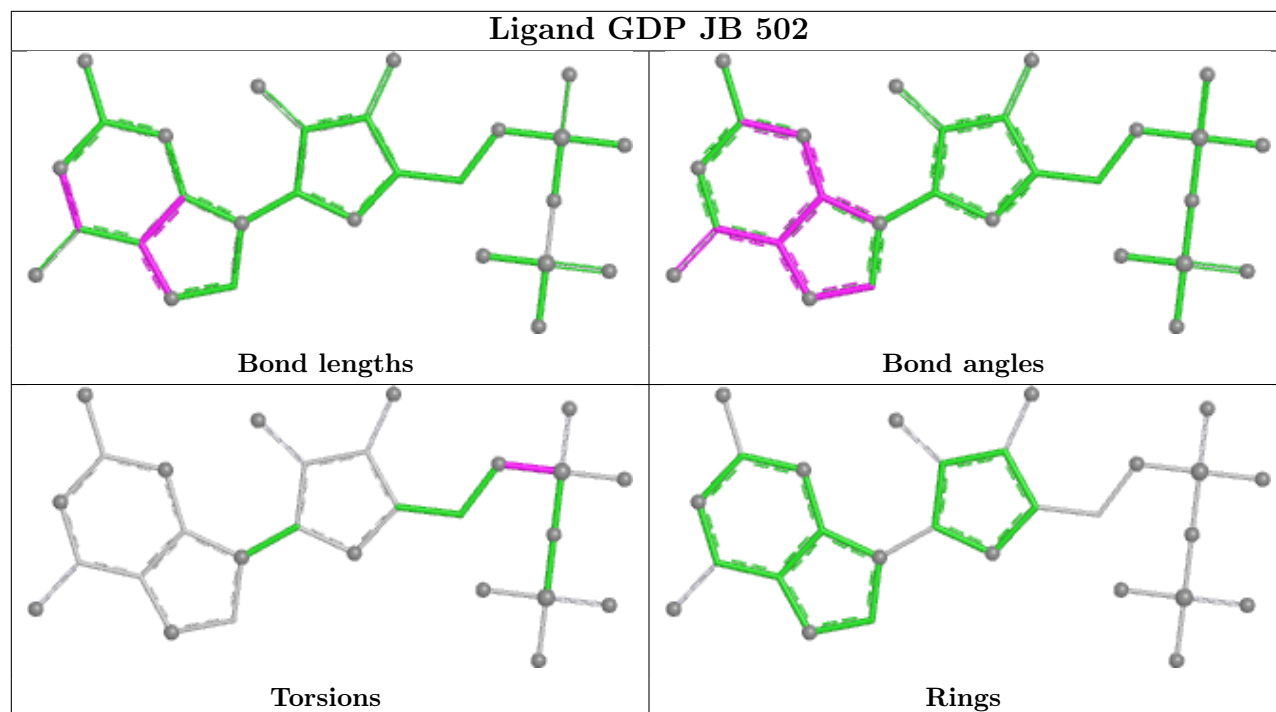


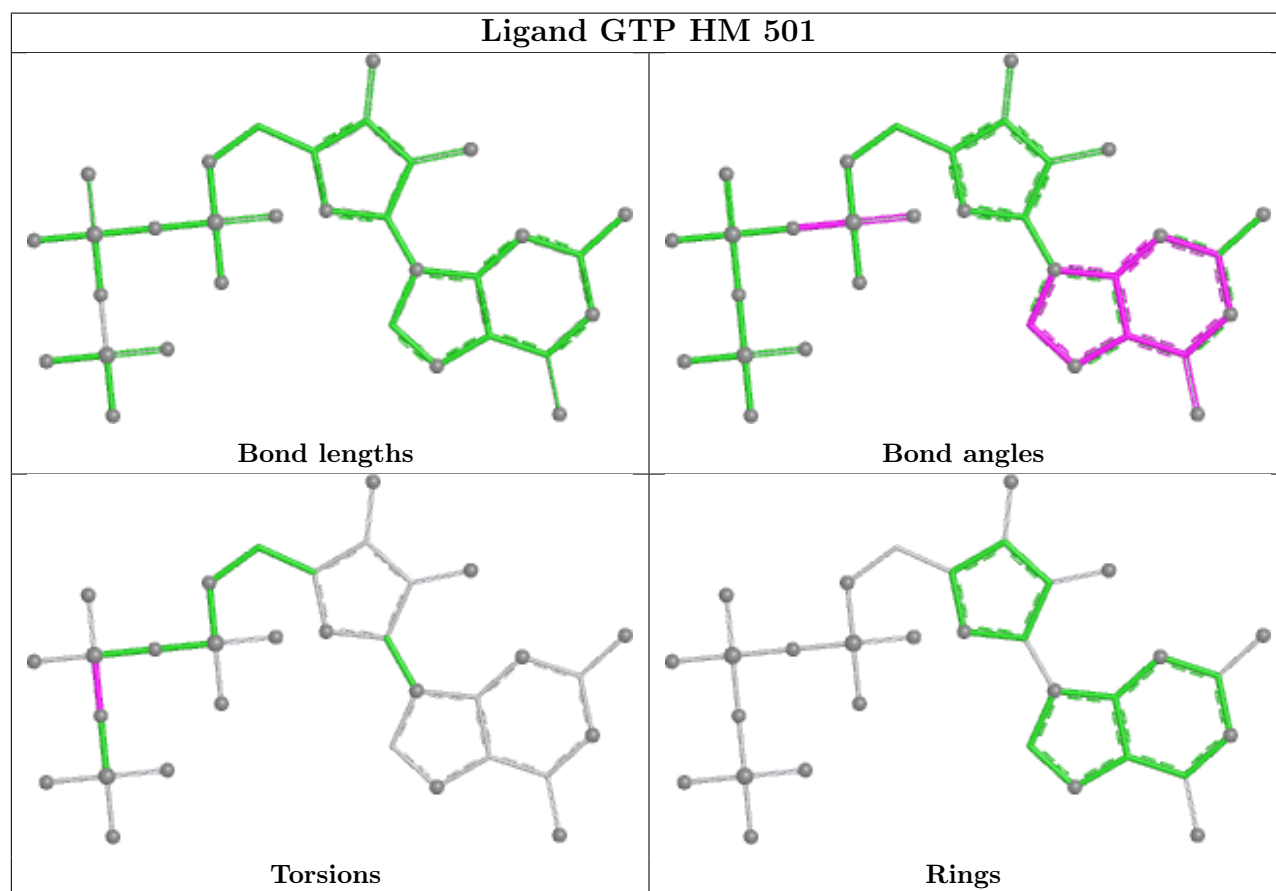
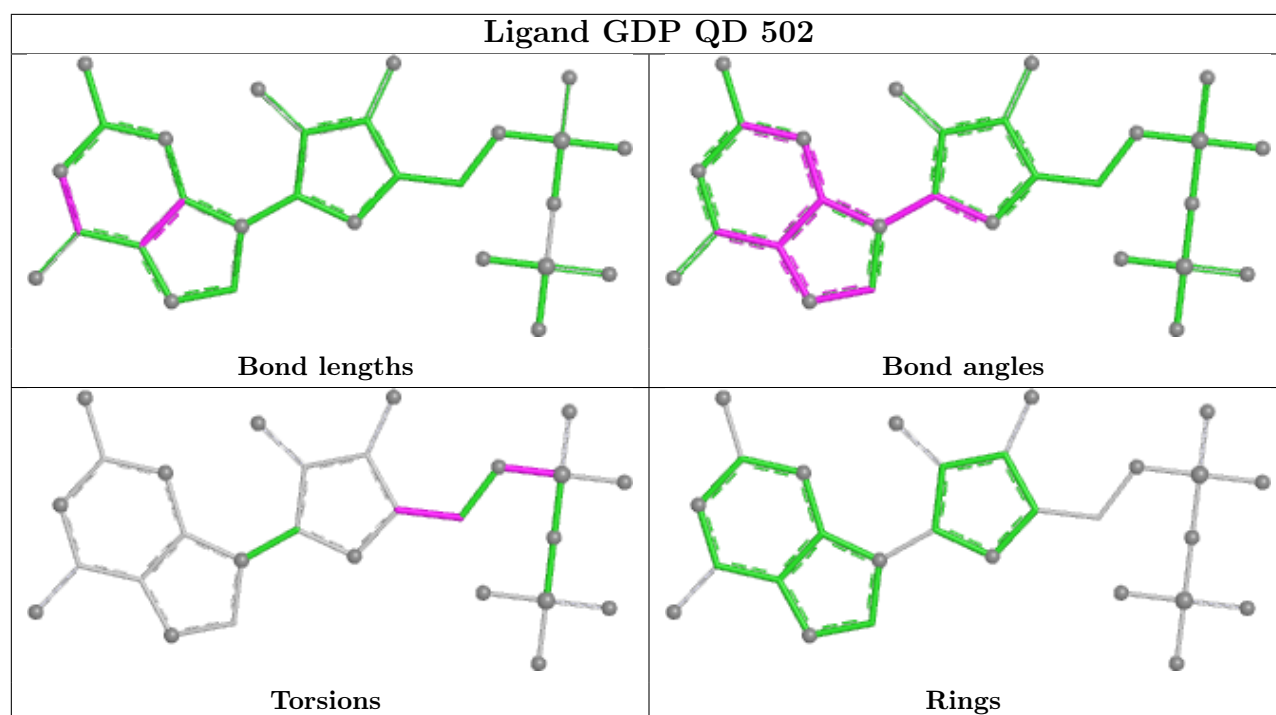


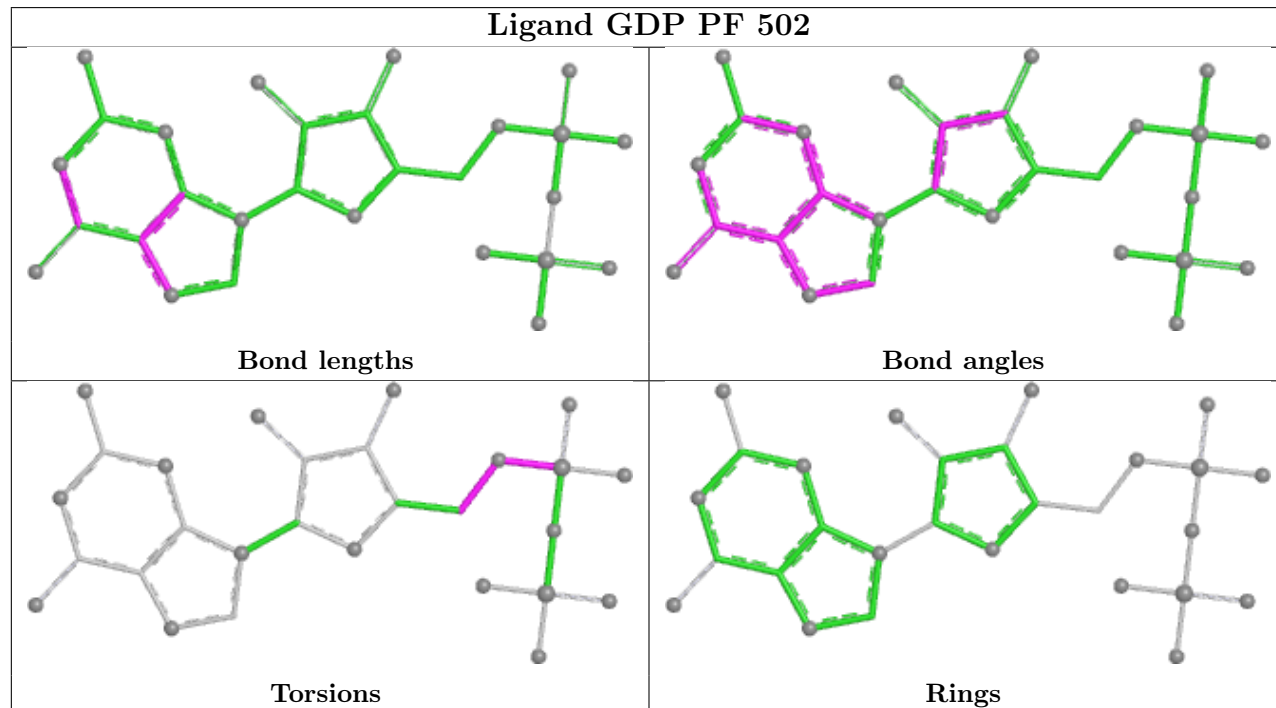
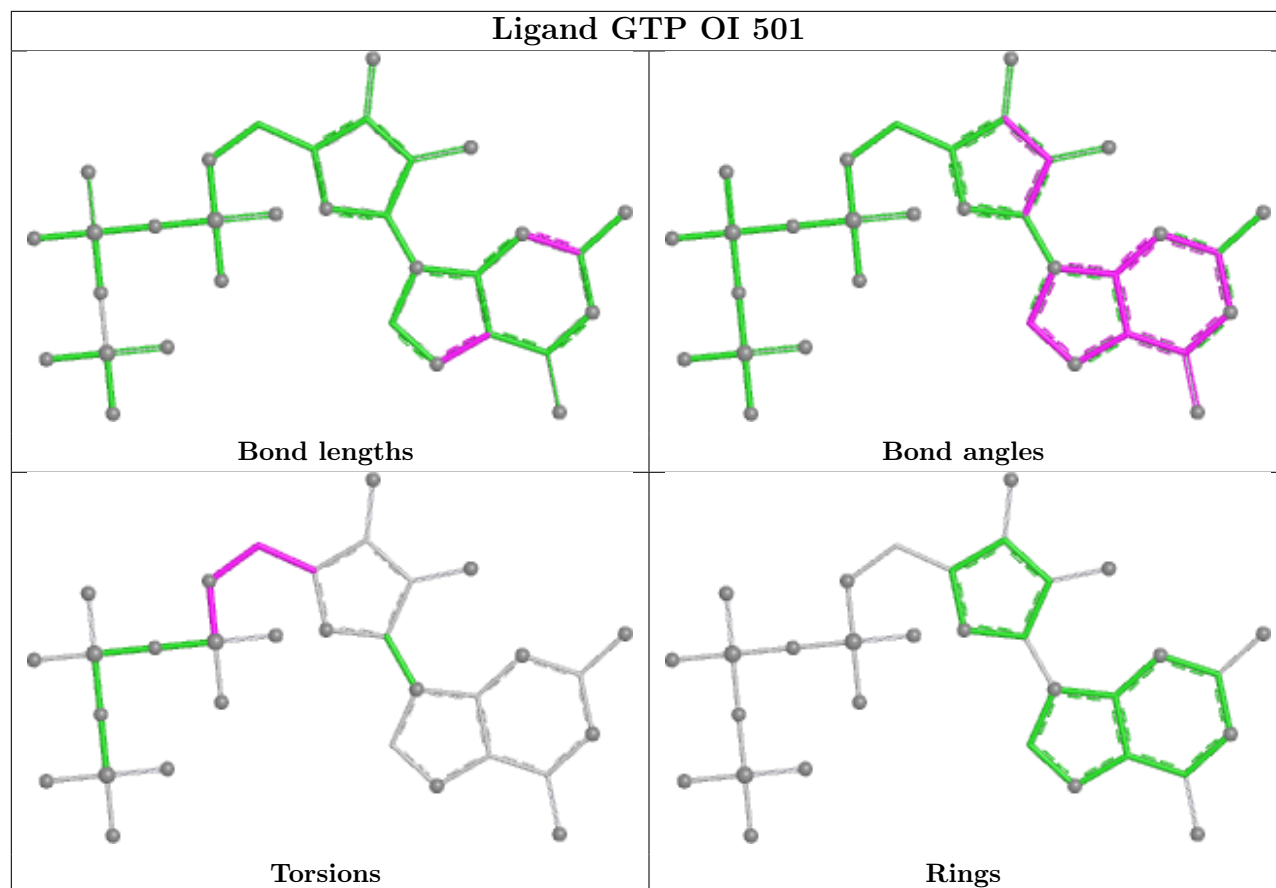


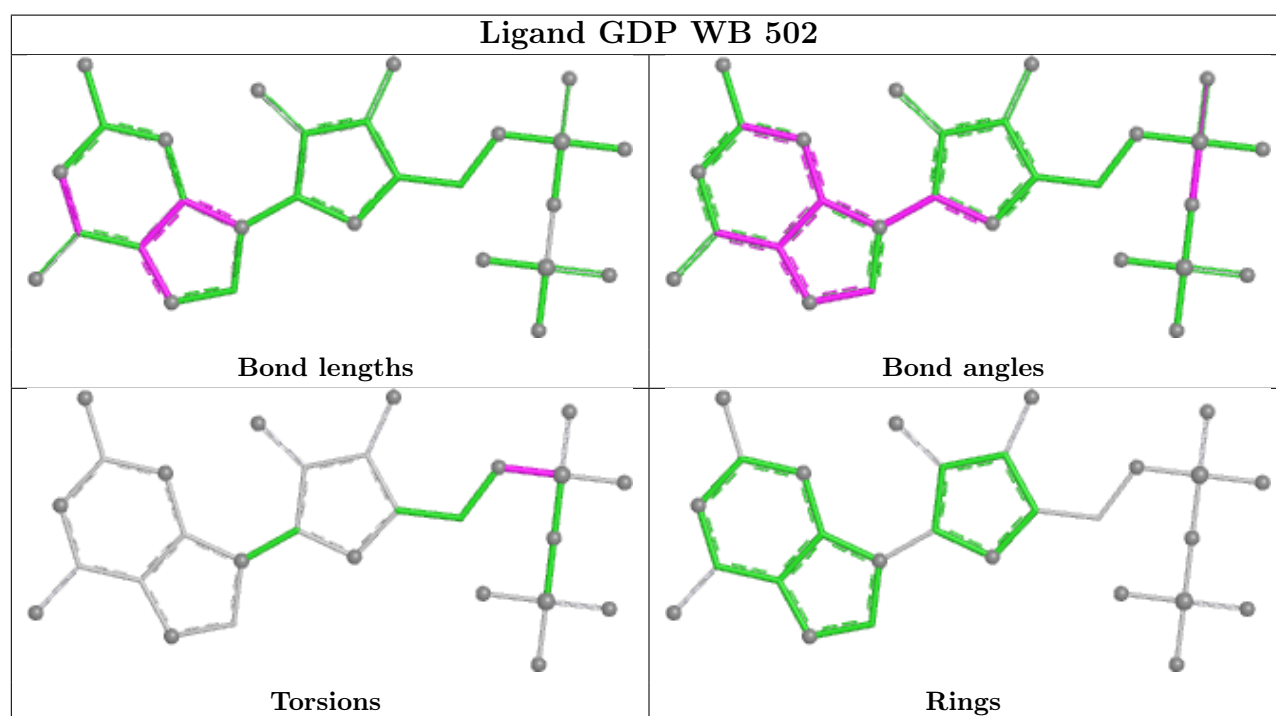
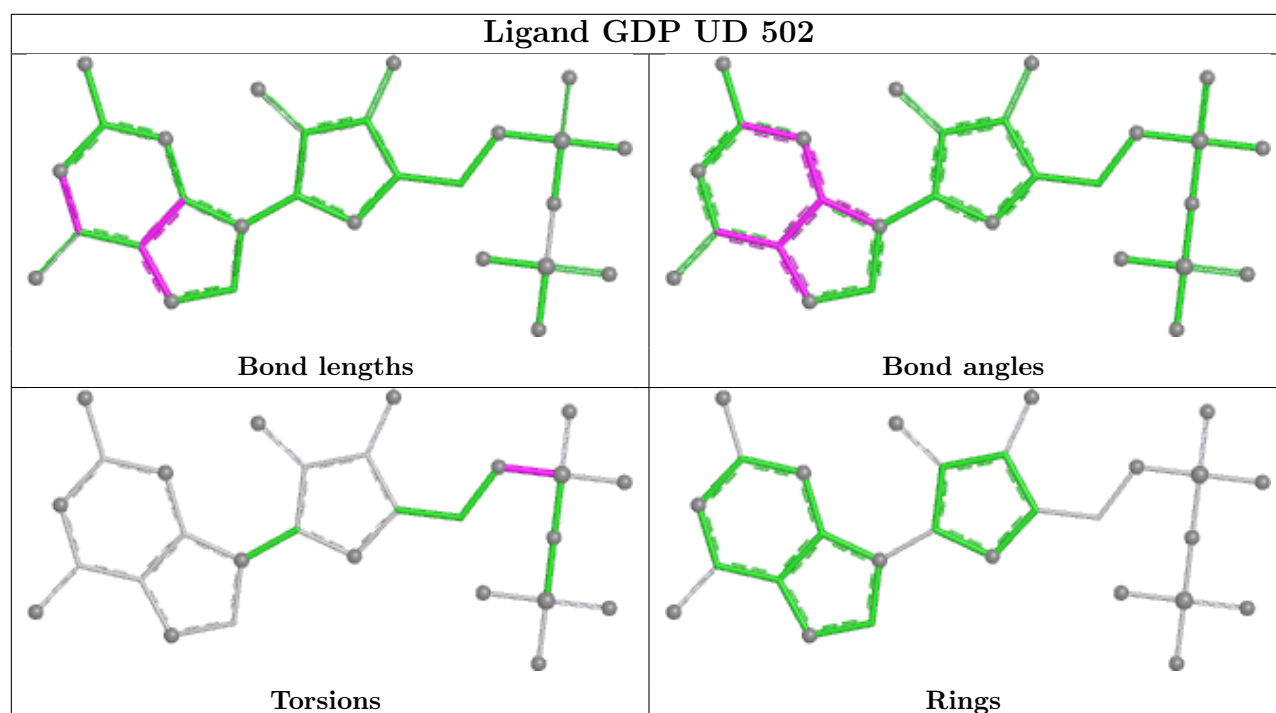


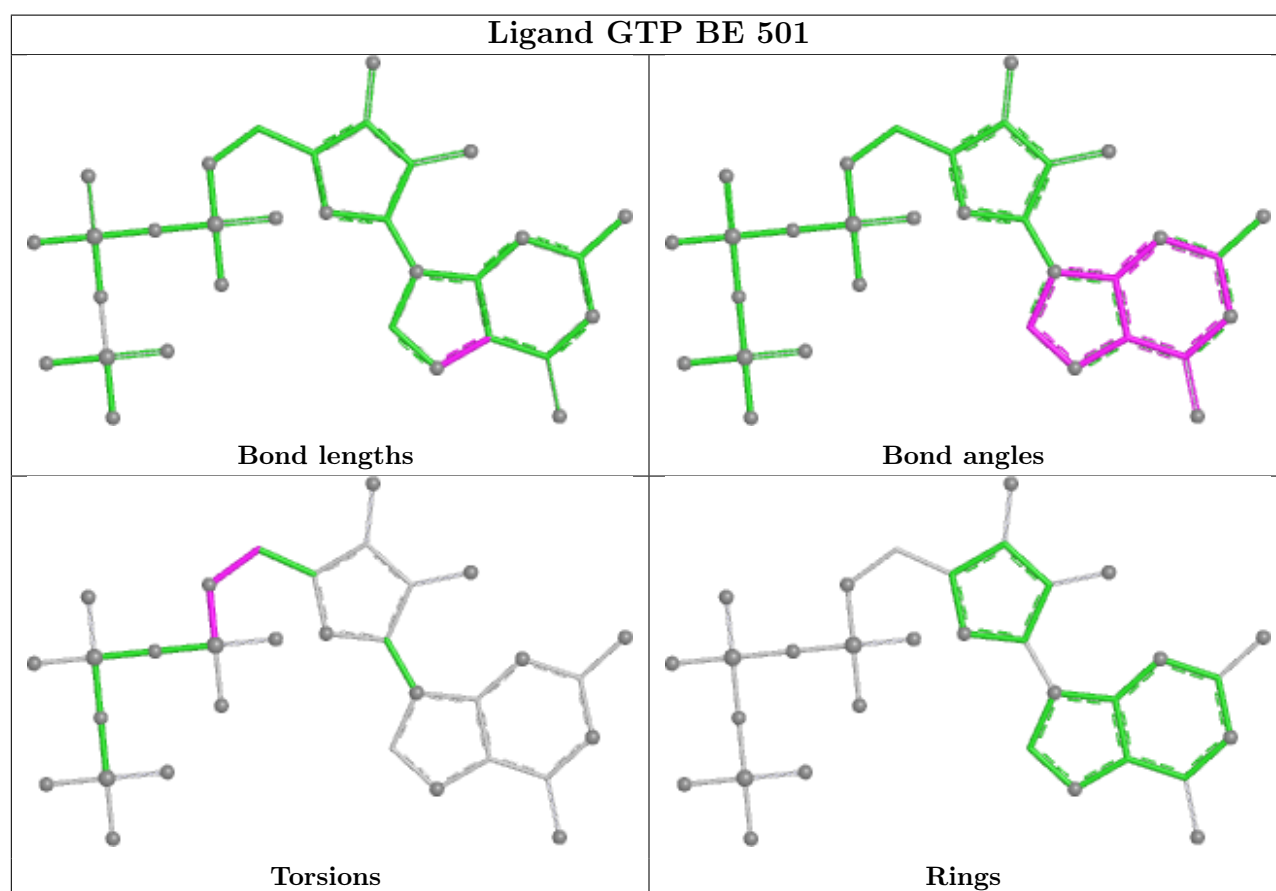
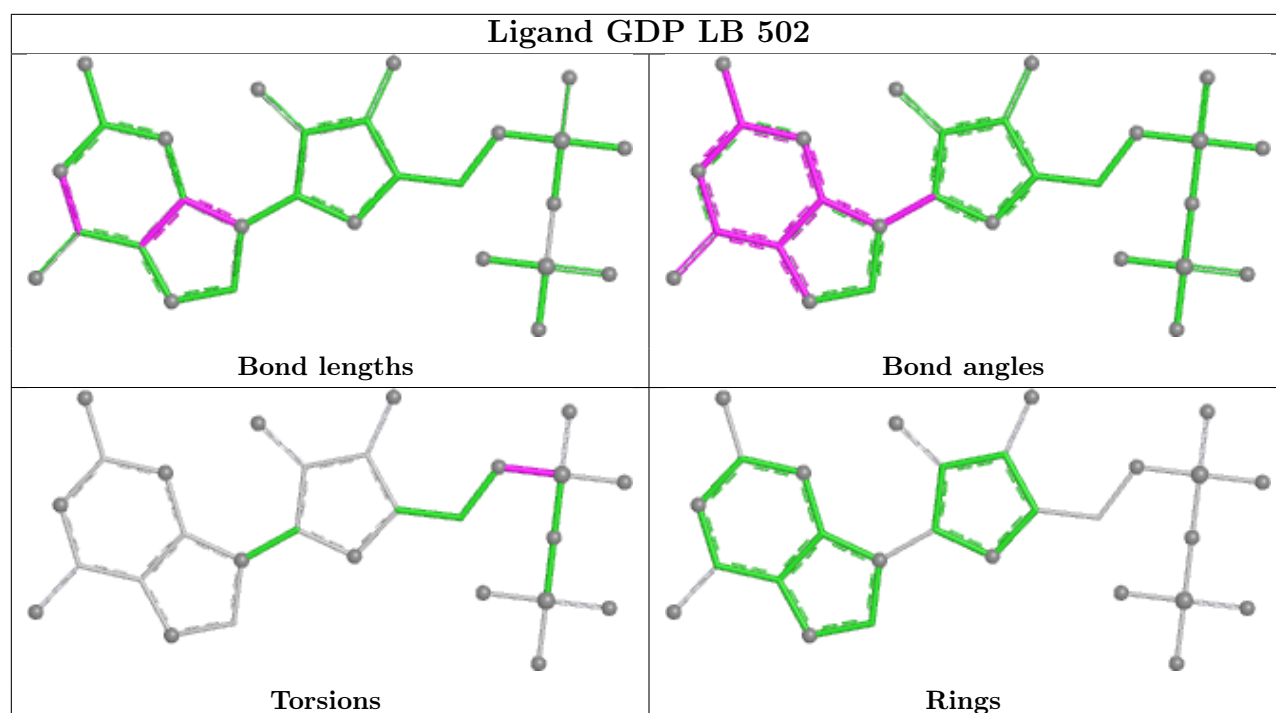




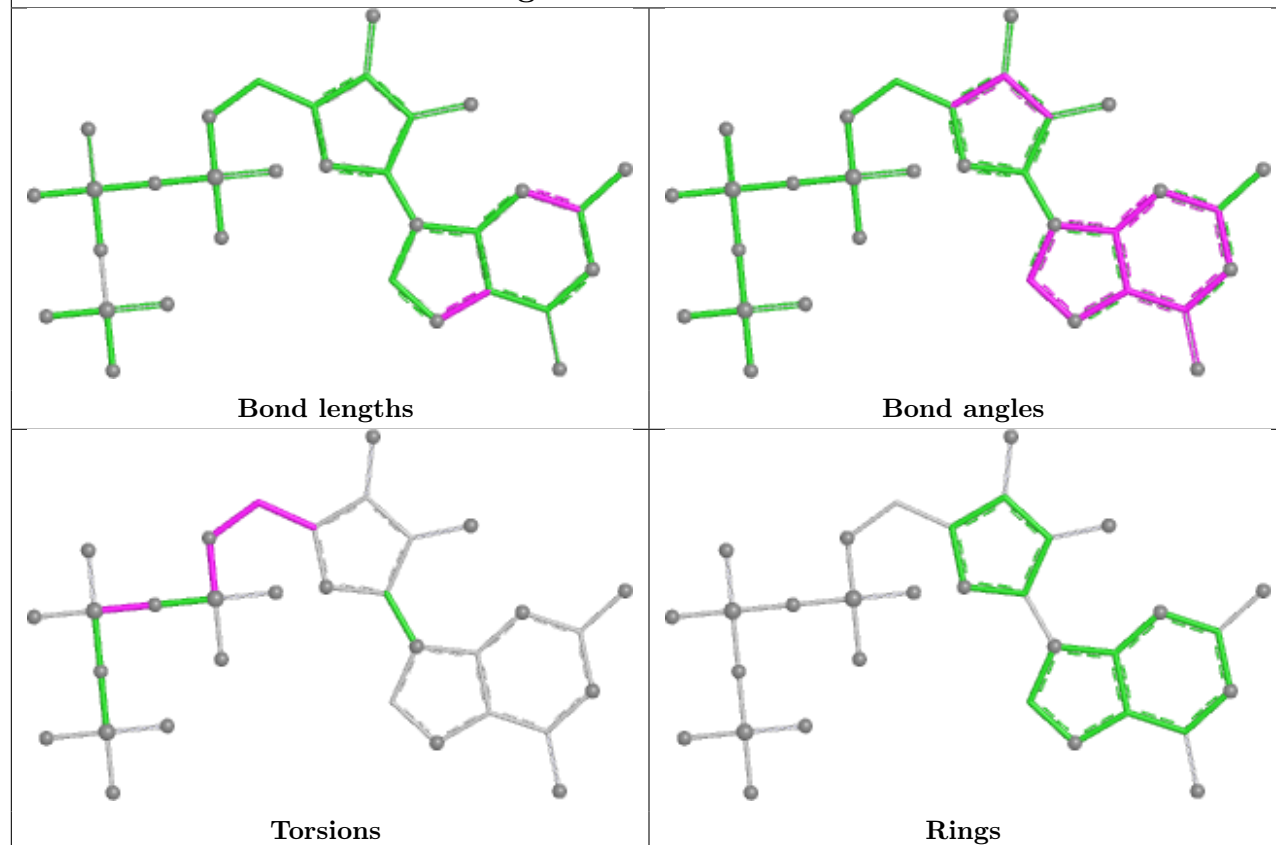




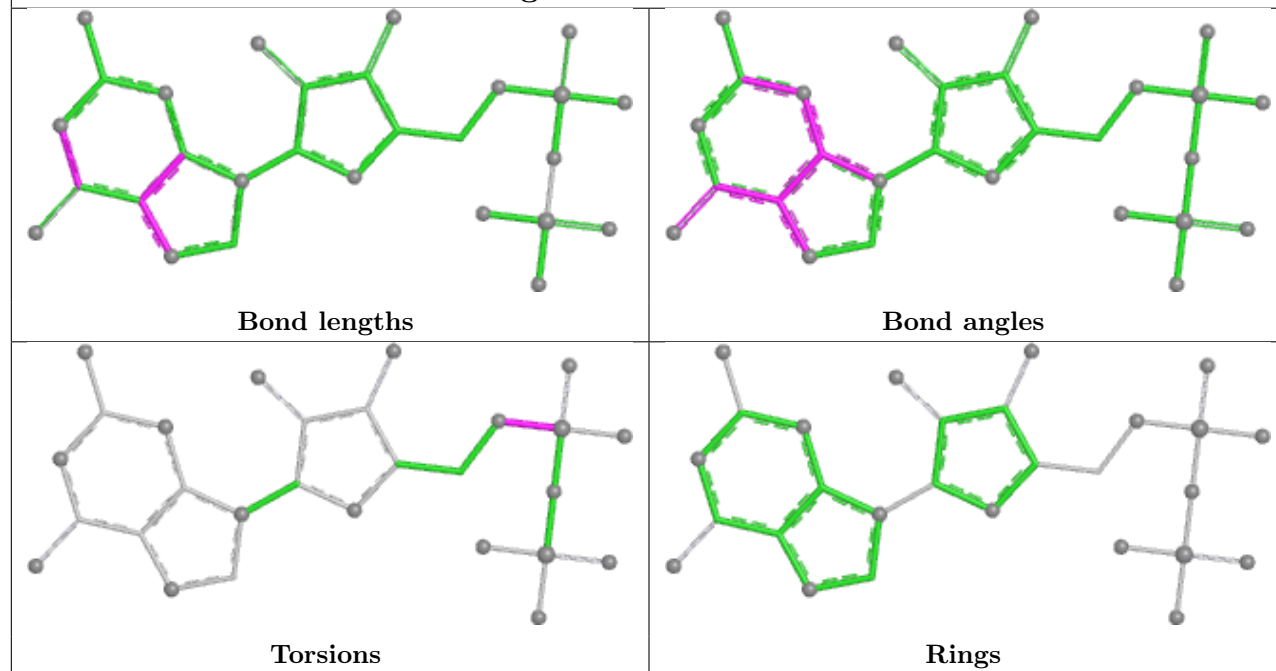


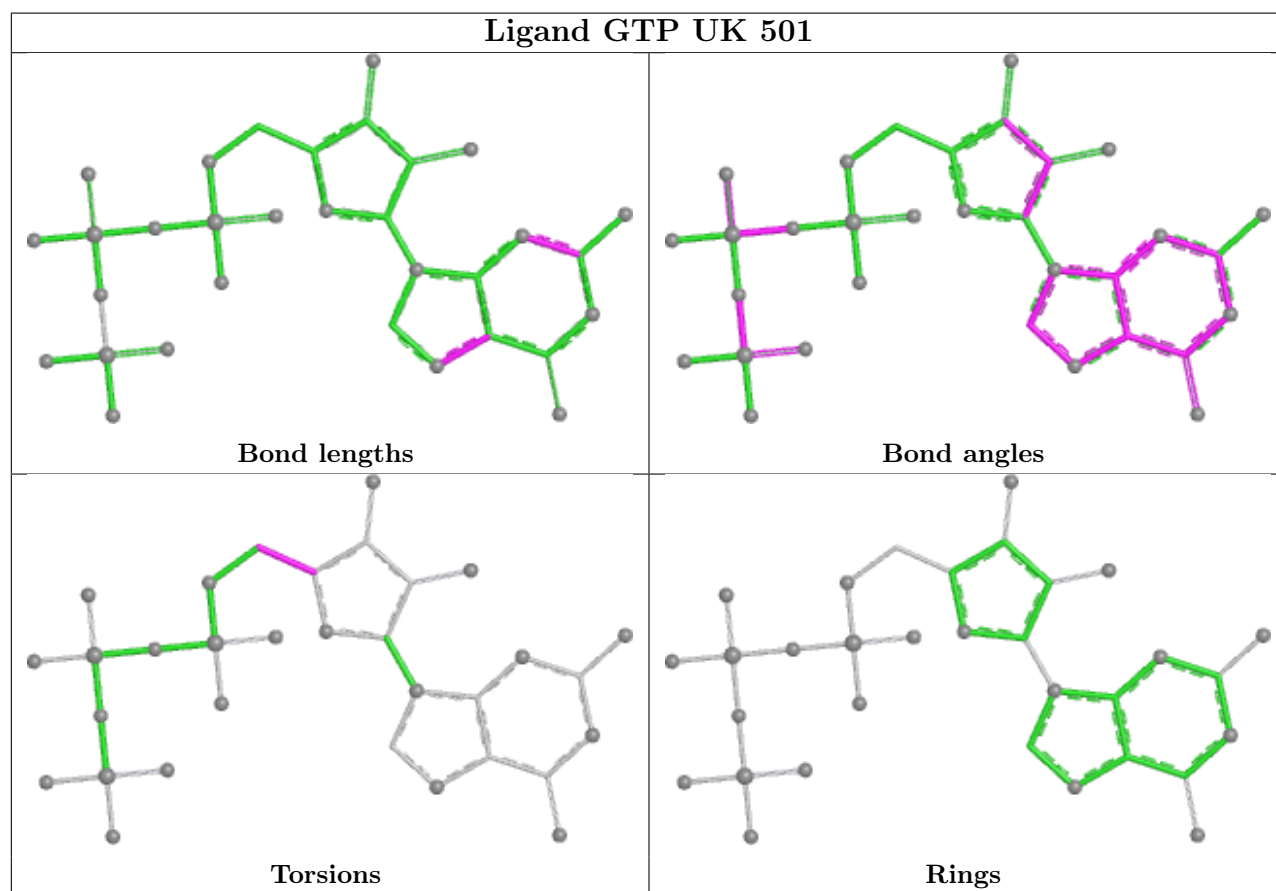
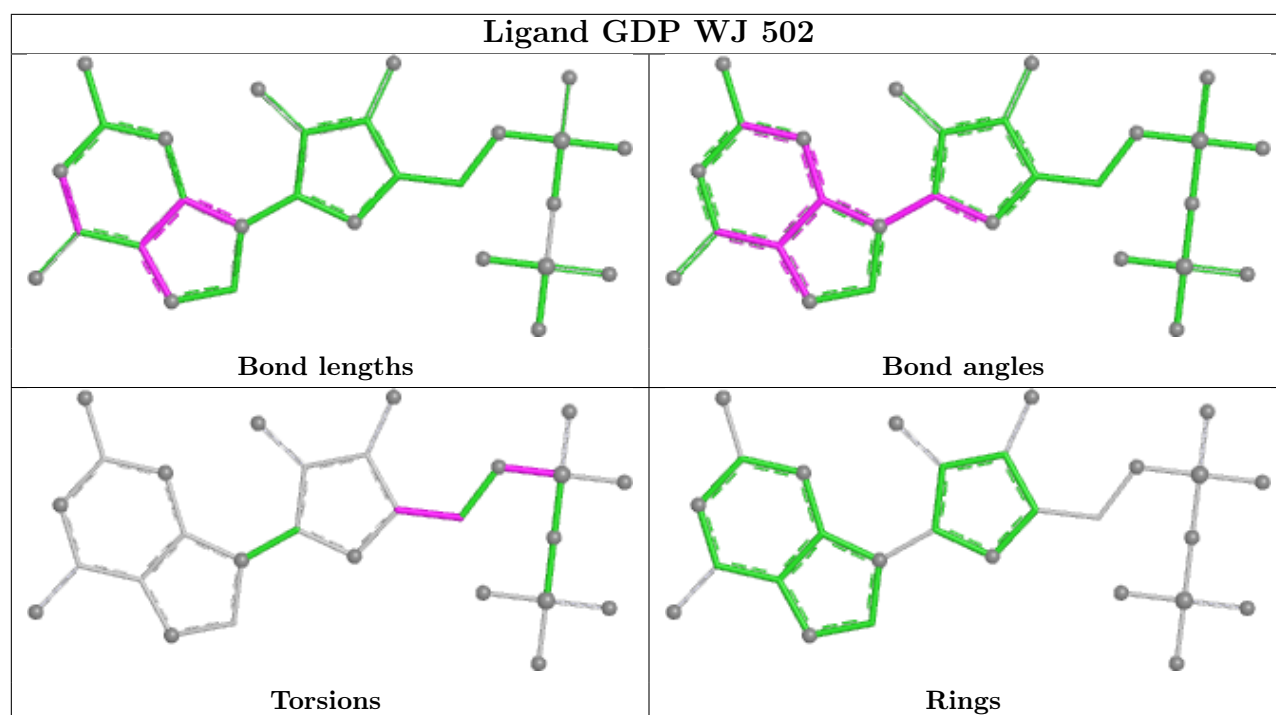


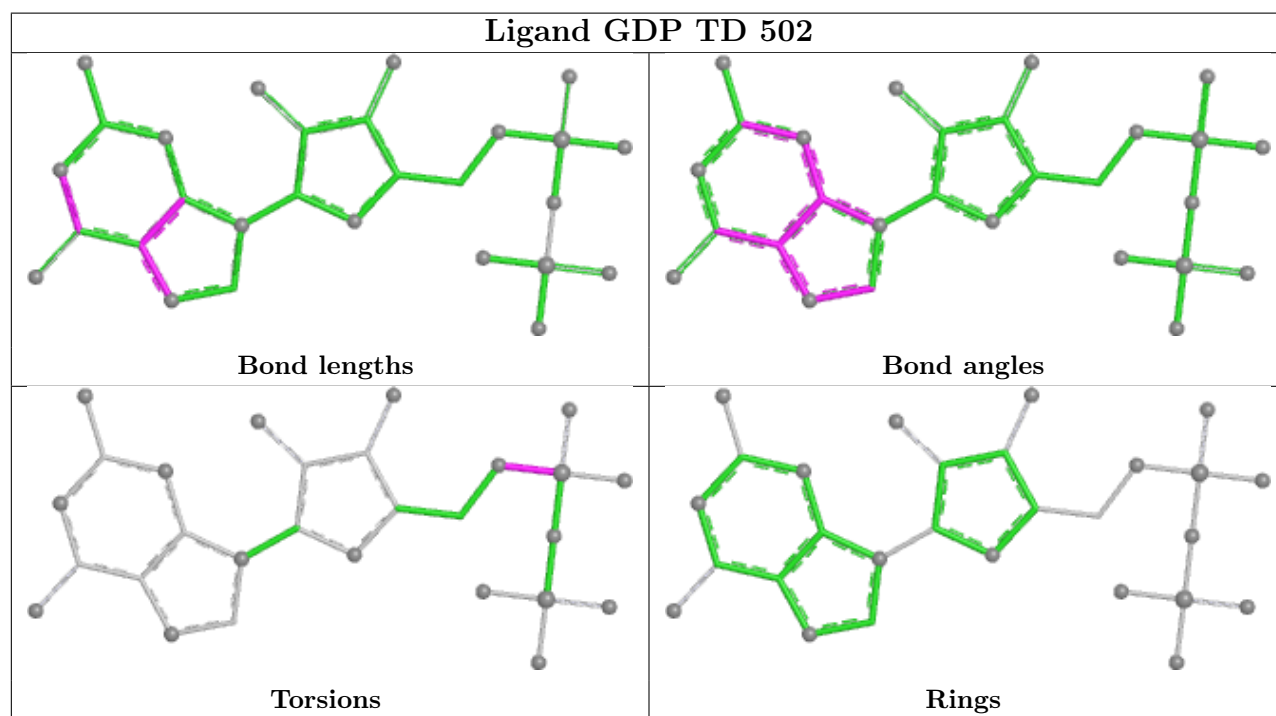
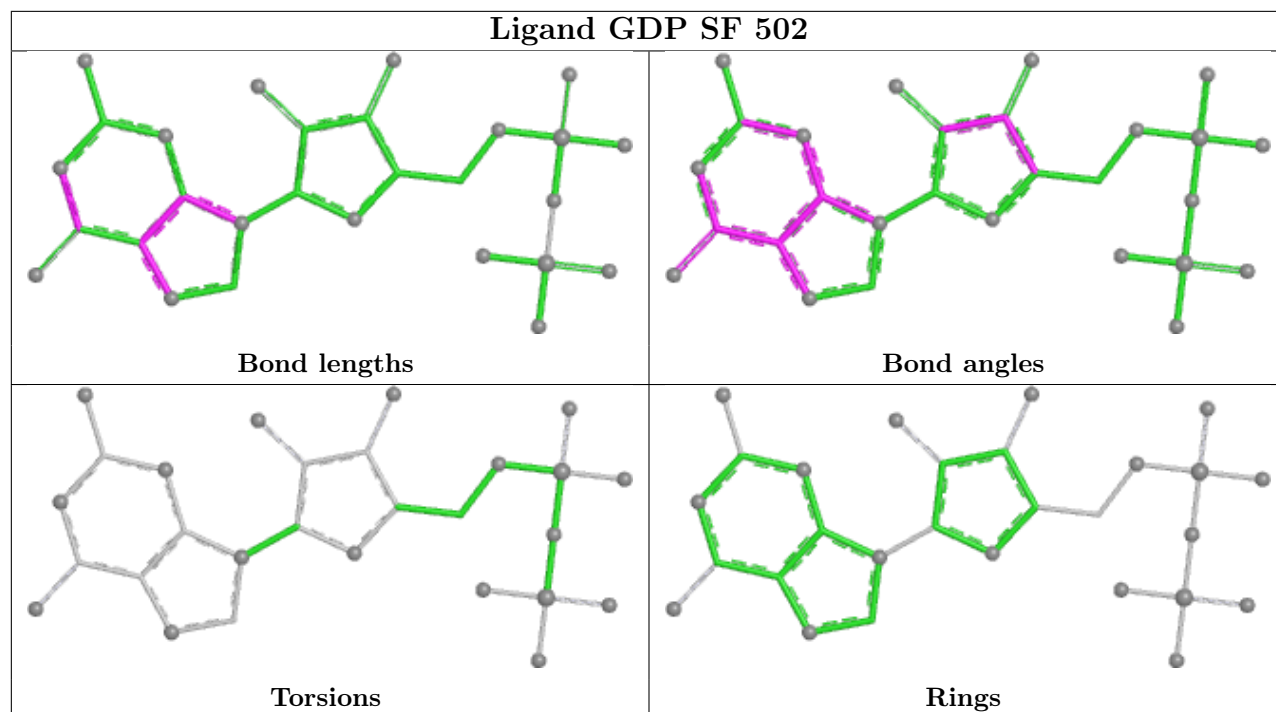
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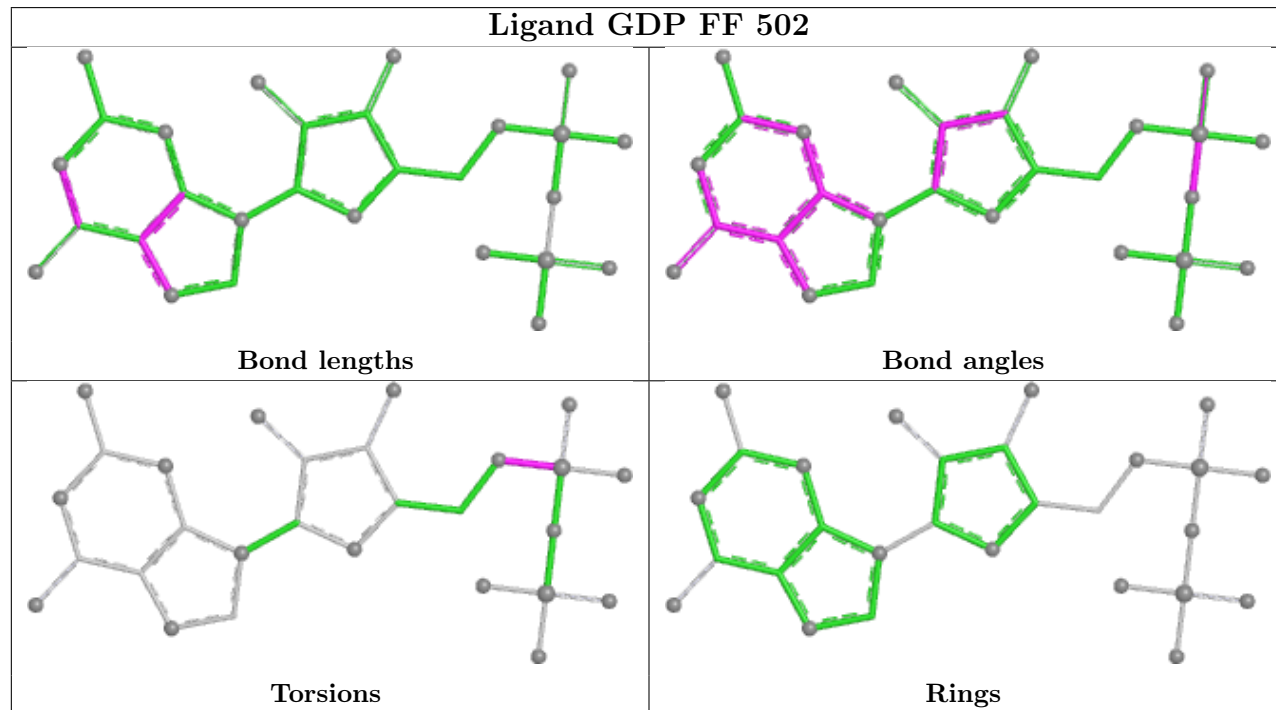
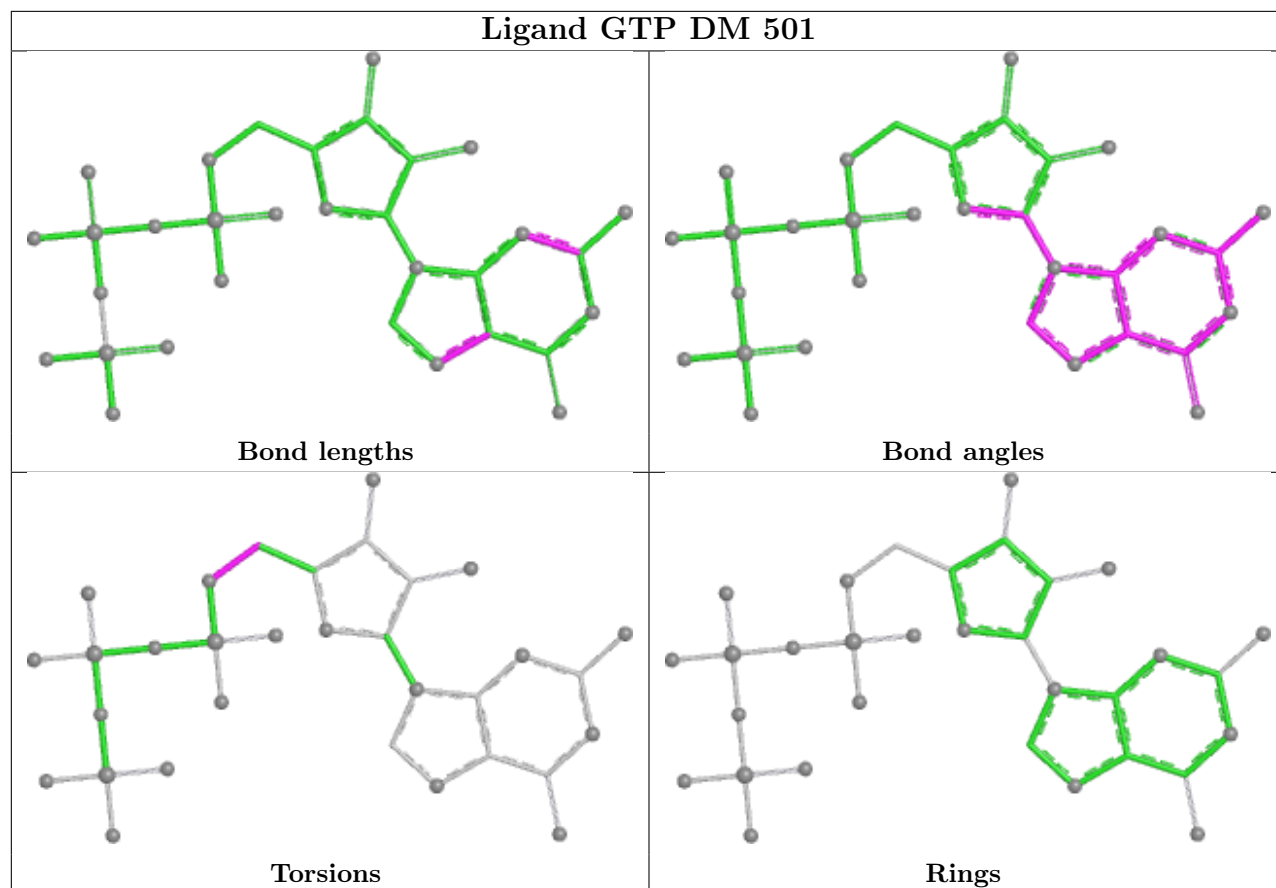


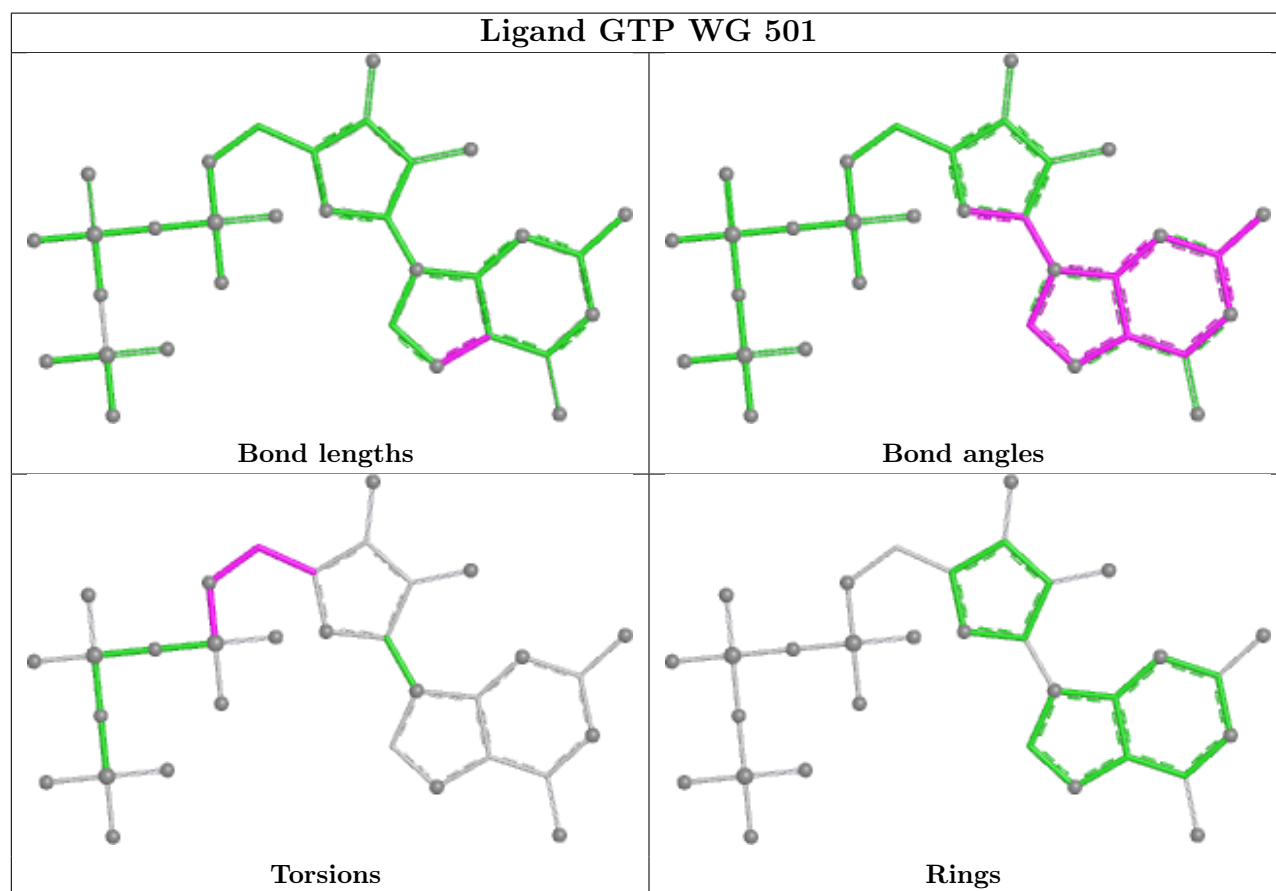
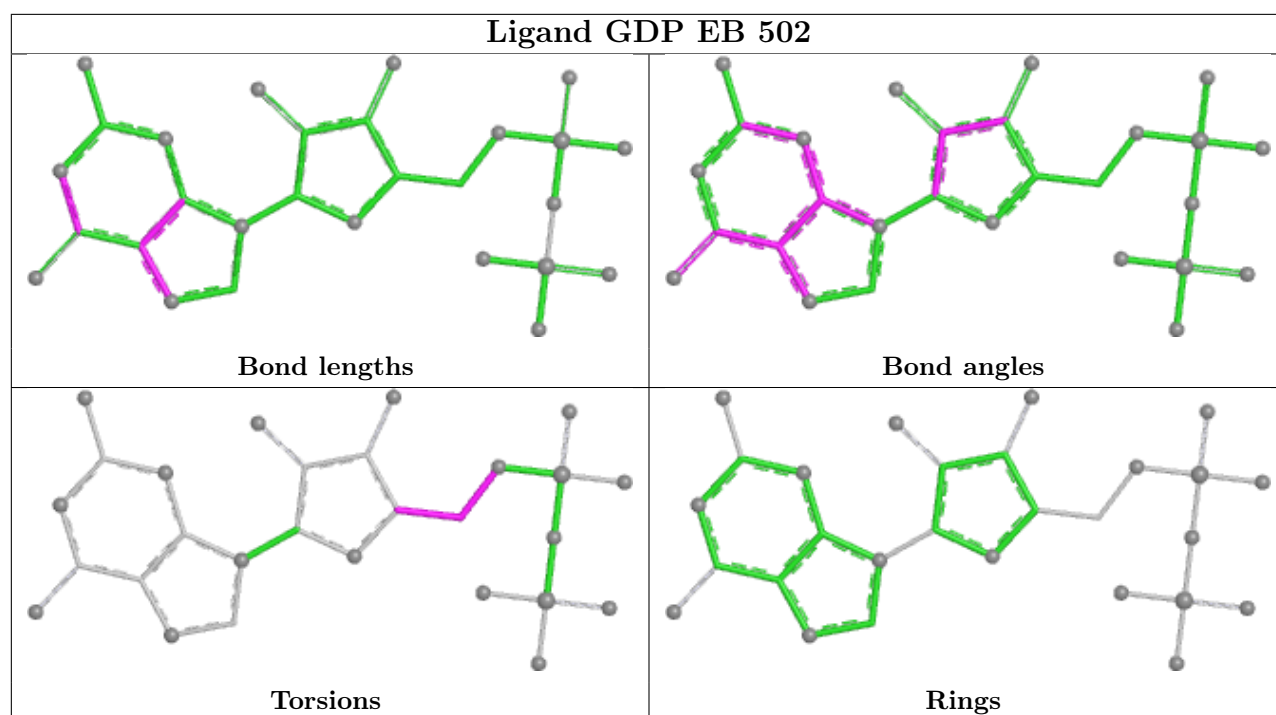
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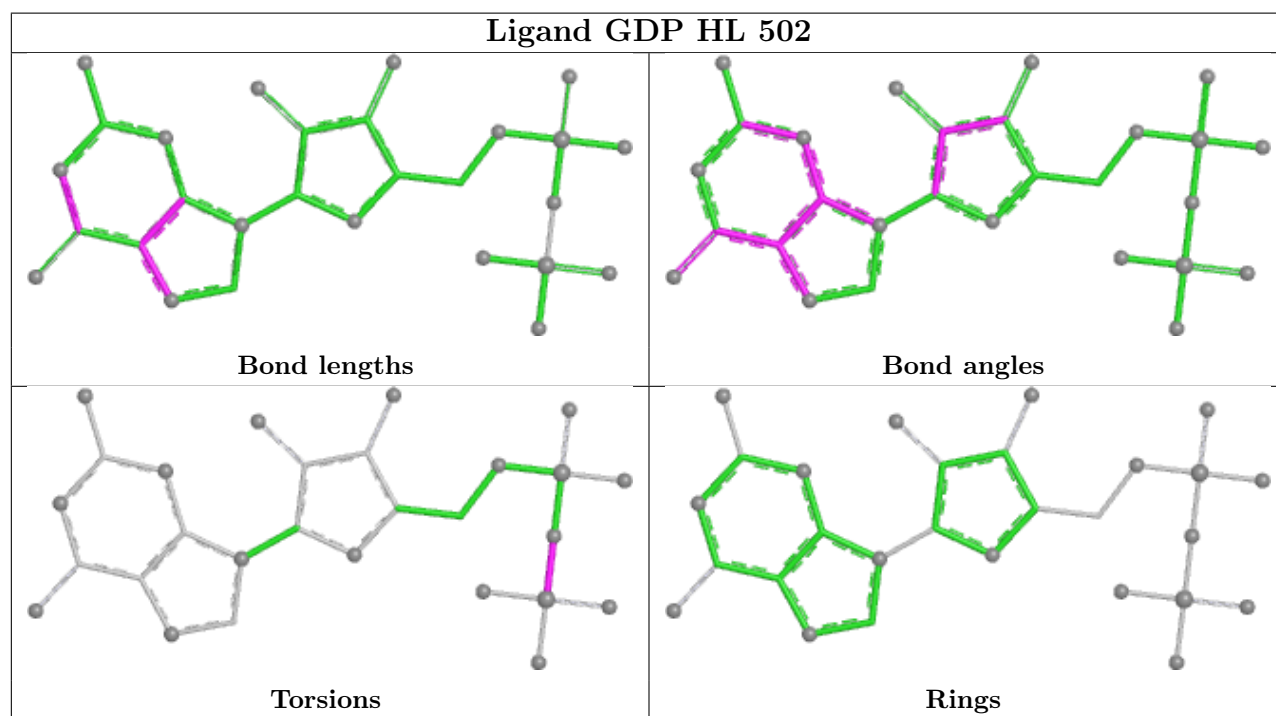
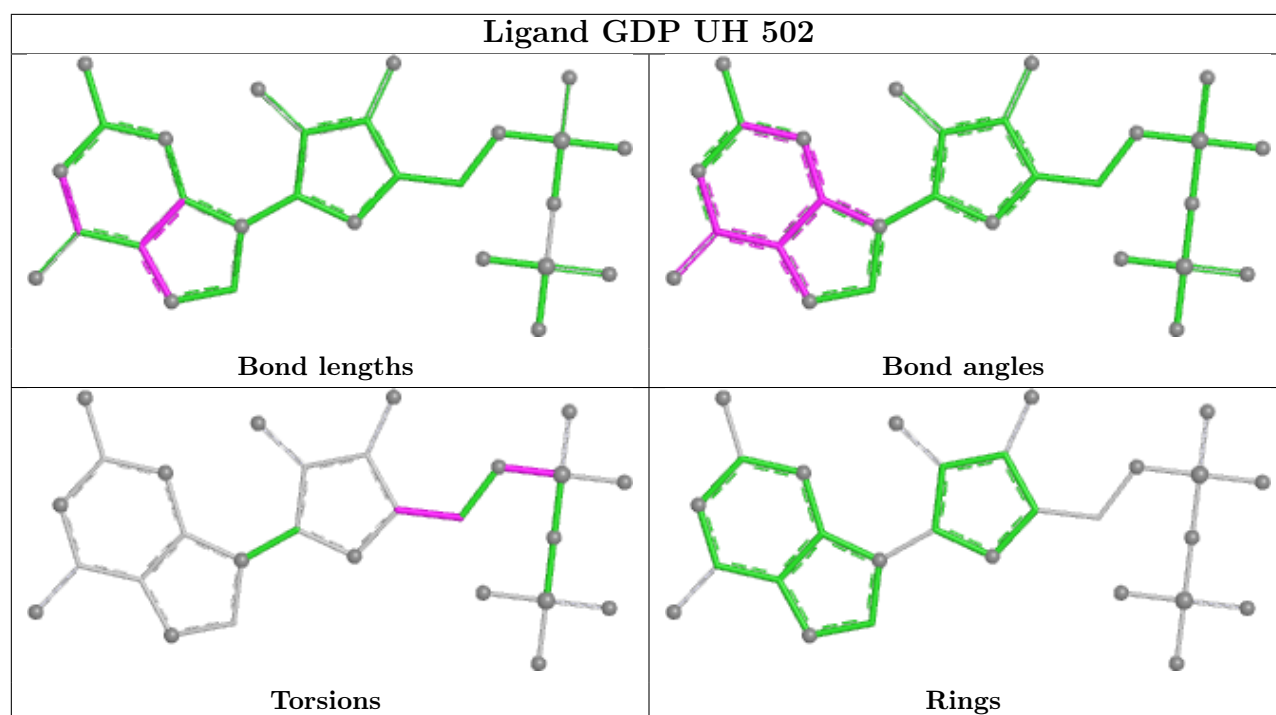


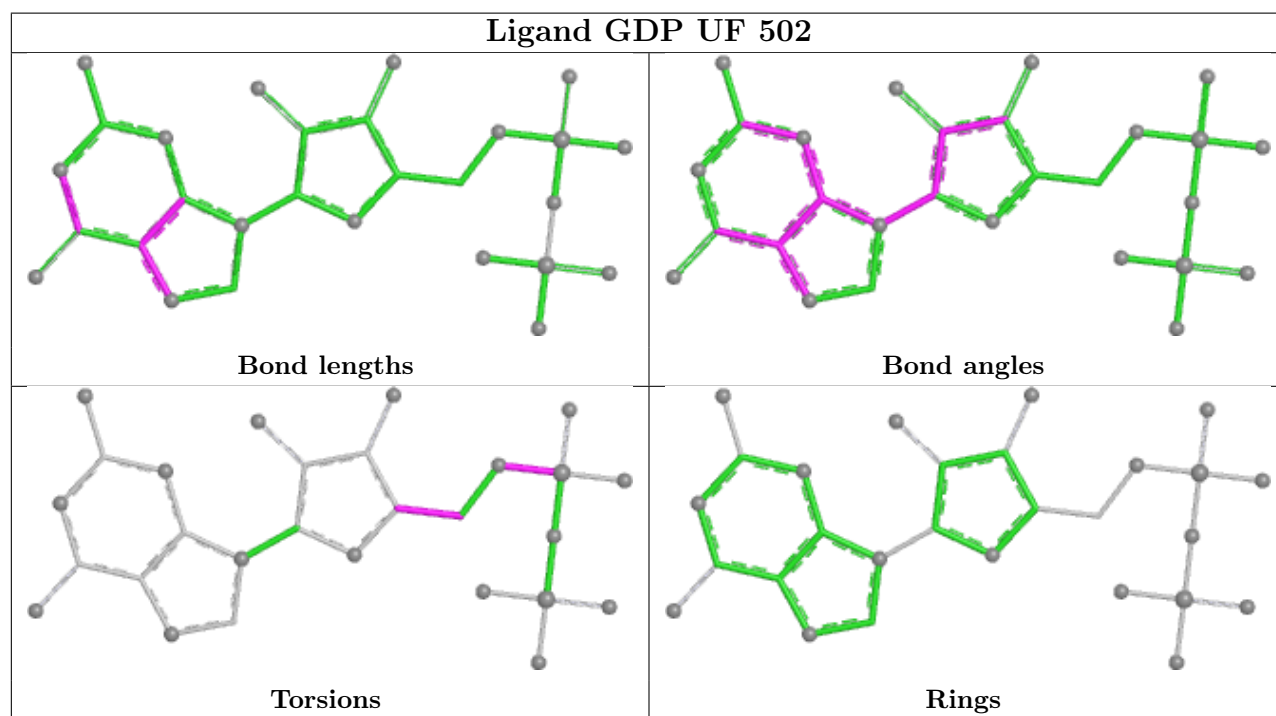
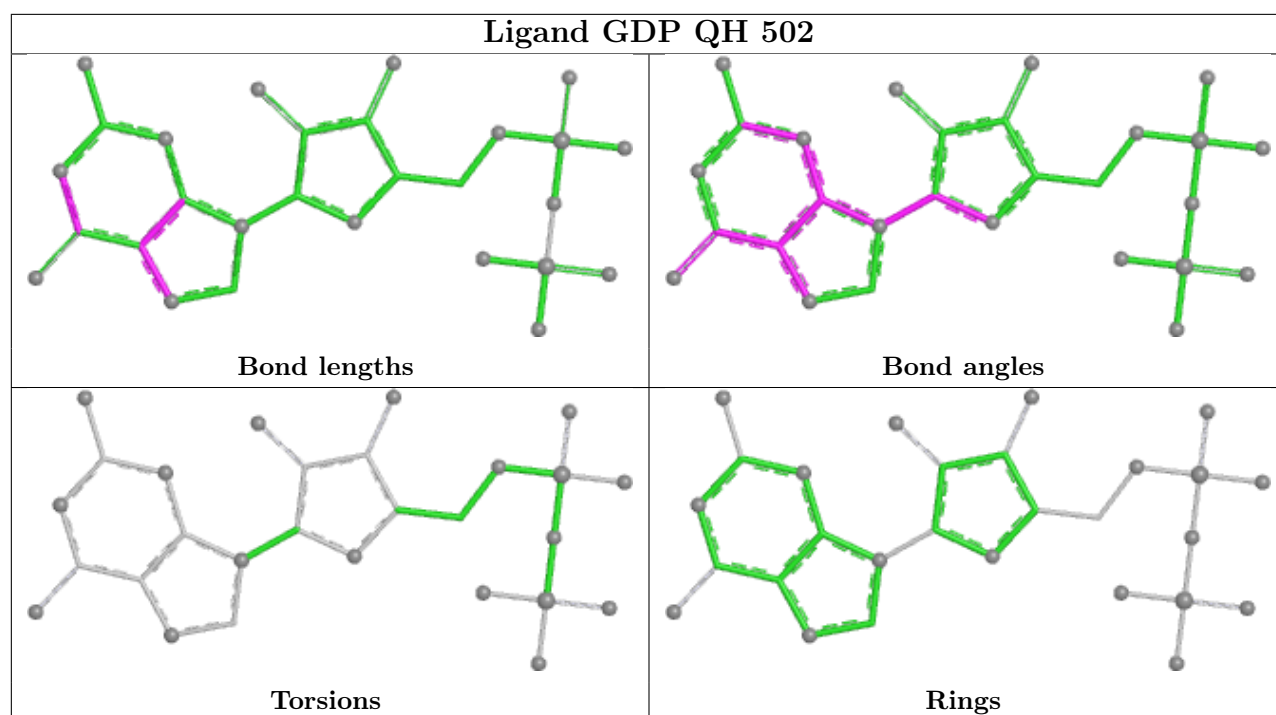


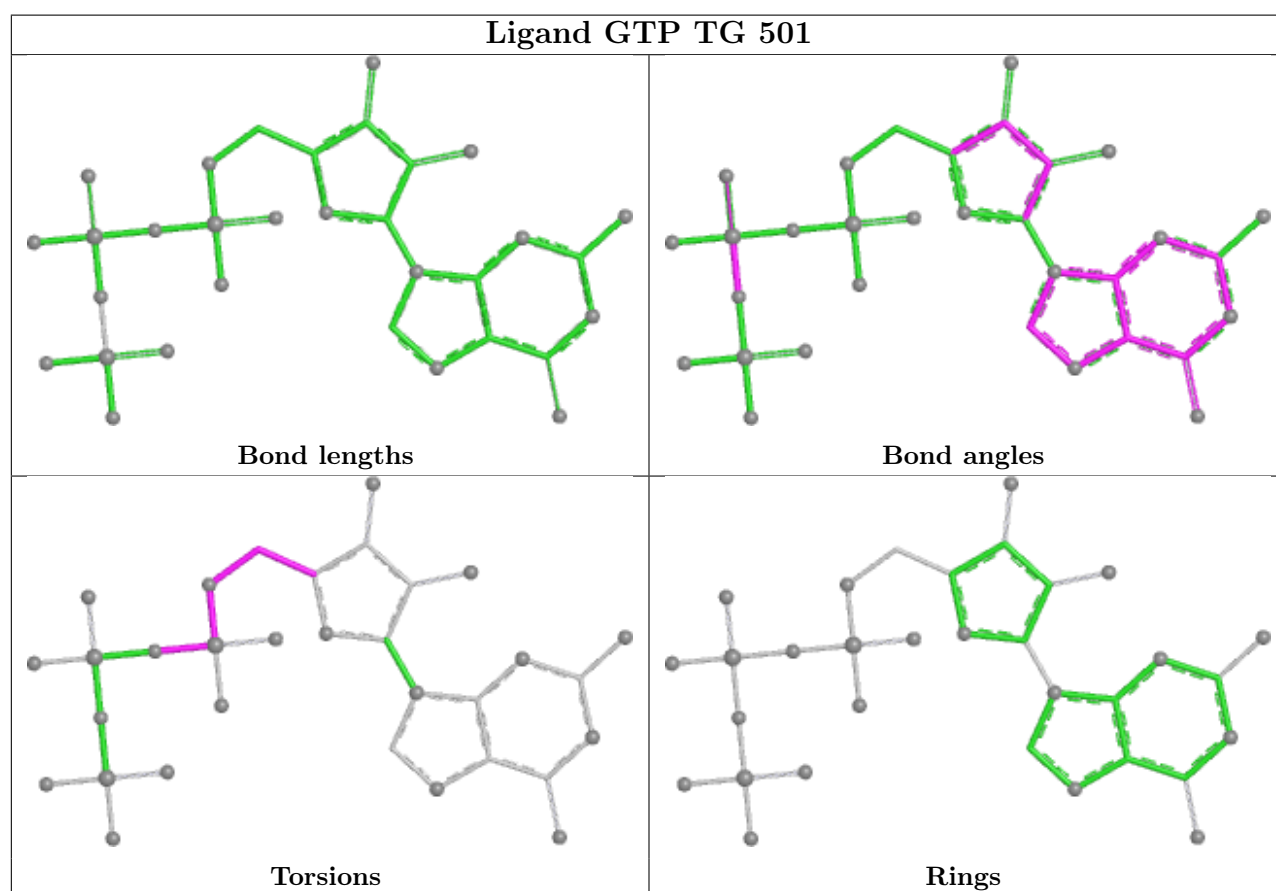
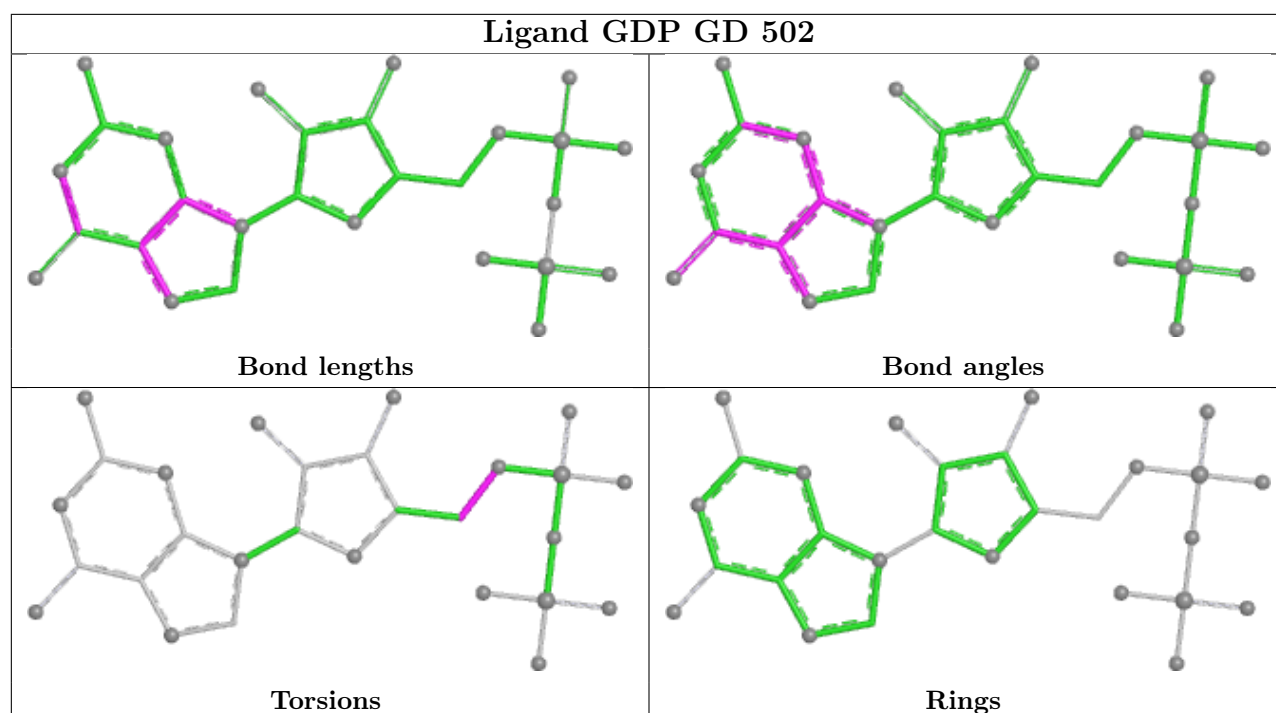


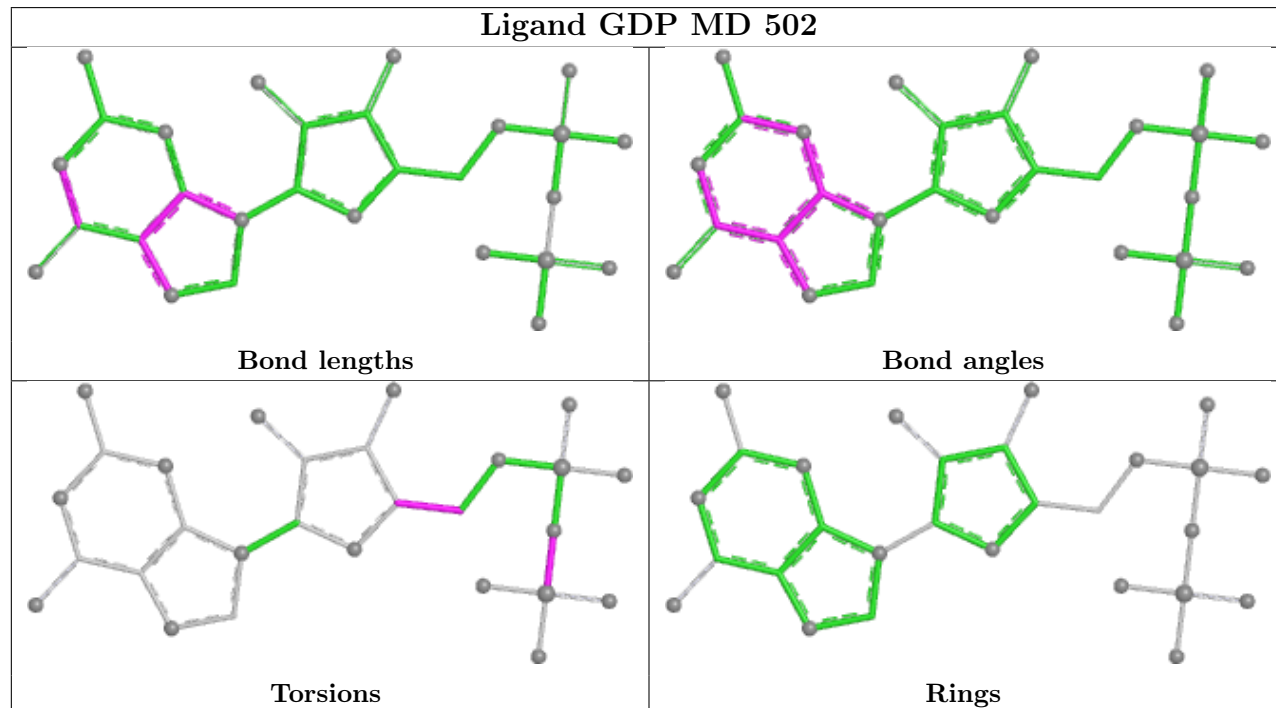
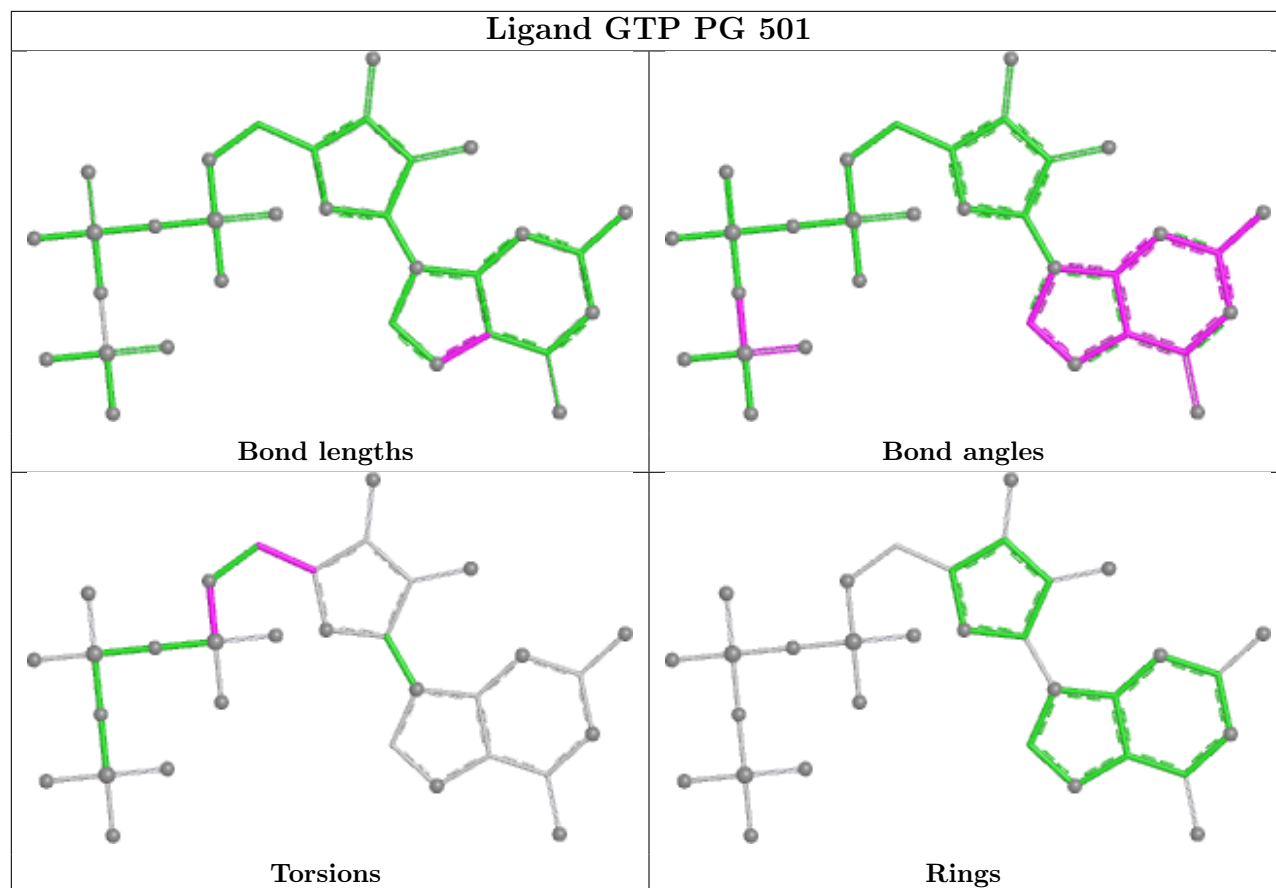


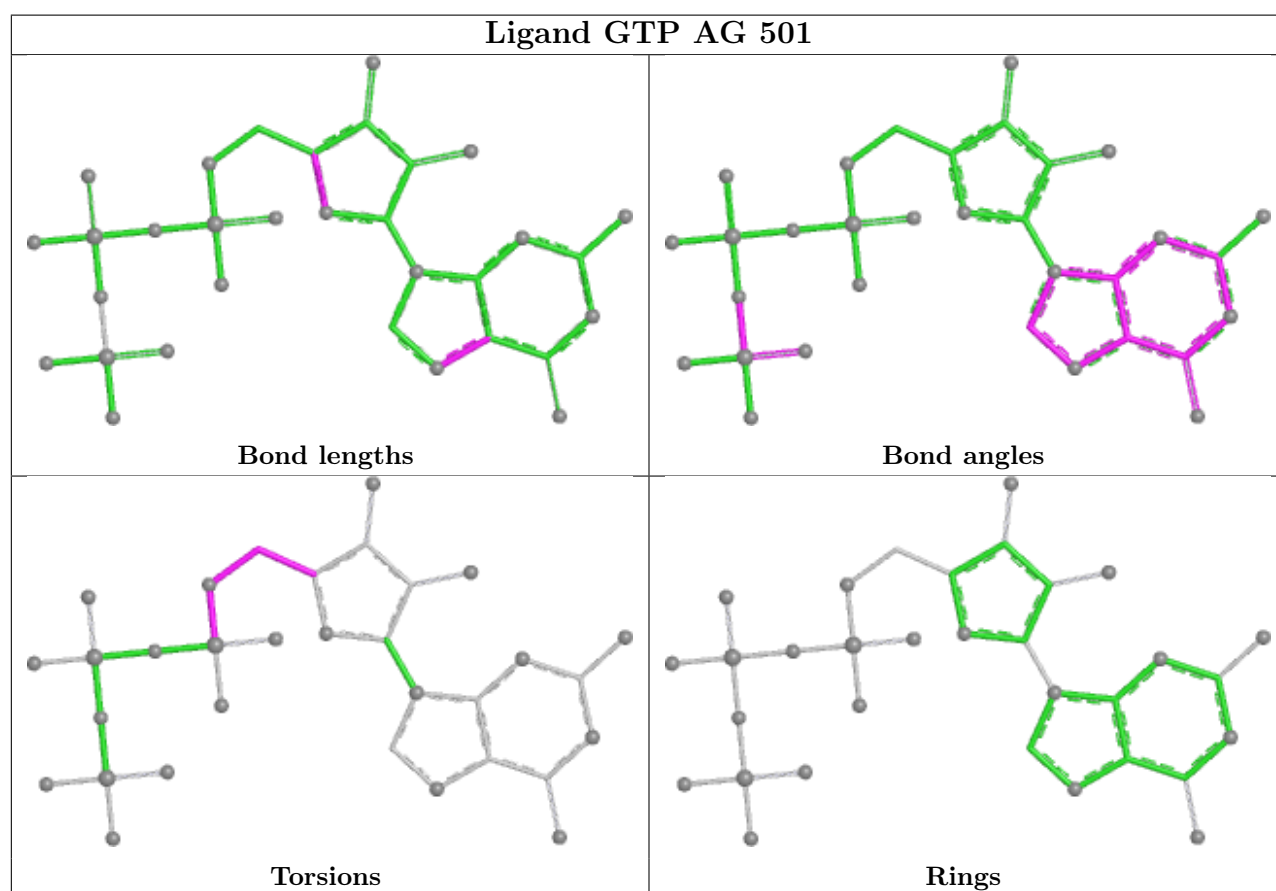
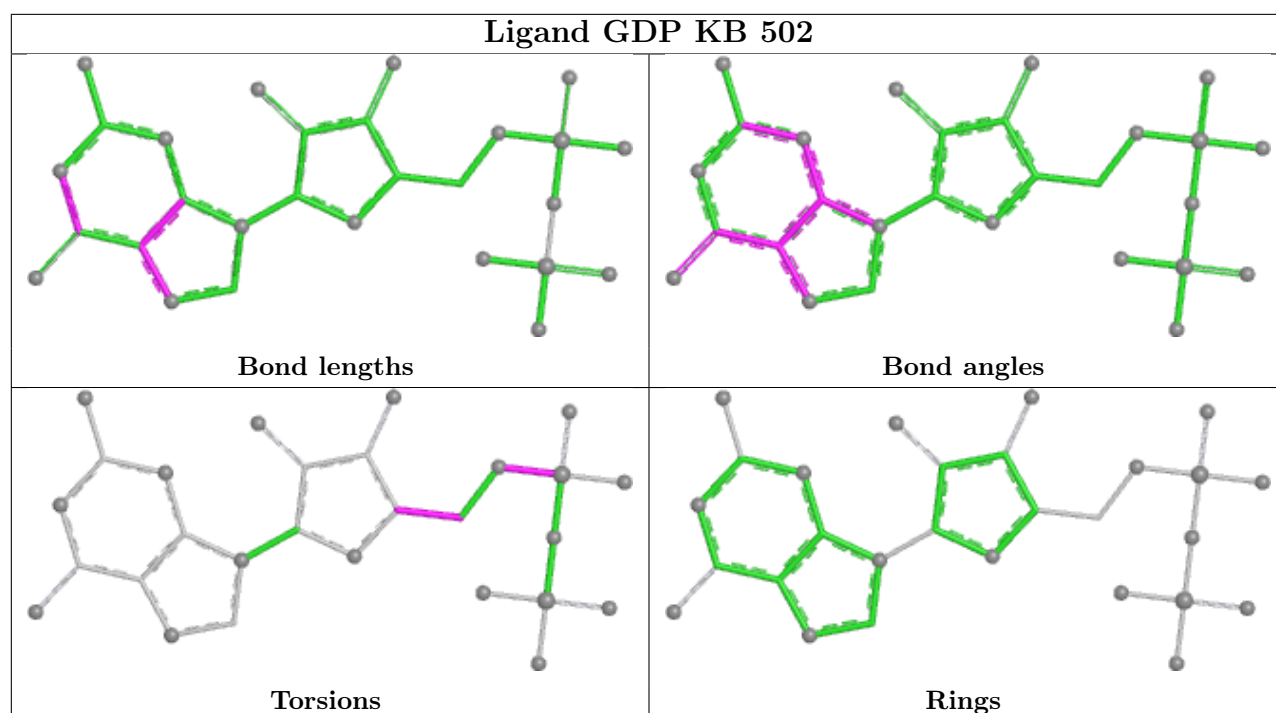


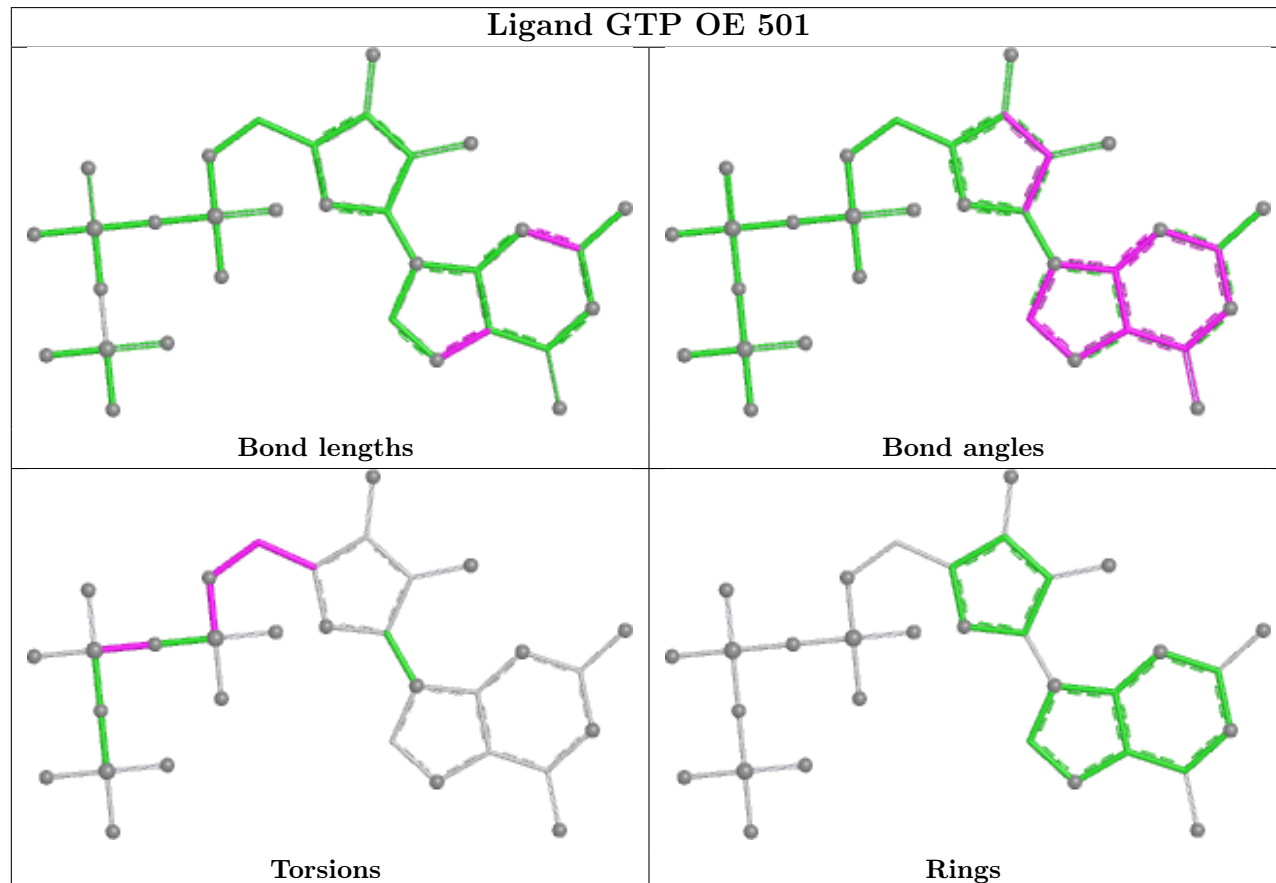
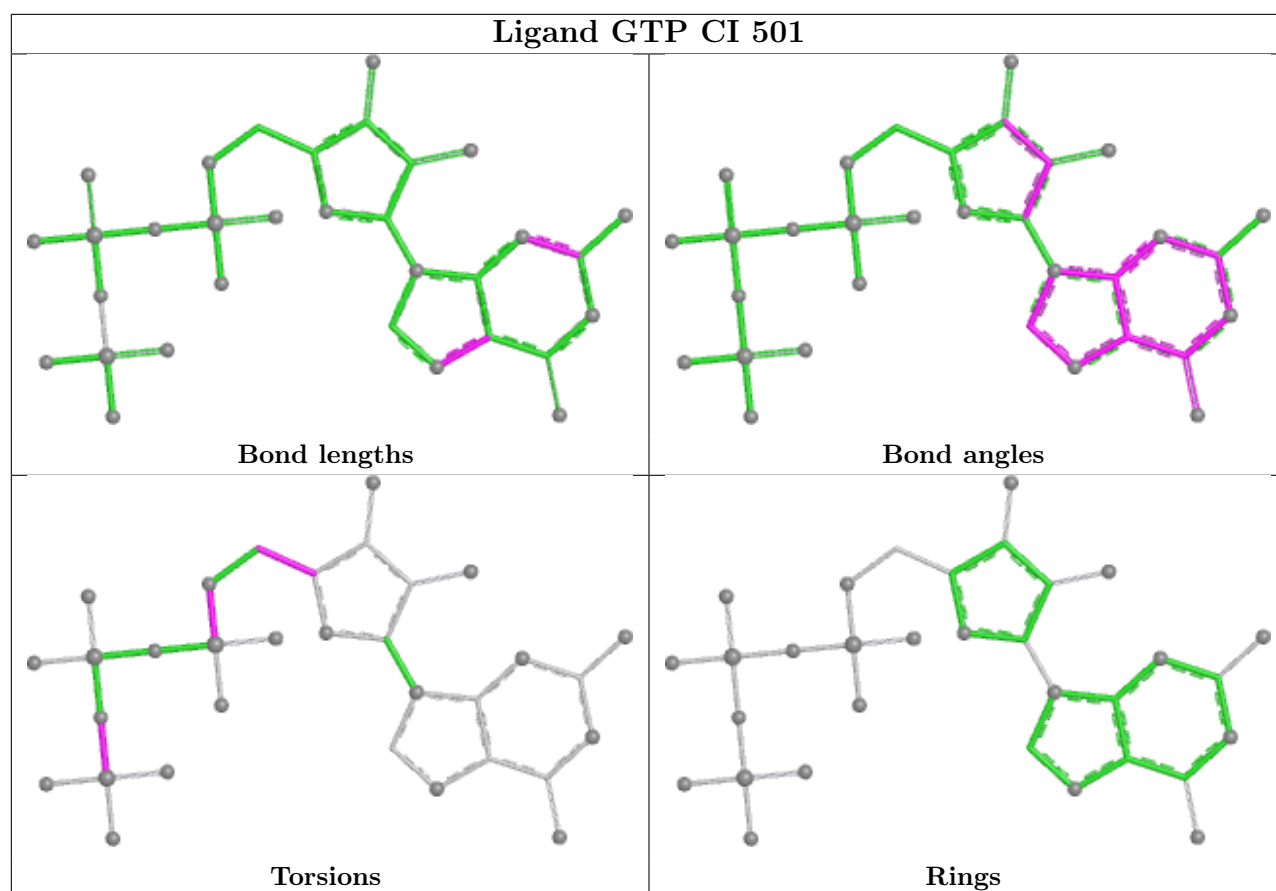


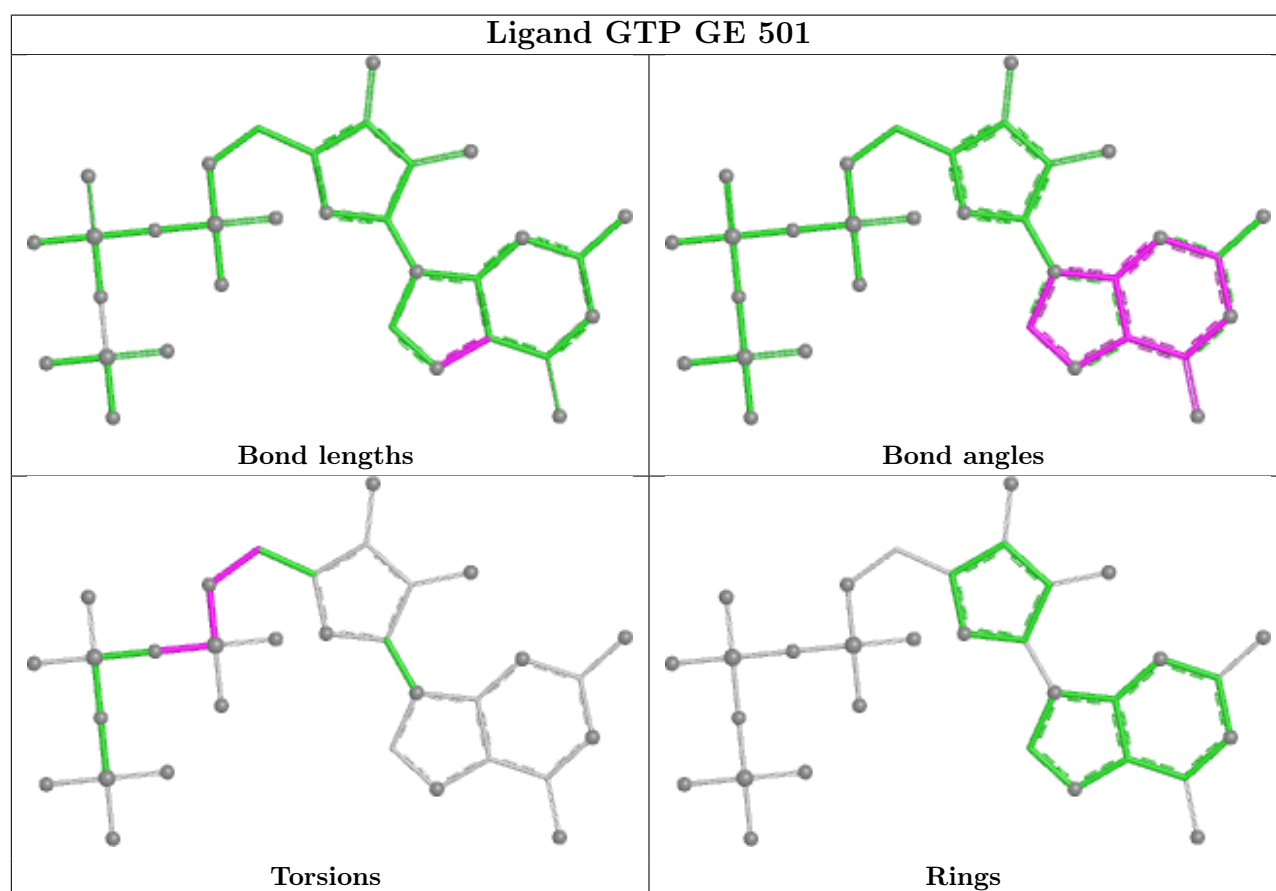
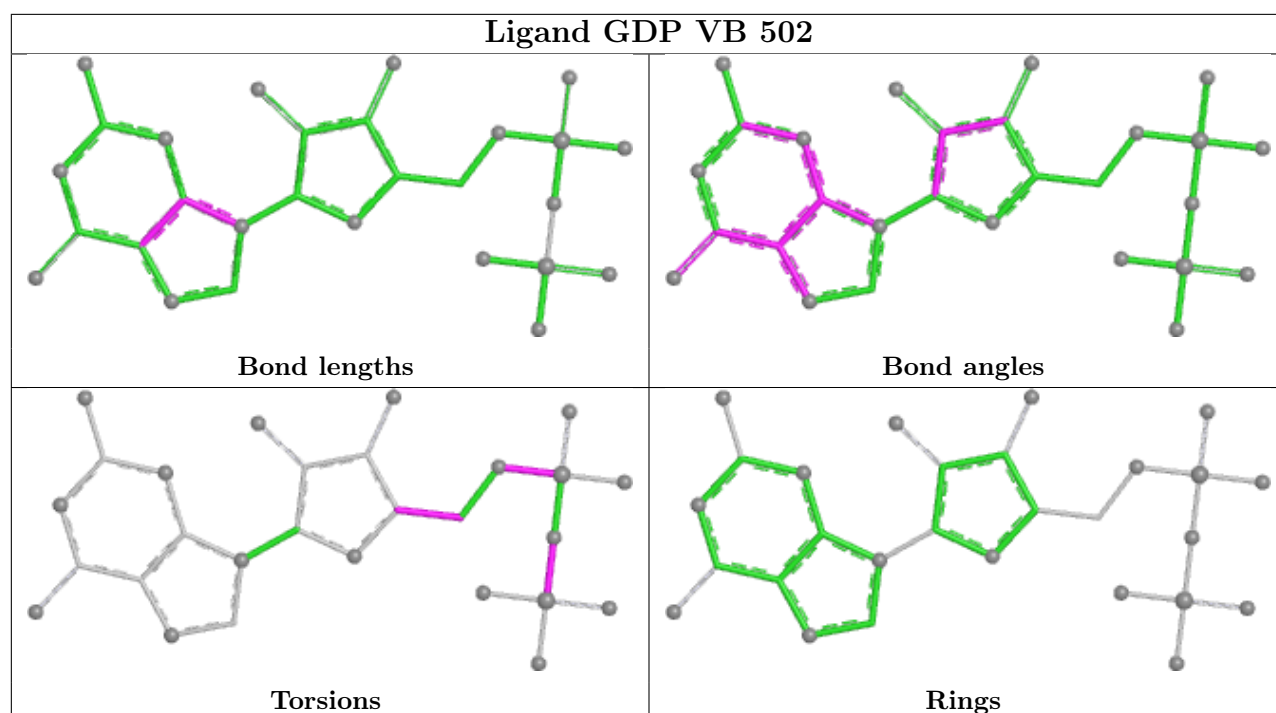


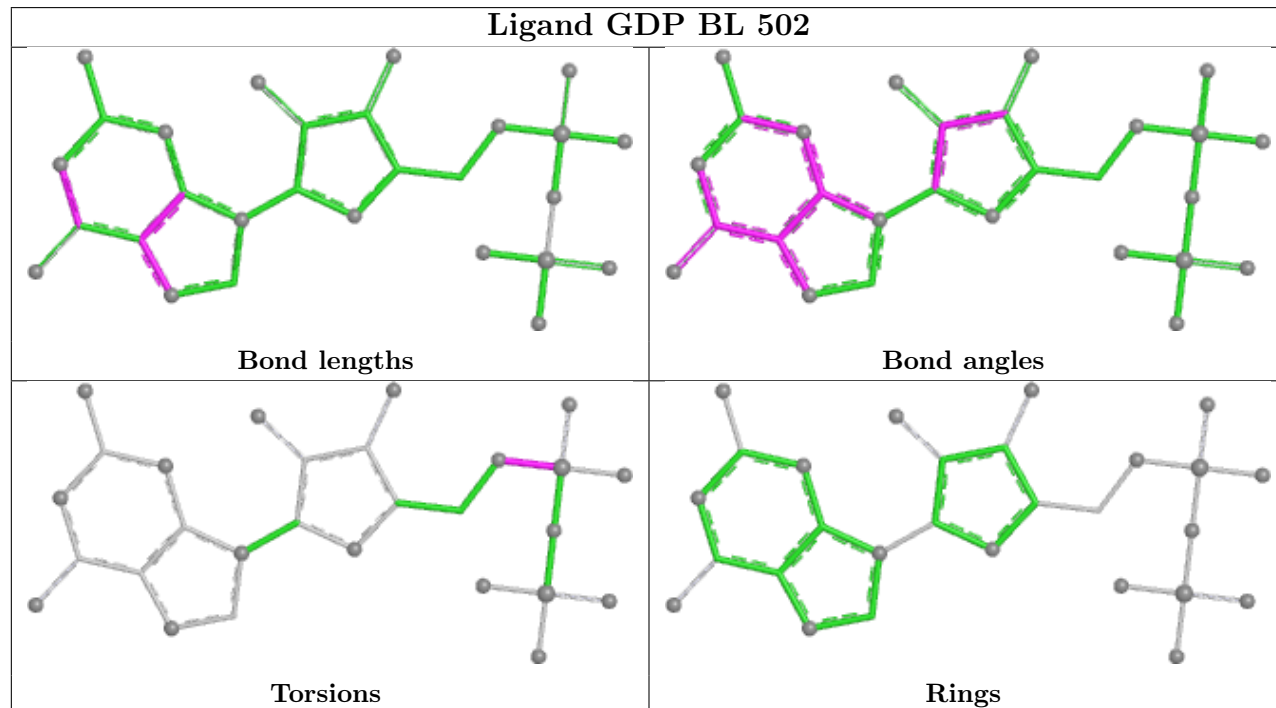
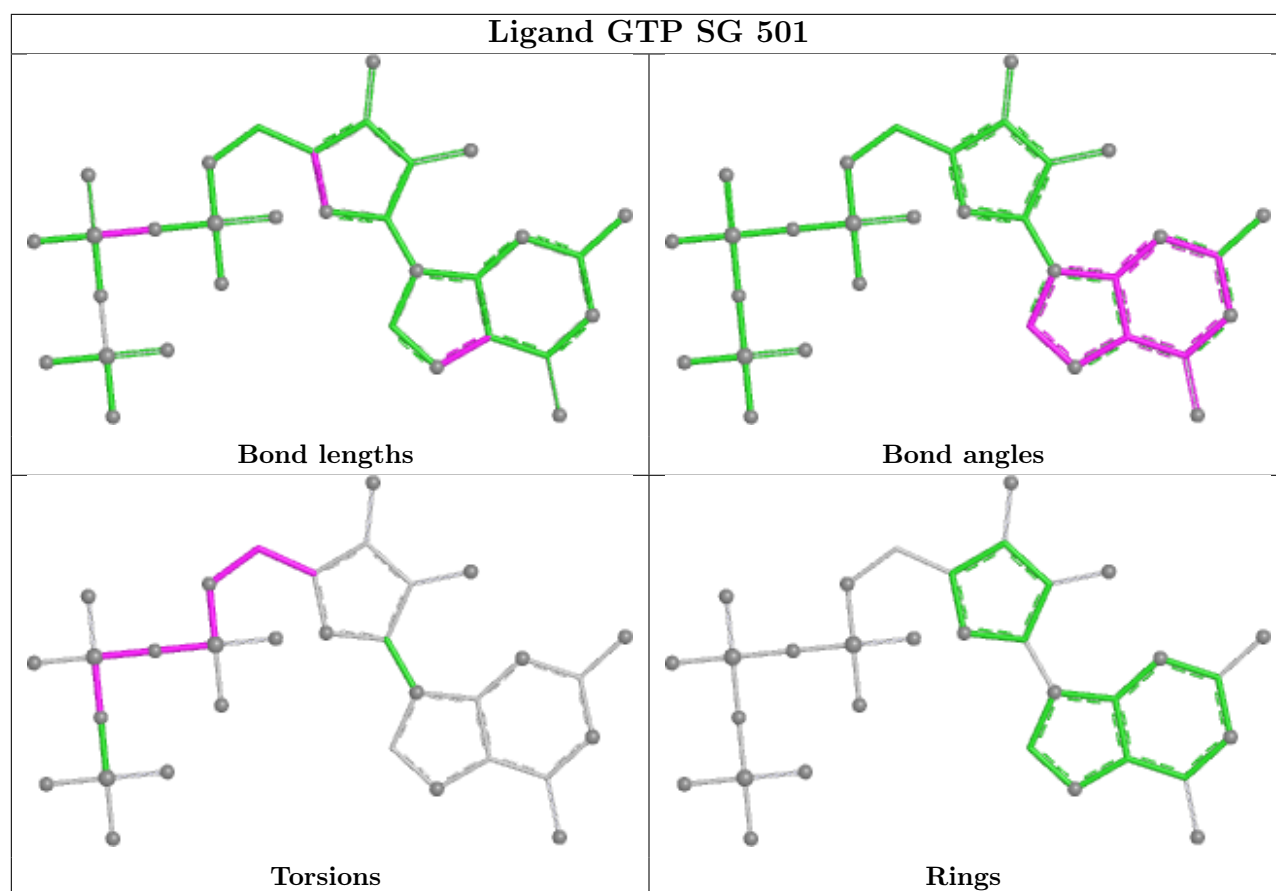


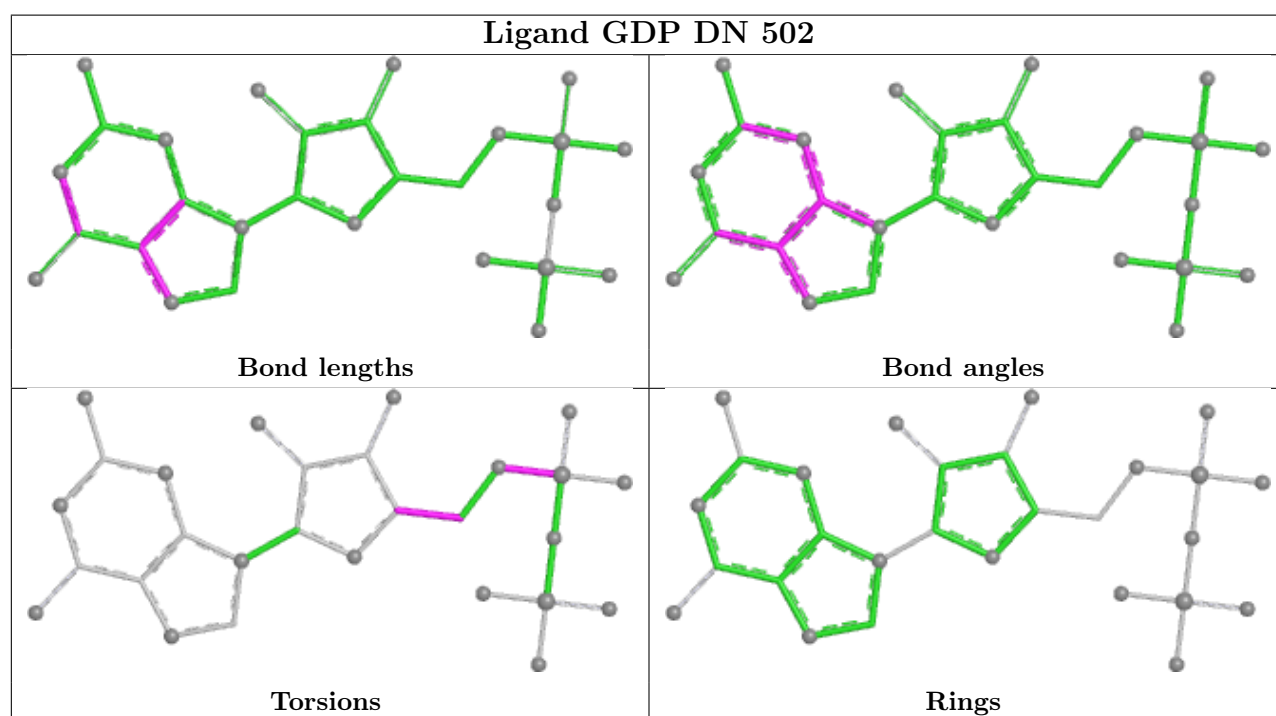
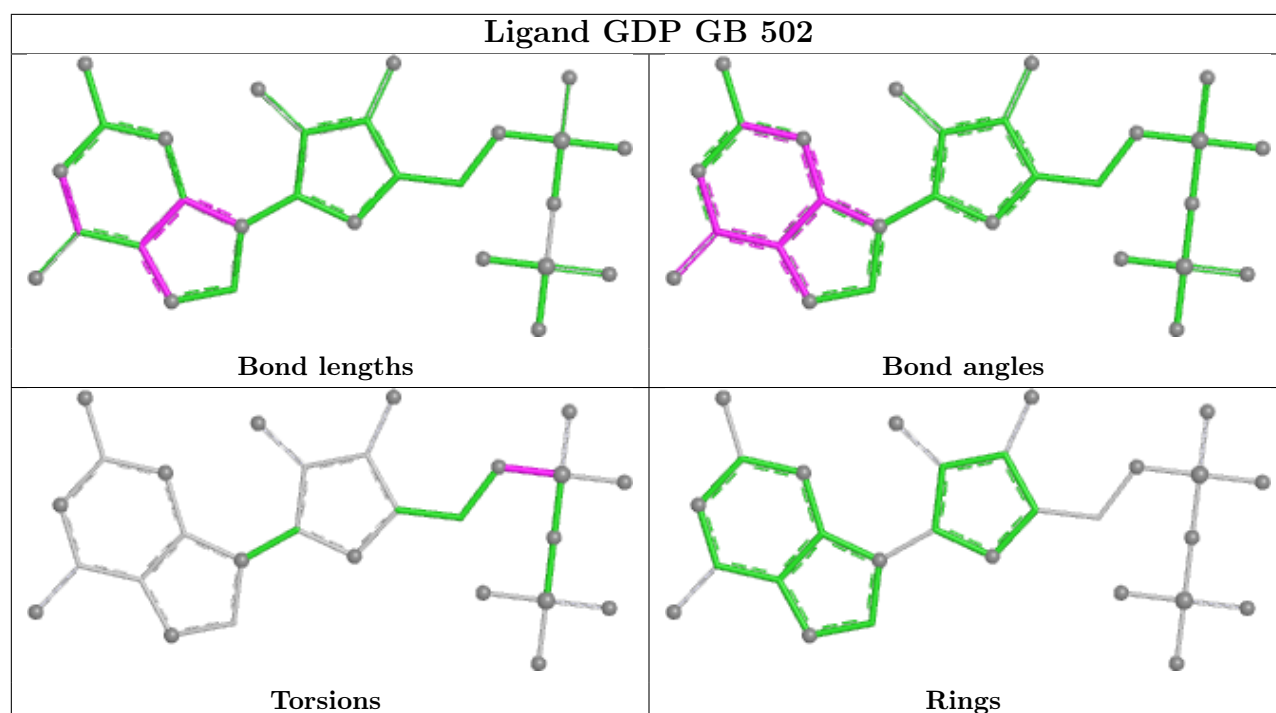


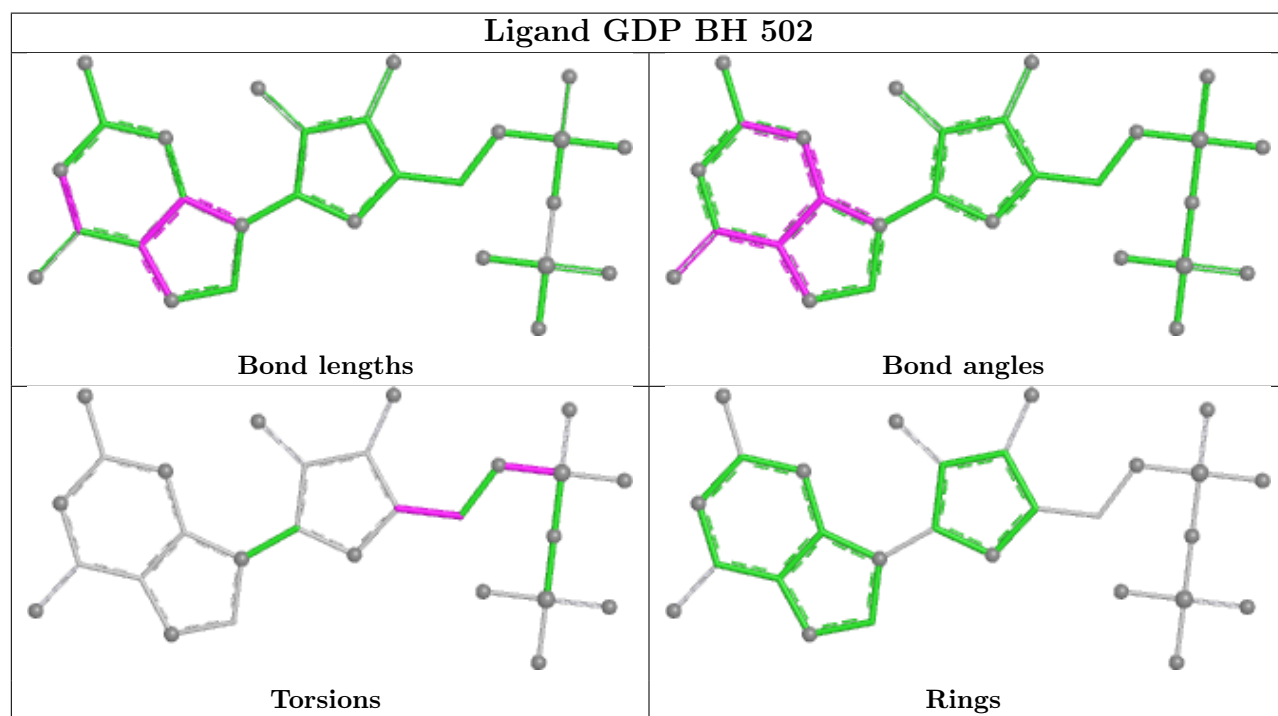
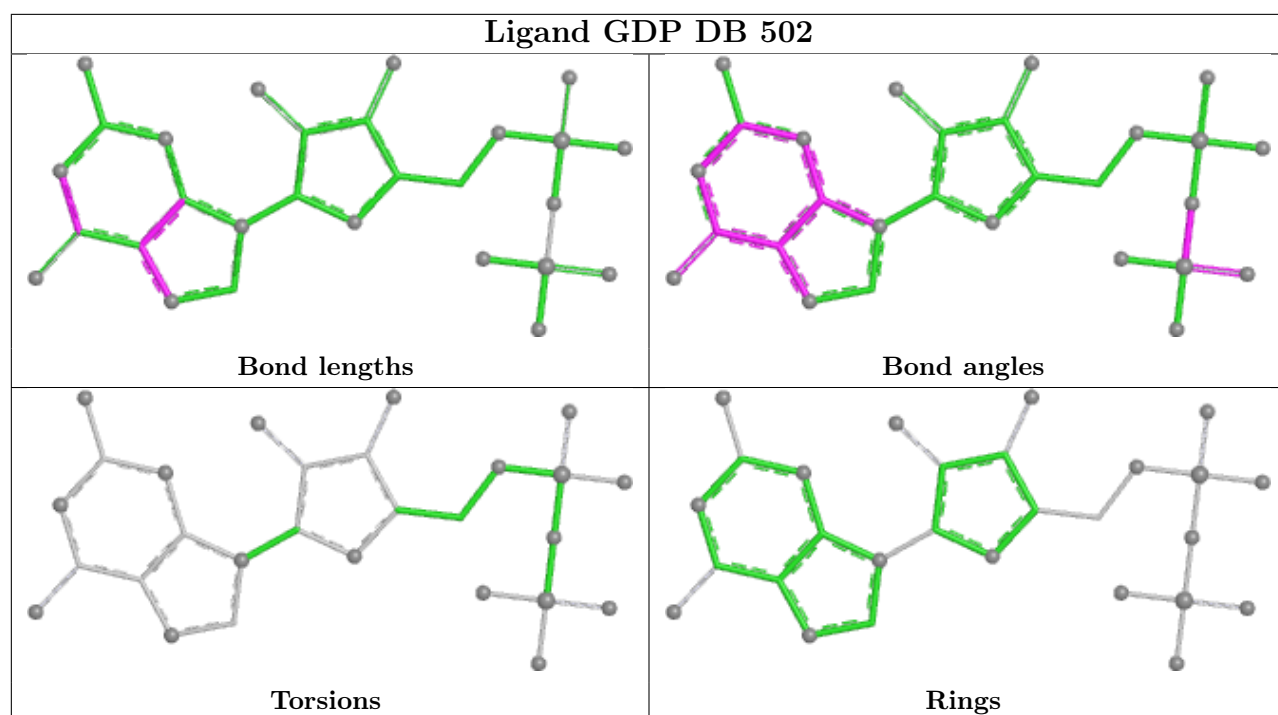


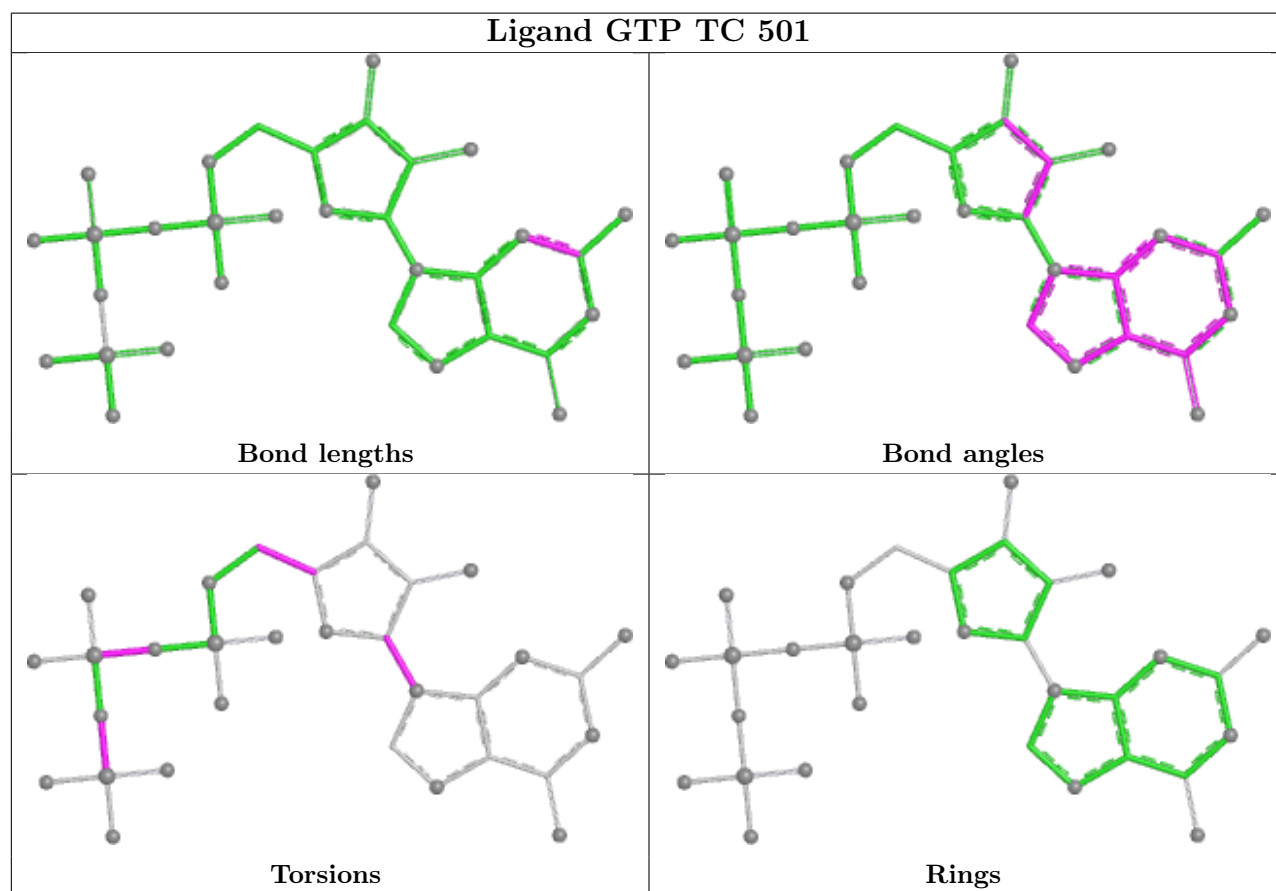
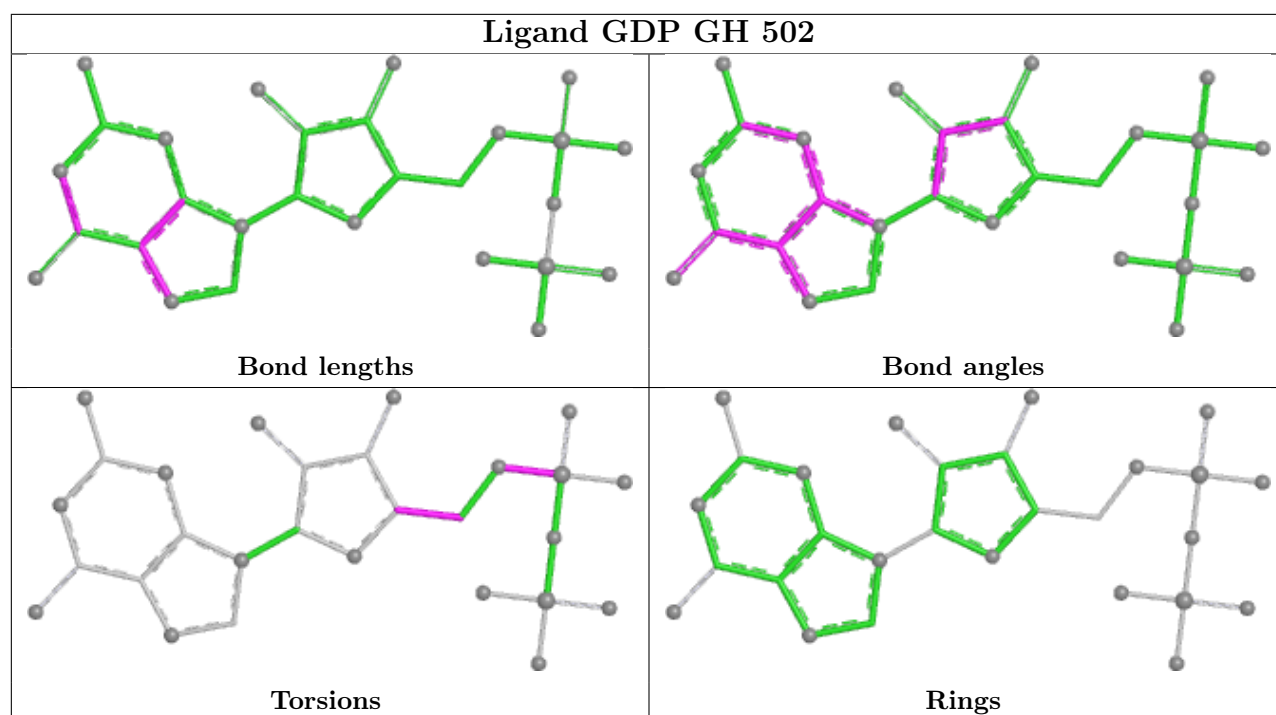


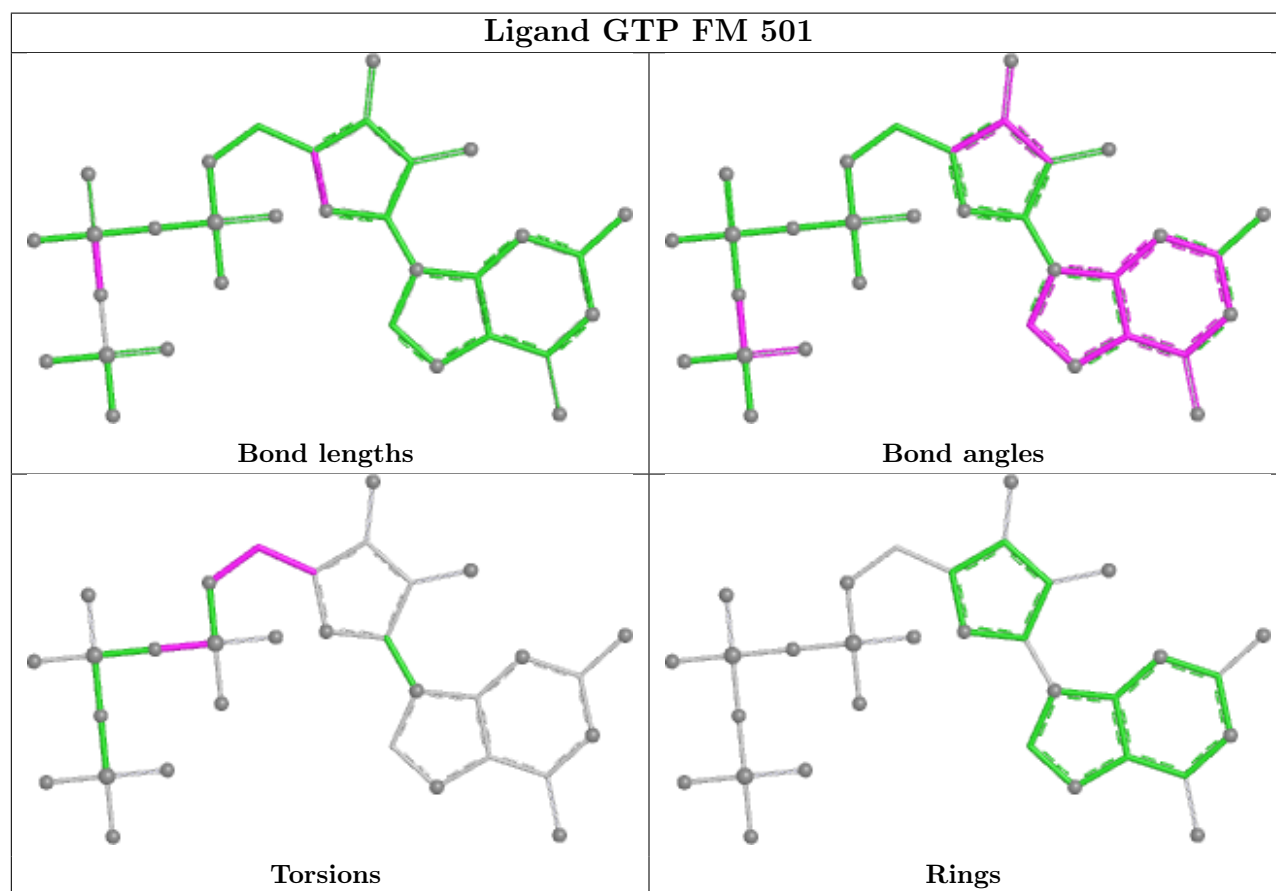
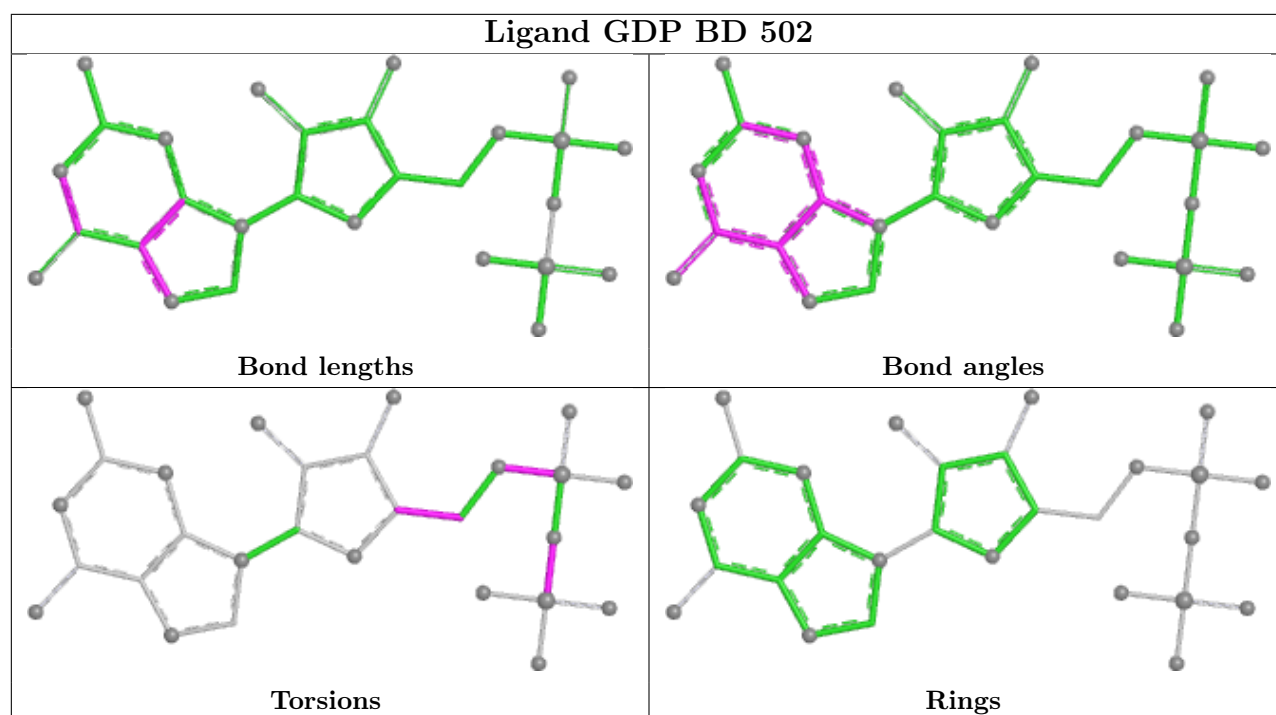


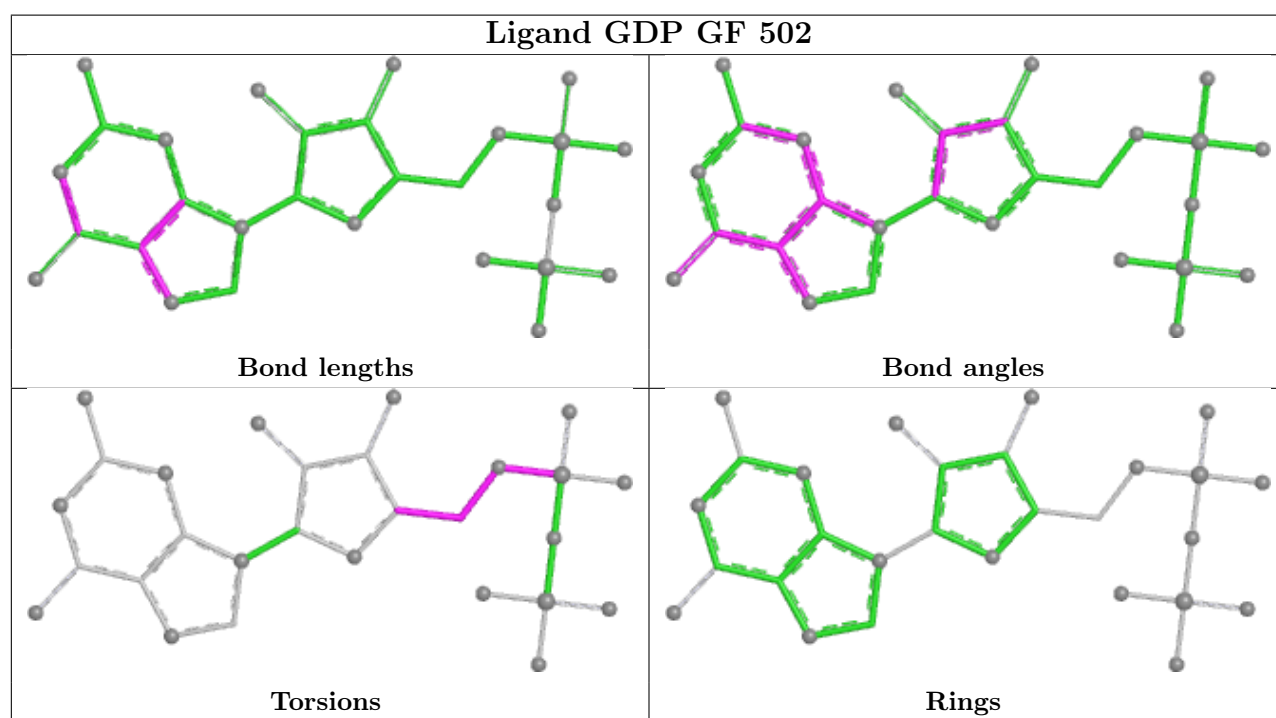
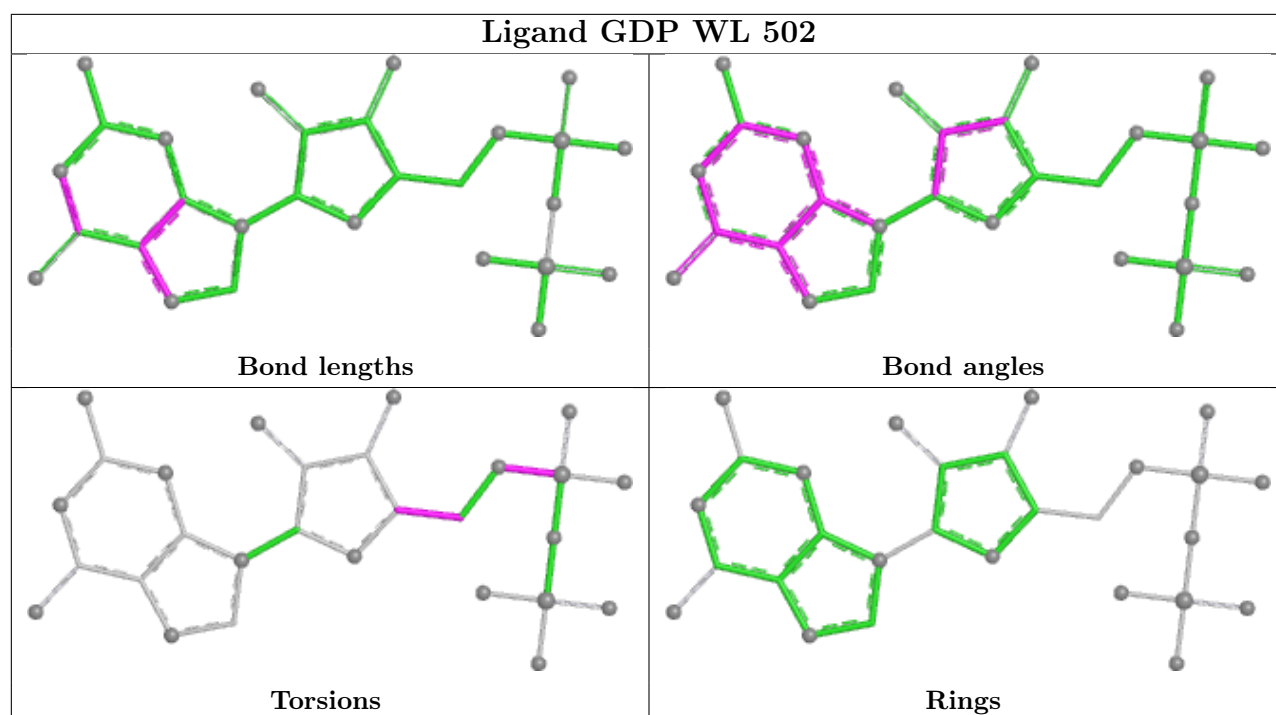


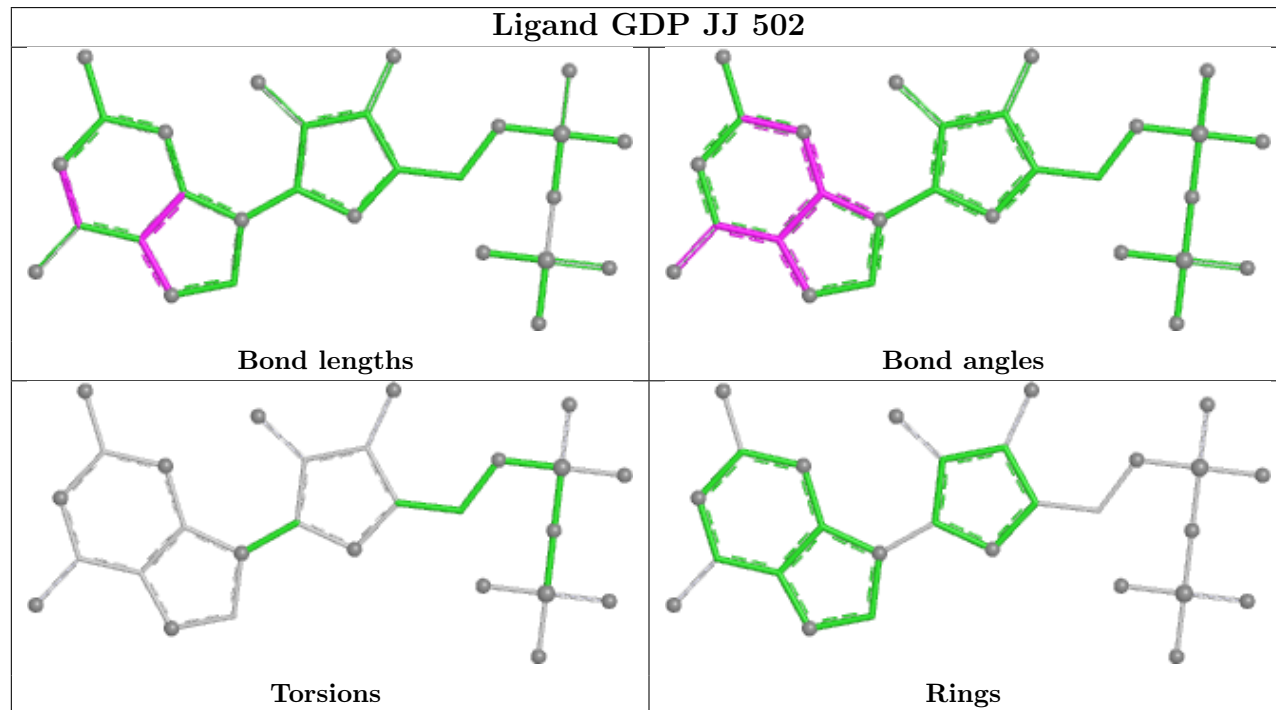
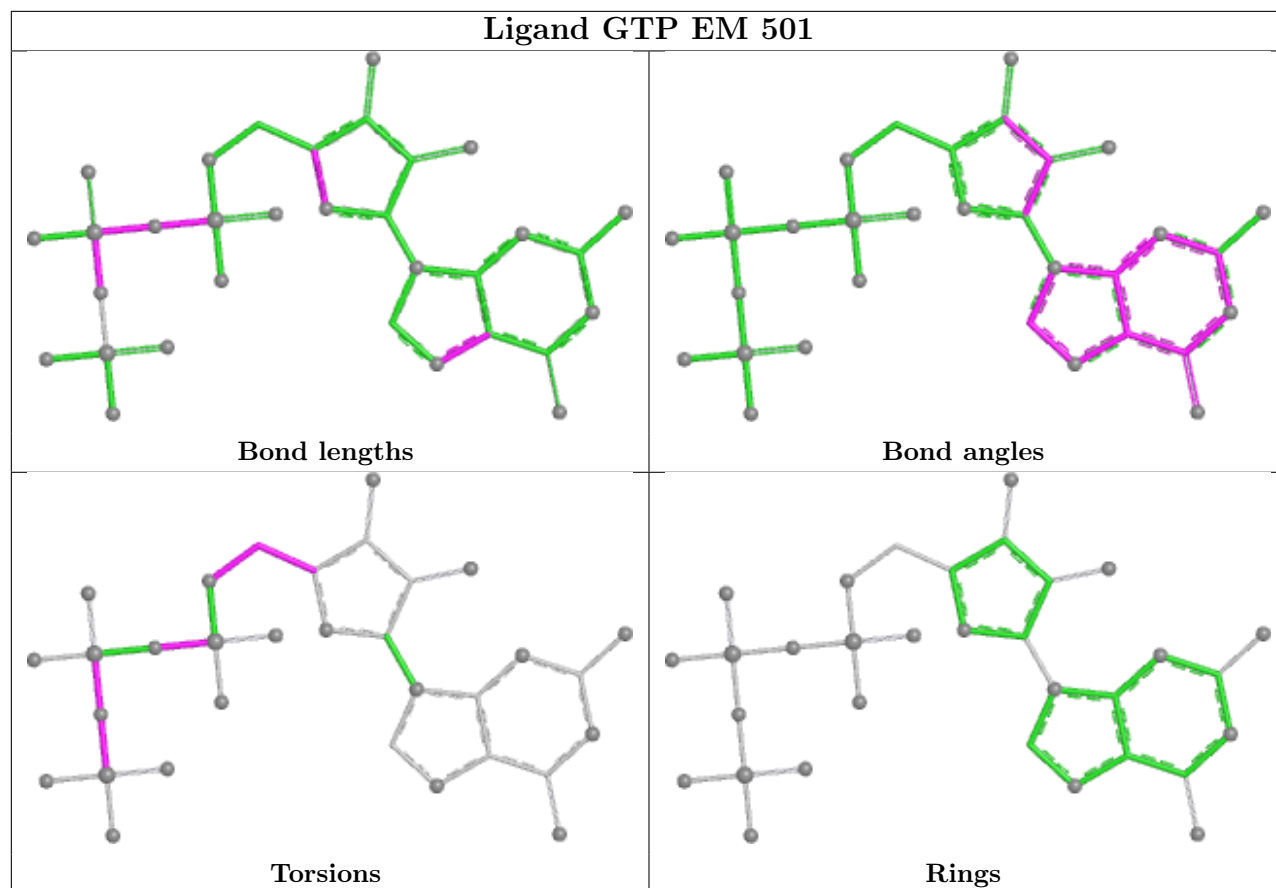




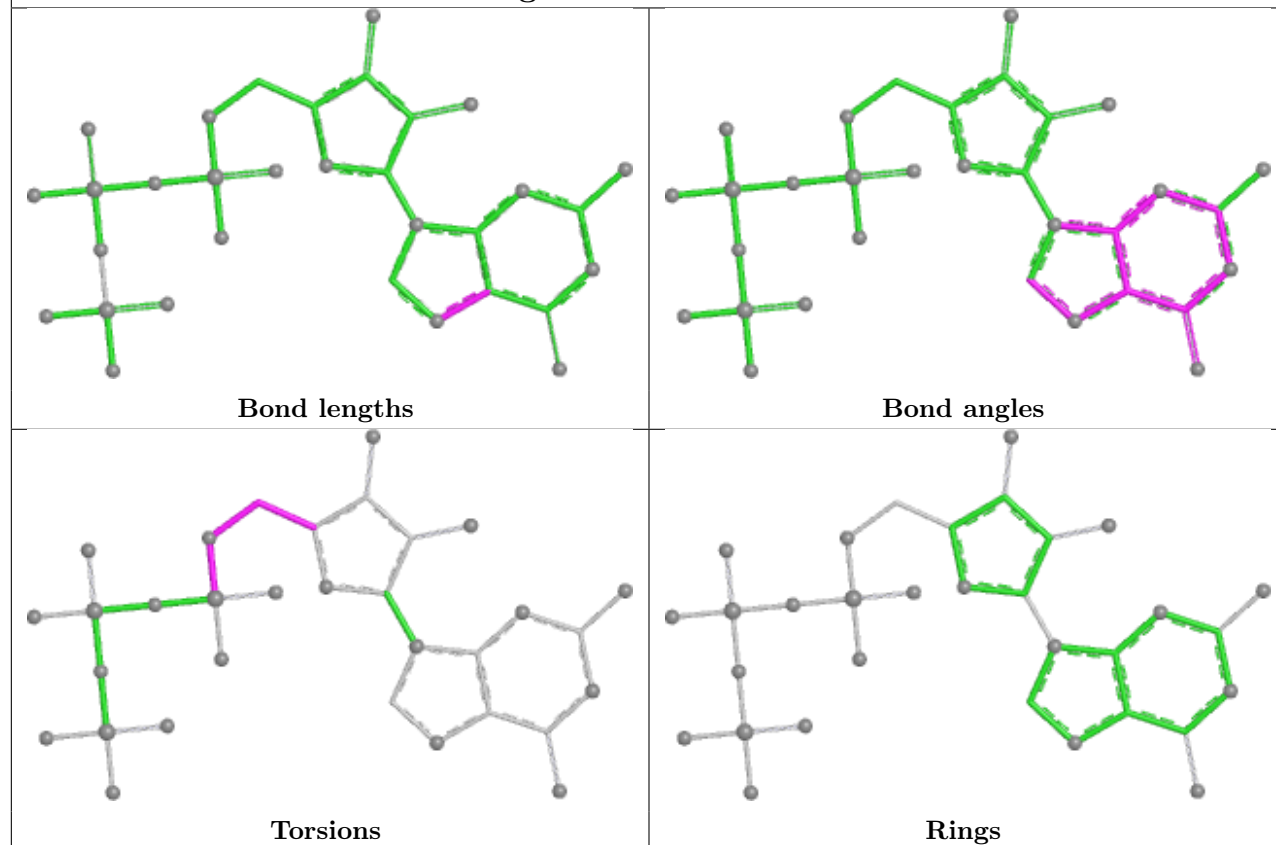




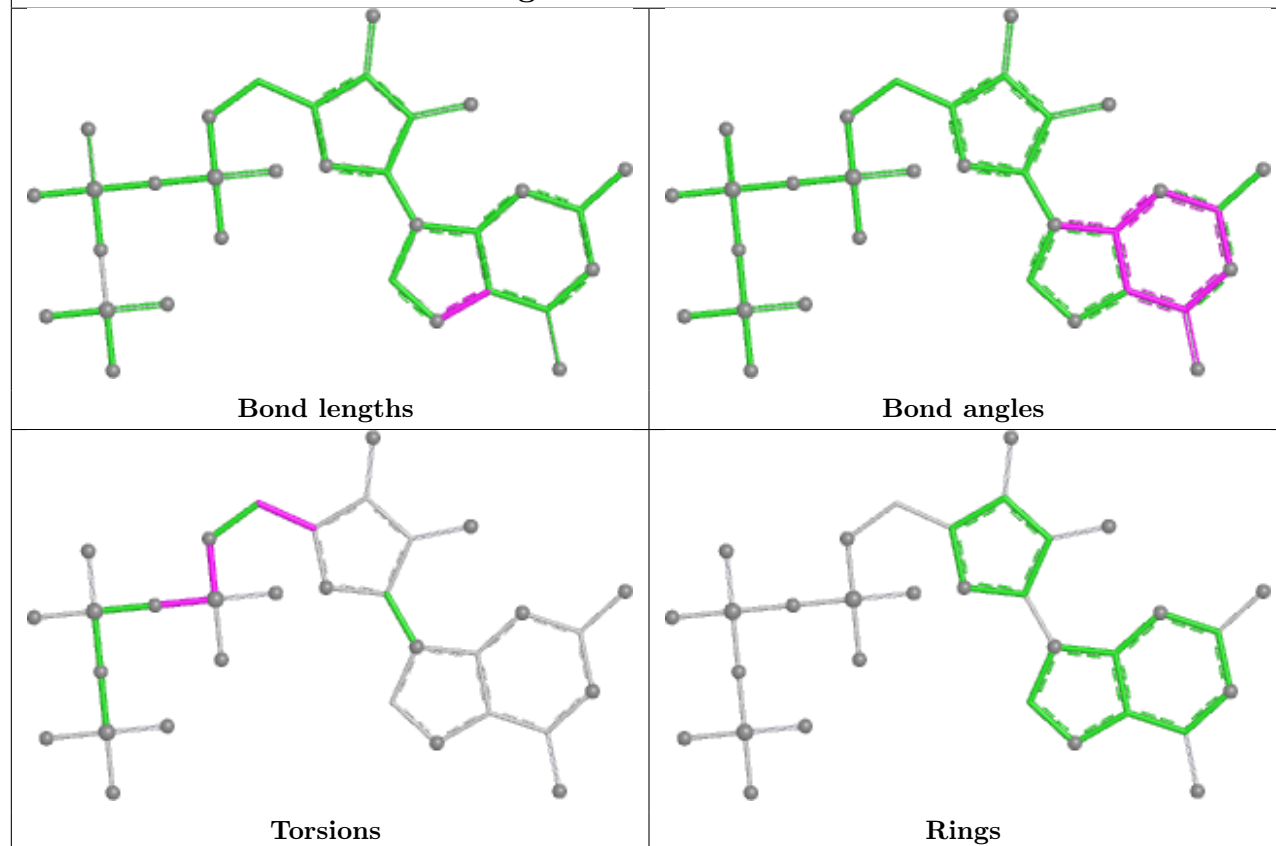


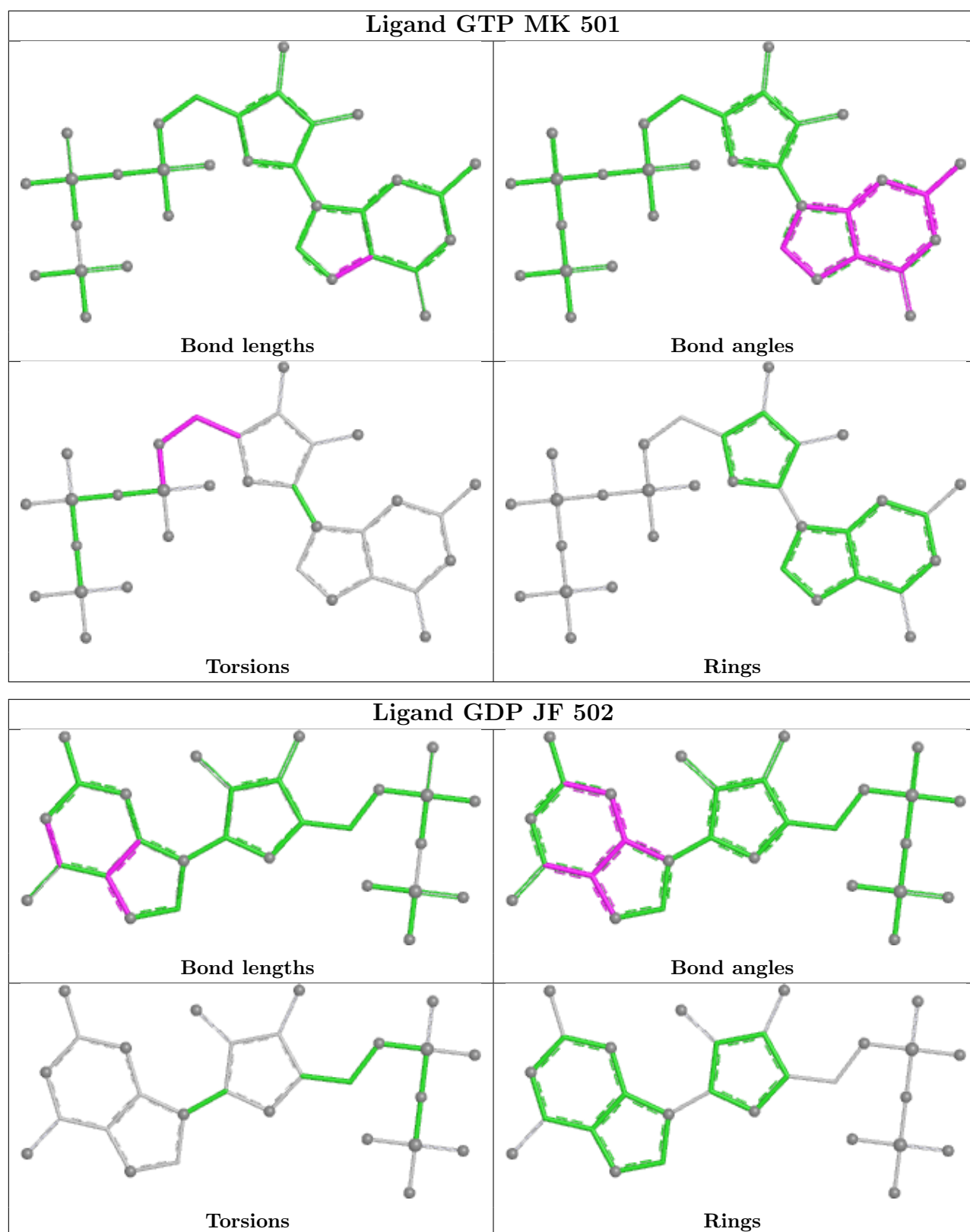


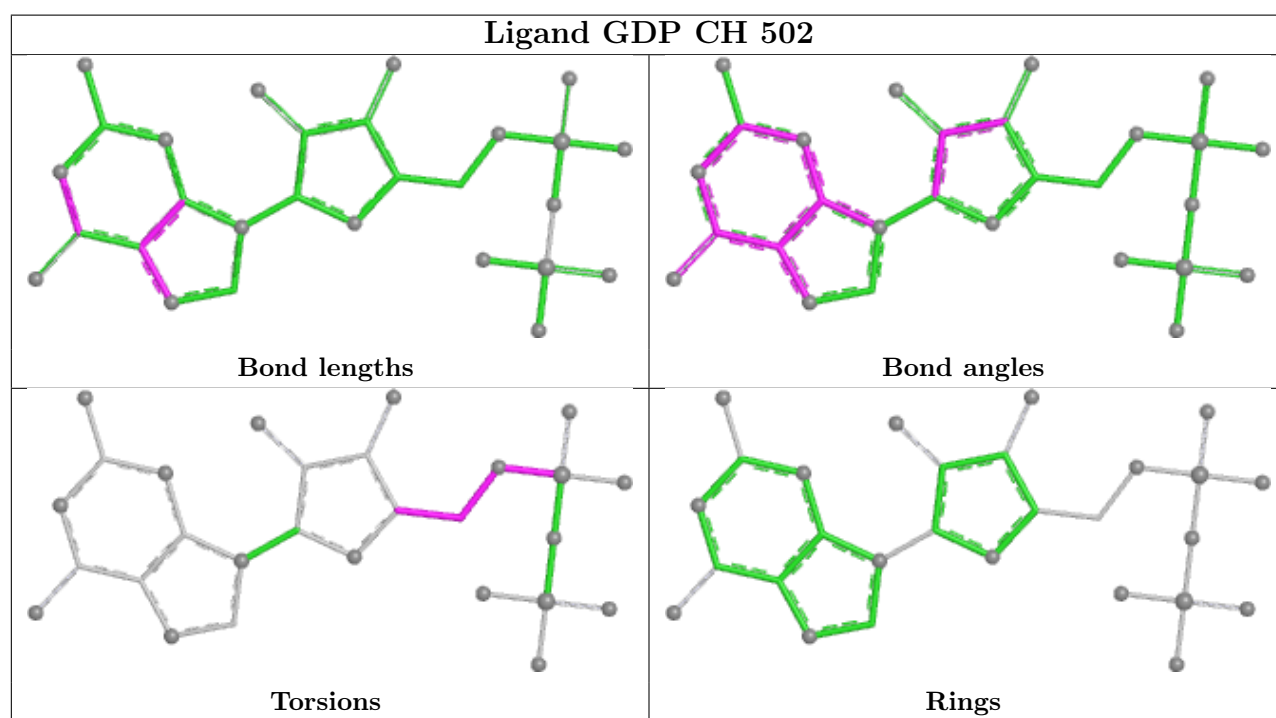
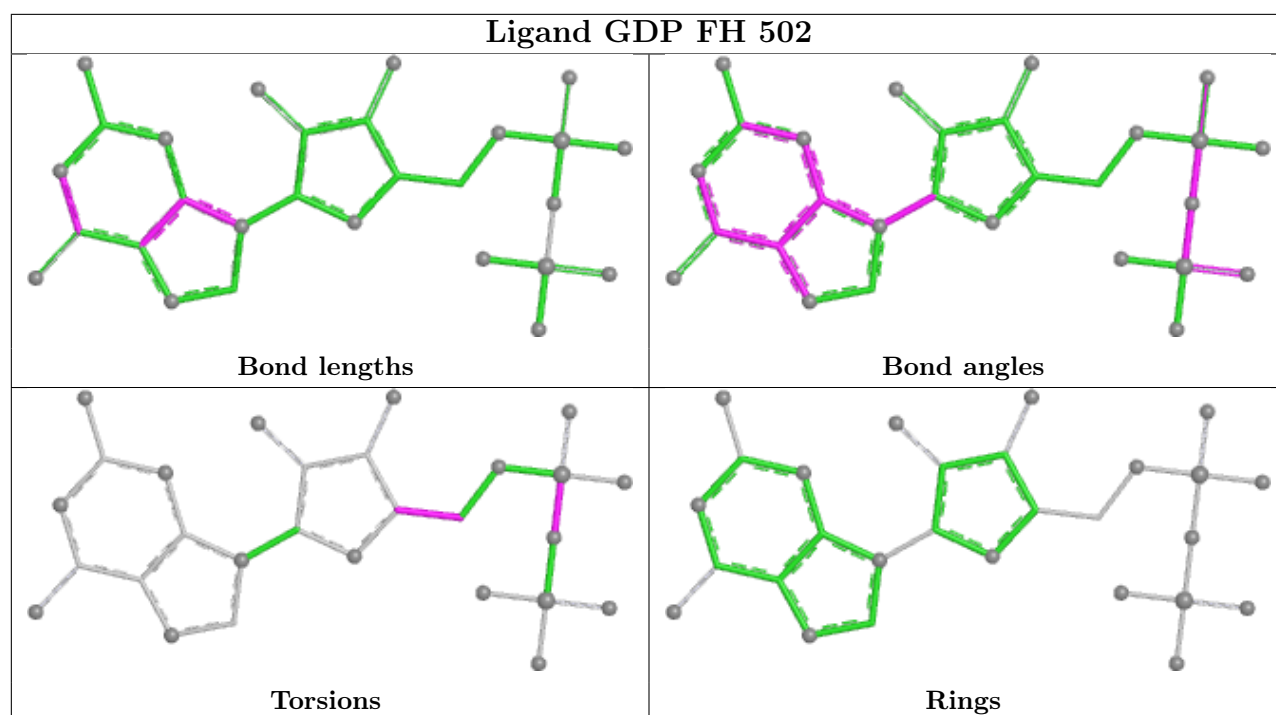
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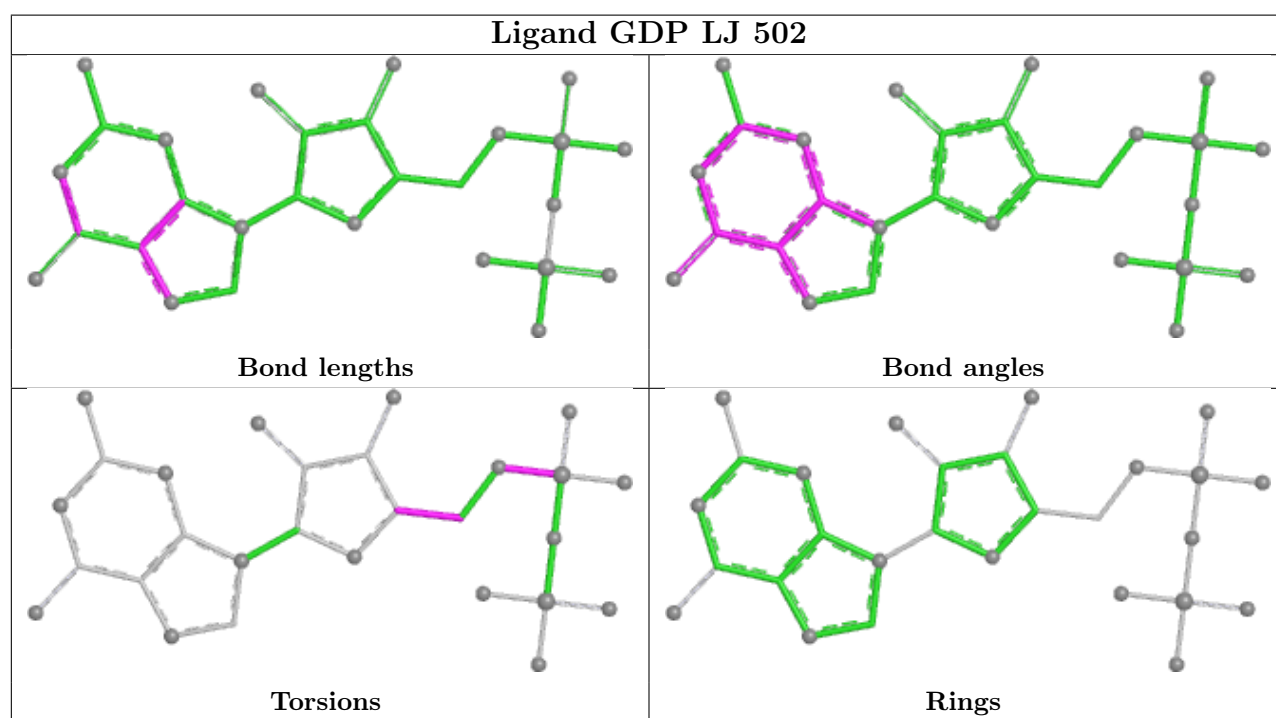
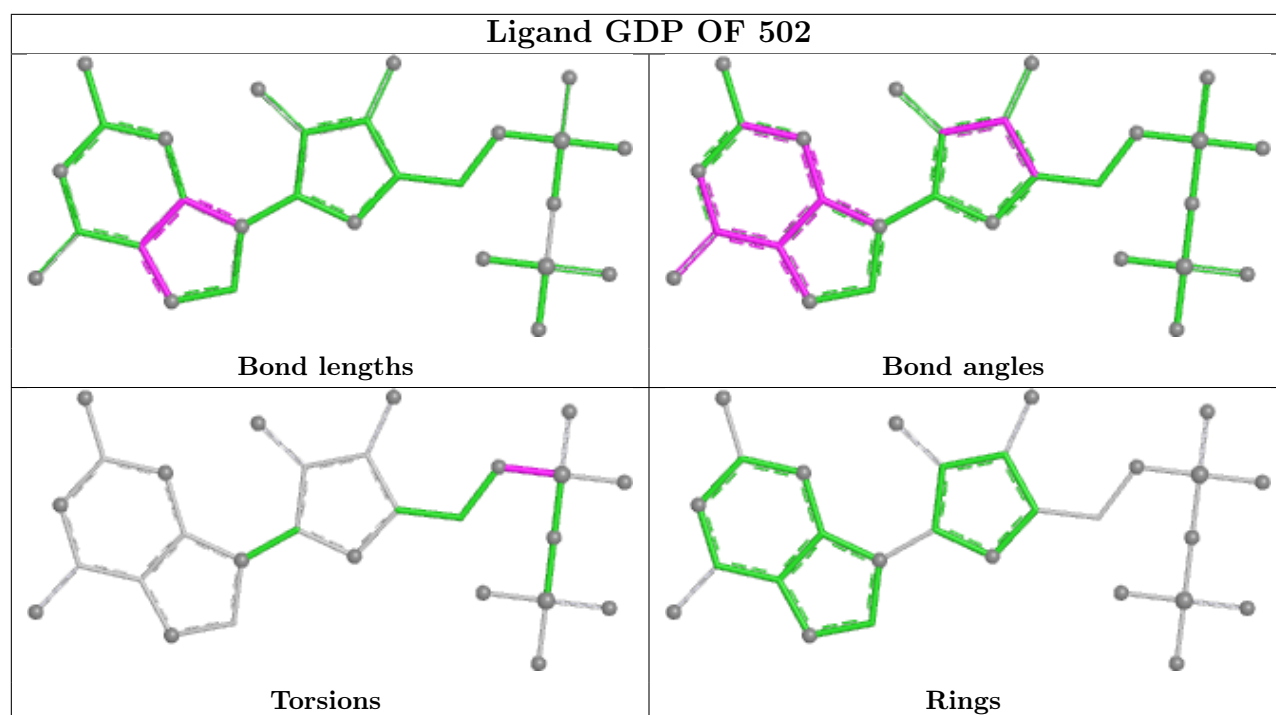


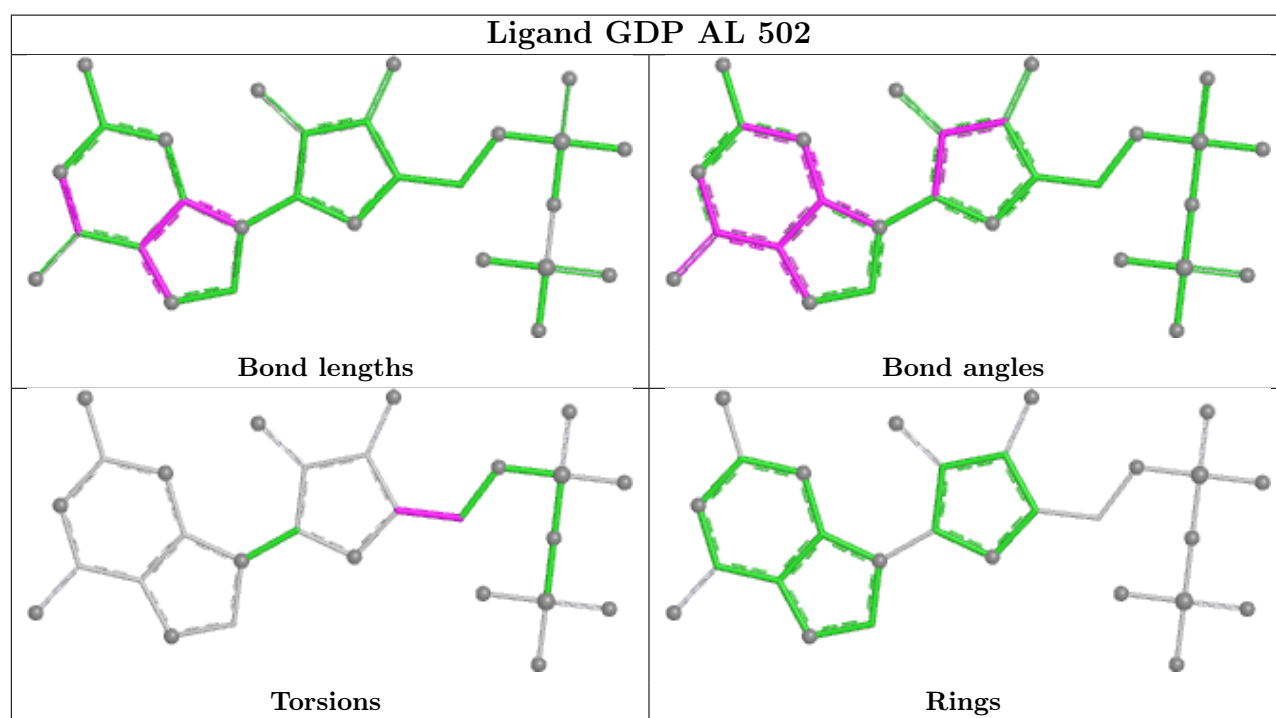
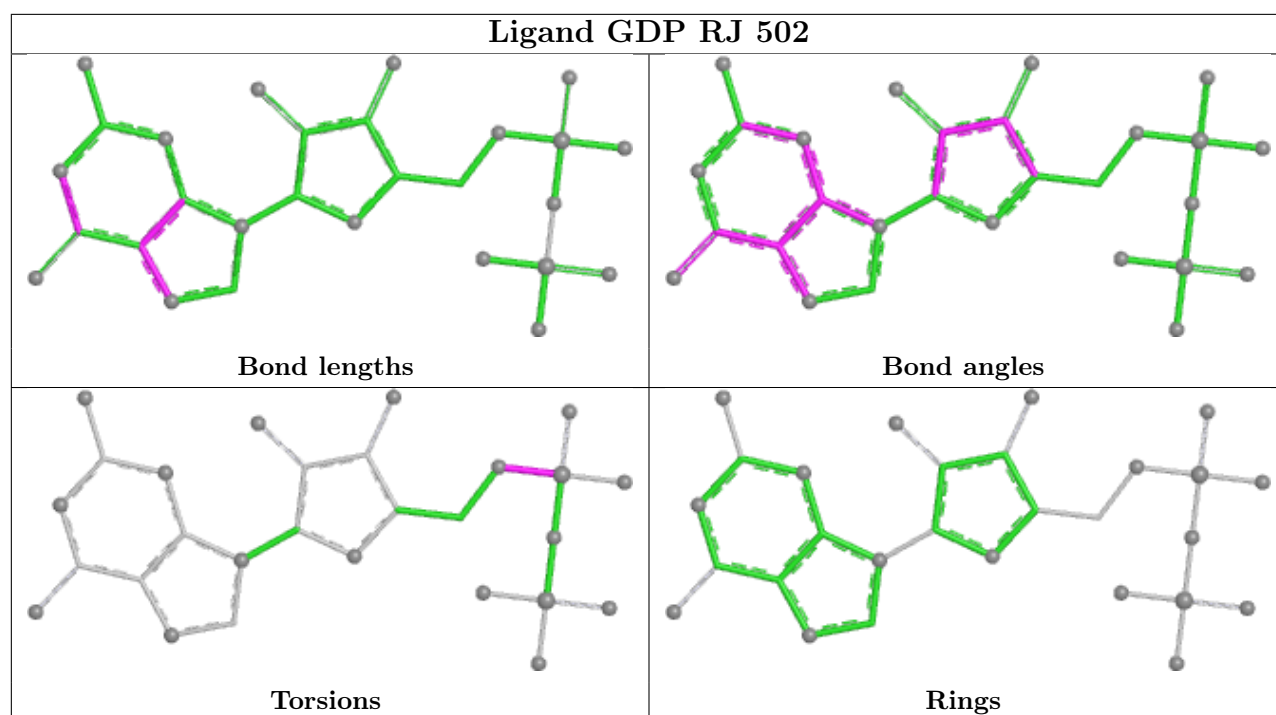
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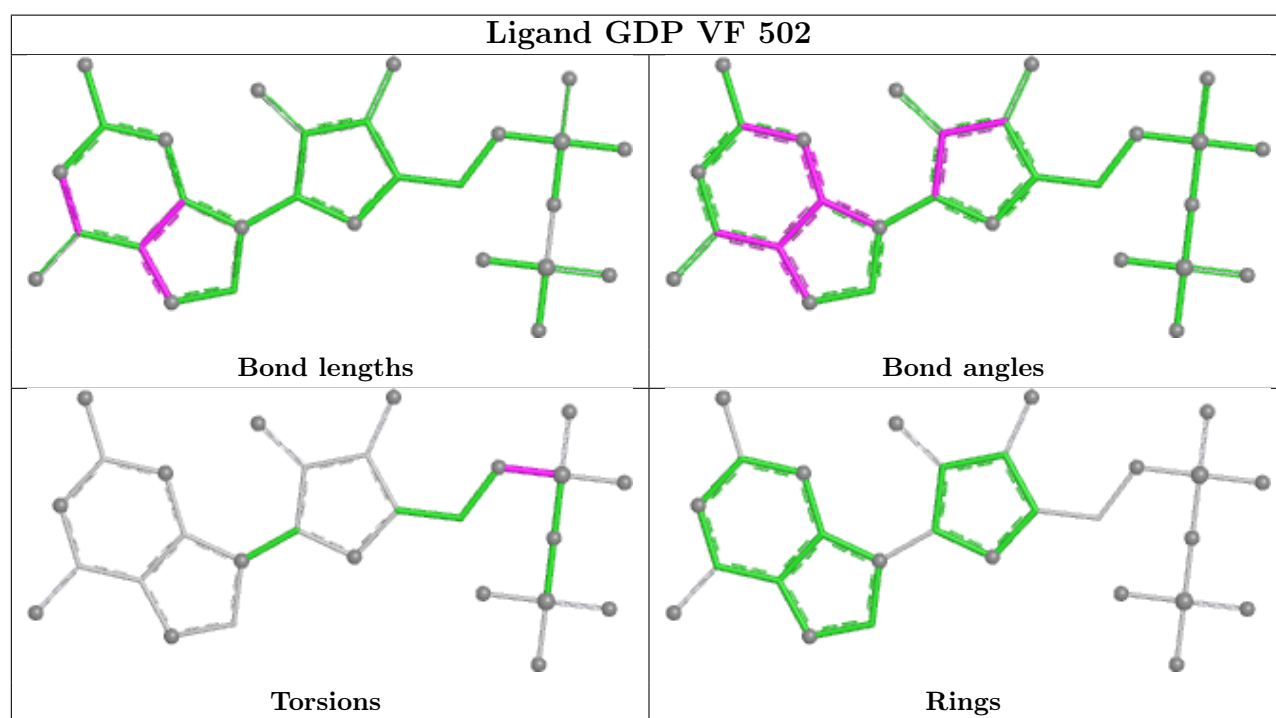
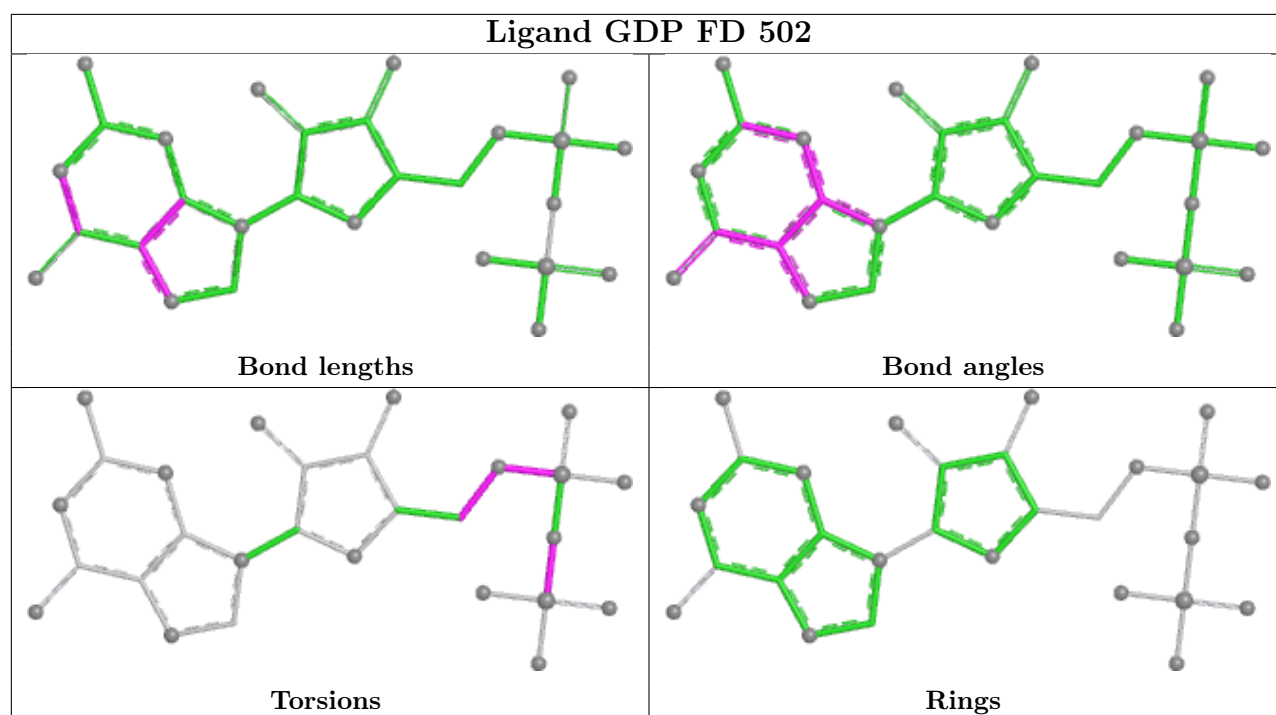


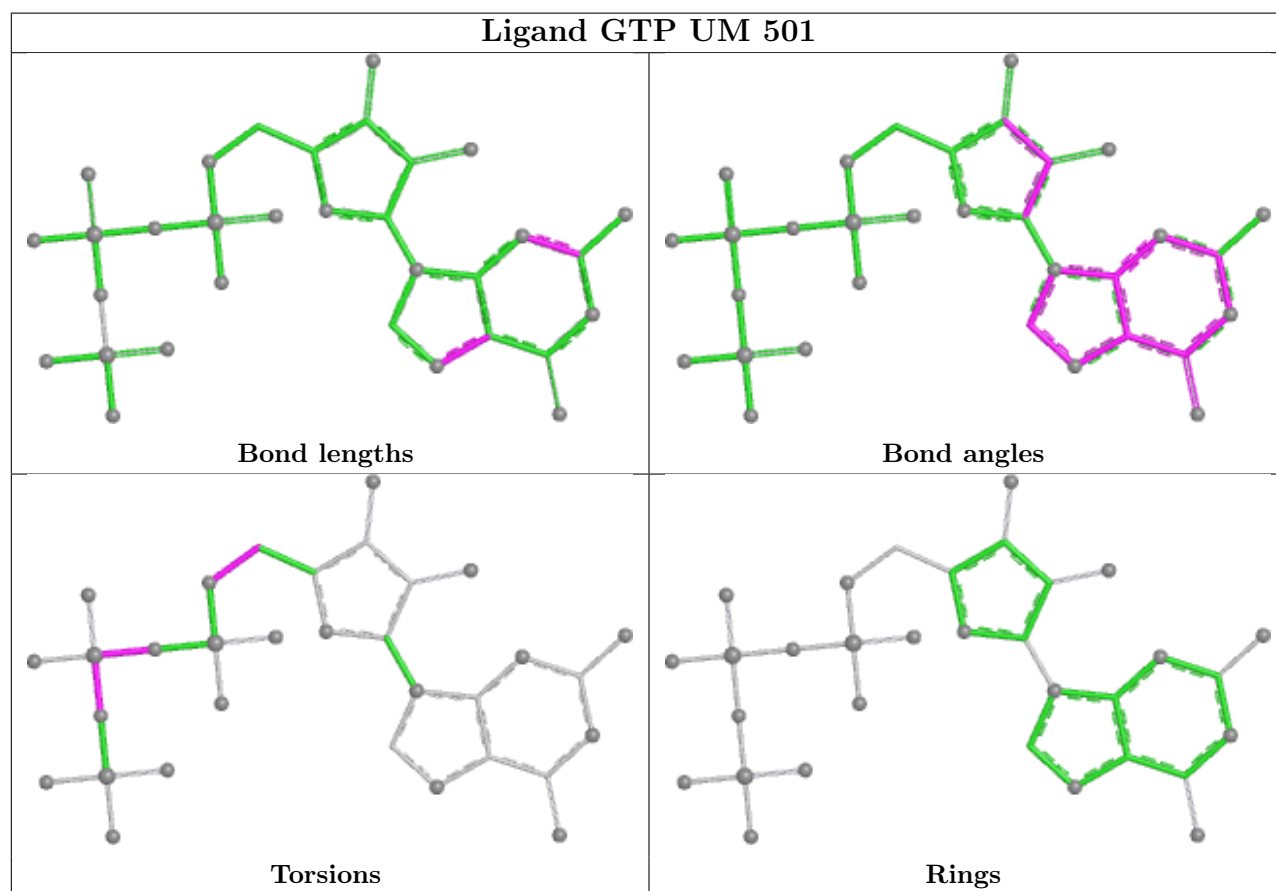
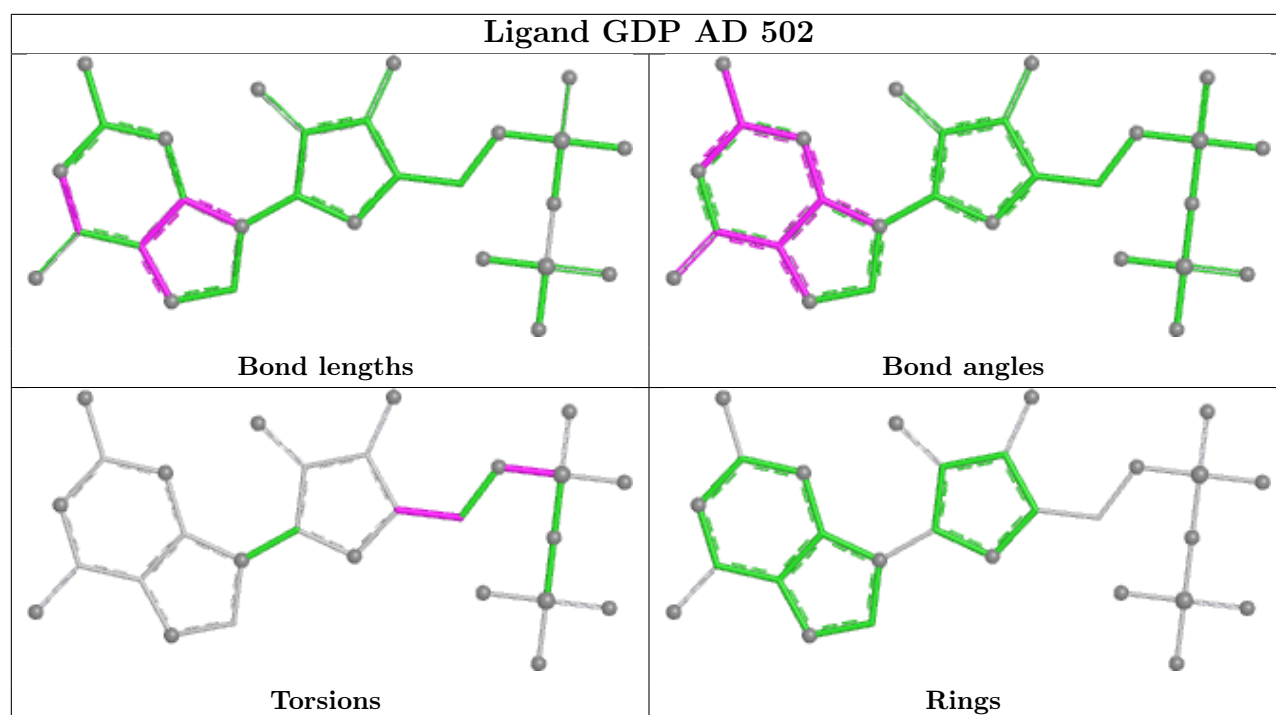


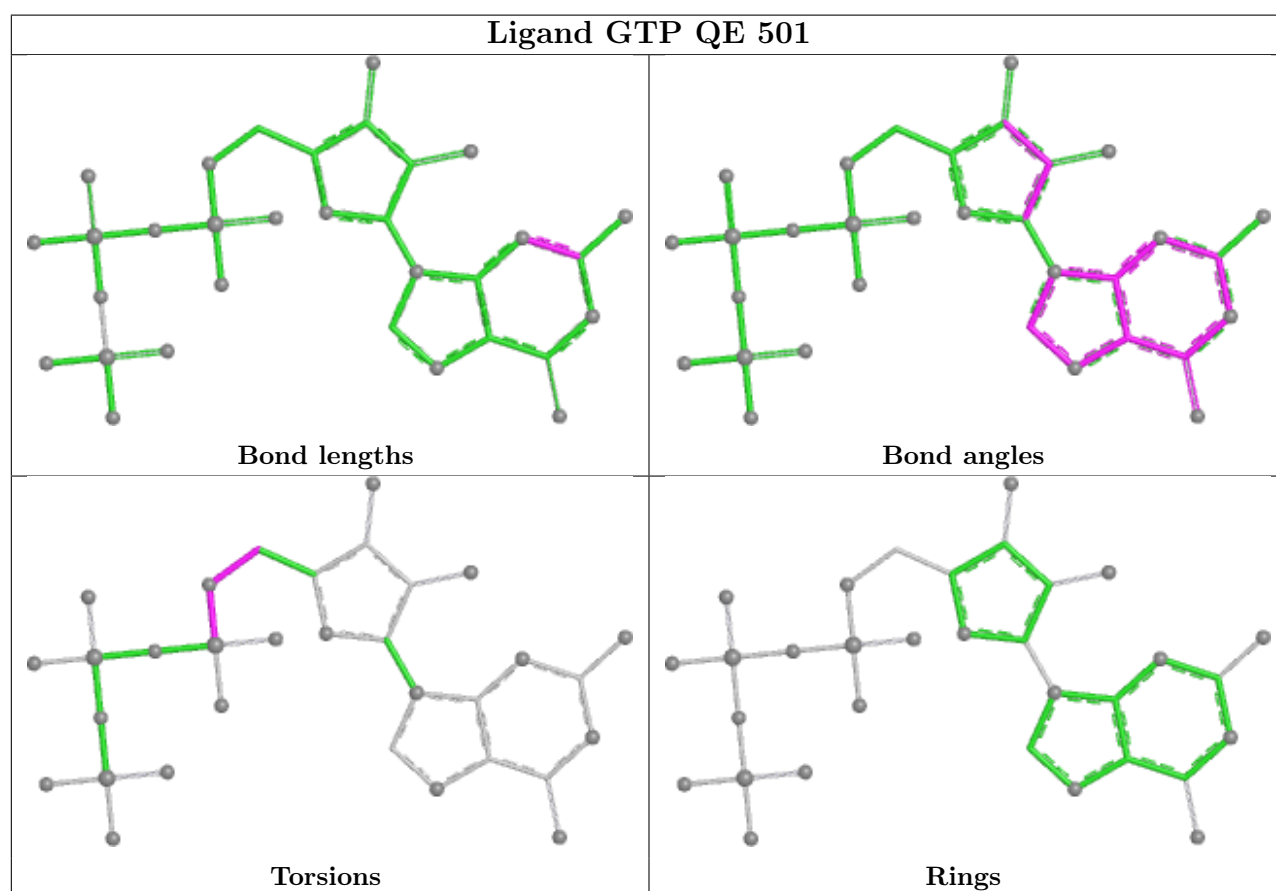
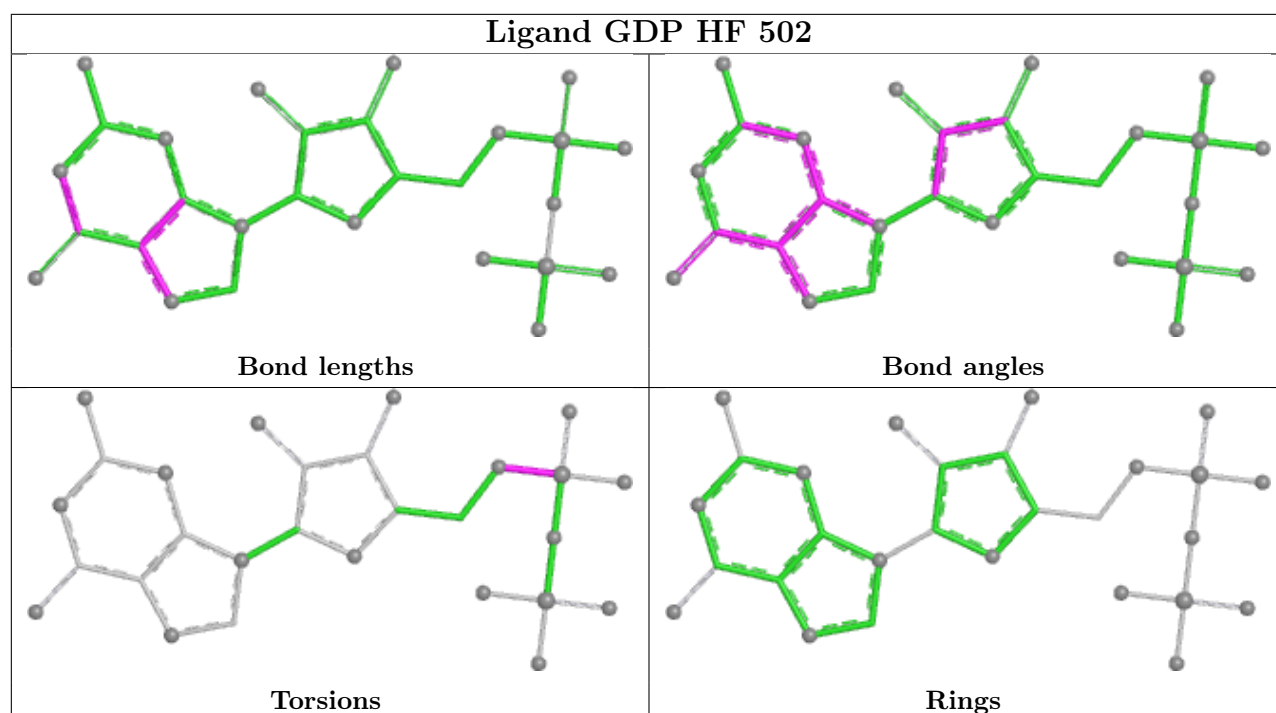




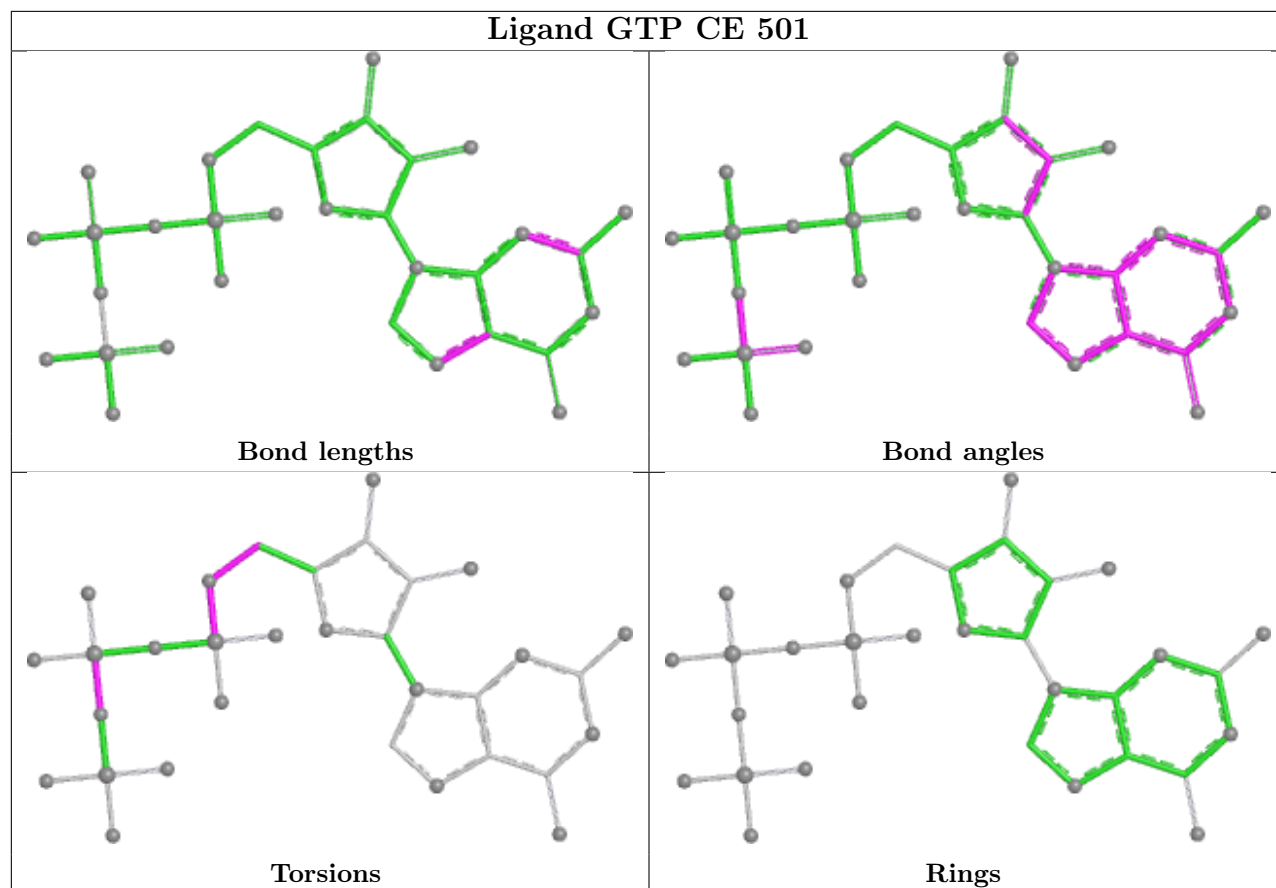




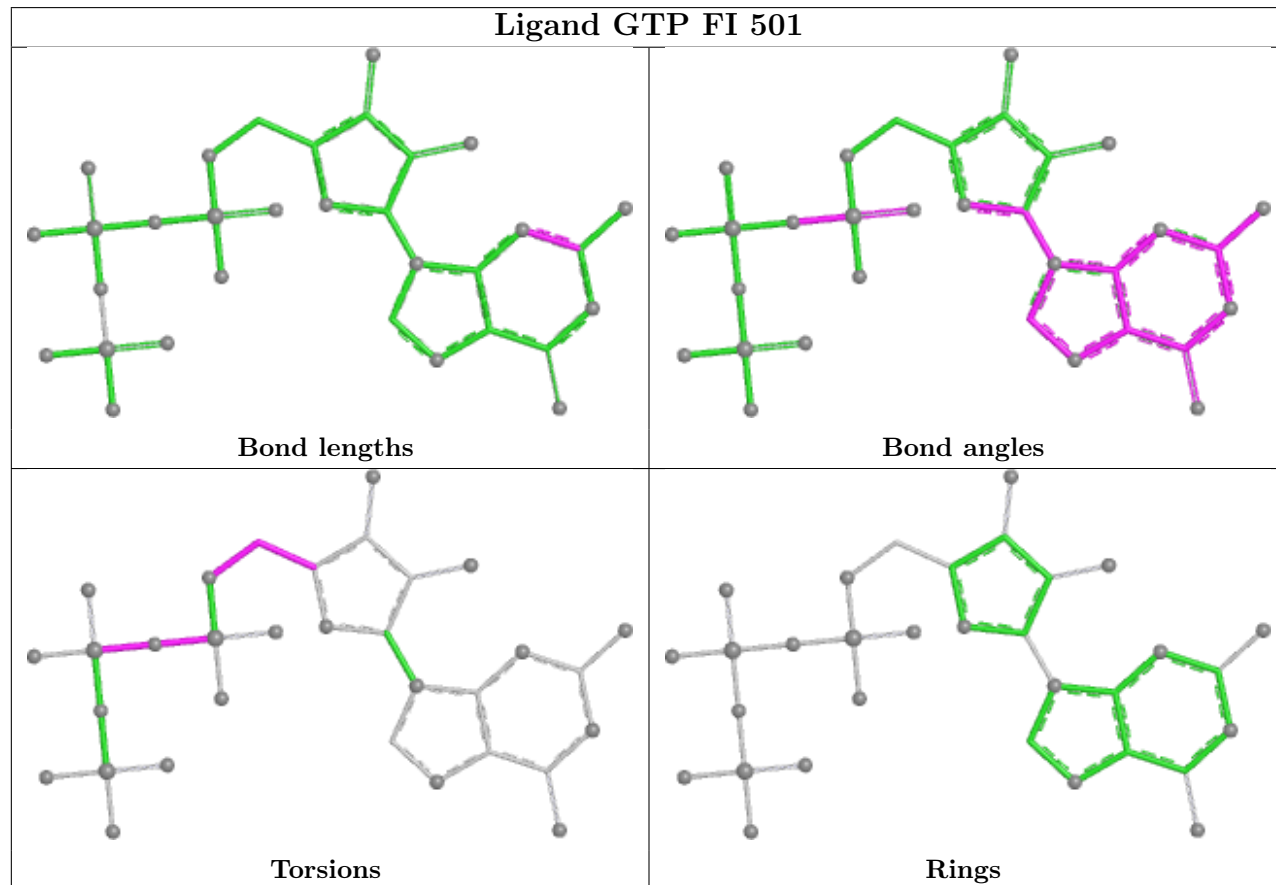


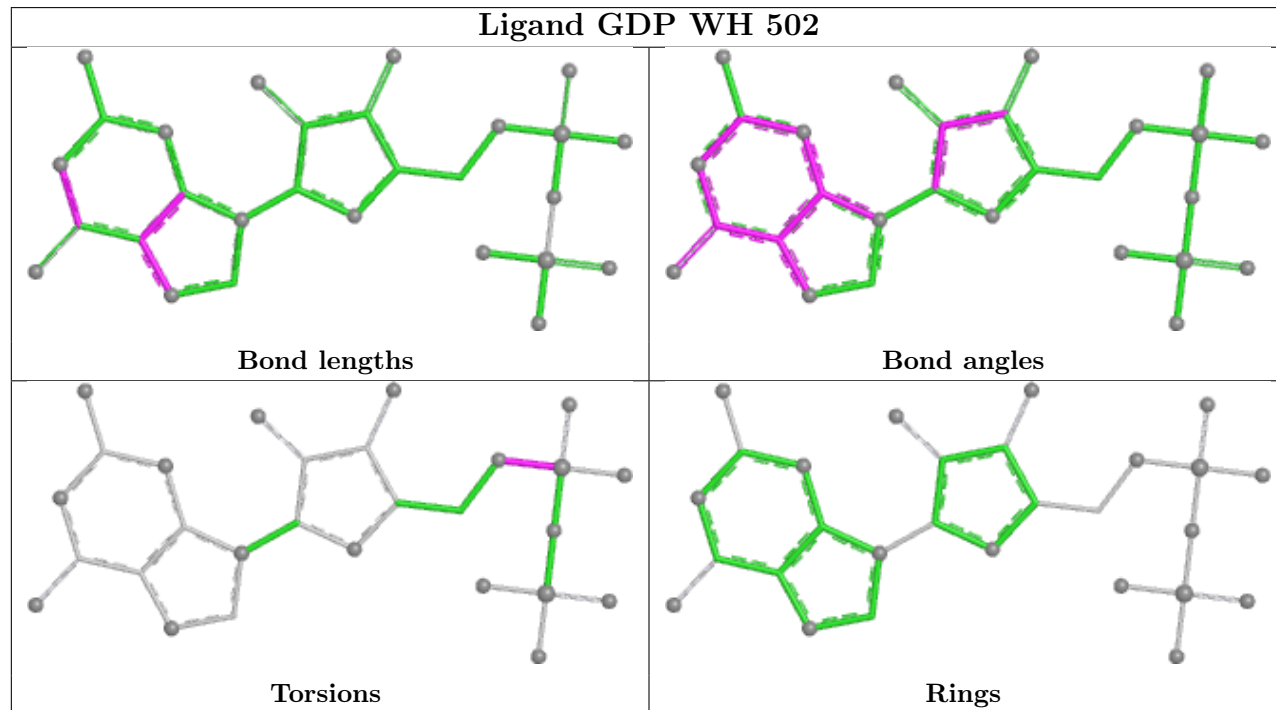
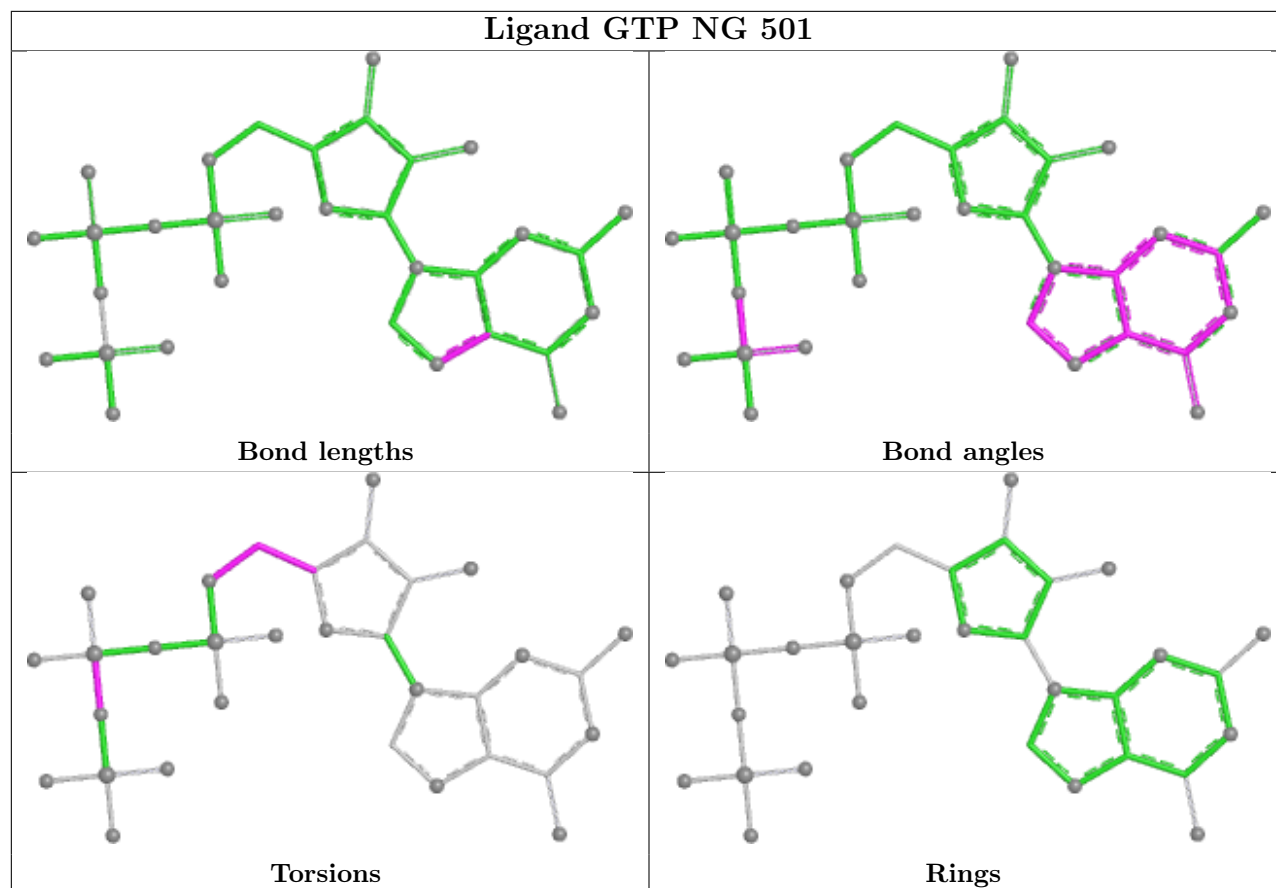


Ligand GTP CE 501

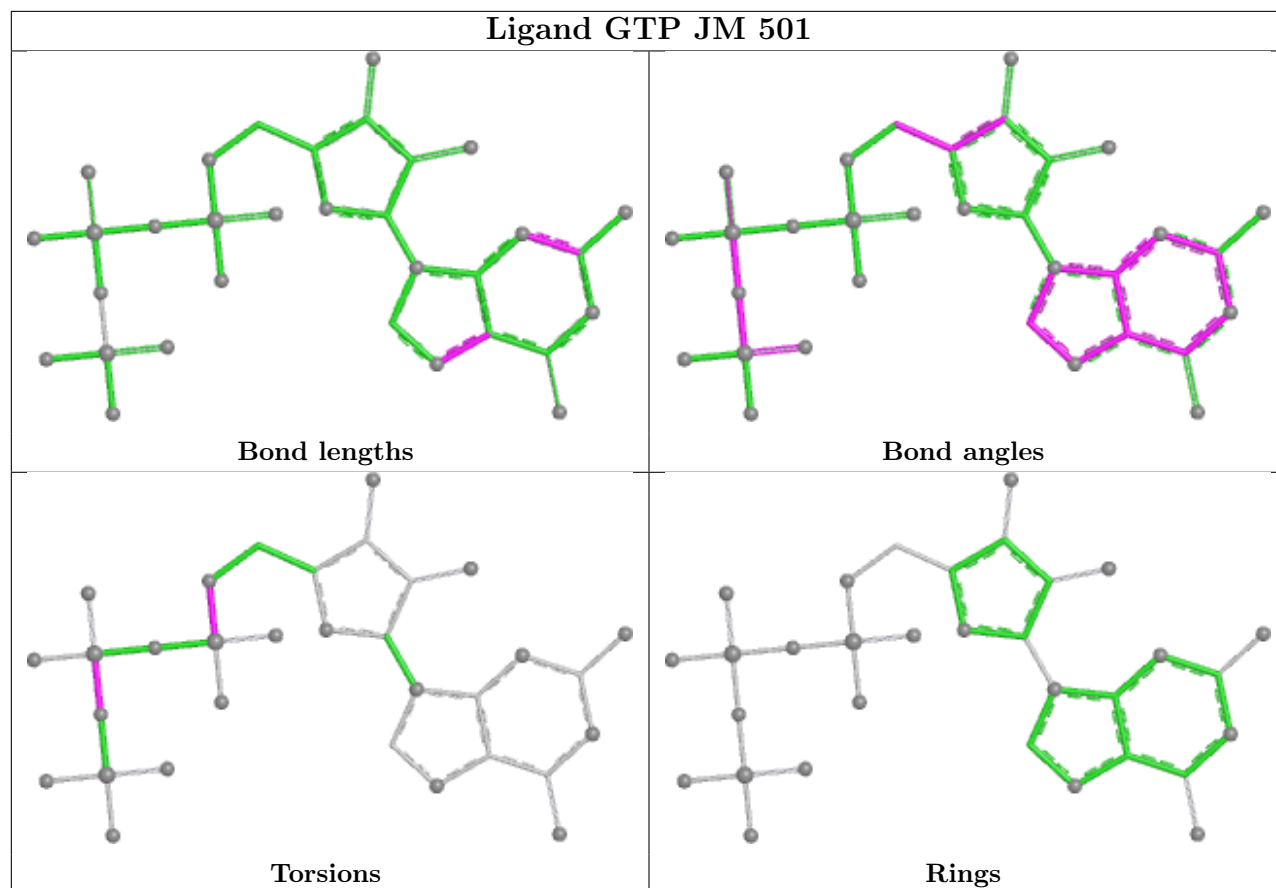


Ligand GTP FI 501

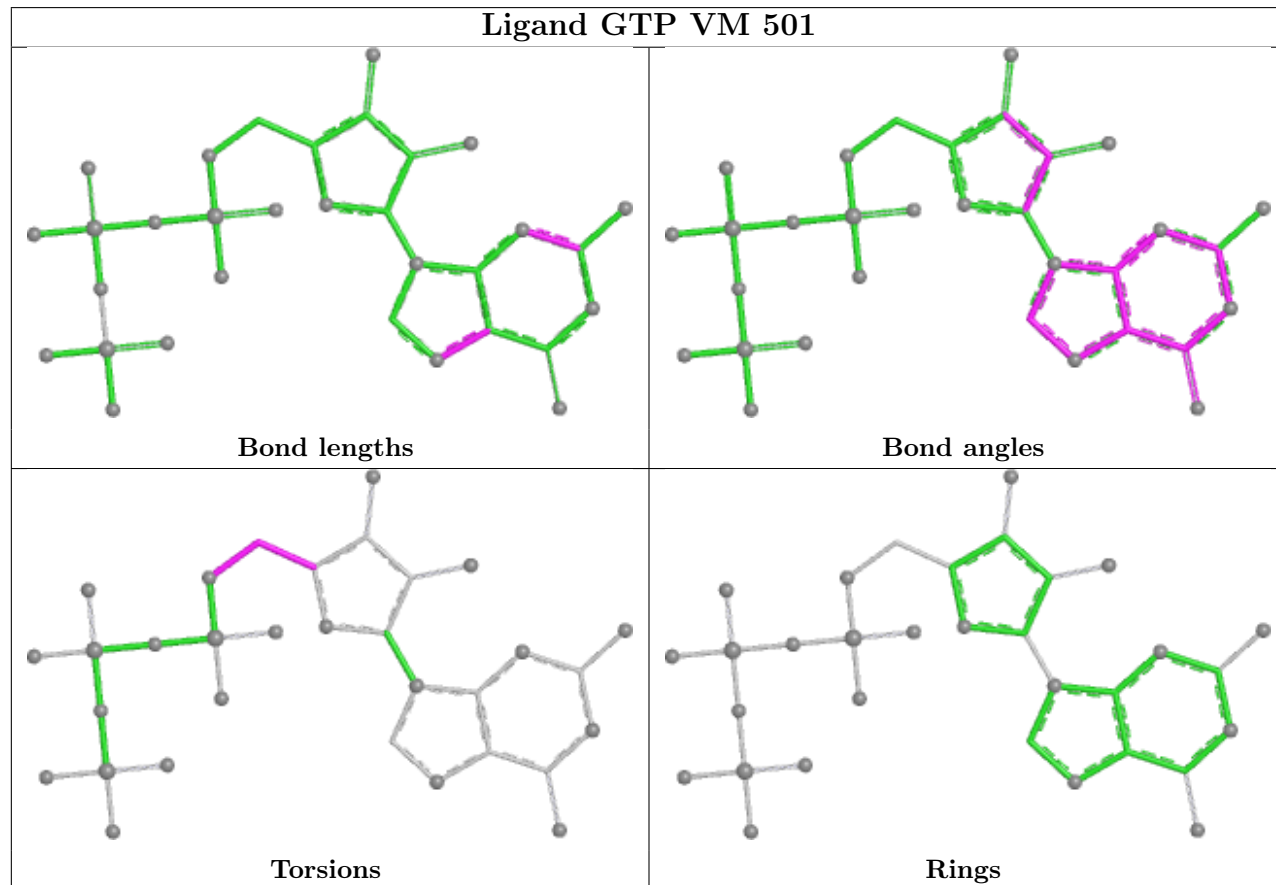




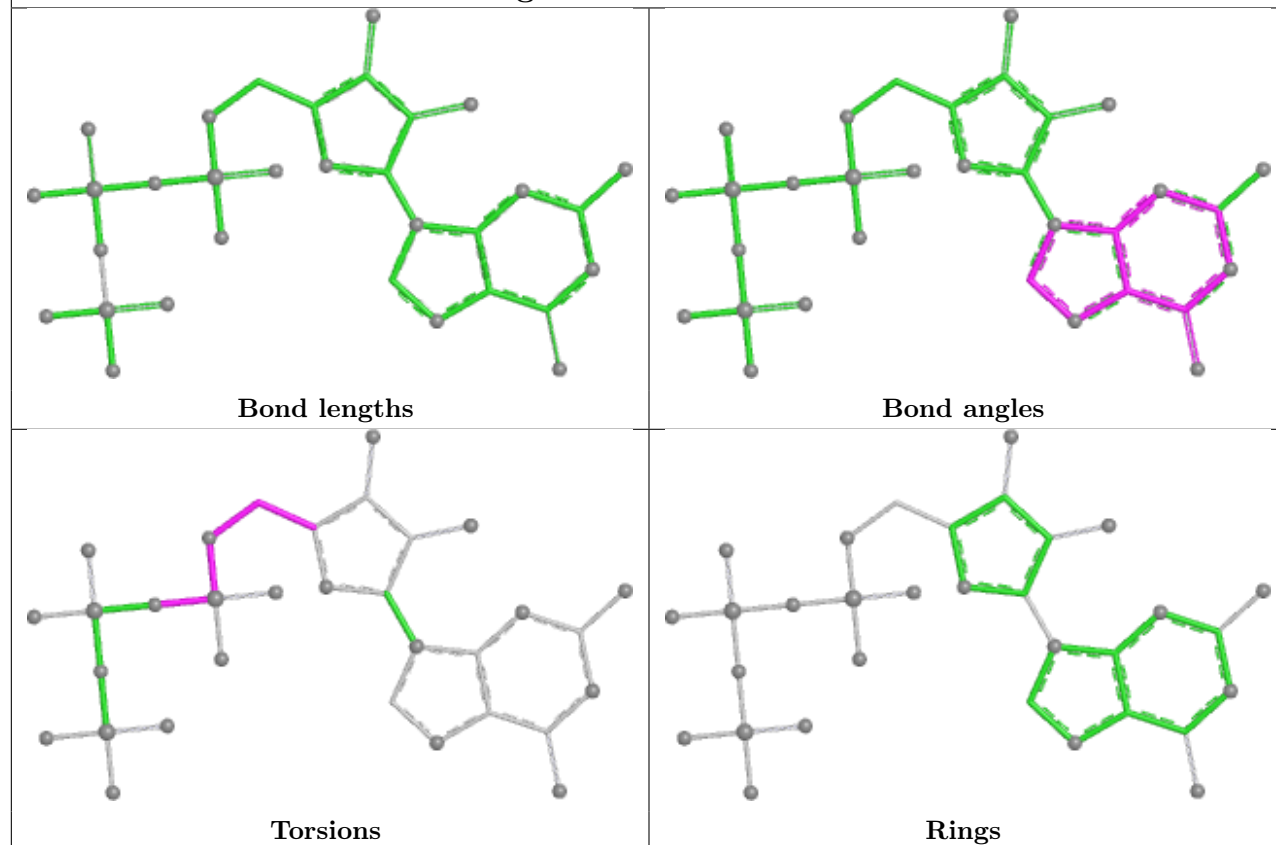
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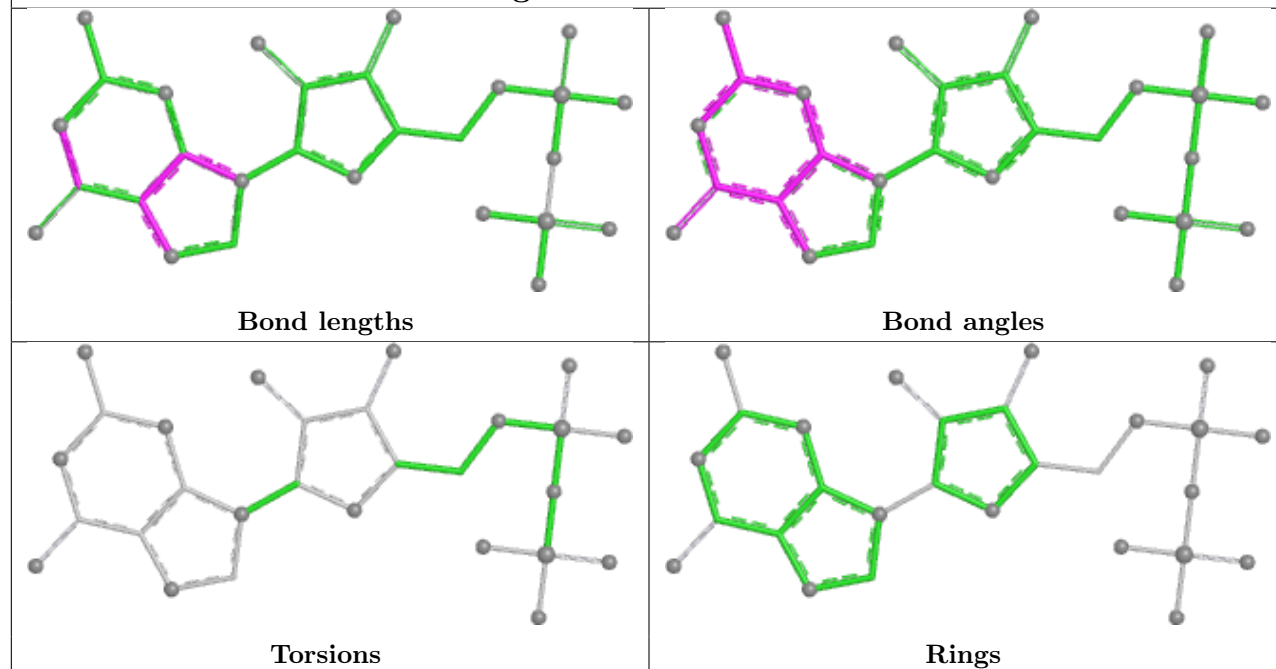
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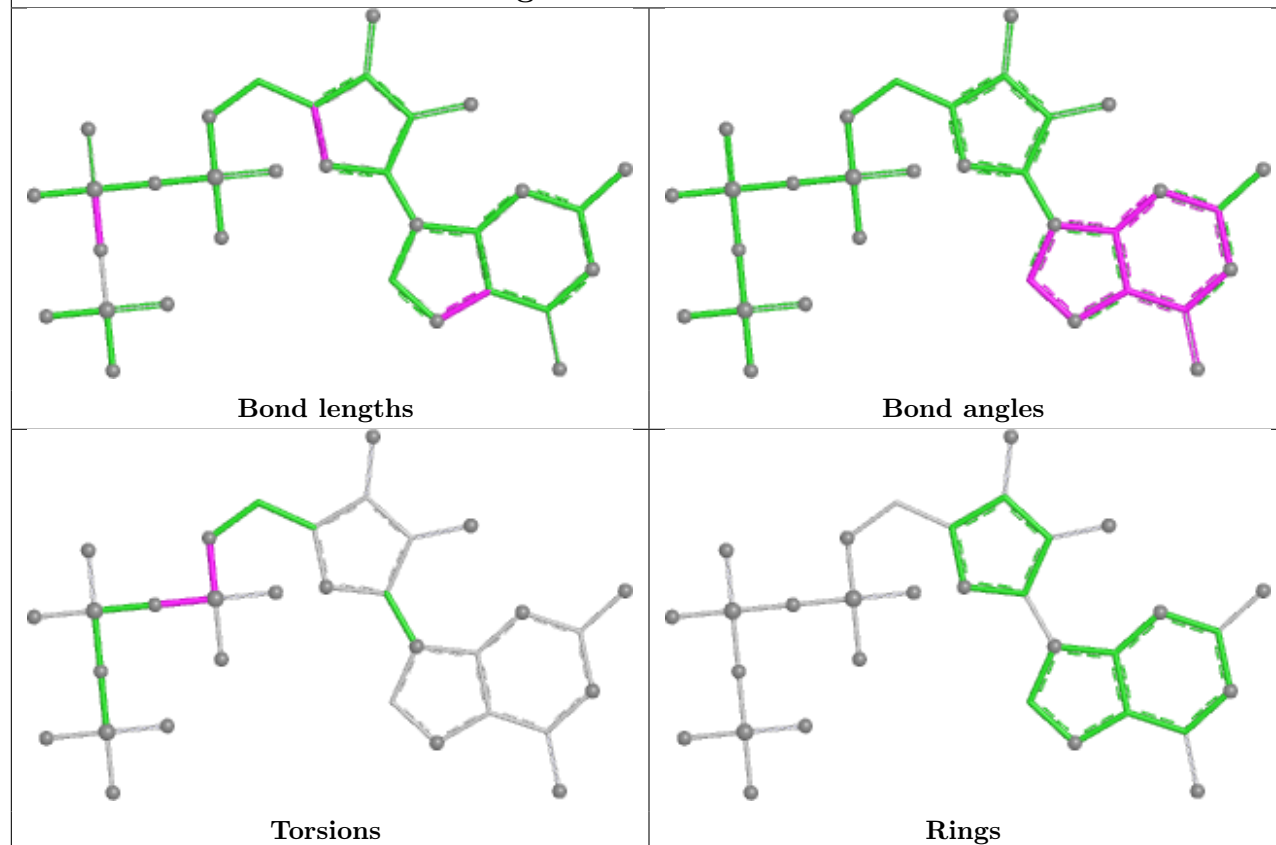
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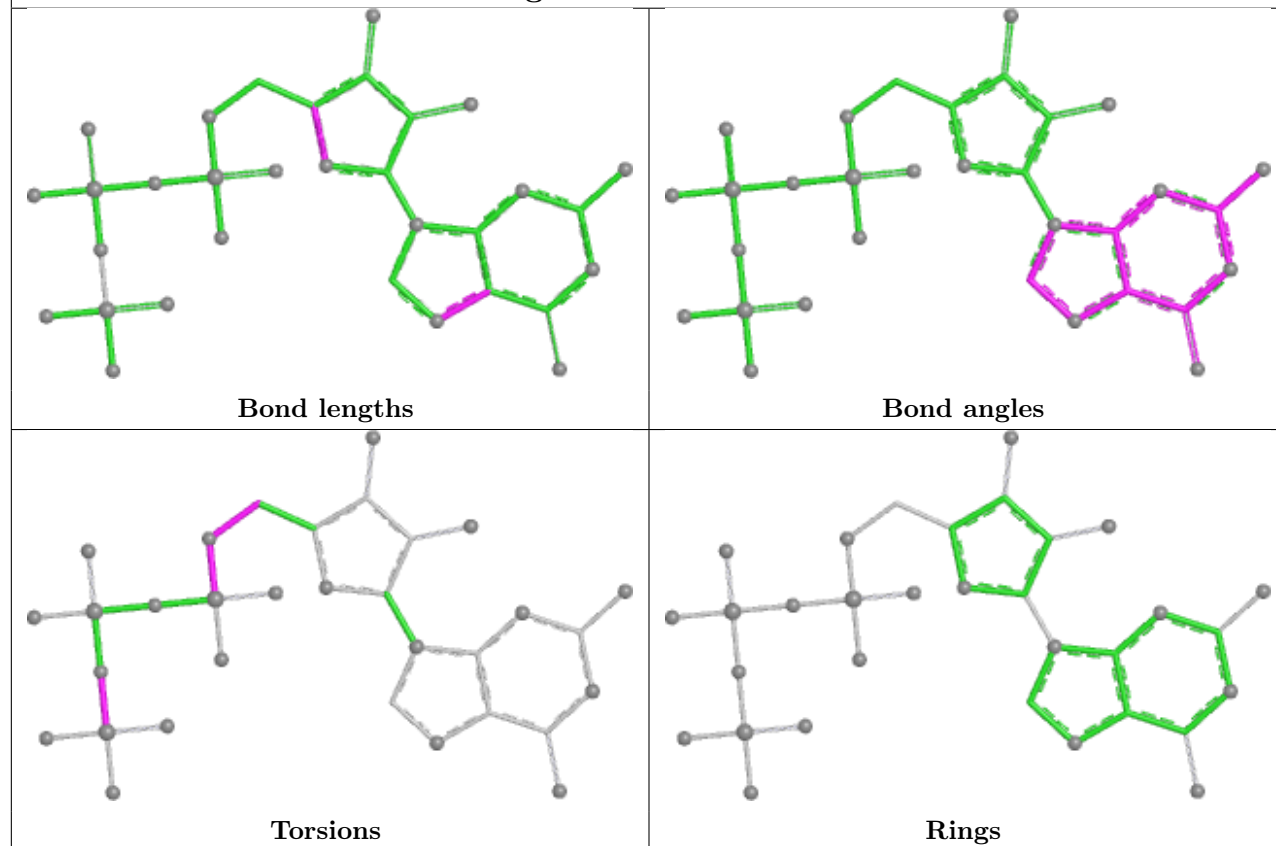
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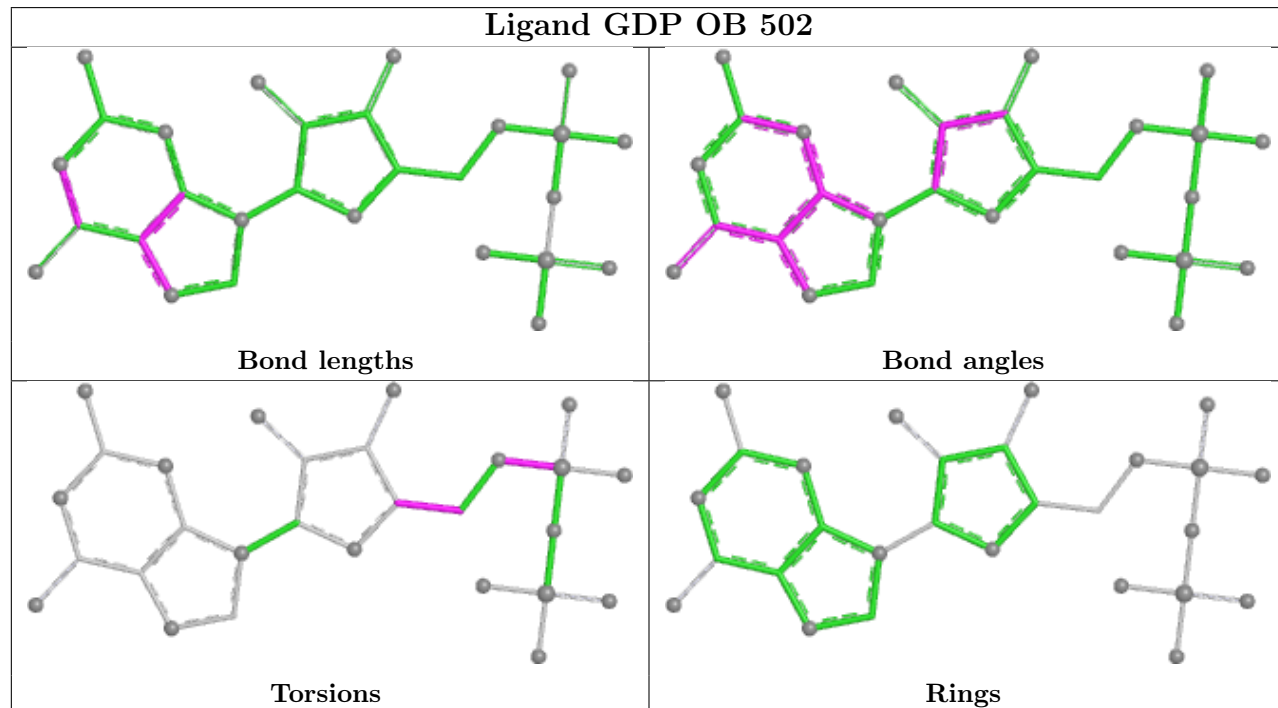
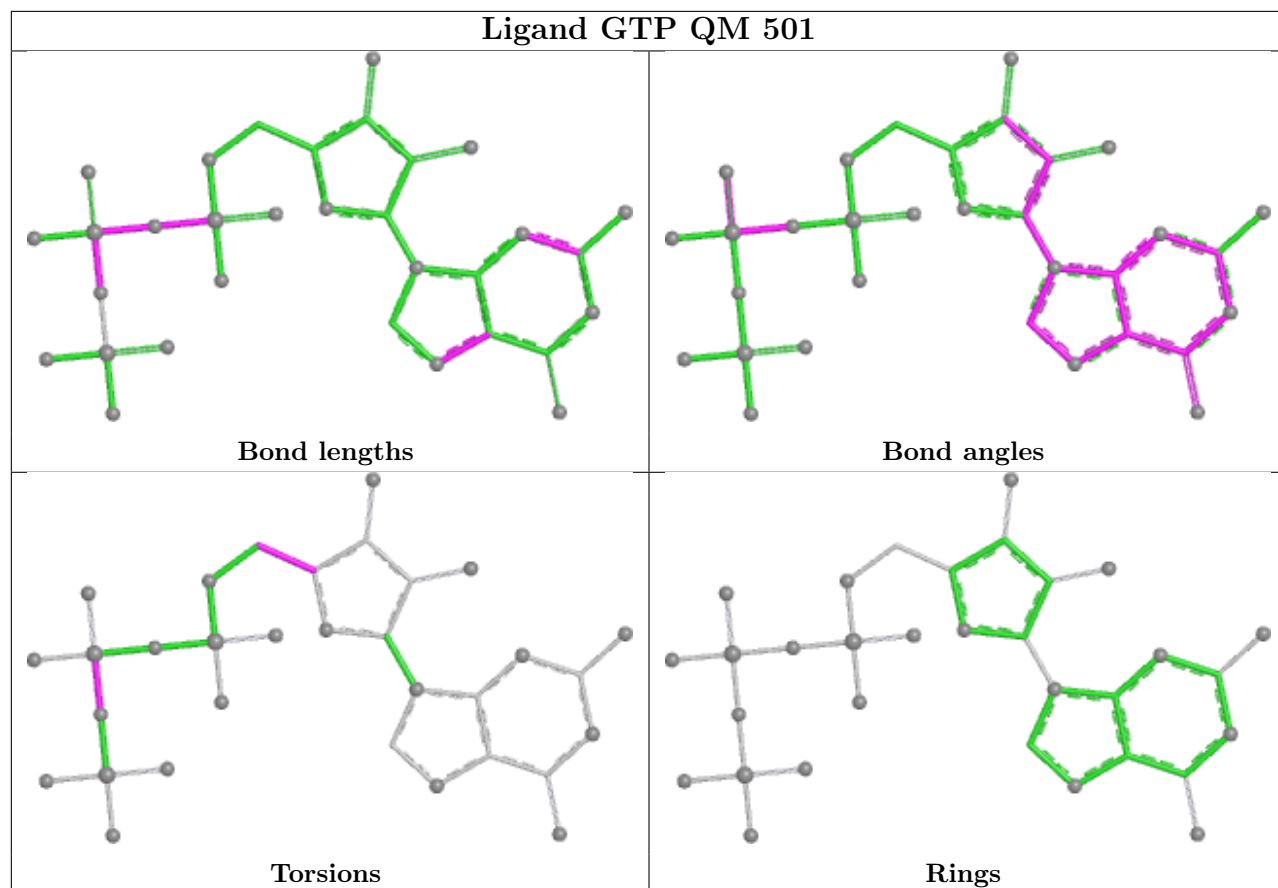


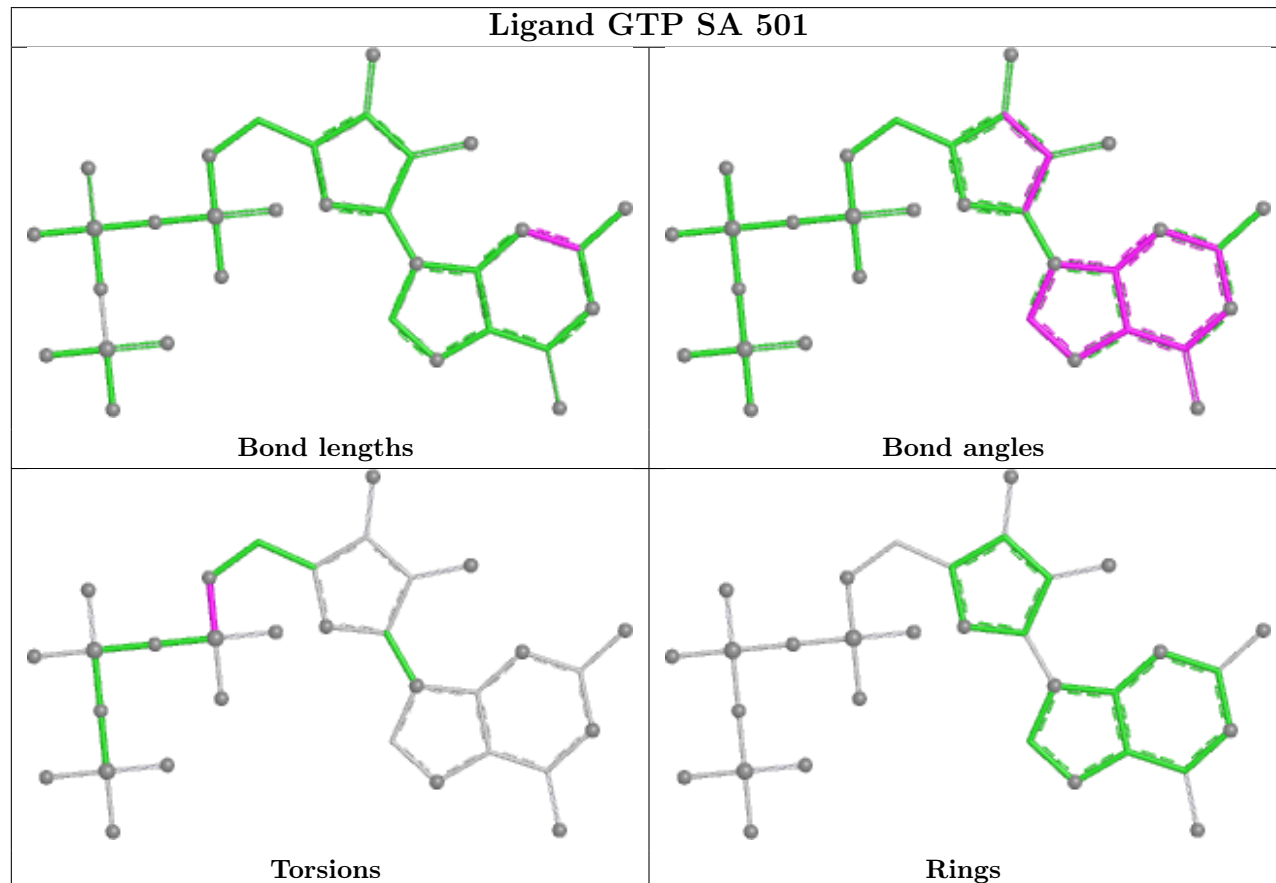
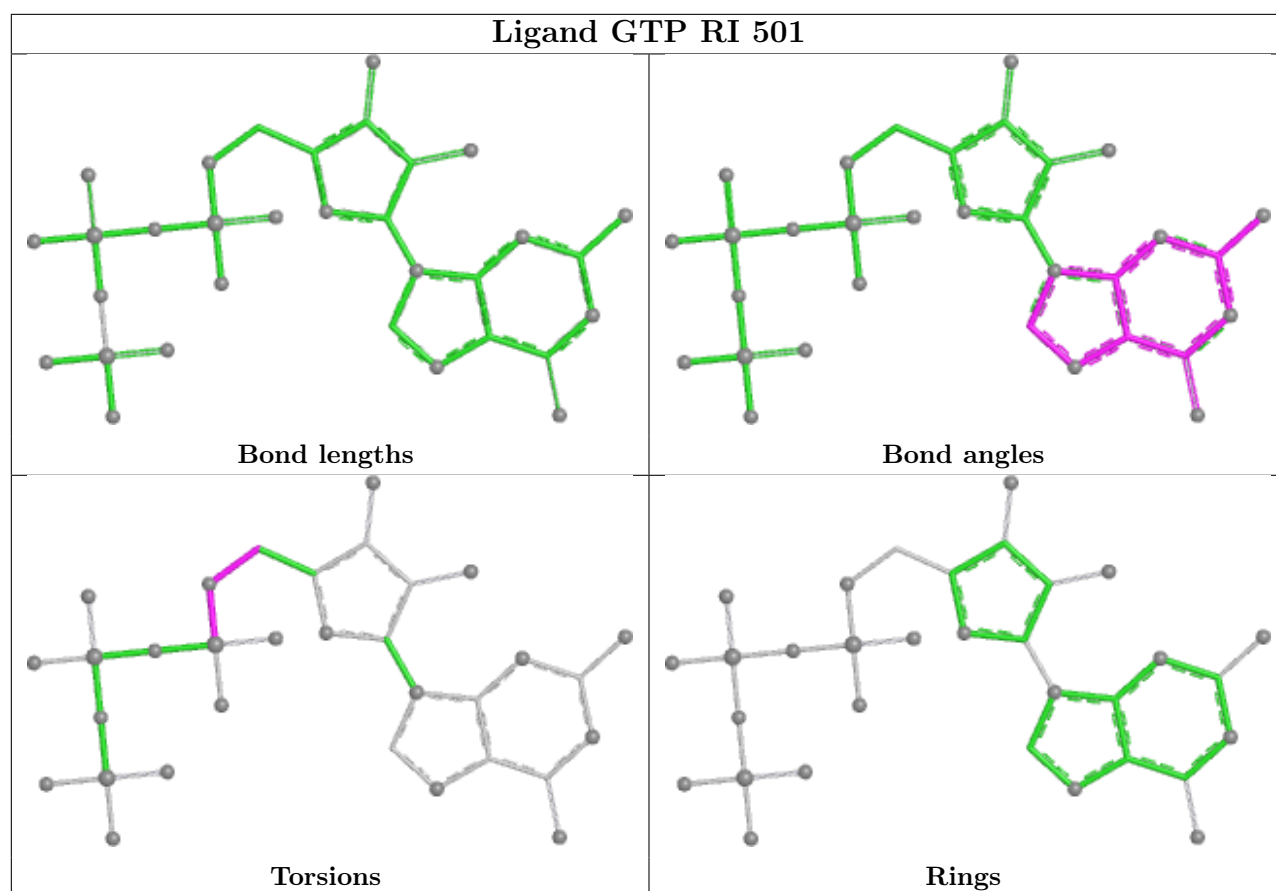
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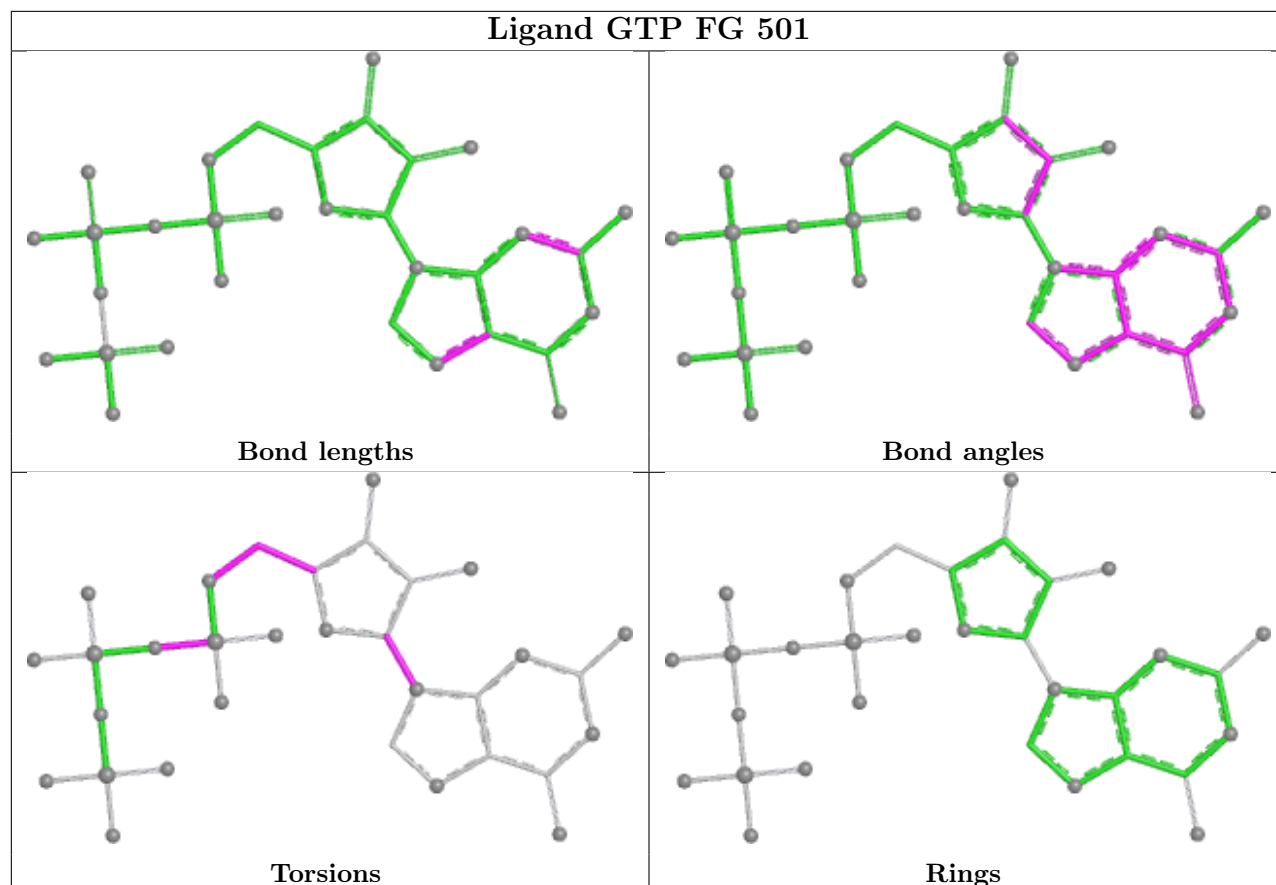
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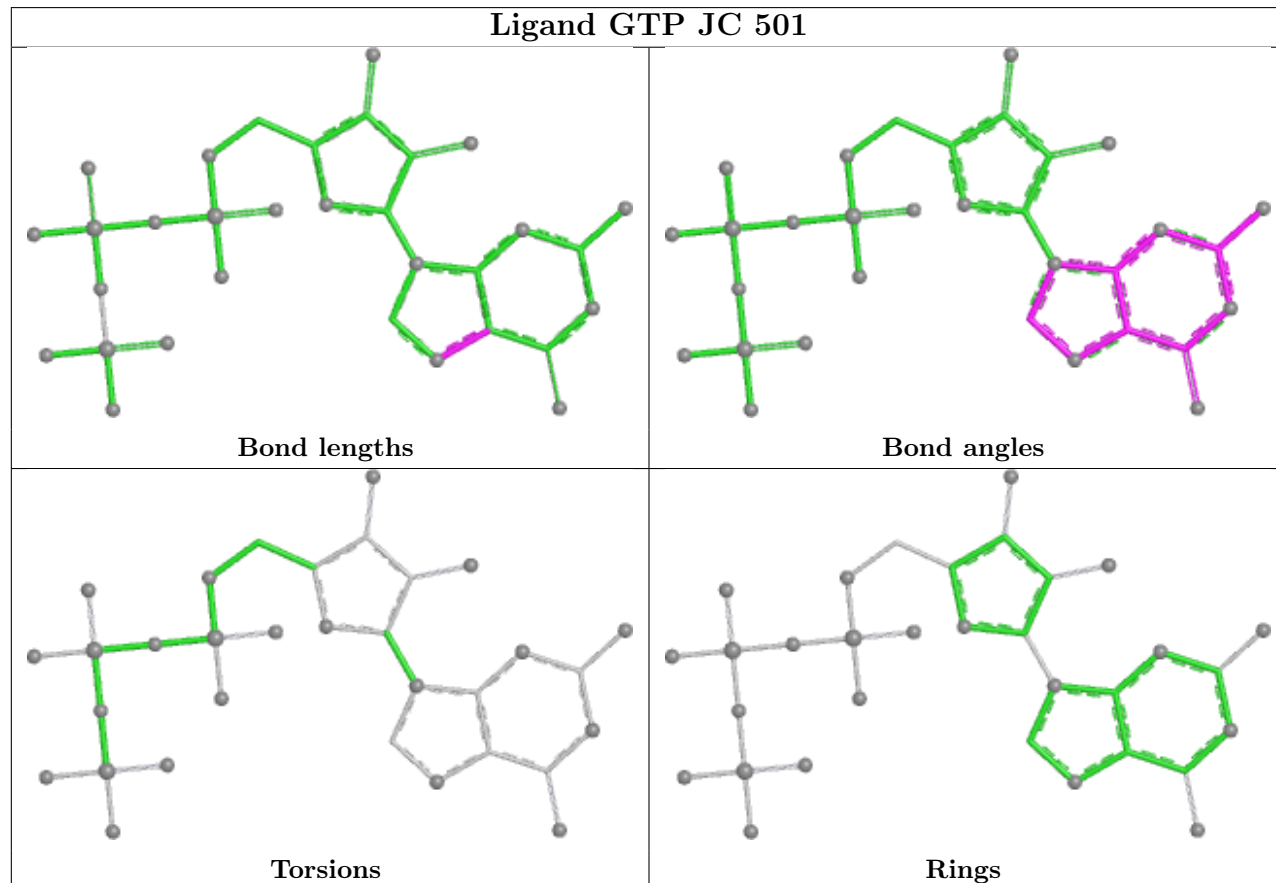




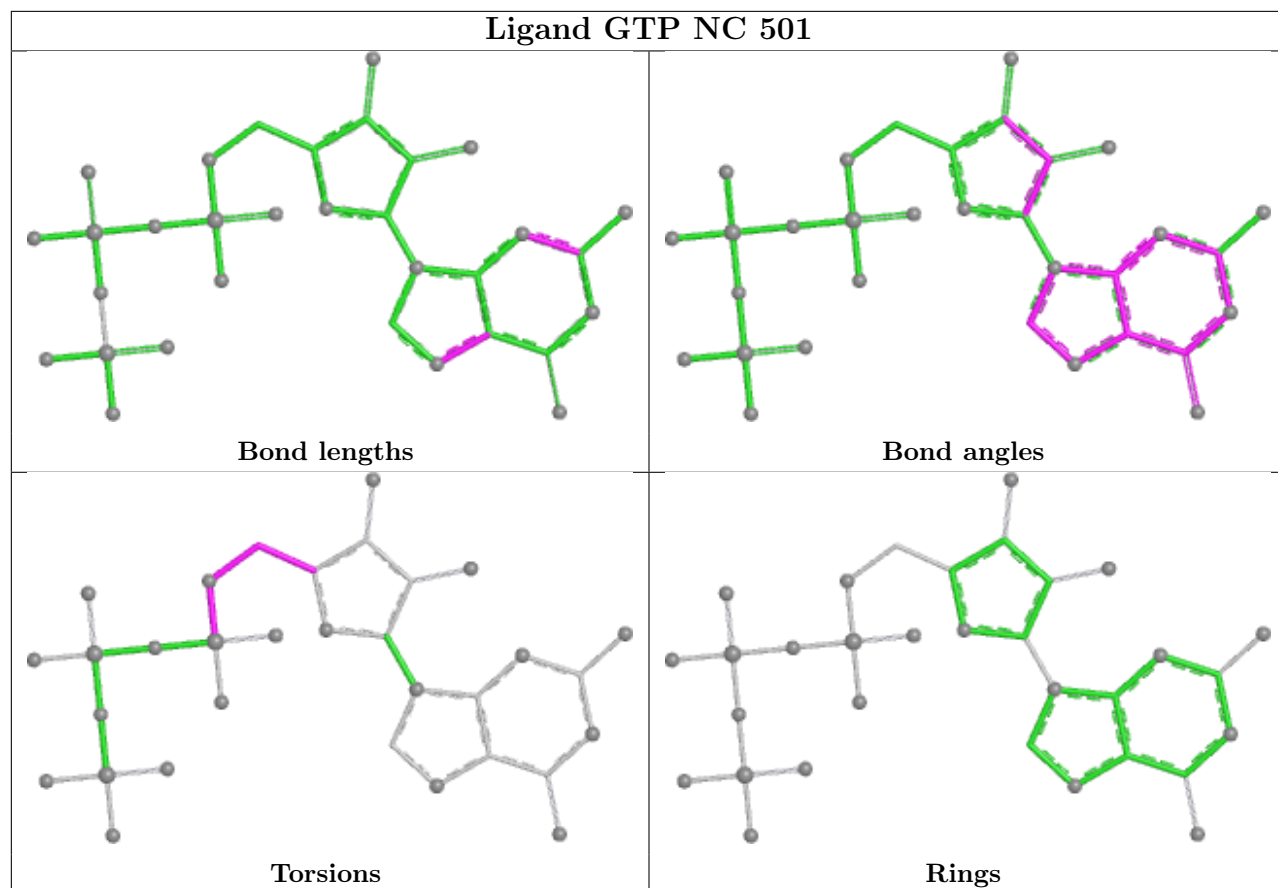
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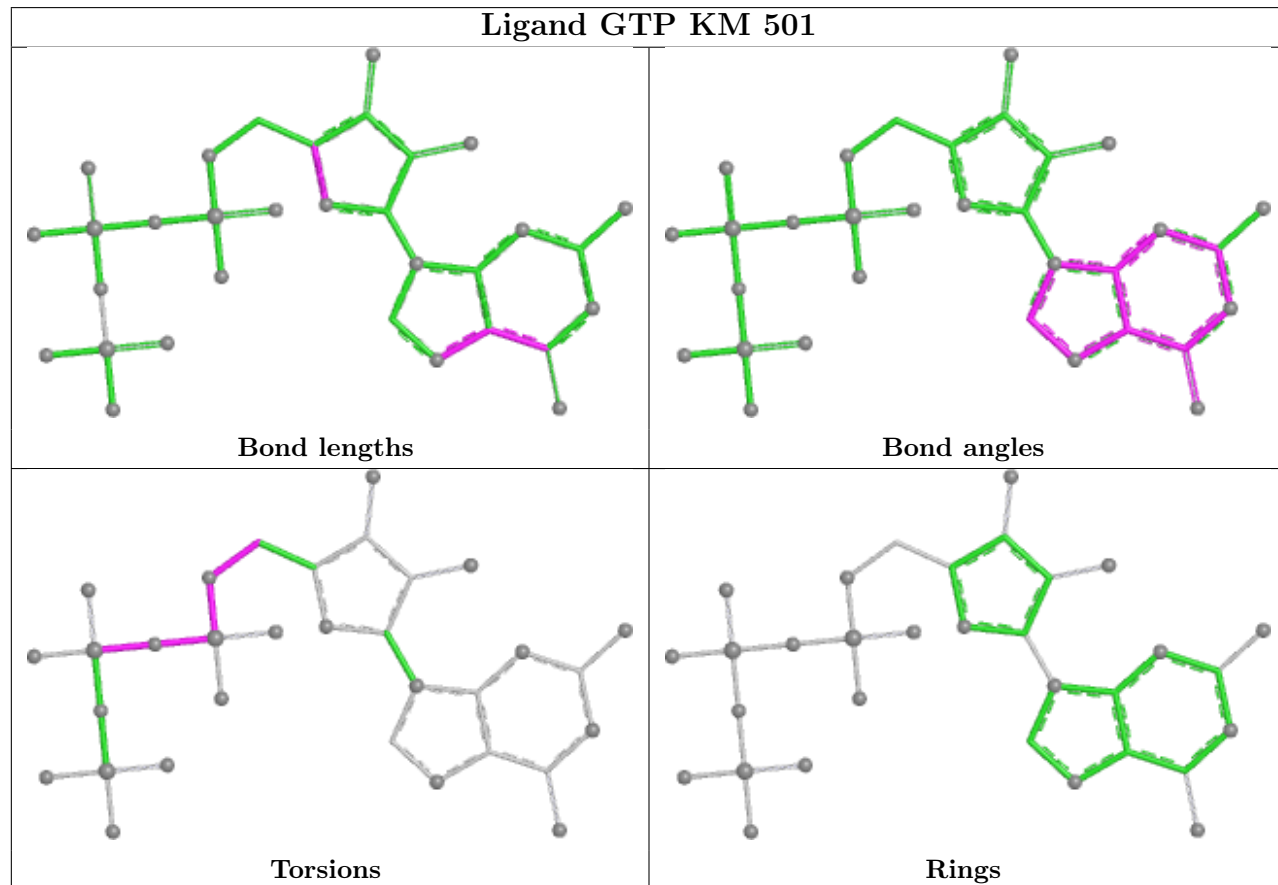
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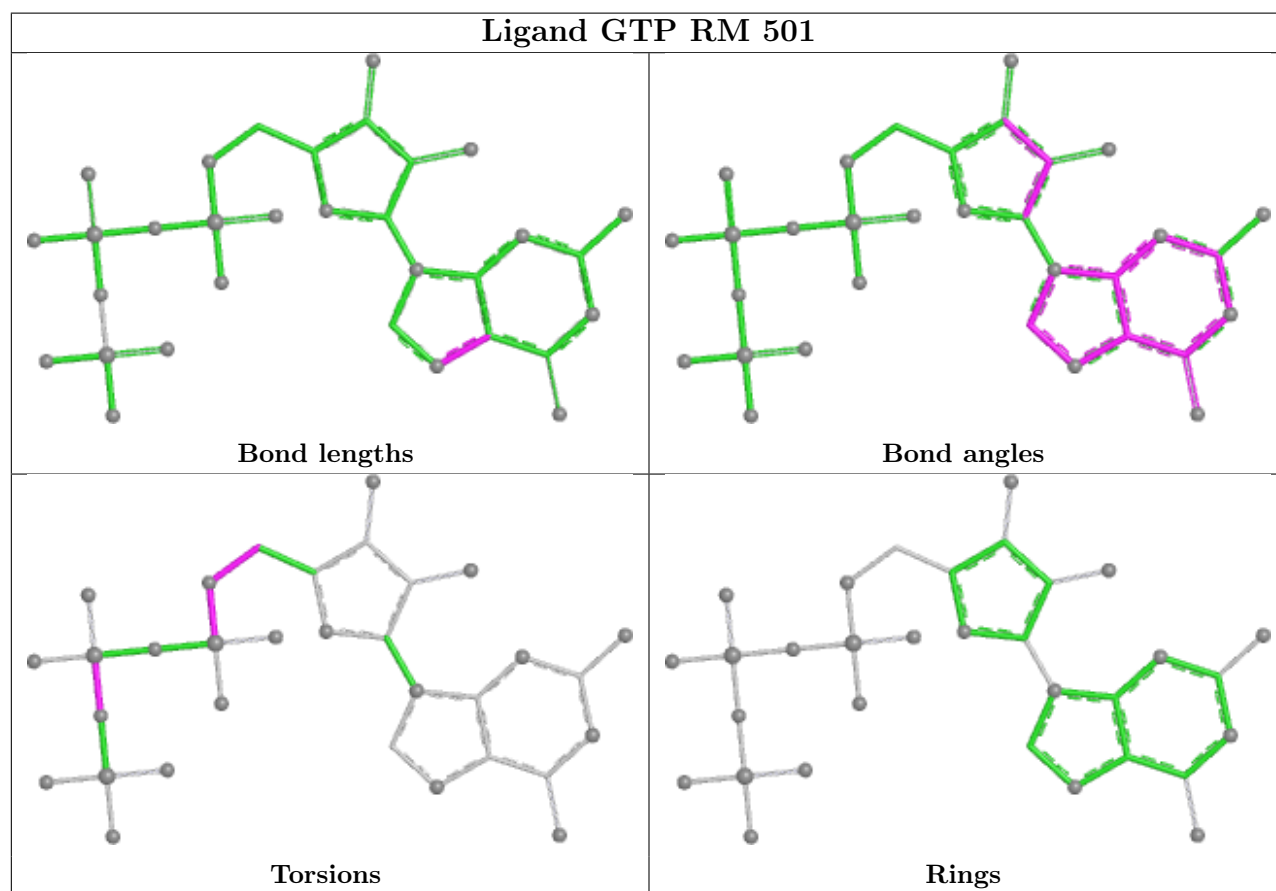
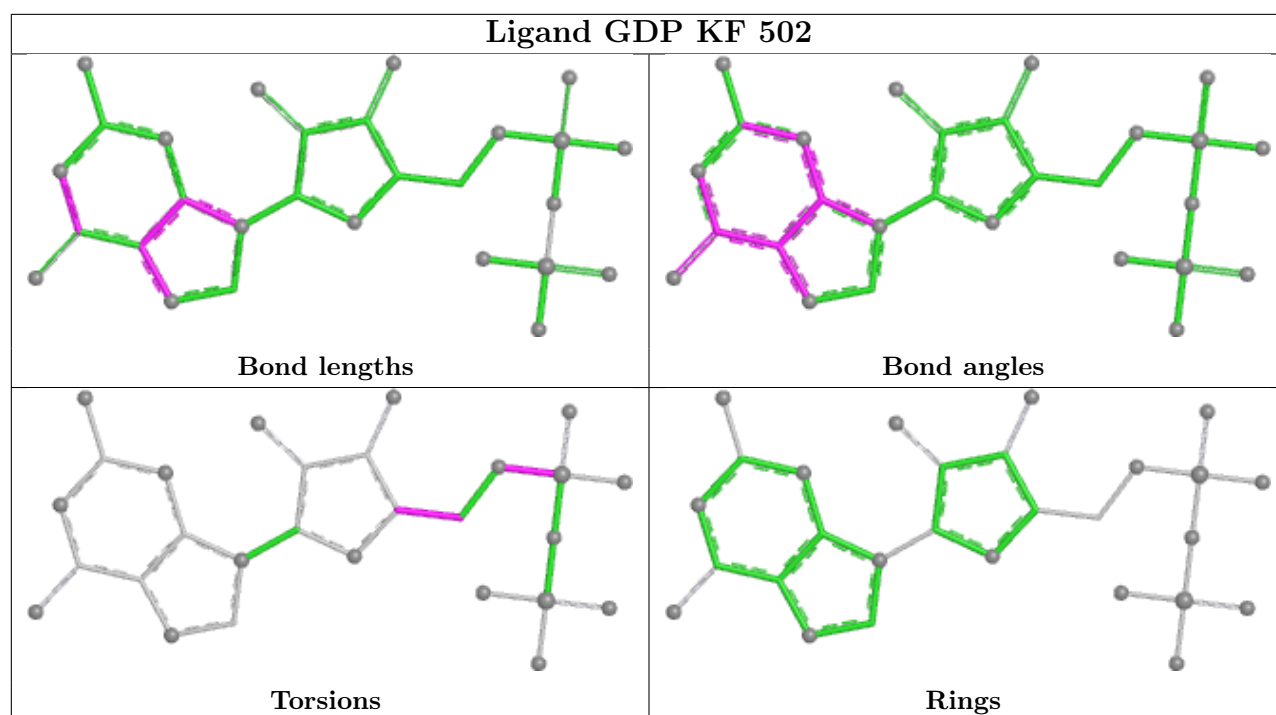


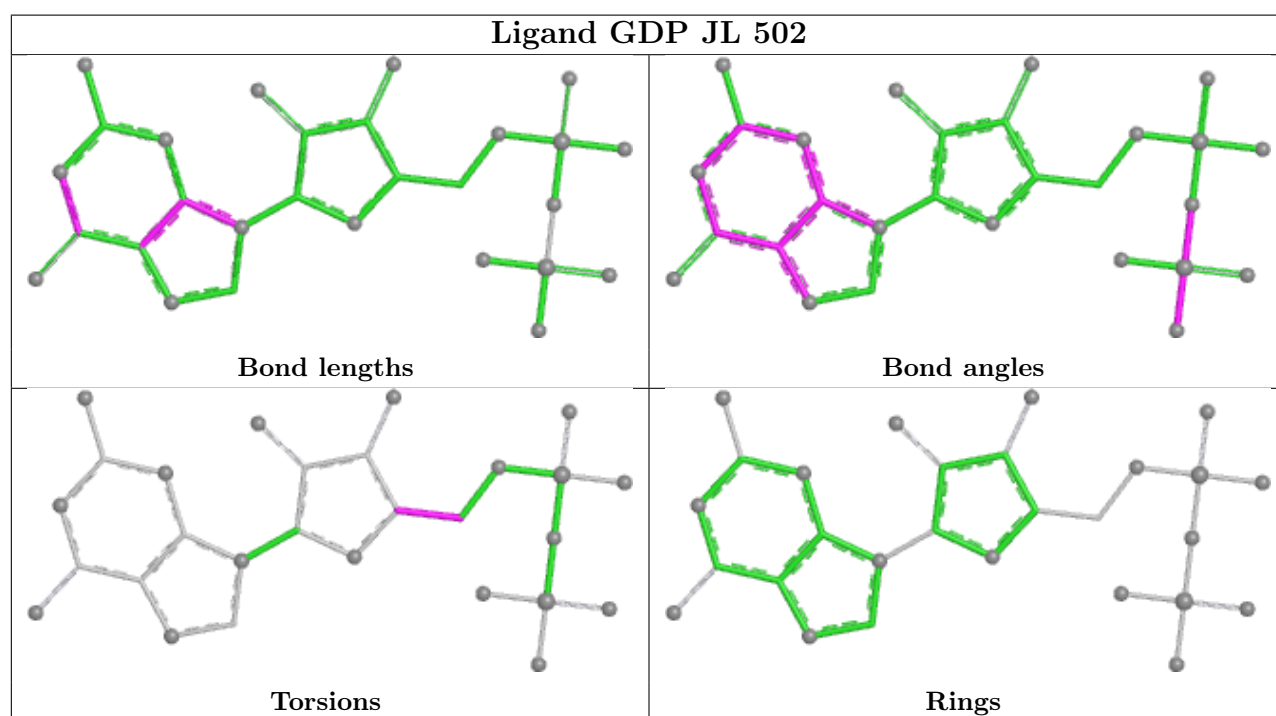
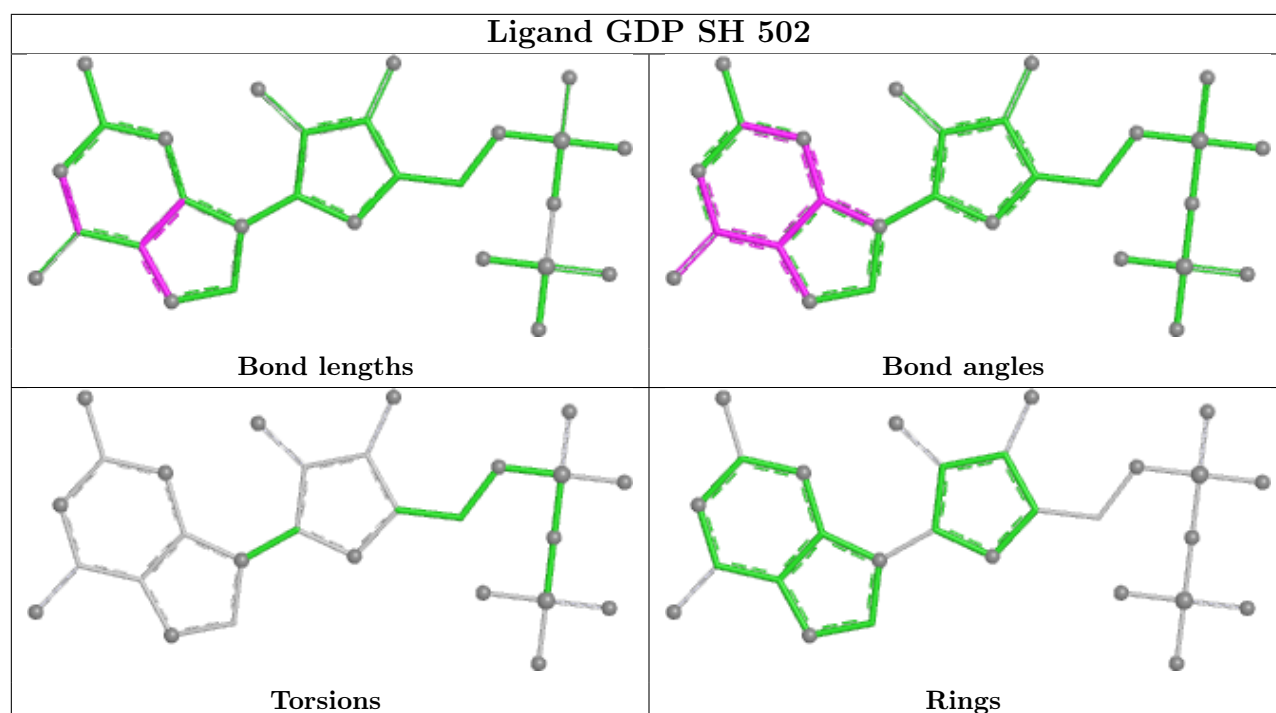
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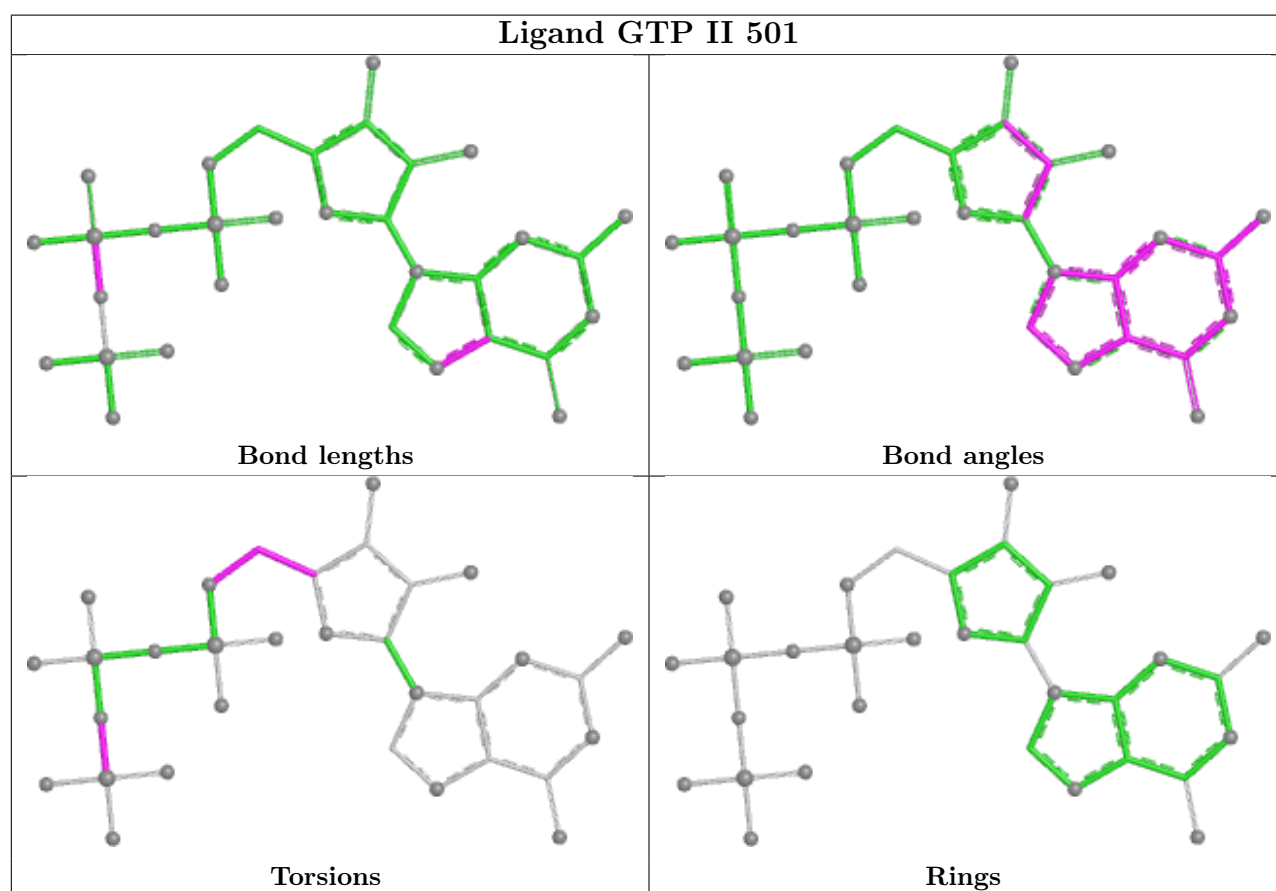
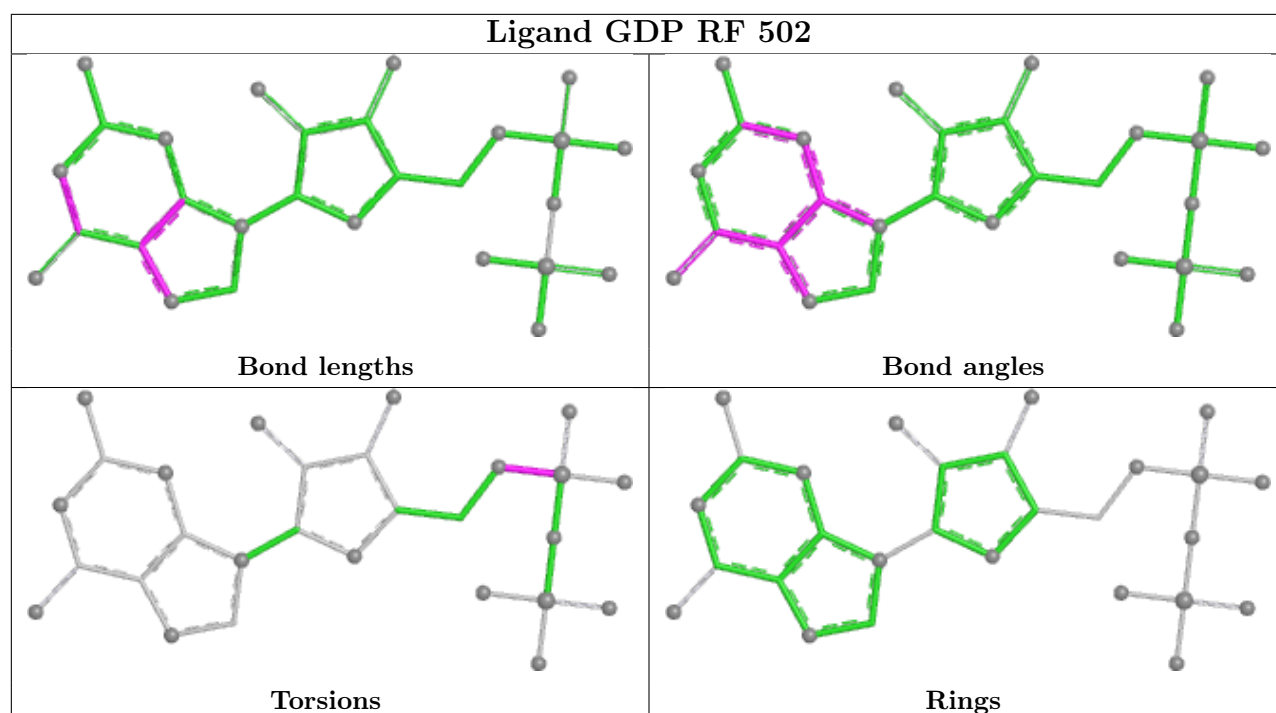


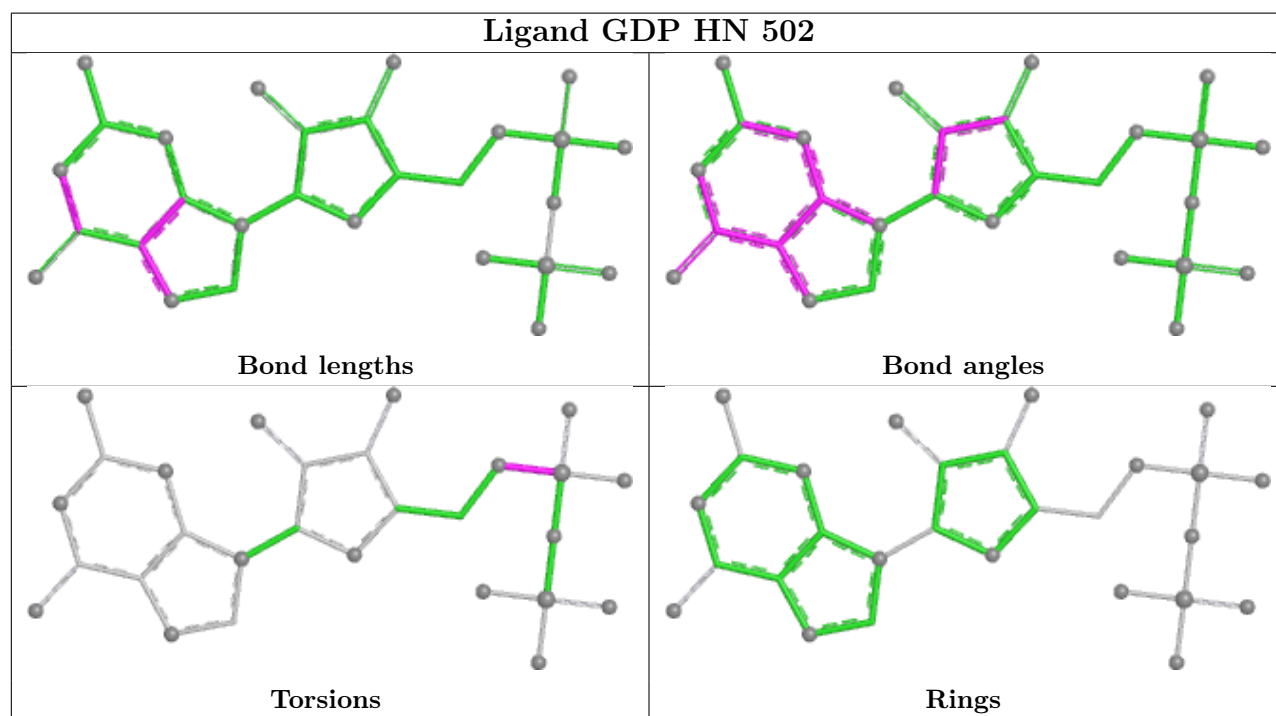
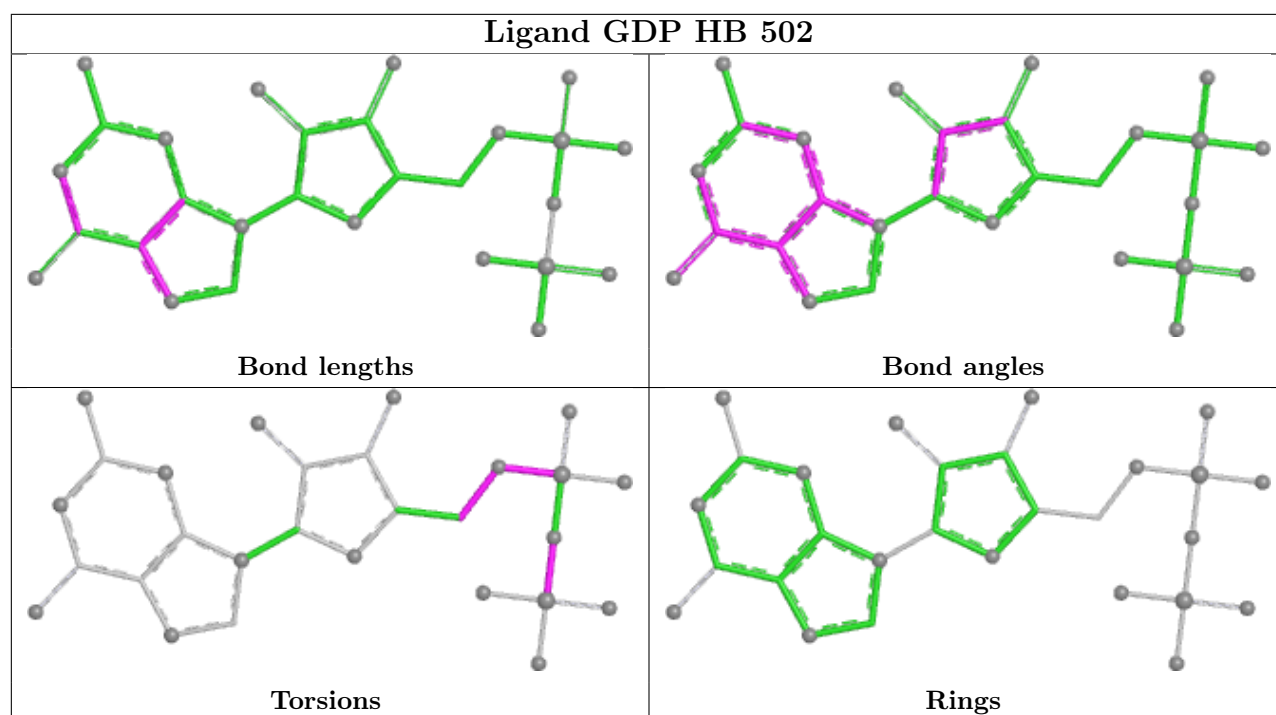
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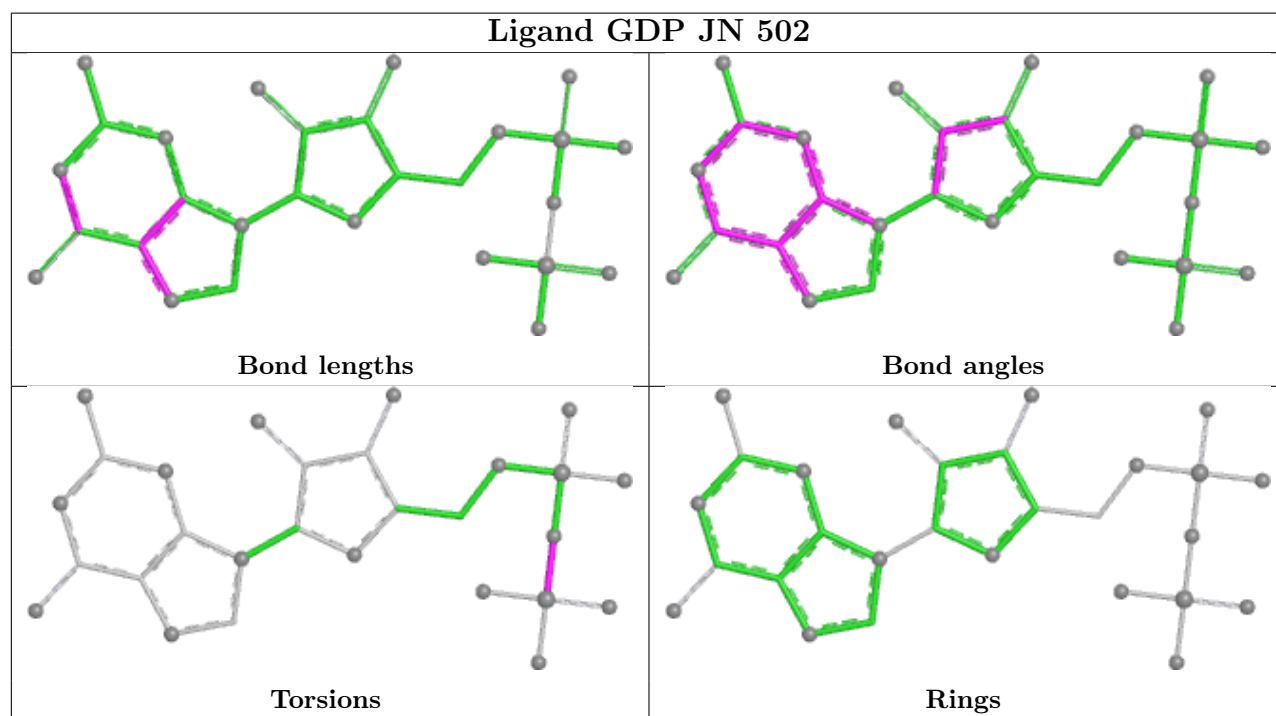
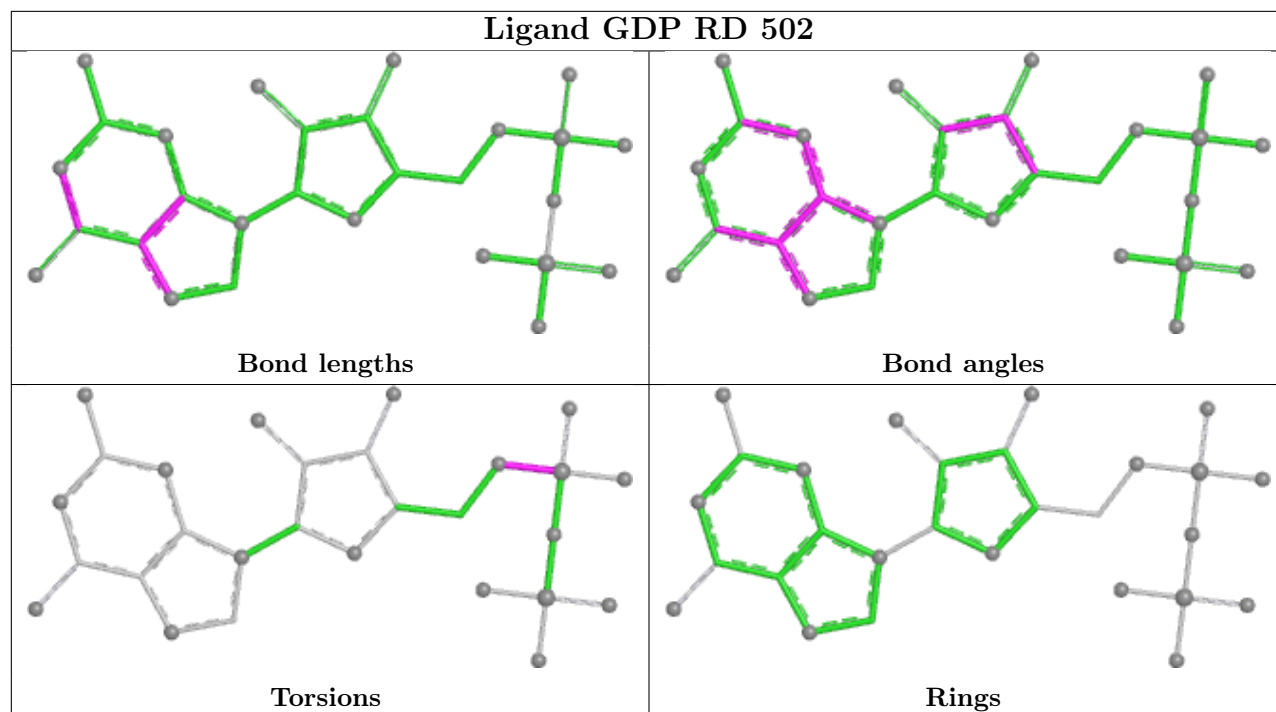


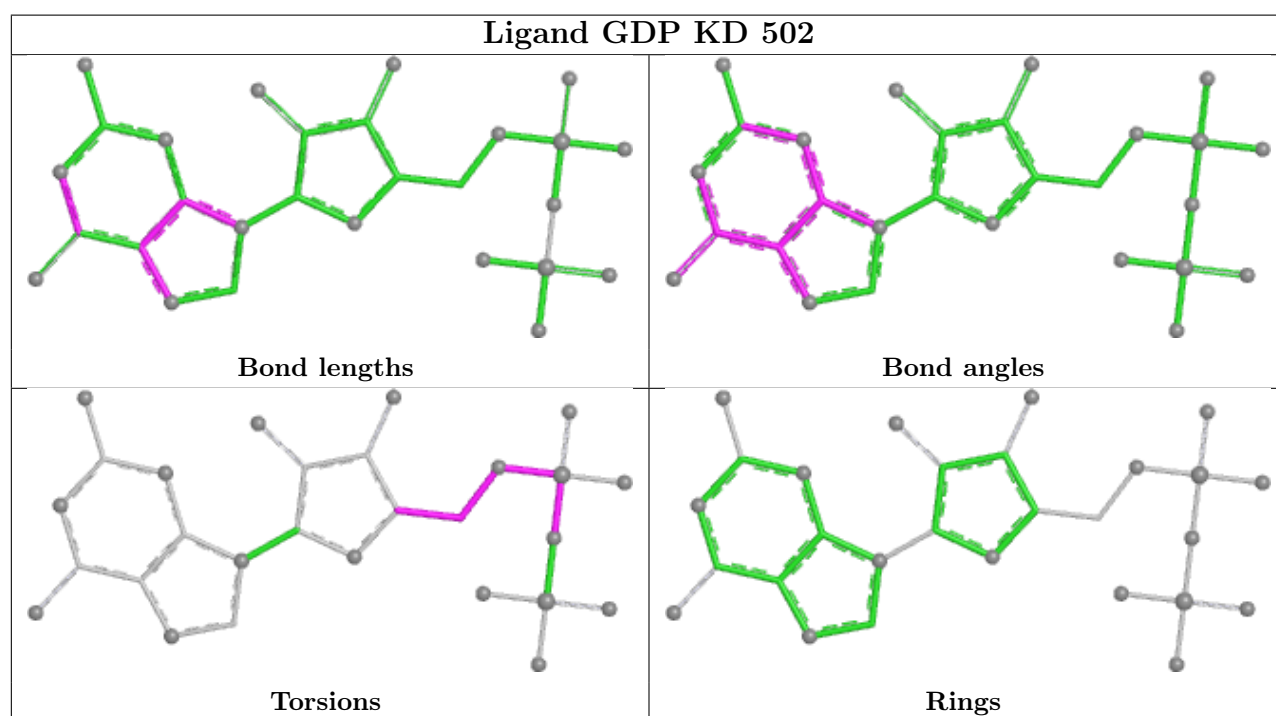
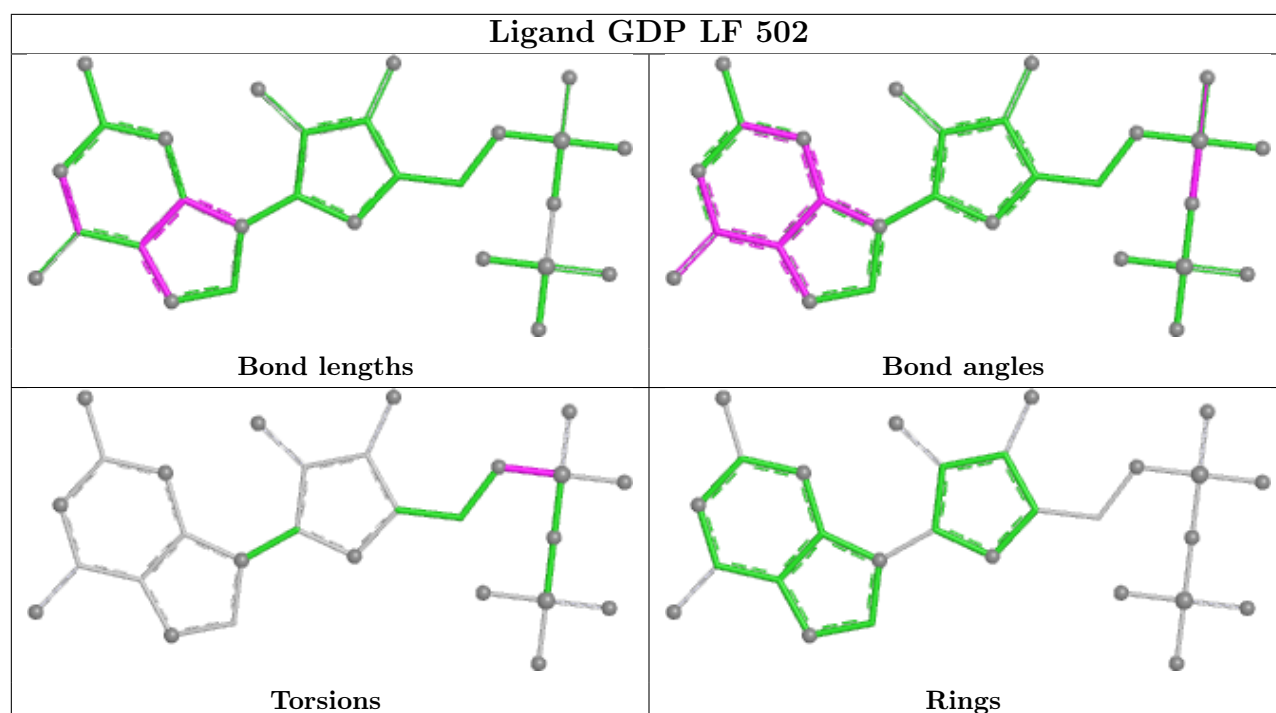


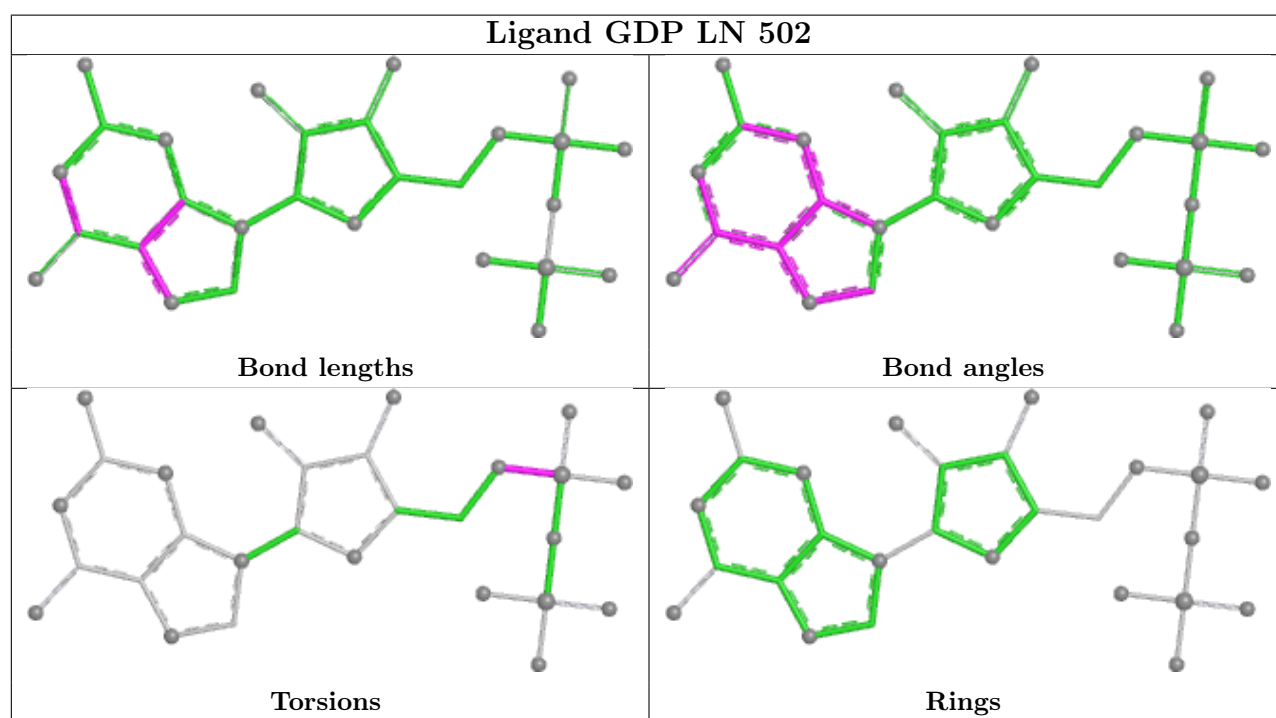
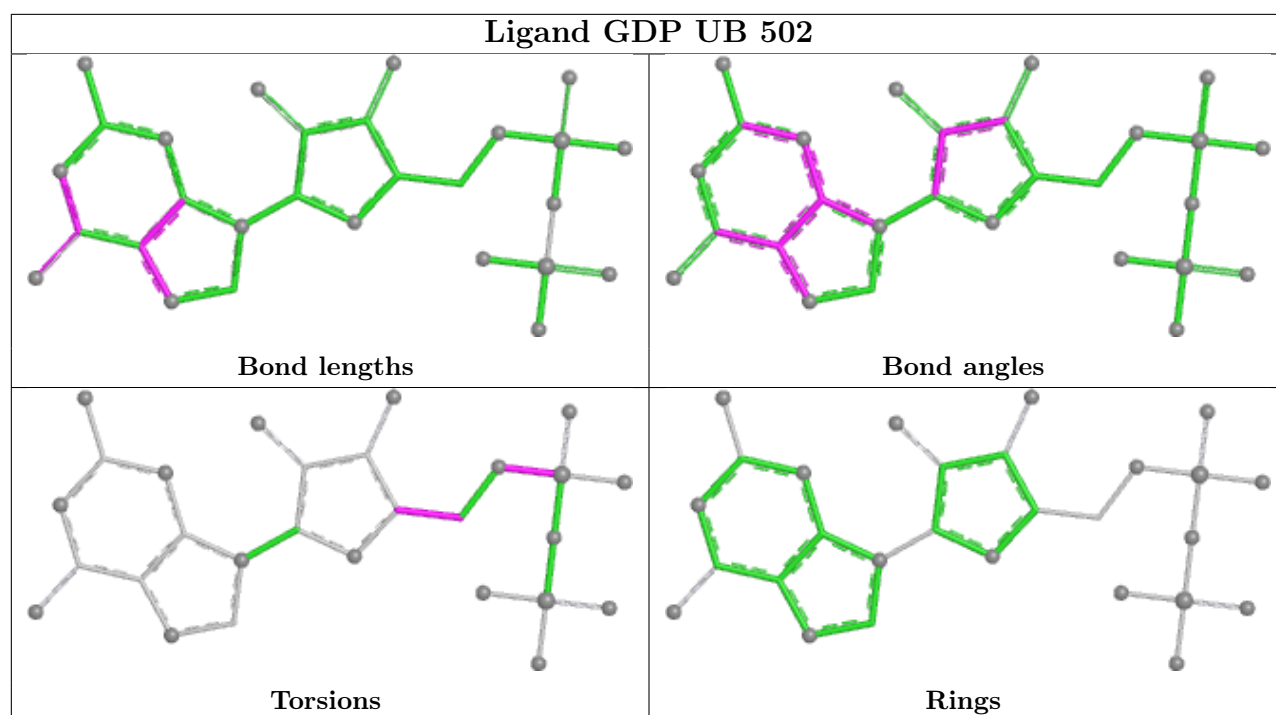


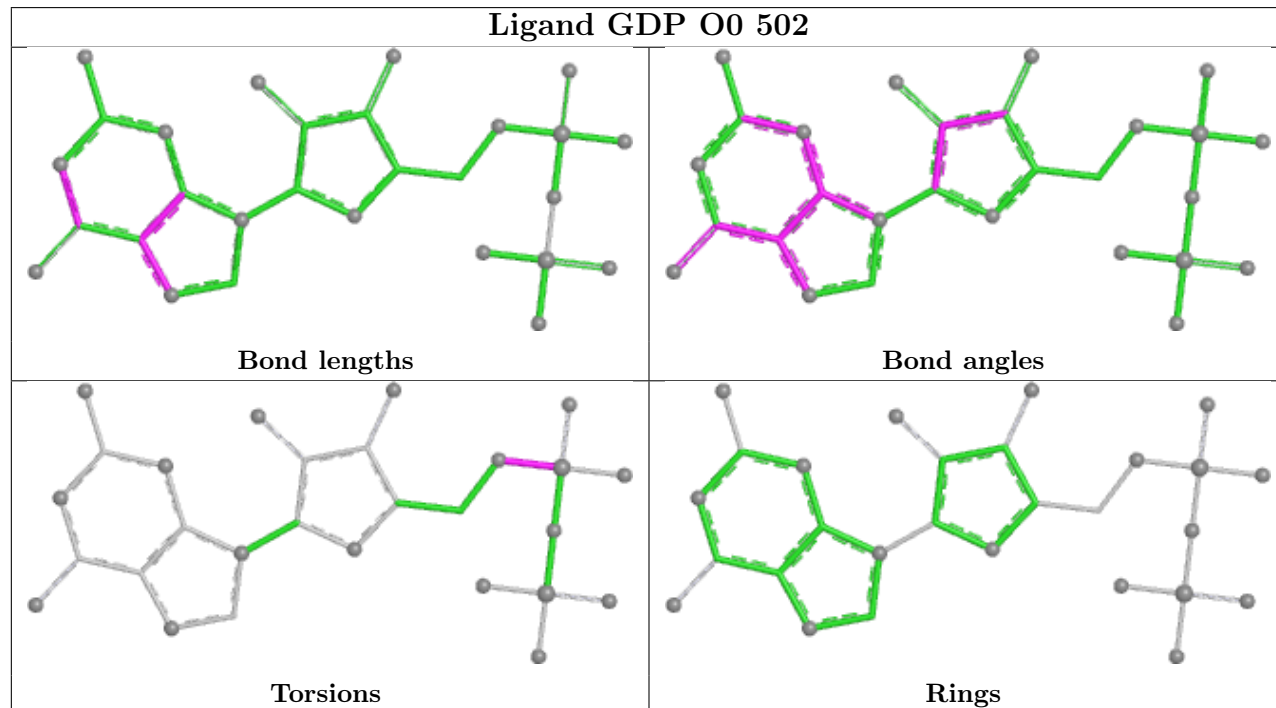
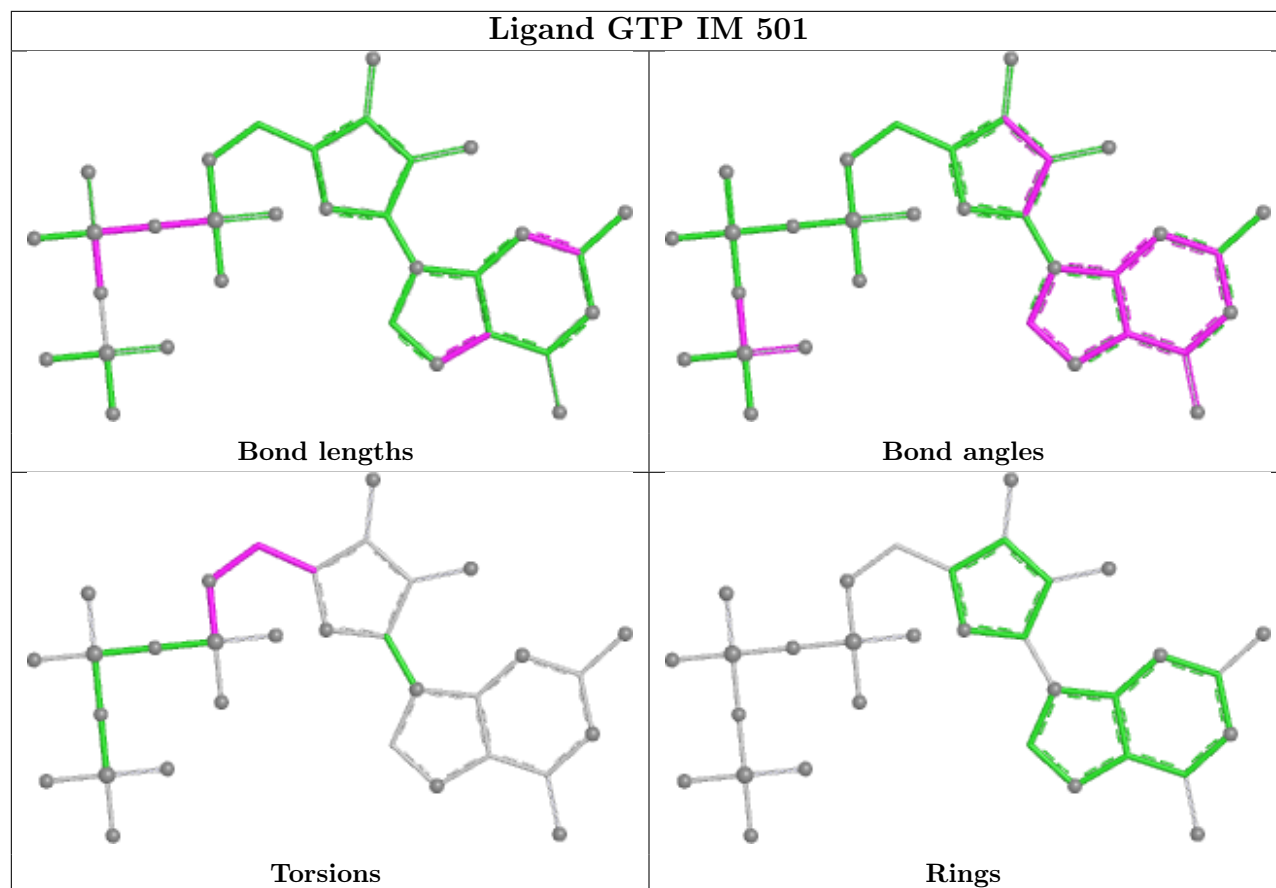




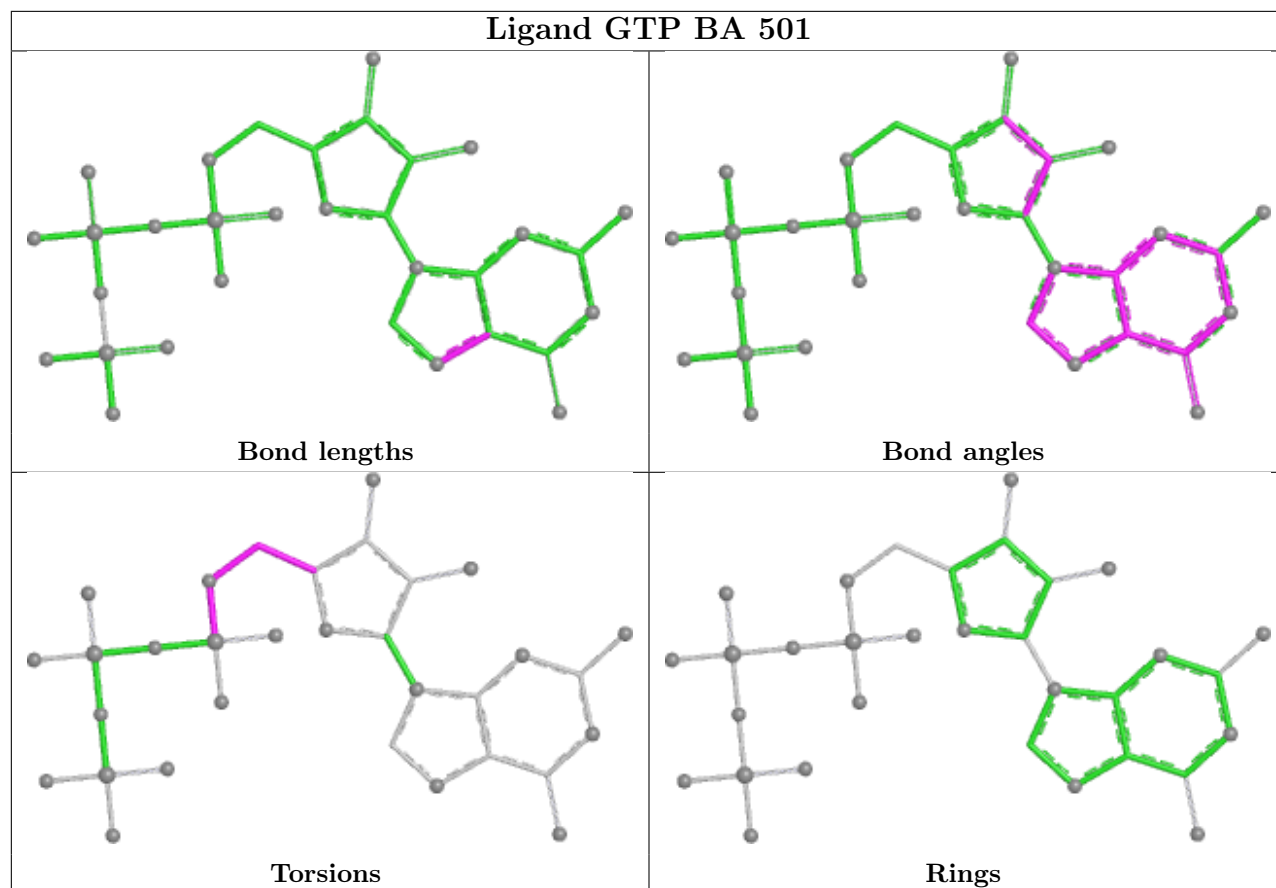




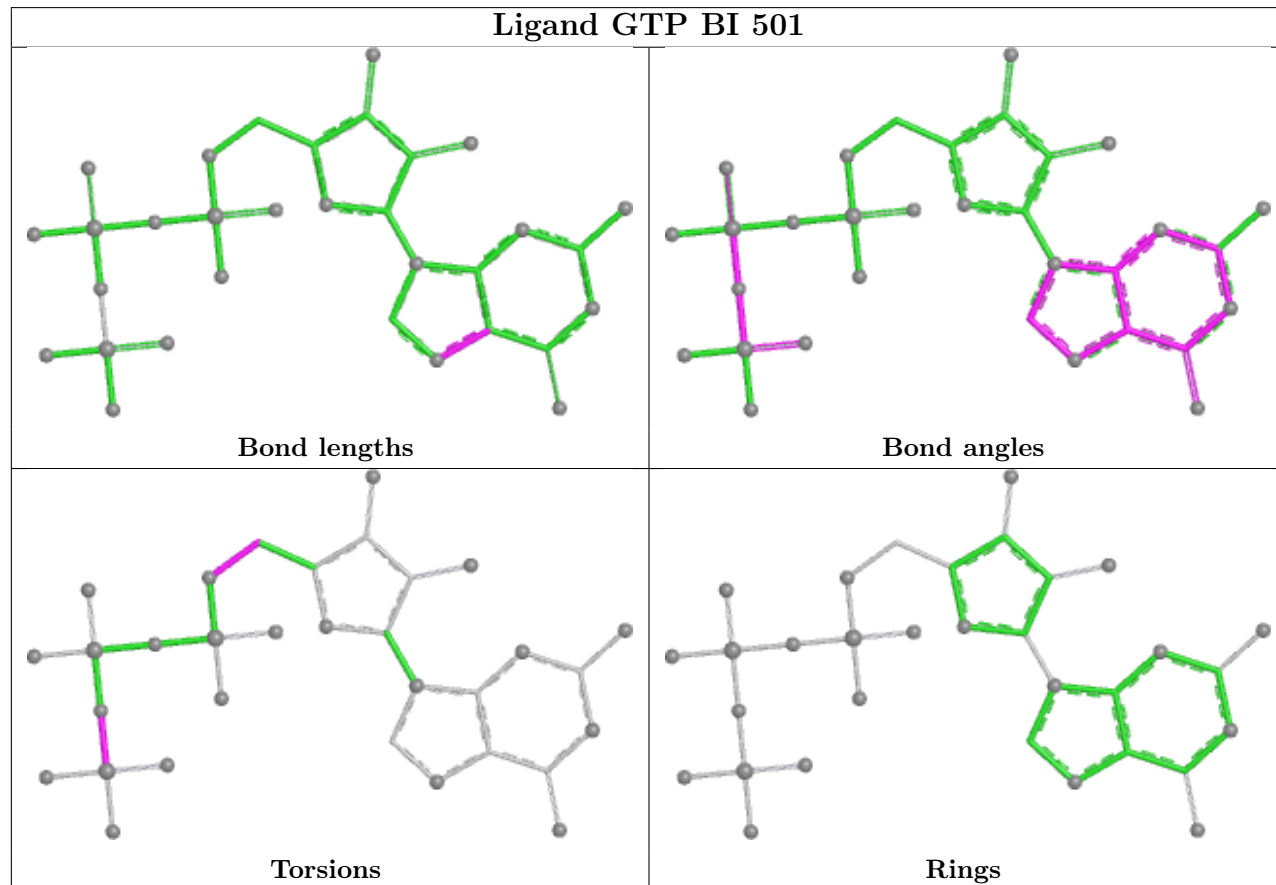


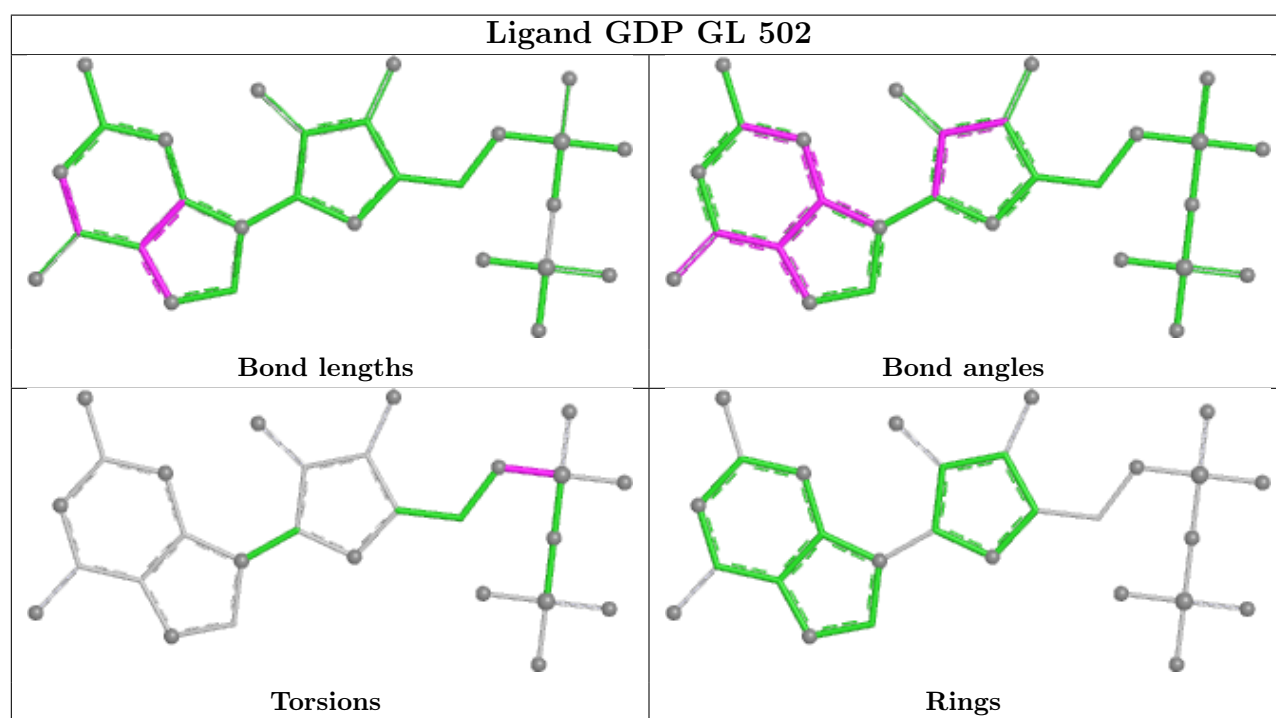
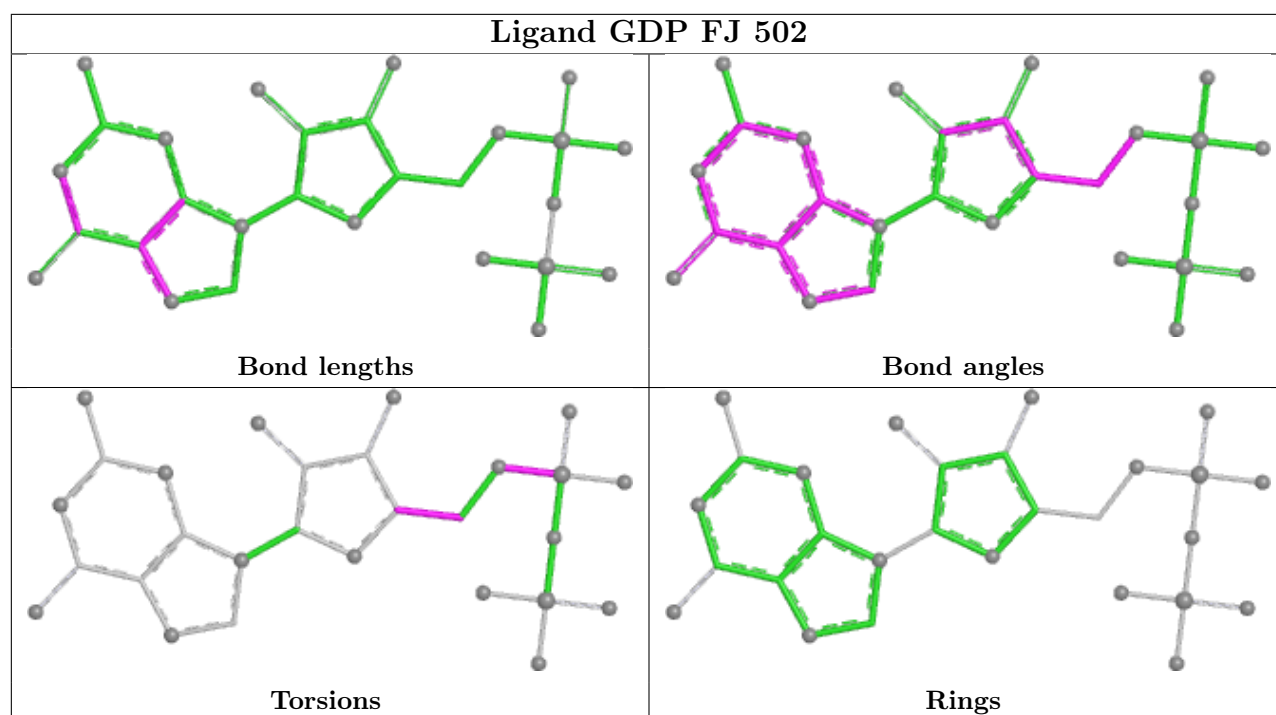


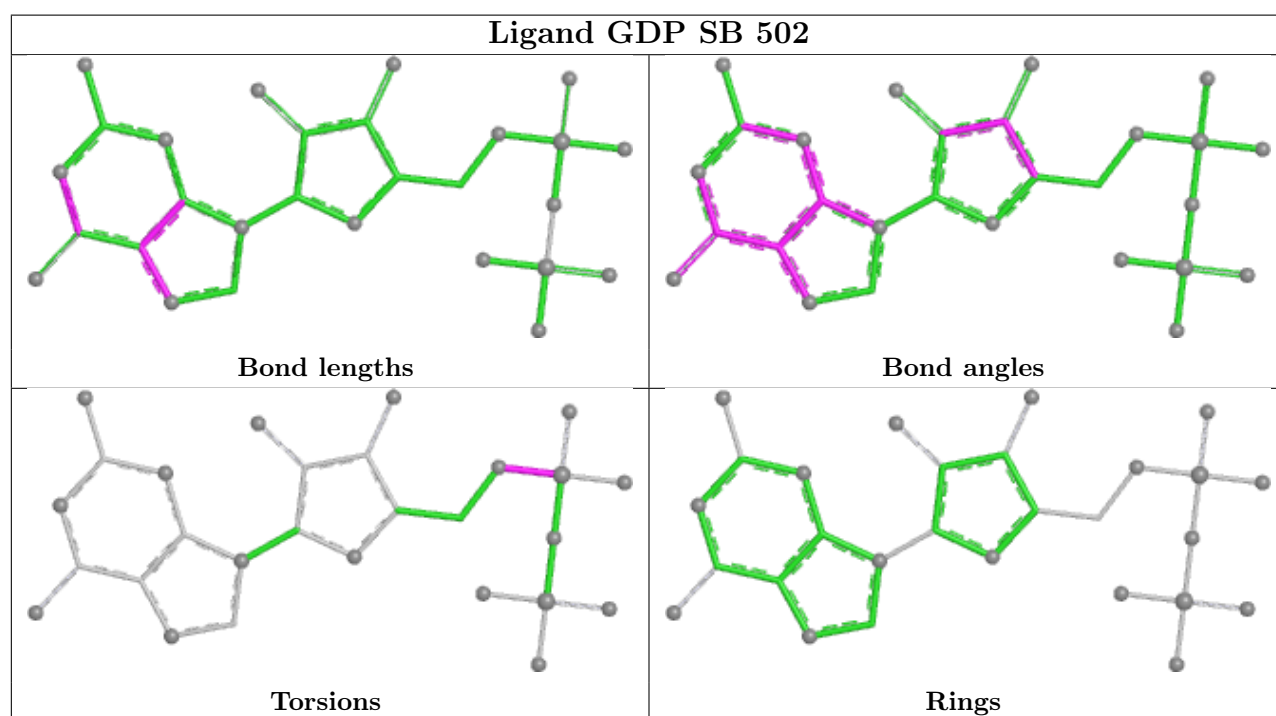
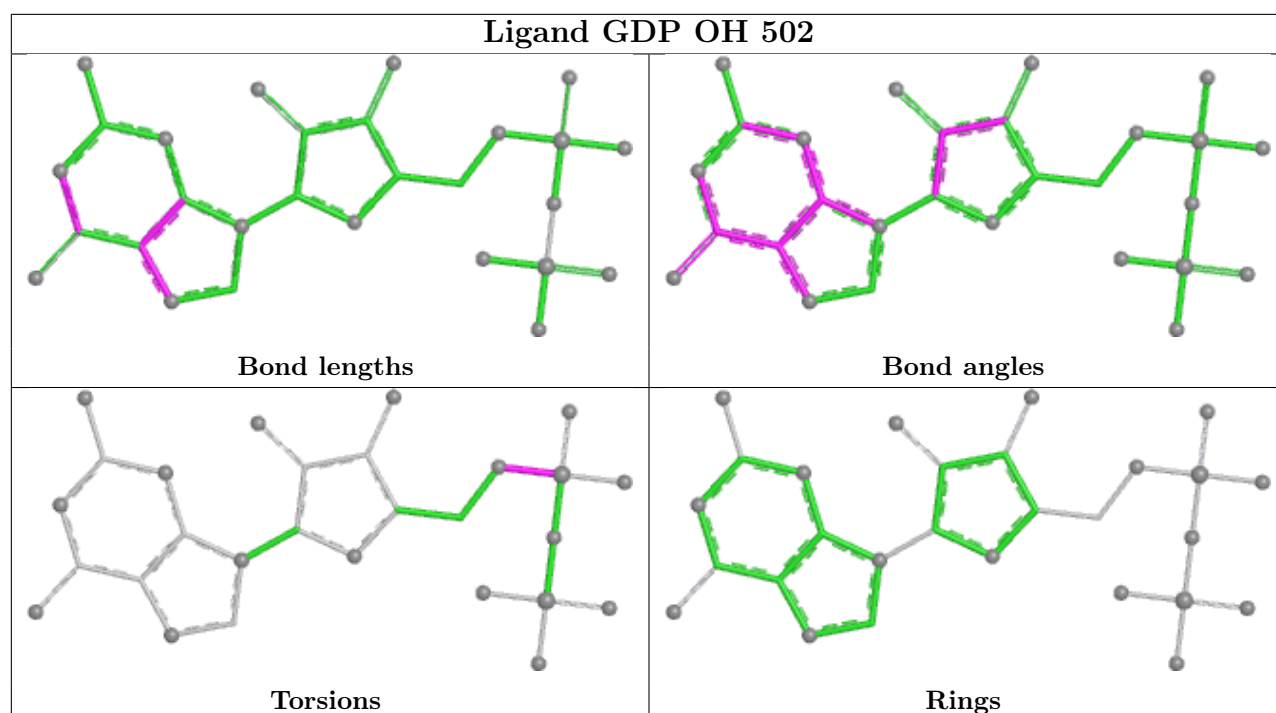
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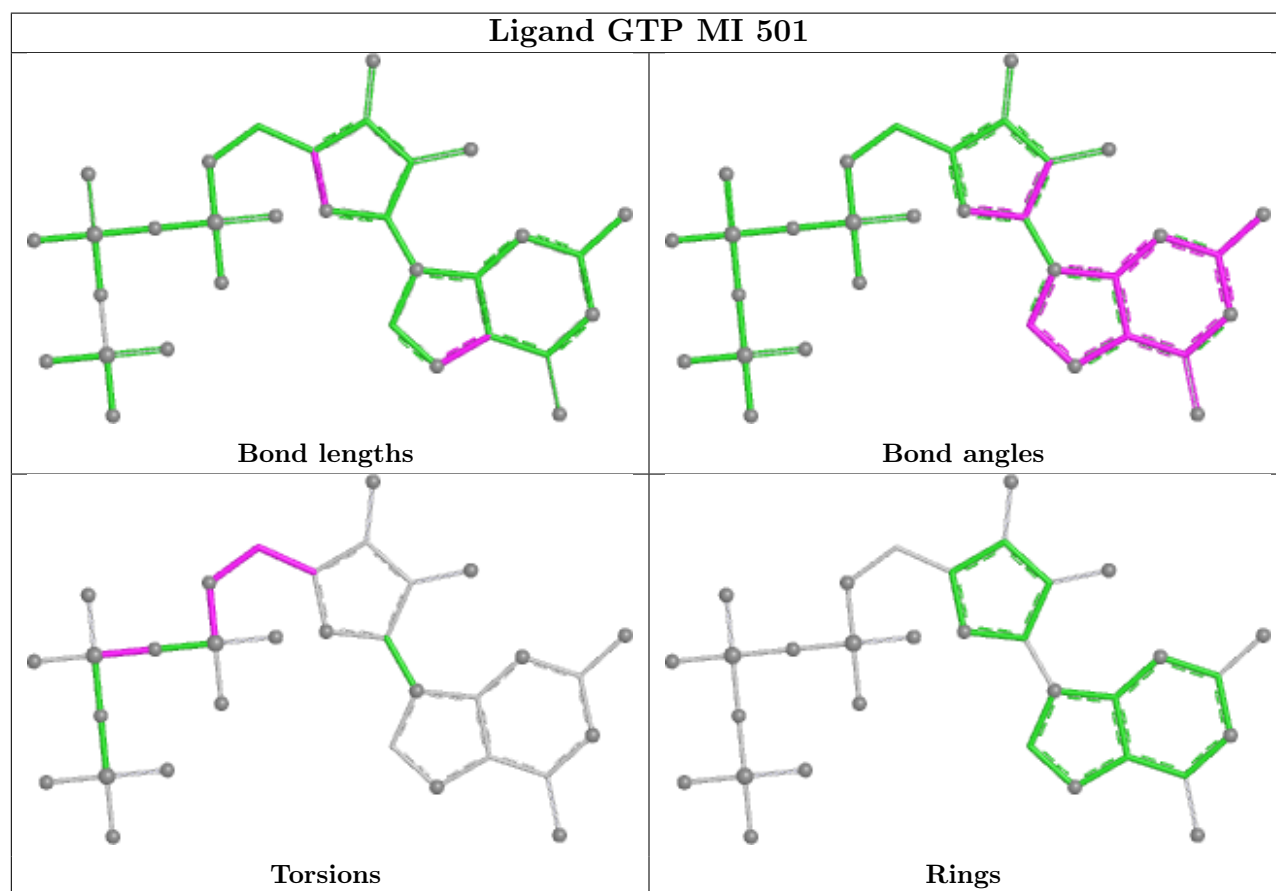
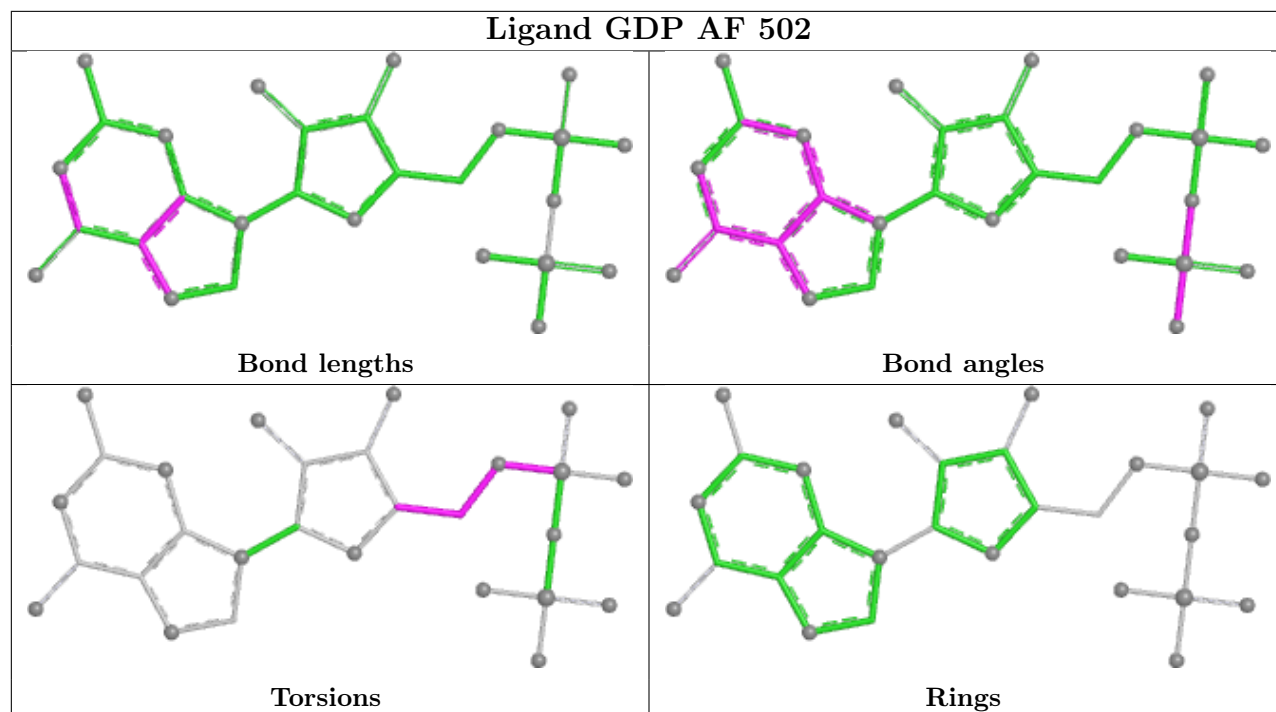


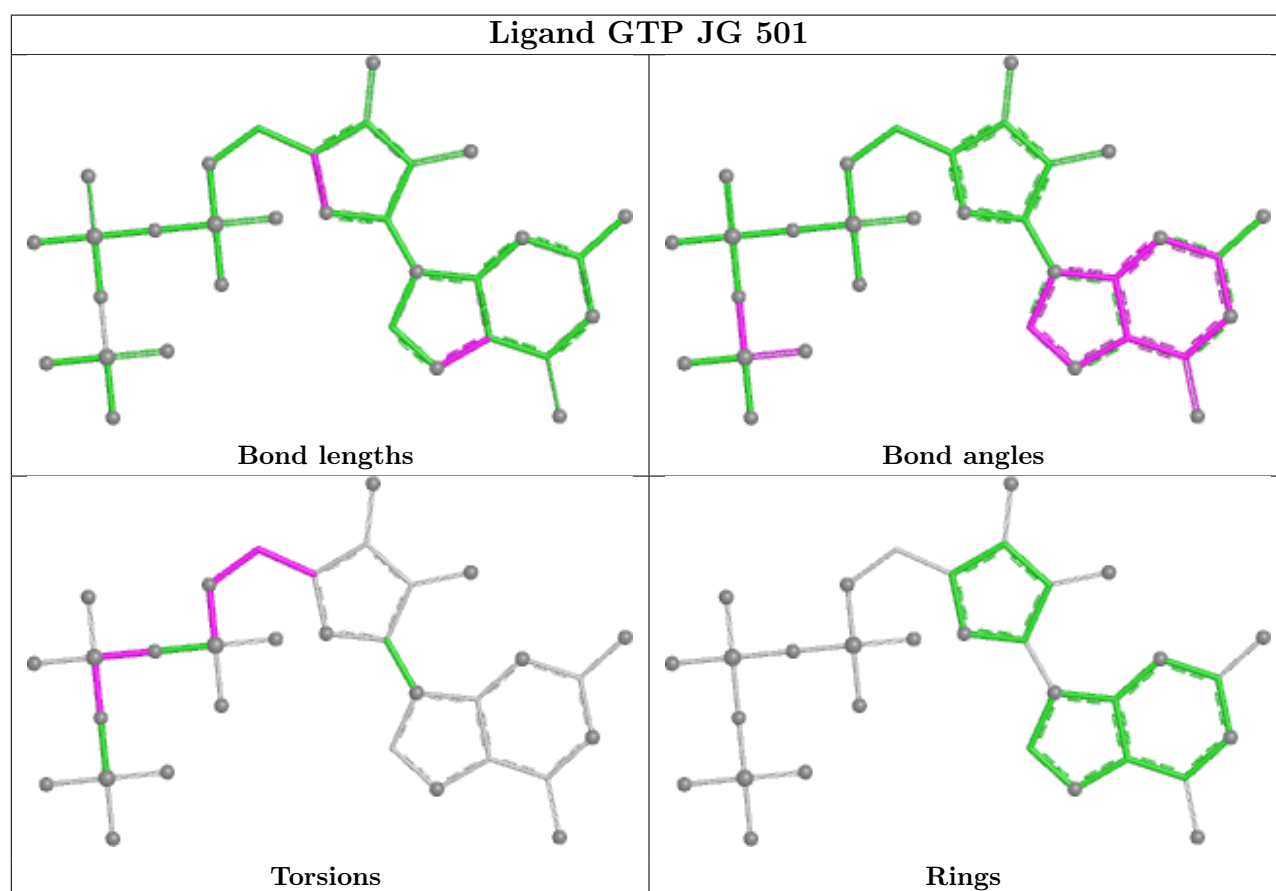
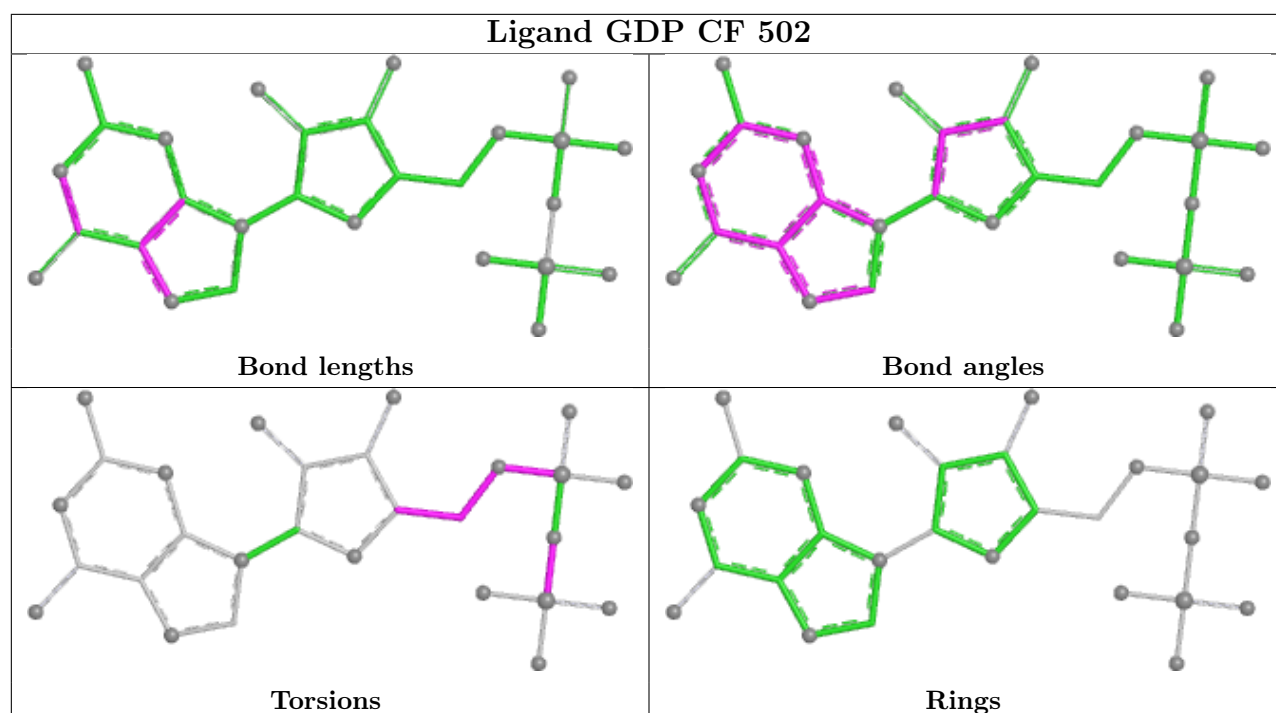
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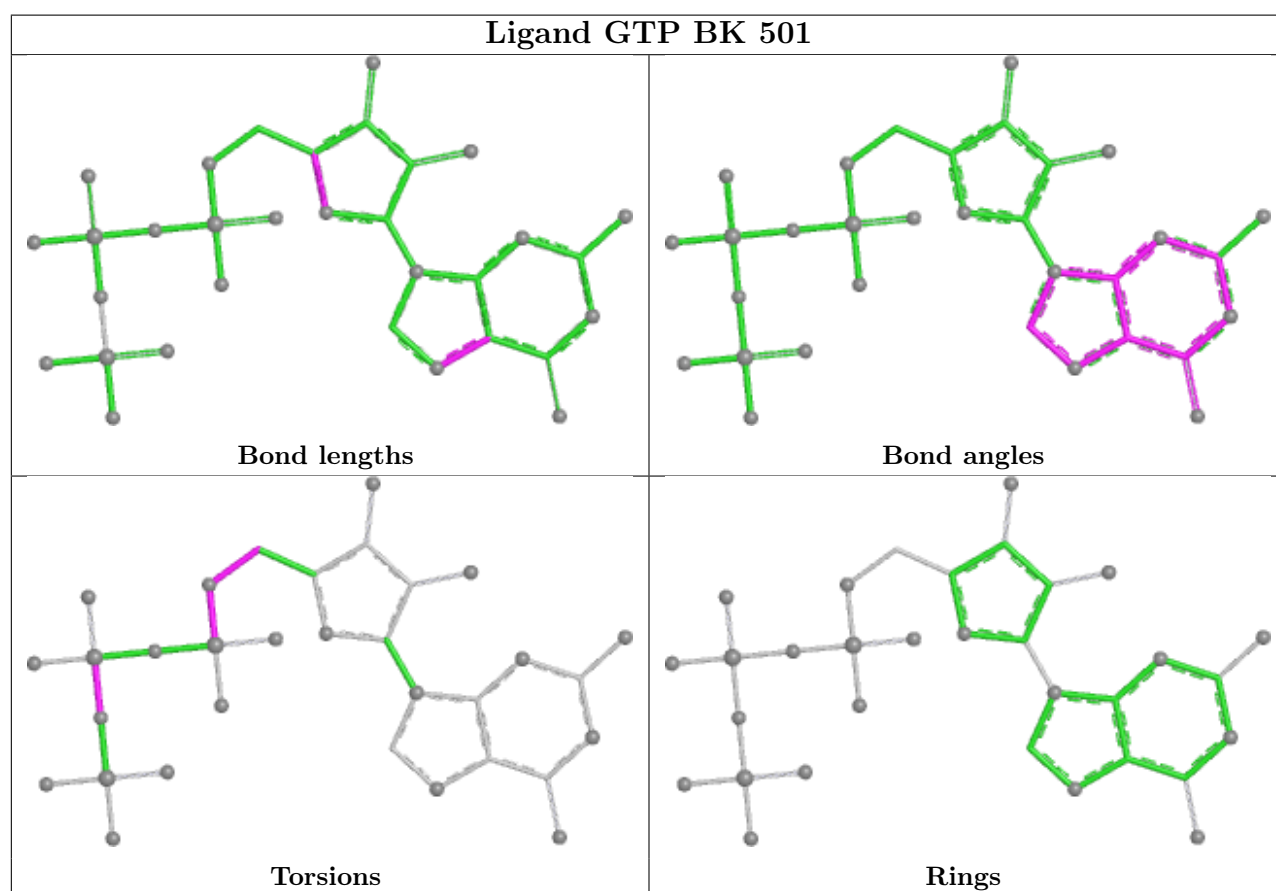
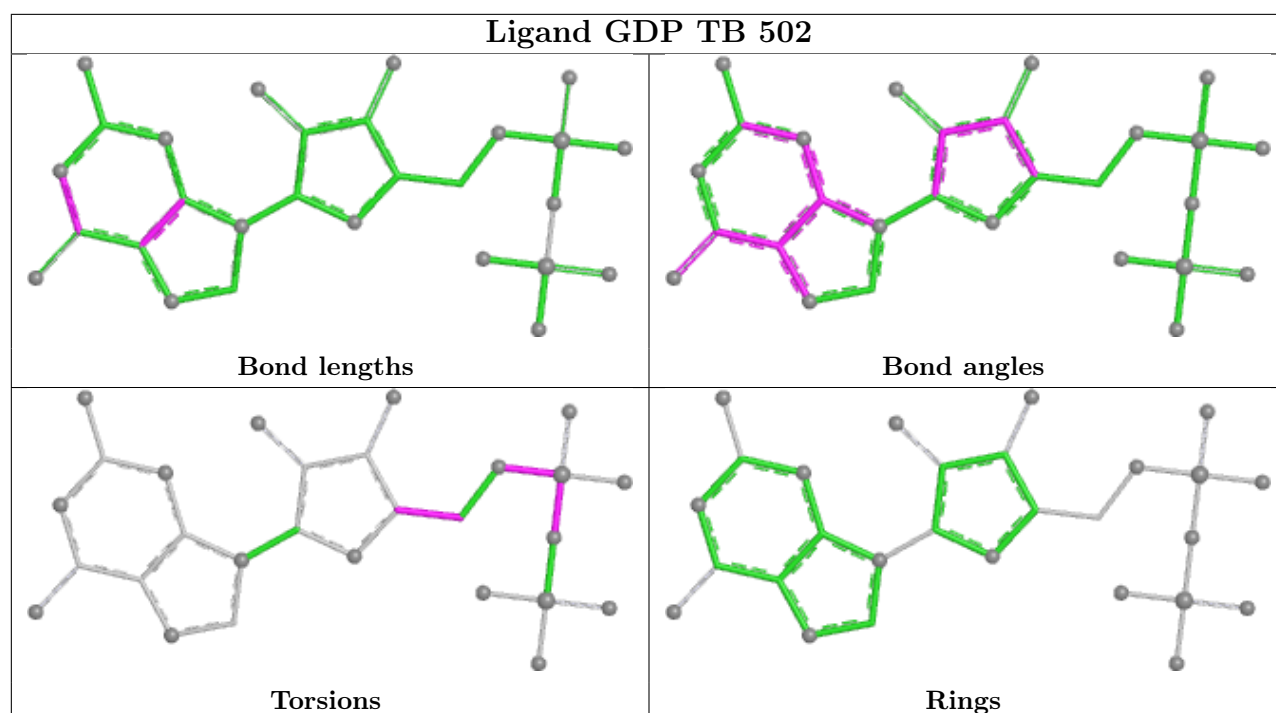


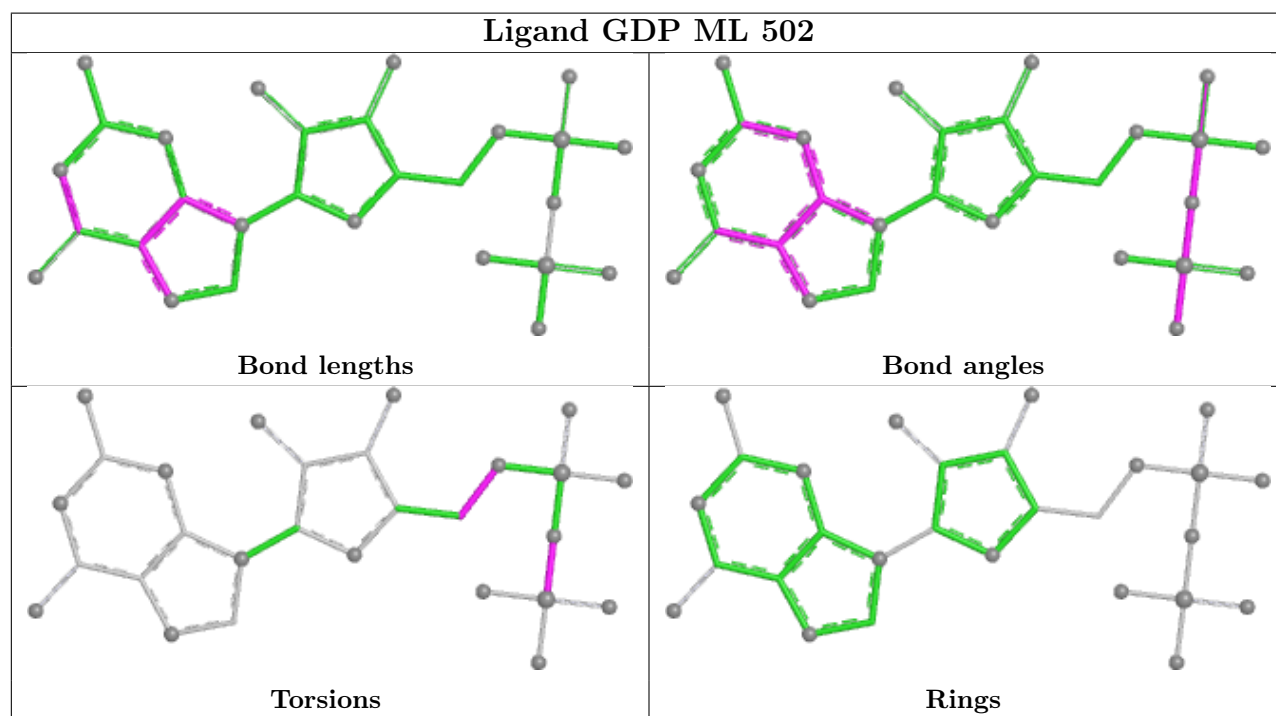
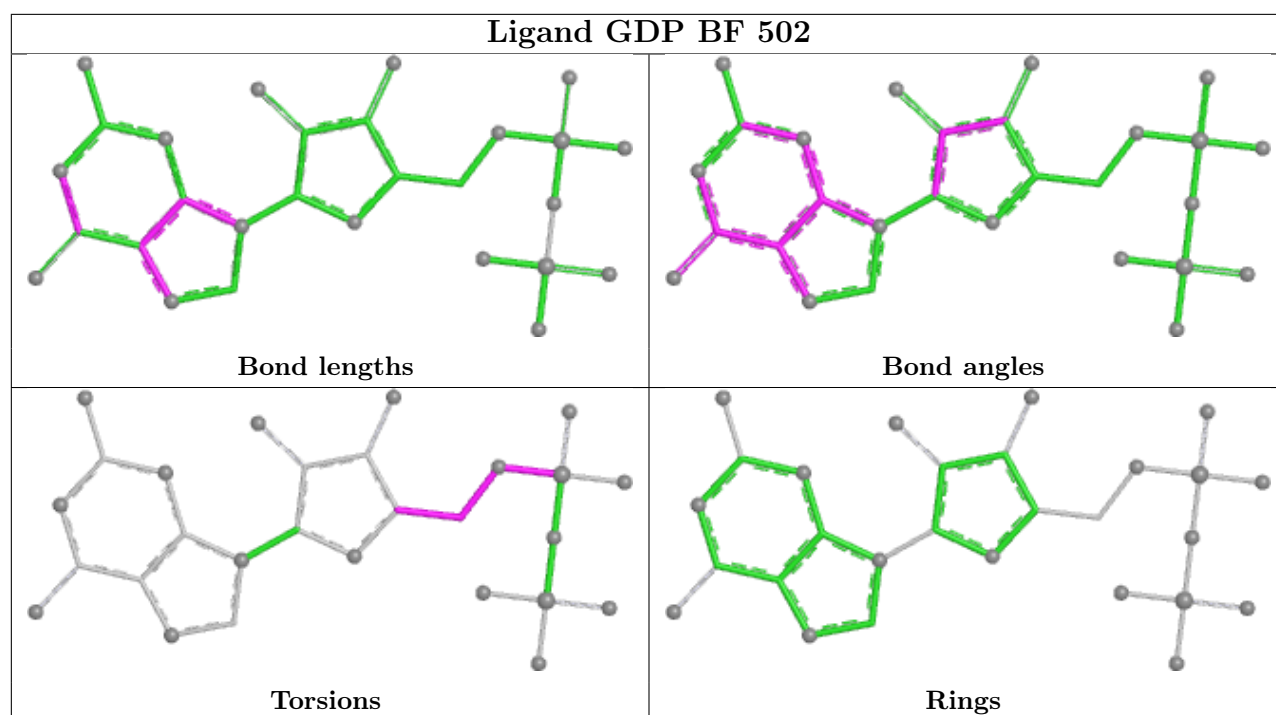


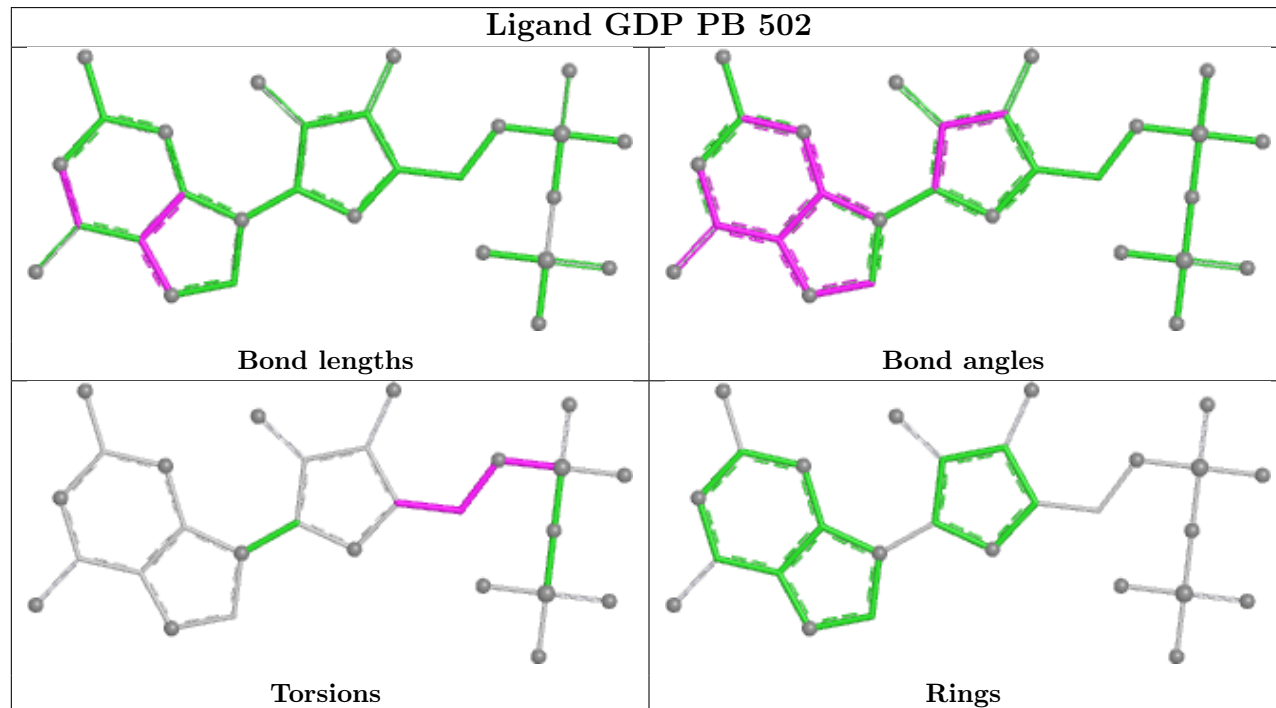
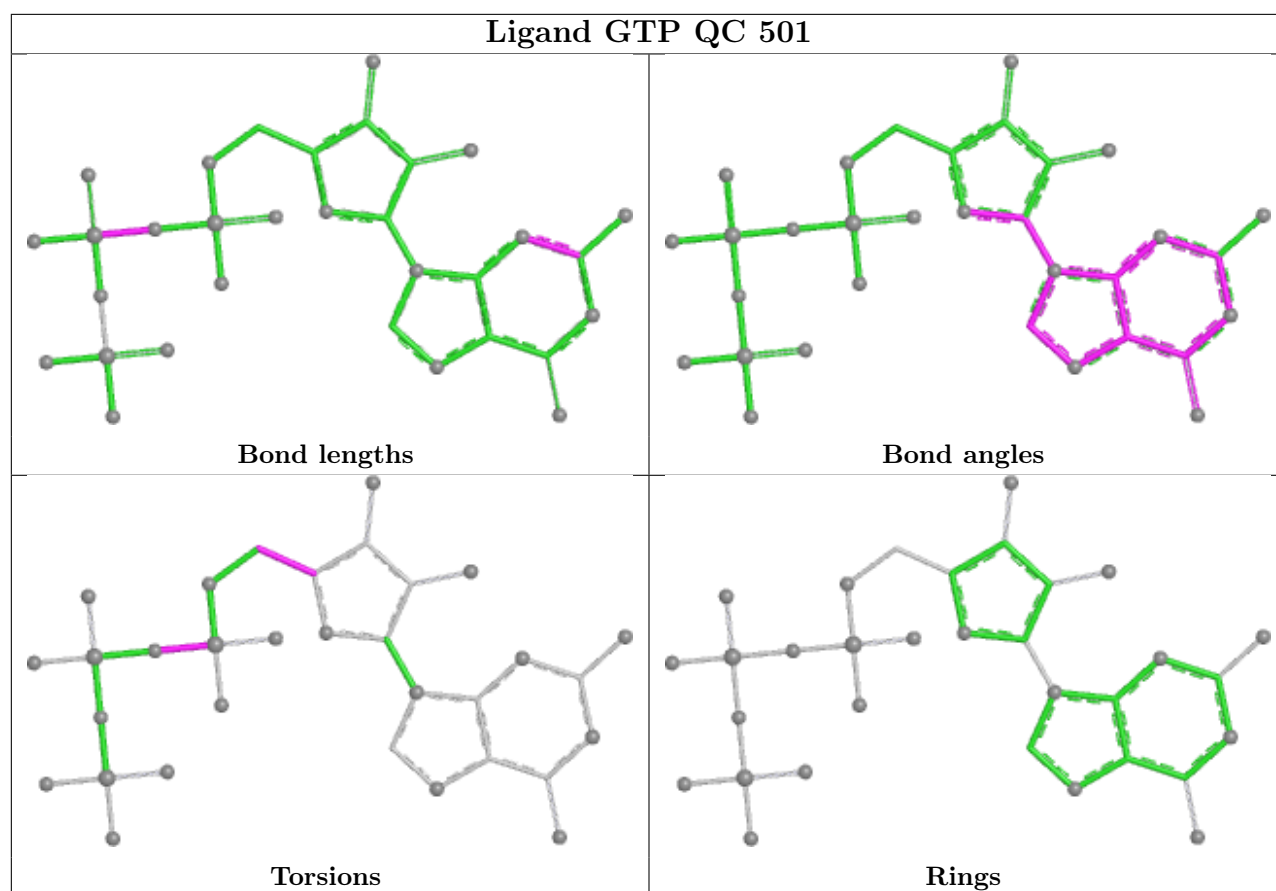


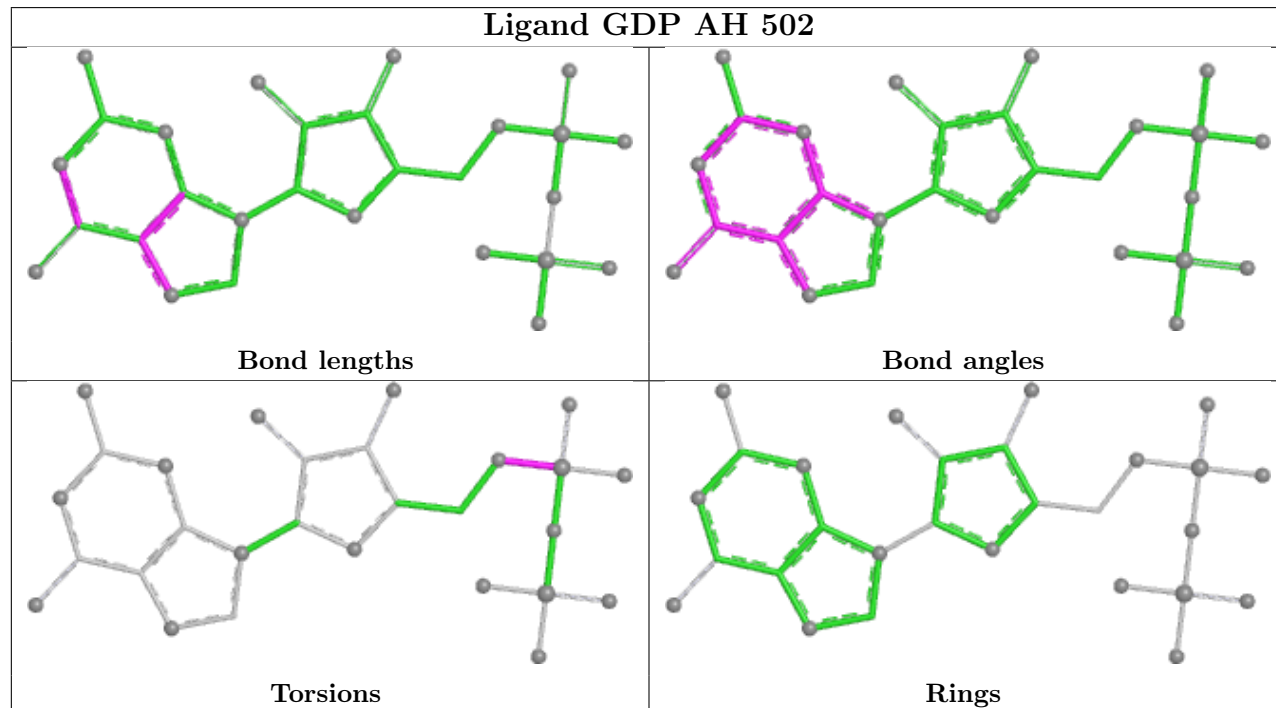
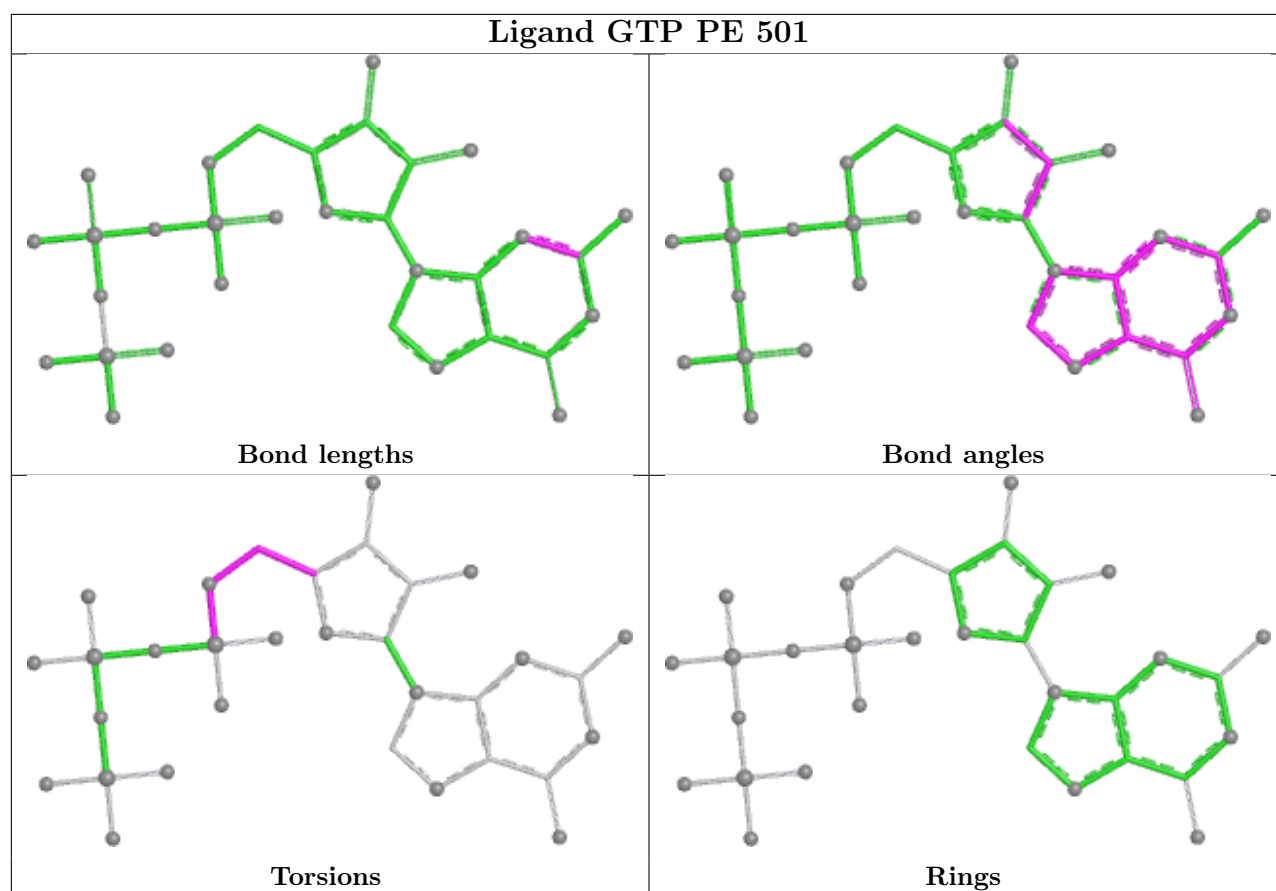


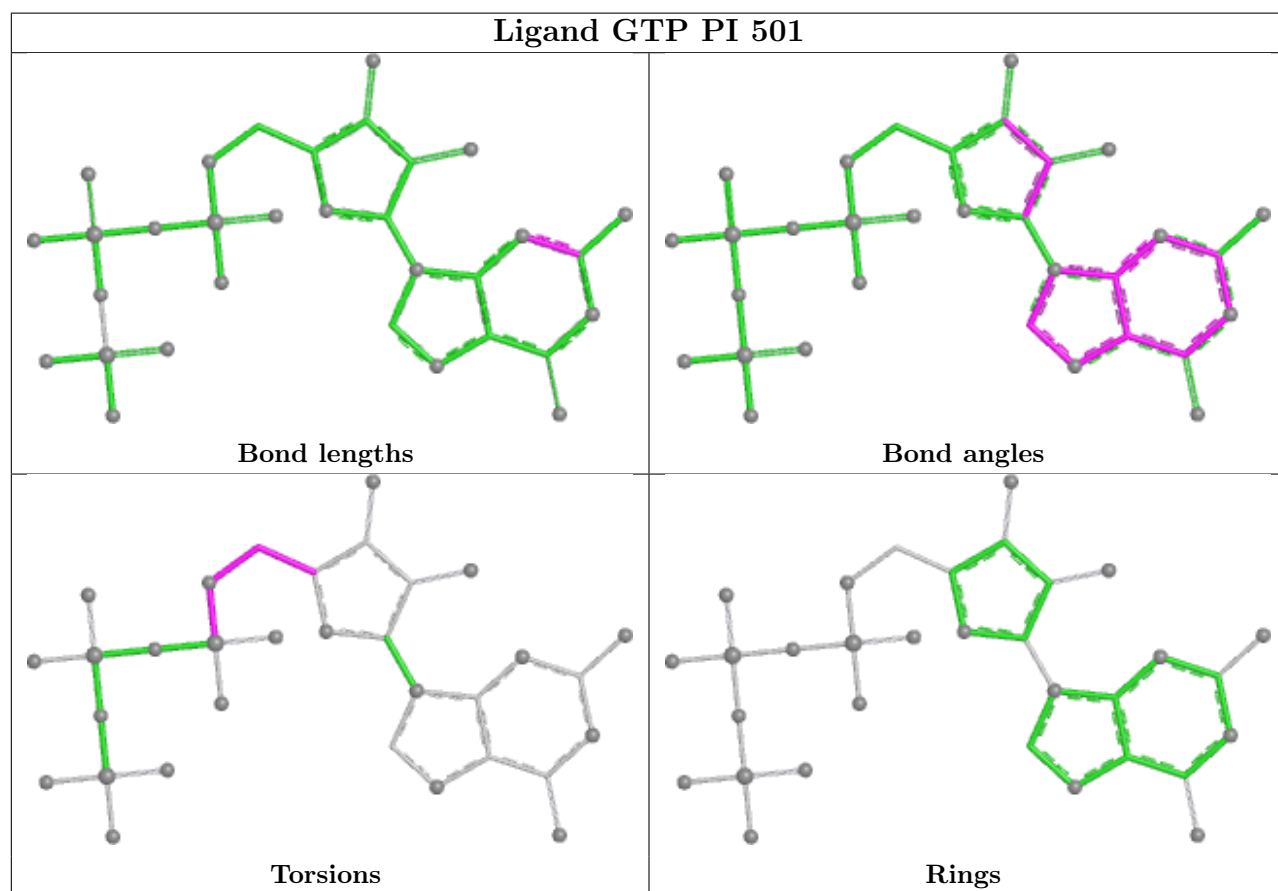
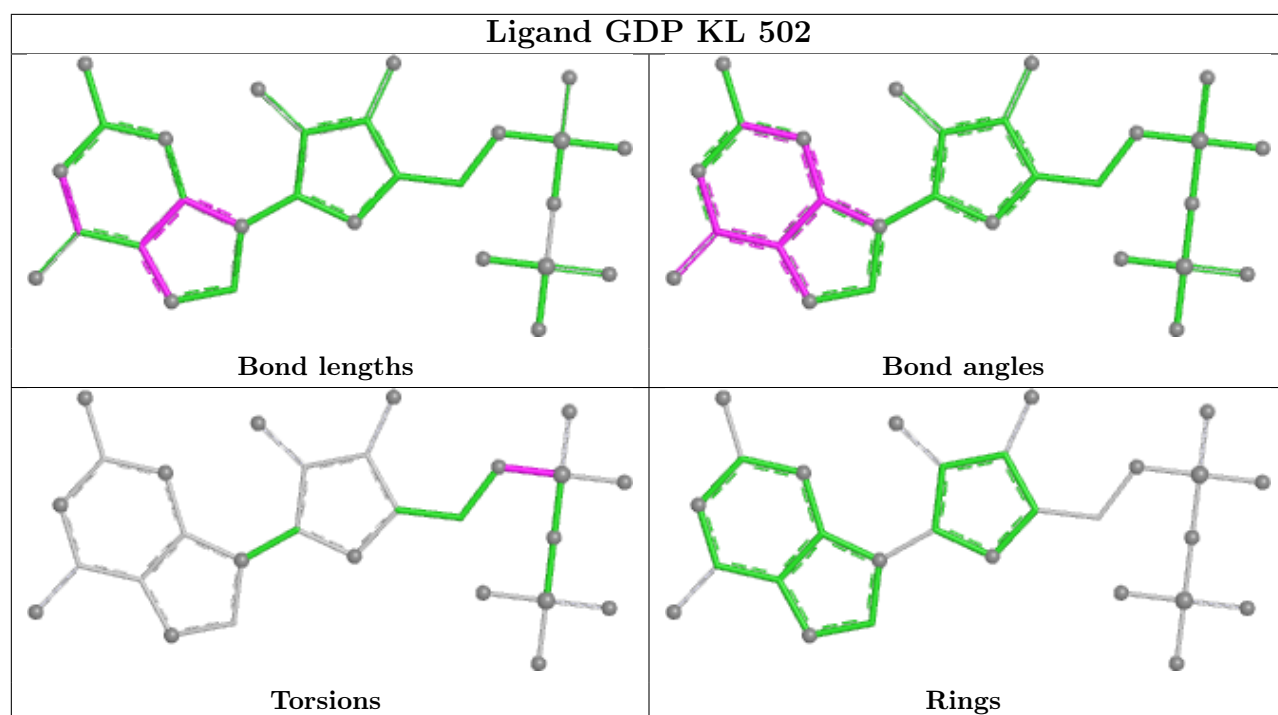


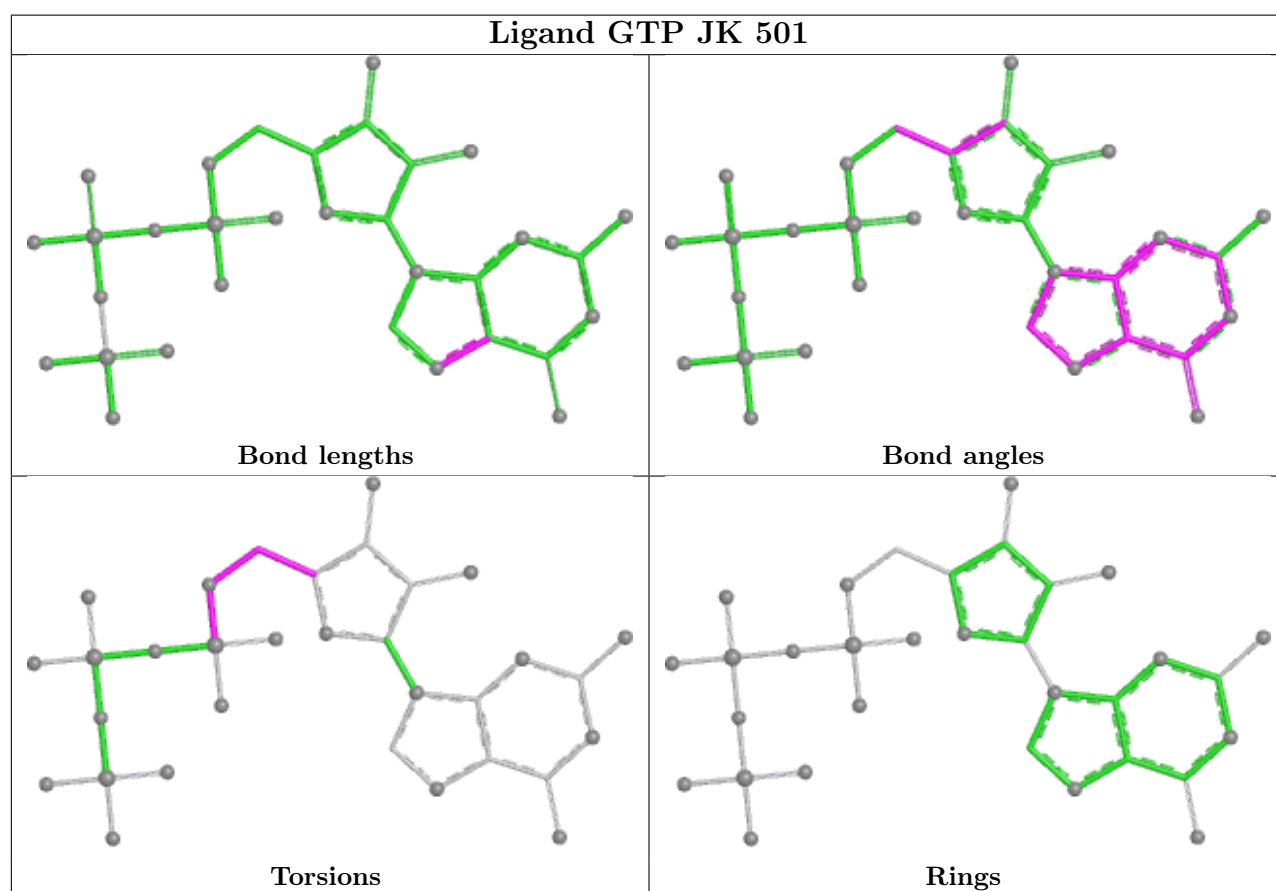
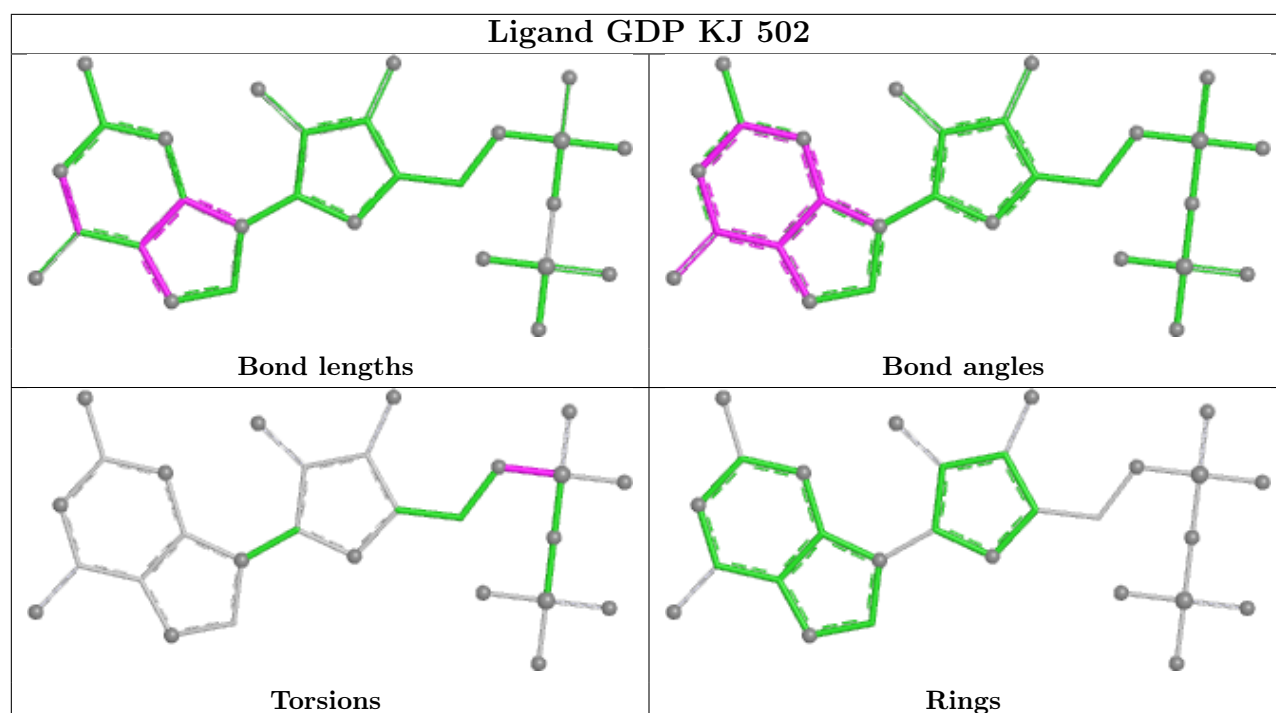




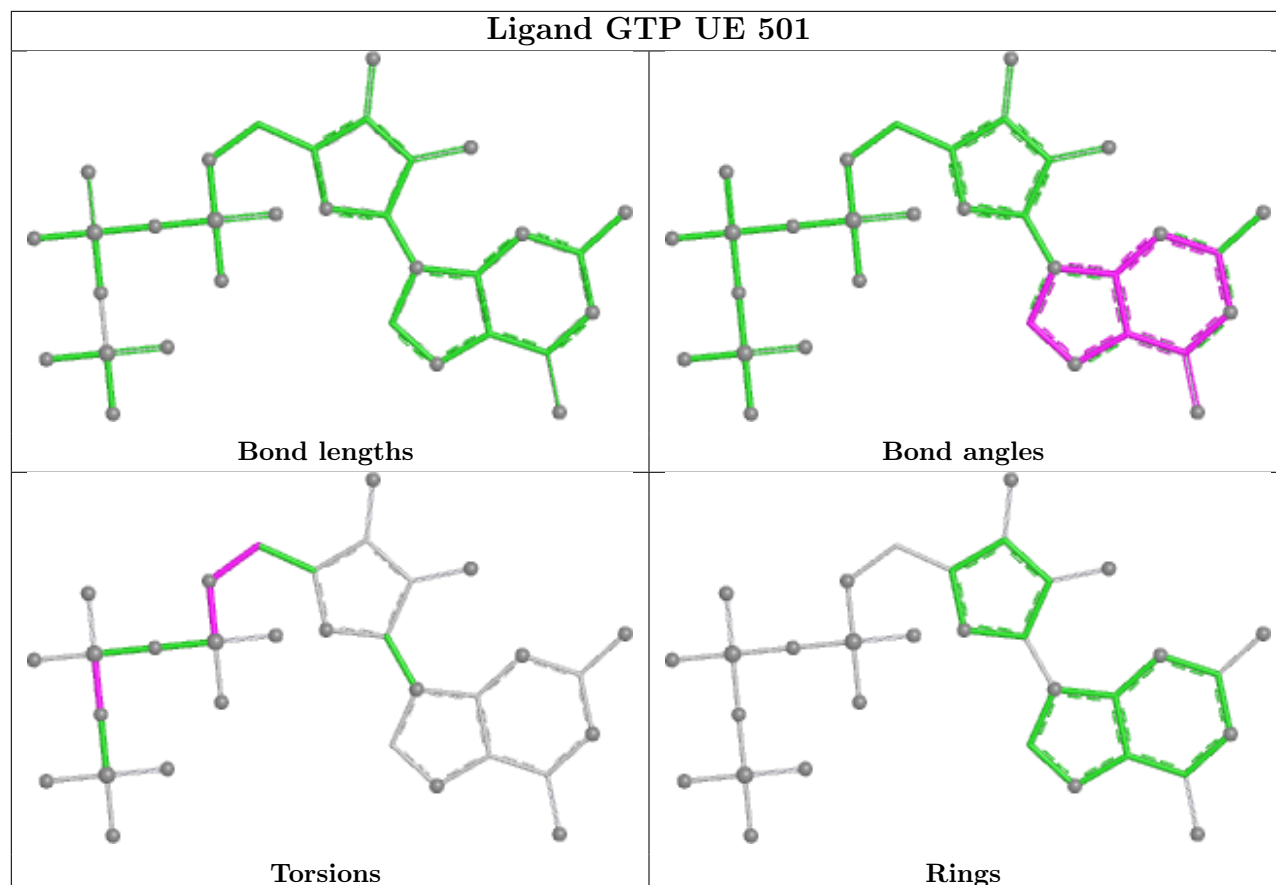




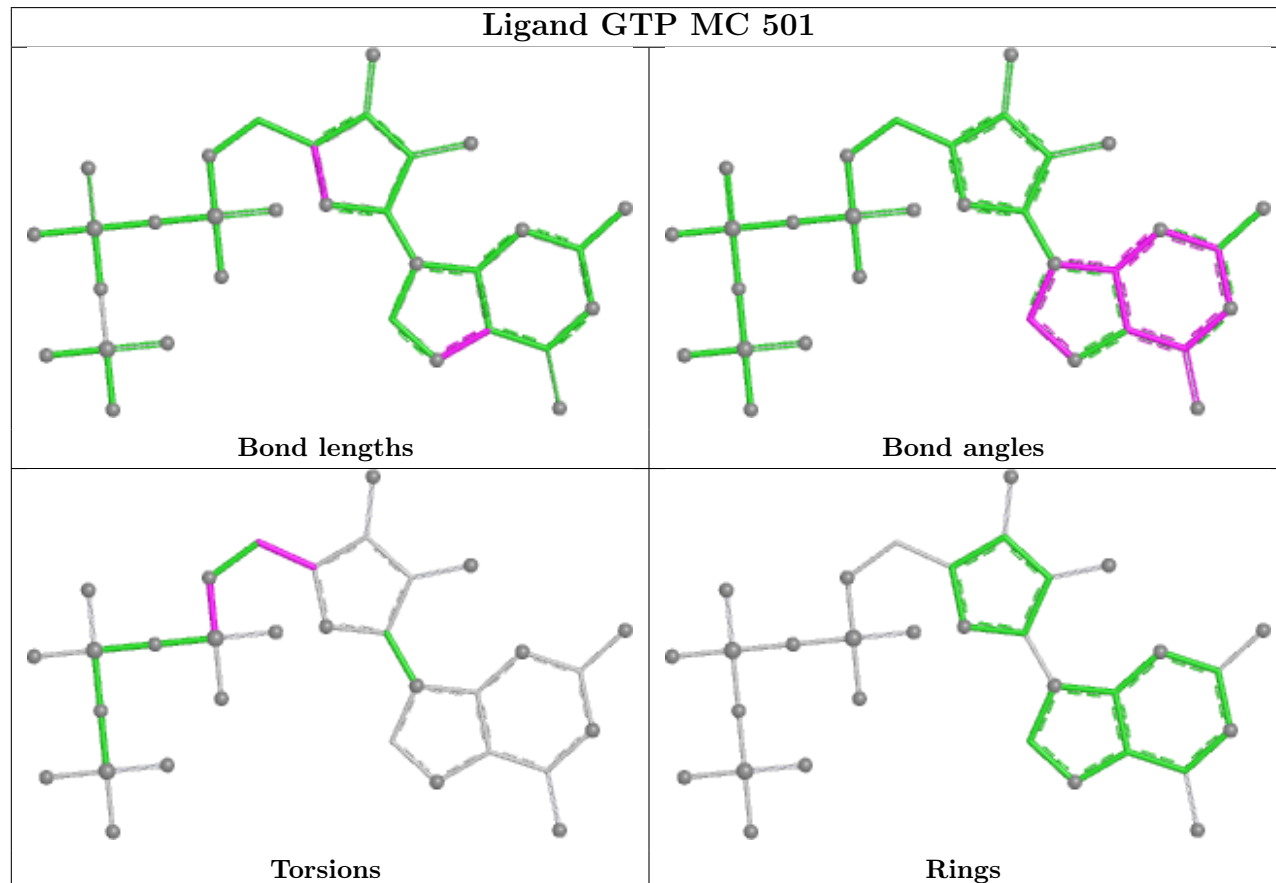




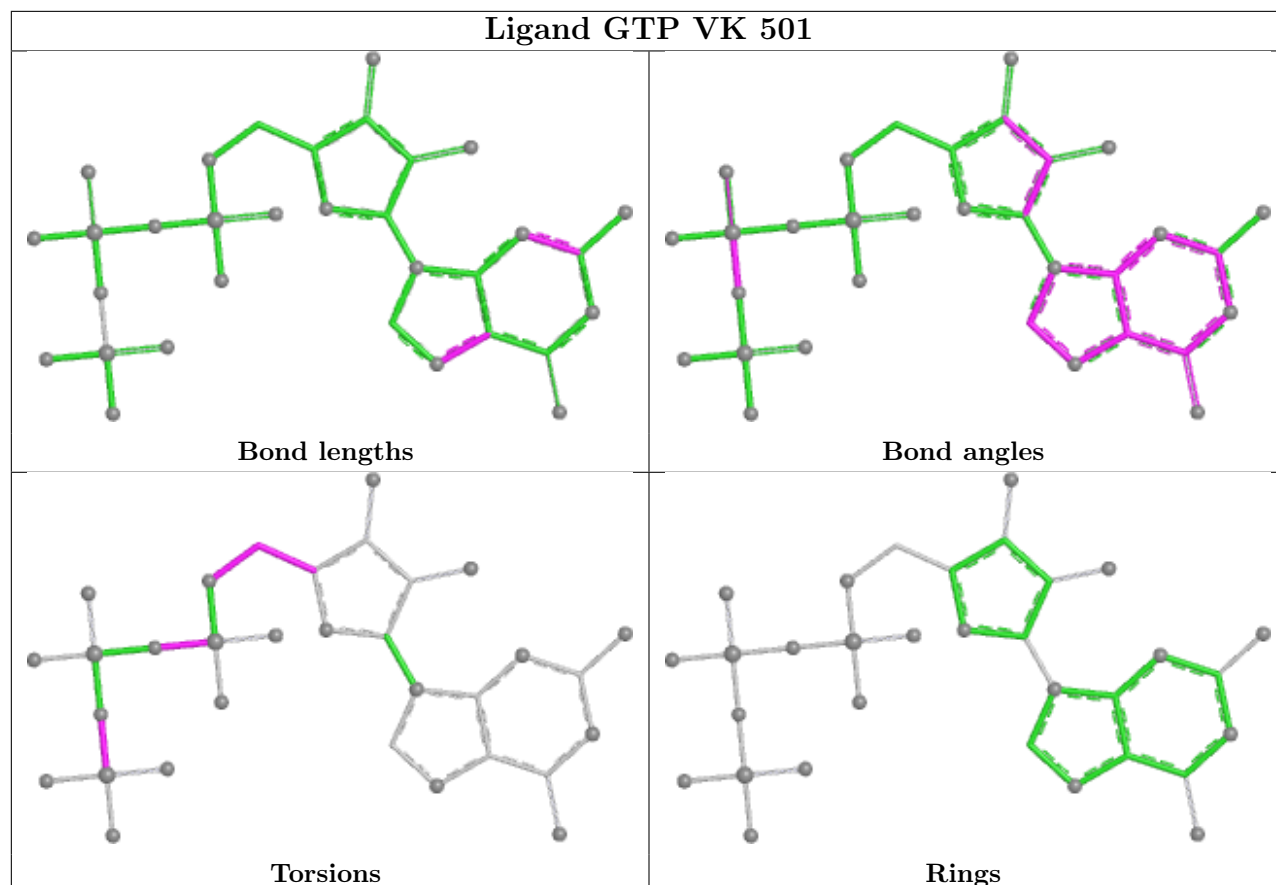
Ligand GTP UE 501



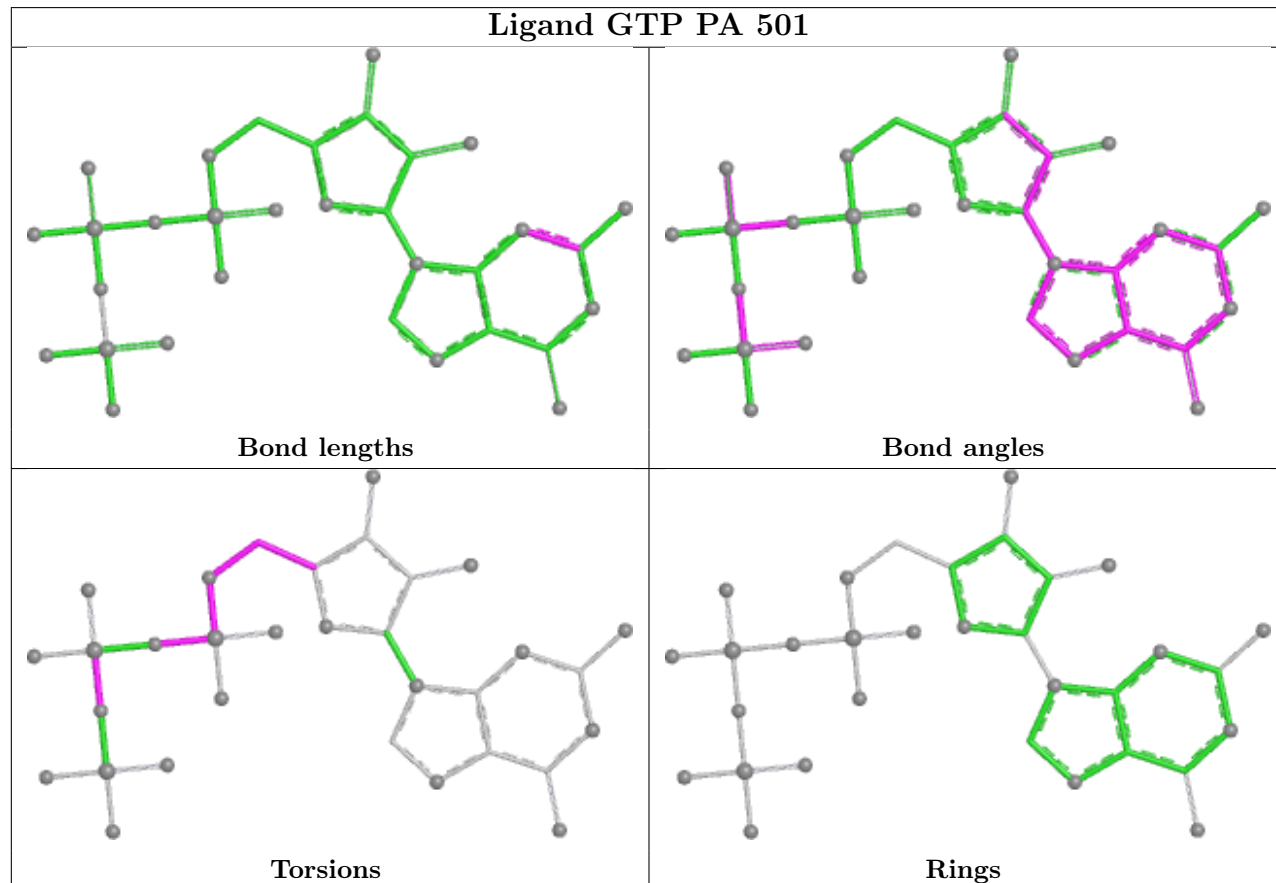
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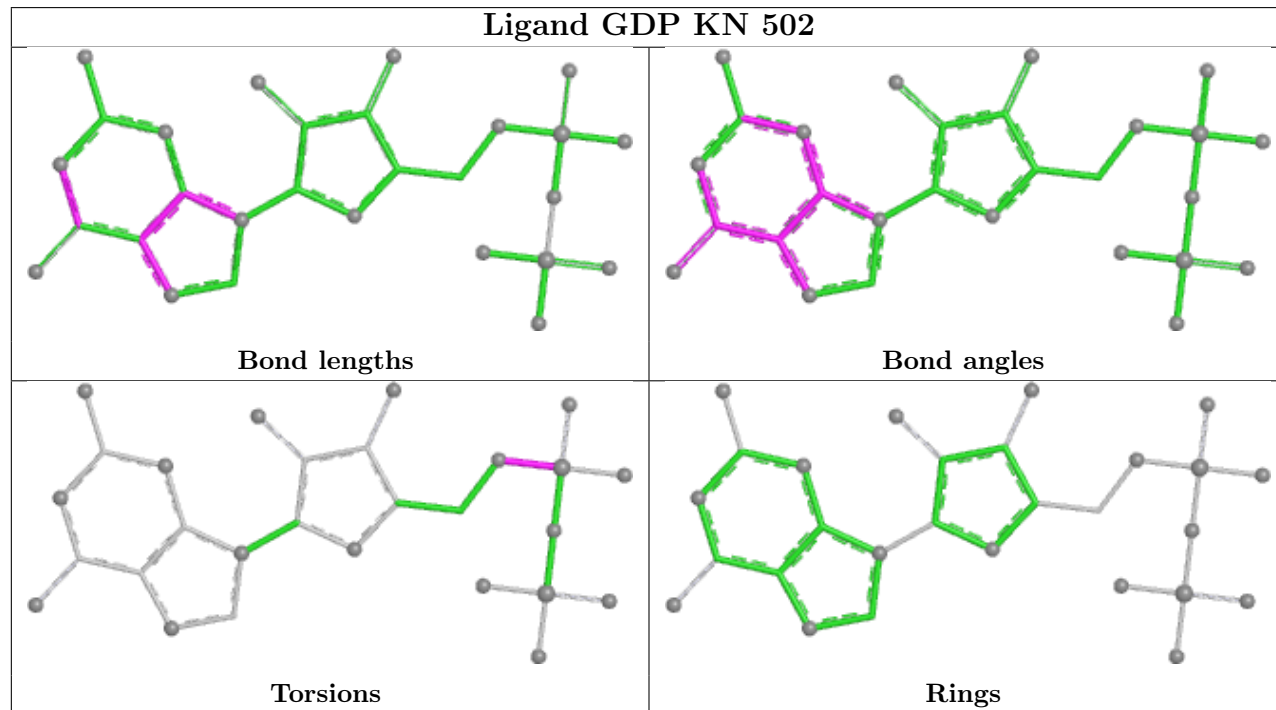
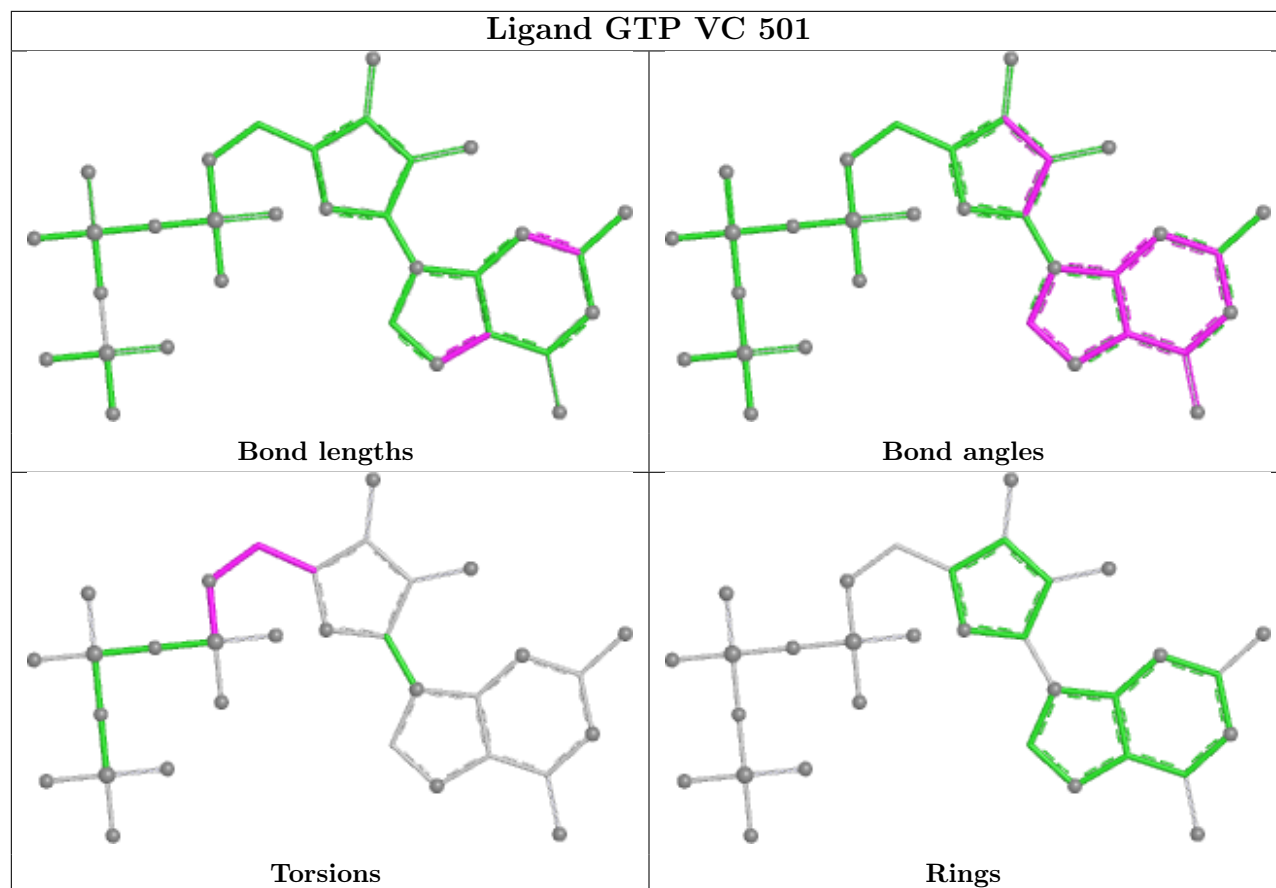


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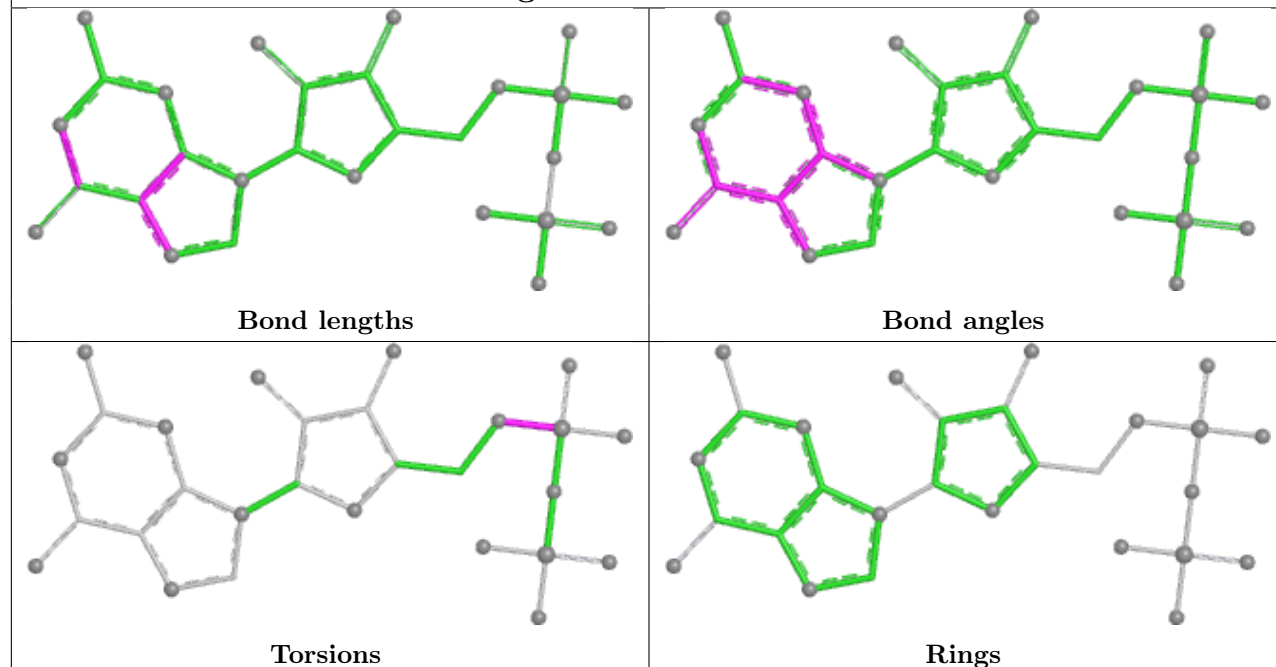


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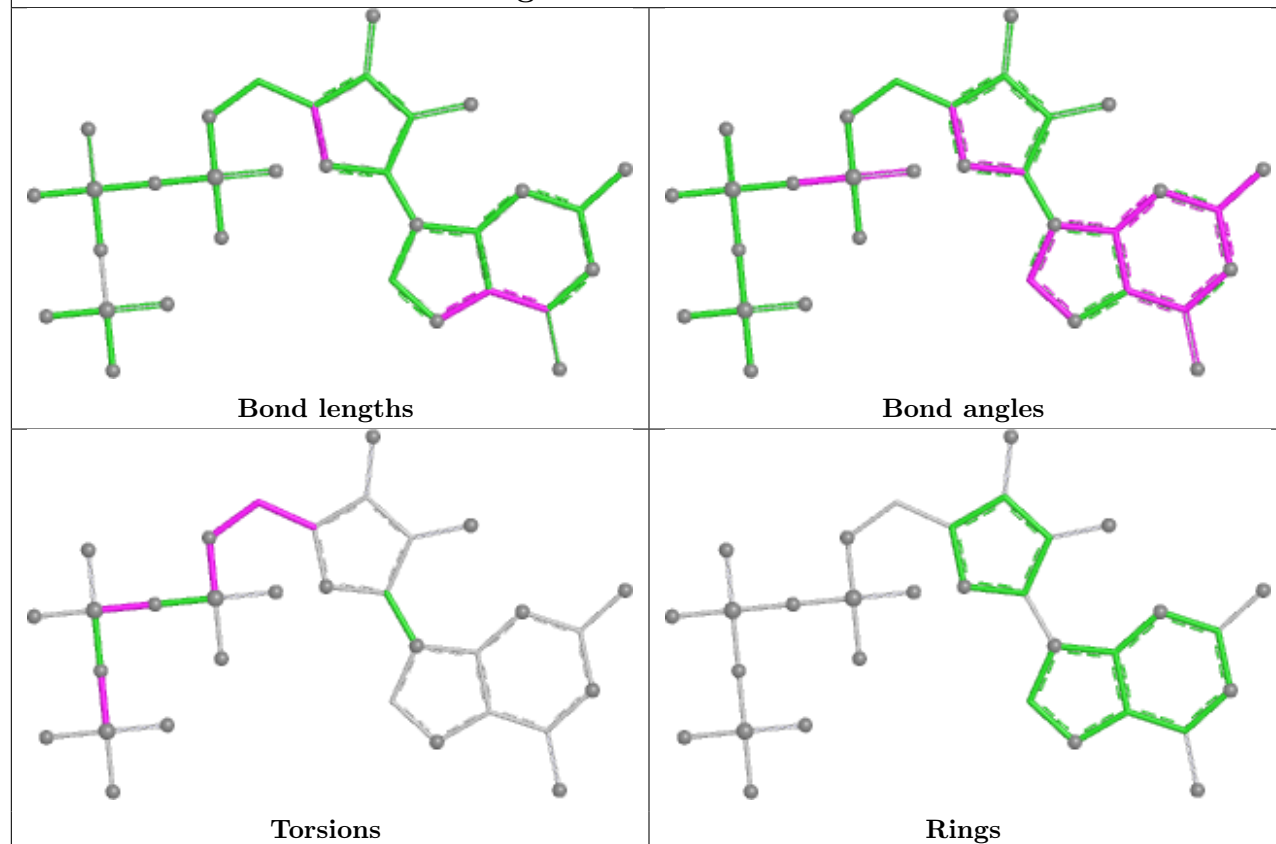


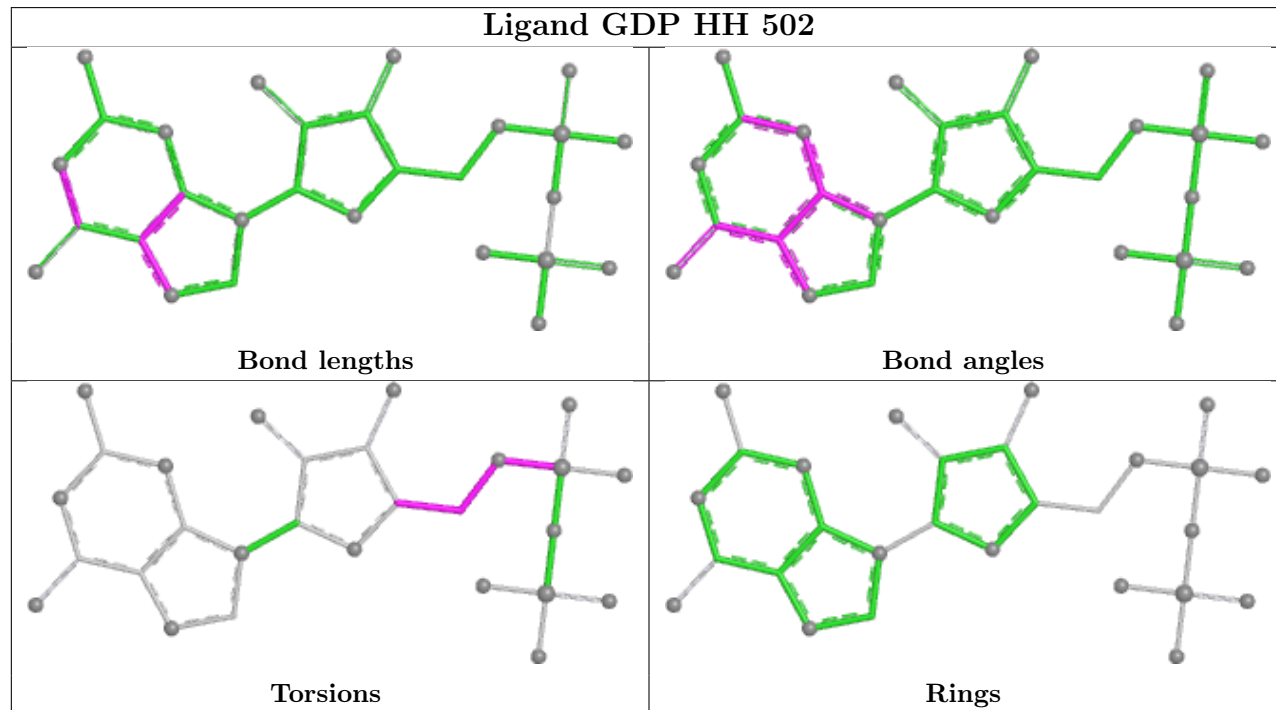
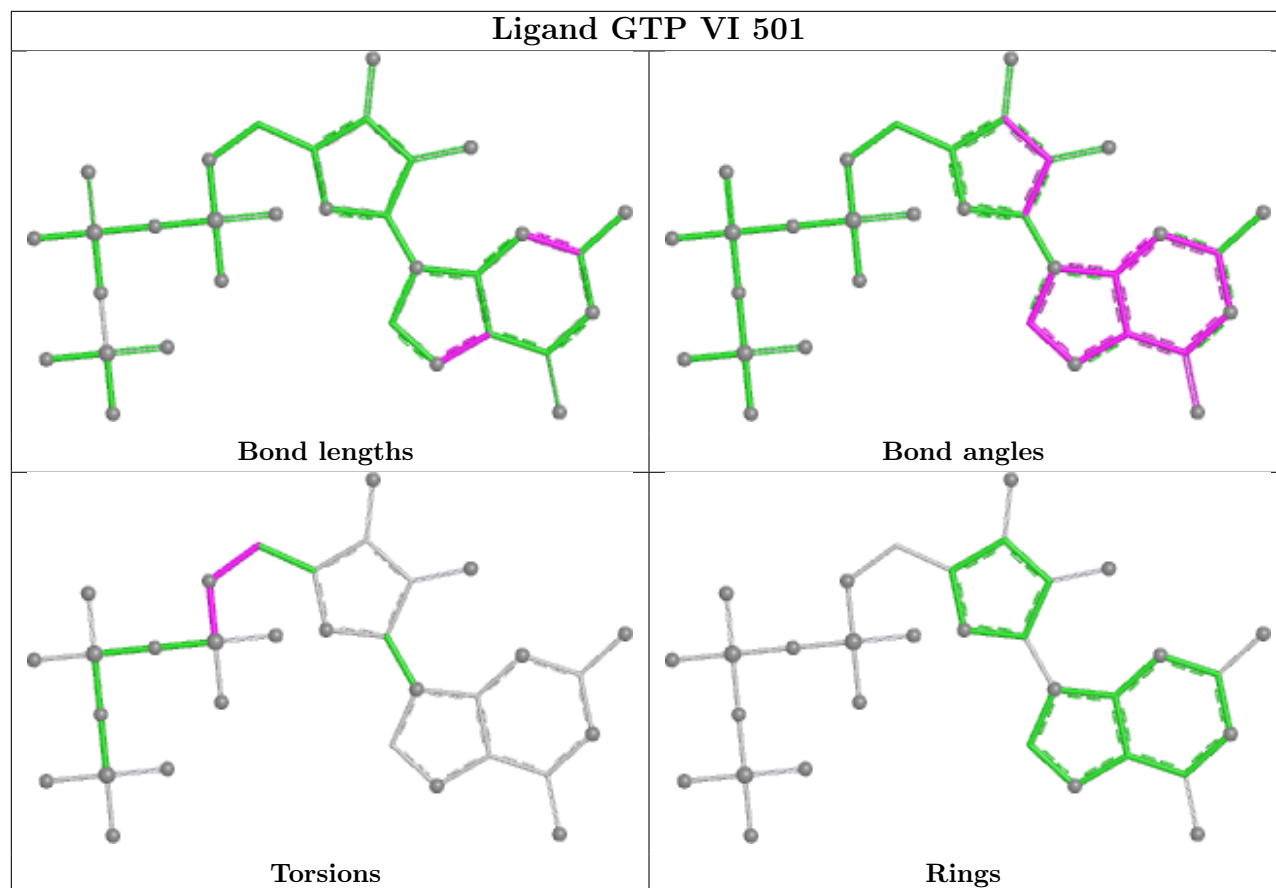


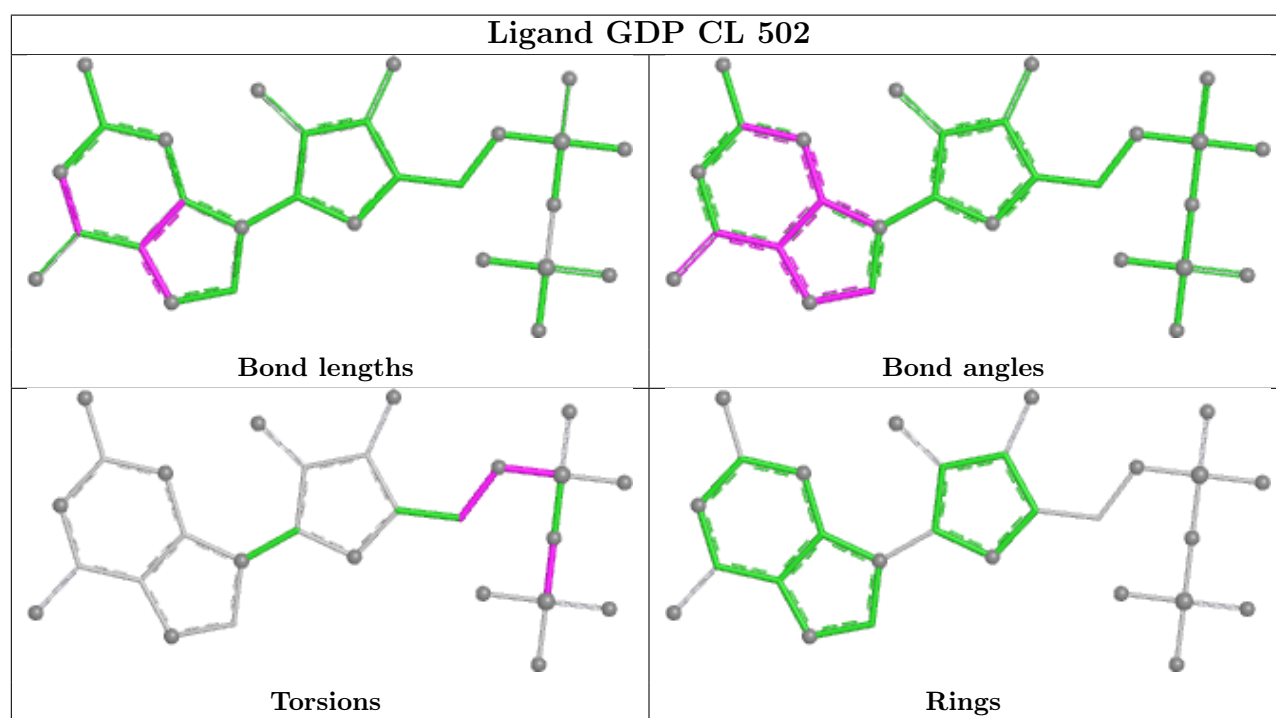
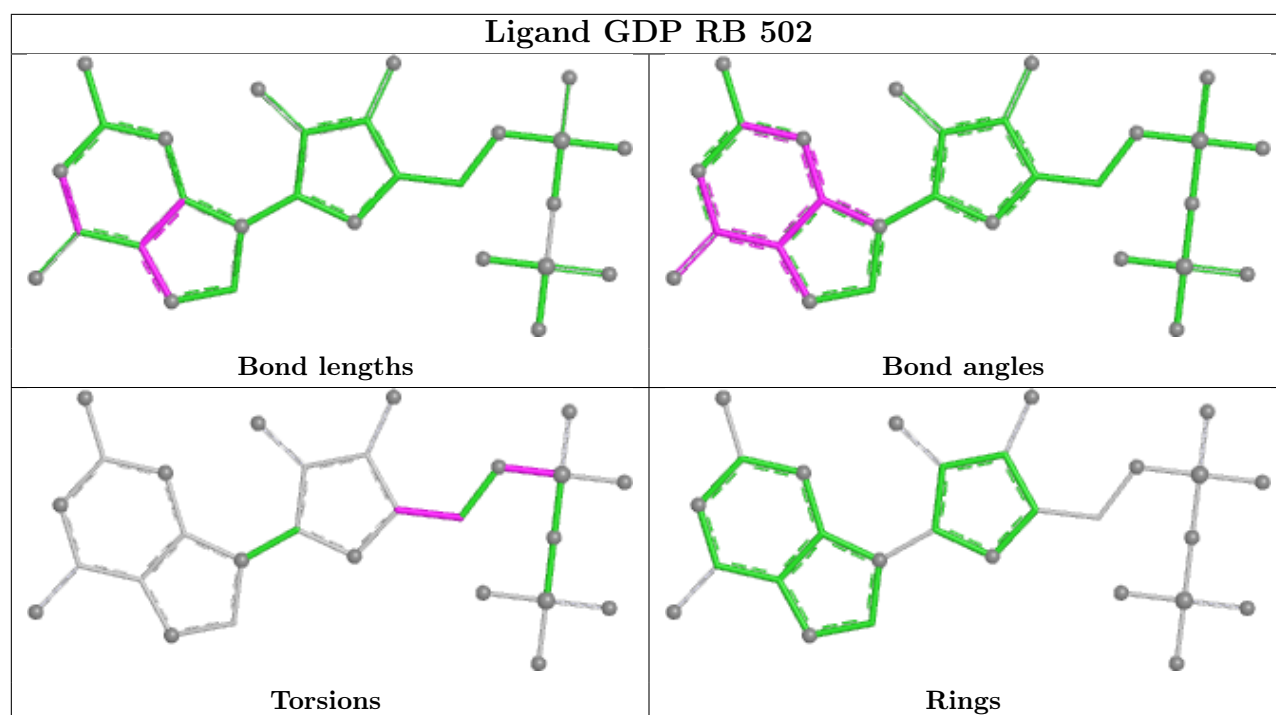
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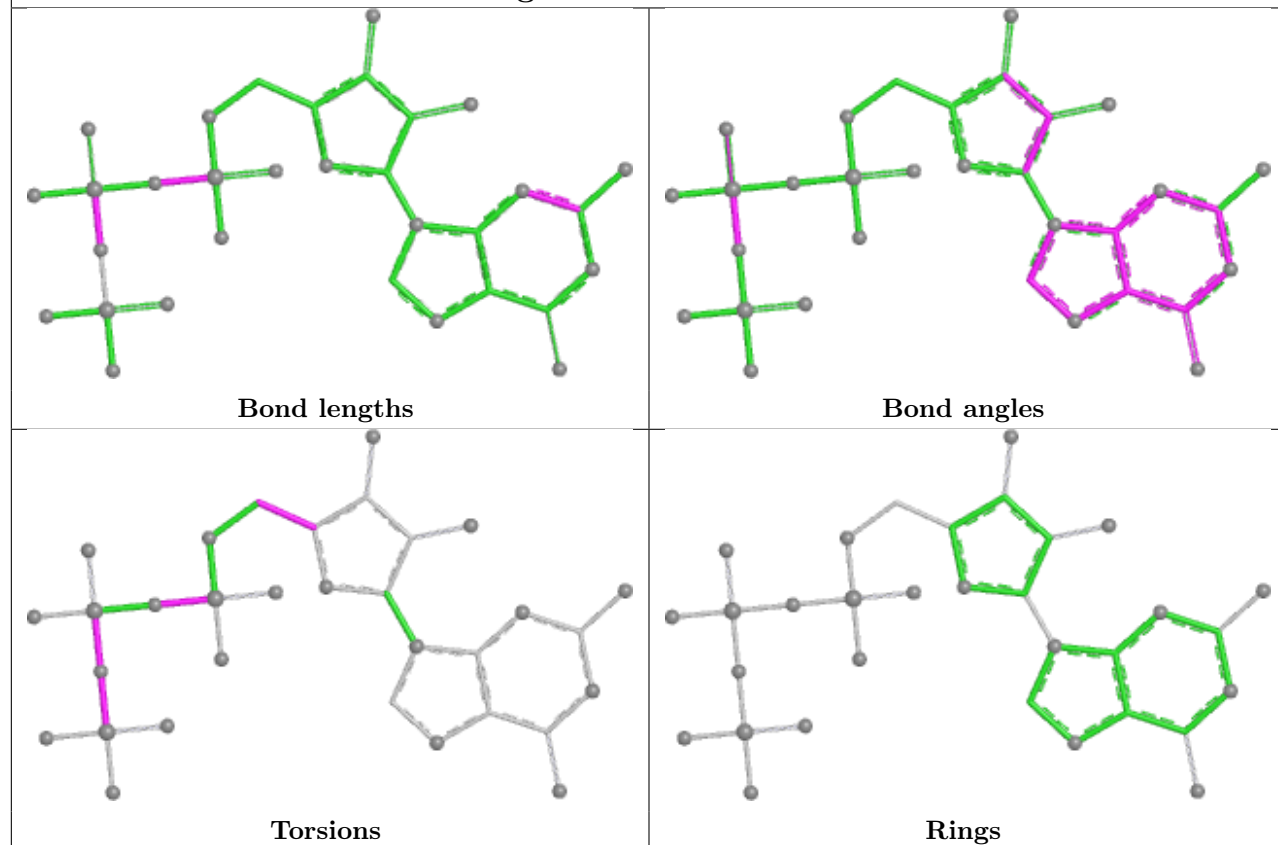
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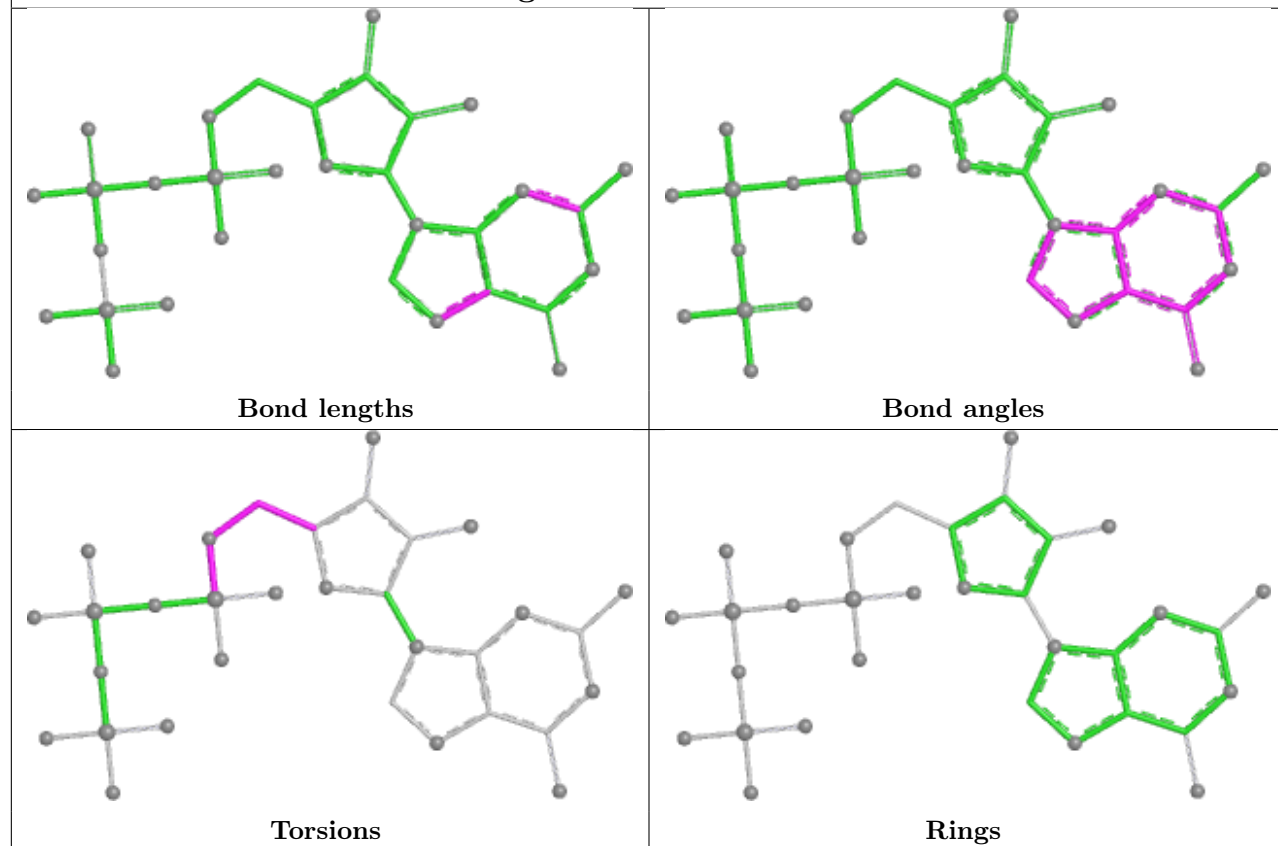


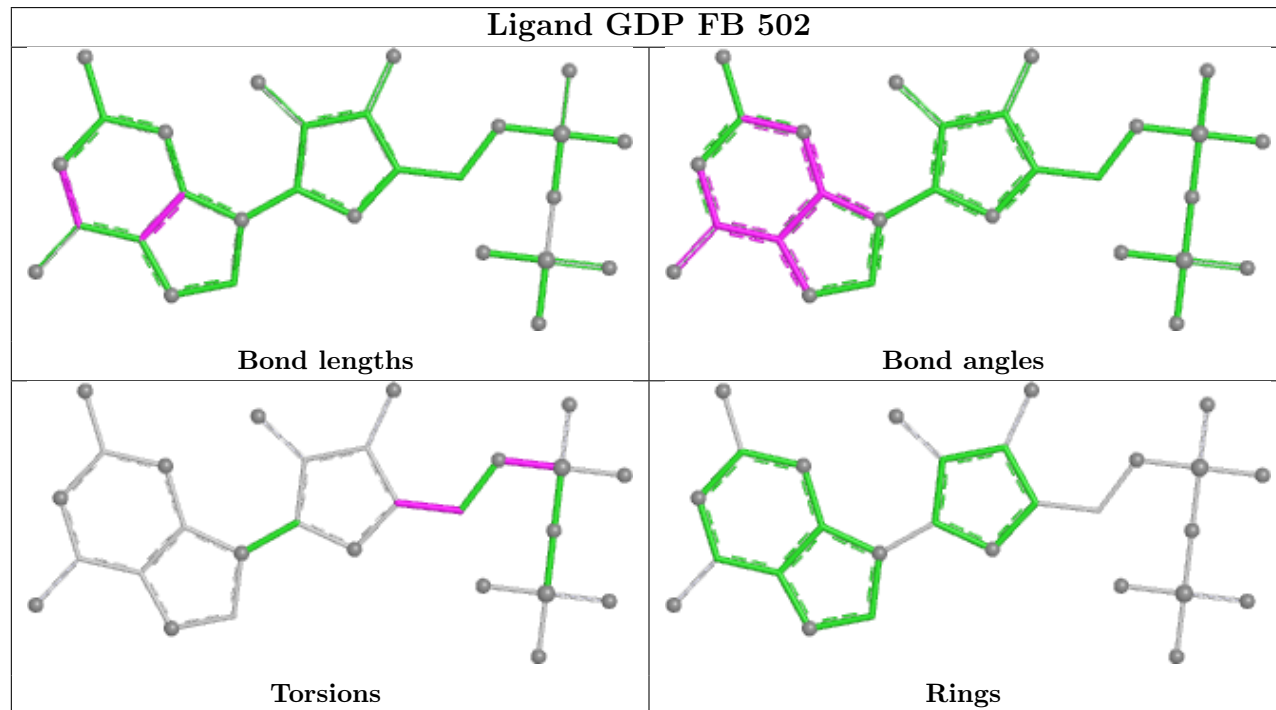
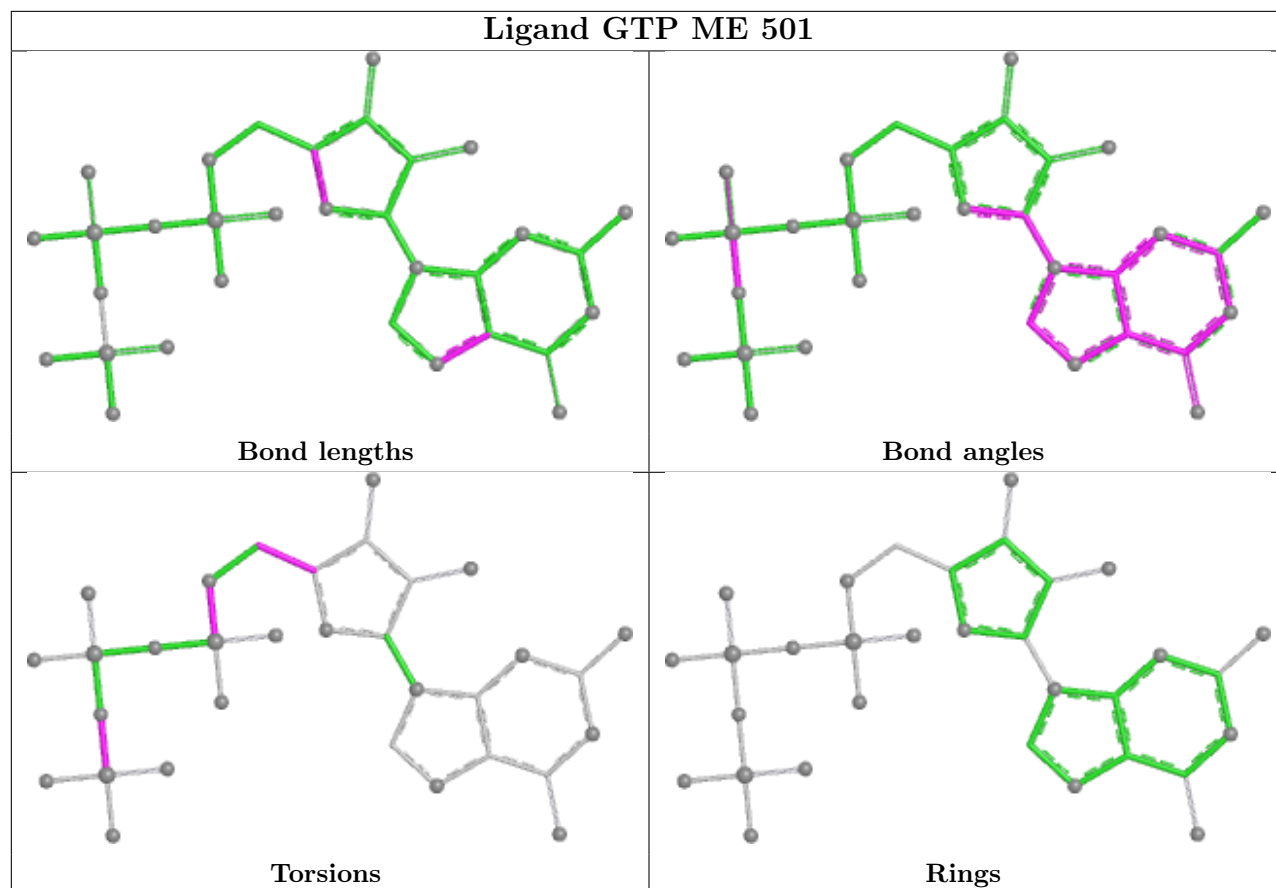


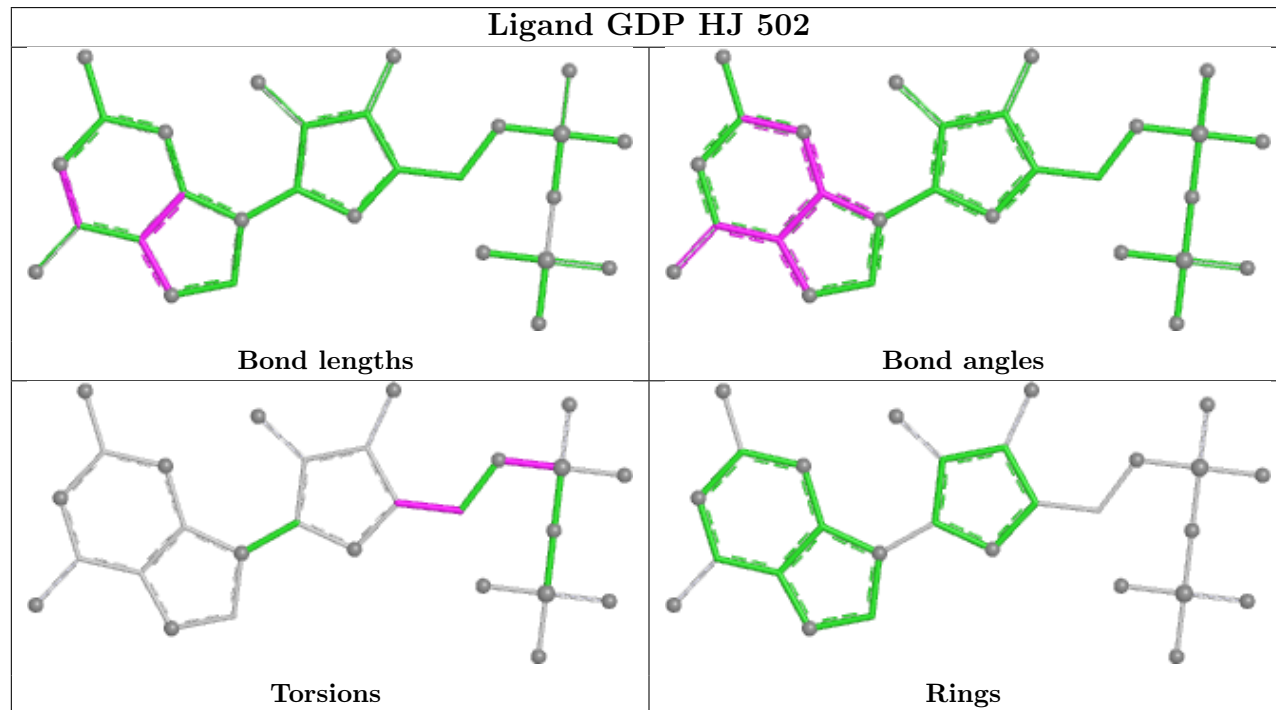
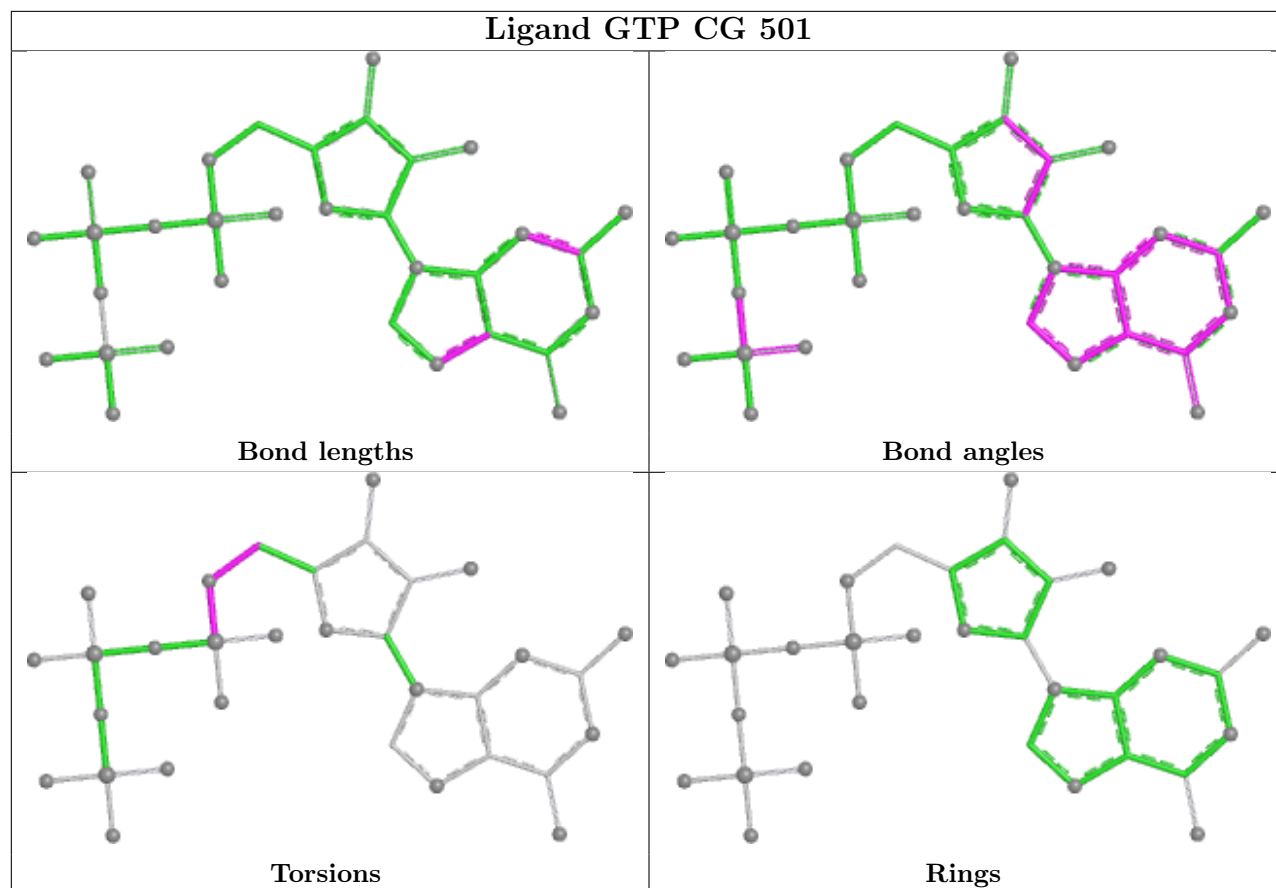
Ligand GTP DA 501

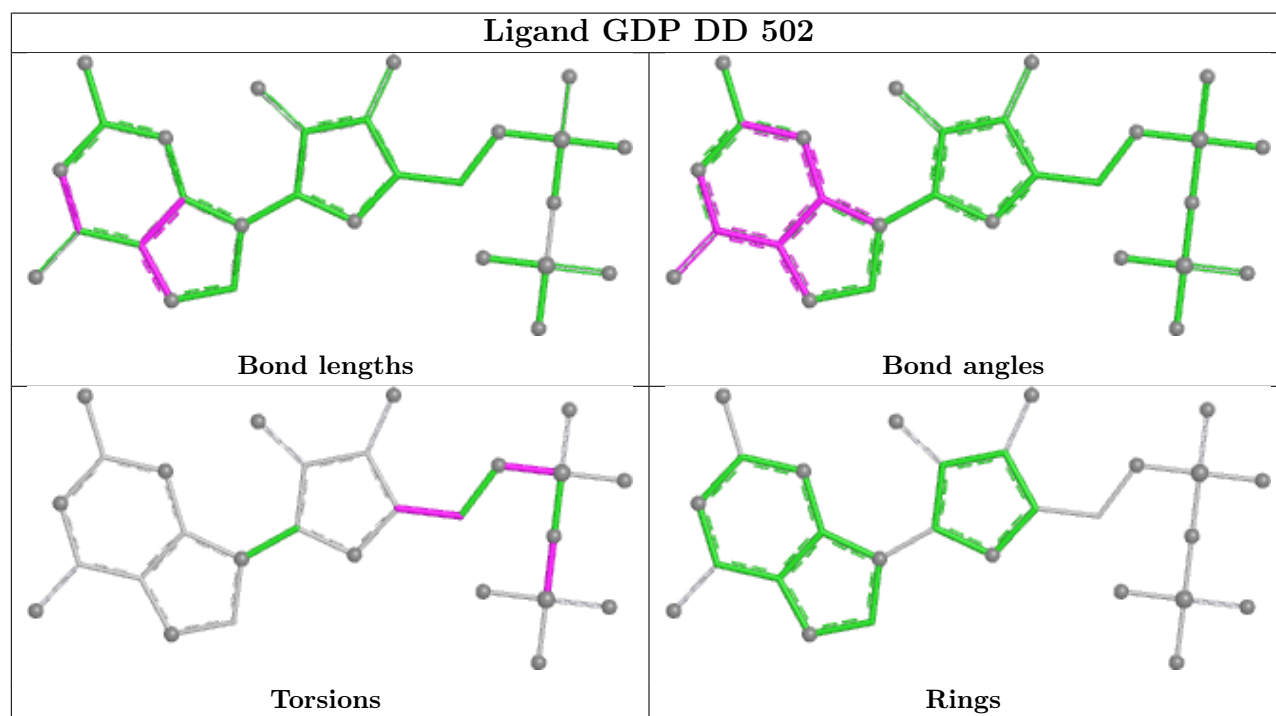
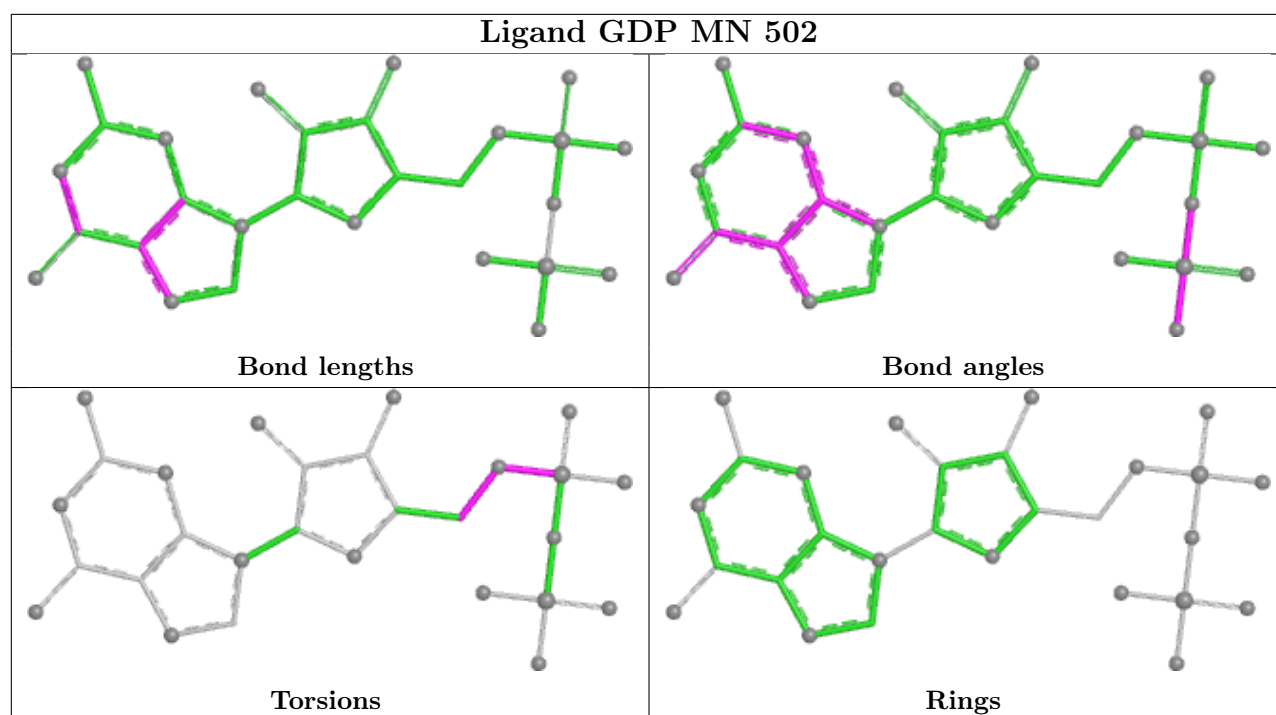


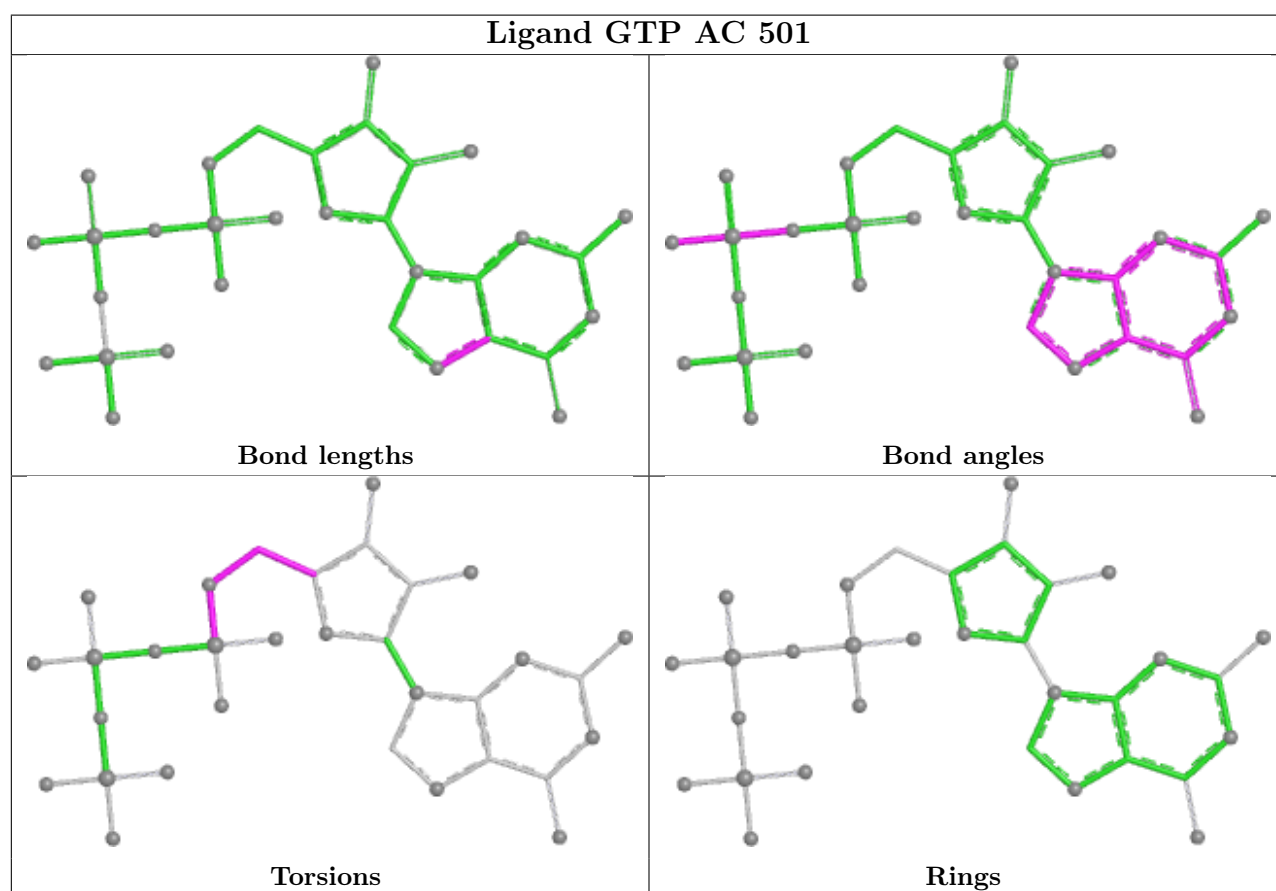
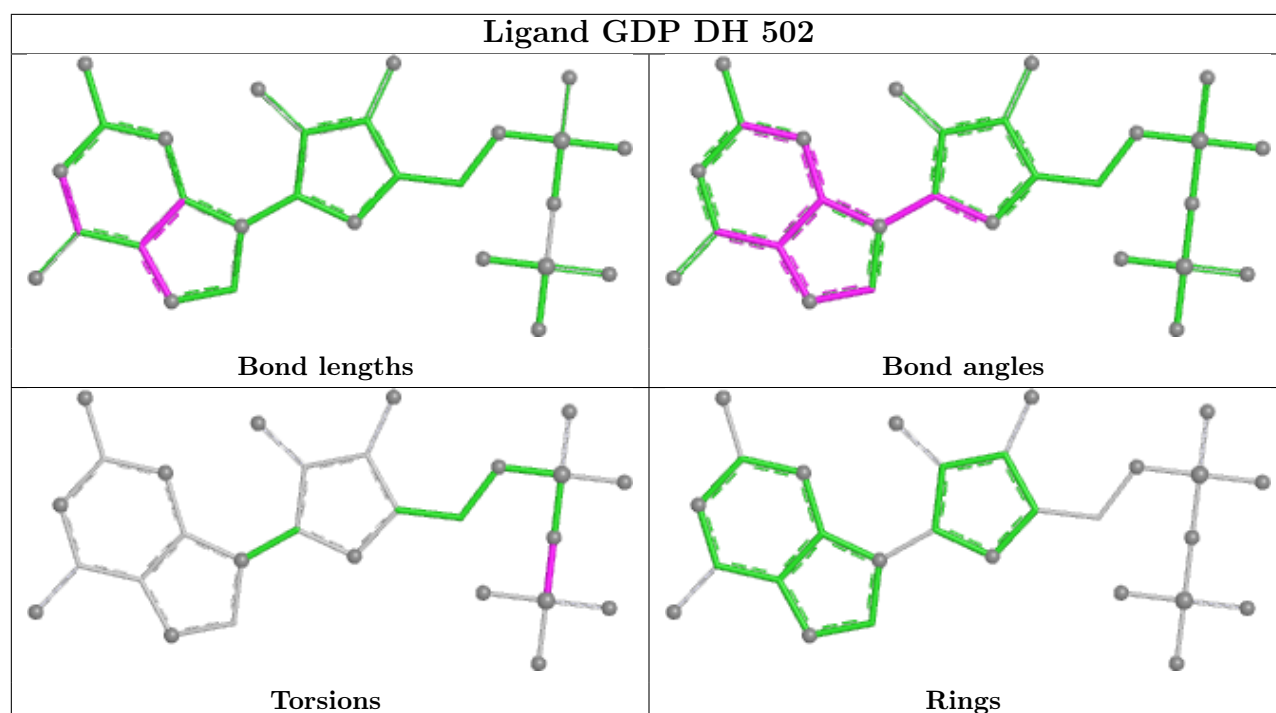
Ligand GTP HE 501

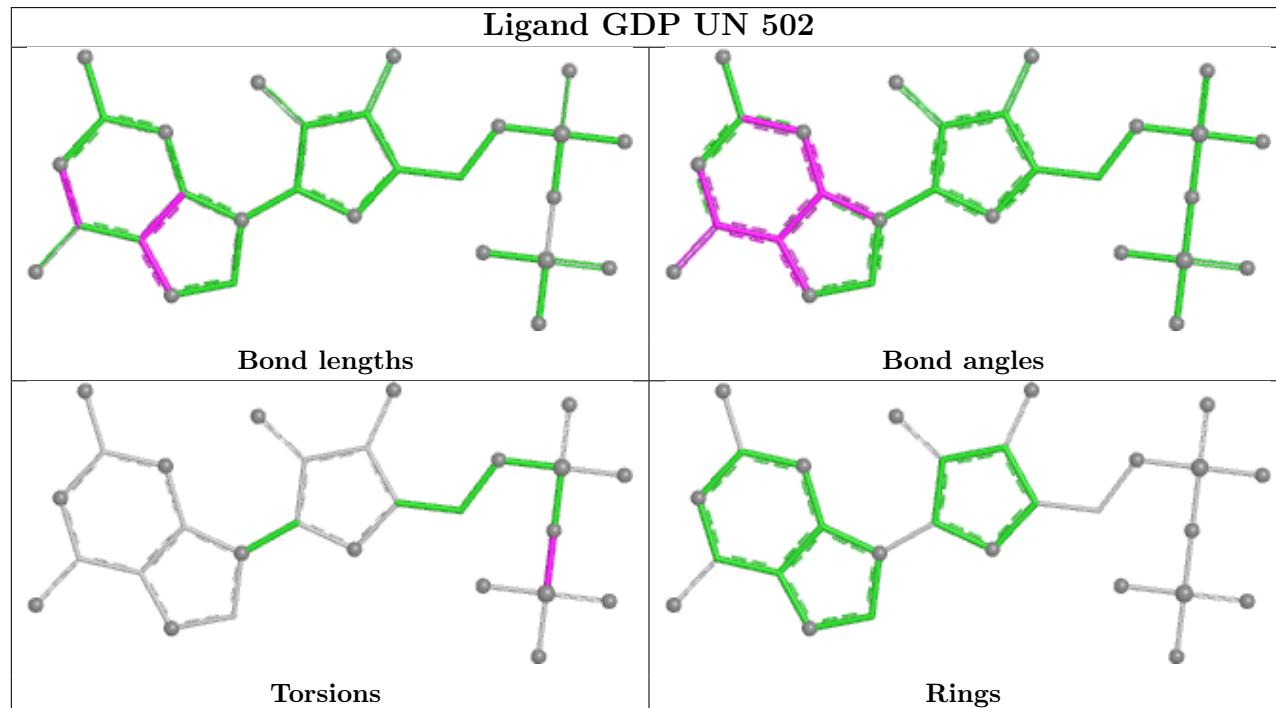
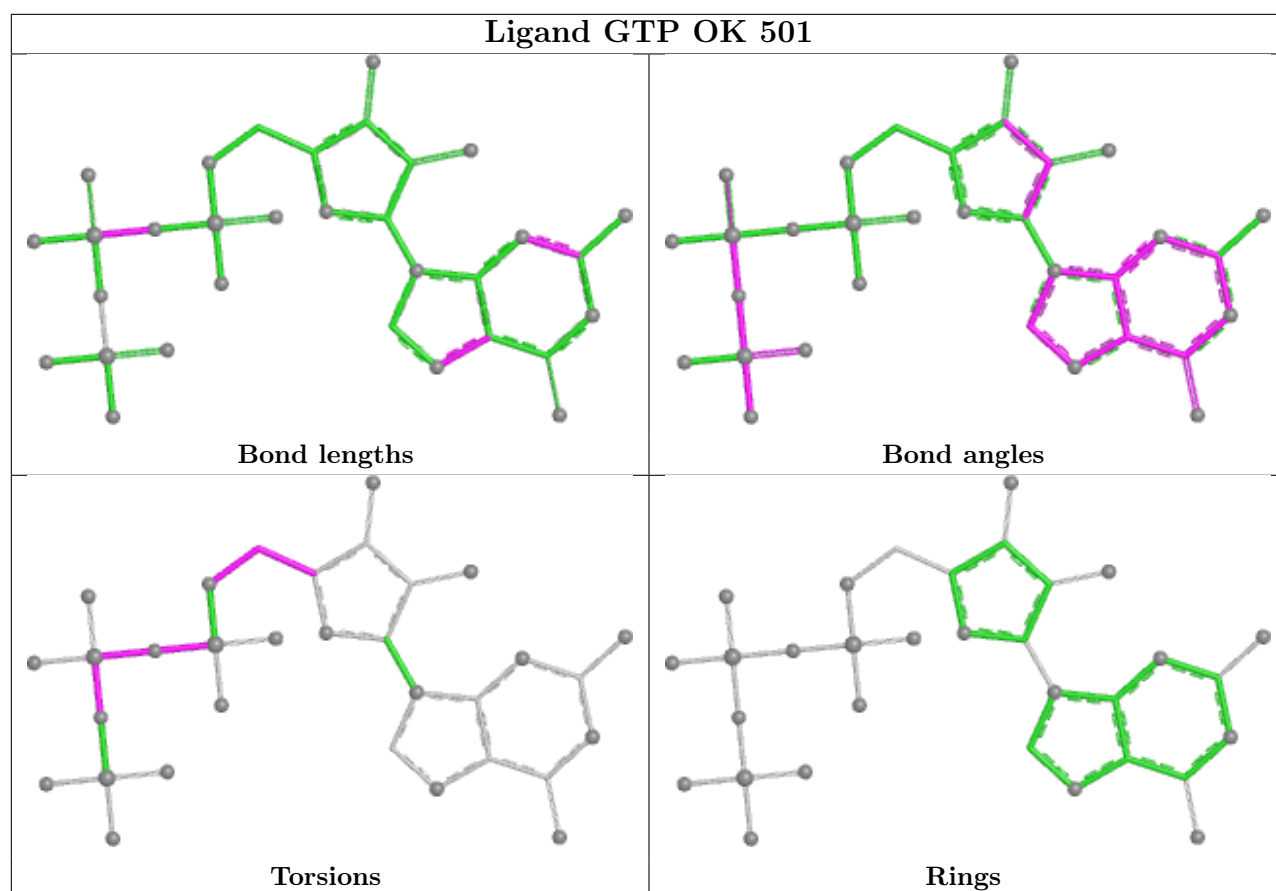


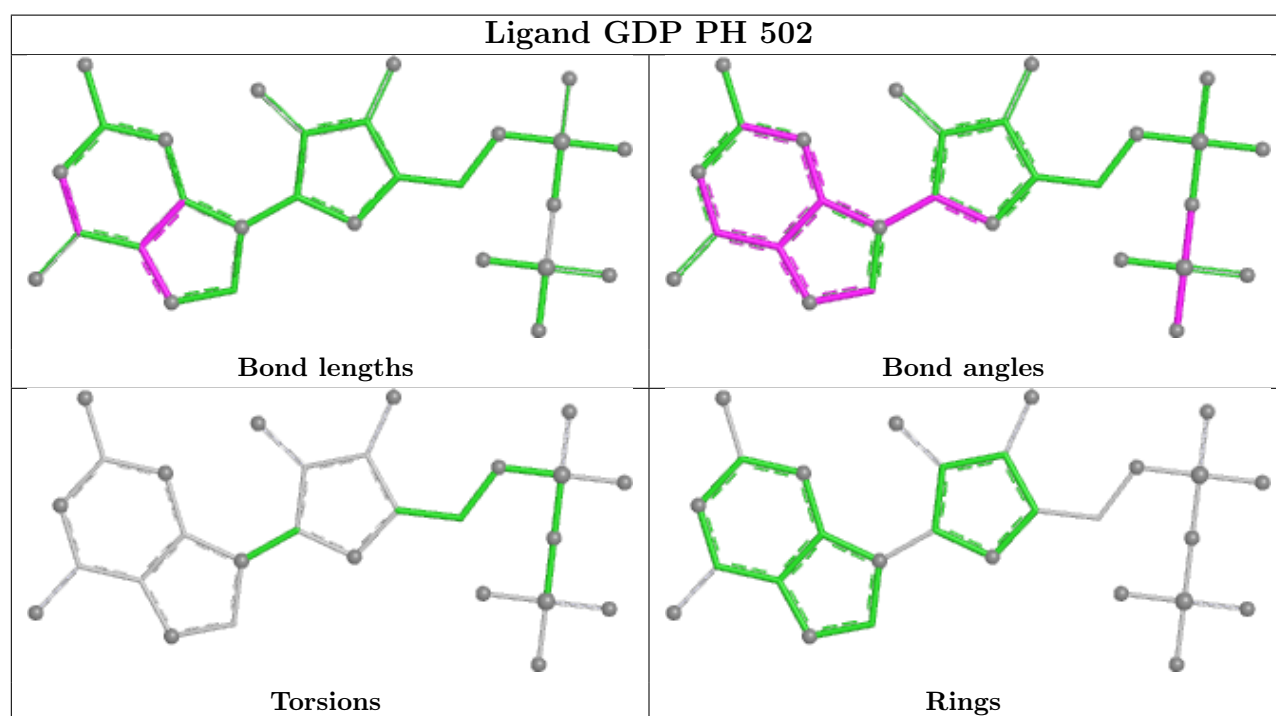
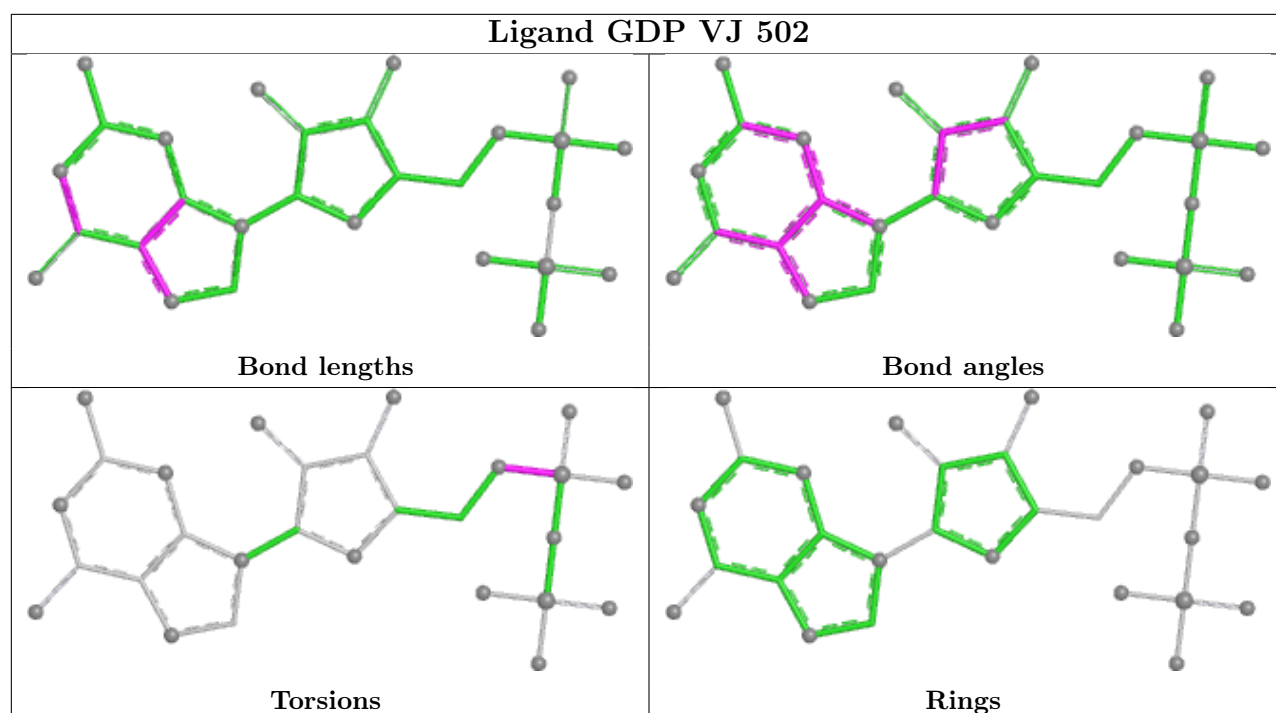


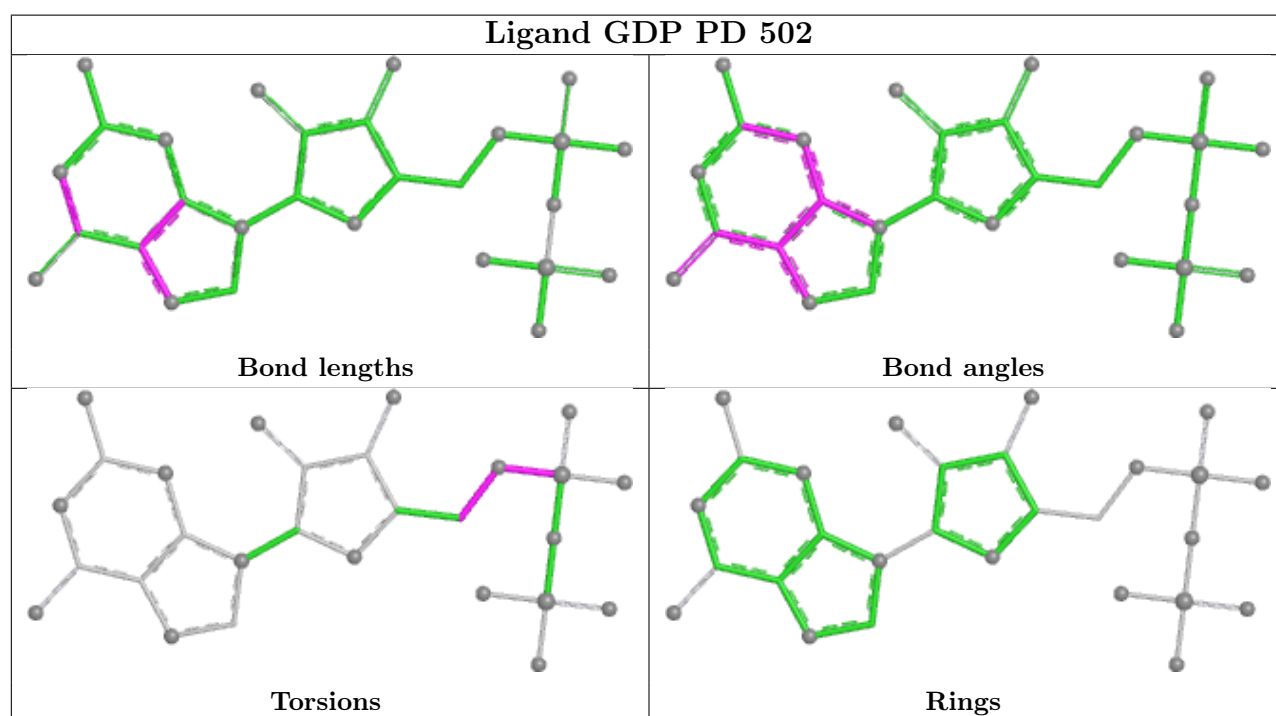
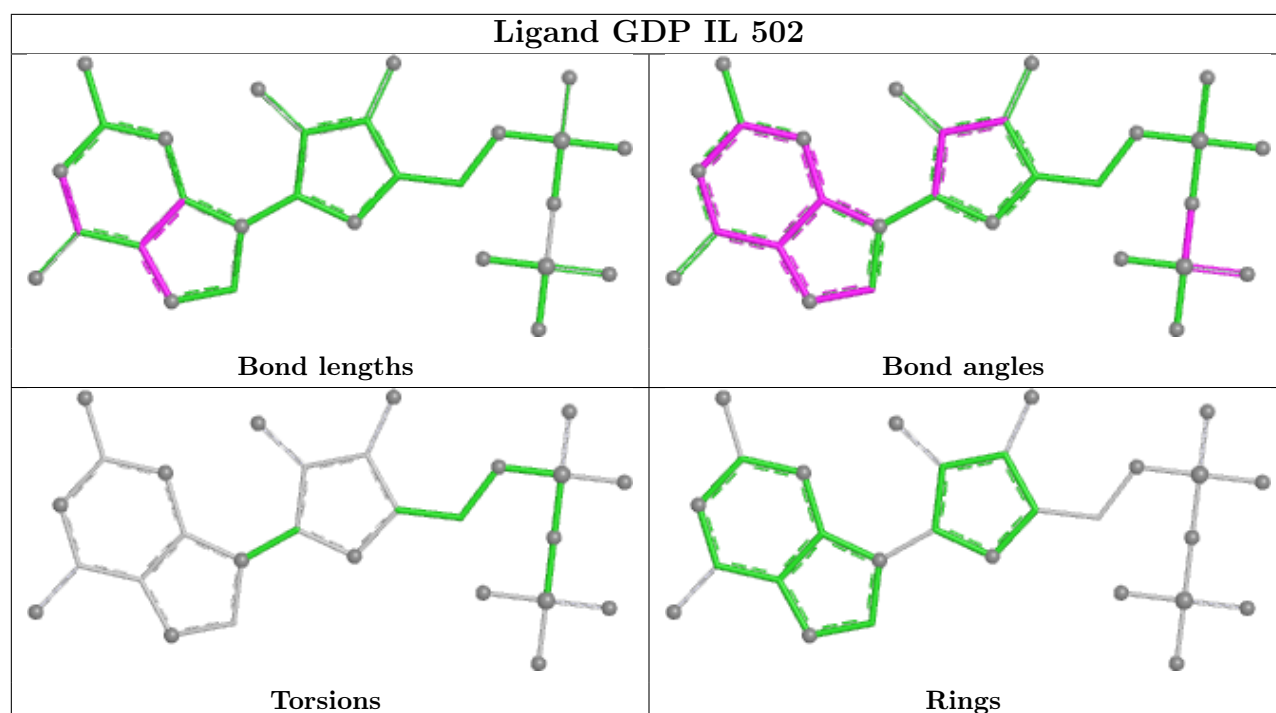


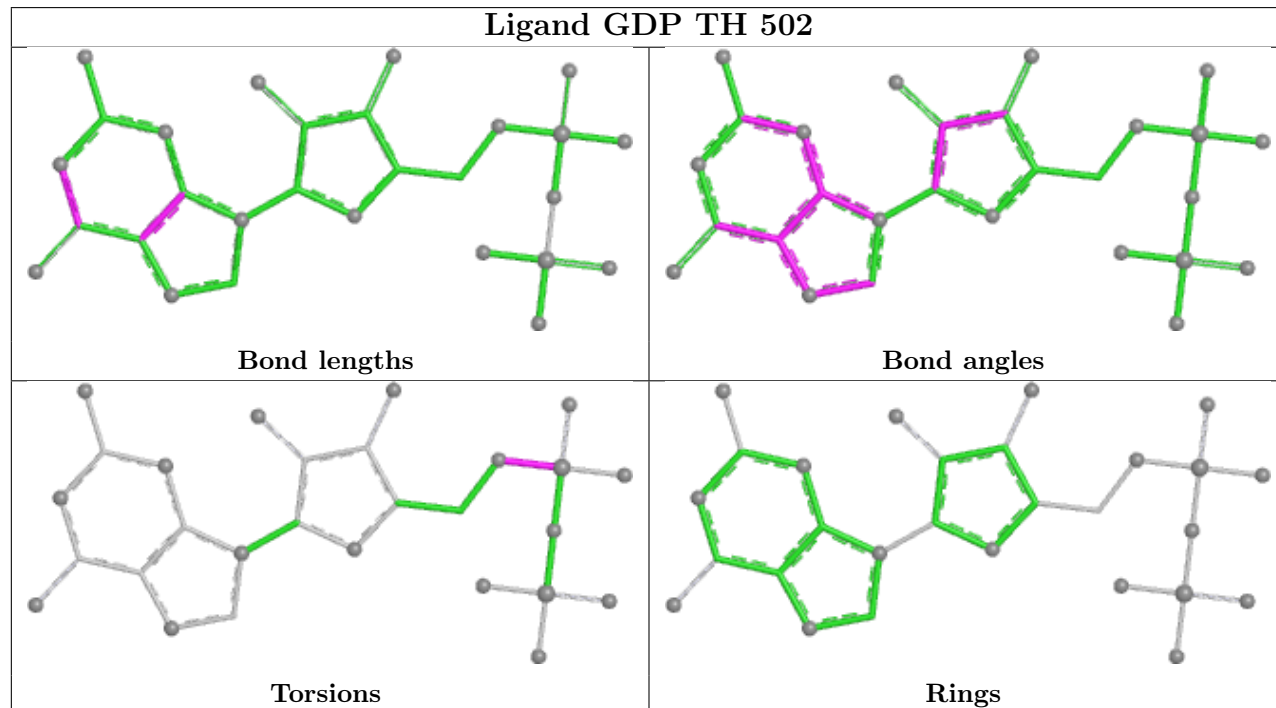
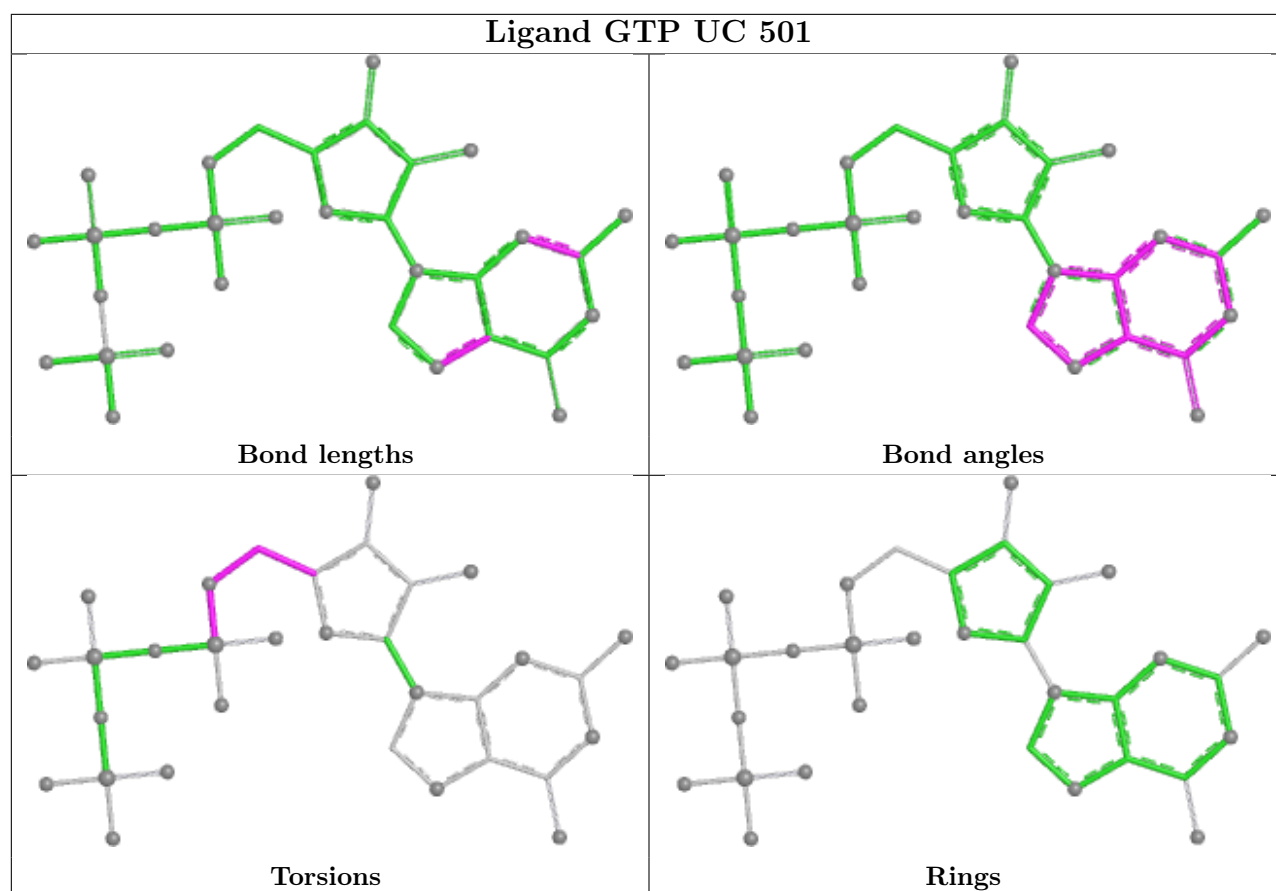


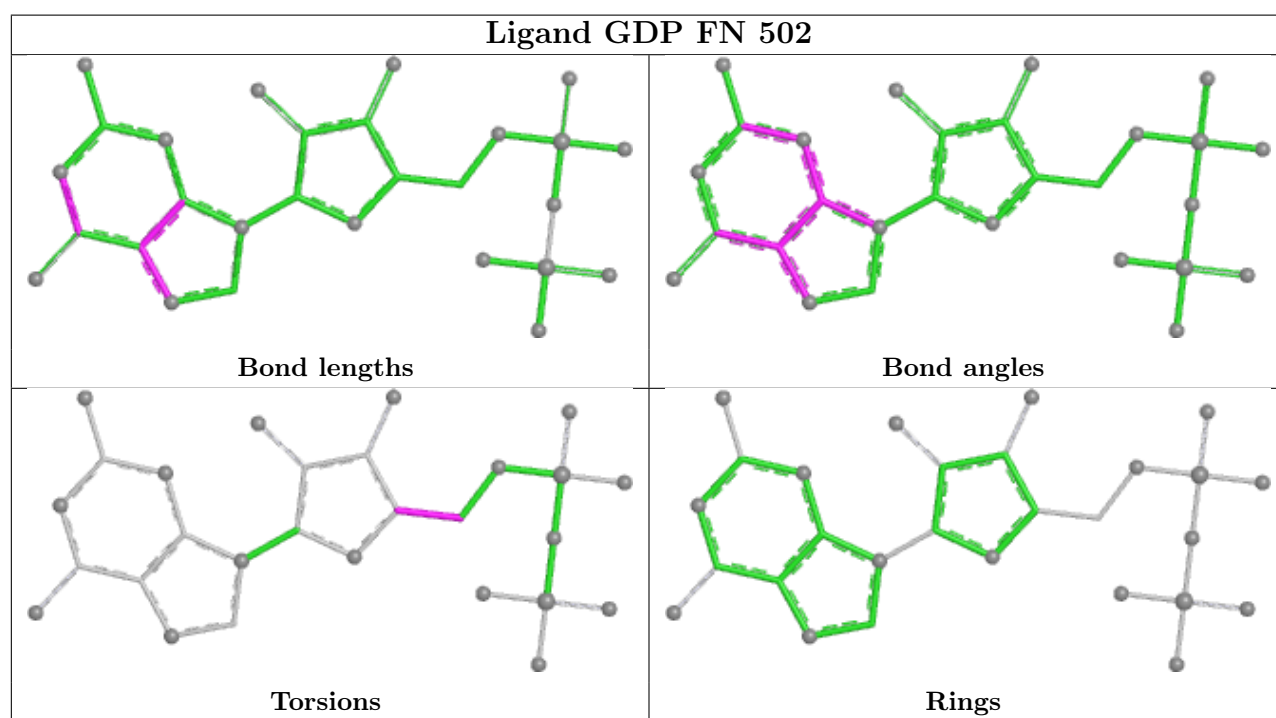
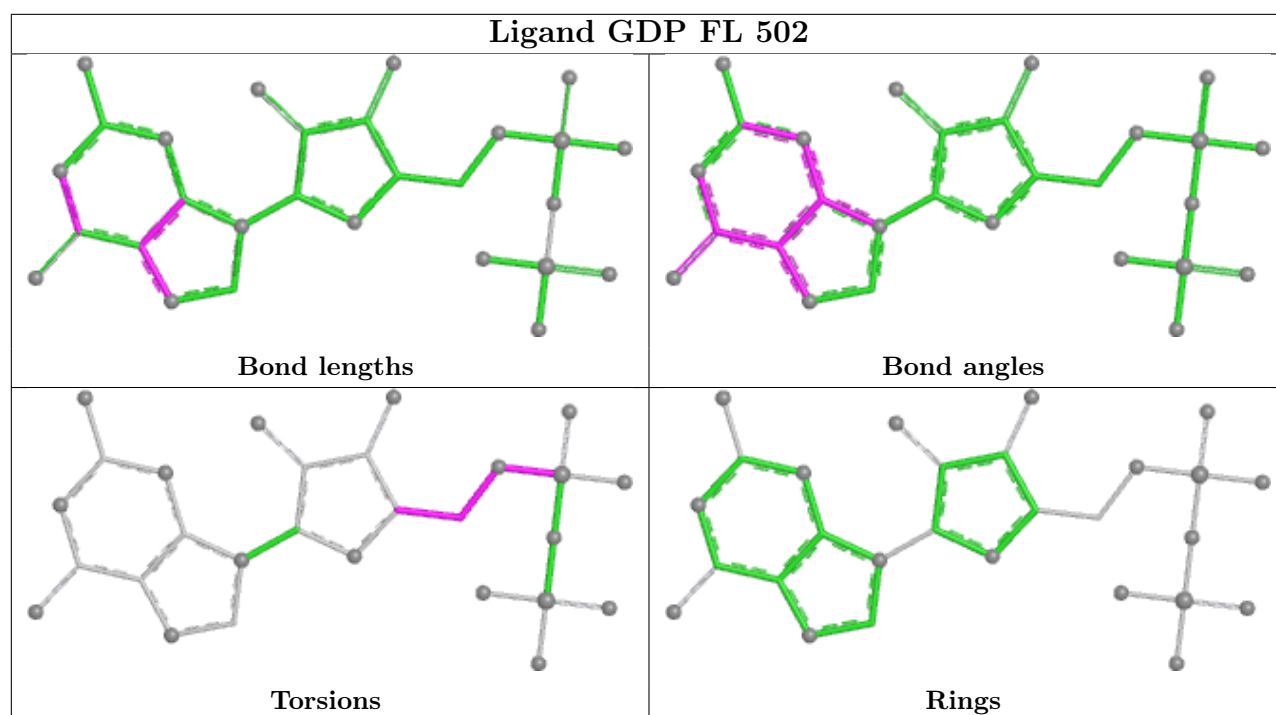


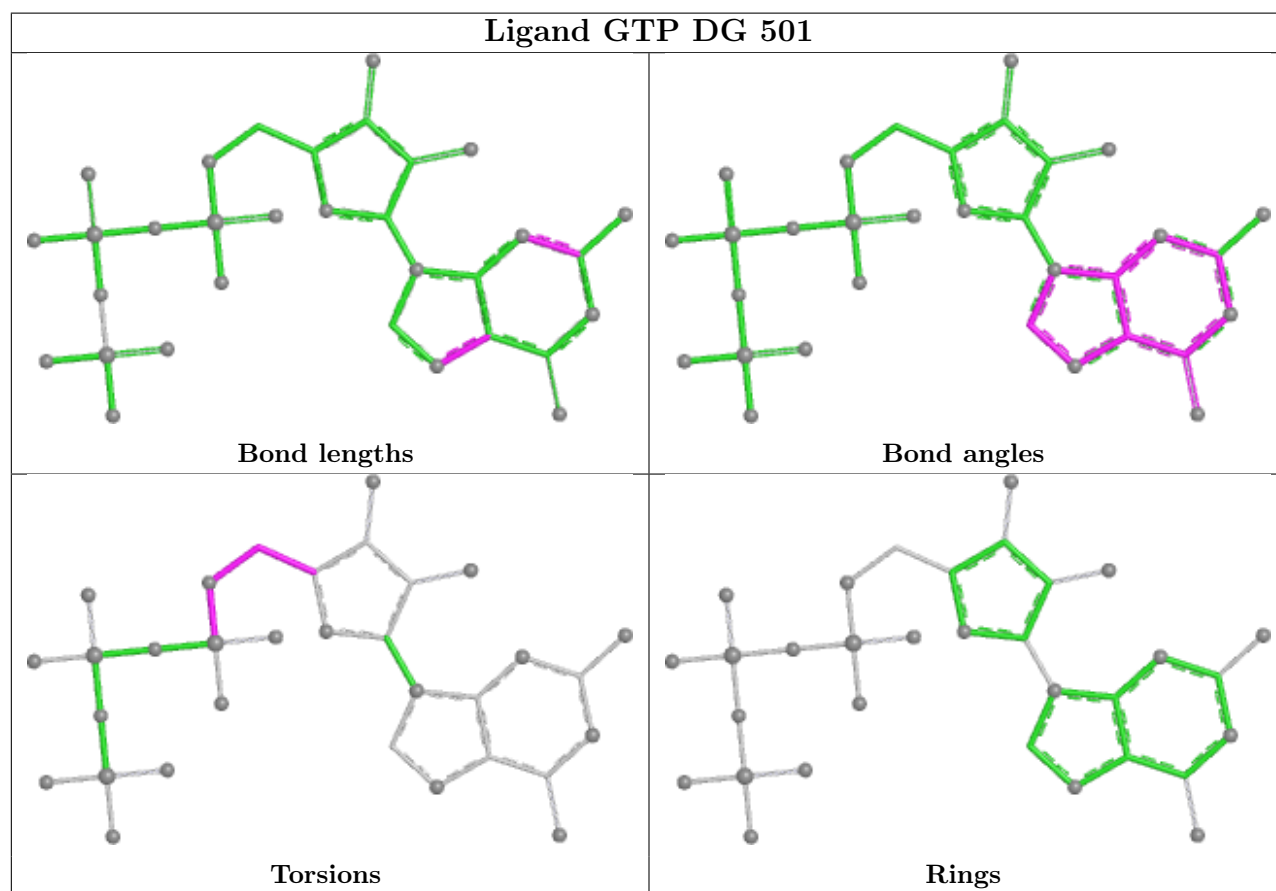
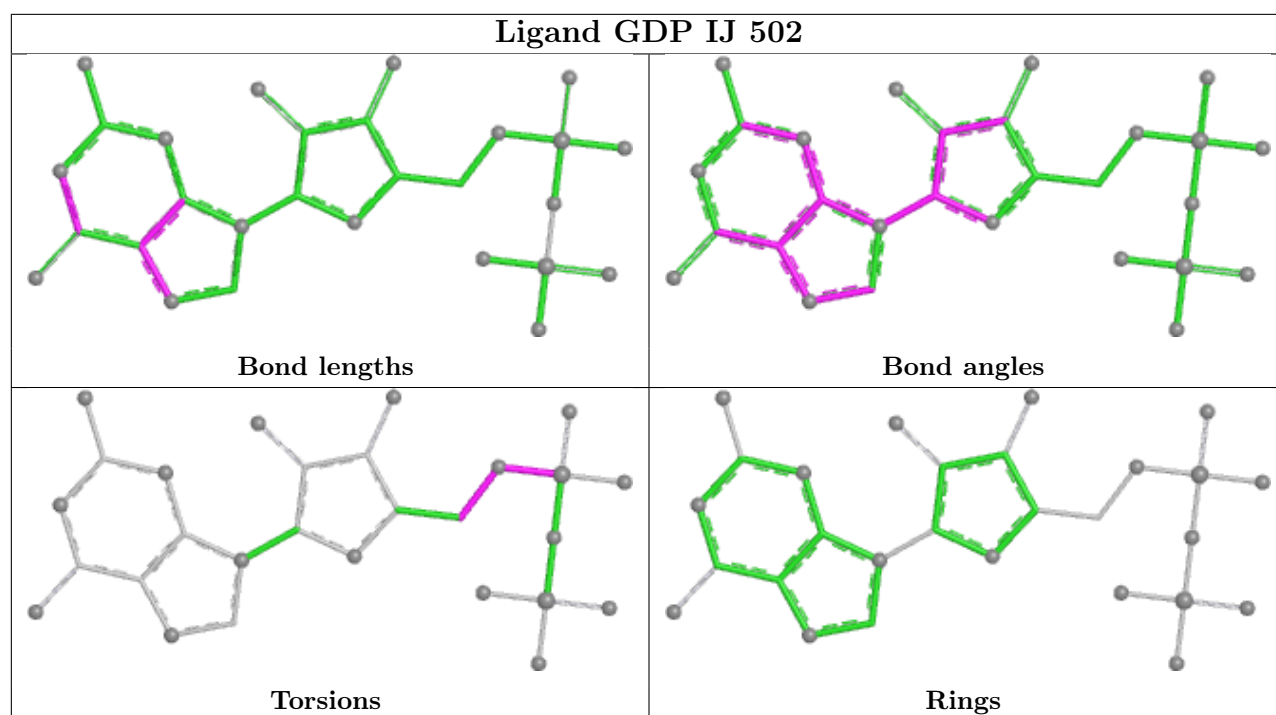




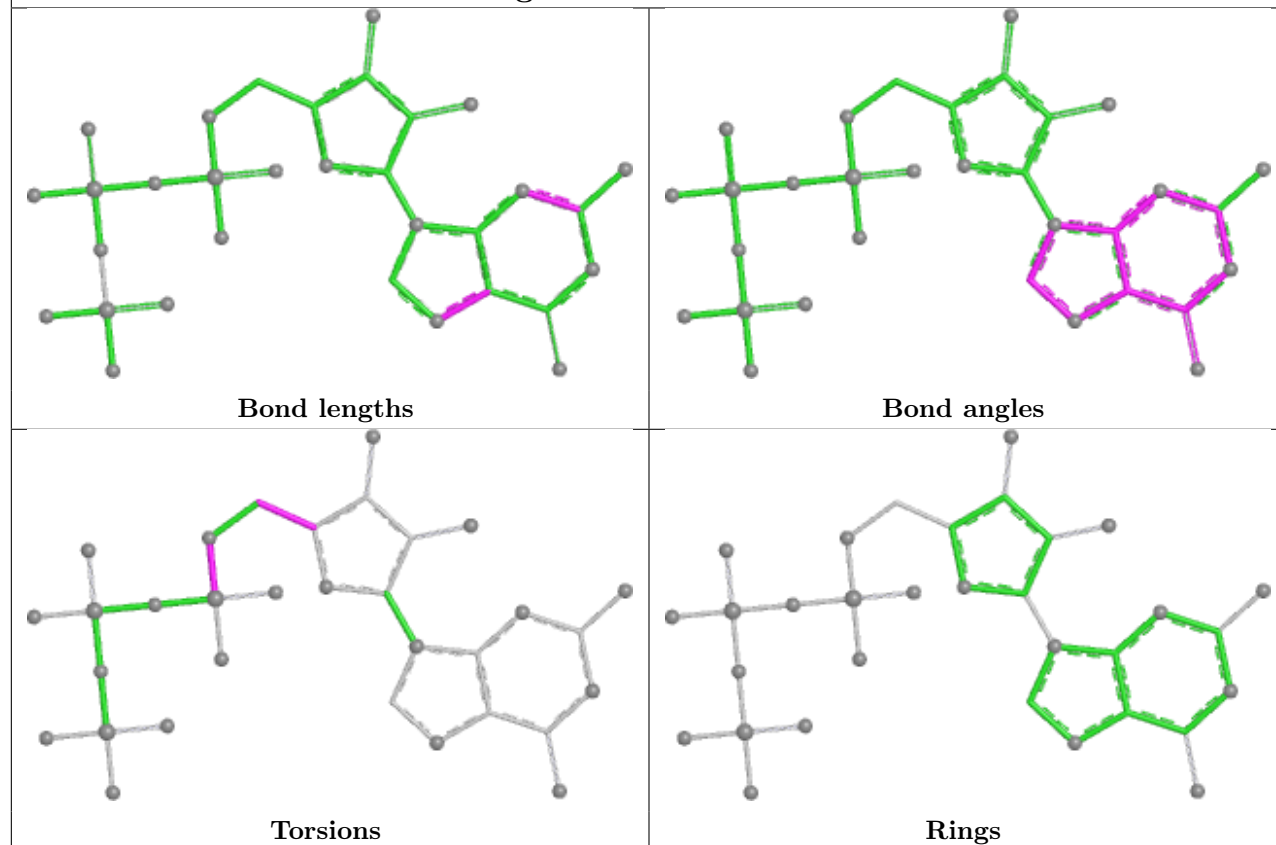




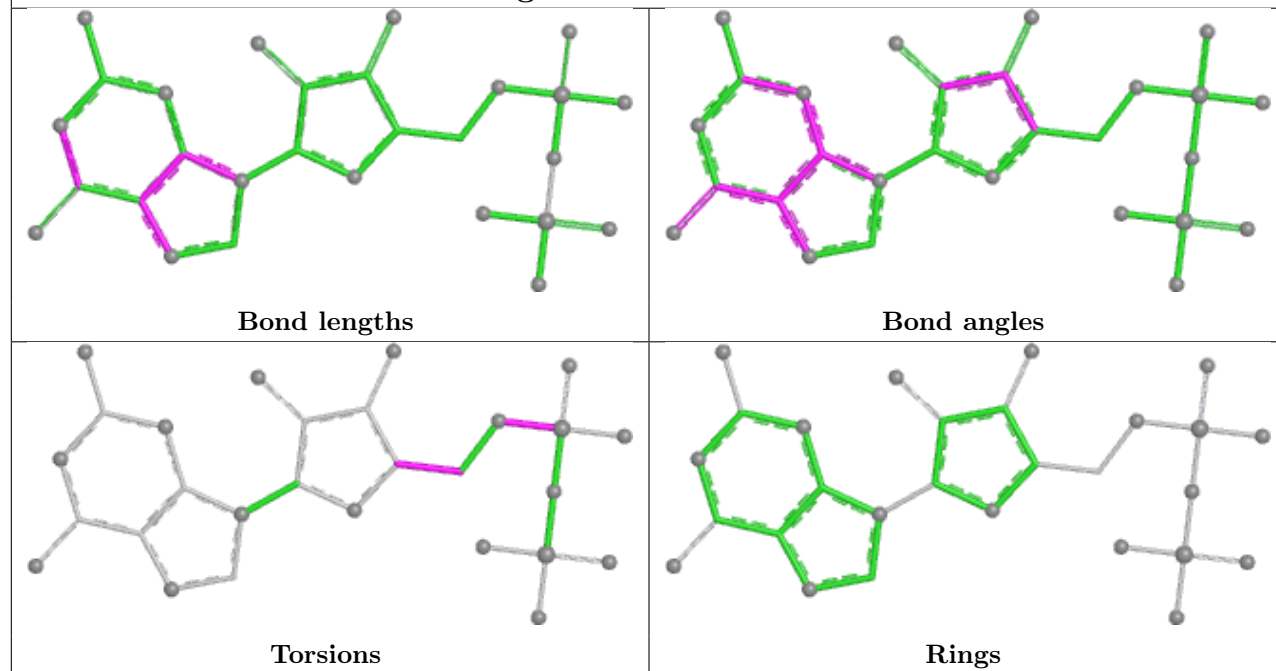


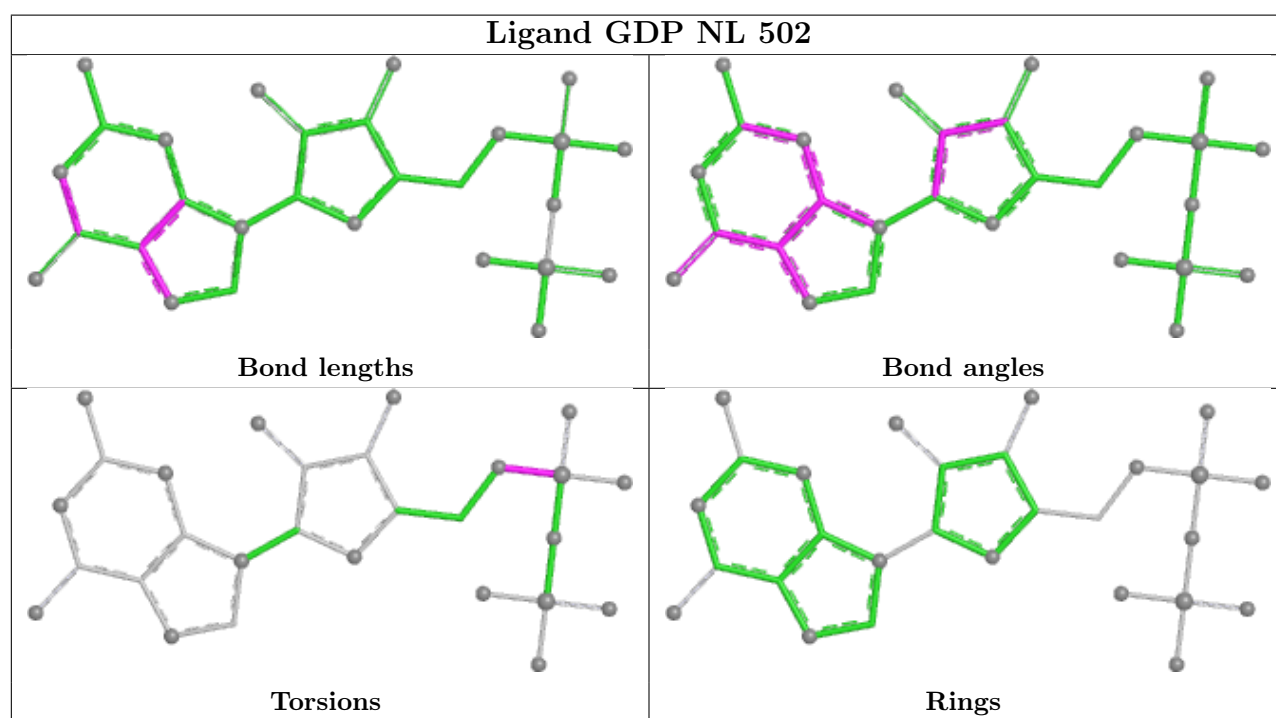
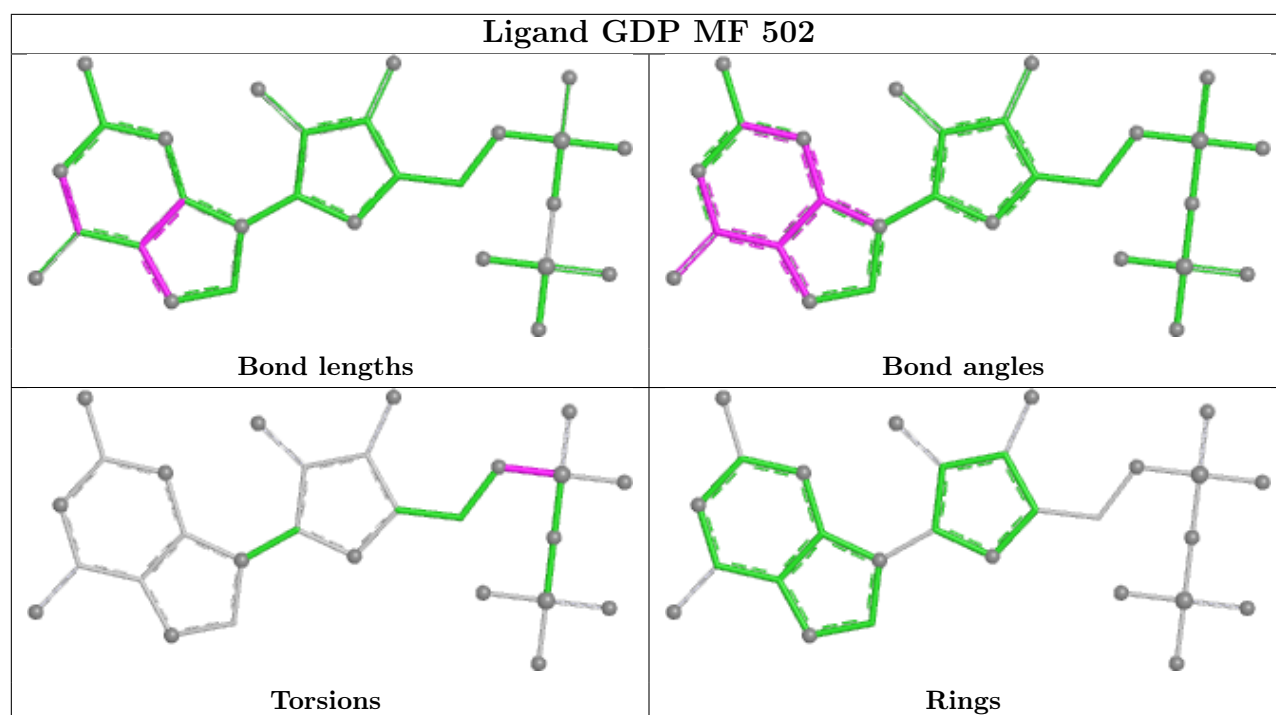


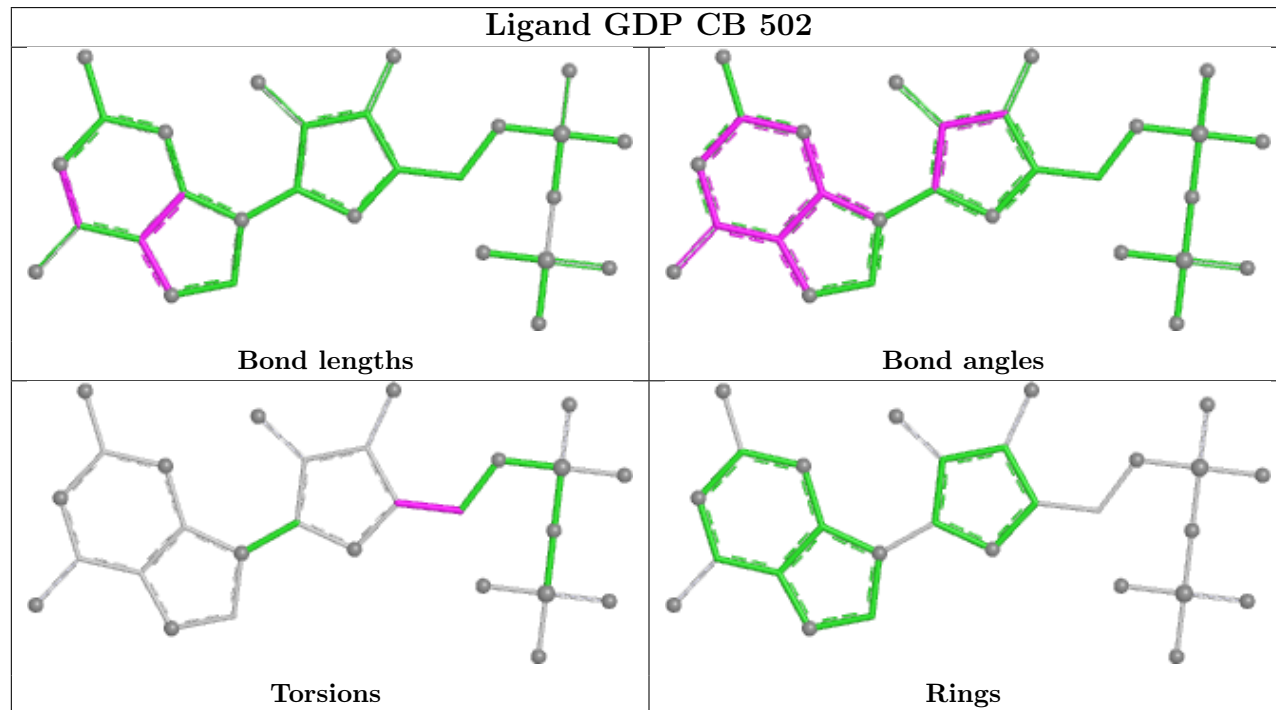
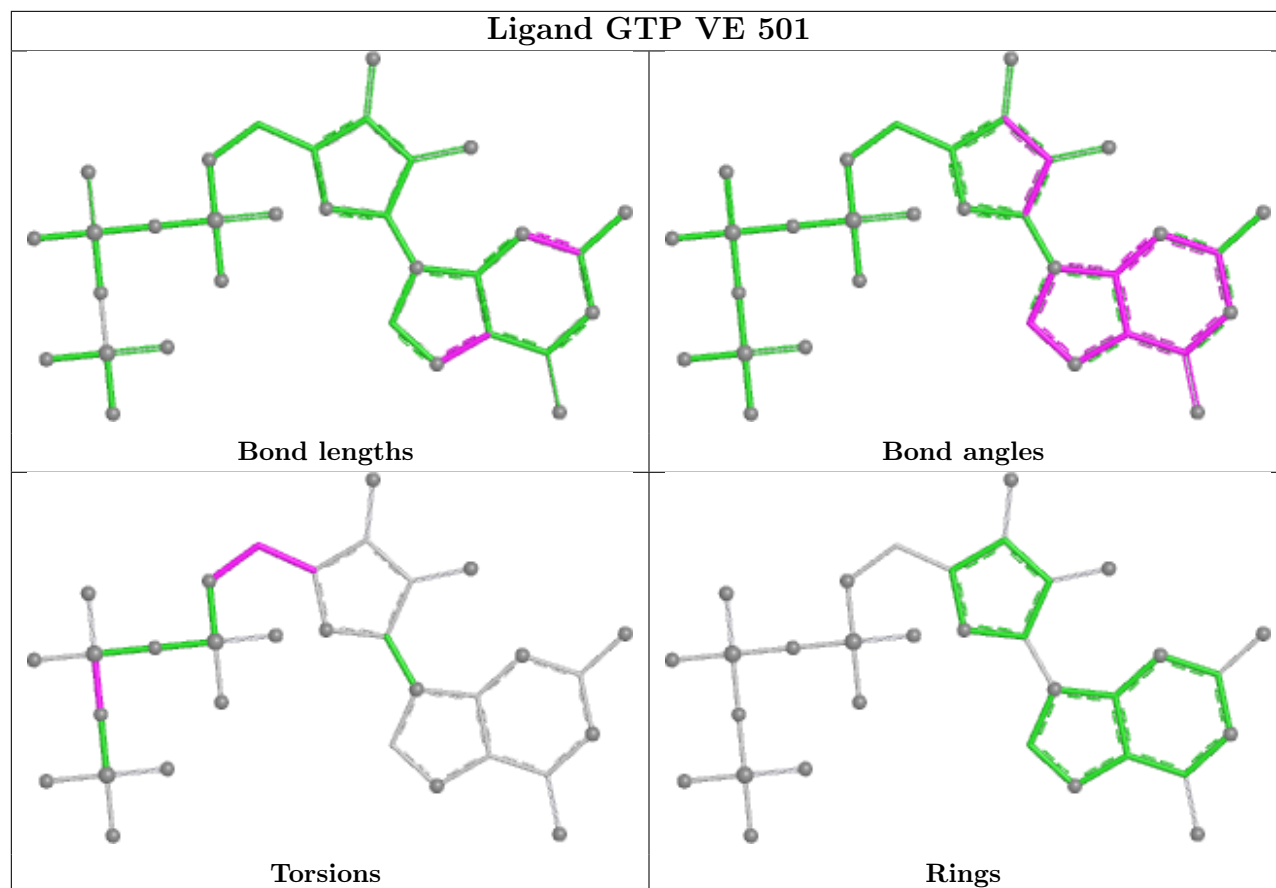
Ligand GTP HG 501

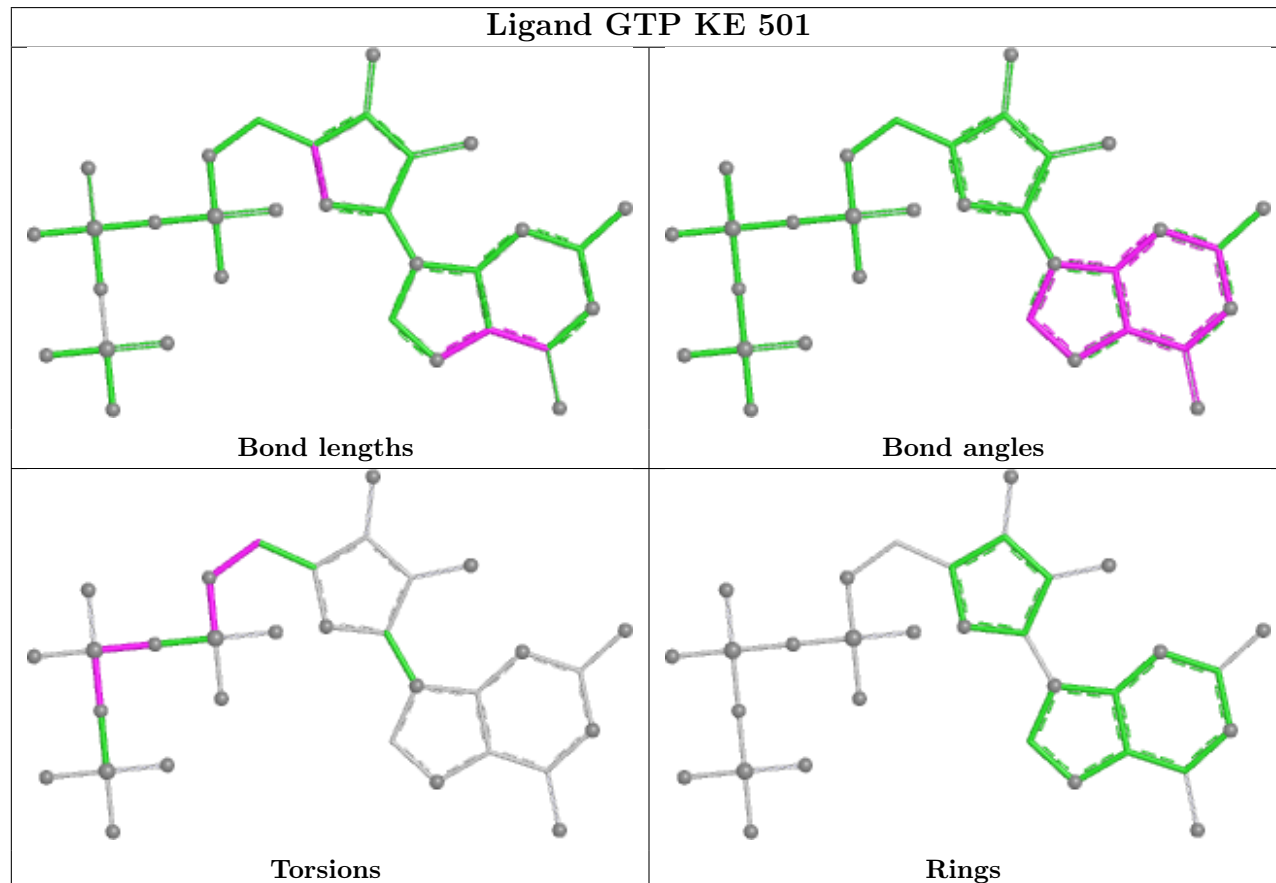
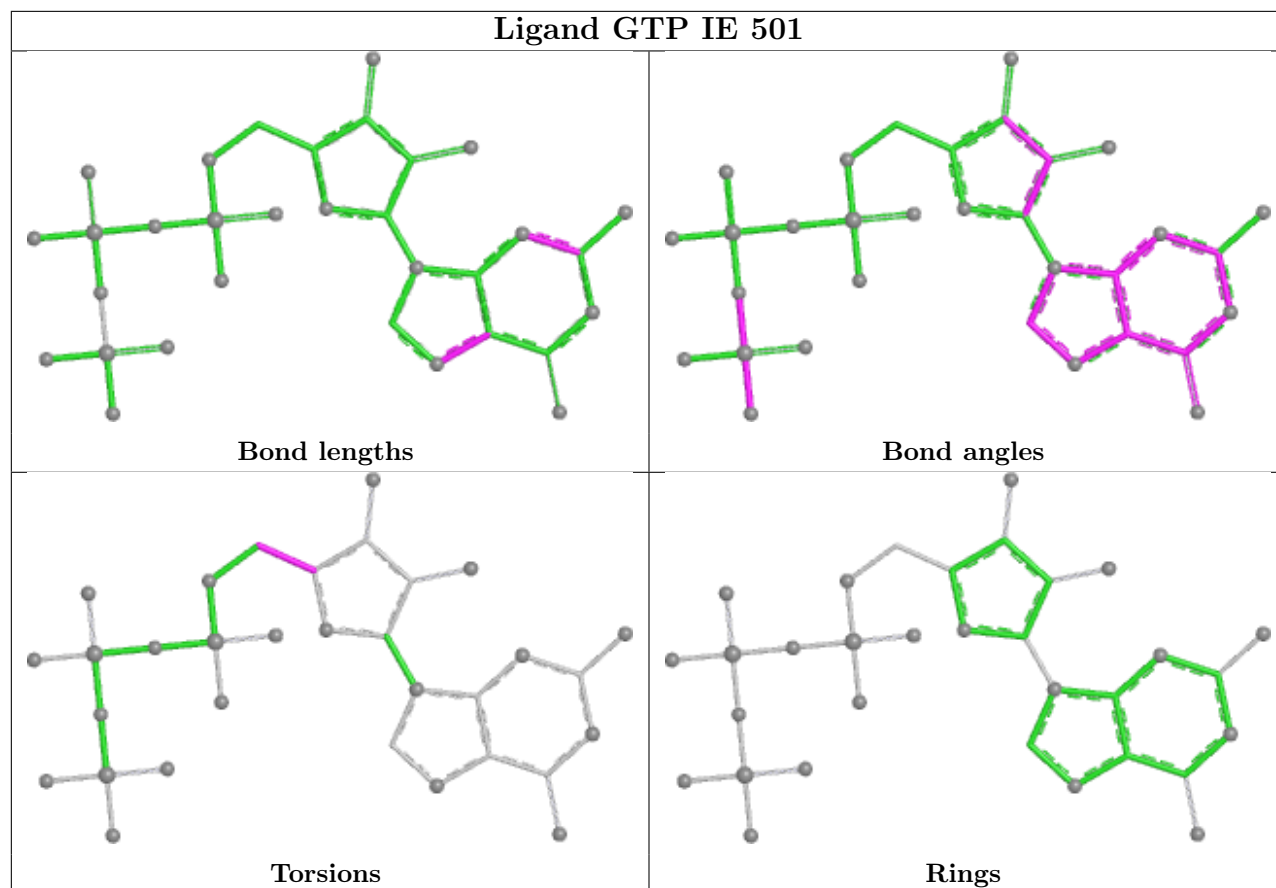


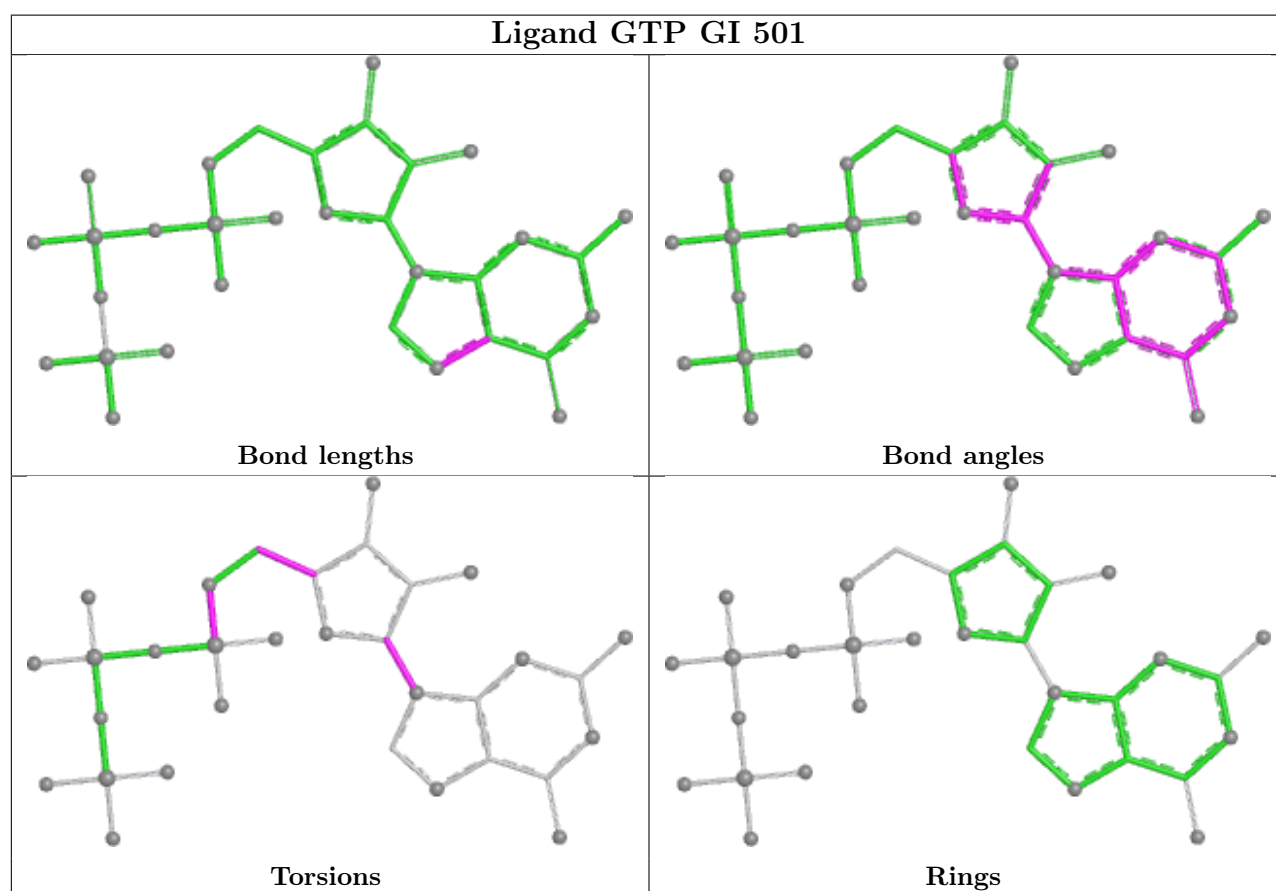
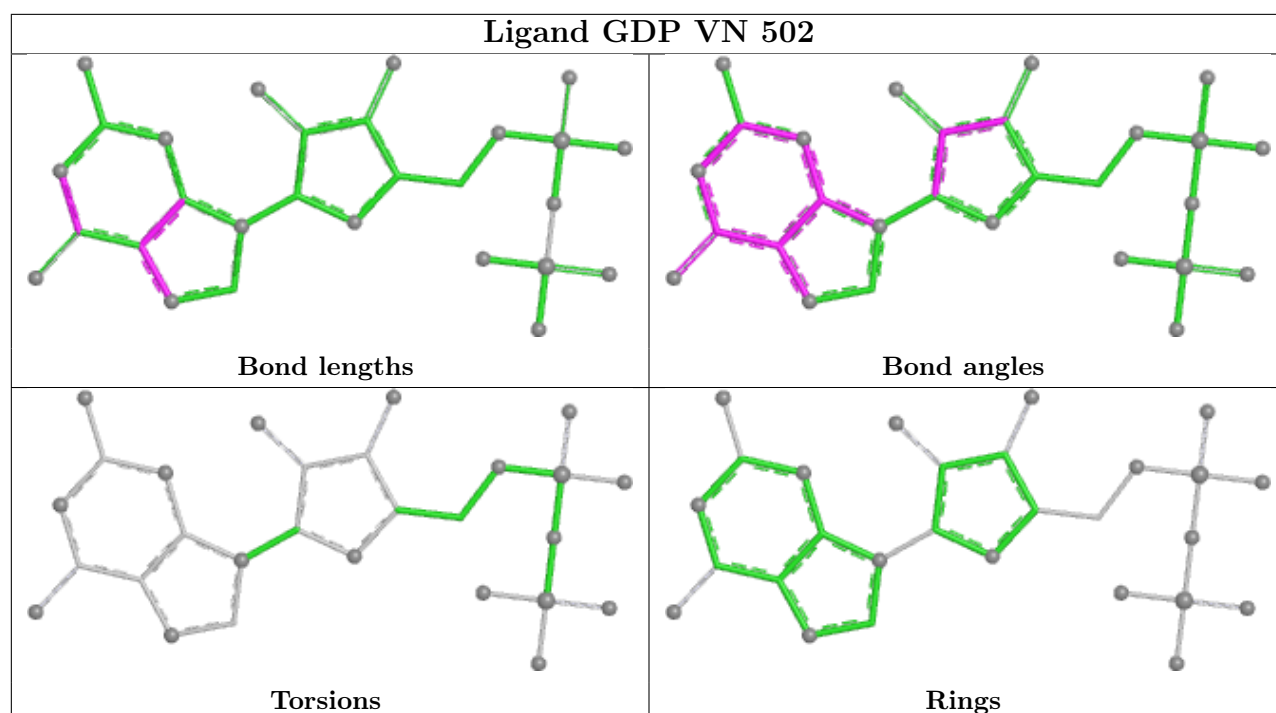
Ligand GDP NF 502

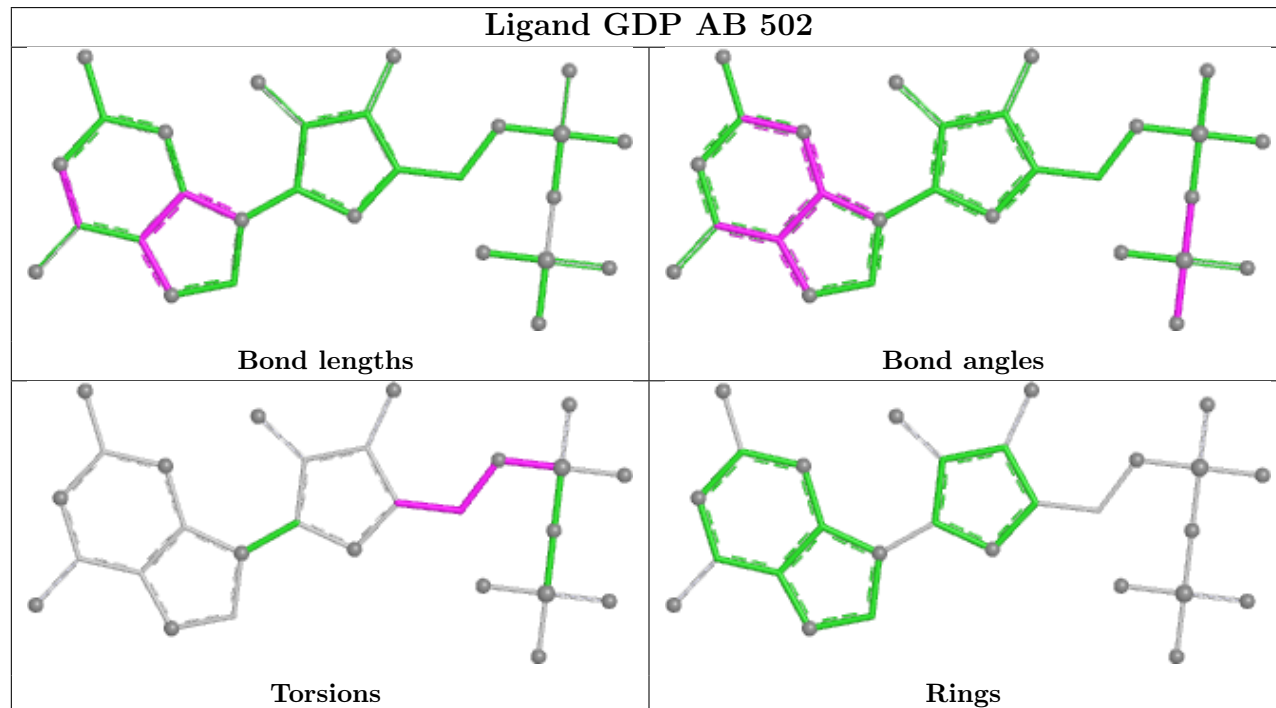
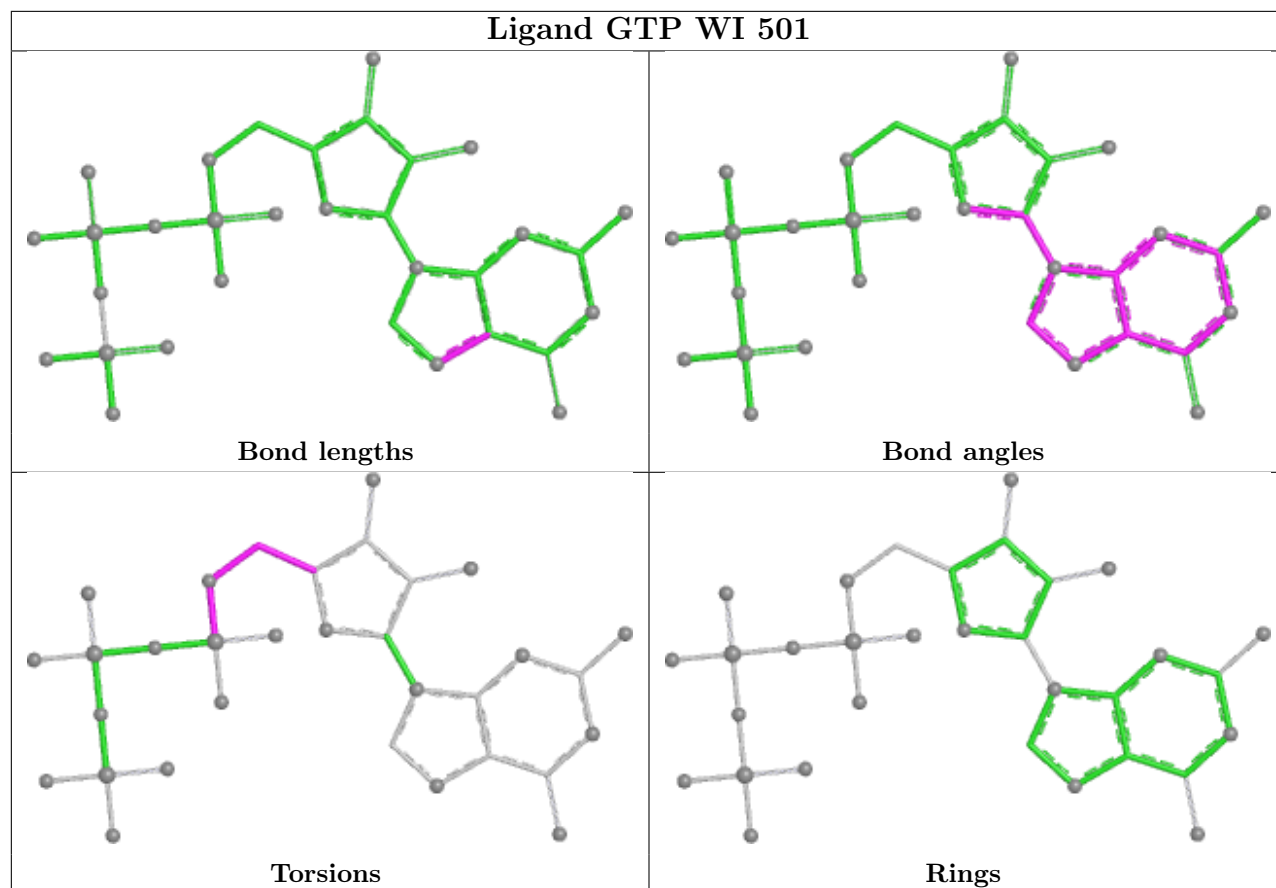


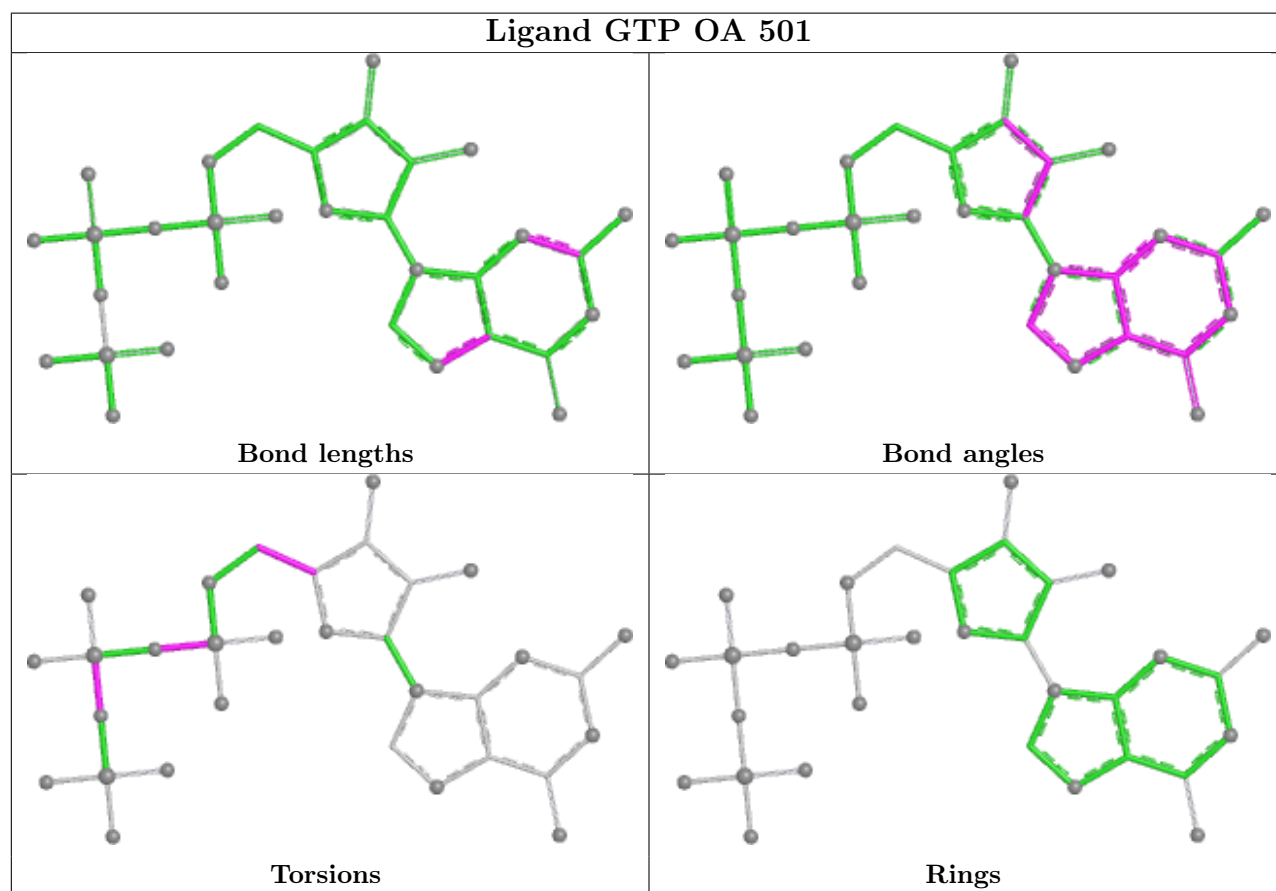
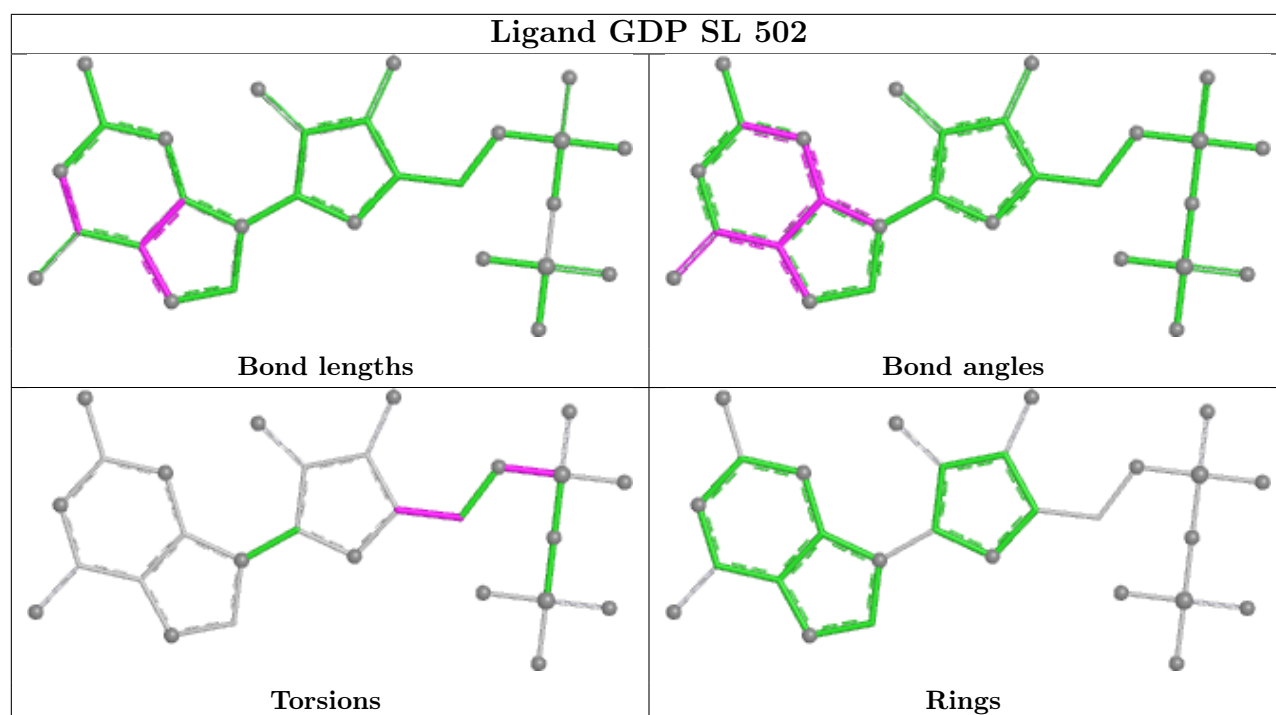




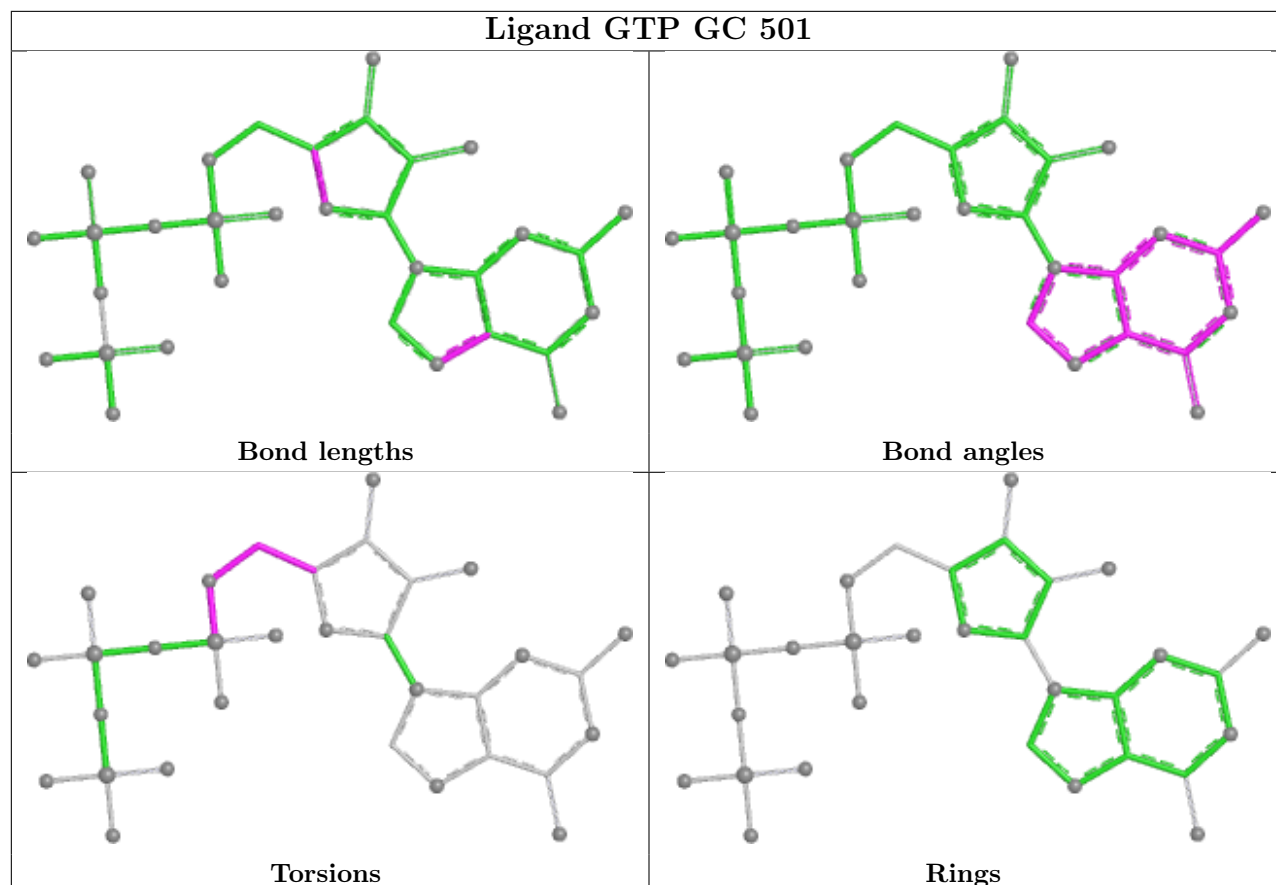




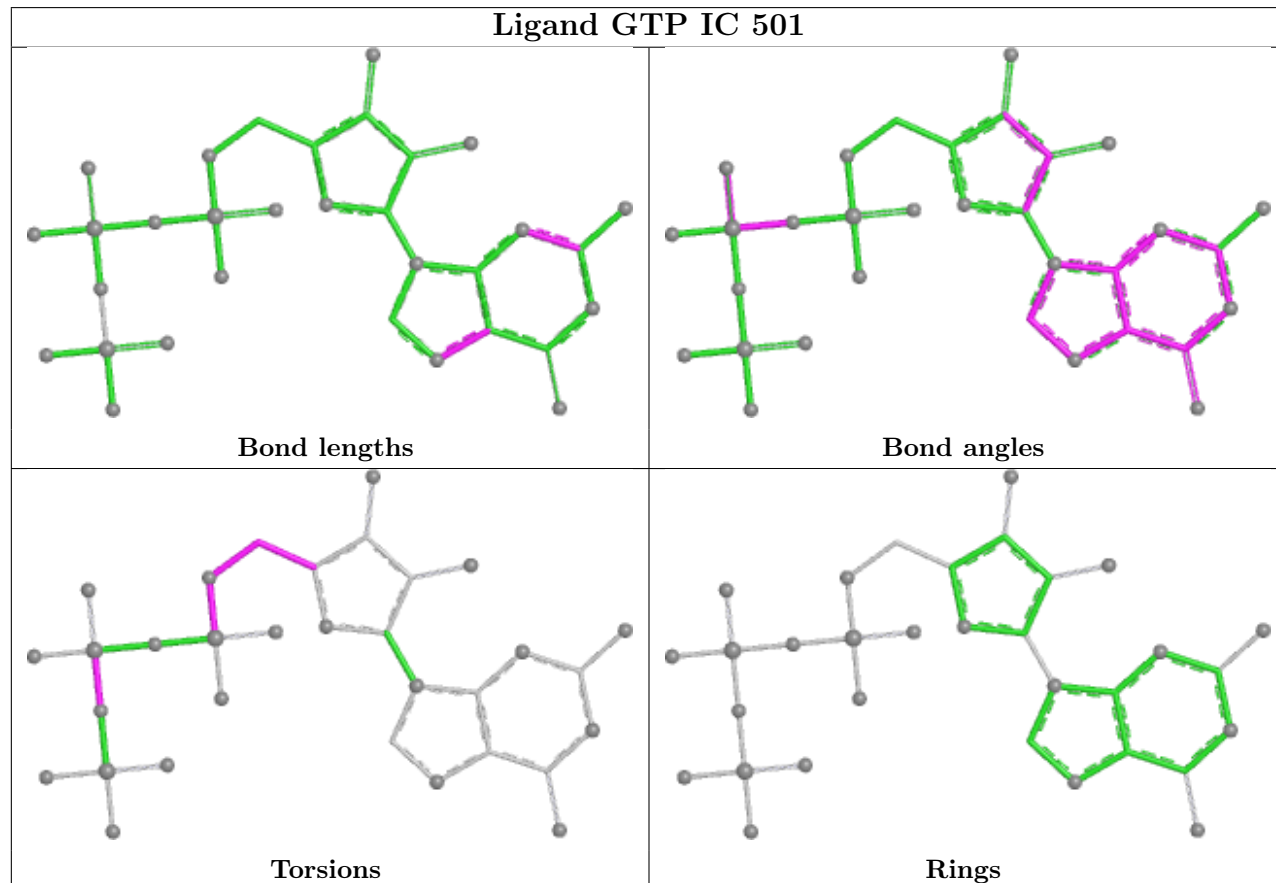


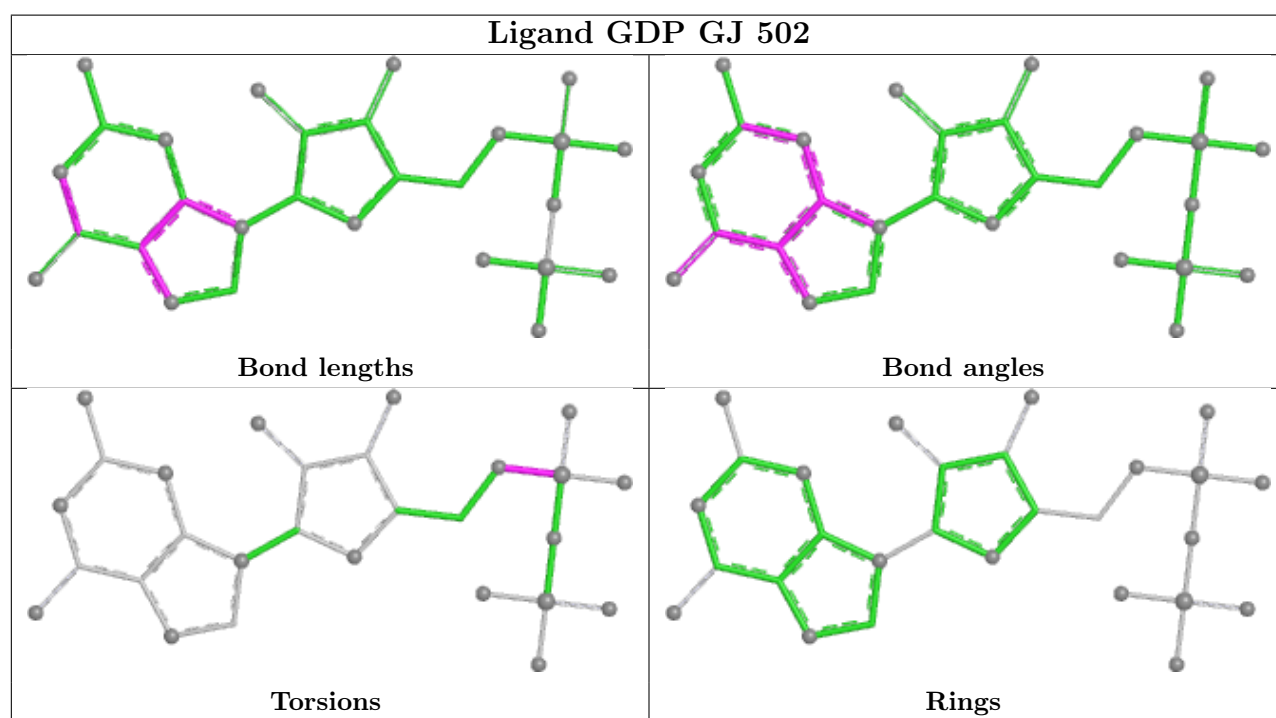
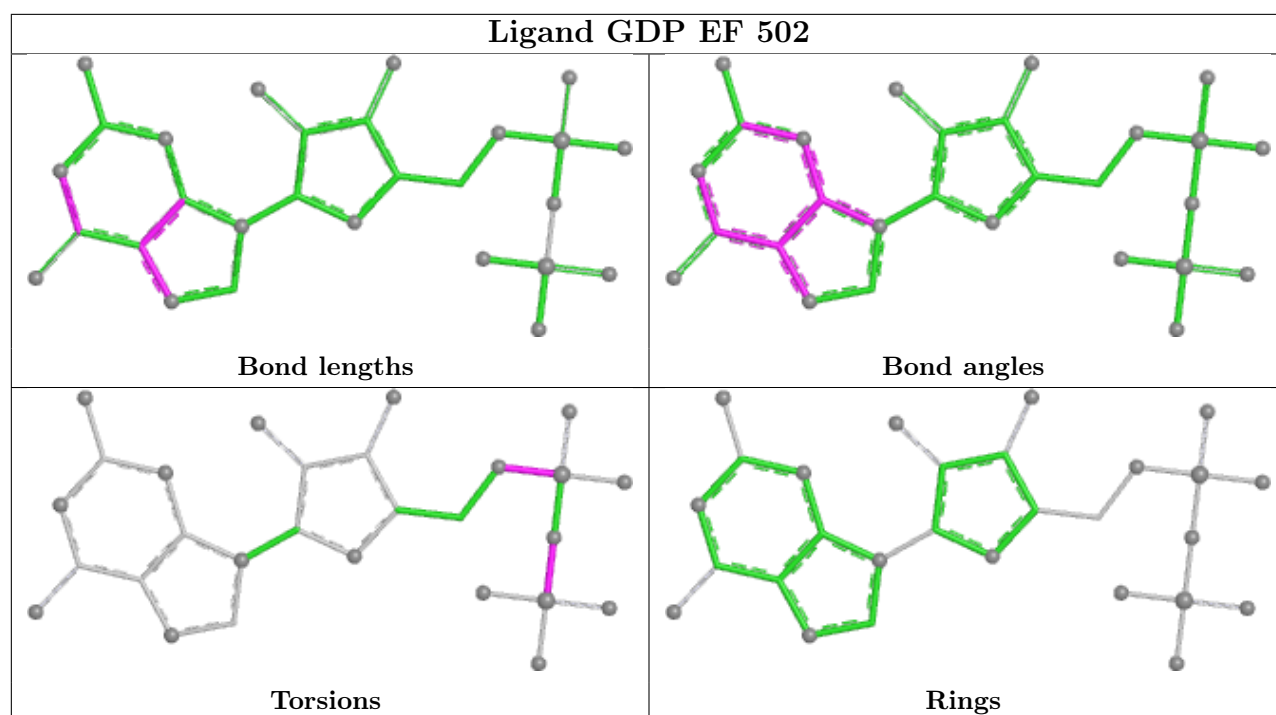


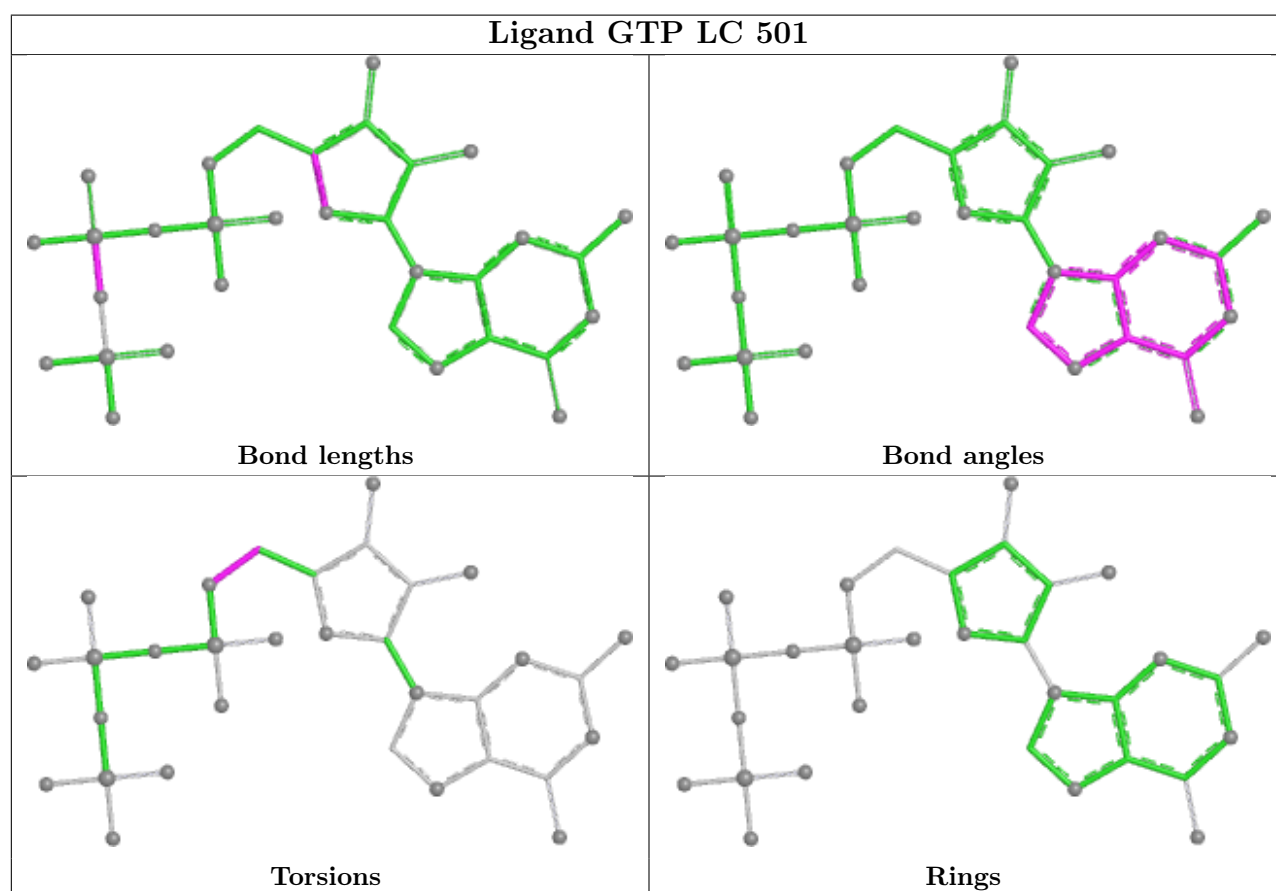
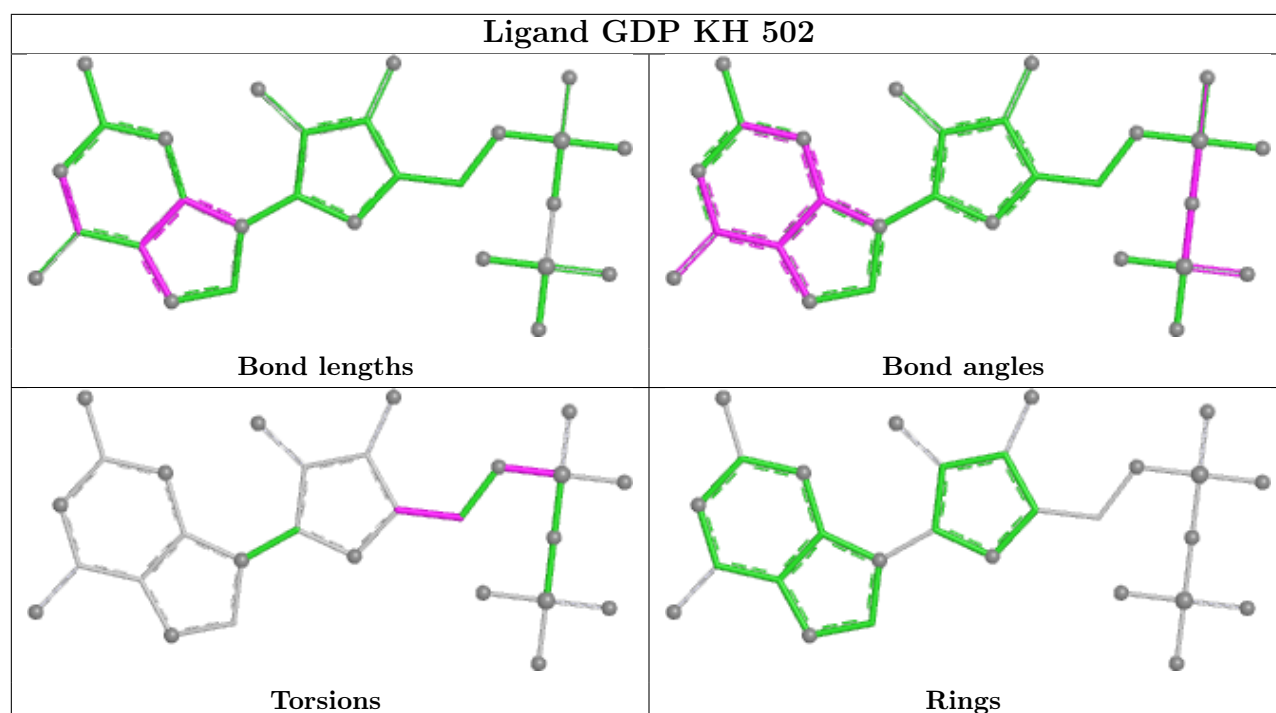
Ligand GTP GC 501

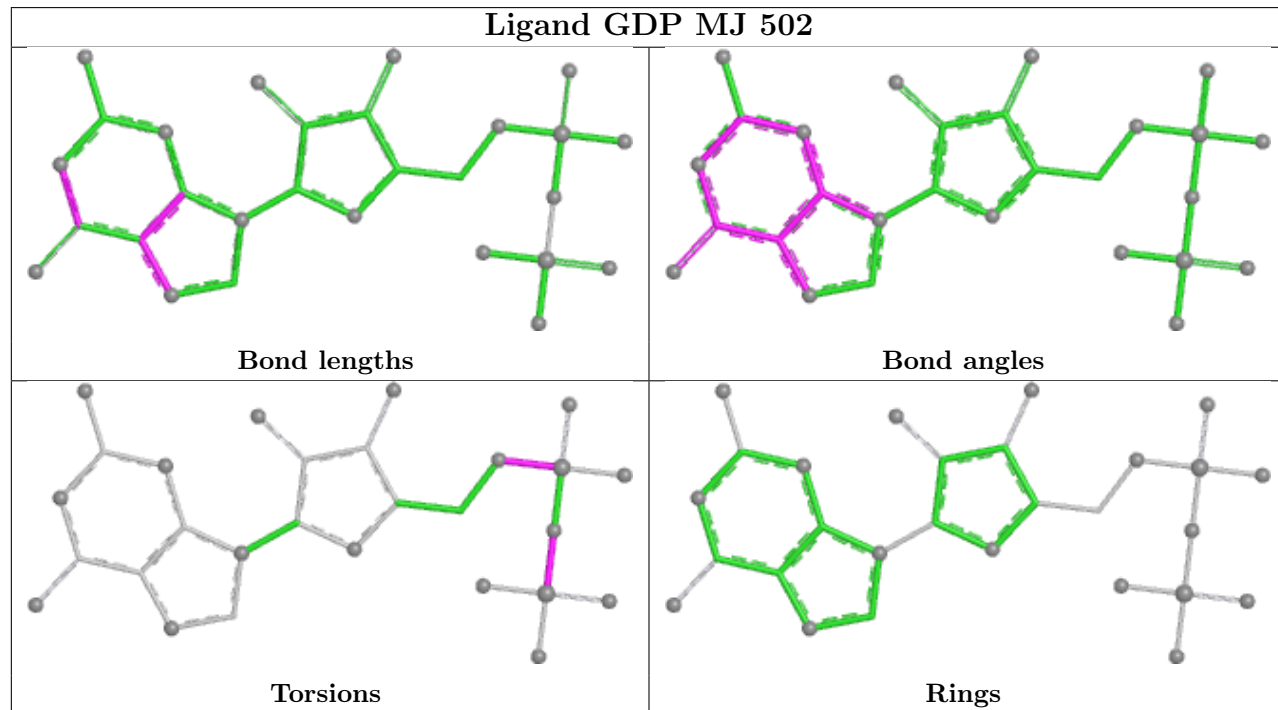
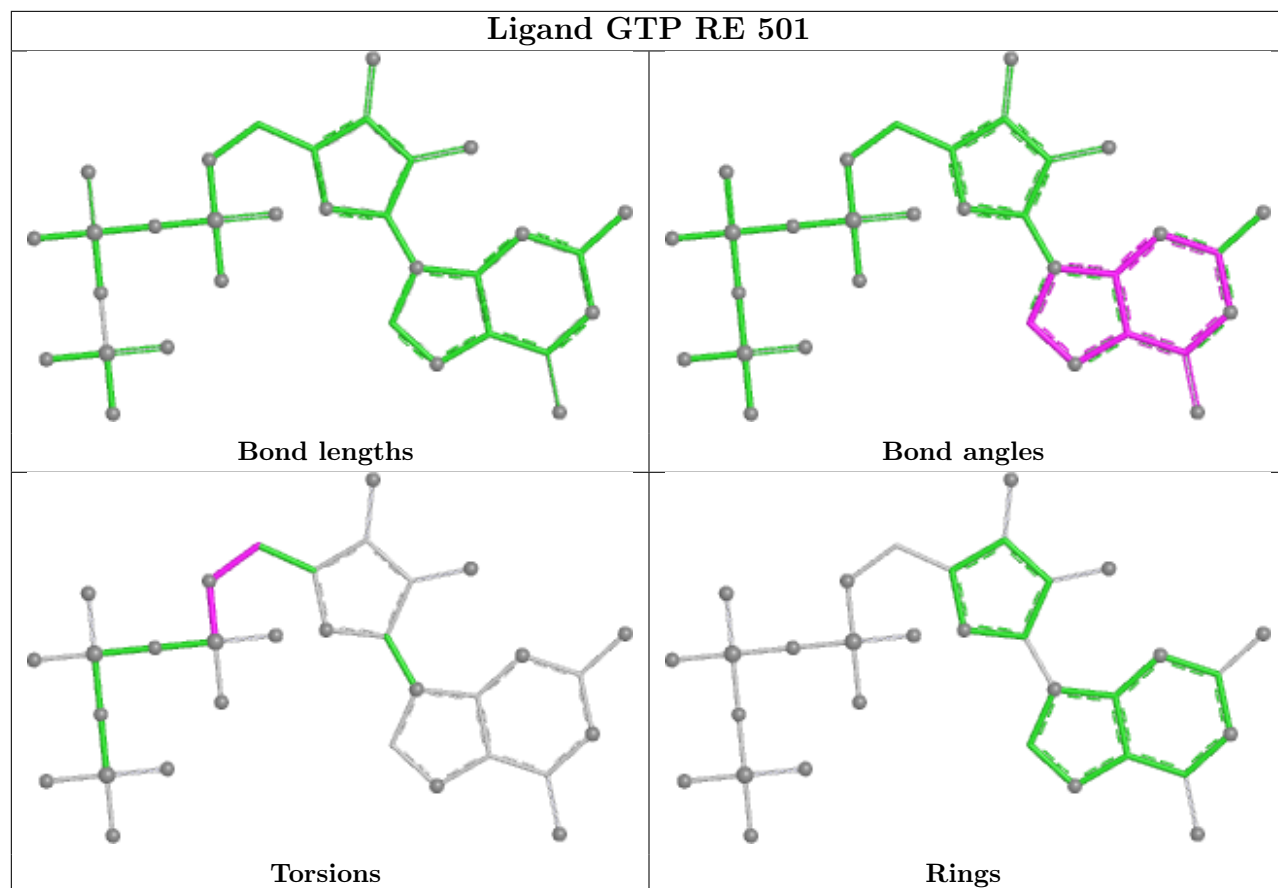


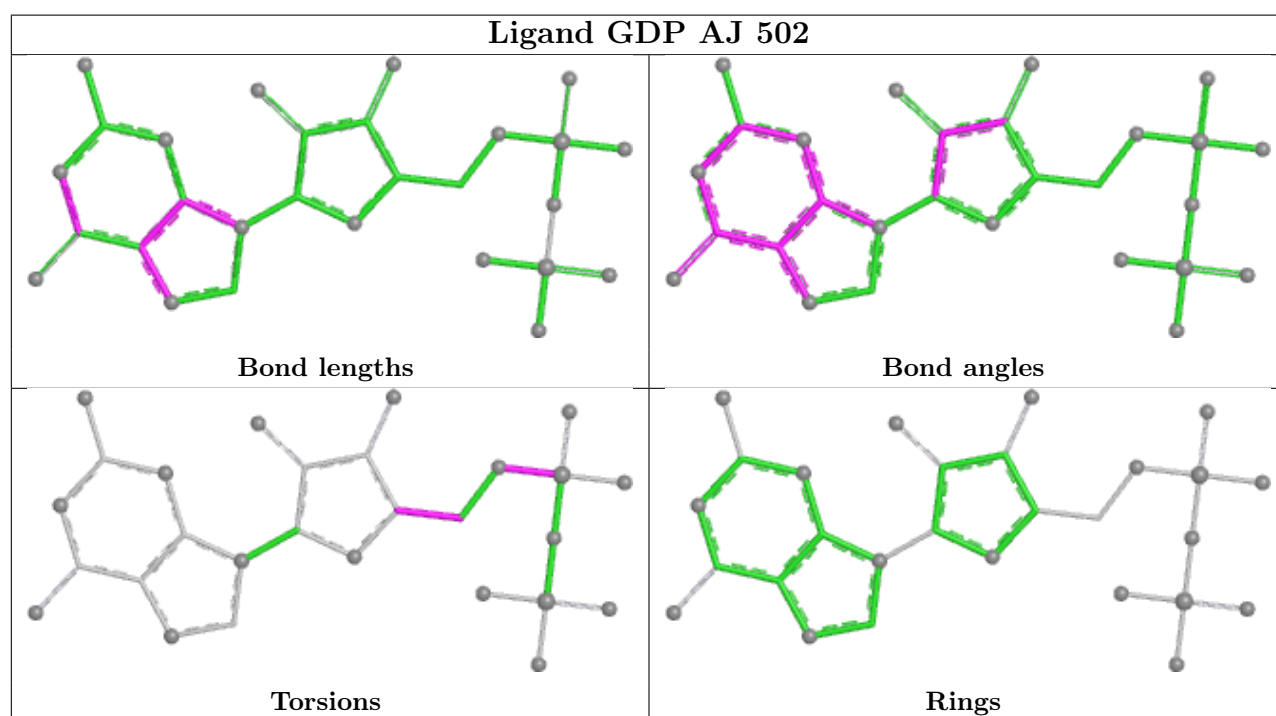
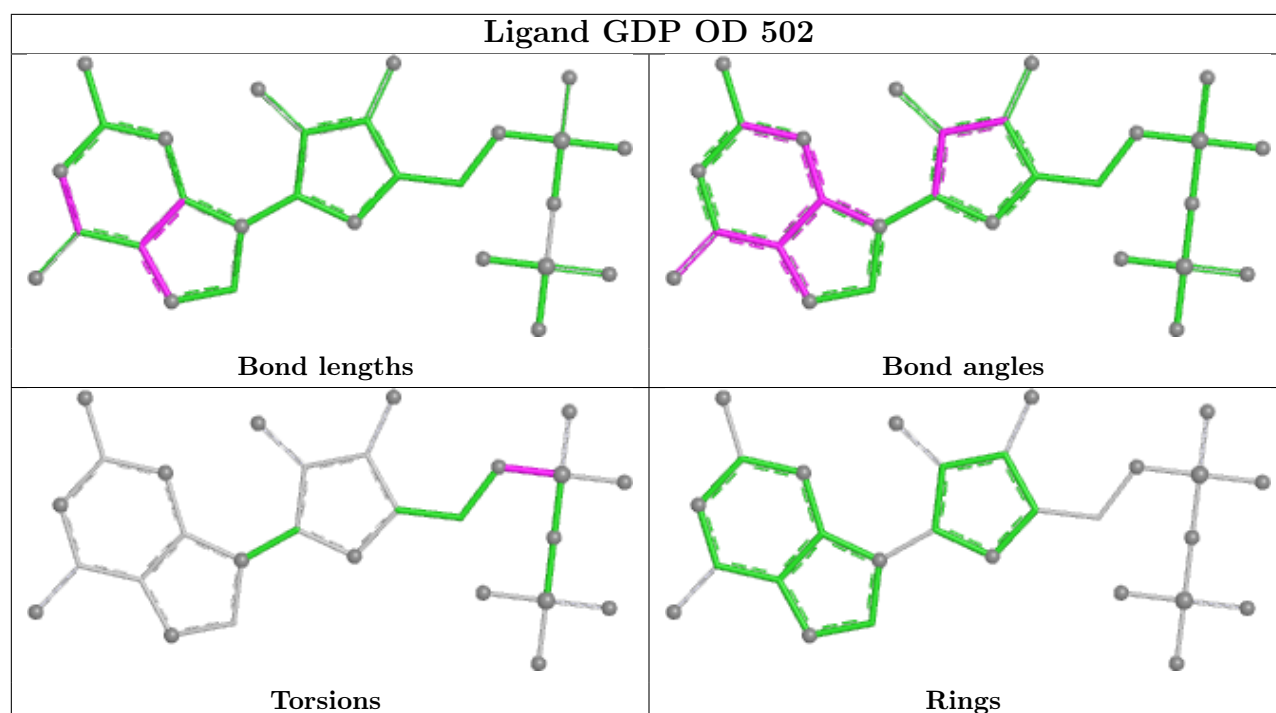
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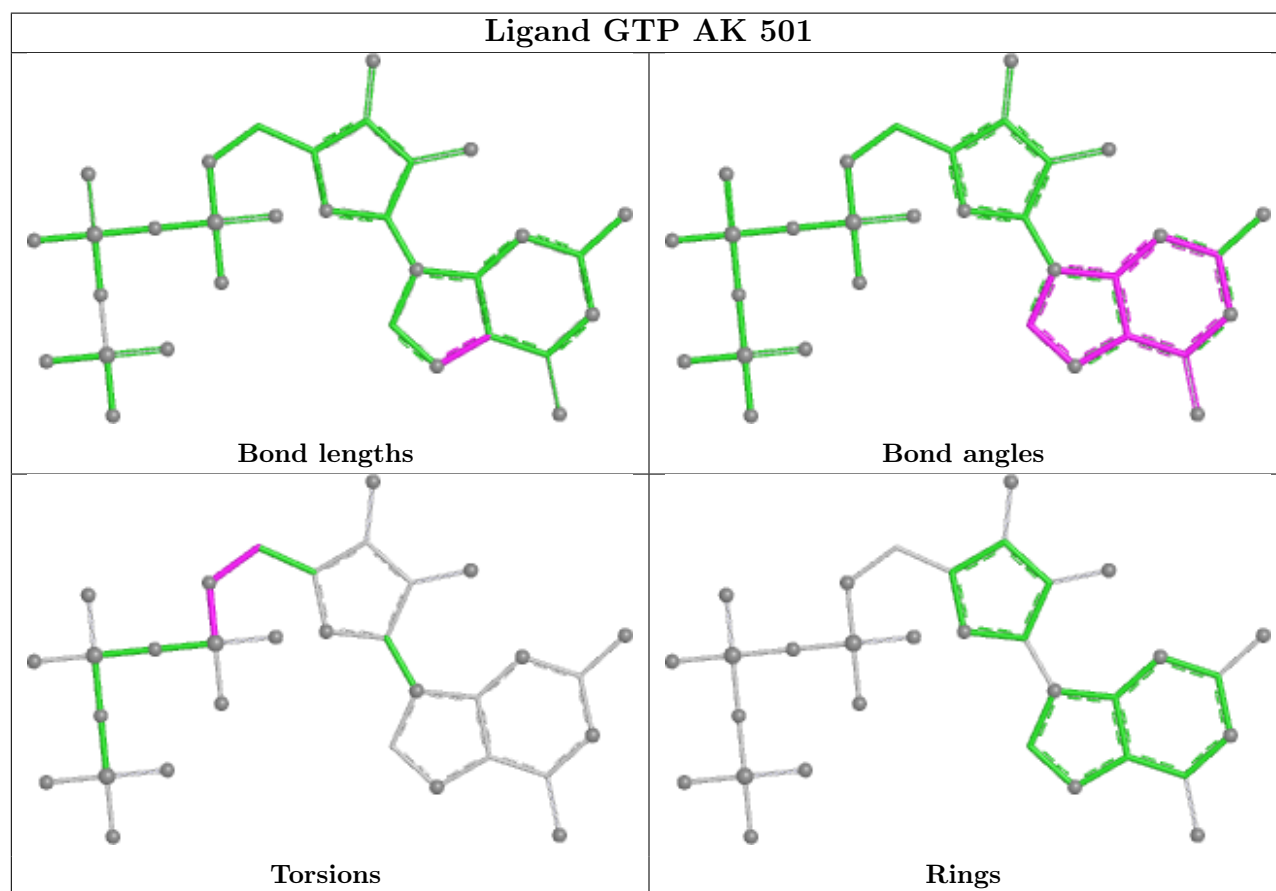
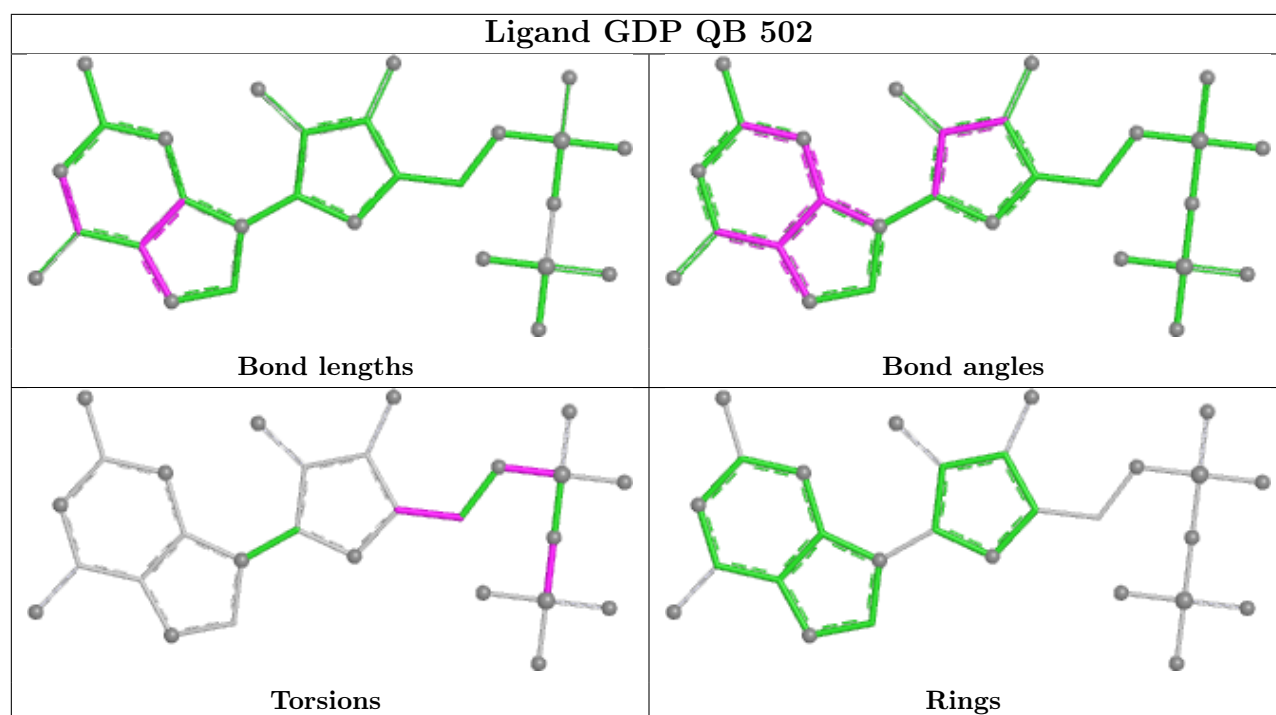




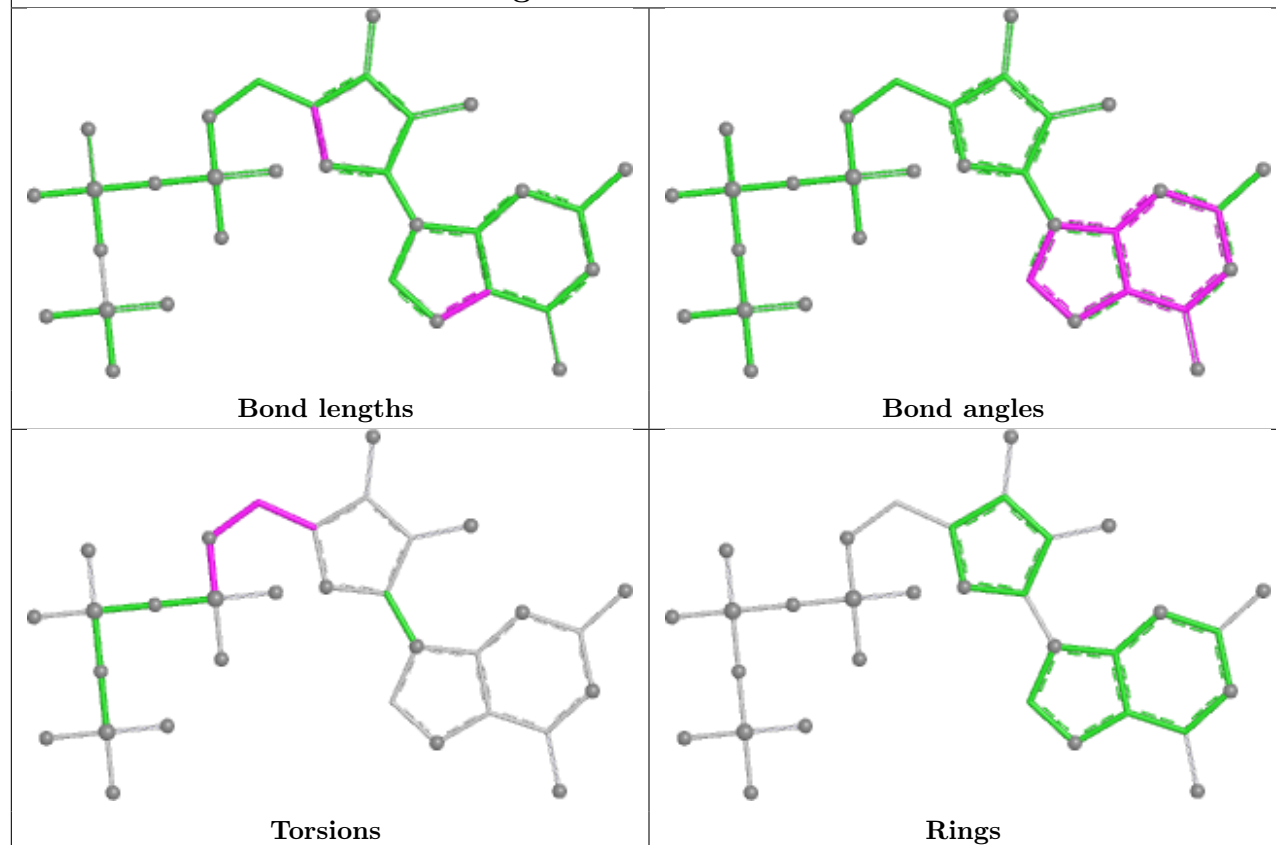




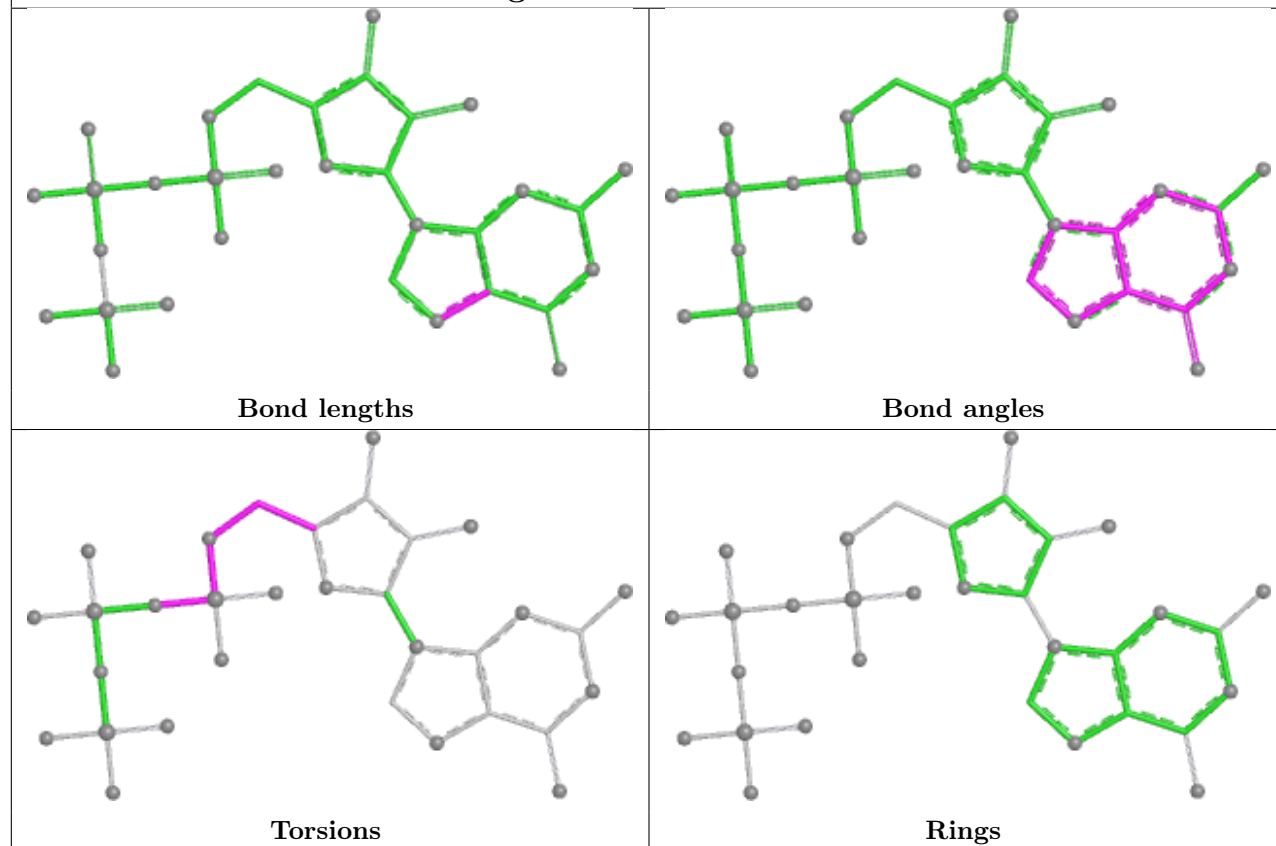


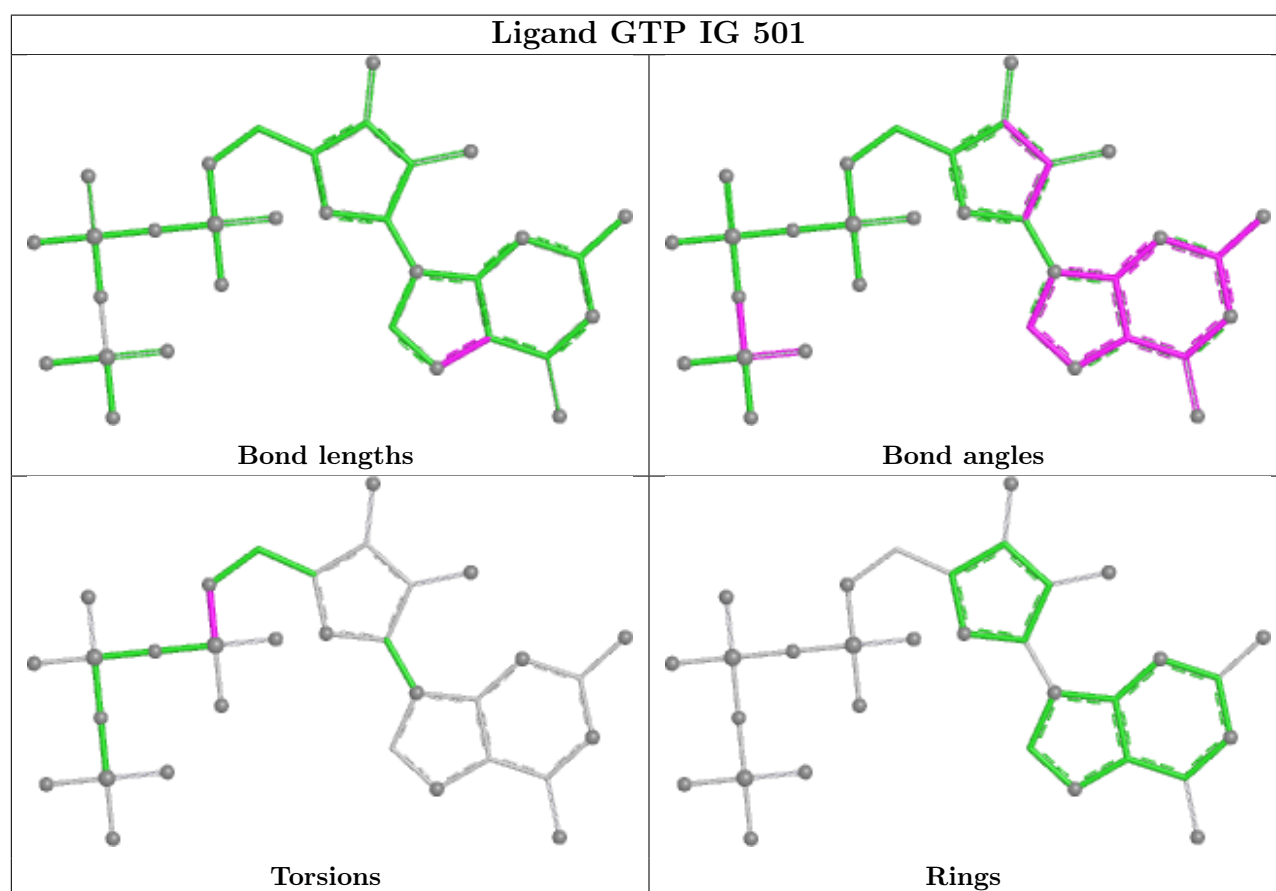
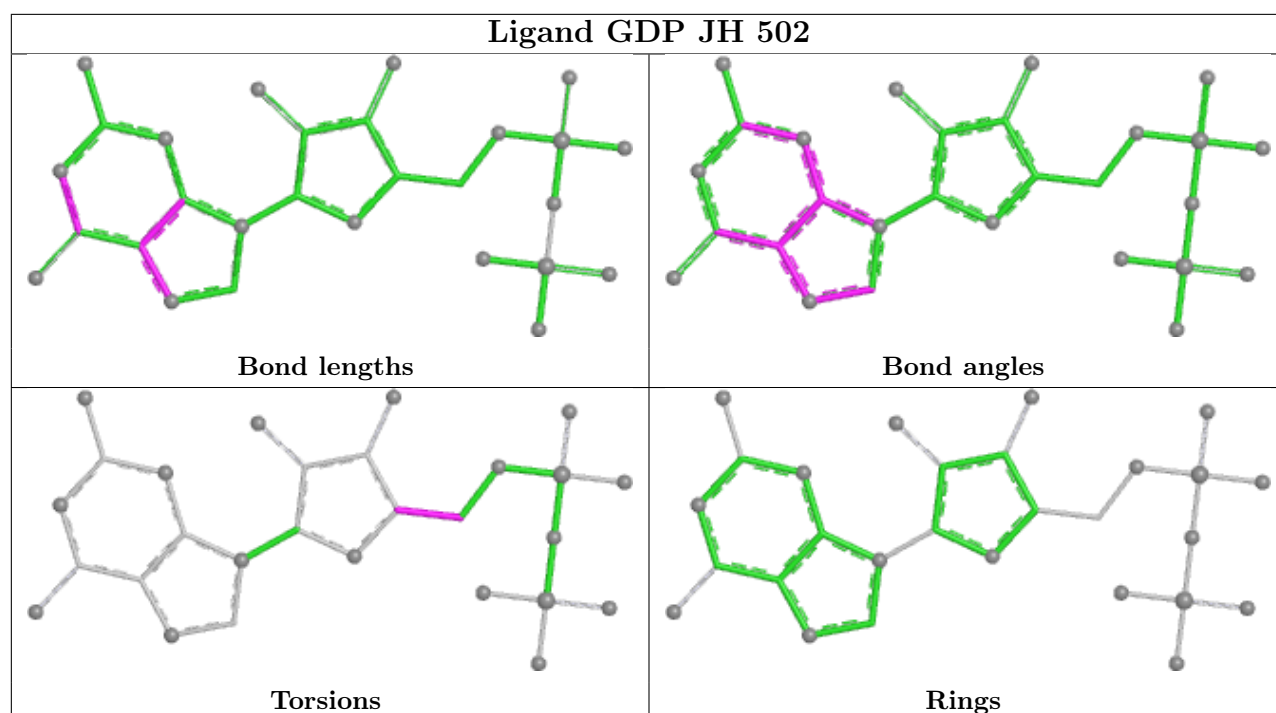


Ligand GTP AM 501

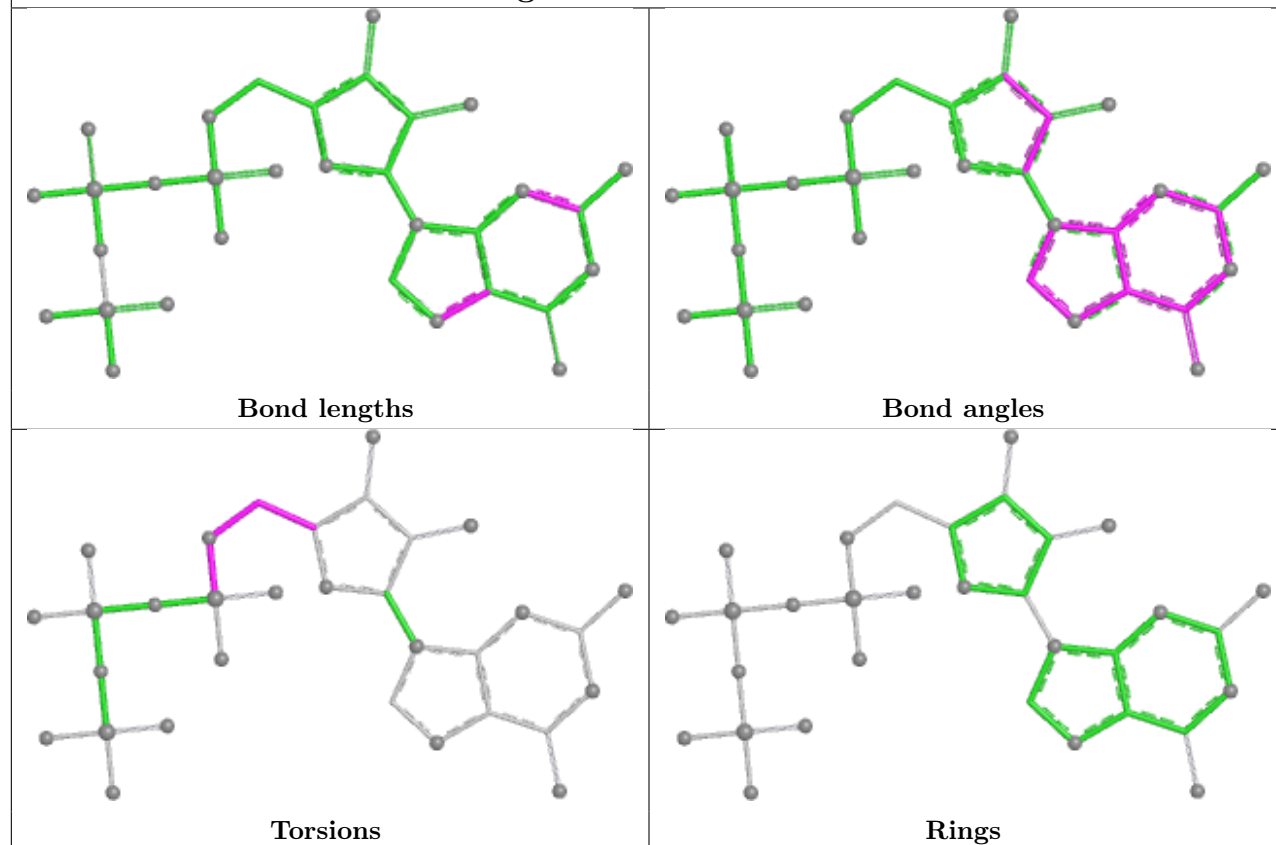


Ligand GTP WM 501

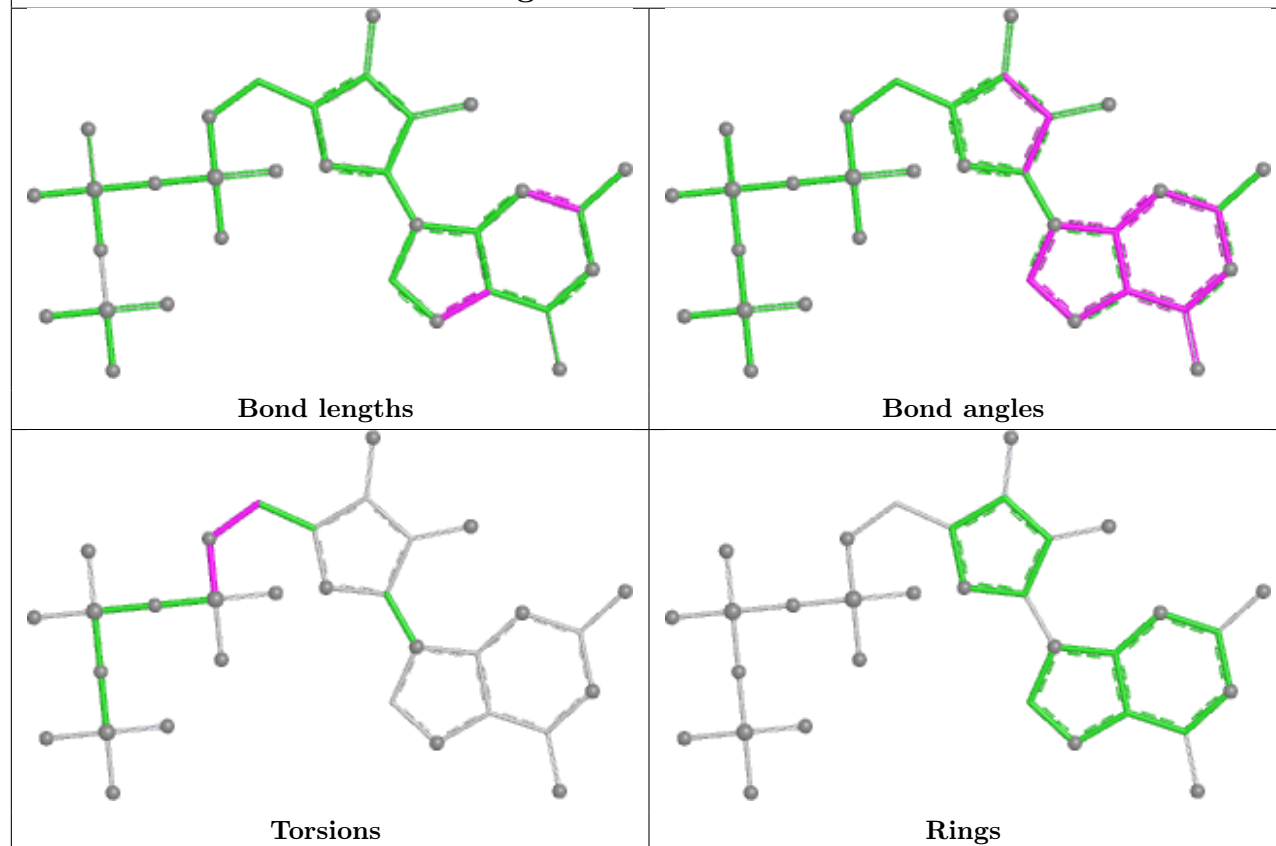




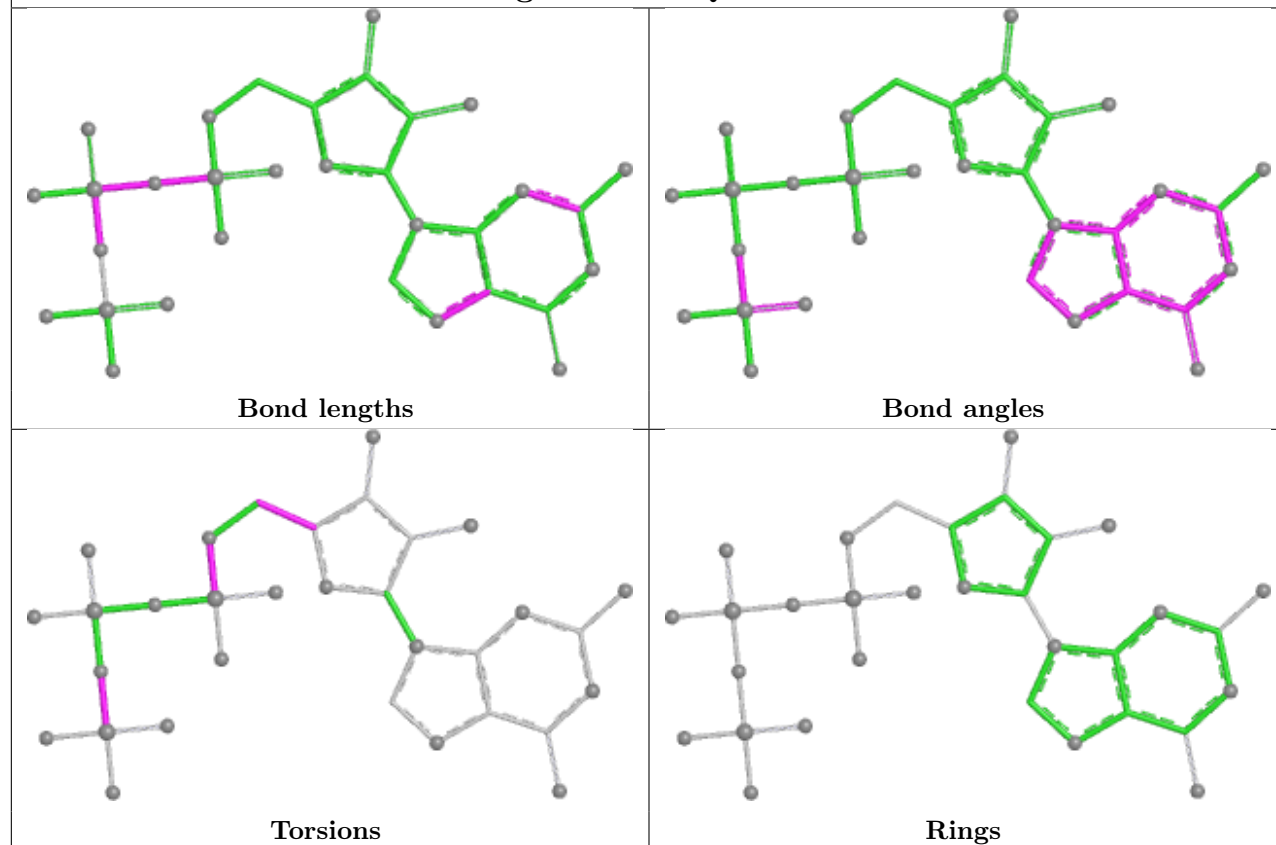
Ligand GTP OC 501



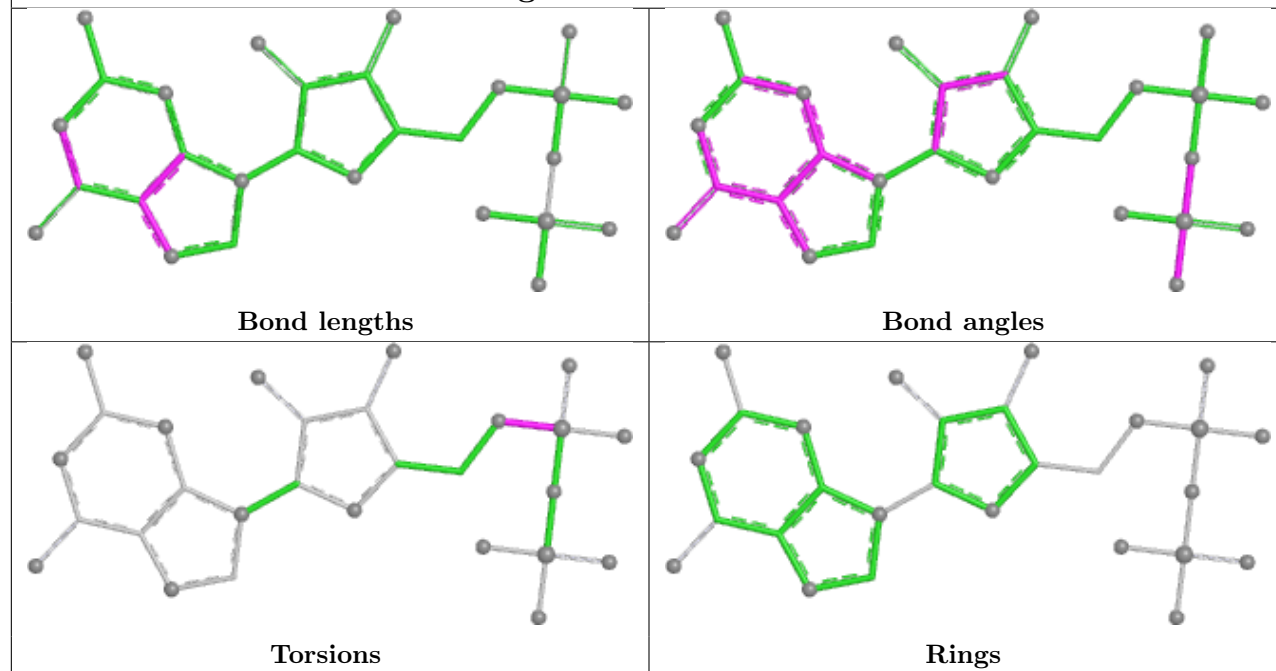
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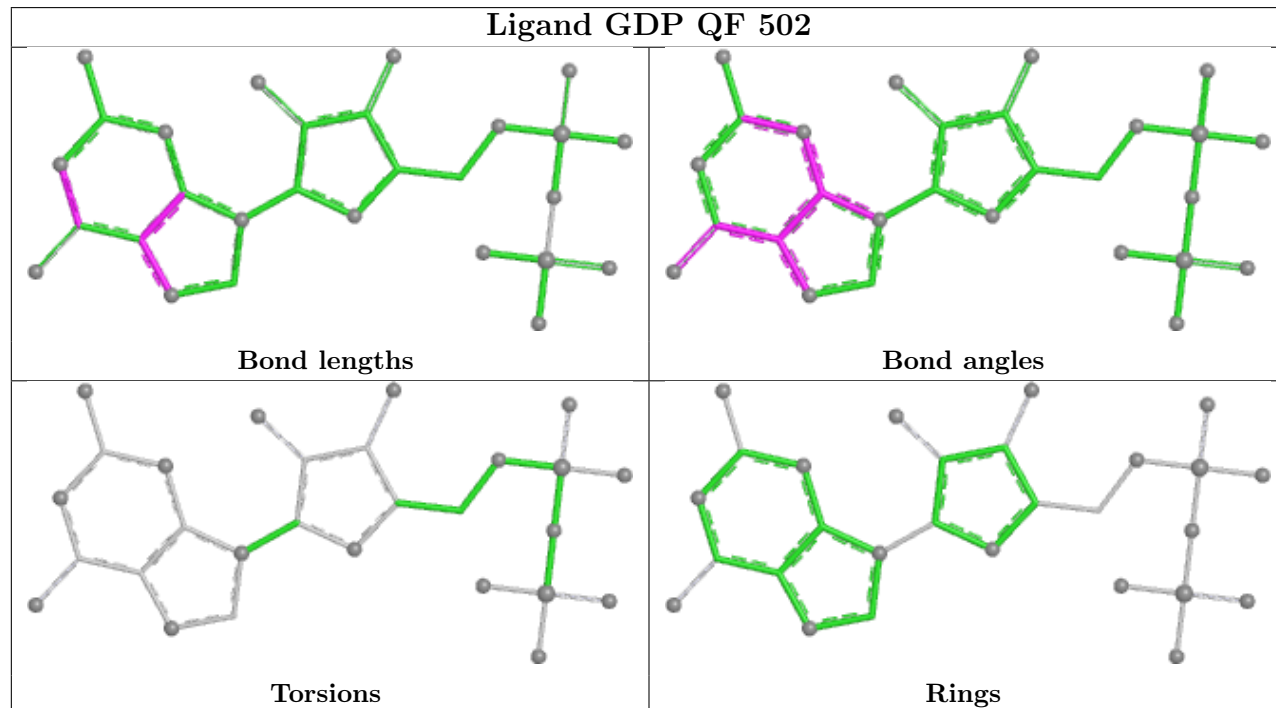
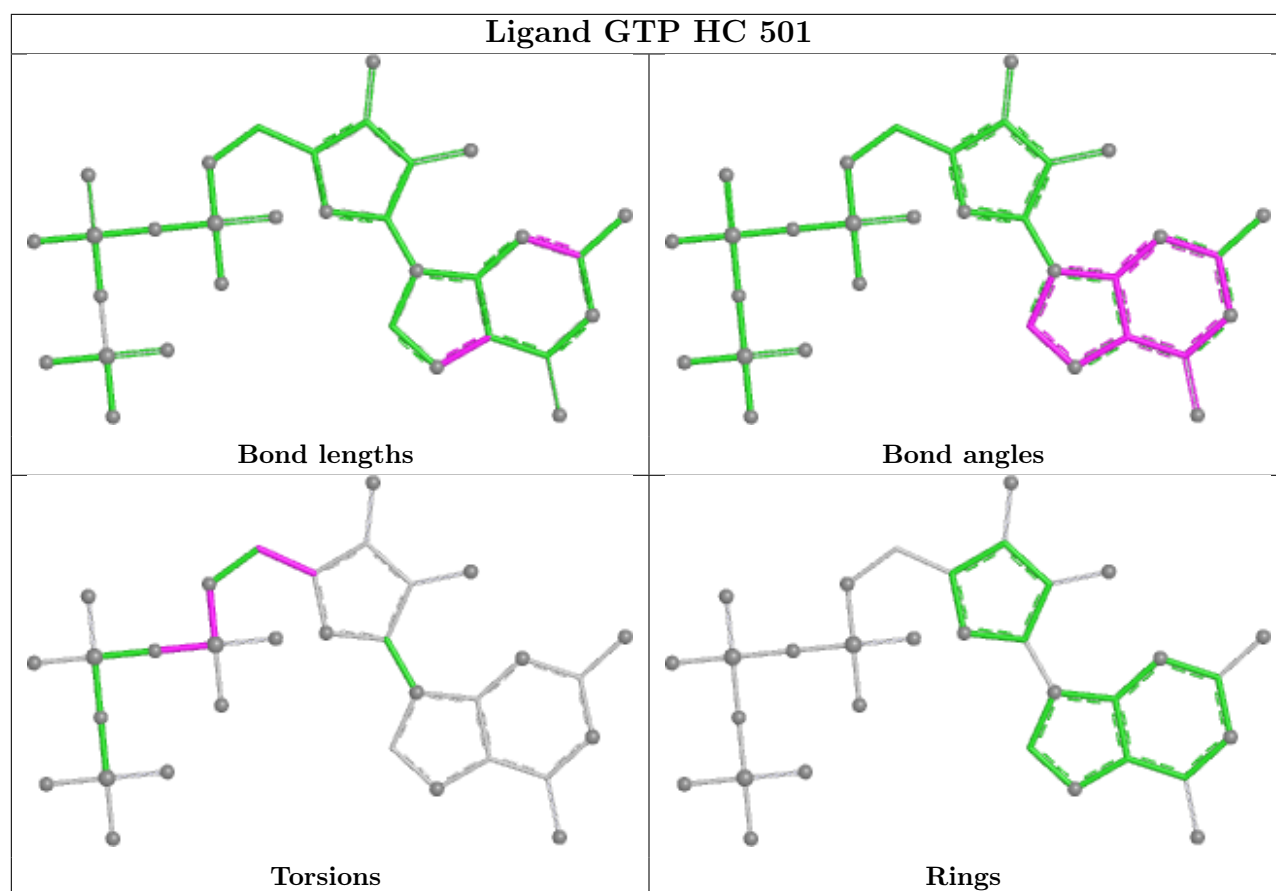


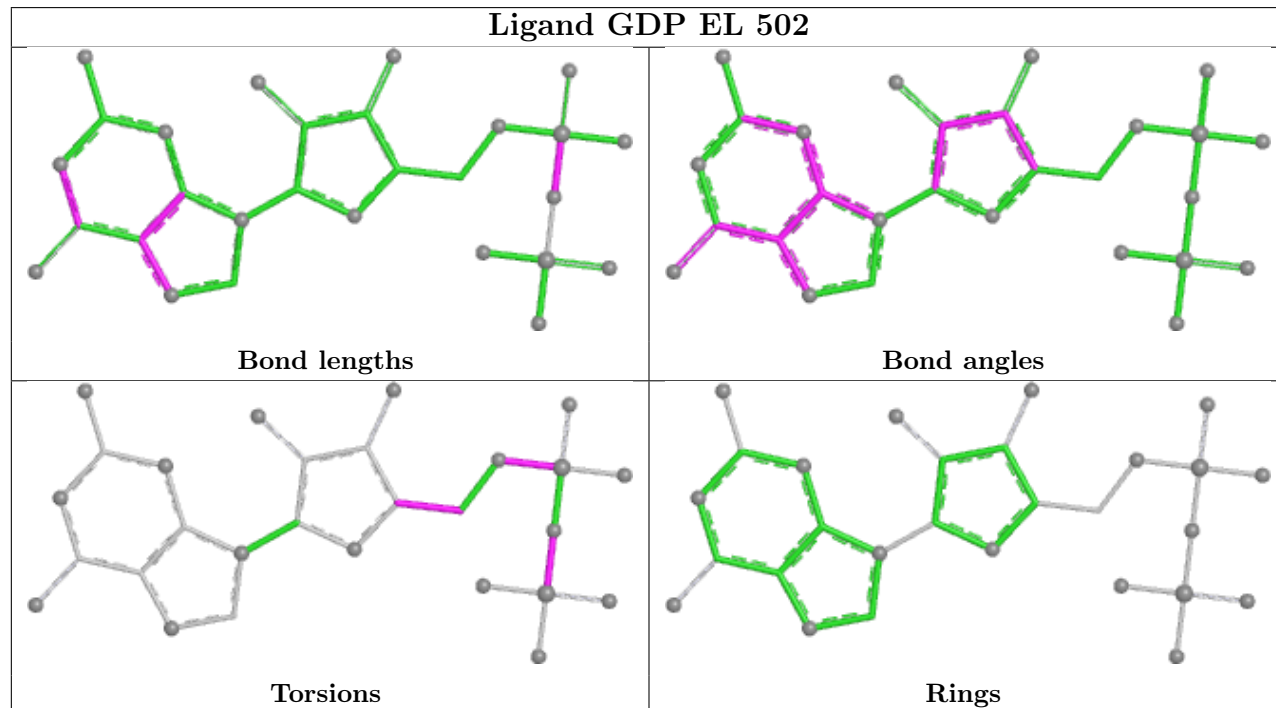
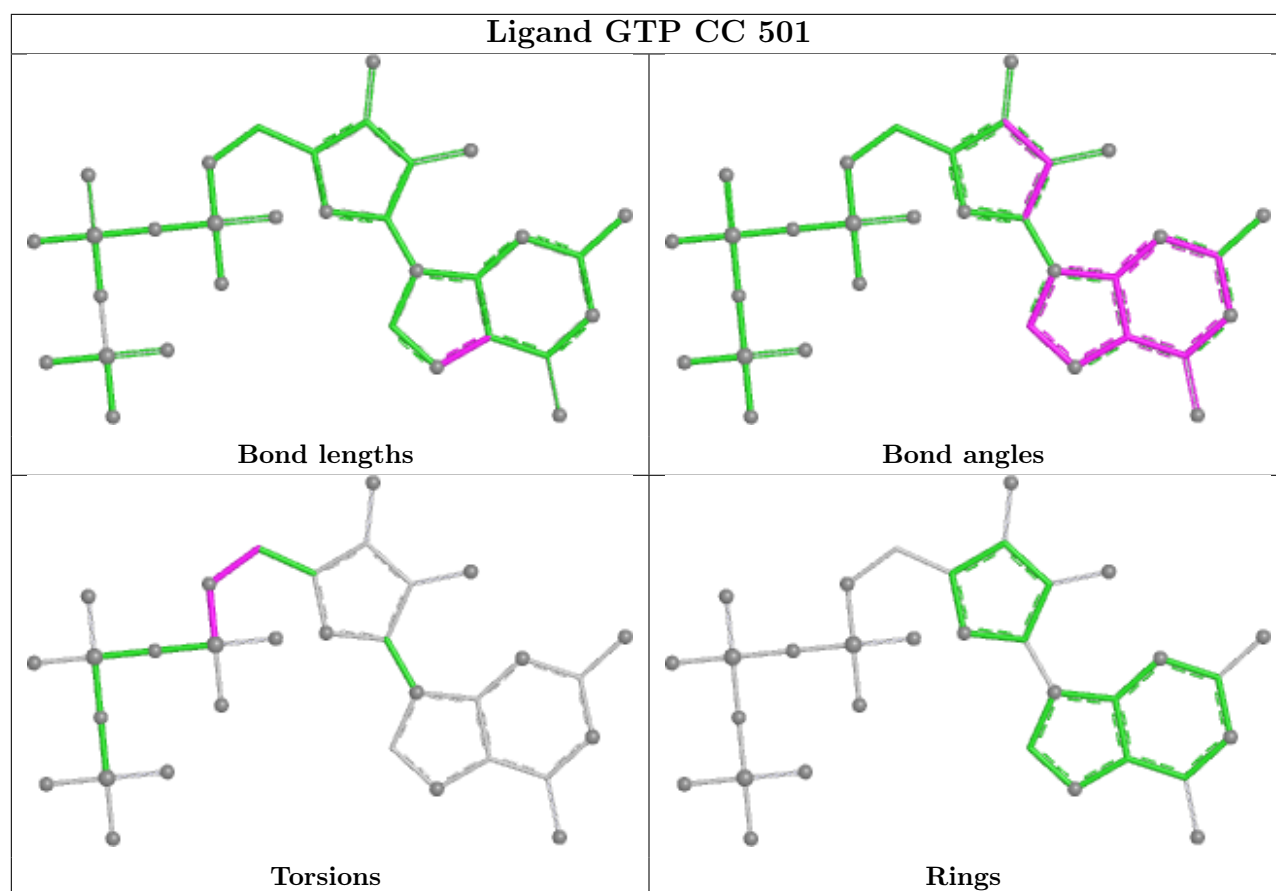
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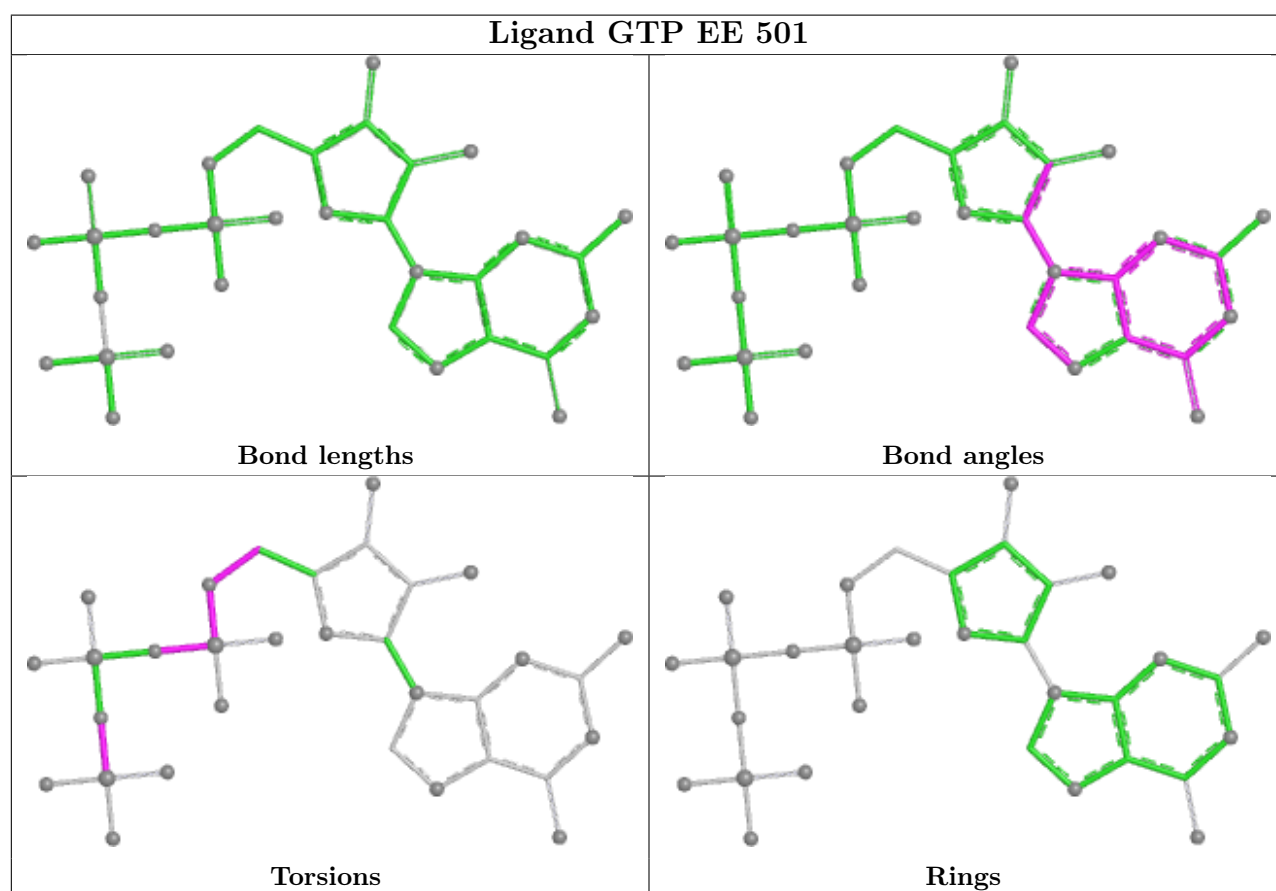
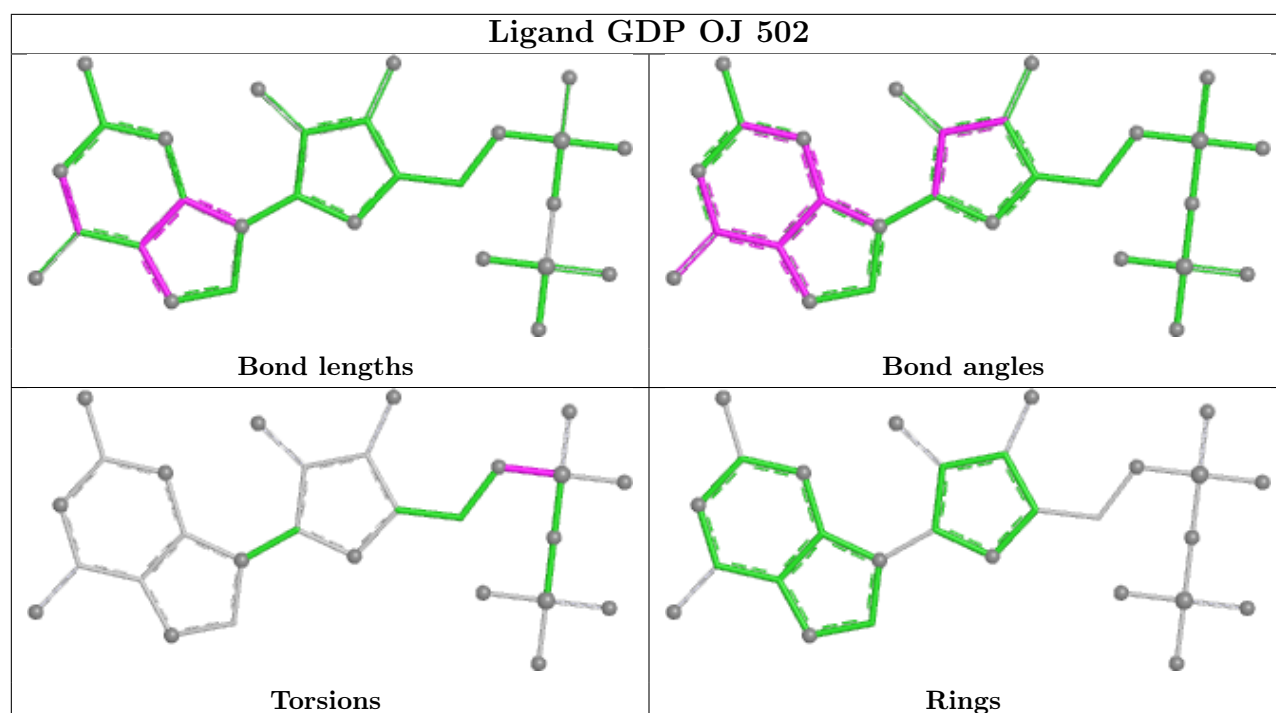


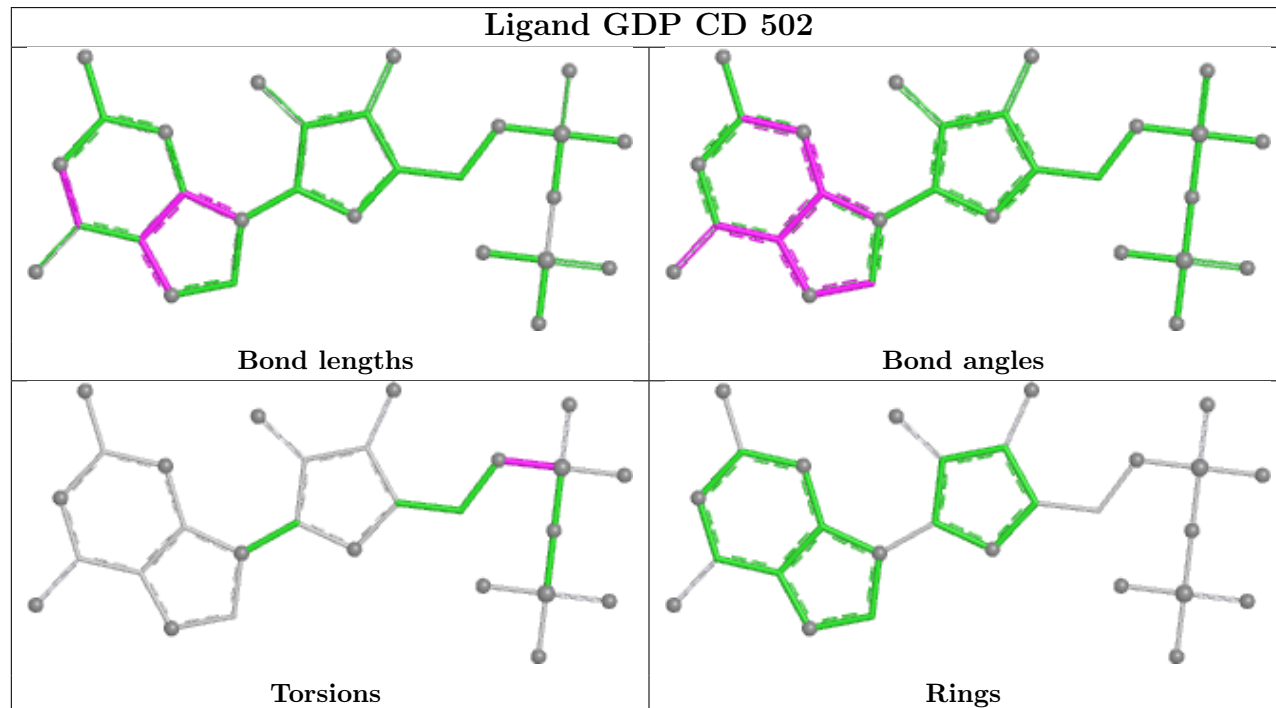
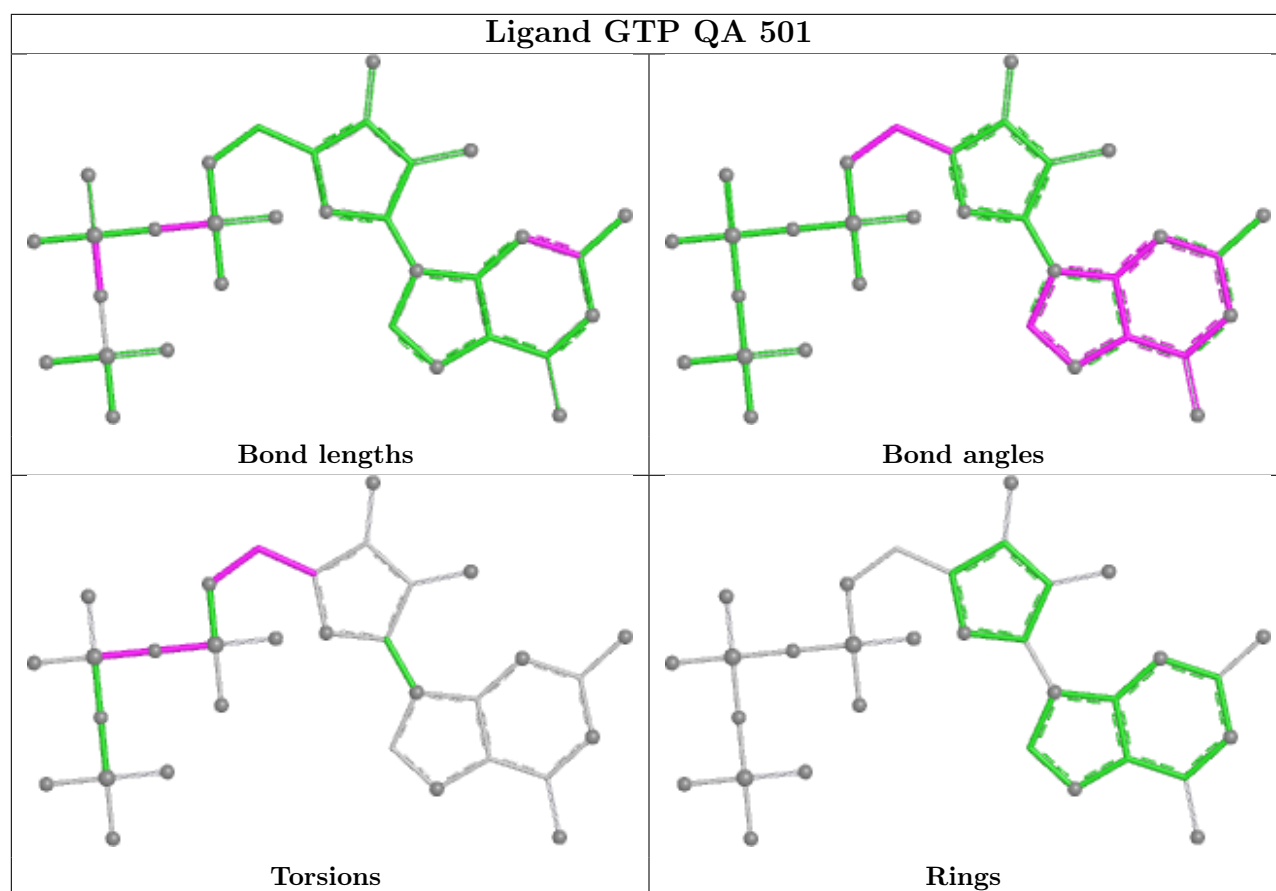
Ligand GDP OL 502



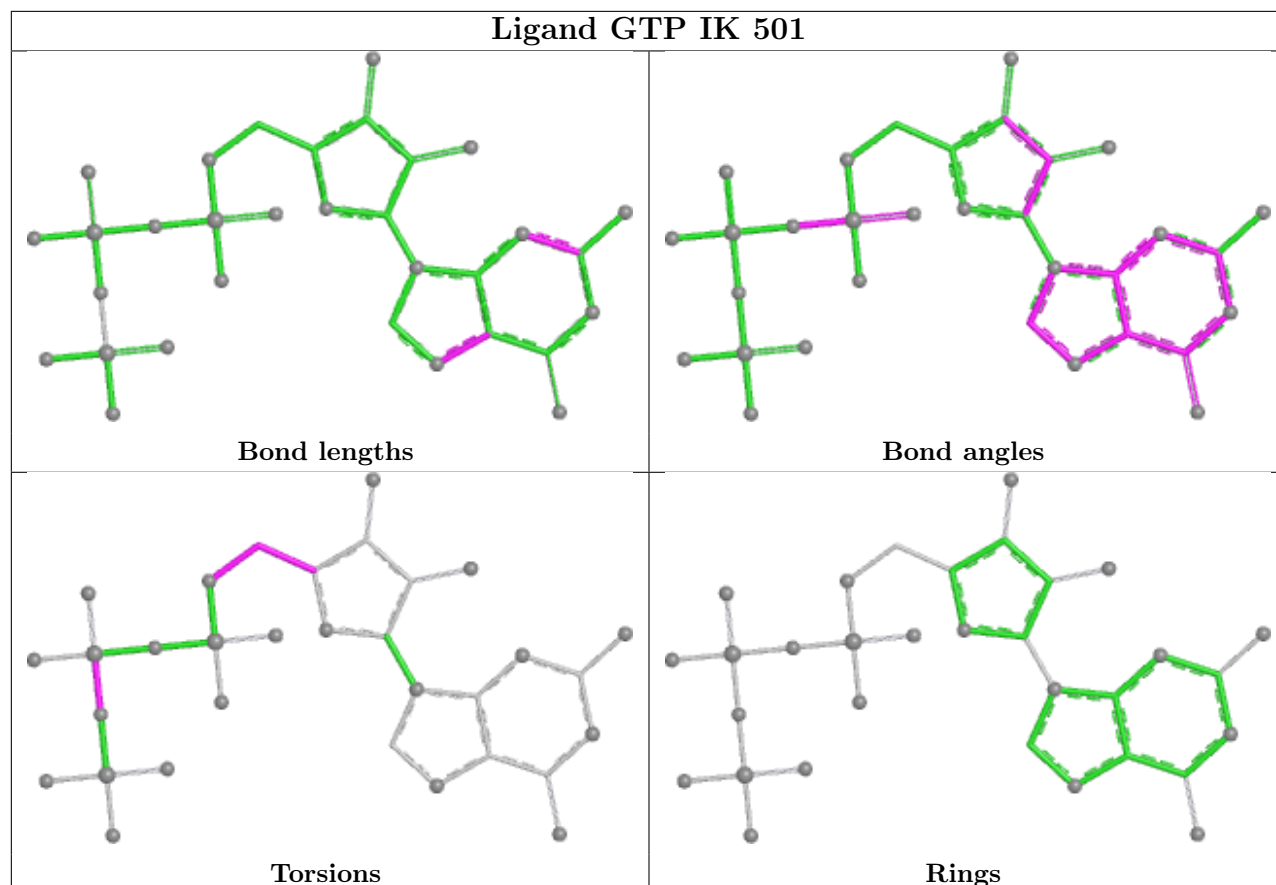




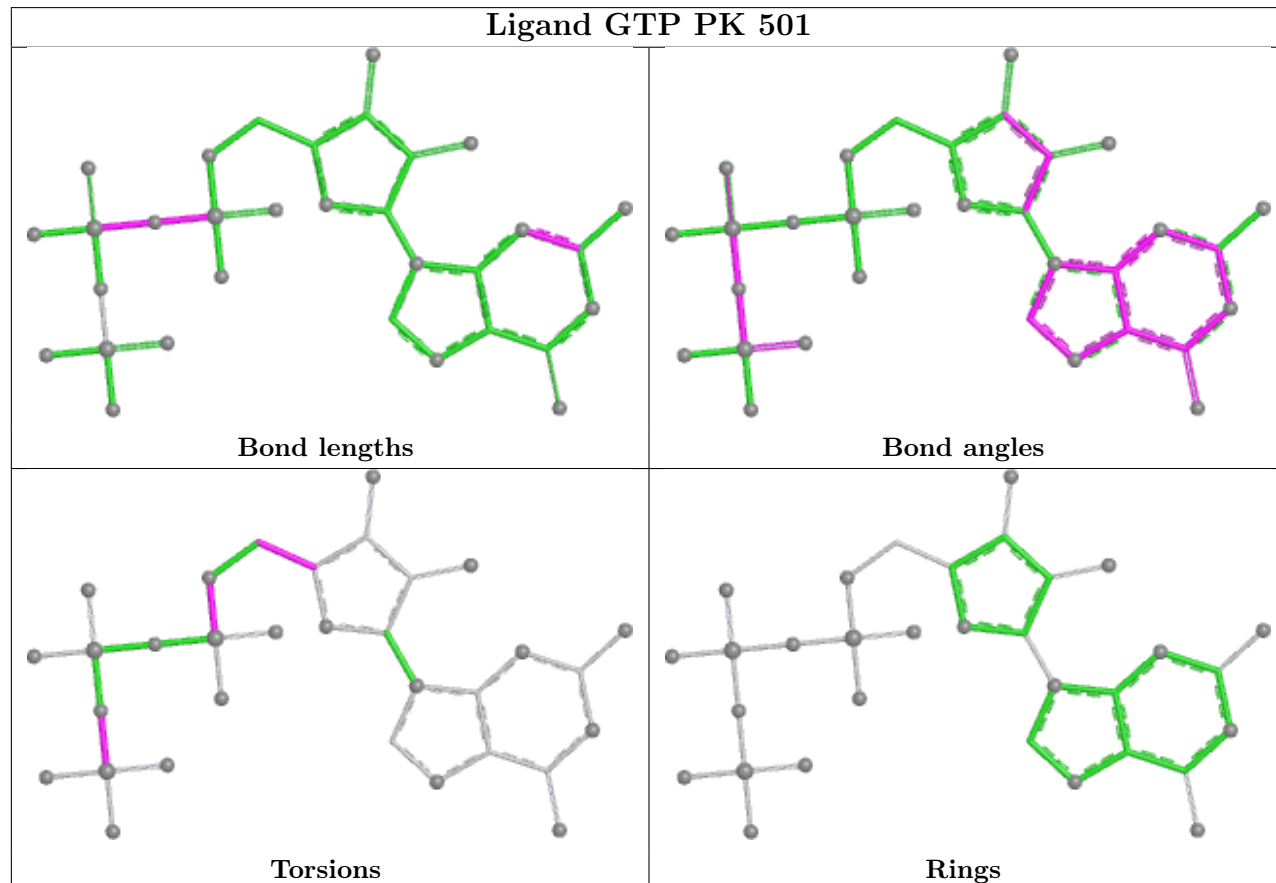




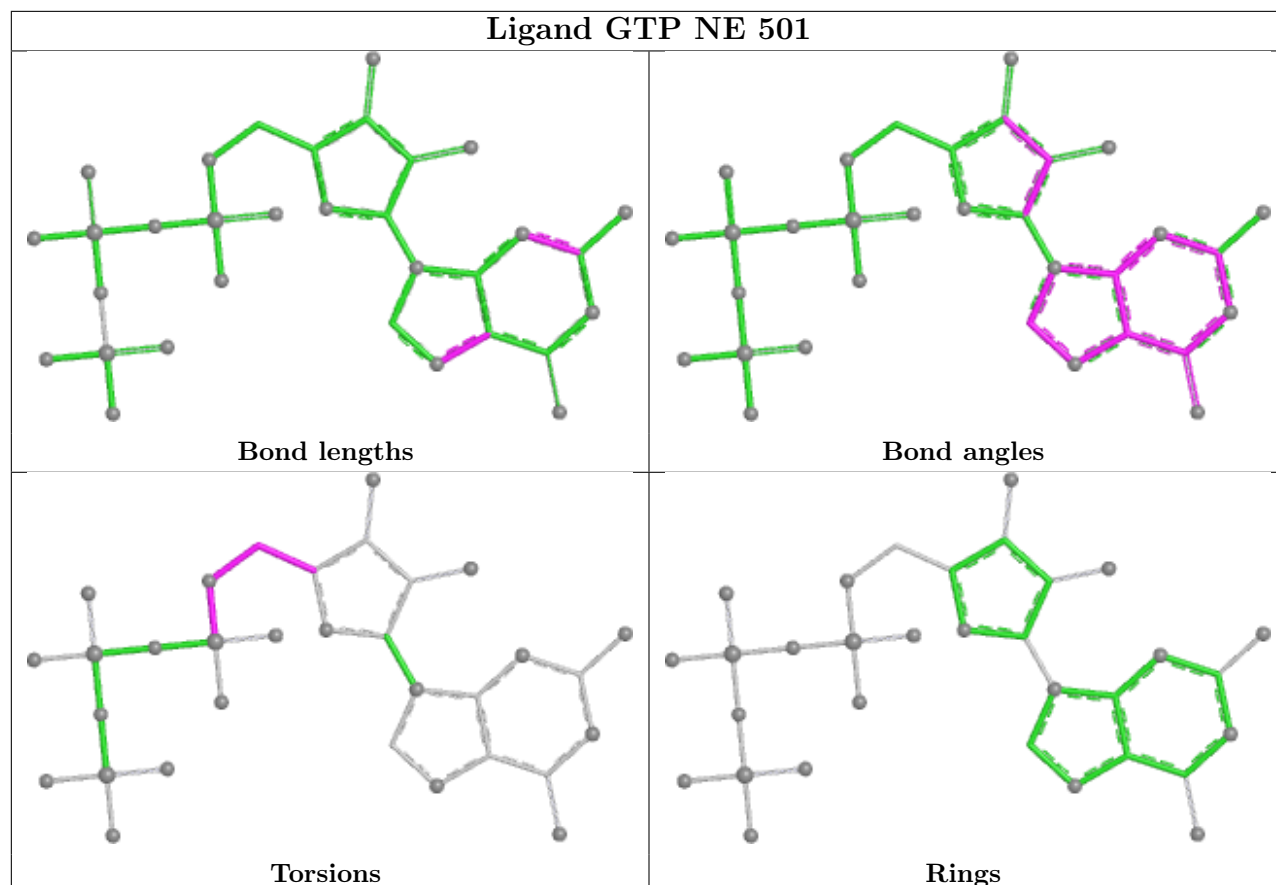
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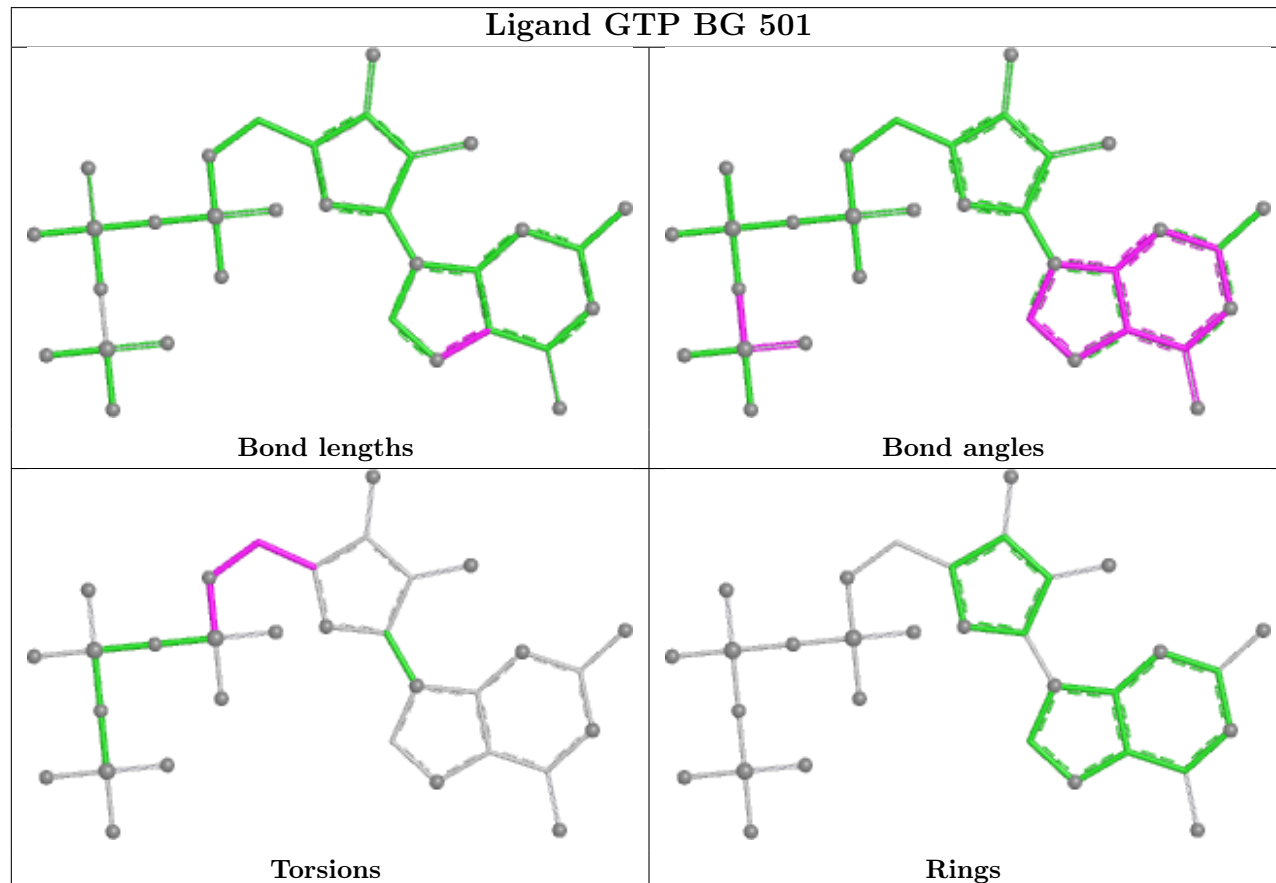
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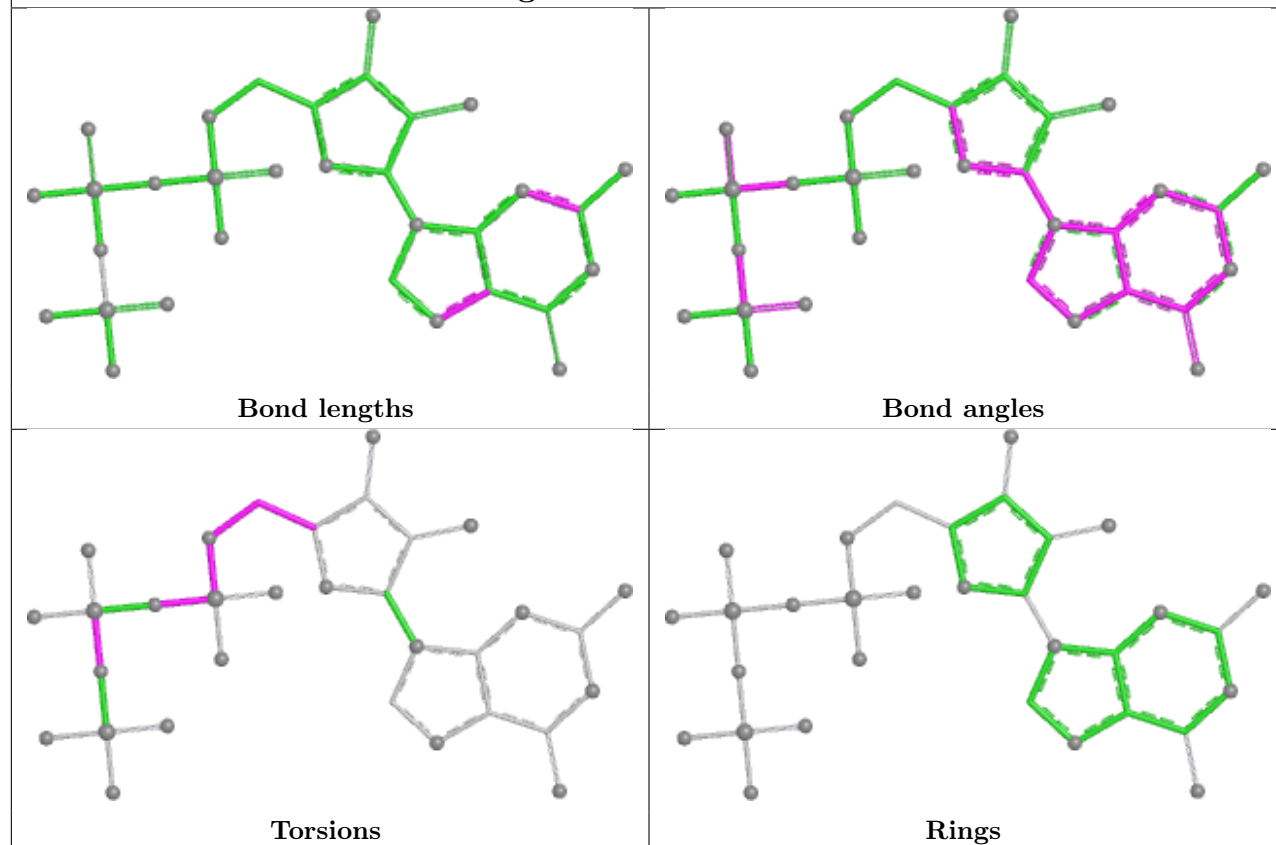
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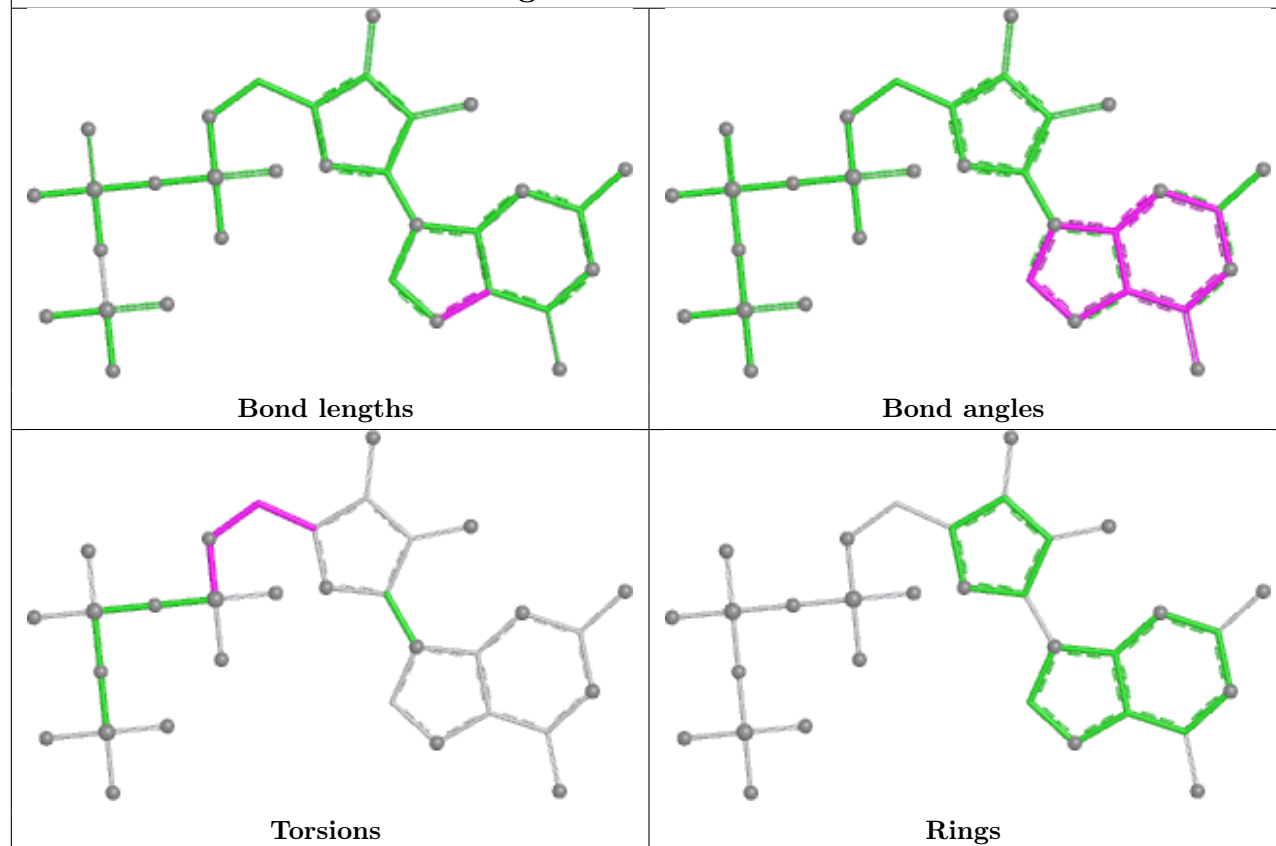
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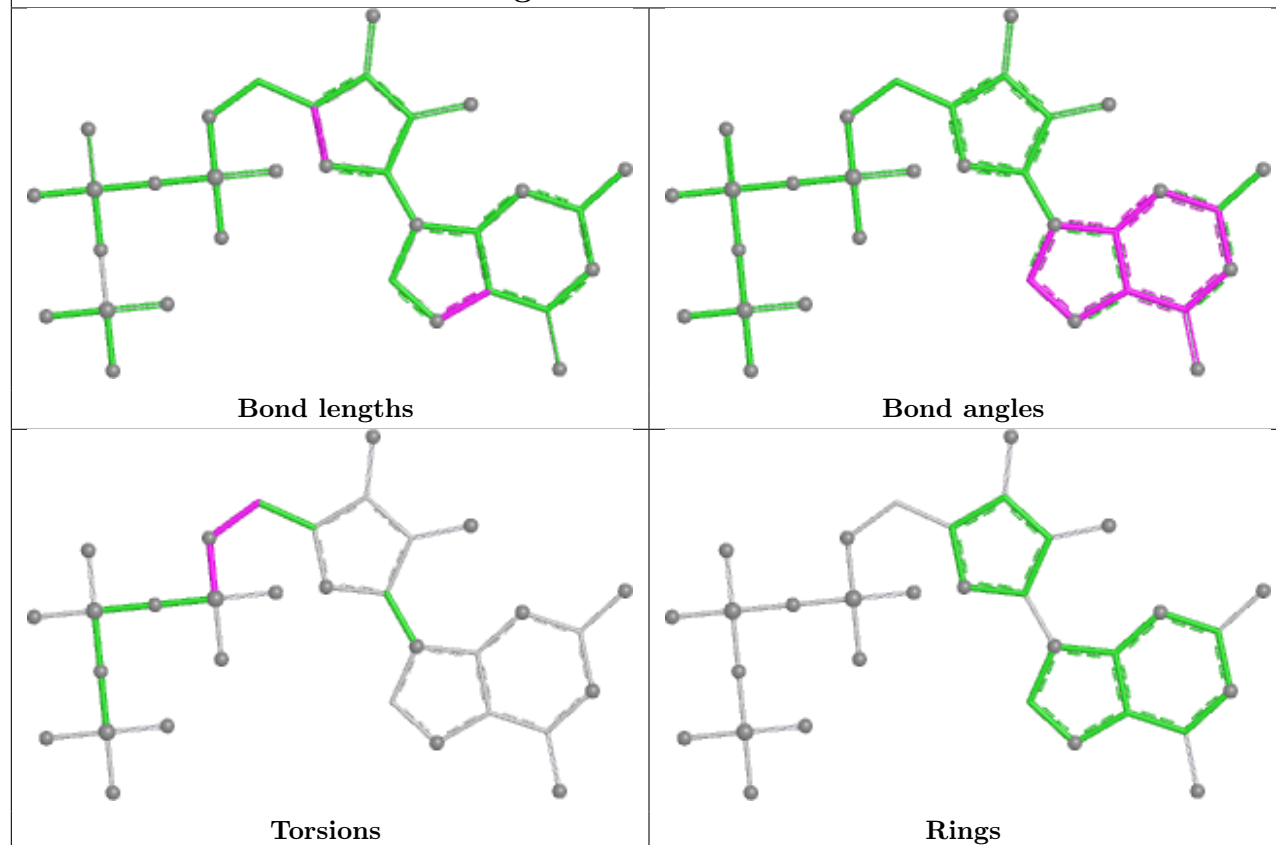
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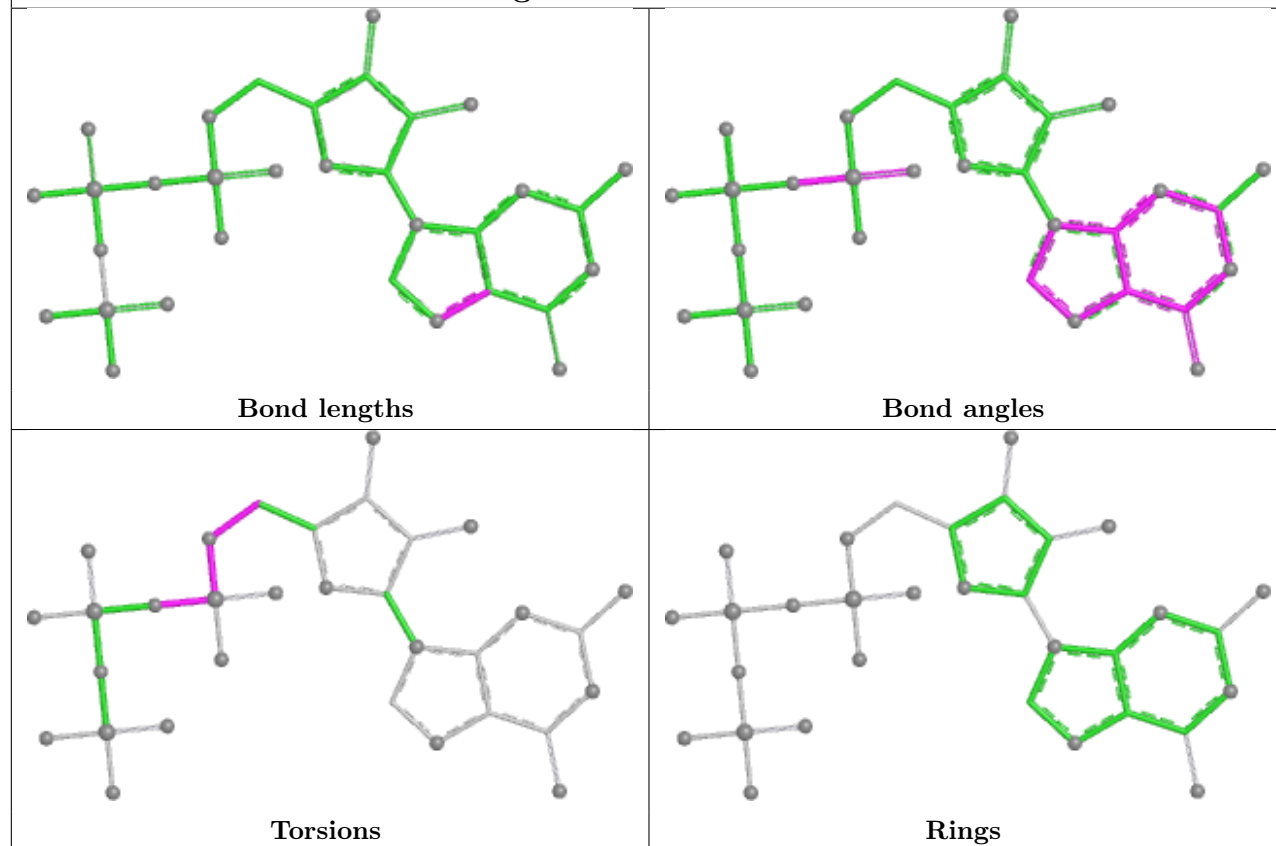
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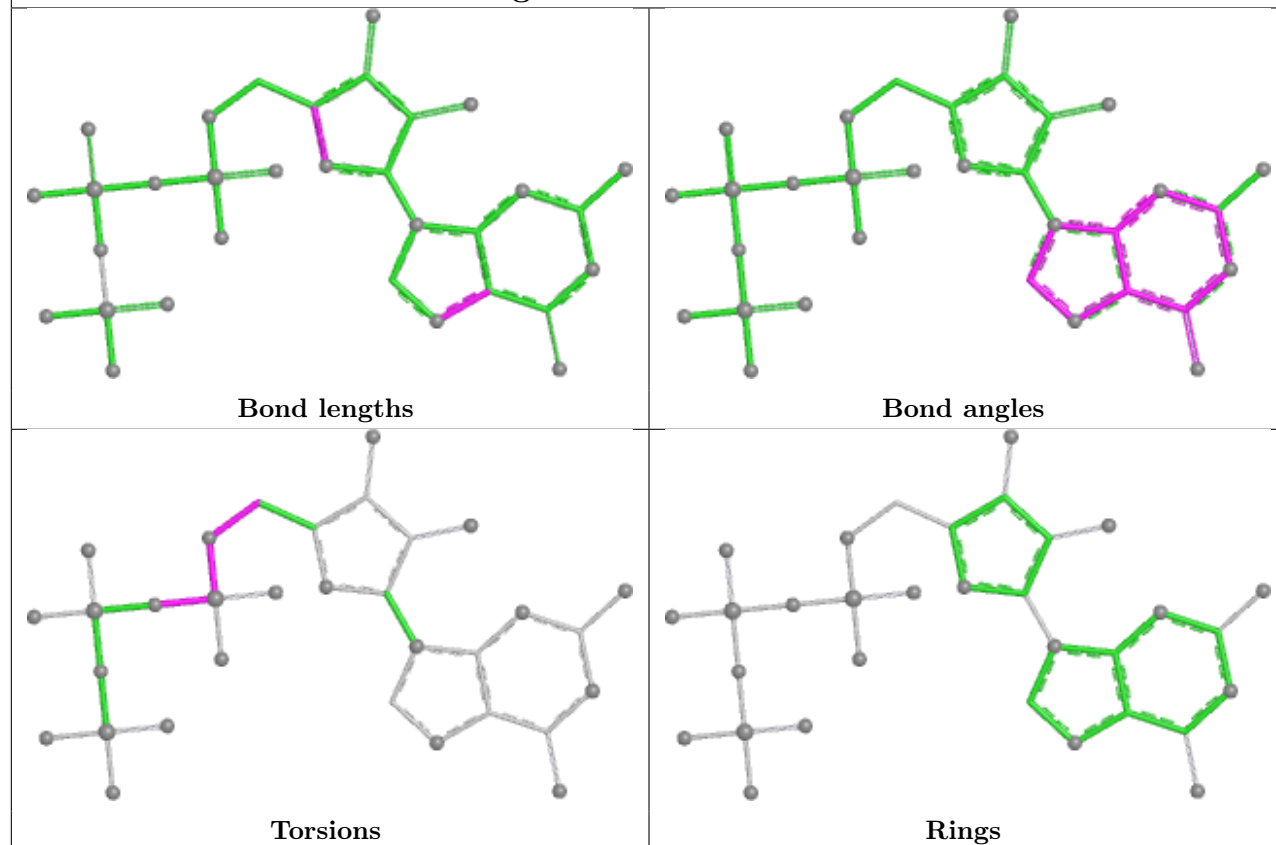
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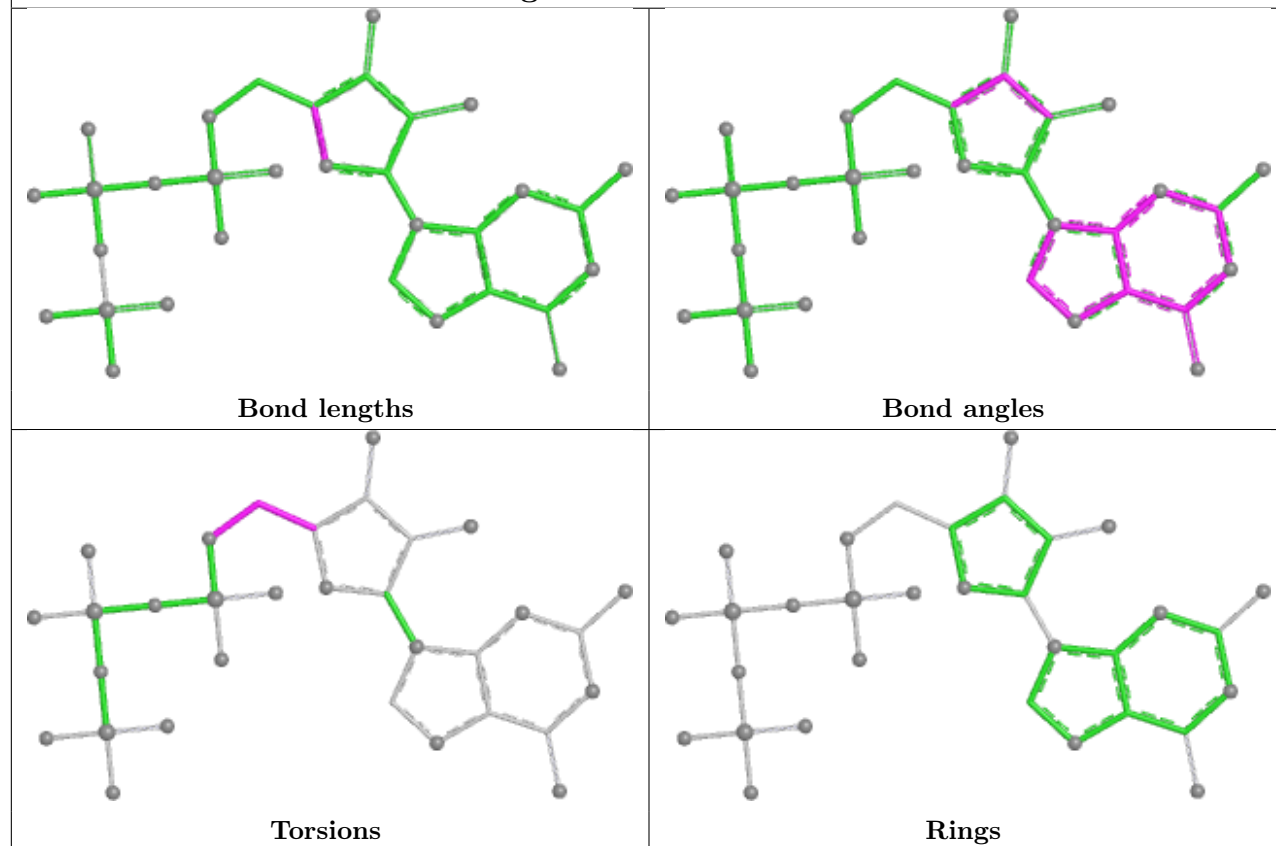
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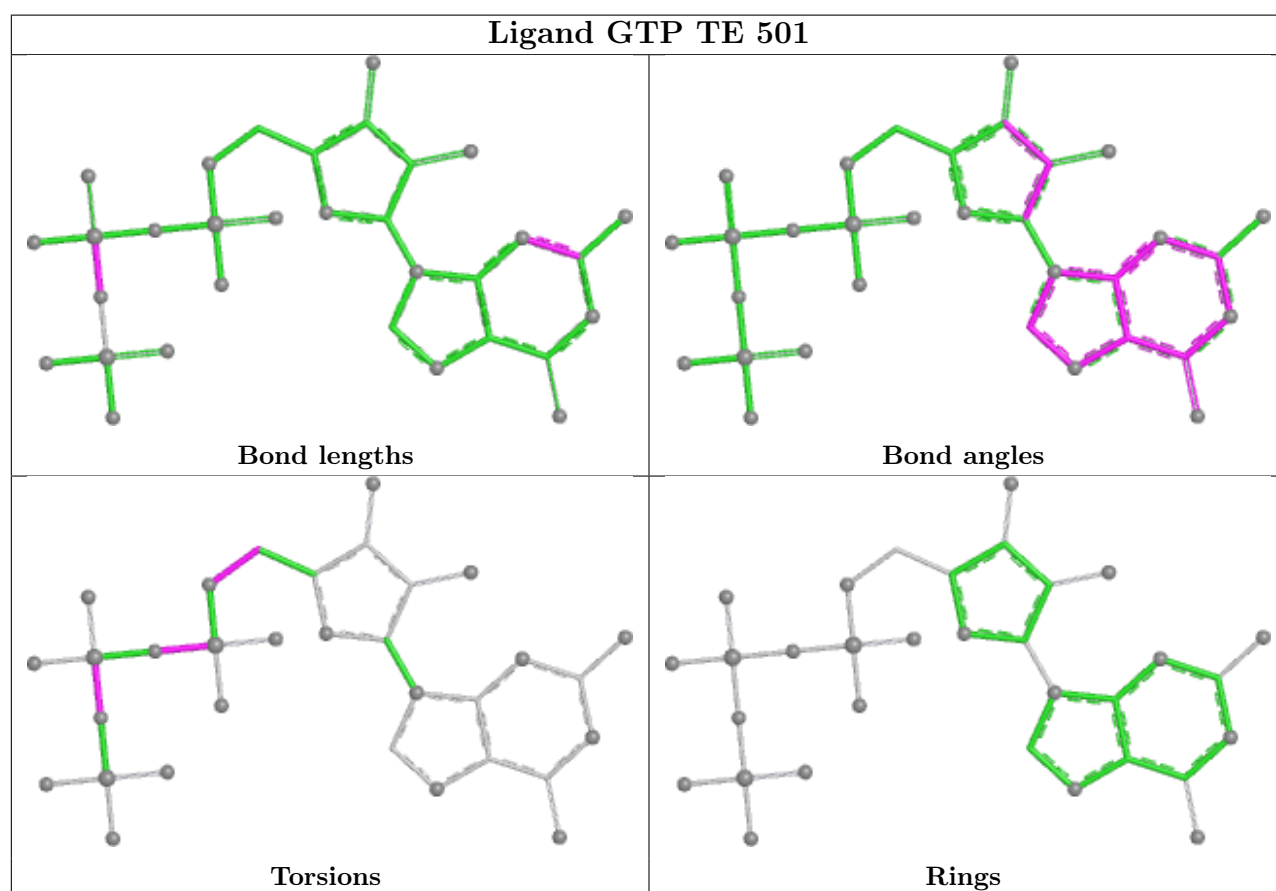
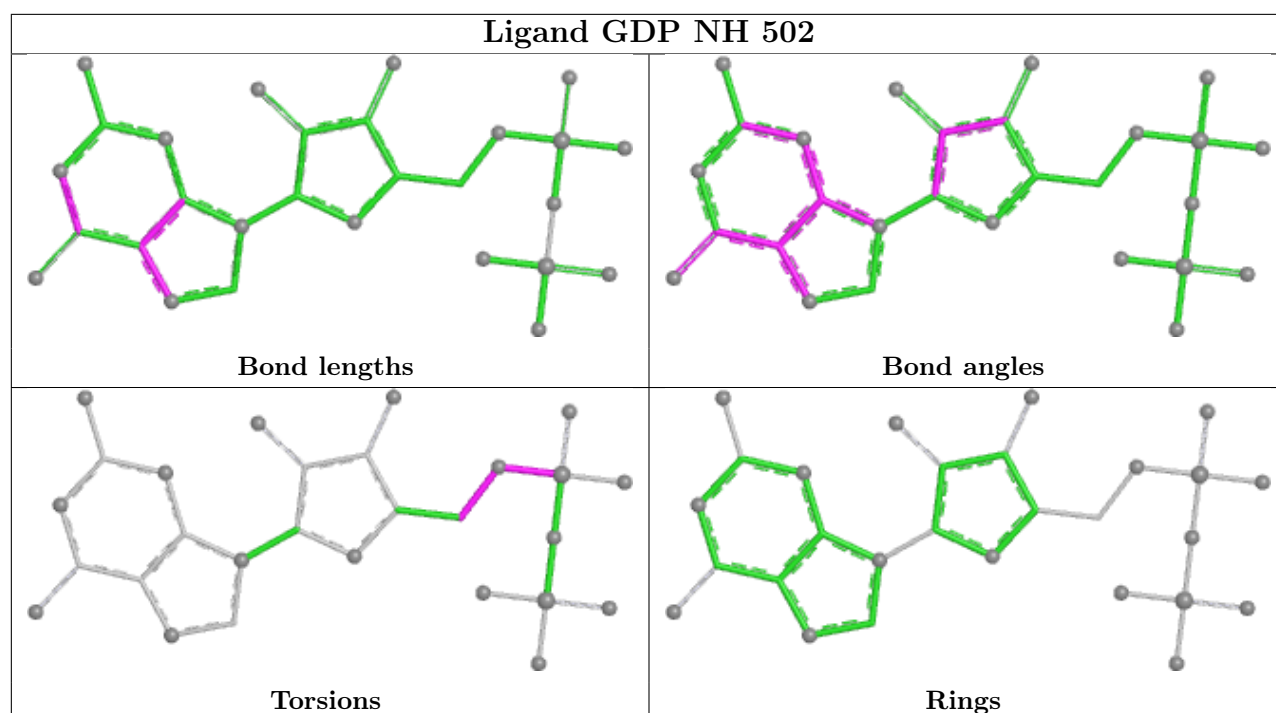


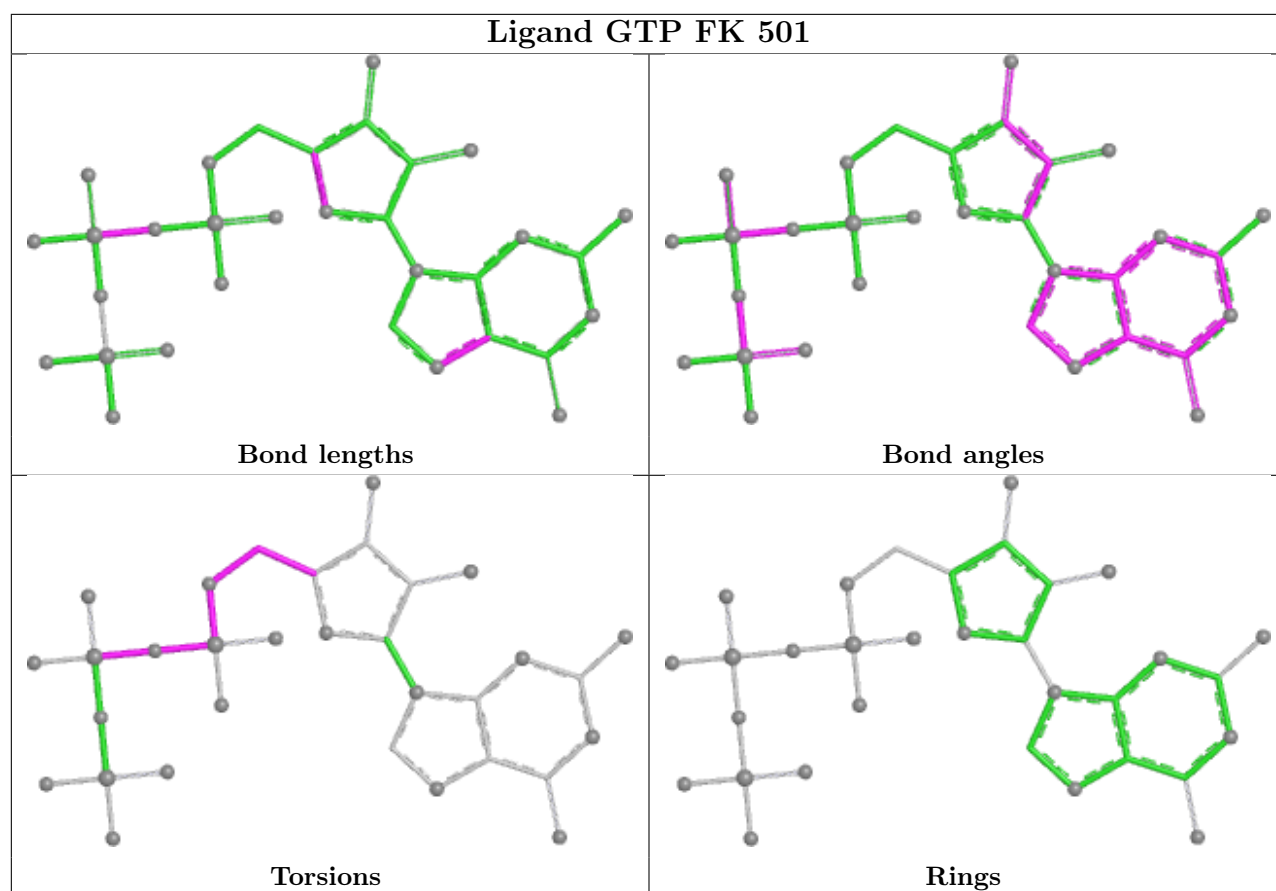
Ligand GTP GM 501



Ligand GTP SC 501







4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-24664. 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.