



## wwPDB EM Validation Summary Report ⓘ

Nov 15, 2022 – 05:56 AM JST

PDB ID : 6KIG  
EMDB ID : EMD-9995  
Title : Structure of cyanobacterial photosystem I-IsiA supercomplex  
Authors : Cao, P.; Cao, D.F.; Si, L.; Su, X.D.; Chang, W.R.; Liu, Z.F.; Zhang, X.Z.; Li, M.  
Deposited on : 2019-07-18  
Resolution : 2.90 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](mailto: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>.

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

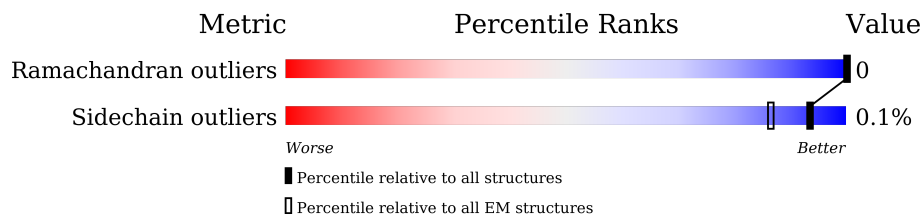
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance

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

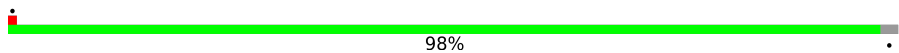
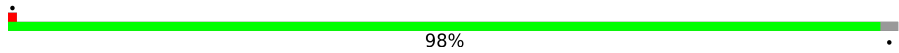
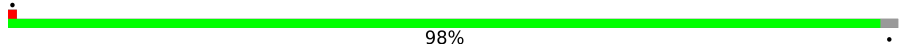
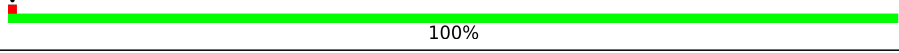
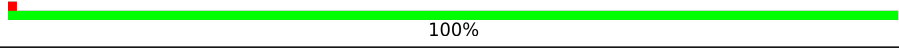
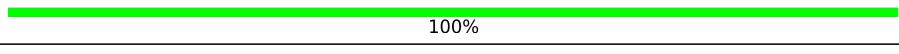
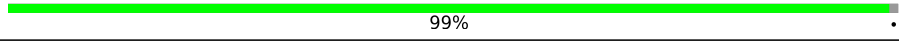
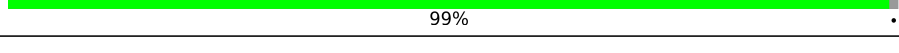
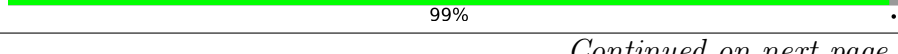
The reported resolution of this entry is 2.90 Å.

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



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

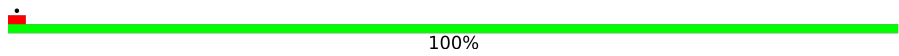
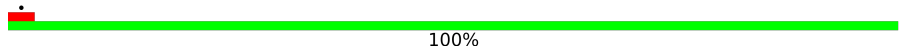
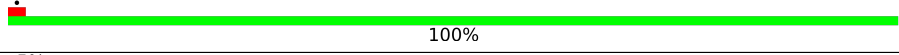
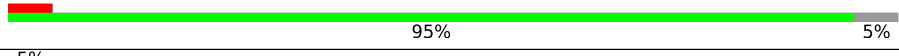
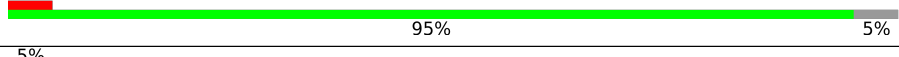
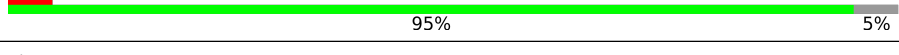


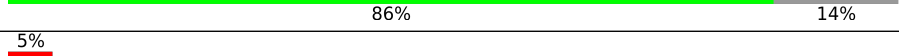
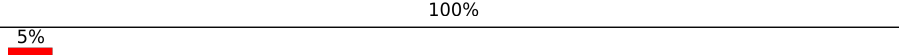
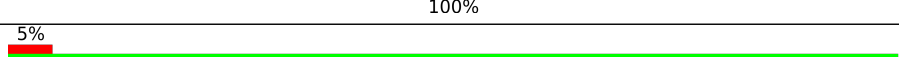
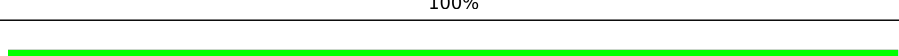
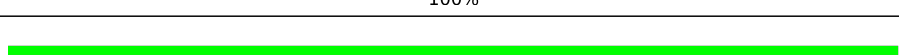
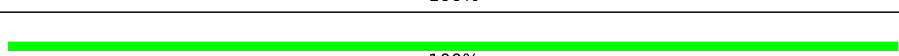
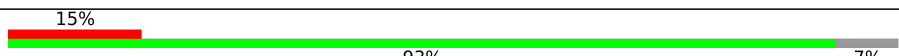
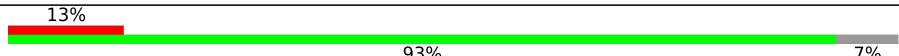
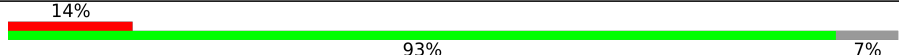
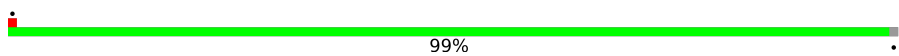
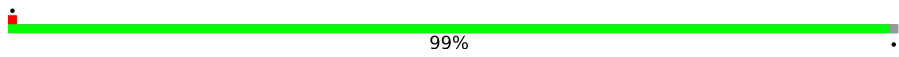
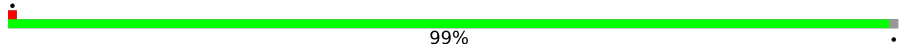
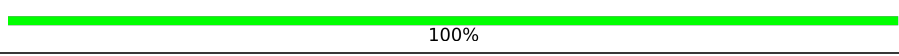
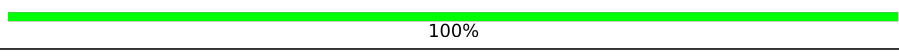
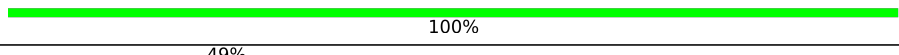
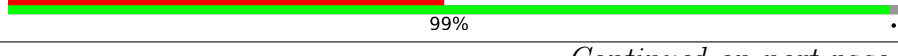

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	763	 98%
1	G	763	 98%
1	e	763	 98%
2	B	734	 100%
2	H	734	 100%
2	f	734	 100%
3	C	81	 99%
3	N	81	 99%
3	g	81	 99%

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Mol	Chain	Length	Quality of chain
4	D	141	 100%
4	O	141	 100%
4	h	141	 100%
5	E	75	 5% 95% 5%
5	Q	75	 5% 95% 5%
5	i	75	 5% 95% 5%
6	F	159	 86% 14%
6	R	159	 86% 14%
6	j	159	 86% 14%
7	I	38	 5% 100%
7	S	38	 5% 100%
7	k	38	 5% 100%
8	J	41	 100%
8	T	41	 100%
8	l	41	 100%
9	K	84	 15% 93% 7%
9	U	84	 13% 93% 7%
9	m	84	 14% 93% 7%
10	L	166	 99%
10	V	166	 99%
10	n	166	 99%
11	M	29	 100%
11	W	29	 100%
11	o	29	 100%
12	1	342	 49% 99%

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Mol	Chain	Length	Quality of chain
12	2	342	40% 99%
12	3	342	59% 99%
12	4	342	94% 99%
12	5	342	98% 99%
12	6	342	91% 99%
12	Y	342	49% 99%
12	Z	342	38% 99%
12	a	342	60% 99%
12	b	342	95% 99%
12	c	342	98% 99%
12	d	342	90% 99%
12	q	342	51% 99%
12	r	342	41% 99%
12	s	342	59% 99%
12	t	342	93% 99%
12	u	342	99% 99%
12	v	342	90% 99%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	1	501	X	-	-	-
13	CLA	1	502	X	-	-	-
13	CLA	1	503	X	-	-	-
13	CLA	1	504	X	-	-	-
13	CLA	1	505	X	-	-	-
13	CLA	1	506	X	-	-	-
13	CLA	1	507	X	-	-	-
13	CLA	1	508	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	1	509	X	-	-	-
13	CLA	1	510	X	-	-	-
13	CLA	1	511	X	-	-	-
13	CLA	1	512	X	-	-	-
13	CLA	1	513	X	-	-	-
13	CLA	1	516	X	-	-	-
13	CLA	1	517	X	-	-	-
13	CLA	1	518	X	-	-	-
13	CLA	1	519	X	-	-	-
13	CLA	2	501	X	-	-	-
13	CLA	2	502	X	-	-	-
13	CLA	2	503	X	-	-	-
13	CLA	2	504	X	-	-	-
13	CLA	2	505	X	-	-	-
13	CLA	2	506	X	-	-	-
13	CLA	2	507	X	-	-	-
13	CLA	2	508	X	-	-	-
13	CLA	2	509	X	-	-	-
13	CLA	2	510	X	-	-	-
13	CLA	2	511	X	-	-	-
13	CLA	2	512	X	-	-	-
13	CLA	2	513	X	-	-	-
13	CLA	2	516	X	-	-	-
13	CLA	2	517	X	-	-	-
13	CLA	2	518	X	-	-	-
13	CLA	2	519	X	-	-	-
13	CLA	3	501	X	-	-	-
13	CLA	3	502	X	-	-	-
13	CLA	3	503	X	-	-	-
13	CLA	3	504	X	-	-	-
13	CLA	3	505	X	-	-	-
13	CLA	3	506	X	-	-	-
13	CLA	3	507	X	-	-	-
13	CLA	3	508	X	-	-	-
13	CLA	3	509	X	-	-	-
13	CLA	3	510	X	-	-	-
13	CLA	3	511	X	-	-	-
13	CLA	3	512	X	-	-	-
13	CLA	3	513	X	-	-	-
13	CLA	3	516	X	-	-	-
13	CLA	3	517	X	-	-	-
13	CLA	3	518	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	3	519	X	-	-	-
13	CLA	4	501	X	-	-	-
13	CLA	4	502	X	-	-	-
13	CLA	4	503	X	-	-	-
13	CLA	4	504	X	-	-	-
13	CLA	4	505	X	-	-	-
13	CLA	4	506	X	-	-	-
13	CLA	4	507	X	-	-	-
13	CLA	4	508	X	-	-	-
13	CLA	4	509	X	-	-	-
13	CLA	4	510	X	-	-	-
13	CLA	4	511	X	-	-	-
13	CLA	4	512	X	-	-	-
13	CLA	4	513	X	-	-	-
13	CLA	4	516	X	-	-	-
13	CLA	4	517	X	-	-	-
13	CLA	4	518	X	-	-	-
13	CLA	4	519	X	-	-	-
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13	CLA	5	502	X	-	-	-
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13	CLA	5	516	X	-	-	-
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13	CLA	5	518	X	-	-	-
13	CLA	5	519	X	-	-	-
13	CLA	6	501	X	-	-	-
13	CLA	6	502	X	-	-	-
13	CLA	6	503	X	-	-	-
13	CLA	6	504	X	-	-	-
13	CLA	6	505	X	-	-	-
13	CLA	6	506	X	-	-	-
13	CLA	6	507	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	6	508	X	-	-	-
13	CLA	6	509	X	-	-	-
13	CLA	6	510	X	-	-	-
13	CLA	6	511	X	-	-	-
13	CLA	6	512	X	-	-	-
13	CLA	6	513	X	-	-	-
13	CLA	6	516	X	-	-	-
13	CLA	6	517	X	-	-	-
13	CLA	6	518	X	-	-	-
13	CLA	6	519	X	-	-	-
13	CLA	A	1011	X	-	-	-
13	CLA	A	1013	X	-	-	-
13	CLA	A	1022	X	-	-	-
13	CLA	A	1101	X	-	-	-
13	CLA	A	1102	X	-	-	-
13	CLA	A	1103	X	-	-	-
13	CLA	A	1104	X	-	-	-
13	CLA	A	1105	X	-	-	-
13	CLA	A	1106	X	-	-	-
13	CLA	A	1107	X	-	-	-
13	CLA	A	1108	X	-	-	-
13	CLA	A	1109	X	-	-	-
13	CLA	A	1110	X	-	-	-
13	CLA	A	1111	X	-	-	-
13	CLA	A	1112	X	-	-	-
13	CLA	A	1113	X	-	-	-
13	CLA	A	1114	X	-	-	-
13	CLA	A	1115	X	-	-	-
13	CLA	A	1116	X	-	-	-
13	CLA	A	1117	X	-	-	-
13	CLA	A	1118	X	-	-	-
13	CLA	A	1119	X	-	-	-
13	CLA	A	1120	X	-	-	-
13	CLA	A	1121	X	-	-	-
13	CLA	A	1122	X	-	-	-
13	CLA	A	1123	X	-	-	-
13	CLA	A	1124	X	-	-	-
13	CLA	A	1125	X	-	-	-
13	CLA	A	1126	X	-	-	-
13	CLA	A	1127	X	-	-	-
13	CLA	A	1128	X	-	-	-
13	CLA	A	1129	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	A	1130	X	-	-	-
13	CLA	A	1131	X	-	-	-
13	CLA	A	1132	X	-	-	-
13	CLA	A	1133	X	-	-	-
13	CLA	A	1134	X	-	-	-
13	CLA	A	1135	X	-	-	-
13	CLA	A	1136	X	-	-	-
13	CLA	A	1137	X	-	-	-
13	CLA	A	1138	X	-	-	-
13	CLA	A	1139	X	-	-	-
13	CLA	A	1140	X	-	-	-
13	CLA	A	1237	X	-	-	-
13	CLA	A	1801	X	-	-	-
13	CLA	B	1012	X	-	-	-
13	CLA	B	1021	X	-	-	-
13	CLA	B	1023	X	-	-	-
13	CLA	B	1201	X	-	-	-
13	CLA	B	1202	X	-	-	-
13	CLA	B	1203	X	-	-	-
13	CLA	B	1204	X	-	-	-
13	CLA	B	1205	X	-	-	-
13	CLA	B	1206	X	-	-	-
13	CLA	B	1207	X	-	-	-
13	CLA	B	1208	X	-	-	-
13	CLA	B	1209	X	-	-	-
13	CLA	B	1210	X	-	-	-
13	CLA	B	1211	X	-	-	-
13	CLA	B	1212	X	-	-	-
13	CLA	B	1213	X	-	-	-
13	CLA	B	1214	X	-	-	-
13	CLA	B	1215	X	-	-	-
13	CLA	B	1216	X	-	-	-
13	CLA	B	1217	X	-	-	-
13	CLA	B	1218	X	-	-	-
13	CLA	B	1219	X	-	-	-
13	CLA	B	1220	X	-	-	-
13	CLA	B	1221	X	-	-	-
13	CLA	B	1222	X	-	-	-
13	CLA	B	1223	X	-	-	-
13	CLA	B	1224	X	-	-	-
13	CLA	B	1225	X	-	-	-
13	CLA	B	1226	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	B	1227	X	-	-	-
13	CLA	B	1228	X	-	-	-
13	CLA	B	1229	X	-	-	-
13	CLA	B	1230	X	-	-	-
13	CLA	B	1231	X	-	-	-
13	CLA	B	1232	X	-	-	-
13	CLA	B	1234	X	-	-	-
13	CLA	B	1235	X	-	-	-
13	CLA	B	1238	X	-	-	-
13	CLA	B	1239	X	-	-	-
13	CLA	F	1301	X	-	-	-
13	CLA	F	1302	X	-	-	-
13	CLA	G	1011	X	-	-	-
13	CLA	G	1013	X	-	-	-
13	CLA	G	1022	X	-	-	-
13	CLA	G	1101	X	-	-	-
13	CLA	G	1102	X	-	-	-
13	CLA	G	1103	X	-	-	-
13	CLA	G	1104	X	-	-	-
13	CLA	G	1105	X	-	-	-
13	CLA	G	1106	X	-	-	-
13	CLA	G	1107	X	-	-	-
13	CLA	G	1108	X	-	-	-
13	CLA	G	1109	X	-	-	-
13	CLA	G	1110	X	-	-	-
13	CLA	G	1111	X	-	-	-
13	CLA	G	1112	X	-	-	-
13	CLA	G	1113	X	-	-	-
13	CLA	G	1114	X	-	-	-
13	CLA	G	1115	X	-	-	-
13	CLA	G	1116	X	-	-	-
13	CLA	G	1117	X	-	-	-
13	CLA	G	1118	X	-	-	-
13	CLA	G	1119	X	-	-	-
13	CLA	G	1120	X	-	-	-
13	CLA	G	1121	X	-	-	-
13	CLA	G	1122	X	-	-	-
13	CLA	G	1123	X	-	-	-
13	CLA	G	1124	X	-	-	-
13	CLA	G	1125	X	-	-	-
13	CLA	G	1126	X	-	-	-
13	CLA	G	1127	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	G	1128	X	-	-	-
13	CLA	G	1129	X	-	-	-
13	CLA	G	1130	X	-	-	-
13	CLA	G	1131	X	-	-	-
13	CLA	G	1132	X	-	-	-
13	CLA	G	1133	X	-	-	-
13	CLA	G	1134	X	-	-	-
13	CLA	G	1135	X	-	-	-
13	CLA	G	1136	X	-	-	-
13	CLA	G	1137	X	-	-	-
13	CLA	G	1138	X	-	-	-
13	CLA	G	1139	X	-	-	-
13	CLA	G	1140	X	-	-	-
13	CLA	G	1237	X	-	-	-
13	CLA	G	1801	X	-	-	-
13	CLA	H	1012	X	-	-	-
13	CLA	H	1021	X	-	-	-
13	CLA	H	1023	X	-	-	-
13	CLA	H	1201	X	-	-	-
13	CLA	H	1202	X	-	-	-
13	CLA	H	1203	X	-	-	-
13	CLA	H	1204	X	-	-	-
13	CLA	H	1205	X	-	-	-
13	CLA	H	1206	X	-	-	-
13	CLA	H	1207	X	-	-	-
13	CLA	H	1208	X	-	-	-
13	CLA	H	1209	X	-	-	-
13	CLA	H	1210	X	-	-	-
13	CLA	H	1211	X	-	-	-
13	CLA	H	1212	X	-	-	-
13	CLA	H	1213	X	-	-	-
13	CLA	H	1214	X	-	-	-
13	CLA	H	1215	X	-	-	-
13	CLA	H	1216	X	-	-	-
13	CLA	H	1217	X	-	-	-
13	CLA	H	1218	X	-	-	-
13	CLA	H	1219	X	-	-	-
13	CLA	H	1220	X	-	-	-
13	CLA	H	1221	X	-	-	-
13	CLA	H	1222	X	-	-	-
13	CLA	H	1223	X	-	-	-
13	CLA	H	1224	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	H	1225	X	-	-	-
13	CLA	H	1226	X	-	-	-
13	CLA	H	1227	X	-	-	-
13	CLA	H	1228	X	-	-	-
13	CLA	H	1229	X	-	-	-
13	CLA	H	1230	X	-	-	-
13	CLA	H	1231	X	-	-	-
13	CLA	H	1232	X	-	-	-
13	CLA	H	1234	X	-	-	-
13	CLA	H	1235	X	-	-	-
13	CLA	H	1238	X	-	-	-
13	CLA	H	1239	X	-	-	-
13	CLA	J	1302	X	-	-	-
13	CLA	J	1303	X	-	-	-
13	CLA	K	1103	X	-	-	-
13	CLA	K	1105	X	-	-	-
13	CLA	K	1401	X	-	-	-
13	CLA	L	1501	X	-	-	-
13	CLA	L	1502	X	-	-	-
13	CLA	L	1503	X	-	-	-
13	CLA	R	1301	X	-	-	-
13	CLA	R	1302	X	-	-	-
13	CLA	T	1302	X	-	-	-
13	CLA	T	1303	X	-	-	-
13	CLA	U	1103	X	-	-	-
13	CLA	U	1105	X	-	-	-
13	CLA	U	1401	X	-	-	-
13	CLA	V	1501	X	-	-	-
13	CLA	V	1502	X	-	-	-
13	CLA	V	1503	X	-	-	-
13	CLA	Y	501	X	-	-	-
13	CLA	Y	502	X	-	-	-
13	CLA	Y	503	X	-	-	-
13	CLA	Y	504	X	-	-	-
13	CLA	Y	505	X	-	-	-
13	CLA	Y	506	X	-	-	-
13	CLA	Y	507	X	-	-	-
13	CLA	Y	508	X	-	-	-
13	CLA	Y	509	X	-	-	-
13	CLA	Y	510	X	-	-	-
13	CLA	Y	511	X	-	-	-
13	CLA	Y	512	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	Y	513	X	-	-	-
13	CLA	Y	516	X	-	-	-
13	CLA	Y	517	X	-	-	-
13	CLA	Y	518	X	-	-	-
13	CLA	Y	519	X	-	-	-
13	CLA	Z	501	X	-	-	-
13	CLA	Z	502	X	-	-	-
13	CLA	Z	503	X	-	-	-
13	CLA	Z	504	X	-	-	-
13	CLA	Z	505	X	-	-	-
13	CLA	Z	506	X	-	-	-
13	CLA	Z	507	X	-	-	-
13	CLA	Z	508	X	-	-	-
13	CLA	Z	509	X	-	-	-
13	CLA	Z	510	X	-	-	-
13	CLA	Z	511	X	-	-	-
13	CLA	Z	512	X	-	-	-
13	CLA	Z	513	X	-	-	-
13	CLA	Z	516	X	-	-	-
13	CLA	Z	517	X	-	-	-
13	CLA	Z	518	X	-	-	-
13	CLA	Z	519	X	-	-	-
13	CLA	a	501	X	-	-	-
13	CLA	a	502	X	-	-	-
13	CLA	a	503	X	-	-	-
13	CLA	a	504	X	-	-	-
13	CLA	a	505	X	-	-	-
13	CLA	a	506	X	-	-	-
13	CLA	a	507	X	-	-	-
13	CLA	a	508	X	-	-	-
13	CLA	a	509	X	-	-	-
13	CLA	a	510	X	-	-	-
13	CLA	a	511	X	-	-	-
13	CLA	a	512	X	-	-	-
13	CLA	a	513	X	-	-	-
13	CLA	a	516	X	-	-	-
13	CLA	a	517	X	-	-	-
13	CLA	a	518	X	-	-	-
13	CLA	a	519	X	-	-	-
13	CLA	b	501	X	-	-	-
13	CLA	b	502	X	-	-	-
13	CLA	b	503	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	b	504	X	-	-	-
13	CLA	b	505	X	-	-	-
13	CLA	b	506	X	-	-	-
13	CLA	b	507	X	-	-	-
13	CLA	b	508	X	-	-	-
13	CLA	b	509	X	-	-	-
13	CLA	b	510	X	-	-	-
13	CLA	b	511	X	-	-	-
13	CLA	b	512	X	-	-	-
13	CLA	b	513	X	-	-	-
13	CLA	b	516	X	-	-	-
13	CLA	b	517	X	-	-	-
13	CLA	b	518	X	-	-	-
13	CLA	b	519	X	-	-	-
13	CLA	c	501	X	-	-	-
13	CLA	c	502	X	-	-	-
13	CLA	c	503	X	-	-	-
13	CLA	c	504	X	-	-	-
13	CLA	c	505	X	-	-	-
13	CLA	c	506	X	-	-	-
13	CLA	c	507	X	-	-	-
13	CLA	c	508	X	-	-	-
13	CLA	c	509	X	-	-	-
13	CLA	c	510	X	-	-	-
13	CLA	c	511	X	-	-	-
13	CLA	c	512	X	-	-	-
13	CLA	c	513	X	-	-	-
13	CLA	c	516	X	-	-	-
13	CLA	c	517	X	-	-	-
13	CLA	c	518	X	-	-	-
13	CLA	c	519	X	-	-	-
13	CLA	d	501	X	-	-	-
13	CLA	d	502	X	-	-	-
13	CLA	d	503	X	-	-	-
13	CLA	d	504	X	-	-	-
13	CLA	d	505	X	-	-	-
13	CLA	d	506	X	-	-	-
13	CLA	d	507	X	-	-	-
13	CLA	d	508	X	-	-	-
13	CLA	d	509	X	-	-	-
13	CLA	d	510	X	-	-	-
13	CLA	d	511	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	d	512	X	-	-	-
13	CLA	d	513	X	-	-	-
13	CLA	d	516	X	-	-	-
13	CLA	d	517	X	-	-	-
13	CLA	d	518	X	-	-	-
13	CLA	d	519	X	-	-	-
13	CLA	e	1011	X	-	-	-
13	CLA	e	1013	X	-	-	-
13	CLA	e	1022	X	-	-	-
13	CLA	e	1101	X	-	-	-
13	CLA	e	1102	X	-	-	-
13	CLA	e	1103	X	-	-	-
13	CLA	e	1104	X	-	-	-
13	CLA	e	1105	X	-	-	-
13	CLA	e	1106	X	-	-	-
13	CLA	e	1107	X	-	-	-
13	CLA	e	1108	X	-	-	-
13	CLA	e	1109	X	-	-	-
13	CLA	e	1110	X	-	-	-
13	CLA	e	1111	X	-	-	-
13	CLA	e	1112	X	-	-	-
13	CLA	e	1113	X	-	-	-
13	CLA	e	1114	X	-	-	-
13	CLA	e	1115	X	-	-	-
13	CLA	e	1116	X	-	-	-
13	CLA	e	1117	X	-	-	-
13	CLA	e	1118	X	-	-	-
13	CLA	e	1119	X	-	-	-
13	CLA	e	1120	X	-	-	-
13	CLA	e	1121	X	-	-	-
13	CLA	e	1122	X	-	-	-
13	CLA	e	1123	X	-	-	-
13	CLA	e	1124	X	-	-	-
13	CLA	e	1125	X	-	-	-
13	CLA	e	1126	X	-	-	-
13	CLA	e	1127	X	-	-	-
13	CLA	e	1128	X	-	-	-
13	CLA	e	1129	X	-	-	-
13	CLA	e	1130	X	-	-	-
13	CLA	e	1131	X	-	-	-
13	CLA	e	1132	X	-	-	-
13	CLA	e	1133	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	e	1134	X	-	-	-
13	CLA	e	1135	X	-	-	-
13	CLA	e	1136	X	-	-	-
13	CLA	e	1137	X	-	-	-
13	CLA	e	1138	X	-	-	-
13	CLA	e	1139	X	-	-	-
13	CLA	e	1140	X	-	-	-
13	CLA	e	1237	X	-	-	-
13	CLA	e	1801	X	-	-	-
13	CLA	f	1012	X	-	-	-
13	CLA	f	1021	X	-	-	-
13	CLA	f	1023	X	-	-	-
13	CLA	f	1201	X	-	-	-
13	CLA	f	1202	X	-	-	-
13	CLA	f	1203	X	-	-	-
13	CLA	f	1204	X	-	-	-
13	CLA	f	1205	X	-	-	-
13	CLA	f	1206	X	-	-	-
13	CLA	f	1207	X	-	-	-
13	CLA	f	1208	X	-	-	-
13	CLA	f	1209	X	-	-	-
13	CLA	f	1210	X	-	-	-
13	CLA	f	1211	X	-	-	-
13	CLA	f	1212	X	-	-	-
13	CLA	f	1213	X	-	-	-
13	CLA	f	1214	X	-	-	-
13	CLA	f	1215	X	-	-	-
13	CLA	f	1216	X	-	-	-
13	CLA	f	1217	X	-	-	-
13	CLA	f	1218	X	-	-	-
13	CLA	f	1219	X	-	-	-
13	CLA	f	1220	X	-	-	-
13	CLA	f	1221	X	-	-	-
13	CLA	f	1222	X	-	-	-
13	CLA	f	1223	X	-	-	-
13	CLA	f	1224	X	-	-	-
13	CLA	f	1225	X	-	-	-
13	CLA	f	1226	X	-	-	-
13	CLA	f	1227	X	-	-	-
13	CLA	f	1228	X	-	-	-
13	CLA	f	1229	X	-	-	-
13	CLA	f	1230	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	f	1231	X	-	-	-
13	CLA	f	1232	X	-	-	-
13	CLA	f	1234	X	-	-	-
13	CLA	f	1235	X	-	-	-
13	CLA	f	1238	X	-	-	-
13	CLA	f	1239	X	-	-	-
13	CLA	j	1301	X	-	-	-
13	CLA	j	1302	X	-	-	-
13	CLA	l	1302	X	-	-	-
13	CLA	l	1303	X	-	-	-
13	CLA	m	1103	X	-	-	-
13	CLA	m	1105	X	-	-	-
13	CLA	m	1401	X	-	-	-
13	CLA	n	1501	X	-	-	-
13	CLA	n	1502	X	-	-	-
13	CLA	n	1503	X	-	-	-
13	CLA	q	501	X	-	-	-
13	CLA	q	502	X	-	-	-
13	CLA	q	503	X	-	-	-
13	CLA	q	504	X	-	-	-
13	CLA	q	505	X	-	-	-
13	CLA	q	506	X	-	-	-
13	CLA	q	507	X	-	-	-
13	CLA	q	508	X	-	-	-
13	CLA	q	509	X	-	-	-
13	CLA	q	510	X	-	-	-
13	CLA	q	511	X	-	-	-
13	CLA	q	512	X	-	-	-
13	CLA	q	513	X	-	-	-
13	CLA	q	516	X	-	-	-
13	CLA	q	517	X	-	-	-
13	CLA	q	518	X	-	-	-
13	CLA	q	519	X	-	-	-
13	CLA	r	501	X	-	-	-
13	CLA	r	502	X	-	-	-
13	CLA	r	503	X	-	-	-
13	CLA	r	504	X	-	-	-
13	CLA	r	505	X	-	-	-
13	CLA	r	506	X	-	-	-
13	CLA	r	507	X	-	-	-
13	CLA	r	508	X	-	-	-
13	CLA	r	509	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	r	510	X	-	-	-
13	CLA	r	511	X	-	-	-
13	CLA	r	512	X	-	-	-
13	CLA	r	513	X	-	-	-
13	CLA	r	516	X	-	-	-
13	CLA	r	517	X	-	-	-
13	CLA	r	518	X	-	-	-
13	CLA	r	519	X	-	-	-
13	CLA	s	501	X	-	-	-
13	CLA	s	502	X	-	-	-
13	CLA	s	503	X	-	-	-
13	CLA	s	504	X	-	-	-
13	CLA	s	505	X	-	-	-
13	CLA	s	506	X	-	-	-
13	CLA	s	507	X	-	-	-
13	CLA	s	508	X	-	-	-
13	CLA	s	509	X	-	-	-
13	CLA	s	510	X	-	-	-
13	CLA	s	511	X	-	-	-
13	CLA	s	512	X	-	-	-
13	CLA	s	513	X	-	-	-
13	CLA	s	516	X	-	-	-
13	CLA	s	517	X	-	-	-
13	CLA	s	518	X	-	-	-
13	CLA	s	519	X	-	-	-
13	CLA	t	501	X	-	-	-
13	CLA	t	502	X	-	-	-
13	CLA	t	503	X	-	-	-
13	CLA	t	504	X	-	-	-
13	CLA	t	505	X	-	-	-
13	CLA	t	506	X	-	-	-
13	CLA	t	507	X	-	-	-
13	CLA	t	508	X	-	-	-
13	CLA	t	509	X	-	-	-
13	CLA	t	510	X	-	-	-
13	CLA	t	511	X	-	-	-
13	CLA	t	512	X	-	-	-
13	CLA	t	513	X	-	-	-
13	CLA	t	516	X	-	-	-
13	CLA	t	517	X	-	-	-
13	CLA	t	518	X	-	-	-
13	CLA	t	519	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	CLA	u	501	X	-	-	-
13	CLA	u	502	X	-	-	-
13	CLA	u	503	X	-	-	-
13	CLA	u	504	X	-	-	-
13	CLA	u	505	X	-	-	-
13	CLA	u	506	X	-	-	-
13	CLA	u	507	X	-	-	-
13	CLA	u	508	X	-	-	-
13	CLA	u	509	X	-	-	-
13	CLA	u	510	X	-	-	-
13	CLA	u	511	X	-	-	-
13	CLA	u	512	X	-	-	-
13	CLA	u	513	X	-	-	-
13	CLA	u	516	X	-	-	-
13	CLA	u	517	X	-	-	-
13	CLA	u	518	X	-	-	-
13	CLA	u	519	X	-	-	-
13	CLA	v	501	X	-	-	-
13	CLA	v	502	X	-	-	-
13	CLA	v	503	X	-	-	-
13	CLA	v	504	X	-	-	-
13	CLA	v	505	X	-	-	-
13	CLA	v	506	X	-	-	-
13	CLA	v	507	X	-	-	-
13	CLA	v	508	X	-	-	-
13	CLA	v	509	X	-	-	-
13	CLA	v	510	X	-	-	-
13	CLA	v	511	X	-	-	-
13	CLA	v	512	X	-	-	-
13	CLA	v	513	X	-	-	-
13	CLA	v	516	X	-	-	-
13	CLA	v	517	X	-	-	-
13	CLA	v	518	X	-	-	-
13	CLA	v	519	X	-	-	-



## 2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 143022 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 Photosystem I P700 chlorophyll a apoprotein A1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	751	Total	C	N	O	S	0	0
			5865	3847	1002	999	17		
1	G	751	Total	C	N	O	S	0	0
			5865	3847	1002	999	17		
1	e	751	Total	C	N	O	S	0	0
			5865	3847	1002	999	17		

- Molecule 2 is a protein called Photosystem I P700 chlorophyll a apoprotein A2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	733	Total	C	N	O	S	0	0
			5789	3811	970	994	14		
2	H	733	Total	C	N	O	S	0	0
			5789	3811	970	994	14		
2	f	733	Total	C	N	O	S	0	0
			5789	3811	970	994	14		

- Molecule 3 is a protein called Photosystem I iron-sulfur center.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	80	Total	C	N	O	S	0	0
			598	368	103	116	11		
3	N	80	Total	C	N	O	S	0	0
			598	368	103	116	11		
3	g	80	Total	C	N	O	S	0	0
			598	368	103	116	11		

- Molecule 4 is a protein called Photosystem I reaction center subunit II.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	141	Total	C	N	O	S	0	0
			1098	702	187	208	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	141	Total	C	N	O	S	0	0
			1098	702	187	208	1		
4	h	141	Total	C	N	O	S	0	0
			1098	702	187	208	1		

- Molecule 5 is a protein called Photosystem I reaction center subunit IV.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	71	Total	C	N	O	0	0	
			543	343	95	105			
5	Q	71	Total	C	N	O	0	0	
			543	343	95	105			
5	i	71	Total	C	N	O	0	0	
			543	343	95	105			

- Molecule 6 is a protein called Photosystem I reaction center subunit III.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	136	Total	C	N	O	S	0	0
			1036	670	174	190	2		
6	R	136	Total	C	N	O	S	0	0
			1036	670	174	190	2		
6	j	136	Total	C	N	O	S	0	0
			1036	670	174	190	2		

- Molecule 7 is a protein called Photosystem I PsaI protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	38	Total	C	N	O	S	0	0
			282	191	38	51	2		
7	S	38	Total	C	N	O	S	0	0
			282	191	38	51	2		
7	k	38	Total	C	N	O	S	0	0
			282	191	38	51	2		

- Molecule 8 is a protein called Photosystem I reaction center subunit IX.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	41	Total	C	N	O	S	0	0
			335	228	52	54	1		
8	T	41	Total	C	N	O	S	0	0
			335	228	52	54	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	l	41	Total	C	N	O	S	0	0
			335	228	52	54	1		

- Molecule 9 is a protein called Photosystem I reaction center subunit Psak.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	78	Total	C	N	O	S	0	0
			549	364	91	93	1		
9	U	78	Total	C	N	O	S	0	0
			549	364	91	93	1		
9	m	78	Total	C	N	O	S	0	0
			549	364	91	93	1		

- Molecule 10 is a protein called Photosystem I reaction center subunit XI.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	164	Total	C	N	O	S	0	0
			1210	782	201	225	2		
10	V	164	Total	C	N	O	S	0	0
			1210	782	201	225	2		
10	n	164	Total	C	N	O	S	0	0
			1210	782	201	225	2		

- Molecule 11 is a protein called Psam.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	29	Total	C	N	O	S	0	0
			228	151	36	40	1		
11	W	29	Total	C	N	O	S	0	0
			228	151	36	40	1		
11	o	29	Total	C	N	O	S	0	0
			228	151	36	40	1		

- Molecule 12 is a protein called Iron stress-induced chlorophyll-binding protein.

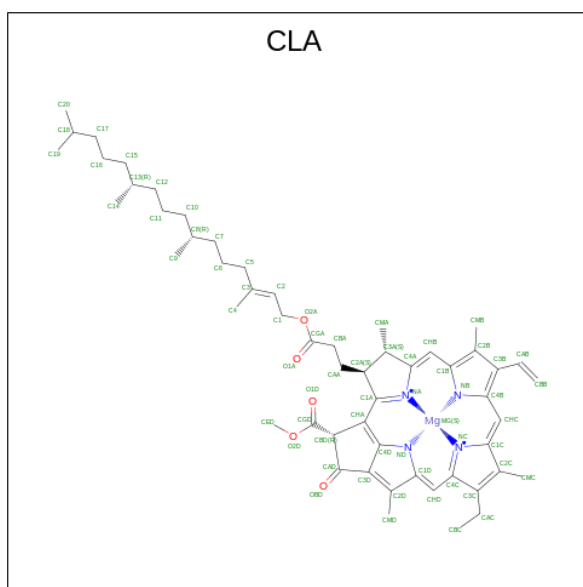
Mol	Chain	Residues	Atoms					AltConf	Trace
12	1	339	Total	C	N	O	S	0	0
			2605	1722	428	448	7		
12	2	339	Total	C	N	O	S	0	0
			2605	1722	428	448	7		
12	3	339	Total	C	N	O	S	0	0
			2605	1722	428	448	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	4	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	5	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	6	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	Y	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	Z	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	a	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	b	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	c	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	d	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	q	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	r	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	s	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	t	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	u	339	Total 2605	C 1722	N 428	O 448	S 7	0	0
12	v	339	Total 2605	C 1722	N 428	O 448	S 7	0	0

- Molecule 13 is CHLOROPHYLL A (three-letter code: CLA) (formula:  $C_{55}H_{72}MgN_4O_5$ ).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0
13	A	1	2728	2278	45	180	225	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	A	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	B	1	Total 2550	C 2140	Mg 41	N 164	O 205	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	B	1	2550	2140	41	164	205	0
13	F	1	110	90	2	8	10	0
13	F	1	110	90	2	8	10	0
13	J	1	123	103	2	8	10	0
13	J	1	123	103	2	8	10	0
13	K	1	150	120	3	12	15	0
13	K	1	150	120	3	12	15	0
13	K	1	150	120	3	12	15	0
13	L	1	190	160	3	12	15	0
13	L	1	190	160	3	12	15	0
13	L	1	190	160	3	12	15	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	1	1	951	781	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	2	1	993	823	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	3	1	950	780	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	4	1	860	690	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	5	1	857	687	17	68	85	0
13	6	1	823	653	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	6	1	823	653	17	68	85	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	G	1	2728	2278	45	180	225	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	H	1	2550	2140	41	164	205	0
13	R	1	110	90	2	8	10	0
13	R	1	110	90	2	8	10	0
13	T	1	123	103	2	8	10	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	T	1	Total 123	C 103	Mg 2	N 8	O 10	0
13	U	1	Total 150	C 120	Mg 3	N 12	O 15	0
13	U	1	Total 150	C 120	Mg 3	N 12	O 15	0
13	U	1	Total 150	C 120	Mg 3	N 12	O 15	0
13	V	1	Total 190	C 160	Mg 3	N 12	O 15	0
13	V	1	Total 190	C 160	Mg 3	N 12	O 15	0
13	V	1	Total 190	C 160	Mg 3	N 12	O 15	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	Y	1	Total 951	C 781	Mg 17	N 68	O 85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	Y	1	951	781	17	68	85	0
13	Y	1	951	781	17	68	85	0
13	Y	1	951	781	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	Z	1	993	823	17	68	85	0
13	a	1	950	780	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	a	1	950	780	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	b	1	860	690	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	c	1	857	687	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0
13	d	1	823	653	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
13	d	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	d	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	d	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	d	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	
13	e	1	Total	C	Mg	N	O	0
			2728	2278	45	180	225	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	e	1	Total 2728	C 2278	Mg 45	N 180	O 225	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0

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Mol	Chain	Residues	Atoms					AltConf
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	
13	f	1	Total	C	Mg	N	O	0
			2550	2140	41	164	205	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	f	1	Total 2550	C 2140	Mg 41	N 164	O 205	0
13	j	1	Total 110	C 90	Mg 2	N 8	O 10	0
13	j	1	Total 110	C 90	Mg 2	N 8	O 10	0
13	l	1	Total 123	C 103	Mg 2	N 8	O 10	0
13	l	1	Total 123	C 103	Mg 2	N 8	O 10	0
13	m	1	Total 150	C 120	Mg 3	N 12	O 15	0
13	m	1	Total 150	C 120	Mg 3	N 12	O 15	0
13	m	1	Total 150	C 120	Mg 3	N 12	O 15	0
13	n	1	Total 190	C 160	Mg 3	N 12	O 15	0
13	n	1	Total 190	C 160	Mg 3	N 12	O 15	0
13	n	1	Total 190	C 160	Mg 3	N 12	O 15	0
13	q	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	q	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	q	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	q	1	Total 951	C 781	Mg 17	N 68	O 85	0
13	q	1	Total 951	C 781	Mg 17	N 68	O 85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	q	1	951	781	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	r	1	993	823	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	s	1	950	780	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0
13	t	1	860	690	17	68	85	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	u	1	857	687	17	68	85	0
13	v	1	823	653	17	68	85	0
13	v	1	823	653	17	68	85	0
13	v	1	823	653	17	68	85	0
13	v	1	823	653	17	68	85	0

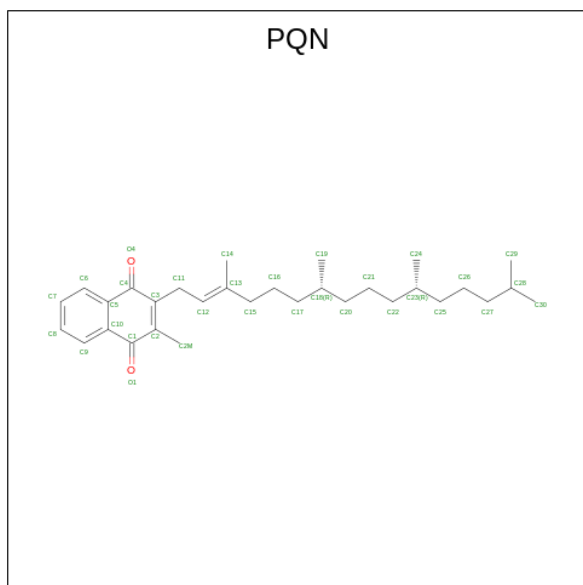
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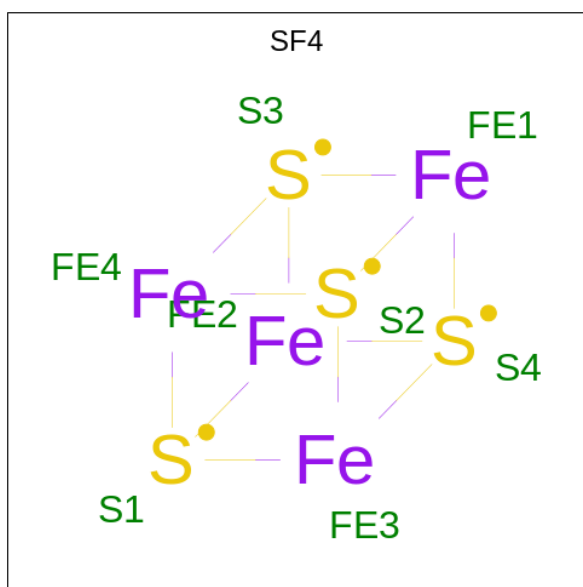
Mol	Chain	Residues	Atoms					AltConf
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	
13	v	1	Total	C	Mg	N	O	0
			823	653	17	68	85	

- Molecule 14 is PHYLLOQUINONE (three-letter code: PQN) (formula: C<sub>31</sub>H<sub>46</sub>O<sub>2</sub>).



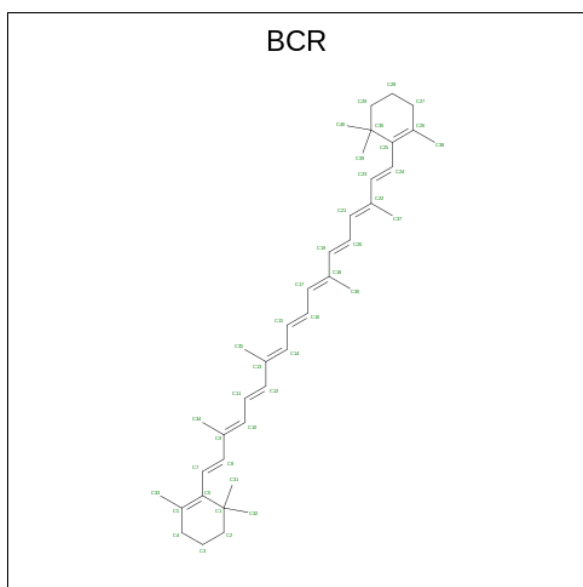
Mol	Chain	Residues	Atoms			AltConf
14	A	1	Total	C	O	0
			33	31	2	
14	B	1	Total	C	O	0
			33	31	2	
14	G	1	Total	C	O	0
			33	31	2	
14	H	1	Total	C	O	0
			33	31	2	
14	e	1	Total	C	O	0
			33	31	2	
14	f	1	Total	C	O	0
			33	31	2	

- Molecule 15 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
15	A	1	8	4	4	0
15	C	1	16	8	8	0
15	C	1	16	8	8	0
15	G	1	8	4	4	0
15	N	1	16	8	8	0
15	N	1	16	8	8	0
15	e	1	8	4	4	0
15	g	1	16	8	8	0
15	g	1	16	8	8	0

- Molecule 16 is BETA-CAROTENE (three-letter code: BCR) (formula: C<sub>40</sub>H<sub>56</sub>).



Mol	Chain	Residues	Atoms	AltConf
16	A	1	Total C 240 240	0
16	A	1	Total C 240 240	0
16	A	1	Total C 240 240	0
16	A	1	Total C 240 240	0
16	A	1	Total C 240 240	0
16	A	1	Total C 240 240	0
16	B	1	Total C 280 280	0
16	B	1	Total C 280 280	0
16	B	1	Total C 280 280	0
16	B	1	Total C 280 280	0
16	B	1	Total C 280 280	0
16	B	1	Total C 280 280	0
16	B	1	Total C 280 280	0
16	F	1	Total C 40 40	0

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Mol	Chain	Residues	Atoms		AltConf
16	I	1	Total 40	C 40	0
16	J	1	Total 120	C 120	0
16	J	1	Total 120	C 120	0
16	J	1	Total 120	C 120	0
16	K	1	Total 40	C 40	0
16	L	1	Total 160	C 160	0
16	L	1	Total 160	C 160	0
16	L	1	Total 160	C 160	0
16	L	1	Total 160	C 160	0
16	M	1	Total 40	C 40	0
16	1	1	Total 160	C 160	0
16	1	1	Total 160	C 160	0
16	1	1	Total 160	C 160	0
16	1	1	Total 160	C 160	0
16	2	1	Total 160	C 160	0
16	2	1	Total 160	C 160	0
16	2	1	Total 160	C 160	0
16	2	1	Total 160	C 160	0
16	3	1	Total 160	C 160	0
16	3	1	Total 160	C 160	0
16	3	1	Total 160	C 160	0

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Mol	Chain	Residues	Atoms		AltConf
16	3	1	Total 160	C 160	0
16	4	1	Total 160	C 160	0
16	4	1	Total 160	C 160	0
16	4	1	Total 160	C 160	0
16	4	1	Total 160	C 160	0
16	5	1	Total 160	C 160	0
16	5	1	Total 160	C 160	0
16	5	1	Total 160	C 160	0
16	5	1	Total 160	C 160	0
16	6	1	Total 160	C 160	0
16	6	1	Total 160	C 160	0
16	6	1	Total 160	C 160	0
16	6	1	Total 160	C 160	0
16	G	1	Total 240	C 240	0
16	G	1	Total 240	C 240	0
16	G	1	Total 240	C 240	0
16	G	1	Total 240	C 240	0
16	G	1	Total 240	C 240	0
16	G	1	Total 240	C 240	0
16	H	1	Total 280	C 280	0
16	H	1	Total 280	C 280	0

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Mol	Chain	Residues	Atoms		AltConf
16	H	1	Total 280	C 280	0
16	H	1	Total 280	C 280	0
16	H	1	Total 280	C 280	0
16	H	1	Total 280	C 280	0
16	H	1	Total 280	C 280	0
16	R	1	Total 40	C 40	0
16	S	1	Total 40	C 40	0
16	T	1	Total 120	C 120	0
16	T	1	Total 120	C 120	0
16	T	1	Total 120	C 120	0
16	U	1	Total 40	C 40	0
16	V	1	Total 160	C 160	0
16	V	1	Total 160	C 160	0
16	V	1	Total 160	C 160	0
16	V	1	Total 160	C 160	0
16	W	1	Total 40	C 40	0
16	Y	1	Total 160	C 160	0
16	Y	1	Total 160	C 160	0
16	Y	1	Total 160	C 160	0
16	Y	1	Total 160	C 160	0
16	Z	1	Total 160	C 160	0

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Mol	Chain	Residues	Atoms		AltConf
16	Z	1	Total 160	C 160	0
16	Z	1	Total 160	C 160	0
16	Z	1	Total 160	C 160	0
16	a	1	Total 160	C 160	0
16	a	1	Total 160	C 160	0
16	a	1	Total 160	C 160	0
16	a	1	Total 160	C 160	0
16	b	1	Total 160	C 160	0
16	b	1	Total 160	C 160	0
16	b	1	Total 160	C 160	0
16	b	1	Total 160	C 160	0
16	c	1	Total 160	C 160	0
16	c	1	Total 160	C 160	0
16	c	1	Total 160	C 160	0
16	c	1	Total 160	C 160	0
16	d	1	Total 160	C 160	0
16	d	1	Total 160	C 160	0
16	d	1	Total 160	C 160	0
16	d	1	Total 160	C 160	0
16	e	1	Total 240	C 240	0
16	e	1	Total 240	C 240	0

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Mol	Chain	Residues	Atoms		AltConf
16	e	1	Total 240	C 240	0
16	e	1	Total 240	C 240	0
16	e	1	Total 240	C 240	0
16	e	1	Total 240	C 240	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	f	1	Total 280	C 280	0
16	j	1	Total 40	C 40	0
16	k	1	Total 40	C 40	0
16	l	1	Total 120	C 120	0
16	l	1	Total 120	C 120	0
16	l	1	Total 120	C 120	0
16	m	1	Total 40	C 40	0
16	n	1	Total 160	C 160	0
16	n	1	Total 160	C 160	0
16	n	1	Total 160	C 160	0
16	n	1	Total 160	C 160	0

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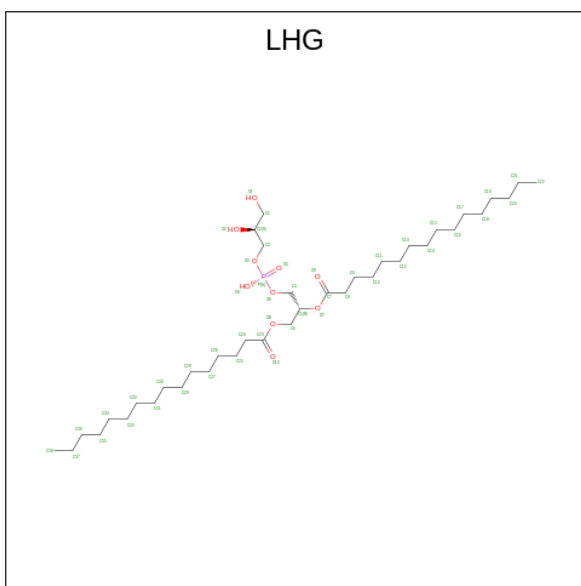
Mol	Chain	Residues	Atoms		AltConf
16	o	1	Total 40	C 40	0
16	q	1	Total 160	C 160	0
16	q	1	Total 160	C 160	0
16	q	1	Total 160	C 160	0
16	q	1	Total 160	C 160	0
16	r	1	Total 160	C 160	0
16	r	1	Total 160	C 160	0
16	r	1	Total 160	C 160	0
16	r	1	Total 160	C 160	0
16	s	1	Total 160	C 160	0
16	s	1	Total 160	C 160	0
16	s	1	Total 160	C 160	0
16	s	1	Total 160	C 160	0
16	t	1	Total 160	C 160	0
16	t	1	Total 160	C 160	0
16	t	1	Total 160	C 160	0
16	t	1	Total 160	C 160	0
16	u	1	Total 160	C 160	0
16	u	1	Total 160	C 160	0
16	u	1	Total 160	C 160	0
16	u	1	Total 160	C 160	0

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Mol	Chain	Residues	Atoms		AltConf
16	v	1	Total	C	0
			160	160	
16	v	1	Total	C	0
			160	160	
16	v	1	Total	C	0
			160	160	
16	v	1	Total	C	0
			160	160	

- Molecule 17 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (three-letter code: LHG) (formula:  $C_{38}H_{75}O_{10}P$ ).



Mol	Chain	Residues	Atoms				AltConf
17	A	1	Total	C	O	P	0
			386	287	90	9	
17	A	1	Total	C	O	P	0
			386	287	90	9	
17	A	1	Total	C	O	P	0
			386	287	90	9	
17	A	1	Total	C	O	P	0
			386	287	90	9	
17	A	1	Total	C	O	P	0
			386	287	90	9	
17	A	1	Total	C	O	P	0
			386	287	90	9	

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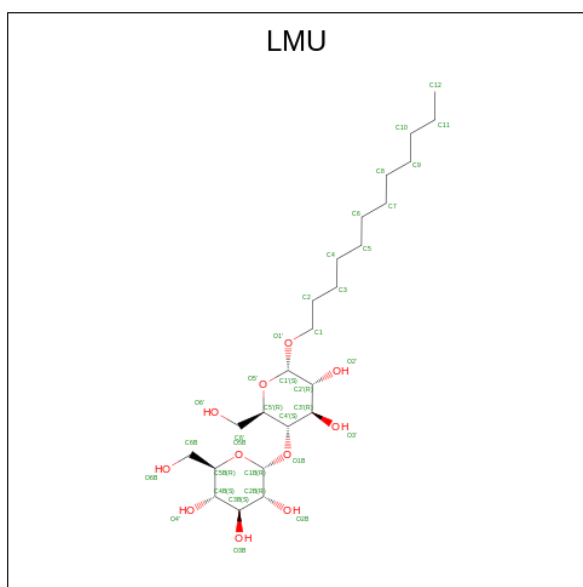
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
17	A	1	386	287	90	9	0
17	A	1	386	287	90	9	0
17	B	1	83	61	20	2	0
17	B	1	83	61	20	2	0
17	I	1	44	33	10	1	0
17	L	1	128	95	30	3	0
17	L	1	128	95	30	3	0
17	L	1	128	95	30	3	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	G	1	386	287	90	9	0
17	H	1	83	61	20	2	0
17	H	1	83	61	20	2	0
17	S	1	44	33	10	1	0
17	V	1	128	95	30	3	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
17	V	1	Total 128	C 95	O 30	P 3	0
17	V	1	Total 128	C 95	O 30	P 3	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	e	1	Total 386	C 287	O 90	P 9	0
17	f	1	Total 83	C 61	O 20	P 2	0
17	f	1	Total 83	C 61	O 20	P 2	0
17	k	1	Total 44	C 33	O 10	P 1	0
17	n	1	Total 128	C 95	O 30	P 3	0
17	n	1	Total 128	C 95	O 30	P 3	0
17	n	1	Total 128	C 95	O 30	P 3	0

- Molecule 18 is DODECYL-ALPHA-D-MALTOSE (three-letter code: LMU) (formula:  $C_{24}H_{46}O_{11}$ ).



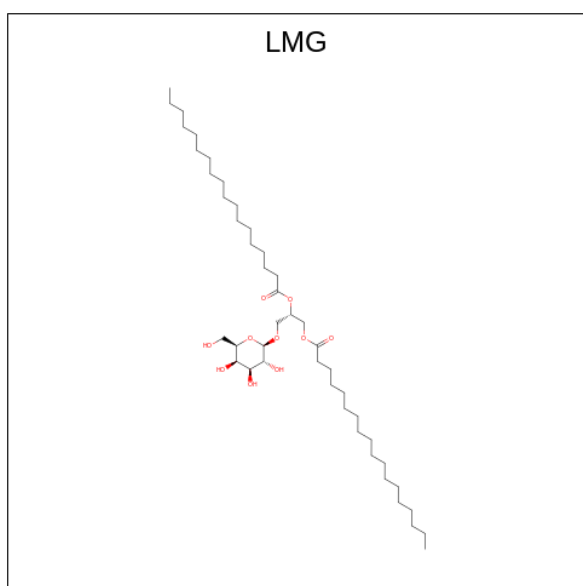
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
18	A	1	58	41	17	0
18	A	1	58	41	17	0
18	B	1	35	24	11	0
18	J	1	22	16	6	0
18	1	1	19	13	6	0
18	2	1	23	17	6	0
18	G	1	58	41	17	0
18	G	1	58	41	17	0
18	H	1	35	24	11	0
18	T	1	22	16	6	0
18	Y	1	19	13	6	0
18	Z	1	23	17	6	0
18	e	1	58	41	17	0
18	e	1	58	41	17	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
18	f	1	35	24	11	0
18	l	1	22	16	6	0
18	q	1	19	13	6	0
18	r	1	23	17	6	0

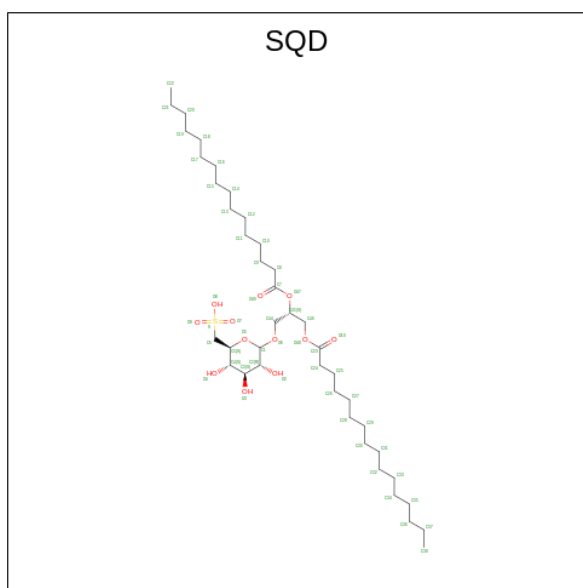
- Molecule 19 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (three-letter code: LMG) (formula: C<sub>45</sub>H<sub>86</sub>O<sub>10</sub>).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
19	B	1	54	44	10	0
19	J	1	35	25	10	0
19	H	1	54	44	10	0
19	T	1	35	25	10	0
19	f	1	54	44	10	0
19	l	1	35	25	10	0

- Molecule 20 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSY

L]-SN-GLYCEROL (three-letter code: SQD) (formula: C<sub>41</sub>H<sub>78</sub>O<sub>12</sub>S).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	S	
20	B	1	Total 45	C 32	O 12	S 1	0
20	L	1	Total 51	C 38	O 12	S 1	0
20	1	1	Total 48	C 35	O 12	S 1	0
20	2	1	Total 43	C 30	O 12	S 1	0
20	3	1	Total 43	C 30	O 12	S 1	0
20	4	1	Total 26	C 13	O 12	S 1	0
20	5	1	Total 29	C 16	O 12	S 1	0
20	6	1	Total 26	C 13	O 12	S 1	0
20	H	1	Total 45	C 32	O 12	S 1	0
20	V	1	Total 51	C 38	O 12	S 1	0
20	Y	1	Total 48	C 35	O 12	S 1	0
20	Z	1	Total 43	C 30	O 12	S 1	0
20	a	1	Total 43	C 30	O 12	S 1	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	S	
20	b	1	26	13	12	1	0
20	c	1	29	16	12	1	0
20	d	1	26	13	12	1	0
20	f	1	45	32	12	1	0
20	n	1	51	38	12	1	0
20	q	1	48	35	12	1	0
20	r	1	43	30	12	1	0
20	s	1	43	30	12	1	0
20	t	1	26	13	12	1	0
20	u	1	29	16	12	1	0
20	v	1	26	13	12	1	0

- Molecule 21 is water.

Mol	Chain	Residues	Atoms		AltConf
21	A	9	Total	O	0
			9	9	
21	B	7	Total	O	0
			7	7	
21	F	1	Total	O	0
			1	1	
21	L	1	Total	O	0
			1	1	
21	G	9	Total	O	0
			9	9	
21	H	7	Total	O	0
			7	7	
21	R	1	Total	O	0
			1	1	
21	V	1	Total	O	0
			1	1	

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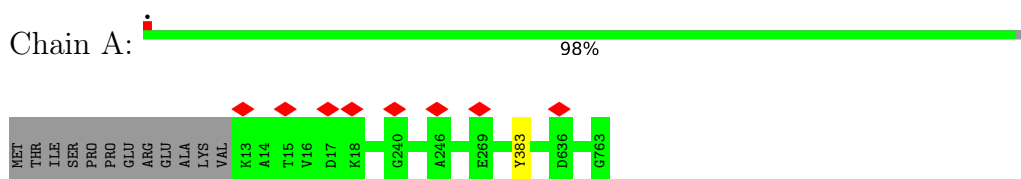
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
21	e	9	Total 9	O 9	0
21	f	7	Total 7	O 7	0
21	j	1	Total 1	O 1	0
21	n	1	Total 1	O 1	0

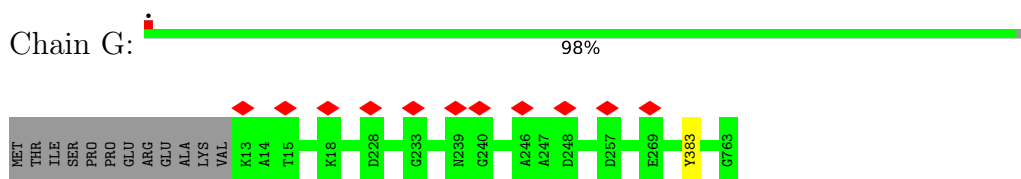
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

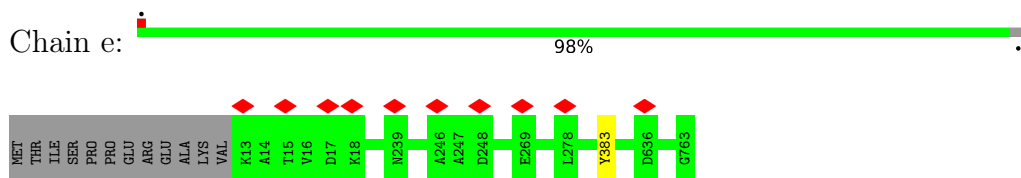
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



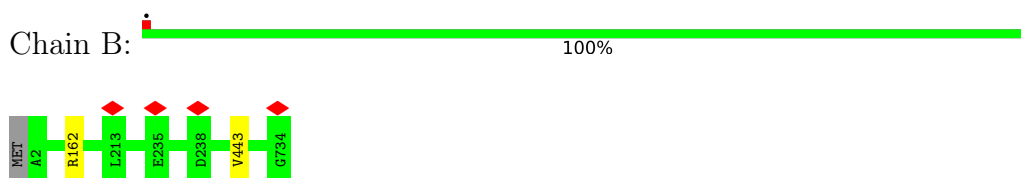
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



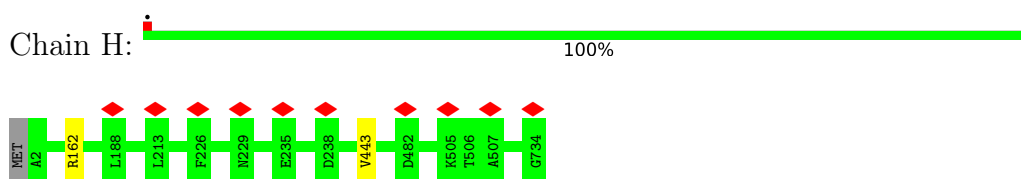
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2

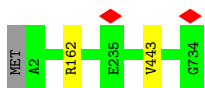


- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2



- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2

Chain f:  100%



- Molecule 3: Photosystem I iron-sulfur center

Chain C:  99%



- Molecule 3: Photosystem I iron-sulfur center

Chain N:  99%



- Molecule 3: Photosystem I iron-sulfur center

Chain g:  99%



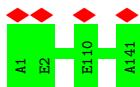
- Molecule 4: Photosystem I reaction center subunit II

Chain D:  100%



- Molecule 4: Photosystem I reaction center subunit II

Chain O:  100%

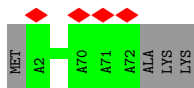
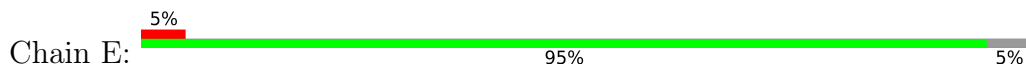


- Molecule 4: Photosystem I reaction center subunit II

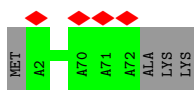
Chain h:  100%



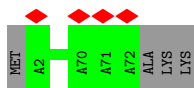
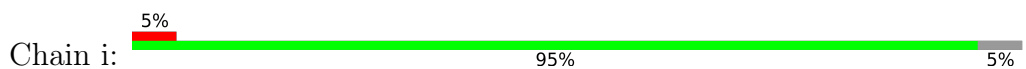
- Molecule 5: Photosystem I reaction center subunit IV



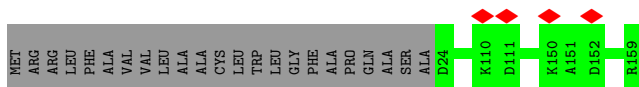
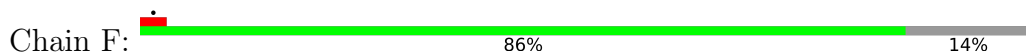
- Molecule 5: Photosystem I reaction center subunit IV



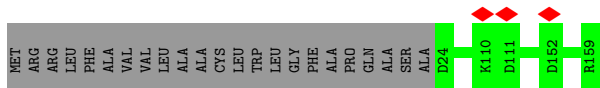
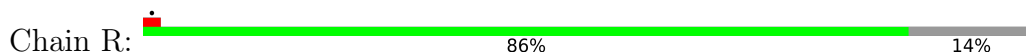
- Molecule 5: Photosystem I reaction center subunit IV



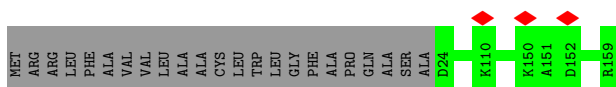
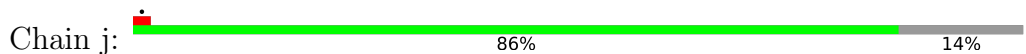
- Molecule 6: Photosystem I reaction center subunit III



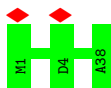
- Molecule 6: Photosystem I reaction center subunit III



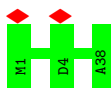
- Molecule 6: Photosystem I reaction center subunit III



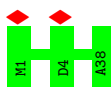
- Molecule 7: Photosystem I PsaI protein



- Molecule 7: Photosystem I PsaI protein



- Molecule 7: Photosystem I PsaI protein



- Molecule 8: Photosystem I reaction center subunit IX



There are no outlier residues recorded for this chain.

- Molecule 8: Photosystem I reaction center subunit IX



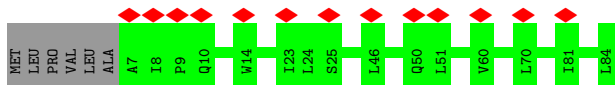
There are no outlier residues recorded for this chain.

- Molecule 8: Photosystem I reaction center subunit IX



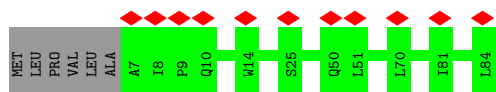
There are no outlier residues recorded for this chain.

- Molecule 9: Photosystem I reaction center subunit PsaK

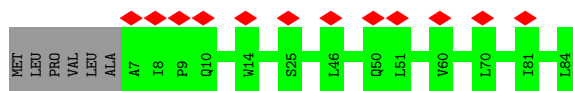
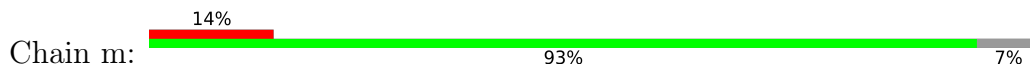


- Molecule 9: Photosystem I reaction center subunit PsaK

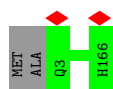




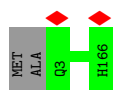
- Molecule 9: Photosystem I reaction center subunit PsaK



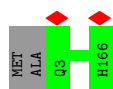
- Molecule 10: Photosystem I reaction center subunit XI



- Molecule 10: Photosystem I reaction center subunit XI



- Molecule 10: Photosystem I reaction center subunit XI



- Molecule 11: PsaM



There are no outlier residues recorded for this chain.

- Molecule 11: PsaM



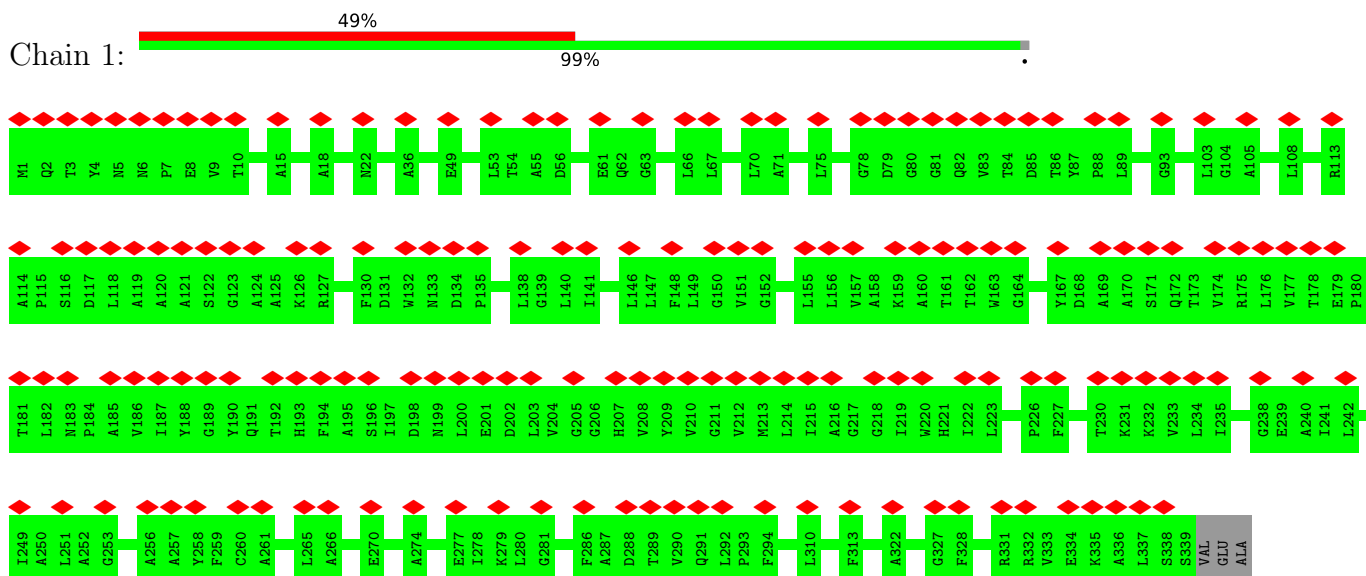
There are no outlier residues recorded for this chain.

- Molecule 11: PsaM

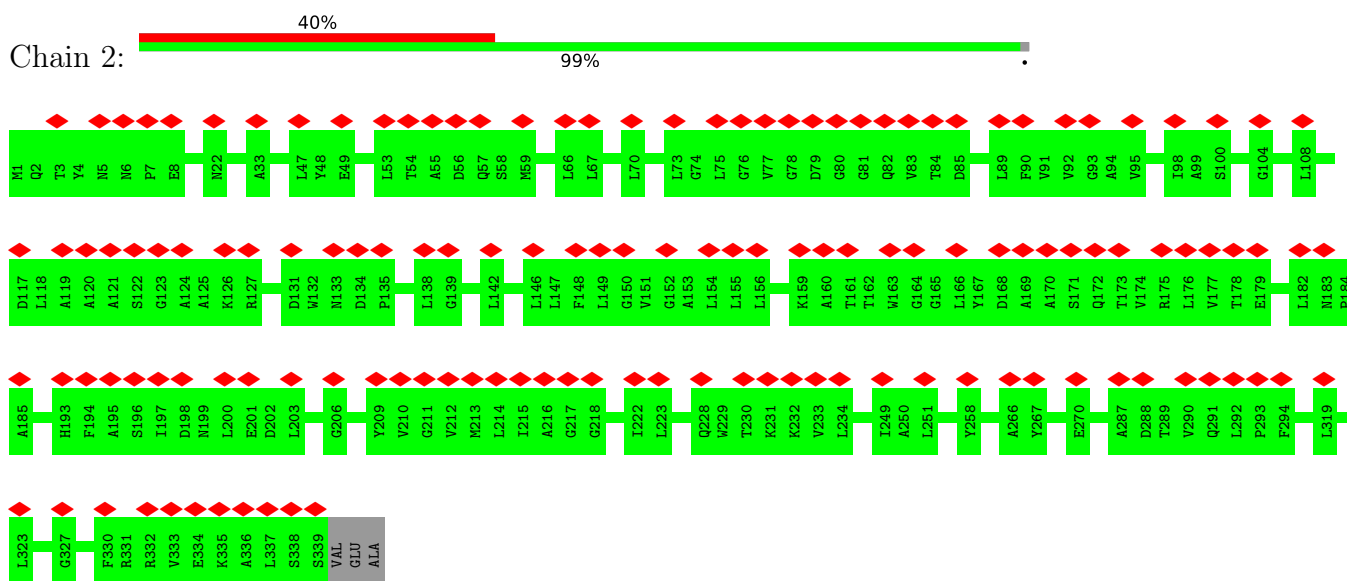


There are no outlier residues recorded for this chain.

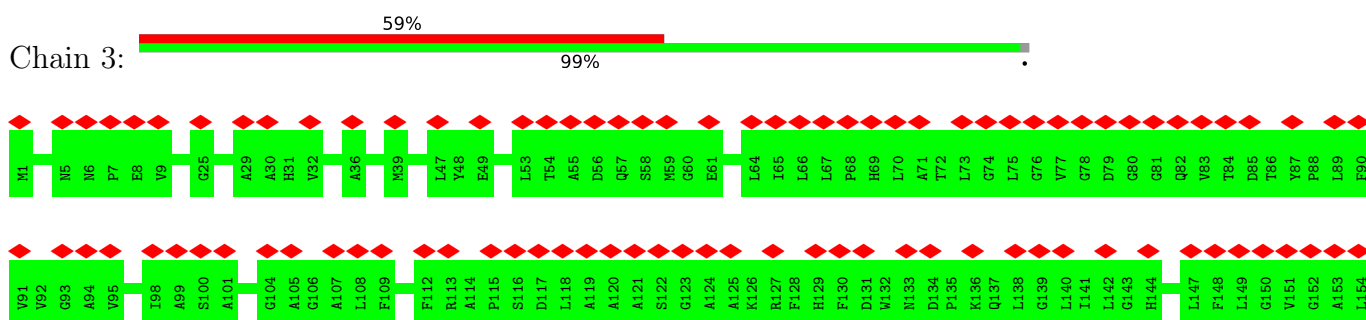
- Molecule 12: Iron stress-induced chlorophyll-binding protein



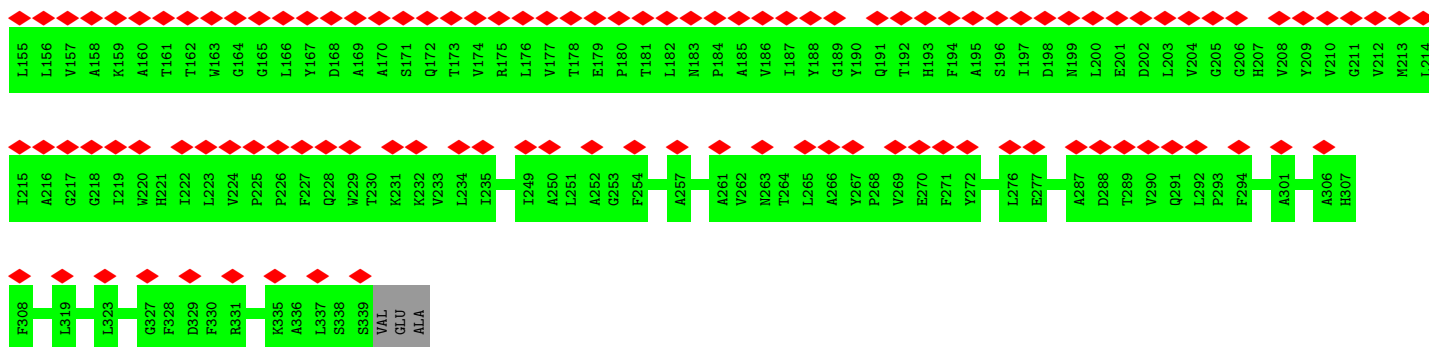
- Molecule 12: Iron stress-induced chlorophyll-binding protein



- Molecule 12: Iron stress-induced chlorophyll-binding protein



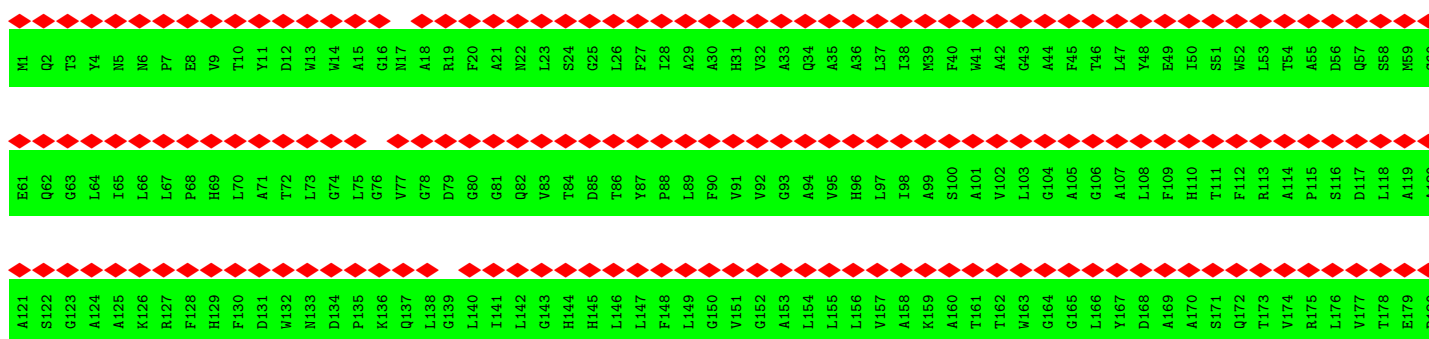


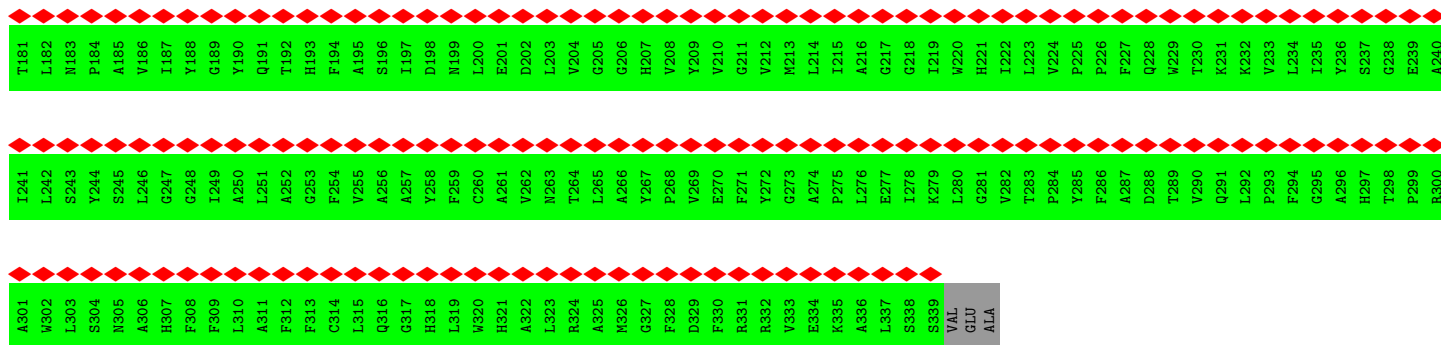


• Molecule 12: Iron stress-induced chlorophyll-binding protein



• Molecule 12: Iron stress-induced chlorophyll-binding protein

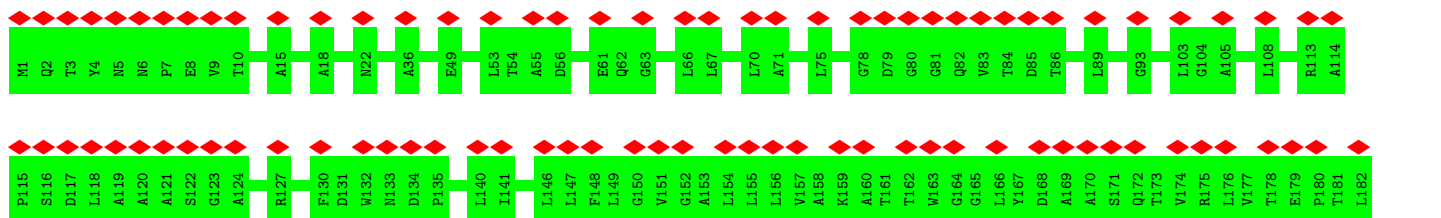


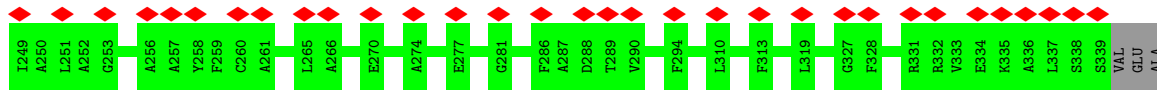


• Molecule 12: Iron stress-induced chlorophyll-binding protein

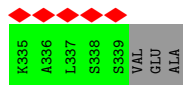
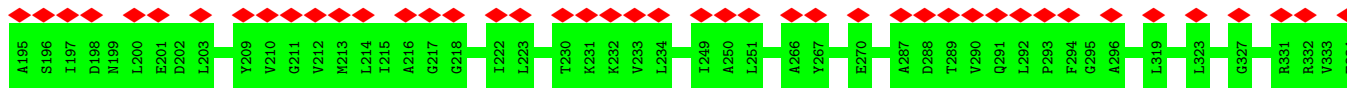
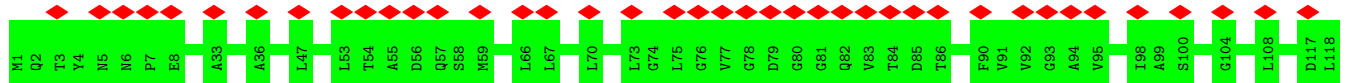


• Molecule 12: Iron stress-induced chlorophyll-binding protein

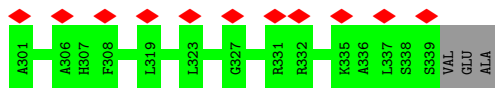
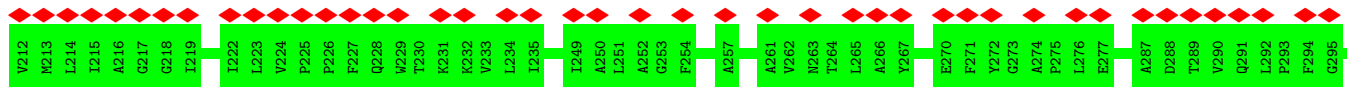
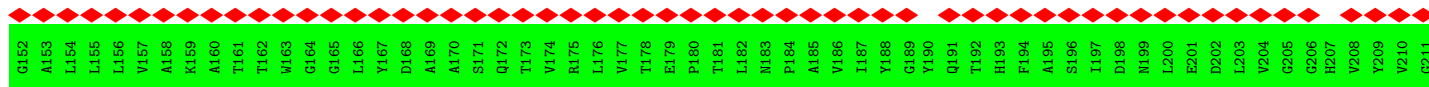
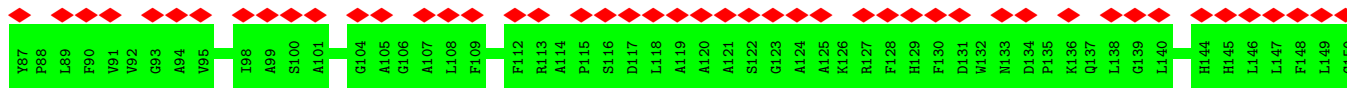
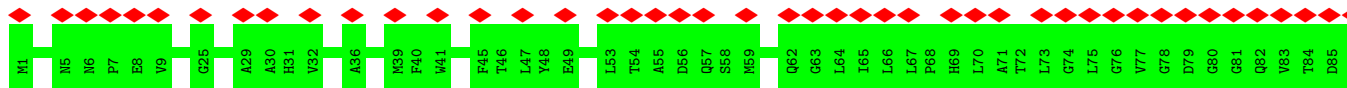




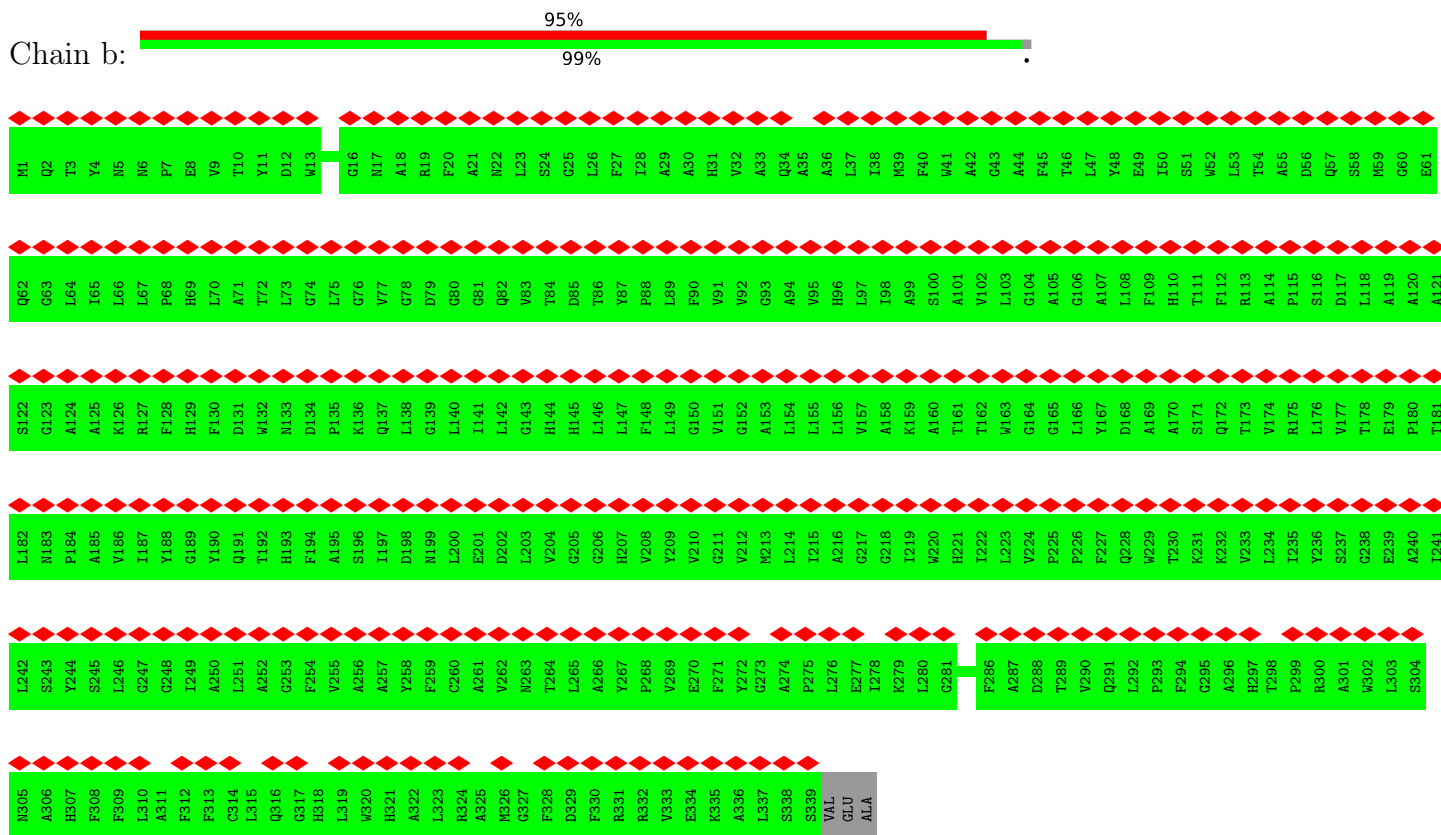
• Molecule 12: Iron stress-induced chlorophyll-binding protein



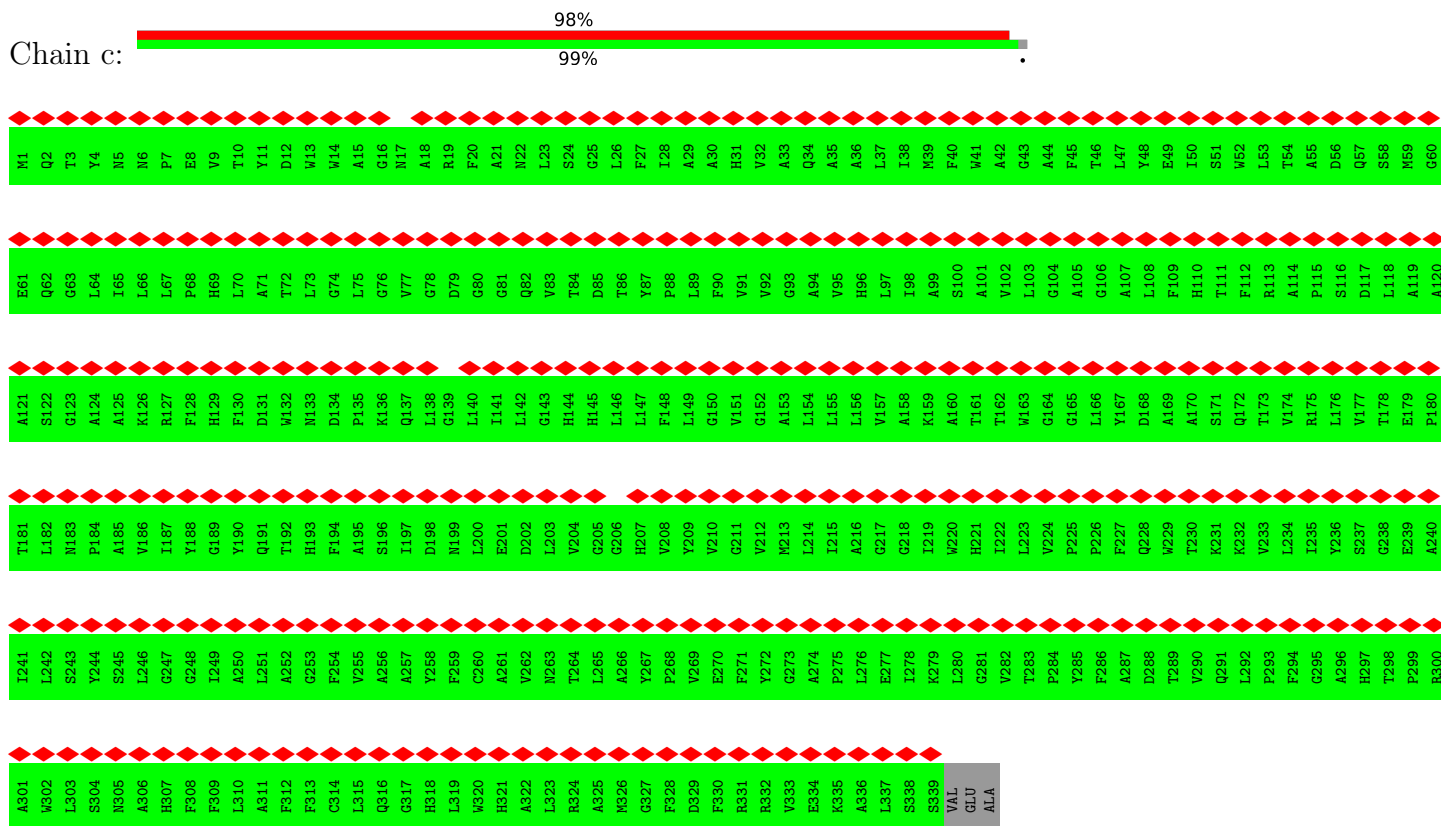
• Molecule 12: Iron stress-induced chlorophyll-binding protein



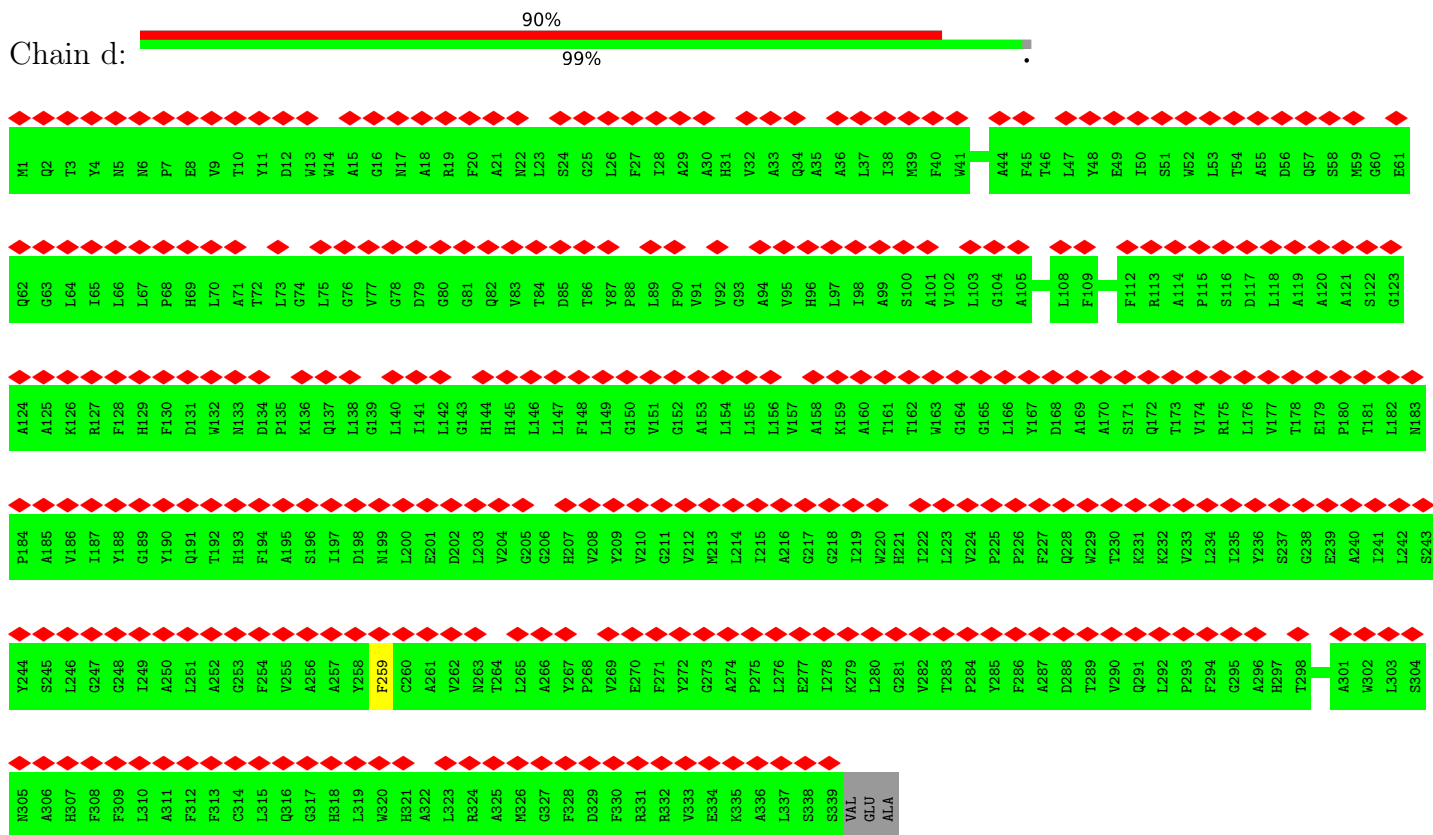
• Molecule 12: Iron stress-induced chlorophyll-binding protein



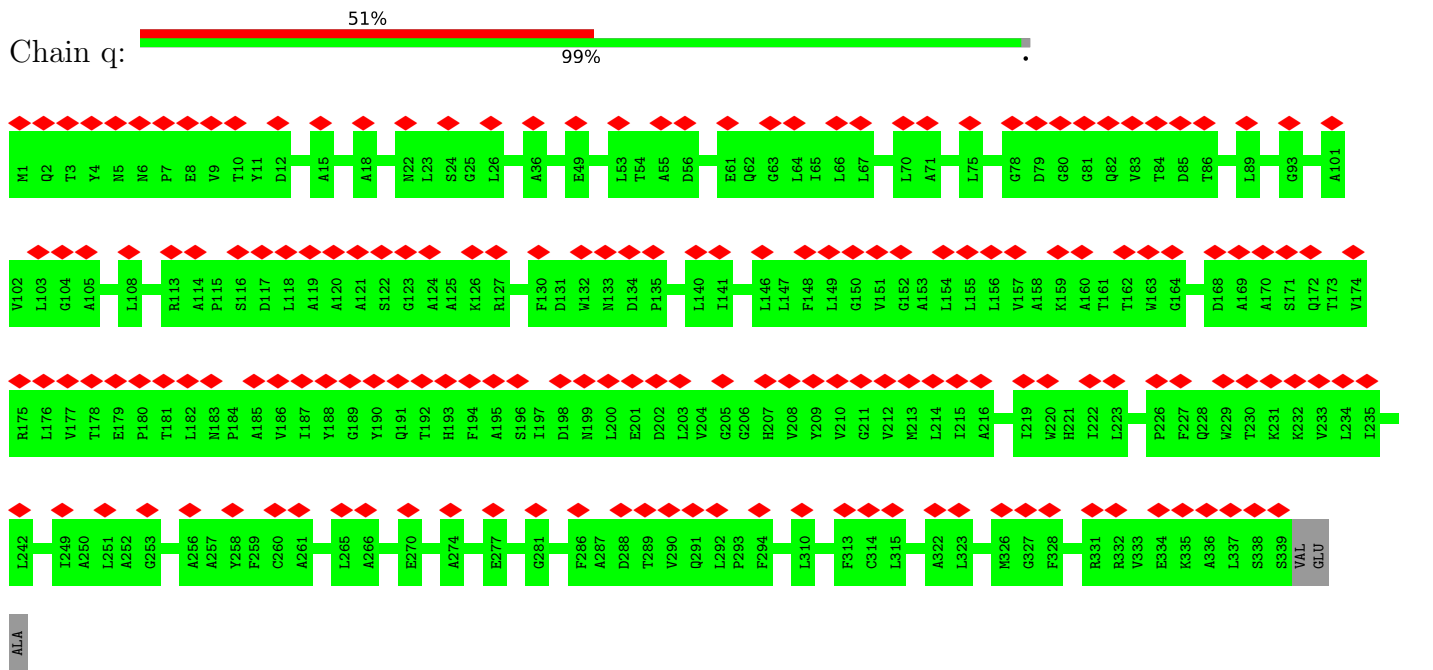
• Molecule 12: Iron stress-induced chlorophyll-binding protein



• Molecule 12: Iron stress-induced chlorophyll-binding protein

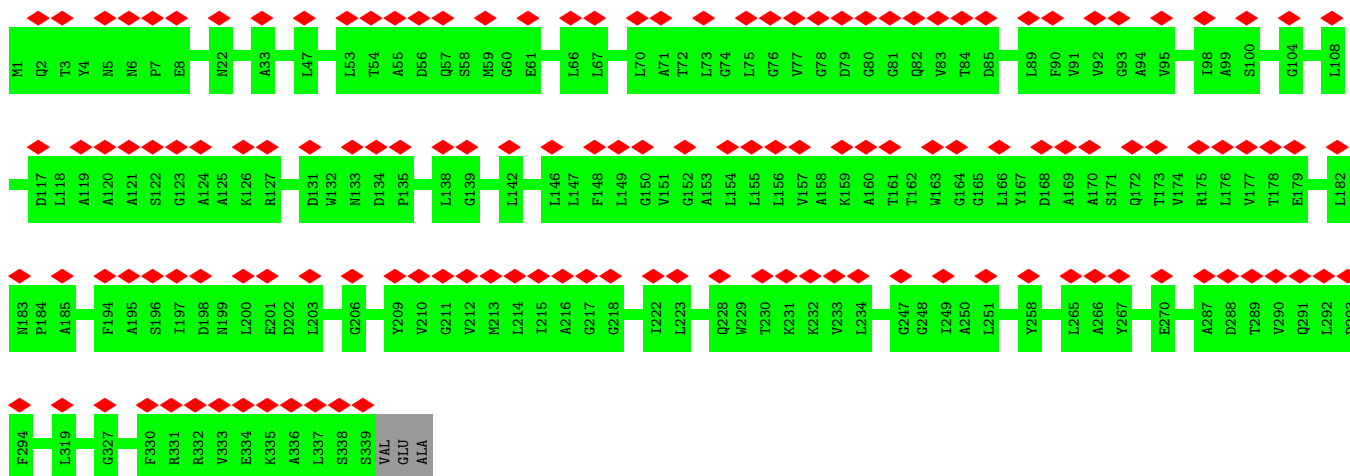


• Molecule 12: Iron stress-induced chlorophyll-binding protein

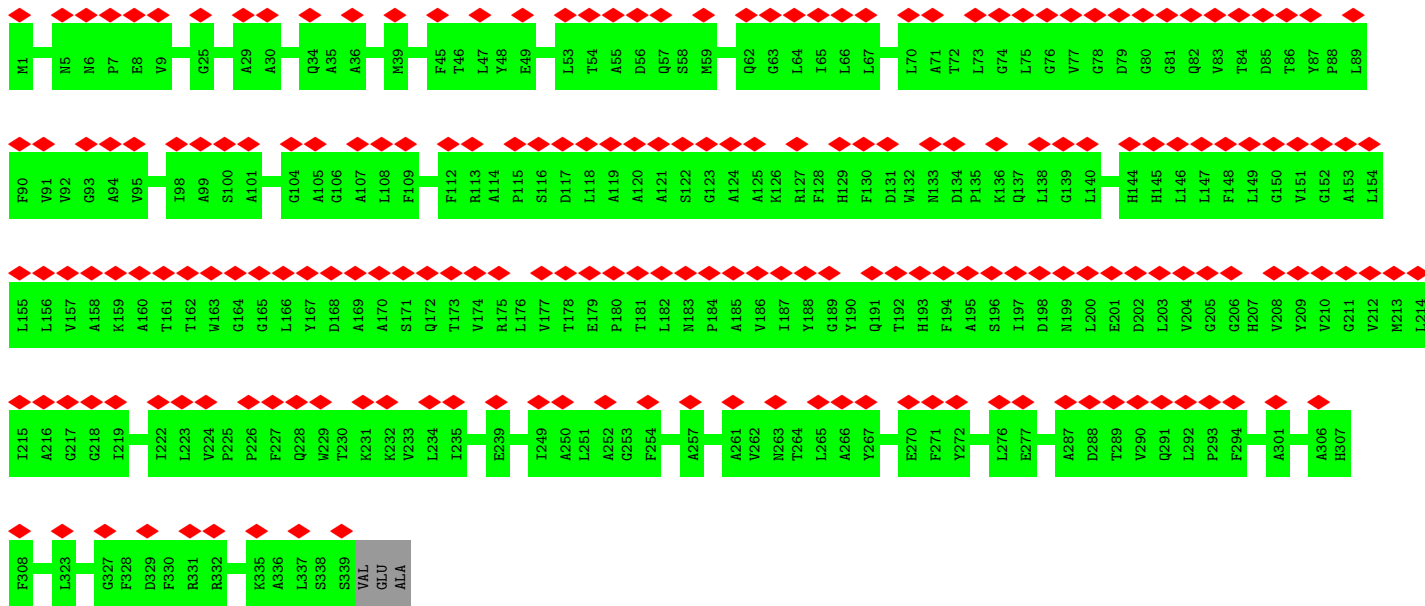


• Molecule 12: Iron stress-induced chlorophyll-binding protein



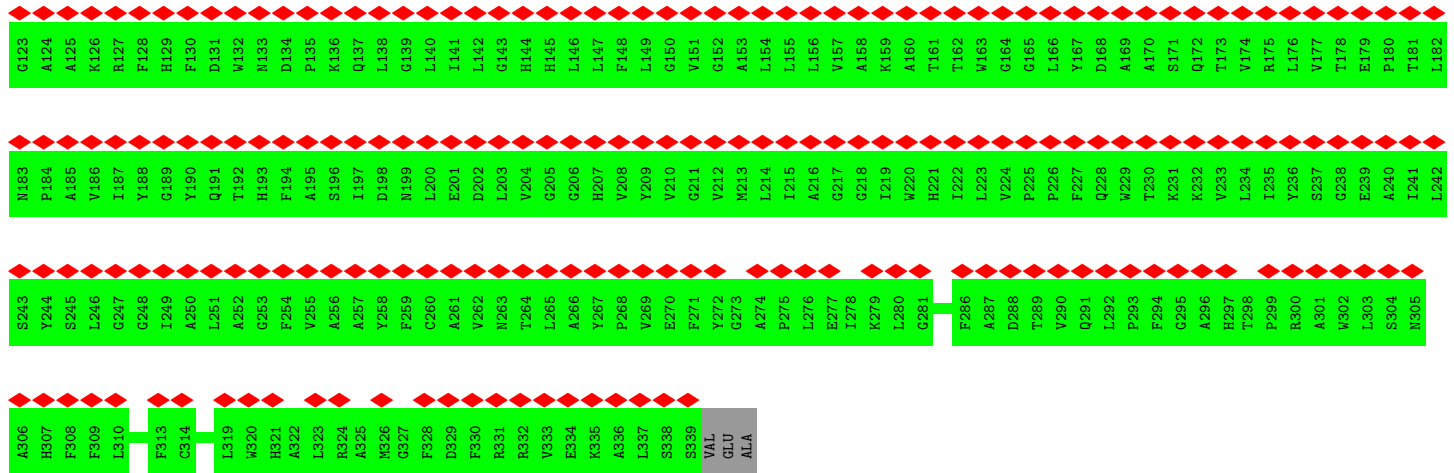


• Molecule 12: Iron stress-induced chlorophyll-binding protein

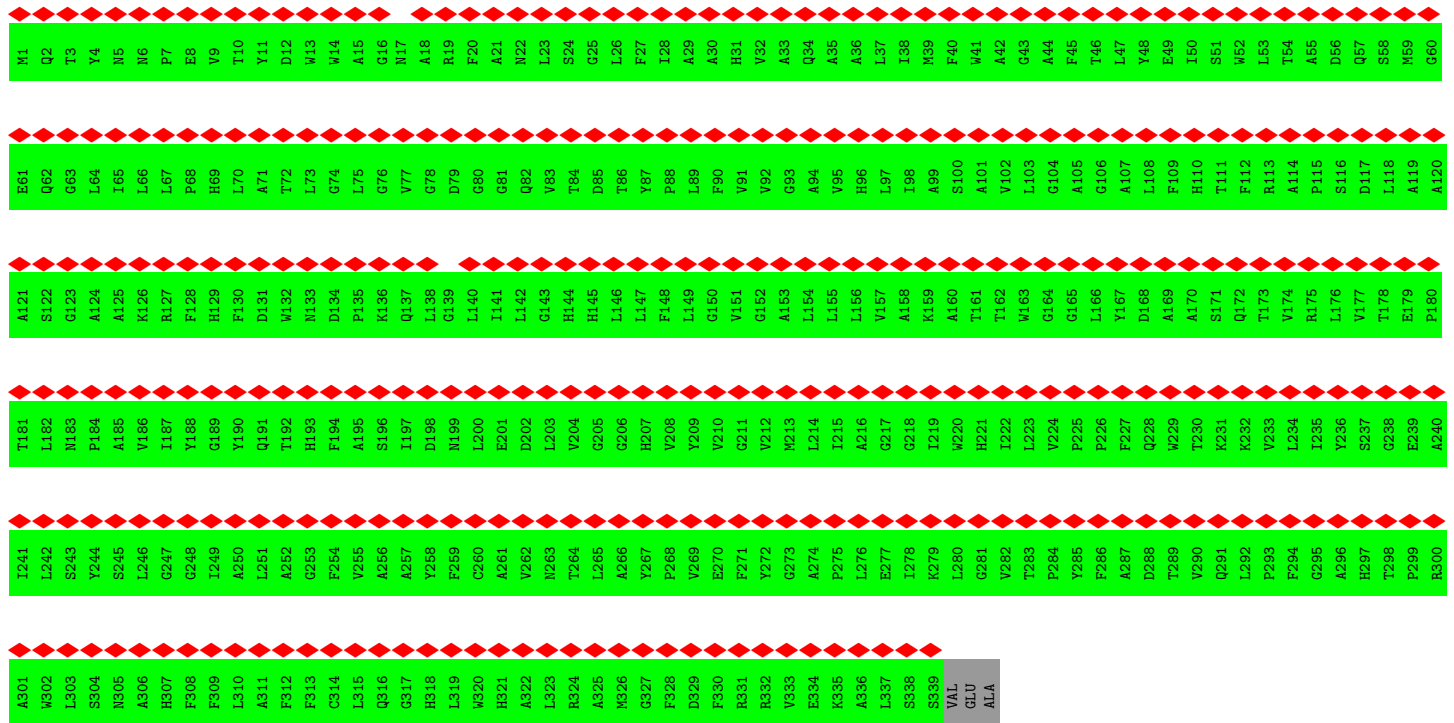


• Molecule 12: Iron stress-induced chlorophyll-binding protein

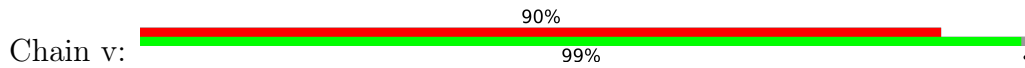




• Molecule 12: Iron stress-induced chlorophyll-binding protein



• Molecule 12: Iron stress-induced chlorophyll-binding protein



A124	A125	K126	R127	F128	H129	F130	D131	W132	M133	D134	P135	K136	Q137	L138	G139	L140	I141	L142	G143	H144	H145	L146	L147	F148	L149	G150	V151	G152	A153	L154	L155	L156	V157	A158	K159	A160	T161	T162	W163	G164	G165	L166	Y167	D168	A169	A170	S171	Q172	T173	V174	R175	L176	V177	T178	E179	P180	T181	L182	N183
P184	A185	V186	I187	Y188	G189	Y190	Q191	T192	H193	F194	A195	S196	I197	D198	N199	L200	E201	D202	L203	V204	G205	G206	H207	V208	Y209	V210	G211	V212	M213	L214	I215	A216	G217	G218	I219	W220	H221	I222	L223	V224	P225	P226	F227	Q228	W229	T230	K231	K232	V233	L234	I235	Y236	S237	G238	E239	A240	I241	L242	S243
Y244	S245	L246	G247	G248	I249	A250	L251	A252	G253	F254	V255	A256	A257	Y258	F259	C260	A261	V262	N263	T264	L265	A266	Y267	P268	V269	E270	F271	Y272	G273	A274	P275	L276	E277	I278	K279	L280	G281	V282	T283	P284	Y285	F286	A287	D288	T289	V290	Q291	L292	P293	F294	G295	A296	H297	T298	A301	W302	L303	S304	
N305	A306	H307	F308	F309	L310	A311	F312	F313	C314	L315	Q316	G317	H318	L319	W320	H321	A322	L323	R324	A325	M326	G327	F328	D329	F330	R331	R332	V333	E334	K335	A336	L337	S338	S339	VAL	GLU	ALA																						



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	63332	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 K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.170	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.022	Depositor
Map size (Å)	499.19998, 499.19998, 499.19998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SQD, SF4, LMU, LHG, CLA, LMG, PQN, BCR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.42	0/6064	0.53	0/8274
1	G	0.42	0/6064	0.53	0/8274
1	e	0.42	0/6064	0.53	0/8274
2	B	0.42	0/5999	0.53	0/8199
2	H	0.42	0/5999	0.53	0/8199
2	f	0.42	0/5999	0.53	0/8199
3	C	0.42	0/608	0.56	0/823
3	N	0.42	0/608	0.56	0/823
3	g	0.43	0/608	0.56	0/823
4	D	0.37	0/1124	0.54	0/1516
4	O	0.37	0/1124	0.54	0/1516
4	h	0.37	0/1124	0.54	0/1516
5	E	0.38	0/553	0.46	0/750
5	Q	0.38	0/553	0.46	0/750
5	i	0.38	0/553	0.46	0/750
6	F	0.36	0/1062	0.50	0/1442
6	R	0.36	0/1062	0.50	0/1442
6	j	0.36	0/1062	0.50	0/1442
7	I	0.38	0/289	0.62	0/393
7	S	0.38	0/289	0.62	0/393
7	k	0.38	0/289	0.62	0/393
8	J	0.41	0/346	0.57	0/469
8	T	0.41	0/346	0.57	0/469
8	l	0.41	0/346	0.57	0/469
9	K	0.31	0/560	0.56	0/765
9	U	0.31	0/560	0.56	0/765
9	m	0.31	0/560	0.56	0/765
10	L	0.36	0/1242	0.51	0/1696
10	V	0.36	0/1242	0.51	0/1696
10	n	0.36	0/1242	0.51	0/1696
11	M	0.37	0/231	0.54	0/314
11	W	0.37	0/231	0.54	0/314

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
11	o	0.37	0/231	0.54	0/314
12	1	0.28	0/2689	0.47	0/3678
12	2	0.28	0/2689	0.48	0/3678
12	3	0.27	0/2689	0.46	0/3678
12	4	0.27	0/2689	0.47	0/3678
12	5	0.27	0/2689	0.46	0/3678
12	6	0.27	0/2689	0.45	0/3678
12	Y	0.29	0/2689	0.47	0/3678
12	Z	0.29	0/2689	0.48	0/3678
12	a	0.27	0/2689	0.46	0/3678
12	b	0.27	0/2689	0.47	0/3678
12	c	0.27	0/2689	0.46	0/3678
12	d	0.27	0/2689	0.45	0/3678
12	q	0.29	0/2689	0.47	0/3678
12	r	0.29	0/2689	0.48	0/3678
12	s	0.27	0/2689	0.46	0/3678
12	t	0.27	0/2689	0.47	0/3678
12	u	0.27	0/2689	0.46	0/3678
12	v	0.27	0/2689	0.45	0/3678
All	All	0.35	0/102636	0.50	0/140127

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	749/763 (98%)	723 (96%)	26 (4%)	0	100	100
1	G	749/763 (98%)	723 (96%)	26 (4%)	0	100	100
1	e	749/763 (98%)	723 (96%)	26 (4%)	0	100	100
2	B	731/734 (100%)	711 (97%)	20 (3%)	0	100	100
2	H	731/734 (100%)	711 (97%)	20 (3%)	0	100	100
2	f	731/734 (100%)	711 (97%)	20 (3%)	0	100	100
3	C	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
3	N	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
3	g	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
4	D	139/141 (99%)	132 (95%)	7 (5%)	0	100	100
4	O	139/141 (99%)	132 (95%)	7 (5%)	0	100	100
4	h	139/141 (99%)	132 (95%)	7 (5%)	0	100	100
5	E	69/75 (92%)	68 (99%)	1 (1%)	0	100	100
5	Q	69/75 (92%)	68 (99%)	1 (1%)	0	100	100
5	i	69/75 (92%)	68 (99%)	1 (1%)	0	100	100
6	F	134/159 (84%)	129 (96%)	5 (4%)	0	100	100
6	R	134/159 (84%)	129 (96%)	5 (4%)	0	100	100
6	j	134/159 (84%)	129 (96%)	5 (4%)	0	100	100
7	I	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
7	S	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
7	k	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
8	J	39/41 (95%)	39 (100%)	0	0	100	100
8	T	39/41 (95%)	39 (100%)	0	0	100	100
8	l	39/41 (95%)	39 (100%)	0	0	100	100
9	K	76/84 (90%)	75 (99%)	1 (1%)	0	100	100
9	U	76/84 (90%)	75 (99%)	1 (1%)	0	100	100
9	m	76/84 (90%)	75 (99%)	1 (1%)	0	100	100
10	L	162/166 (98%)	157 (97%)	5 (3%)	0	100	100
10	V	162/166 (98%)	157 (97%)	5 (3%)	0	100	100
10	n	162/166 (98%)	157 (97%)	5 (3%)	0	100	100
11	M	27/29 (93%)	27 (100%)	0	0	100	100
11	W	27/29 (93%)	27 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	o	27/29 (93%)	27 (100%)	0	0	100	100
12	1	337/342 (98%)	328 (97%)	9 (3%)	0	100	100
12	2	337/342 (98%)	329 (98%)	8 (2%)	0	100	100
12	3	337/342 (98%)	330 (98%)	7 (2%)	0	100	100
12	4	337/342 (98%)	327 (97%)	10 (3%)	0	100	100
12	5	337/342 (98%)	326 (97%)	11 (3%)	0	100	100
12	6	337/342 (98%)	328 (97%)	9 (3%)	0	100	100
12	Y	337/342 (98%)	328 (97%)	9 (3%)	0	100	100
12	Z	337/342 (98%)	329 (98%)	8 (2%)	0	100	100
12	a	337/342 (98%)	330 (98%)	7 (2%)	0	100	100
12	b	337/342 (98%)	327 (97%)	10 (3%)	0	100	100
12	c	337/342 (98%)	326 (97%)	11 (3%)	0	100	100
12	d	337/342 (98%)	328 (97%)	9 (3%)	0	100	100
12	q	337/342 (98%)	328 (97%)	9 (3%)	0	100	100
12	r	337/342 (98%)	329 (98%)	8 (2%)	0	100	100
12	s	337/342 (98%)	330 (98%)	7 (2%)	0	100	100
12	t	337/342 (98%)	327 (97%)	10 (3%)	0	100	100
12	u	337/342 (98%)	326 (97%)	11 (3%)	0	100	100
12	v	337/342 (98%)	328 (97%)	9 (3%)	0	100	100
All	All	12786/13089 (98%)	12420 (97%)	366 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	600/611 (98%)	599 (100%)	1 (0%)	93	98
1	G	600/611 (98%)	599 (100%)	1 (0%)	93	98

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	e	600/611 (98%)	599 (100%)	1 (0%)	93	98
2	B	583/584 (100%)	581 (100%)	2 (0%)	92	98
2	H	583/584 (100%)	581 (100%)	2 (0%)	92	98
2	f	583/584 (100%)	581 (100%)	2 (0%)	92	98
3	C	67/68 (98%)	67 (100%)	0	100	100
3	N	67/68 (98%)	67 (100%)	0	100	100
3	g	67/68 (98%)	67 (100%)	0	100	100
4	D	114/114 (100%)	114 (100%)	0	100	100
4	O	114/114 (100%)	114 (100%)	0	100	100
4	h	114/114 (100%)	114 (100%)	0	100	100
5	E	56/59 (95%)	56 (100%)	0	100	100
5	Q	56/59 (95%)	56 (100%)	0	100	100
5	i	56/59 (95%)	56 (100%)	0	100	100
6	F	105/121 (87%)	105 (100%)	0	100	100
6	R	105/121 (87%)	105 (100%)	0	100	100
6	j	105/121 (87%)	105 (100%)	0	100	100
7	I	30/30 (100%)	30 (100%)	0	100	100
7	S	30/30 (100%)	30 (100%)	0	100	100
7	k	30/30 (100%)	30 (100%)	0	100	100
8	J	35/35 (100%)	35 (100%)	0	100	100
8	T	35/35 (100%)	35 (100%)	0	100	100
8	l	35/35 (100%)	35 (100%)	0	100	100
9	K	56/61 (92%)	56 (100%)	0	100	100
9	U	56/61 (92%)	56 (100%)	0	100	100
9	m	56/61 (92%)	56 (100%)	0	100	100
10	L	127/128 (99%)	127 (100%)	0	100	100
10	V	127/128 (99%)	127 (100%)	0	100	100
10	n	127/128 (99%)	127 (100%)	0	100	100
11	M	24/24 (100%)	24 (100%)	0	100	100
11	W	24/24 (100%)	24 (100%)	0	100	100
11	o	24/24 (100%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	1	257/259 (99%)	257 (100%)	0	100	100
12	2	257/259 (99%)	257 (100%)	0	100	100
12	3	257/259 (99%)	257 (100%)	0	100	100
12	4	257/259 (99%)	257 (100%)	0	100	100
12	5	257/259 (99%)	257 (100%)	0	100	100
12	6	257/259 (99%)	256 (100%)	1 (0%)	91	97
12	Y	257/259 (99%)	257 (100%)	0	100	100
12	Z	257/259 (99%)	257 (100%)	0	100	100
12	a	257/259 (99%)	257 (100%)	0	100	100
12	b	257/259 (99%)	257 (100%)	0	100	100
12	c	257/259 (99%)	257 (100%)	0	100	100
12	d	257/259 (99%)	256 (100%)	1 (0%)	91	97
12	q	257/259 (99%)	257 (100%)	0	100	100
12	r	257/259 (99%)	257 (100%)	0	100	100
12	s	257/259 (99%)	257 (100%)	0	100	100
12	t	257/259 (99%)	257 (100%)	0	100	100
12	u	257/259 (99%)	257 (100%)	0	100	100
12	v	257/259 (99%)	256 (100%)	1 (0%)	91	97
All	All	10017/10167 (98%)	10005 (100%)	12 (0%)	93	98

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	d	259	PHE
1	e	383	TYR
12	v	259	PHE
2	f	162	ARG
12	6	259	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	e	179	HIS
2	f	603	GLN
1	e	192	ASN

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Mol	Chain	Res	Type
2	f	34	HIS
10	n	3	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

846 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
13	CLA	3	512	12	45,53,73	1.74	7 (15%)	52,89,113	1.61	5 (9%)
13	CLA	G	1130	1	65,73,73	1.47	7 (10%)	76,113,113	1.52	10 (13%)
13	CLA	A	1134	1	56,64,73	1.57	8 (14%)	65,102,113	1.55	8 (12%)
16	BCR	S	4018	-	41,41,41	0.77	0	56,56,56	1.84	15 (26%)
18	LMU	T	5105	-	22,22,36	1.14	1 (4%)	27,27,47	0.81	0
13	CLA	G	1127	1	65,73,73	1.41	7 (10%)	76,113,113	1.50	9 (11%)
17	LHG	A	5007	-	46,46,48	0.67	1 (2%)	49,52,54	1.24	5 (10%)
13	CLA	G	1101	1	65,73,73	1.49	8 (12%)	76,113,113	1.45	9 (11%)
13	CLA	G	1237	21	65,73,73	1.48	9 (13%)	76,113,113	1.50	11 (14%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	e	1133	1	65,73,73	1.39	7 (10%)	76,113,113	1.48	6 (7%)
13	CLA	G	1117	1	65,73,73	1.43	10 (15%)	76,113,113	1.69	12 (15%)
13	CLA	B	1226	2	65,73,73	1.56	10 (15%)	76,113,113	1.82	14 (18%)
13	CLA	b	502	12	50,58,73	1.69	6 (12%)	58,95,113	1.59	7 (12%)
13	CLA	e	1140	1	65,73,73	1.49	7 (10%)	76,113,113	1.47	12 (15%)
13	CLA	H	1226	2	65,73,73	1.56	10 (15%)	76,113,113	1.82	13 (17%)
13	CLA	f	1238	21	65,73,73	1.41	7 (10%)	76,113,113	1.57	10 (13%)
13	CLA	G	1108	1	54,62,73	1.61	7 (12%)	62,99,113	1.48	6 (9%)
18	LMU	A	1849	-	23,23,36	1.17	1 (4%)	28,28,47	1.00	1 (3%)
15	SF4	N	3003	3	0,12,12	-	-	-	-	-
13	CLA	f	1206	2	65,73,73	1.44	10 (15%)	76,113,113	1.58	7 (9%)
13	CLA	B	1225	2	65,73,73	1.42	9 (13%)	76,113,113	1.45	7 (9%)
13	CLA	e	1121	1	55,63,73	1.59	7 (12%)	64,101,113	1.58	11 (17%)
13	CLA	Z	510	12	65,73,73	1.46	7 (10%)	76,113,113	1.44	6 (7%)
13	CLA	l	503	12	64,72,73	1.50	6 (9%)	74,111,113	1.46	7 (9%)
13	CLA	6	512	12	45,53,73	1.77	6 (13%)	52,89,113	1.58	5 (9%)
13	CLA	H	1229	2	65,73,73	1.43	7 (10%)	76,113,113	1.57	10 (13%)
13	CLA	a	501	12	65,73,73	1.44	7 (10%)	76,113,113	1.53	7 (9%)
16	BCR	q	521	-	41,41,41	0.65	0	56,56,56	1.80	11 (19%)
13	CLA	G	1118	1	60,68,73	1.49	8 (13%)	70,107,113	1.49	8 (11%)
18	LMU	r	901	-	23,23,36	1.10	1 (4%)	28,28,47	0.94	0
16	BCR	l	522	-	41,41,41	0.73	0	56,56,56	1.91	19 (33%)
13	CLA	4	501	12	60,68,73	1.54	5 (8%)	70,107,113	1.45	6 (8%)
13	CLA	u	504	-	45,53,73	1.78	6 (13%)	52,89,113	1.64	7 (13%)
13	CLA	t	517	-	45,53,73	1.77	7 (15%)	52,89,113	1.66	8 (15%)
13	CLA	L	1502	10	65,73,73	1.43	7 (10%)	76,113,113	1.49	8 (10%)
13	CLA	d	507	-	45,53,73	1.77	6 (13%)	52,89,113	1.66	8 (15%)
13	CLA	c	507	-	45,53,73	1.74	6 (13%)	52,89,113	1.69	8 (15%)
13	CLA	f	1217	2	57,65,73	1.51	7 (12%)	66,103,113	1.54	8 (12%)
13	CLA	r	512	12	53,61,73	1.61	7 (13%)	61,98,113	1.47	5 (8%)
13	CLA	b	511	12	45,53,73	1.80	6 (13%)	52,89,113	1.69	7 (13%)
20	SQD	Y	822	-	47,48,54	0.99	5 (10%)	56,59,65	1.74	13 (23%)
13	CLA	B	1235	2	65,73,73	1.43	7 (10%)	76,113,113	1.54	10 (13%)
16	BCR	B	4004	-	41,41,41	0.72	0	56,56,56	1.85	13 (23%)
16	BCR	t	522	-	41,41,41	0.73	0	56,56,56	1.85	18 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
20	SQD	u	822	-	28,29,54	1.26	5 (17%)	37,40,65	1.92	13 (35%)
13	CLA	f	1230	2	60,68,73	1.53	9 (15%)	70,107,113	1.53	10 (14%)
13	CLA	Z	517	-	45,53,73	1.77	7 (15%)	52,89,113	1.62	6 (11%)
13	CLA	u	519	12	46,54,73	1.75	9 (19%)	53,90,113	1.55	6 (11%)
13	CLA	A	1131	1	65,73,73	1.45	9 (13%)	76,113,113	1.43	9 (11%)
16	BCR	H	4006	-	41,41,41	0.73	0	56,56,56	1.98	19 (33%)
13	CLA	v	511	12	45,53,73	1.78	6 (13%)	52,89,113	1.67	6 (11%)
16	BCR	G	4002	-	41,41,41	0.81	1 (2%)	56,56,56	1.85	14 (25%)
13	CLA	A	1106	1	65,73,73	1.41	9 (13%)	76,113,113	1.54	9 (11%)
16	BCR	a	521	-	41,41,41	0.68	0	56,56,56	1.75	10 (17%)
13	CLA	5	501	12	65,73,73	1.46	6 (9%)	76,113,113	1.47	7 (9%)
13	CLA	2	507	-	65,73,73	1.44	6 (9%)	76,113,113	1.48	7 (9%)
13	CLA	e	1113	1	45,53,73	1.67	7 (15%)	52,89,113	1.77	6 (11%)
13	CLA	Z	508	12	55,63,73	1.63	8 (14%)	64,101,113	1.58	9 (14%)
13	CLA	B	1023	-	65,73,73	1.41	8 (12%)	76,113,113	1.85	14 (18%)
16	BCR	k	4018	-	41,41,41	0.77	0	56,56,56	1.84	15 (26%)
13	CLA	6	505	12	65,73,73	1.47	6 (9%)	76,113,113	1.43	7 (9%)
16	BCR	n	4219	-	41,41,41	0.78	0	56,56,56	1.81	12 (21%)
13	CLA	Z	511	12	55,63,73	1.62	6 (10%)	64,101,113	1.57	7 (10%)
13	CLA	q	508	12	55,63,73	1.60	7 (12%)	64,101,113	1.70	9 (14%)
13	CLA	c	509	12	65,73,73	1.46	7 (10%)	76,113,113	1.49	8 (10%)
16	BCR	s	522	-	41,41,41	0.68	0	56,56,56	1.91	15 (26%)
13	CLA	r	511	12	55,63,73	1.62	6 (10%)	64,101,113	1.56	7 (10%)
13	CLA	t	516	12	45,53,73	1.78	6 (13%)	52,89,113	1.59	7 (13%)
16	BCR	t	521	-	41,41,41	0.65	0	56,56,56	1.78	11 (19%)
18	LMU	f	1843	-	36,36,36	1.19	2 (5%)	47,47,47	1.11	3 (6%)
20	SQD	2	822	-	42,43,54	1.06	5 (11%)	51,54,65	1.61	10 (19%)
13	CLA	A	1136	1	60,68,73	1.52	8 (13%)	70,107,113	1.56	11 (15%)
13	CLA	c	516	12	45,53,73	1.79	6 (13%)	52,89,113	1.60	6 (11%)
13	CLA	A	1119	21	65,73,73	1.46	9 (13%)	76,113,113	1.52	9 (11%)
13	CLA	f	1203	2	65,73,73	1.44	8 (12%)	76,113,113	1.46	7 (9%)
20	SQD	r	822	-	42,43,54	1.07	5 (11%)	51,54,65	1.61	10 (19%)
13	CLA	t	501	12	60,68,73	1.55	5 (8%)	70,107,113	1.44	6 (8%)
13	CLA	2	513	12	65,73,73	1.50	8 (12%)	76,113,113	1.38	6 (7%)
13	CLA	u	503	12	55,63,73	1.63	6 (10%)	64,101,113	1.53	8 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	s	510	12	65,73,73	1.47	6 (9%)	76,113,113	1.46	9 (11%)
13	CLA	T	1302	8	58,66,73	1.53	8 (13%)	67,104,113	1.51	8 (11%)
13	CLA	e	1124	21	56,64,73	1.58	6 (10%)	65,102,113	1.62	12 (18%)
17	LHG	A	5003	13	40,40,48	0.74	1 (2%)	43,46,54	1.34	6 (13%)
13	CLA	Y	506	12	45,53,73	1.77	6 (13%)	52,89,113	1.68	6 (11%)
13	CLA	3	502	12	50,58,73	1.69	7 (14%)	58,95,113	1.62	8 (13%)
13	CLA	s	506	12	50,58,73	1.69	7 (14%)	58,95,113	1.67	6 (10%)
18	LMU	2	901	-	23,23,36	1.10	1 (4%)	28,28,47	0.94	0
17	LHG	A	5002	-	38,38,48	0.70	1 (2%)	41,44,54	1.22	5 (12%)
18	LMU	Z	901	-	23,23,36	1.10	1 (4%)	28,28,47	0.94	0
13	CLA	H	1234	2	65,73,73	1.43	8 (12%)	76,113,113	1.68	13 (17%)
16	BCR	H	4009	-	41,41,41	0.81	0	56,56,56	1.91	21 (37%)
16	BCR	v	523	-	41,41,41	0.70	0	56,56,56	1.73	14 (25%)
13	CLA	B	1230	2	60,68,73	1.54	9 (15%)	70,107,113	1.53	10 (14%)
13	CLA	s	516	12	45,53,73	1.78	6 (13%)	52,89,113	1.85	12 (23%)
13	CLA	f	1228	2	55,63,73	1.53	7 (12%)	64,101,113	1.67	8 (12%)
13	CLA	l	501	12	65,73,73	1.49	7 (10%)	76,113,113	1.44	8 (10%)
13	CLA	r	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.48	7 (9%)
16	BCR	W	4021	-	41,41,41	0.71	0	56,56,56	1.82	14 (25%)
16	BCR	u	524	-	41,41,41	0.68	0	56,56,56	1.67	14 (25%)
17	LHG	A	5008	-	34,34,48	0.76	1 (2%)	37,40,54	1.28	4 (10%)
13	CLA	G	1105	1	55,63,73	1.51	7 (12%)	64,101,113	1.70	9 (14%)
16	BCR	A	4007	-	41,41,41	0.74	0	56,56,56	2.11	18 (32%)
16	BCR	B	4009	-	41,41,41	0.81	0	56,56,56	1.91	21 (37%)
13	CLA	f	1202	2	65,73,73	1.44	7 (10%)	76,113,113	1.65	10 (13%)
13	CLA	F	1301	21	65,73,73	1.46	7 (10%)	76,113,113	1.39	8 (10%)
13	CLA	A	1115	1	60,68,73	1.47	7 (11%)	70,107,113	1.59	8 (11%)
13	CLA	2	518	12	65,73,73	1.46	6 (9%)	76,113,113	1.48	7 (9%)
16	BCR	j	4016	-	41,41,41	0.74	0	56,56,56	1.79	13 (23%)
13	CLA	5	513	12	45,53,73	1.81	8 (17%)	52,89,113	1.57	6 (11%)
16	BCR	T	4013	-	41,41,41	0.76	0	56,56,56	1.96	15 (26%)
16	BCR	r	523	-	41,41,41	0.71	0	56,56,56	1.75	15 (26%)
13	CLA	b	509	12	65,73,73	1.47	6 (9%)	76,113,113	1.50	9 (11%)
16	BCR	l	4015	-	41,41,41	0.79	0	56,56,56	1.82	14 (25%)
17	LHG	A	5006	-	44,44,48	0.62	0	47,50,54	1.26	5 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	4	512	12	45,53,73	1.79	6 (13%)	52,89,113	1.62	6 (11%)
13	CLA	G	1113	1	45,53,73	1.68	7 (15%)	52,89,113	1.76	6 (11%)
13	CLA	1	504	-	45,53,73	1.79	8 (17%)	52,89,113	1.61	8 (15%)
13	CLA	f	1231	21	65,73,73	1.38	7 (10%)	76,113,113	1.57	8 (10%)
13	CLA	4	503	12	55,63,73	1.63	6 (10%)	64,101,113	1.54	11 (17%)
13	CLA	q	507	-	60,68,73	1.53	6 (10%)	70,107,113	1.54	9 (12%)
13	CLA	H	1235	2	65,73,73	1.43	8 (12%)	76,113,113	1.54	10 (13%)
13	CLA	f	1219	2	65,73,73	1.47	7 (10%)	76,113,113	1.33	9 (11%)
13	CLA	G	1107	1	65,73,73	1.47	10 (15%)	76,113,113	1.43	9 (11%)
16	BCR	R	4016	-	41,41,41	0.75	0	56,56,56	1.78	13 (23%)
13	CLA	e	1108	1	54,62,73	1.61	7 (12%)	62,99,113	1.49	6 (9%)
13	CLA	1	508	12	55,63,73	1.60	7 (12%)	64,101,113	1.70	9 (14%)
13	CLA	A	1022	21	65,73,73	1.47	10 (15%)	76,113,113	1.49	9 (11%)
13	CLA	2	505	12	65,73,73	1.44	6 (9%)	76,113,113	1.41	8 (10%)
13	CLA	a	511	12	50,58,73	1.70	6 (12%)	58,95,113	1.61	6 (10%)
13	CLA	e	1104	1	65,73,73	1.40	7 (10%)	76,113,113	1.52	10 (13%)
13	CLA	G	1125	1	65,73,73	1.43	7 (10%)	76,113,113	1.55	9 (11%)
13	CLA	Y	510	12	65,73,73	1.46	6 (9%)	76,113,113	1.40	7 (9%)
13	CLA	Z	505	12	65,73,73	1.44	6 (9%)	76,113,113	1.41	8 (10%)
13	CLA	u	510	12	45,53,73	1.77	6 (13%)	52,89,113	1.60	7 (13%)
13	CLA	H	1023	-	65,73,73	1.40	8 (12%)	76,113,113	1.85	15 (19%)
13	CLA	d	519	12	46,54,73	1.76	6 (13%)	53,90,113	1.59	6 (11%)
13	CLA	t	510	12	50,58,73	1.68	6 (12%)	58,95,113	1.62	7 (12%)
13	CLA	c	510	12	45,53,73	1.76	6 (13%)	52,89,113	1.60	7 (13%)
16	BCR	Y	521	-	41,41,41	0.65	0	56,56,56	1.80	11 (19%)
13	CLA	f	1220	2	55,63,73	1.54	9 (16%)	64,101,113	1.67	11 (17%)
13	CLA	j	1302	6	45,53,73	1.76	7 (15%)	52,89,113	1.58	6 (11%)
13	CLA	u	506	12	45,53,73	1.78	6 (13%)	52,89,113	1.66	7 (13%)
13	CLA	s	504	-	45,53,73	1.75	6 (13%)	52,89,113	1.69	6 (11%)
13	CLA	H	1236	2	55,63,73	1.63	7 (12%)	64,101,113	1.42	8 (12%)
13	CLA	6	507	-	45,53,73	1.77	6 (13%)	52,89,113	1.66	8 (15%)
20	SQD	s	822	-	42,43,54	1.06	5 (11%)	51,54,65	1.59	12 (23%)
13	CLA	G	1011	1	65,73,73	1.46	6 (9%)	76,113,113	1.63	12 (15%)
17	LHG	G	5009	-	48,48,48	0.62	1 (2%)	51,54,54	1.27	6 (11%)
17	LHG	I	5001	-	43,43,48	0.64	0	46,49,54	1.22	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
16	BCR	L	4219	-	41,41,41	0.78	0	56,56,56	1.80	12 (21%)
13	CLA	Z	506	12	55,63,73	1.61	7 (12%)	64,101,113	1.55	6 (9%)
13	CLA	6	518	12	55,63,73	1.61	6 (10%)	64,101,113	1.49	7 (10%)
13	CLA	q	519	12	50,58,73	1.66	10 (20%)	58,95,113	1.50	8 (13%)
13	CLA	2	519	12	55,63,73	1.61	9 (16%)	64,101,113	1.46	9 (14%)
13	CLA	6	511	12	45,53,73	1.78	6 (13%)	52,89,113	1.66	6 (11%)
13	CLA	5	511	12	55,63,73	1.61	6 (10%)	64,101,113	1.52	7 (10%)
15	SF4	A	3001	1,2	0,12,12	-	-	-	-	-
13	CLA	4	509	12	65,73,73	1.47	6 (9%)	76,113,113	1.51	8 (10%)
17	LHG	e	5003	13	40,40,48	0.74	1 (2%)	43,46,54	1.33	6 (13%)
13	CLA	6	504	-	45,53,73	1.78	5 (11%)	52,89,113	1.68	8 (15%)
13	CLA	A	1135	1	52,60,73	1.53	8 (15%)	60,97,113	1.72	10 (16%)
13	CLA	e	1101	1	65,73,73	1.49	8 (12%)	76,113,113	1.45	9 (11%)
16	BCR	B	4005	-	41,41,41	0.70	0	56,56,56	1.78	11 (19%)
13	CLA	r	507	-	65,73,73	1.44	7 (10%)	76,113,113	1.48	7 (9%)
13	CLA	s	512	12	45,53,73	1.74	7 (15%)	52,89,113	1.62	5 (9%)
20	SQD	1	822	-	47,48,54	0.99	5 (10%)	56,59,65	1.74	13 (23%)
13	CLA	a	502	12	50,58,73	1.68	7 (14%)	58,95,113	1.62	8 (13%)
13	CLA	l	1302	8	58,66,73	1.52	8 (13%)	67,104,113	1.53	8 (11%)
13	CLA	G	1111	1	65,73,73	1.47	7 (10%)	76,113,113	1.49	7 (9%)
13	CLA	A	1126	1	65,73,73	1.39	7 (10%)	76,113,113	1.60	8 (10%)
13	CLA	5	505	12	61,69,73	1.51	6 (9%)	71,108,113	1.39	6 (8%)
13	CLA	f	1216	21	60,68,73	1.57	10 (16%)	70,107,113	1.44	6 (8%)
13	CLA	n	1502	10	65,73,73	1.43	7 (10%)	76,113,113	1.48	8 (10%)
16	BCR	V	4019	-	41,41,41	0.74	0	56,56,56	1.92	14 (25%)
20	SQD	t	822	-	25,26,54	1.31	4 (16%)	34,37,65	1.84	9 (26%)
13	CLA	B	1206	2	65,73,73	1.44	10 (15%)	76,113,113	1.58	7 (9%)
13	CLA	V	1503	21	60,68,73	1.49	7 (11%)	70,107,113	1.56	7 (10%)
16	BCR	e	4007	-	41,41,41	0.74	0	56,56,56	2.11	18 (32%)
13	CLA	1	511	12	55,63,73	1.60	6 (10%)	64,101,113	1.58	8 (12%)
13	CLA	H	1240	17	65,73,73	1.47	6 (9%)	76,113,113	1.44	9 (11%)
13	CLA	c	502	12	50,58,73	1.71	8 (16%)	58,95,113	1.54	7 (12%)
17	LHG	B	1842	13	38,38,48	0.66	0	41,44,54	1.23	4 (9%)
20	SQD	n	5216	-	50,51,54	0.97	5 (10%)	59,62,65	1.63	11 (18%)
13	CLA	5	510	12	45,53,73	1.76	6 (13%)	52,89,113	1.60	7 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	q	512	12	52,60,73	1.64	6 (11%)	60,97,113	1.53	6 (10%)
17	LHG	H	1842	13	38,38,48	0.66	0	41,44,54	1.23	4 (9%)
13	CLA	r	505	12	65,73,73	1.44	6 (9%)	76,113,113	1.40	8 (10%)
13	CLA	f	1012	21	65,73,73	1.46	9 (13%)	76,113,113	1.54	8 (10%)
13	CLA	B	1215	2	65,73,73	1.44	8 (12%)	76,113,113	1.57	8 (10%)
13	CLA	B	1209	2	52,60,73	1.66	8 (15%)	60,97,113	1.67	8 (13%)
13	CLA	q	503	12	64,72,73	1.50	6 (9%)	74,111,113	1.46	8 (10%)
13	CLA	H	1220	2	55,63,73	1.55	9 (16%)	64,101,113	1.67	11 (17%)
13	CLA	Z	519	12	55,63,73	1.61	9 (16%)	64,101,113	1.46	9 (14%)
13	CLA	b	517	-	45,53,73	1.78	6 (13%)	52,89,113	1.66	8 (15%)
13	CLA	Y	518	12	60,68,73	1.52	9 (15%)	70,107,113	1.52	8 (11%)
13	CLA	f	1232	21	50,58,73	1.62	7 (14%)	58,95,113	1.82	6 (10%)
13	CLA	G	1136	1	60,68,73	1.52	8 (13%)	70,107,113	1.55	11 (15%)
13	CLA	s	517	-	45,53,73	1.77	7 (15%)	52,89,113	1.58	6 (11%)
16	BCR	B	4014	-	41,41,41	0.74	0	56,56,56	1.85	13 (23%)
13	CLA	A	1140	1	65,73,73	1.49	8 (12%)	76,113,113	1.47	12 (15%)
16	BCR	B	4017	-	41,41,41	0.80	0	56,56,56	1.57	11 (19%)
13	CLA	B	1239	2	65,73,73	1.49	7 (10%)	76,113,113	1.63	14 (18%)
18	LMU	q	902	-	19,19,36	1.22	1 (5%)	24,24,47	1.10	3 (12%)
13	CLA	Y	507	-	60,68,73	1.52	6 (10%)	70,107,113	1.53	9 (12%)
13	CLA	r	506	12	55,63,73	1.61	6 (10%)	64,101,113	1.55	6 (9%)
13	CLA	l	502	12	60,68,73	1.55	7 (11%)	70,107,113	1.47	7 (10%)
13	CLA	B	1222	21	60,68,73	1.50	7 (11%)	70,107,113	1.54	10 (14%)
13	CLA	B	1207	2	65,73,73	1.46	9 (13%)	76,113,113	1.38	6 (7%)
13	CLA	G	1126	1	65,73,73	1.38	6 (9%)	76,113,113	1.60	8 (10%)
13	CLA	c	511	12	55,63,73	1.61	6 (10%)	64,101,113	1.53	7 (10%)
13	CLA	f	1239	2	65,73,73	1.49	7 (10%)	76,113,113	1.62	14 (18%)
13	CLA	s	505	12	65,73,73	1.46	6 (9%)	76,113,113	1.37	6 (7%)
17	LHG	G	5005	-	44,44,48	0.67	1 (2%)	47,50,54	1.27	6 (12%)
13	CLA	s	502	12	50,58,73	1.68	7 (14%)	58,95,113	1.62	8 (13%)
13	CLA	Y	504	-	45,53,73	1.80	8 (17%)	52,89,113	1.61	8 (15%)
13	CLA	s	513	12	65,73,73	1.47	6 (9%)	76,113,113	1.44	7 (9%)
13	CLA	B	1238	21	65,73,73	1.41	7 (10%)	76,113,113	1.57	10 (13%)
13	CLA	B	1221	21	65,73,73	1.48	8 (12%)	76,113,113	1.66	12 (15%)
13	CLA	e	1128	1	65,73,73	1.54	10 (15%)	76,113,113	1.61	7 (9%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	e	1137	1	65,73,73	1.45	7 (10%)	76,113,113	1.50	8 (10%)
13	CLA	H	1213	2	65,73,73	1.40	7 (10%)	76,113,113	1.54	10 (13%)
13	CLA	f	1213	2	65,73,73	1.40	7 (10%)	76,113,113	1.54	10 (13%)
17	LHG	L	5220	-	40,40,48	0.65	0	43,46,54	1.23	4 (9%)
13	CLA	B	1223	2	65,73,73	1.41	7 (10%)	76,113,113	1.56	6 (7%)
13	CLA	G	1139	21	65,73,73	1.45	7 (10%)	76,113,113	1.33	9 (11%)
13	CLA	r	518	12	65,73,73	1.46	7 (10%)	76,113,113	1.48	7 (9%)
13	CLA	e	1117	1	65,73,73	1.43	10 (15%)	76,113,113	1.69	12 (15%)
16	BCR	n	4022	-	41,41,41	0.75	0	56,56,56	1.90	15 (26%)
16	BCR	v	521	-	41,41,41	0.66	0	56,56,56	1.91	12 (21%)
13	CLA	f	1229	2	65,73,73	1.44	7 (10%)	76,113,113	1.57	10 (13%)
16	BCR	H	4005	-	41,41,41	0.70	0	56,56,56	1.78	11 (19%)
13	CLA	e	1125	1	65,73,73	1.42	8 (12%)	76,113,113	1.56	9 (11%)
13	CLA	a	507	-	65,73,73	1.46	6 (9%)	76,113,113	1.44	8 (10%)
13	CLA	1	513	12	55,63,73	1.61	7 (12%)	64,101,113	1.49	6 (9%)
18	LMU	l	5105	-	22,22,36	1.14	1 (4%)	27,27,47	0.81	0
16	BCR	3	521	-	41,41,41	0.67	0	56,56,56	1.76	10 (17%)
13	CLA	A	1102	1	65,73,73	1.42	6 (9%)	76,113,113	1.49	7 (9%)
13	CLA	H	1223	2	65,73,73	1.40	7 (10%)	76,113,113	1.55	6 (7%)
16	BCR	Y	523	-	41,41,41	0.71	0	56,56,56	1.64	16 (28%)
13	CLA	t	502	12	50,58,73	1.68	7 (14%)	58,95,113	1.59	7 (12%)
13	CLA	H	1206	2	65,73,73	1.44	10 (15%)	76,113,113	1.58	7 (9%)
13	CLA	e	1112	1	50,58,73	1.63	9 (18%)	58,95,113	1.72	8 (13%)
16	BCR	1	521	-	41,41,41	0.66	0	56,56,56	1.81	11 (19%)
13	CLA	3	519	12	55,63,73	1.61	9 (16%)	64,101,113	1.50	7 (10%)
13	CLA	v	517	-	45,53,73	1.79	6 (13%)	52,89,113	1.59	6 (11%)
13	CLA	f	1240	17	65,73,73	1.47	6 (9%)	76,113,113	1.44	9 (11%)
14	PQN	G	2001	-	34,34,34	2.87	11 (32%)	42,45,45	2.12	7 (16%)
13	CLA	d	516	12	45,53,73	1.79	6 (13%)	52,89,113	1.61	8 (15%)
13	CLA	B	1210	2	65,73,73	1.42	8 (12%)	76,113,113	1.53	12 (15%)
16	BCR	d	524	-	41,41,41	0.75	0	56,56,56	1.87	13 (23%)
13	CLA	H	1232	21	50,58,73	1.62	7 (14%)	58,95,113	1.82	6 (10%)
13	CLA	3	518	12	55,63,73	1.61	7 (12%)	64,101,113	1.48	7 (10%)
16	BCR	q	524	-	41,41,41	0.73	0	56,56,56	1.82	15 (26%)
13	CLA	d	508	12	45,53,73	1.77	7 (15%)	52,89,113	1.67	7 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	J	1302	8	58,66,73	1.52	8 (13%)	67,104,113	1.51	8 (11%)
13	CLA	e	1105	1	55,63,73	1.52	7 (12%)	64,101,113	1.69	9 (14%)
13	CLA	2	506	12	55,63,73	1.61	7 (12%)	64,101,113	1.55	6 (9%)
13	CLA	q	506	12	45,53,73	1.77	7 (15%)	52,89,113	1.69	6 (11%)
16	BCR	G	4011	-	41,41,41	0.71	0	56,56,56	1.84	13 (23%)
13	CLA	Y	517	-	45,53,73	1.78	7 (15%)	52,89,113	1.58	6 (11%)
16	BCR	u	523	-	41,41,41	0.74	0	56,56,56	1.78	16 (28%)
15	SF4	C	3002	3	0,12,12	-	-	-	-	-
13	CLA	G	1120	1	53,61,73	1.56	7 (13%)	61,98,113	1.68	7 (11%)
13	CLA	Y	502	12	60,68,73	1.55	7 (11%)	70,107,113	1.47	7 (10%)
20	SQD	4	822	-	25,26,54	1.31	4 (16%)	34,37,65	1.84	9 (26%)
13	CLA	A	1124	21	56,64,73	1.58	6 (10%)	65,102,113	1.63	12 (18%)
13	CLA	H	1239	2	65,73,73	1.48	7 (10%)	76,113,113	1.63	14 (18%)
13	CLA	e	1114	21	50,58,73	1.68	8 (16%)	58,95,113	1.64	7 (12%)
16	BCR	H	4017	-	41,41,41	0.79	0	56,56,56	1.58	11 (19%)
16	BCR	f	4006	-	41,41,41	0.72	0	56,56,56	1.98	20 (35%)
13	CLA	a	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.50	8 (10%)
13	CLA	6	513	12	45,53,73	1.83	5 (11%)	52,89,113	1.54	6 (11%)
13	CLA	2	516	12	45,53,73	1.77	6 (13%)	52,89,113	1.64	7 (13%)
13	CLA	a	512	12	45,53,73	1.75	7 (15%)	52,89,113	1.62	5 (9%)
17	LHG	e	5005	-	44,44,48	0.67	1 (2%)	47,50,54	1.27	6 (12%)
13	CLA	H	1222	21	60,68,73	1.49	7 (11%)	70,107,113	1.54	10 (14%)
13	CLA	H	1207	2	65,73,73	1.47	9 (13%)	76,113,113	1.39	6 (7%)
13	CLA	G	1102	1	65,73,73	1.42	6 (9%)	76,113,113	1.49	7 (9%)
13	CLA	G	1104	1	65,73,73	1.40	7 (10%)	76,113,113	1.53	10 (13%)
13	CLA	B	1218	2	60,68,73	1.47	7 (11%)	70,107,113	1.52	7 (10%)
13	CLA	H	1221	21	65,73,73	1.48	8 (12%)	76,113,113	1.66	12 (15%)
13	CLA	q	501	12	65,73,73	1.50	7 (10%)	76,113,113	1.43	8 (10%)
13	CLA	q	504	-	45,53,73	1.79	7 (15%)	52,89,113	1.61	8 (15%)
16	BCR	M	4021	-	41,41,41	0.71	0	56,56,56	1.82	14 (25%)
13	CLA	4	519	12	55,63,73	1.58	9 (16%)	64,101,113	1.49	6 (9%)
16	BCR	A	4003	-	41,41,41	0.78	0	56,56,56	1.73	11 (19%)
13	CLA	5	509	12	65,73,73	1.46	7 (10%)	76,113,113	1.48	8 (10%)
13	CLA	u	512	12	45,53,73	1.77	7 (15%)	52,89,113	1.59	7 (13%)
16	BCR	J	4013	-	41,41,41	0.76	0	56,56,56	1.96	15 (26%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
16	BCR	G	4007	-	41,41,41	0.75	0	56,56,56	2.10	18 (32%)
13	CLA	s	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.51	8 (10%)
18	LMU	B	1843	-	36,36,36	1.19	2 (5%)	47,47,47	1.11	3 (6%)
16	BCR	Z	521	-	41,41,41	0.66	0	56,56,56	1.86	11 (19%)
13	CLA	A	1113	1	45,53,73	1.67	7 (15%)	52,89,113	1.77	6 (11%)
13	CLA	J	1303	8	65,73,73	1.44	7 (10%)	76,113,113	1.51	12 (15%)
13	CLA	4	516	12	45,53,73	1.78	6 (13%)	52,89,113	1.58	7 (13%)
13	CLA	f	1234	2	65,73,73	1.42	8 (12%)	76,113,113	1.69	13 (17%)
16	BCR	b	523	-	41,41,41	0.70	0	56,56,56	1.65	12 (21%)
16	BCR	4	523	-	41,41,41	0.69	0	56,56,56	1.65	12 (21%)
13	CLA	G	1135	1	52,60,73	1.53	8 (15%)	60,97,113	1.71	10 (16%)
19	LMG	J	5104	-	35,35,55	0.99	1 (2%)	43,43,63	1.25	7 (16%)
16	BCR	c	524	-	41,41,41	0.69	0	56,56,56	1.67	15 (26%)
13	CLA	d	504	-	45,53,73	1.77	5 (11%)	52,89,113	1.68	7 (13%)
13	CLA	3	507	-	65,73,73	1.46	6 (9%)	76,113,113	1.44	8 (10%)
19	LMG	B	5002	-	54,54,55	0.79	2 (3%)	62,62,63	1.43	10 (16%)
13	CLA	m	1103	9	50,58,73	1.66	9 (18%)	58,95,113	1.68	12 (20%)
13	CLA	v	518	12	55,63,73	1.61	6 (10%)	64,101,113	1.49	7 (10%)
13	CLA	H	1212	2	55,63,73	1.54	8 (14%)	64,101,113	1.64	8 (12%)
13	CLA	A	1103	1	65,73,73	1.43	7 (10%)	76,113,113	1.64	8 (10%)
13	CLA	q	516	12	45,53,73	1.79	6 (13%)	52,89,113	1.79	10 (19%)
16	BCR	e	4003	-	41,41,41	0.78	0	56,56,56	1.73	11 (19%)
13	CLA	v	507	-	45,53,73	1.77	6 (13%)	52,89,113	1.66	8 (15%)
16	BCR	f	4017	-	41,41,41	0.80	0	56,56,56	1.57	11 (19%)
18	LMU	e	1848	-	36,36,36	1.14	2 (5%)	47,47,47	1.07	2 (4%)
13	CLA	t	513	12	45,53,73	1.80	7 (15%)	52,89,113	1.62	6 (11%)
13	CLA	a	510	12	65,73,73	1.47	6 (9%)	76,113,113	1.47	9 (11%)
13	CLA	B	1217	2	57,65,73	1.52	7 (12%)	66,103,113	1.54	8 (12%)
13	CLA	G	1137	1	65,73,73	1.44	7 (10%)	76,113,113	1.51	8 (10%)
17	LHG	e	5002	-	38,38,48	0.70	1 (2%)	41,44,54	1.22	5 (12%)
13	CLA	3	511	12	50,58,73	1.70	6 (12%)	58,95,113	1.62	6 (10%)
13	CLA	f	1235	2	65,73,73	1.42	8 (12%)	76,113,113	1.54	10 (13%)
13	CLA	v	504	-	45,53,73	1.76	5 (11%)	52,89,113	1.68	8 (15%)
14	PQN	f	2002	-	34,34,34	2.87	11 (32%)	42,45,45	2.18	4 (9%)
13	CLA	c	505	12	61,69,73	1.51	6 (9%)	71,108,113	1.40	6 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	e	1011	1	65,73,73	1.45	6 (9%)	76,113,113	1.63	12 (15%)
13	CLA	Z	501	12	65,73,73	1.48	7 (10%)	76,113,113	1.47	7 (9%)
16	BCR	c	521	-	41,41,41	0.69	0	56,56,56	1.94	16 (28%)
13	CLA	3	513	12	65,73,73	1.47	6 (9%)	76,113,113	1.43	7 (9%)
13	CLA	G	1013	-	65,73,73	1.43	8 (12%)	76,113,113	1.75	9 (11%)
13	CLA	t	509	12	65,73,73	1.48	6 (9%)	76,113,113	1.50	8 (10%)
16	BCR	l	4013	-	41,41,41	0.76	0	56,56,56	1.96	15 (26%)
13	CLA	3	505	12	65,73,73	1.46	6 (9%)	76,113,113	1.36	6 (7%)
13	CLA	f	1023	-	65,73,73	1.41	8 (12%)	76,113,113	1.84	14 (18%)
13	CLA	r	513	12	65,73,73	1.50	8 (12%)	76,113,113	1.38	6 (7%)
16	BCR	e	4008	-	41,41,41	0.84	1 (2%)	56,56,56	2.02	17 (30%)
17	LHG	e	5006	-	44,44,48	0.62	0	47,50,54	1.26	5 (10%)
16	BCR	T	4012	-	41,41,41	0.70	0	56,56,56	1.66	13 (23%)
13	CLA	H	1218	2	60,68,73	1.47	7 (11%)	70,107,113	1.52	6 (8%)
13	CLA	f	1218	2	60,68,73	1.47	7 (11%)	70,107,113	1.53	6 (8%)
16	BCR	q	522	-	41,41,41	0.74	0	56,56,56	1.90	19 (33%)
19	LMG	T	5104	-	35,35,55	0.99	1 (2%)	43,43,63	1.25	7 (16%)
16	BCR	J	4012	-	41,41,41	0.70	0	56,56,56	1.66	13 (23%)
13	CLA	c	519	12	46,54,73	1.76	9 (19%)	53,90,113	1.56	6 (11%)
13	CLA	U	1105	9	45,53,73	1.79	8 (17%)	52,89,113	1.85	11 (21%)
20	SQD	q	822	-	47,48,54	0.99	5 (10%)	56,59,65	1.74	13 (23%)
16	BCR	t	523	-	41,41,41	0.69	0	56,56,56	1.65	13 (23%)
13	CLA	m	1401	-	55,63,73	1.59	8 (14%)	64,101,113	1.56	9 (14%)
13	CLA	c	506	12	45,53,73	1.77	5 (11%)	52,89,113	1.66	7 (13%)
13	CLA	d	503	12	52,60,73	1.66	6 (11%)	60,97,113	1.57	9 (15%)
13	CLA	B	1211	2	56,64,73	1.53	7 (12%)	65,102,113	1.78	6 (9%)
13	CLA	f	1214	2	65,73,73	1.49	9 (13%)	76,113,113	1.51	7 (9%)
13	CLA	K	1103	9	50,58,73	1.64	9 (18%)	58,95,113	1.68	12 (20%)
13	CLA	H	1238	21	65,73,73	1.41	7 (10%)	76,113,113	1.57	10 (13%)
16	BCR	U	4104	-	41,41,41	0.74	0	56,56,56	1.86	15 (26%)
13	CLA	b	519	12	55,63,73	1.58	9 (16%)	64,101,113	1.49	6 (9%)
18	LMU	H	1843	-	36,36,36	1.19	2 (5%)	47,47,47	1.10	3 (6%)
16	BCR	V	4022	-	41,41,41	0.76	0	56,56,56	1.90	14 (25%)
13	CLA	Y	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.51	7 (9%)
16	BCR	t	524	-	41,41,41	0.68	0	56,56,56	1.84	15 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	6	509	12	45,53,73	1.77	6 (13%)	52,89,113	1.63	6 (11%)
13	CLA	Z	512	12	53,61,73	1.61	6 (11%)	61,98,113	1.48	5 (8%)
13	CLA	H	1208	2	65,73,73	1.42	7 (10%)	76,113,113	1.43	8 (10%)
13	CLA	A	1117	1	65,73,73	1.43	10 (15%)	76,113,113	1.69	12 (15%)
13	CLA	A	1111	1	65,73,73	1.46	7 (10%)	76,113,113	1.49	7 (9%)
13	CLA	e	1136	1	60,68,73	1.53	8 (13%)	70,107,113	1.56	11 (15%)
13	CLA	c	508	12	45,53,73	1.77	7 (15%)	52,89,113	1.73	6 (11%)
13	CLA	5	507	-	45,53,73	1.75	6 (13%)	52,89,113	1.68	8 (15%)
17	LHG	L	5218	-	37,37,48	0.75	2 (5%)	40,43,54	1.23	4 (10%)
13	CLA	H	1205	2	65,73,73	1.46	9 (13%)	76,113,113	1.54	9 (11%)
13	CLA	e	1120	1	53,61,73	1.56	7 (13%)	61,98,113	1.68	7 (11%)
13	CLA	6	516	12	45,53,73	1.79	6 (13%)	52,89,113	1.60	8 (15%)
13	CLA	A	1108	1	54,62,73	1.61	7 (12%)	62,99,113	1.48	6 (9%)
15	SF4	g	3002	3	0,12,12	-	-	-	-	-
16	BCR	6	523	-	41,41,41	0.70	0	56,56,56	1.73	14 (25%)
13	CLA	G	1128	1	65,73,73	1.53	10 (15%)	76,113,113	1.61	6 (7%)
13	CLA	e	1131	1	65,73,73	1.44	9 (13%)	76,113,113	1.43	9 (11%)
13	CLA	A	1130	1	65,73,73	1.47	7 (10%)	76,113,113	1.52	10 (13%)
13	CLA	s	508	12	55,63,73	1.63	7 (12%)	64,101,113	1.59	8 (12%)
13	CLA	u	501	12	65,73,73	1.47	6 (9%)	76,113,113	1.47	7 (9%)
13	CLA	u	517	-	45,53,73	1.80	7 (15%)	52,89,113	1.56	6 (11%)
18	LMU	l	902	-	19,19,36	1.22	1 (5%)	24,24,47	1.10	3 (12%)
13	CLA	c	503	12	55,63,73	1.64	6 (10%)	64,101,113	1.53	8 (12%)
13	CLA	q	510	12	65,73,73	1.47	5 (7%)	76,113,113	1.41	7 (9%)
14	PQN	H	2002	-	34,34,34	2.87	11 (32%)	42,45,45	2.17	4 (9%)
16	BCR	e	4011	-	41,41,41	0.71	0	56,56,56	1.84	13 (23%)
13	CLA	H	1217	2	57,65,73	1.52	7 (12%)	66,103,113	1.54	9 (13%)
16	BCR	q	523	-	41,41,41	0.71	0	56,56,56	1.64	16 (28%)
13	CLA	d	511	12	45,53,73	1.79	6 (13%)	52,89,113	1.66	6 (11%)
13	CLA	a	518	12	55,63,73	1.61	7 (12%)	64,101,113	1.47	7 (10%)
13	CLA	l	518	12	60,68,73	1.53	10 (16%)	70,107,113	1.53	8 (11%)
13	CLA	V	1502	10	65,73,73	1.43	7 (10%)	76,113,113	1.49	8 (10%)
13	CLA	v	505	12	65,73,73	1.47	6 (9%)	76,113,113	1.43	7 (9%)
13	CLA	Z	513	12	65,73,73	1.50	8 (12%)	76,113,113	1.38	7 (9%)
16	BCR	e	4001	-	41,41,41	0.76	0	56,56,56	1.72	11 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	b	503	12	55,63,73	1.64	6 (10%)	64,101,113	1.55	11 (17%)
13	CLA	e	1139	21	65,73,73	1.46	7 (10%)	76,113,113	1.34	9 (11%)
13	CLA	u	509	12	65,73,73	1.45	7 (10%)	76,113,113	1.49	8 (10%)
13	CLA	G	1131	1	65,73,73	1.45	9 (13%)	76,113,113	1.43	9 (11%)
16	BCR	A	4002	-	41,41,41	0.81	1 (2%)	56,56,56	1.85	15 (26%)
16	BCR	d	521	-	41,41,41	0.66	0	56,56,56	1.91	12 (21%)
13	CLA	r	508	12	55,63,73	1.63	8 (14%)	64,101,113	1.59	9 (14%)
13	CLA	d	505	12	65,73,73	1.47	6 (9%)	76,113,113	1.43	7 (9%)
16	BCR	a	524	-	41,41,41	0.74	0	56,56,56	1.81	17 (30%)
13	CLA	q	505	12	65,73,73	1.46	6 (9%)	76,113,113	1.40	7 (9%)
13	CLA	d	510	12	45,53,73	1.80	5 (11%)	52,89,113	1.57	7 (13%)
13	CLA	e	1115	1	60,68,73	1.46	7 (11%)	70,107,113	1.59	8 (11%)
13	CLA	v	519	12	46,54,73	1.76	6 (13%)	53,90,113	1.59	6 (11%)
16	BCR	b	524	-	41,41,41	0.67	0	56,56,56	1.85	15 (26%)
16	BCR	b	522	-	41,41,41	0.74	0	56,56,56	1.85	18 (32%)
13	CLA	A	1801	17	45,53,73	1.72	7 (15%)	52,89,113	1.83	8 (15%)
13	CLA	e	1126	1	65,73,73	1.39	7 (10%)	76,113,113	1.60	8 (10%)
16	BCR	F	4016	-	41,41,41	0.74	0	56,56,56	1.78	13 (23%)
20	SQD	b	822	-	25,26,54	1.31	4 (16%)	34,37,65	1.85	9 (26%)
13	CLA	t	507	-	45,53,73	1.77	6 (13%)	52,89,113	1.69	8 (15%)
13	CLA	d	506	12	45,53,73	1.79	6 (13%)	52,89,113	1.65	6 (11%)
13	CLA	4	517	-	45,53,73	1.79	6 (13%)	52,89,113	1.66	8 (15%)
18	LMU	G	1848	-	36,36,36	1.15	2 (5%)	47,47,47	1.07	2 (4%)
13	CLA	G	1109	1	65,73,73	1.41	7 (10%)	76,113,113	1.52	7 (9%)
13	CLA	5	518	12	55,63,73	1.60	6 (10%)	64,101,113	1.45	7 (10%)
13	CLA	H	1225	2	65,73,73	1.41	9 (13%)	76,113,113	1.44	7 (9%)
13	CLA	d	512	12	45,53,73	1.77	6 (13%)	52,89,113	1.59	5 (9%)
13	CLA	A	1013	-	65,73,73	1.42	8 (12%)	76,113,113	1.75	9 (11%)
13	CLA	e	1129	1	51,59,73	1.60	10 (19%)	59,96,113	1.61	8 (13%)
13	CLA	n	1501	10	65,73,73	1.46	8 (12%)	76,113,113	1.52	9 (11%)
16	BCR	V	4219	-	41,41,41	0.77	0	56,56,56	1.80	12 (21%)
13	CLA	G	1114	21	50,58,73	1.67	8 (16%)	58,95,113	1.64	7 (12%)
13	CLA	a	505	12	65,73,73	1.45	6 (9%)	76,113,113	1.36	6 (7%)
13	CLA	t	511	12	45,53,73	1.80	6 (13%)	52,89,113	1.70	7 (13%)
13	CLA	r	519	12	55,63,73	1.61	8 (14%)	64,101,113	1.46	9 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
16	BCR	Z	524	-	41,41,41	0.74	0	56,56,56	1.67	12 (21%)
17	LHG	V	5221	-	48,48,48	0.65	2 (4%)	51,54,54	1.30	6 (11%)
13	CLA	A	1110	1	51,59,73	1.66	7 (13%)	59,96,113	1.60	7 (11%)
13	CLA	q	502	12	60,68,73	1.54	7 (11%)	70,107,113	1.47	7 (10%)
13	CLA	2	502	12	60,68,73	1.56	8 (13%)	70,107,113	1.45	7 (10%)
13	CLA	1	507	-	60,68,73	1.52	6 (10%)	70,107,113	1.53	9 (12%)
13	CLA	e	1102	1	65,73,73	1.42	7 (10%)	76,113,113	1.49	7 (9%)
13	CLA	H	1215	2	65,73,73	1.44	8 (12%)	76,113,113	1.57	8 (10%)
16	BCR	f	4005	-	41,41,41	0.70	0	56,56,56	1.78	11 (19%)
13	CLA	s	507	-	65,73,73	1.47	6 (9%)	76,113,113	1.43	8 (10%)
13	CLA	A	1127	1	65,73,73	1.41	7 (10%)	76,113,113	1.50	9 (11%)
16	BCR	L	4019	-	41,41,41	0.73	0	56,56,56	1.92	14 (25%)
13	CLA	v	503	12	52,60,73	1.67	6 (11%)	60,97,113	1.58	9 (15%)
13	CLA	2	504	-	50,58,73	1.68	7 (14%)	58,95,113	1.59	8 (13%)
17	LHG	G	5001	-	48,48,48	0.78	1 (2%)	51,54,54	1.26	6 (11%)
13	CLA	a	519	12	55,63,73	1.61	7 (12%)	64,101,113	1.50	7 (10%)
13	CLA	b	510	12	50,58,73	1.69	6 (12%)	58,95,113	1.62	7 (12%)
16	BCR	d	522	-	41,41,41	0.70	0	56,56,56	1.84	14 (25%)
13	CLA	r	504	-	50,58,73	1.68	7 (14%)	58,95,113	1.58	8 (13%)
17	LHG	e	5004	-	35,35,48	0.74	1 (2%)	38,41,54	1.25	4 (10%)
16	BCR	L	4020	-	41,41,41	0.83	0	56,56,56	1.95	16 (28%)
16	BCR	v	522	-	41,41,41	0.69	0	56,56,56	1.84	15 (26%)
13	CLA	G	1116	1	60,68,73	1.51	8 (13%)	70,107,113	1.50	7 (10%)
13	CLA	G	1115	1	60,68,73	1.47	7 (11%)	70,107,113	1.59	8 (11%)
13	CLA	s	511	12	50,58,73	1.71	6 (12%)	58,95,113	1.62	6 (10%)
13	CLA	b	506	12	45,53,73	1.79	6 (13%)	52,89,113	1.63	6 (11%)
13	CLA	e	1111	1	65,73,73	1.46	7 (10%)	76,113,113	1.48	7 (9%)
13	CLA	1	517	-	45,53,73	1.78	7 (15%)	52,89,113	1.58	6 (11%)
13	CLA	a	516	12	45,53,73	1.77	6 (13%)	52,89,113	1.85	12 (23%)
13	CLA	4	504	-	45,53,73	1.77	6 (13%)	52,89,113	1.63	7 (13%)
16	BCR	a	523	-	41,41,41	0.69	0	56,56,56	1.76	15 (26%)
13	CLA	3	506	12	50,58,73	1.70	7 (14%)	58,95,113	1.67	6 (10%)
13	CLA	3	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.51	8 (10%)
13	CLA	r	503	12	65,73,73	1.48	7 (10%)	76,113,113	1.45	7 (9%)
19	LMG	f	5002	-	54,54,55	0.80	3 (5%)	62,62,63	1.43	10 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	B	1227	2	65,73,73	1.46	9 (13%)	76,113,113	1.47	9 (11%)
13	CLA	c	501	12	65,73,73	1.46	7 (10%)	76,113,113	1.48	7 (9%)
13	CLA	u	518	12	55,63,73	1.60	6 (10%)	64,101,113	1.45	7 (10%)
13	CLA	e	1135	1	52,60,73	1.54	8 (15%)	60,97,113	1.71	10 (16%)
13	CLA	t	518	12	55,63,73	1.62	7 (12%)	64,101,113	1.49	7 (10%)
13	CLA	v	509	12	45,53,73	1.77	6 (13%)	52,89,113	1.63	6 (11%)
13	CLA	G	1122	1	60,68,73	1.50	9 (15%)	70,107,113	1.53	8 (11%)
13	CLA	u	507	-	45,53,73	1.75	6 (13%)	52,89,113	1.68	8 (15%)
13	CLA	4	508	12	45,53,73	1.82	8 (17%)	52,89,113	1.75	10 (19%)
16	BCR	3	523	-	41,41,41	0.69	0	56,56,56	1.76	15 (26%)
16	BCR	o	4021	-	41,41,41	0.71	0	56,56,56	1.81	14 (25%)
13	CLA	f	1222	21	60,68,73	1.50	7 (11%)	70,107,113	1.54	10 (14%)
13	CLA	B	1234	2	65,73,73	1.43	8 (12%)	76,113,113	1.69	13 (17%)
16	BCR	f	4009	-	41,41,41	0.81	0	56,56,56	1.91	21 (37%)
13	CLA	e	1118	1	60,68,73	1.50	7 (11%)	70,107,113	1.49	8 (11%)
13	CLA	G	1134	1	56,64,73	1.57	7 (12%)	65,102,113	1.55	8 (12%)
18	LMU	e	1849	-	23,23,36	1.16	1 (4%)	28,28,47	1.00	2 (7%)
13	CLA	B	1202	2	65,73,73	1.44	7 (10%)	76,113,113	1.65	9 (11%)
13	CLA	5	519	12	46,54,73	1.76	9 (19%)	53,90,113	1.55	6 (11%)
16	BCR	b	521	-	41,41,41	0.64	0	56,56,56	1.78	11 (19%)
13	CLA	1	519	12	50,58,73	1.66	10 (20%)	58,95,113	1.50	8 (13%)
13	CLA	Z	507	-	65,73,73	1.44	6 (9%)	76,113,113	1.48	7 (9%)
17	LHG	G	5007	-	46,46,48	0.67	1 (2%)	49,52,54	1.24	5 (10%)
13	CLA	B	1224	2	60,68,73	1.47	7 (11%)	70,107,113	1.59	8 (11%)
13	CLA	f	1221	21	65,73,73	1.49	8 (12%)	76,113,113	1.65	12 (15%)
16	BCR	e	4002	-	41,41,41	0.81	0	56,56,56	1.85	14 (25%)
17	LHG	A	5001	-	48,48,48	0.78	1 (2%)	51,54,54	1.26	6 (11%)
13	CLA	K	1401	-	55,63,73	1.59	8 (14%)	64,101,113	1.55	9 (14%)
17	LHG	S	5001	-	43,43,48	0.64	0	46,49,54	1.22	4 (8%)
13	CLA	6	517	-	45,53,73	1.78	7 (15%)	52,89,113	1.59	6 (11%)
13	CLA	H	1209	2	52,60,73	1.66	8 (15%)	60,97,113	1.67	8 (13%)
20	SQD	L	5216	-	50,51,54	0.97	5 (10%)	59,62,65	1.63	11 (18%)
13	CLA	t	505	12	65,73,73	1.46	6 (9%)	76,113,113	1.36	6 (7%)
17	LHG	f	1855	-	43,43,48	0.64	1 (2%)	46,49,54	1.22	5 (10%)
13	CLA	Y	513	12	55,63,73	1.62	7 (12%)	64,101,113	1.49	6 (9%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	Z	518	12	65,73,73	1.46	6 (9%)	76,113,113	1.48	7 (9%)
13	CLA	f	1223	2	65,73,73	1.42	7 (10%)	76,113,113	1.56	6 (7%)
13	CLA	u	513	12	45,53,73	1.82	8 (17%)	52,89,113	1.56	7 (13%)
13	CLA	G	1138	1	65,73,73	1.44	7 (10%)	76,113,113	1.45	8 (10%)
13	CLA	2	517	-	45,53,73	1.77	7 (15%)	52,89,113	1.63	6 (11%)
13	CLA	A	1011	1	65,73,73	1.45	6 (9%)	76,113,113	1.63	12 (15%)
13	CLA	f	1201	2	60,68,73	1.48	7 (11%)	70,107,113	1.66	8 (11%)
13	CLA	r	501	12	65,73,73	1.49	7 (10%)	76,113,113	1.47	7 (9%)
13	CLA	4	510	12	50,58,73	1.68	6 (12%)	58,95,113	1.62	7 (12%)
16	BCR	2	522	-	41,41,41	0.71	0	56,56,56	1.75	18 (32%)
13	CLA	e	1103	1	65,73,73	1.43	7 (10%)	76,113,113	1.64	8 (10%)
13	CLA	v	506	12	45,53,73	1.79	7 (15%)	52,89,113	1.65	6 (11%)
13	CLA	s	519	12	55,63,73	1.60	8 (14%)	64,101,113	1.49	7 (10%)
13	CLA	e	1123	21	65,73,73	1.40	7 (10%)	76,113,113	1.51	8 (10%)
16	BCR	T	4015	-	41,41,41	0.78	0	56,56,56	1.82	14 (25%)
13	CLA	3	501	12	65,73,73	1.44	7 (10%)	76,113,113	1.53	7 (9%)
13	CLA	A	1112	1	50,58,73	1.63	9 (18%)	58,95,113	1.72	9 (15%)
20	SQD	B	1852	-	44,45,54	1.02	4 (9%)	53,56,65	1.84	14 (26%)
20	SQD	Z	822	-	42,43,54	1.07	5 (11%)	51,54,65	1.61	10 (19%)
13	CLA	3	510	12	65,73,73	1.46	6 (9%)	76,113,113	1.46	9 (11%)
13	CLA	Y	503	12	64,72,73	1.49	6 (9%)	74,111,113	1.45	8 (10%)
19	LMG	l	5104	-	35,35,55	0.99	1 (2%)	43,43,63	1.24	7 (16%)
13	CLA	G	1112	1	50,58,73	1.63	9 (18%)	58,95,113	1.72	9 (15%)
13	CLA	b	508	12	45,53,73	1.82	8 (17%)	52,89,113	1.75	10 (19%)
17	LHG	A	5005	-	44,44,48	0.67	1 (2%)	47,50,54	1.27	6 (12%)
13	CLA	f	1212	2	55,63,73	1.53	7 (12%)	64,101,113	1.65	8 (12%)
13	CLA	2	503	12	65,73,73	1.47	6 (9%)	76,113,113	1.45	7 (9%)
16	BCR	Y	524	-	41,41,41	0.73	0	56,56,56	1.82	15 (26%)
16	BCR	V	4020	-	41,41,41	0.83	0	56,56,56	1.95	16 (28%)
13	CLA	Z	503	12	65,73,73	1.47	6 (9%)	76,113,113	1.44	7 (9%)
13	CLA	G	1106	1	65,73,73	1.41	9 (13%)	76,113,113	1.55	9 (11%)
13	CLA	f	1225	2	65,73,73	1.41	9 (13%)	76,113,113	1.45	7 (9%)
17	LHG	L	5221	-	48,48,48	0.65	2 (4%)	51,54,54	1.30	6 (11%)
13	CLA	Y	516	12	45,53,73	1.79	6 (13%)	52,89,113	1.78	10 (19%)
13	CLA	H	1227	2	65,73,73	1.46	9 (13%)	76,113,113	1.46	9 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
20	SQD	c	822	-	28,29,54	1.25	5 (17%)	37,40,65	1.92	13 (35%)
17	LHG	G	5003	13	40,40,48	0.74	0	43,46,54	1.34	6 (13%)
13	CLA	f	1236	2	55,63,73	1.63	7 (12%)	64,101,113	1.43	8 (12%)
16	BCR	5	524	-	41,41,41	0.68	0	56,56,56	1.67	14 (25%)
13	CLA	c	513	12	45,53,73	1.81	8 (17%)	52,89,113	1.57	6 (11%)
13	CLA	e	1022	21	65,73,73	1.48	9 (13%)	76,113,113	1.48	9 (11%)
16	BCR	H	4014	-	41,41,41	0.74	0	56,56,56	1.84	13 (23%)
18	LMU	G	1849	-	23,23,36	1.17	1 (4%)	28,28,47	1.00	2 (7%)
13	CLA	q	517	-	45,53,73	1.78	7 (15%)	52,89,113	1.57	6 (11%)
13	CLA	B	1201	2	60,68,73	1.48	7 (11%)	70,107,113	1.65	8 (11%)
17	LHG	G	5002	-	38,38,48	0.70	1 (2%)	41,44,54	1.22	5 (12%)
15	SF4	C	3003	3	0,12,12	-	-	-	-	-
13	CLA	A	1101	1	65,73,73	1.49	8 (12%)	76,113,113	1.45	9 (11%)
13	CLA	R	1302	6	45,53,73	1.76	7 (15%)	52,89,113	1.59	6 (11%)
20	SQD	v	822	-	25,26,54	1.29	4 (16%)	34,37,65	1.91	10 (29%)
13	CLA	H	1224	2	60,68,73	1.47	7 (11%)	70,107,113	1.58	8 (11%)
13	CLA	f	1224	2	60,68,73	1.47	7 (11%)	70,107,113	1.59	8 (11%)
16	BCR	B	4010	-	41,41,41	0.94	3 (7%)	56,56,56	2.28	23 (41%)
13	CLA	Z	504	-	50,58,73	1.68	6 (12%)	58,95,113	1.58	8 (13%)
13	CLA	B	1231	21	65,73,73	1.37	7 (10%)	76,113,113	1.56	8 (10%)
13	CLA	Y	511	12	55,63,73	1.61	6 (10%)	64,101,113	1.58	8 (12%)
13	CLA	4	505	12	65,73,73	1.47	6 (9%)	76,113,113	1.37	7 (9%)
13	CLA	u	511	12	55,63,73	1.62	6 (10%)	64,101,113	1.53	7 (10%)
13	CLA	f	1210	2	65,73,73	1.43	8 (12%)	76,113,113	1.53	12 (15%)
16	BCR	I	4018	-	41,41,41	0.77	0	56,56,56	1.84	15 (26%)
16	BCR	l	4012	-	41,41,41	0.70	0	56,56,56	1.66	13 (23%)
13	CLA	4	502	12	50,58,73	1.69	6 (12%)	58,95,113	1.60	7 (12%)
13	CLA	c	512	12	45,53,73	1.75	6 (13%)	52,89,113	1.59	7 (13%)
17	LHG	n	5221	-	48,48,48	0.65	2 (4%)	51,54,54	1.30	6 (11%)
13	CLA	2	501	12	65,73,73	1.48	7 (10%)	76,113,113	1.47	7 (9%)
16	BCR	6	522	-	41,41,41	0.70	0	56,56,56	1.84	14 (25%)
13	CLA	A	1122	1	60,68,73	1.50	9 (15%)	70,107,113	1.53	8 (11%)
13	CLA	e	1237	21	65,73,73	1.49	9 (13%)	76,113,113	1.50	11 (14%)
13	CLA	a	506	12	50,58,73	1.70	7 (14%)	58,95,113	1.67	6 (10%)
16	BCR	5	522	-	41,41,41	0.74	0	56,56,56	1.93	20 (35%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	e	1110	1	51,59,73	1.66	7 (13%)	59,96,113	1.61	7 (11%)
17	LHG	G	5006	-	44,44,48	0.62	0	47,50,54	1.25	5 (10%)
17	LHG	e	5001	-	48,48,48	0.78	1 (2%)	51,54,54	1.26	6 (11%)
13	CLA	G	1110	1	51,59,73	1.65	7 (13%)	59,96,113	1.60	7 (11%)
16	BCR	5	521	-	41,41,41	0.68	0	56,56,56	1.94	16 (28%)
13	CLA	t	519	12	55,63,73	1.59	9 (16%)	64,101,113	1.50	6 (9%)
16	BCR	H	4010	-	41,41,41	0.94	3 (7%)	56,56,56	2.28	23 (41%)
16	BCR	c	523	-	41,41,41	0.74	0	56,56,56	1.78	16 (28%)
18	LMU	J	5105	-	22,22,36	1.14	1 (4%)	27,27,47	0.81	0
13	CLA	e	1116	1	60,68,73	1.51	8 (13%)	70,107,113	1.49	7 (10%)
13	CLA	e	1107	1	65,73,73	1.46	10 (15%)	76,113,113	1.43	10 (13%)
13	CLA	v	512	12	45,53,73	1.77	6 (13%)	52,89,113	1.58	5 (9%)
13	CLA	5	503	12	55,63,73	1.63	6 (10%)	64,101,113	1.53	8 (12%)
13	CLA	F	1302	6	45,53,73	1.76	7 (15%)	52,89,113	1.59	6 (11%)
13	CLA	A	1105	1	55,63,73	1.52	7 (12%)	64,101,113	1.69	9 (14%)
16	BCR	2	521	-	41,41,41	0.66	0	56,56,56	1.87	11 (19%)
13	CLA	A	1139	21	65,73,73	1.45	7 (10%)	76,113,113	1.33	9 (11%)
13	CLA	G	1129	1	51,59,73	1.61	10 (19%)	59,96,113	1.61	8 (13%)
13	CLA	A	1104	1	65,73,73	1.40	7 (10%)	76,113,113	1.53	10 (13%)
13	CLA	5	506	12	45,53,73	1.78	6 (13%)	52,89,113	1.66	7 (13%)
13	CLA	d	518	12	55,63,73	1.61	6 (10%)	64,101,113	1.50	7 (10%)
20	SQD	5	822	-	28,29,54	1.25	5 (17%)	37,40,65	1.92	13 (35%)
16	BCR	n	4019	-	41,41,41	0.73	0	56,56,56	1.92	14 (25%)
16	BCR	A	4008	-	41,41,41	0.84	1 (2%)	56,56,56	2.03	17 (30%)
20	SQD	d	822	-	25,26,54	1.30	4 (16%)	34,37,65	1.91	10 (29%)
13	CLA	1	506	12	45,53,73	1.77	6 (13%)	52,89,113	1.68	6 (11%)
13	CLA	1	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.50	7 (9%)
13	CLA	U	1103	9	50,58,73	1.64	9 (18%)	58,95,113	1.69	11 (18%)
13	CLA	e	1122	1	60,68,73	1.49	9 (15%)	70,107,113	1.53	8 (11%)
13	CLA	f	1227	2	65,73,73	1.47	9 (13%)	76,113,113	1.47	9 (11%)
16	BCR	n	4020	-	41,41,41	0.82	0	56,56,56	1.95	15 (26%)
15	SF4	g	3003	3	0,12,12	-	-	-	-	-
13	CLA	b	505	12	65,73,73	1.47	6 (9%)	76,113,113	1.37	6 (7%)
16	BCR	G	4003	-	41,41,41	0.78	0	56,56,56	1.73	11 (19%)
13	CLA	v	513	12	45,53,73	1.82	6 (13%)	52,89,113	1.54	6 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	s	503	12	65,73,73	1.50	6 (9%)	76,113,113	1.41	9 (11%)
16	BCR	Y	522	-	41,41,41	0.73	0	56,56,56	1.91	20 (35%)
13	CLA	G	1022	21	65,73,73	1.48	9 (13%)	76,113,113	1.48	9 (11%)
13	CLA	Z	502	12	60,68,73	1.56	8 (13%)	70,107,113	1.44	7 (10%)
16	BCR	1	523	-	41,41,41	0.71	0	56,56,56	1.63	16 (28%)
16	BCR	6	524	-	41,41,41	0.75	0	56,56,56	1.86	13 (23%)
17	LHG	e	5007	-	46,46,48	0.66	1 (2%)	49,52,54	1.24	5 (10%)
16	BCR	u	522	-	41,41,41	0.74	0	56,56,56	1.93	20 (35%)
14	PQN	B	2002	-	34,34,34	2.88	11 (32%)	42,45,45	2.18	4 (9%)
13	CLA	H	1201	2	60,68,73	1.48	7 (11%)	70,107,113	1.66	8 (11%)
16	BCR	2	524	-	41,41,41	0.73	0	56,56,56	1.67	12 (21%)
13	CLA	e	1109	1	65,73,73	1.42	7 (10%)	76,113,113	1.52	7 (9%)
16	BCR	H	4004	-	41,41,41	0.72	0	56,56,56	1.85	13 (23%)
13	CLA	2	508	12	55,63,73	1.62	8 (14%)	64,101,113	1.59	9 (14%)
13	CLA	H	1210	2	65,73,73	1.42	8 (12%)	76,113,113	1.53	12 (15%)
13	CLA	H	1231	21	65,73,73	1.37	7 (10%)	76,113,113	1.56	8 (10%)
17	LHG	B	1855	-	43,43,48	0.64	1 (2%)	46,49,54	1.21	5 (10%)
13	CLA	q	513	12	55,63,73	1.61	7 (12%)	64,101,113	1.50	6 (9%)
13	CLA	A	1120	1	53,61,73	1.56	7 (13%)	61,98,113	1.67	7 (11%)
13	CLA	K	1105	9	45,53,73	1.79	8 (17%)	52,89,113	1.86	11 (21%)
13	CLA	m	1105	9	45,53,73	1.79	9 (20%)	52,89,113	1.85	11 (21%)
13	CLA	B	1204	2	65,73,73	1.38	8 (12%)	76,113,113	1.43	9 (11%)
13	CLA	v	510	12	45,53,73	1.80	6 (13%)	52,89,113	1.58	7 (13%)
13	CLA	t	506	12	45,53,73	1.80	6 (13%)	52,89,113	1.65	7 (13%)
13	CLA	H	1204	2	65,73,73	1.38	8 (12%)	76,113,113	1.43	9 (11%)
13	CLA	b	516	12	45,53,73	1.77	6 (13%)	52,89,113	1.58	7 (13%)
16	BCR	A	4011	-	41,41,41	0.71	0	56,56,56	1.84	13 (23%)
16	BCR	r	522	-	41,41,41	0.70	0	56,56,56	1.75	17 (30%)
14	PQN	A	2001	-	34,34,34	2.88	11 (32%)	42,45,45	2.11	7 (16%)
13	CLA	B	1203	2	65,73,73	1.44	9 (13%)	76,113,113	1.46	7 (9%)
13	CLA	a	508	12	55,63,73	1.65	7 (12%)	64,101,113	1.60	8 (12%)
16	BCR	6	521	-	41,41,41	0.66	0	56,56,56	1.91	12 (21%)
13	CLA	e	1127	1	65,73,73	1.42	7 (10%)	76,113,113	1.50	9 (11%)
17	LHG	n	5218	-	37,37,48	0.75	2 (5%)	40,43,54	1.23	4 (10%)
13	CLA	f	1211	2	56,64,73	1.53	7 (12%)	65,102,113	1.77	6 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	Y	501	12	65,73,73	1.49	7 (10%)	76,113,113	1.43	8 (10%)
13	CLA	B	1021	2	65,73,73	1.42	8 (12%)	76,113,113	1.44	9 (11%)
13	CLA	B	1214	2	65,73,73	1.49	9 (13%)	76,113,113	1.50	7 (9%)
13	CLA	f	1207	2	65,73,73	1.46	9 (13%)	76,113,113	1.38	6 (7%)
13	CLA	a	513	12	65,73,73	1.47	6 (9%)	76,113,113	1.44	7 (9%)
13	CLA	v	516	12	45,53,73	1.78	5 (11%)	52,89,113	1.60	8 (15%)
16	BCR	A	4001	-	41,41,41	0.76	0	56,56,56	1.72	11 (19%)
16	BCR	s	521	-	41,41,41	0.66	0	56,56,56	1.76	10 (17%)
17	LHG	V	5218	-	37,37,48	0.75	2 (5%)	40,43,54	1.23	4 (10%)
17	LHG	n	5220	-	40,40,48	0.65	0	43,46,54	1.23	4 (9%)
13	CLA	B	1228	2	55,63,73	1.52	7 (12%)	64,101,113	1.68	8 (12%)
13	CLA	6	510	12	45,53,73	1.80	6 (13%)	52,89,113	1.57	7 (13%)
13	CLA	l	510	12	65,73,73	1.47	6 (9%)	76,113,113	1.40	7 (9%)
13	CLA	c	504	-	45,53,73	1.77	5 (11%)	52,89,113	1.63	7 (13%)
13	CLA	q	509	12	65,73,73	1.46	7 (10%)	76,113,113	1.50	7 (9%)
13	CLA	s	501	12	65,73,73	1.45	7 (10%)	76,113,113	1.52	7 (9%)
16	BCR	v	524	-	41,41,41	0.76	0	56,56,56	1.87	13 (23%)
16	BCR	4	522	-	41,41,41	0.74	0	56,56,56	1.85	18 (32%)
13	CLA	e	1134	1	56,64,73	1.57	8 (14%)	65,102,113	1.54	8 (12%)
13	CLA	f	1205	2	65,73,73	1.45	9 (13%)	76,113,113	1.53	9 (11%)
16	BCR	f	4014	-	41,41,41	0.74	0	56,56,56	1.84	13 (23%)
13	CLA	6	519	12	46,54,73	1.76	6 (13%)	53,90,113	1.59	6 (11%)
15	SF4	G	3001	1,2	0,12,12	-	-	-	-	-
16	BCR	2	523	-	41,41,41	0.71	0	56,56,56	1.75	15 (26%)
13	CLA	b	512	12	45,53,73	1.78	6 (13%)	52,89,113	1.62	6 (11%)
13	CLA	6	506	12	45,53,73	1.79	5 (11%)	52,89,113	1.66	6 (11%)
13	CLA	d	501	12	60,68,73	1.53	6 (10%)	70,107,113	1.51	7 (10%)
13	CLA	d	517	-	45,53,73	1.78	7 (15%)	52,89,113	1.58	6 (11%)
13	CLA	v	508	12	45,53,73	1.77	7 (15%)	52,89,113	1.68	7 (13%)
13	CLA	L	1501	10	65,73,73	1.47	7 (10%)	76,113,113	1.52	9 (11%)
13	CLA	l	516	12	45,53,73	1.79	6 (13%)	52,89,113	1.79	10 (19%)
13	CLA	r	516	12	45,53,73	1.77	6 (13%)	52,89,113	1.66	7 (13%)
13	CLA	Y	505	12	65,73,73	1.45	6 (9%)	76,113,113	1.39	7 (9%)
13	CLA	d	502	12	50,58,73	1.68	6 (12%)	58,95,113	1.60	7 (12%)
13	CLA	G	1103	1	65,73,73	1.43	7 (10%)	76,113,113	1.64	8 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	H	1230	2	60,68,73	1.53	9 (15%)	70,107,113	1.52	10 (14%)
13	CLA	6	508	12	45,53,73	1.77	7 (15%)	52,89,113	1.67	7 (13%)
16	BCR	G	4001	-	41,41,41	0.76	0	56,56,56	1.72	11 (19%)
13	CLA	A	1118	1	60,68,73	1.49	8 (13%)	70,107,113	1.49	8 (11%)
13	CLA	5	508	12	45,53,73	1.78	7 (15%)	52,89,113	1.73	6 (11%)
17	LHG	G	5004	-	35,35,48	0.74	1 (2%)	38,41,54	1.25	4 (10%)
13	CLA	A	1129	1	51,59,73	1.61	10 (19%)	59,96,113	1.61	8 (13%)
16	BCR	4	524	-	41,41,41	0.67	0	56,56,56	1.84	15 (26%)
13	CLA	A	1137	1	65,73,73	1.44	7 (10%)	76,113,113	1.50	8 (10%)
13	CLA	3	503	12	65,73,73	1.50	6 (9%)	76,113,113	1.41	9 (11%)
13	CLA	e	1130	1	65,73,73	1.47	7 (10%)	76,113,113	1.52	10 (13%)
13	CLA	q	511	12	55,63,73	1.60	6 (10%)	64,101,113	1.57	8 (12%)
16	BCR	r	524	-	41,41,41	0.73	0	56,56,56	1.67	12 (21%)
13	CLA	2	511	12	55,63,73	1.62	6 (10%)	64,101,113	1.57	7 (10%)
17	LHG	H	1855	-	43,43,48	0.64	1 (2%)	46,49,54	1.21	5 (10%)
13	CLA	G	1133	1	65,73,73	1.39	7 (10%)	76,113,113	1.49	6 (7%)
16	BCR	u	521	-	41,41,41	0.68	0	56,56,56	1.94	16 (28%)
17	LHG	e	5008	-	34,34,48	0.77	1 (2%)	37,40,54	1.28	4 (10%)
13	CLA	L	1503	21	60,68,73	1.49	7 (11%)	70,107,113	1.55	7 (10%)
13	CLA	6	503	12	52,60,73	1.67	6 (11%)	60,97,113	1.58	9 (15%)
16	BCR	s	523	-	41,41,41	0.69	0	56,56,56	1.76	15 (26%)
13	CLA	R	1301	21	65,73,73	1.47	7 (10%)	76,113,113	1.39	8 (10%)
13	CLA	t	504	-	45,53,73	1.77	6 (13%)	52,89,113	1.63	7 (13%)
13	CLA	A	1132	1	65,73,73	1.43	10 (15%)	76,113,113	1.48	10 (13%)
13	CLA	H	1219	2	65,73,73	1.48	7 (10%)	76,113,113	1.33	9 (11%)
13	CLA	4	506	12	45,53,73	1.80	6 (13%)	52,89,113	1.64	6 (11%)
13	CLA	c	518	12	55,63,73	1.60	6 (10%)	64,101,113	1.45	7 (10%)
16	BCR	Z	522	-	41,41,41	0.71	0	56,56,56	1.75	18 (32%)
13	CLA	B	1208	2	65,73,73	1.43	7 (10%)	76,113,113	1.42	8 (10%)
13	CLA	5	512	12	45,53,73	1.76	7 (15%)	52,89,113	1.58	7 (13%)
13	CLA	1	512	12	52,60,73	1.64	6 (11%)	60,97,113	1.53	6 (10%)
13	CLA	B	1219	2	65,73,73	1.48	7 (10%)	76,113,113	1.33	9 (11%)
13	CLA	H	1203	2	65,73,73	1.44	8 (12%)	76,113,113	1.46	7 (9%)
17	LHG	G	5008	-	34,34,48	0.76	1 (2%)	37,40,54	1.28	4 (10%)
13	CLA	f	1209	2	52,60,73	1.66	8 (15%)	60,97,113	1.67	8 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	u	508	12	45,53,73	1.78	7 (15%)	52,89,113	1.73	6 (11%)
13	CLA	B	1205	2	65,73,73	1.46	9 (13%)	76,113,113	1.53	9 (11%)
13	CLA	Z	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.48	7 (9%)
13	CLA	H	1021	2	65,73,73	1.42	8 (12%)	76,113,113	1.43	9 (11%)
13	CLA	H	1214	2	65,73,73	1.49	9 (13%)	76,113,113	1.51	7 (9%)
13	CLA	f	1021	2	65,73,73	1.42	8 (12%)	76,113,113	1.44	9 (11%)
13	CLA	t	508	12	45,53,73	1.82	8 (17%)	52,89,113	1.75	10 (19%)
13	CLA	H	1228	2	55,63,73	1.52	7 (12%)	64,101,113	1.68	9 (14%)
13	CLA	2	510	12	65,73,73	1.46	6 (9%)	76,113,113	1.44	6 (7%)
13	CLA	t	503	12	55,63,73	1.63	6 (10%)	64,101,113	1.54	12 (18%)
16	BCR	5	523	-	41,41,41	0.75	0	56,56,56	1.78	16 (28%)
13	CLA	e	1106	1	65,73,73	1.41	9 (13%)	76,113,113	1.54	9 (11%)
16	BCR	r	521	-	41,41,41	0.66	0	56,56,56	1.86	11 (19%)
14	PQN	e	2001	-	34,34,34	2.88	11 (32%)	42,45,45	2.11	7 (16%)
20	SQD	6	822	-	25,26,54	1.29	4 (16%)	34,37,65	1.91	10 (29%)
13	CLA	Z	516	12	45,53,73	1.77	7 (15%)	52,89,113	1.64	7 (13%)
13	CLA	j	1301	21	65,73,73	1.46	7 (10%)	76,113,113	1.38	8 (10%)
13	CLA	5	502	12	50,58,73	1.71	8 (16%)	58,95,113	1.54	7 (12%)
19	LMG	H	5002	-	54,54,55	0.79	2 (3%)	62,62,63	1.43	10 (16%)
13	CLA	Y	508	12	55,63,73	1.60	7 (12%)	64,101,113	1.71	10 (15%)
13	CLA	5	516	12	45,53,73	1.78	6 (13%)	52,89,113	1.59	6 (11%)
13	CLA	G	1123	21	65,73,73	1.40	7 (10%)	76,113,113	1.50	8 (10%)
16	BCR	Z	523	-	41,41,41	0.71	0	56,56,56	1.75	15 (26%)
13	CLA	e	1119	21	65,73,73	1.45	9 (13%)	76,113,113	1.52	9 (11%)
13	CLA	A	1128	1	65,73,73	1.53	10 (15%)	76,113,113	1.61	7 (9%)
16	BCR	4	521	-	41,41,41	0.64	0	56,56,56	1.78	11 (19%)
13	CLA	t	512	12	45,53,73	1.79	6 (13%)	52,89,113	1.62	6 (11%)
13	CLA	e	1132	1	65,73,73	1.43	10 (15%)	76,113,113	1.47	10 (13%)
13	CLA	G	1121	1	55,63,73	1.58	8 (14%)	64,101,113	1.59	11 (17%)
16	BCR	3	522	-	41,41,41	0.67	0	56,56,56	1.91	16 (28%)
13	CLA	G	1124	21	56,64,73	1.58	6 (10%)	65,102,113	1.64	12 (18%)
13	CLA	H	1202	2	65,73,73	1.44	7 (10%)	76,113,113	1.65	9 (11%)
13	CLA	d	513	12	45,53,73	1.84	6 (13%)	52,89,113	1.54	6 (11%)
13	CLA	1	505	12	65,73,73	1.46	6 (9%)	76,113,113	1.40	7 (9%)
13	CLA	G	1140	1	65,73,73	1.49	8 (12%)	76,113,113	1.48	12 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	U	1401	-	55,63,73	1.59	7 (12%)	64,101,113	1.55	9 (14%)
13	CLA	A	1138	1	65,73,73	1.44	7 (10%)	76,113,113	1.46	8 (10%)
13	CLA	n	1503	21	60,68,73	1.49	7 (11%)	70,107,113	1.55	7 (10%)
16	BCR	J	4015	-	41,41,41	0.78	0	56,56,56	1.82	14 (25%)
13	CLA	B	1220	2	55,63,73	1.54	9 (16%)	64,101,113	1.67	11 (17%)
13	CLA	T	1303	8	65,73,73	1.44	7 (10%)	76,113,113	1.51	11 (14%)
16	BCR	3	524	-	41,41,41	0.74	0	56,56,56	1.81	17 (30%)
18	LMU	Y	902	-	19,19,36	1.22	1 (5%)	24,24,47	1.10	3 (12%)
13	CLA	Y	519	12	50,58,73	1.65	10 (20%)	58,95,113	1.50	8 (13%)
13	CLA	a	504	-	45,53,73	1.75	6 (13%)	52,89,113	1.69	6 (11%)
13	CLA	d	509	12	45,53,73	1.77	6 (13%)	52,89,113	1.62	6 (11%)
13	CLA	B	1216	21	60,68,73	1.56	10 (16%)	70,107,113	1.43	7 (10%)
13	CLA	B	1212	2	55,63,73	1.53	7 (12%)	64,101,113	1.64	8 (12%)
13	CLA	e	1801	17	45,53,73	1.72	7 (15%)	52,89,113	1.83	8 (15%)
13	CLA	6	502	12	50,58,73	1.68	6 (12%)	58,95,113	1.60	7 (12%)
13	CLA	b	501	12	60,68,73	1.54	5 (8%)	70,107,113	1.46	6 (8%)
13	CLA	A	1133	1	65,73,73	1.39	8 (12%)	76,113,113	1.49	6 (7%)
17	LHG	A	5009	-	48,48,48	0.62	1 (2%)	51,54,54	1.27	6 (11%)
16	BCR	d	523	-	41,41,41	0.70	0	56,56,56	1.73	14 (25%)
13	CLA	f	1215	2	65,73,73	1.44	8 (12%)	76,113,113	1.57	7 (9%)
13	CLA	B	1012	21	65,73,73	1.46	9 (13%)	76,113,113	1.54	8 (10%)
13	CLA	s	518	12	55,63,73	1.61	7 (12%)	64,101,113	1.48	7 (10%)
13	CLA	c	517	-	45,53,73	1.81	6 (13%)	52,89,113	1.55	6 (11%)
17	LHG	A	5004	-	35,35,48	0.74	1 (2%)	38,41,54	1.25	4 (10%)
13	CLA	A	1116	1	60,68,73	1.51	7 (11%)	70,107,113	1.50	7 (10%)
13	CLA	G	1801	17	45,53,73	1.72	7 (15%)	52,89,113	1.83	8 (15%)
17	LHG	f	1842	13	38,38,48	0.65	0	41,44,54	1.23	4 (9%)
13	CLA	5	504	-	45,53,73	1.77	5 (11%)	52,89,113	1.64	7 (13%)
13	CLA	A	1121	1	55,63,73	1.58	7 (12%)	64,101,113	1.58	11 (17%)
16	BCR	1	524	-	41,41,41	0.73	0	56,56,56	1.82	15 (26%)
13	CLA	4	513	12	45,53,73	1.80	7 (15%)	52,89,113	1.62	6 (11%)
13	CLA	6	501	12	60,68,73	1.53	6 (10%)	70,107,113	1.51	7 (10%)
13	CLA	r	517	-	45,53,73	1.77	7 (15%)	52,89,113	1.64	6 (11%)
13	CLA	B	1213	2	65,73,73	1.40	7 (10%)	76,113,113	1.54	10 (13%)
13	CLA	r	510	12	65,73,73	1.46	7 (10%)	76,113,113	1.43	6 (7%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
18	LMU	A	1848	-	36,36,36	1.15	2 (5%)	47,47,47	1.07	2 (4%)
13	CLA	V	1501	10	65,73,73	1.46	7 (10%)	76,113,113	1.52	9 (11%)
13	CLA	Y	512	12	52,60,73	1.65	6 (11%)	60,97,113	1.53	6 (10%)
13	CLA	e	1138	1	65,73,73	1.44	7 (10%)	76,113,113	1.46	8 (10%)
13	CLA	q	518	12	60,68,73	1.52	9 (15%)	70,107,113	1.53	8 (11%)
13	CLA	r	502	12	60,68,73	1.57	8 (13%)	70,107,113	1.44	8 (11%)
13	CLA	u	505	12	61,69,73	1.51	6 (9%)	71,108,113	1.40	6 (8%)
13	CLA	b	518	12	55,63,73	1.62	7 (12%)	64,101,113	1.49	7 (10%)
16	BCR	G	4008	-	41,41,41	0.84	1 (2%)	56,56,56	2.03	16 (28%)
17	LHG	V	5220	-	40,40,48	0.64	0	43,46,54	1.23	4 (9%)
13	CLA	A	1123	21	65,73,73	1.40	7 (10%)	76,113,113	1.51	8 (10%)
13	CLA	4	507	-	45,53,73	1.76	6 (13%)	52,89,113	1.68	8 (15%)
13	CLA	b	507	-	45,53,73	1.75	6 (13%)	52,89,113	1.68	8 (15%)
20	SQD	V	5216	-	50,51,54	0.97	5 (10%)	59,62,65	1.64	10 (16%)
15	SF4	N	3002	3	0,12,12	-	-	-	-	-
13	CLA	A	1125	1	65,73,73	1.43	8 (12%)	76,113,113	1.55	9 (11%)
13	CLA	f	1226	2	65,73,73	1.56	10 (15%)	76,113,113	1.82	14 (18%)
13	CLA	b	504	-	45,53,73	1.76	6 (13%)	52,89,113	1.63	7 (13%)
13	CLA	3	516	12	45,53,73	1.77	6 (13%)	52,89,113	1.85	12 (23%)
13	CLA	B	1232	21	50,58,73	1.62	7 (14%)	58,95,113	1.82	6 (10%)
16	BCR	L	4022	-	41,41,41	0.76	0	56,56,56	1.90	14 (25%)
13	CLA	B	1236	2	55,63,73	1.63	7 (12%)	64,101,113	1.43	8 (12%)
13	CLA	B	1229	2	65,73,73	1.43	7 (10%)	76,113,113	1.57	10 (13%)
13	CLA	4	518	12	55,63,73	1.61	6 (10%)	64,101,113	1.48	7 (10%)
13	CLA	l	1303	8	65,73,73	1.43	7 (10%)	76,113,113	1.51	12 (15%)
20	SQD	H	1852	-	44,45,54	1.02	4 (9%)	53,56,65	1.84	14 (26%)
20	SQD	f	1852	-	44,45,54	1.01	4 (9%)	53,56,65	1.84	14 (26%)
16	BCR	K	4104	-	41,41,41	0.74	0	56,56,56	1.86	15 (26%)
13	CLA	f	1204	2	65,73,73	1.38	8 (12%)	76,113,113	1.43	9 (11%)
13	CLA	A	1109	1	65,73,73	1.41	7 (10%)	76,113,113	1.52	7 (9%)
13	CLA	4	511	12	45,53,73	1.79	6 (13%)	52,89,113	1.70	7 (13%)
13	CLA	B	1240	17	65,73,73	1.47	6 (9%)	76,113,113	1.44	9 (11%)
13	CLA	a	517	-	45,53,73	1.77	7 (15%)	52,89,113	1.58	6 (11%)
13	CLA	2	509	12	65,73,73	1.47	7 (10%)	76,113,113	1.48	7 (9%)
13	CLA	e	1013	-	65,73,73	1.42	8 (12%)	76,113,113	1.75	9 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
13	CLA	A	1114	21	50,58,73	1.68	8 (16%)	58,95,113	1.64	7 (12%)
13	CLA	2	512	12	53,61,73	1.61	7 (13%)	61,98,113	1.48	5 (8%)
16	BCR	a	522	-	41,41,41	0.67	0	56,56,56	1.91	16 (28%)
13	CLA	f	1208	2	65,73,73	1.42	7 (10%)	76,113,113	1.42	8 (10%)
20	SQD	3	822	-	42,43,54	1.06	5 (11%)	51,54,65	1.59	12 (23%)
13	CLA	v	501	12	60,68,73	1.53	7 (11%)	70,107,113	1.51	7 (10%)
13	CLA	H	1216	21	60,68,73	1.56	10 (16%)	70,107,113	1.43	6 (8%)
20	SQD	a	822	-	42,43,54	1.06	5 (11%)	51,54,65	1.59	12 (23%)
13	CLA	A	1237	21	65,73,73	1.49	9 (13%)	76,113,113	1.50	11 (14%)
16	BCR	m	4104	-	41,41,41	0.74	0	56,56,56	1.86	15 (26%)
13	CLA	b	513	12	45,53,73	1.80	7 (15%)	52,89,113	1.62	6 (11%)
15	SF4	e	3001	1,2	0,12,12	-	-	-	-	-
13	CLA	u	502	12	50,58,73	1.71	8 (16%)	58,95,113	1.55	7 (12%)
13	CLA	G	1119	21	65,73,73	1.46	9 (13%)	76,113,113	1.51	9 (11%)
16	BCR	s	524	-	41,41,41	0.73	0	56,56,56	1.82	17 (30%)
16	BCR	B	4006	-	41,41,41	0.72	0	56,56,56	1.99	19 (33%)
13	CLA	u	516	12	45,53,73	1.78	6 (13%)	52,89,113	1.59	6 (11%)
13	CLA	3	504	-	45,53,73	1.75	6 (13%)	52,89,113	1.69	6 (11%)
13	CLA	v	502	12	50,58,73	1.68	6 (12%)	58,95,113	1.60	6 (10%)
13	CLA	H	1211	2	56,64,73	1.53	7 (12%)	65,102,113	1.79	6 (9%)
13	CLA	3	517	-	45,53,73	1.78	7 (15%)	52,89,113	1.58	6 (11%)
16	BCR	f	4004	-	41,41,41	0.72	0	56,56,56	1.85	13 (23%)
17	LHG	k	5001	-	43,43,48	0.64	0	46,49,54	1.22	4 (8%)
13	CLA	a	503	12	65,73,73	1.50	6 (9%)	76,113,113	1.41	9 (11%)
13	CLA	H	1012	21	65,73,73	1.46	9 (13%)	76,113,113	1.54	8 (10%)
13	CLA	A	1107	1	65,73,73	1.47	10 (15%)	76,113,113	1.43	9 (11%)
13	CLA	5	517	-	45,53,73	1.80	7 (15%)	52,89,113	1.55	6 (11%)
13	CLA	G	1132	1	65,73,73	1.42	9 (13%)	76,113,113	1.47	10 (13%)
16	BCR	f	4010	-	41,41,41	0.94	3 (7%)	56,56,56	2.28	23 (41%)
17	LHG	e	5009	-	48,48,48	0.62	1 (2%)	51,54,54	1.27	6 (11%)
13	CLA	3	508	12	55,63,73	1.65	7 (12%)	64,101,113	1.60	8 (12%)
16	BCR	c	522	-	41,41,41	0.74	0	56,56,56	1.93	20 (35%)

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
13	CLA	3	512	12	1/1/11/20	3/13/91/115	-
13	CLA	G	1130	1	1/1/15/20	7/37/115/115	-
13	CLA	A	1134	1	1/1/13/20	11/27/105/115	-
16	BCR	S	4018	-	-	1/29/63/63	0/2/2/2
18	LMU	T	5105	-	-	8/13/33/61	0/1/1/2
13	CLA	G	1127	1	1/1/15/20	12/37/115/115	-
17	LHG	A	5007	-	-	24/51/51/53	-
13	CLA	G	1101	1	1/1/15/20	13/37/115/115	-
13	CLA	G	1237	21	1/1/15/20	18/37/115/115	-
13	CLA	e	1133	1	1/1/15/20	15/37/115/115	-
13	CLA	G	1117	1	1/1/15/20	12/37/115/115	-
13	CLA	B	1226	2	1/1/15/20	12/37/115/115	-
13	CLA	b	502	12	1/1/12/20	5/19/97/115	-
13	CLA	e	1140	1	1/1/15/20	11/37/115/115	-
13	CLA	H	1226	2	1/1/15/20	12/37/115/115	-
13	CLA	f	1238	21	1/1/15/20	4/37/115/115	-
13	CLA	G	1108	1	1/1/12/20	16/24/102/115	-
18	LMU	A	1849	-	-	6/14/34/61	0/1/1/2
15	SF4	N	3003	3	-	-	0/6/5/5
13	CLA	f	1206	2	1/1/15/20	15/37/115/115	-
13	CLA	B	1225	2	1/1/15/20	8/37/115/115	-
13	CLA	e	1121	1	1/1/13/20	6/25/103/115	-
13	CLA	Z	510	12	1/1/15/20	9/37/115/115	-
13	CLA	1	503	12	1/1/14/20	9/36/114/115	-
13	CLA	6	512	12	1/1/11/20	6/13/91/115	-
13	CLA	H	1229	2	1/1/15/20	13/37/115/115	-
13	CLA	a	501	12	1/1/15/20	6/37/115/115	-
16	BCR	q	521	-	-	7/29/63/63	0/2/2/2
13	CLA	G	1118	1	1/1/14/20	12/31/109/115	-
18	LMU	r	901	-	-	8/14/34/61	0/1/1/2
16	BCR	1	522	-	-	6/29/63/63	0/2/2/2
13	CLA	4	501	12	1/1/14/20	12/31/109/115	-
13	CLA	u	504	-	1/1/11/20	3/13/91/115	-
13	CLA	t	517	-	1/1/11/20	5/13/91/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	L	1502	10	1/1/15/20	8/37/115/115	-
13	CLA	d	507	-	1/1/11/20	4/13/91/115	-
13	CLA	c	507	-	1/1/11/20	5/13/91/115	-
13	CLA	f	1217	2	1/1/13/20	12/28/106/115	-
13	CLA	r	512	12	1/1/12/20	5/23/101/115	-
13	CLA	b	511	12	1/1/11/20	3/13/91/115	-
20	SQD	Y	822	-	-	20/43/63/69	0/1/1/1
13	CLA	B	1235	2	1/1/15/20	6/37/115/115	-
16	BCR	B	4004	-	-	8/29/63/63	0/2/2/2
16	BCR	t	522	-	-	4/29/63/63	0/2/2/2
20	SQD	u	822	-	-	7/24/44/69	0/1/1/1
13	CLA	f	1230	2	1/1/14/20	10/31/109/115	-
13	CLA	Z	517	-	1/1/11/20	4/13/91/115	-
13	CLA	u	519	12	1/1/11/20	8/15/93/115	-
13	CLA	A	1131	1	1/1/15/20	6/37/115/115	-
16	BCR	H	4006	-	-	4/29/63/63	0/2/2/2
13	CLA	v	511	12	1/1/11/20	4/13/91/115	-
16	BCR	G	4002	-	-	0/29/63/63	0/2/2/2
13	CLA	A	1106	1	1/1/15/20	21/37/115/115	-
16	BCR	a	521	-	-	7/29/63/63	0/2/2/2
13	CLA	5	501	12	1/1/15/20	19/37/115/115	-
13	CLA	2	507	-	1/1/15/20	14/37/115/115	-
13	CLA	e	1113	1	1/1/11/20	5/13/91/115	-
13	CLA	Z	508	12	1/1/13/20	6/25/103/115	-
13	CLA	B	1023	-	1/1/15/20	10/37/115/115	-
16	BCR	k	4018	-	-	1/29/63/63	0/2/2/2
13	CLA	6	505	12	1/1/15/20	15/37/115/115	-
16	BCR	n	4219	-	-	2/29/63/63	0/2/2/2
13	CLA	Z	511	12	1/1/13/20	4/25/103/115	-
13	CLA	q	508	12	1/1/13/20	9/25/103/115	-
13	CLA	c	509	12	1/1/15/20	12/37/115/115	-
16	BCR	s	522	-	-	5/29/63/63	0/2/2/2
13	CLA	r	511	12	1/1/13/20	4/25/103/115	-
13	CLA	t	516	12	1/1/11/20	7/13/91/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	BCR	t	521	-	-	10/29/63/63	0/2/2/2
18	LMU	f	1843	-	-	12/21/61/61	0/2/2/2
20	SQD	2	822	-	-	13/38/58/69	0/1/1/1
13	CLA	A	1136	1	1/1/14/20	5/31/109/115	-
13	CLA	c	516	12	1/1/11/20	2/13/91/115	-
13	CLA	A	1119	21	1/1/15/20	15/37/115/115	-
13	CLA	f	1203	2	1/1/15/20	16/37/115/115	-
20	SQD	r	822	-	-	13/38/58/69	0/1/1/1
13	CLA	t	501	12	1/1/14/20	12/31/109/115	-
13	CLA	2	513	12	1/1/15/20	15/37/115/115	-
13	CLA	u	503	12	1/1/13/20	10/25/103/115	-
13	CLA	s	510	12	1/1/15/20	17/37/115/115	-
13	CLA	T	1302	8	1/1/13/20	13/29/107/115	-
13	CLA	e	1124	21	1/1/13/20	11/27/105/115	-
17	LHG	A	5003	13	-	17/45/45/53	-
13	CLA	Y	506	12	1/1/11/20	6/13/91/115	-
13	CLA	3	502	12	1/1/12/20	4/19/97/115	-
13	CLA	s	506	12	1/1/12/20	5/19/97/115	-
18	LMU	2	901	-	-	8/14/34/61	0/1/1/2
17	LHG	A	5002	-	-	26/43/43/53	-
18	LMU	Z	901	-	-	8/14/34/61	0/1/1/2
13	CLA	H	1234	2	1/1/15/20	13/37/115/115	-
16	BCR	H	4009	-	-	1/29/63/63	0/2/2/2
16	BCR	v	523	-	-	4/29/63/63	0/2/2/2
13	CLA	B	1230	2	1/1/14/20	10/31/109/115	-
13	CLA	s	516	12	1/1/11/20	9/13/91/115	-
13	CLA	f	1228	2	1/1/13/20	8/25/103/115	-
13	CLA	l	501	12	1/1/15/20	18/37/115/115	-
13	CLA	r	509	12	1/1/15/20	6/37/115/115	-
16	BCR	W	4021	-	-	7/29/63/63	0/2/2/2
16	BCR	u	524	-	-	2/29/63/63	0/2/2/2
17	LHG	A	5008	-	-	19/39/39/53	-
13	CLA	G	1105	1	1/1/13/20	6/25/103/115	-
16	BCR	A	4007	-	-	0/29/63/63	0/2/2/2
16	BCR	B	4009	-	-	1/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	f	1202	2	1/1/15/20	13/37/115/115	-
13	CLA	F	1301	21	1/1/15/20	11/37/115/115	-
13	CLA	A	1115	1	1/1/14/20	10/31/109/115	-
13	CLA	2	518	12	1/1/15/20	16/37/115/115	-
16	BCR	j	4016	-	-	2/29/63/63	0/2/2/2
13	CLA	5	513	12	1/1/11/20	4/13/91/115	-
16	BCR	T	4013	-	-	4/29/63/63	0/2/2/2
16	BCR	r	523	-	-	6/29/63/63	0/2/2/2
13	CLA	b	509	12	1/1/15/20	7/37/115/115	-
16	BCR	l	4015	-	-	5/29/63/63	0/2/2/2
17	LHG	A	5006	-	-	24/49/49/53	-
13	CLA	4	512	12	1/1/11/20	3/13/91/115	-
13	CLA	G	1113	1	1/1/11/20	5/13/91/115	-
13	CLA	1	504	-	1/1/11/20	5/13/91/115	-
13	CLA	f	1231	21	1/1/15/20	8/37/115/115	-
13	CLA	4	503	12	1/1/13/20	1/25/103/115	-
13	CLA	q	507	-	1/1/14/20	15/31/109/115	-
13	CLA	H	1235	2	1/1/15/20	6/37/115/115	-
13	CLA	f	1219	2	1/1/15/20	17/37/115/115	-
13	CLA	G	1107	1	1/1/15/20	14/37/115/115	-
16	BCR	R	4016	-	-	2/29/63/63	0/2/2/2
13	CLA	e	1108	1	1/1/12/20	16/24/102/115	-
13	CLA	1	508	12	1/1/13/20	9/25/103/115	-
13	CLA	A	1022	21	1/1/15/20	8/37/115/115	-
13	CLA	2	505	12	1/1/15/20	14/37/115/115	-
13	CLA	a	511	12	1/1/12/20	5/19/97/115	-
13	CLA	e	1104	1	1/1/15/20	12/37/115/115	-
13	CLA	G	1125	1	1/1/15/20	14/37/115/115	-
13	CLA	Y	510	12	1/1/15/20	11/37/115/115	-
13	CLA	Z	505	12	1/1/15/20	14/37/115/115	-
13	CLA	u	510	12	1/1/11/20	7/13/91/115	-
13	CLA	H	1023	-	1/1/15/20	10/37/115/115	-
13	CLA	d	519	12	1/1/11/20	6/15/93/115	-
13	CLA	t	510	12	1/1/12/20	5/19/97/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	c	510	12	1/1/11/20	7/13/91/115	-
16	BCR	Y	521	-	-	6/29/63/63	0/2/2/2
13	CLA	f	1220	2	1/1/13/20	9/25/103/115	-
13	CLA	j	1302	6	1/1/11/20	8/13/91/115	-
13	CLA	u	506	12	1/1/11/20	5/13/91/115	-
13	CLA	s	504	-	1/1/11/20	6/13/91/115	-
13	CLA	H	1236	2	-	3/25/103/115	-
13	CLA	6	507	-	1/1/11/20	4/13/91/115	-
20	SQD	s	822	-	-	21/38/58/69	0/1/1/1
13	CLA	G	1011	1	1/1/15/20	10/37/115/115	-
17	LHG	G	5009	-	-	28/53/53/53	-
17	LHG	I	5001	-	-	22/48/48/53	-
16	BCR	L	4219	-	-	2/29/63/63	0/2/2/2
13	CLA	Z	506	12	1/1/13/20	8/25/103/115	-
13	CLA	6	518	12	1/1/13/20	10/25/103/115	-
13	CLA	q	519	12	1/1/12/20	6/19/97/115	-
13	CLA	2	519	12	1/1/13/20	9/25/103/115	-
13	CLA	6	511	12	1/1/11/20	4/13/91/115	-
13	CLA	5	511	12	1/1/13/20	5/25/103/115	-
15	SF4	A	3001	1,2	-	-	0/6/5/5
13	CLA	4	509	12	1/1/15/20	7/37/115/115	-
17	LHG	e	5003	13	-	17/45/45/53	-
13	CLA	6	504	-	1/1/11/20	6/13/91/115	-
13	CLA	A	1135	1	1/1/12/20	10/22/100/115	-
13	CLA	e	1101	1	1/1/15/20	13/37/115/115	-
16	BCR	B	4005	-	-	6/29/63/63	0/2/2/2
13	CLA	r	507	-	1/1/15/20	14/37/115/115	-
13	CLA	s	512	12	1/1/11/20	3/13/91/115	-
20	SQD	1	822	-	-	20/43/63/69	0/1/1/1
13	CLA	a	502	12	1/1/12/20	4/19/97/115	-
13	CLA	l	1302	8	1/1/13/20	13/29/107/115	-
13	CLA	G	1111	1	1/1/15/20	14/37/115/115	-
13	CLA	A	1126	1	1/1/15/20	18/37/115/115	-
13	CLA	5	505	12	1/1/14/20	16/33/111/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	f	1216	21	1/1/14/20	5/31/109/115	-
13	CLA	n	1502	10	1/1/15/20	8/37/115/115	-
16	BCR	V	4019	-	-	6/29/63/63	0/2/2/2
20	SQD	t	822	-	-	8/19/39/69	0/1/1/1
13	CLA	B	1206	2	1/1/15/20	15/37/115/115	-
13	CLA	V	1503	21	1/1/14/20	10/31/109/115	-
16	BCR	e	4007	-	-	0/29/63/63	0/2/2/2
13	CLA	l	511	12	1/1/13/20	4/25/103/115	-
13	CLA	H	1240	17	-	13/37/115/115	-
13	CLA	c	502	12	1/1/12/20	5/19/97/115	-
17	LHG	B	1842	13	-	22/43/43/53	-
20	SQD	n	5216	-	-	17/46/66/69	0/1/1/1
13	CLA	5	510	12	1/1/11/20	7/13/91/115	-
13	CLA	q	512	12	1/1/12/20	10/22/100/115	-
17	LHG	H	1842	13	-	22/43/43/53	-
13	CLA	r	505	12	1/1/15/20	14/37/115/115	-
13	CLA	f	1012	21	1/1/15/20	16/37/115/115	-
13	CLA	B	1215	2	1/1/15/20	19/37/115/115	-
13	CLA	B	1209	2	1/1/12/20	8/22/100/115	-
13	CLA	q	503	12	1/1/14/20	9/36/114/115	-
13	CLA	H	1220	2	1/1/13/20	9/25/103/115	-
13	CLA	Z	519	12	1/1/13/20	9/25/103/115	-
13	CLA	b	517	-	1/1/11/20	5/13/91/115	-
13	CLA	Y	518	12	1/1/14/20	15/31/109/115	-
13	CLA	f	1232	21	1/1/12/20	6/19/97/115	-
13	CLA	G	1136	1	1/1/14/20	5/31/109/115	-
13	CLA	s	517	-	1/1/11/20	7/13/91/115	-
16	BCR	B	4014	-	-	9/29/63/63	0/2/2/2
13	CLA	A	1140	1	1/1/15/20	11/37/115/115	-
16	BCR	B	4017	-	-	2/29/63/63	0/2/2/2
13	CLA	B	1239	2	1/1/15/20	15/37/115/115	-
18	LMU	q	902	-	-	6/10/30/61	0/1/1/2
13	CLA	Y	507	-	1/1/14/20	15/31/109/115	-
13	CLA	r	506	12	1/1/13/20	8/25/103/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	1	502	12	1/1/14/20	14/31/109/115	-
13	CLA	B	1222	21	1/1/14/20	7/31/109/115	-
13	CLA	B	1207	2	1/1/15/20	14/37/115/115	-
13	CLA	G	1126	1	1/1/15/20	18/37/115/115	-
13	CLA	c	511	12	1/1/13/20	5/25/103/115	-
13	CLA	f	1239	2	1/1/15/20	15/37/115/115	-
13	CLA	s	505	12	1/1/15/20	18/37/115/115	-
17	LHG	G	5005	-	-	29/49/49/53	-
13	CLA	s	502	12	1/1/12/20	4/19/97/115	-
13	CLA	Y	504	-	1/1/11/20	5/13/91/115	-
13	CLA	s	513	12	1/1/15/20	13/37/115/115	-
13	CLA	B	1238	21	1/1/15/20	4/37/115/115	-
13	CLA	B	1221	21	1/1/15/20	14/37/115/115	-
13	CLA	e	1128	1	1/1/15/20	12/37/115/115	-
13	CLA	e	1137	1	1/1/15/20	19/37/115/115	-
13	CLA	H	1213	2	1/1/15/20	14/37/115/115	-
13	CLA	f	1213	2	1/1/15/20	14/37/115/115	-
17	LHG	L	5220	-	-	24/45/45/53	-
13	CLA	B	1223	2	1/1/15/20	14/37/115/115	-
13	CLA	G	1139	21	1/1/15/20	12/37/115/115	-
13	CLA	r	518	12	1/1/15/20	16/37/115/115	-
13	CLA	e	1117	1	1/1/15/20	12/37/115/115	-
16	BCR	n	4022	-	-	2/29/63/63	0/2/2/2
16	BCR	v	521	-	-	5/29/63/63	0/2/2/2
13	CLA	f	1229	2	1/1/15/20	13/37/115/115	-
16	BCR	H	4005	-	-	6/29/63/63	0/2/2/2
13	CLA	e	1125	1	1/1/15/20	14/37/115/115	-
13	CLA	a	507	-	1/1/15/20	13/37/115/115	-
13	CLA	1	513	12	1/1/13/20	2/25/103/115	-
18	LMU	l	5105	-	-	8/13/33/61	0/1/1/2
16	BCR	3	521	-	-	7/29/63/63	0/2/2/2
13	CLA	A	1102	1	1/1/15/20	11/37/115/115	-
13	CLA	H	1223	2	1/1/15/20	14/37/115/115	-
16	BCR	Y	523	-	-	6/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	t	502	12	1/1/12/20	5/19/97/115	-
13	CLA	H	1206	2	1/1/15/20	15/37/115/115	-
13	CLA	e	1112	1	1/1/12/20	3/19/97/115	-
16	BCR	1	521	-	-	7/29/63/63	0/2/2/2
13	CLA	3	519	12	1/1/13/20	8/25/103/115	-
13	CLA	v	517	-	1/1/11/20	9/13/91/115	-
13	CLA	f	1240	17	-	13/37/115/115	-
14	PQN	G	2001	-	-	14/23/43/43	0/2/2/2
13	CLA	d	516	12	1/1/11/20	8/13/91/115	-
13	CLA	B	1210	2	1/1/15/20	19/37/115/115	-
16	BCR	d	524	-	-	5/29/63/63	0/2/2/2
13	CLA	H	1232	21	1/1/12/20	6/19/97/115	-
13	CLA	3	518	12	1/1/13/20	10/25/103/115	-
16	BCR	q	524	-	-	2/29/63/63	0/2/2/2
13	CLA	d	508	12	1/1/11/20	3/13/91/115	-
13	CLA	J	1302	8	1/1/13/20	13/29/107/115	-
13	CLA	e	1105	1	1/1/13/20	6/25/103/115	-
13	CLA	2	506	12	1/1/13/20	8/25/103/115	-
13	CLA	q	506	12	1/1/11/20	6/13/91/115	-
16	BCR	G	4011	-	-	12/29/63/63	0/2/2/2
13	CLA	Y	517	-	1/1/11/20	4/13/91/115	-
16	BCR	u	523	-	-	4/29/63/63	0/2/2/2
15	SF4	C	3002	3	-	-	0/6/5/5
13	CLA	G	1120	1	1/1/12/20	4/23/101/115	-
13	CLA	Y	502	12	1/1/14/20	14/31/109/115	-
20	SQD	4	822	-	-	8/19/39/69	0/1/1/1
13	CLA	A	1124	21	1/1/13/20	11/27/105/115	-
13	CLA	H	1239	2	1/1/15/20	15/37/115/115	-
13	CLA	e	1114	21	1/1/12/20	2/19/97/115	-
16	BCR	H	4017	-	-	2/29/63/63	0/2/2/2
16	BCR	f	4006	-	-	4/29/63/63	0/2/2/2
13	CLA	a	509	12	1/1/15/20	4/37/115/115	-
13	CLA	6	513	12	1/1/11/20	3/13/91/115	-
13	CLA	2	516	12	1/1/11/20	8/13/91/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	a	512	12	1/1/11/20	3/13/91/115	-
17	LHG	e	5005	-	-	29/49/49/53	-
13	CLA	H	1222	21	1/1/14/20	7/31/109/115	-
13	CLA	H	1207	2	1/1/15/20	14/37/115/115	-
13	CLA	G	1102	1	1/1/15/20	11/37/115/115	-
13	CLA	G	1104	1	1/1/15/20	12/37/115/115	-
13	CLA	B	1218	2	1/1/14/20	7/31/109/115	-
13	CLA	H	1221	21	1/1/15/20	14/37/115/115	-
13	CLA	q	501	12	1/1/15/20	18/37/115/115	-
13	CLA	q	504	-	1/1/11/20	5/13/91/115	-
16	BCR	M	4021	-	-	7/29/63/63	0/2/2/2
13	CLA	4	519	12	1/1/13/20	12/25/103/115	-
16	BCR	A	4003	-	-	0/29/63/63	0/2/2/2
13	CLA	5	509	12	1/1/15/20	12/37/115/115	-
13	CLA	u	512	12	1/1/11/20	5/13/91/115	-
16	BCR	J	4013	-	-	4/29/63/63	0/2/2/2
16	BCR	G	4007	-	-	0/29/63/63	0/2/2/2
13	CLA	s	509	12	1/1/15/20	4/37/115/115	-
18	LMU	B	1843	-	-	12/21/61/61	0/2/2/2
16	BCR	Z	521	-	-	4/29/63/63	0/2/2/2
13	CLA	A	1113	1	1/1/11/20	5/13/91/115	-
13	CLA	J	1303	8	1/1/15/20	18/37/115/115	-
13	CLA	4	516	12	1/1/11/20	7/13/91/115	-
13	CLA	f	1234	2	1/1/15/20	13/37/115/115	-
16	BCR	b	523	-	-	5/29/63/63	0/2/2/2
16	BCR	4	523	-	-	5/29/63/63	0/2/2/2
13	CLA	G	1135	1	1/1/12/20	10/22/100/115	-
19	LMG	J	5104	-	-	17/30/50/70	0/1/1/1
16	BCR	c	524	-	-	2/29/63/63	0/2/2/2
13	CLA	d	504	-	1/1/11/20	6/13/91/115	-
13	CLA	3	507	-	1/1/15/20	13/37/115/115	-
19	LMG	B	5002	-	-	24/49/69/70	0/1/1/1
13	CLA	m	1103	9	1/1/12/20	7/19/97/115	-
13	CLA	v	518	12	1/1/13/20	10/25/103/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	H	1212	2	1/1/13/20	11/25/103/115	-
13	CLA	A	1103	1	1/1/15/20	20/37/115/115	-
13	CLA	q	516	12	1/1/11/20	13/13/91/115	-
16	BCR	e	4003	-	-	0/29/63/63	0/2/2/2
13	CLA	v	507	-	1/1/11/20	4/13/91/115	-
16	BCR	f	4017	-	-	2/29/63/63	0/2/2/2
18	LMU	e	1848	-	-	7/21/61/61	0/2/2/2
13	CLA	t	513	12	1/1/11/20	7/13/91/115	-
13	CLA	a	510	12	1/1/15/20	17/37/115/115	-
13	CLA	B	1217	2	1/1/13/20	12/28/106/115	-
13	CLA	G	1137	1	1/1/15/20	19/37/115/115	-
17	LHG	e	5002	-	-	26/43/43/53	-
13	CLA	3	511	12	1/1/12/20	5/19/97/115	-
13	CLA	f	1235	2	1/1/15/20	6/37/115/115	-
13	CLA	v	504	-	1/1/11/20	6/13/91/115	-
14	PQN	f	2002	-	-	9/23/43/43	0/2/2/2
13	CLA	c	505	12	1/1/14/20	16/33/111/115	-
13	CLA	e	1011	1	1/1/15/20	10/37/115/115	-
13	CLA	Z	501	12	1/1/15/20	12/37/115/115	-
16	BCR	c	521	-	-	7/29/63/63	0/2/2/2
13	CLA	3	513	12	1/1/15/20	13/37/115/115	-
13	CLA	G	1013	-	1/1/15/20	11/37/115/115	-
13	CLA	t	509	12	1/1/15/20	7/37/115/115	-
16	BCR	l	4013	-	-	4/29/63/63	0/2/2/2
13	CLA	3	505	12	1/1/15/20	17/37/115/115	-
13	CLA	f	1023	-	1/1/15/20	10/37/115/115	-
13	CLA	r	513	12	1/1/15/20	15/37/115/115	-
16	BCR	e	4008	-	-	7/29/63/63	0/2/2/2
17	LHG	e	5006	-	-	24/49/49/53	-
16	BCR	T	4012	-	-	9/29/63/63	0/2/2/2
13	CLA	H	1218	2	1/1/14/20	7/31/109/115	-
13	CLA	f	1218	2	1/1/14/20	7/31/109/115	-
16	BCR	q	522	-	-	6/29/63/63	0/2/2/2
19	LMG	T	5104	-	-	17/30/50/70	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	BCR	J	4012	-	-	9/29/63/63	0/2/2/2
13	CLA	c	519	12	1/1/11/20	8/15/93/115	-
13	CLA	U	1105	9	1/1/11/20	9/13/91/115	-
20	SQD	q	822	-	-	20/43/63/69	0/1/1/1
16	BCR	t	523	-	-	5/29/63/63	0/2/2/2
13	CLA	m	1401	-	1/1/13/20	8/25/103/115	-
13	CLA	c	506	12	1/1/11/20	5/13/91/115	-
13	CLA	d	503	12	1/1/12/20	8/22/100/115	-
13	CLA	B	1211	2	1/1/13/20	4/27/105/115	-
13	CLA	f	1214	2	1/1/15/20	13/37/115/115	-
13	CLA	K	1103	9	1/1/12/20	7/19/97/115	-
13	CLA	H	1238	21	1/1/15/20	4/37/115/115	-
16	BCR	U	4104	-	-	2/29/63/63	0/2/2/2
13	CLA	b	519	12	1/1/13/20	12/25/103/115	-
18	LMU	H	1843	-	-	12/21/61/61	0/2/2/2
16	BCR	V	4022	-	-	2/29/63/63	0/2/2/2
13	CLA	Y	509	12	1/1/15/20	6/37/115/115	-
16	BCR	t	524	-	-	4/29/63/63	0/2/2/2
13	CLA	6	509	12	1/1/11/20	5/13/91/115	-
13	CLA	Z	512	12	1/1/12/20	5/23/101/115	-
13	CLA	H	1208	2	1/1/15/20	15/37/115/115	-
13	CLA	A	1117	1	1/1/15/20	12/37/115/115	-
13	CLA	A	1111	1	1/1/15/20	14/37/115/115	-
13	CLA	e	1136	1	1/1/14/20	5/31/109/115	-
13	CLA	c	508	12	1/1/11/20	4/13/91/115	-
13	CLA	5	507	-	1/1/11/20	5/13/91/115	-
17	LHG	L	5218	-	-	23/42/42/53	-
13	CLA	H	1205	2	1/1/15/20	10/37/115/115	-
13	CLA	e	1120	1	1/1/12/20	4/23/101/115	-
13	CLA	6	516	12	1/1/11/20	8/13/91/115	-
13	CLA	A	1108	1	1/1/12/20	16/24/102/115	-
15	SF4	g	3002	3	-	-	0/6/5/5
16	BCR	6	523	-	-	4/29/63/63	0/2/2/2
13	CLA	G	1128	1	1/1/15/20	12/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	e	1131	1	1/1/15/20	6/37/115/115	-
13	CLA	A	1130	1	1/1/15/20	7/37/115/115	-
13	CLA	s	508	12	1/1/13/20	7/25/103/115	-
13	CLA	u	501	12	1/1/15/20	19/37/115/115	-
13	CLA	u	517	-	1/1/11/20	9/13/91/115	-
18	LMU	l	902	-	-	6/10/30/61	0/1/1/2
13	CLA	c	503	12	1/1/13/20	10/25/103/115	-
13	CLA	q	510	12	1/1/15/20	11/37/115/115	-
14	PQN	H	2002	-	-	9/23/43/43	0/2/2/2
16	BCR	e	4011	-	-	13/29/63/63	0/2/2/2
13	CLA	H	1217	2	1/1/13/20	12/28/106/115	-
16	BCR	q	523	-	-	6/29/63/63	0/2/2/2
13	CLA	d	511	12	1/1/11/20	4/13/91/115	-
13	CLA	a	518	12	1/1/13/20	10/25/103/115	-
13	CLA	l	518	12	1/1/14/20	15/31/109/115	-
13	CLA	V	1502	10	1/1/15/20	8/37/115/115	-
13	CLA	v	505	12	1/1/15/20	15/37/115/115	-
13	CLA	Z	513	12	1/1/15/20	15/37/115/115	-
16	BCR	e	4001	-	-	8/29/63/63	0/2/2/2
13	CLA	b	503	12	1/1/13/20	1/25/103/115	-
13	CLA	e	1139	21	1/1/15/20	12/37/115/115	-
13	CLA	u	509	12	1/1/15/20	12/37/115/115	-
13	CLA	G	1131	1	1/1/15/20	6/37/115/115	-
16	BCR	A	4002	-	-	0/29/63/63	0/2/2/2
16	BCR	d	521	-	-	5/29/63/63	0/2/2/2
13	CLA	r	508	12	1/1/13/20	6/25/103/115	-
13	CLA	d	505	12	1/1/15/20	15/37/115/115	-
16	BCR	a	524	-	-	5/29/63/63	0/2/2/2
13	CLA	q	505	12	1/1/15/20	11/37/115/115	-
13	CLA	d	510	12	1/1/11/20	7/13/91/115	-
13	CLA	e	1115	1	1/1/14/20	10/31/109/115	-
13	CLA	v	519	12	1/1/11/20	6/15/93/115	-
16	BCR	b	524	-	-	4/29/63/63	0/2/2/2
16	BCR	b	522	-	-	4/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	A	1801	17	1/1/11/20	5/13/91/115	-
13	CLA	e	1126	1	1/1/15/20	18/37/115/115	-
16	BCR	F	4016	-	-	2/29/63/63	0/2/2/2
20	SQD	b	822	-	-	8/19/39/69	0/1/1/1
13	CLA	t	507	-	1/1/11/20	6/13/91/115	-
13	CLA	d	506	12	1/1/11/20	5/13/91/115	-
13	CLA	4	517	-	1/1/11/20	5/13/91/115	-
18	LMU	G	1848	-	-	7/21/61/61	0/2/2/2
13	CLA	G	1109	1	1/1/15/20	9/37/115/115	-
13	CLA	5	518	12	1/1/13/20	11/25/103/115	-
13	CLA	H	1225	2	1/1/15/20	7/37/115/115	-
13	CLA	d	512	12	1/1/11/20	6/13/91/115	-
13	CLA	A	1013	-	1/1/15/20	11/37/115/115	-
13	CLA	e	1129	1	1/1/12/20	5/21/99/115	-
13	CLA	n	1501	10	1/1/15/20	18/37/115/115	-
16	BCR	V	4219	-	-	2/29/63/63	0/2/2/2
13	CLA	G	1114	21	1/1/12/20	2/19/97/115	-
13	CLA	a	505	12	1/1/15/20	17/37/115/115	-
13	CLA	t	511	12	1/1/11/20	3/13/91/115	-
13	CLA	r	519	12	1/1/13/20	9/25/103/115	-
16	BCR	Z	524	-	-	2/29/63/63	0/2/2/2
17	LHG	V	5221	-	-	30/53/53/53	-
13	CLA	A	1110	1	1/1/12/20	9/21/99/115	-
13	CLA	q	502	12	1/1/14/20	14/31/109/115	-
13	CLA	2	502	12	1/1/14/20	11/31/109/115	-
13	CLA	1	507	-	1/1/14/20	15/31/109/115	-
13	CLA	e	1102	1	1/1/15/20	11/37/115/115	-
13	CLA	H	1215	2	1/1/15/20	19/37/115/115	-
16	BCR	f	4005	-	-	6/29/63/63	0/2/2/2
13	CLA	s	507	-	1/1/15/20	13/37/115/115	-
13	CLA	A	1127	1	1/1/15/20	12/37/115/115	-
16	BCR	L	4019	-	-	6/29/63/63	0/2/2/2
13	CLA	v	503	12	1/1/12/20	8/22/100/115	-
13	CLA	2	504	-	1/1/12/20	5/19/97/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	LHG	G	5001	-	-	25/53/53/53	-
13	CLA	a	519	12	1/1/13/20	8/25/103/115	-
13	CLA	b	510	12	1/1/12/20	5/19/97/115	-
16	BCR	d	522	-	-	5/29/63/63	0/2/2/2
13	CLA	r	504	-	1/1/12/20	5/19/97/115	-
17	LHG	e	5004	-	-	21/40/40/53	-
16	BCR	L	4020	-	-	4/29/63/63	0/2/2/2
16	BCR	v	522	-	-	5/29/63/63	0/2/2/2
13	CLA	G	1116	1	1/1/14/20	15/31/109/115	-
13	CLA	G	1115	1	1/1/14/20	10/31/109/115	-
13	CLA	s	511	12	1/1/12/20	5/19/97/115	-
13	CLA	b	506	12	1/1/11/20	2/13/91/115	-
13	CLA	e	1111	1	1/1/15/20	14/37/115/115	-
13	CLA	l	517	-	1/1/11/20	4/13/91/115	-
13	CLA	a	516	12	1/1/11/20	9/13/91/115	-
13	CLA	4	504	-	1/1/11/20	5/13/91/115	-
16	BCR	a	523	-	-	4/29/63/63	0/2/2/2
13	CLA	3	506	12	1/1/12/20	5/19/97/115	-
13	CLA	3	509	12	1/1/15/20	4/37/115/115	-
13	CLA	r	503	12	1/1/15/20	9/37/115/115	-
19	LMG	f	5002	-	-	24/49/69/70	0/1/1/1
13	CLA	B	1227	2	1/1/15/20	12/37/115/115	-
13	CLA	c	501	12	1/1/15/20	19/37/115/115	-
13	CLA	u	518	12	1/1/13/20	11/25/103/115	-
13	CLA	e	1135	1	1/1/12/20	10/22/100/115	-
13	CLA	t	518	12	1/1/13/20	8/25/103/115	-
13	CLA	v	509	12	1/1/11/20	6/13/91/115	-
13	CLA	G	1122	1	1/1/14/20	14/31/109/115	-
13	CLA	u	507	-	1/1/11/20	5/13/91/115	-
13	CLA	4	508	12	1/1/11/20	4/13/91/115	-
16	BCR	3	523	-	-	4/29/63/63	0/2/2/2
16	BCR	o	4021	-	-	7/29/63/63	0/2/2/2
13	CLA	f	1222	21	1/1/14/20	7/31/109/115	-
13	CLA	B	1234	2	1/1/15/20	13/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	BCR	f	4009	-	-	1/29/63/63	0/2/2/2
13	CLA	e	1118	1	1/1/14/20	12/31/109/115	-
13	CLA	G	1134	1	1/1/13/20	11/27/105/115	-
18	LMU	e	1849	-	-	6/14/34/61	0/1/1/2
13	CLA	B	1202	2	1/1/15/20	13/37/115/115	-
13	CLA	5	519	12	1/1/11/20	8/15/93/115	-
16	BCR	b	521	-	-	10/29/63/63	0/2/2/2
13	CLA	1	519	12	1/1/12/20	6/19/97/115	-
13	CLA	Z	507	-	1/1/15/20	14/37/115/115	-
17	LHG	G	5007	-	-	24/51/51/53	-
13	CLA	B	1224	2	1/1/14/20	13/31/109/115	-
13	CLA	f	1221	21	1/1/15/20	14/37/115/115	-
16	BCR	e	4002	-	-	0/29/63/63	0/2/2/2
17	LHG	A	5001	-	-	25/53/53/53	-
13	CLA	K	1401	-	1/1/13/20	8/25/103/115	-
17	LHG	S	5001	-	-	22/48/48/53	-
13	CLA	6	517	-	1/1/11/20	9/13/91/115	-
13	CLA	H	1209	2	1/1/12/20	8/22/100/115	-
20	SQD	L	5216	-	-	17/46/66/69	0/1/1/1
13	CLA	t	505	12	1/1/15/20	11/37/115/115	-
17	LHG	f	1855	-	-	28/48/48/53	-
13	CLA	Y	513	12	1/1/13/20	2/25/103/115	-
13	CLA	Z	518	12	1/1/15/20	16/37/115/115	-
13	CLA	f	1223	2	1/1/15/20	14/37/115/115	-
13	CLA	u	513	12	1/1/11/20	4/13/91/115	-
13	CLA	G	1138	1	1/1/15/20	12/37/115/115	-
13	CLA	2	517	-	1/1/11/20	4/13/91/115	-
13	CLA	A	1011	1	1/1/15/20	10/37/115/115	-
13	CLA	f	1201	2	1/1/14/20	11/31/109/115	-
13	CLA	r	501	12	1/1/15/20	12/37/115/115	-
13	CLA	4	510	12	1/1/12/20	5/19/97/115	-
16	BCR	2	522	-	-	6/29/63/63	0/2/2/2
13	CLA	e	1103	1	1/1/15/20	20/37/115/115	-
13	CLA	v	506	12	1/1/11/20	5/13/91/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	s	519	12	1/1/13/20	8/25/103/115	-
13	CLA	e	1123	21	1/1/15/20	11/37/115/115	-
16	BCR	T	4015	-	-	5/29/63/63	0/2/2/2
13	CLA	3	501	12	1/1/15/20	6/37/115/115	-
13	CLA	A	1112	1	1/1/12/20	3/19/97/115	-
20	SQD	B	1852	-	-	19/40/60/69	0/1/1/1
20	SQD	Z	822	-	-	13/38/58/69	0/1/1/1
13	CLA	3	510	12	1/1/15/20	17/37/115/115	-
13	CLA	Y	503	12	1/1/14/20	9/36/114/115	-
19	LMG	l	5104	-	-	17/30/50/70	0/1/1/1
13	CLA	G	1112	1	1/1/12/20	3/19/97/115	-
13	CLA	b	508	12	1/1/11/20	4/13/91/115	-
17	LHG	A	5005	-	-	29/49/49/53	-
13	CLA	f	1212	2	1/1/13/20	11/25/103/115	-
13	CLA	2	503	12	1/1/15/20	9/37/115/115	-
16	BCR	Y	524	-	-	2/29/63/63	0/2/2/2
16	BCR	V	4020	-	-	4/29/63/63	0/2/2/2
13	CLA	Z	503	12	1/1/15/20	9/37/115/115	-
13	CLA	G	1106	1	1/1/15/20	21/37/115/115	-
13	CLA	f	1225	2	1/1/15/20	7/37/115/115	-
17	LHG	L	5221	-	-	30/53/53/53	-
13	CLA	Y	516	12	1/1/11/20	13/13/91/115	-
13	CLA	H	1227	2	1/1/15/20	12/37/115/115	-
20	SQD	c	822	-	-	7/24/44/69	0/1/1/1
17	LHG	G	5003	13	-	16/45/45/53	-
13	CLA	f	1236	2	-	3/25/103/115	-
16	BCR	5	524	-	-	2/29/63/63	0/2/2/2
13	CLA	c	513	12	1/1/11/20	4/13/91/115	-
13	CLA	e	1022	21	1/1/15/20	8/37/115/115	-
16	BCR	H	4014	-	-	9/29/63/63	0/2/2/2
18	LMU	G	1849	-	-	6/14/34/61	0/1/1/2
13	CLA	q	517	-	1/1/11/20	4/13/91/115	-
13	CLA	B	1201	2	1/1/14/20	11/31/109/115	-
17	LHG	G	5002	-	-	26/43/43/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	SF4	C	3003	3	-	-	0/6/5/5
13	CLA	A	1101	1	1/1/15/20	13/37/115/115	-
13	CLA	R	1302	6	1/1/11/20	8/13/91/115	-
20	SQD	v	822	-	-	9/19/39/69	0/1/1/1
13	CLA	H	1224	2	1/1/14/20	13/31/109/115	-
13	CLA	f	1224	2	1/1/14/20	13/31/109/115	-
16	BCR	B	4010	-	-	5/29/63/63	0/2/2/2
13	CLA	Z	504	-	1/1/12/20	5/19/97/115	-
13	CLA	B	1231	21	1/1/15/20	8/37/115/115	-
13	CLA	Y	511	12	1/1/13/20	4/25/103/115	-
13	CLA	4	505	12	1/1/15/20	11/37/115/115	-
13	CLA	u	511	12	1/1/13/20	5/25/103/115	-
13	CLA	f	1210	2	1/1/15/20	19/37/115/115	-
16	BCR	I	4018	-	-	1/29/63/63	0/2/2/2
16	BCR	l	4012	-	-	9/29/63/63	0/2/2/2
13	CLA	4	502	12	1/1/12/20	5/19/97/115	-
13	CLA	c	512	12	1/1/11/20	5/13/91/115	-
17	LHG	n	5221	-	-	30/53/53/53	-
13	CLA	2	501	12	1/1/15/20	12/37/115/115	-
16	BCR	6	522	-	-	5/29/63/63	0/2/2/2
13	CLA	A	1122	1	1/1/14/20	14/31/109/115	-
13	CLA	e	1237	21	1/1/15/20	19/37/115/115	-
13	CLA	a	506	12	1/1/12/20	5/19/97/115	-
16	BCR	5	522	-	-	5/29/63/63	0/2/2/2
13	CLA	e	1110	1	1/1/12/20	9/21/99/115	-
17	LHG	G	5006	-	-	24/49/49/53	-
17	LHG	e	5001	-	-	25/53/53/53	-
13	CLA	G	1110	1	1/1/12/20	9/21/99/115	-
16	BCR	5	521	-	-	7/29/63/63	0/2/2/2
13	CLA	t	519	12	1/1/13/20	12/25/103/115	-
16	BCR	H	4010	-	-	5/29/63/63	0/2/2/2
16	BCR	c	523	-	-	4/29/63/63	0/2/2/2
18	LMU	J	5105	-	-	8/13/33/61	0/1/1/2
13	CLA	e	1116	1	1/1/14/20	15/31/109/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	e	1107	1	1/1/15/20	14/37/115/115	-
13	CLA	v	512	12	1/1/11/20	6/13/91/115	-
13	CLA	5	503	12	1/1/13/20	10/25/103/115	-
13	CLA	F	1302	6	1/1/11/20	8/13/91/115	-
13	CLA	A	1105	1	1/1/13/20	6/25/103/115	-
16	BCR	2	521	-	-	4/29/63/63	0/2/2/2
13	CLA	A	1139	21	1/1/15/20	12/37/115/115	-
13	CLA	G	1129	1	1/1/12/20	5/21/99/115	-
13	CLA	A	1104	1	1/1/15/20	12/37/115/115	-
13	CLA	5	506	12	1/1/11/20	5/13/91/115	-
13	CLA	d	518	12	1/1/13/20	10/25/103/115	-
20	SQD	5	822	-	-	7/24/44/69	0/1/1/1
16	BCR	n	4019	-	-	6/29/63/63	0/2/2/2
16	BCR	A	4008	-	-	7/29/63/63	0/2/2/2
20	SQD	d	822	-	-	9/19/39/69	0/1/1/1
13	CLA	1	506	12	1/1/11/20	6/13/91/115	-
13	CLA	1	509	12	1/1/15/20	6/37/115/115	-
13	CLA	U	1103	9	1/1/12/20	7/19/97/115	-
13	CLA	e	1122	1	1/1/14/20	14/31/109/115	-
13	CLA	f	1227	2	1/1/15/20	12/37/115/115	-
16	BCR	n	4020	-	-	4/29/63/63	0/2/2/2
15	SF4	g	3003	3	-	-	0/6/5/5
13	CLA	b	505	12	1/1/15/20	11/37/115/115	-
16	BCR	G	4003	-	-	0/29/63/63	0/2/2/2
13	CLA	v	513	12	1/1/11/20	3/13/91/115	-
13	CLA	s	503	12	1/1/15/20	7/37/115/115	-
16	BCR	Y	522	-	-	6/29/63/63	0/2/2/2
13	CLA	G	1022	21	1/1/15/20	8/37/115/115	-
13	CLA	Z	502	12	1/1/14/20	11/31/109/115	-
16	BCR	1	523	-	-	6/29/63/63	0/2/2/2
16	BCR	6	524	-	-	5/29/63/63	0/2/2/2
17	LHG	e	5007	-	-	24/51/51/53	-
16	BCR	u	522	-	-	5/29/63/63	0/2/2/2
14	PQN	B	2002	-	-	9/23/43/43	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	H	1201	2	1/1/14/20	11/31/109/115	-
16	BCR	2	524	-	-	2/29/63/63	0/2/2/2
13	CLA	e	1109	1	1/1/15/20	9/37/115/115	-
16	BCR	H	4004	-	-	8/29/63/63	0/2/2/2
13	CLA	2	508	12	1/1/13/20	6/25/103/115	-
13	CLA	H	1210	2	1/1/15/20	19/37/115/115	-
13	CLA	H	1231	21	1/1/15/20	8/37/115/115	-
17	LHG	B	1855	-	-	28/48/48/53	-
13	CLA	q	513	12	1/1/13/20	2/25/103/115	-
13	CLA	A	1120	1	1/1/12/20	4/23/101/115	-
13	CLA	K	1105	9	1/1/11/20	9/13/91/115	-
13	CLA	m	1105	9	1/1/11/20	9/13/91/115	-
13	CLA	B	1204	2	1/1/15/20	12/37/115/115	-
13	CLA	v	510	12	1/1/11/20	7/13/91/115	-
13	CLA	t	506	12	1/1/11/20	2/13/91/115	-
13	CLA	H	1204	2	1/1/15/20	12/37/115/115	-
13	CLA	b	516	12	1/1/11/20	7/13/91/115	-
16	BCR	A	4011	-	-	12/29/63/63	0/2/2/2
16	BCR	r	522	-	-	6/29/63/63	0/2/2/2
14	PQN	A	2001	-	-	14/23/43/43	0/2/2/2
13	CLA	B	1203	2	1/1/15/20	16/37/115/115	-
13	CLA	a	508	12	1/1/13/20	7/25/103/115	-
16	BCR	6	521	-	-	5/29/63/63	0/2/2/2
13	CLA	e	1127	1	1/1/15/20	12/37/115/115	-
17	LHG	n	5218	-	-	23/42/42/53	-
13	CLA	f	1211	2	1/1/13/20	4/27/105/115	-
13	CLA	Y	501	12	1/1/15/20	18/37/115/115	-
13	CLA	B	1021	2	1/1/15/20	10/37/115/115	-
13	CLA	B	1214	2	1/1/15/20	13/37/115/115	-
13	CLA	f	1207	2	1/1/15/20	14/37/115/115	-
13	CLA	a	513	12	1/1/15/20	13/37/115/115	-
13	CLA	v	516	12	1/1/11/20	8/13/91/115	-
16	BCR	A	4001	-	-	8/29/63/63	0/2/2/2
16	BCR	s	521	-	-	7/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	LHG	V	5218	-	-	23/42/42/53	-
17	LHG	n	5220	-	-	24/45/45/53	-
13	CLA	B	1228	2	1/1/13/20	8/25/103/115	-
13	CLA	6	510	12	1/1/11/20	7/13/91/115	-
13	CLA	1	510	12	1/1/15/20	11/37/115/115	-
13	CLA	c	504	-	1/1/11/20	3/13/91/115	-
13	CLA	q	509	12	1/1/15/20	6/37/115/115	-
13	CLA	s	501	12	1/1/15/20	6/37/115/115	-
16	BCR	v	524	-	-	5/29/63/63	0/2/2/2
16	BCR	4	522	-	-	4/29/63/63	0/2/2/2
13	CLA	e	1134	1	1/1/13/20	11/27/105/115	-
13	CLA	f	1205	2	1/1/15/20	10/37/115/115	-
16	BCR	f	4014	-	-	9/29/63/63	0/2/2/2
13	CLA	6	519	12	1/1/11/20	6/15/93/115	-
15	SF4	G	3001	1,2	-	-	0/6/5/5
16	BCR	2	523	-	-	6/29/63/63	0/2/2/2
13	CLA	b	512	12	1/1/11/20	3/13/91/115	-
13	CLA	6	506	12	1/1/11/20	5/13/91/115	-
13	CLA	d	501	12	1/1/14/20	16/31/109/115	-
13	CLA	d	517	-	1/1/11/20	9/13/91/115	-
13	CLA	v	508	12	1/1/11/20	3/13/91/115	-
13	CLA	L	1501	10	1/1/15/20	18/37/115/115	-
13	CLA	1	516	12	1/1/11/20	13/13/91/115	-
13	CLA	r	516	12	1/1/11/20	8/13/91/115	-
13	CLA	Y	505	12	1/1/15/20	11/37/115/115	-
13	CLA	d	502	12	1/1/12/20	5/19/97/115	-
13	CLA	G	1103	1	1/1/15/20	20/37/115/115	-
13	CLA	H	1230	2	1/1/14/20	10/31/109/115	-
13	CLA	6	508	12	1/1/11/20	3/13/91/115	-
16	BCR	G	4001	-	-	8/29/63/63	0/2/2/2
13	CLA	A	1118	1	1/1/14/20	12/31/109/115	-
13	CLA	5	508	12	1/1/11/20	4/13/91/115	-
17	LHG	G	5004	-	-	21/40/40/53	-
13	CLA	A	1129	1	1/1/12/20	5/21/99/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	BCR	4	524	-	-	4/29/63/63	0/2/2/2
13	CLA	A	1137	1	1/1/15/20	19/37/115/115	-
13	CLA	3	503	12	1/1/15/20	7/37/115/115	-
13	CLA	e	1130	1	1/1/15/20	7/37/115/115	-
13	CLA	q	511	12	1/1/13/20	4/25/103/115	-
16	BCR	r	524	-	-	2/29/63/63	0/2/2/2
13	CLA	2	511	12	1/1/13/20	4/25/103/115	-
17	LHG	H	1855	-	-	28/48/48/53	-
13	CLA	G	1133	1	1/1/15/20	15/37/115/115	-
16	BCR	u	521	-	-	7/29/63/63	0/2/2/2
17	LHG	e	5008	-	-	19/39/39/53	-
13	CLA	L	1503	21	1/1/14/20	10/31/109/115	-
13	CLA	6	503	12	1/1/12/20	8/22/100/115	-
16	BCR	s	523	-	-	4/29/63/63	0/2/2/2
13	CLA	R	1301	21	1/1/15/20	11/37/115/115	-
13	CLA	t	504	-	1/1/11/20	5/13/91/115	-
13	CLA	A	1132	1	1/1/15/20	15/37/115/115	-
13	CLA	H	1219	2	1/1/15/20	17/37/115/115	-
13	CLA	4	506	12	1/1/11/20	2/13/91/115	-
13	CLA	c	518	12	1/1/13/20	11/25/103/115	-
16	BCR	Z	522	-	-	6/29/63/63	0/2/2/2
13	CLA	B	1208	2	1/1/15/20	15/37/115/115	-
13	CLA	5	512	12	1/1/11/20	5/13/91/115	-
13	CLA	1	512	12	1/1/12/20	10/22/100/115	-
13	CLA	B	1219	2	1/1/15/20	17/37/115/115	-
13	CLA	H	1203	2	1/1/15/20	16/37/115/115	-
17	LHG	G	5008	-	-	19/39/39/53	-
13	CLA	f	1209	2	1/1/12/20	8/22/100/115	-
13	CLA	u	508	12	1/1/11/20	4/13/91/115	-
13	CLA	B	1205	2	1/1/15/20	10/37/115/115	-
13	CLA	Z	509	12	1/1/15/20	6/37/115/115	-
13	CLA	H	1021	2	1/1/15/20	11/37/115/115	-
13	CLA	H	1214	2	1/1/15/20	13/37/115/115	-
13	CLA	f	1021	2	1/1/15/20	11/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	t	508	12	1/1/11/20	4/13/91/115	-
13	CLA	H	1228	2	1/1/13/20	8/25/103/115	-
13	CLA	2	510	12	1/1/15/20	9/37/115/115	-
13	CLA	t	503	12	1/1/13/20	1/25/103/115	-
16	BCR	5	523	-	-	4/29/63/63	0/2/2/2
13	CLA	e	1106	1	1/1/15/20	21/37/115/115	-
16	BCR	r	521	-	-	4/29/63/63	0/2/2/2
14	PQN	e	2001	-	-	14/23/43/43	0/2/2/2
20	SQD	6	822	-	-	9/19/39/69	0/1/1/1
13	CLA	Z	516	12	1/1/11/20	8/13/91/115	-
13	CLA	j	1301	21	1/1/15/20	11/37/115/115	-
13	CLA	5	502	12	1/1/12/20	5/19/97/115	-
19	LMG	H	5002	-	-	24/49/69/70	0/1/1/1
13	CLA	Y	508	12	1/1/13/20	9/25/103/115	-
13	CLA	5	516	12	1/1/11/20	2/13/91/115	-
13	CLA	G	1123	21	1/1/15/20	11/37/115/115	-
16	BCR	Z	523	-	-	6/29/63/63	0/2/2/2
13	CLA	e	1119	21	1/1/15/20	15/37/115/115	-
13	CLA	A	1128	1	1/1/15/20	12/37/115/115	-
16	BCR	4	521	-	-	10/29/63/63	0/2/2/2
13	CLA	t	512	12	1/1/11/20	3/13/91/115	-
13	CLA	e	1132	1	1/1/15/20	15/37/115/115	-
13	CLA	G	1121	1	1/1/13/20	6/25/103/115	-
16	BCR	3	522	-	-	5/29/63/63	0/2/2/2
13	CLA	G	1124	21	1/1/13/20	11/27/105/115	-
13	CLA	H	1202	2	1/1/15/20	13/37/115/115	-
13	CLA	d	513	12	1/1/11/20	3/13/91/115	-
13	CLA	l	505	12	1/1/15/20	11/37/115/115	-
13	CLA	G	1140	1	1/1/15/20	11/37/115/115	-
13	CLA	U	1401	-	1/1/13/20	8/25/103/115	-
13	CLA	A	1138	1	1/1/15/20	12/37/115/115	-
13	CLA	n	1503	21	1/1/14/20	10/31/109/115	-
16	BCR	J	4015	-	-	5/29/63/63	0/2/2/2
13	CLA	B	1220	2	1/1/13/20	9/25/103/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	T	1303	8	1/1/15/20	18/37/115/115	-
16	BCR	3	524	-	-	5/29/63/63	0/2/2/2
18	LMU	Y	902	-	-	6/10/30/61	0/1/1/2
13	CLA	Y	519	12	1/1/12/20	6/19/97/115	-
13	CLA	a	504	-	1/1/11/20	6/13/91/115	-
13	CLA	d	509	12	1/1/11/20	6/13/91/115	-
13	CLA	B	1216	21	1/1/14/20	5/31/109/115	-
13	CLA	B	1212	2	1/1/13/20	11/25/103/115	-
13	CLA	e	1801	17	1/1/11/20	5/13/91/115	-
13	CLA	6	502	12	1/1/12/20	5/19/97/115	-
13	CLA	b	501	12	1/1/14/20	12/31/109/115	-
13	CLA	A	1133	1	1/1/15/20	15/37/115/115	-
17	LHG	A	5009	-	-	28/53/53/53	-
16	BCR	d	523	-	-	4/29/63/63	0/2/2/2
13	CLA	f	1215	2	1/1/15/20	19/37/115/115	-
13	CLA	B	1012	21	1/1/15/20	16/37/115/115	-
13	CLA	s	518	12	1/1/13/20	10/25/103/115	-
13	CLA	c	517	-	1/1/11/20	9/13/91/115	-
17	LHG	A	5004	-	-	21/40/40/53	-
13	CLA	A	1116	1	1/1/14/20	15/31/109/115	-
13	CLA	G	1801	17	1/1/11/20	5/13/91/115	-
17	LHG	f	1842	13	-	22/43/43/53	-
13	CLA	5	504	-	1/1/11/20	3/13/91/115	-
13	CLA	A	1121	1	1/1/13/20	6/25/103/115	-
16	BCR	1	524	-	-	2/29/63/63	0/2/2/2
13	CLA	4	513	12	1/1/11/20	7/13/91/115	-
13	CLA	6	501	12	1/1/14/20	16/31/109/115	-
13	CLA	r	517	-	1/1/11/20	4/13/91/115	-
13	CLA	B	1213	2	1/1/15/20	14/37/115/115	-
13	CLA	r	510	12	1/1/15/20	9/37/115/115	-
18	LMU	A	1848	-	-	7/21/61/61	0/2/2/2
13	CLA	V	1501	10	1/1/15/20	18/37/115/115	-
13	CLA	Y	512	12	1/1/12/20	9/22/100/115	-
13	CLA	e	1138	1	1/1/15/20	12/37/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	q	518	12	1/1/14/20	15/31/109/115	-
13	CLA	r	502	12	1/1/14/20	11/31/109/115	-
13	CLA	u	505	12	1/1/14/20	16/33/111/115	-
13	CLA	b	518	12	1/1/13/20	8/25/103/115	-
16	BCR	G	4008	-	-	7/29/63/63	0/2/2/2
17	LHG	V	5220	-	-	24/45/45/53	-
13	CLA	A	1123	21	1/1/15/20	11/37/115/115	-
13	CLA	4	507	-	1/1/11/20	6/13/91/115	-
13	CLA	b	507	-	1/1/11/20	6/13/91/115	-
20	SQD	V	5216	-	-	17/46/66/69	0/1/1/1
15	SF4	N	3002	3	-	-	0/6/5/5
13	CLA	A	1125	1	1/1/15/20	14/37/115/115	-
13	CLA	f	1226	2	1/1/15/20	12/37/115/115	-
13	CLA	b	504	-	1/1/11/20	5/13/91/115	-
13	CLA	3	516	12	1/1/11/20	9/13/91/115	-
13	CLA	B	1232	21	1/1/12/20	6/19/97/115	-
16	BCR	L	4022	-	-	2/29/63/63	0/2/2/2
13	CLA	4	518	12	1/1/13/20	8/25/103/115	-
13	CLA	B	1229	2	1/1/15/20	13/37/115/115	-
13	CLA	l	1303	8	1/1/15/20	18/37/115/115	-
13	CLA	B	1236	2	-	3/25/103/115	-
20	SQD	H	1852	-	-	19/40/60/69	0/1/1/1
20	SQD	f	1852	-	-	19/40/60/69	0/1/1/1
16	BCR	K	4104	-	-	2/29/63/63	0/2/2/2
13	CLA	f	1204	2	1/1/15/20	12/37/115/115	-
13	CLA	A	1109	1	1/1/15/20	9/37/115/115	-
13	CLA	4	511	12	1/1/11/20	3/13/91/115	-
13	CLA	a	517	-	1/1/11/20	7/13/91/115	-
13	CLA	B	1240	17	-	13/37/115/115	-
13	CLA	2	509	12	1/1/15/20	6/37/115/115	-
13	CLA	e	1013	-	1/1/15/20	11/37/115/115	-
13	CLA	A	1114	21	1/1/12/20	2/19/97/115	-
13	CLA	2	512	12	1/1/12/20	5/23/101/115	-
16	BCR	a	522	-	-	5/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	CLA	f	1208	2	1/1/15/20	15/37/115/115	-
20	SQD	3	822	-	-	21/38/58/69	0/1/1/1
13	CLA	v	501	12	1/1/14/20	16/31/109/115	-
13	CLA	H	1216	21	1/1/14/20	5/31/109/115	-
20	SQD	a	822	-	-	21/38/58/69	0/1/1/1
13	CLA	A	1237	21	1/1/15/20	19/37/115/115	-
16	BCR	m	4104	-	-	2/29/63/63	0/2/2/2
13	CLA	b	513	12	1/1/11/20	7/13/91/115	-
15	SF4	e	3001	1,2	-	-	0/6/5/5
13	CLA	u	502	12	1/1/12/20	5/19/97/115	-
13	CLA	G	1119	21	1/1/15/20	15/37/115/115	-
16	BCR	s	524	-	-	5/29/63/63	0/2/2/2
16	BCR	B	4006	-	-	4/29/63/63	0/2/2/2
13	CLA	u	516	12	1/1/11/20	2/13/91/115	-
13	CLA	3	504	-	1/1/11/20	6/13/91/115	-
13	CLA	v	502	12	1/1/12/20	5/19/97/115	-
13	CLA	H	1211	2	1/1/13/20	4/27/105/115	-
13	CLA	3	517	-	1/1/11/20	7/13/91/115	-
16	BCR	f	4004	-	-	8/29/63/63	0/2/2/2
17	LHG	k	5001	-	-	22/48/48/53	-
13	CLA	a	503	12	1/1/15/20	7/37/115/115	-
13	CLA	H	1012	21	1/1/15/20	16/37/115/115	-
13	CLA	A	1107	1	1/1/15/20	14/37/115/115	-
13	CLA	5	517	-	1/1/11/20	9/13/91/115	-
13	CLA	G	1132	1	1/1/15/20	15/37/115/115	-
16	BCR	f	4010	-	-	5/29/63/63	0/2/2/2
17	LHG	e	5009	-	-	28/53/53/53	-
13	CLA	3	508	12	1/1/13/20	7/25/103/115	-
16	BCR	c	522	-	-	5/29/63/63	0/2/2/2

The worst 5 of 4509 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	2002	PQN	C12-C13	8.71	1.53	1.33
14	f	2002	PQN	C12-C13	8.70	1.53	1.33
14	H	2002	PQN	C12-C13	8.70	1.53	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	G	2001	PQN	C12-C13	8.66	1.53	1.33
14	e	2001	PQN	C12-C13	8.66	1.53	1.33

The worst 5 of 7438 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	f	2002	PQN	C11-C12-C13	-9.00	111.81	126.79
14	B	2002	PQN	C11-C12-C13	-9.00	111.81	126.79
13	H	1211	CLA	C4A-NA-C1A	8.99	110.75	106.71
14	H	2002	PQN	C11-C12-C13	-8.98	111.85	126.79
13	B	1211	CLA	C4A-NA-C1A	8.88	110.70	106.71

5 of 588 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	A	1011	CLA	ND
13	A	1013	CLA	ND
13	A	1102	CLA	ND
13	A	1103	CLA	ND
13	A	1104	CLA	ND

5 of 8073 torsion outliers are listed below:

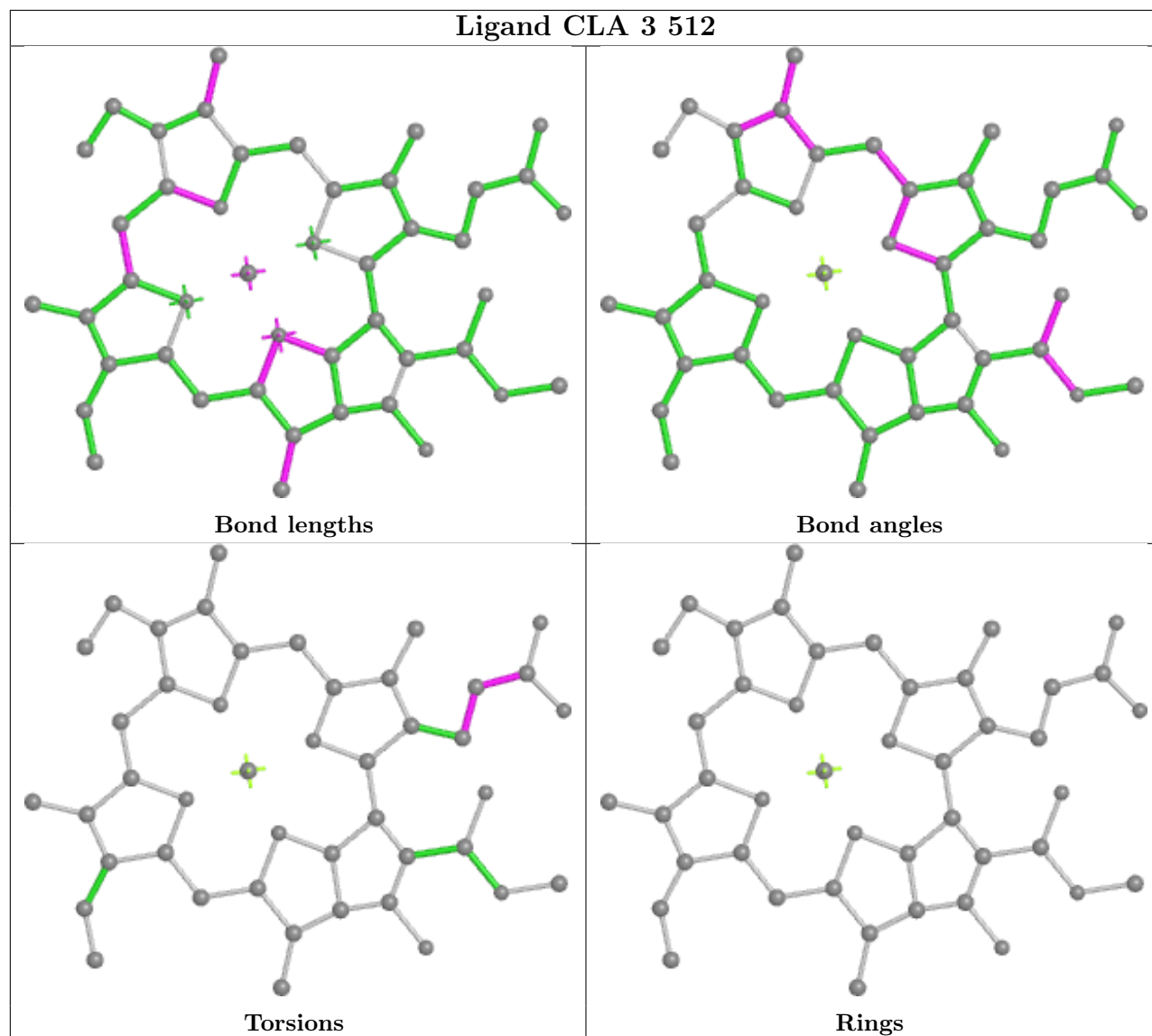
Mol	Chain	Res	Type	Atoms
13	A	1011	CLA	CHA-CBD-CGD-O1D
13	A	1102	CLA	C3A-C2A-CAA-CBA
13	A	1103	CLA	C1A-C2A-CAA-CBA
13	A	1103	CLA	CHA-CBD-CGD-O1D
13	A	1103	CLA	CHA-CBD-CGD-O2D

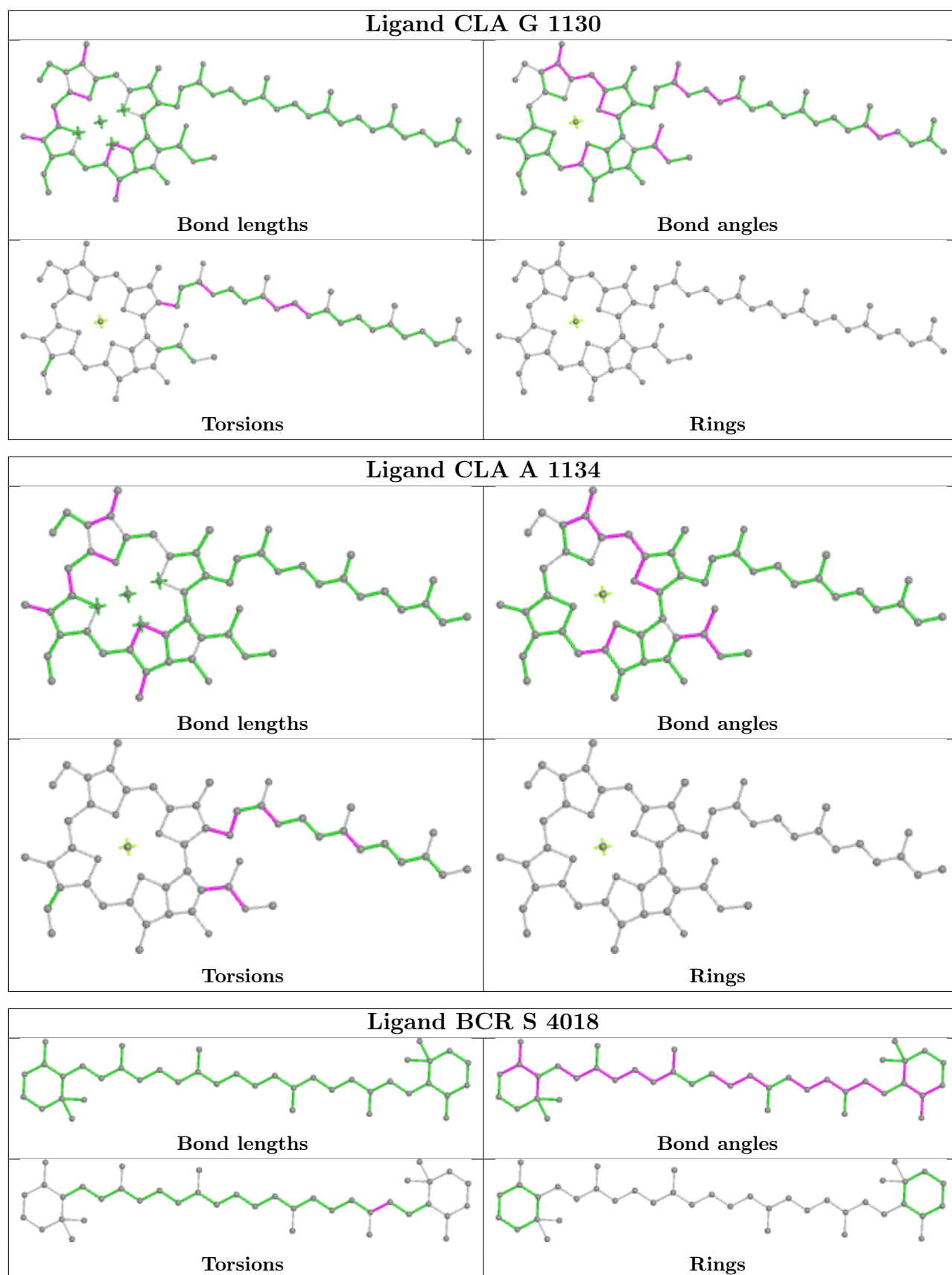
There are no ring outliers.

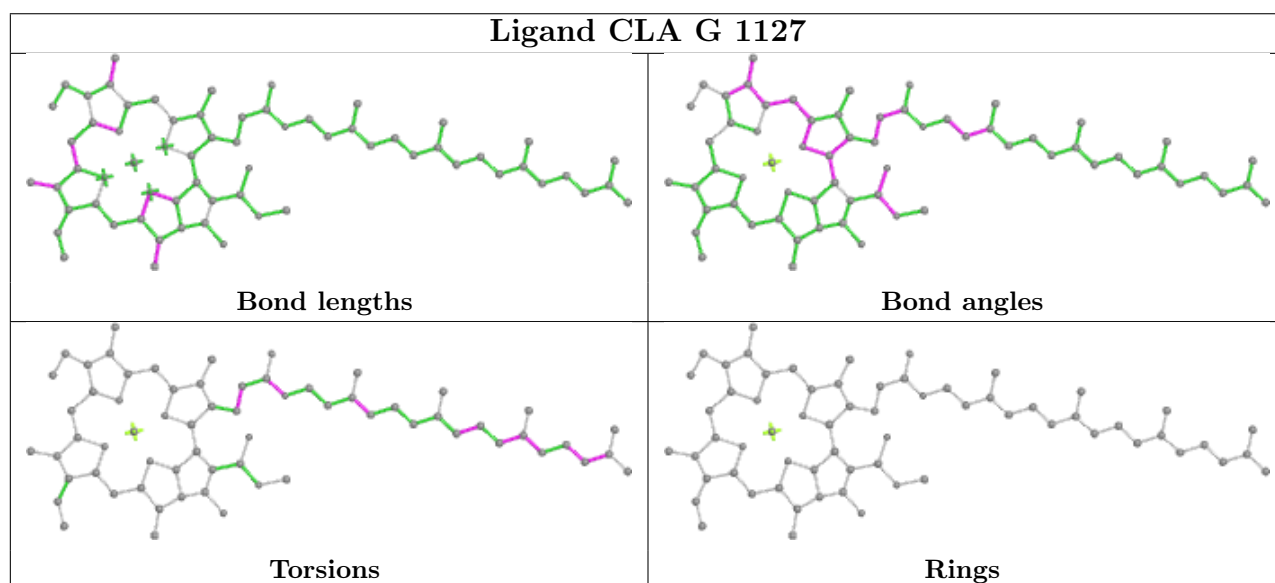
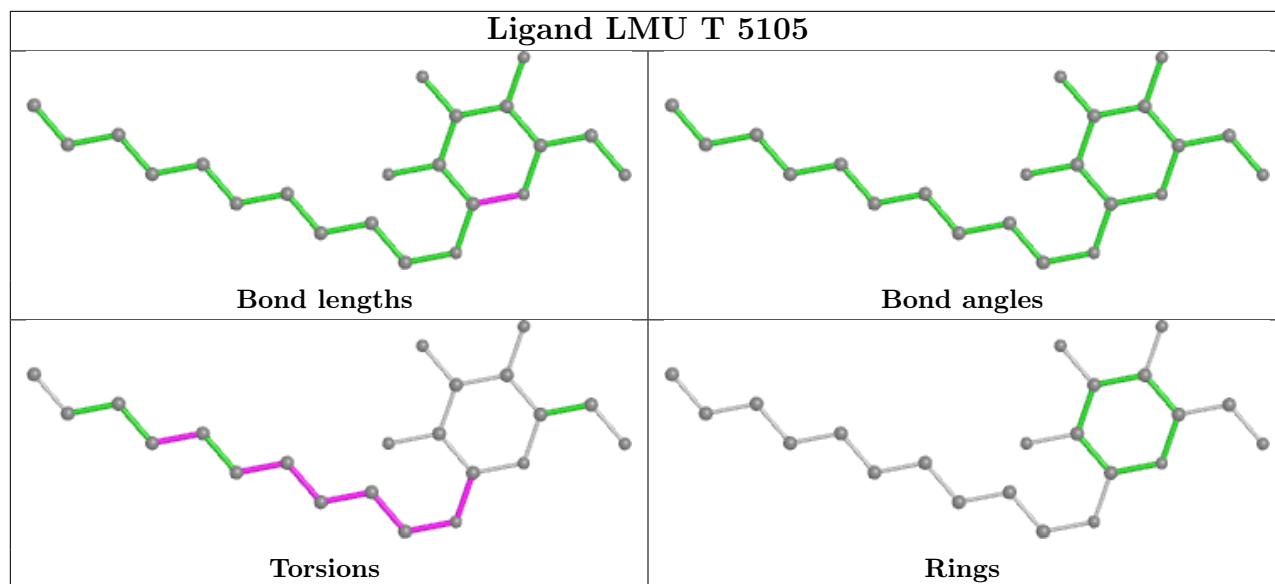
No monomer is involved in short contacts.

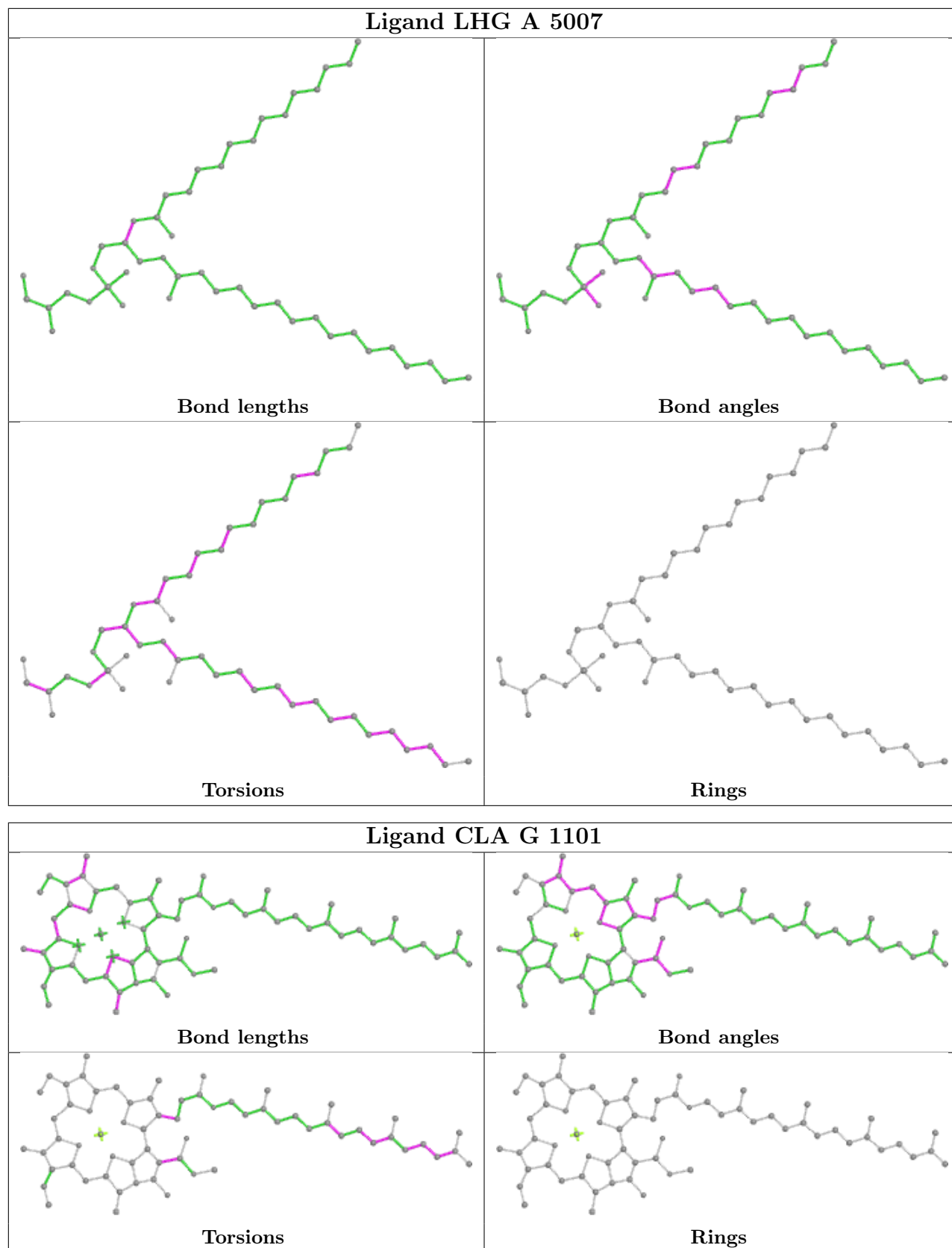
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

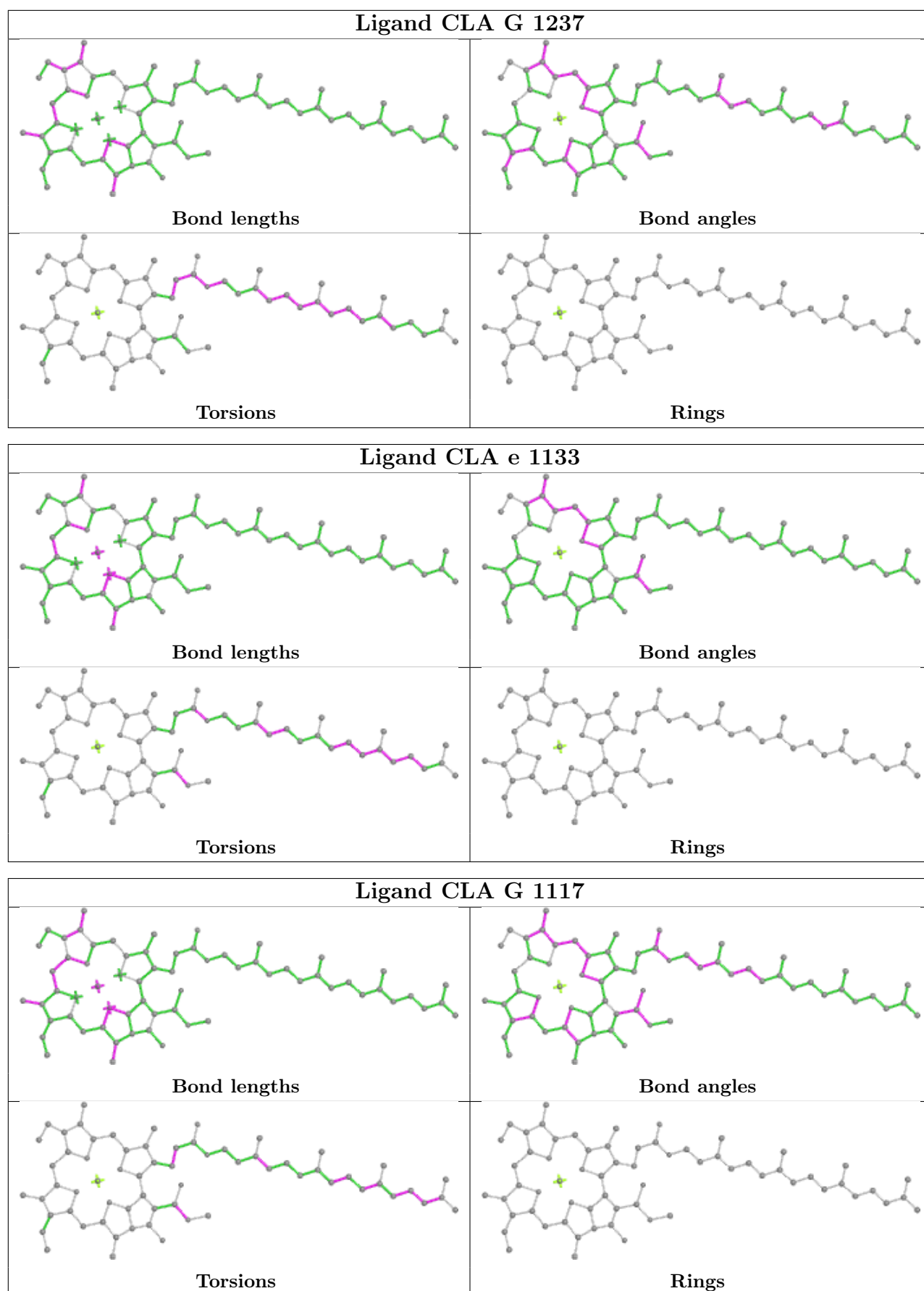
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

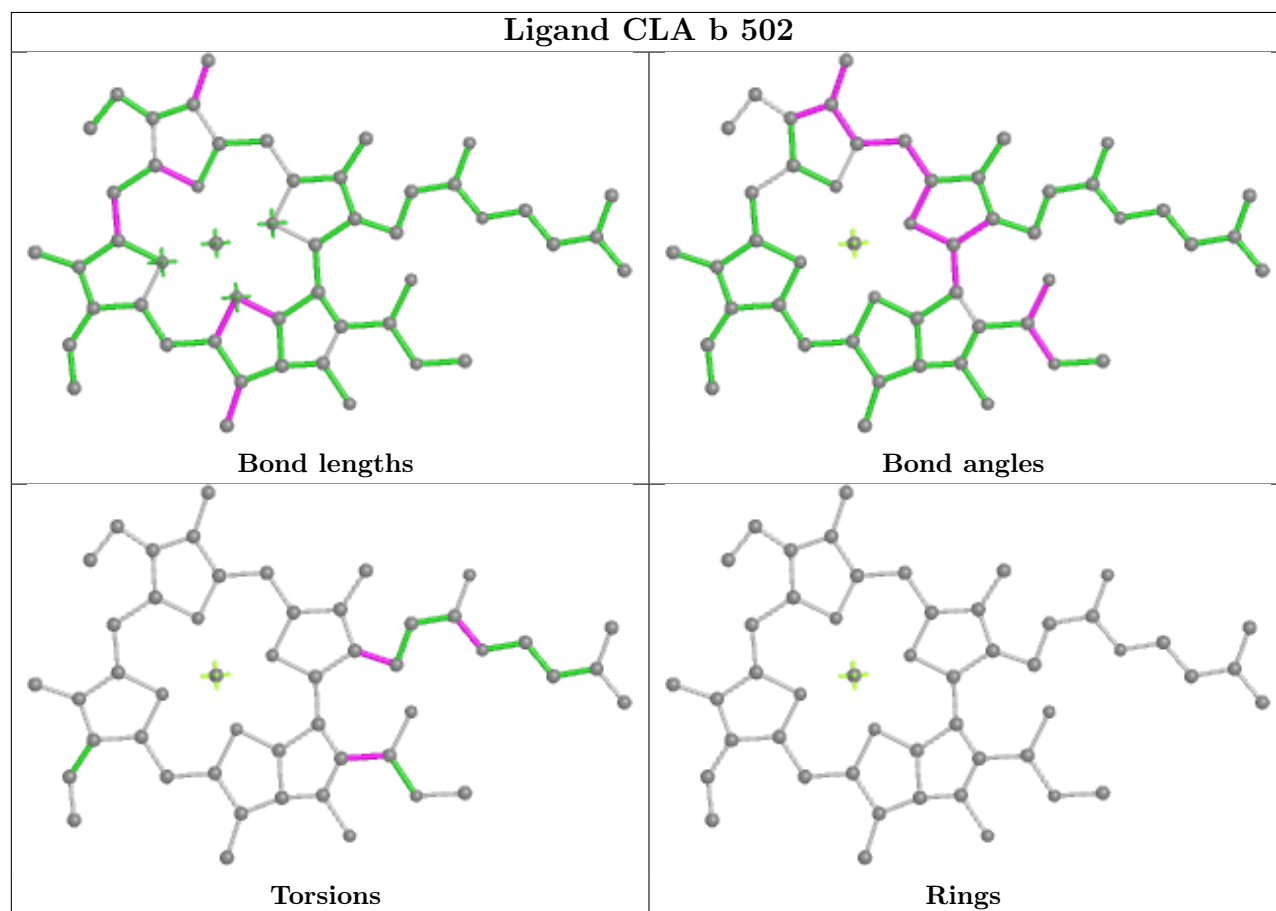
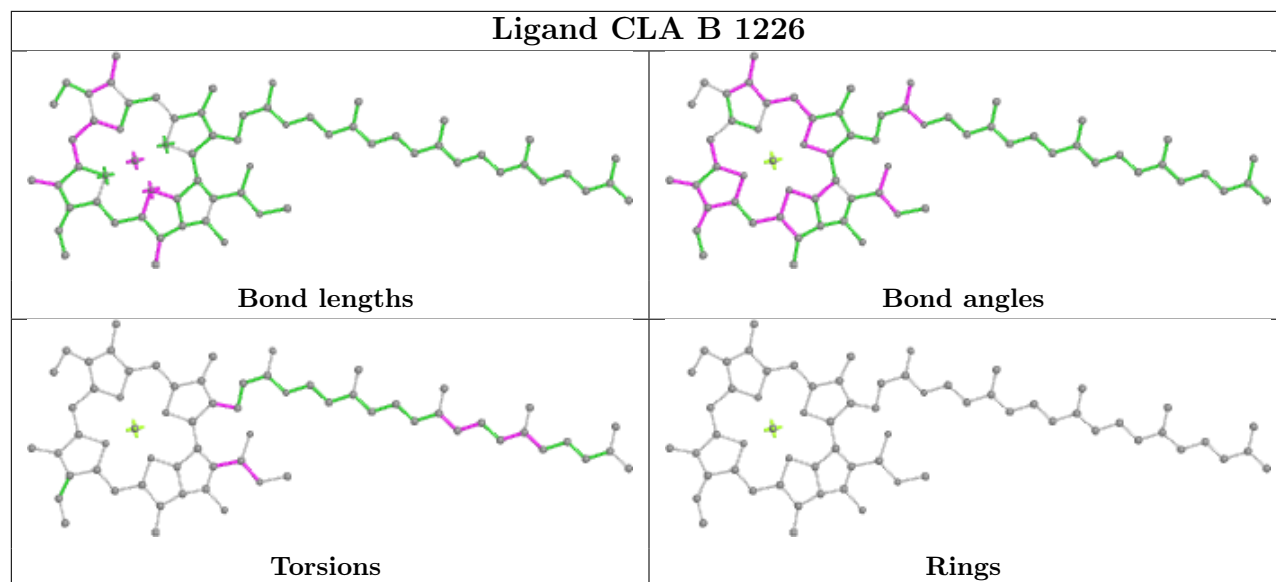




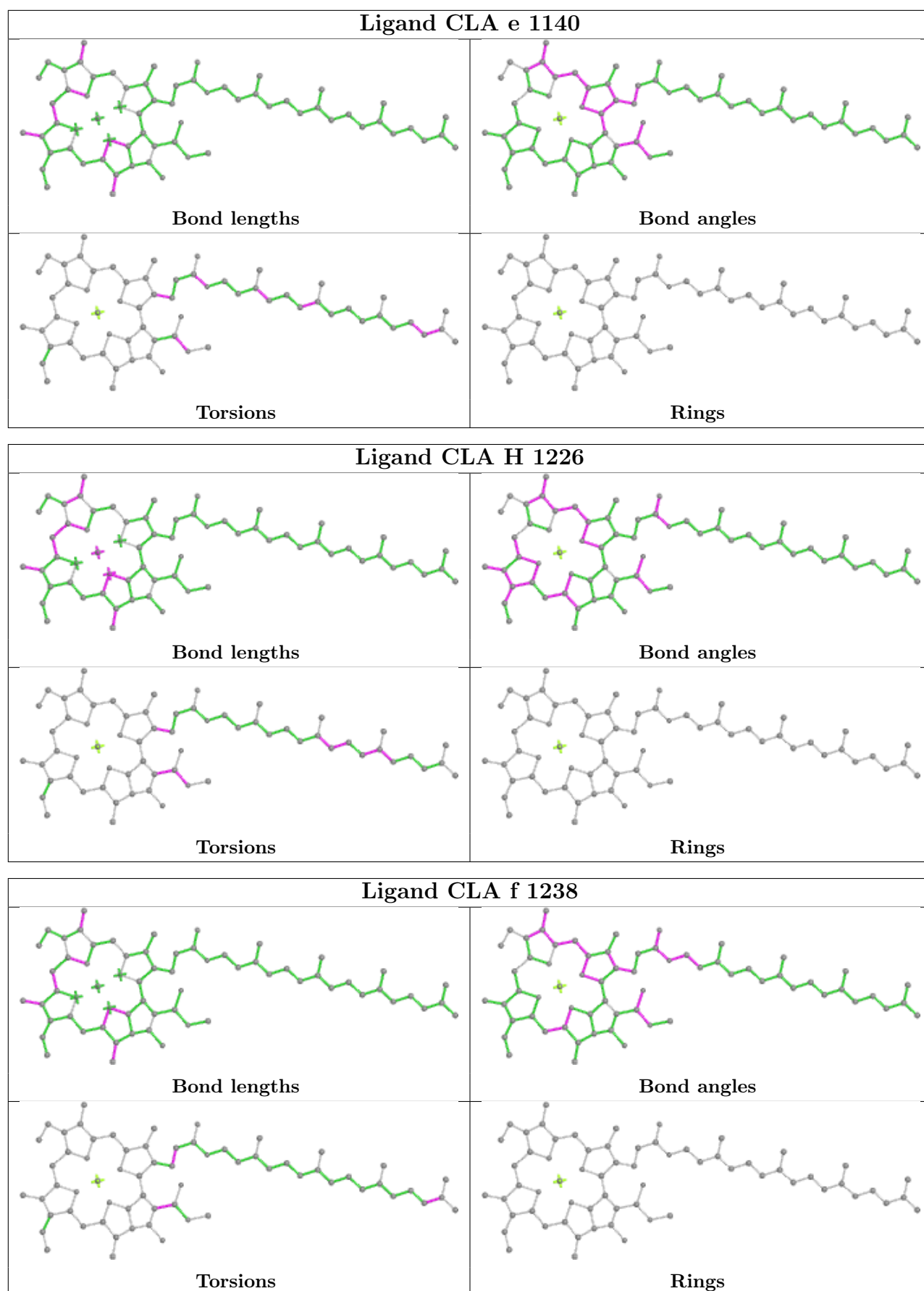


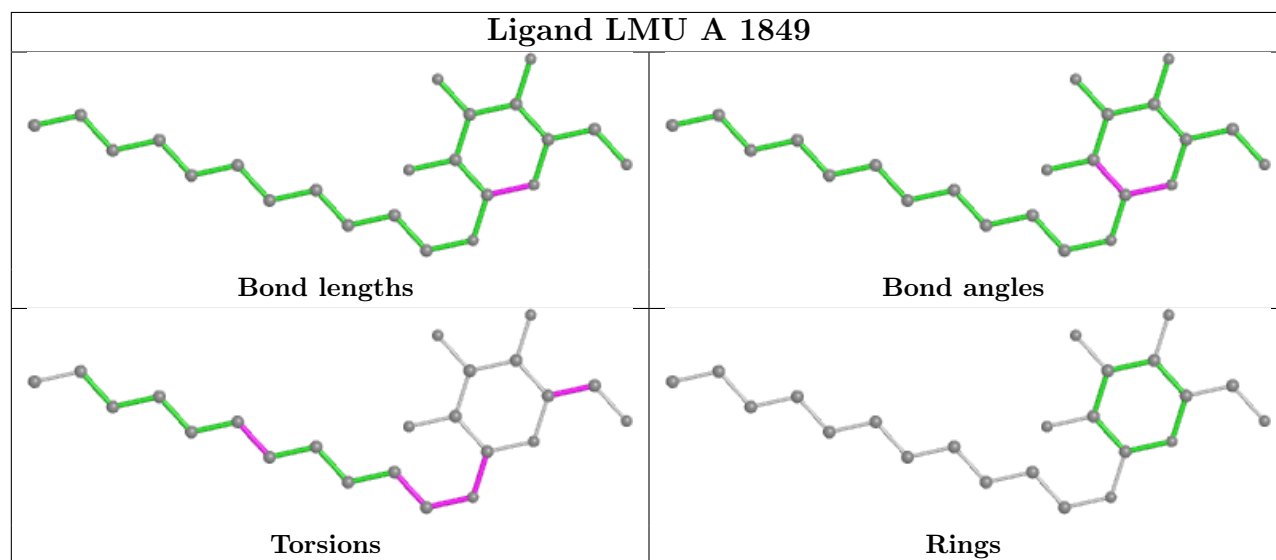
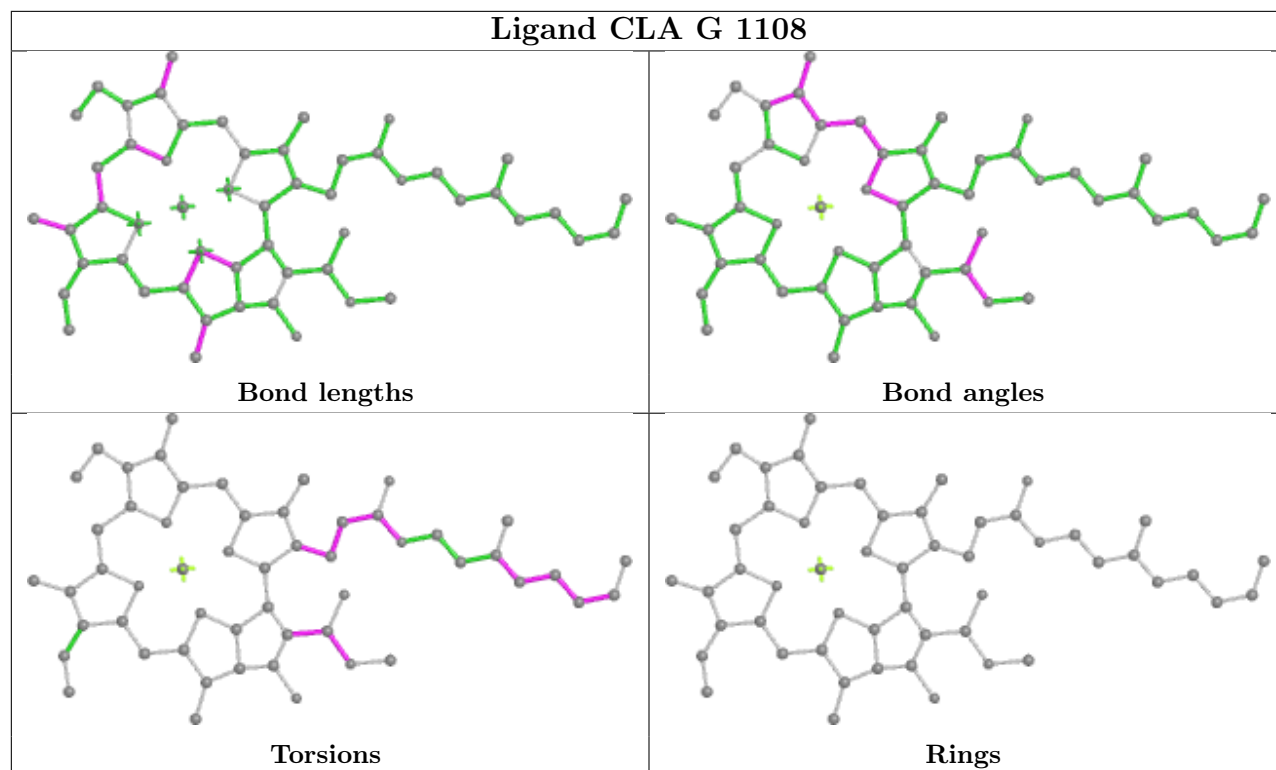


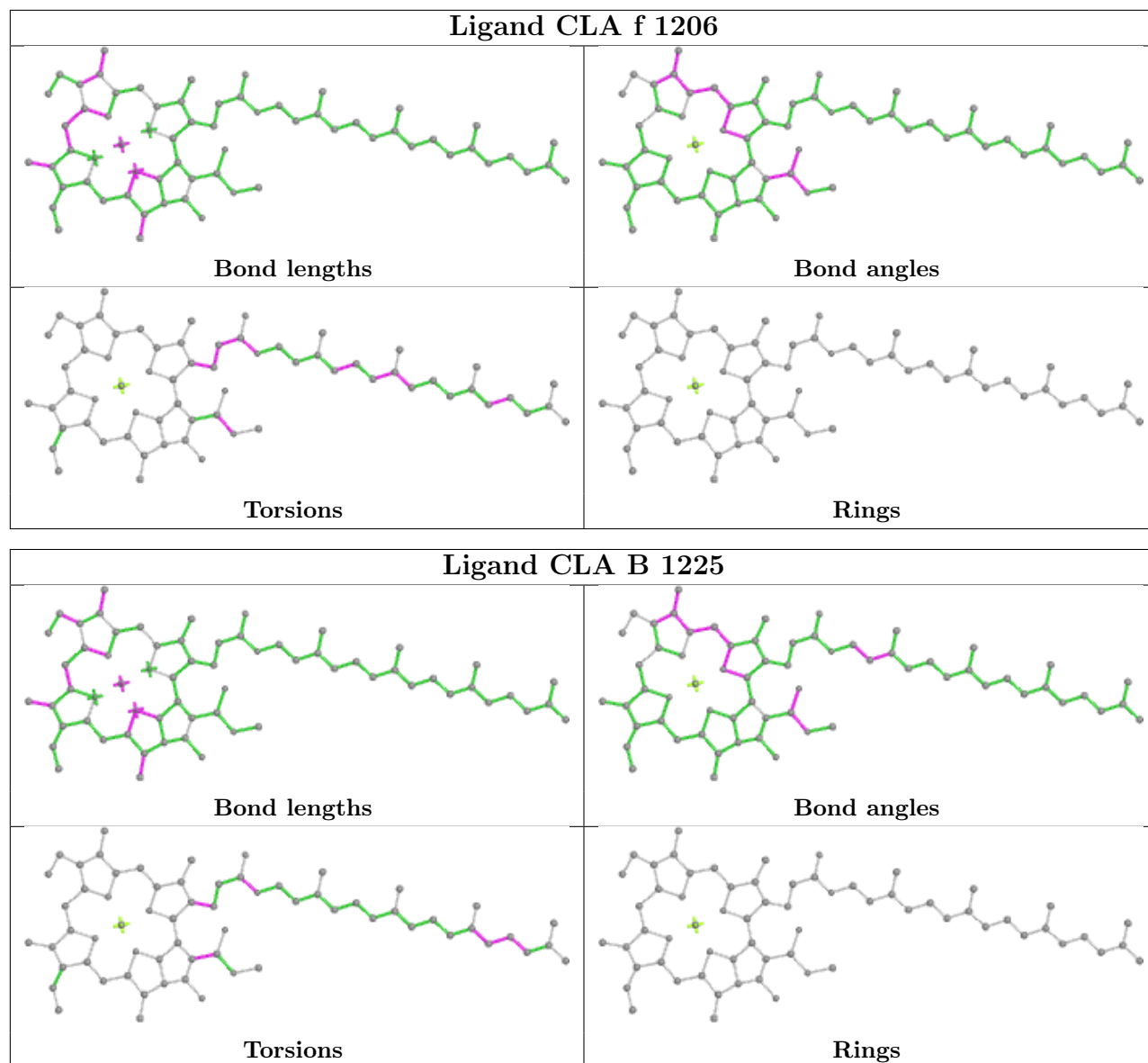


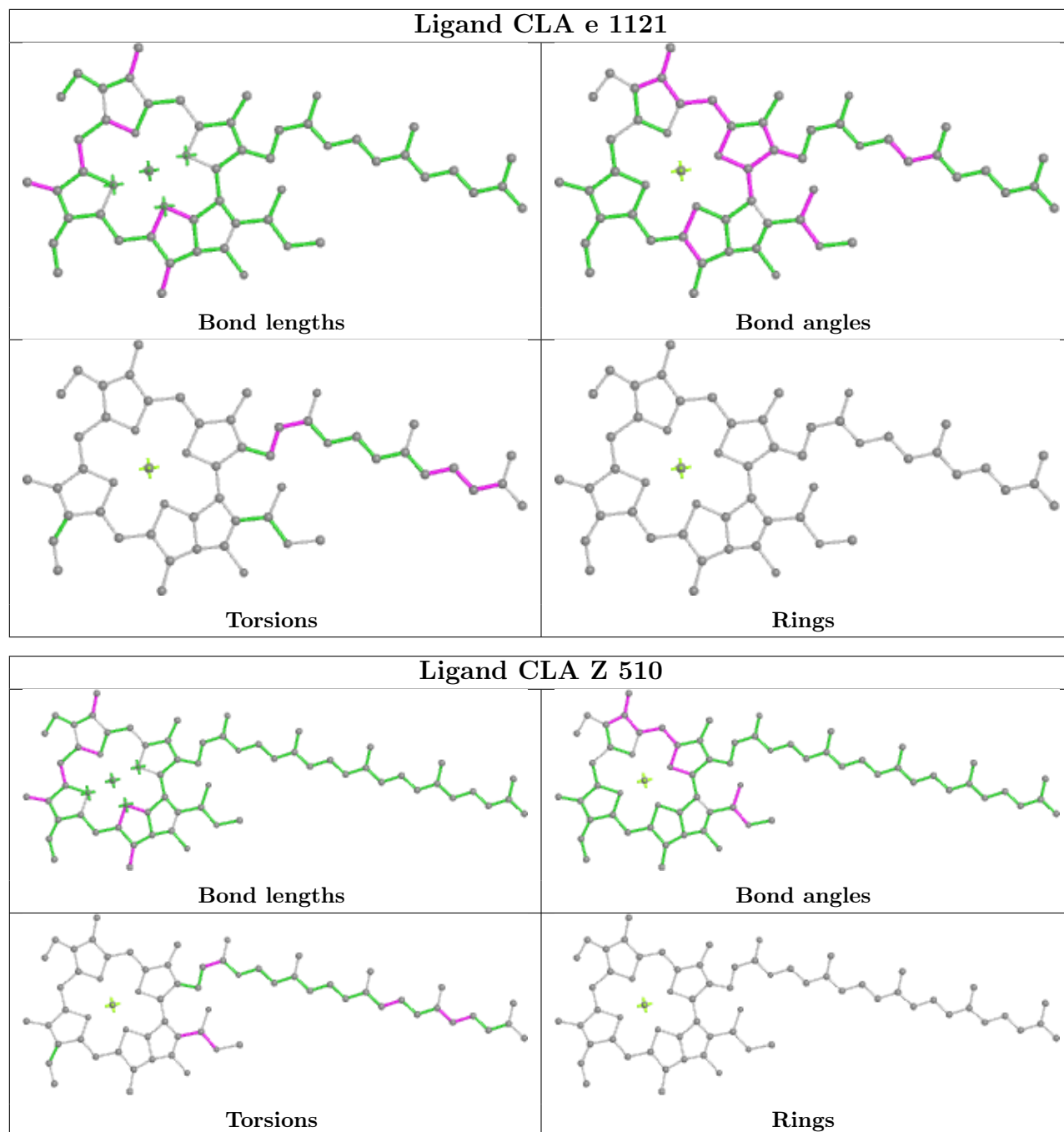


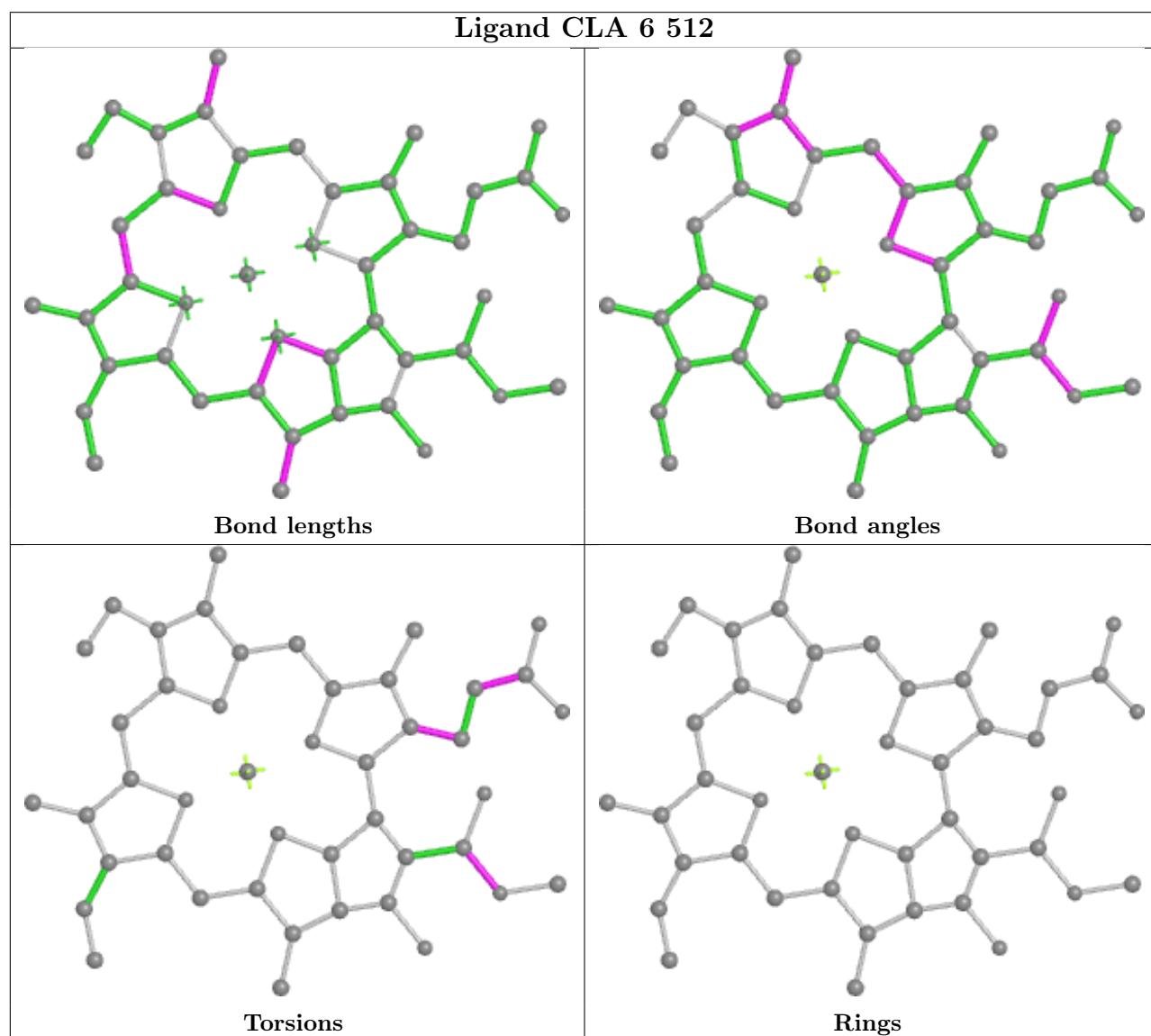
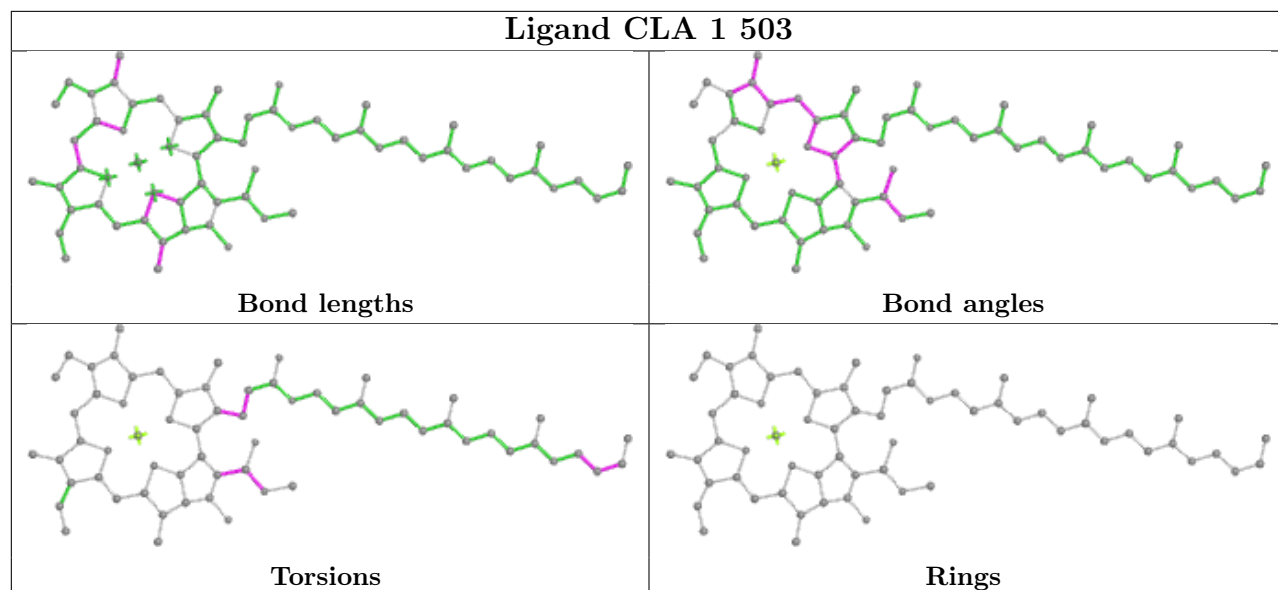


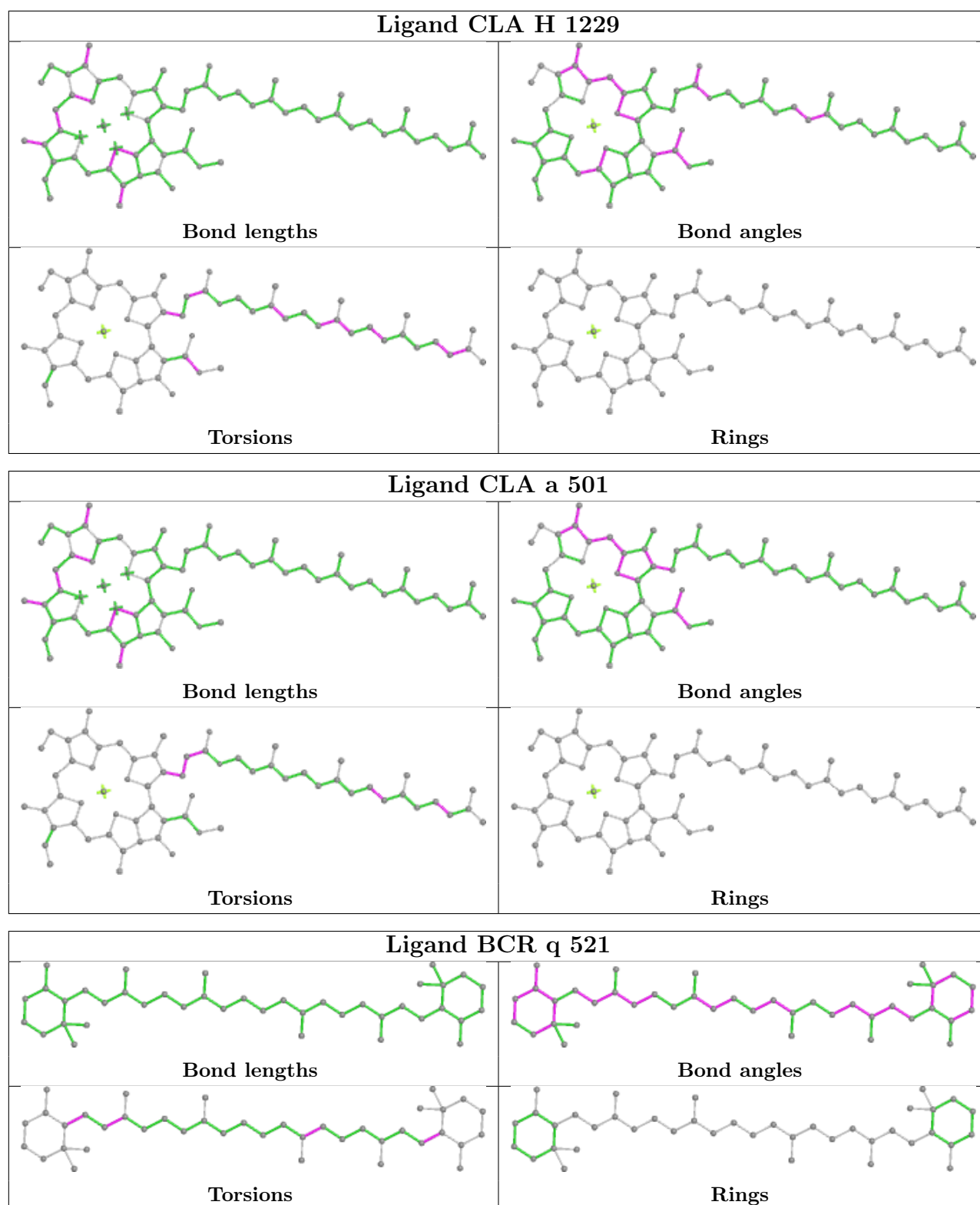


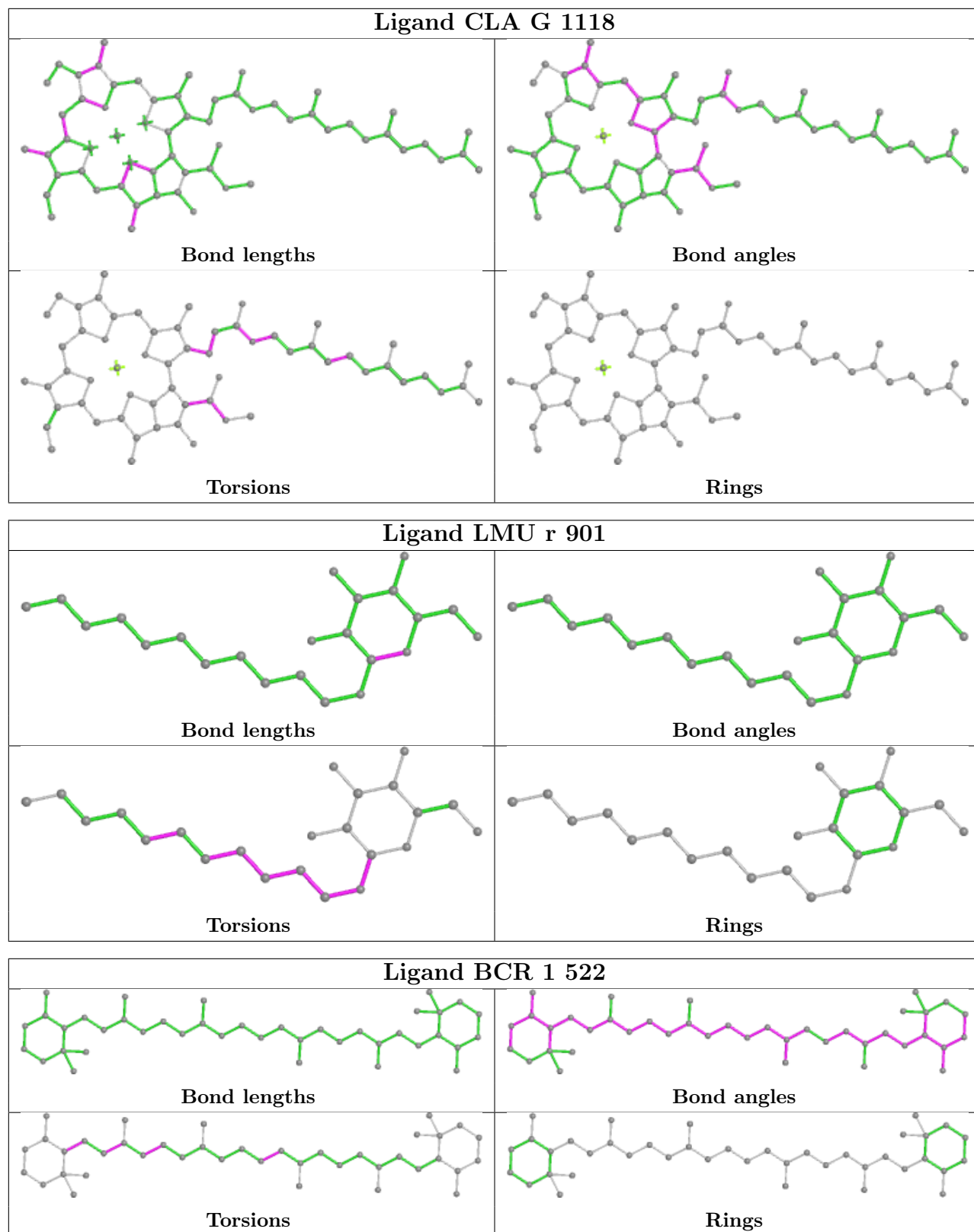


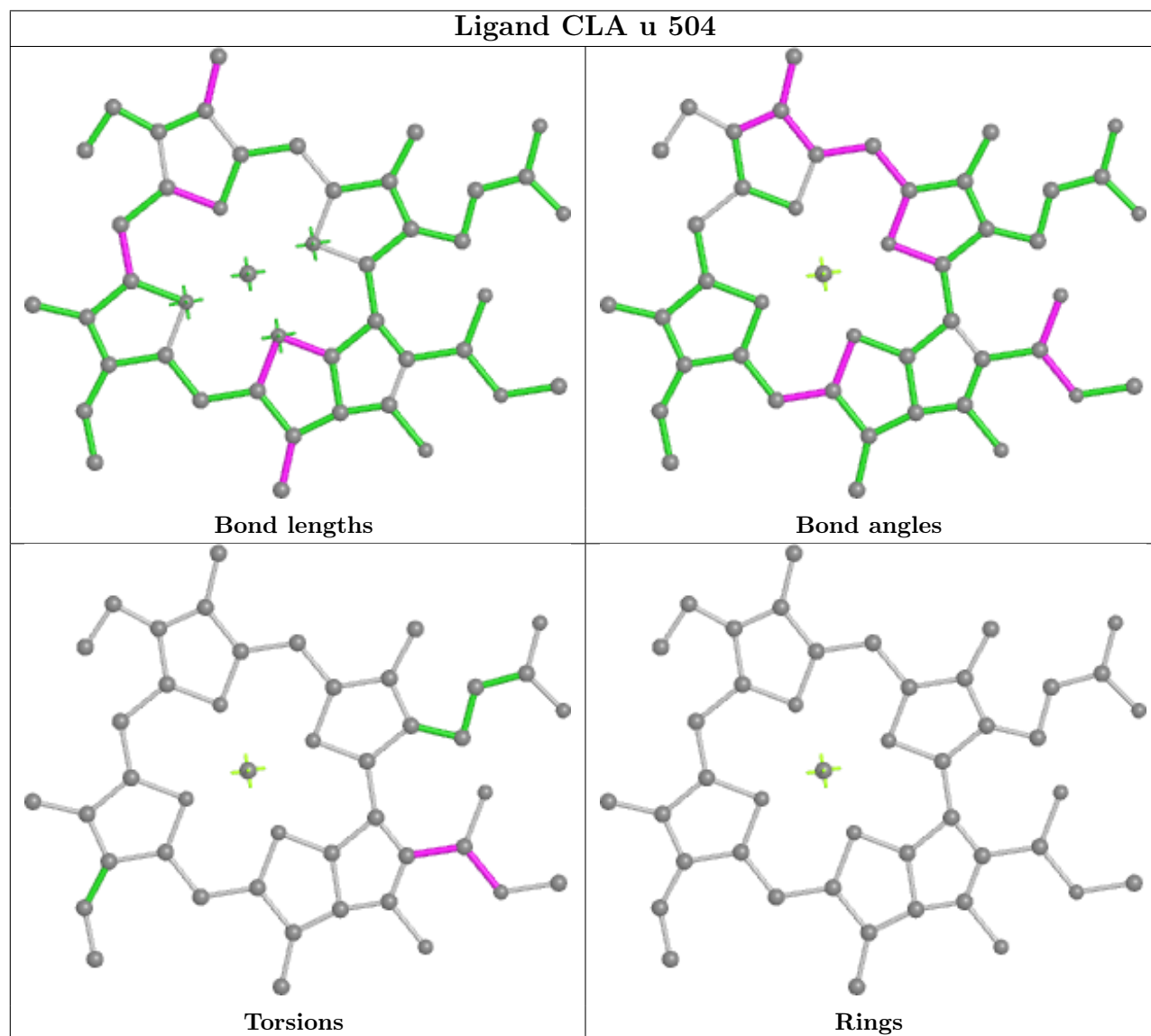
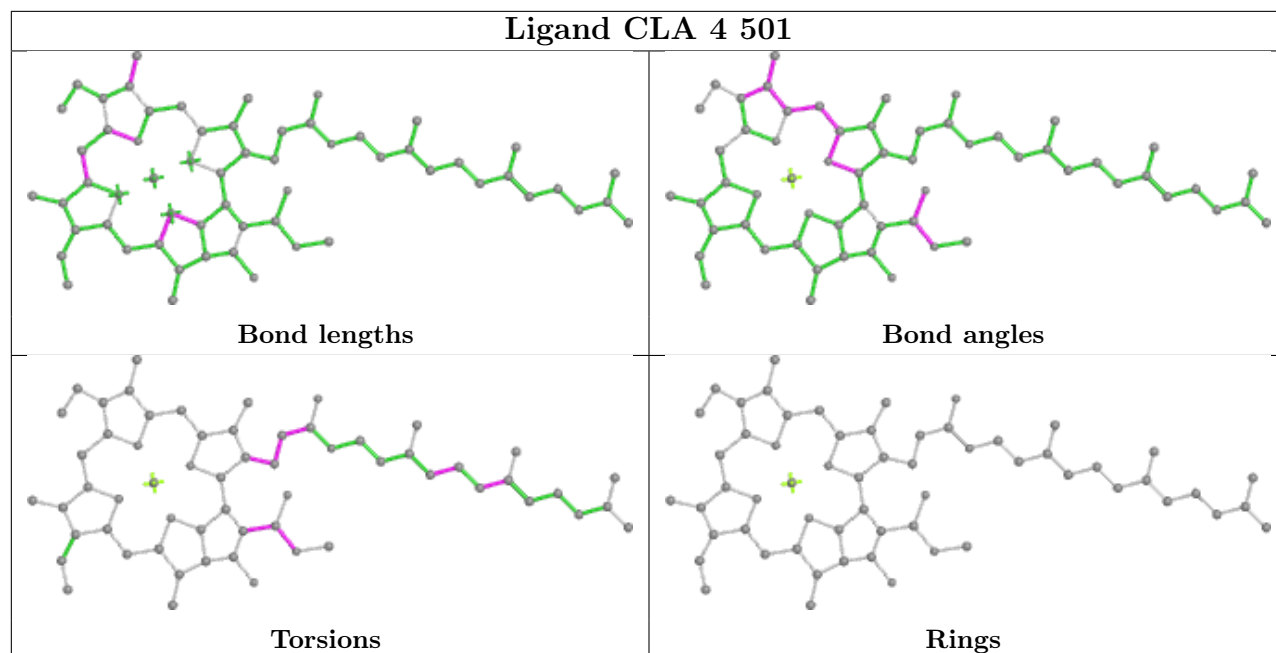




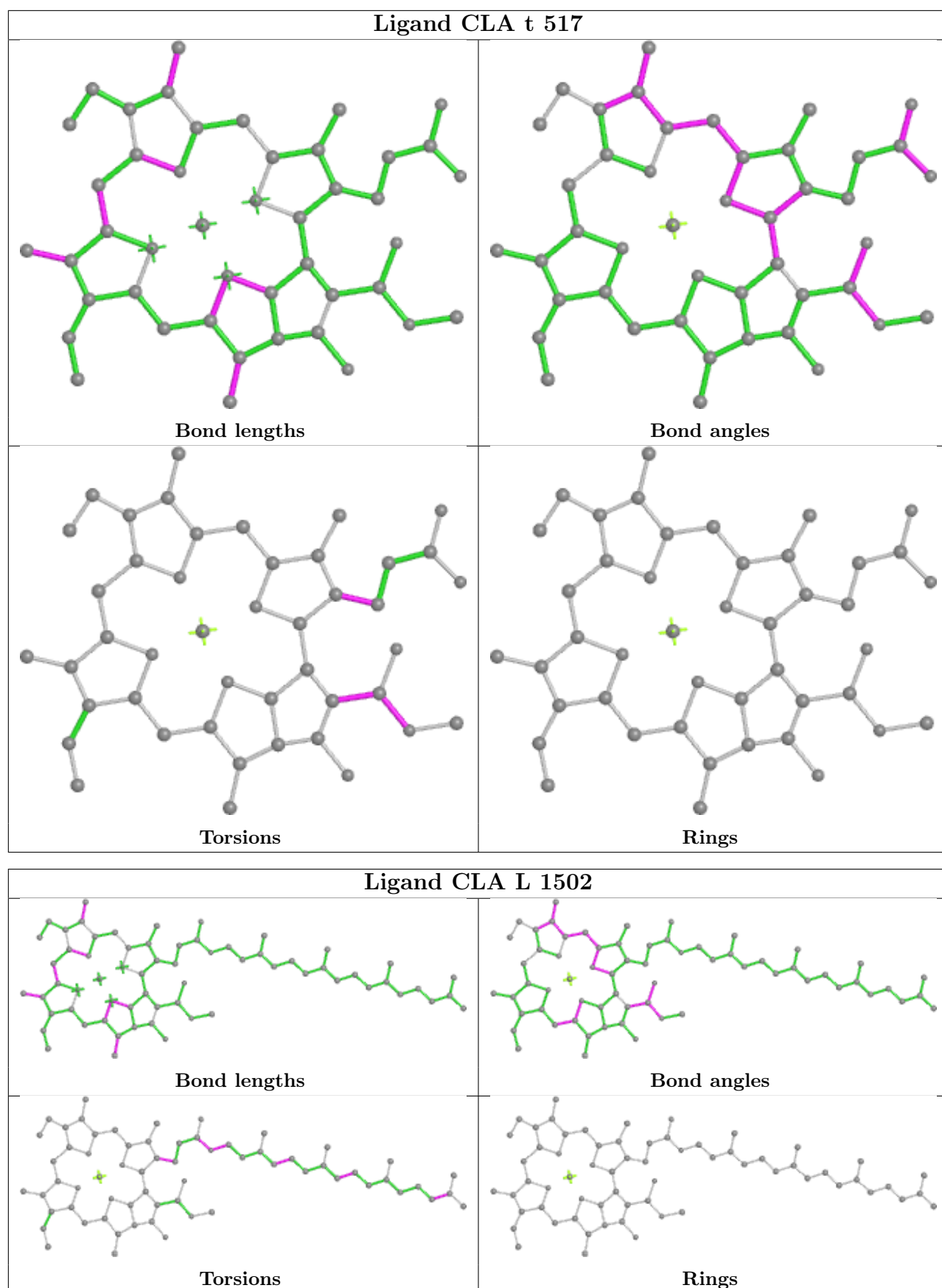


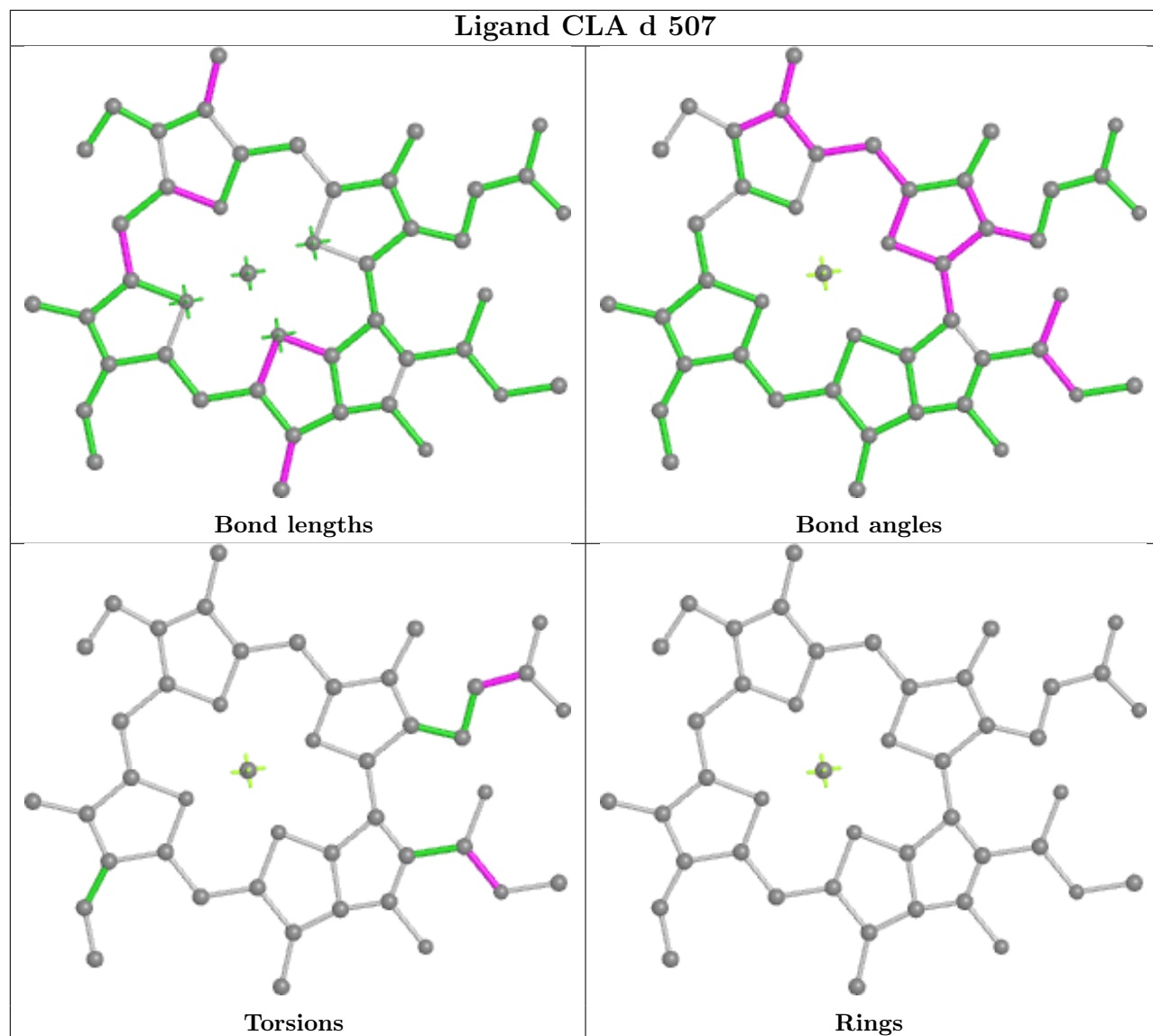


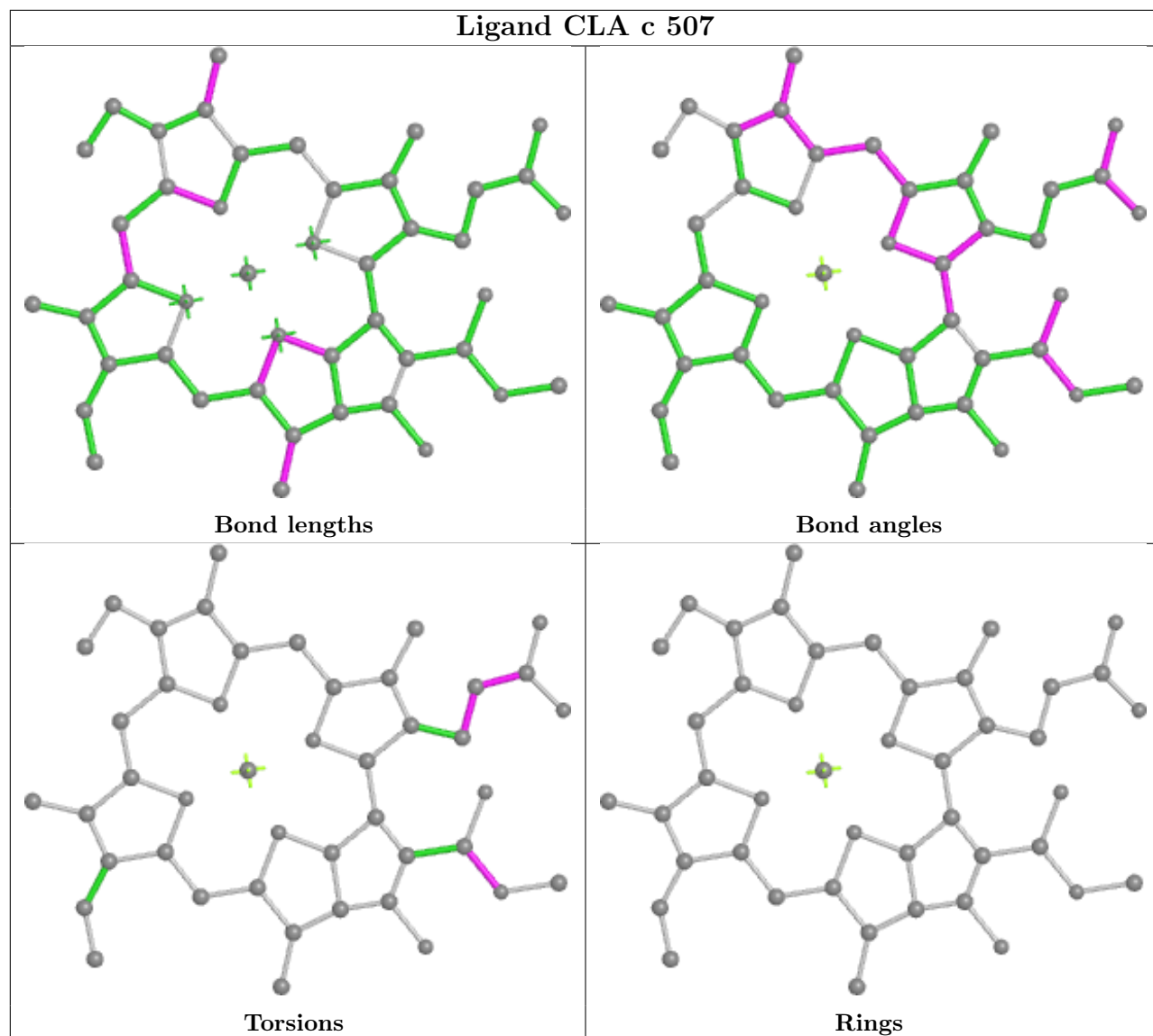


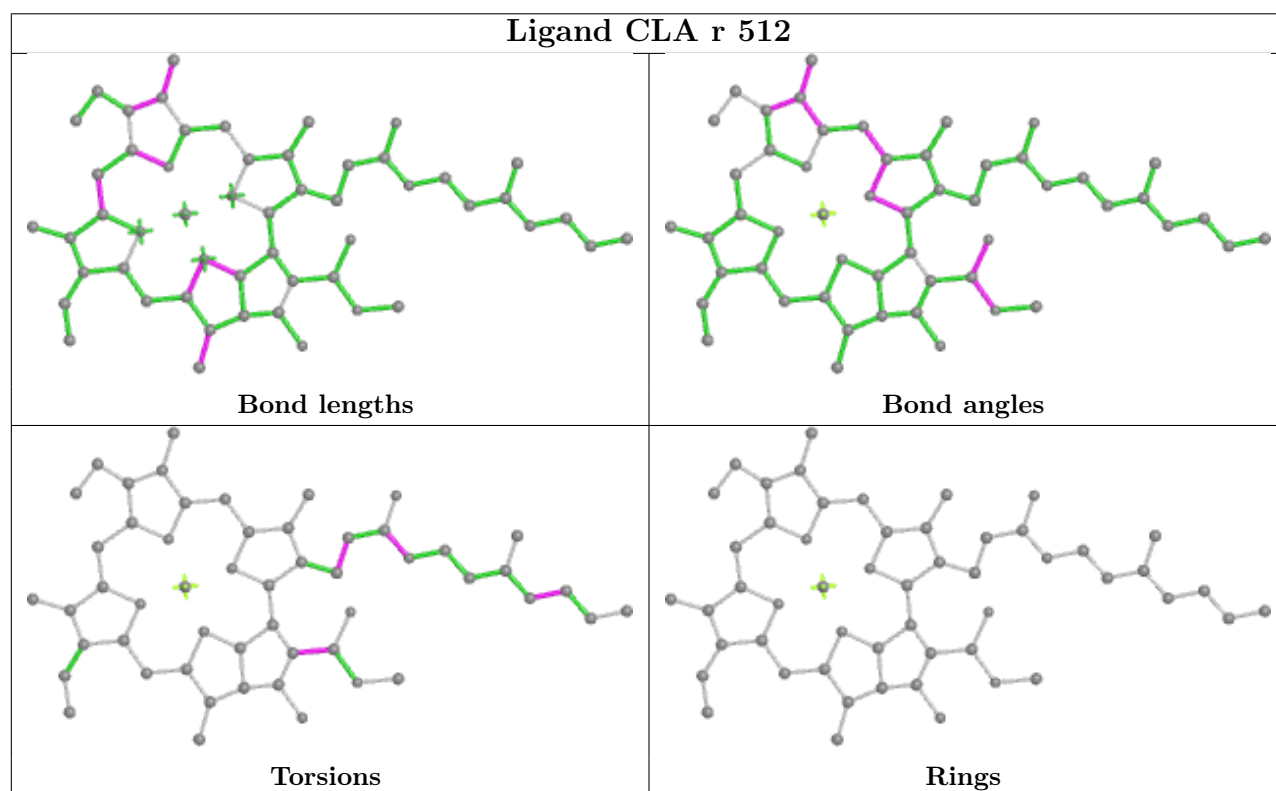
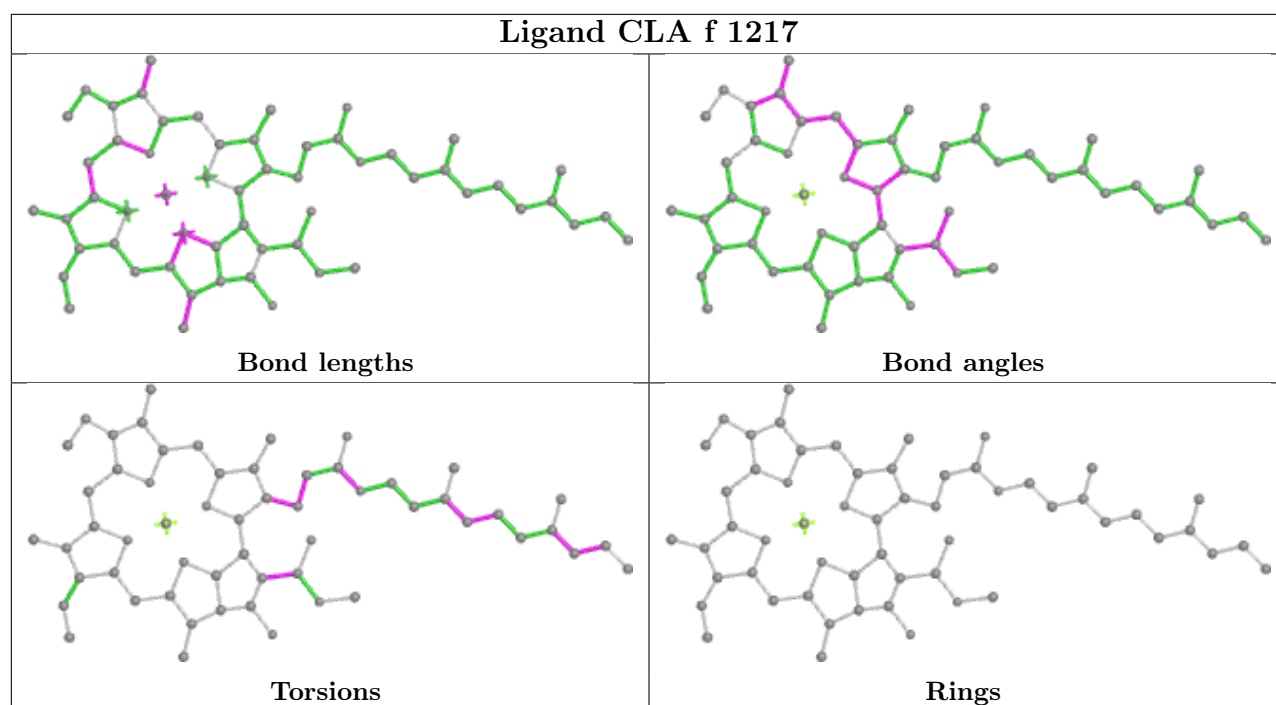


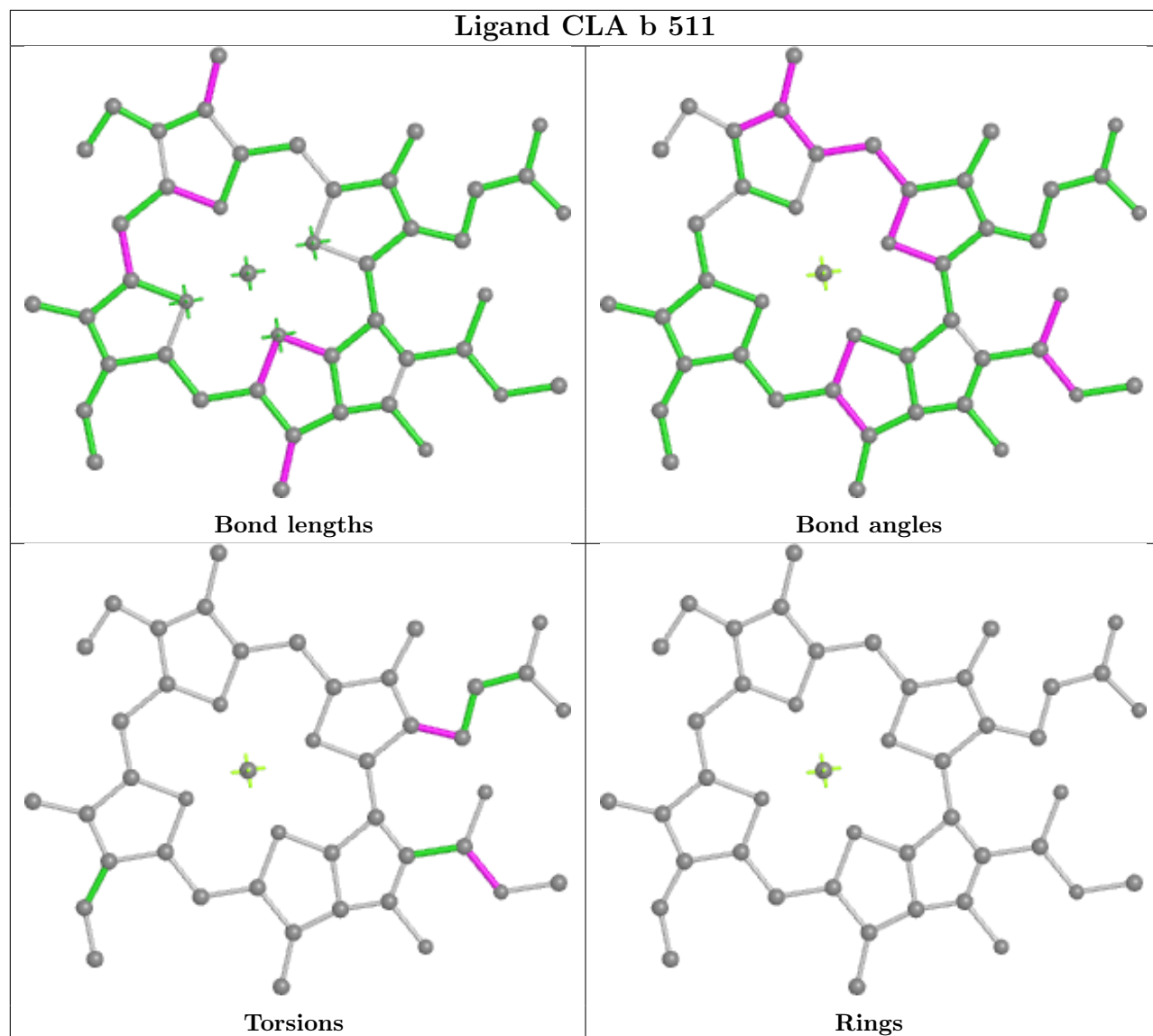


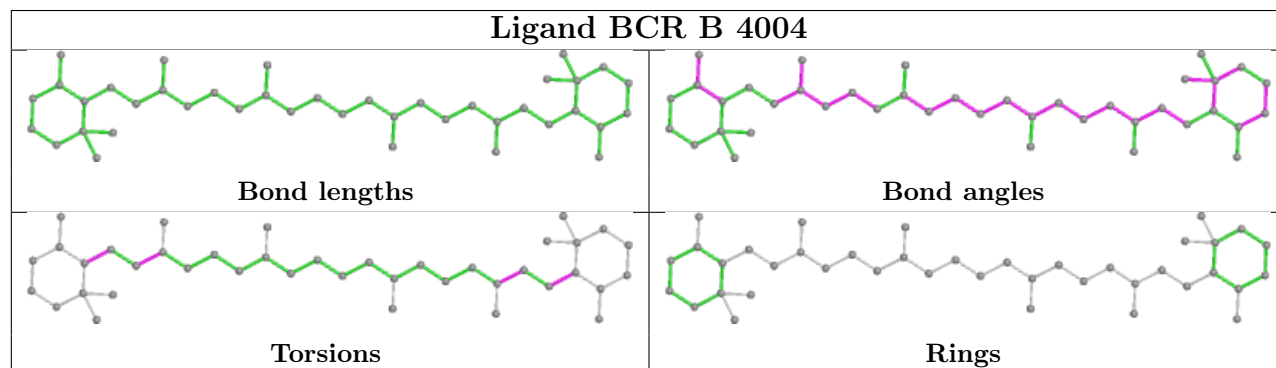
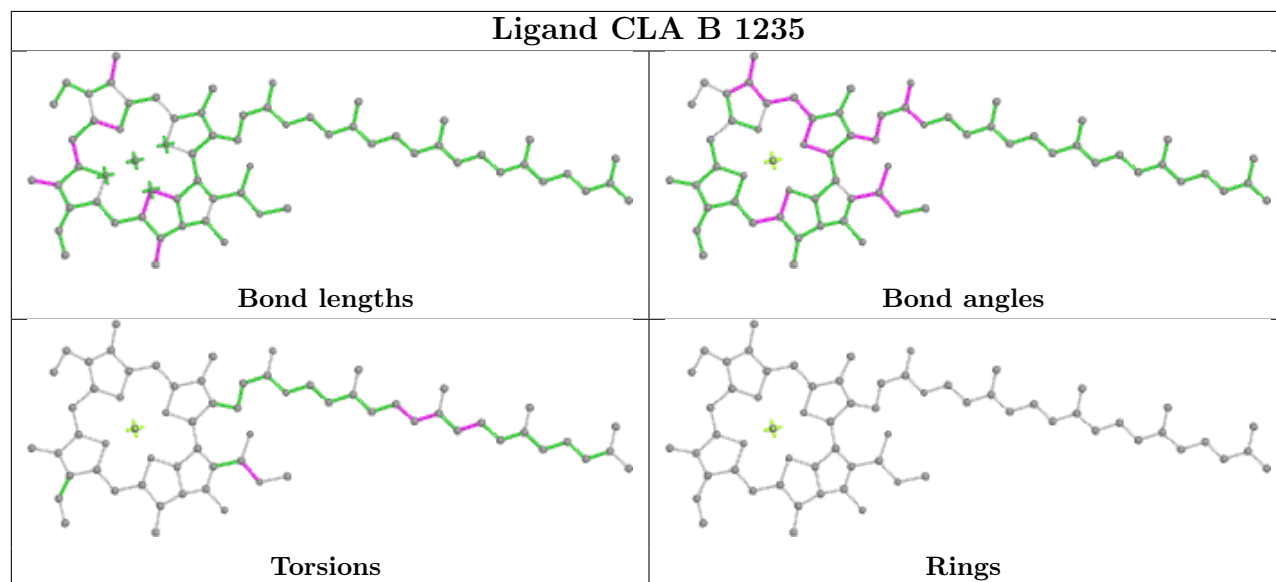
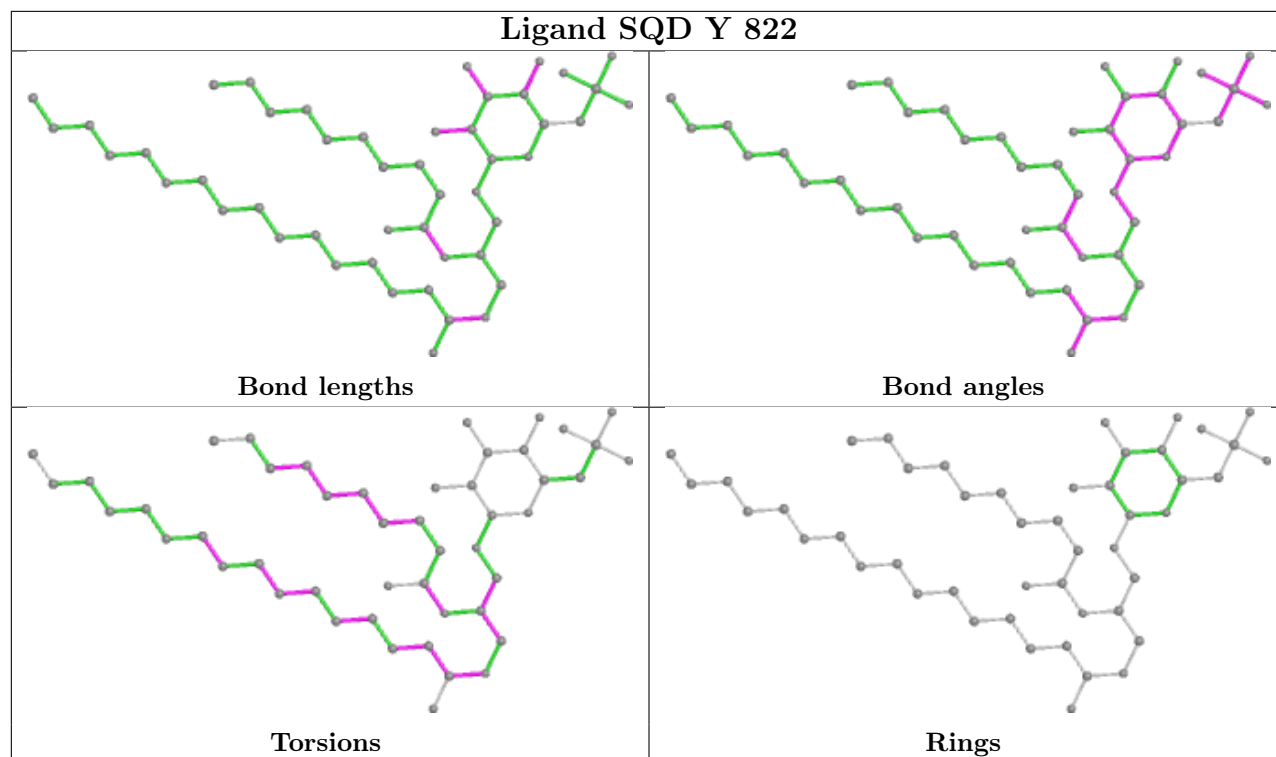


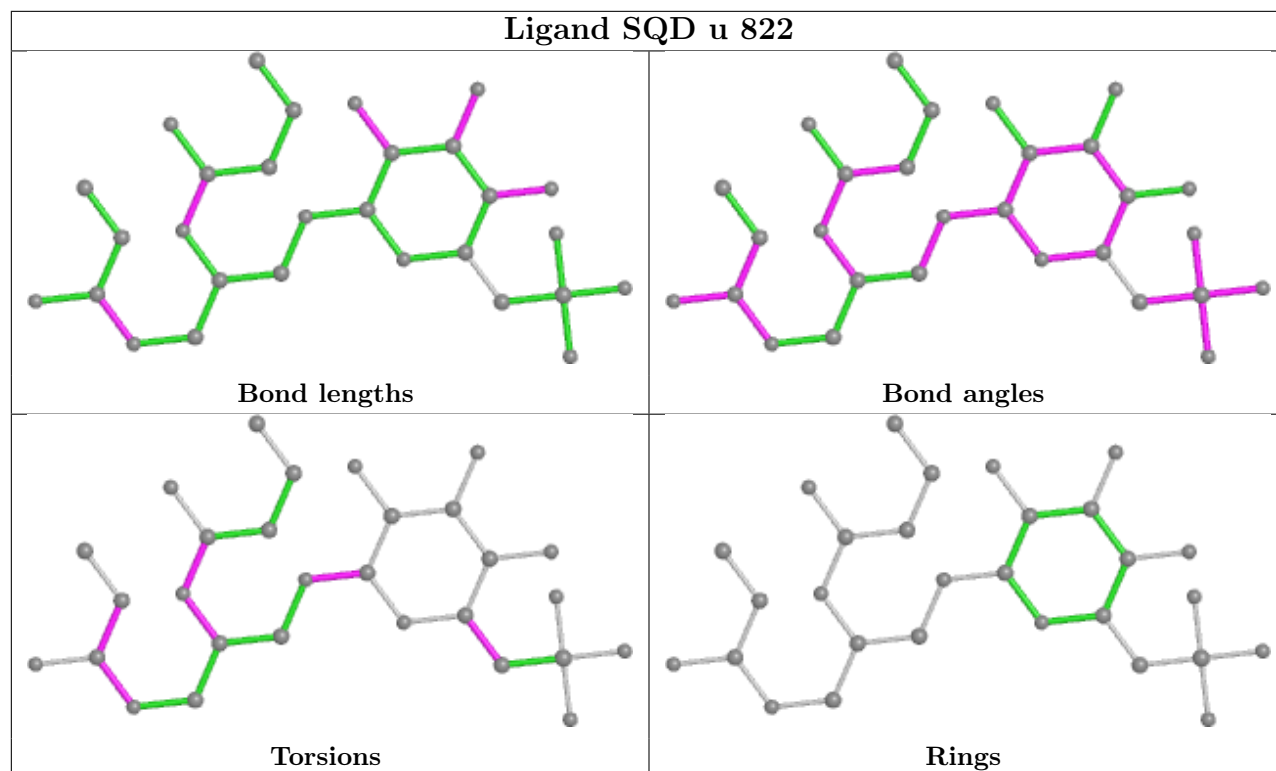
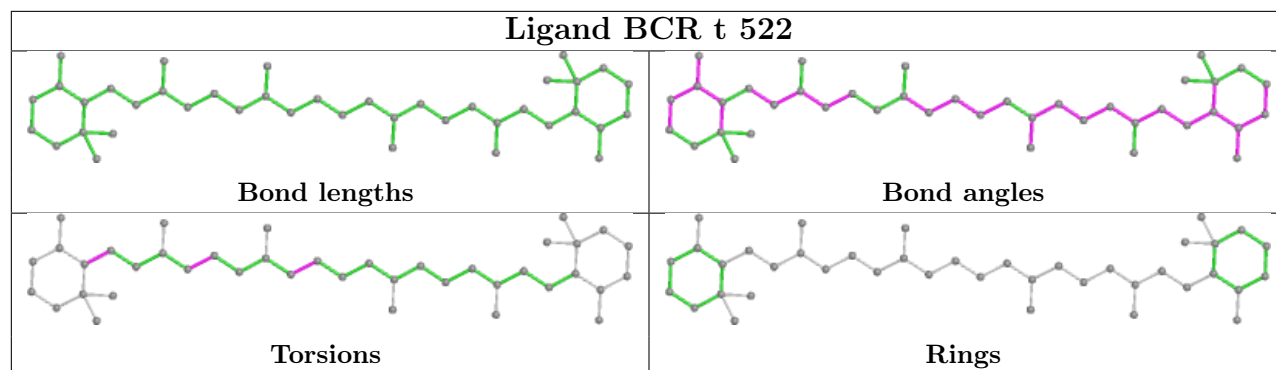


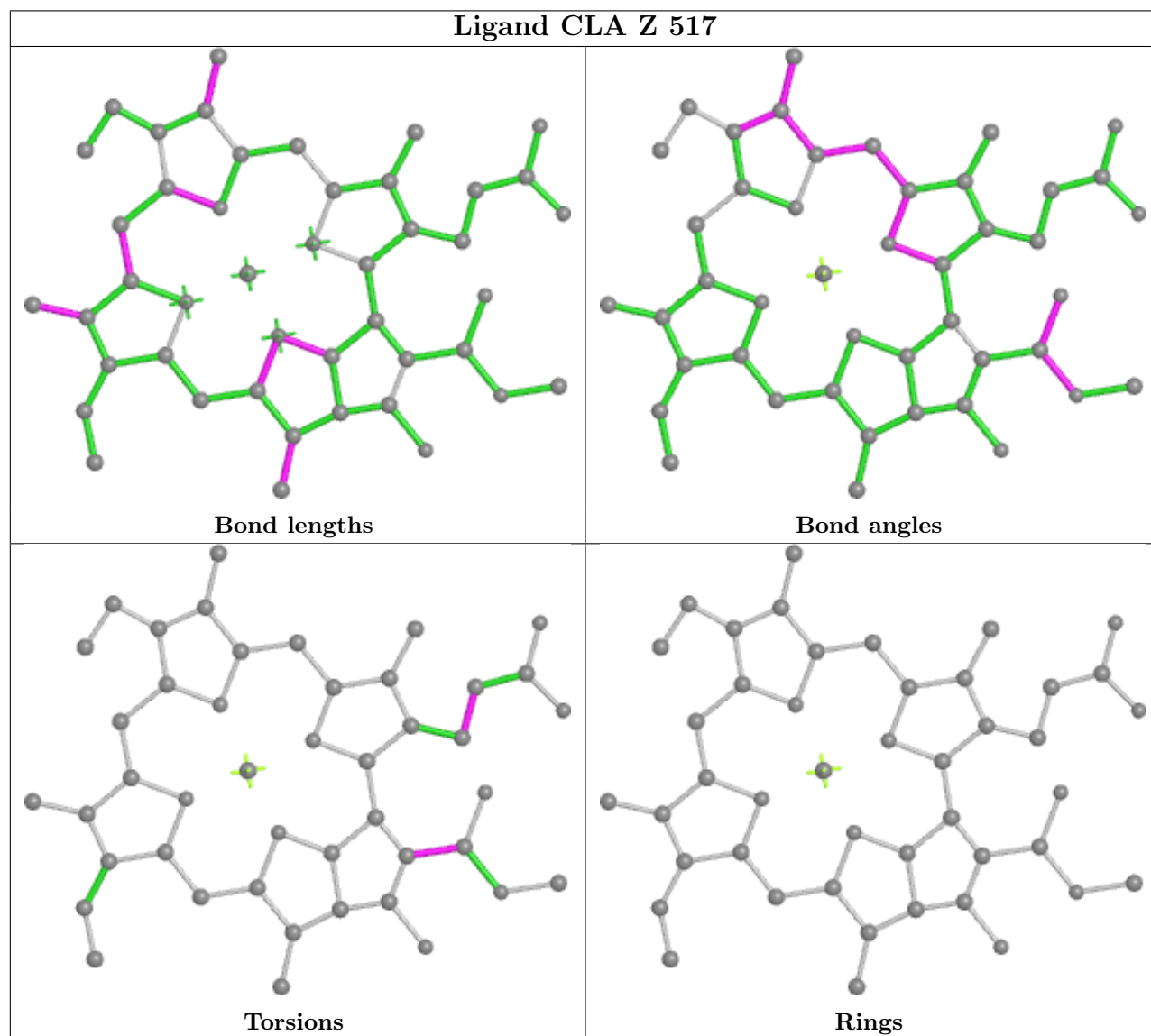
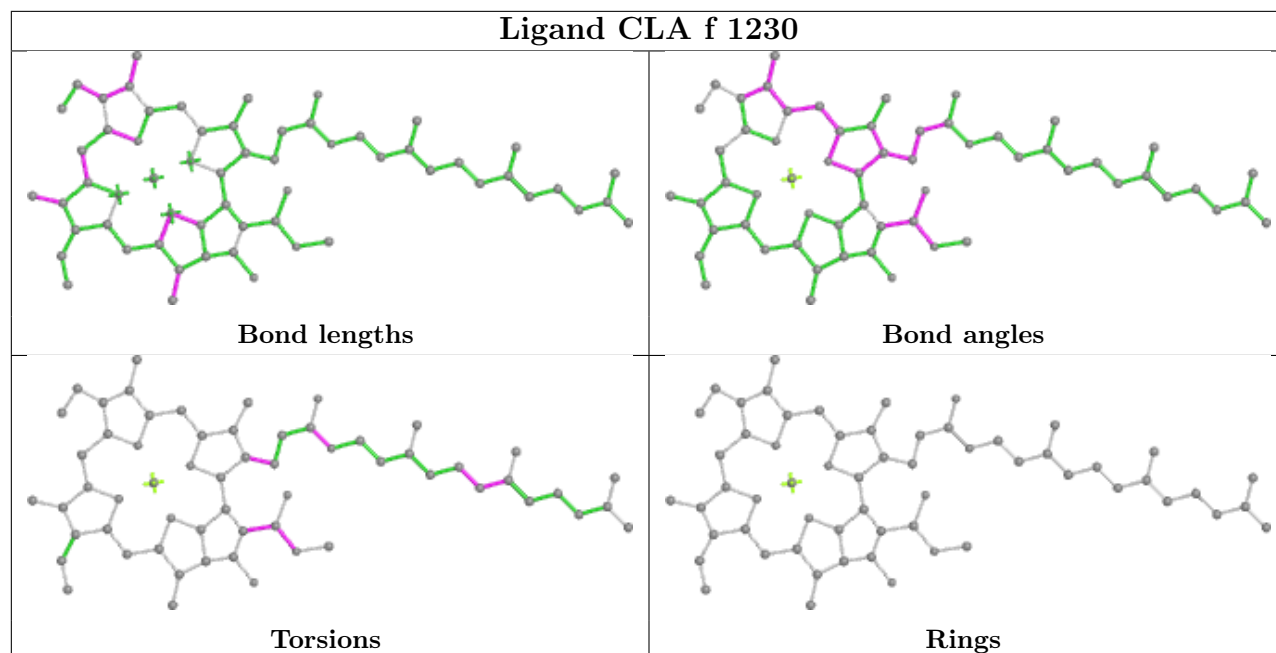




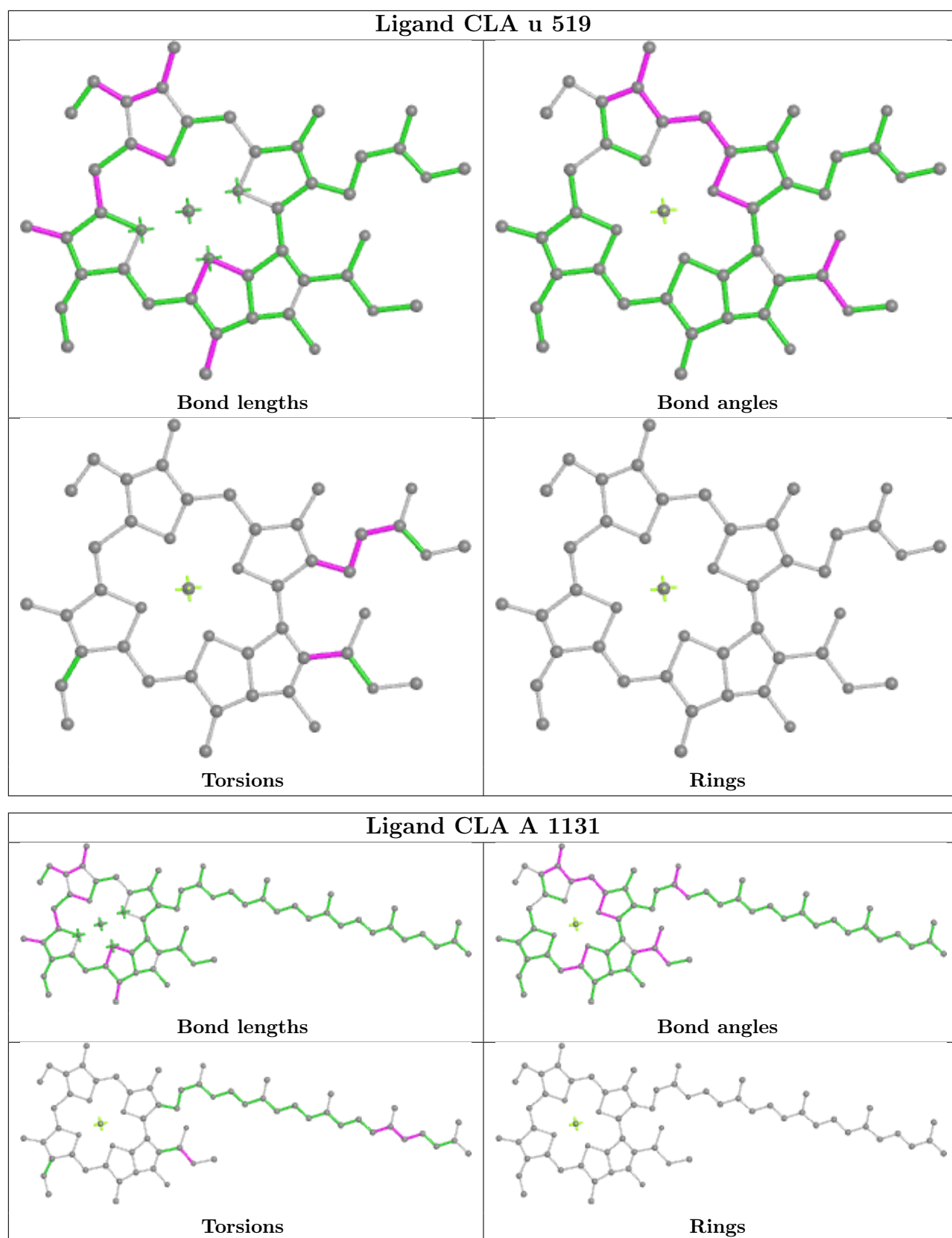


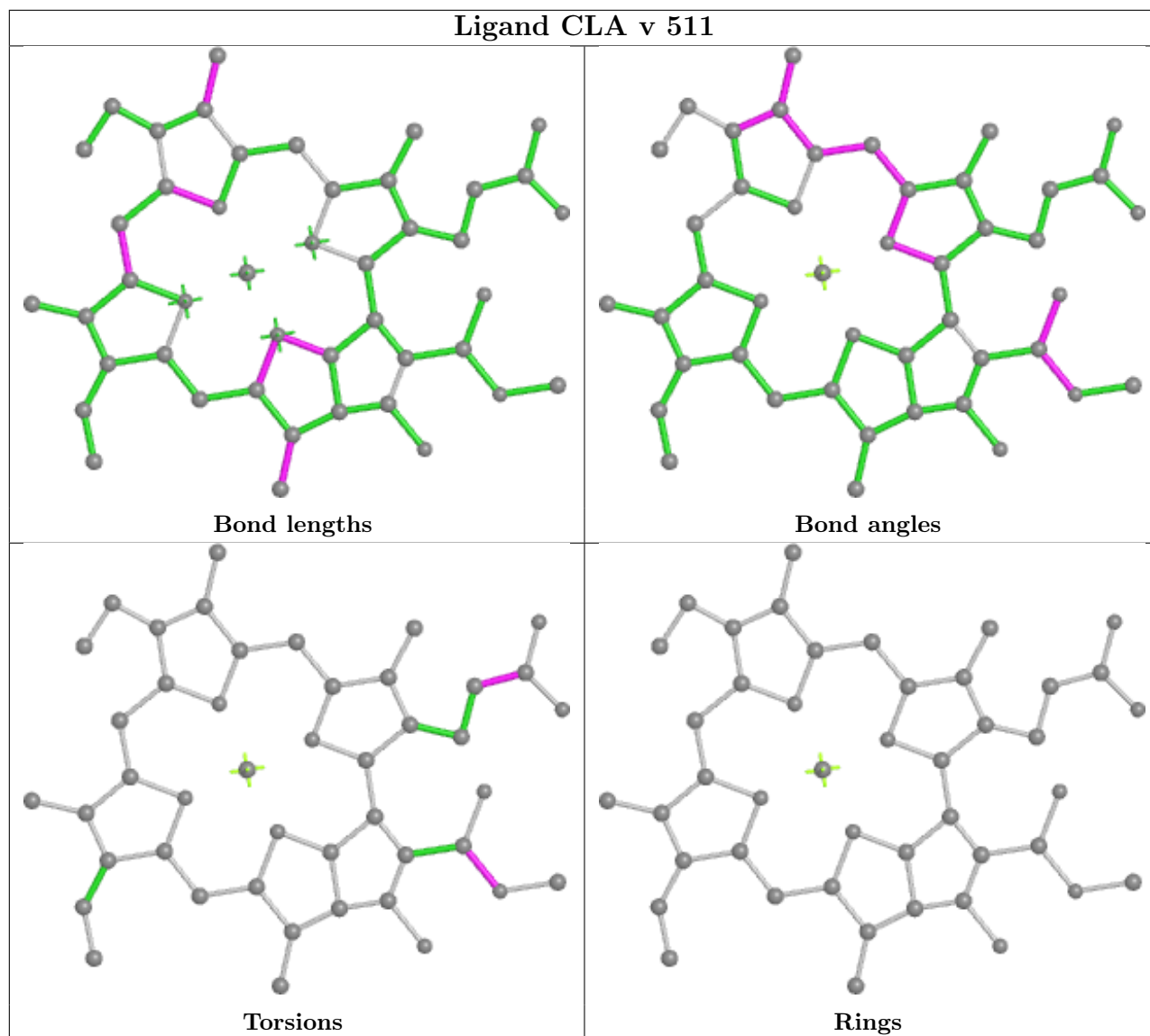
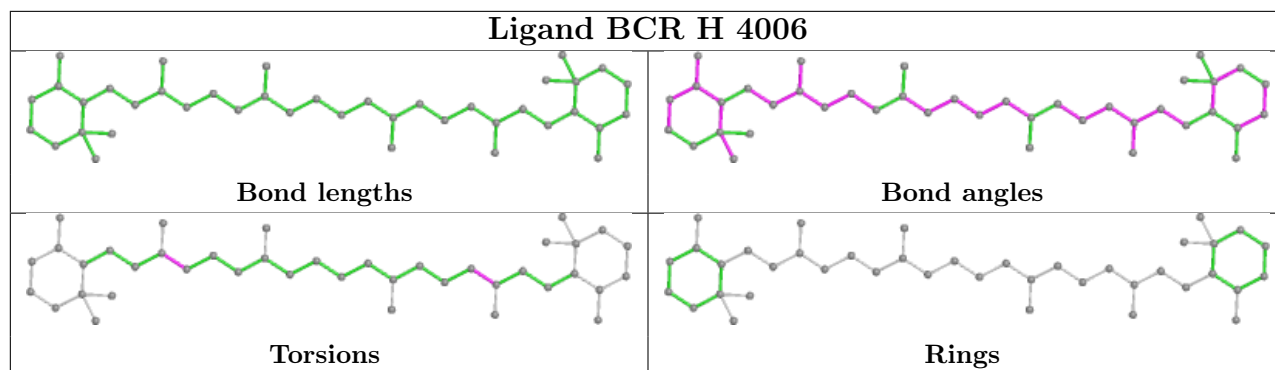


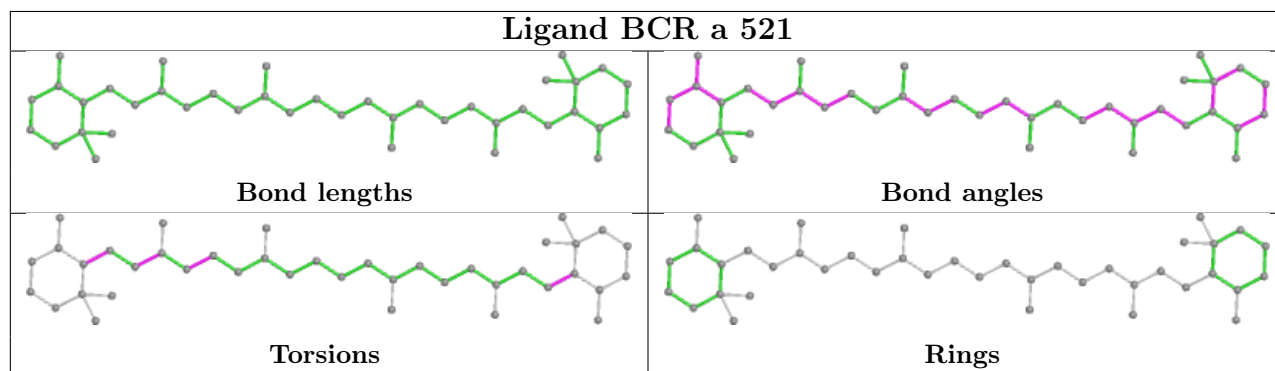
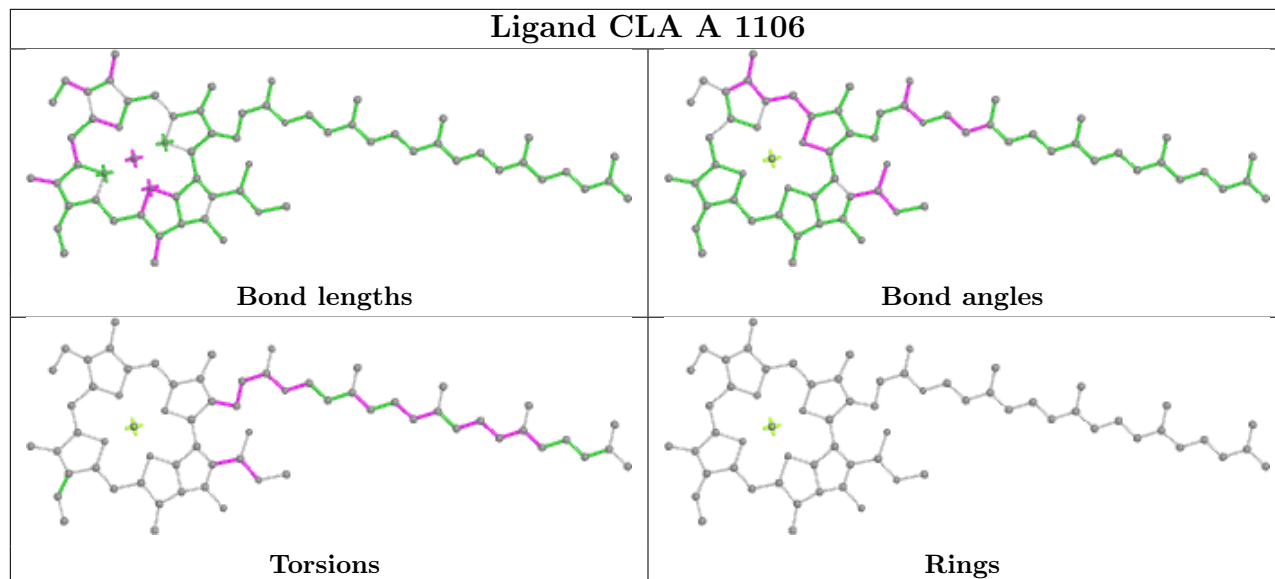
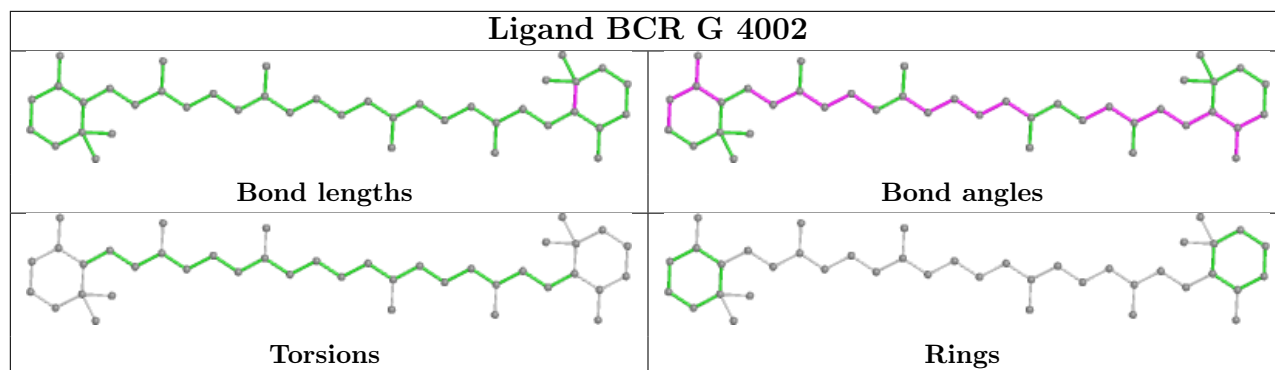


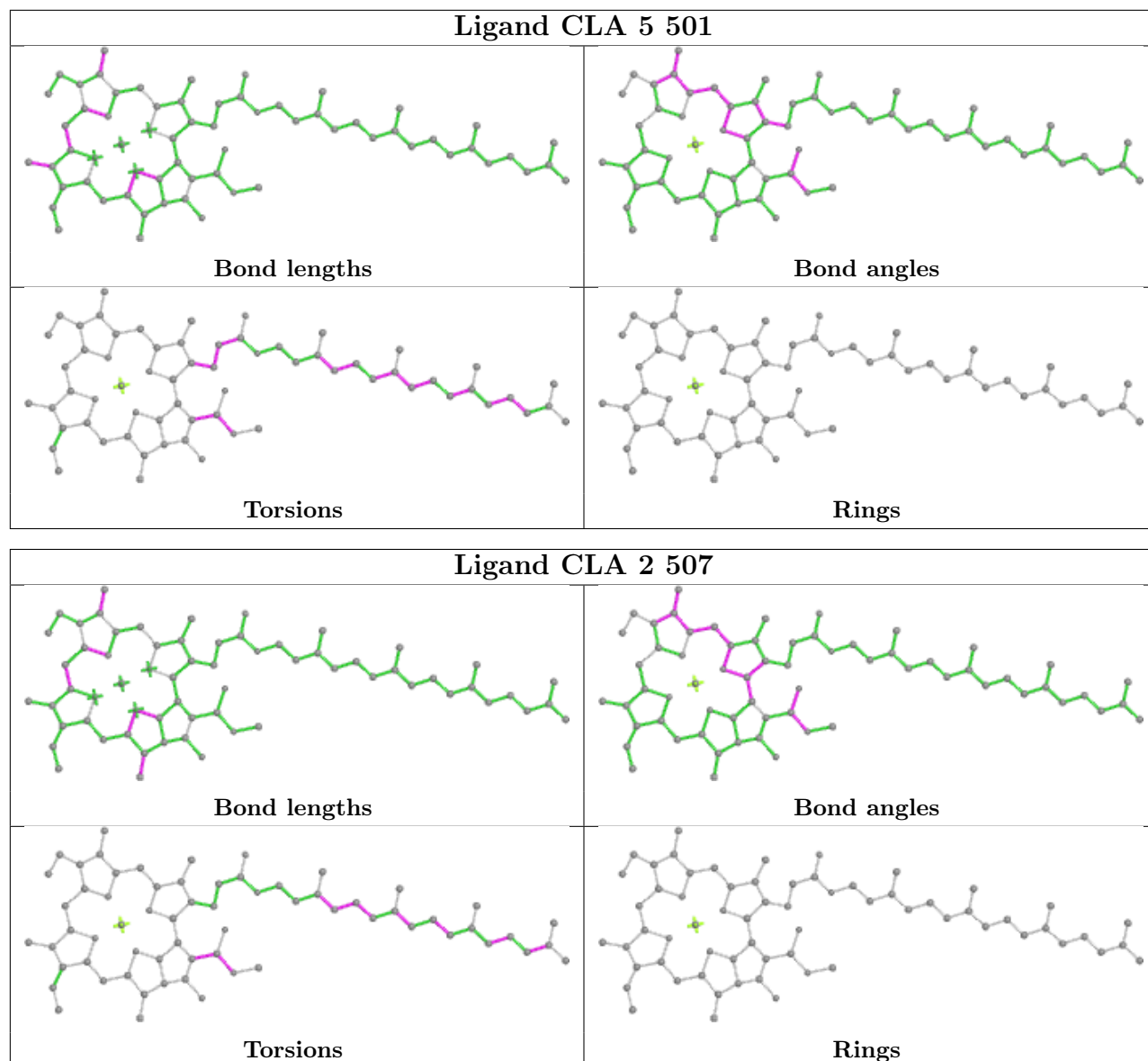


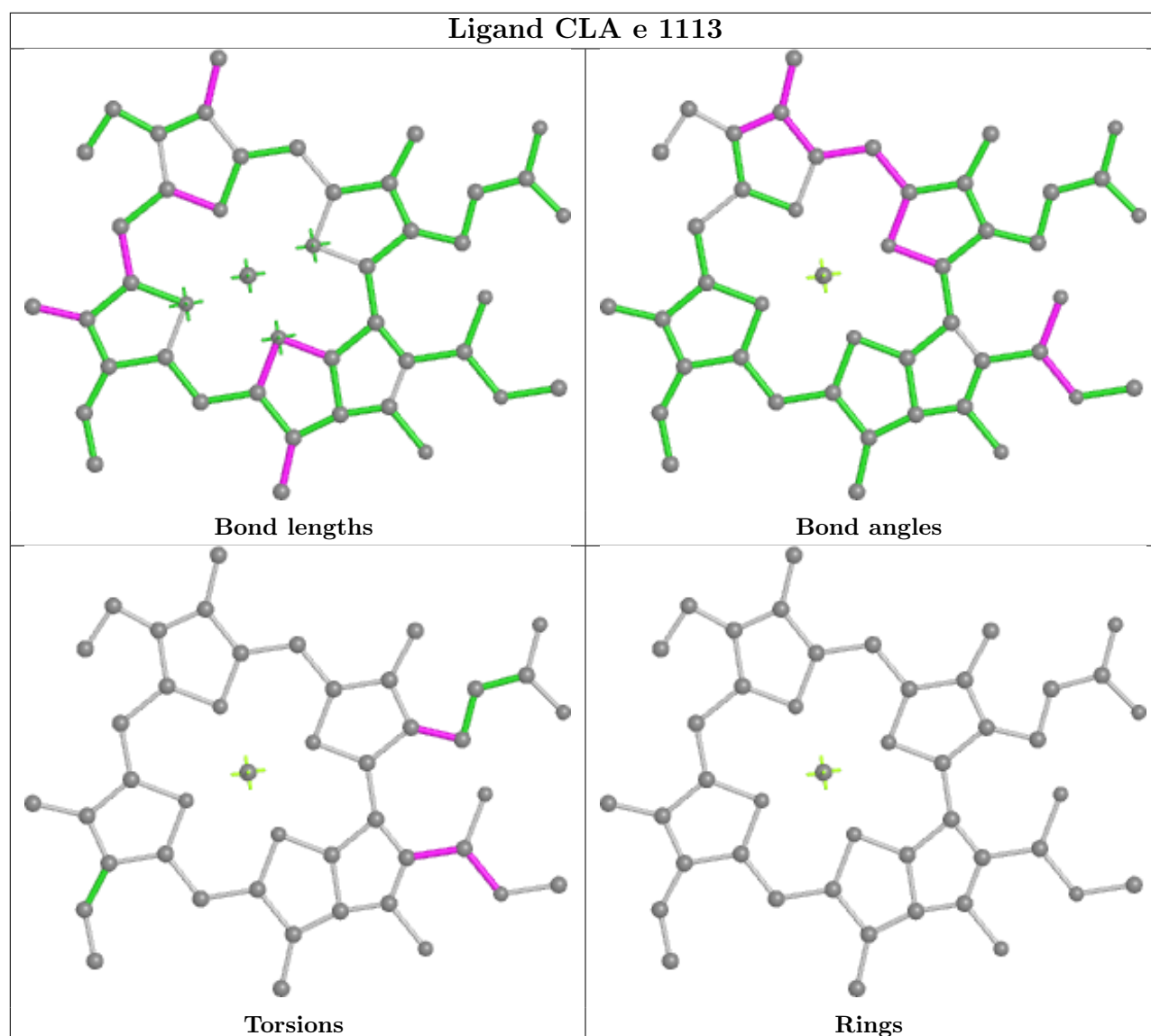


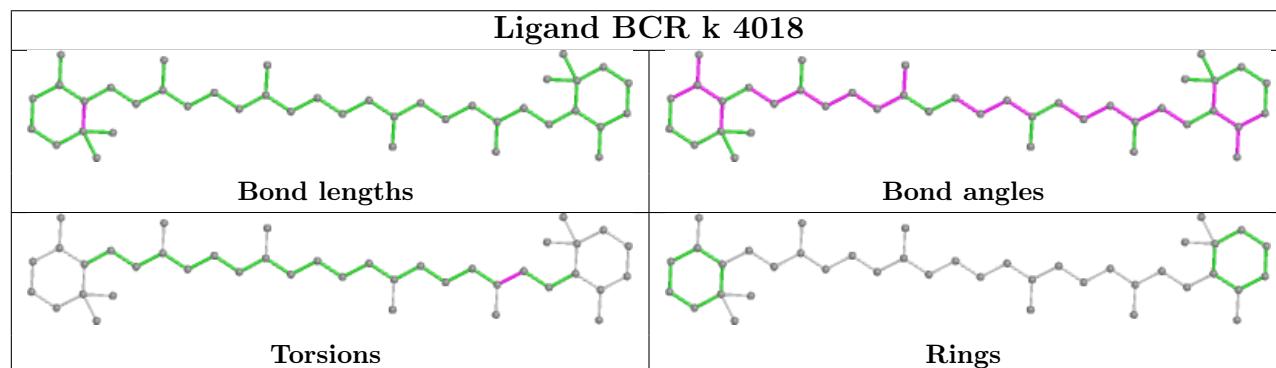
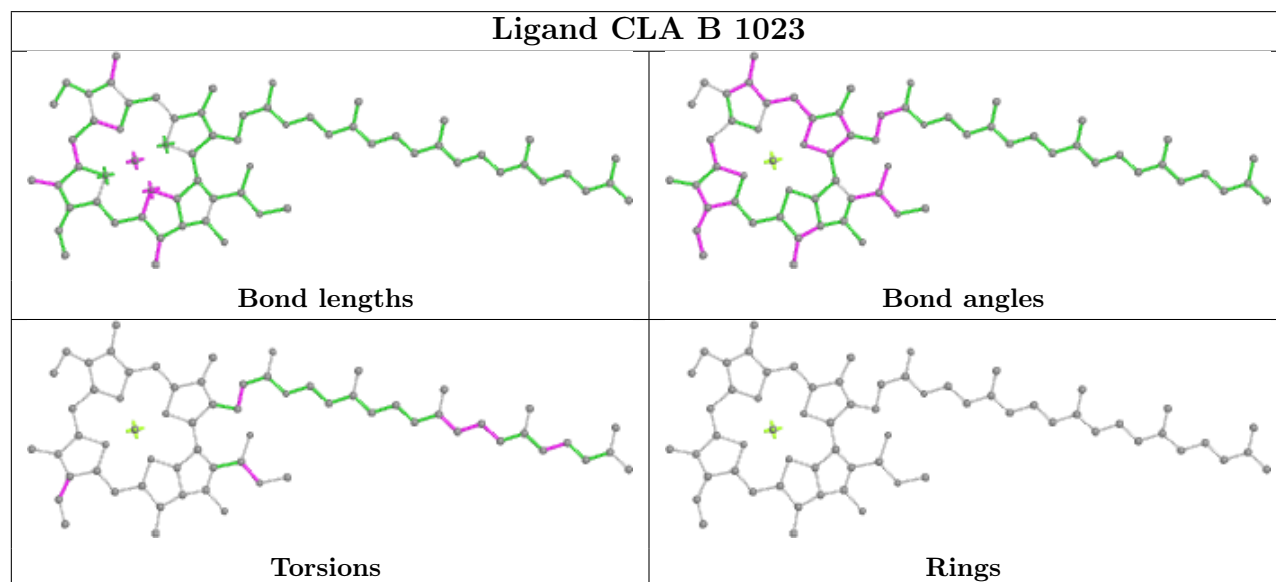
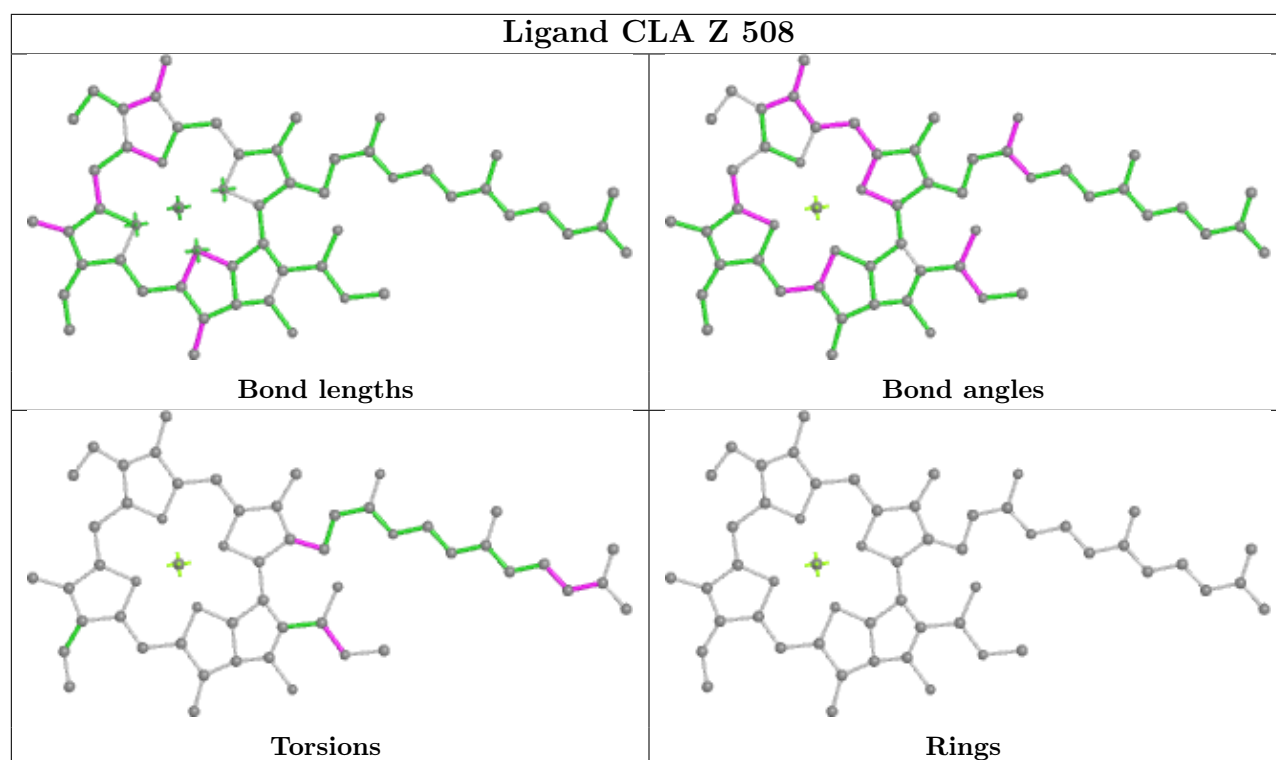


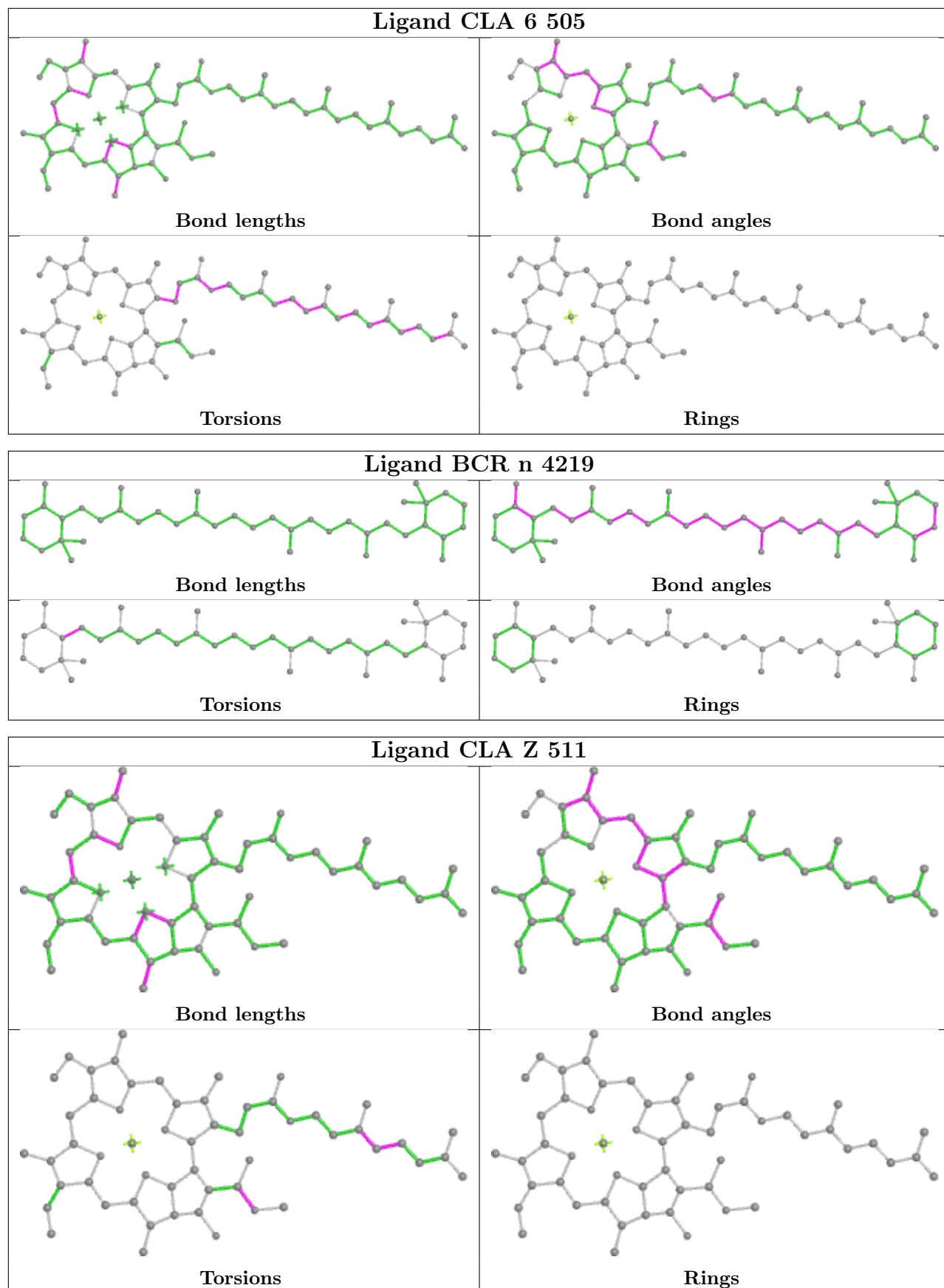


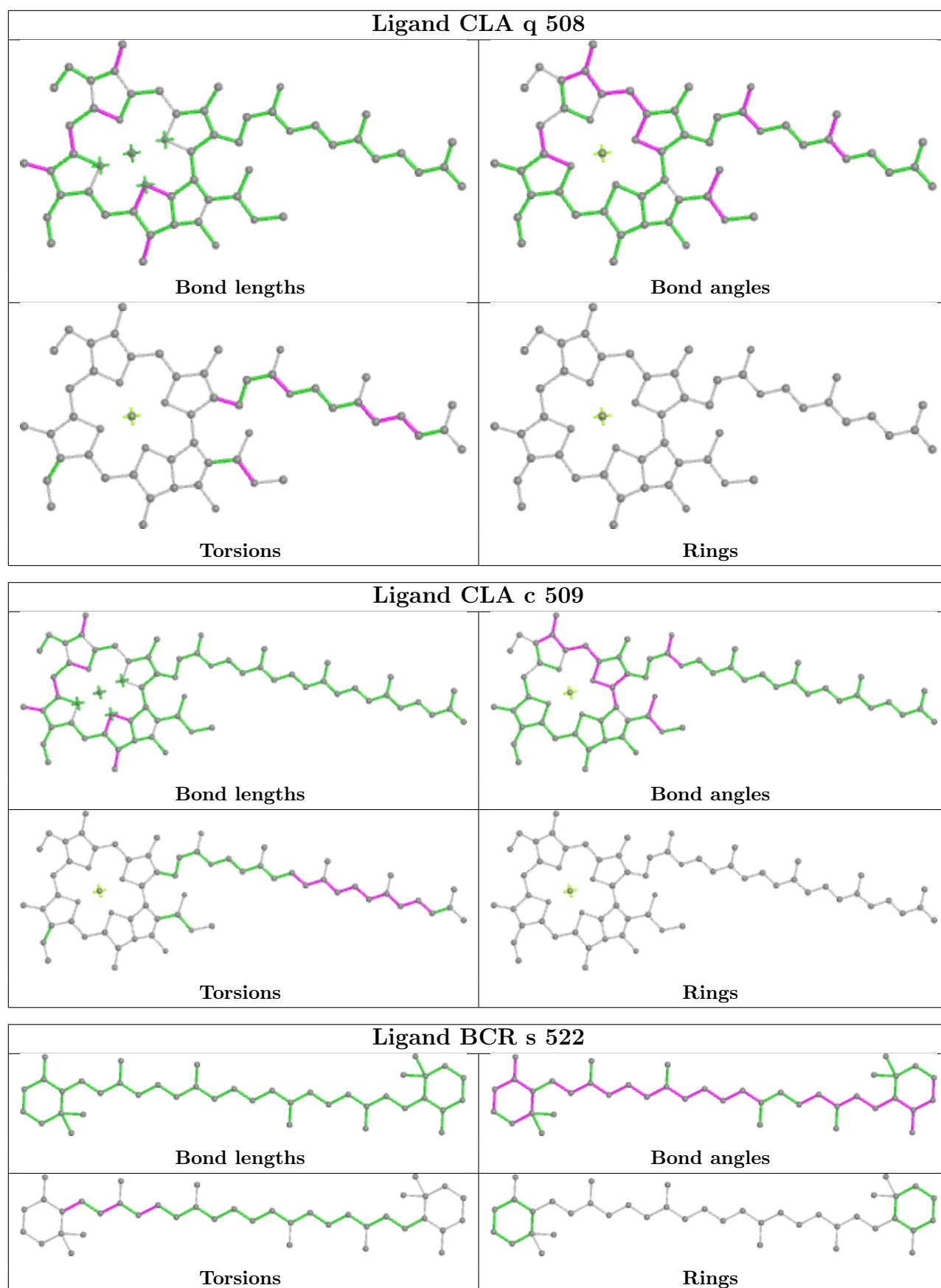




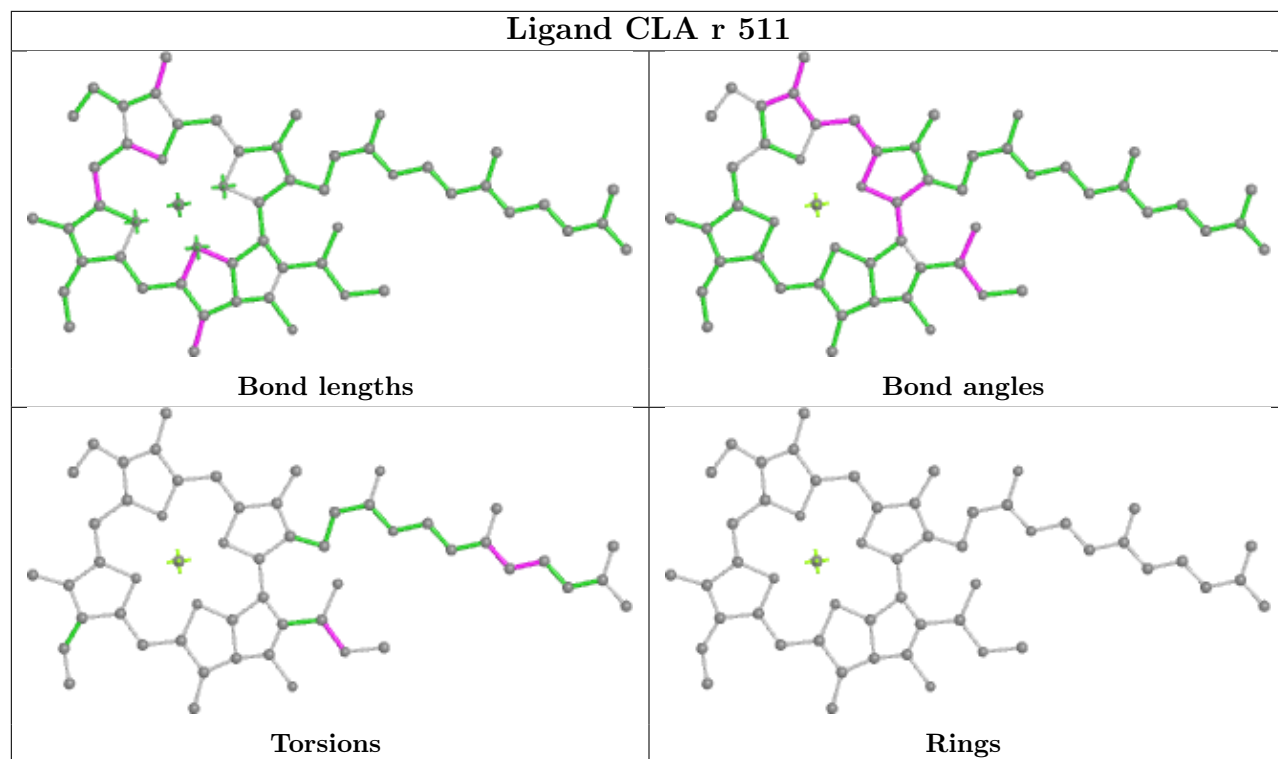


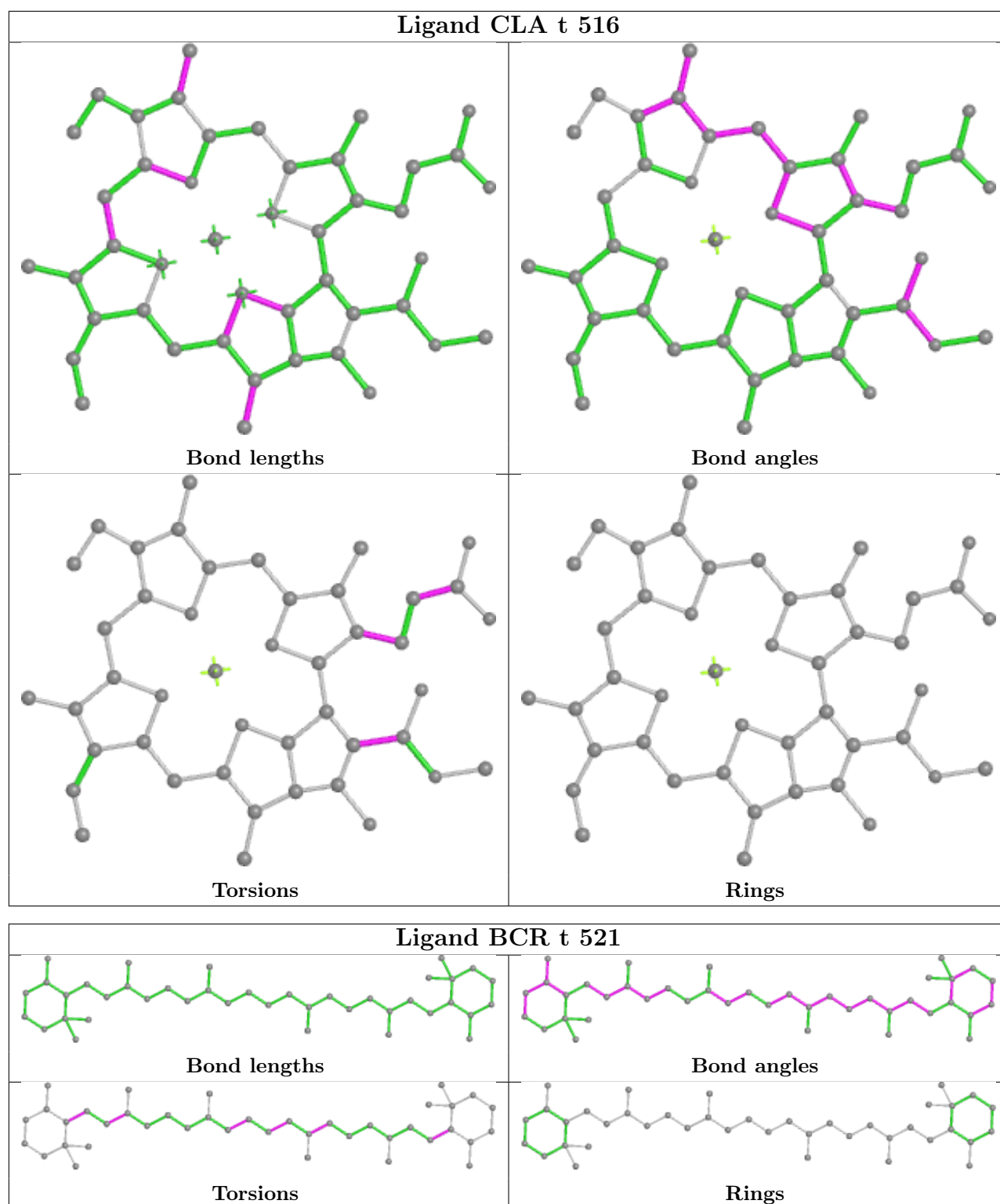


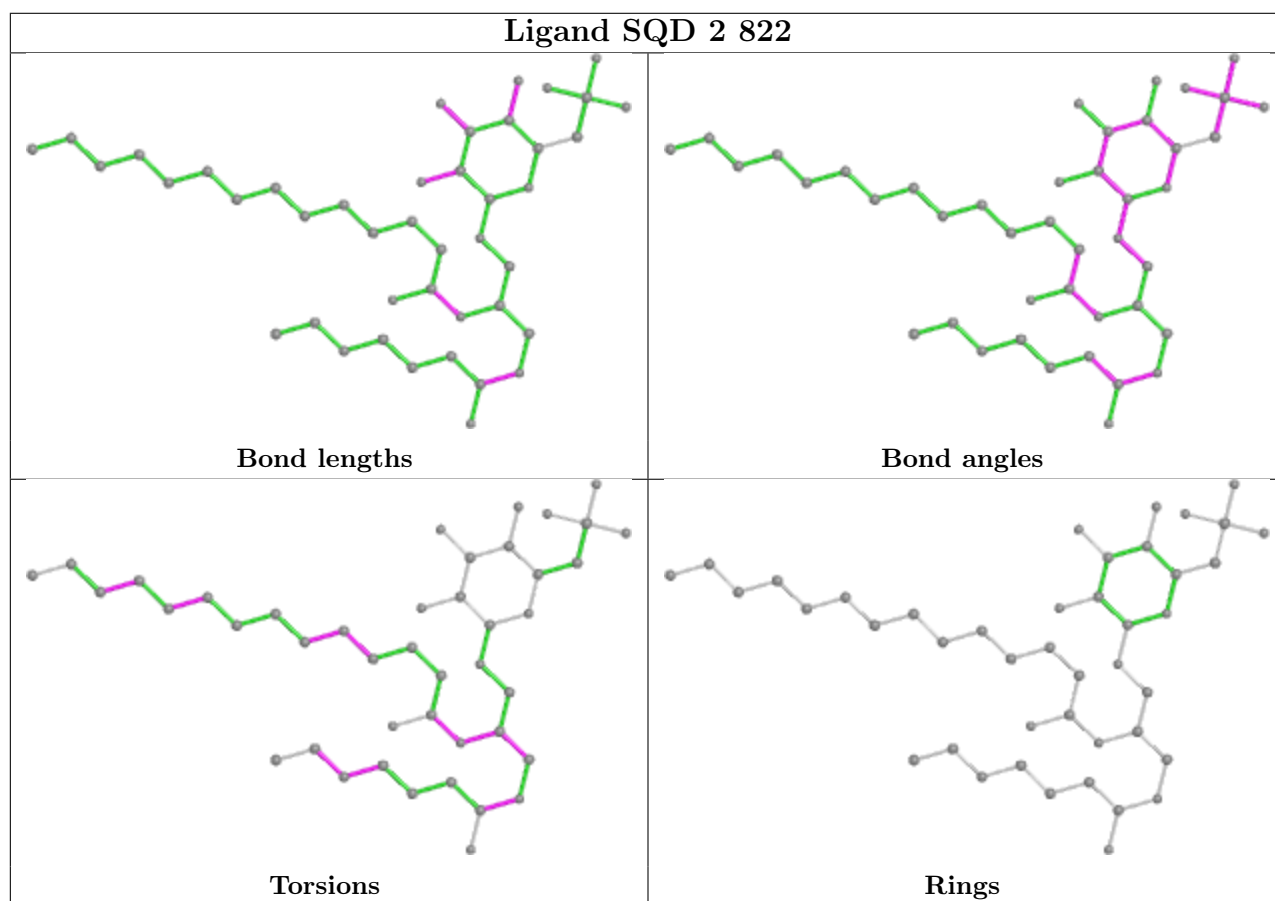
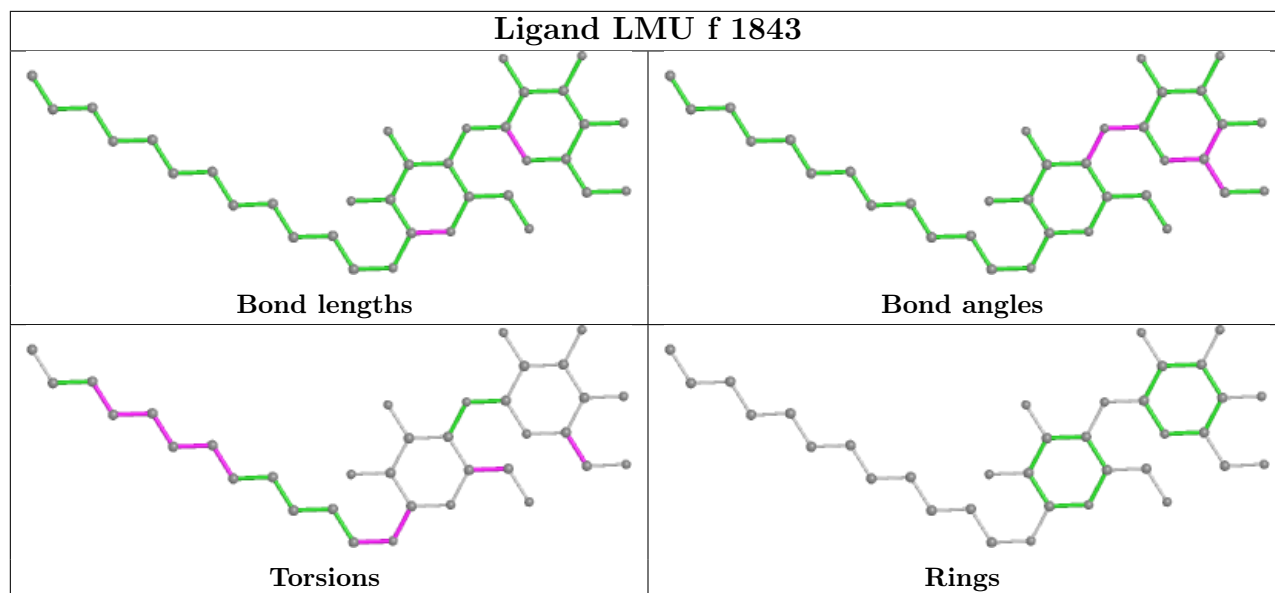


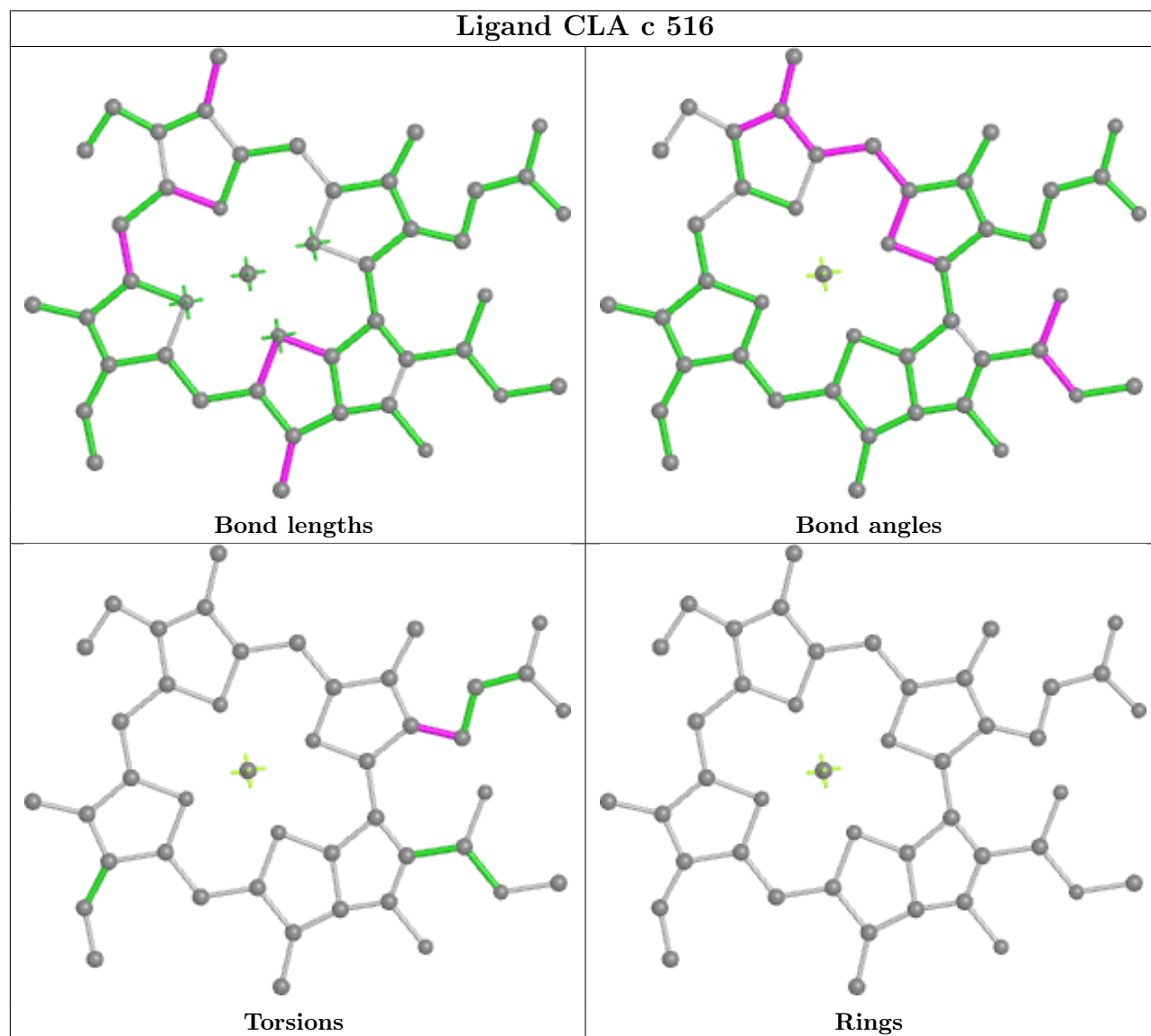
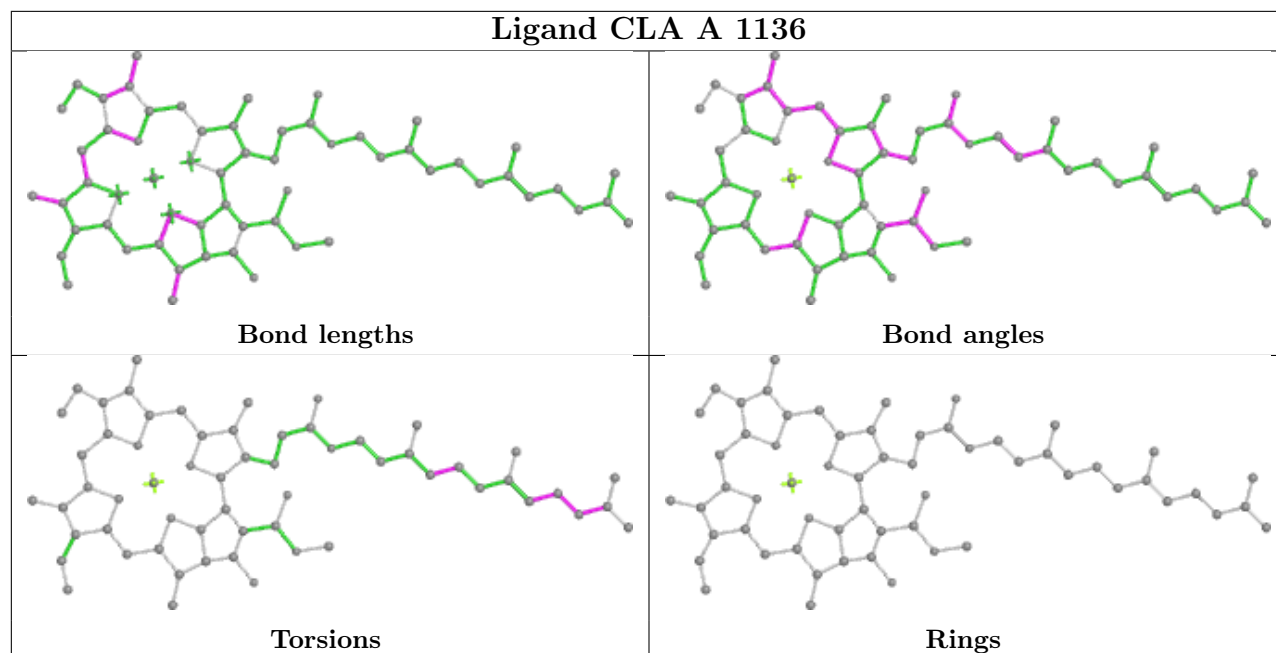


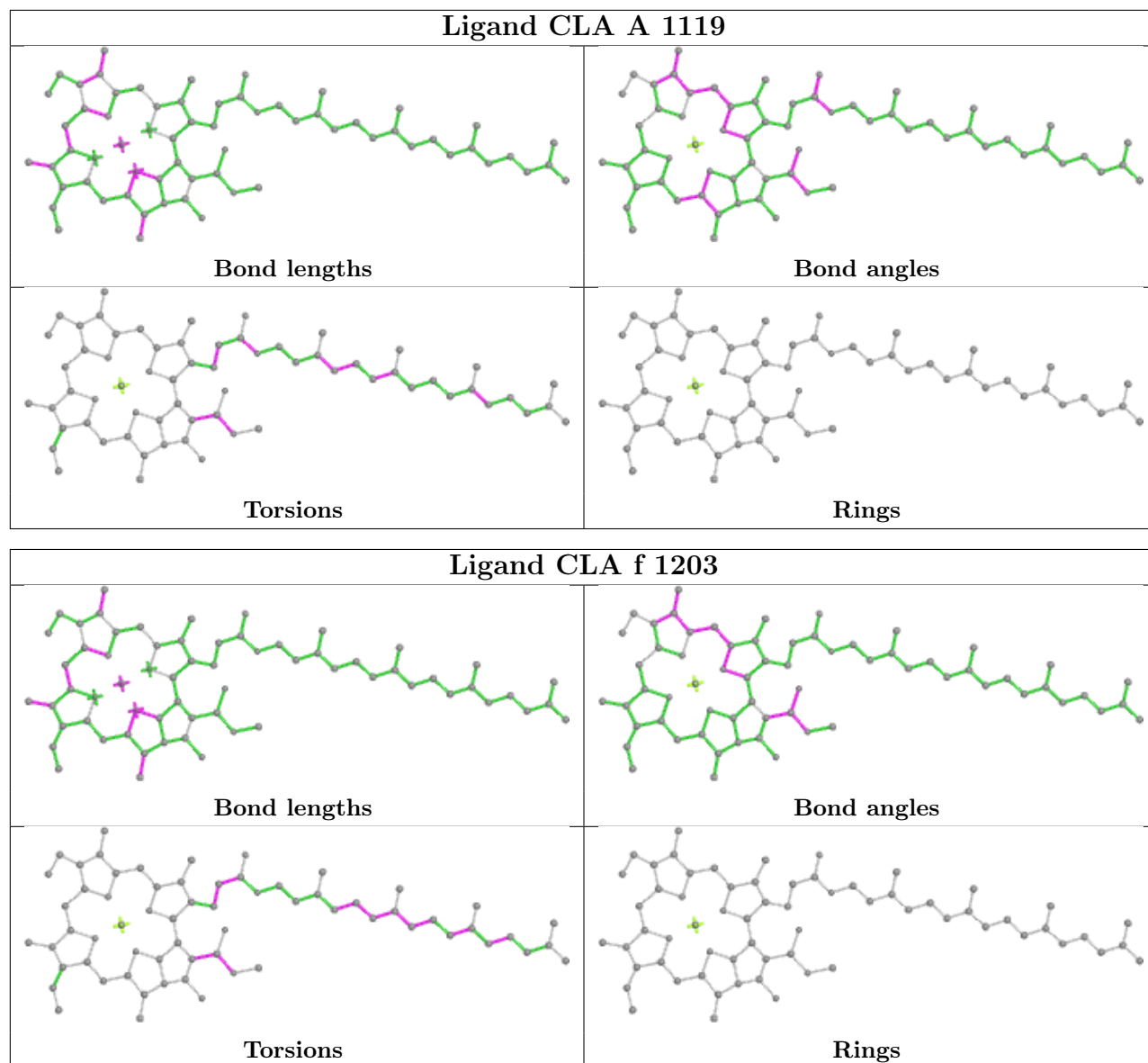


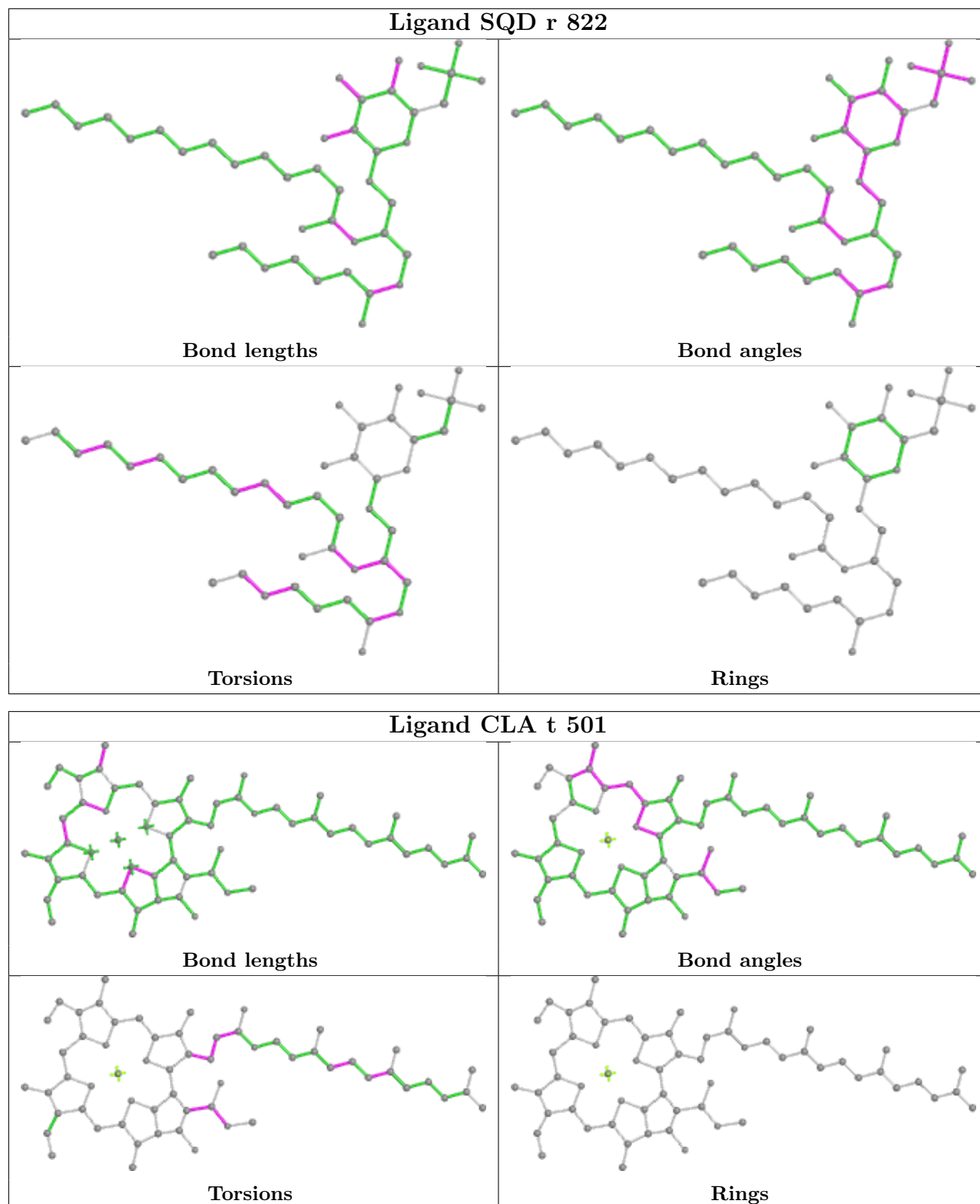


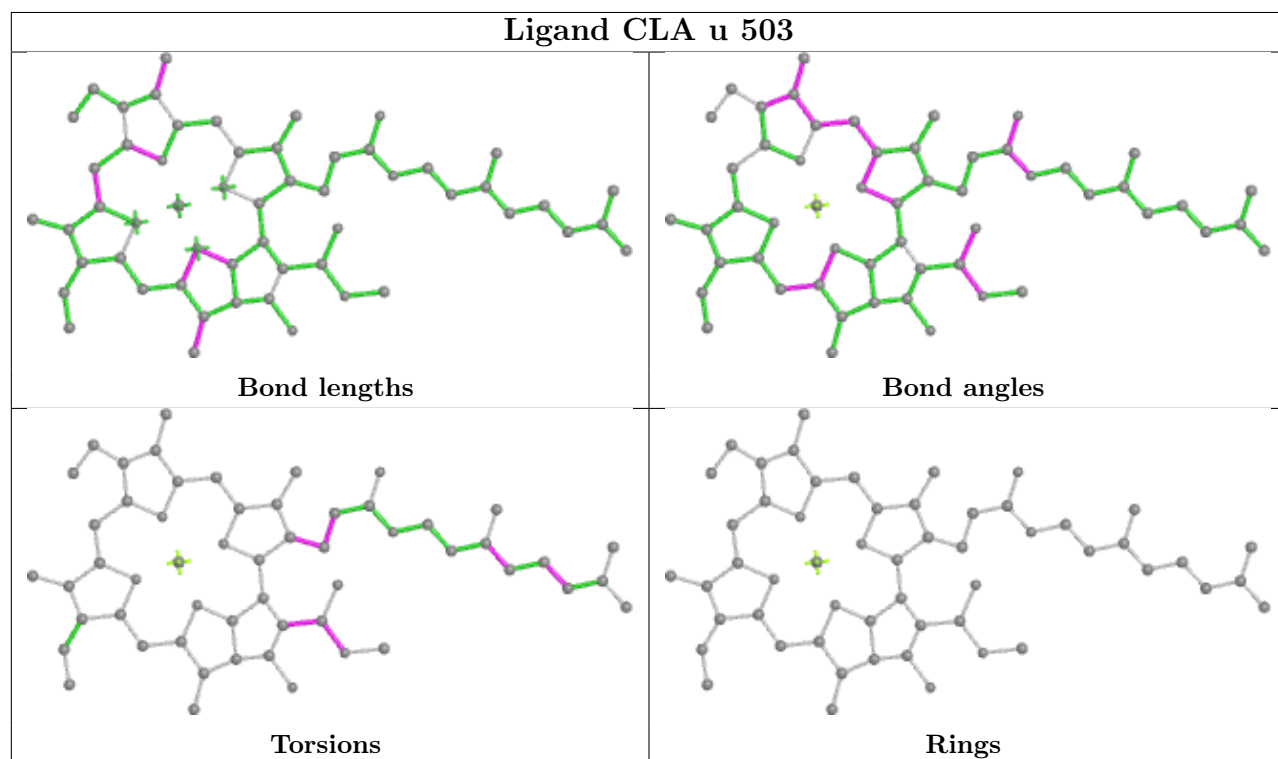
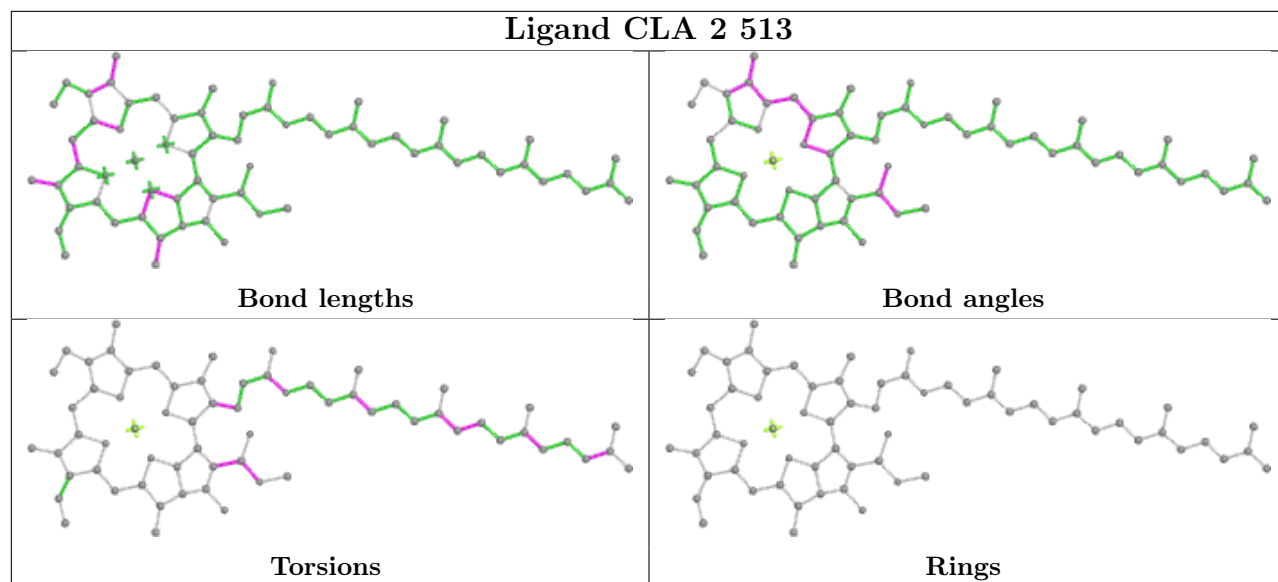


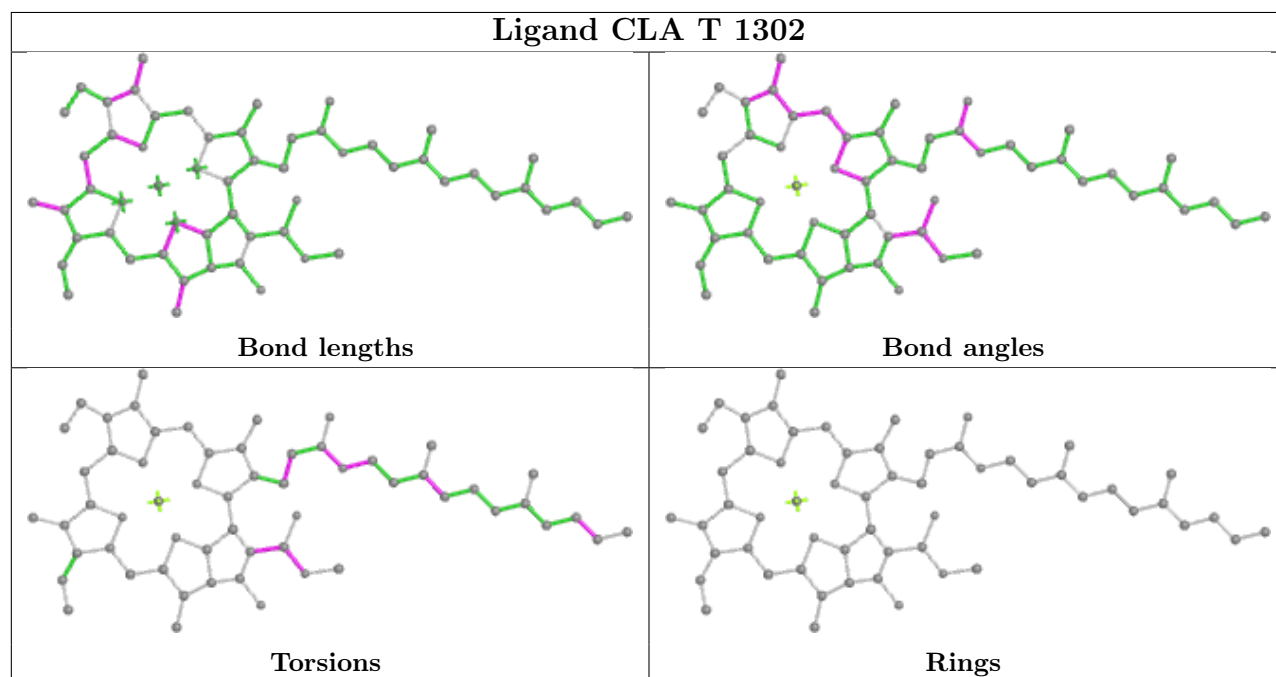
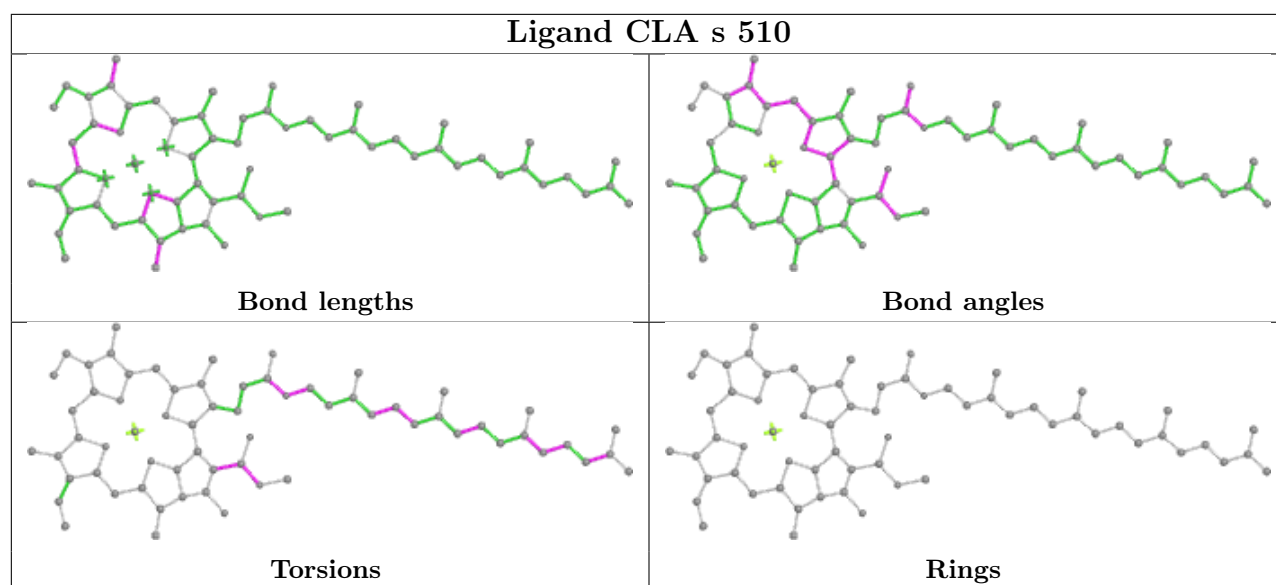




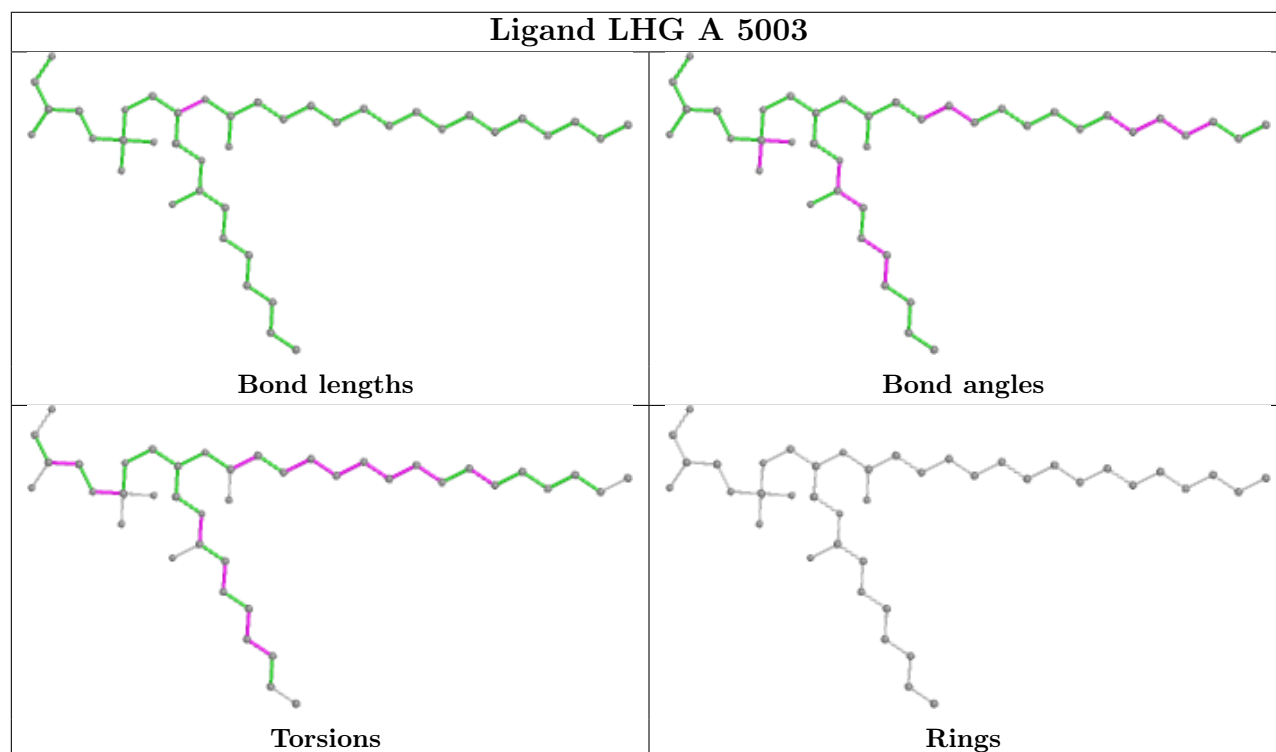
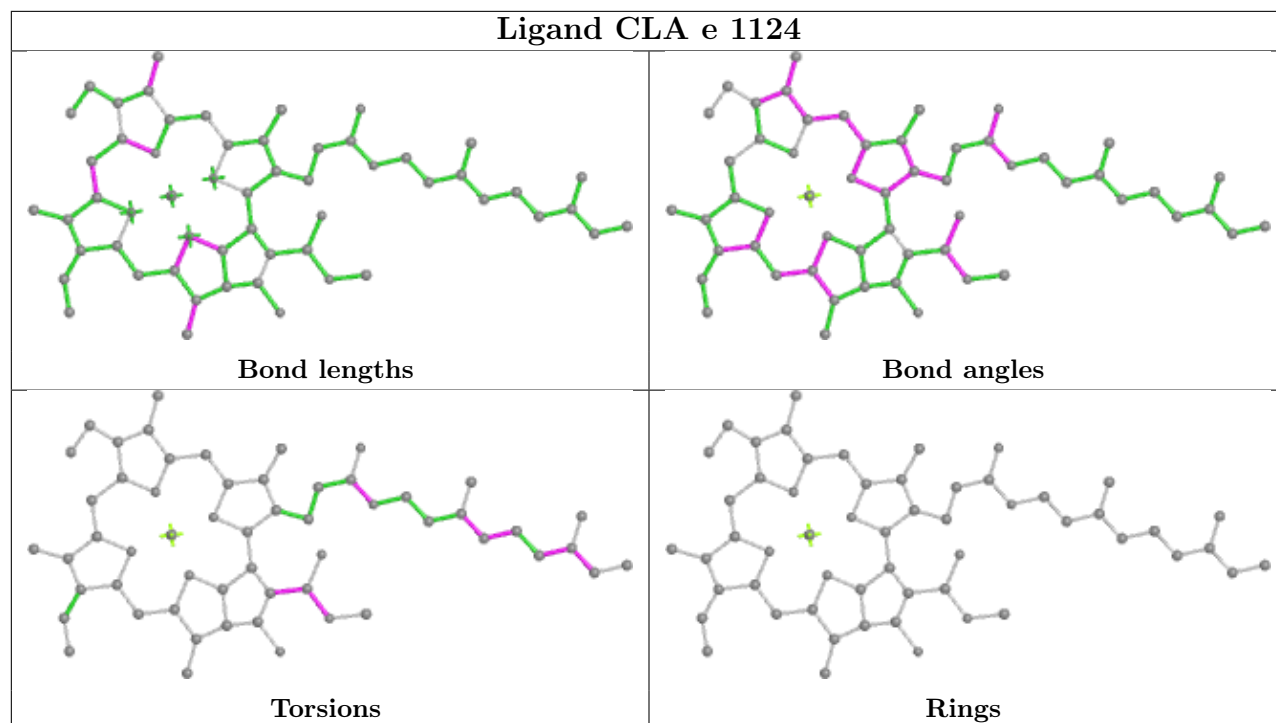


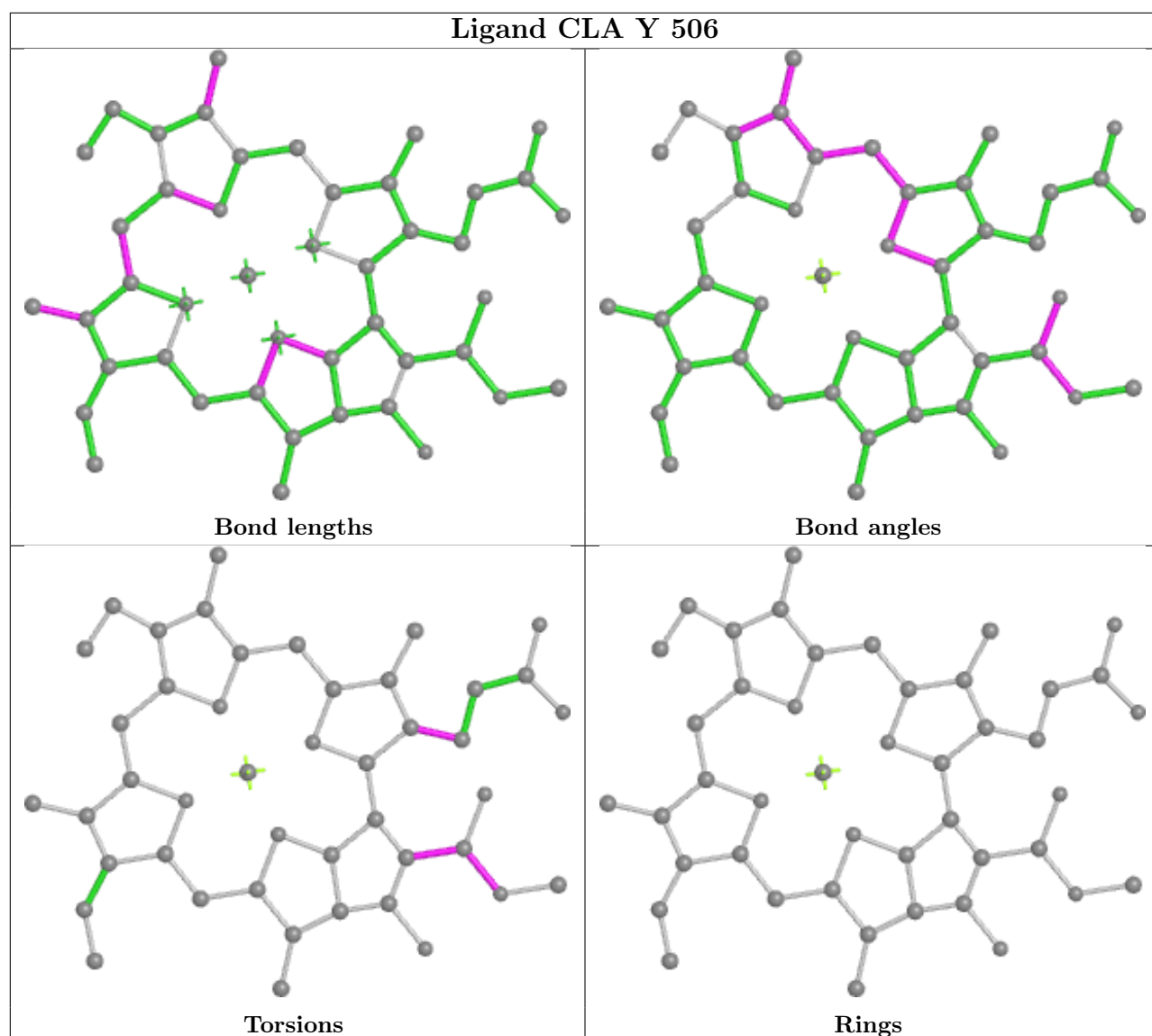


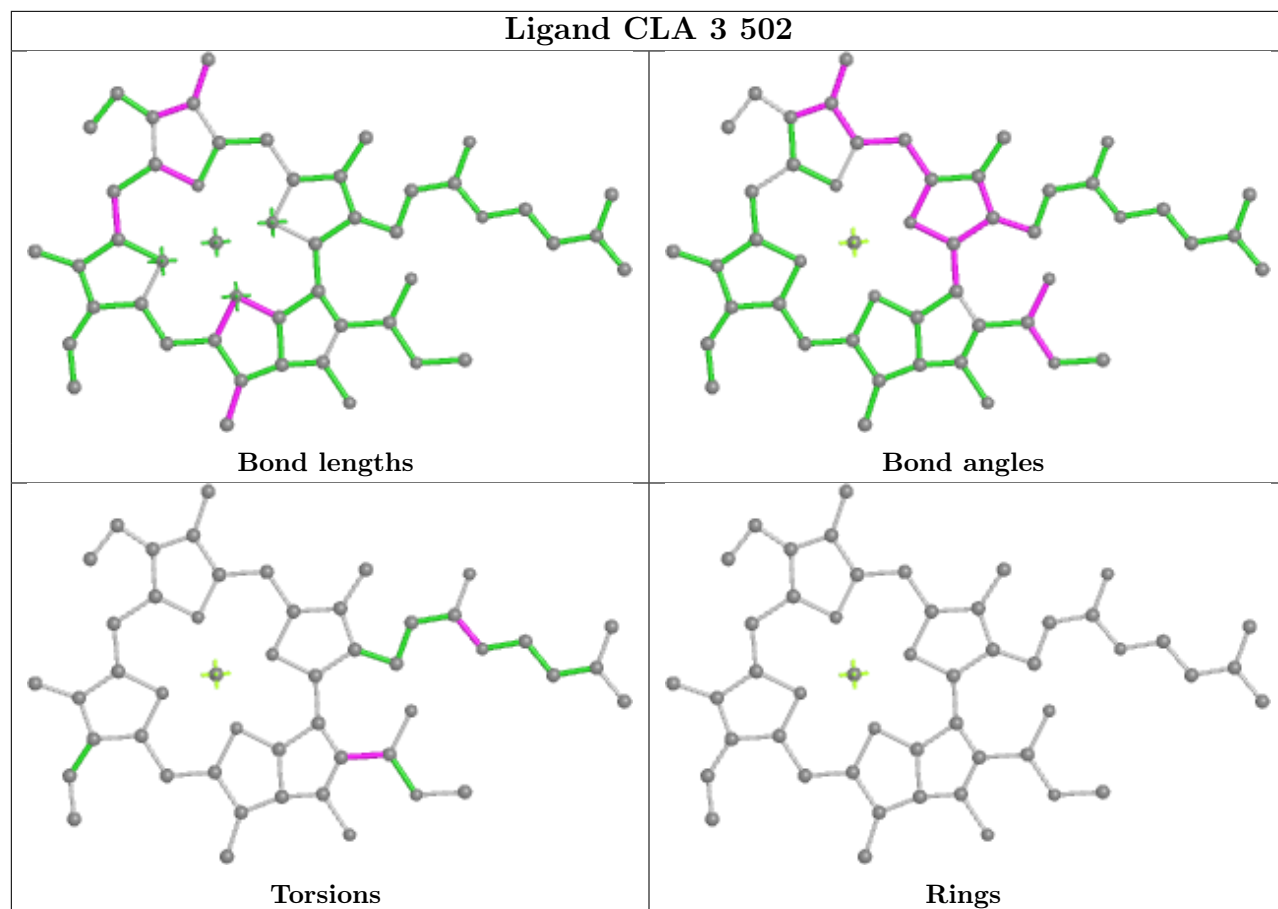


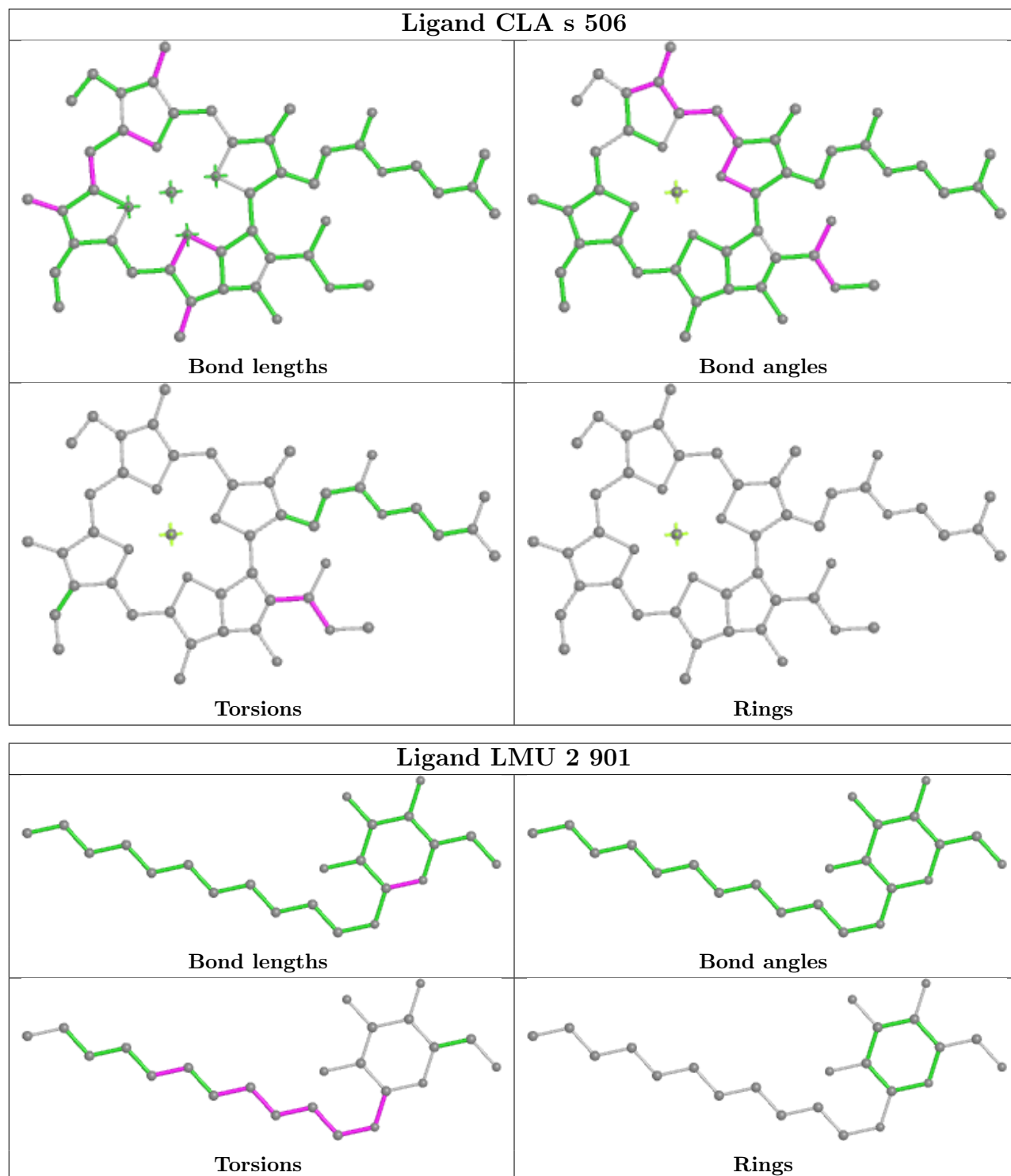


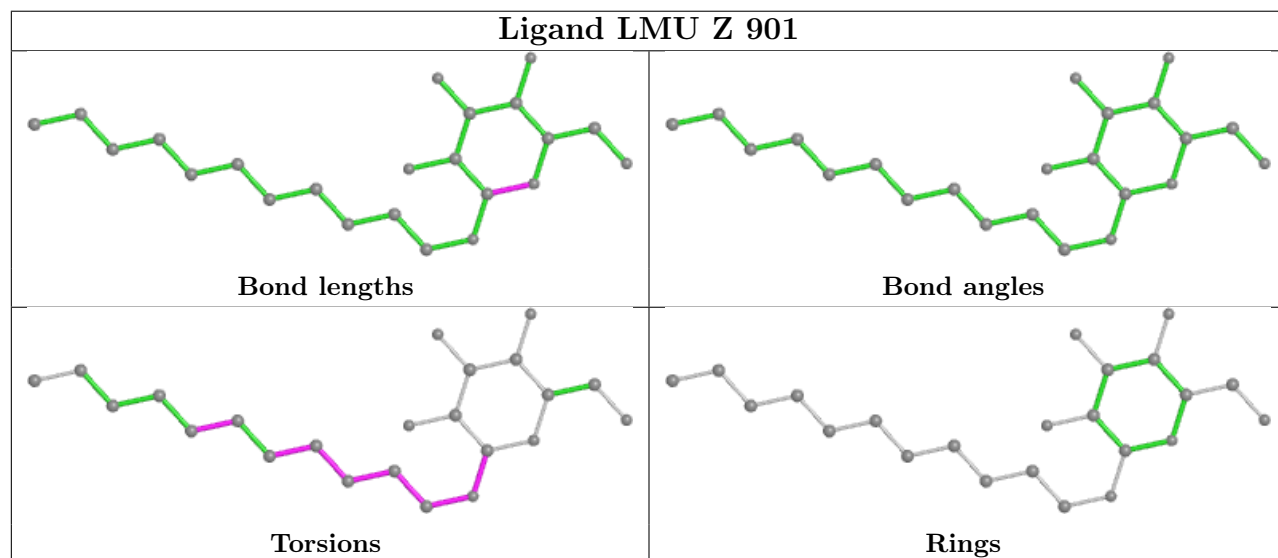
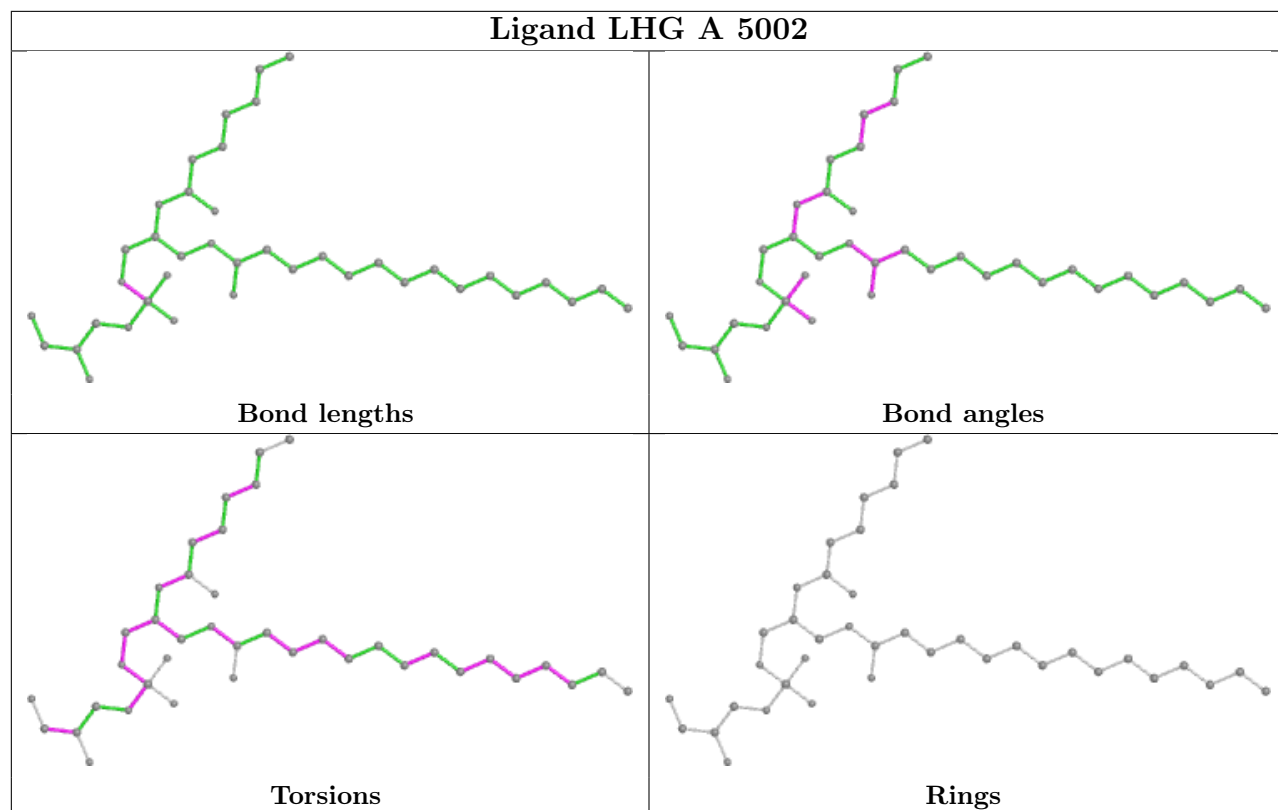


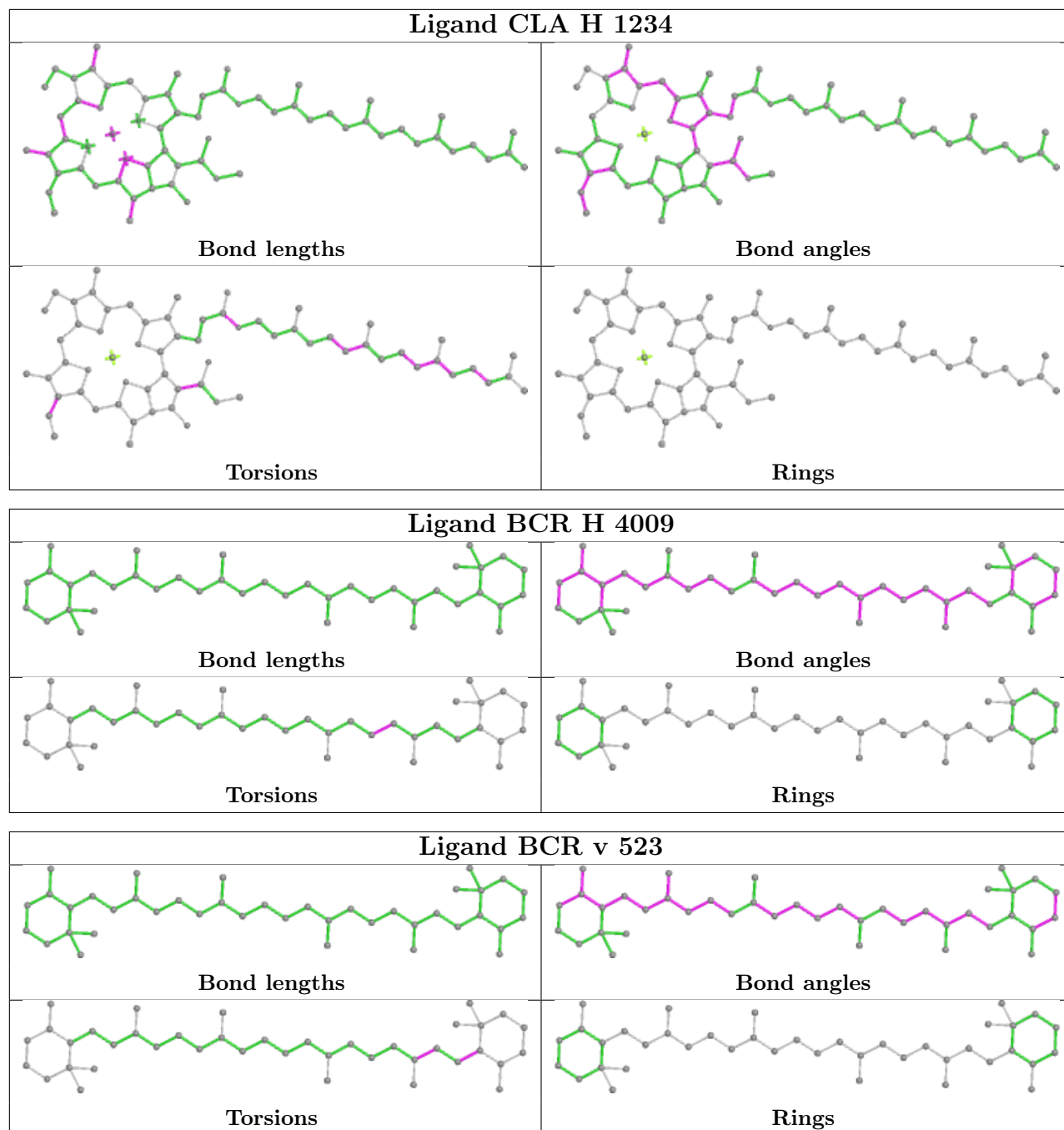


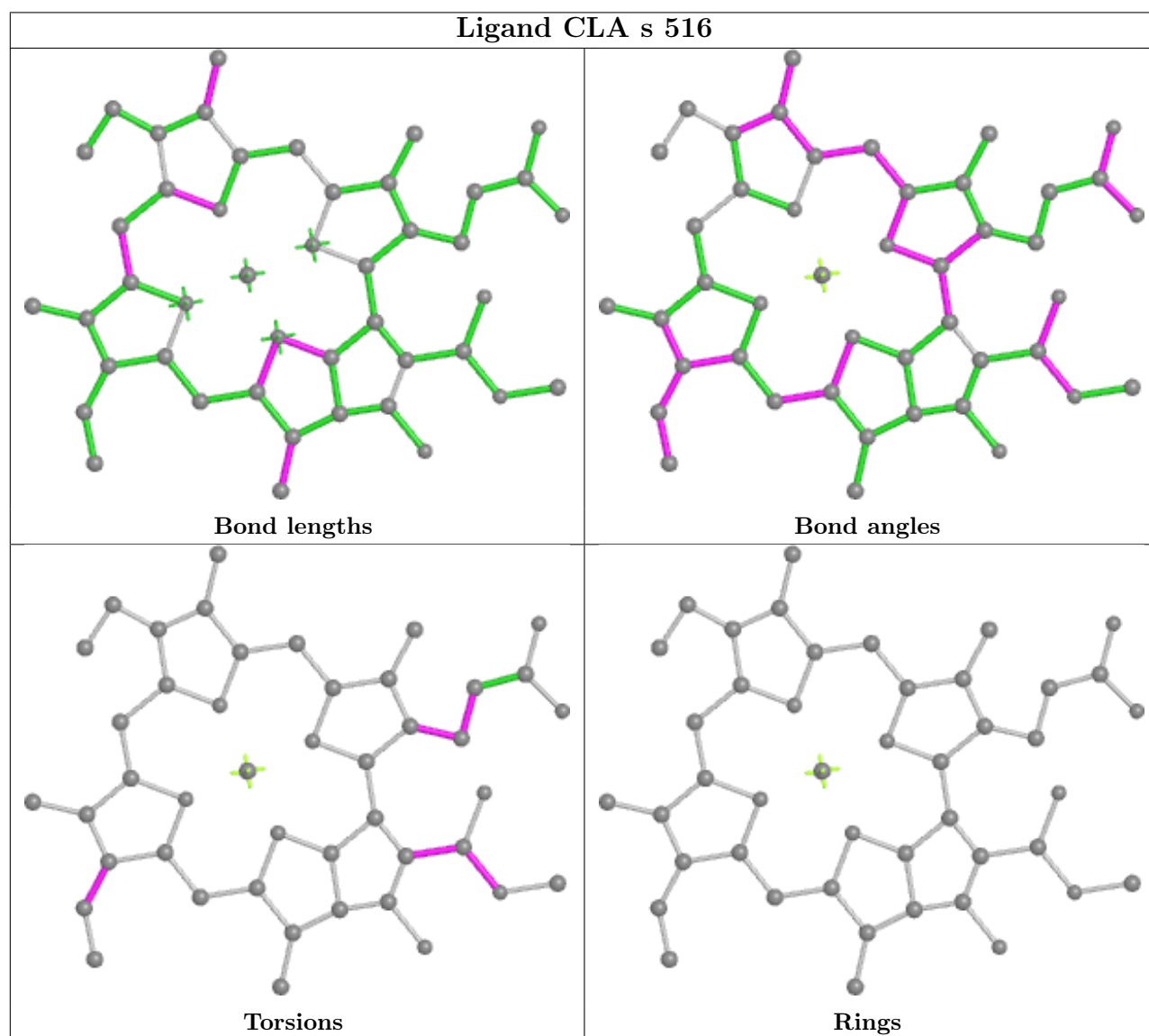
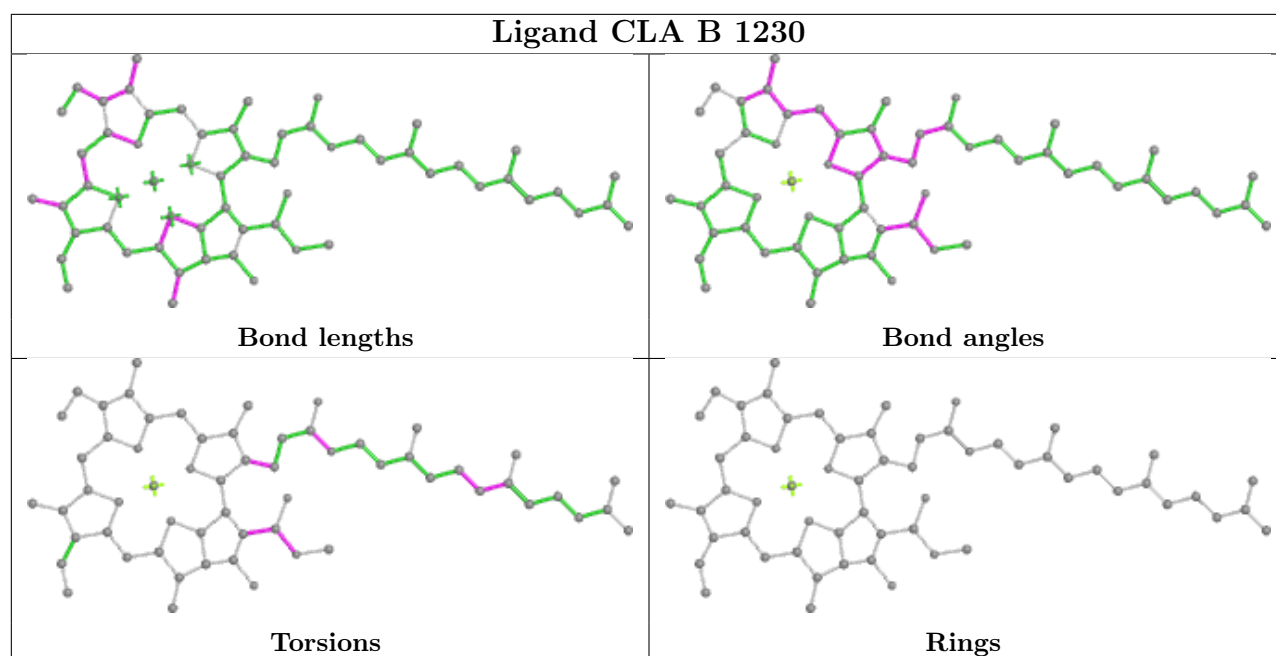


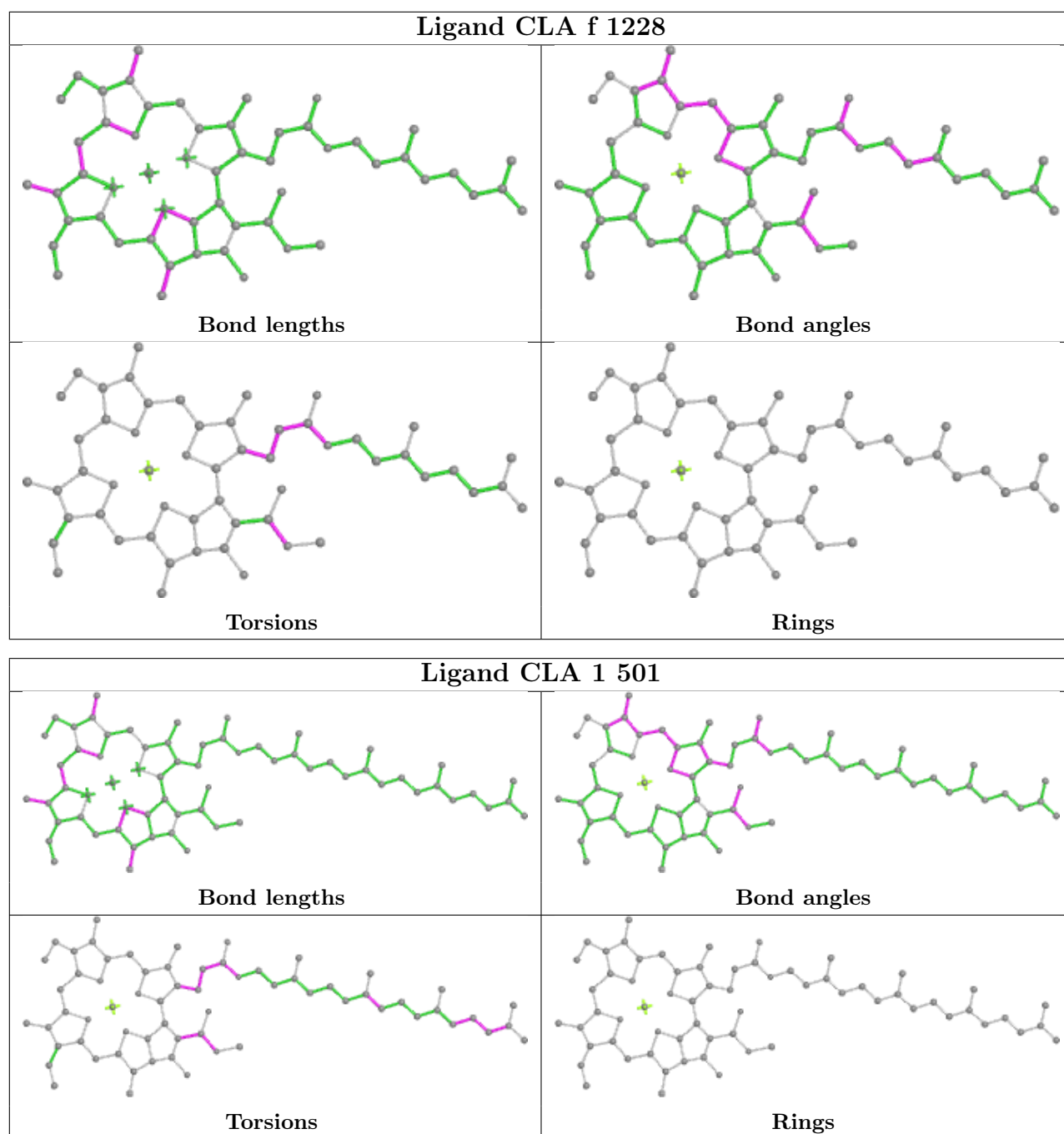




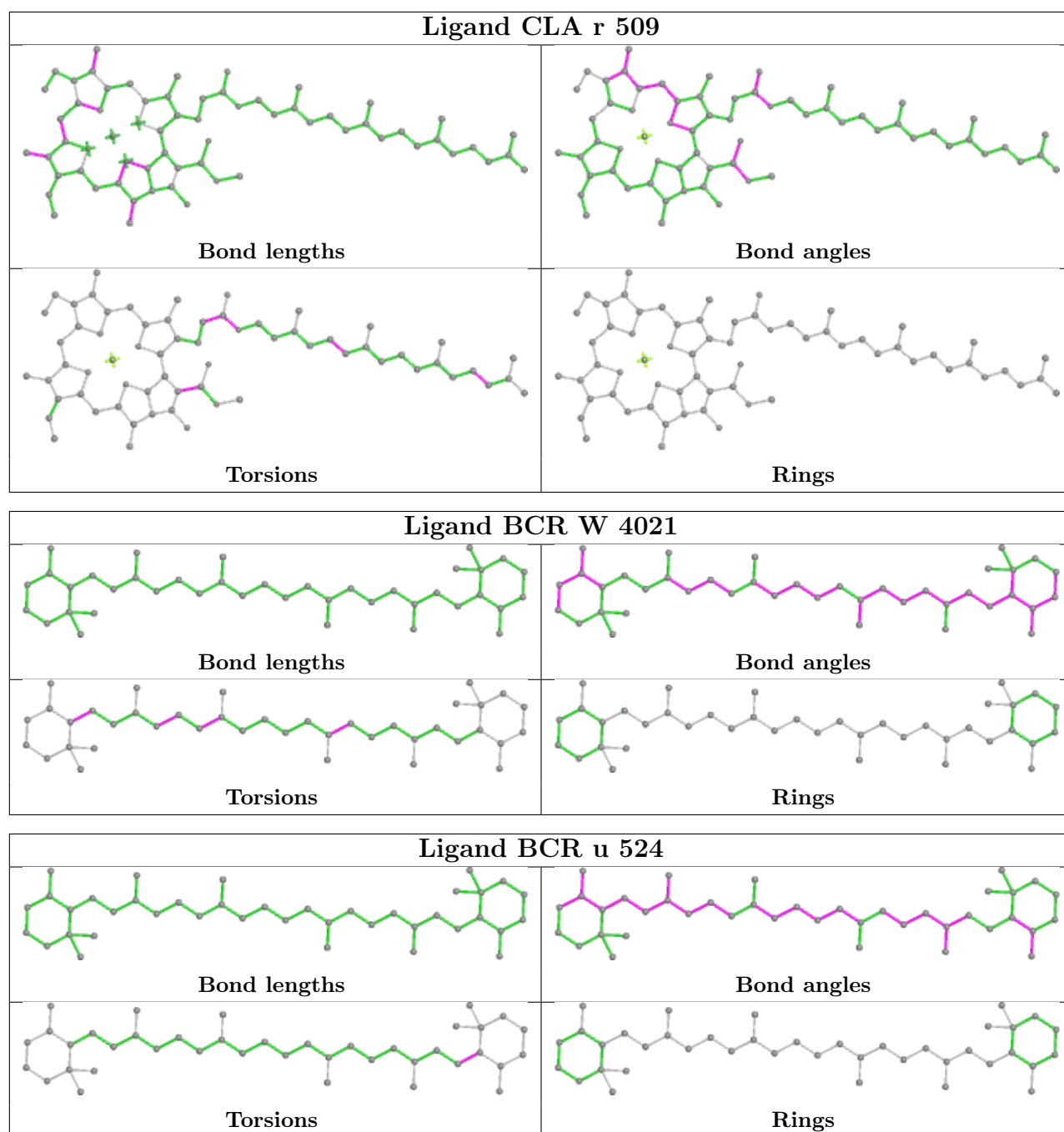


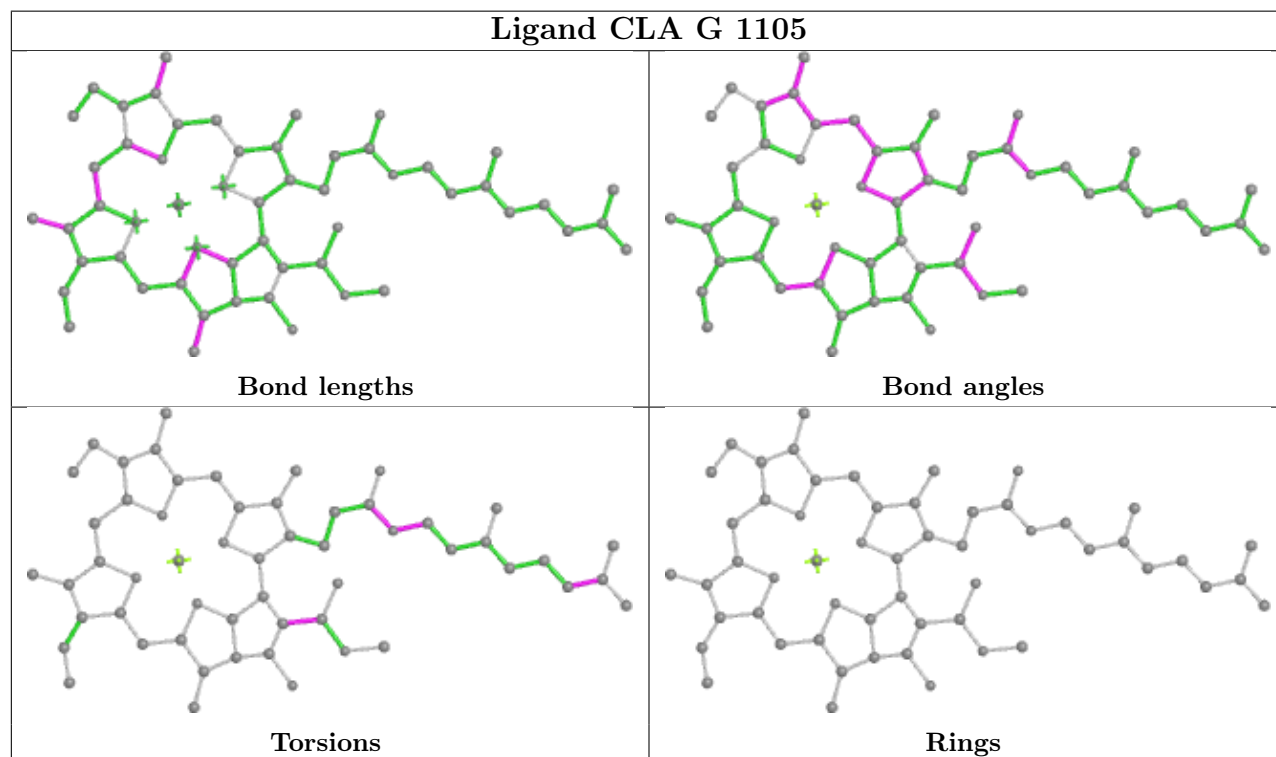
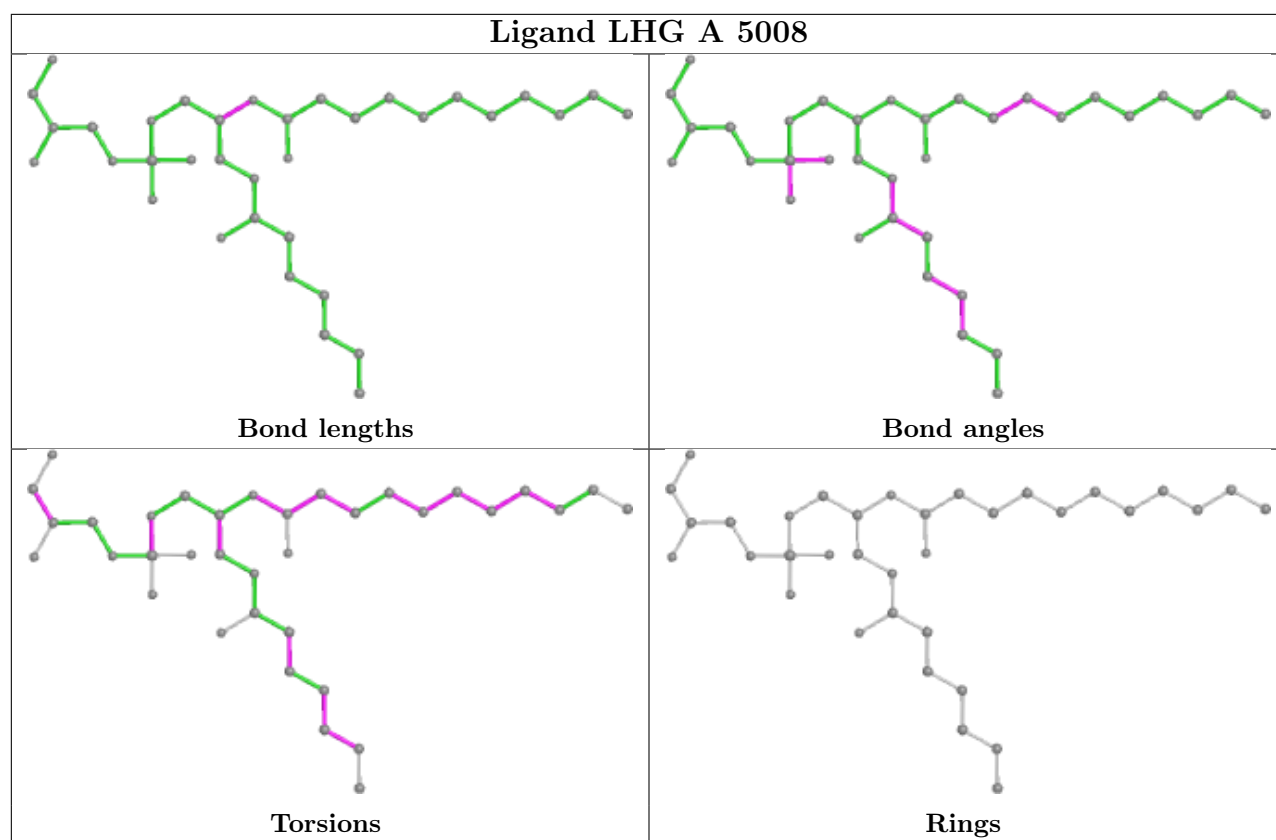


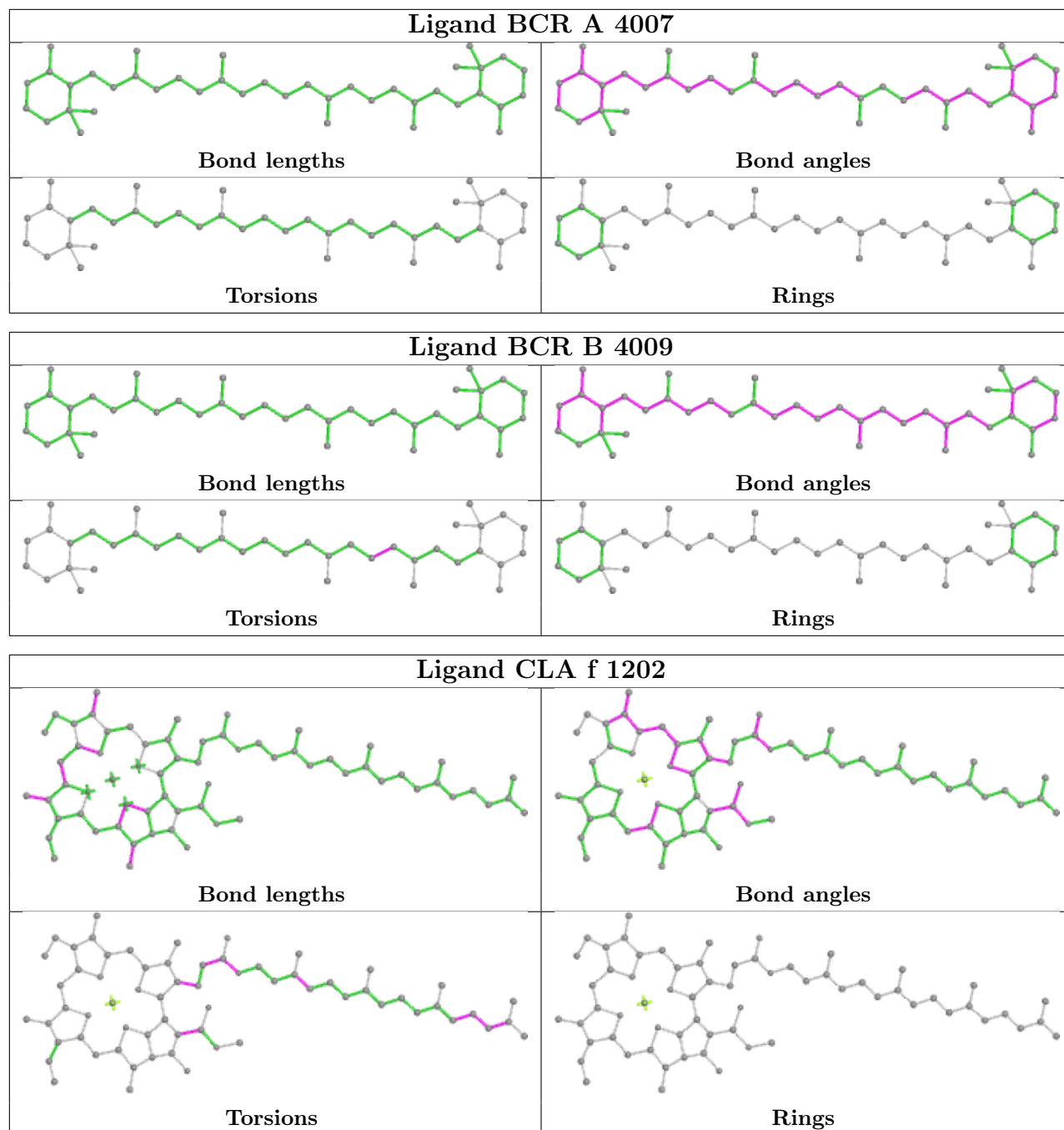


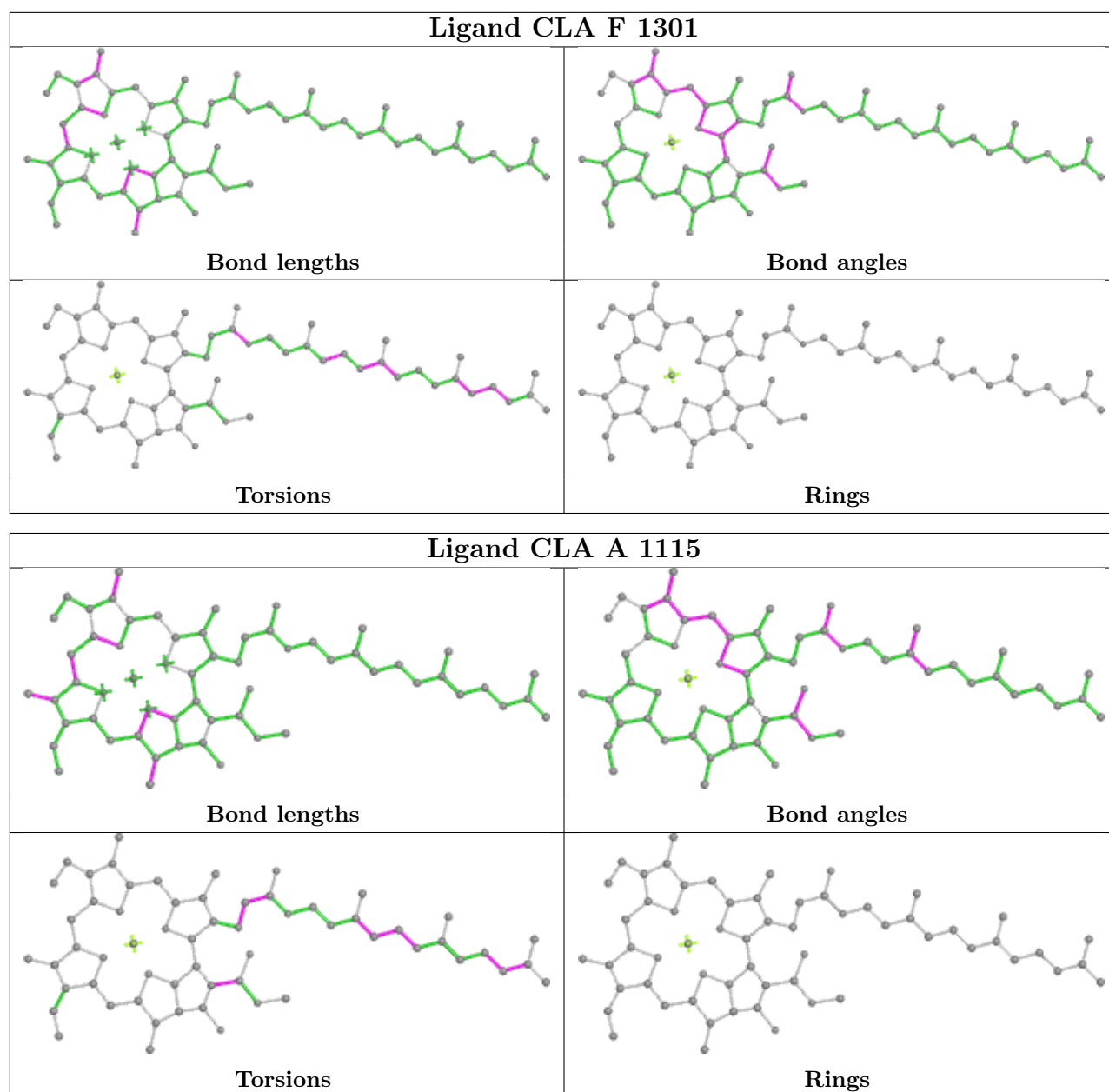


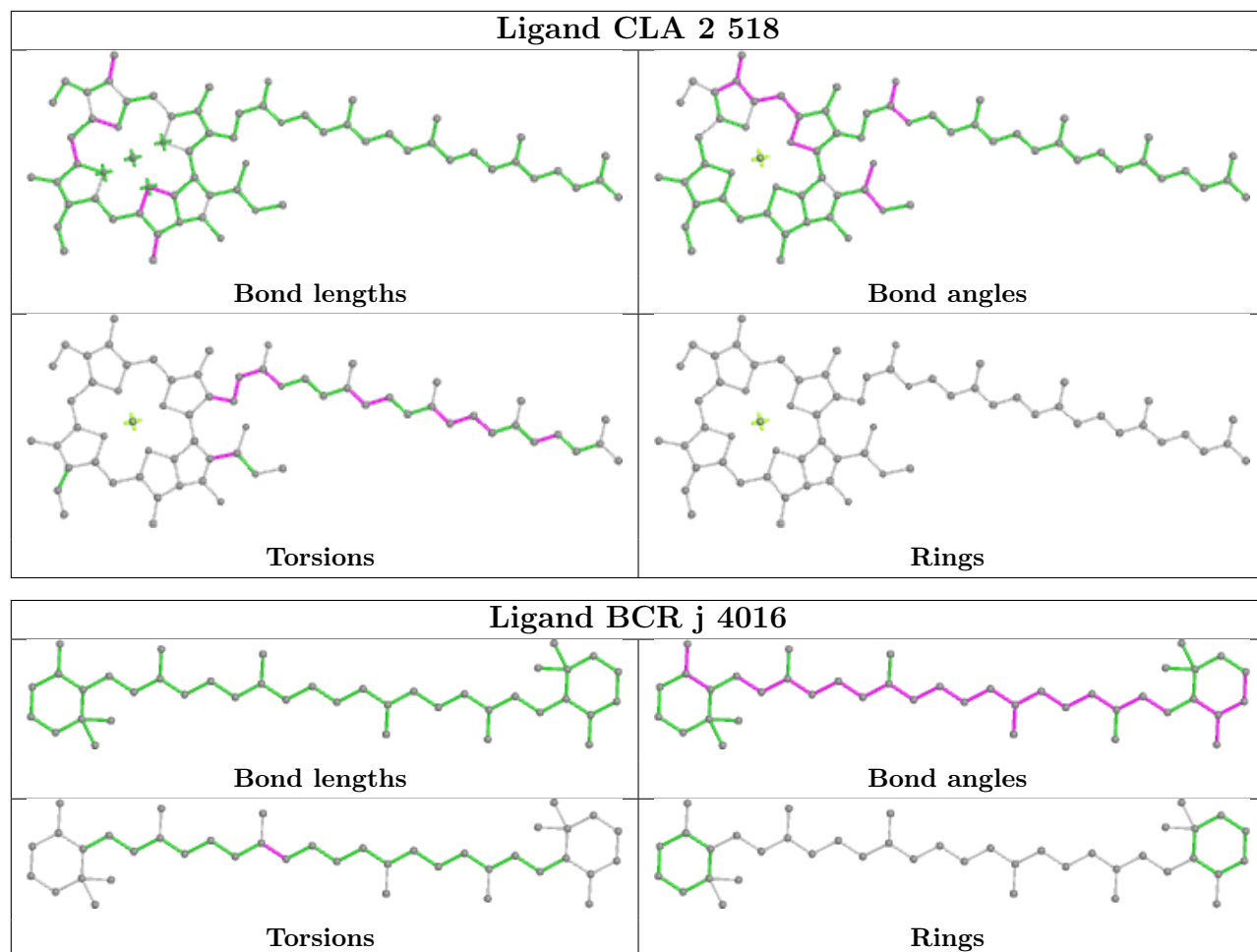


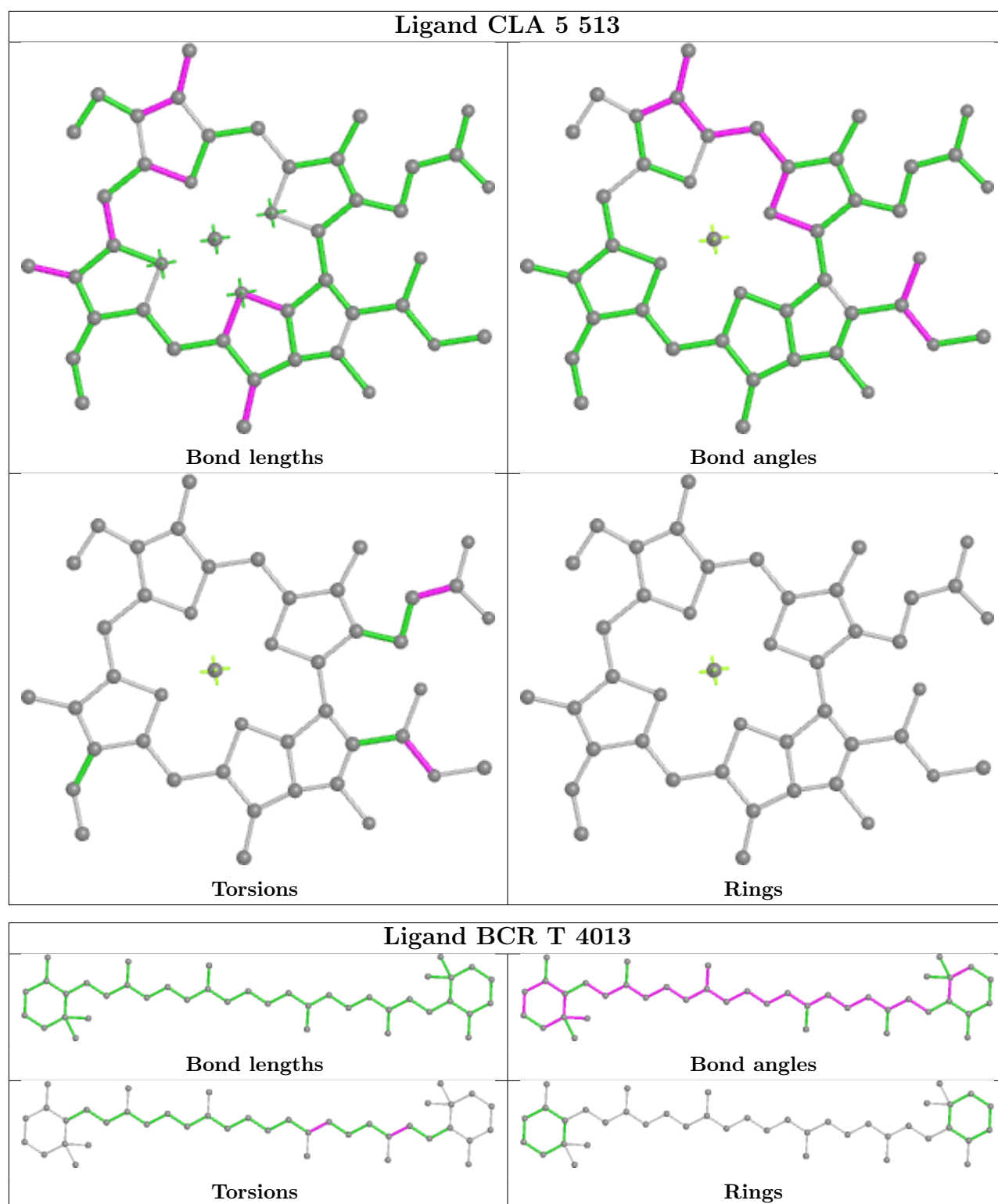


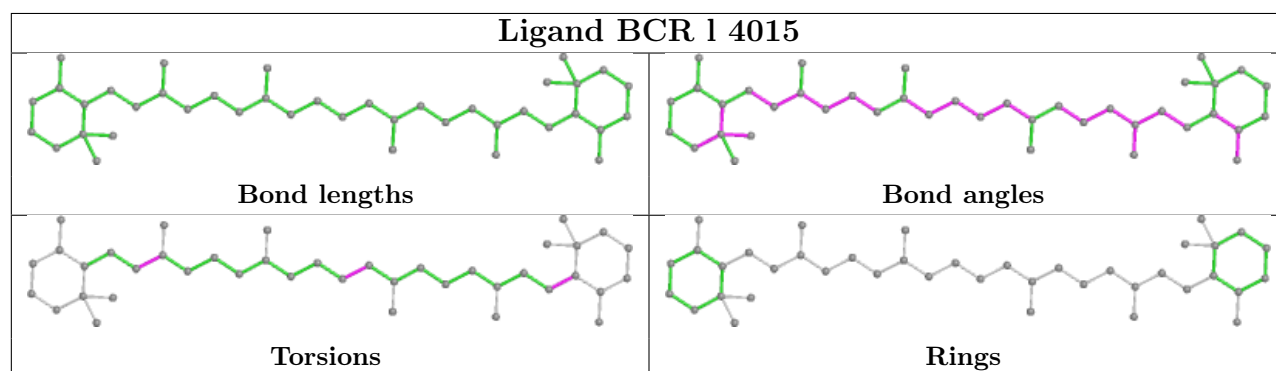
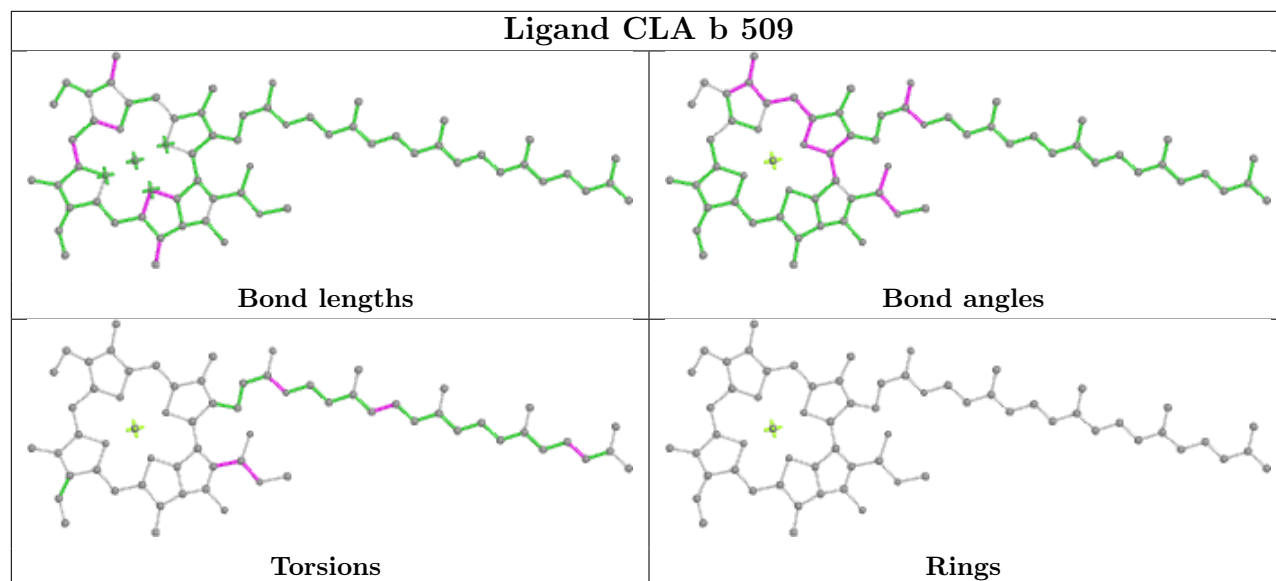
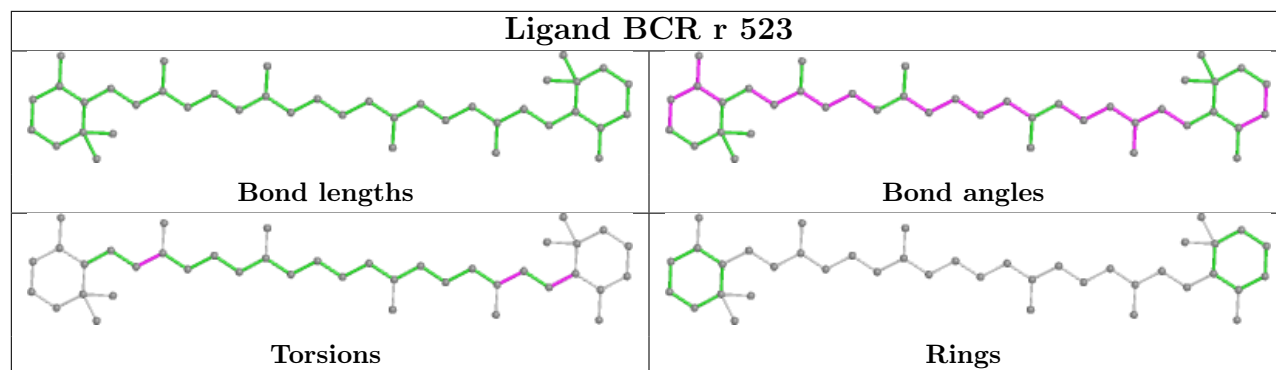


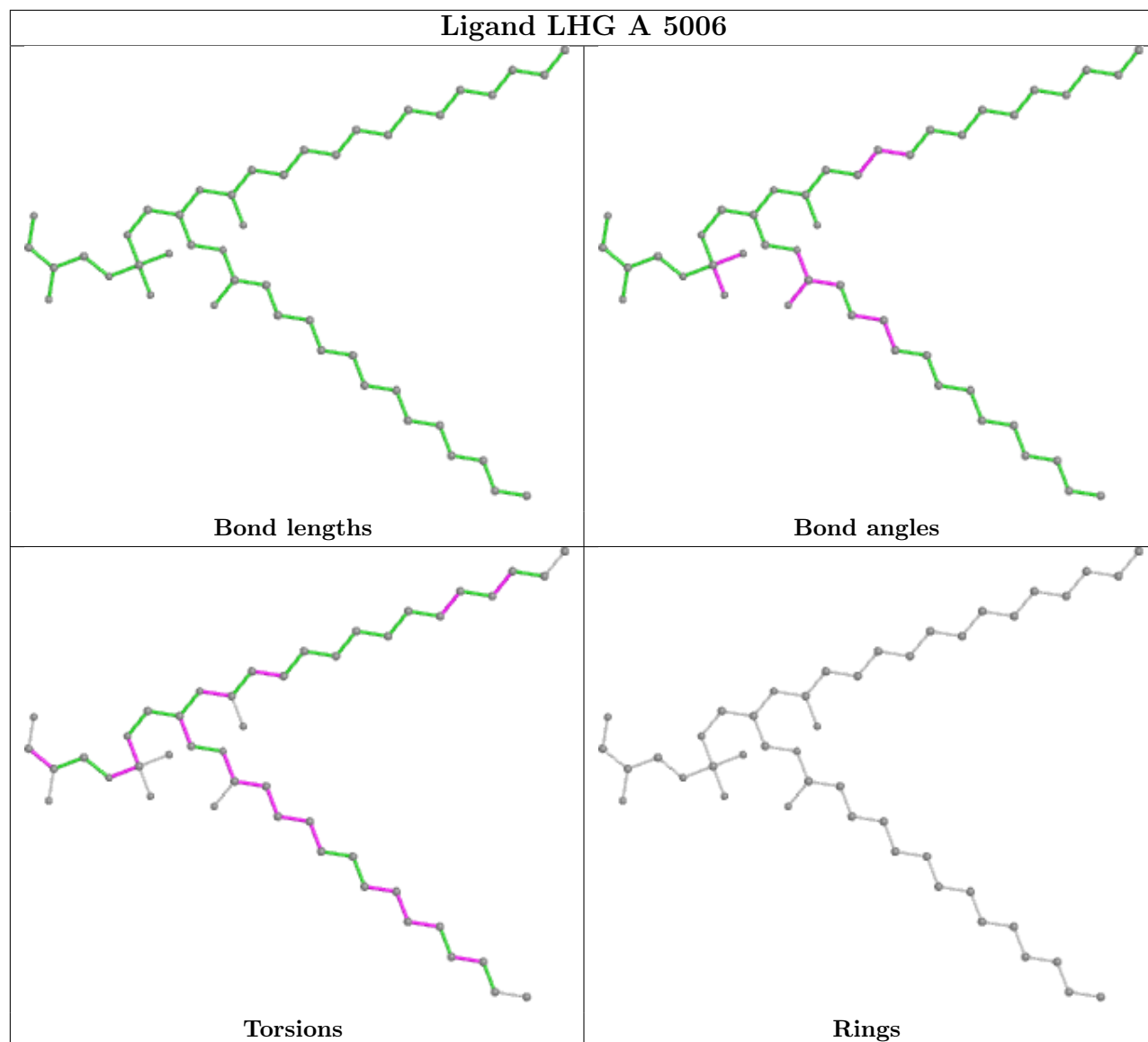




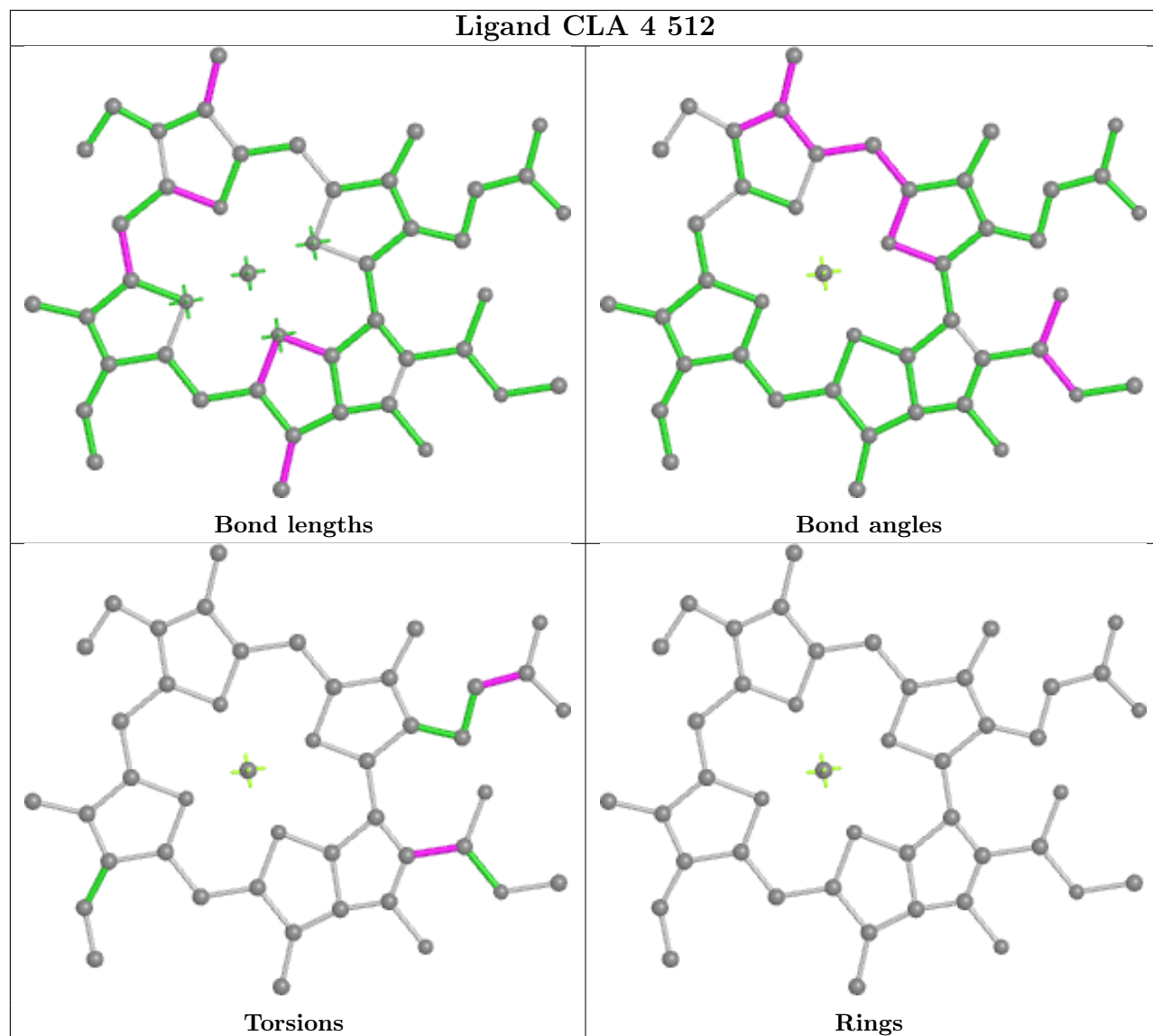


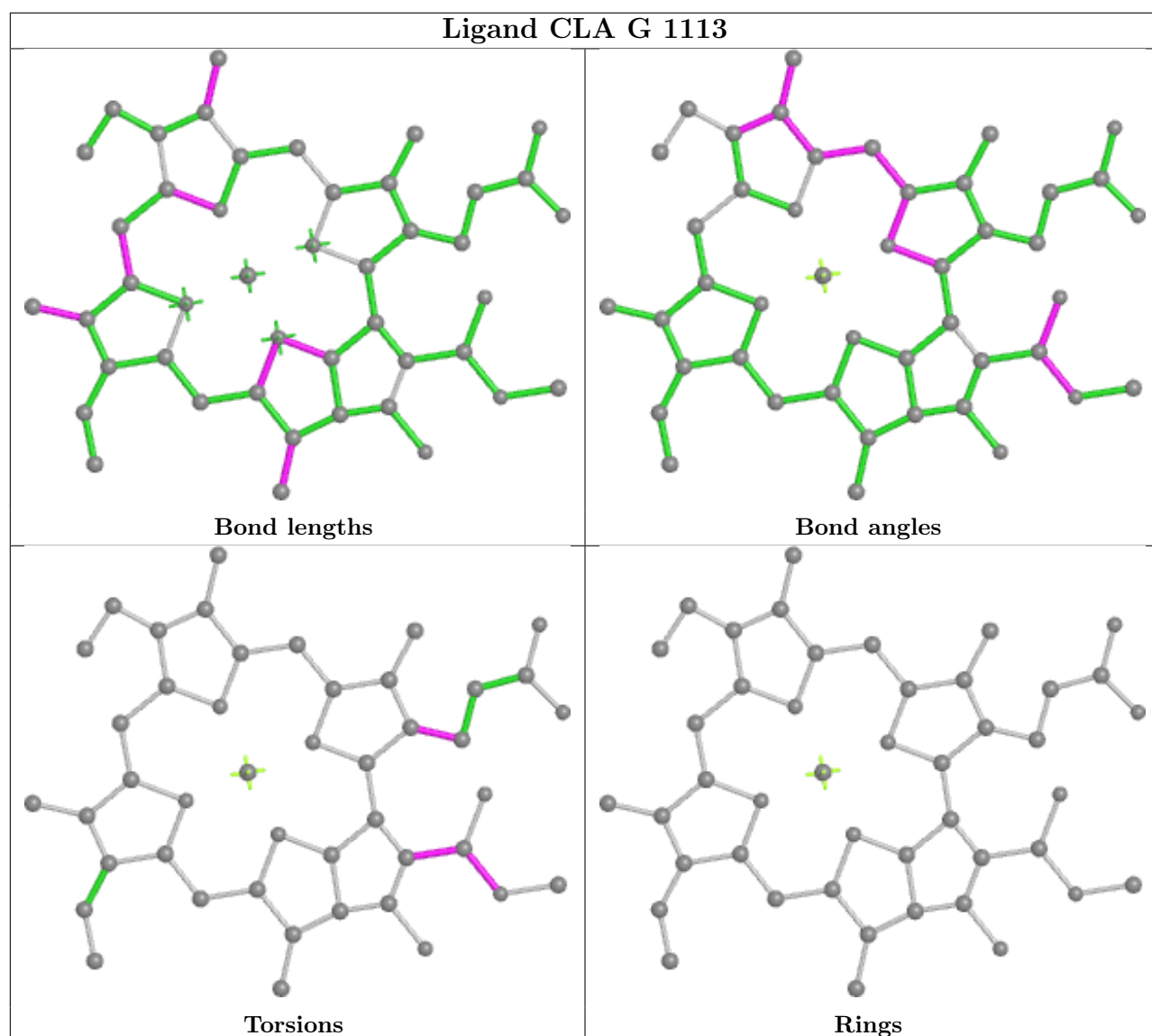


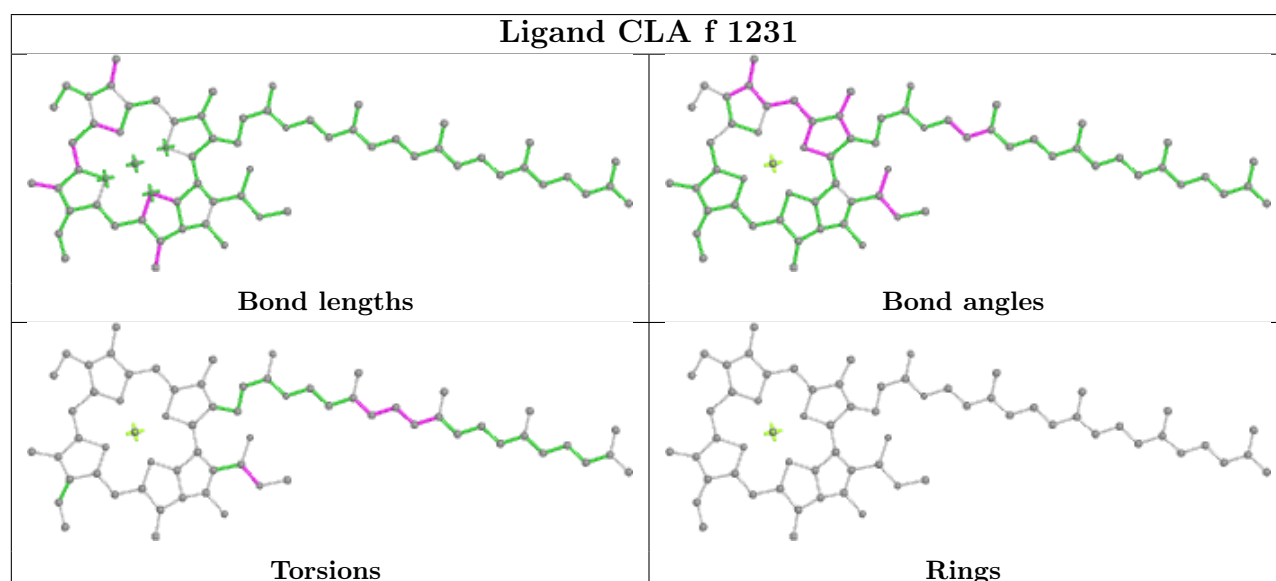
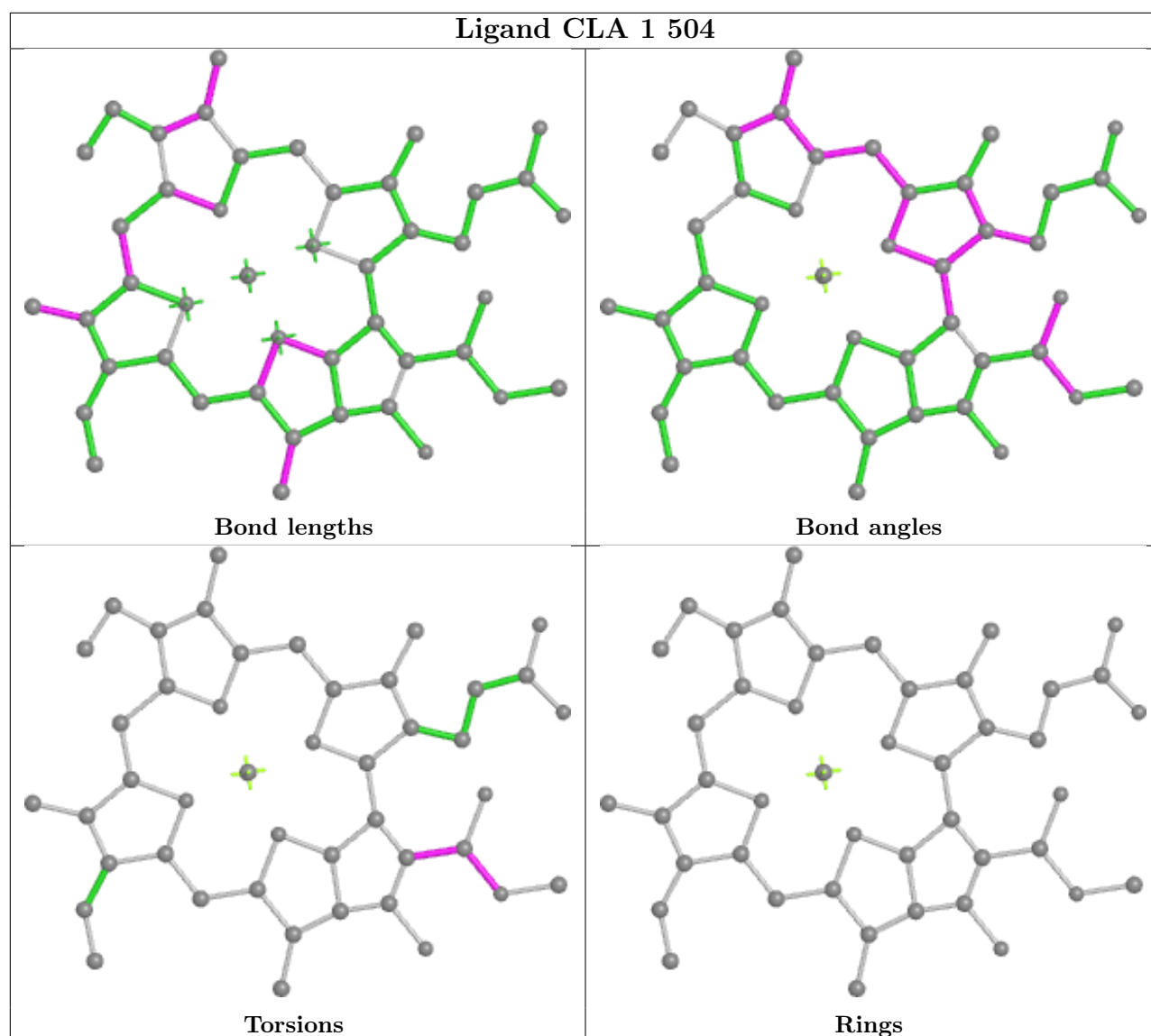


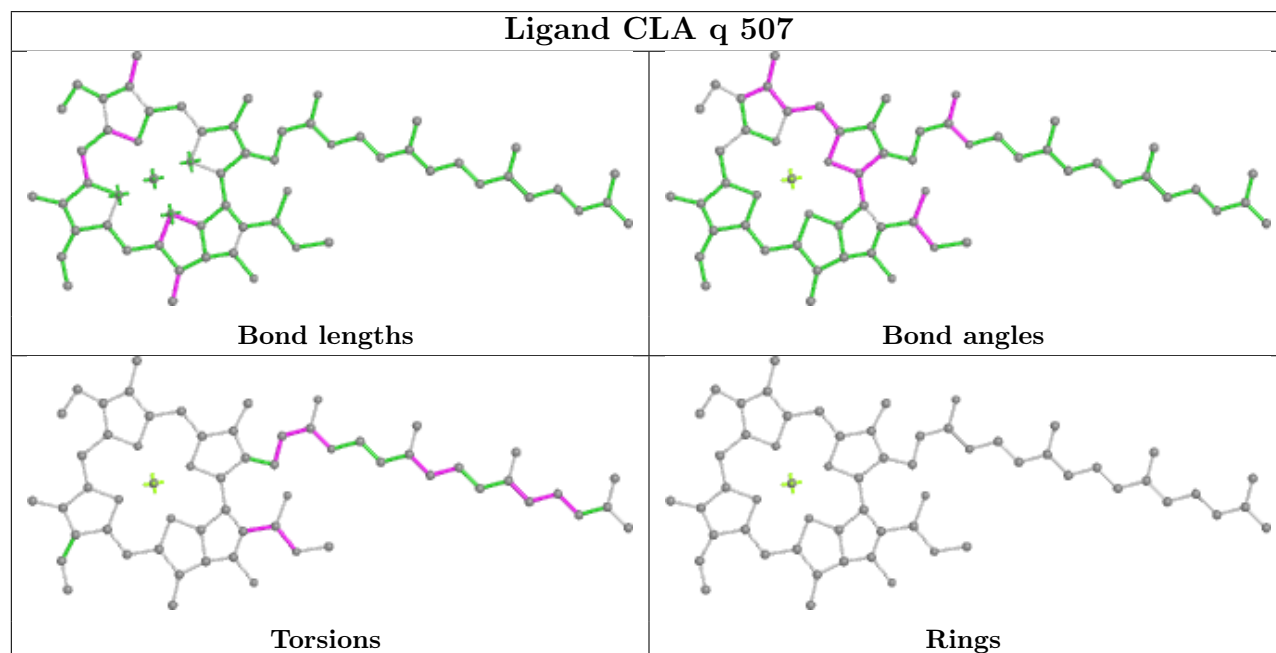
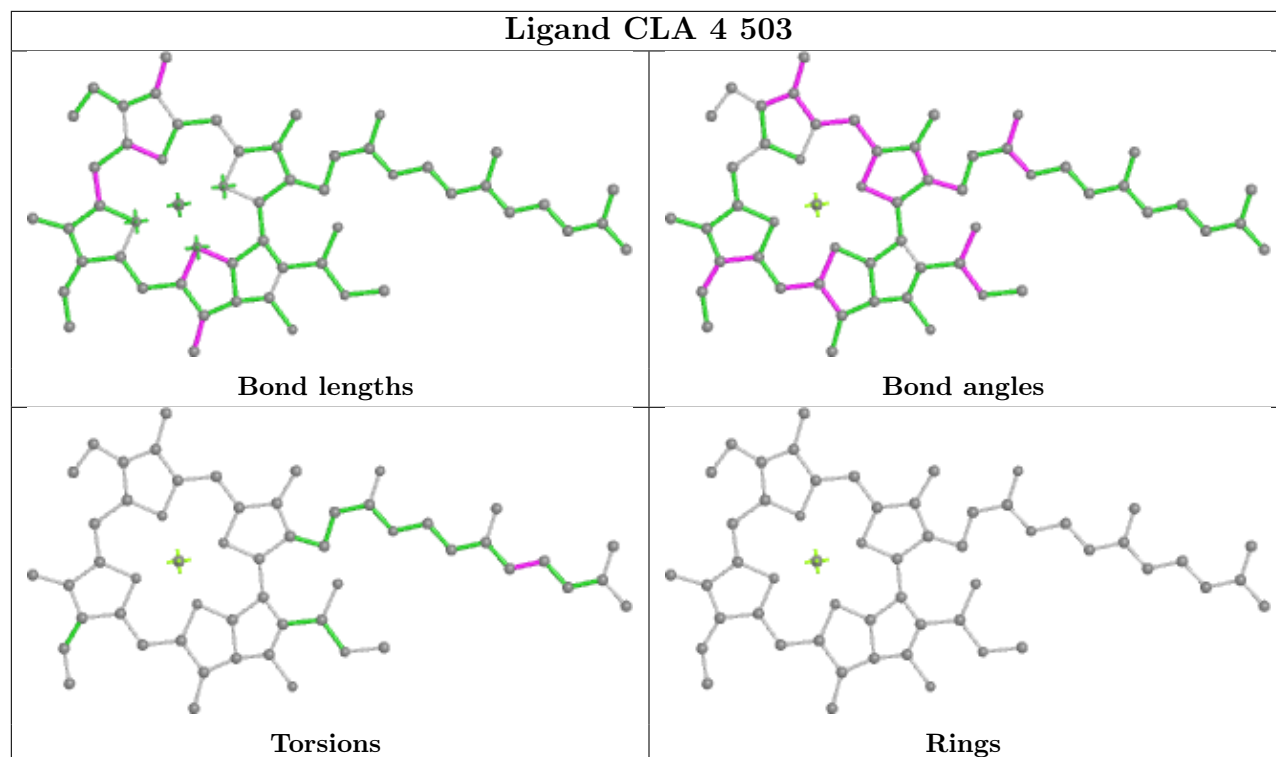


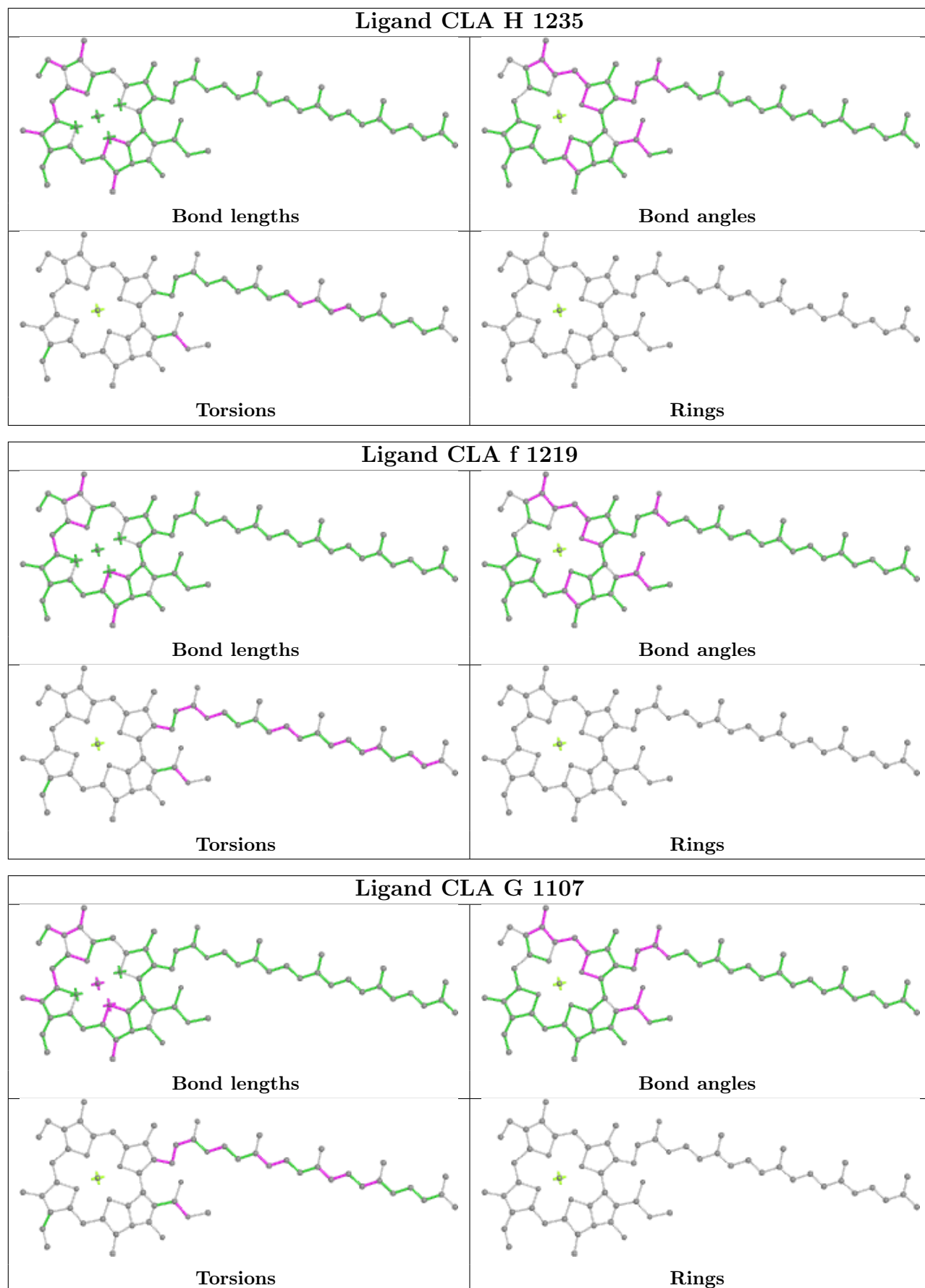


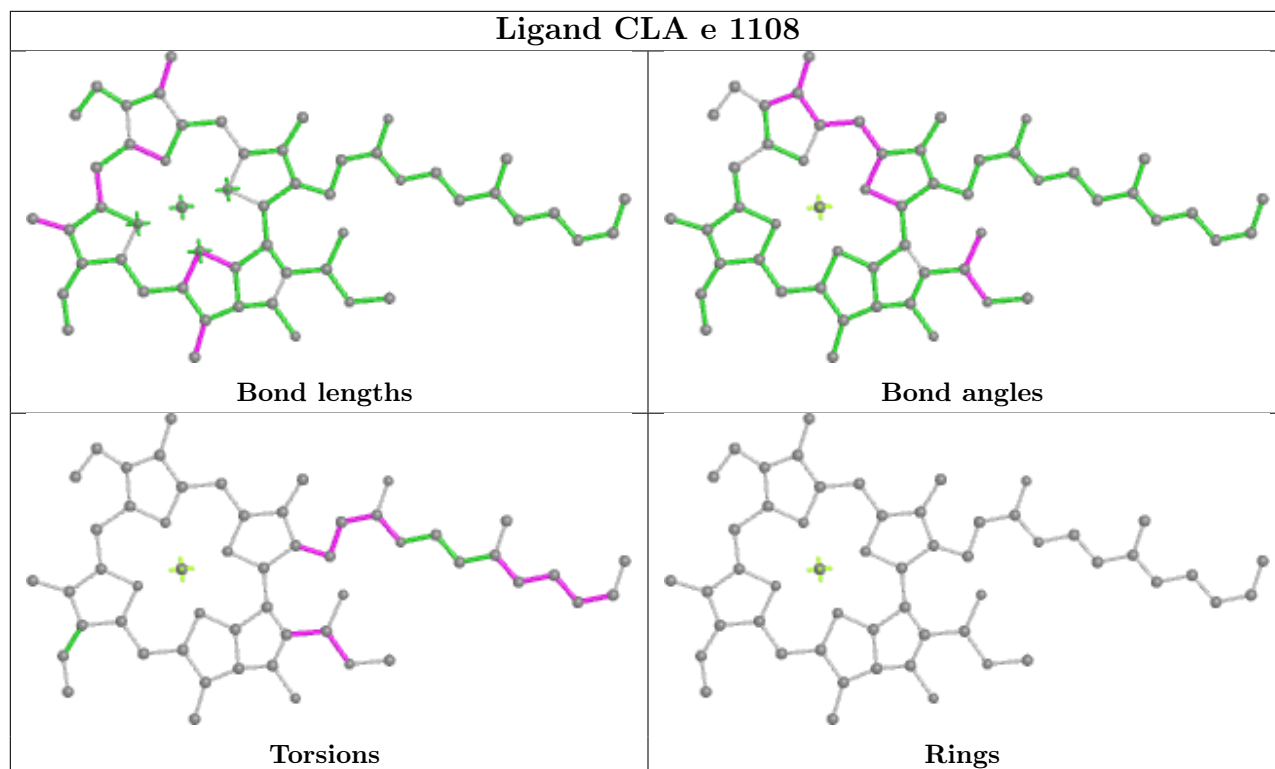
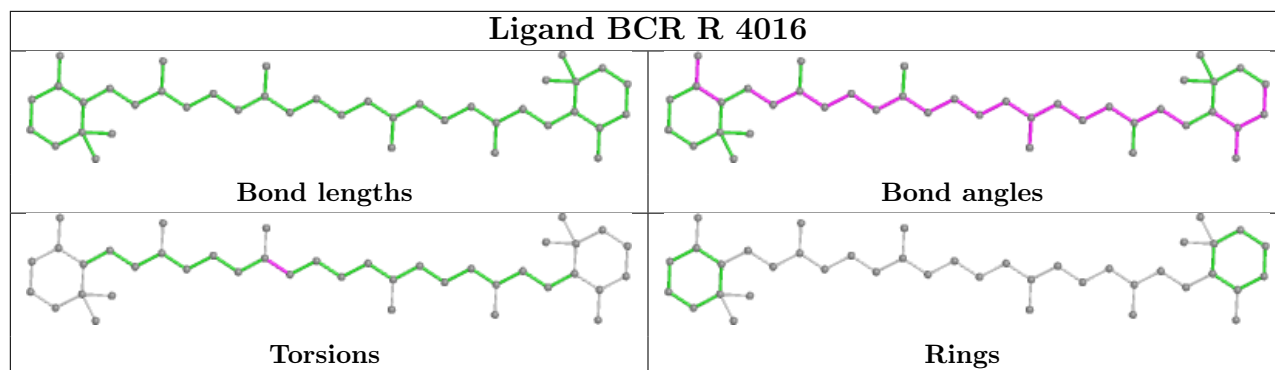


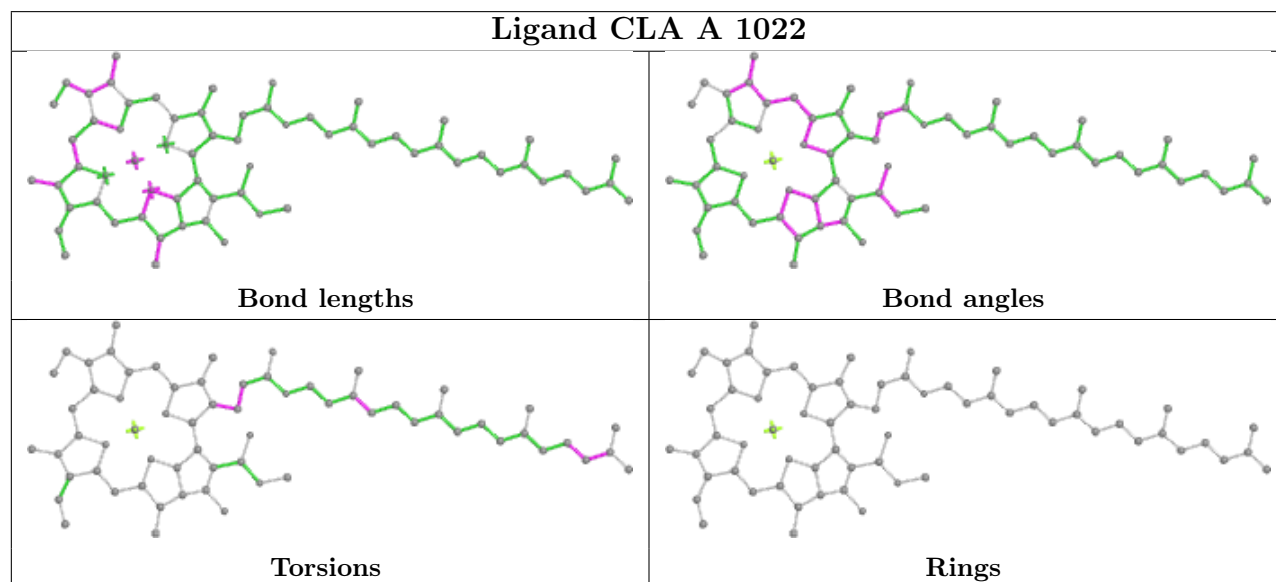
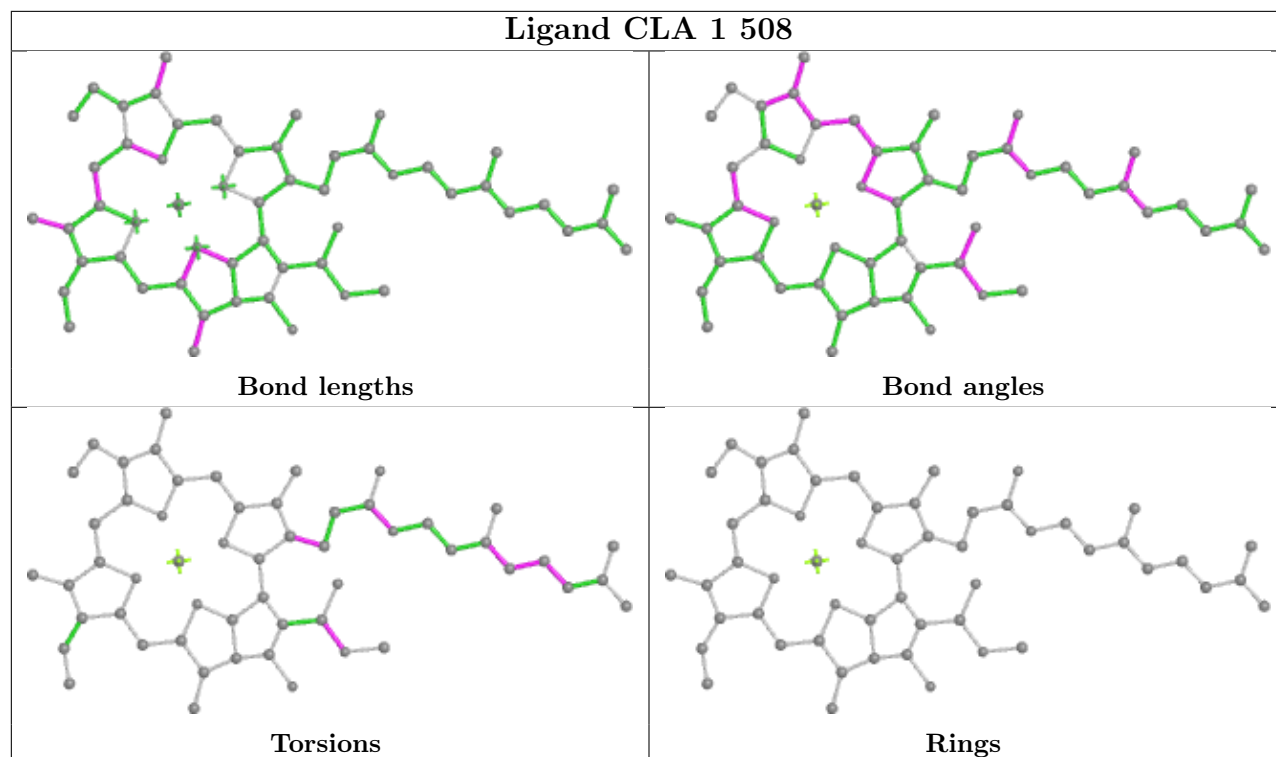


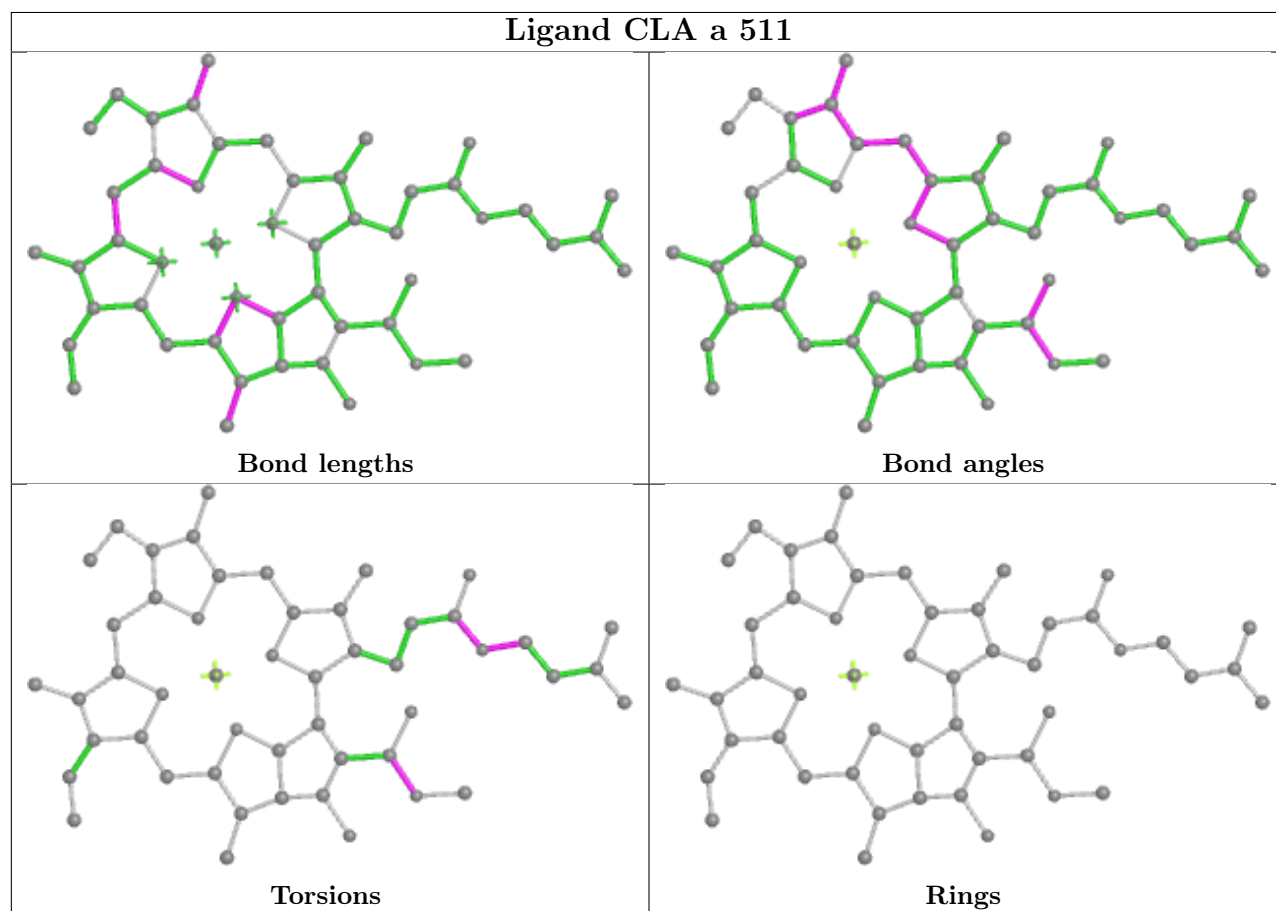
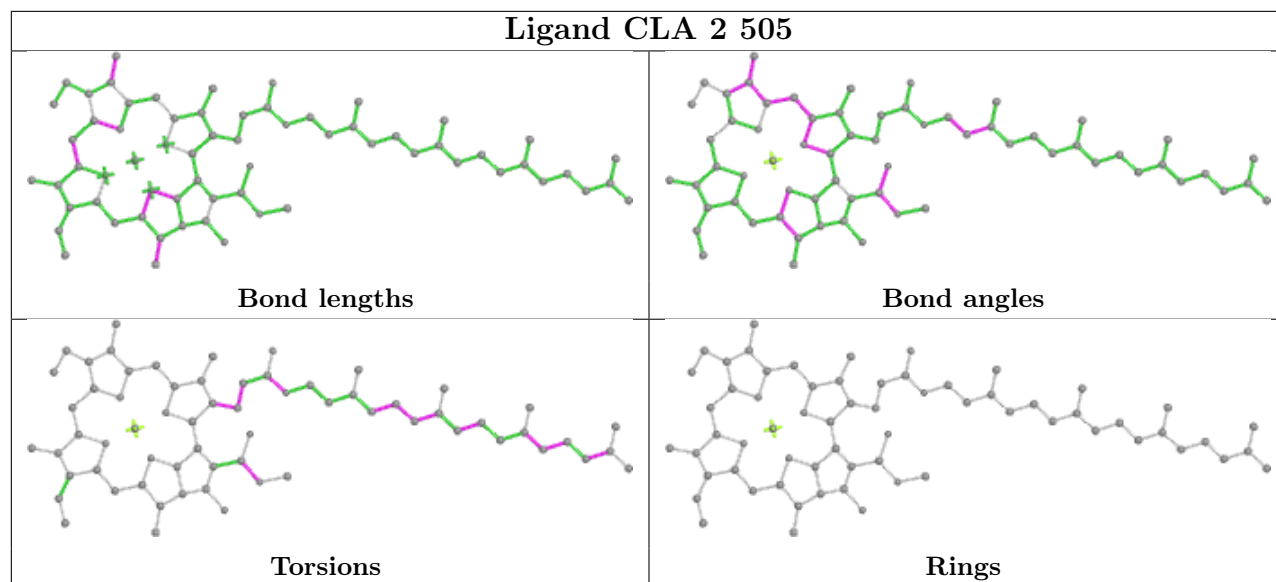




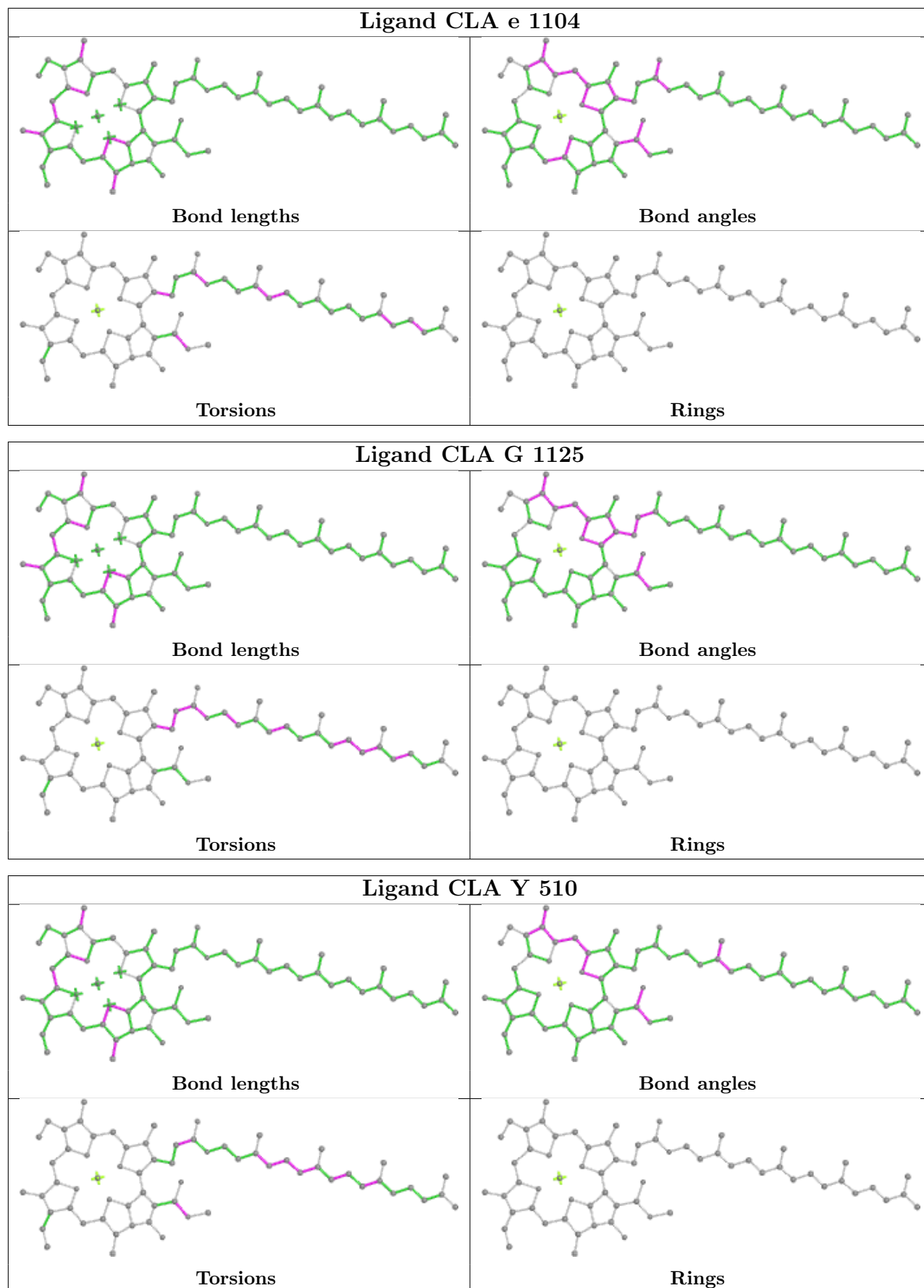


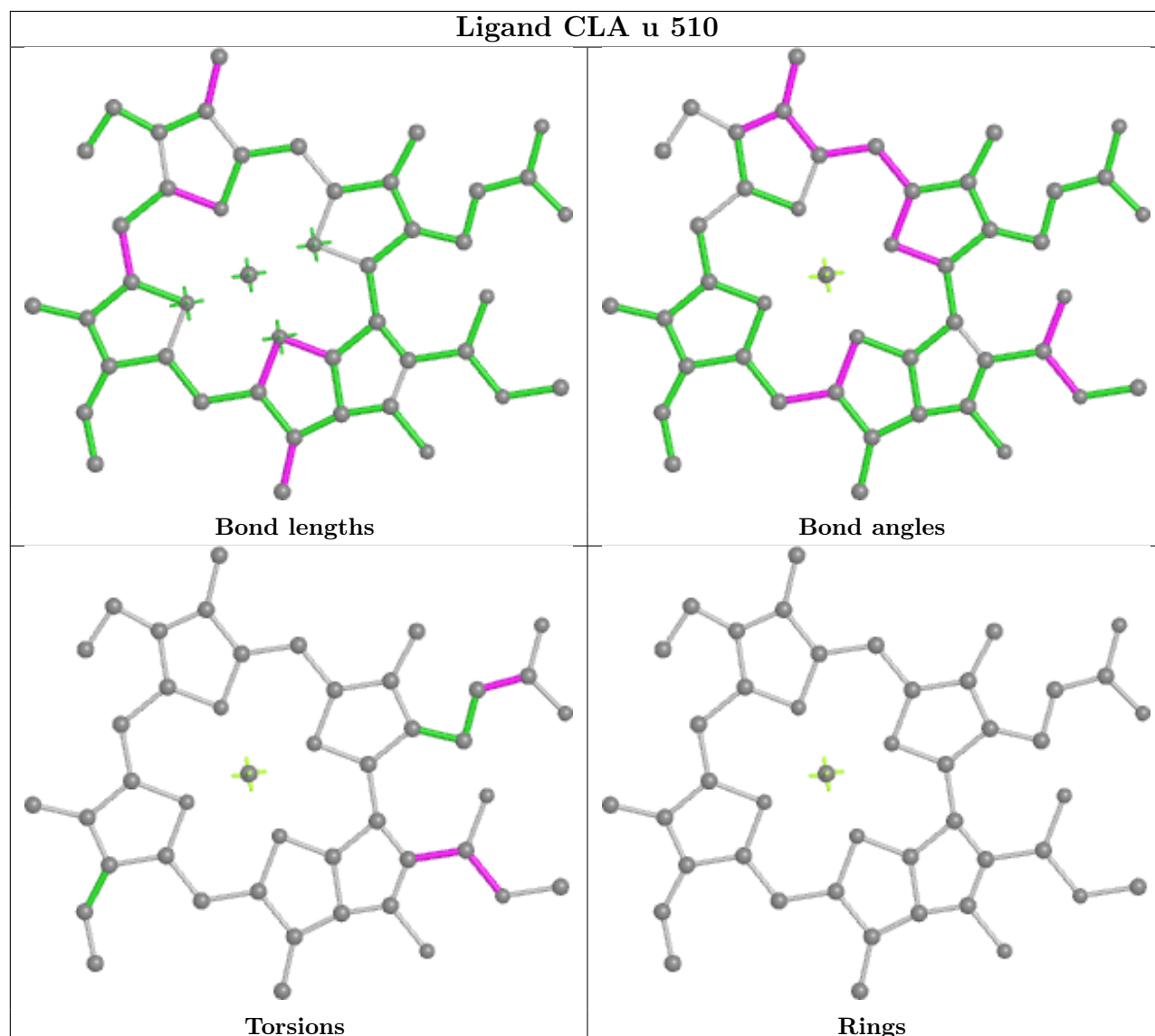
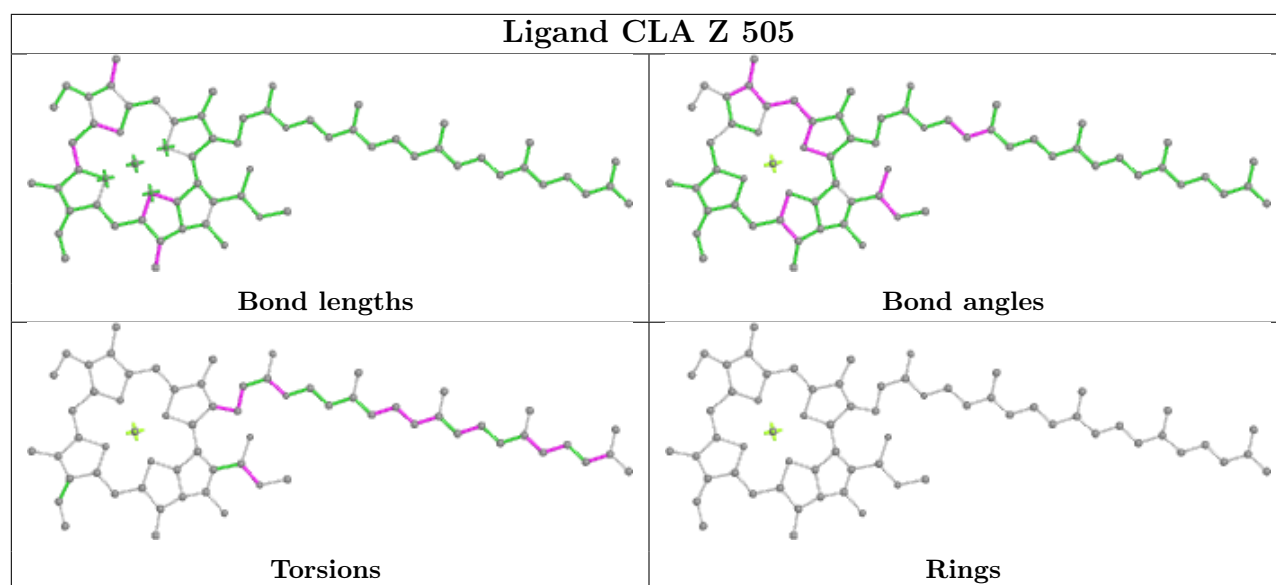


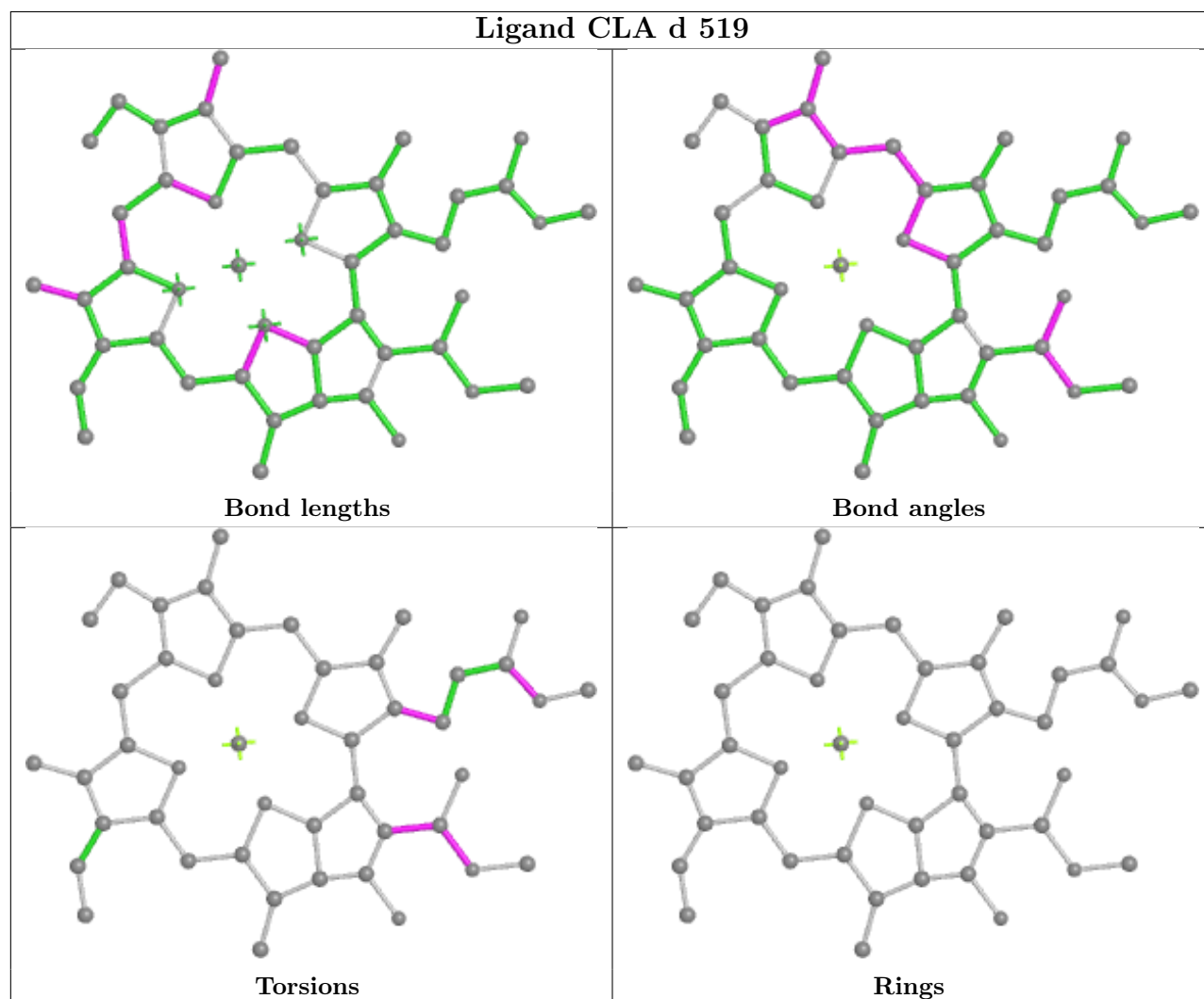
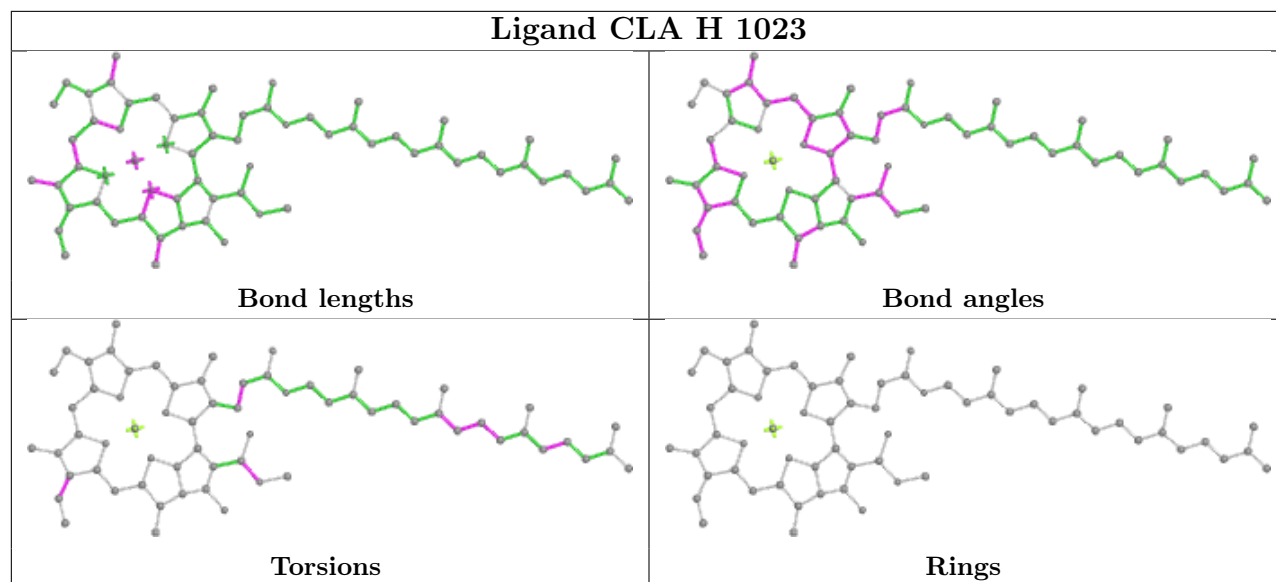


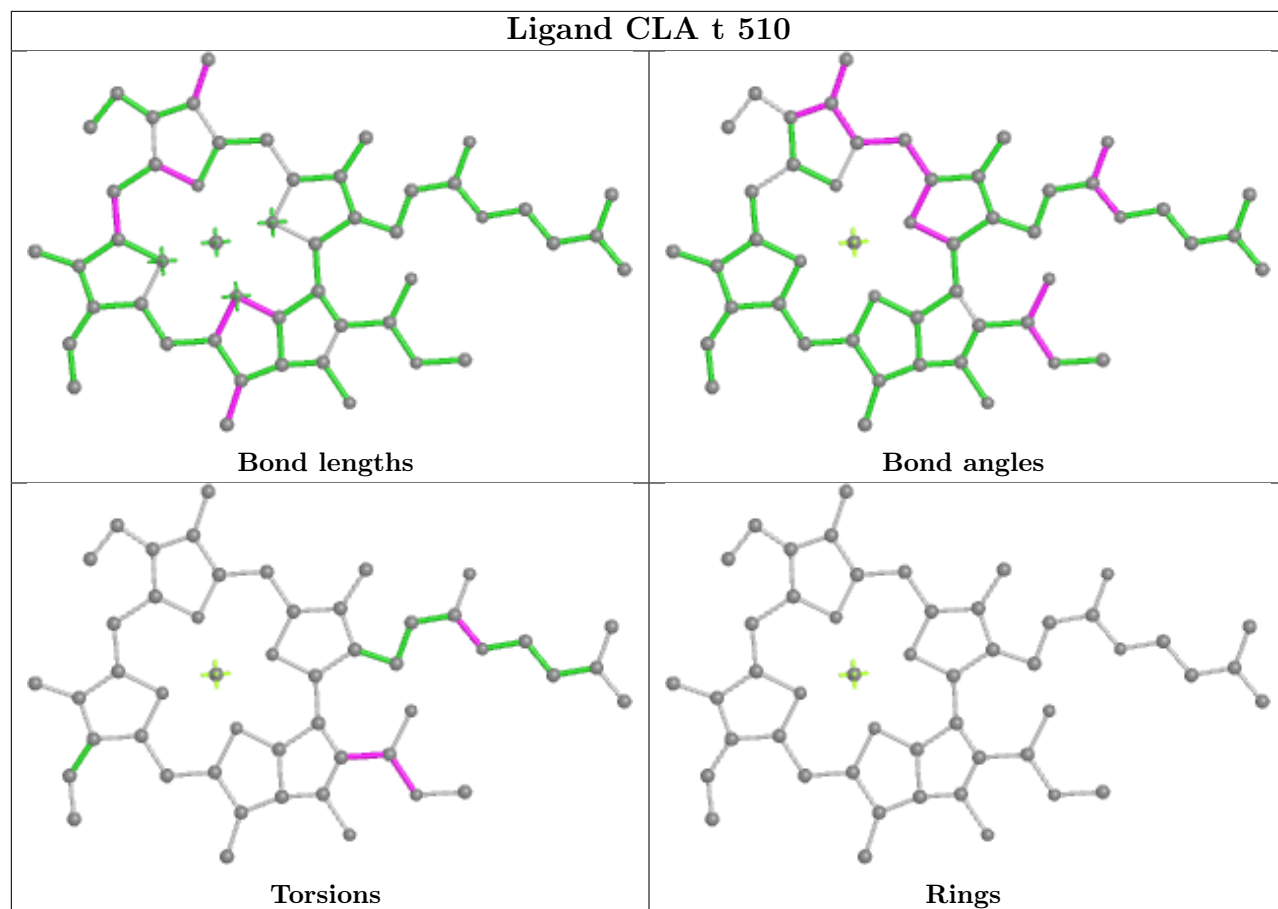


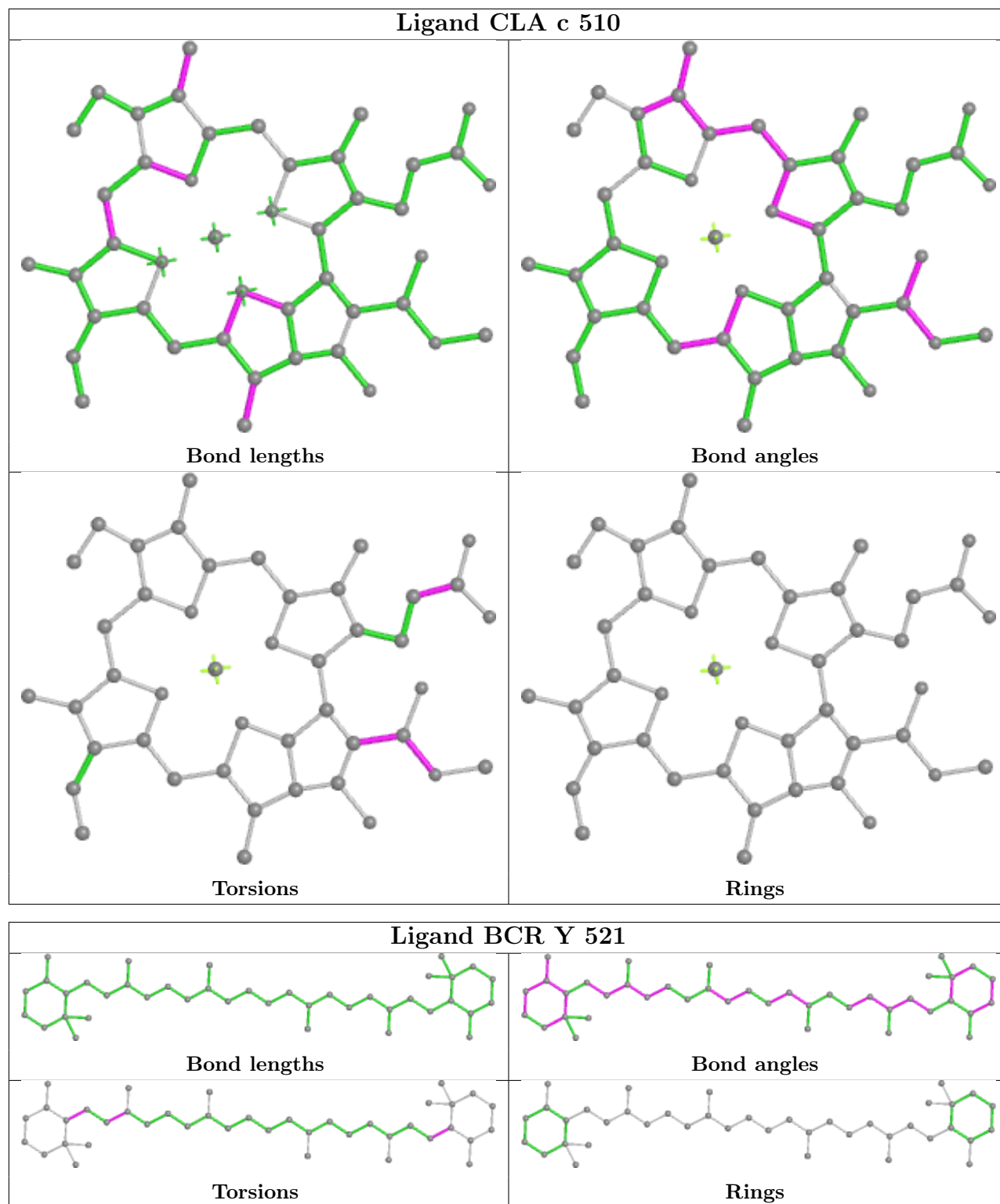


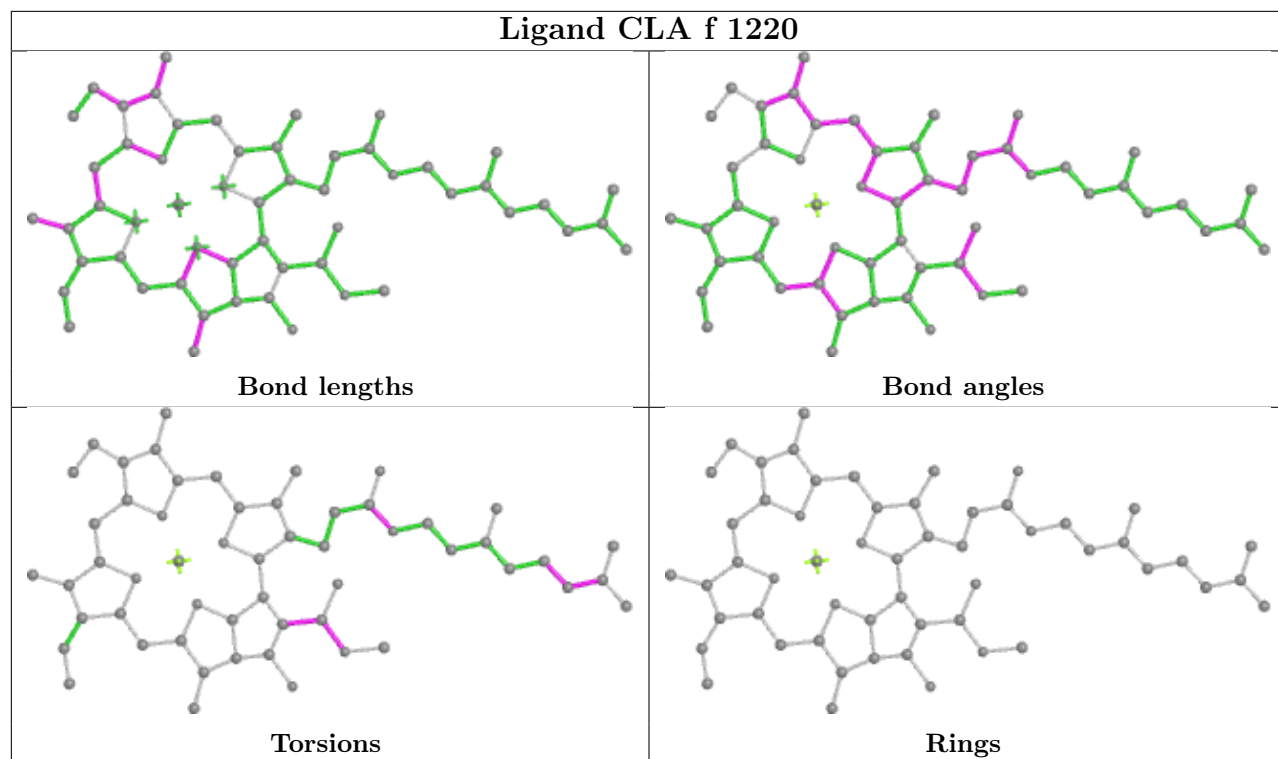


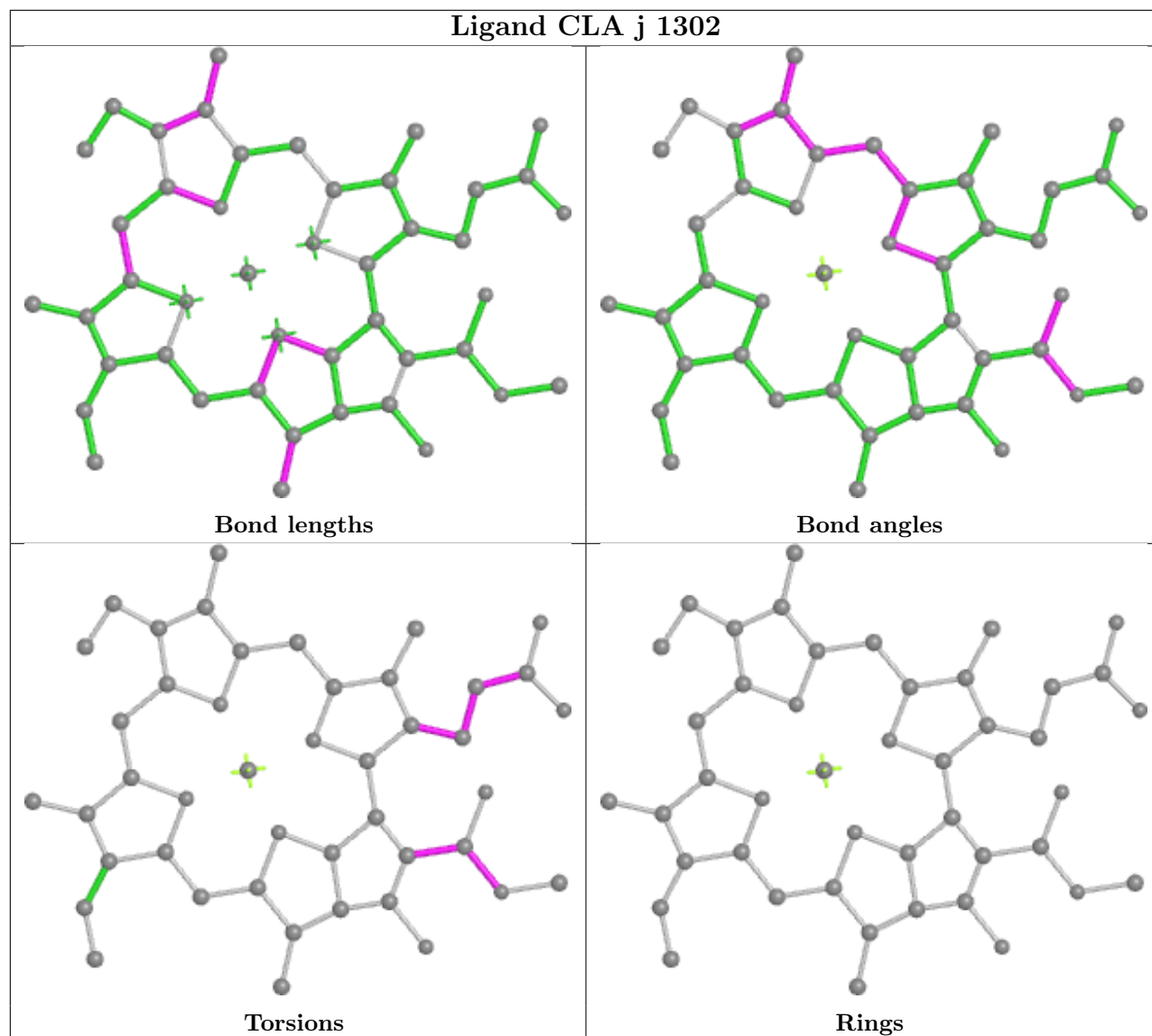


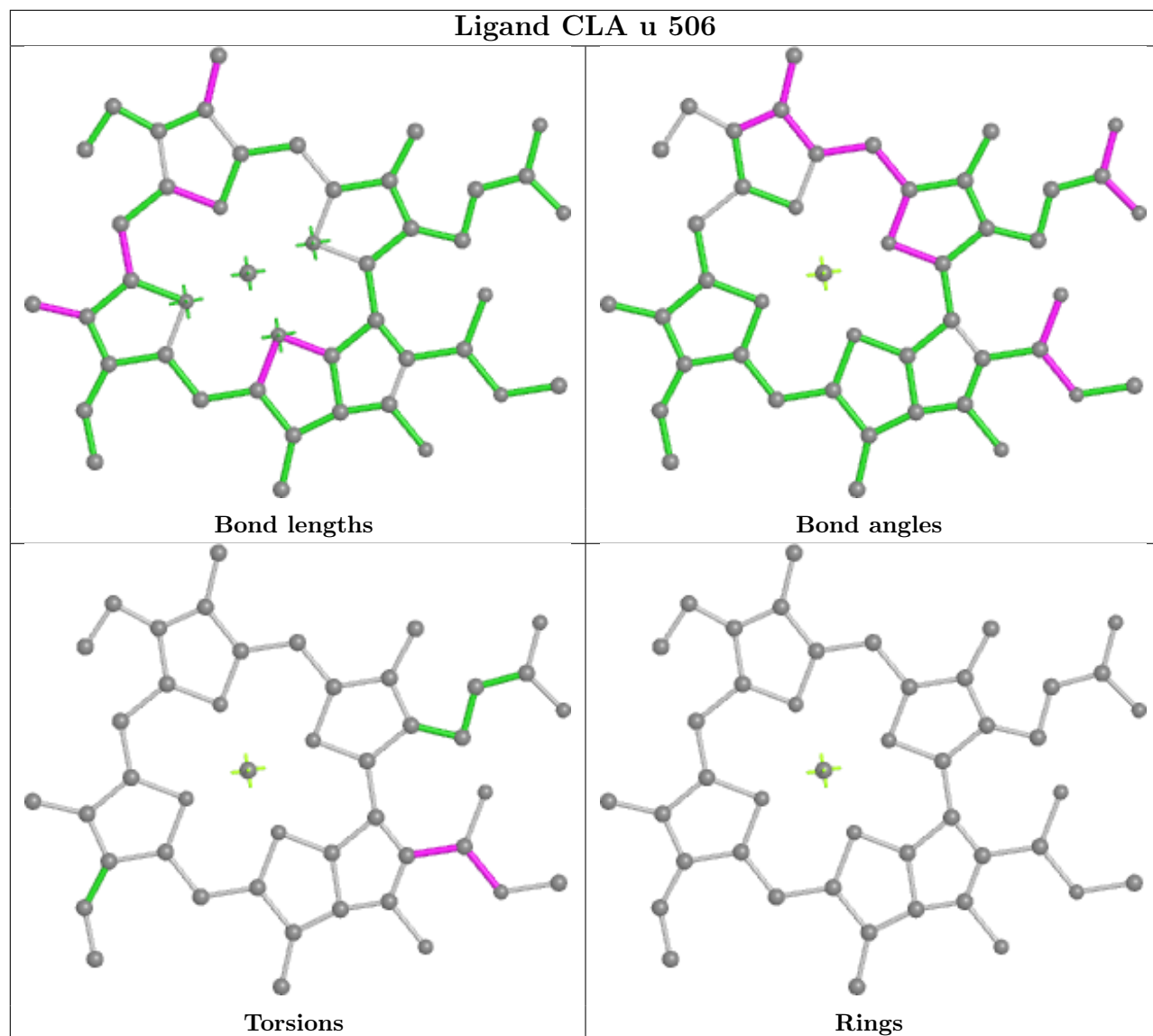




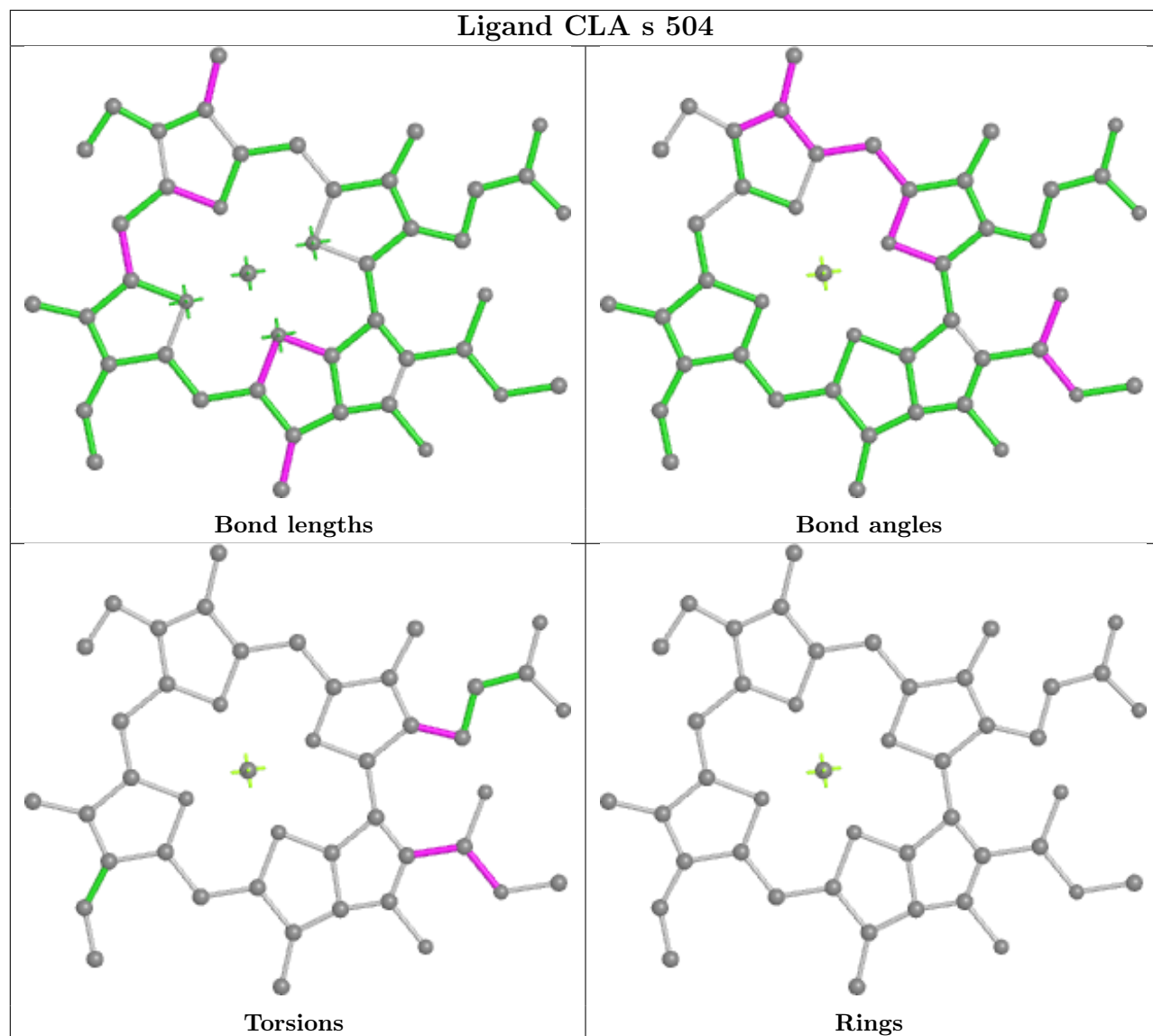


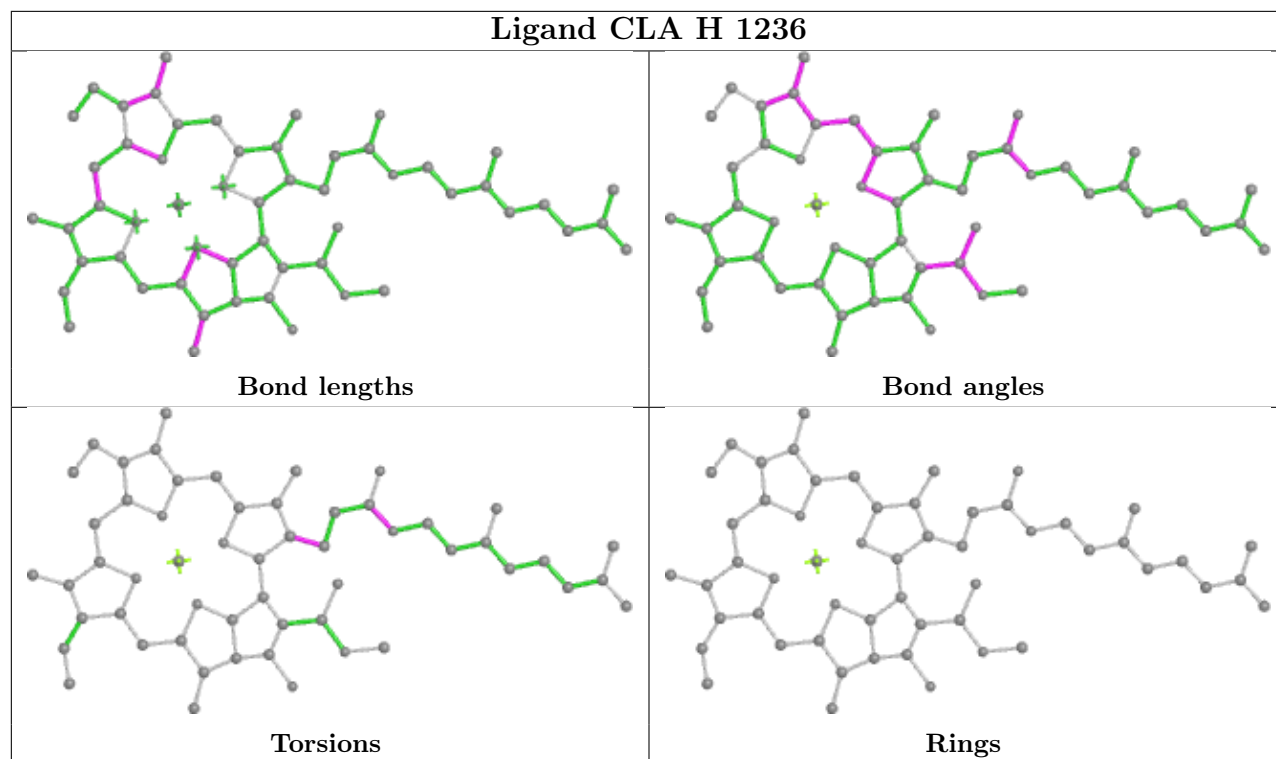


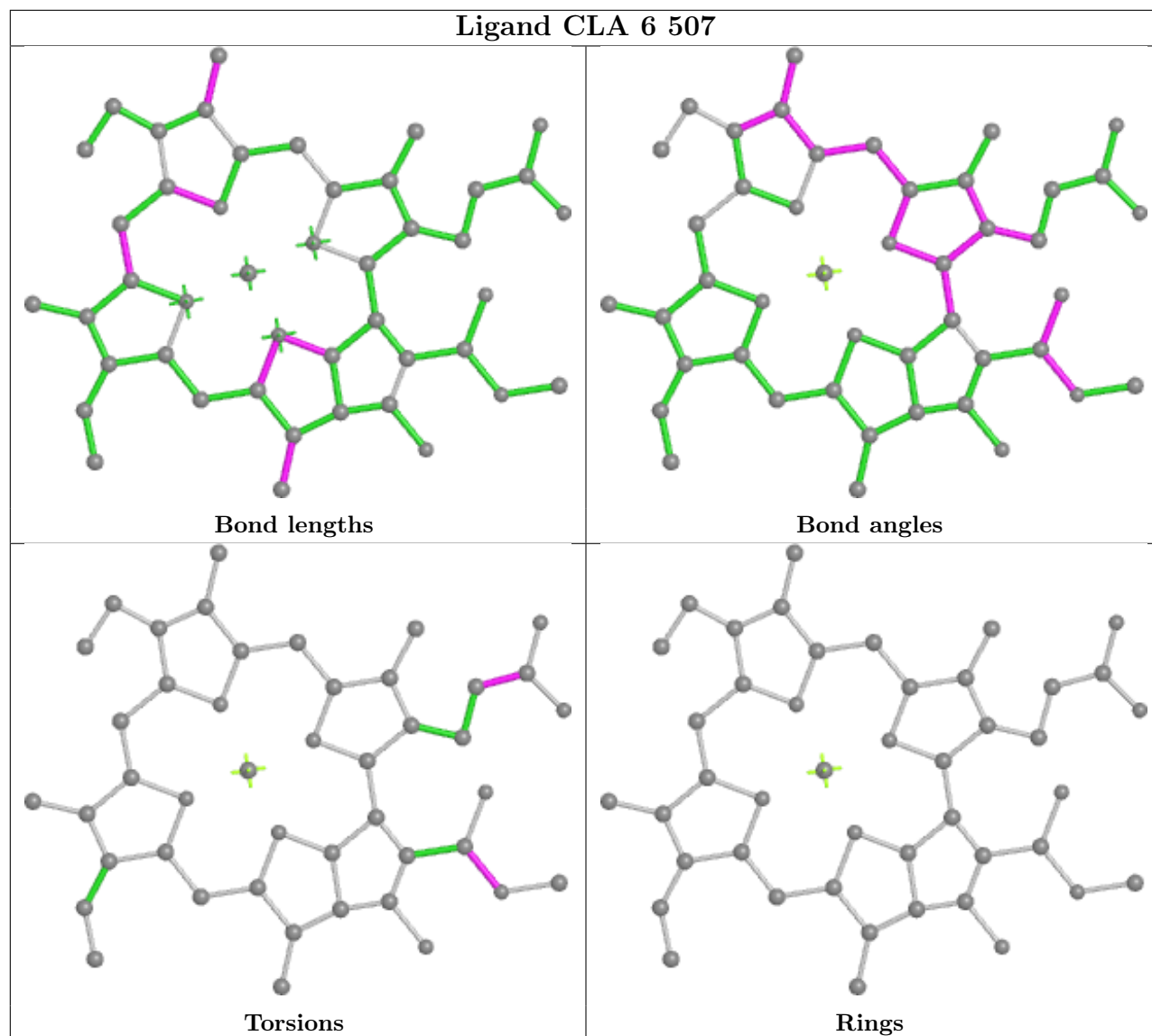


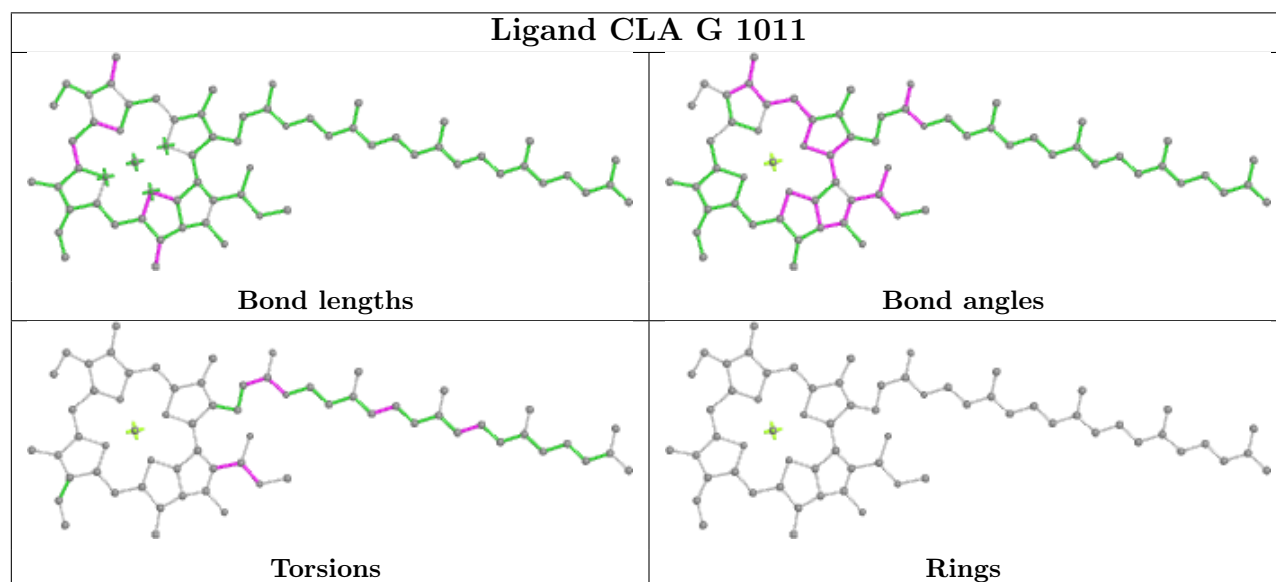
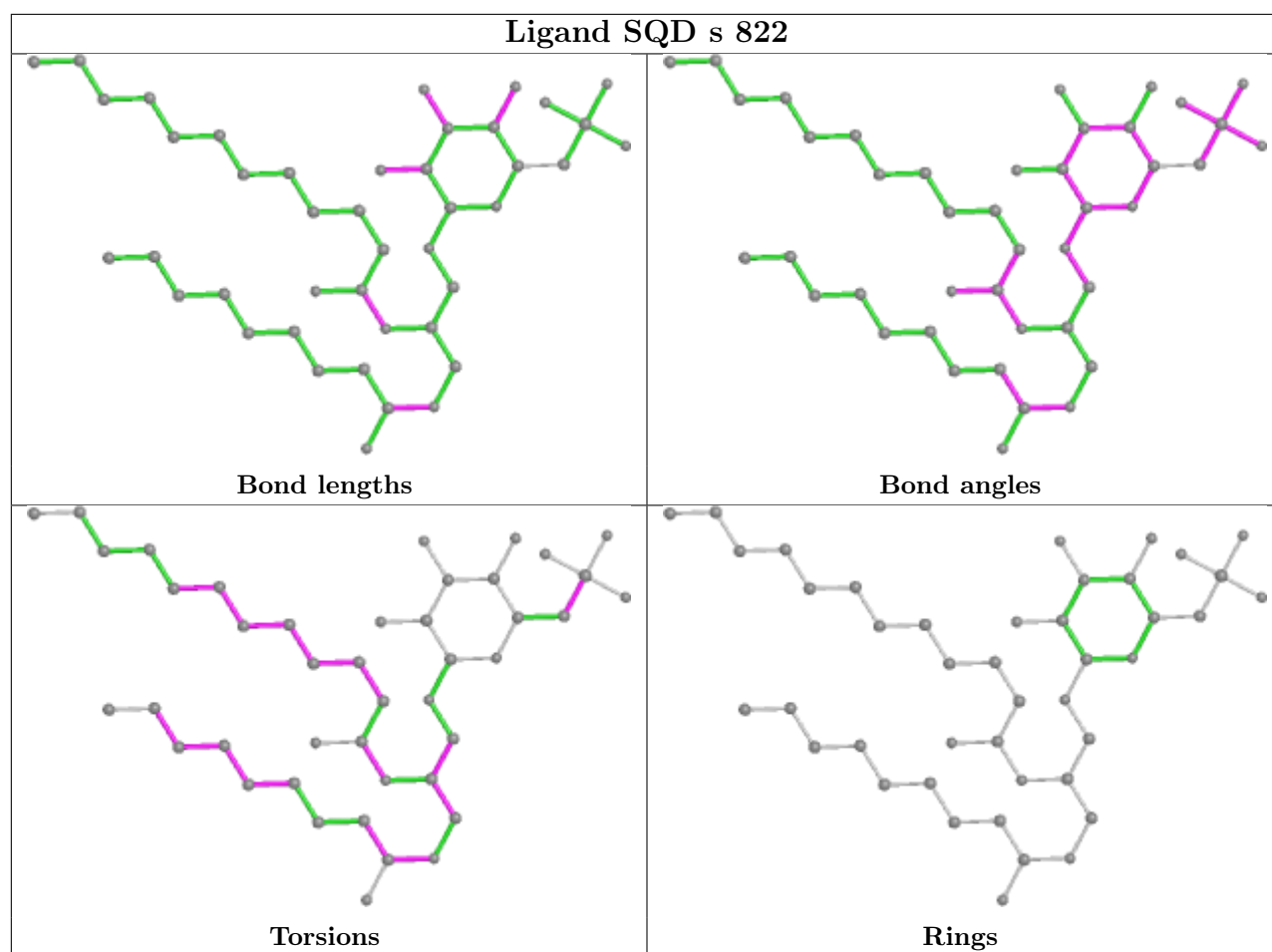


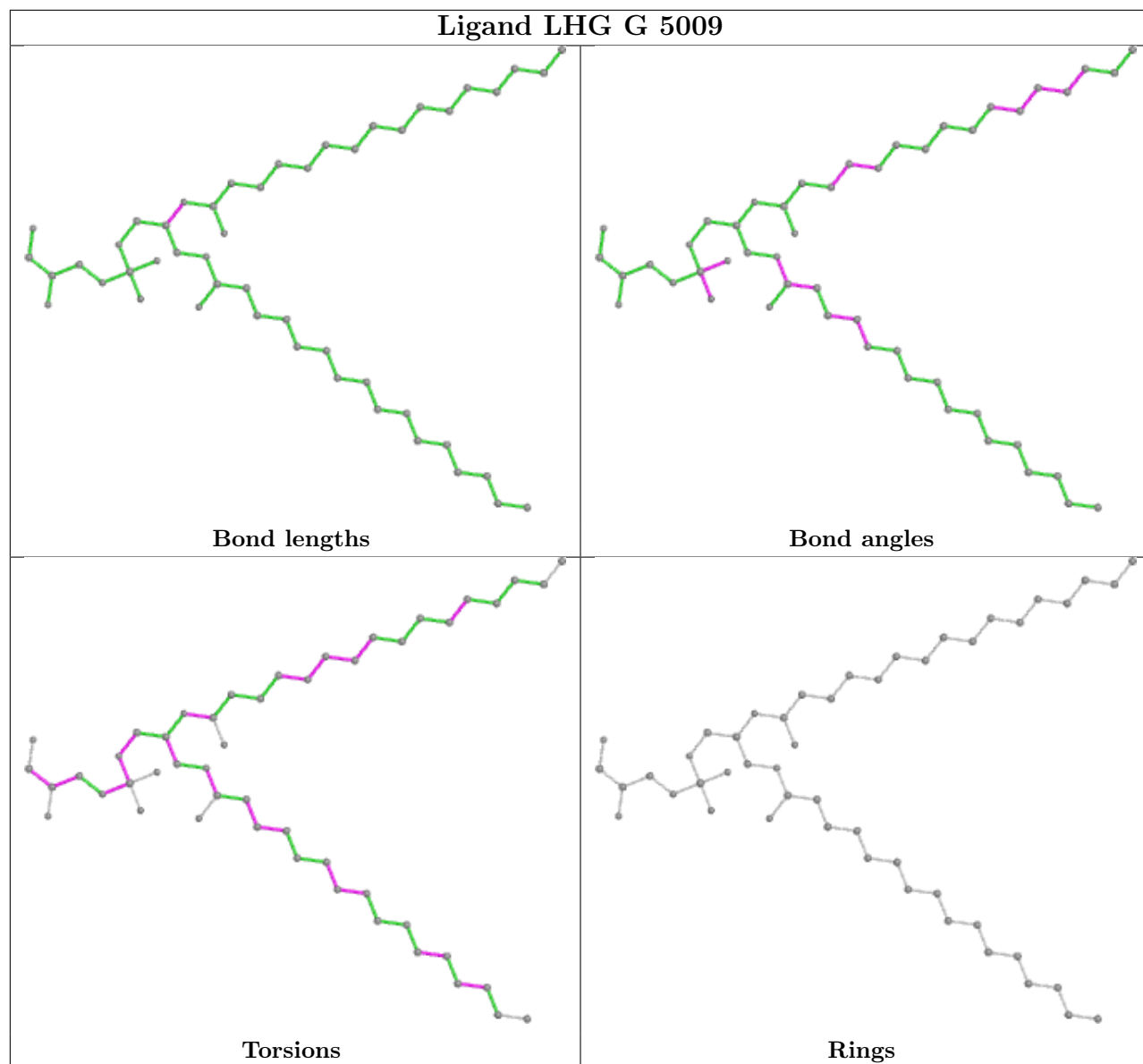


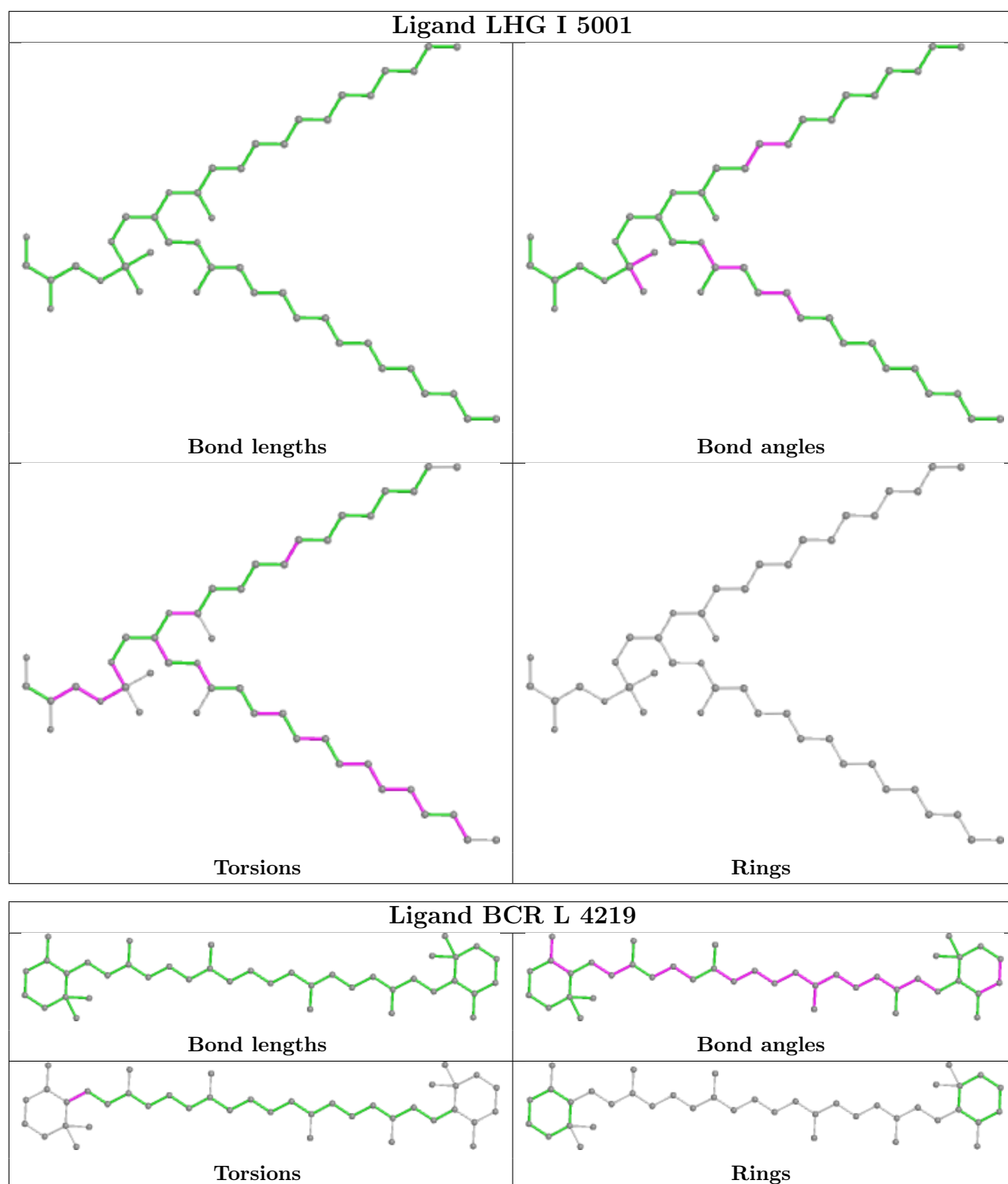


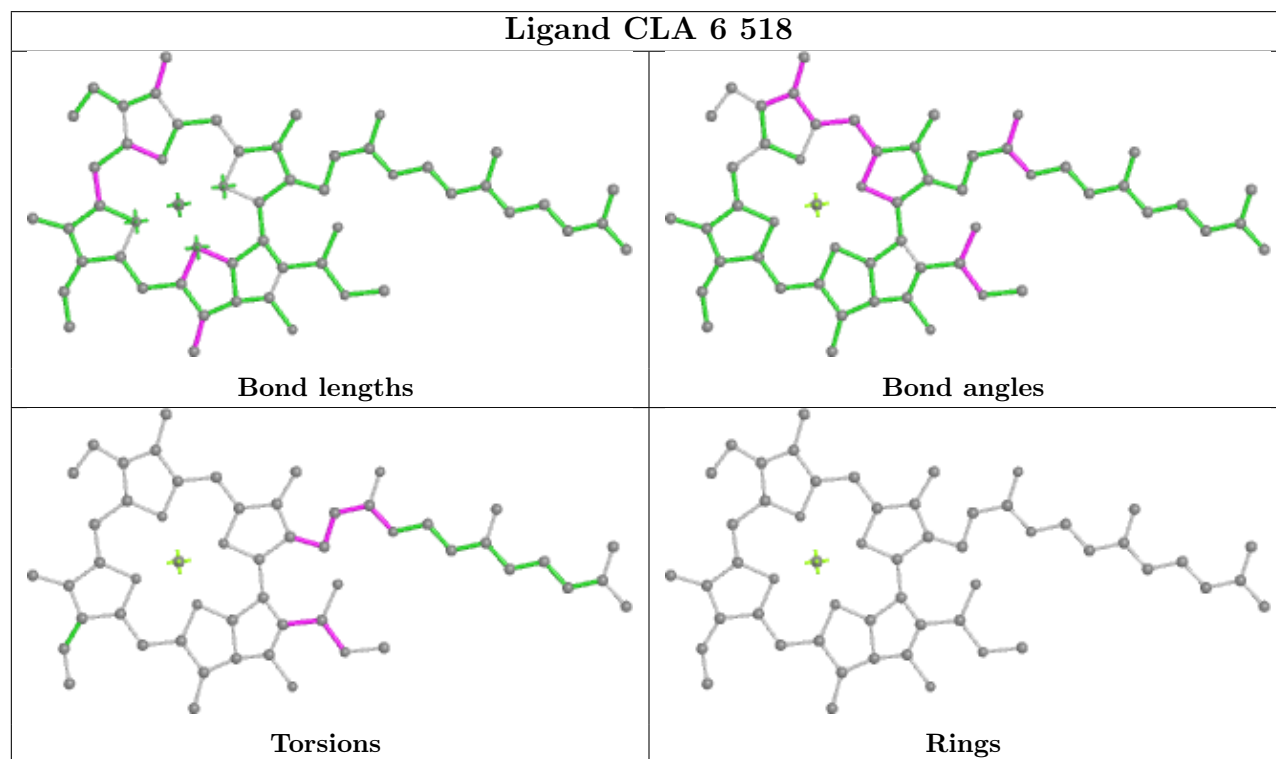
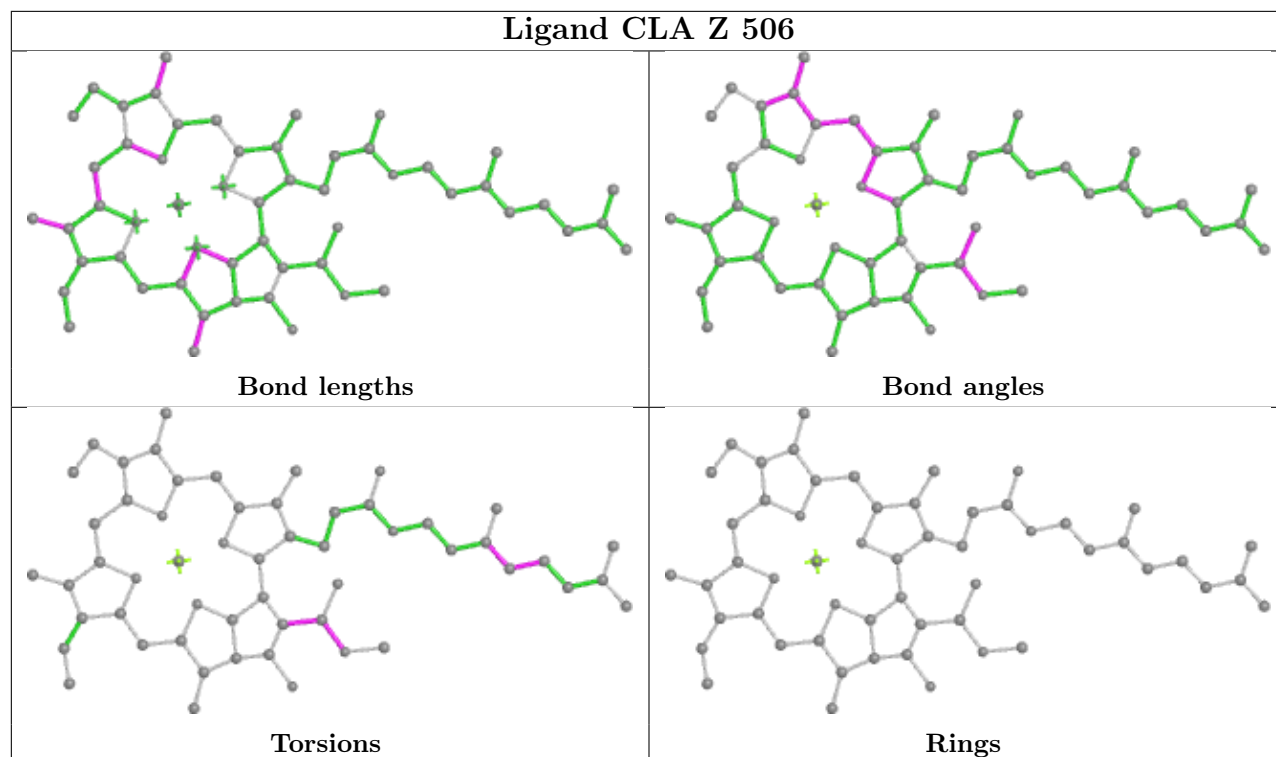


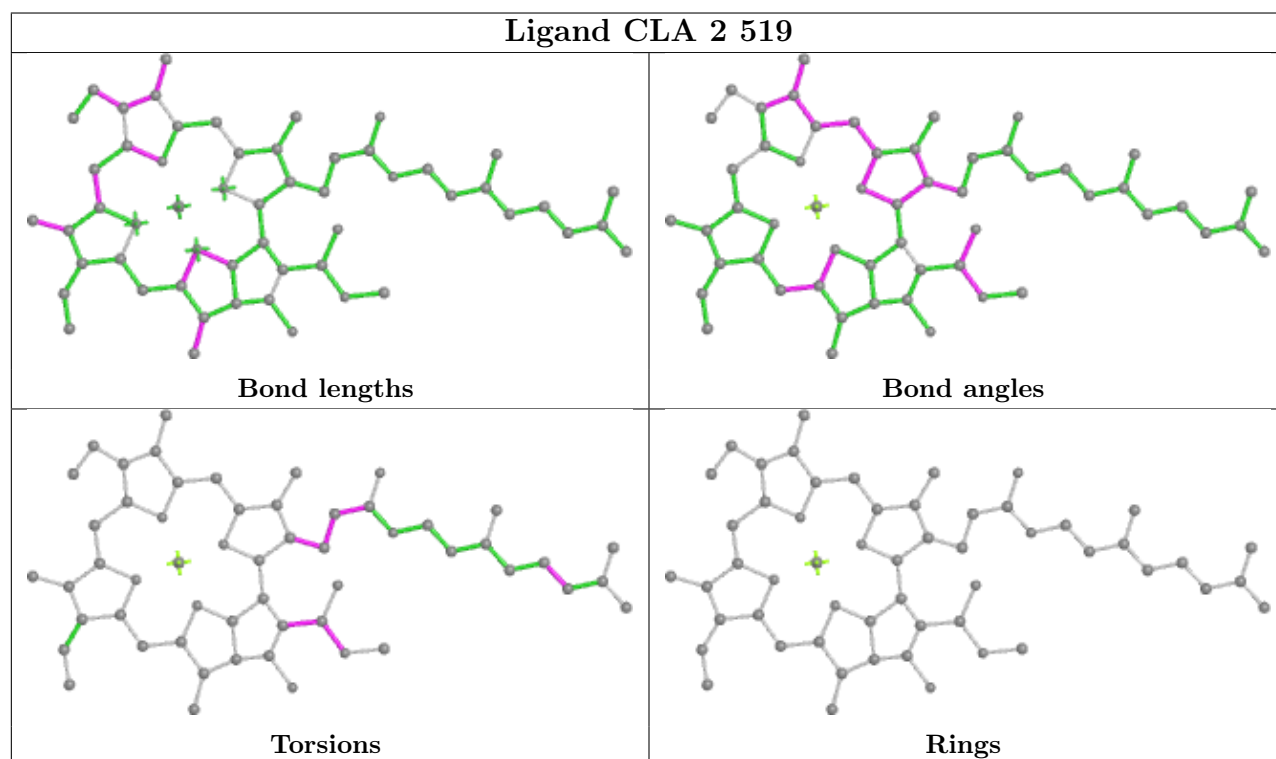
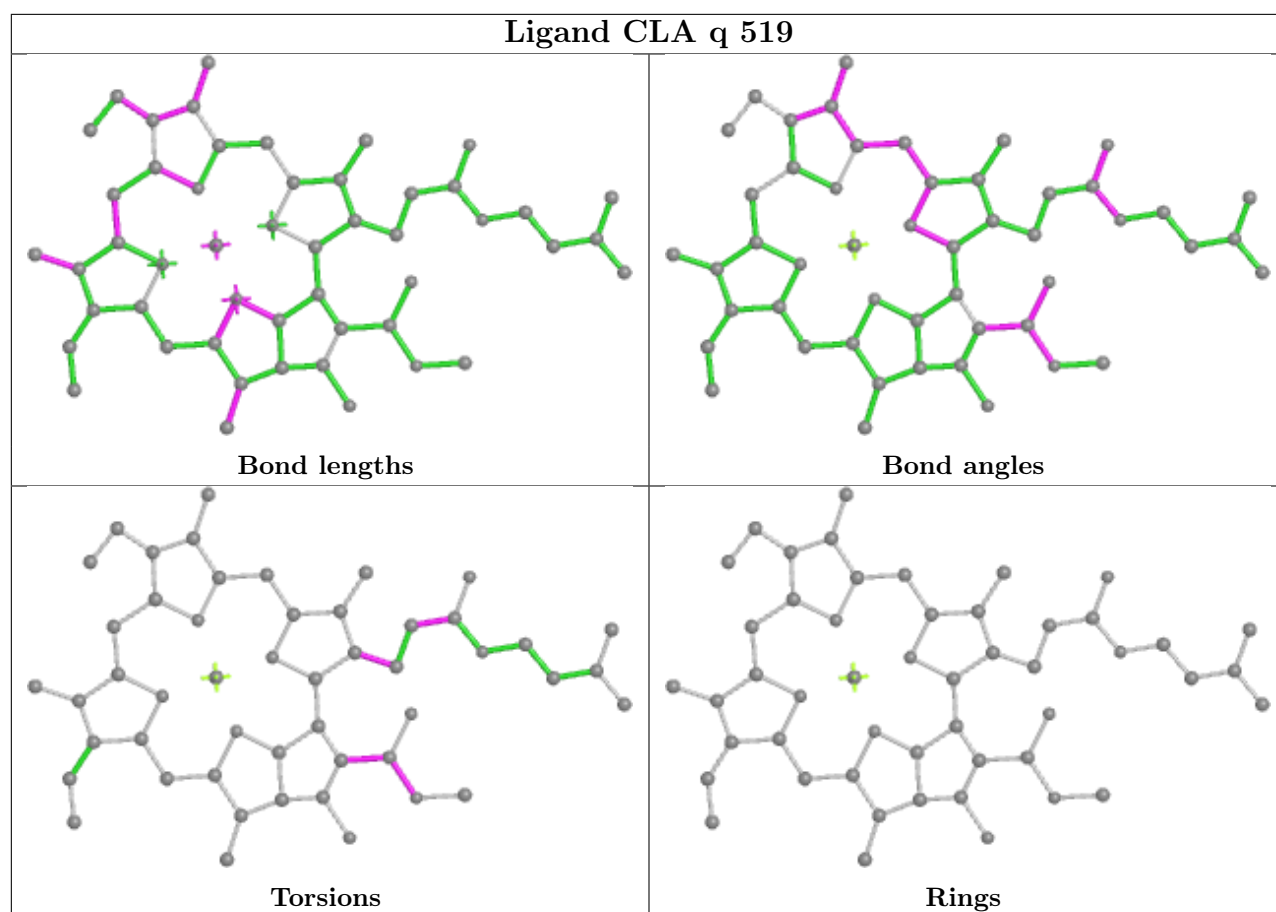




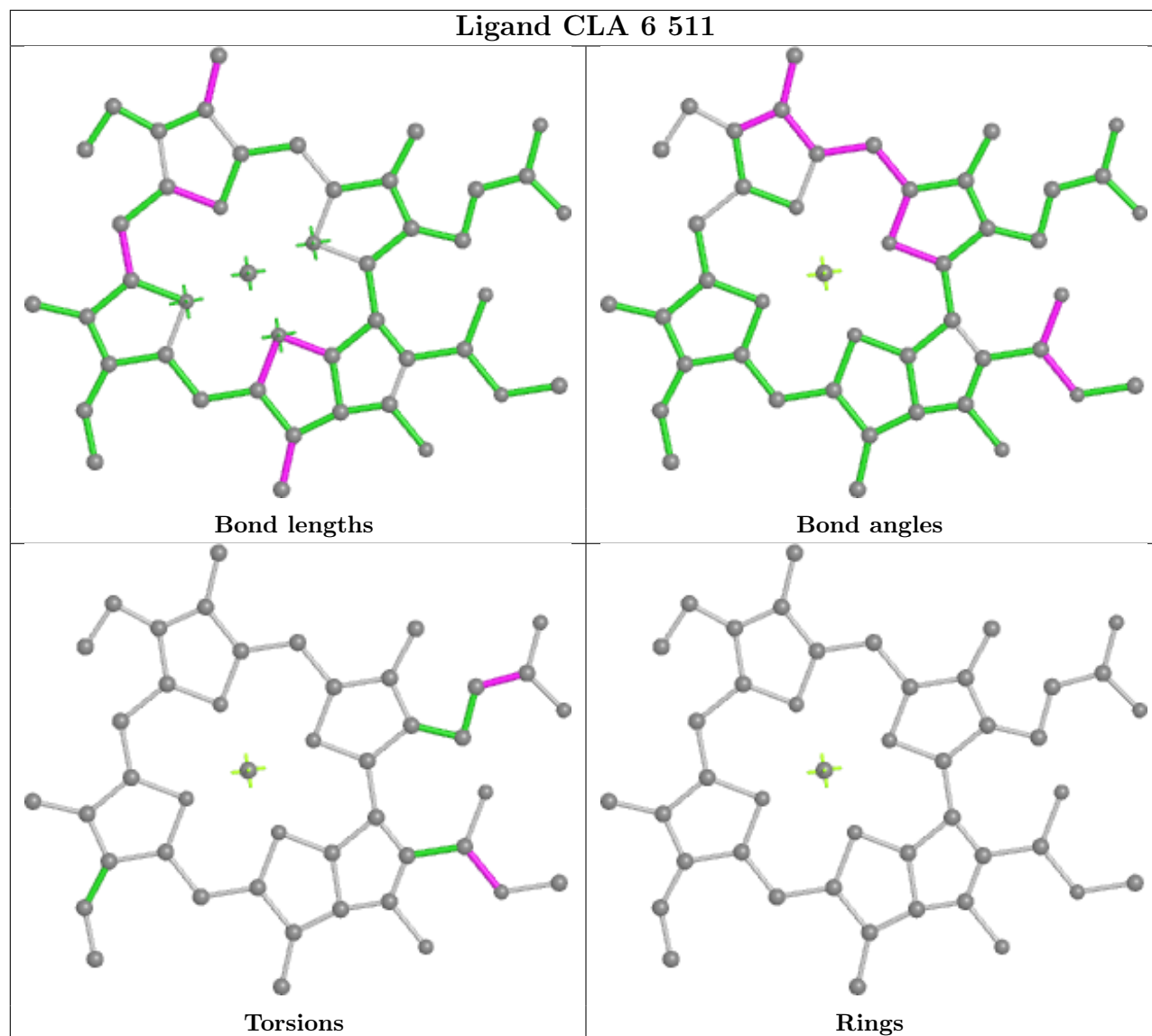


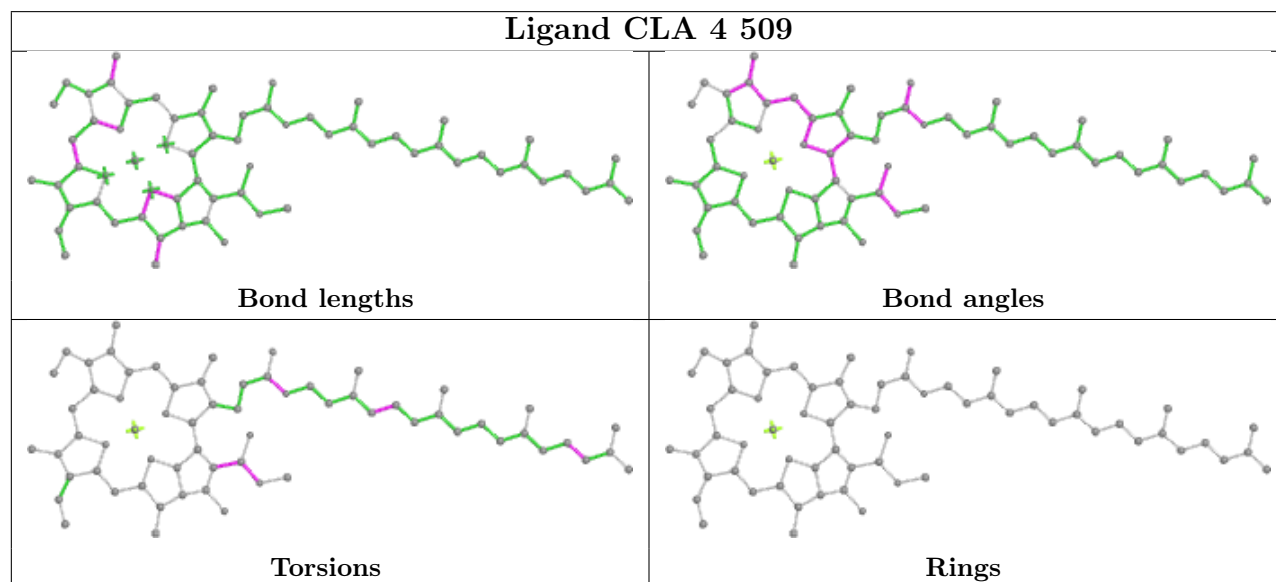
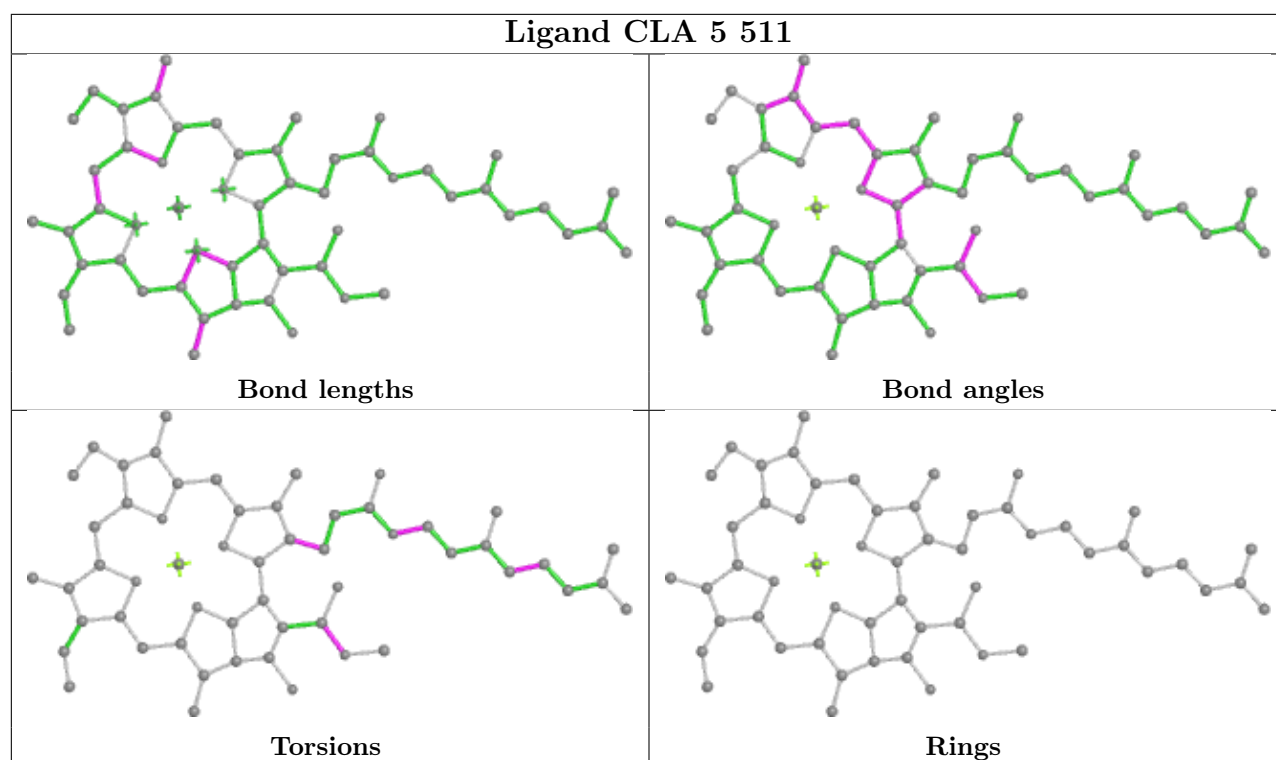


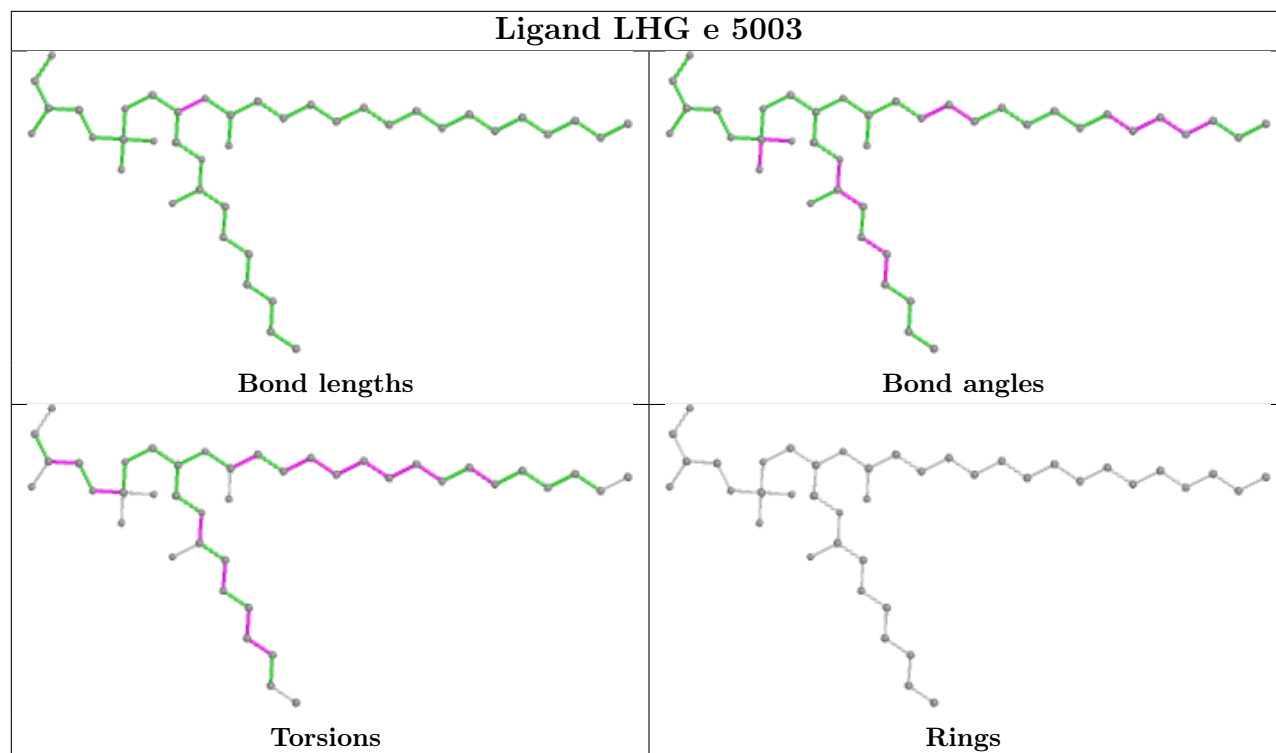


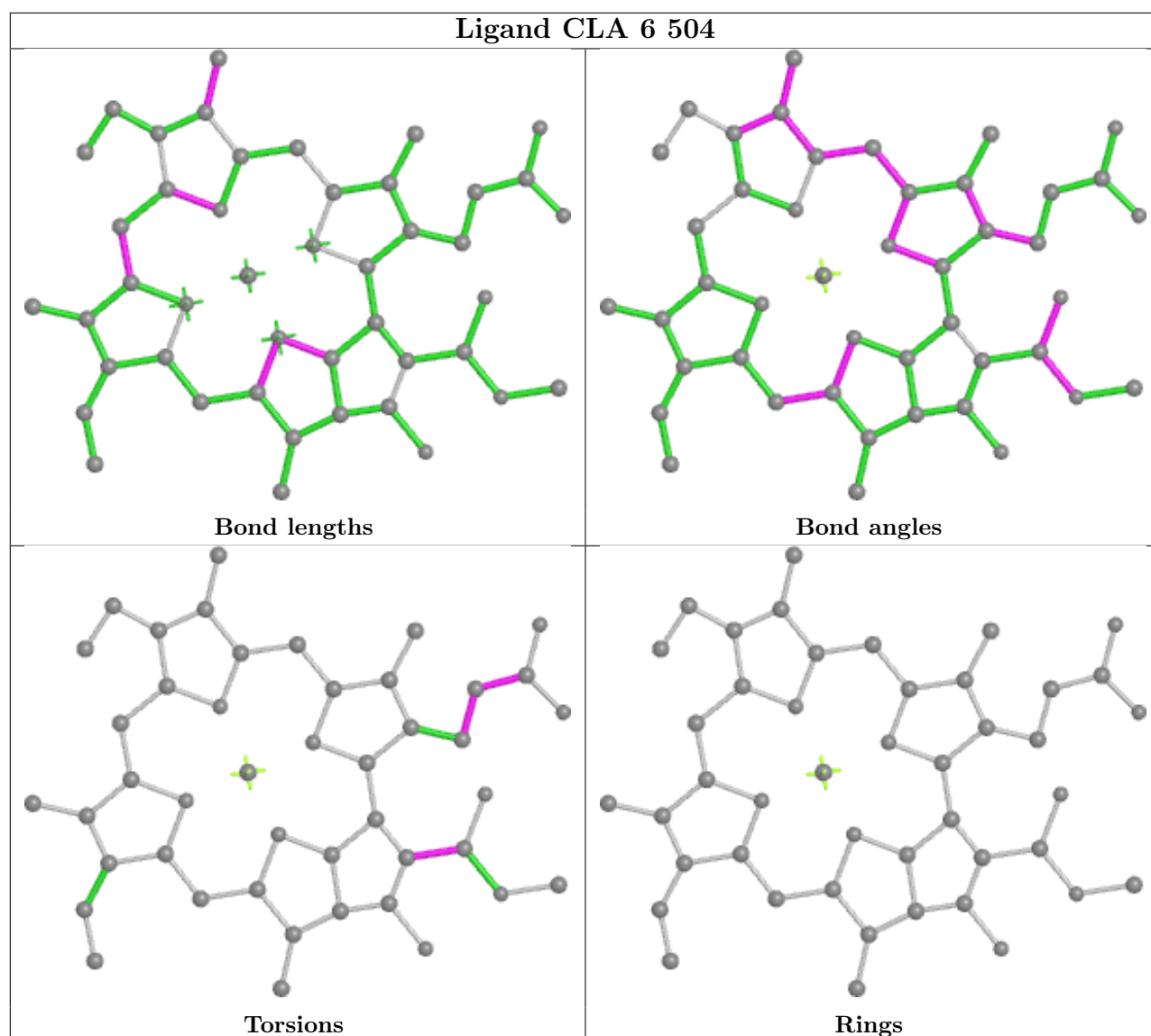


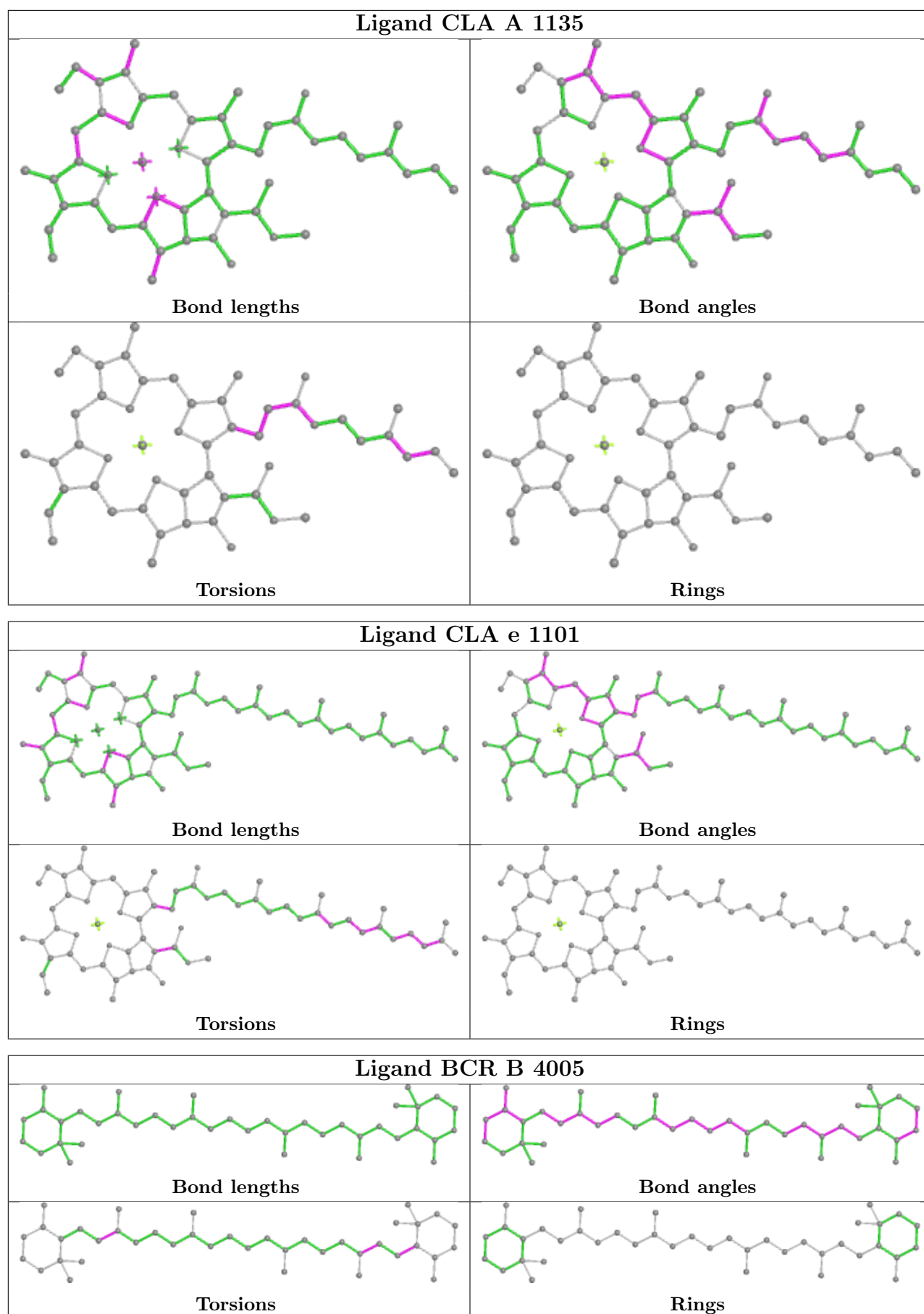


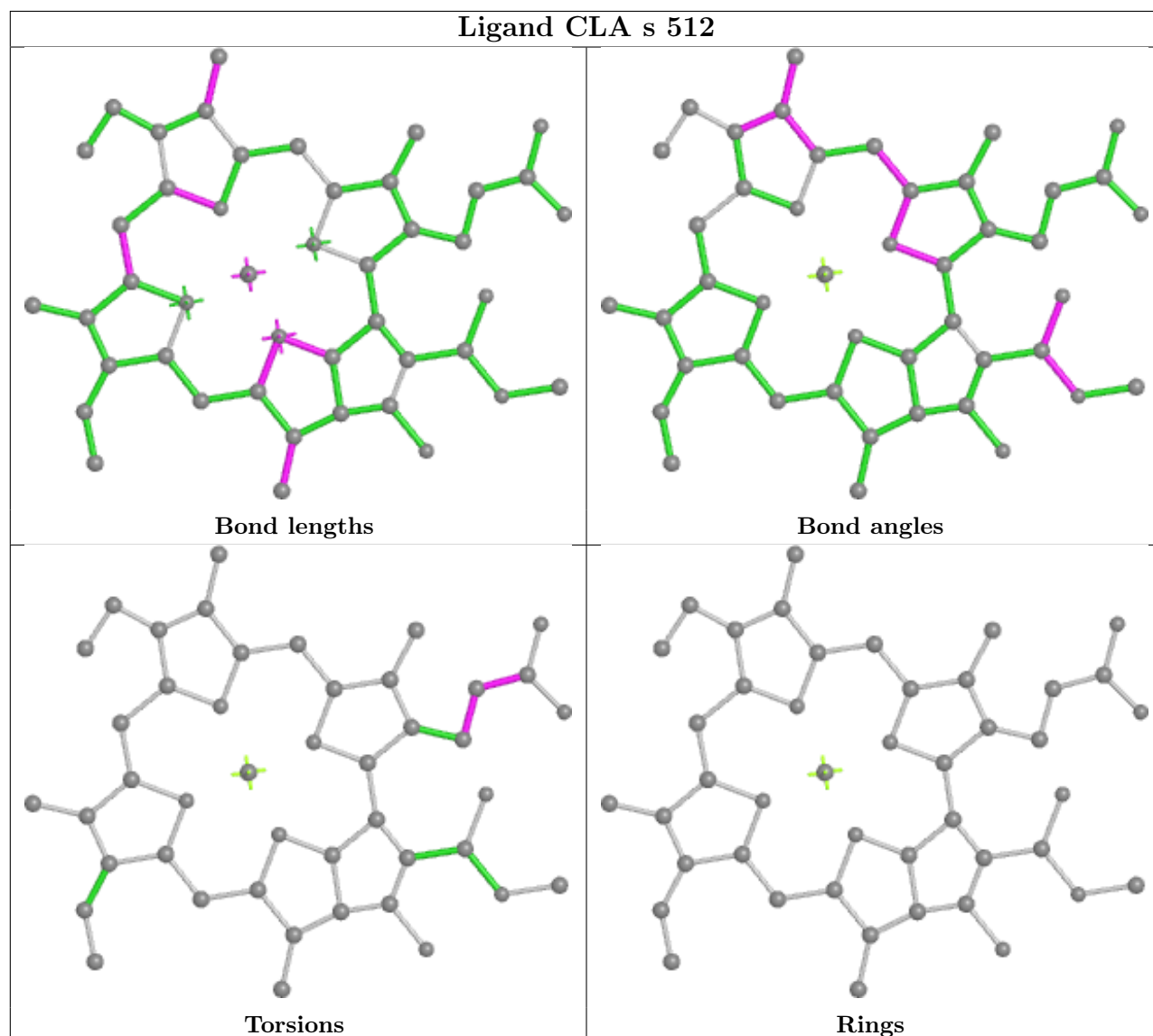
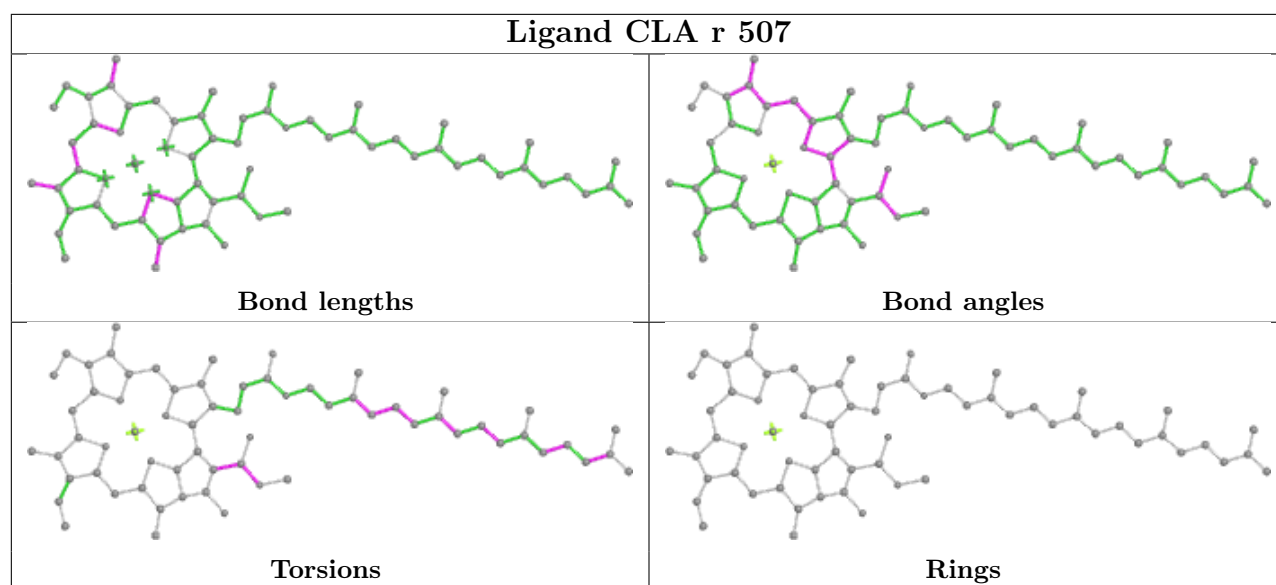


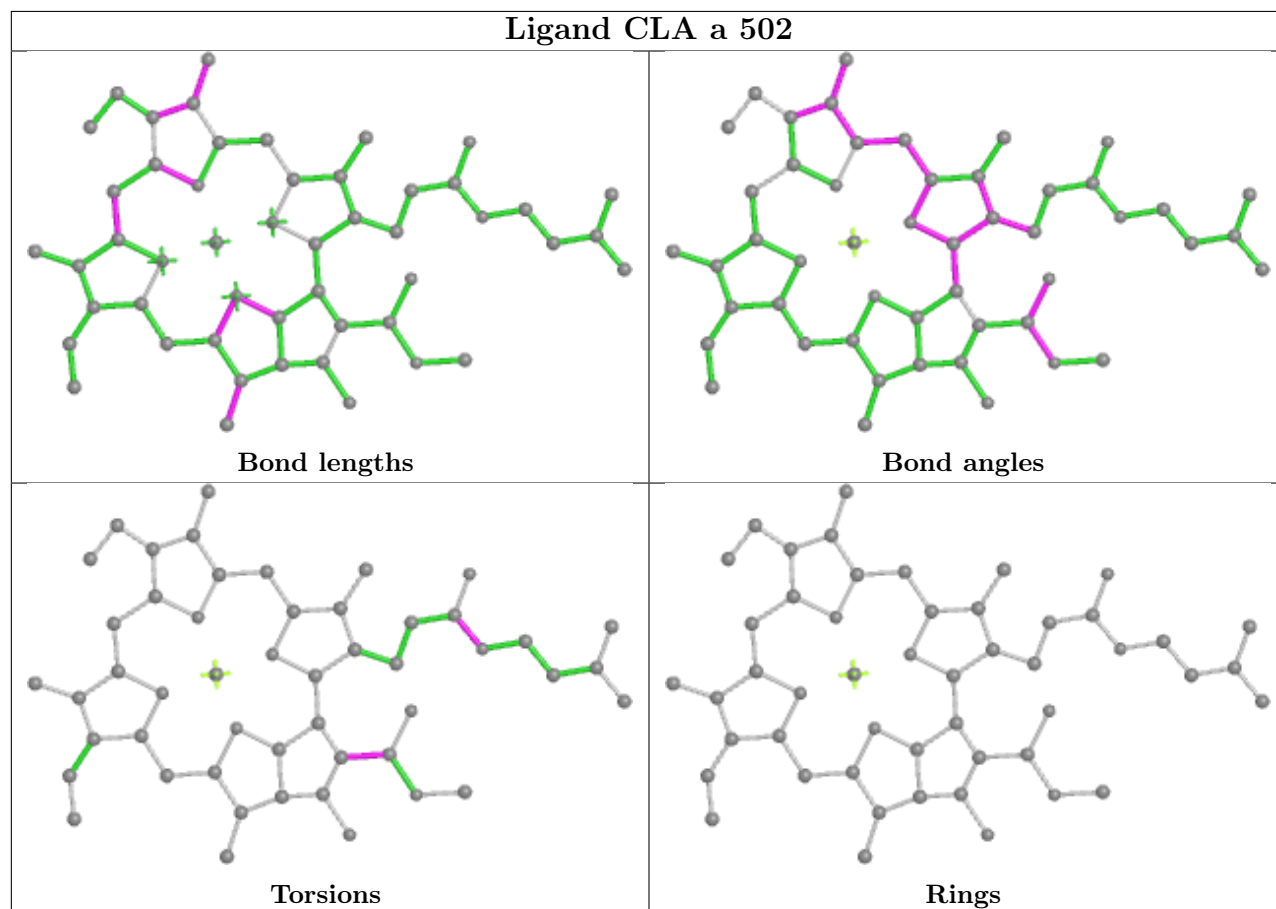
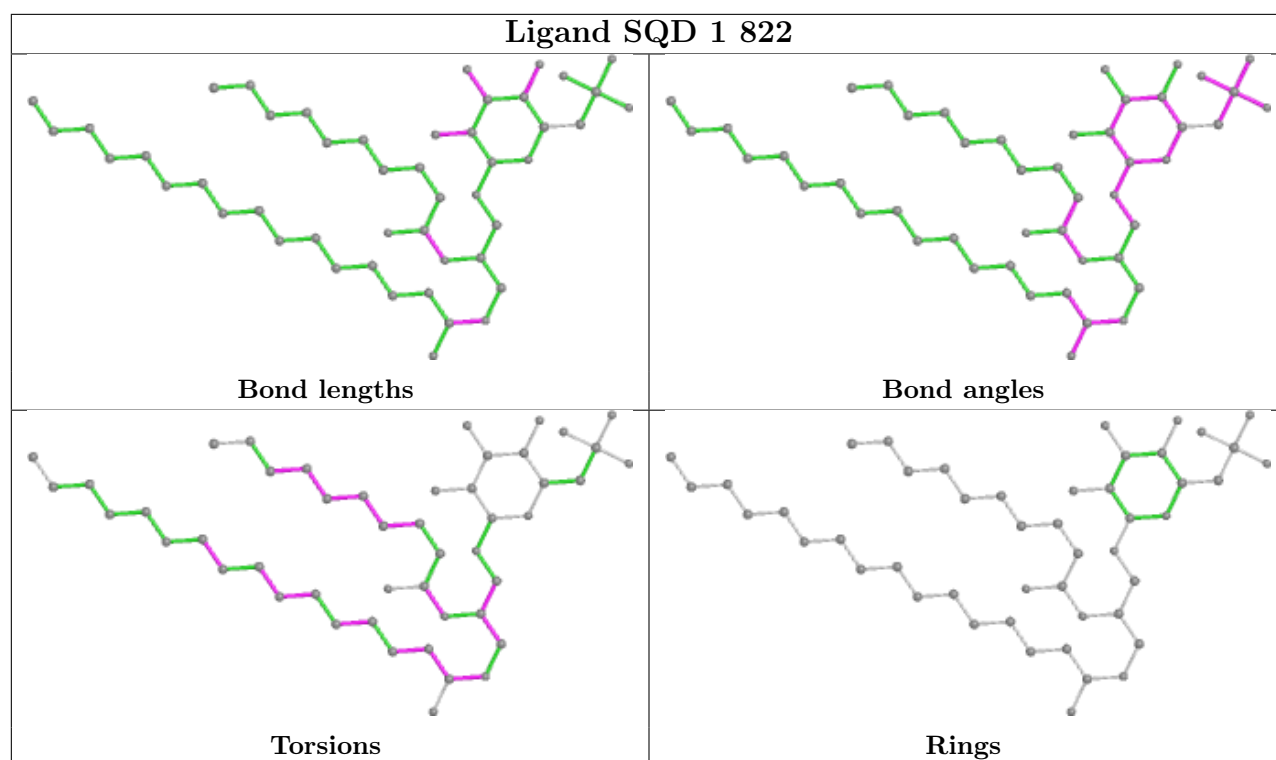


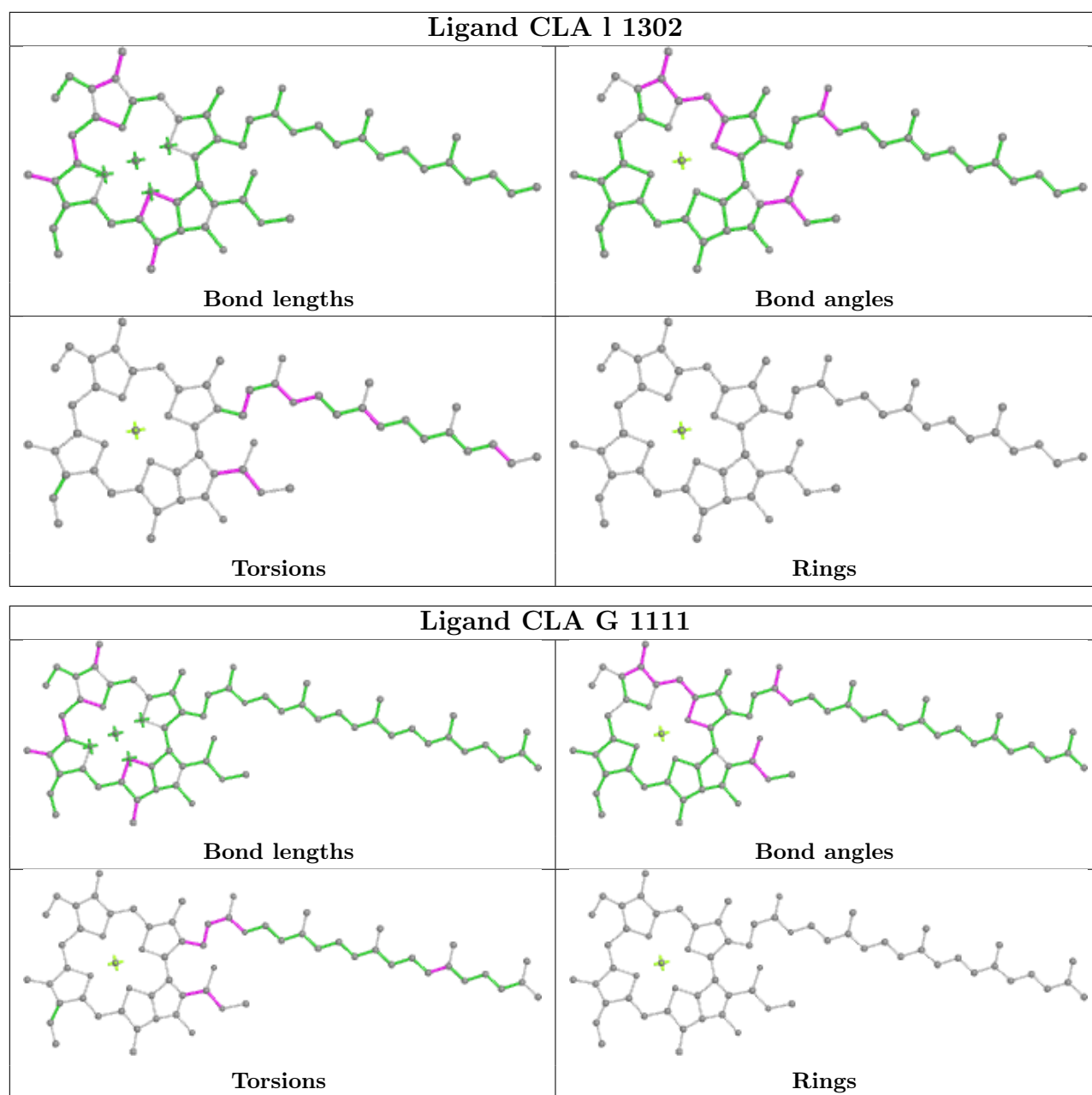




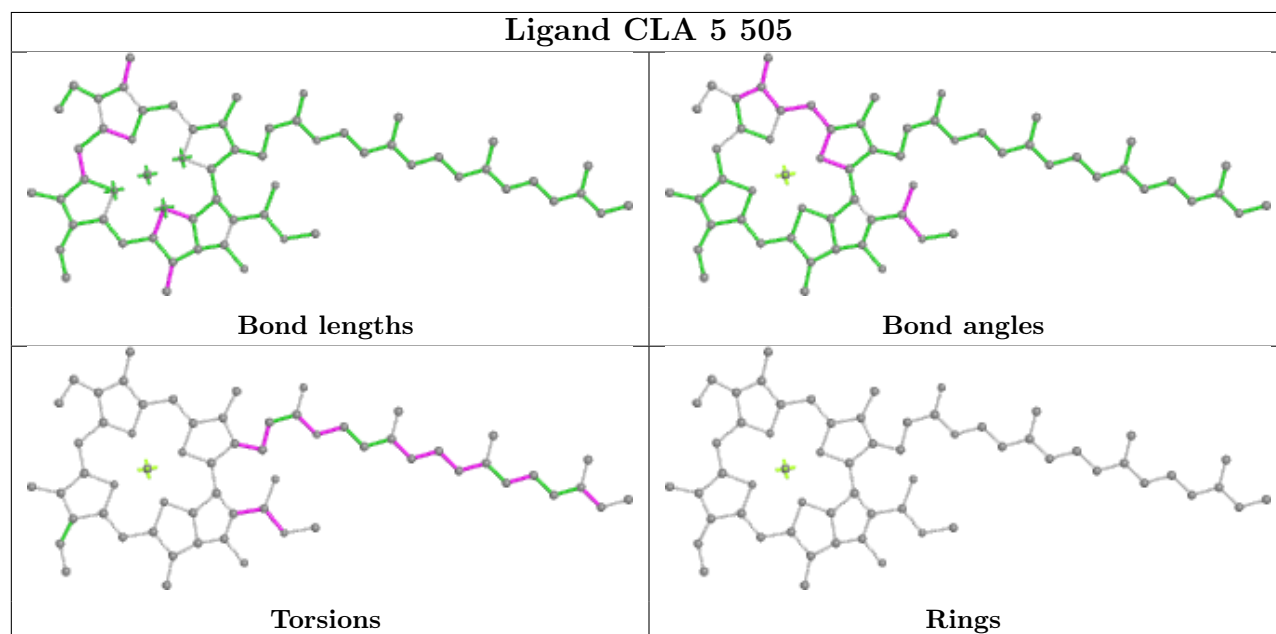
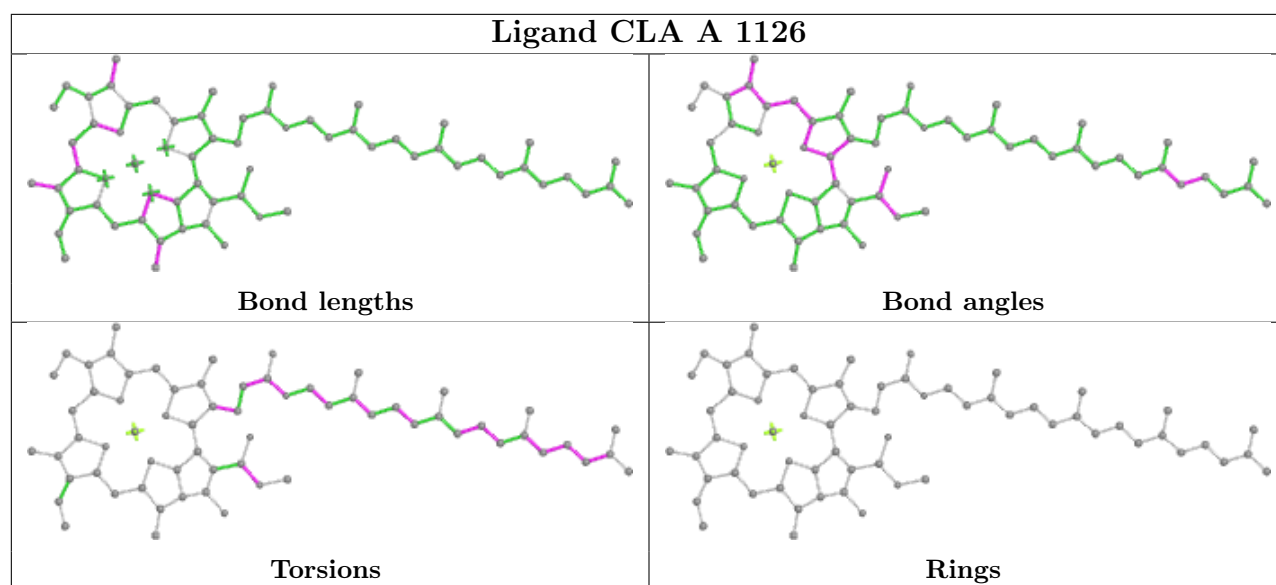


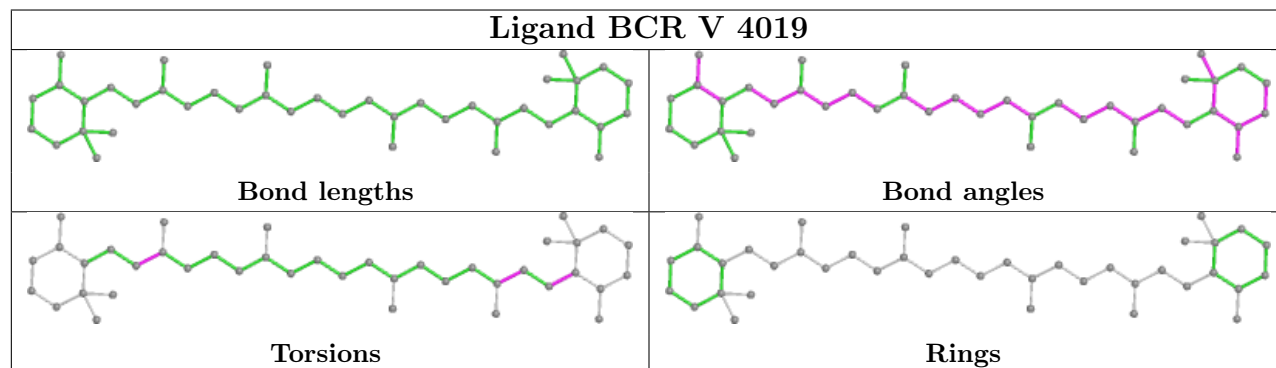
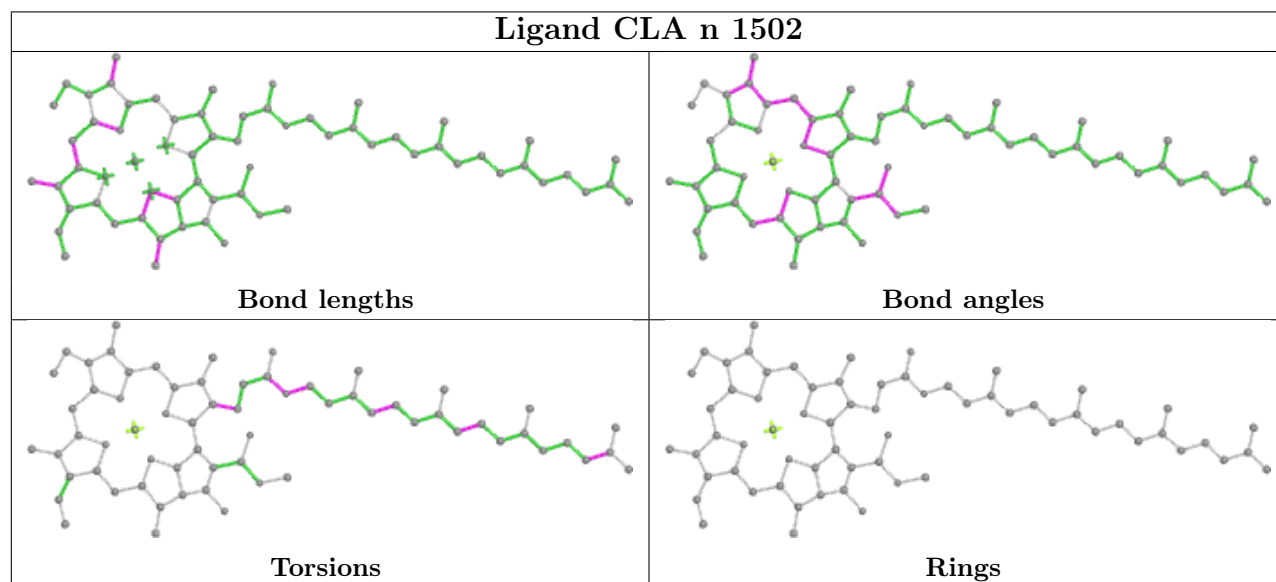
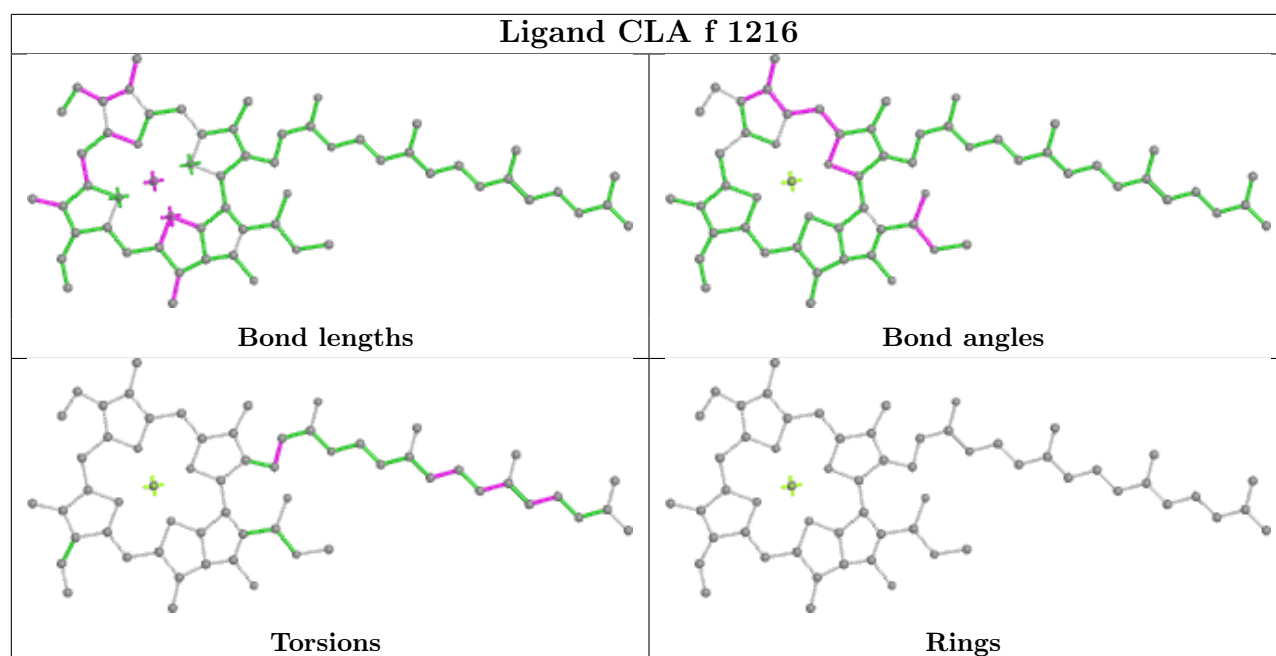


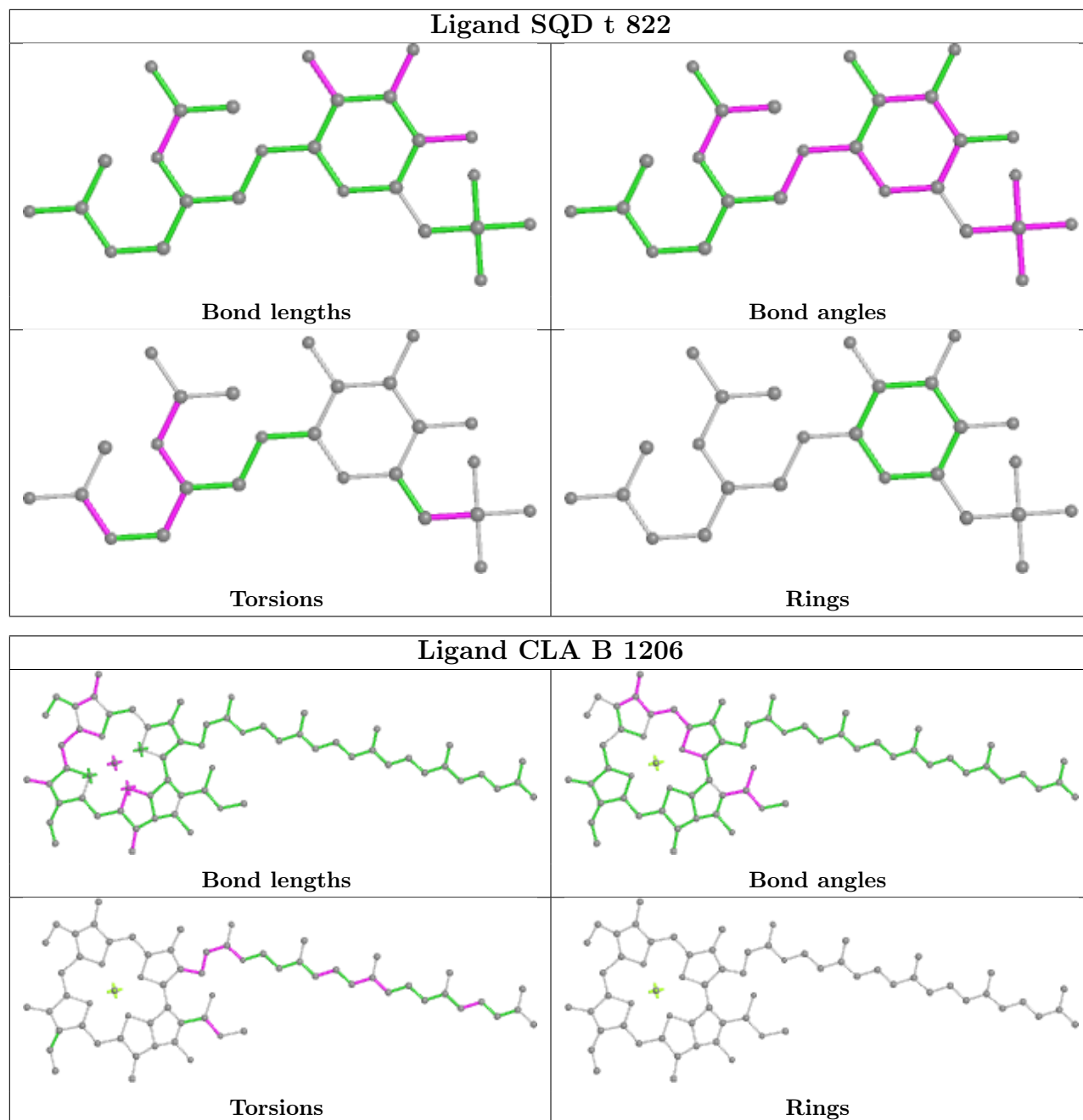


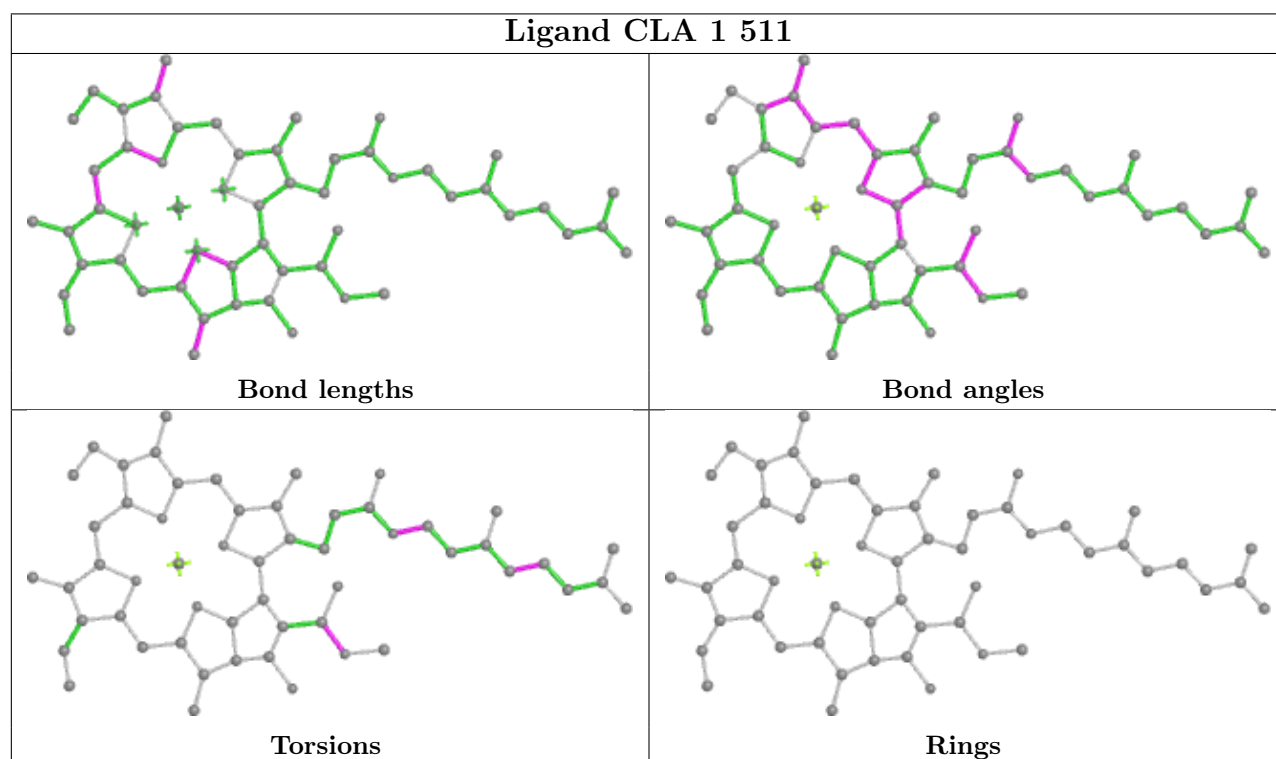
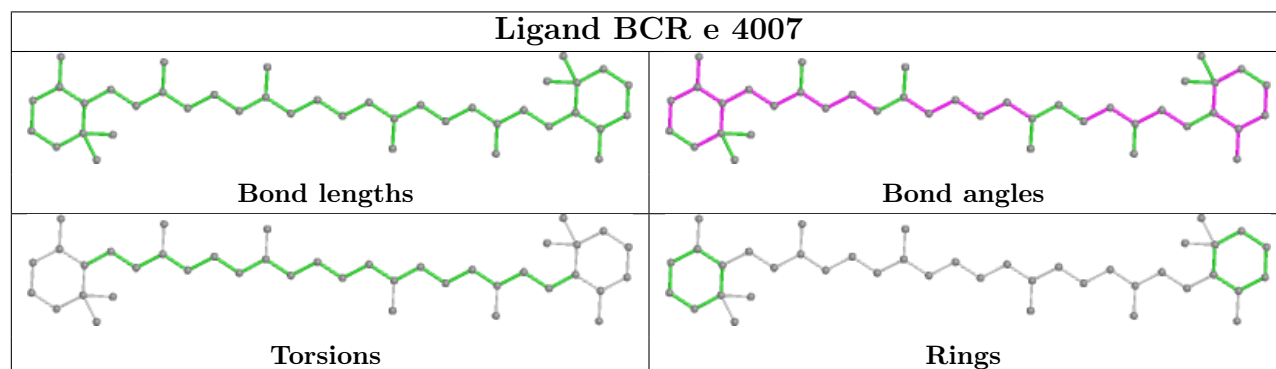
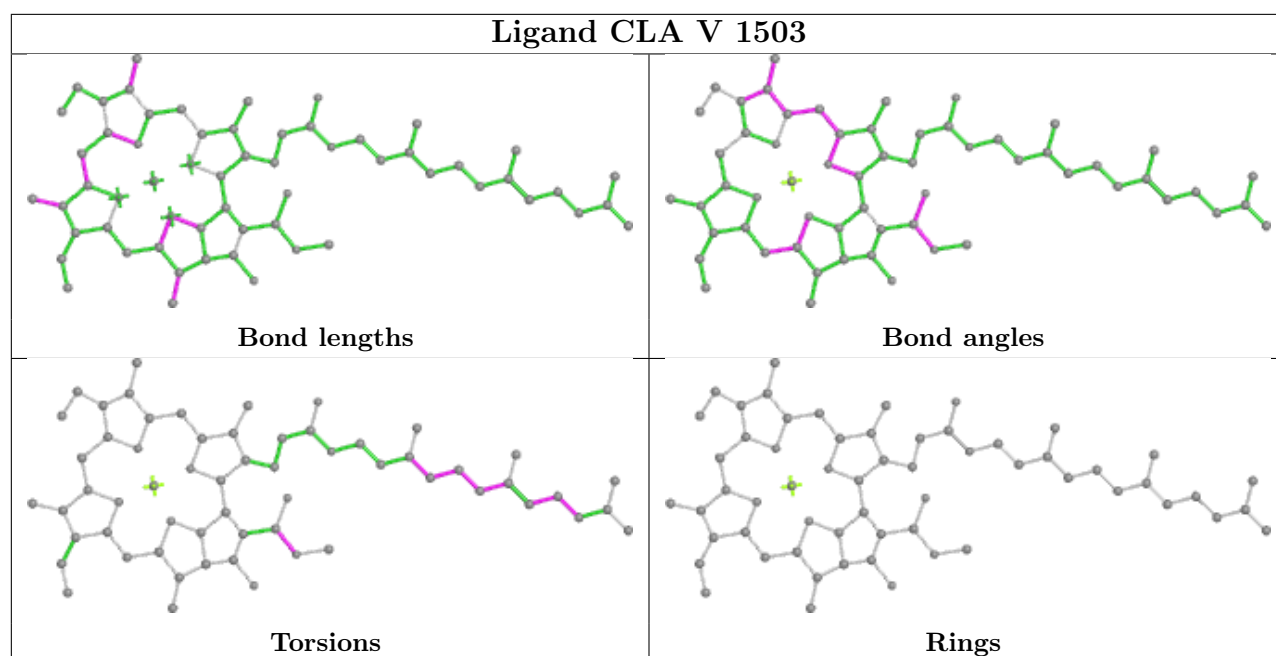


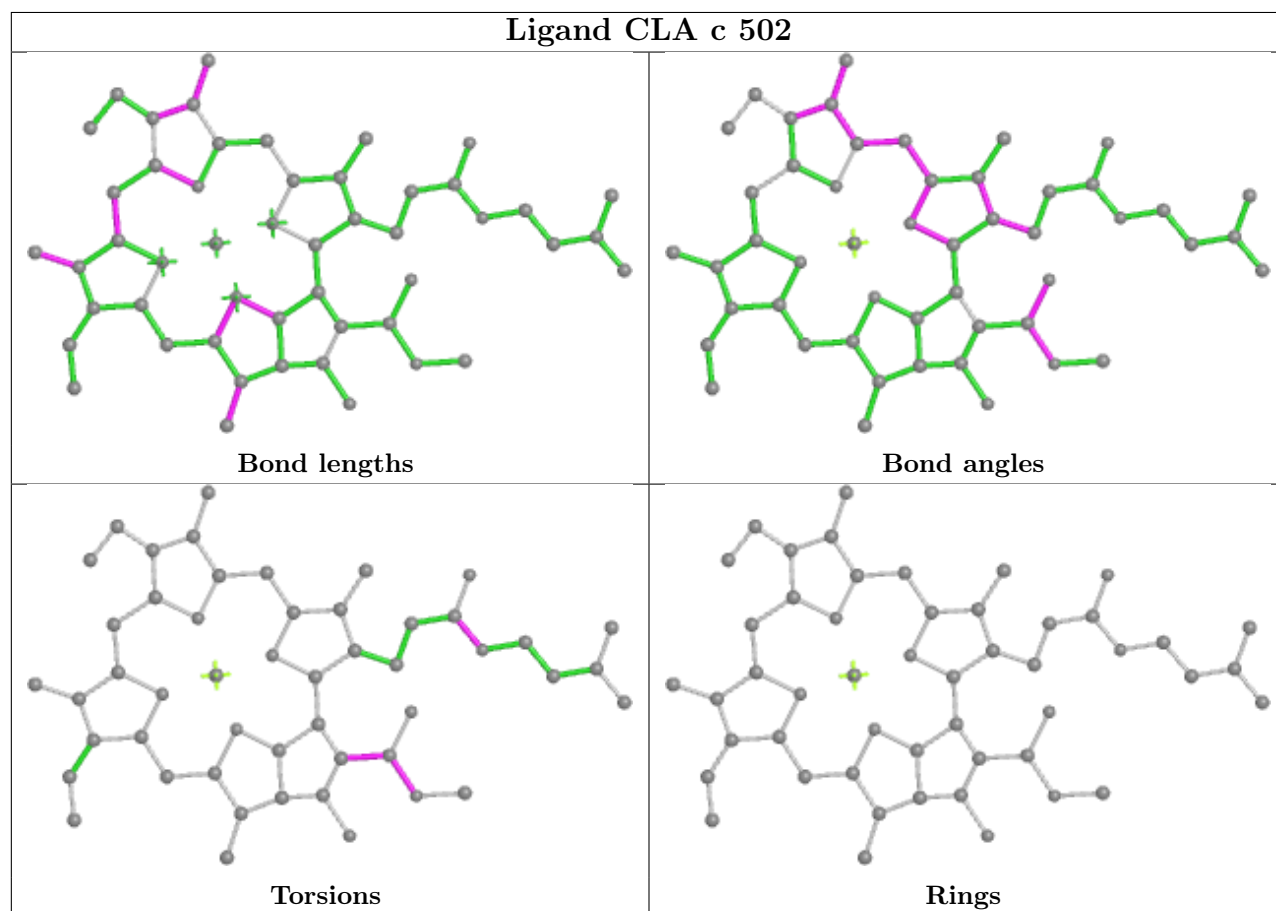
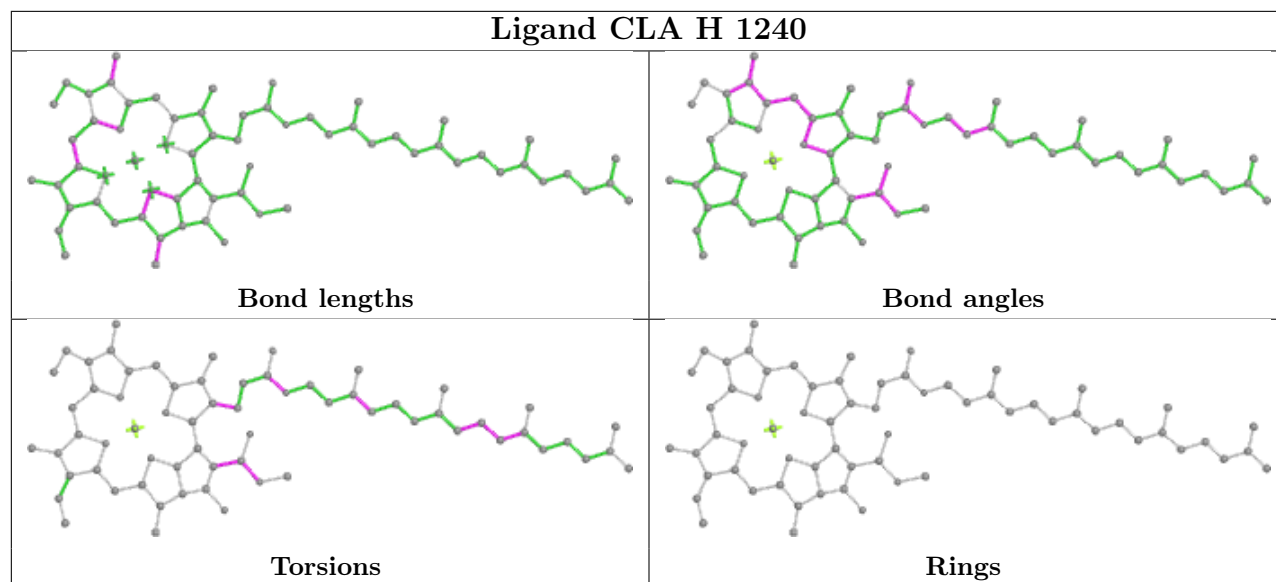


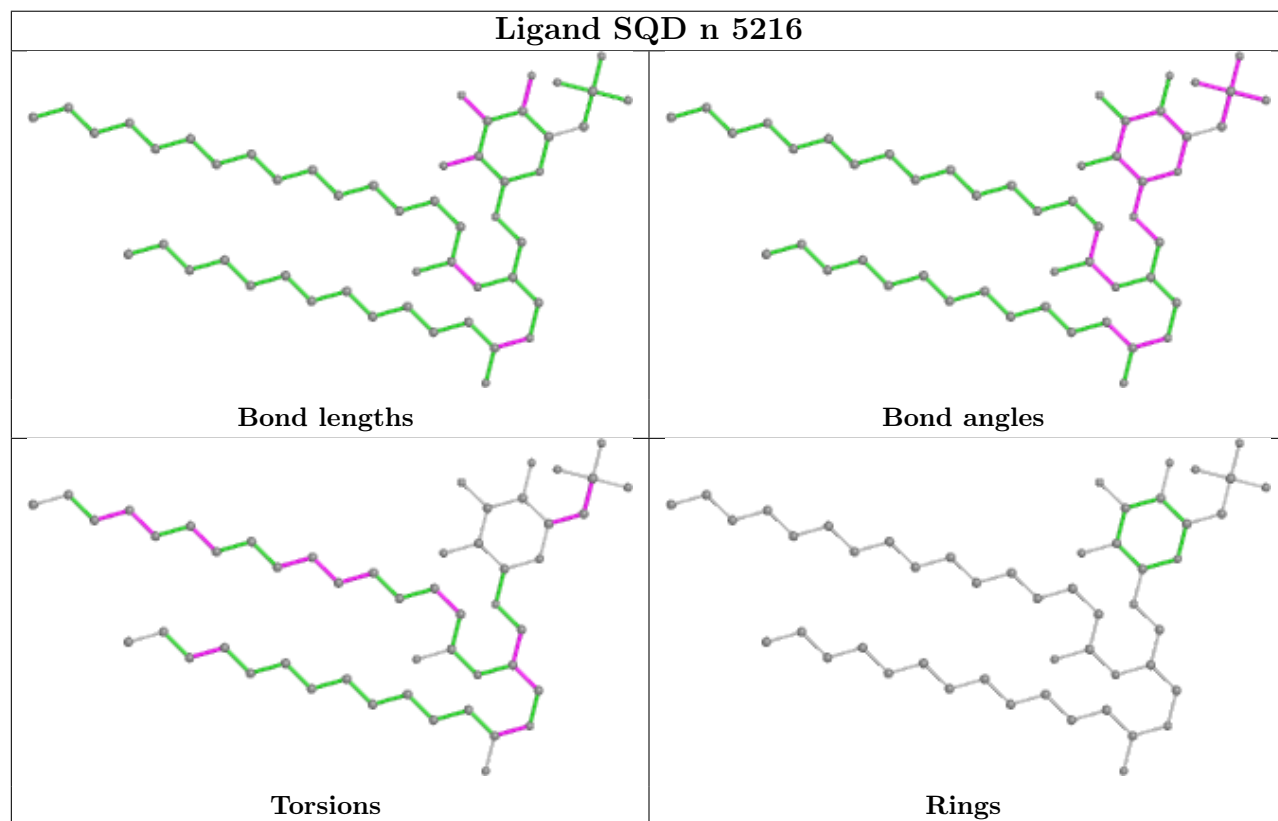
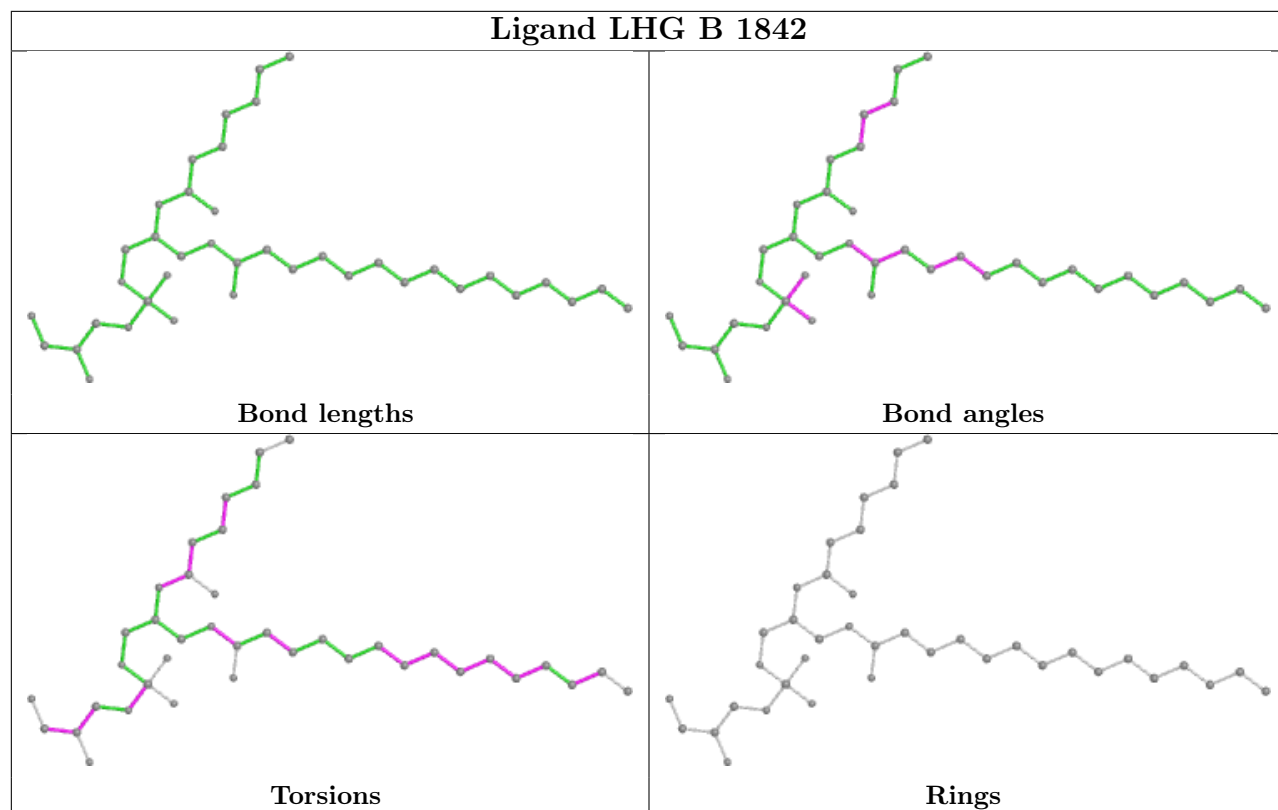


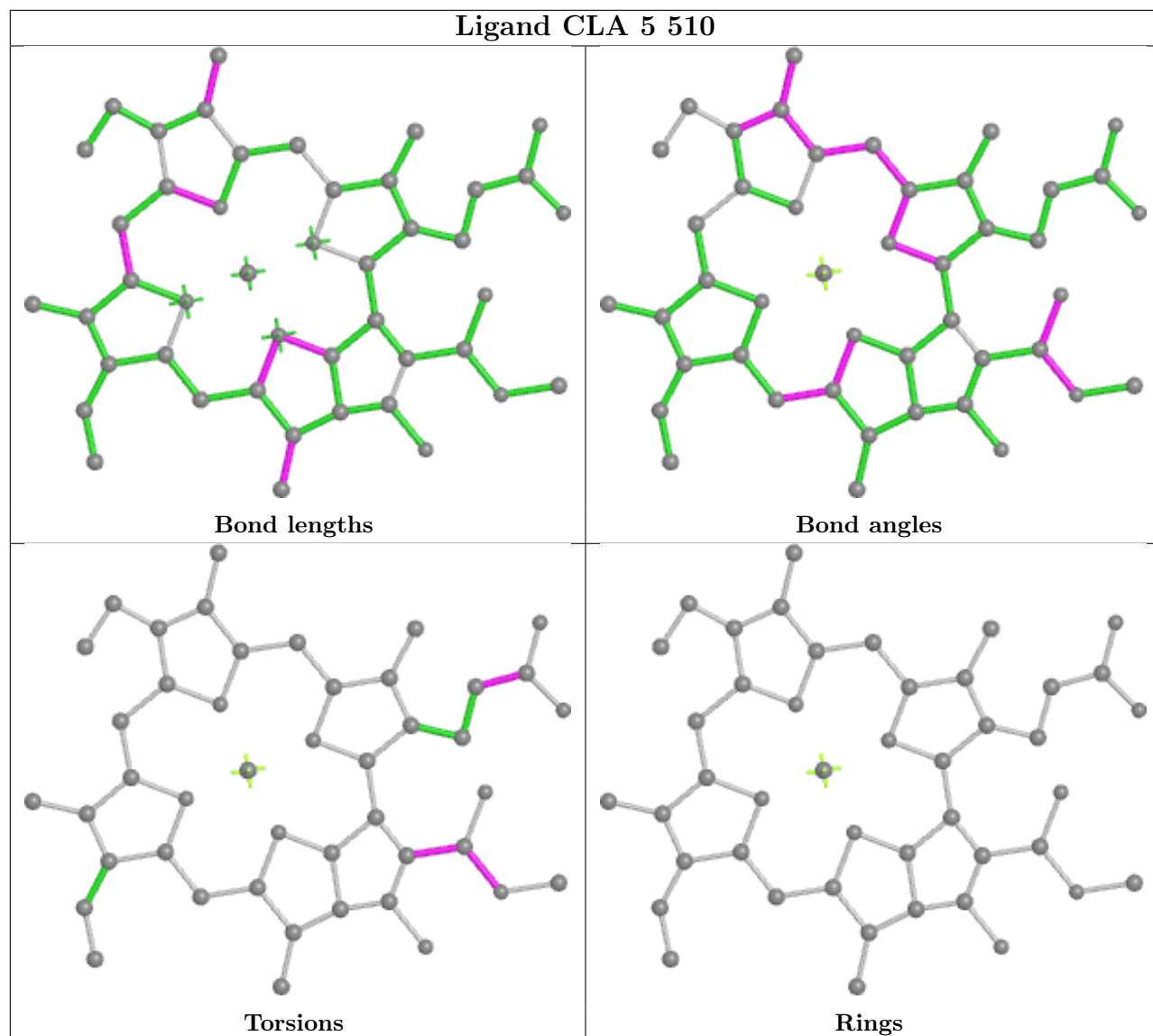


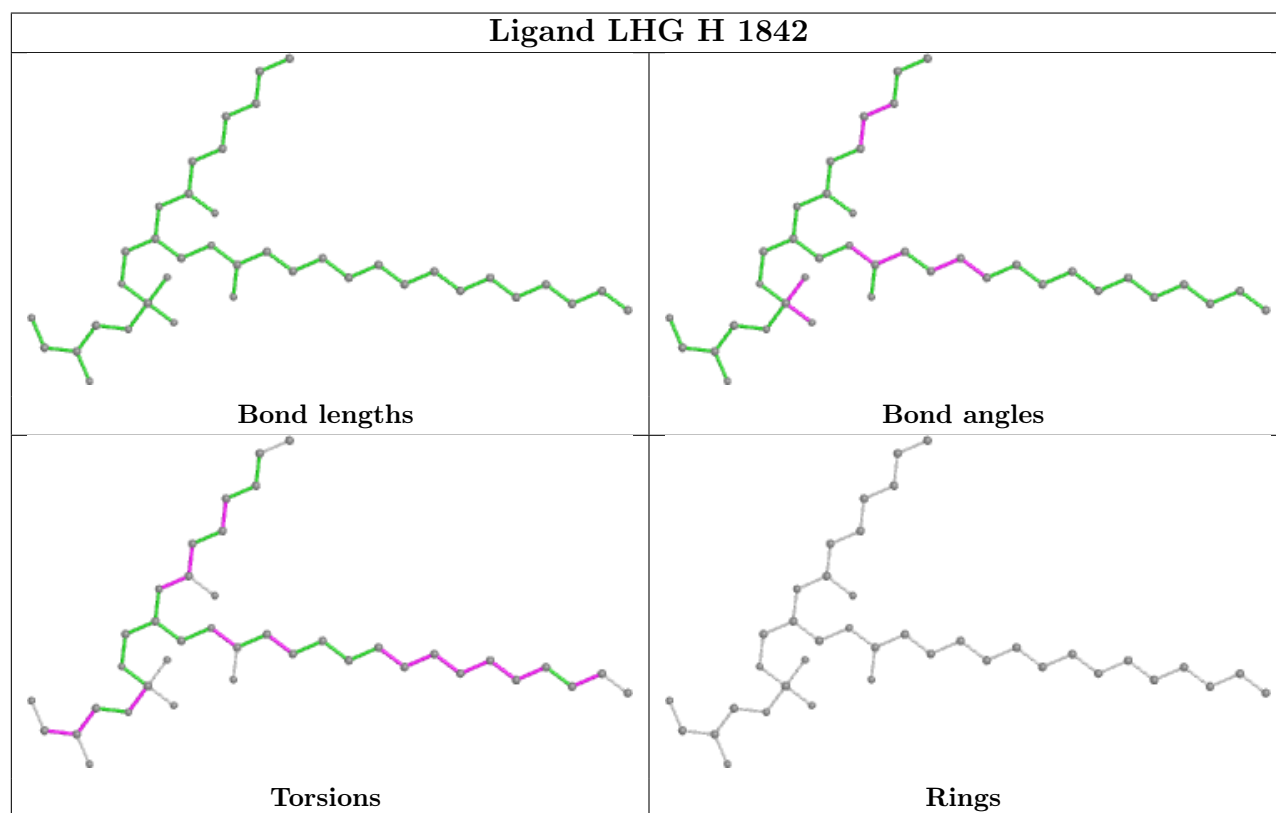
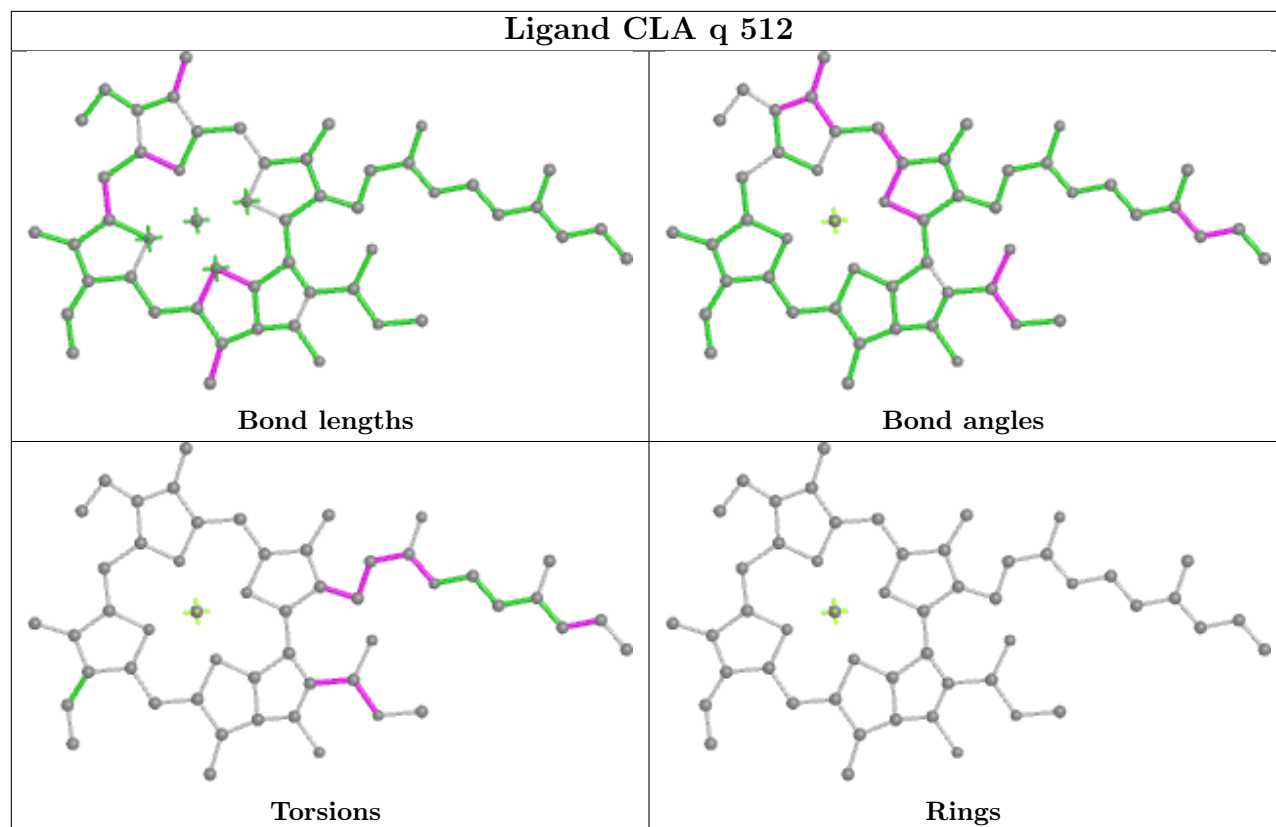




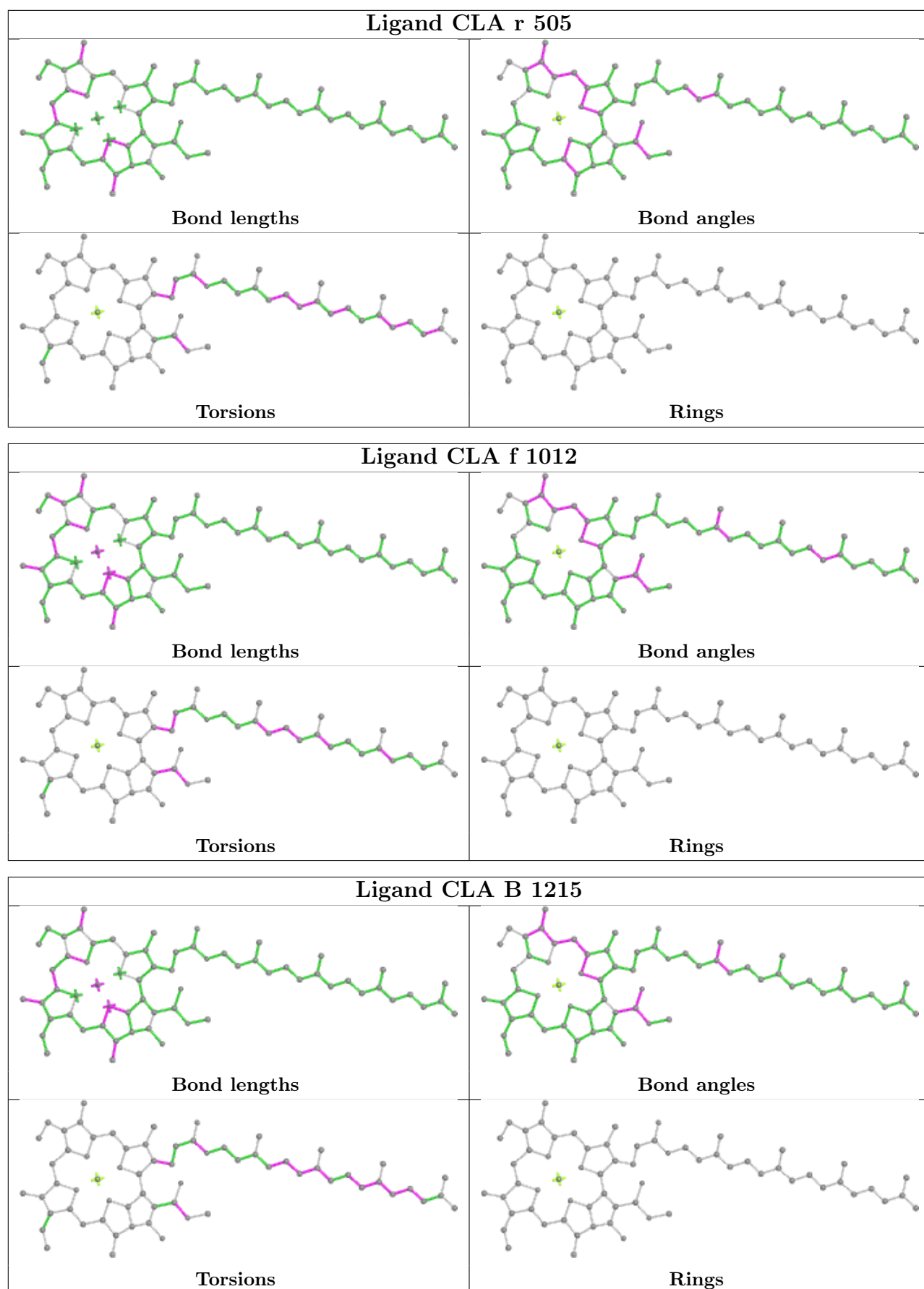


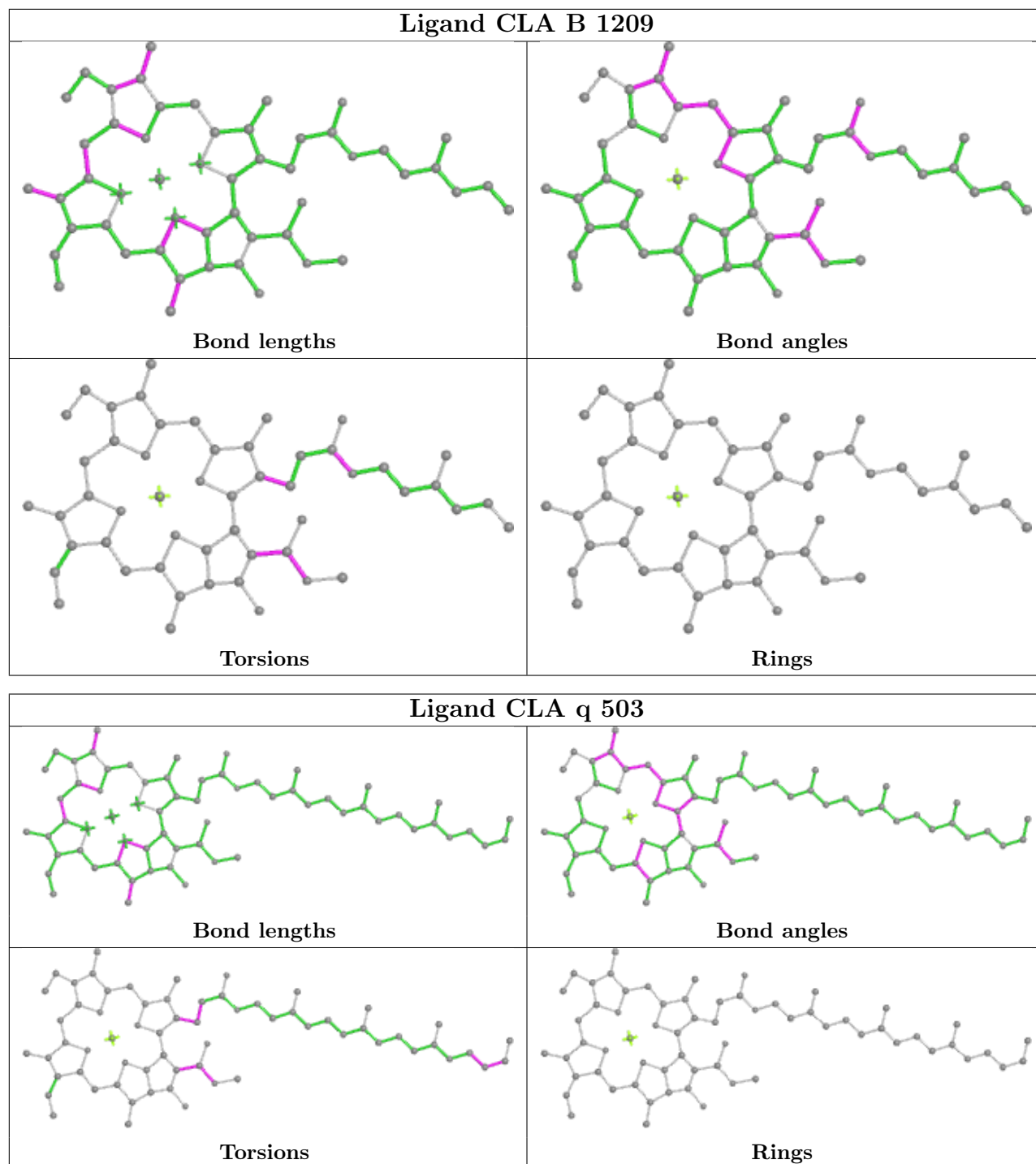


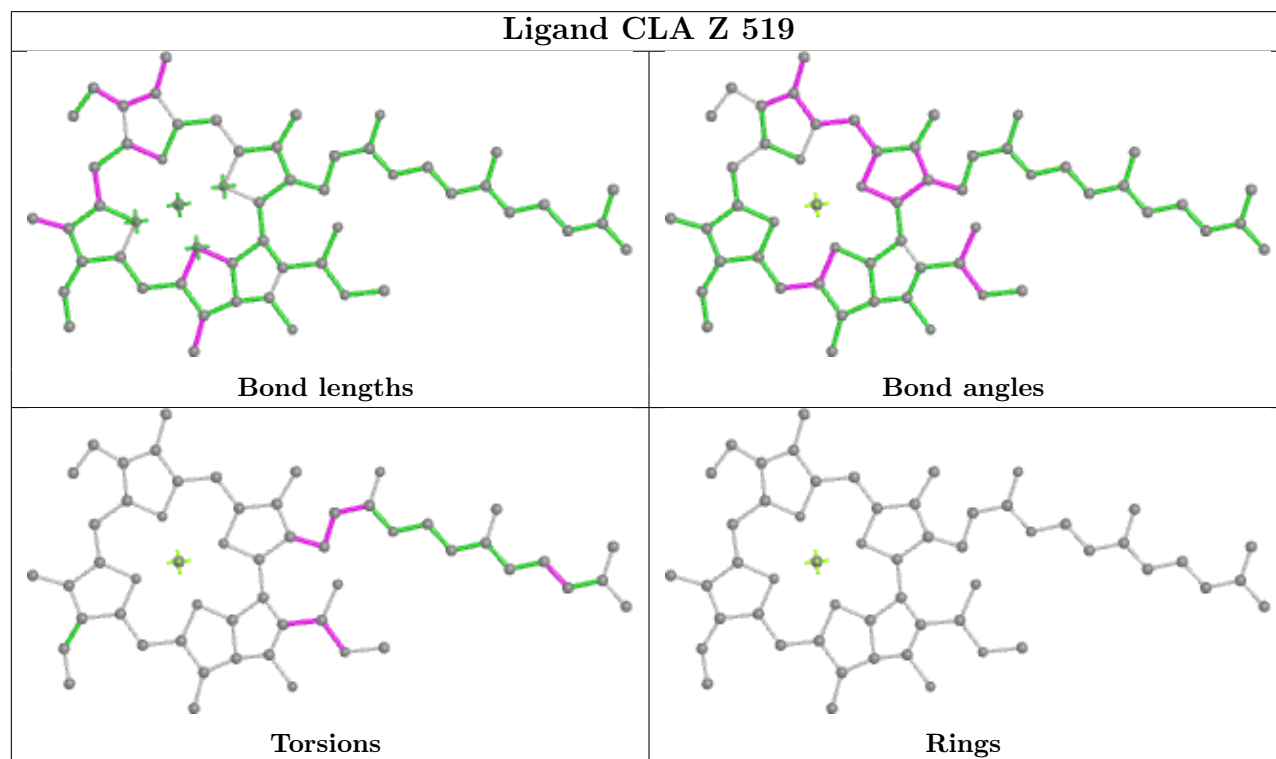
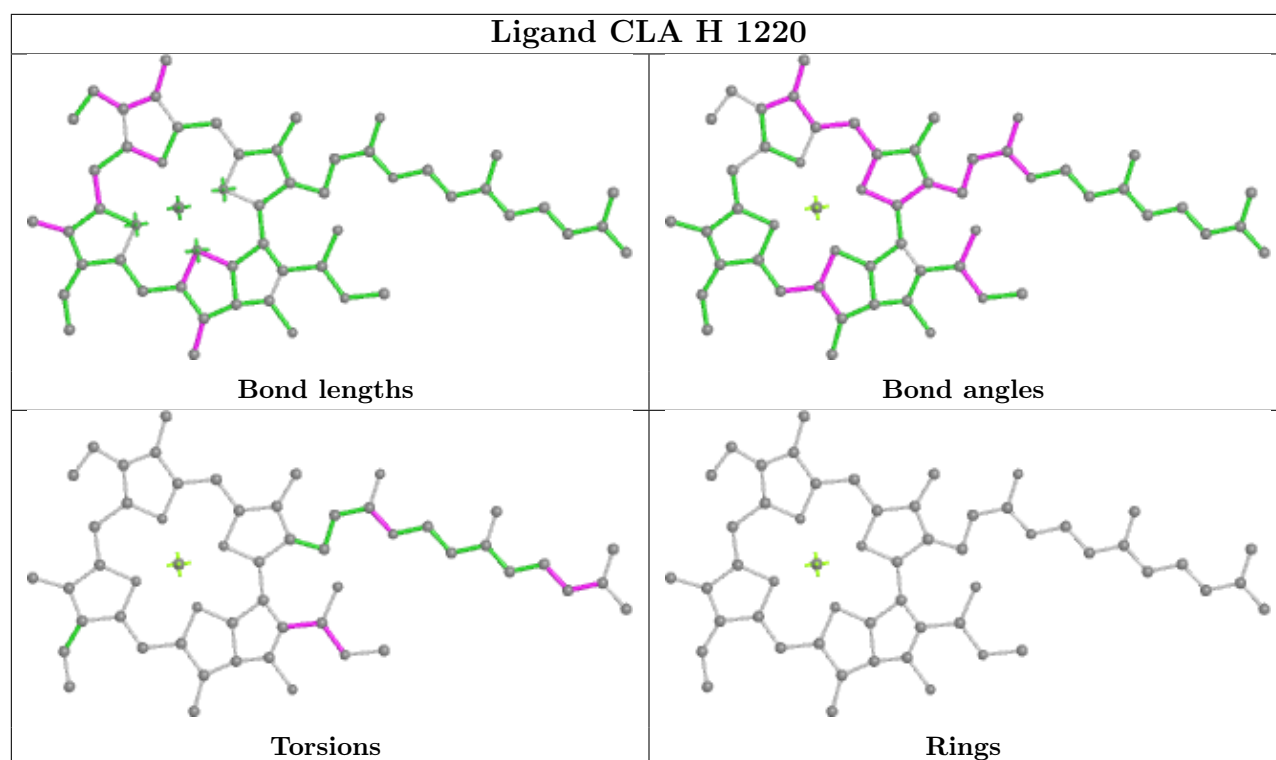


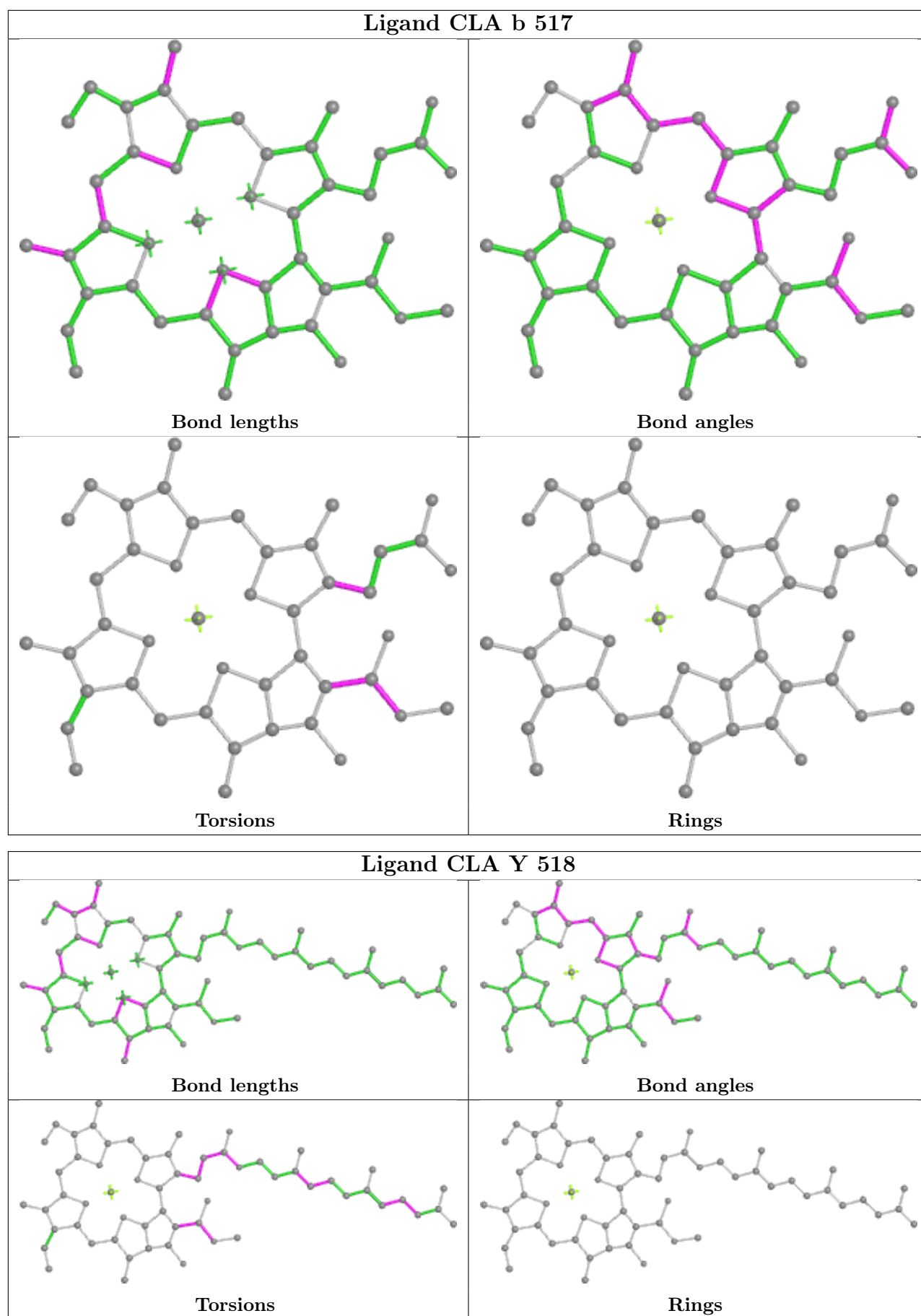


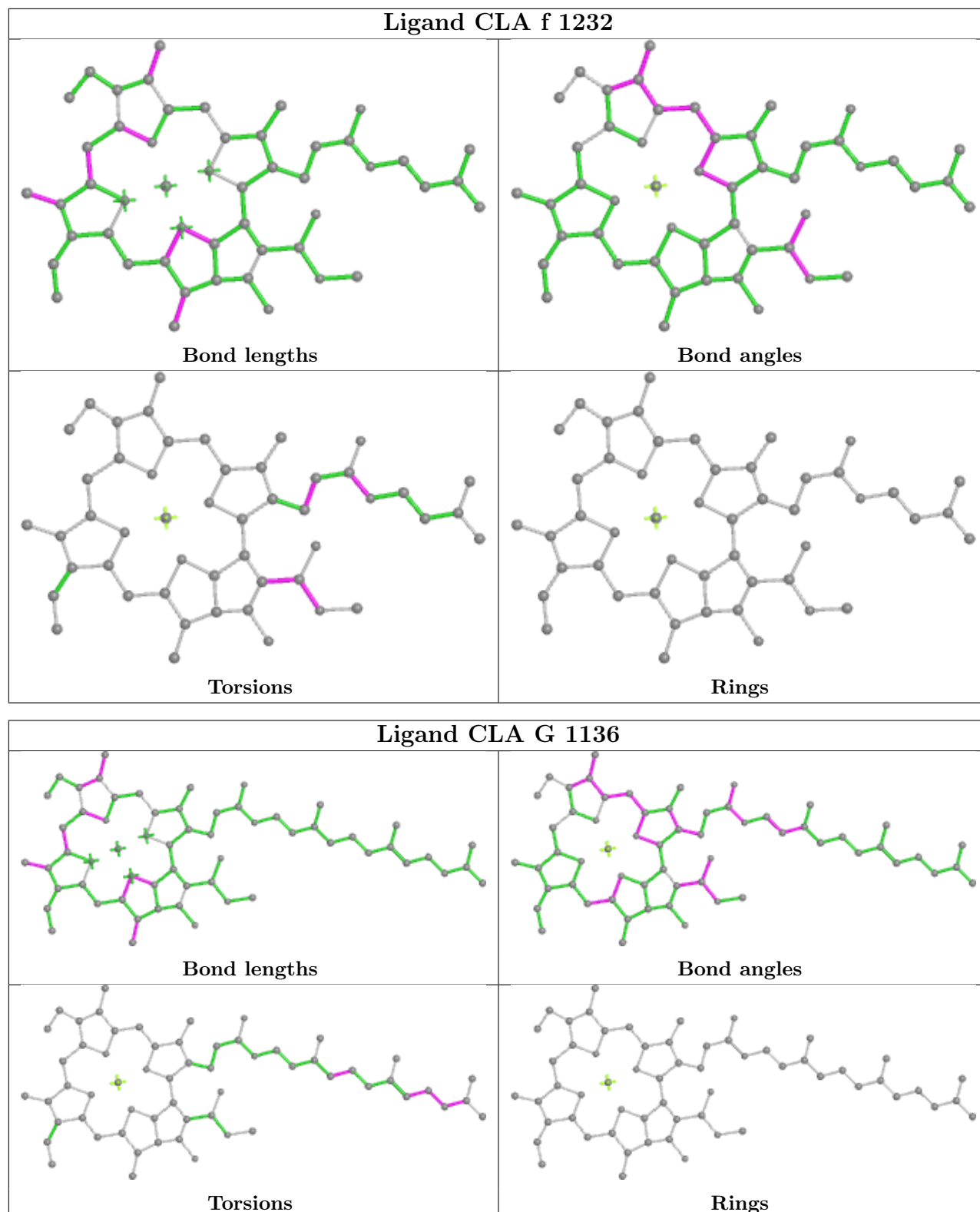


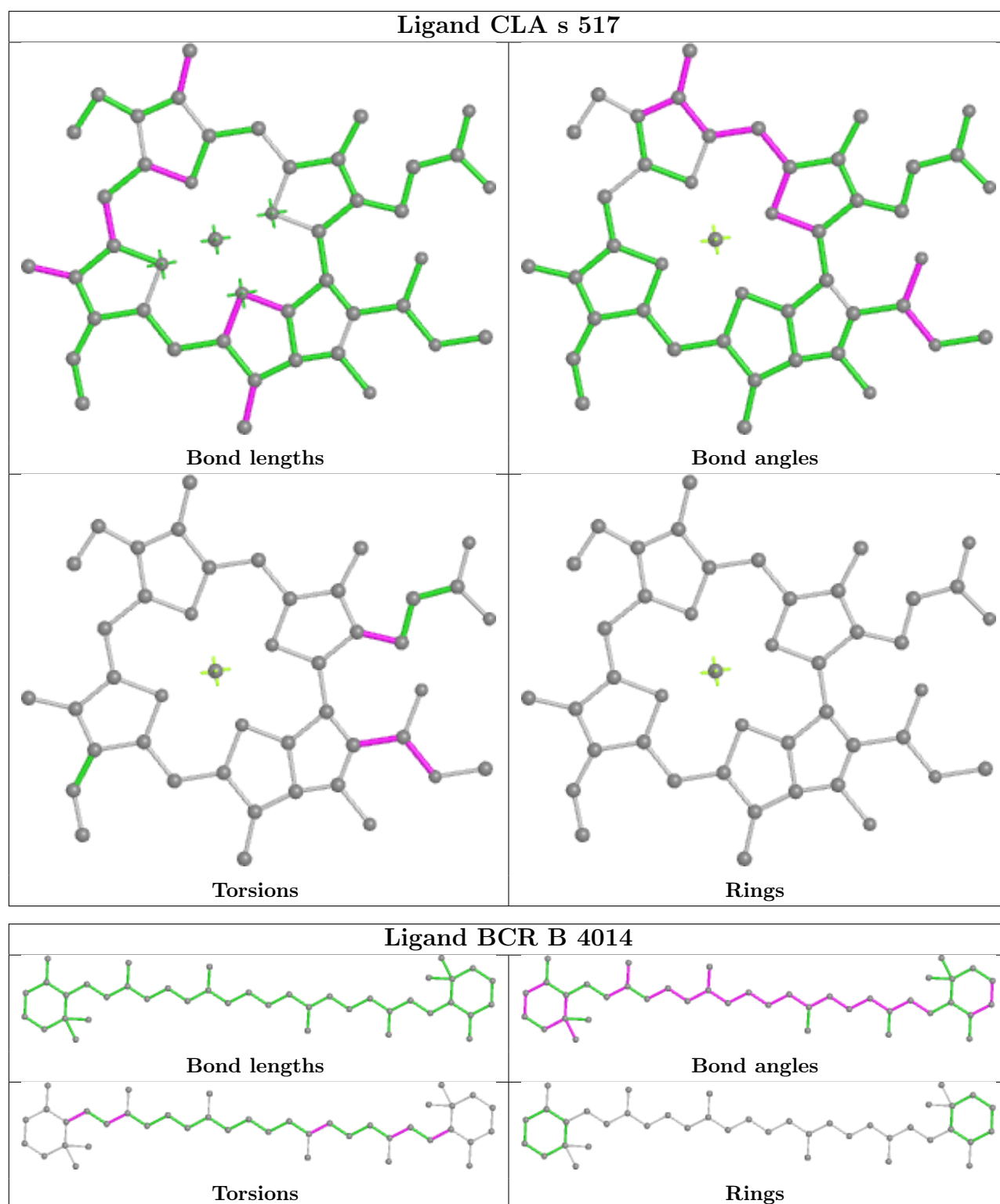


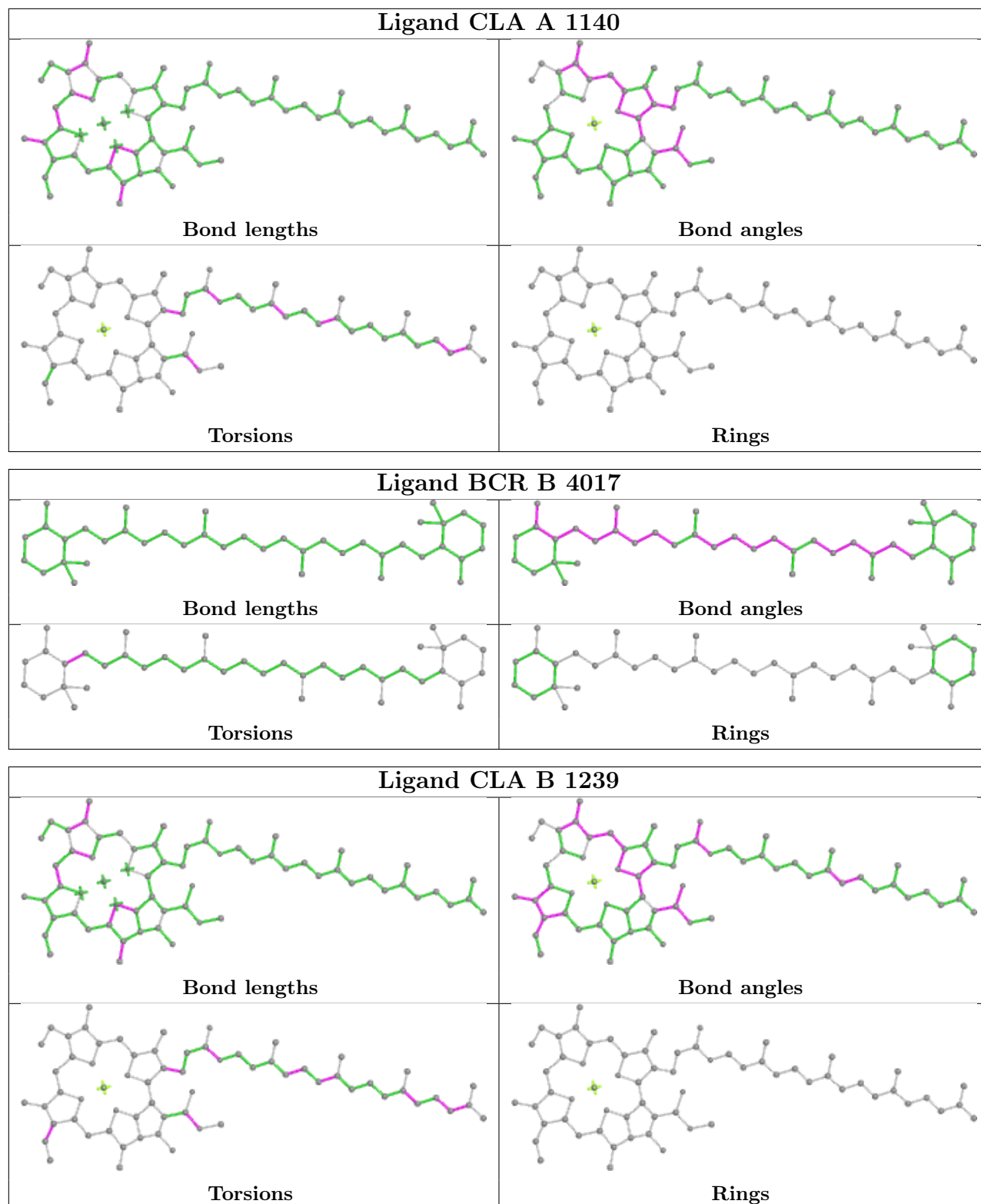


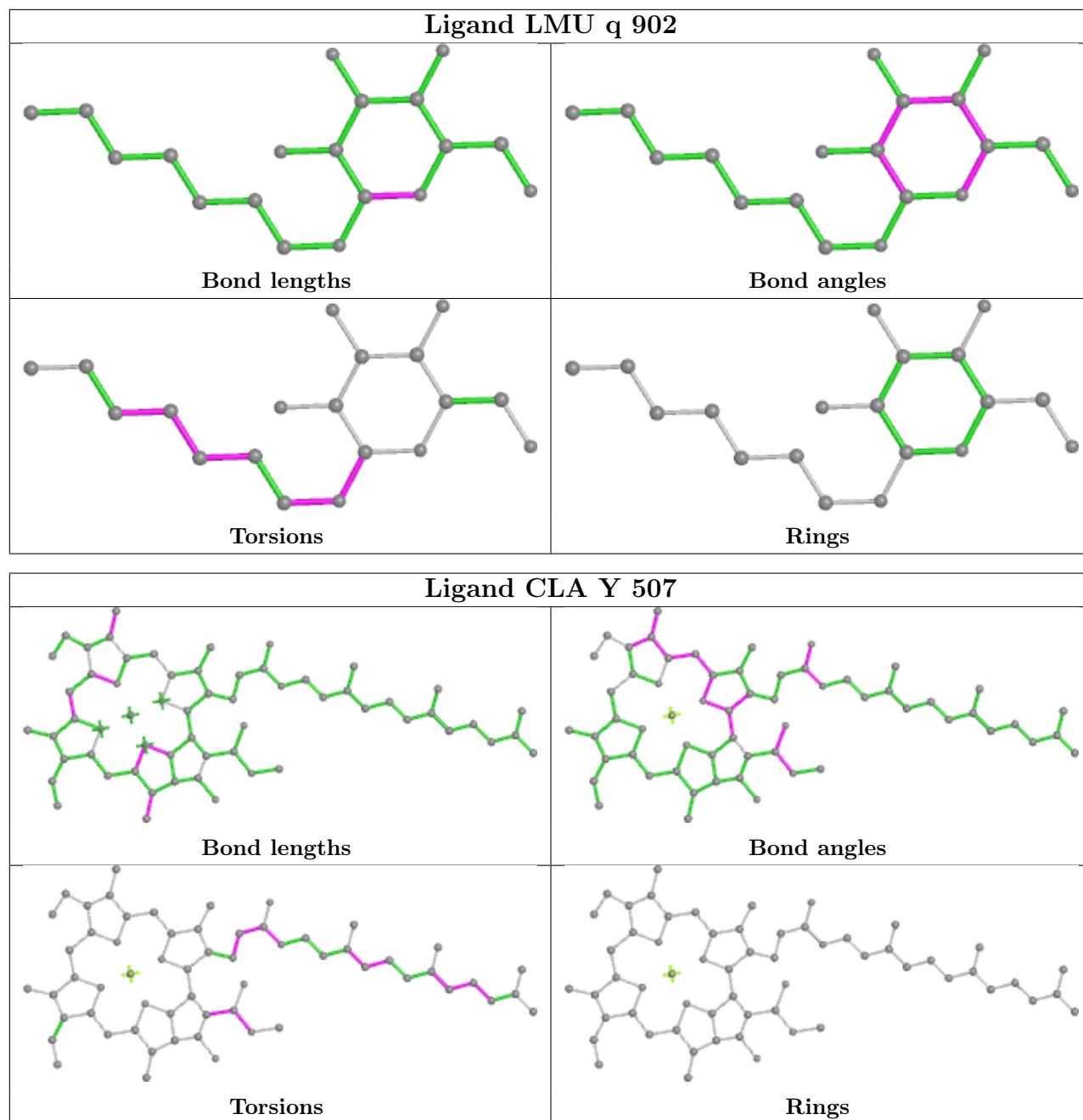




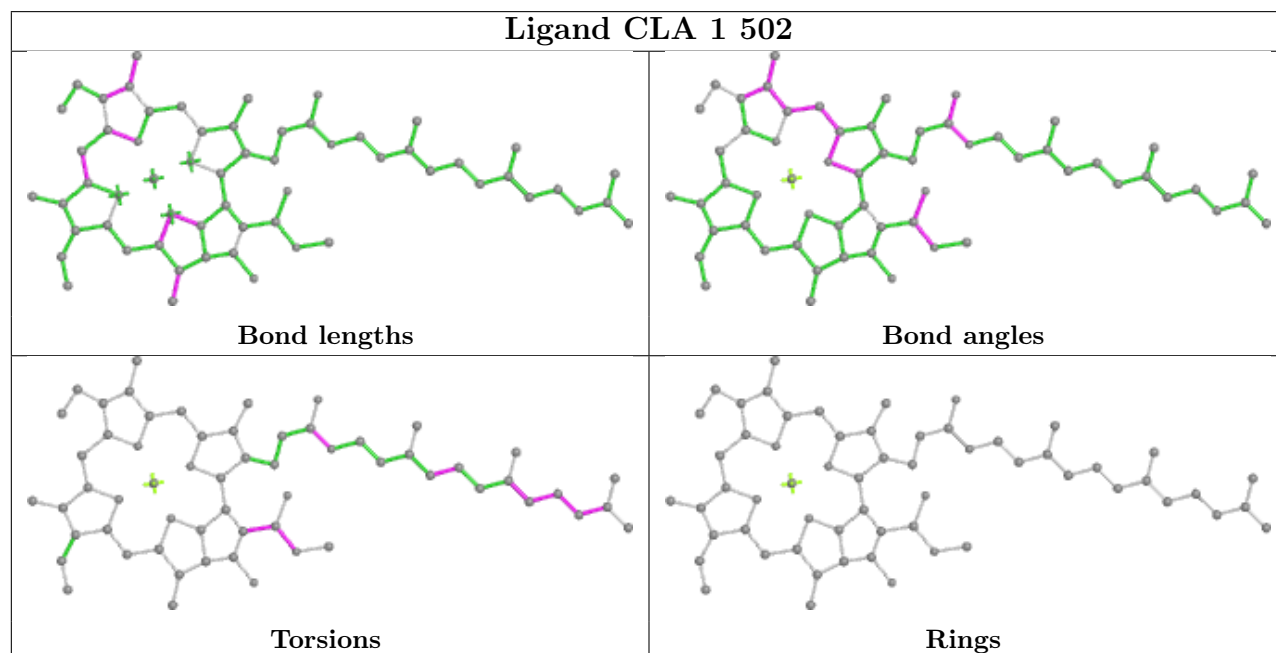
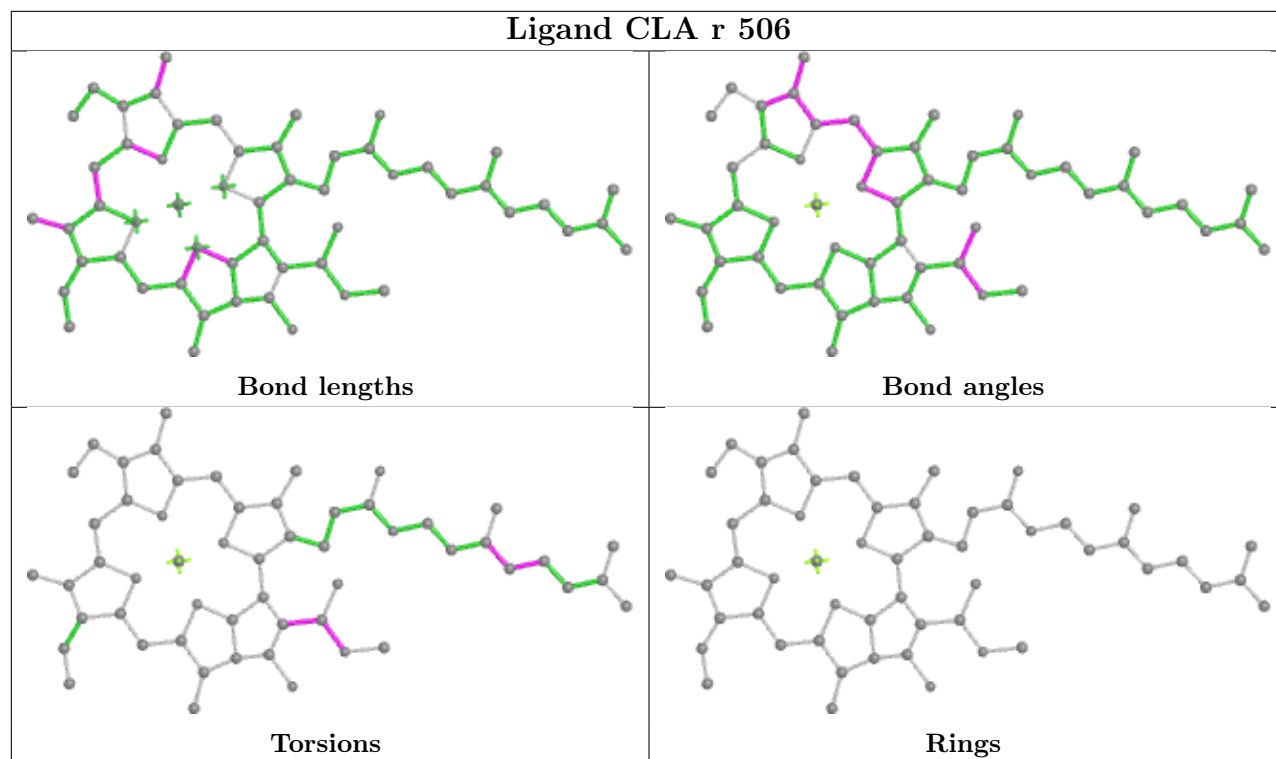


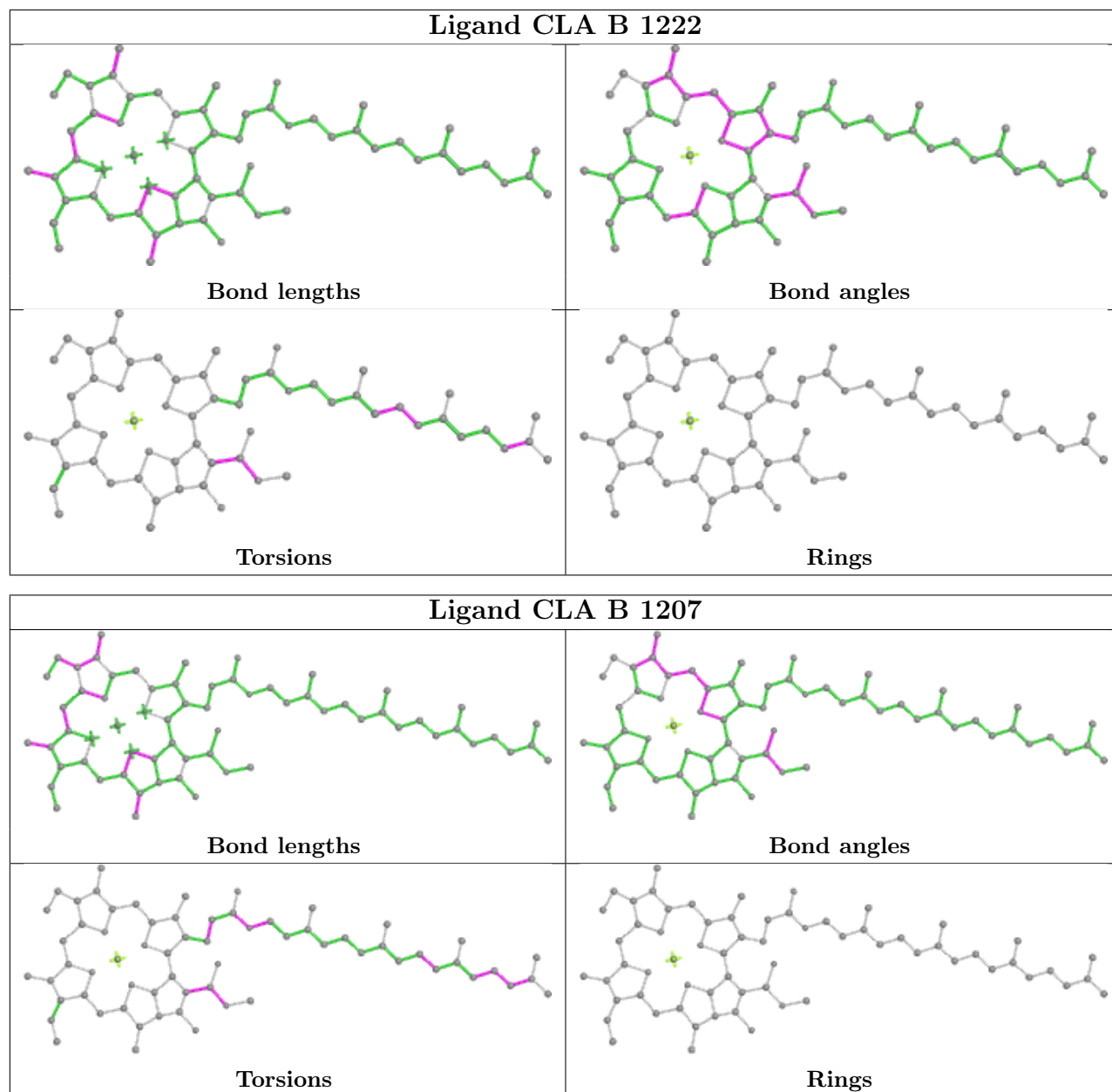


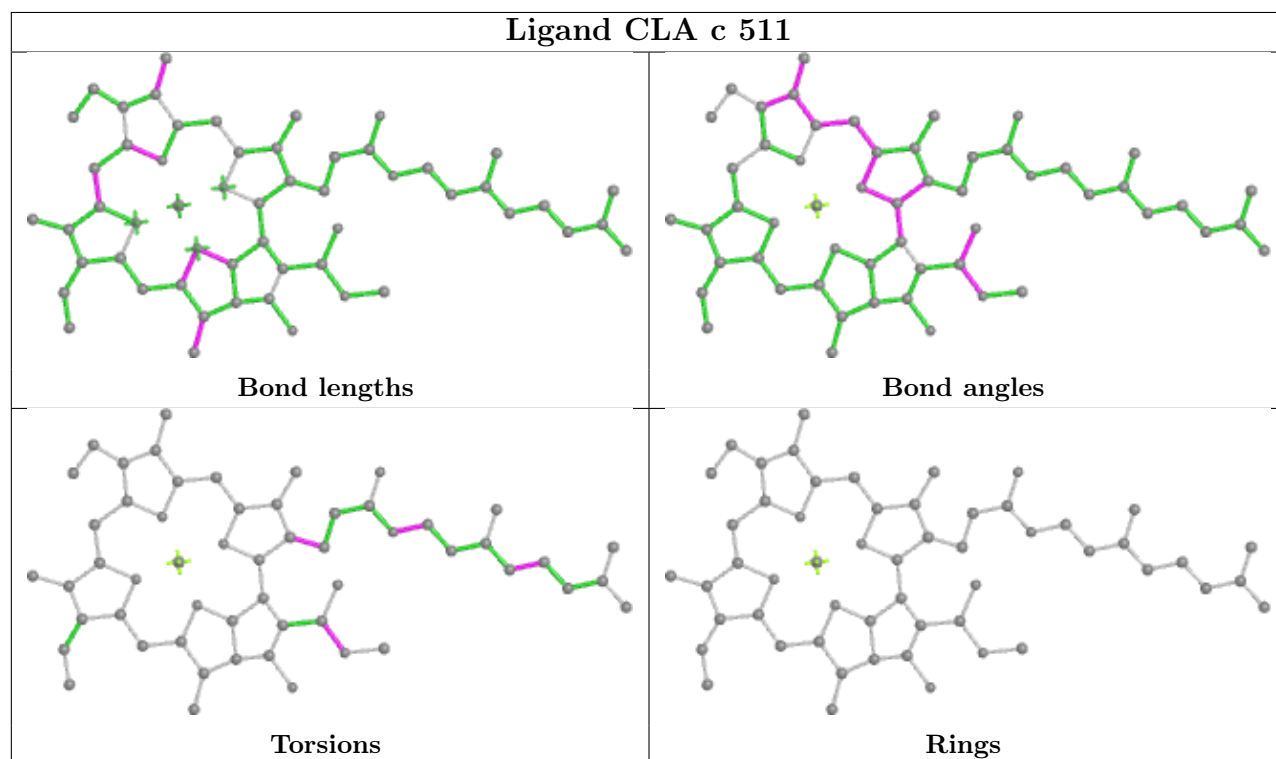
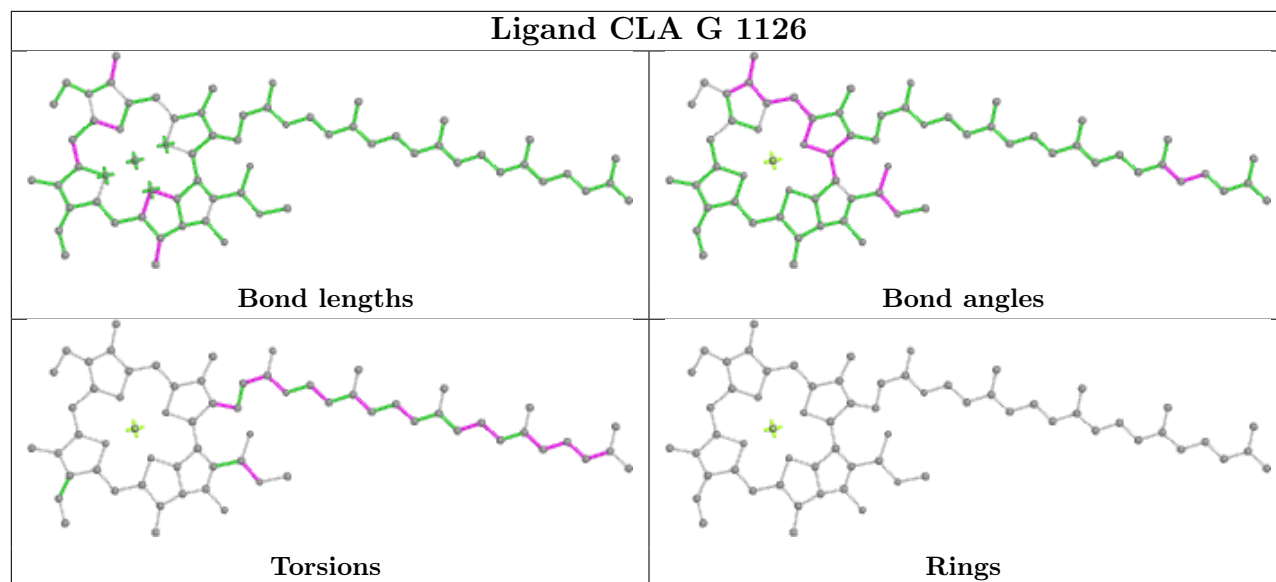


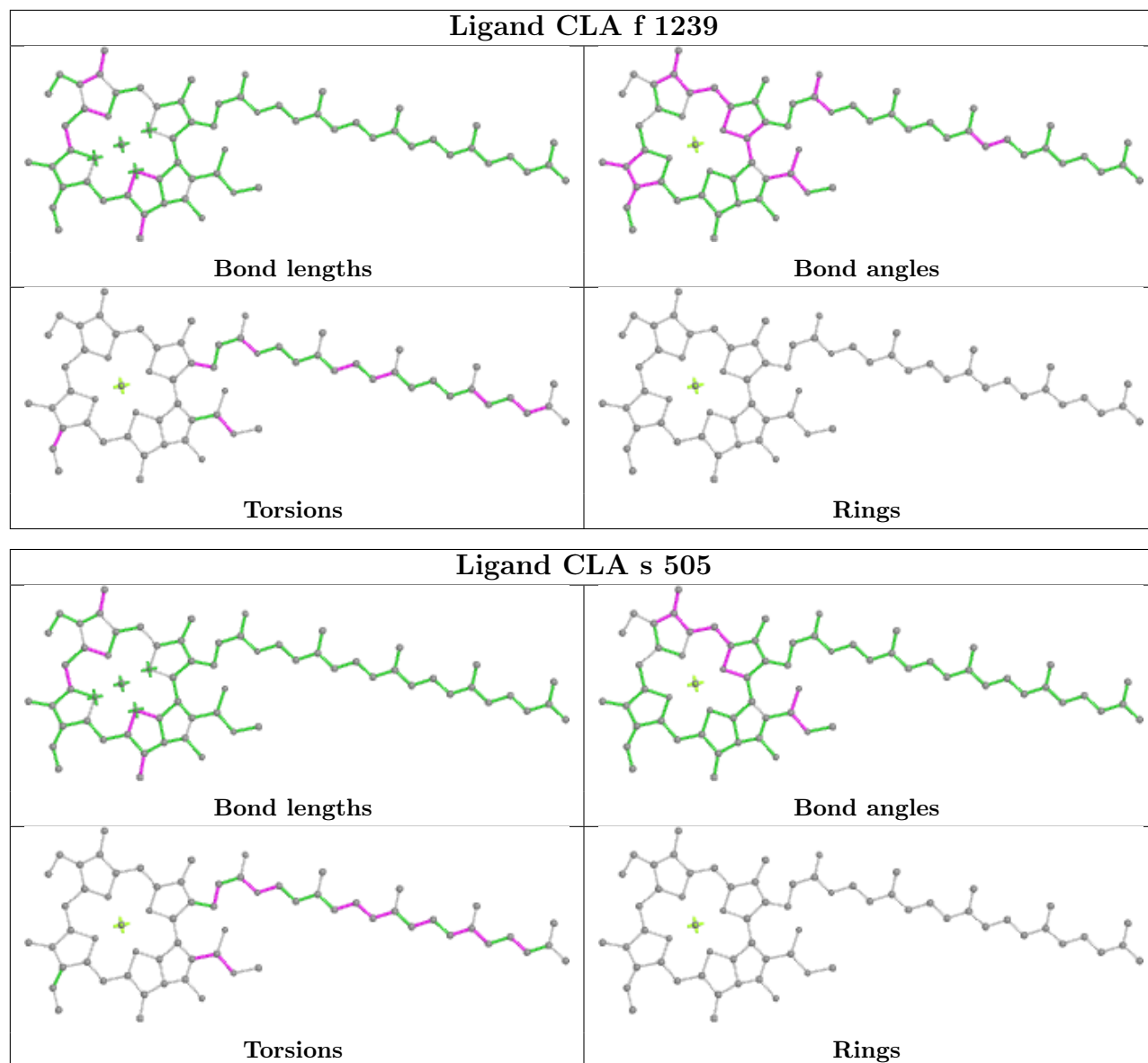


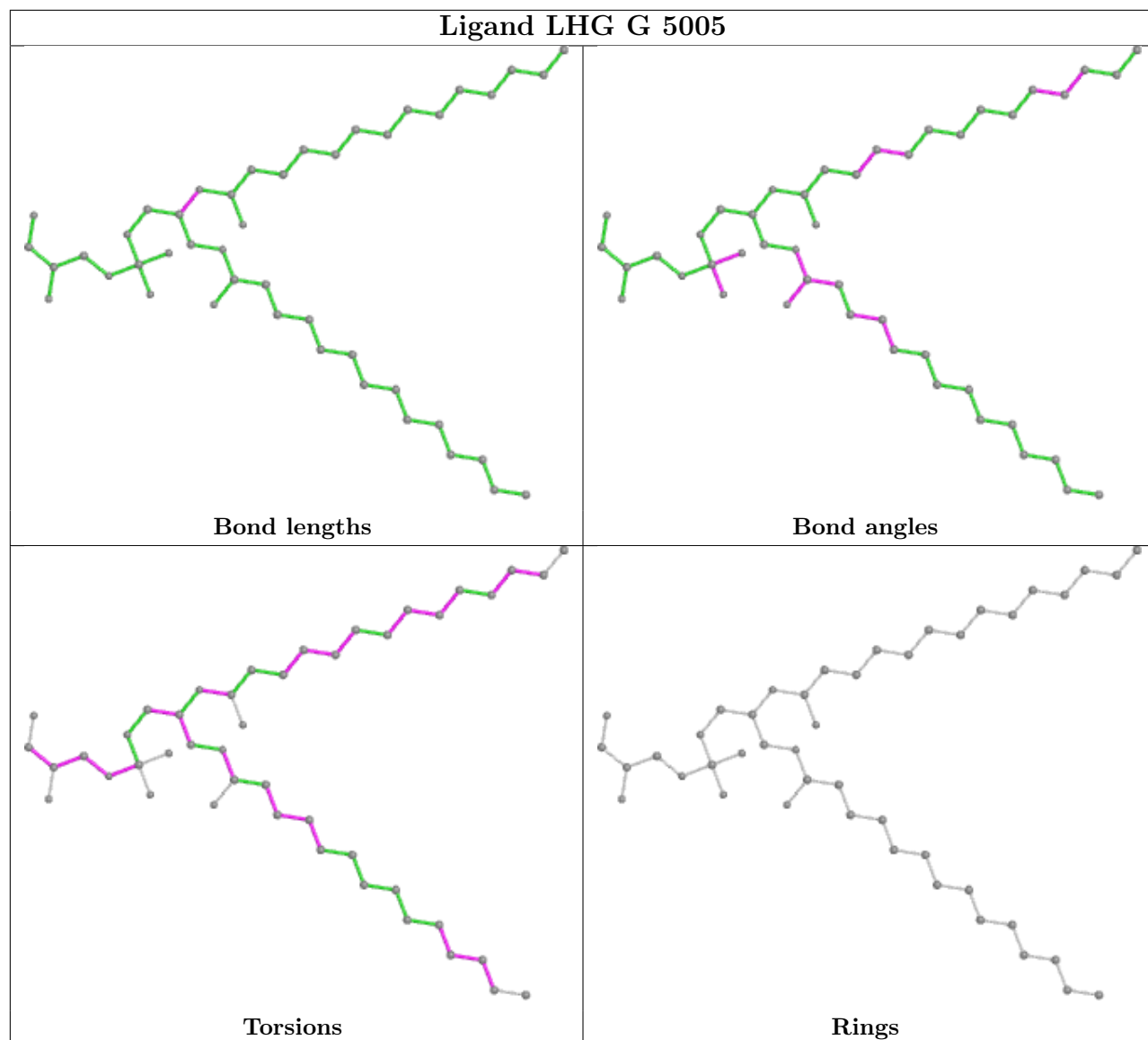


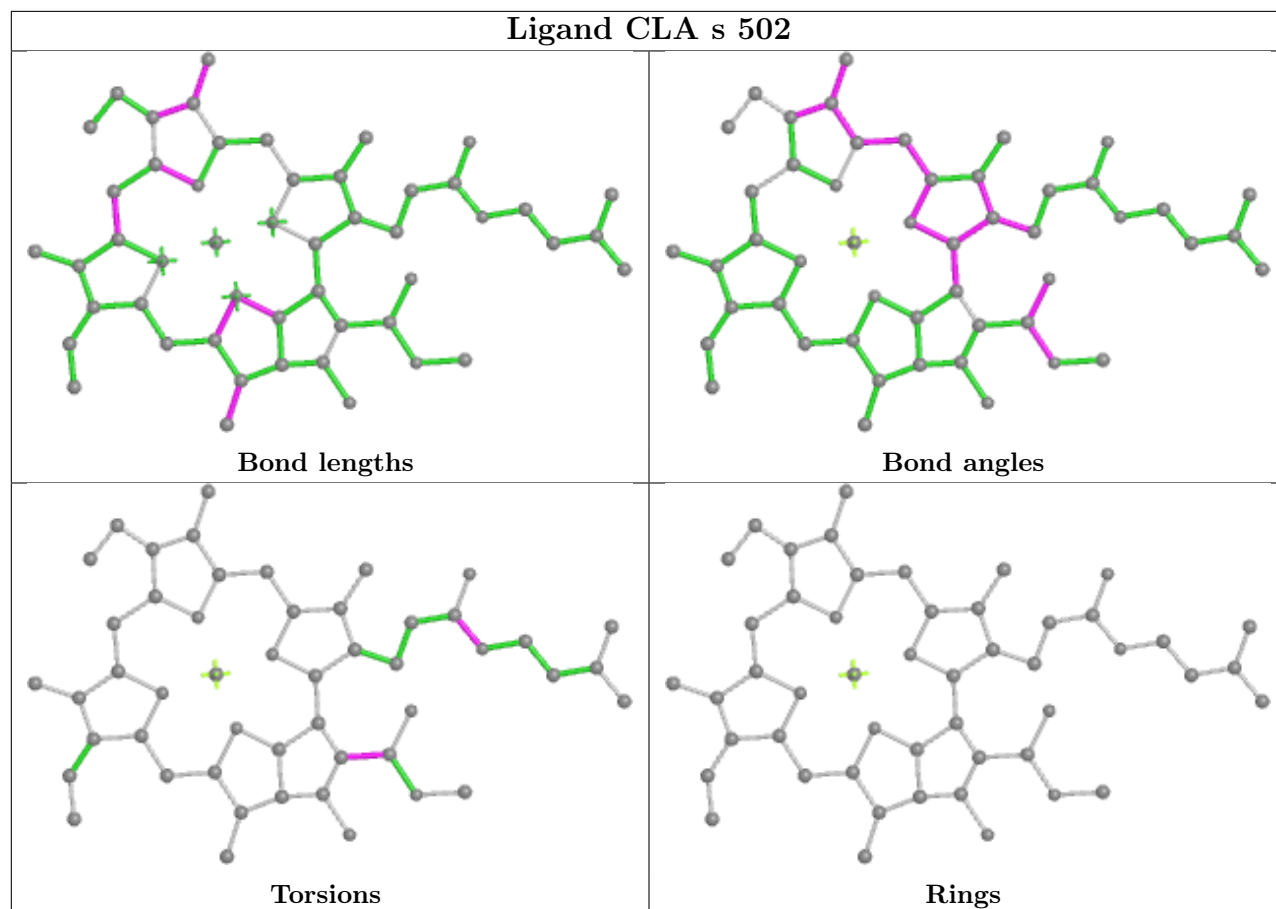


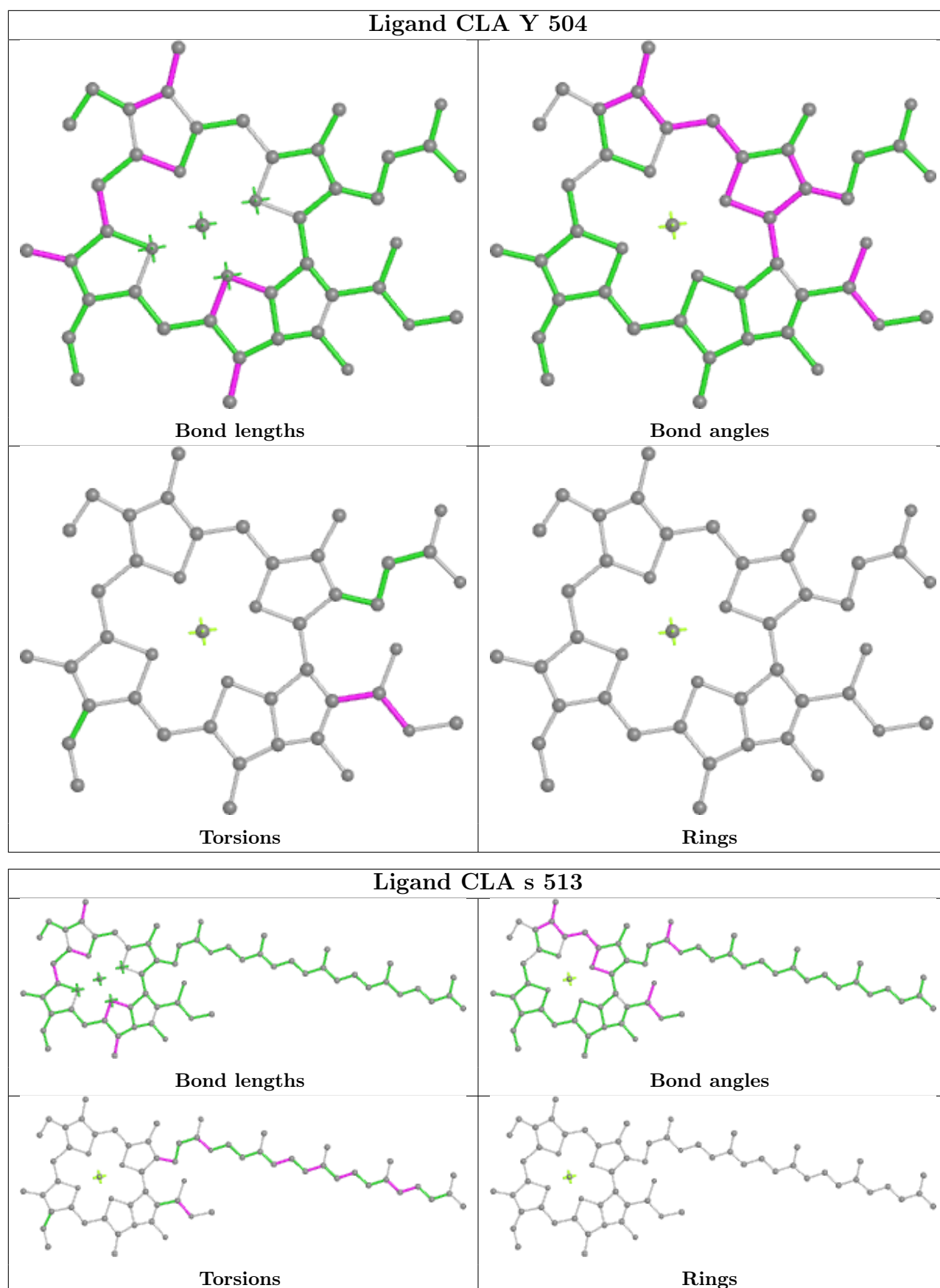


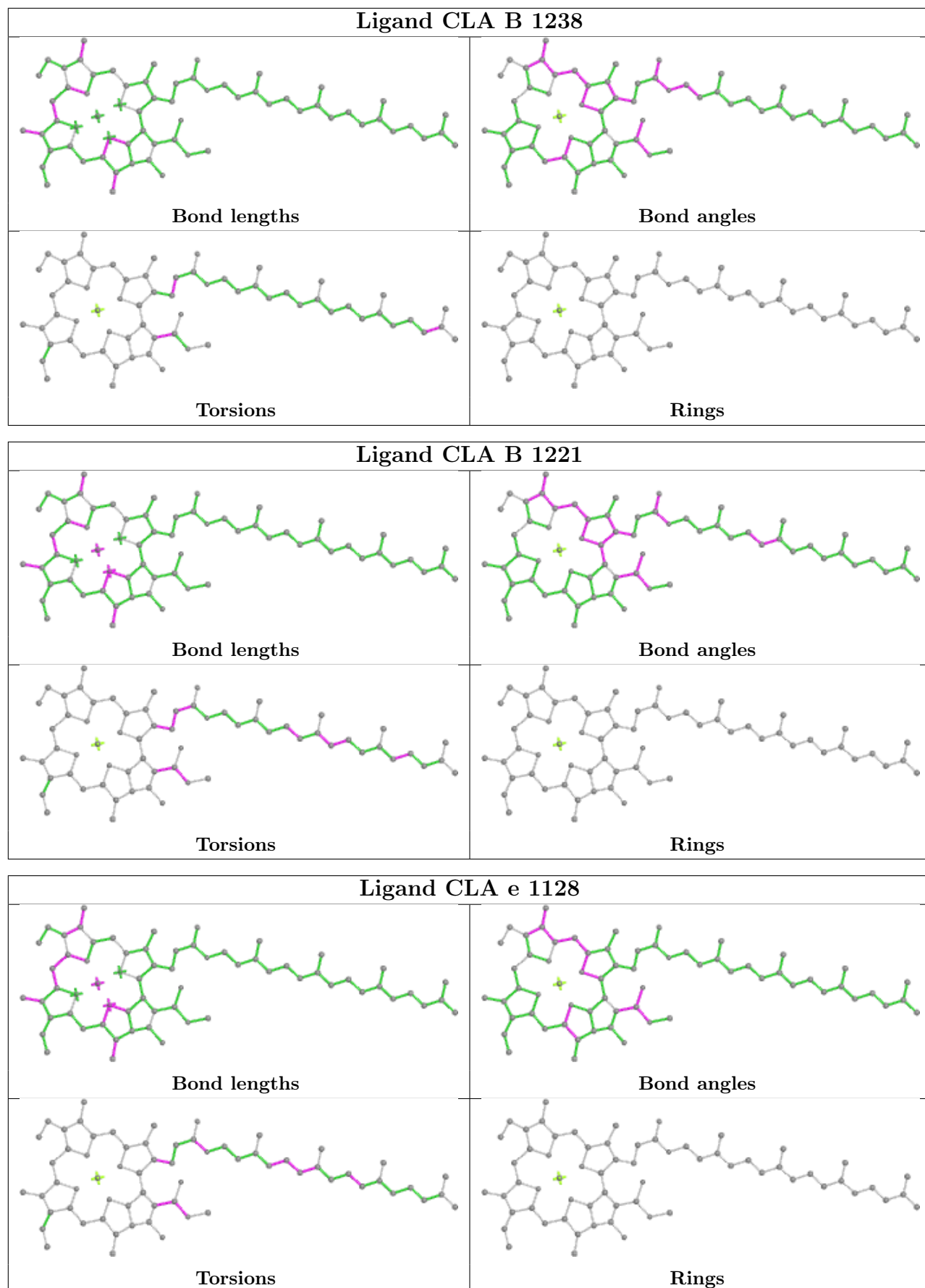




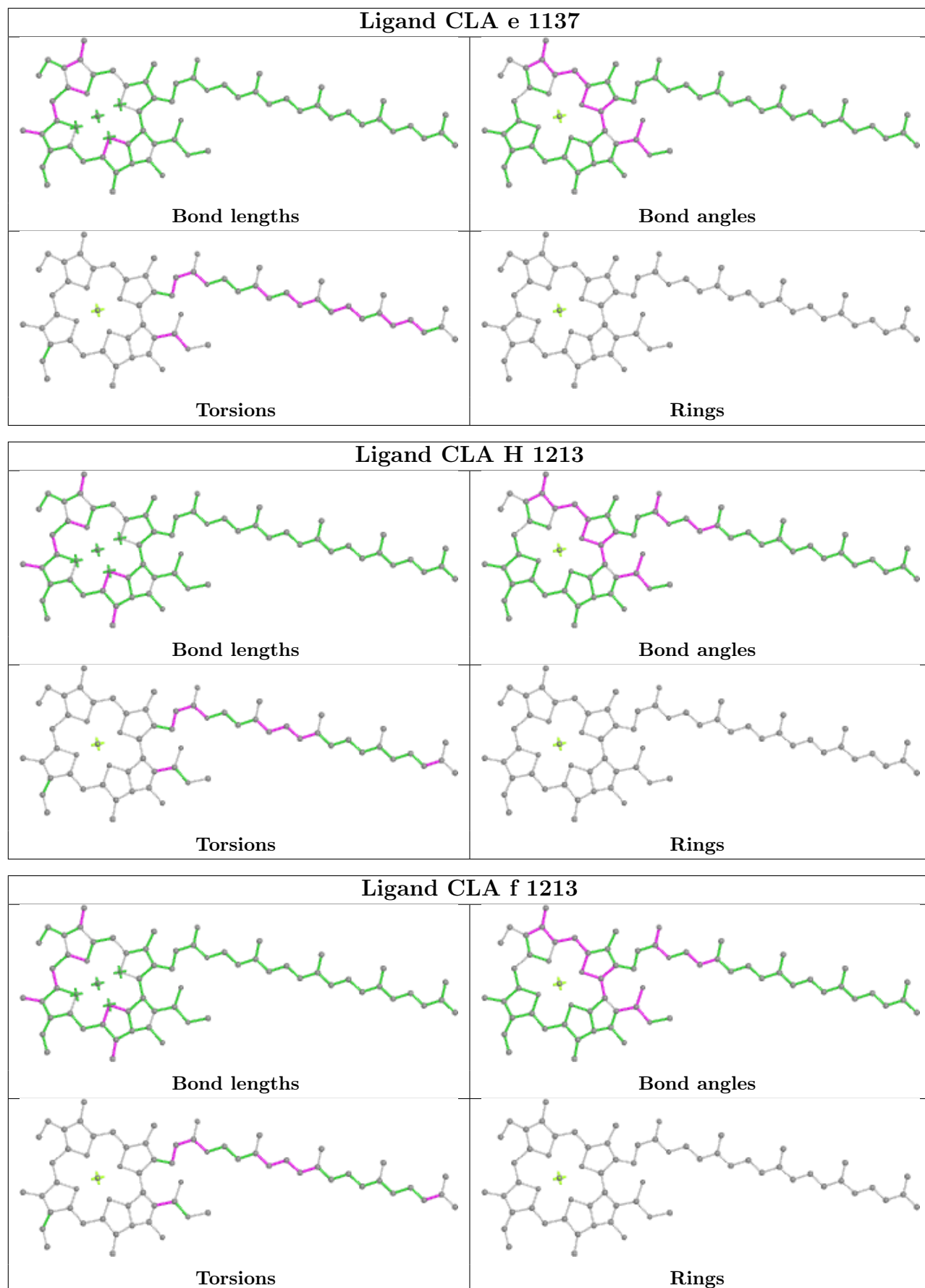


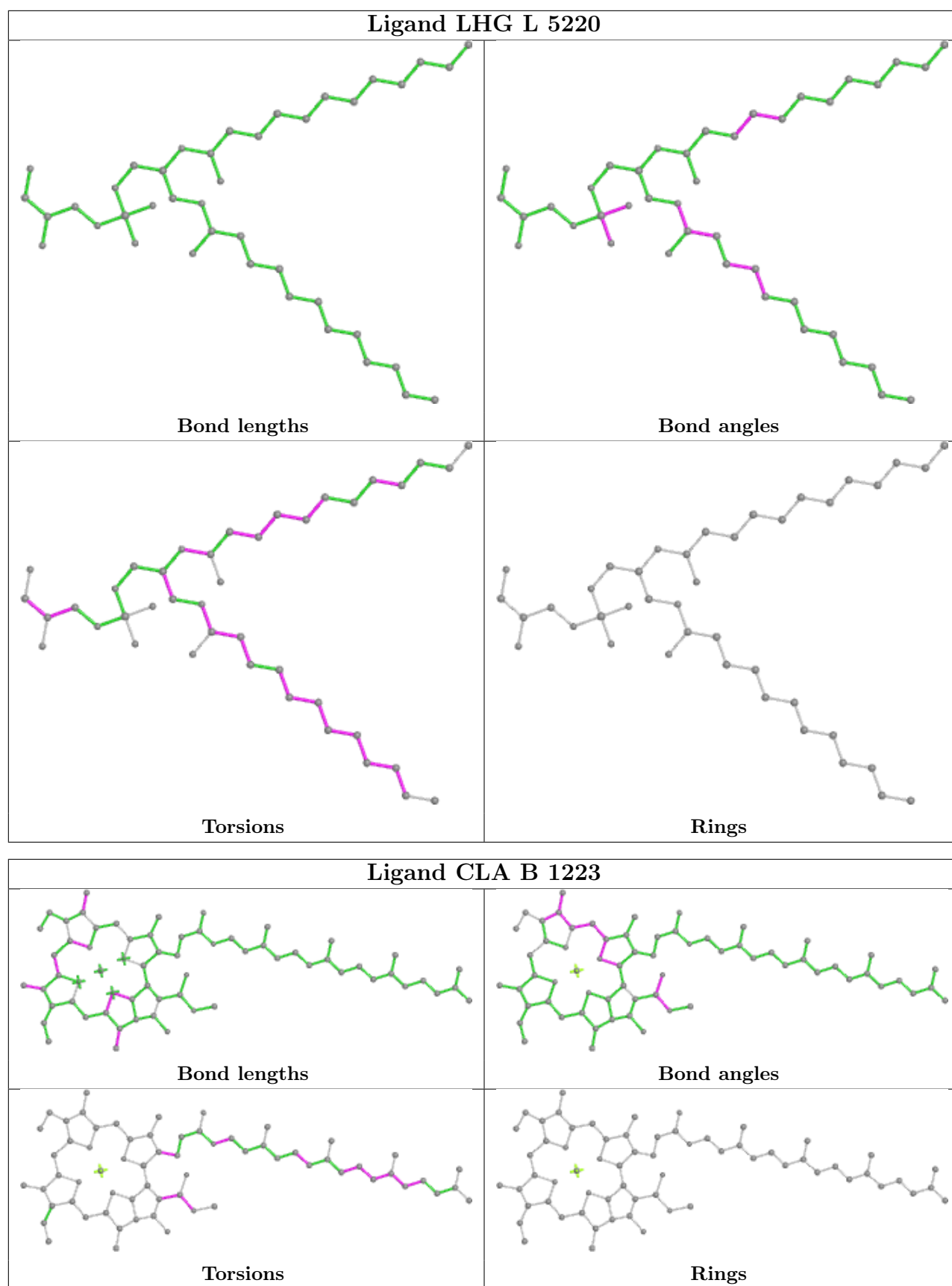


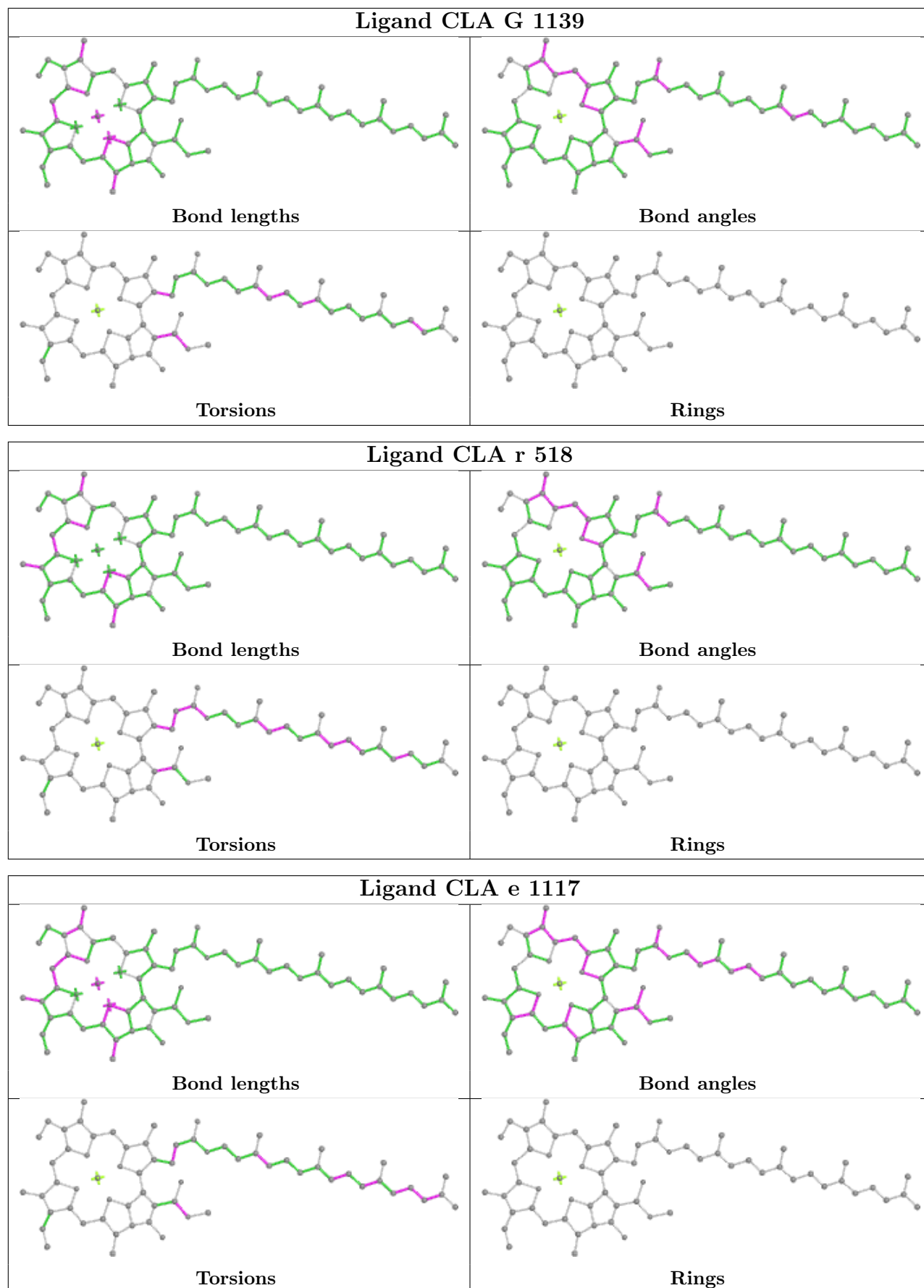


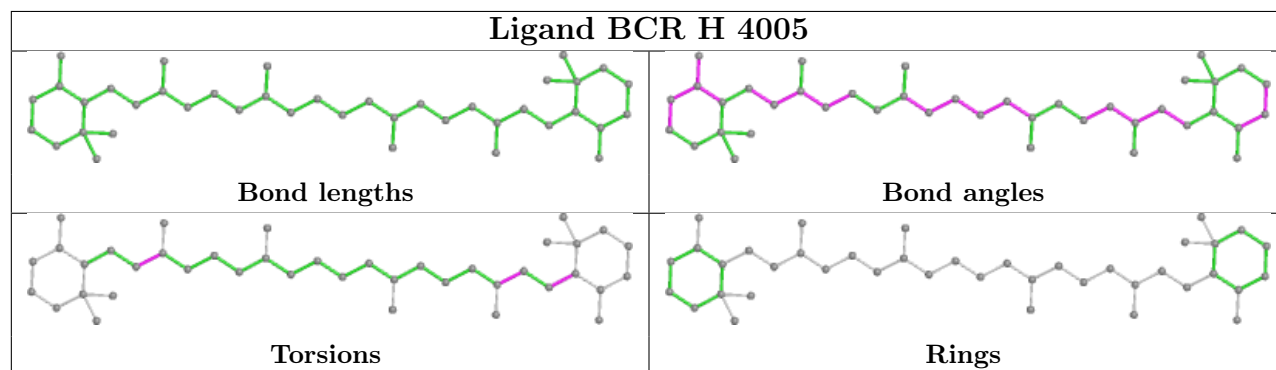
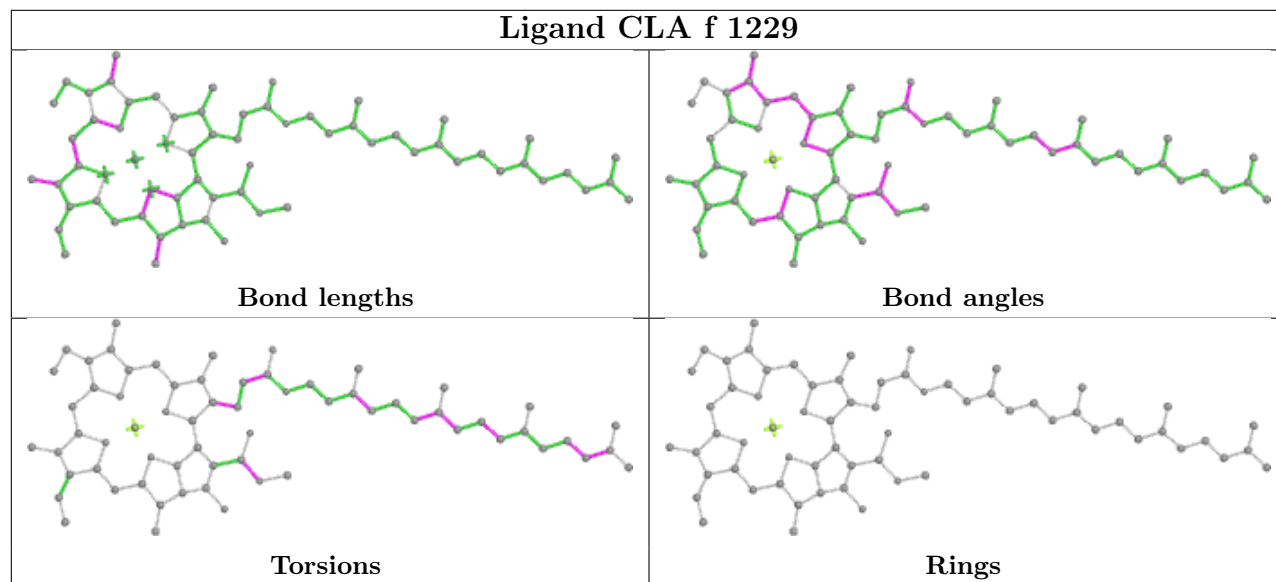
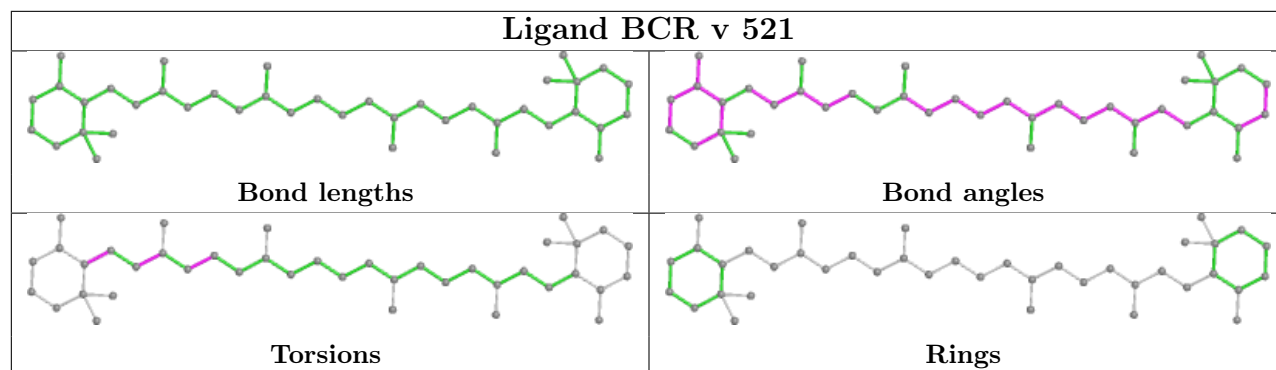
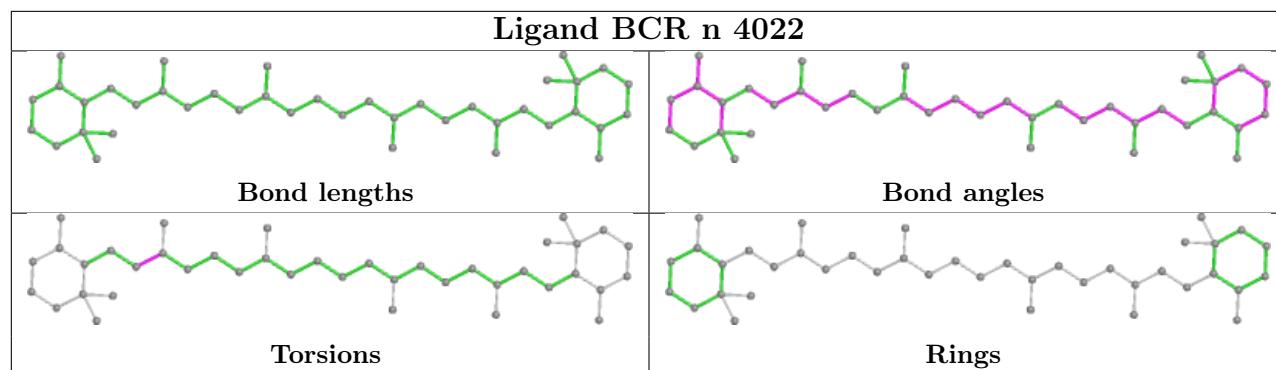


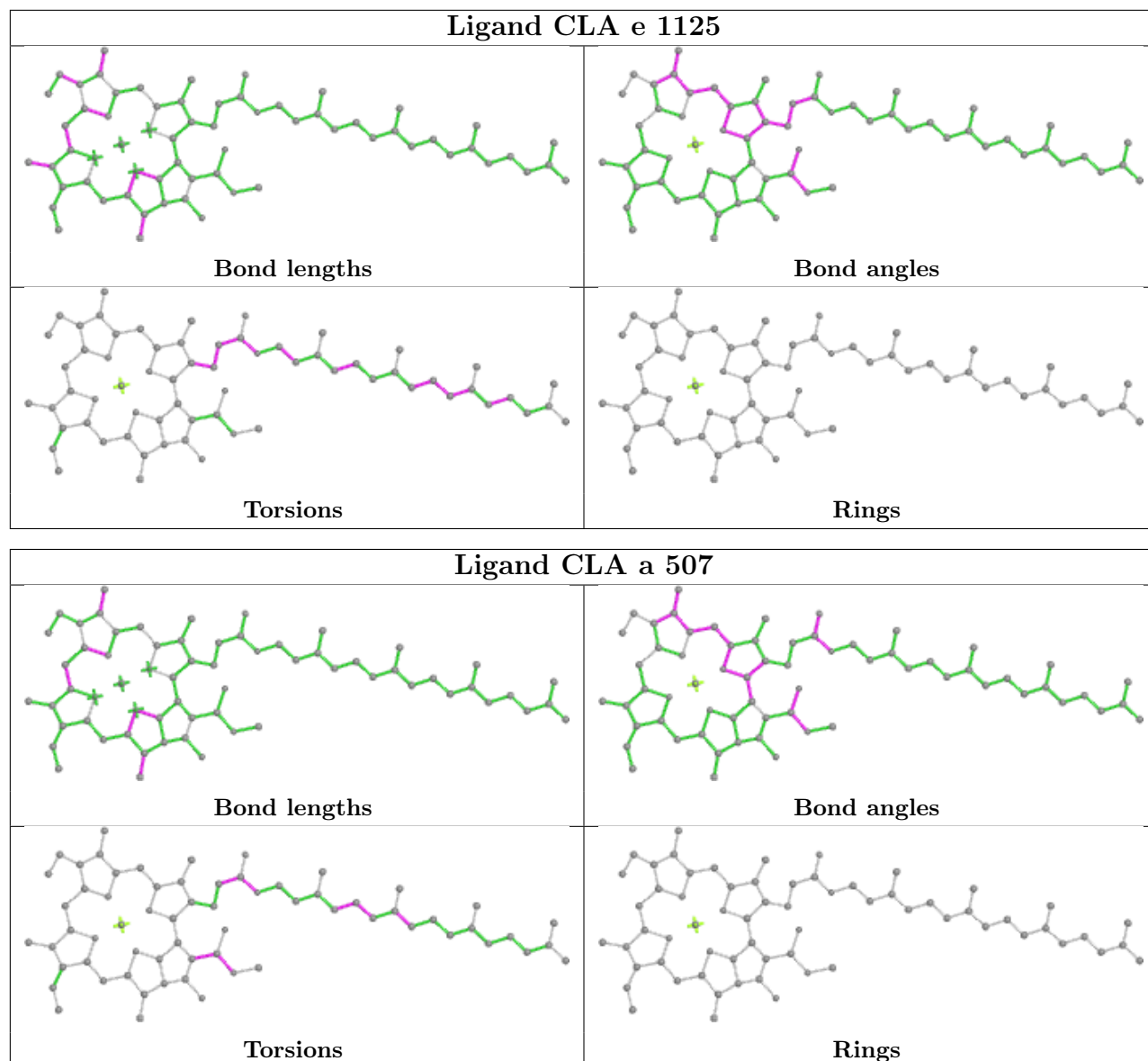


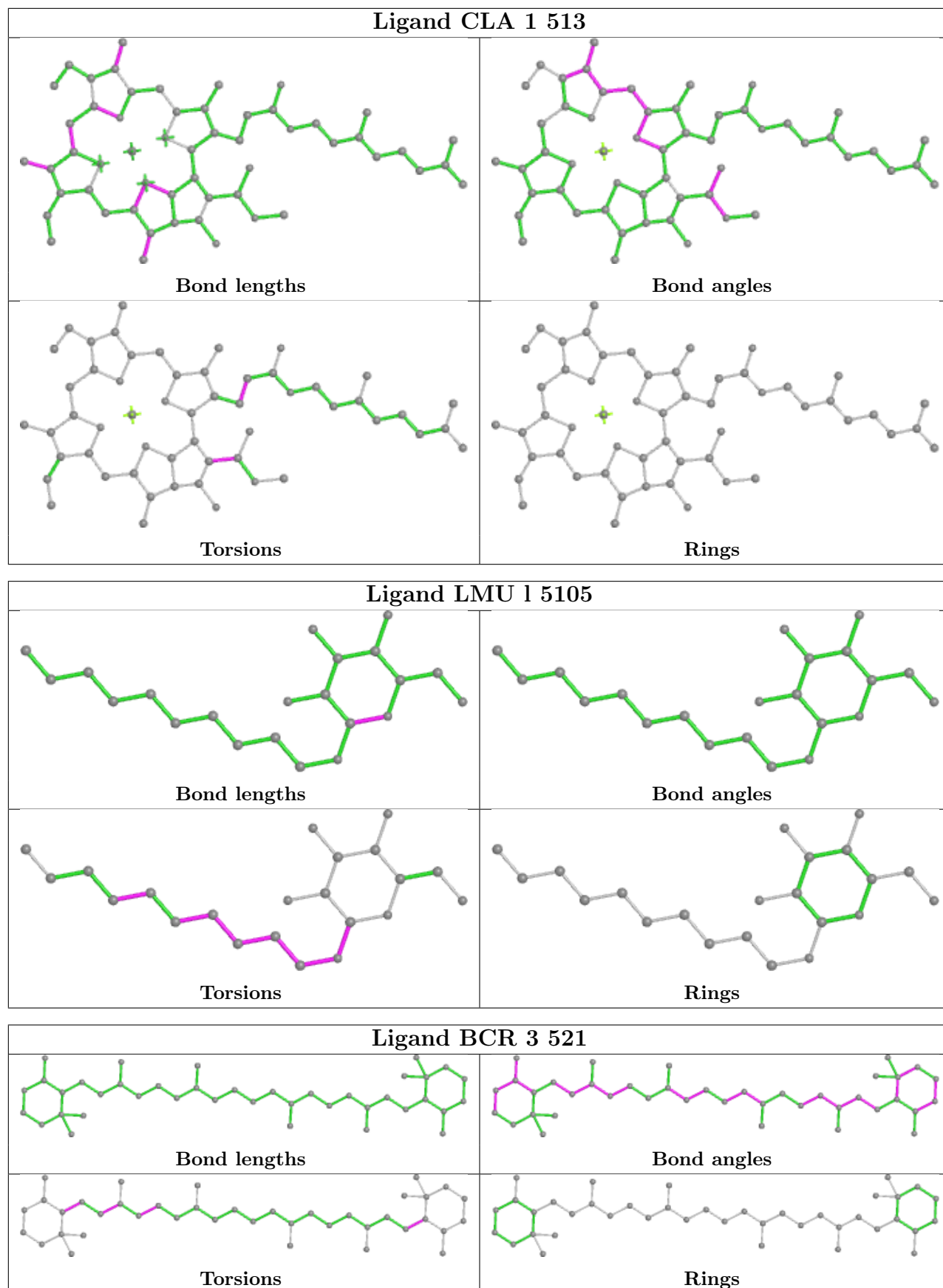


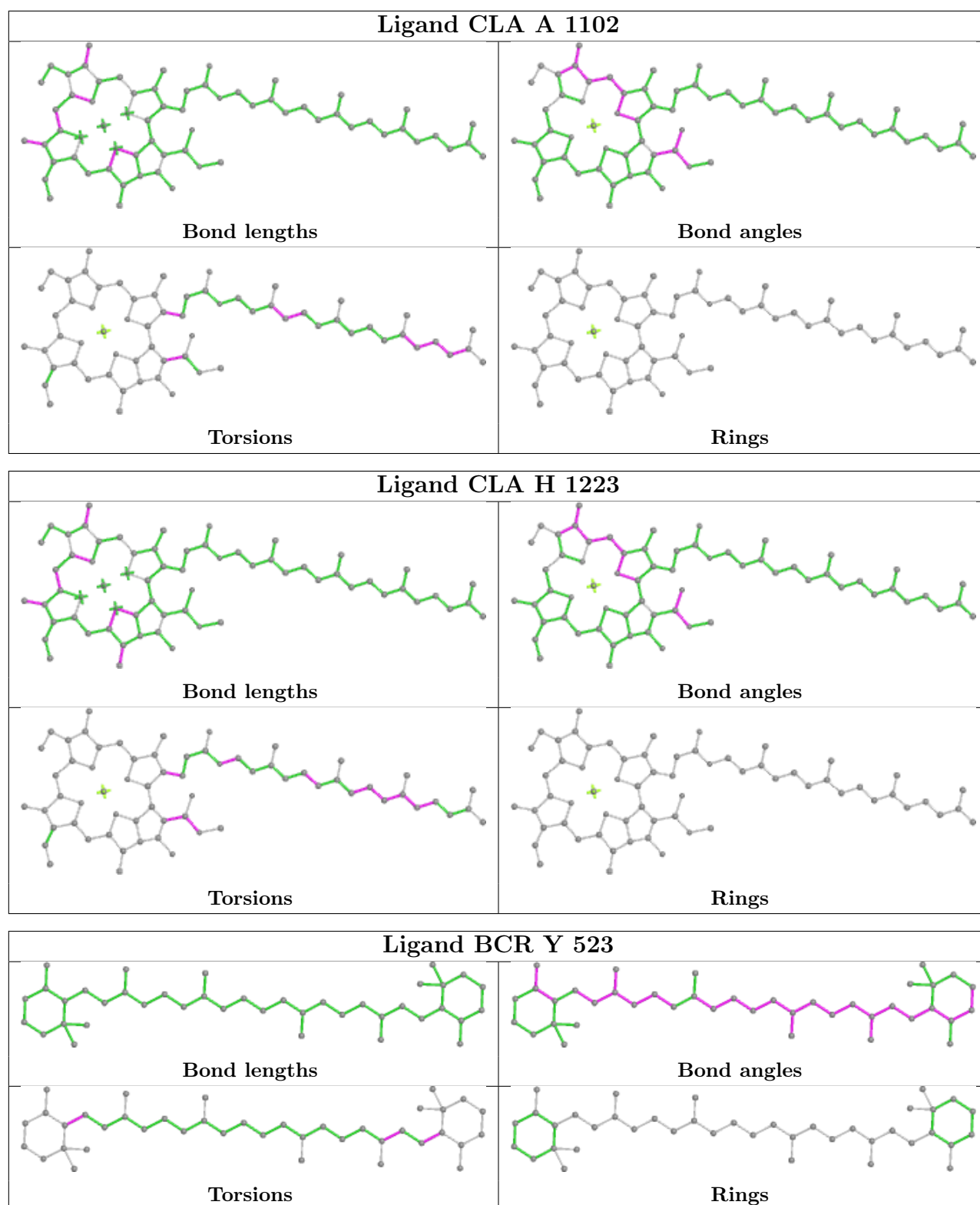


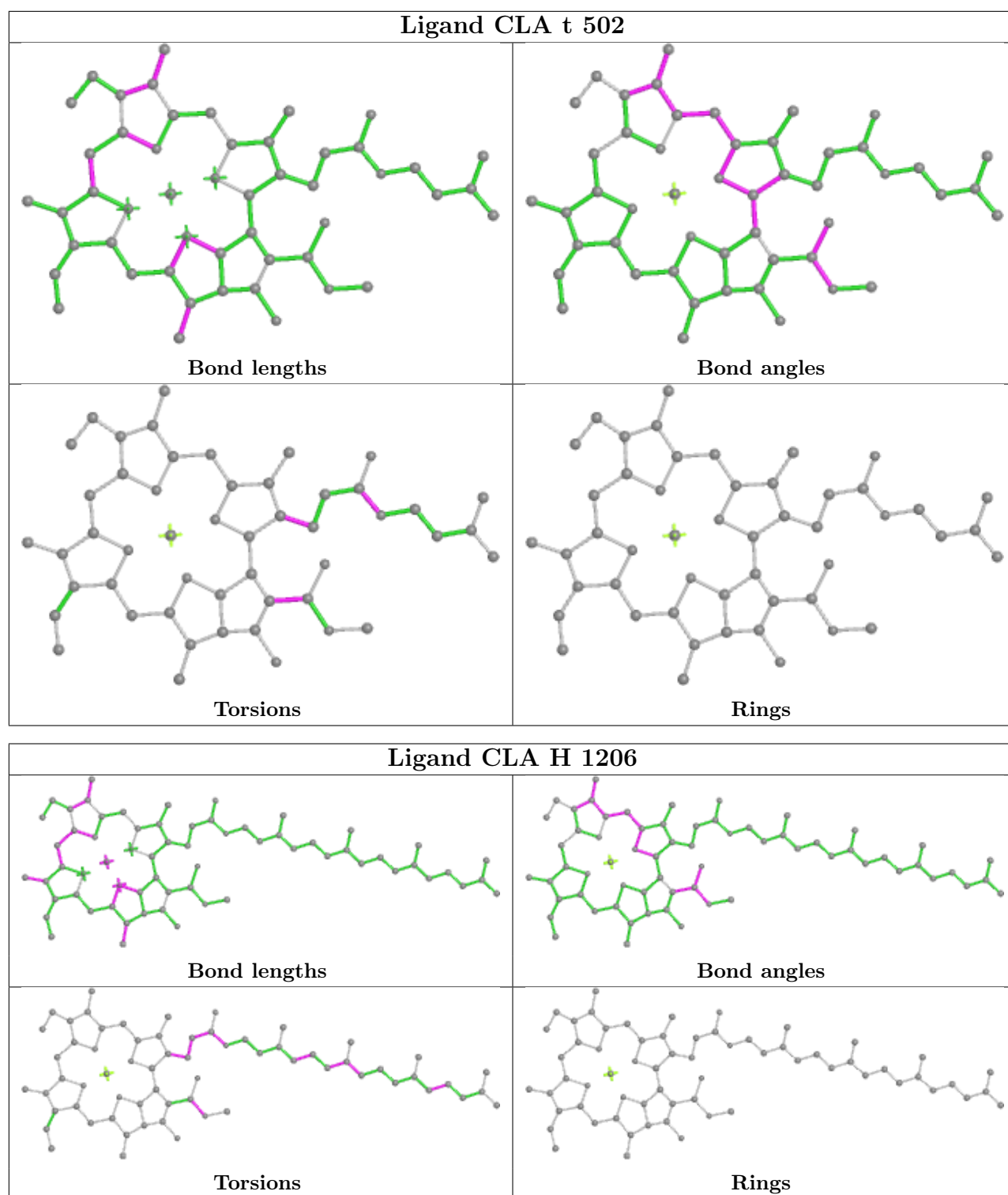




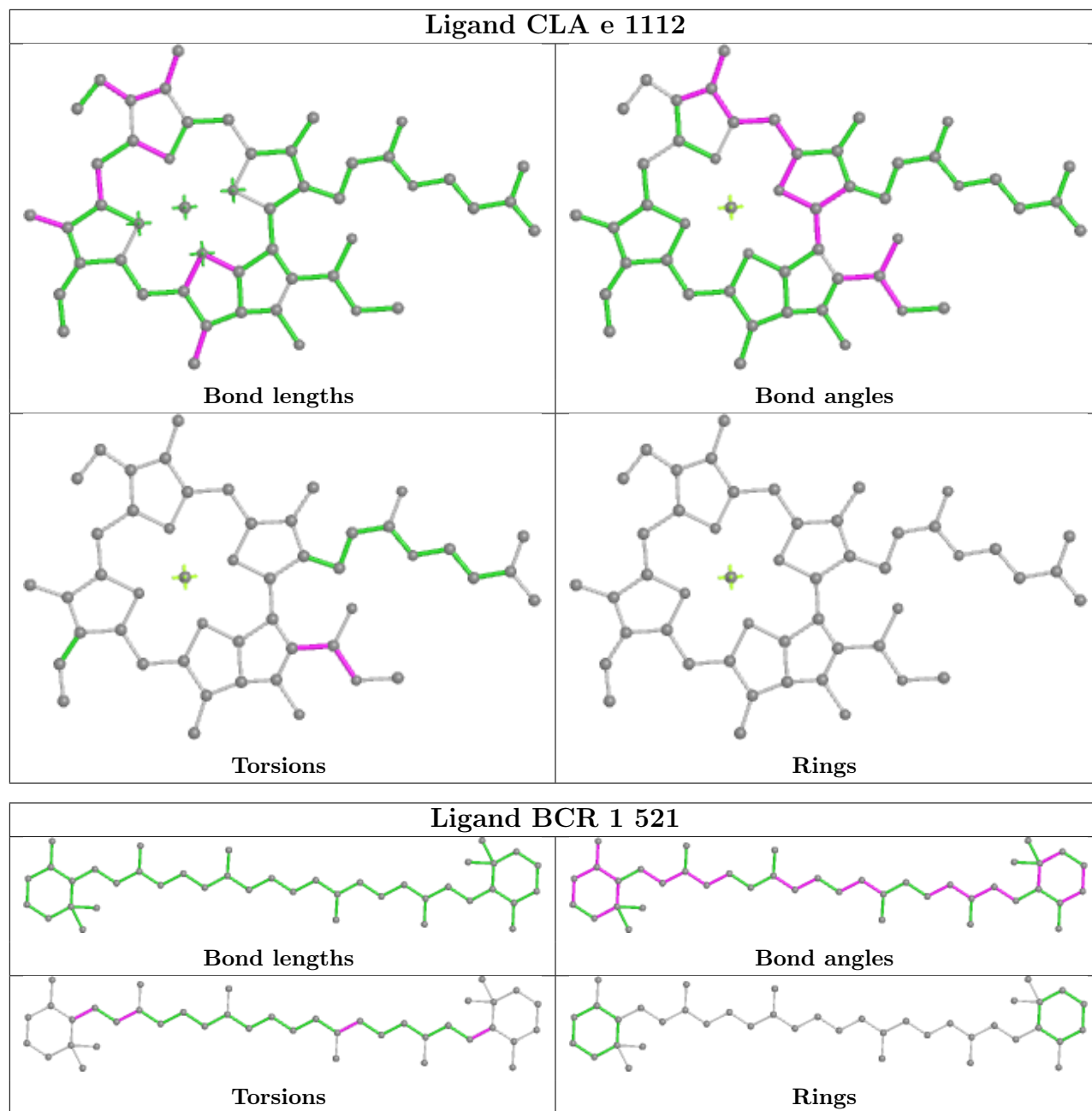


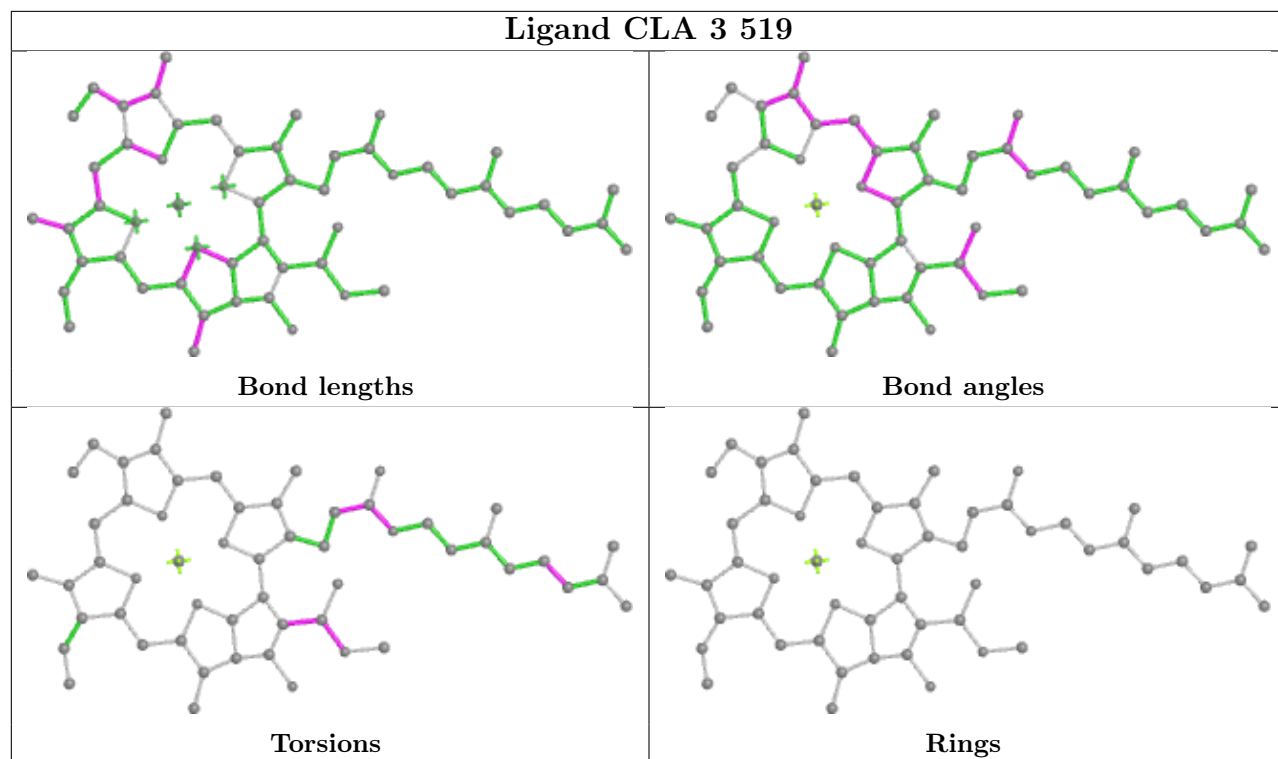


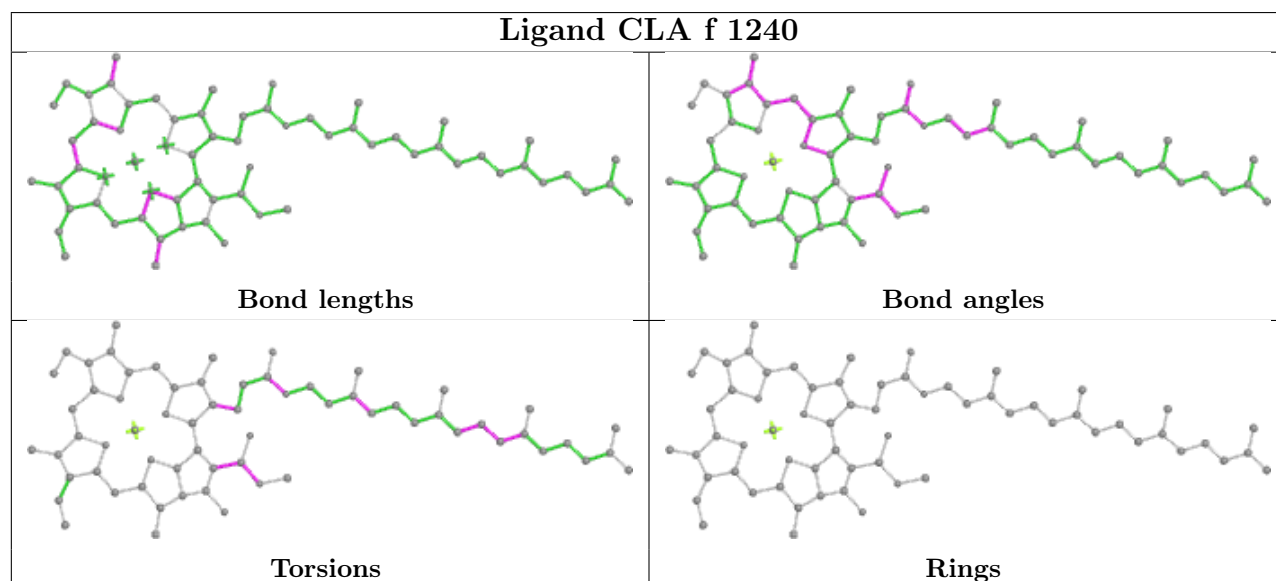
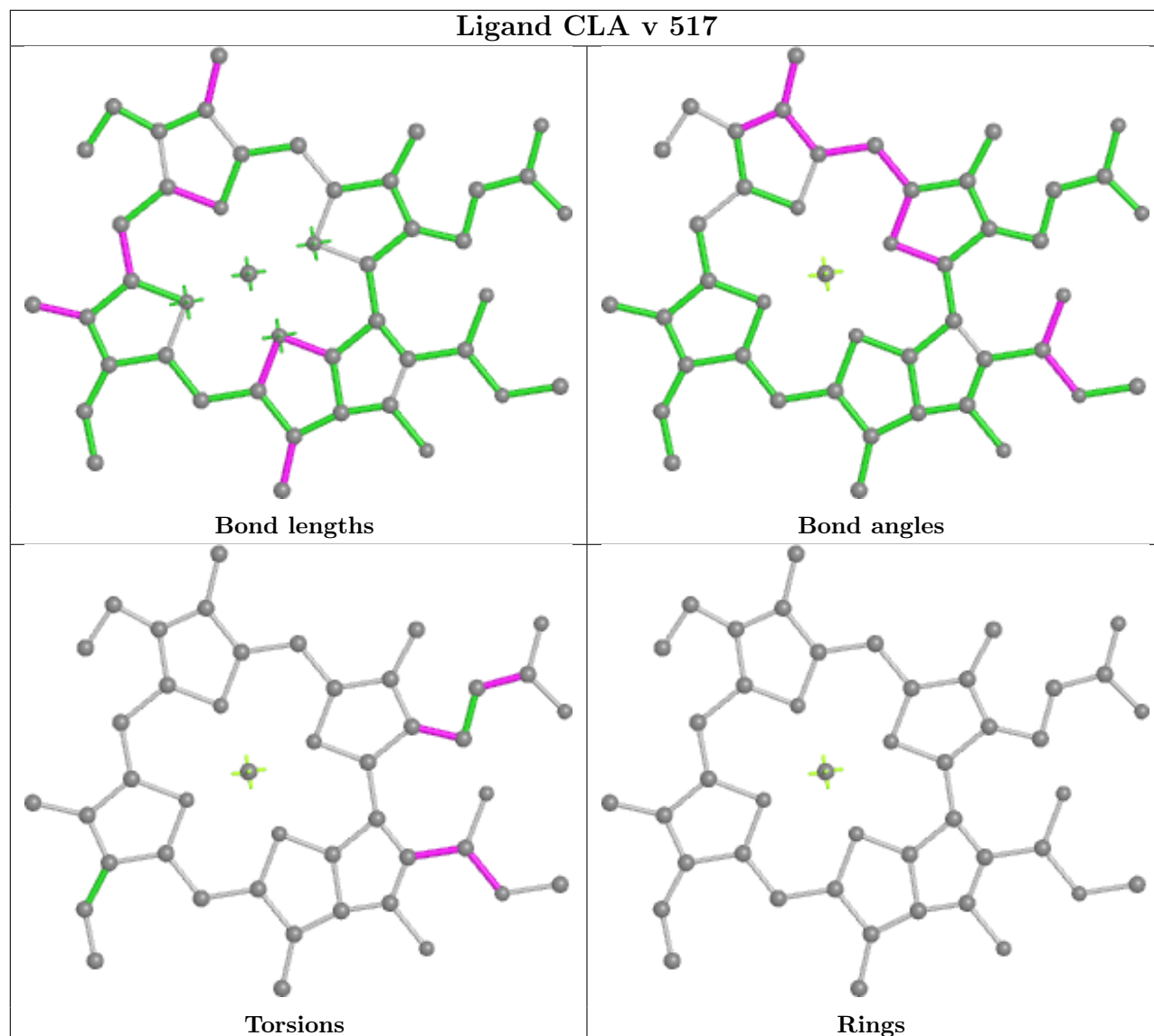


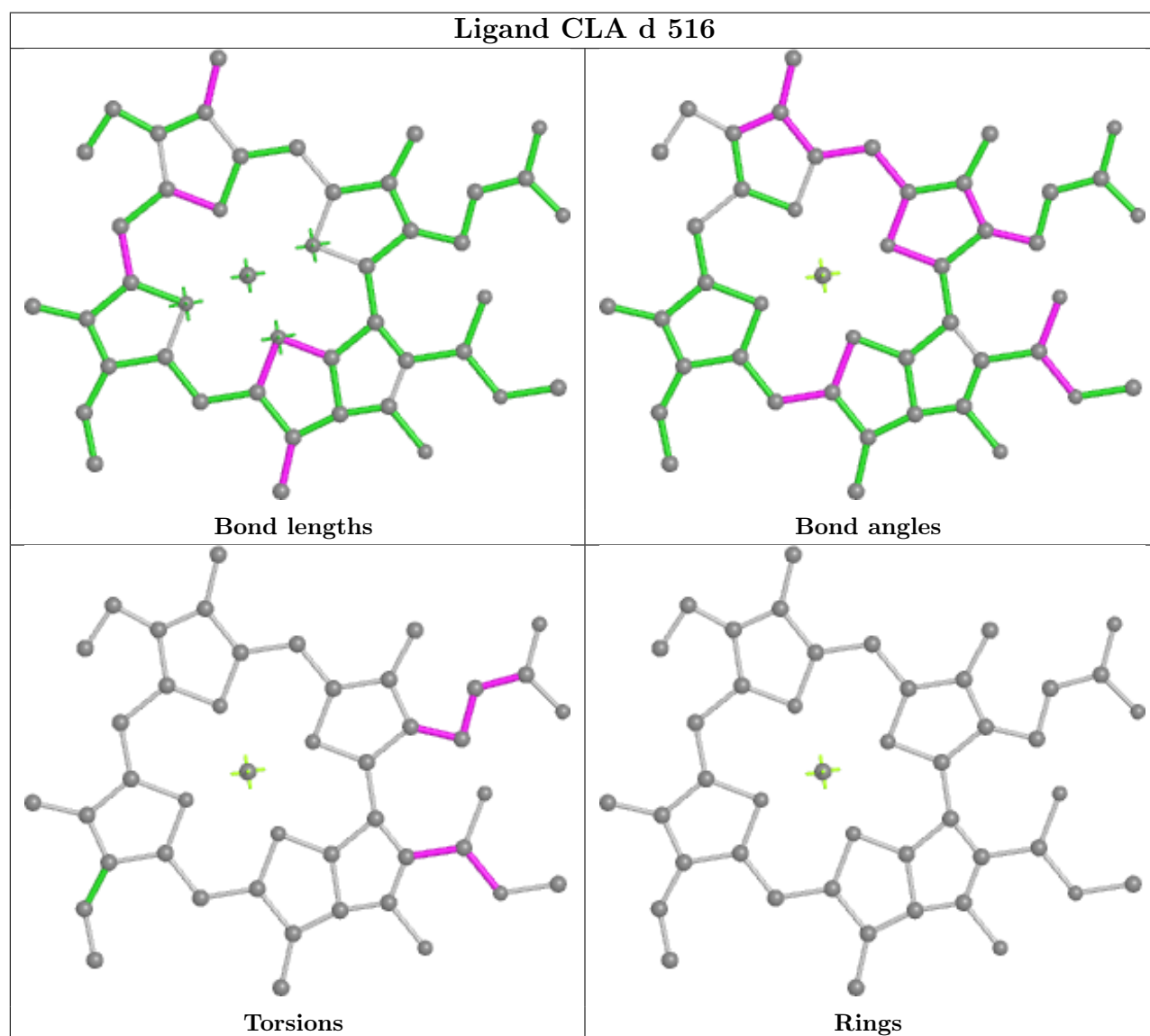
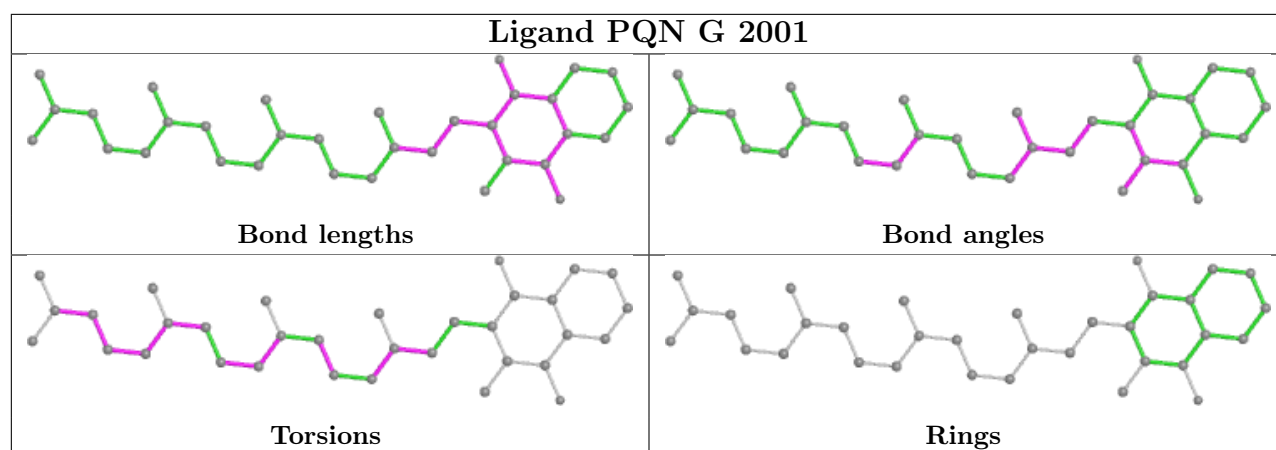


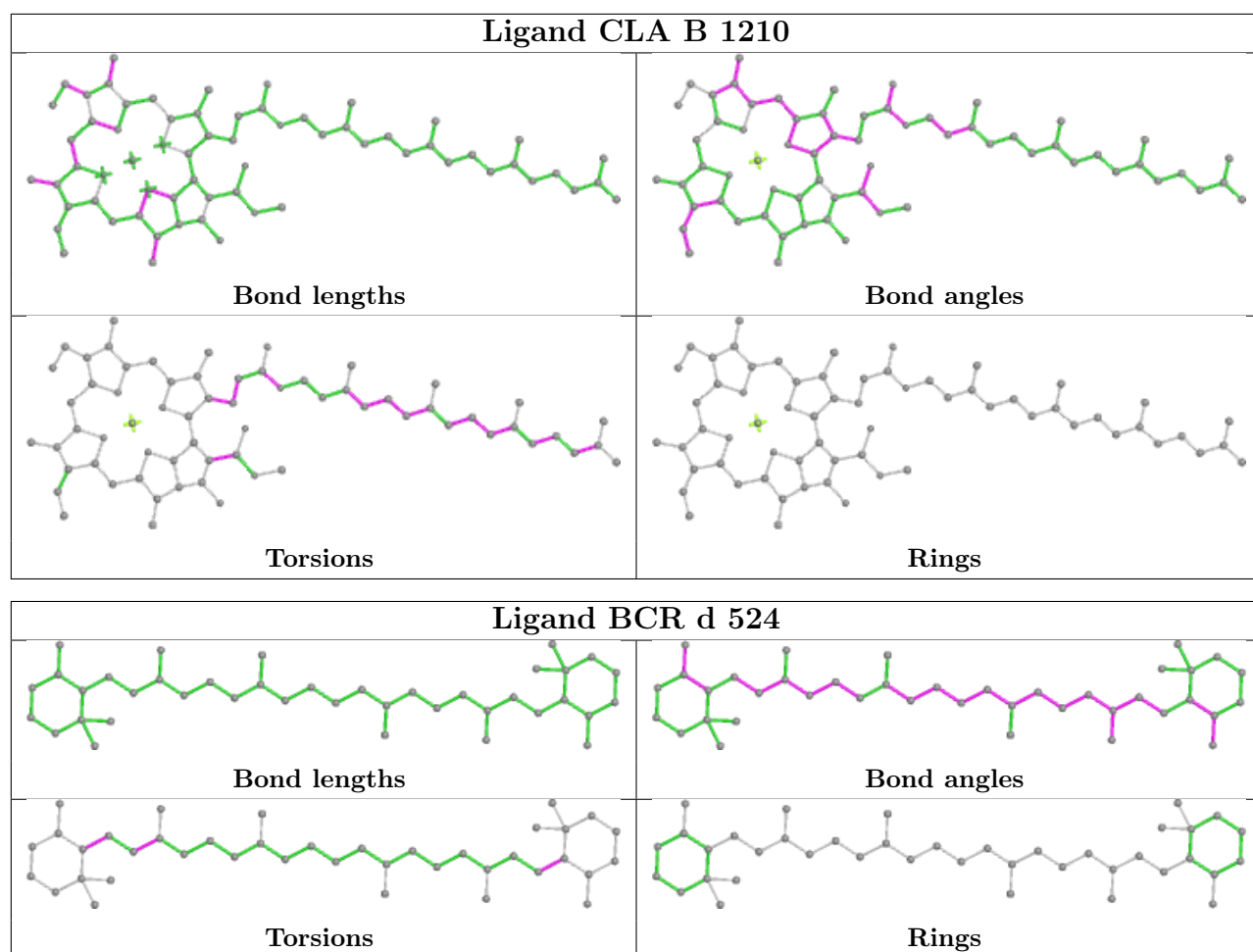


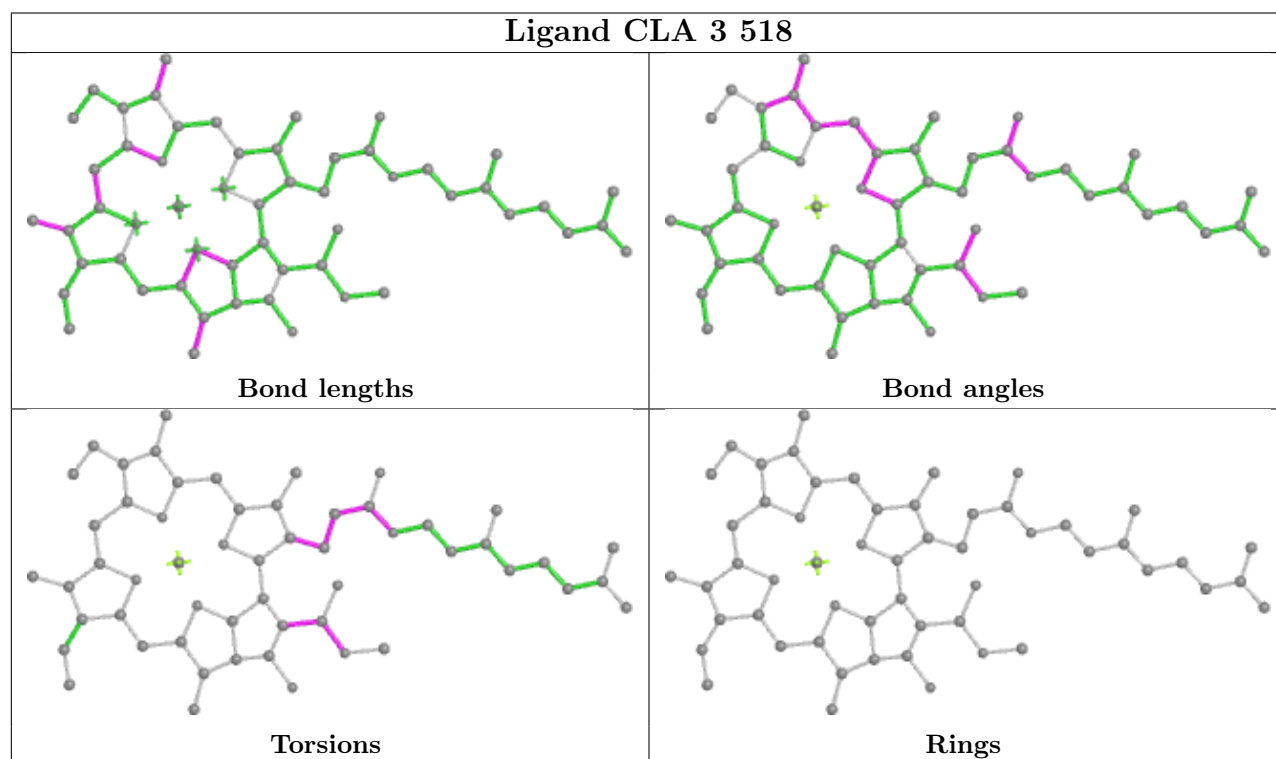
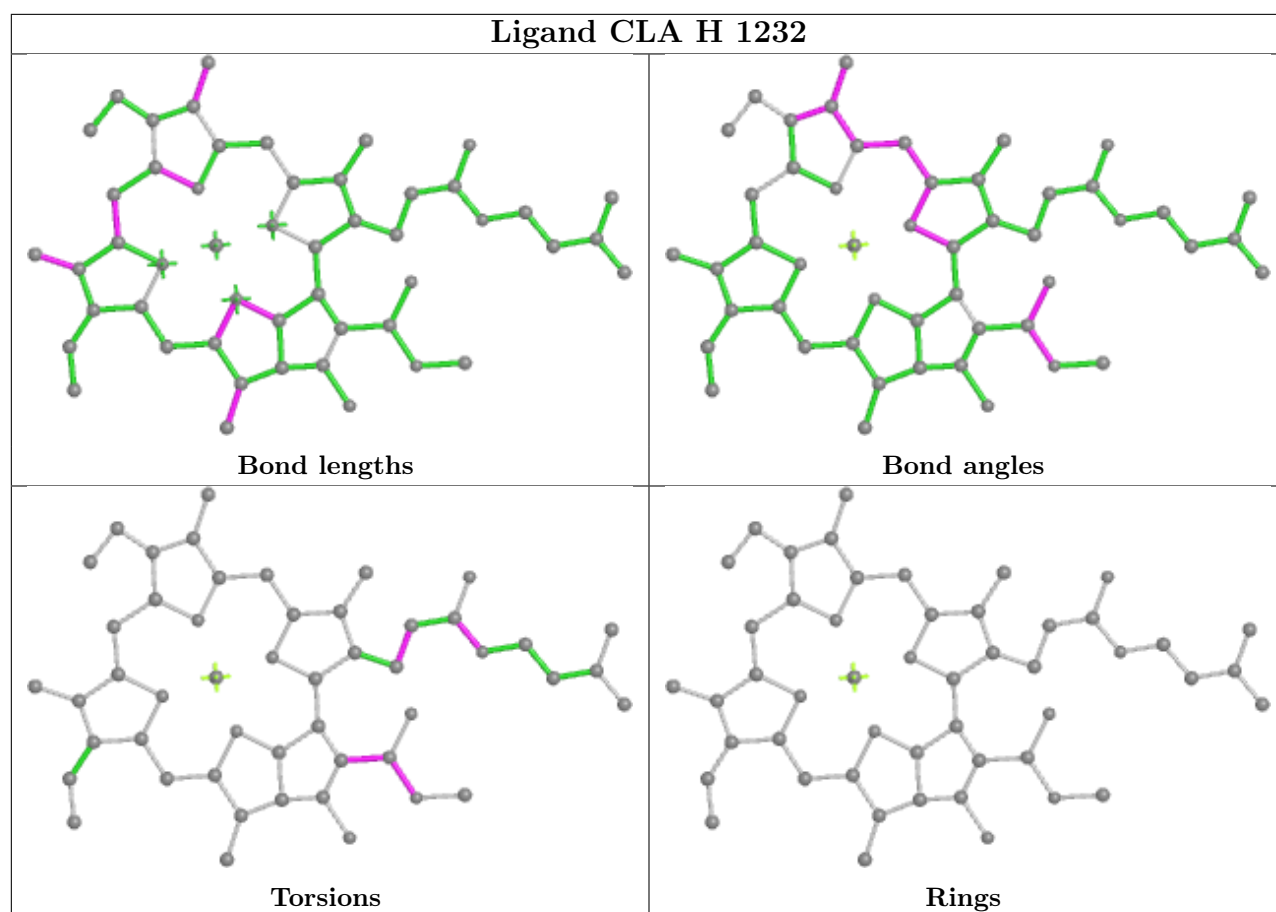


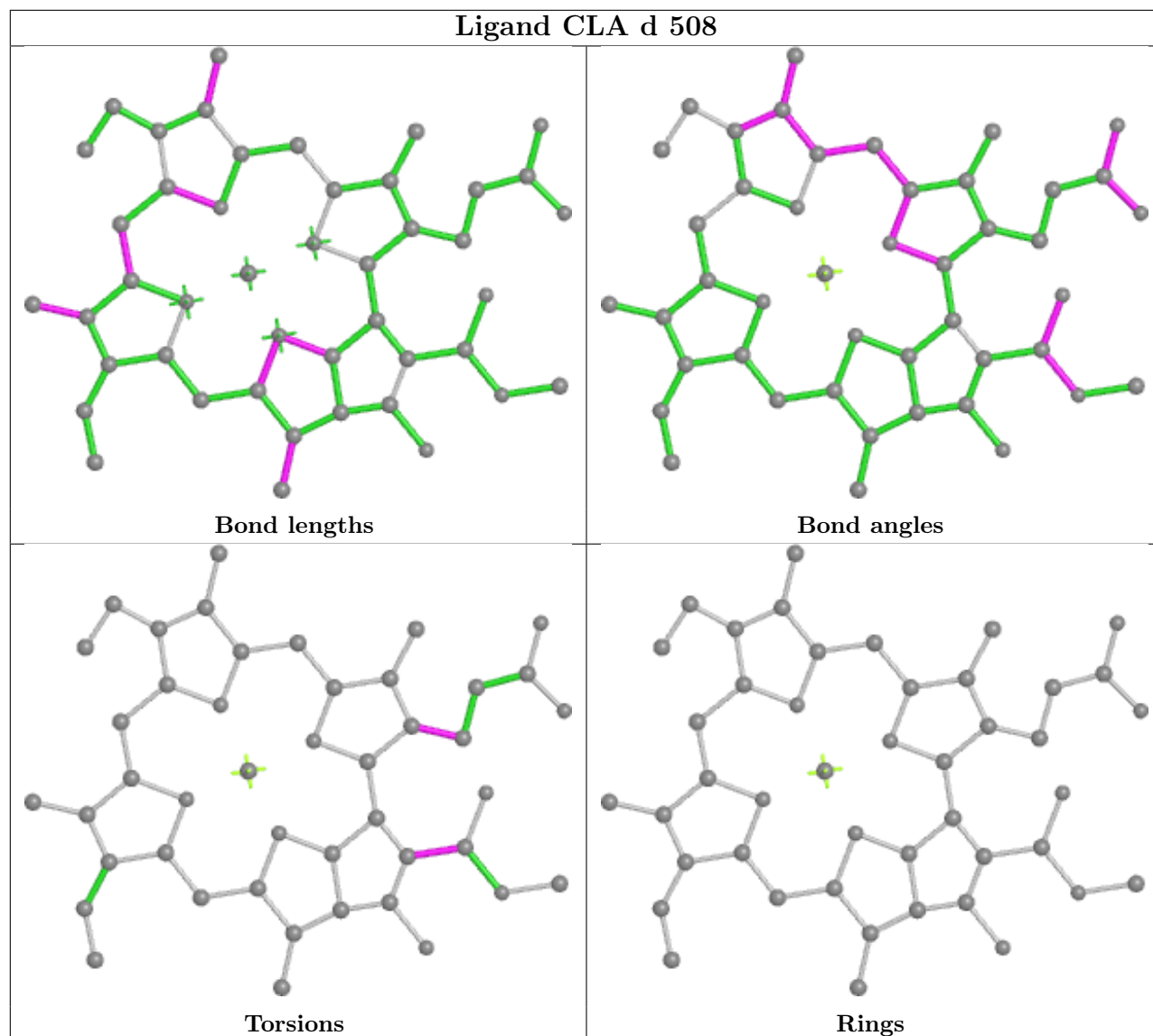
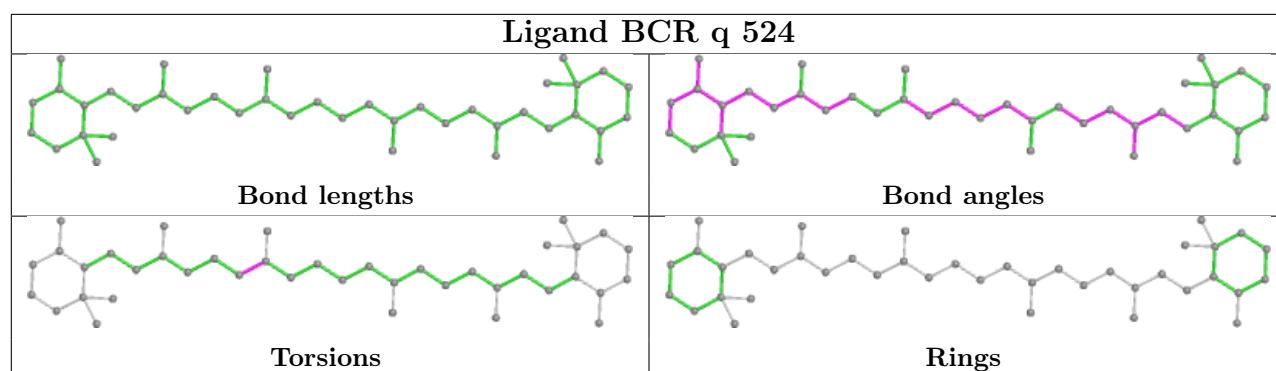


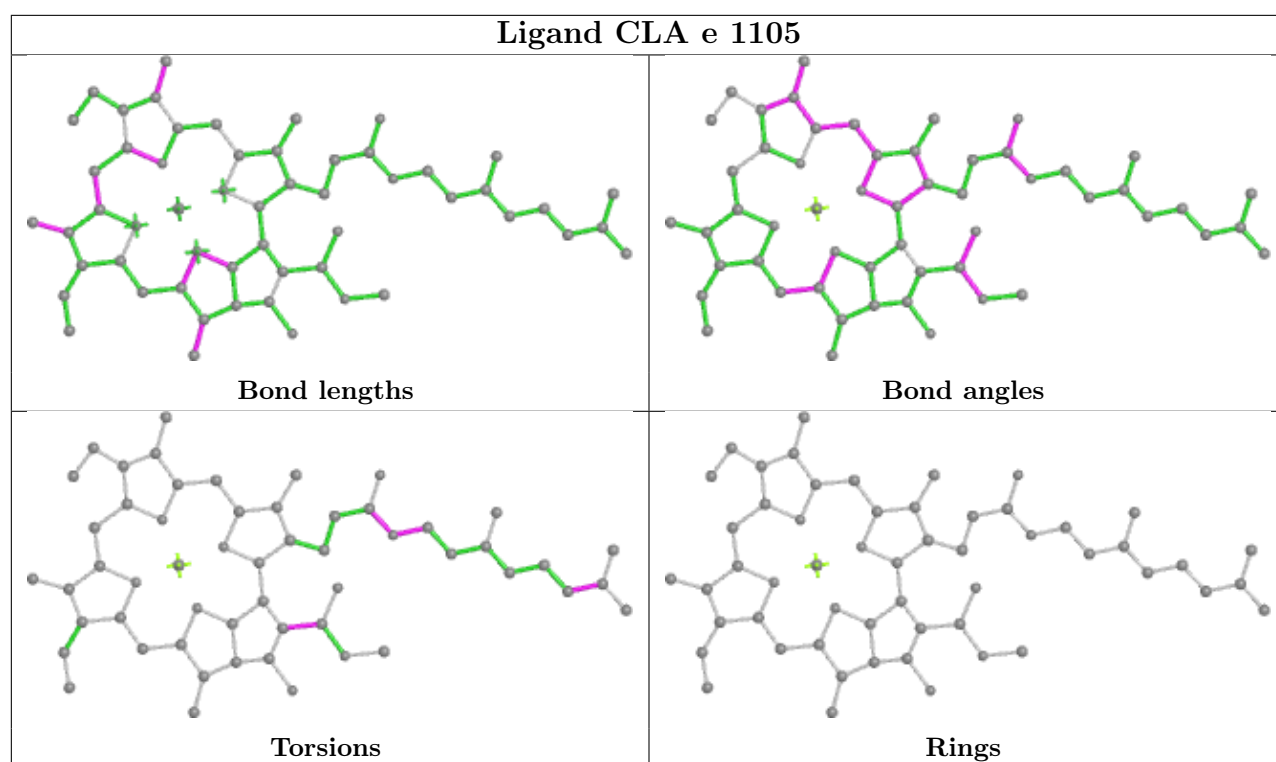
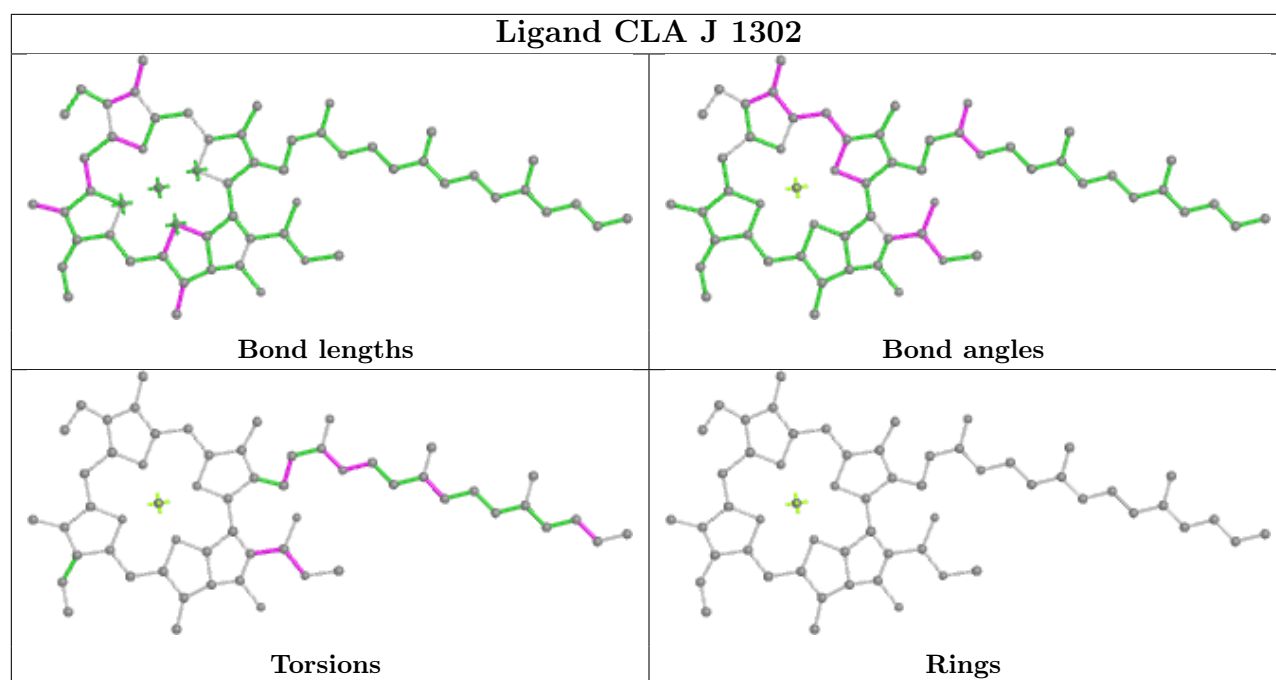




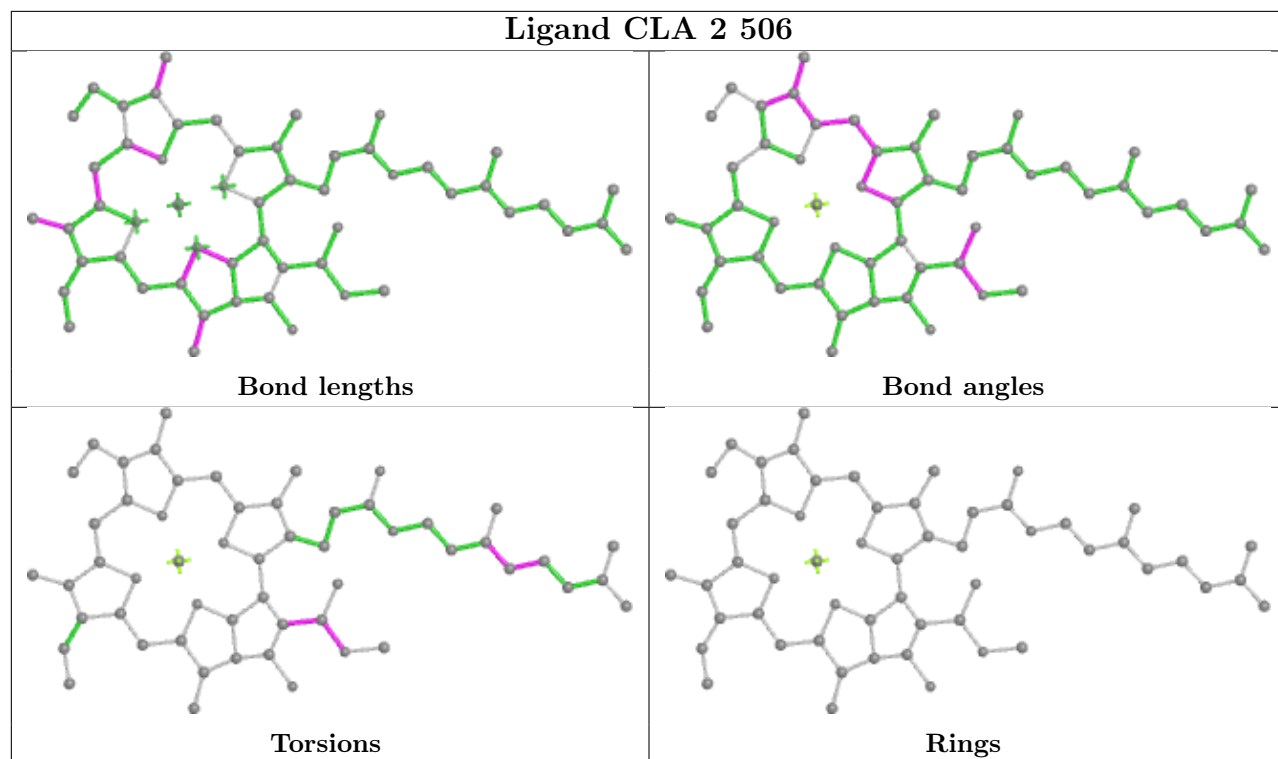


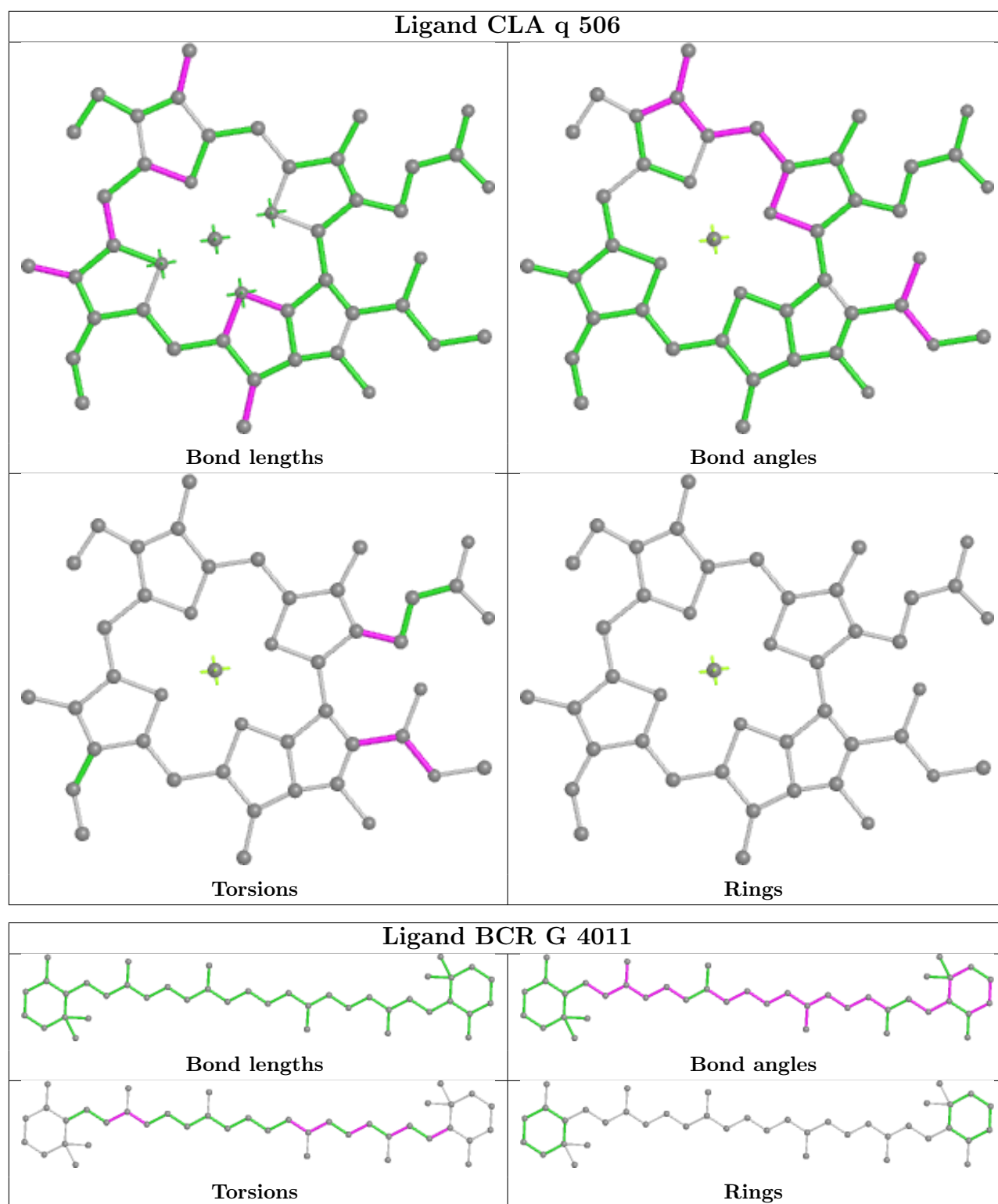


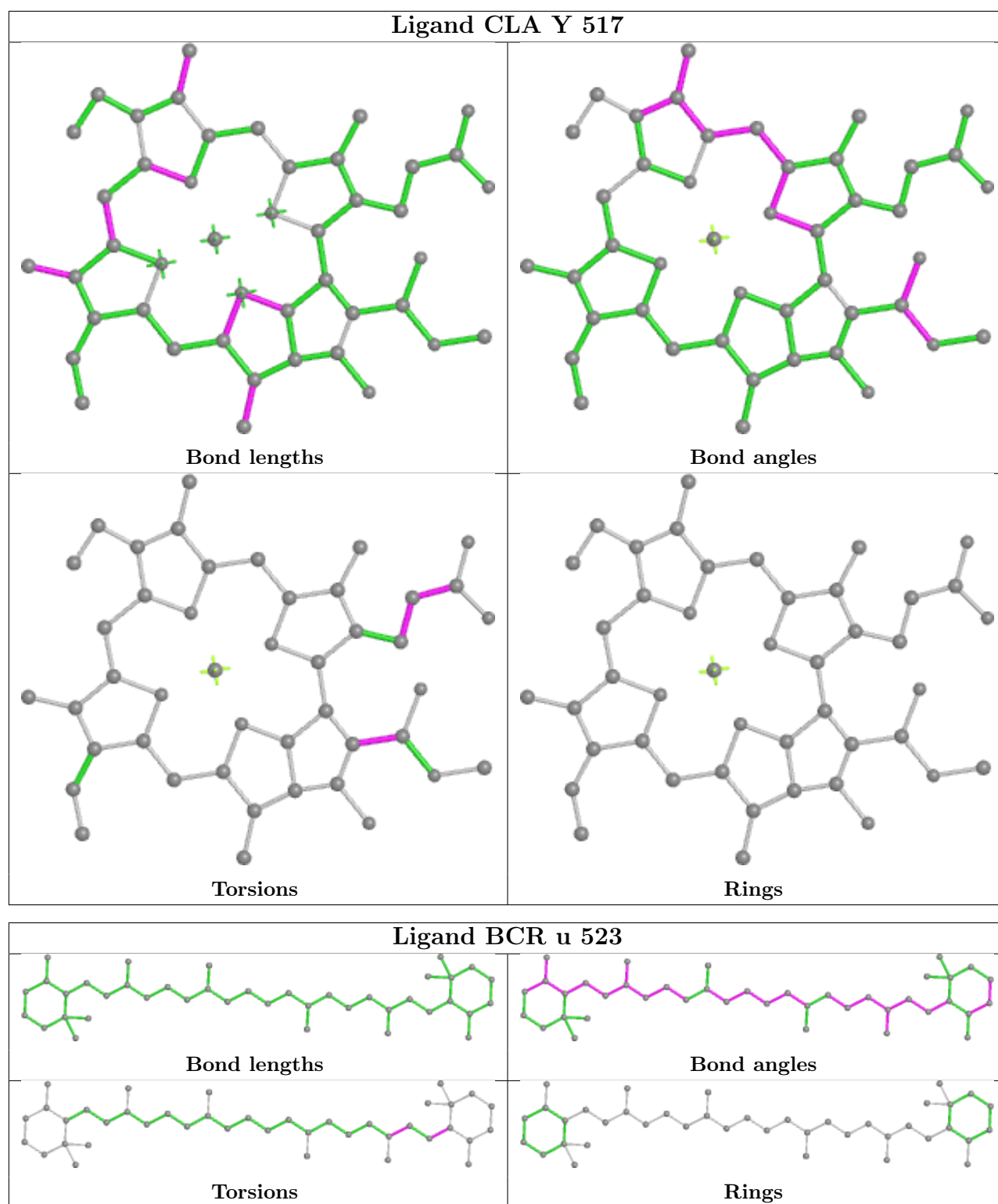


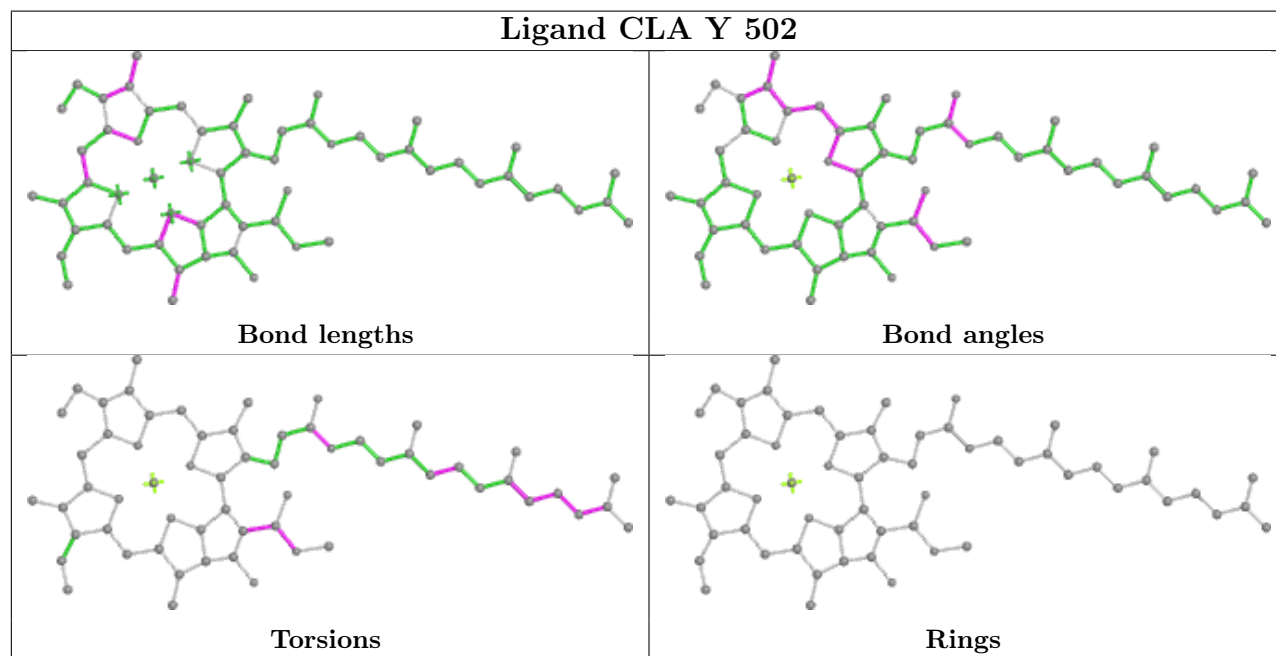
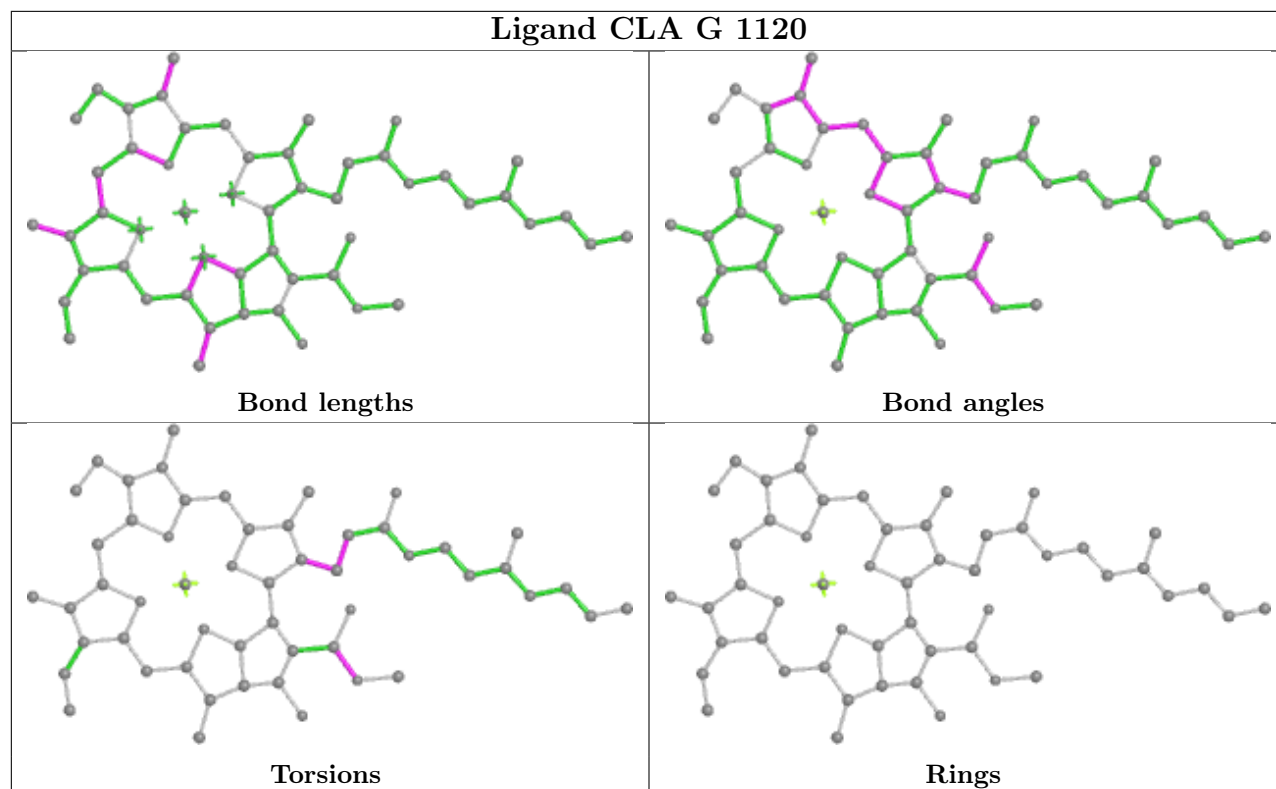


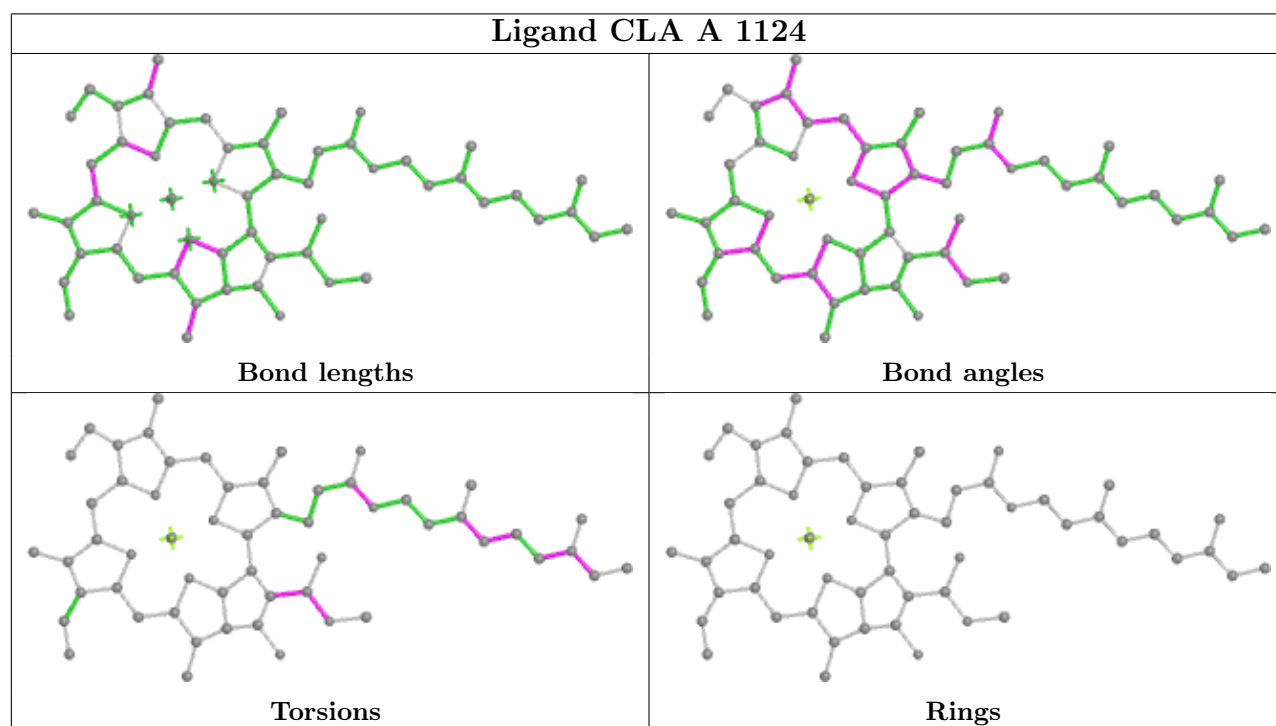
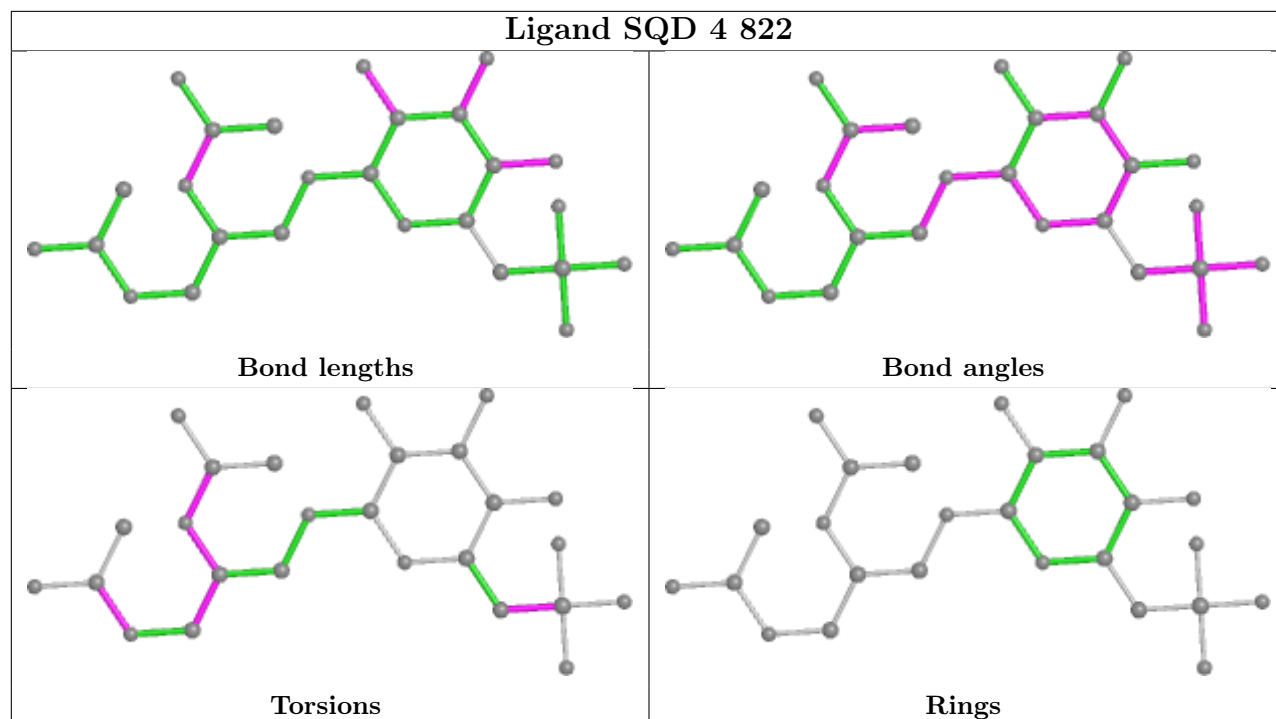


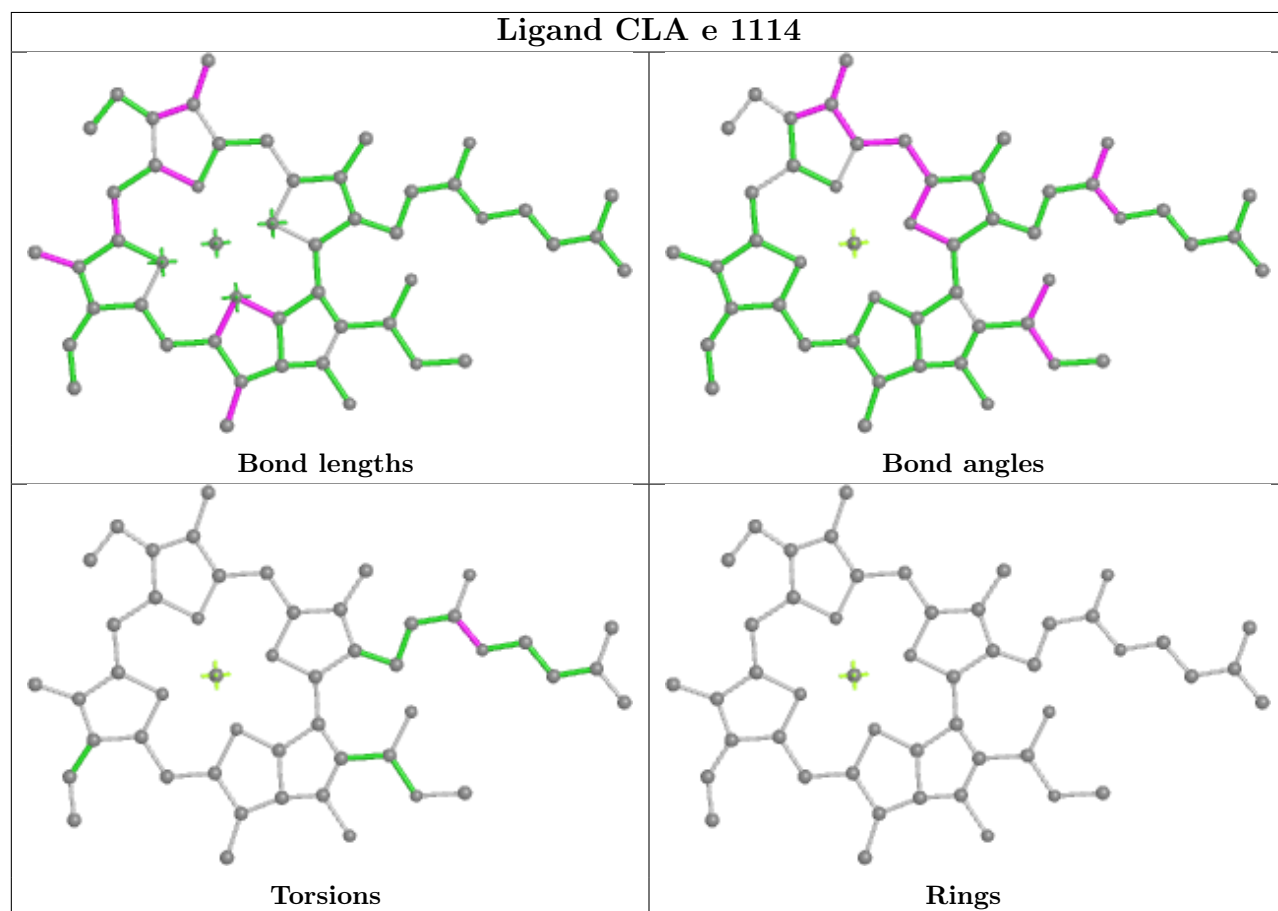
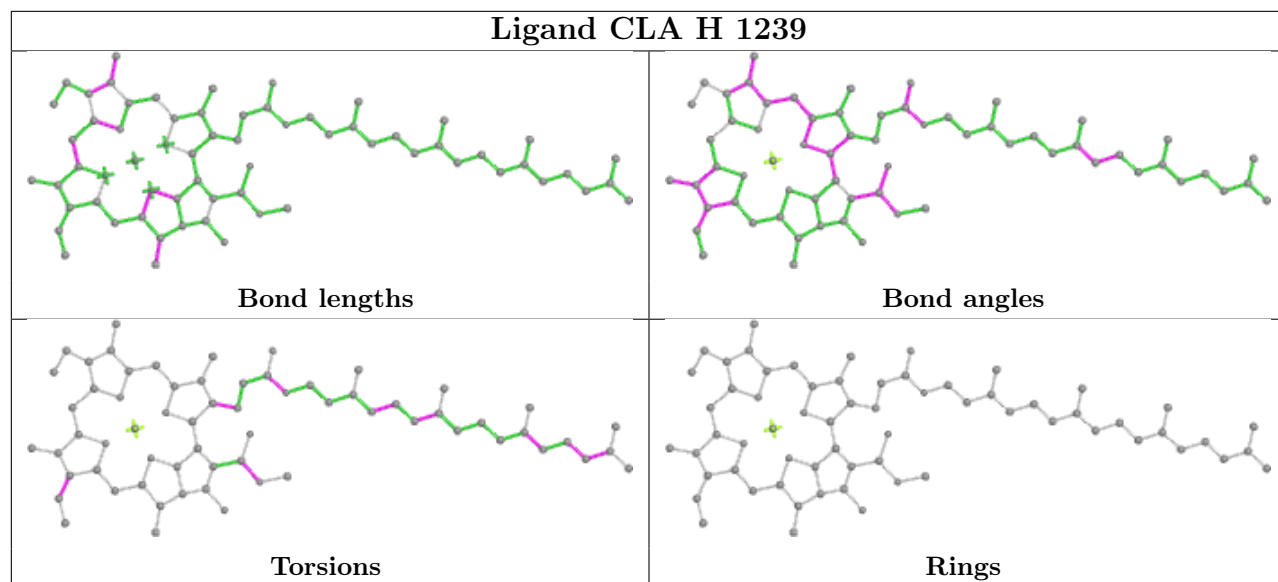


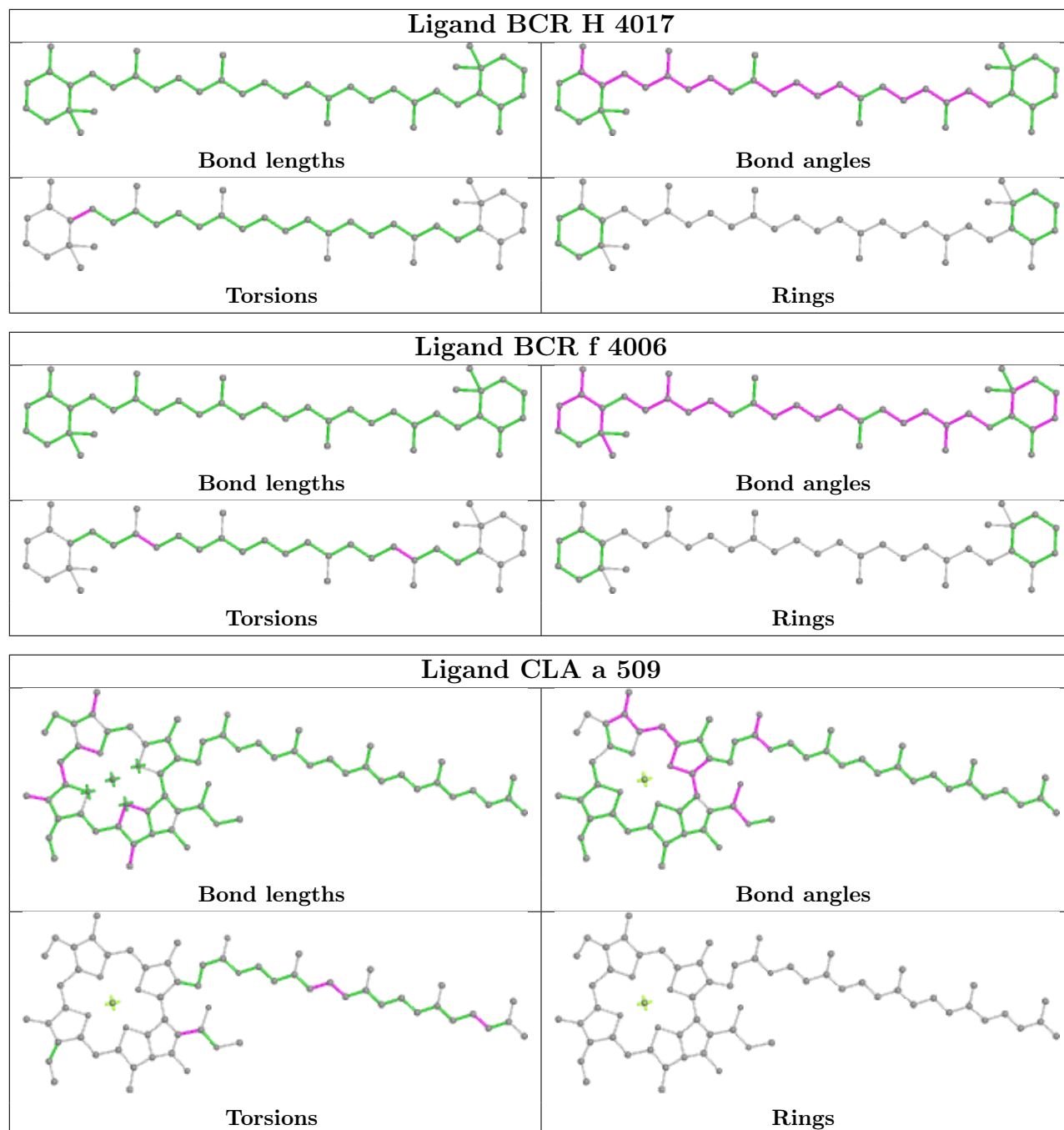


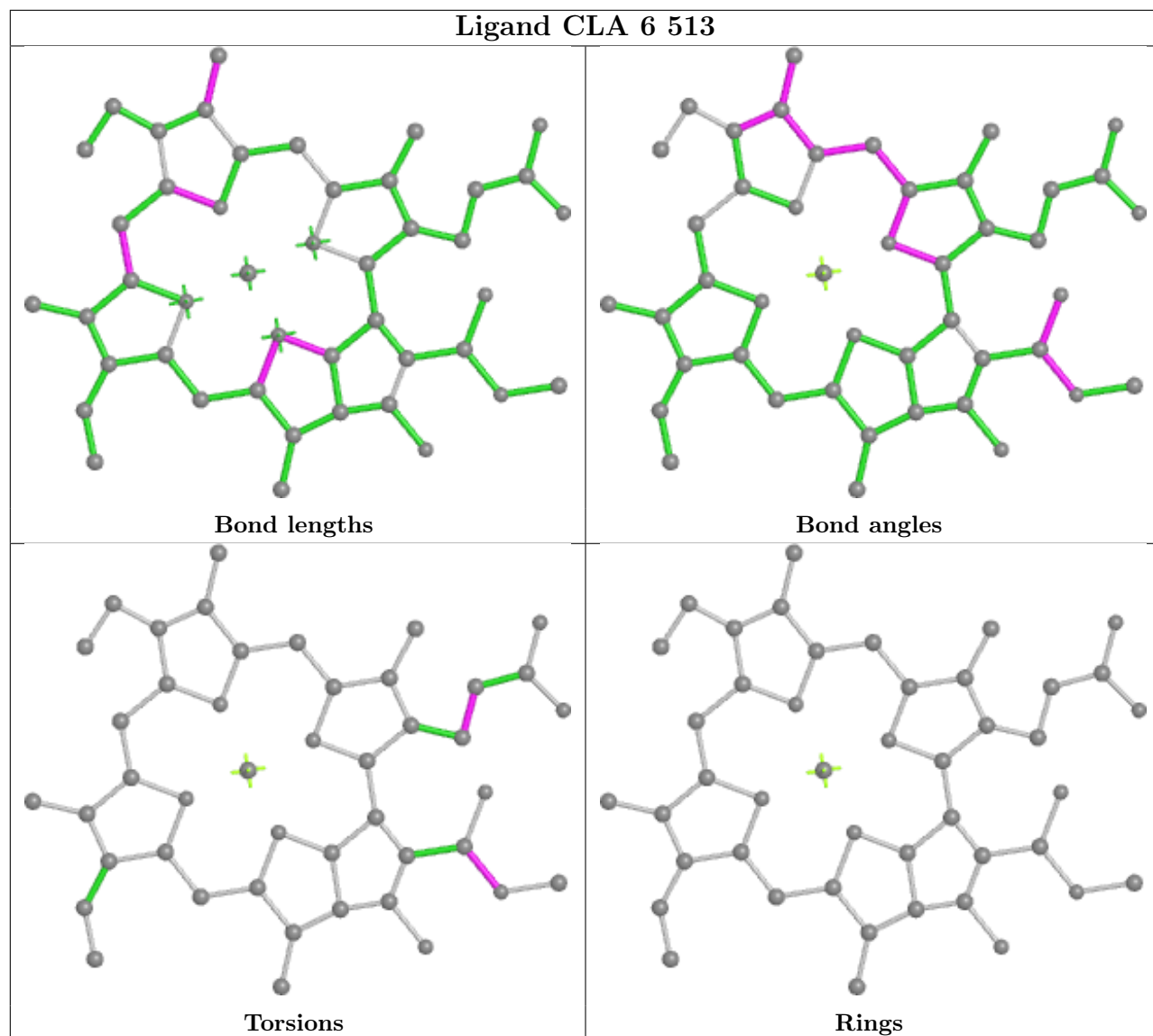




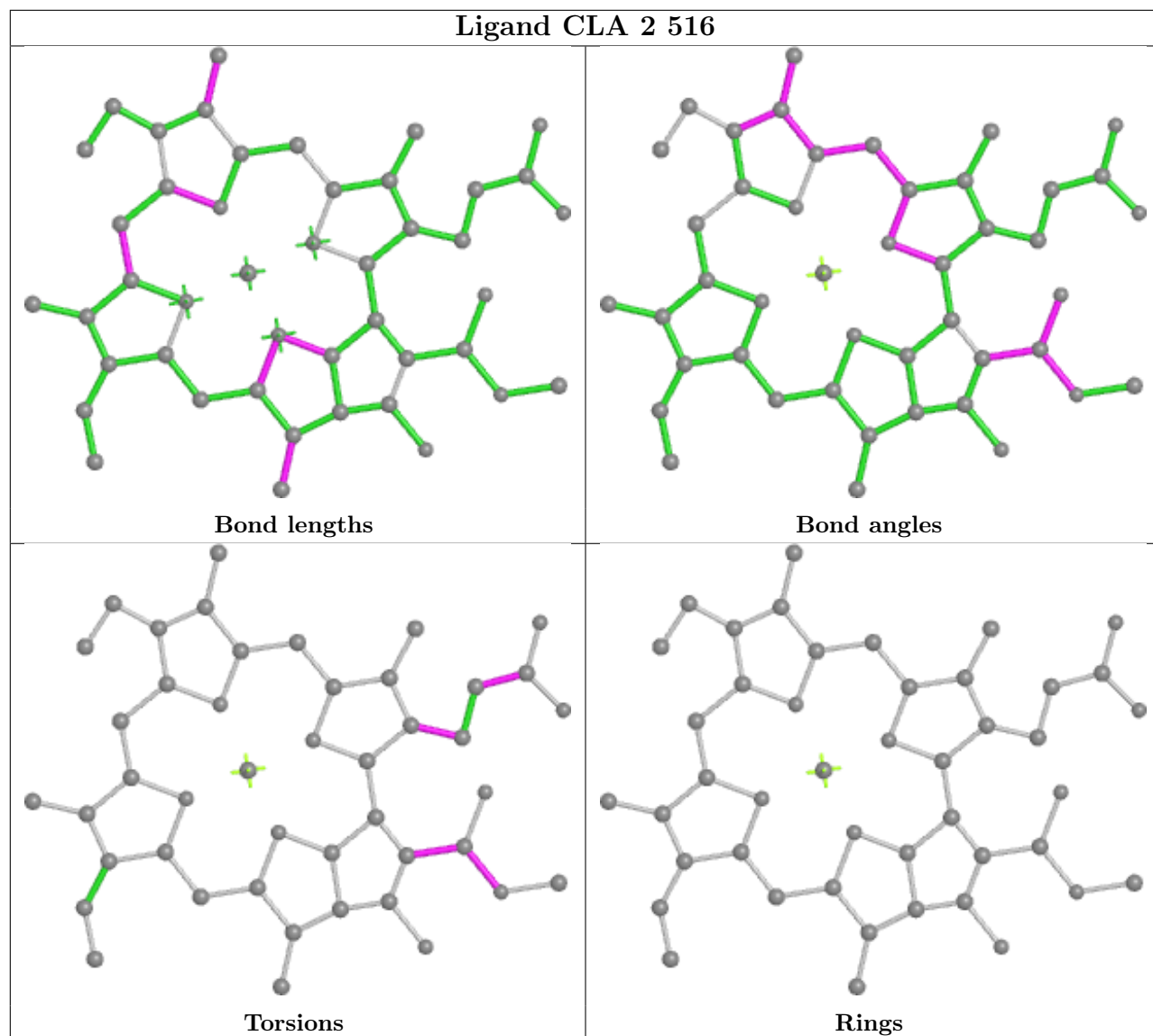


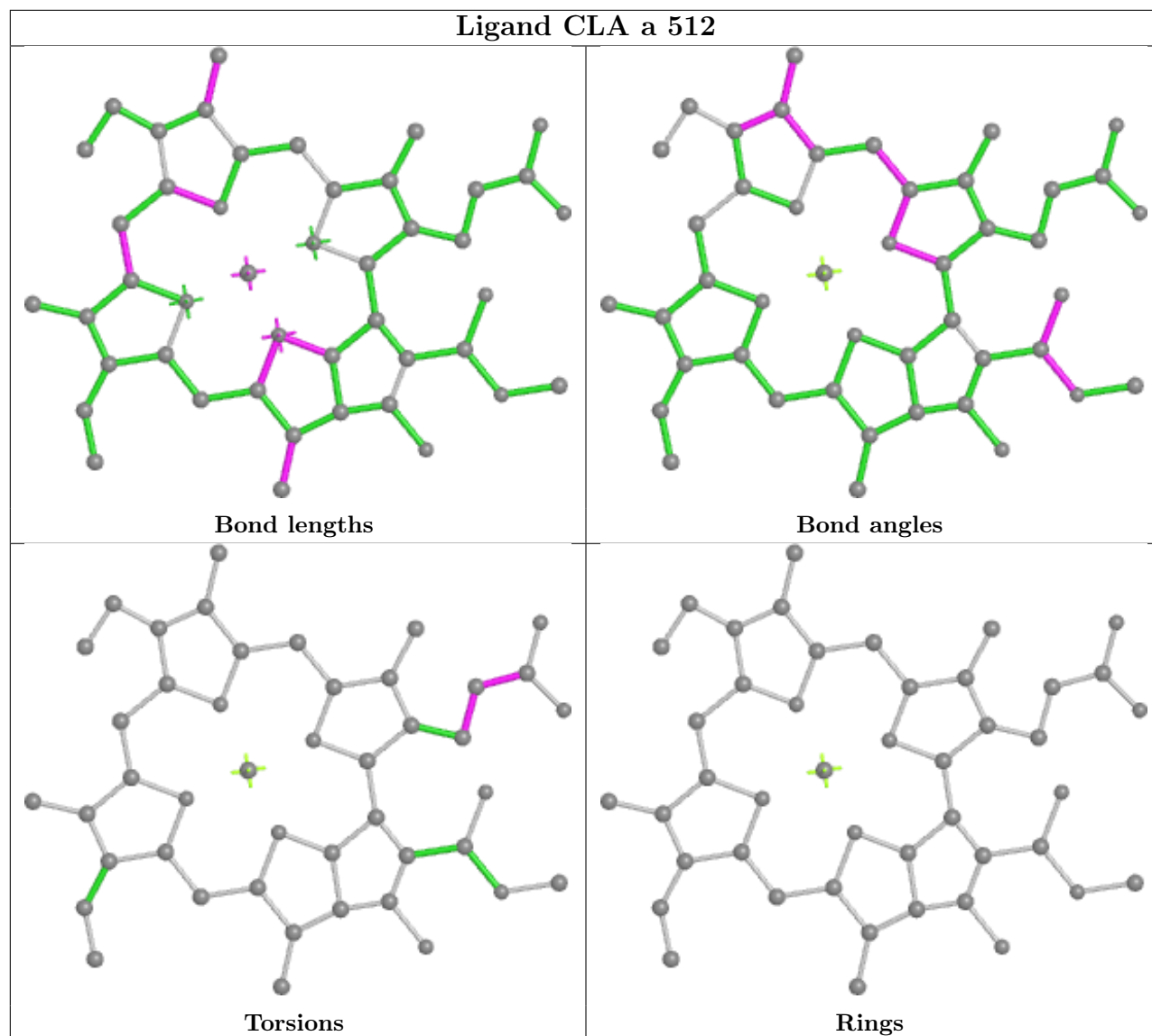


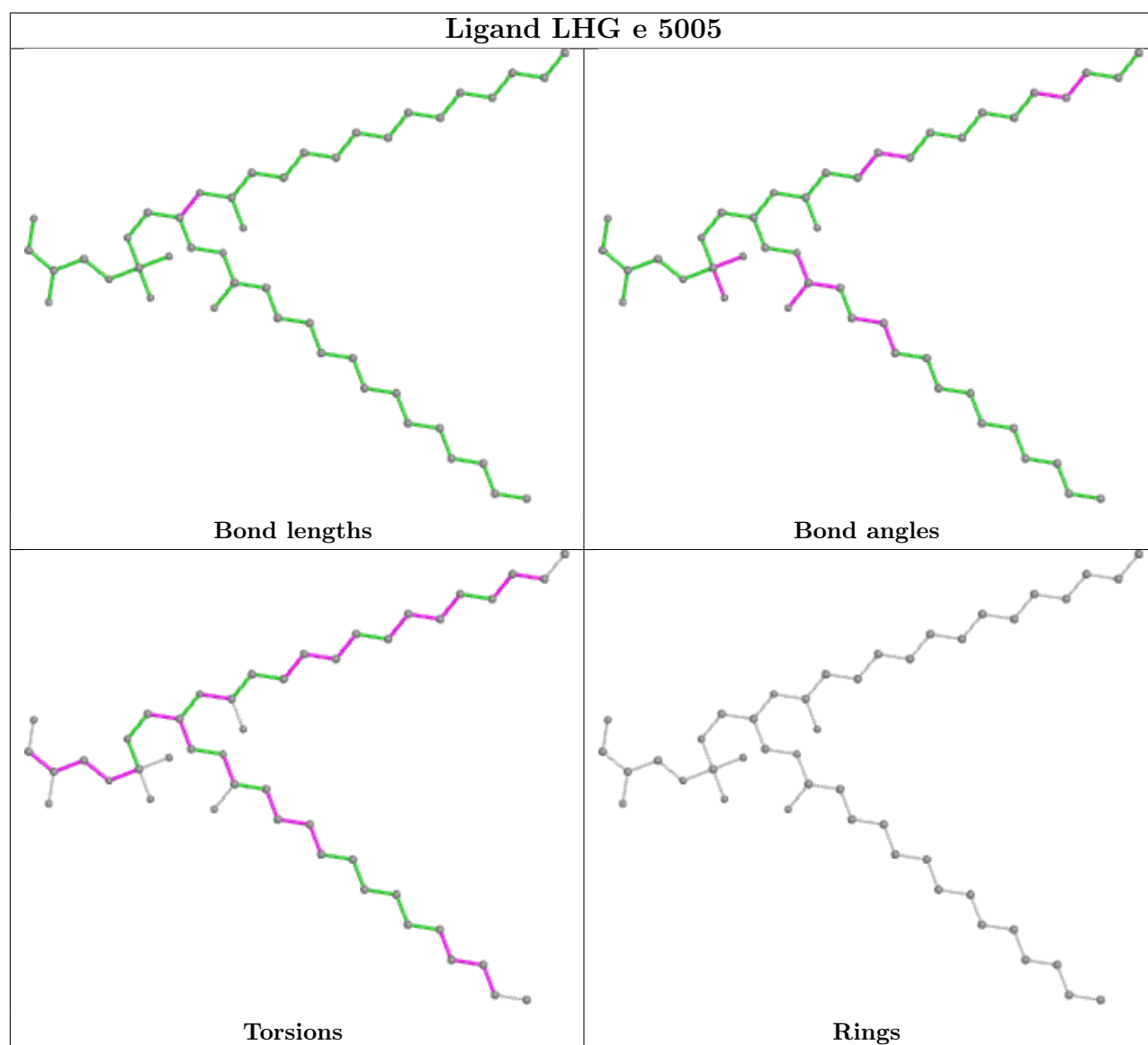


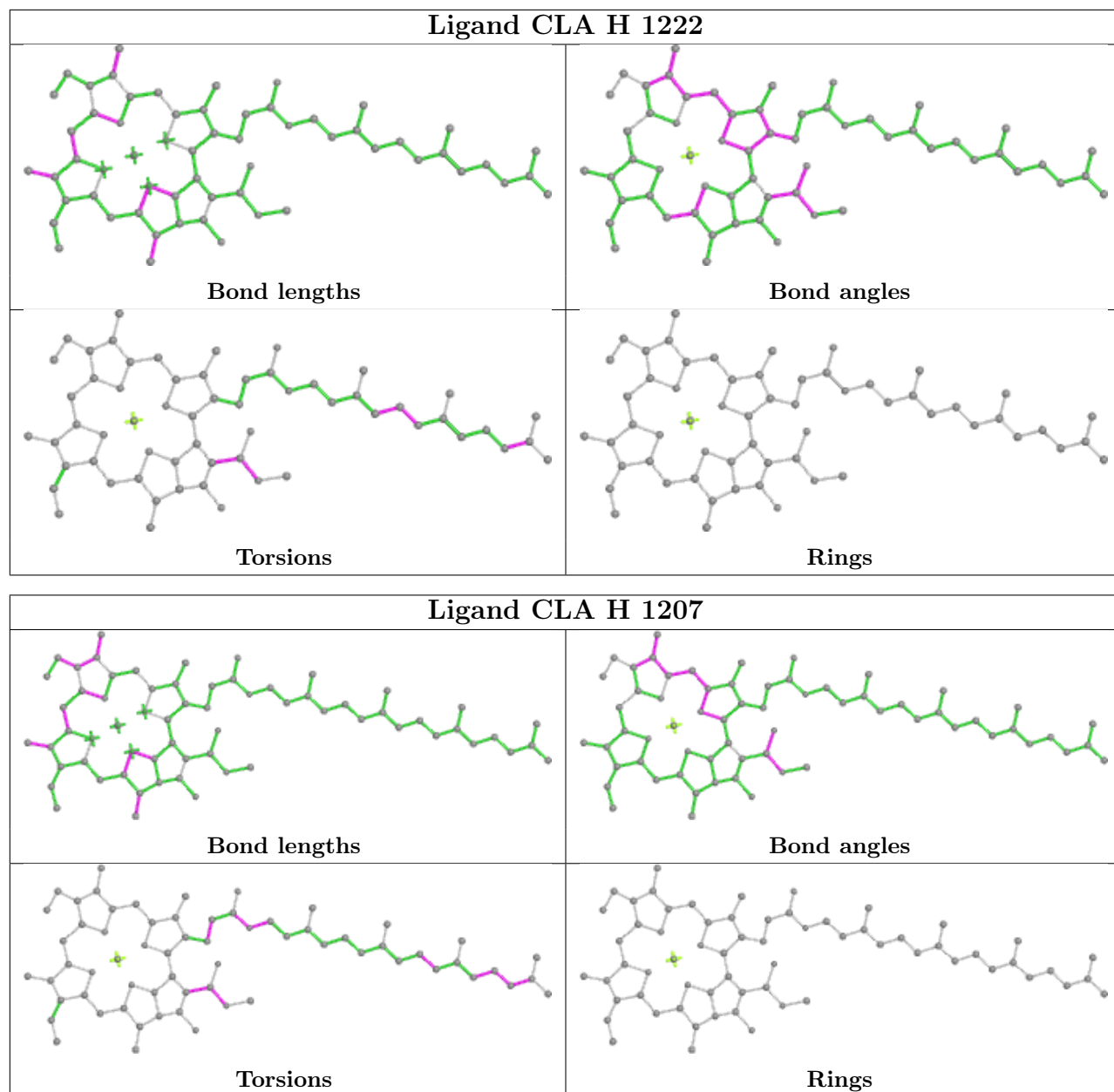


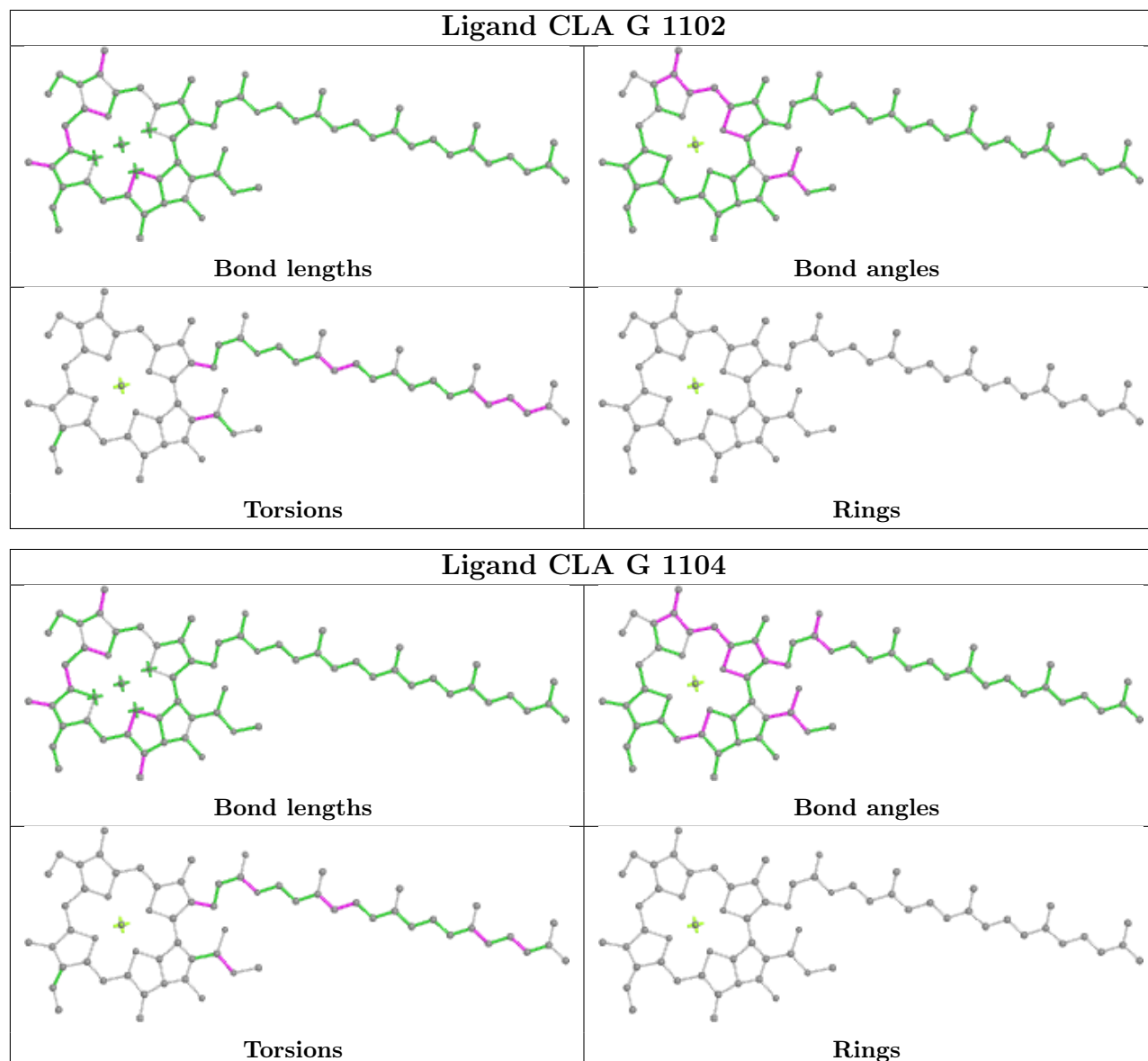


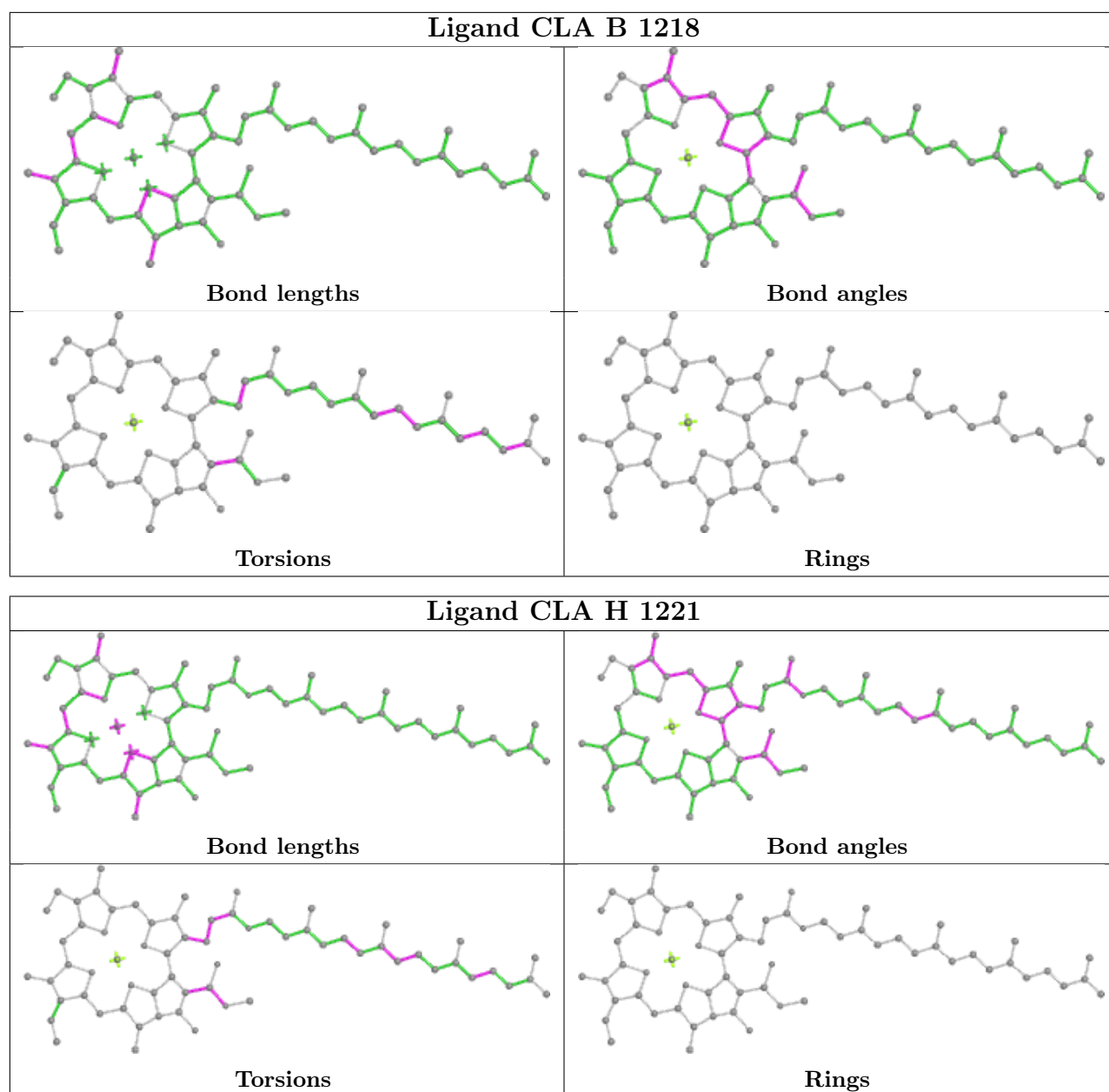


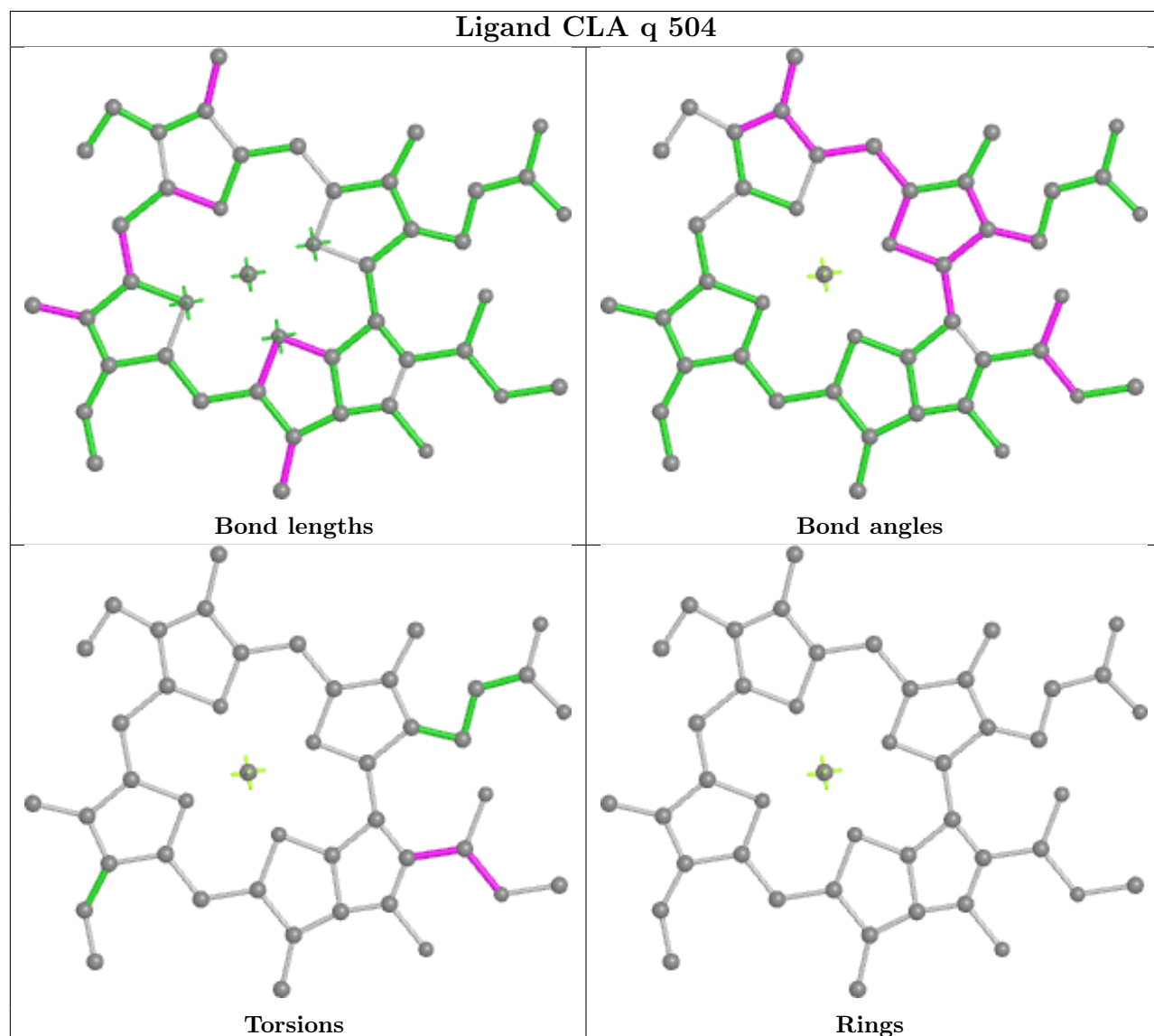
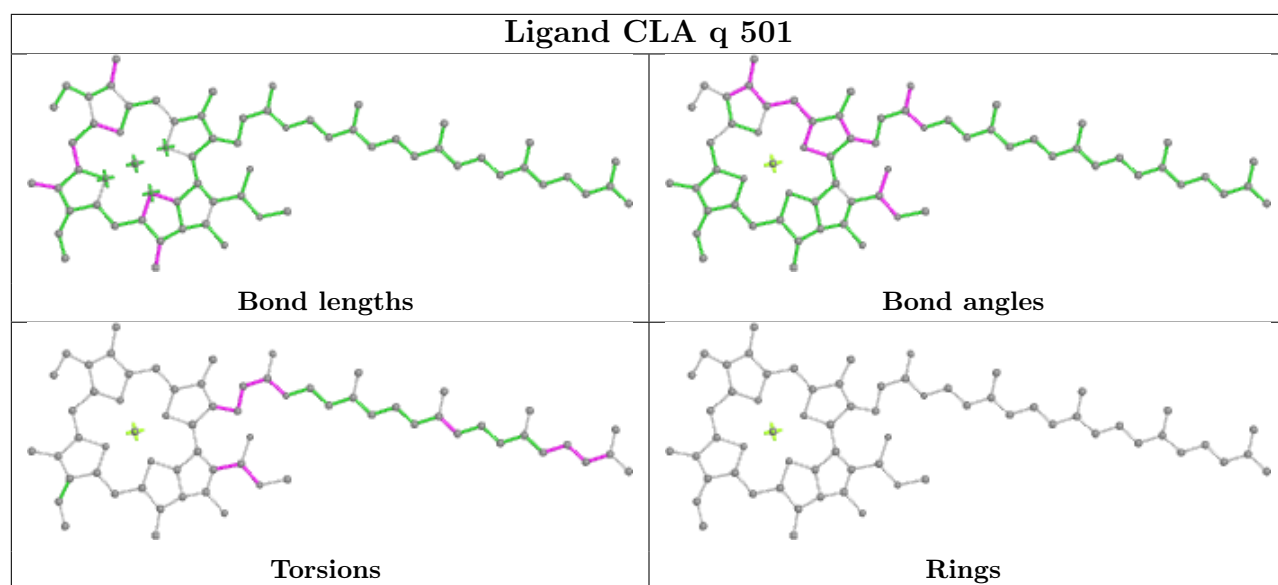


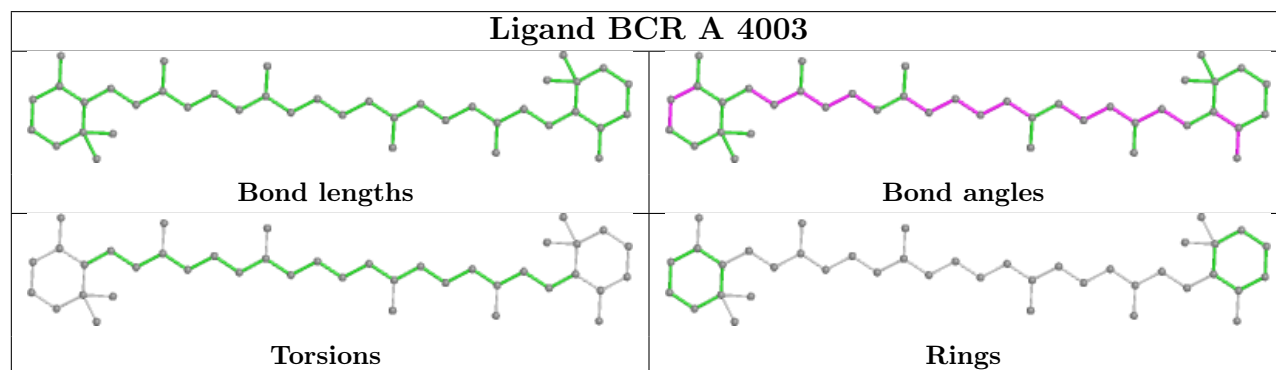
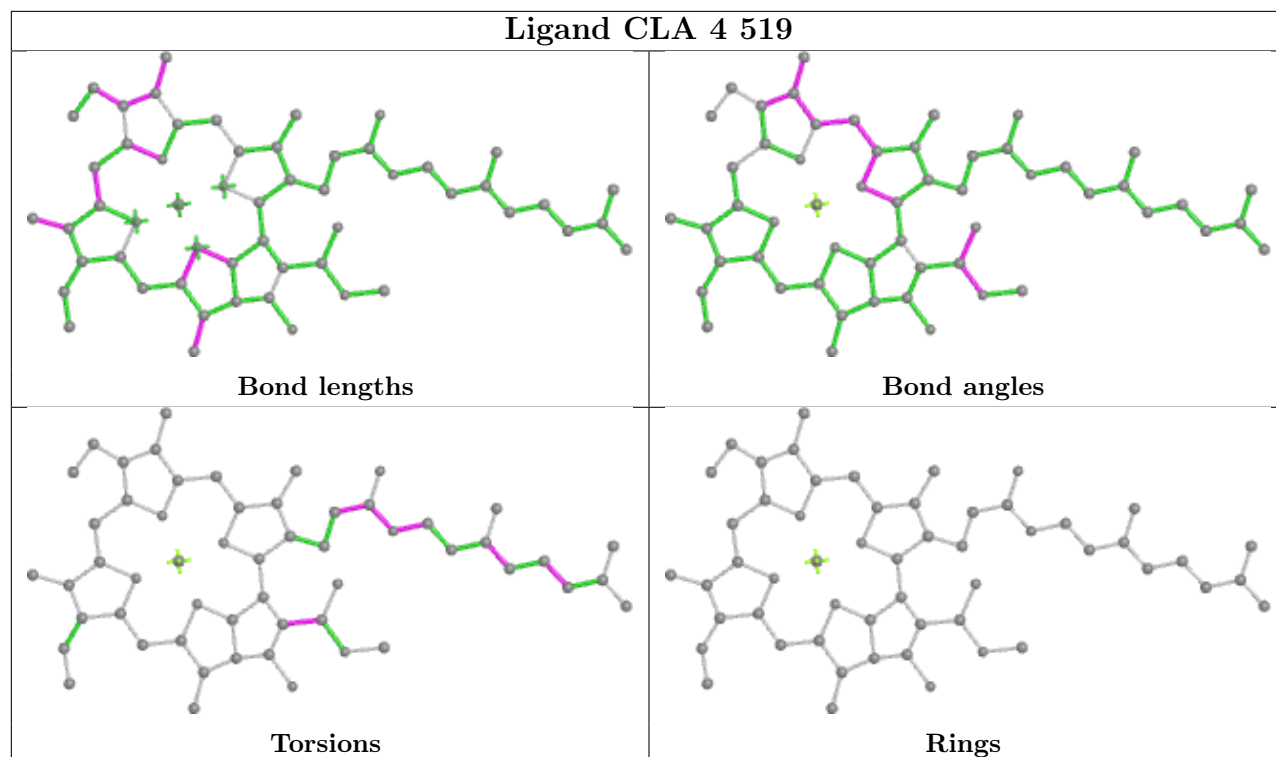
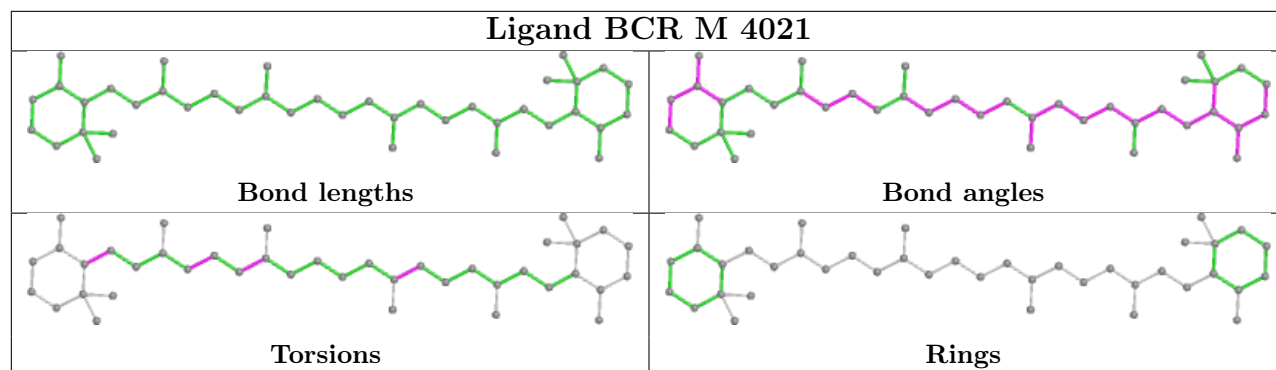




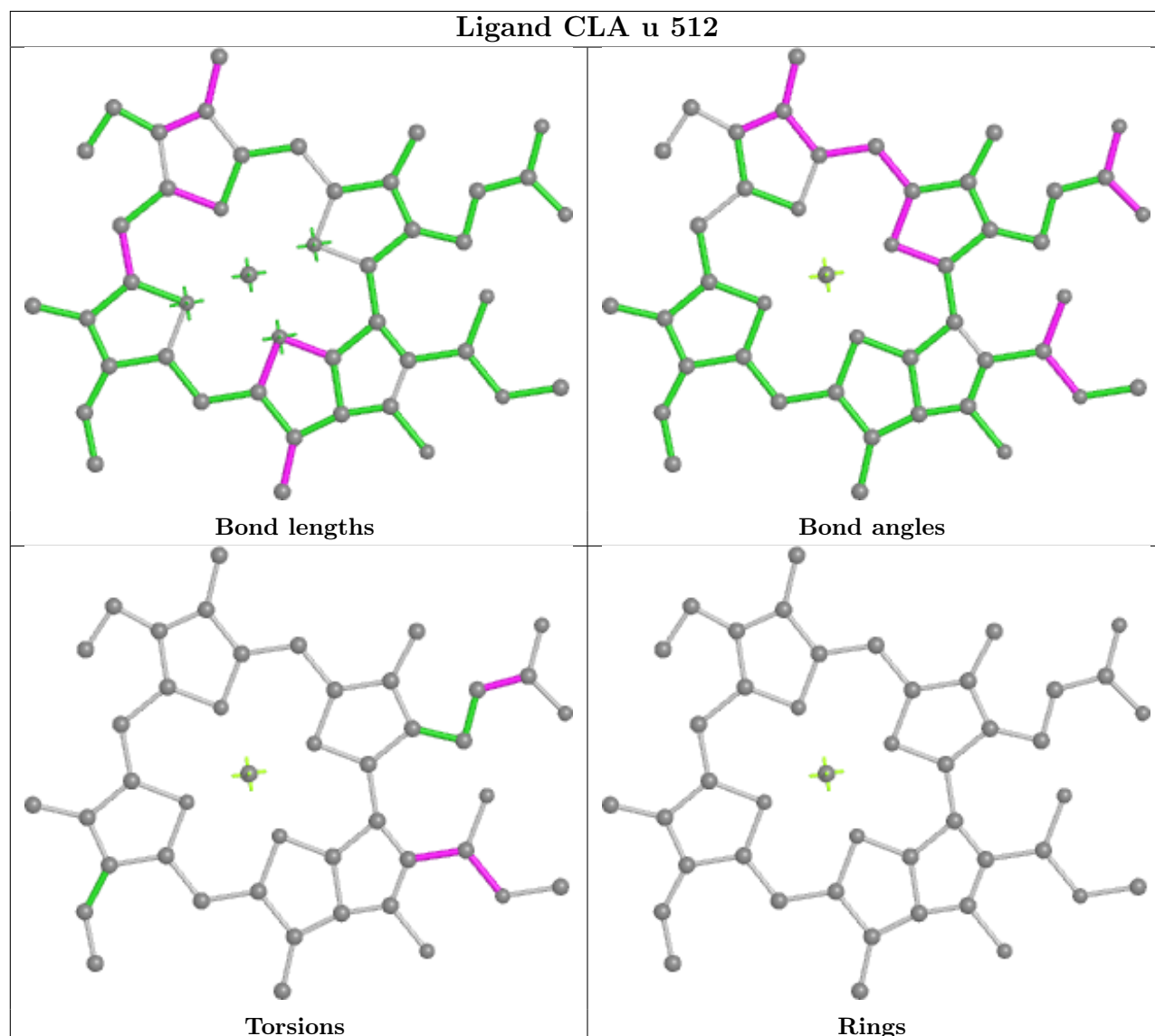
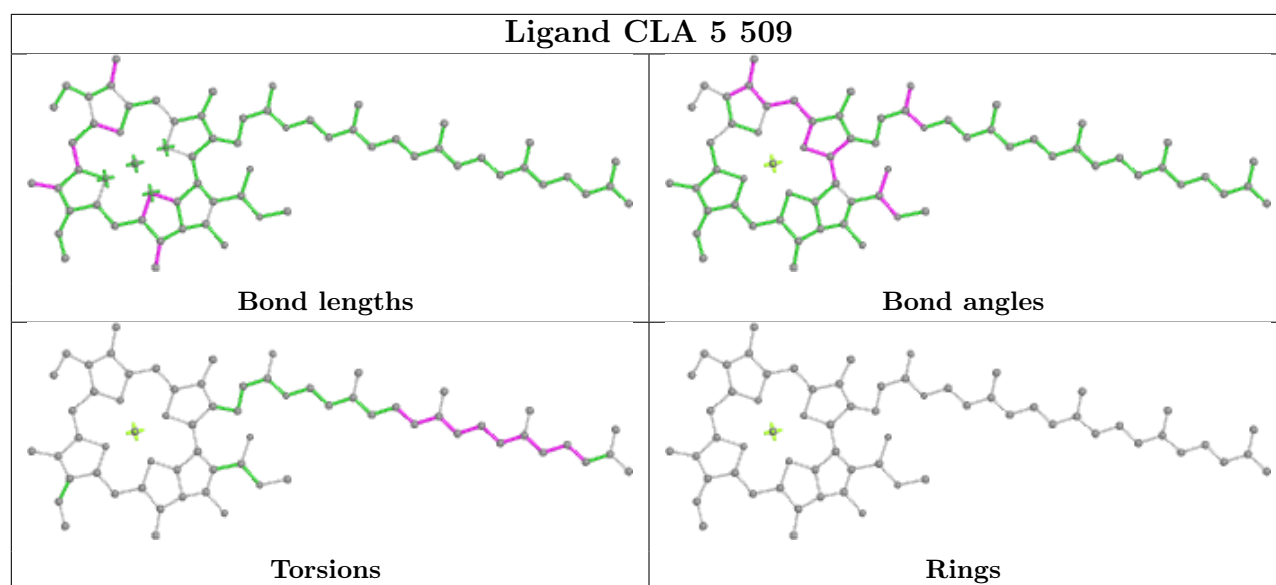


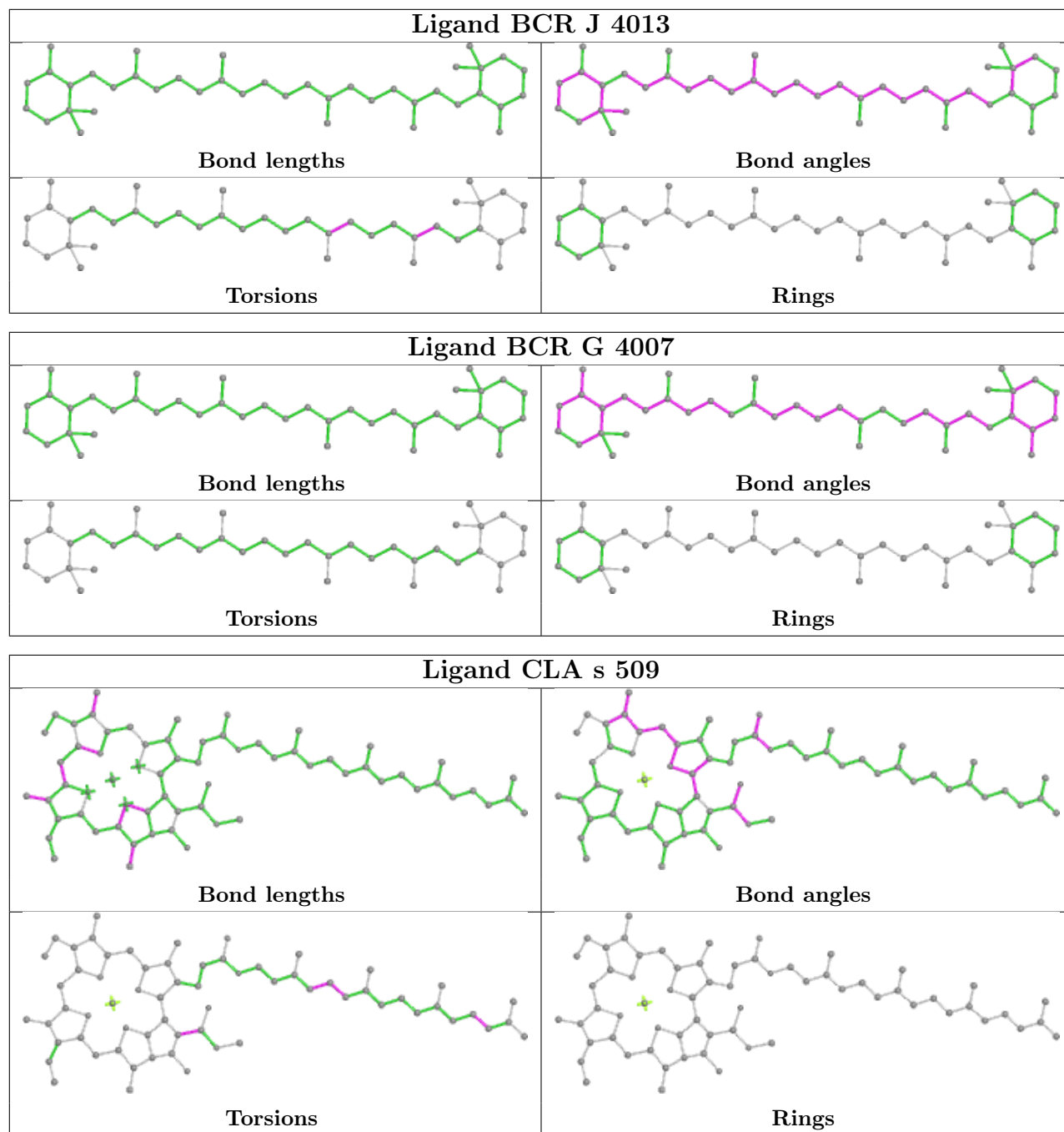


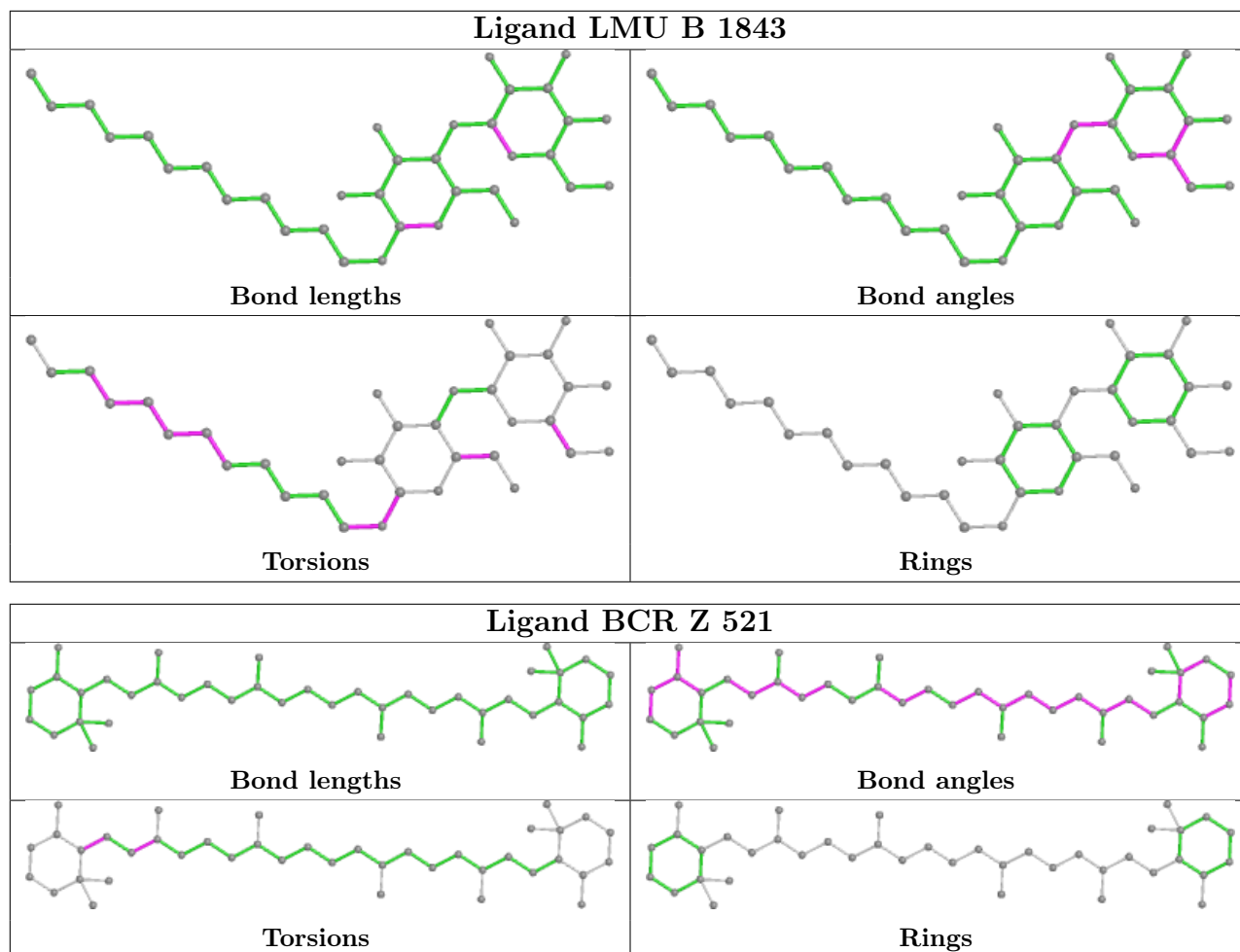


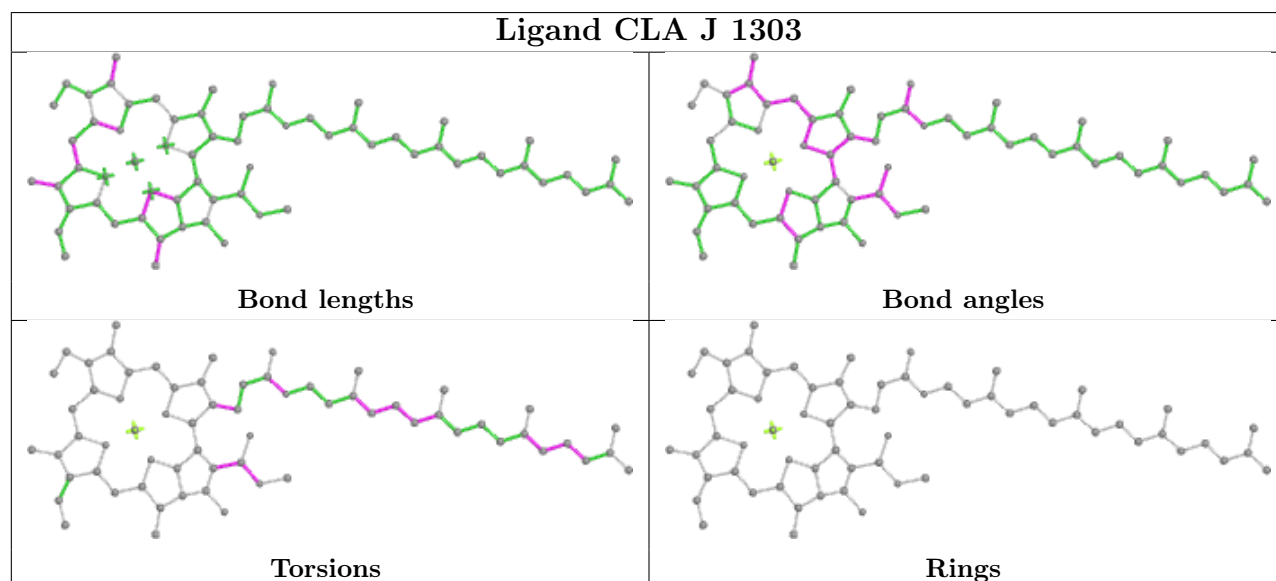
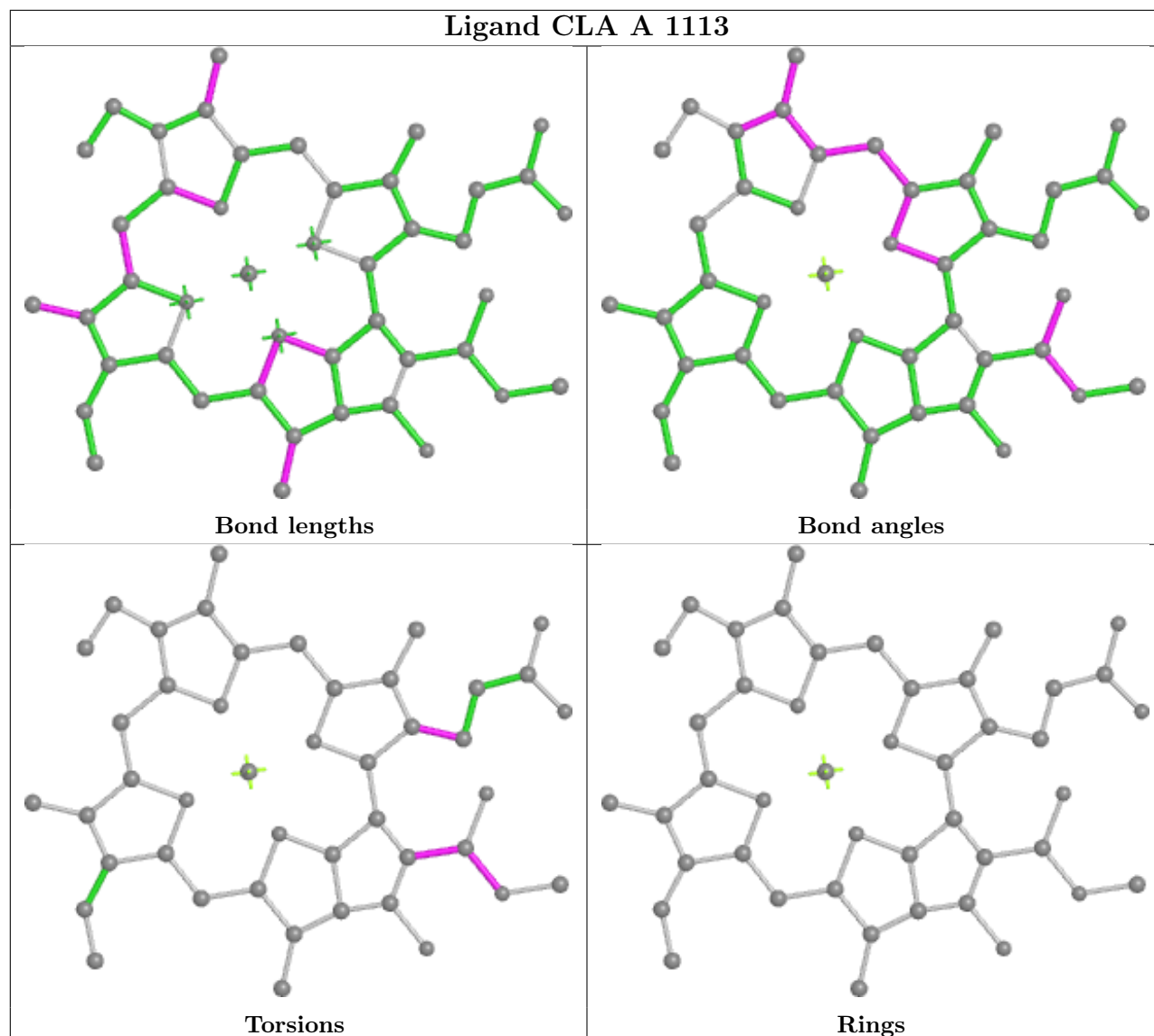


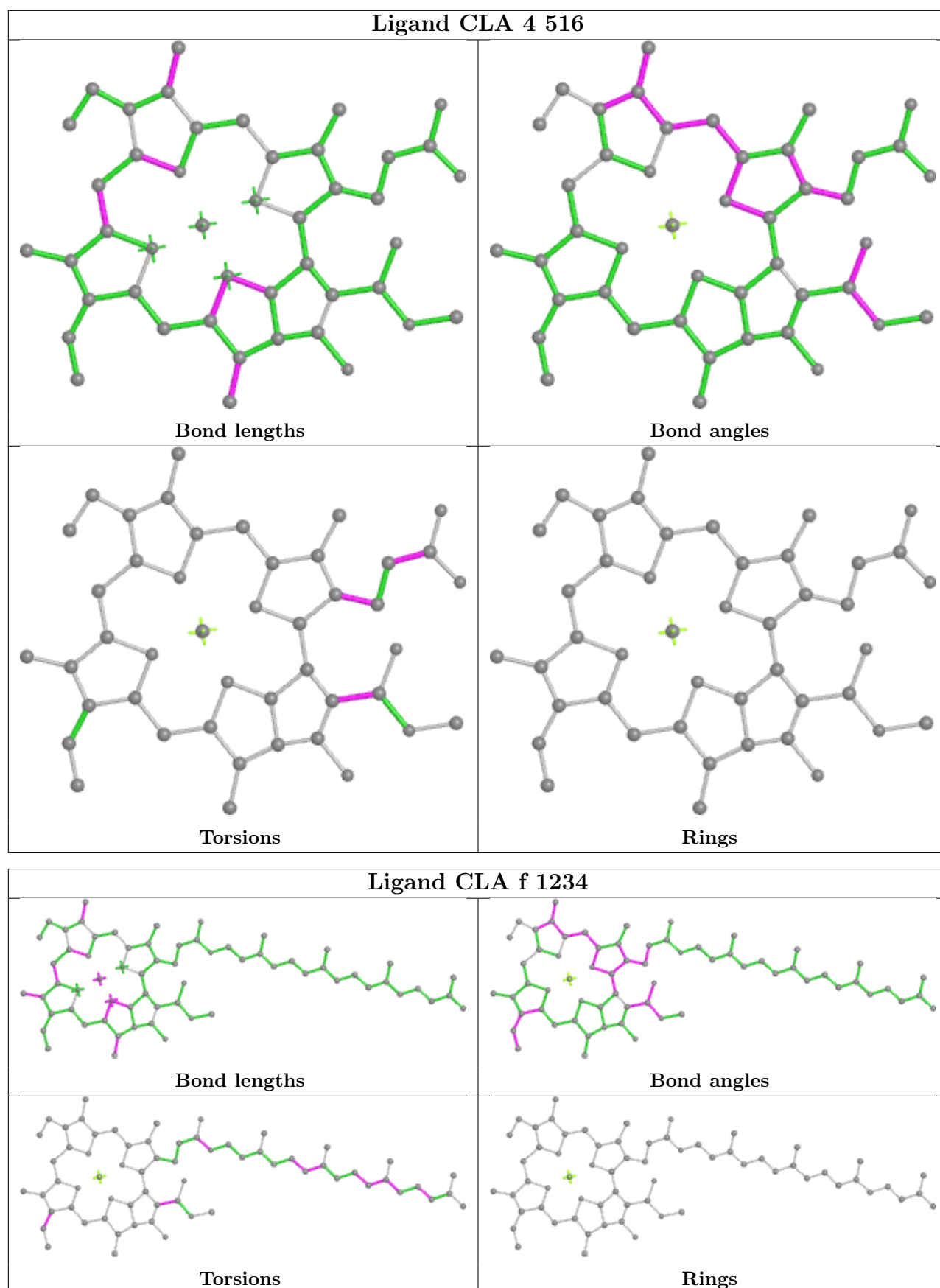


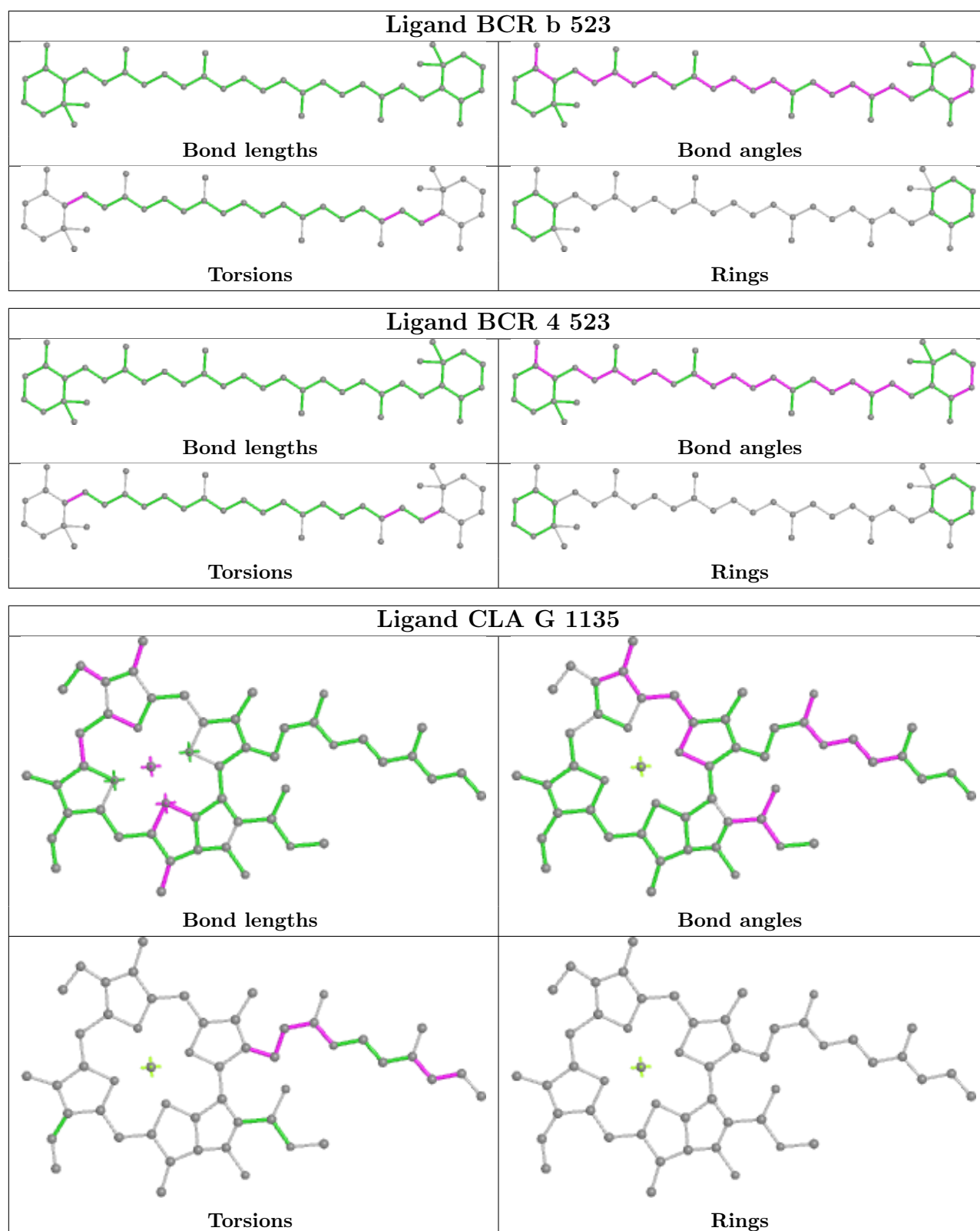


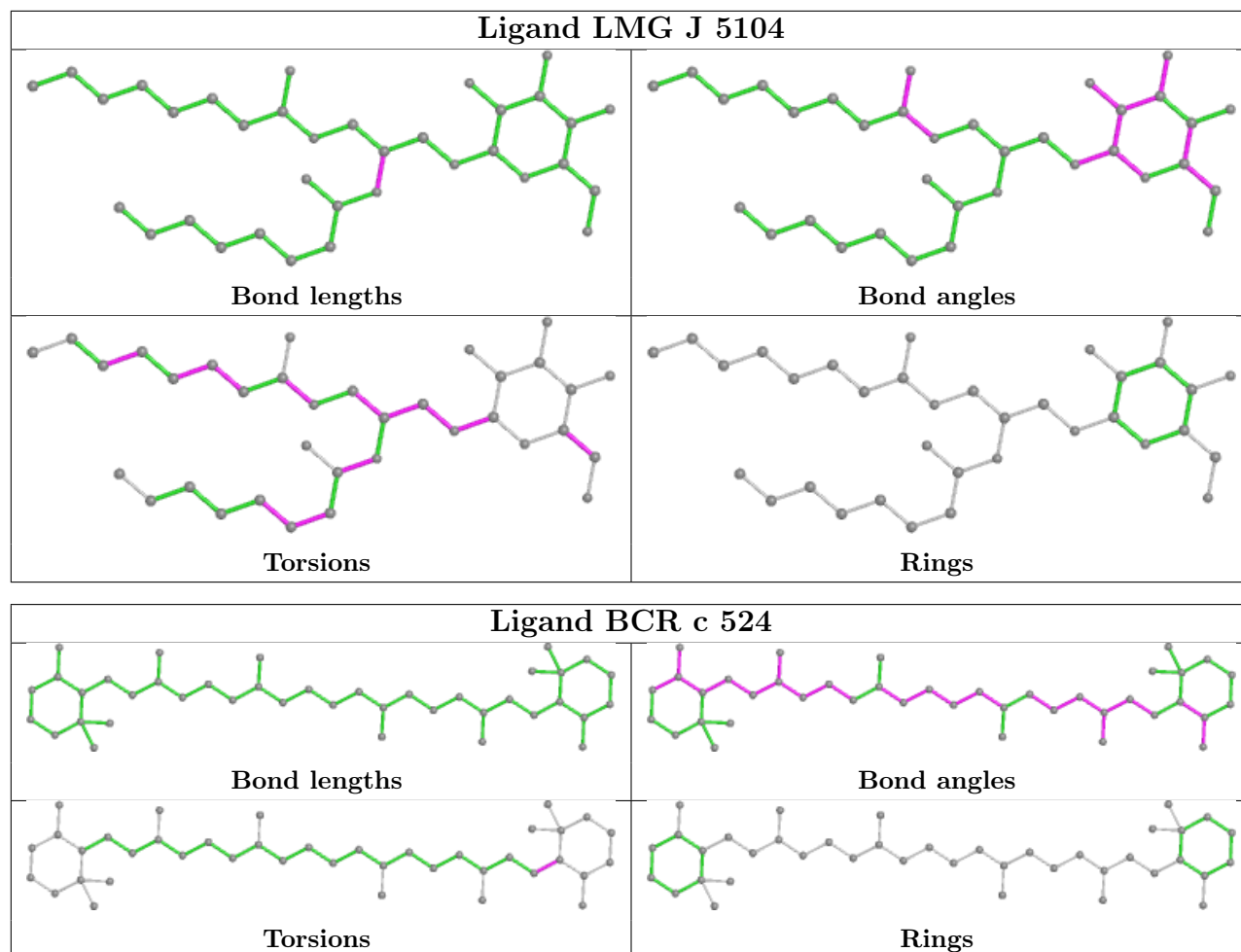


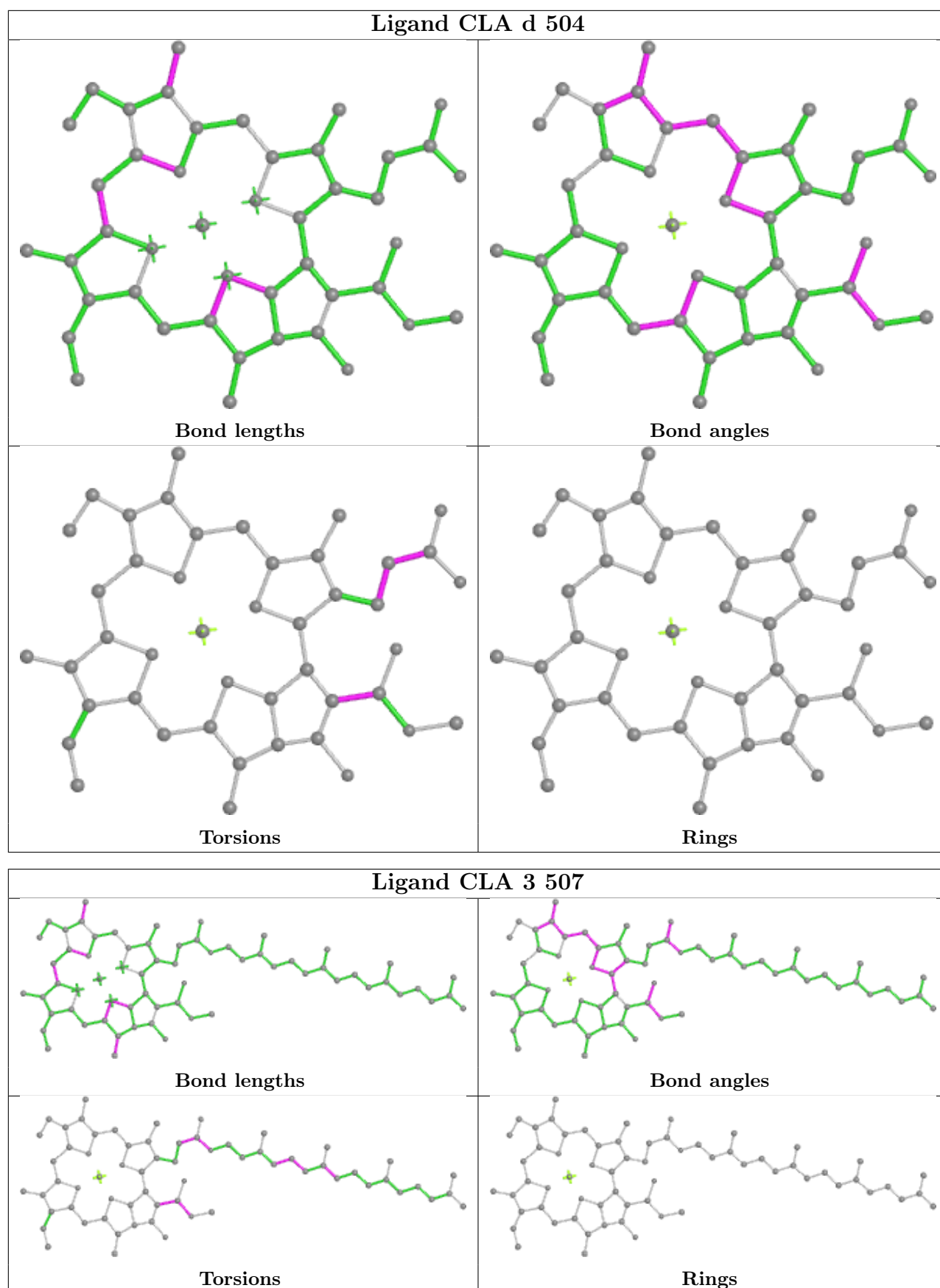




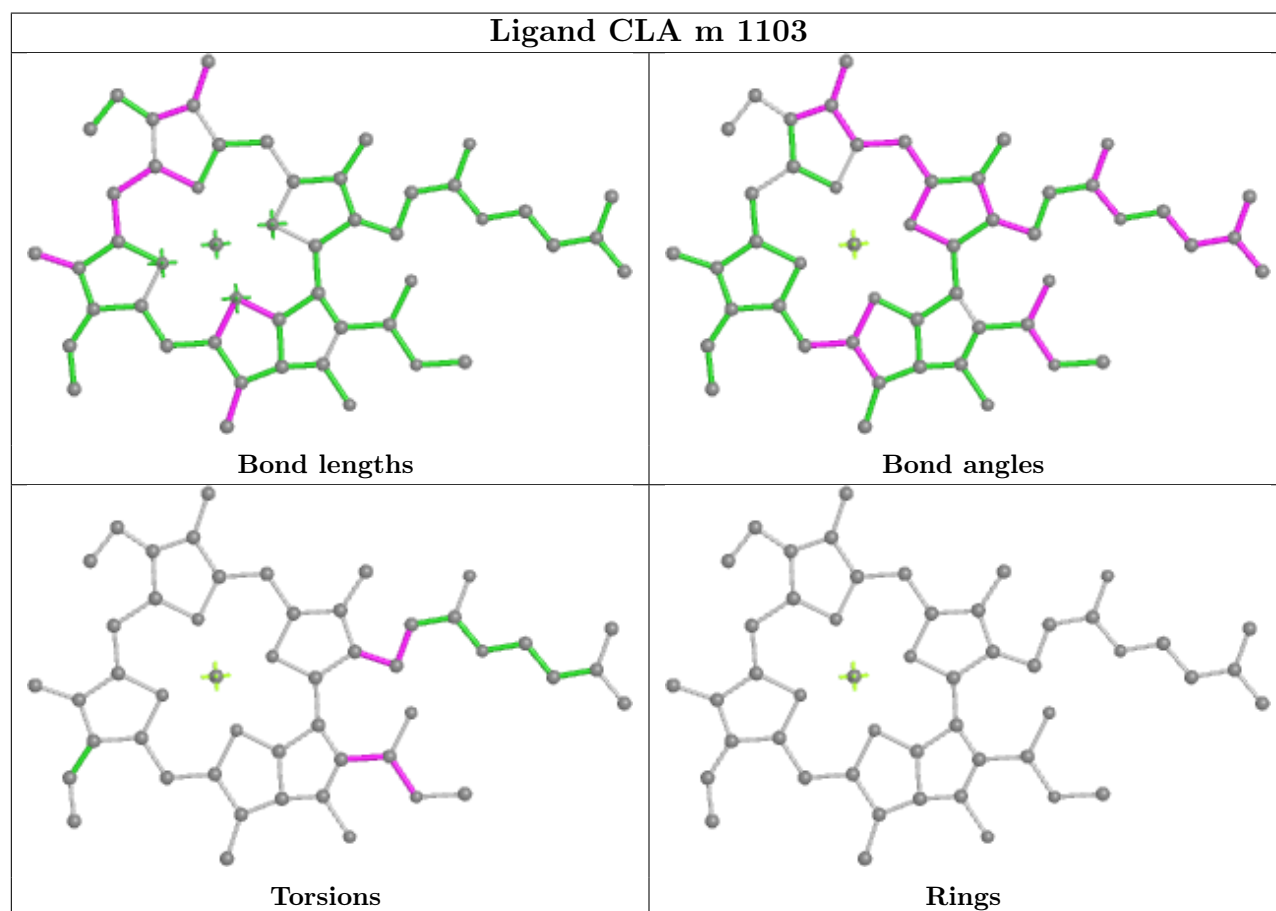
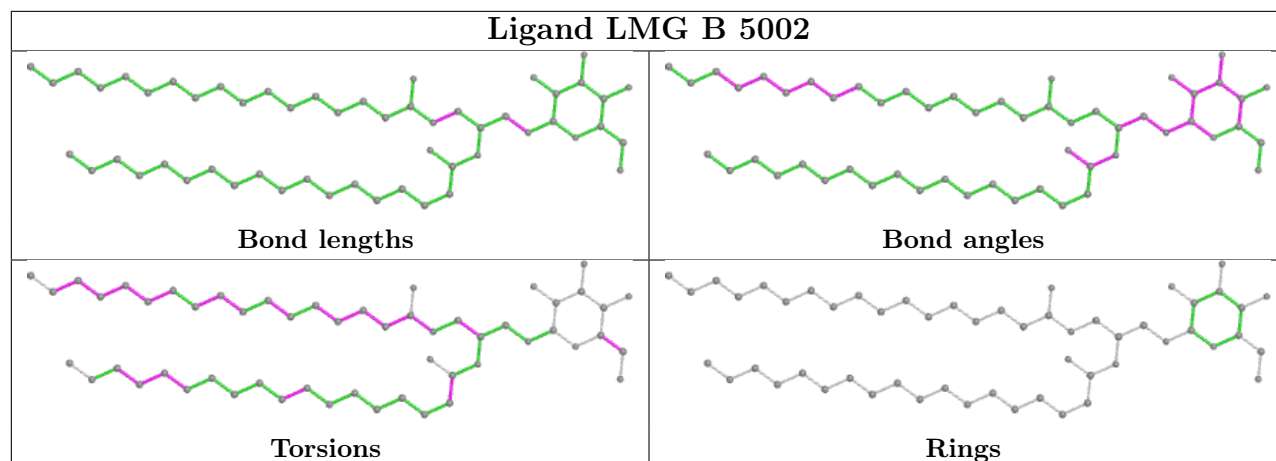


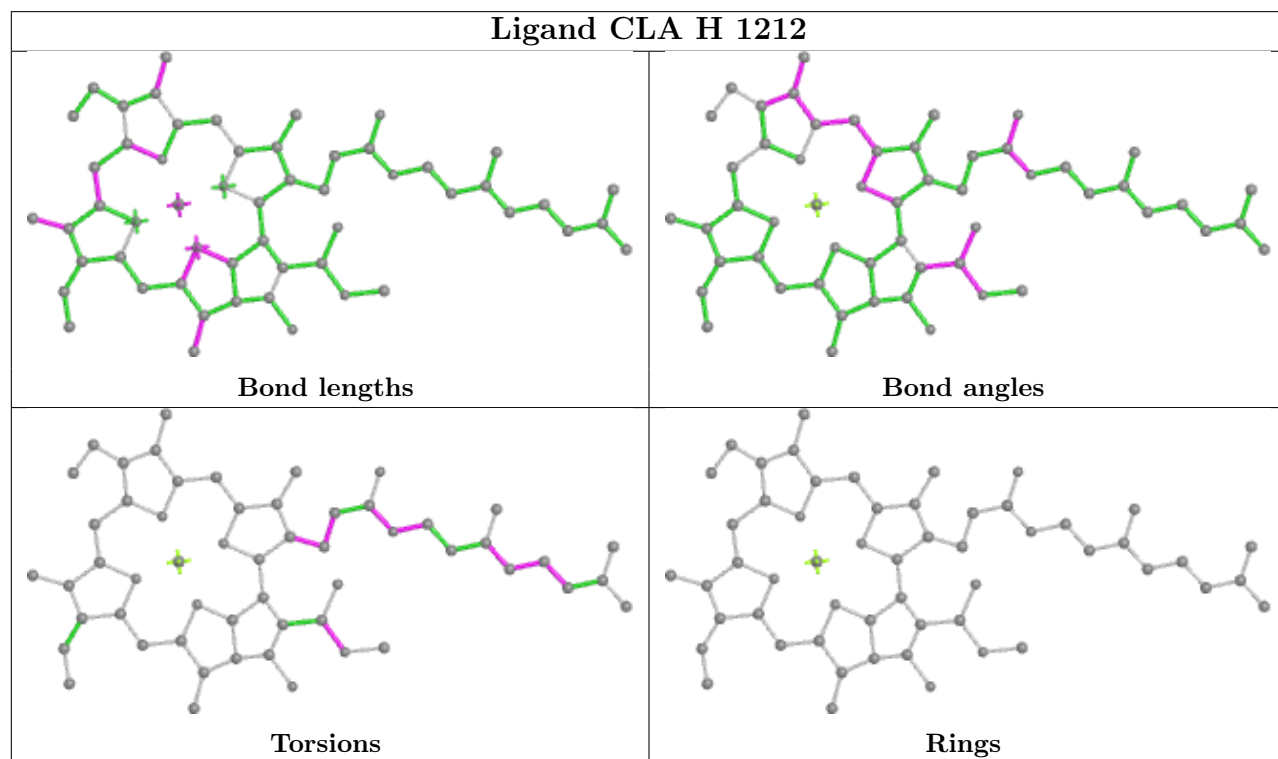
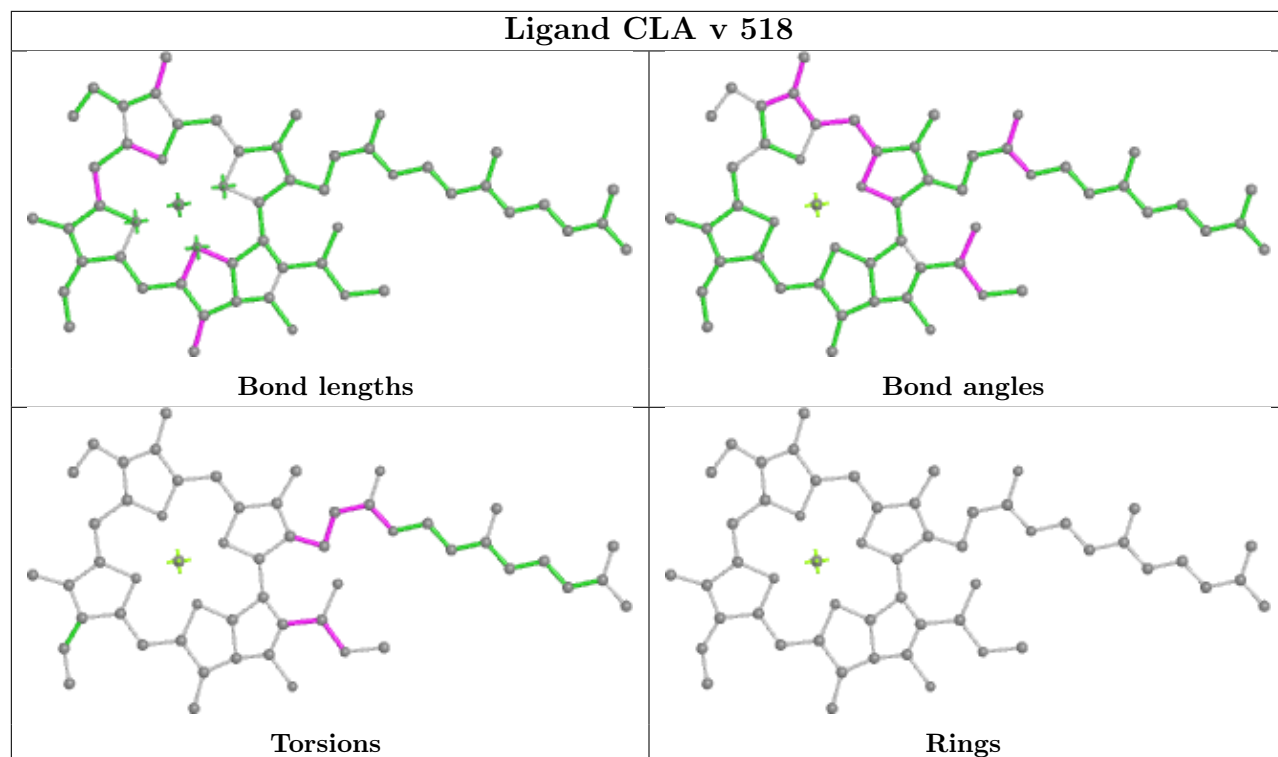


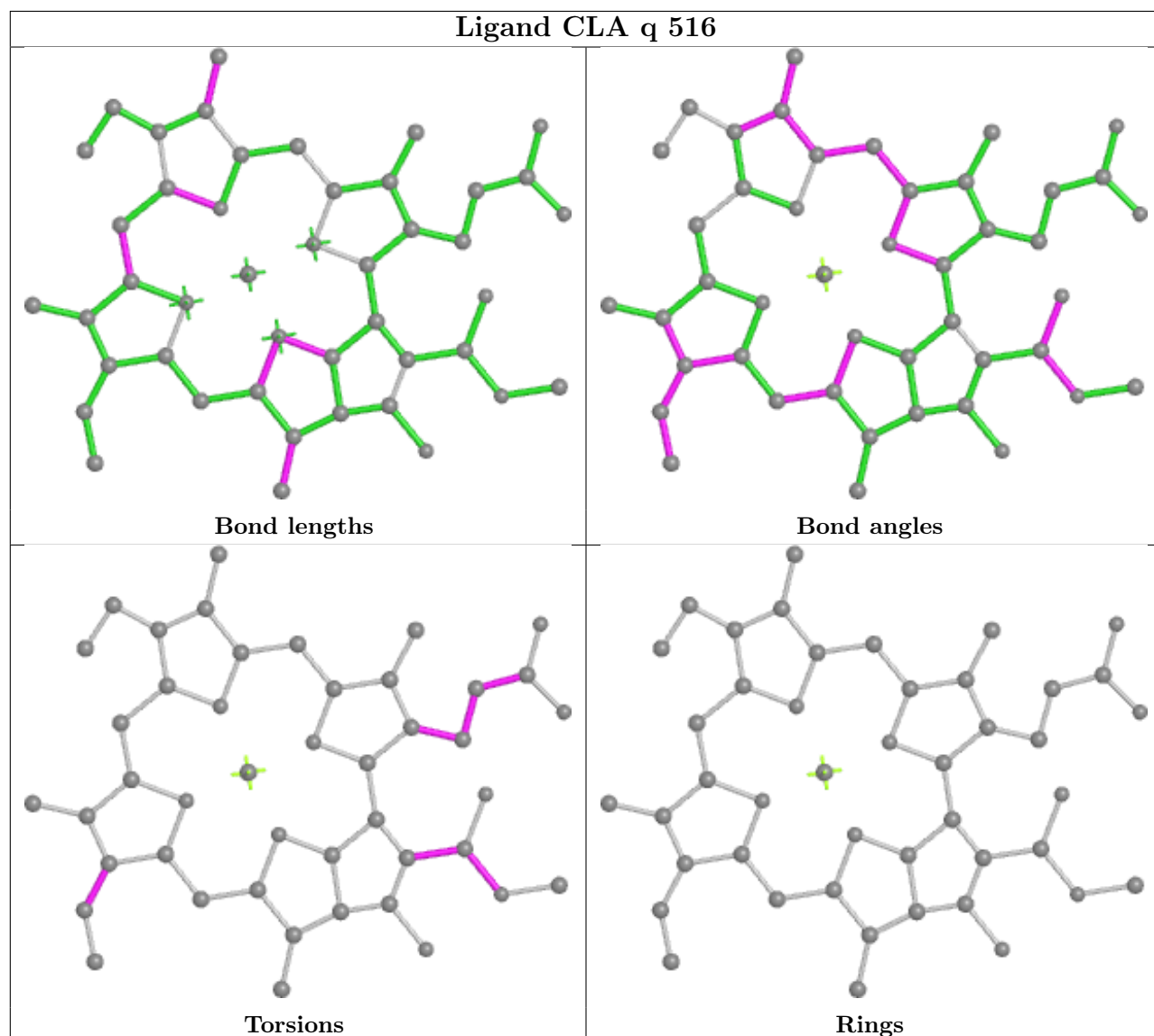
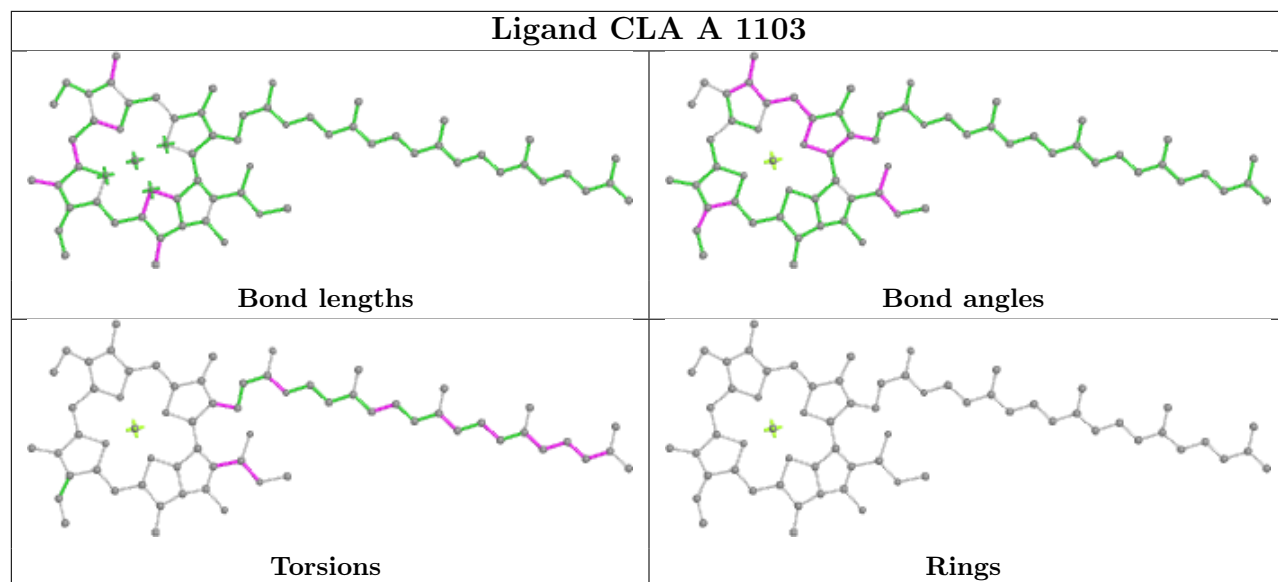


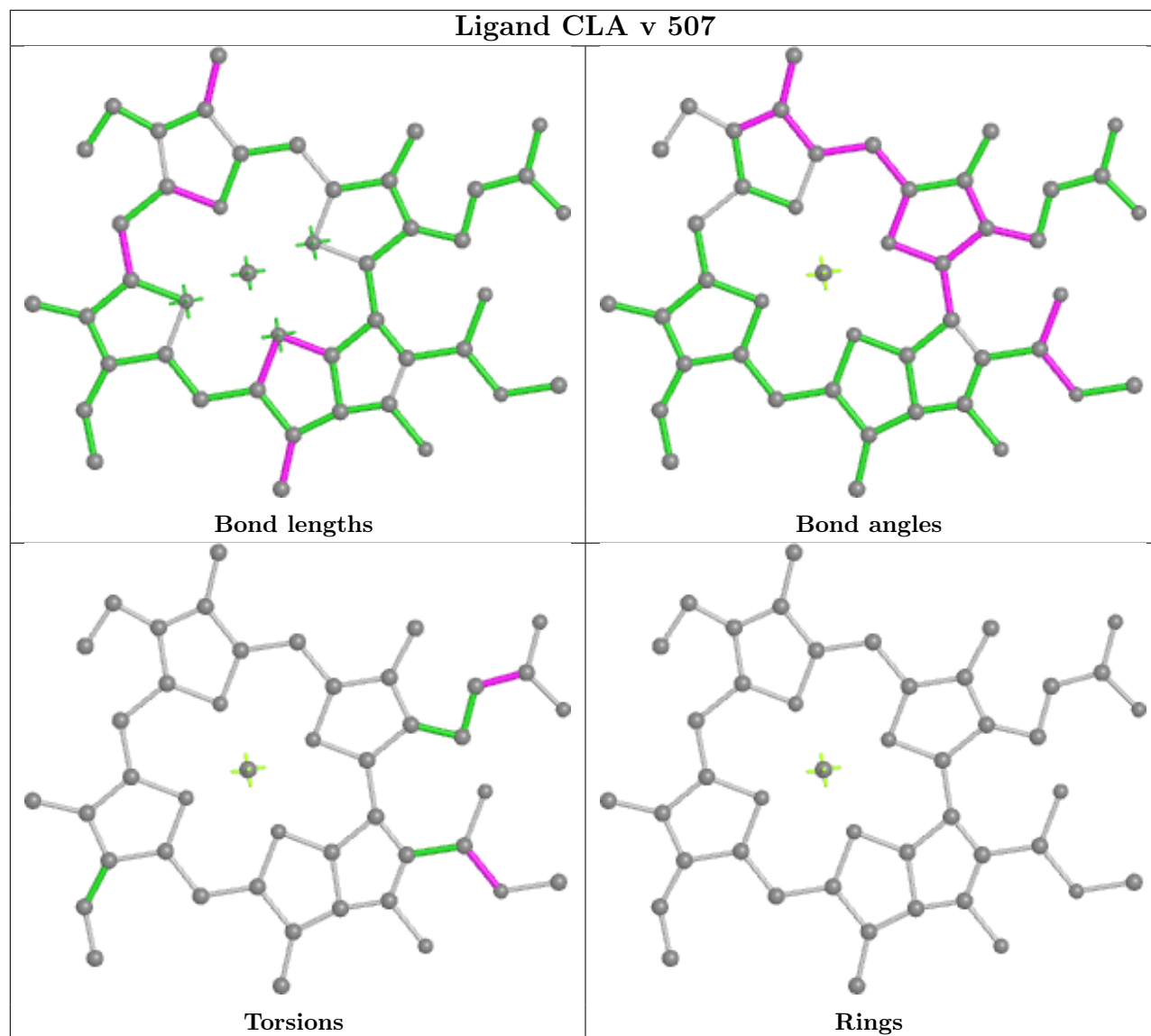
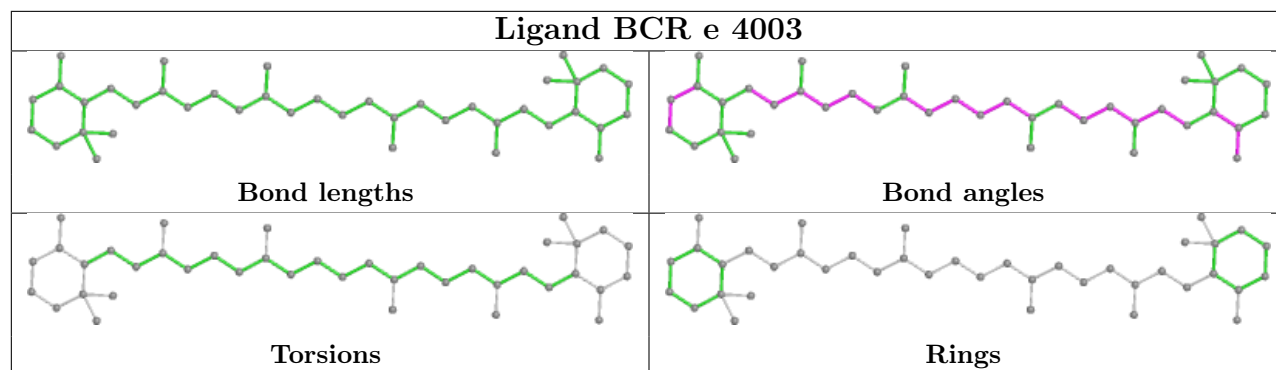


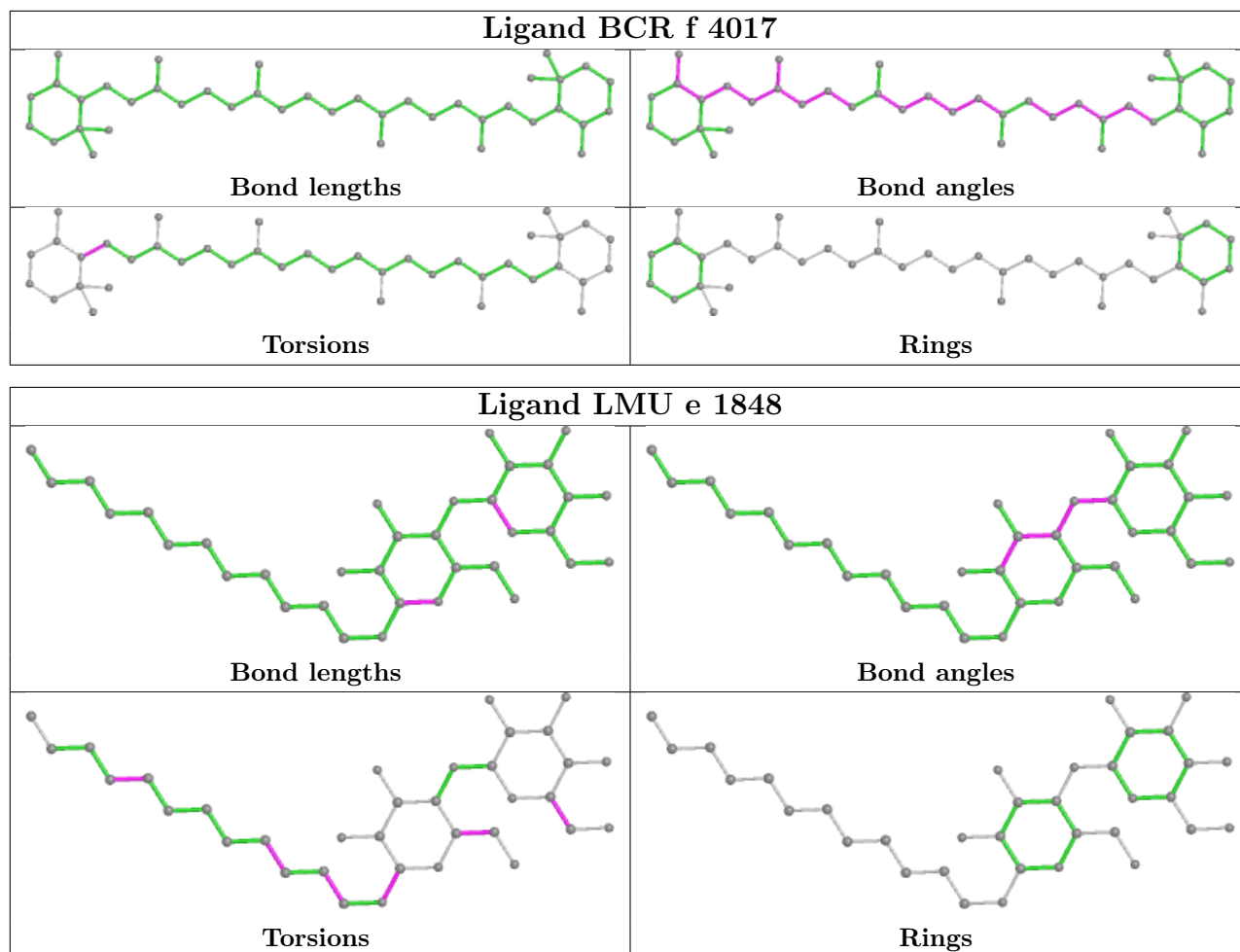


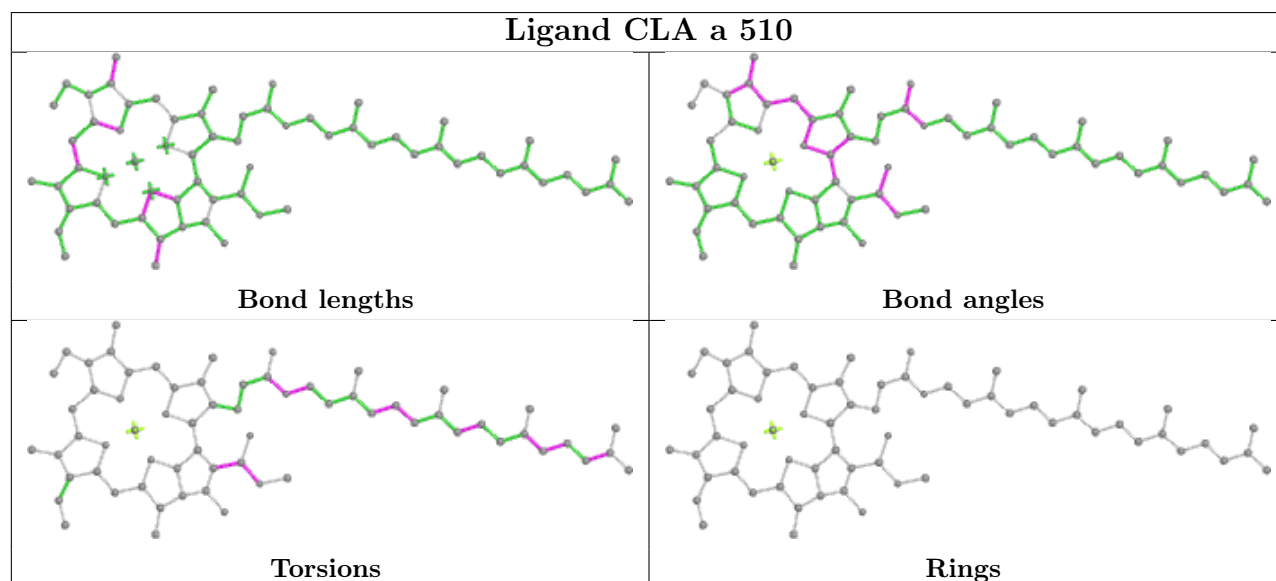
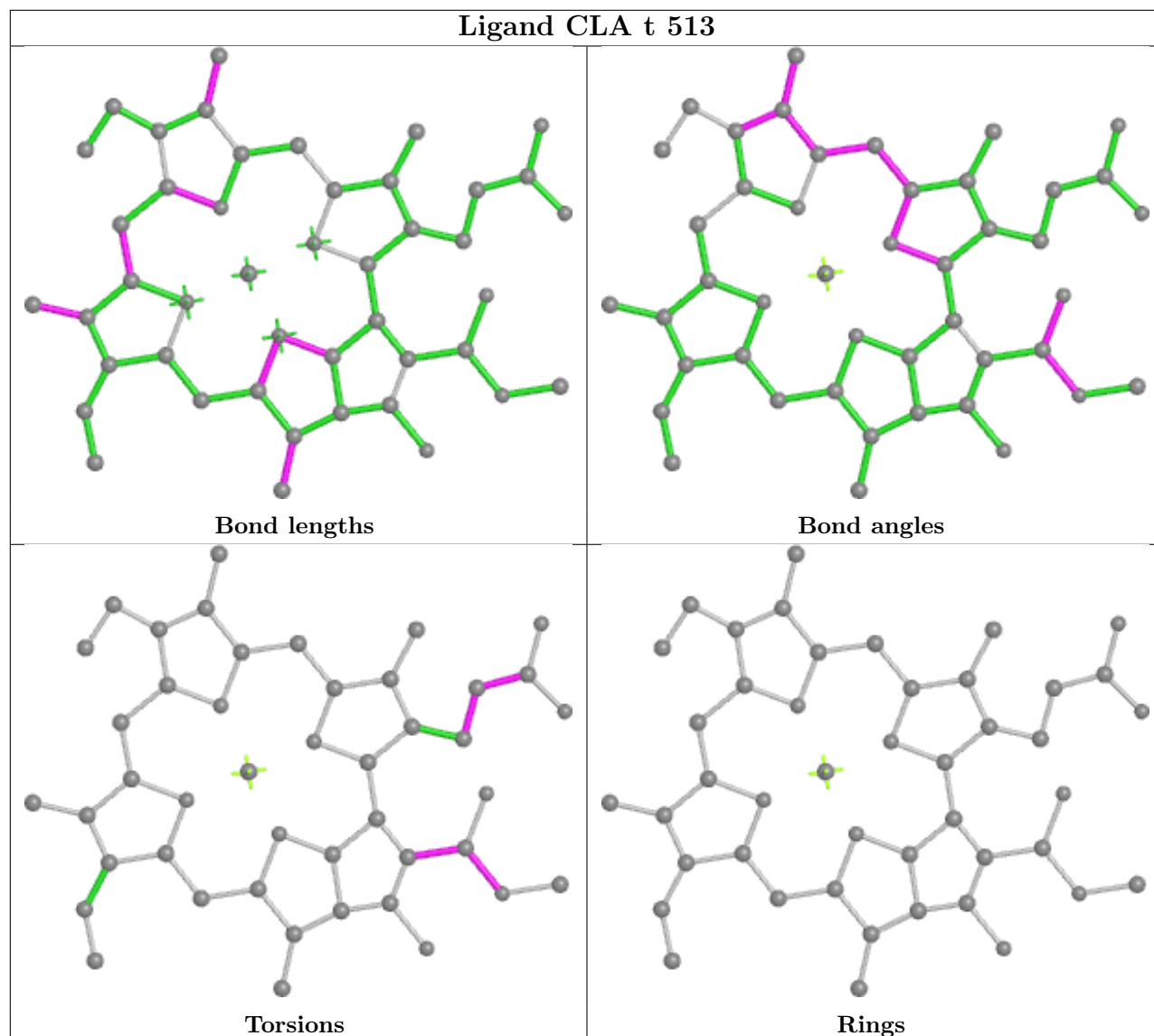


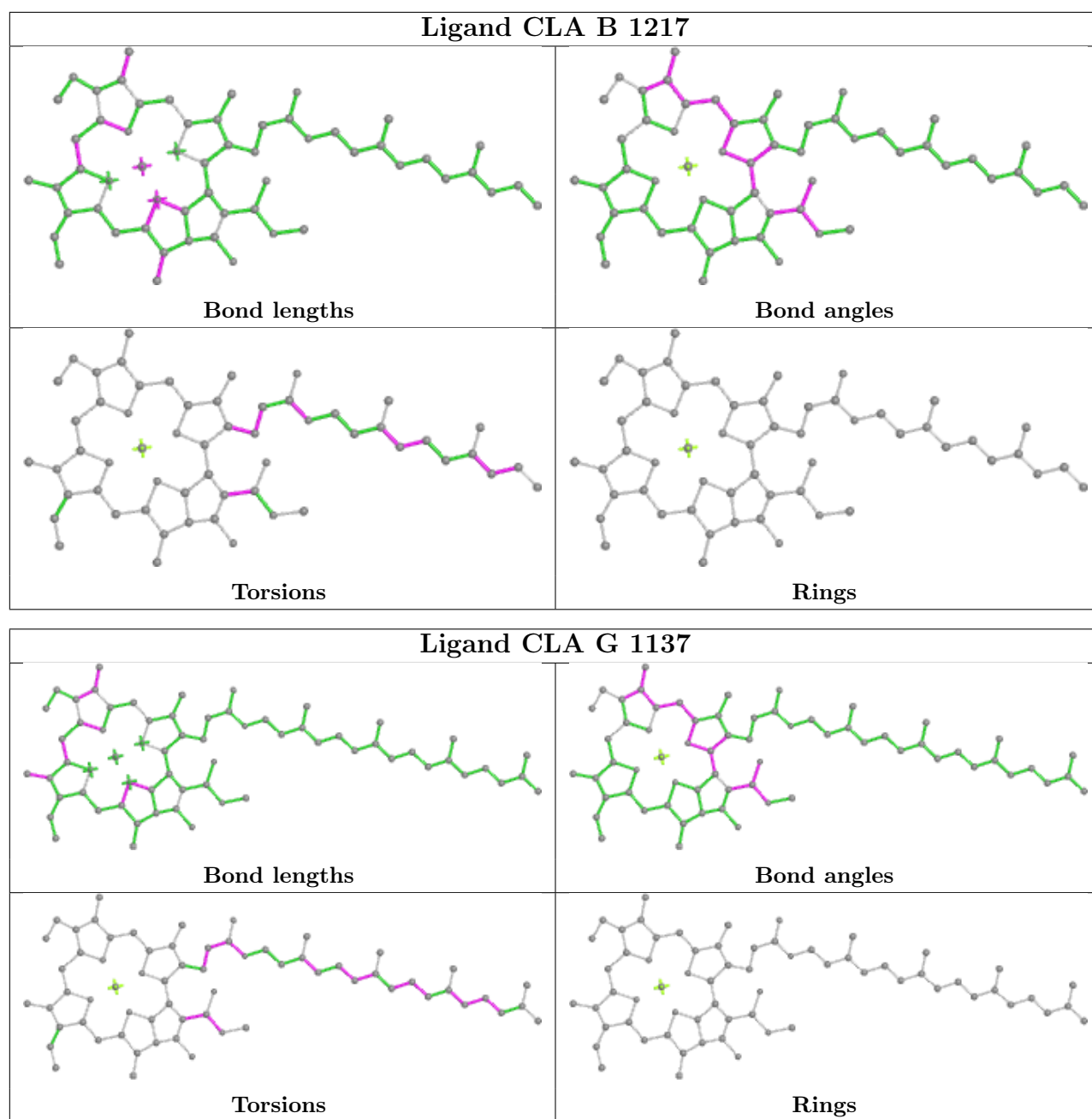


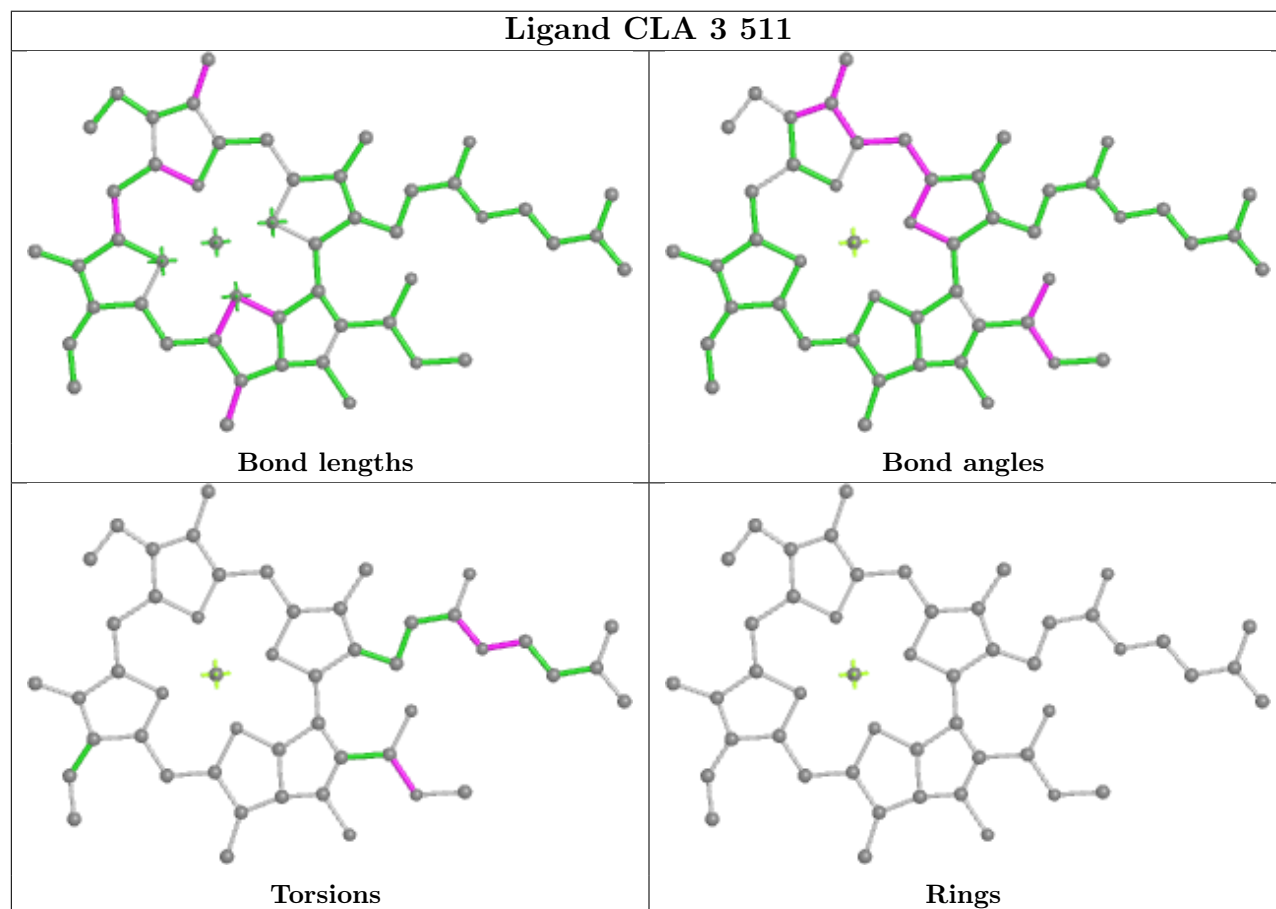
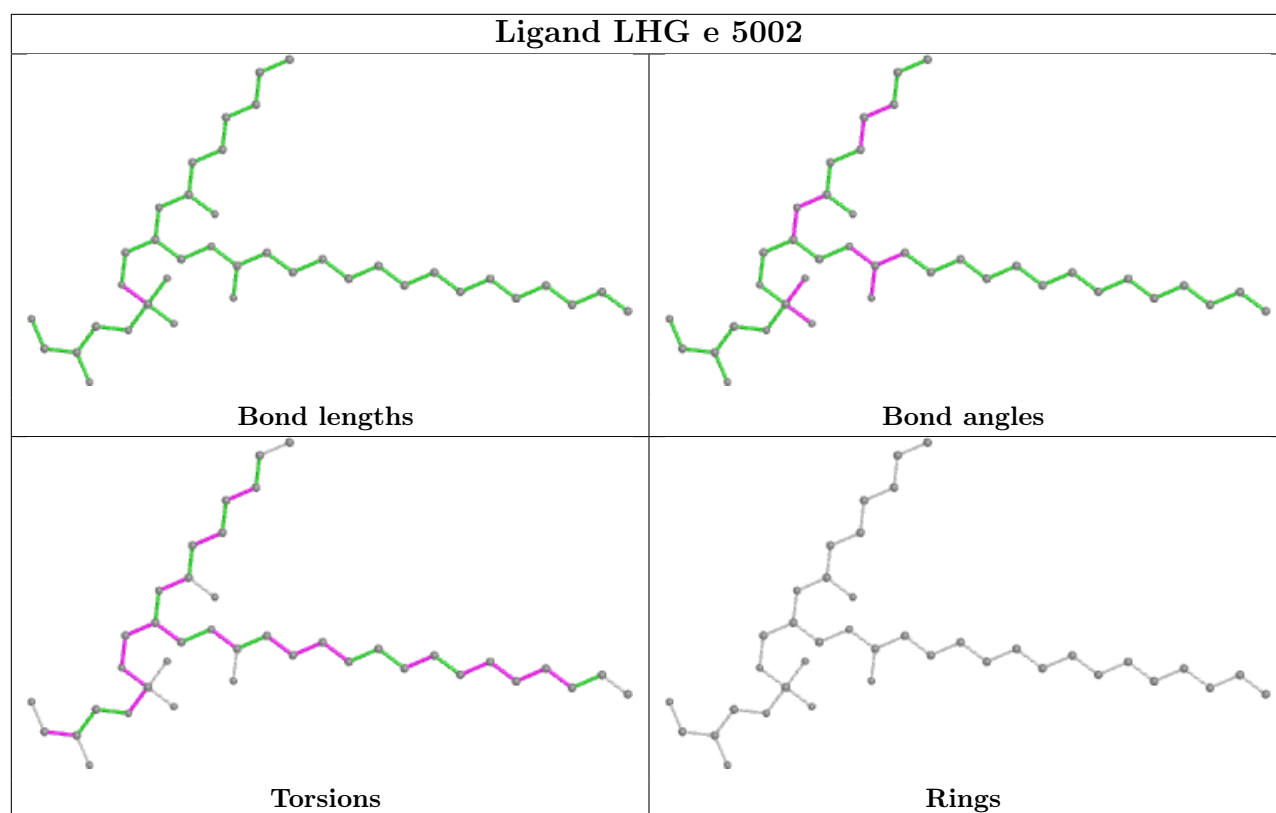




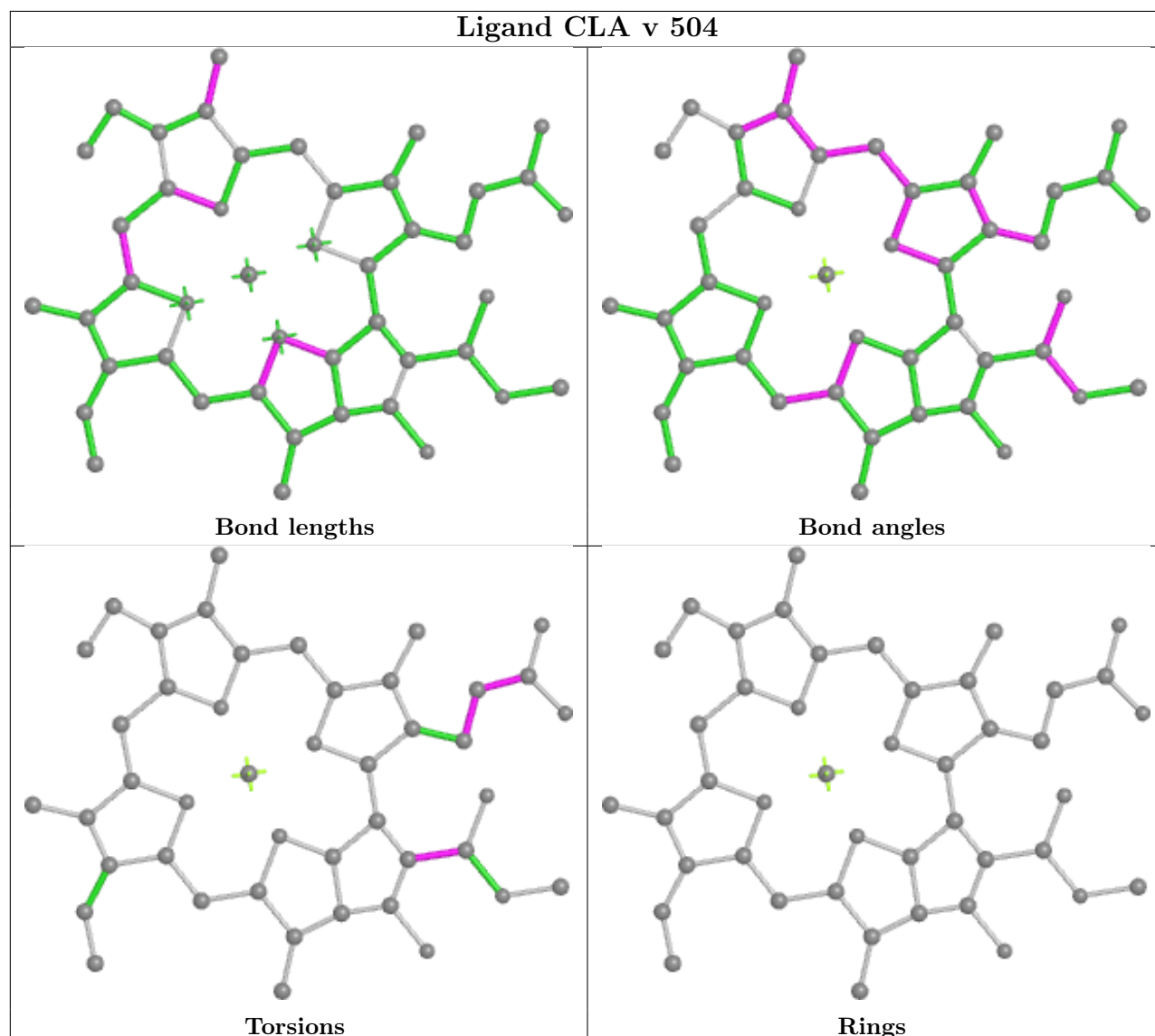
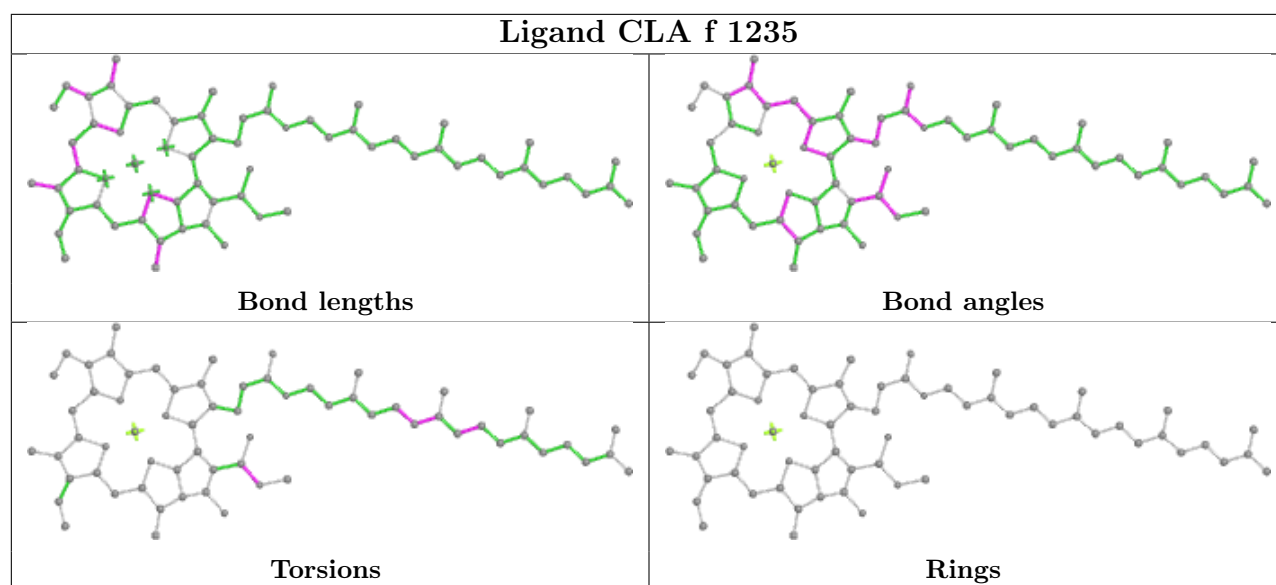


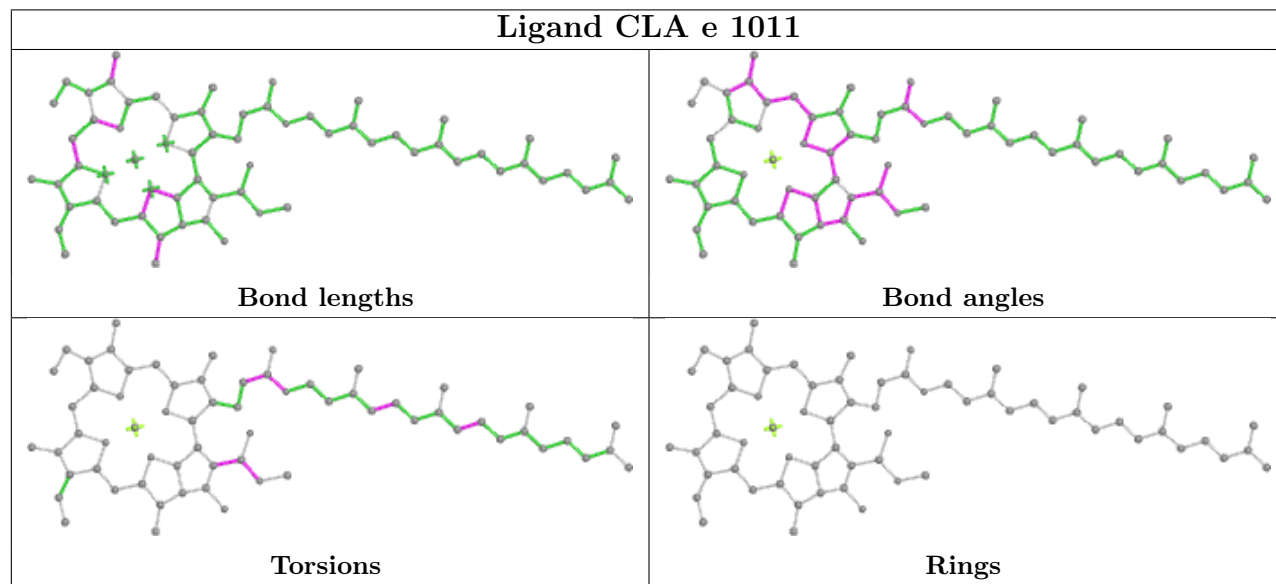
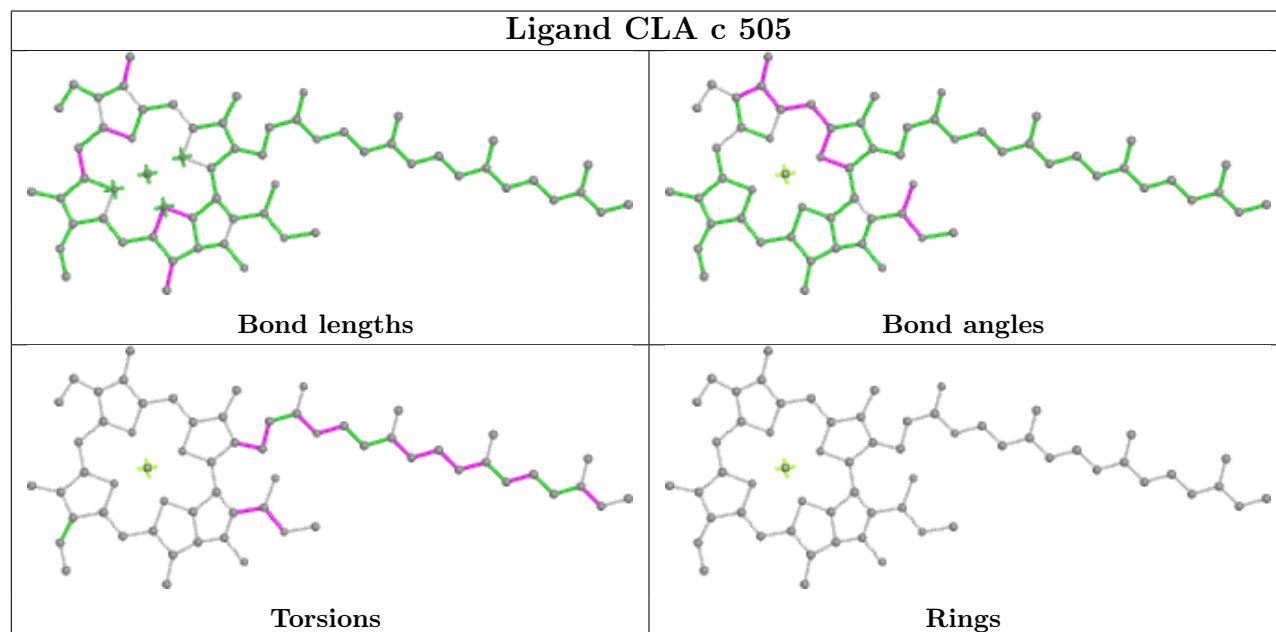
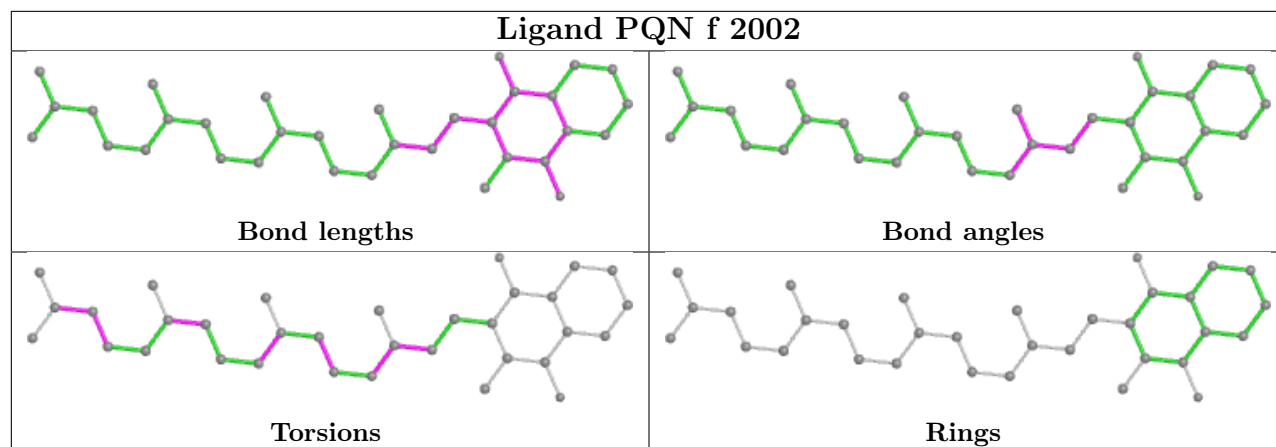


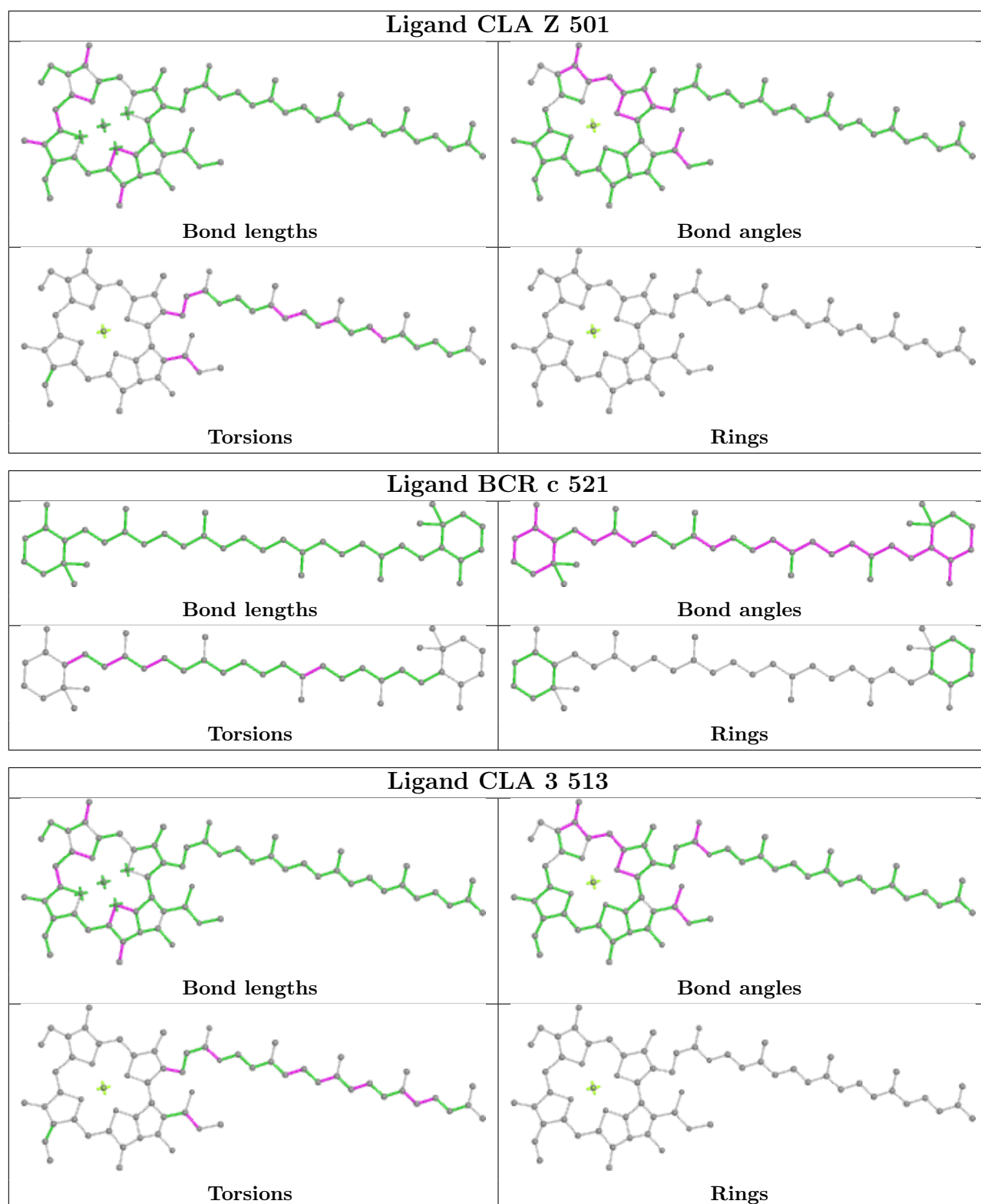


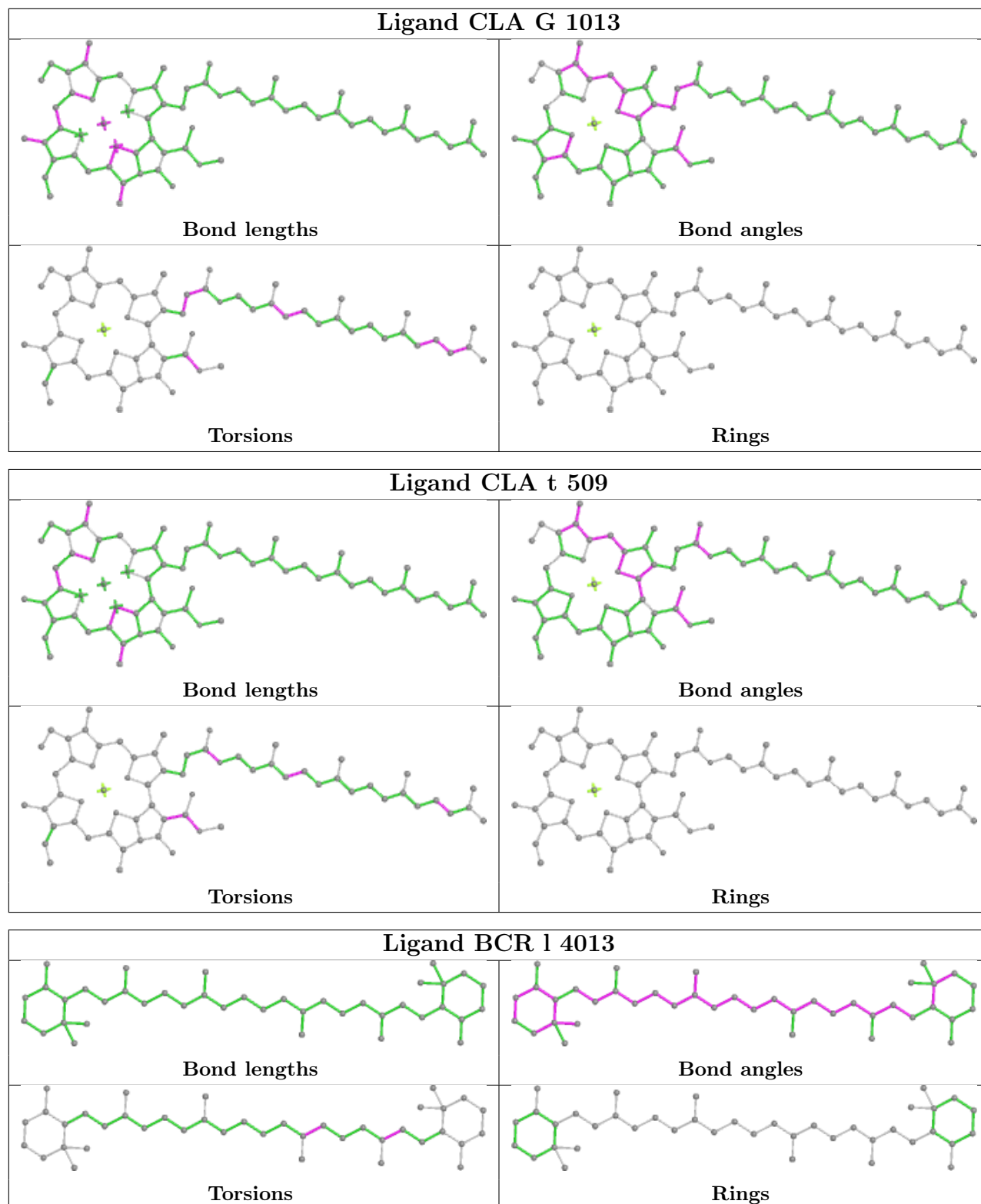


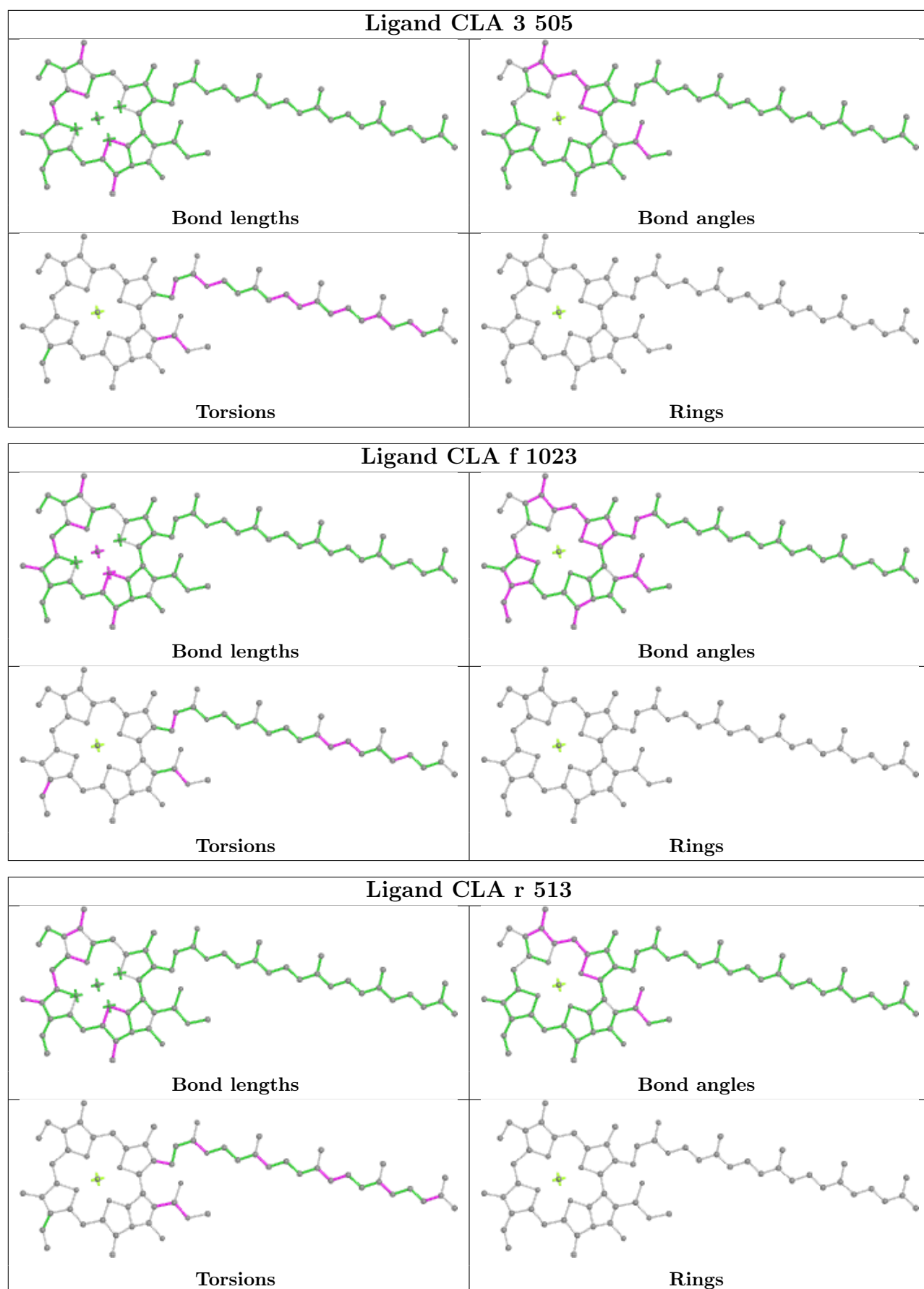


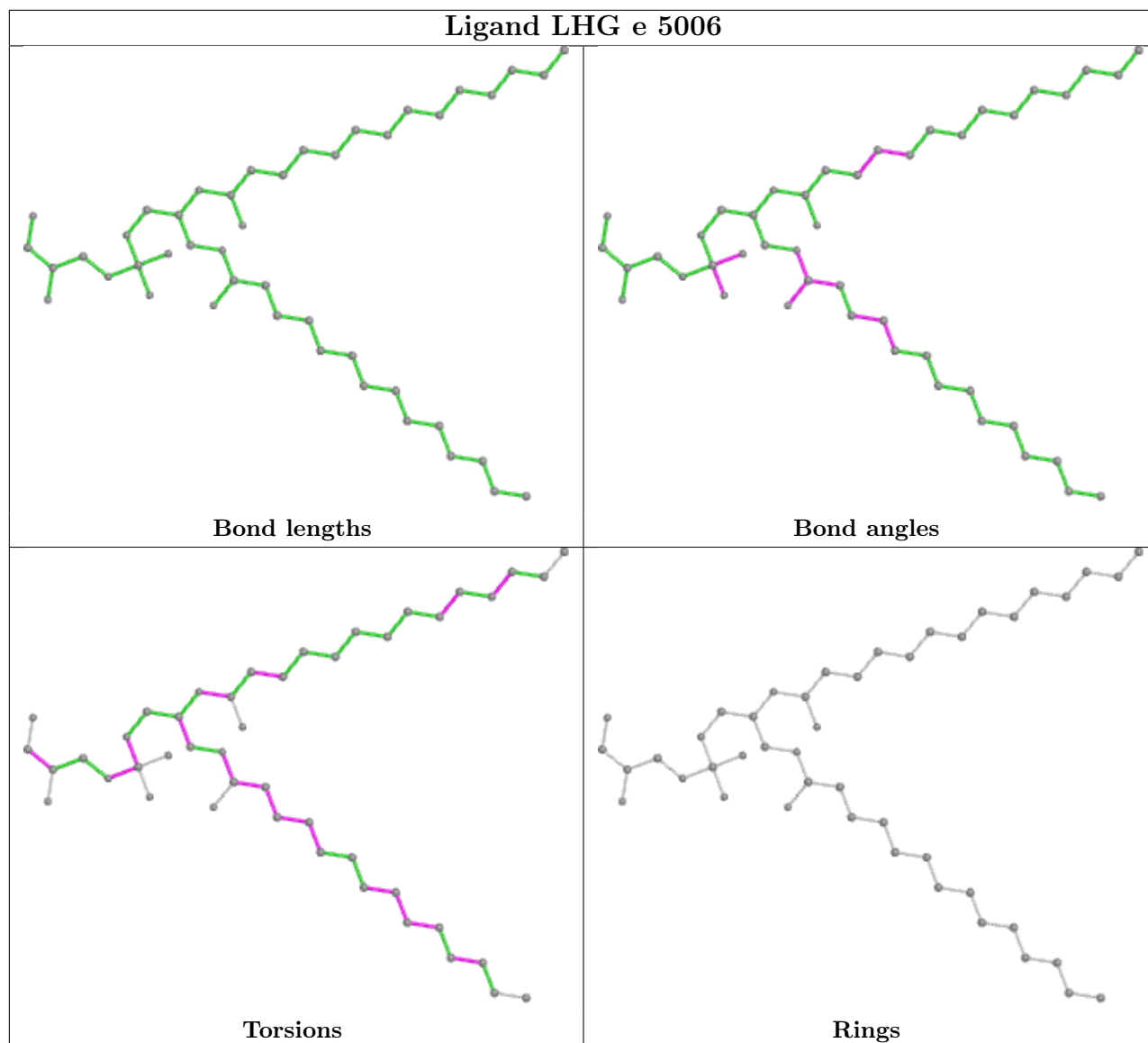
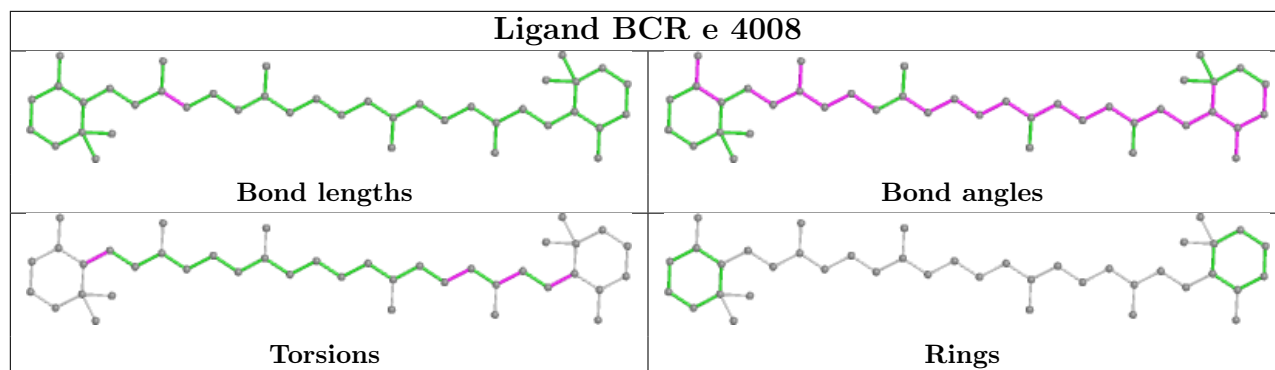


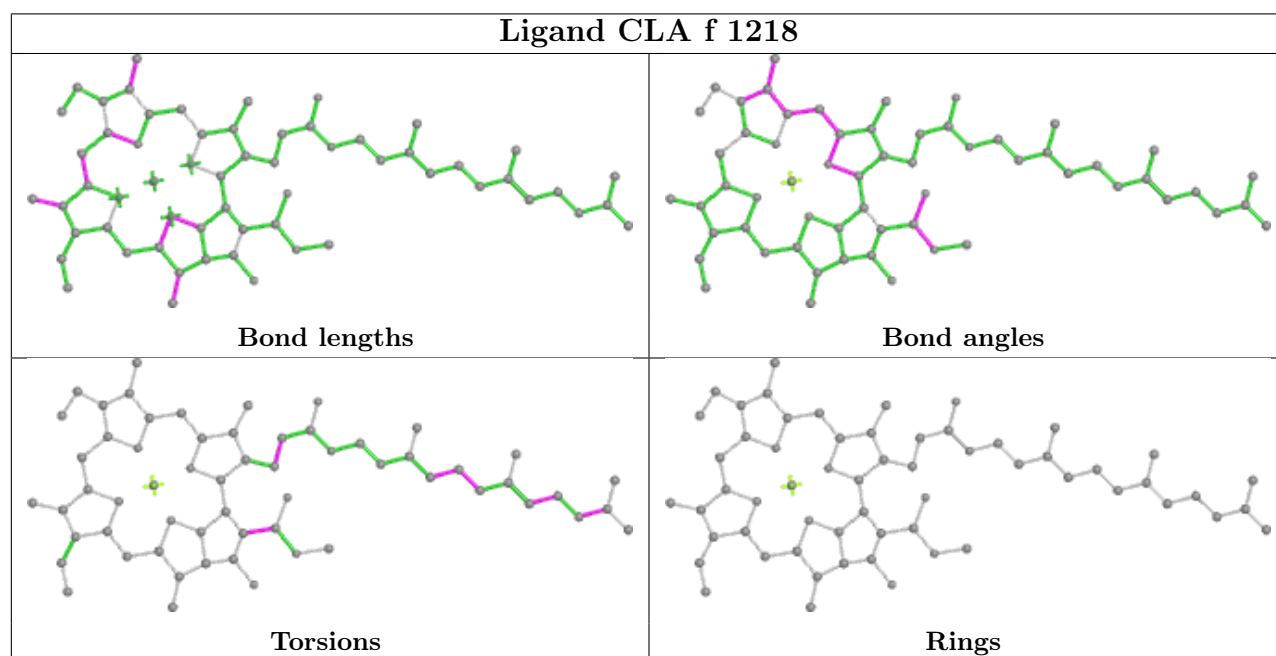
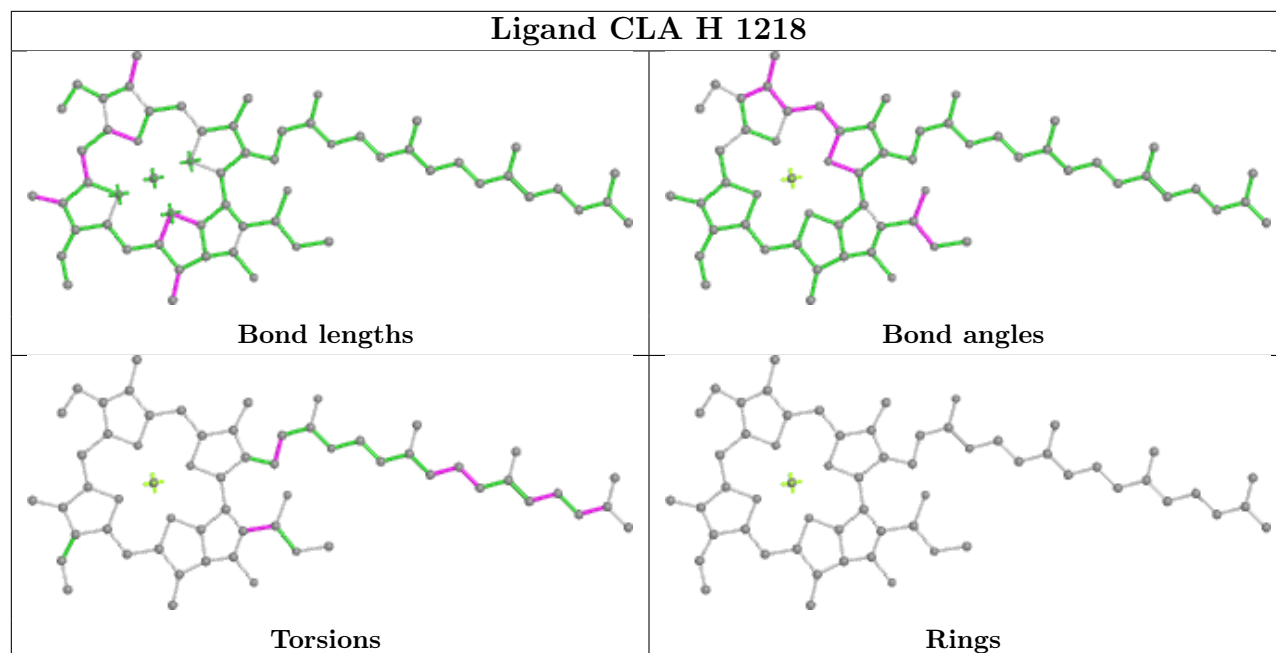
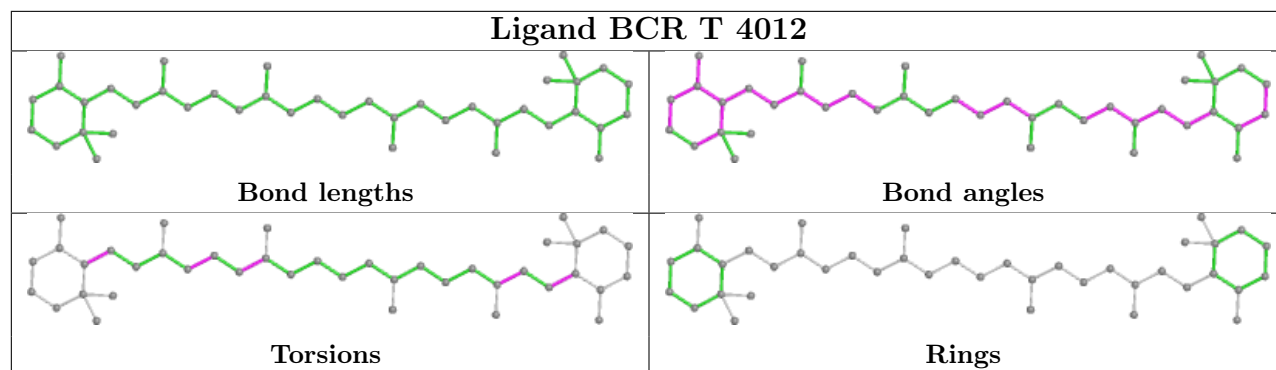


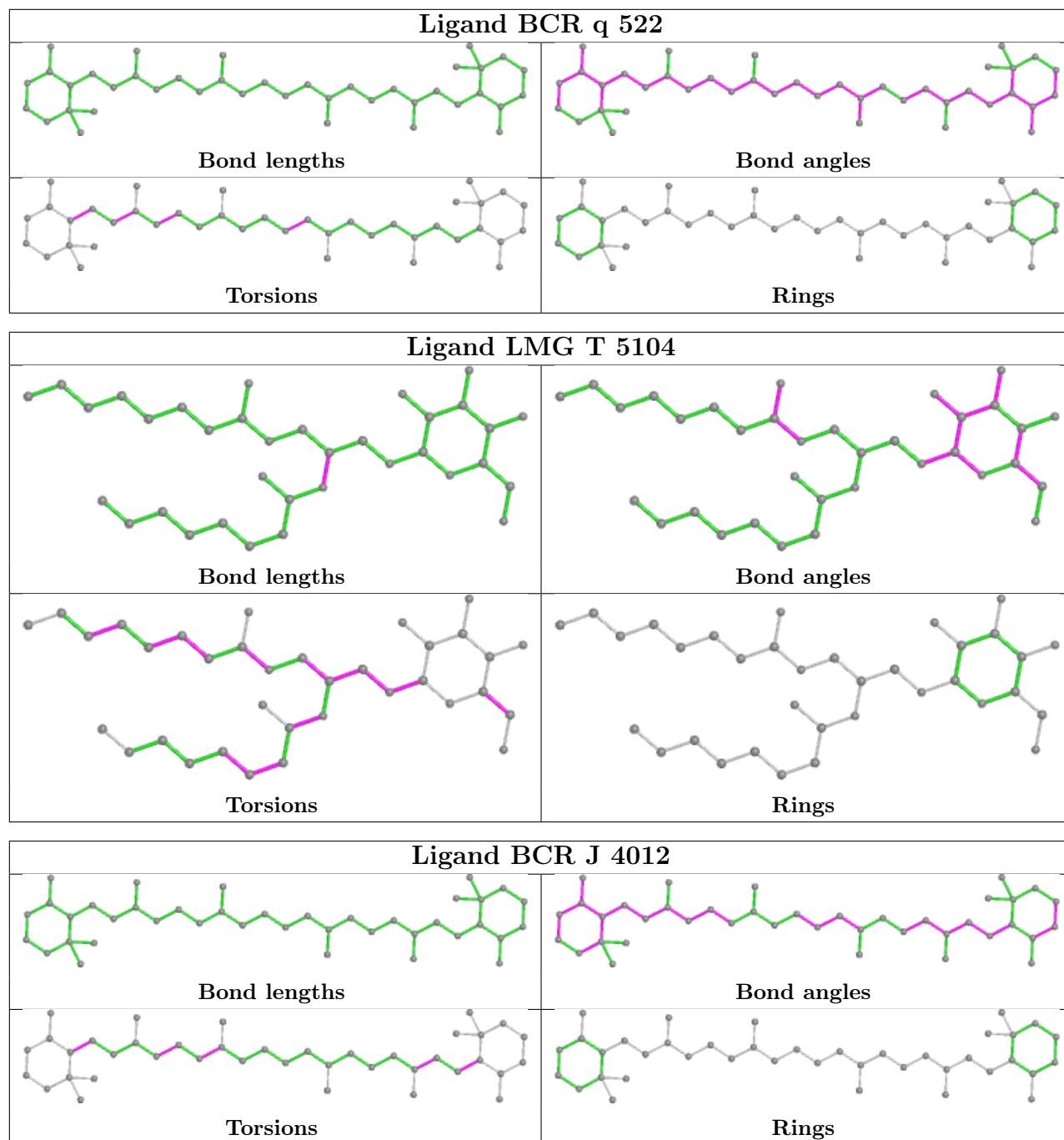




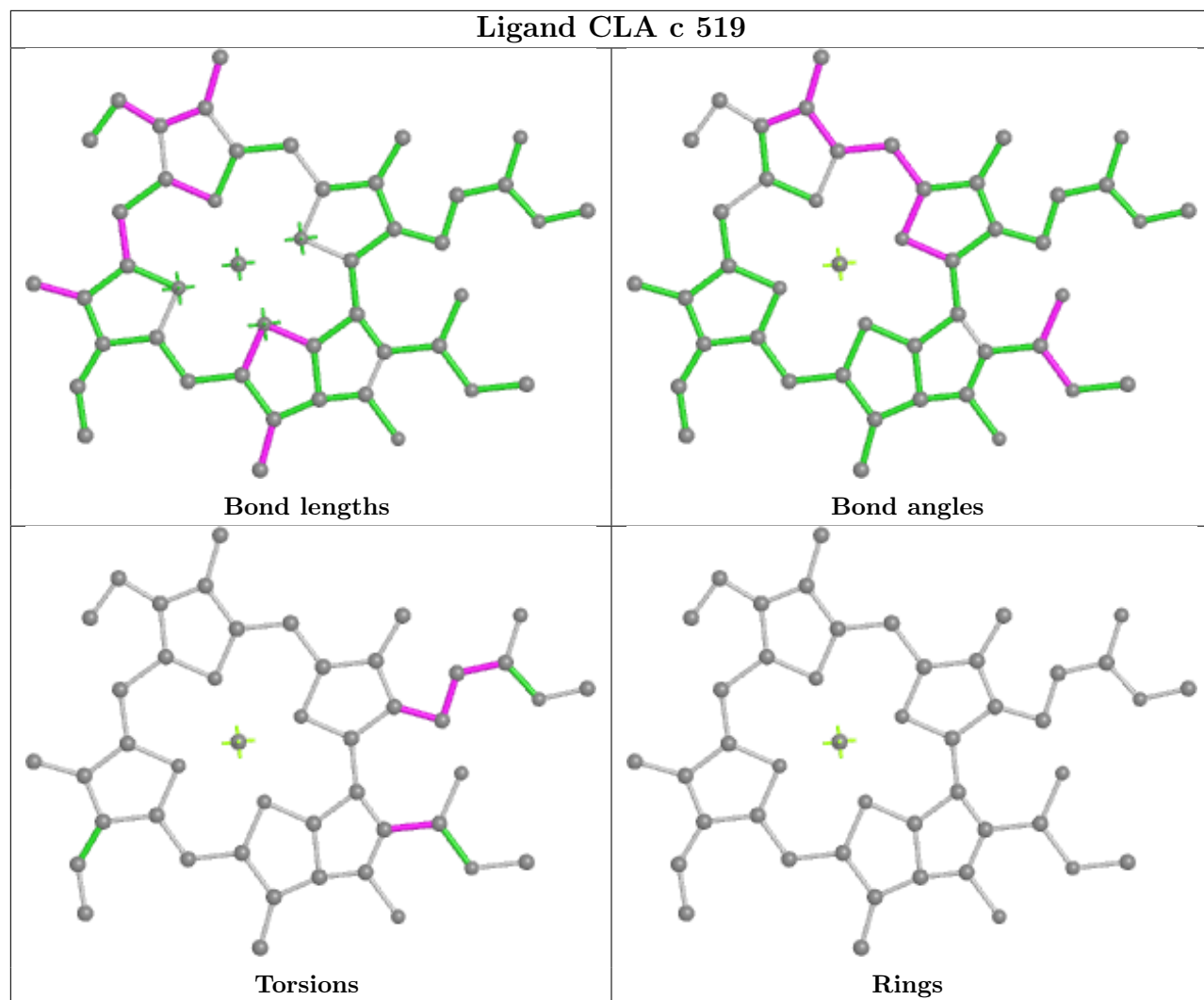


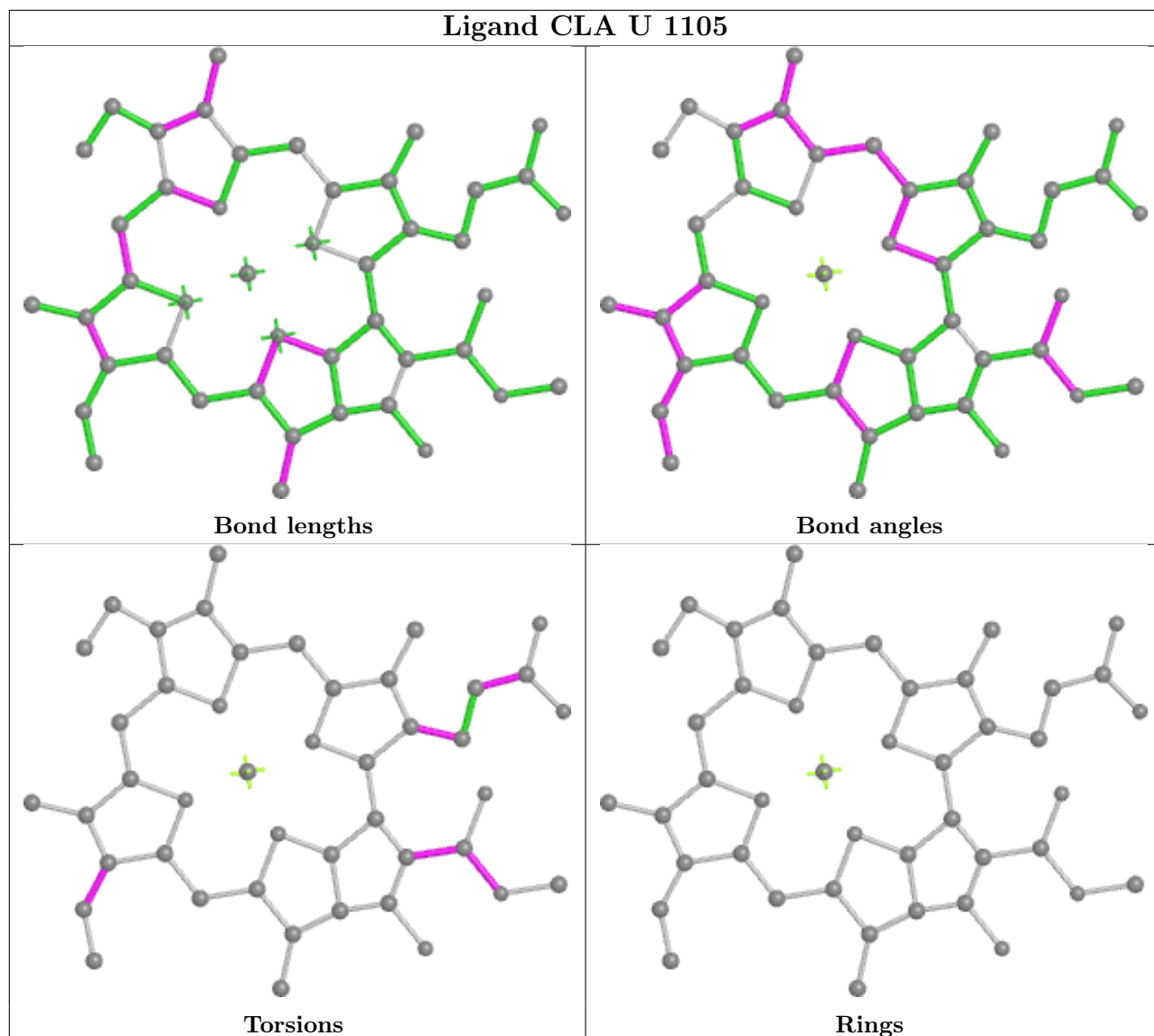


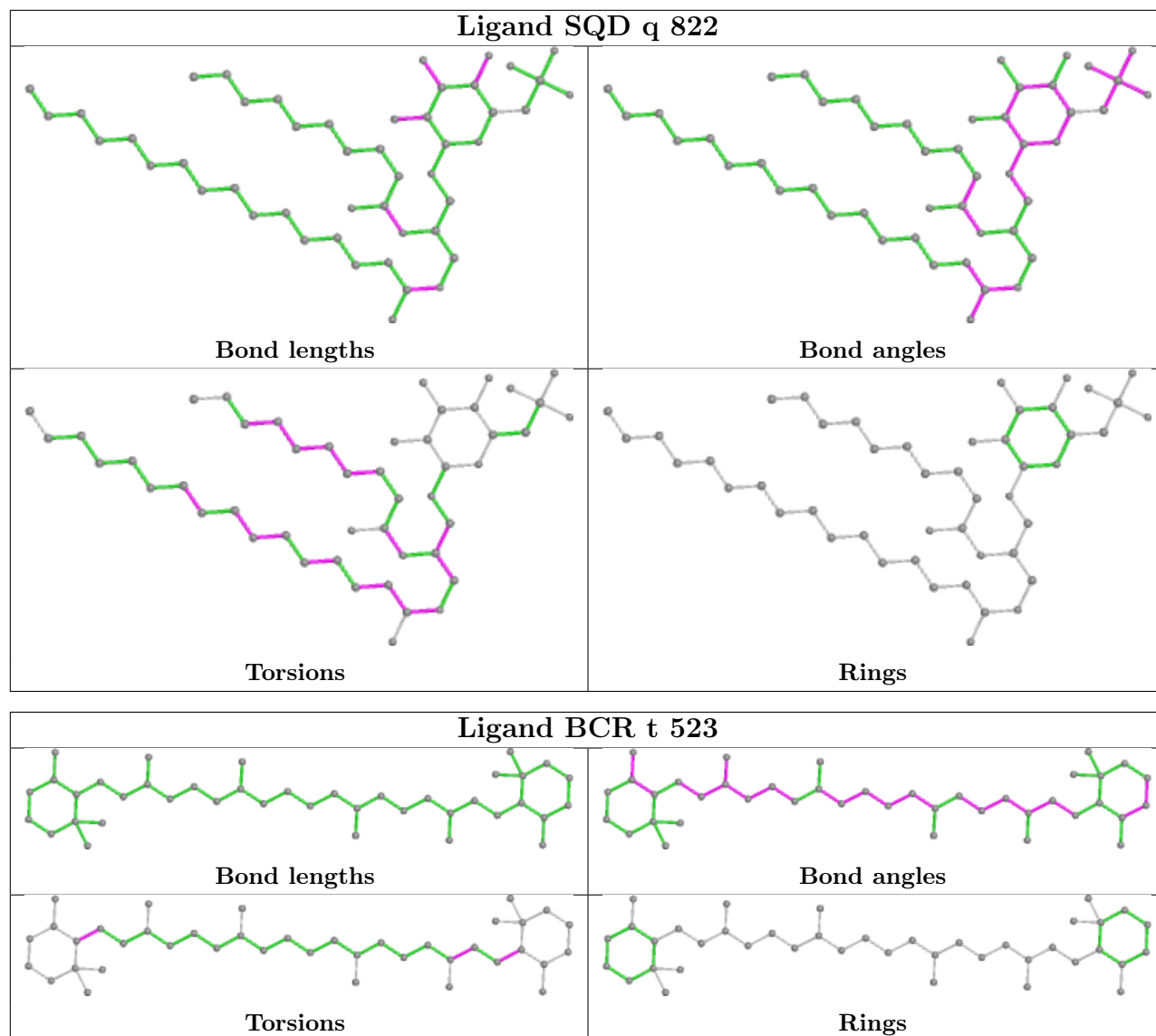


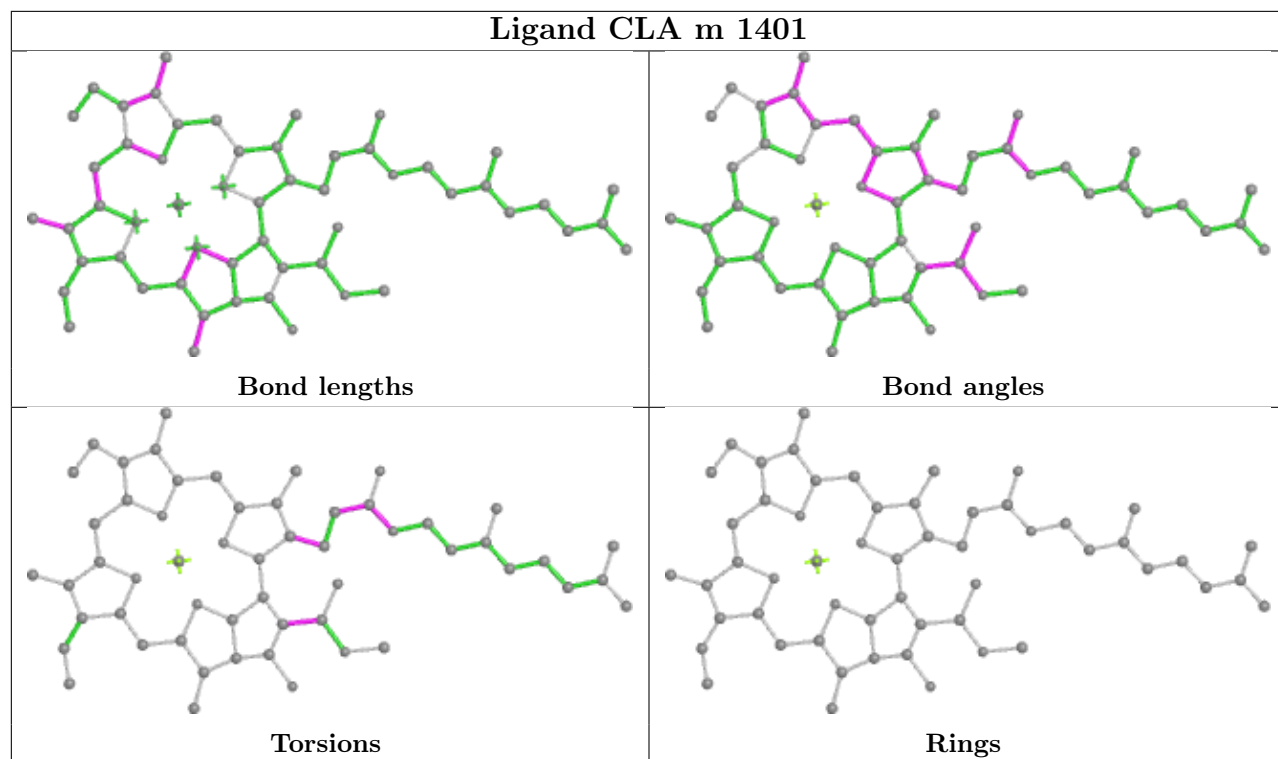


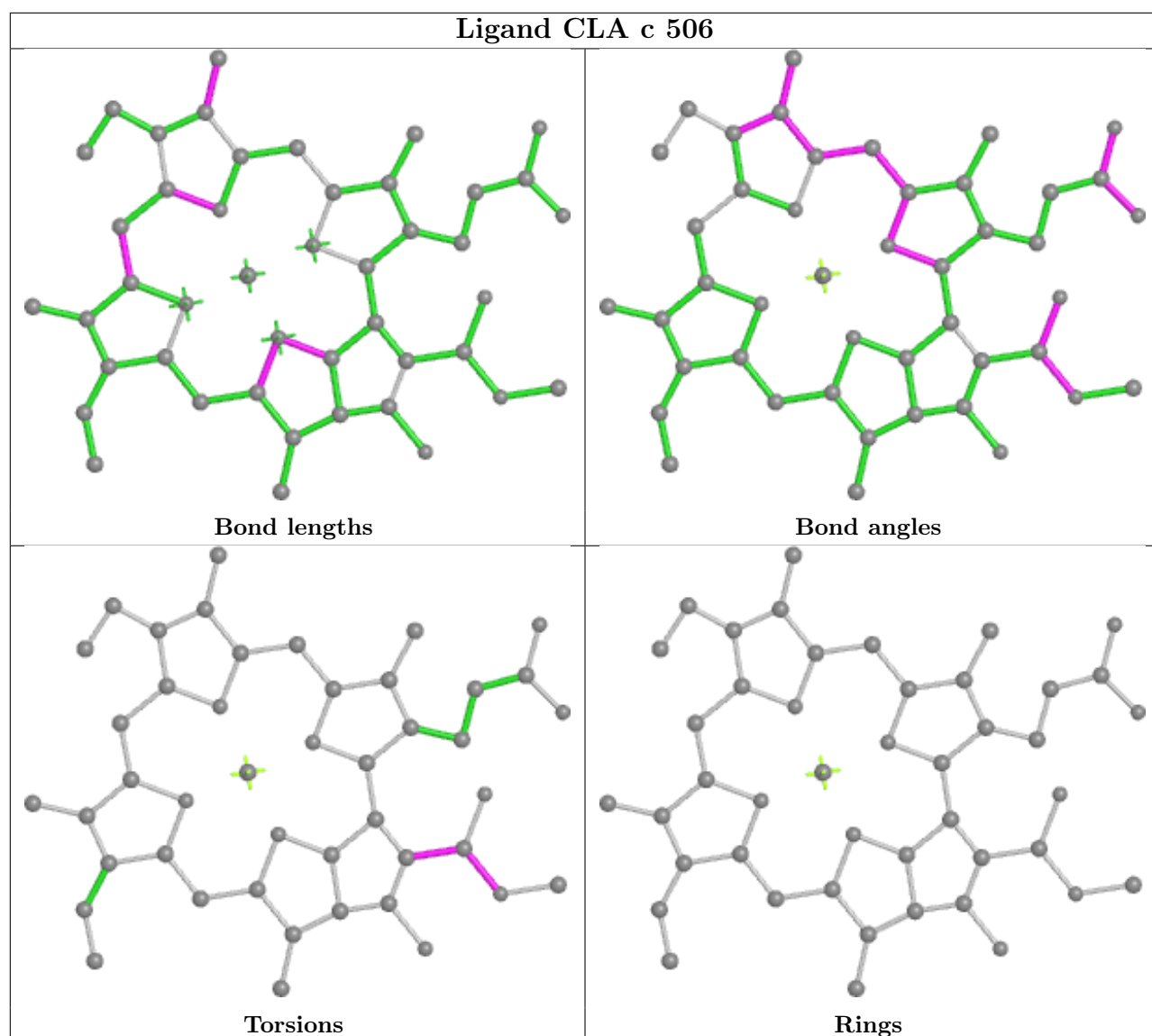


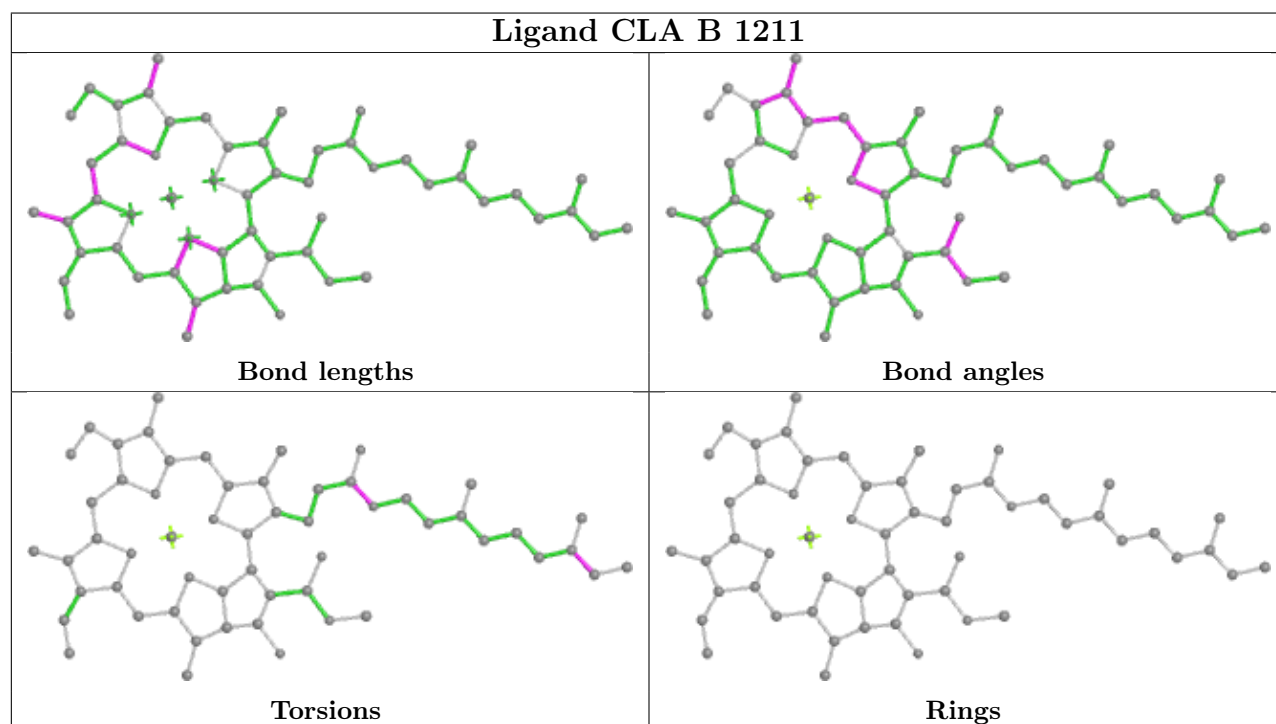
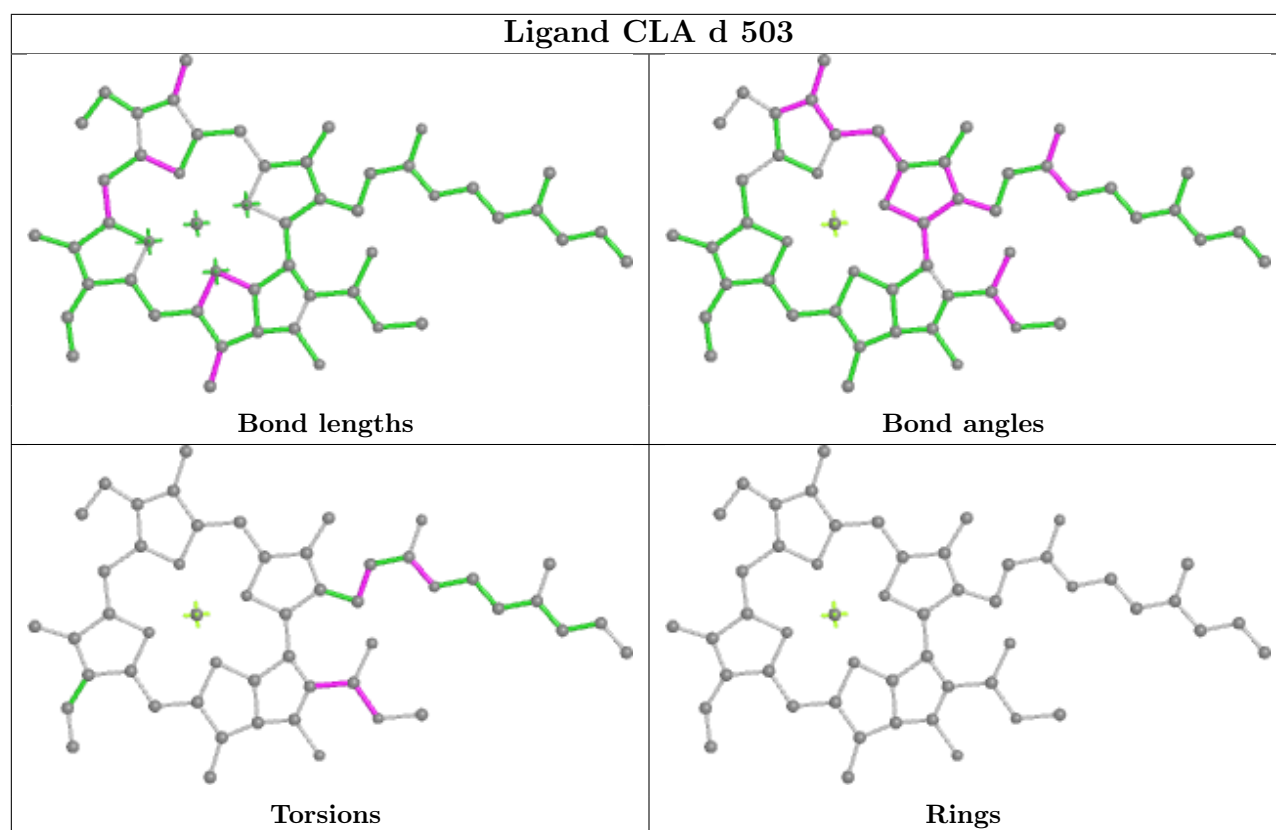


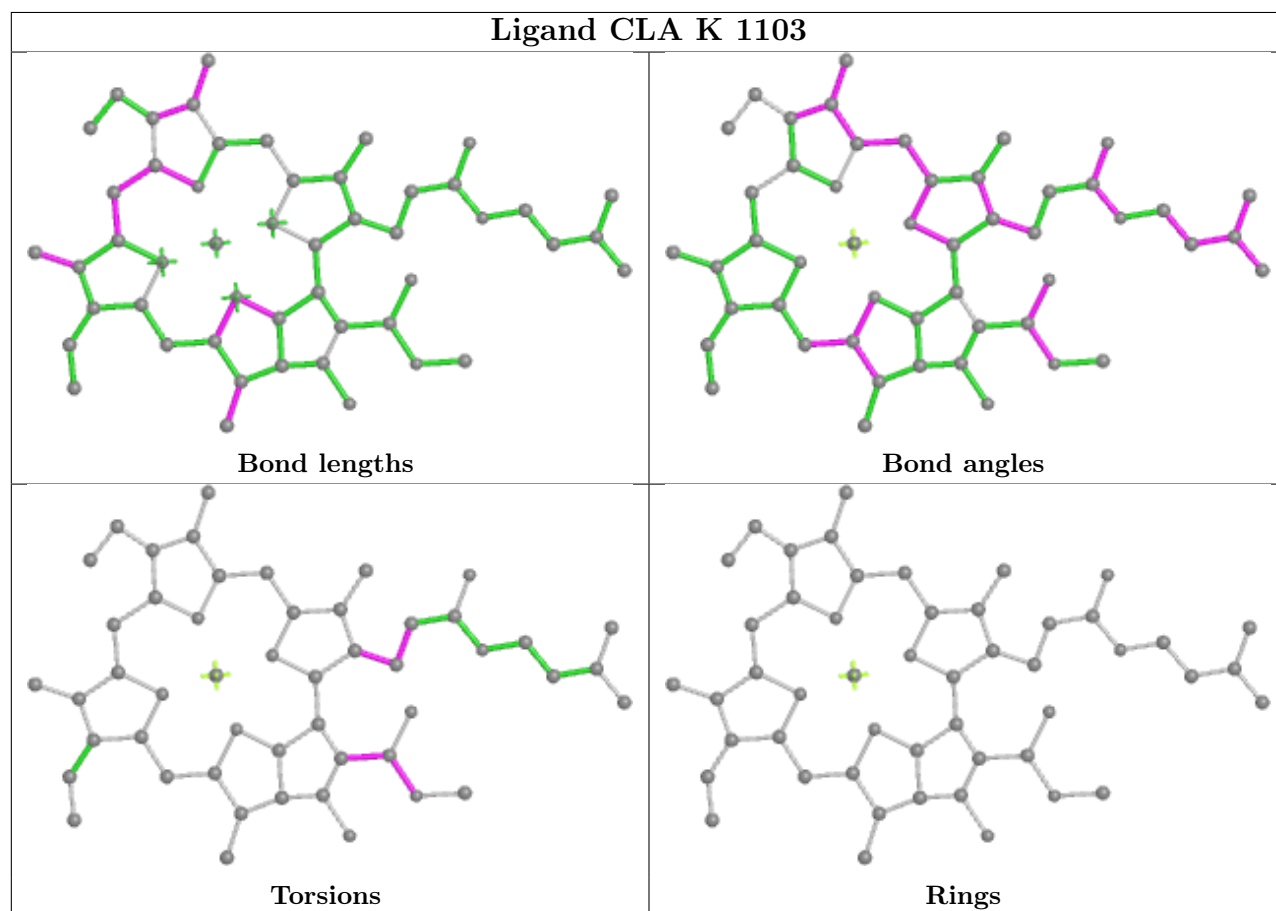
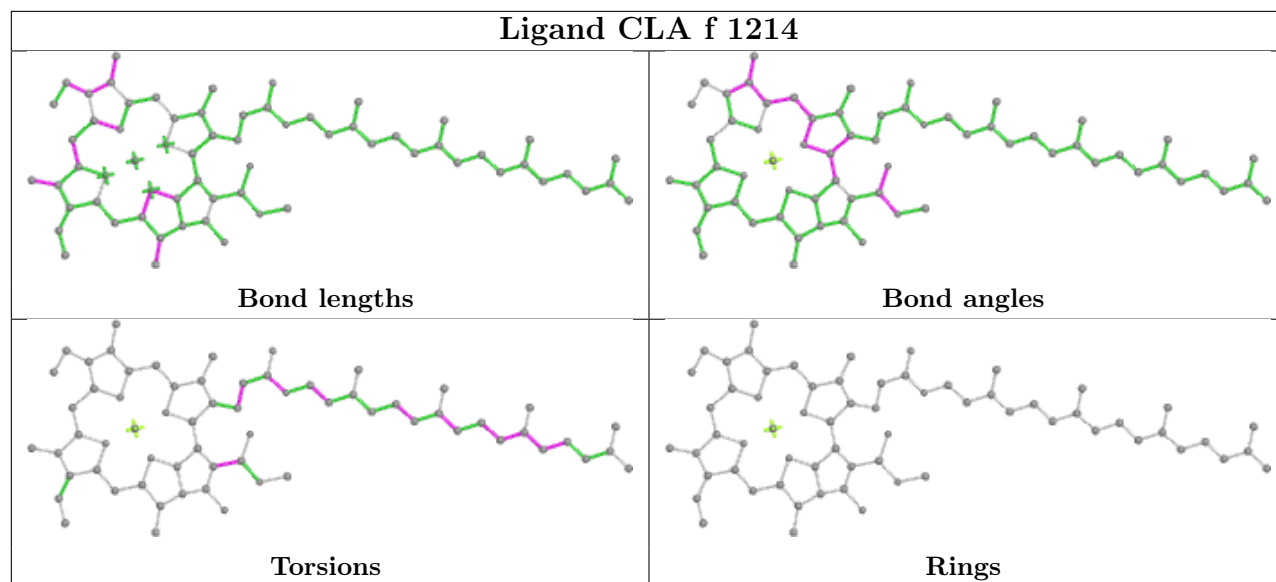


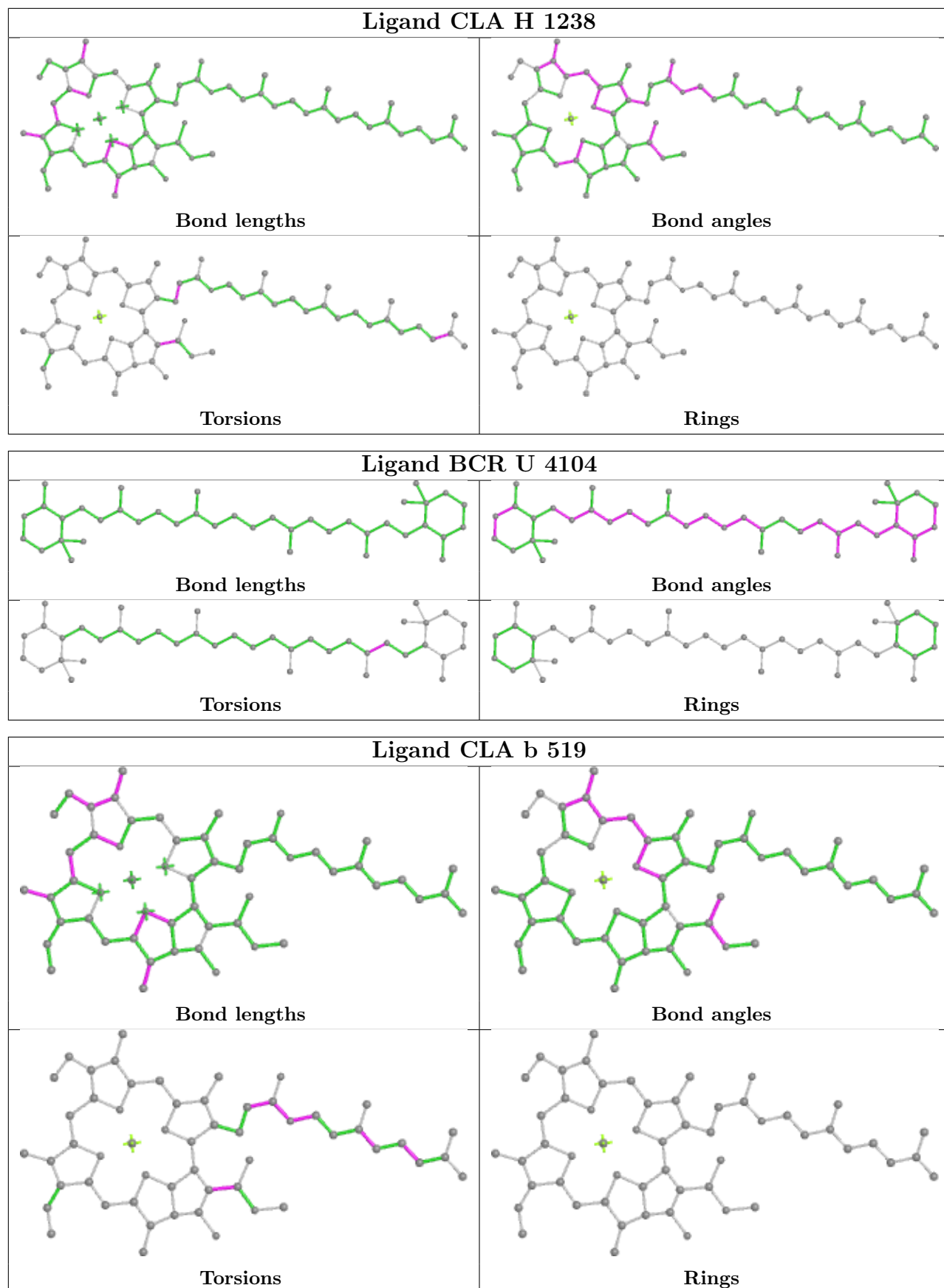




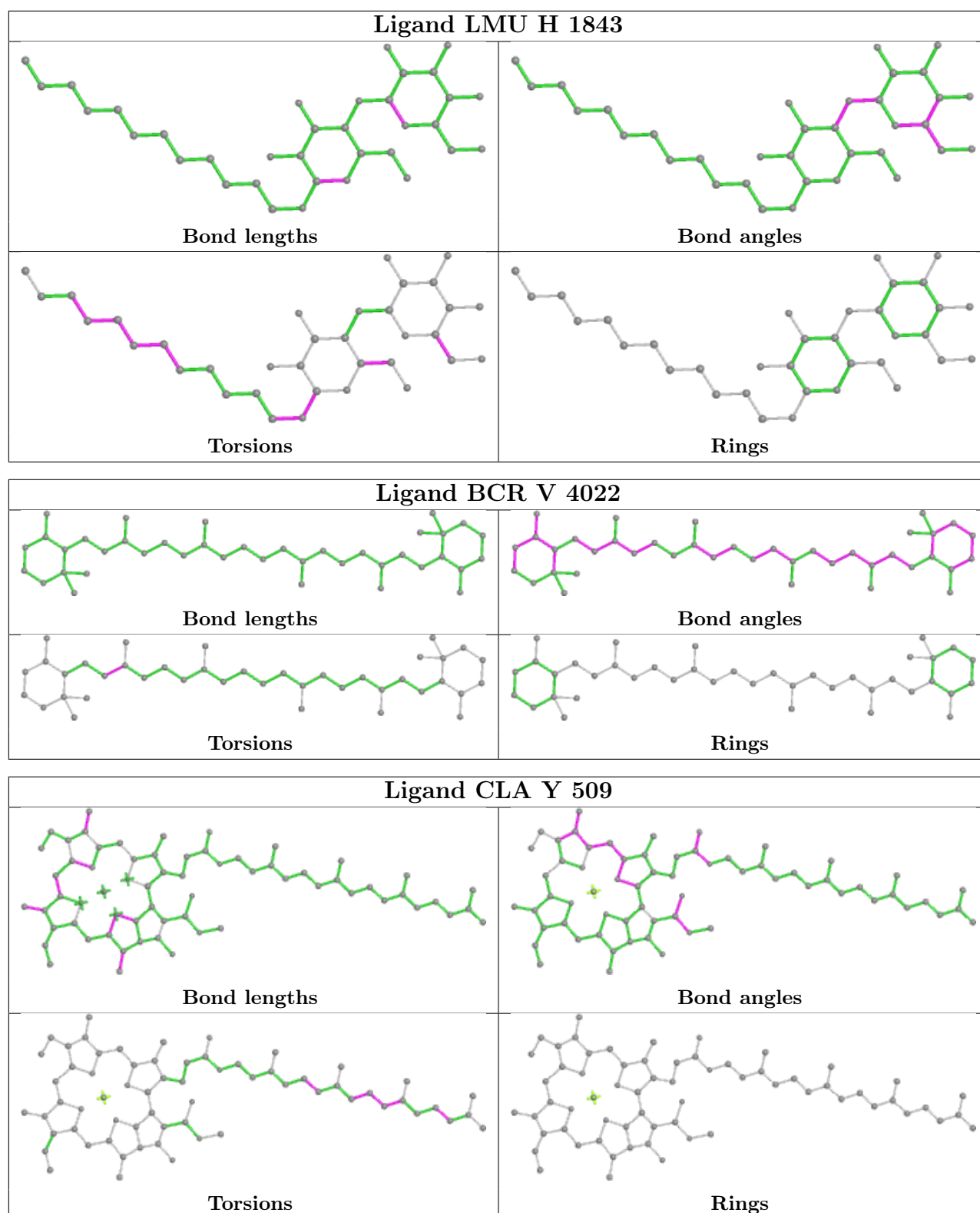


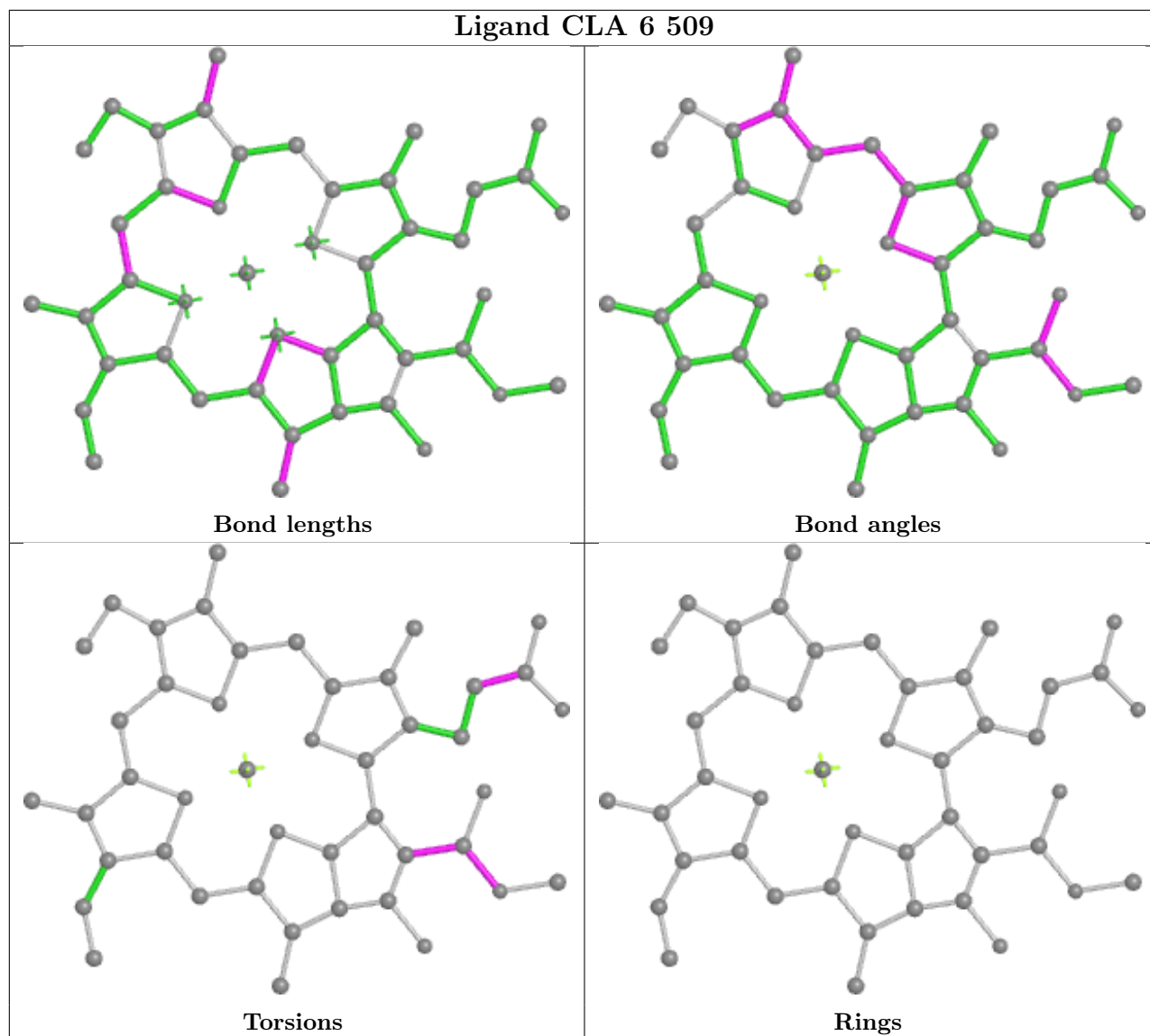
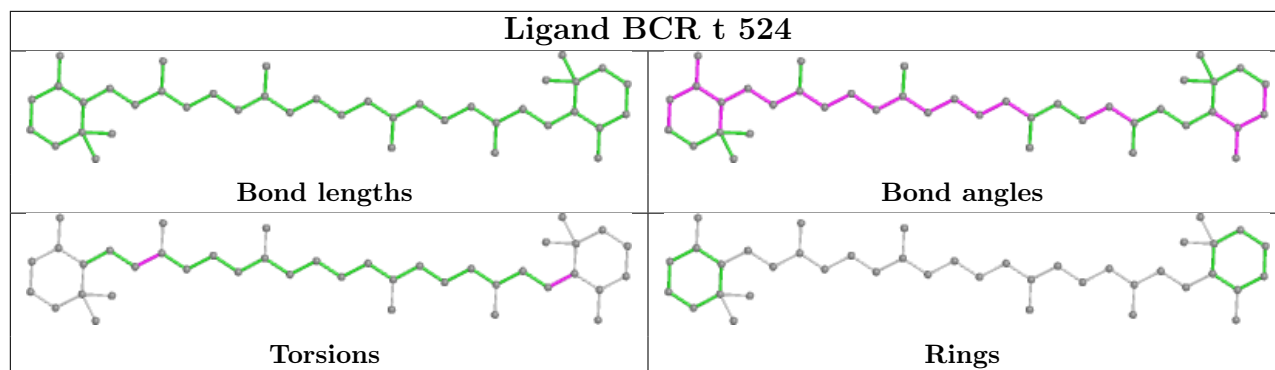


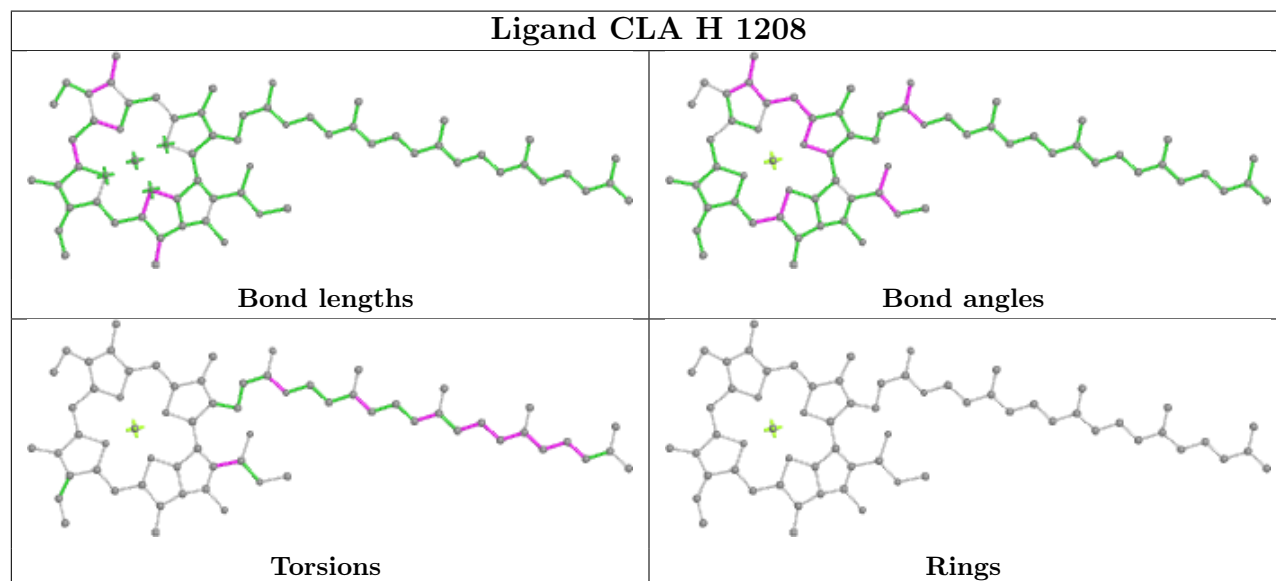
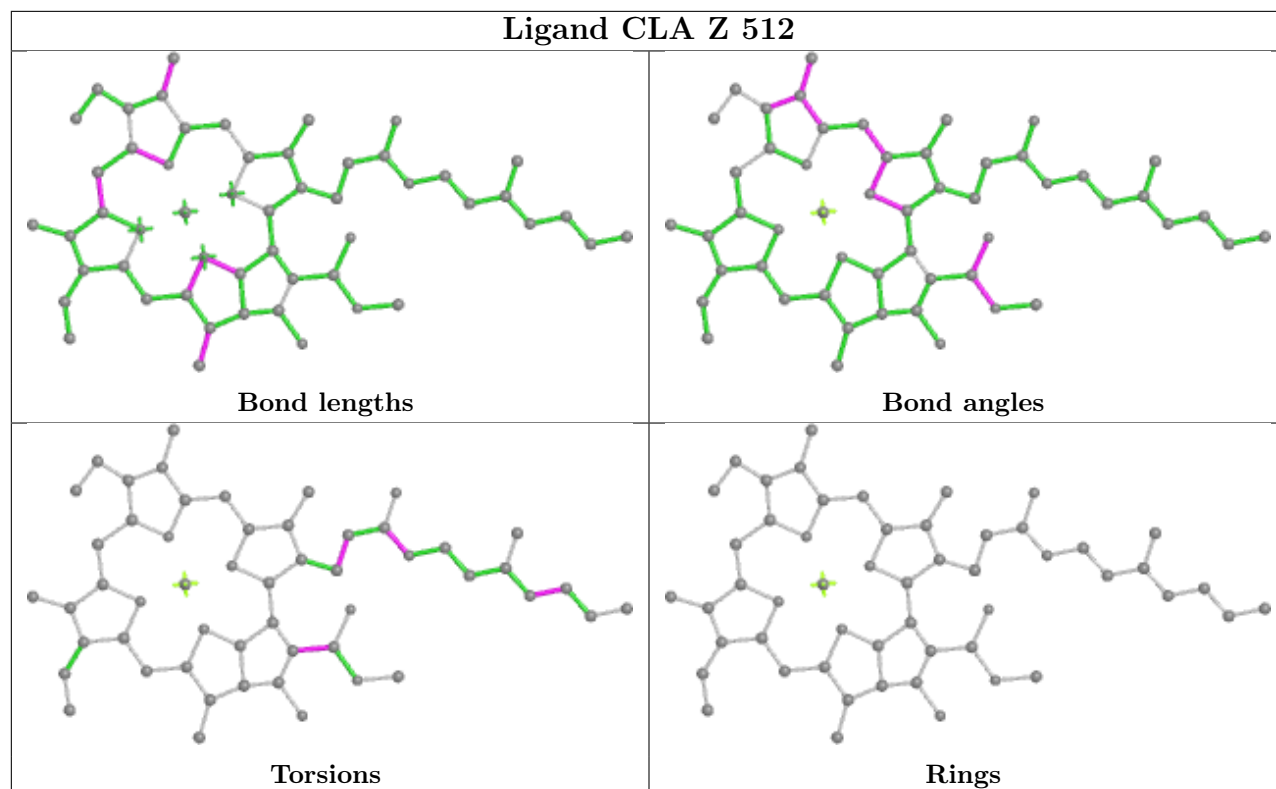


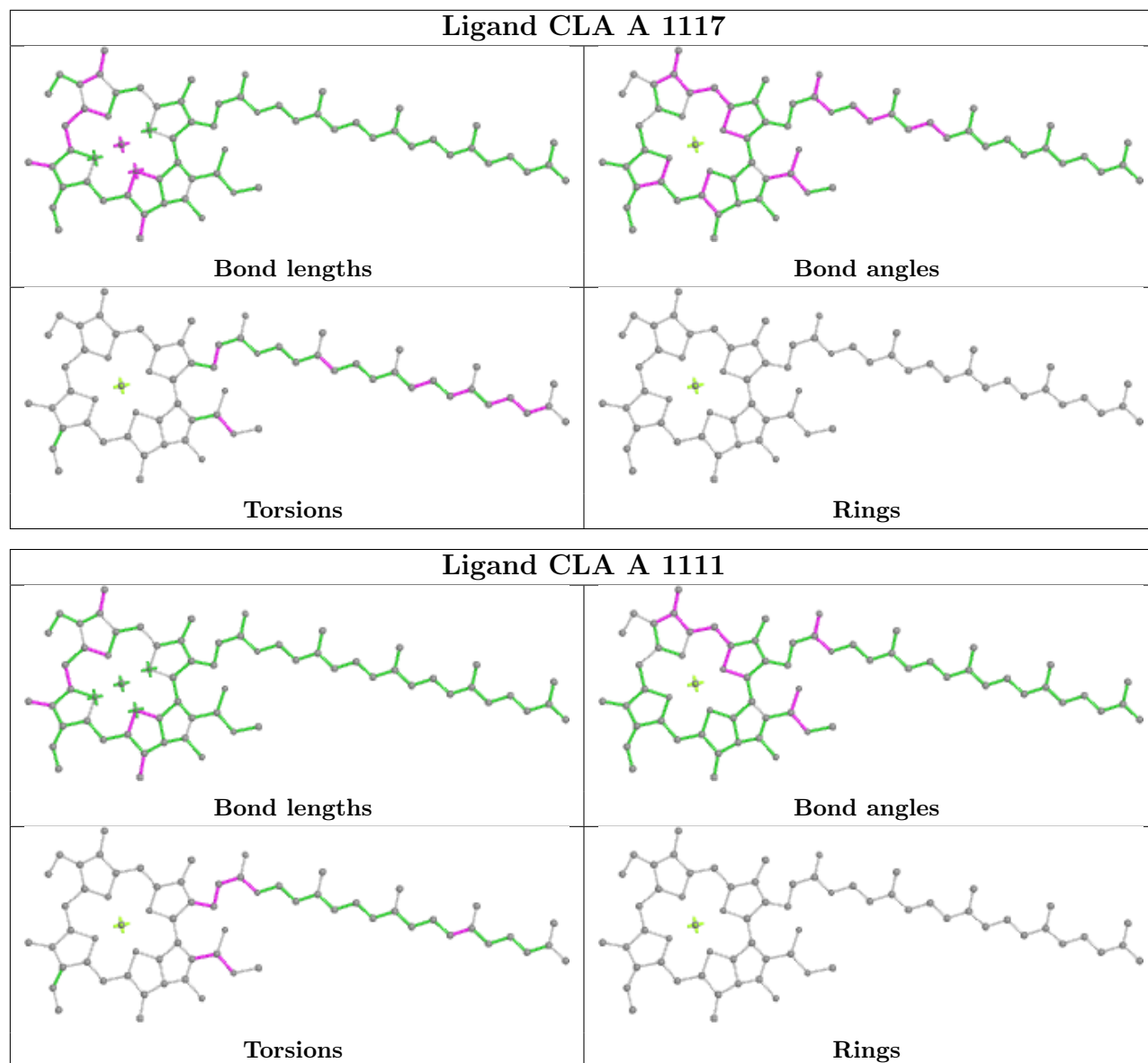


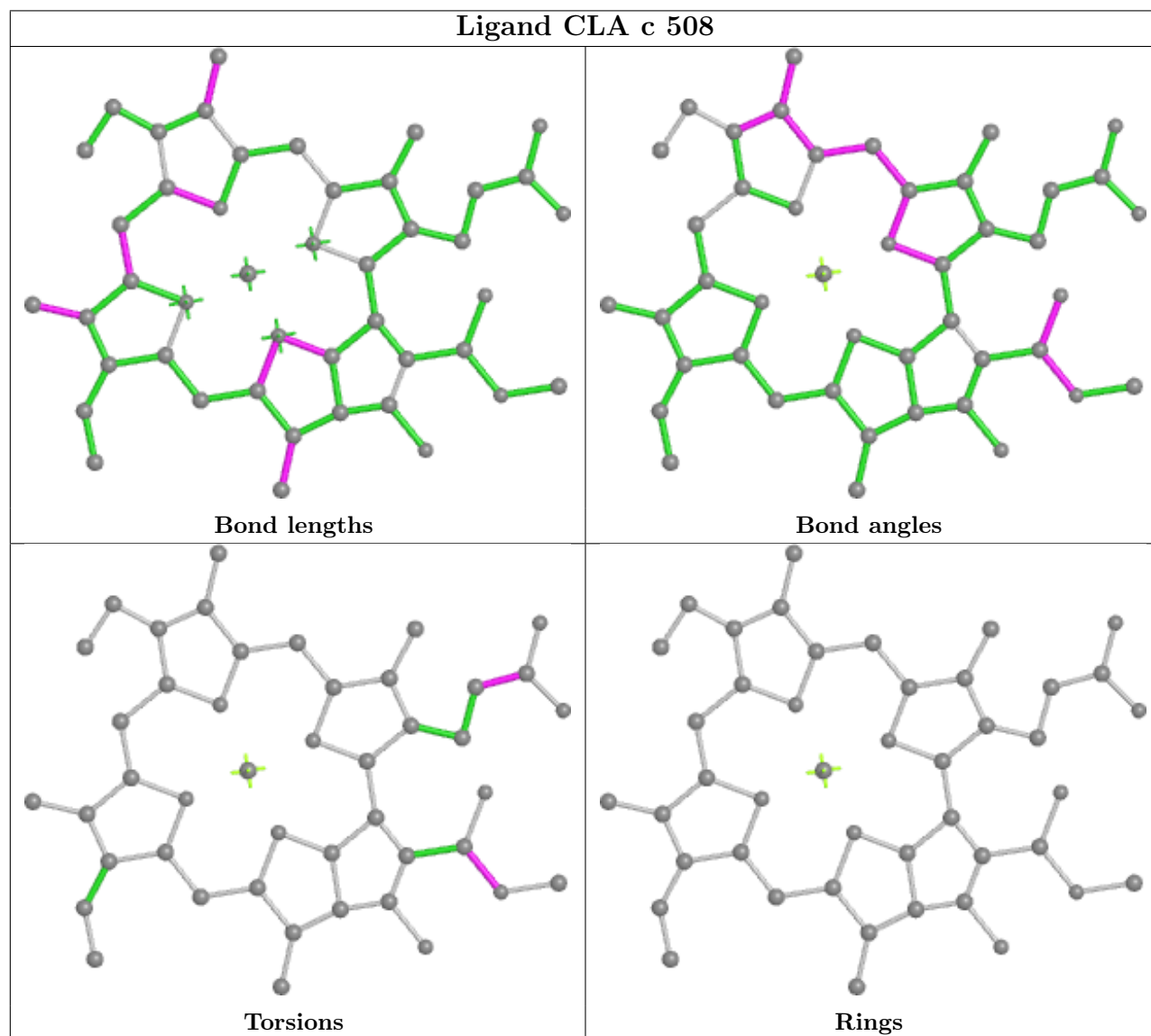
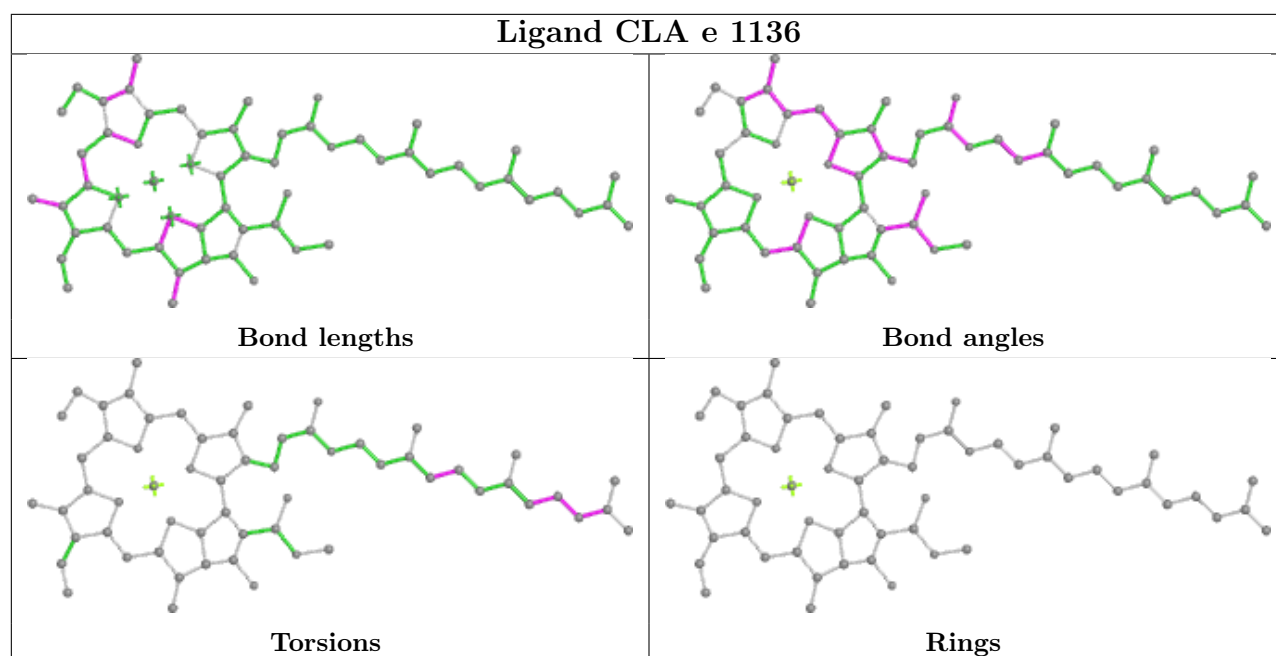


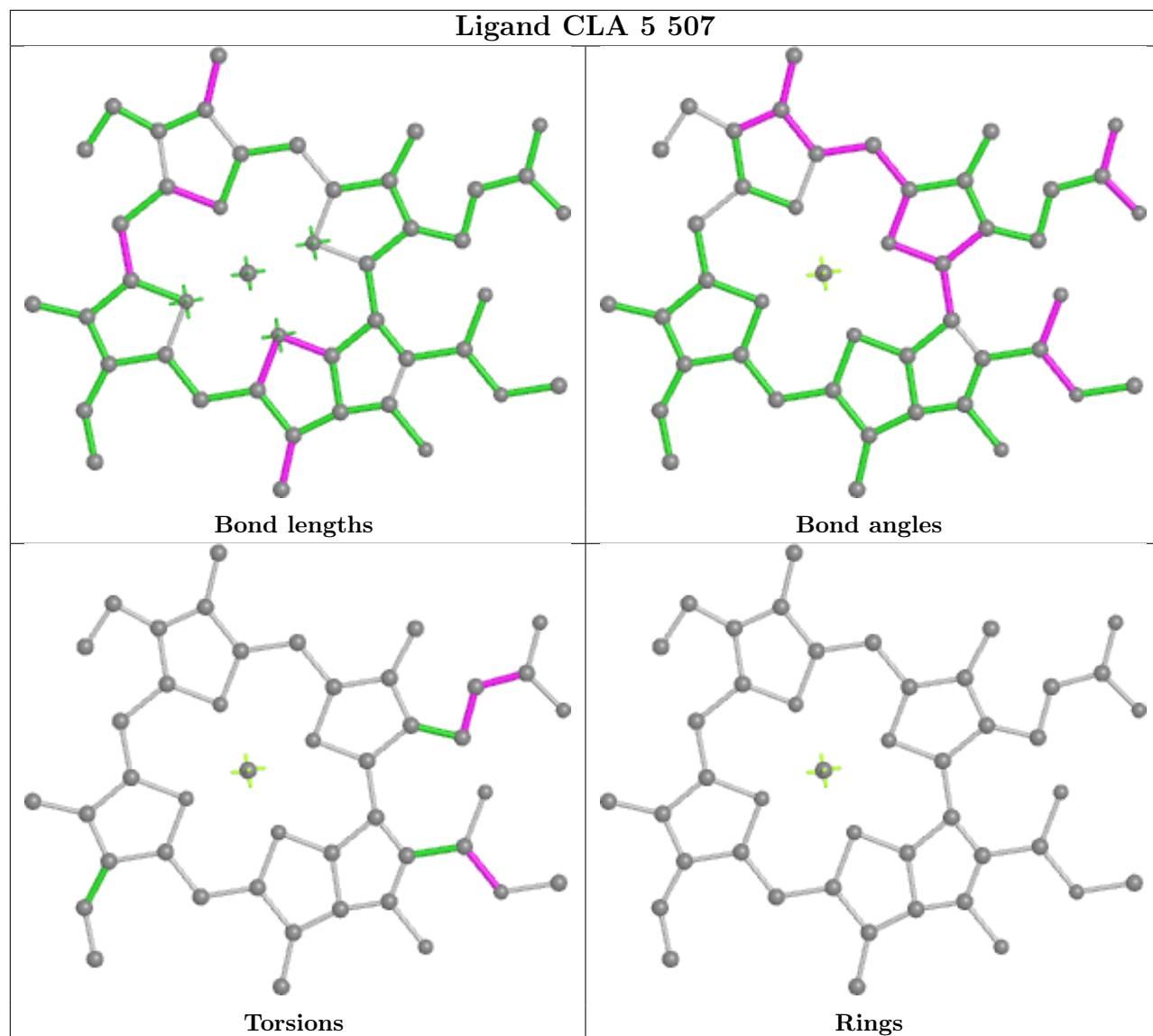


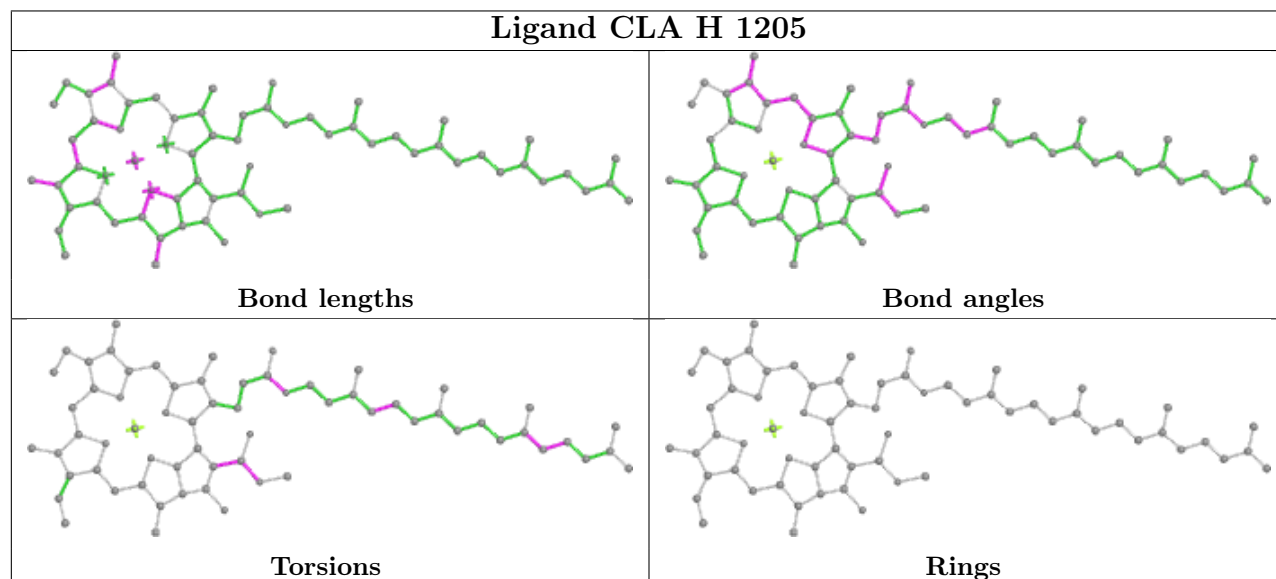
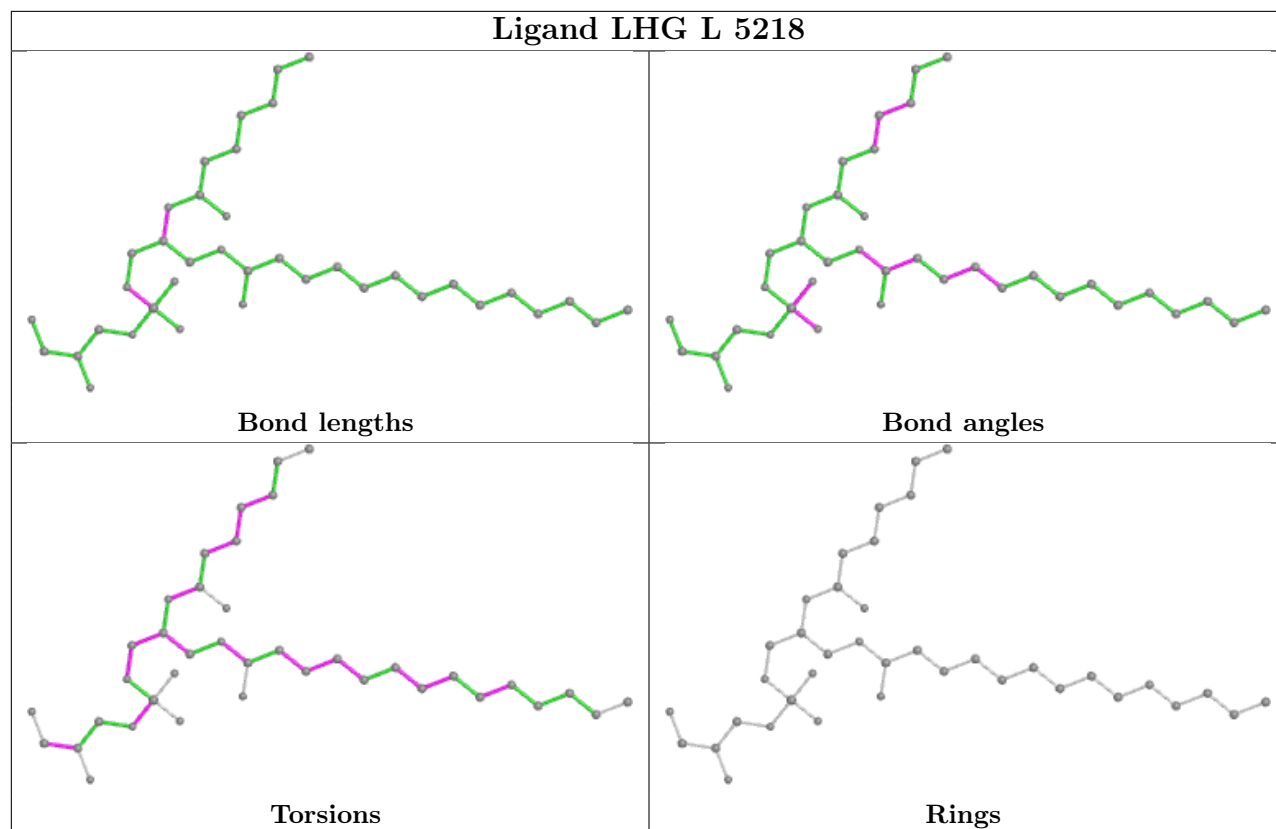


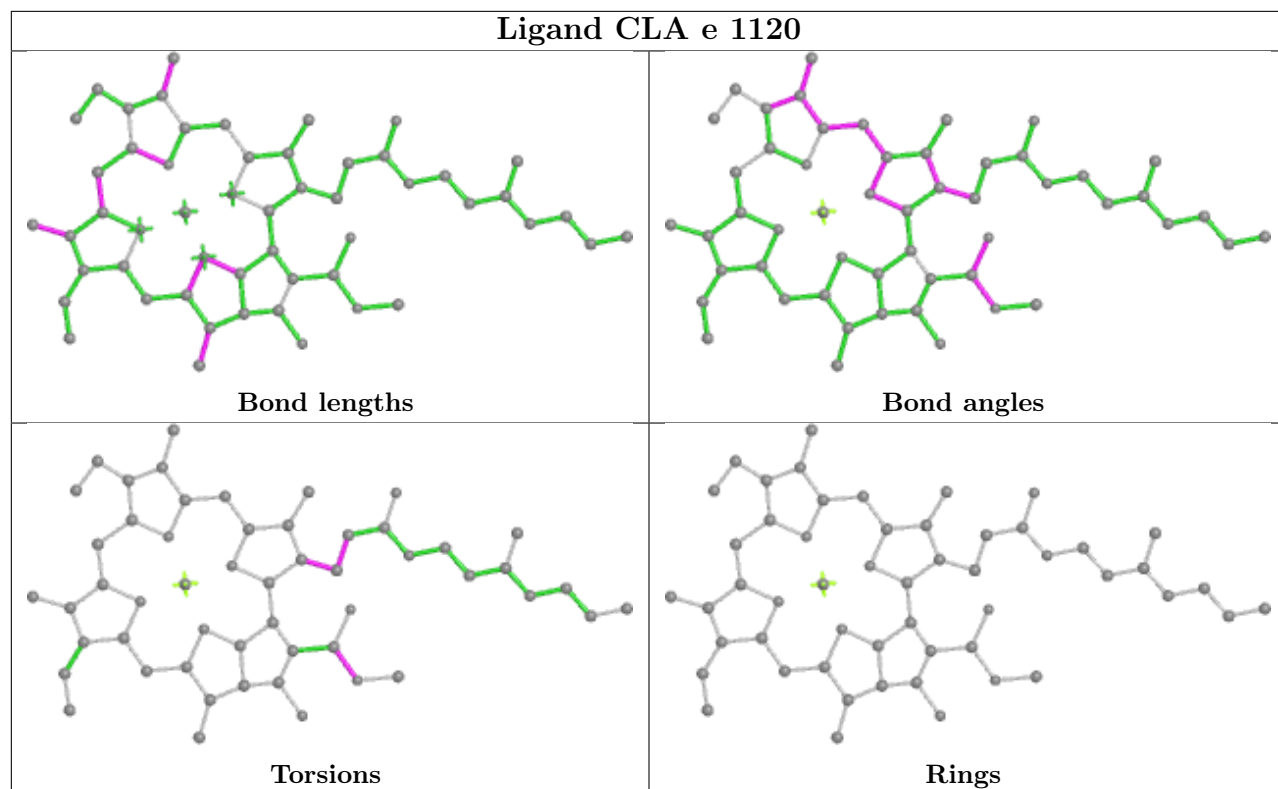




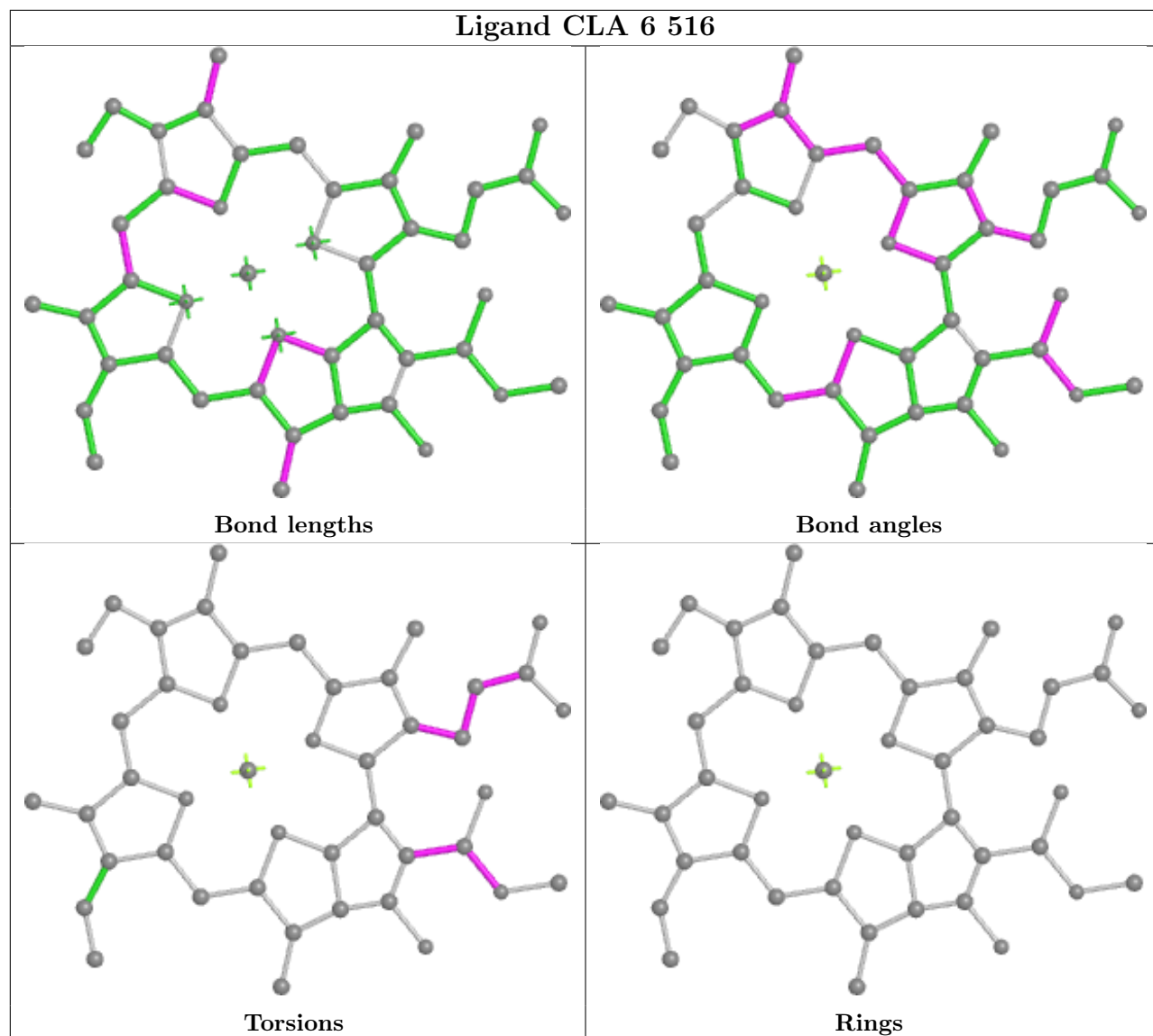


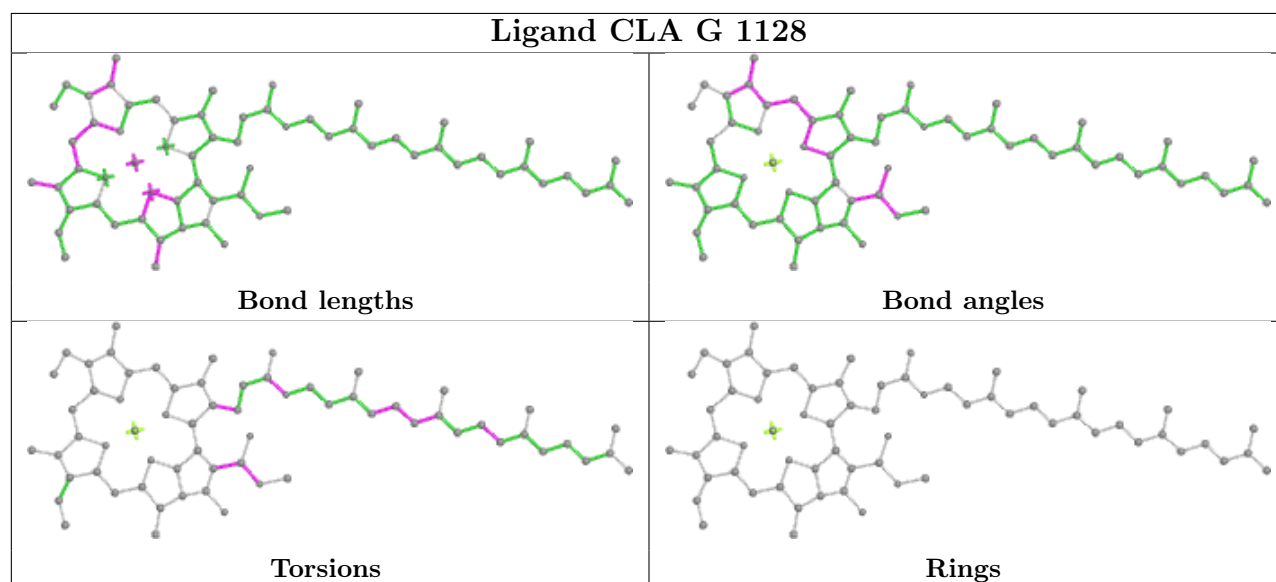
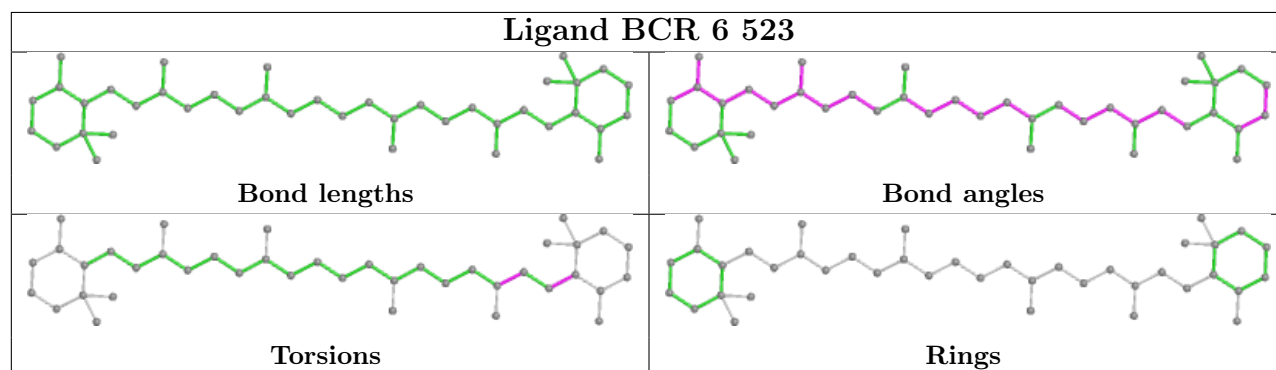
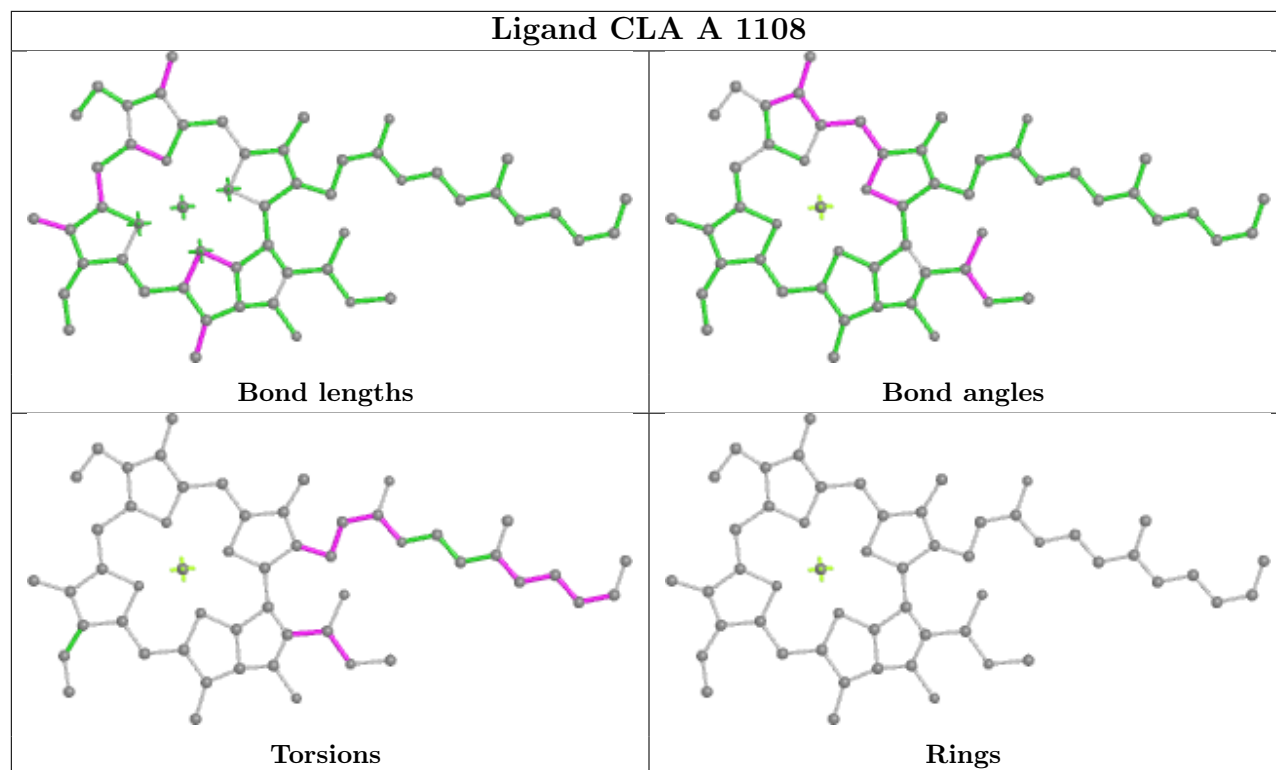


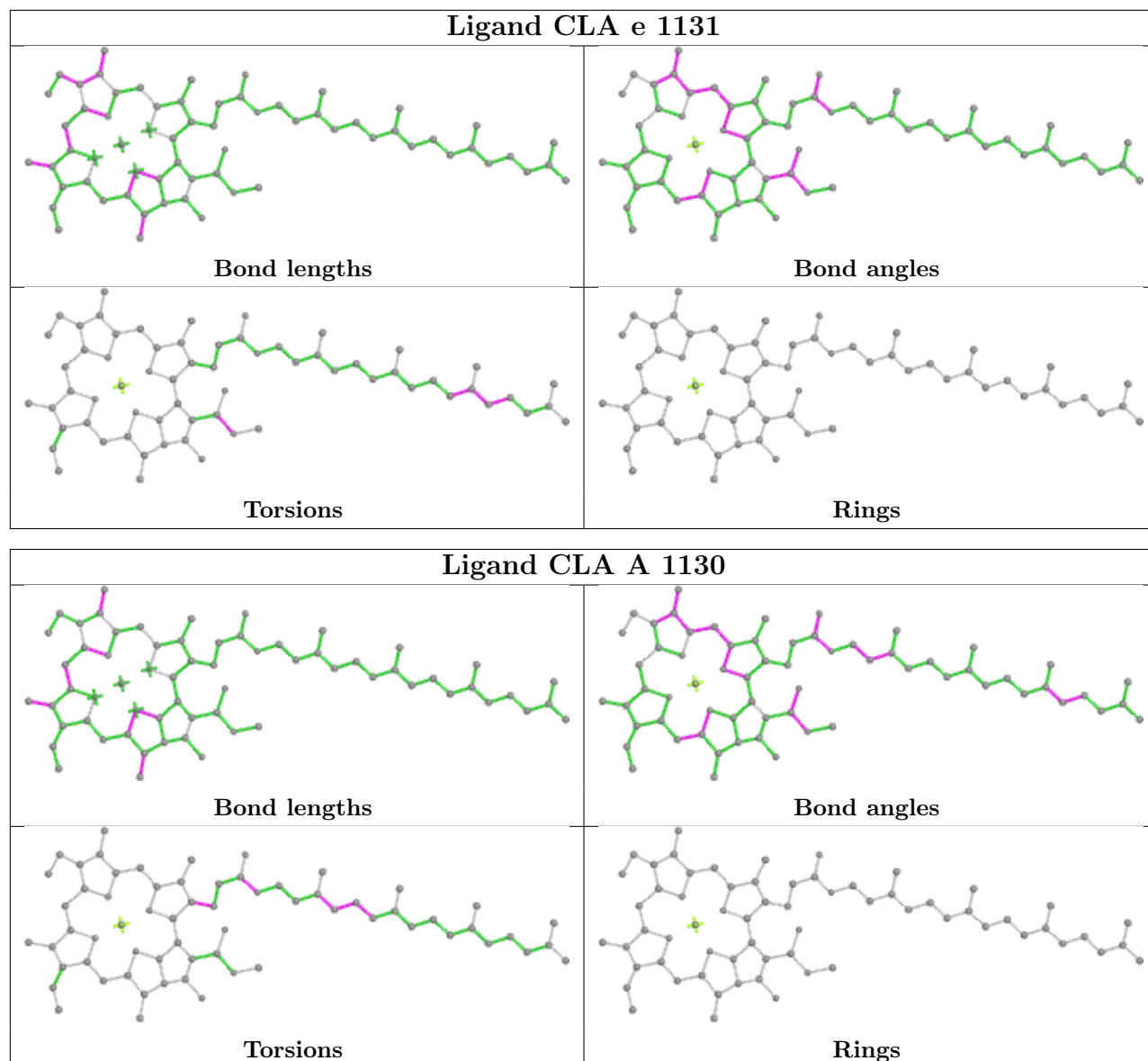


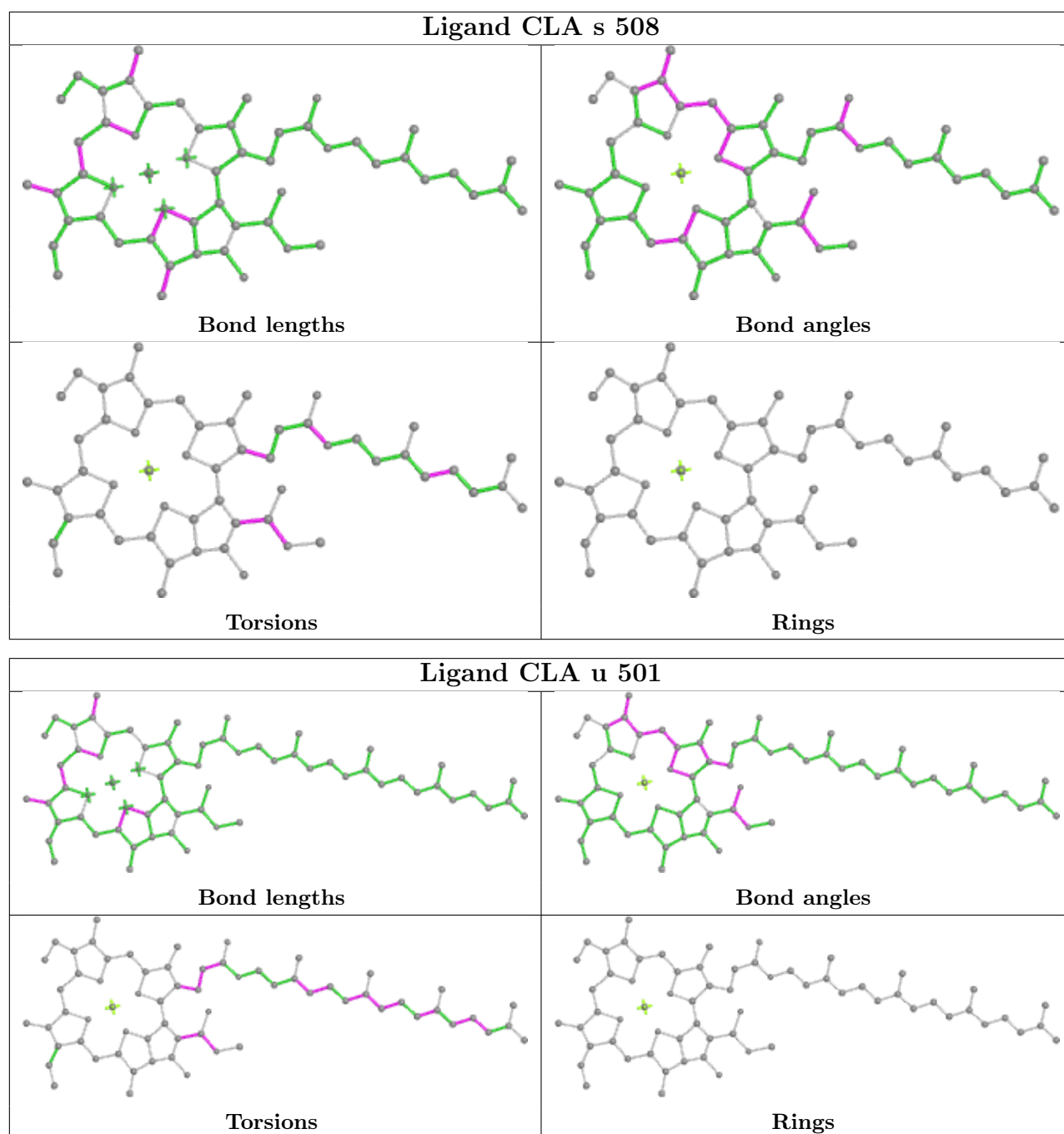


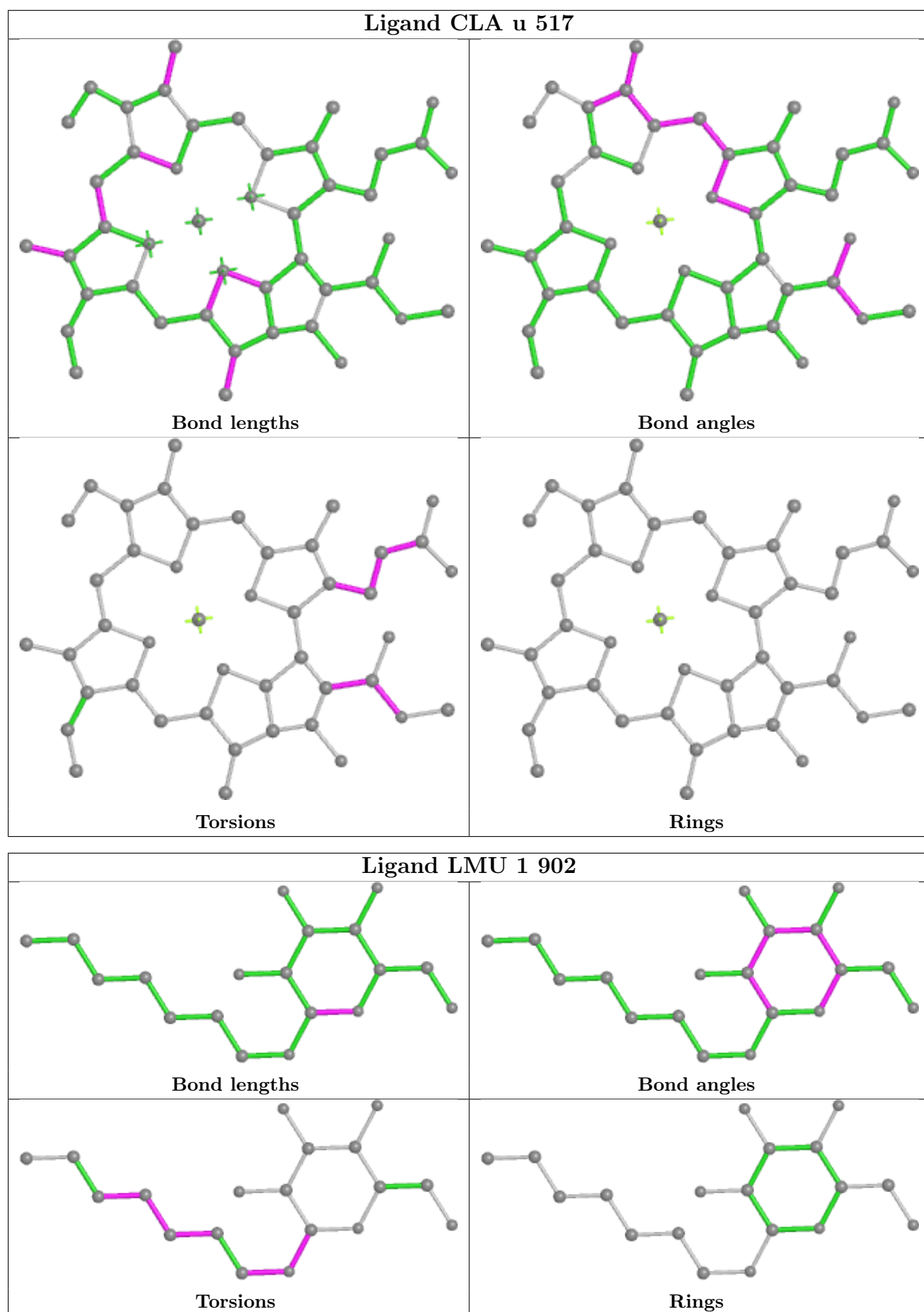


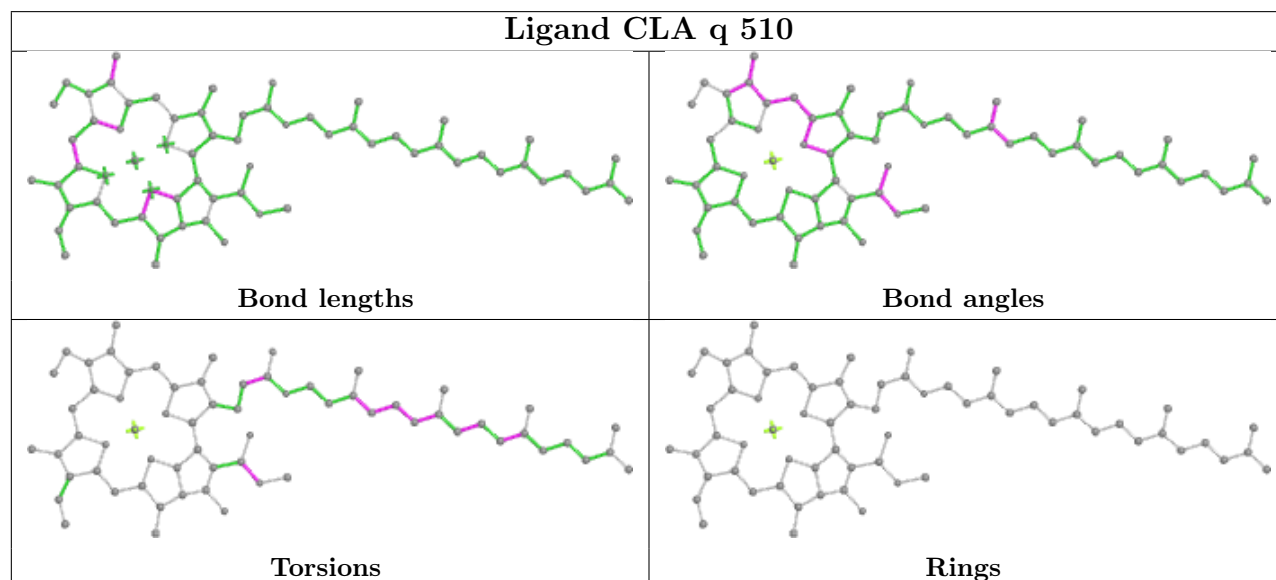
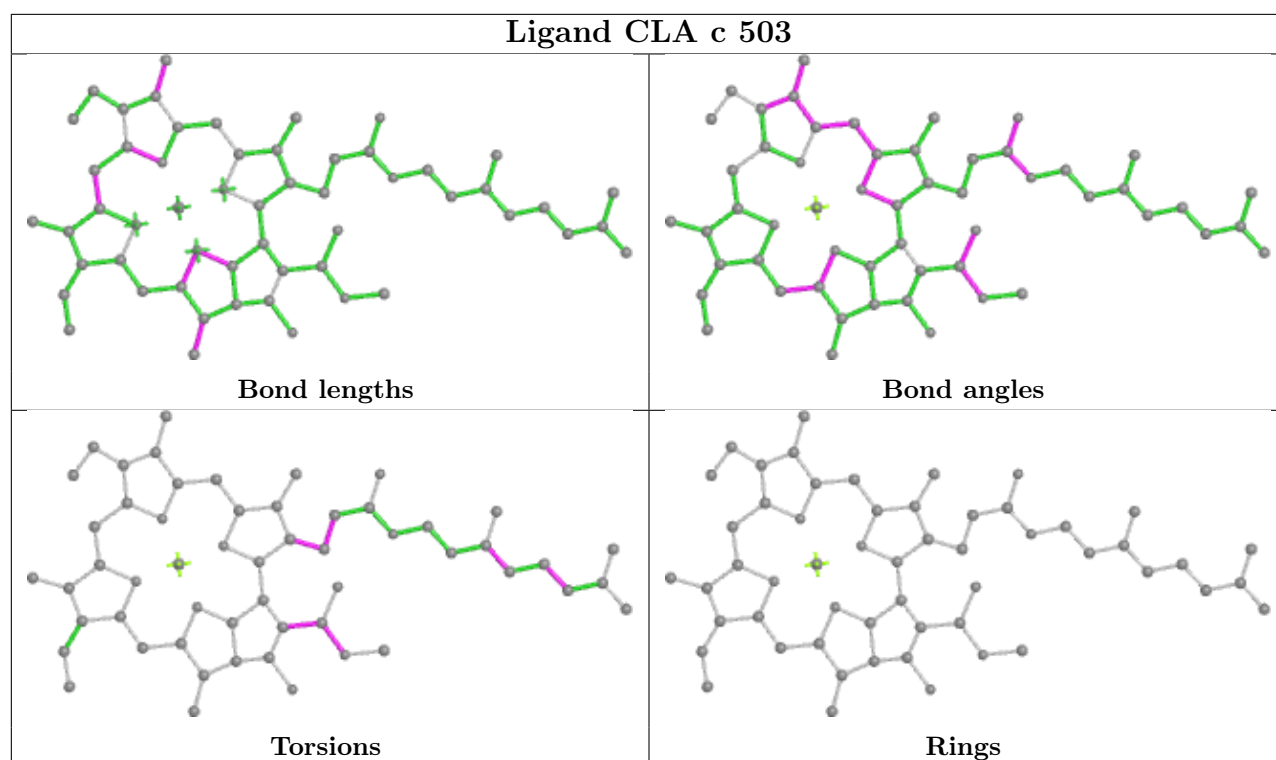


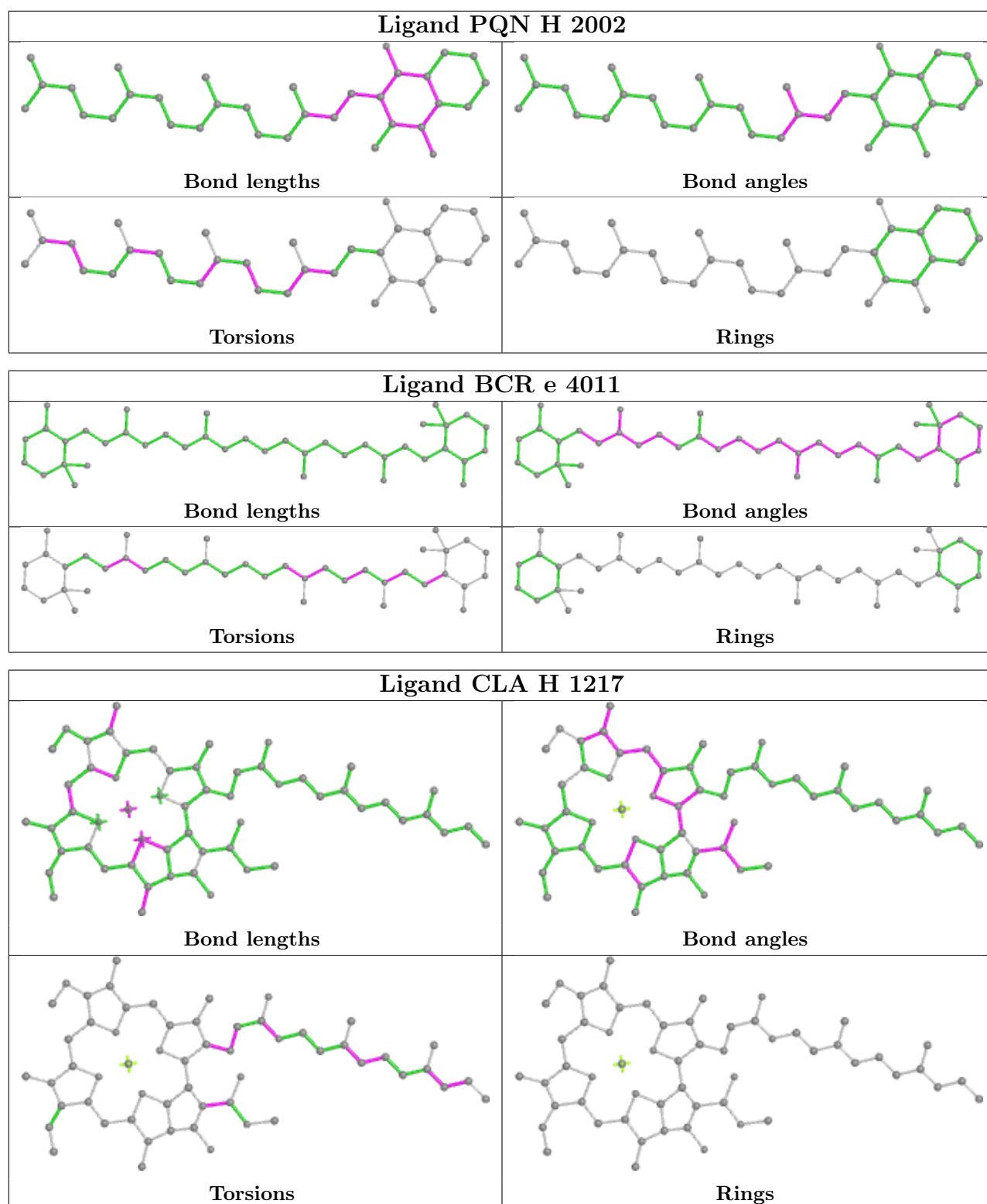


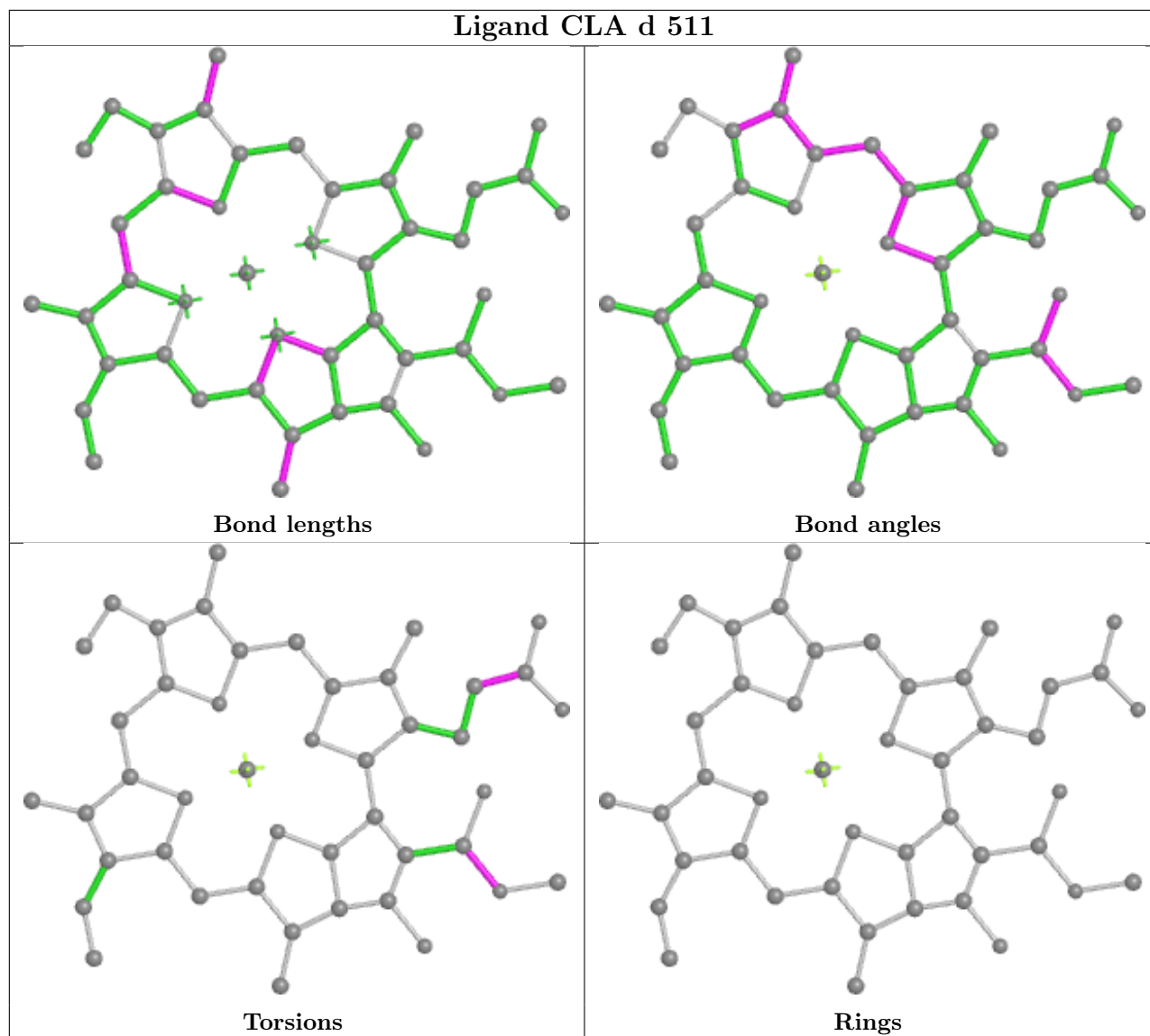
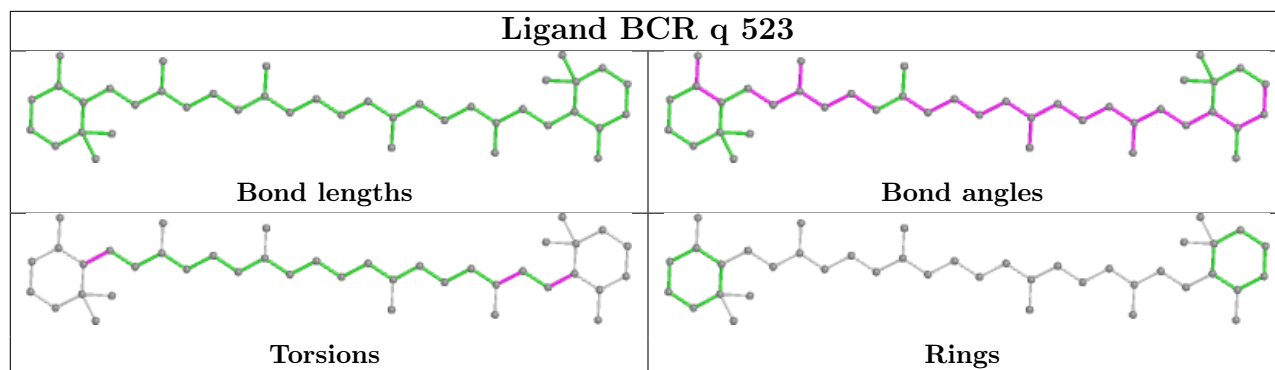




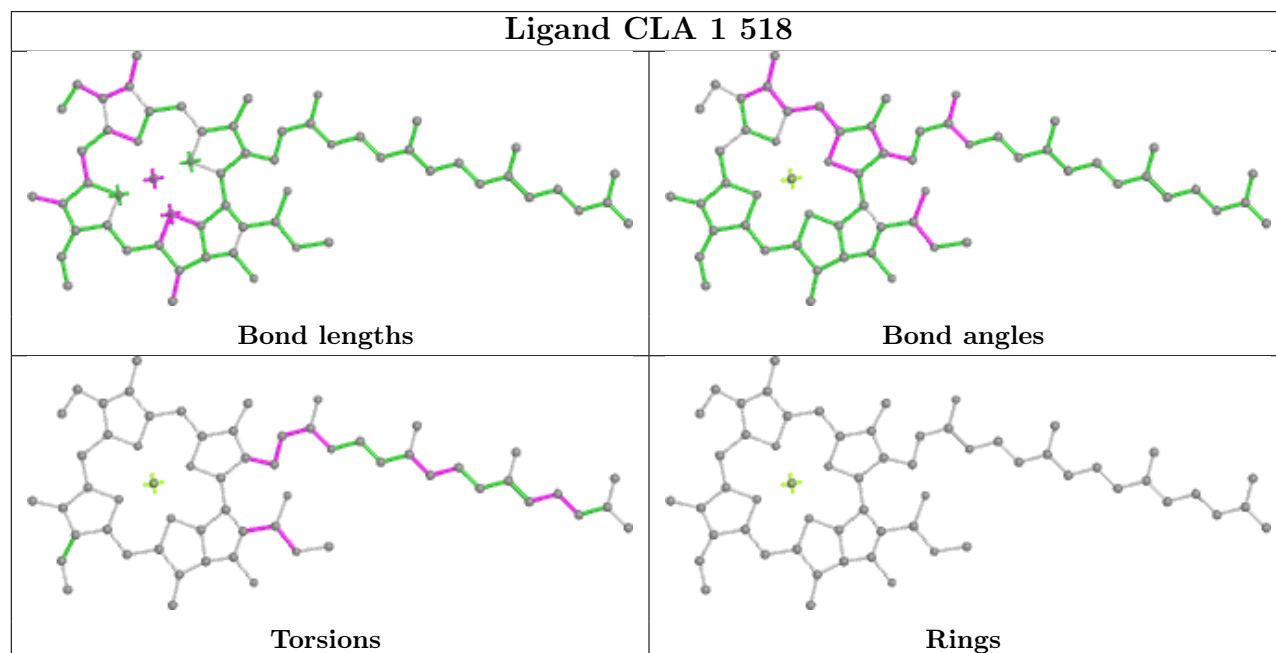
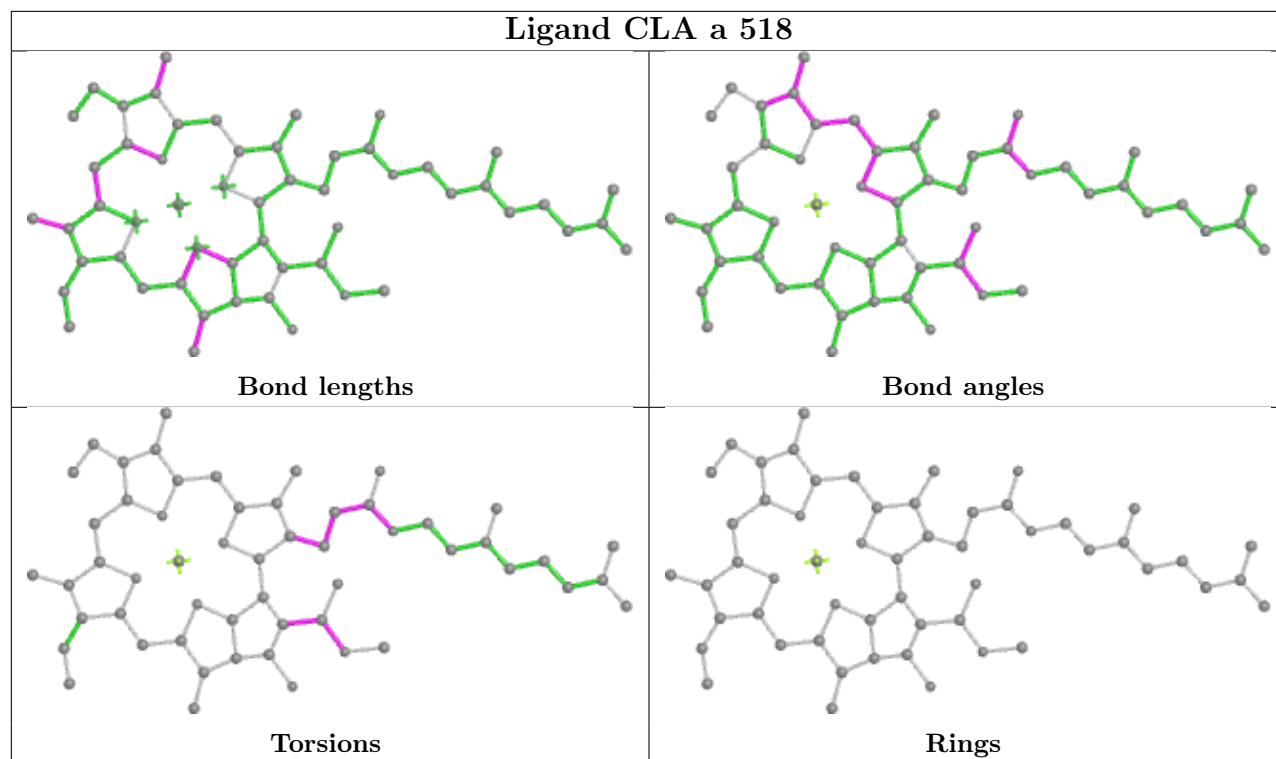


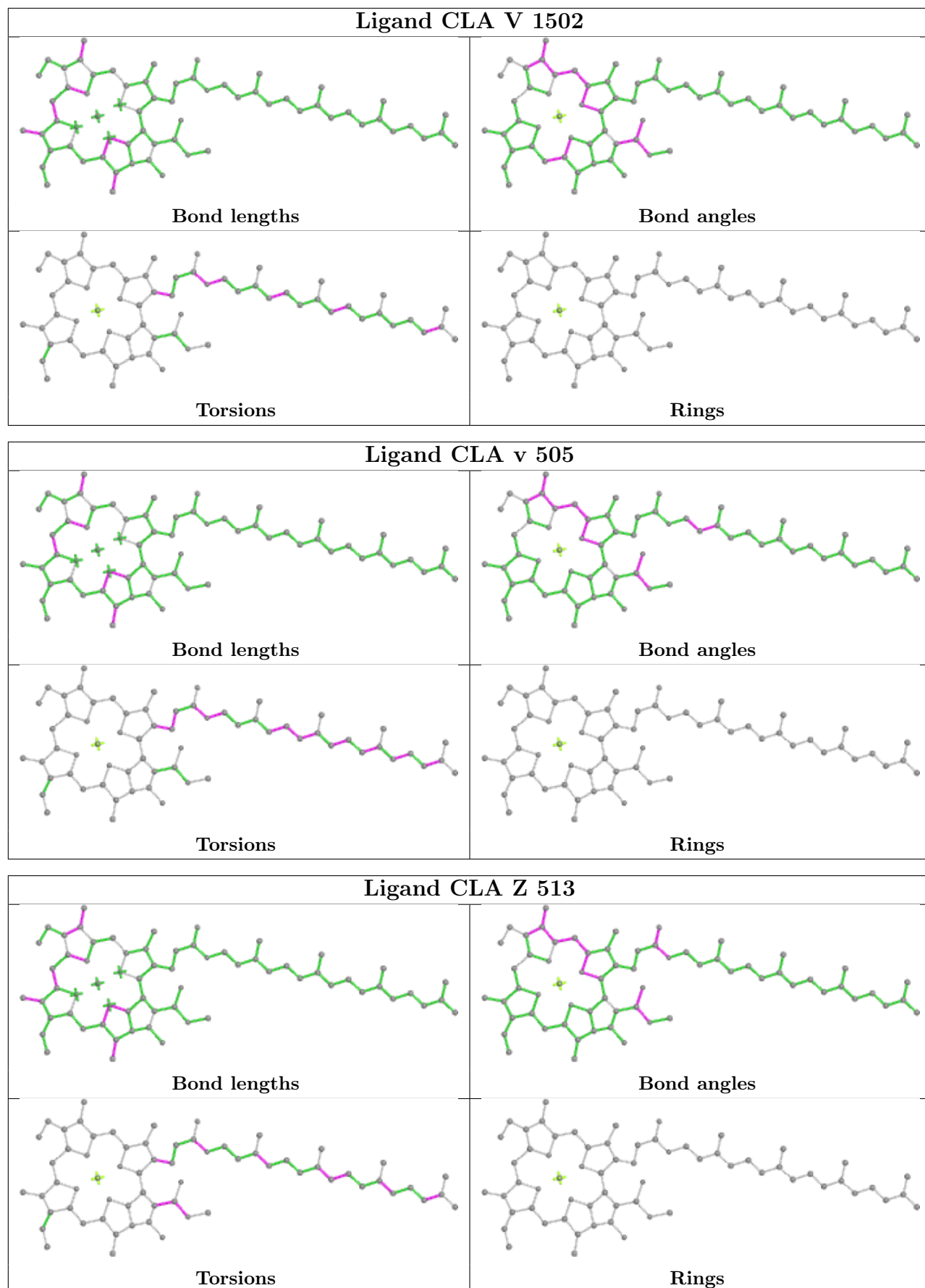


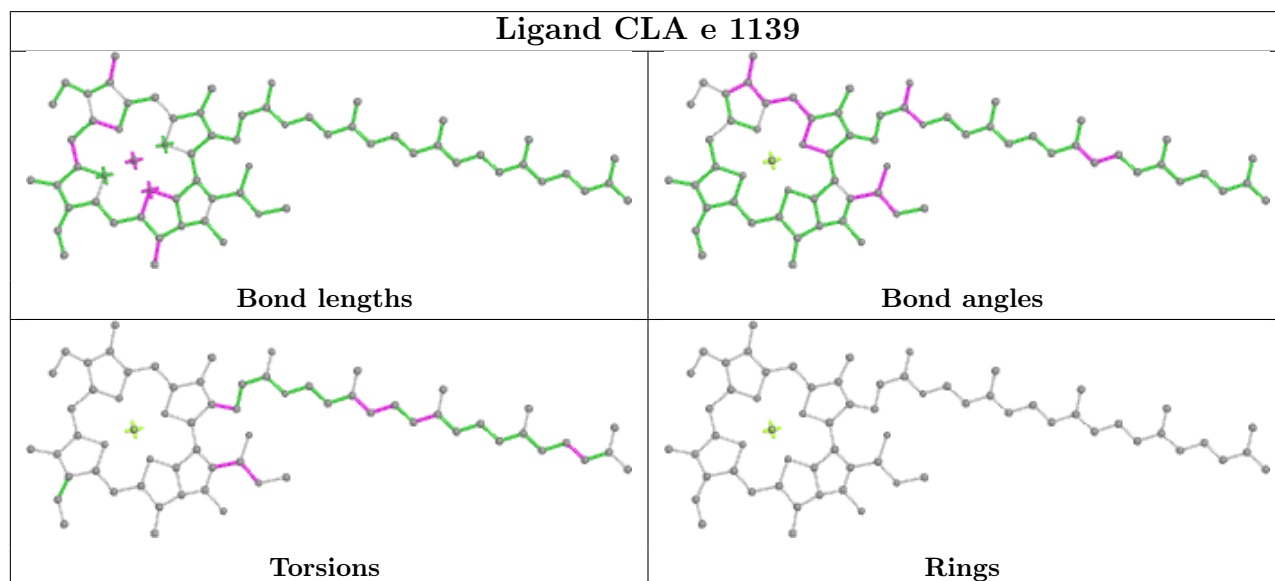
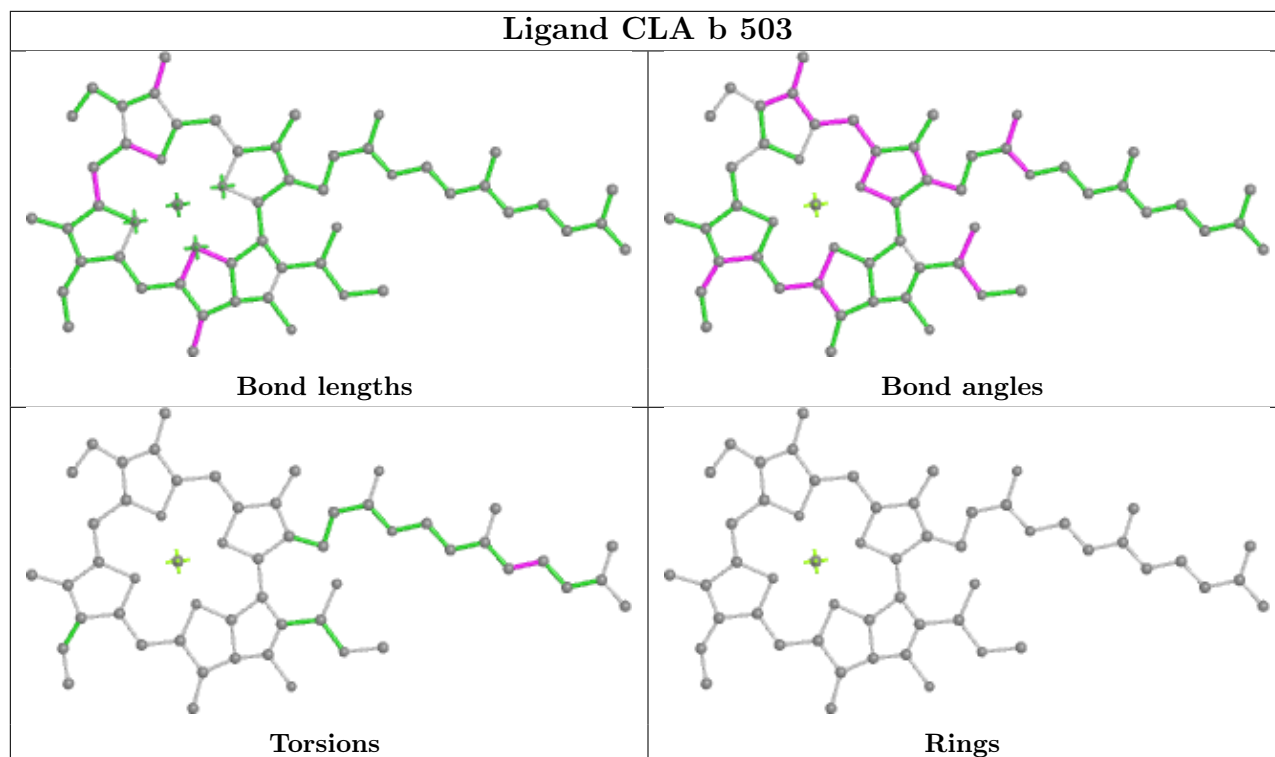
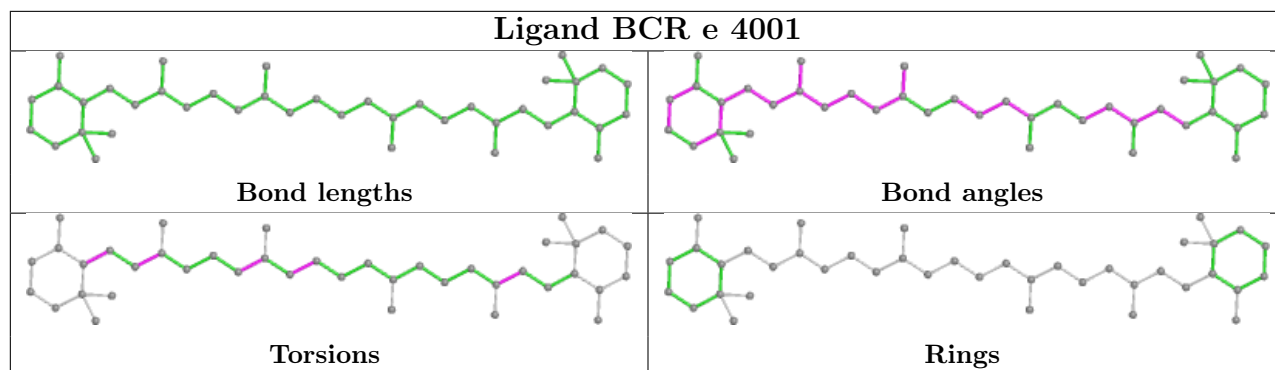


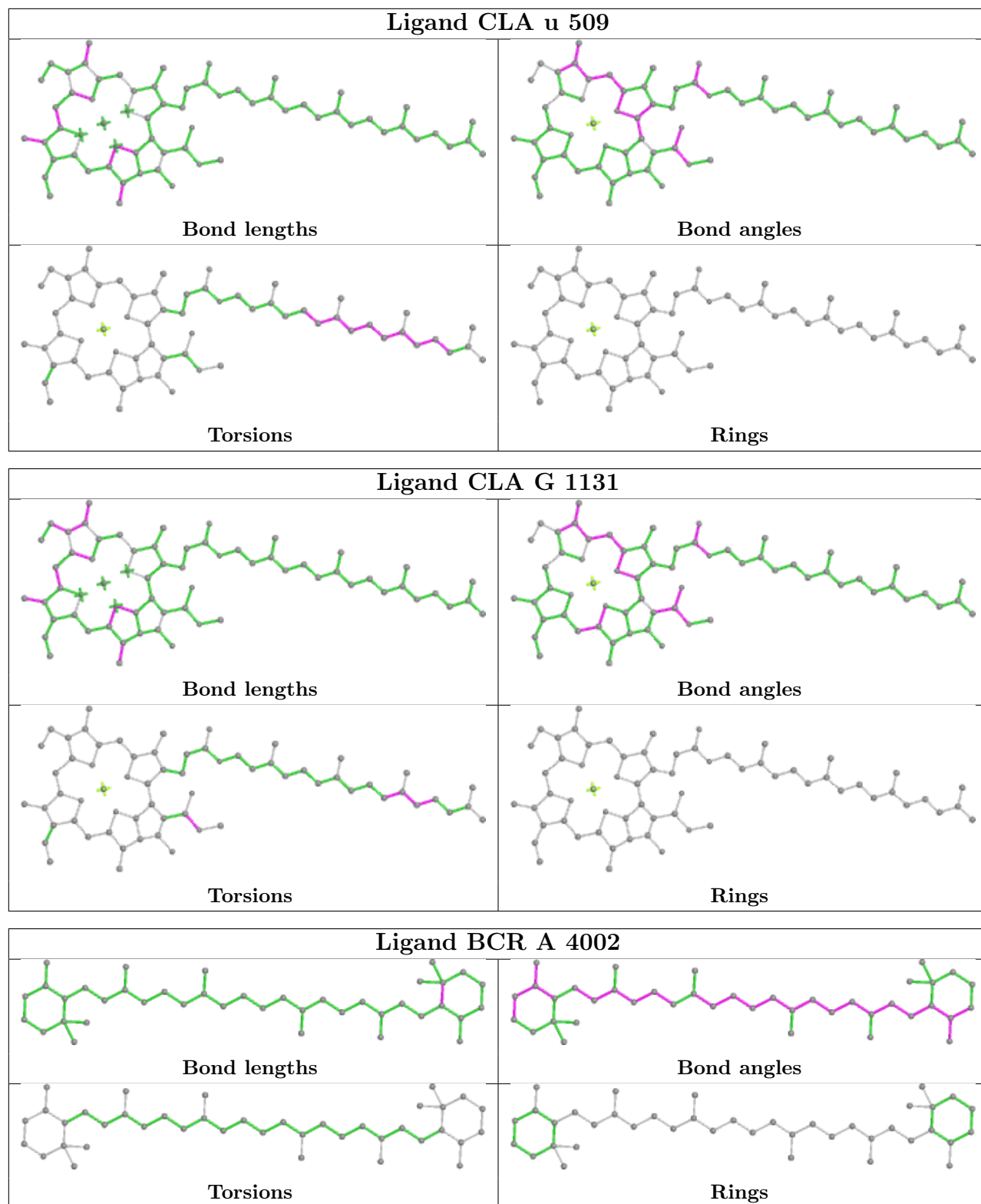


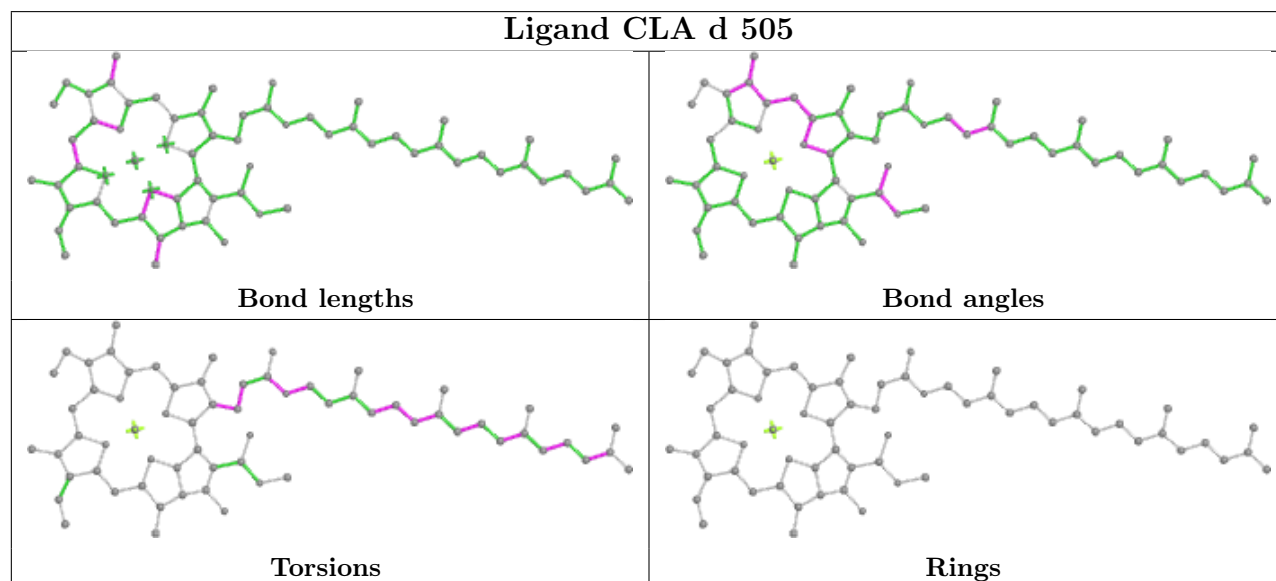
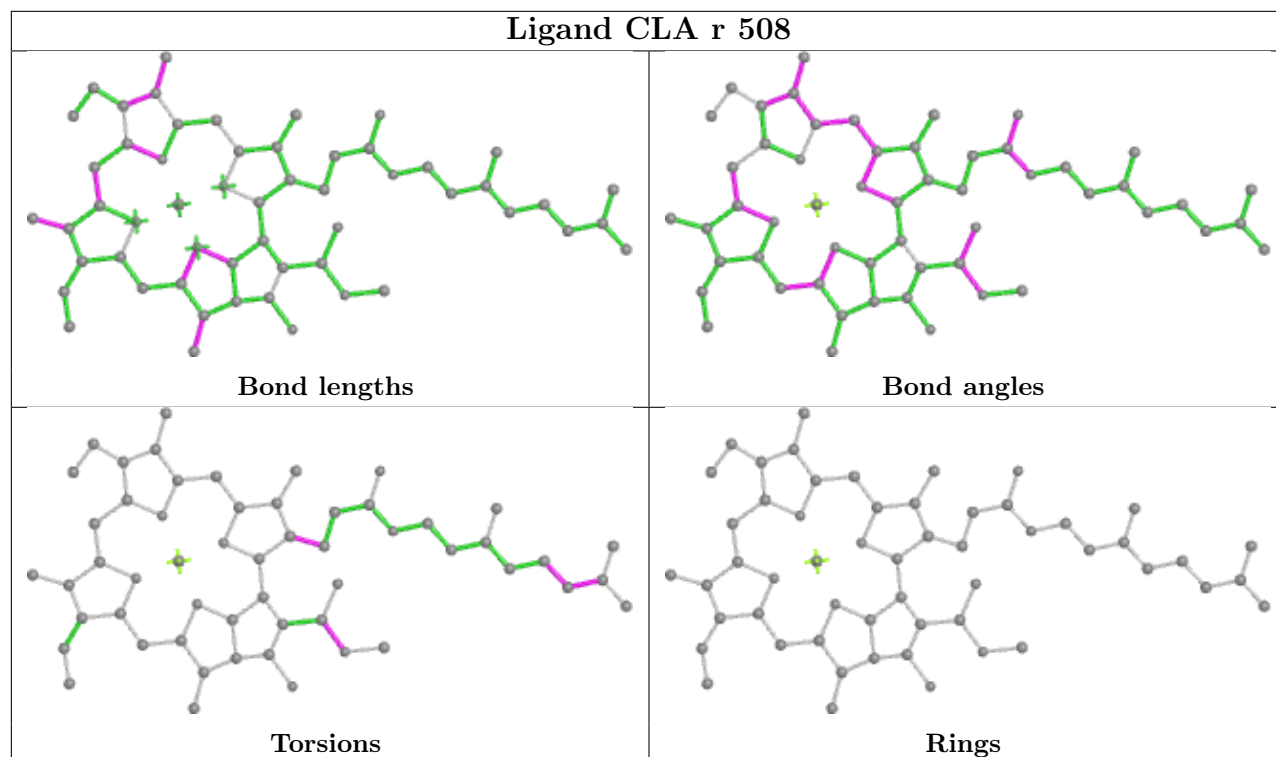
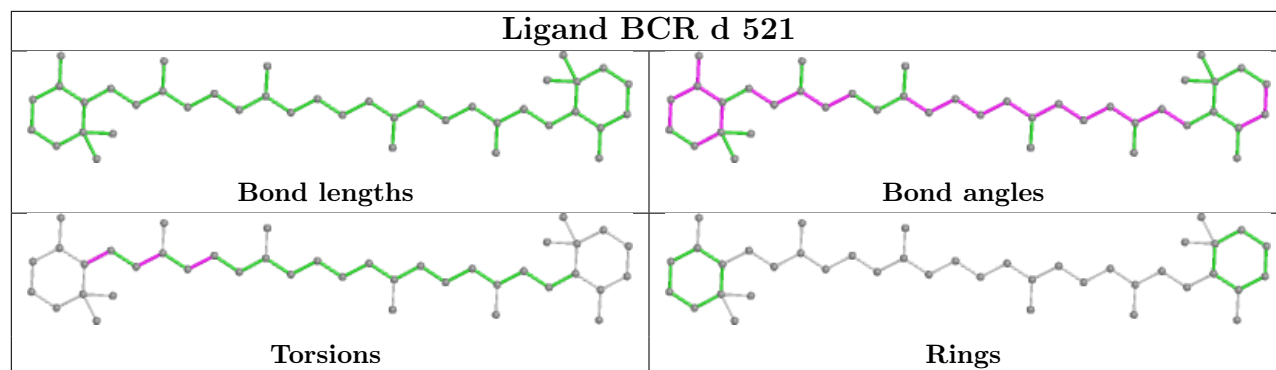


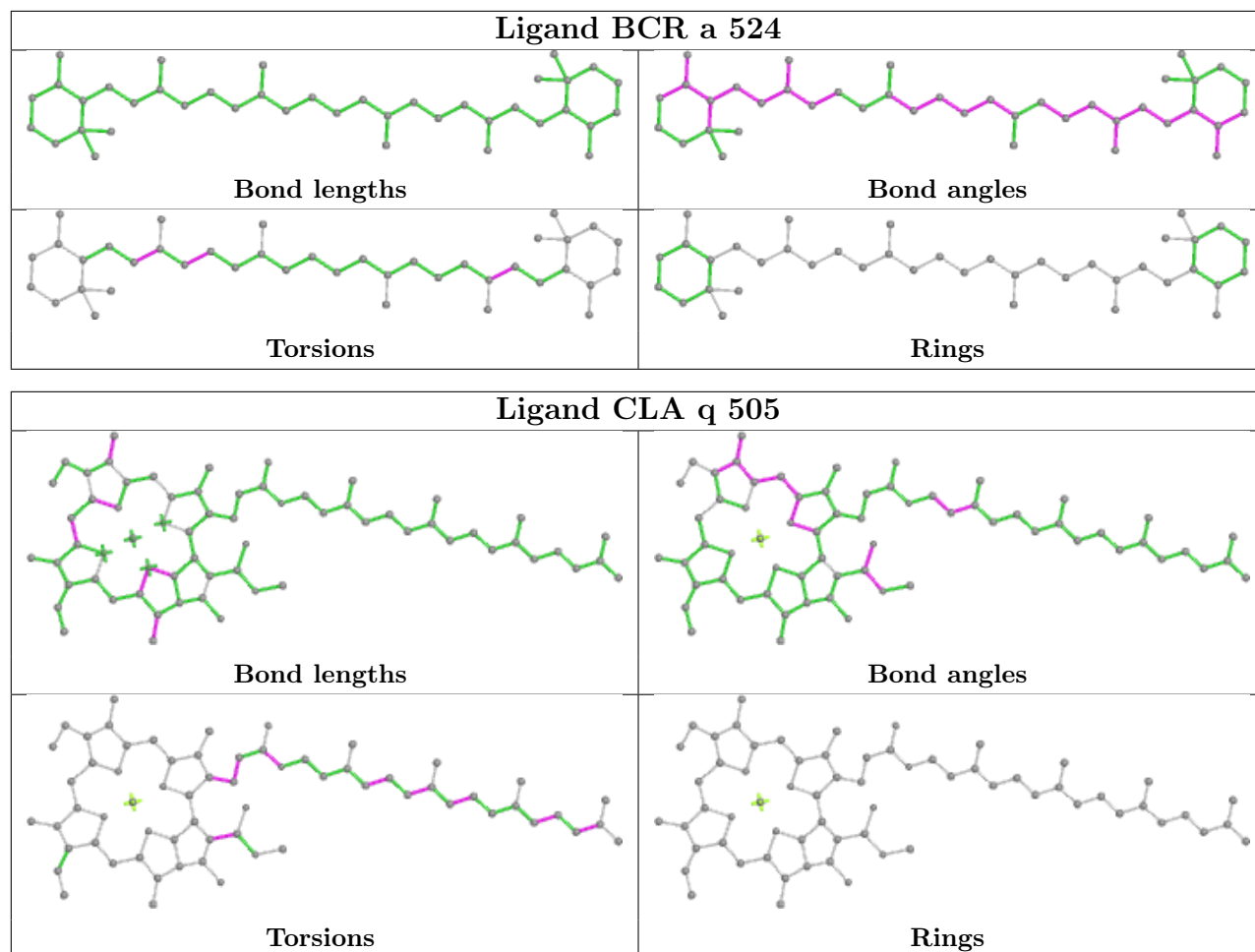


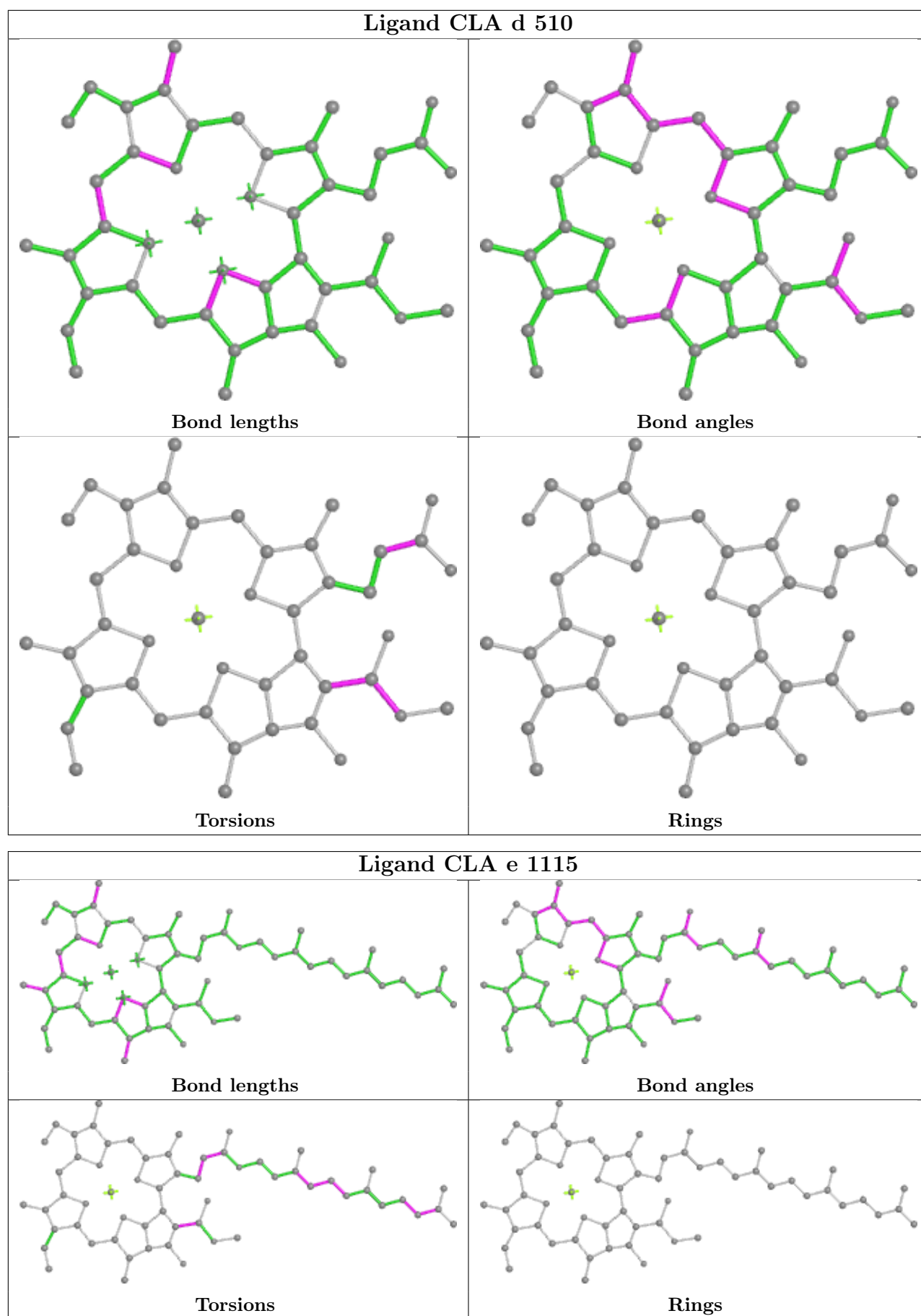


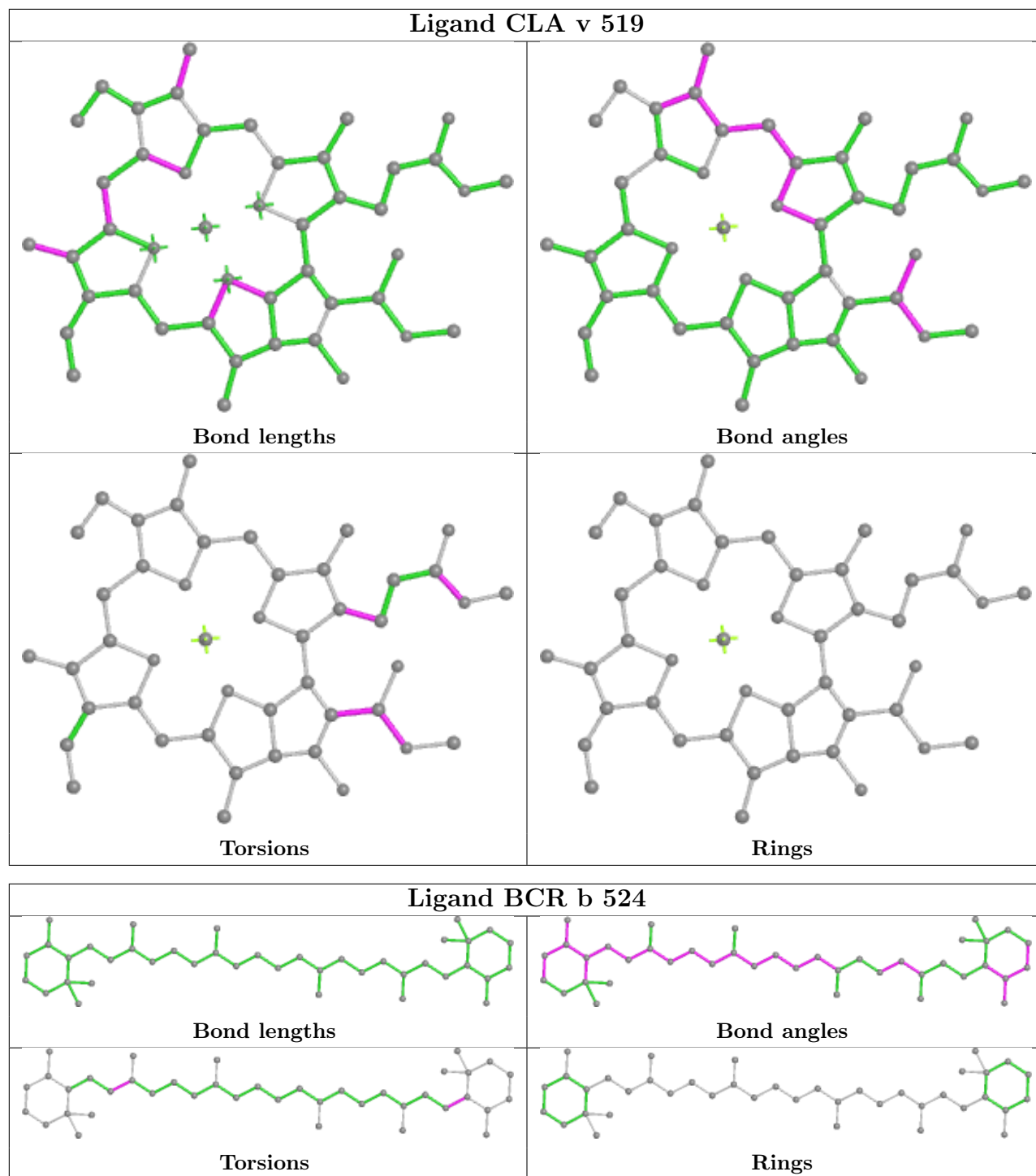




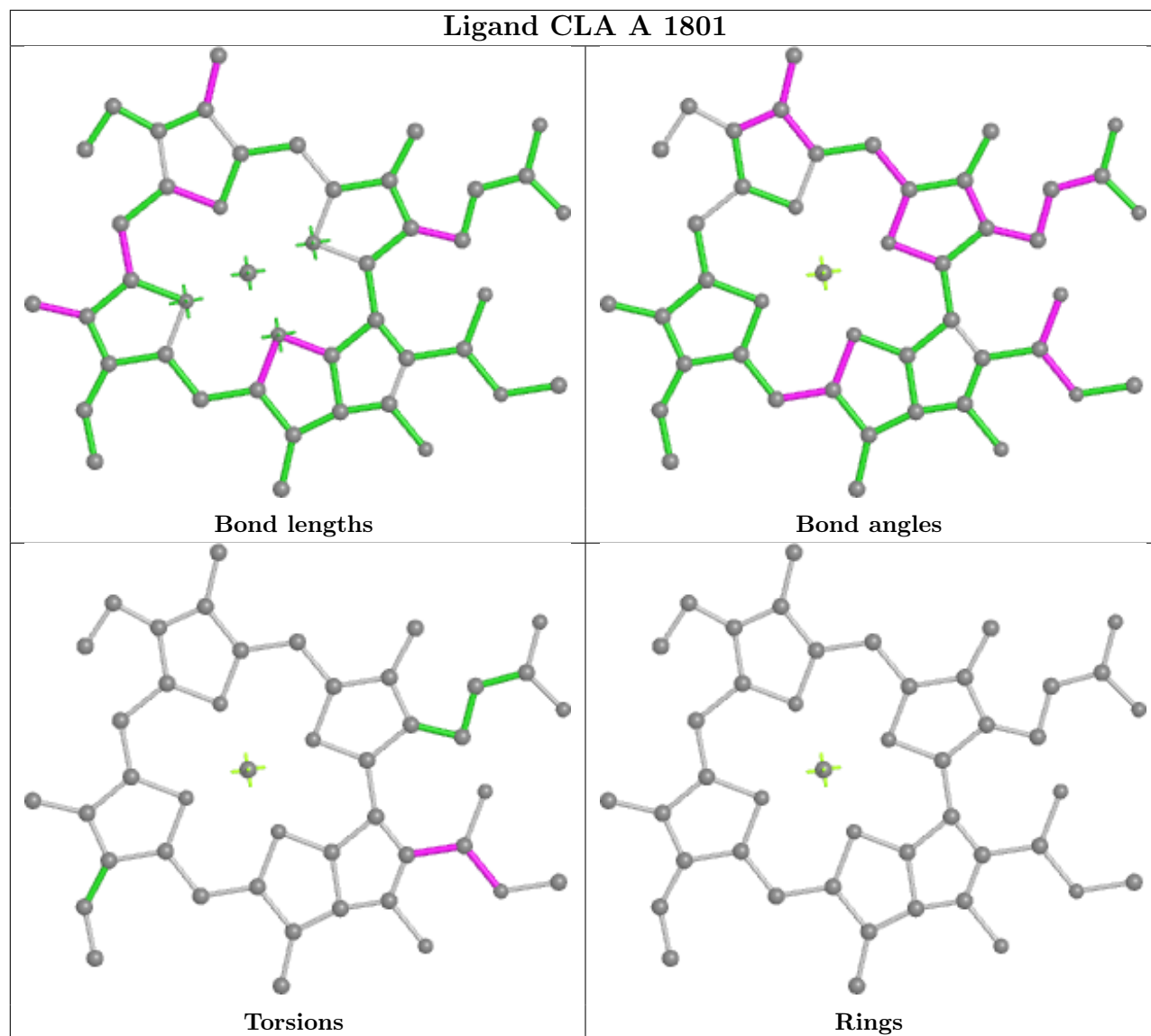
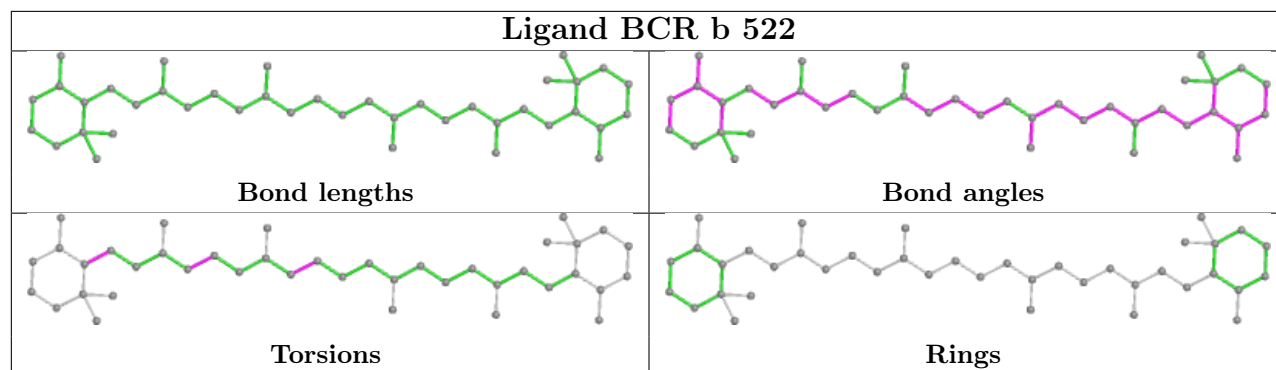


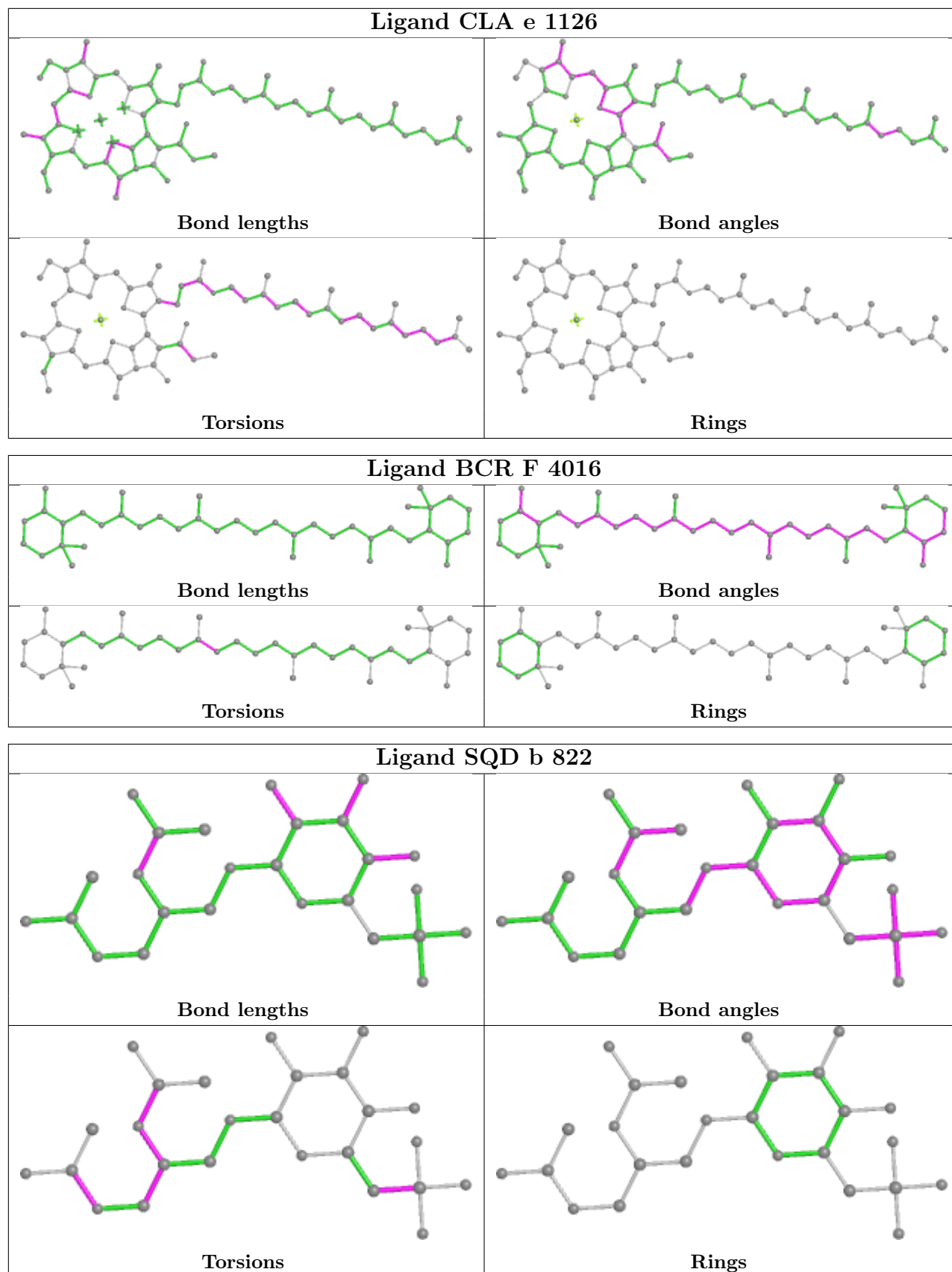


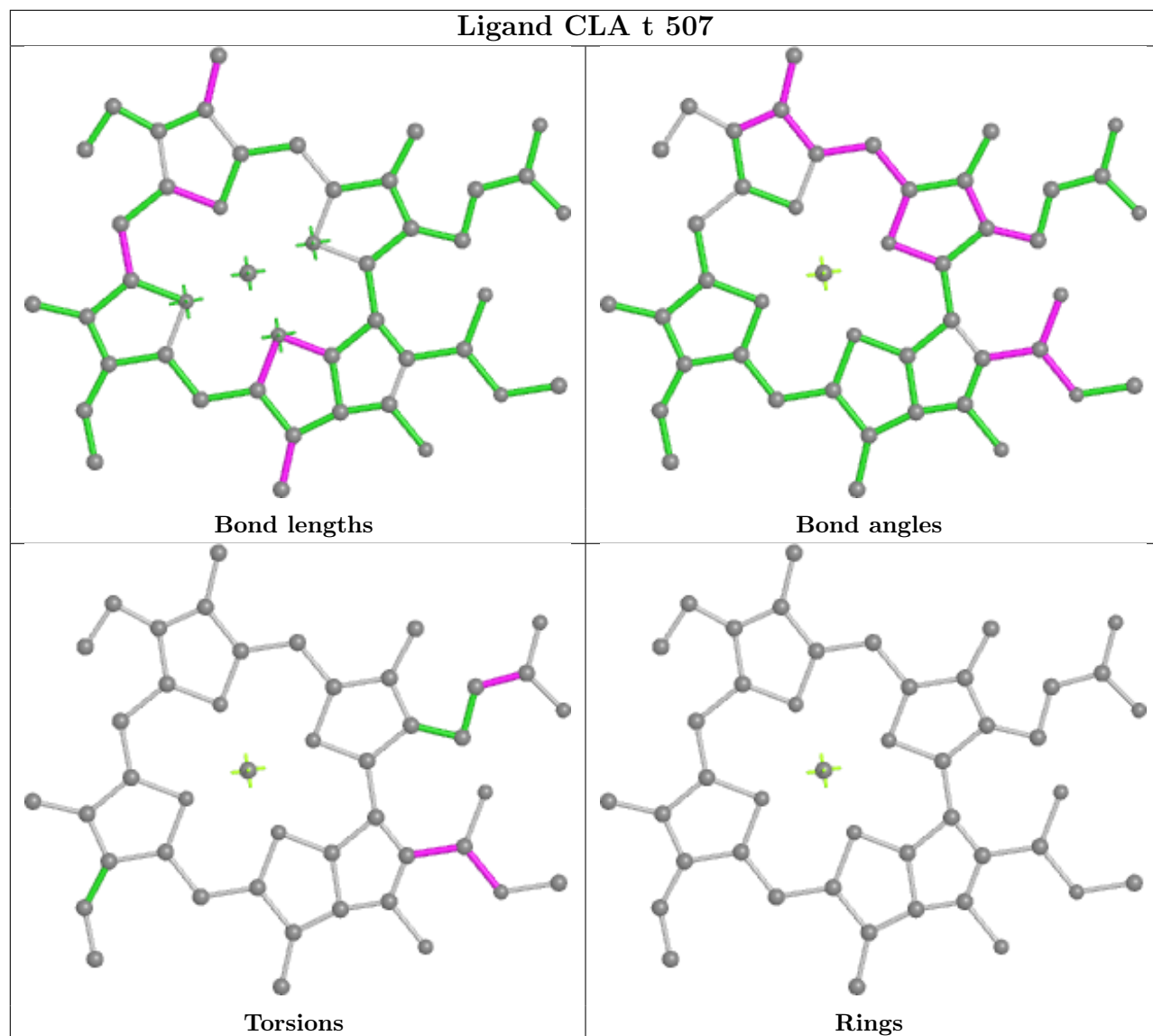


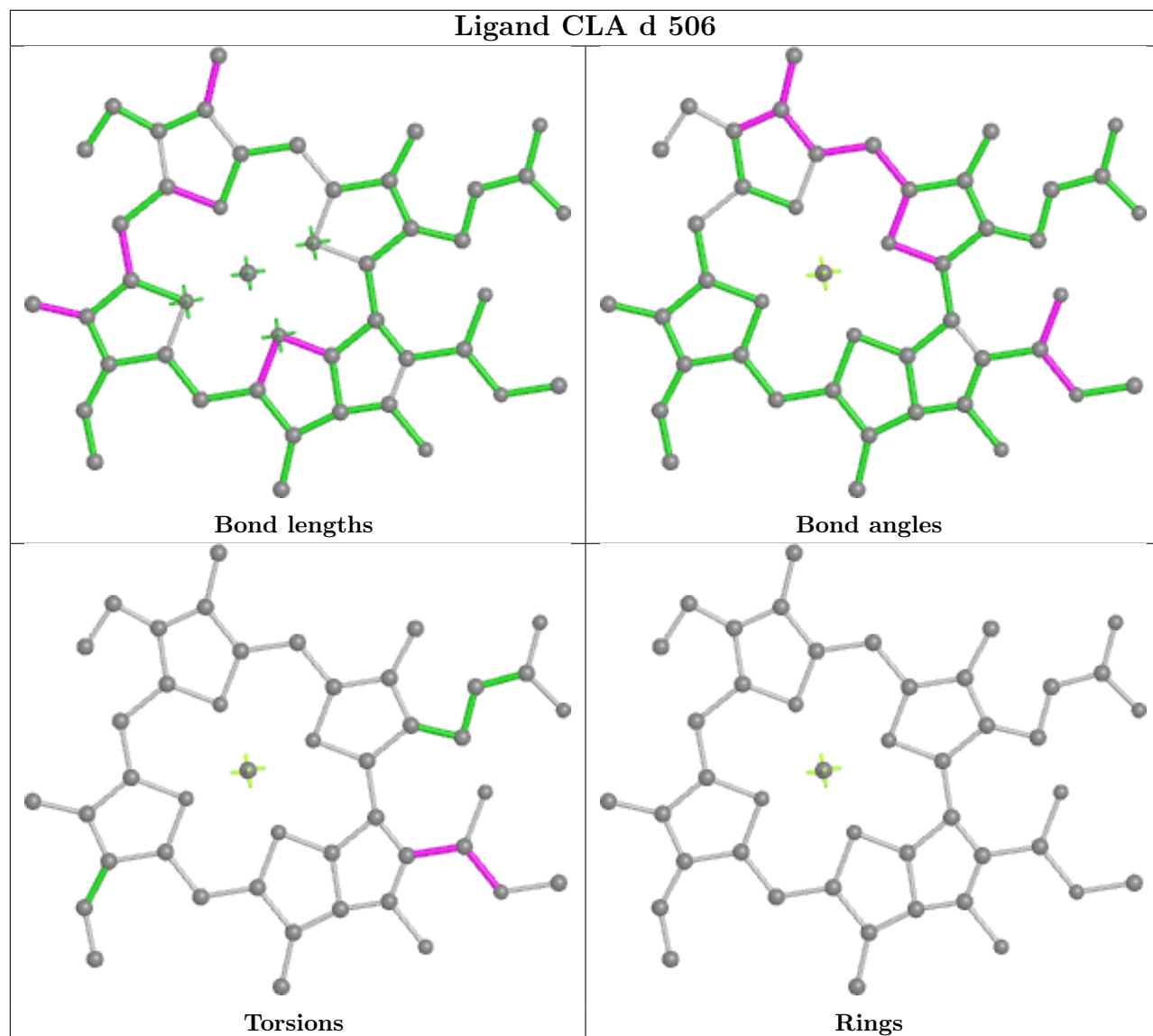


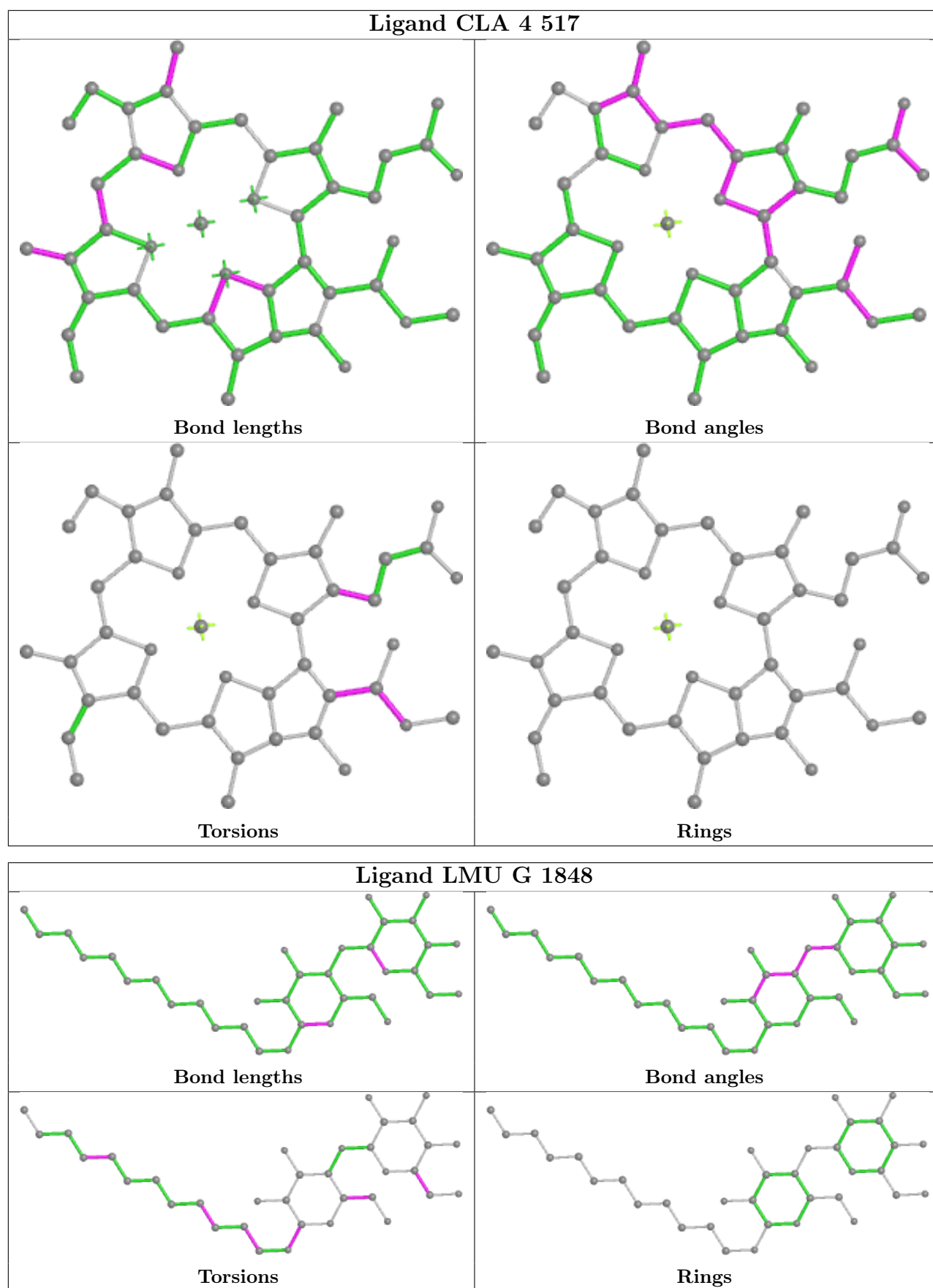


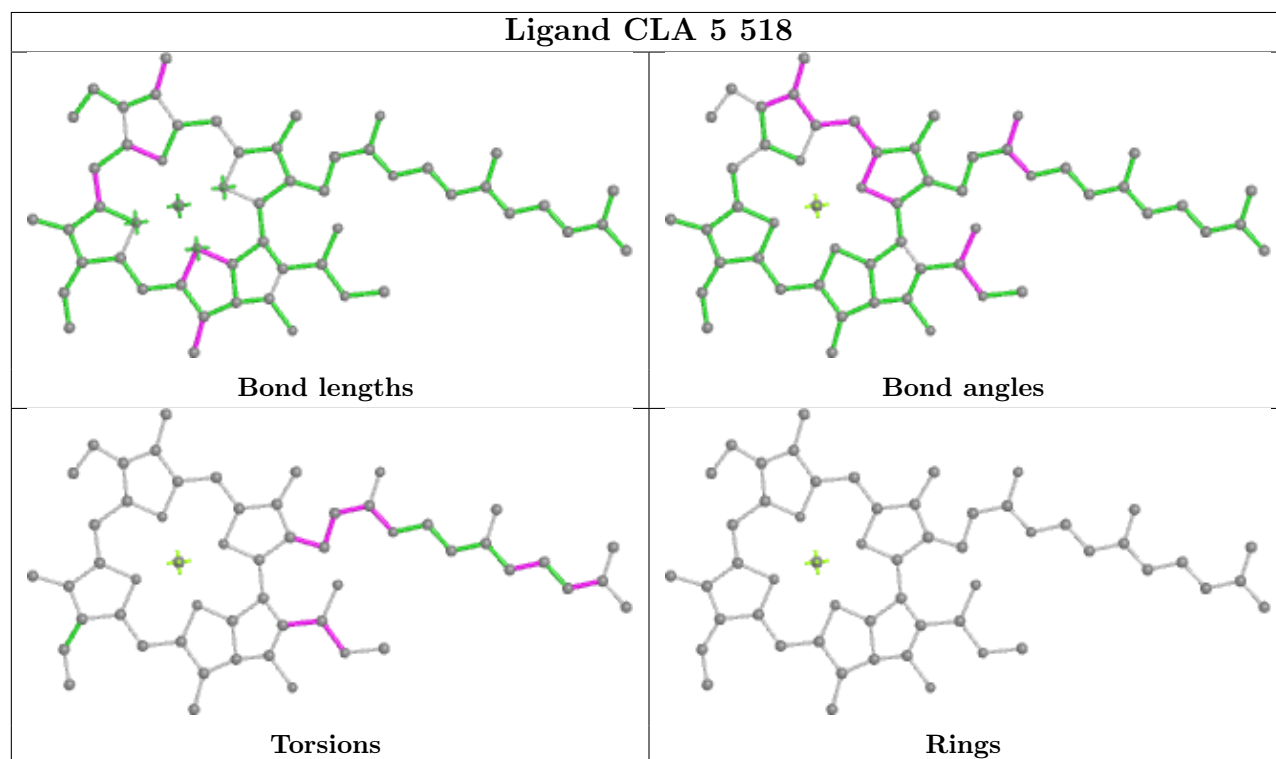
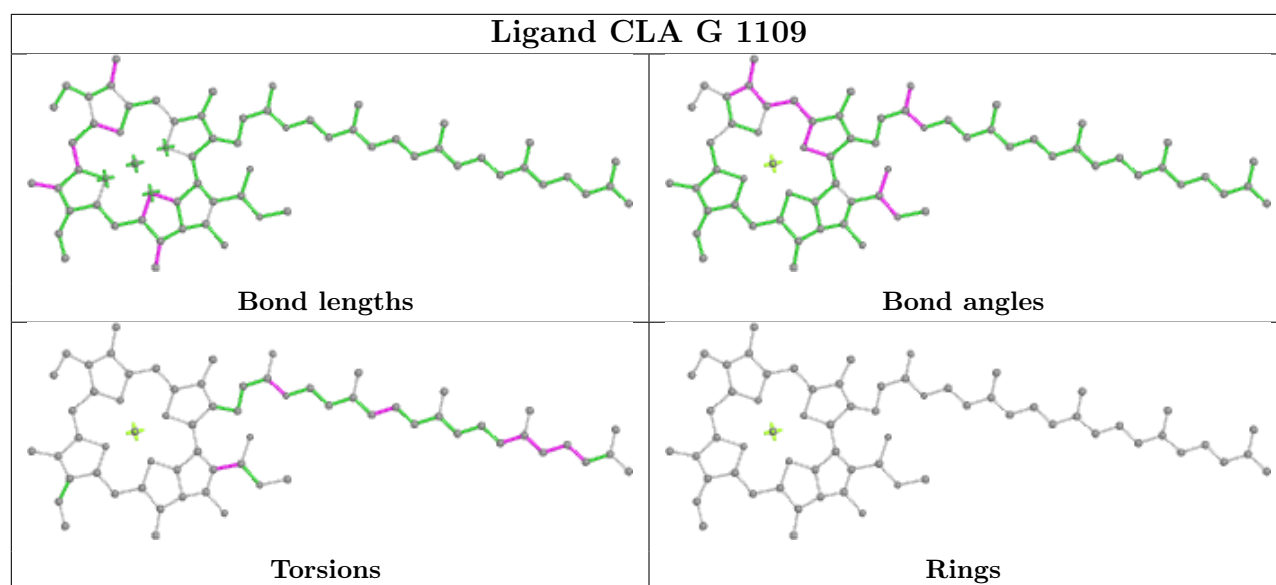


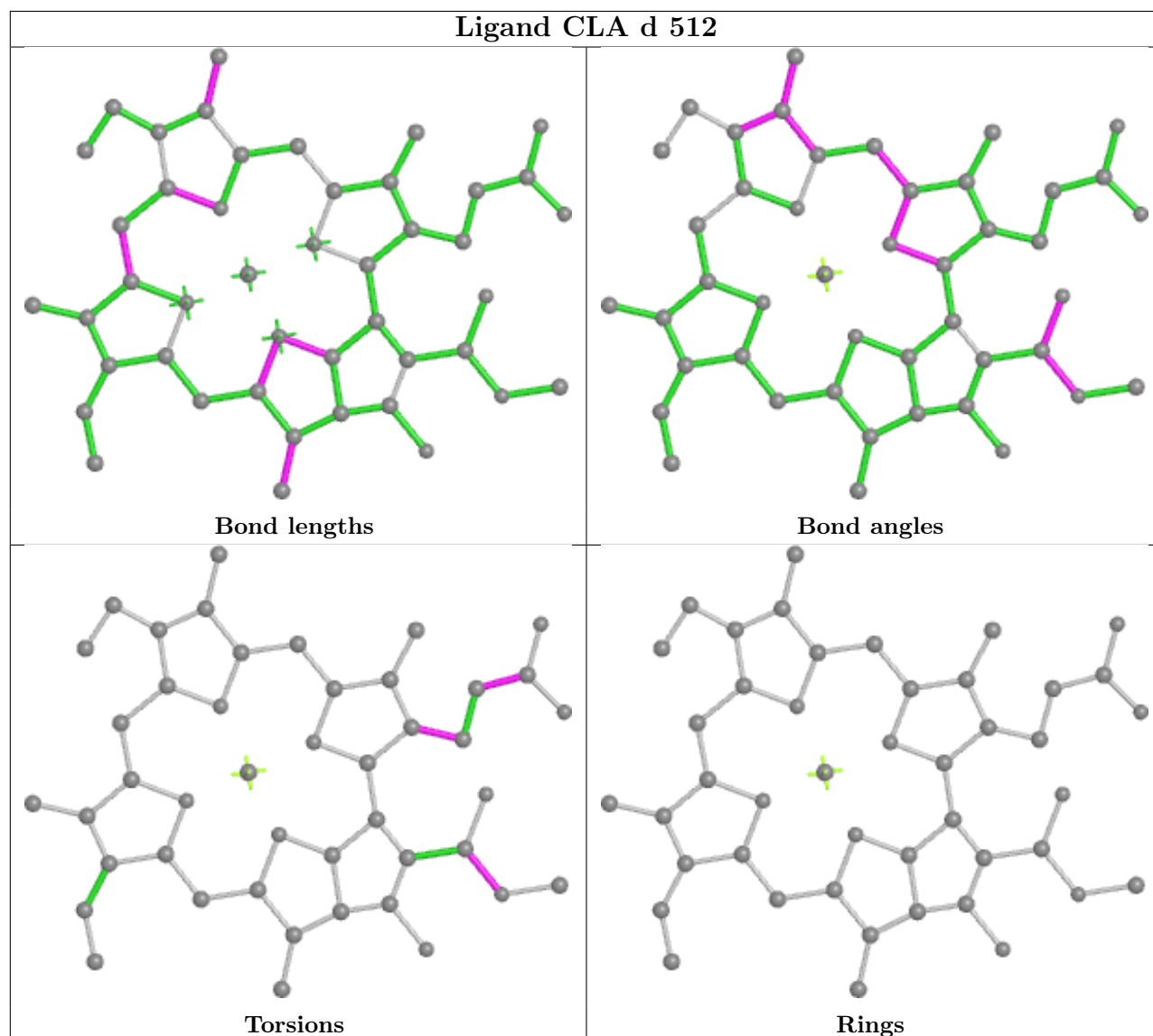
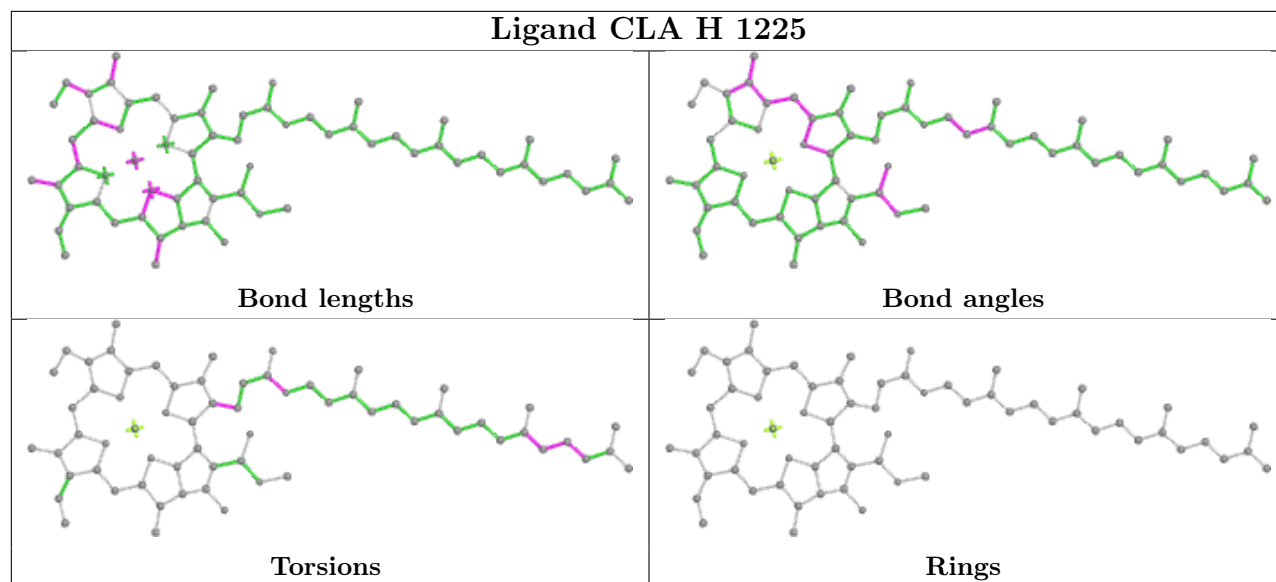


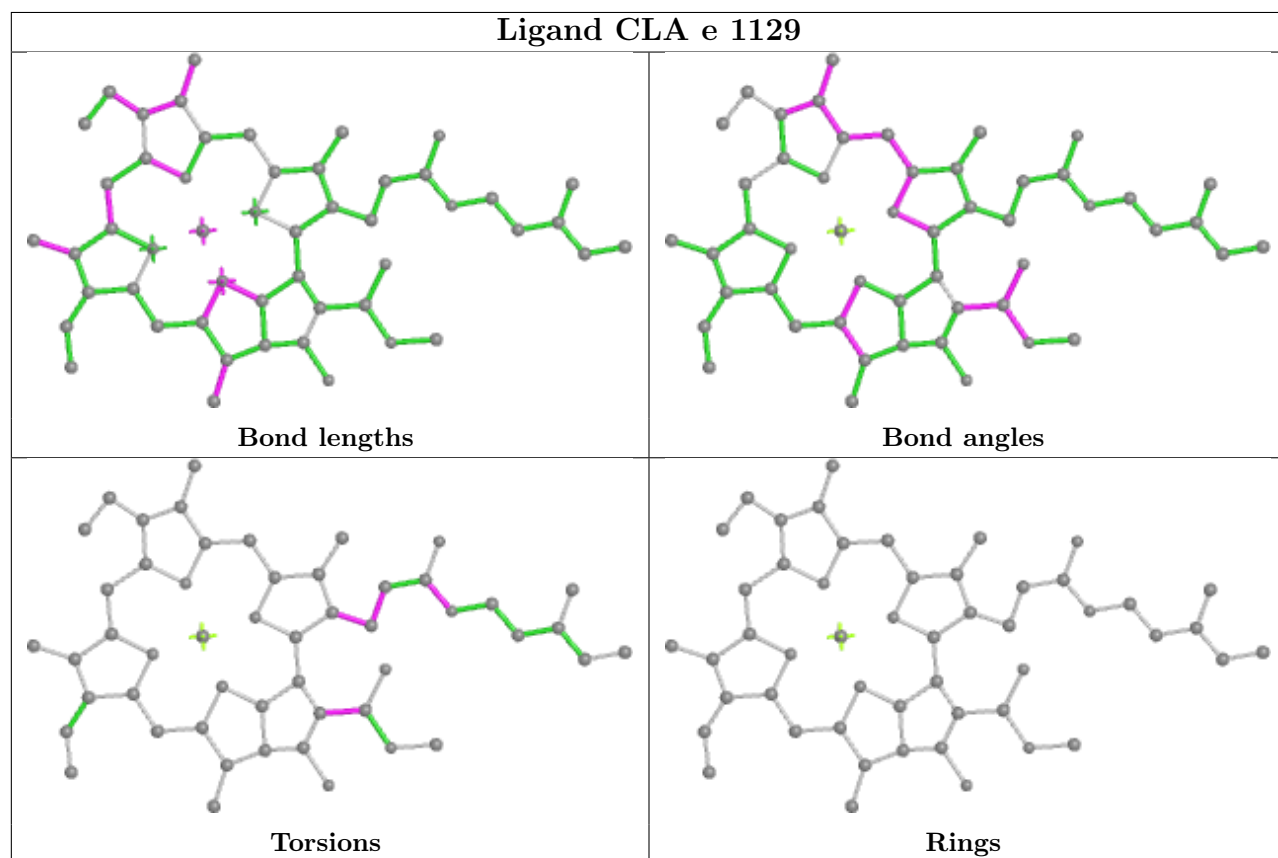
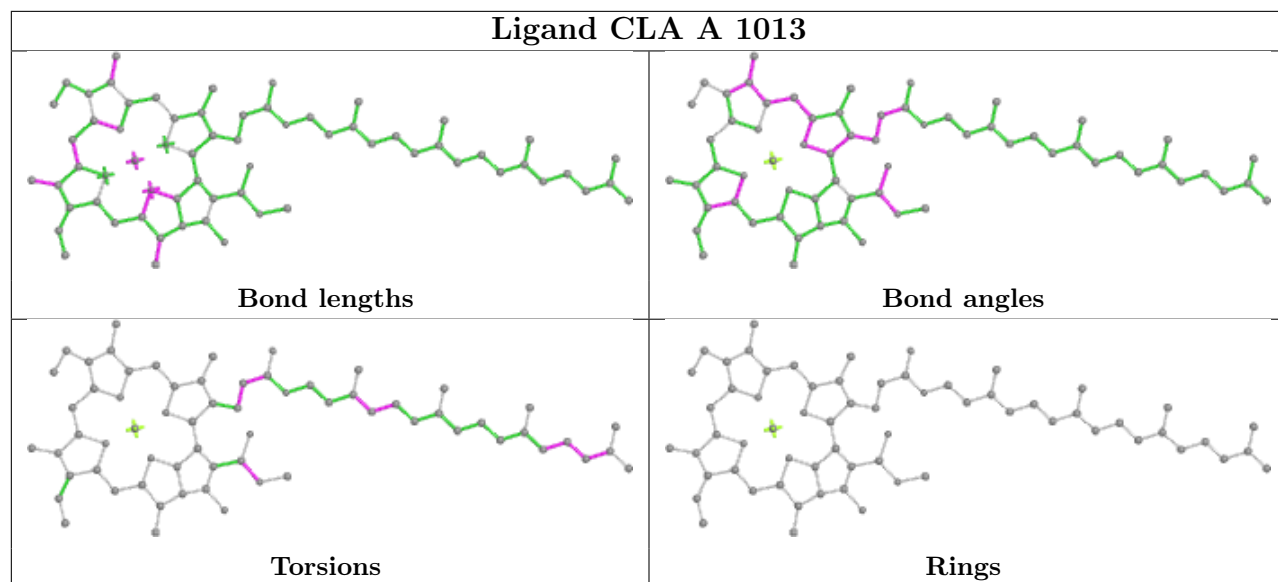




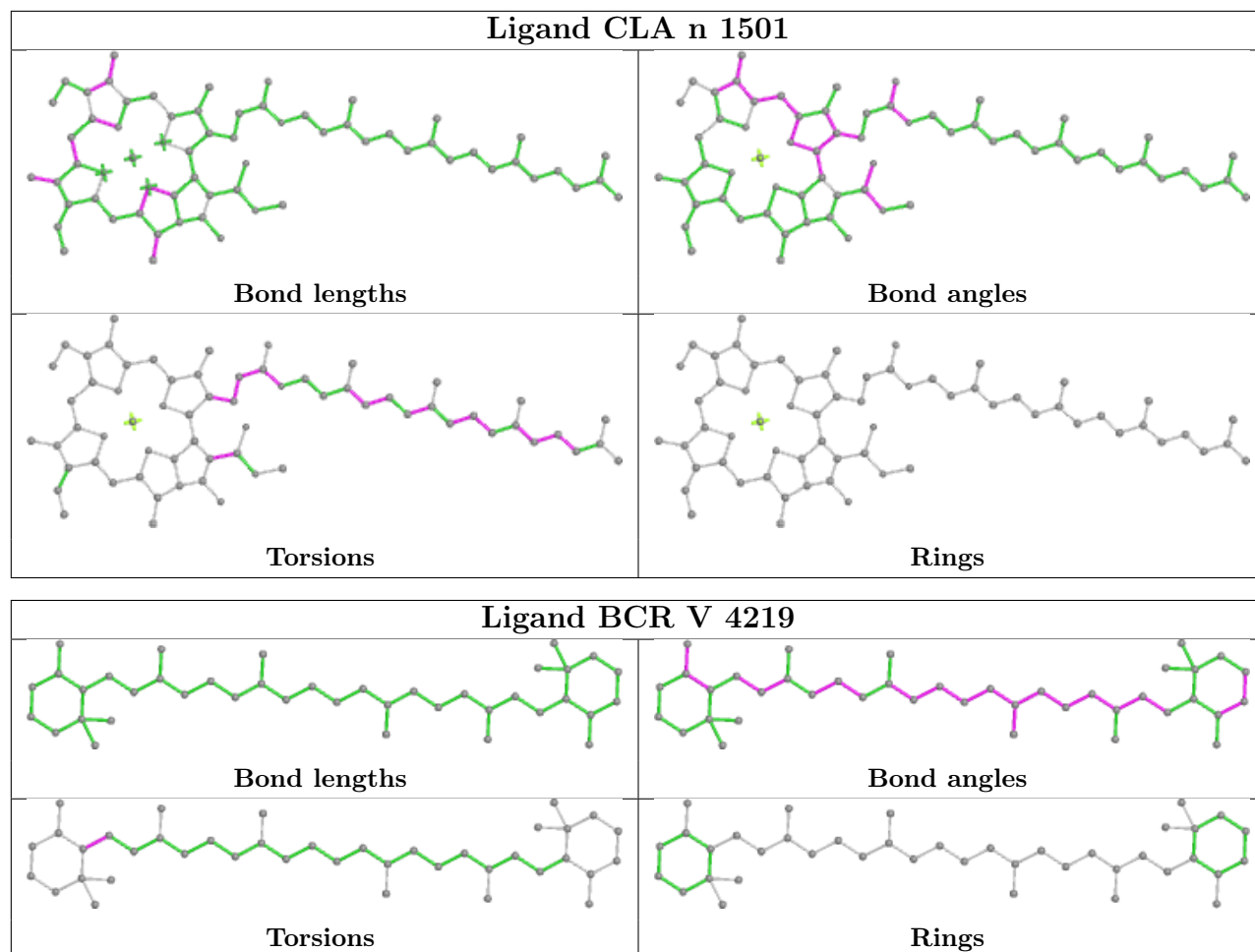


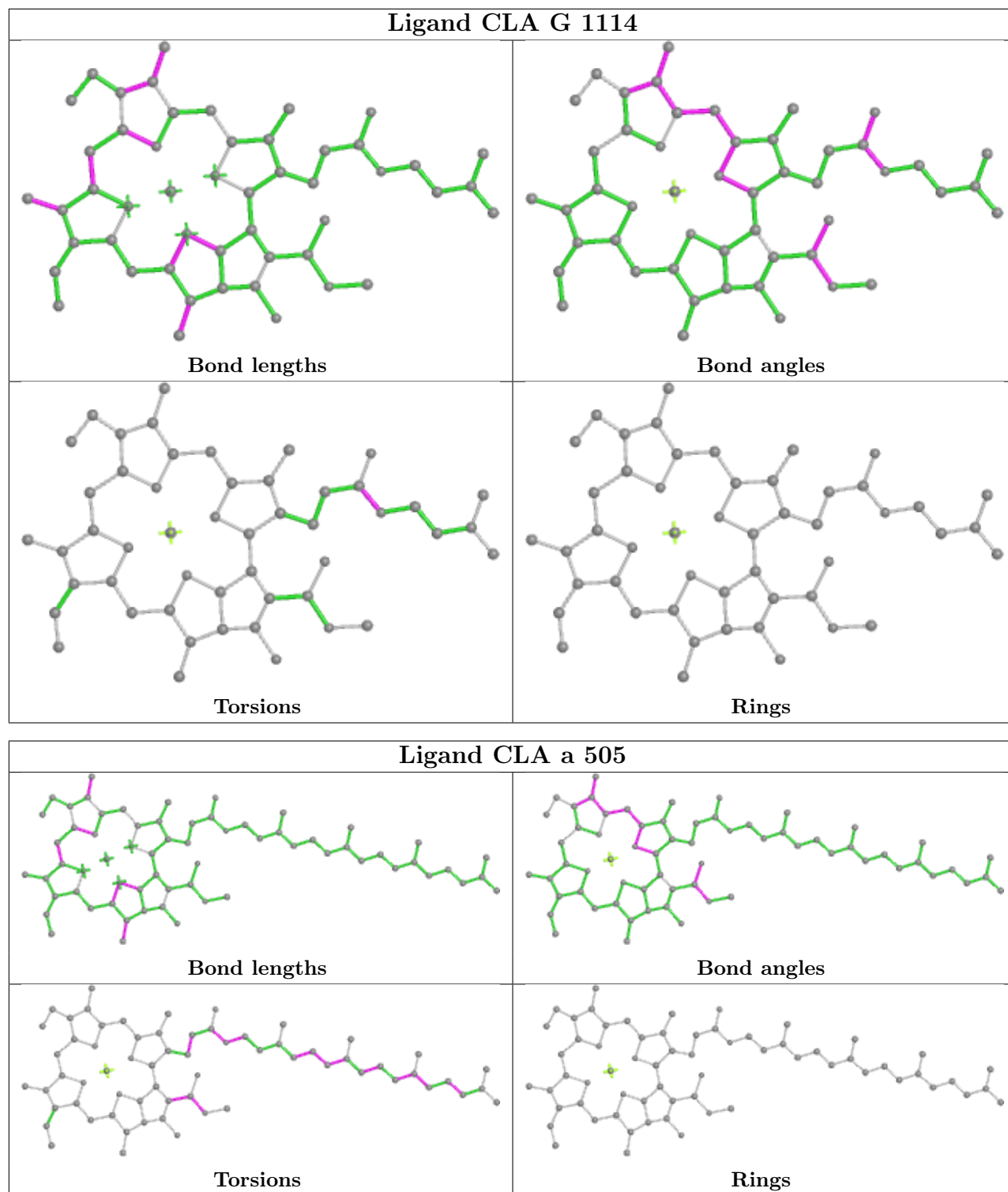


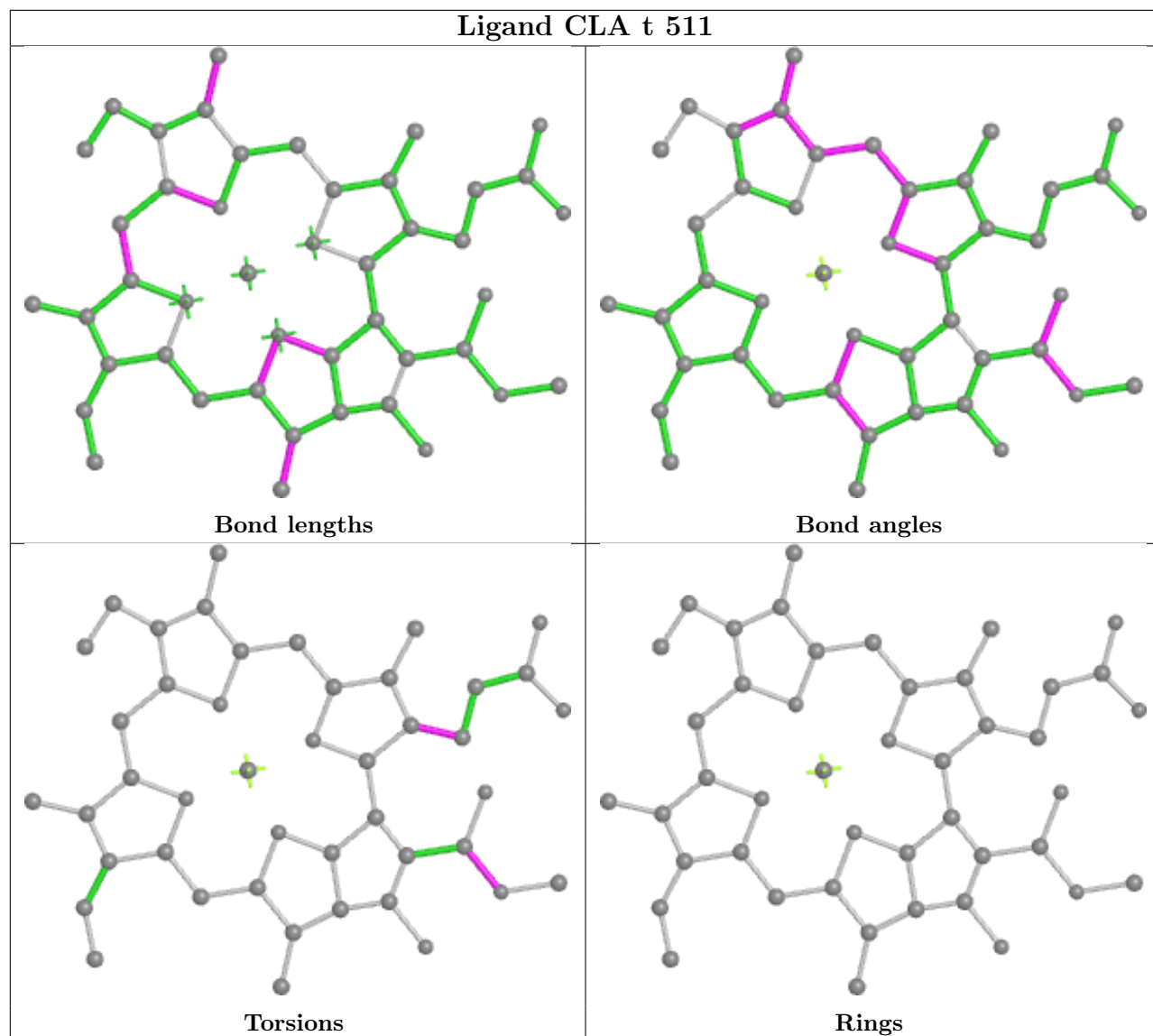


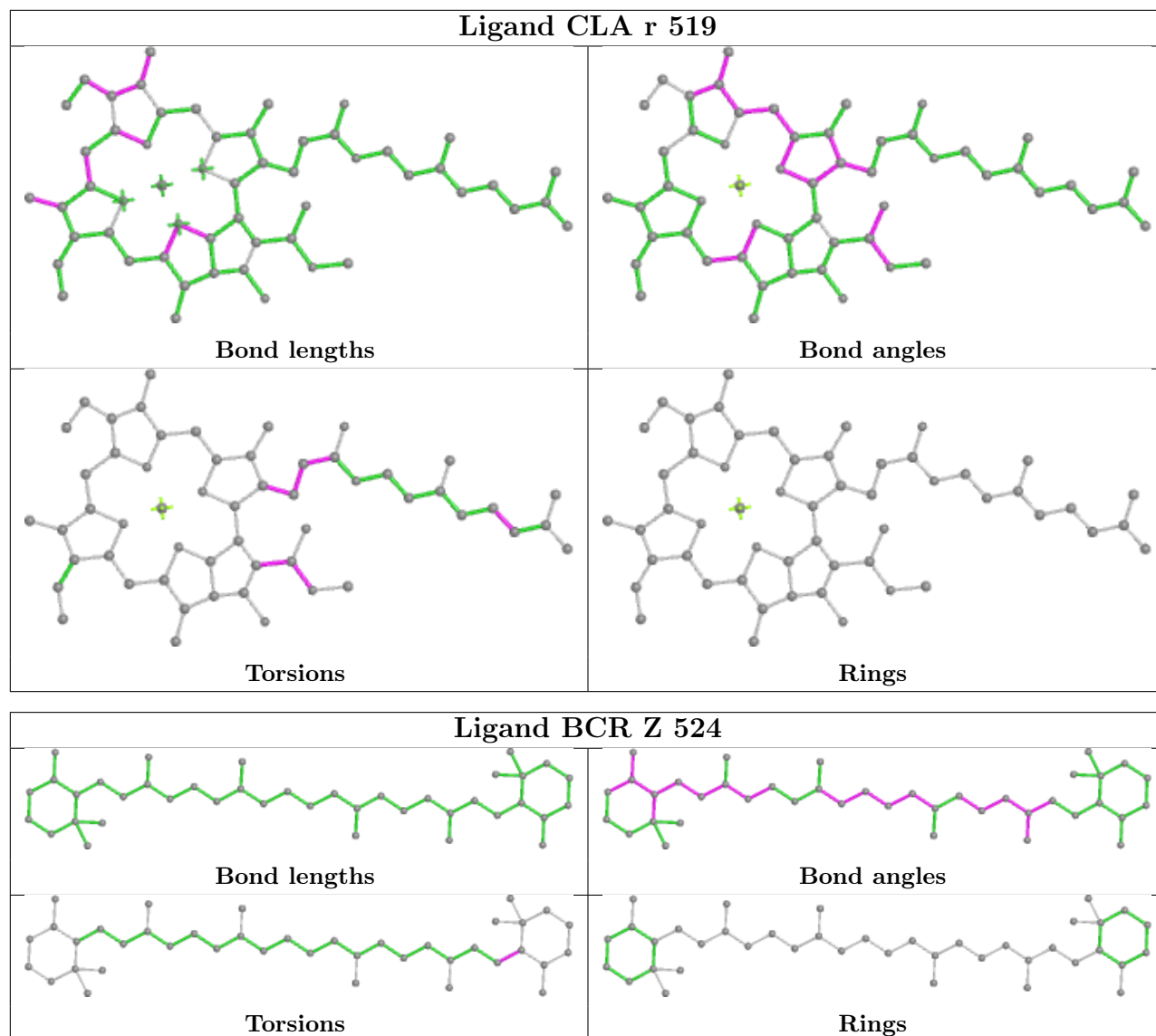


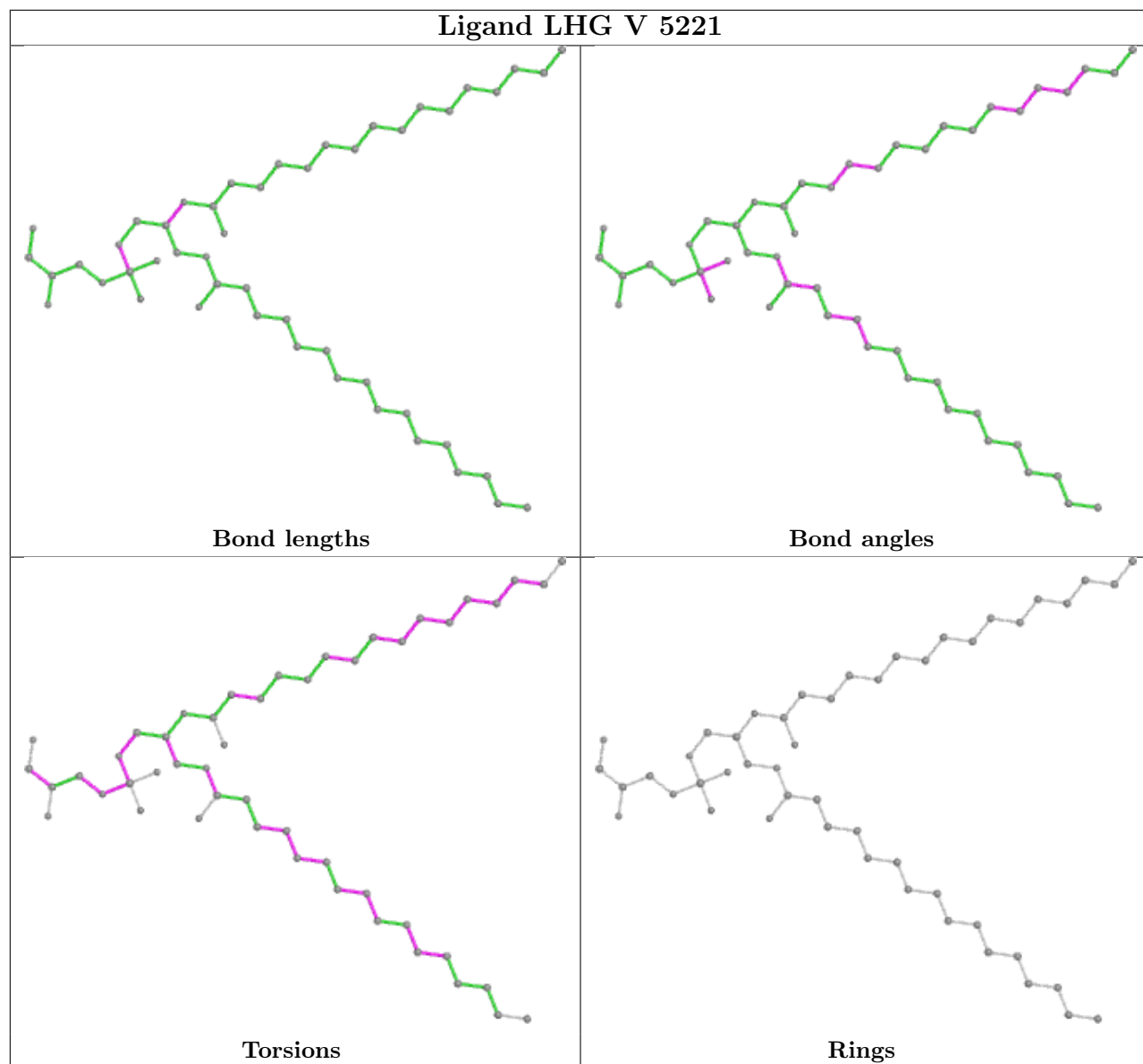


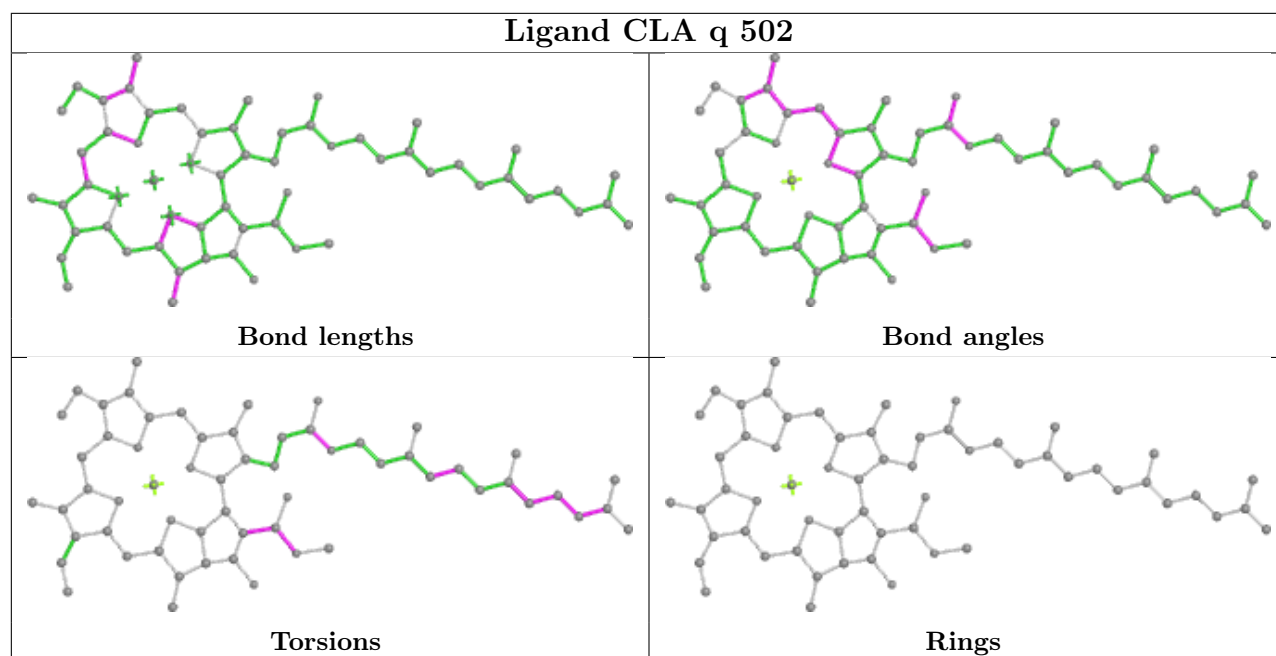
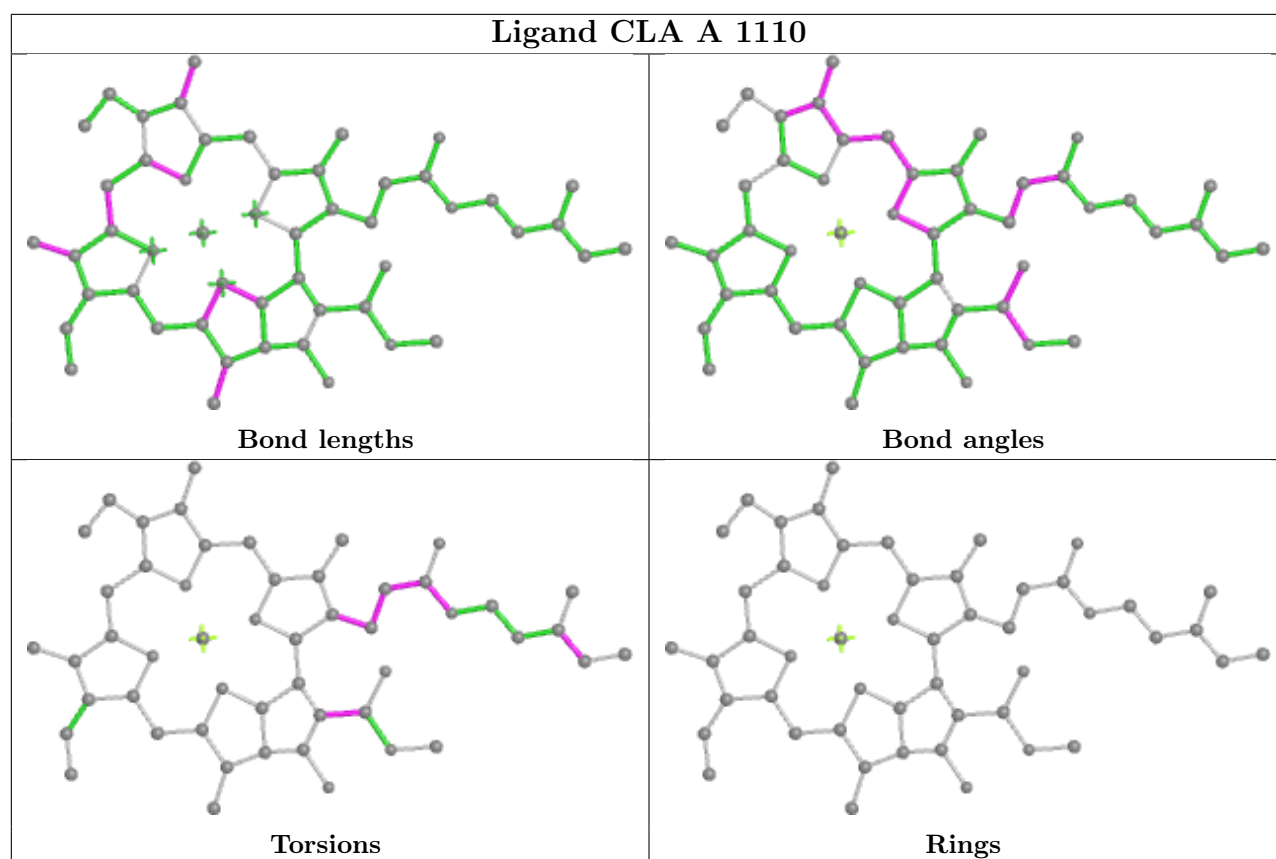


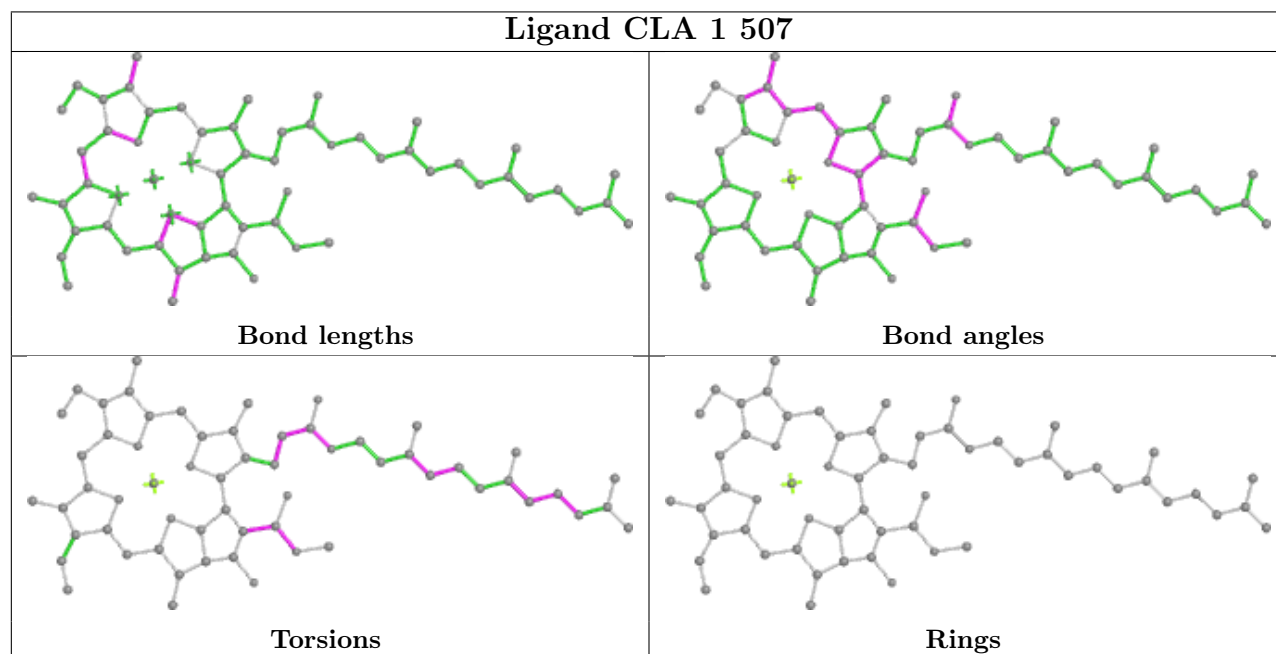
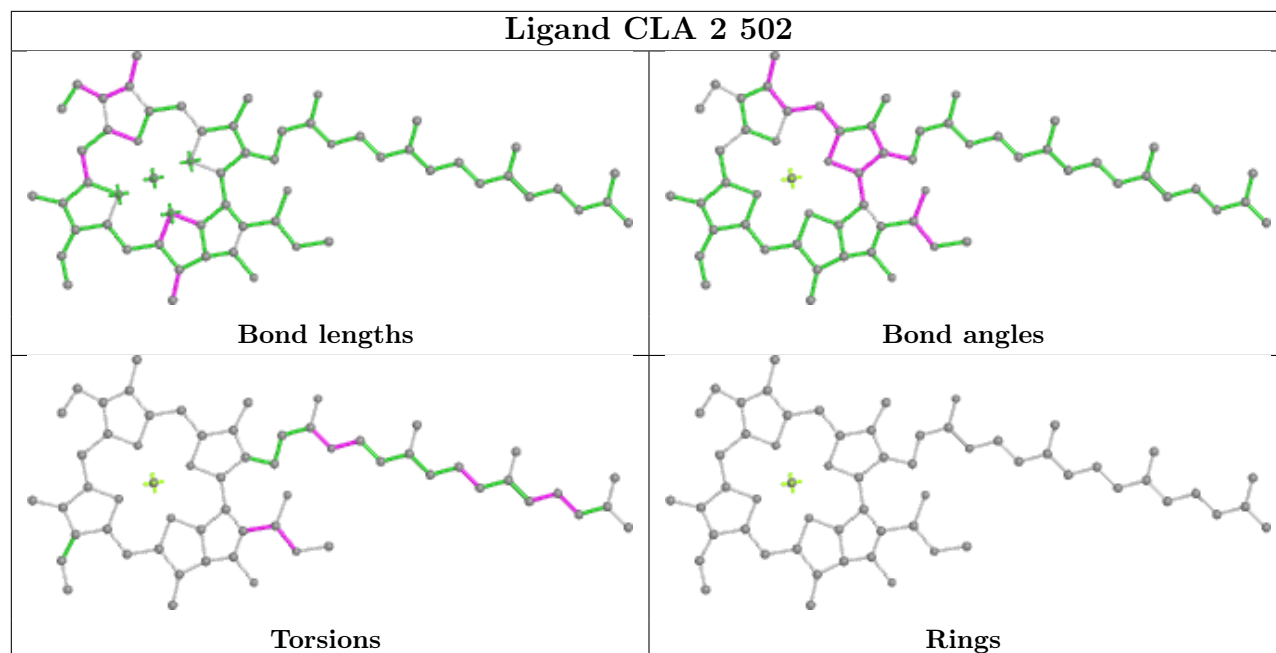


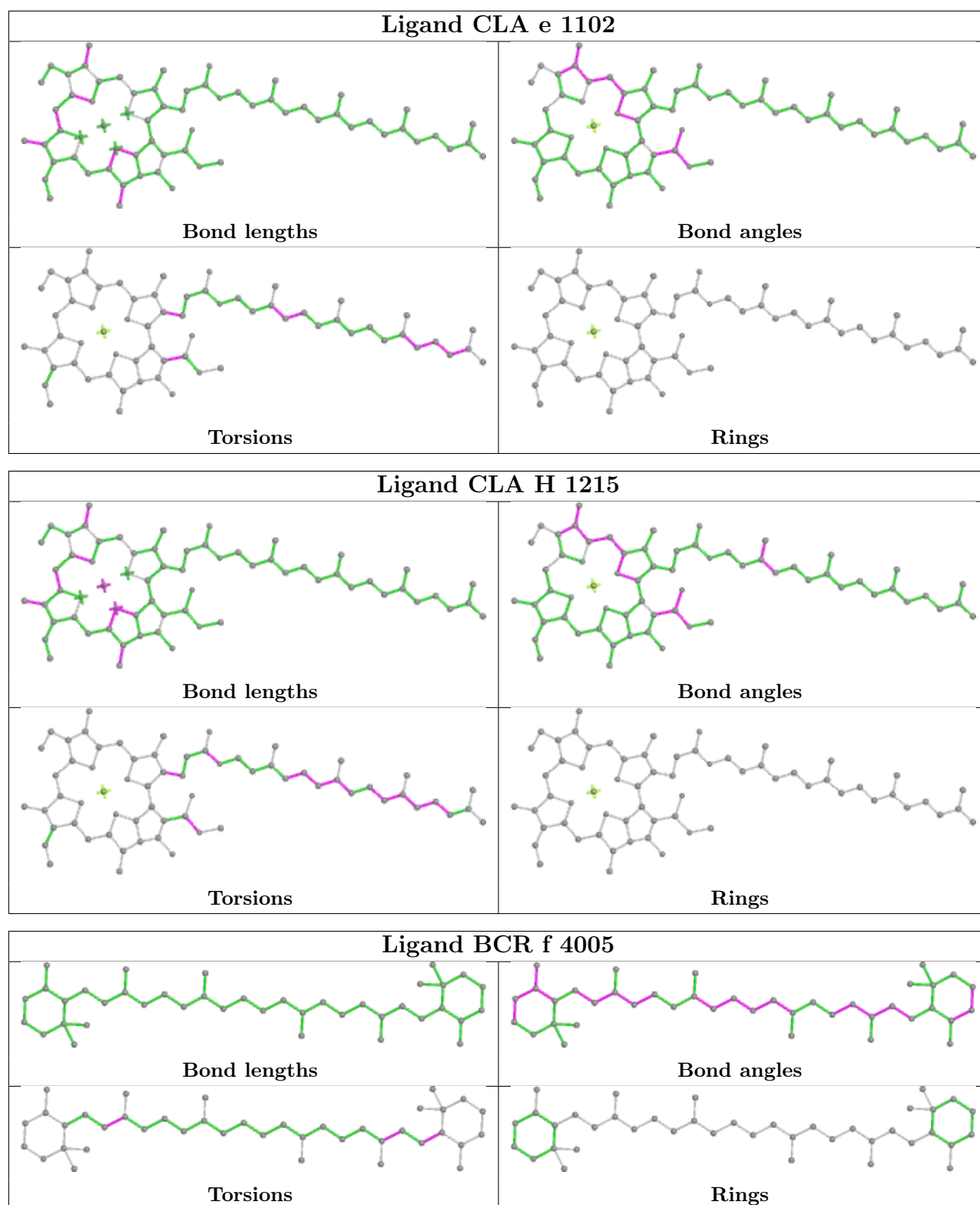




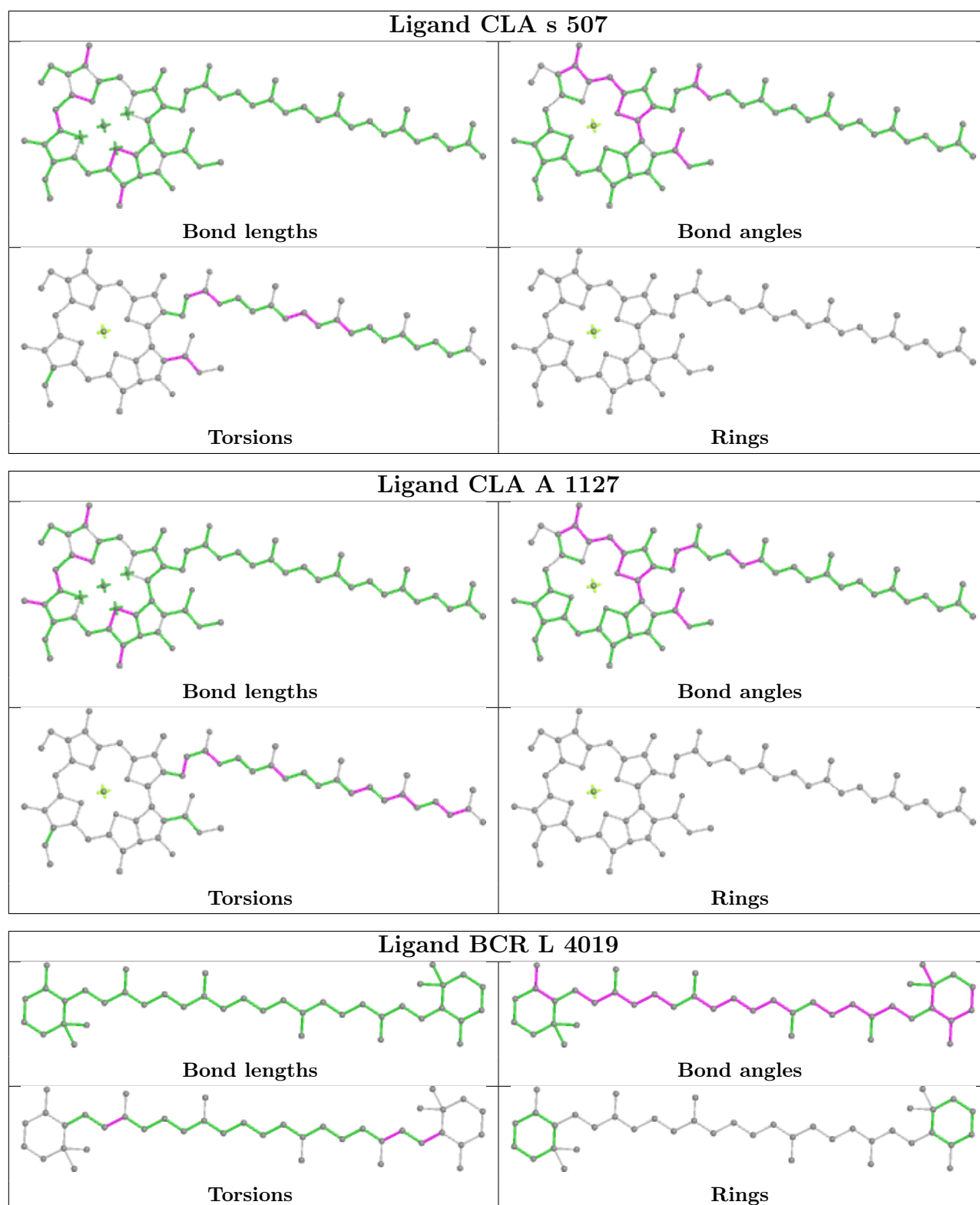


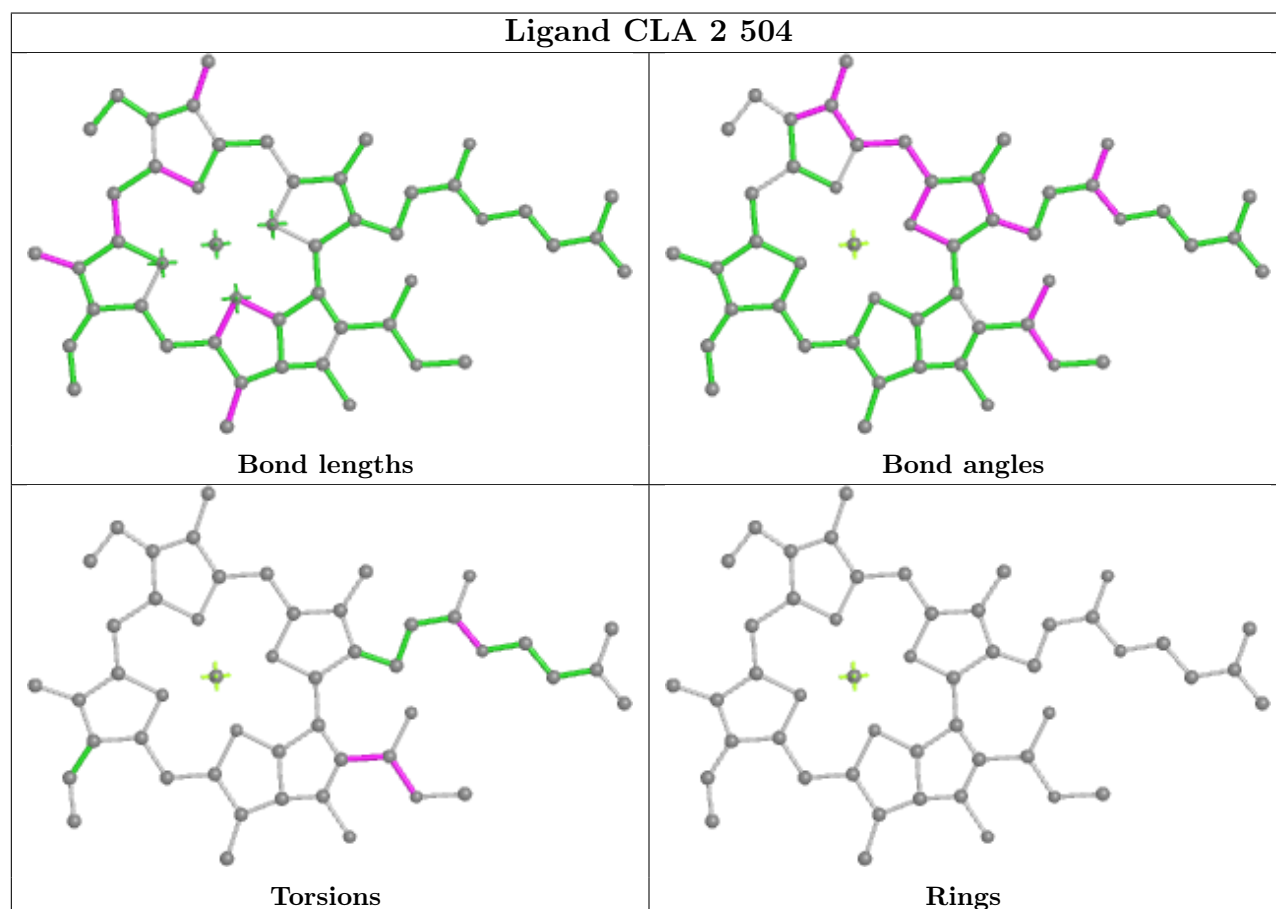
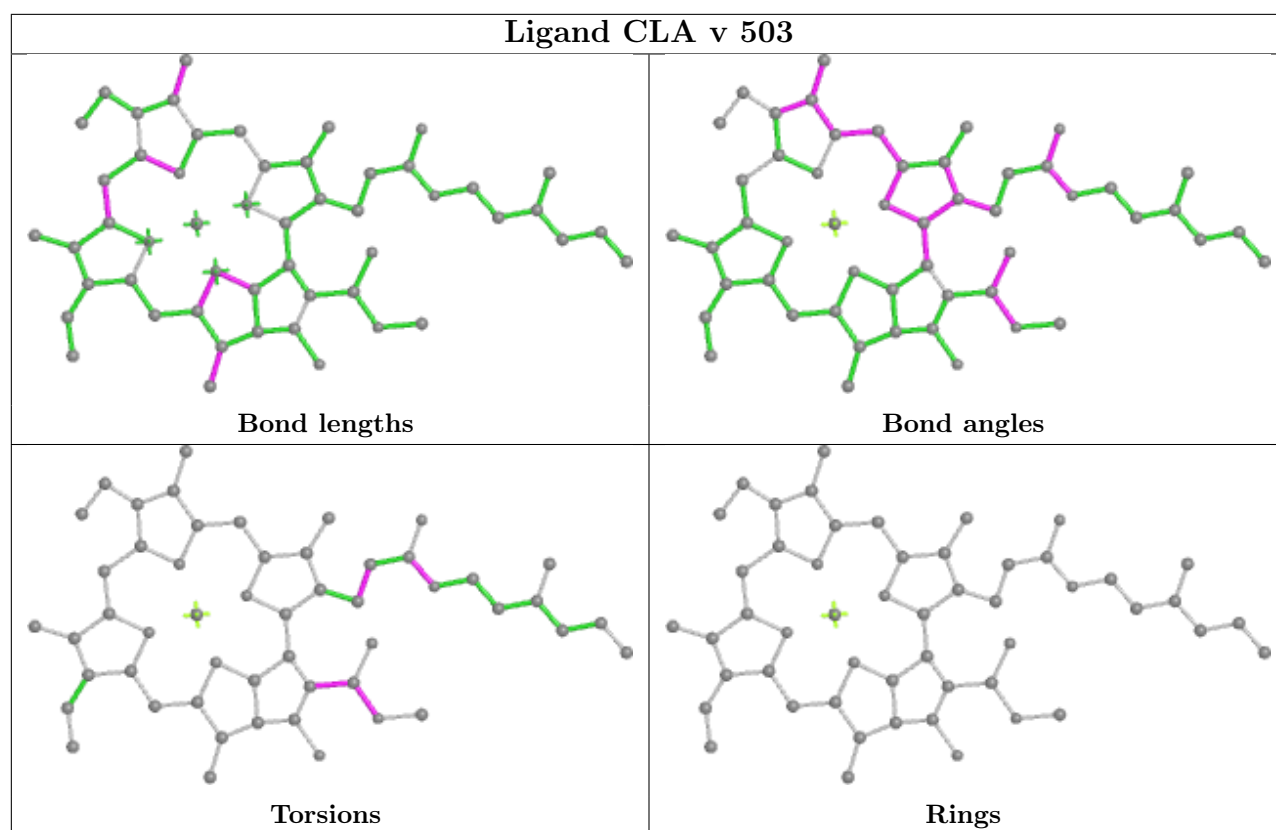


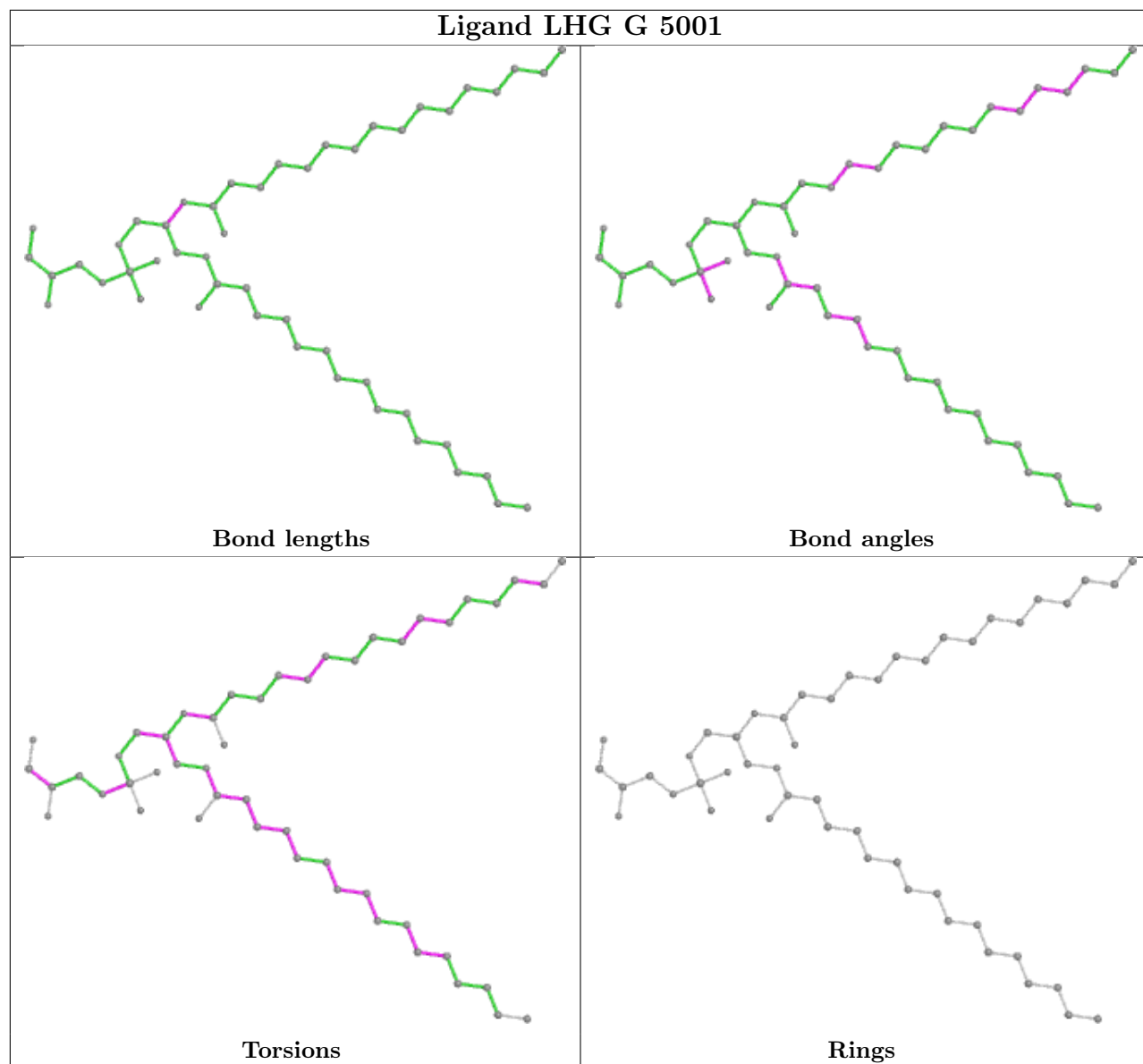


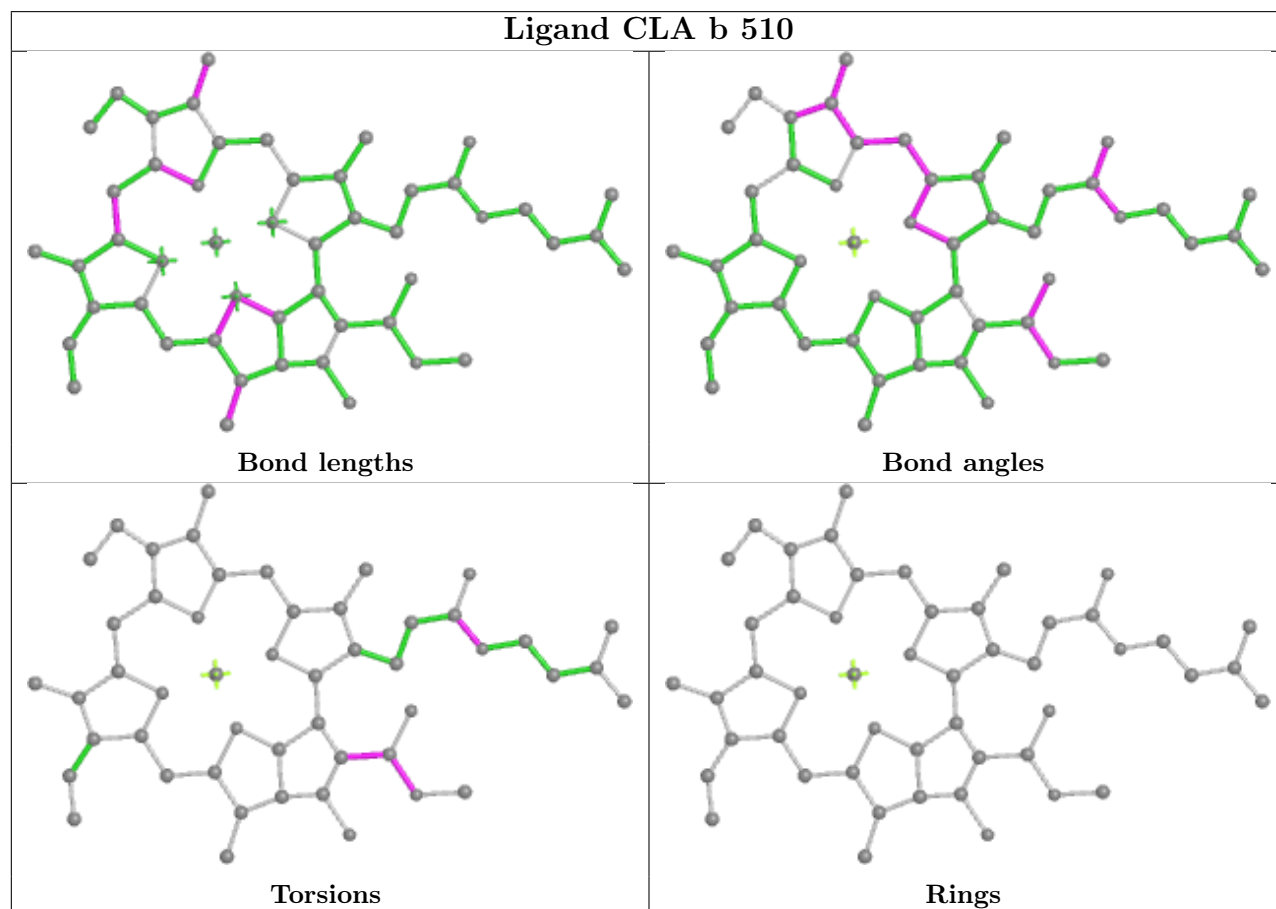
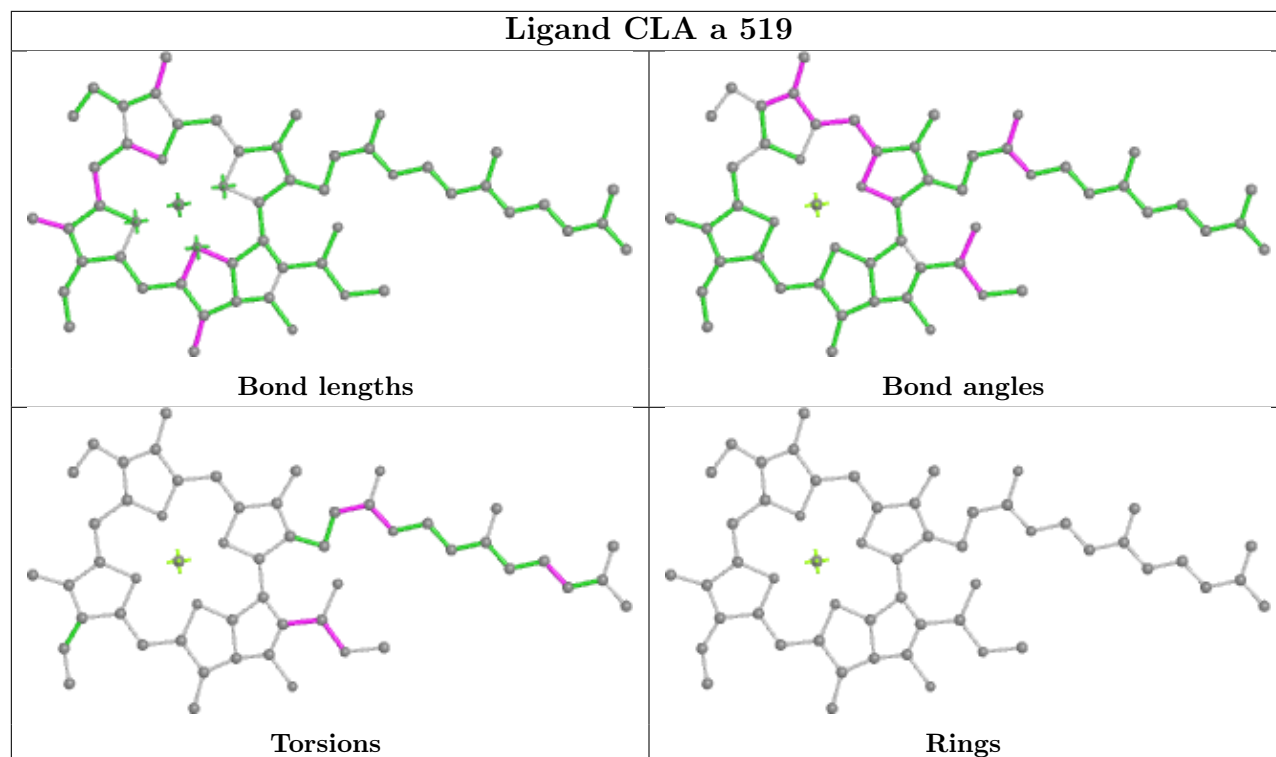


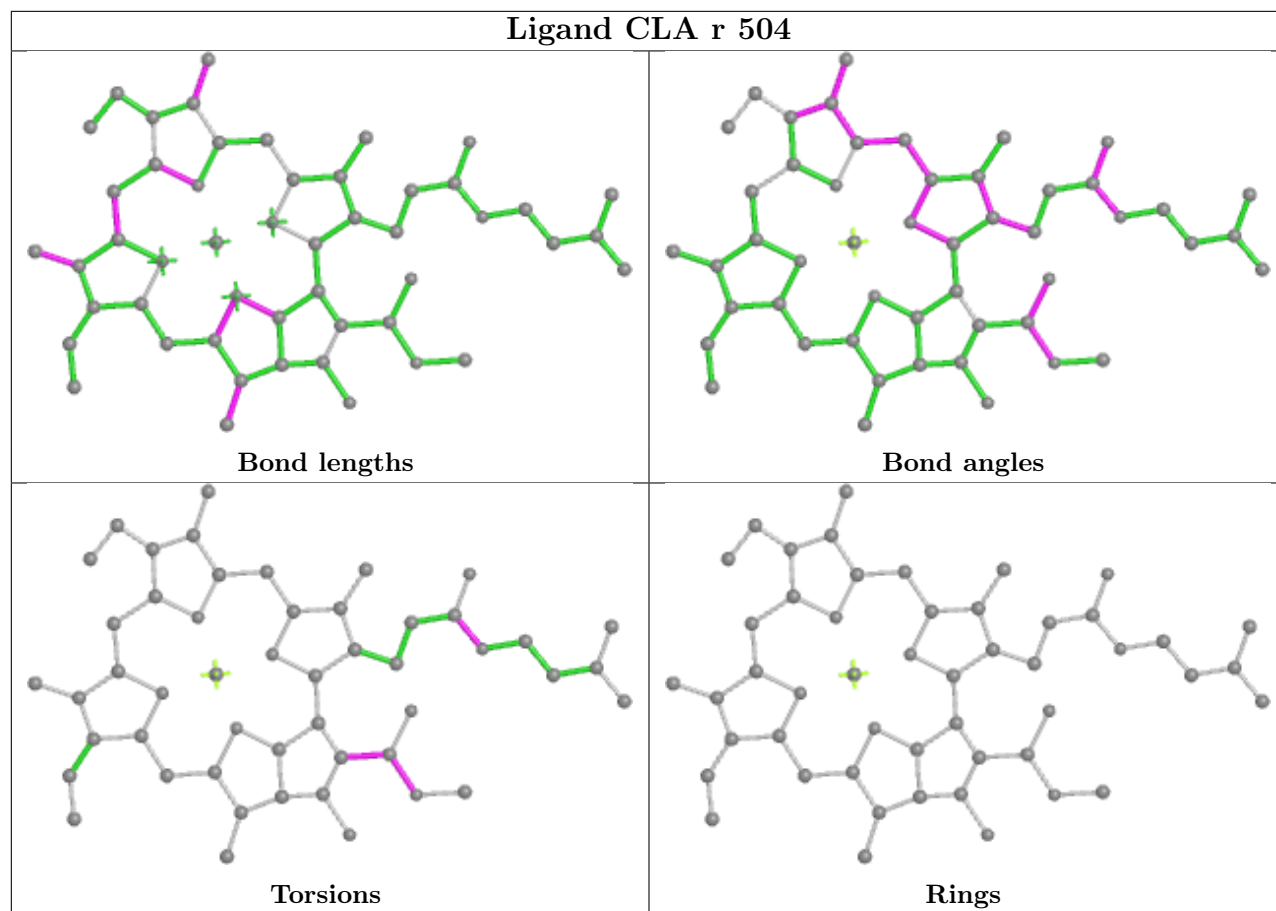
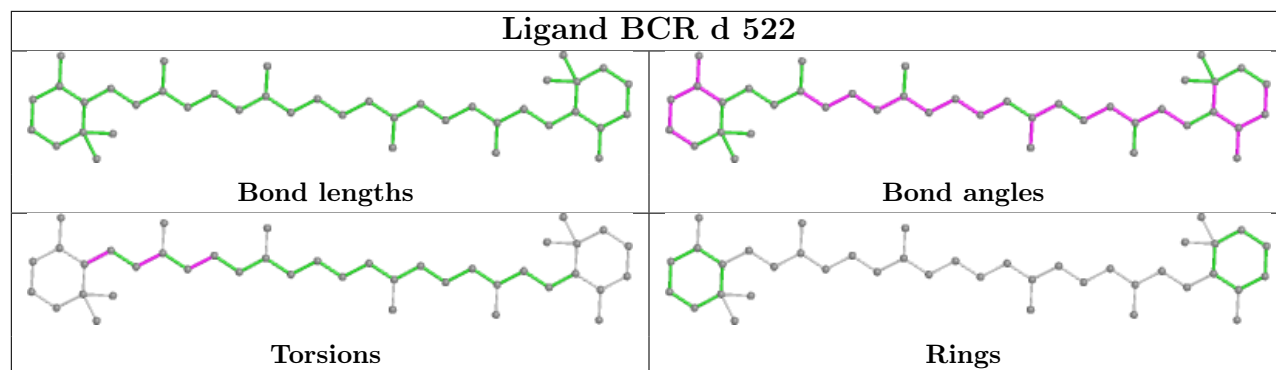


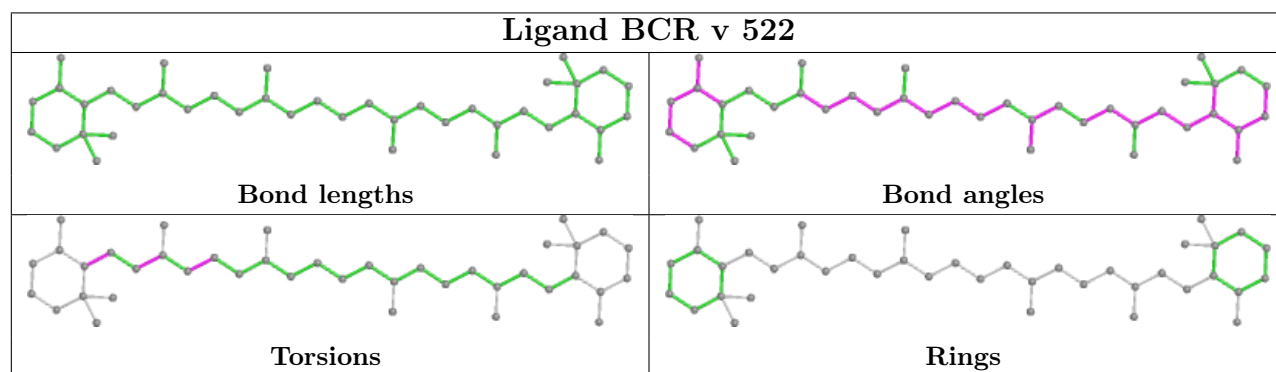
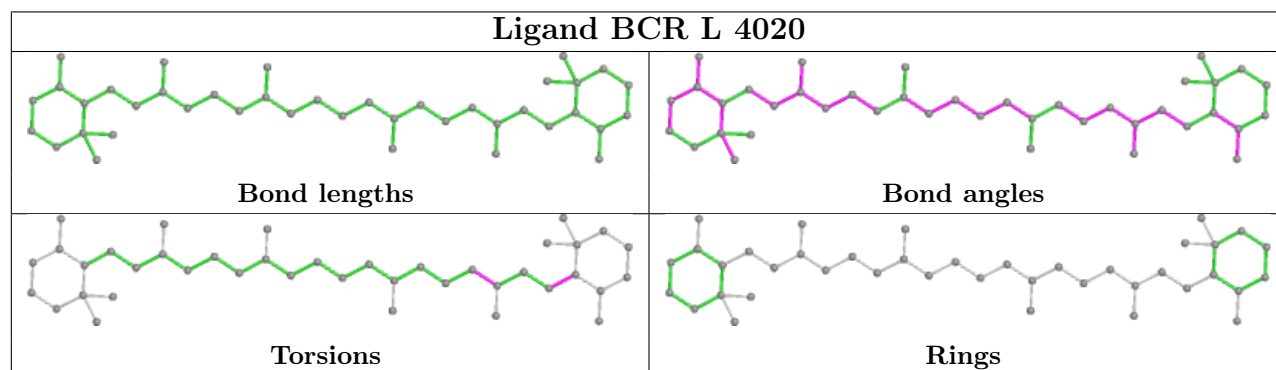
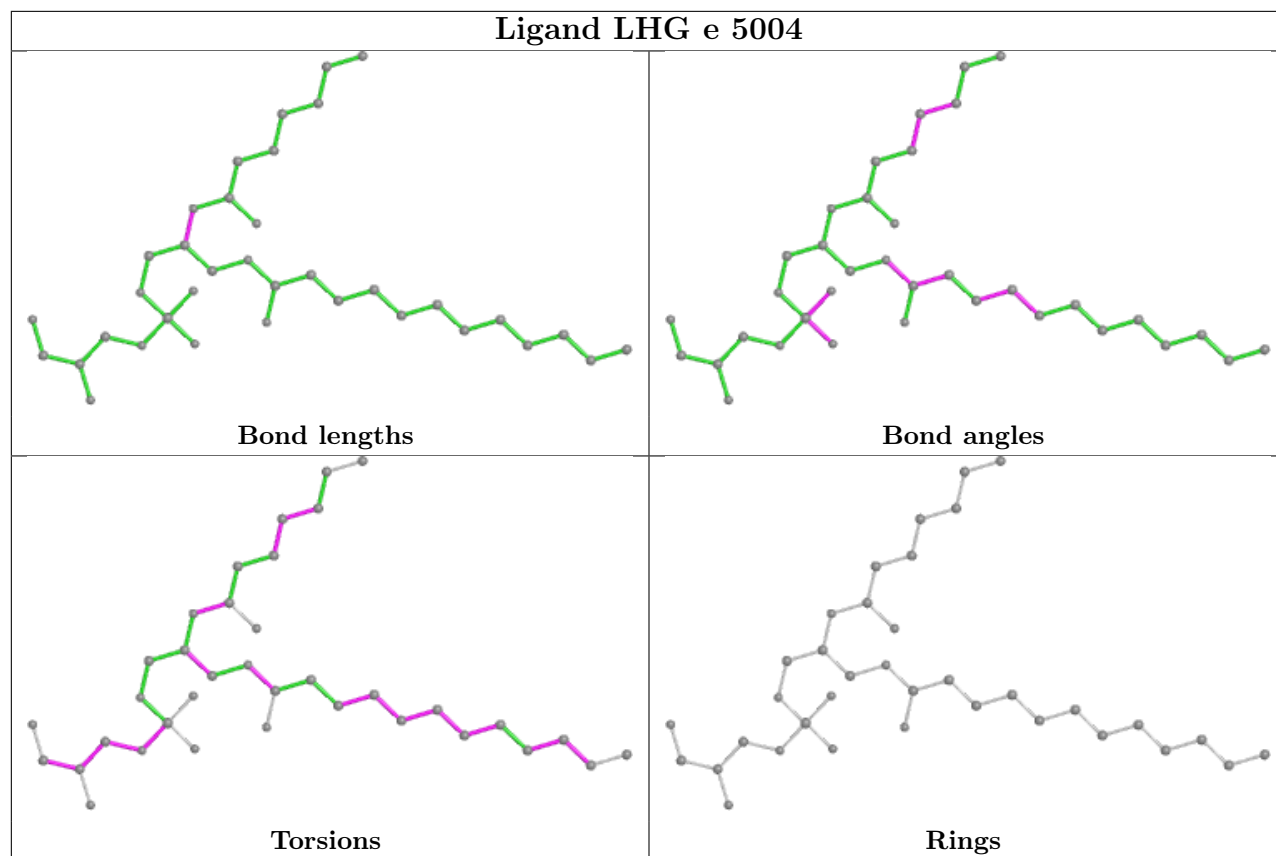


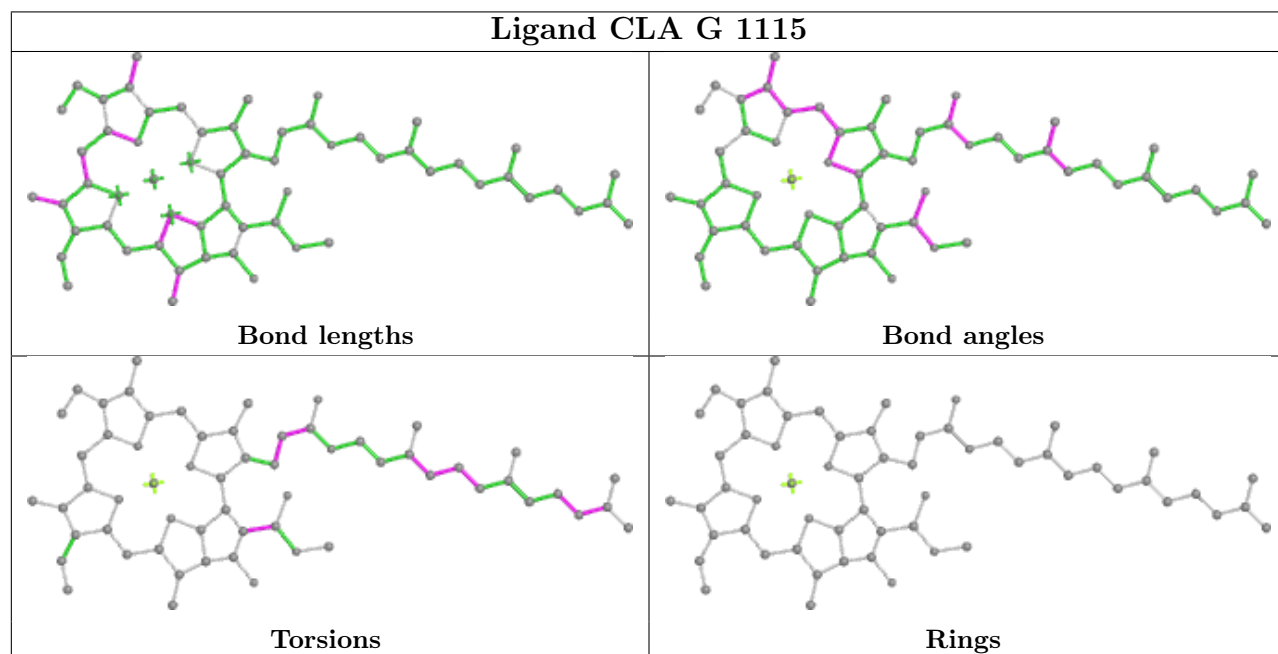
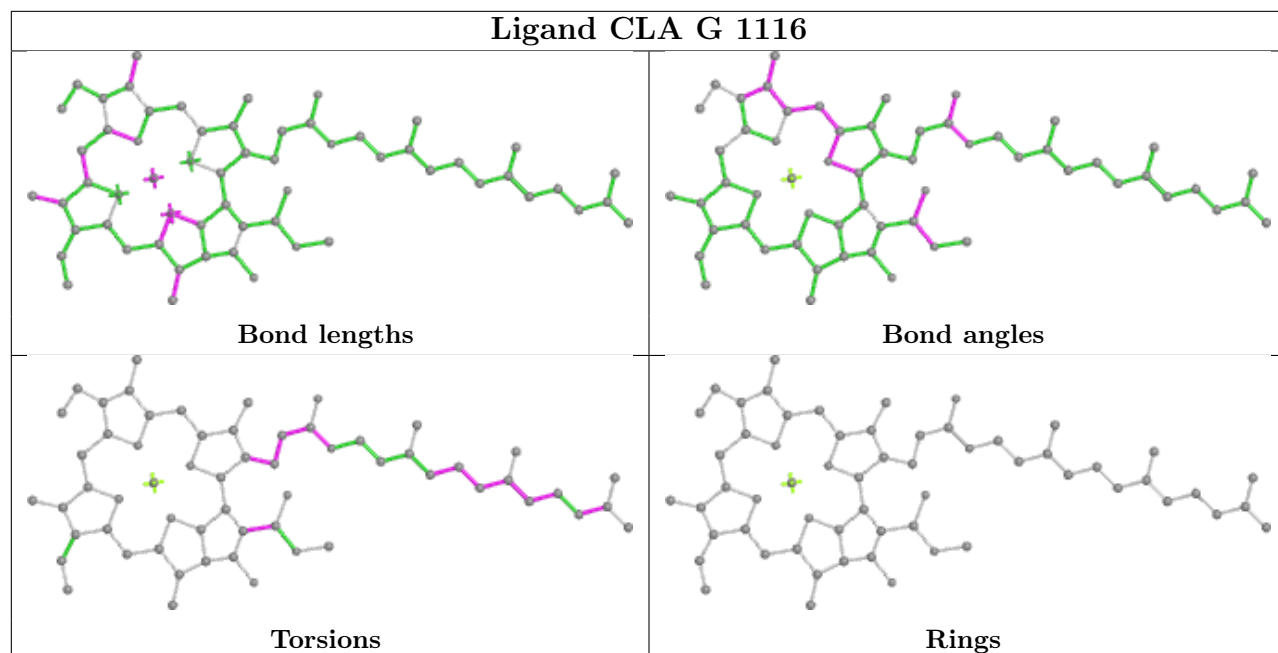


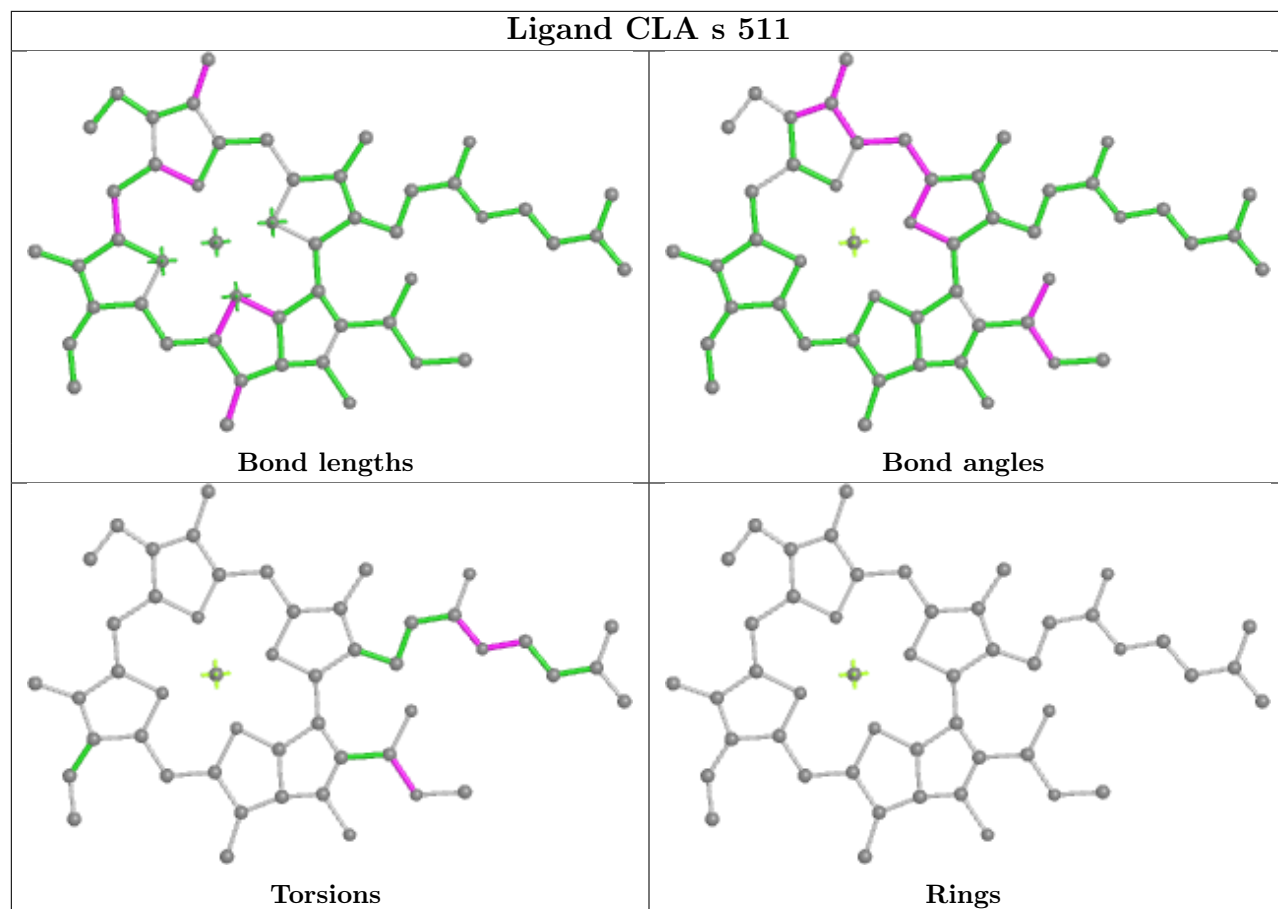




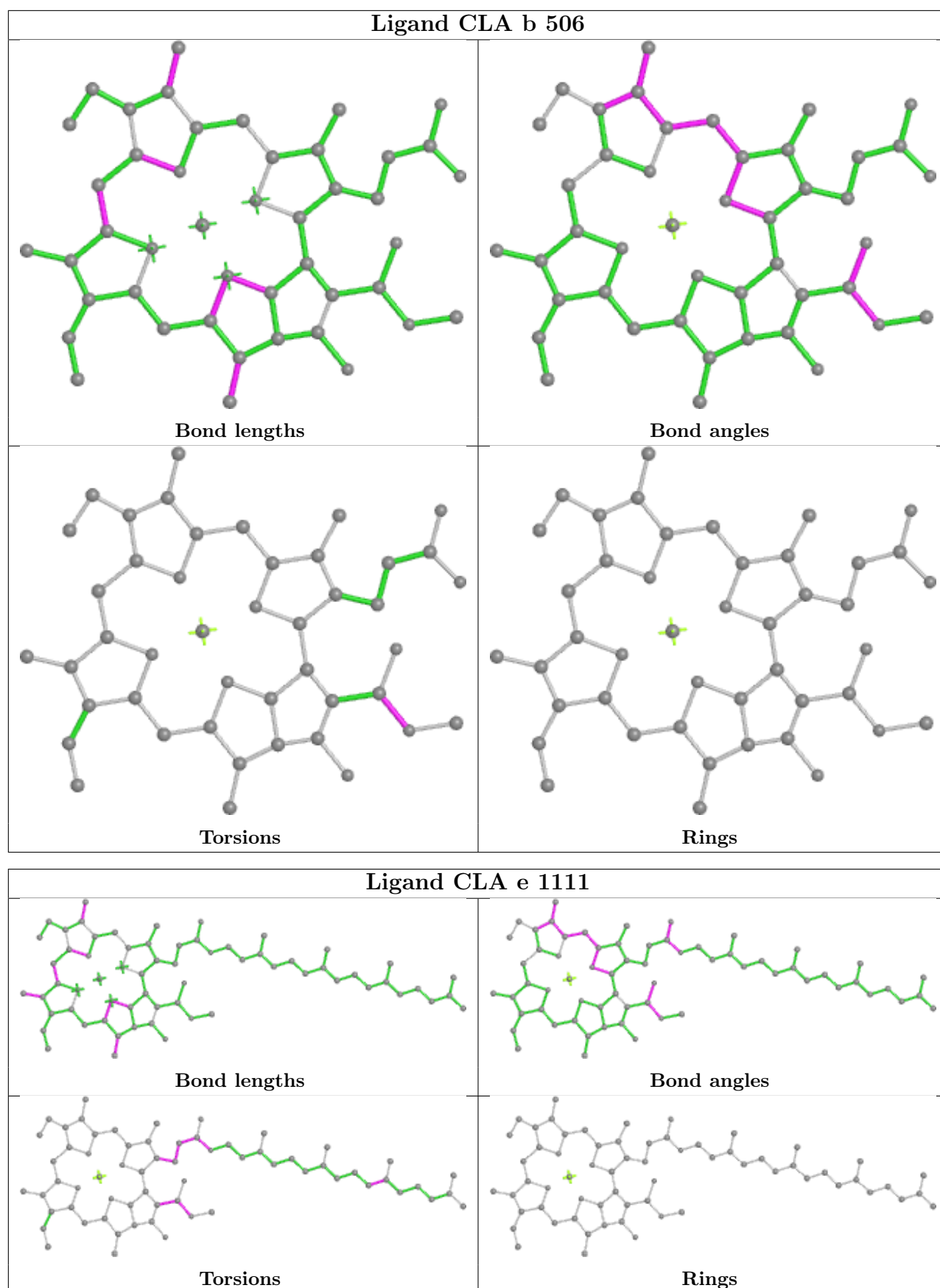


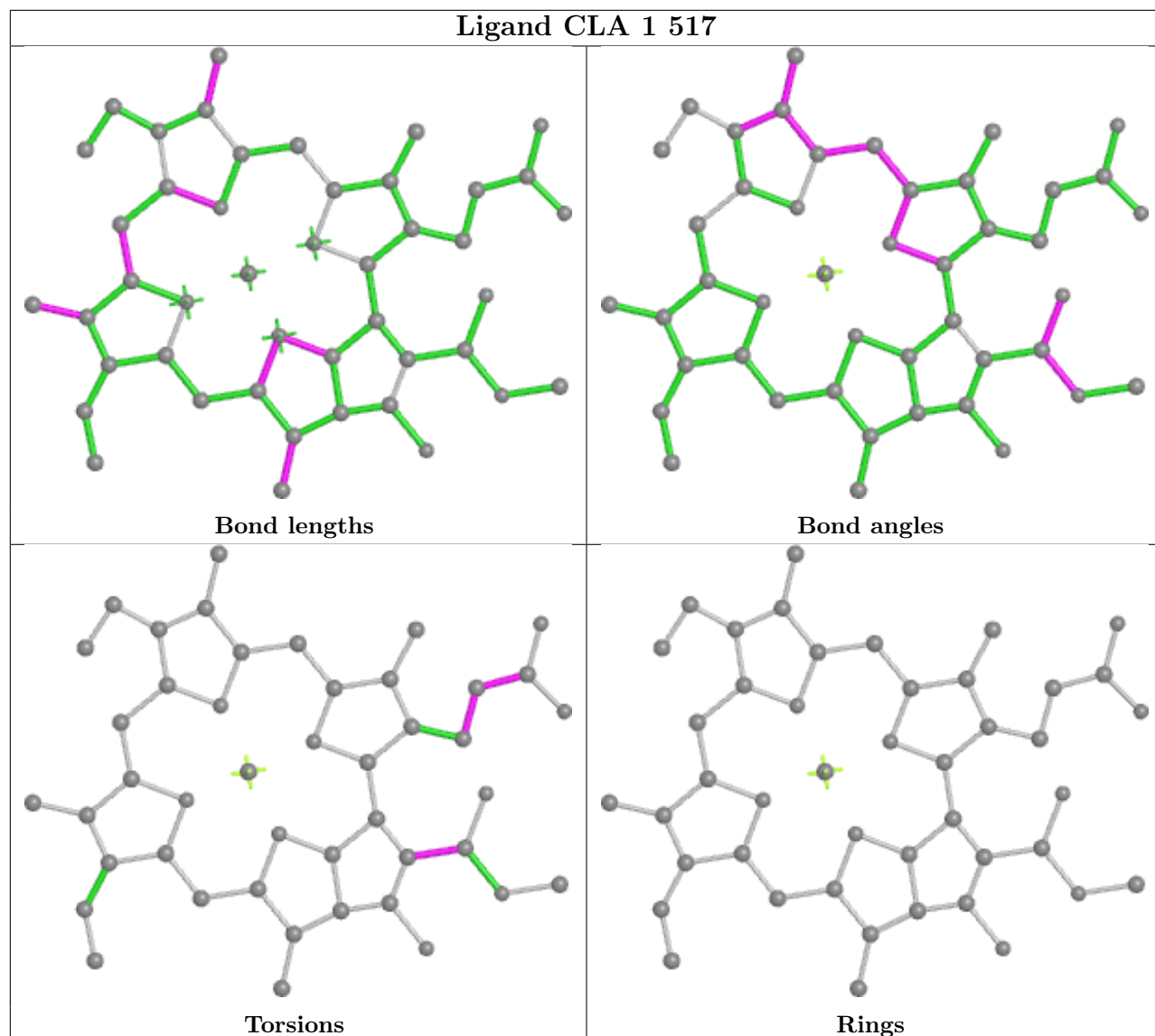


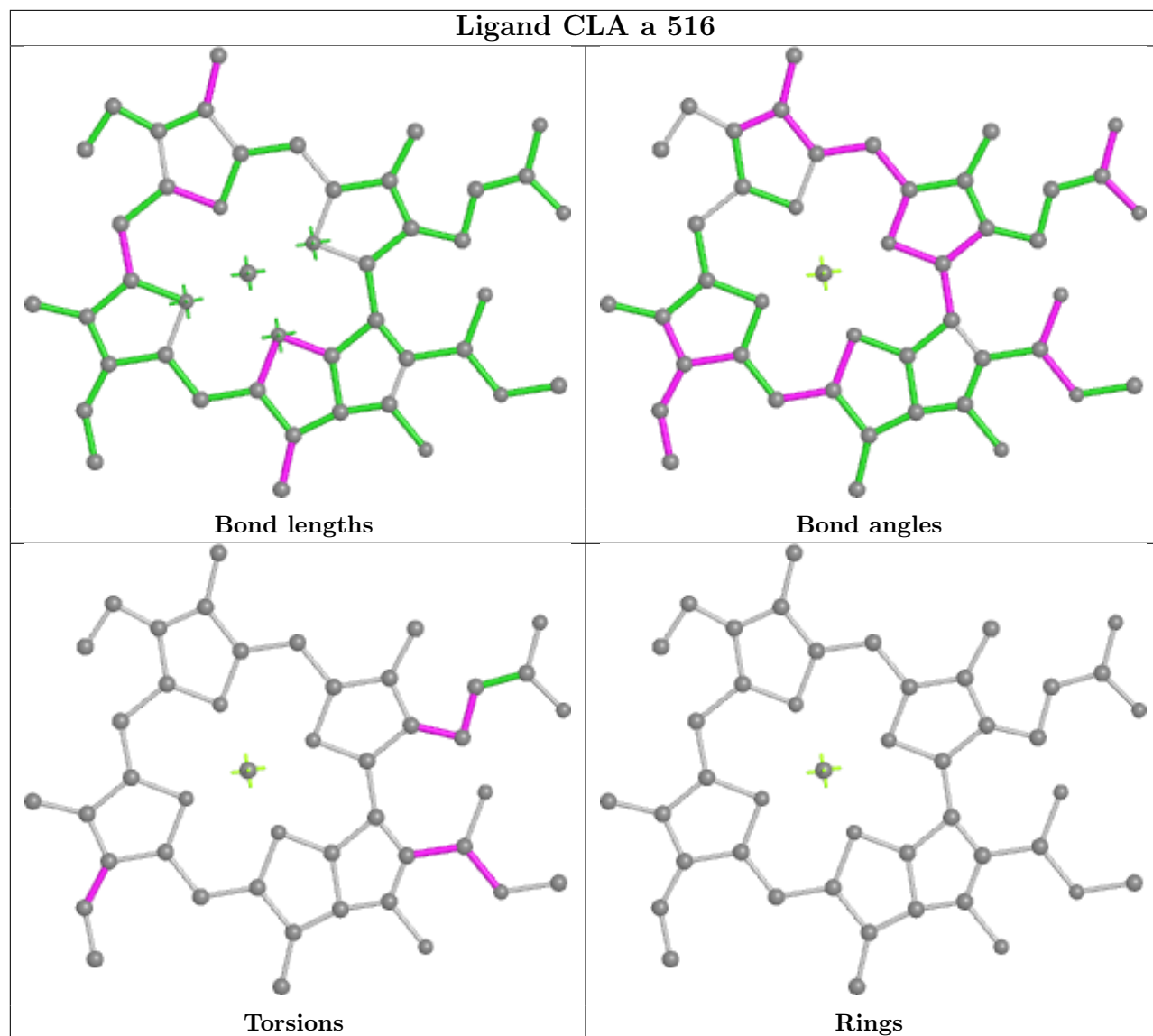


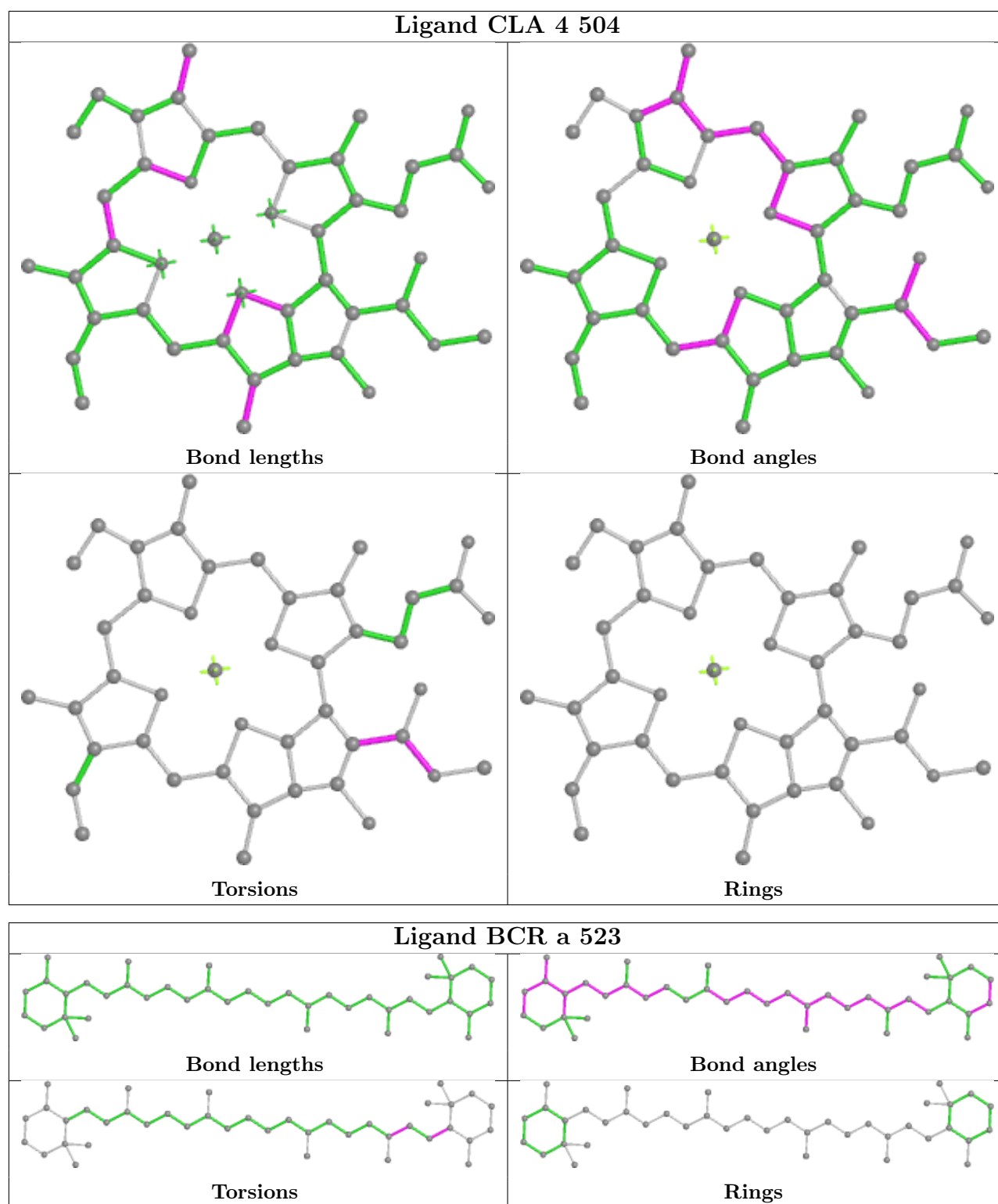


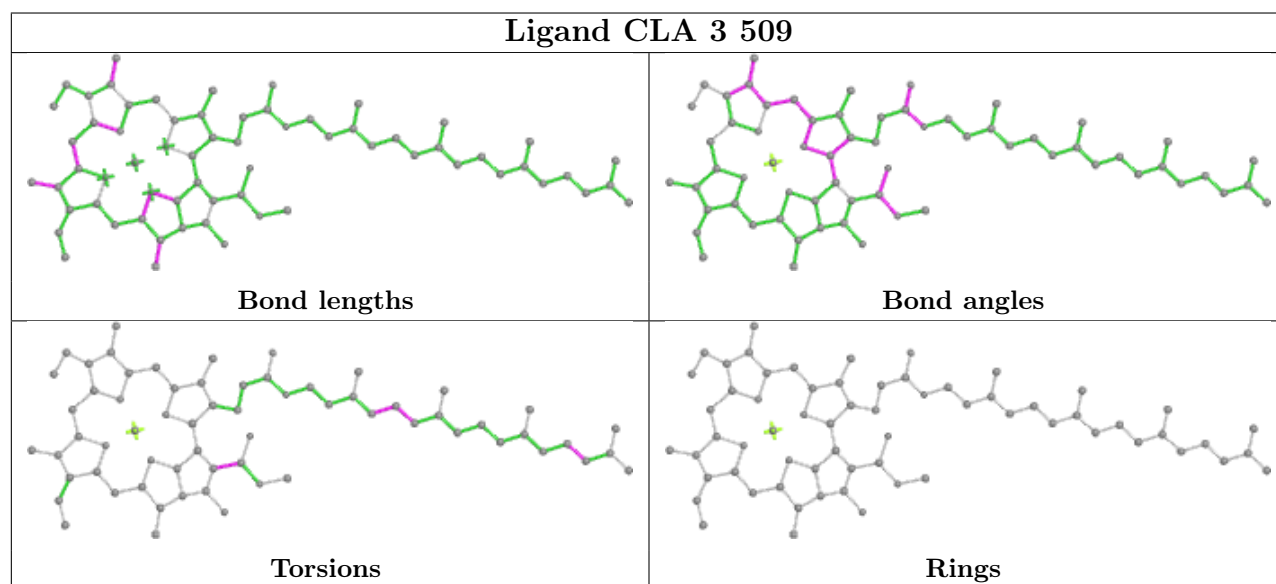
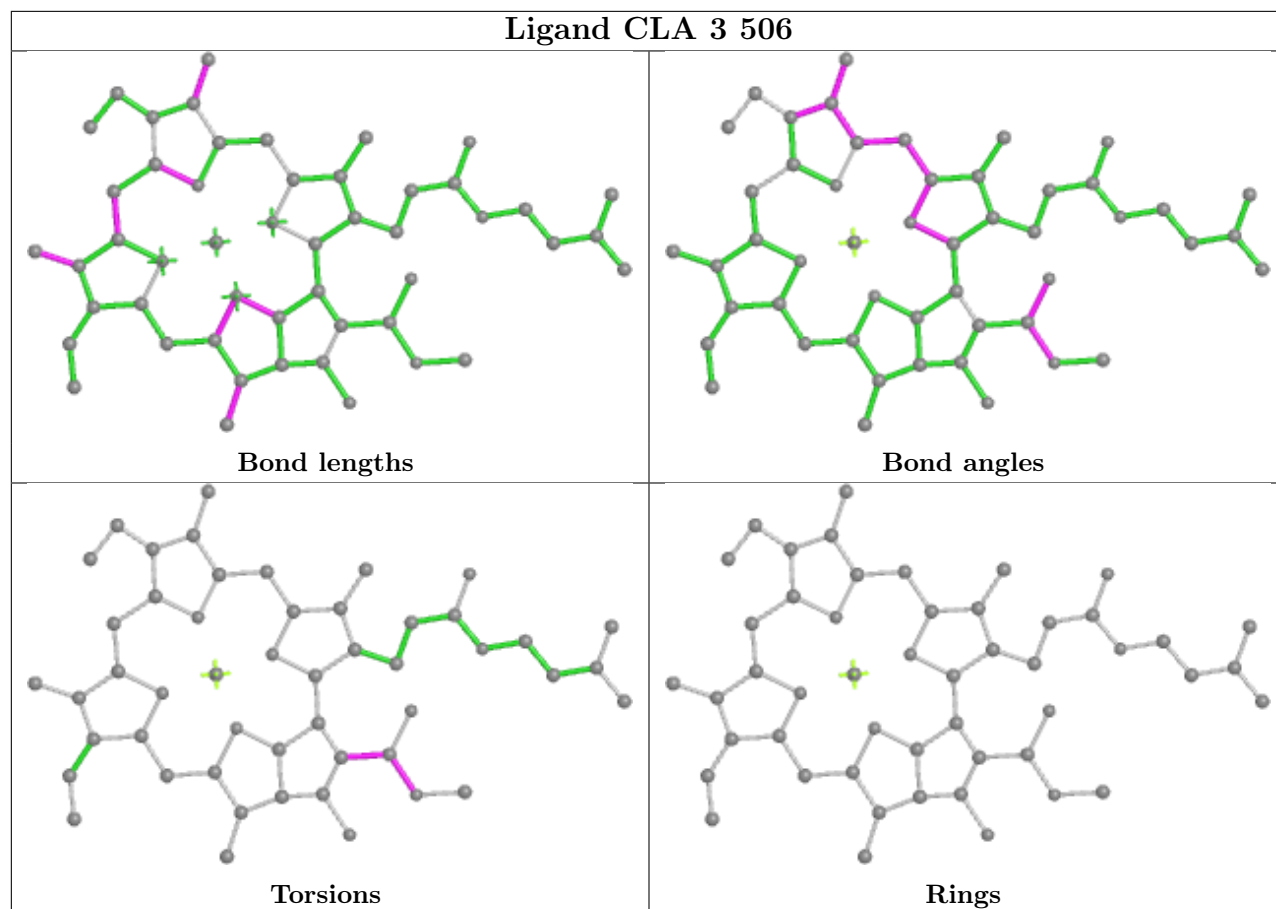


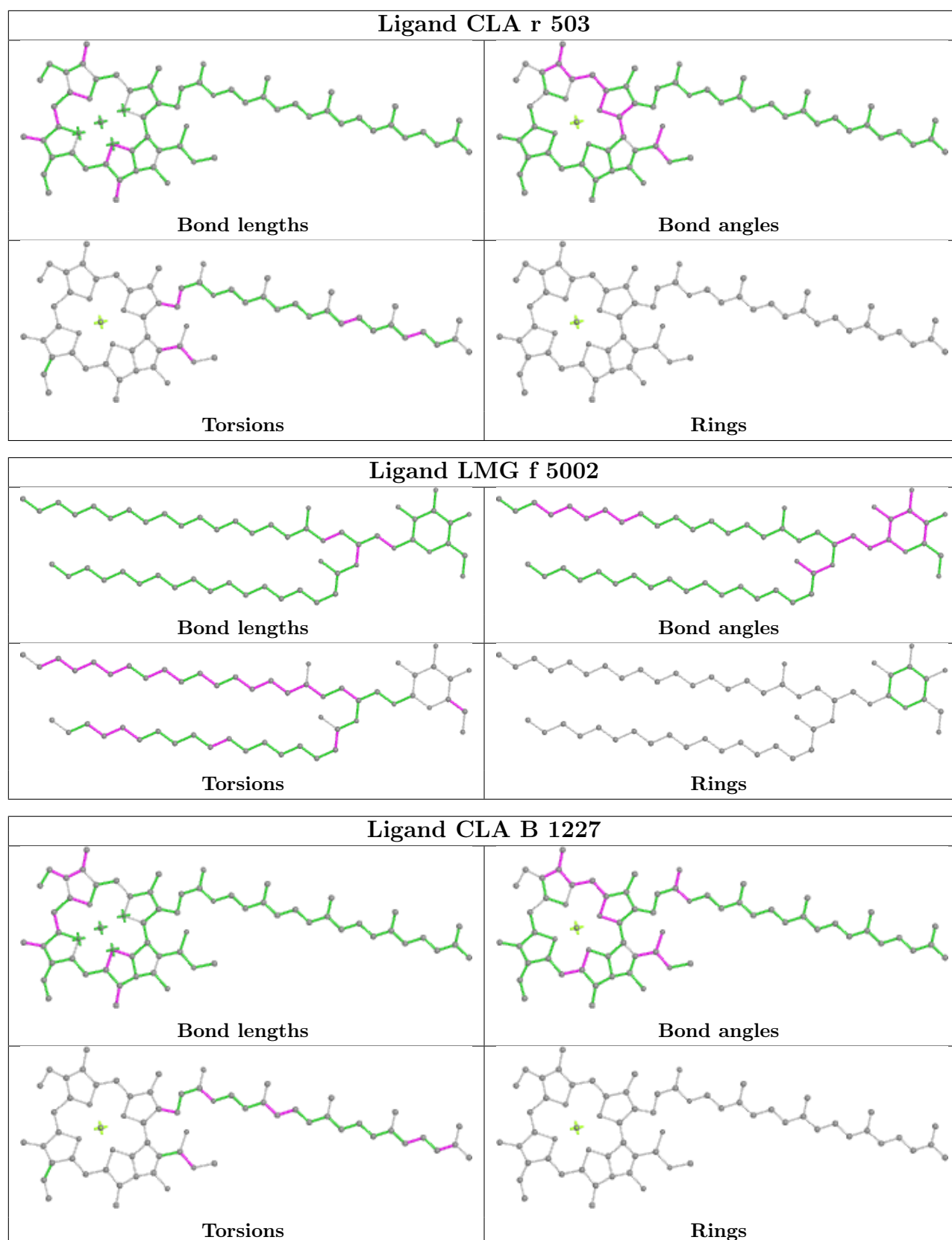


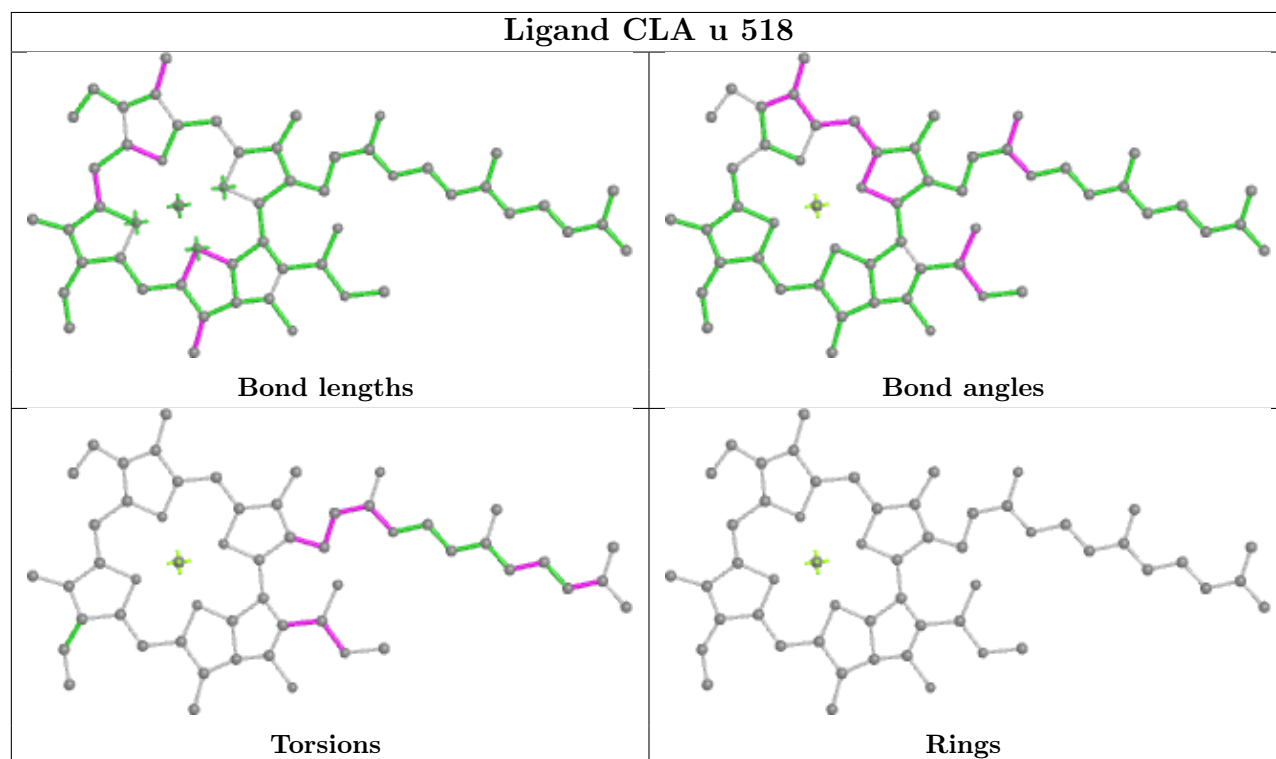
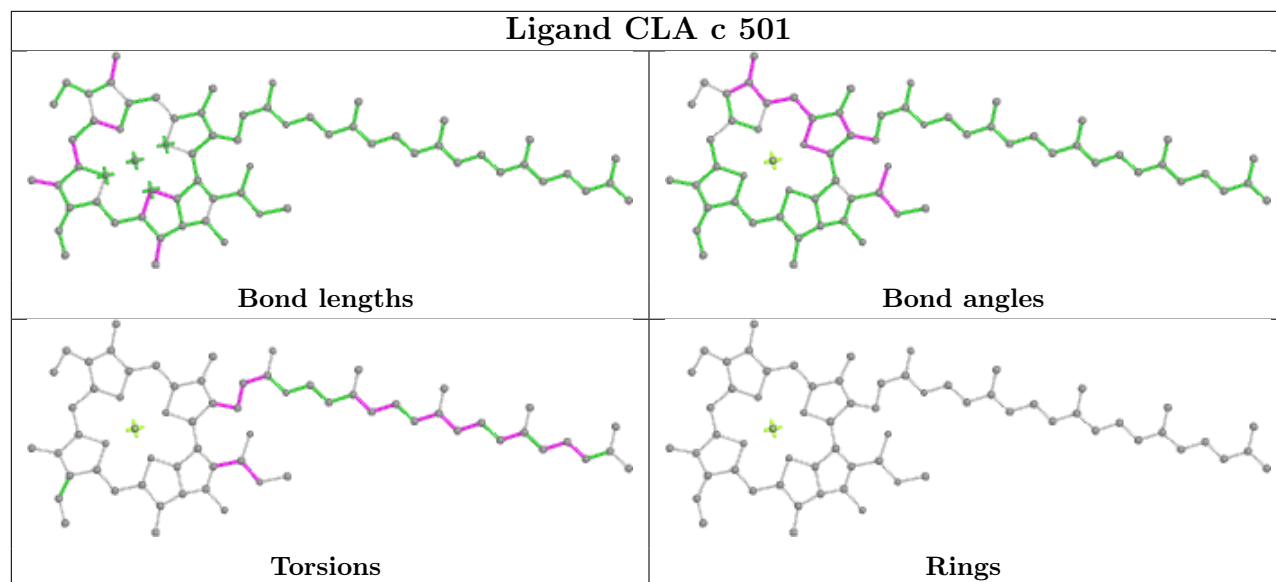


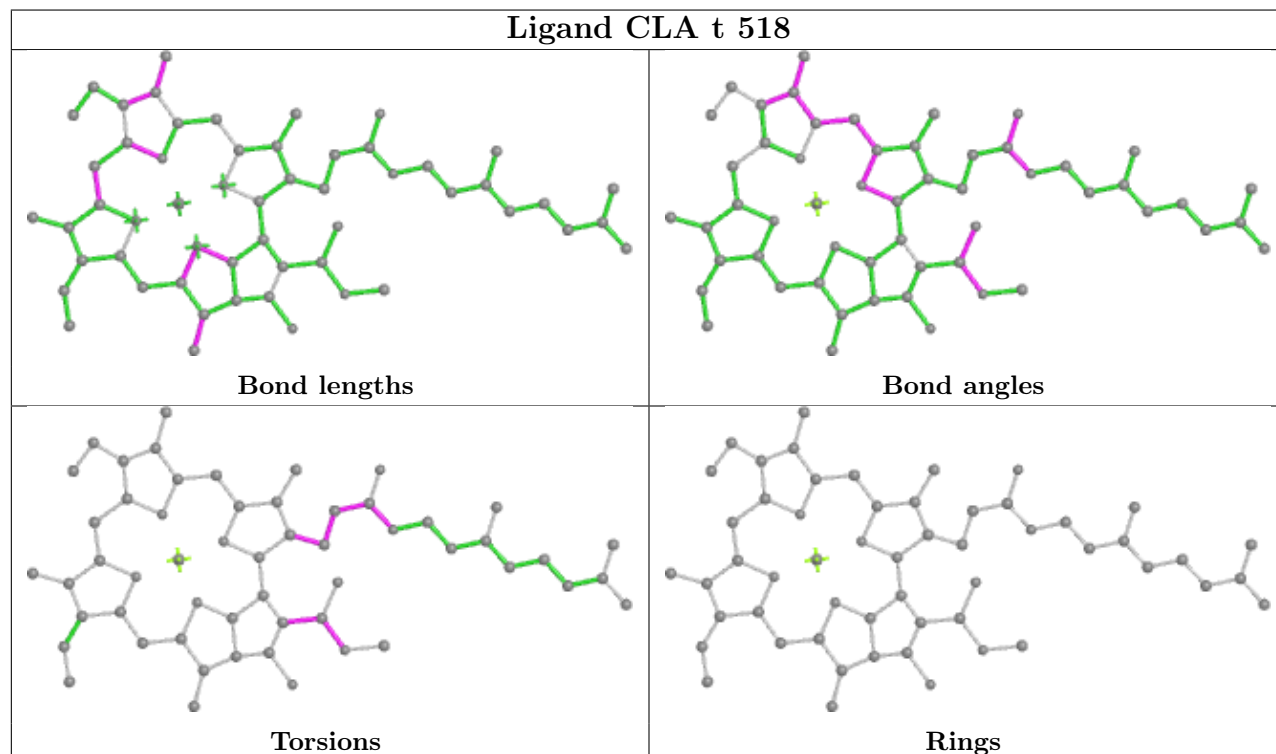
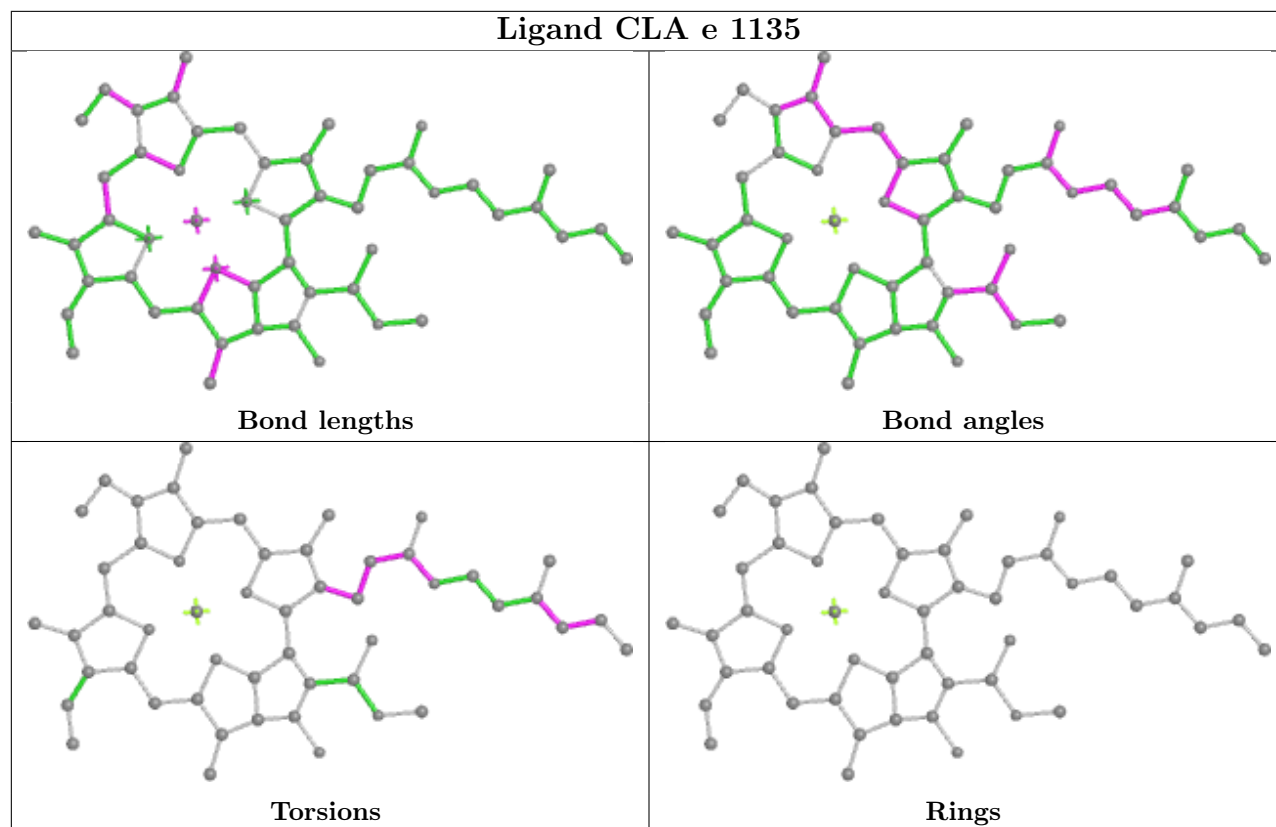




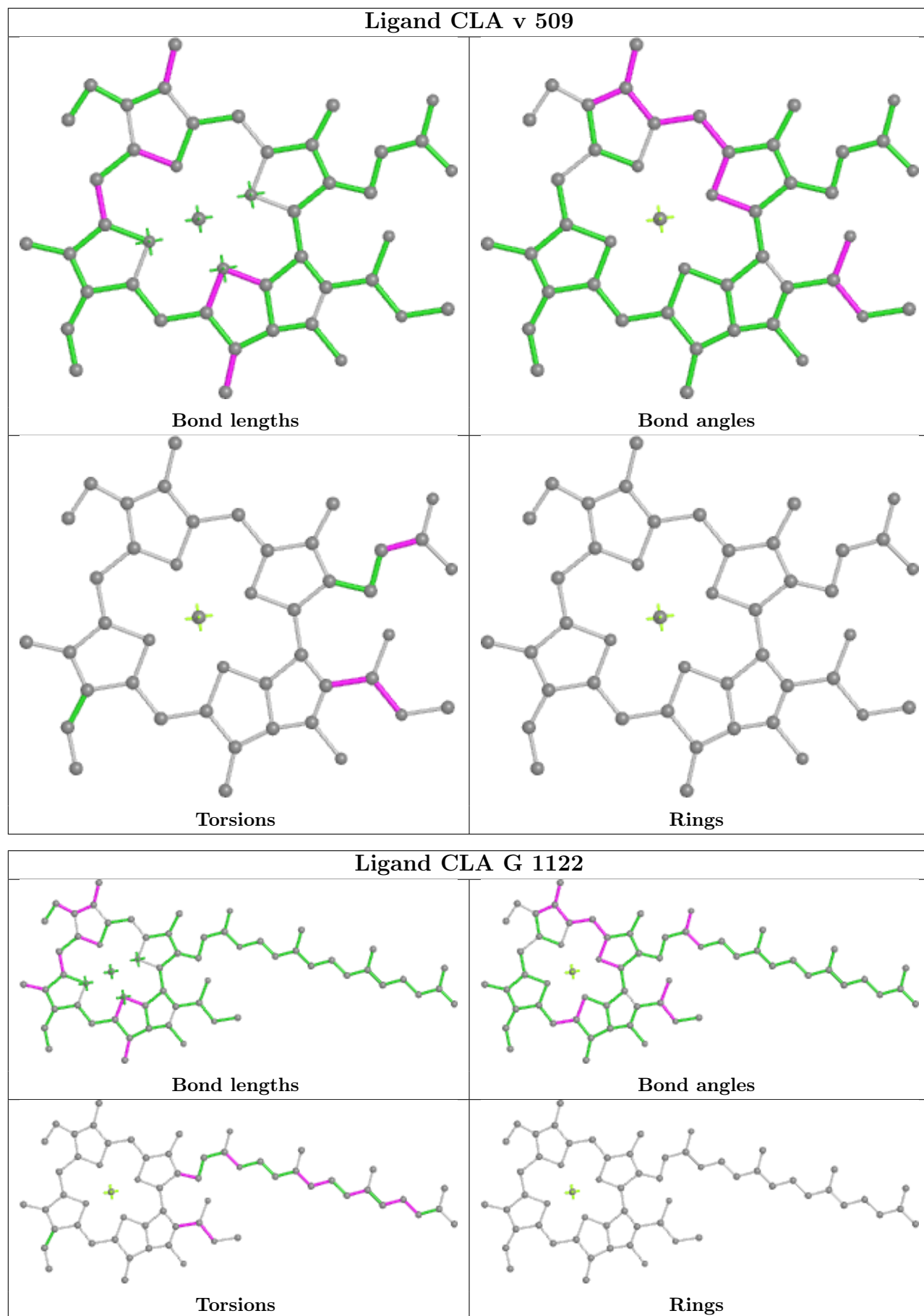


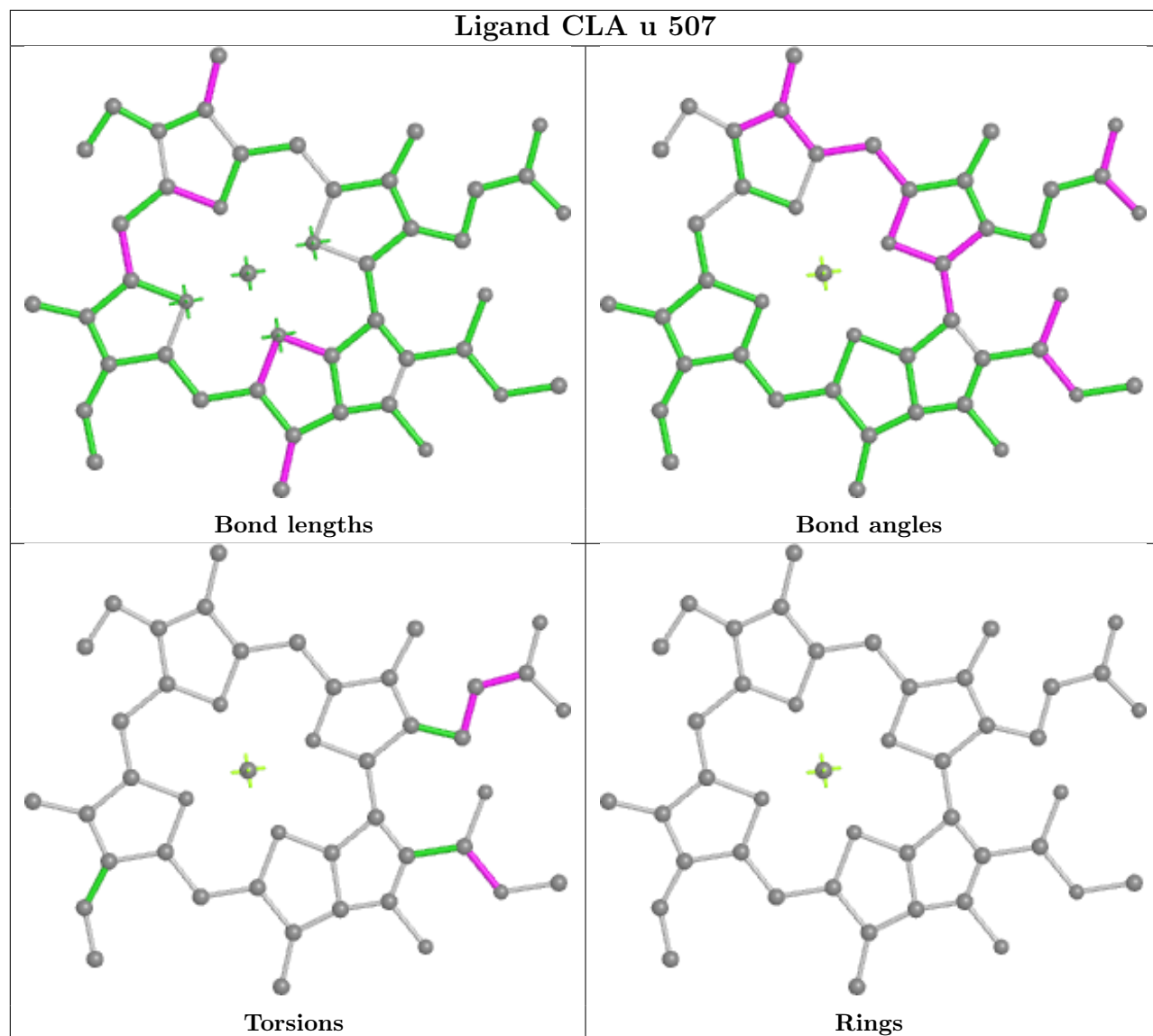


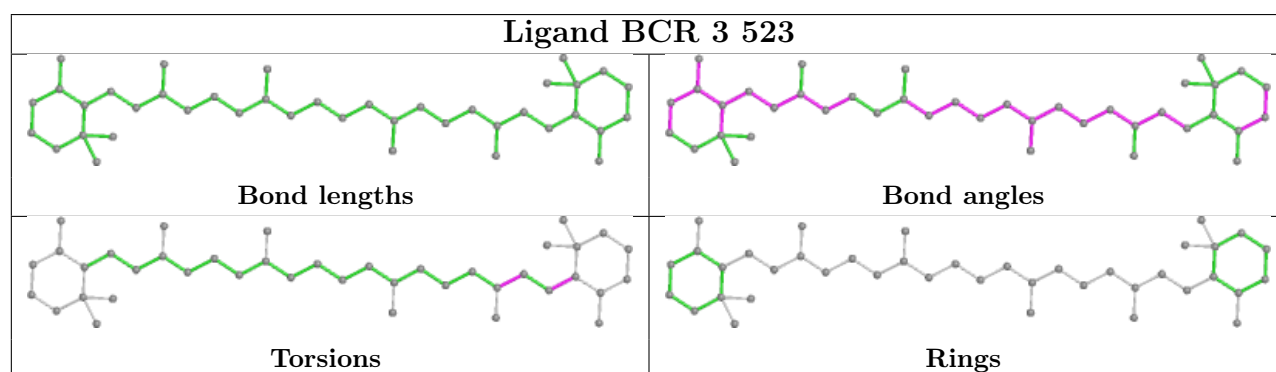
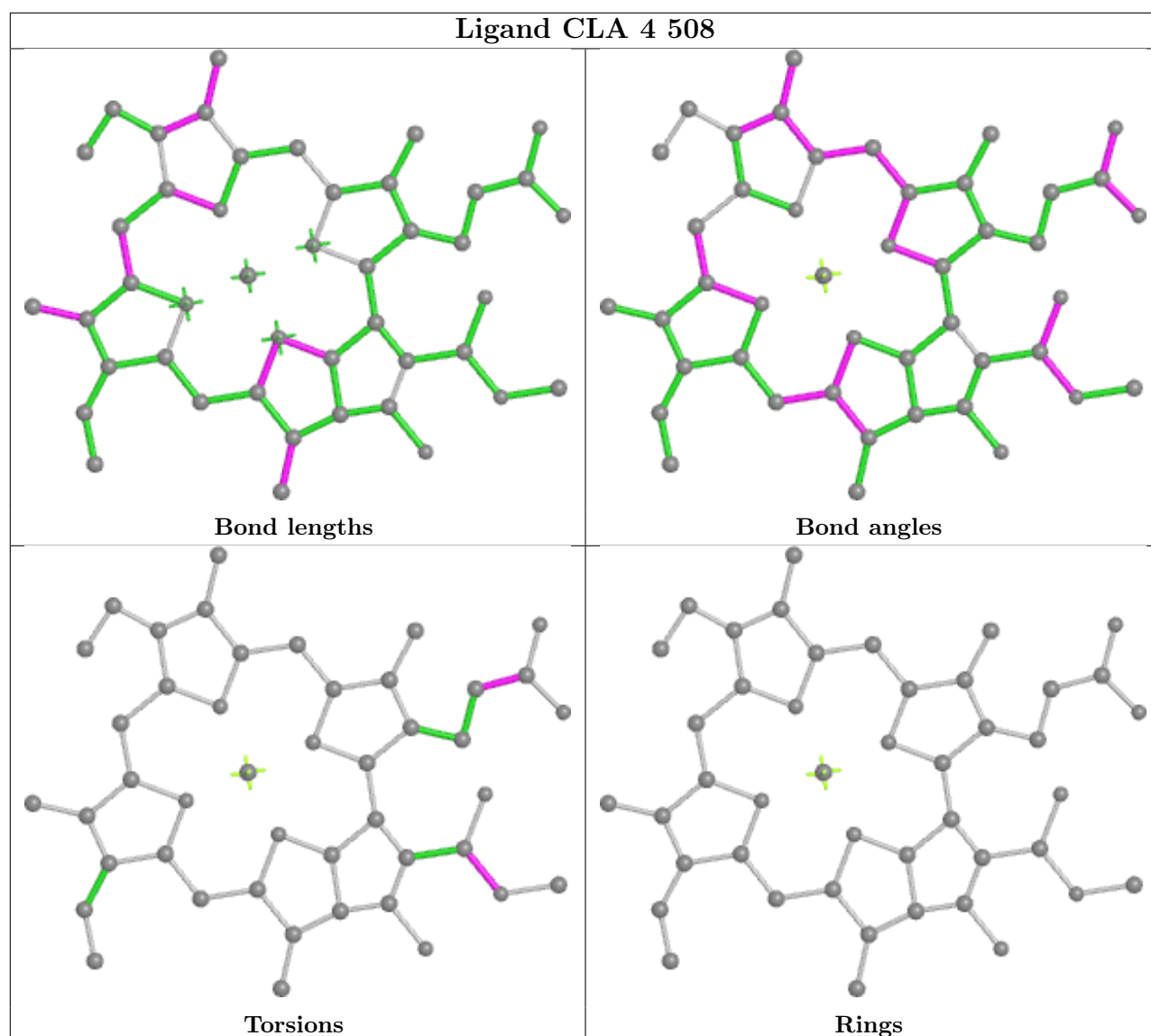


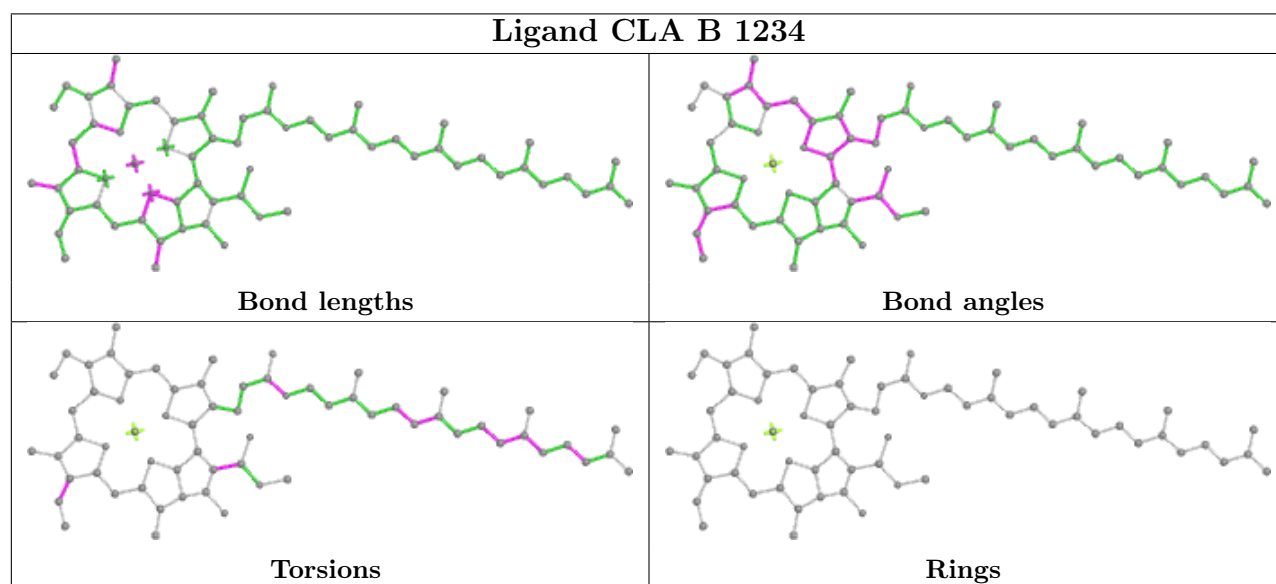
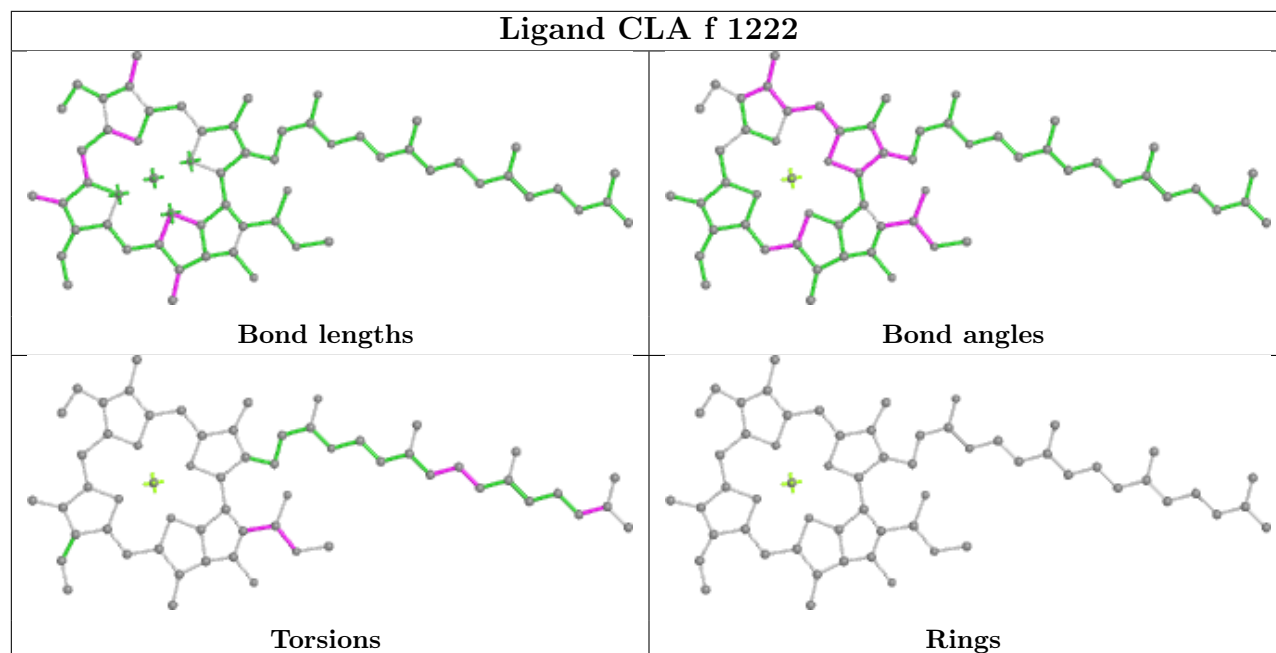
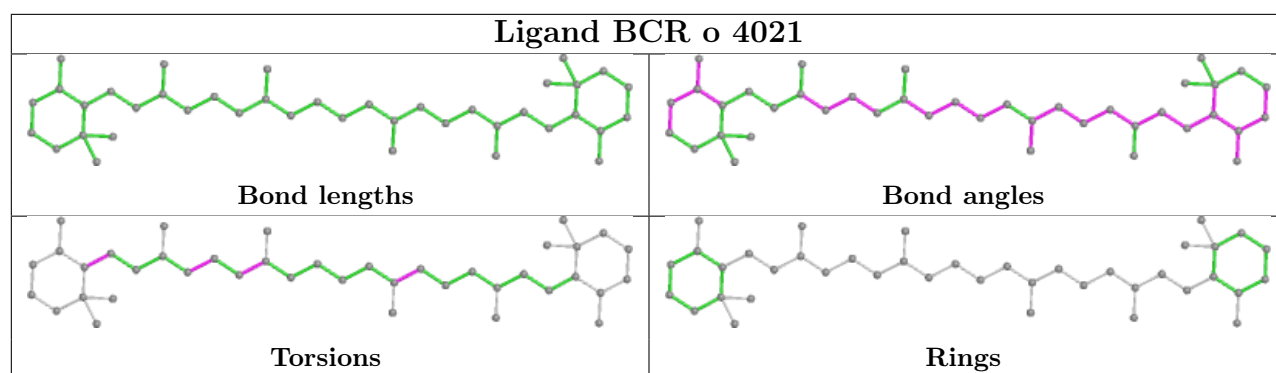


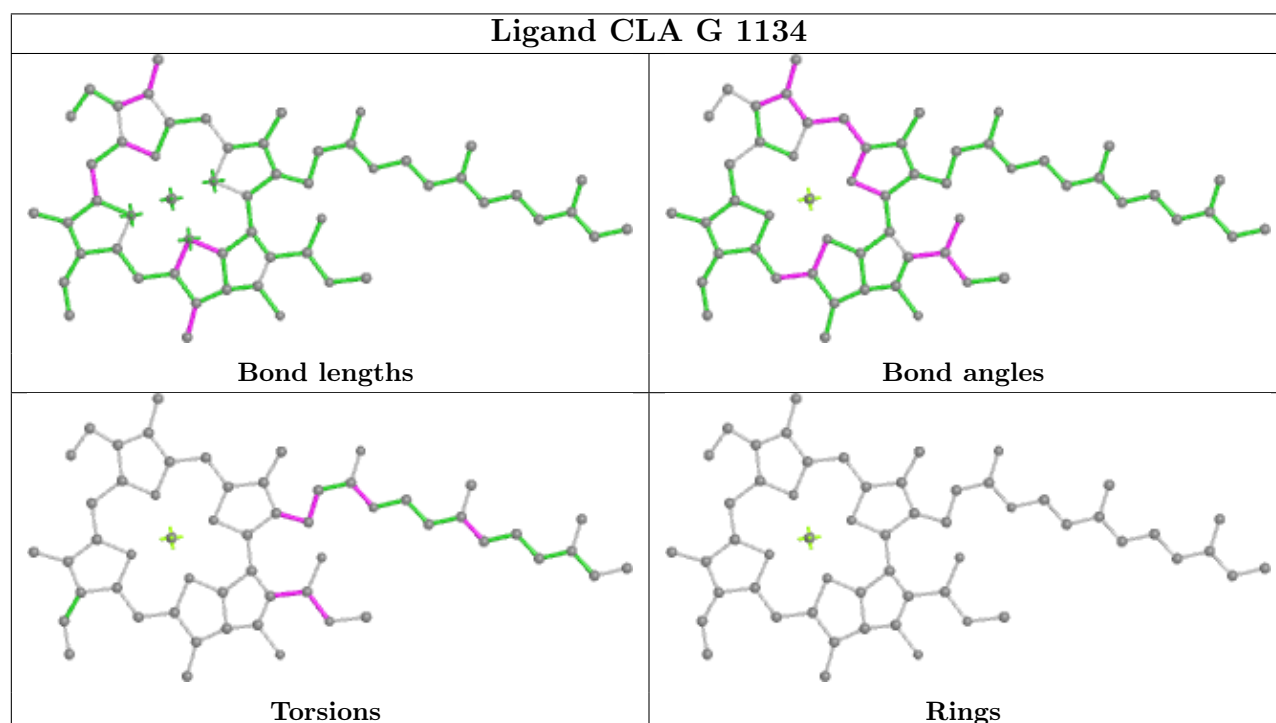
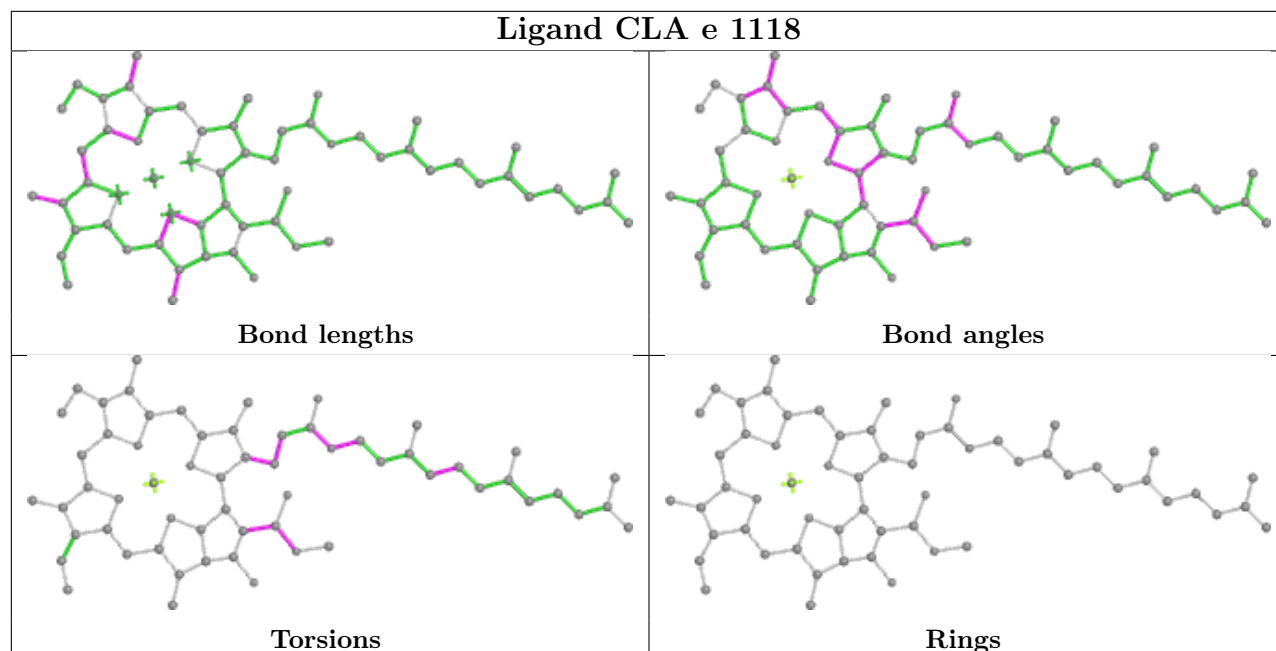
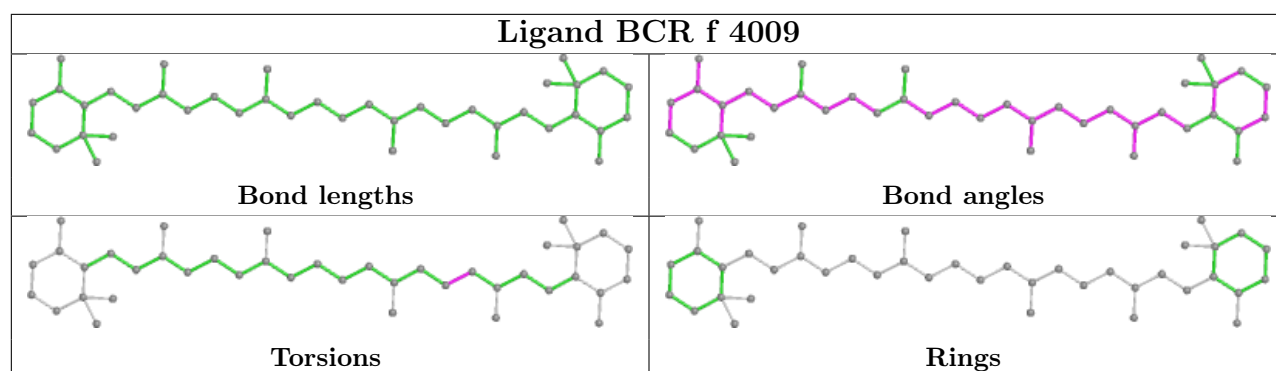


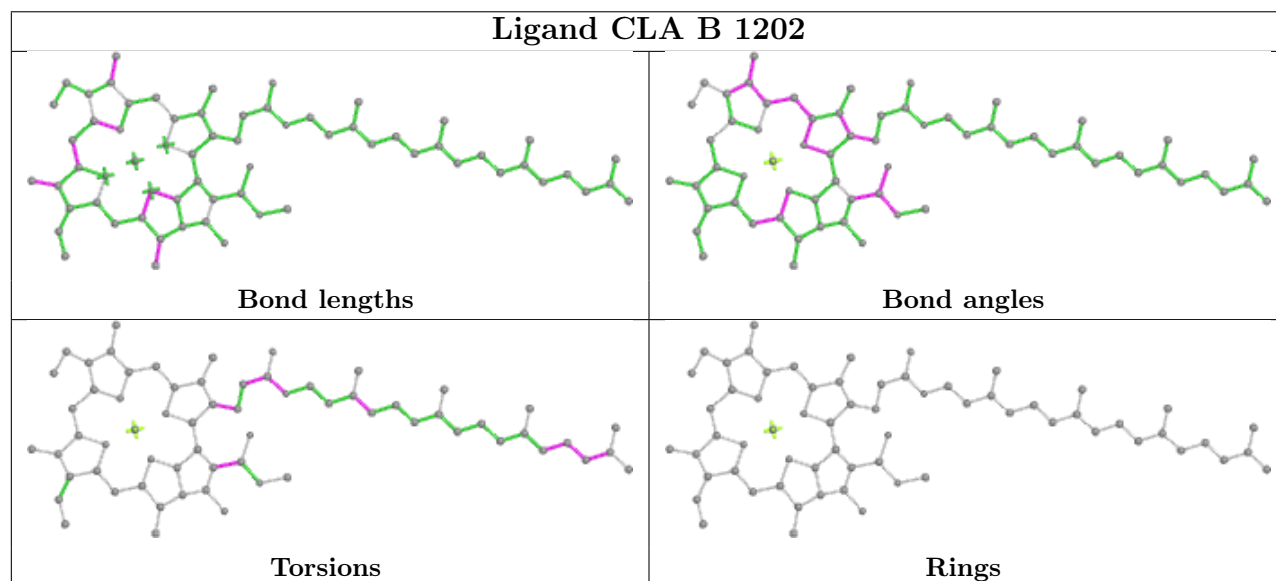
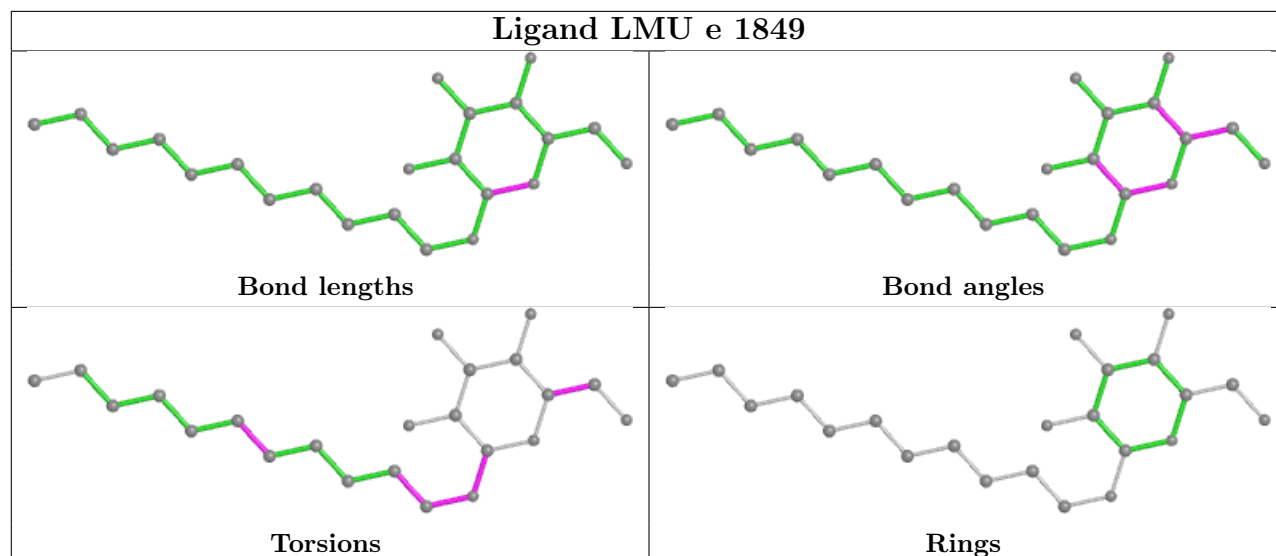


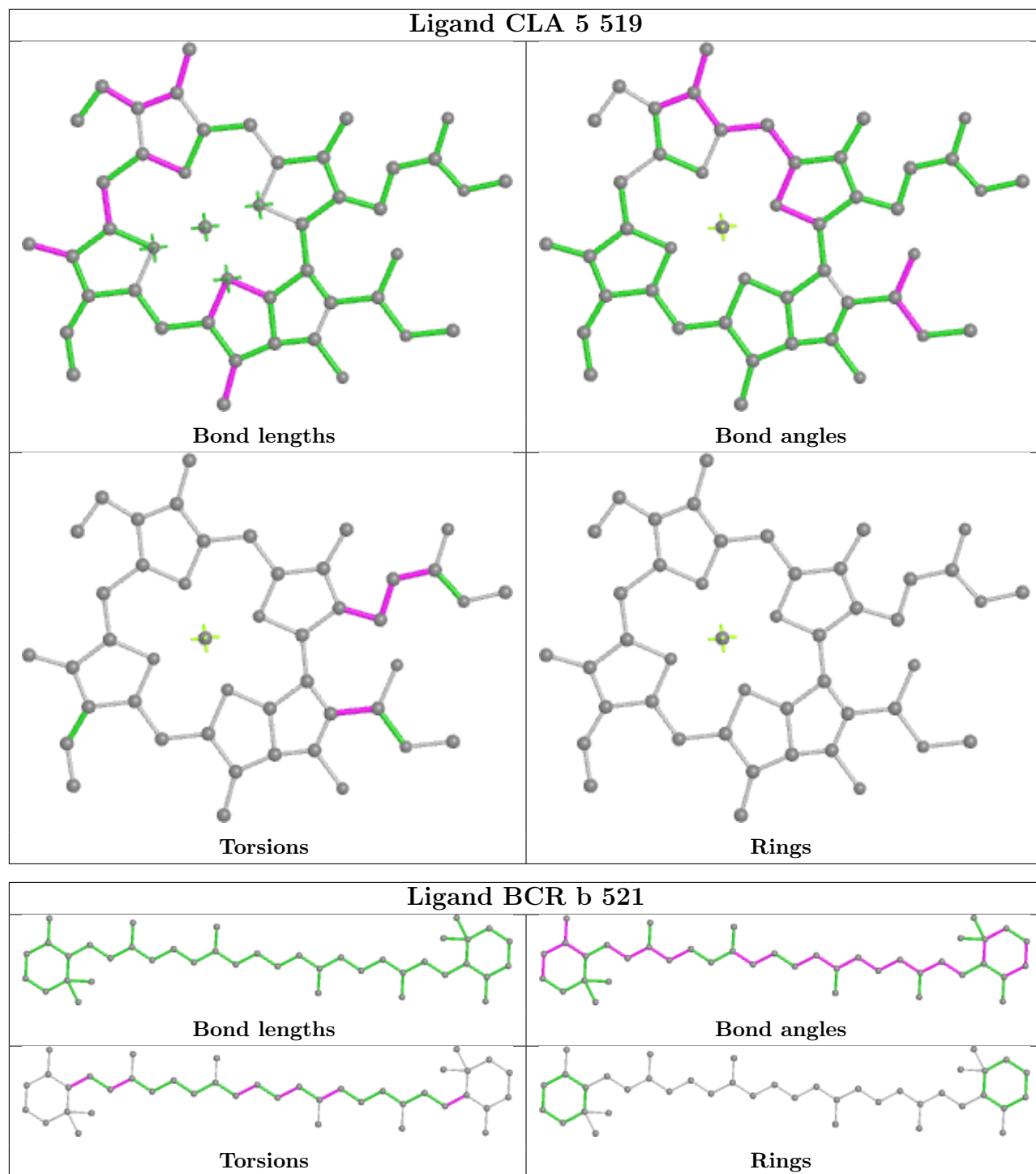


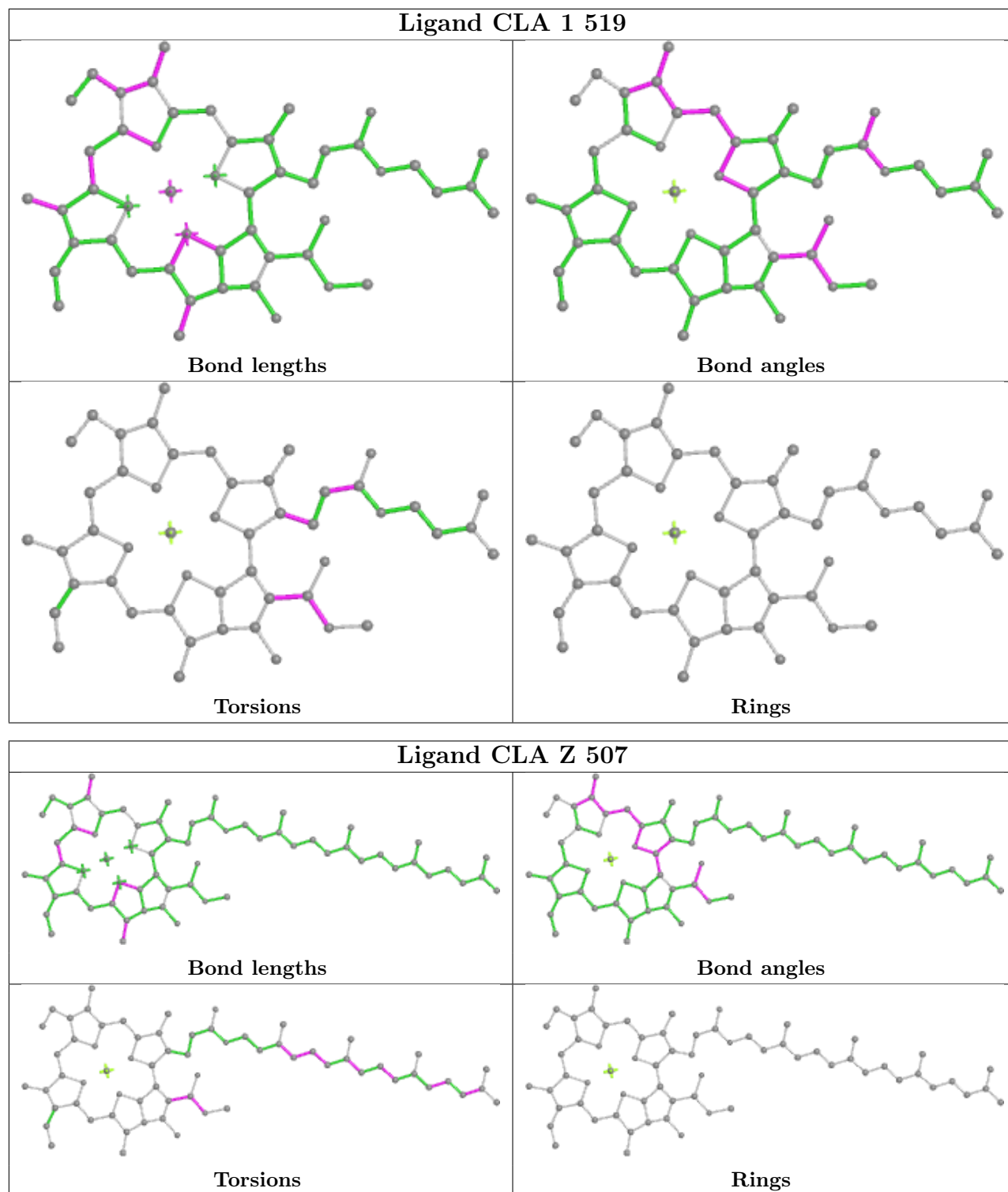




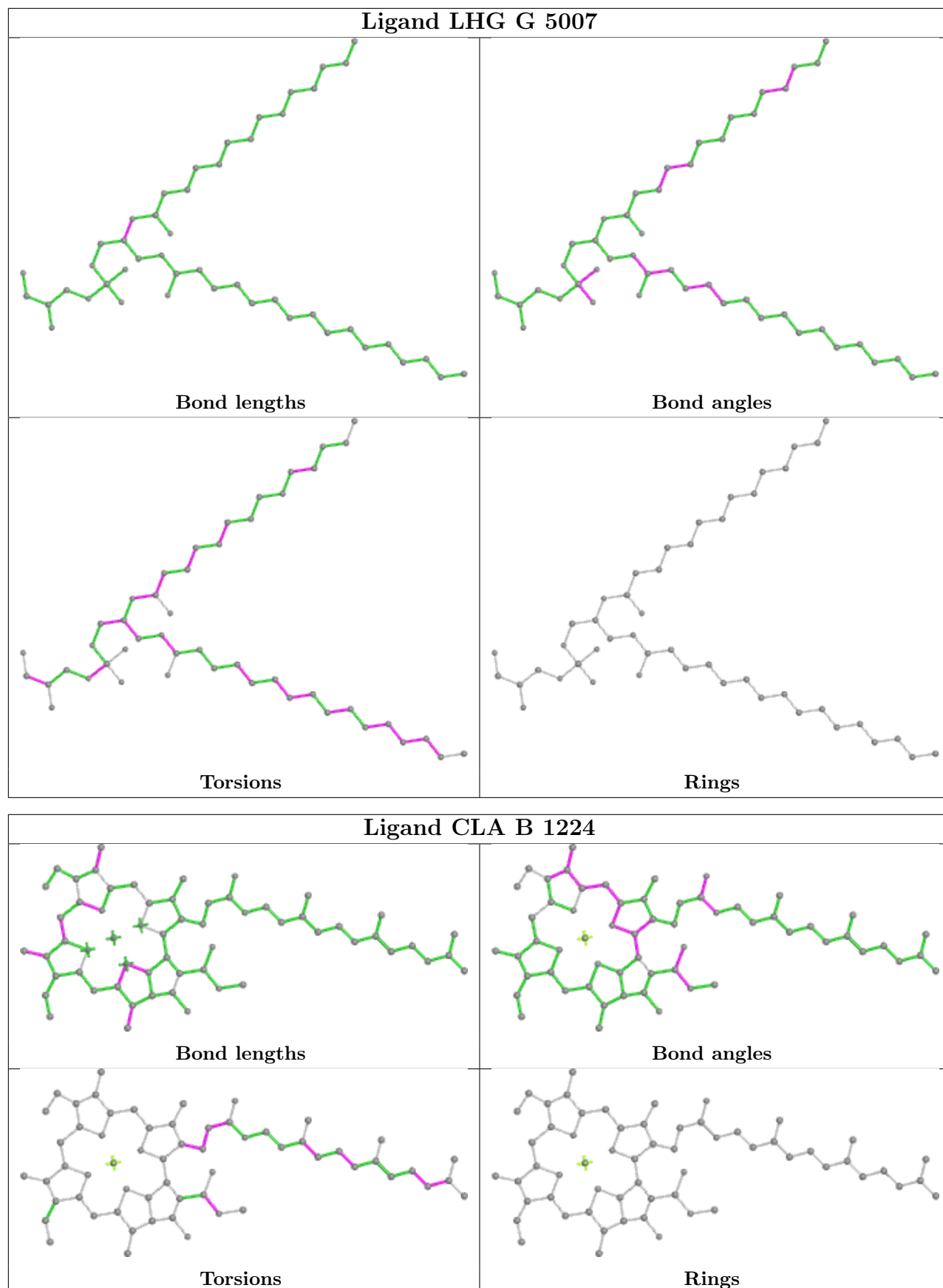


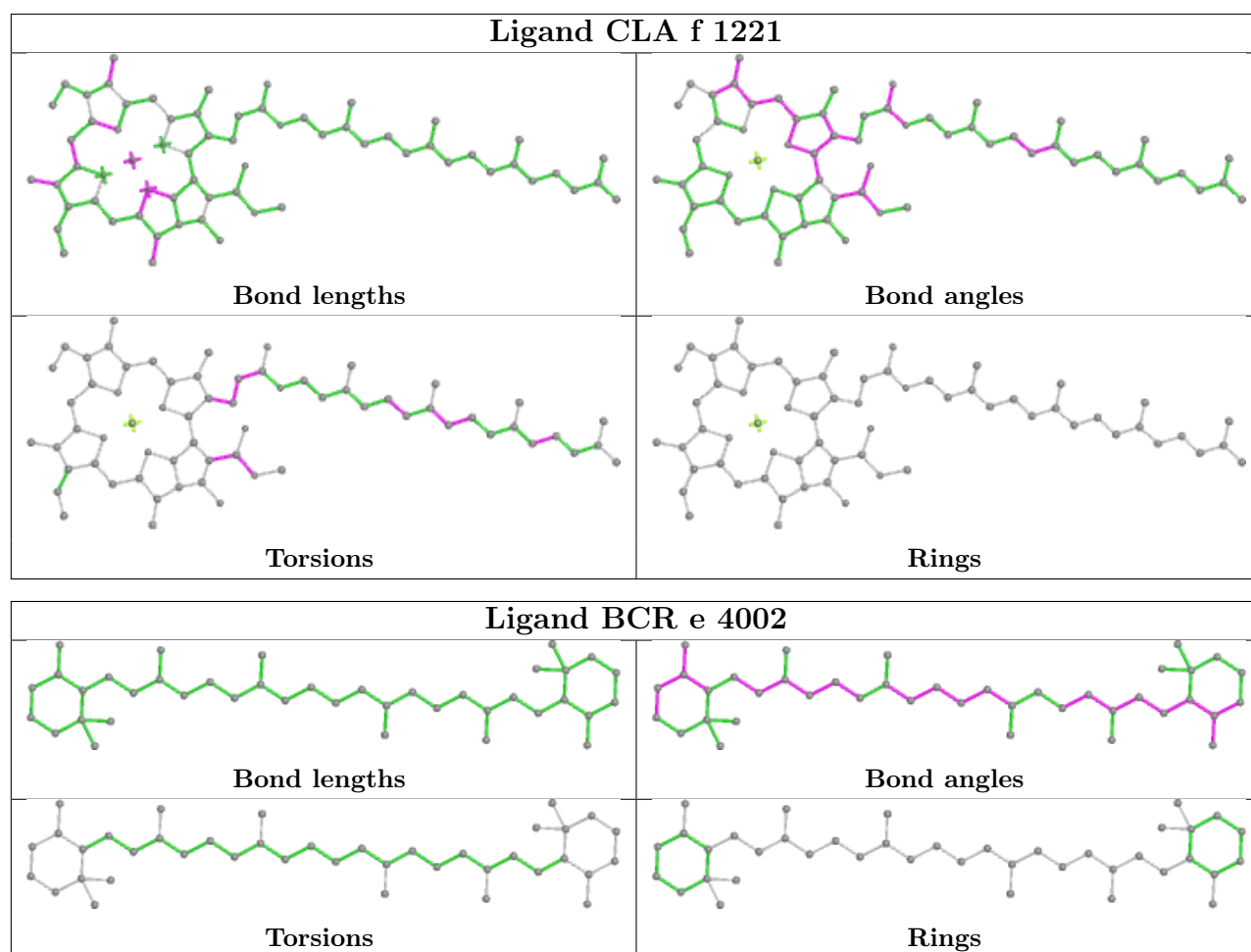


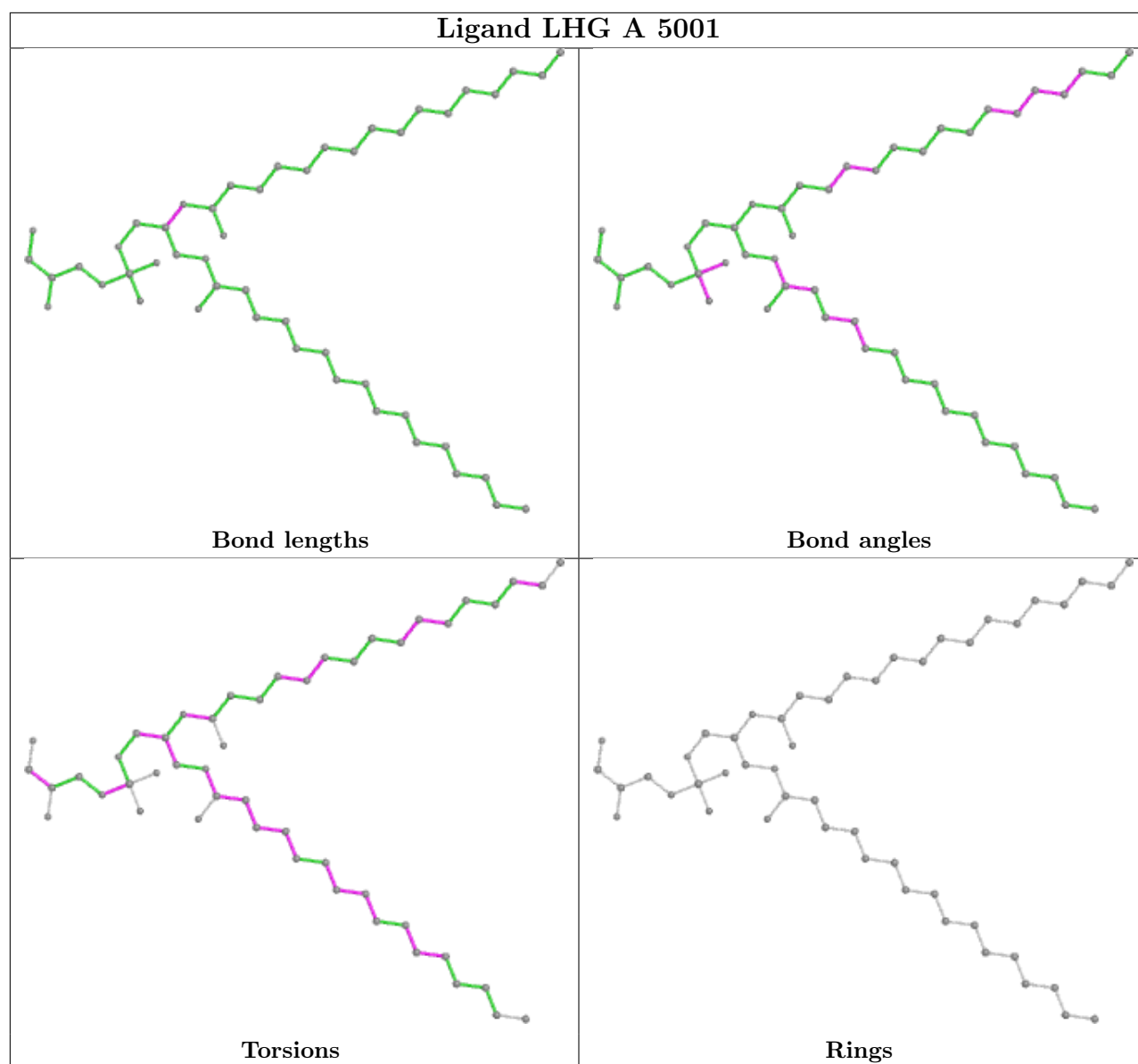


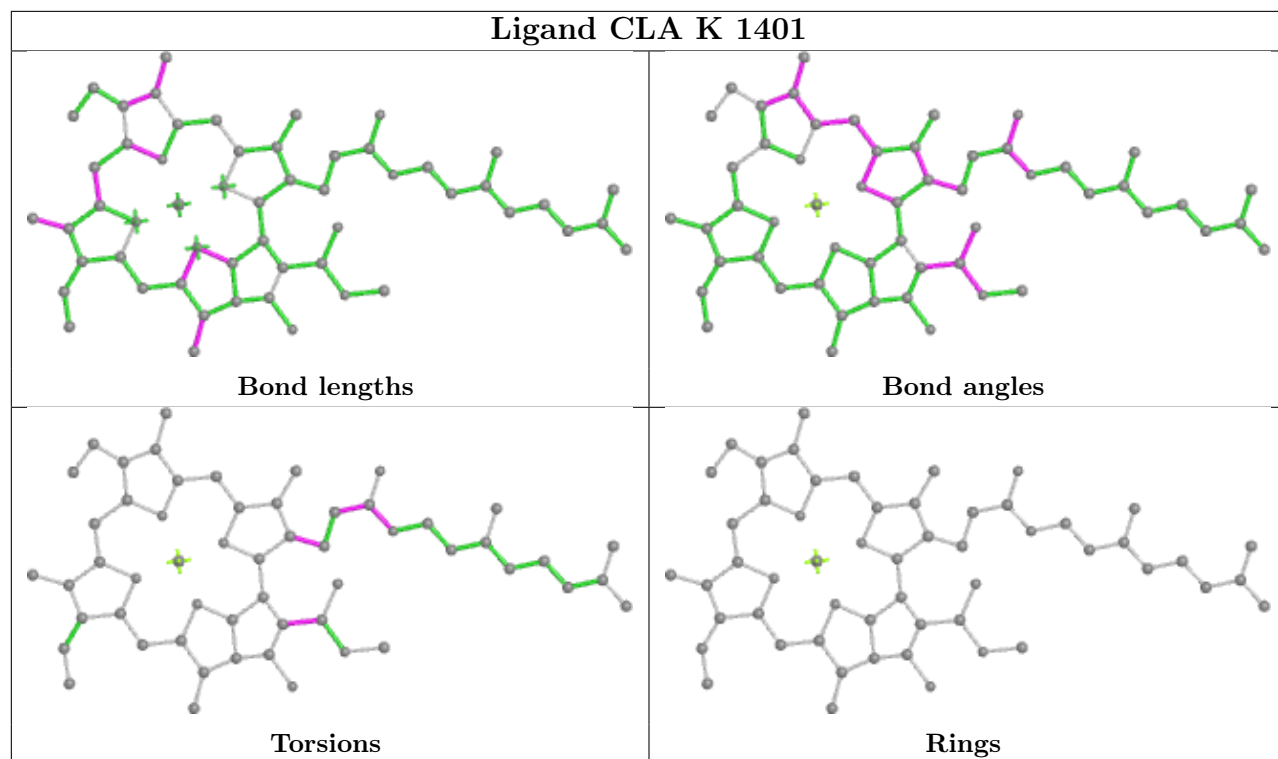


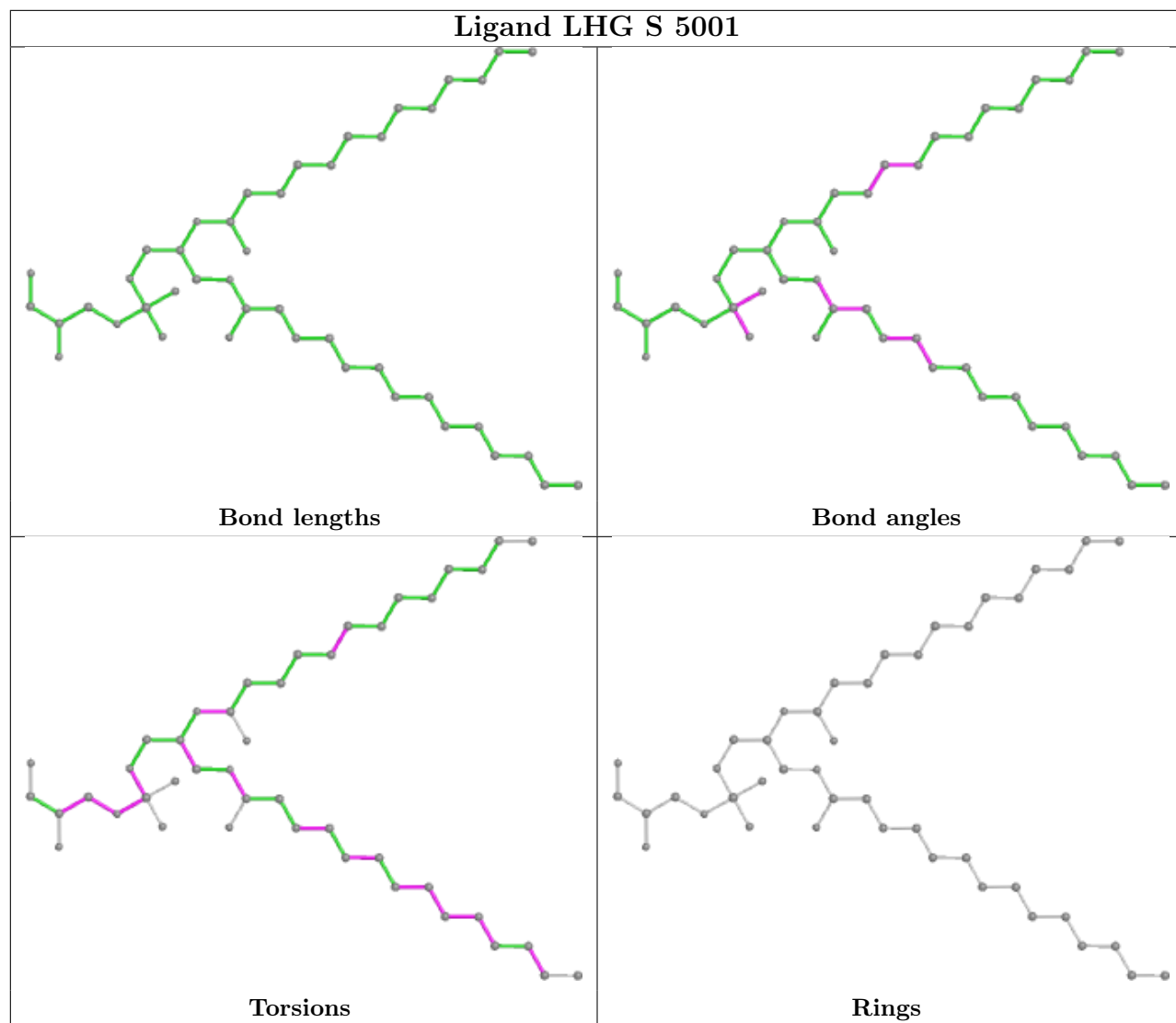


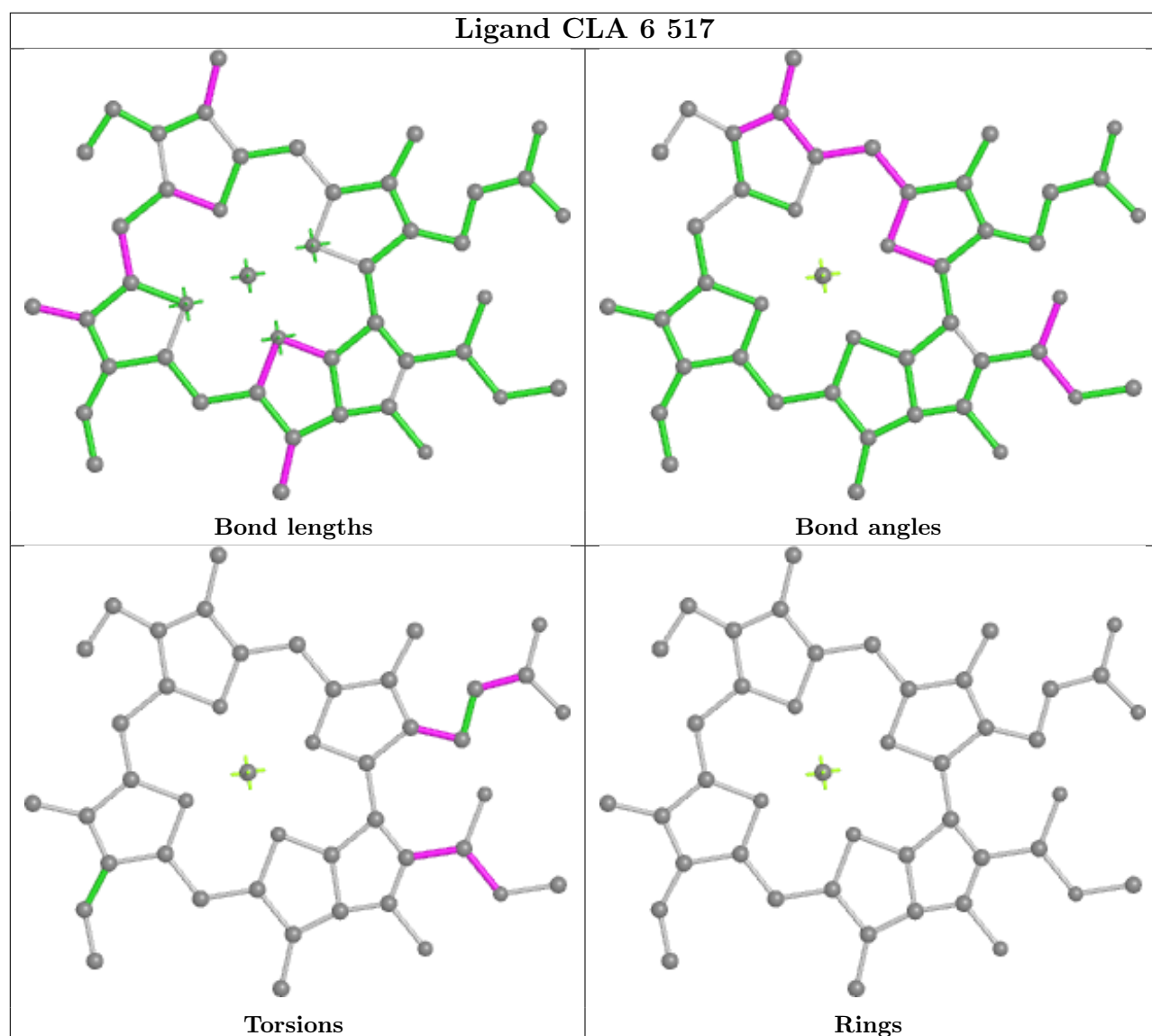


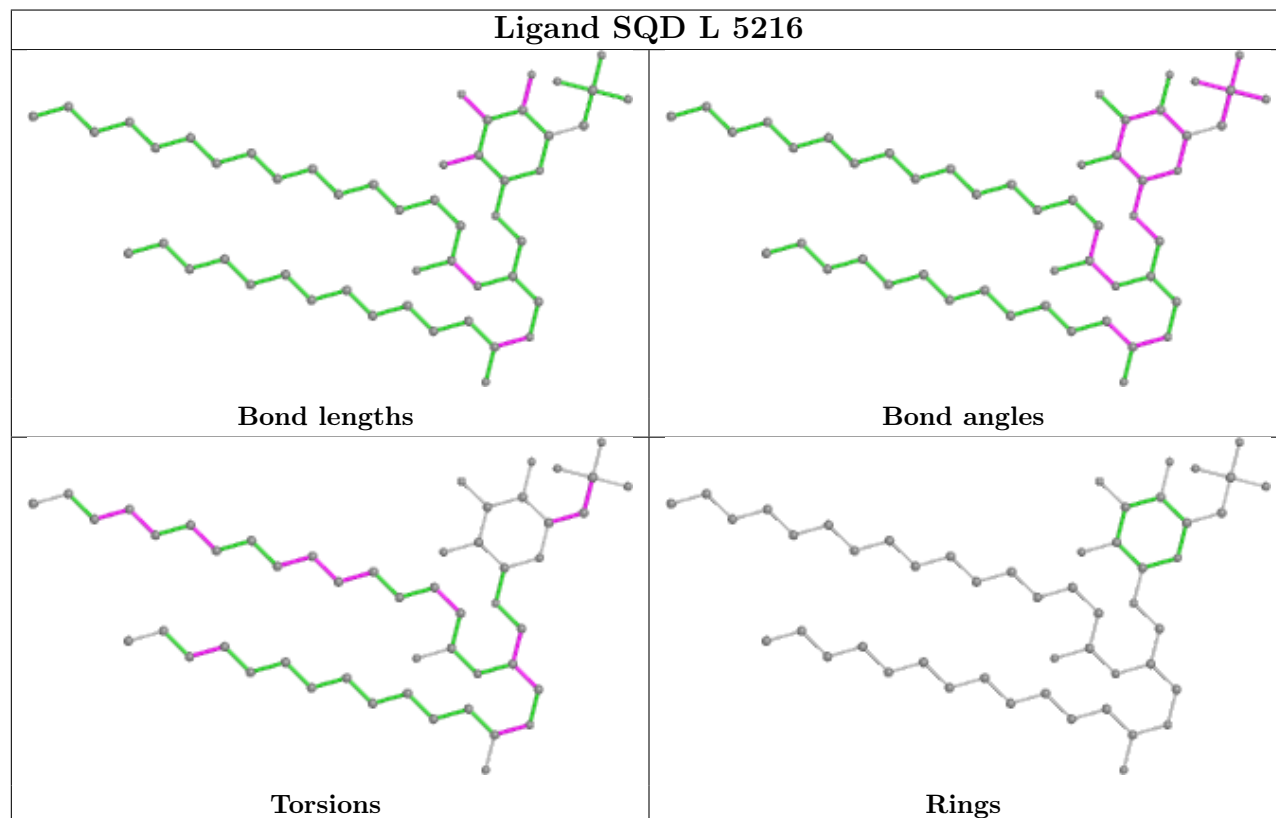
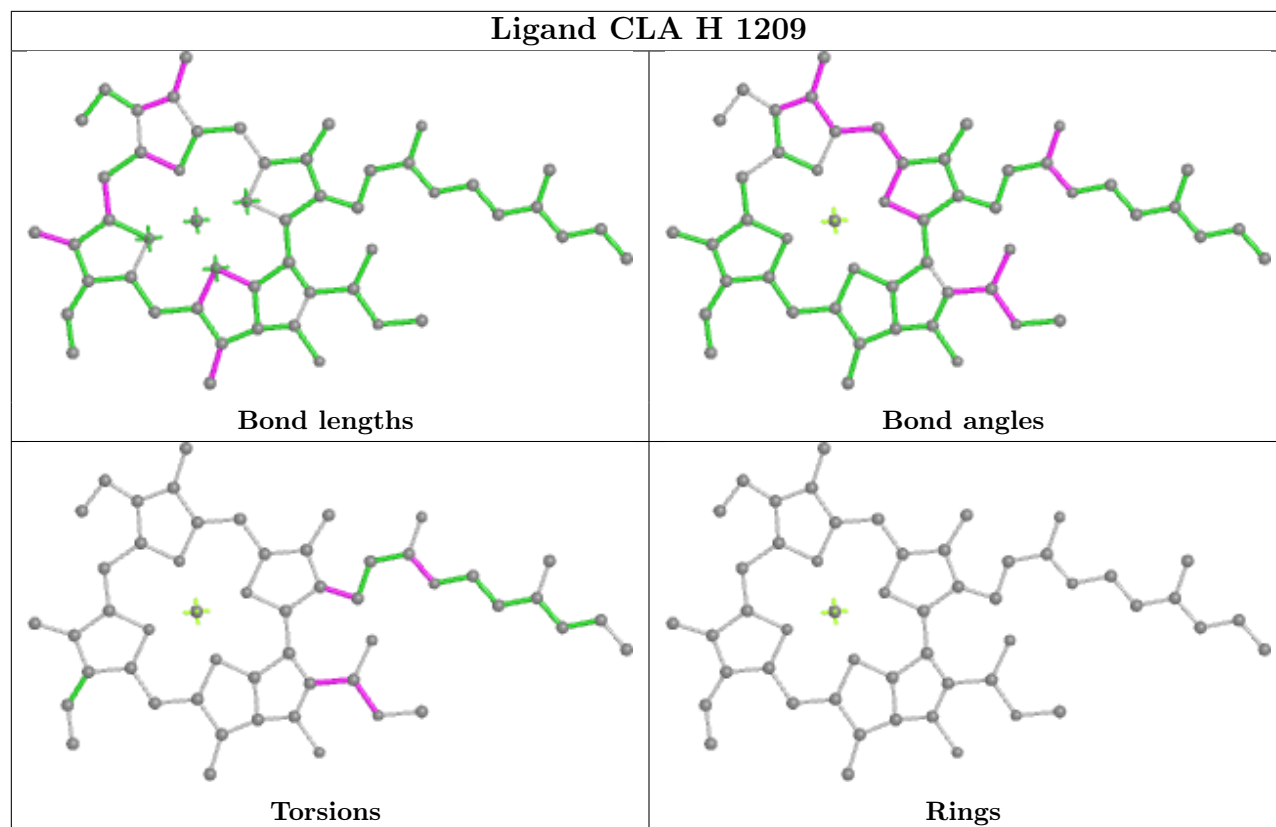


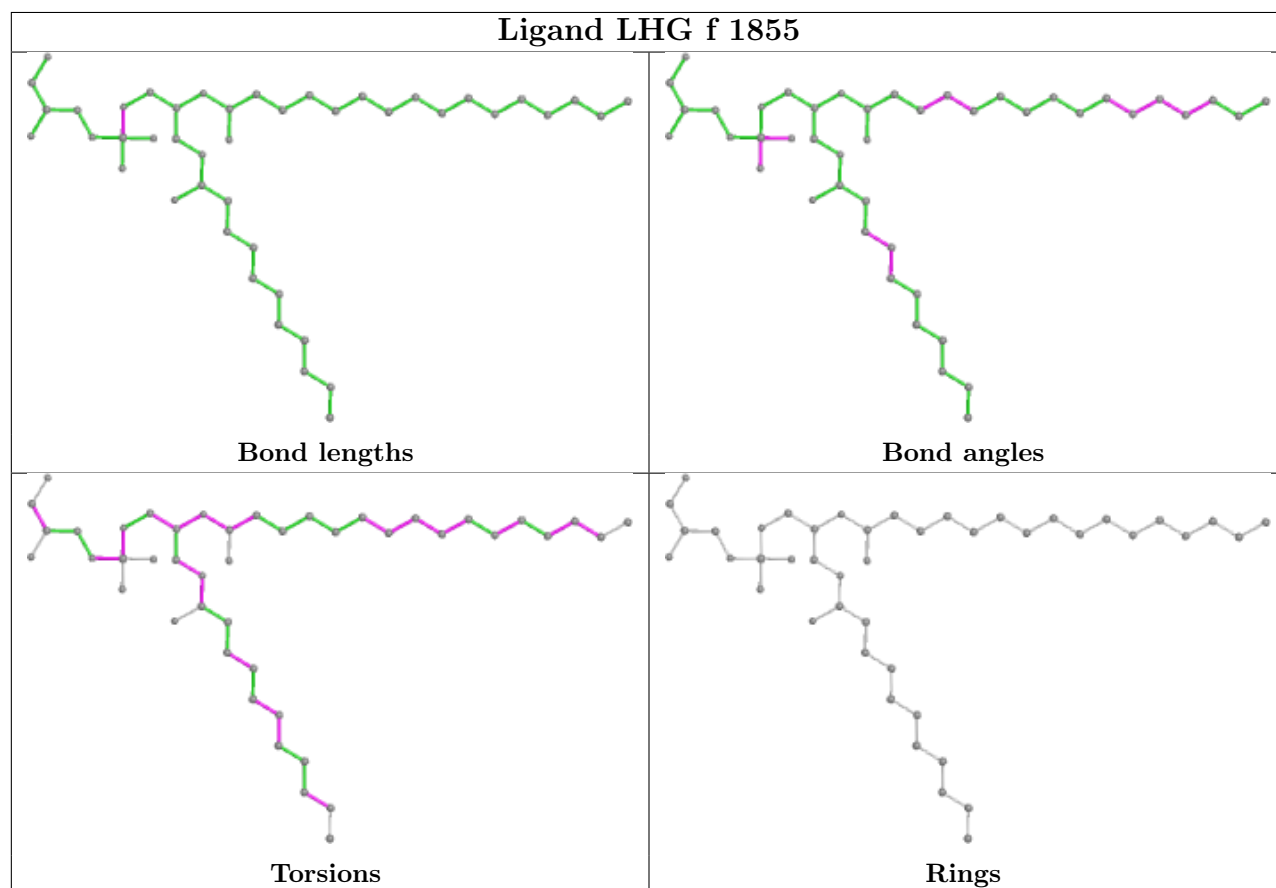
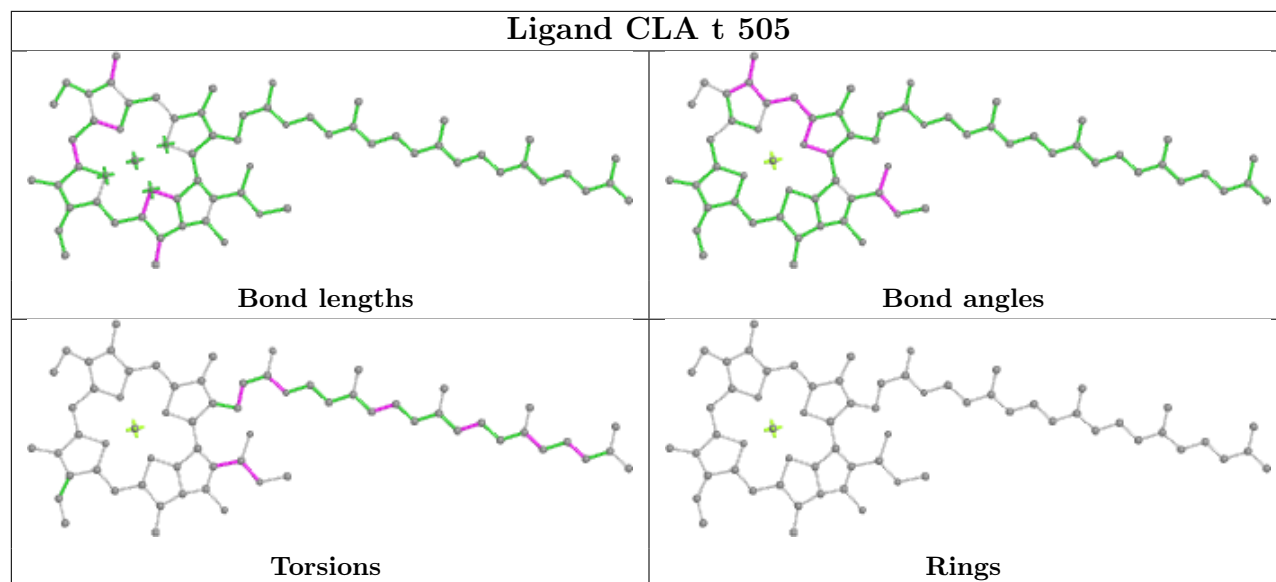




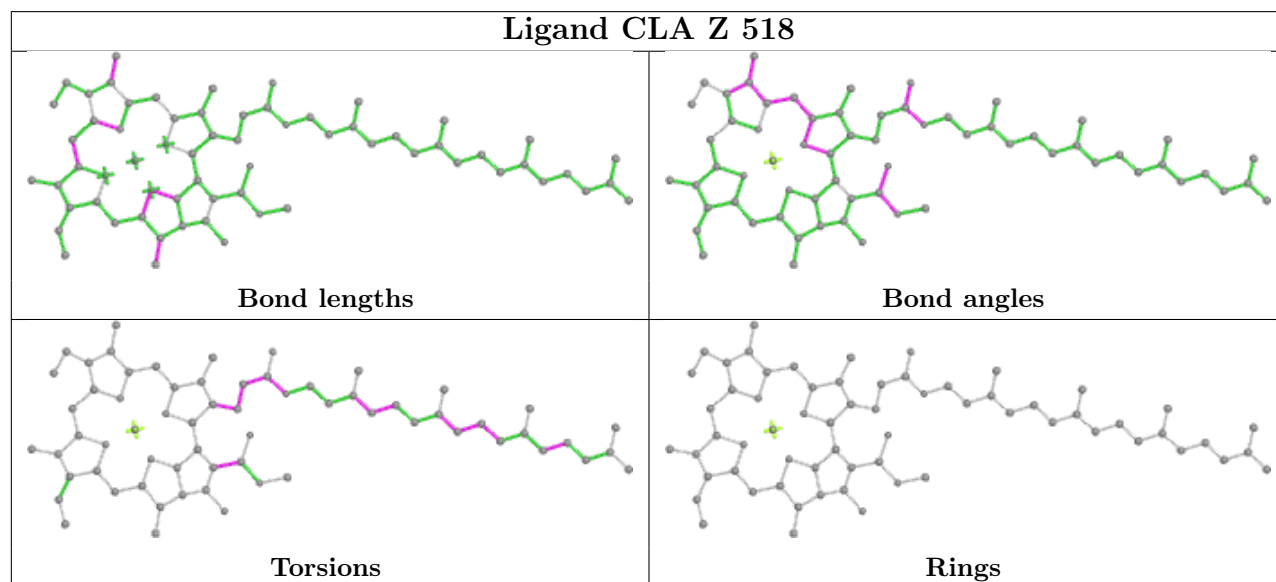
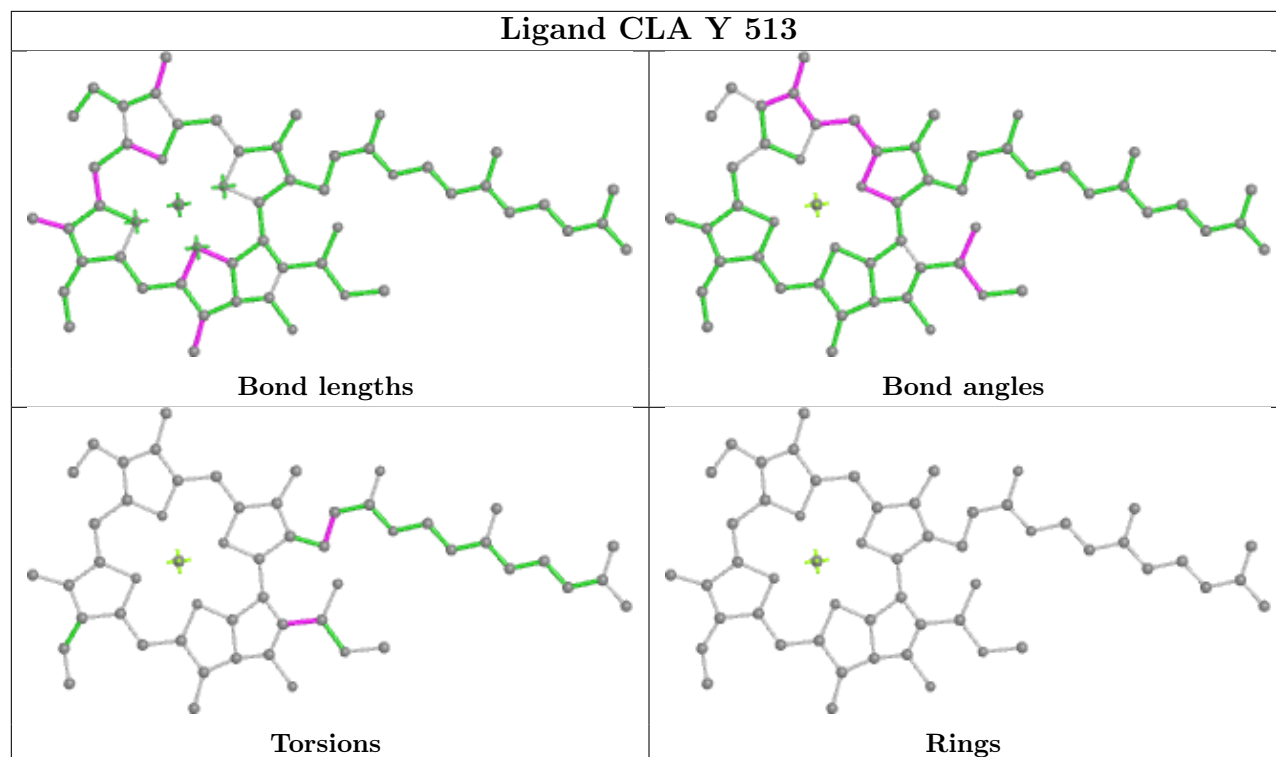


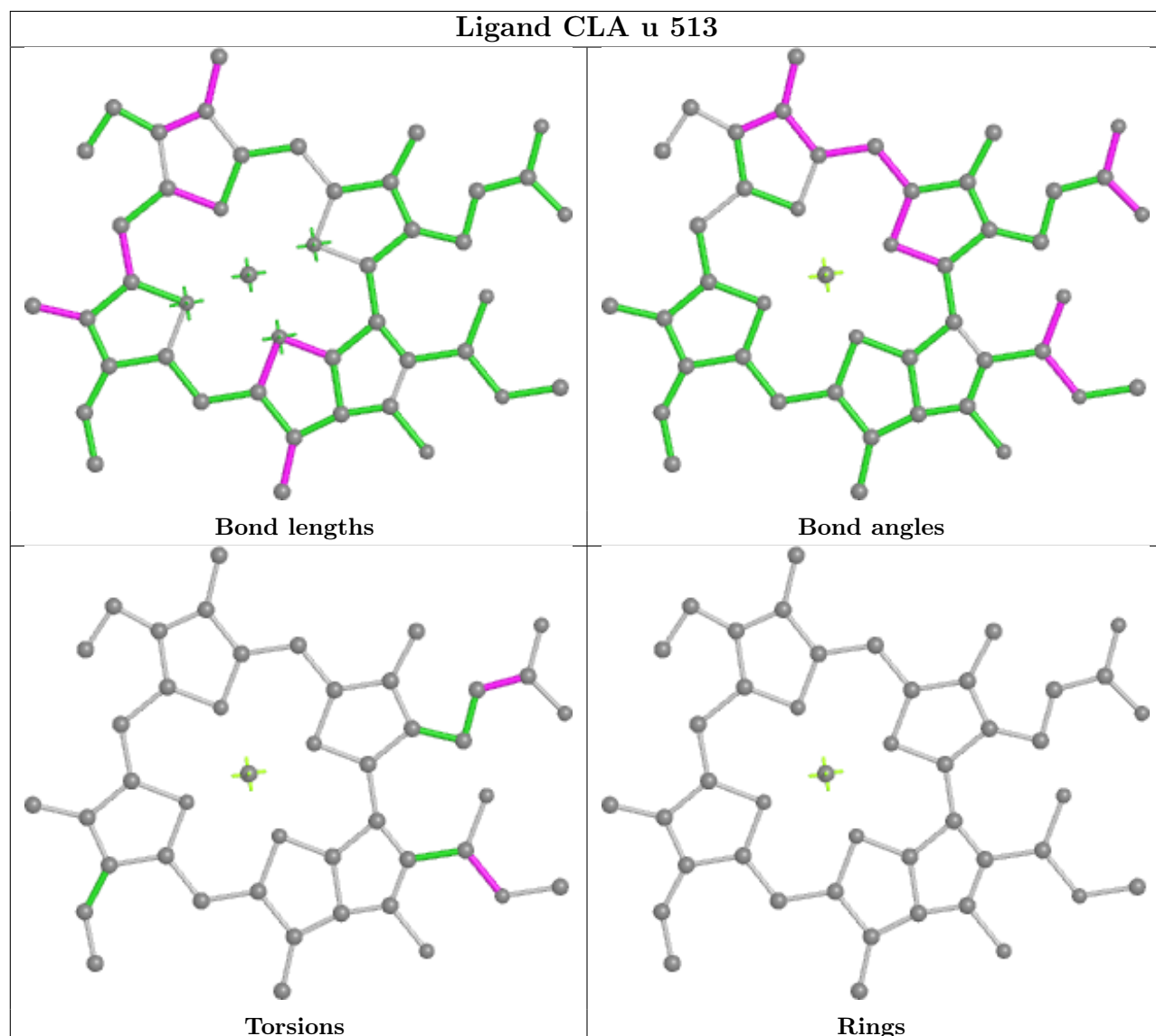
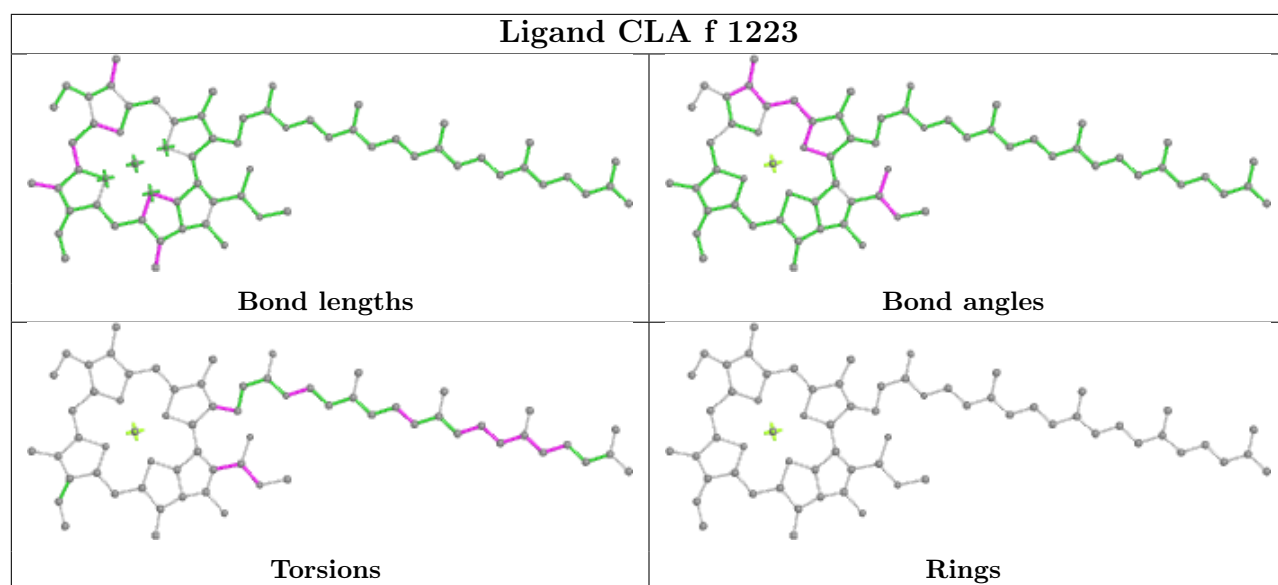


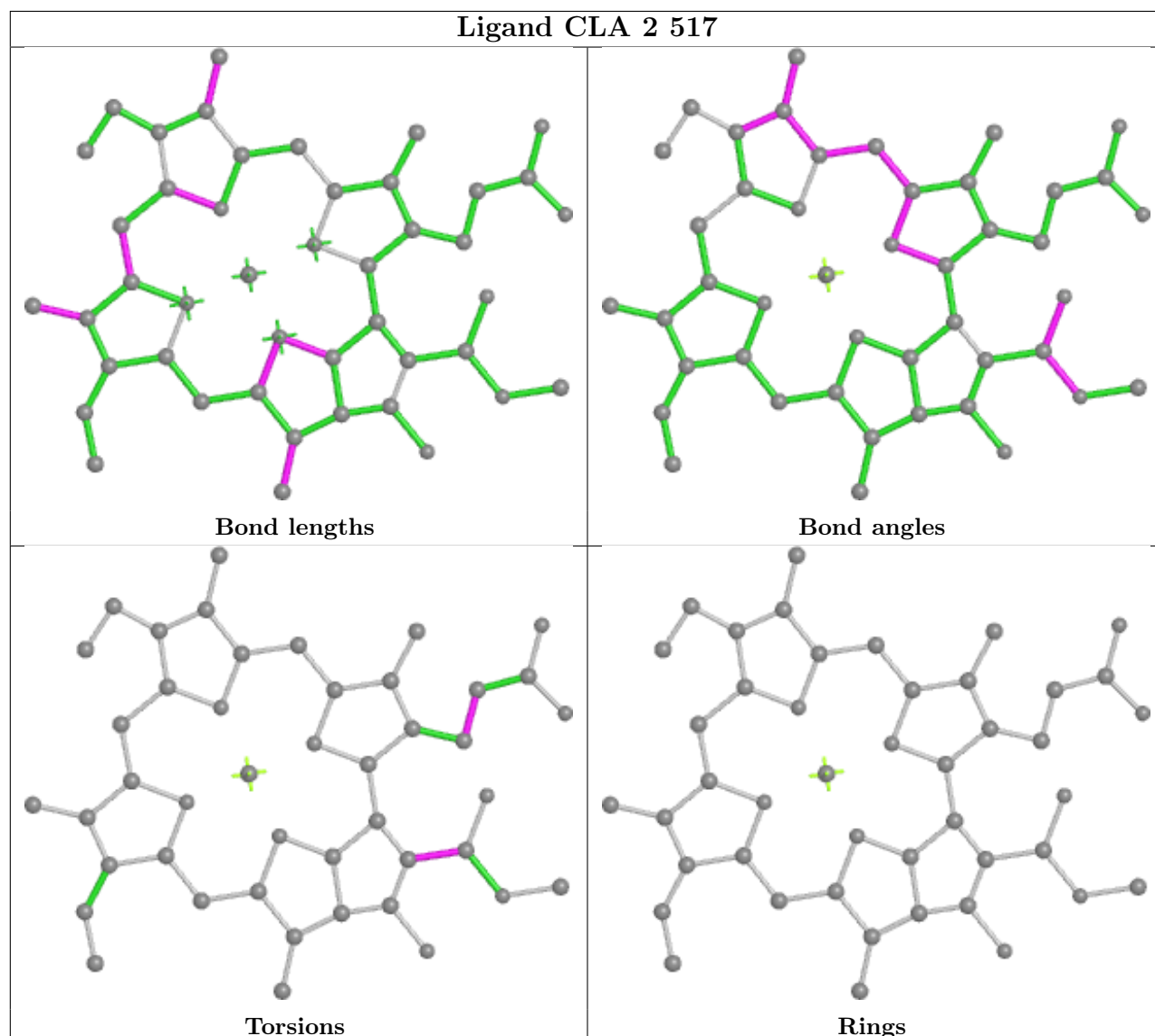
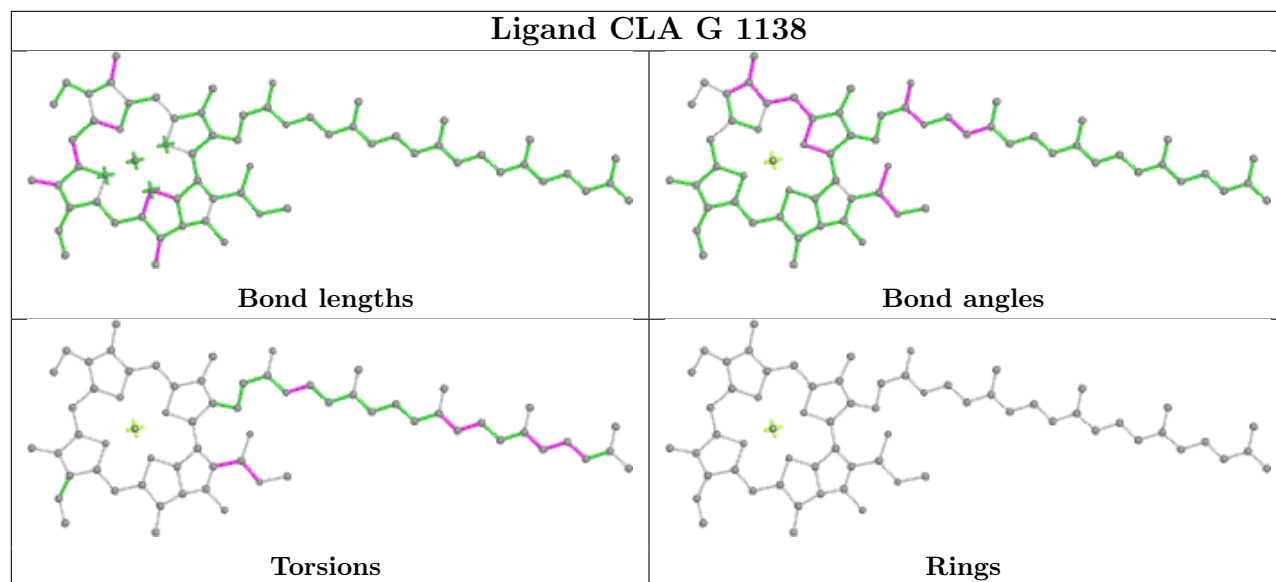


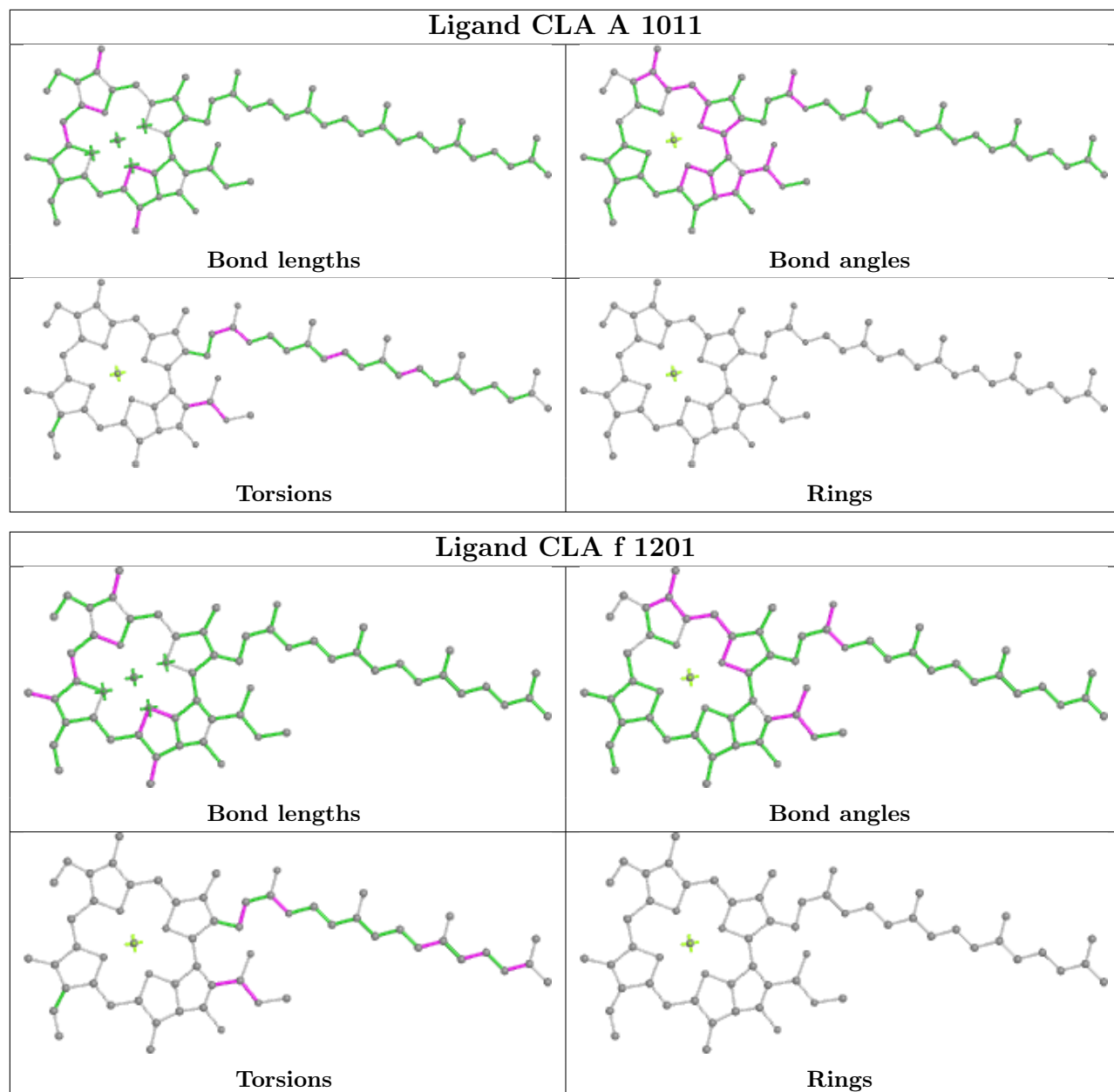


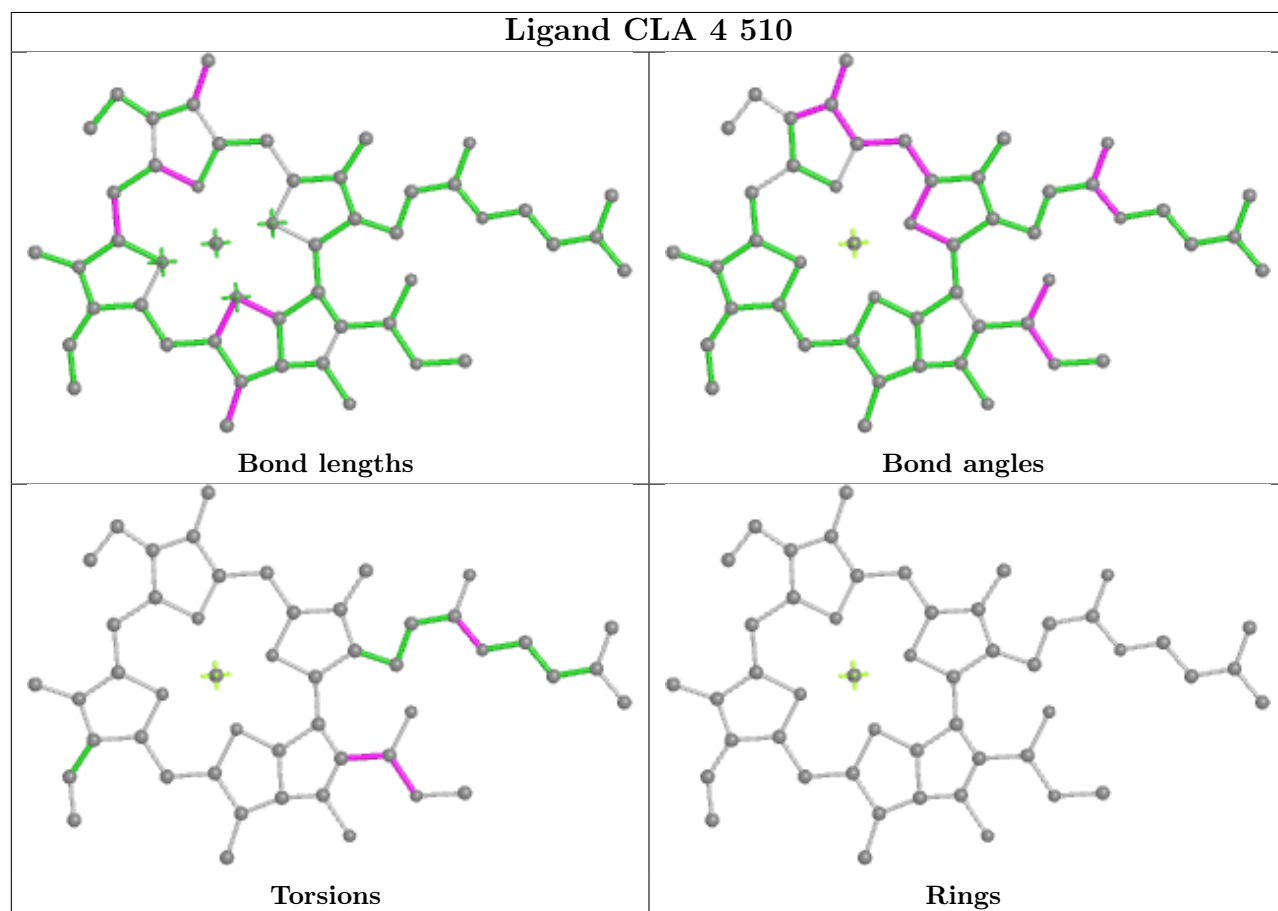
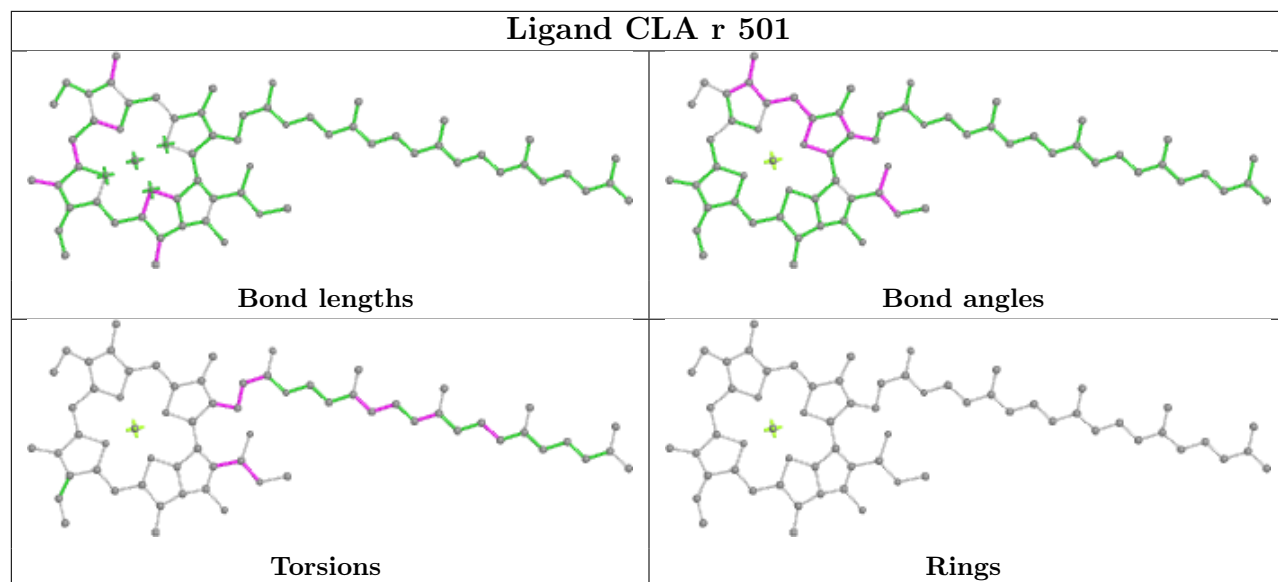


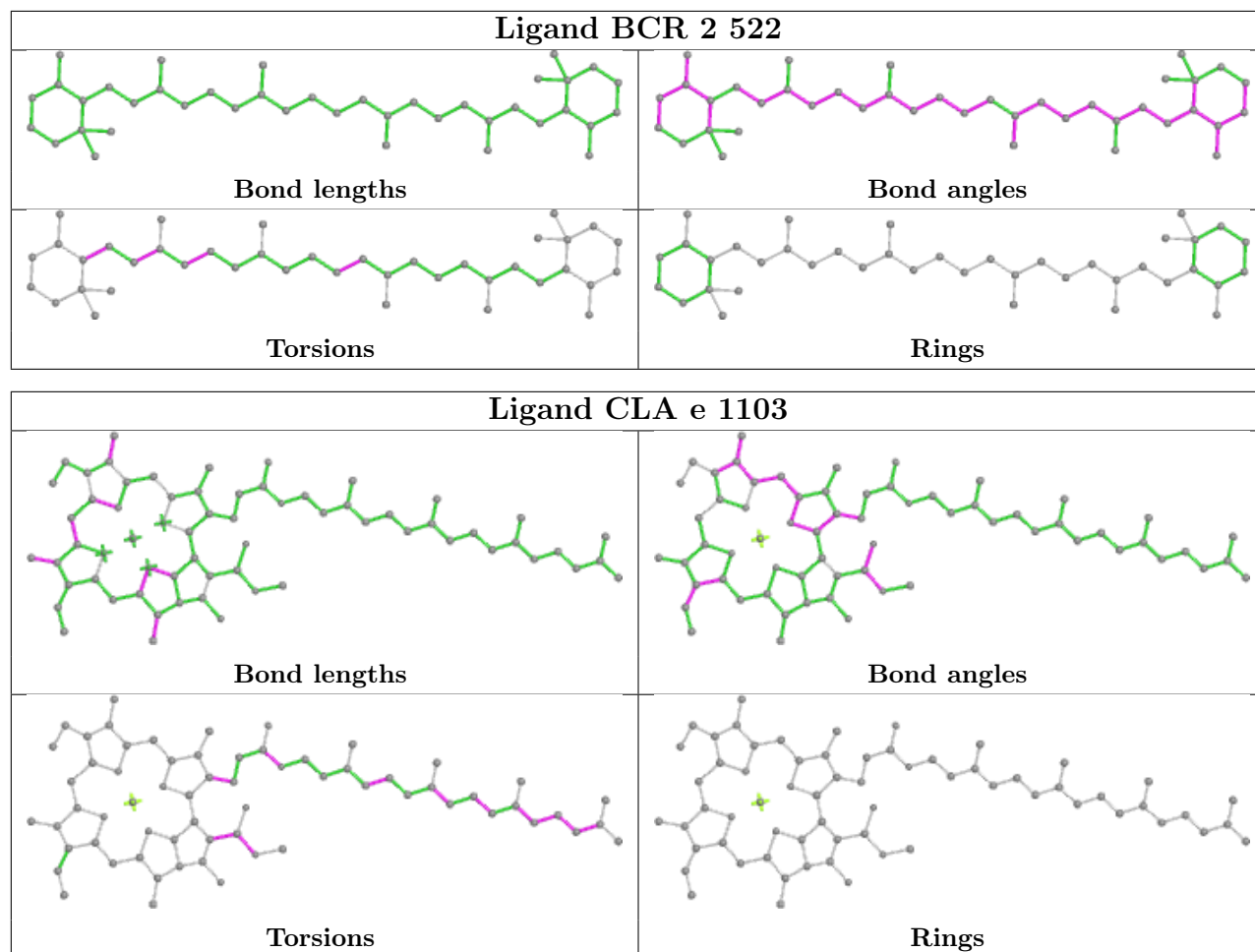


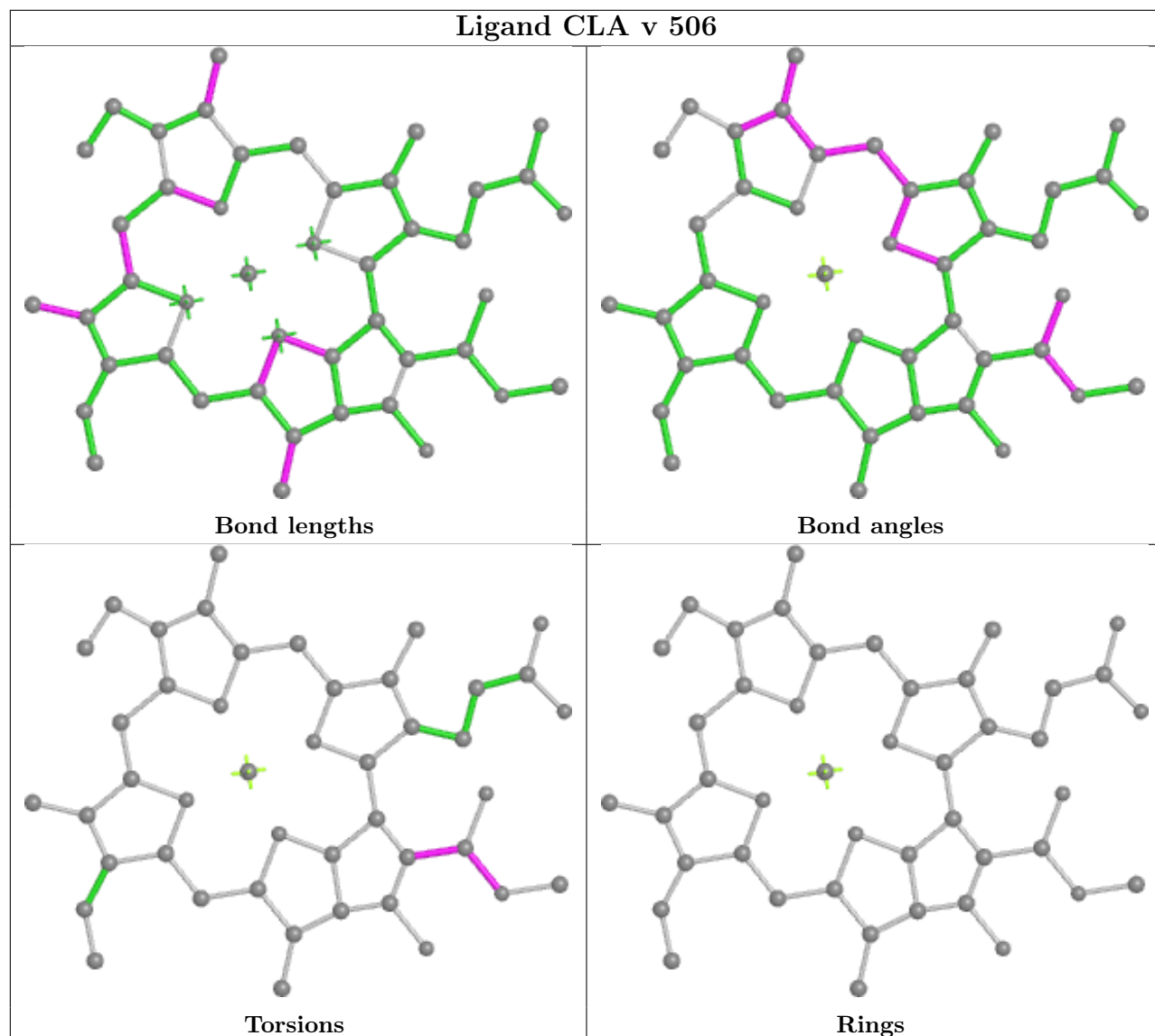


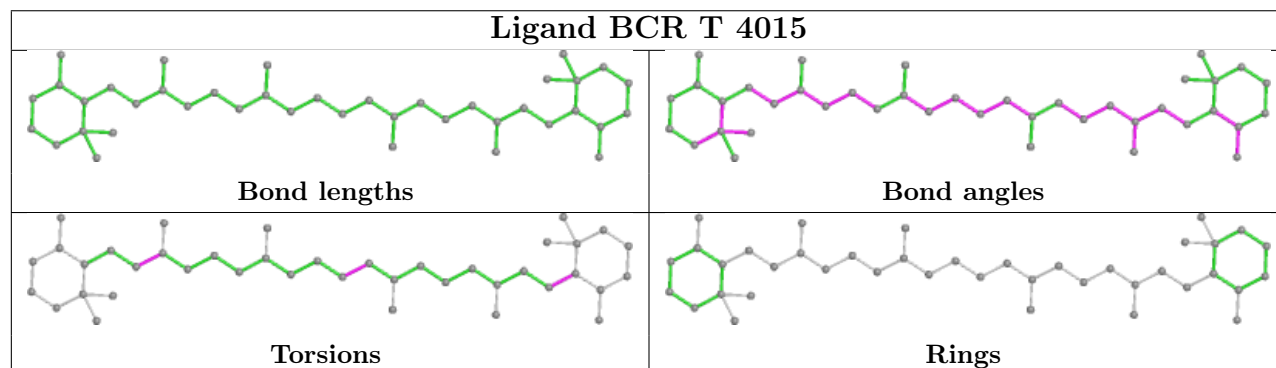
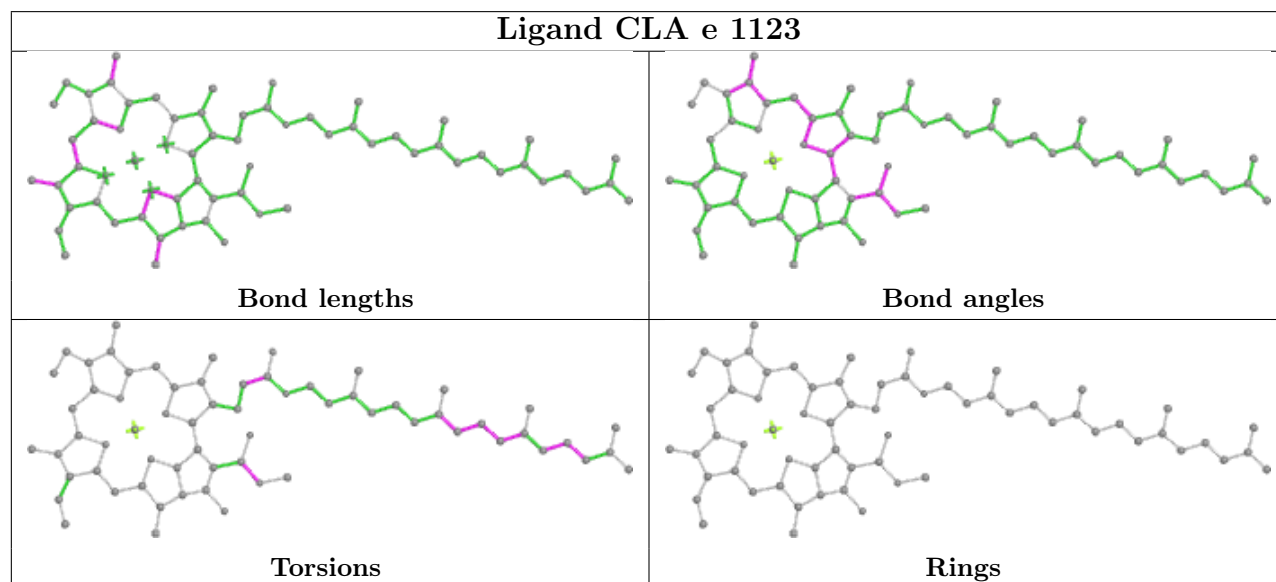
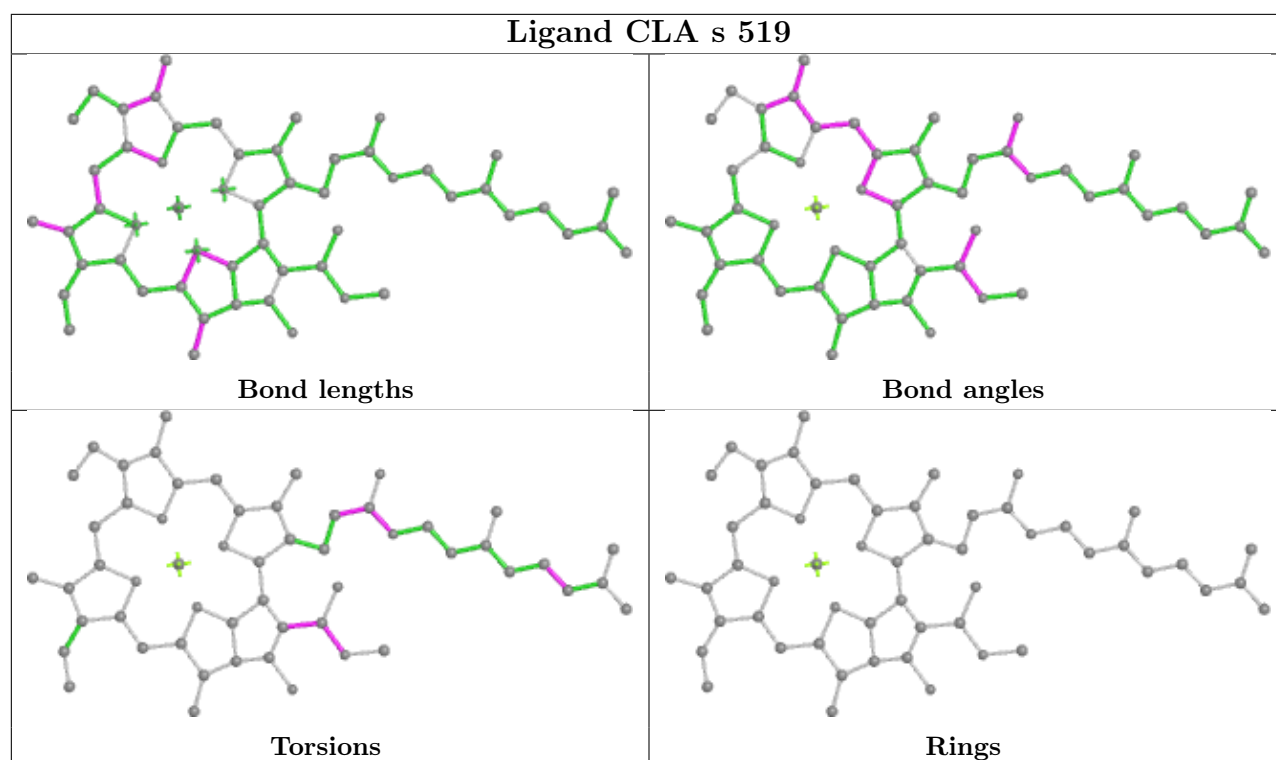




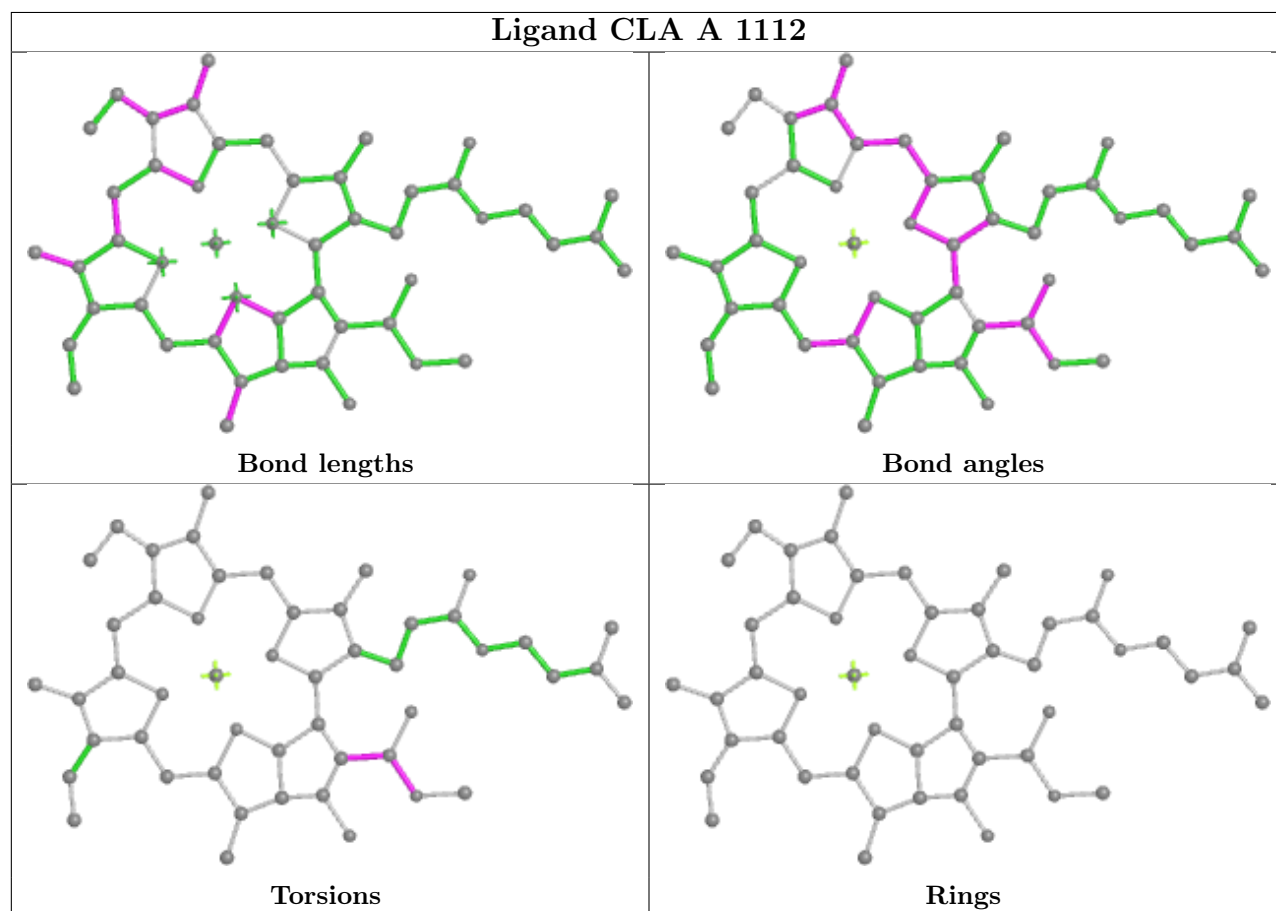
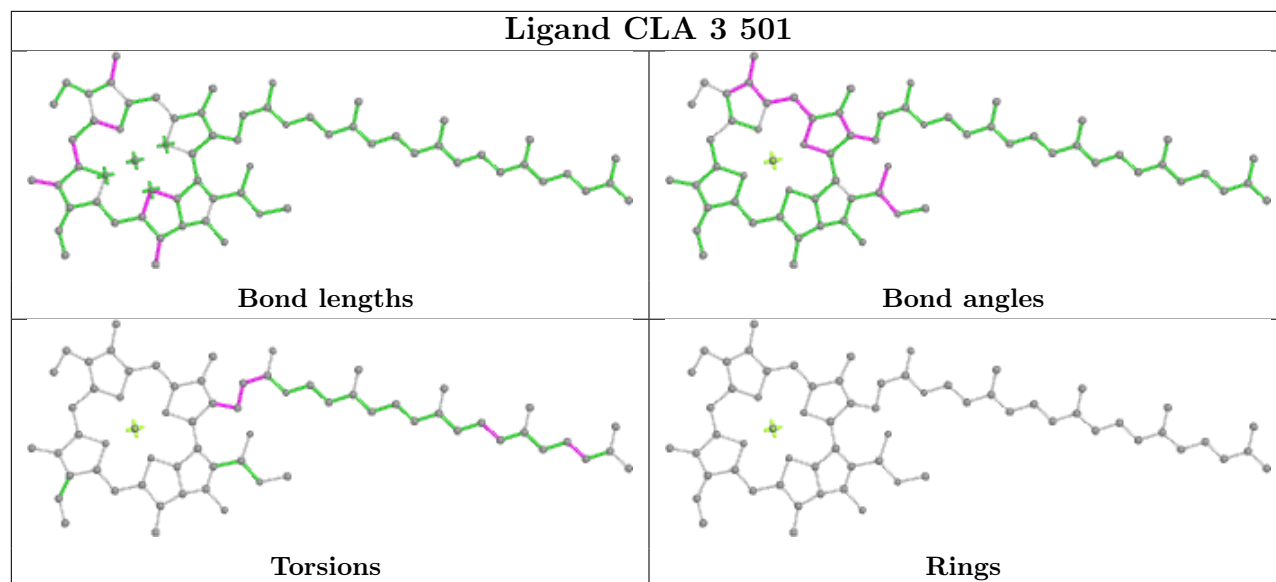


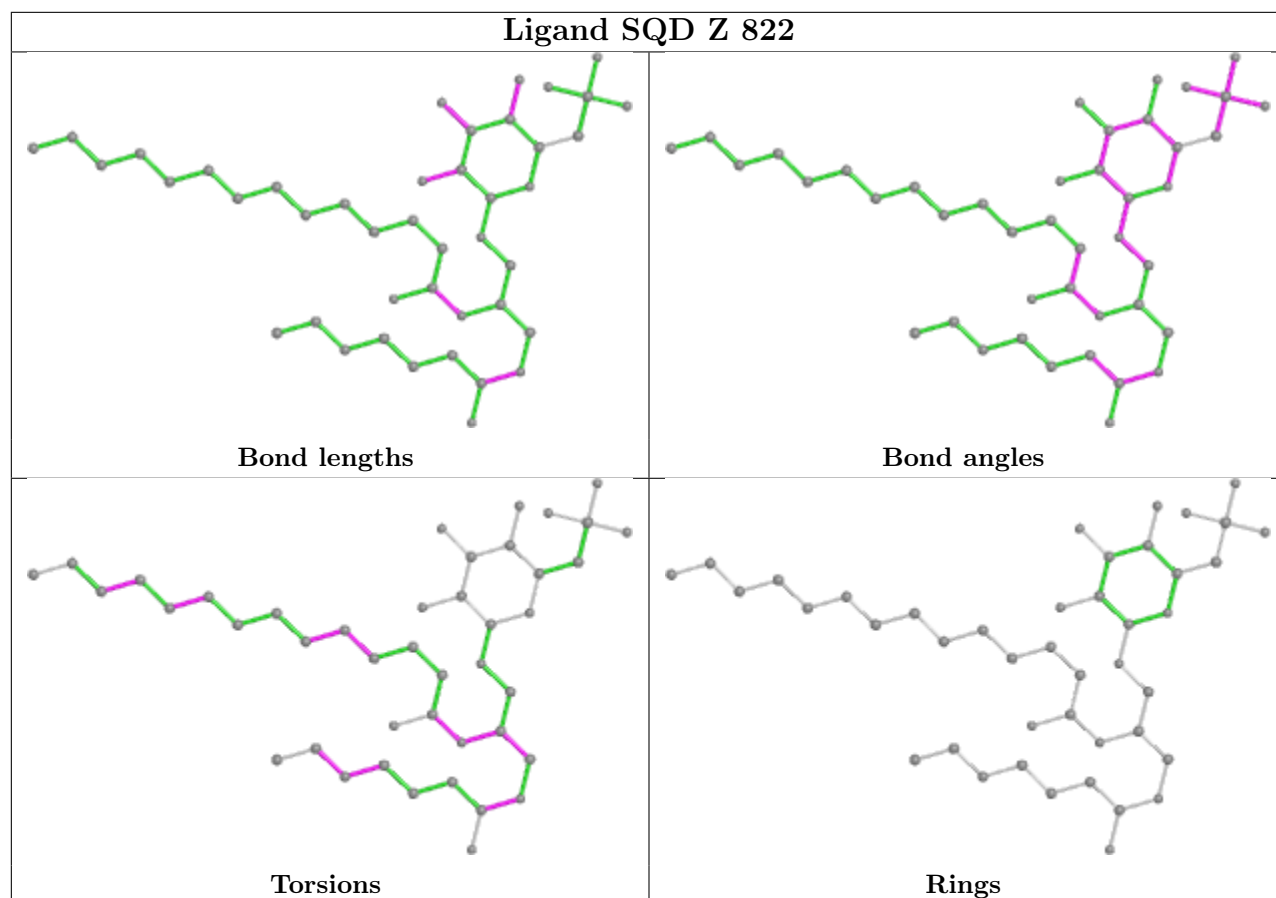
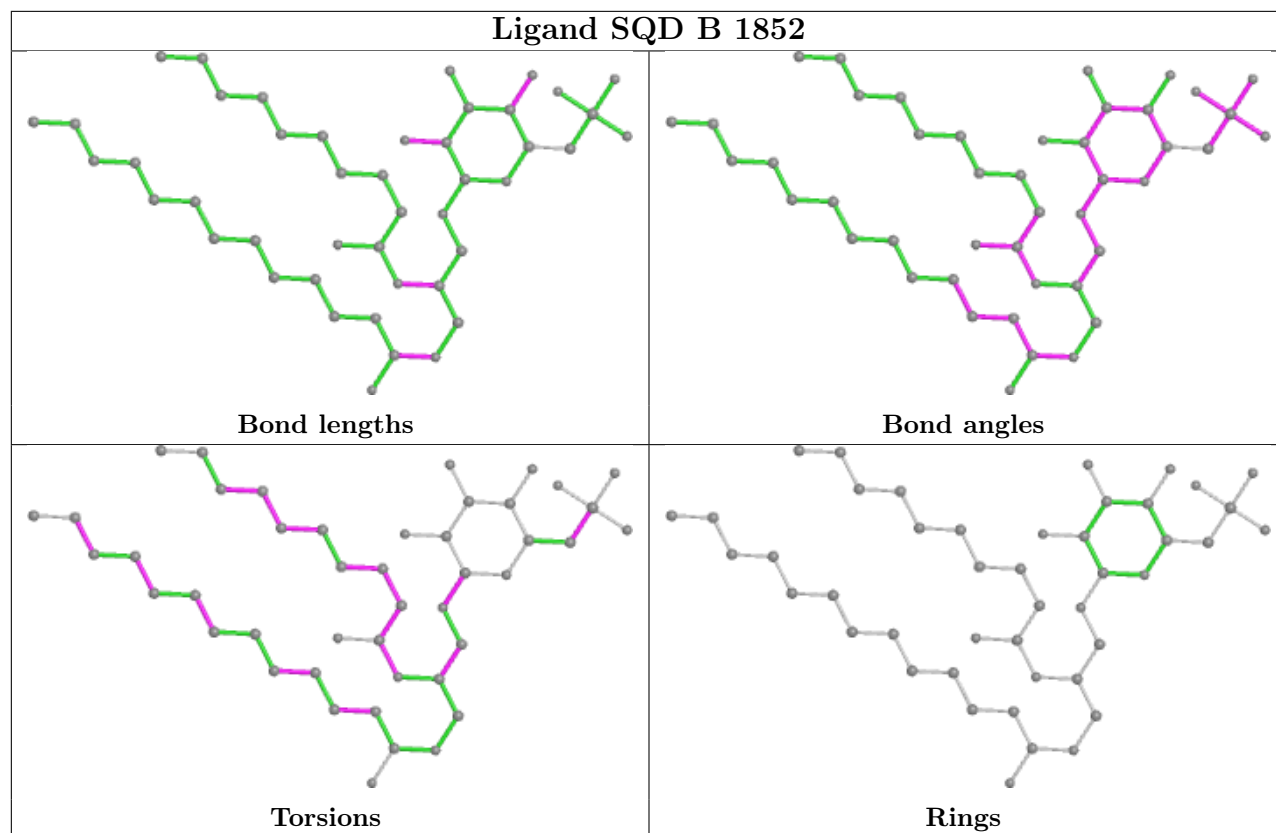


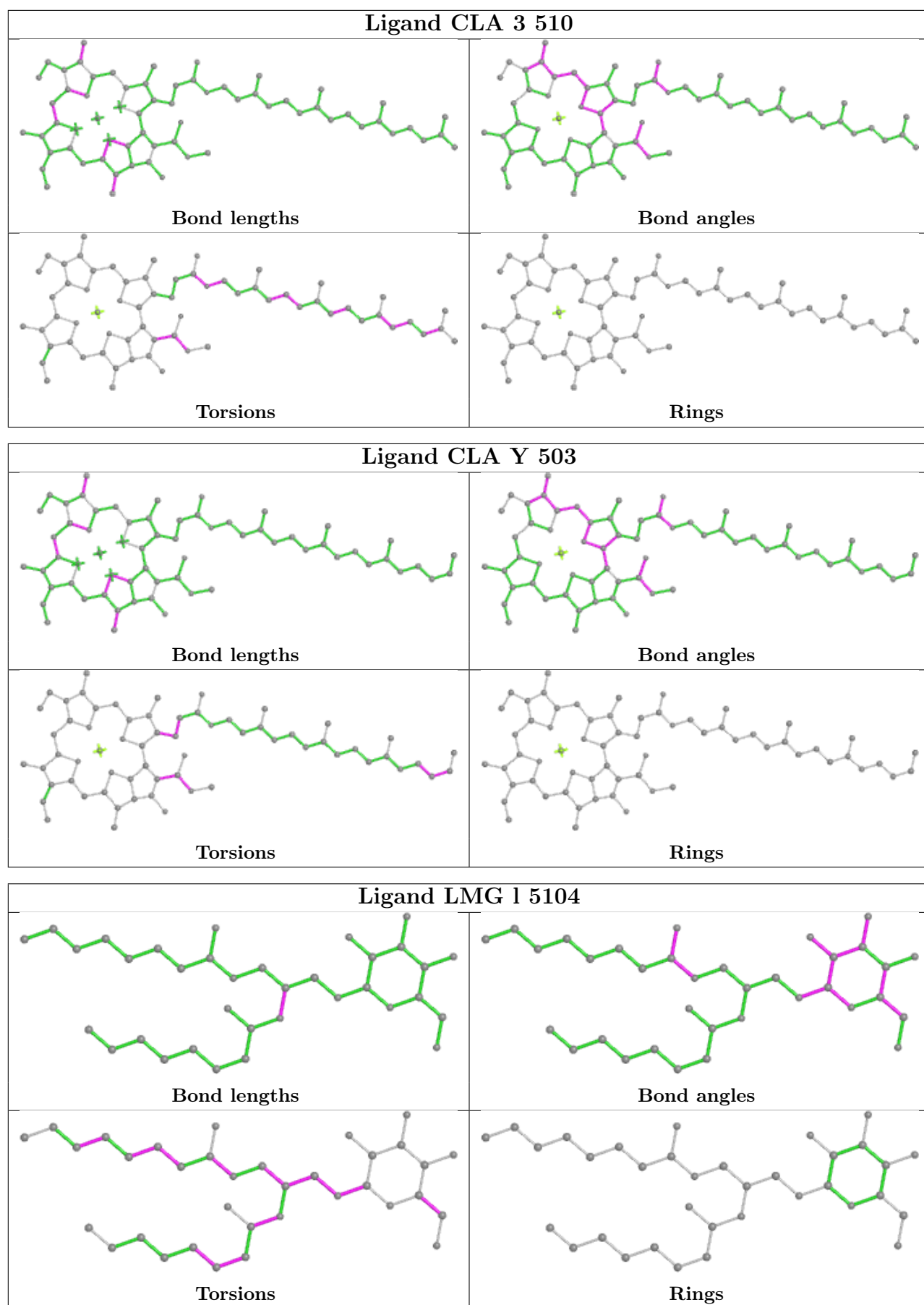


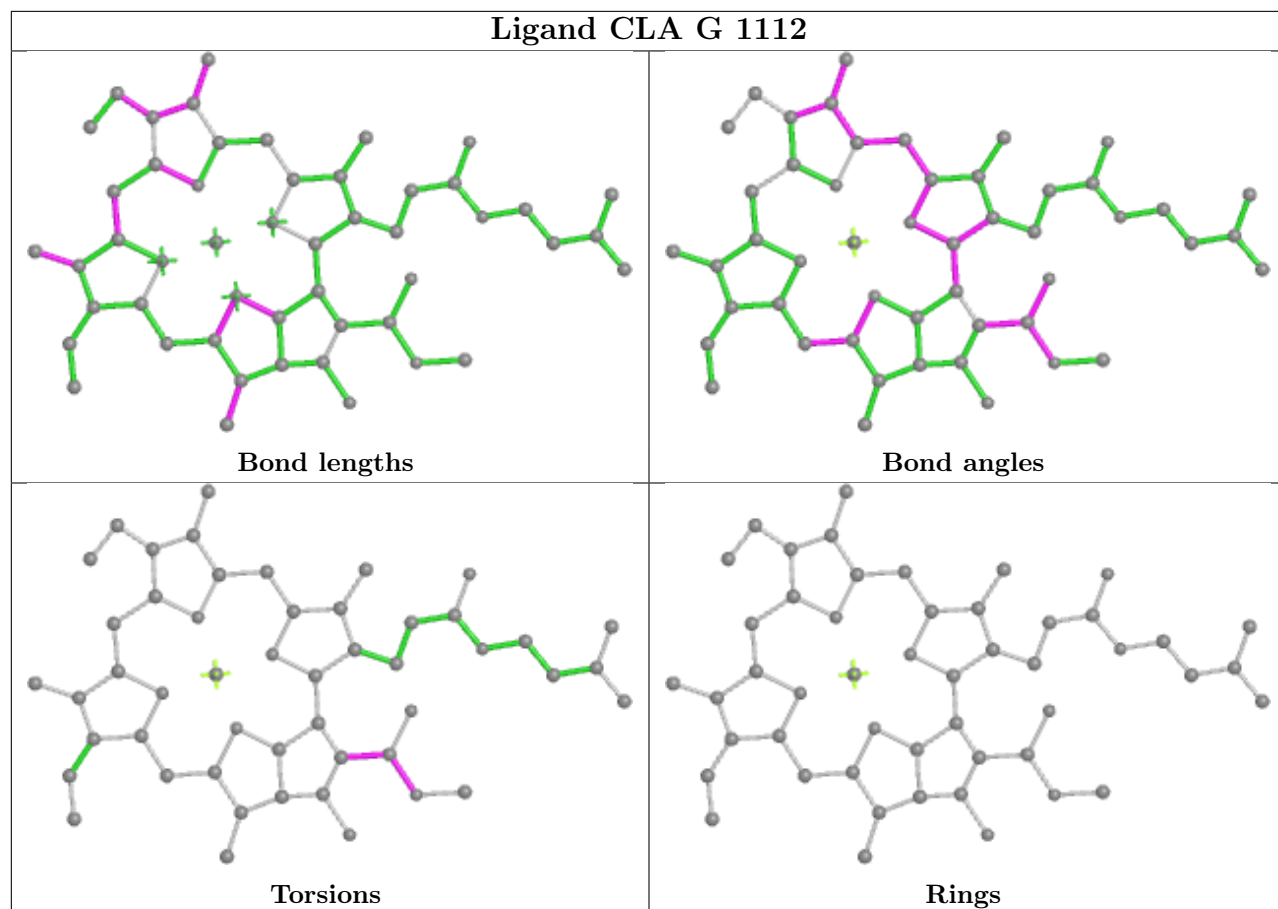


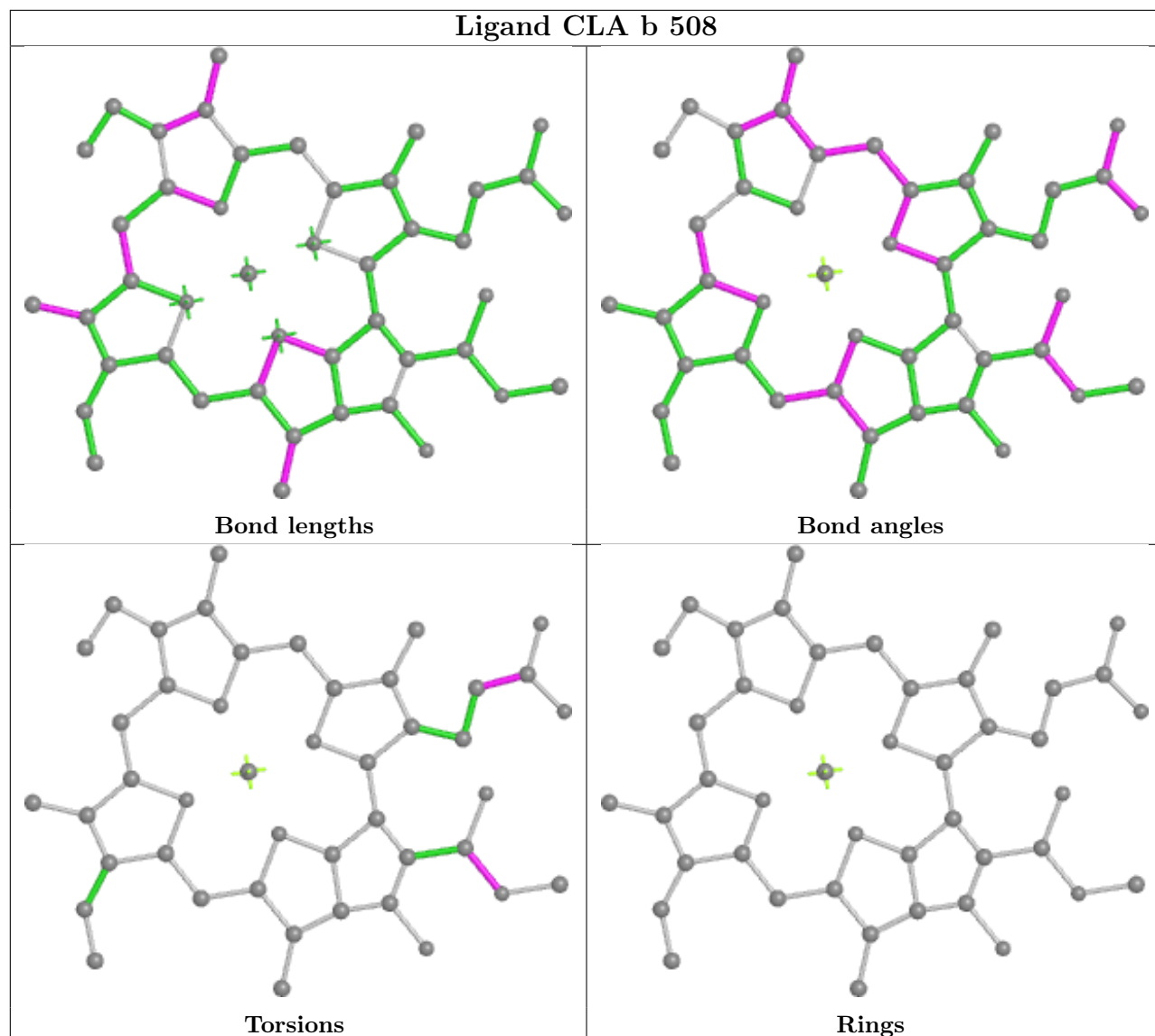


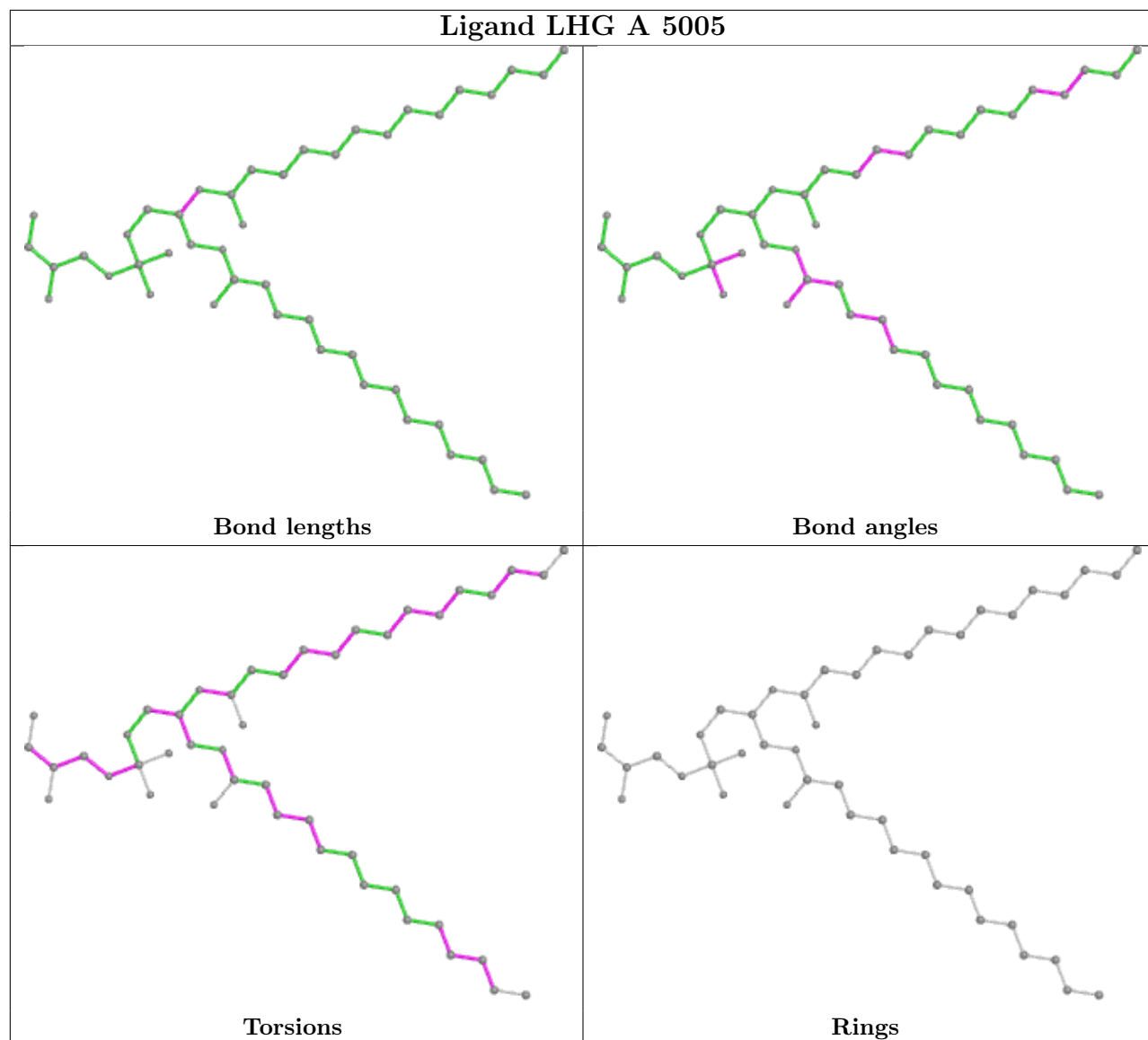


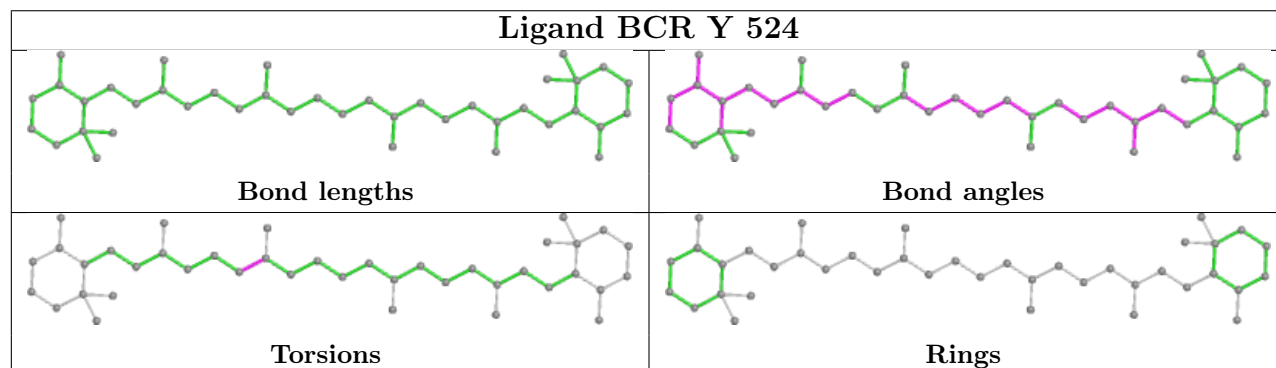
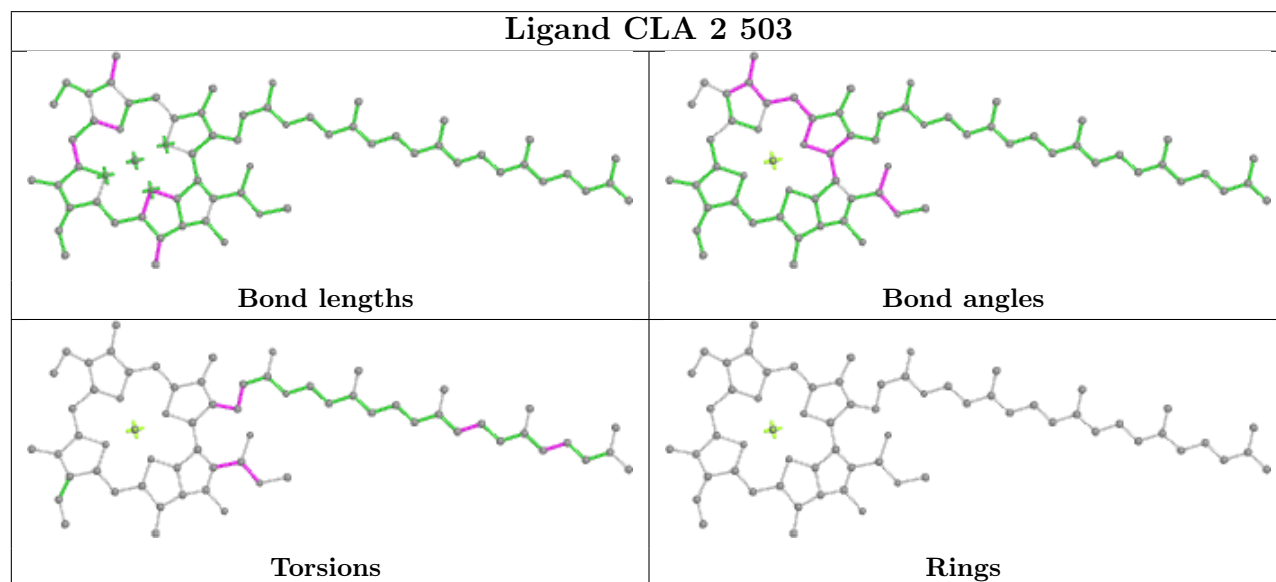
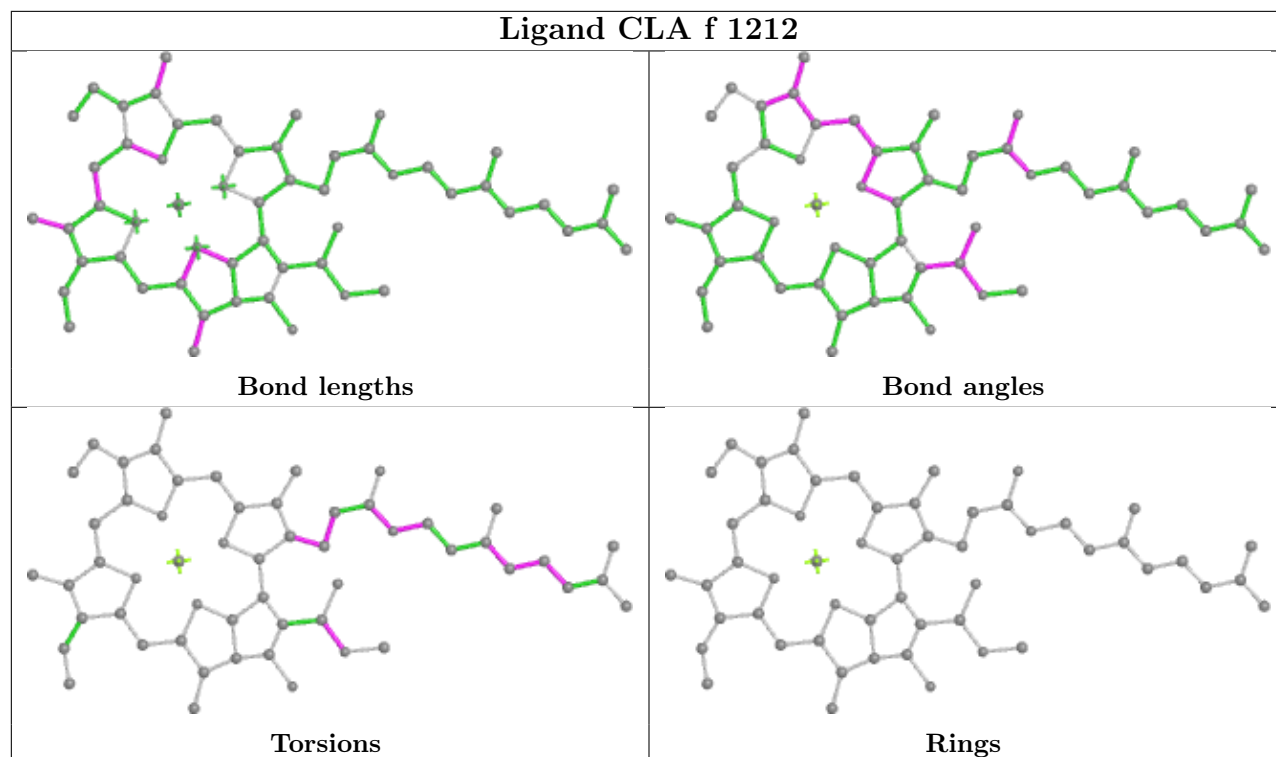


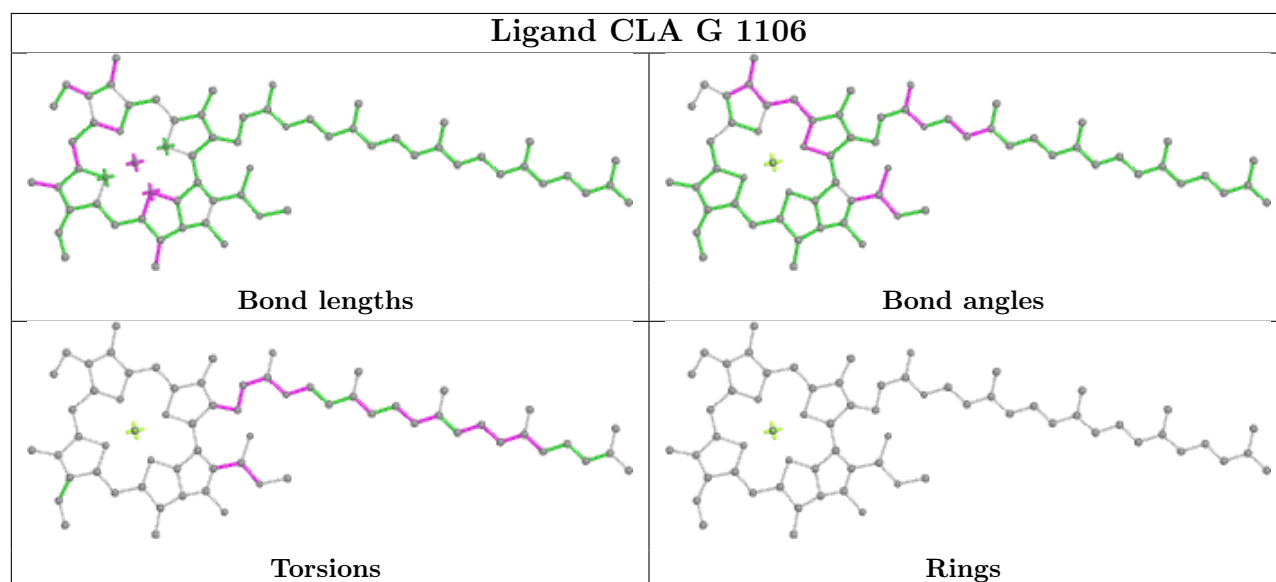
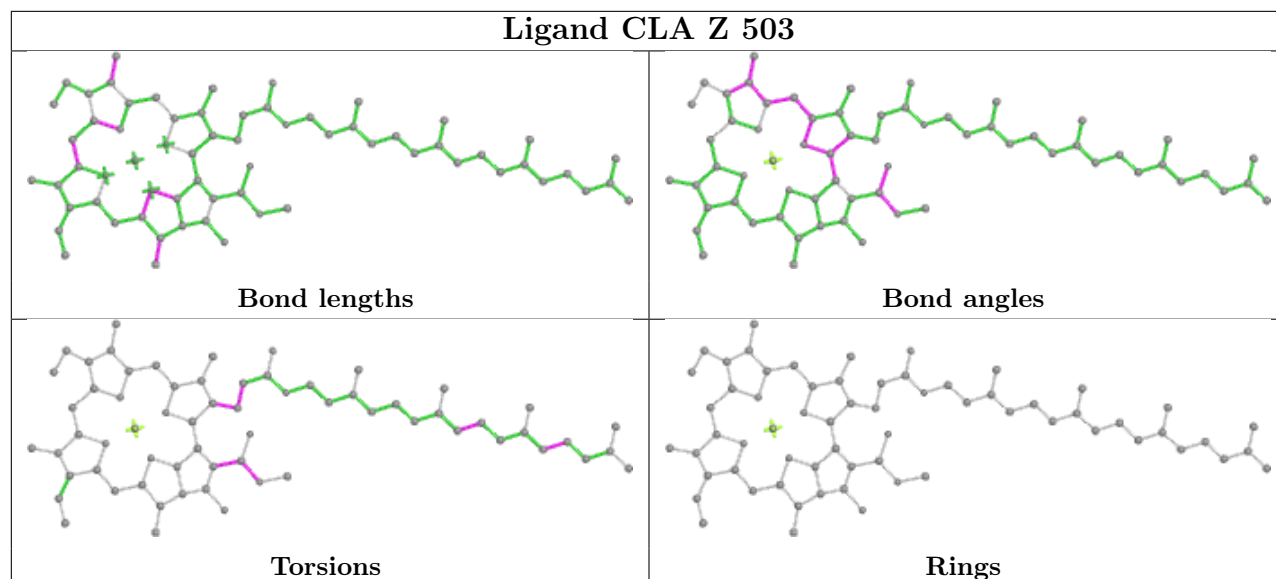
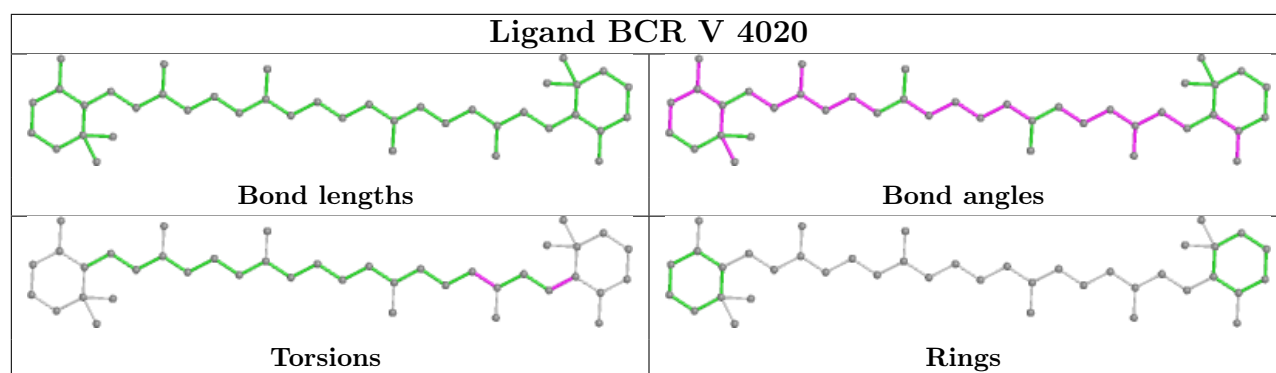




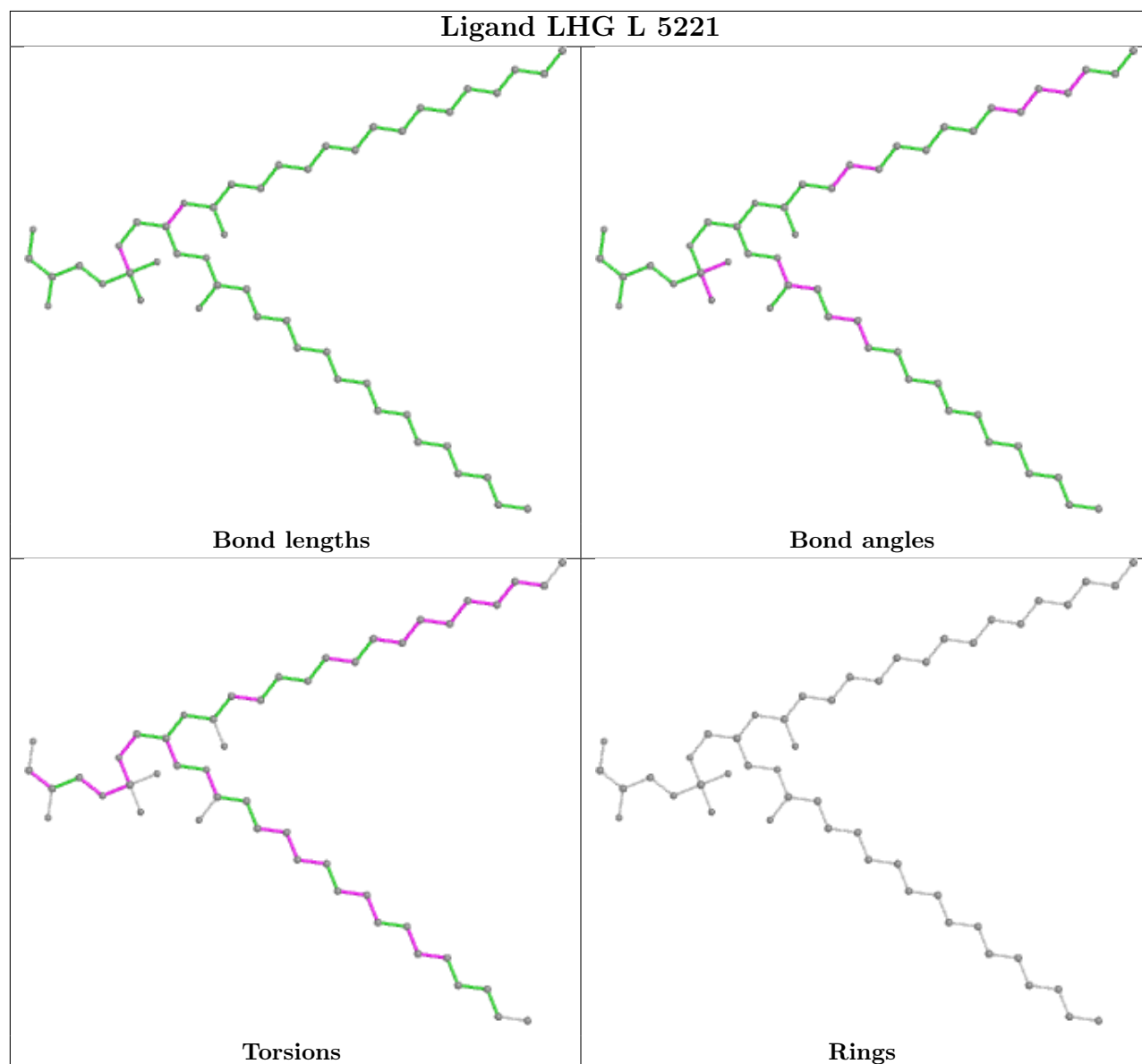
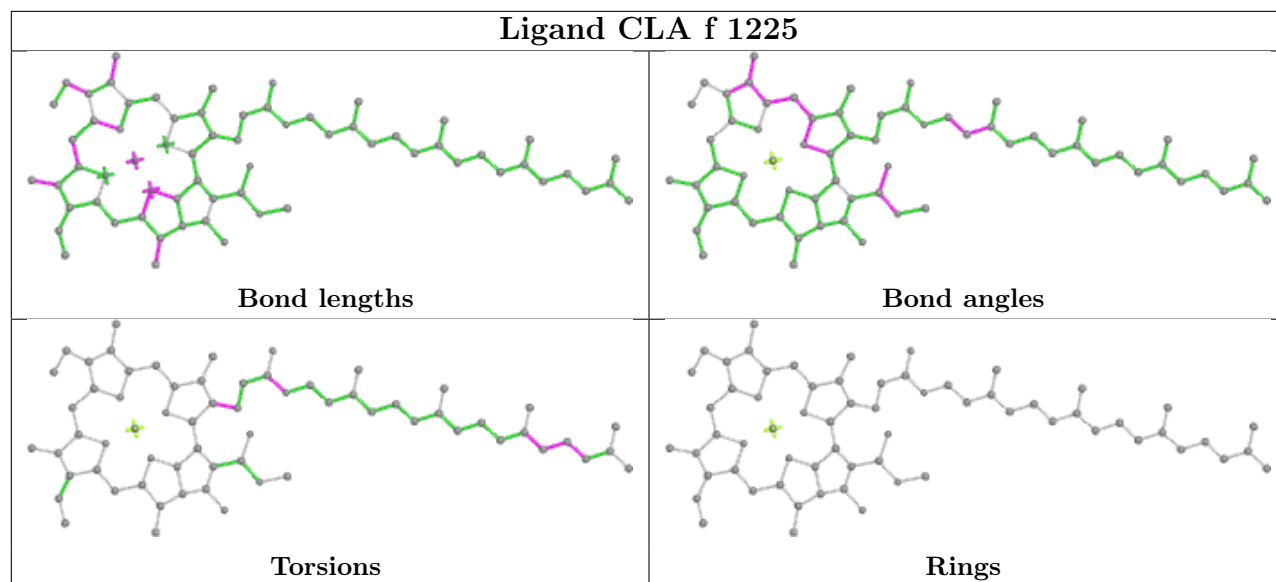


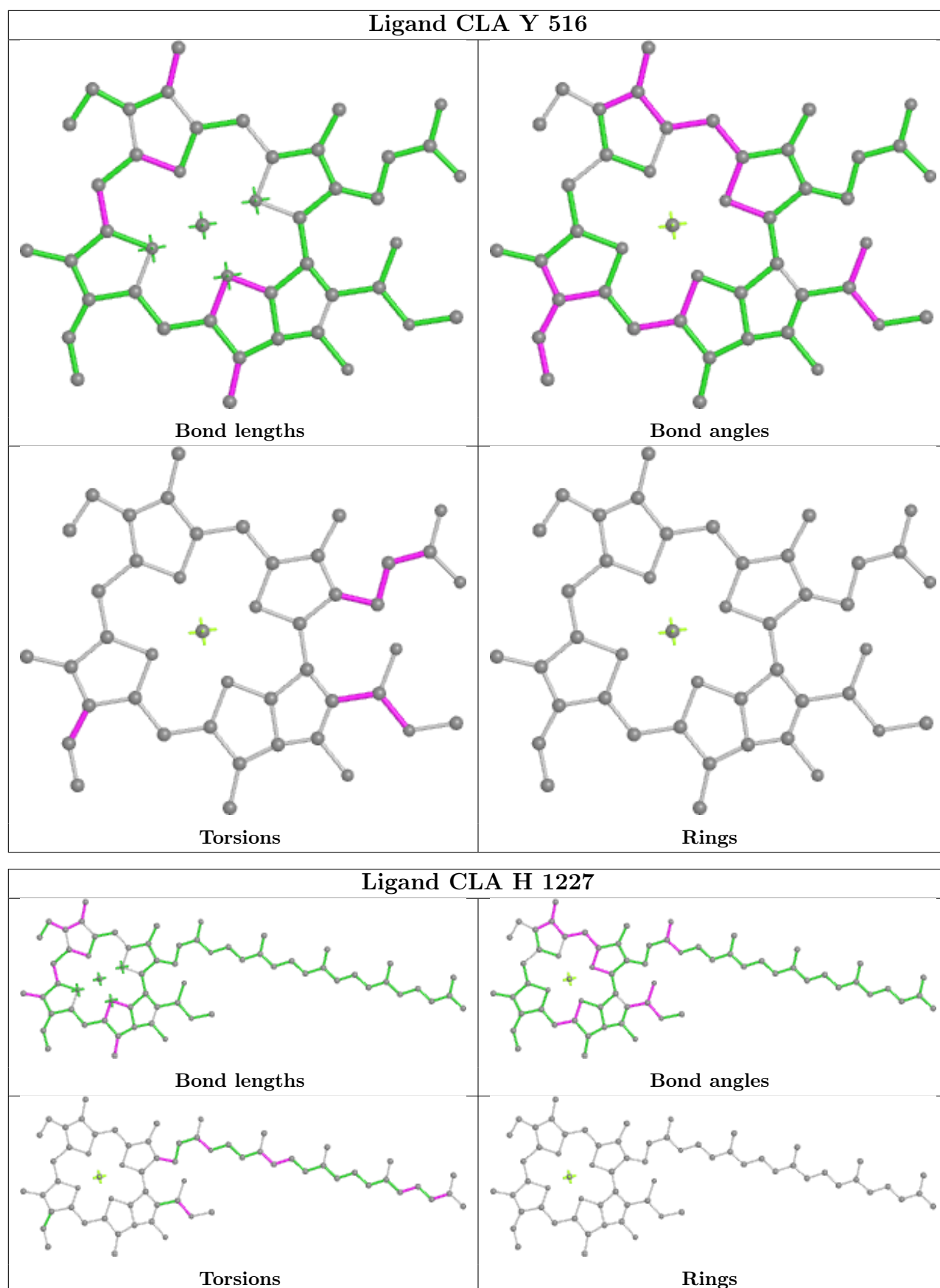


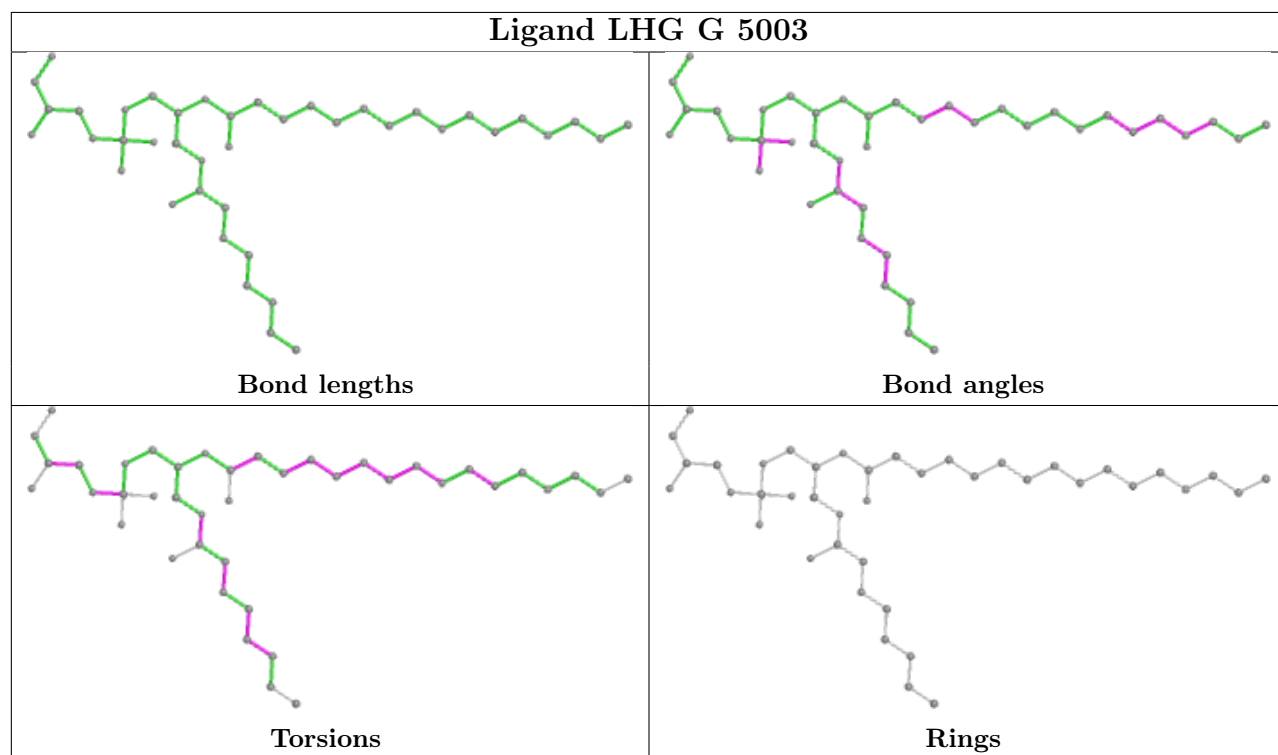
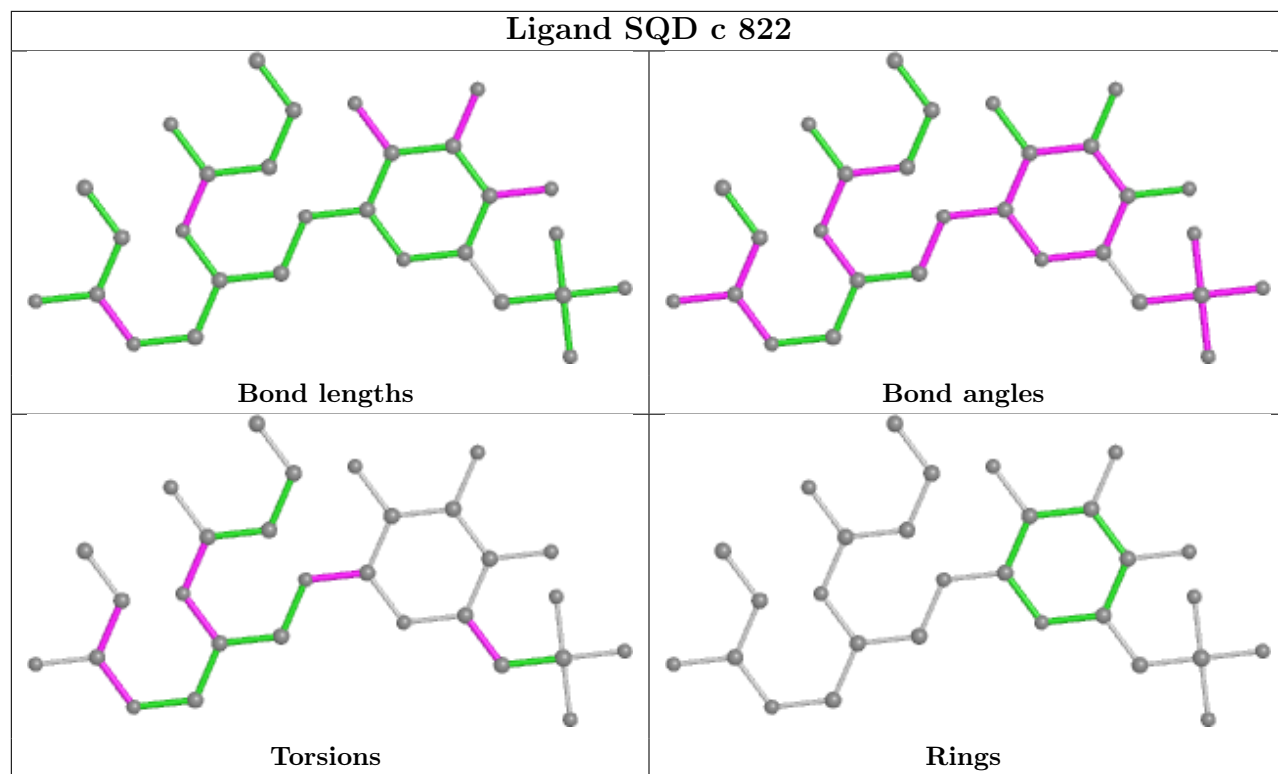


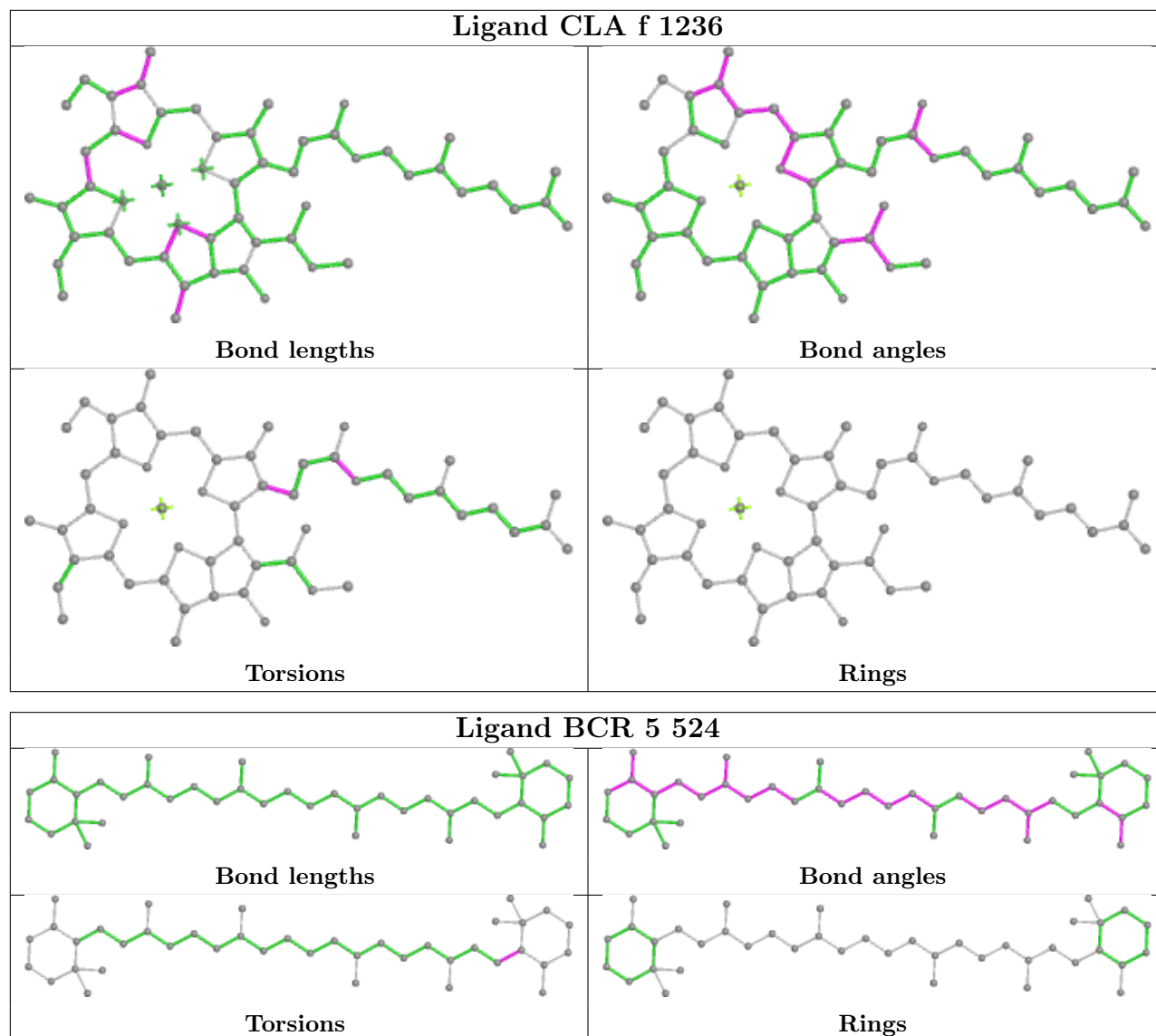


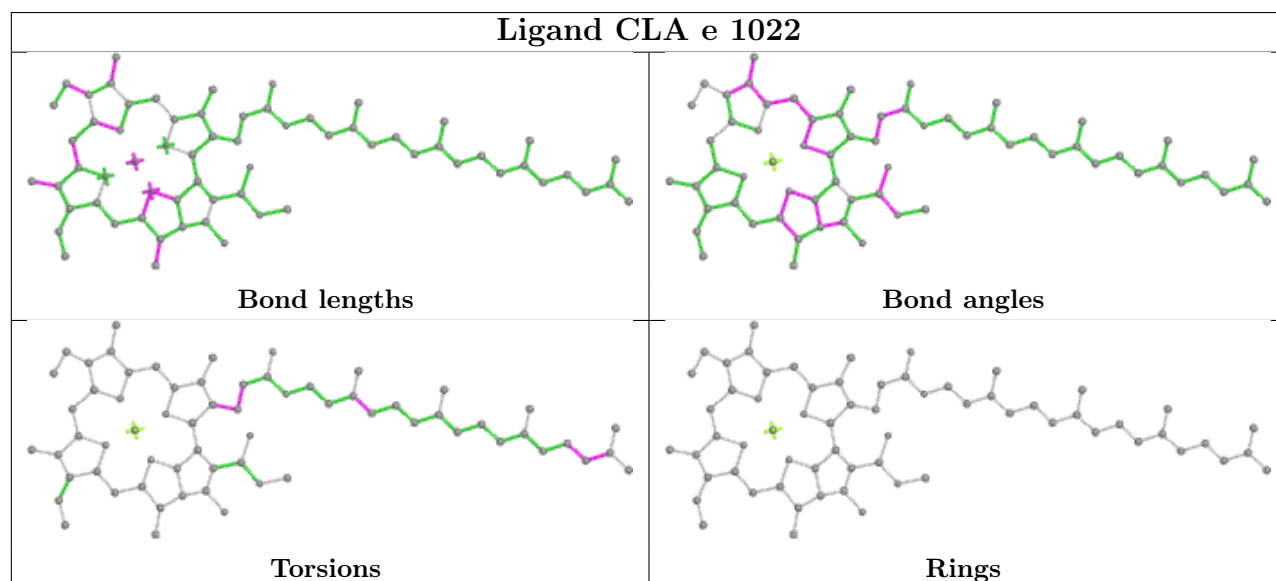
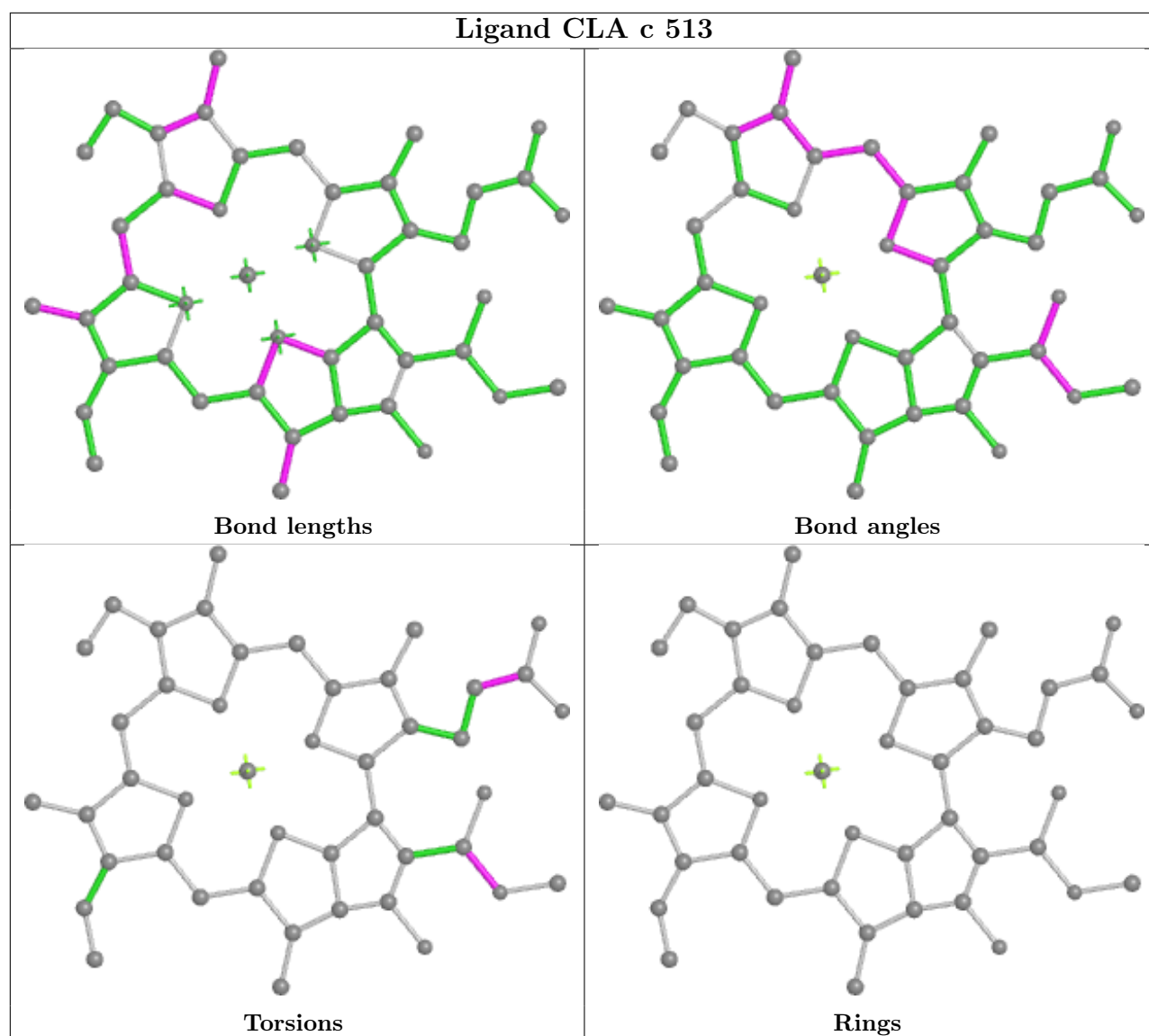


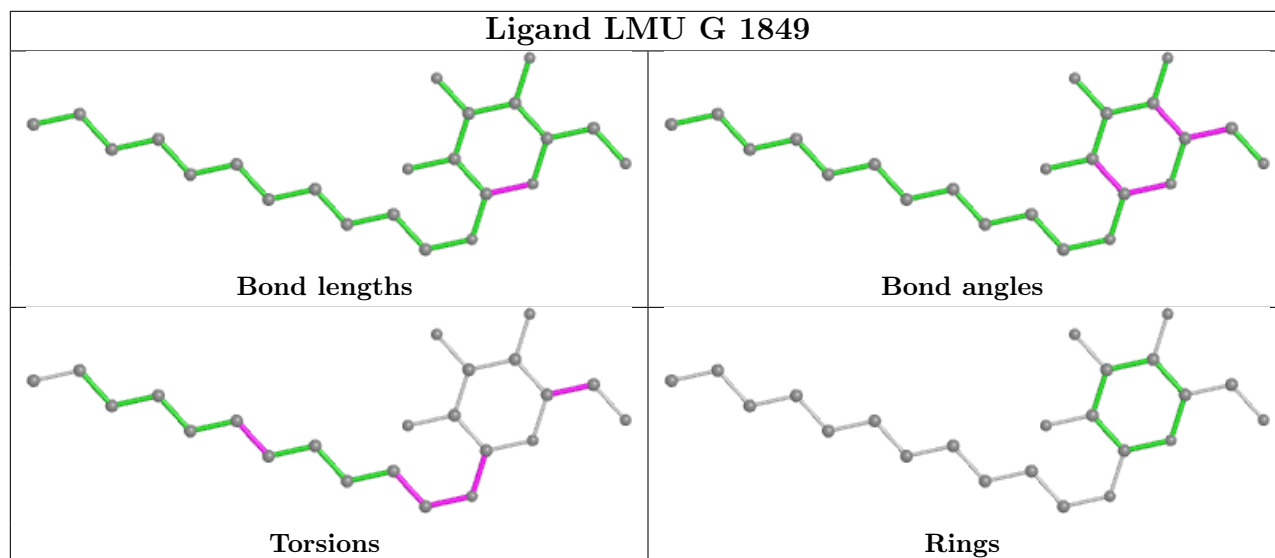
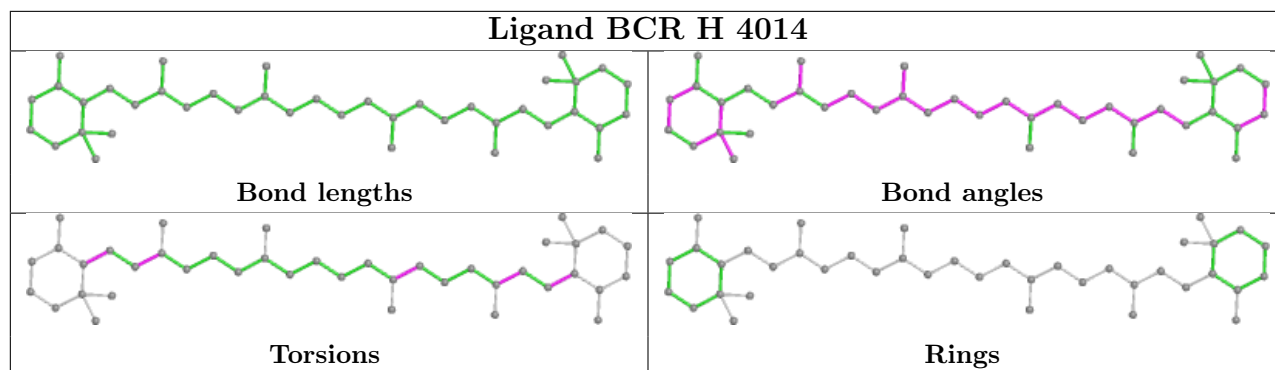


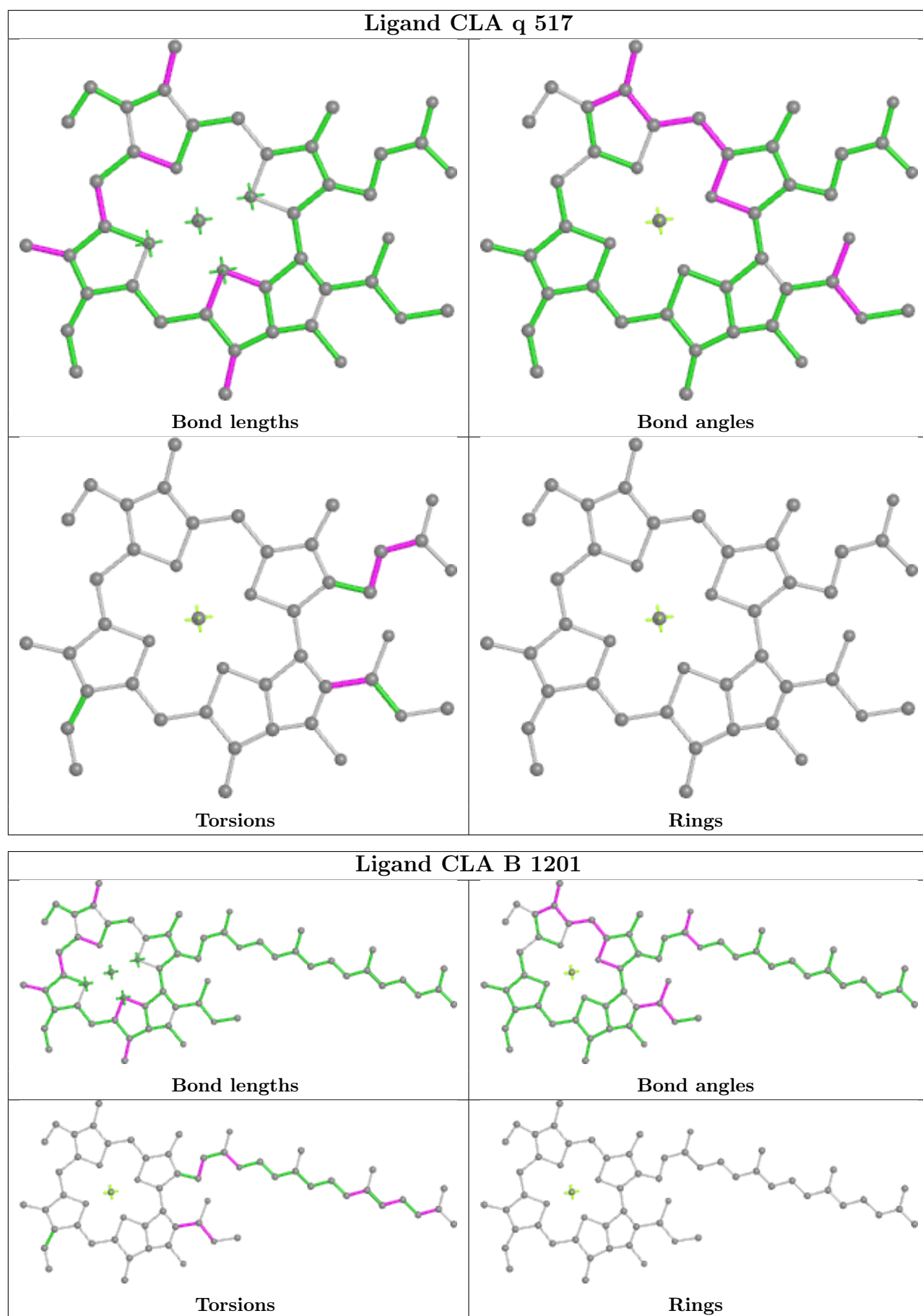


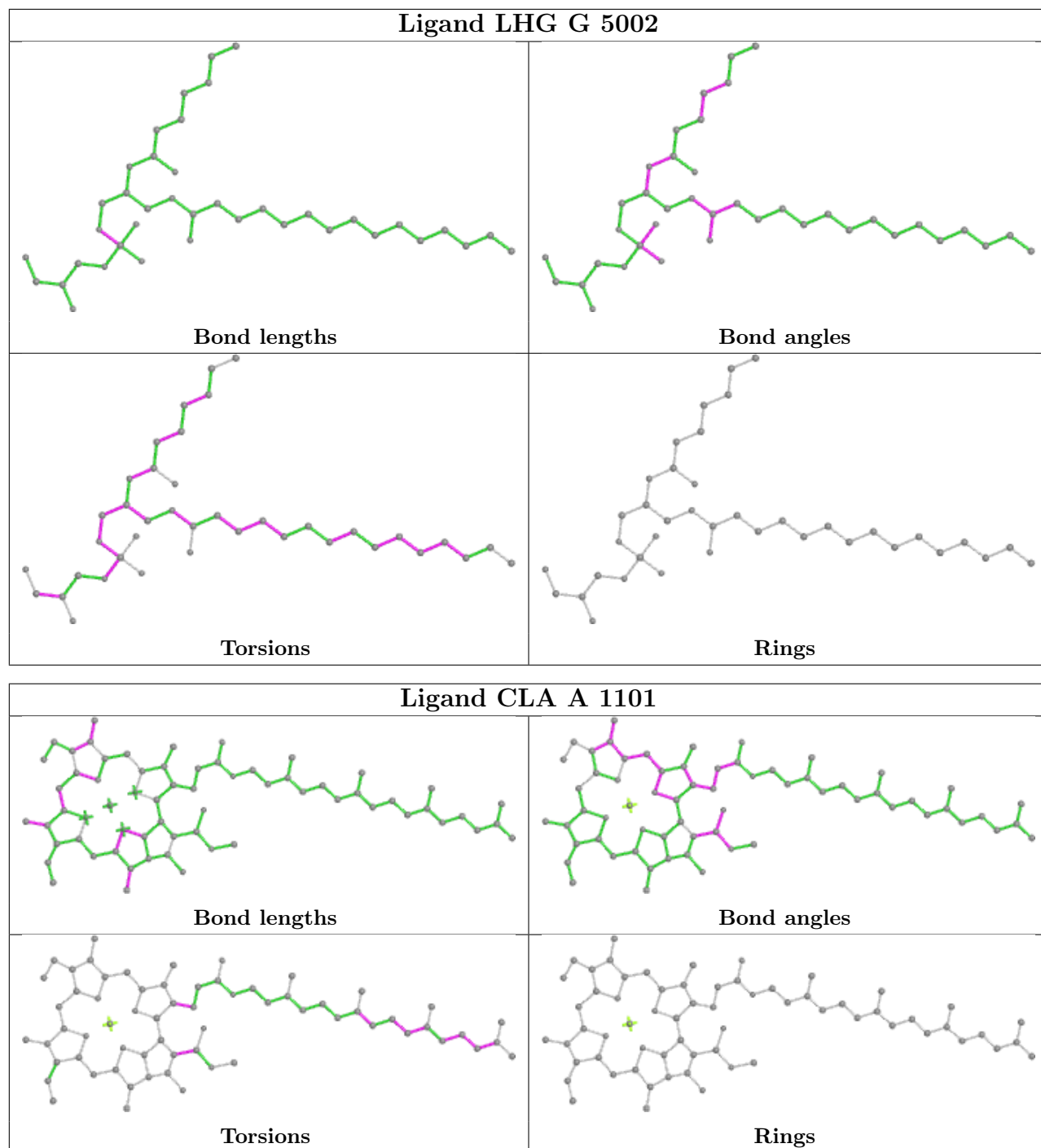




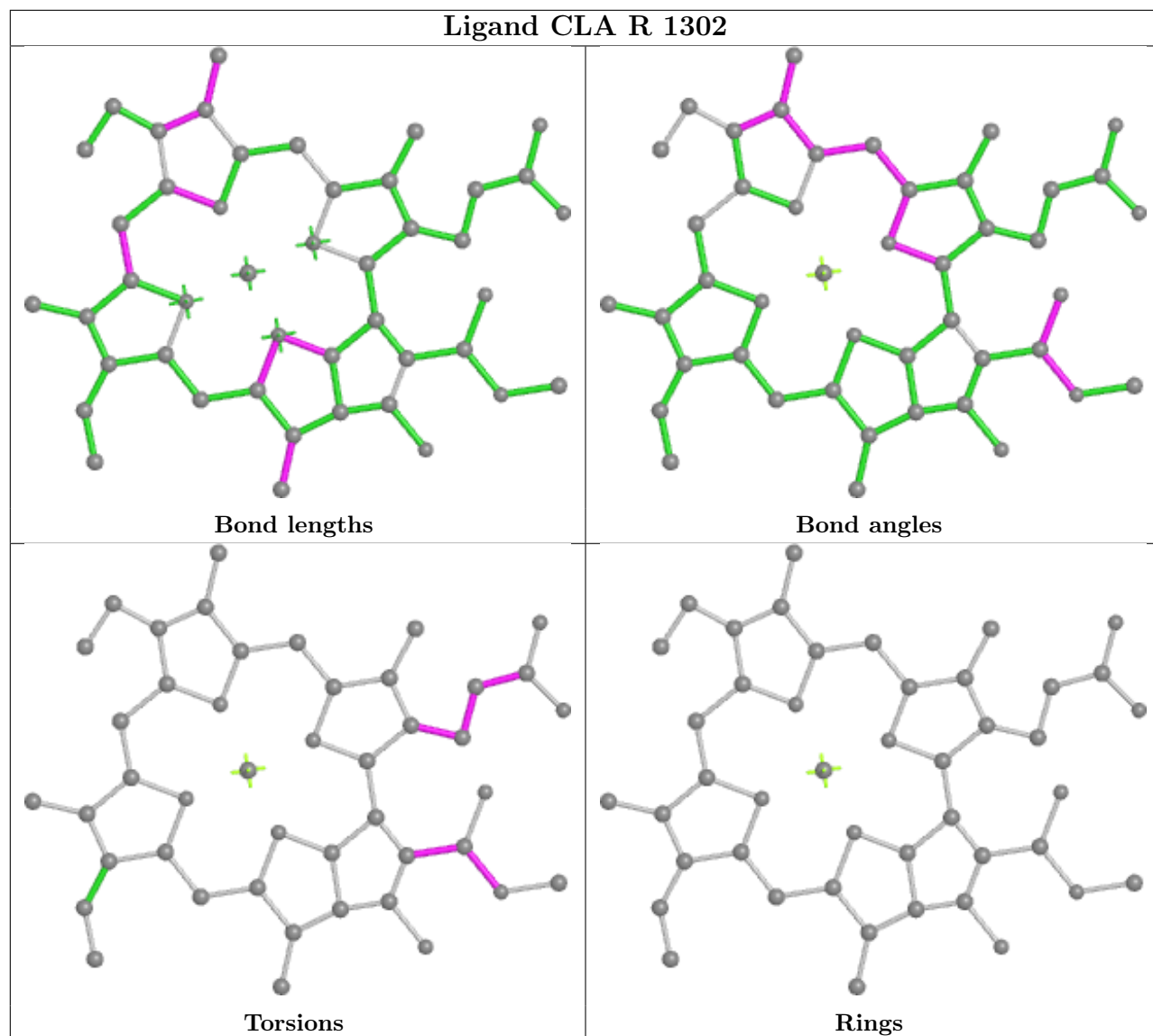


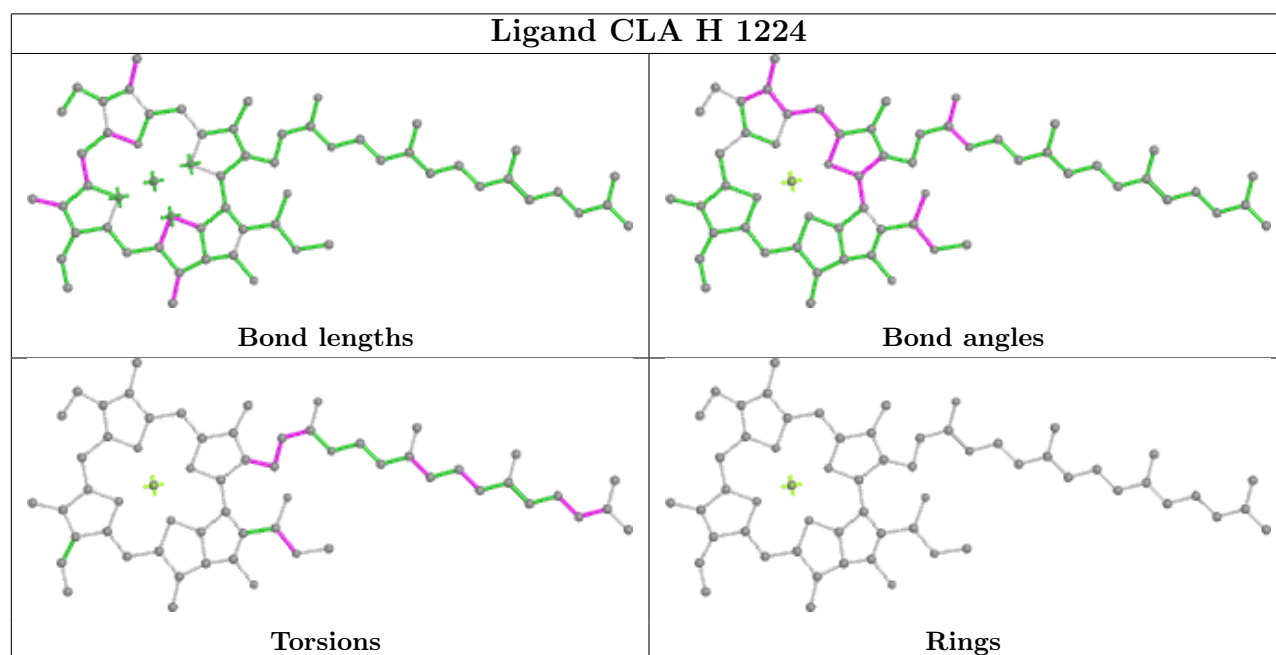
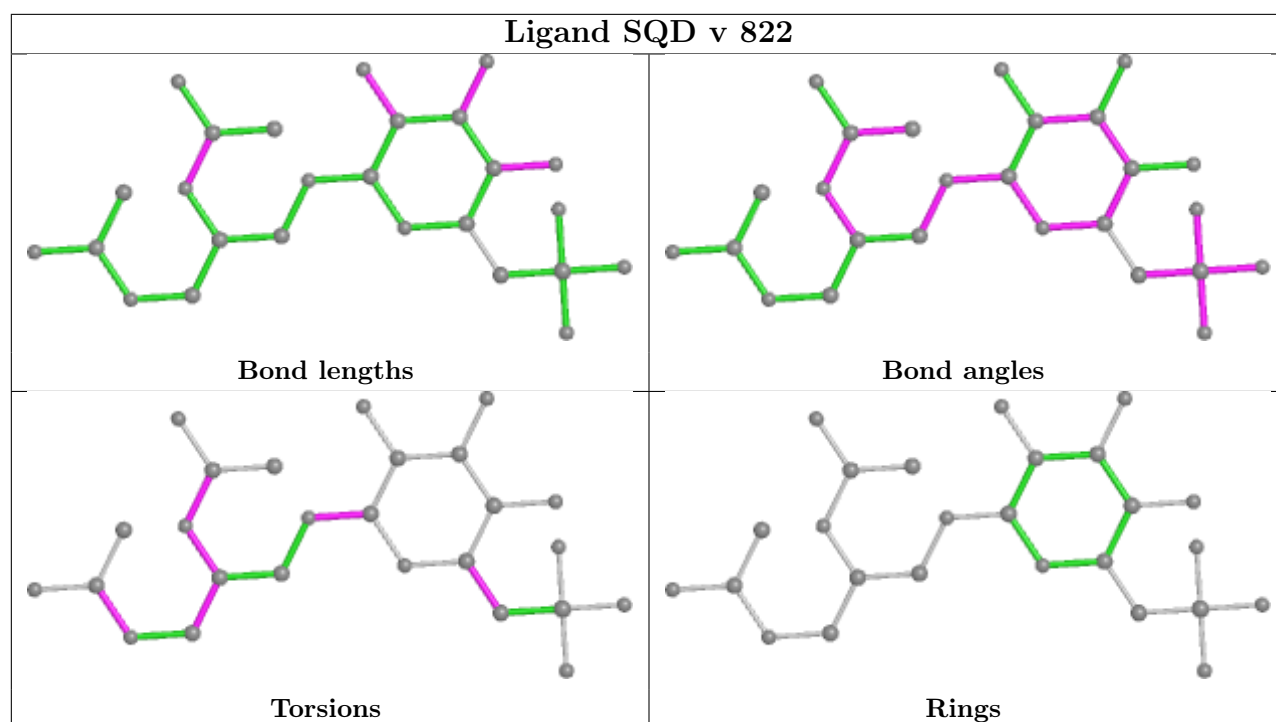


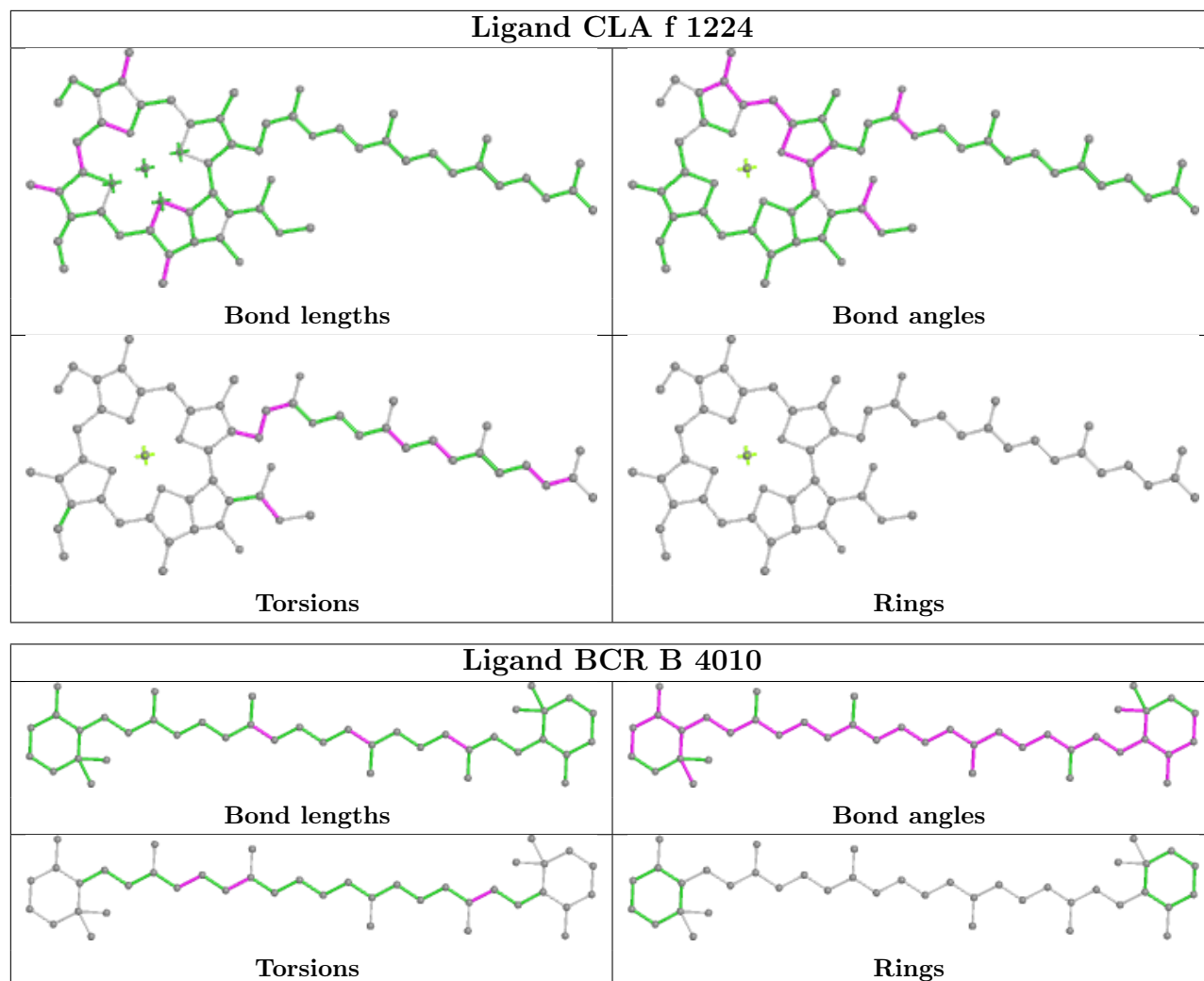


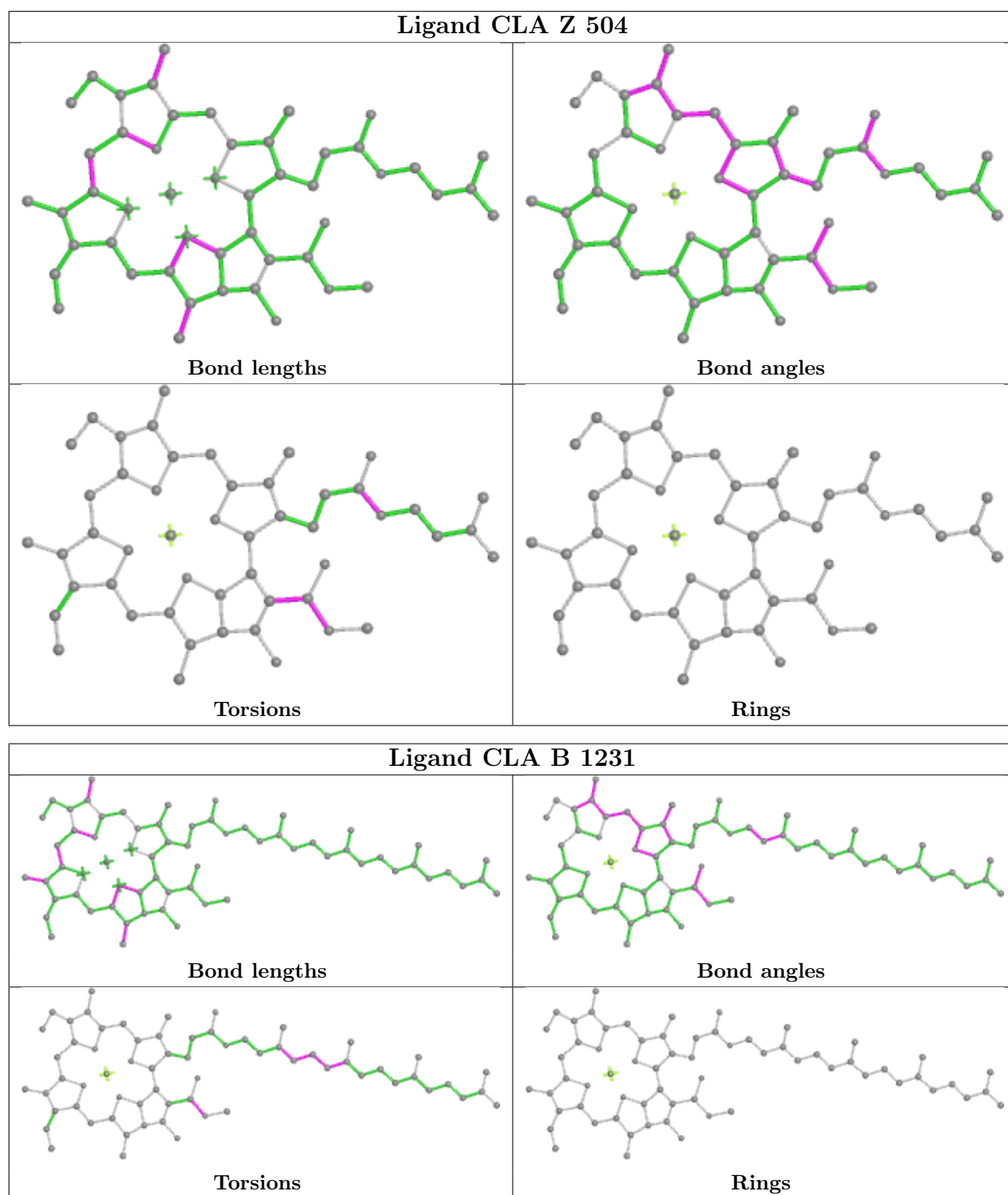


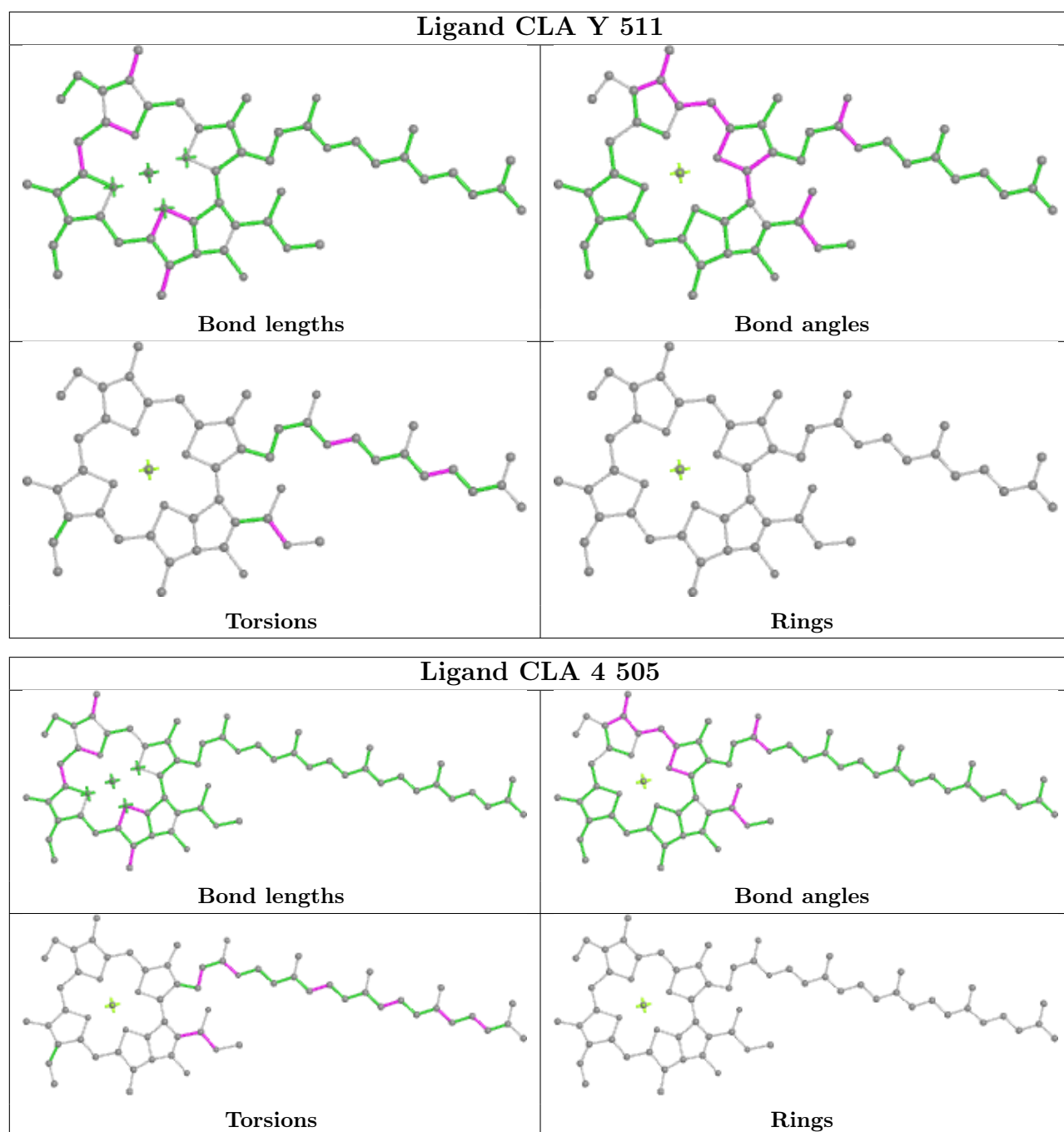


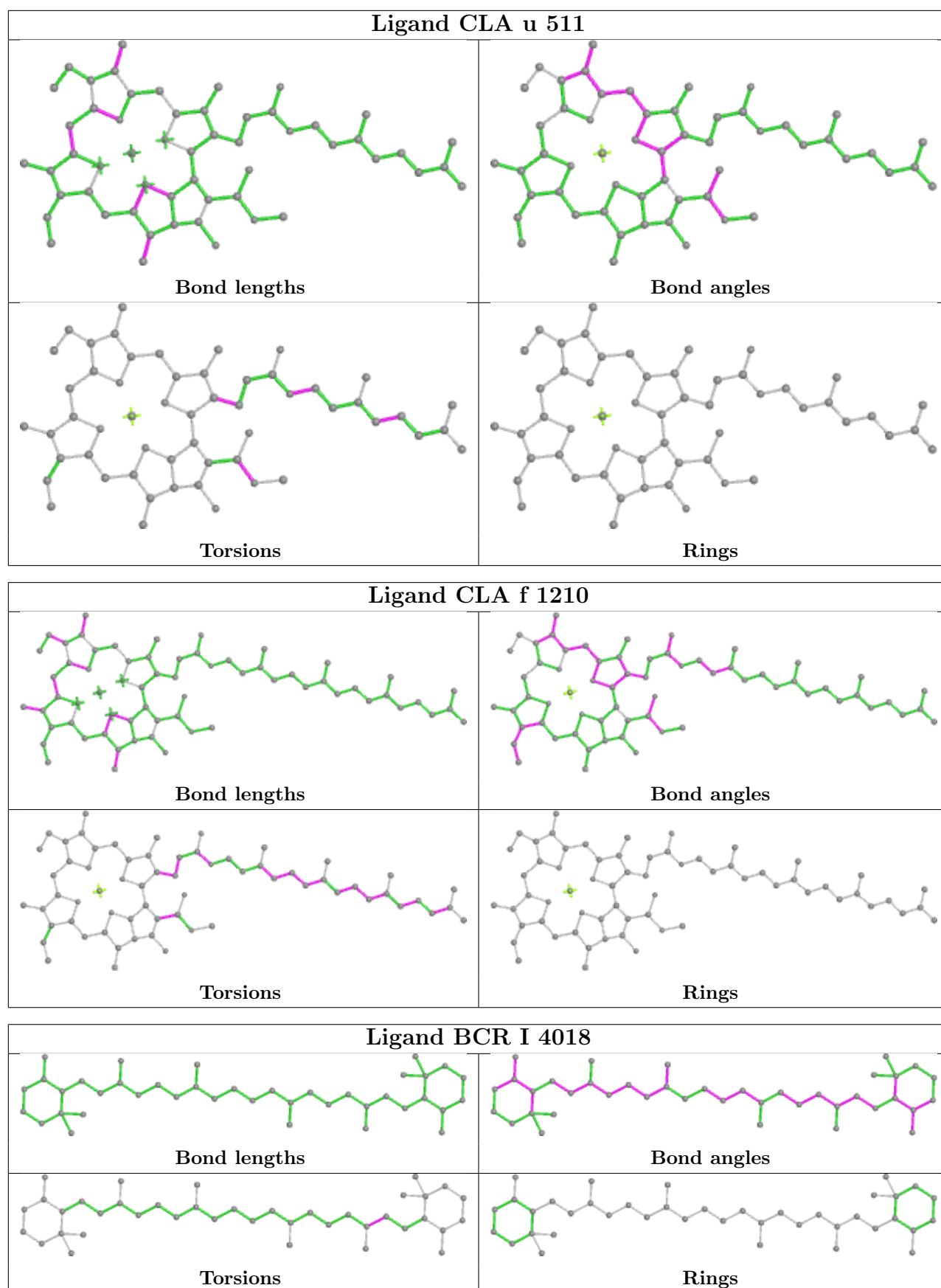


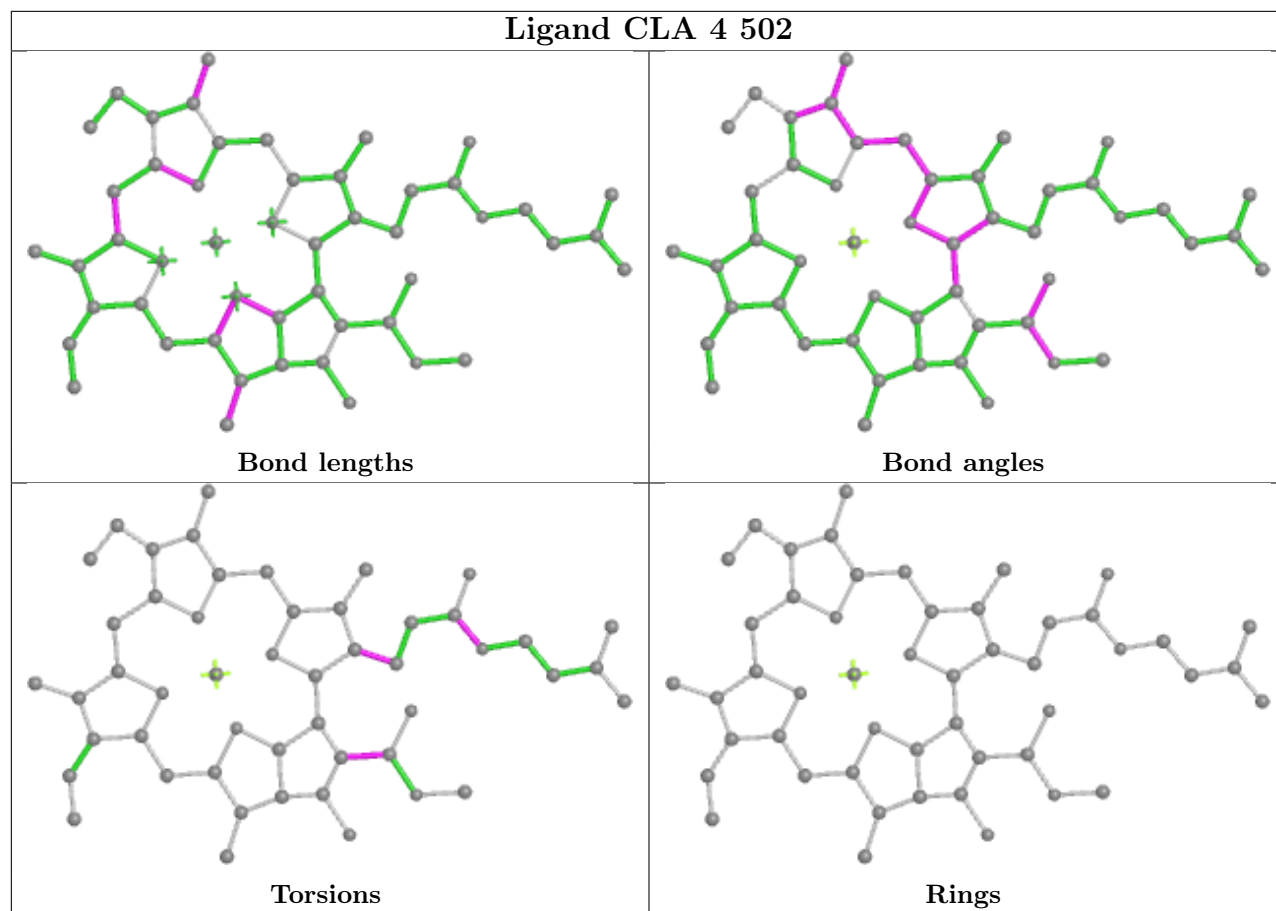
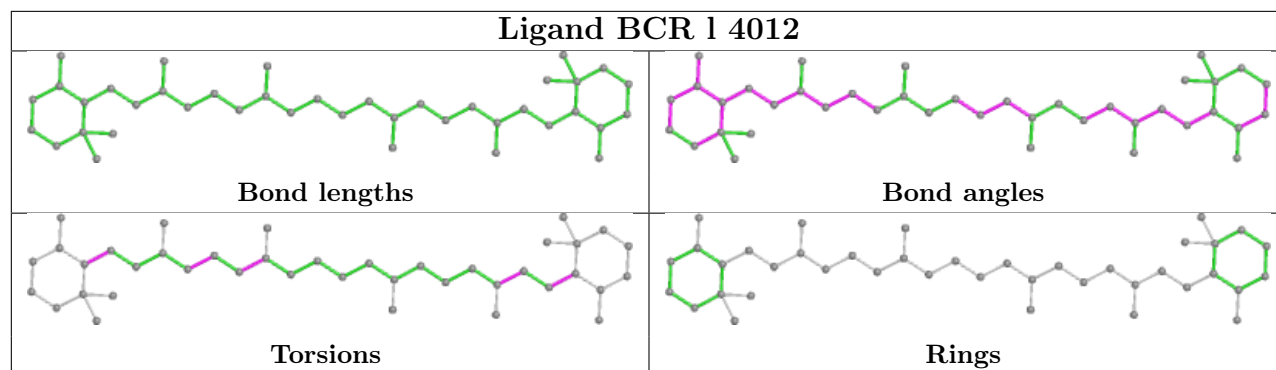


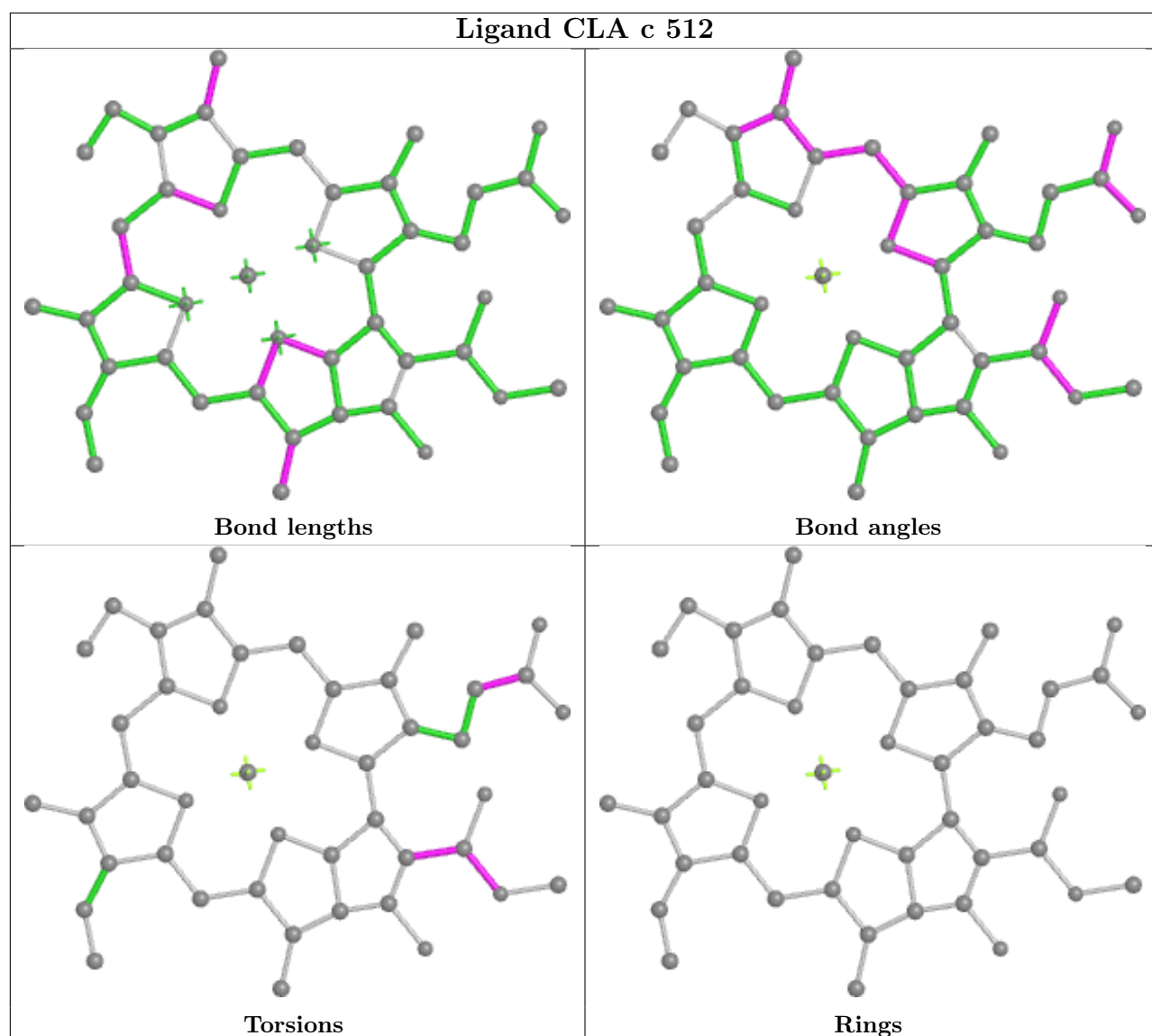




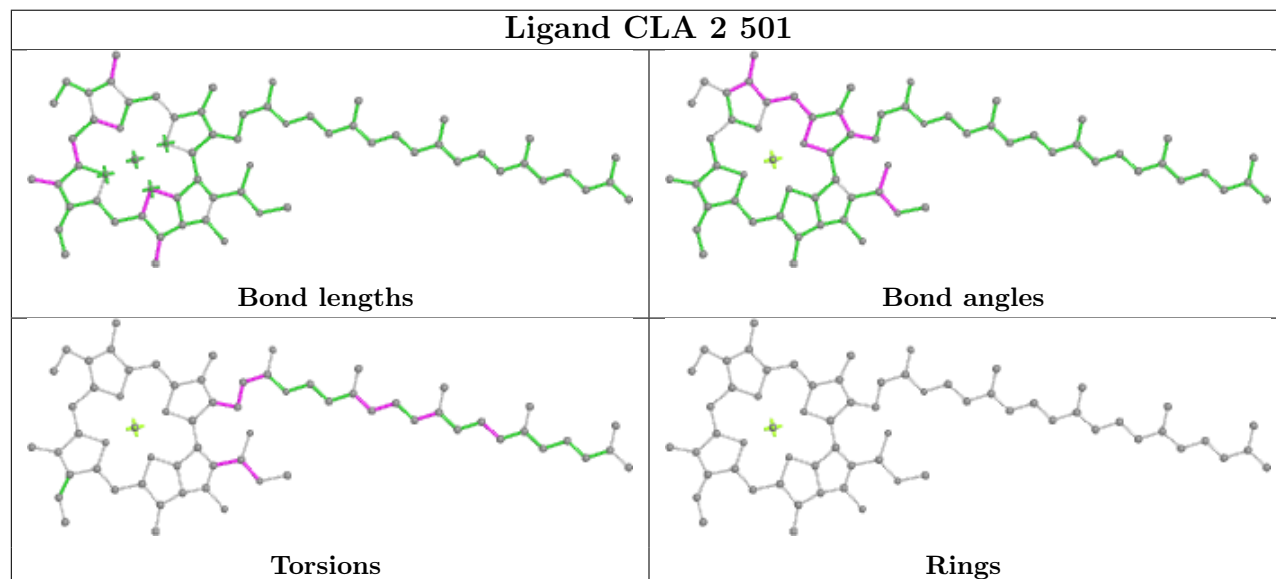
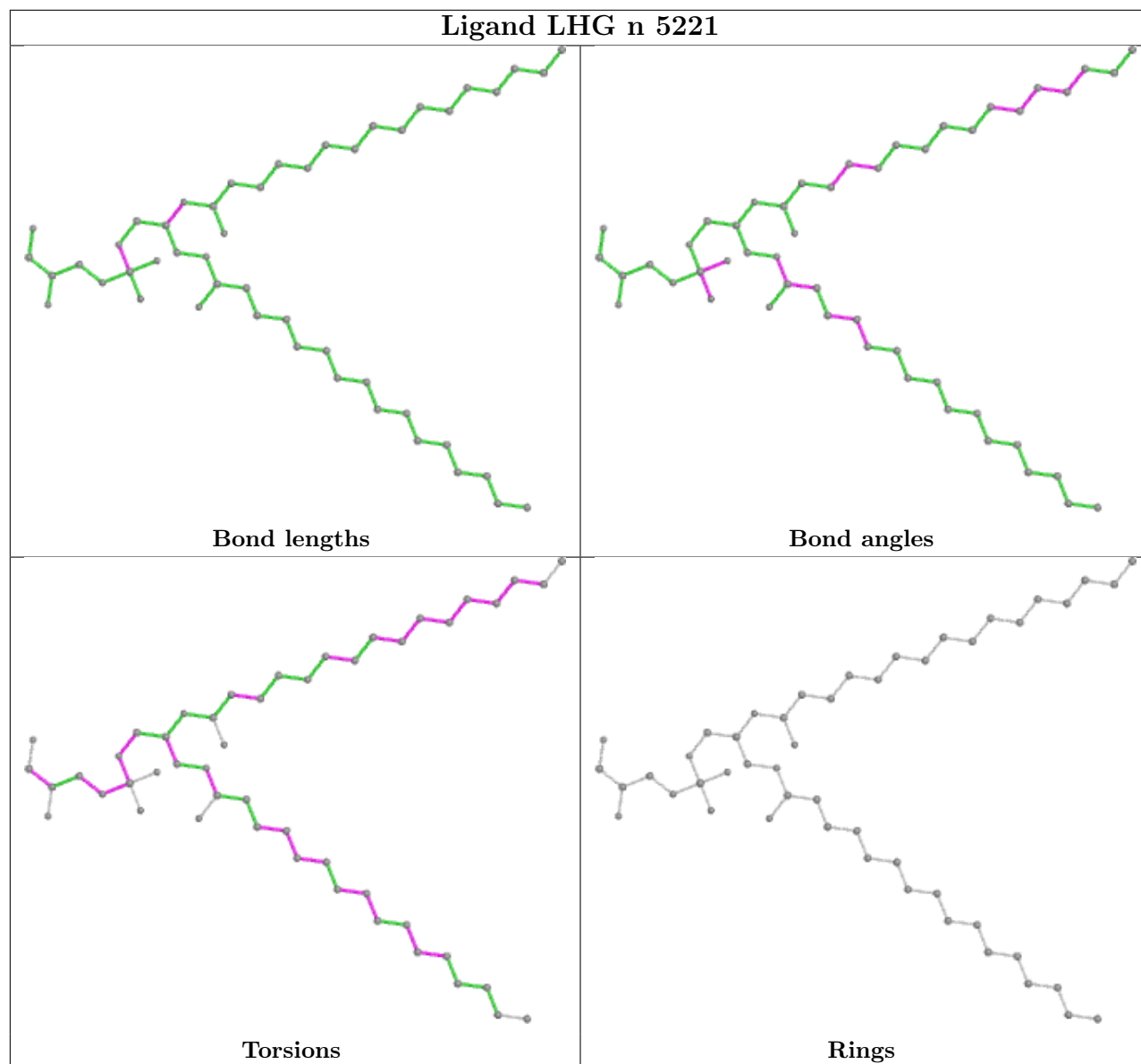


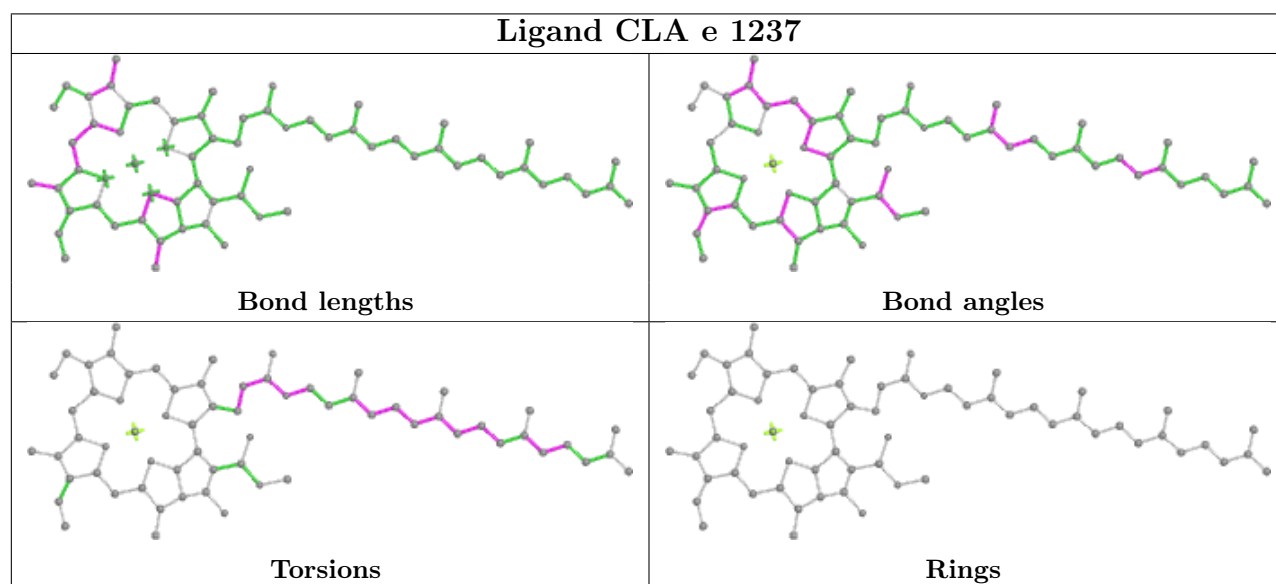
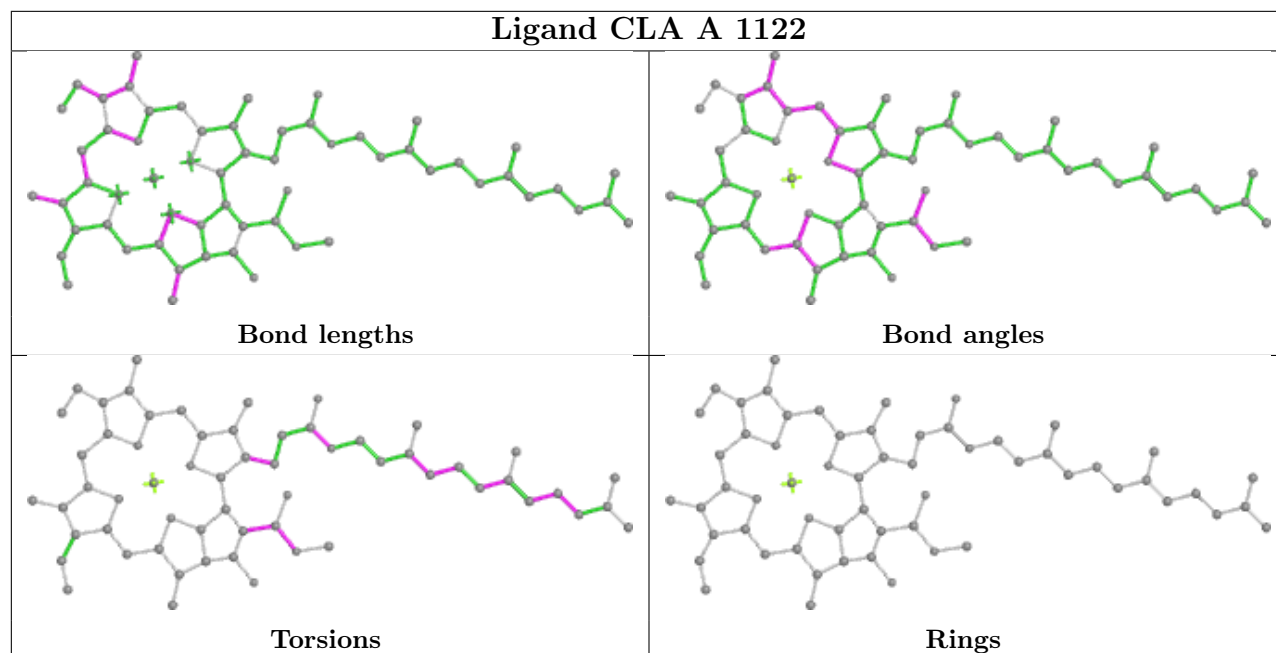
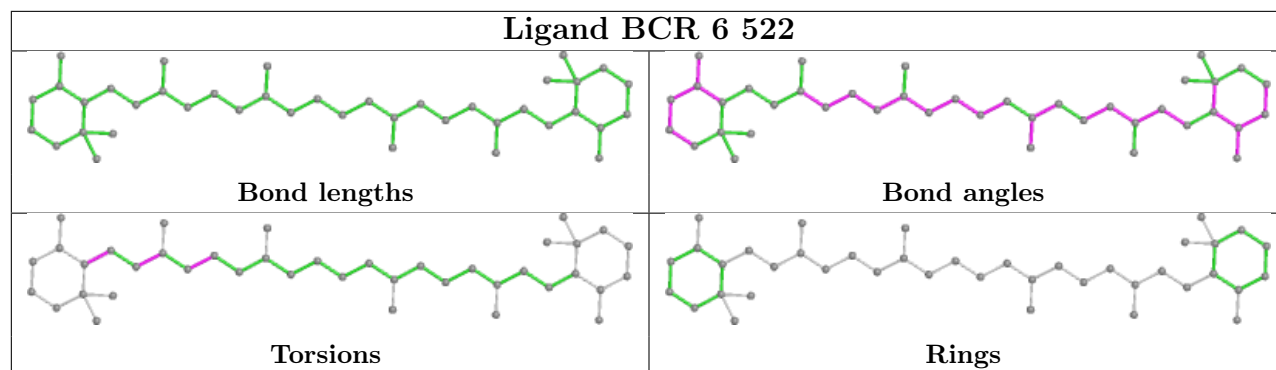


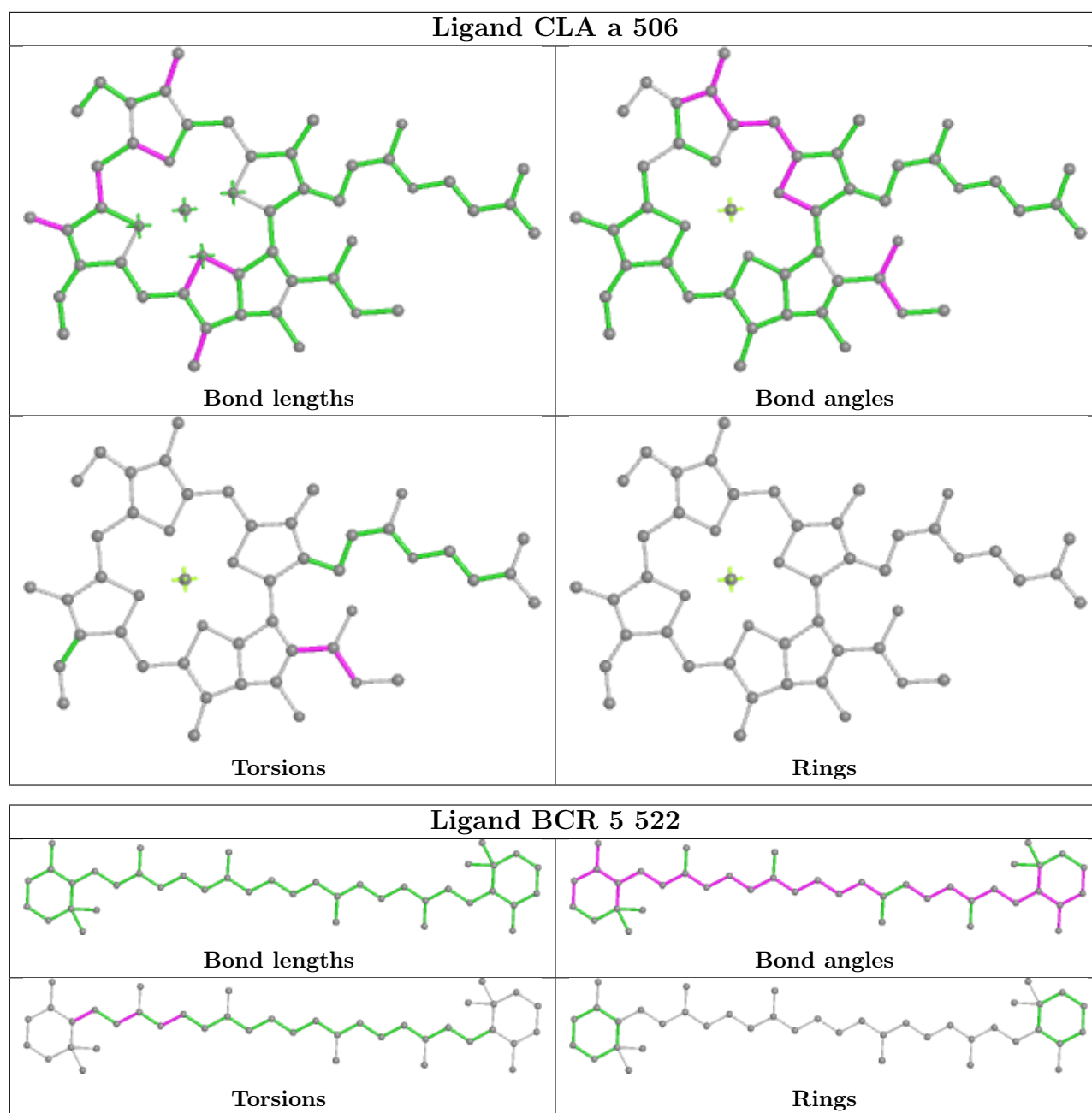


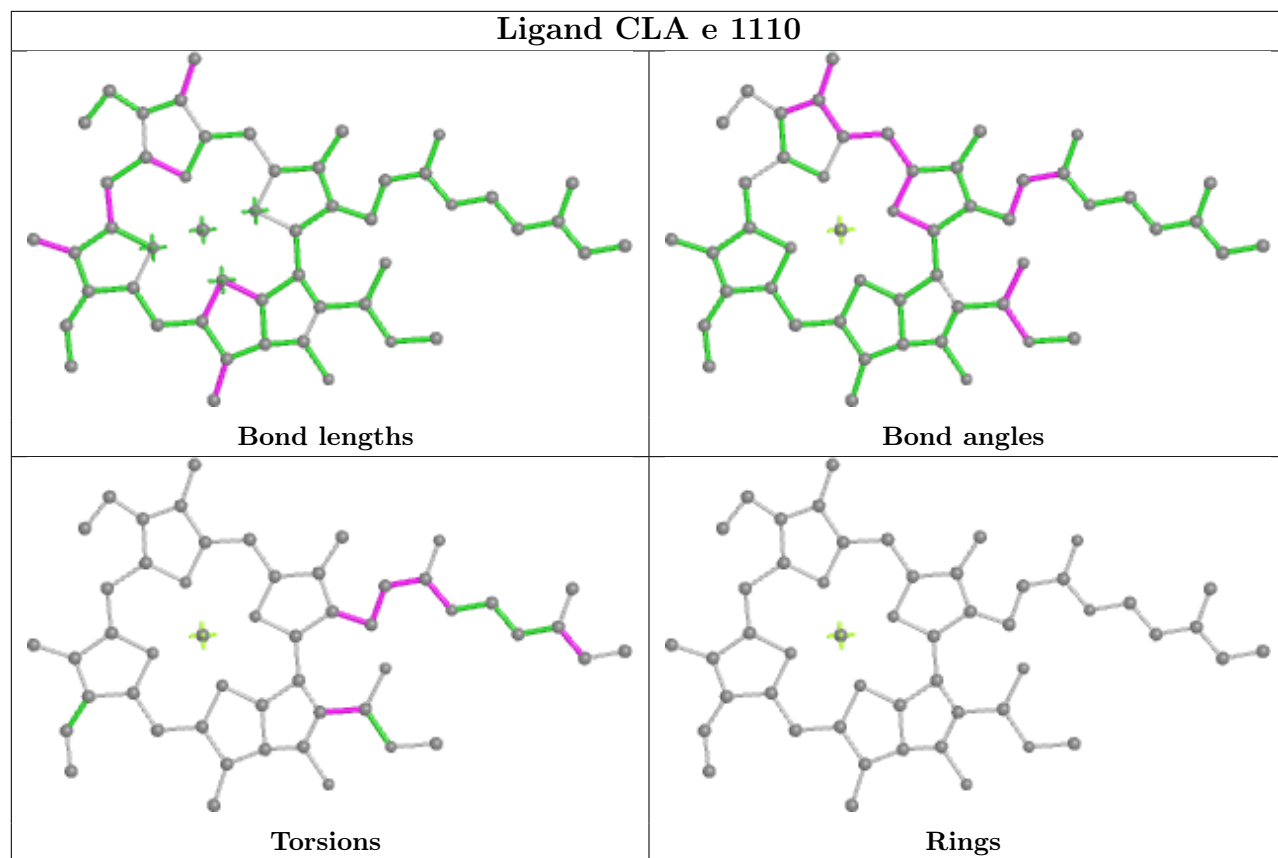


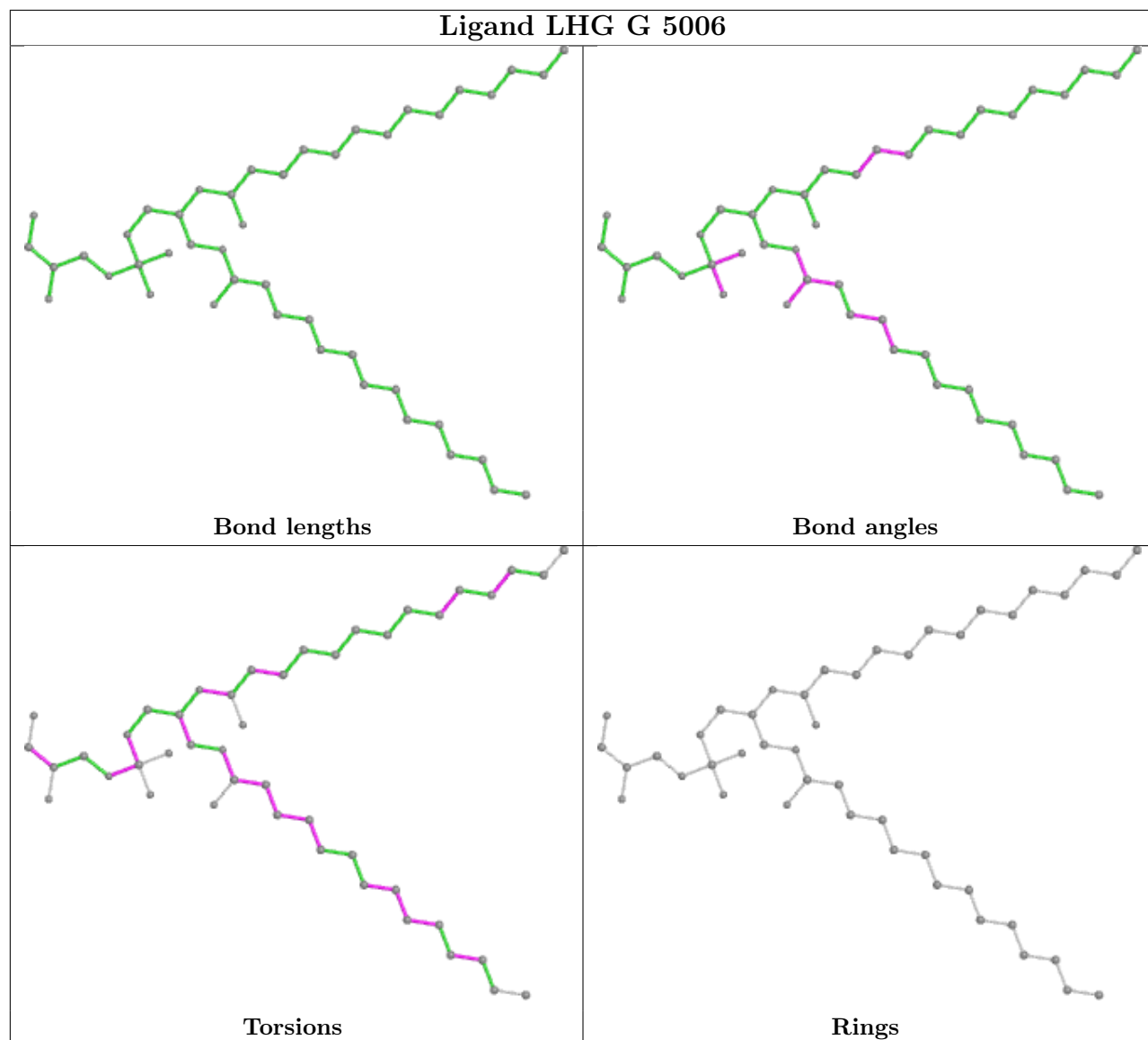


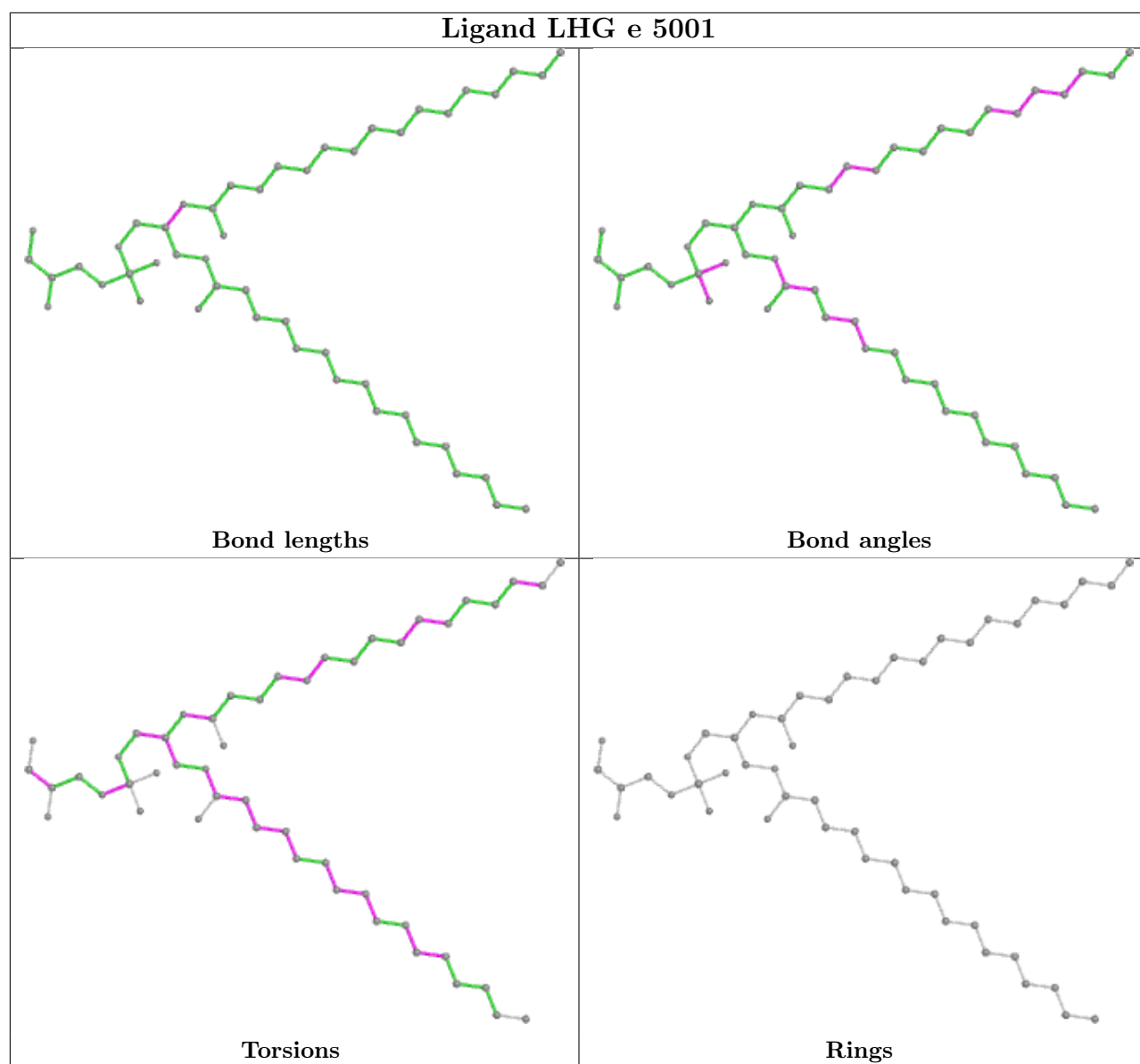


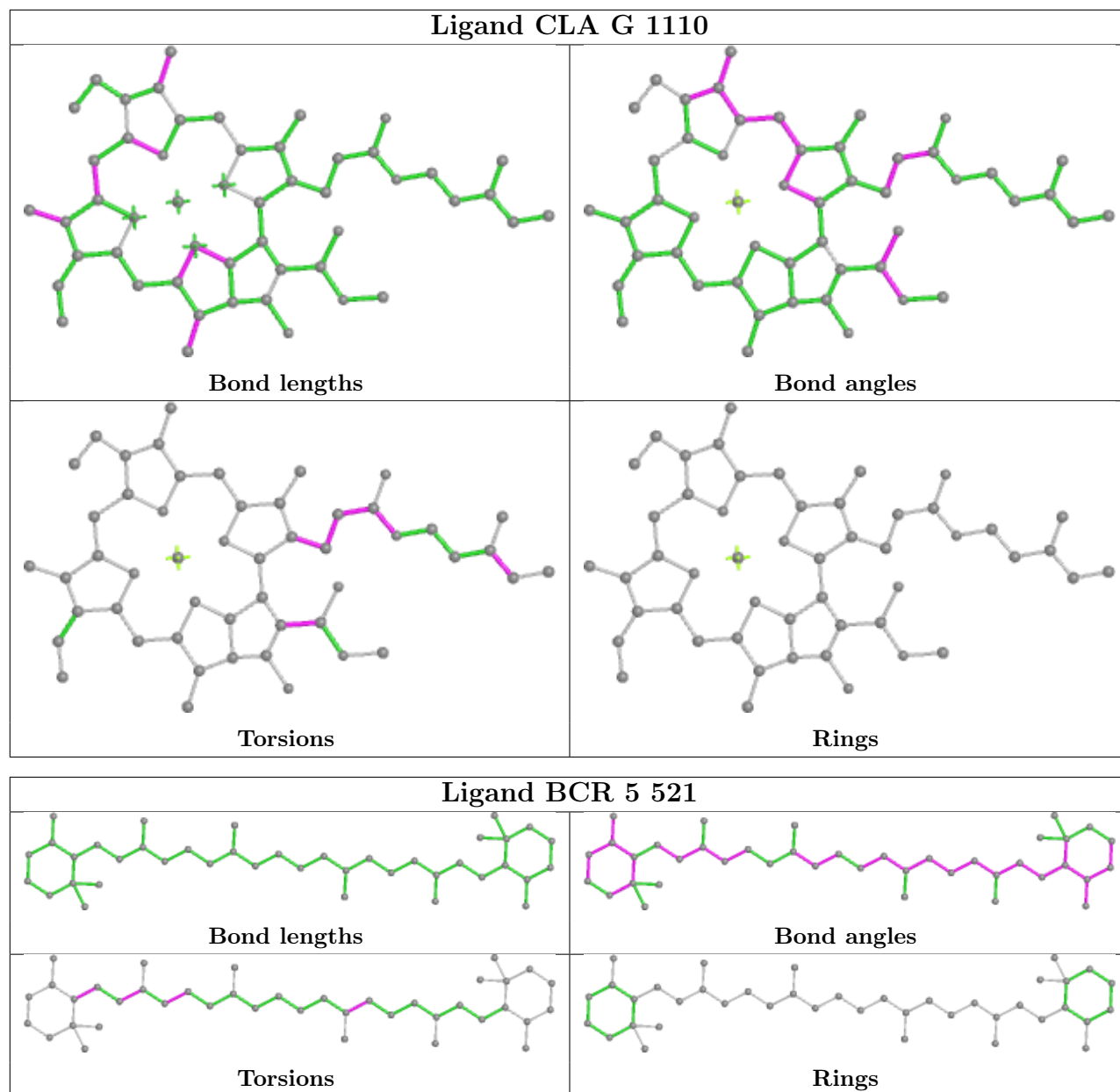


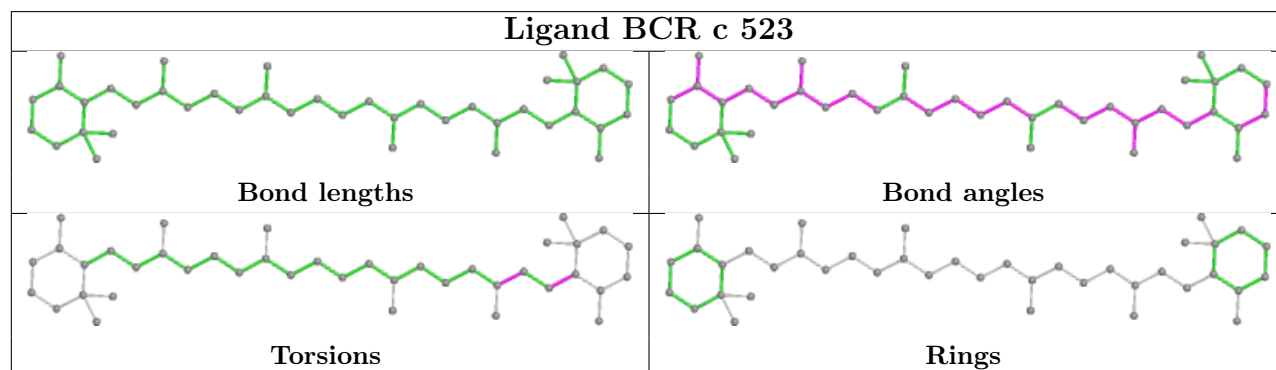
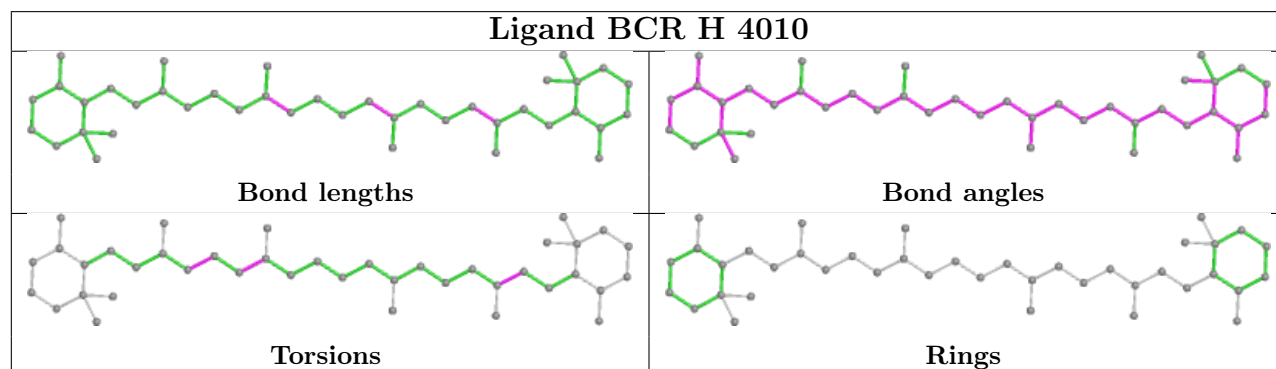
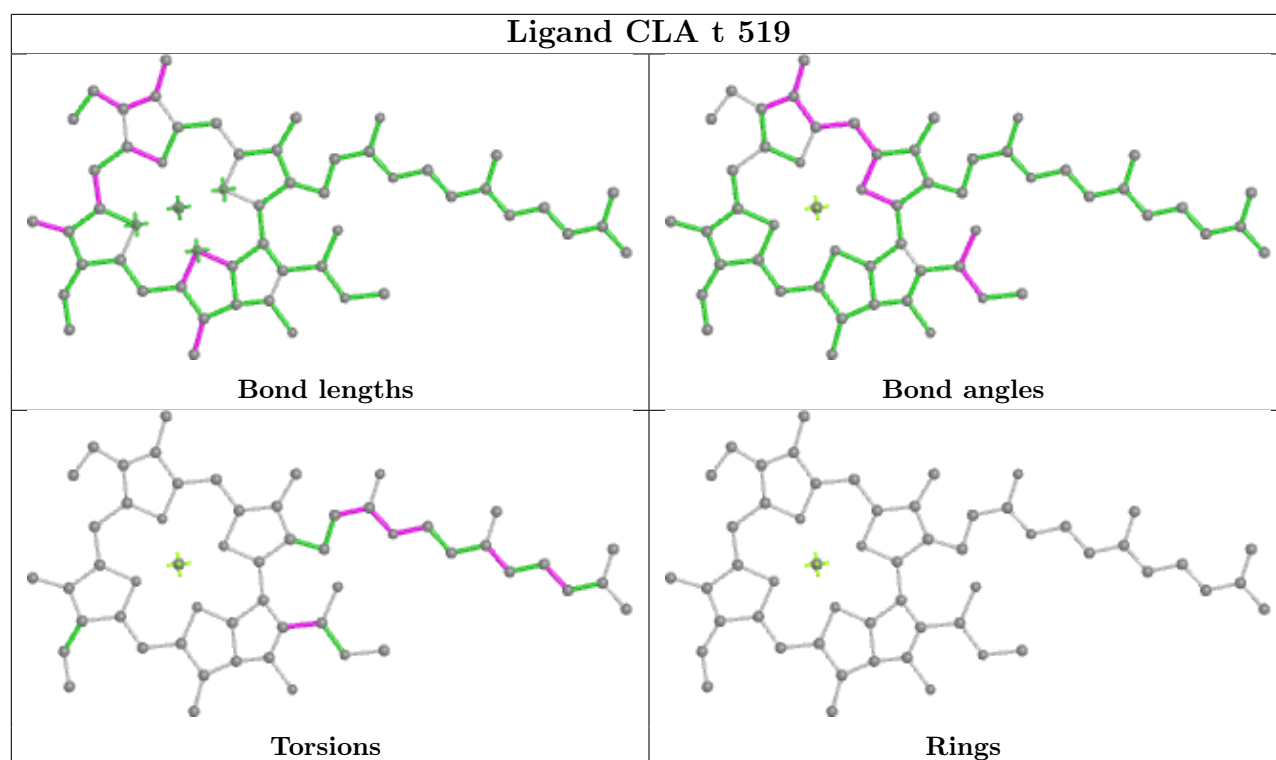




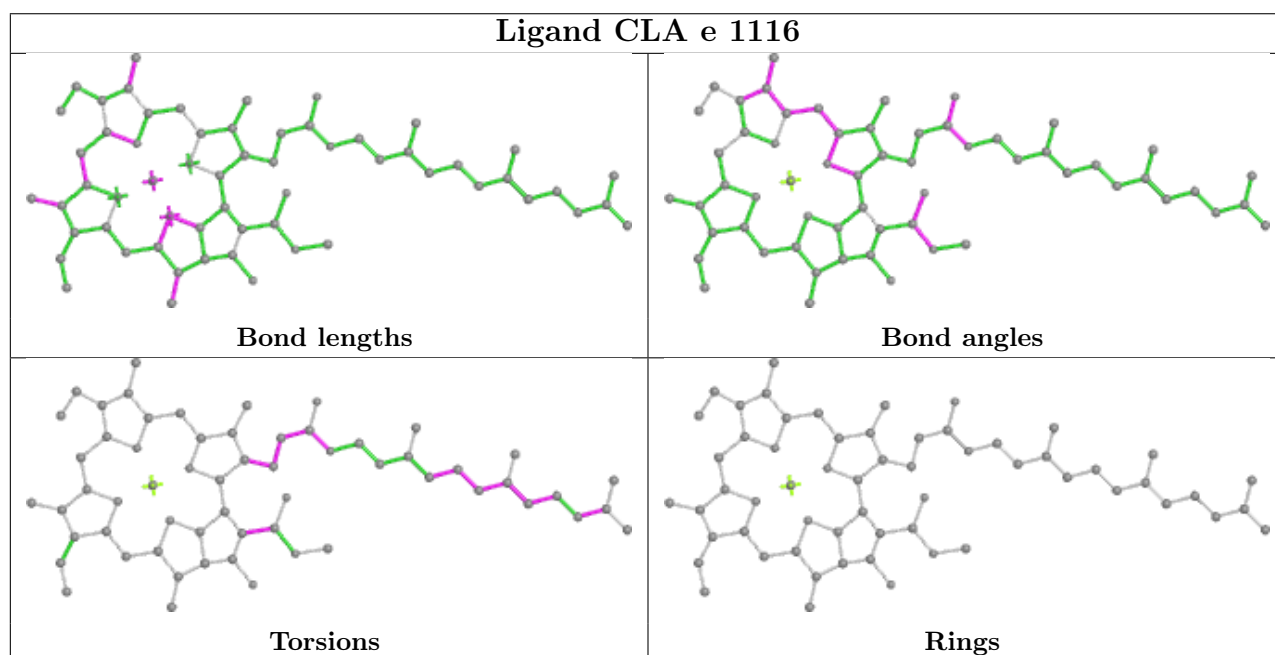
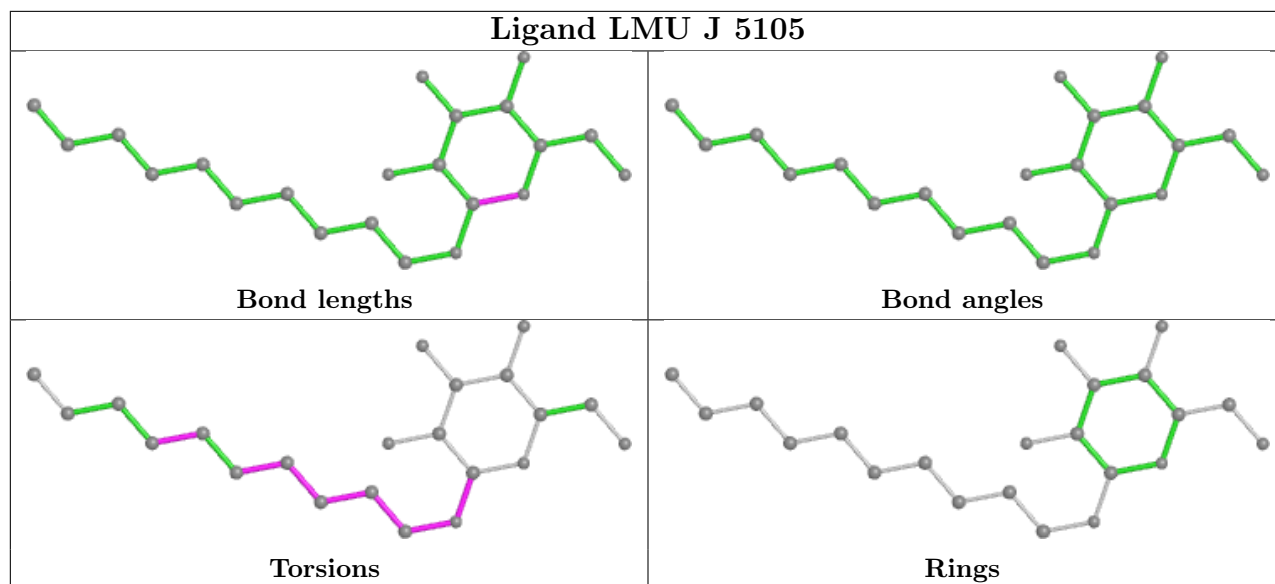


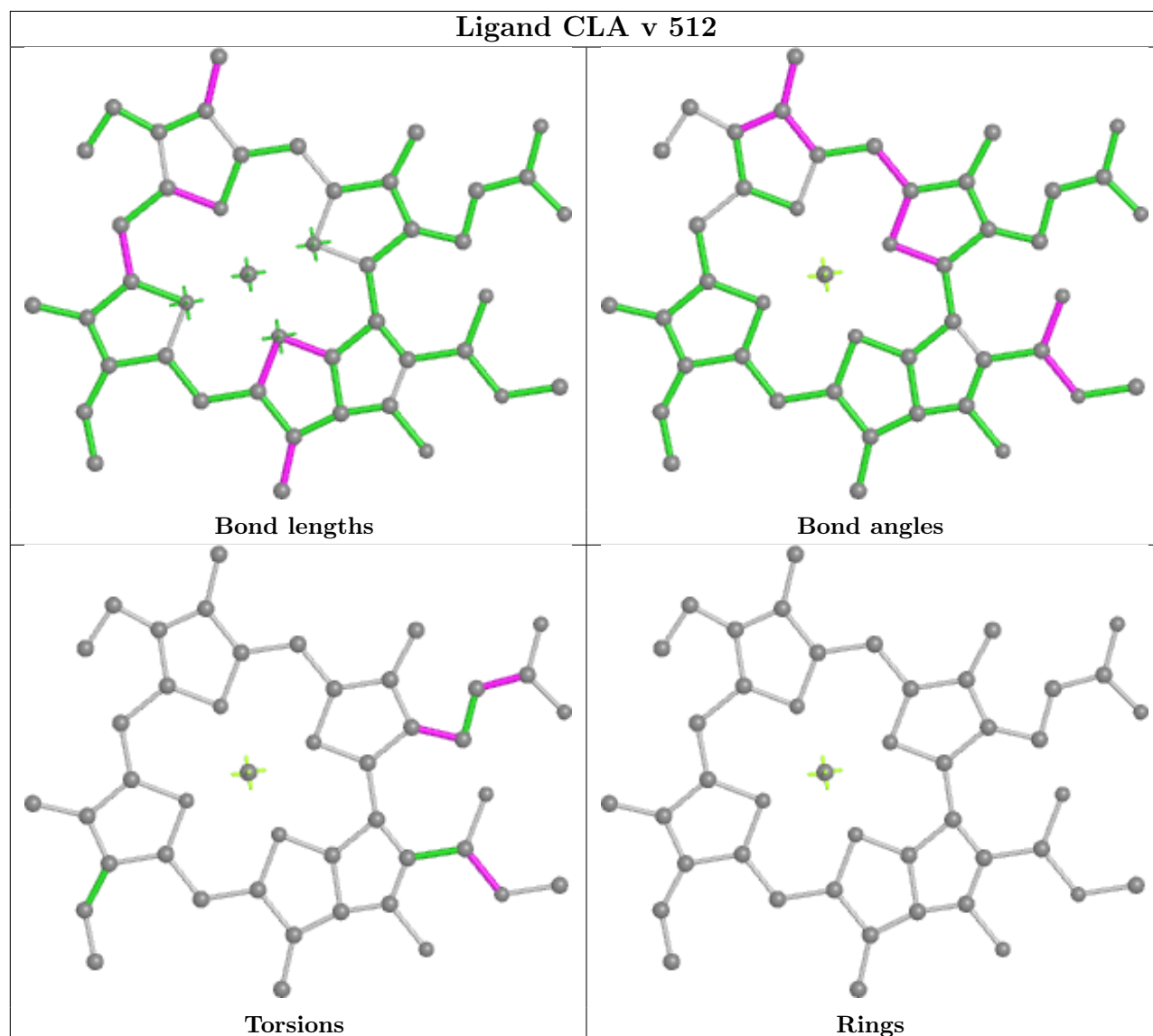
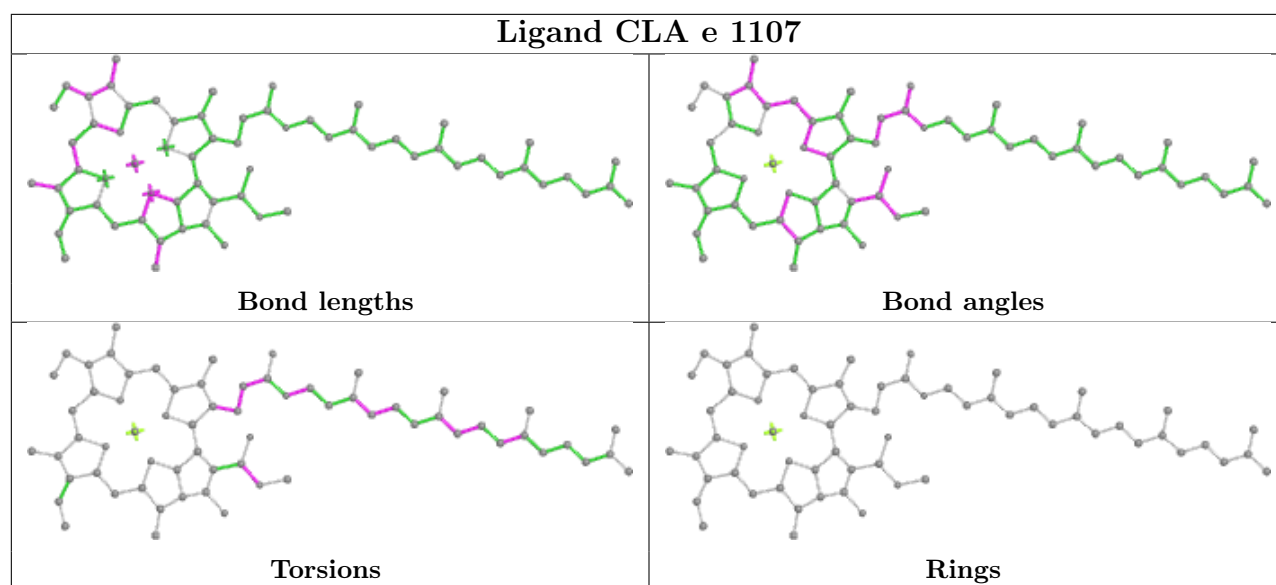


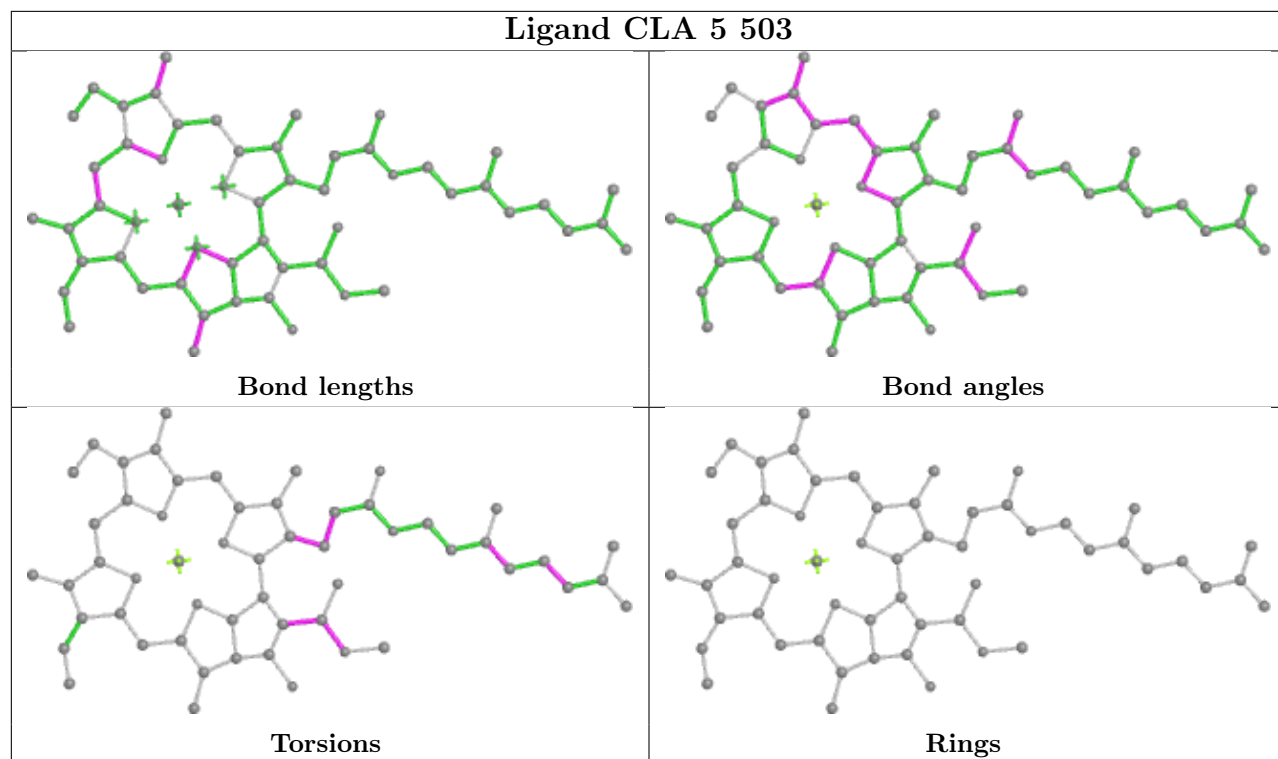


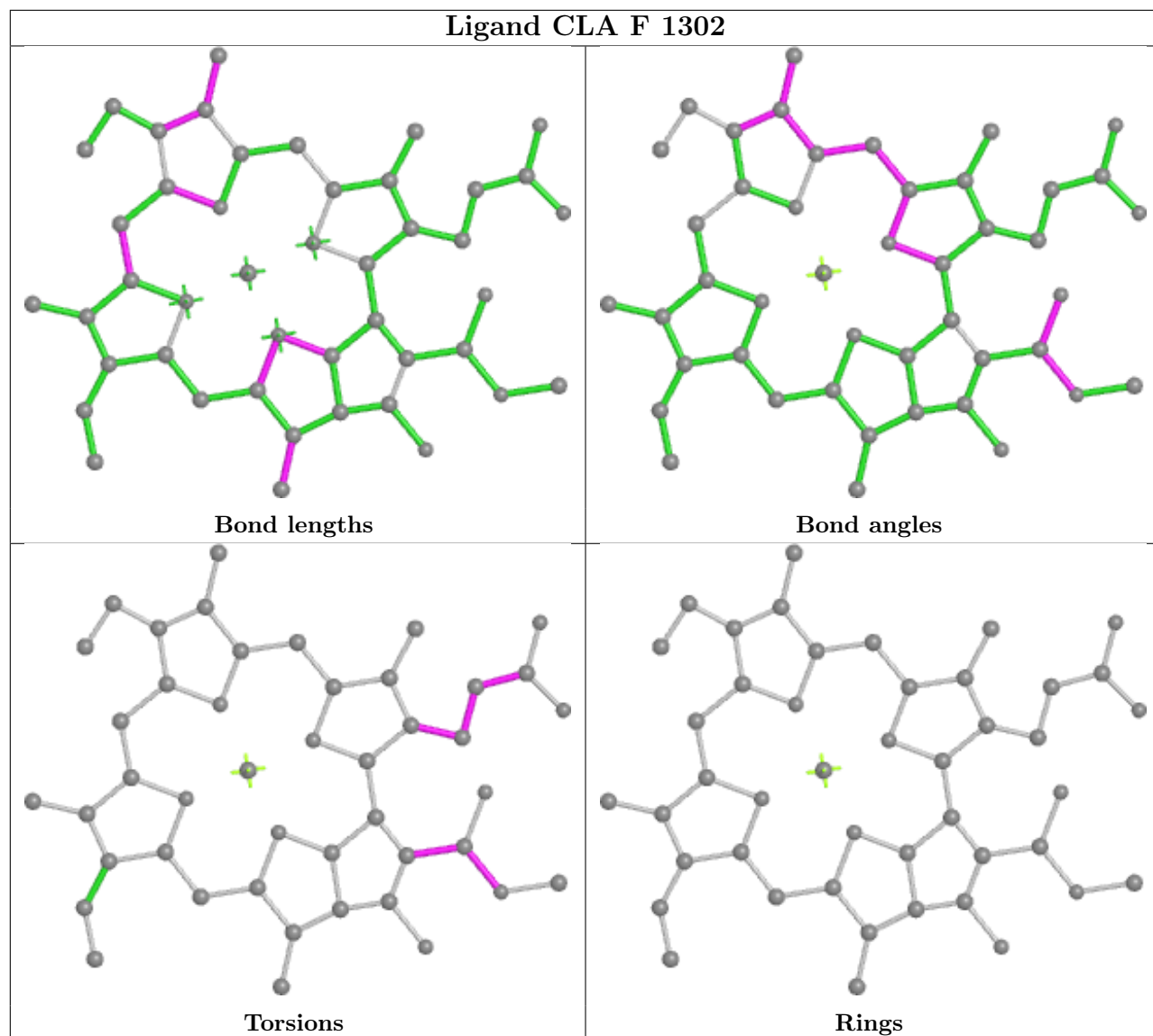


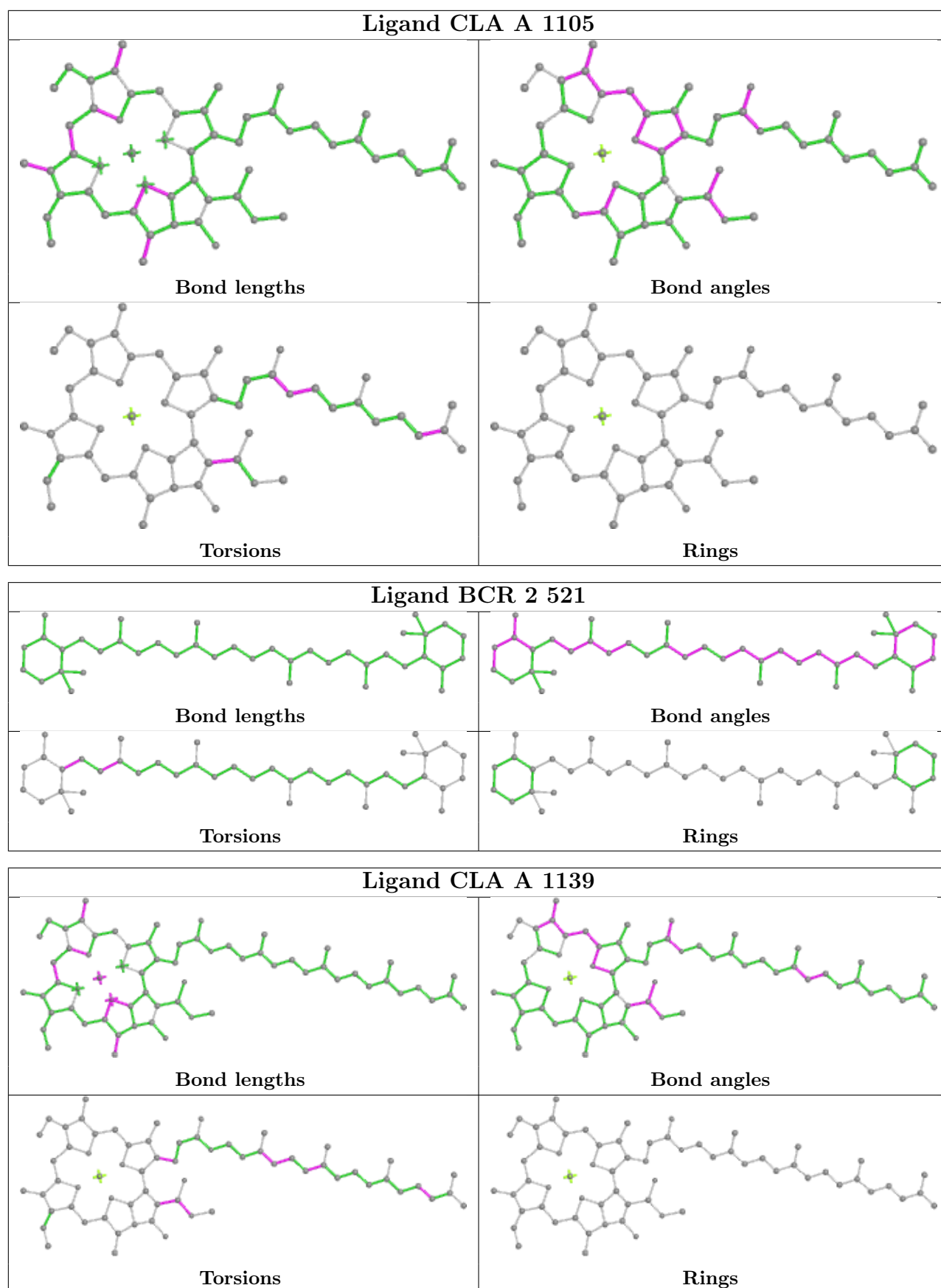


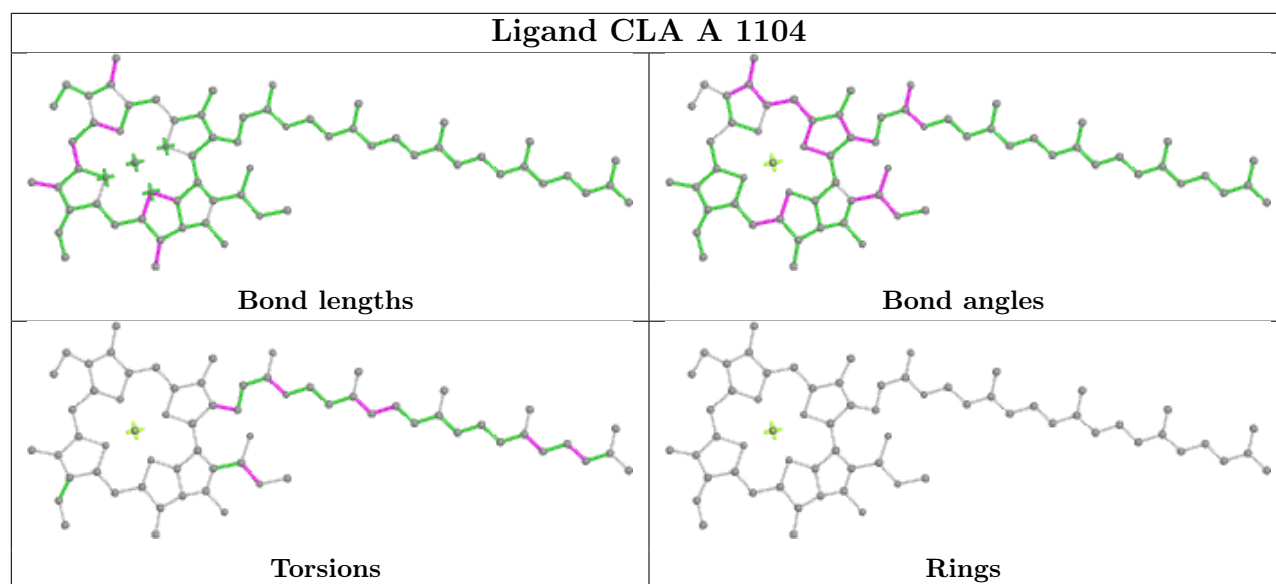
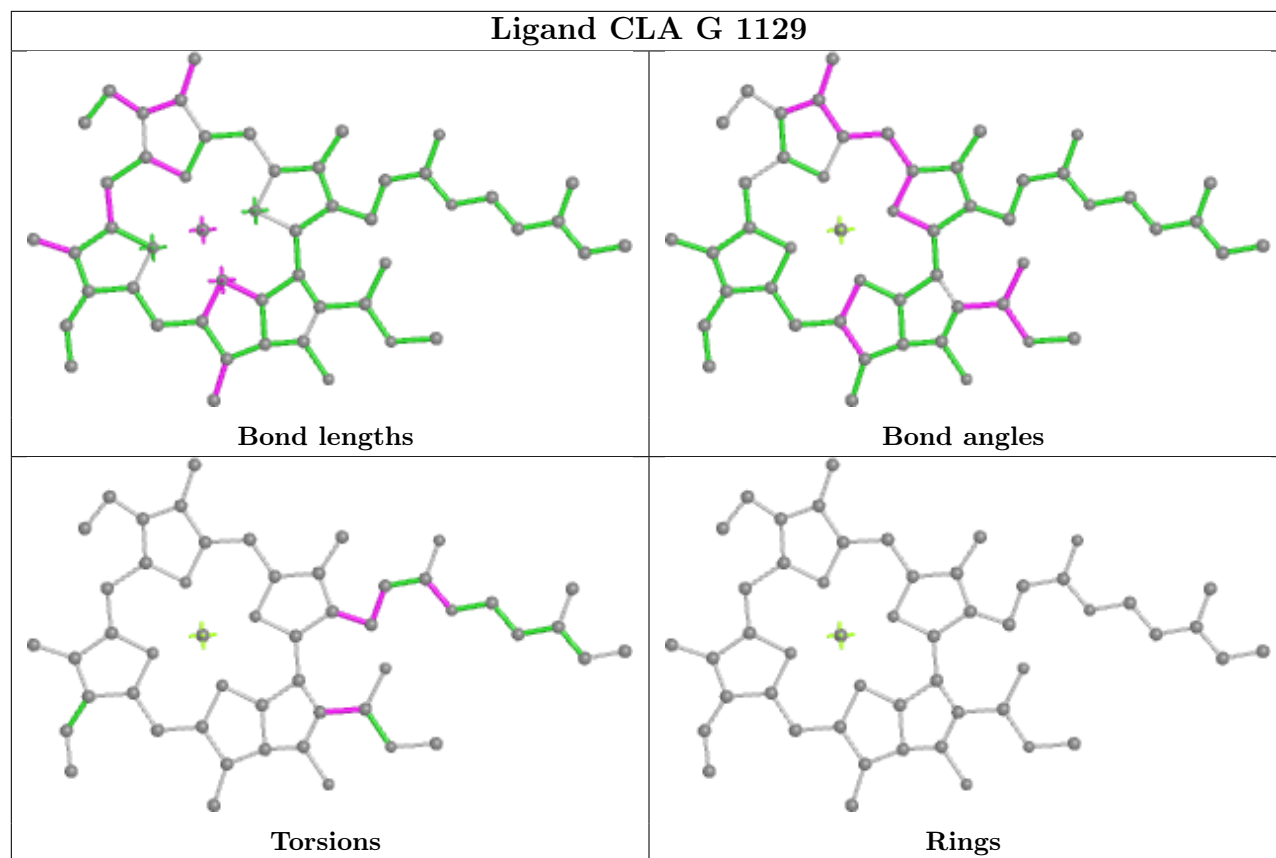


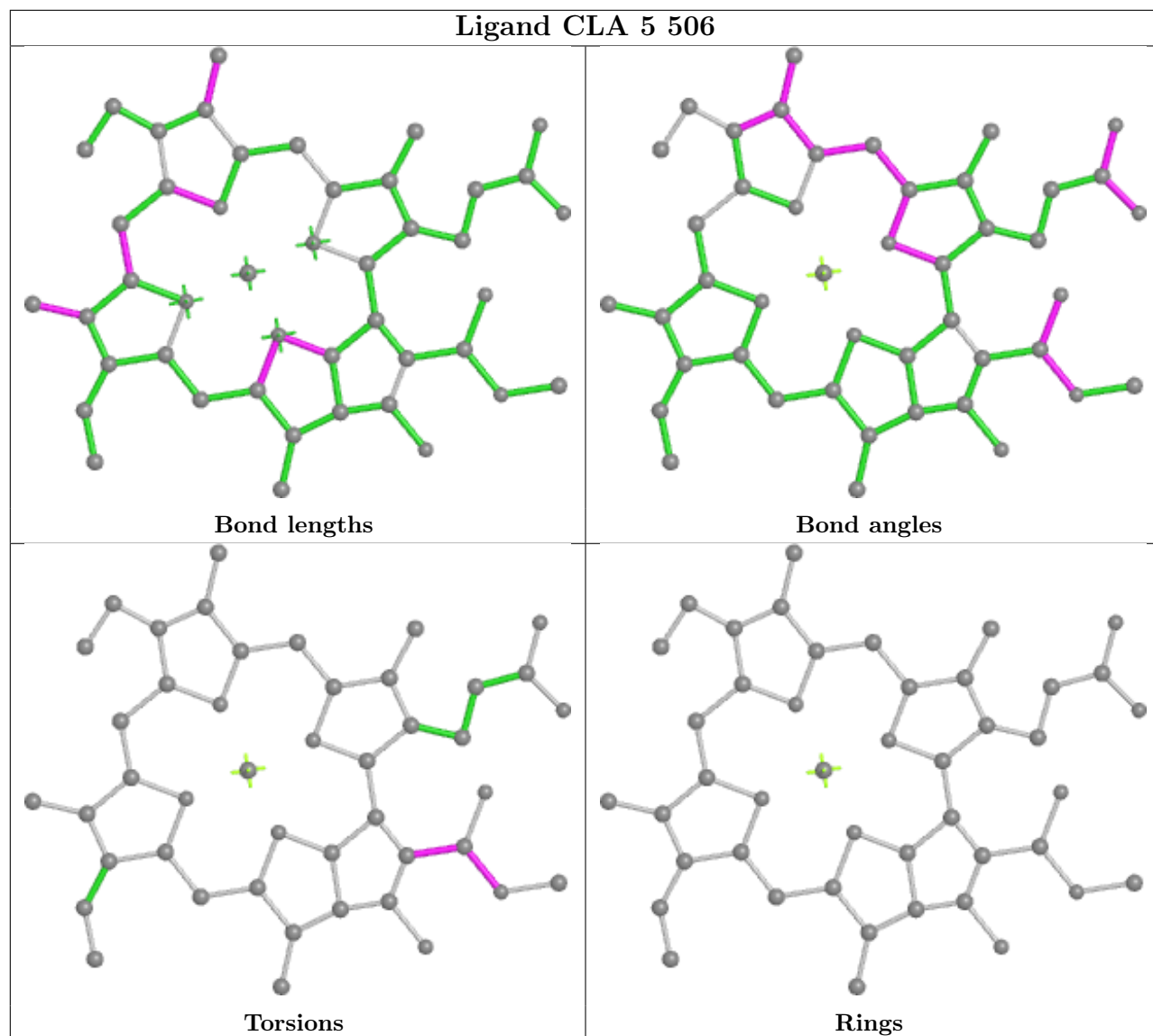


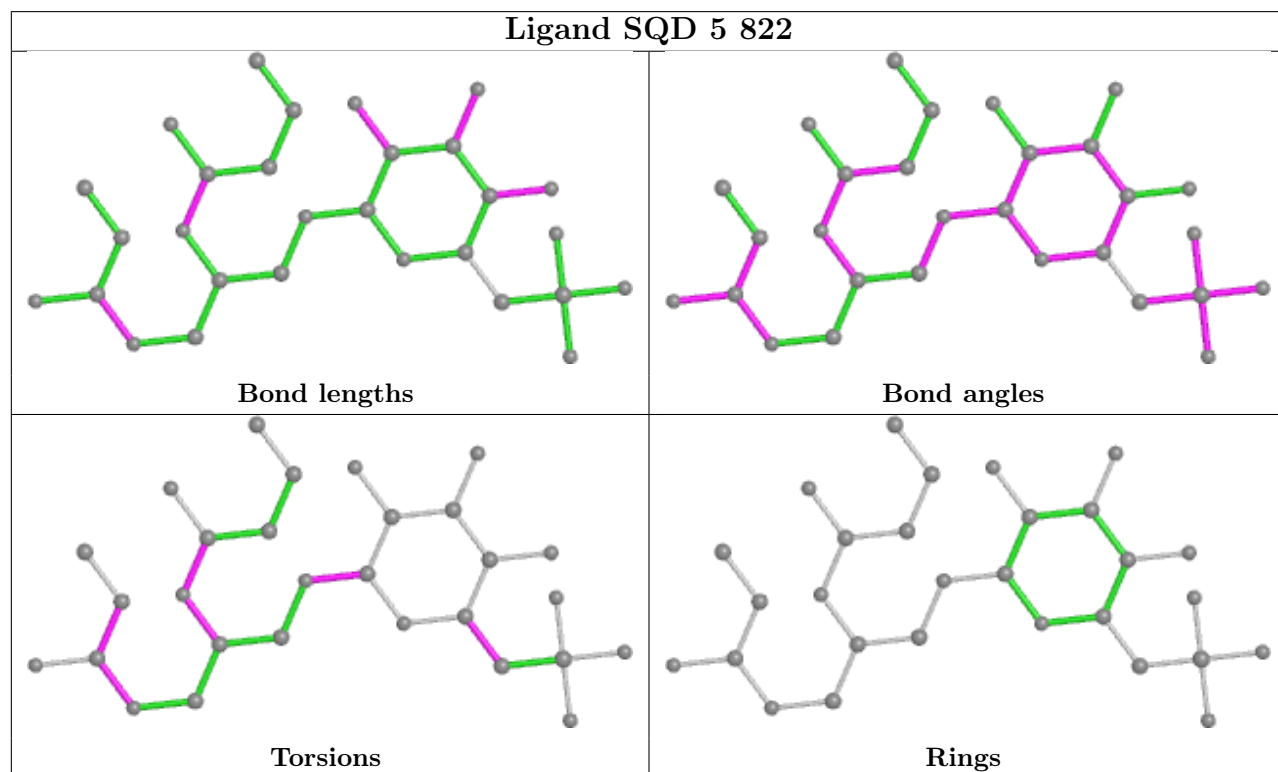
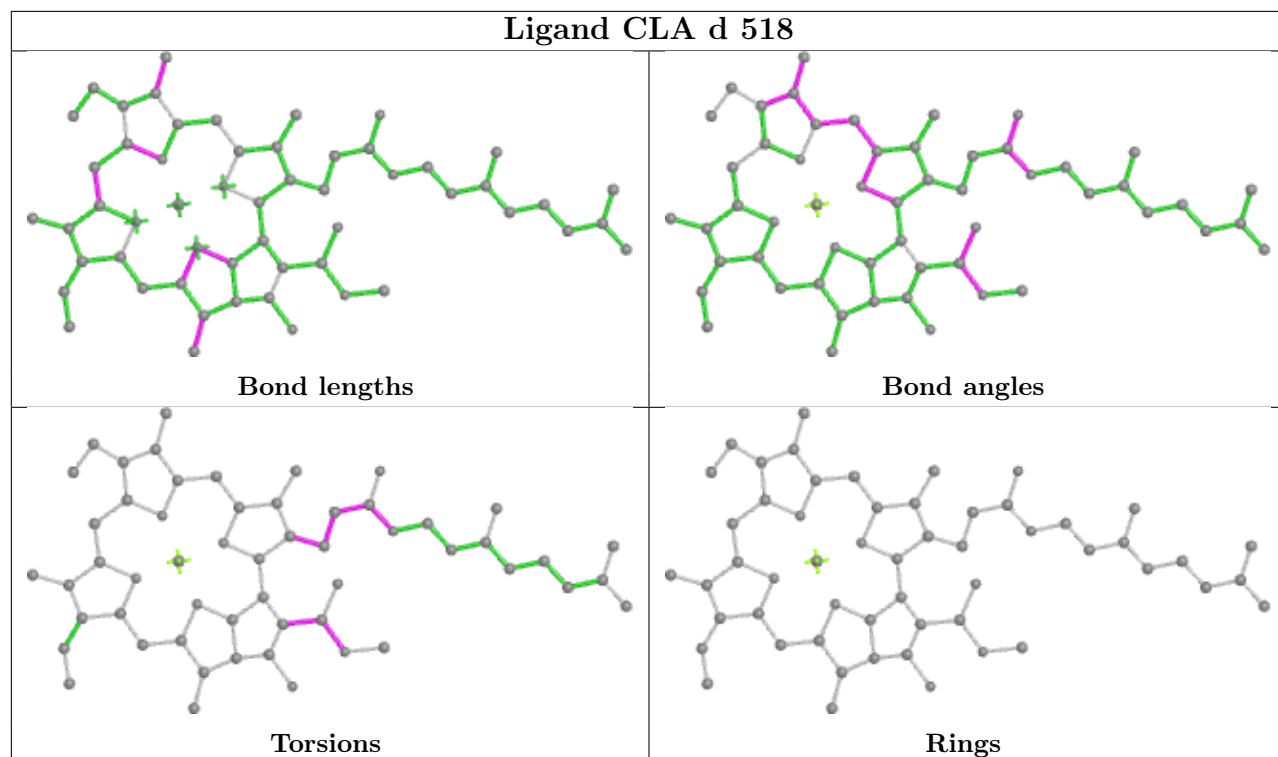




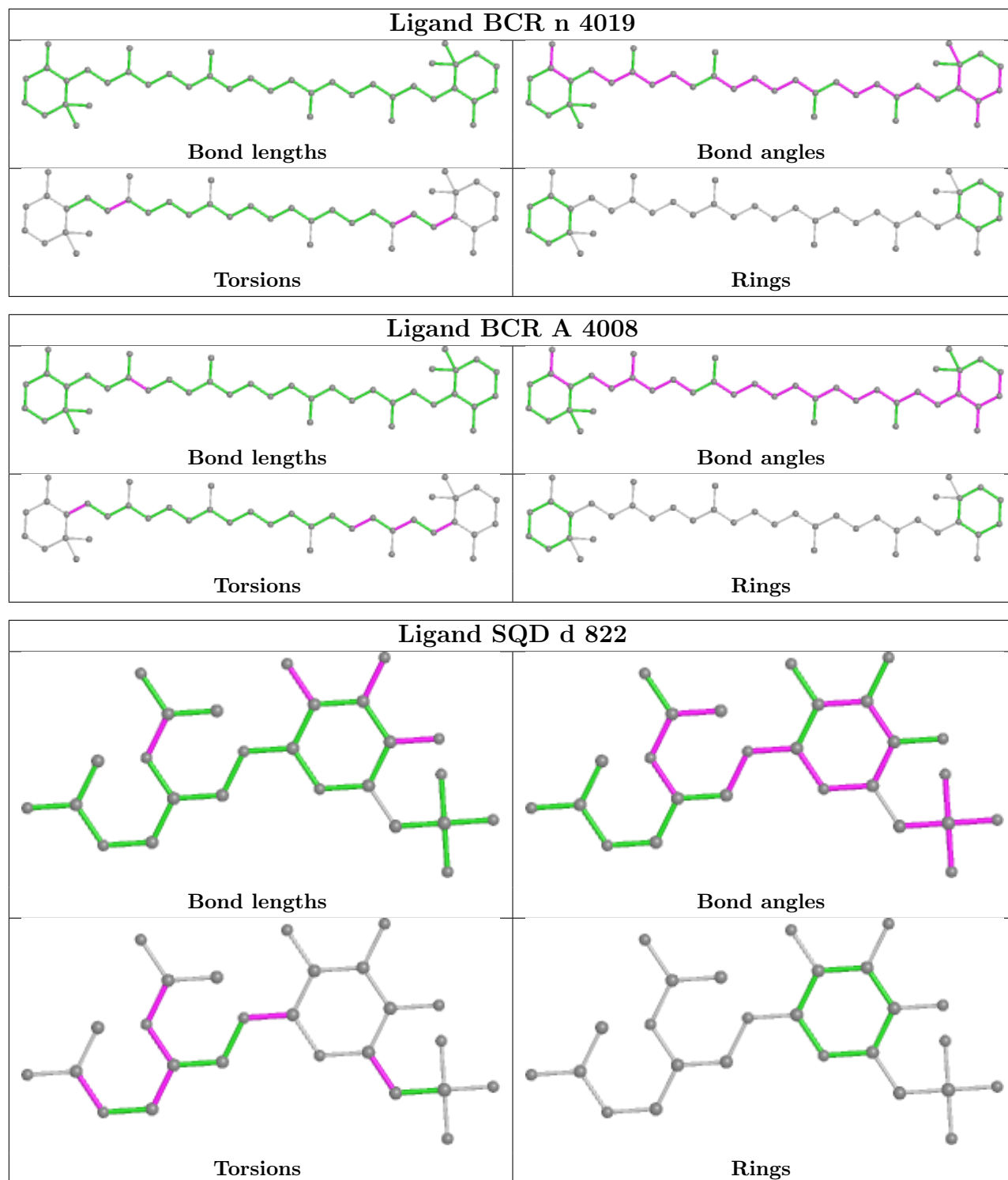


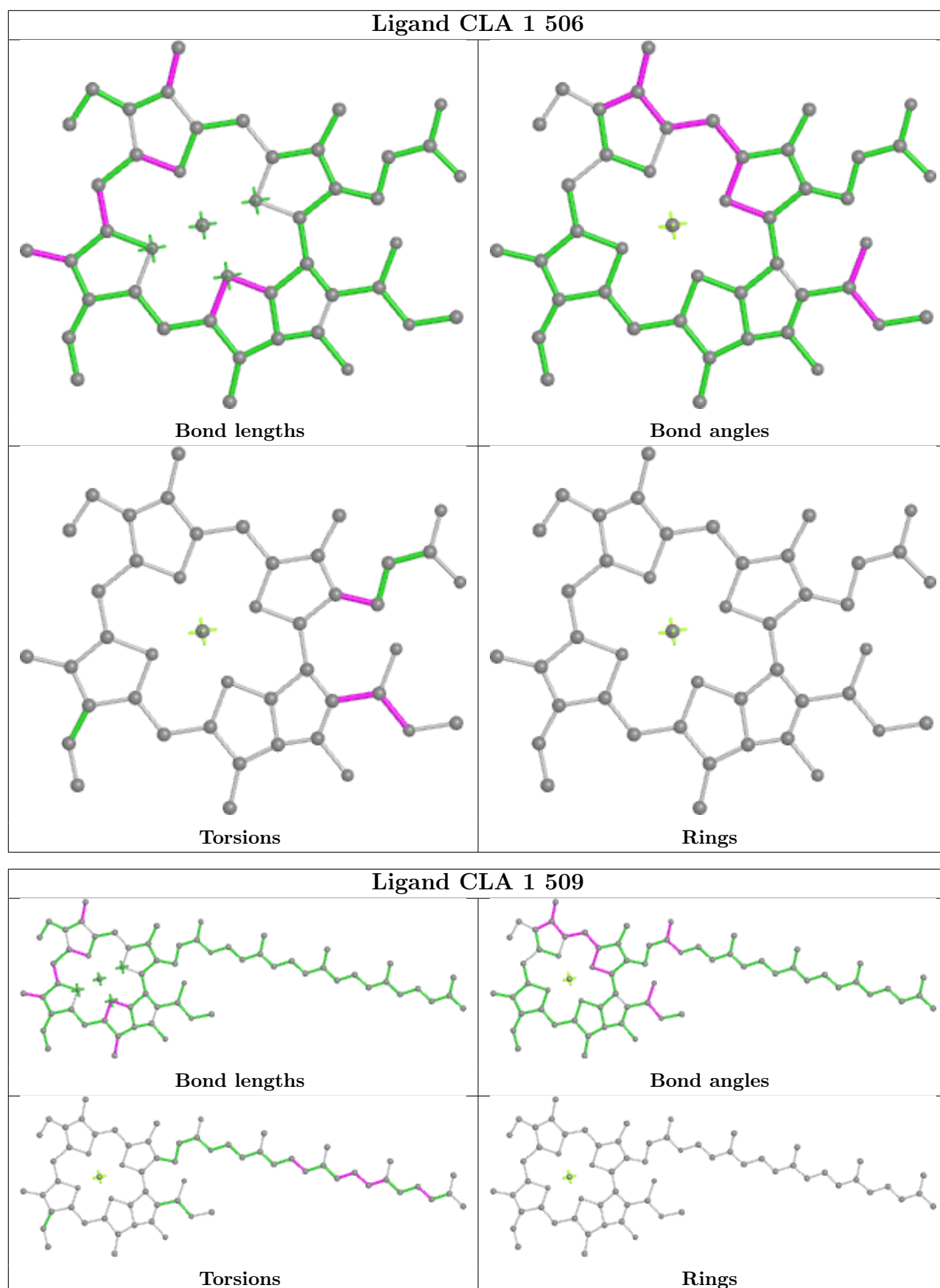


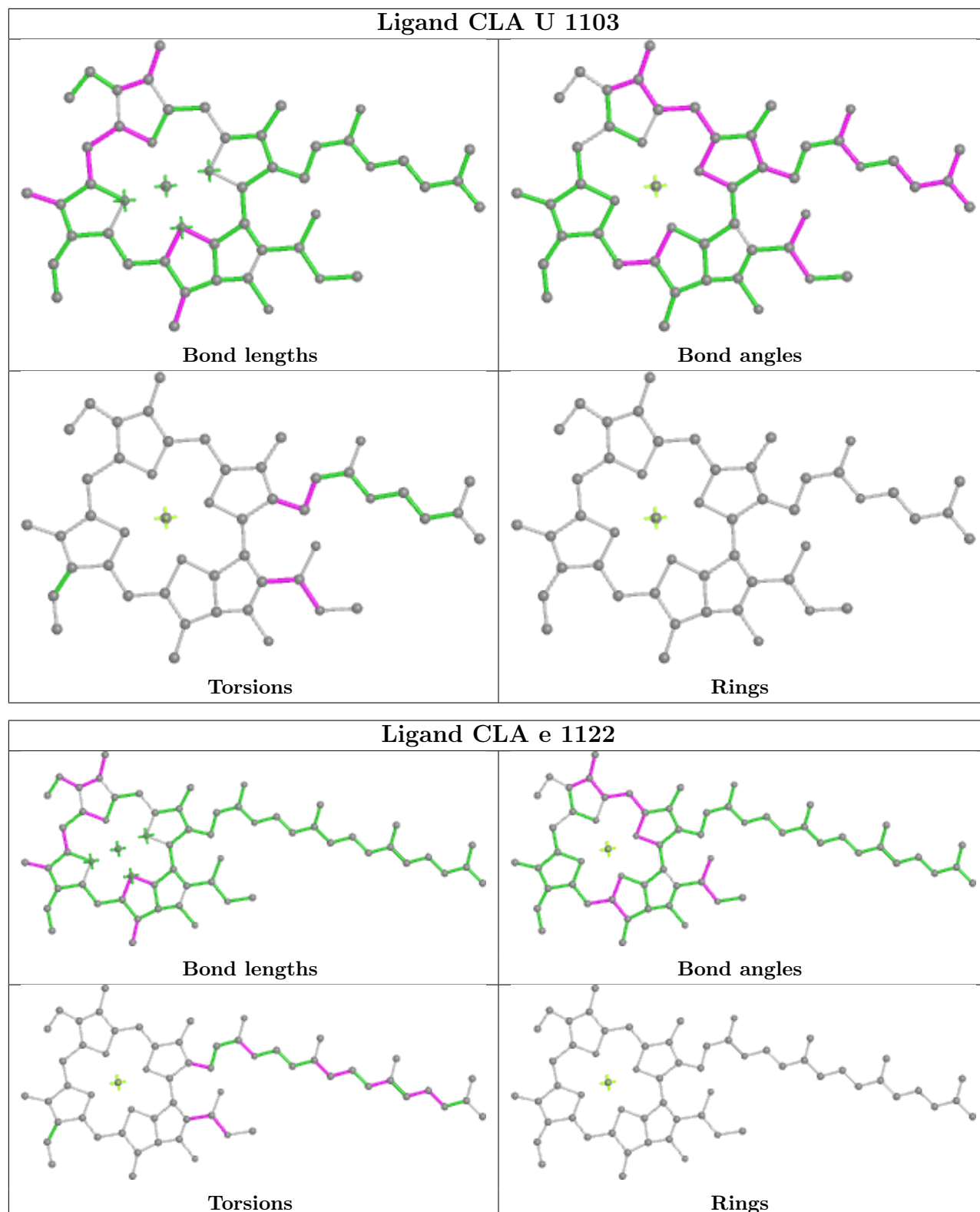


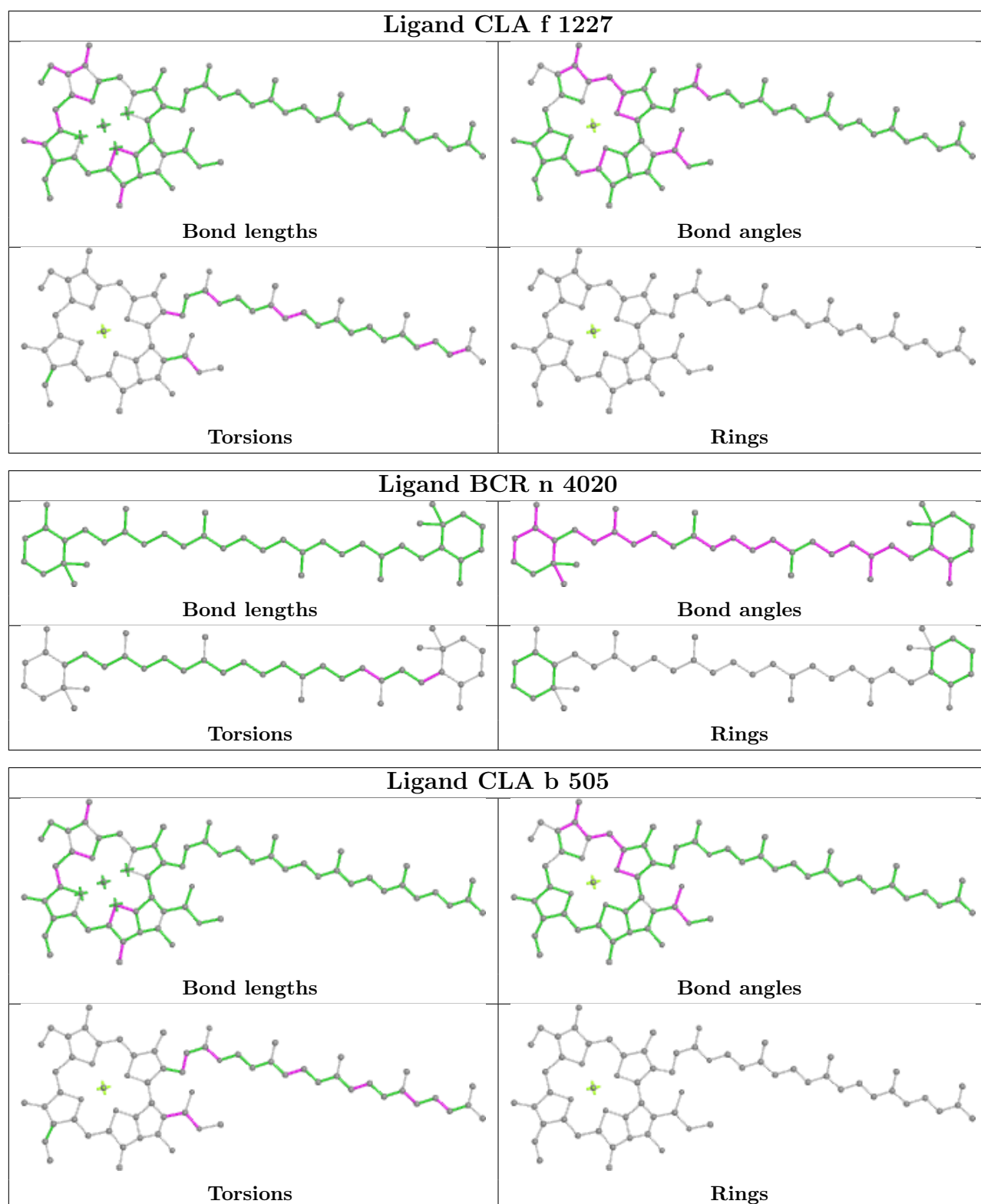


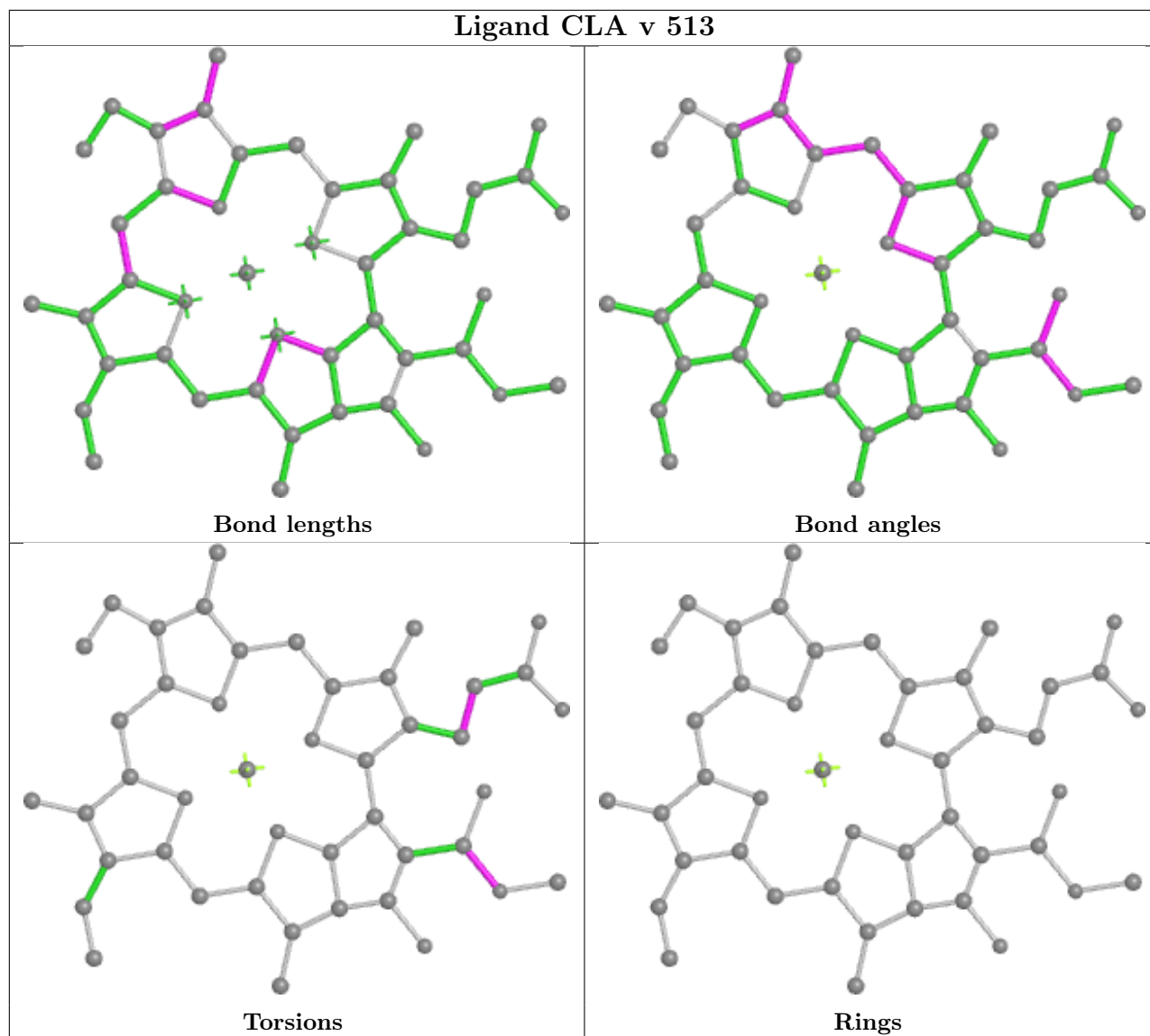
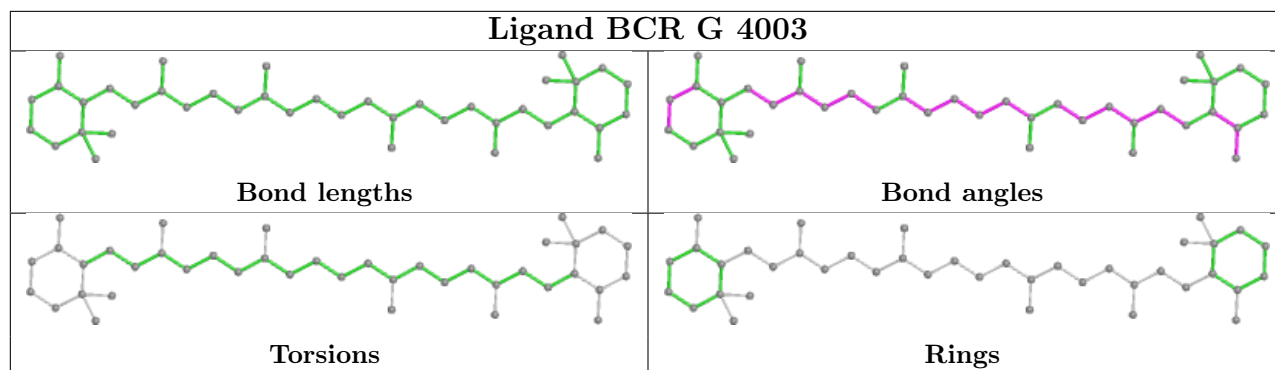


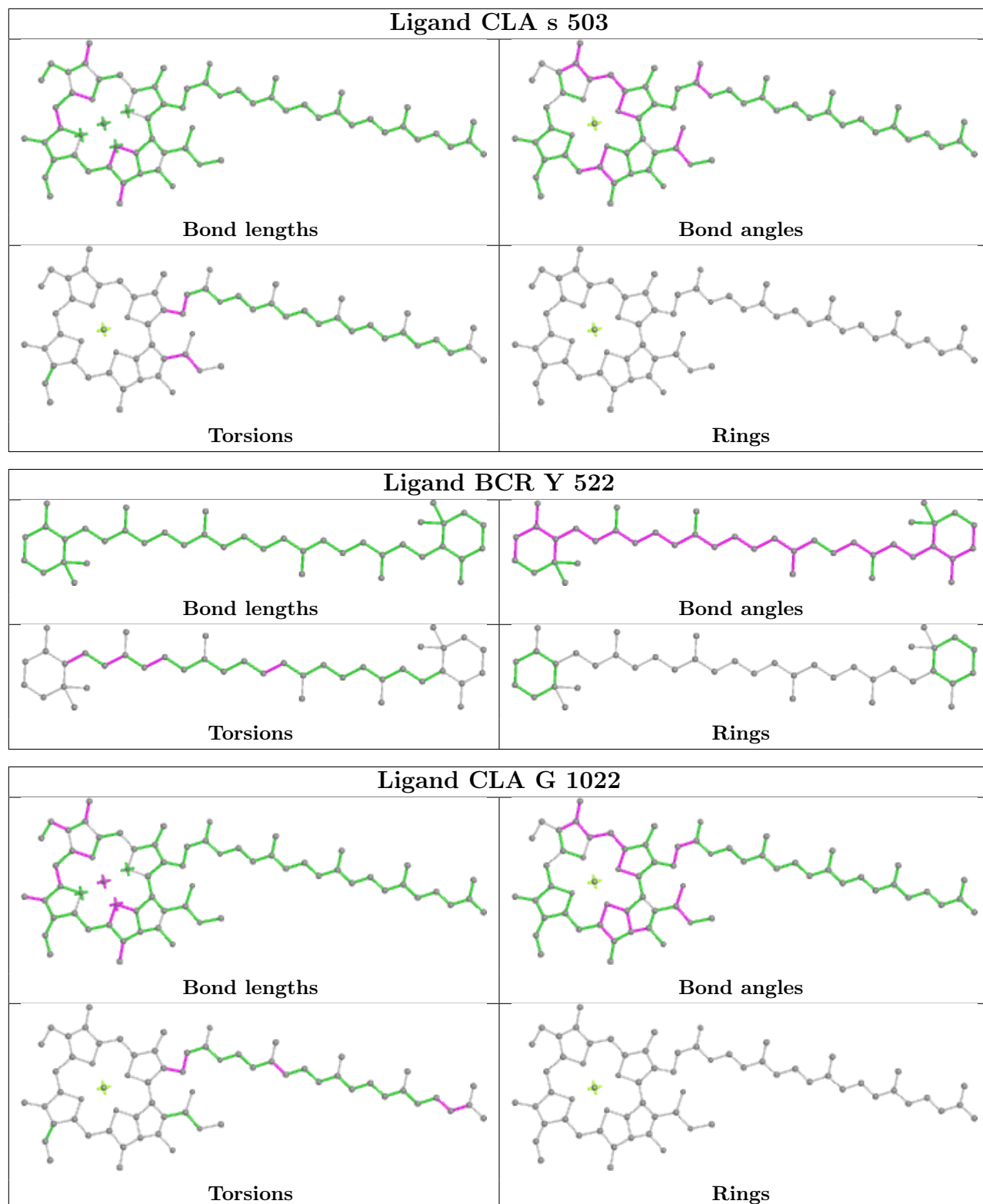


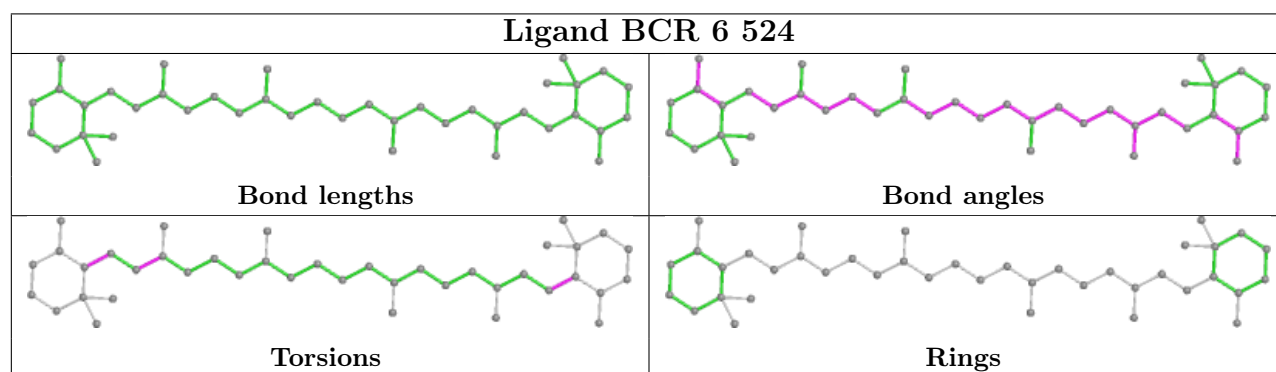
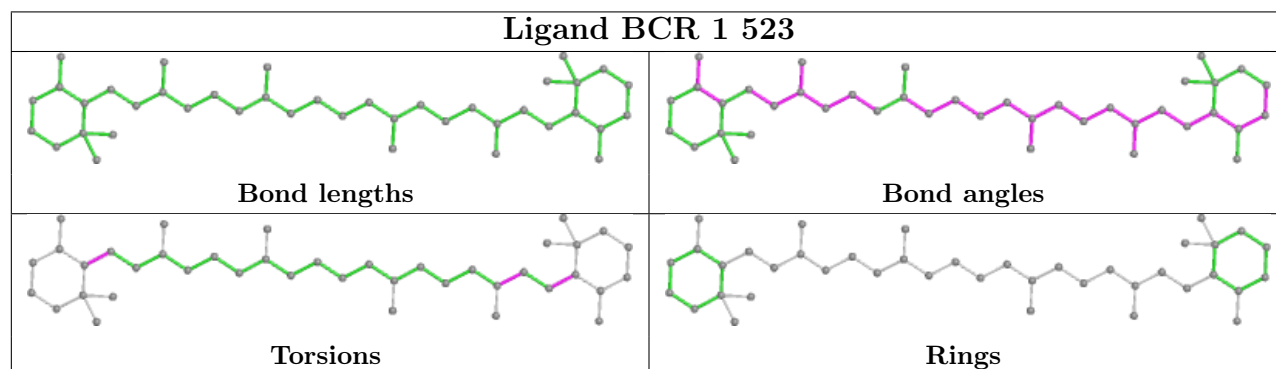
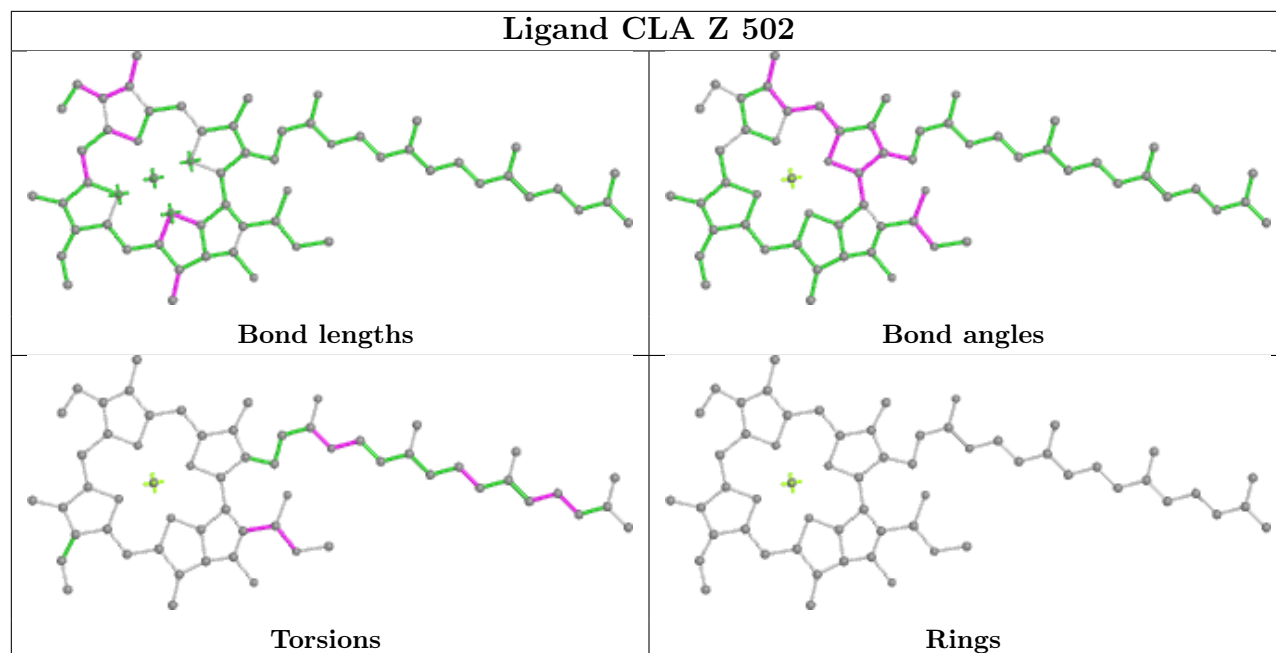


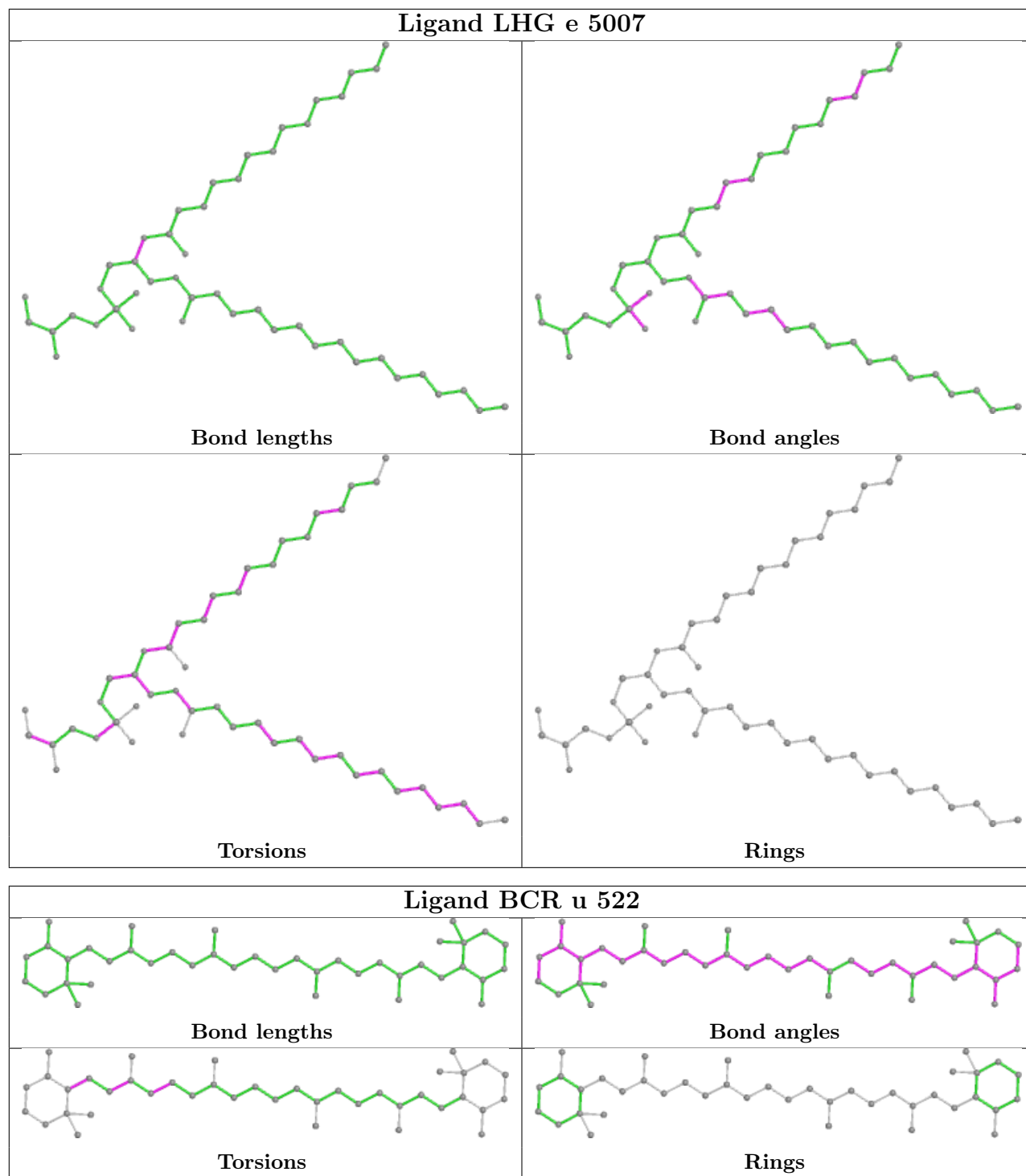




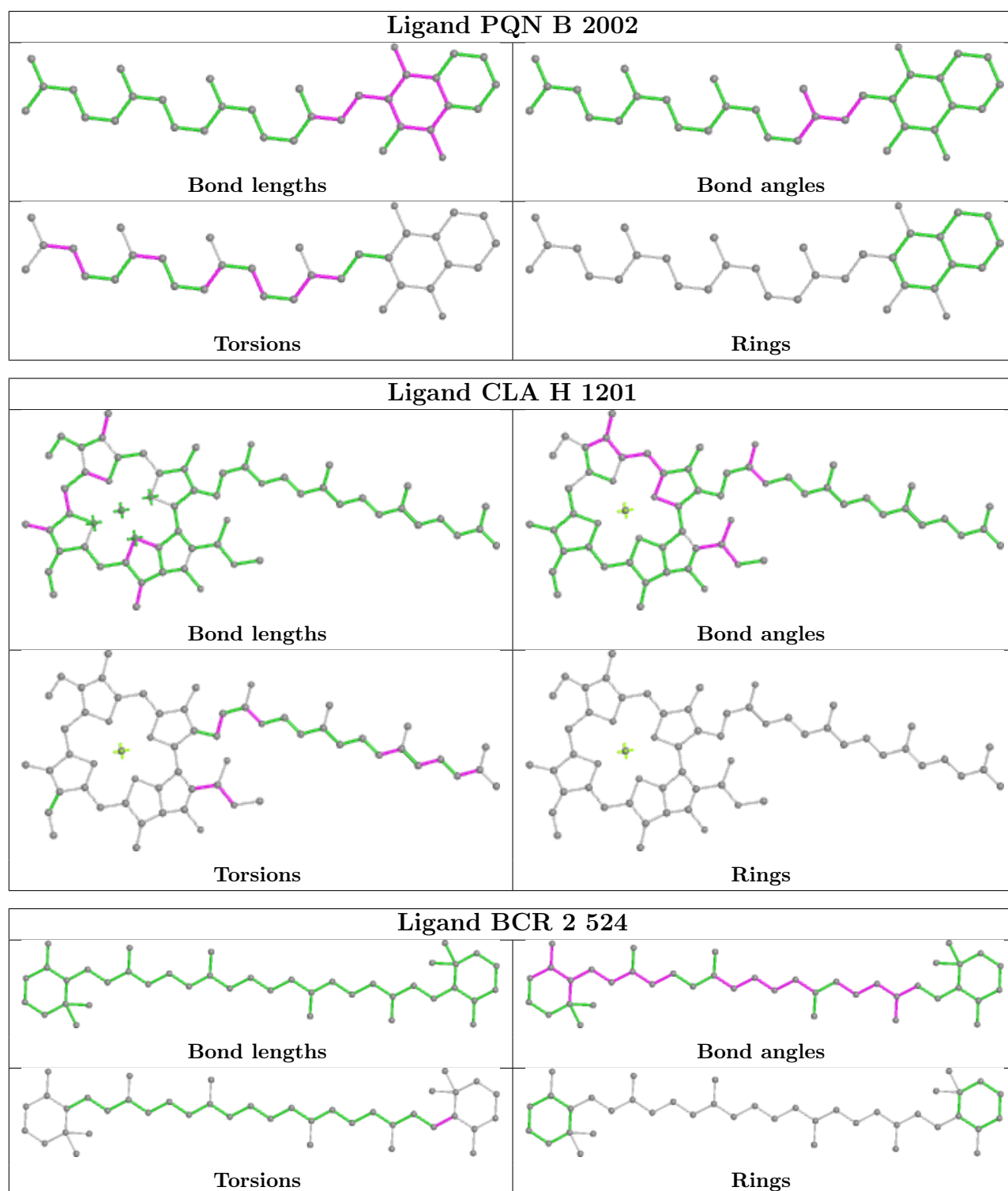


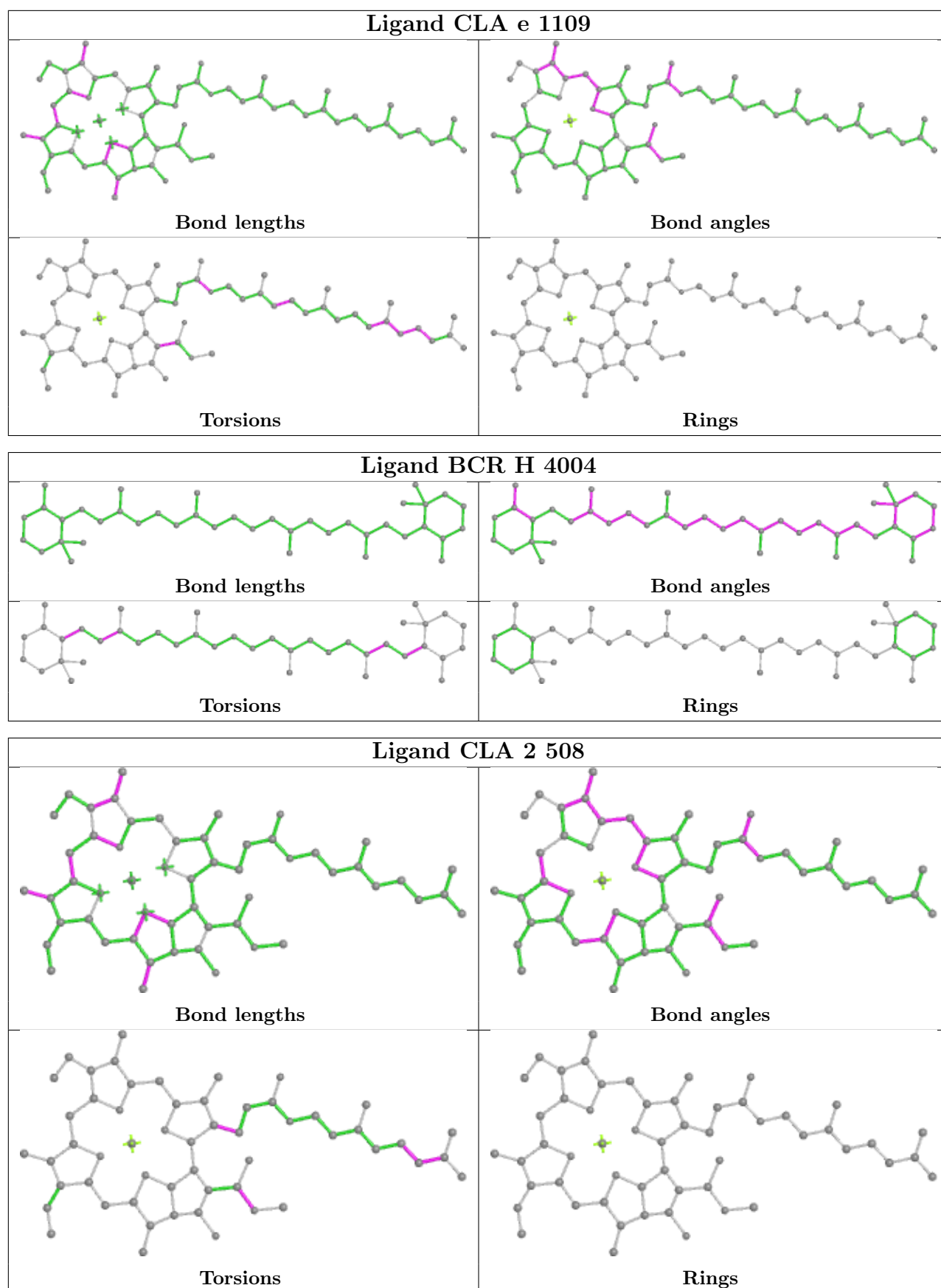


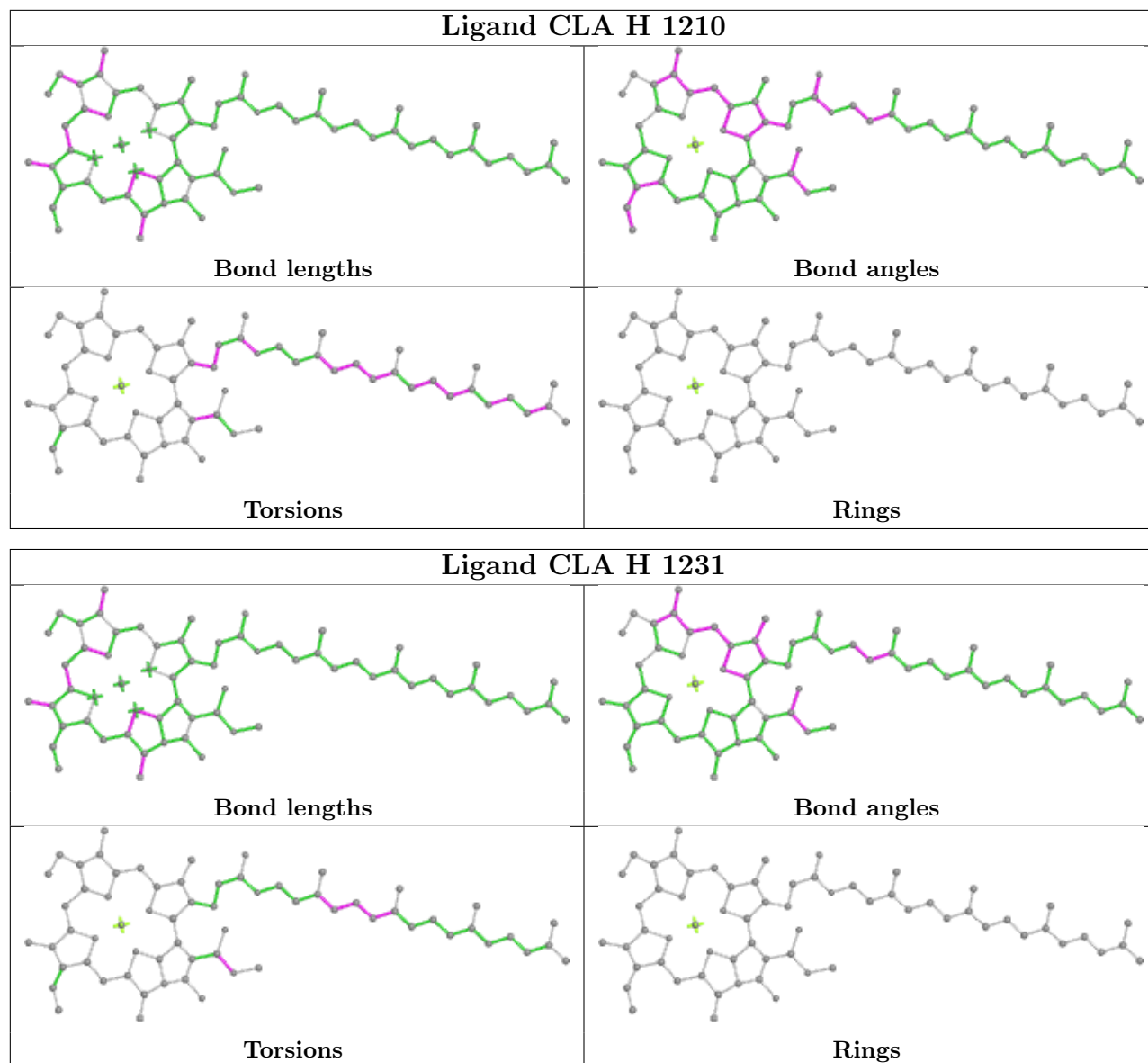


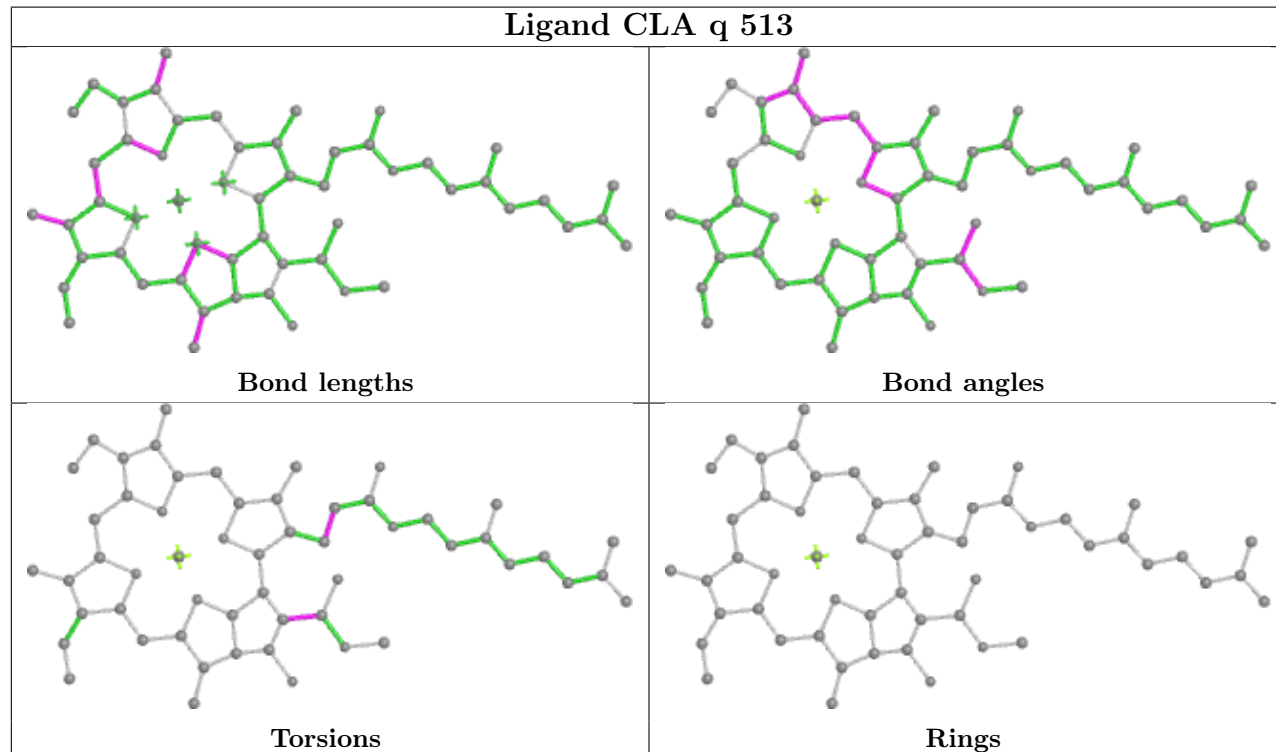
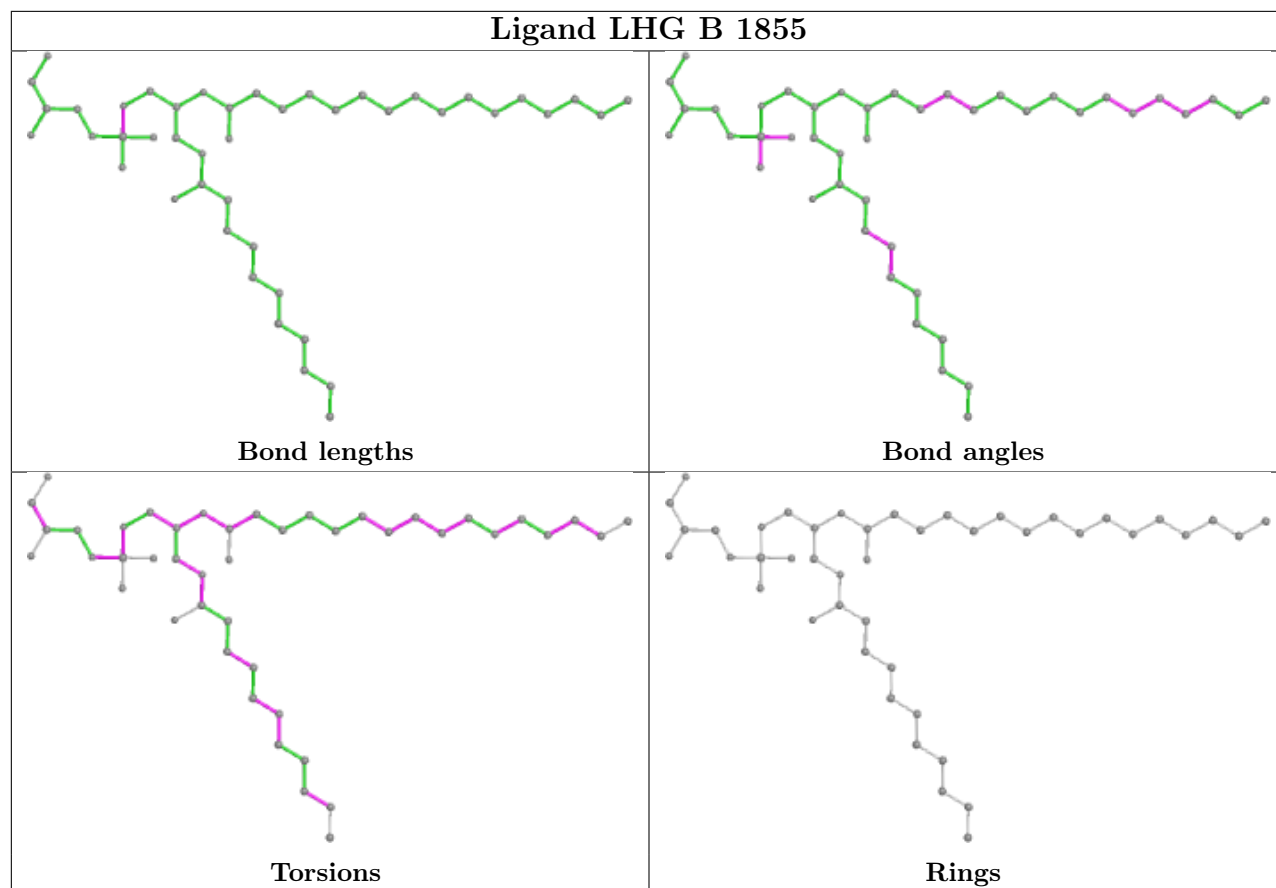


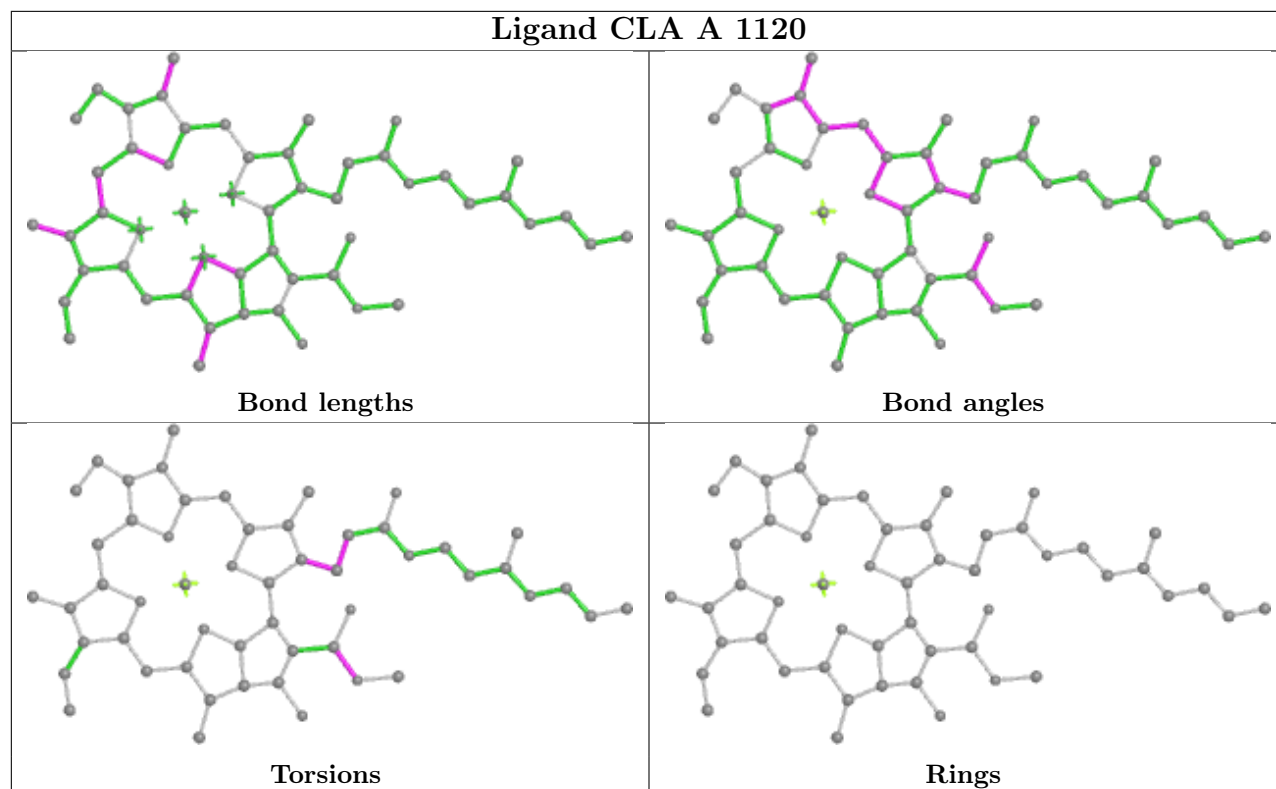


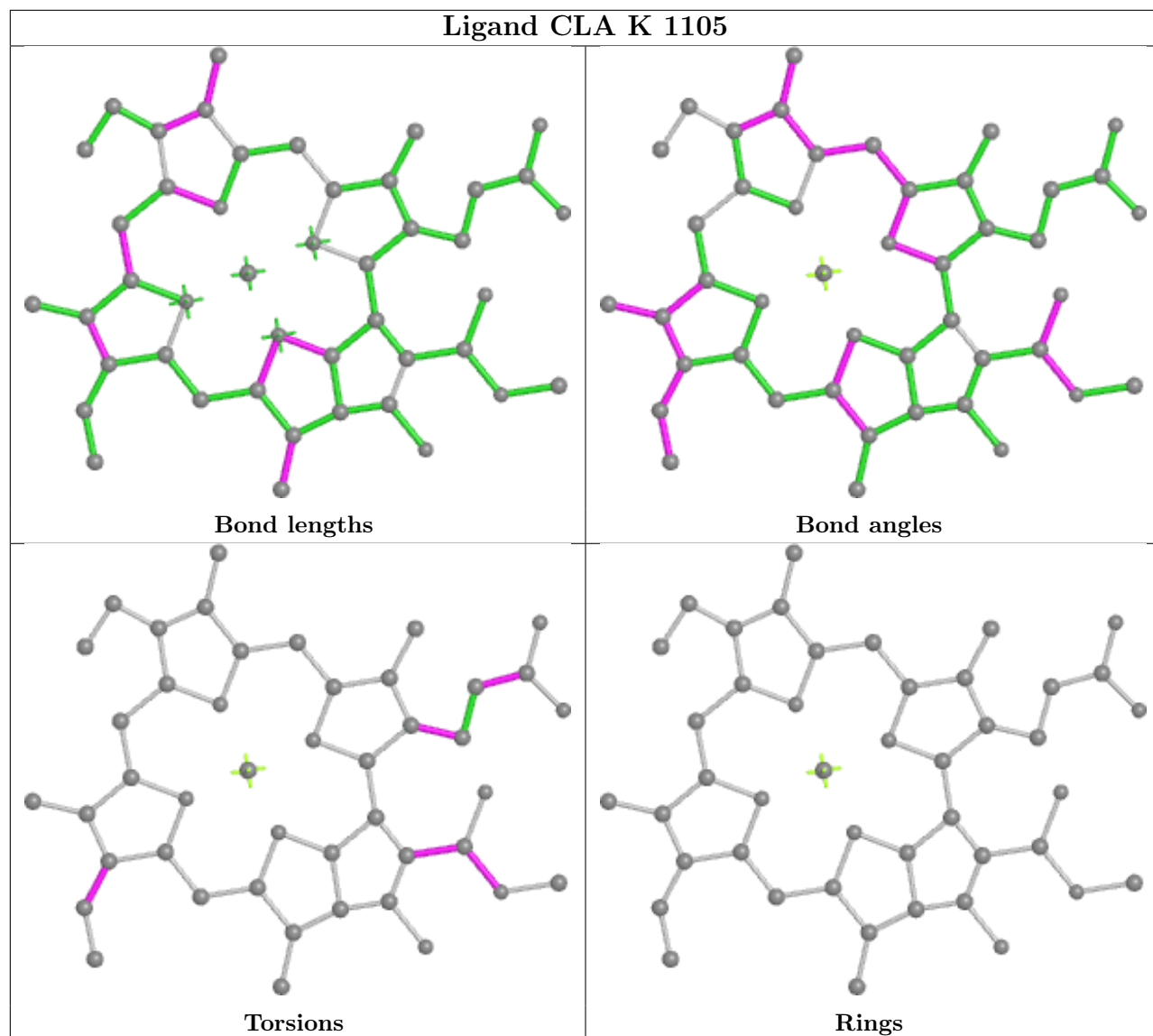


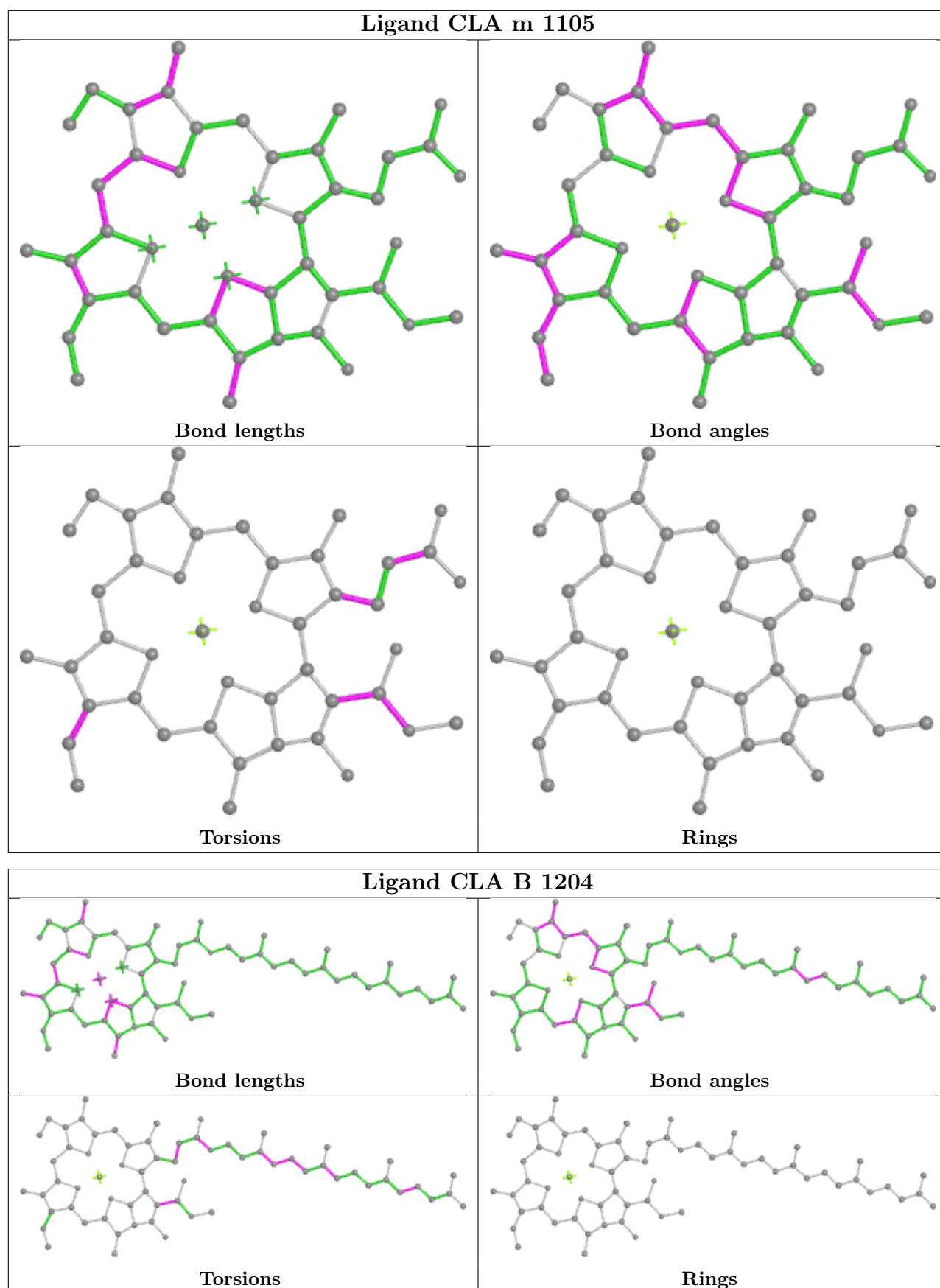


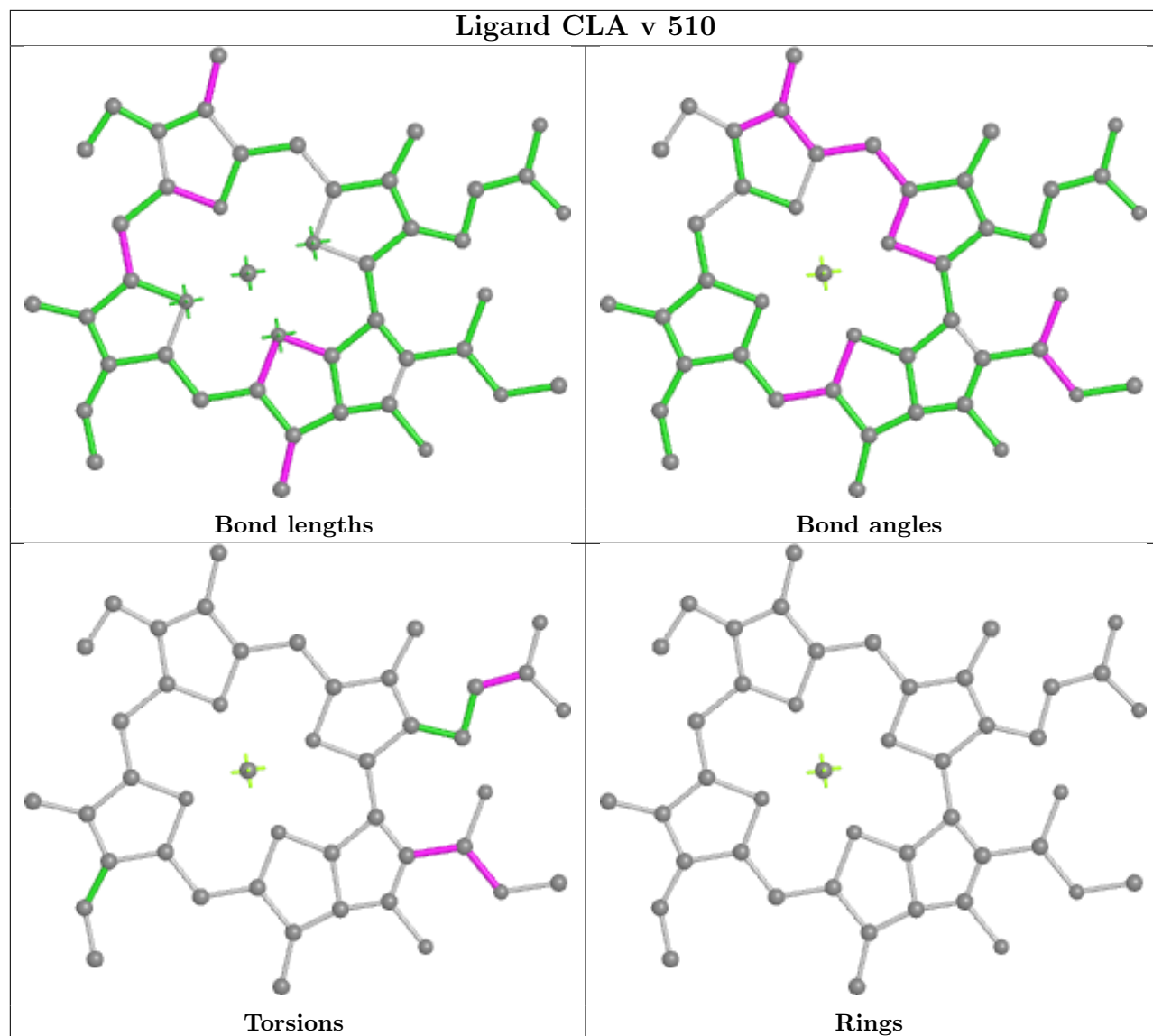




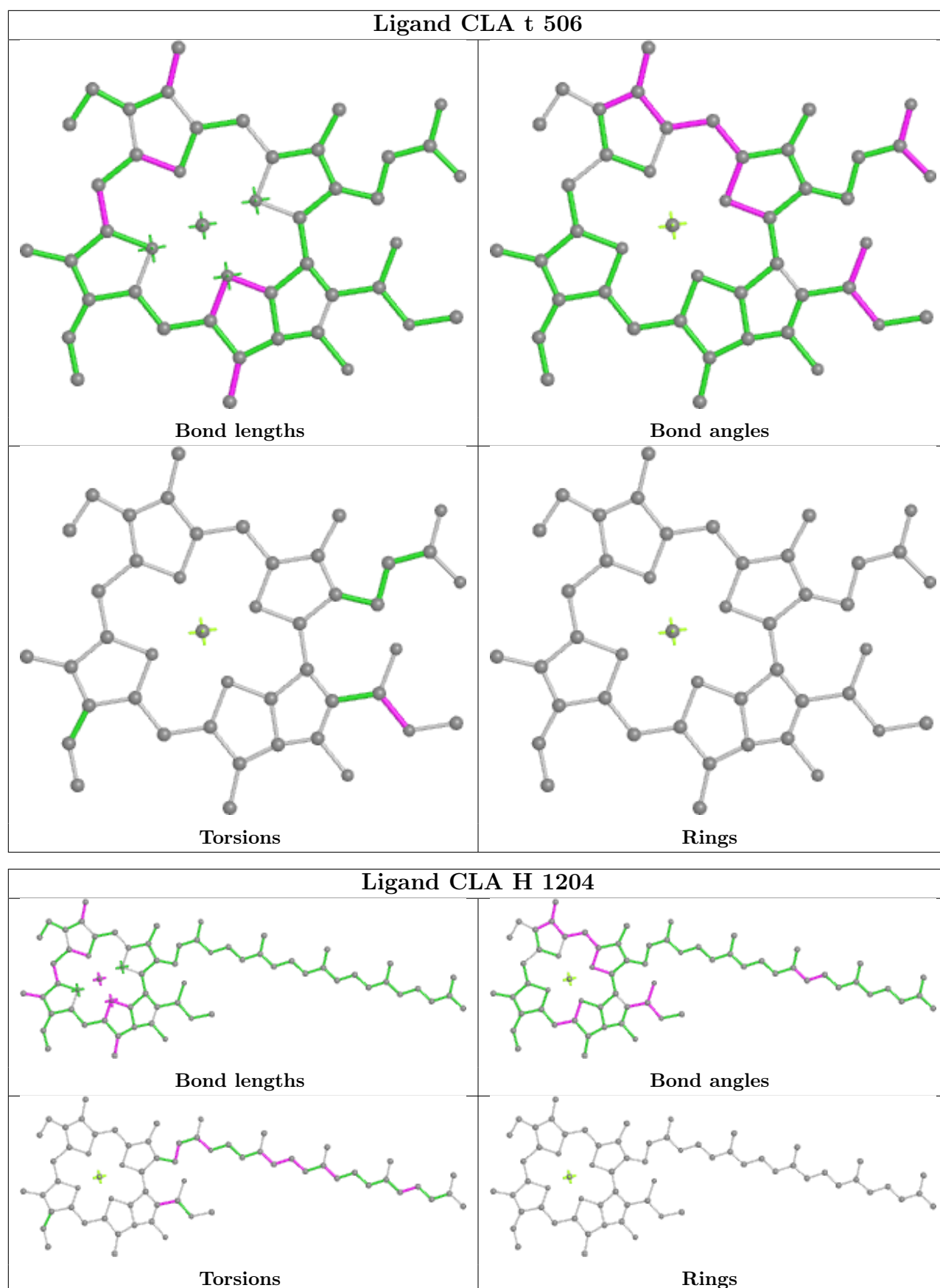


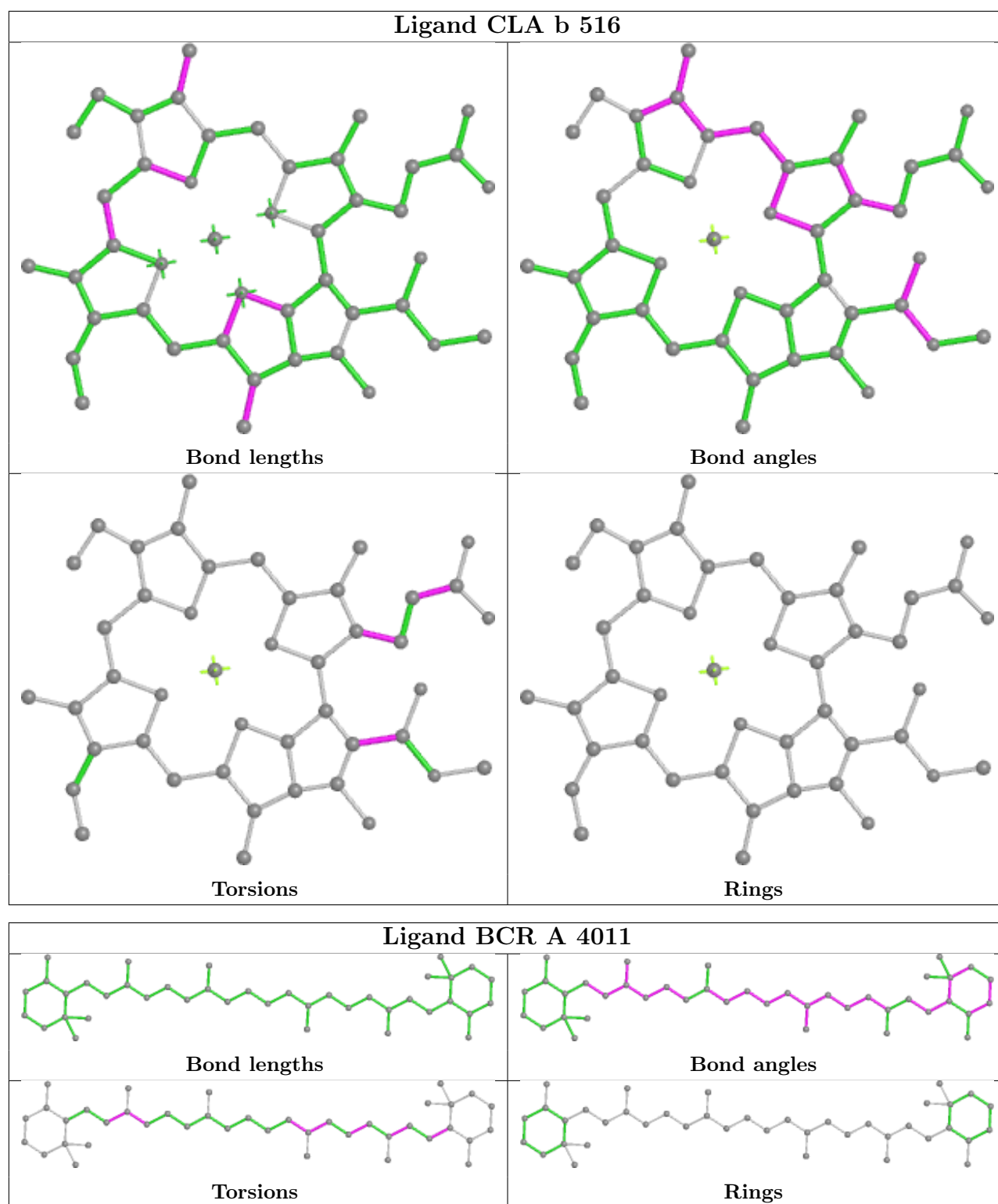


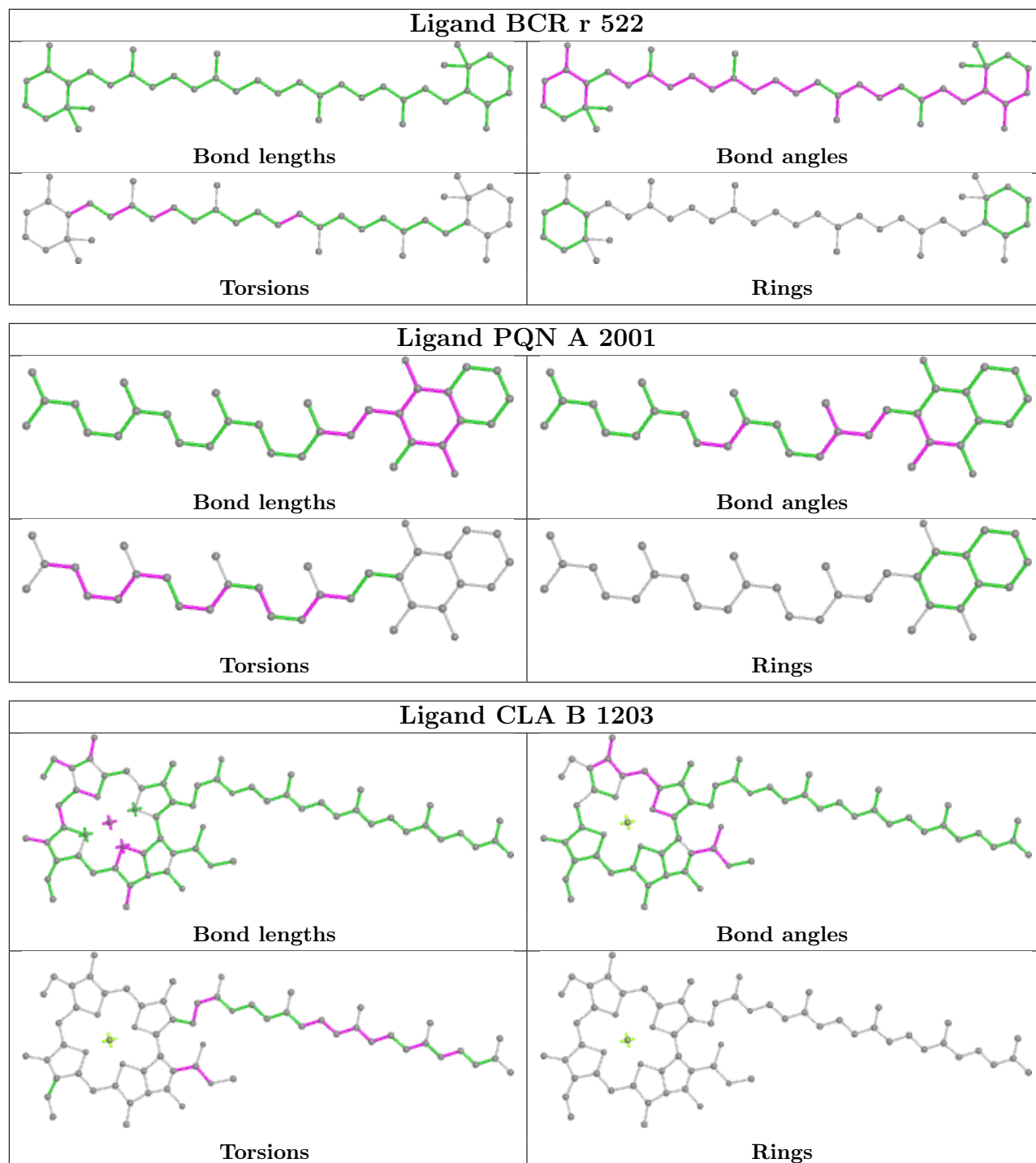


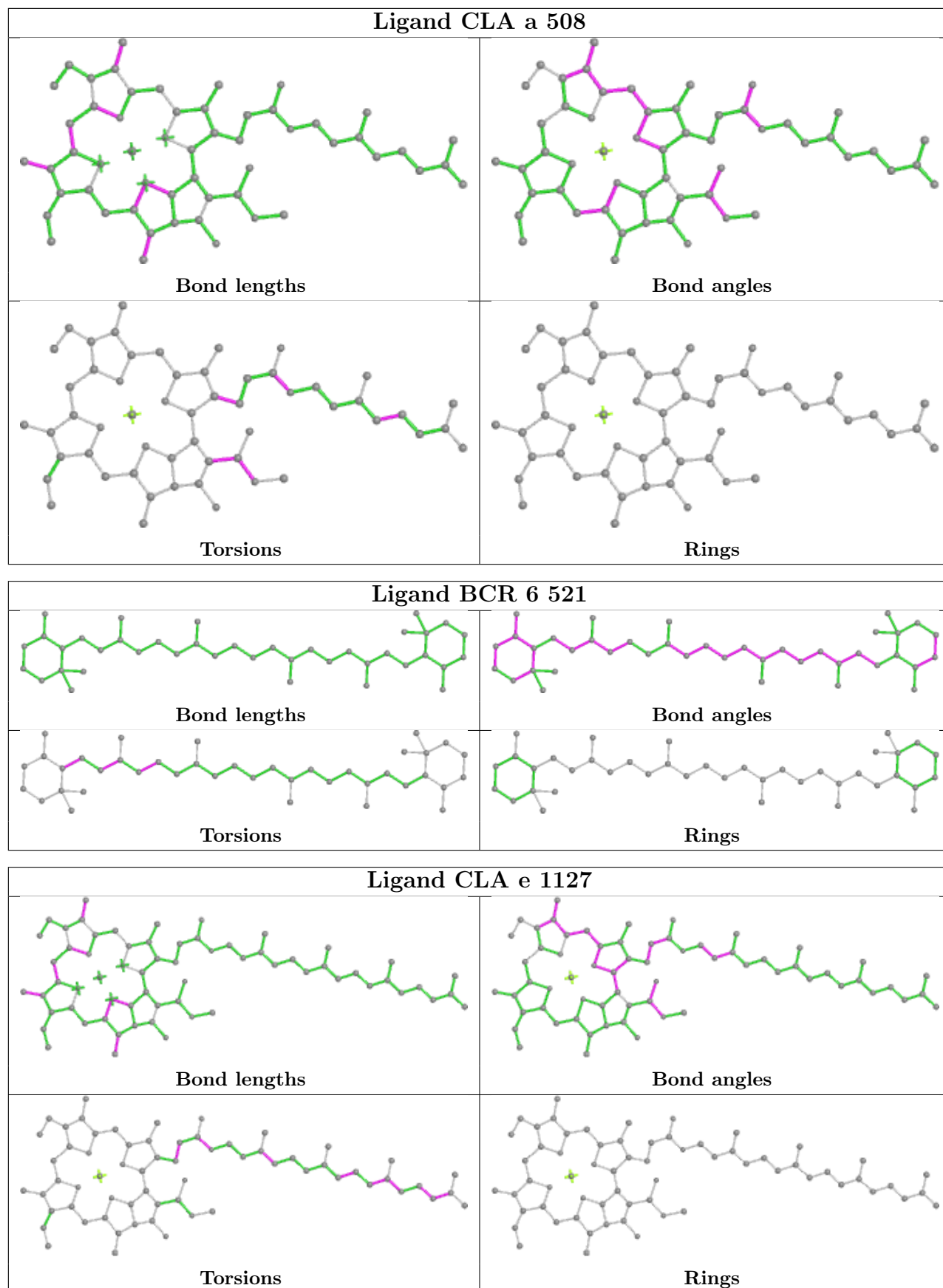


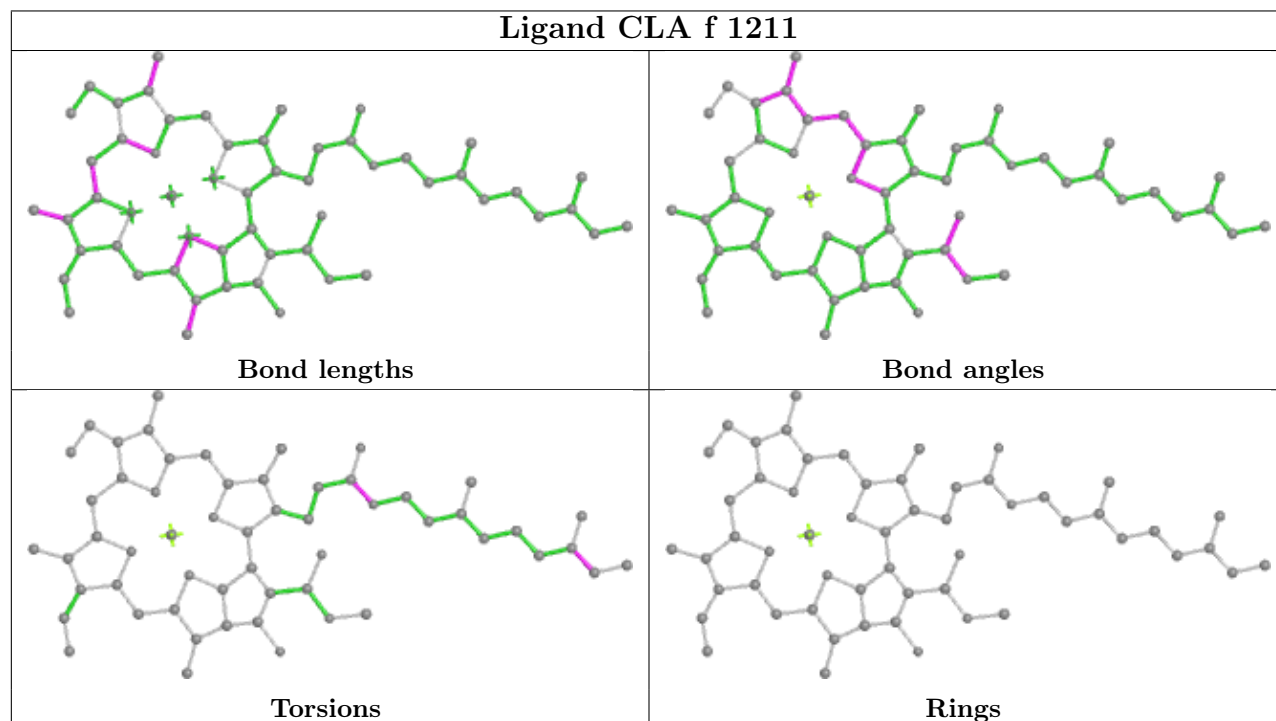
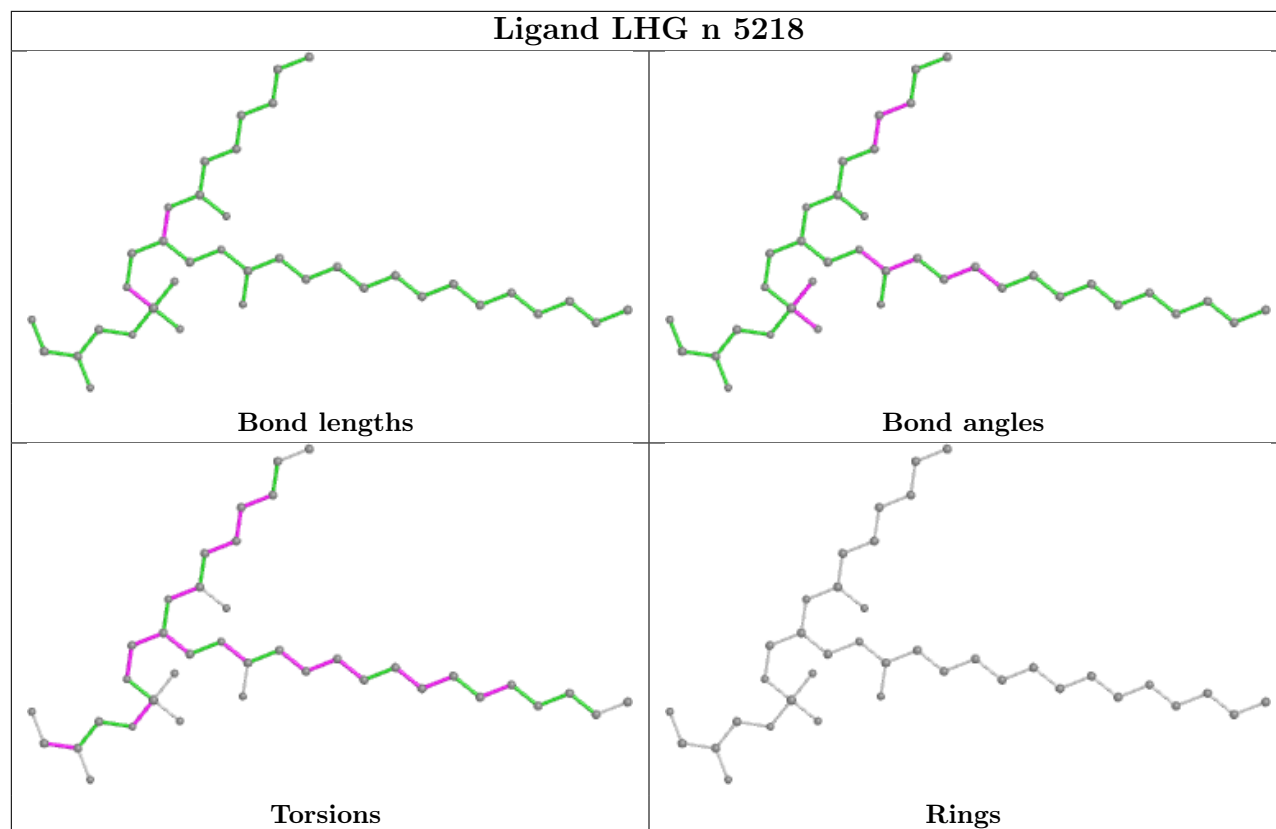


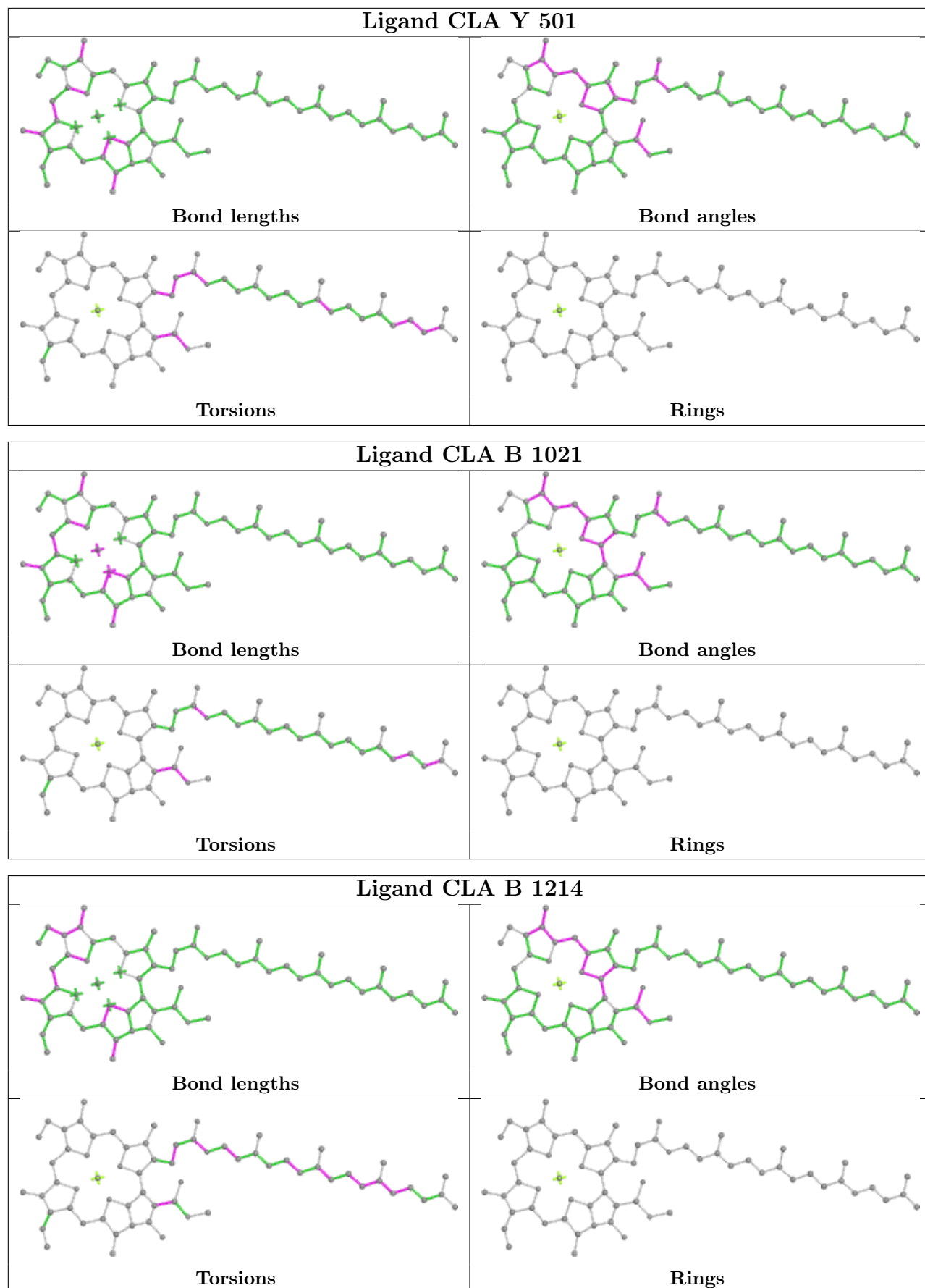


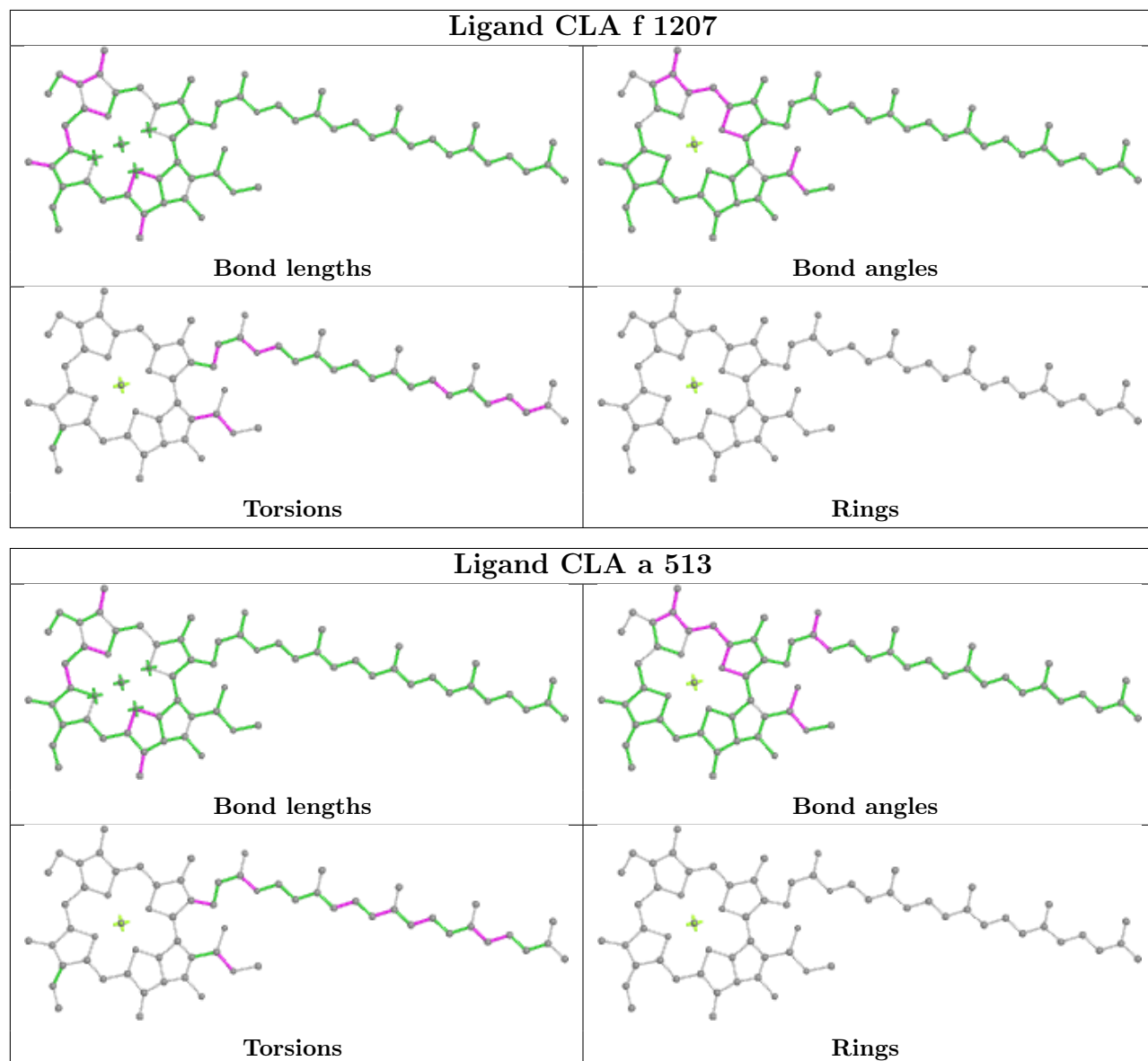


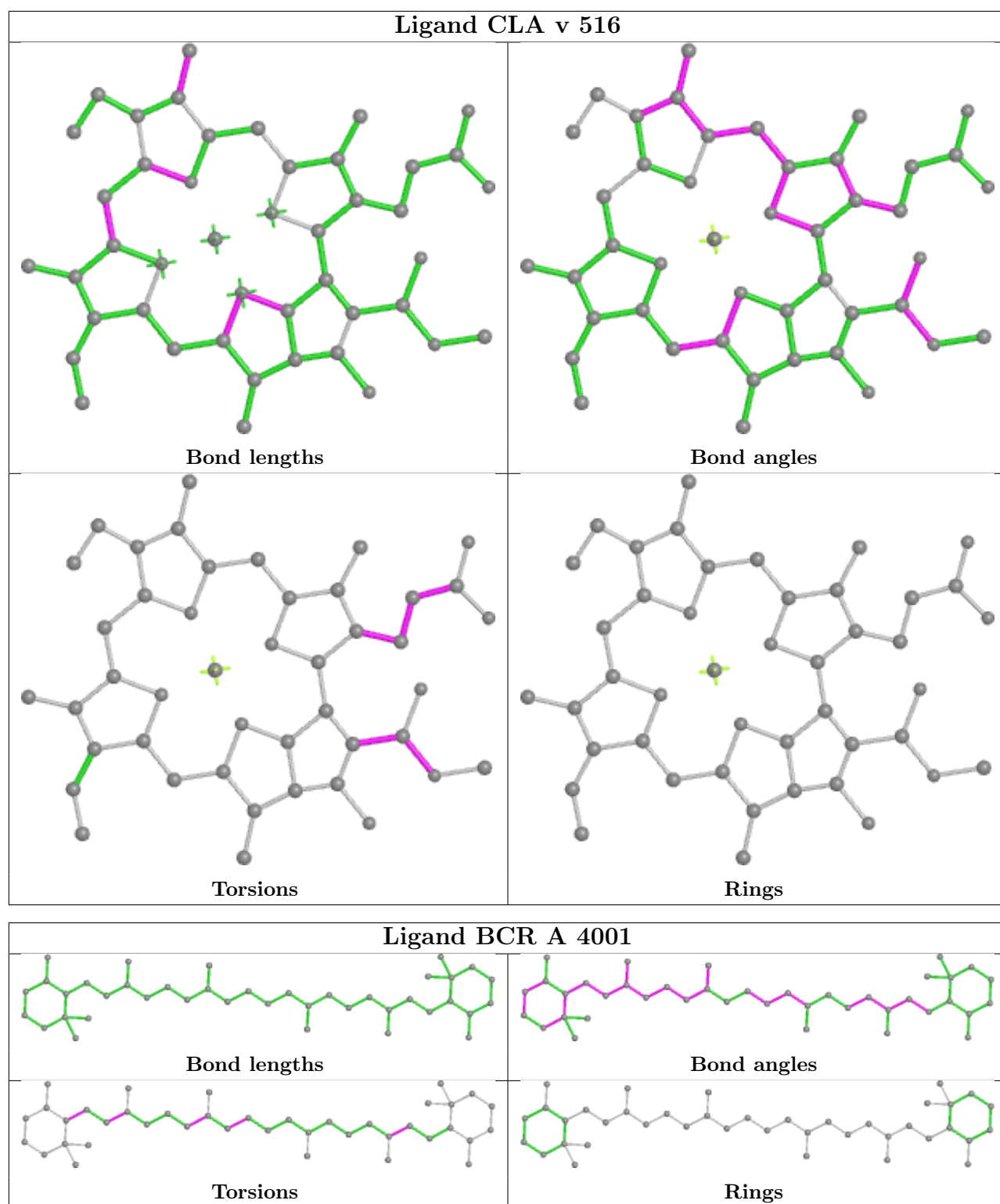




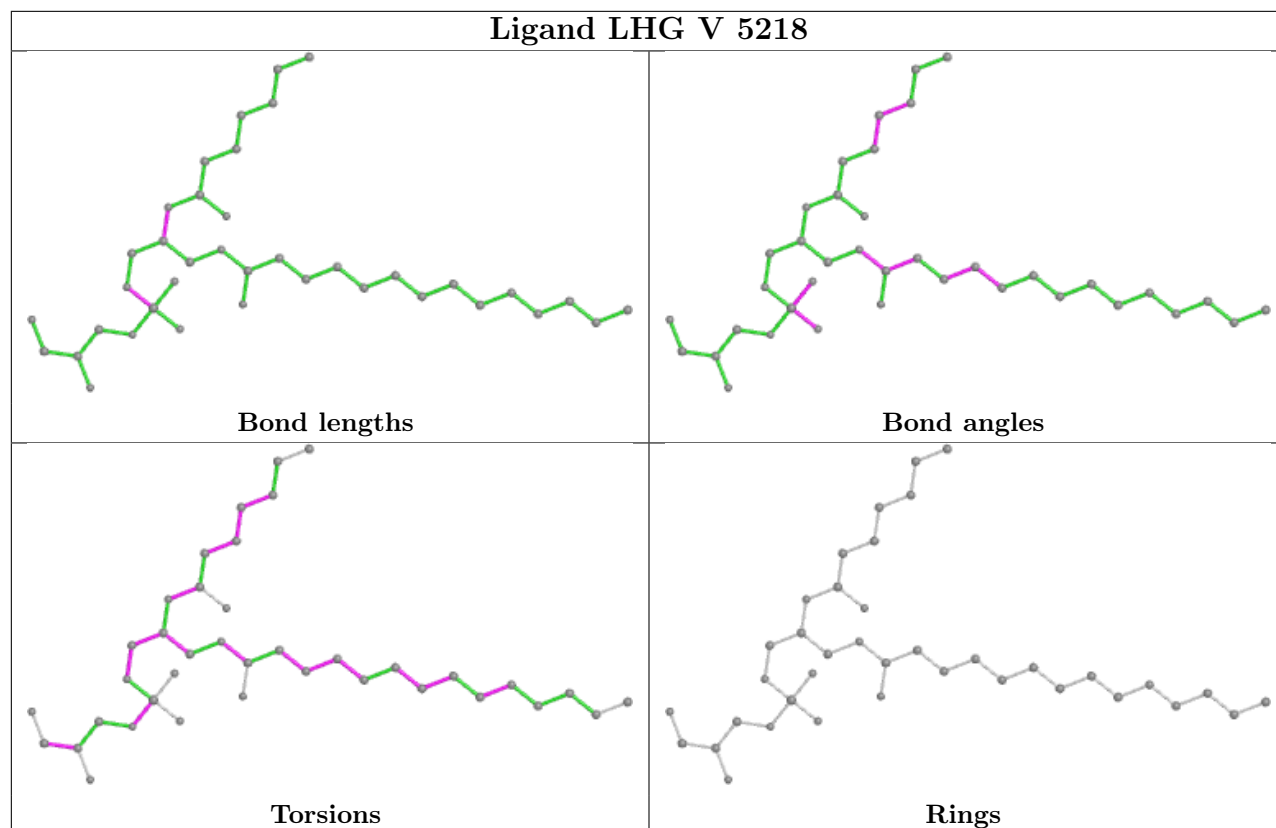
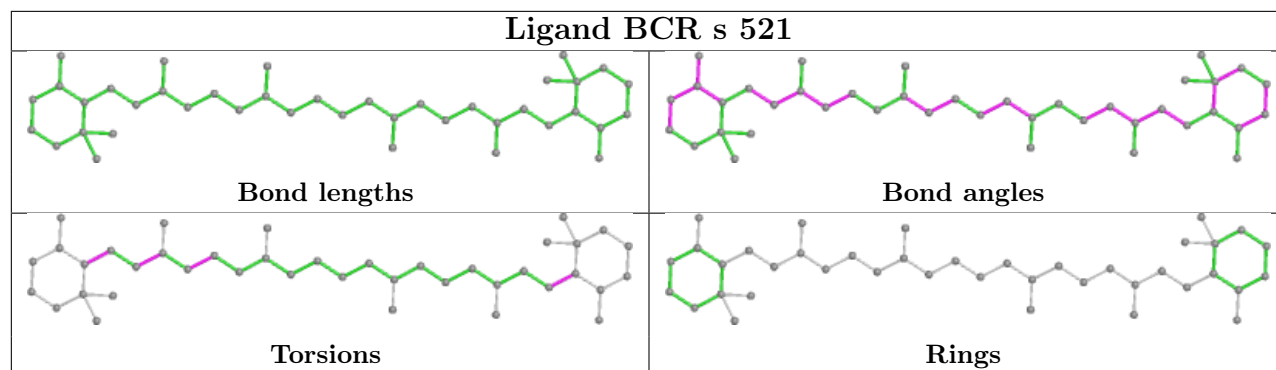


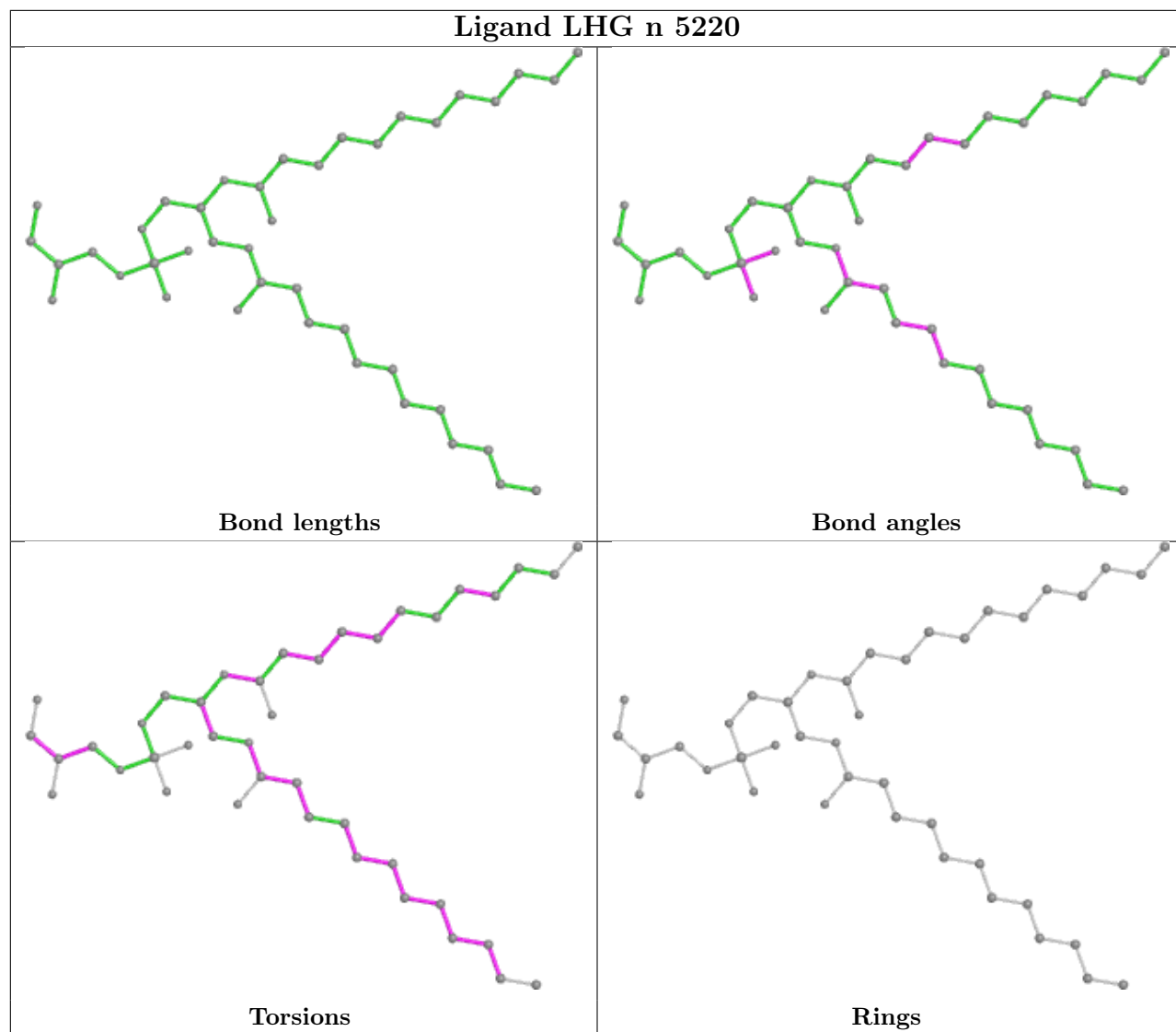


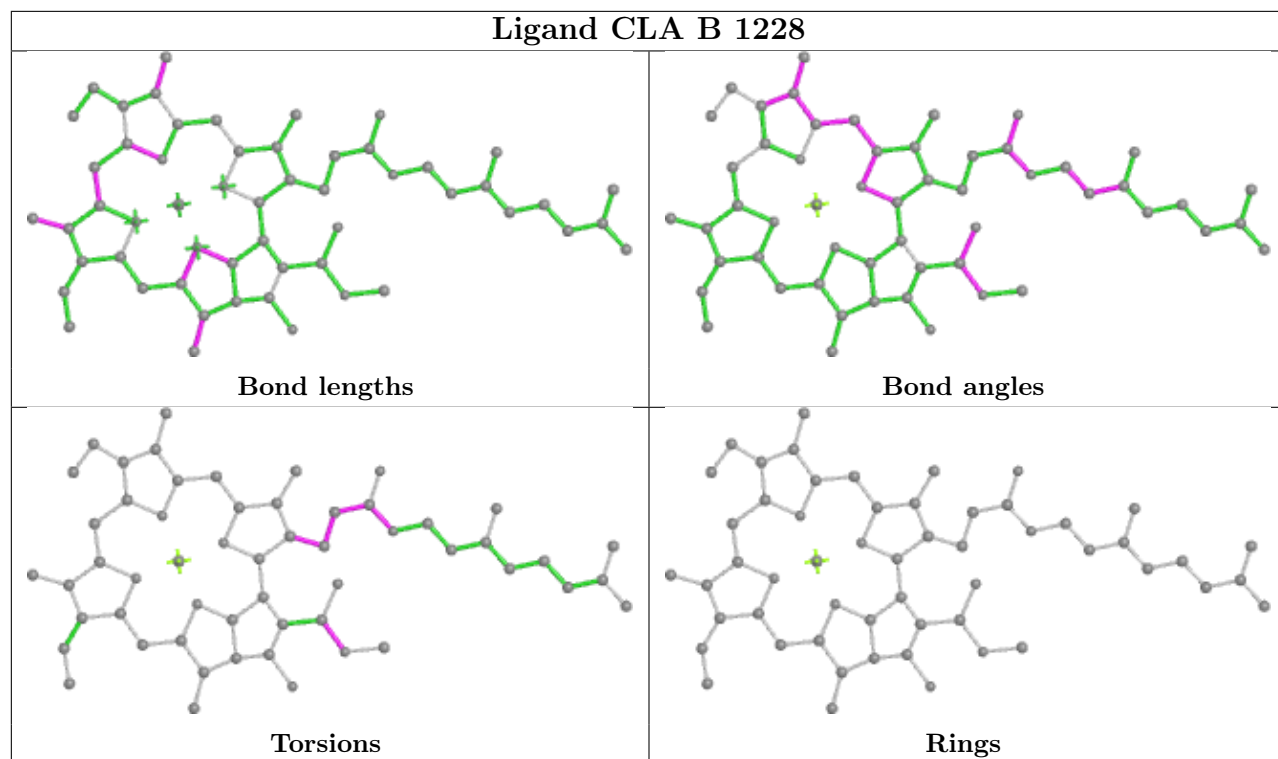


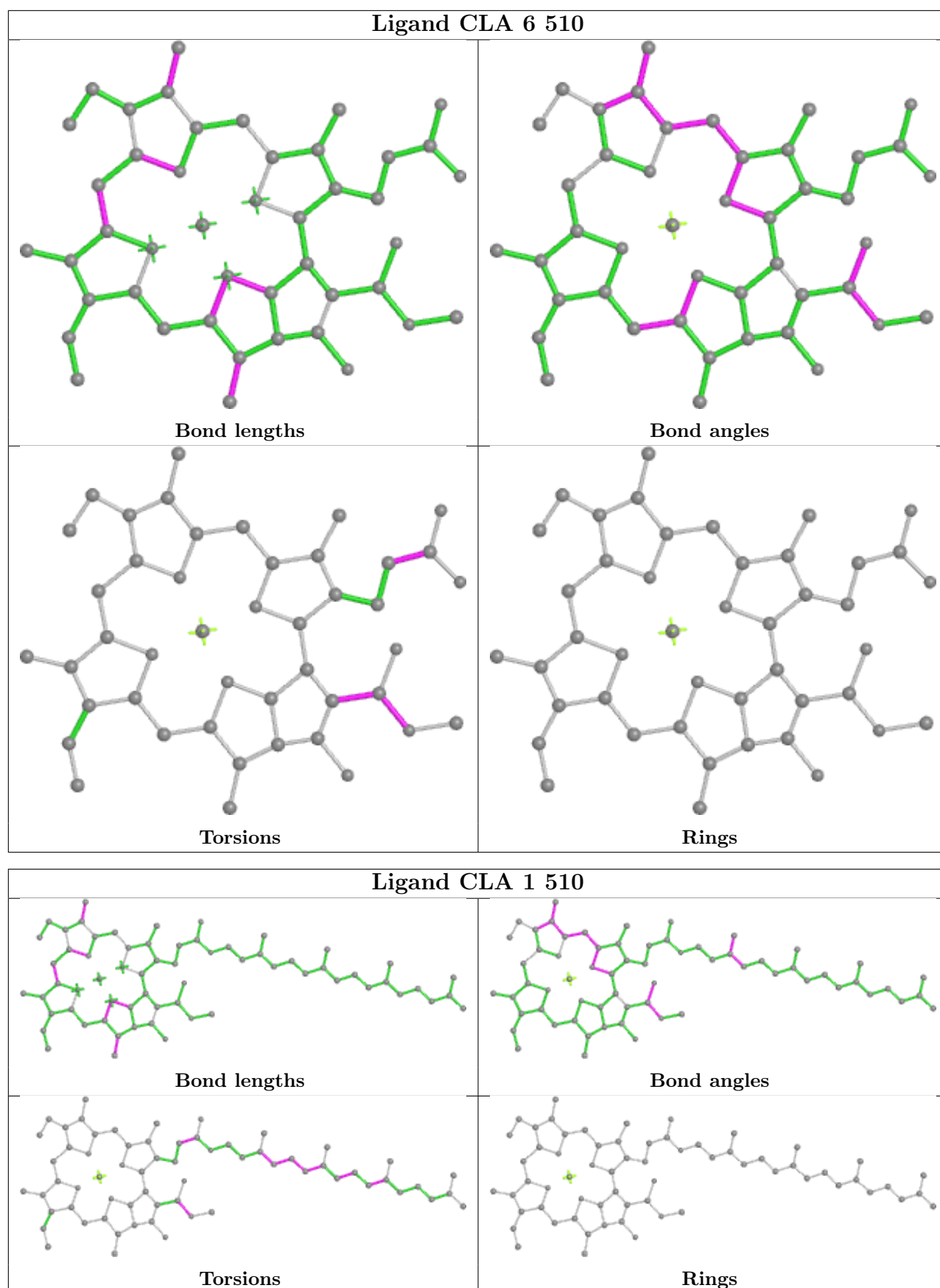


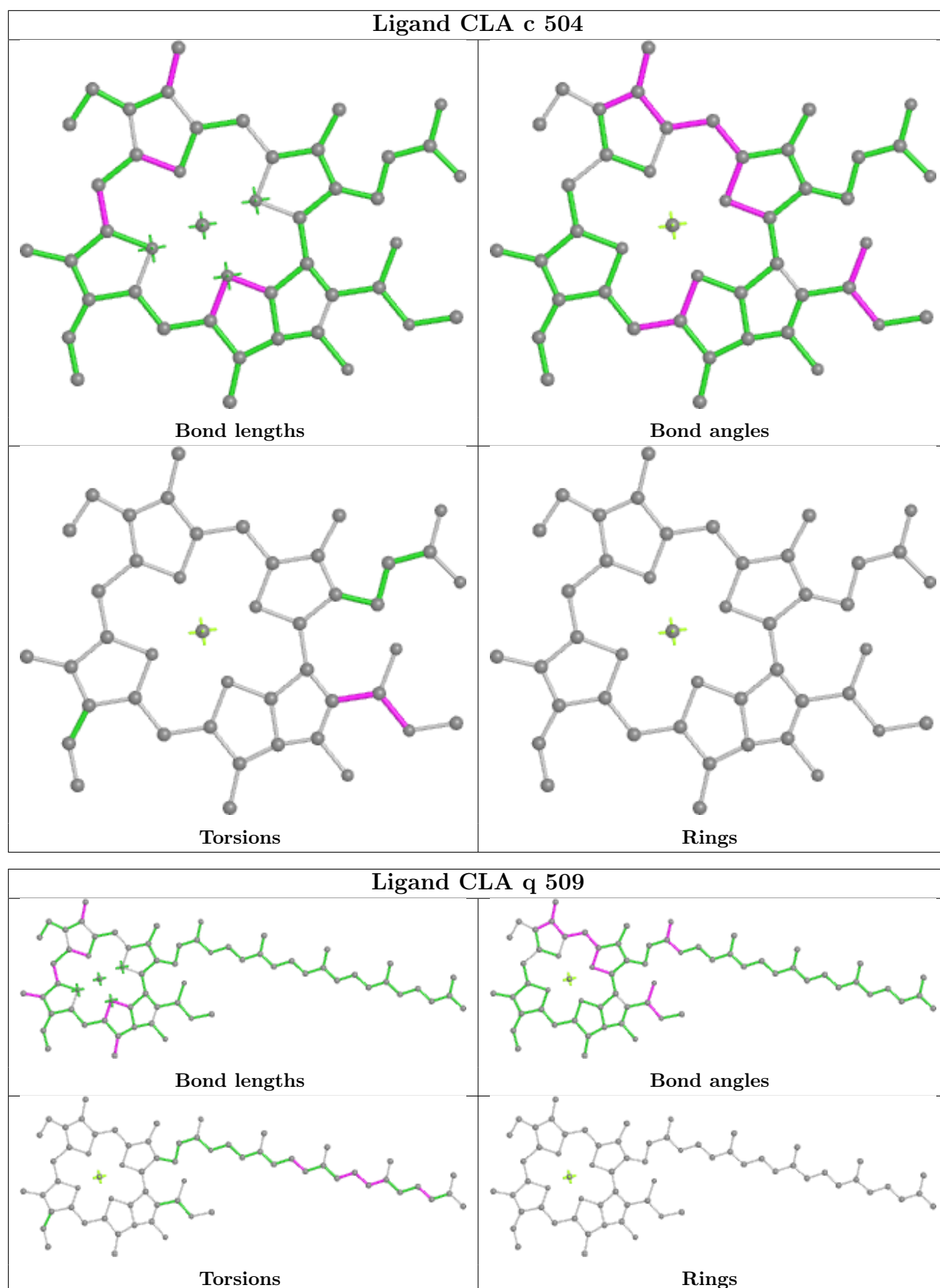


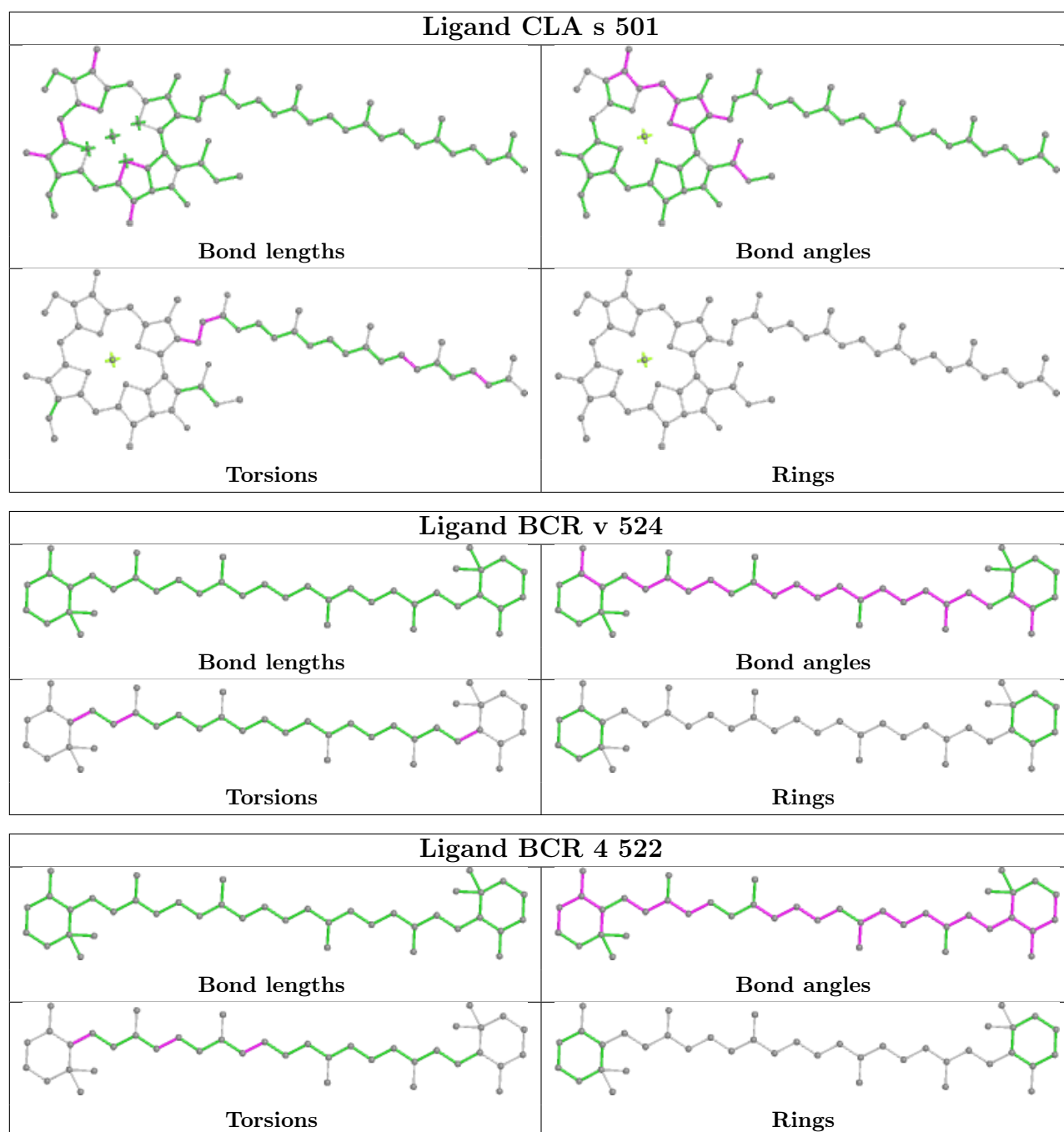


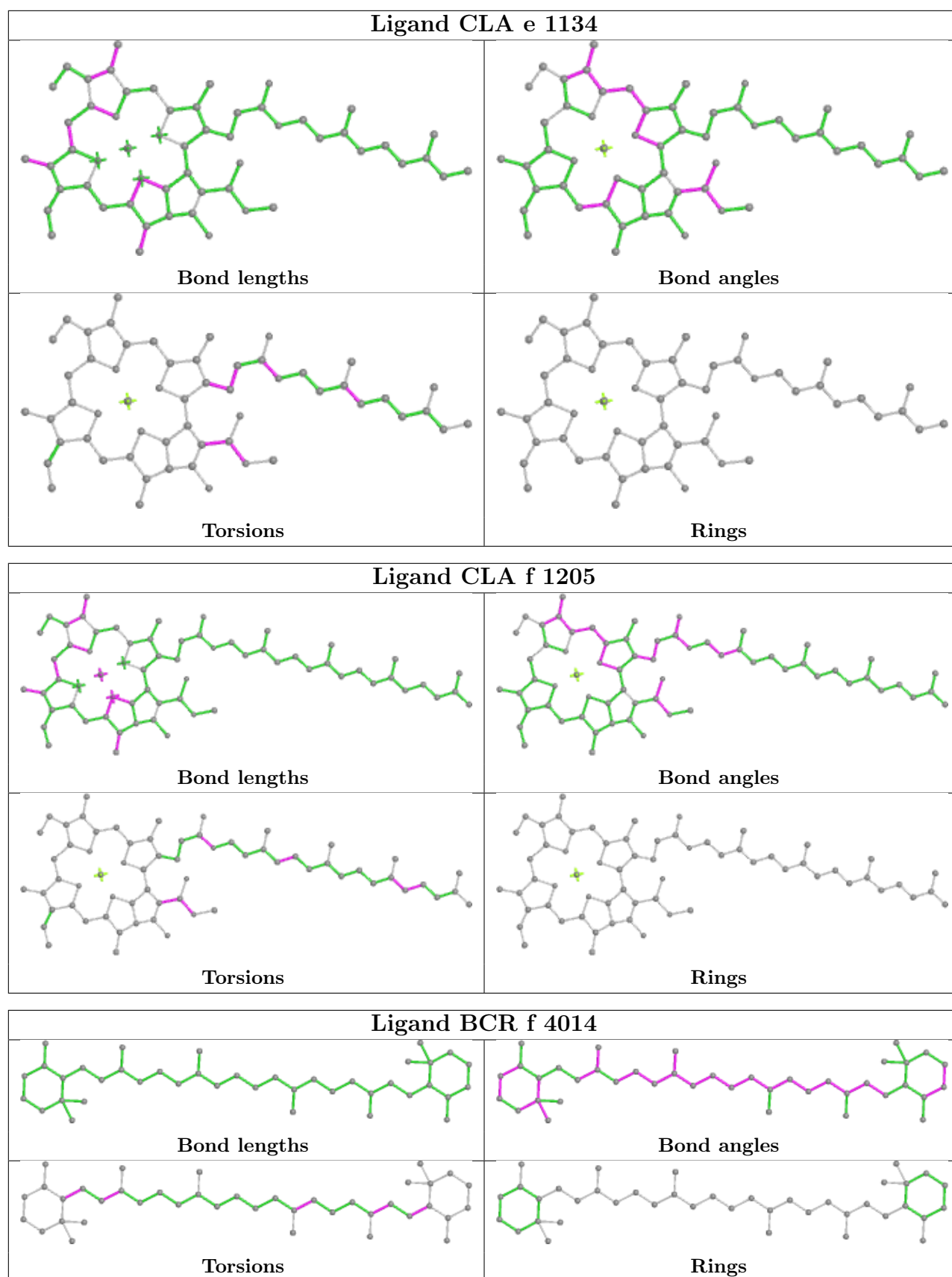


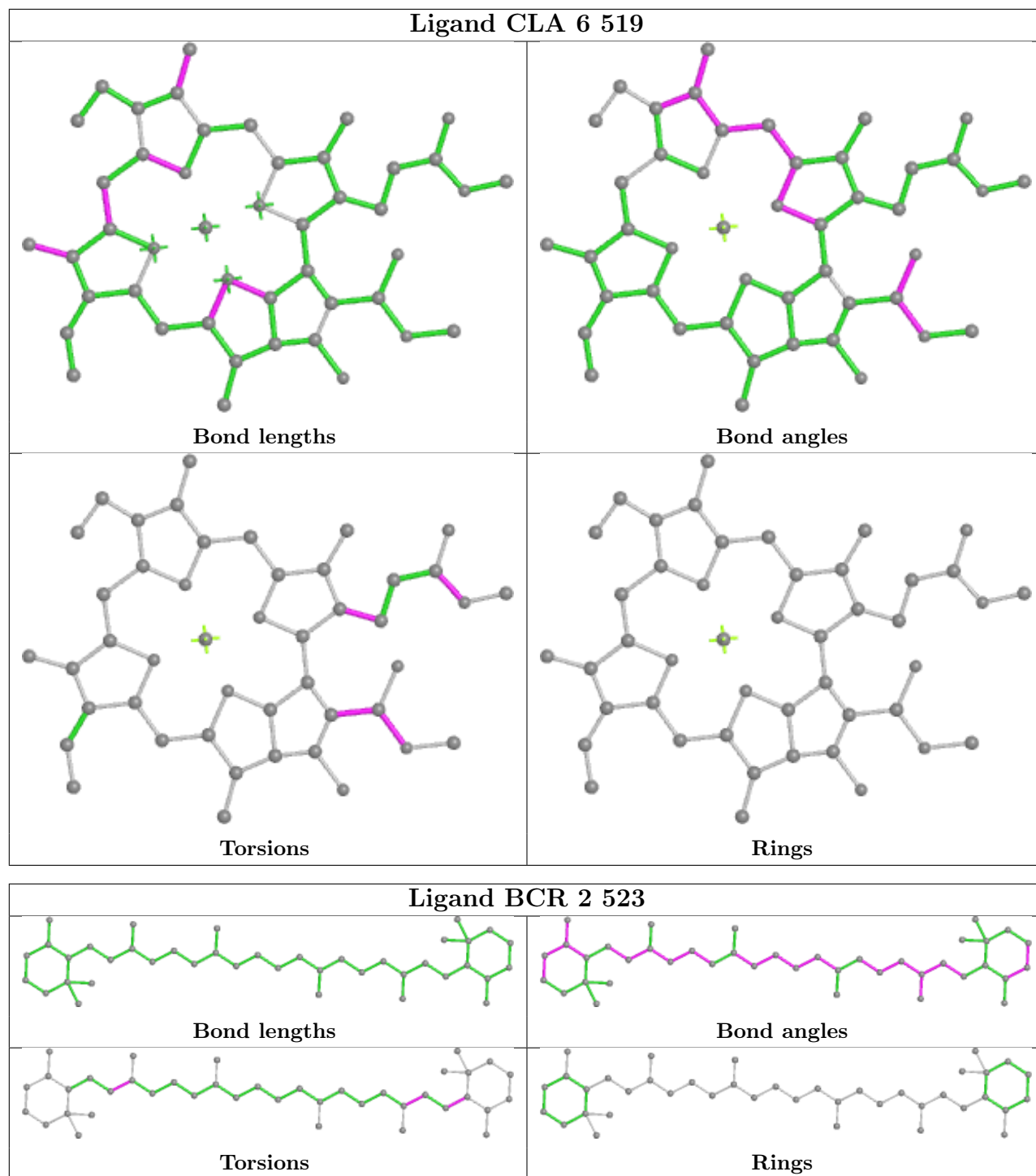




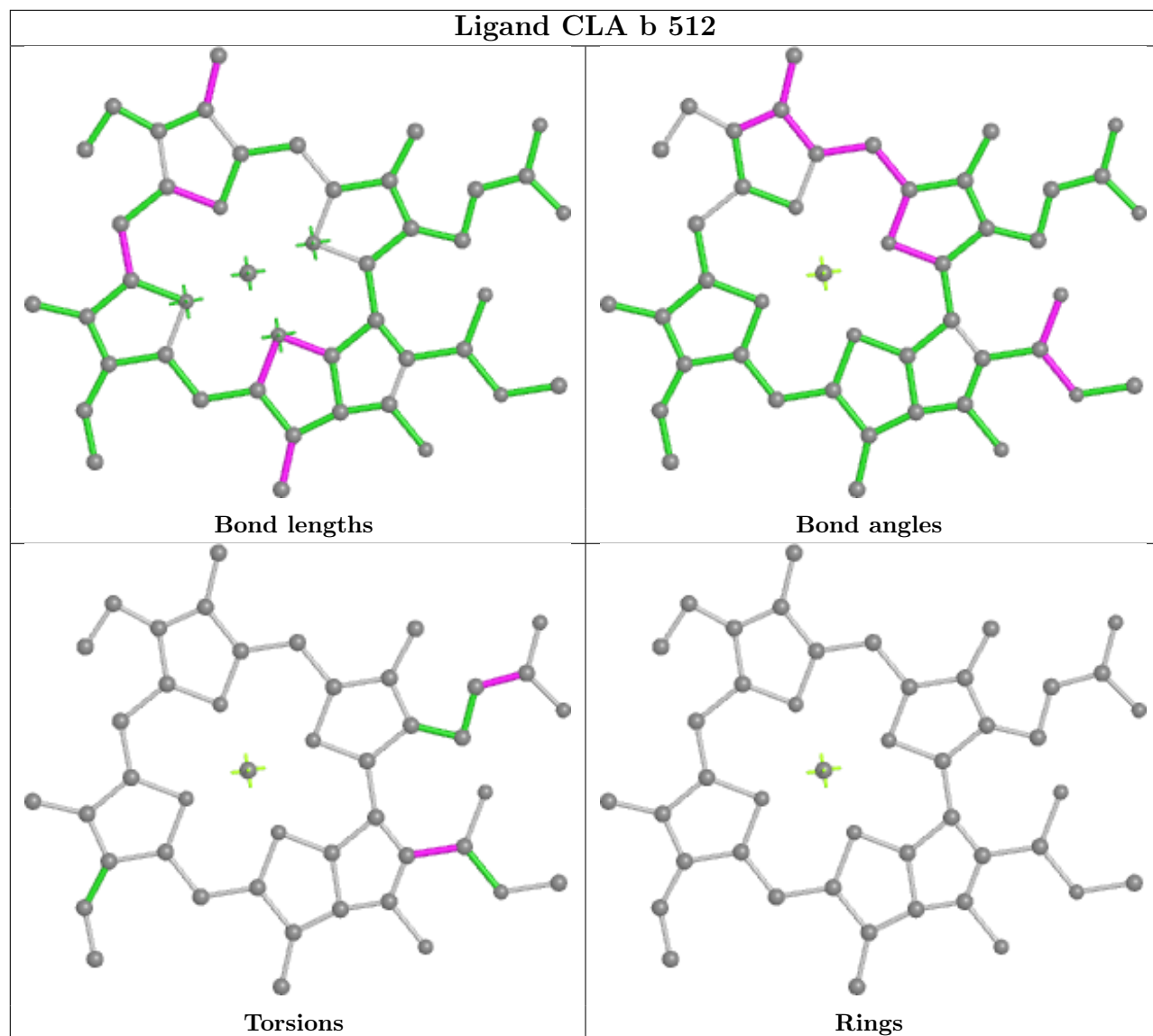


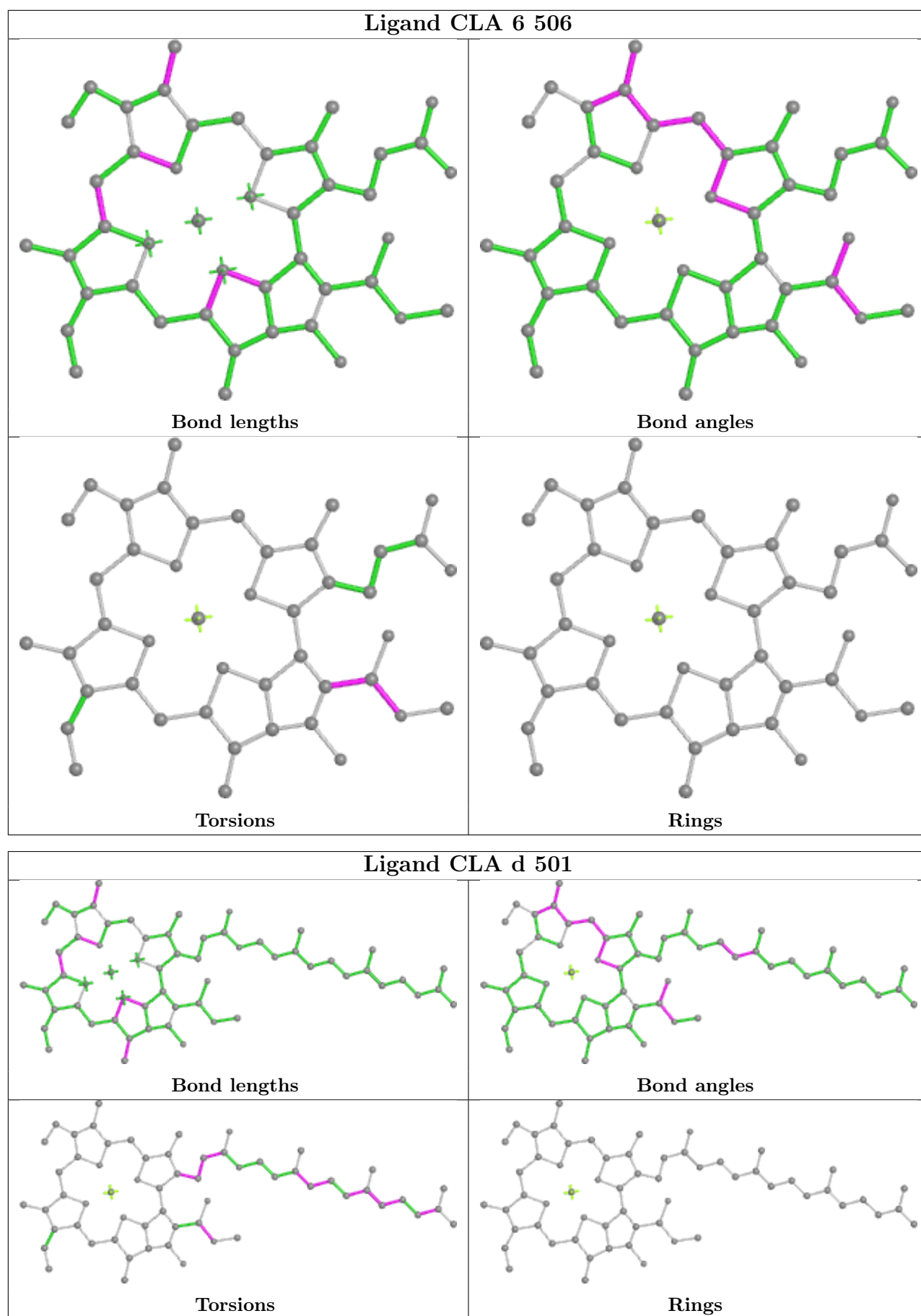


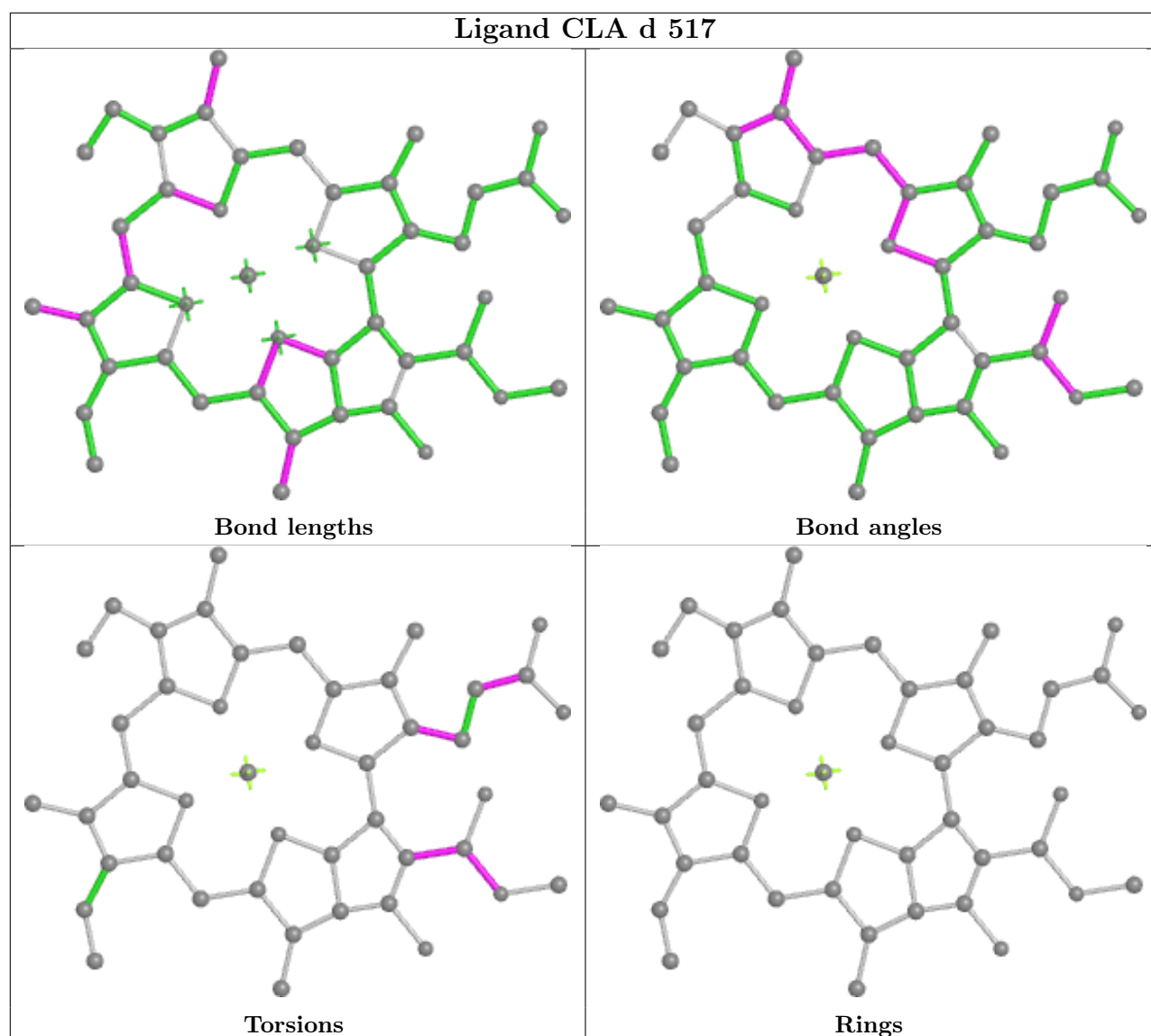


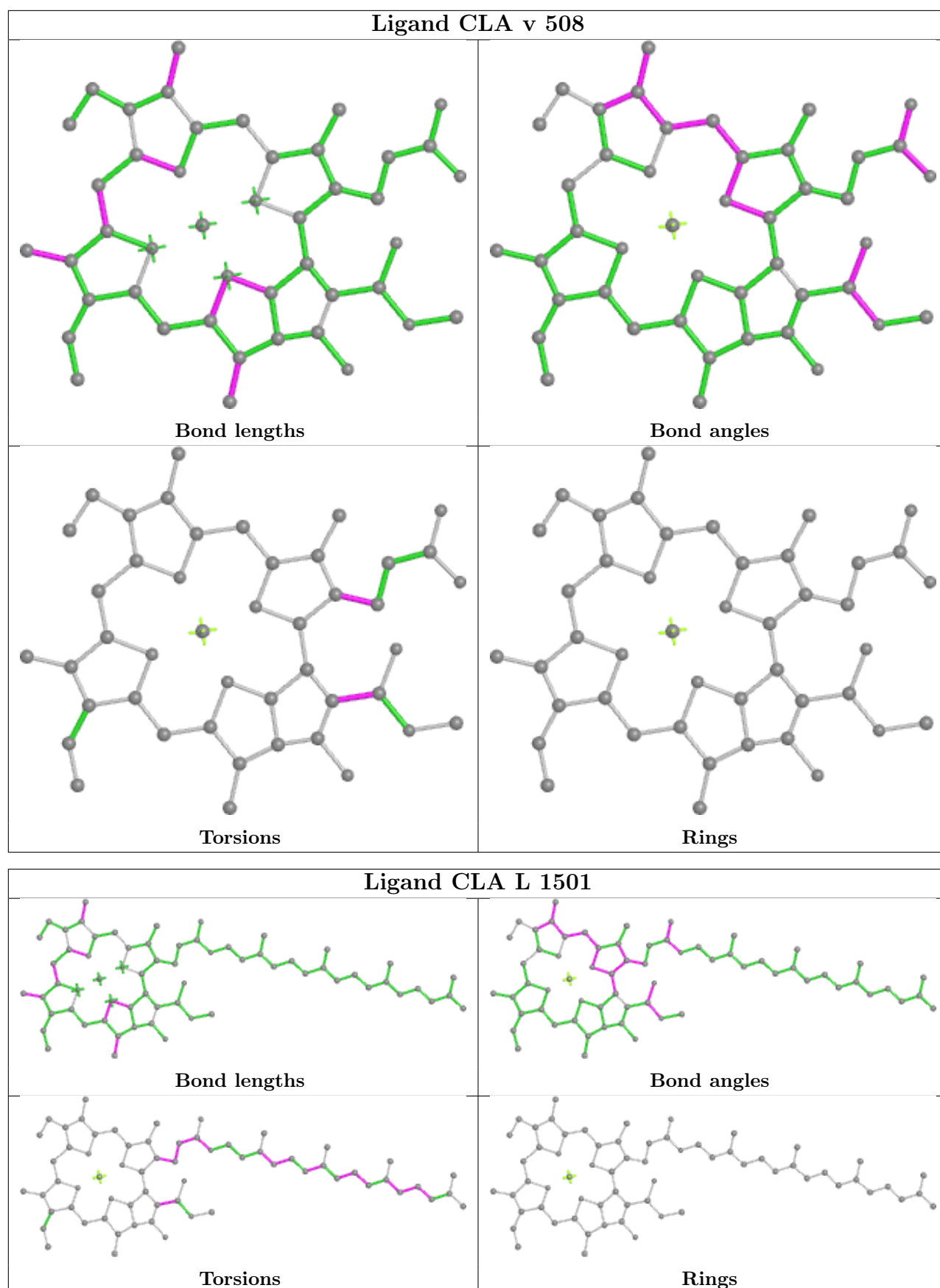


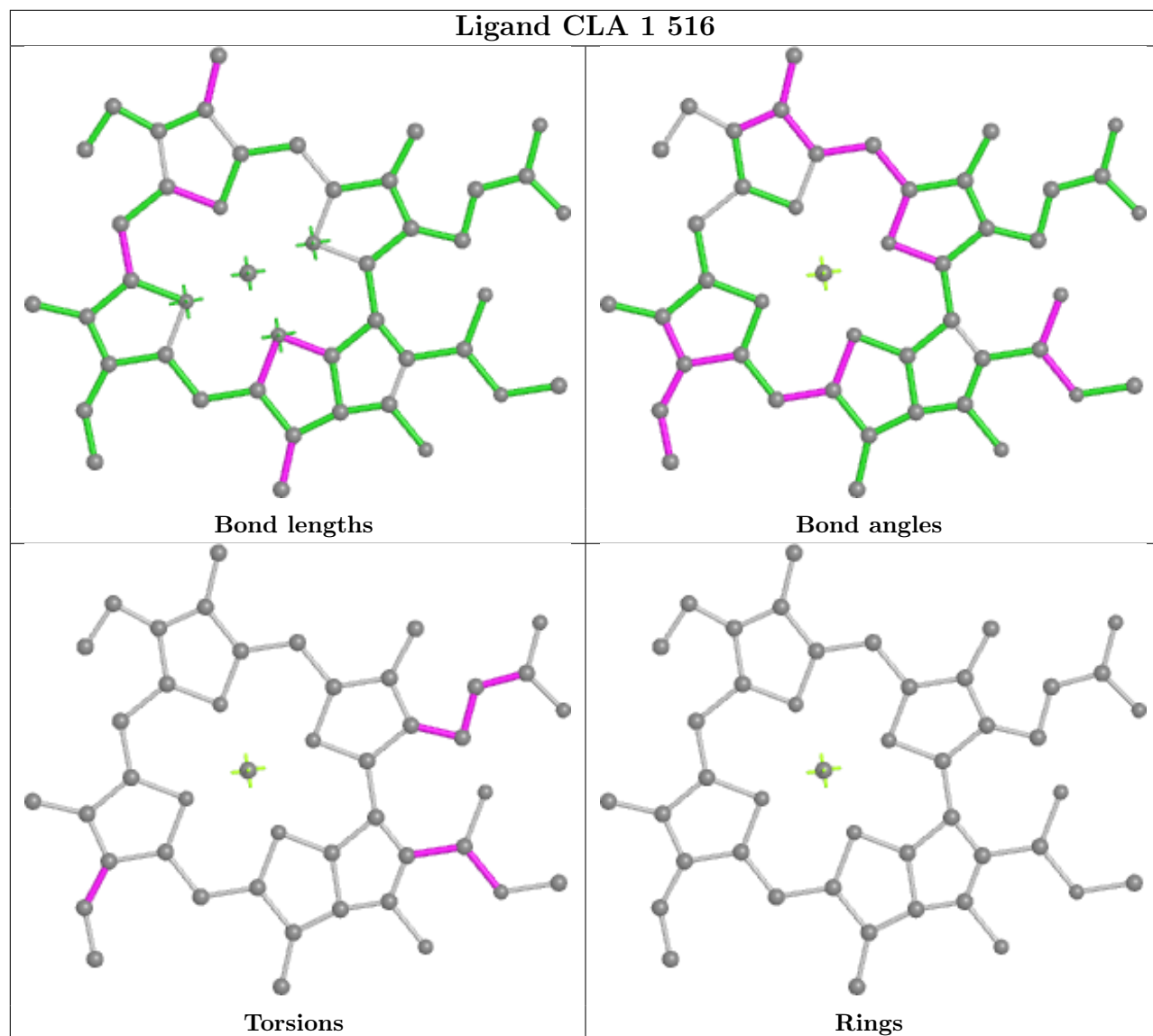


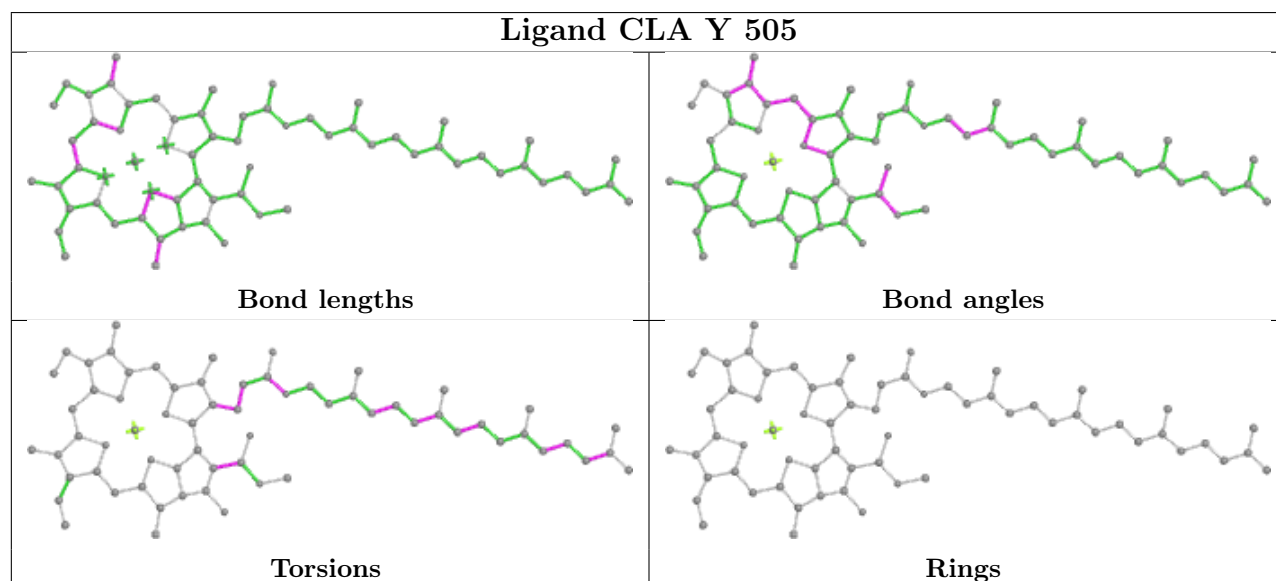
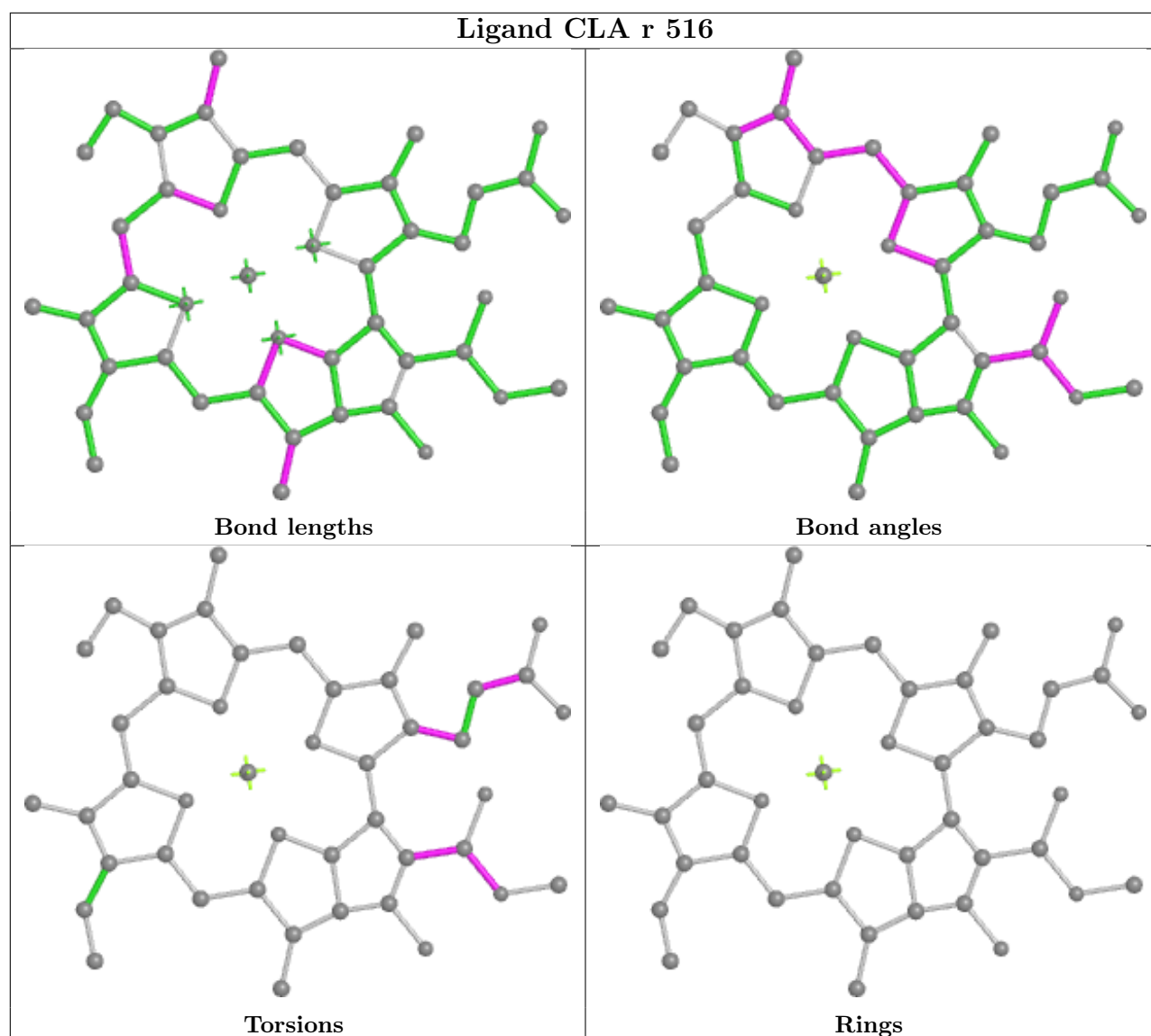


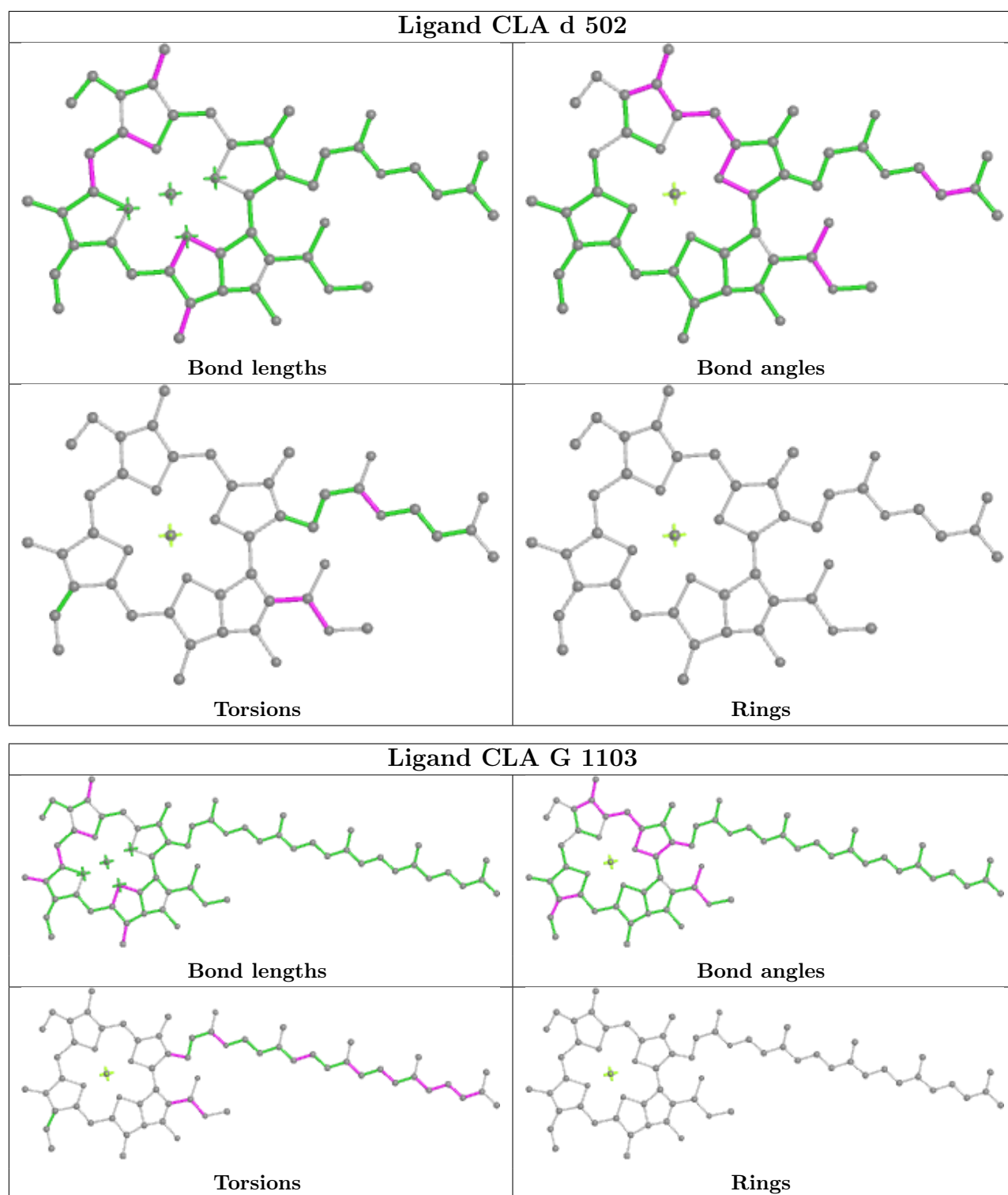


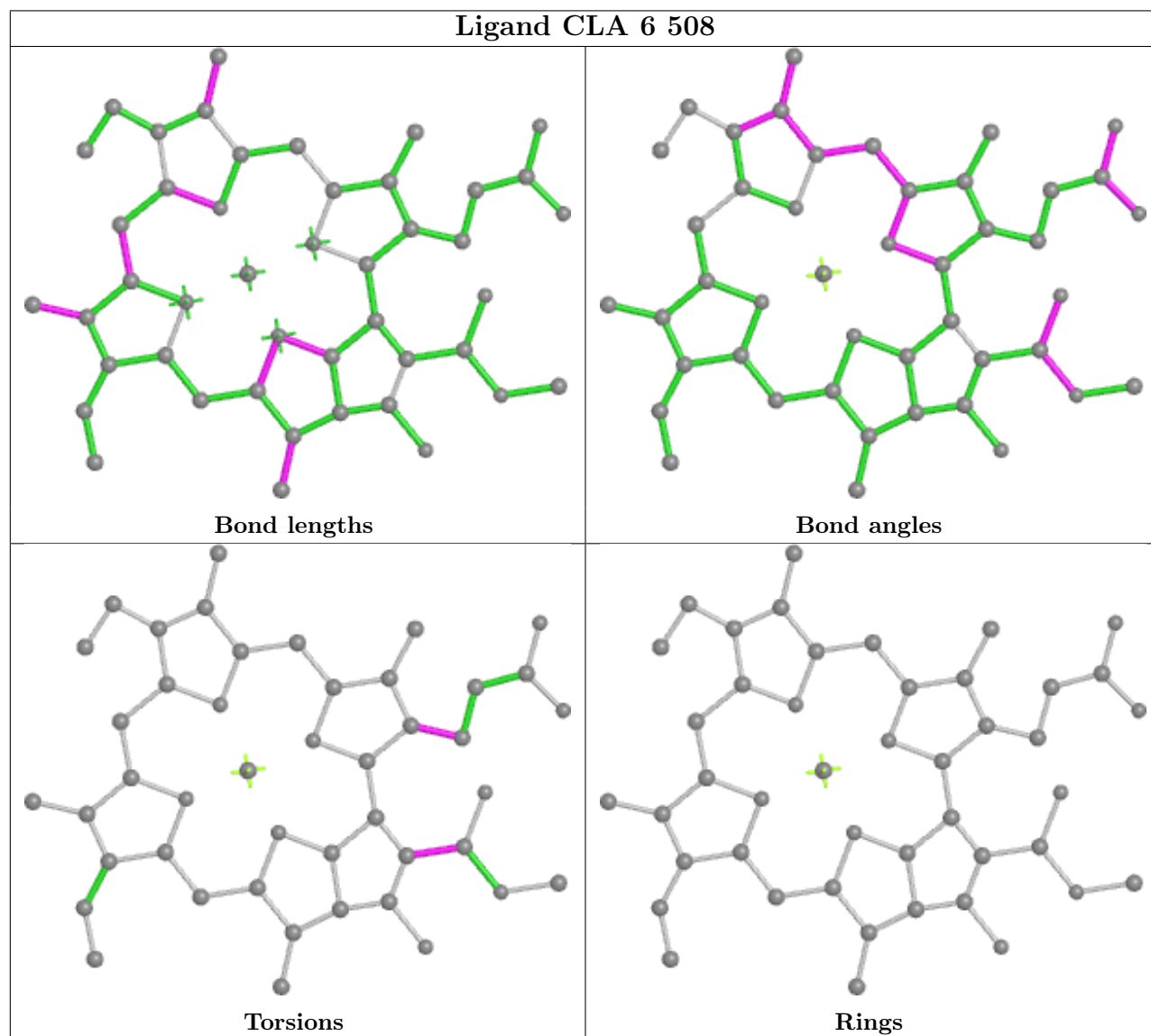
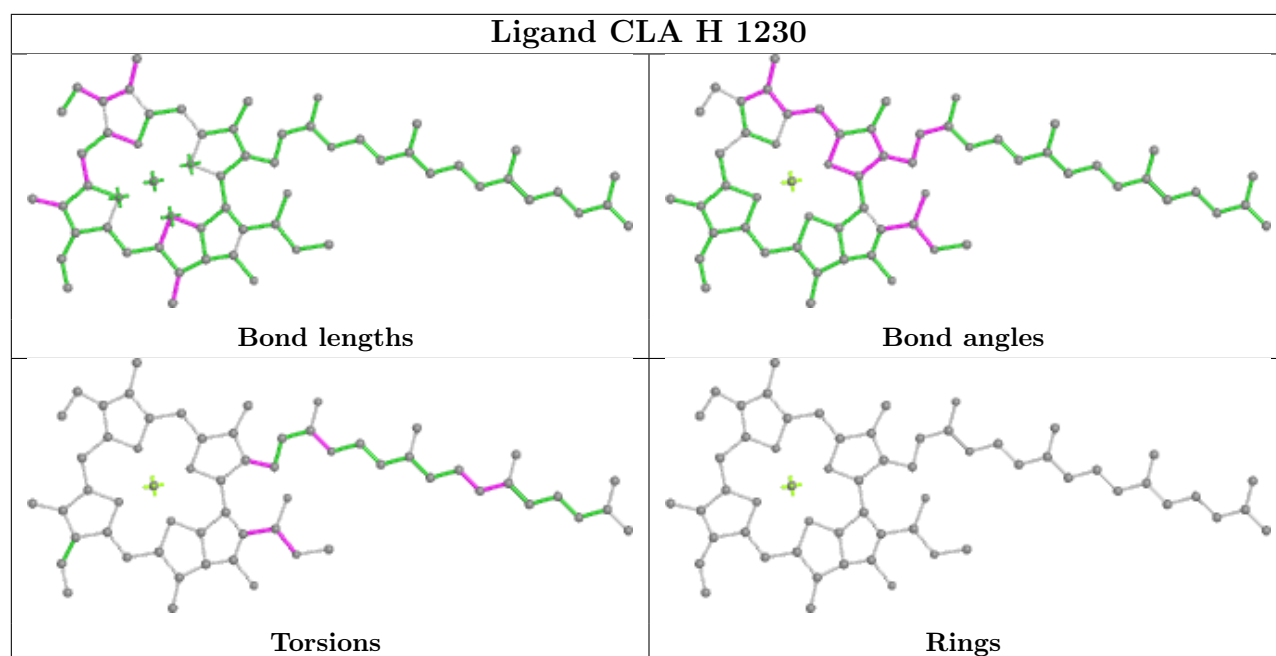




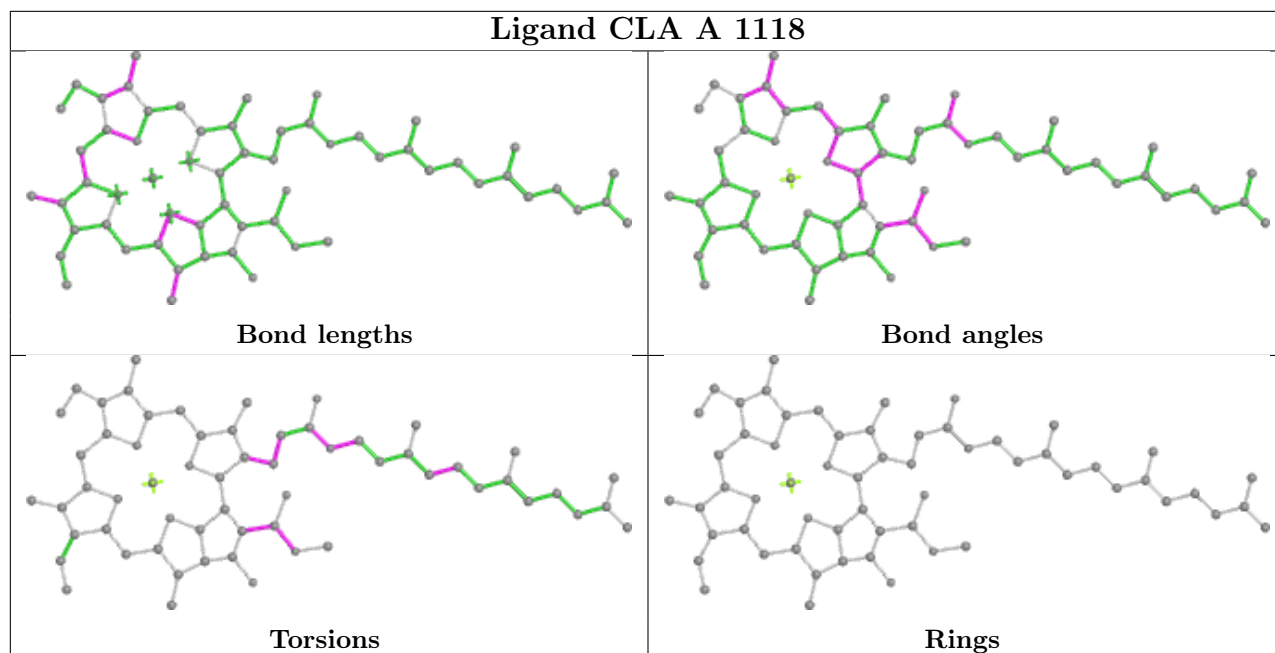
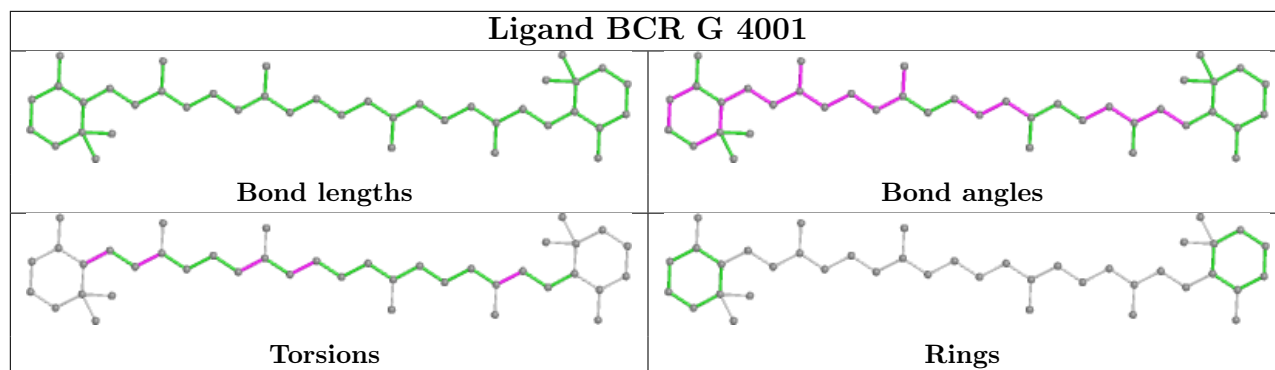


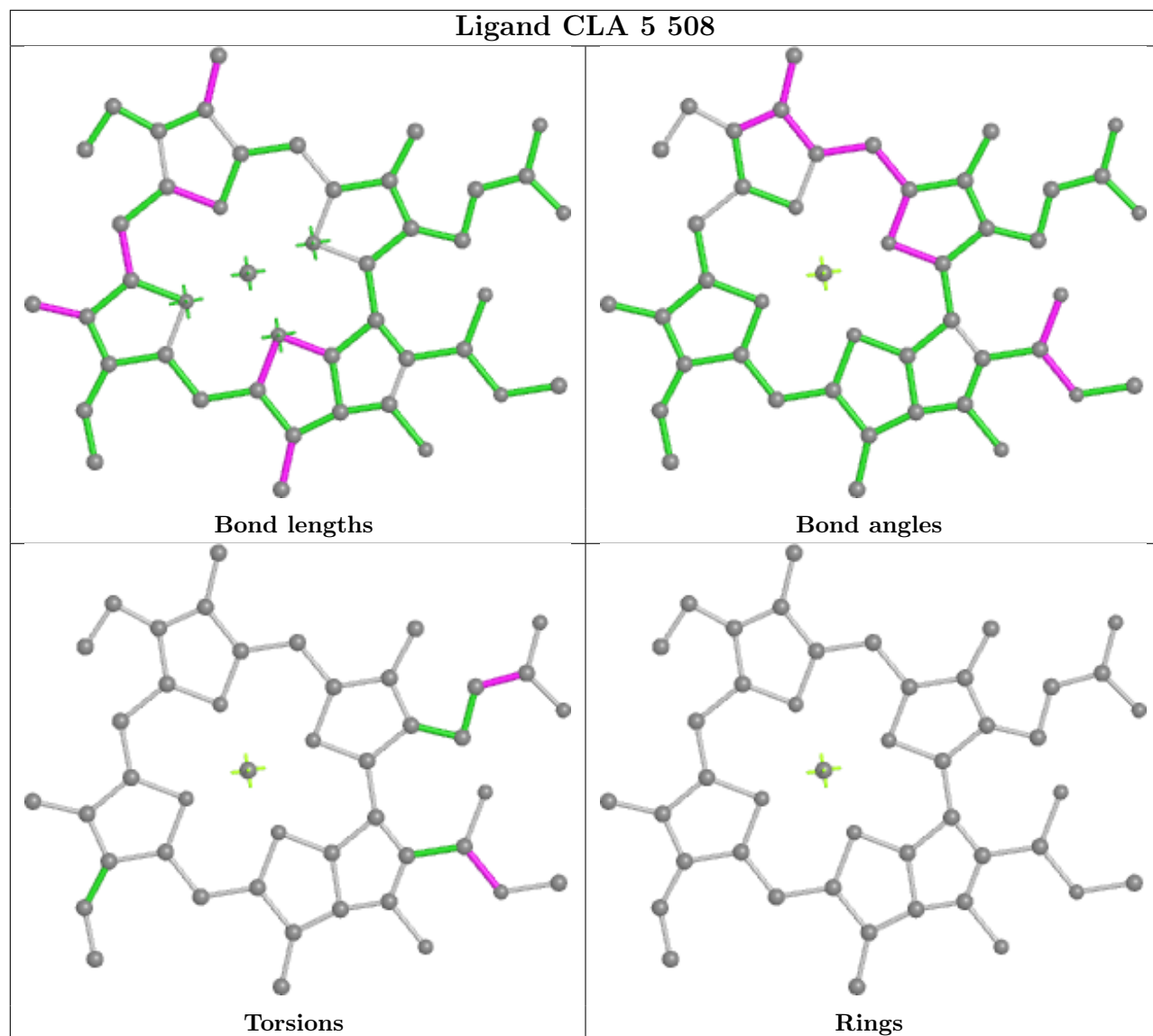


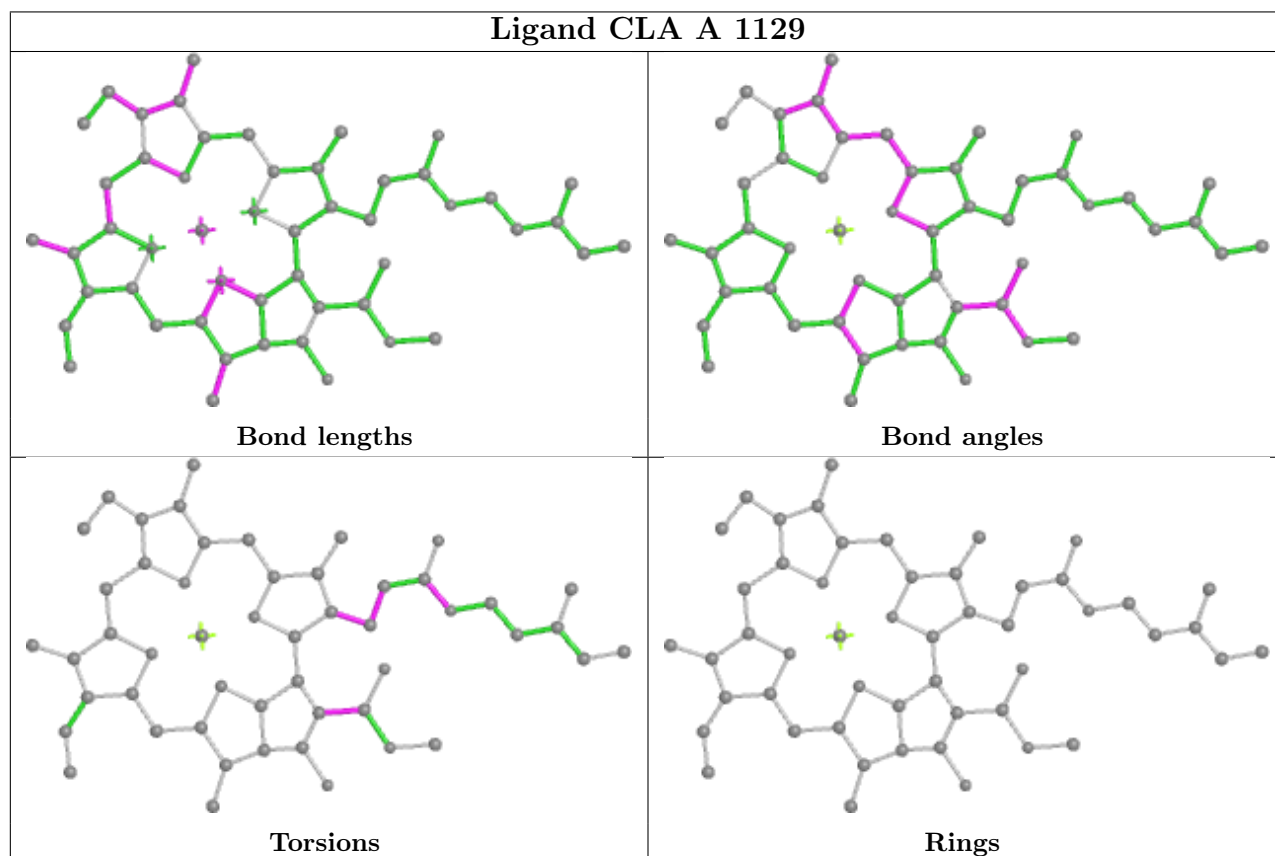
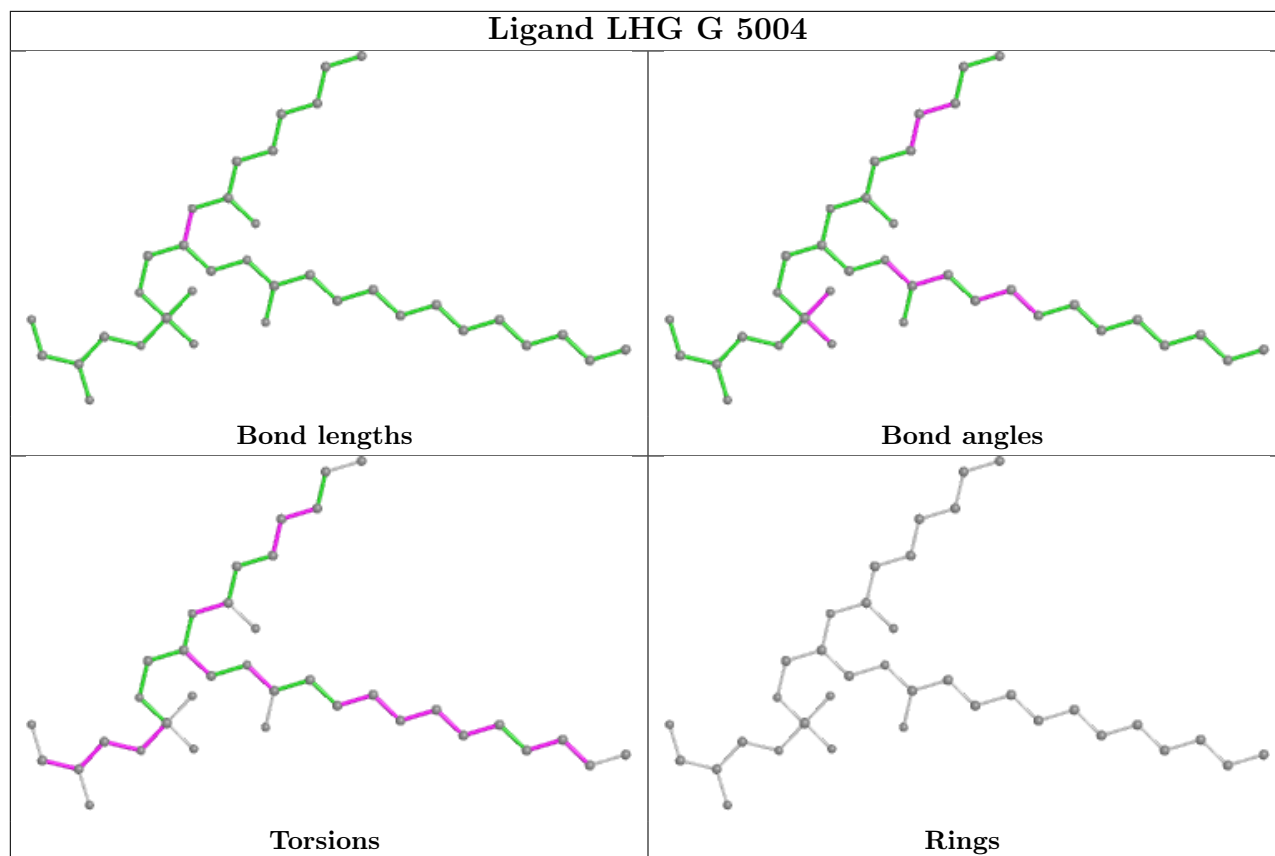


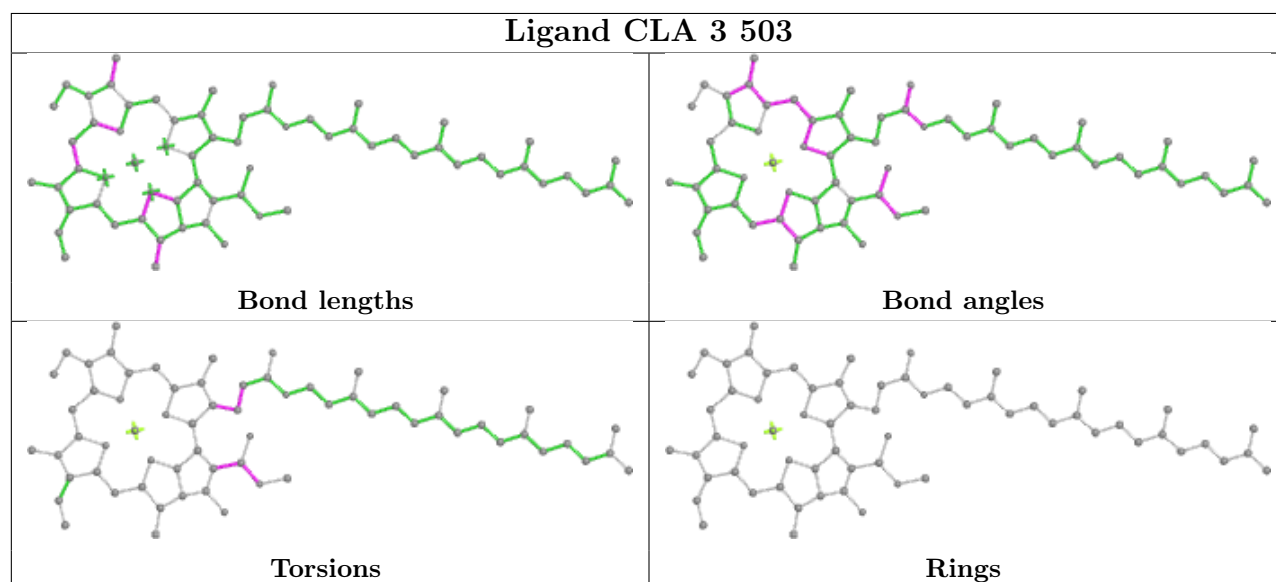
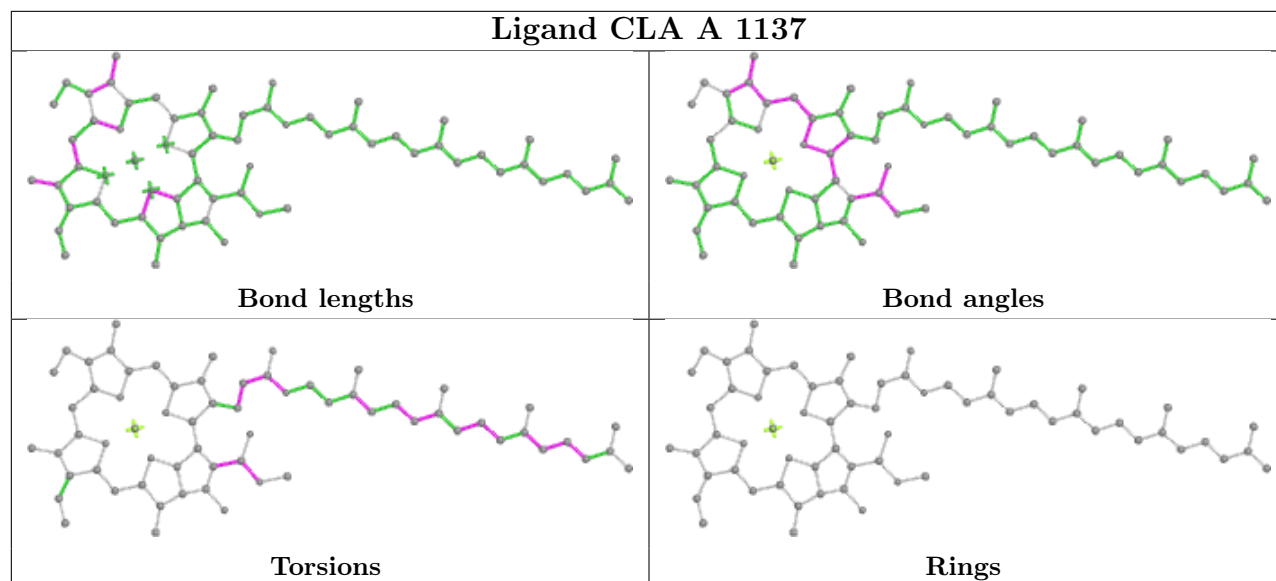
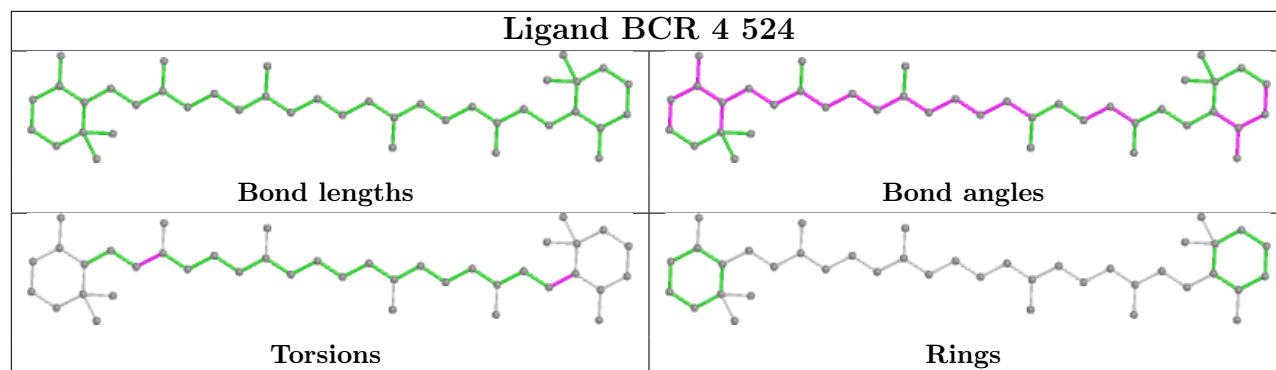


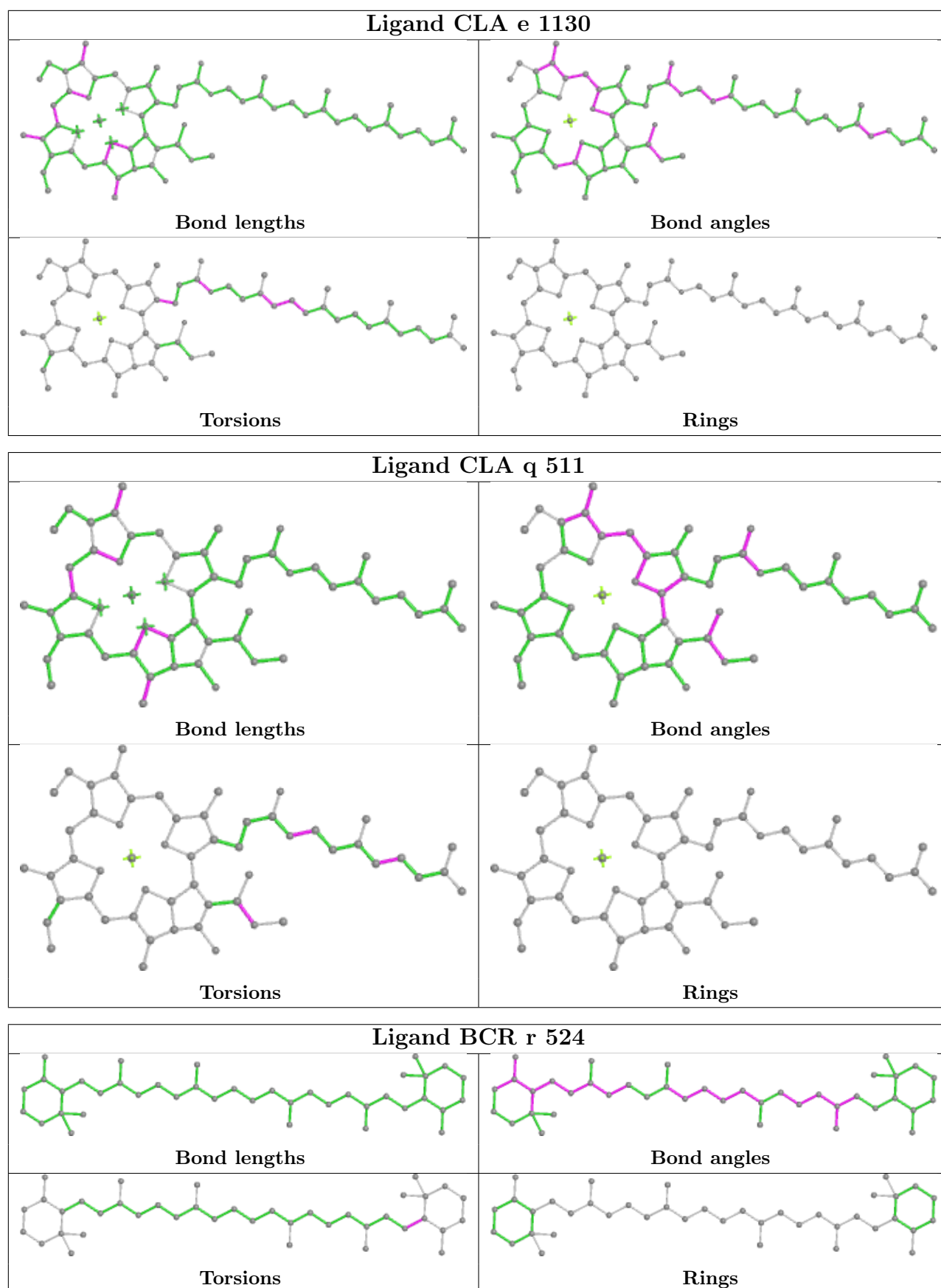


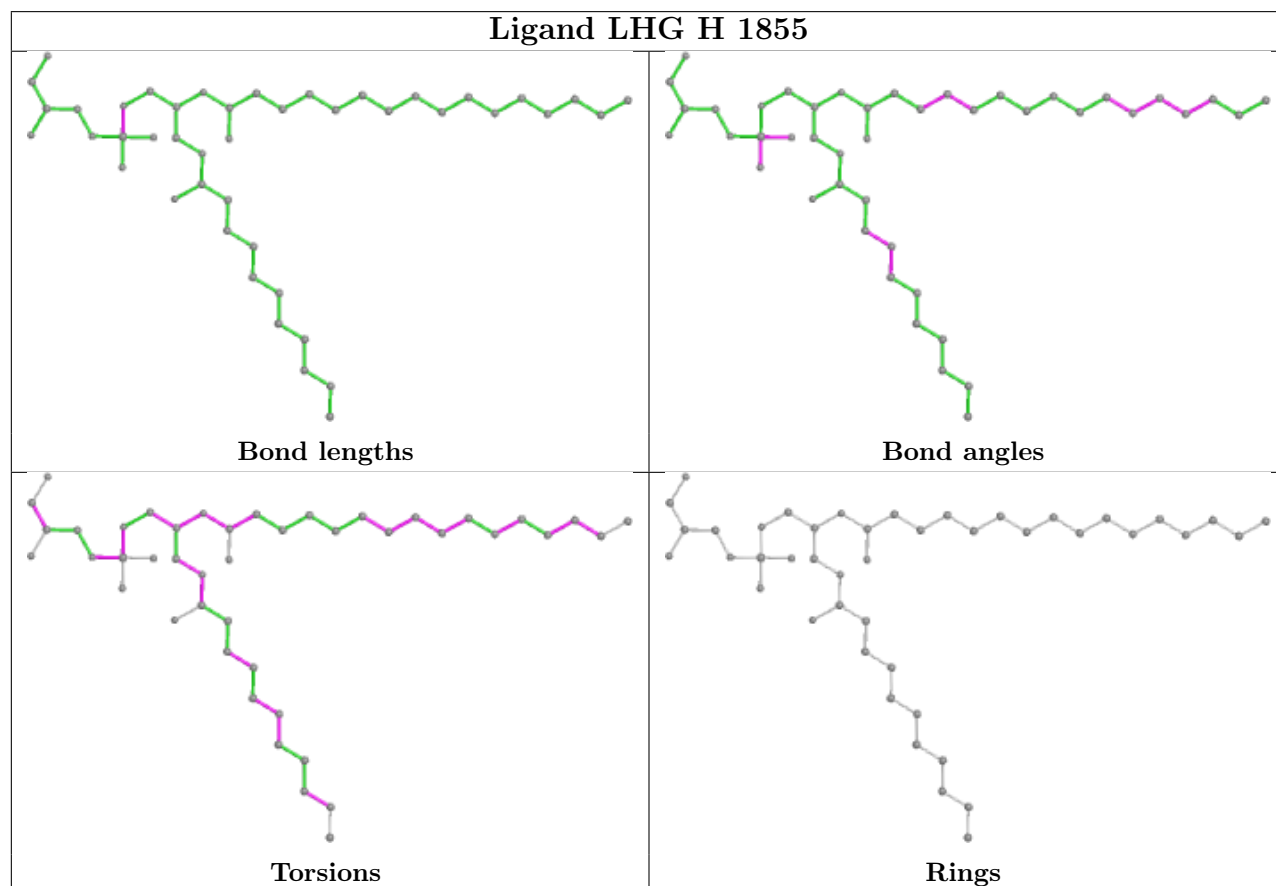
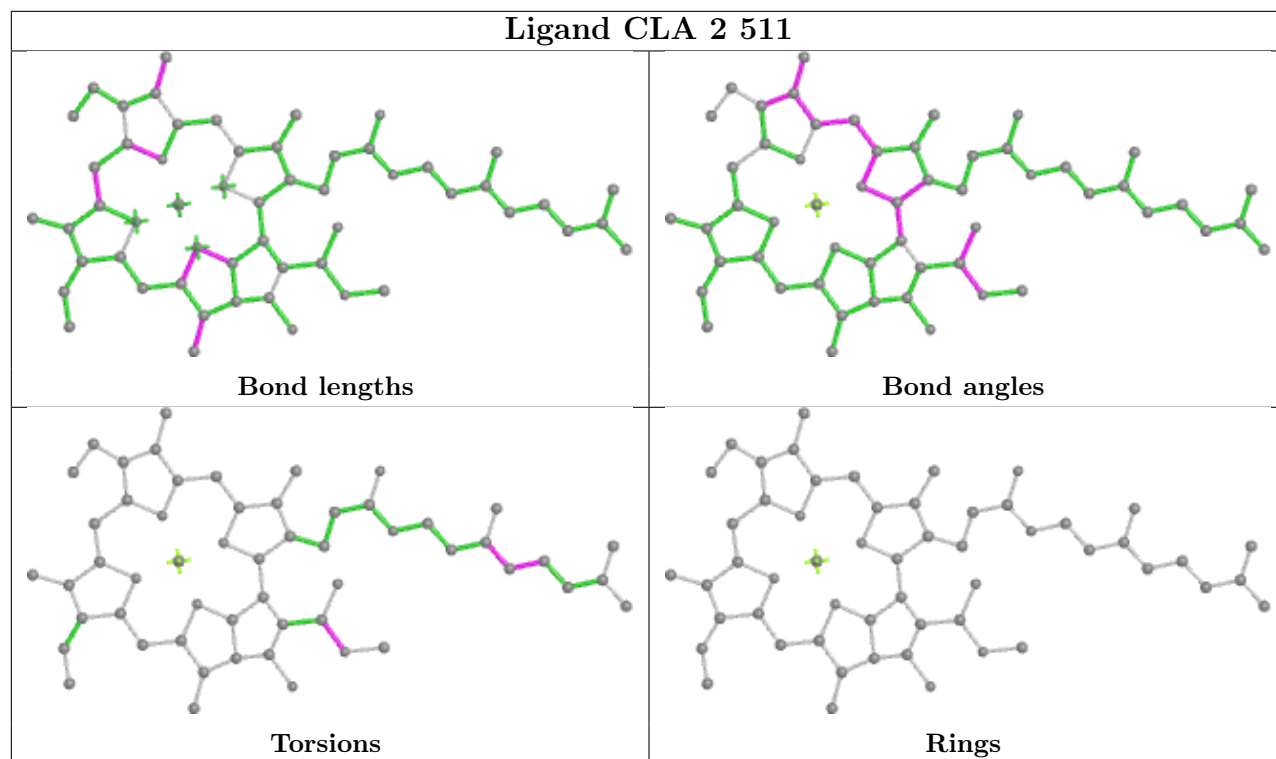


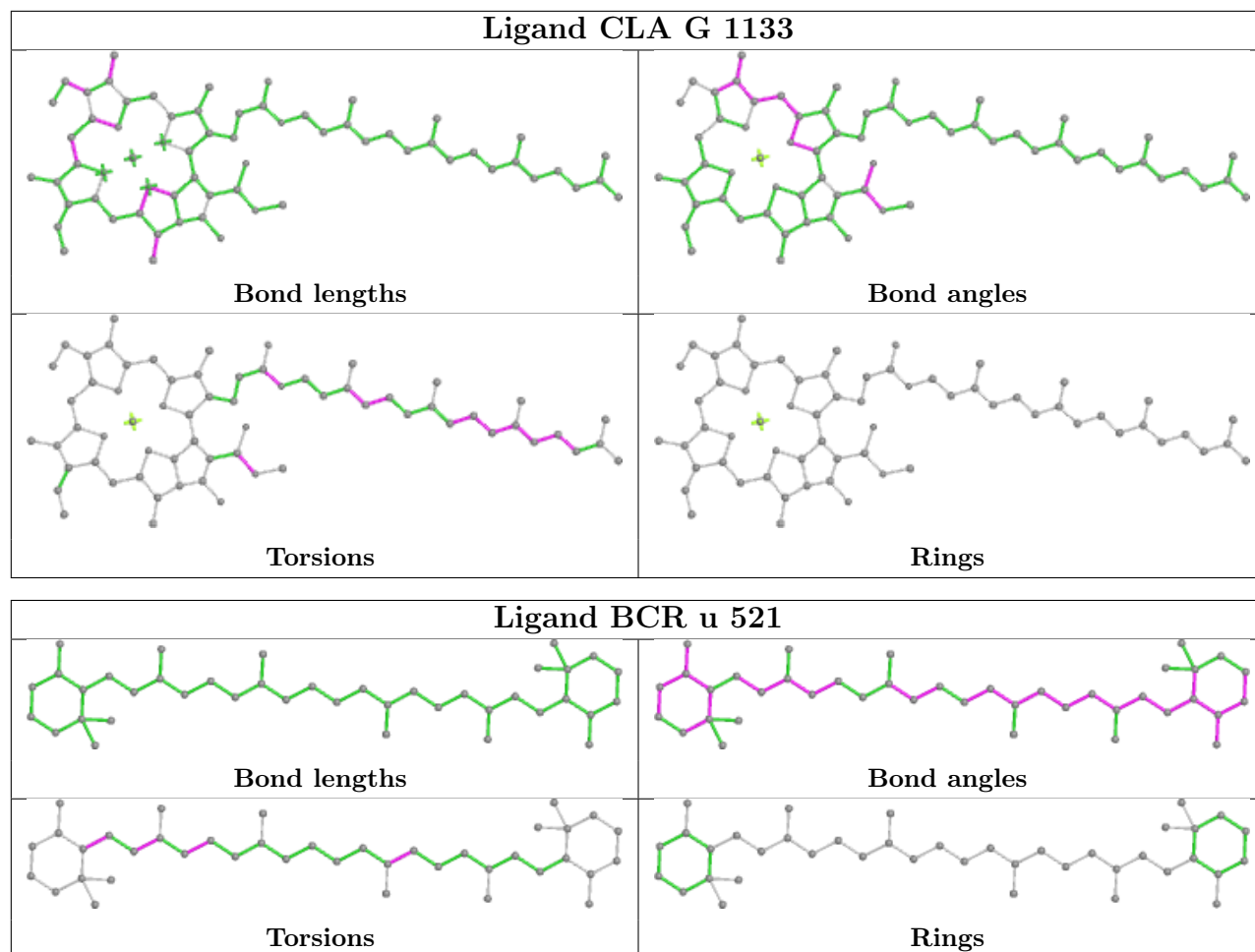


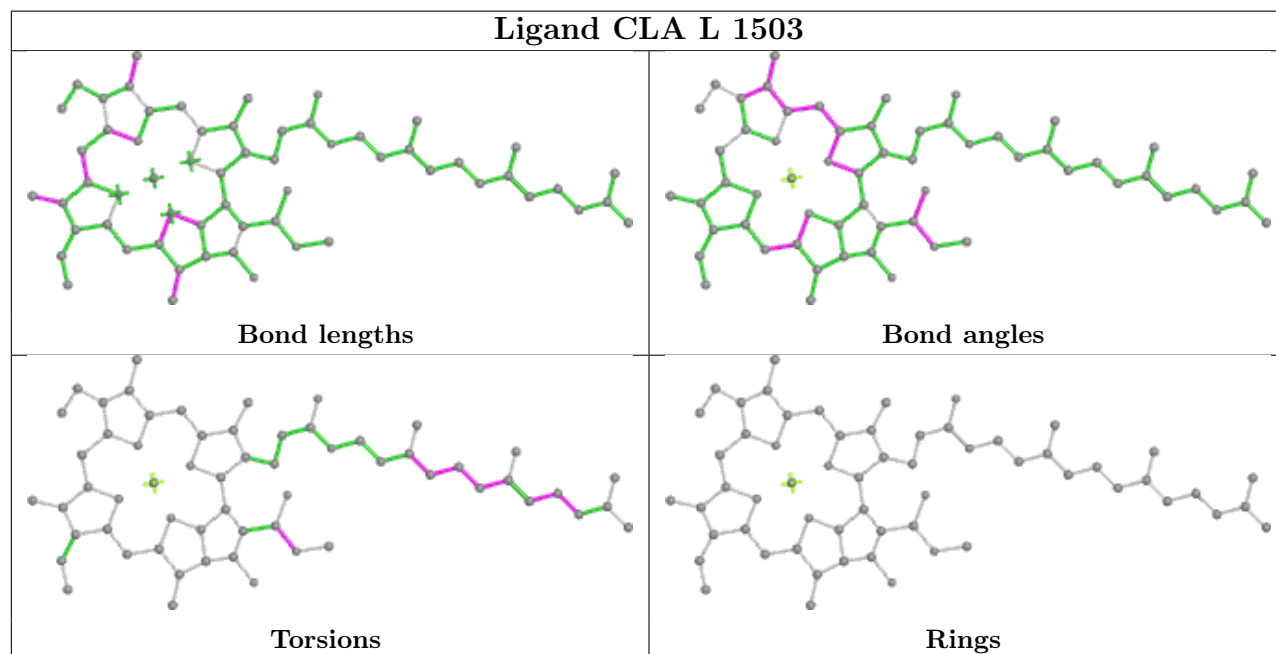
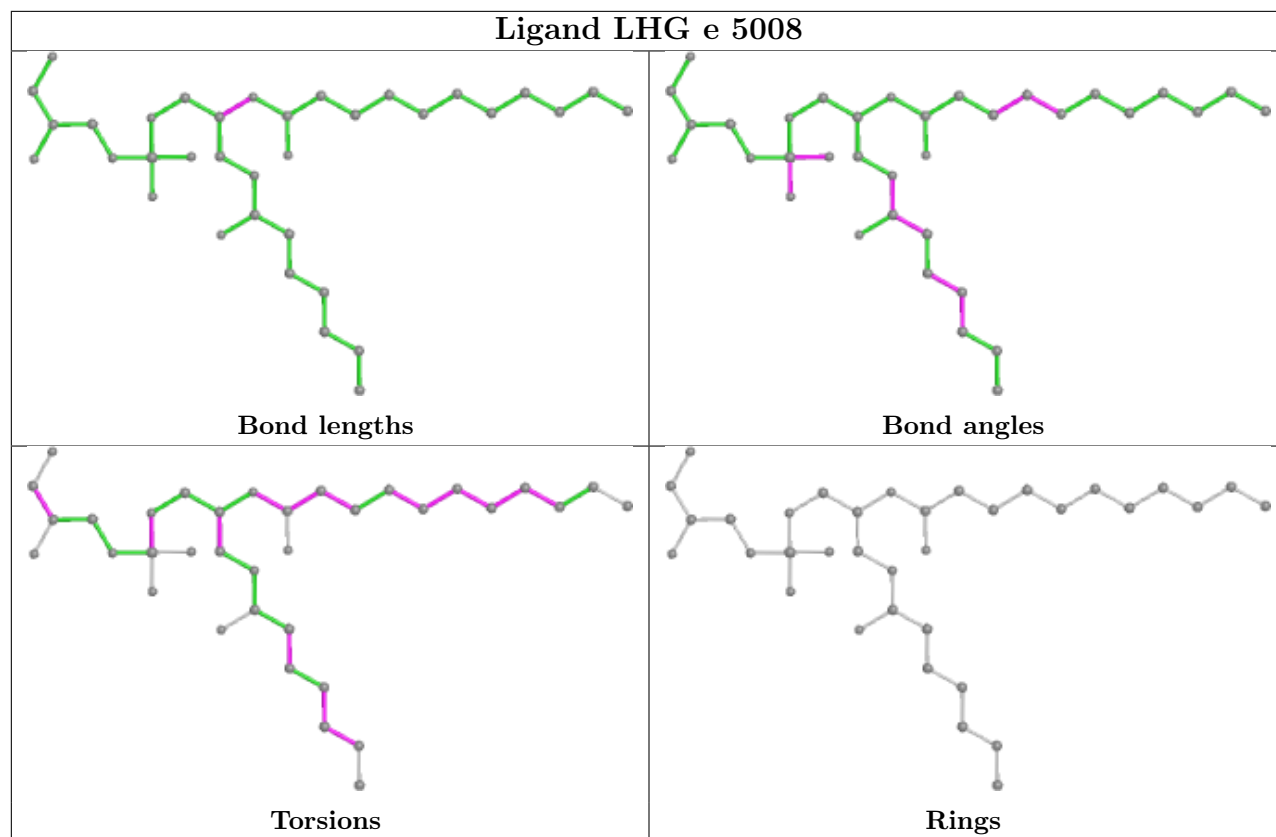




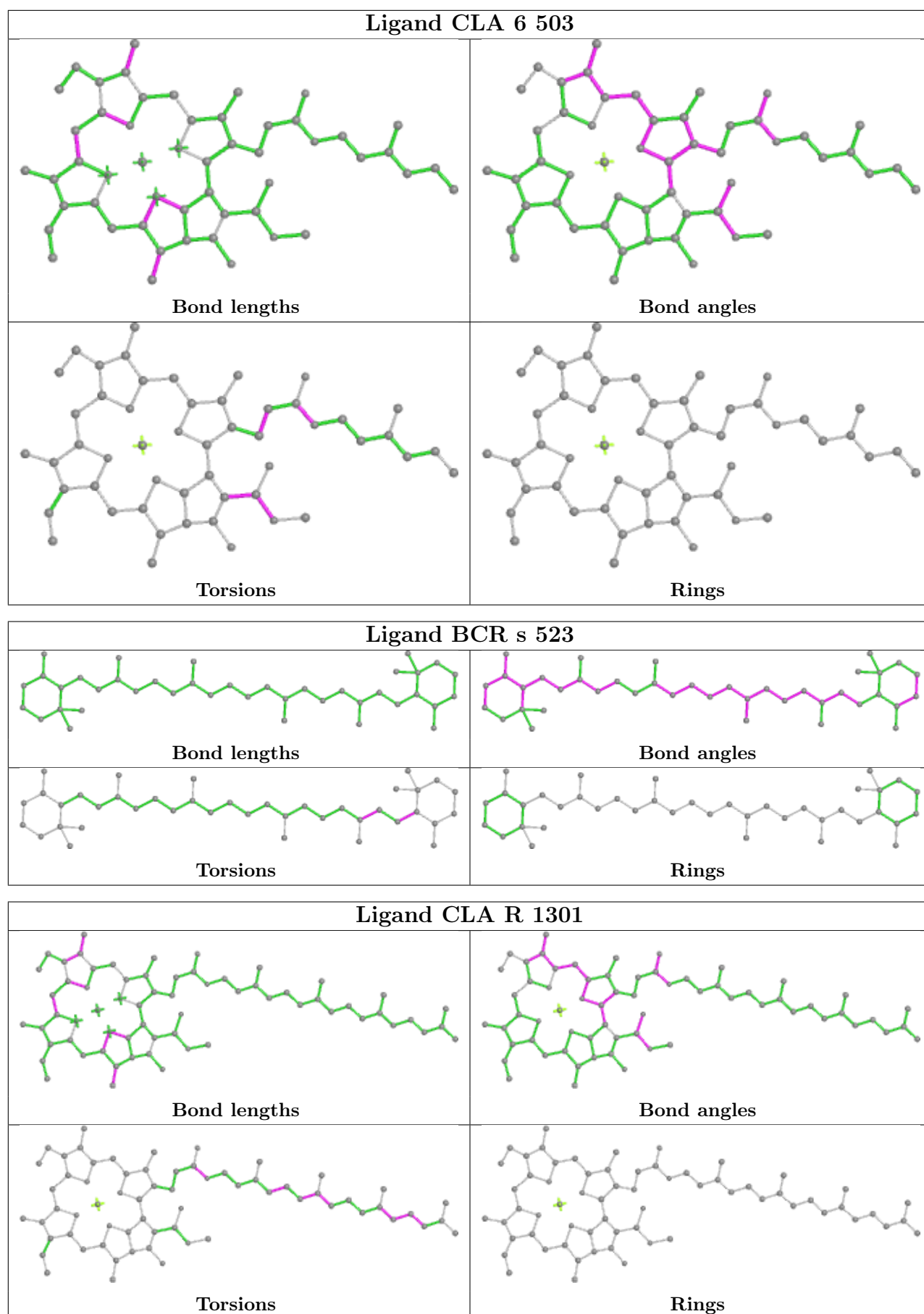


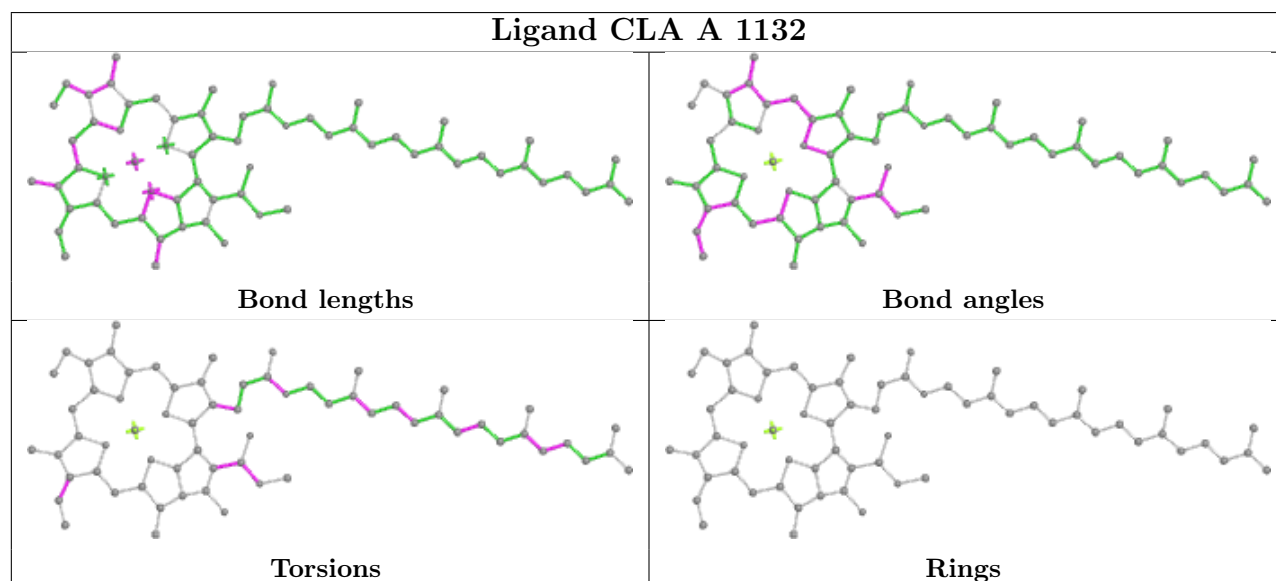
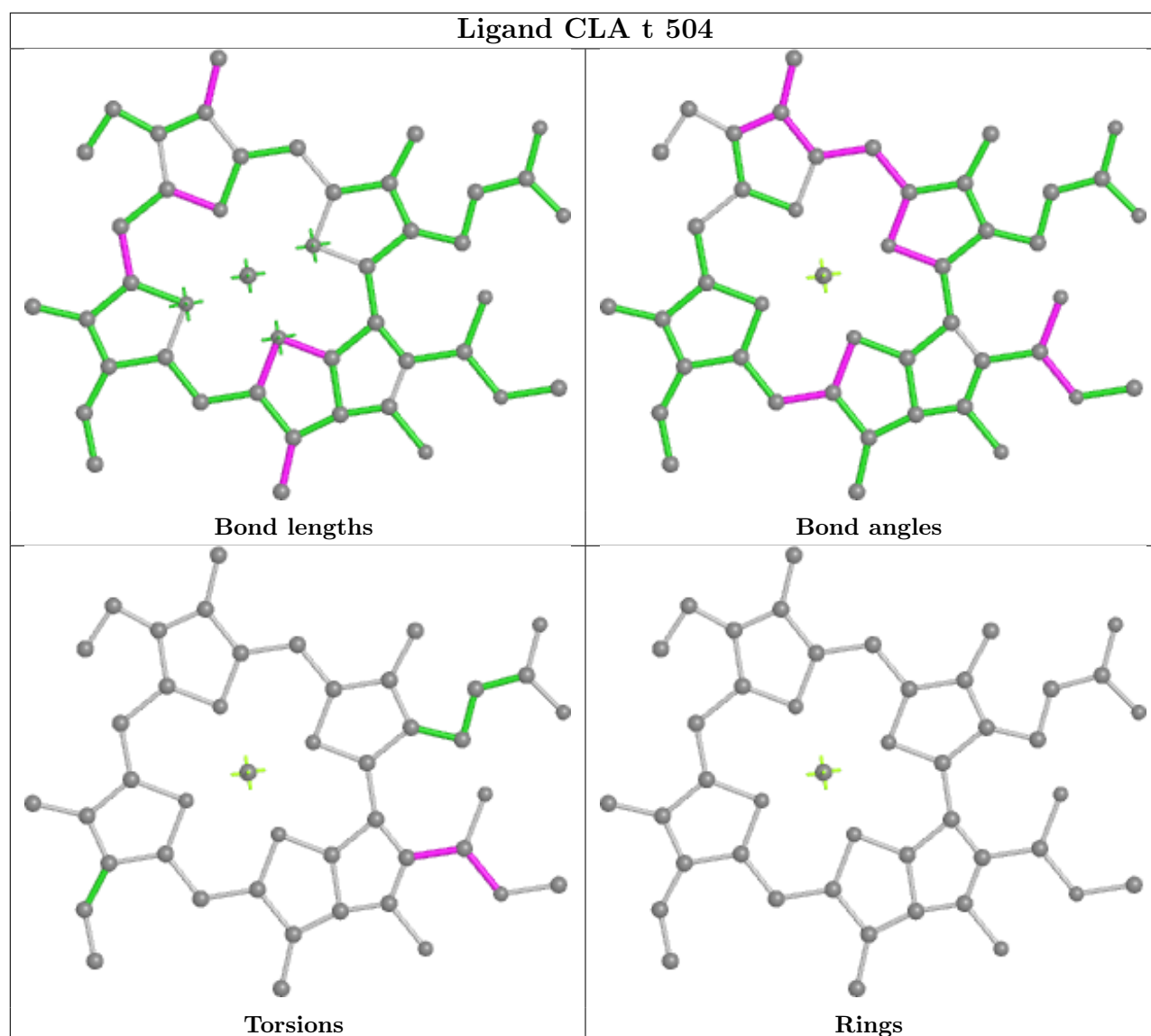


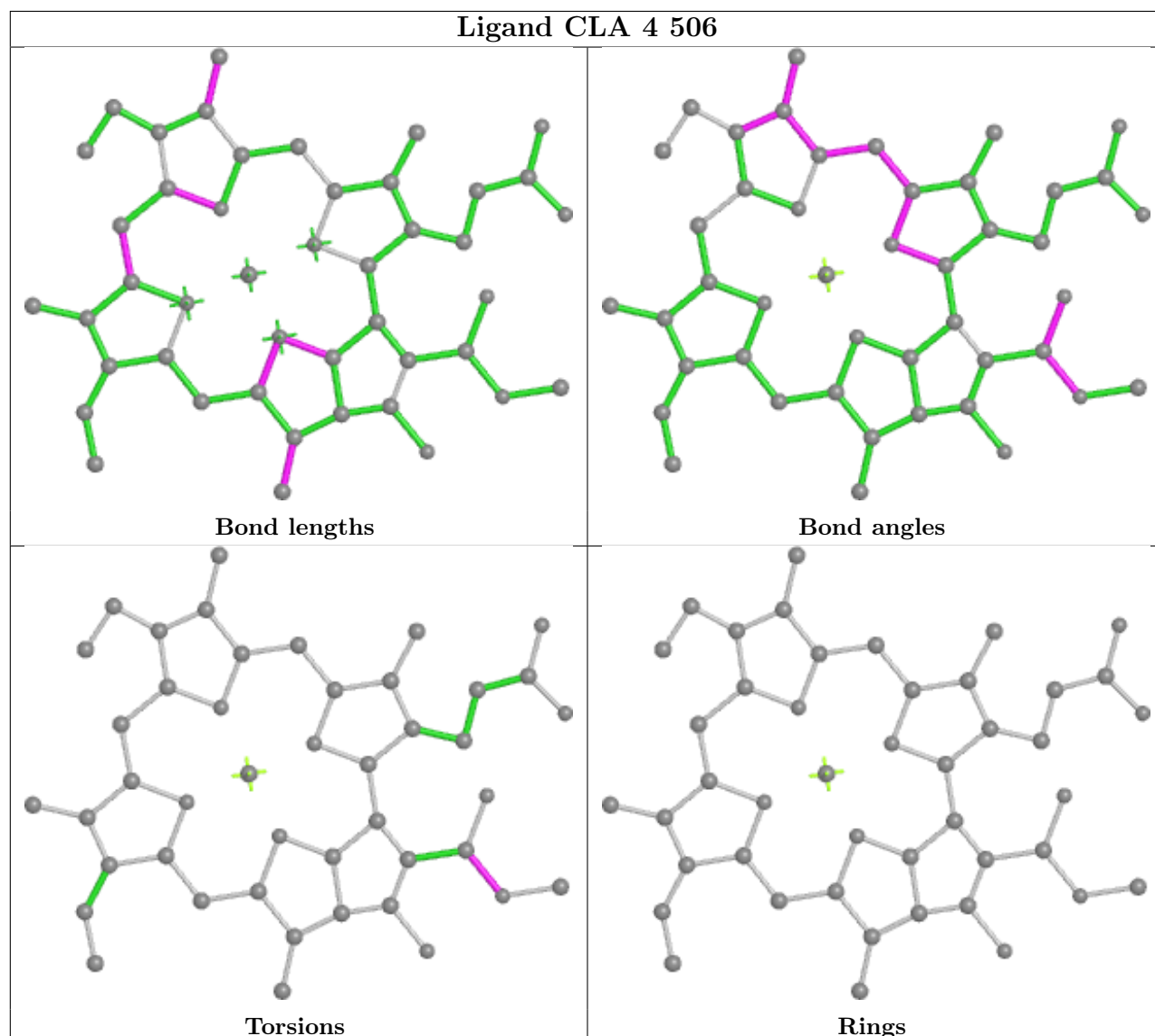
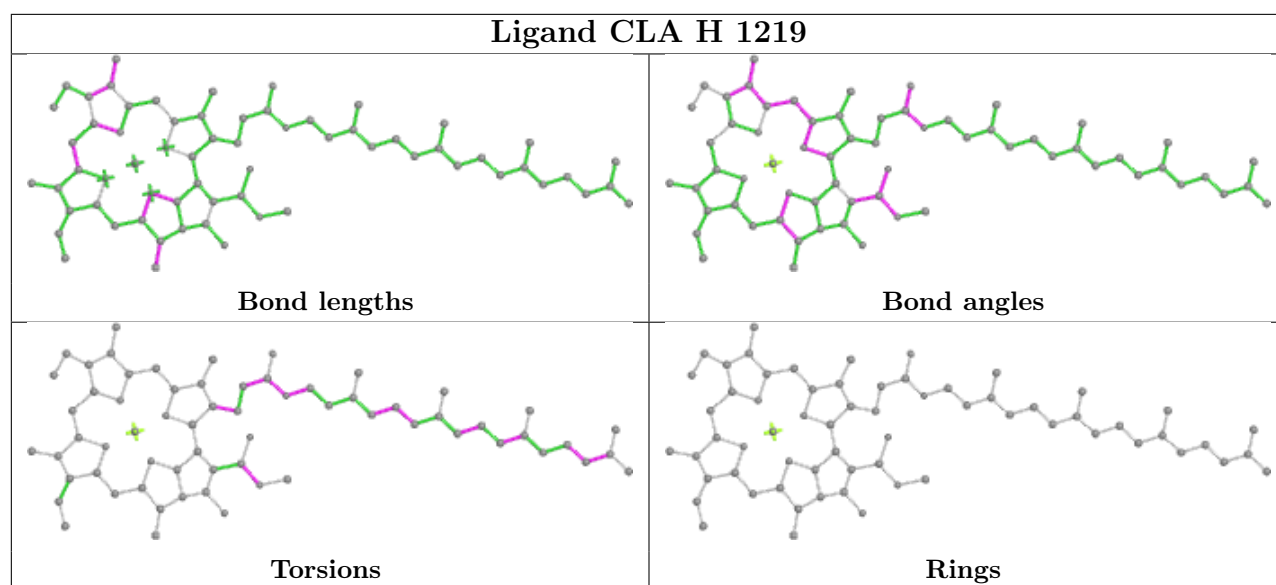


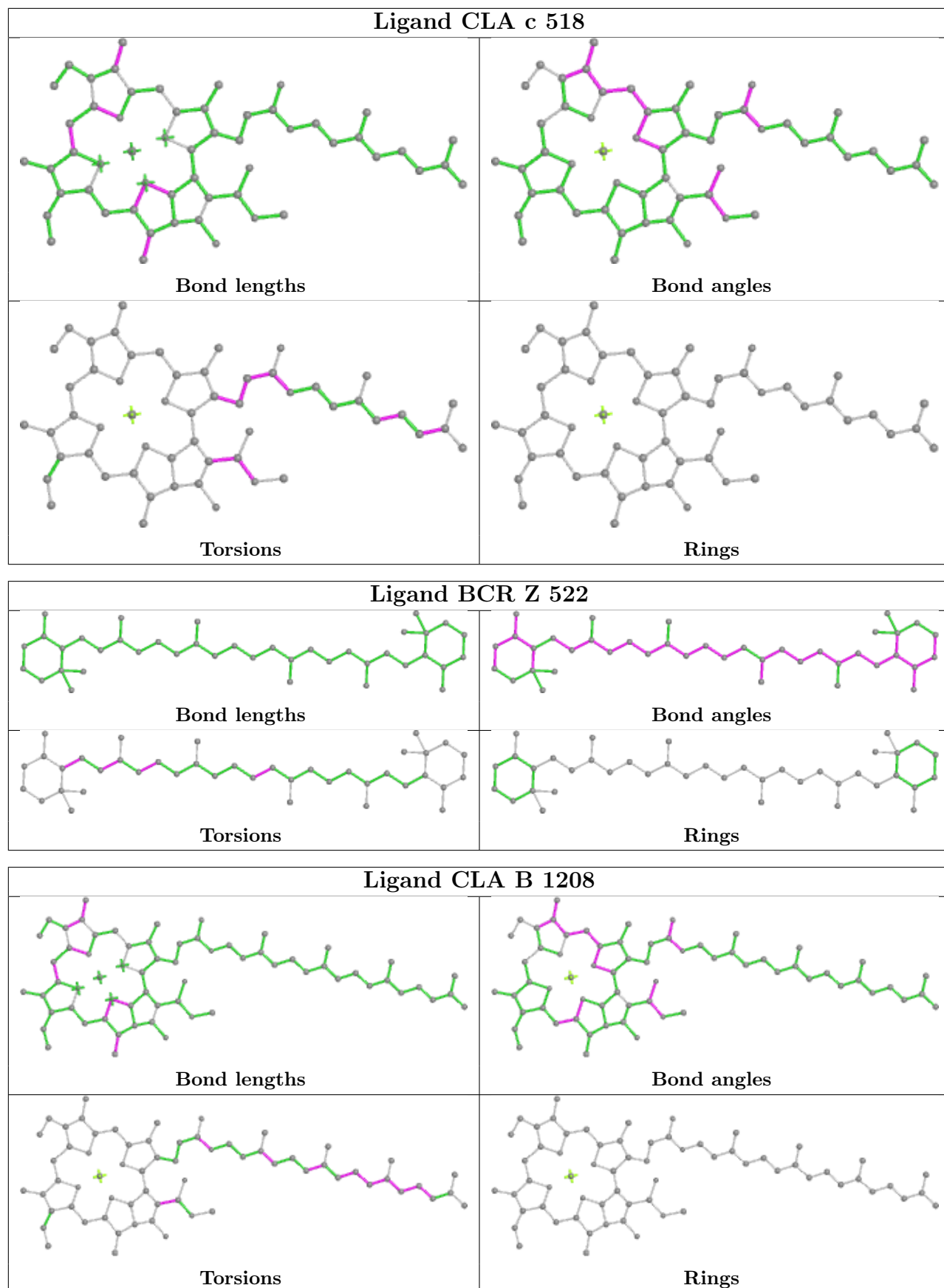


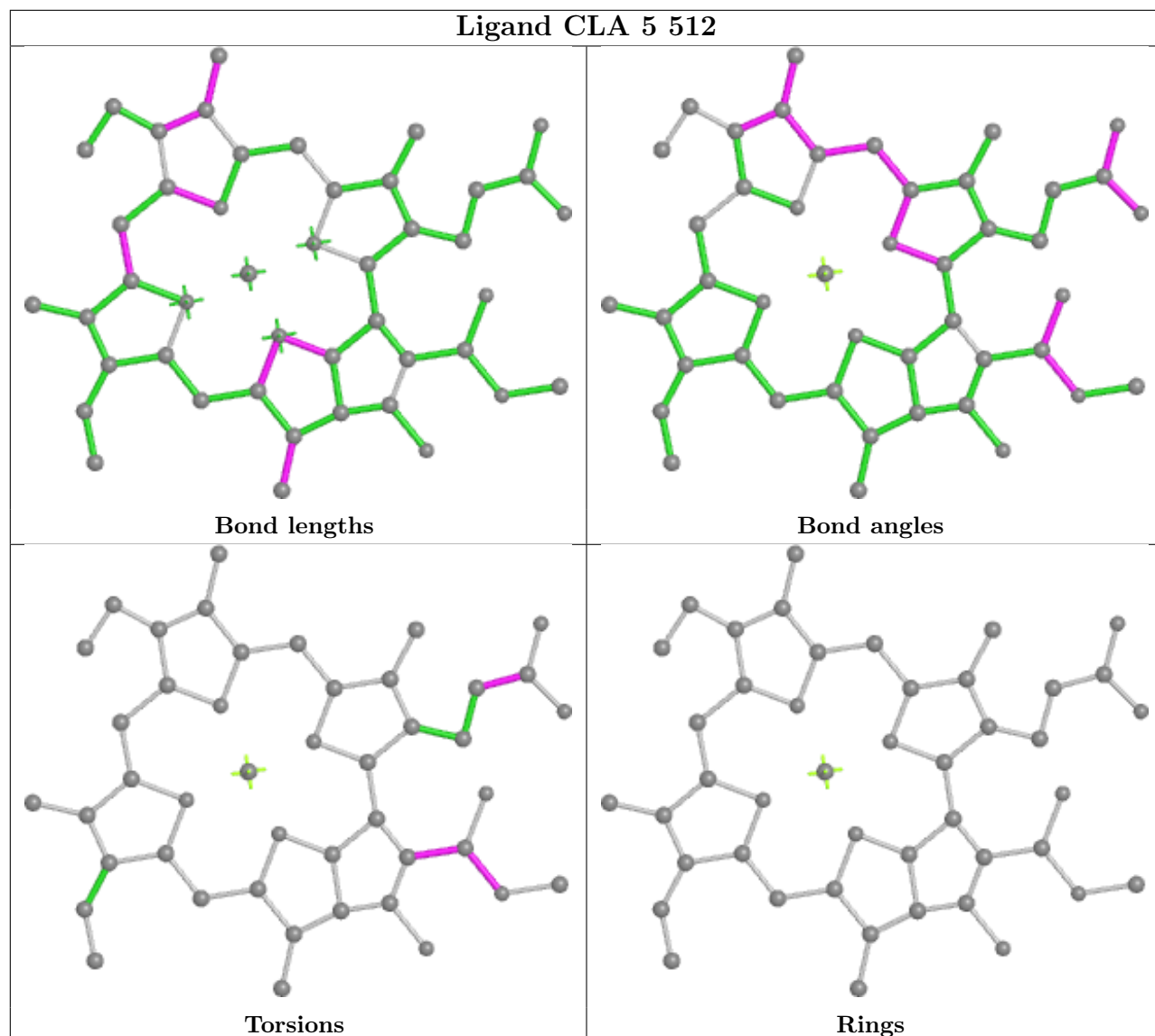


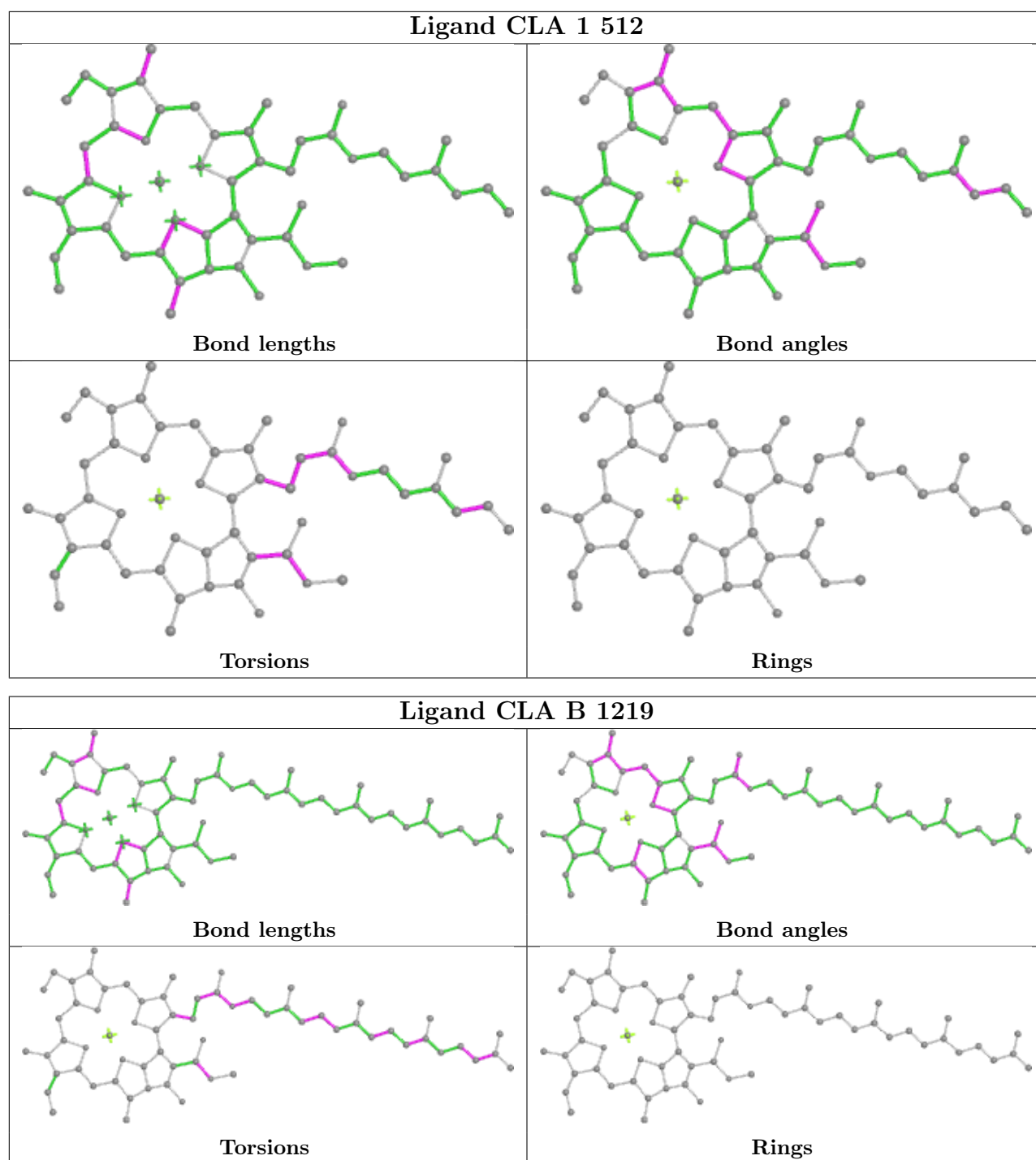


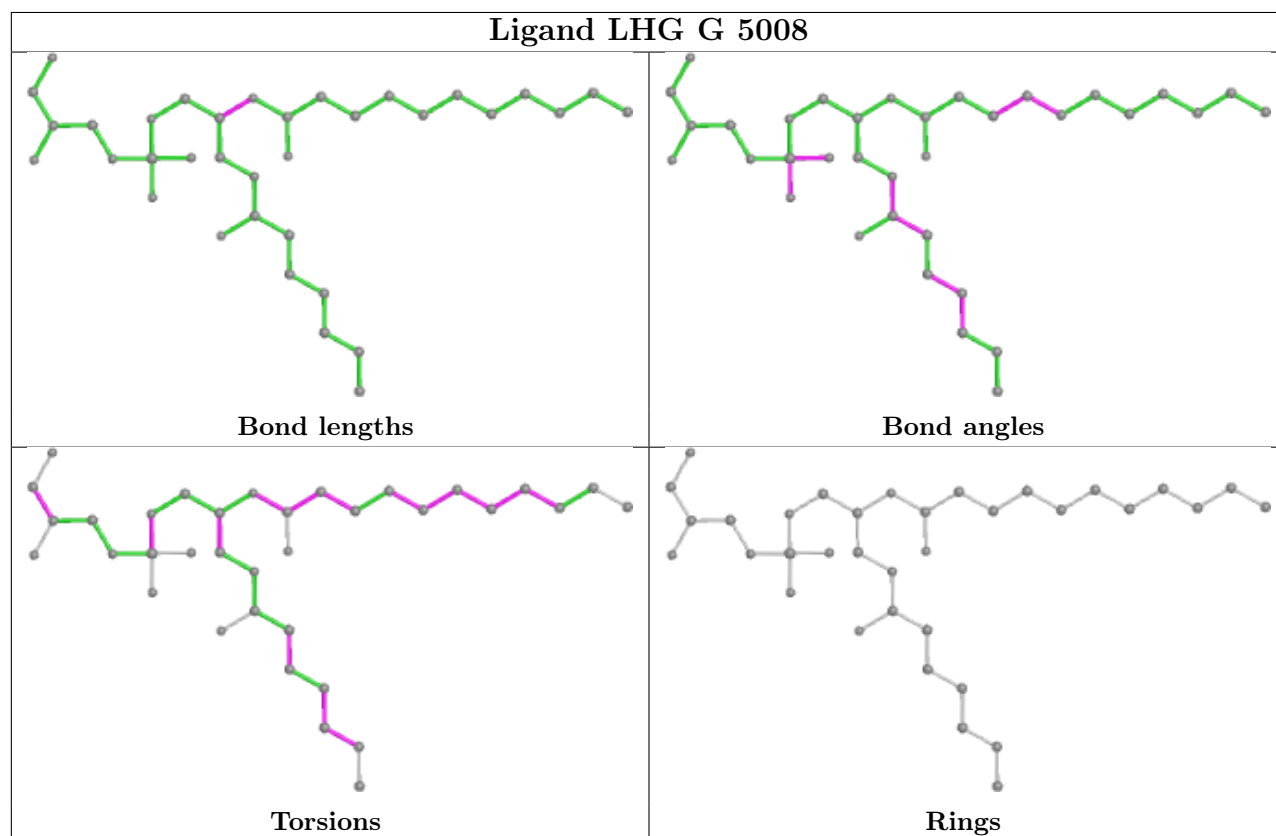
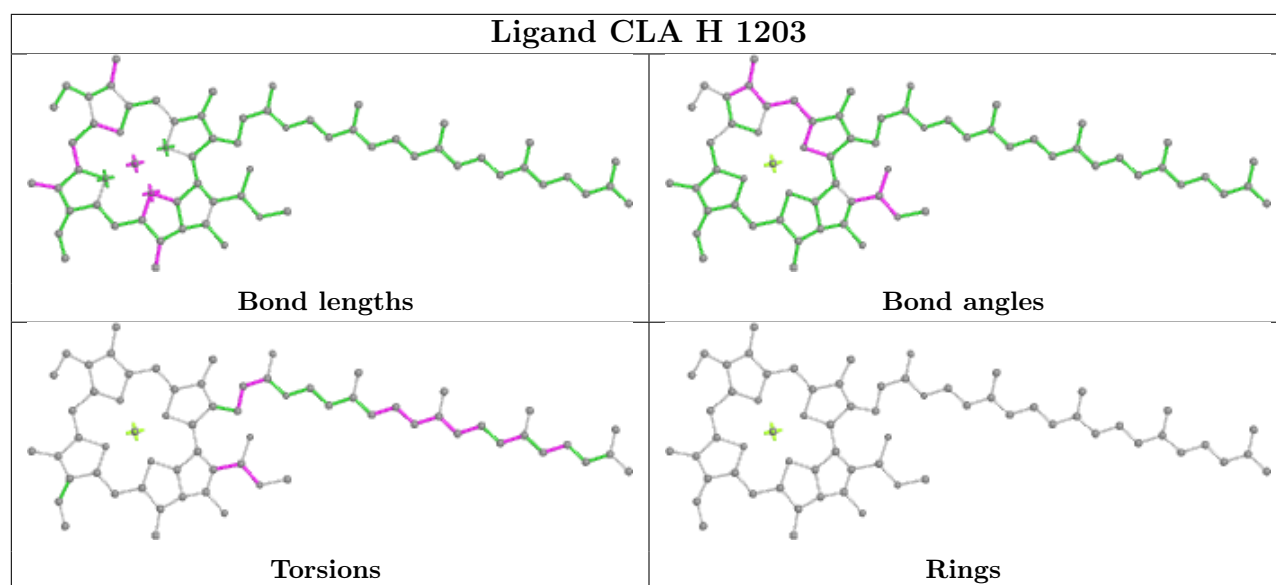


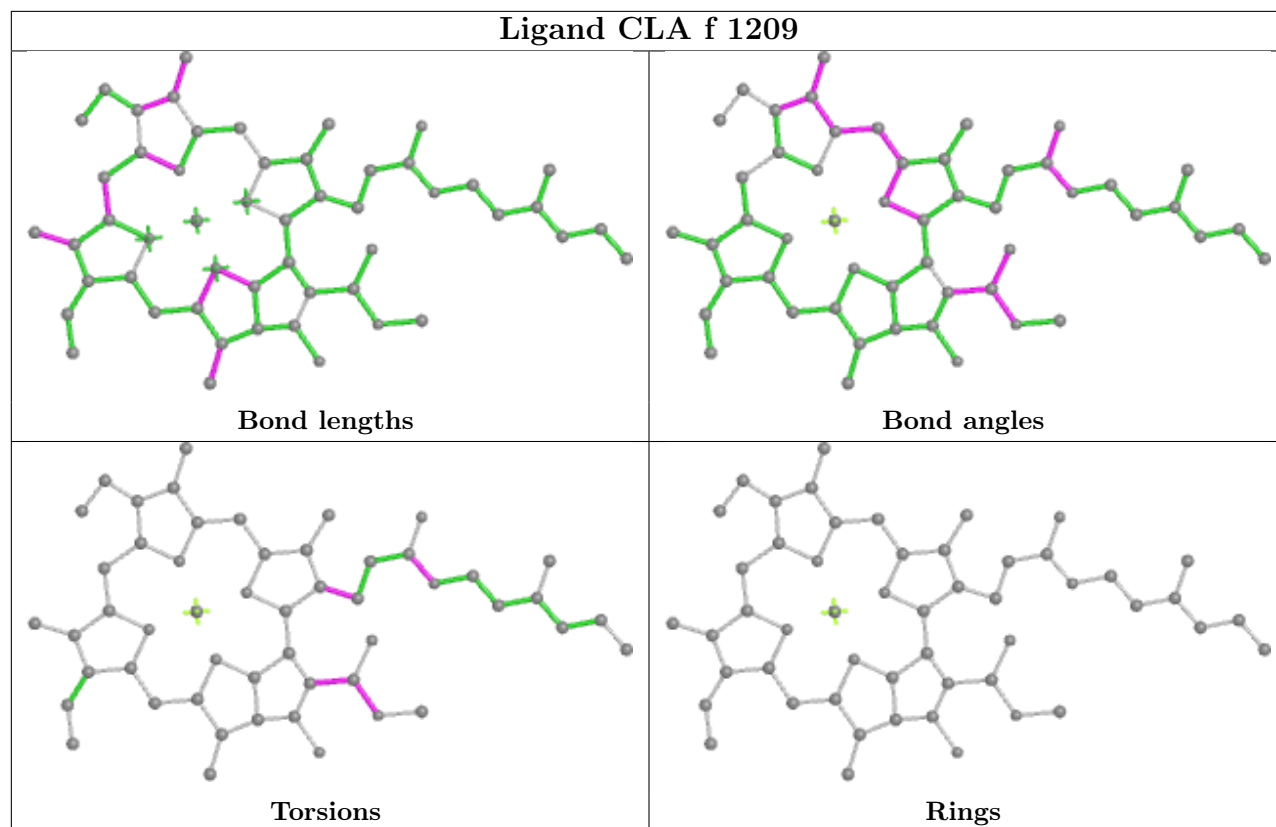




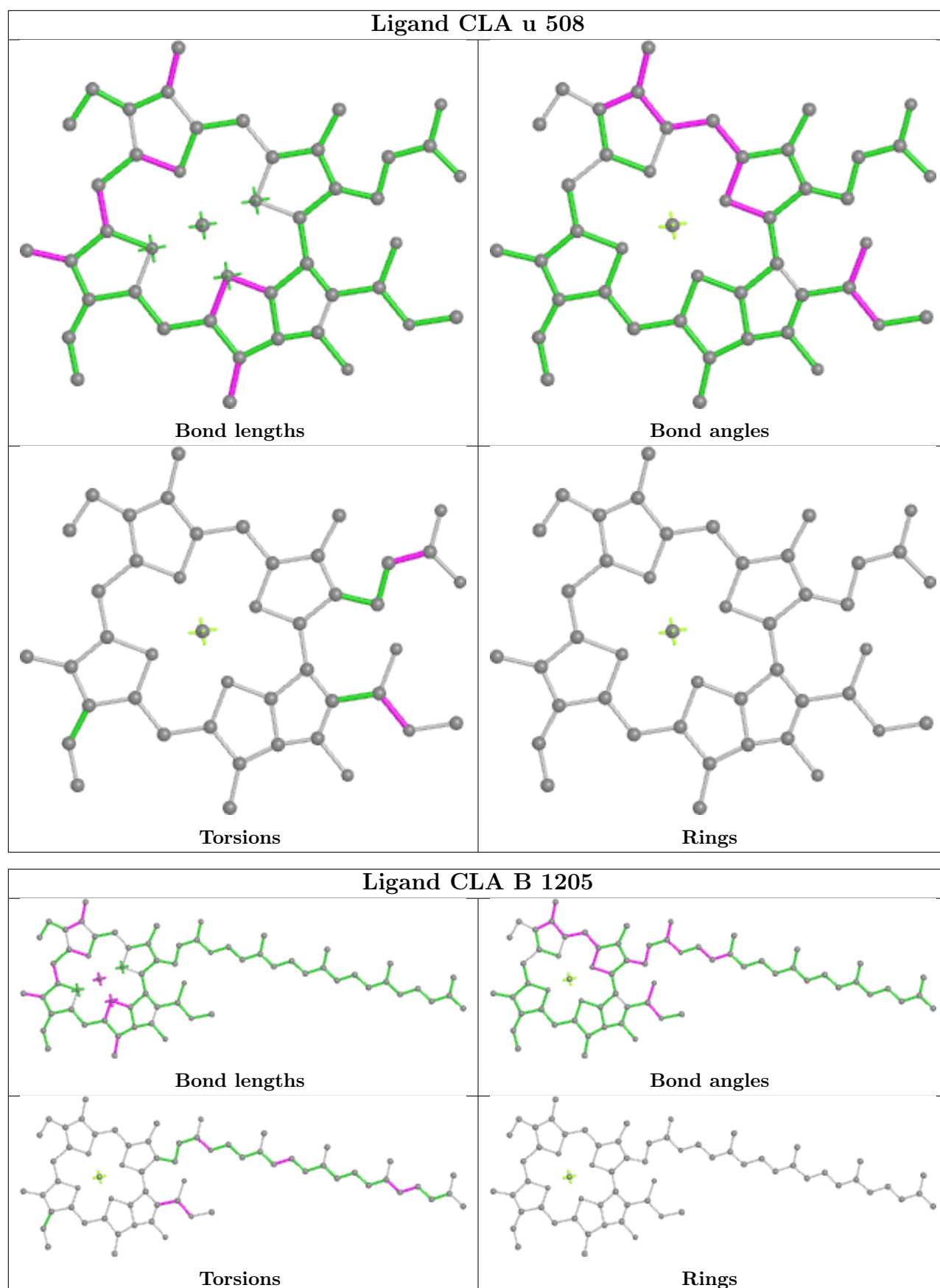


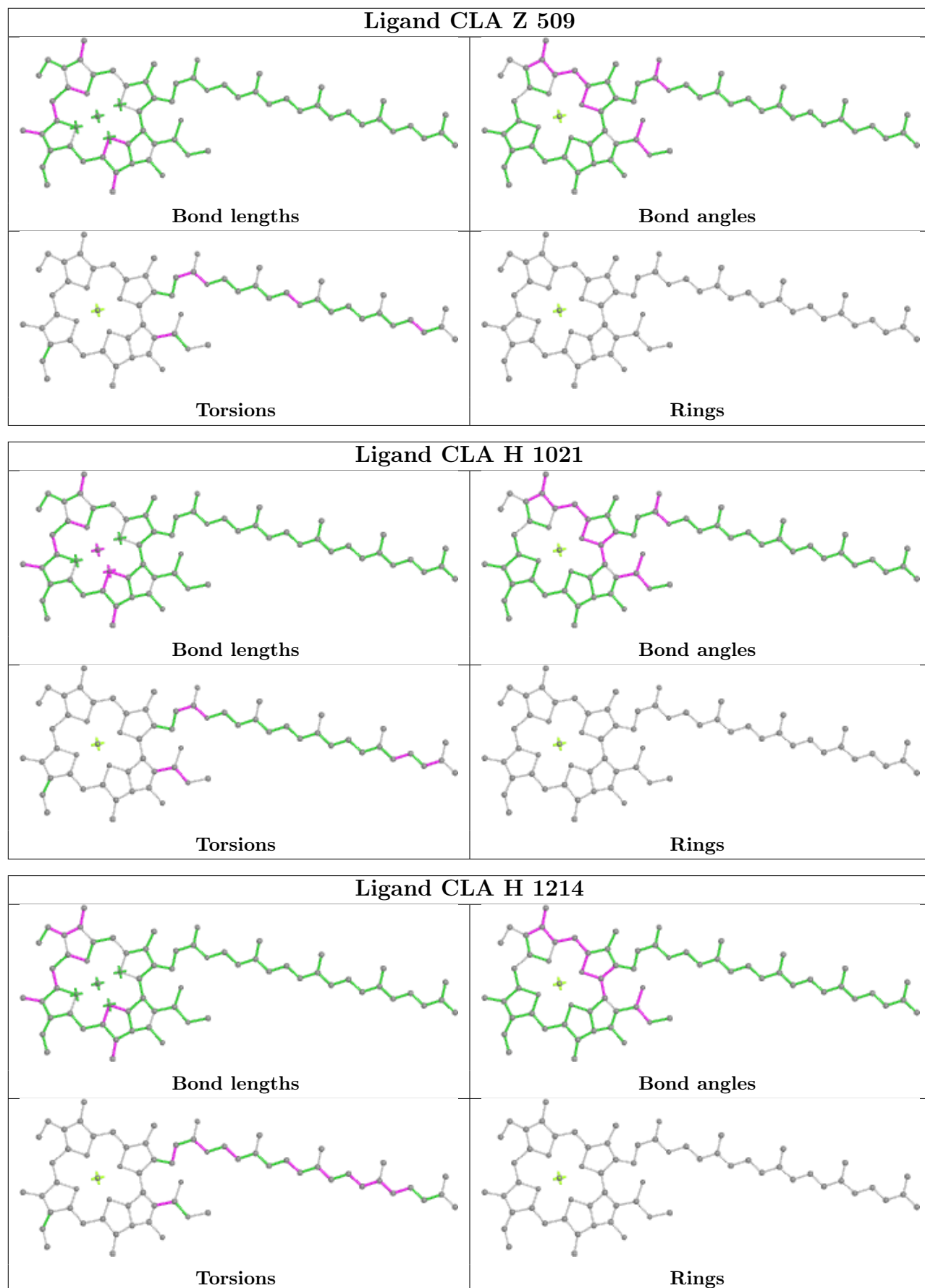


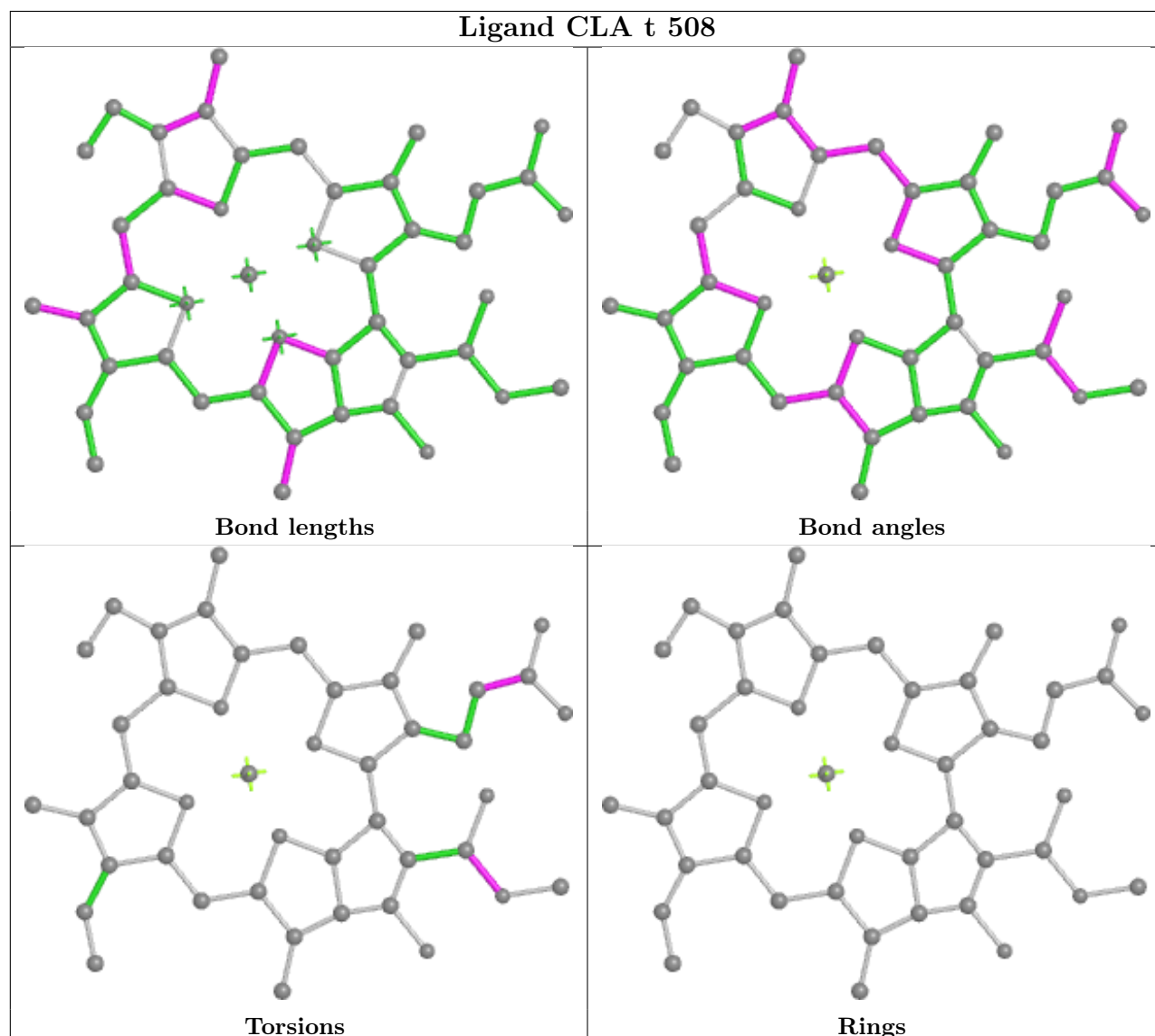
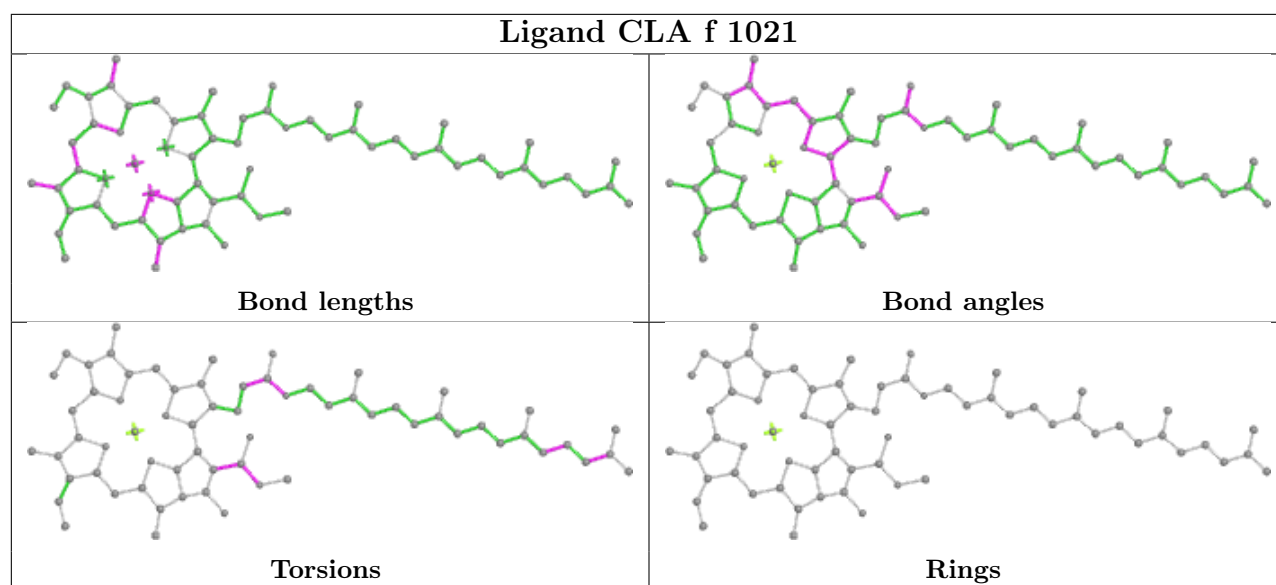


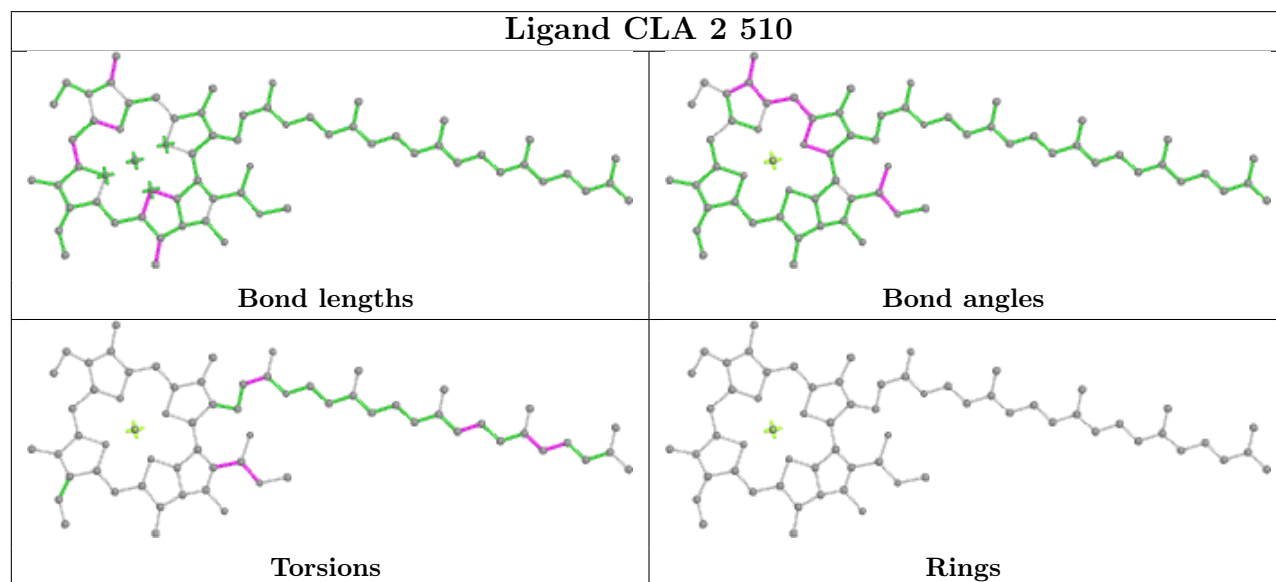
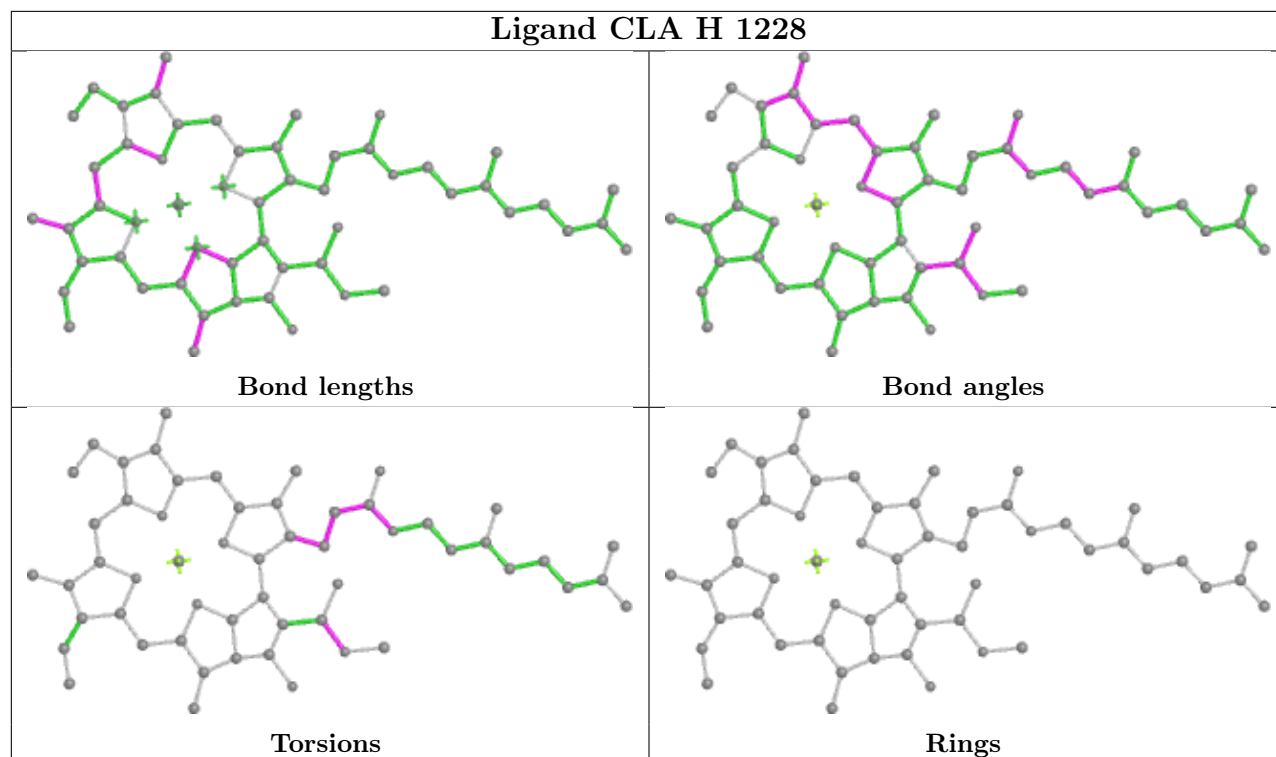


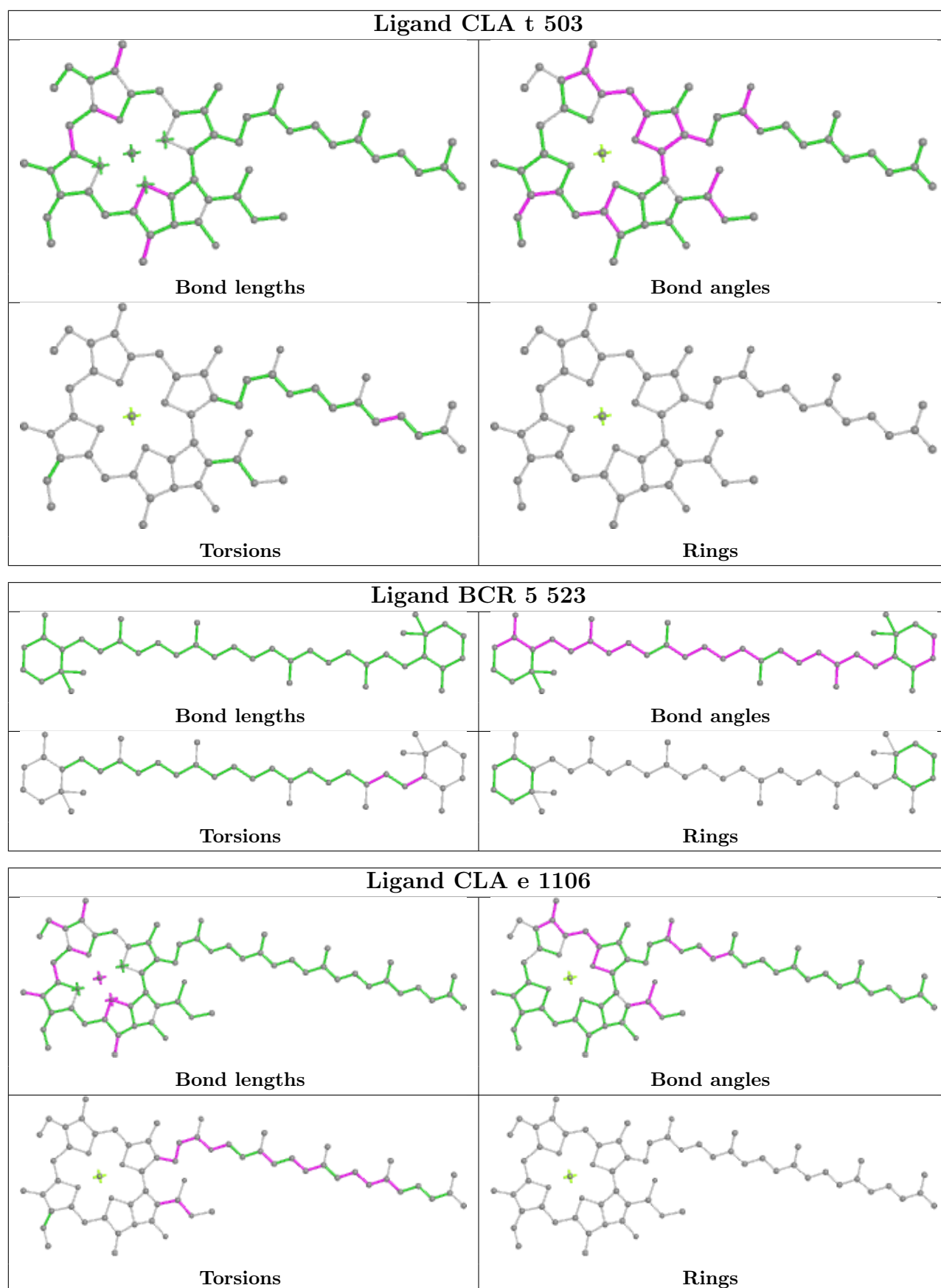


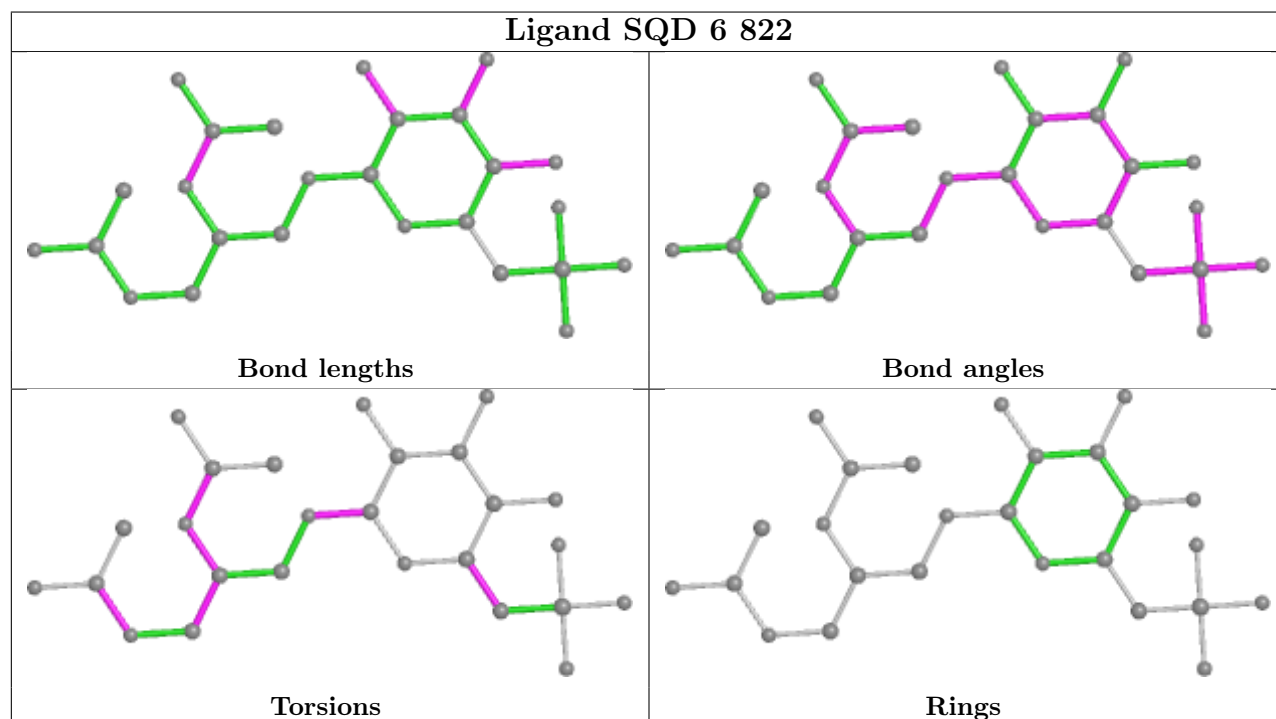
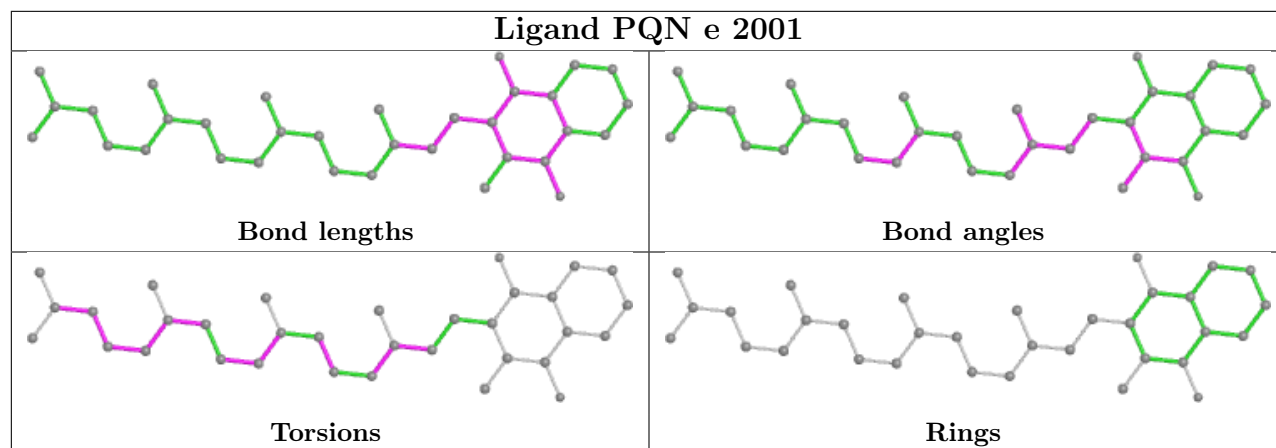
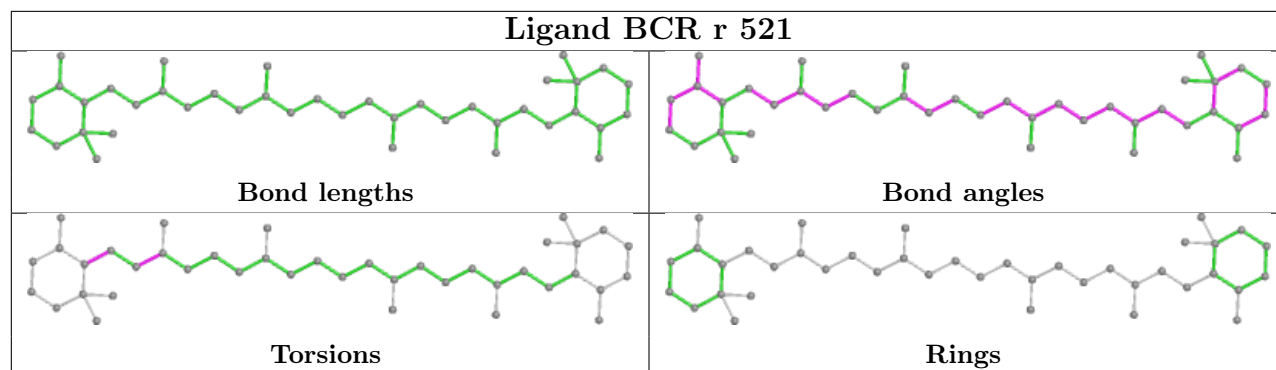


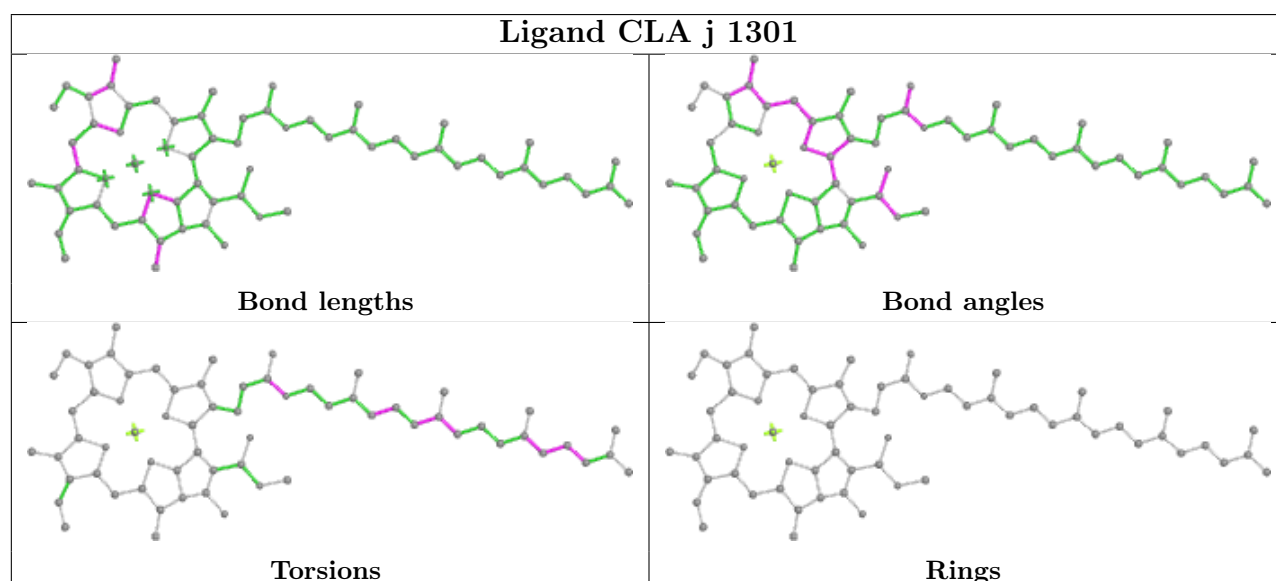
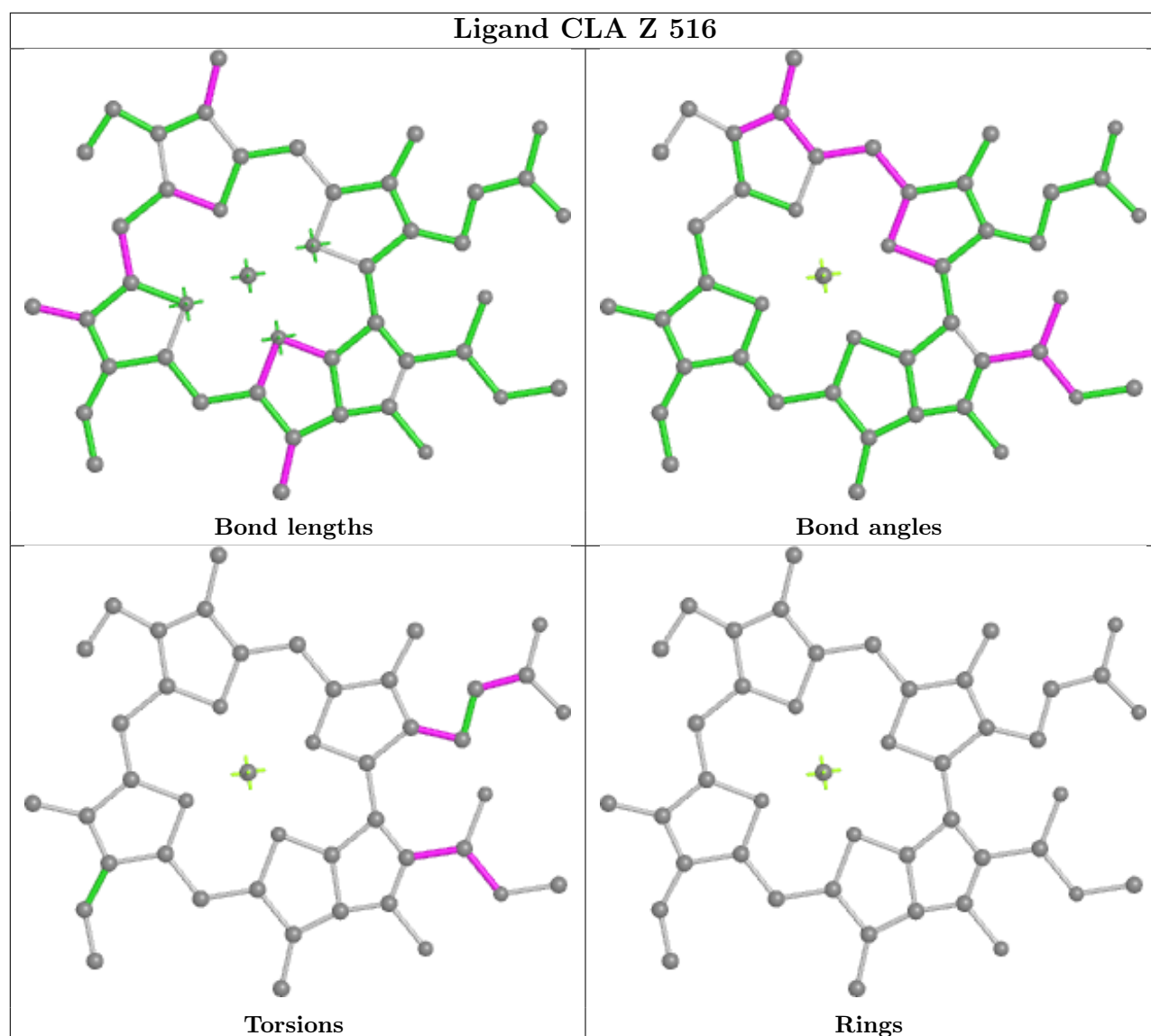


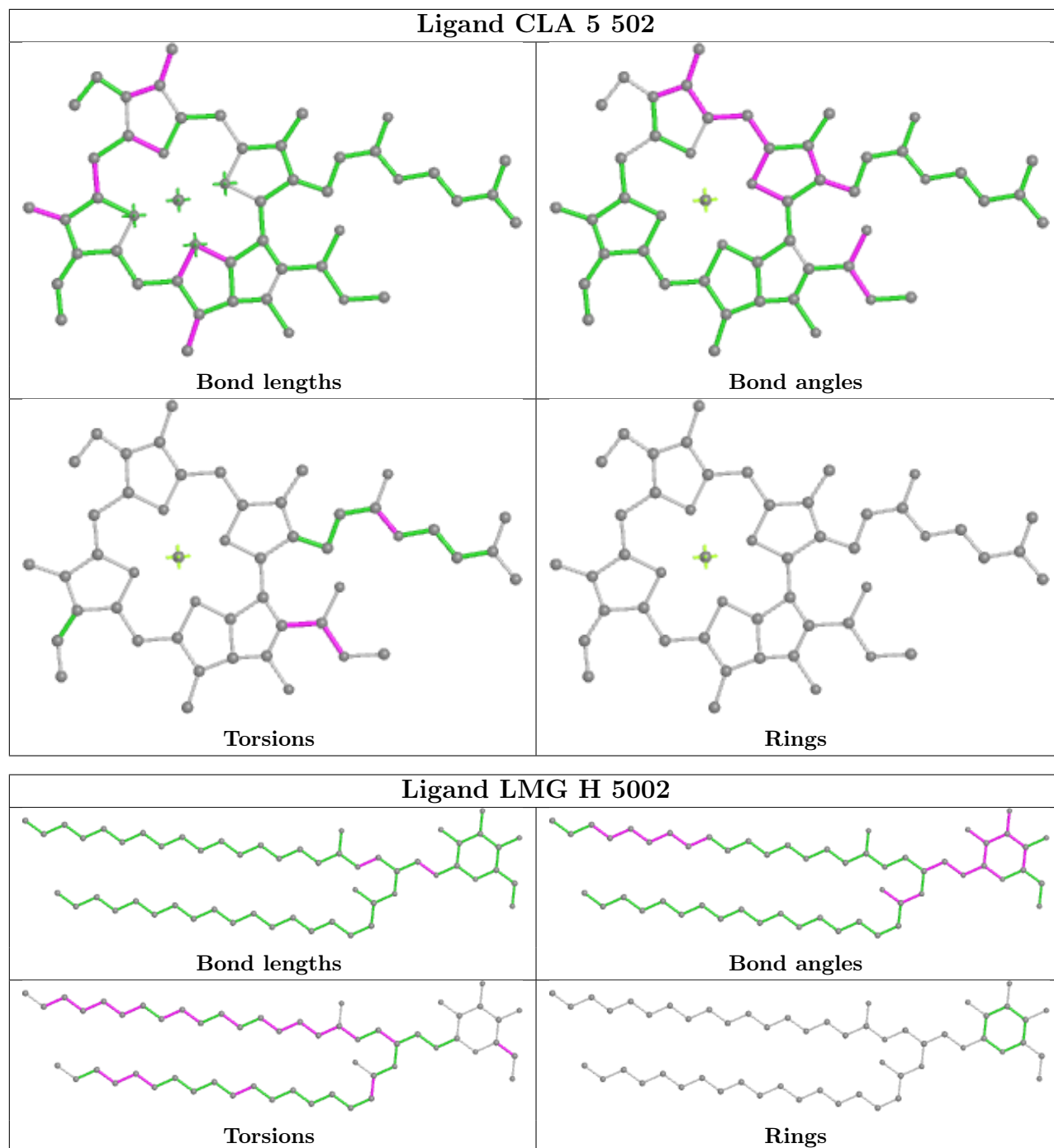




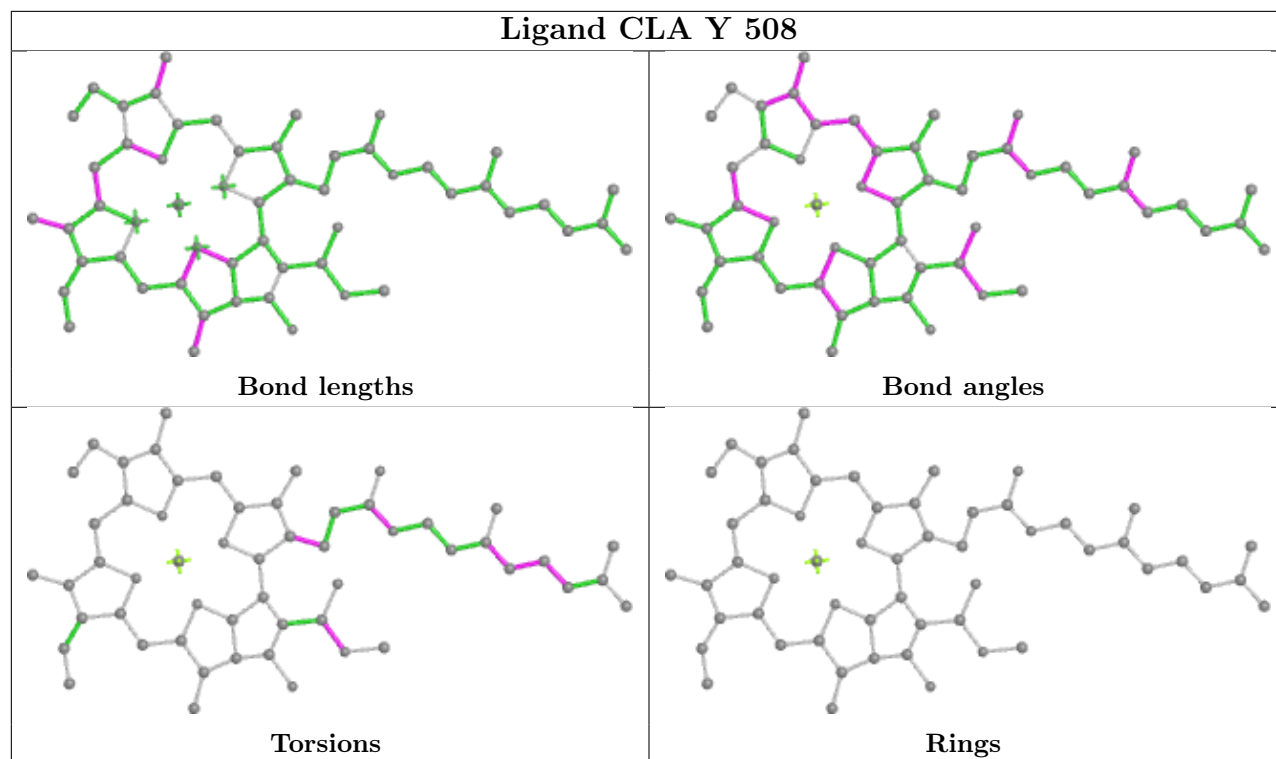


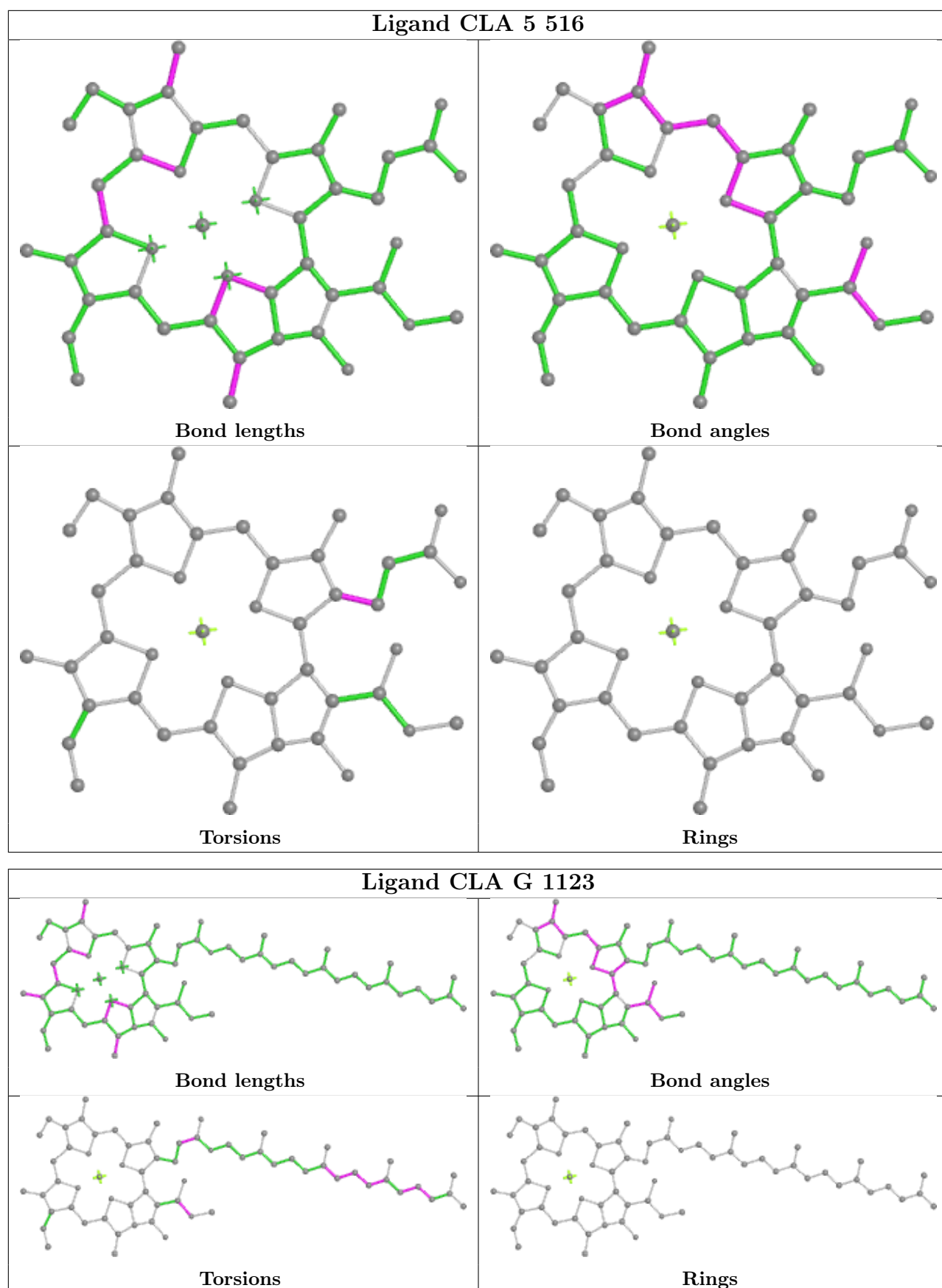


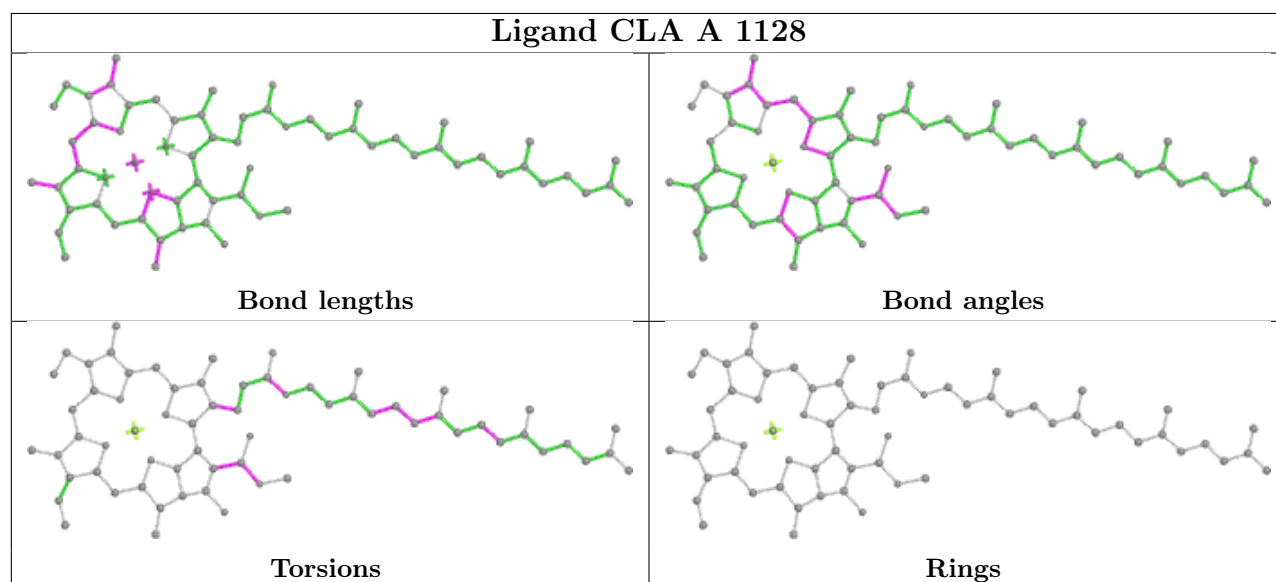
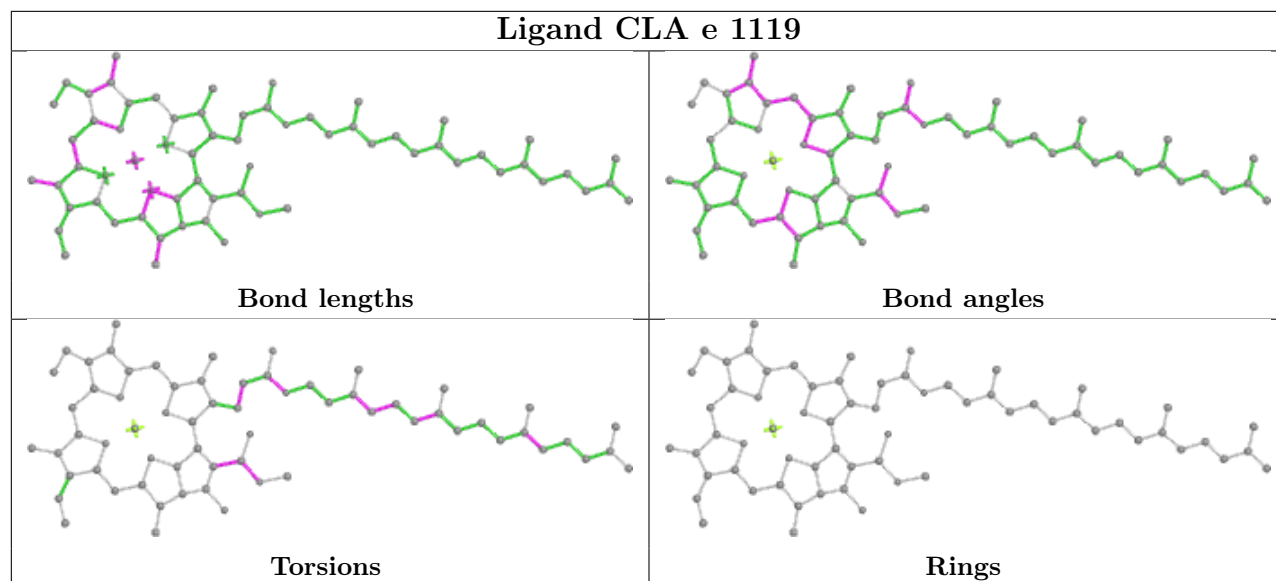
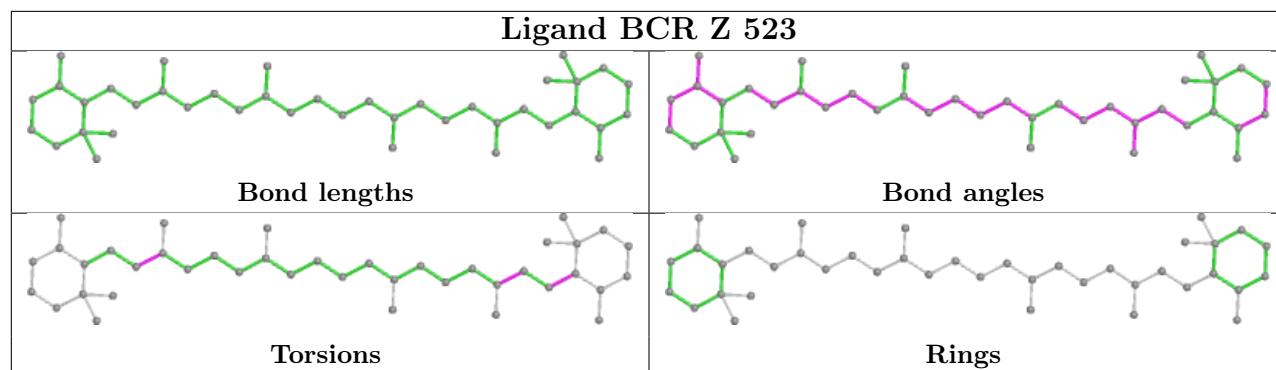


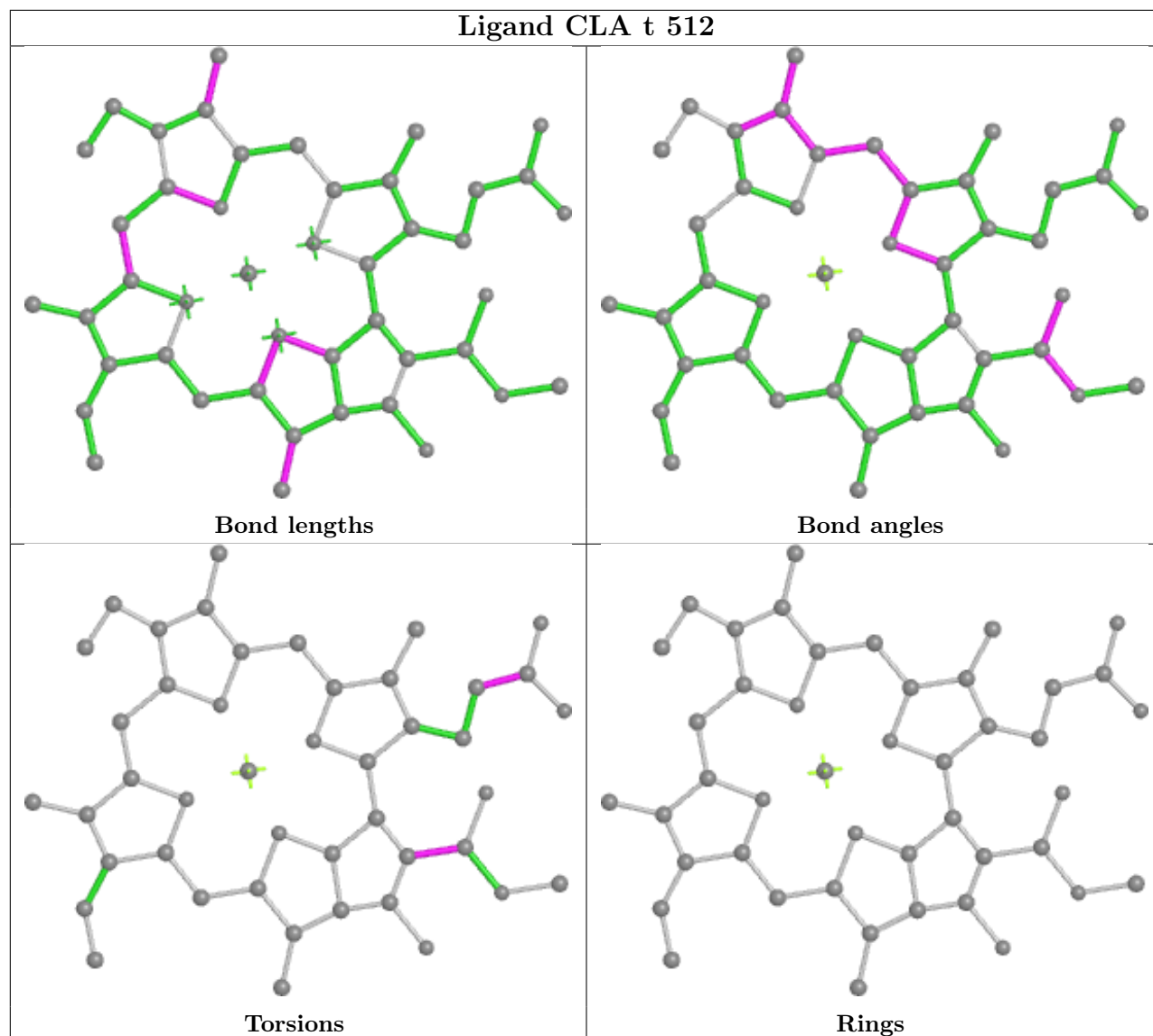
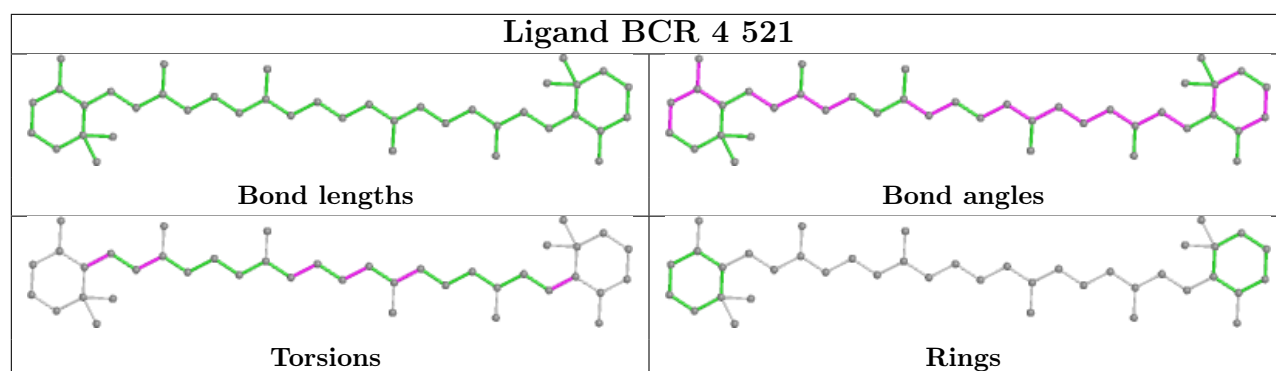


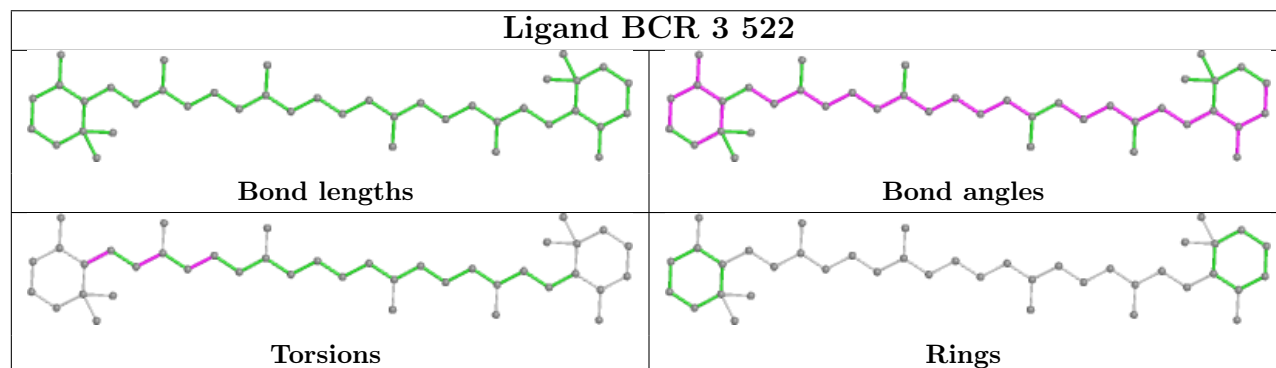
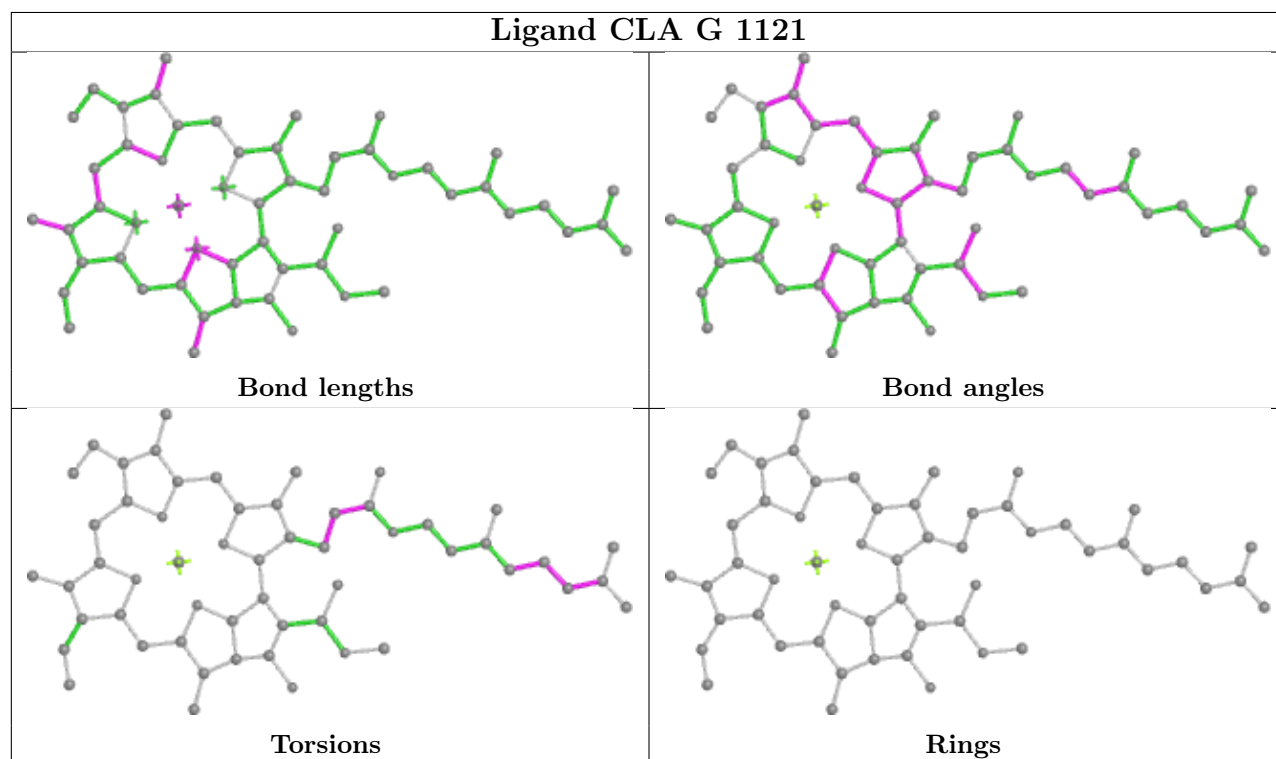
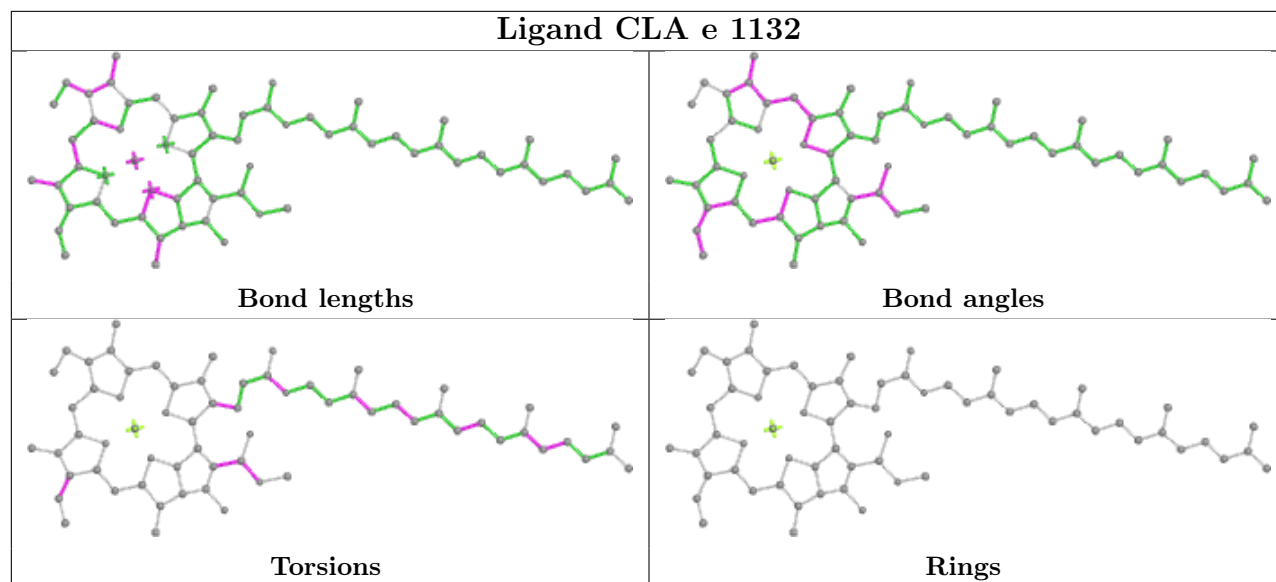


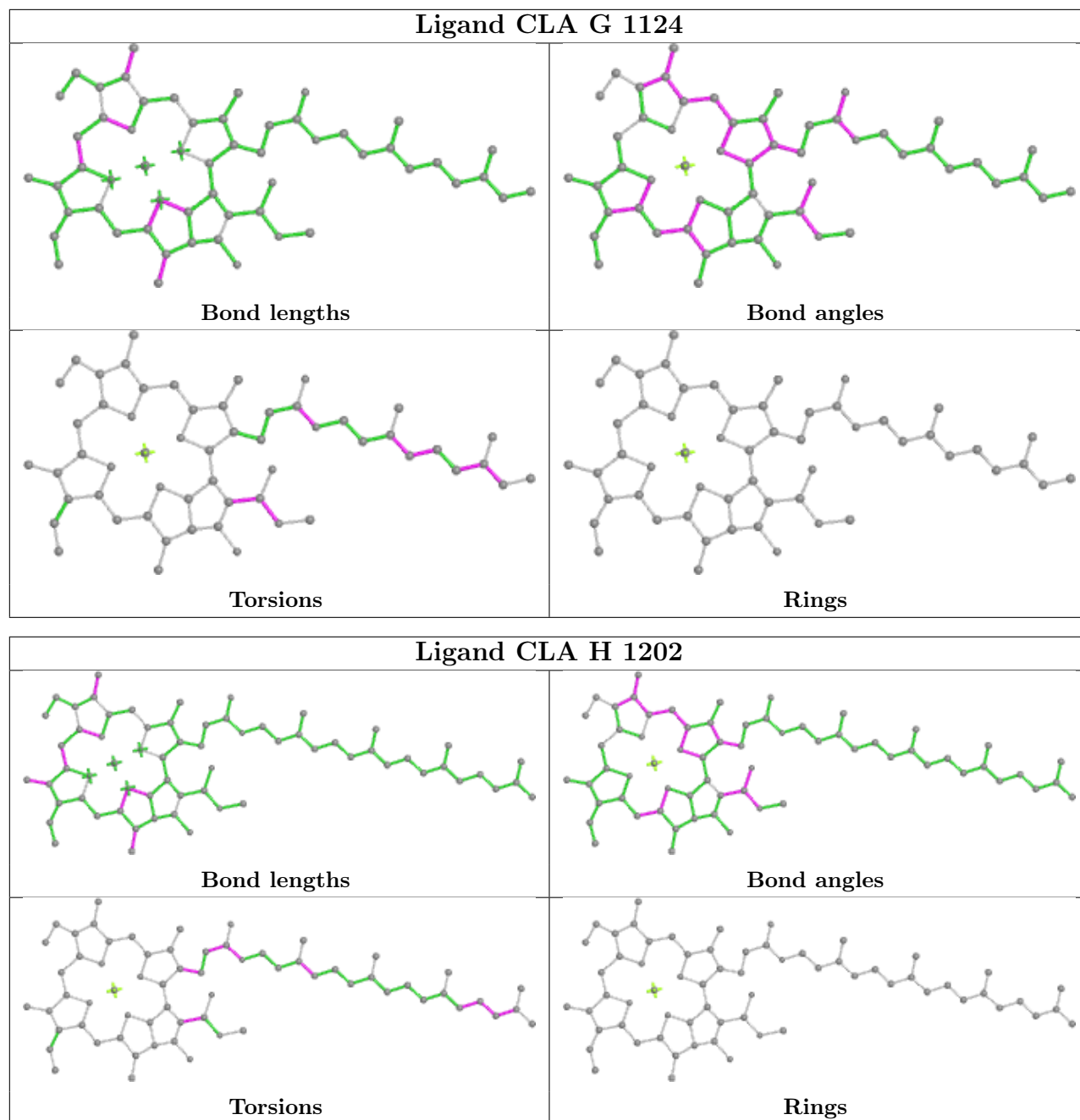


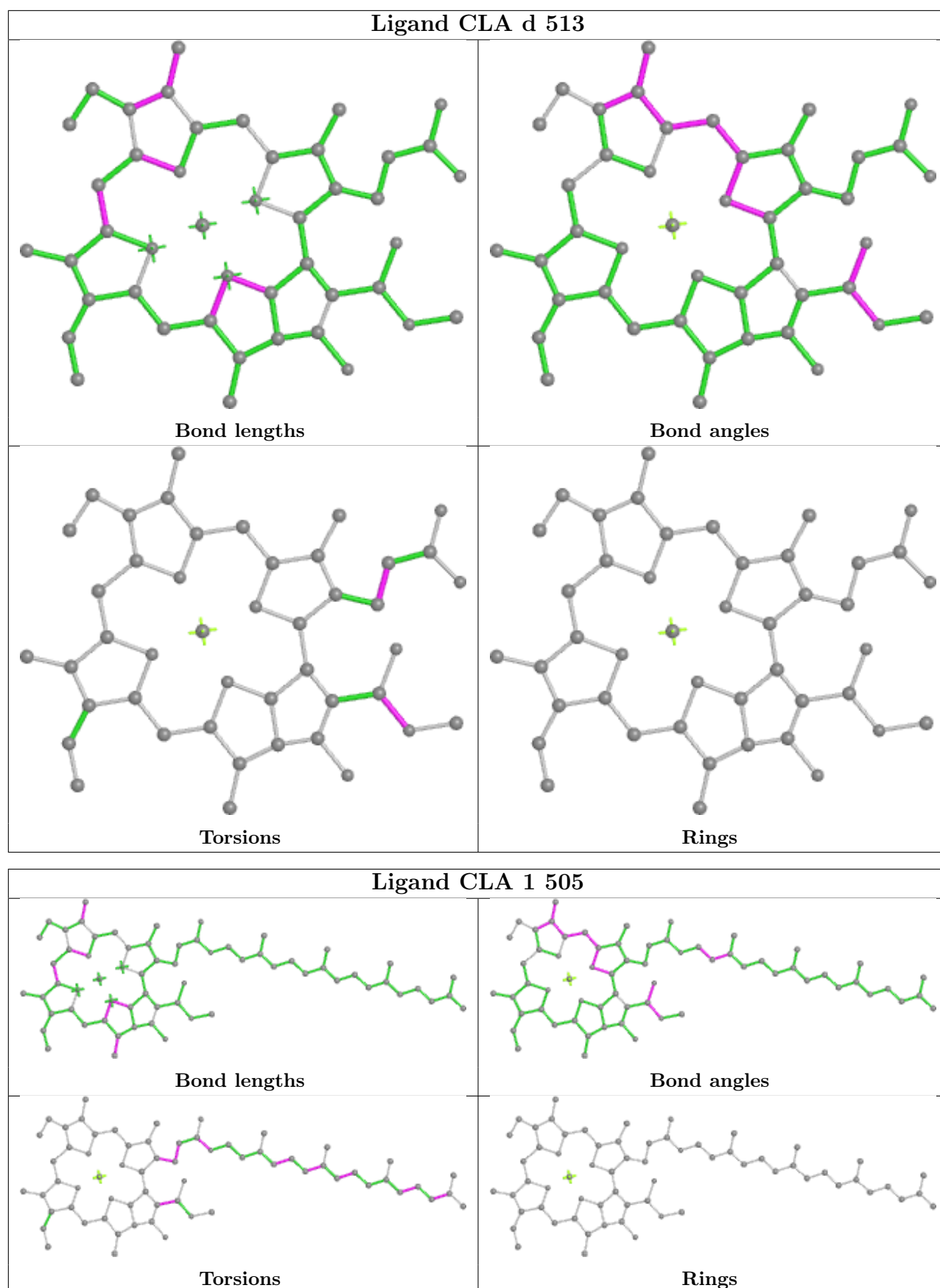


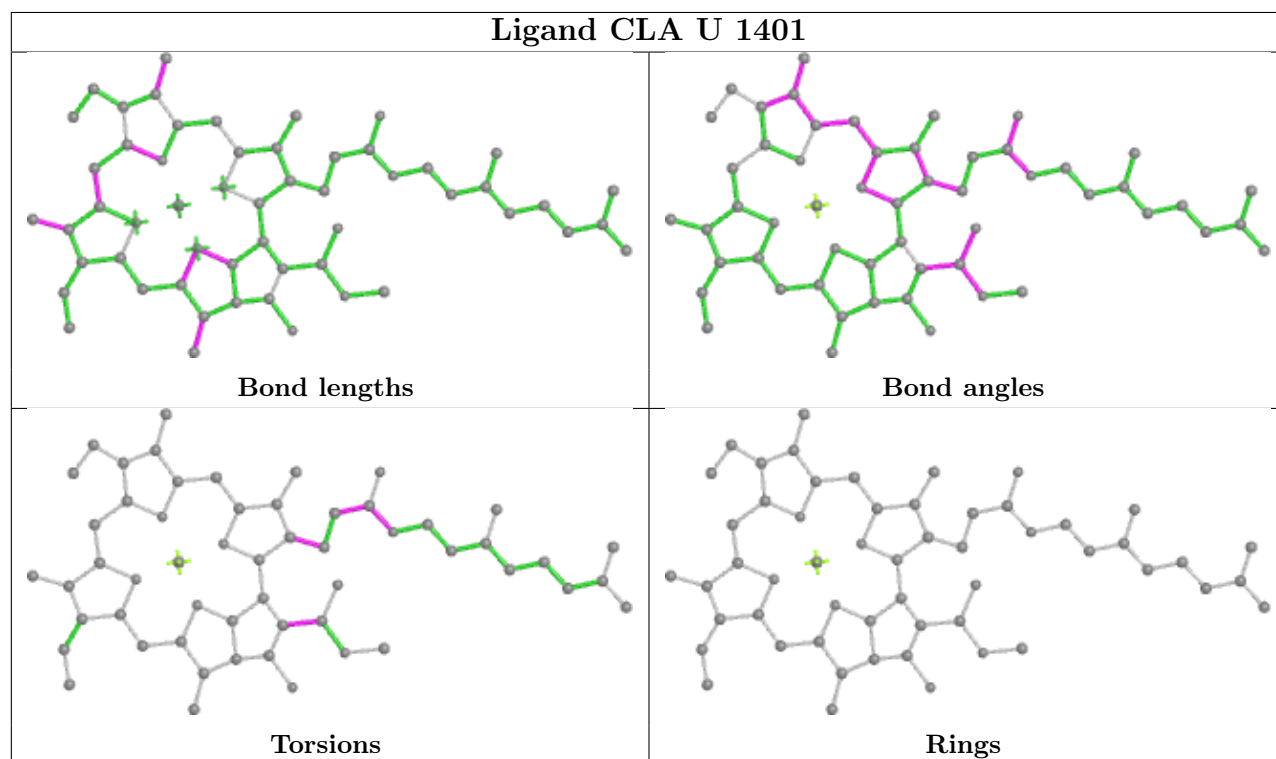
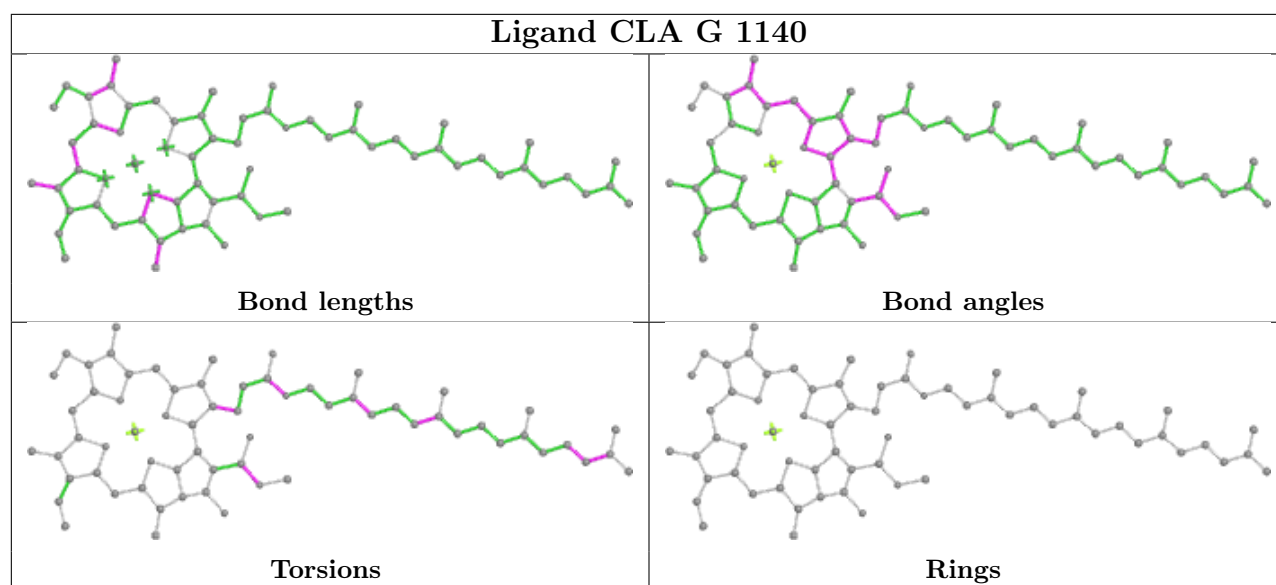




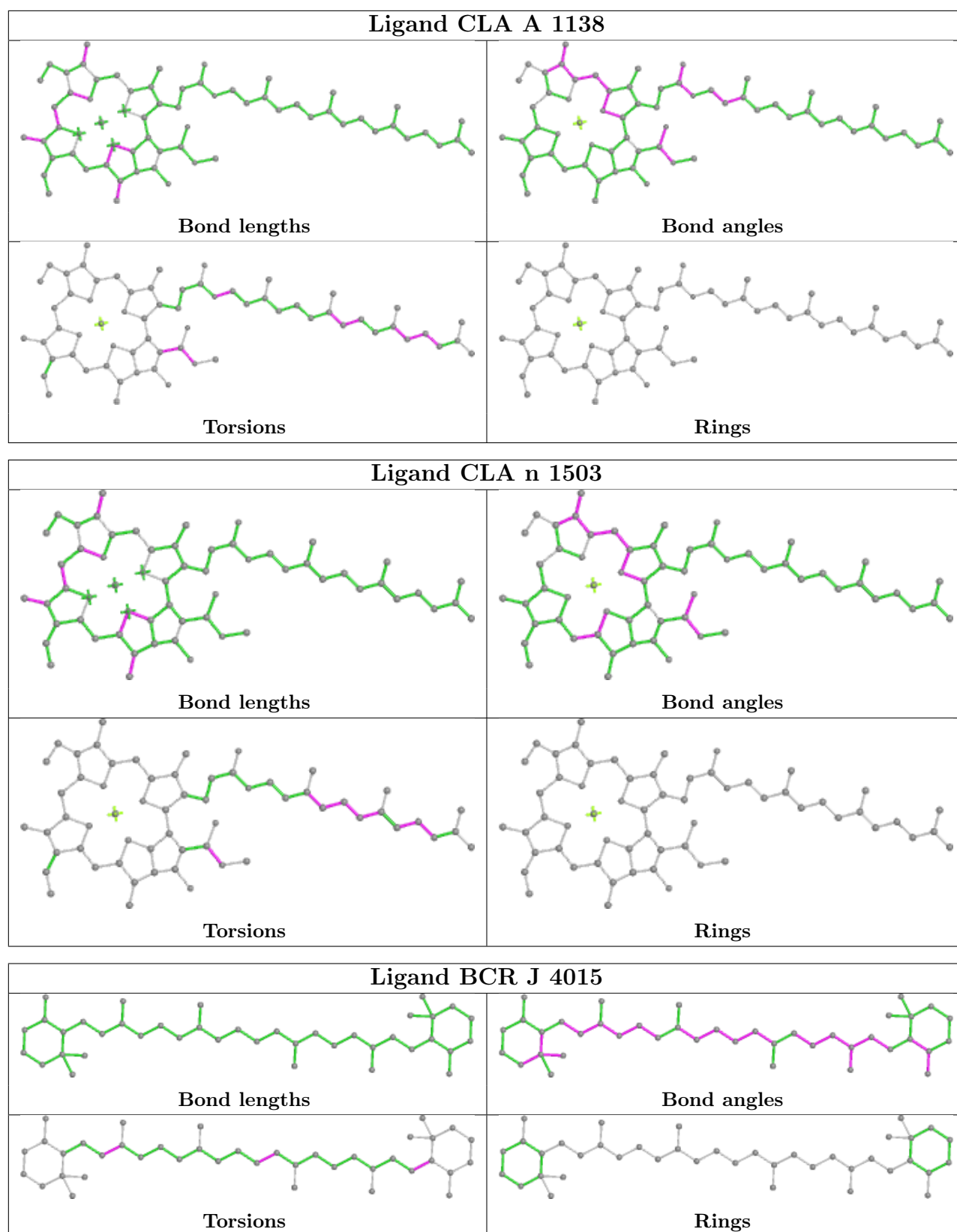


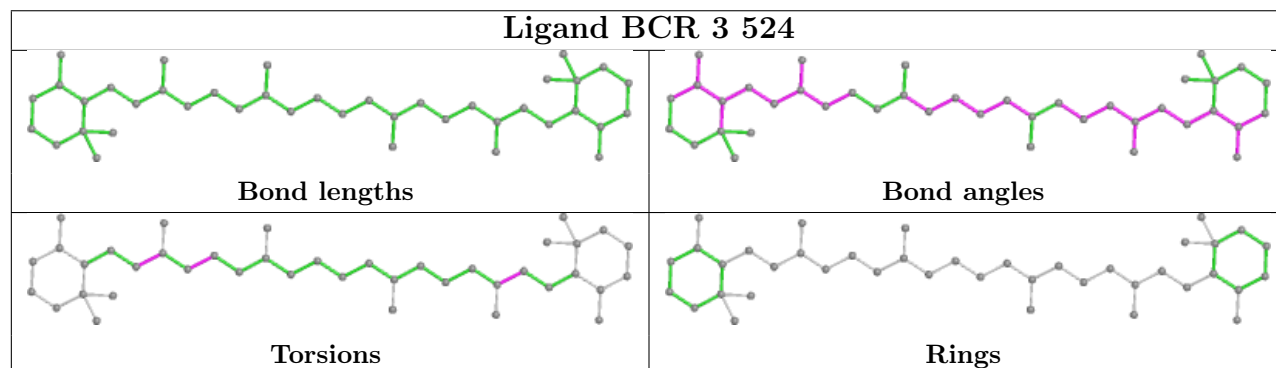
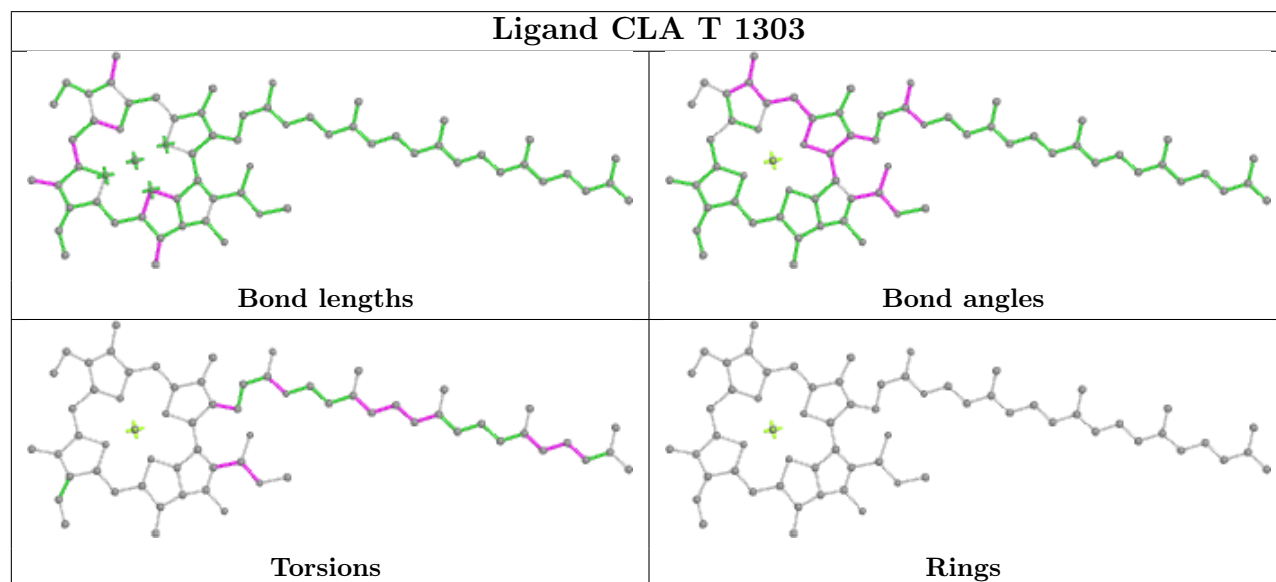
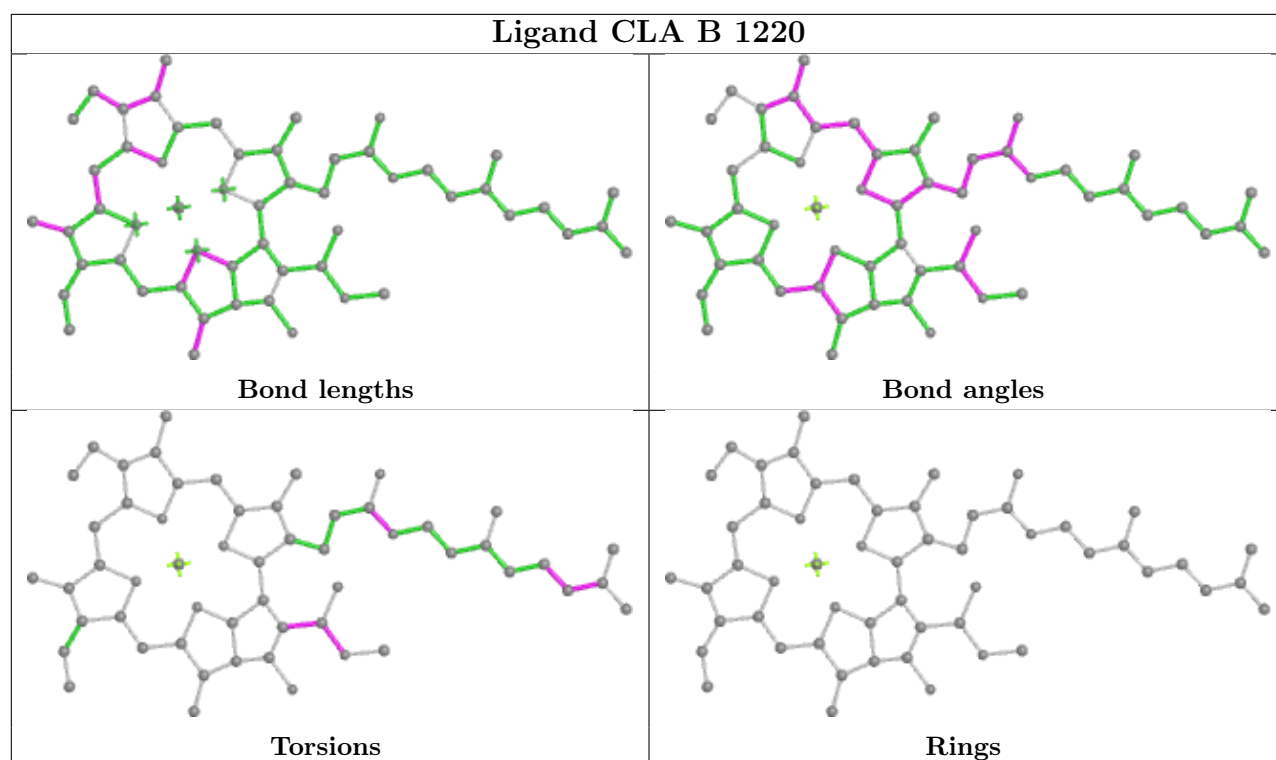


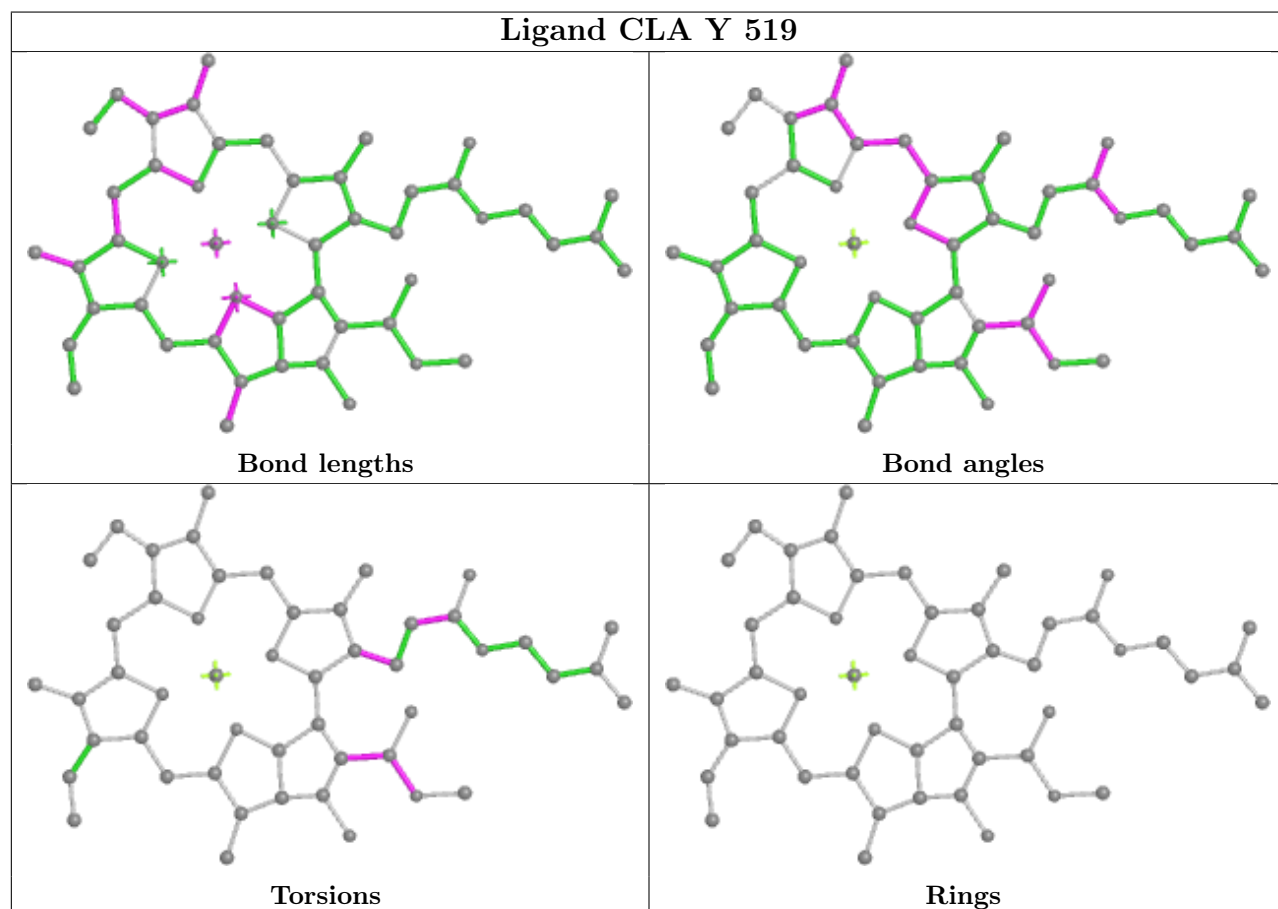
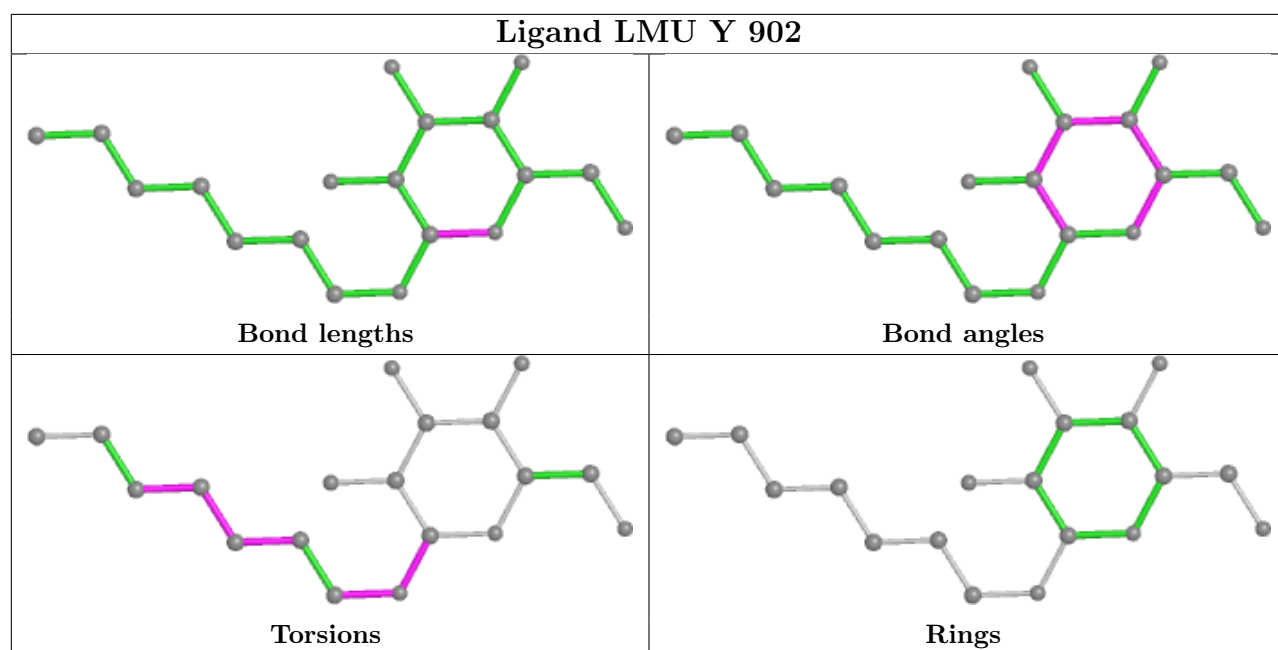


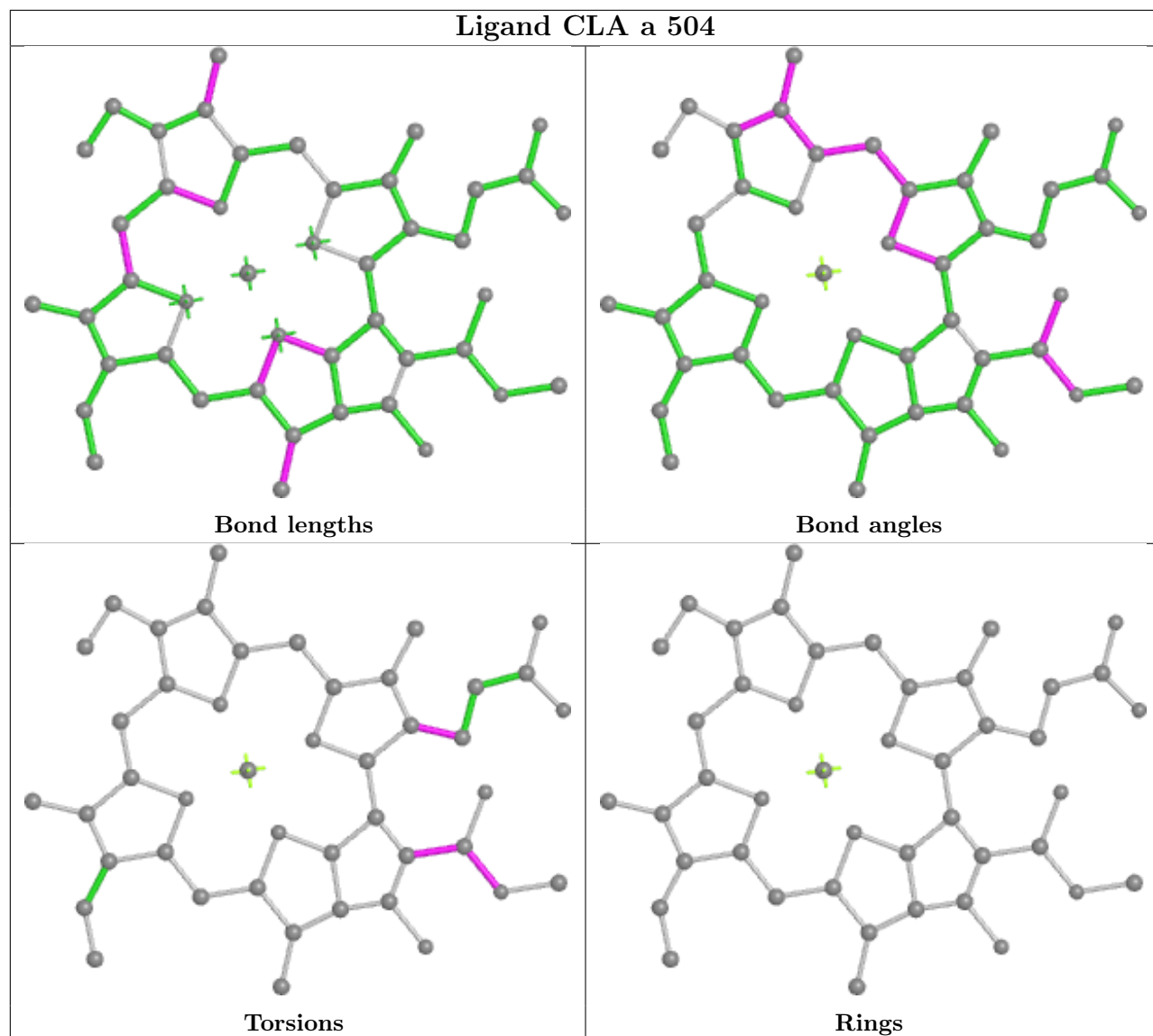


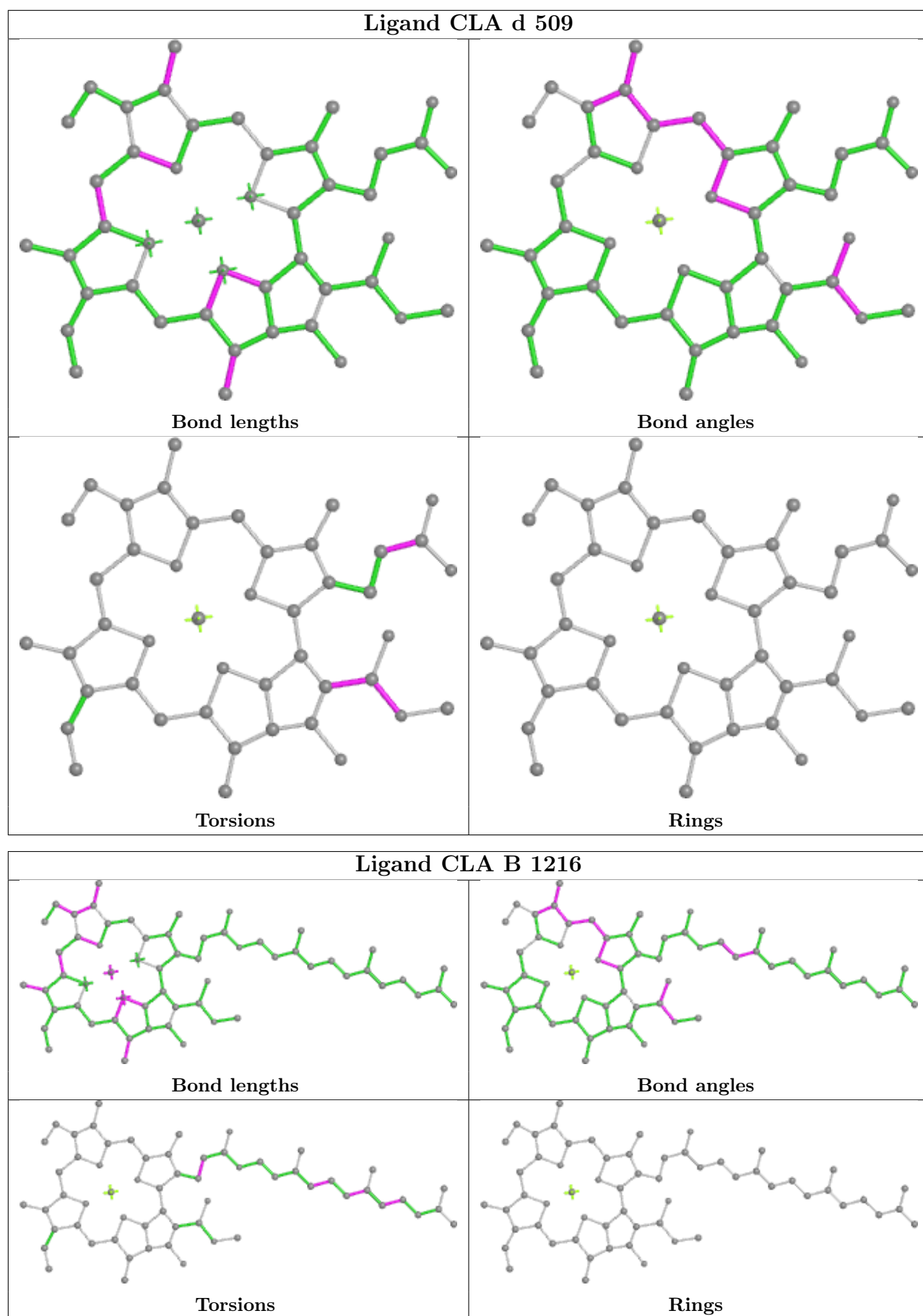


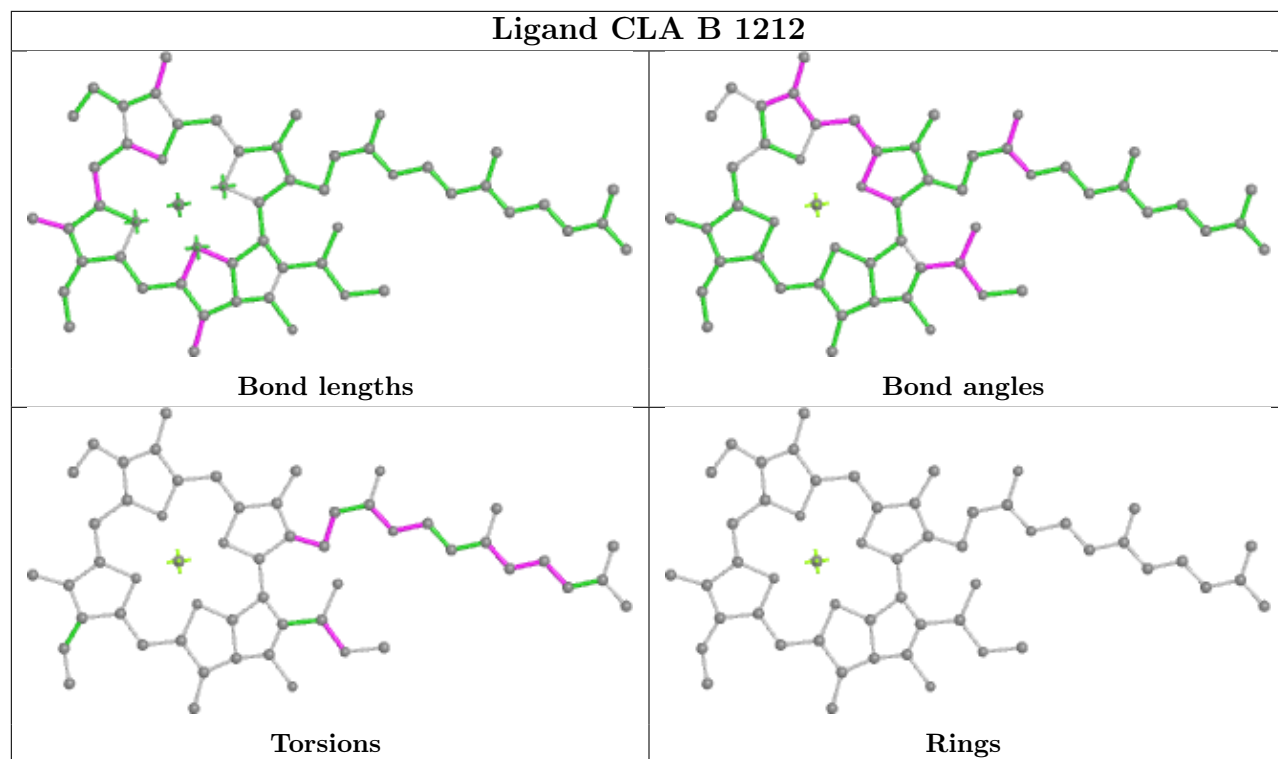


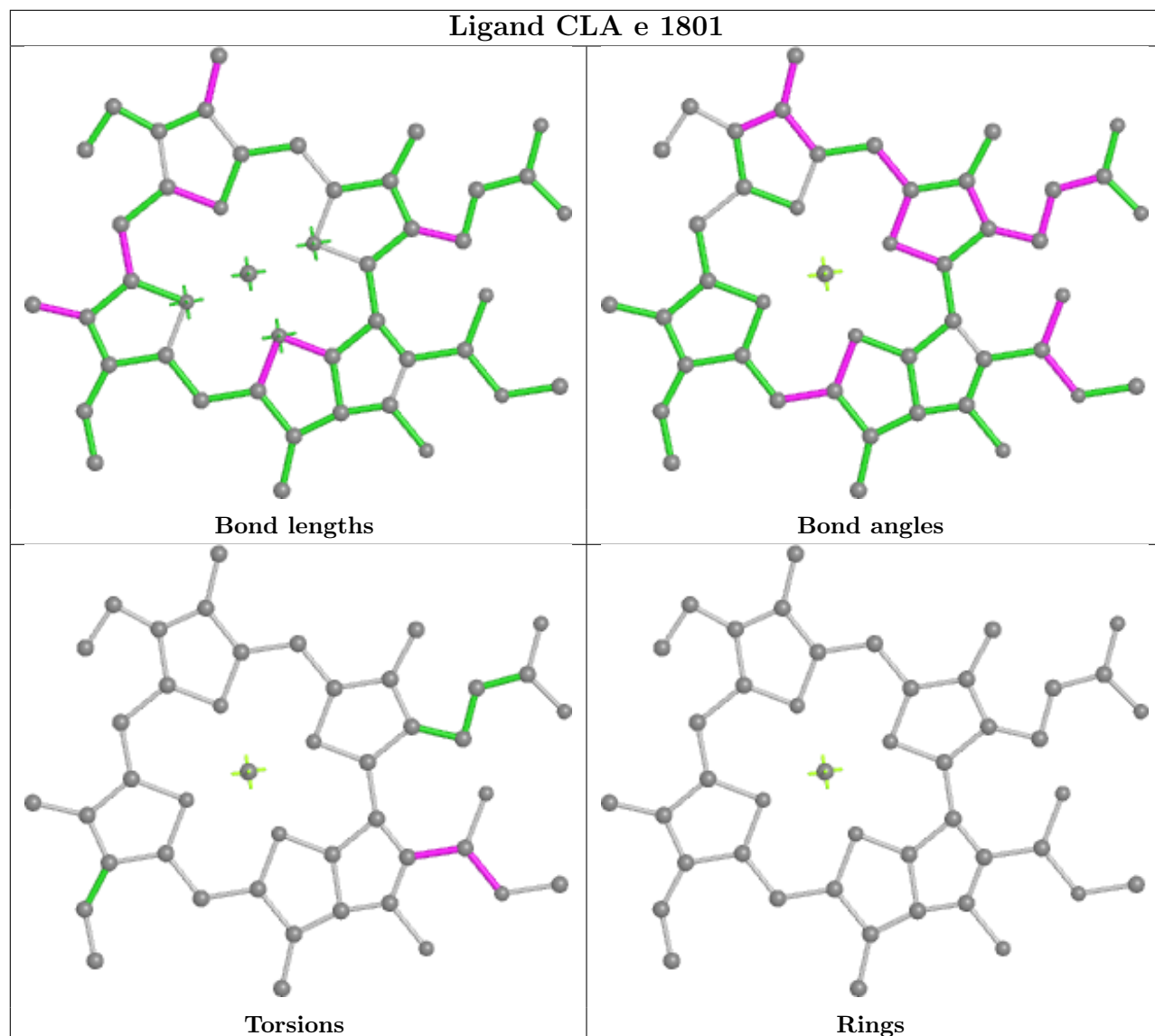


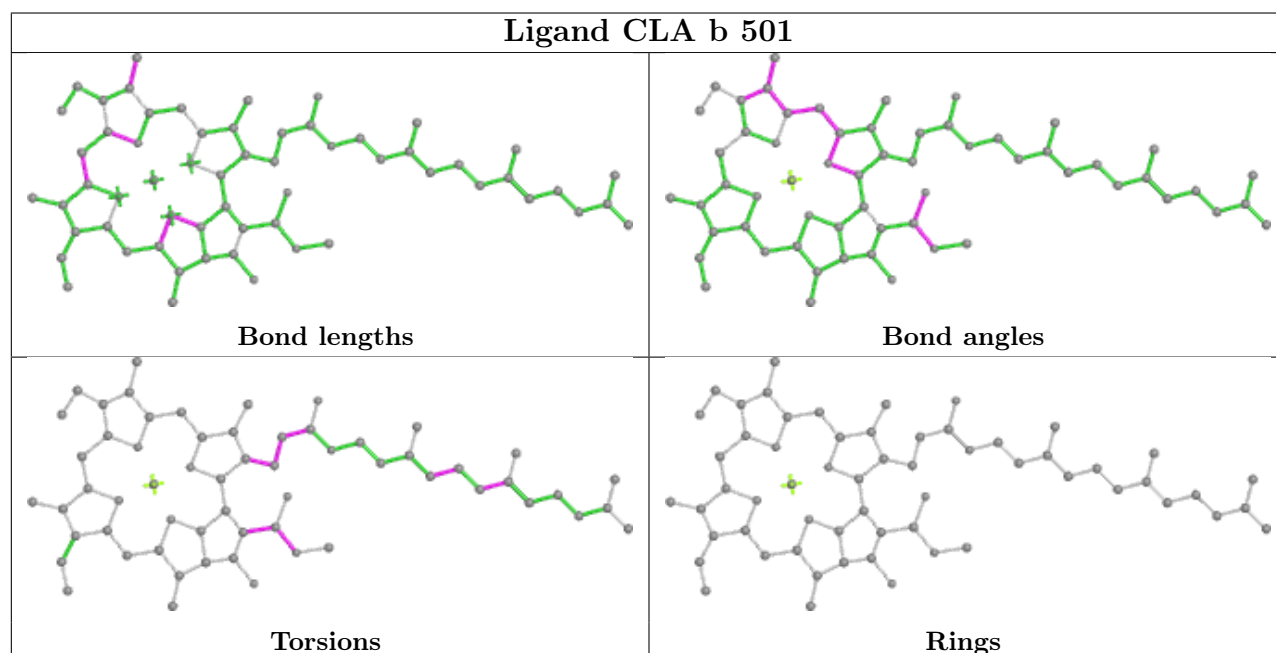
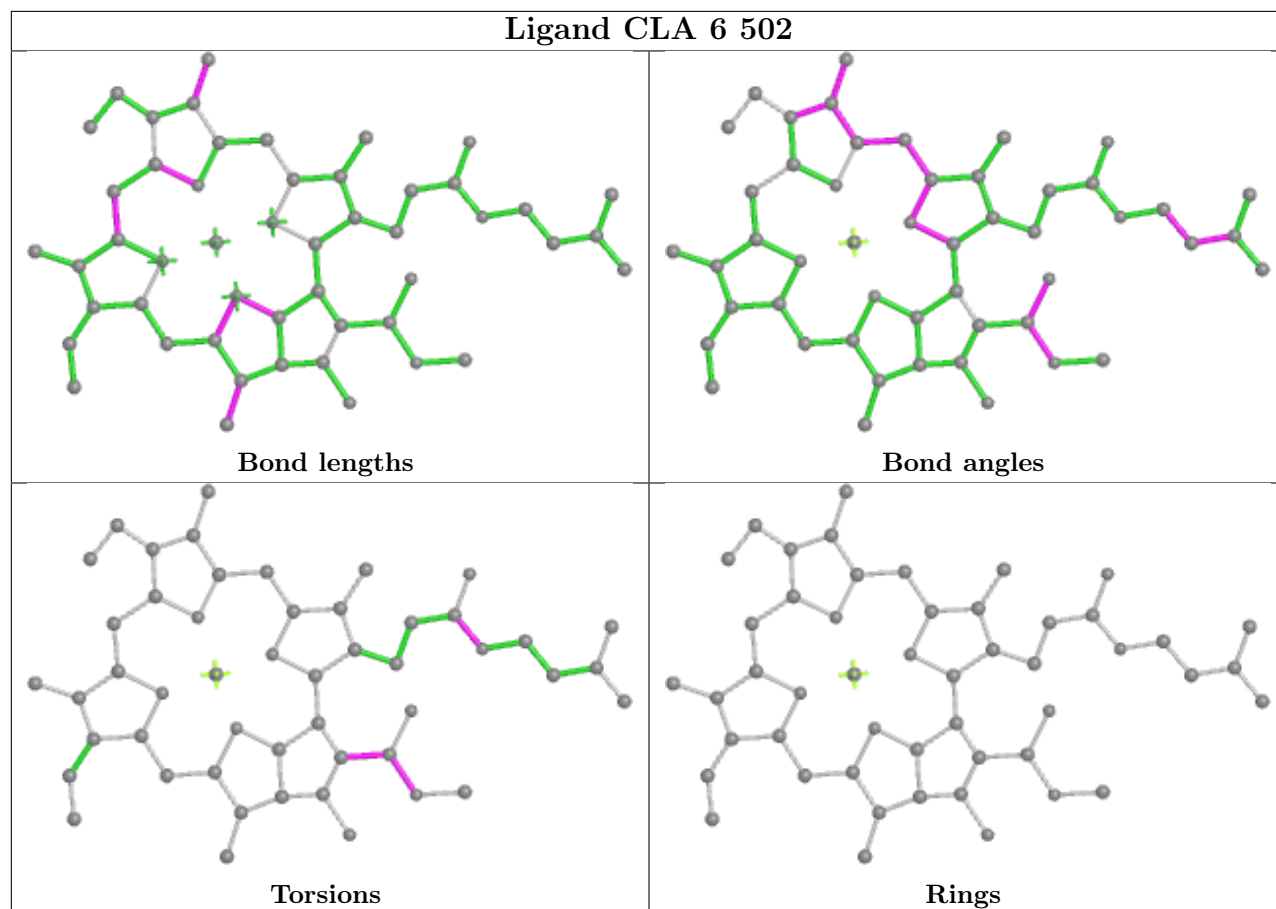




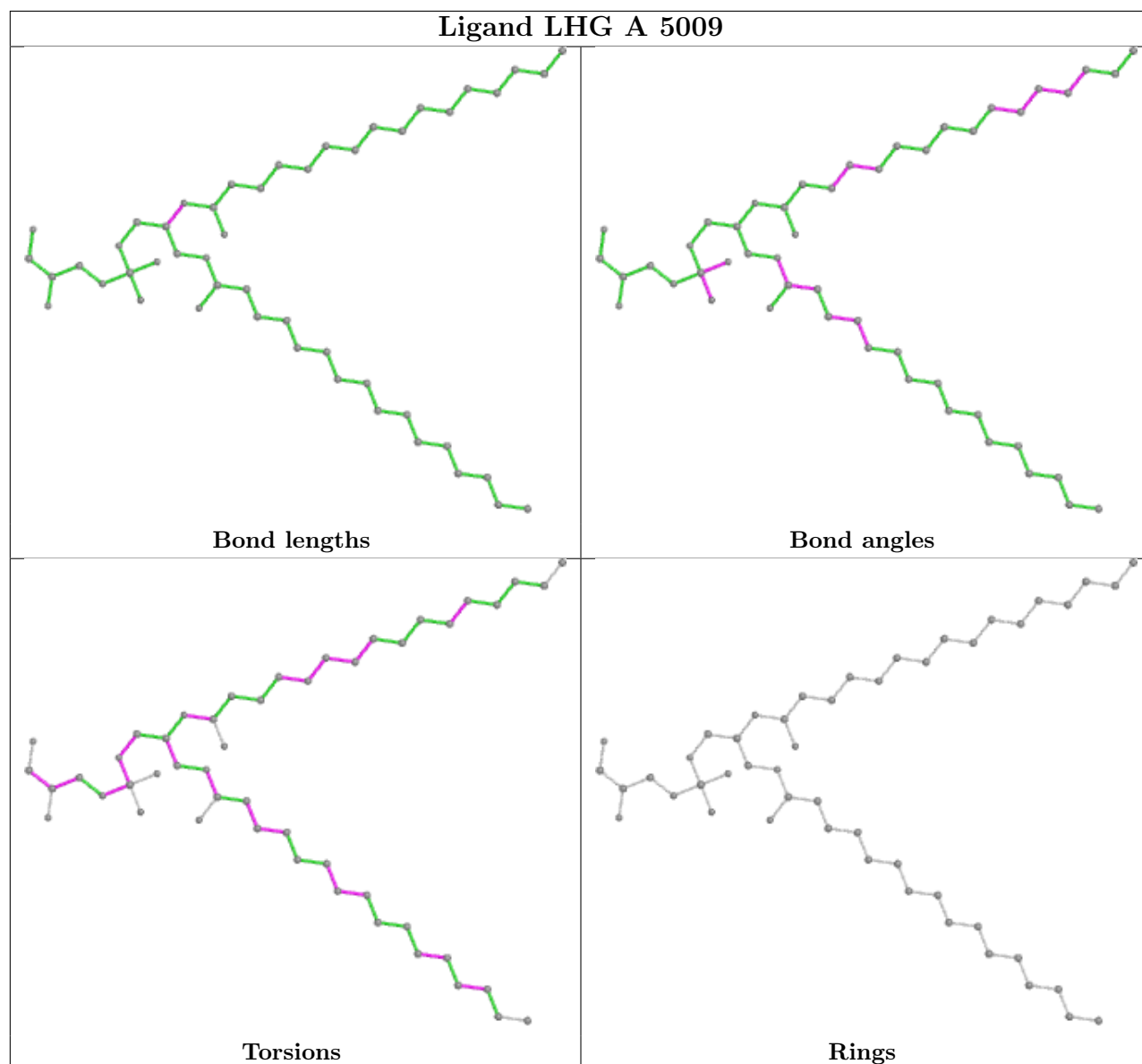
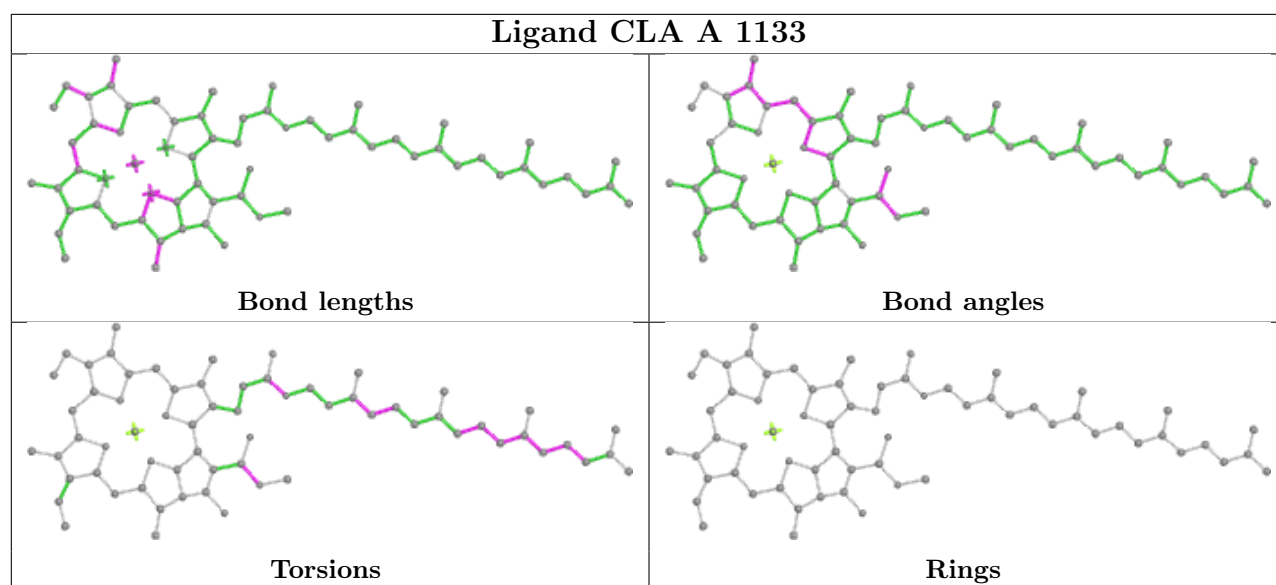


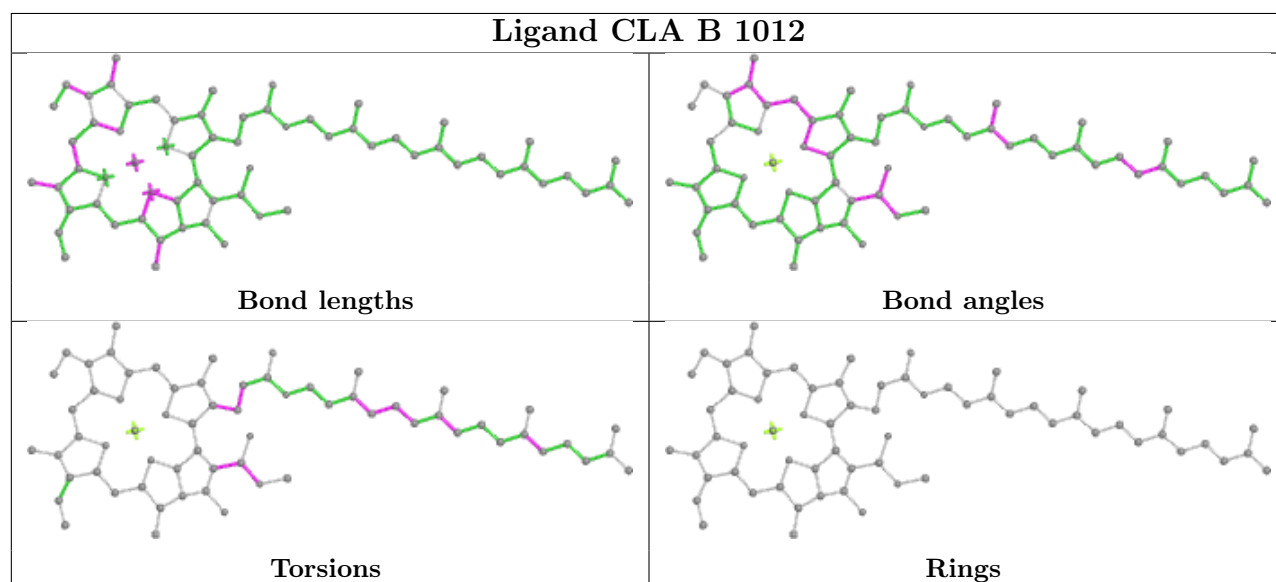
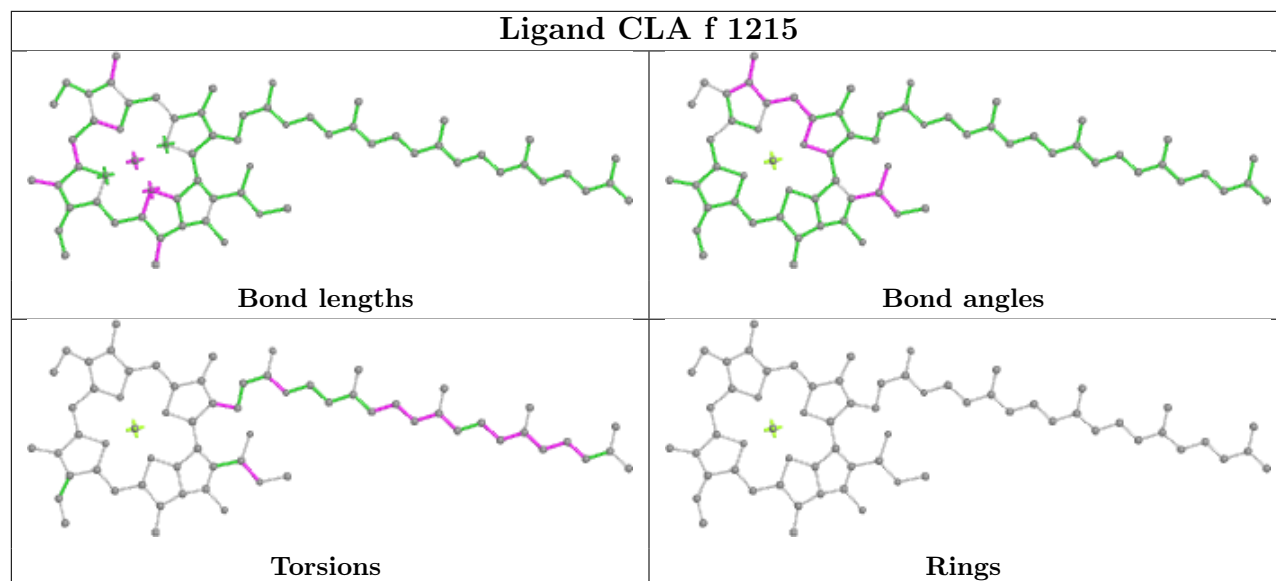
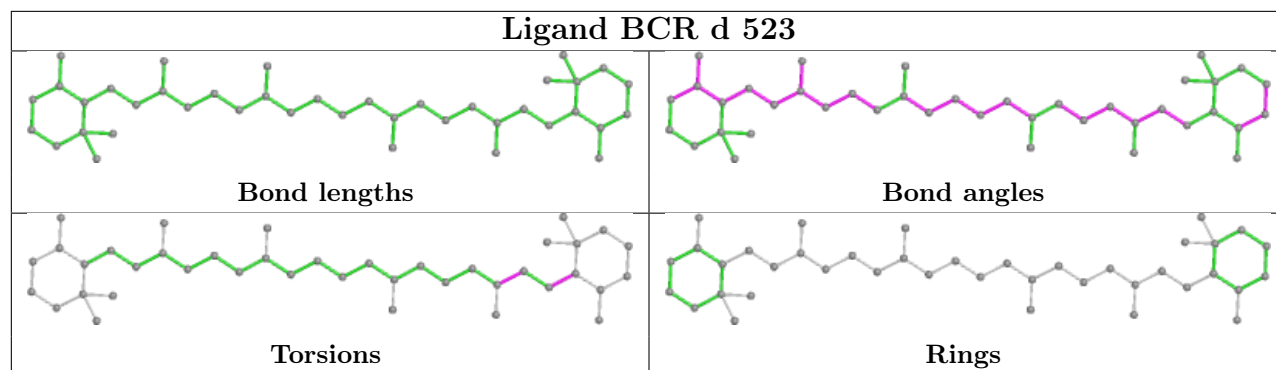


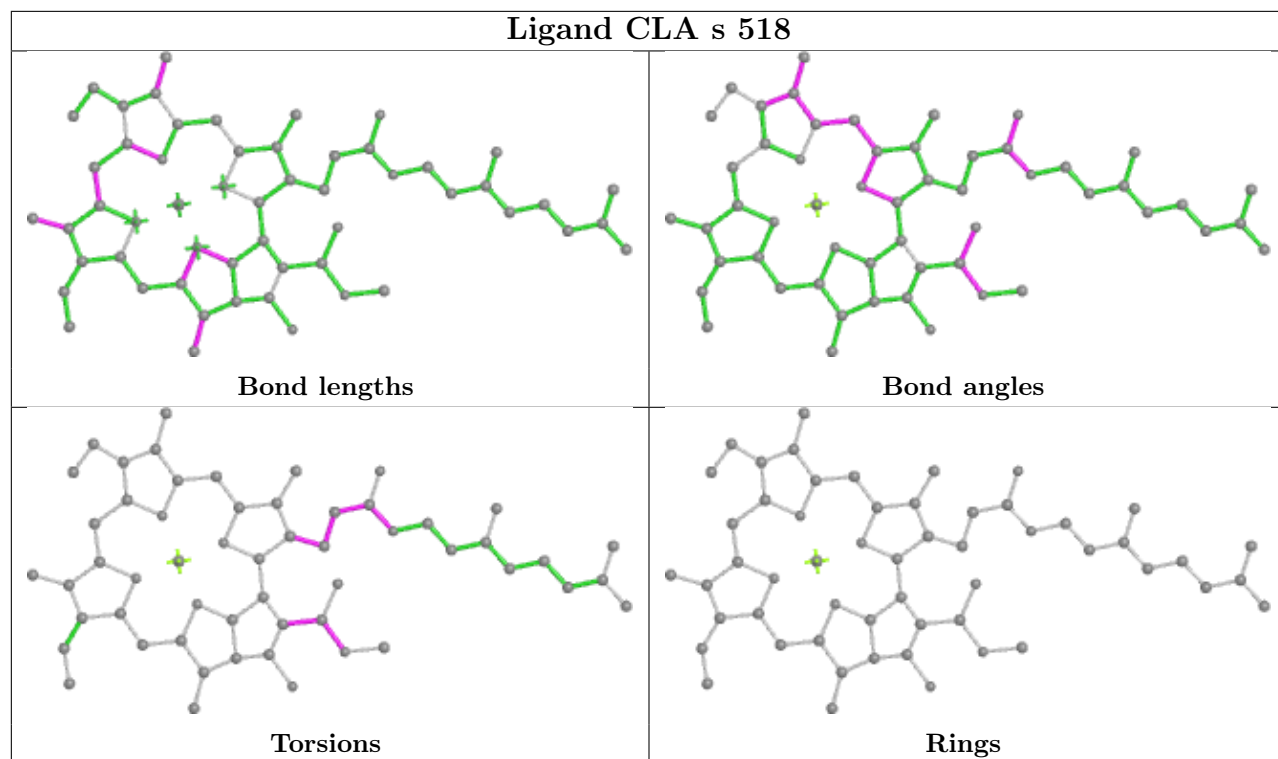


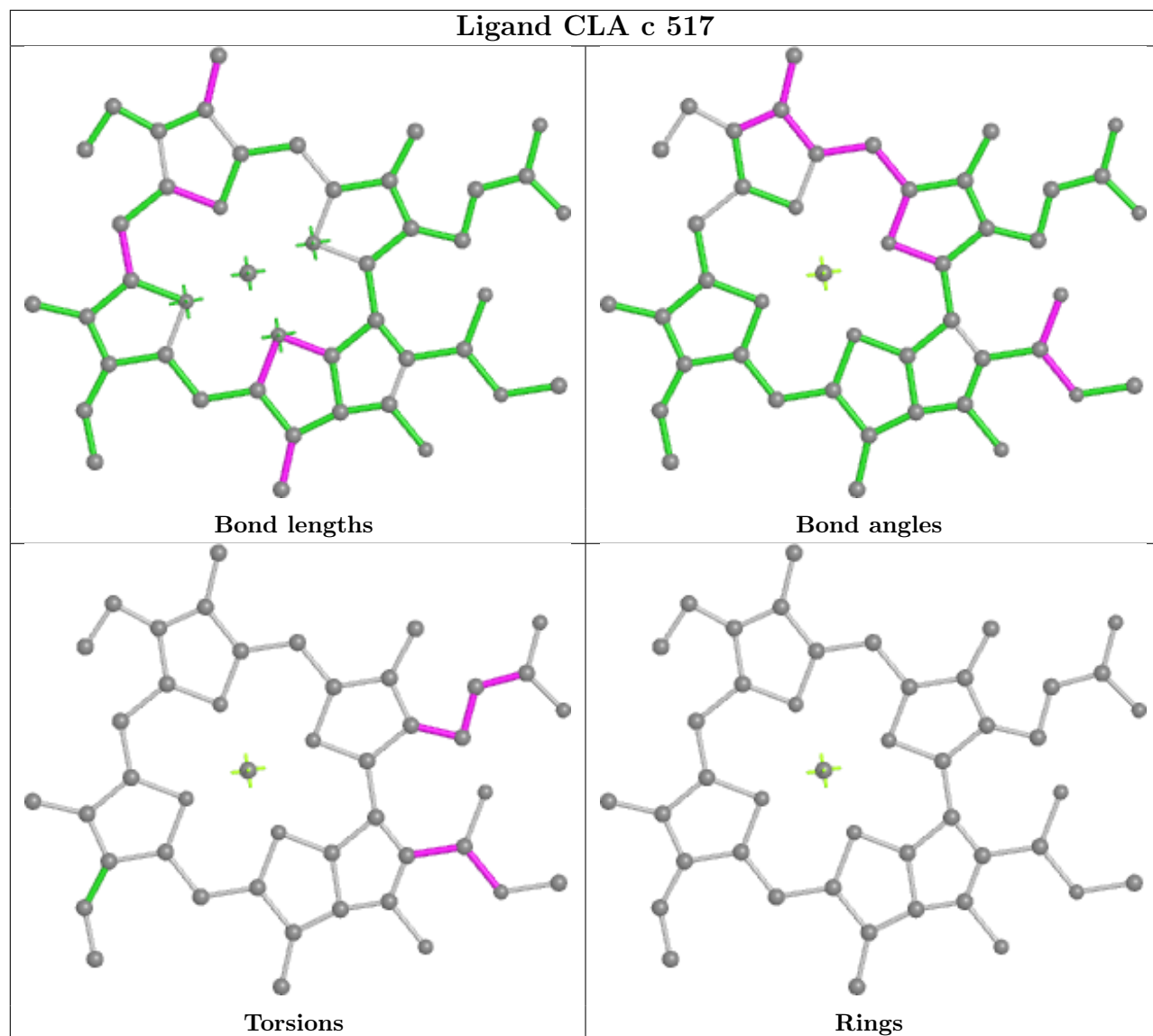


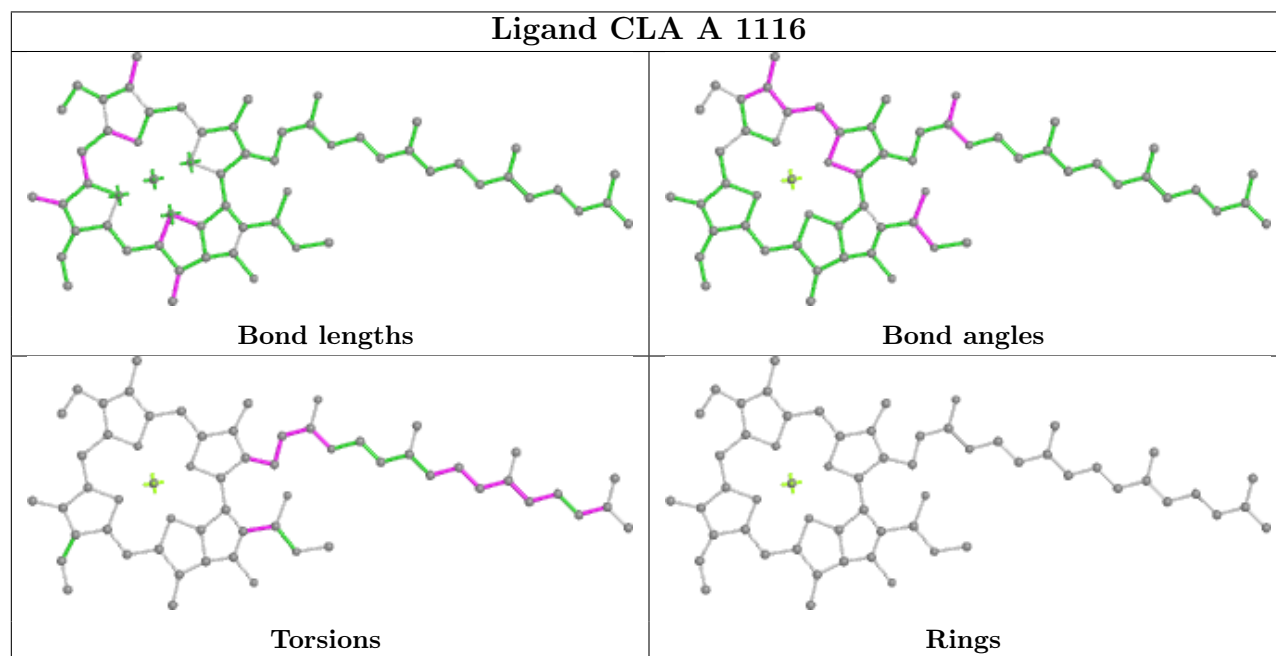
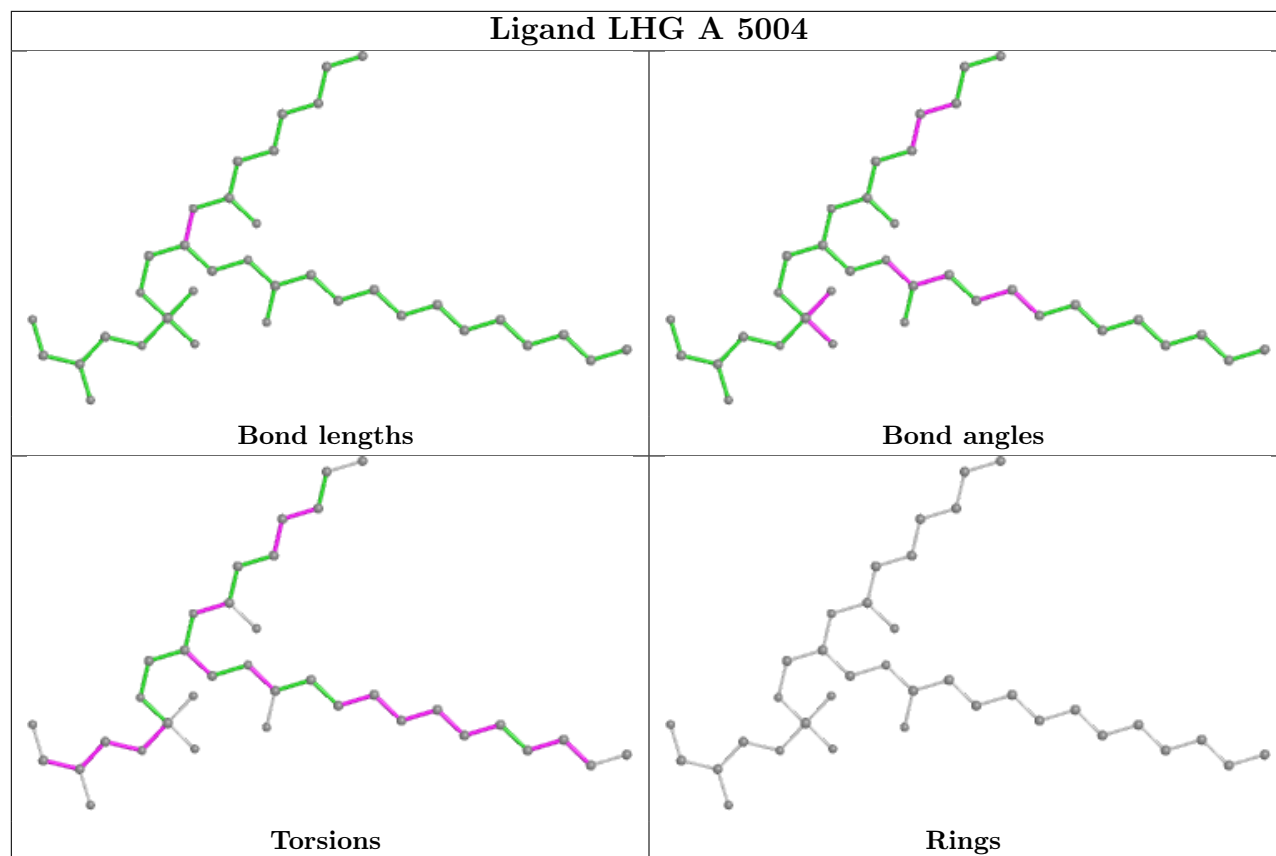


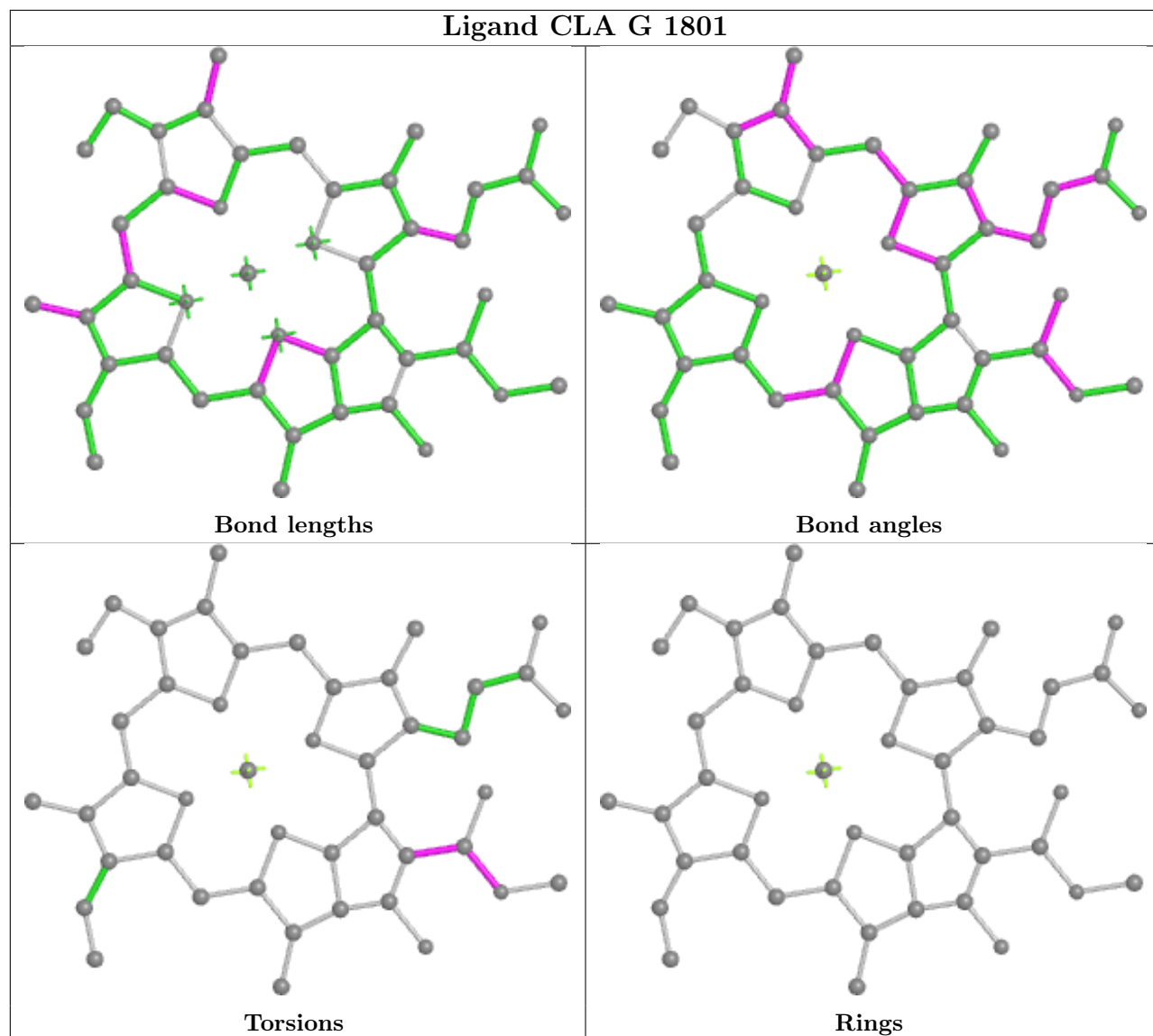


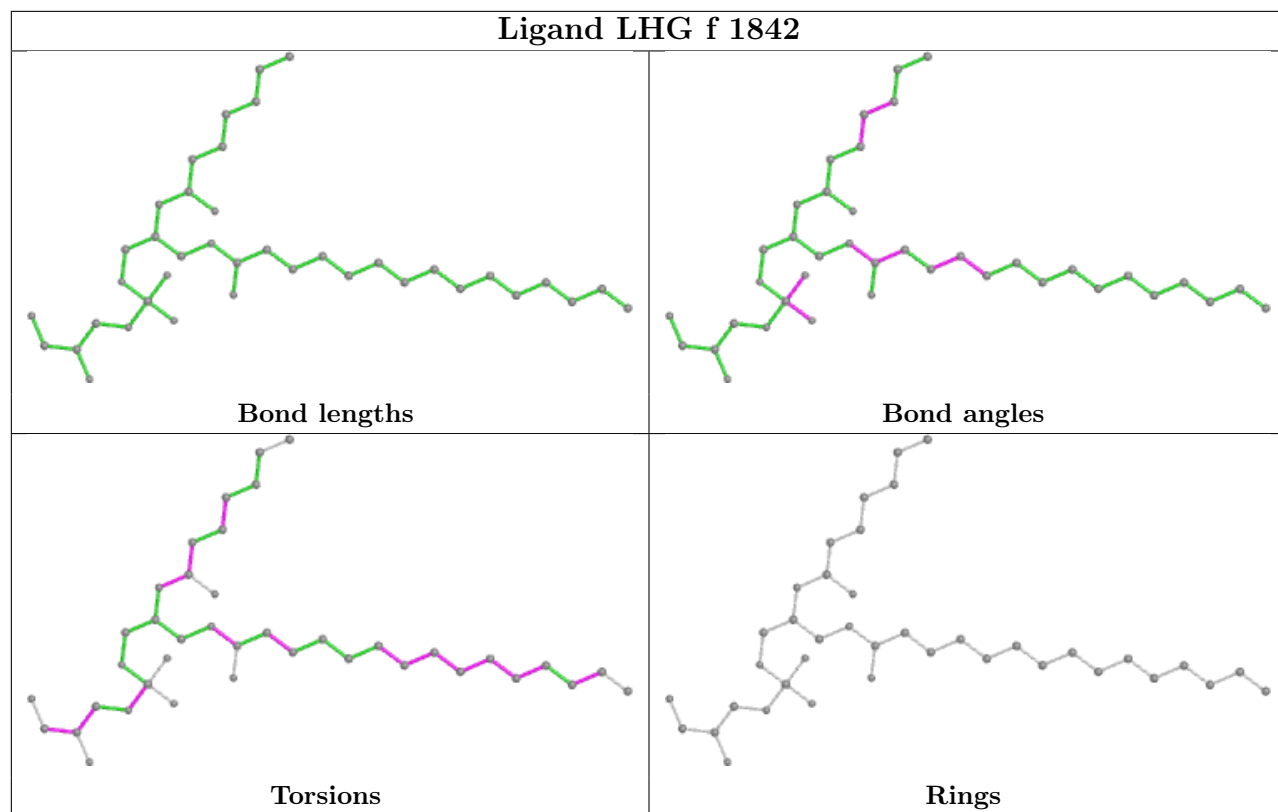


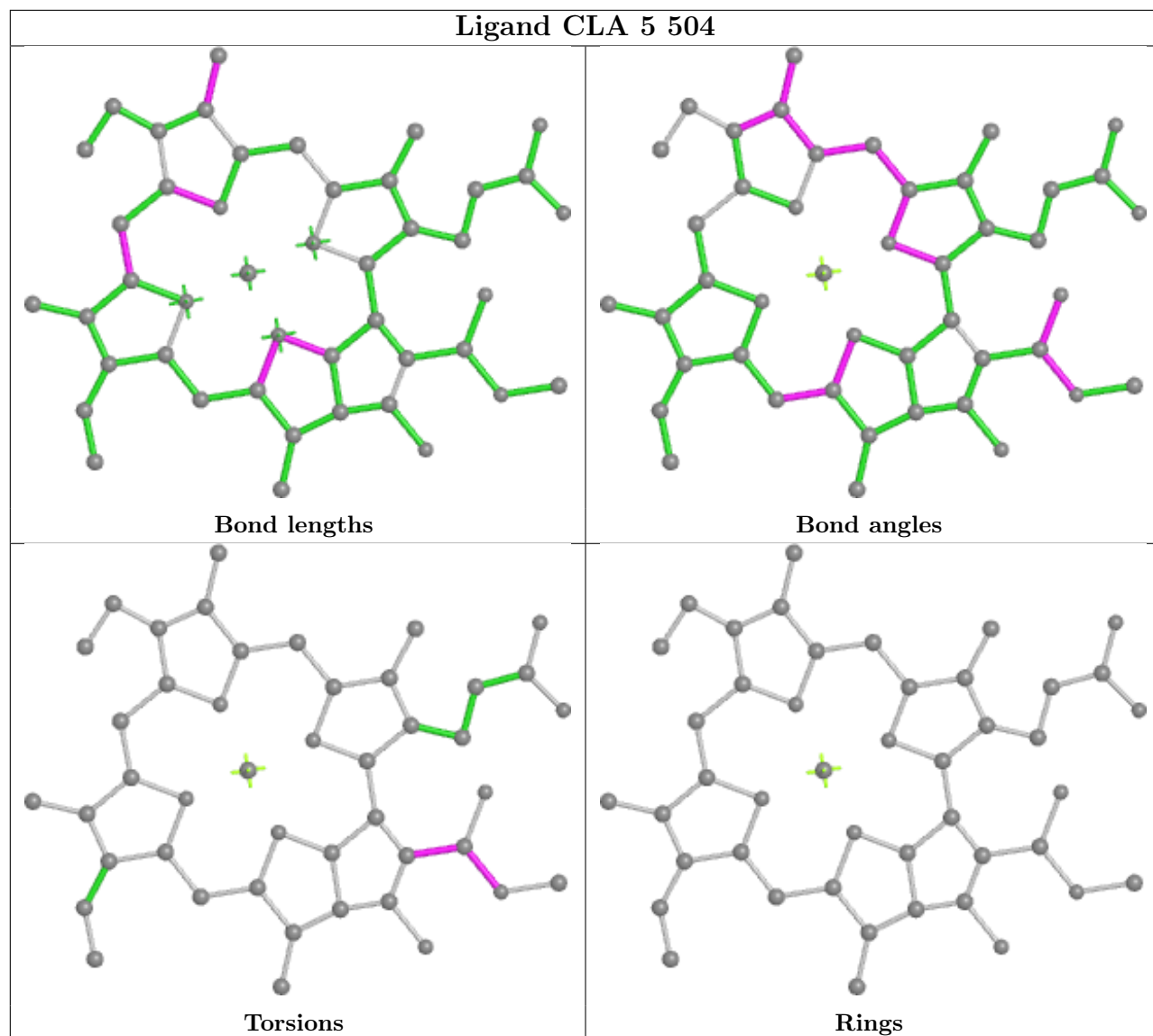




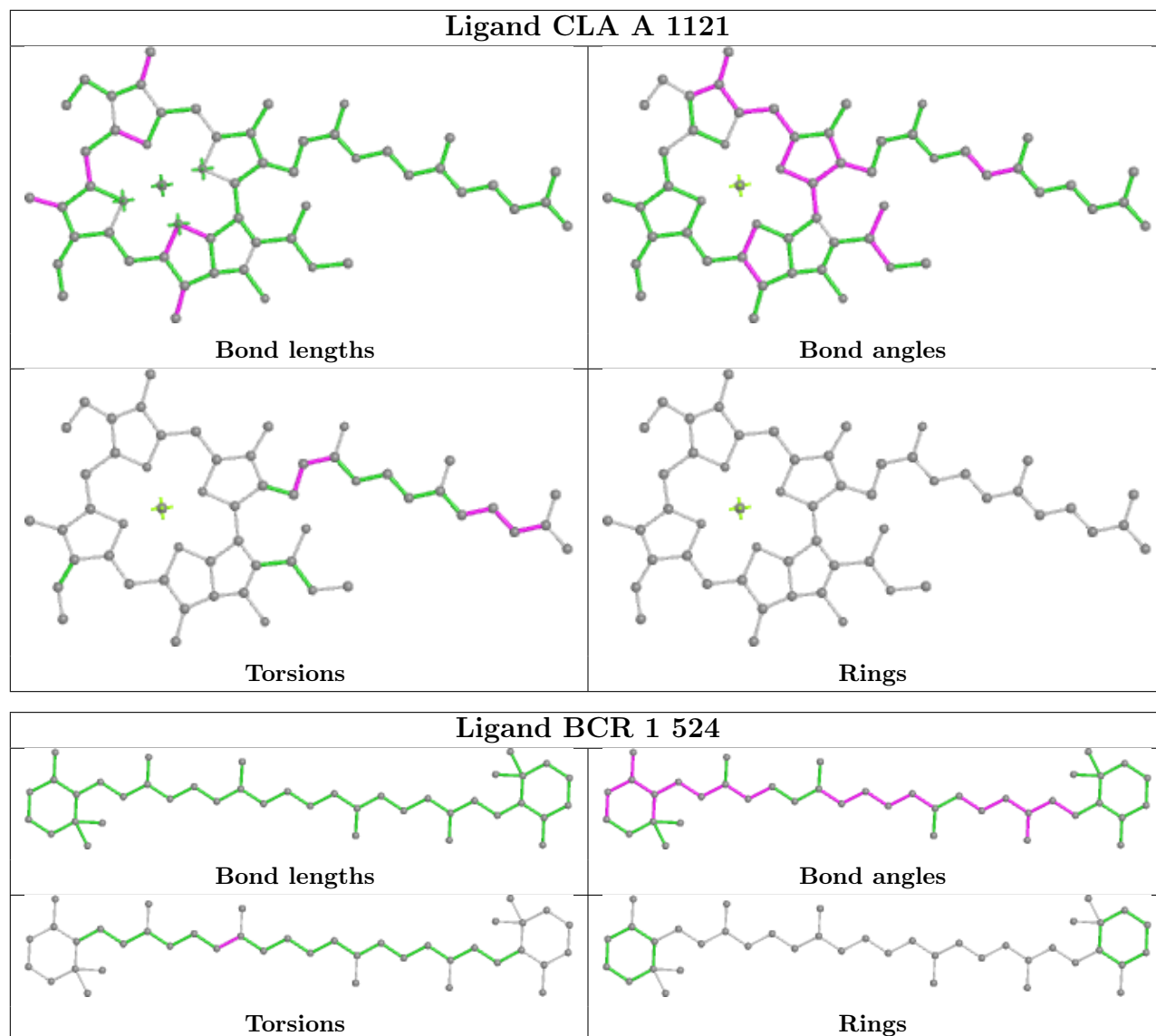




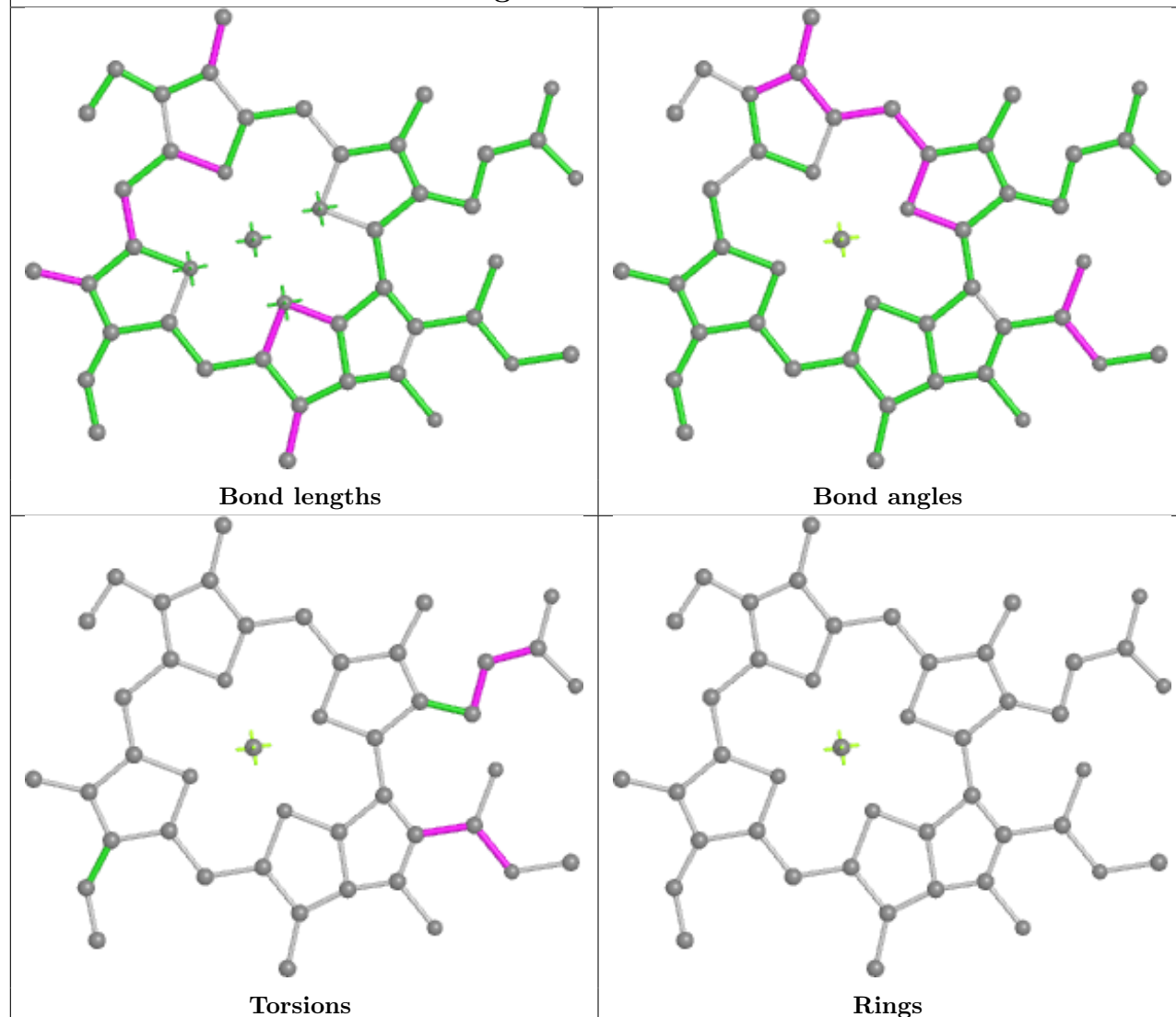




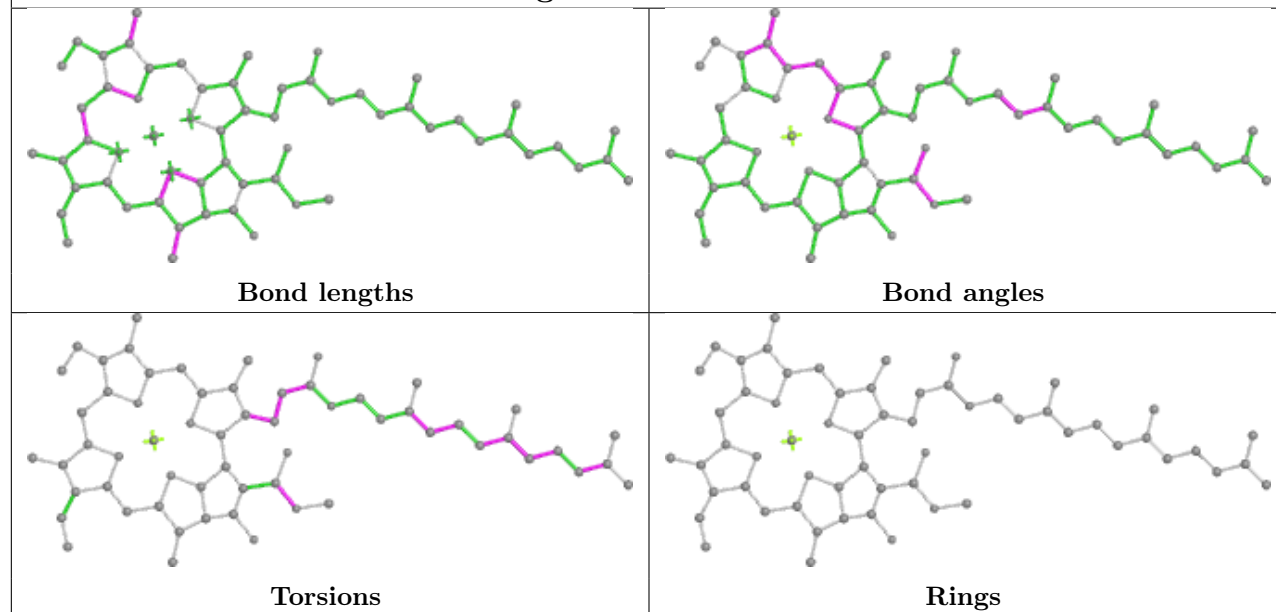


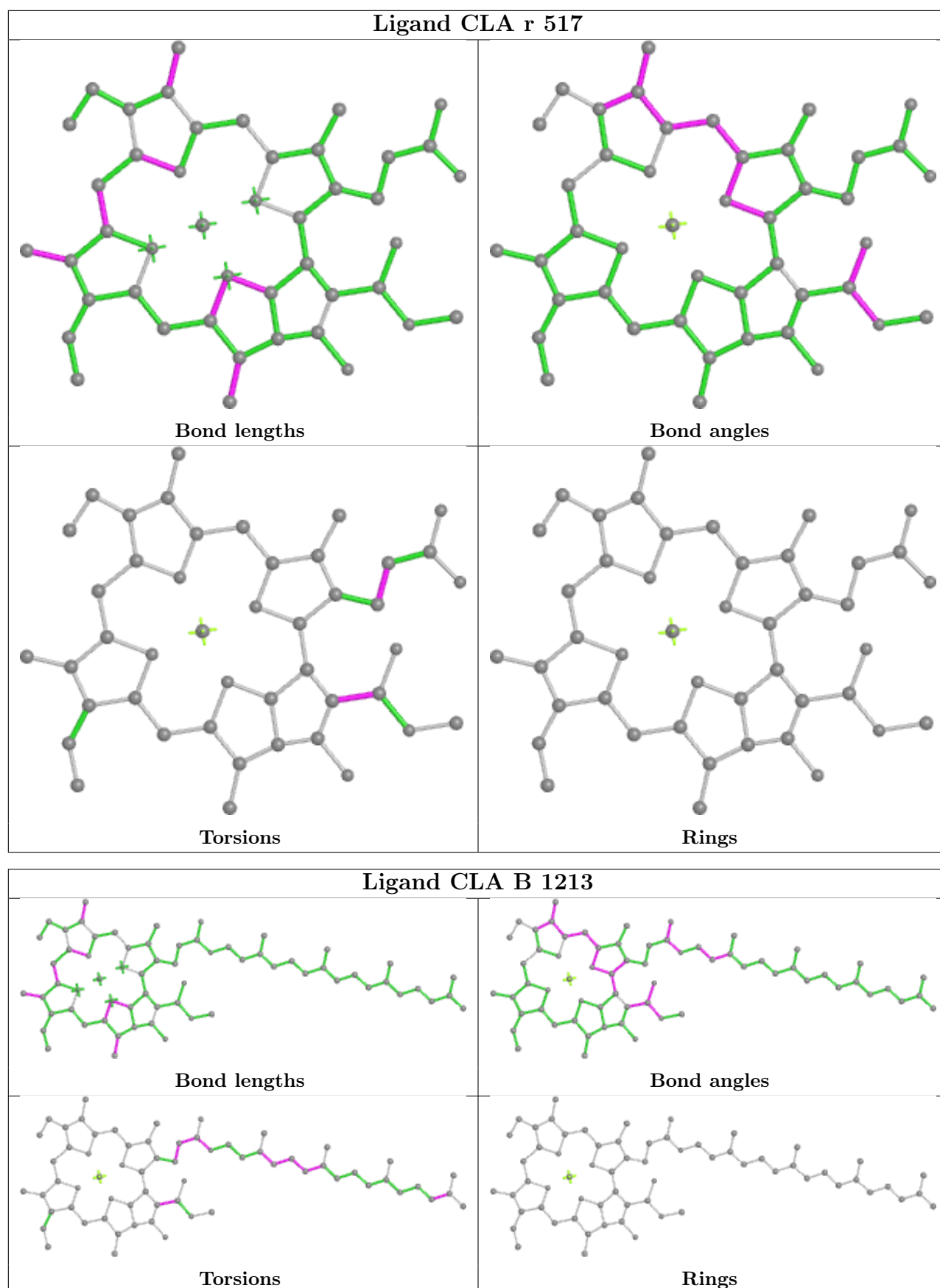


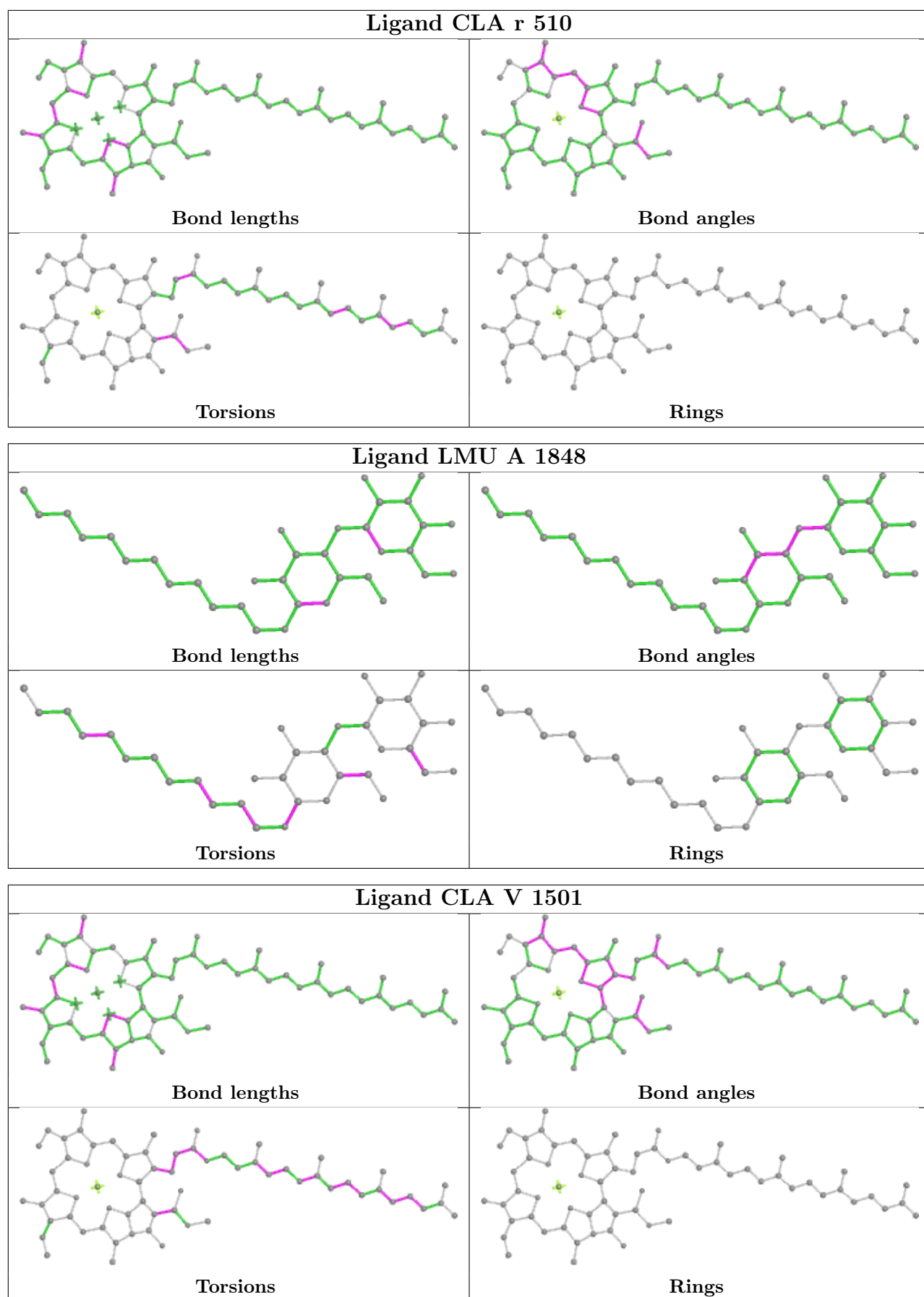
## Ligand CLA 4 513

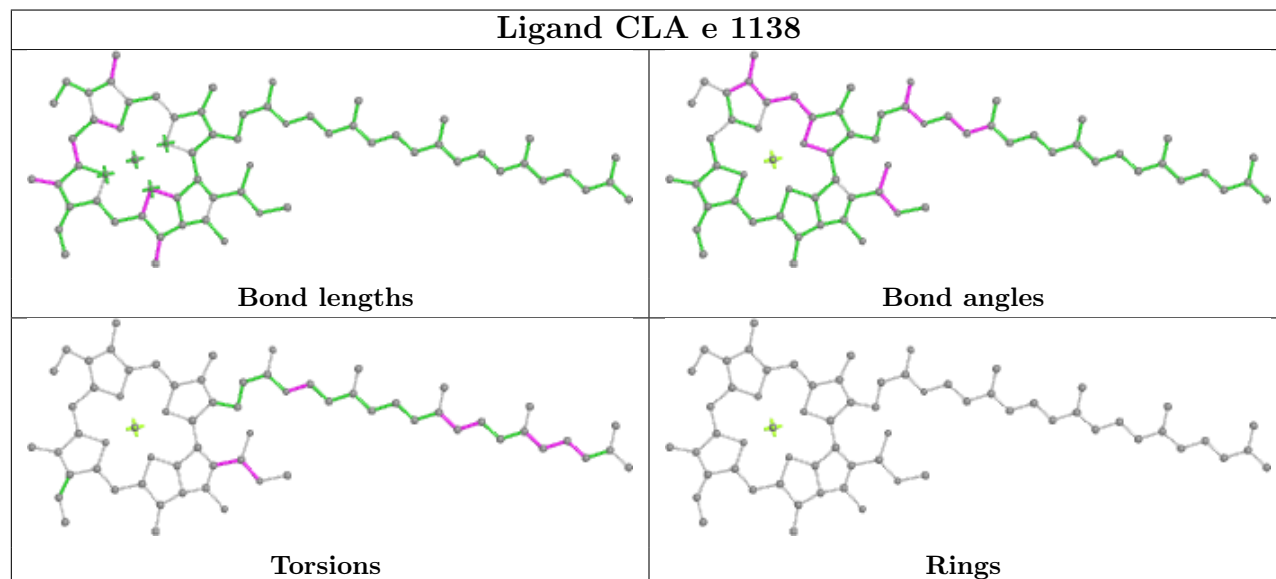
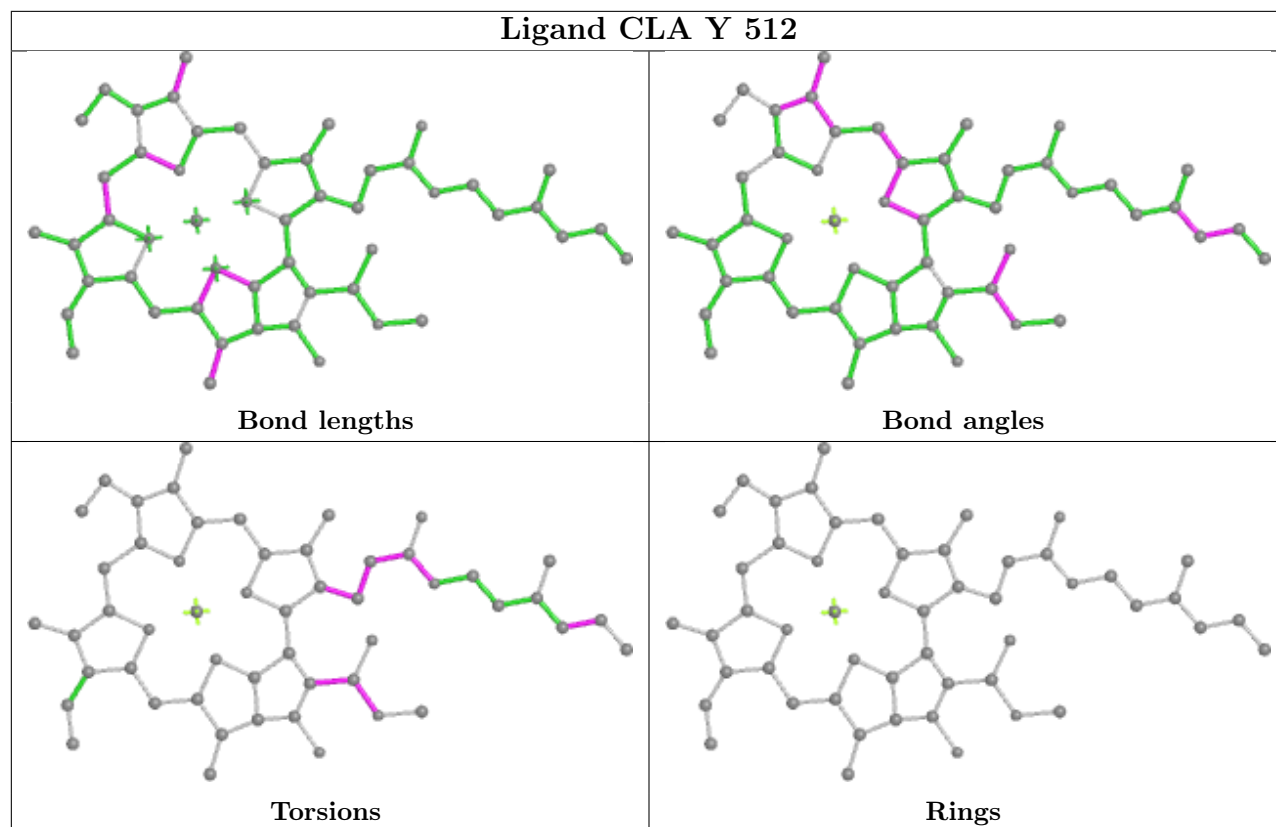


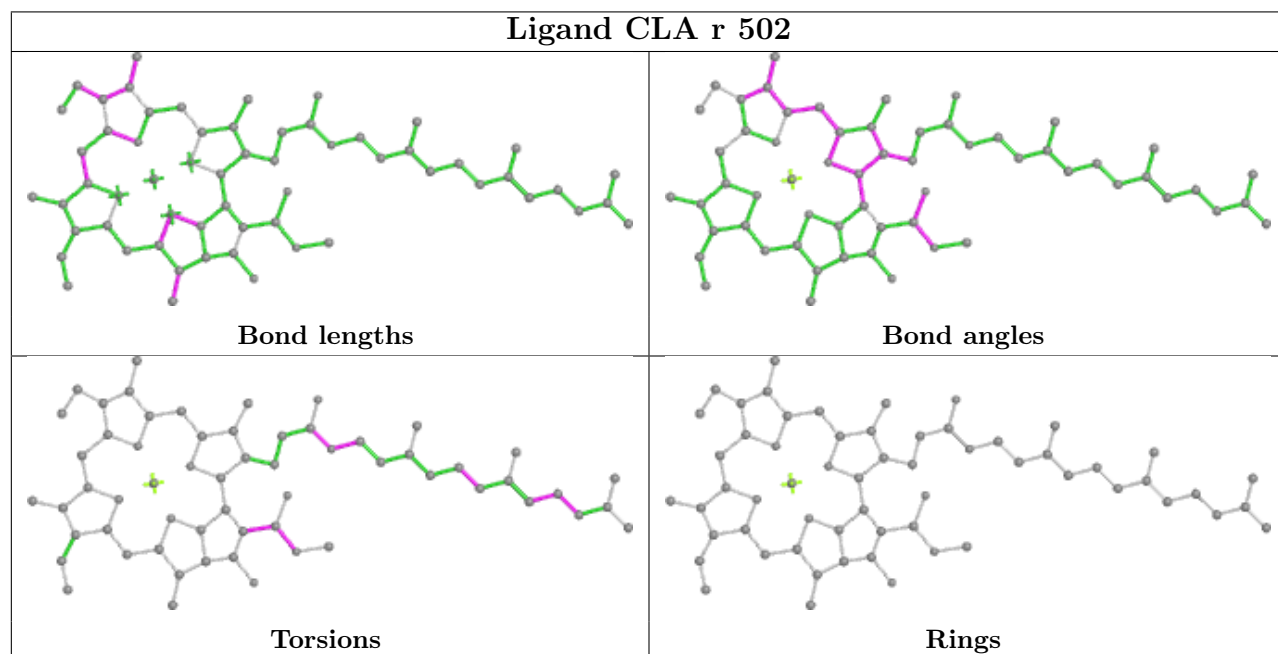
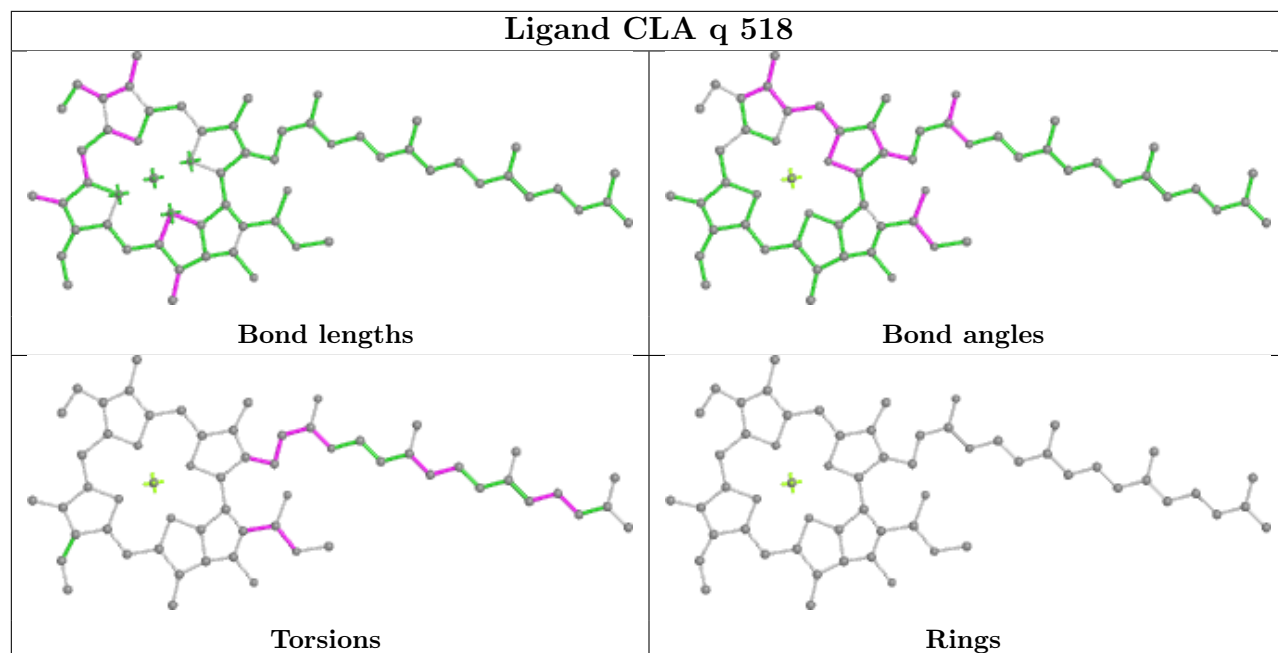
## Ligand CLA 6 501

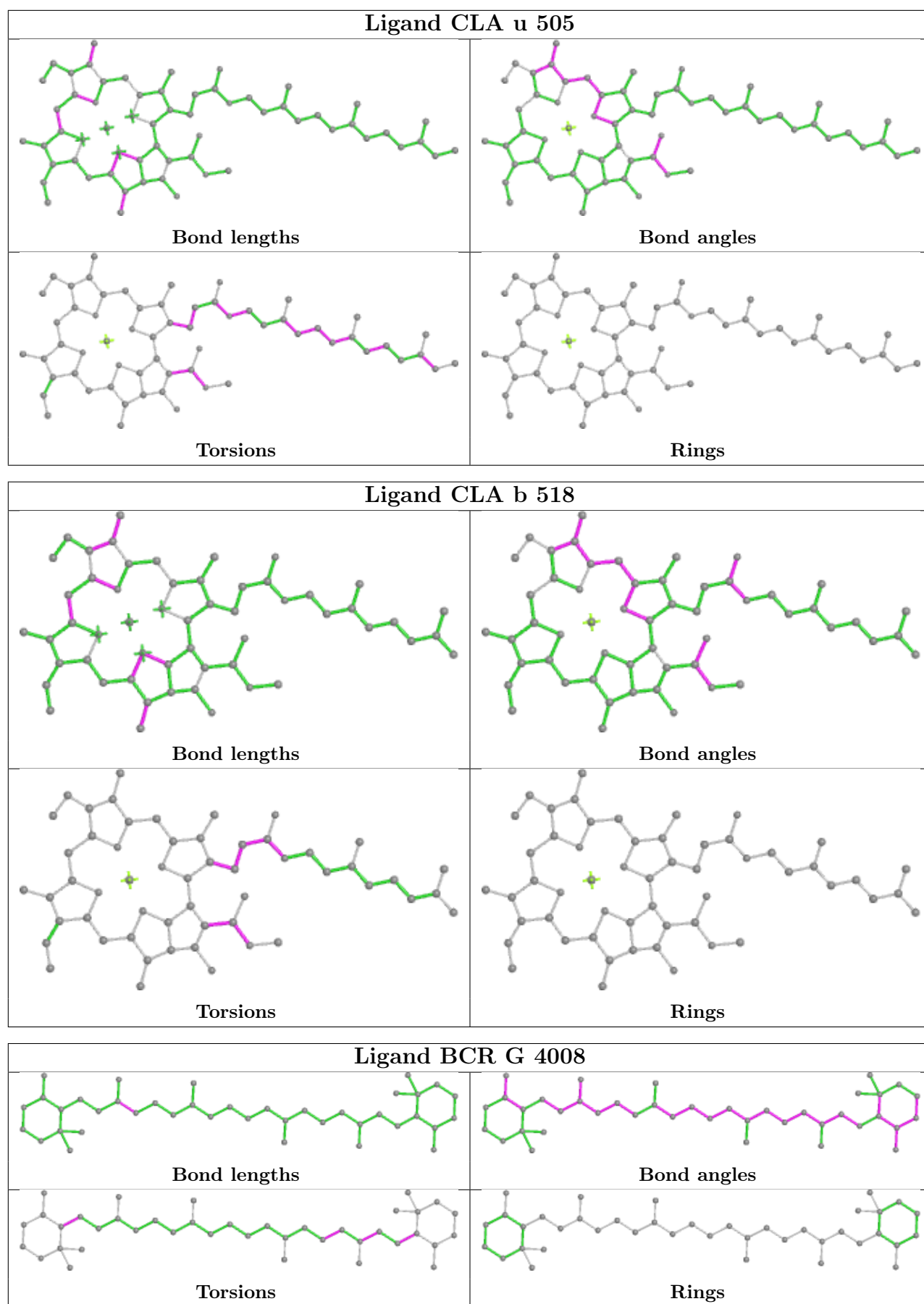


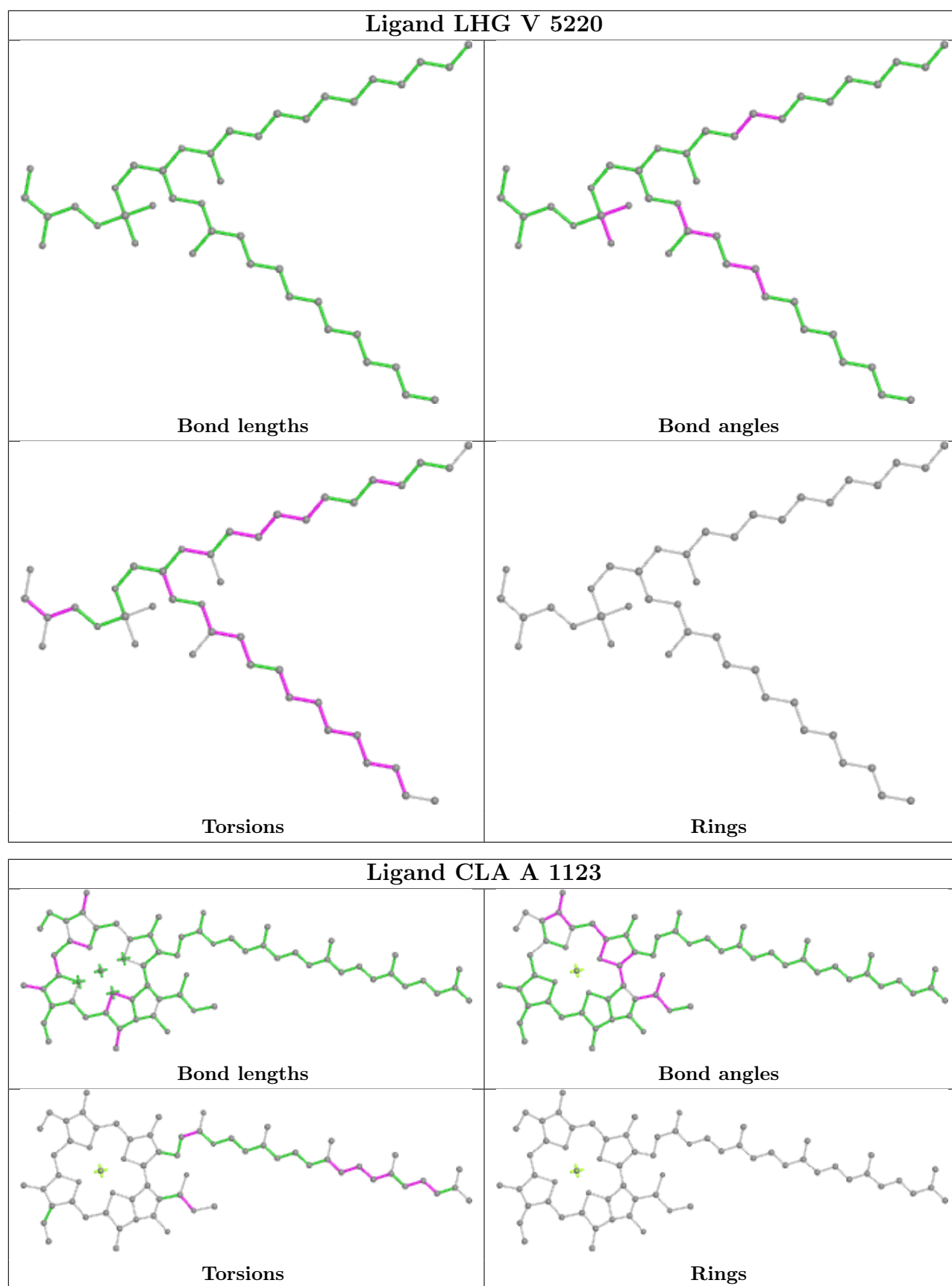




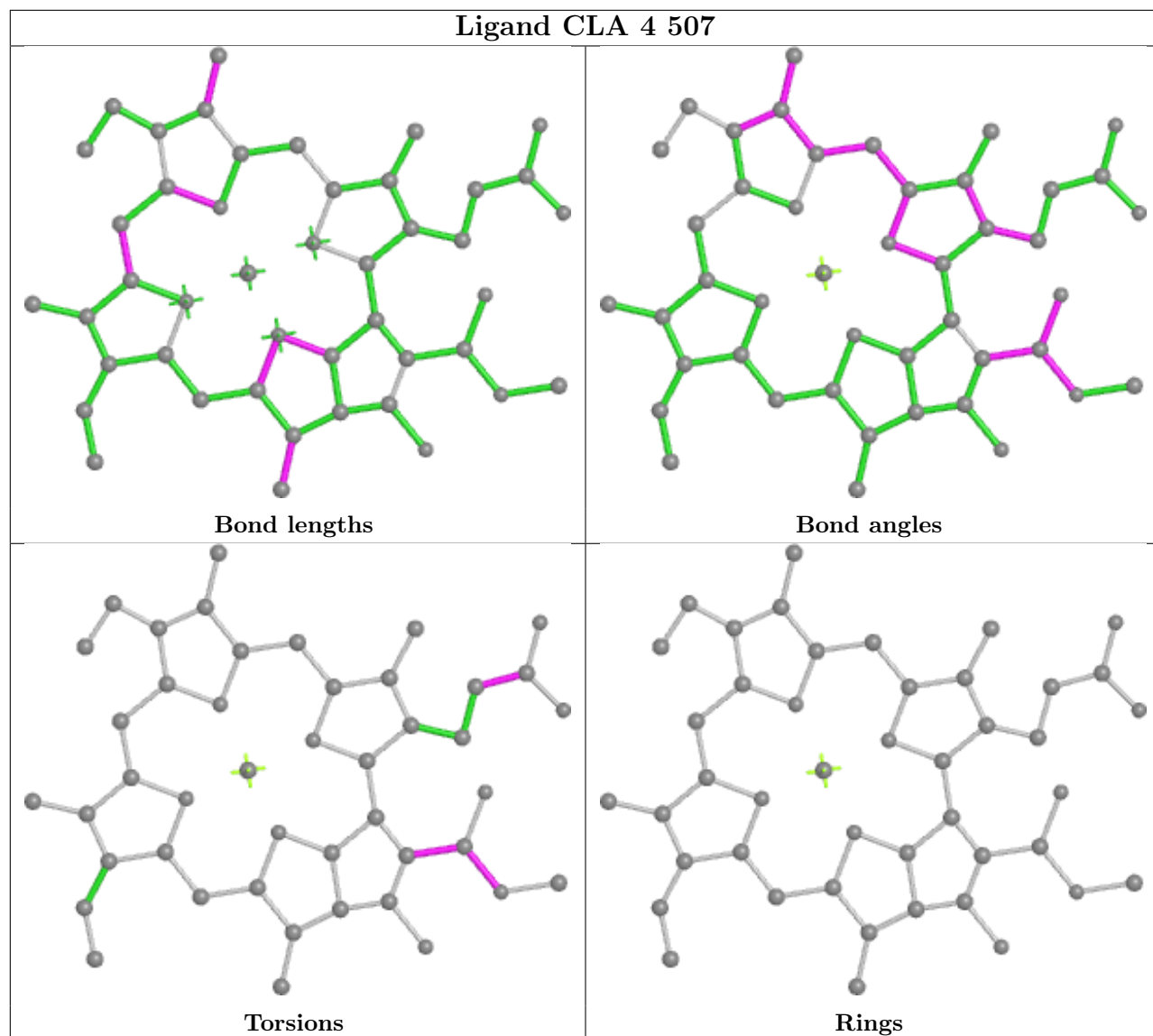


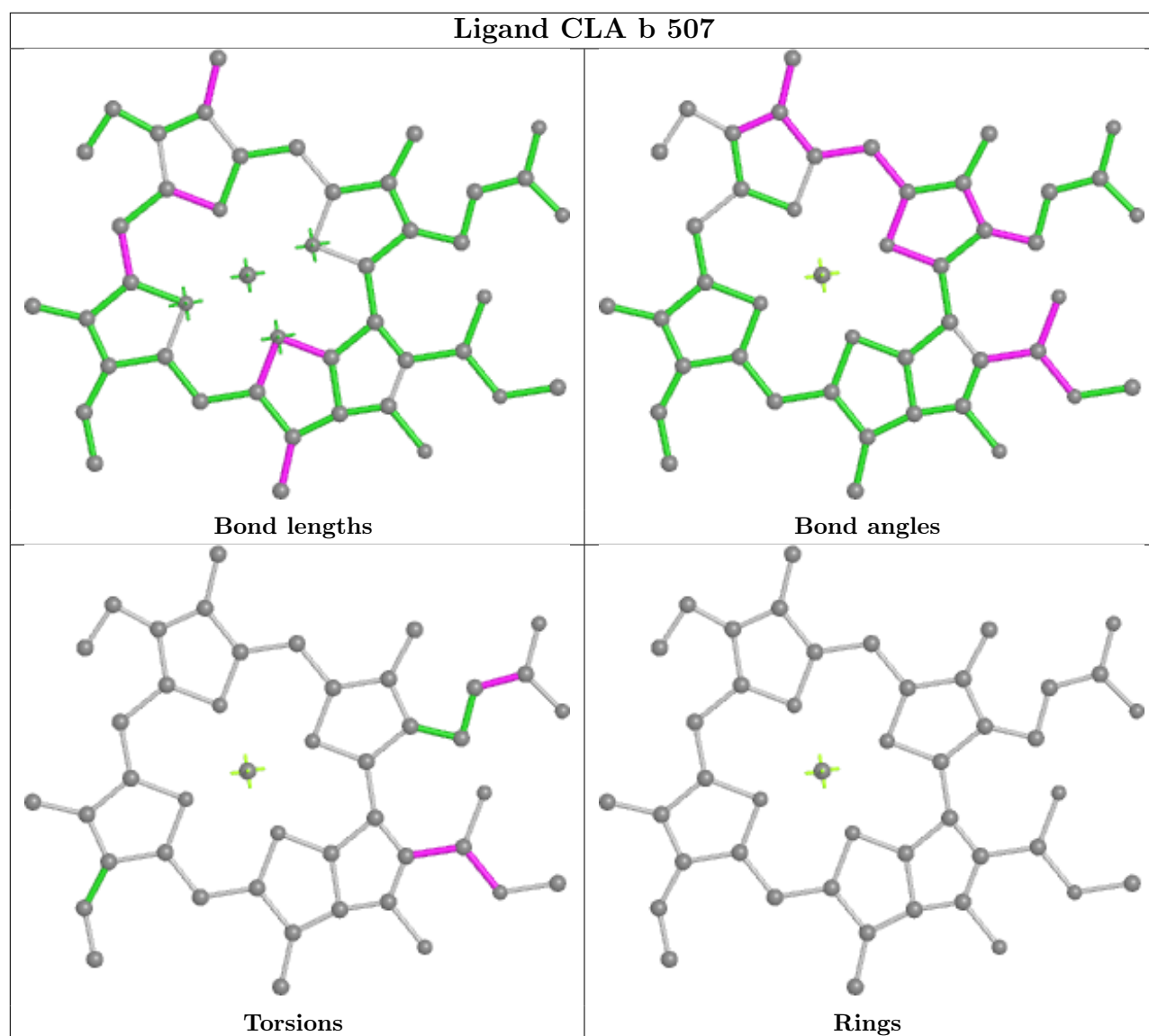


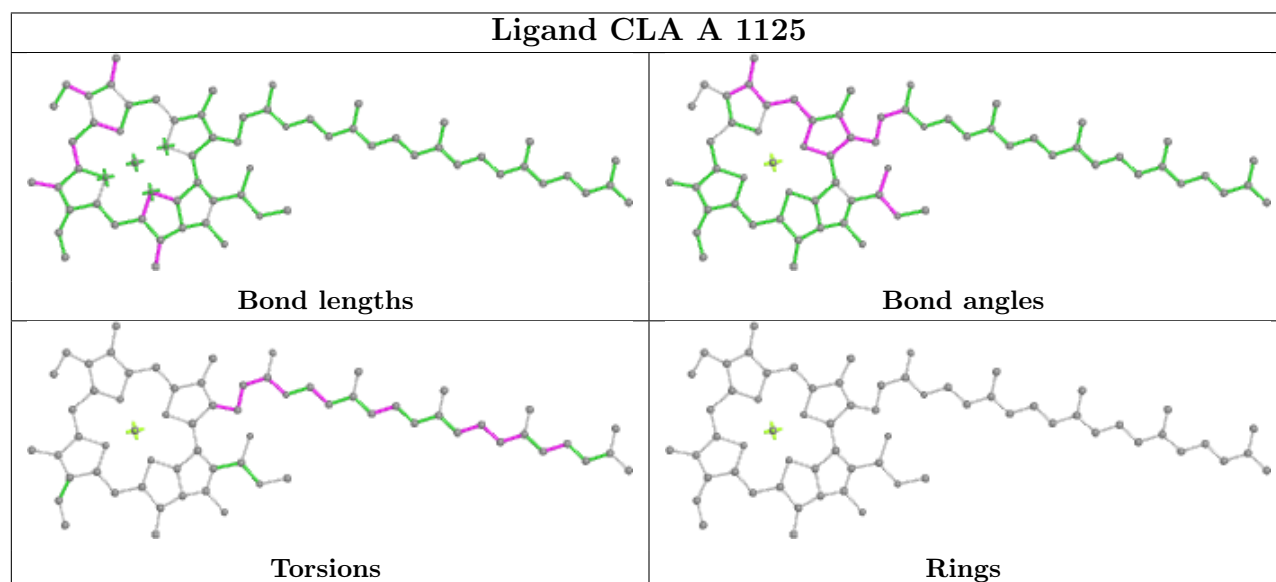
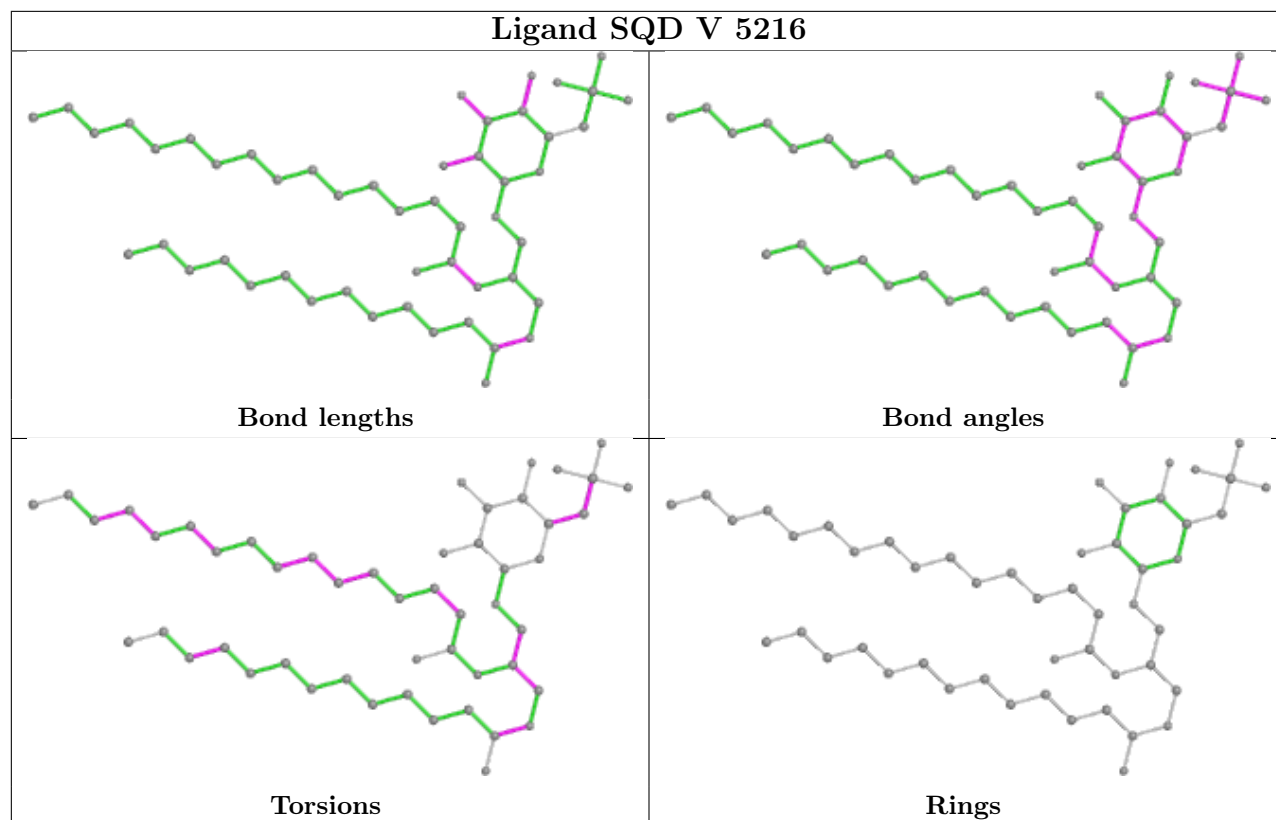


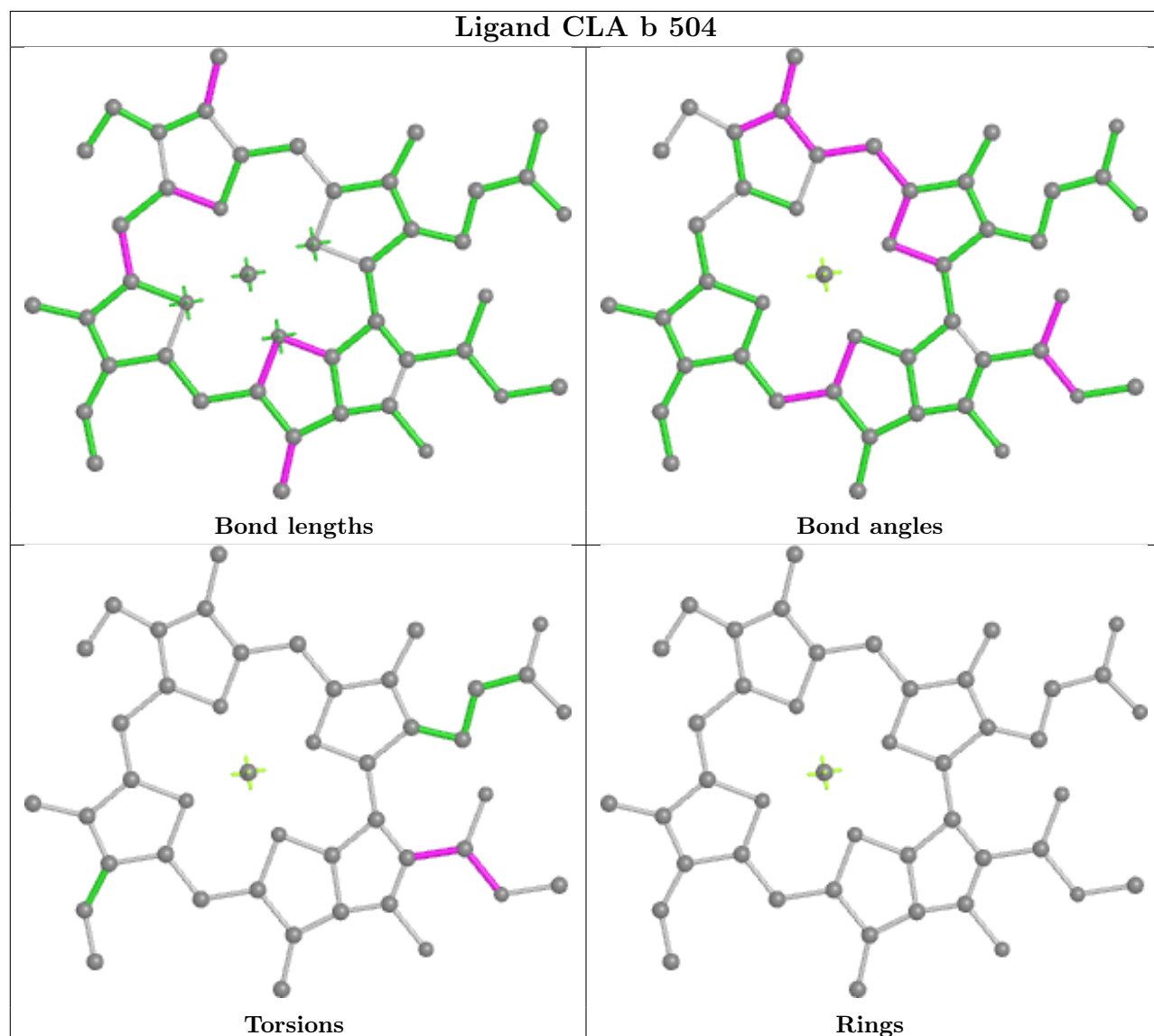
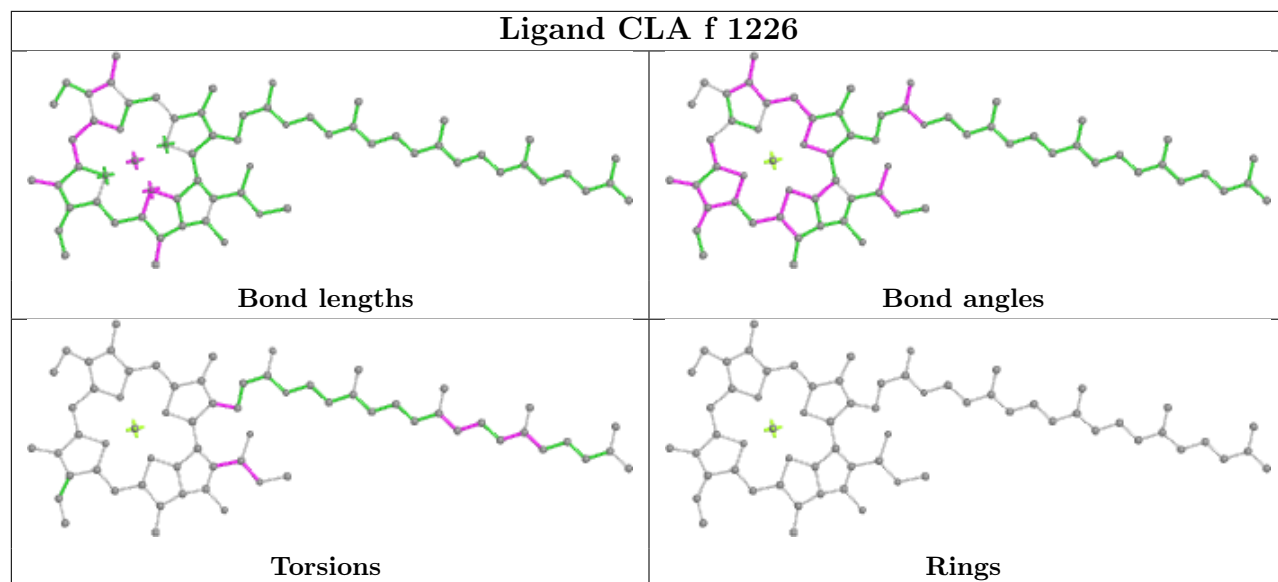


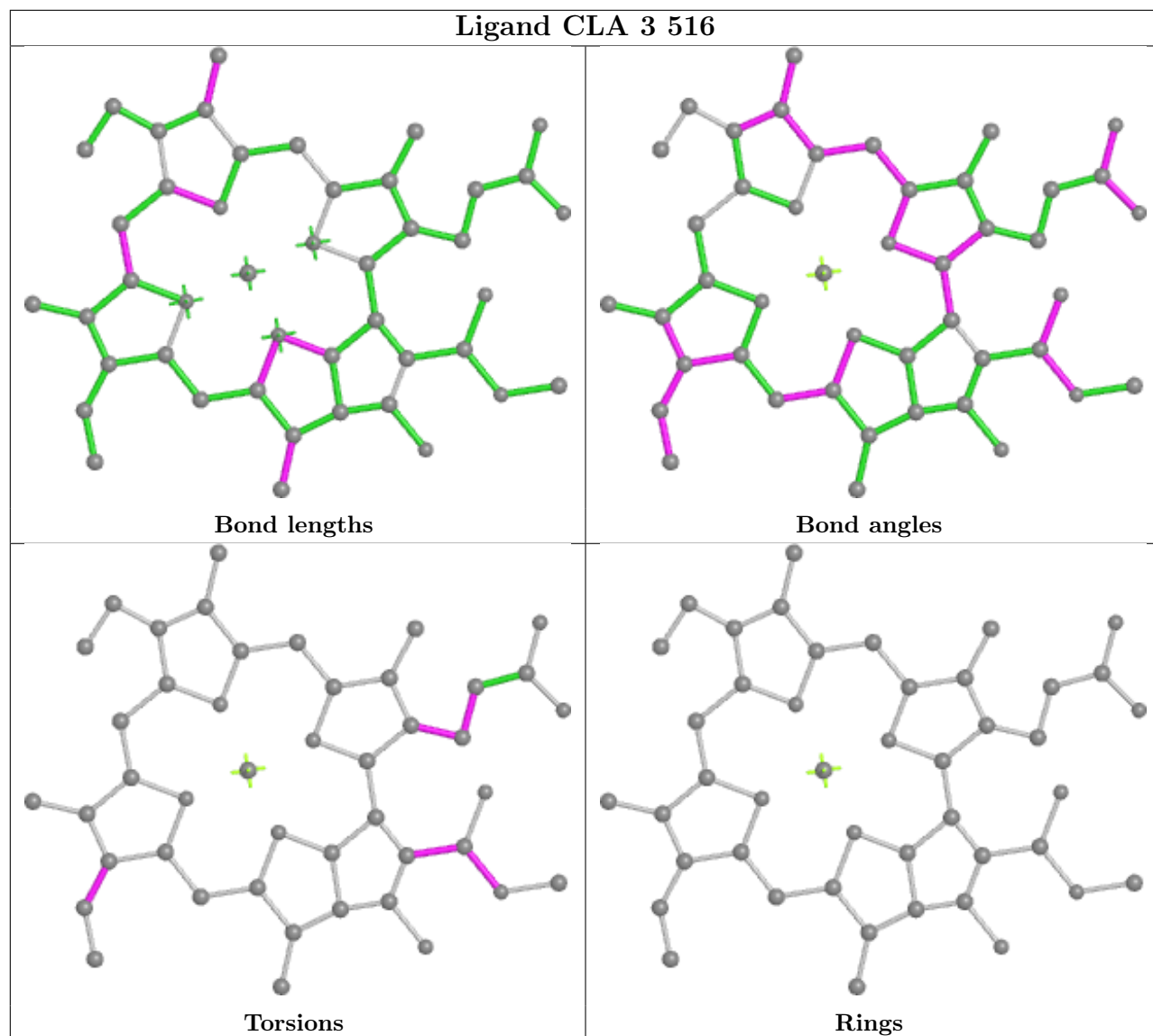


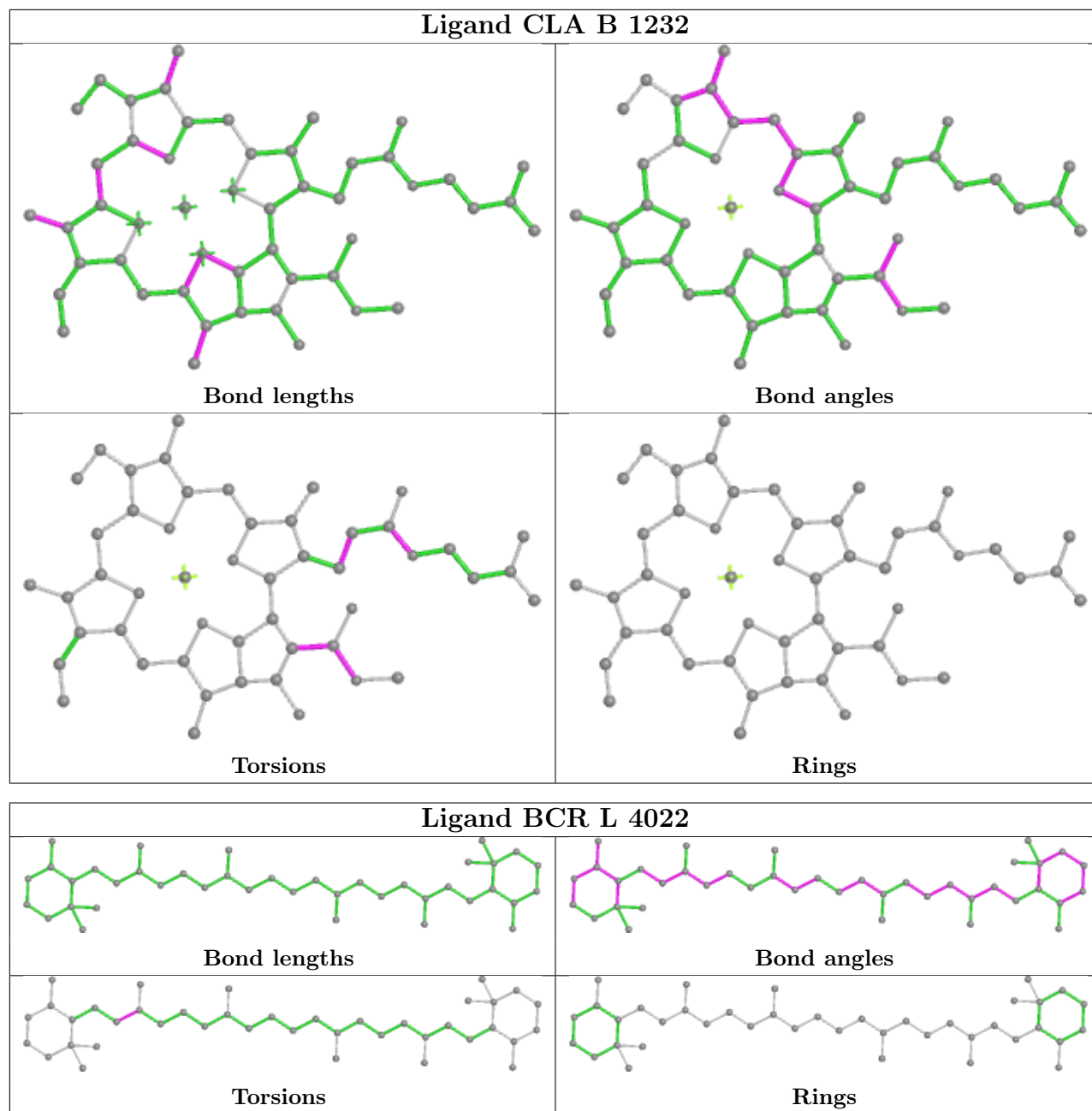


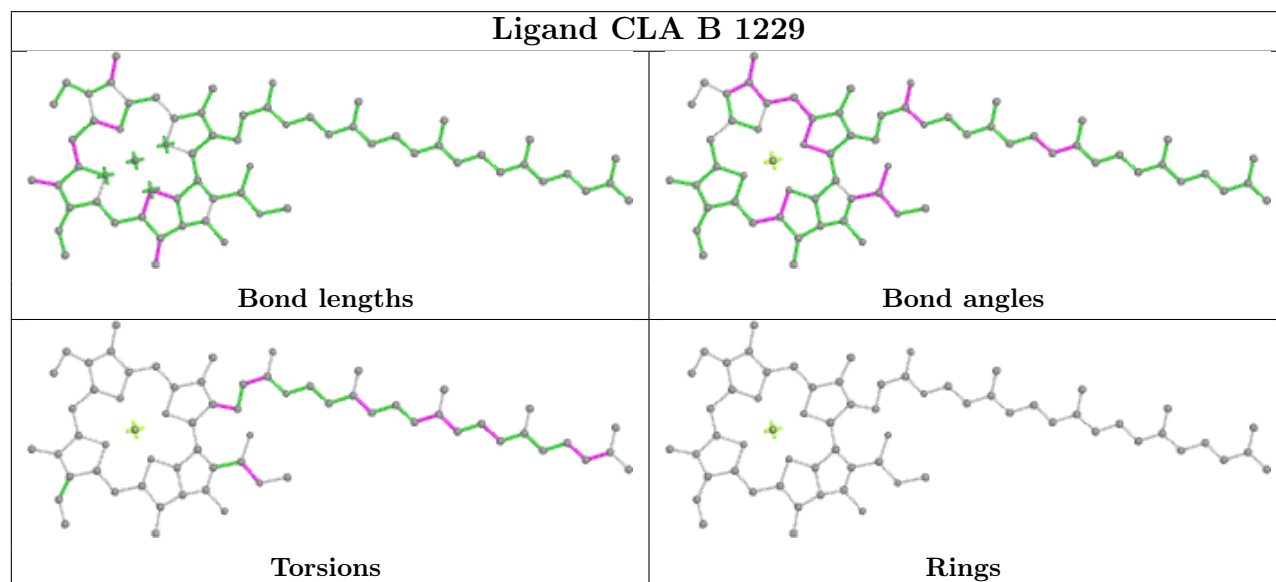
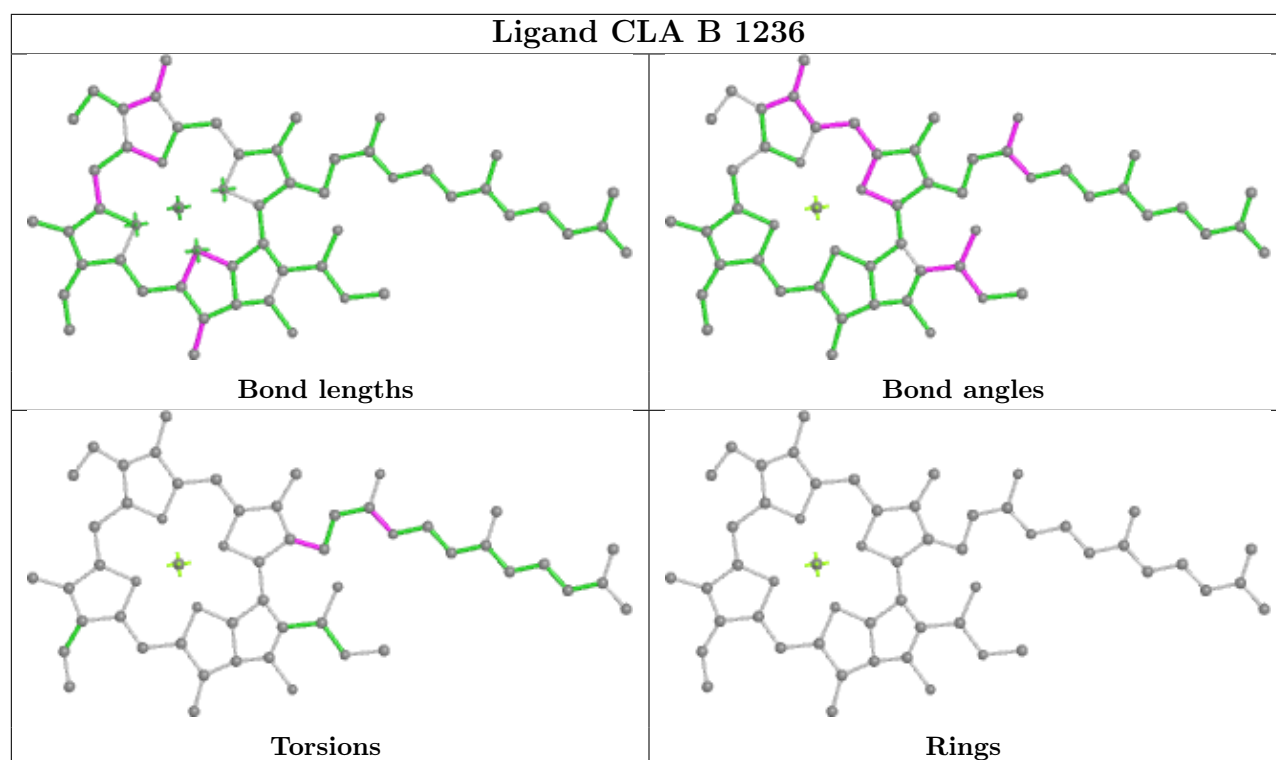


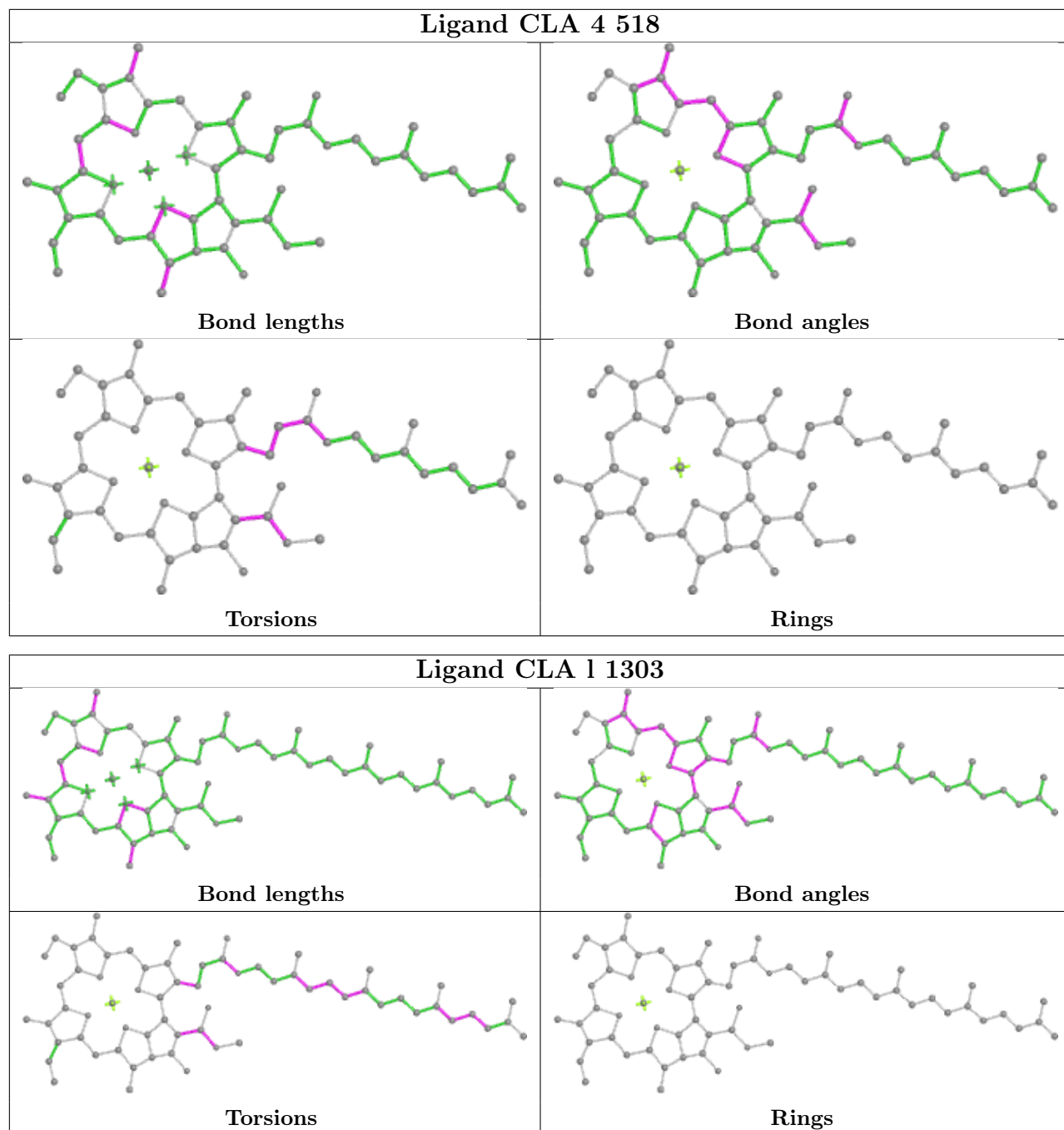




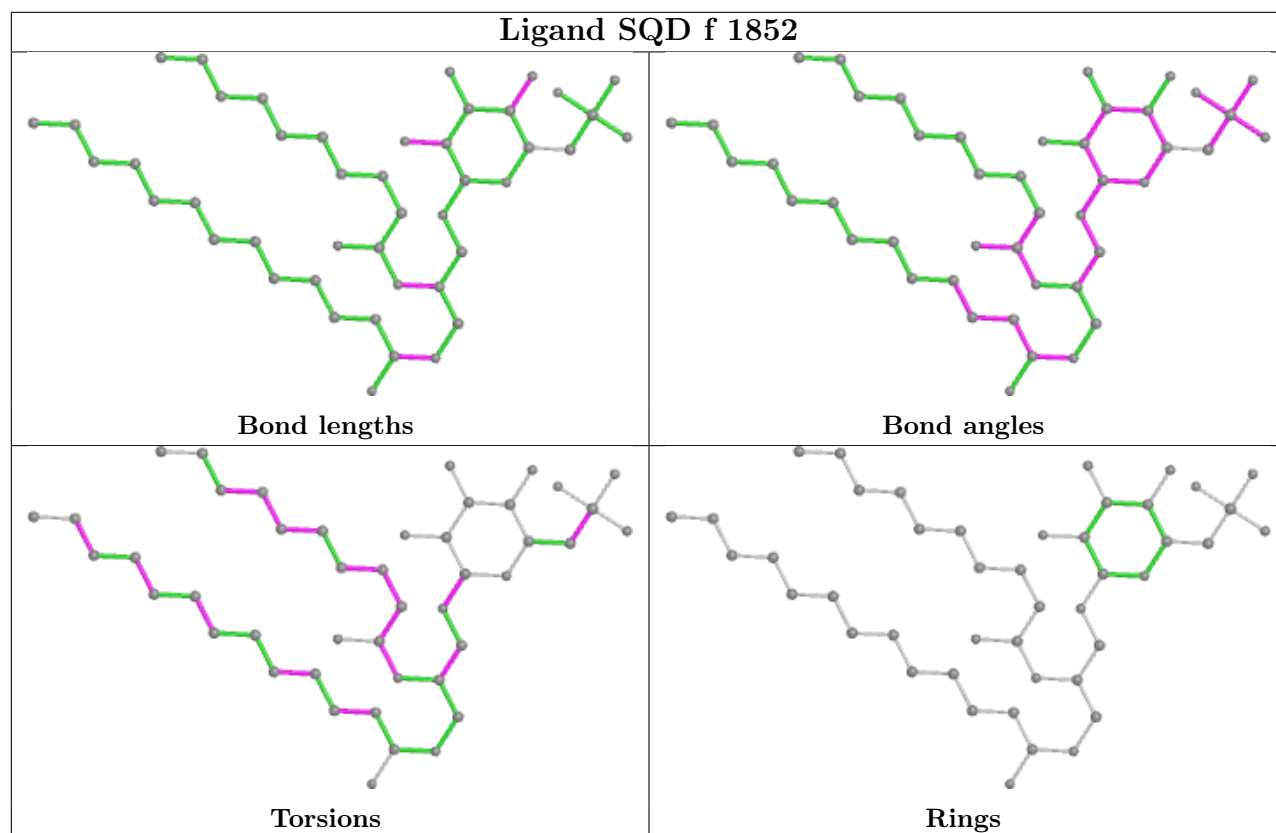
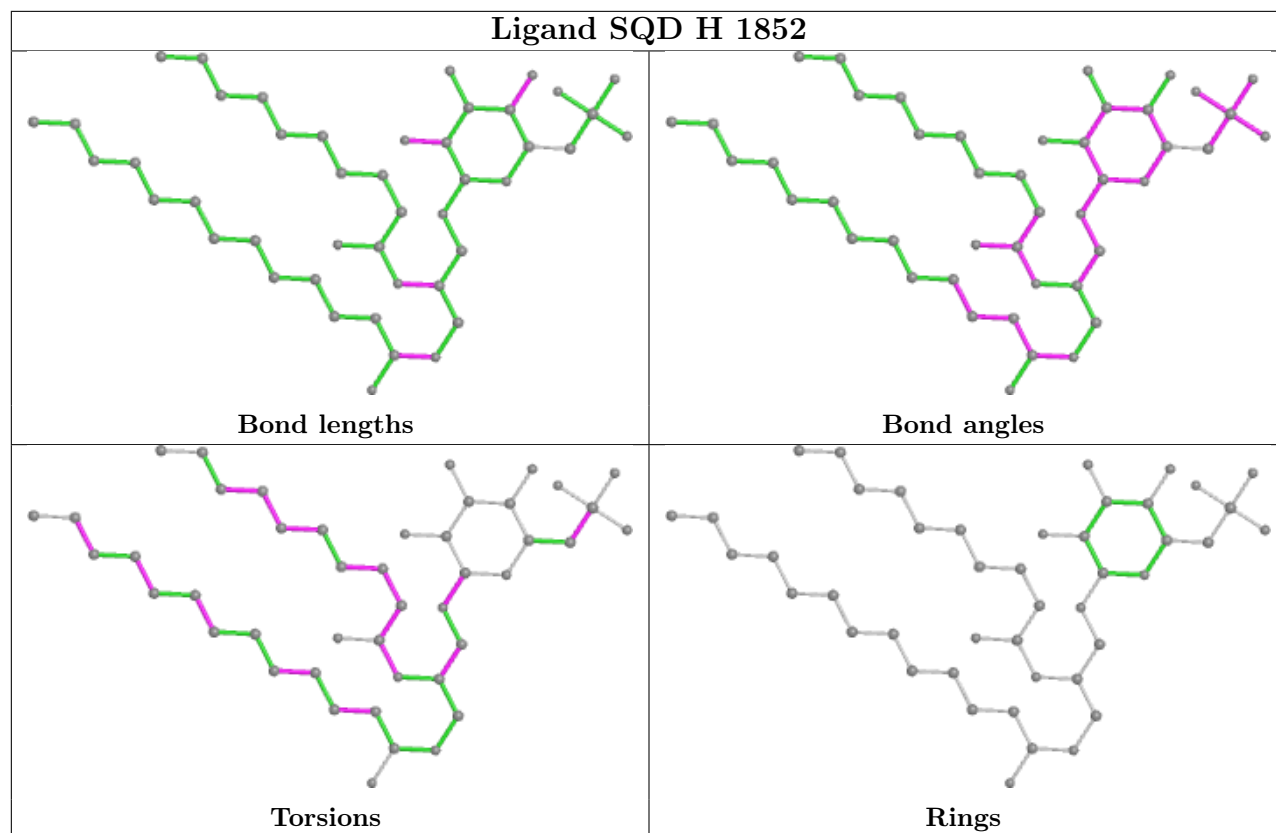


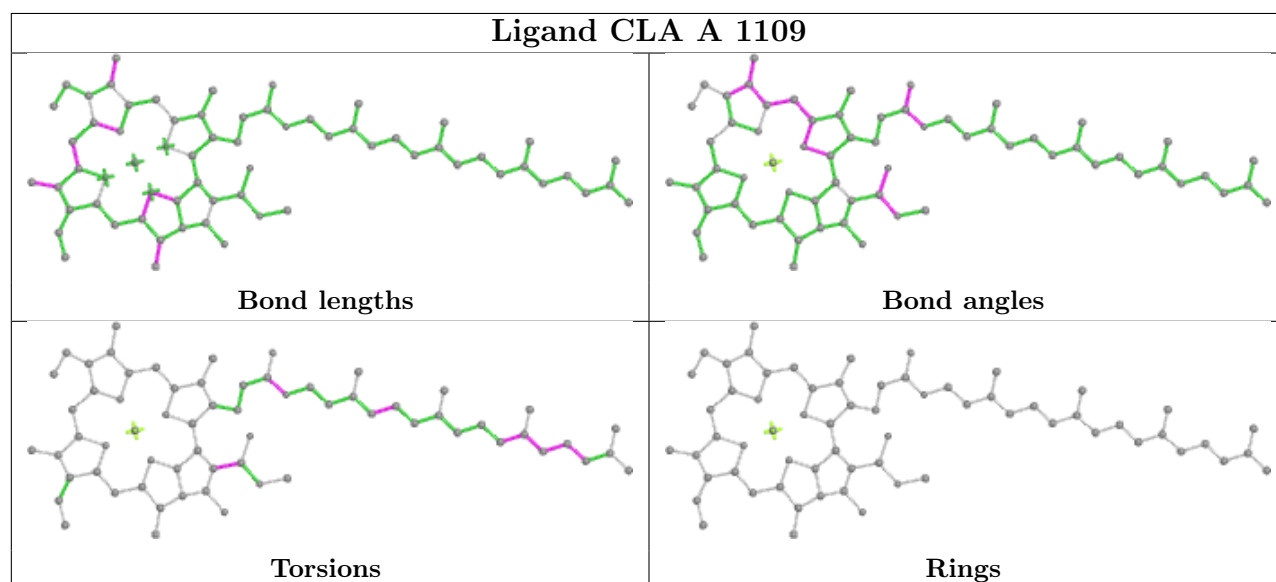
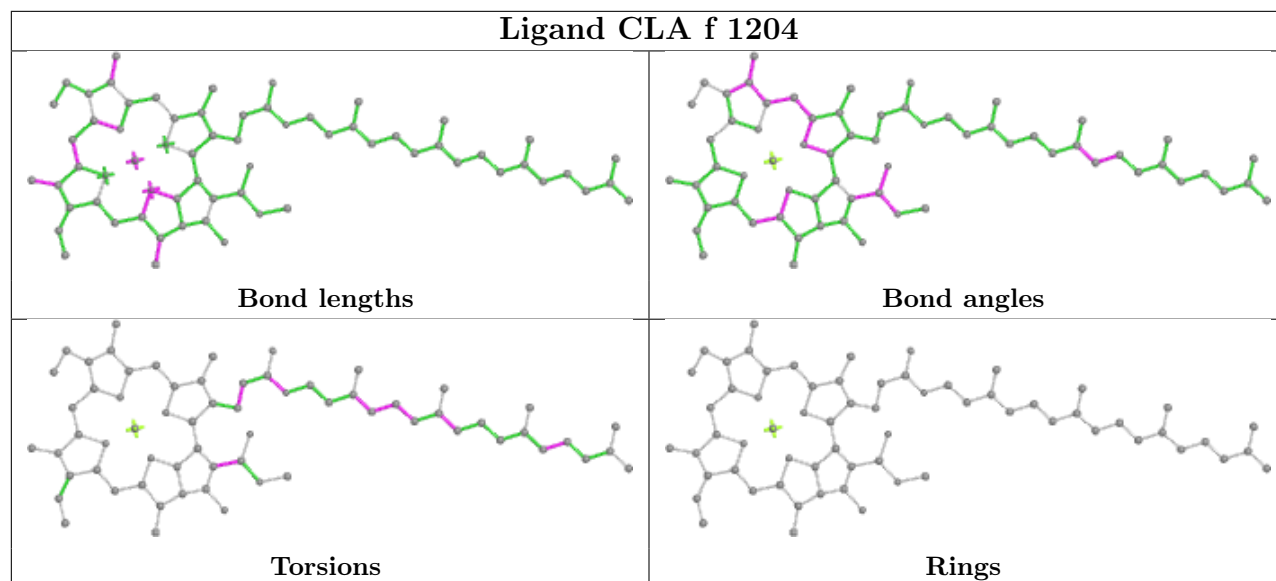
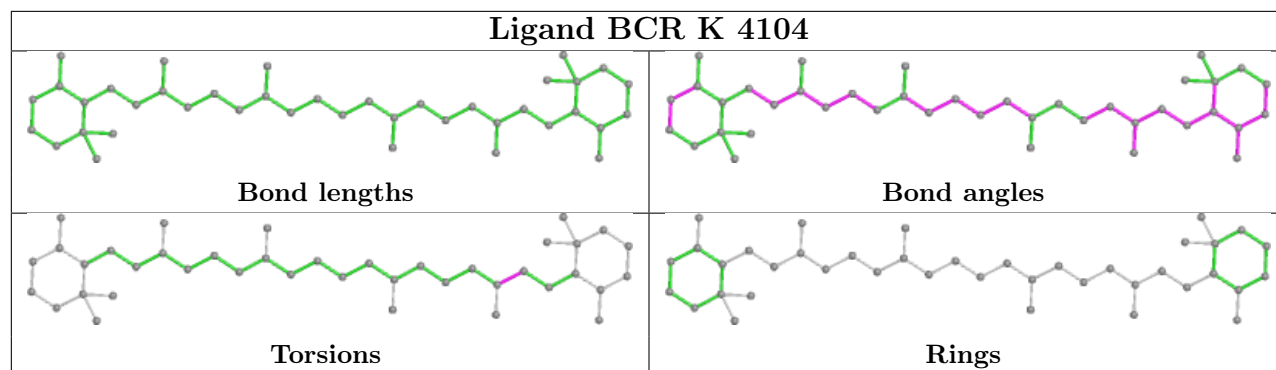


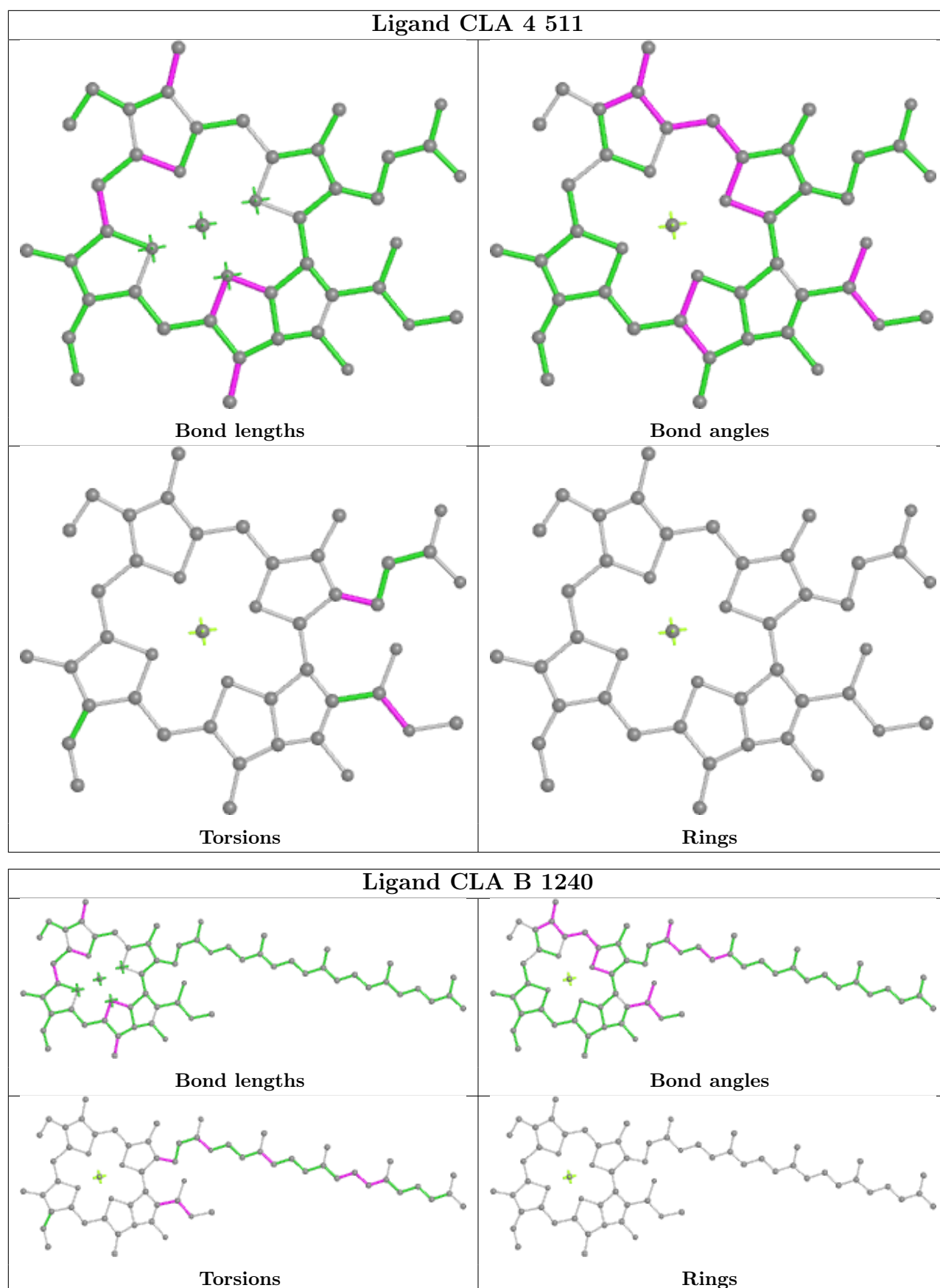


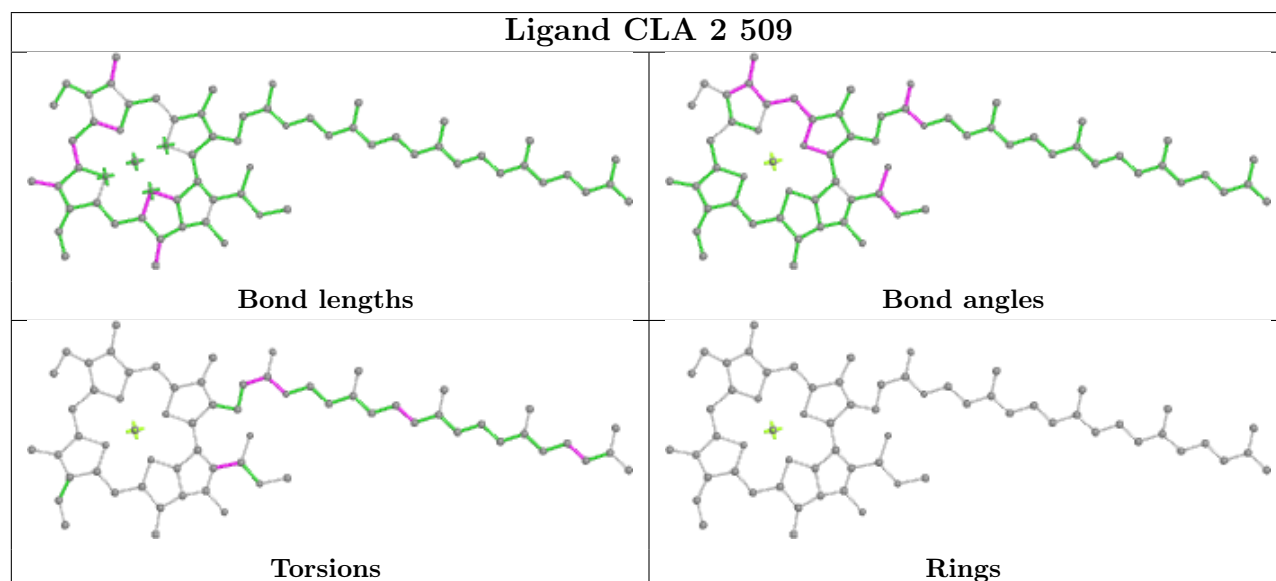
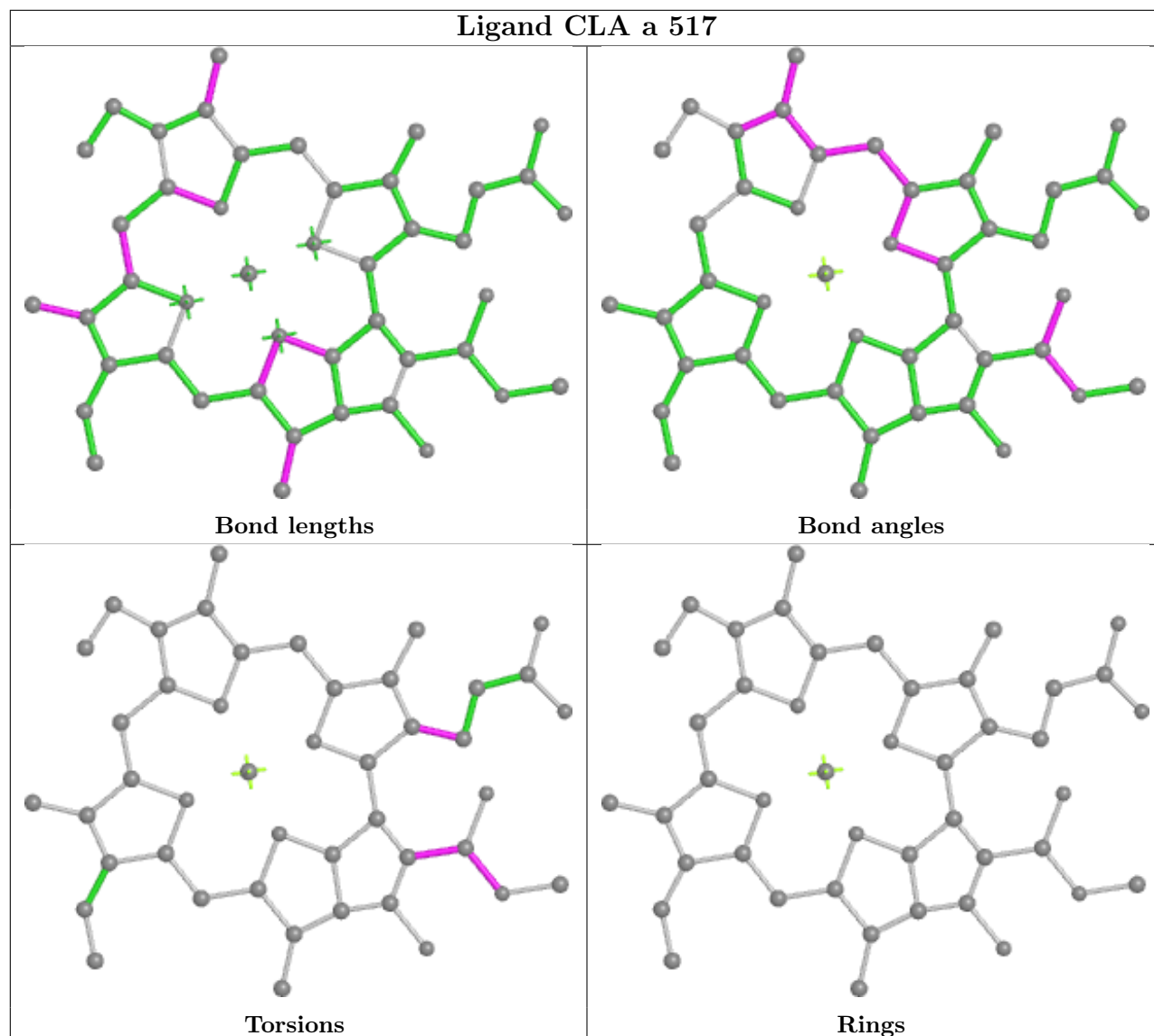


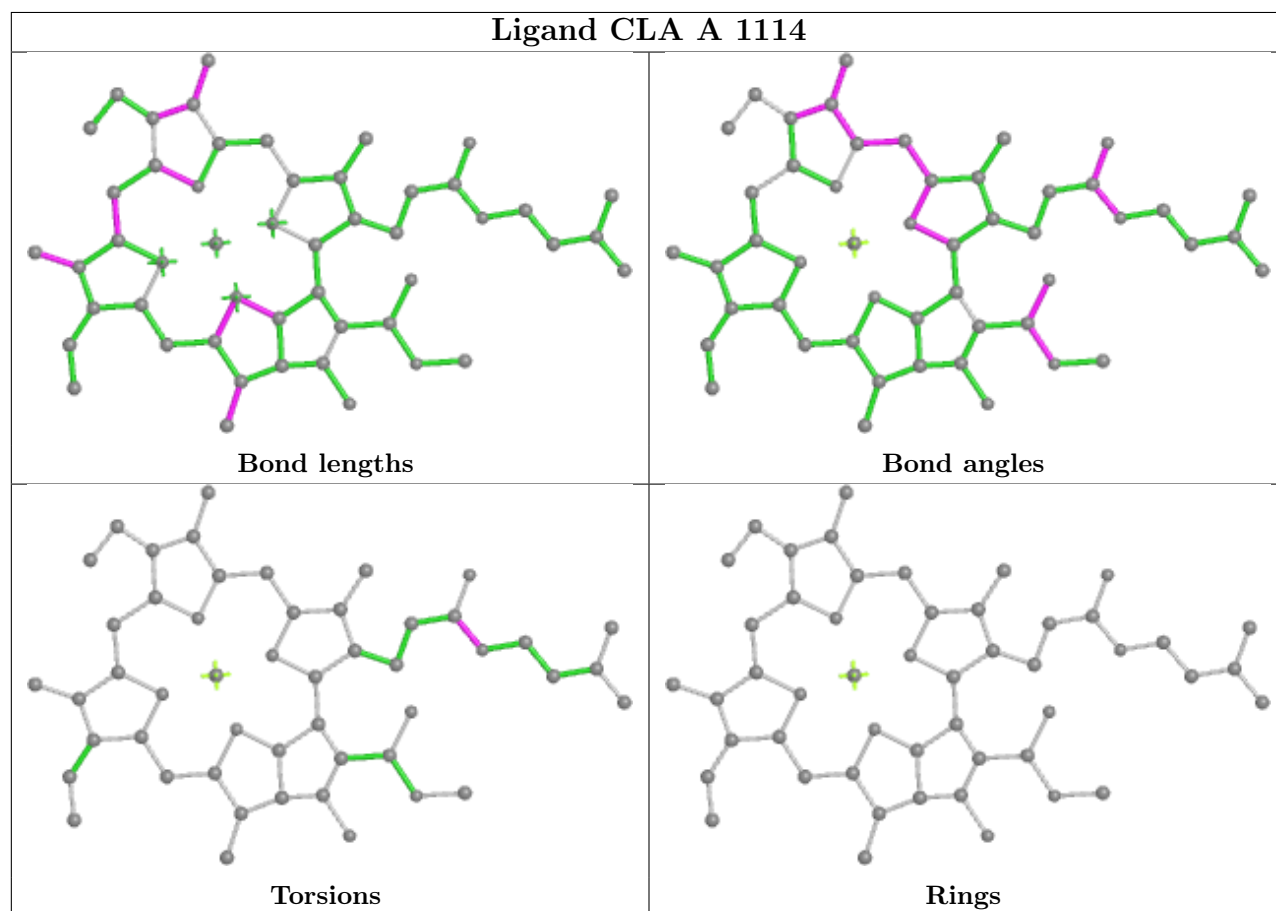
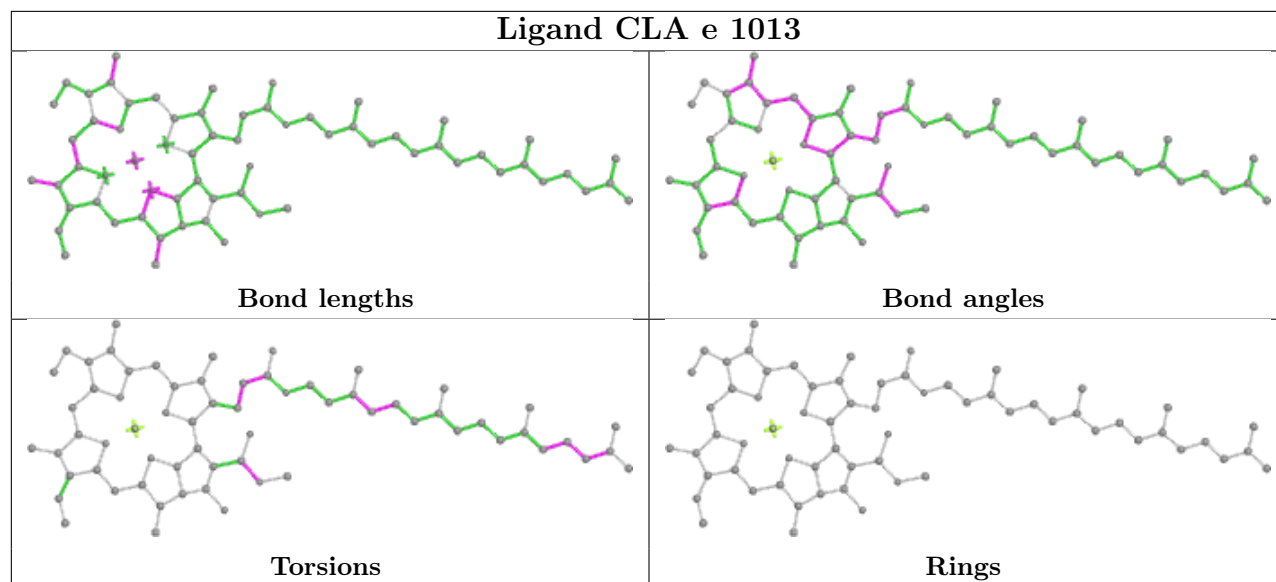


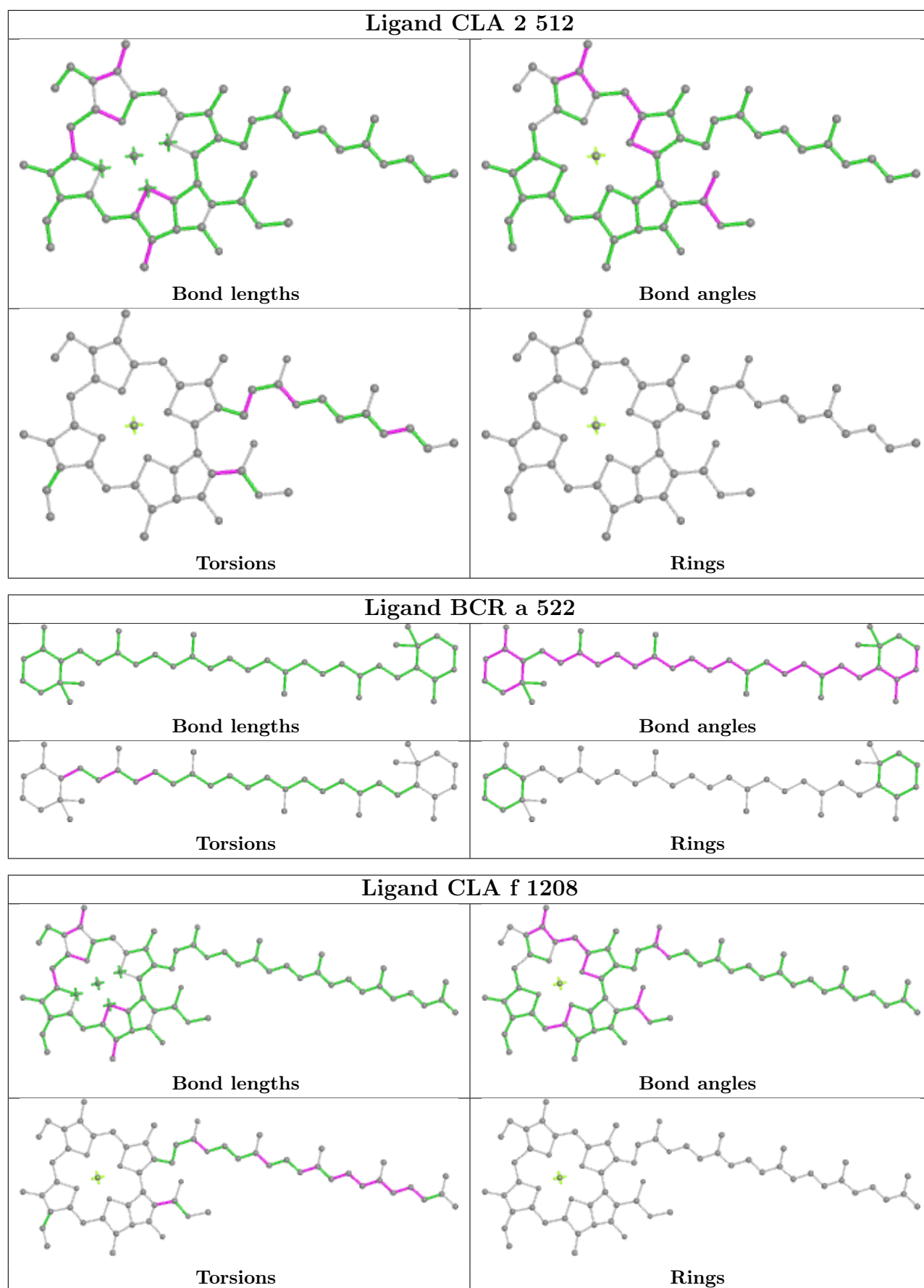


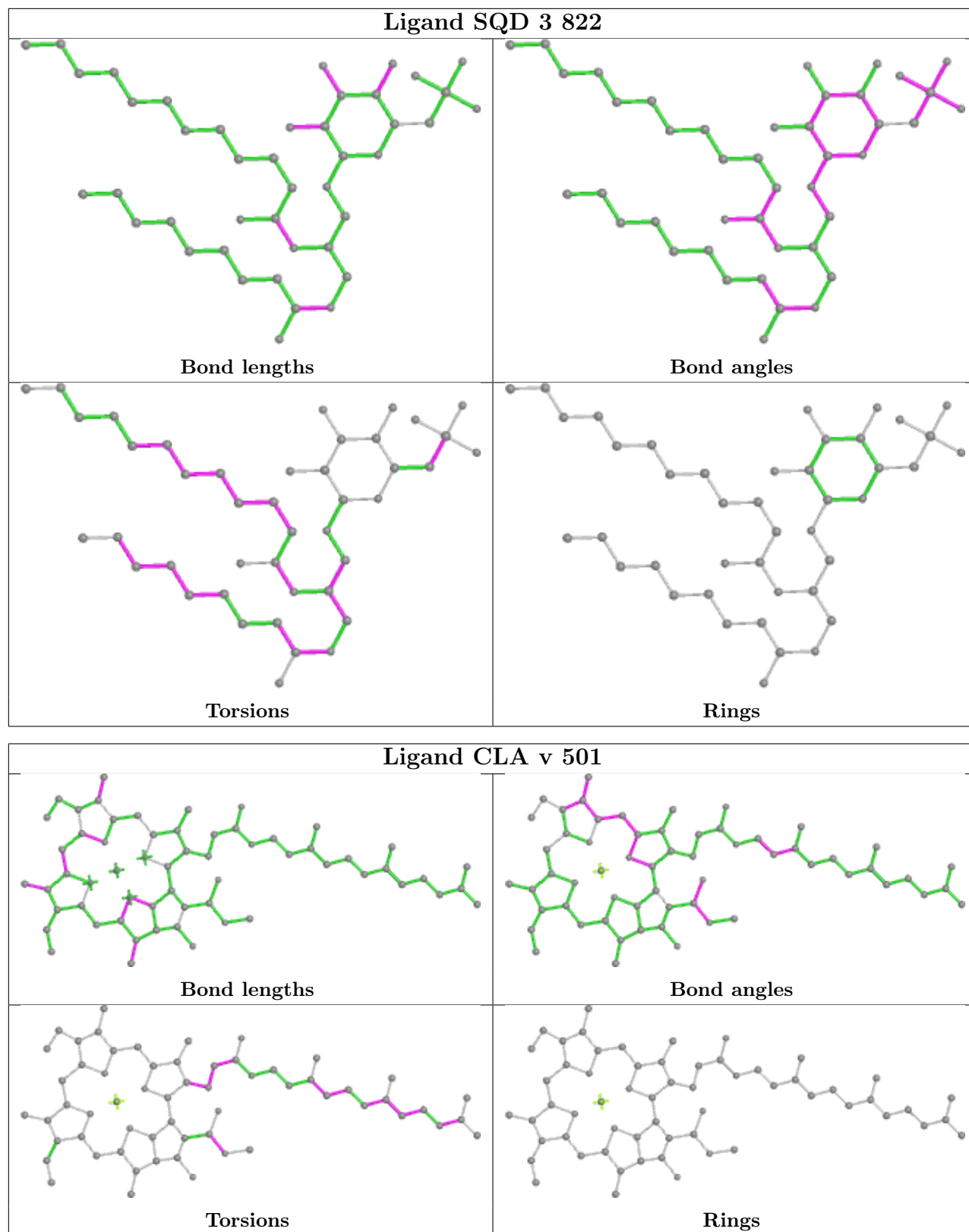


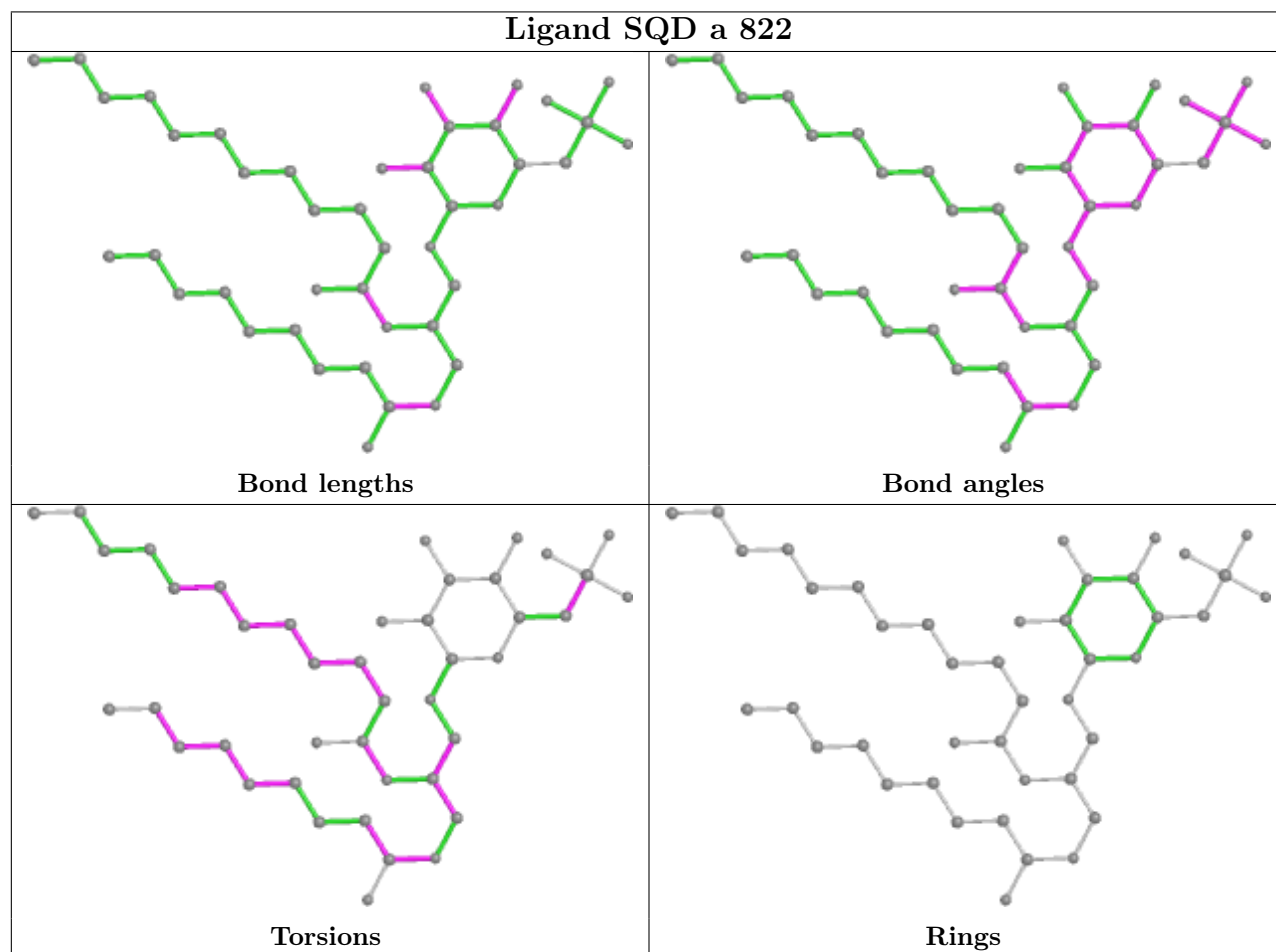
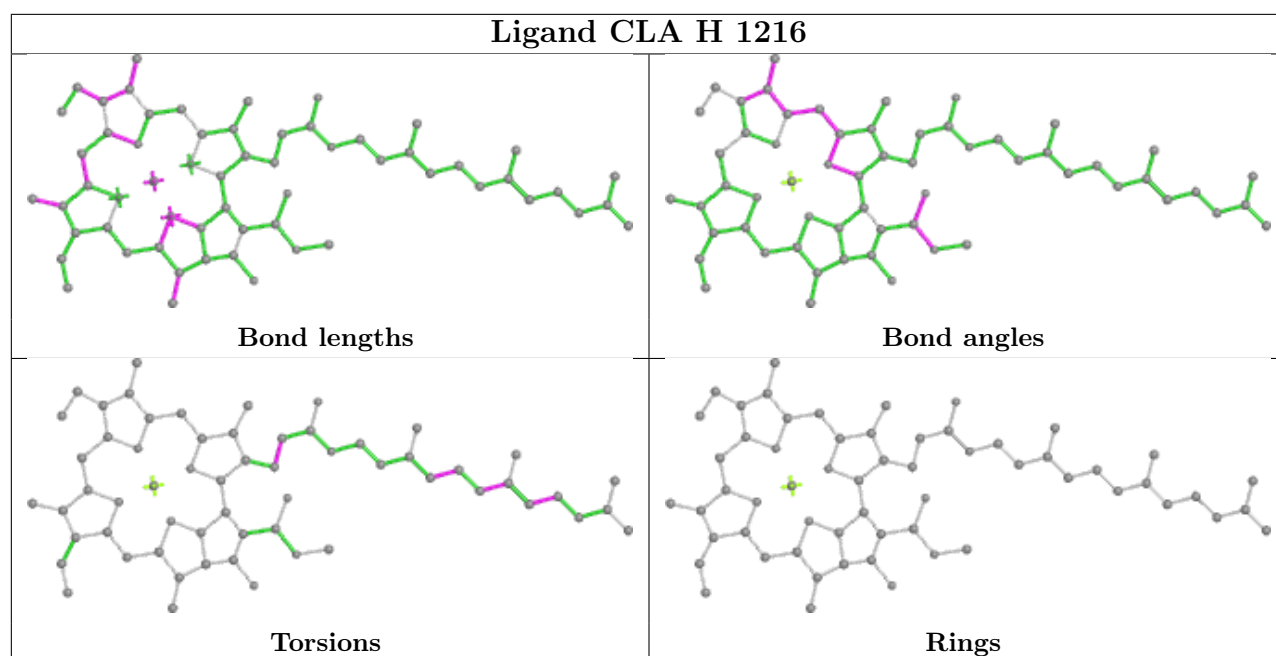




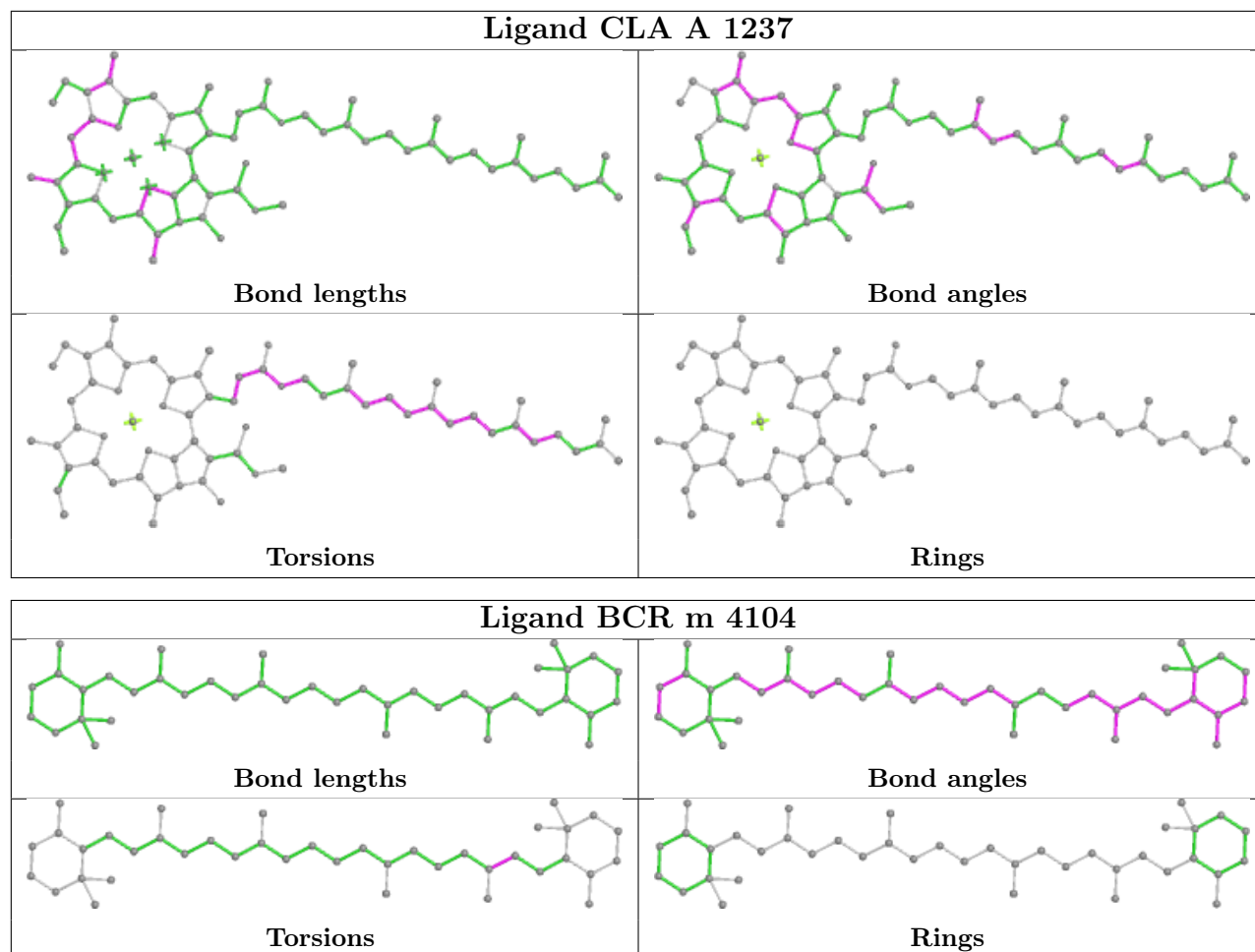


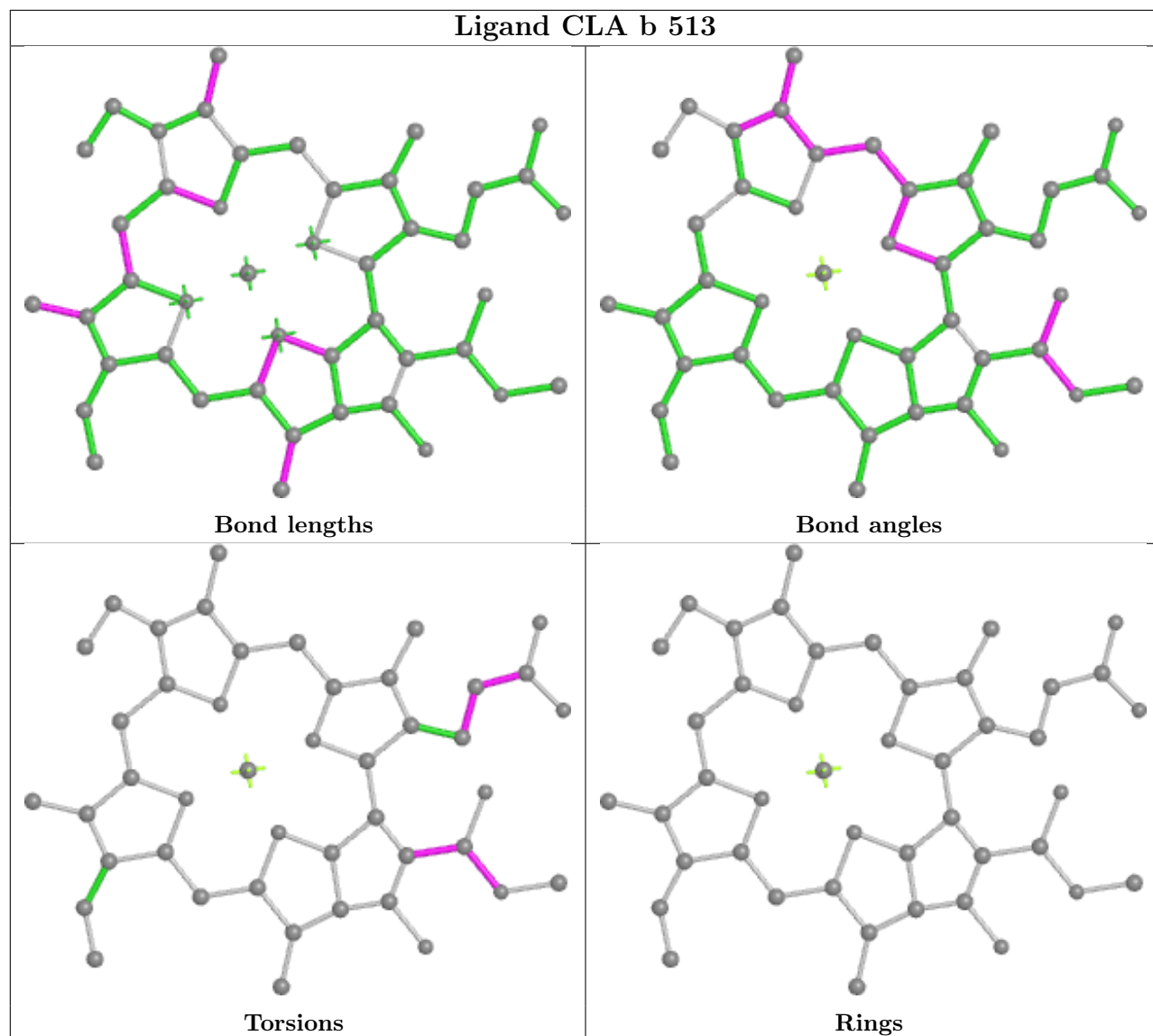


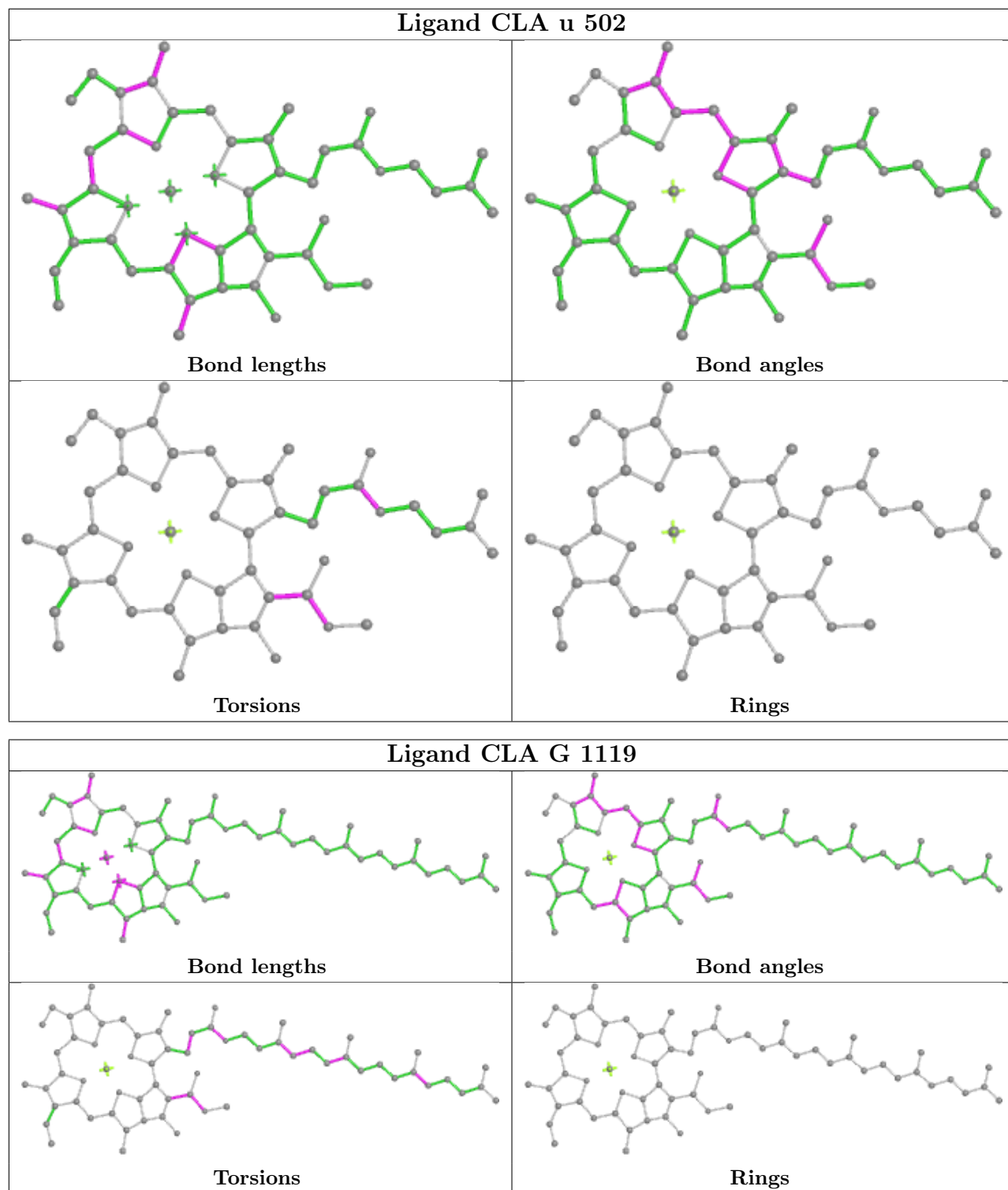


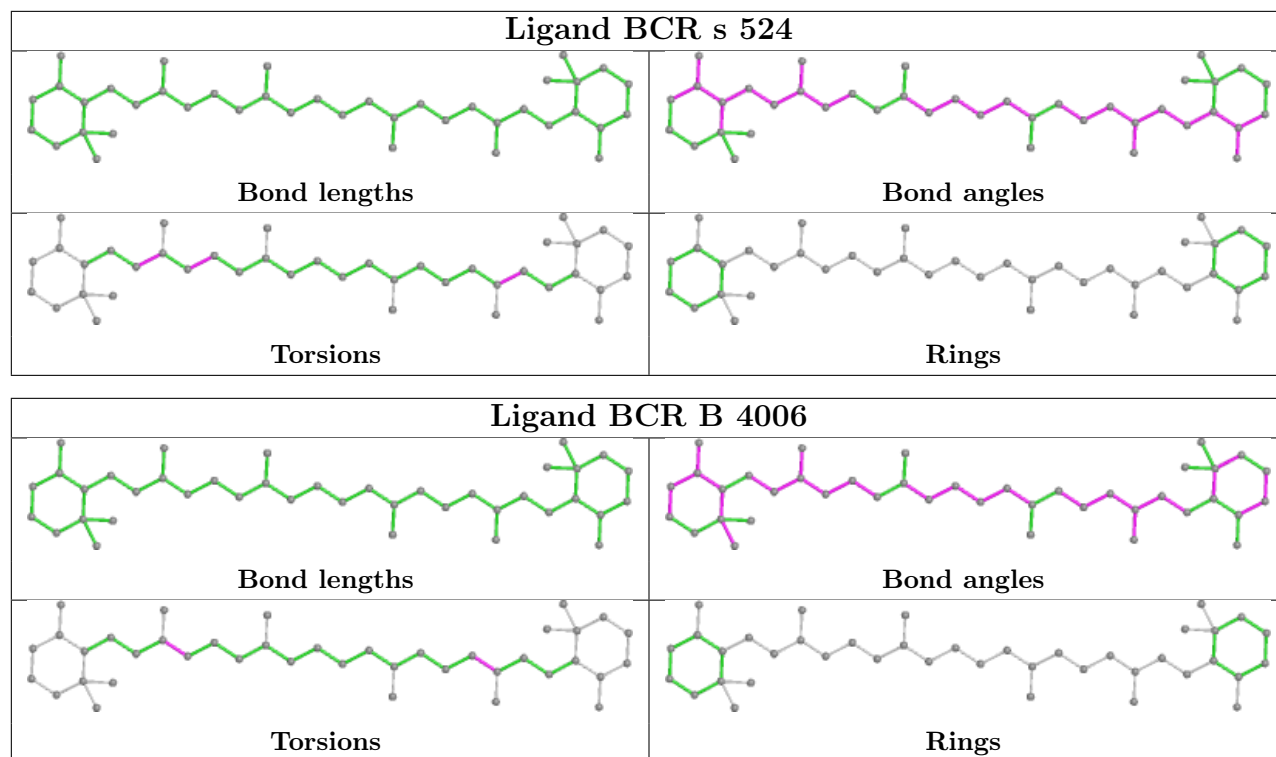


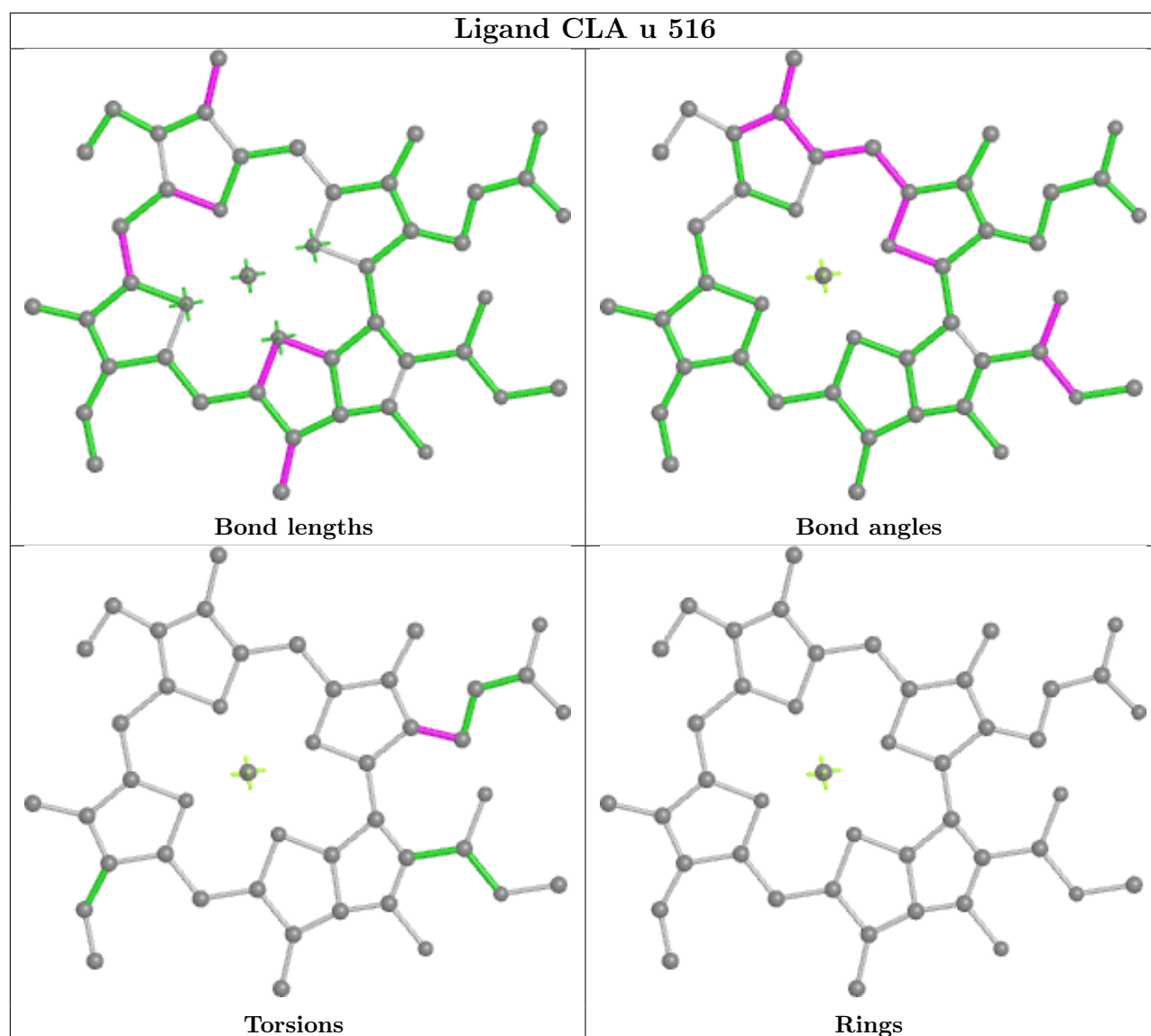


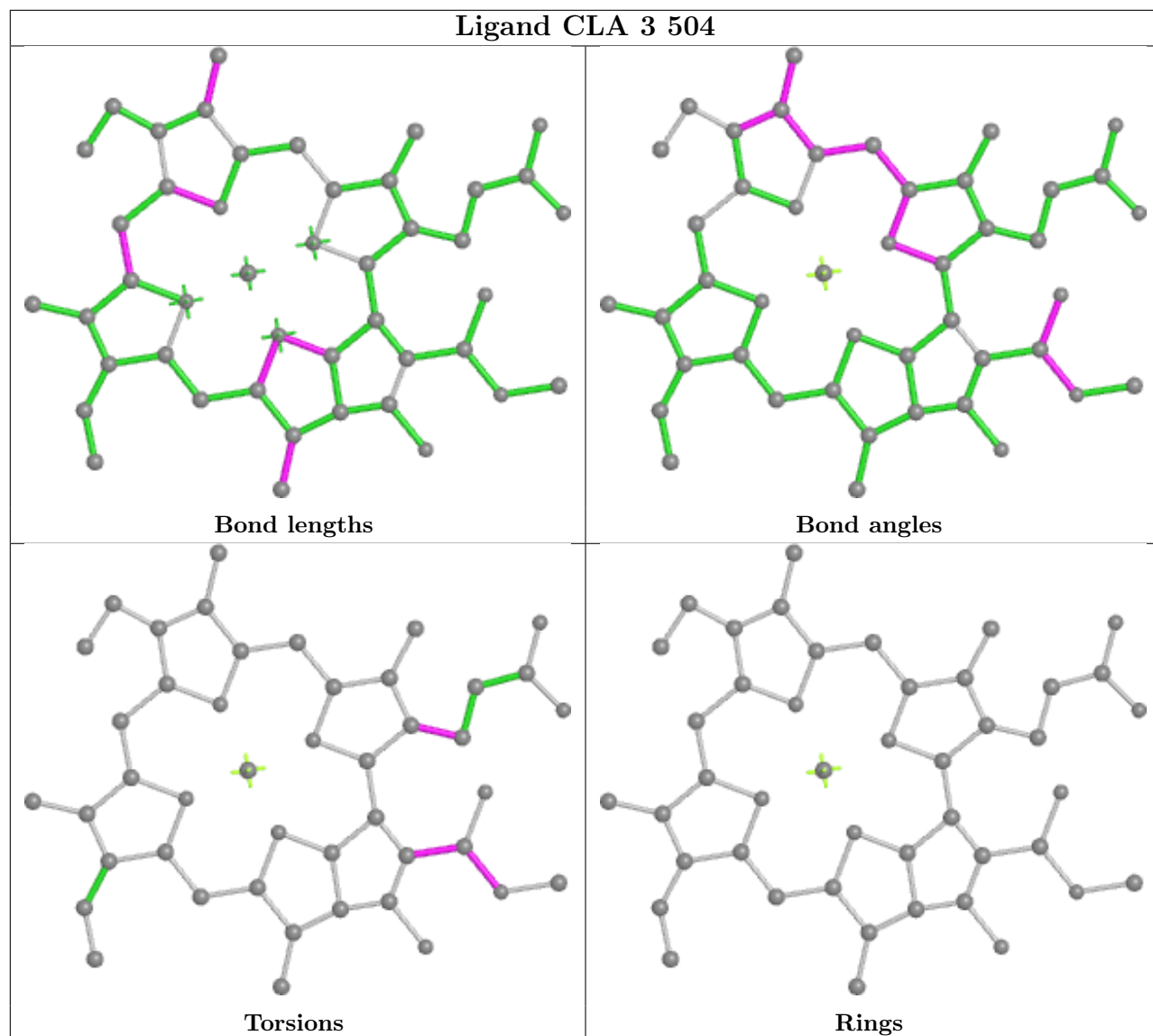


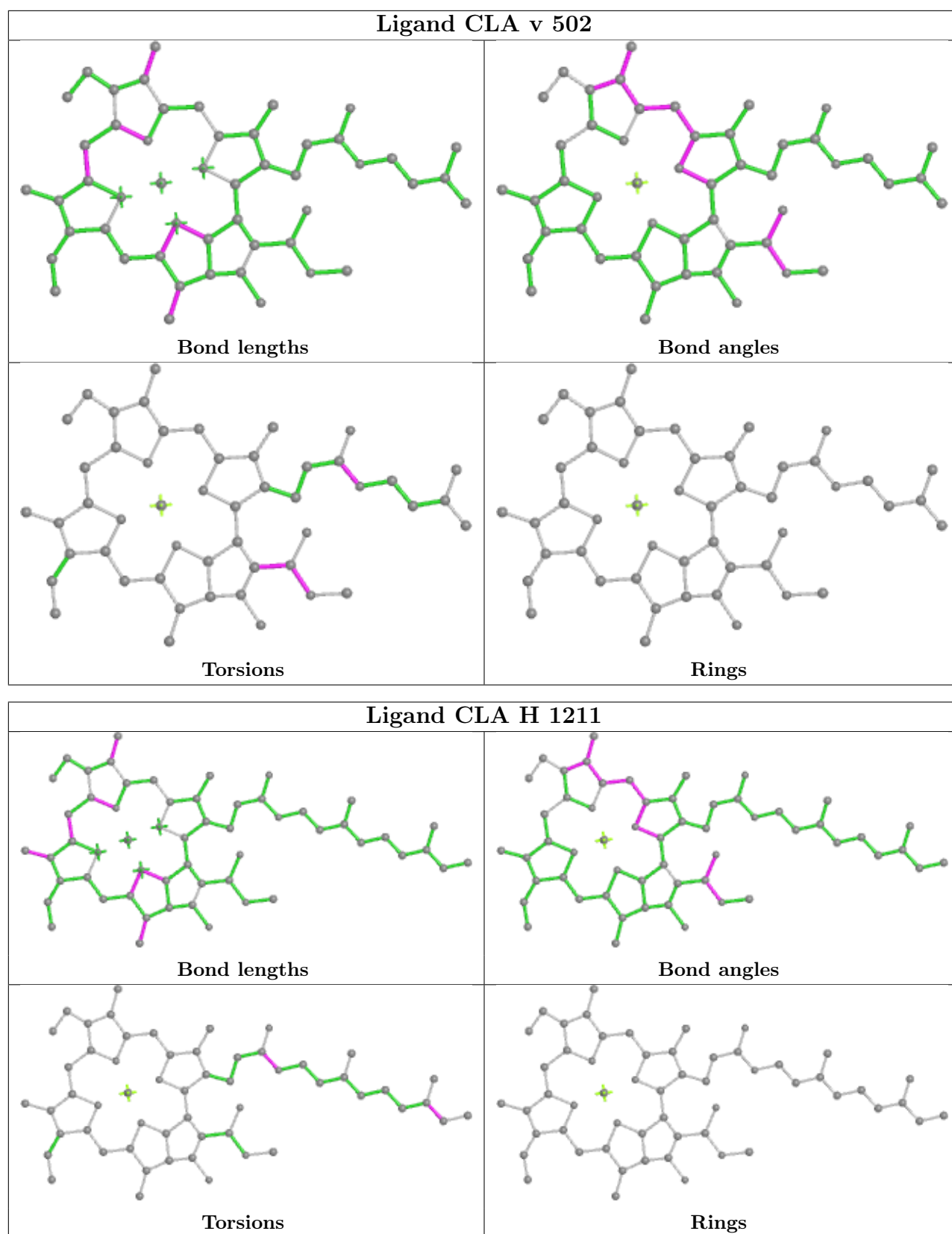


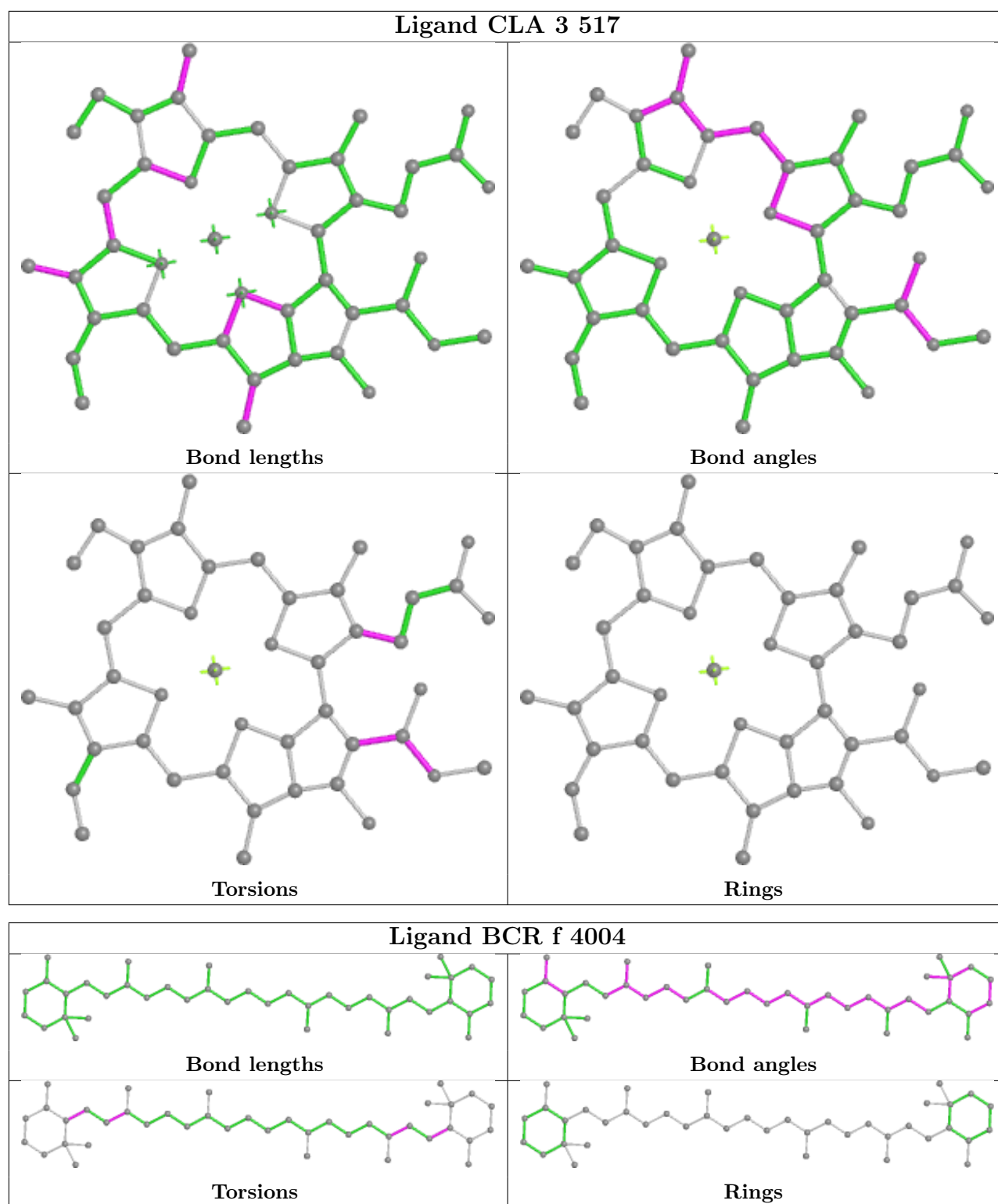




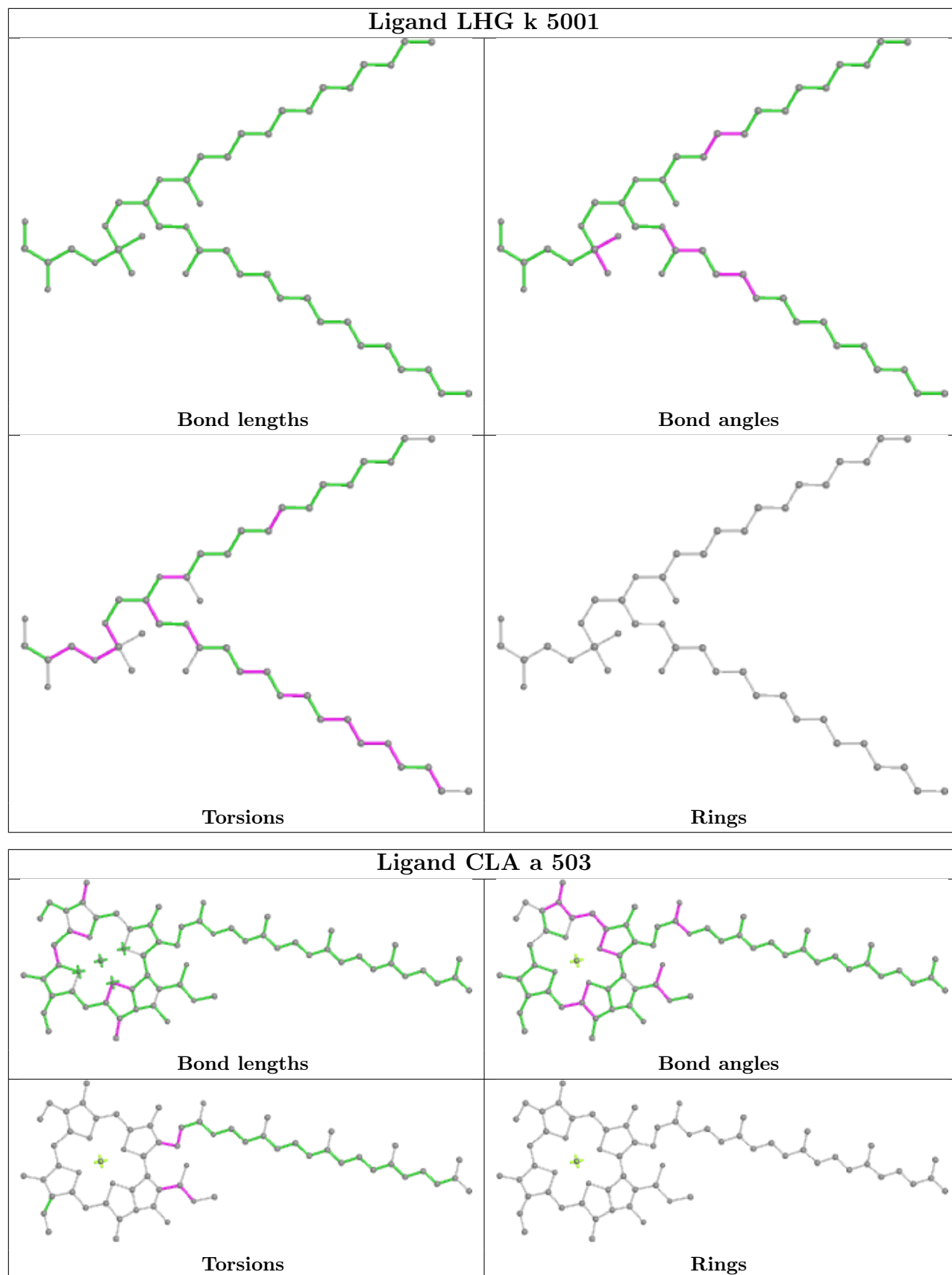


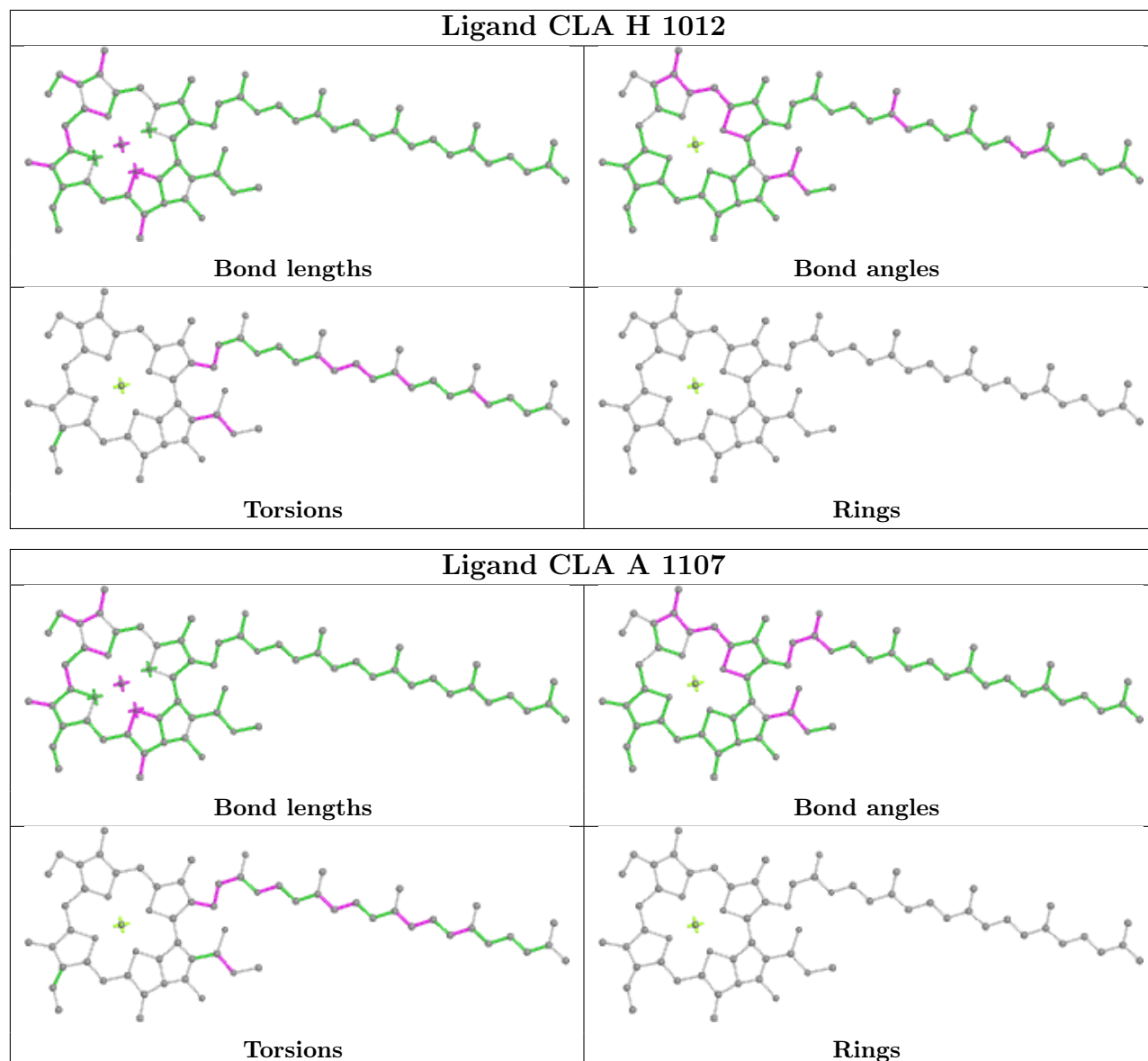


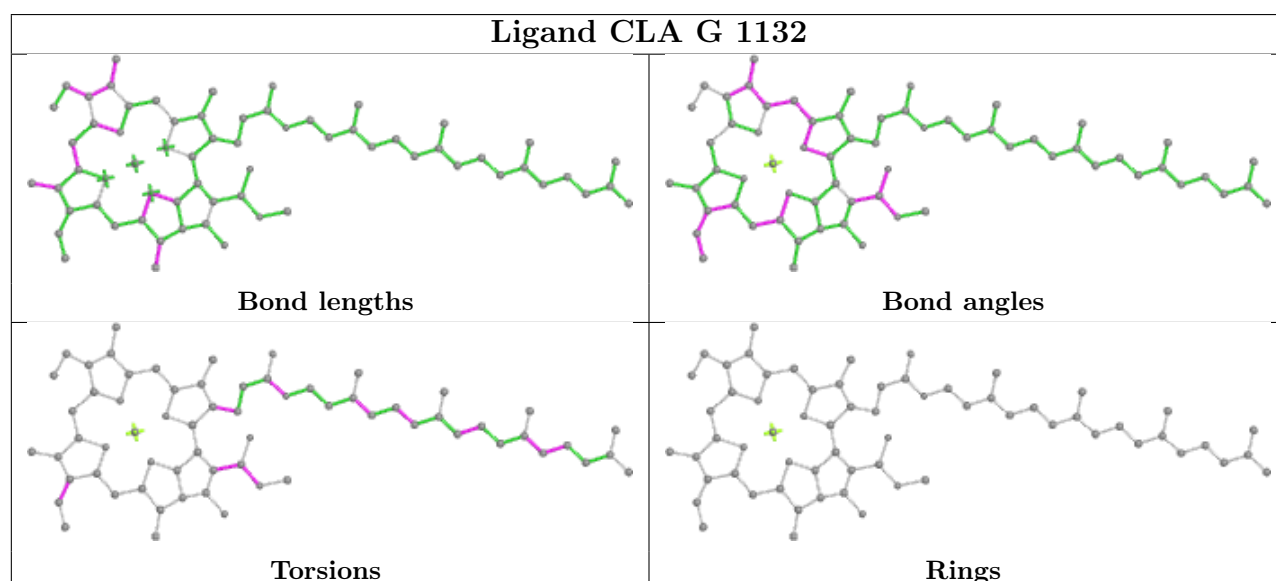
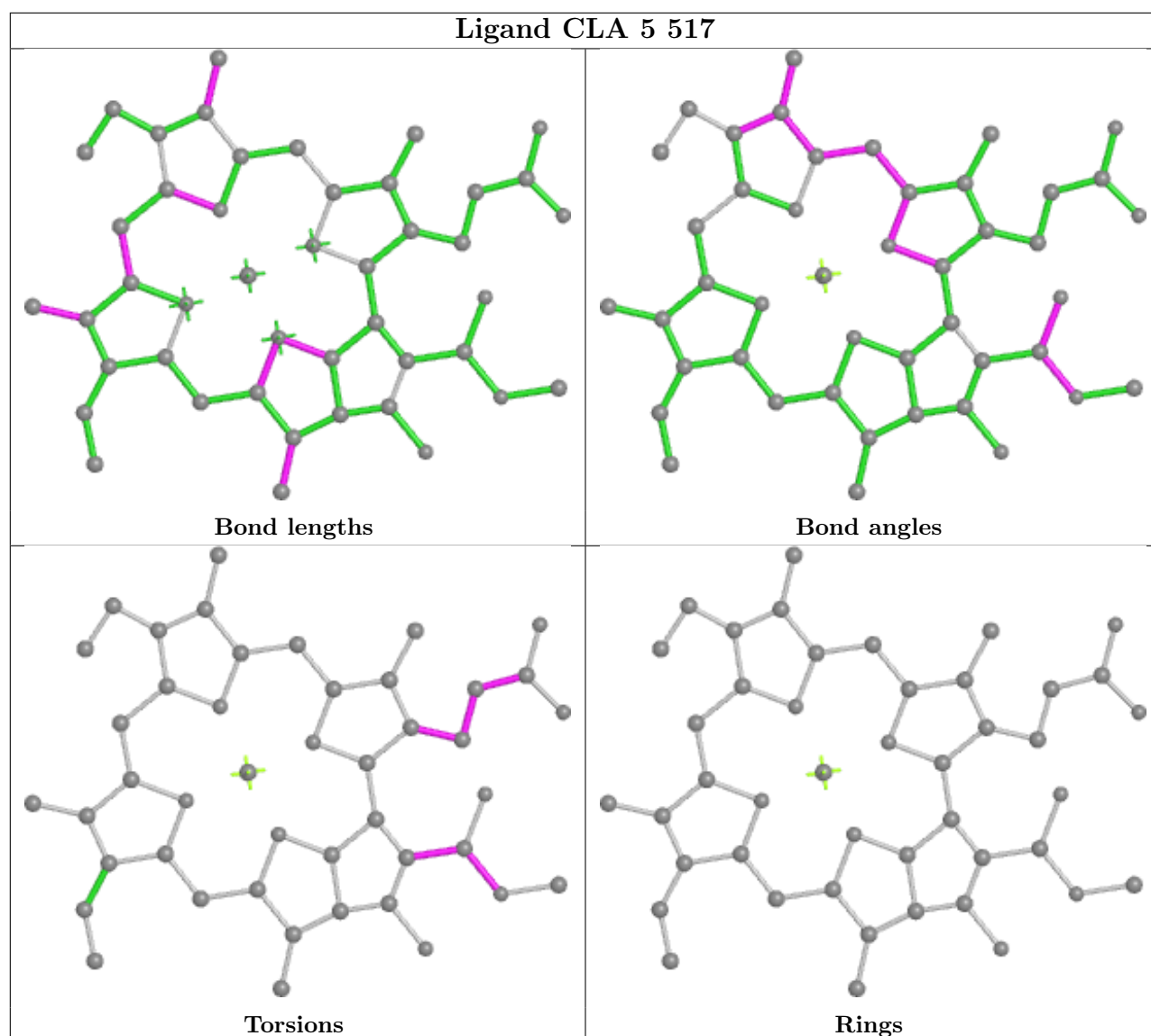


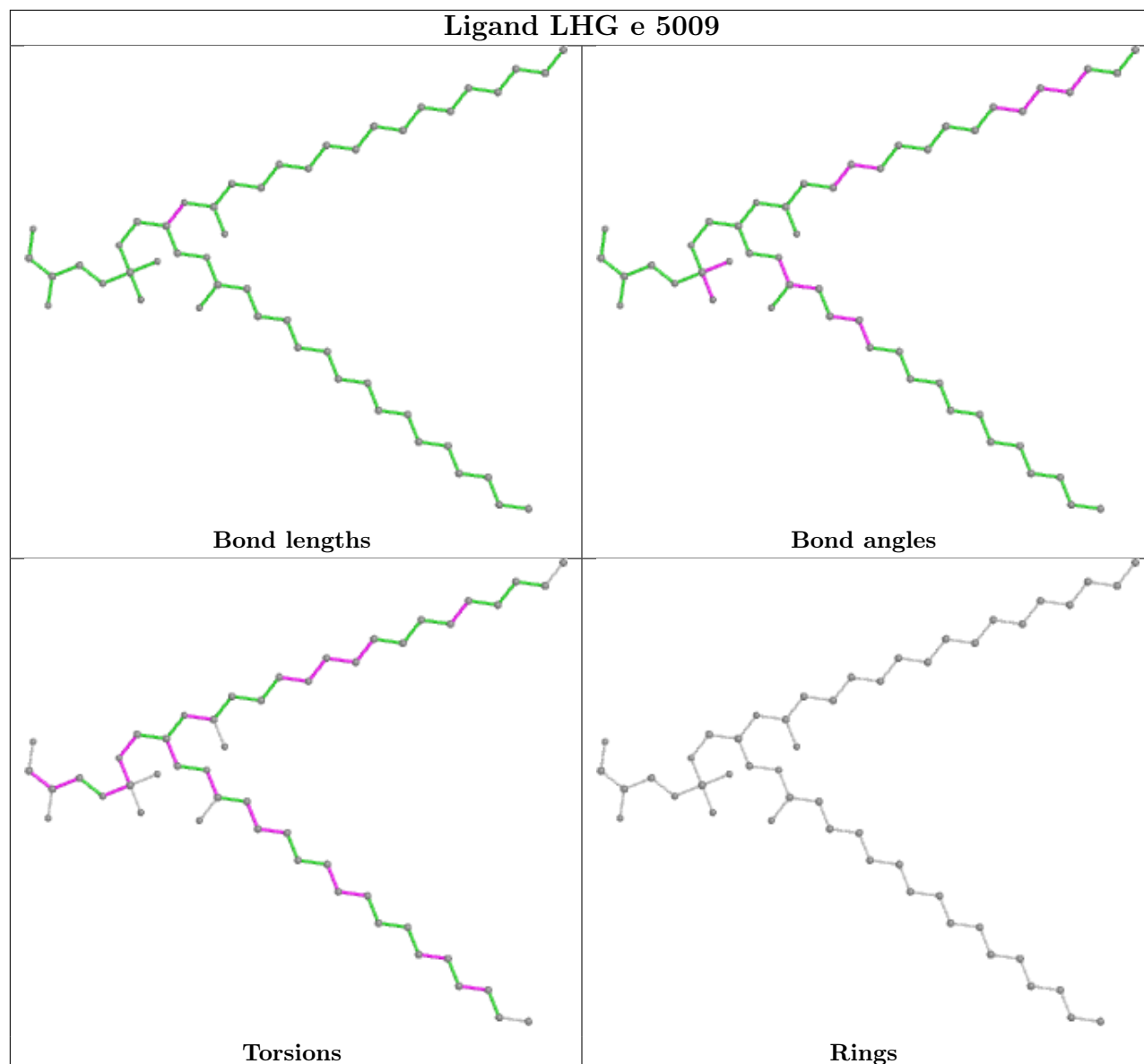
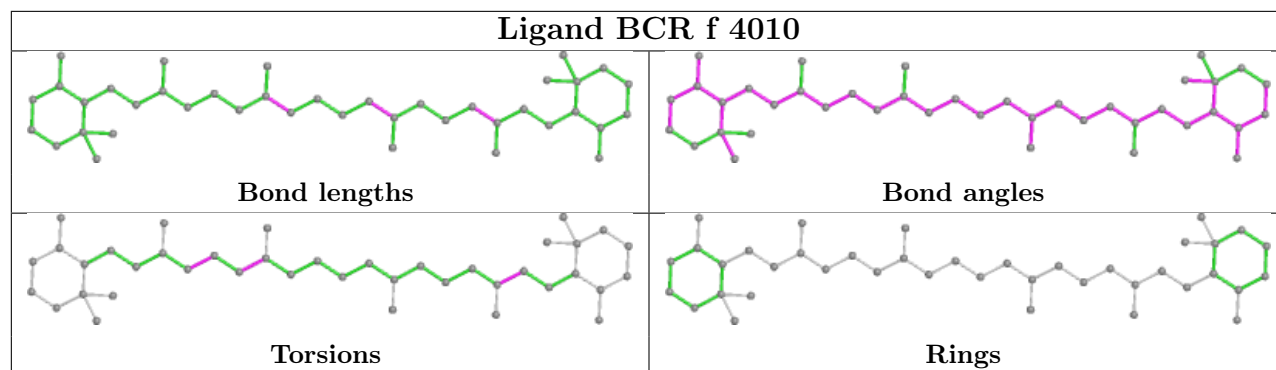


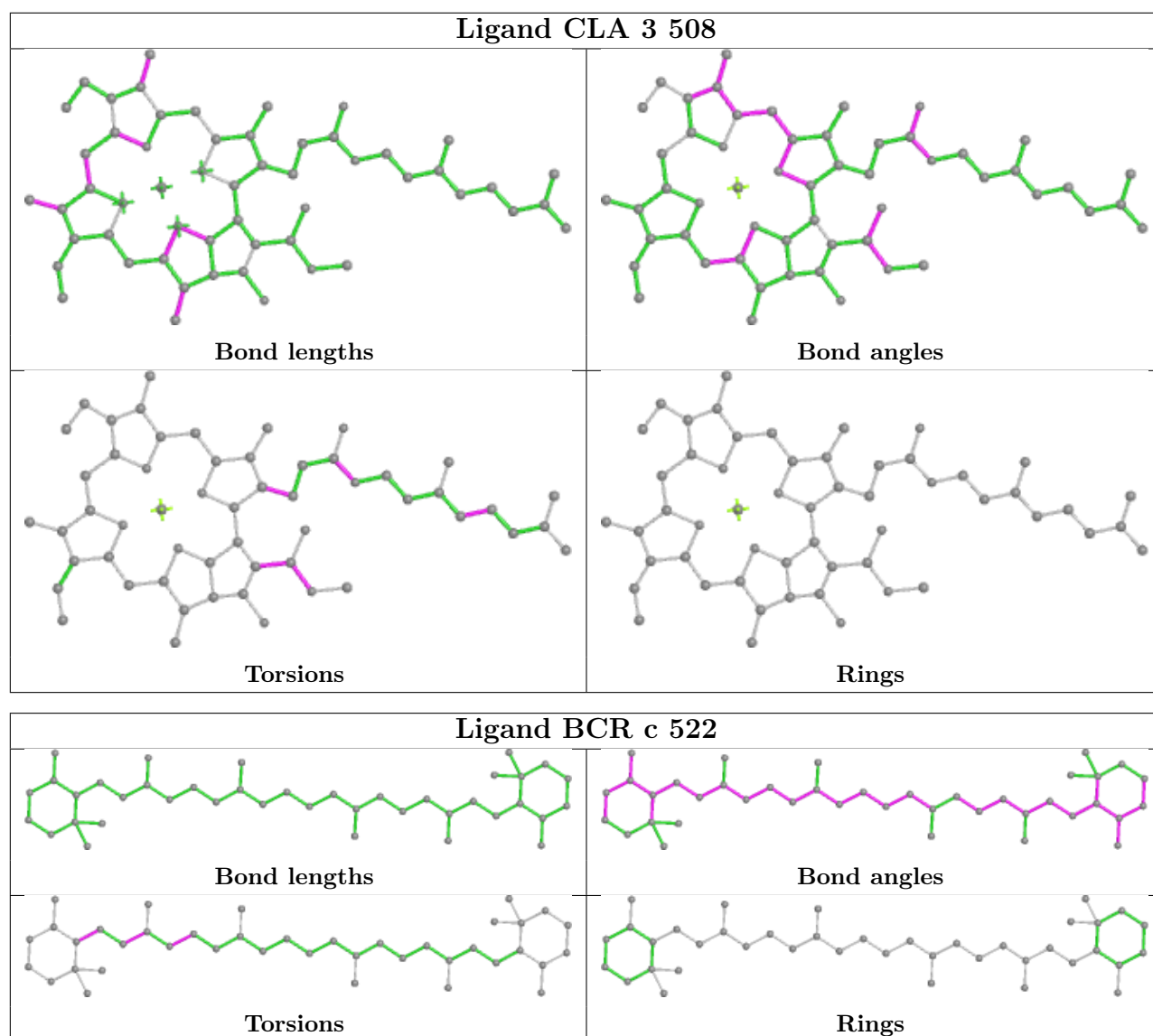












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

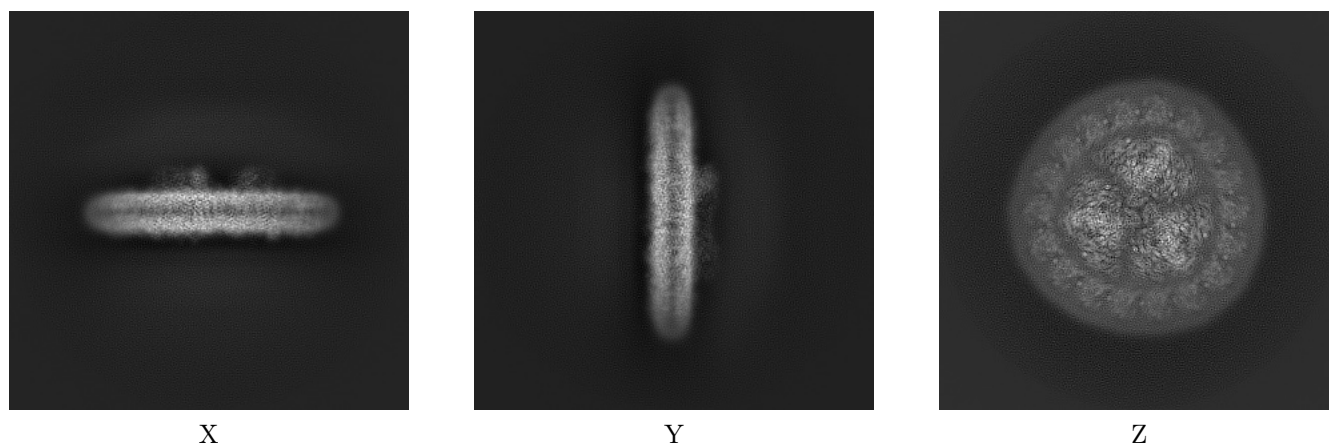
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9995. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

### 6.1 Orthogonal projections [i](#)

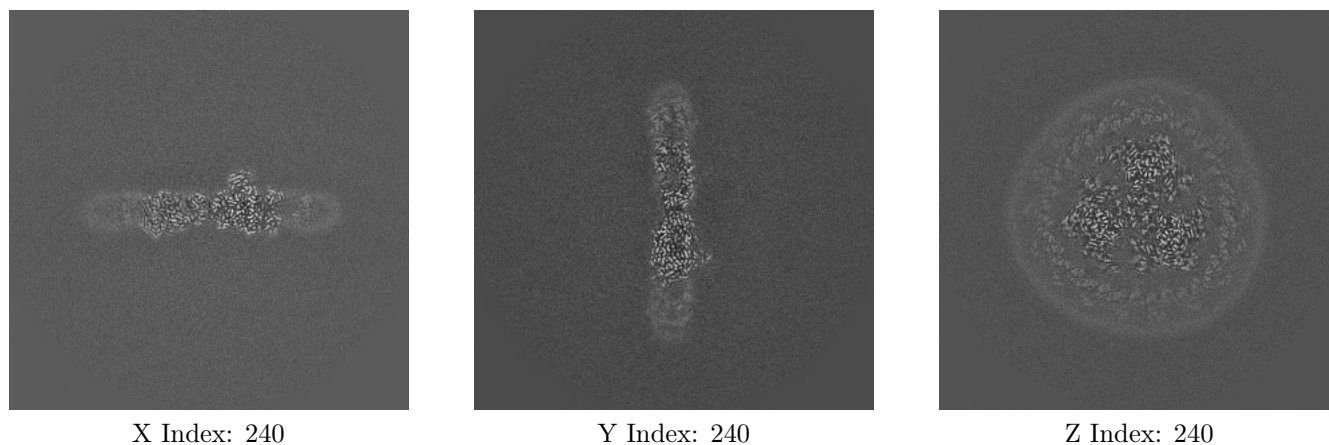
#### 6.1.1 Primary map



The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

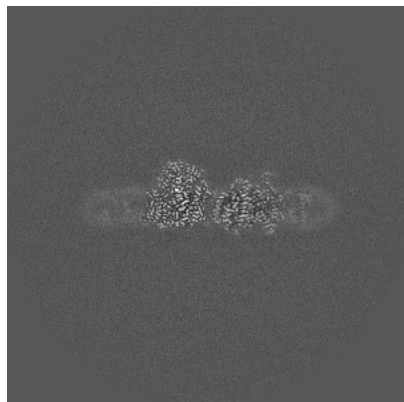
#### 6.2.1 Primary map



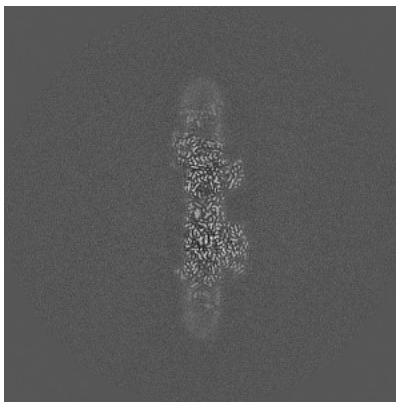
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

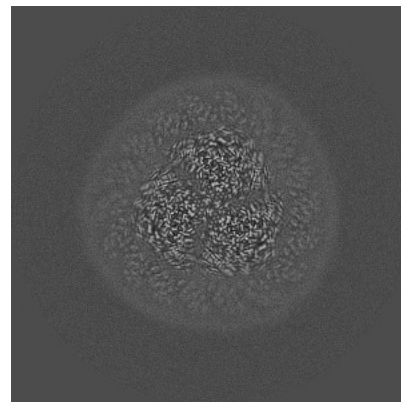
### 6.3.1 Primary map



X Index: 276



Y Index: 224

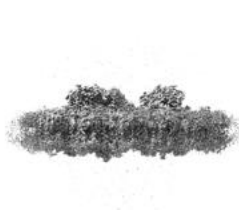


Z Index: 229

The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

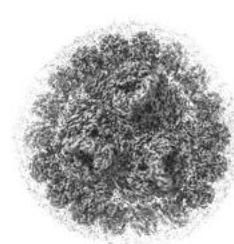
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

## 6.5 Mask visualisation

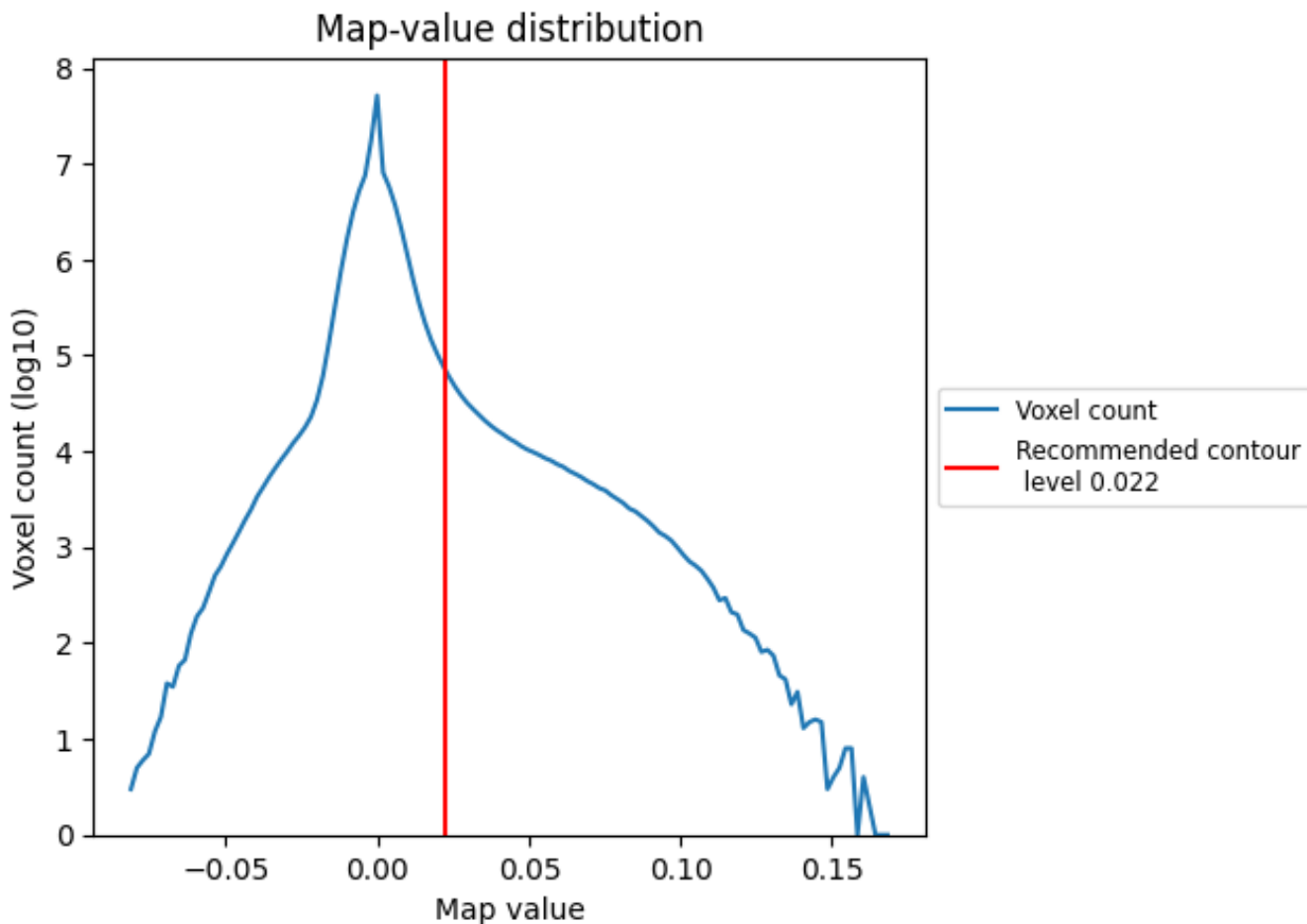
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

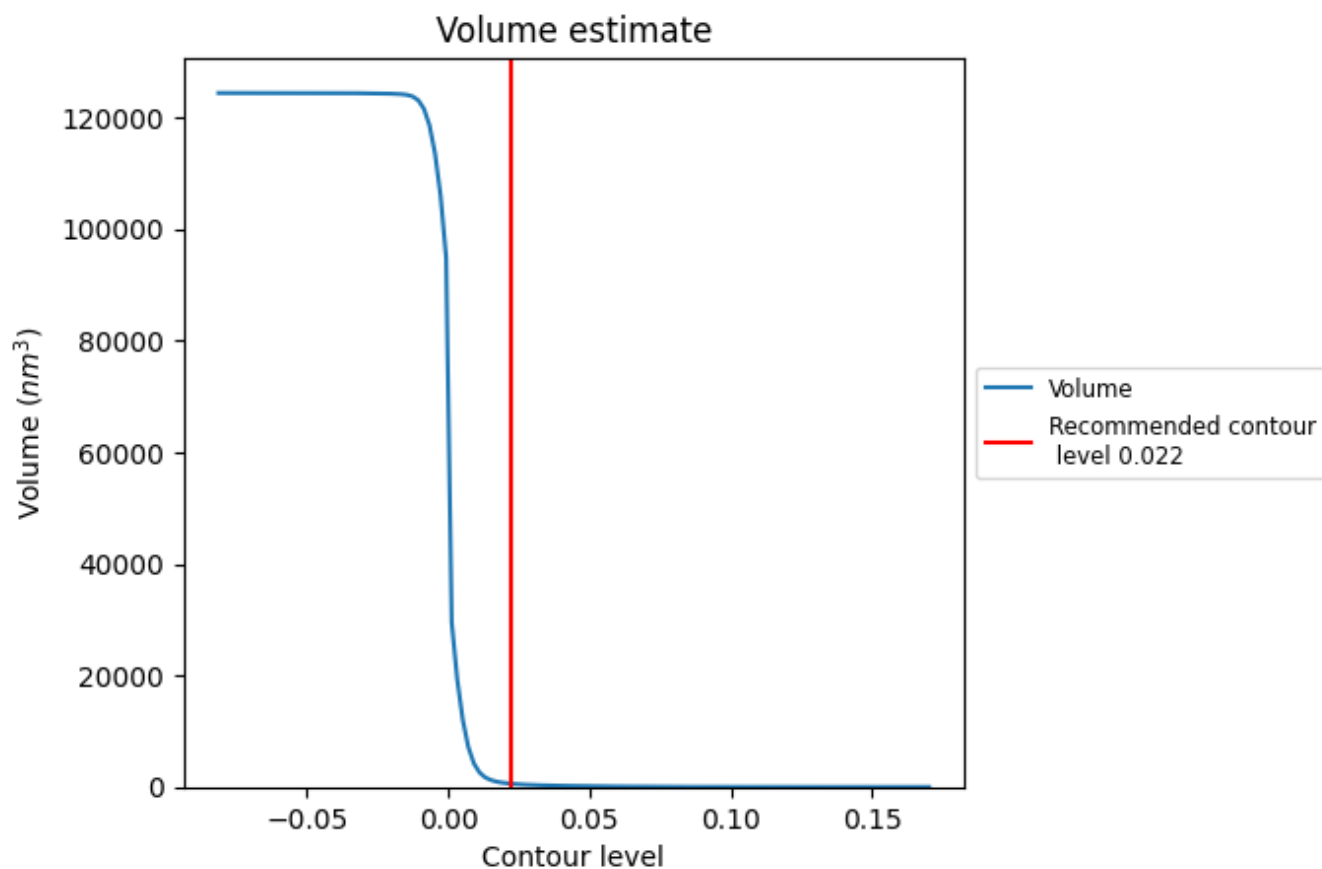
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

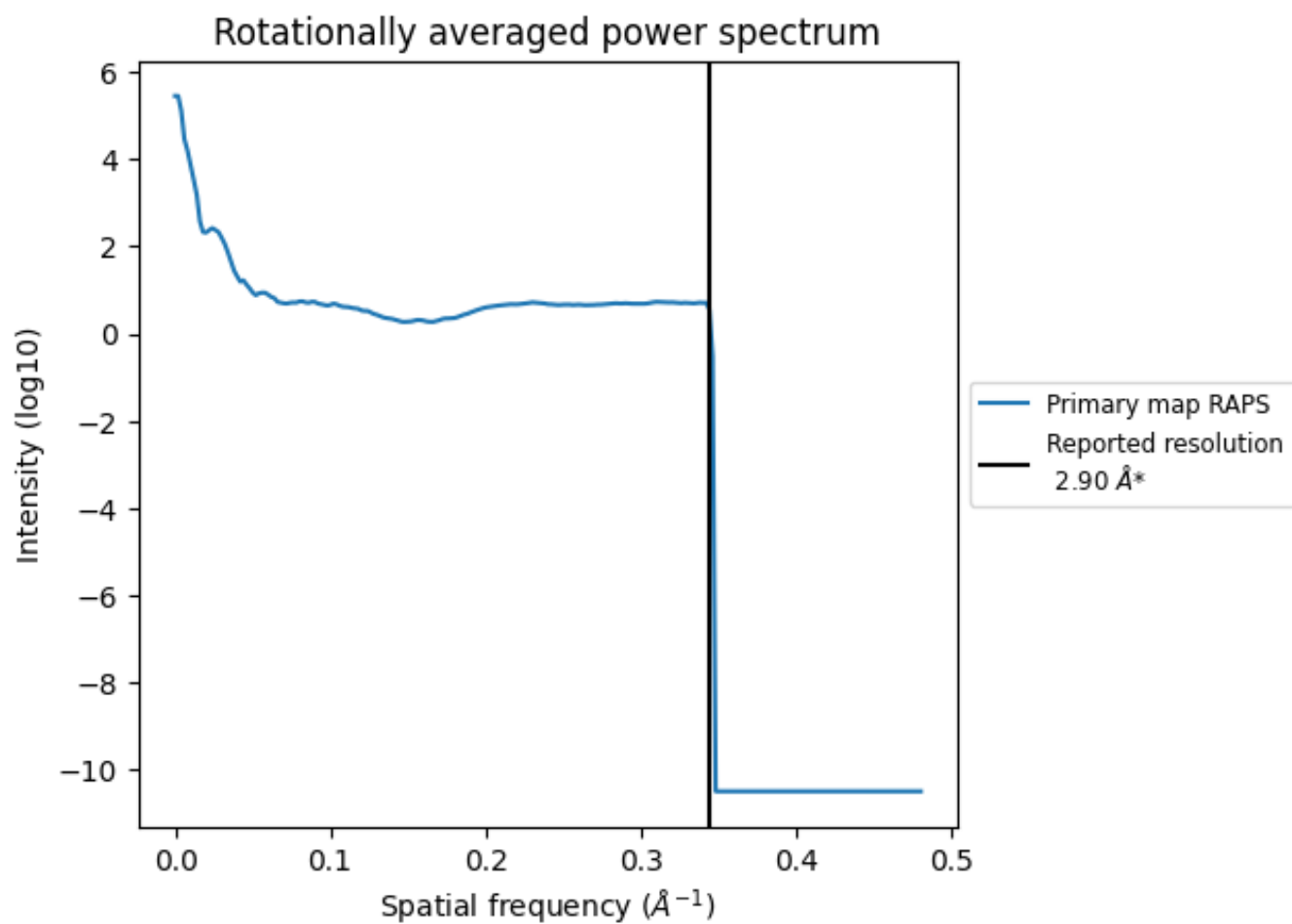
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 595  $\text{nm}^3$ ; this corresponds to an approximate mass of 538 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

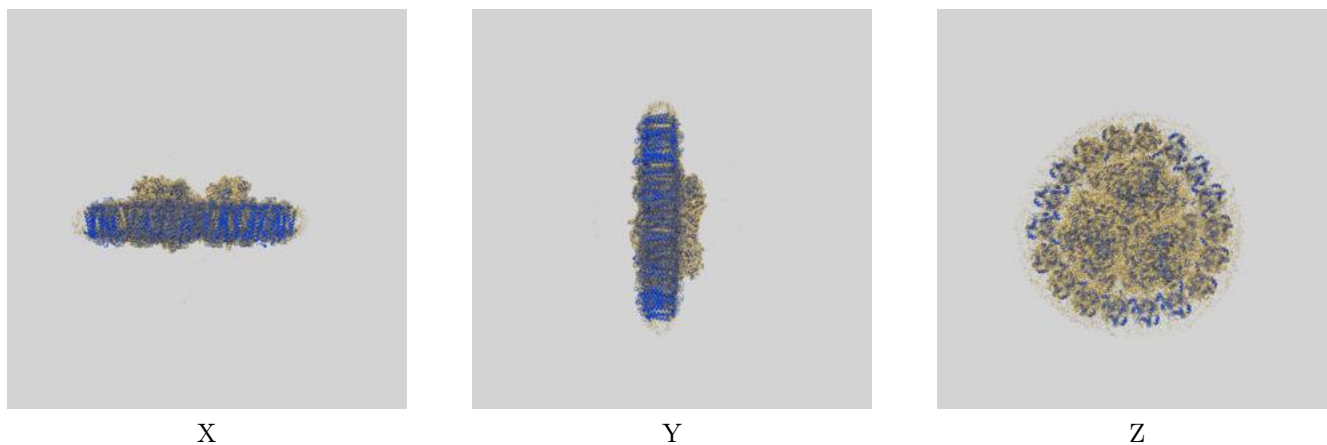
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

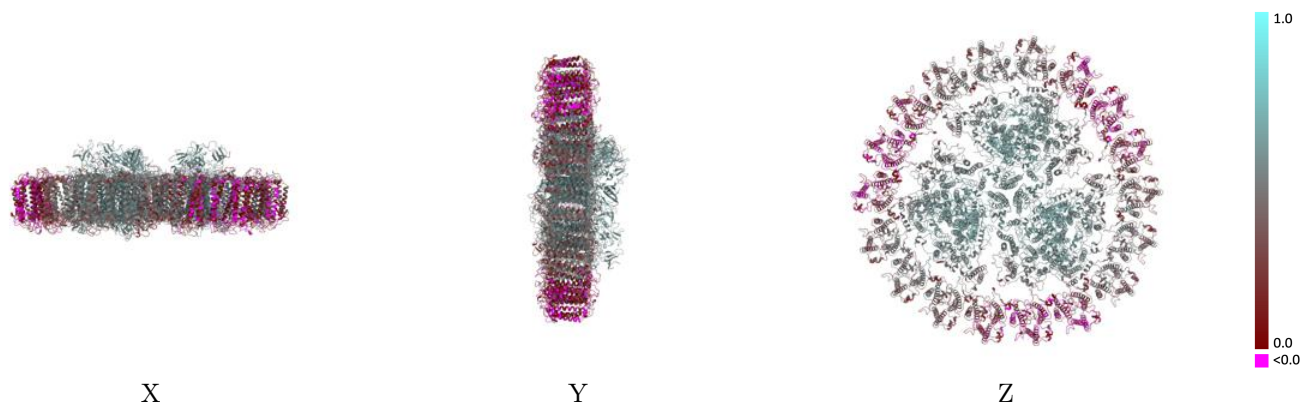
This section contains information regarding the fit between EMDB map EMD-9995 and PDB model 6KIG. Per-residue inclusion information can be found in section 3 on page 69.

### 9.1 Map-model overlay [i](#)



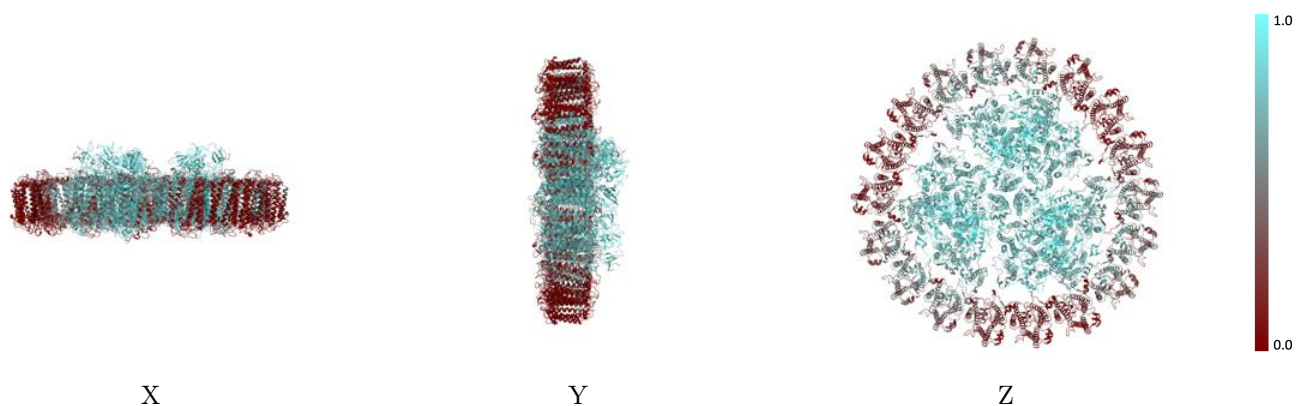
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



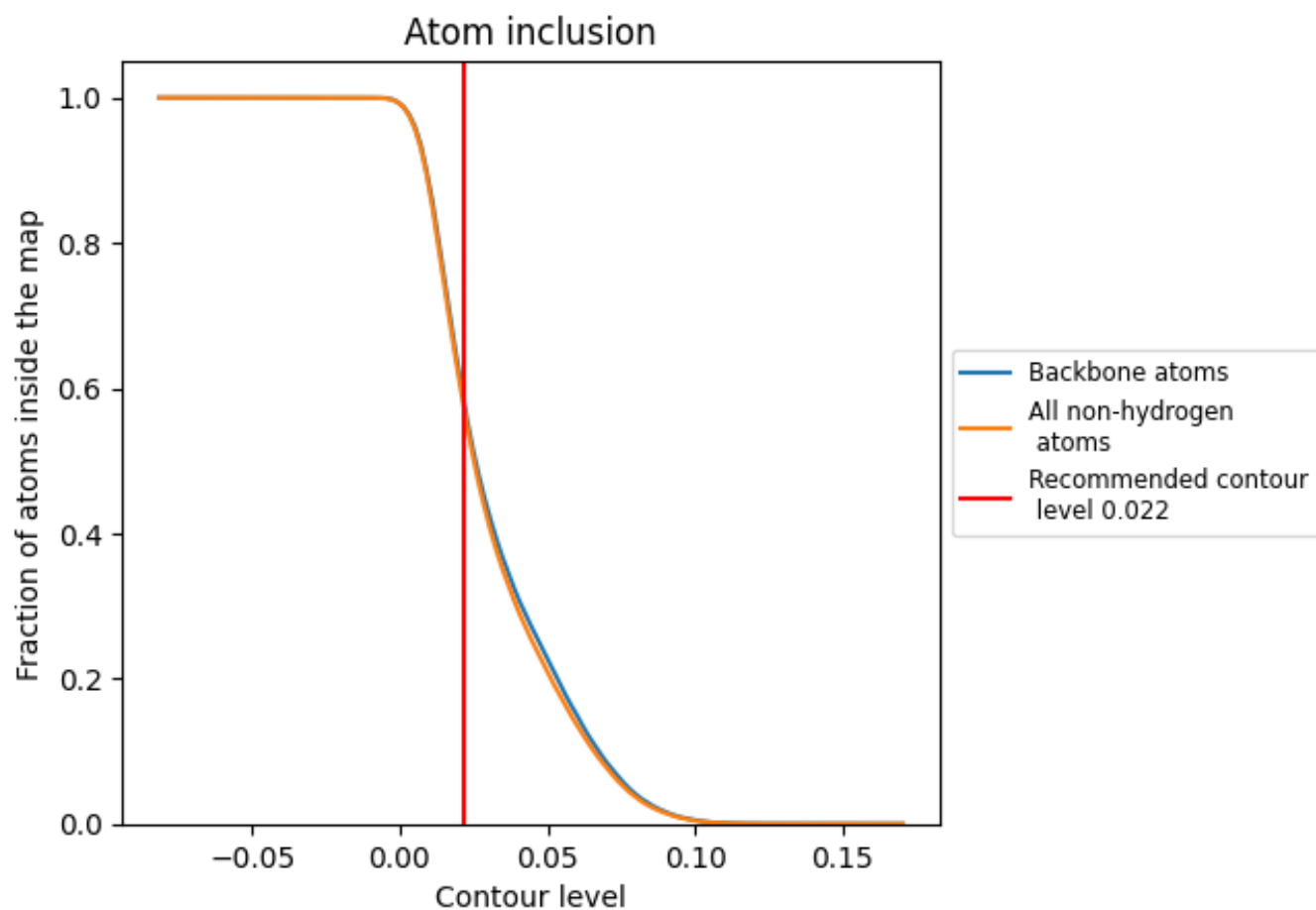
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.022).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.022) and Q-score for the entire model and for each chain.



































Chain	Atom inclusion	Q-score
All	 0.5647	 0.4190
1	 0.4068	 0.3640
2	 0.4699	 0.4180
3	 0.3896	 0.3830
4	 0.1067	 0.1410
5	 0.0559	 0.0860
6	 0.1523	 0.1850
A	 0.8491	 0.5780
B	 0.8269	 0.5450
C	 0.9417	 0.6070
D	 0.8582	 0.5770
E	 0.7872	 0.5410
F	 0.7466	 0.5290
G	 0.8453	 0.5770
H	 0.8162	 0.5370
I	 0.8329	 0.5720
J	 0.7552	 0.5460
K	 0.5868	 0.3890
L	 0.8653	 0.5930
M	 0.7977	 0.5290
N	 0.9450	 0.6070
O	 0.8591	 0.5780
Q	 0.7815	 0.5500
R	 0.7440	 0.5230
S	 0.8247	 0.5780
T	 0.7359	 0.5460
U	 0.5813	 0.3860
V	 0.8689	 0.5940
W	 0.7786	 0.5320
Y	 0.4057	 0.3660
Z	 0.4669	 0.4160
a	 0.3874	 0.3780
b	 0.1036	 0.1380
c	 0.0531	 0.0780
d	 0.1449	 0.1710



*Continued on next page...*



*Continued from previous page...*

Chain	Atom inclusion	Q-score
e	 0.8419	 0.5750
f	 0.8211	 0.5420
g	 0.9417	 0.6070
h	 0.8693	 0.5800
i	 0.7947	 0.5480
j	 0.7500	 0.5280
k	 0.8411	 0.5750
l	 0.7472	 0.5450
m	 0.5785	 0.3770
n	 0.8665	 0.5940
o	 0.7824	 0.5300
q	 0.3921	 0.3580
r	 0.4580	 0.4140
s	 0.3907	 0.3860
t	 0.1104	 0.1390
u	 0.0559	 0.0810
v	 0.1543	 0.1840