



wwPDB EM Validation Summary Report ⓘ

Dec 18, 2022 – 06:20 am GMT

PDB ID : 6ZZY
EMDB ID : EMD-11589
Title : Structure of high-light grown *Chlorella ohadii* photosystem I
Authors : Caspy, I.; Nelson, N.; Nechushtai, R.; Shkolnisky, Y.; Neumann, E.
Deposited on : 2020-08-05
Resolution : 3.16 Å (reported)
Based on initial model : 6IJO

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, 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) : 2.31.3

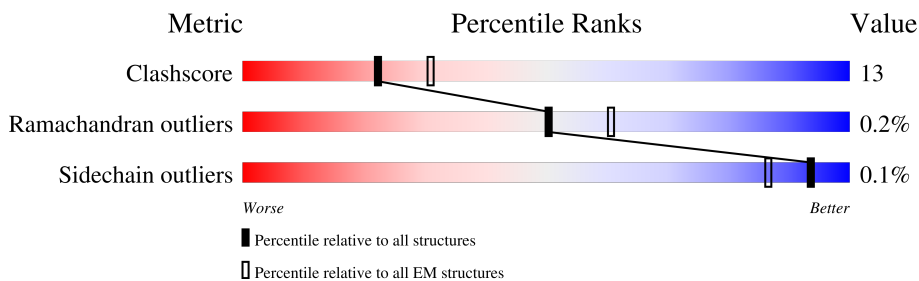
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.16 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	741	
2	B	731	
3	C	80	
4	D	143	
5	E	64	
6	F	165	
7	G	99	
8	J	41	

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Mol	Chain	Length	Quality of chain
9	K	86	
10	M	31	
11	I	35	
12	H	94	
13	L	157	
14	1	192	
14	a	192	
15	3	241	
16	4	207	
17	5	227	
18	6	231	
19	7	221	
20	8	219	
21	2	215	
22	9	182	

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
23	CL0	A	1011	X	-	-	-
24	CLA	1	601	X	-	-	-
24	CLA	1	602	X	-	-	-
24	CLA	1	603	X	-	-	-
24	CLA	1	604	X	-	-	-
24	CLA	1	605	X	-	-	-
24	CLA	1	606	X	-	-	-
24	CLA	1	607	X	-	-	-
24	CLA	1	608	X	-	-	-
24	CLA	1	610	X	-	-	-
24	CLA	1	611	X	-	-	-
24	CLA	1	612	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	1	615	X	-	-	-
24	CLA	2	601	X	-	-	-
24	CLA	2	602	X	-	-	-
24	CLA	2	603	X	-	-	-
24	CLA	2	604	X	-	-	-
24	CLA	2	605	X	-	-	-
24	CLA	2	606	X	-	-	-
24	CLA	2	607	X	-	-	-
24	CLA	2	608	X	-	-	-
24	CLA	2	609	X	-	-	-
24	CLA	2	610	X	-	-	-
24	CLA	2	612	X	-	-	-
24	CLA	2	613	X	-	-	-
24	CLA	2	615	X	-	-	-
24	CLA	2	621	X	-	-	-
24	CLA	3	601	X	-	-	-
24	CLA	3	602	X	-	-	-
24	CLA	3	603	X	-	-	-
24	CLA	3	604	X	-	-	-
24	CLA	3	605	X	-	-	-
24	CLA	3	606	X	-	-	-
24	CLA	3	607	X	-	-	-
24	CLA	3	610	X	-	-	-
24	CLA	3	612	X	-	-	-
24	CLA	3	613	X	-	-	-
24	CLA	3	616	X	-	-	-
24	CLA	3	618	X	-	-	-
24	CLA	4	601	X	-	-	-
24	CLA	4	602	X	-	-	-
24	CLA	4	603	X	-	-	-
24	CLA	4	604	X	-	-	-
24	CLA	4	605	X	-	-	-
24	CLA	4	606	X	-	-	-
24	CLA	4	607	X	-	-	-
24	CLA	4	608	X	-	-	-
24	CLA	4	610	X	-	-	-
24	CLA	4	611	X	-	-	-
24	CLA	4	612	X	-	-	-
24	CLA	4	615	X	-	-	-
24	CLA	4	616	X	-	-	-
24	CLA	4	617	X	-	-	-
24	CLA	5	601	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	5	602	X	-	-	-
24	CLA	5	603	X	-	-	-
24	CLA	5	604	X	-	-	-
24	CLA	5	605	X	-	-	-
24	CLA	5	606	X	-	-	-
24	CLA	5	607	X	-	-	-
24	CLA	5	608	X	-	-	-
24	CLA	5	609	X	-	-	-
24	CLA	5	612	X	-	-	-
24	CLA	5	614	X	-	-	-
24	CLA	5	616	X	-	-	-
24	CLA	5	617	X	-	-	-
24	CLA	5	618	X	-	-	-
24	CLA	6	601	X	-	-	-
24	CLA	6	602	X	-	-	-
24	CLA	6	603	X	-	-	-
24	CLA	6	604	X	-	-	-
24	CLA	6	605	X	-	-	-
24	CLA	6	606	X	-	-	-
24	CLA	6	607	X	-	-	-
24	CLA	6	608	X	-	-	-
24	CLA	6	609	X	-	-	-
24	CLA	6	612	X	-	-	-
24	CLA	6	615	X	-	-	-
24	CLA	6	617	X	-	-	-
24	CLA	6	618	X	-	-	-
24	CLA	7	601	X	-	-	-
24	CLA	7	602	X	-	-	-
24	CLA	7	603	X	-	-	-
24	CLA	7	604	X	-	-	-
24	CLA	7	605	X	-	-	-
24	CLA	7	606	X	-	-	-
24	CLA	7	607	X	-	-	-
24	CLA	7	608	X	-	-	-
24	CLA	7	609	X	-	-	-
24	CLA	7	610	X	-	-	-
24	CLA	7	611	X	-	-	-
24	CLA	7	612	X	-	-	-
24	CLA	7	615	X	-	-	-
24	CLA	7	617	X	-	-	-
24	CLA	8	602	X	-	-	-
24	CLA	8	603	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	8	605	X	-	-	-
24	CLA	8	606	X	-	-	-
24	CLA	8	607	X	-	-	-
24	CLA	8	608	X	-	-	-
24	CLA	8	609	X	-	-	-
24	CLA	8	610	X	-	-	-
24	CLA	8	611	X	-	-	-
24	CLA	8	612	X	-	-	-
24	CLA	8	615	X	-	-	-
24	CLA	8	618	X	-	-	-
24	CLA	8	620	X	-	-	-
24	CLA	9	601	X	-	-	-
24	CLA	9	602	X	-	-	-
24	CLA	9	603	X	-	-	-
24	CLA	9	604	X	-	-	-
24	CLA	9	605	X	-	-	-
24	CLA	9	606	X	-	-	-
24	CLA	9	607	X	-	-	-
24	CLA	9	608	X	-	-	-
24	CLA	9	609	X	-	-	-
24	CLA	9	612	X	-	-	-
24	CLA	A	1012	X	-	-	-
24	CLA	A	1013	X	-	-	-
24	CLA	A	1101	X	-	-	-
24	CLA	A	1102	X	-	-	-
24	CLA	A	1103	X	-	-	-
24	CLA	A	1104	X	-	-	-
24	CLA	A	1105	X	-	-	-
24	CLA	A	1106	X	-	-	-
24	CLA	A	1107	X	-	-	-
24	CLA	A	1108	X	-	-	-
24	CLA	A	1109	X	-	-	-
24	CLA	A	1110	X	-	-	-
24	CLA	A	1111	X	-	-	-
24	CLA	A	1112	X	-	-	-
24	CLA	A	1113	X	-	-	-
24	CLA	A	1114	X	-	-	-
24	CLA	A	1115	X	-	-	-
24	CLA	A	1116	X	-	-	-
24	CLA	A	1117	X	-	-	-
24	CLA	A	1118	X	-	-	-
24	CLA	A	1119	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	A	1120	X	-	-	-
24	CLA	A	1121	X	-	-	-
24	CLA	A	1122	X	-	-	-
24	CLA	A	1123	X	-	-	-
24	CLA	A	1124	X	-	-	-
24	CLA	A	1125	X	-	-	-
24	CLA	A	1126	X	-	-	-
24	CLA	A	1127	X	-	-	-
24	CLA	A	1128	X	-	-	-
24	CLA	A	1129	X	-	-	-
24	CLA	A	1130	X	-	-	-
24	CLA	A	1131	X	-	-	-
24	CLA	A	1132	X	-	-	-
24	CLA	A	1133	X	-	-	-
24	CLA	A	1134	X	-	-	-
24	CLA	A	1135	X	-	-	-
24	CLA	A	1136	X	-	-	-
24	CLA	A	1137	X	-	-	-
24	CLA	A	1138	X	-	-	-
24	CLA	A	1139	X	-	-	-
24	CLA	A	1140	X	-	-	-
24	CLA	A	1141	X	-	-	-
24	CLA	B	1021	X	-	-	-
24	CLA	B	1022	X	-	-	-
24	CLA	B	1023	X	-	-	-
24	CLA	B	1201	X	-	-	-
24	CLA	B	1202	X	-	-	-
24	CLA	B	1203	X	-	-	-
24	CLA	B	1204	X	-	-	-
24	CLA	B	1205	X	-	-	-
24	CLA	B	1206	X	-	-	-
24	CLA	B	1207	X	-	-	-
24	CLA	B	1208	X	-	-	-
24	CLA	B	1209	X	-	-	-
24	CLA	B	1210	X	-	-	-
24	CLA	B	1211	X	-	-	-
24	CLA	B	1212	X	-	-	-
24	CLA	B	1213	X	-	-	-
24	CLA	B	1214	X	-	-	-
24	CLA	B	1215	X	-	-	-
24	CLA	B	1216	X	-	-	-
24	CLA	B	1217	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	B	1218	X	-	-	-
24	CLA	B	1219	X	-	-	-
24	CLA	B	1220	X	-	-	-
24	CLA	B	1221	X	-	-	-
24	CLA	B	1222	X	-	-	-
24	CLA	B	1223	X	-	-	-
24	CLA	B	1224	X	-	-	-
24	CLA	B	1225	X	-	-	-
24	CLA	B	1226	X	-	-	-
24	CLA	B	1227	X	-	-	-
24	CLA	B	1228	X	-	-	-
24	CLA	B	1229	X	-	-	-
24	CLA	B	1230	X	-	-	-
24	CLA	B	1231	X	-	-	-
24	CLA	B	1232	X	-	-	-
24	CLA	B	1234	X	-	-	-
24	CLA	B	1235	X	-	-	-
24	CLA	B	1236	X	-	-	-
24	CLA	B	1237	X	-	-	-
24	CLA	B	1238	X	-	-	-
24	CLA	B	1239	X	-	-	-
24	CLA	B	1240	X	-	-	-
24	CLA	F	1301	X	-	-	-
24	CLA	F	1302	X	-	-	-
24	CLA	G	1601	X	-	-	-
24	CLA	G	1602	X	-	-	-
24	CLA	G	1603	X	-	-	-
24	CLA	H	1701	X	-	-	-
24	CLA	H	1702	X	-	-	-
24	CLA	H	1703	X	-	-	-
24	CLA	J	1901	X	-	-	-
24	CLA	K	1401	X	-	-	-
24	CLA	K	1402	X	-	-	-
24	CLA	K	1403	X	-	-	-
24	CLA	K	1404	X	-	-	-
24	CLA	L	1501	X	-	-	-
24	CLA	L	1502	X	-	-	-
24	CLA	L	1503	X	-	-	-
24	CLA	a	601	X	-	-	-
24	CLA	a	602	X	-	-	-
24	CLA	a	603	X	-	-	-
24	CLA	a	604	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	CLA	a	605	X	-	-	-
24	CLA	a	607	X	-	-	-
24	CLA	a	608	X	-	-	-
24	CLA	a	611	X	-	-	-
24	CLA	a	612	X	-	-	-
24	CLA	a	615	X	-	-	-
36	ERG	G	5002	X	-	-	-
37	RRX	J	4002	X	-	-	-
40	LUT	1	503	X	-	-	-
40	LUT	6	501	X	-	-	-
40	LUT	6	502	X	-	-	-
40	LUT	7	501	X	-	-	-
40	LUT	9	502	X	-	-	-
41	CHL	1	609	X	-	-	-
41	CHL	1	613	X	-	-	-
41	CHL	3	608	X	-	-	-
41	CHL	3	611	X	-	-	-
41	CHL	4	609	X	-	-	-
41	CHL	4	613	X	-	-	-
41	CHL	4	618	X	-	-	-
41	CHL	5	610	X	-	-	-
41	CHL	5	611	X	-	-	-
41	CHL	5	613	X	-	-	-
41	CHL	6	610	X	-	-	-
41	CHL	6	611	X	-	-	-
41	CHL	6	613	X	-	-	-
41	CHL	6	619	X	-	-	-
41	CHL	7	613	X	-	-	-
41	CHL	8	601	X	-	-	-
41	CHL	8	604	X	-	-	-
41	CHL	8	613	X	-	-	-
41	CHL	9	610	X	-	-	-
41	CHL	9	613	X	-	-	-
41	CHL	a	606	X	-	-	-
41	CHL	a	609	X	-	-	-
41	CHL	a	610	X	-	-	-
41	CHL	a	613	X	-	-	-
43	QTB	3	506	X	-	-	-
43	QTB	a	504	X	-	-	-
48	XAT	7	502	X	-	-	-
49	C7Z	7	504	X	-	-	-

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 54609 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	741	5824	3815	988	1001	20	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	368	ALA	SER	variant	UNP W8SY74
A	437	ILE	MET	variant	UNP W8SY74

- 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	731	5796	3807	980	994	15	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	5	LEU	-	insertion	UNP W8SUA3
B	241	ALA	VAL	conflict	UNP W8SUA3
B	402	ALA	GLU	conflict	UNP W8SUA3
B	403	GLN	ALA	conflict	UNP W8SUA3

- 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	601	367	104	119	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	143	1124	716	196	208	4	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	188	ALA	VAL	variant	UNP A0A2P6TKF8
D	320	ILE	VAL	variant	UNP A0A2P6TKF8

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	64	509	323	91	95		0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	44	GLN	THR	variant	UNP A0A2P6U4S6
E	48	LEU	MET	variant	UNP A0A2P6U4S6
E	96	VAL	GLU	variant	UNP A0A2P6U4S6
E	97	ALA	GLU	variant	UNP A0A2P6U4S6
E	98	ALA	VAL	variant	UNP A0A2P6U4S6

- Molecule 6 is a protein called PSI-F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	165	1277	830	216	228	3	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	346	LEU	MET	variant	UNP A0A2P6TPV8
F	348	ASN	LYS	variant	UNP A0A2P6TPV8
F	351	ALA	GLU	variant	UNP A0A2P6TPV8
F	352	ASP	GLY	variant	UNP A0A2P6TPV8
F	360	LYS	GLN	variant	UNP A0A2P6TPV8
F	364	ALA	ASP	variant	UNP A0A2P6TPV8
F	367	GLU	ASN	variant	UNP A0A2P6TPV8
F	430	ALA	SER	variant	UNP A0A2P6TPV8
F	431	ALA	SER	variant	UNP A0A2P6TPV8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	432	THR	MET	variant	UNP A0A2P6TPV8
F	433	ALA	THR	variant	UNP A0A2P6TPV8

- Molecule 7 is a protein called Photosystem I reaction center subunit chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	99	Total	C	N	O	S	0	0
			727	466	127	130	4		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	1229	ALA	SER	variant	UNP A0A2P6TZI8
G	1272	LEU	MET	variant	UNP A0A2P6TZI8
G	1285	ILE	VAL	variant	UNP A0A2P6TZI8
G	1313	ILE	LEU	variant	UNP A0A2P6TZI8
G	1317	SER	HIS	variant	UNP A0A2P6TZI8
G	1320	GLY	GLN	variant	UNP A0A2P6TZI8
G	1321	LEU	VAL	variant	UNP A0A2P6TZI8
G	1324	ASN	VAL	variant	UNP A0A2P6TZI8

- 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
			316	212	46	57	1		

- Molecule 9 is a protein called PSI-K.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	86	Total	C	N	O	S	0	0
			613	390	106	115	2		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	74	ALA	GLU	variant	UNP A0A2P6U0J1
K	103	LEU	ILE	variant	UNP A0A2P6U0J1
K	105	CYS	VAL	variant	UNP A0A2P6U0J1
K	107	ILE	VAL	variant	UNP A0A2P6U0J1
K	108	VAL	ILE	variant	UNP A0A2P6U0J1

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Chain	Residue	Modelled	Actual	Comment	Reference
K	112	LYS	ARG	variant	UNP A0A2P6U0J1
K	113	SER	GLY	variant	UNP A0A2P6U0J1

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	31	Total	C	N	O	S	0	0
			239	163	36	39	1		

- Molecule 11 is a protein called Photosystem I reaction center subunit VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	35	Total	C	N	O	S	0	0
			270	183	37	47	3		

- Molecule 12 is a protein called Photosystem I reaction center subunit VI-chloroplastic-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	94	Total	C	N	O	S	0	0
			729	457	132	139	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	92	ILE	VAL	conflict	UNP A0A2P6TPU7
H	102	GLY	LEU	conflict	UNP A0A2P6TPU7
H	105	ALA	SER	conflict	UNP A0A2P6TPU7
H	106	ALA	SER	conflict	UNP A0A2P6TPU7
H	109	ARG	SER	conflict	UNP A0A2P6TPU7
H	?	-	ILE	deletion	UNP A0A2P6TPU7
H	113	VAL	LYS	conflict	UNP A0A2P6TPU7

- Molecule 13 is a protein called PSI subunit V.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	157	Total	C	N	O	S	0	0
			1165	758	192	211	4		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	350	TYR	PHE	conflict	UNP A0A2P6TC44
L	364	ASP	ASN	conflict	UNP A0A2P6TC44
L	?	-	ALA	deletion	UNP A0A2P6TC44
L	421	ASP	GLU	conflict	UNP A0A2P6TC44
L	443	LEU	ILE	conflict	UNP A0A2P6TC44

- Molecule 14 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1	192	Total	C	N	O	S	0	0
			1405	900	237	261	7		
14	a	192	Total	C	N	O	S	0	0
			1405	900	237	261	7		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	166	SER	LEU	conflict	UNP A0A2P6TT36
1	167	LYS	GLU	conflict	UNP A0A2P6TT36
1	171	THR	VAL	conflict	UNP A0A2P6TT36
1	194	THR	ASN	conflict	UNP A0A2P6TT36
1	196	ALA	GLN	conflict	UNP A0A2P6TT36
1	204	SER	ALA	conflict	UNP A0A2P6TT36
1	210	MET	LEU	conflict	UNP A0A2P6TT36
a	166	SER	LEU	conflict	UNP A0A2P6TT36
a	167	LYS	GLU	conflict	UNP A0A2P6TT36
a	171	THR	VAL	conflict	UNP A0A2P6TT36
a	194	THR	ASN	conflict	UNP A0A2P6TT36
a	196	ALA	GLN	conflict	UNP A0A2P6TT36
a	204	SER	ALA	conflict	UNP A0A2P6TT36
a	210	MET	LEU	conflict	UNP A0A2P6TT36

- Molecule 15 is a protein called Glutathione reductase.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	3	241	Total	C	N	O	S	0	0
			1844	1194	302	337	11		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	314	CYS	GLY	conflict	UNP A0A2P6TMT4
3	329	ILE	VAL	conflict	UNP A0A2P6TMT4

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Chain	Residue	Modelled	Actual	Comment	Reference
3	339	THR	SER	conflict	UNP A0A2P6TMT4
3	359	LYS	ASN	conflict	UNP A0A2P6TMT4
3	405	GLY	ALA	conflict	UNP A0A2P6TMT4
3	429	GLU	ALA	conflict	UNP A0A2P6TMT4
3	484	THR	ARG	conflict	UNP A0A2P6TMT4
3	485	ILE	ARG	conflict	UNP A0A2P6TMT4
3	486	LEU	ARG	conflict	UNP A0A2P6TMT4
3	487	LYS	ALA	conflict	UNP A0A2P6TMT4

- Molecule 16 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	4	207	1631	1056	277	294	4	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	37	GLU	ASP	conflict	UNP A0A2P6TQ14
4	109	ASP	ASN	conflict	UNP A0A2P6TQ14
4	112	ASN	ASP	conflict	UNP A0A2P6TQ14
4	213	GLY	SER	conflict	UNP A0A2P6TQ14
4	218	ASN	ASP	conflict	UNP A0A2P6TQ14
4	?	-	LEU	deletion	UNP A0A2P6TQ14
4	236	ASN	ARG	variant	UNP A0A2P6TQ14

- Molecule 17 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	5	227	1769	1136	307	314	12	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	32	LYS	ASP	conflict	UNP A0A2P6U4K1
5	38	VAL	ALA	conflict	UNP A0A2P6U4K1
5	40	ALA	SER	conflict	UNP A0A2P6U4K1
5	42	GLY	ALA	conflict	UNP A0A2P6U4K1
5	113	SER	GLY	conflict	UNP A0A2P6U4K1
5	127	ILE	LEU	conflict	UNP A0A2P6U4K1
5	195	VAL	ILE	conflict	UNP A0A2P6U4K1

- Molecule 18 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	6	231	1787	1168	295	314	10	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	83	CYS	ALA	conflict	UNP A0A2P6TPR7
6	94	LEU	MET	conflict	UNP A0A2P6TPR7
6	196	ILE	VAL	conflict	UNP A0A2P6TPR7
6	201	ALA	GLY	conflict	UNP A0A2P6TPR7
6	250	GLN	ASN	conflict	UNP A0A2P6TPR7

- Molecule 19 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	7	221	1698	1090	294	308	6	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	6	VAL	ASP	conflict	UNP A0A2P6TS63
7	8	GLU	PRO	conflict	UNP A0A2P6TS63
7	17	VAL	ALA	conflict	UNP A0A2P6TS63
7	82	PHE	TYR	conflict	UNP A0A2P6TS63
7	96	ASP	SER	conflict	UNP A0A2P6TS63
7	107	MET	LEU	conflict	UNP A0A2P6TS63
7	154	TYR	PHE	conflict	UNP A0A2P6TS63
7	205	VAL	ILE	conflict	UNP A0A2P6TS63
7	209	ALA	SER	conflict	UNP A0A2P6TS63
7	218	HIS	TYR	conflict	UNP A0A2P6TS63

- Molecule 20 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	8	219	1669	1073	285	305	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	103	GLU	ASP	conflict	UNP A0A2P6TZ50

- Molecule 21 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	2	215	1666	1074	277	309	6	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	64	ASP	GLU	conflict	UNP A0A2P6TMX4
2	97	PRO	ASN	conflict	UNP A0A2P6TMX4

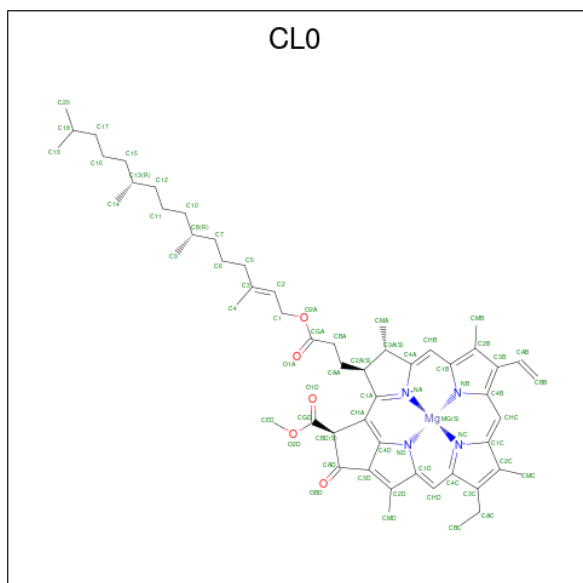
- Molecule 22 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	9	182	1397	906	231	254	6	0	0

There is a discrepancy between the modelled and reference sequences:

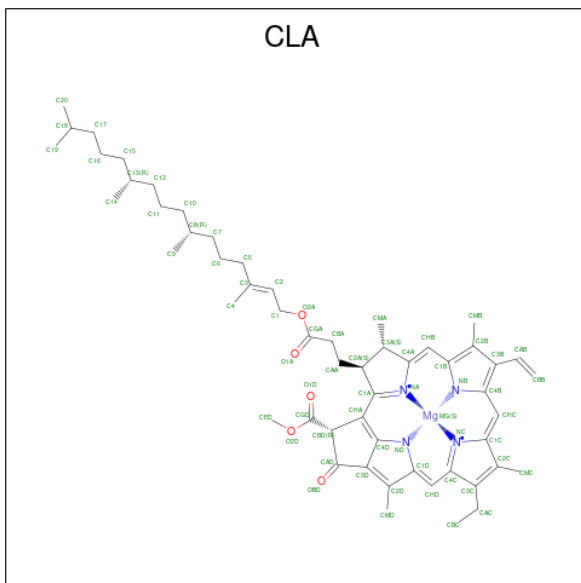
Chain	Residue	Modelled	Actual	Comment	Reference
9	257	TYR	HIS	conflict	UNP A0A2P6TMI2

- Molecule 23 is CHLOROPHYLL A ISOMER (three-letter code: CL0) (formula: $C_{55}H_{72}MgN_4O_5$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
23	A	1	65	55	1	4	5	0

- Molecule 24 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	
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0
24	A	1	2621	2191	43	172	215	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	A	1	Total 2621	C 2191	Mg 43	N 172	O 215	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	B	1	Total 2583	C 2163	Mg 42	N 168	O 210	0
24	F	1	Total 105	C 85	Mg 2	N 8	O 10	0
24	F	1	Total 105	C 85	Mg 2	N 8	O 10	0
24	G	1	Total 141	C 111	Mg 3	N 12	O 15	0
24	G	1	Total 141	C 111	Mg 3	N 12	O 15	0
24	G	1	Total 141	C 111	Mg 3	N 12	O 15	0
24	J	1	Total 42	C 34	Mg 1	N 4	O 3	0
24	K	1	Total 204	C 164	Mg 4	N 16	O 20	0
24	K	1	Total 204	C 164	Mg 4	N 16	O 20	0
24	K	1	Total 204	C 164	Mg 4	N 16	O 20	0
24	K	1	Total 204	C 164	Mg 4	N 16	O 20	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	H	1	156	126	3	12	15	0
24	H	1	156	126	3	12	15	0
24	H	1	156	126	3	12	15	0
24	L	1	155	125	3	12	15	0
24	L	1	155	125	3	12	15	0
24	L	1	155	125	3	12	15	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	1	1	693	573	12	48	60	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	a	1	571	471	10	40	50	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	3	1	719	599	12	48	60	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	4	1	768	628	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	5	1	739	599	14	56	70	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	6	1	711	581	13	52	65	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	7	1	778	641	14	56	67	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0

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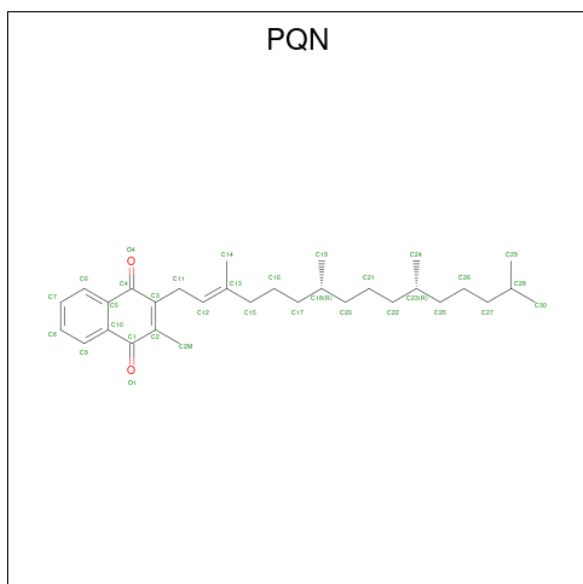
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	8	1	699	569	13	52	65	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	2	1	724	586	14	56	68	0
24	9	1	549	449	10	40	50	0
24	9	1	549	449	10	40	50	0
24	9	1	549	449	10	40	50	0
24	9	1	549	449	10	40	50	0

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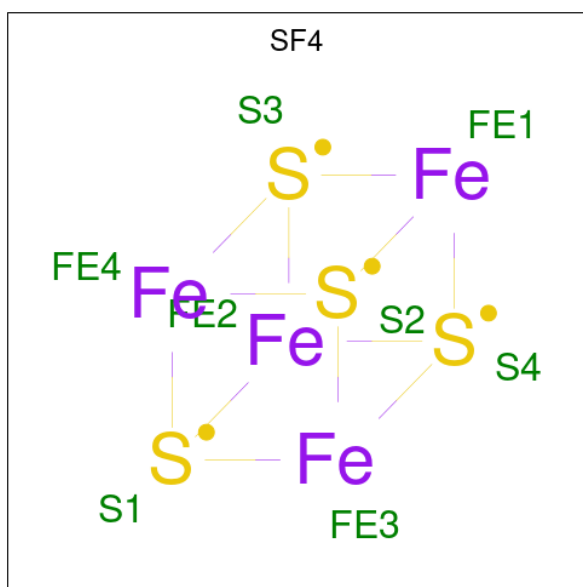
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
24	9	1	Total 549	C 449	Mg 10	N 40	O 50	0
24	9	1	Total 549	C 449	Mg 10	N 40	O 50	0
24	9	1	Total 549	C 449	Mg 10	N 40	O 50	0
24	9	1	Total 549	C 449	Mg 10	N 40	O 50	0
24	9	1	Total 549	C 449	Mg 10	N 40	O 50	0
24	9	1	Total 549	C 449	Mg 10	N 40	O 50	0

- Molecule 25 is PHYLLOQUINONE (three-letter code: PQN) (formula: $C_{31}H_{46}O_2$).



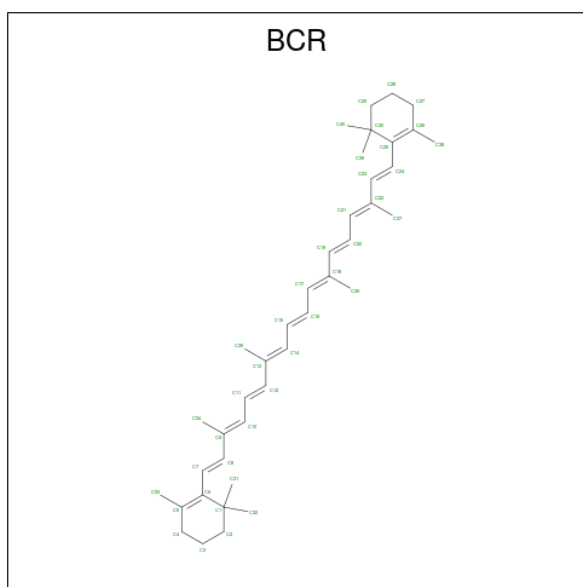
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
25	A	1	Total 33	C 31	O 2	0
25	B	1	Total 33	C 31	O 2	0

- Molecule 26 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	AltConf
26	A	1	Total Fe S 8 4 4	0
26	C	1	Total Fe S 16 8 8	0
26	C	1	Total Fe S 16 8 8	0

- Molecule 27 is BETA-CAROTENE (three-letter code: BCR) (formula: $C_{40}H_{56}$).



Mol	Chain	Residues	Atoms	AltConf
27	A	1	Total C 200 200	0

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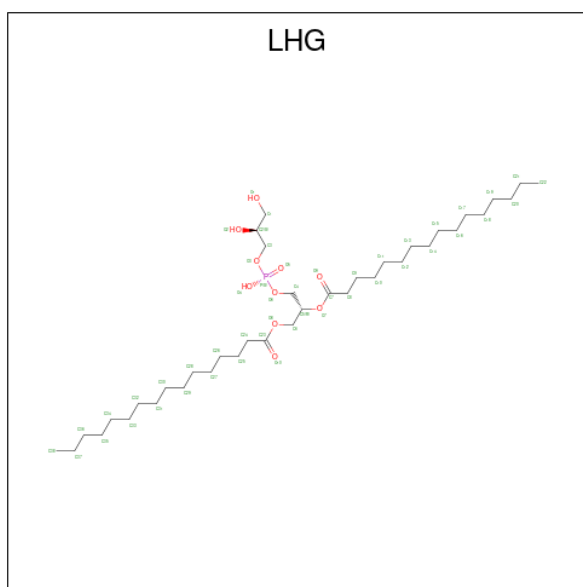
Mol	Chain	Residues	Atoms		AltConf
27	A	1	Total 200	C 200	0
27	A	1	Total 200	C 200	0
27	A	1	Total 200	C 200	0
27	A	1	Total 200	C 200	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	B	1	Total 280	C 280	0
27	F	1	Total 40	C 40	0
27	G	1	Total 40	C 40	0
27	J	1	Total 40	C 40	0
27	K	1	Total 80	C 80	0
27	K	1	Total 80	C 80	0
27	I	1	Total 40	C 40	0
27	H	1	Total 40	C 40	0
27	L	1	Total 120	C 120	0
27	L	1	Total 120	C 120	0
27	L	1	Total 120	C 120	0

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Mol	Chain	Residues	Atoms		AltConf
27	3	1	Total	C	0
			120	120	
27	3	1	Total	C	0
			120	120	
27	3	1	Total	C	0
			120	120	
27	4	1	Total	C	0
			40	40	
27	5	1	Total	C	0
			80	80	
27	5	1	Total	C	0
			80	80	
27	6	1	Total	C	0
			80	80	
27	6	1	Total	C	0
			80	80	
27	7	1	Total	C	0
			40	40	
27	8	1	Total	C	0
			40	40	

- Molecule 28 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (three-letter code: LHG) (formula: $C_{38}H_{75}O_{10}P$).



Mol	Chain	Residues	Atoms				AltConf
28	A	1	Total	C	O	P	0
			120	87	30	3	

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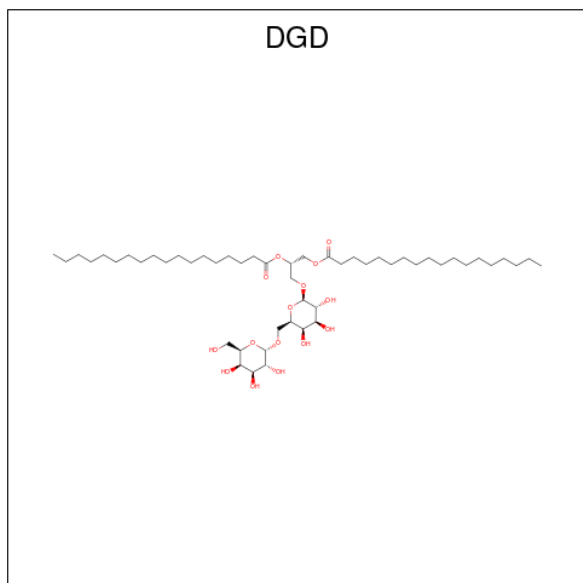
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
28	A	1	120	87	30	3	0
28	A	1	120	87	30	3	0
28	B	1	95	73	20	2	0
28	B	1	95	73	20	2	0
28	F	1	79	57	20	2	0
28	F	1	79	57	20	2	0
28	1	1	77	55	20	2	0
28	1	1	77	55	20	2	0
28	a	1	35	24	10	1	0
28	3	1	49	38	10	1	0
28	4	1	81	59	20	2	0
28	4	1	81	59	20	2	0
28	5	1	49	38	10	1	0
28	6	1	86	64	20	2	0
28	6	1	86	64	20	2	0
28	7	1	128	95	30	3	0
28	7	1	128	95	30	3	0
28	7	1	128	95	30	3	0
28	8	1	37	26	10	1	0
28	2	1	98	76	20	2	0
28	2	1	98	76	20	2	0

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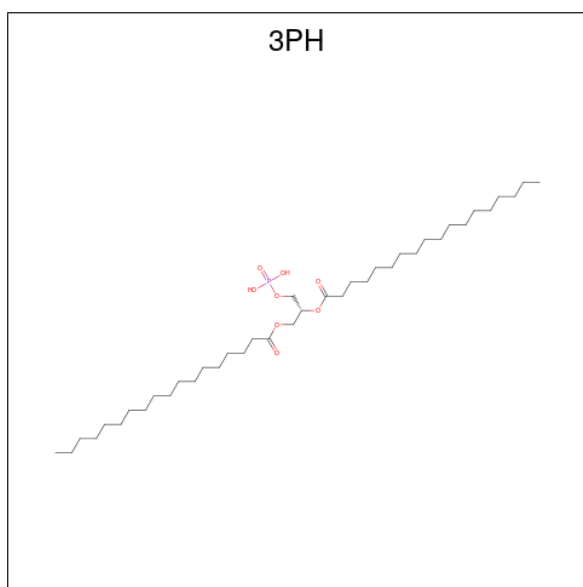
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
28	9	1	82	60	20	2	0
28	9	1	82	60	20	2	0

- Molecule 29 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (three-letter code: DGD) (formula: $C_{51}H_{96}O_{15}$).



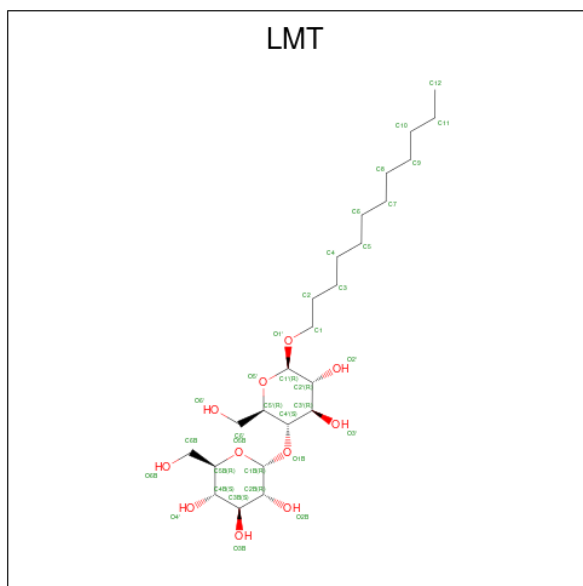
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
29	A	1	51	36	15	0
29	B	1	66	51	15	0
29	8	1	66	51	15	0

- Molecule 30 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: $C_{39}H_{77}O_8P$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
30	A	1	33	24	8	1	0

- Molecule 31 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



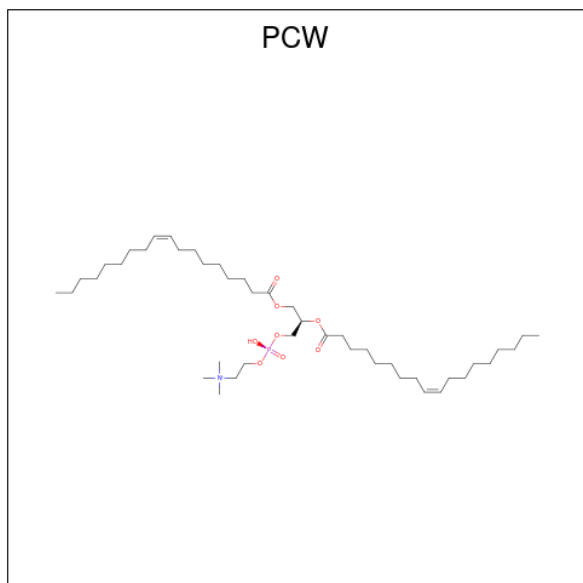
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
31	A	1	35	24	11	0
31	B	1	35	24	11	0

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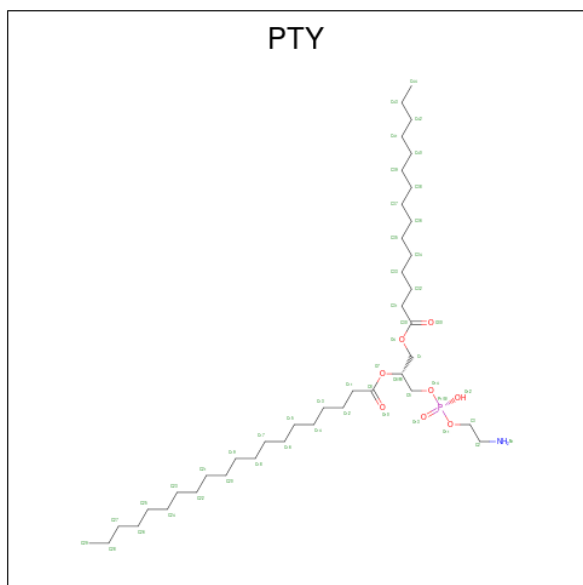
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
31	1	1	35	24	11	0
31	2	1	35	24	11	0

- Molecule 32 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PCW) (formula: $C_{44}H_{85}NO_8P$).



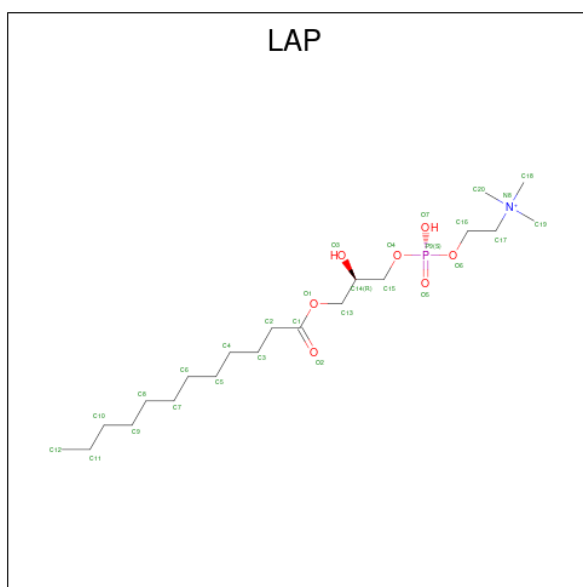
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
32	B	1	30	20	1	8	1	0
32	6	1	36	26	1	8	1	0

- Molecule 33 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula: $C_{40}H_{80}NO_8P$).



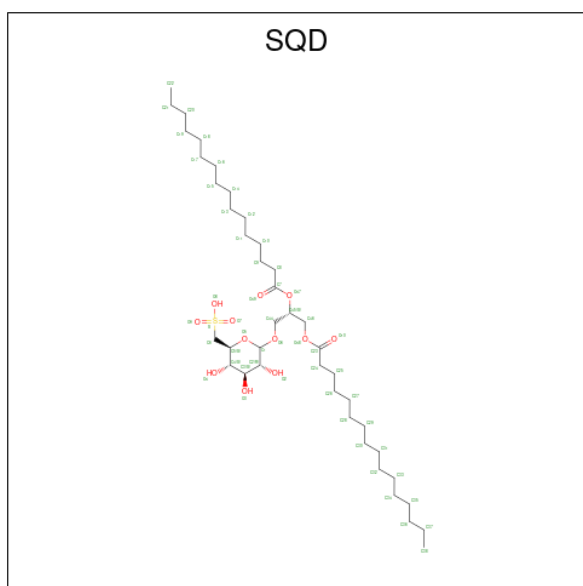
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
33	B	1	41	31	1	8	1	0
33	3	1	38	28	1	8	1	0
33	5	1	38	28	1	8	1	0
33	7	1	33	23	1	8	1	0
33	8	1	35	25	1	8	1	0
33	9	1	48	38	1	8	1	0

- Molecule 34 is [2-((1-OXODODECANOXY-(2-HYDROXY-3-PROPANYL))-PHOSPHONATE-OXY)-ETHYL]-TRIMETHYLAMMONIUM (three-letter code: LAP) (formula: $C_{20}H_{43}NO_7P$).



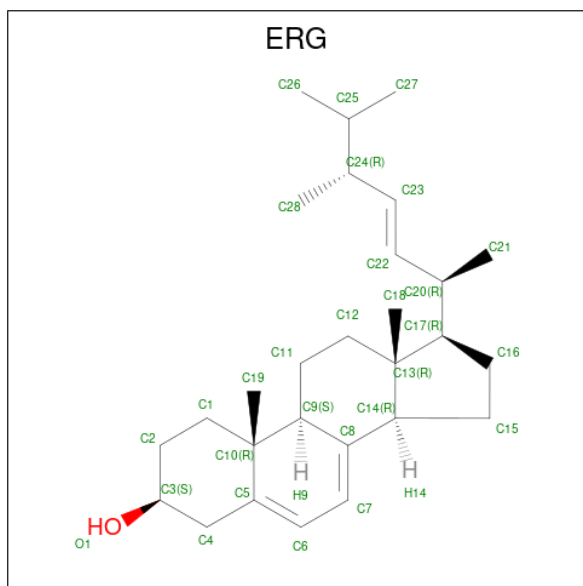
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
34	B	1	29	20	1	7	1	0
34	F	1	29	20	1	7	1	0
34	K	1	29	20	1	7	1	0

- Molecule 35 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: $C_{41}H_{78}O_{12}S$).



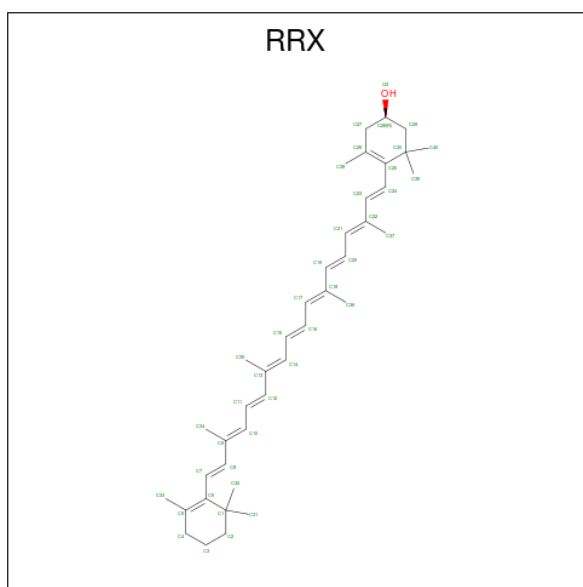
Mol	Chain	Residues	Atoms				AltConf
35	G	1	Total	C	O	S	0
			46	33	12	1	
35	H	1	Total	C	O	S	0
			45	32	12	1	
35	7	1	Total	C	O	S	0
			39	26	12	1	

- Molecule 36 is ERGOSTEROL (three-letter code: ERG) (formula: $C_{28}H_{44}O$).



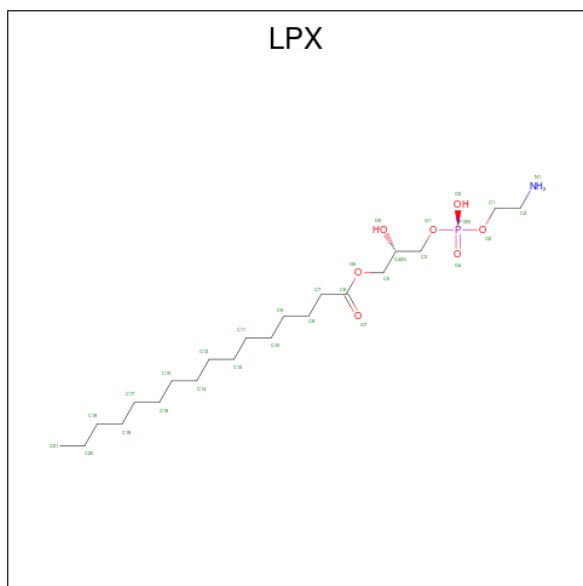
Mol	Chain	Residues	Atoms			AltConf
36	G	1	Total	C	O	0
			29	28	1	

- Molecule 37 is (3R)-beta,beta-caroten-3-ol (three-letter code: RRX) (formula: $C_{40}H_{56}O$).



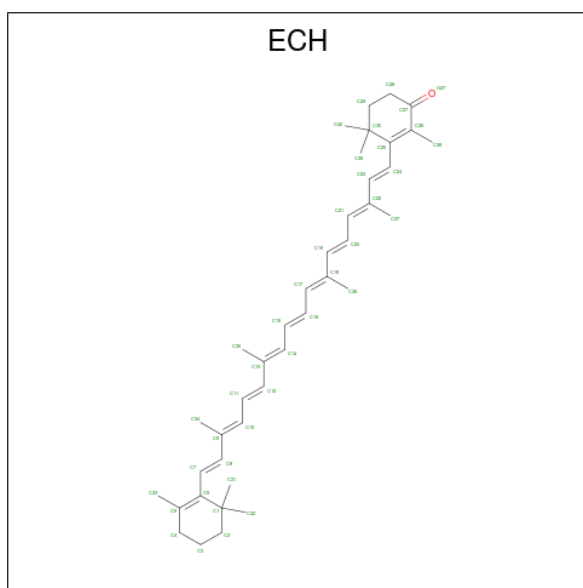
Mol	Chain	Residues	Atoms			AltConf
37	J	1	Total	C	O	0
			41	40	1	

- Molecule 38 is (2S)-3-[[[(R)-(2-aminoethoxy)(hydroxy)phosphoryl]oxy]-2-hydroxypropyl hexadecanoate (three-letter code: LPX) (formula: C₂₁H₄₄NO₇P).



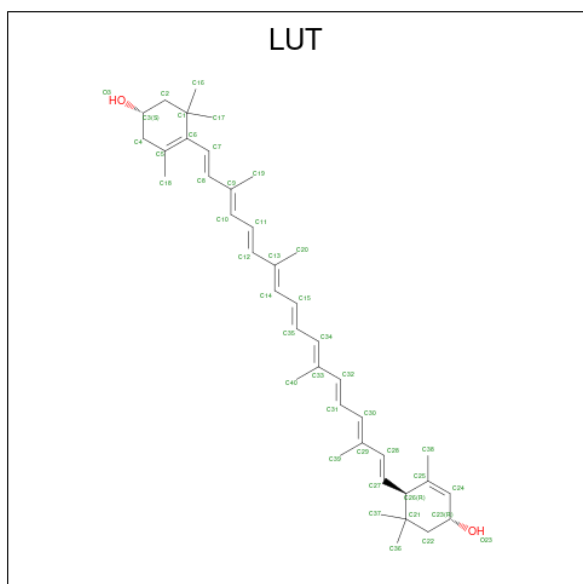
Mol	Chain	Residues	Atoms					AltConf
38	J	1	Total	C	N	O	P	0
			17	8	1	7	1	
38	a	1	Total	C	N	O	P	0
			30	21	1	7	1	

- Molecule 39 is beta,beta-caroten-4-one (three-letter code: ECH) (formula: C₄₀H₅₄O).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
39	M	1	41	40	1	0

- Molecule 40 is (3R,3'R,6S)-4,5-DIDEHYDRO-5,6-DIHYDRO-BETA,BETA-CAROTENE-3,3'-DIOL (three-letter code: LUT) (formula: C₄₀H₅₆O₂).



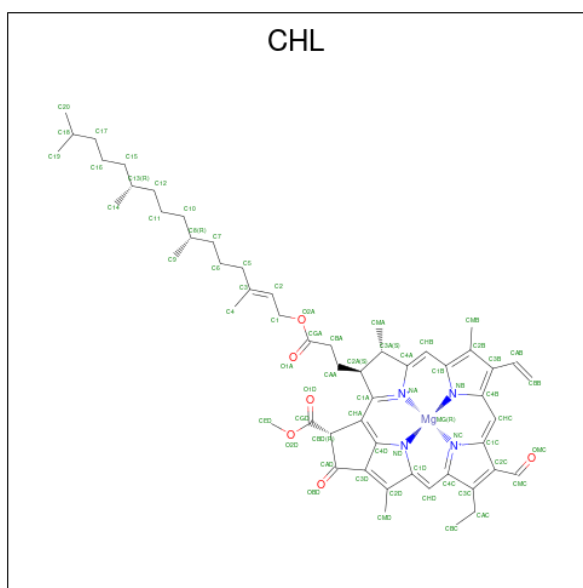
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
40	1	1	126	120	6	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
40	1	1	126	120	6	0
40	1	1	126	120	6	0
40	a	1	126	120	6	0
40	a	1	126	120	6	0
40	a	1	126	120	6	0
40	3	1	84	80	4	0
40	3	1	84	80	4	0
40	4	1	84	80	4	0
40	4	1	84	80	4	0
40	5	1	126	120	6	0
40	5	1	126	120	6	0
40	5	1	126	120	6	0
40	6	1	84	80	4	0
40	6	1	84	80	4	0
40	7	1	42	40	2	0
40	8	1	84	80	4	0
40	8	1	84	80	4	0
40	2	1	84	80	4	0
40	2	1	84	80	4	0
40	9	1	84	80	4	0
40	9	1	84	80	4	0

- Molecule 41 is CHLOROPHYLL B (three-letter code: CHL) (formula: $C_{55}H_{70}MgN_4O_6$).



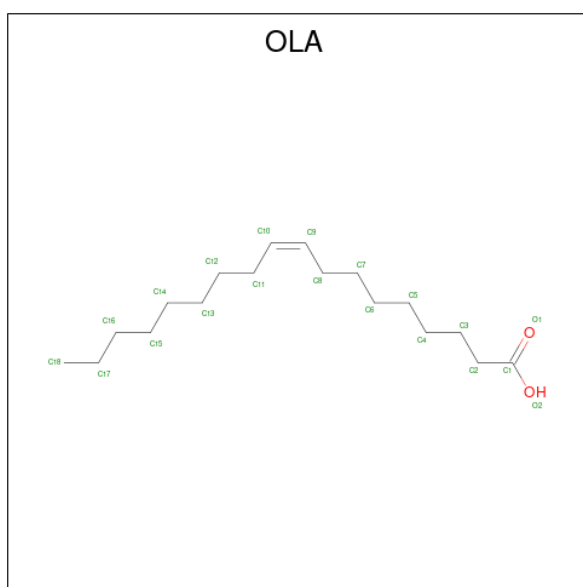
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
41	1	1	Total	C	Mg	N	O	0
			114	92	2	8	12	
41	1	1	Total	C	Mg	N	O	0
			114	92	2	8	12	
41	a	1	Total	C	Mg	N	O	0
			203	159	4	16	24	
41	a	1	Total	C	Mg	N	O	0
			203	159	4	16	24	
41	a	1	Total	C	Mg	N	O	0
			203	159	4	16	24	
41	a	1	Total	C	Mg	N	O	0
			203	159	4	16	24	
41	3	1	Total	C	Mg	N	O	0
			98	78	2	8	10	
41	3	1	Total	C	Mg	N	O	0
			98	78	2	8	10	
41	4	1	Total	C	Mg	N	O	0
			174	141	3	12	18	
41	4	1	Total	C	Mg	N	O	0
			174	141	3	12	18	
41	4	1	Total	C	Mg	N	O	0
			174	141	3	12	18	
41	5	1	Total	C	Mg	N	O	0
			173	140	3	12	18	
41	5	1	Total	C	Mg	N	O	0
			173	140	3	12	18	

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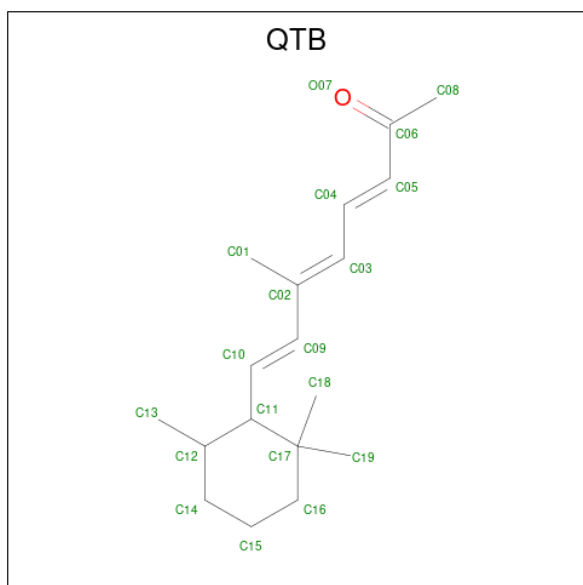
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
41	5	1	Total 173	C 140	Mg 3	N 12	O 18	0
41	6	1	Total 224	C 180	Mg 4	N 16	O 24	0
41	6	1	Total 224	C 180	Mg 4	N 16	O 24	0
41	6	1	Total 224	C 180	Mg 4	N 16	O 24	0
41	6	1	Total 224	C 180	Mg 4	N 16	O 24	0
41	7	1	Total 66	C 55	Mg 1	N 4	O 6	0
41	8	1	Total 174	C 141	Mg 3	N 12	O 18	0
41	8	1	Total 174	C 141	Mg 3	N 12	O 18	0
41	8	1	Total 174	C 141	Mg 3	N 12	O 18	0
41	9	1	Total 93	C 73	Mg 2	N 8	O 10	0
41	9	1	Total 93	C 73	Mg 2	N 8	O 10	0

- Molecule 42 is OLEIC ACID (three-letter code: OLA) (formula: C₁₈H₃₄O₂).



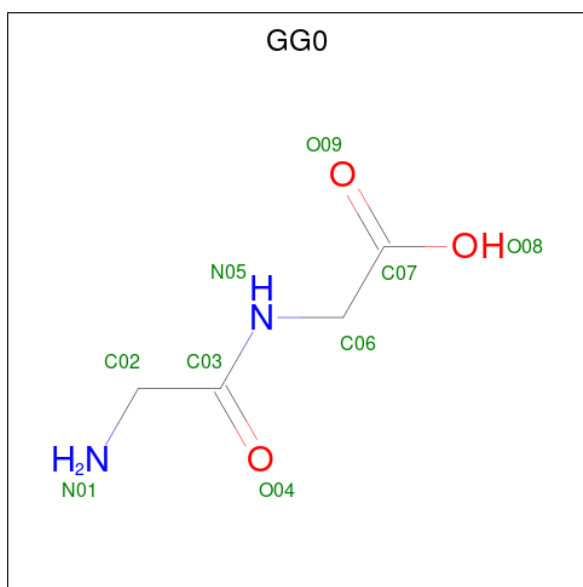
Mol	Chain	Residues	Atoms			AltConf
42	1	1	Total	C	O	0
			20	18	2	
42	8	1	Total	C	O	0
			20	18	2	

- Molecule 43 is (3 {E},5 {E},7 {E})-6-methyl-8-[(6 {R})-2,2,6-trimethylcyclohexyl]octa-3,5,7-trien-2-one (three-letter code: QTB) (formula: C₁₈H₂₈O).



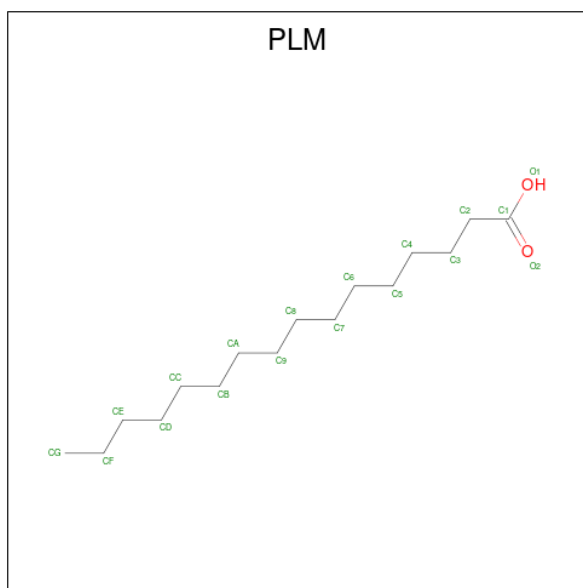
Mol	Chain	Residues	Atoms			AltConf
43	a	1	Total	C	O	0
			19	18	1	
43	3	1	Total	C	O	0
			19	18	1	

- Molecule 44 is 2-(2-azanylethanoylamino)ethanoic acid (three-letter code: GG0) (formula: C₄H₈N₂O₃).



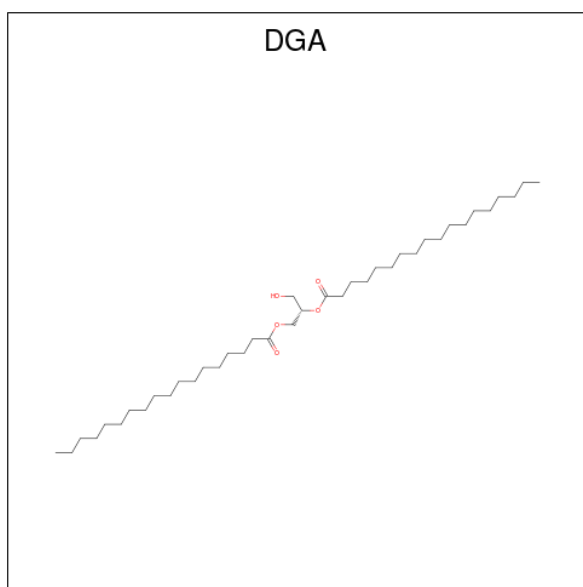
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
44	a	1	9	4	2	3	0

- Molecule 45 is PALMITIC ACID (three-letter code: PLM) (formula: $C_{16}H_{32}O_2$).



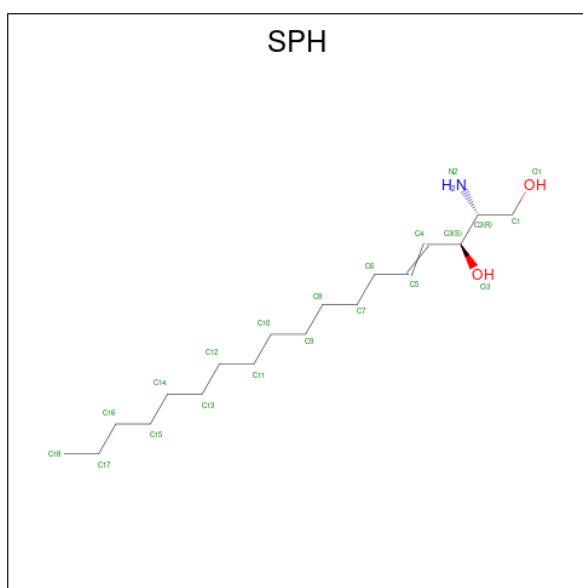
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
45	4	1	17	16	1	0
45	6	1	18	16	2	0

- Molecule 46 is DIACYL GLYCEROL (three-letter code: DGA) (formula: $C_{39}H_{76}O_5$).



Mol	Chain	Residues	Atoms			AltConf
46	5	1	Total	C	O	0
			23	18	5	
46	8	1	Total	C	O	0
			30	25	5	

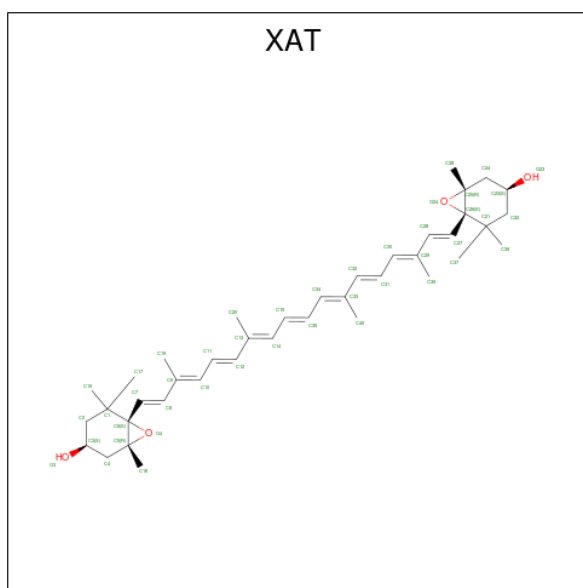
- Molecule 47 is SPHINGOSINE (three-letter code: SPH) (formula: $C_{18}H_{37}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
47	6	1	Total	C	N	O	0
			21	18	1	2	

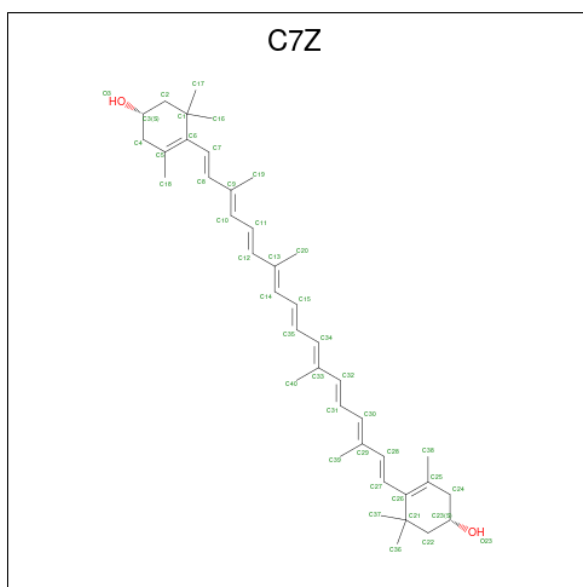
- Molecule 48 is (3S,5R,6S,3'S,5'R,6'S)-5,6,5',6'-DIEPOXY-5,6,5',6'- TETRAHYDRO-BETA

,BETA-CAROTENE-3,3'-DIOL (three-letter code: XAT) (formula: C₄₀H₅₆O₄).



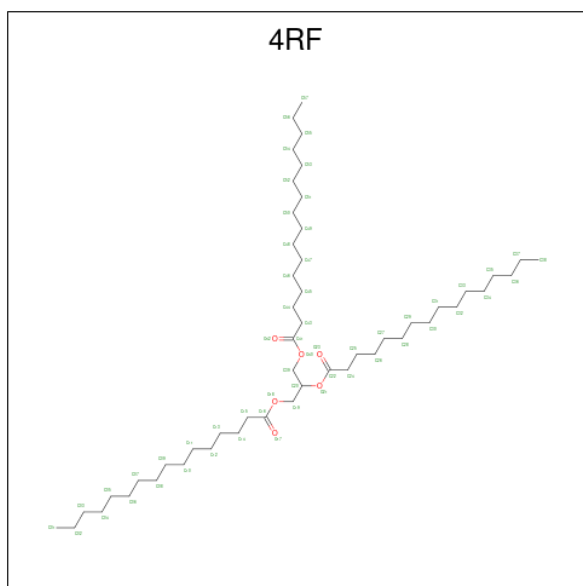
Mol	Chain	Residues	Atoms		AltConf
			Total	C O	
48	7	1	44	40 4	0

- Molecule 49 is (1 {S})-3,5,5-trimethyl-4-[(1 {E},3 {E},5 {E},7 {E},9 {E},11 {E},13 {E},15 {E},17 {E})-3,7,12,16-tetramethyl-18-[(4 {S})-2,6,6-trimethyl-4-oxidanyl-cyclohexen-1-yl]octadeca-1,3,5,7,9,11,13,15,17-nonaenyl]cyclohex-3-en-1-ol (three-letter code: C7Z) (formula: C₄₀H₅₆O₂).



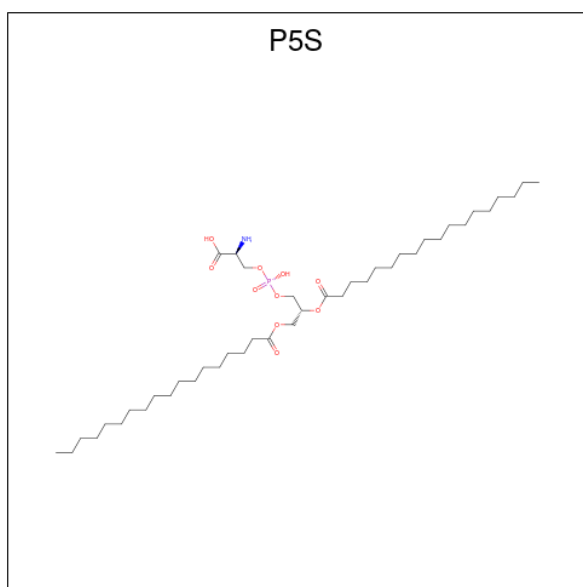
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
49	7	1	42	40	2	0

- Molecule 50 is Tripalmitoylglycerol (three-letter code: 4RF) (formula: $C_{51}H_{98}O_6$).



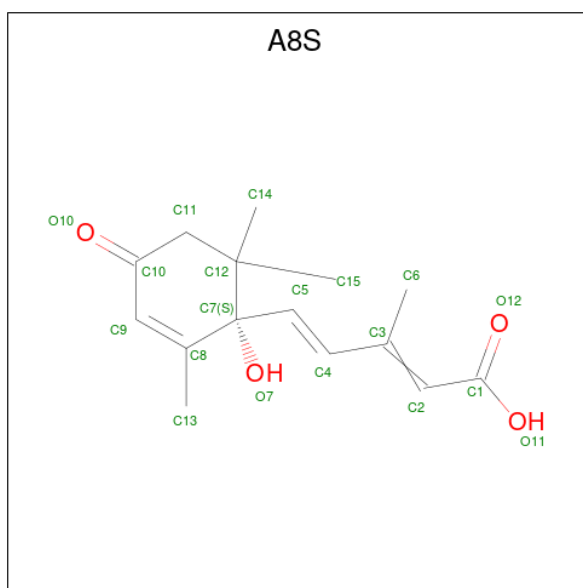
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
50	7	1	32	26	6	0
50	8	1	96	84	12	0
50	8	1	96	84	12	0

- Molecule 51 is O-[(R)-{[(2R)-2,3-bis(octadecanoyloxy)propyl]oxy}(hydroxy)phosphoryl]-L-serine (three-letter code: P5S) (formula: $C_{42}H_{82}NO_{10}P$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
51	8	1	37	25	1	10	1	0

- Molecule 52 is (2Z,4E)-5-[(1S)-1-hydroxy-2,6,6-trimethyl-4-oxocyclohex-2-en-1-yl]-3-methyl penta-2,4-dienoic acid (three-letter code: A8S) (formula: C₁₅H₂₀O₄).

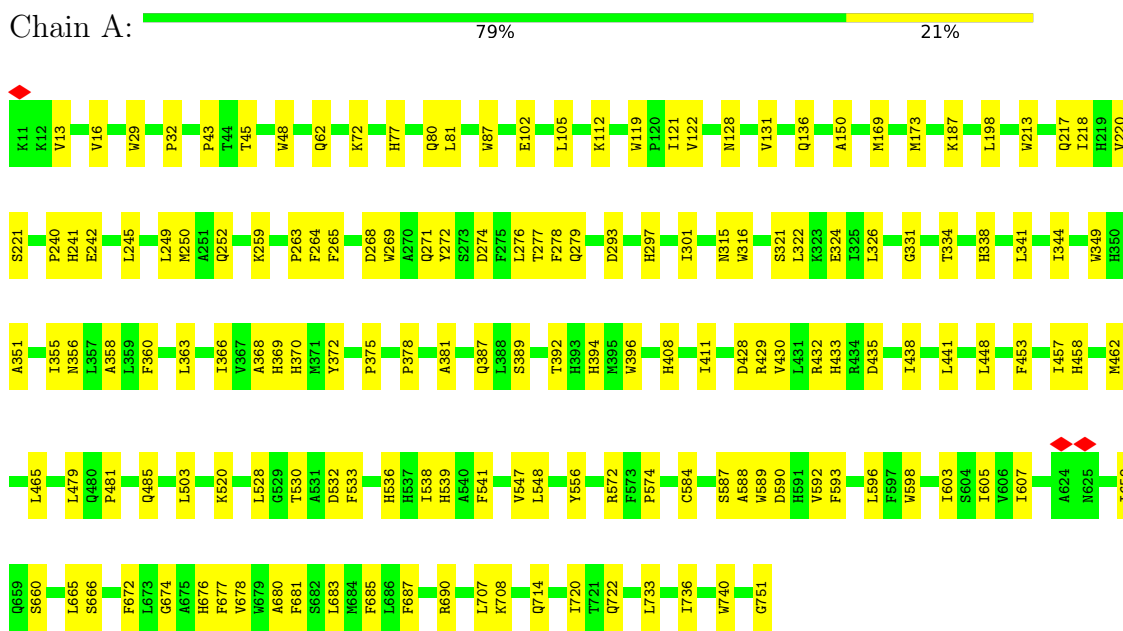


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
52	9	1	19	15	4	0

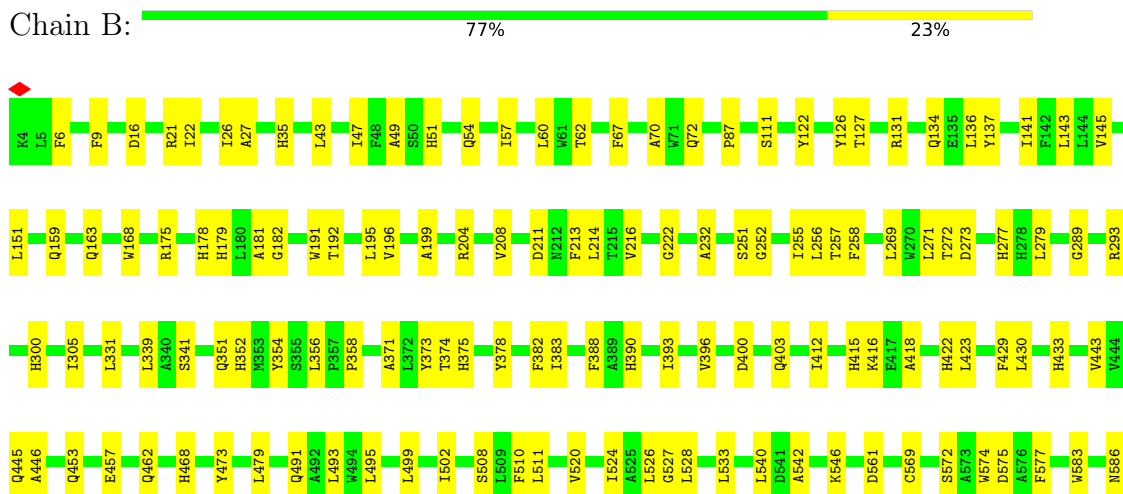
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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

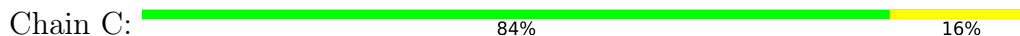


- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2

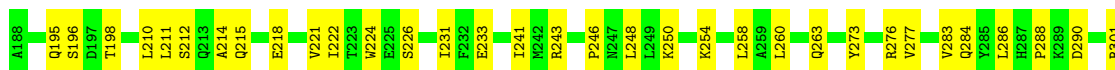




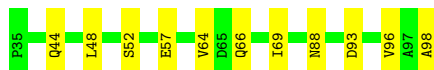
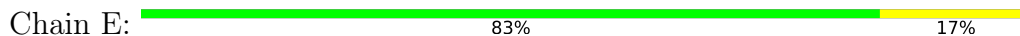
- Molecule 3: Photosystem I iron-sulfur center



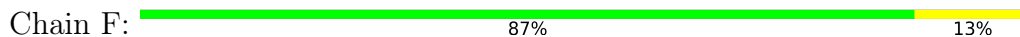
- Molecule 4: Photosystem I reaction center subunit chloroplastic



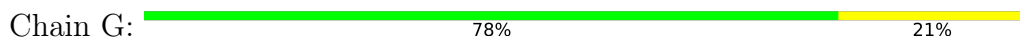
- Molecule 5: Photosystem I reaction center subunit IV



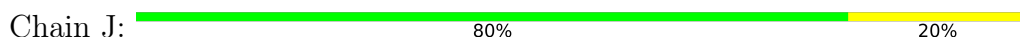
- Molecule 6: PSI-F

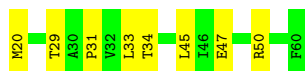


- Molecule 7: Photosystem I reaction center subunit chloroplastic

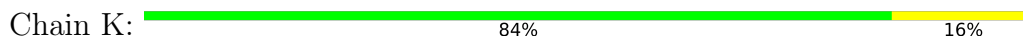


- Molecule 8: Photosystem I reaction center subunit IX

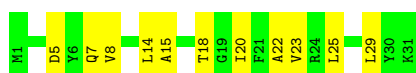




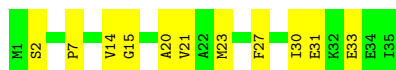
- Molecule 9: PSI-K



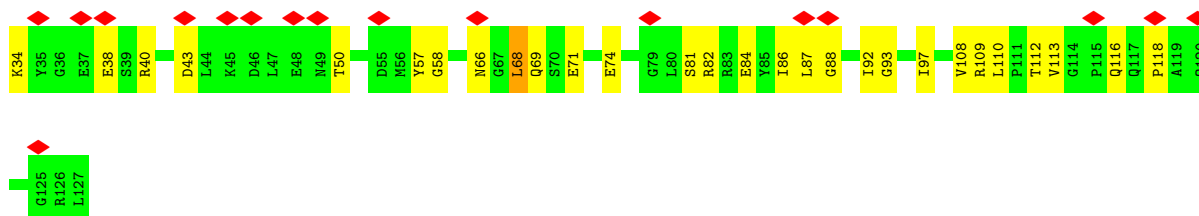
- Molecule 10: Photosystem I reaction center subunit XII



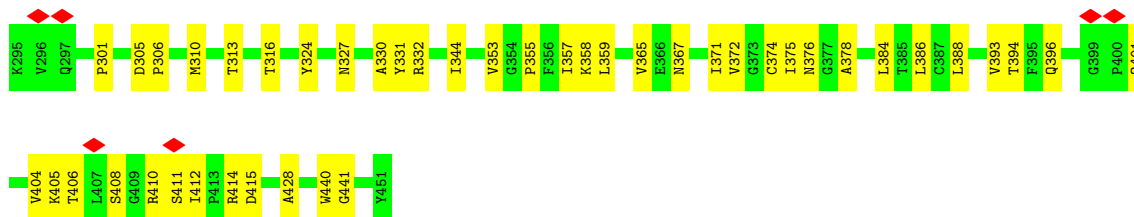
- Molecule 11: Photosystem I reaction center subunit VIII



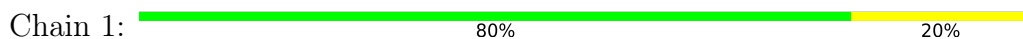
- Molecule 12: Photosystem I reaction center subunit VI-chloroplastic-like

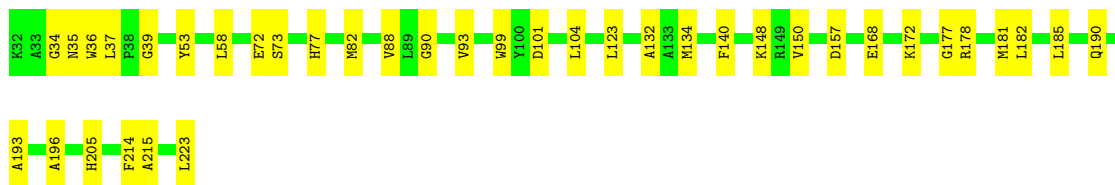


- Molecule 13: PSI subunit V

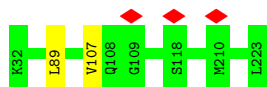


- Molecule 14: Chlorophyll a-b binding protein, chloroplastic

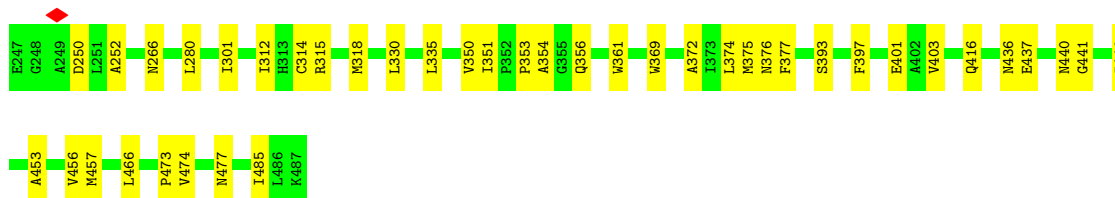
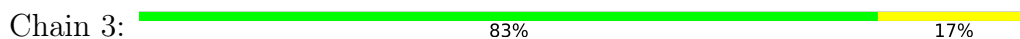




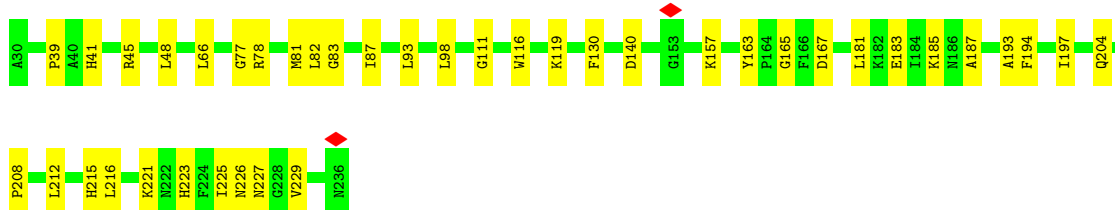
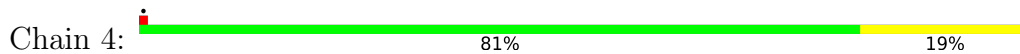
- Molecule 14: Chlorophyll a-b binding protein, chloroplastic



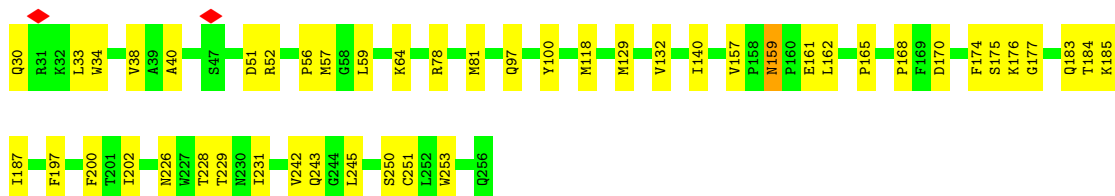
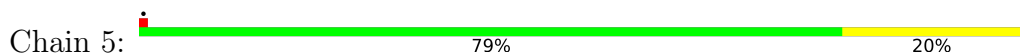
- Molecule 15: Glutathione reductase



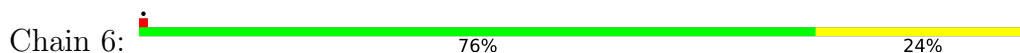
- Molecule 16: Chlorophyll a-b binding protein, chloroplastic

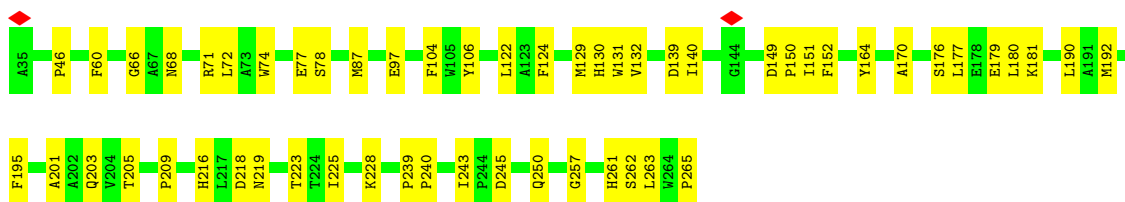


- Molecule 17: Chlorophyll a-b binding protein, chloroplastic

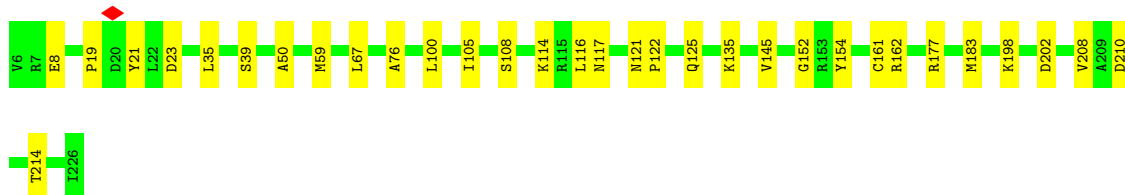
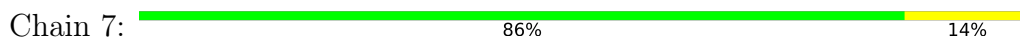


- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

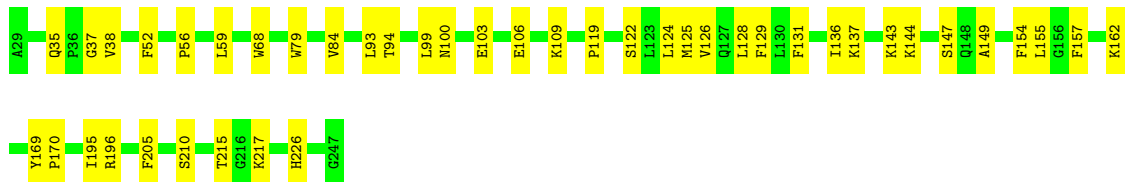
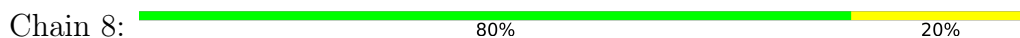




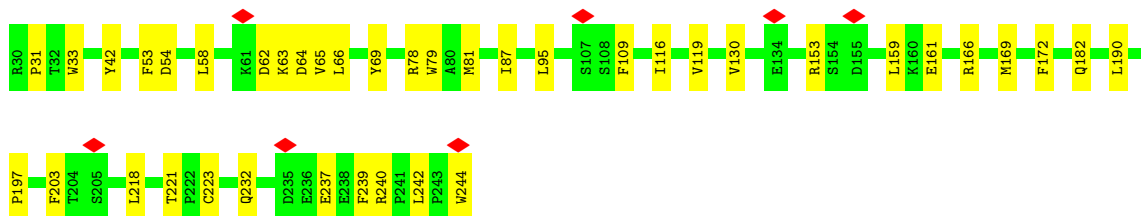
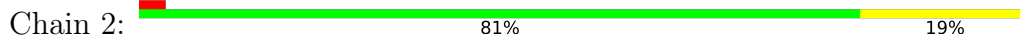
• Molecule 19: Chlorophyll a-b binding protein, chloroplastic



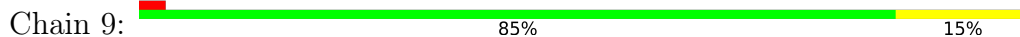
• Molecule 20: Chlorophyll a-b binding protein, chloroplastic



• Molecule 21: Chlorophyll a-b binding protein, chloroplastic



• Molecule 22: Chlorophyll a-b binding protein, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75049	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.04	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	165000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.082	Depositor
Minimum map value	-0.041	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.007	Depositor
Map size (\AA)	414.72, 414.72, 414.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.81, 0.81, 0.81	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: LHG, P5S, LAP, QTB, PTY, 3PH, LMT, CL0, RRX, LUT, PQN, SF4, BCR, DGA, 4RF, CLA, SPH, PCW, PLM, LPX, GG0, XAT, ECH, CHL, OLA, DGD, C7Z, SQD, A8S, ERG

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	0.27	0/6022	0.47	0/8215
2	B	0.27	0/6006	0.47	0/8205
3	C	0.25	0/611	0.54	0/828
4	D	0.27	0/1150	0.51	0/1551
5	E	0.28	0/520	0.54	0/705
6	F	0.26	0/1309	0.49	0/1771
7	G	0.27	0/743	0.55	0/1007
8	J	0.25	0/322	0.51	0/439
9	K	0.26	0/622	0.49	0/844
10	M	0.27	0/244	0.46	0/330
11	I	0.29	0/276	0.51	0/373
12	H	0.27	0/744	0.58	1/1000 (0.1%)
13	L	0.27	0/1195	0.54	0/1635
14	1	0.29	0/1443	0.50	0/1960
14	a	0.29	0/1443	0.55	1/1960 (0.1%)
15	3	0.28	0/1896	0.49	0/2573
16	4	0.27	0/1681	0.49	0/2285
17	5	0.26	0/1825	0.51	0/2483
18	6	0.28	0/1845	0.50	1/2515 (0.0%)
19	7	0.27	0/1748	0.48	0/2372
20	8	0.27	0/1717	0.45	0/2330
21	2	0.28	0/1708	0.54	0/2318
22	9	0.28	0/1435	0.54	0/1946
All	All	0.27	0/36505	0.50	3/49645 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
-----	-------	-----	------	-------	---	-------------	----------

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	6	139	ASP	CB-CG-OD1	6.49	124.14	118.30
12	H	68	LEU	CB-CG-CD2	6.05	121.28	111.00
14	a	89	LEU	CA-CB-CG	5.06	126.93	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5824	0	5675	126	0
2	B	5796	0	5576	153	0
3	C	601	0	576	15	0
4	D	1124	0	1129	27	0
5	E	509	0	507	8	0
6	F	1277	0	1296	20	0
7	G	727	0	724	21	0
8	J	316	0	332	8	0
9	K	613	0	639	12	0
10	M	239	0	255	13	0
11	I	270	0	287	14	0
12	H	729	0	705	26	0
13	L	1165	0	1181	40	0
14	1	1405	0	1370	30	0
14	a	1405	0	1370	0	0
15	3	1844	0	1805	36	0
16	4	1631	0	1575	40	0
17	5	1769	0	1719	39	0
18	6	1787	0	1762	43	0
19	7	1698	0	1640	30	0
20	8	1669	0	1619	43	0
21	2	1666	0	1657	34	0
22	9	1397	0	1374	25	0
23	A	65	0	72	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	1	693	0	673	45	0
24	2	724	0	608	42	0
24	3	719	0	724	36	0
24	4	768	0	683	41	0
24	5	739	0	635	23	0
24	6	711	0	648	38	0
24	7	778	0	716	38	0
24	8	699	0	619	32	0
24	9	549	0	499	27	0
24	A	2621	0	2693	174	0
24	B	2583	0	2673	171	0
24	F	105	0	87	6	0
24	G	141	0	104	5	0
24	H	156	0	129	10	0
24	J	42	0	30	0	0
24	K	204	0	165	7	0
24	L	155	0	130	8	0
24	a	571	0	538	0	0
25	A	33	0	46	4	0
25	B	33	0	46	5	0
26	A	8	0	0	0	0
26	C	16	0	0	1	0
27	3	120	0	159	9	0
27	4	40	0	51	0	0
27	5	80	0	106	6	0
27	6	80	0	105	4	0
27	7	40	0	52	2	0
27	8	40	0	53	1	0
27	A	200	0	264	27	0
27	B	280	0	369	31	0
27	F	40	0	53	7	0
27	G	40	0	53	3	0
27	H	40	0	52	2	0
27	I	40	0	53	6	0
27	J	40	0	53	4	0
27	K	80	0	106	8	0
27	L	120	0	159	11	0
28	1	77	0	97	6	0
28	2	98	0	148	6	0
28	3	49	0	74	5	0
28	4	81	0	108	3	0
28	5	49	0	74	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	6	86	0	118	7	0
28	7	128	0	175	7	0
28	8	37	0	44	0	0
28	9	82	0	110	6	0
28	A	120	0	159	10	0
28	B	95	0	139	6	0
28	F	79	0	101	6	0
28	a	35	0	40	0	0
29	8	66	0	96	8	0
29	A	51	0	60	3	0
29	B	66	0	96	10	0
30	A	33	0	39	0	0
31	1	35	0	45	1	0
31	2	35	0	46	1	0
31	A	35	0	45	3	0
31	B	35	0	45	6	0
32	6	36	0	44	2	0
32	B	30	0	34	2	0
33	3	38	0	49	1	0
33	5	38	0	49	3	0
33	7	33	0	39	1	0
33	8	35	0	43	2	0
33	9	48	0	72	2	0
33	B	41	0	55	2	0
34	B	29	0	42	0	0
34	F	29	0	42	3	0
34	K	29	0	42	2	0
35	7	39	0	41	1	0
35	G	46	0	55	2	0
35	H	45	0	53	7	0
36	G	29	0	38	7	0
37	J	41	0	56	5	0
38	J	17	0	14	1	0
38	a	30	0	43	0	0
39	M	41	0	54	4	0
40	1	126	0	165	12	0
40	2	84	0	110	13	0
40	3	84	0	110	10	0
40	4	84	0	110	14	0
40	5	126	0	165	14	0
40	6	84	0	110	12	0
40	7	42	0	55	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	8	84	0	110	15	0
40	9	84	0	110	11	0
40	a	126	0	165	0	0
41	1	114	0	101	11	0
41	3	98	0	73	9	0
41	4	174	0	156	10	0
41	5	173	0	152	13	0
41	6	224	0	188	11	0
41	7	66	0	69	3	0
41	8	174	0	150	12	0
41	9	93	0	62	3	0
41	a	203	0	148	0	0
42	1	20	0	33	2	0
42	8	20	0	33	3	0
43	3	19	0	0	0	0
43	a	19	0	0	0	0
44	a	9	0	0	0	0
45	4	17	0	31	0	0
45	6	18	0	31	2	0
46	5	23	0	28	1	0
46	8	30	0	42	2	0
47	6	21	0	37	1	0
48	7	44	0	56	3	0
49	7	42	0	0	0	0
50	7	32	0	39	1	0
50	8	96	0	142	4	0
51	8	37	0	40	0	0
52	9	19	0	19	1	0
All	All	54609	0	54543	1327	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 1327 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:G:5002:ERG:O1	36:G:5002:ERG:C3	1.70	1.38
24:A:1131:CLA:HBB1	24:A:1132:CLA:H2	1.44	0.97
40:4:502:LUT:H32	24:4:604:CLA:HAB	1.49	0.95
1:A:396:TRP:CD1	24:A:1126:CLA:HAB	2.13	0.84
24:B:1220:CLA:HAB	24:B:1227:CLA:HMD2	1.60	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	739/741 (100%)	715 (97%)	24 (3%)	0	100	100
2	B	729/731 (100%)	697 (96%)	32 (4%)	0	100	100
3	C	78/80 (98%)	76 (97%)	2 (3%)	0	100	100
4	D	141/143 (99%)	133 (94%)	8 (6%)	0	100	100
5	E	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
6	F	163/165 (99%)	158 (97%)	5 (3%)	0	100	100
7	G	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
8	J	39/41 (95%)	39 (100%)	0	0	100	100
9	K	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
10	M	29/31 (94%)	29 (100%)	0	0	100	100
11	I	33/35 (94%)	30 (91%)	3 (9%)	0	100	100
12	H	92/94 (98%)	75 (82%)	15 (16%)	2 (2%)	6	32
13	L	155/157 (99%)	141 (91%)	13 (8%)	1 (1%)	25	62
14	1	190/192 (99%)	174 (92%)	15 (8%)	1 (0%)	29	65
14	a	190/192 (99%)	169 (89%)	20 (10%)	1 (0%)	29	65
15	3	239/241 (99%)	221 (92%)	17 (7%)	1 (0%)	34	68
16	4	205/207 (99%)	188 (92%)	17 (8%)	0	100	100
17	5	225/227 (99%)	204 (91%)	21 (9%)	0	100	100
18	6	229/231 (99%)	208 (91%)	20 (9%)	1 (0%)	34	68
19	7	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
20	8	217/219 (99%)	203 (94%)	14 (6%)	0	100	100
21	2	213/215 (99%)	199 (93%)	13 (6%)	1 (0%)	29	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	9	180/182 (99%)	166 (92%)	14 (8%)	0	100	100
All	All	4548/4594 (99%)	4261 (94%)	279 (6%)	8 (0%)	50	78

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	H	118	PRO
14	1	36	TRP
14	a	107	VAL
18	6	46	PRO
12	H	110	LEU

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	600/600 (100%)	600 (100%)	0	100	100
2	B	588/588 (100%)	588 (100%)	0	100	100
3	C	69/69 (100%)	69 (100%)	0	100	100
4	D	121/121 (100%)	121 (100%)	0	100	100
5	E	55/55 (100%)	55 (100%)	0	100	100
6	F	126/126 (100%)	126 (100%)	0	100	100
7	G	71/71 (100%)	70 (99%)	1 (1%)	67	85
8	J	35/35 (100%)	35 (100%)	0	100	100
9	K	66/66 (100%)	66 (100%)	0	100	100
10	M	23/23 (100%)	23 (100%)	0	100	100
11	I	30/30 (100%)	30 (100%)	0	100	100
12	H	71/71 (100%)	71 (100%)	0	100	100
13	L	122/122 (100%)	122 (100%)	0	100	100
14	1	134/134 (100%)	134 (100%)	0	100	100
14	a	134/134 (100%)	134 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	3	186/186 (100%)	186 (100%)	0	100	100
16	4	165/165 (100%)	165 (100%)	0	100	100
17	5	183/183 (100%)	182 (100%)	1 (0%)	88	95
18	6	187/187 (100%)	187 (100%)	0	100	100
19	7	176/176 (100%)	176 (100%)	0	100	100
20	8	168/168 (100%)	168 (100%)	0	100	100
21	2	173/173 (100%)	173 (100%)	0	100	100
22	9	140/140 (100%)	140 (100%)	0	100	100
All	All	3623/3623 (100%)	3621 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	1323	ARG
17	5	159	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	468	HIS
19	7	167	GLN
2	B	604	GLN
21	2	182	GLN
15	3	465	ASN

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

379 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
35	SQD	H	5001	-	44,45,54	0.85	0	53,56,65	0.96	2 (3%)
50	4RF	8	808	-	53,53,56	0.89	6 (11%)	56,56,59	0.93	3 (5%)
24	CLA	L	1503	-	45,53,73	1.62	9 (20%)	52,89,113	2.18	13 (25%)
24	CLA	B	1240	-	65,73,73	1.35	8 (12%)	76,113,113	2.04	20 (26%)
24	CLA	7	608	-	42,50,73	1.69	8 (19%)	48,85,113	2.24	12 (25%)
43	QTB	a	504	-	19,19,19	2.45	5 (26%)	20,26,26	2.77	8 (40%)
27	BCR	L	4001	-	41,41,41	1.84	4 (9%)	56,56,56	4.39	16 (28%)
24	CLA	A	1137	-	60,68,73	1.42	8 (13%)	70,107,113	2.08	20 (28%)
24	CLA	6	608	-	45,53,73	1.62	9 (20%)	52,89,113	2.17	14 (26%)
24	CLA	B	1239	-	65,73,73	1.34	7 (10%)	76,113,113	2.02	18 (23%)
28	LHG	8	801	-	36,36,48	0.44	0	39,42,54	1.15	3 (7%)
24	CLA	5	616	-	46,54,73	1.62	9 (19%)	53,90,113	2.09	13 (24%)
24	CLA	5	612	-	65,73,73	1.34	8 (12%)	76,113,113	1.99	16 (21%)
24	CLA	A	1103	-	65,73,73	1.34	7 (10%)	76,113,113	2.01	16 (21%)
24	CLA	B	1225	-	65,73,73	1.38	8 (12%)	76,113,113	1.87	14 (18%)
27	BCR	8	503	-	41,41,41	1.85	4 (9%)	56,56,56	4.41	18 (32%)
23	CL0	A	1011	-	65,73,73	2.36	17 (26%)	76,113,113	2.52	24 (31%)
27	BCR	3	505	-	41,41,41	1.85	4 (9%)	56,56,56	4.34	14 (25%)
28	LHG	1	802	-	41,41,48	0.42	0	44,47,54	1.08	3 (6%)
31	LMT	A	5008	-	36,36,36	1.12	5 (13%)	47,47,47	1.02	3 (6%)
48	XAT	7	502	-	39,47,47	0.69	1 (2%)	54,74,74	1.82	11 (20%)
24	CLA	3	610	15	60,68,73	1.39	8 (13%)	70,107,113	2.04	19 (27%)
24	CLA	6	605	-	46,54,73	1.58	8 (17%)	53,90,113	2.29	16 (30%)
24	CLA	9	607	-	47,55,73	1.61	10 (21%)	54,91,113	2.21	14 (25%)
24	CLA	A	1133	-	65,73,73	1.37	9 (13%)	76,113,113	1.88	14 (18%)
30	3PH	A	5007	-	32,32,47	1.03	4 (12%)	36,37,52	1.21	2 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	K	1404	-	52,60,73	1.52	9 (17%)	60,97,113	2.22	19 (31%)
49	C7Z	7	504	-	43,43,43	5.35	26 (60%)	58,60,60	2.72	20 (34%)
25	PQN	A	2001	-	34,34,34	0.38	0	42,45,45	1.11	3 (7%)
24	CLA	6	606	-	52,60,73	1.51	8 (15%)	60,97,113	2.22	17 (28%)
41	CHL	6	613	-	51,59,74	0.85	2 (3%)	55,96,114	1.42	12 (21%)
24	CLA	L	1501	13	50,58,73	1.53	8 (16%)	58,95,113	2.23	15 (25%)
24	CLA	A	1139	-	55,63,73	1.49	8 (14%)	64,101,113	2.08	16 (25%)
27	BCR	3	504	-	41,41,41	1.86	4 (9%)	56,56,56	4.23	17 (30%)
24	CLA	6	603	-	65,73,73	1.36	9 (13%)	76,113,113	2.01	17 (22%)
24	CLA	2	608	-	45,53,73	1.61	8 (17%)	52,89,113	2.16	14 (26%)
27	BCR	A	4002	-	41,41,41	1.82	4 (9%)	56,56,56	4.28	14 (25%)
40	LUT	5	501	-	42,43,43	2.36	1 (2%)	51,60,60	1.96	15 (29%)
34	LAP	K	5001	-	28,28,28	1.22	2 (7%)	33,35,35	0.97	1 (3%)
28	LHG	7	801	-	48,48,48	0.39	0	51,54,54	1.09	3 (5%)
24	CLA	8	611	-	50,58,73	1.52	7 (14%)	58,95,113	2.25	17 (29%)
24	CLA	6	601	-	60,68,73	1.40	8 (13%)	70,107,113	2.09	18 (25%)
24	CLA	2	610	-	46,54,73	1.61	10 (21%)	53,90,113	2.15	13 (24%)
24	CLA	4	601	-	60,68,73	1.40	8 (13%)	70,107,113	2.06	17 (24%)
24	CLA	1	601	-	60,68,73	1.42	9 (15%)	70,107,113	2.10	20 (28%)
46	DGA	8	803	-	29,29,43	1.29	2 (6%)	31,31,45	1.34	3 (9%)
24	CLA	A	1105	-	57,65,73	1.44	8 (14%)	66,103,113	2.13	17 (25%)
28	LHG	2	801	-	48,48,48	0.37	0	51,54,54	1.11	2 (3%)
40	LUT	9	502	-	42,43,43	2.36	1 (2%)	51,60,60	2.02	15 (29%)
25	PQN	B	2002	-	34,34,34	0.36	0	42,45,45	1.13	3 (7%)
24	CLA	A	1141	28	45,53,73	1.62	9 (20%)	52,89,113	2.18	13 (25%)
36	ERG	G	5002	-	31,32,32	7.94	19 (61%)	47,50,50	3.55	19 (40%)
27	BCR	A	4004	-	41,41,41	1.84	4 (9%)	56,56,56	4.29	15 (26%)
24	CLA	8	606	-	57,65,73	1.43	7 (12%)	66,103,113	2.08	15 (22%)
24	CLA	B	1228	-	65,73,73	1.35	8 (12%)	76,113,113	1.94	19 (25%)
45	PLM	4	803	-	16,16,17	0.43	0	15,15,17	0.93	0
24	CLA	A	1115	-	60,68,73	1.41	9 (15%)	70,107,113	2.07	16 (22%)
24	CLA	7	607	-	59,67,73	1.44	9 (15%)	68,105,113	2.04	15 (22%)
24	CLA	A	1111	-	65,73,73	1.34	7 (10%)	76,113,113	2.01	18 (23%)
24	CLA	7	601	-	60,68,73	1.42	9 (15%)	70,107,113	2.07	18 (25%)
24	CLA	H	1701	-	55,63,73	1.46	9 (16%)	64,101,113	2.27	15 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	3	601	-	65,73,73	1.36	7 (10%)	76,113,113	2.05	18 (23%)
41	CHL	a	609	-	53,61,74	0.85	2 (3%)	57,98,114	1.37	12 (21%)
31	LMT	1	804	-	36,36,36	1.16	6 (16%)	47,47,47	1.01	2 (4%)
40	LUT	a	501	-	42,43,43	2.38	1 (2%)	51,60,60	2.00	14 (27%)
24	CLA	A	1120	-	49,57,73	1.56	9 (18%)	55,93,113	2.33	15 (27%)
24	CLA	a	612	-	57,65,73	1.45	9 (15%)	66,103,113	2.07	16 (24%)
24	CLA	B	1023	-	65,73,73	1.37	7 (10%)	76,113,113	1.94	17 (22%)
24	CLA	1	610	-	45,53,73	1.62	7 (15%)	52,89,113	2.11	12 (23%)
32	PCW	6	803	-	35,35,53	1.30	4 (11%)	41,43,61	1.13	2 (4%)
24	CLA	4	603	-	56,64,73	1.46	9 (16%)	65,102,113	2.13	16 (24%)
27	BCR	I	4001	-	41,41,41	1.83	4 (9%)	56,56,56	4.25	19 (33%)
24	CLA	1	603	-	65,73,73	1.35	9 (13%)	76,113,113	2.00	17 (22%)
24	CLA	8	615	-	46,54,73	1.62	8 (17%)	53,90,113	2.14	14 (26%)
24	CLA	4	612	-	62,70,73	1.38	8 (12%)	72,109,113	2.09	19 (26%)
41	CHL	5	610	-	66,74,74	0.82	3 (4%)	73,114,114	1.32	12 (16%)
24	CLA	B	1204	-	65,73,73	1.35	9 (13%)	76,113,113	2.05	17 (22%)
27	BCR	L	4003	-	41,41,41	1.87	4 (9%)	56,56,56	4.41	15 (26%)
24	CLA	B	1229	-	65,73,73	1.35	8 (12%)	76,113,113	1.99	20 (26%)
24	CLA	G	1602	-	46,54,73	1.63	9 (19%)	53,90,113	2.18	16 (30%)
43	QTB	3	506	-	19,19,19	2.46	4 (21%)	20,26,26	2.79	8 (40%)
40	LUT	1	501	-	42,43,43	2.36	1 (2%)	51,60,60	2.06	16 (31%)
41	CHL	3	611	-	55,63,74	1.04	3 (5%)	59,100,114	1.48	11 (18%)
24	CLA	1	605	-	65,73,73	1.35	7 (10%)	76,113,113	2.06	19 (25%)
24	CLA	5	606	-	50,58,73	1.54	8 (16%)	58,95,113	2.22	17 (29%)
24	CLA	L	1502	-	60,68,73	1.41	8 (13%)	70,107,113	2.09	18 (25%)
24	CLA	2	613	-	41,49,73	1.70	8 (19%)	47,84,113	2.28	14 (29%)
24	CLA	B	1022	-	65,73,73	1.41	9 (13%)	76,113,113	1.89	18 (23%)
27	BCR	G	4001	-	41,41,41	1.84	4 (9%)	56,56,56	4.27	13 (23%)
24	CLA	B	1213	-	60,68,73	1.41	7 (11%)	70,107,113	2.11	19 (27%)
35	SQD	7	805	-	38,39,54	0.91	0	47,50,65	1.00	3 (6%)
24	CLA	5	602	-	52,60,73	1.52	8 (15%)	60,97,113	2.16	17 (28%)
24	CLA	A	1122	-	65,73,73	1.37	9 (13%)	76,113,113	1.98	16 (21%)
41	CHL	a	606	-	56,64,74	0.95	3 (5%)	61,102,114	1.32	10 (16%)
28	LHG	F	5001	-	42,42,48	0.42	0	45,48,54	1.11	3 (6%)
24	CLA	K	1401	-	46,54,73	1.61	9 (19%)	53,90,113	2.18	14 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	A	1121	-	57,65,73	1.45	9 (15%)	66,103,113	2.30	18 (27%)
31	LMT	B	5006	-	36,36,36	1.18	6 (16%)	47,47,47	0.97	1 (2%)
24	CLA	A	1135	-	65,73,73	1.38	9 (13%)	76,113,113	1.97	17 (22%)
24	CLA	B	1236	-	53,61,73	1.50	8 (15%)	61,98,113	2.10	14 (22%)
26	SF4	C	3003	3	0,12,12	-	-	-	-	-
50	4RF	8	807	-	41,41,56	1.00	6 (14%)	44,44,59	1.07	3 (6%)
24	CLA	4	615	16	60,68,73	1.43	9 (15%)	70,107,113	2.06	16 (22%)
24	CLA	B	1217	-	56,64,73	1.46	9 (16%)	65,102,113	2.17	15 (23%)
24	CLA	5	618	17	52,60,73	1.52	9 (17%)	60,97,113	2.18	17 (28%)
24	CLA	B	1231	-	65,73,73	1.35	9 (13%)	76,113,113	1.98	17 (22%)
24	CLA	2	609	21	55,63,73	1.46	7 (12%)	64,101,113	2.14	18 (28%)
24	CLA	2	604	-	56,64,73	1.49	9 (16%)	65,102,113	2.22	18 (27%)
28	LHG	9	802	-	48,48,48	0.38	0	51,54,54	1.09	4 (7%)
41	CHL	8	601	-	61,69,74	0.98	4 (6%)	67,108,114	1.33	8 (11%)
24	CLA	A	1101	-	65,73,73	1.35	7 (10%)	76,113,113	2.11	19 (25%)
24	CLA	G	1603	-	45,53,73	1.63	9 (20%)	52,89,113	2.15	13 (25%)
41	CHL	a	610	-	48,56,74	0.95	3 (6%)	51,92,114	1.50	13 (25%)
24	CLA	6	607	-	55,63,73	1.47	8 (14%)	64,101,113	2.11	15 (23%)
41	CHL	8	613	-	51,59,74	0.98	3 (5%)	55,96,114	1.35	12 (21%)
24	CLA	5	614	-	46,54,73	1.62	9 (19%)	53,90,113	2.15	14 (26%)
27	BCR	B	4002	-	41,41,41	1.86	4 (9%)	56,56,56	4.45	17 (30%)
24	CLA	1	607	-	65,73,73	1.37	8 (12%)	76,113,113	1.98	17 (22%)
27	BCR	7	503	-	41,41,41	1.84	4 (9%)	56,56,56	4.36	13 (23%)
40	LUT	2	501	-	42,43,43	2.36	1 (2%)	51,60,60	2.08	10 (19%)
28	LHG	A	5003	-	41,41,48	0.41	0	44,47,54	1.13	2 (4%)
27	BCR	L	4002	-	41,41,41	1.83	4 (9%)	56,56,56	4.30	16 (28%)
24	CLA	B	1226	-	65,73,73	1.39	8 (12%)	76,113,113	2.04	18 (23%)
24	CLA	4	606	-	50,58,73	1.53	7 (14%)	58,95,113	2.22	19 (32%)
24	CLA	7	610	-	55,63,73	1.50	10 (18%)	64,101,113	2.11	17 (26%)
24	CLA	a	611	-	50,58,73	1.55	9 (18%)	58,95,113	2.15	17 (29%)
24	CLA	3	618	-	46,54,73	1.62	10 (21%)	53,90,113	2.19	15 (28%)
27	BCR	B	4005	-	41,41,41	1.87	5 (12%)	56,56,56	4.48	13 (23%)
24	CLA	a	602	-	50,58,73	1.56	8 (16%)	58,95,113	2.18	16 (27%)
24	CLA	B	1227	-	50,58,73	1.55	8 (16%)	58,95,113	2.19	16 (27%)
33	PTY	3	802	-	37,37,49	0.99	4 (10%)	40,42,54	1.08	2 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	CHL	3	608	-	43,51,74	0.96	2 (4%)	45,86,114	1.46	8 (17%)
41	CHL	7	613	-	66,74,74	0.89	4 (6%)	73,114,114	1.16	8 (10%)
27	BCR	F	4001	-	41,41,41	1.77	4 (9%)	56,56,56	4.09	14 (25%)
24	CLA	A	1107	1	55,63,73	1.46	7 (12%)	64,101,113	2.15	18 (28%)
24	CLA	8	603	-	65,73,73	1.35	8 (12%)	76,113,113	2.01	15 (19%)
24	CLA	5	601	-	60,68,73	1.43	8 (13%)	70,107,113	2.10	20 (28%)
28	LHG	7	802	-	35,35,48	0.44	0	38,41,54	1.11	2 (5%)
24	CLA	6	615	-	65,73,73	1.36	8 (12%)	76,113,113	2.00	16 (21%)
24	CLA	9	604	-	60,68,73	1.41	7 (11%)	70,107,113	2.09	20 (28%)
27	BCR	H	4001	-	41,41,41	1.86	4 (9%)	56,56,56	4.60	18 (32%)
24	CLA	A	1131	-	65,73,73	1.35	8 (12%)	76,113,113	1.98	16 (21%)
40	LUT	3	501	-	42,43,43	2.38	1 (2%)	51,60,60	2.07	16 (31%)
27	BCR	K	4001	-	41,41,41	1.84	4 (9%)	56,56,56	4.36	13 (23%)
24	CLA	2	621	-	50,58,73	1.56	9 (18%)	58,95,113	2.27	16 (27%)
24	CLA	3	604	-	60,68,73	1.37	6 (10%)	70,107,113	2.07	20 (28%)
33	PTY	9	803	-	47,47,49	0.89	4 (8%)	50,52,54	1.10	2 (4%)
40	LUT	6	502	-	42,43,43	2.37	1 (2%)	51,60,60	2.14	16 (31%)
40	LUT	9	501	-	42,43,43	2.35	1 (2%)	51,60,60	1.92	12 (23%)
40	LUT	4	502	-	42,43,43	2.33	1 (2%)	51,60,60	1.82	11 (21%)
24	CLA	9	605	-	60,68,73	1.43	9 (15%)	70,107,113	2.06	18 (25%)
24	CLA	8	607	-	46,54,73	1.62	8 (17%)	53,90,113	2.16	12 (22%)
24	CLA	4	610	-	65,73,73	1.41	9 (13%)	76,113,113	1.95	15 (19%)
24	CLA	8	602	-	52,60,73	1.53	8 (15%)	60,97,113	2.15	16 (26%)
24	CLA	2	602	-	52,60,73	1.52	9 (17%)	60,97,113	2.20	18 (30%)
24	CLA	B	1202	-	65,73,73	1.36	7 (10%)	76,113,113	1.94	17 (22%)
29	DGD	8	802	-	67,67,67	1.18	7 (10%)	81,81,81	1.06	2 (2%)
24	CLA	G	1601	-	50,58,73	1.55	9 (18%)	58,95,113	2.20	16 (27%)
42	OLA	8	809	-	19,19,19	0.57	0	19,19,19	1.03	0
24	CLA	7	604	-	65,73,73	1.35	7 (10%)	76,113,113	1.99	19 (25%)
24	CLA	8	605	-	45,53,73	1.62	8 (17%)	52,89,113	2.14	15 (28%)
24	CLA	A	1129	-	50,58,73	1.56	8 (16%)	58,95,113	2.19	18 (31%)
24	CLA	B	1210	-	65,73,73	1.36	7 (10%)	76,113,113	1.97	17 (22%)
24	CLA	A	1118	-	55,63,73	1.47	8 (14%)	64,101,113	2.09	16 (25%)
24	CLA	5	609	17	51,59,73	1.53	9 (17%)	59,96,113	2.19	16 (27%)
24	CLA	9	602	-	46,54,73	1.60	8 (17%)	53,90,113	2.13	14 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	B	1235	-	65,73,73	1.35	8 (12%)	76,113,113	2.06	17 (22%)
24	CLA	B	1208	-	60,68,73	1.41	7 (11%)	70,107,113	2.13	22 (31%)
28	LHG	9	801	-	32,32,48	0.46	0	35,38,54	1.16	3 (8%)
24	CLA	3	607	-	65,73,73	1.35	9 (13%)	76,113,113	1.96	14 (18%)
41	CHL	6	611	-	51,59,74	0.95	3 (5%)	55,96,114	1.50	12 (21%)
24	CLA	B	1206	-	55,63,73	1.46	7 (12%)	64,101,113	2.17	16 (25%)
24	CLA	a	601	-	60,68,73	1.42	9 (15%)	70,107,113	2.02	18 (25%)
24	CLA	A	1136	-	65,73,73	1.36	8 (12%)	76,113,113	1.96	17 (22%)
27	BCR	B	4006	-	41,41,41	1.82	4 (9%)	56,56,56	4.43	13 (23%)
24	CLA	1	604	-	65,73,73	1.35	7 (10%)	76,113,113	1.95	18 (23%)
27	BCR	J	4001	-	41,41,41	1.82	4 (9%)	56,56,56	4.27	16 (28%)
24	CLA	7	609	19	60,68,73	1.42	8 (13%)	70,107,113	2.16	18 (25%)
24	CLA	A	1126	-	65,73,73	1.36	8 (12%)	76,113,113	1.98	16 (21%)
41	CHL	9	610	-	51,59,74	0.95	3 (5%)	55,96,114	1.38	11 (20%)
24	CLA	B	1205	-	65,73,73	1.35	8 (12%)	76,113,113	2.06	17 (22%)
28	LHG	3	801	-	48,48,48	0.39	0	51,54,54	1.02	3 (5%)
26	SF4	C	3002	3	0,12,12	-	-	-	-	-
27	BCR	6	504	-	41,41,41	1.84	4 (9%)	56,56,56	4.37	15 (26%)
24	CLA	B	1211	-	55,63,73	1.46	8 (14%)	64,101,113	2.11	19 (29%)
24	CLA	2	612	-	50,58,73	1.54	7 (14%)	58,95,113	2.30	16 (27%)
28	LHG	B	5002	-	48,48,48	0.39	0	51,54,54	1.02	3 (5%)
27	BCR	3	503	-	41,41,41	1.87	4 (9%)	56,56,56	4.41	17 (30%)
33	PTY	B	5005	-	40,40,49	0.96	4 (10%)	43,45,54	1.18	2 (4%)
24	CLA	A	1108	-	65,73,73	1.36	8 (12%)	76,113,113	2.04	17 (22%)
24	CLA	B	1238	-	65,73,73	1.34	8 (12%)	76,113,113	2.01	18 (23%)
24	CLA	4	611	-	56,64,73	1.45	7 (12%)	65,102,113	2.10	17 (26%)
40	LUT	8	502	-	42,43,43	2.31	1 (2%)	51,60,60	1.88	16 (31%)
28	LHG	B	5001	-	45,45,48	0.40	0	48,51,54	1.07	3 (6%)
38	LPX	a	804	-	29,29,29	1.02	2 (6%)	31,33,33	0.97	1 (3%)
41	CHL	4	609	16	66,74,74	0.91	4 (6%)	73,114,114	1.21	9 (12%)
28	LHG	4	801	-	48,48,48	0.40	0	51,54,54	1.01	3 (5%)
24	CLA	5	605	-	46,54,73	1.62	8 (17%)	53,90,113	2.14	14 (26%)
32	PCW	B	5004	-	29,29,53	1.38	4 (13%)	35,37,61	1.10	2 (5%)
24	CLA	B	1230	-	58,66,73	1.43	7 (12%)	67,104,113	2.08	15 (22%)
41	CHL	9	613	-	42,50,74	1.06	3 (7%)	44,85,114	1.51	11 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	A	1013	-	65,73,73	1.33	7 (10%)	76,113,113	1.94	17 (22%)
28	LHG	F	5002	-	35,35,48	0.45	0	38,41,54	1.17	3 (7%)
24	CLA	8	608	-	52,60,73	1.50	7 (13%)	60,97,113	2.37	19 (31%)
24	CLA	A	1132	-	65,73,73	1.34	7 (10%)	76,113,113	1.99	17 (22%)
24	CLA	7	617	19	54,62,73	1.51	8 (14%)	63,100,113	2.13	17 (26%)
24	CLA	J	1901	8	42,50,73	1.69	10 (23%)	48,85,113	2.23	15 (31%)
29	DGD	B	5003	-	67,67,67	1.18	7 (10%)	81,81,81	0.93	2 (2%)
24	CLA	A	1113	-	52,60,73	1.49	7 (13%)	60,97,113	2.24	19 (31%)
24	CLA	a	605	-	65,73,73	1.36	8 (12%)	76,113,113	1.97	17 (22%)
42	OLA	1	803	-	19,19,19	0.57	0	19,19,19	1.03	1 (5%)
24	CLA	2	601	-	60,68,73	1.41	8 (13%)	70,107,113	4.52	21 (30%)
24	CLA	B	1234	-	56,64,73	1.49	10 (17%)	65,102,113	2.06	18 (27%)
24	CLA	A	1119	-	65,73,73	1.36	8 (12%)	76,113,113	1.80	13 (17%)
24	CLA	A	1104	-	65,73,73	1.36	9 (13%)	76,113,113	1.96	15 (19%)
24	CLA	A	1130	-	56,64,73	1.50	8 (14%)	65,102,113	2.16	16 (24%)
24	CLA	A	1127	-	65,73,73	1.39	9 (13%)	76,113,113	1.87	15 (19%)
28	LHG	7	803	-	42,42,48	0.41	0	45,48,54	1.06	3 (6%)
41	CHL	6	619	18	66,74,74	0.85	3 (4%)	73,114,114	1.20	10 (13%)
24	CLA	H	1702	-	46,54,73	1.61	10 (21%)	53,90,113	2.18	13 (24%)
24	CLA	7	605	-	43,52,73	1.67	9 (20%)	49,88,113	2.05	13 (26%)
24	CLA	B	1201	-	65,73,73	1.34	7 (10%)	76,113,113	2.02	22 (28%)
24	CLA	5	617	-	50,58,73	1.56	9 (18%)	58,95,113	2.16	16 (27%)
37	RRX	J	4002	-	42,42,42	4.90	24 (57%)	57,58,58	2.31	20 (35%)
28	LHG	5	801	-	48,48,48	0.39	0	51,54,54	1.07	4 (7%)
27	BCR	5	503	-	41,41,41	1.85	4 (9%)	56,56,56	4.38	16 (28%)
27	BCR	A	4001	-	41,41,41	1.82	4 (9%)	56,56,56	4.23	19 (33%)
24	CLA	1	615	14	46,54,73	1.61	10 (21%)	53,90,113	2.19	14 (26%)
24	CLA	A	1140	-	55,63,73	1.49	8 (14%)	64,101,113	2.02	15 (23%)
24	CLA	5	603	-	56,64,73	1.46	9 (16%)	65,102,113	2.15	16 (24%)
24	CLA	6	612	-	50,58,73	1.54	9 (18%)	58,95,113	2.20	17 (29%)
24	CLA	5	604	-	65,73,73	1.35	7 (10%)	76,113,113	2.01	19 (25%)
24	CLA	4	616	-	50,58,73	1.56	10 (20%)	58,95,113	2.23	18 (31%)
24	CLA	A	1112	-	55,63,73	1.47	7 (12%)	64,101,113	2.15	17 (26%)
24	CLA	B	1220	-	60,68,73	1.42	8 (13%)	70,107,113	2.06	17 (24%)
39	ECH	M	4001	-	42,42,42	0.96	1 (2%)	55,58,58	2.20	12 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	CHL	6	610	-	56,64,74	0.85	2 (3%)	61,102,114	1.41	13 (21%)
41	CHL	5	613	-	56,64,74	0.84	2 (3%)	61,102,114	1.32	11 (18%)
24	CLA	A	1114	-	65,73,73	1.37	7 (10%)	76,113,113	2.01	17 (22%)
24	CLA	A	1124	-	55,63,73	1.48	8 (14%)	64,101,113	2.11	18 (28%)
40	LUT	7	501	-	42,43,43	2.39	1 (2%)	51,60,60	1.97	14 (27%)
24	CLA	9	608	-	45,53,73	1.63	9 (20%)	52,89,113	2.11	12 (23%)
24	CLA	A	1110	-	60,68,73	1.41	8 (13%)	70,107,113	2.01	16 (22%)
24	CLA	a	603	-	65,73,73	1.35	9 (13%)	76,113,113	2.03	15 (19%)
24	CLA	B	1215	-	60,68,73	1.42	7 (11%)	70,107,113	1.98	14 (20%)
29	DGD	A	5005	-	52,52,67	0.90	2 (3%)	66,66,81	1.02	4 (6%)
40	LUT	6	501	-	42,43,43	2.38	1 (2%)	51,60,60	3.24	23 (45%)
24	CLA	a	604	-	65,73,73	1.35	9 (13%)	76,113,113	1.97	19 (25%)
24	CLA	B	1232	-	45,53,73	1.64	9 (20%)	52,89,113	2.13	14 (26%)
27	BCR	B	4001	-	41,41,41	1.84	4 (9%)	56,56,56	4.23	16 (28%)
24	CLA	4	604	-	60,68,73	1.38	7 (11%)	70,107,113	2.08	21 (30%)
24	CLA	8	620	20	65,73,73	1.34	8 (12%)	76,113,113	1.97	18 (23%)
41	CHL	4	618	16	56,64,74	0.95	3 (5%)	61,102,114	1.26	10 (16%)
40	LUT	2	502	-	42,43,43	2.30	1 (2%)	51,60,60	2.17	12 (23%)
28	LHG	1	801	-	34,34,48	0.45	0	37,40,54	1.20	4 (10%)
24	CLA	B	1219	-	59,67,73	1.42	8 (13%)	68,105,113	2.11	16 (23%)
27	BCR	K	4002	-	41,41,41	1.87	4 (9%)	56,56,56	4.32	14 (25%)
24	CLA	B	1223	-	65,73,73	1.38	9 (13%)	76,113,113	2.01	18 (23%)
24	CLA	9	609	-	46,54,73	1.60	8 (17%)	53,90,113	2.11	12 (22%)
27	BCR	B	4007	-	41,41,41	1.85	4 (9%)	56,56,56	4.31	14 (25%)
24	CLA	A	1117	-	65,73,73	1.36	7 (10%)	76,113,113	1.99	16 (21%)
26	SF4	A	3001	2,1	0,12,12	-	-	-	-	-
24	CLA	B	1209	-	65,73,73	1.35	7 (10%)	76,113,113	1.99	16 (21%)
24	CLA	2	615	-	57,65,73	1.43	9 (15%)	66,103,113	2.13	16 (24%)
24	CLA	6	617	-	45,53,73	1.63	9 (20%)	52,89,113	2.14	14 (26%)
24	CLA	B	1212	-	65,73,73	1.35	8 (12%)	76,113,113	2.00	18 (23%)
24	CLA	A	1123	-	65,73,73	1.35	8 (12%)	76,113,113	2.06	18 (23%)
24	CLA	8	609	20	60,68,73	1.40	8 (13%)	70,107,113	2.05	16 (22%)
40	LUT	4	501	-	42,43,43	2.36	1 (2%)	51,60,60	2.05	15 (29%)
41	CHL	1	613	-	48,56,74	0.89	2 (4%)	51,92,114	1.45	10 (19%)
52	A8S	9	504	-	17,19,19	0.73	0	17,29,29	1.62	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	3	616	-	56,64,73	1.47	8 (14%)	65,102,113	2.11	17 (26%)
24	CLA	7	603	-	65,73,73	1.36	9 (13%)	76,113,113	1.99	16 (21%)
40	LUT	a	503	-	42,43,43	2.39	1 (2%)	51,60,60	2.42	13 (25%)
24	CLA	7	612	-	60,68,73	1.41	8 (13%)	70,107,113	2.04	17 (24%)
24	CLA	5	607	-	55,63,73	1.49	10 (18%)	64,101,113	2.10	17 (26%)
27	BCR	4	503	-	41,41,41	1.89	4 (9%)	56,56,56	4.31	21 (37%)
24	CLA	2	603	-	60,68,73	1.41	8 (13%)	70,107,113	2.09	19 (27%)
41	CHL	a	613	-	46,54,74	0.95	3 (6%)	49,90,114	1.58	10 (20%)
24	CLA	A	1125	-	65,73,73	1.37	6 (9%)	76,113,113	2.06	22 (28%)
24	CLA	A	1102	24	65,73,73	1.33	8 (12%)	76,113,113	2.06	19 (25%)
24	CLA	1	606	-	57,65,73	1.42	7 (12%)	66,103,113	2.10	17 (25%)
24	CLA	6	602	-	52,60,73	1.52	8 (15%)	60,97,113	2.15	17 (28%)
47	SPH	6	806	-	19,20,20	0.63	0	18,21,21	1.12	1 (5%)
40	LUT	8	501	-	42,43,43	2.33	1 (2%)	51,60,60	1.96	15 (29%)
34	LAP	F	5003	-	28,28,28	1.22	2 (7%)	33,35,35	0.96	1 (3%)
40	LUT	1	503	-	42,43,43	2.38	1 (2%)	51,60,60	2.24	14 (27%)
28	LHG	A	5001	24	28,28,48	0.48	0	31,34,54	1.23	3 (9%)
24	CLA	B	1203	-	65,73,73	1.34	7 (10%)	76,113,113	1.96	19 (25%)
24	CLA	B	1218	-	55,63,73	1.46	8 (14%)	64,101,113	2.24	19 (29%)
24	CLA	1	612	-	65,73,73	1.35	10 (15%)	76,113,113	1.96	16 (21%)
24	CLA	4	617	-	45,53,73	1.64	9 (20%)	52,89,113	2.16	13 (25%)
28	LHG	6	801	-	48,48,48	0.39	0	51,54,54	1.06	3 (5%)
28	LHG	2	802	-	48,48,48	0.39	0	51,54,54	1.06	3 (5%)
24	CLA	3	613	-	61,69,73	1.37	6 (9%)	71,108,113	2.04	18 (25%)
24	CLA	A	1012	-	65,73,73	1.39	9 (13%)	76,113,113	1.91	16 (21%)
24	CLA	A	1116	-	60,68,73	1.42	8 (13%)	70,107,113	2.04	19 (27%)
27	BCR	B	4003	-	41,41,41	1.85	4 (9%)	56,56,56	4.48	17 (30%)
27	BCR	A	4003	-	41,41,41	1.84	4 (9%)	56,56,56	4.51	17 (30%)
40	LUT	5	502	-	42,43,43	2.38	2 (4%)	51,60,60	2.03	18 (35%)
24	CLA	B	1216	-	61,69,73	1.43	7 (11%)	71,108,113	1.96	15 (21%)
24	CLA	B	1237	-	65,73,73	1.37	7 (10%)	76,113,113	1.91	14 (18%)
28	LHG	4	802	-	31,31,48	0.47	0	34,37,54	1.13	3 (8%)
24	CLA	a	607	-	58,66,73	1.44	10 (17%)	67,104,113	2.12	18 (26%)
24	CLA	B	1207	-	60,68,73	1.40	7 (11%)	70,107,113	1.99	16 (22%)
27	BCR	6	503	-	41,41,41	1.84	4 (9%)	56,56,56	4.33	14 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	7	611	-	60,68,73	1.38	6 (10%)	70,107,113	2.07	17 (24%)
24	CLA	6	618	-	46,54,73	1.62	9 (19%)	53,90,113	2.10	13 (24%)
46	DGA	5	803	-	22,22,43	1.44	3 (13%)	24,24,45	1.36	2 (8%)
24	CLA	7	602	-	44,52,73	1.65	9 (20%)	49,87,113	2.18	14 (28%)
24	CLA	3	603	-	65,73,73	1.37	8 (12%)	76,113,113	1.97	17 (22%)
33	PTY	7	804	-	32,32,49	1.05	4 (12%)	35,37,54	1.19	2 (5%)
35	SQD	G	5001	-	45,46,54	0.83	0	54,57,65	0.97	2 (3%)
28	LHG	a	801	-	34,34,48	0.45	0	37,40,54	1.23	3 (8%)
24	CLA	4	608	-	51,59,73	1.52	8 (15%)	59,96,113	2.25	17 (28%)
24	CLA	4	607	-	55,63,73	1.50	9 (16%)	64,101,113	2.15	16 (25%)
41	CHL	8	604	-	62,70,74	0.98	4 (6%)	68,109,114	1.33	10 (14%)
24	CLA	4	602	-	52,60,73	1.53	9 (17%)	60,97,113	2.18	18 (30%)
24	CLA	1	602	-	45,53,73	1.63	8 (17%)	52,89,113	2.12	14 (26%)
24	CLA	9	603	-	65,73,73	1.37	8 (12%)	76,113,113	2.05	19 (25%)
28	LHG	6	802	-	36,36,48	0.44	0	39,42,54	1.14	3 (7%)
24	CLA	B	1214	-	62,70,73	1.39	8 (12%)	72,109,113	1.98	17 (23%)
40	LUT	5	505	-	42,43,43	2.40	1 (2%)	51,60,60	2.43	18 (35%)
24	CLA	6	609	18	65,73,73	1.36	8 (12%)	76,113,113	2.05	17 (22%)
24	CLA	A	1128	-	65,73,73	1.37	7 (10%)	76,113,113	2.04	18 (23%)
24	CLA	9	601	-	60,68,73	1.44	9 (15%)	70,107,113	2.05	17 (24%)
41	CHL	5	611	-	51,59,74	0.90	2 (3%)	55,96,114	1.48	12 (21%)
24	CLA	2	606	-	46,54,73	1.61	9 (19%)	53,90,113	2.14	13 (24%)
24	CLA	B	1222	-	58,66,73	1.43	7 (12%)	67,104,113	2.14	21 (31%)
24	CLA	8	618	-	60,68,73	1.42	7 (11%)	70,107,113	2.03	17 (24%)
24	CLA	F	1301	-	50,58,73	1.56	9 (18%)	58,95,113	2.21	16 (27%)
24	CLA	8	610	-	55,63,73	1.49	8 (14%)	64,101,113	2.10	16 (25%)
24	CLA	a	615	-	46,54,73	1.61	8 (17%)	53,90,113	2.09	13 (24%)
24	CLA	5	608	-	45,53,73	1.63	10 (22%)	52,89,113	2.28	14 (26%)
24	CLA	3	602	-	46,54,73	1.59	8 (17%)	53,90,113	2.15	16 (30%)
24	CLA	7	615	19	55,63,73	1.49	8 (14%)	64,101,113	2.06	15 (23%)
24	CLA	7	606	-	55,63,73	1.47	8 (14%)	64,101,113	2.12	18 (28%)
31	LMT	2	804	-	36,36,36	1.17	6 (16%)	47,47,47	0.98	2 (4%)
24	CLA	3	612	-	65,73,73	1.35	7 (10%)	76,113,113	2.00	16 (21%)
38	LPX	J	5001	-	16,16,29	1.30	2 (12%)	18,20,33	1.11	2 (11%)
24	CLA	B	1021	-	65,73,73	1.37	8 (12%)	76,113,113	1.91	16 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	F	1302	-	55,63,73	1.48	8 (14%)	64,101,113	2.11	17 (26%)
40	LUT	a	502	-	42,43,43	2.30	1 (2%)	51,60,60	2.03	14 (27%)
24	CLA	9	606	-	55,63,73	1.47	8 (14%)	64,101,113	2.08	18 (28%)
24	CLA	B	1221	-	65,73,73	1.37	9 (13%)	76,113,113	1.99	15 (19%)
27	BCR	A	4005	-	41,41,41	1.84	4 (9%)	56,56,56	4.29	16 (28%)
24	CLA	A	1138	-	65,73,73	1.34	7 (10%)	76,113,113	1.95	14 (18%)
33	PTY	8	891	-	34,34,49	1.03	4 (11%)	37,39,54	1.14	2 (5%)
24	CLA	3	605	-	65,73,73	1.36	7 (10%)	76,113,113	1.97	18 (23%)
24	CLA	A	1109	24	65,73,73	1.34	8 (12%)	76,113,113	2.07	16 (21%)
27	BCR	B	4004	-	41,41,41	1.84	4 (9%)	56,56,56	4.34	12 (21%)
50	4RF	7	807	-	31,31,56	1.15	6 (19%)	34,34,59	1.26	3 (8%)
41	CHL	1	609	14	66,74,74	0.76	2 (3%)	73,114,114	1.30	10 (13%)
24	CLA	A	1134	1	60,68,73	1.41	8 (13%)	70,107,113	2.02	17 (24%)
41	CHL	4	613	-	52,60,74	0.94	3 (5%)	56,97,114	1.40	10 (17%)
34	LAP	B	5007	-	28,28,28	1.23	2 (7%)	33,35,35	0.96	1 (3%)
24	CLA	4	605	-	46,54,73	1.63	9 (19%)	53,90,113	2.10	12 (22%)
40	LUT	1	502	-	42,43,43	2.33	1 (2%)	51,60,60	2.10	18 (35%)
24	CLA	A	1106	-	65,73,73	1.36	8 (12%)	76,113,113	2.02	19 (25%)
24	CLA	K	1402	-	60,68,73	1.42	9 (15%)	70,107,113	2.08	18 (25%)
51	P5S	8	806	-	35,36,53	1.18	3 (8%)	39,43,60	1.21	2 (5%)
24	CLA	6	604	-	65,73,73	1.35	8 (12%)	76,113,113	2.02	16 (21%)
24	CLA	2	607	-	46,54,73	1.62	10 (21%)	53,90,113	2.10	12 (22%)
27	BCR	5	504	-	41,41,41	1.84	4 (9%)	56,56,56	4.49	19 (33%)
45	PLM	6	804	-	17,17,17	0.58	0	17,17,17	1.11	0
24	CLA	8	612	20	46,54,73	1.62	8 (17%)	53,90,113	2.08	11 (20%)
33	PTY	5	802	-	37,37,49	0.99	4 (10%)	40,42,54	1.10	2 (5%)
28	LHG	A	5002	-	48,48,48	0.39	0	51,54,54	0.99	2 (3%)
24	CLA	1	608	-	60,68,73	1.41	8 (13%)	70,107,113	2.05	16 (22%)
24	CLA	K	1403	9	46,54,73	1.60	8 (17%)	53,90,113	2.15	13 (24%)
24	CLA	B	1224	-	65,73,73	1.36	8 (12%)	76,113,113	2.00	17 (22%)
24	CLA	3	606	-	65,73,73	1.35	7 (10%)	76,113,113	1.98	15 (19%)
40	LUT	3	502	-	42,43,43	2.34	1 (2%)	51,60,60	1.97	13 (25%)
24	CLA	1	611	-	55,63,73	1.45	7 (12%)	64,101,113	2.17	19 (29%)
44	GG0	a	805	-	7,8,8	1.44	2 (28%)	6,9,9	0.78	0
24	CLA	9	612	-	65,73,73	1.37	8 (12%)	76,113,113	2.02	17 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	CLA	2	605	-	60,68,73	1.41	7 (11%)	70,107,113	2.07	19 (27%)
24	CLA	H	1703	-	55,63,73	1.48	9 (16%)	64,101,113	2.13	14 (21%)
24	CLA	a	608	-	55,63,73	1.49	9 (16%)	64,101,113	2.10	17 (26%)

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
35	SQD	H	5001	-	-	8/40/60/69	0/1/1/1
50	4RF	8	808	-	-	24/56/56/59	-
24	CLA	L	1503	-	1/1/11/20	6/13/91/115	-
24	CLA	B	1240	-	1/1/15/20	15/37/115/115	-
24	CLA	7	608	-	1/1/10/20	5/10/88/115	-
43	QTB	a	504	-	1/1/5/10	4/11/28/28	0/1/1/1
27	BCR	L	4001	-	-	12/29/63/63	0/2/2/2
24	CLA	A	1137	-	1/1/14/20	13/31/109/115	-
24	CLA	6	608	-	1/1/11/20	3/13/91/115	-
24	CLA	B	1239	-	1/1/15/20	13/37/115/115	-
28	LHG	8	801	-	-	28/41/41/53	-
24	CLA	5	616	-	1/1/11/20	9/15/93/115	-
24	CLA	5	612	-	1/1/15/20	16/37/115/115	-
24	CLA	A	1103	-	1/1/15/20	24/37/115/115	-
24	CLA	B	1225	-	1/1/15/20	7/37/115/115	-
27	BCR	8	503	-	-	11/29/63/63	0/2/2/2
23	CL0	A	1011	-	3/3/20/25	7/37/135/135	-
27	BCR	3	505	-	-	11/29/63/63	0/2/2/2
28	LHG	1	802	-	-	29/46/46/53	-
31	LMT	A	5008	-	-	8/21/61/61	0/2/2/2
48	XAT	7	502	-	2/2/12/26	1/31/93/93	0/4/4/4
24	CLA	3	610	15	1/1/14/20	12/31/109/115	-
24	CLA	6	605	-	1/1/11/20	4/15/93/115	-
24	CLA	9	607	-	1/1/11/20	11/16/94/115	-
24	CLA	A	1133	-	1/1/15/20	15/37/115/115	-
30	3PH	A	5007	-	-	17/34/34/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	K	1404	-	1/1/12/20	8/22/100/115	-
49	C7Z	7	504	-	1/1/12/26	10/29/67/67	0/2/2/2
25	PQN	A	2001	-	-	8/23/43/43	0/2/2/2
24	CLA	6	606	-	1/1/12/20	12/22/100/115	-
41	CHL	6	613	-	3/3/17/26	4/21/119/137	-
24	CLA	L	1501	13	1/1/12/20	11/19/97/115	-
24	CLA	A	1139	-	1/1/13/20	12/25/103/115	-
27	BCR	3	504	-	-	12/29/63/63	0/2/2/2
24	CLA	6	603	-	1/1/15/20	16/37/115/115	-
24	CLA	2	608	-	1/1/11/20	5/13/91/115	-
27	BCR	A	4002	-	-	9/29/63/63	0/2/2/2
40	LUT	5	501	-	-	3/29/67/67	0/2/2/2
34	LAP	K	5001	-	-	12/30/30/30	-
28	LHG	7	801	-	-	24/53/53/53	-
24	CLA	8	611	-	1/1/12/20	8/19/97/115	-
24	CLA	6	601	-	1/1/14/20	17/31/109/115	-
24	CLA	2	610	-	1/1/11/20	7/15/93/115	-
24	CLA	4	601	-	1/1/14/20	10/31/109/115	-
24	CLA	1	601	-	1/1/14/20	10/31/109/115	-
46	DGA	8	803	-	-	18/31/31/45	-
24	CLA	A	1105	-	1/1/13/20	11/28/106/115	-
40	LUT	9	502	-	1/1/12/27	7/29/67/67	0/2/2/2
28	LHG	2	801	-	-	35/53/53/53	-
25	PQN	B	2002	-	-	5/23/43/43	0/2/2/2
24	CLA	A	1141	28	1/1/11/20	10/13/91/115	-
36	ERG	G	5002	-	4/4/11/15	7/13/71/71	0/4/4/4
27	BCR	A	4004	-	-	12/29/63/63	0/2/2/2
24	CLA	8	606	-	1/1/13/20	15/28/106/115	-
24	CLA	B	1228	-	1/1/15/20	18/37/115/115	-
45	PLM	4	803	-	-	2/13/14/15	-
24	CLA	A	1115	-	1/1/14/20	16/31/109/115	-
24	CLA	7	607	-	1/1/13/20	16/29/107/115	-
24	CLA	A	1111	-	1/1/15/20	19/37/115/115	-
24	CLA	7	601	-	1/1/14/20	15/31/109/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	H	1701	-	1/1/13/20	10/25/103/115	-
24	CLA	3	601	-	1/1/15/20	15/37/115/115	-
41	CHL	a	609	-	3/3/17/26	5/24/122/137	-
31	LMT	1	804	-	-	8/21/61/61	0/2/2/2
40	LUT	a	501	-	-	8/29/67/67	0/2/2/2
24	CLA	A	1120	-	1/1/11/20	8/18/96/115	-
24	CLA	a	612	-	1/1/13/20	10/28/106/115	-
24	CLA	B	1023	-	1/1/15/20	11/37/115/115	-
24	CLA	1	610	-	1/1/11/20	9/13/91/115	-
32	PCW	6	803	-	-	16/39/39/57	-
24	CLA	4	603	-	1/1/13/20	12/27/105/115	-
27	BCR	I	4001	-	-	12/29/63/63	0/2/2/2
24	CLA	1	603	-	1/1/15/20	19/37/115/115	-
24	CLA	8	615	-	1/1/11/20	7/15/93/115	-
24	CLA	4	612	-	1/1/14/20	19/34/112/115	-
41	CHL	5	610	-	4/4/20/26	7/39/137/137	-
24	CLA	B	1204	-	1/1/15/20	18/37/115/115	-
27	BCR	L	4003	-	-	12/29/63/63	0/2/2/2
24	CLA	B	1229	-	1/1/15/20	13/37/115/115	-
24	CLA	G	1602	-	1/1/11/20	8/15/93/115	-
43	QTB	3	506	-	2/2/5/10	0/11/28/28	0/1/1/1
40	LUT	1	501	-	-	5/29/67/67	0/2/2/2
41	CHL	3	611	-	3/3/17/26	5/26/124/137	-
24	CLA	1	605	-	1/1/15/20	19/37/115/115	-
24	CLA	5	606	-	1/1/12/20	7/19/97/115	-
24	CLA	L	1502	-	1/1/14/20	15/31/109/115	-
24	CLA	2	613	-	1/1/10/20	2/8/86/115	-
24	CLA	B	1022	-	1/1/15/20	12/37/115/115	-
27	BCR	G	4001	-	-	14/29/63/63	0/2/2/2
24	CLA	B	1213	-	1/1/14/20	11/31/109/115	-
35	SQD	7	805	-	-	15/34/54/69	0/1/1/1
24	CLA	5	602	-	1/1/12/20	7/22/100/115	-
24	CLA	A	1122	-	1/1/15/20	15/37/115/115	-
41	CHL	a	606	-	4/4/18/26	7/27/125/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	LHG	F	5001	-	-	24/47/47/53	-
24	CLA	K	1401	-	1/1/11/20	6/15/93/115	-
24	CLA	A	1121	-	1/1/13/20	14/28/106/115	-
31	LMT	B	5006	-	-	15/21/61/61	0/2/2/2
24	CLA	A	1135	-	1/1/15/20	17/37/115/115	-
24	CLA	B	1236	-	1/1/12/20	9/23/101/115	-
26	SF4	C	3003	3	-	-	0/6/5/5
50	4RF	8	807	-	-	25/44/44/59	-
24	CLA	4	615	16	1/1/14/20	16/31/109/115	-
24	CLA	B	1217	-	1/1/13/20	13/27/105/115	-
24	CLA	5	618	17	1/1/12/20	6/22/100/115	-
24	CLA	B	1231	-	1/1/15/20	15/37/115/115	-
24	CLA	2	609	21	1/1/13/20	10/25/103/115	-
24	CLA	2	604	-	1/1/13/20	14/27/105/115	-
28	LHG	9	802	-	-	31/53/53/53	-
41	CHL	8	601	-	4/4/19/26	6/33/131/137	-
24	CLA	A	1101	-	1/1/15/20	15/37/115/115	-
24	CLA	G	1603	-	1/1/11/20	5/13/91/115	-
41	CHL	a	610	-	4/4/16/26	1/18/116/137	-
24	CLA	6	607	-	1/1/13/20	10/25/103/115	-
41	CHL	8	613	-	3/3/17/26	3/21/119/137	-
24	CLA	5	614	-	1/1/11/20	4/15/93/115	-
27	BCR	B	4002	-	-	13/29/63/63	0/2/2/2
24	CLA	1	607	-	1/1/15/20	8/37/115/115	-
27	BCR	7	503	-	-	10/29/63/63	0/2/2/2
40	LUT	2	501	-	-	3/29/67/67	0/2/2/2
28	LHG	A	5003	-	-	24/46/46/53	-
27	BCR	L	4002	-	-	7/29/63/63	0/2/2/2
24	CLA	B	1226	-	1/1/15/20	14/37/115/115	-
24	CLA	4	606	-	1/1/12/20	6/19/97/115	-
24	CLA	7	610	-	1/1/13/20	12/25/103/115	-
24	CLA	a	611	-	1/1/12/20	8/19/97/115	-
24	CLA	3	618	-	1/1/11/20	6/15/93/115	-
27	BCR	B	4005	-	-	11/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	a	602	-	1/1/12/20	7/19/97/115	-
24	CLA	B	1227	-	1/1/12/20	9/19/97/115	-
41	CHL	3	608	-	3/3/15/26	6/12/110/137	-
33	PTY	3	802	-	-	14/41/41/53	-
41	CHL	7	613	-	4/4/20/26	6/39/137/137	-
27	BCR	F	4001	-	-	14/29/63/63	0/2/2/2
24	CLA	A	1107	1	1/1/13/20	10/25/103/115	-
24	CLA	8	603	-	1/1/15/20	17/37/115/115	-
24	CLA	5	601	-	1/1/14/20	11/31/109/115	-
28	LHG	7	802	-	-	20/40/40/53	-
24	CLA	6	615	-	1/1/15/20	18/37/115/115	-
24	CLA	9	604	-	1/1/14/20	9/31/109/115	-
27	BCR	H	4001	-	-	11/29/63/63	0/2/2/2
24	CLA	A	1131	-	1/1/15/20	14/37/115/115	-
40	LUT	3	501	-	-	3/29/67/67	0/2/2/2
27	BCR	K	4001	-	-	10/29/63/63	0/2/2/2
24	CLA	2	621	-	1/1/12/20	10/19/97/115	-
24	CLA	3	604	-	1/1/14/20	9/31/109/115	-
33	PTY	9	803	-	-	27/51/51/53	-
40	LUT	6	502	-	1/1/12/27	7/29/67/67	0/2/2/2
40	LUT	9	501	-	-	2/29/67/67	0/2/2/2
40	LUT	4	502	-	-	3/29/67/67	0/2/2/2
24	CLA	9	605	-	1/1/14/20	13/31/109/115	-
24	CLA	8	607	-	1/1/11/20	4/15/93/115	-
24	CLA	4	610	-	1/1/15/20	24/37/115/115	-
24	CLA	8	602	-	1/1/12/20	9/22/100/115	-
24	CLA	2	602	-	1/1/12/20	7/22/100/115	-
24	CLA	B	1202	-	1/1/15/20	17/37/115/115	-
29	DGD	8	802	-	-	19/55/95/95	0/2/2/2
24	CLA	G	1601	-	1/1/12/20	10/19/97/115	-
42	OLA	8	809	-	-	10/17/17/17	-
24	CLA	7	604	-	1/1/15/20	11/37/115/115	-
24	CLA	8	605	-	1/1/11/20	6/13/91/115	-
24	CLA	A	1129	-	1/1/12/20	10/19/97/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	B	1210	-	1/1/15/20	20/37/115/115	-
24	CLA	A	1118	-	1/1/13/20	14/25/103/115	-
24	CLA	5	609	17	1/1/12/20	11/21/99/115	-
24	CLA	9	602	-	1/1/11/20	4/15/93/115	-
24	CLA	B	1235	-	1/1/15/20	11/37/115/115	-
24	CLA	B	1208	-	1/1/14/20	15/31/109/115	-
28	LHG	9	801	-	-	22/37/37/53	-
24	CLA	3	607	-	1/1/15/20	16/37/115/115	-
41	CHL	6	611	-	3/3/17/26	2/21/119/137	-
24	CLA	B	1206	-	1/1/13/20	14/25/103/115	-
24	CLA	a	601	-	1/1/14/20	11/31/109/115	-
24	CLA	A	1136	-	1/1/15/20	18/37/115/115	-
27	BCR	B	4006	-	-	11/29/63/63	0/2/2/2
24	CLA	1	604	-	1/1/15/20	21/37/115/115	-
27	BCR	J	4001	-	-	10/29/63/63	0/2/2/2
24	CLA	7	609	19	1/1/14/20	15/31/109/115	-
24	CLA	A	1126	-	1/1/15/20	22/37/115/115	-
41	CHL	9	610	-	3/3/17/26	3/21/119/137	-
24	CLA	B	1205	-	1/1/15/20	8/37/115/115	-
28	LHG	3	801	-	-	31/53/53/53	-
27	BCR	6	504	-	-	9/29/63/63	0/2/2/2
26	SF4	C	3002	3	-	-	0/6/5/5
24	CLA	B	1211	-	1/1/13/20	14/25/103/115	-
24	CLA	2	612	-	1/1/12/20	8/19/97/115	-
28	LHG	B	5002	-	-	28/53/53/53	-
27	BCR	3	503	-	-	12/29/63/63	0/2/2/2
33	PTY	B	5005	-	-	26/44/44/53	-
24	CLA	A	1108	-	1/1/15/20	20/37/115/115	-
24	CLA	B	1238	-	1/1/15/20	13/37/115/115	-
24	CLA	4	611	-	1/1/13/20	11/27/105/115	-
40	LUT	8	502	-	-	2/29/67/67	0/2/2/2
28	LHG	B	5001	-	-	30/50/50/53	-
38	LPX	a	804	-	-	8/31/31/31	-
41	CHL	4	609	16	4/4/20/26	9/39/137/137	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	LHG	4	801	-	-	28/53/53/53	-
24	CLA	5	605	-	1/1/11/20	5/15/93/115	-
32	PCW	B	5004	-	-	19/33/33/57	-
24	CLA	B	1230	-	1/1/13/20	13/29/107/115	-
41	CHL	9	613	-	3/3/15/26	0/10/108/137	-
24	CLA	A	1013	-	1/1/15/20	13/37/115/115	-
28	LHG	F	5002	-	-	27/40/40/53	-
24	CLA	8	608	-	1/1/12/20	9/22/100/115	-
24	CLA	A	1132	-	1/1/15/20	13/37/115/115	-
24	CLA	7	617	19	1/1/13/20	13/23/101/115	-
24	CLA	J	1901	8	1/1/10/20	5/10/88/115	-
29	DGD	B	5003	-	-	16/55/95/95	0/2/2/2
24	CLA	A	1113	-	1/1/12/20	7/22/100/115	-
24	CLA	a	605	-	1/1/15/20	17/37/115/115	-
42	OLA	1	803	-	-	5/17/17/17	-
24	CLA	2	601	-	1/1/14/20	15/31/109/115	-
24	CLA	B	1234	-	1/1/13/20	9/27/105/115	-
24	CLA	A	1119	-	1/1/15/20	18/37/115/115	-
24	CLA	A	1104	-	1/1/15/20	16/37/115/115	-
24	CLA	A	1130	-	1/1/13/20	13/27/105/115	-
24	CLA	A	1127	-	1/1/15/20	16/37/115/115	-
28	LHG	7	803	-	-	25/47/47/53	-
41	CHL	6	619	18	4/4/20/26	12/39/137/137	-
24	CLA	H	1702	-	1/1/11/20	7/15/93/115	-
24	CLA	7	605	-	1/1/11/20	1/11/89/115	-
24	CLA	B	1201	-	1/1/15/20	14/37/115/115	-
24	CLA	5	617	-	1/1/12/20	9/19/97/115	-
37	RRX	J	4002	-	1/1/11/25	9/29/65/65	0/2/2/2
28	LHG	5	801	-	-	26/53/53/53	-
27	BCR	5	503	-	-	13/29/63/63	0/2/2/2
27	BCR	A	4001	-	-	14/29/63/63	0/2/2/2
24	CLA	1	615	14	1/1/11/20	9/15/93/115	-
24	CLA	A	1140	-	1/1/13/20	10/25/103/115	-
24	CLA	5	603	-	1/1/13/20	18/27/105/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	6	612	-	1/1/12/20	10/19/97/115	-
24	CLA	5	604	-	1/1/15/20	16/37/115/115	-
24	CLA	4	616	-	1/1/12/20	6/19/97/115	-
24	CLA	A	1112	-	1/1/13/20	13/25/103/115	-
24	CLA	B	1220	-	1/1/14/20	17/31/109/115	-
39	ECH	M	4001	-	-	5/29/66/66	0/2/2/2
41	CHL	6	610	-	4/4/18/26	6/27/125/137	-
41	CHL	5	613	-	4/4/18/26	1/27/125/137	-
24	CLA	A	1114	-	1/1/15/20	15/37/115/115	-
24	CLA	A	1124	-	1/1/13/20	5/25/103/115	-
40	LUT	7	501	-	1/1/12/27	6/29/67/67	0/2/2/2
24	CLA	9	608	-	1/1/11/20	4/13/91/115	-
24	CLA	A	1110	-	1/1/14/20	13/31/109/115	-
24	CLA	a	603	-	1/1/15/20	13/37/115/115	-
24	CLA	B	1215	-	1/1/14/20	20/31/109/115	-
40	LUT	6	501	-	1/1/12/27	8/29/67/67	0/2/2/2
29	DGD	A	5005	-	-	12/40/80/95	0/2/2/2
24	CLA	a	604	-	1/1/15/20	16/37/115/115	-
24	CLA	B	1232	-	1/1/11/20	7/13/91/115	-
27	BCR	B	4001	-	-	10/29/63/63	0/2/2/2
24	CLA	4	604	-	1/1/14/20	12/31/109/115	-
24	CLA	8	620	20	1/1/15/20	18/37/115/115	-
41	CHL	4	618	16	4/4/18/26	6/27/125/137	-
40	LUT	2	502	-	-	3/29/67/67	0/2/2/2
28	LHG	1	801	-	-	26/39/39/53	-
24	CLA	B	1219	-	1/1/13/20	11/30/108/115	-
27	BCR	K	4002	-	-	12/29/63/63	0/2/2/2
24	CLA	B	1223	-	1/1/15/20	18/37/115/115	-
24	CLA	9	609	-	1/1/11/20	6/15/93/115	-
27	BCR	B	4007	-	-	13/29/63/63	0/2/2/2
24	CLA	A	1117	-	1/1/15/20	21/37/115/115	-
26	SF4	A	3001	2,1	-	-	0/6/5/5
24	CLA	B	1209	-	1/1/15/20	16/37/115/115	-
24	CLA	2	615	-	1/1/13/20	13/28/106/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	6	617	-	1/1/11/20	5/13/91/115	-
24	CLA	B	1212	-	1/1/15/20	20/37/115/115	-
24	CLA	A	1123	-	1/1/15/20	20/37/115/115	-
24	CLA	8	609	20	1/1/14/20	20/31/109/115	-
41	CHL	1	613	-	3/3/16/26	5/18/116/137	-
40	LUT	4	501	-	-	2/29/67/67	0/2/2/2
52	A8S	9	504	-	-	2/10/34/34	0/1/1/1
24	CLA	3	616	-	1/1/13/20	11/27/105/115	-
24	CLA	7	603	-	1/1/15/20	21/37/115/115	-
40	LUT	a	503	-	-	5/29/67/67	0/2/2/2
24	CLA	7	612	-	1/1/14/20	12/31/109/115	-
24	CLA	5	607	-	1/1/13/20	10/25/103/115	-
27	BCR	4	503	-	-	13/29/63/63	0/2/2/2
24	CLA	2	603	-	1/1/14/20	13/31/109/115	-
41	CHL	a	613	-	4/4/16/26	4/15/113/137	-
24	CLA	A	1125	-	1/1/15/20	21/37/115/115	-
24	CLA	A	1102	24	1/1/15/20	18/37/115/115	-
24	CLA	1	606	-	1/1/13/20	16/28/106/115	-
24	CLA	6	602	-	1/1/12/20	4/22/100/115	-
47	SPH	6	806	-	-	7/21/21/21	-
40	LUT	8	501	-	-	2/29/67/67	0/2/2/2
34	LAP	F	5003	-	-	17/30/30/30	-
40	LUT	1	503	-	1/1/12/27	4/29/67/67	0/2/2/2
28	LHG	A	5001	24	-	15/33/33/53	-
24	CLA	B	1203	-	1/1/15/20	17/37/115/115	-
24	CLA	B	1218	-	1/1/13/20	9/25/103/115	-
24	CLA	1	612	-	1/1/15/20	22/37/115/115	-
24	CLA	4	617	-	1/1/11/20	7/13/91/115	-
28	LHG	6	801	-	-	29/53/53/53	-
28	LHG	2	802	-	-	35/53/53/53	-
24	CLA	3	613	-	1/1/14/20	11/33/111/115	-
24	CLA	A	1012	-	1/1/15/20	15/37/115/115	-
24	CLA	A	1116	-	1/1/14/20	14/31/109/115	-
27	BCR	B	4003	-	-	12/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	BCR	A	4003	-	-	11/29/63/63	0/2/2/2
40	LUT	5	502	-	-	5/29/67/67	0/2/2/2
24	CLA	B	1216	-	1/1/14/20	18/33/111/115	-
24	CLA	B	1237	-	1/1/15/20	19/37/115/115	-
28	LHG	4	802	-	-	22/36/36/53	-
24	CLA	a	607	-	1/1/13/20	13/29/107/115	-
24	CLA	B	1207	-	1/1/14/20	14/31/109/115	-
27	BCR	6	503	-	-	12/29/63/63	0/2/2/2
24	CLA	7	611	-	1/1/14/20	11/31/109/115	-
24	CLA	6	618	-	1/1/11/20	9/15/93/115	-
46	DGA	5	803	-	-	13/24/24/45	-
24	CLA	7	602	-	1/1/10/20	5/11/90/115	-
24	CLA	3	603	-	1/1/15/20	13/37/115/115	-
33	PTY	7	804	-	-	17/36/36/53	-
35	SQD	G	5001	-	-	16/41/61/69	0/1/1/1
28	LHG	a	801	-	-	23/39/39/53	-
24	CLA	4	608	-	1/1/12/20	6/21/99/115	-
24	CLA	4	607	-	1/1/13/20	13/25/103/115	-
41	CHL	8	604	-	4/4/19/26	13/35/133/137	-
24	CLA	4	602	-	1/1/12/20	5/22/100/115	-
24	CLA	1	602	-	1/1/11/20	7/13/91/115	-
24	CLA	9	603	-	1/1/15/20	13/37/115/115	-
28	LHG	6	802	-	-	23/41/41/53	-
24	CLA	B	1214	-	1/1/14/20	19/34/112/115	-
40	LUT	5	505	-	-	7/29/67/67	0/2/2/2
24	CLA	6	609	18	1/1/15/20	19/37/115/115	-
24	CLA	A	1128	-	1/1/15/20	15/37/115/115	-
24	CLA	9	601	-	1/1/14/20	14/31/109/115	-
41	CHL	5	611	-	3/3/17/26	2/21/119/137	-
24	CLA	2	606	-	1/1/11/20	8/15/93/115	-
24	CLA	B	1222	-	1/1/13/20	4/29/107/115	-
24	CLA	8	618	-	1/1/14/20	15/31/109/115	-
24	CLA	F	1301	-	1/1/12/20	7/19/97/115	-
24	CLA	8	610	-	1/1/13/20	16/25/103/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	CLA	a	615	-	1/1/11/20	4/15/93/115	-
24	CLA	5	608	-	1/1/11/20	5/13/91/115	-
24	CLA	3	602	-	1/1/11/20	5/15/93/115	-
24	CLA	7	615	19	1/1/13/20	11/25/103/115	-
24	CLA	7	606	-	1/1/13/20	15/25/103/115	-
31	LMT	2	804	-	-	6/21/61/61	0/2/2/2
24	CLA	3	612	-	1/1/15/20	12/37/115/115	-
38	LPX	J	5001	-	-	11/18/18/31	-
24	CLA	B	1021	-	1/1/15/20	19/37/115/115	-
24	CLA	F	1302	-	1/1/13/20	11/25/103/115	-
40	LUT	a	502	-	-	1/29/67/67	0/2/2/2
24	CLA	9	606	-	1/1/13/20	6/25/103/115	-
24	CLA	B	1221	-	1/1/15/20	13/37/115/115	-
27	BCR	A	4005	-	-	15/29/63/63	0/2/2/2
24	CLA	A	1138	-	1/1/15/20	10/37/115/115	-
33	PTY	8	891	-	-	14/38/38/53	-
24	CLA	3	605	-	1/1/15/20	19/37/115/115	-
24	CLA	A	1109	24	1/1/15/20	16/37/115/115	-
27	BCR	B	4004	-	-	12/29/63/63	0/2/2/2
50	4RF	7	807	-	-	10/34/34/59	-
41	CHL	1	609	14	4/4/20/26	10/39/137/137	-
24	CLA	A	1134	1	1/1/14/20	15/31/109/115	-
41	CHL	4	613	-	3/3/17/26	3/23/121/137	-
34	LAP	B	5007	-	-	15/30/30/30	-
24	CLA	4	605	-	1/1/11/20	5/15/93/115	-
40	LUT	1	502	-	-	1/29/67/67	0/2/2/2
24	CLA	A	1106	-	1/1/15/20	13/37/115/115	-
24	CLA	K	1402	-	1/1/14/20	15/31/109/115	-
51	P5S	8	806	-	-	16/42/42/59	-
24	CLA	6	604	-	1/1/15/20	14/37/115/115	-
24	CLA	2	607	-	1/1/11/20	6/15/93/115	-
27	BCR	5	504	-	-	11/29/63/63	0/2/2/2
45	PLM	6	804	-	-	4/15/15/15	-
24	CLA	8	612	20	1/1/11/20	11/15/93/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	PTY	5	802	-	-	19/41/41/53	-
28	LHG	A	5002	-	-	32/53/53/53	-
24	CLA	1	608	-	1/1/14/20	15/31/109/115	-
24	CLA	K	1403	9	1/1/11/20	9/15/93/115	-
24	CLA	B	1224	-	1/1/15/20	21/37/115/115	-
24	CLA	3	606	-	1/1/15/20	19/37/115/115	-
40	LUT	3	502	-	-	1/29/67/67	0/2/2/2
24	CLA	1	611	-	1/1/13/20	10/25/103/115	-
44	GG0	a	805	-	-	2/7/7/7	-
24	CLA	9	612	-	1/1/15/20	21/37/115/115	-
24	CLA	2	605	-	1/1/14/20	16/31/109/115	-
24	CLA	H	1703	-	1/1/13/20	8/25/103/115	-
24	CLA	a	608	-	1/1/13/20	14/25/103/115	-

The worst 5 of 2283 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	G	5002	ERG	C1-C10	-23.39	1.09	1.54
36	G	5002	ERG	C10-C9	-21.00	1.27	1.55
49	7	504	C7Z	C25-C26	15.58	1.61	1.34
37	J	4002	RRX	C26-C25	15.42	1.61	1.34
49	7	504	C7Z	C5-C6	15.18	1.60	1.34

The worst 5 of 5090 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	2	601	CLA	C4-C3-C5	-22.53	77.37	115.27
24	2	601	CLA	C5-C3-C2	18.93	159.43	121.12
27	F	4001	BCR	C10-C11-C12	18.18	179.95	123.22
27	5	504	BCR	C10-C11-C12	17.97	179.29	123.22
27	H	4001	BCR	C10-C11-C12	17.82	178.83	123.22

5 of 331 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	A	1011	CL0	ND
23	A	1011	CL0	NC
23	A	1011	CL0	NA
24	A	1012	CLA	ND

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Mol	Chain	Res	Type	Atom
24	A	1013	CLA	ND

5 of 4533 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	A	1011	CL0	C2-C1-O2A-CGA
24	A	1101	CLA	C2A-CAA-CBA-CGA
24	A	1101	CLA	CBA-CGA-O2A-C1
24	A	1101	CLA	O1A-CGA-O2A-C1
24	A	1101	CLA	CHA-CBD-CGD-O1D

There are no ring outliers.

326 monomers are involved in 956 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	H	5001	SQD	7	0
50	8	808	4RF	2	0
24	L	1503	CLA	2	0
24	B	1240	CLA	7	0
24	7	608	CLA	3	0
27	L	4001	BCR	5	0
24	A	1137	CLA	4	0
24	B	1239	CLA	4	0
24	5	616	CLA	1	0
24	5	612	CLA	6	0
24	A	1103	CLA	7	0
24	B	1225	CLA	7	0
27	8	503	BCR	1	0
23	A	1011	CL0	5	0
27	3	505	BCR	2	0
28	1	802	LHG	2	0
31	A	5008	LMT	3	0
48	7	502	XAT	3	0
24	3	610	CLA	3	0
24	6	605	CLA	3	0
24	A	1133	CLA	8	0
24	K	1404	CLA	2	0
25	A	2001	PQN	4	0
41	6	613	CHL	3	0
24	L	1501	CLA	3	0
24	A	1139	CLA	3	0
27	3	504	BCR	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	6	603	CLA	3	0
24	2	608	CLA	2	0
27	A	4002	BCR	4	0
40	5	501	LUT	3	0
34	K	5001	LAP	2	0
28	7	801	LHG	6	0
24	8	611	CLA	2	0
24	6	601	CLA	9	0
24	4	601	CLA	8	0
24	1	601	CLA	4	0
46	8	803	DGA	2	0
24	A	1105	CLA	2	0
28	2	801	LHG	4	0
40	9	502	LUT	7	0
25	B	2002	PQN	5	0
24	A	1141	CLA	3	0
36	G	5002	ERG	7	0
27	A	4004	BCR	6	0
24	8	606	CLA	3	0
24	B	1228	CLA	5	0
24	A	1115	CLA	2	0
24	7	607	CLA	3	0
24	A	1111	CLA	5	0
24	7	601	CLA	5	0
24	H	1701	CLA	3	0
24	3	601	CLA	3	0
31	1	804	LMT	1	0
24	A	1120	CLA	3	0
24	B	1023	CLA	10	0
24	1	610	CLA	1	0
32	6	803	PCW	2	0
24	4	603	CLA	5	0
27	I	4001	BCR	6	0
24	1	603	CLA	7	0
24	8	615	CLA	1	0
24	4	612	CLA	5	0
41	5	610	CHL	9	0
24	B	1204	CLA	7	0
27	L	4003	BCR	2	0
24	B	1229	CLA	5	0
24	G	1602	CLA	2	0
40	1	501	LUT	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	3	611	CHL	4	0
24	1	605	CLA	5	0
24	5	606	CLA	1	0
24	L	1502	CLA	4	0
24	B	1022	CLA	4	0
27	G	4001	BCR	3	0
24	B	1213	CLA	1	0
35	7	805	SQD	1	0
24	A	1122	CLA	6	0
28	F	5001	LHG	4	0
24	K	1401	CLA	2	0
24	A	1121	CLA	3	0
31	B	5006	LMT	6	0
24	A	1135	CLA	5	0
24	B	1236	CLA	1	0
26	C	3003	SF4	1	0
50	8	807	4RF	2	0
24	4	615	CLA	2	0
24	B	1217	CLA	3	0
24	5	618	CLA	1	0
24	B	1231	CLA	6	0
24	2	609	CLA	4	0
24	2	604	CLA	11	0
28	9	802	LHG	3	0
41	8	601	CHL	5	0
24	A	1101	CLA	6	0
24	G	1603	CLA	3	0
41	8	613	CHL	3	0
27	B	4002	BCR	4	0
24	1	607	CLA	3	0
27	7	503	BCR	2	0
40	2	501	LUT	4	0
28	A	5003	LHG	5	0
27	L	4002	BCR	4	0
24	B	1226	CLA	3	0
24	4	606	CLA	1	0
24	7	610	CLA	2	0
27	B	4005	BCR	2	0
24	B	1227	CLA	2	0
33	3	802	PTY	1	0
41	3	608	CHL	5	0
41	7	613	CHL	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	F	4001	BCR	7	0
24	A	1107	CLA	4	0
24	8	603	CLA	2	0
24	5	601	CLA	4	0
24	6	615	CLA	6	0
24	9	604	CLA	5	0
27	H	4001	BCR	2	0
24	A	1131	CLA	5	0
40	3	501	LUT	6	0
27	K	4001	BCR	7	0
24	2	621	CLA	5	0
24	3	604	CLA	2	0
33	9	803	PTY	2	0
40	6	502	LUT	5	0
40	9	501	LUT	4	0
40	4	502	LUT	4	0
24	8	607	CLA	2	0
24	4	610	CLA	4	0
24	8	602	CLA	1	0
24	B	1202	CLA	7	0
29	8	802	DGD	8	0
42	8	809	OLA	3	0
24	7	604	CLA	7	0
24	8	605	CLA	1	0
24	A	1129	CLA	2	0
24	B	1210	CLA	6	0
24	A	1118	CLA	4	0
24	B	1235	CLA	6	0
24	B	1208	CLA	3	0
28	9	801	LHG	3	0
24	3	607	CLA	2	0
41	6	611	CHL	3	0
24	B	1206	CLA	2	0
24	A	1136	CLA	7	0
27	B	4006	BCR	8	0
24	1	604	CLA	7	0
27	J	4001	BCR	4	0
24	7	609	CLA	3	0
24	A	1126	CLA	14	0
41	9	610	CHL	2	0
24	B	1205	CLA	4	0
28	3	801	LHG	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	6	504	BCR	3	0
24	B	1211	CLA	1	0
24	2	612	CLA	4	0
28	B	5002	LHG	2	0
27	3	503	BCR	4	0
33	B	5005	PTY	2	0
24	A	1108	CLA	5	0
24	B	1238	CLA	3	0
24	4	611	CLA	5	0
40	8	502	LUT	11	0
28	B	5001	LHG	4	0
41	4	609	CHL	5	0
28	4	801	LHG	3	0
24	5	605	CLA	1	0
32	B	5004	PCW	2	0
24	B	1230	CLA	5	0
41	9	613	CHL	1	0
24	A	1013	CLA	9	0
28	F	5002	LHG	2	0
24	8	608	CLA	1	0
24	A	1132	CLA	5	0
24	7	617	CLA	3	0
29	B	5003	DGD	10	0
24	A	1113	CLA	1	0
42	1	803	OLA	2	0
24	2	601	CLA	4	0
24	B	1234	CLA	5	0
24	A	1119	CLA	7	0
24	A	1104	CLA	3	0
24	A	1130	CLA	1	0
24	A	1127	CLA	7	0
28	7	803	LHG	1	0
41	6	619	CHL	3	0
24	H	1702	CLA	3	0
24	7	605	CLA	3	0
24	B	1201	CLA	3	0
24	5	617	CLA	4	0
37	J	4002	RRX	5	0
28	5	801	LHG	1	0
27	5	503	BCR	2	0
27	A	4001	BCR	4	0
24	1	615	CLA	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1140	CLA	2	0
24	5	603	CLA	2	0
24	6	612	CLA	4	0
24	5	604	CLA	2	0
24	A	1112	CLA	3	0
24	B	1220	CLA	7	0
39	M	4001	ECH	4	0
41	6	610	CHL	4	0
41	5	613	CHL	1	0
24	A	1114	CLA	6	0
24	A	1124	CLA	3	0
40	7	501	LUT	3	0
24	9	608	CLA	1	0
24	A	1110	CLA	3	0
24	B	1215	CLA	4	0
29	A	5005	DGD	3	0
40	6	501	LUT	7	0
24	B	1232	CLA	2	0
27	B	4001	BCR	6	0
24	4	604	CLA	7	0
24	8	620	CLA	2	0
41	4	618	CHL	2	0
40	2	502	LUT	9	0
28	1	801	LHG	4	0
24	B	1219	CLA	4	0
27	K	4002	BCR	1	0
24	B	1223	CLA	4	0
24	9	609	CLA	1	0
27	B	4007	BCR	2	0
24	A	1117	CLA	11	0
24	B	1209	CLA	6	0
24	2	615	CLA	4	0
24	6	617	CLA	3	0
24	B	1212	CLA	4	0
24	A	1123	CLA	6	0
24	8	609	CLA	6	0
40	4	501	LUT	10	0
41	1	613	CHL	3	0
52	9	504	A8S	1	0
24	3	616	CLA	5	0
24	7	603	CLA	1	0
24	7	612	CLA	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	5	607	CLA	1	0
24	2	603	CLA	6	0
24	A	1125	CLA	3	0
24	A	1102	CLA	7	0
24	1	606	CLA	3	0
24	6	602	CLA	3	0
47	6	806	SPH	1	0
40	8	501	LUT	4	0
34	F	5003	LAP	3	0
40	1	503	LUT	3	0
28	A	5001	LHG	3	0
24	B	1203	CLA	3	0
24	B	1218	CLA	3	0
24	1	612	CLA	8	0
28	6	801	LHG	6	0
28	2	802	LHG	2	0
24	3	613	CLA	4	0
24	A	1012	CLA	4	0
24	A	1116	CLA	11	0
27	B	4003	BCR	4	0
27	A	4003	BCR	5	0
40	5	502	LUT	4	0
24	B	1216	CLA	4	0
24	B	1237	CLA	2	0
24	B	1207	CLA	13	0
27	6	503	BCR	1	0
24	7	611	CLA	4	0
24	6	618	CLA	2	0
46	5	803	DGA	1	0
24	3	603	CLA	6	0
33	7	804	PTY	1	0
35	G	5001	SQD	2	0
24	4	608	CLA	3	0
24	4	607	CLA	2	0
41	8	604	CHL	4	0
24	4	602	CLA	1	0
24	1	602	CLA	3	0
24	9	603	CLA	5	0
28	6	802	LHG	1	0
24	B	1214	CLA	6	0
40	5	505	LUT	7	0
24	6	609	CLA	4	0

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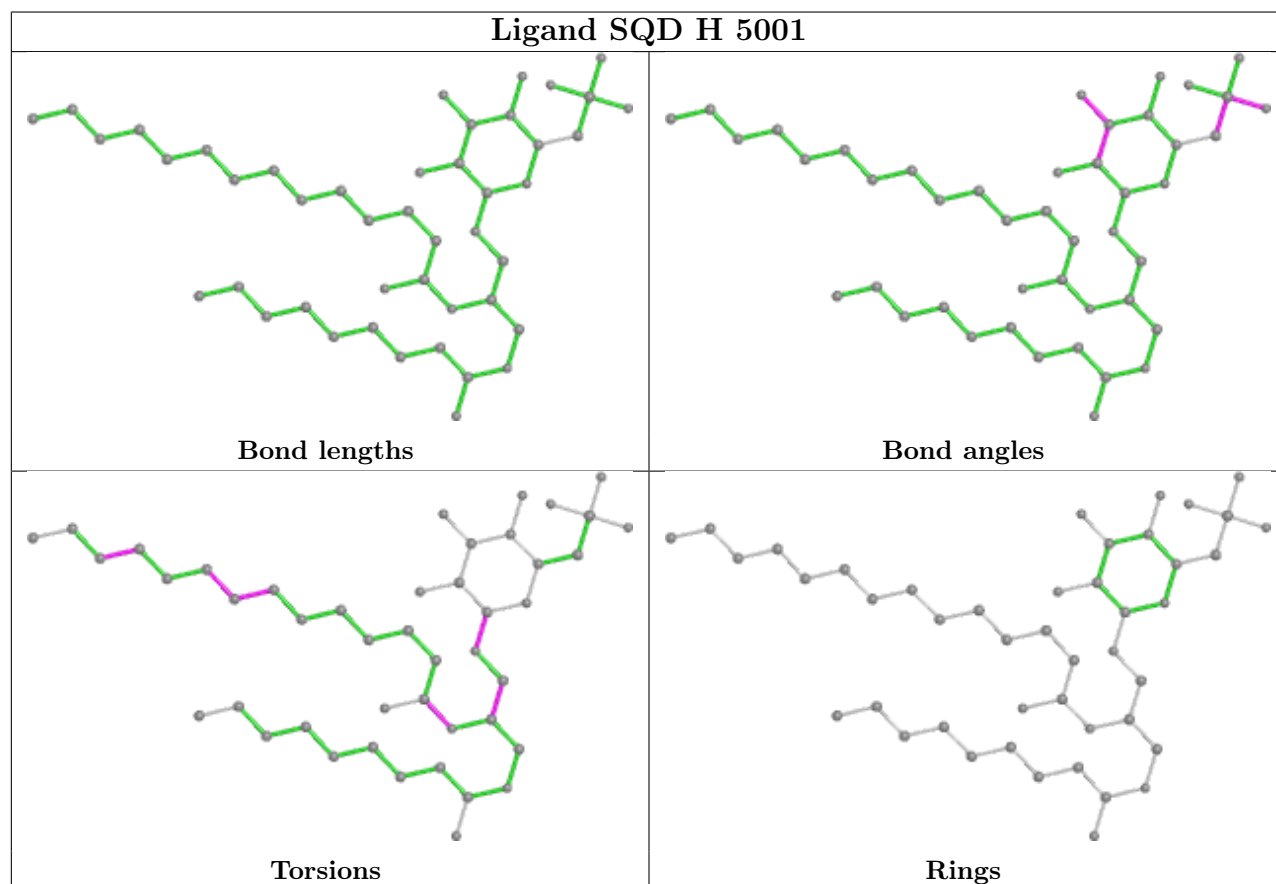
Mol	Chain	Res	Type	Clashes	Symm-Clashes
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24	9	601	CLA	5	0
41	5	611	CHL	3	0
24	B	1222	CLA	5	0
24	8	618	CLA	3	0
24	F	1301	CLA	3	0
24	8	610	CLA	6	0
24	5	608	CLA	1	0
24	7	615	CLA	1	0
24	7	606	CLA	1	0
31	2	804	LMT	1	0
24	3	612	CLA	8	0
38	J	5001	LPX	1	0
24	B	1021	CLA	6	0
24	F	1302	CLA	3	0
24	9	606	CLA	2	0
24	B	1221	CLA	6	0
27	A	4005	BCR	8	0
24	A	1138	CLA	4	0
33	8	891	PTY	2	0
24	3	605	CLA	5	0
24	A	1109	CLA	6	0
27	B	4004	BCR	6	0
50	7	807	4RF	1	0
41	1	609	CHL	8	0
24	A	1134	CLA	4	0
41	4	613	CHL	3	0
24	4	605	CLA	2	0
40	1	502	LUT	4	0
24	A	1106	CLA	6	0
24	K	1402	CLA	2	0
24	6	604	CLA	5	0
24	2	607	CLA	1	0
27	5	504	BCR	4	0
45	6	804	PLM	2	0
24	8	612	CLA	4	0
33	5	802	PTY	3	0
28	A	5002	LHG	2	0
24	1	608	CLA	4	0
24	K	1403	CLA	1	0
24	B	1224	CLA	8	0
24	3	606	CLA	3	0

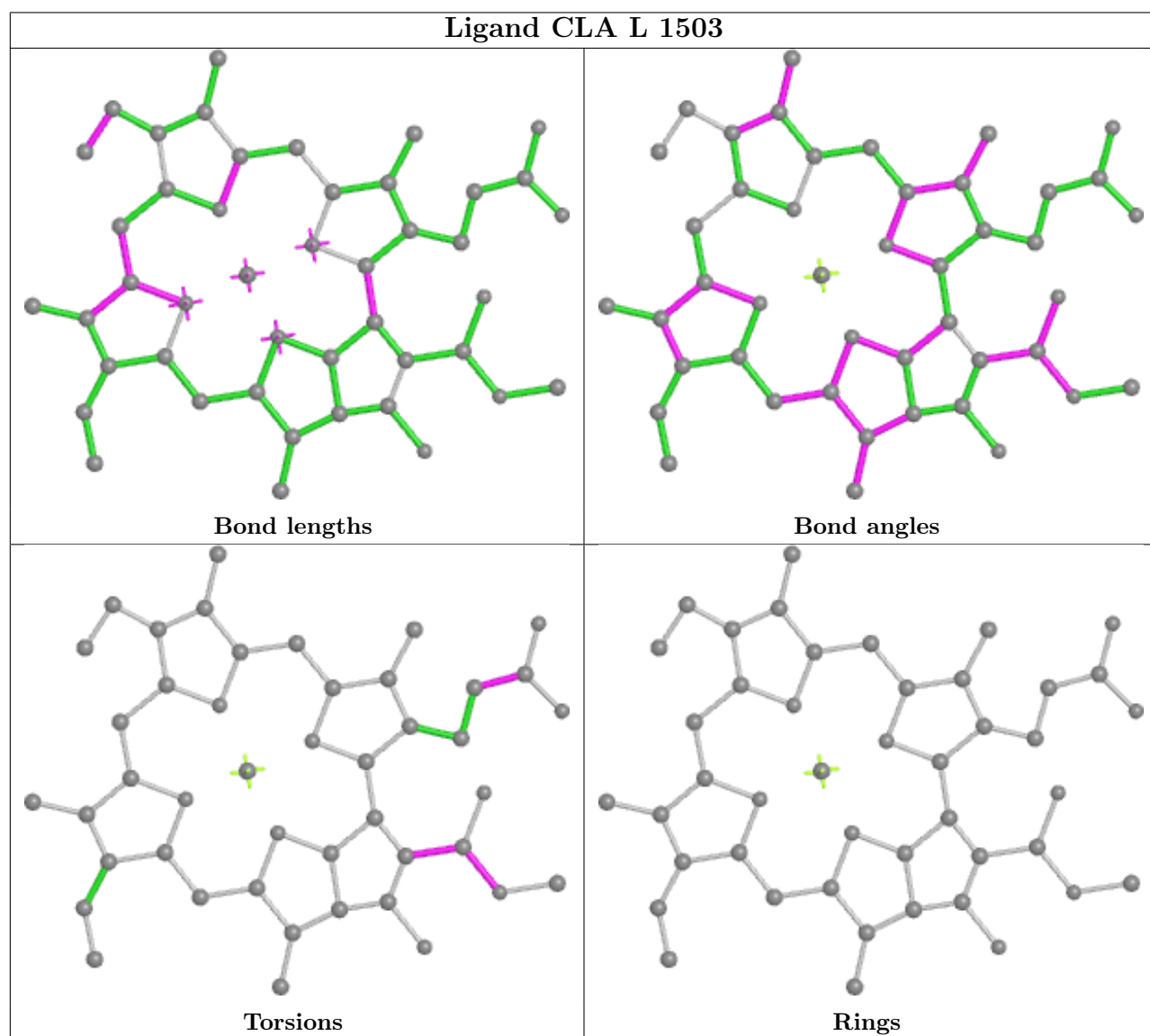
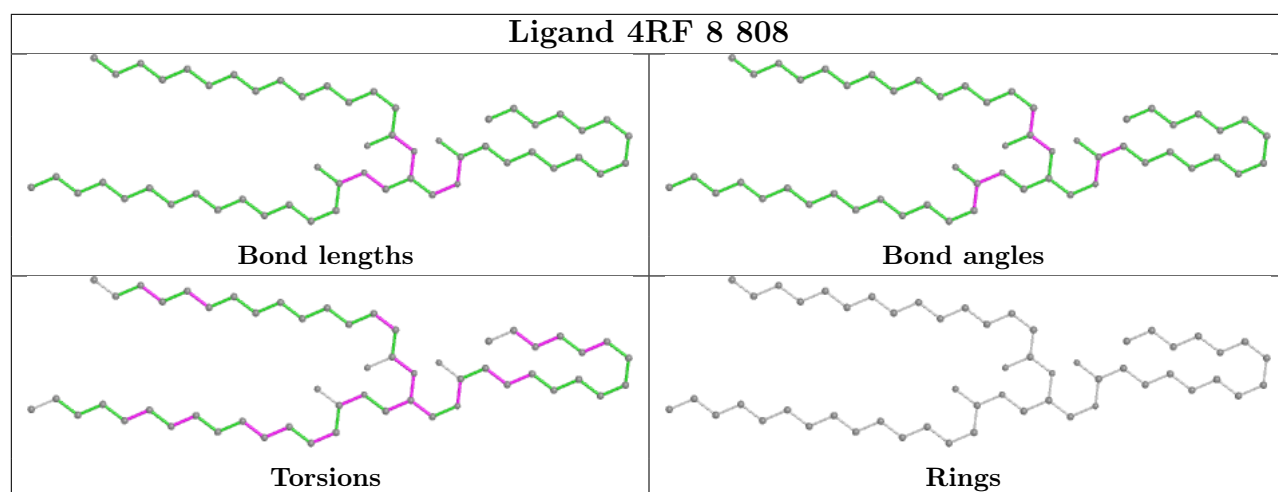
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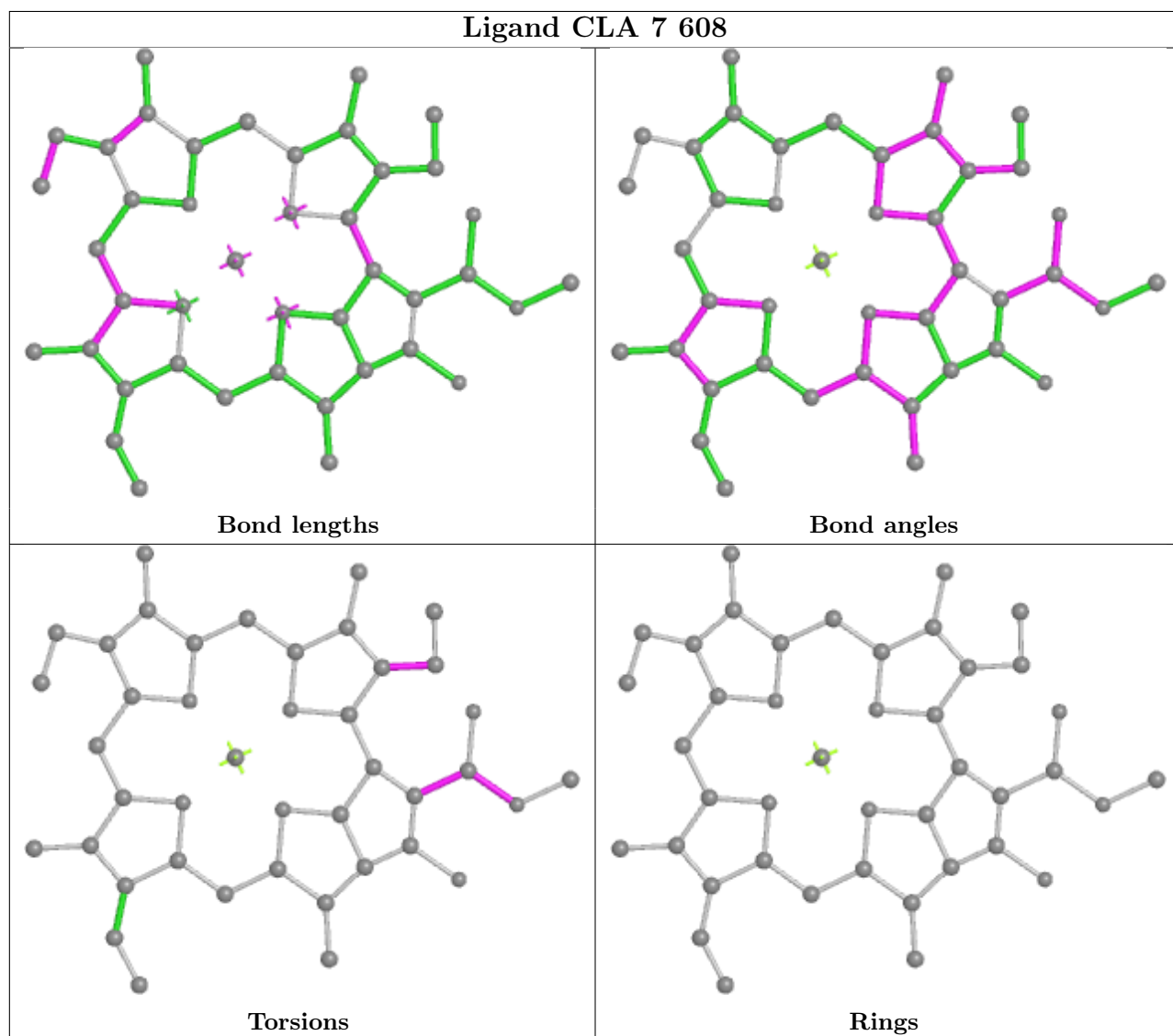
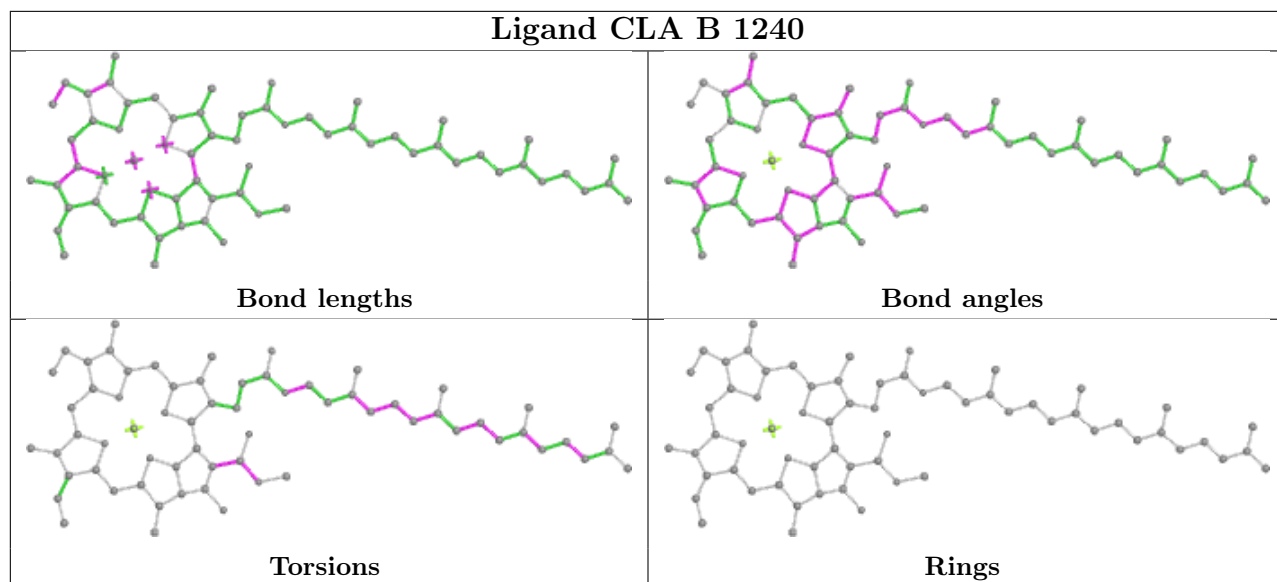
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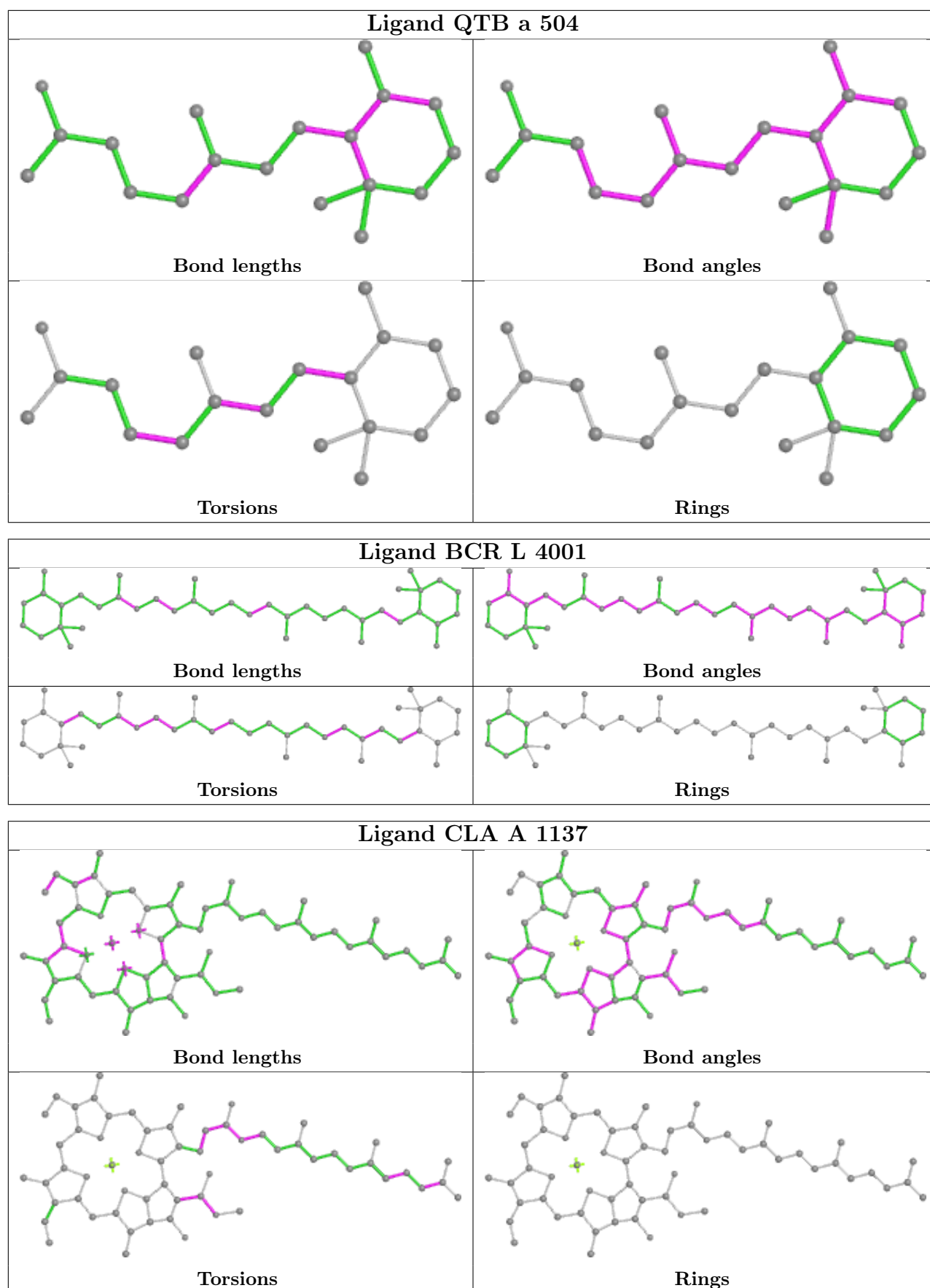
Mol	Chain	Res	Type	Clashes	Symm-Clashes
40	3	502	LUT	4	0
24	1	611	CLA	4	0
24	9	612	CLA	8	0
24	2	605	CLA	2	0
24	H	1703	CLA	4	0

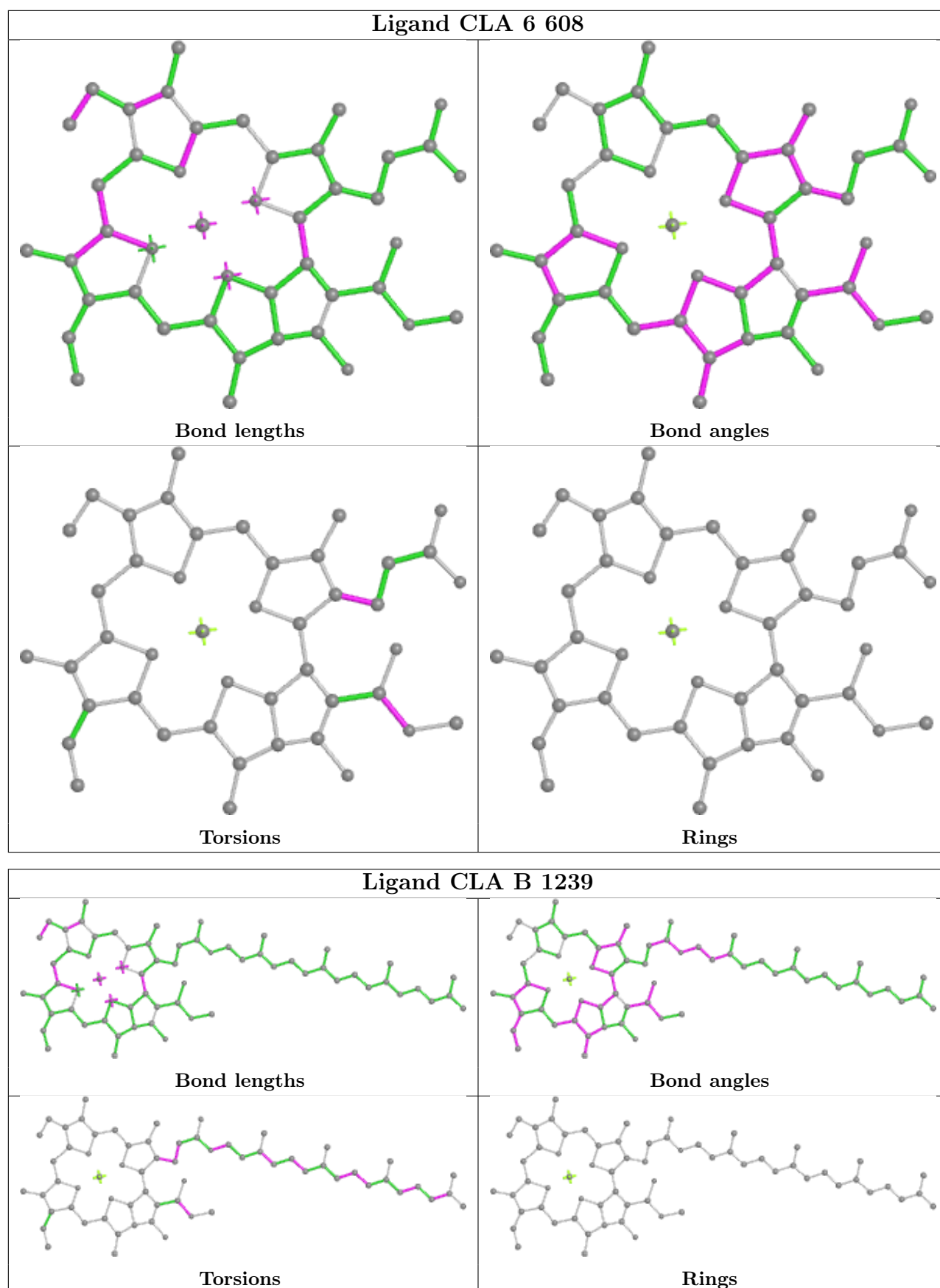
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

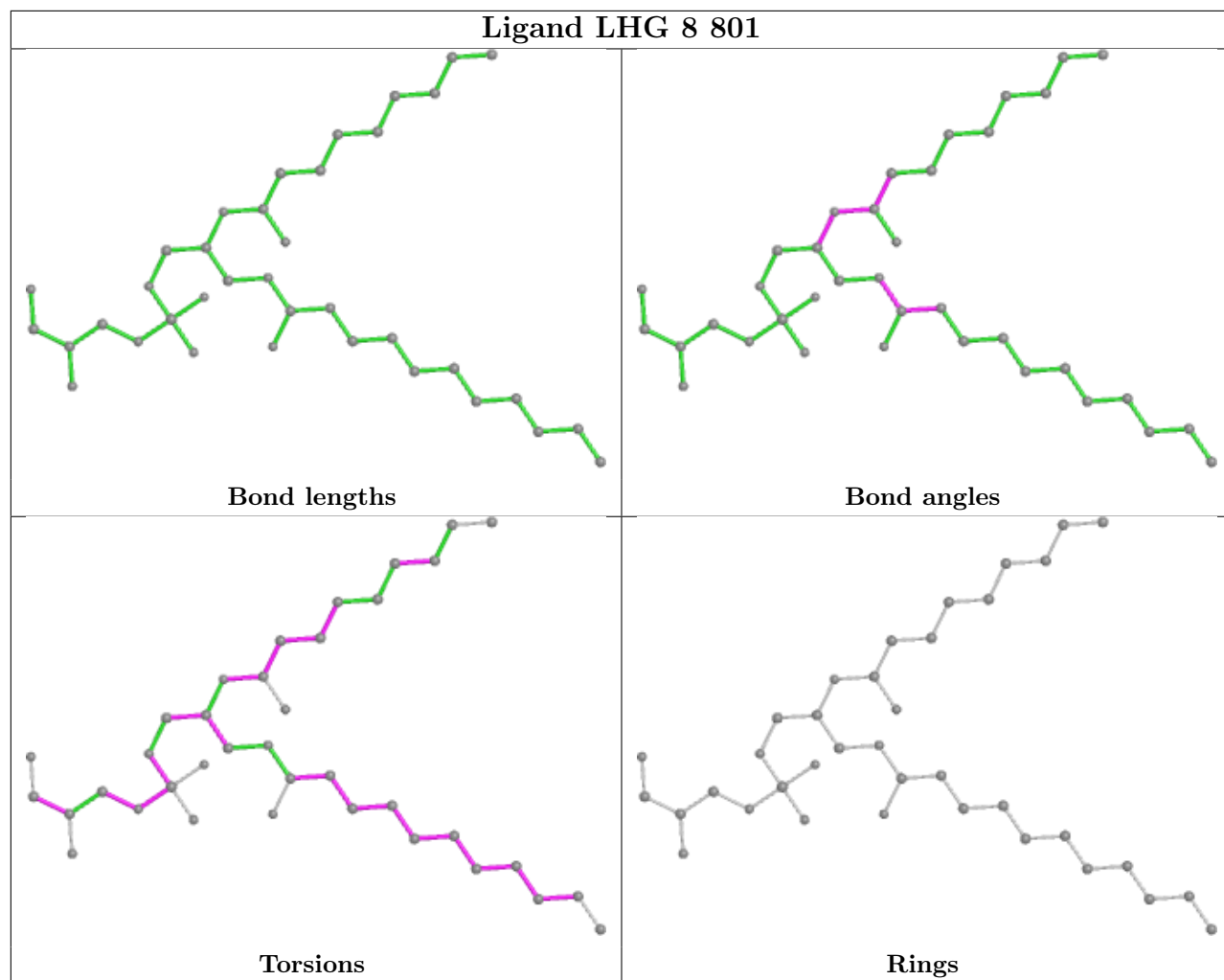


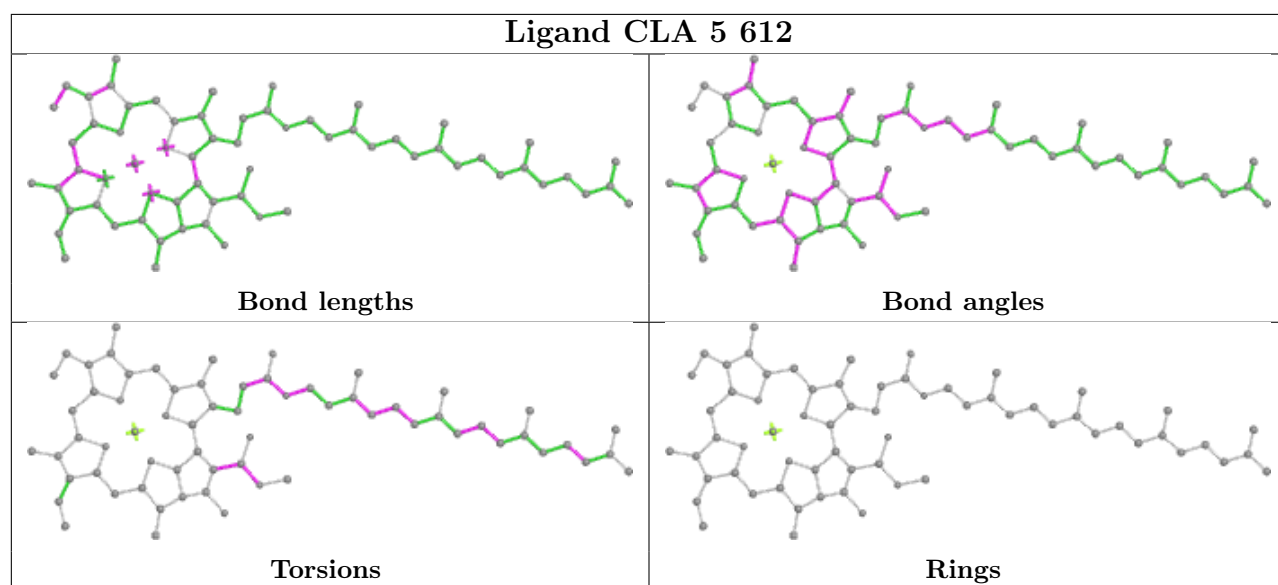
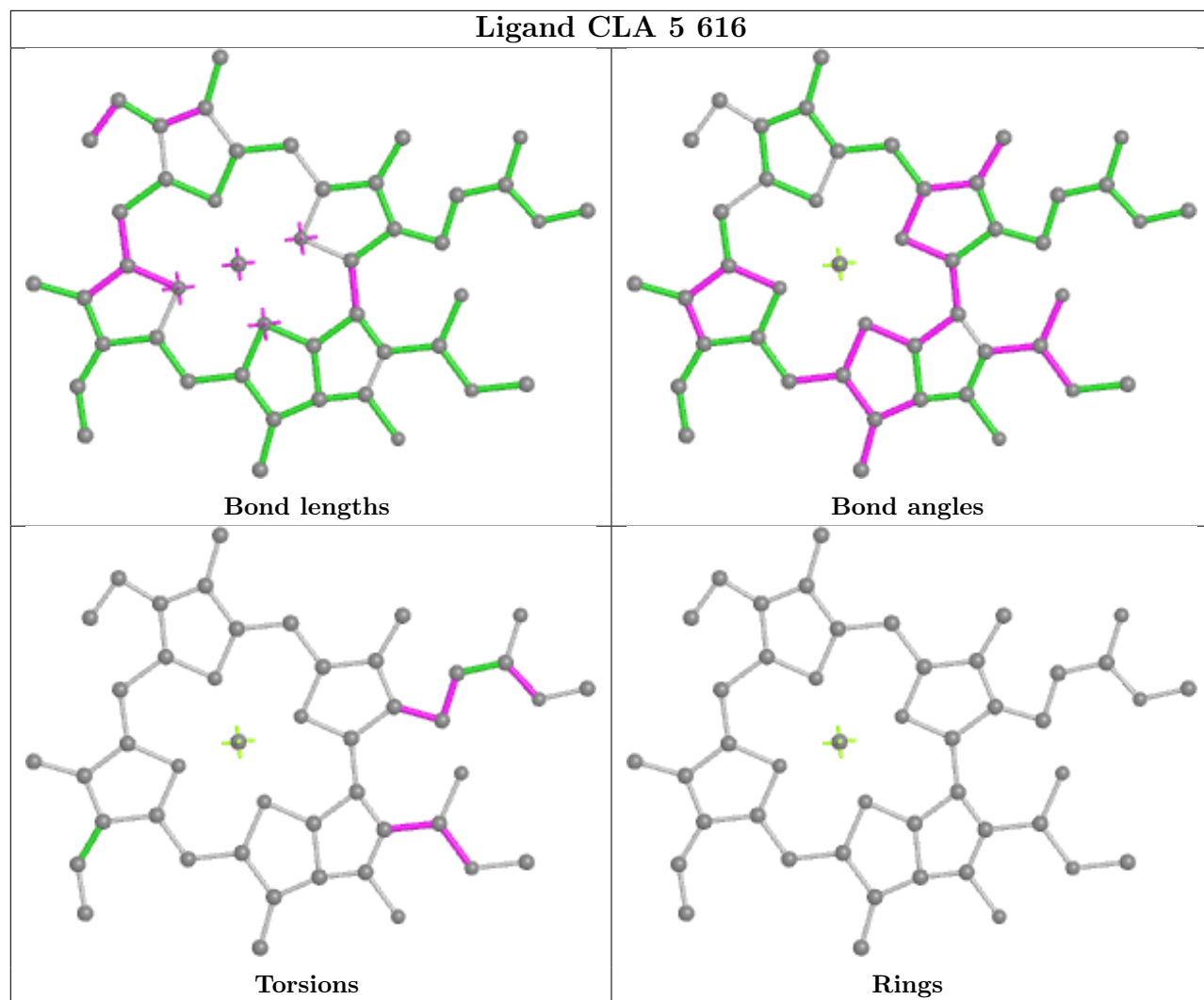


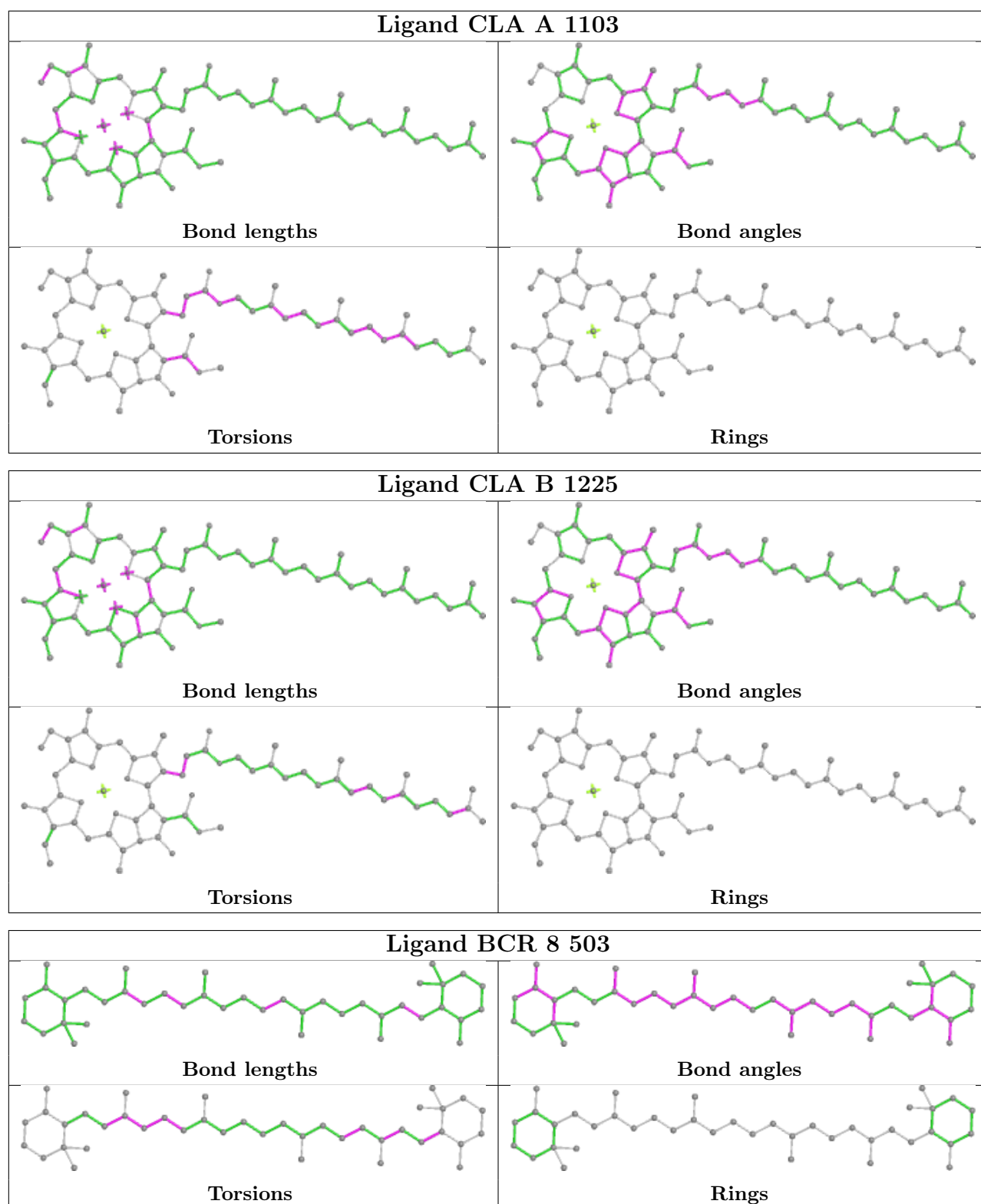


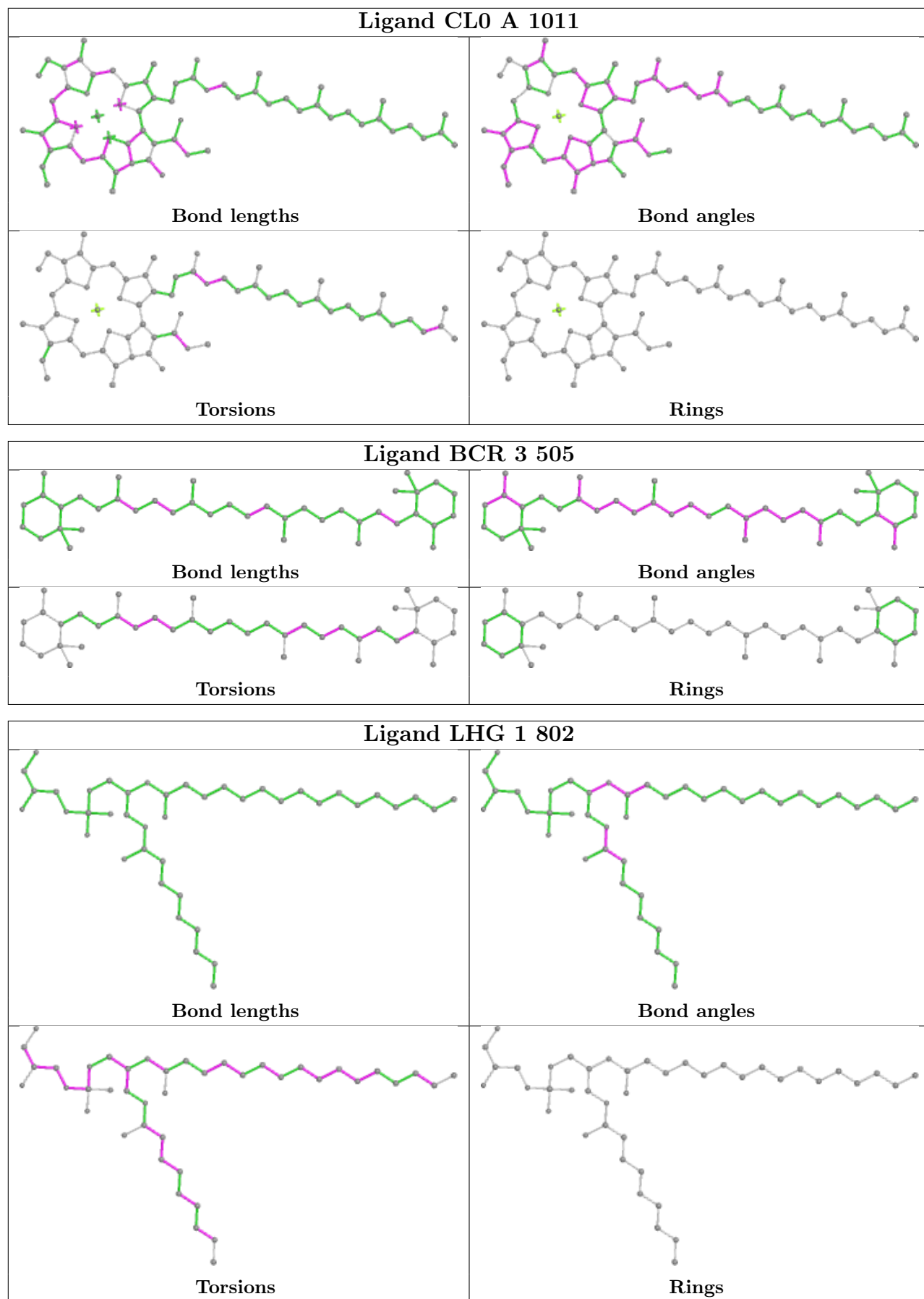


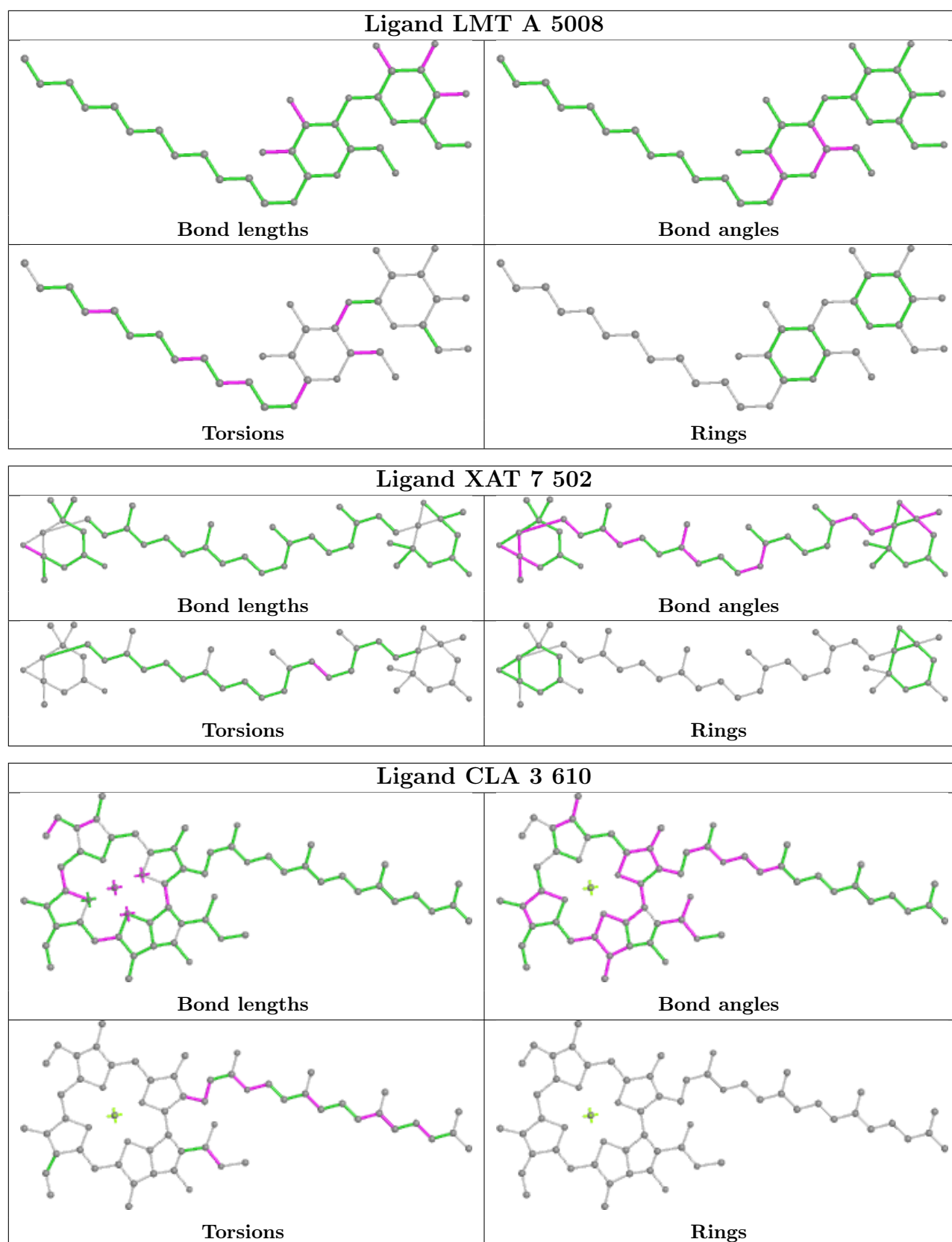


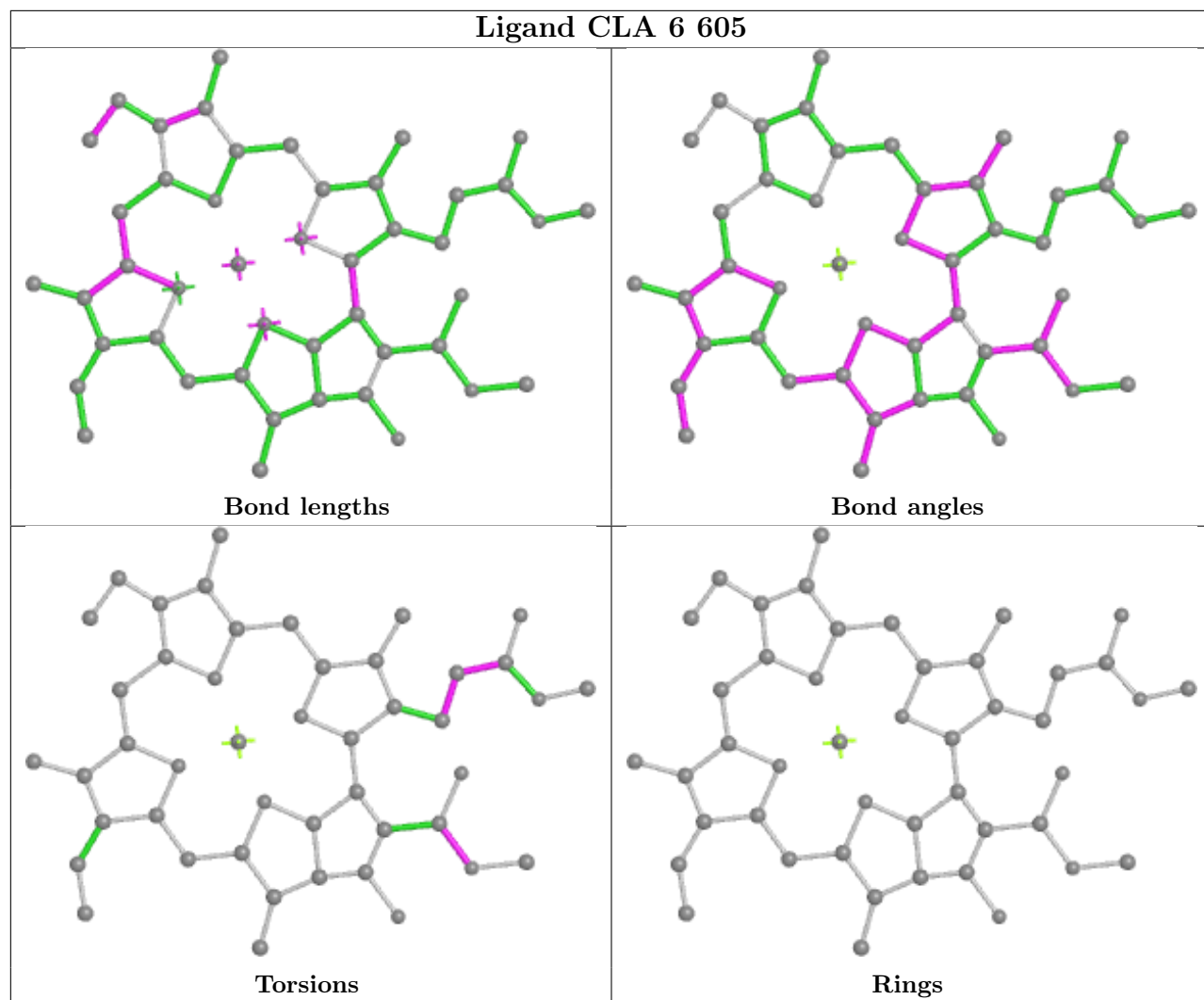


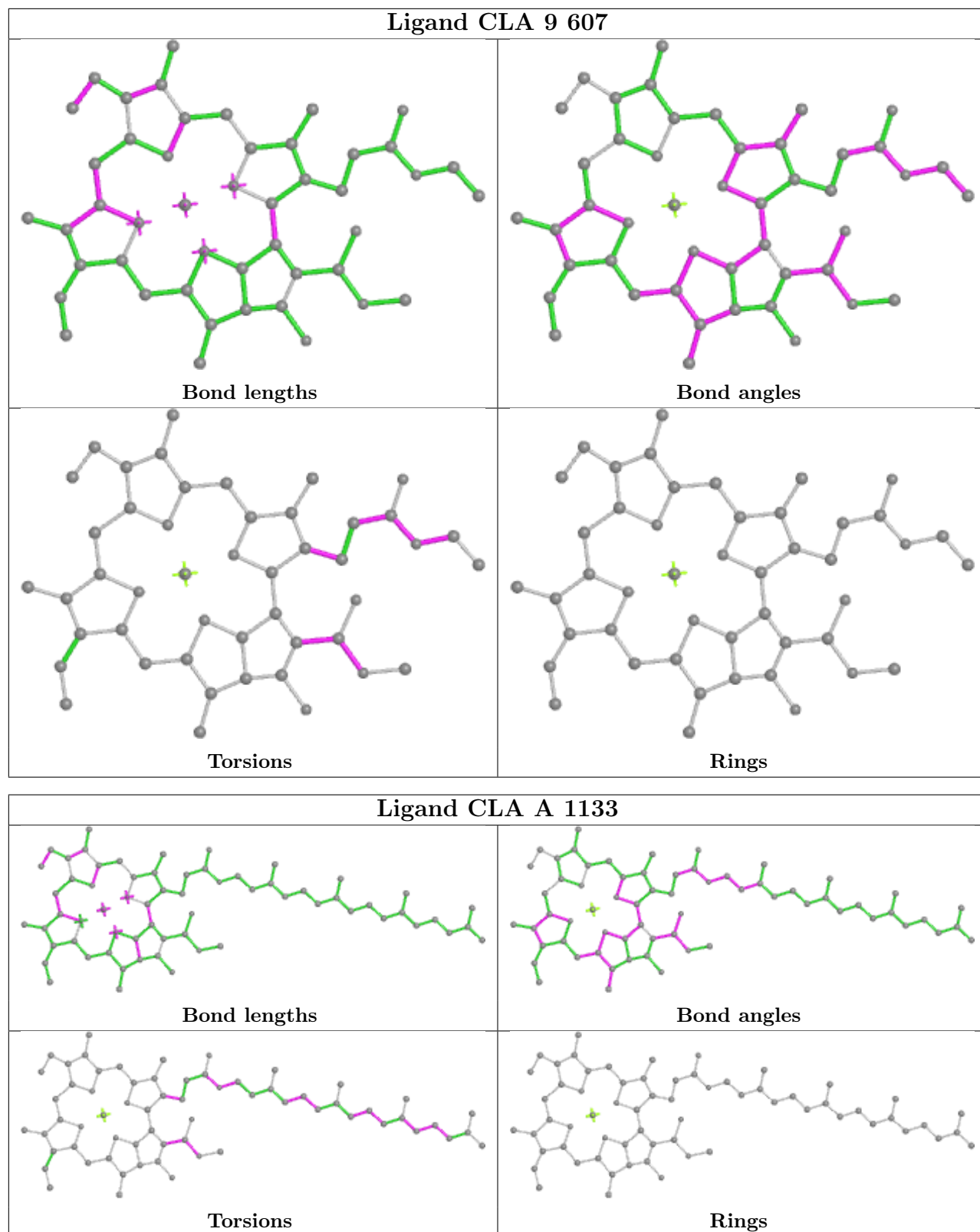


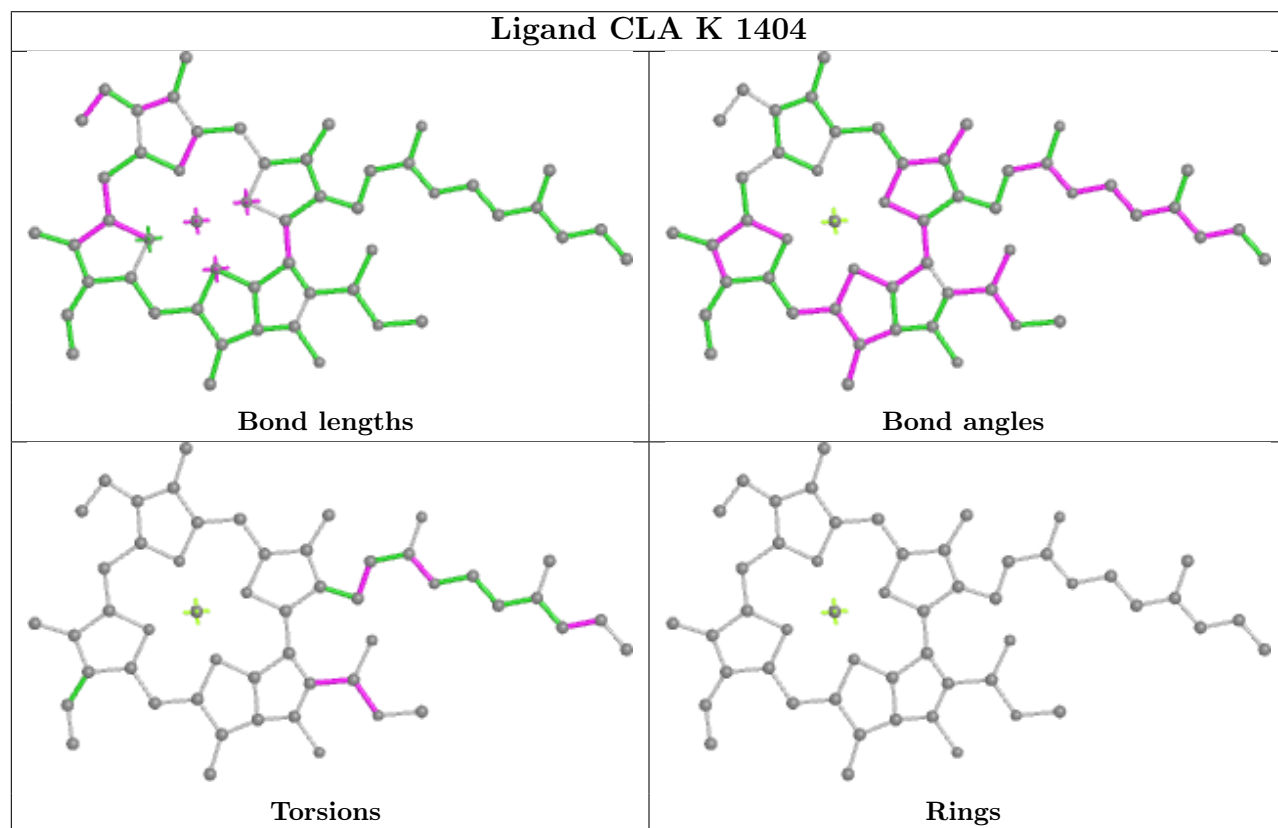
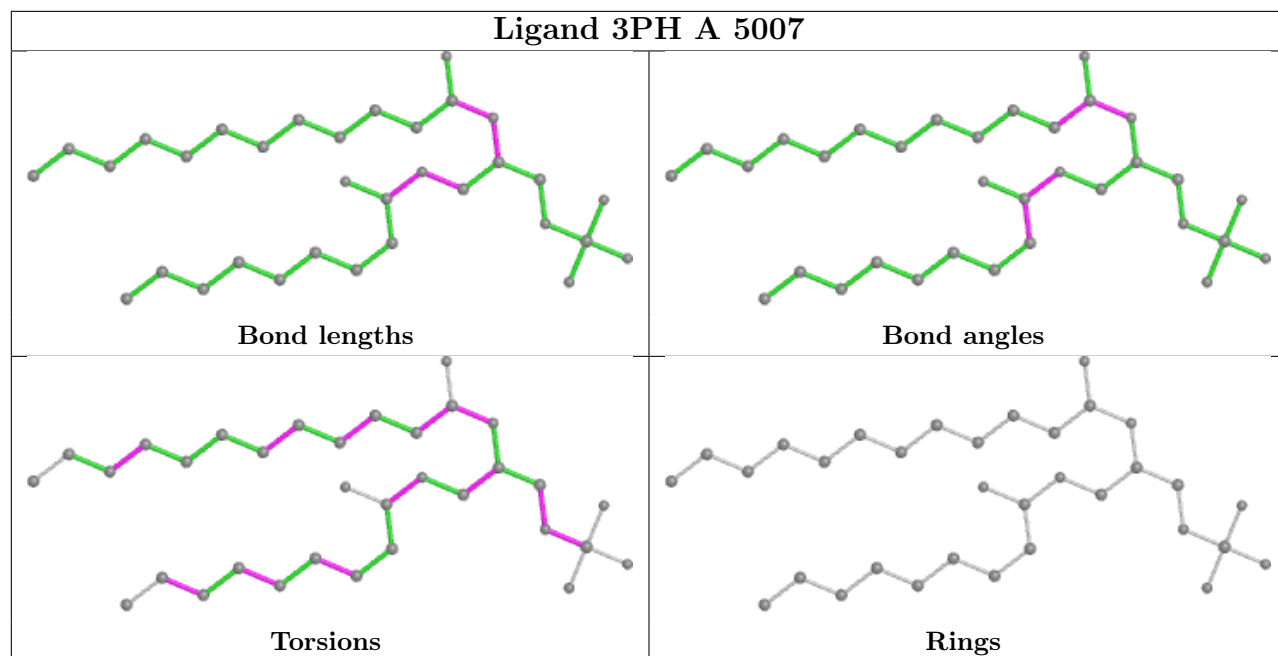


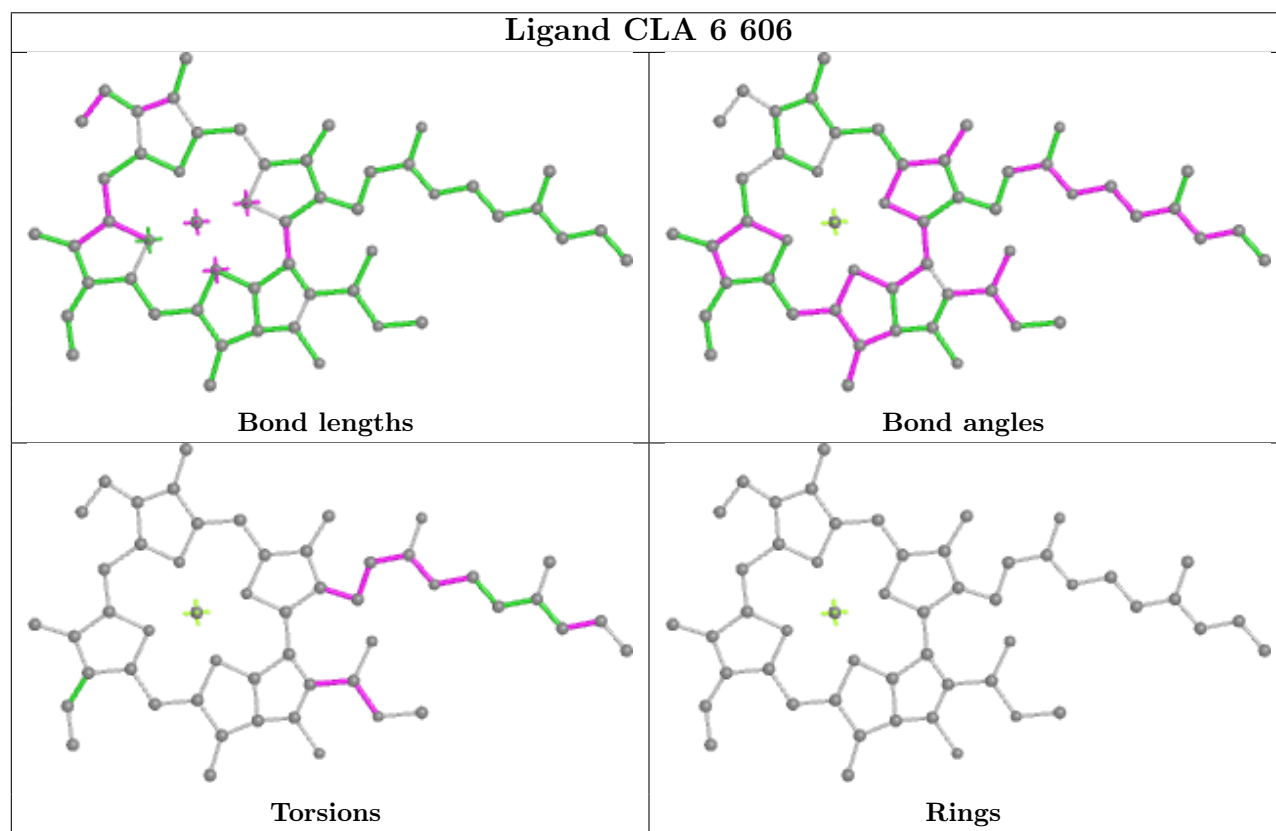
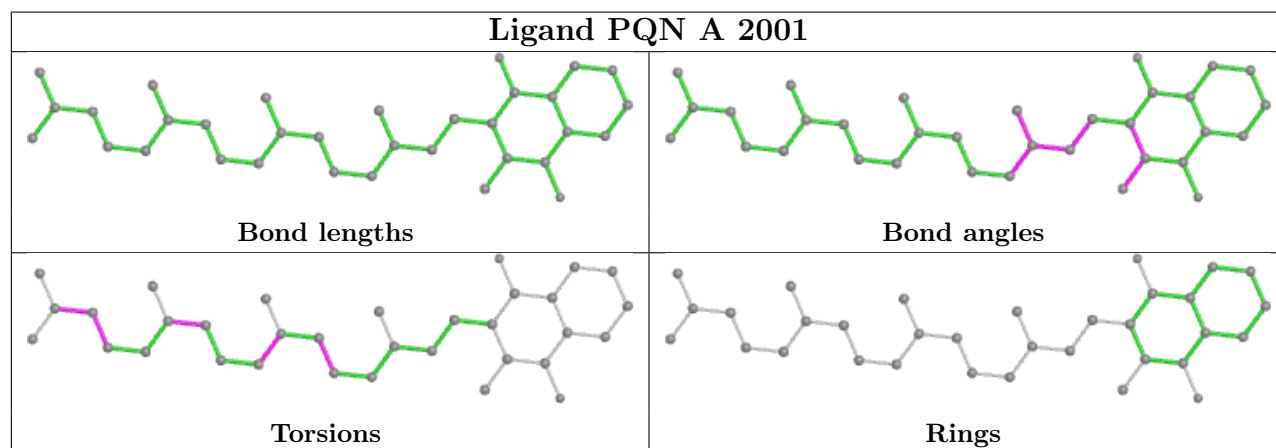
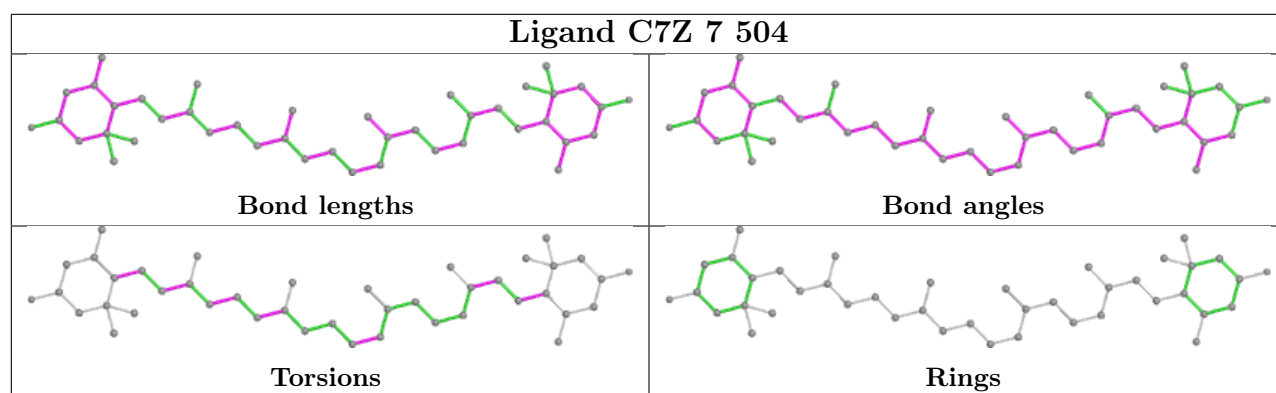


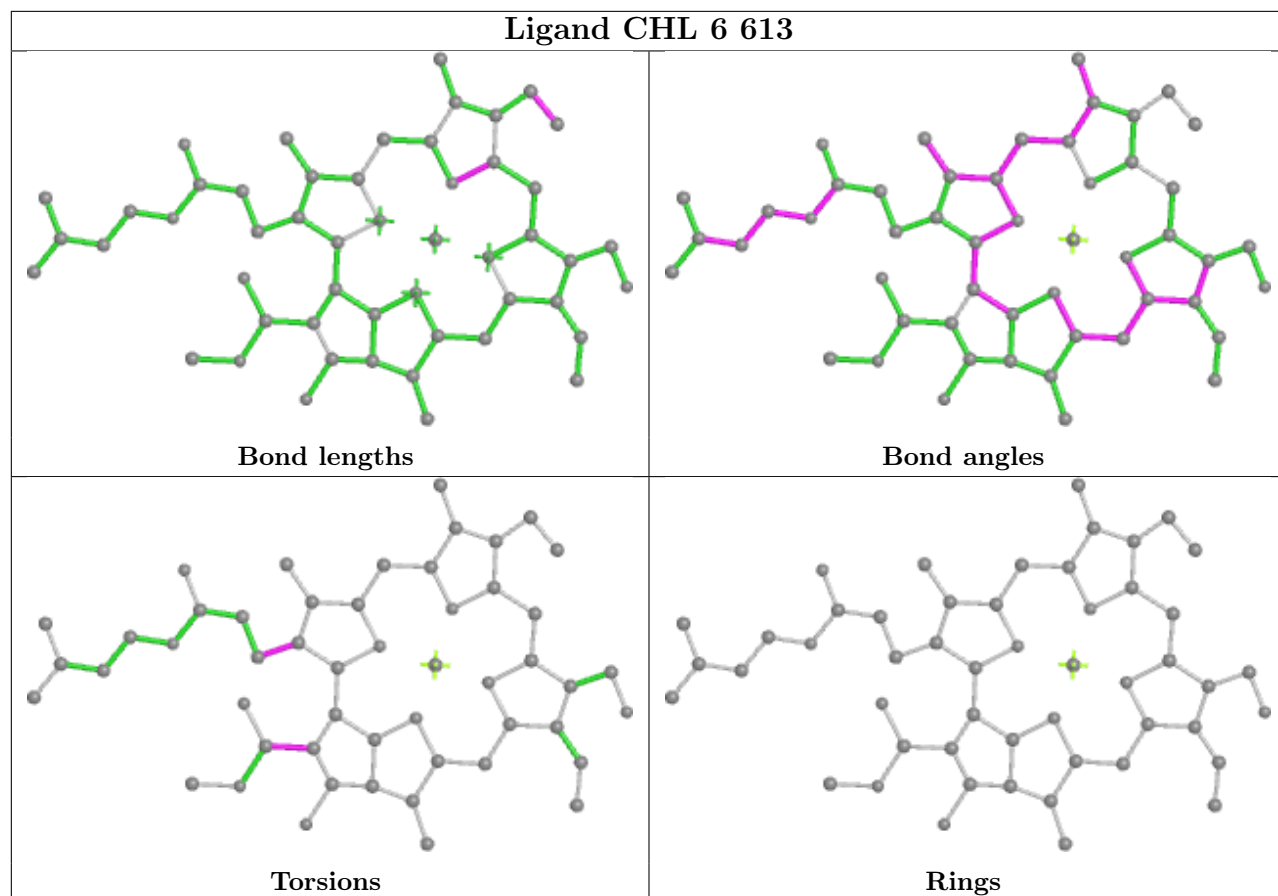


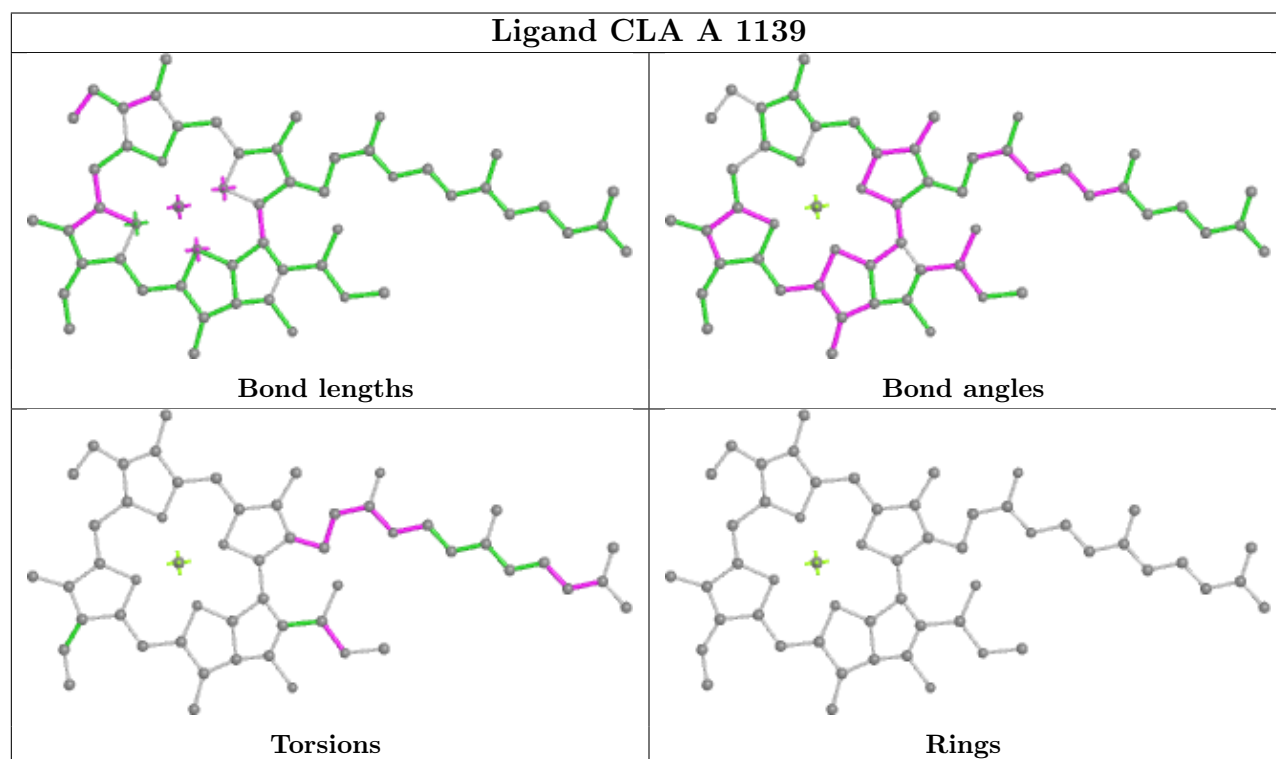
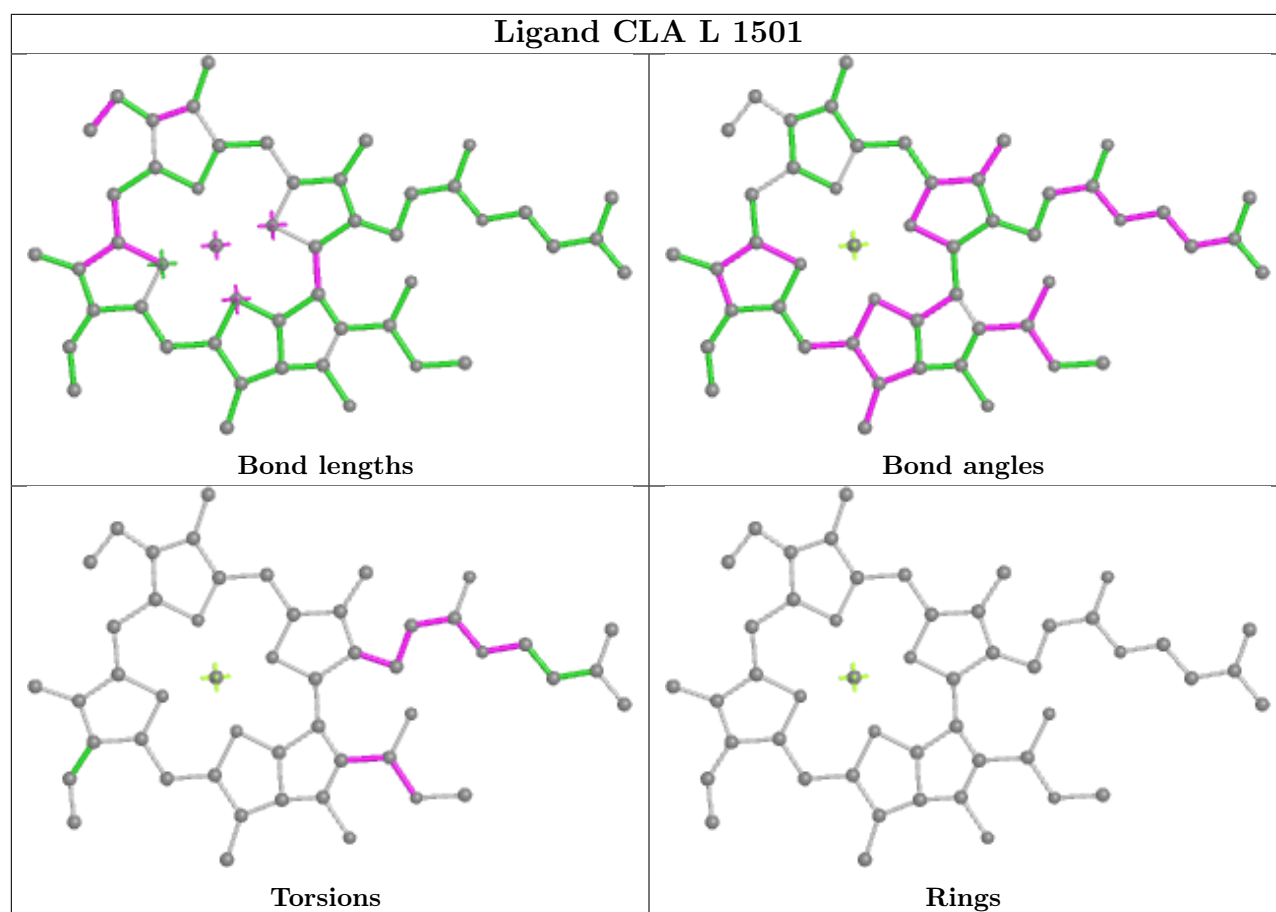


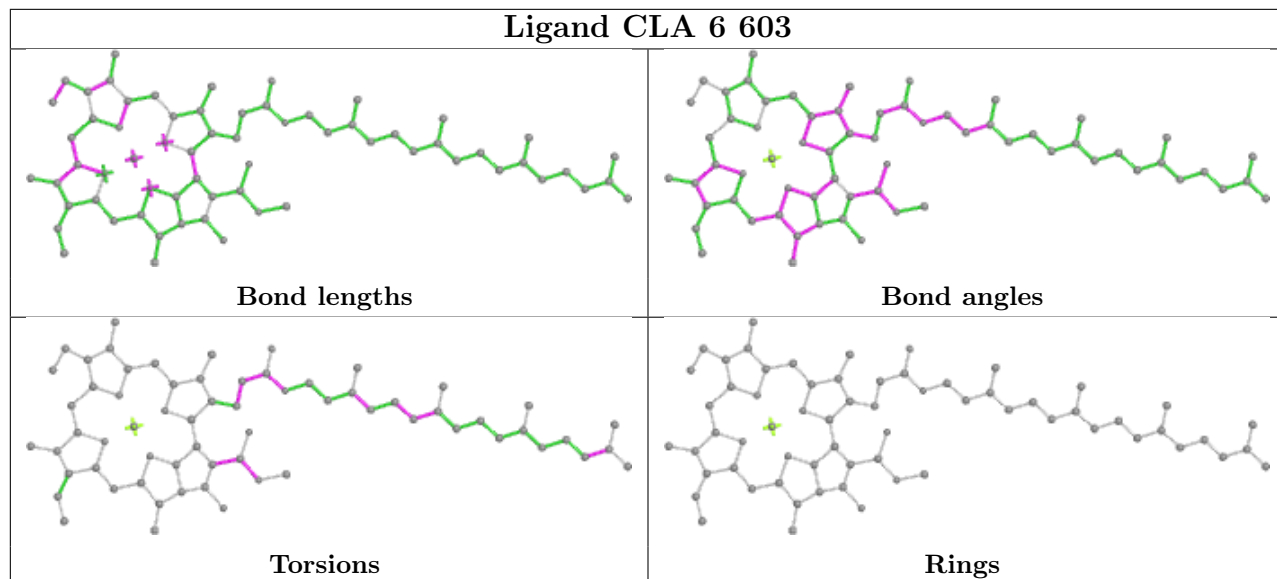
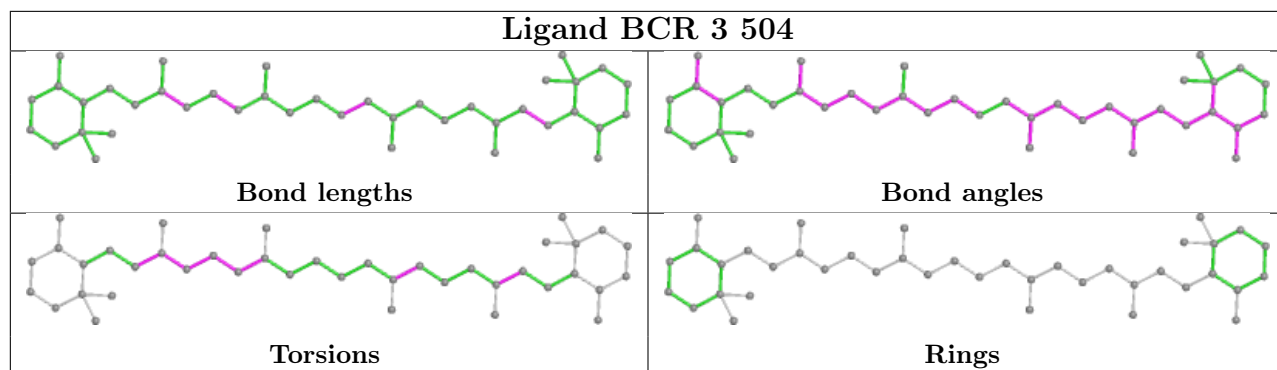


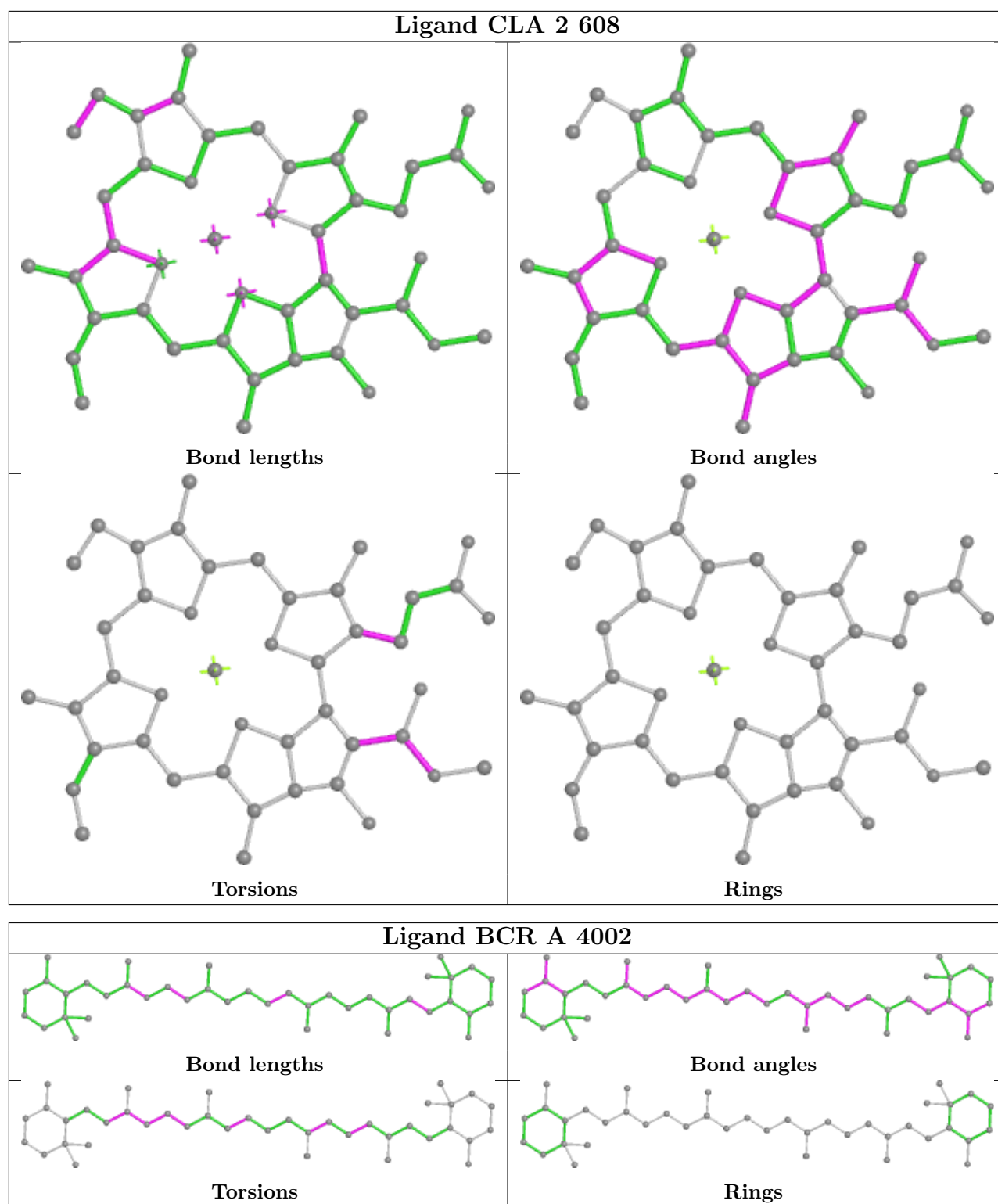


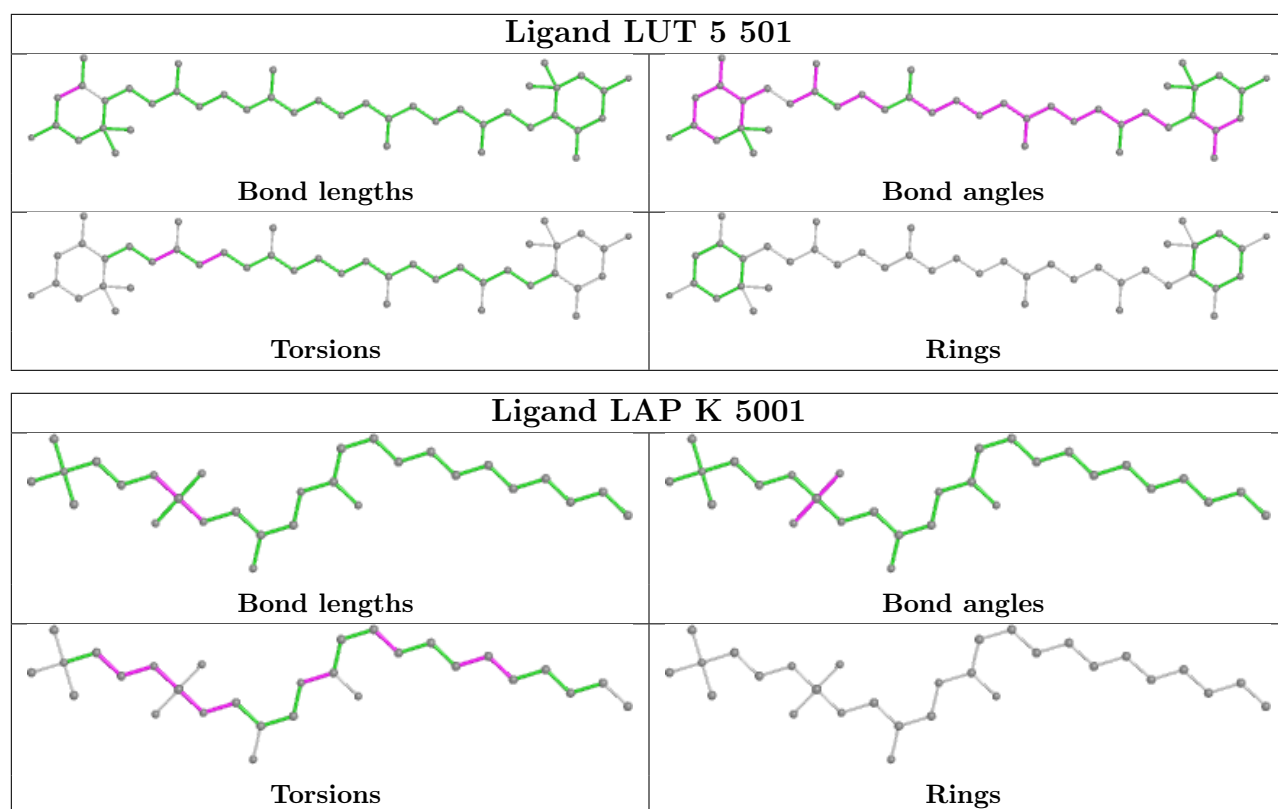


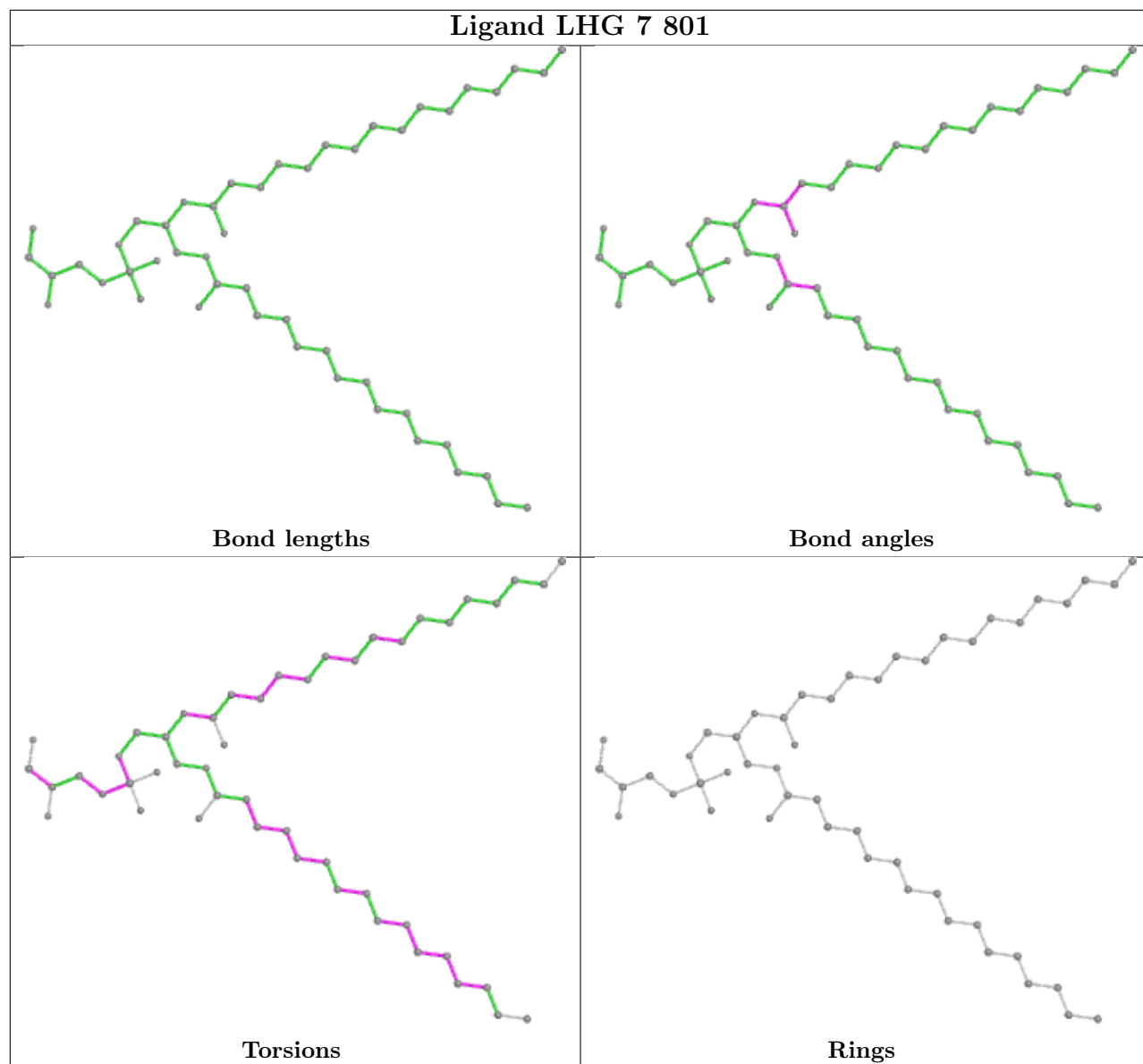


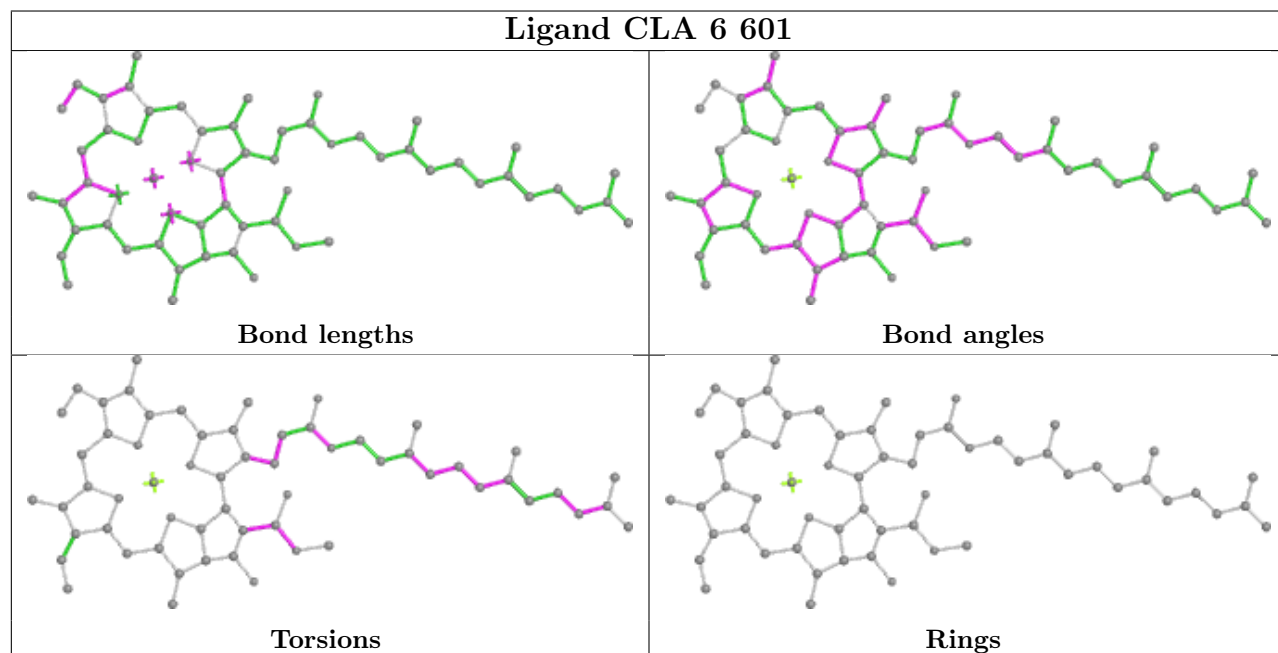
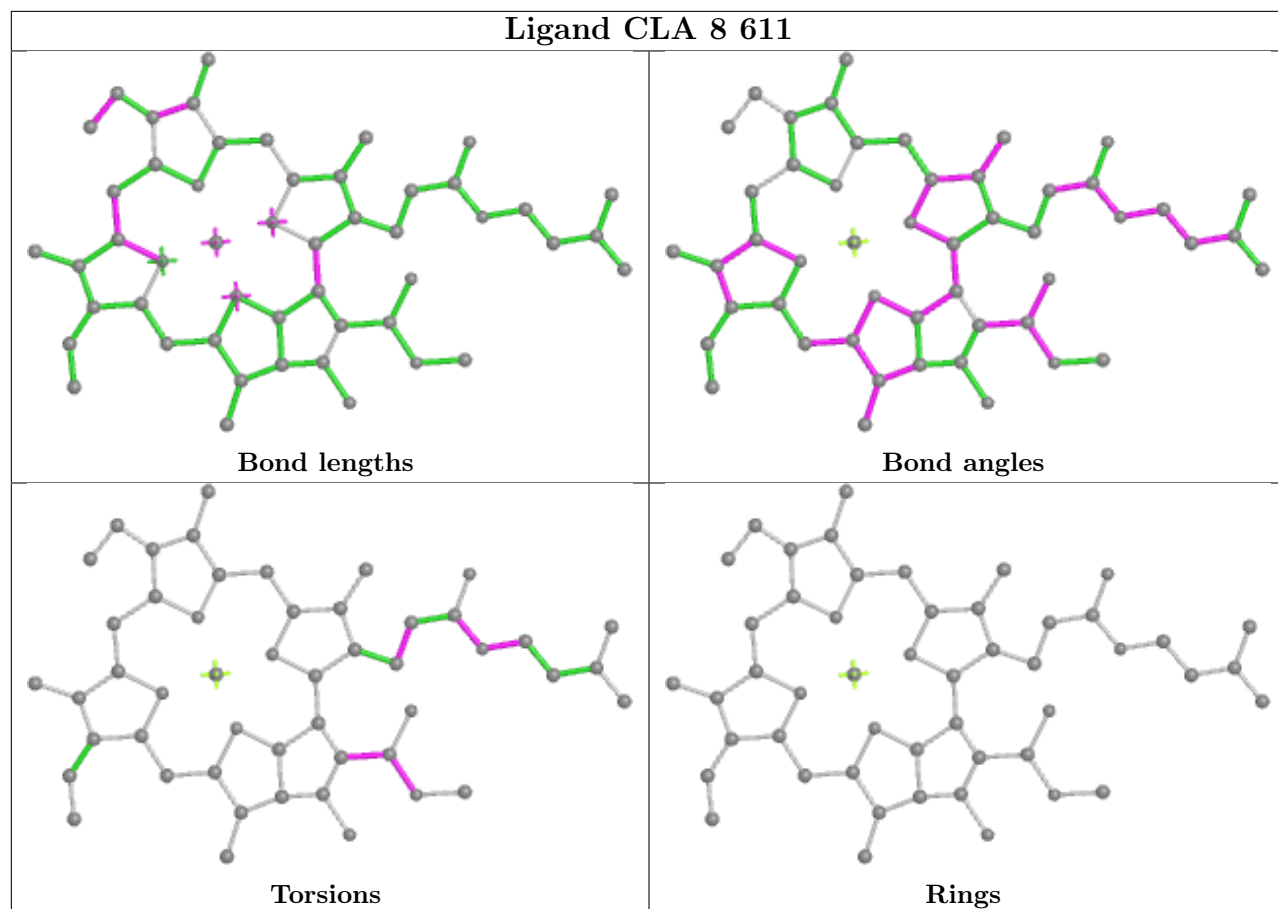


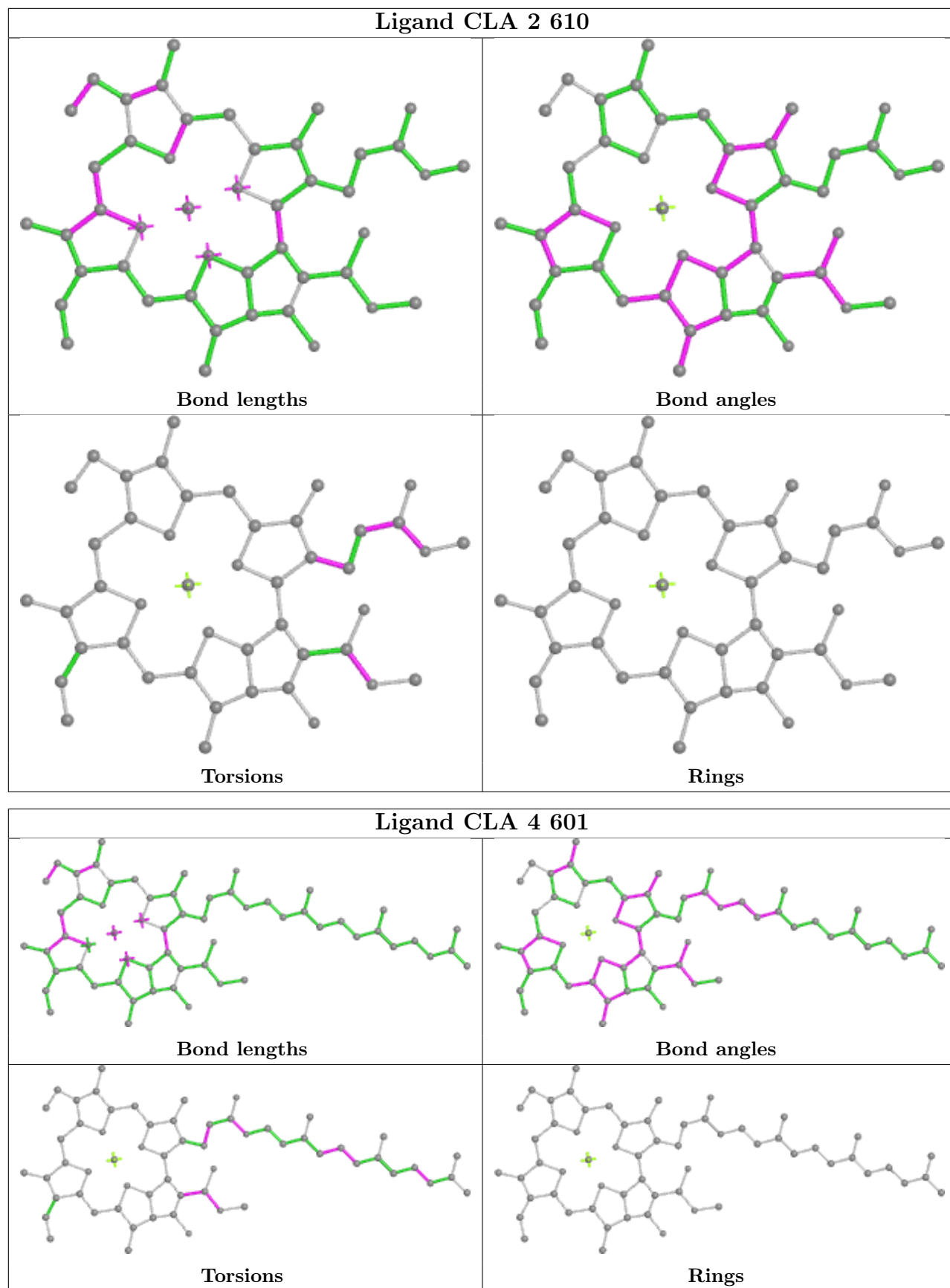


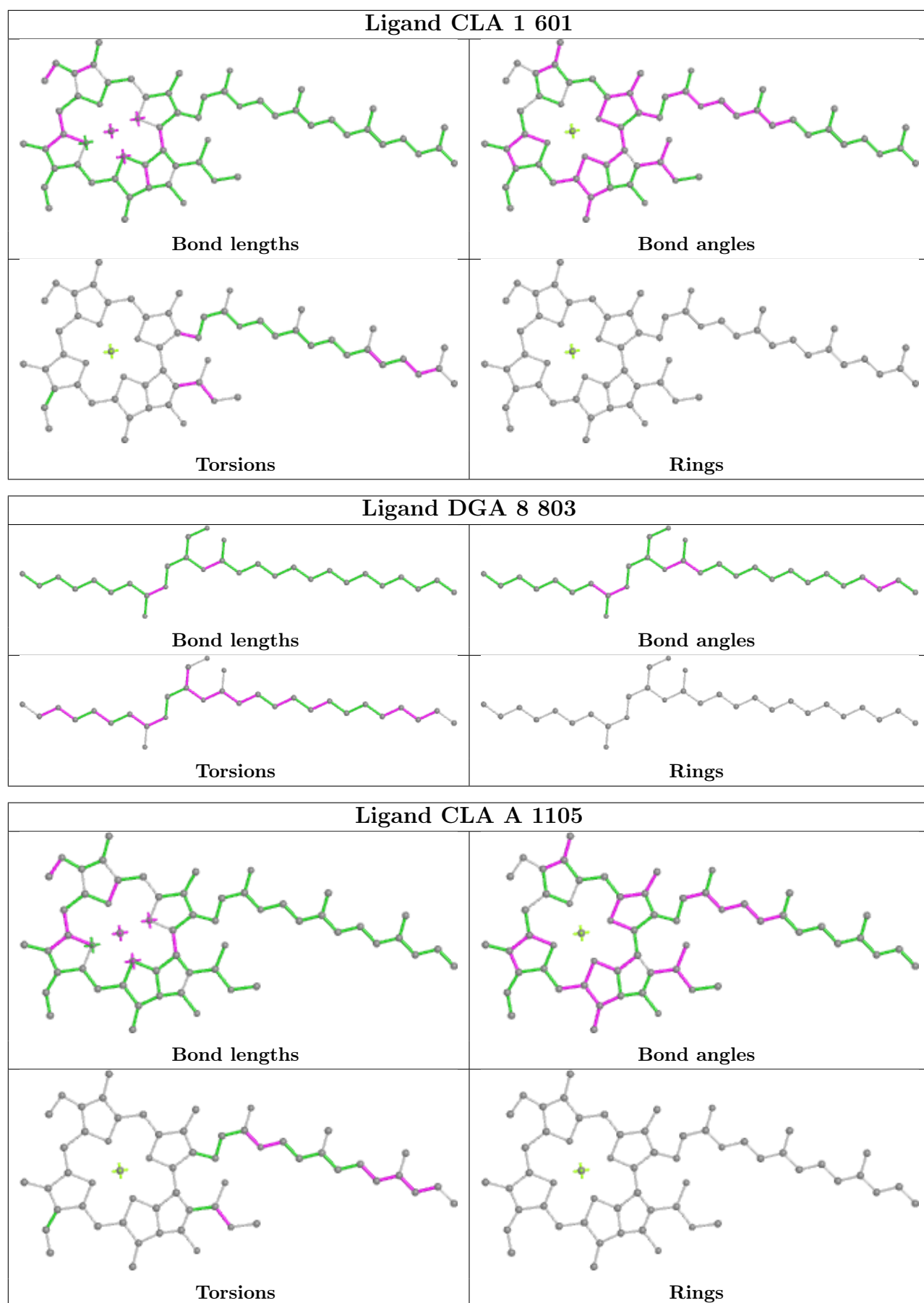


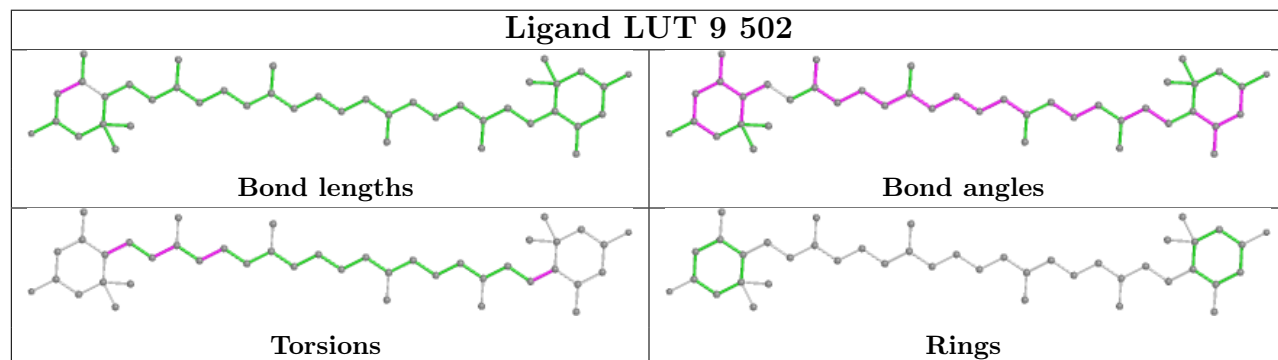
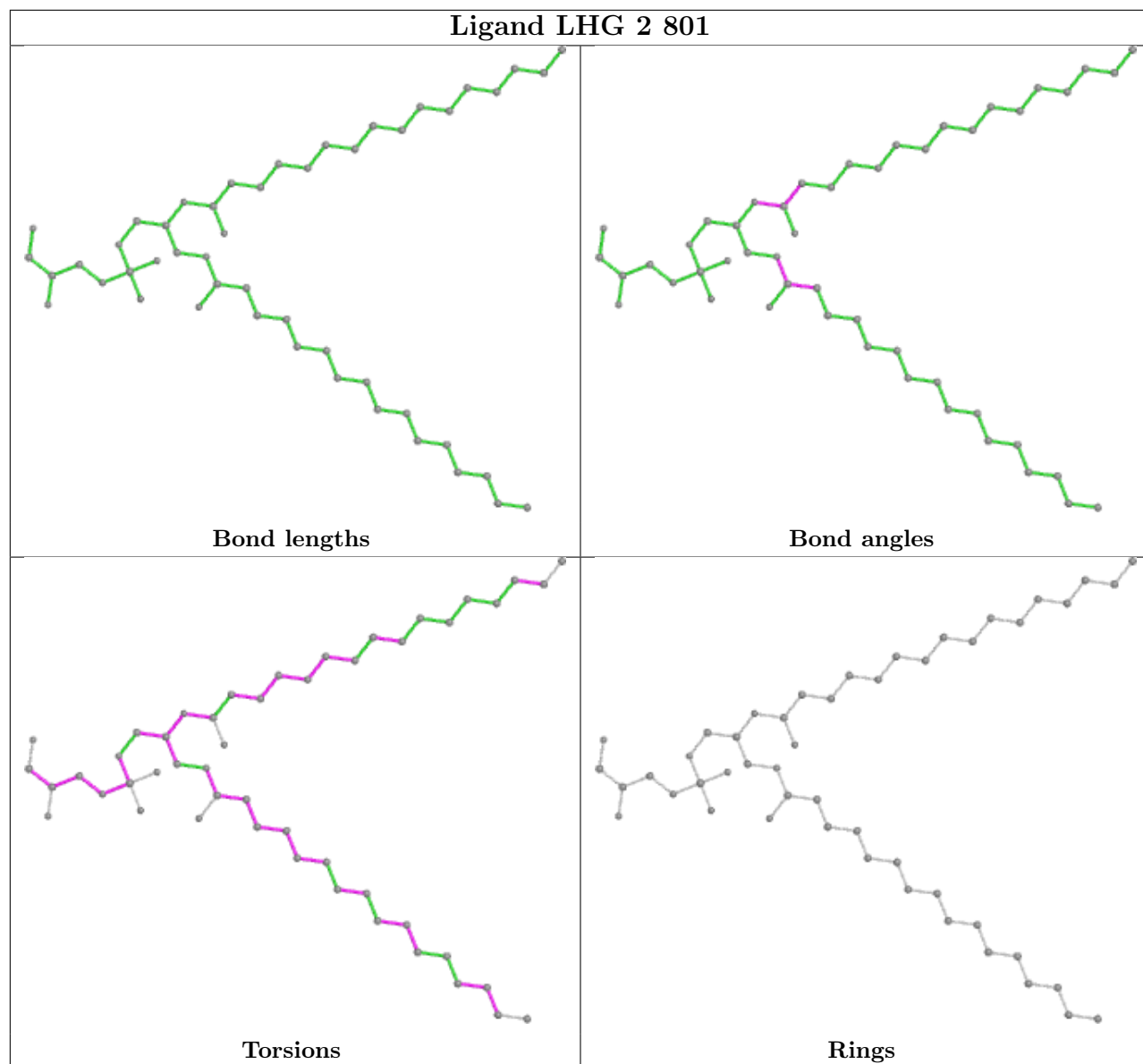


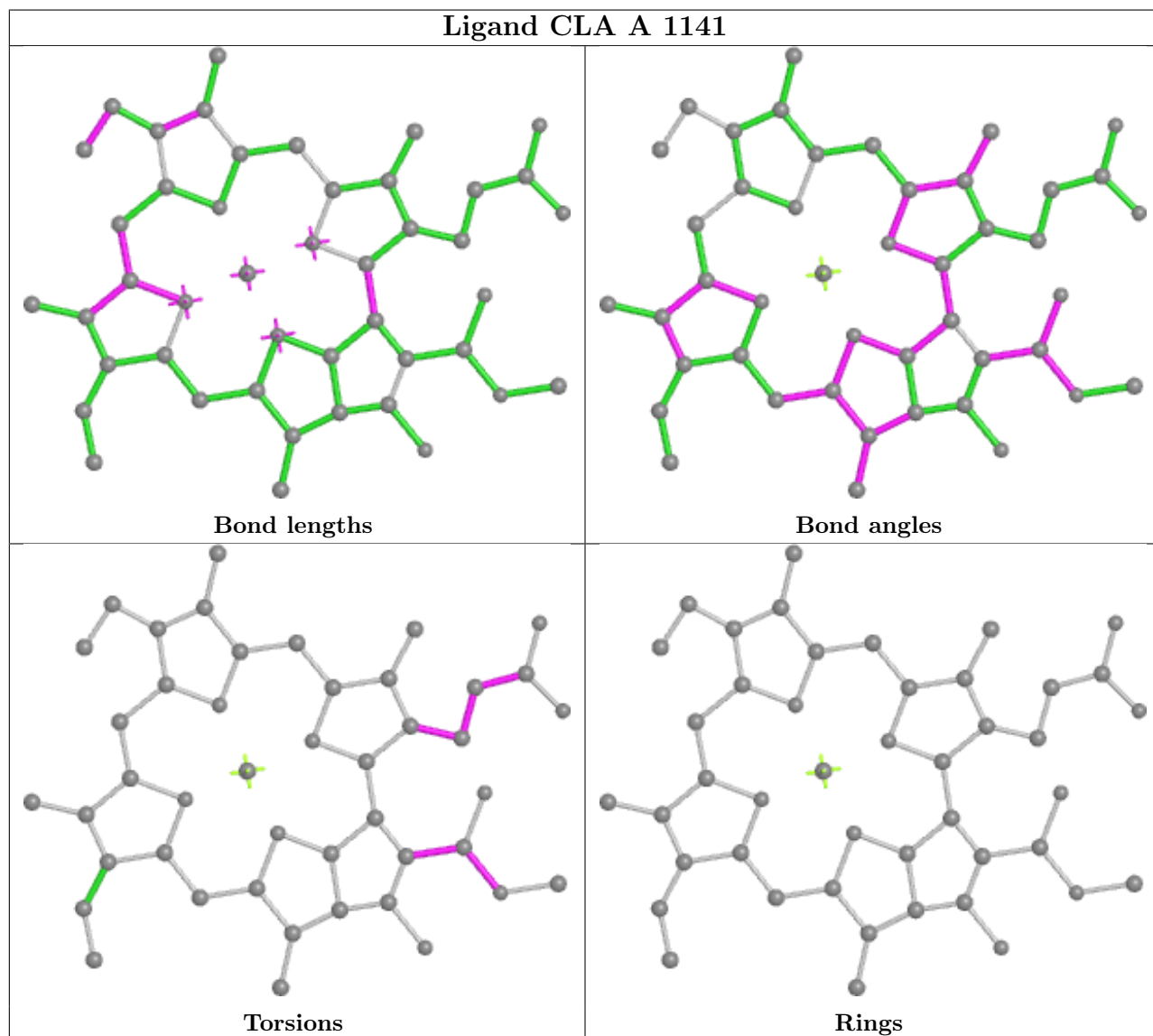
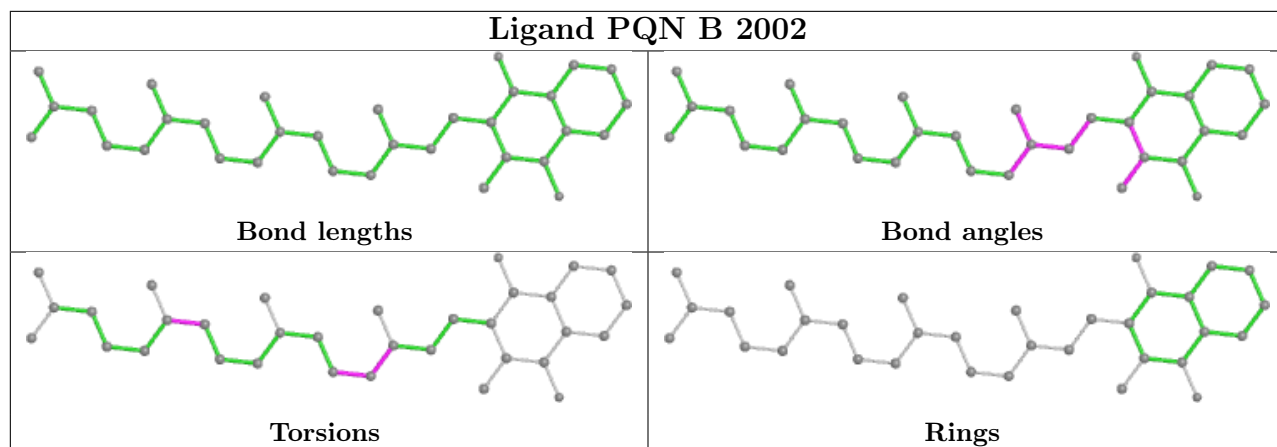


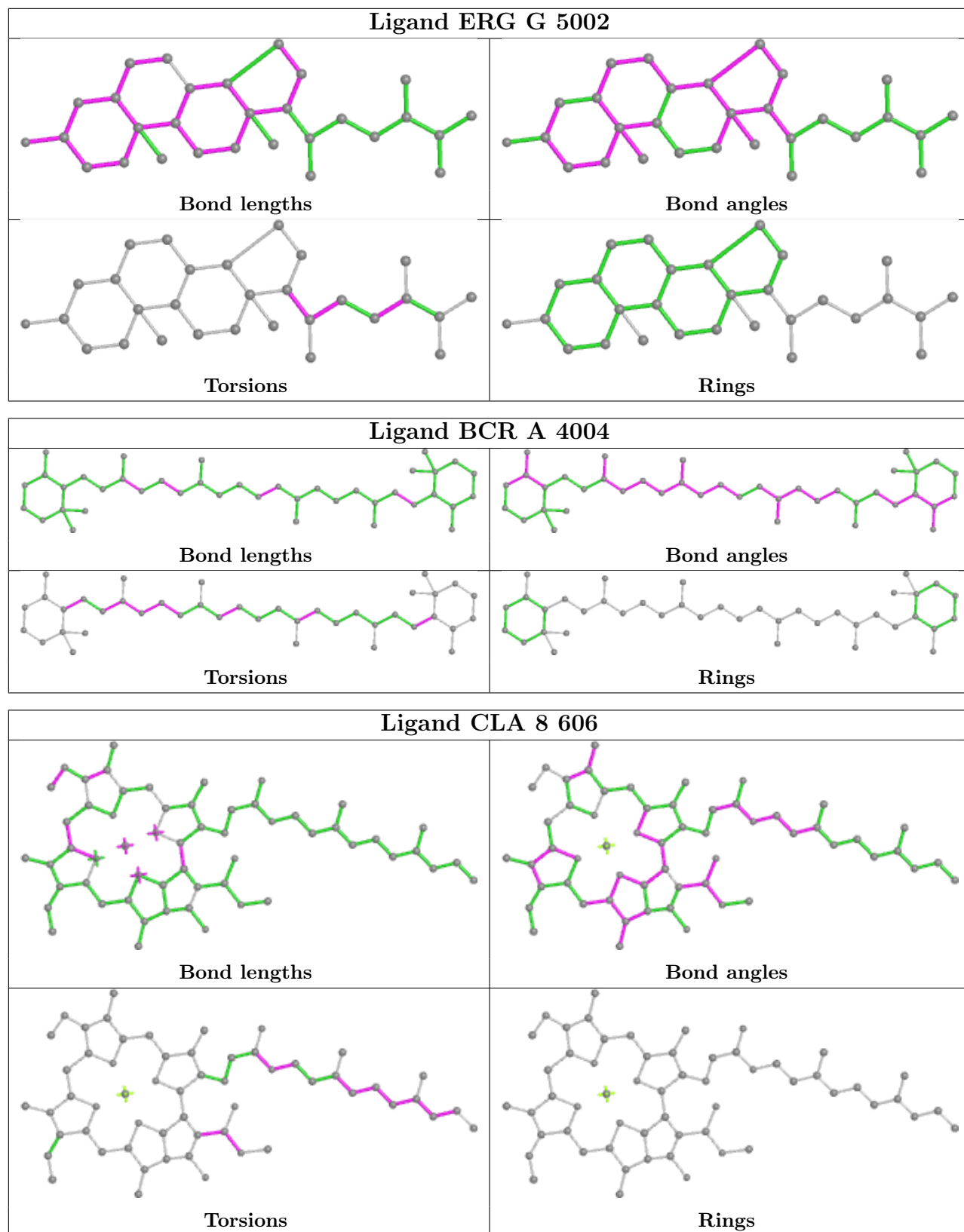


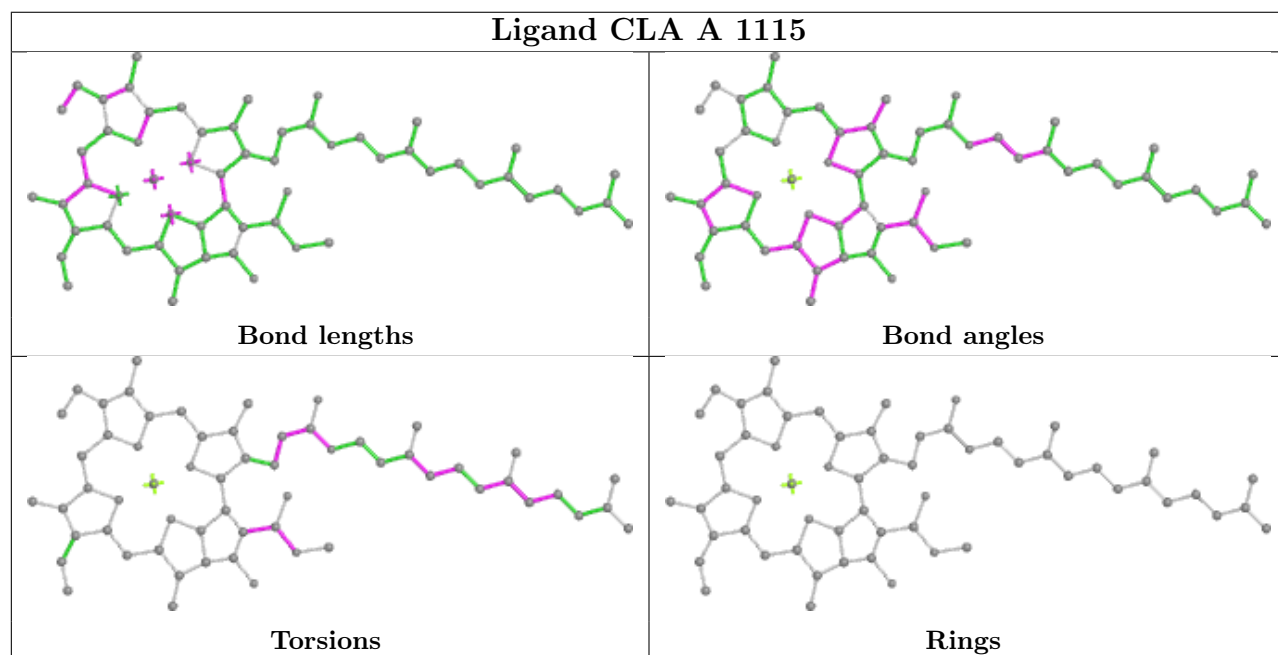
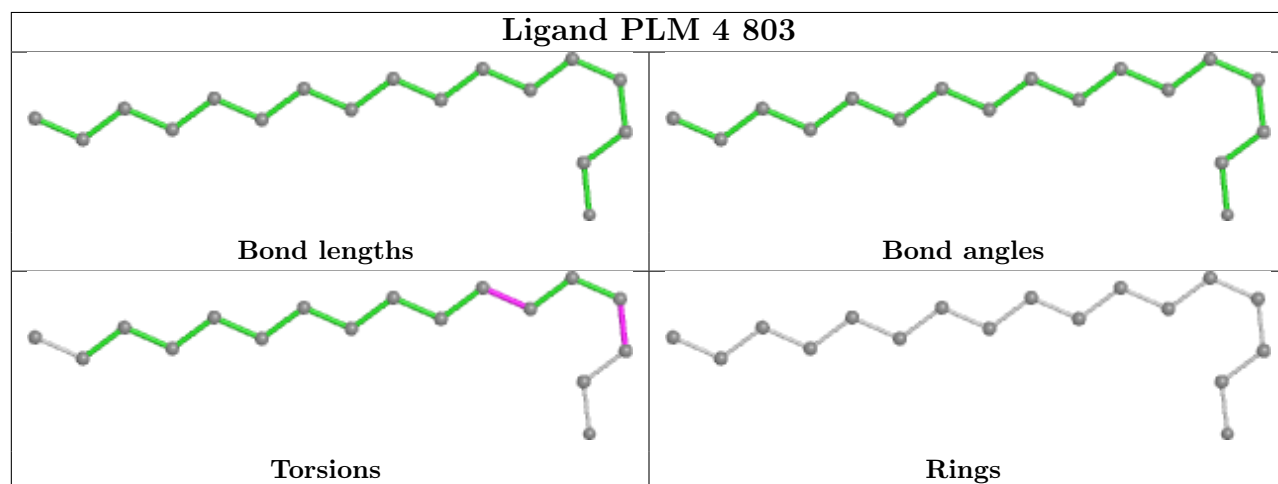
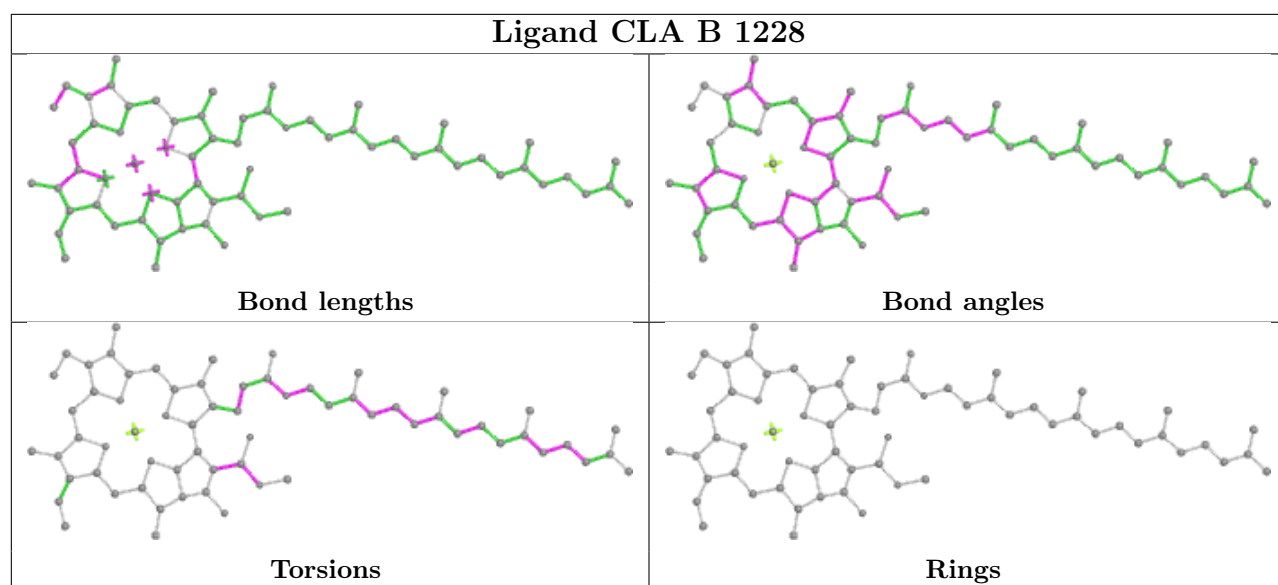


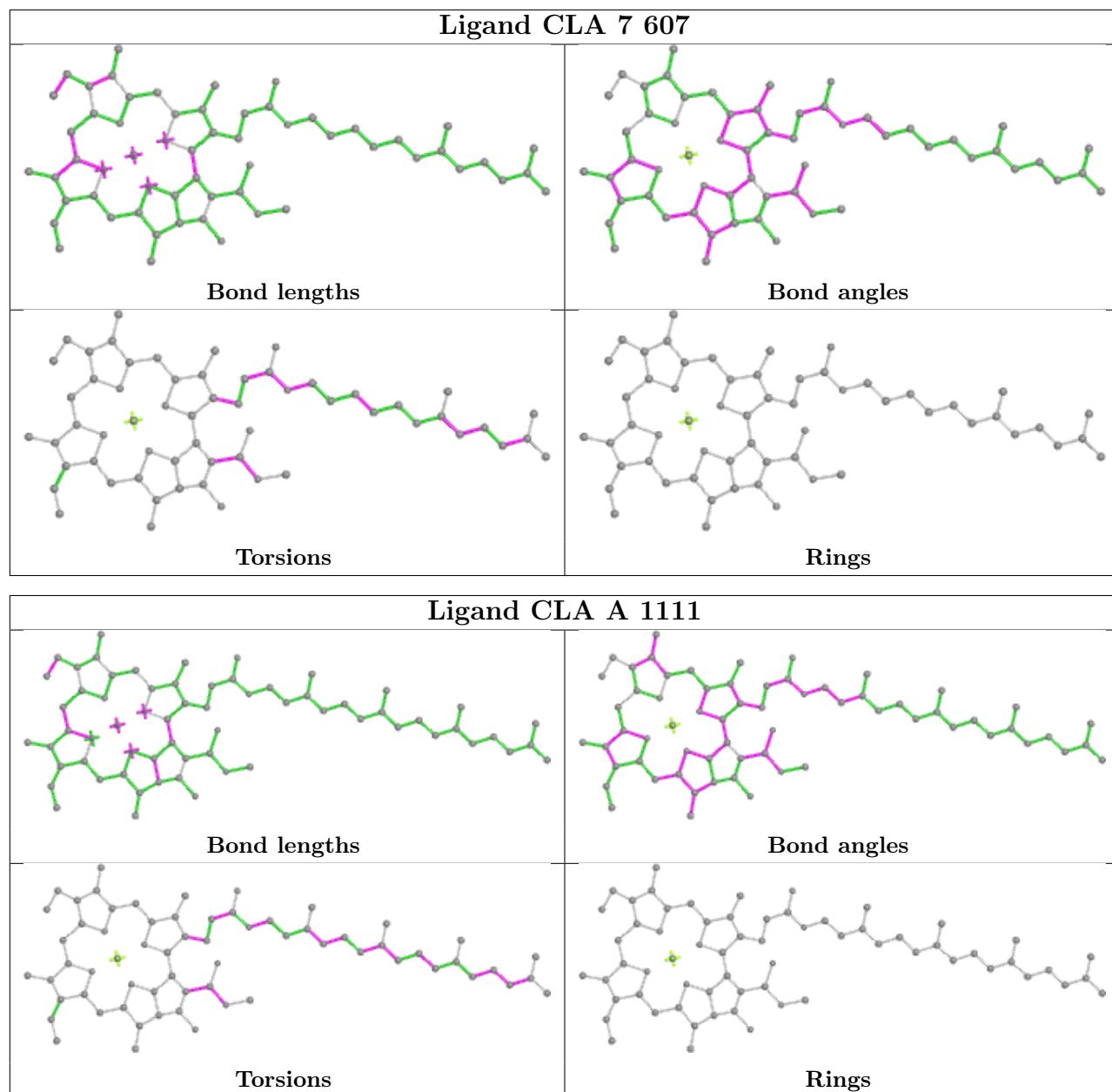


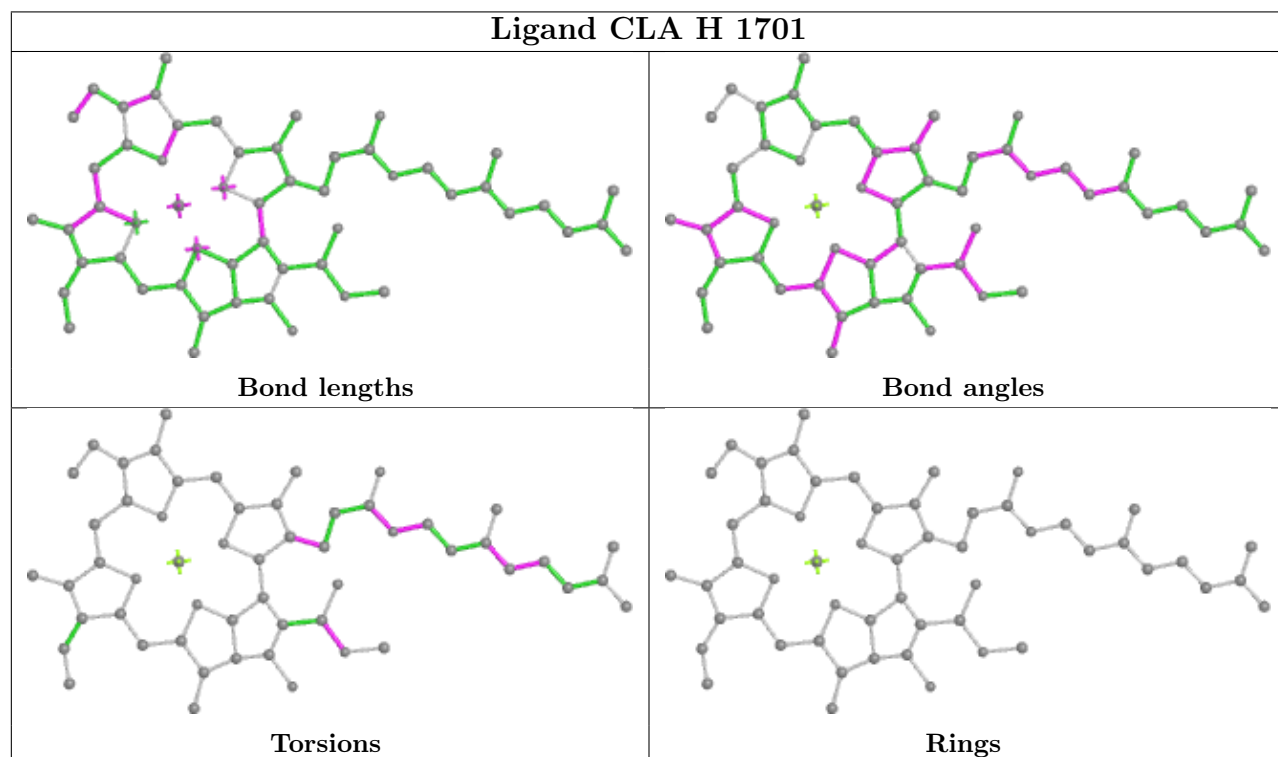
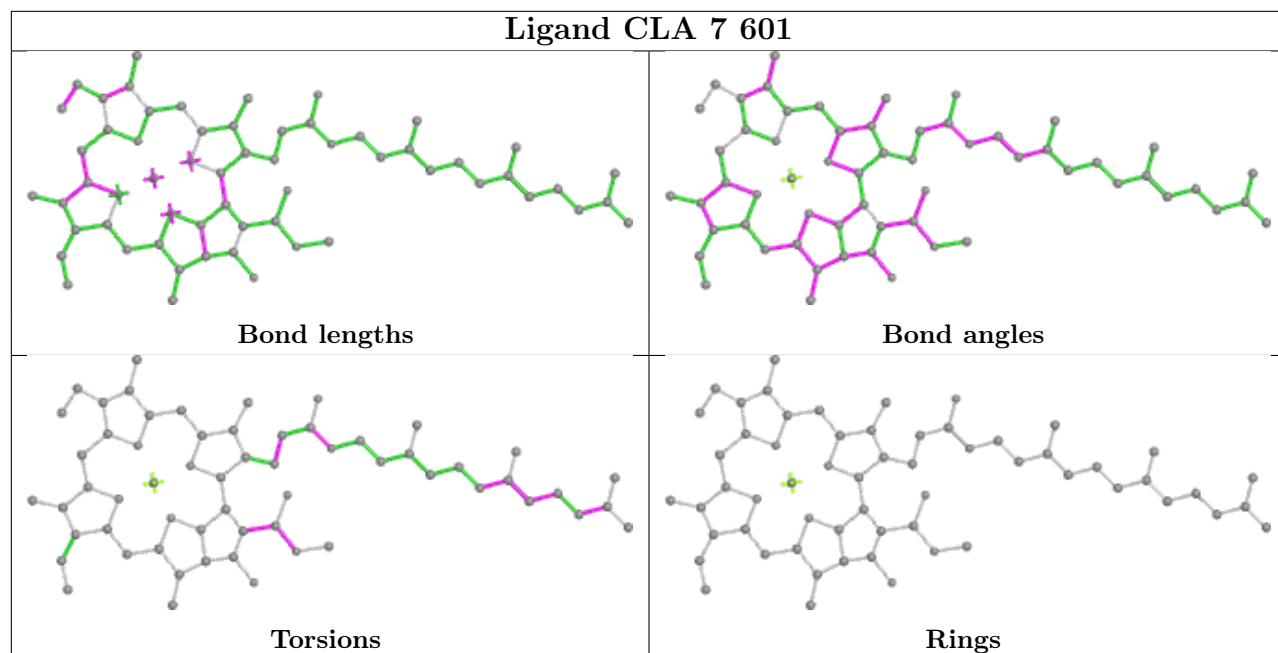


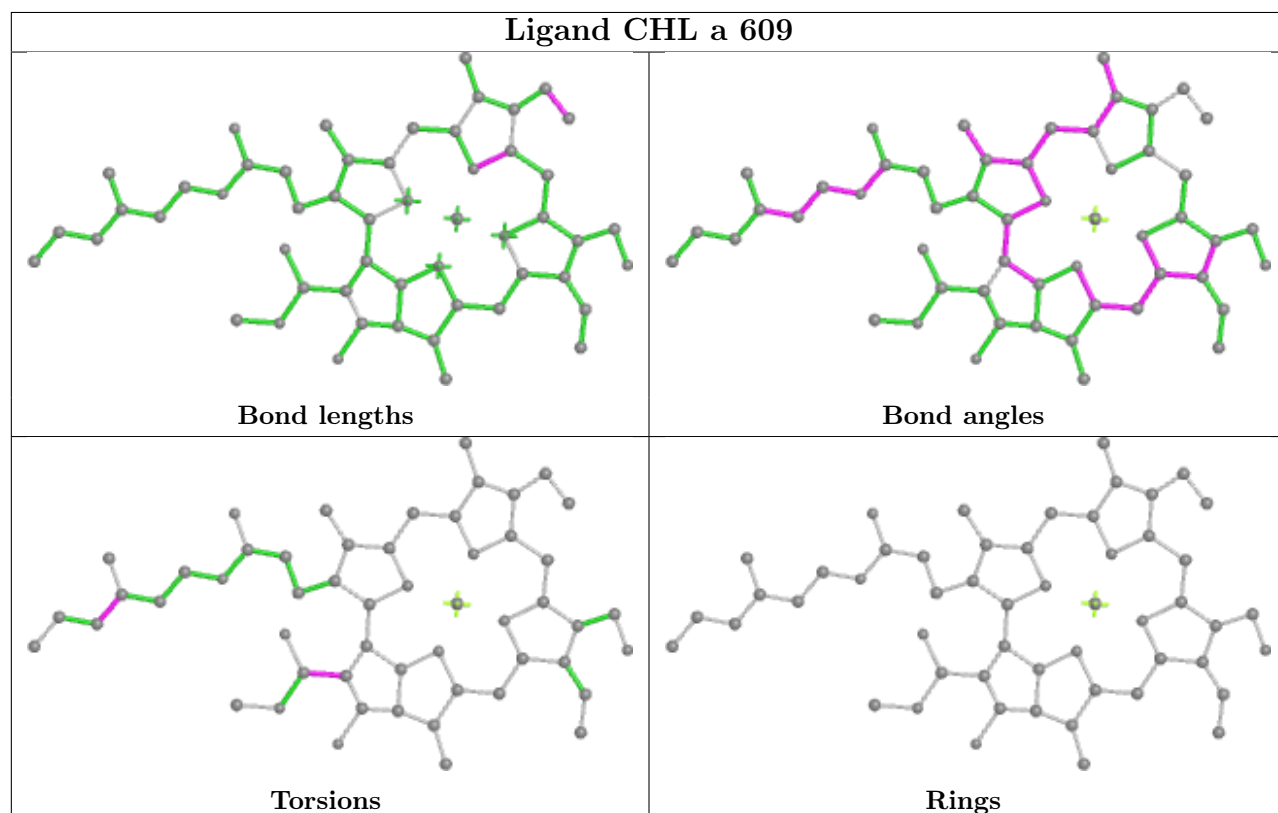
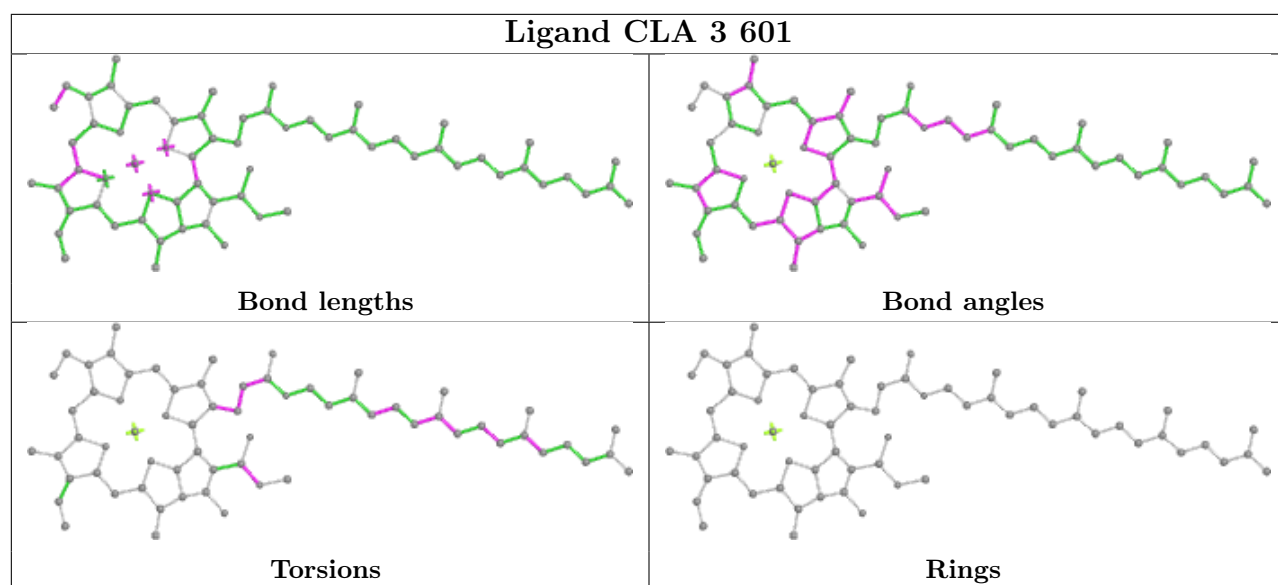


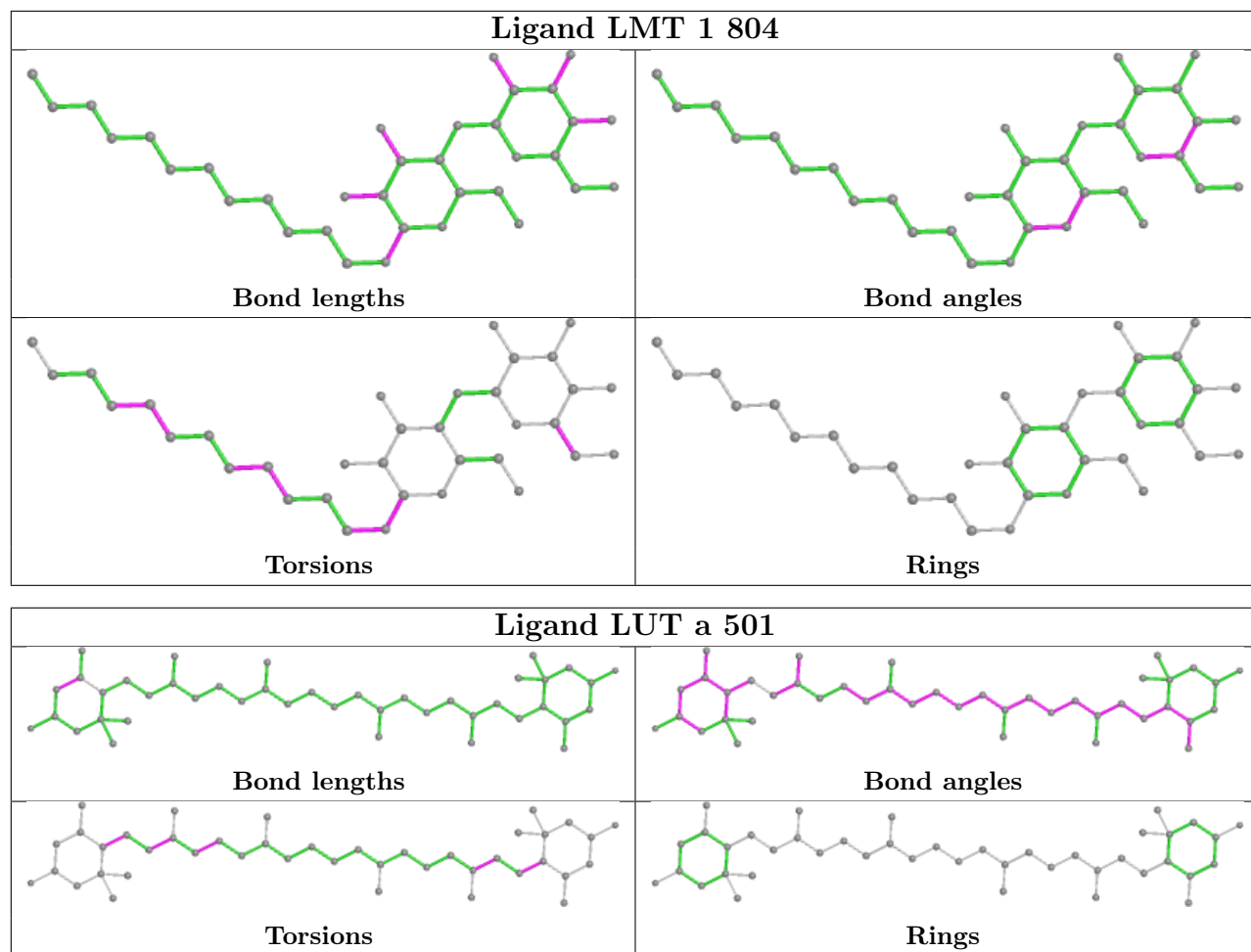


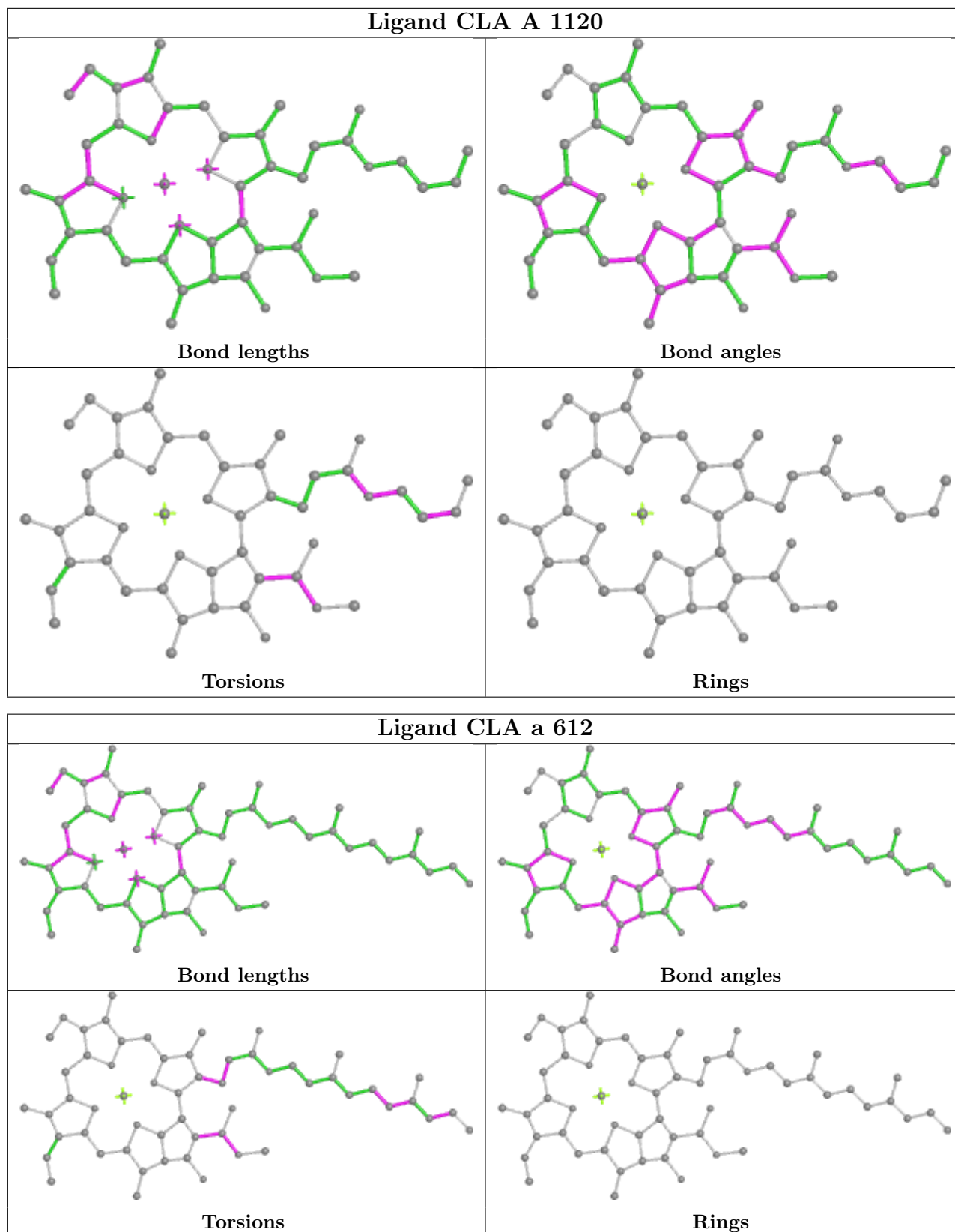


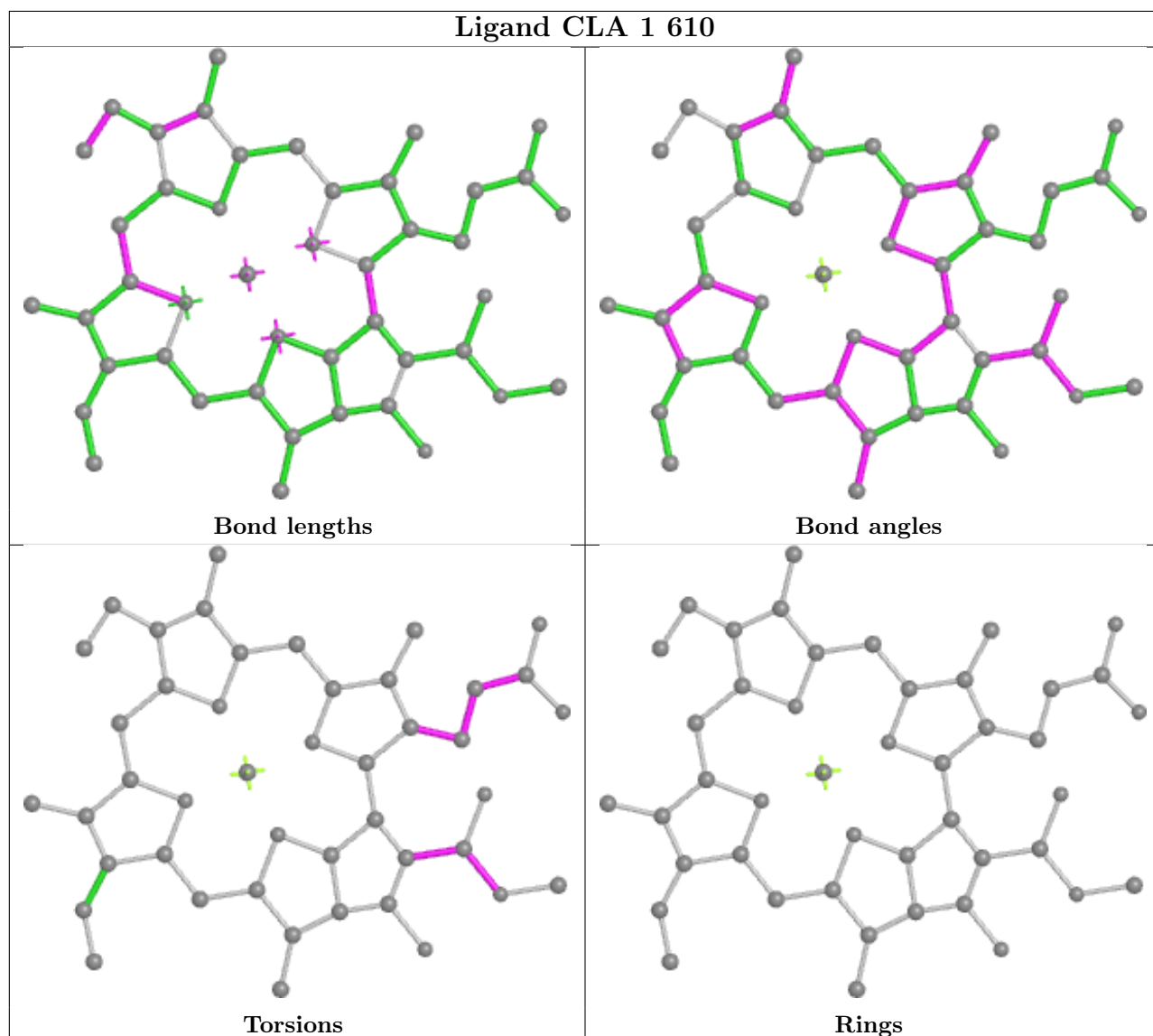
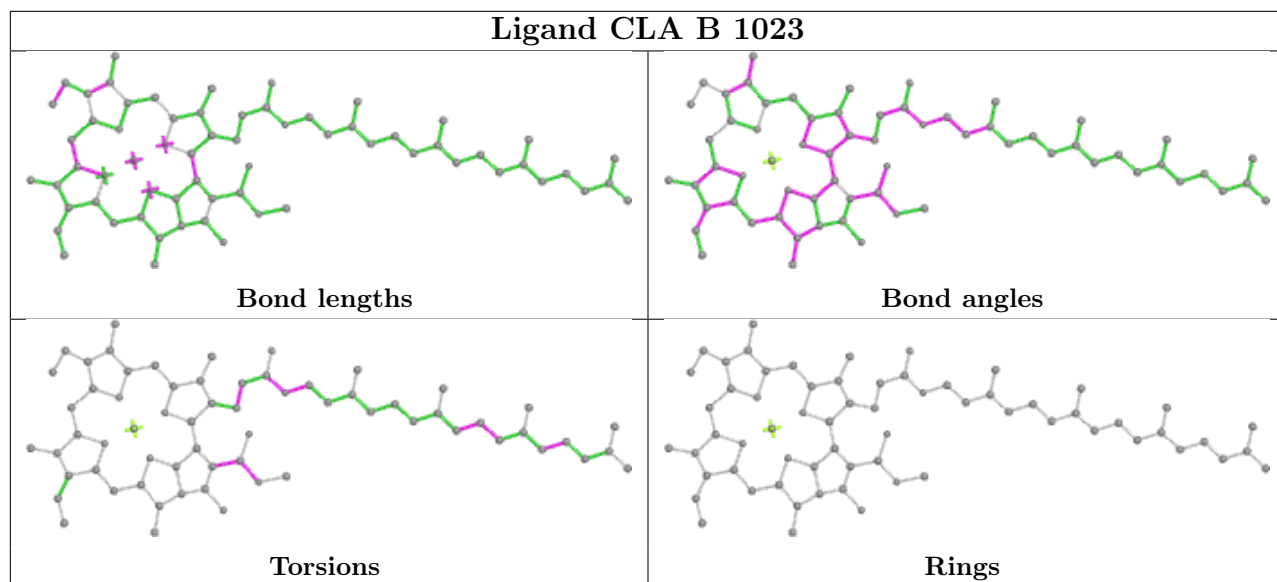


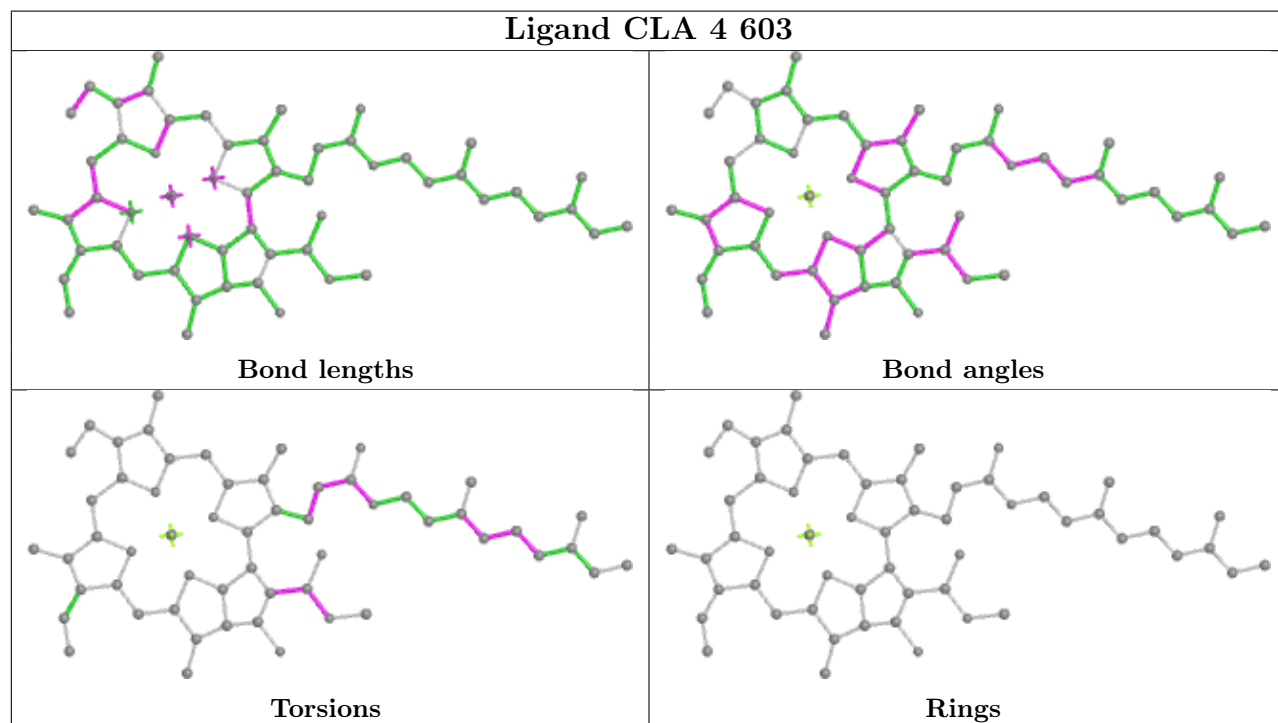
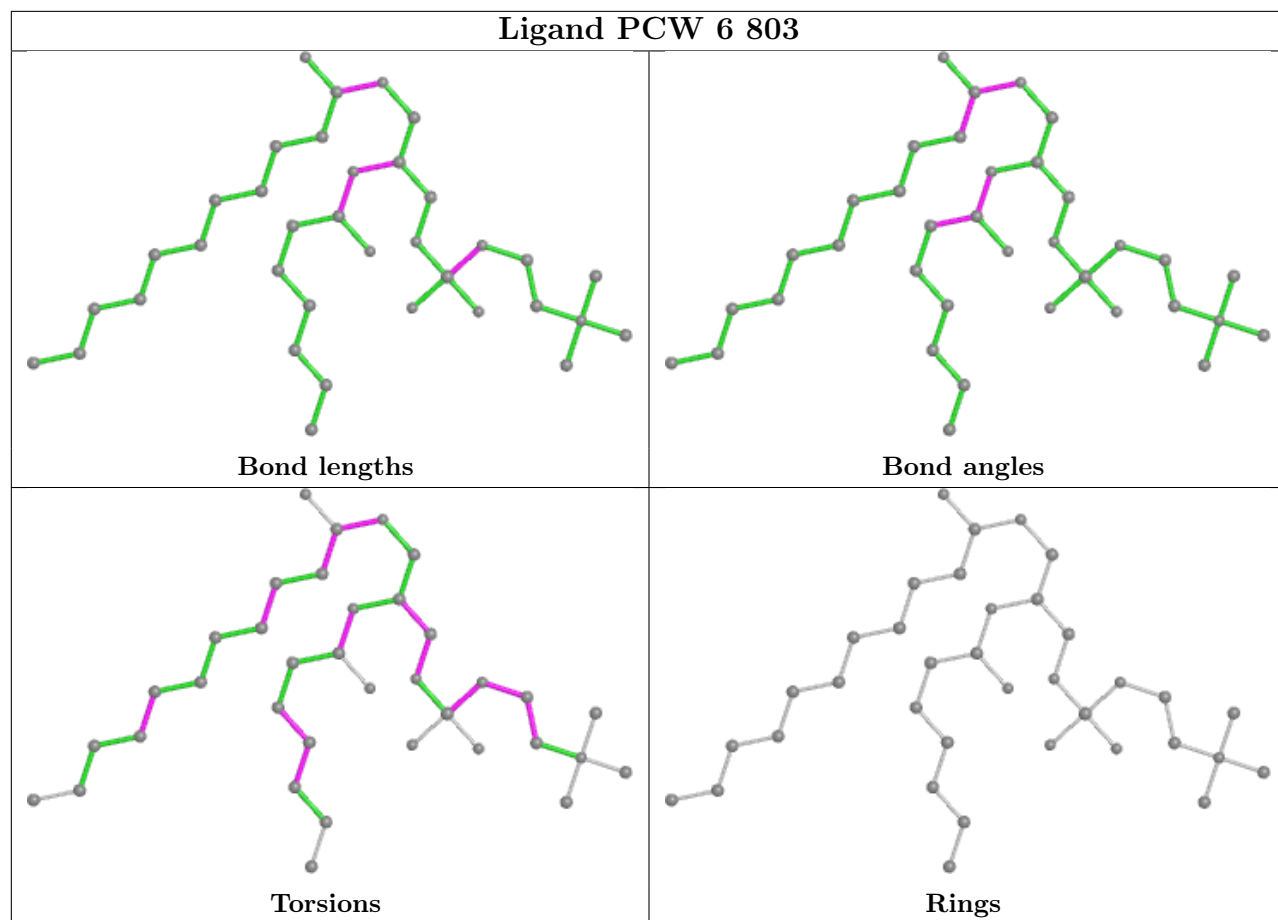


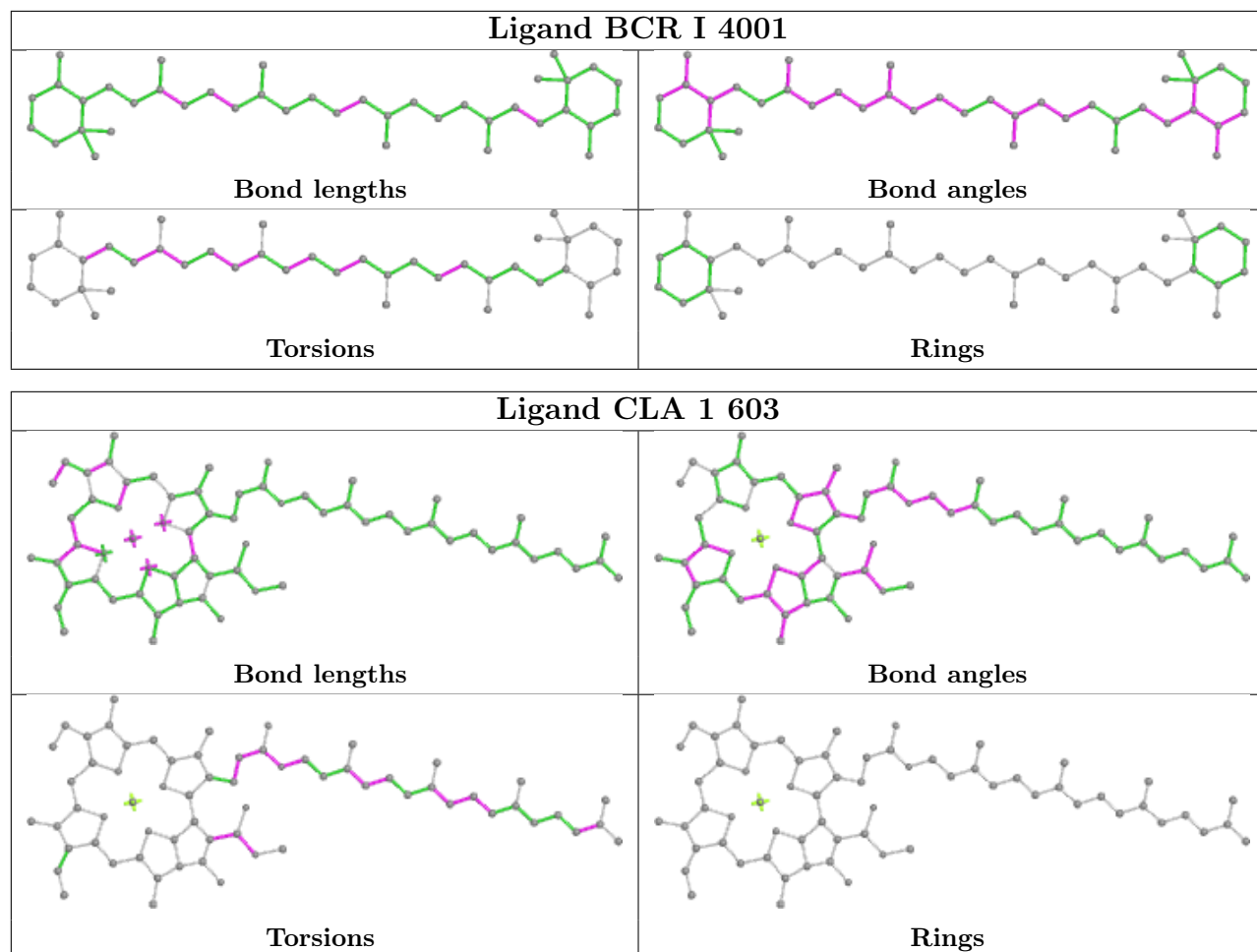


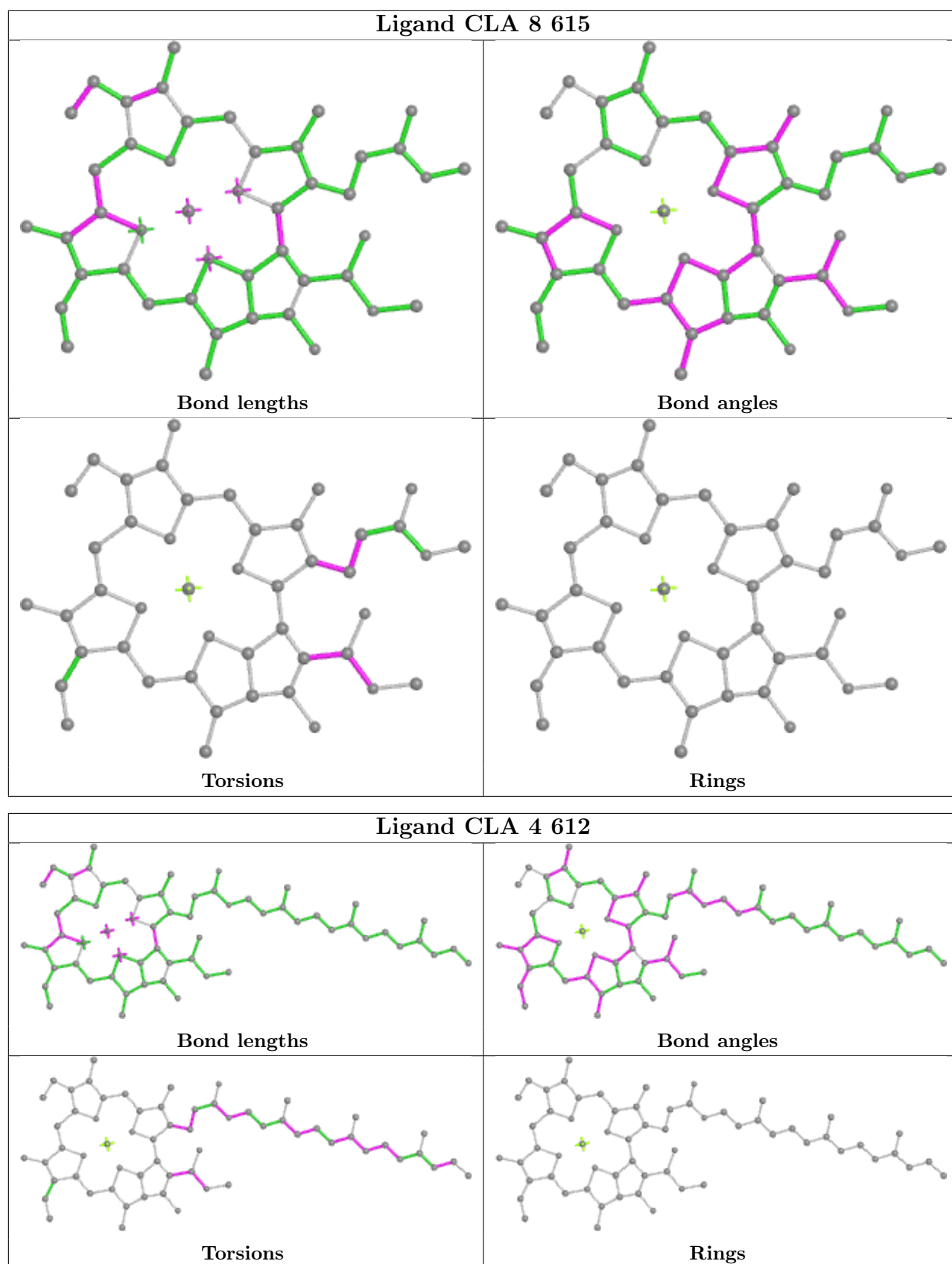


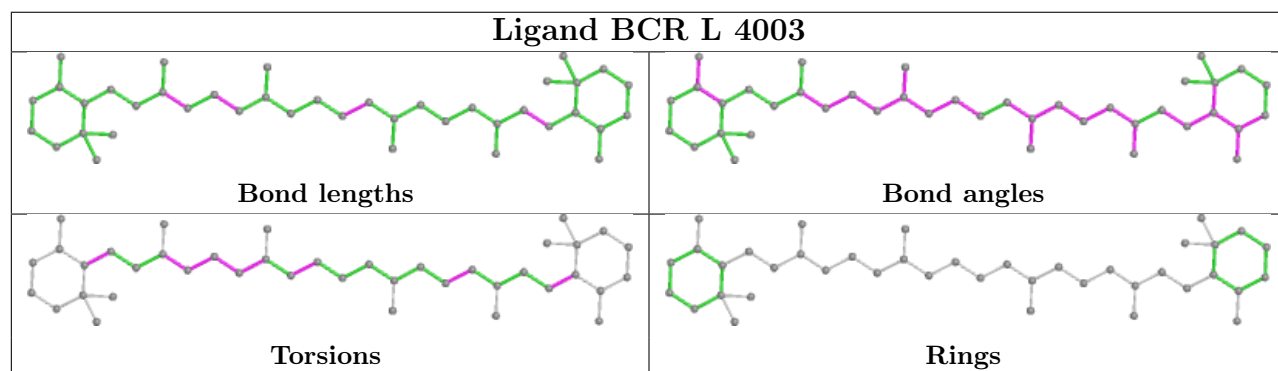
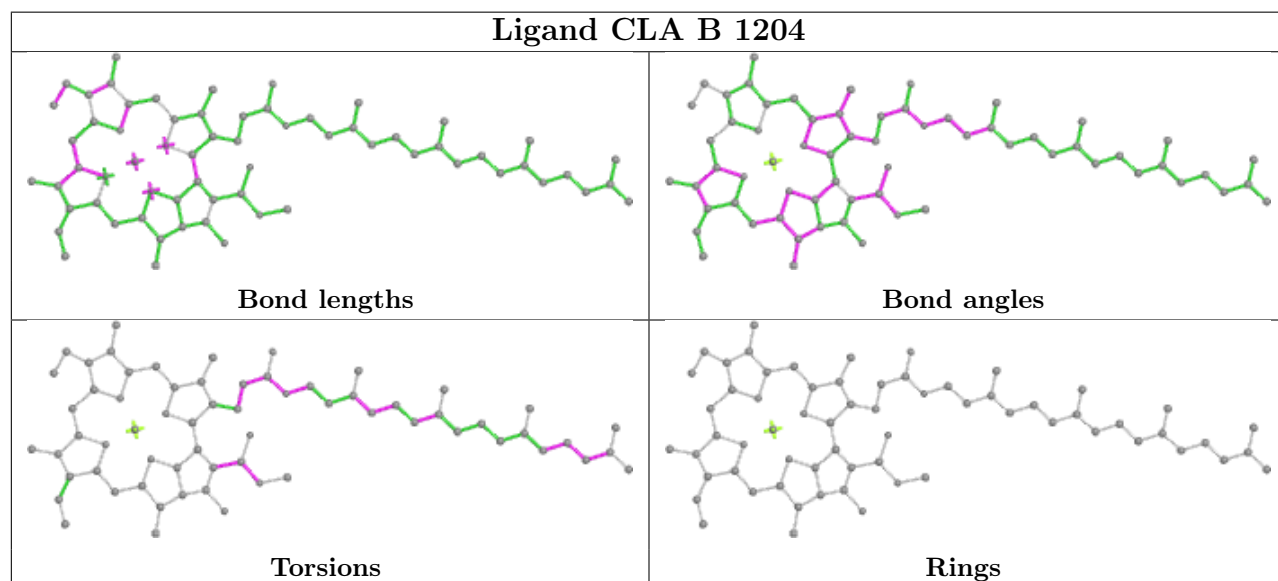
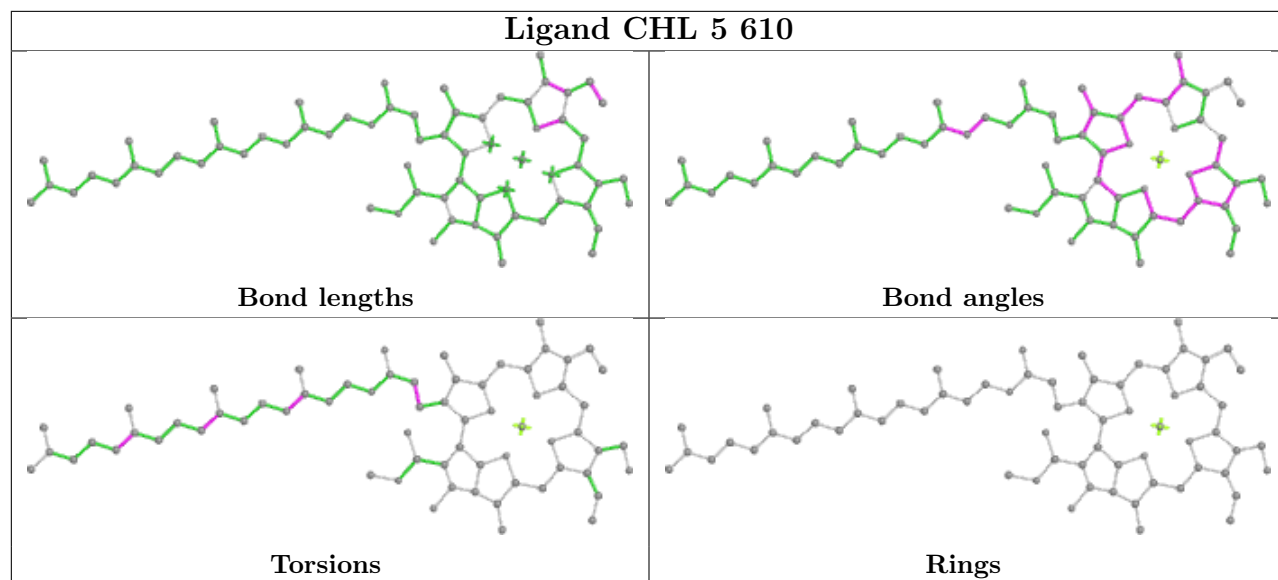


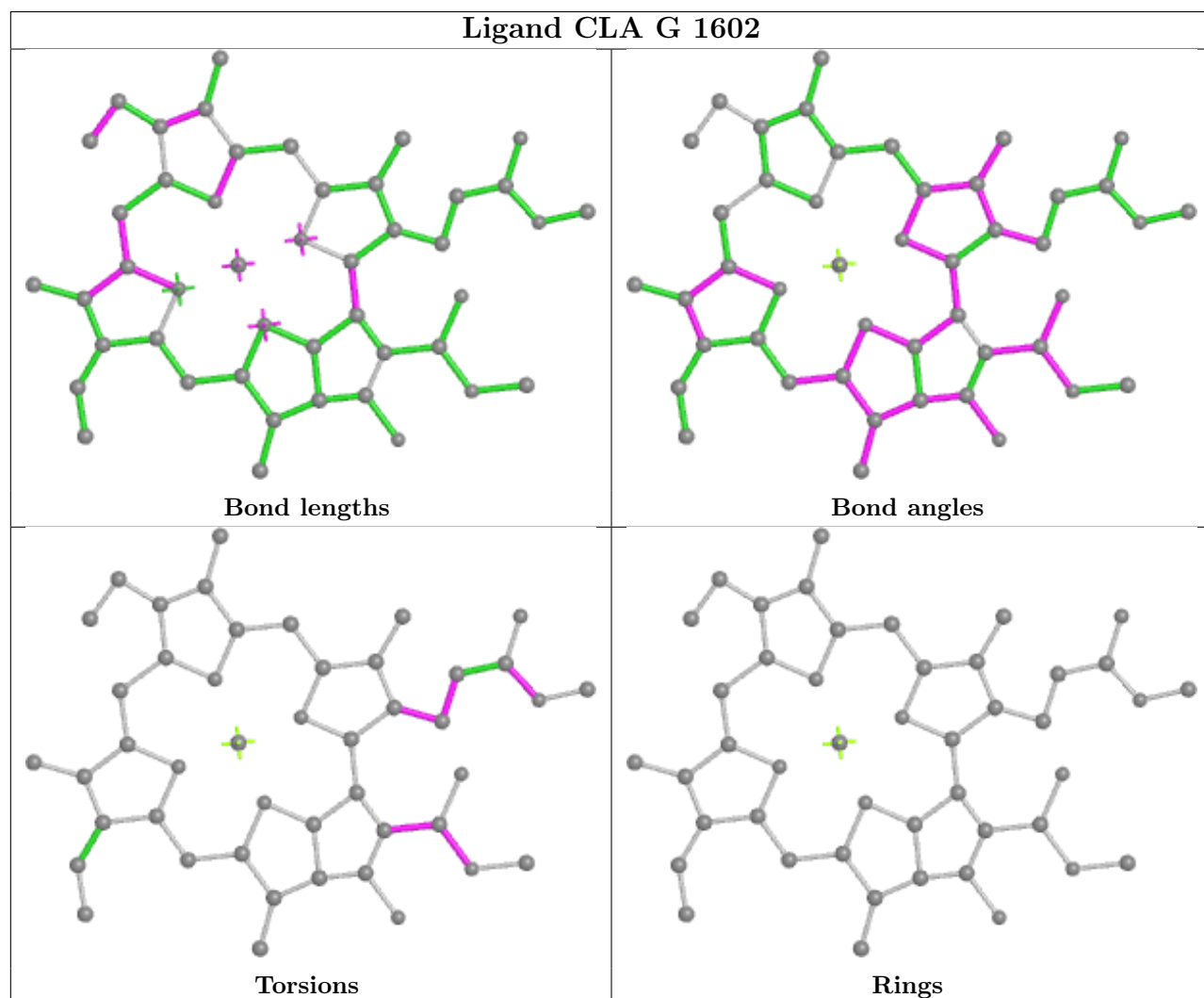
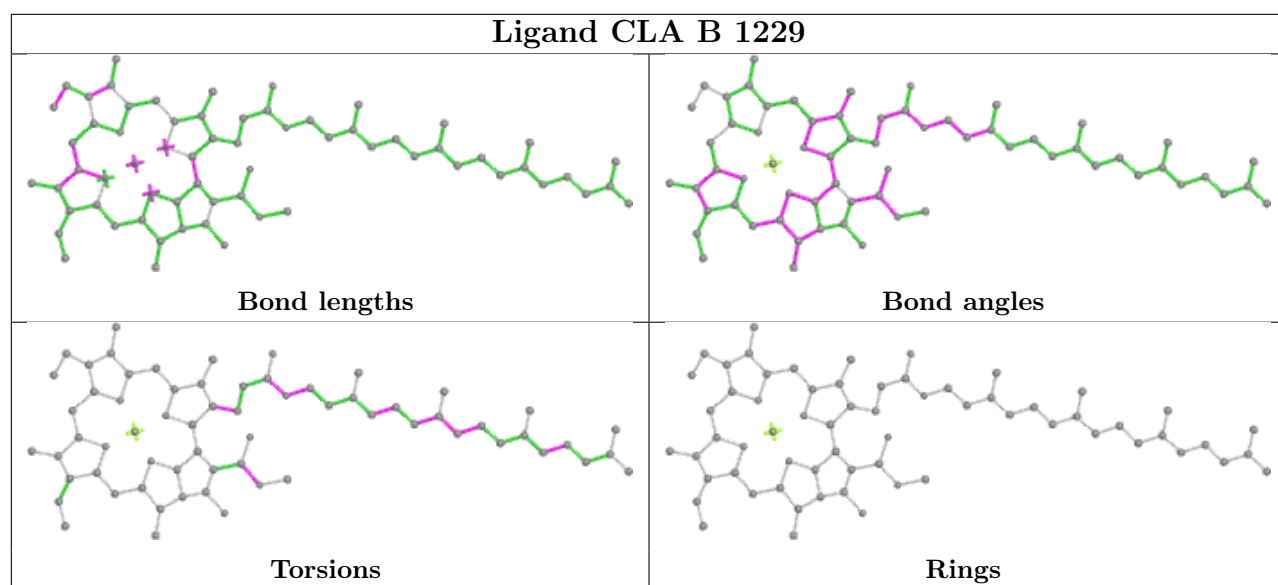


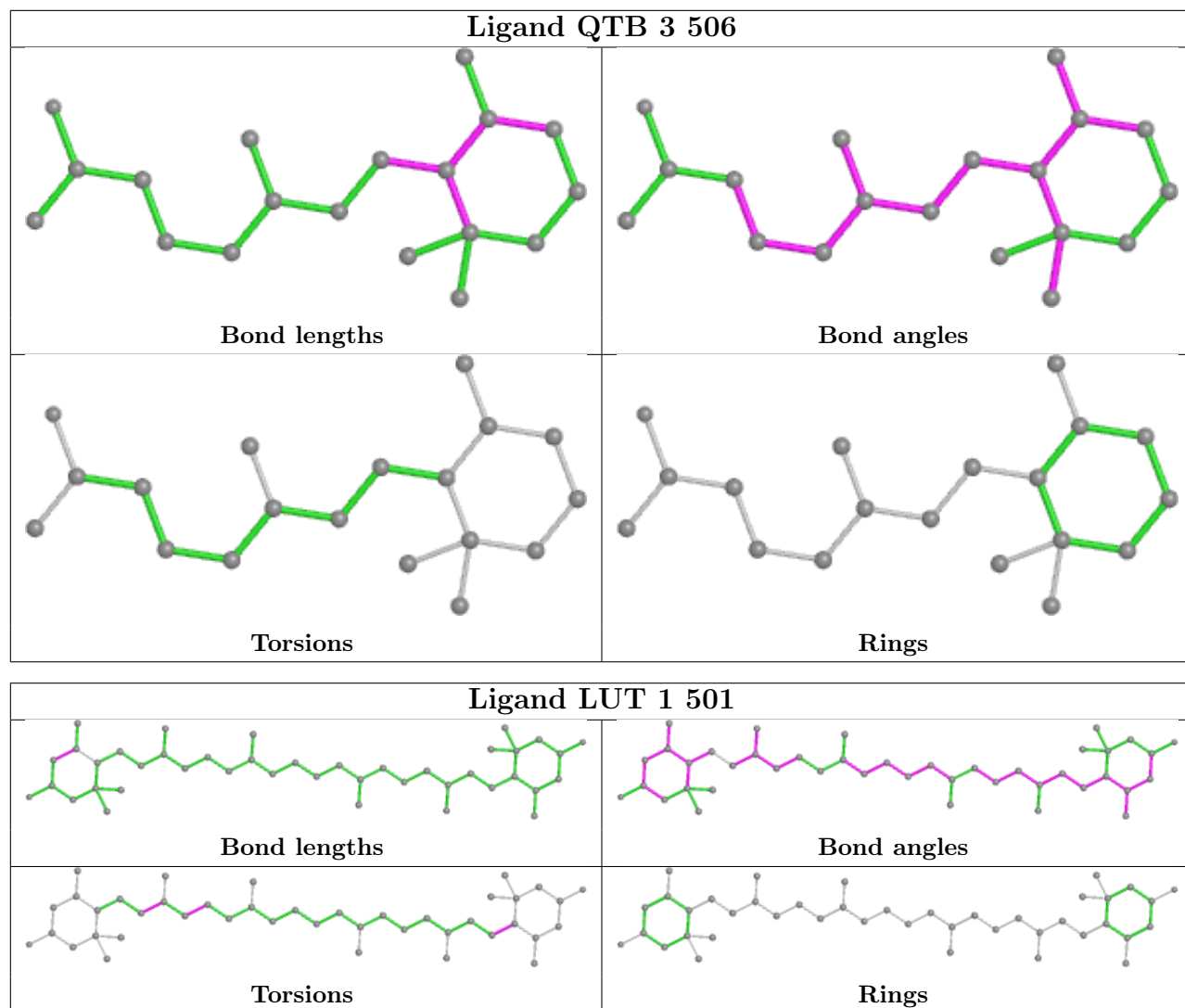


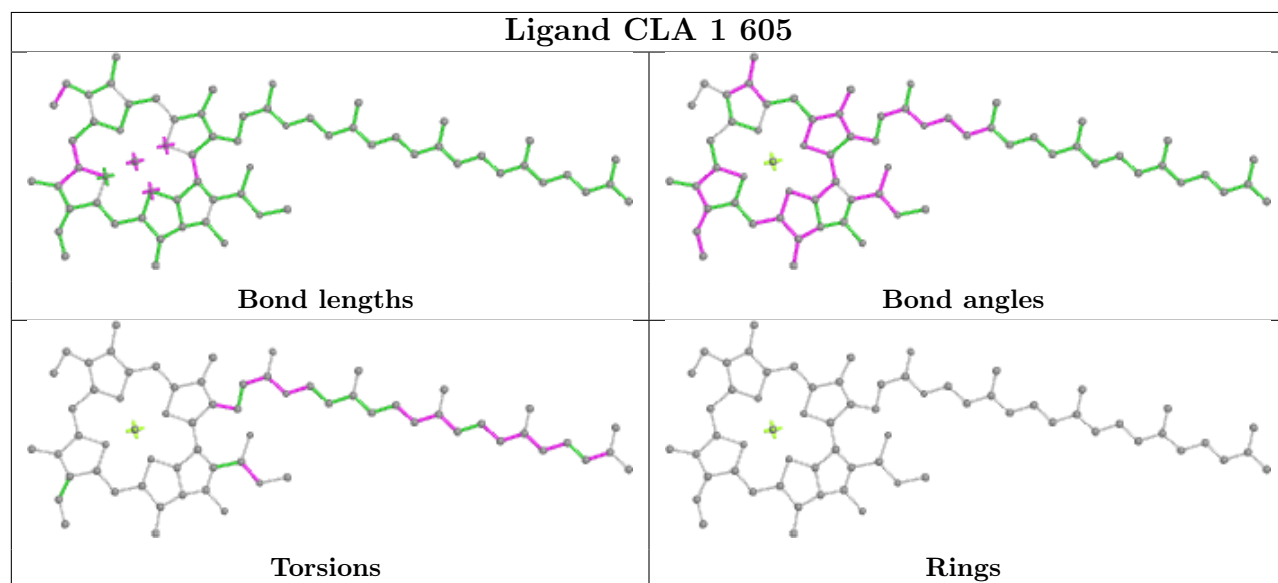
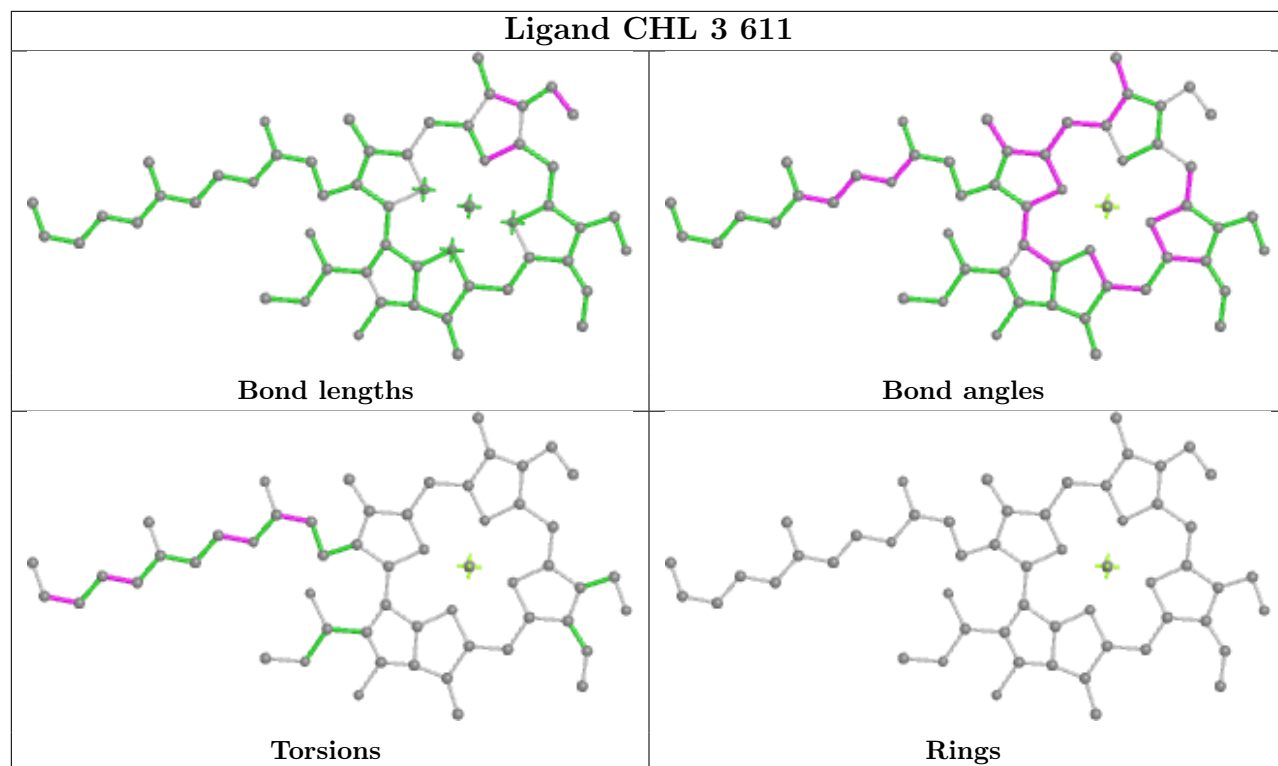


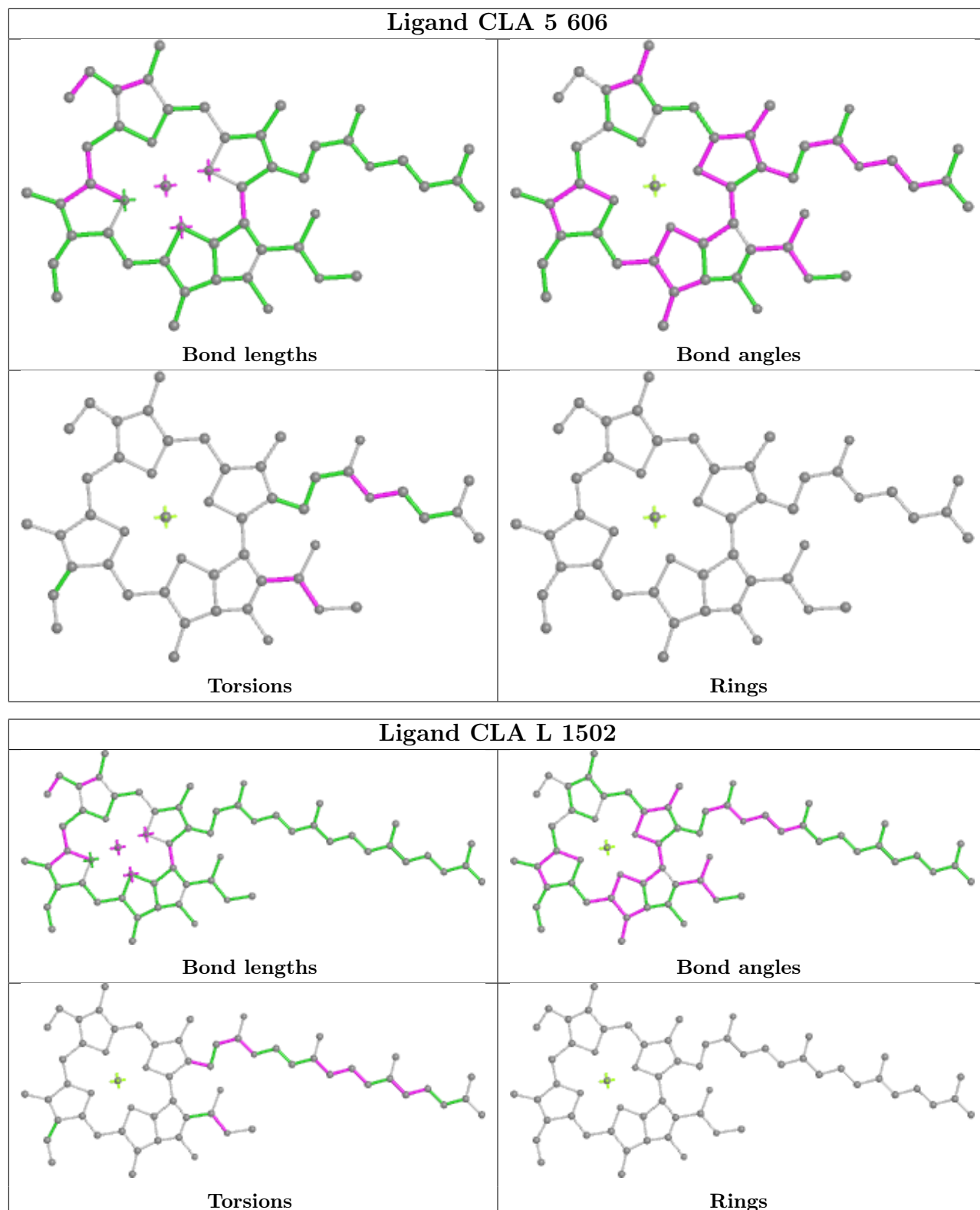


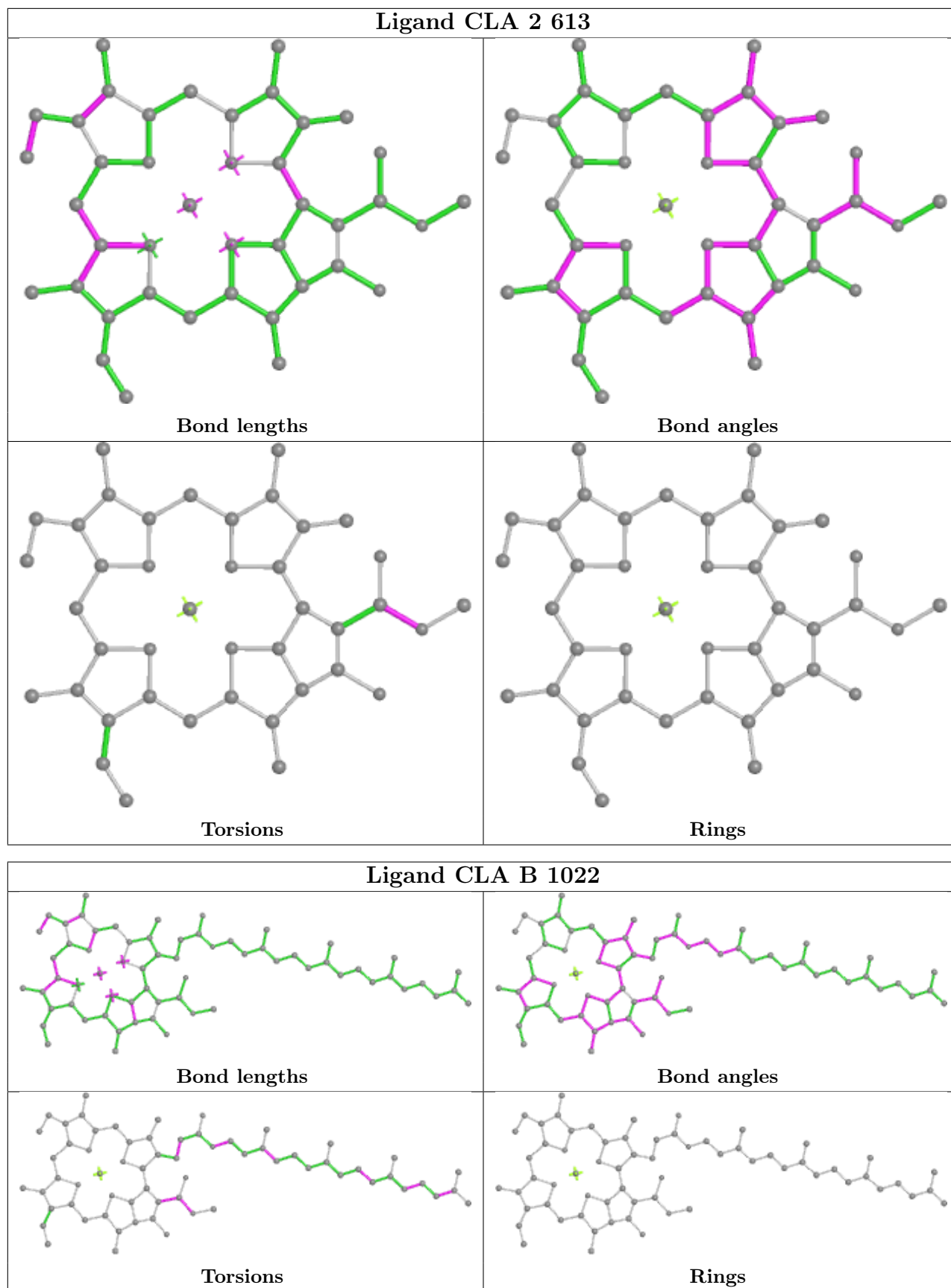


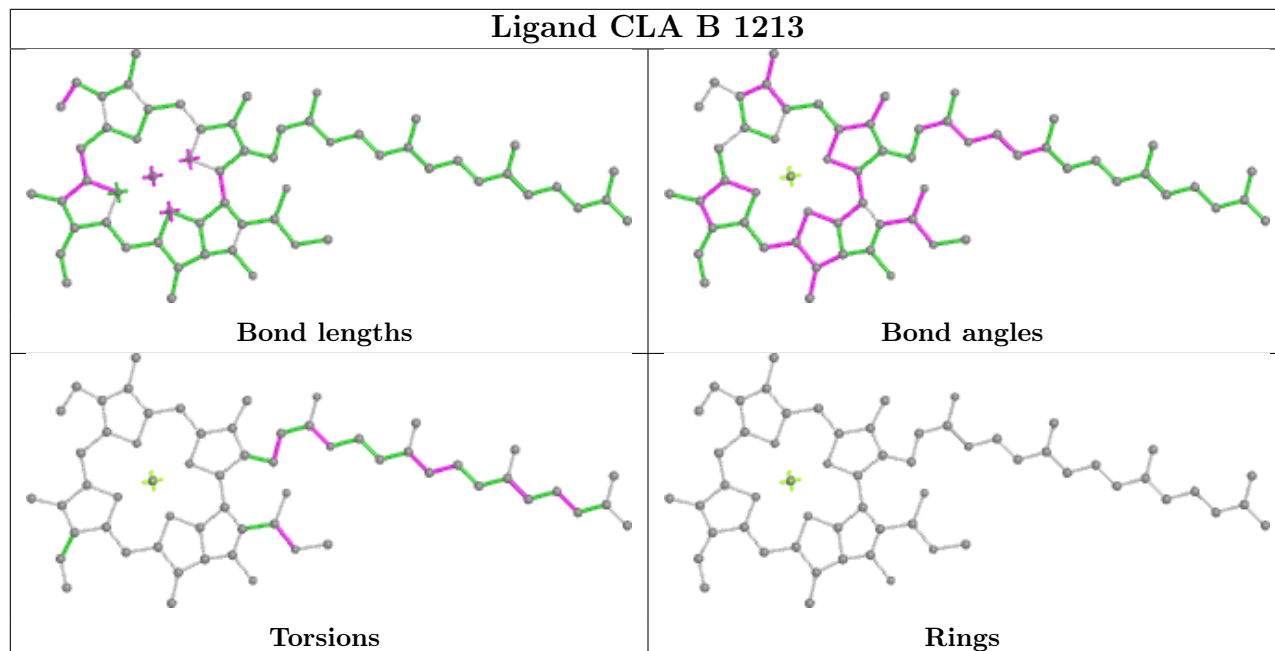
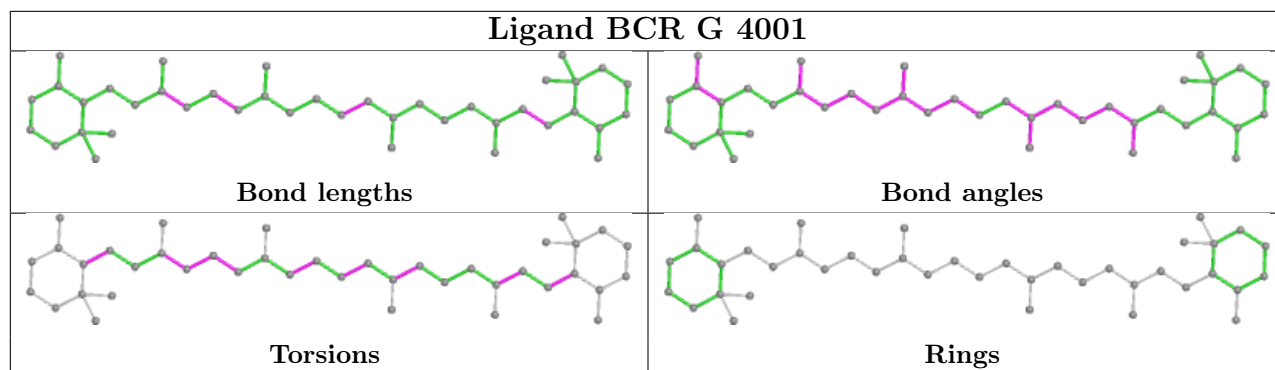


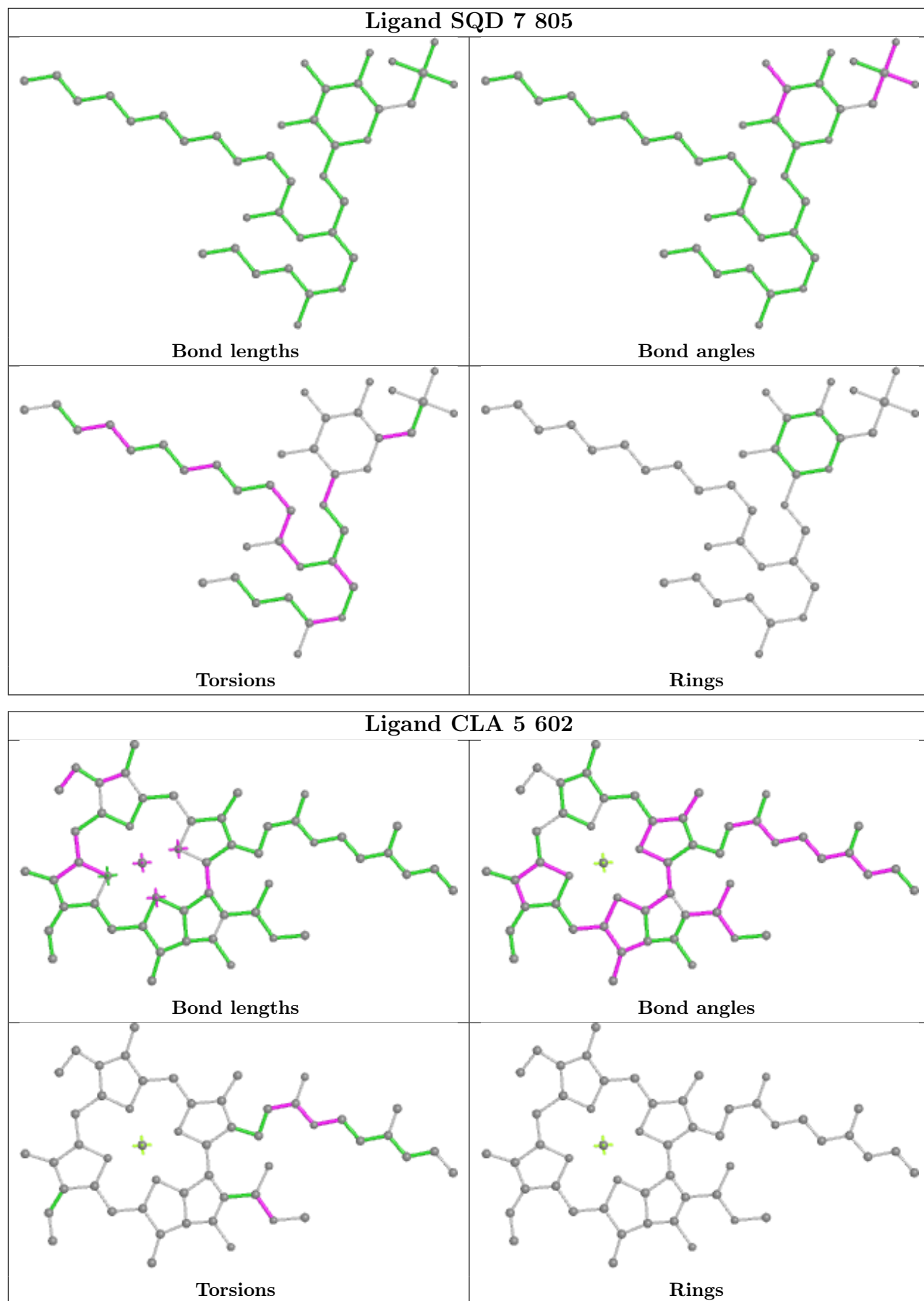


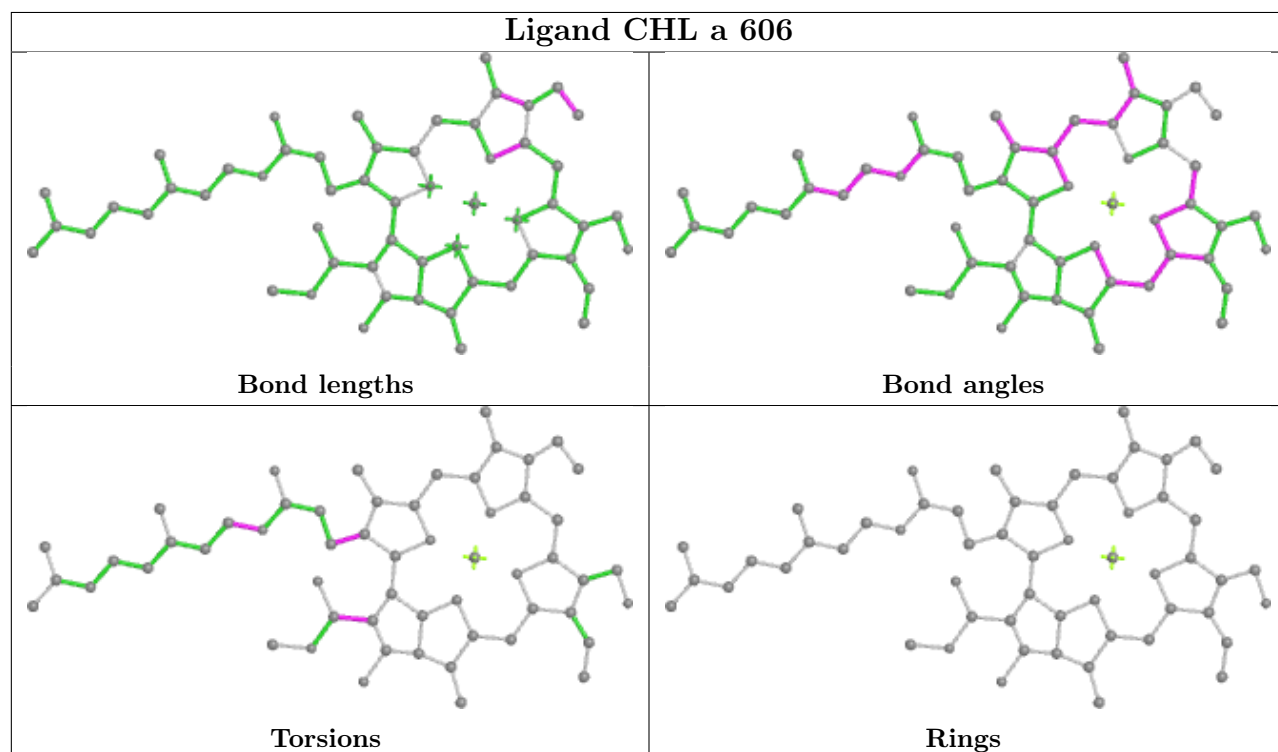
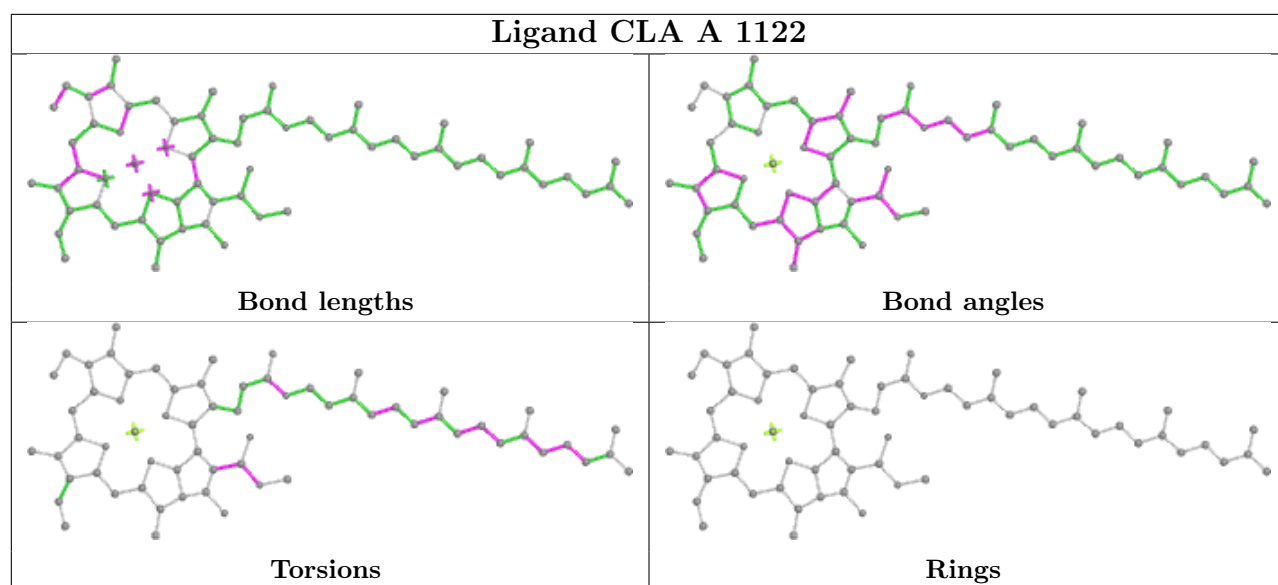


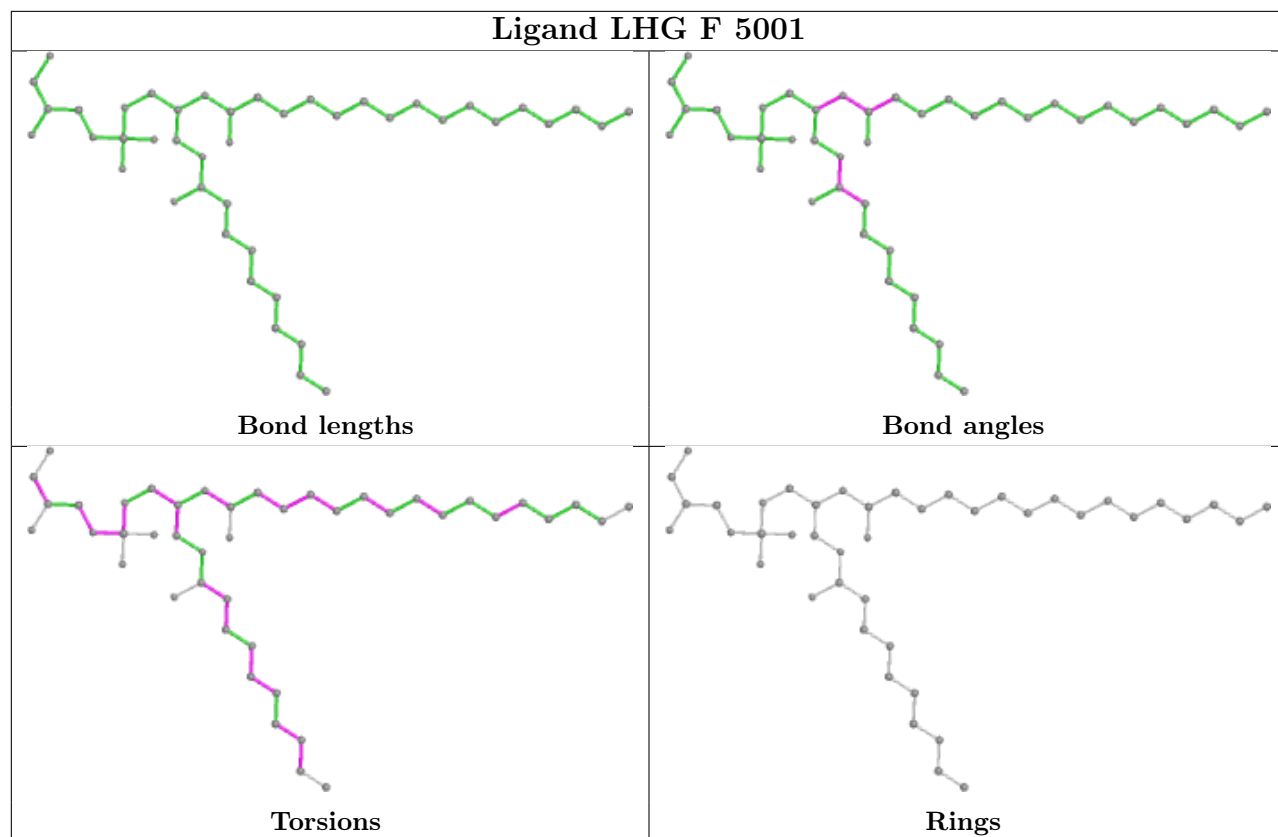


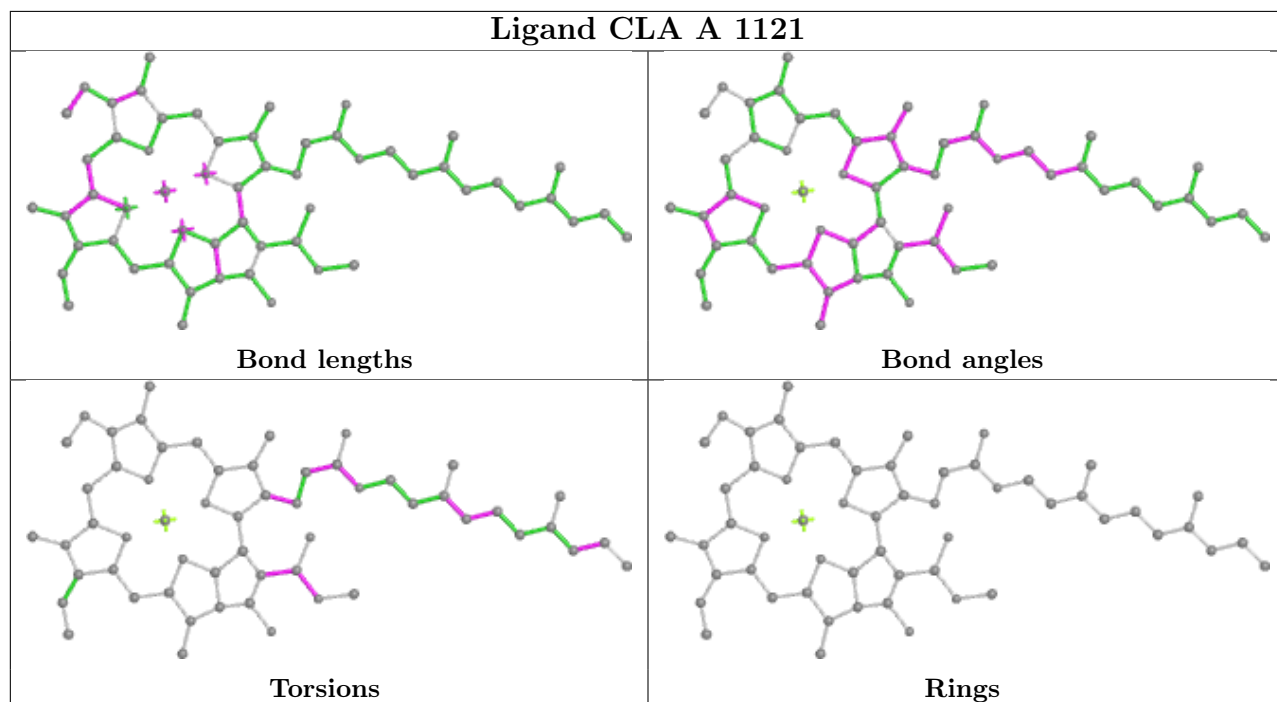
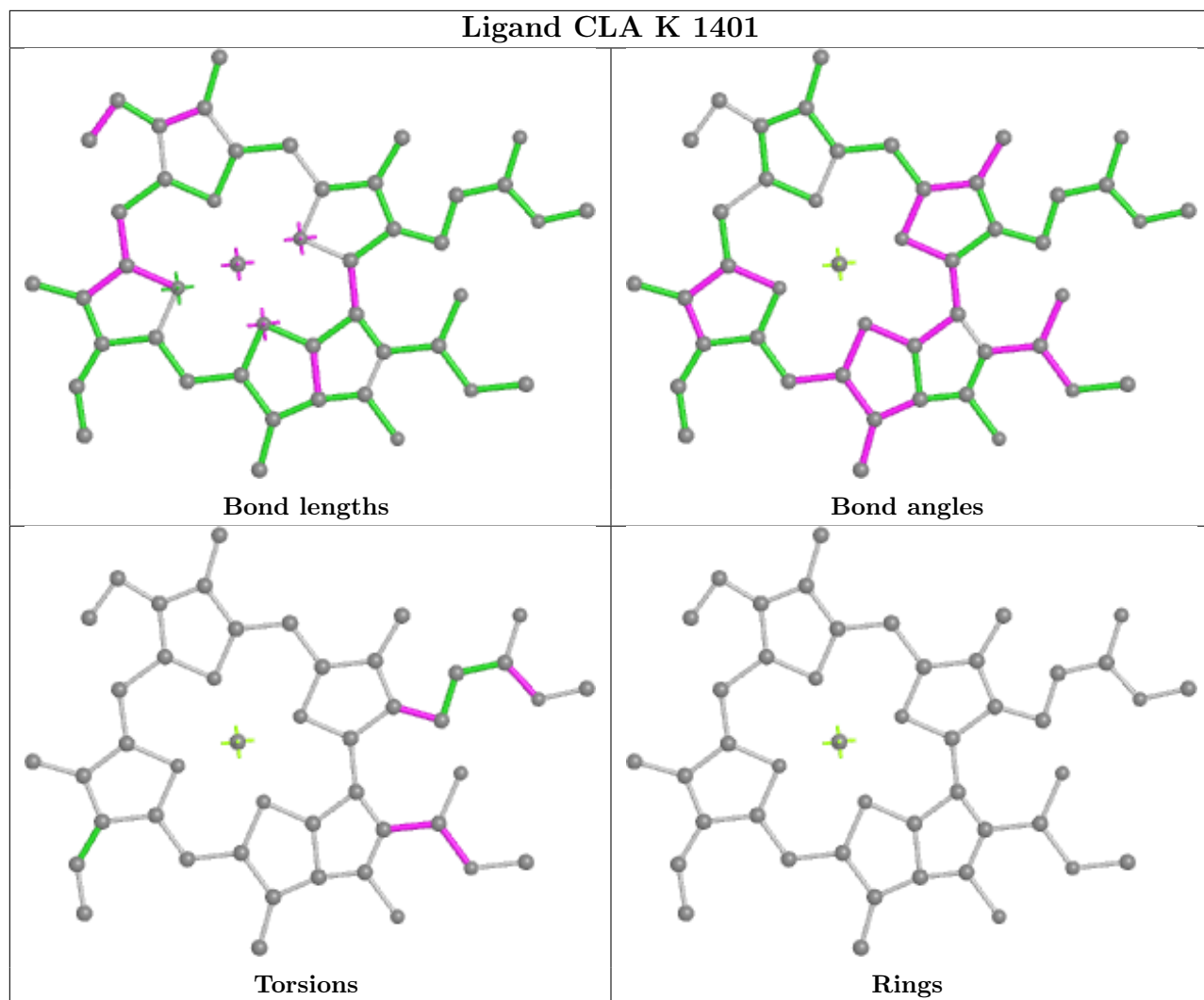


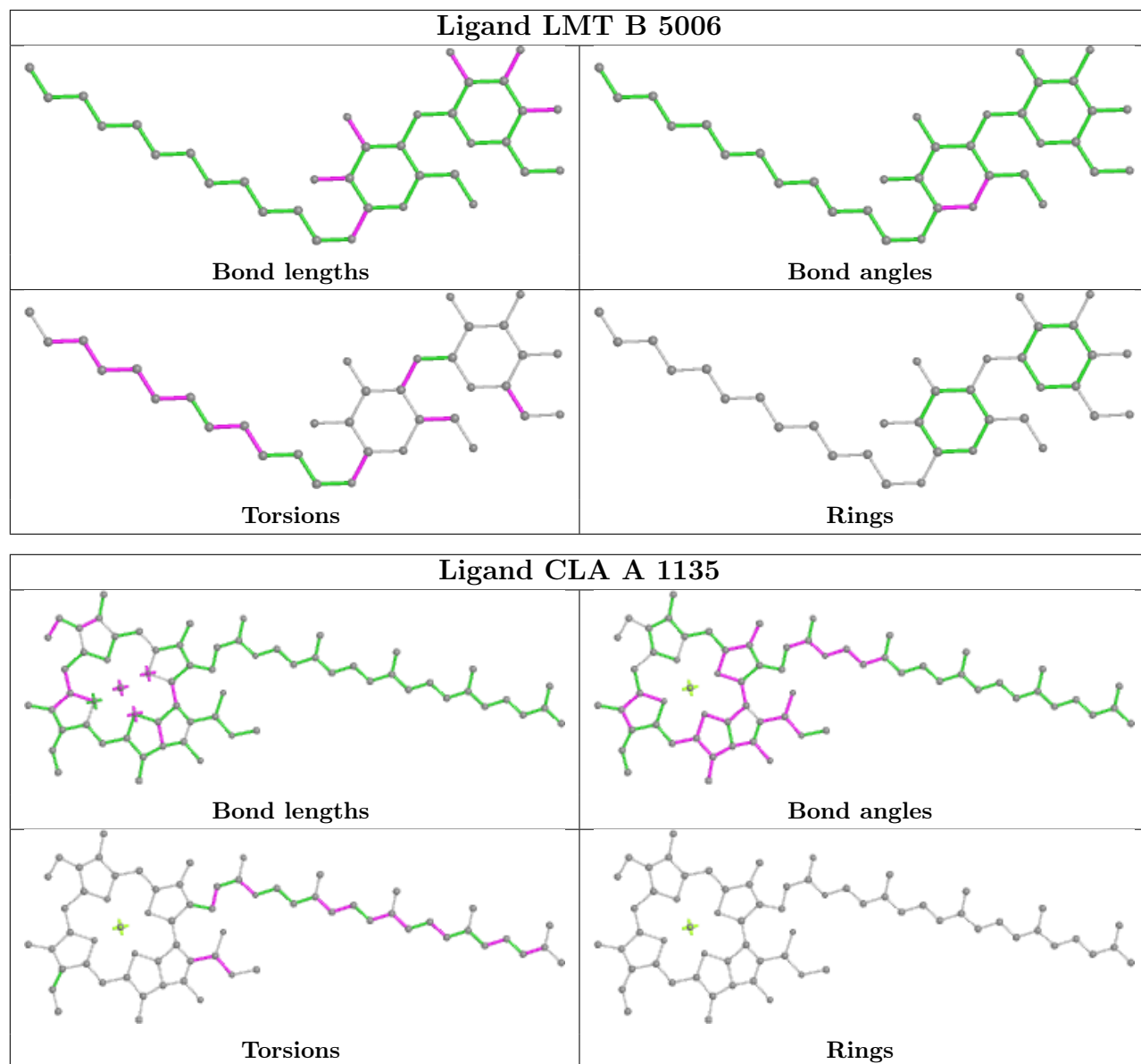


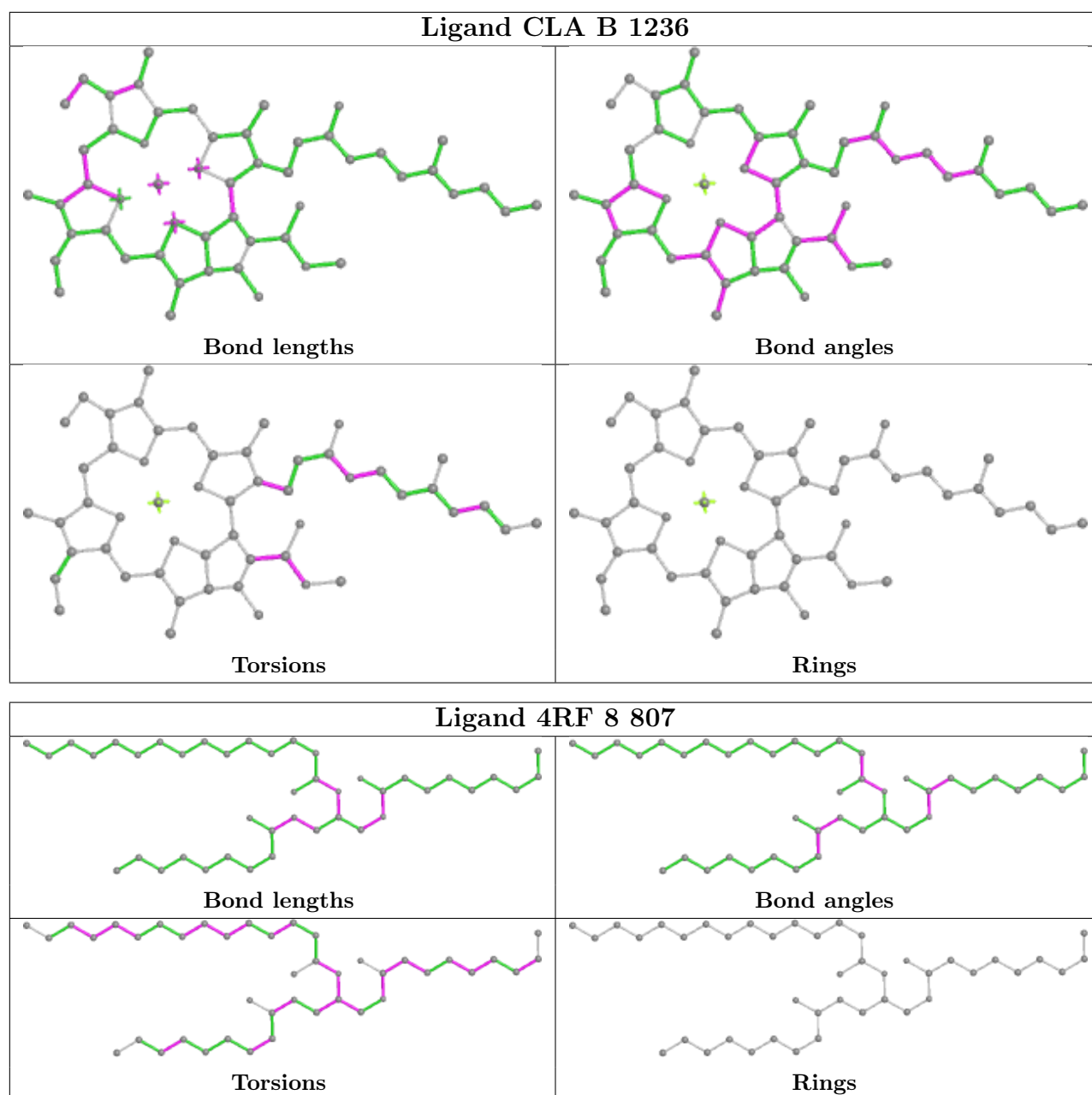


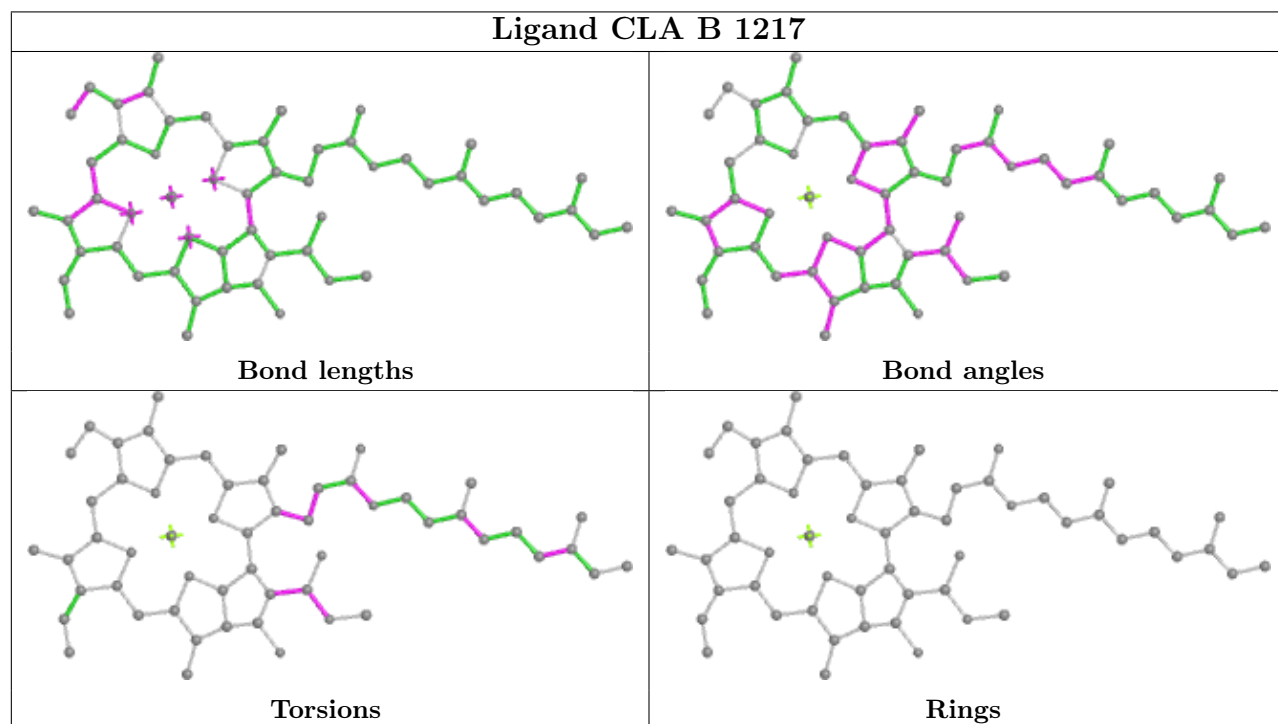
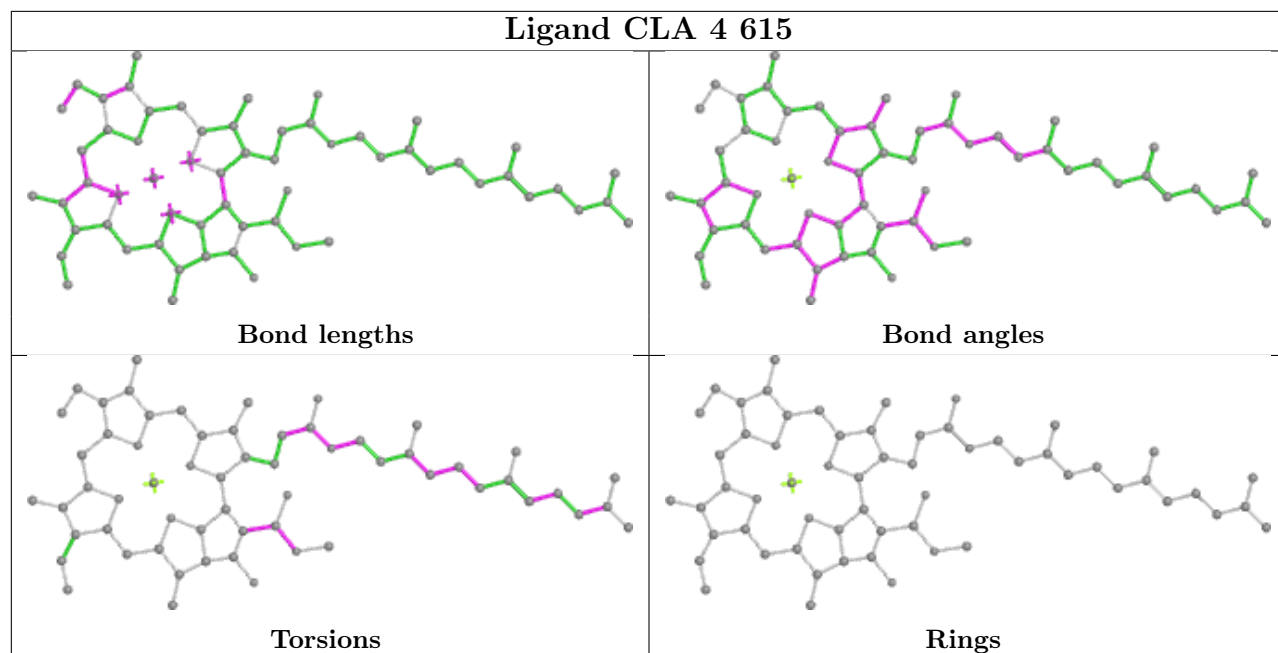


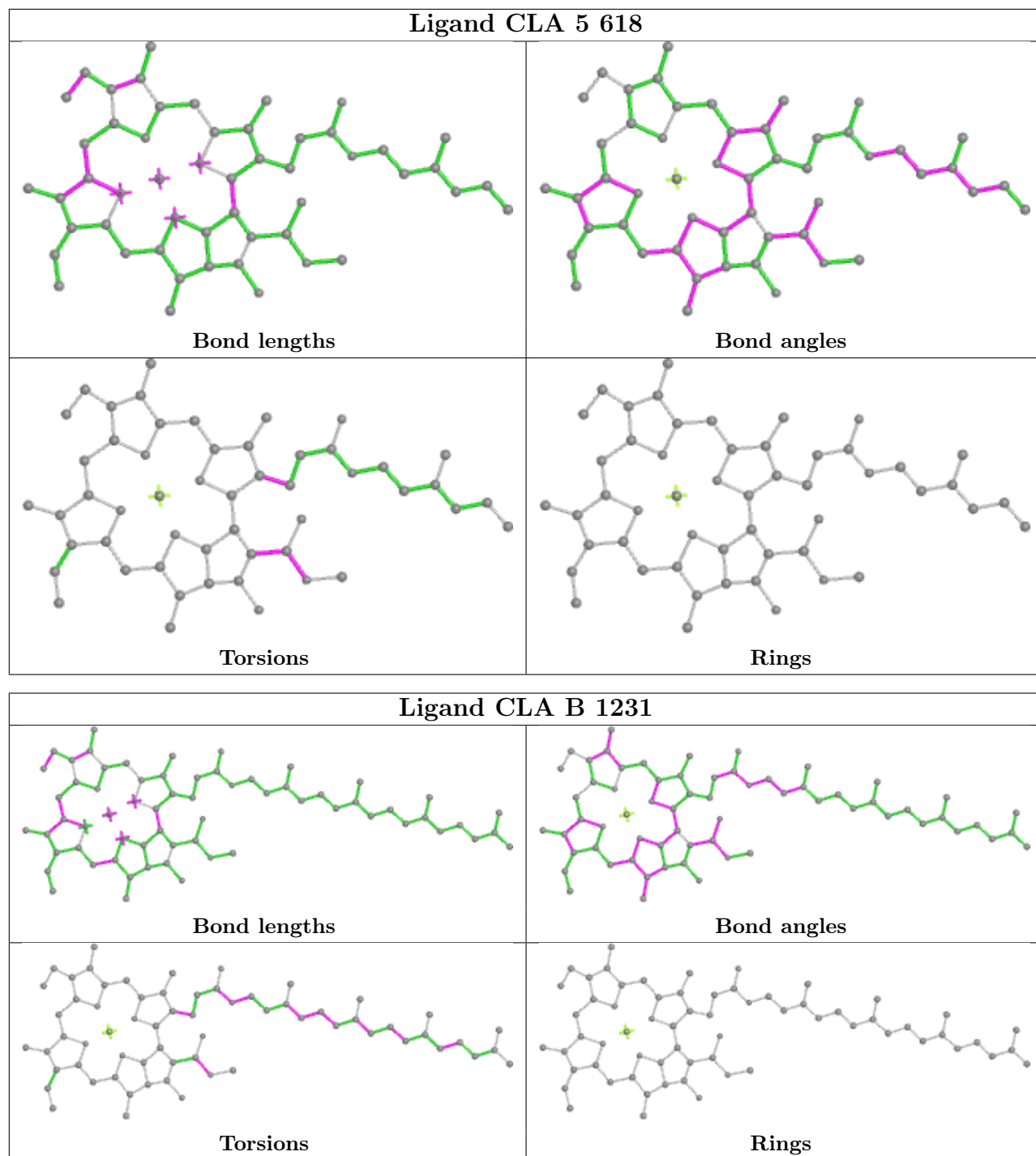


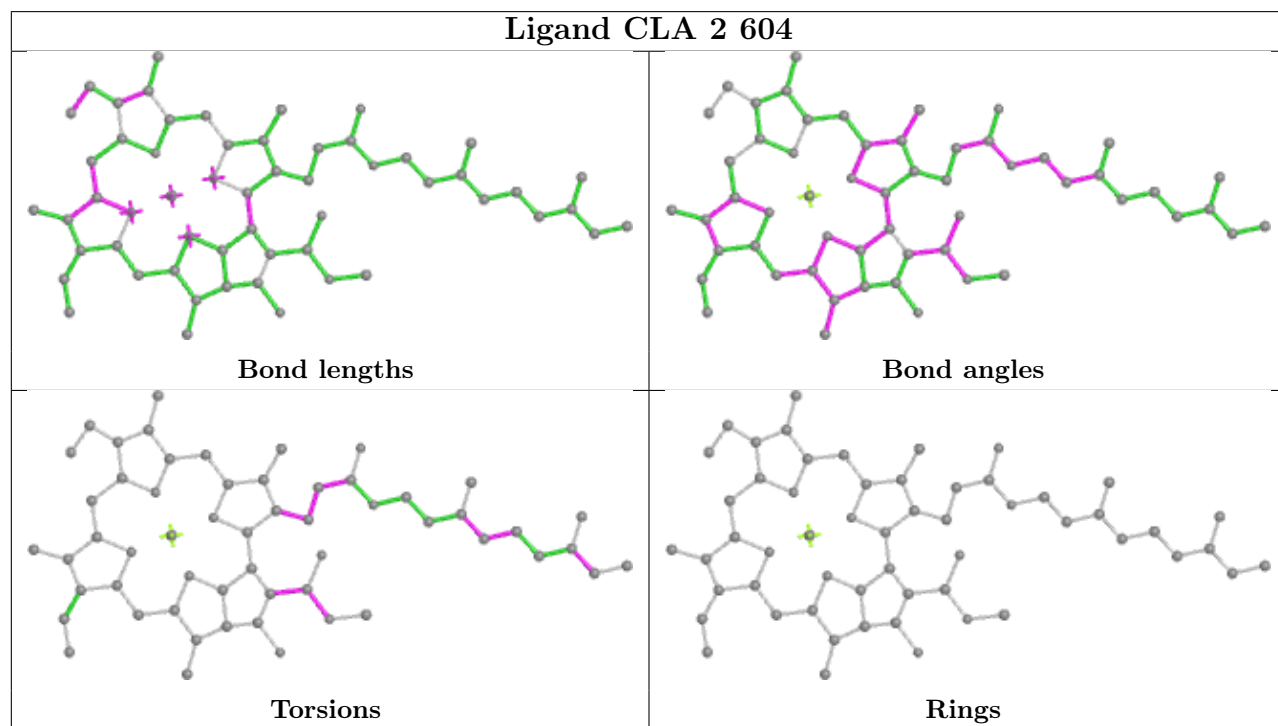
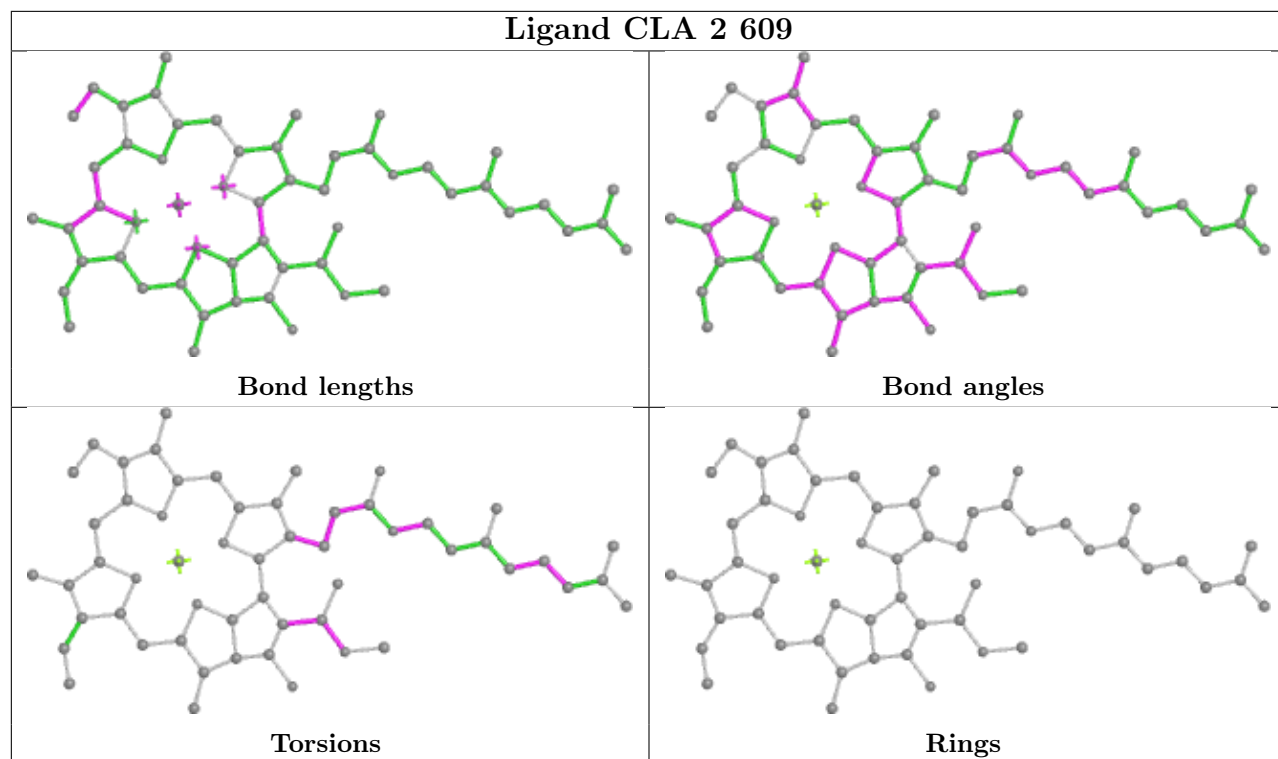


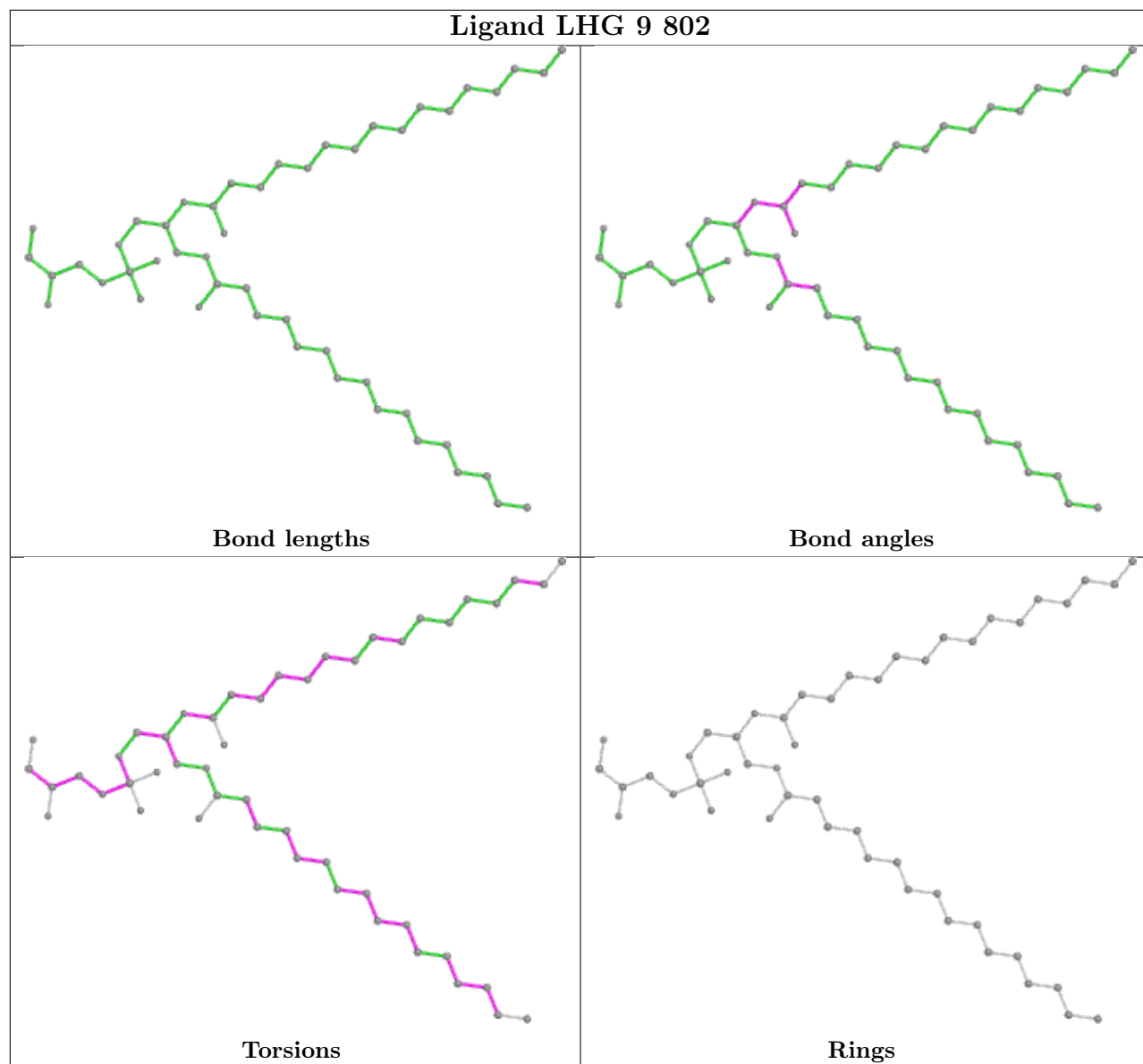


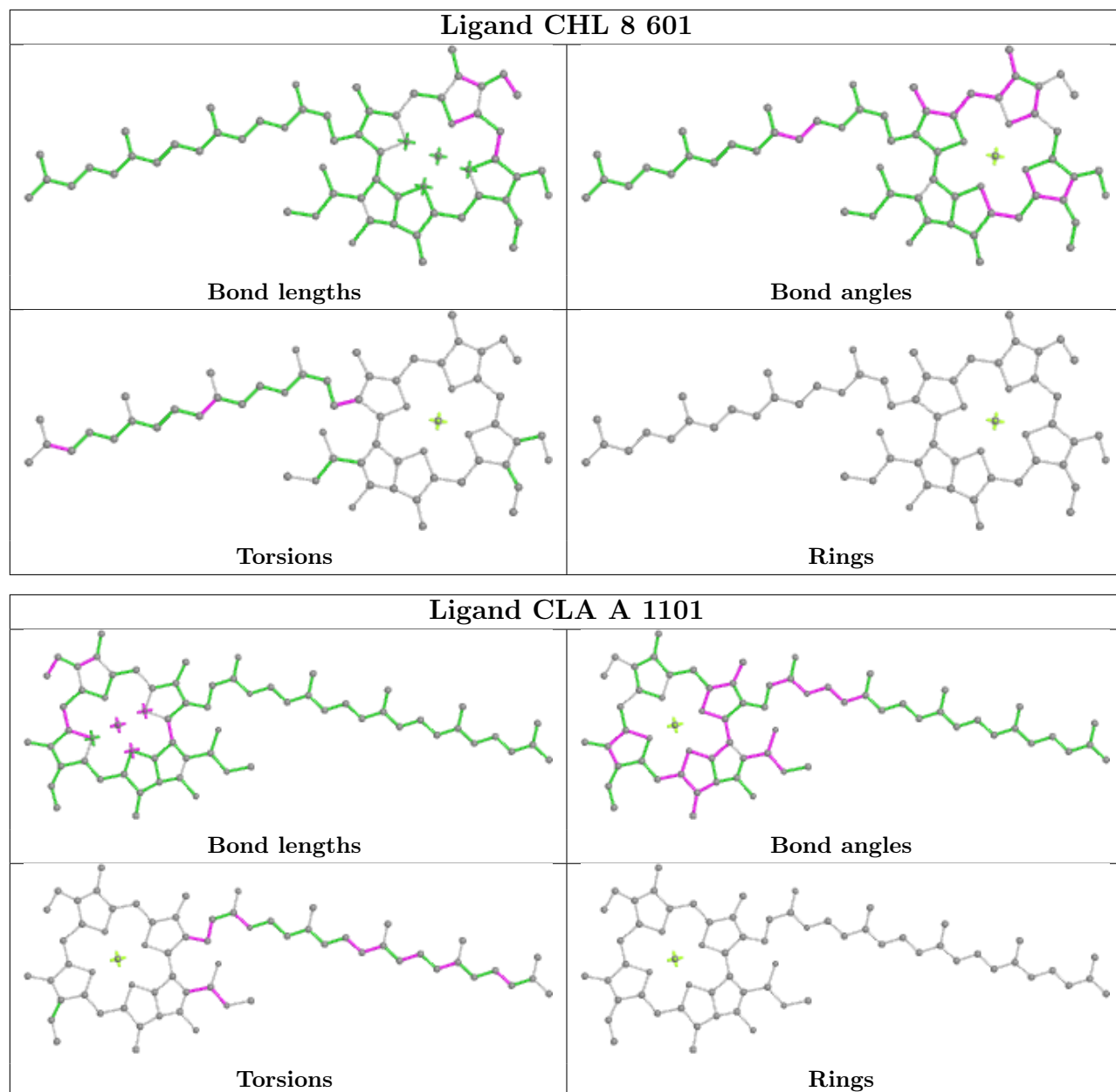


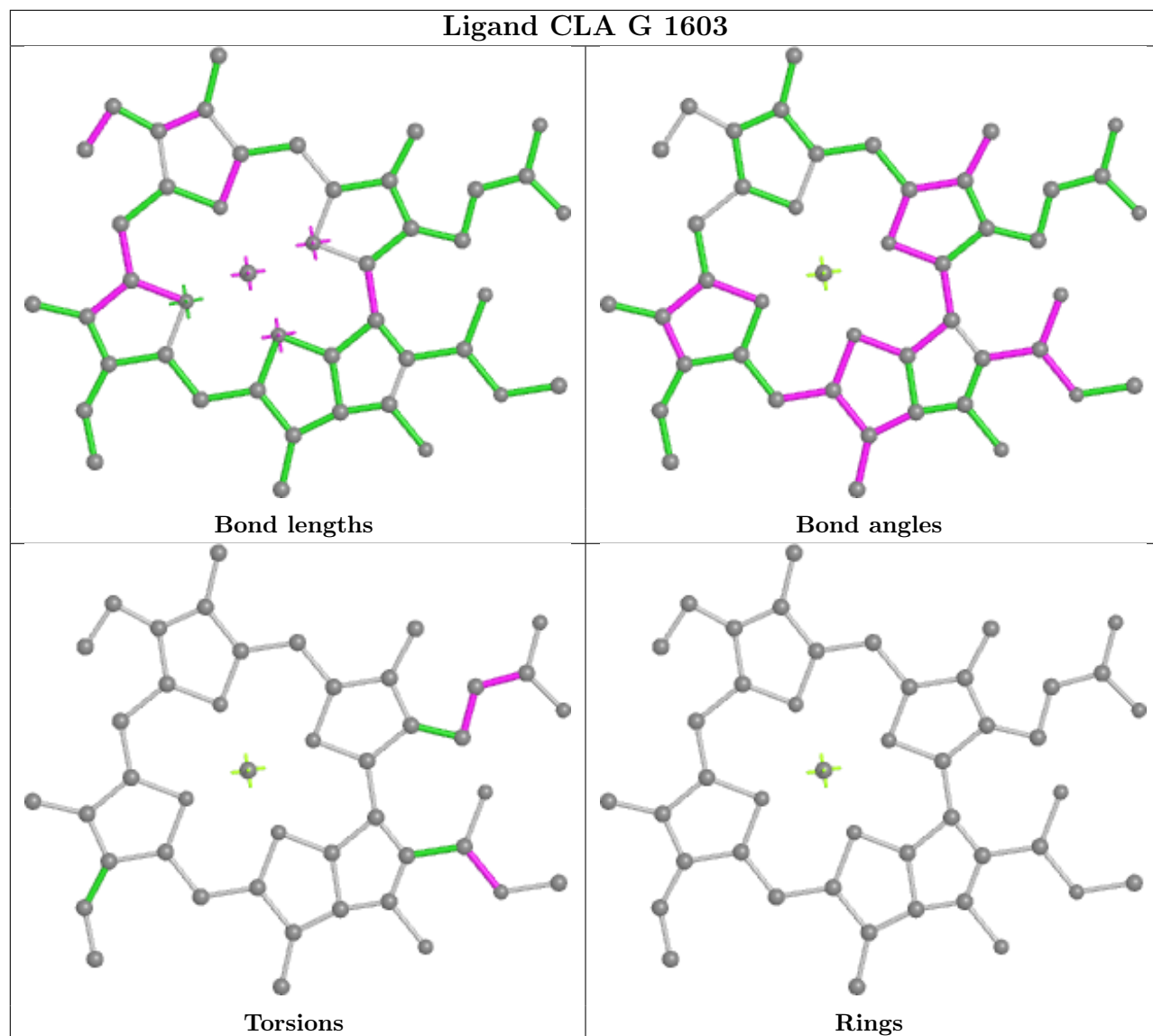


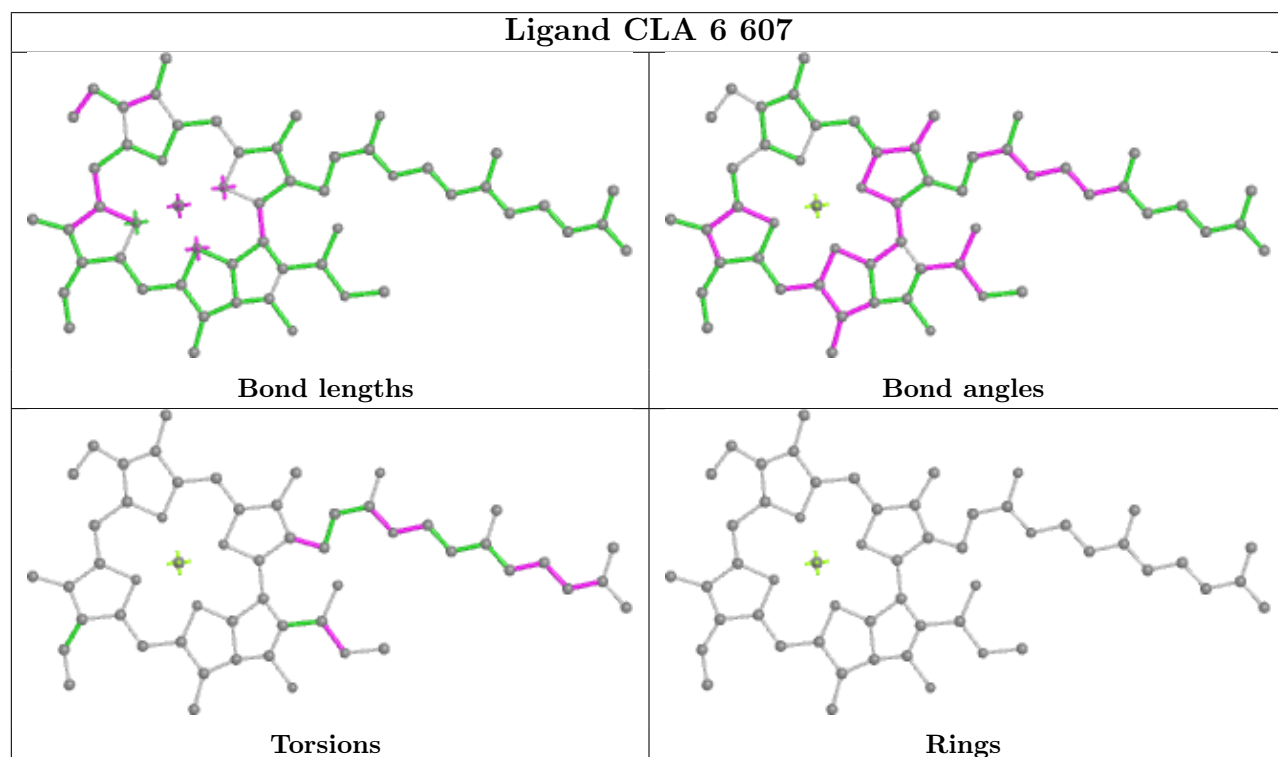
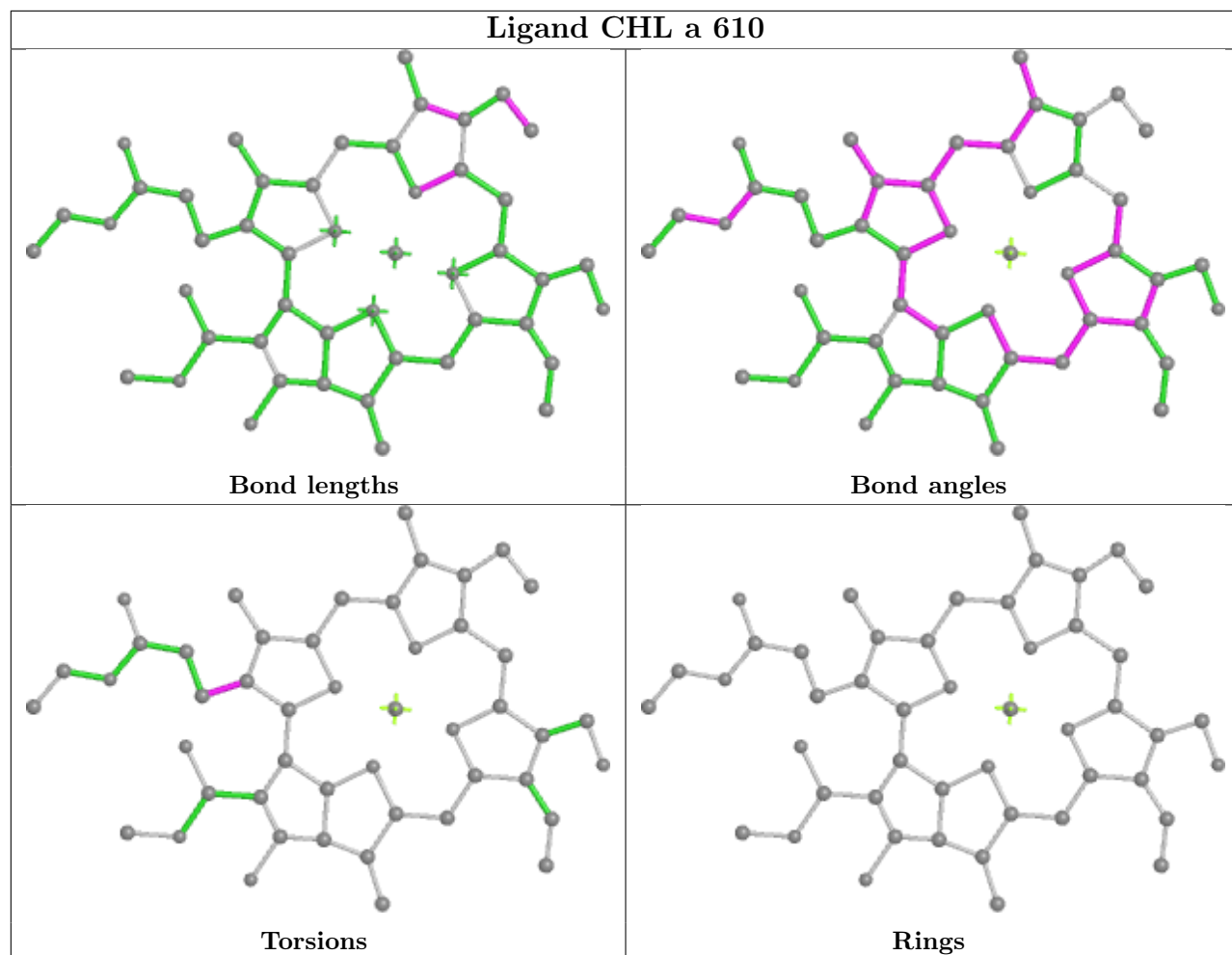


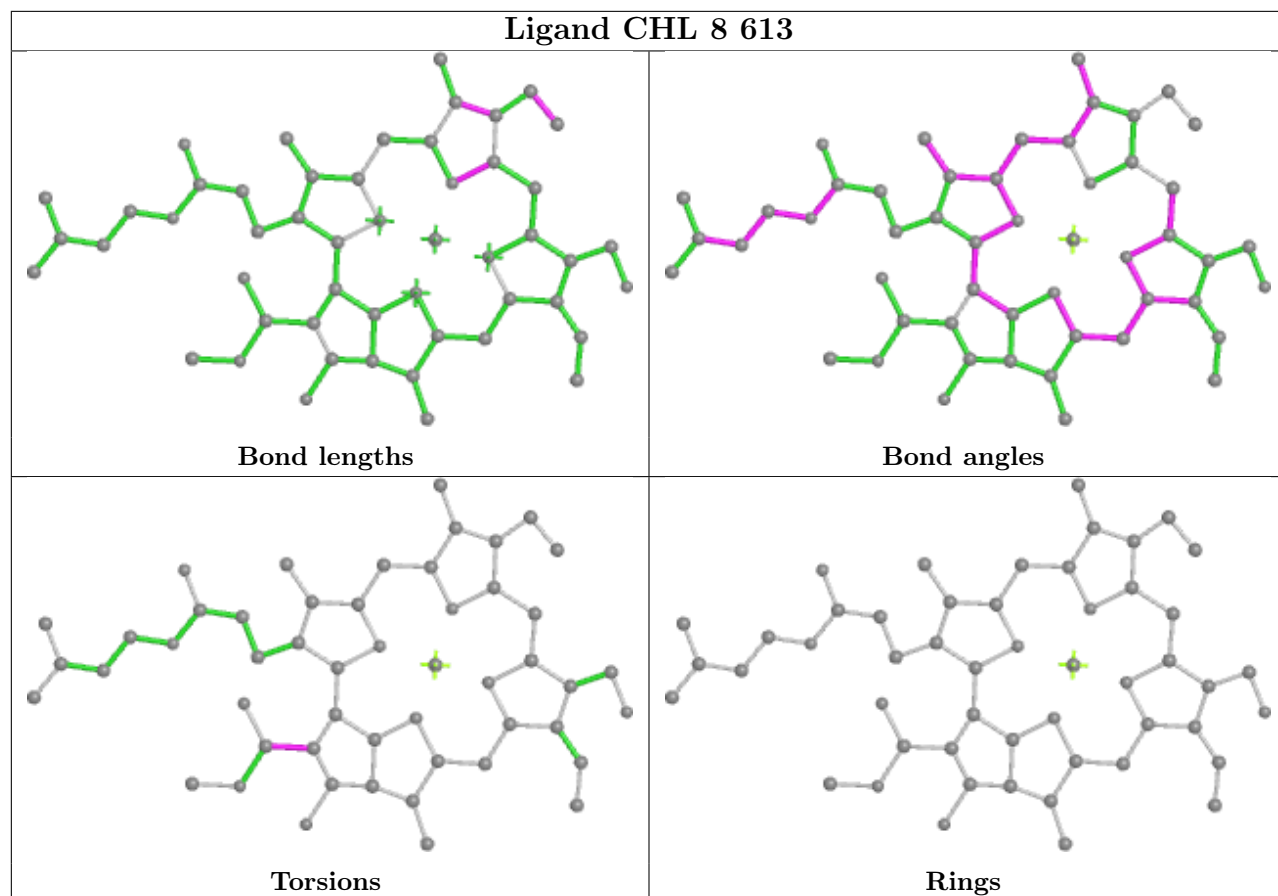


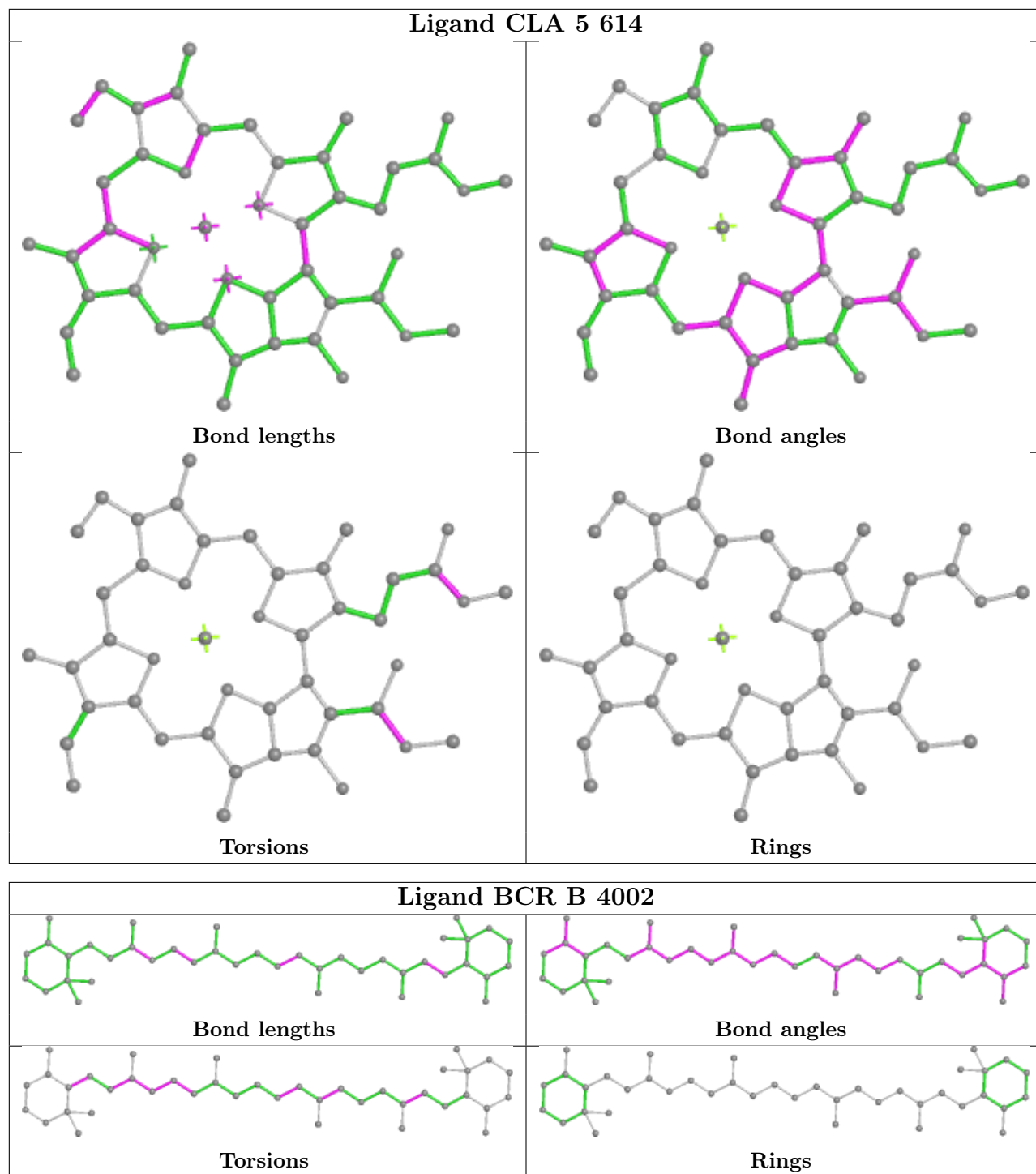


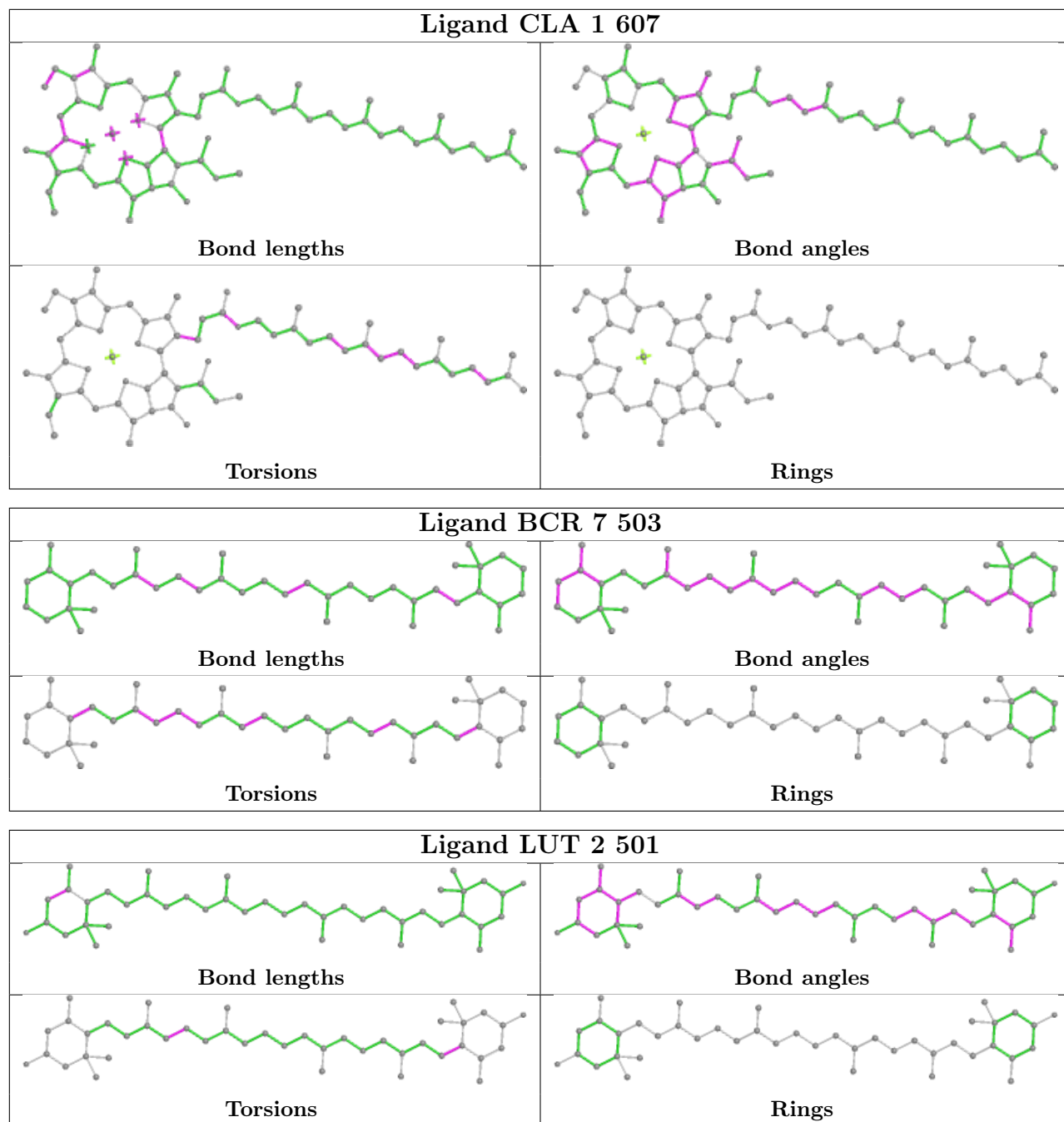


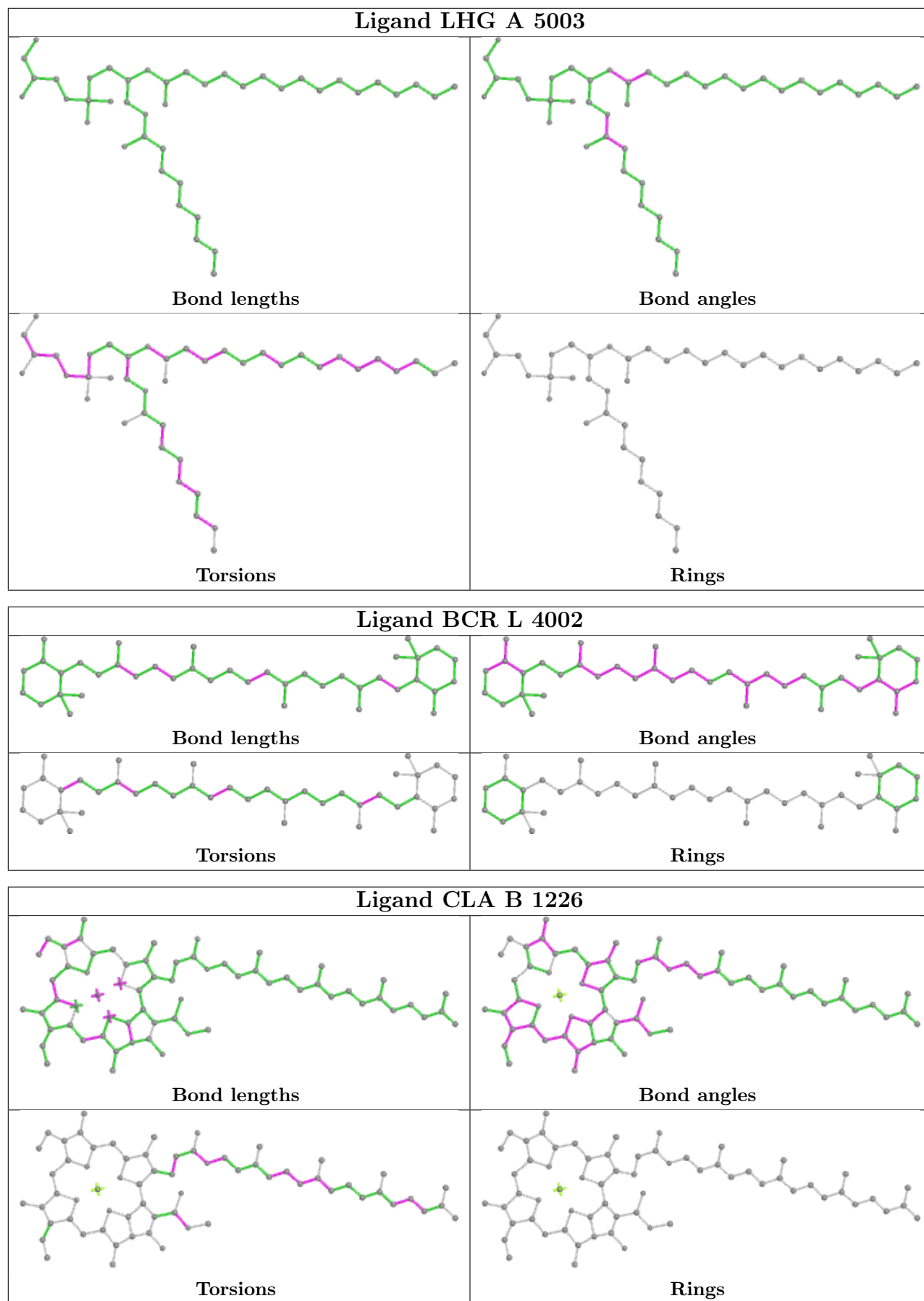


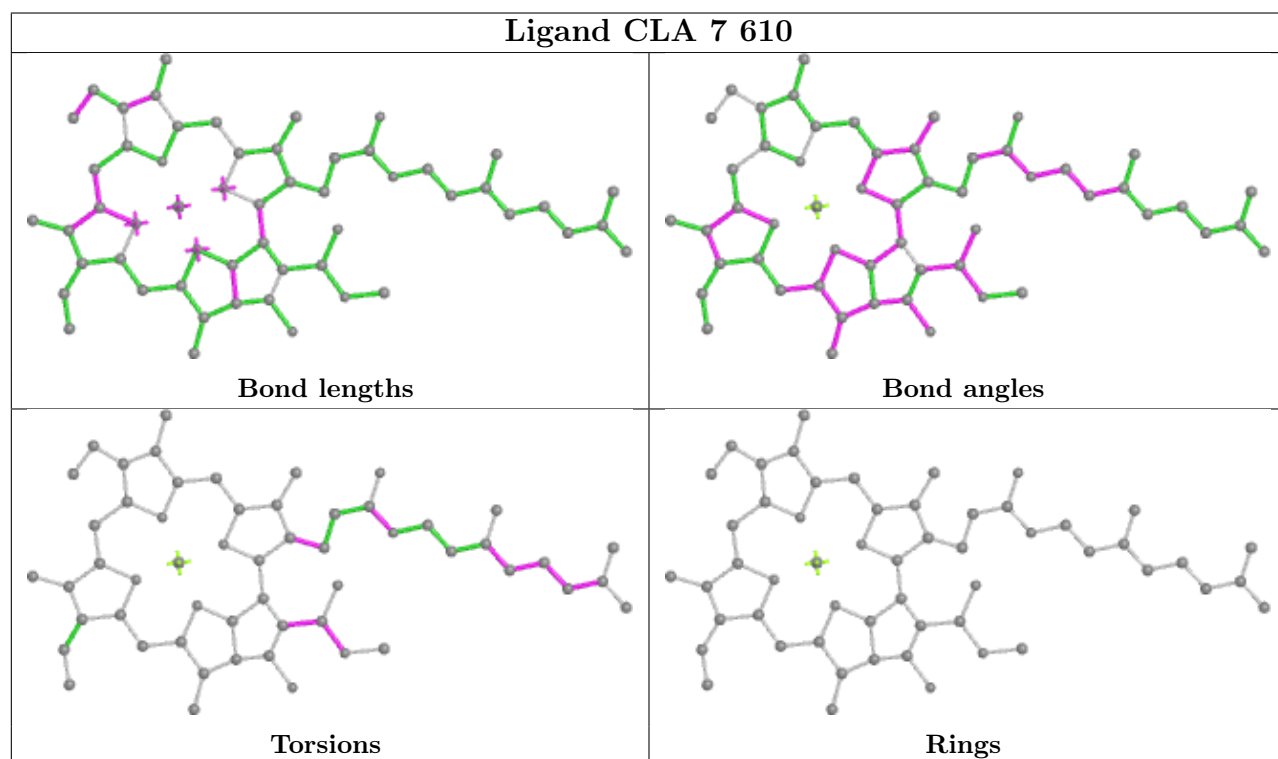
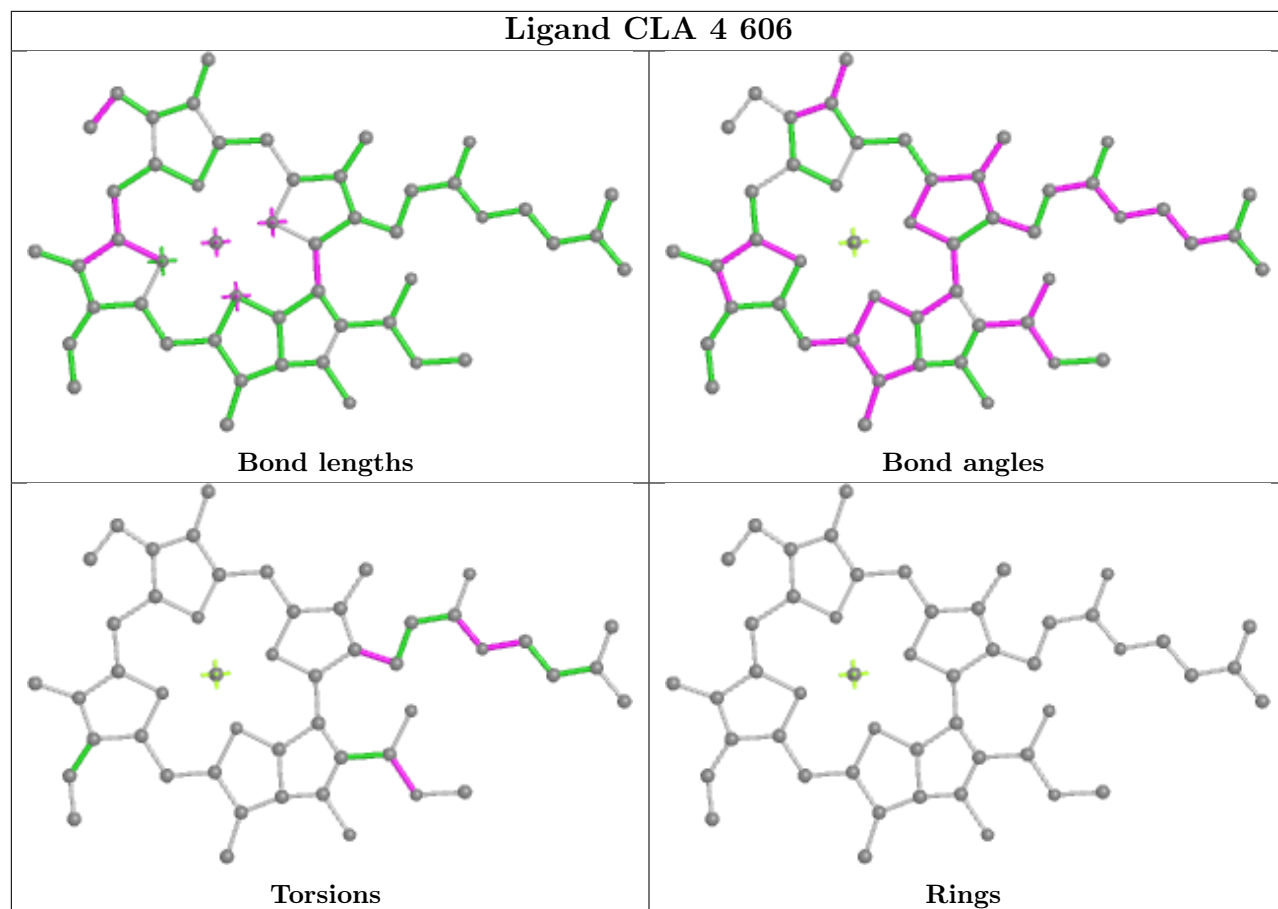


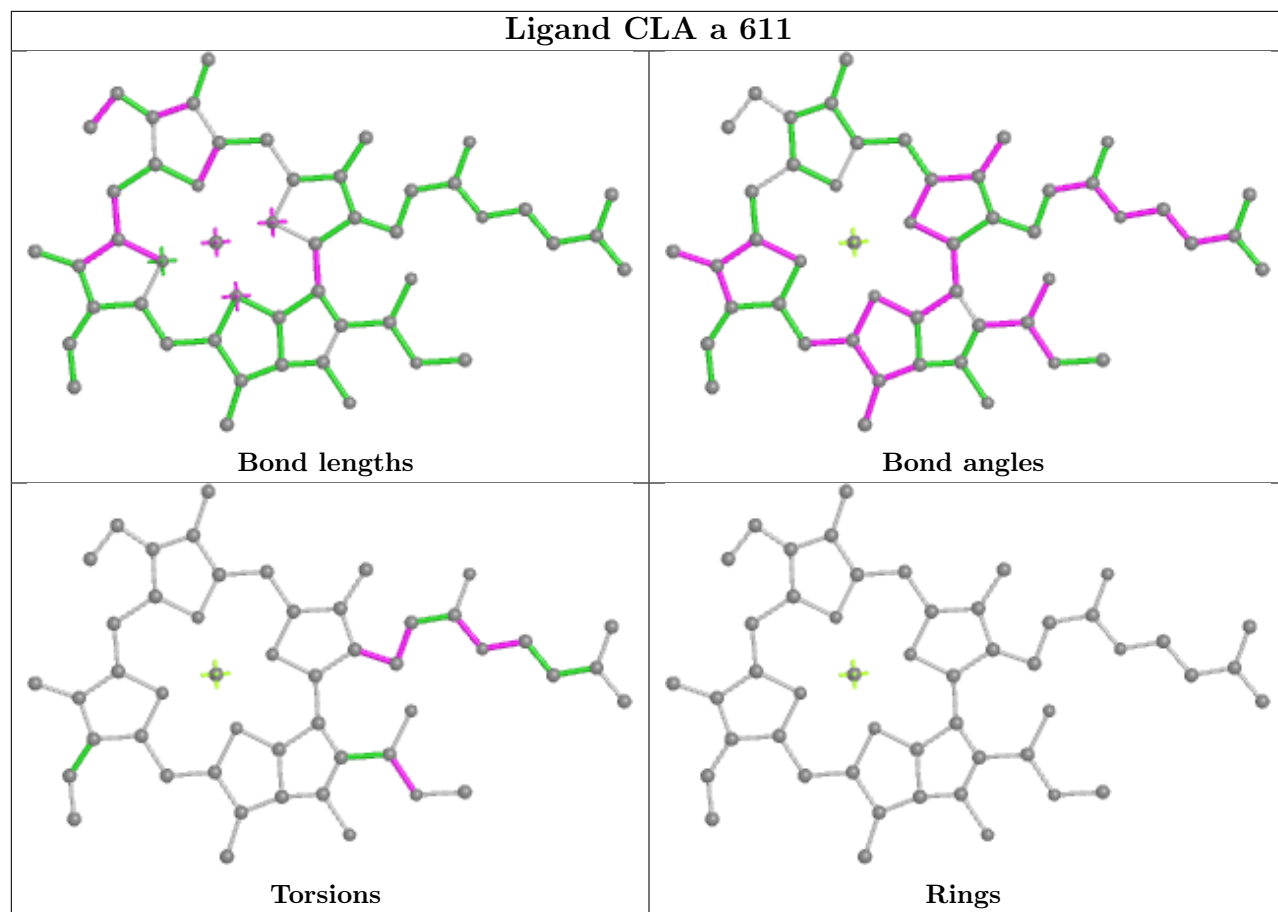


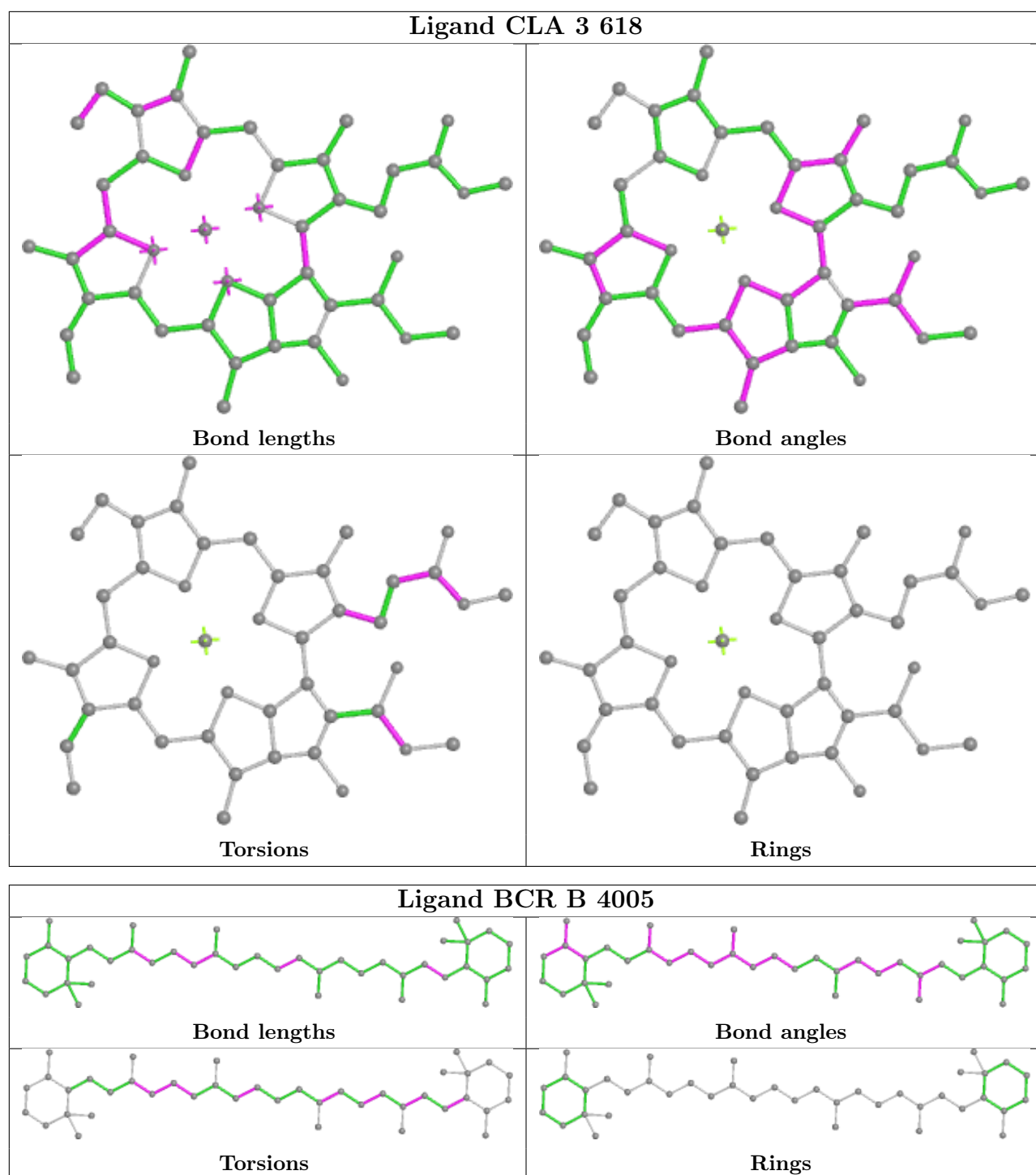


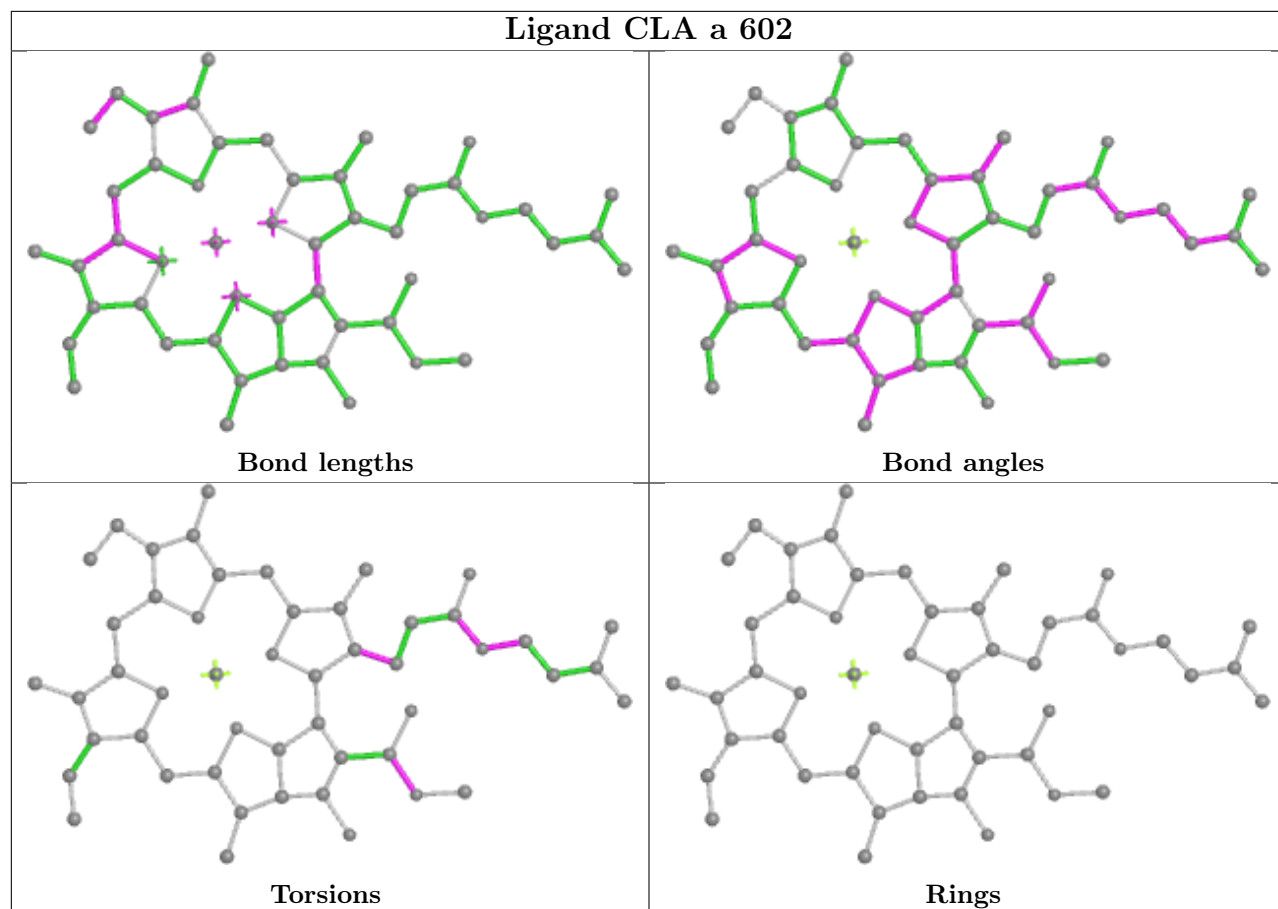


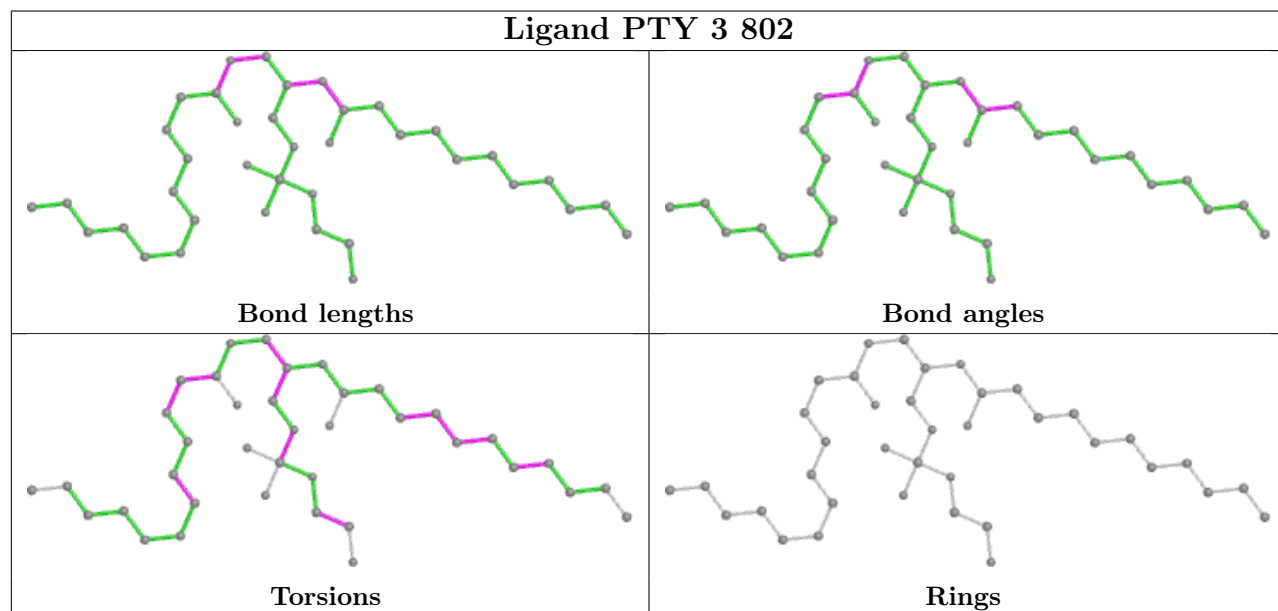
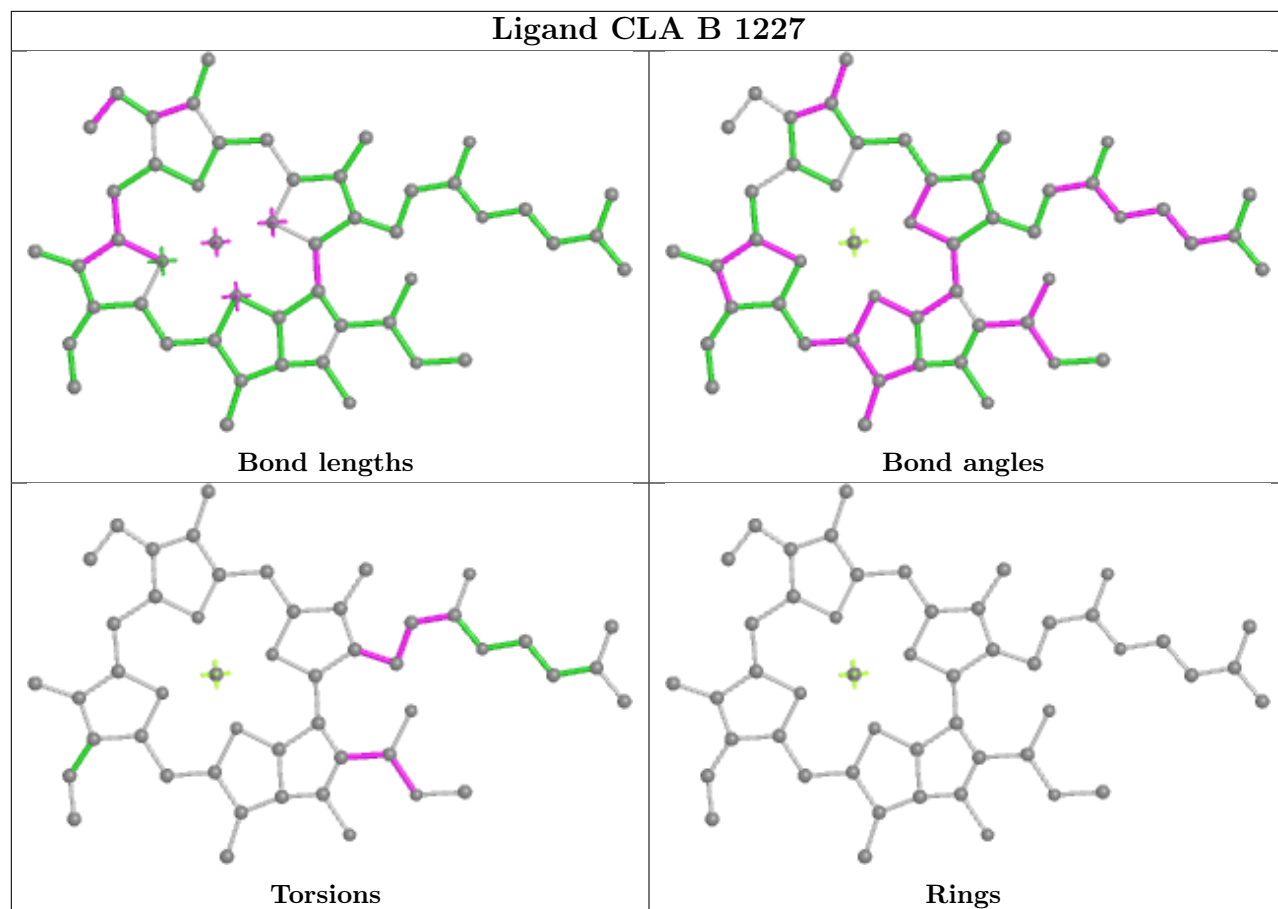


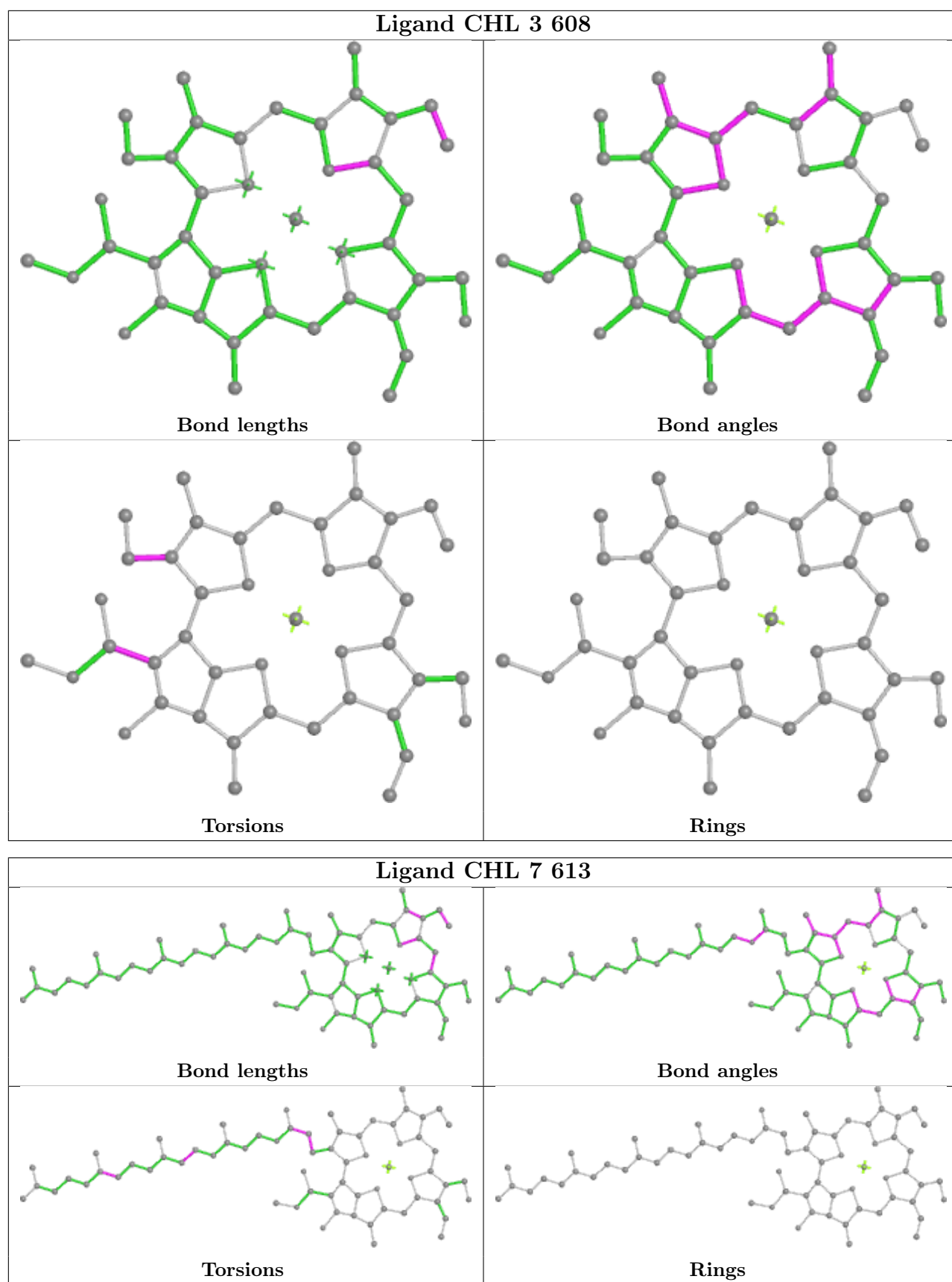


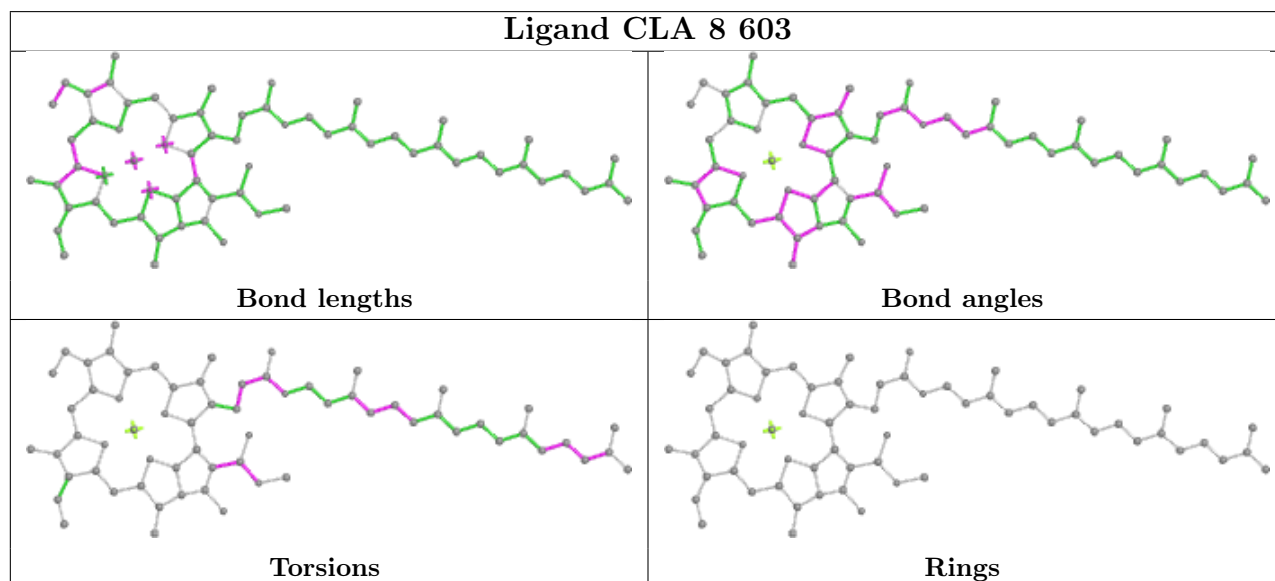
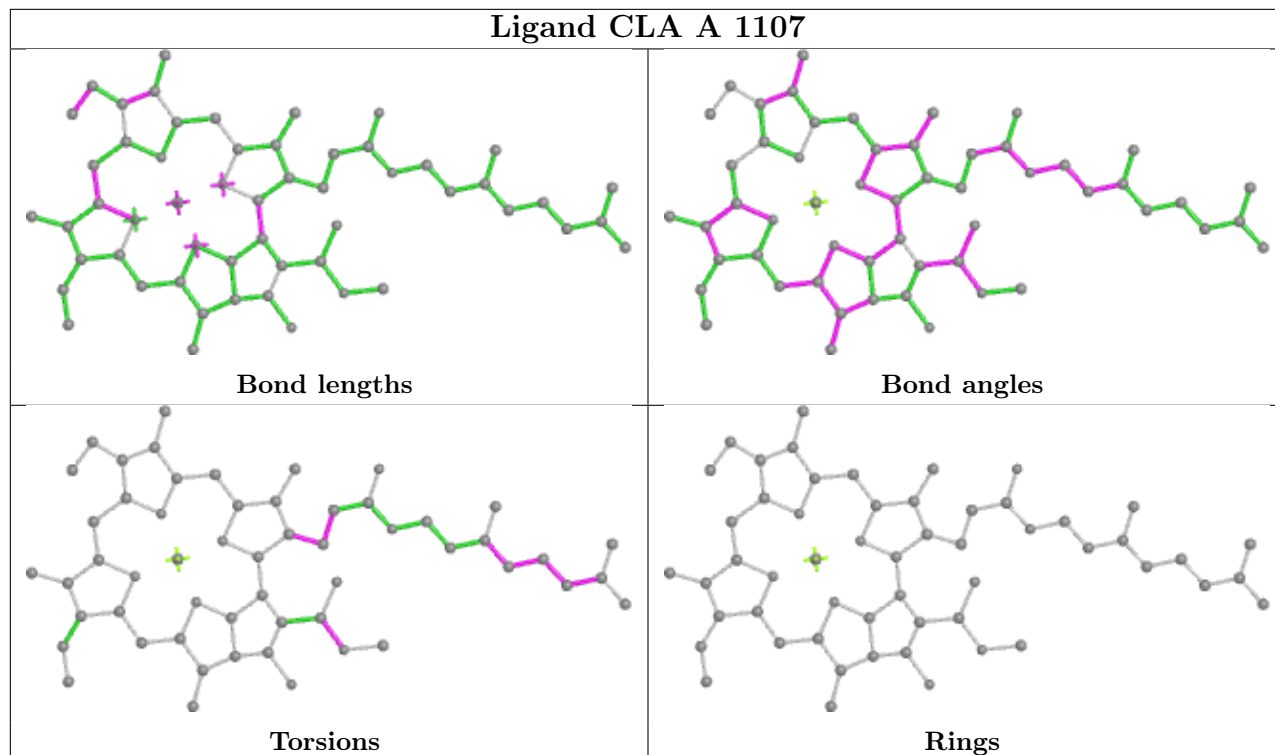
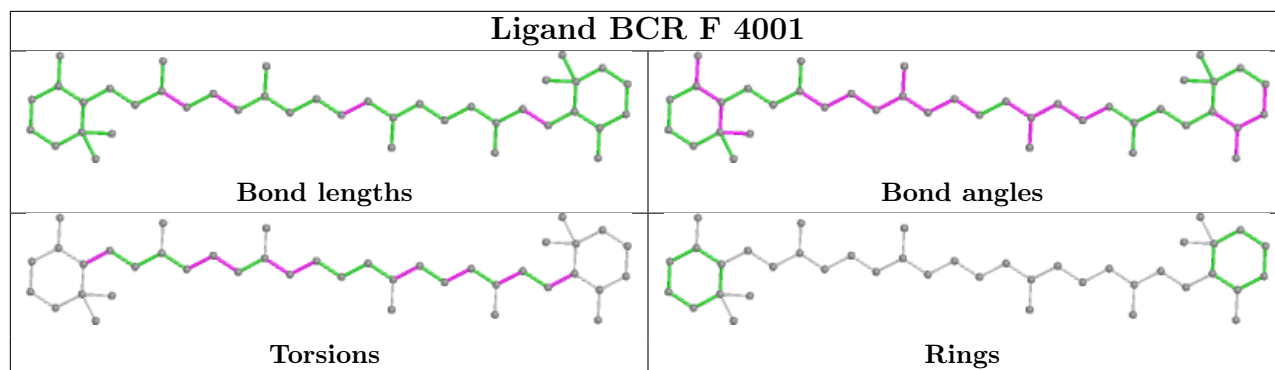


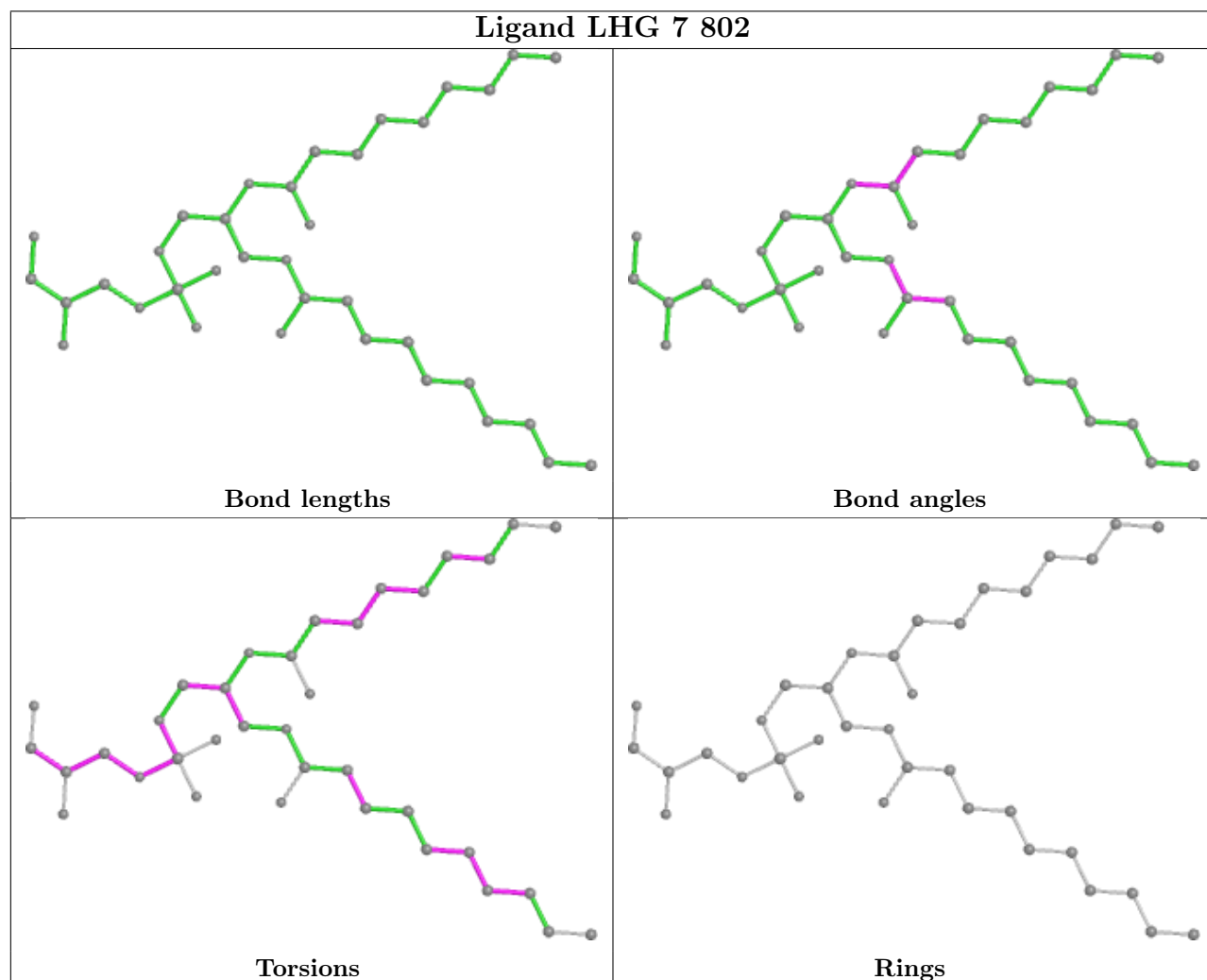
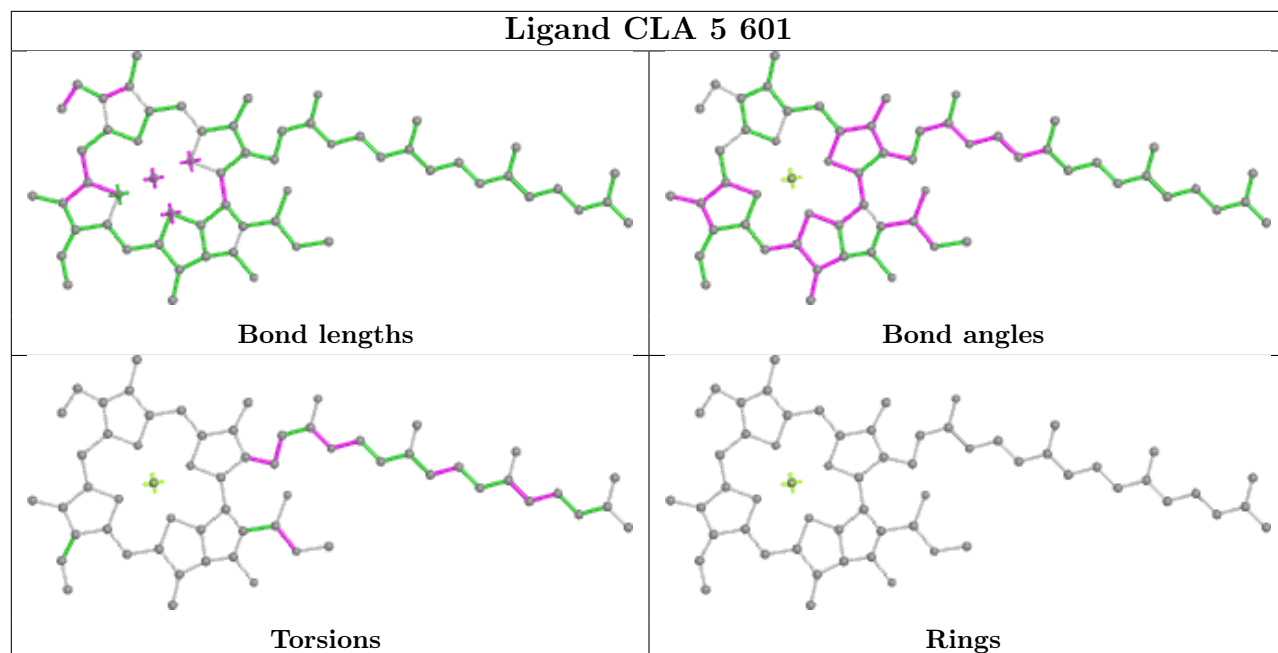


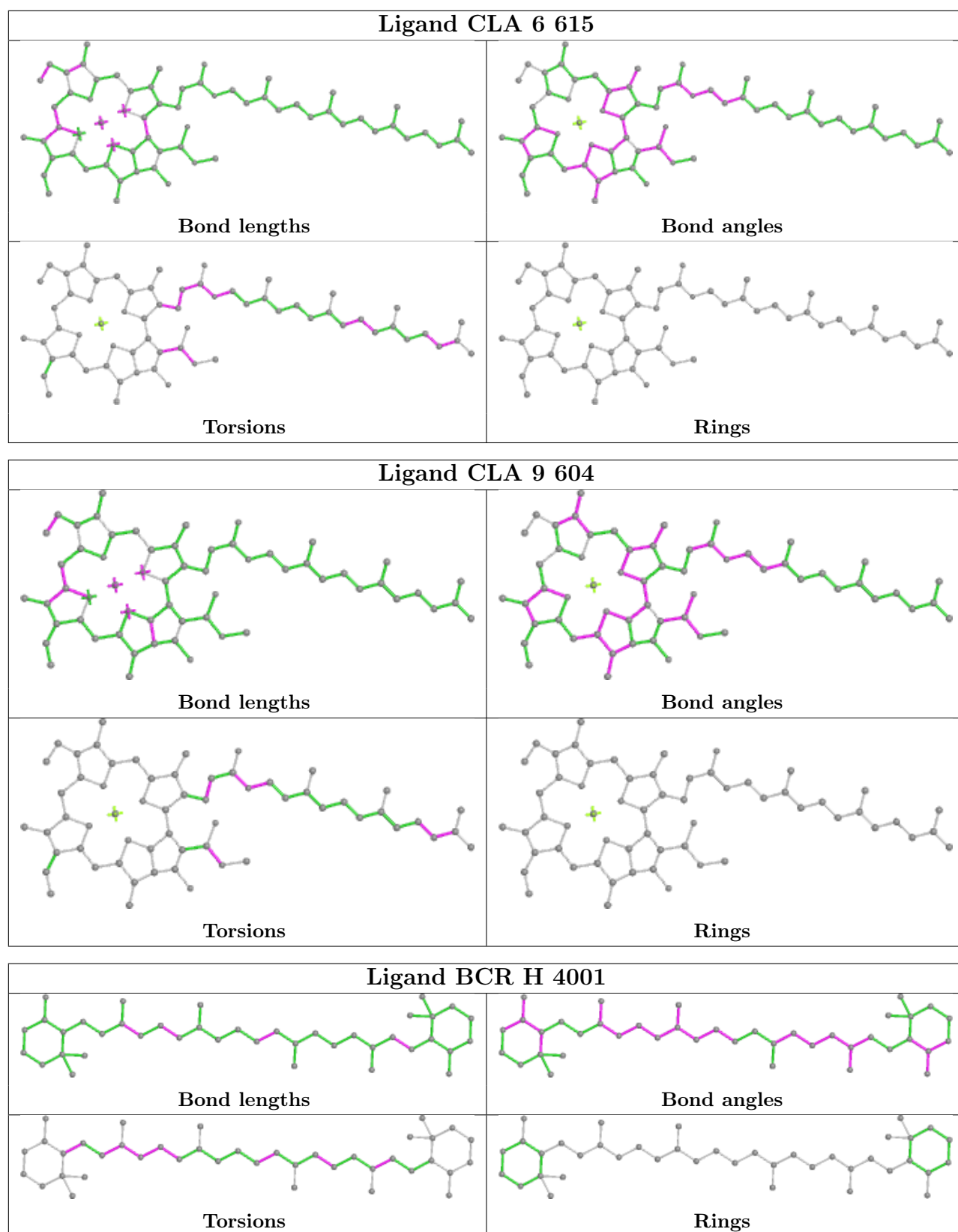


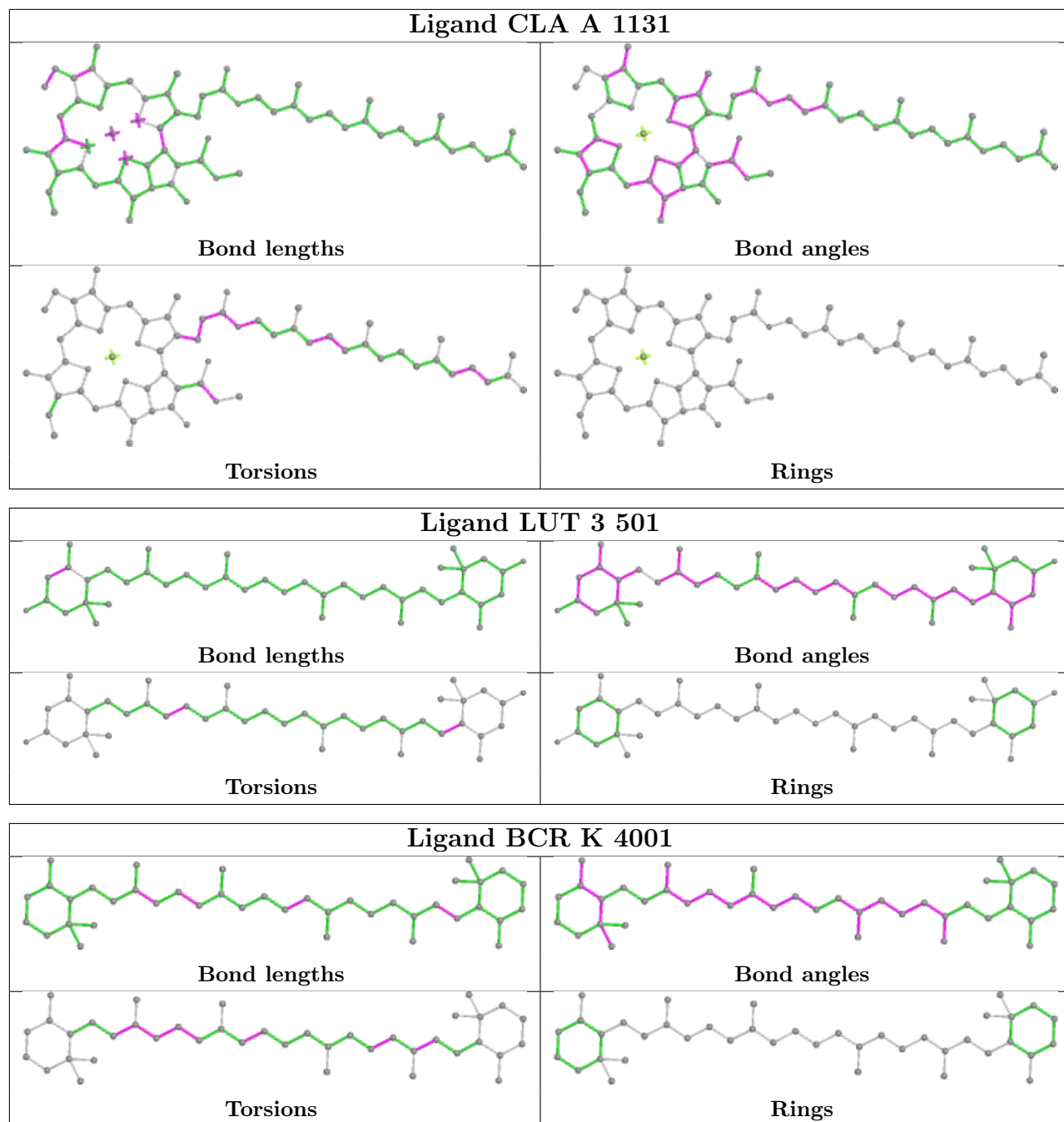


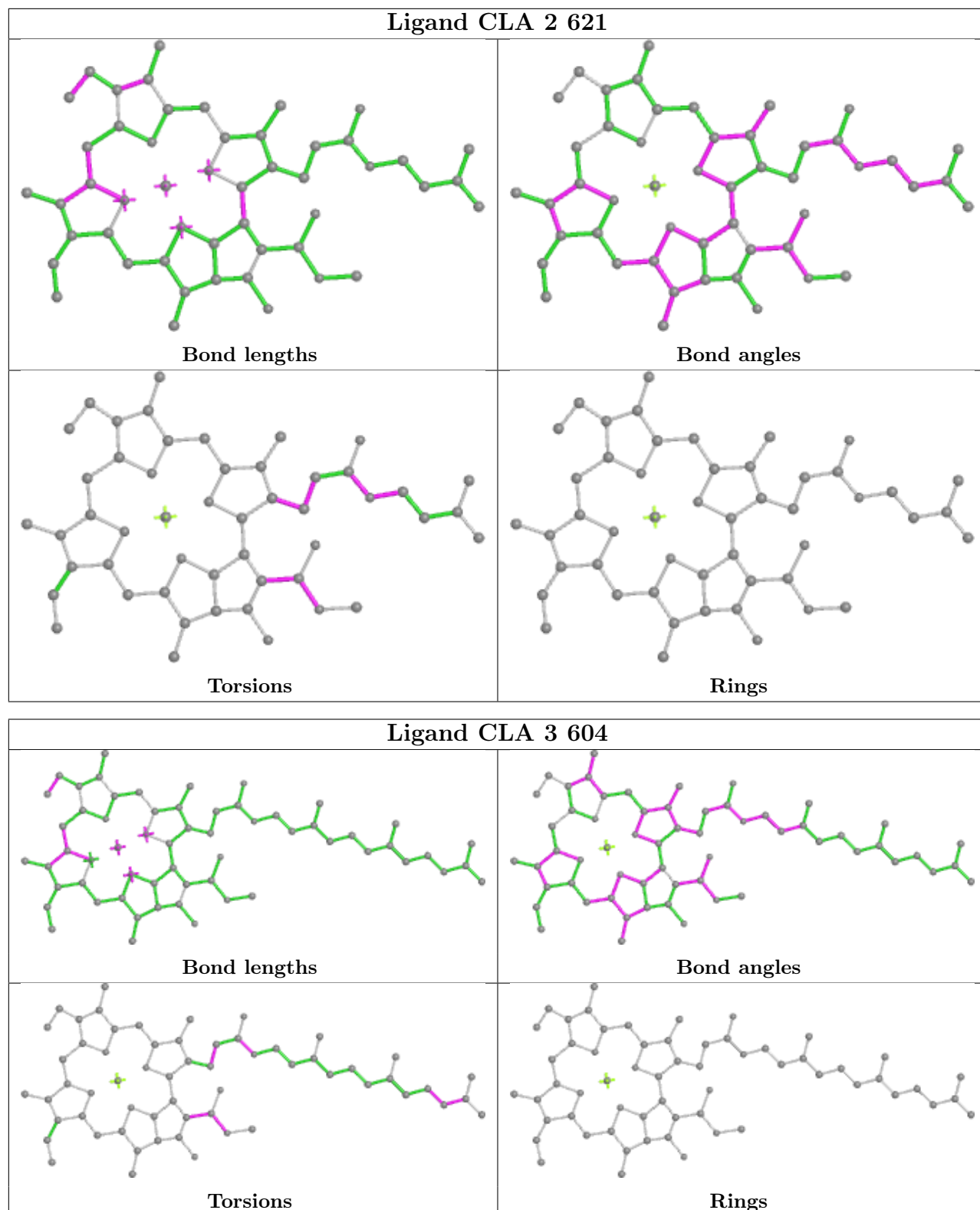


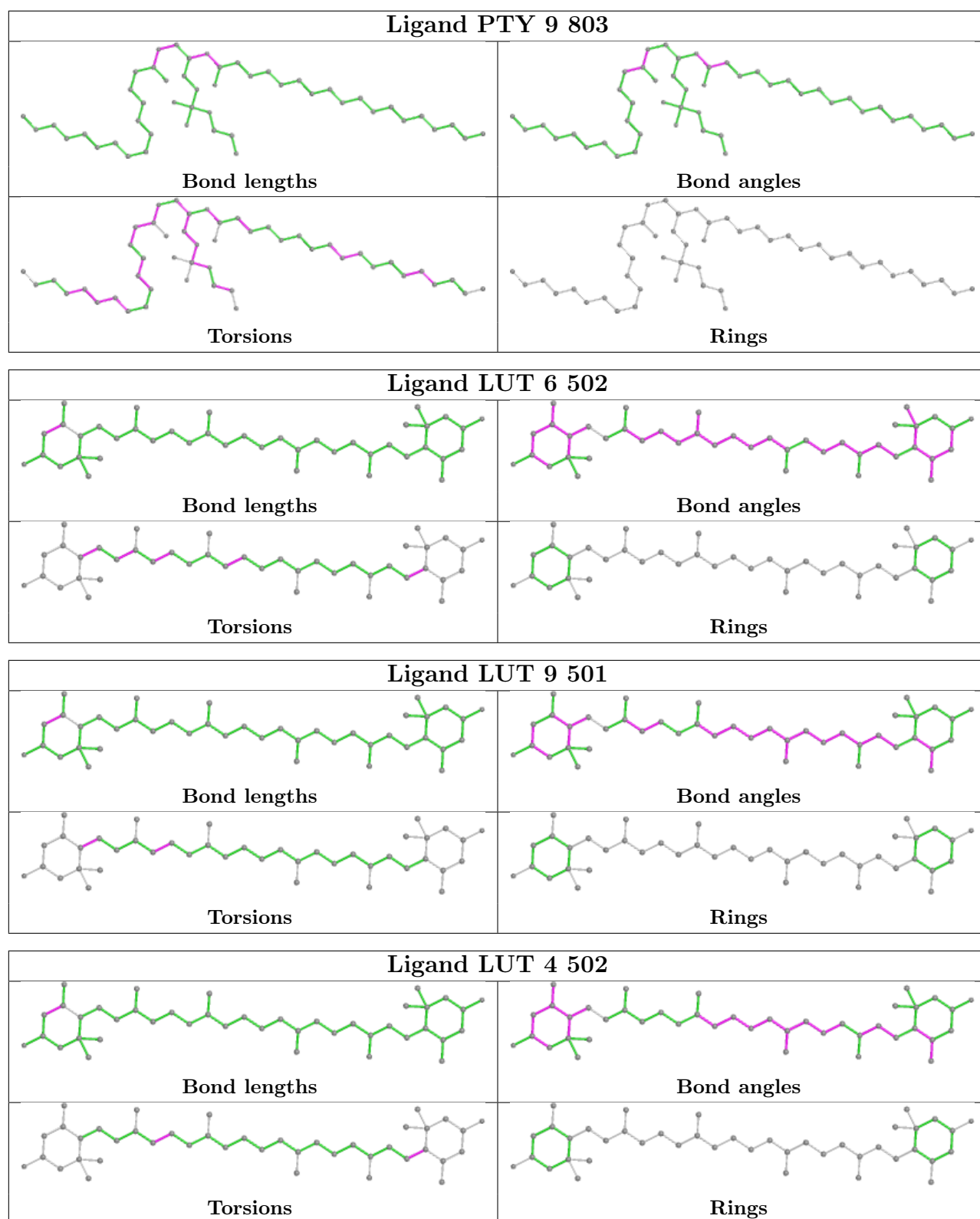


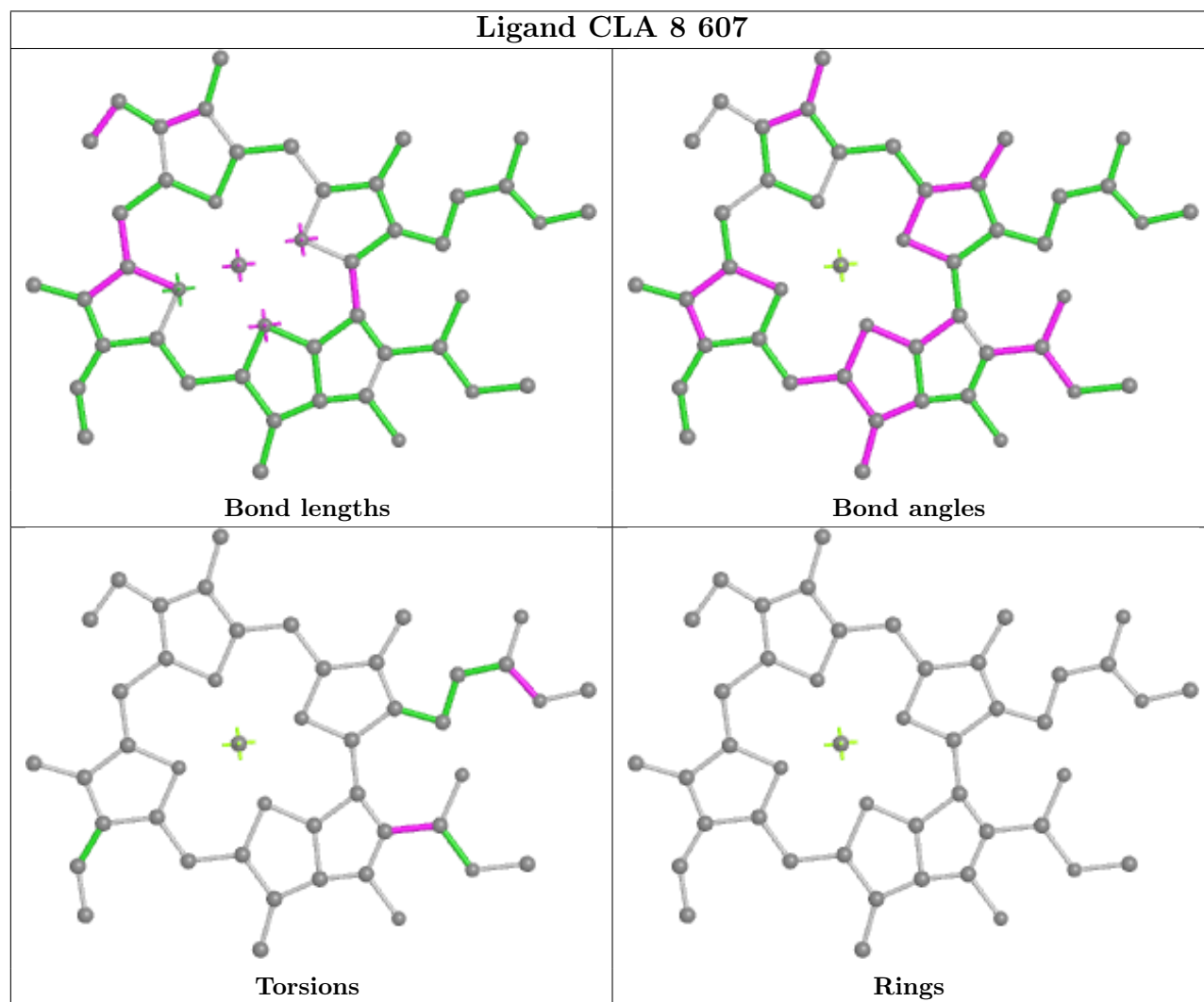
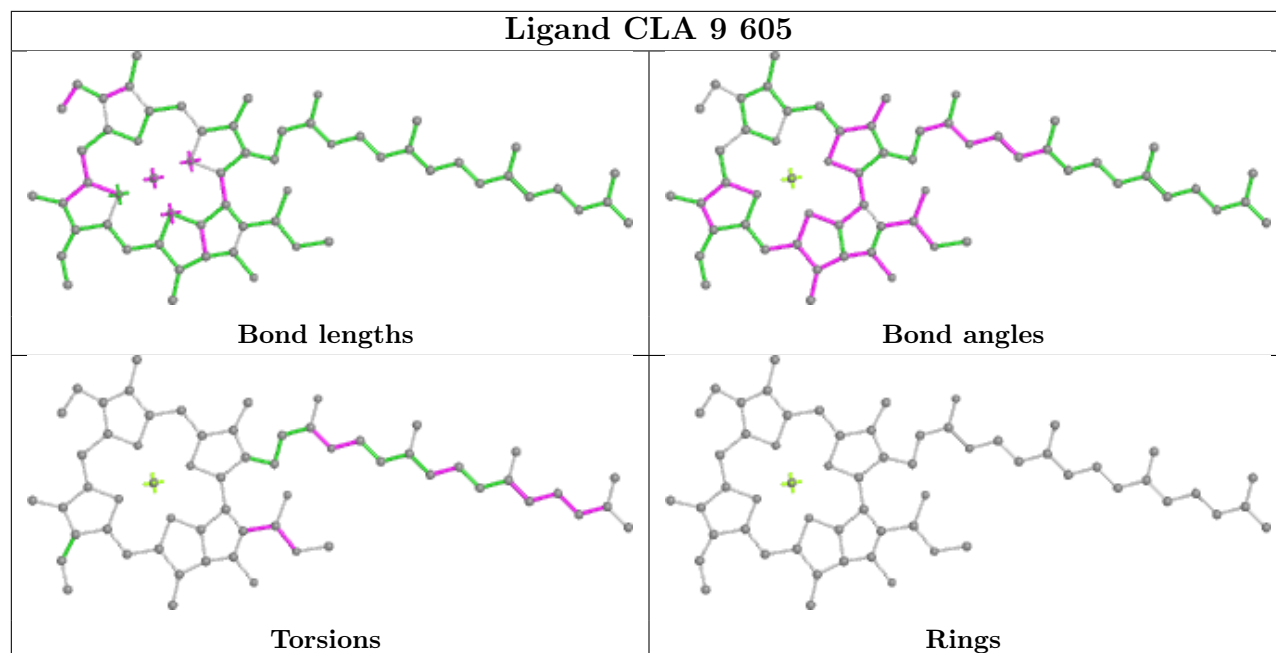


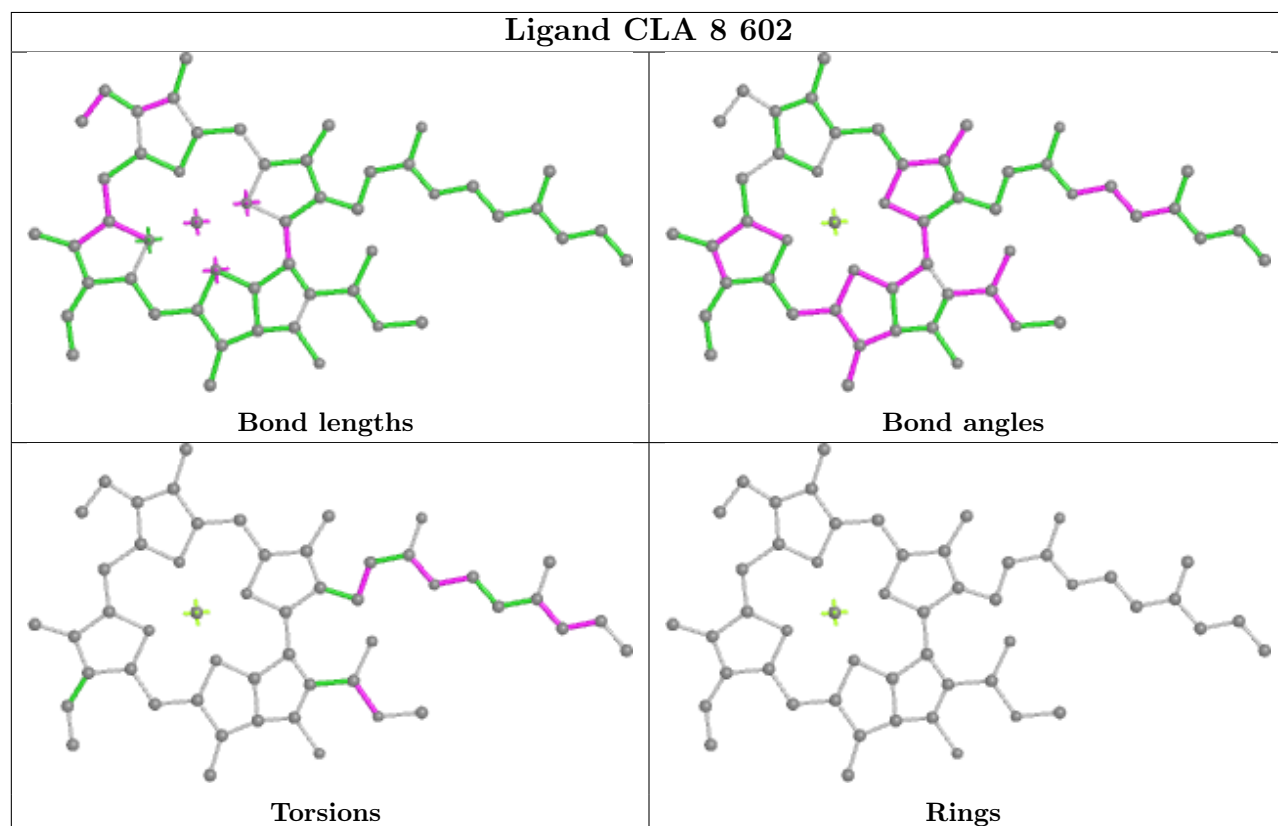
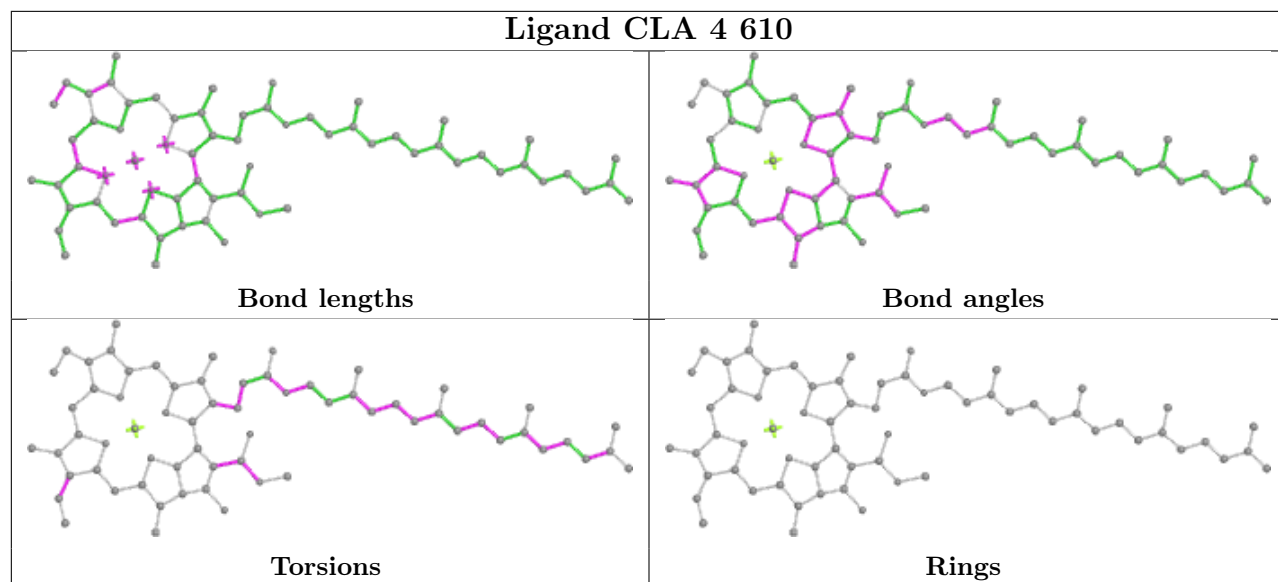


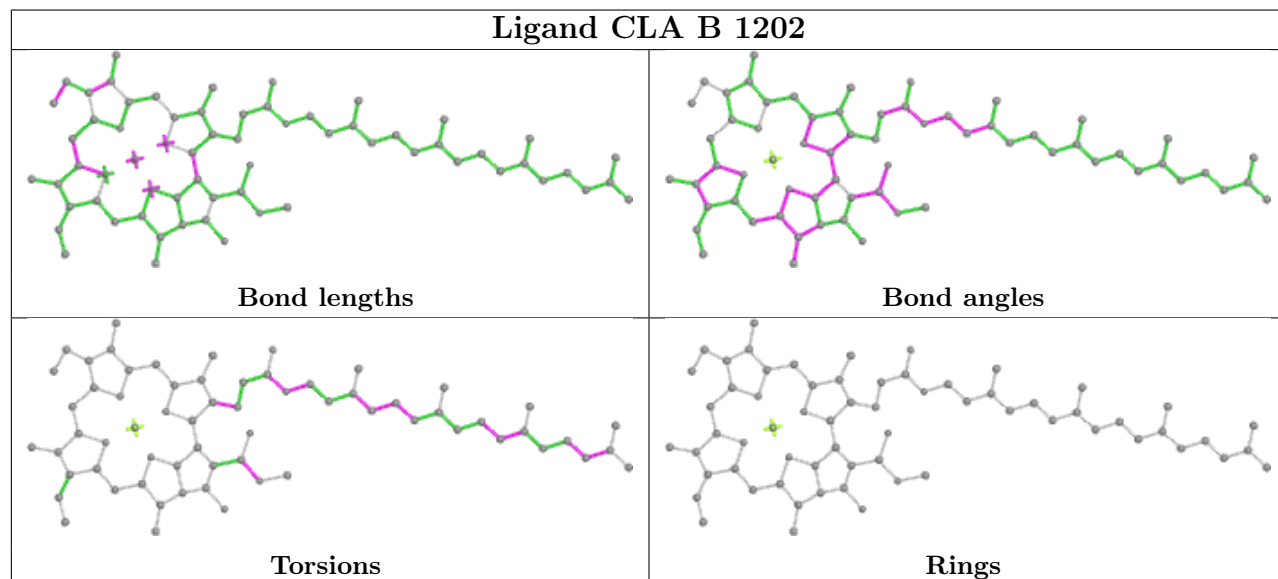
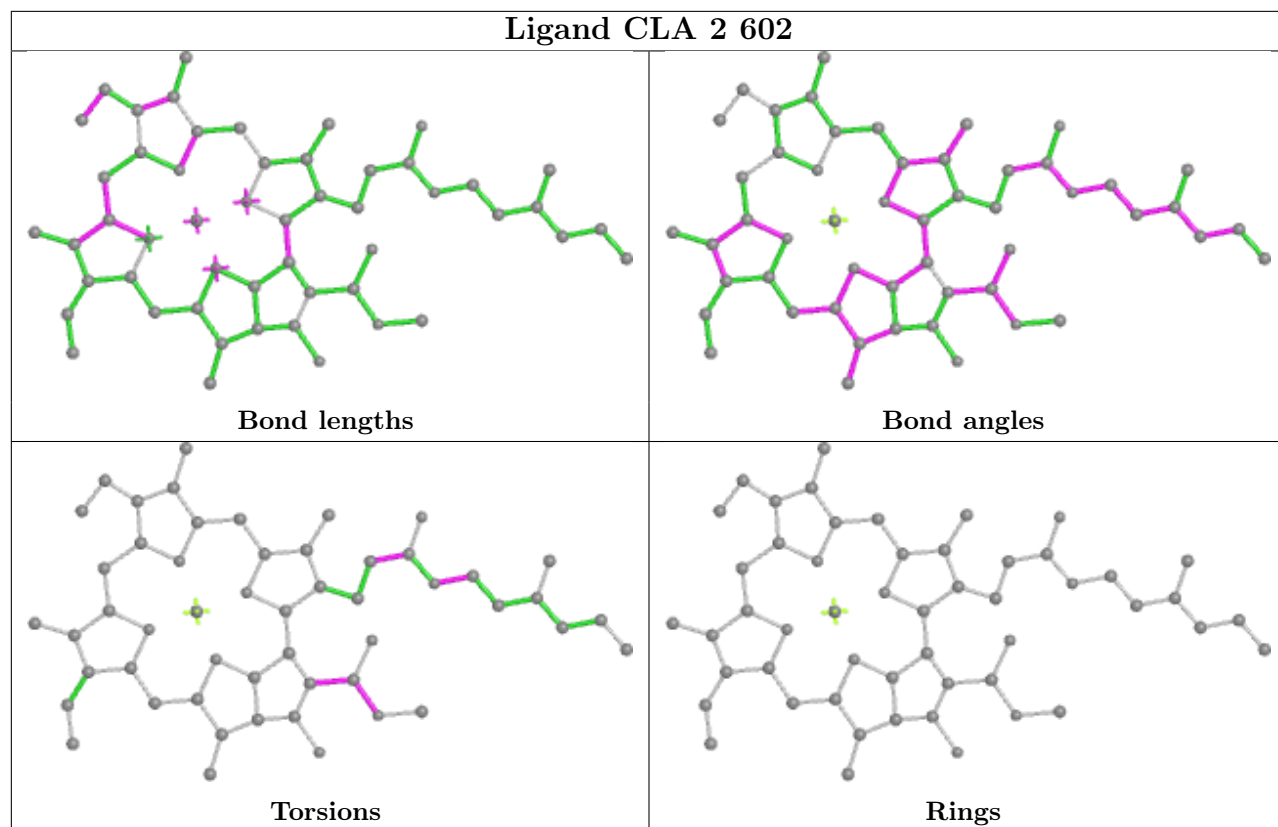


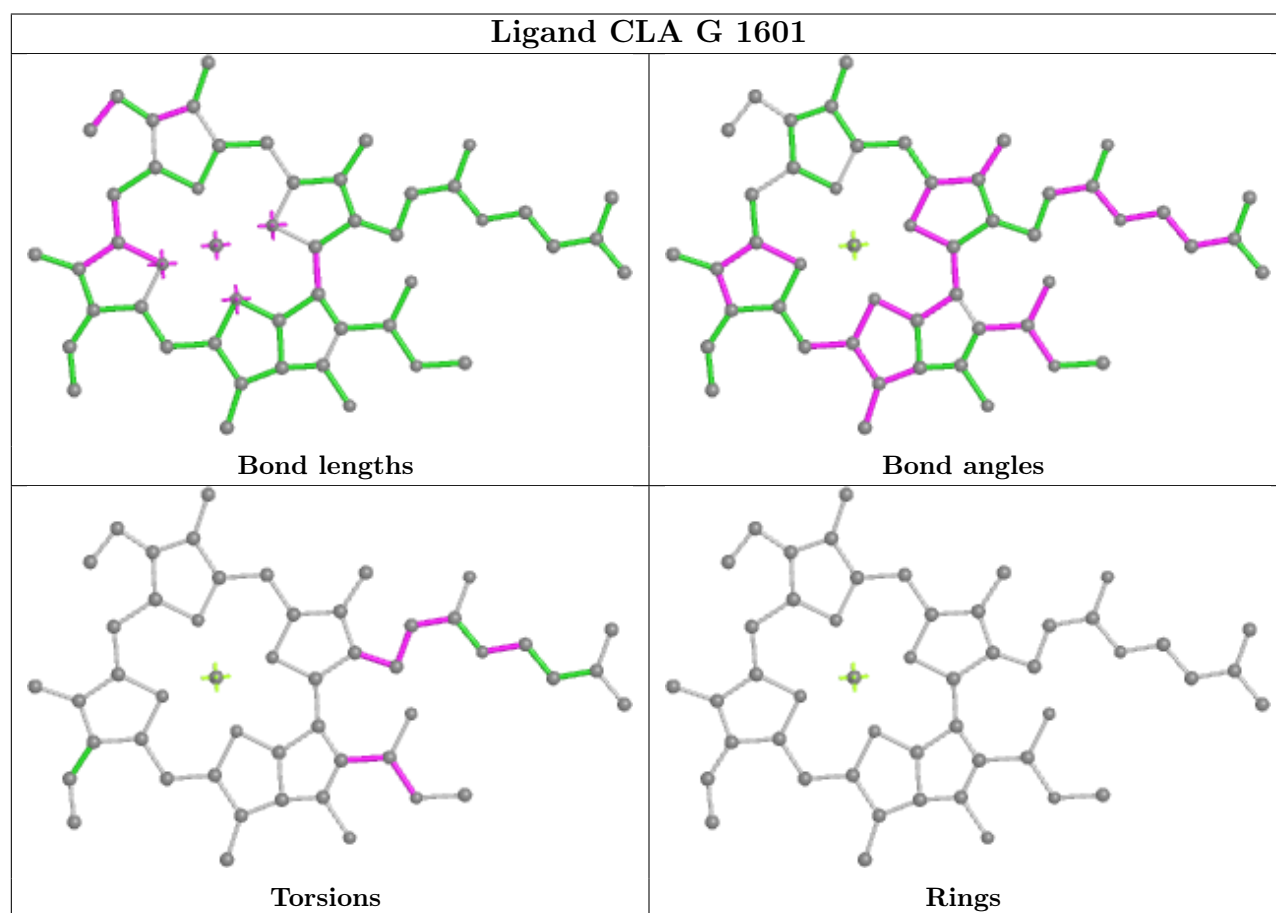
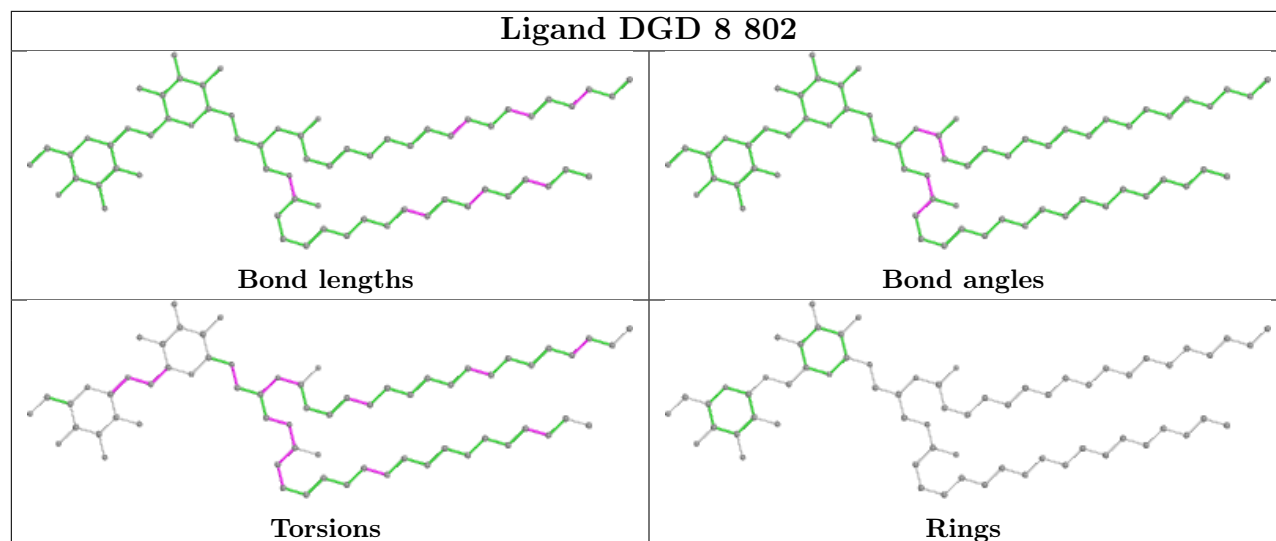


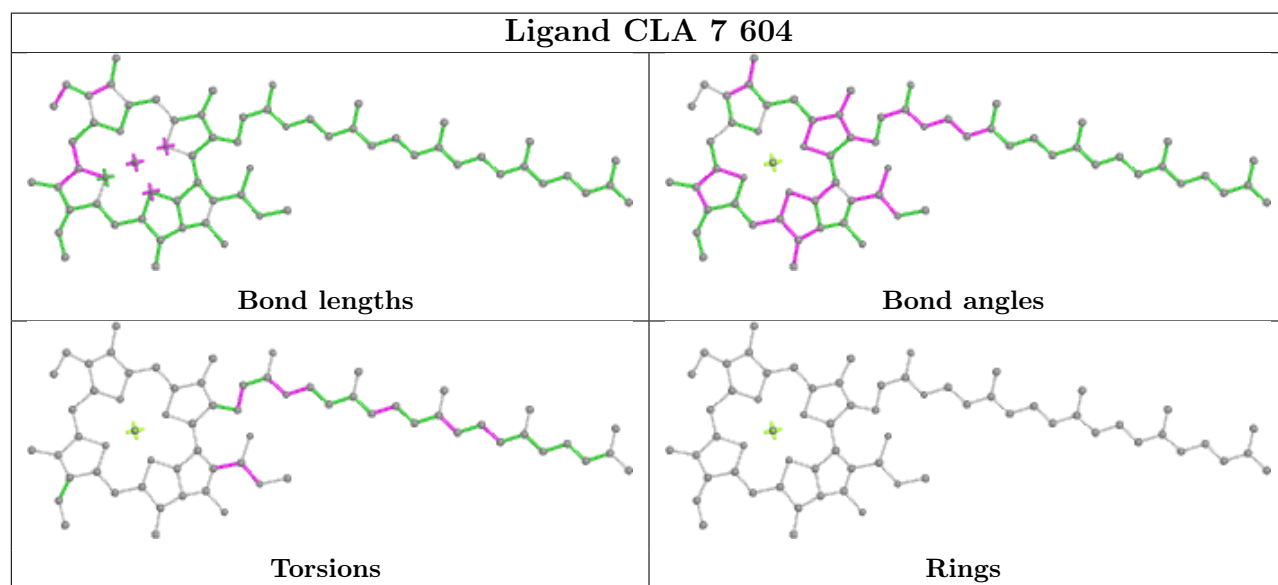
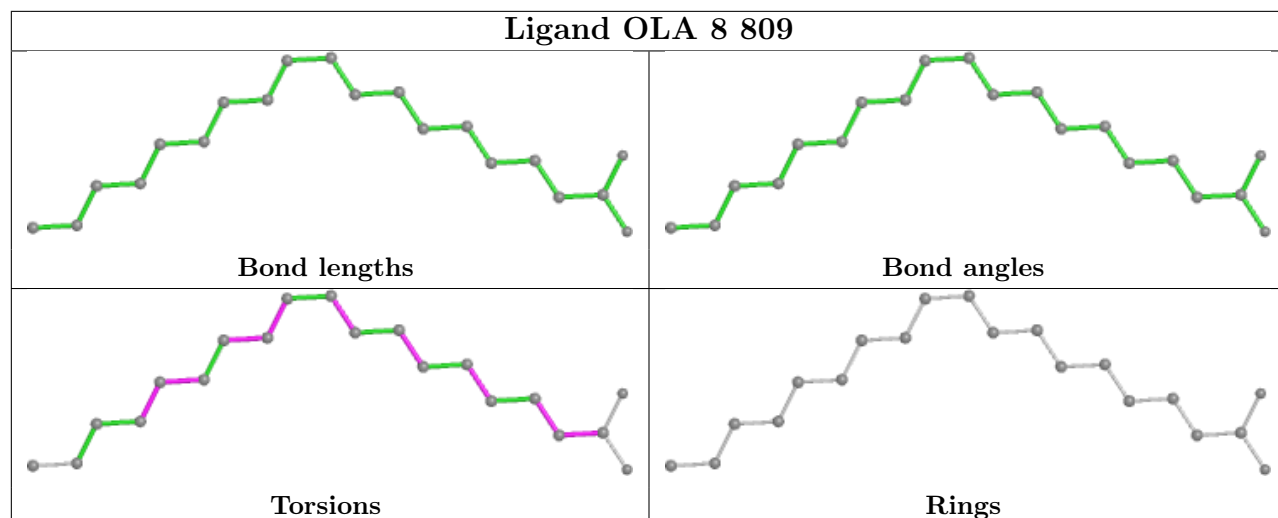


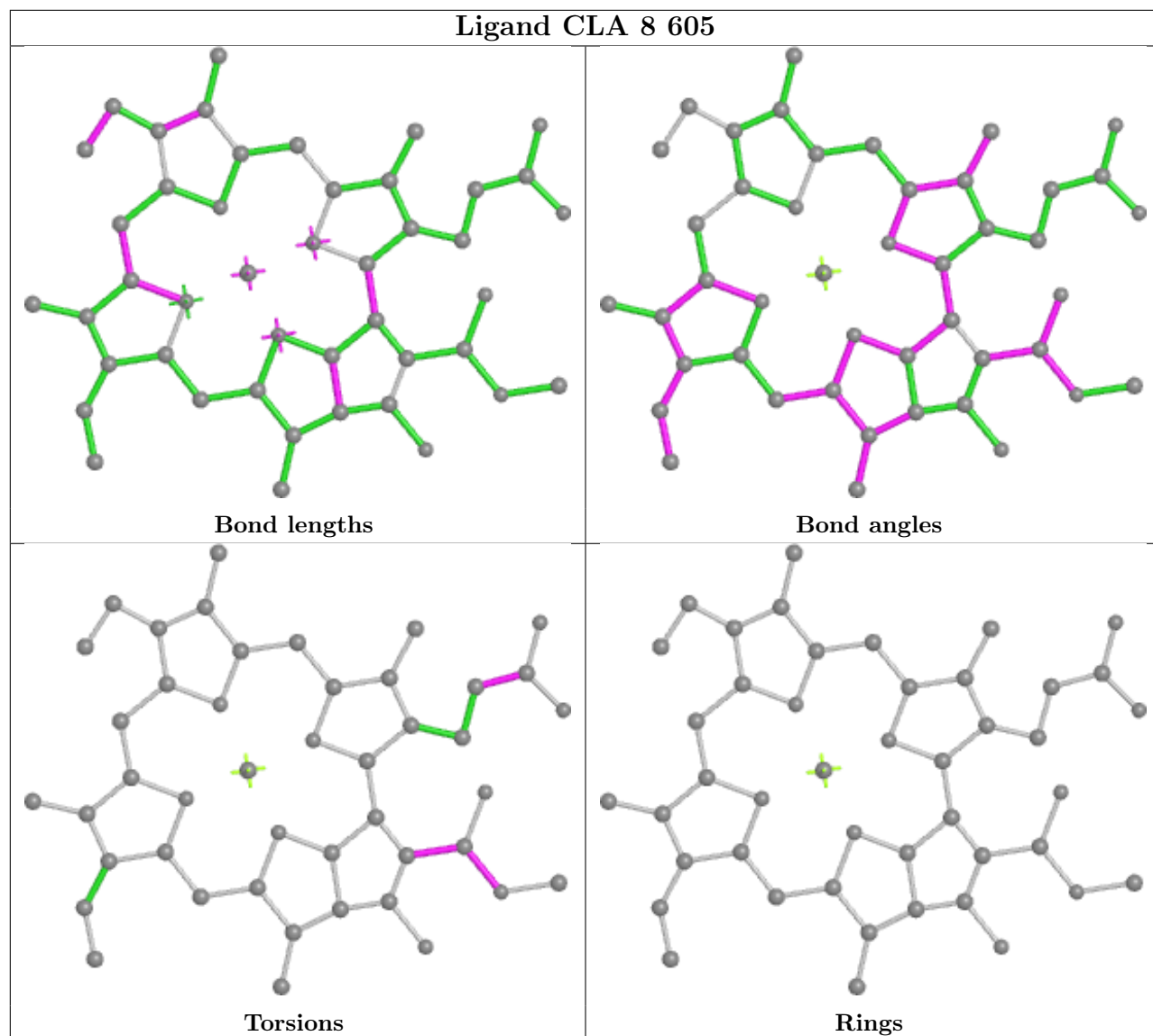


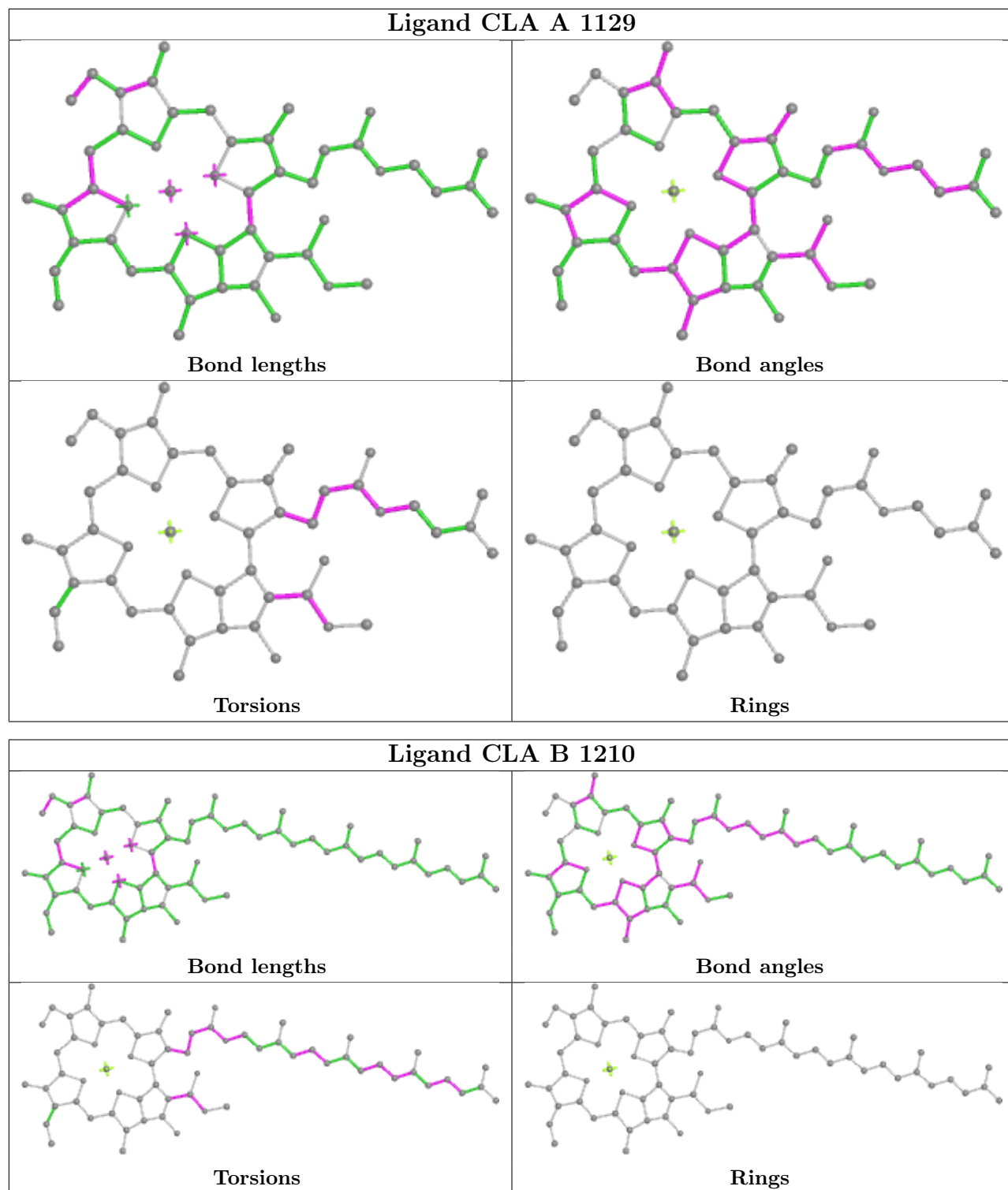


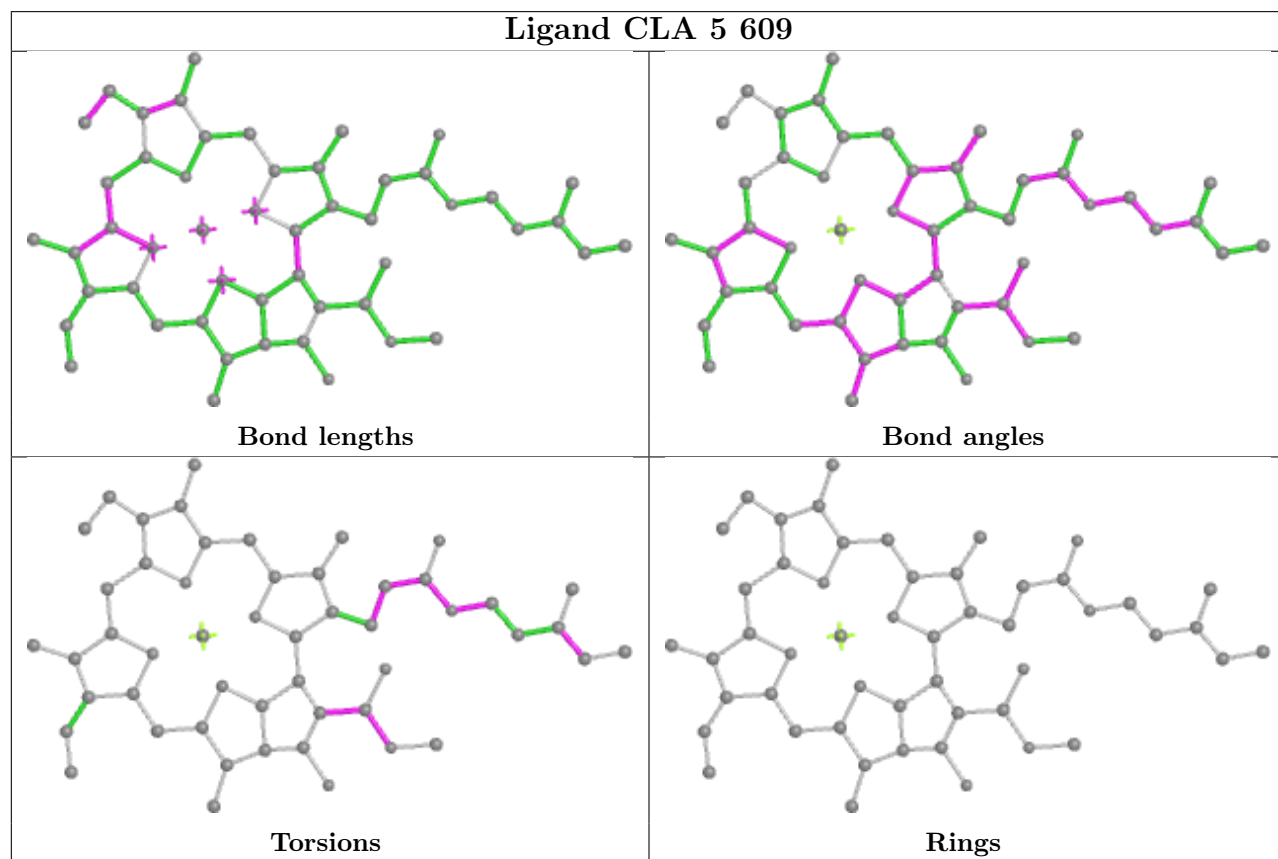
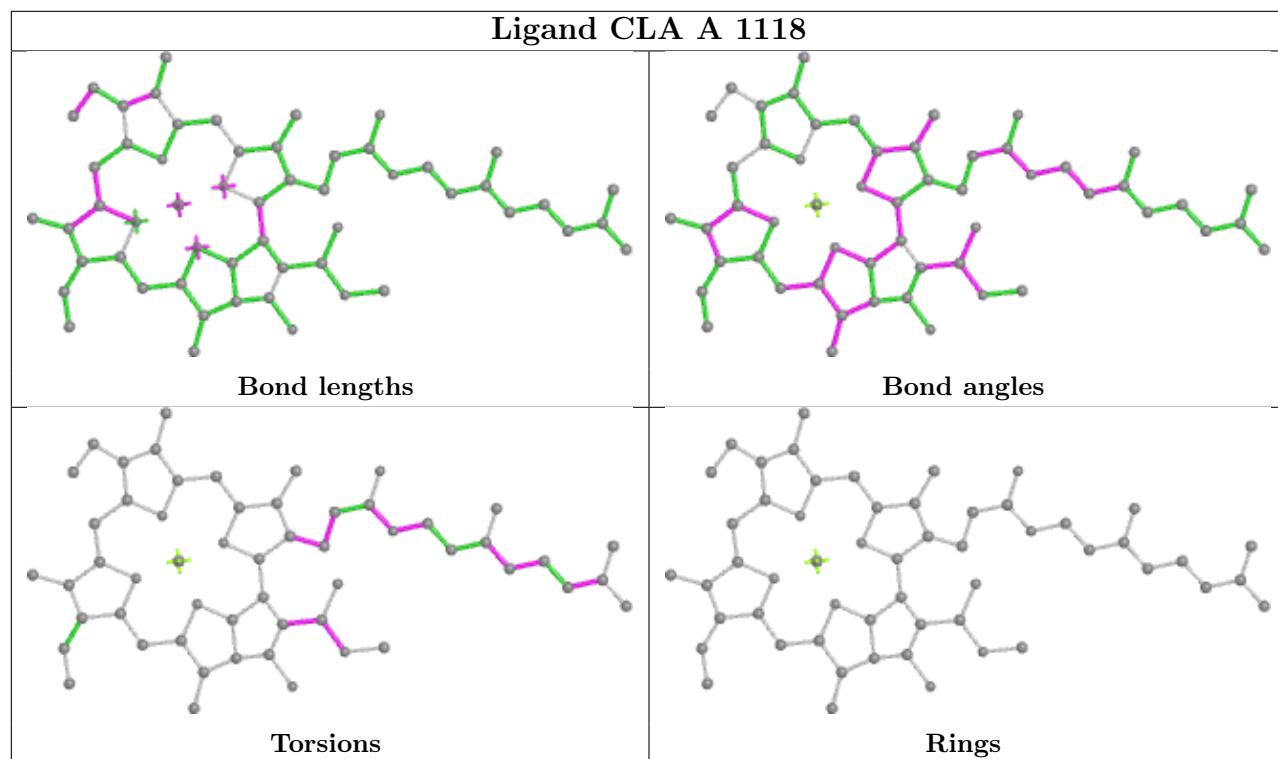


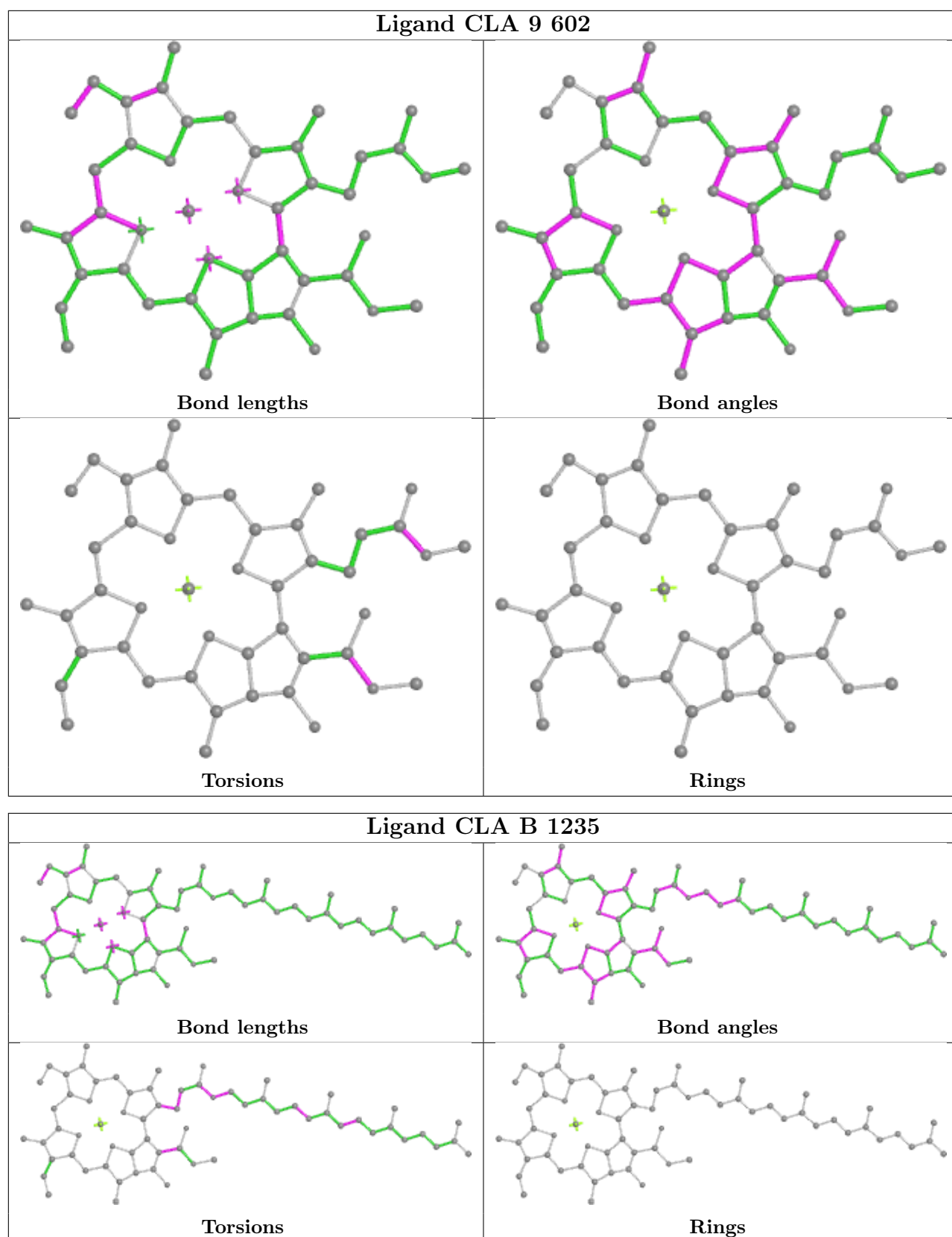


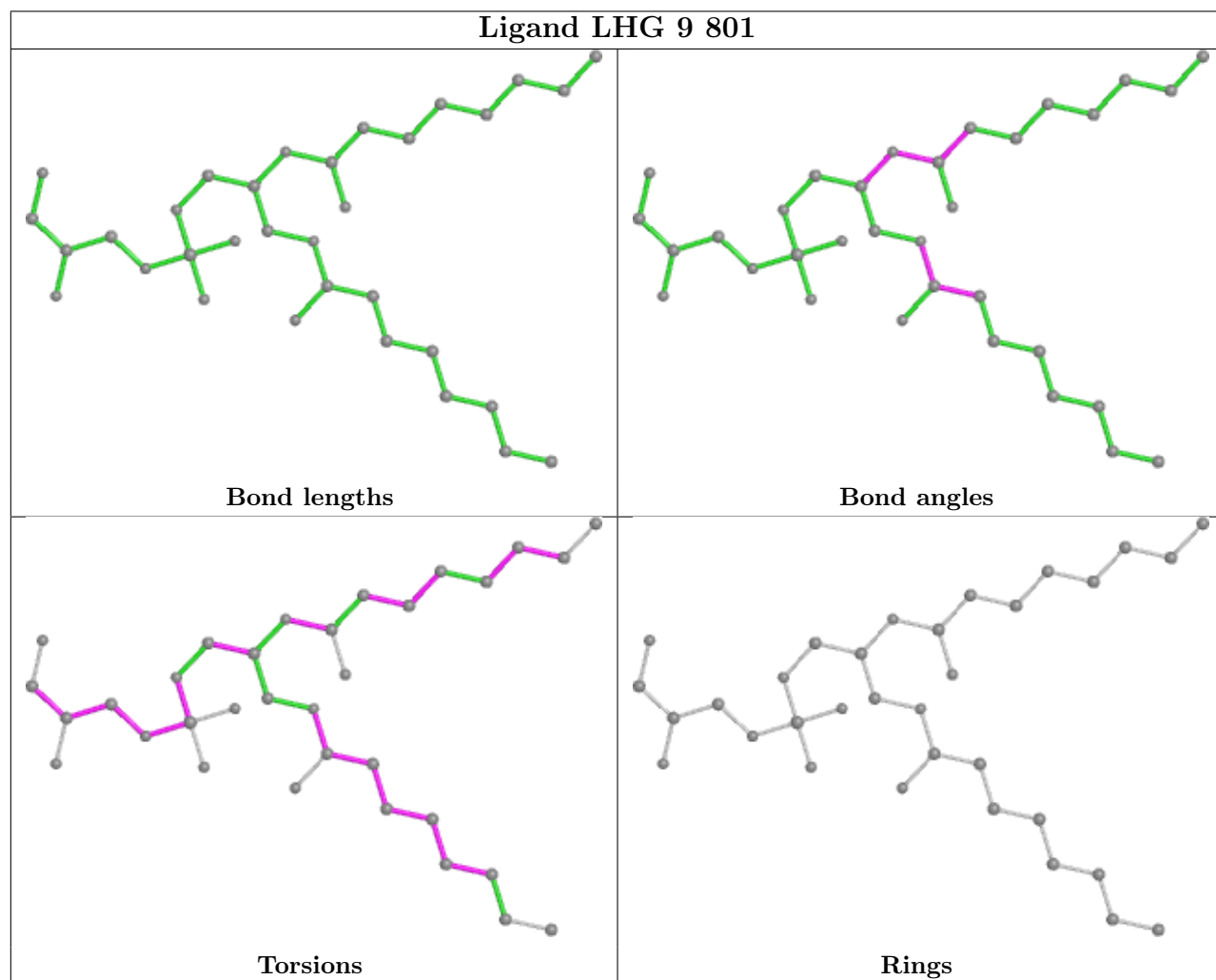
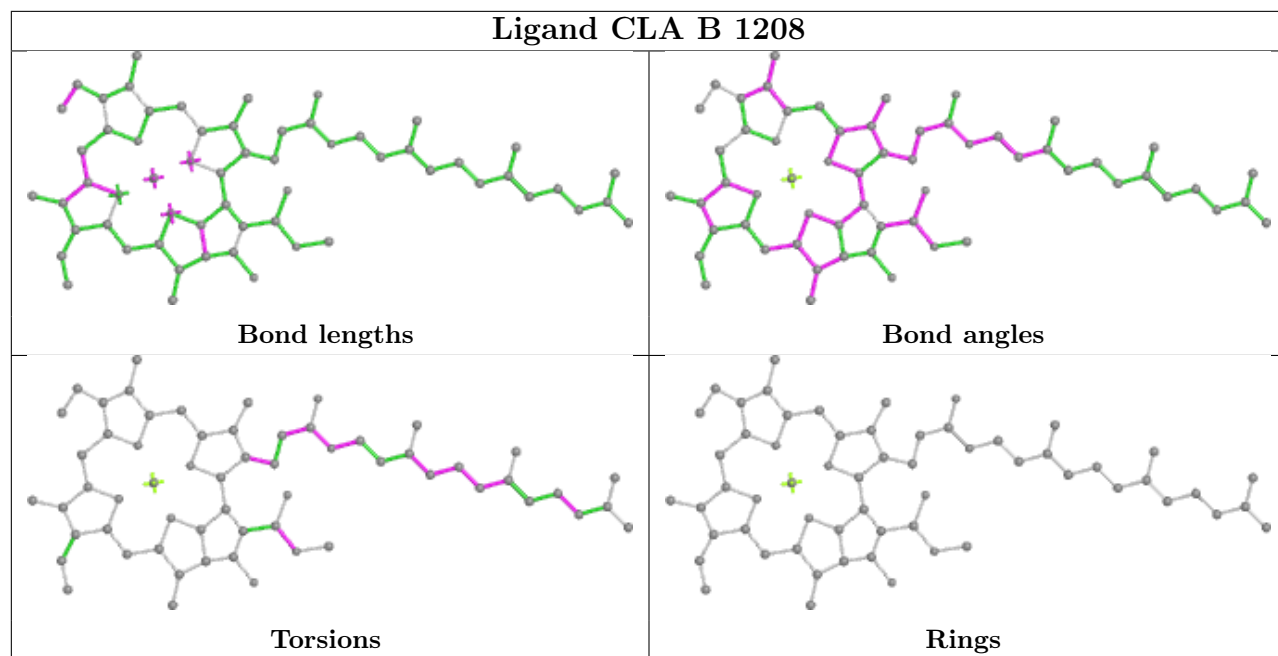


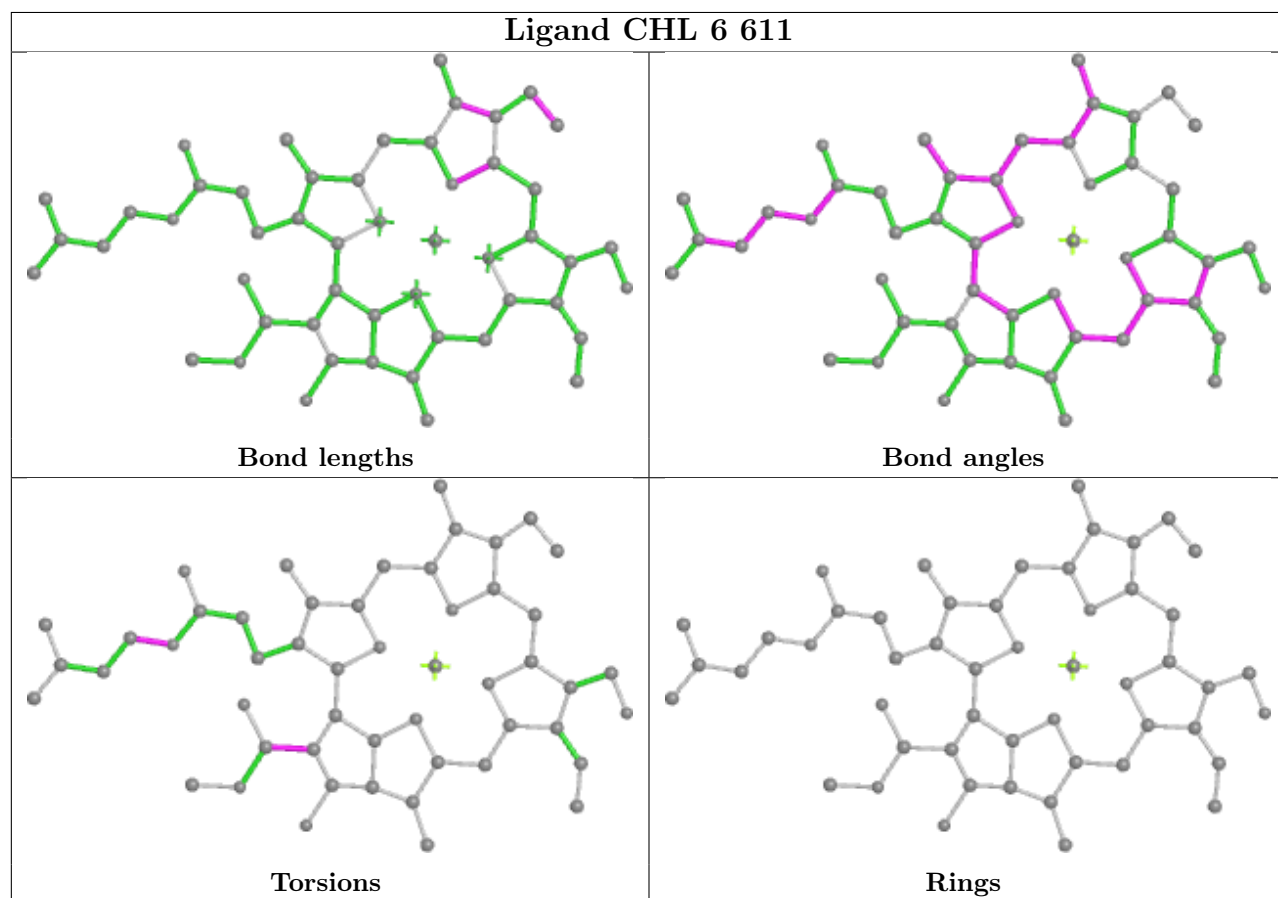
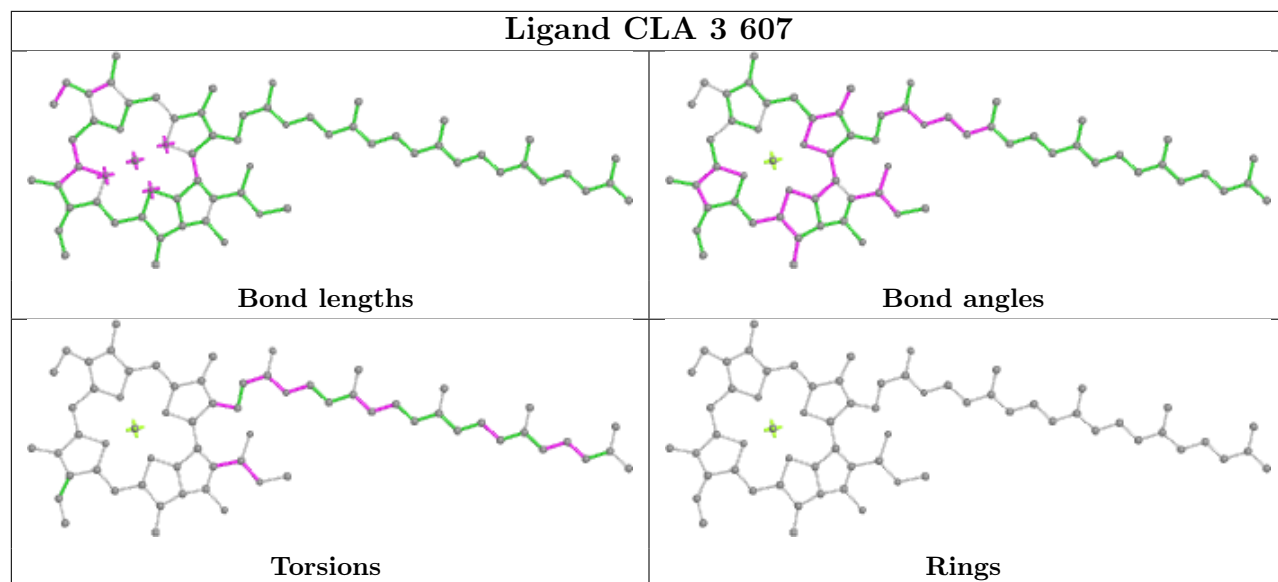


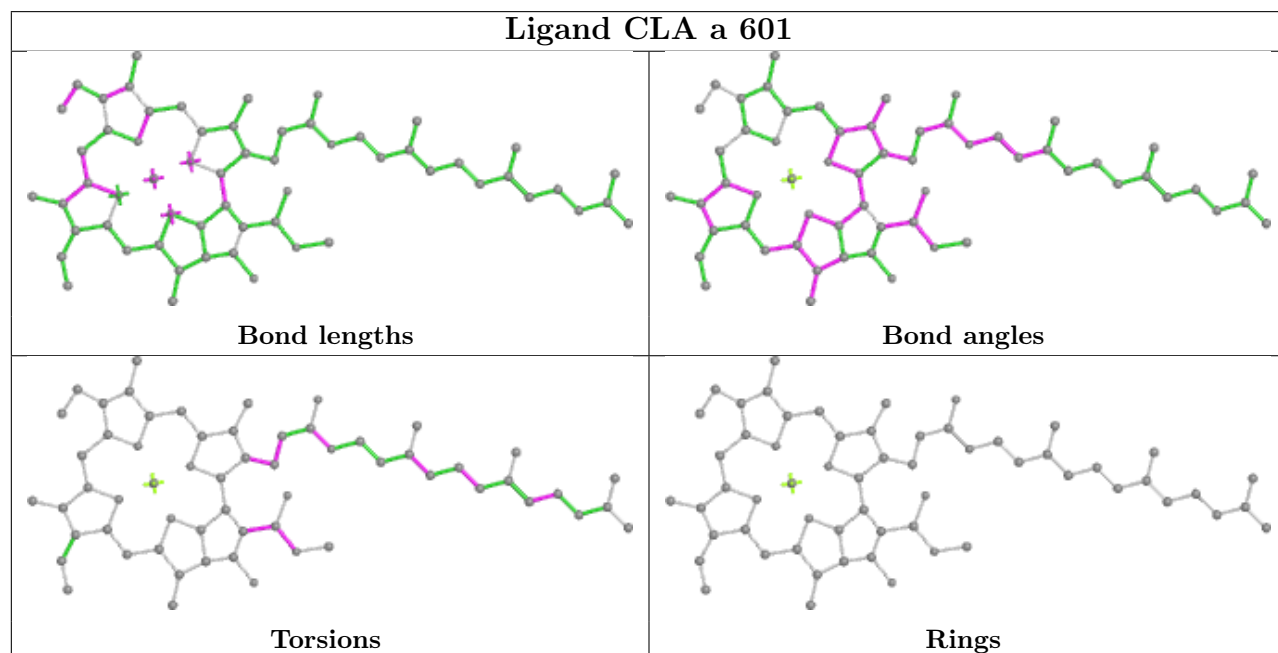
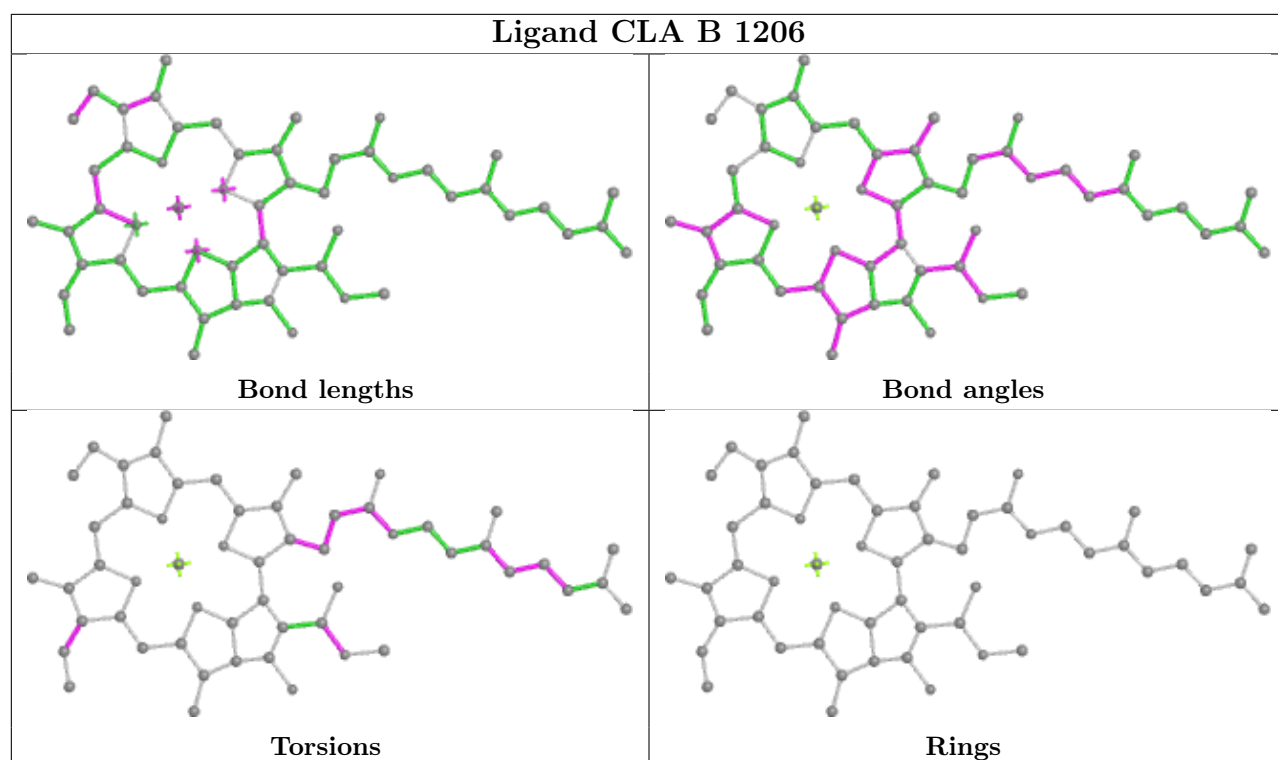


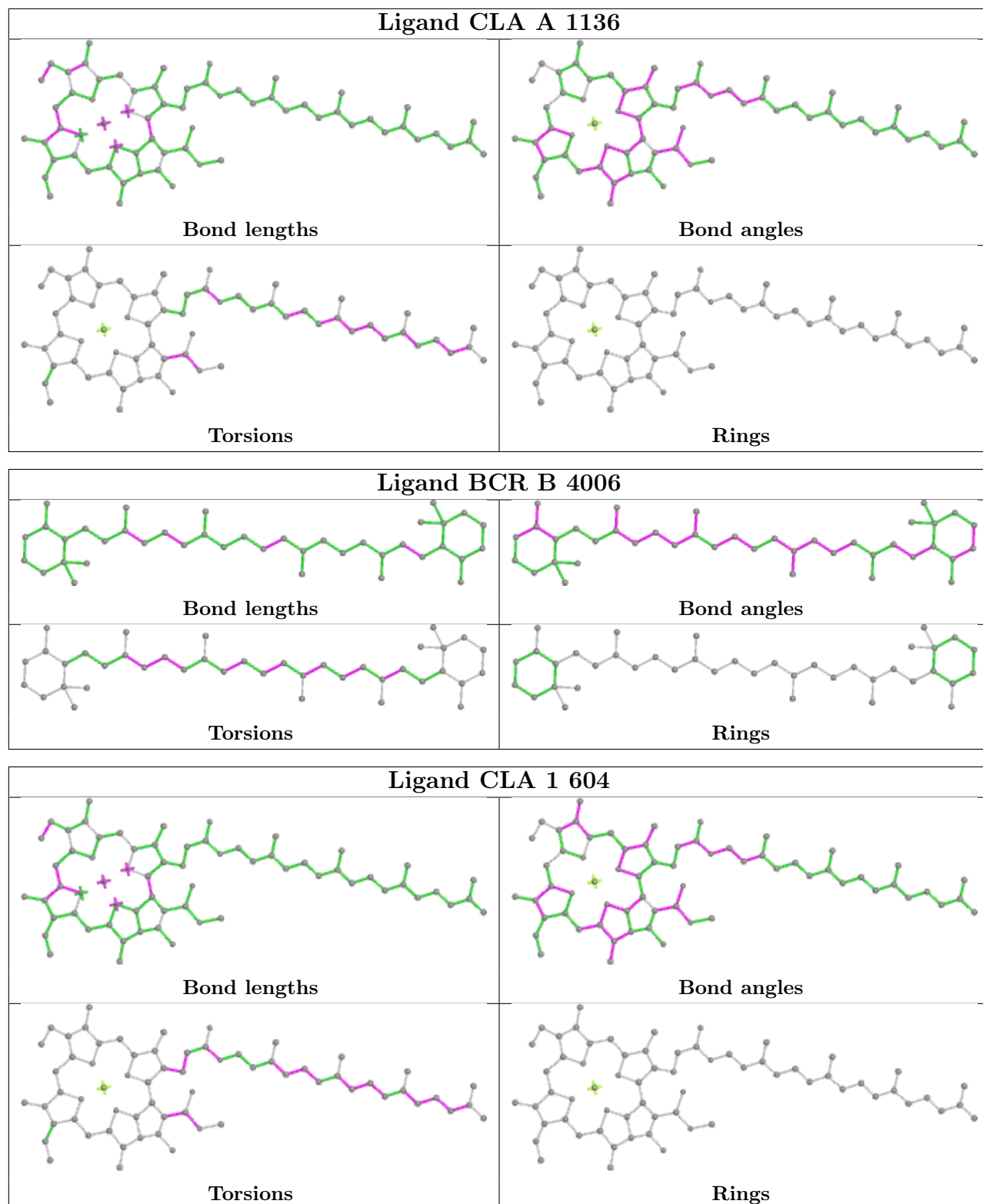


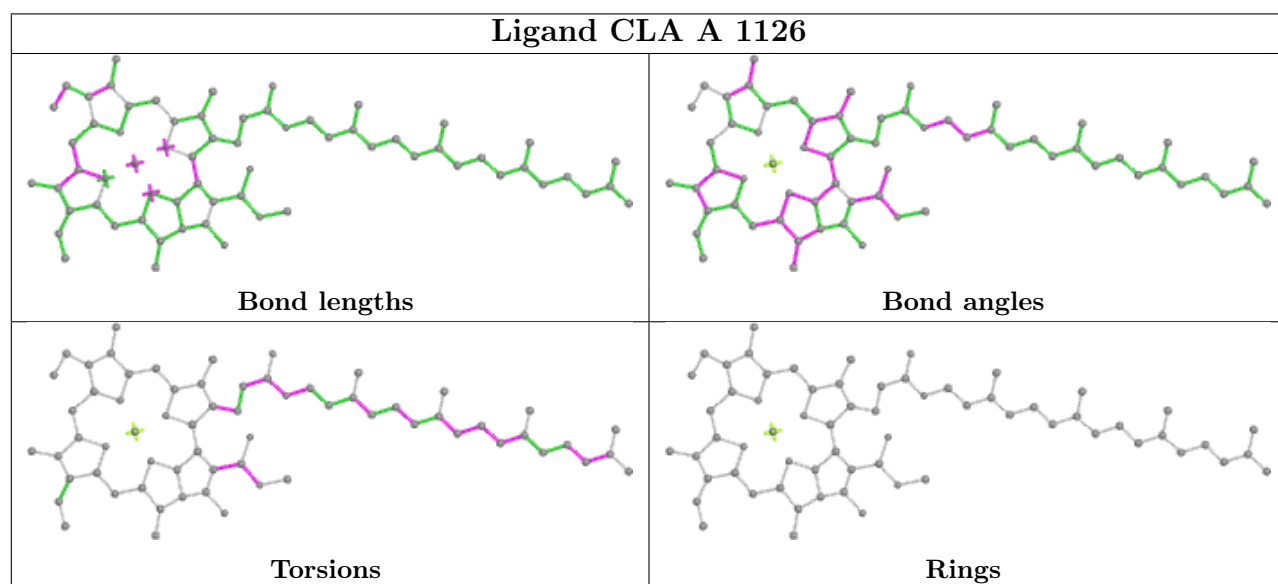
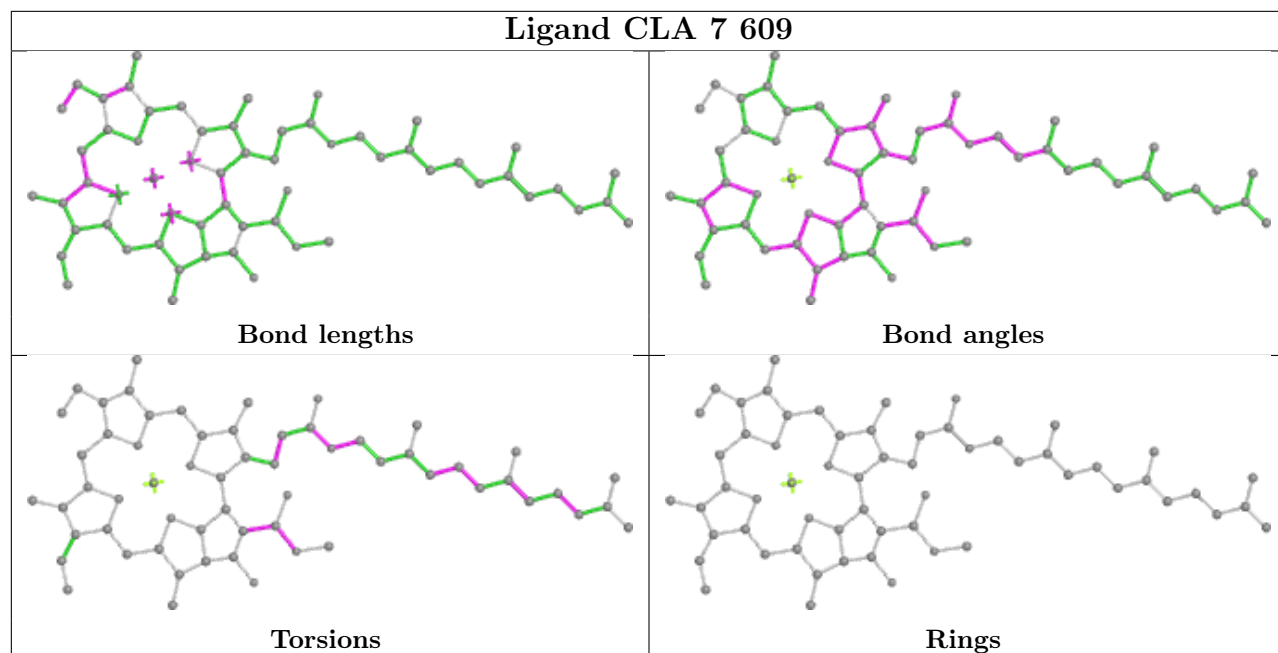
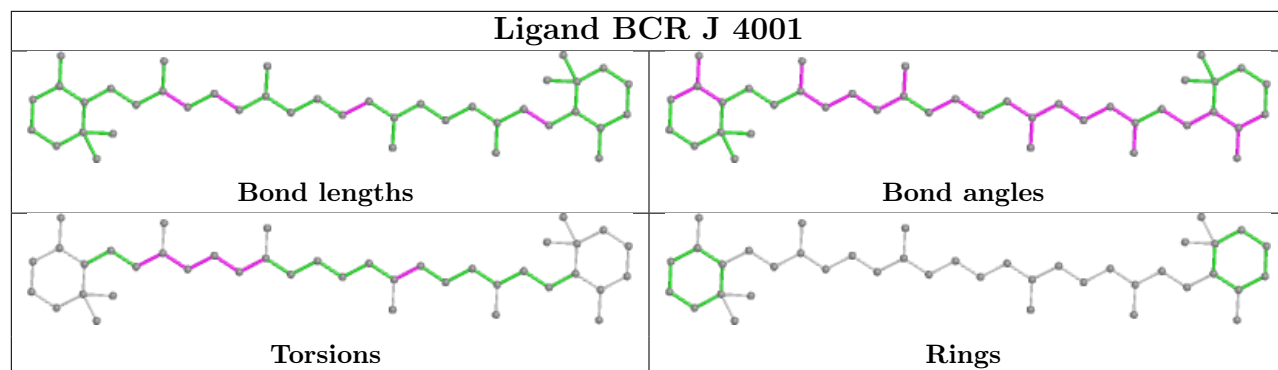


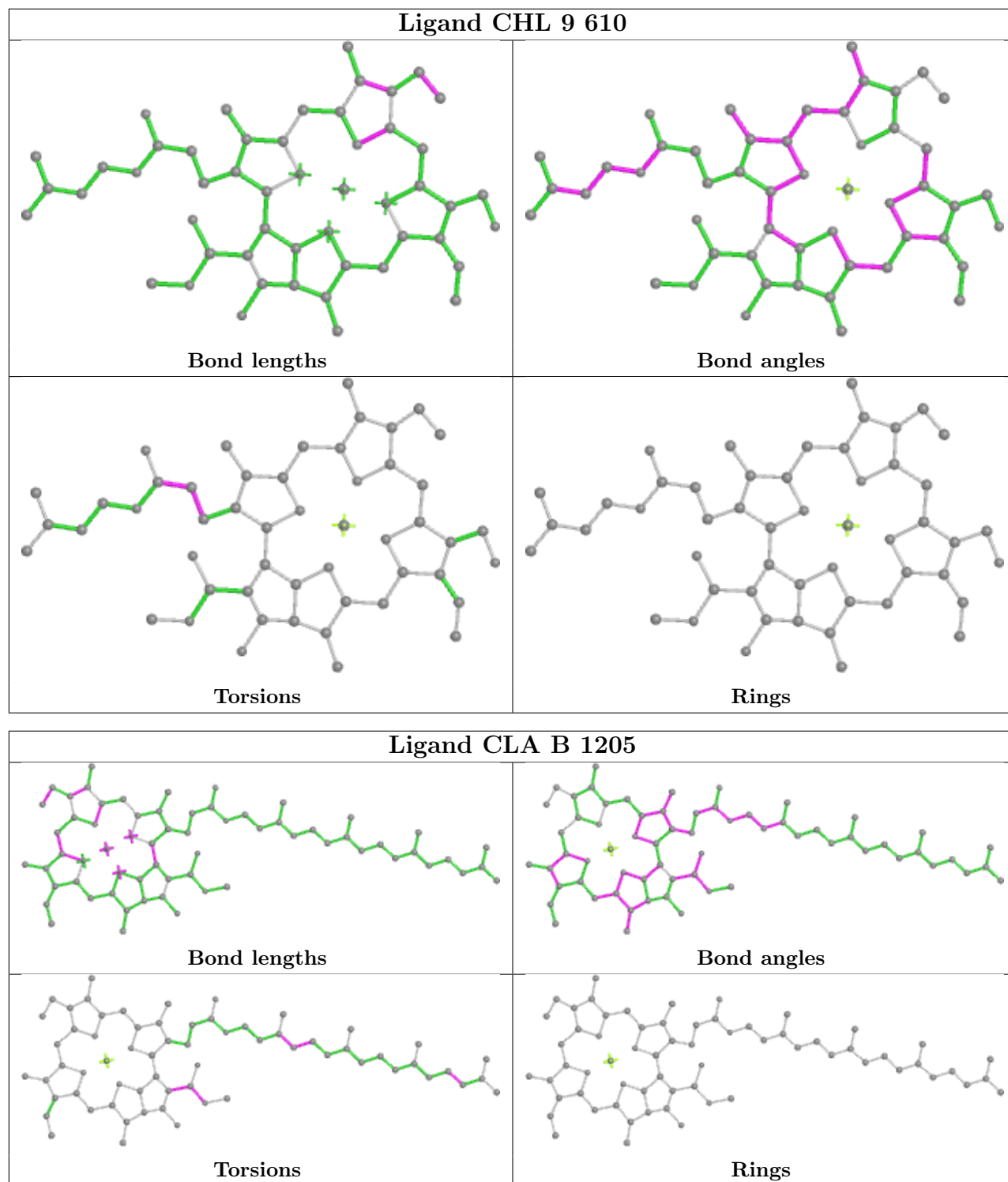


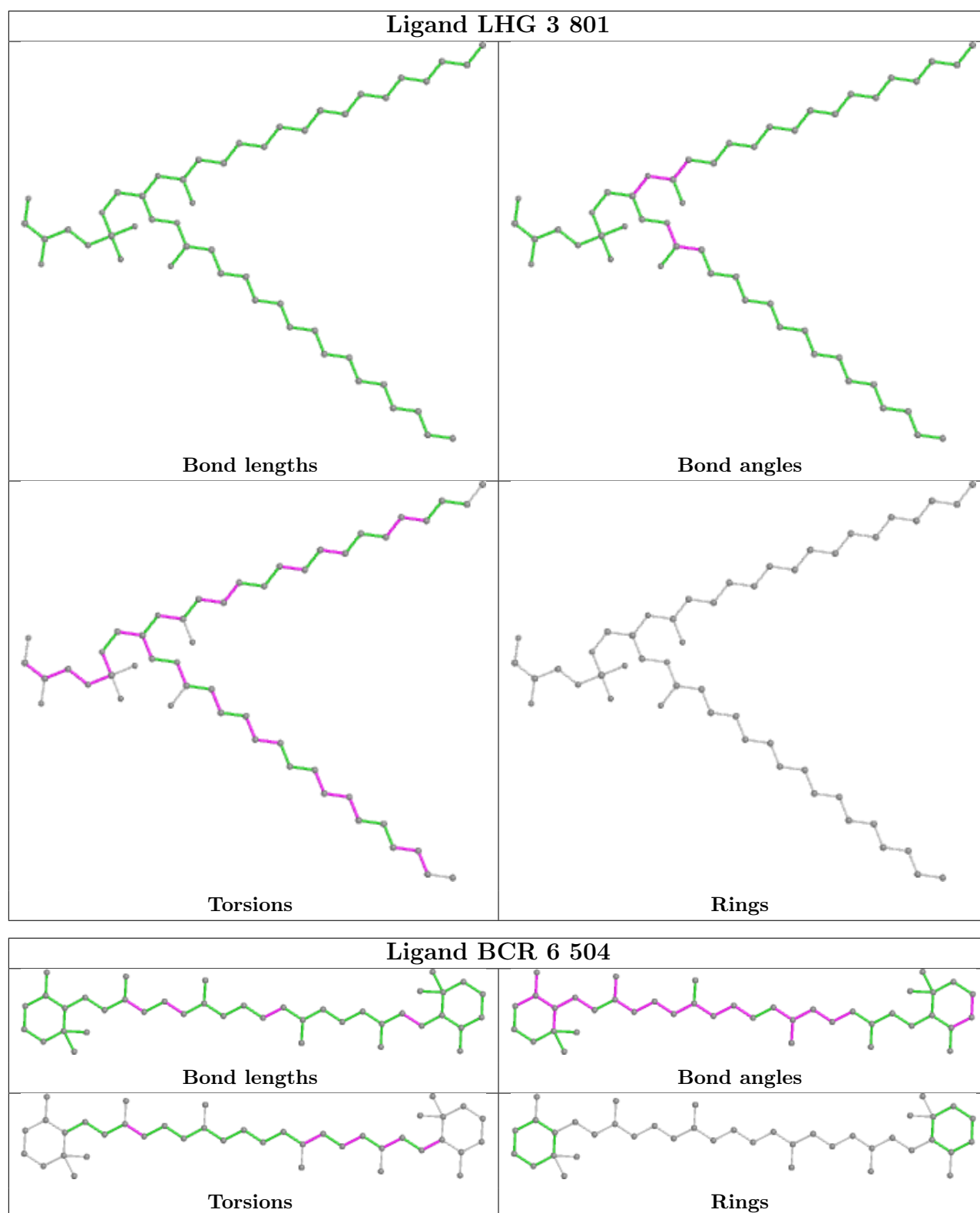


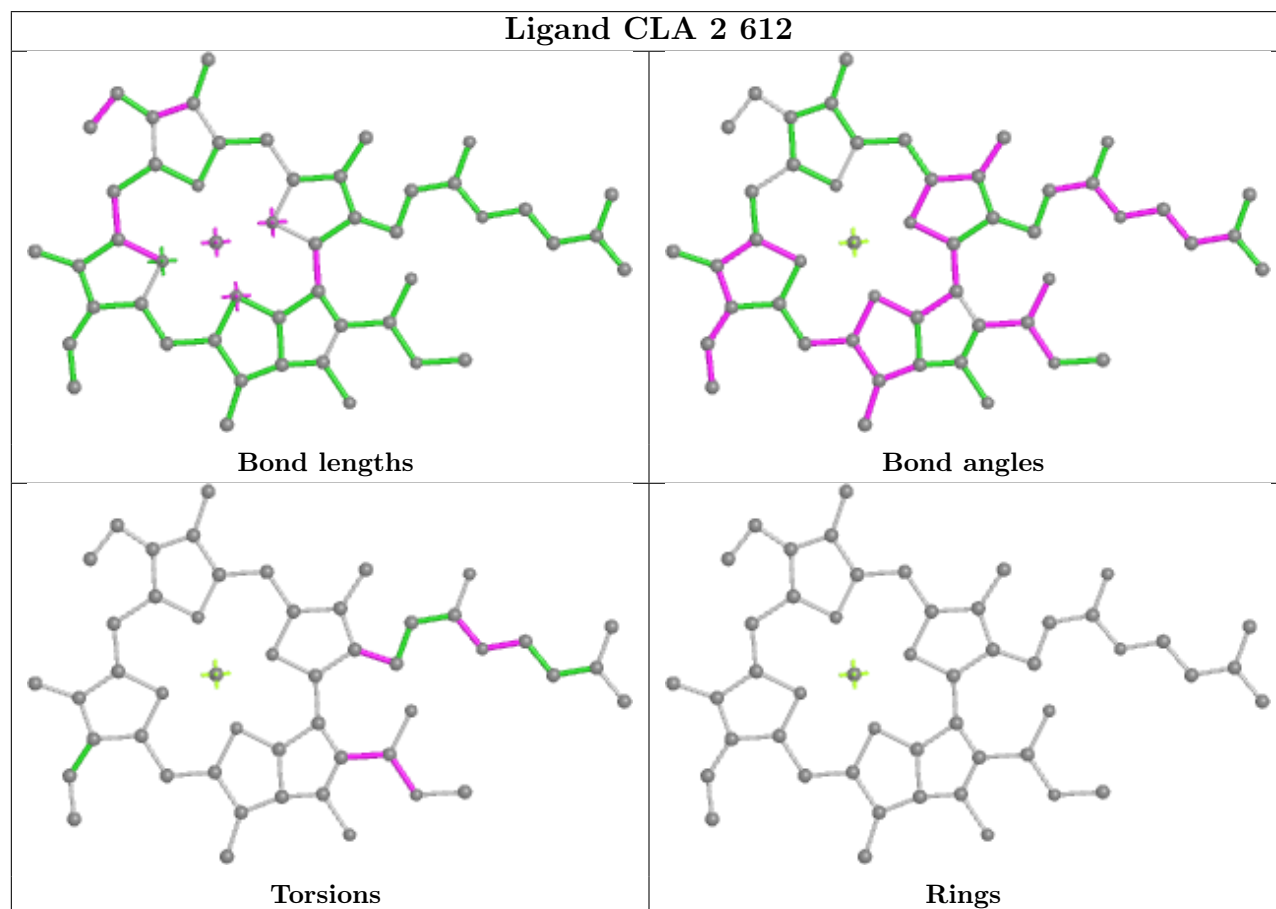
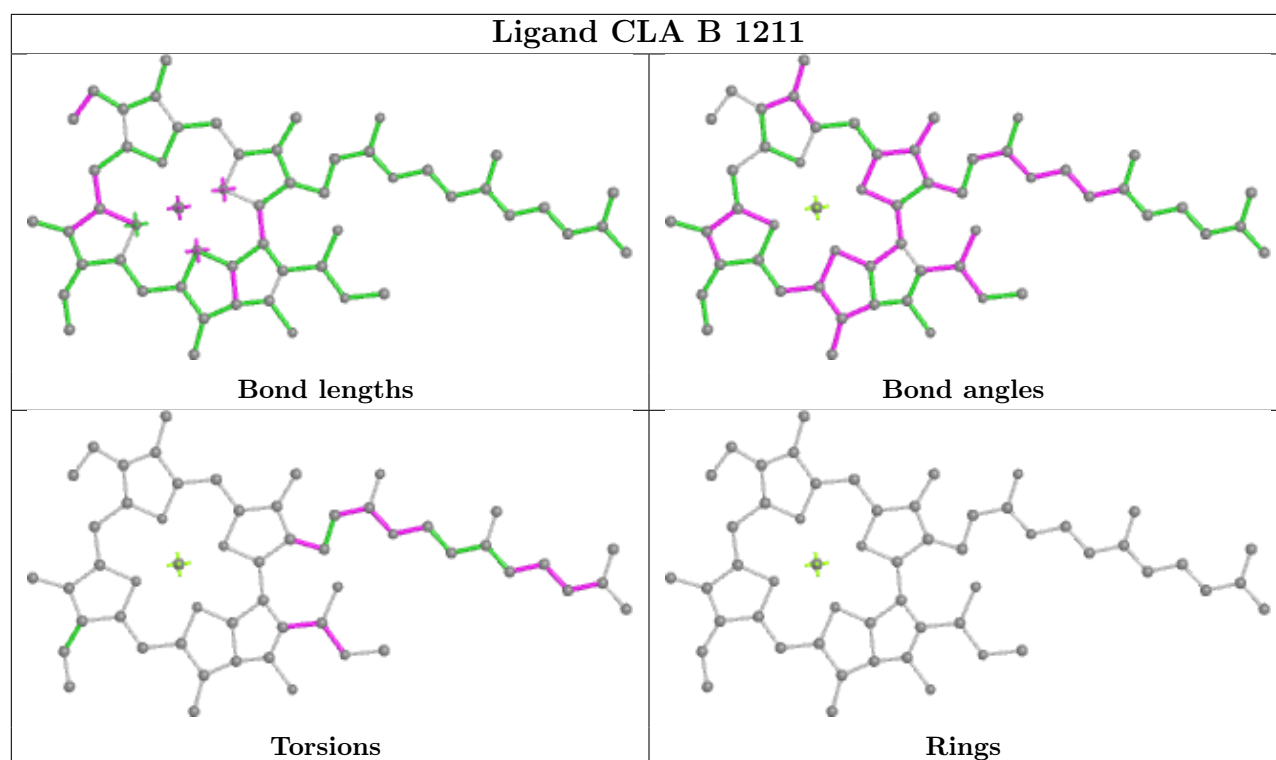


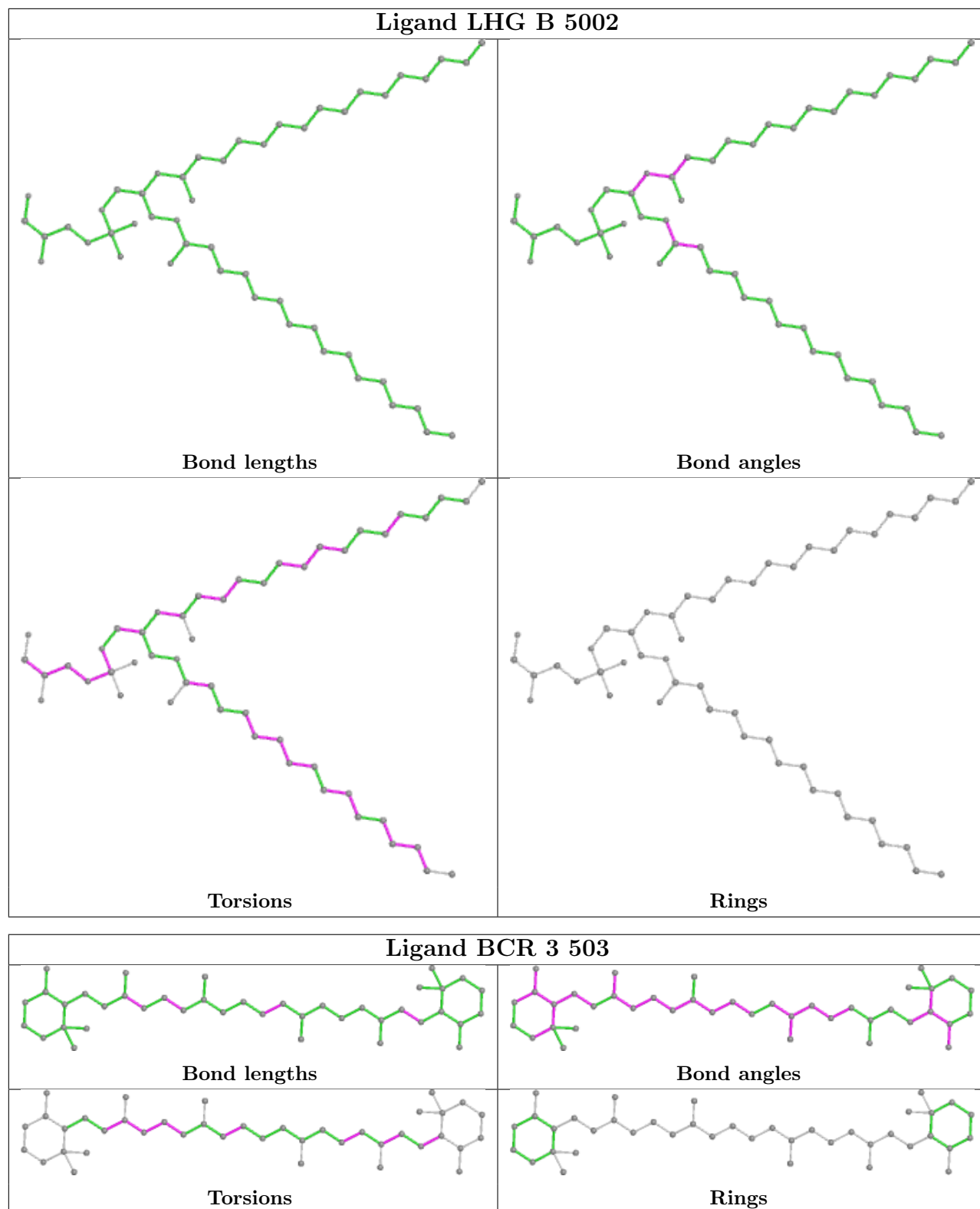


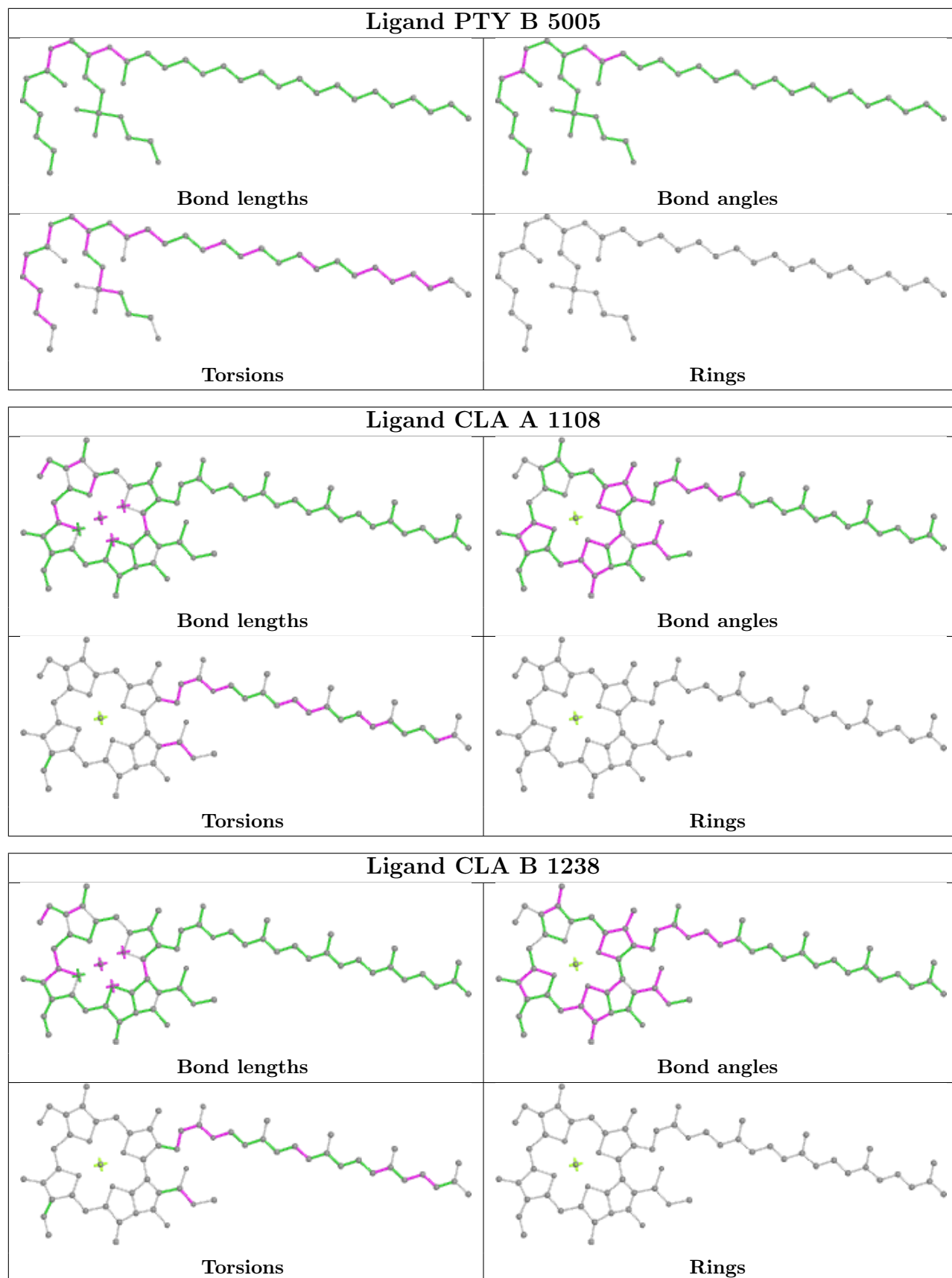


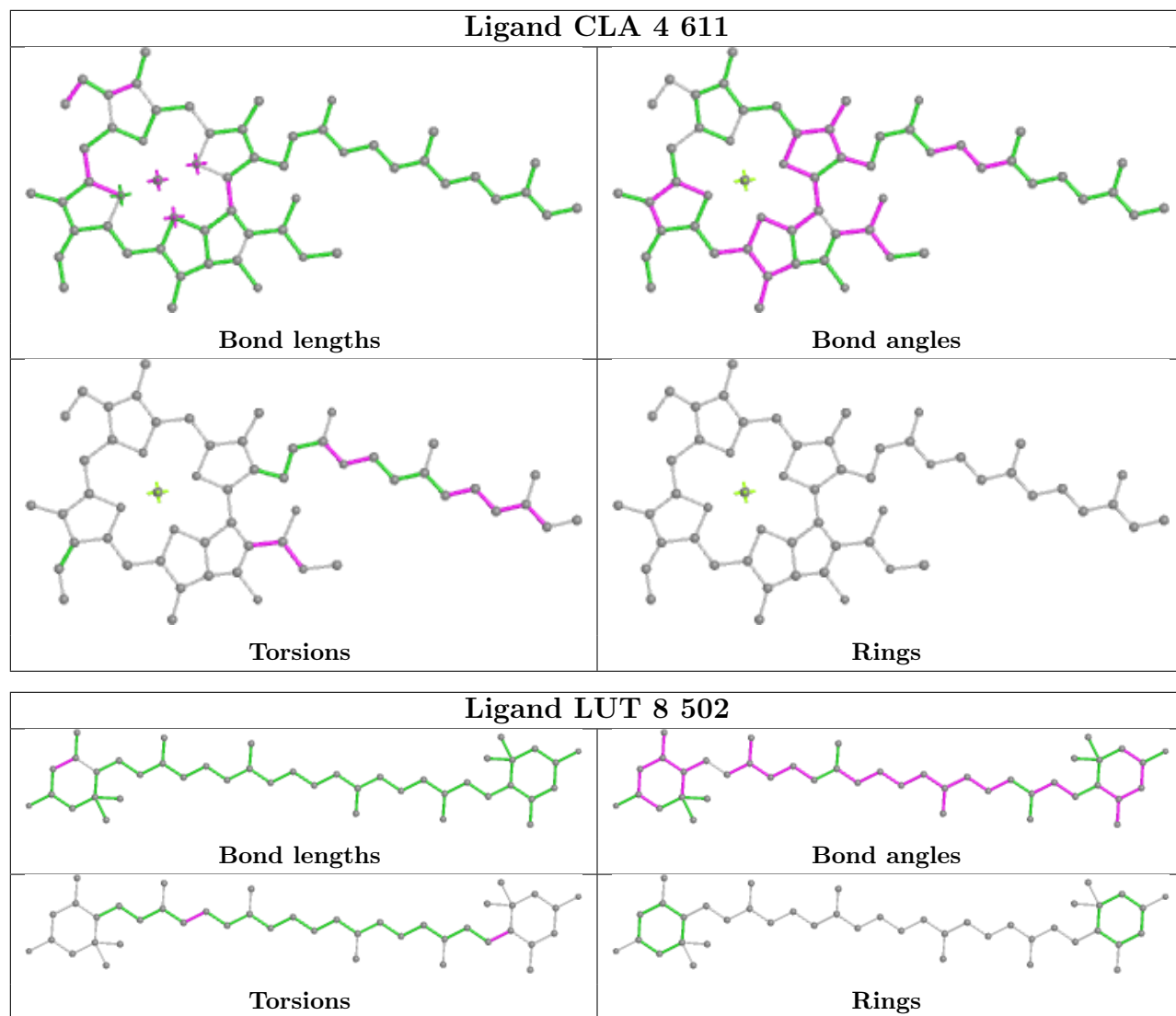


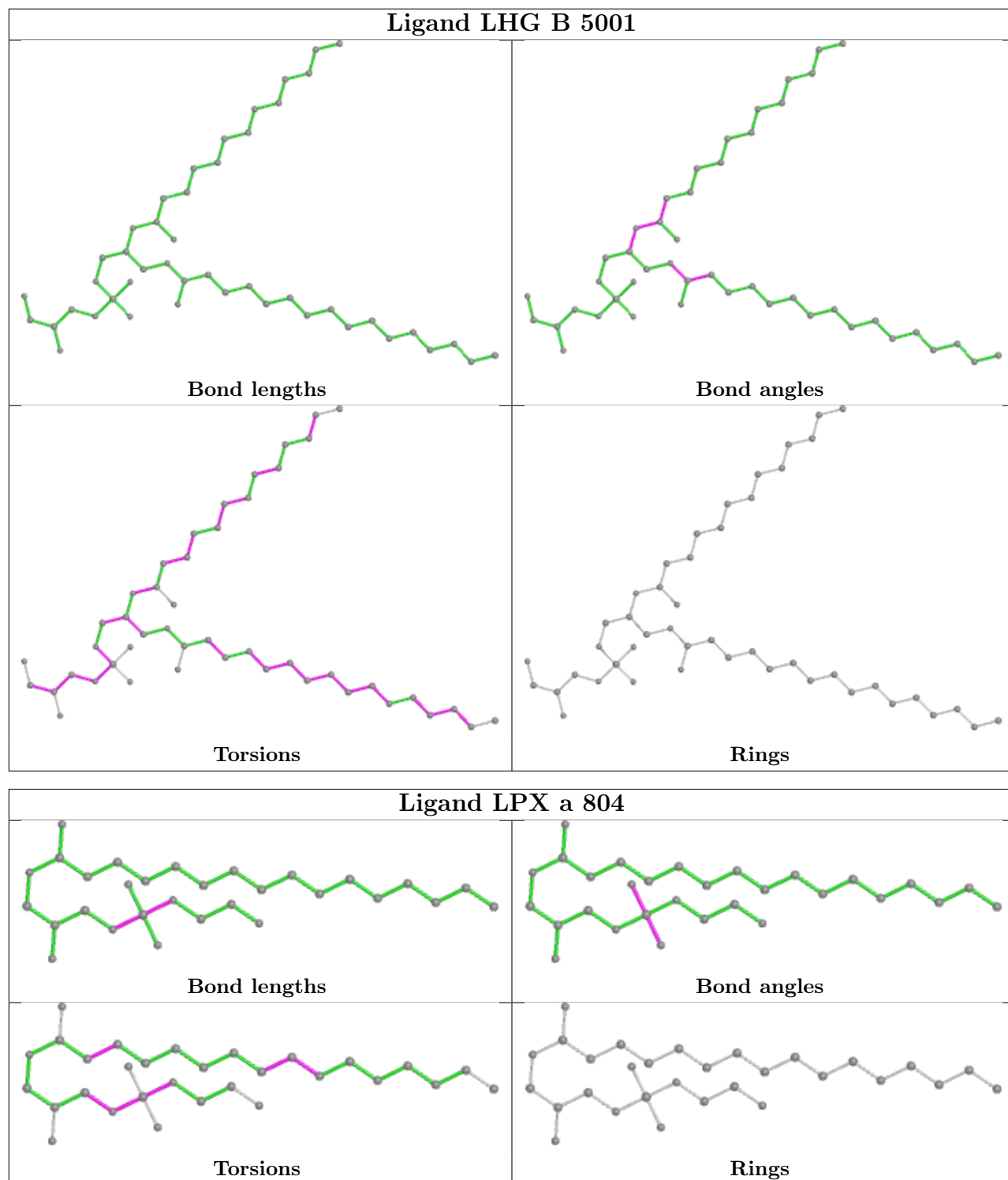


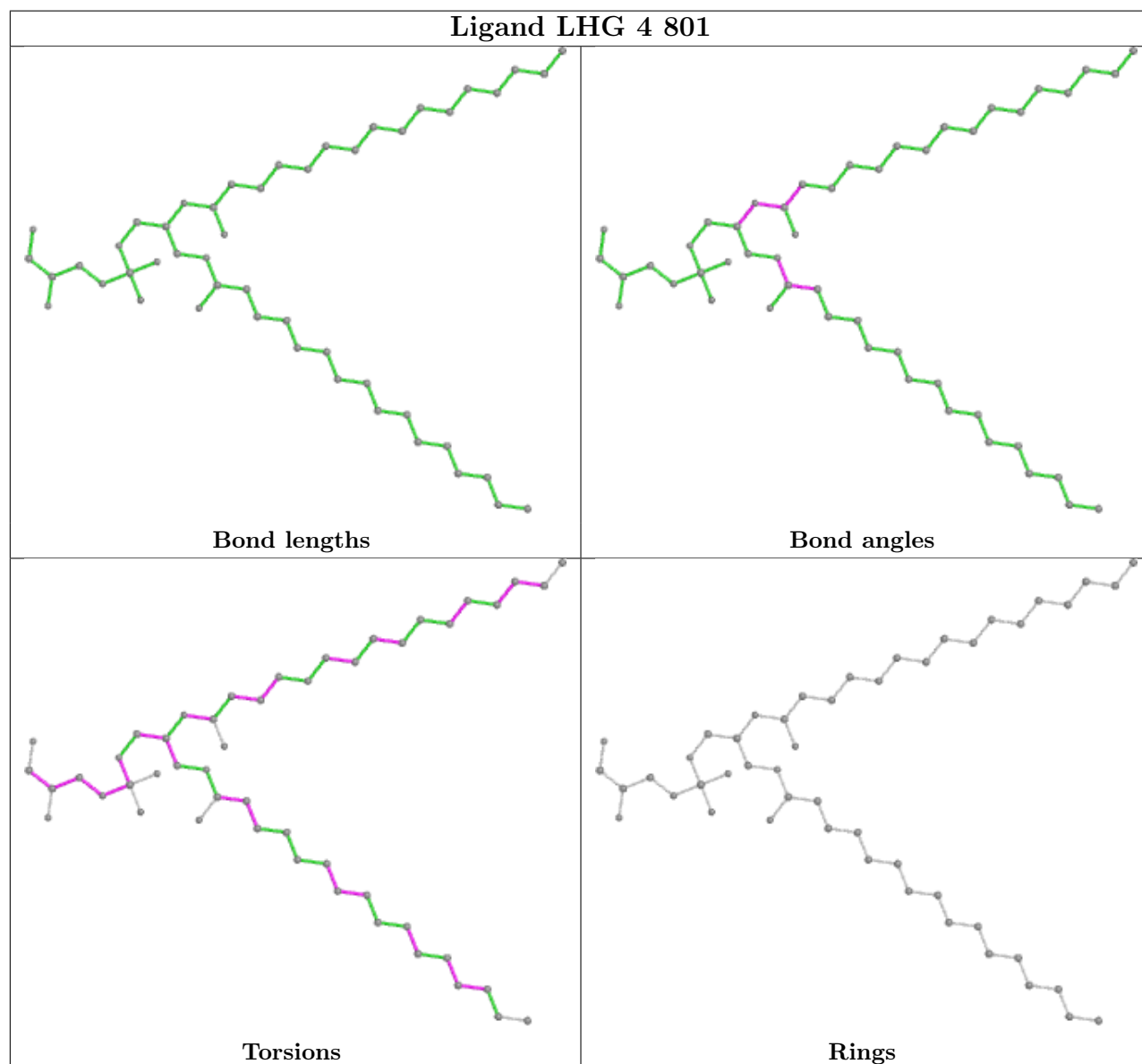
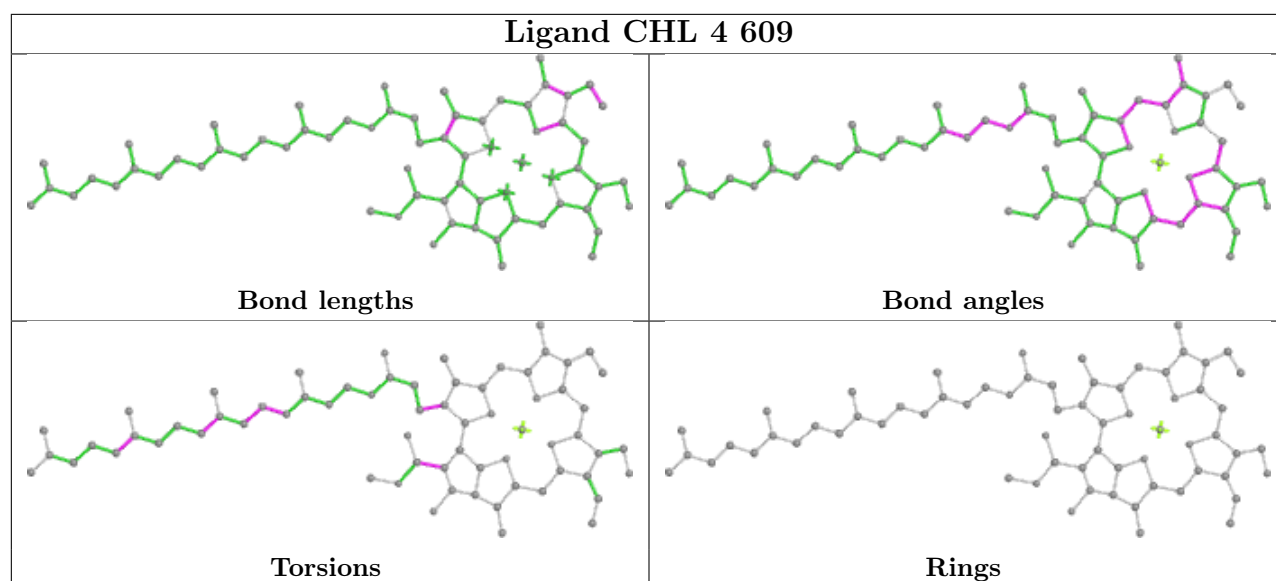


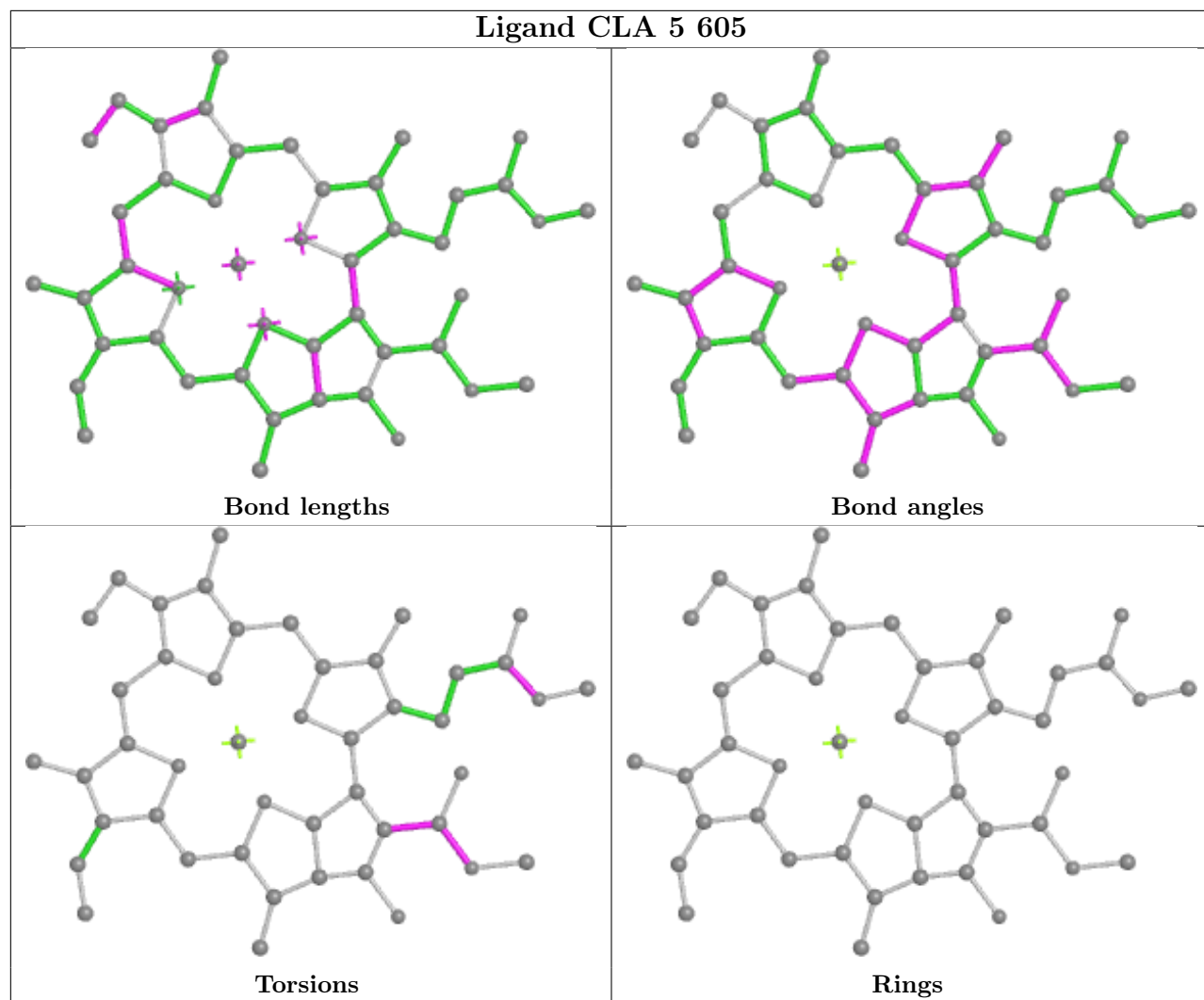


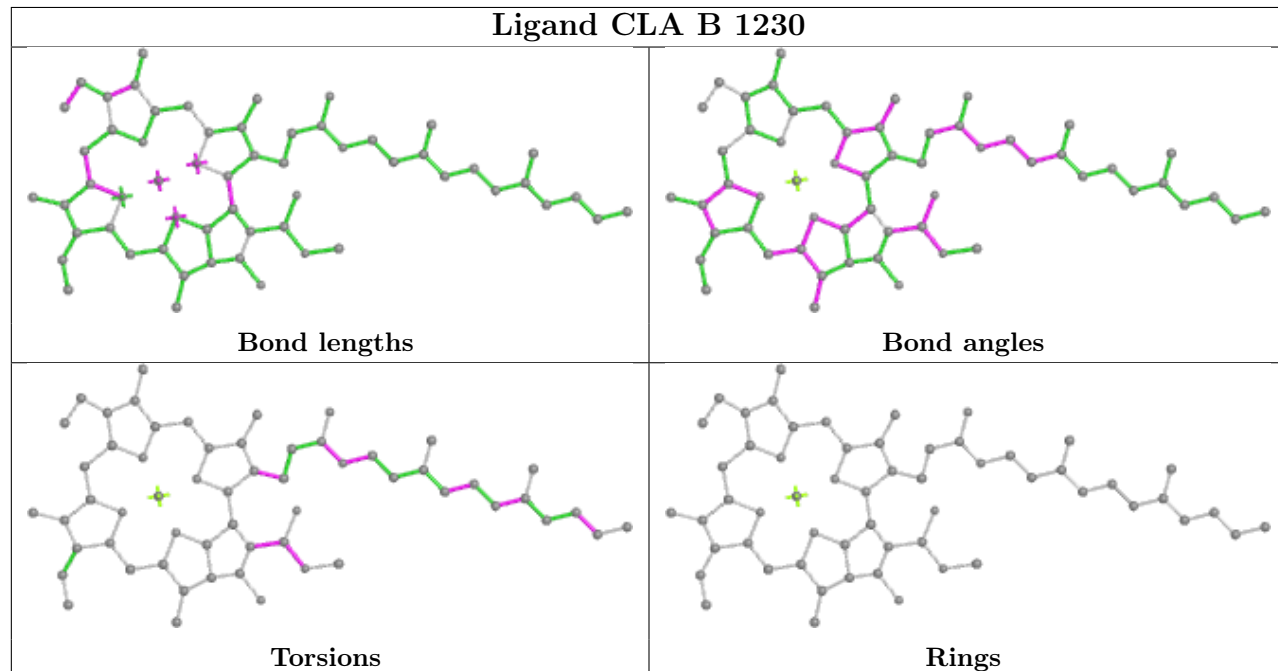
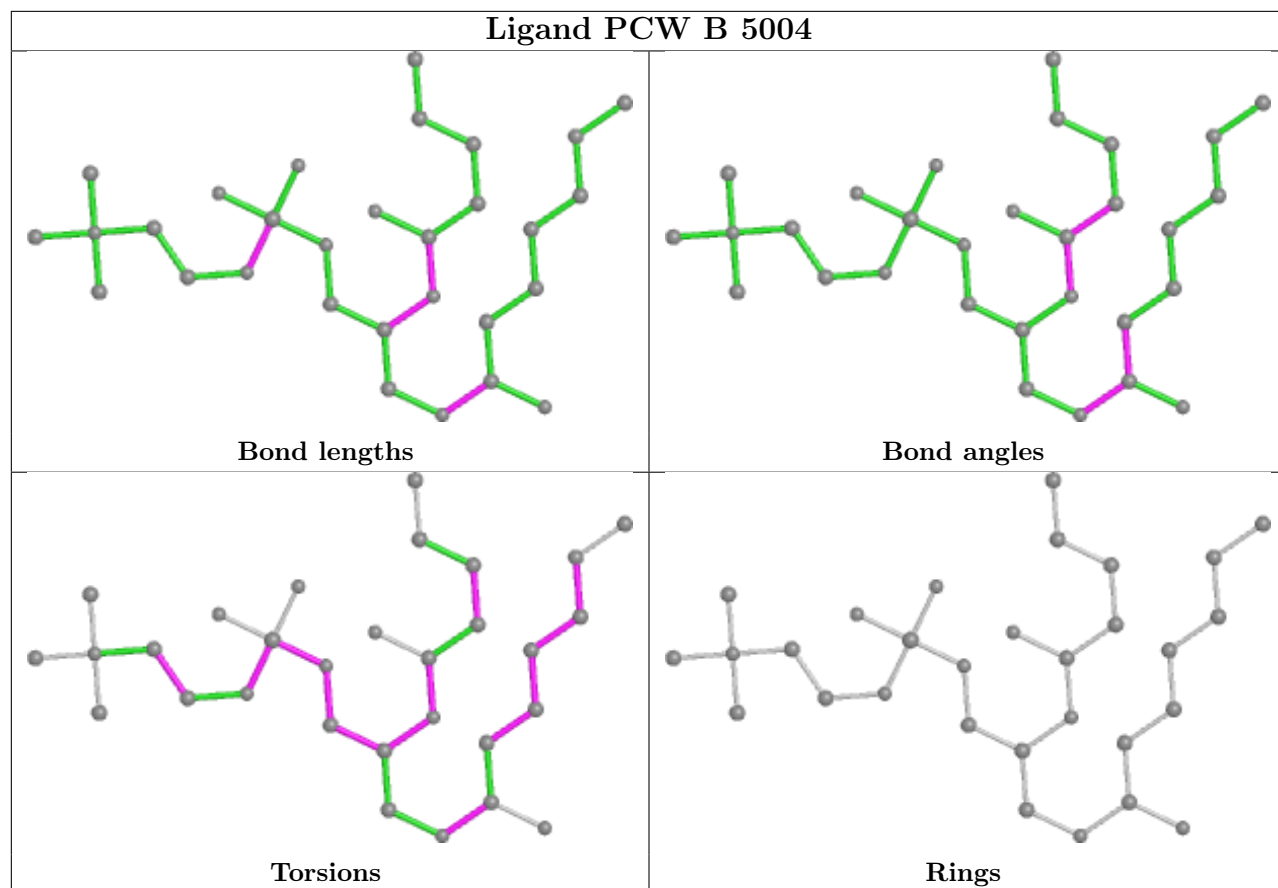


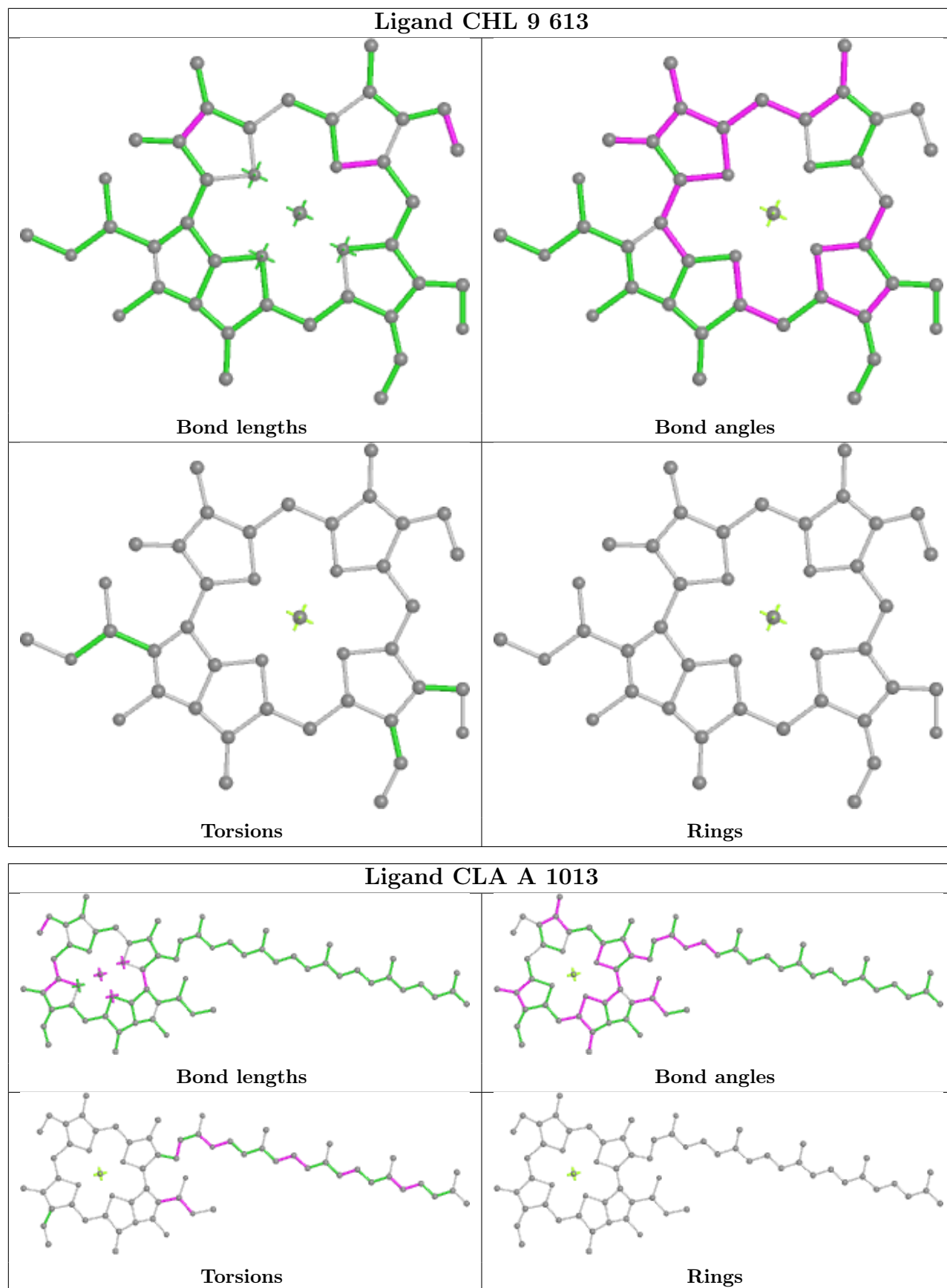


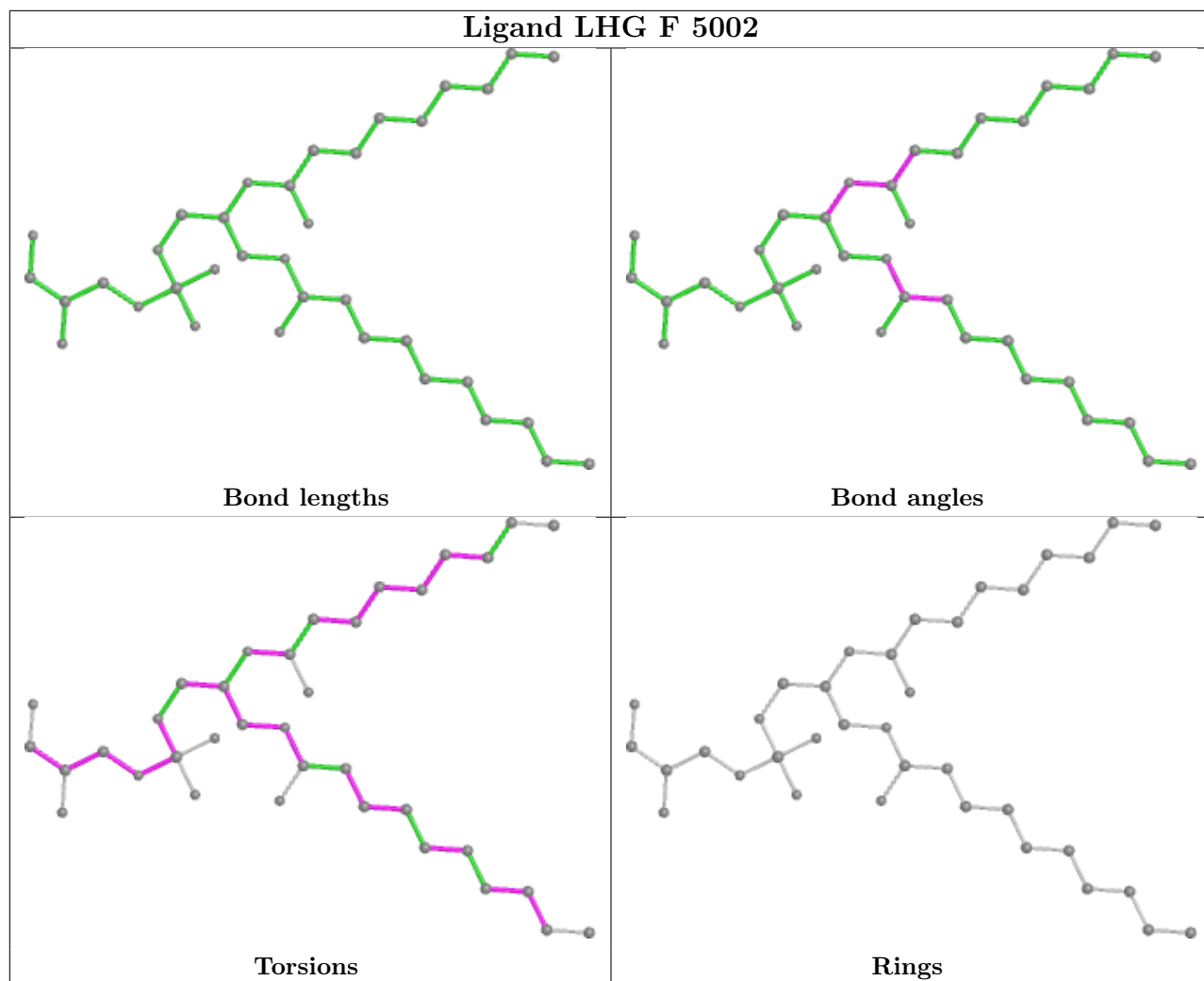


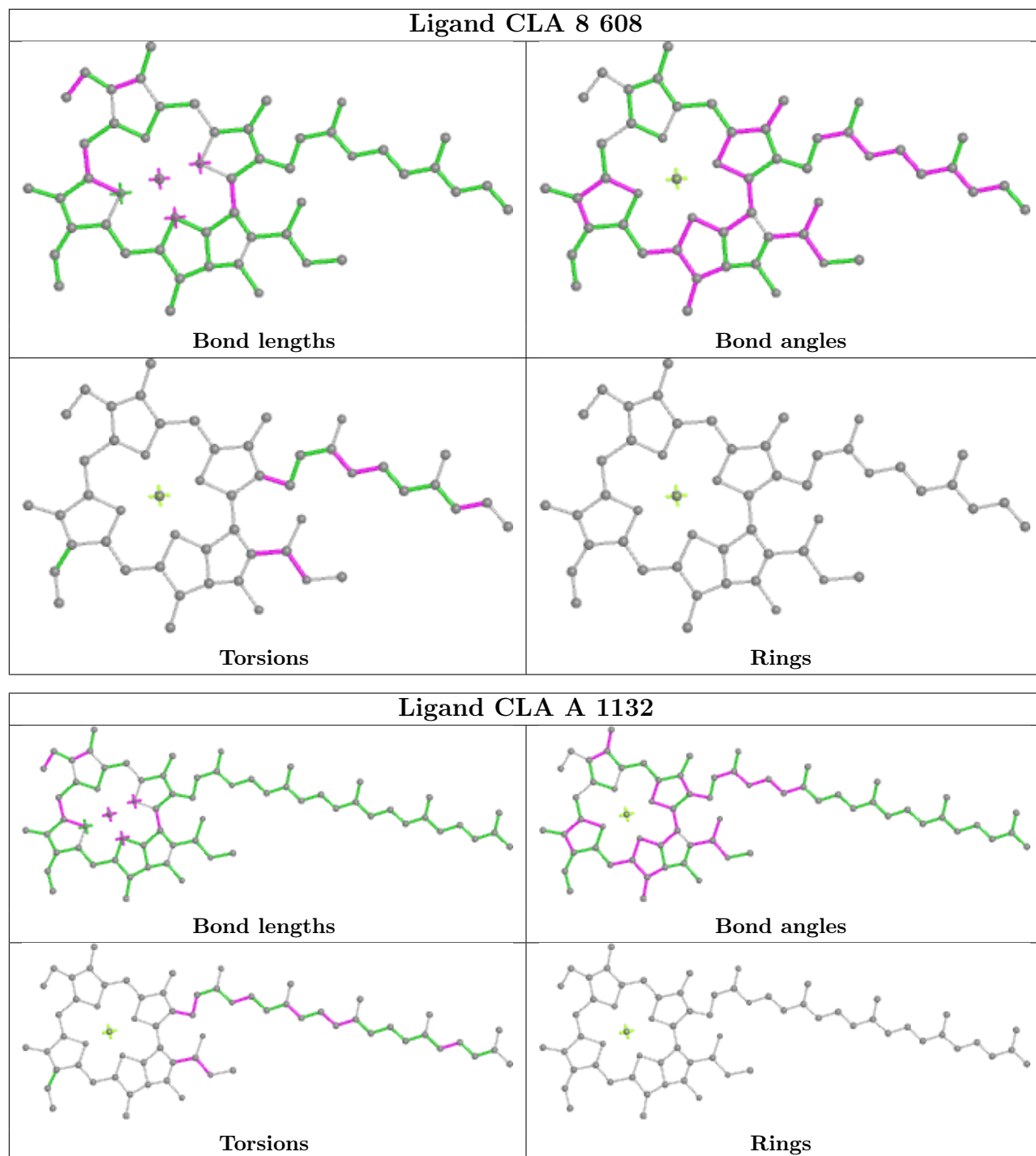


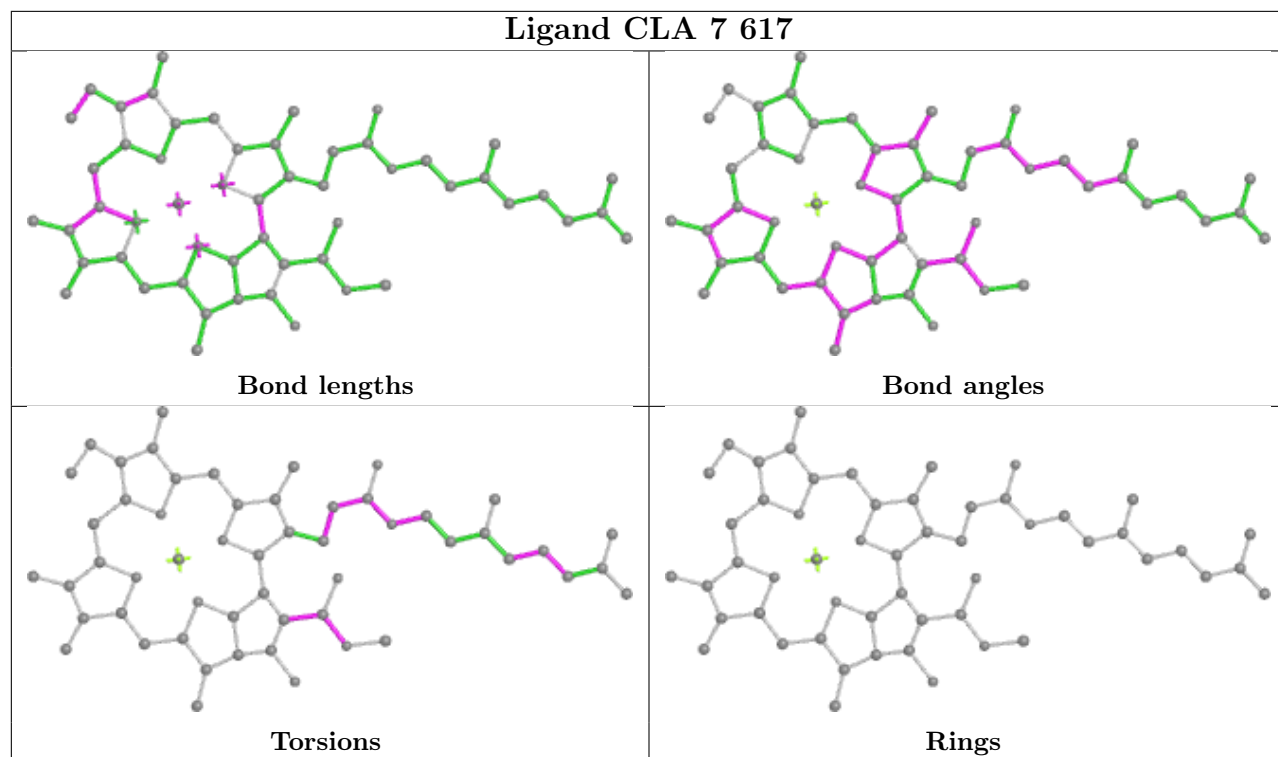


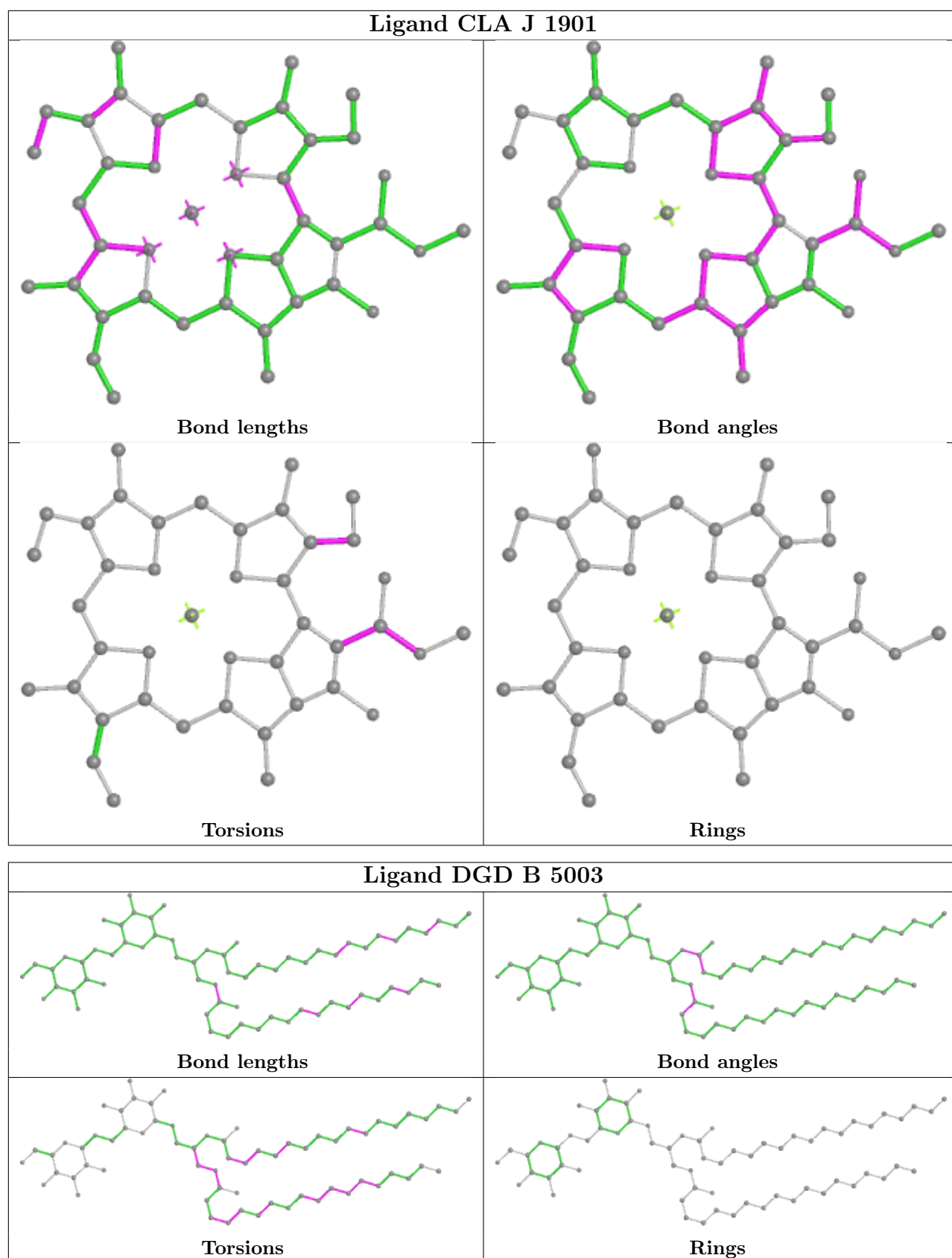


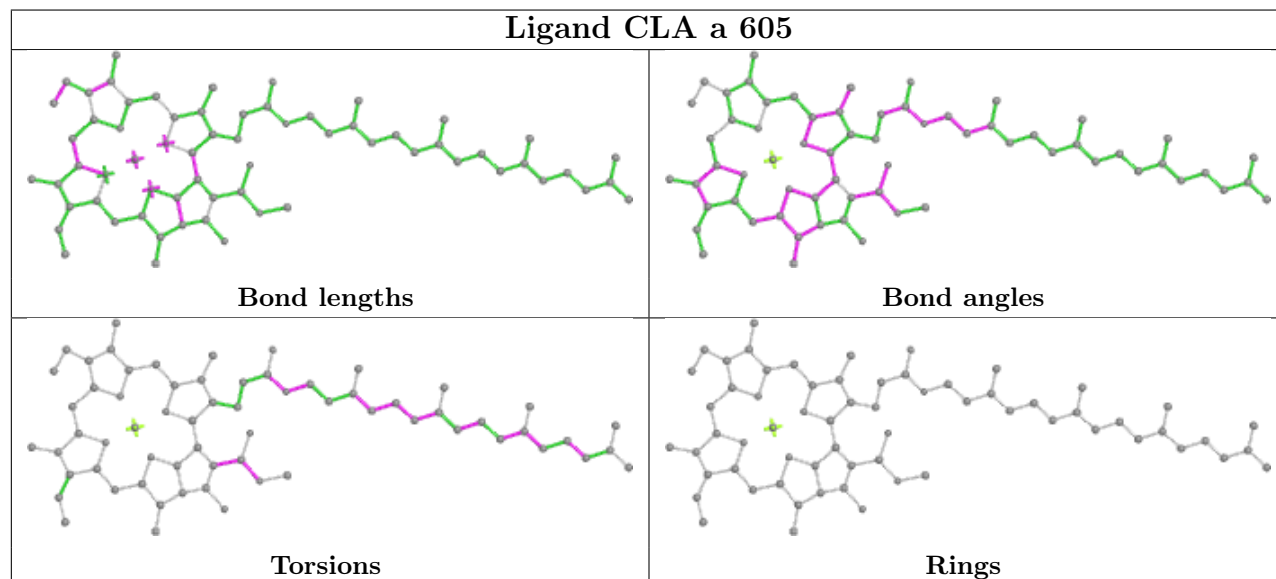
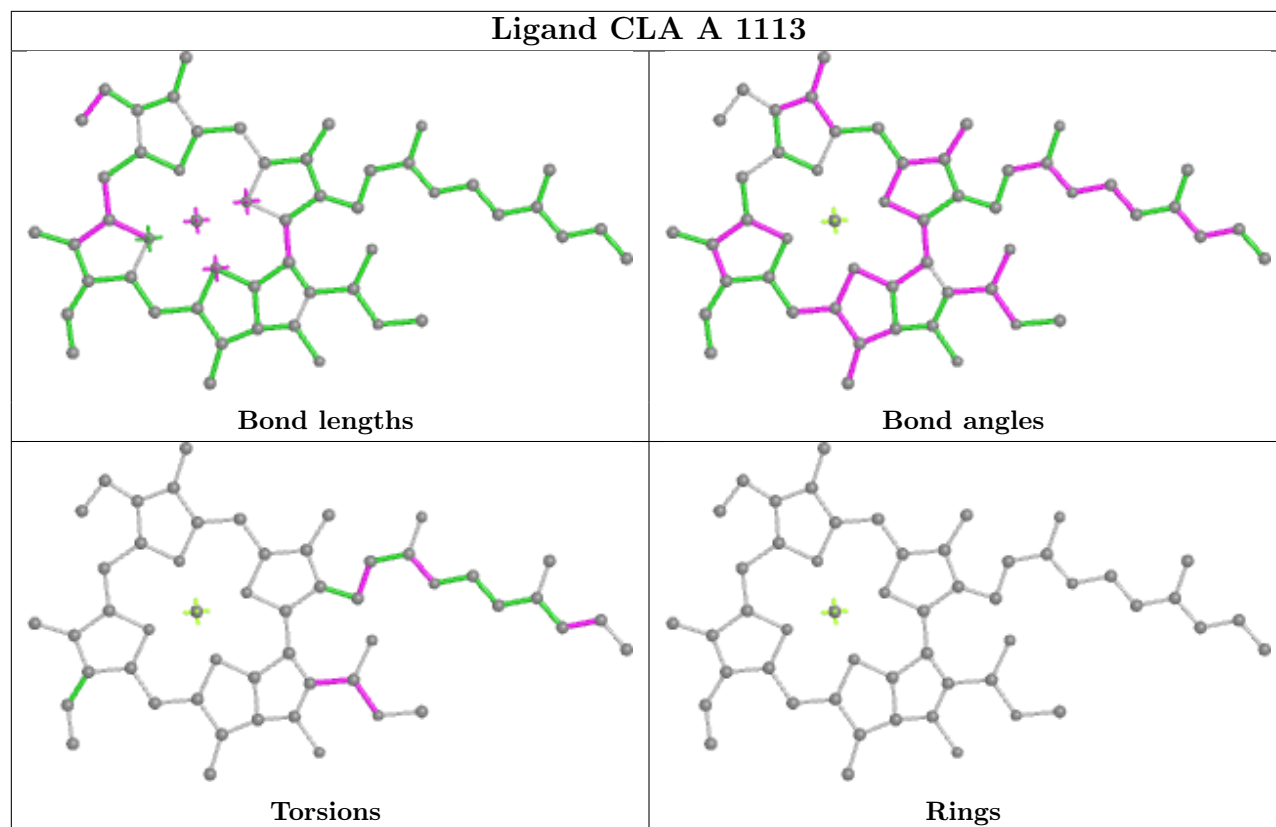


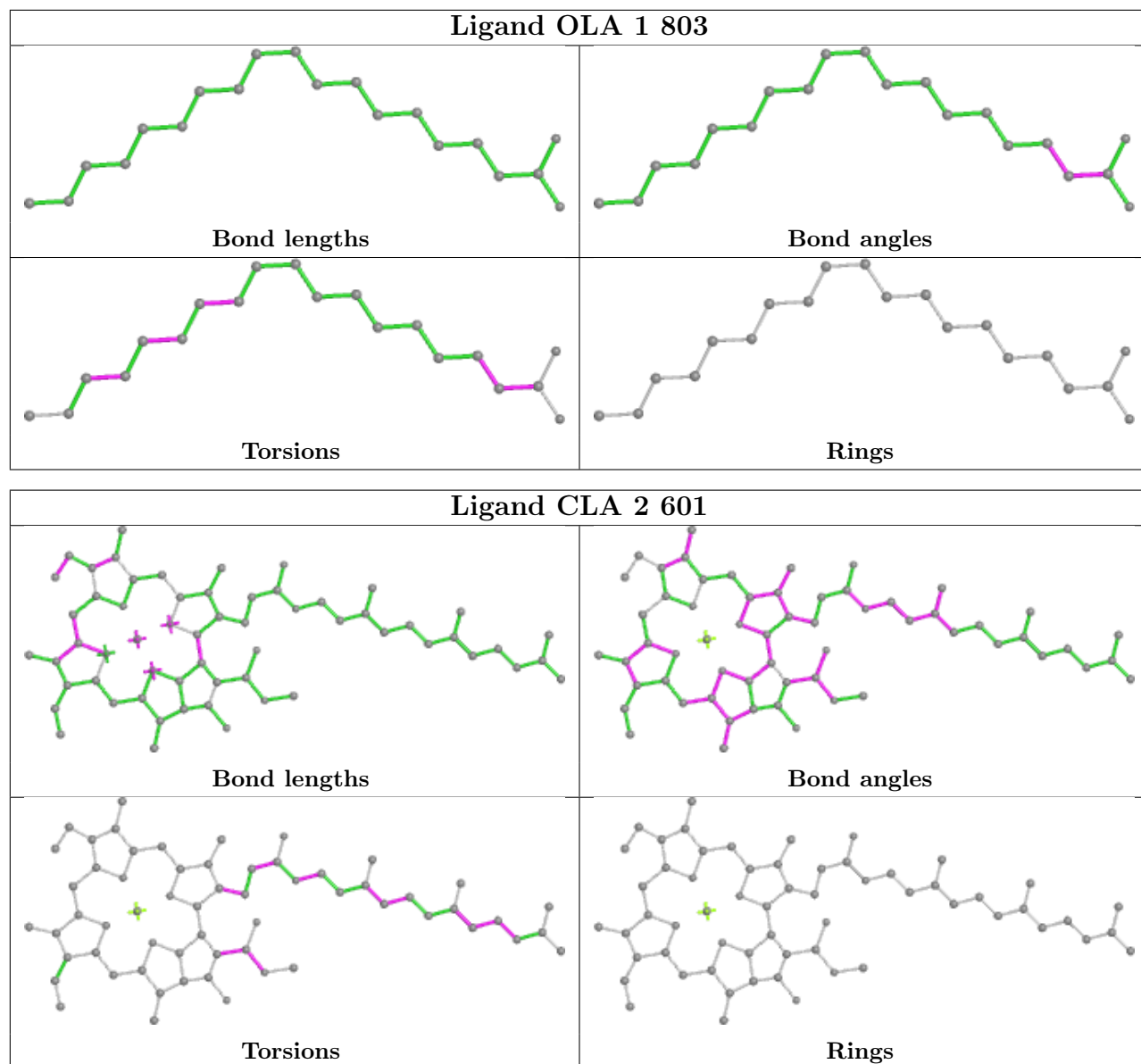


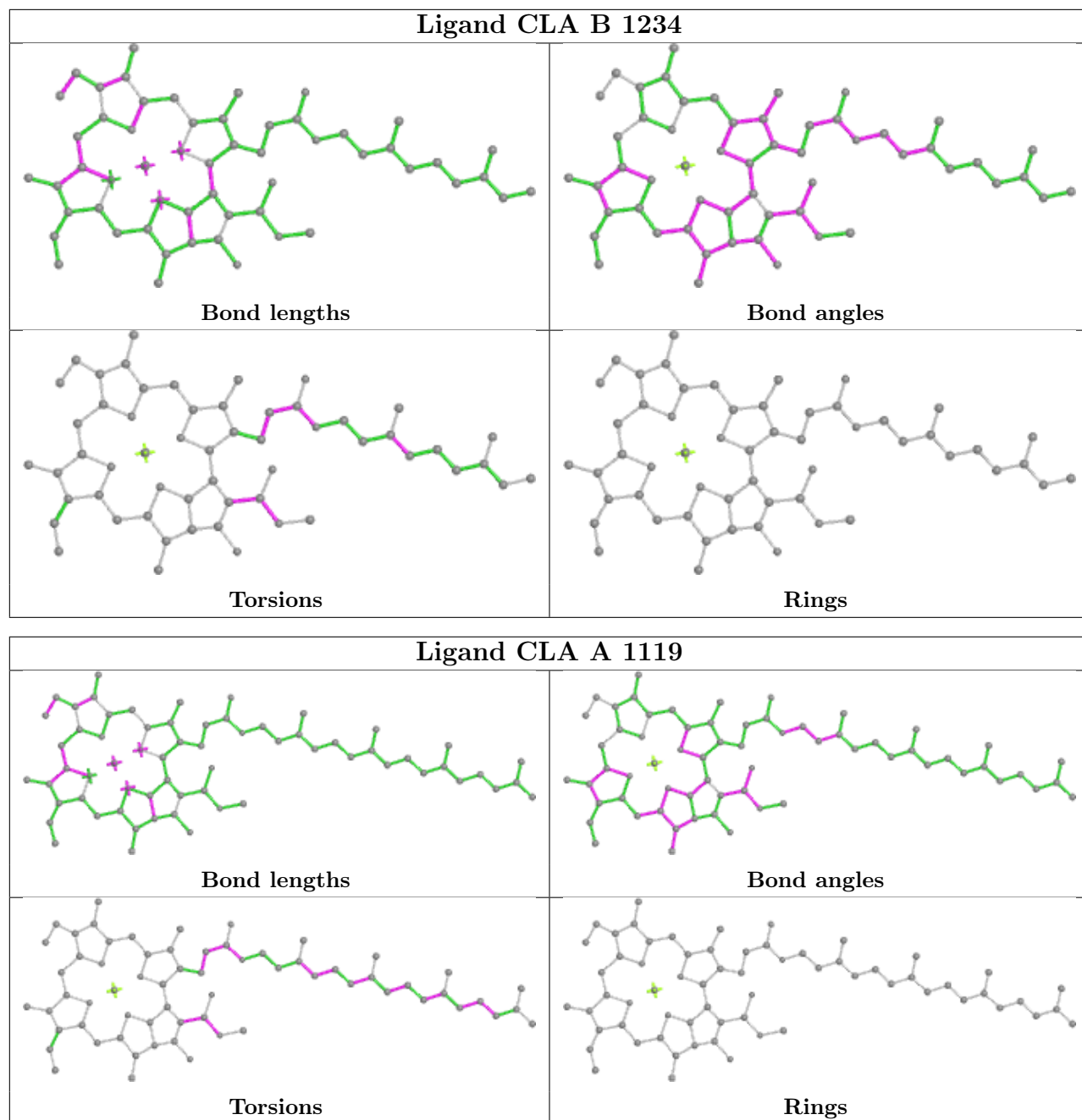


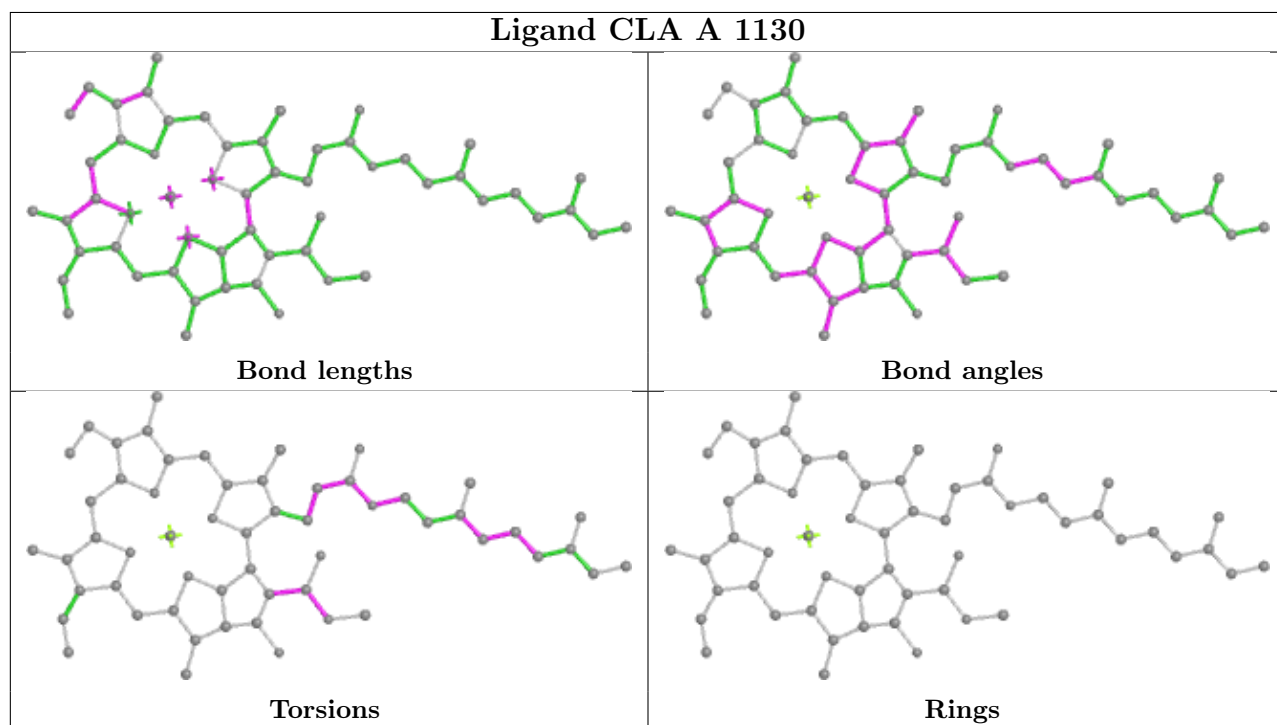
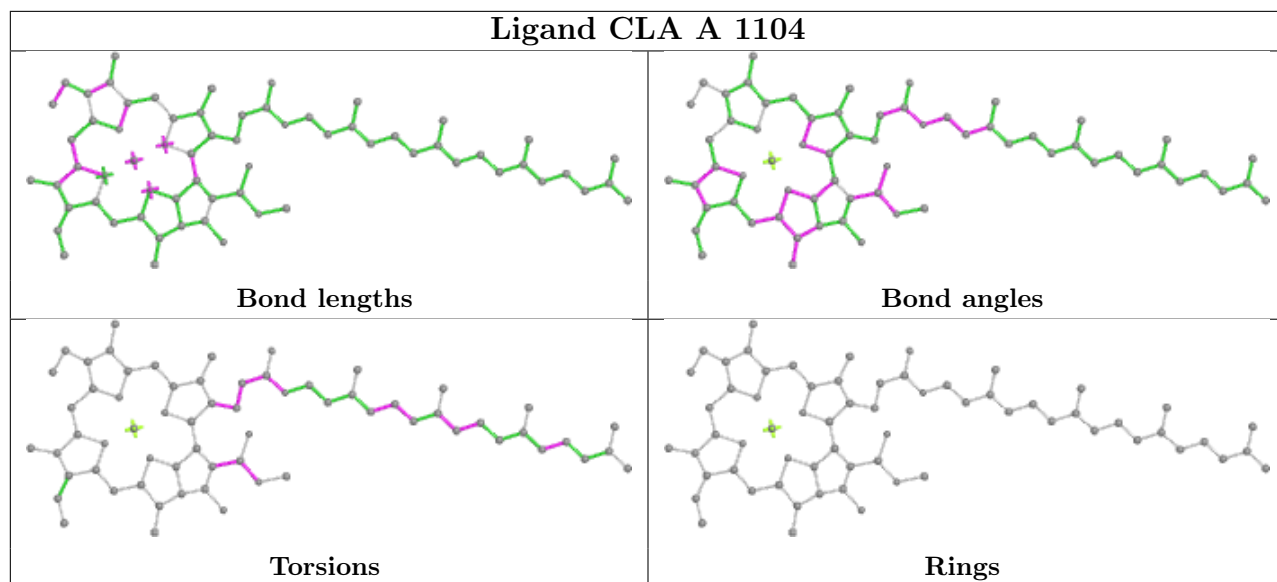


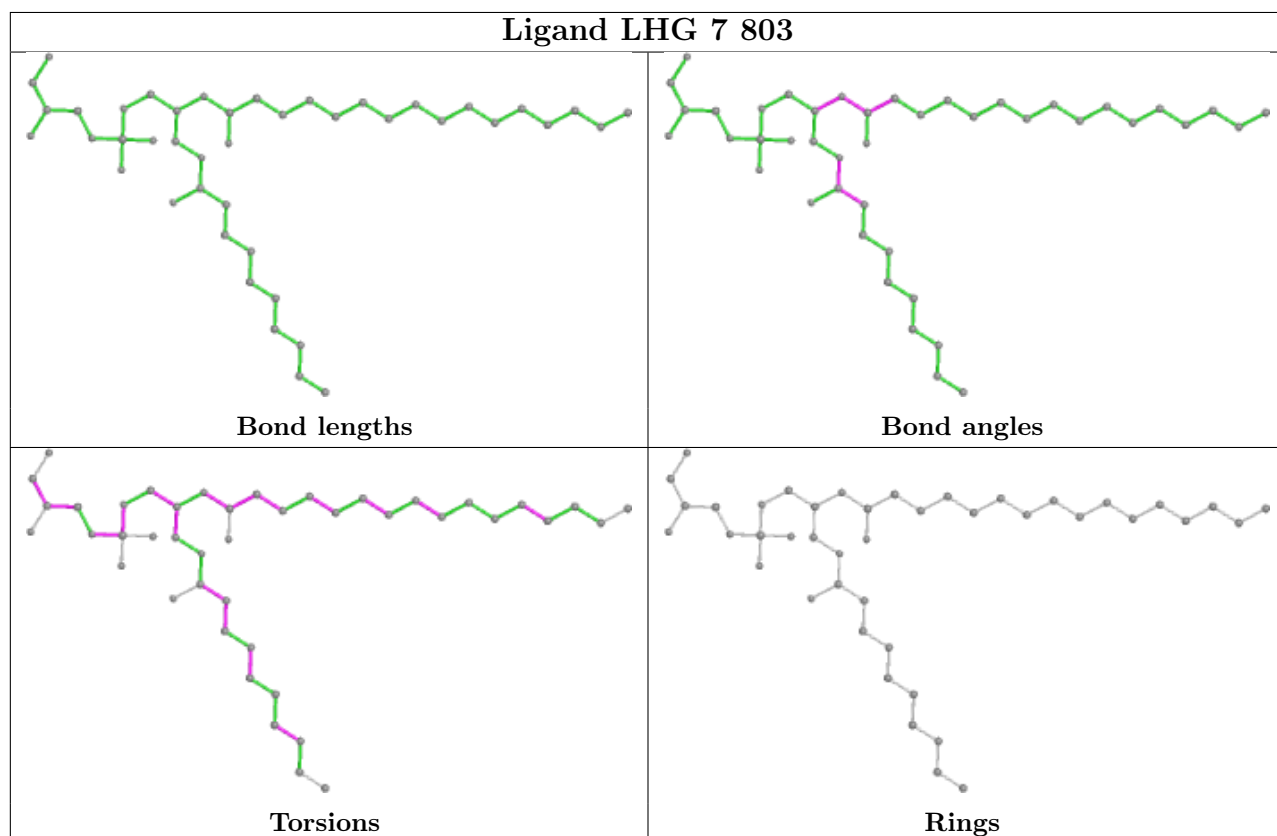
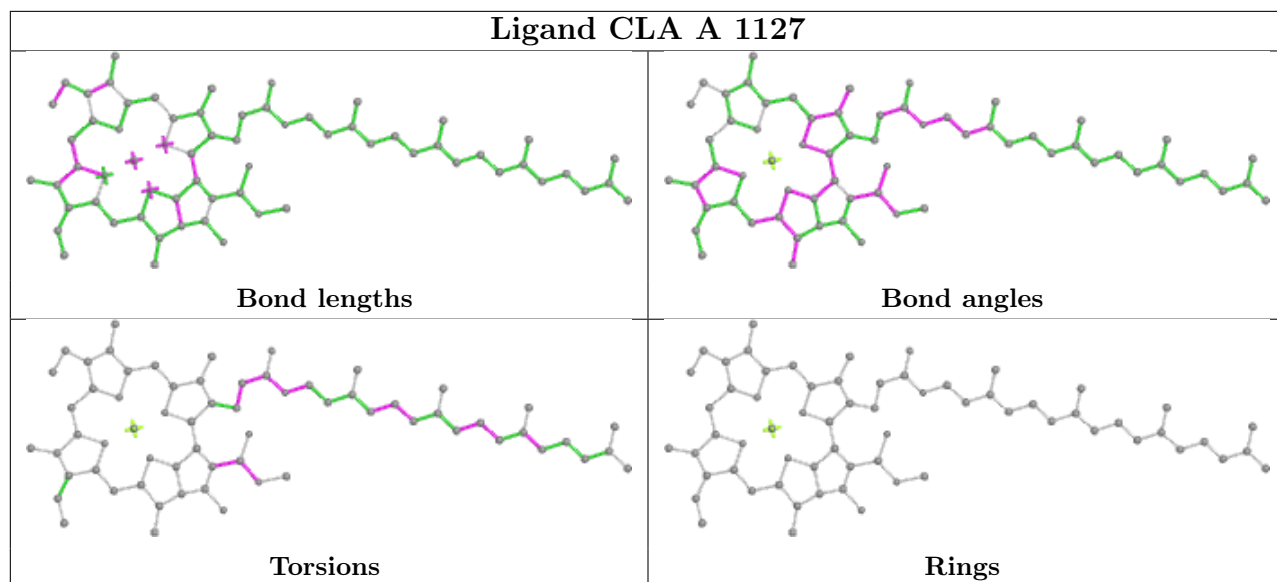


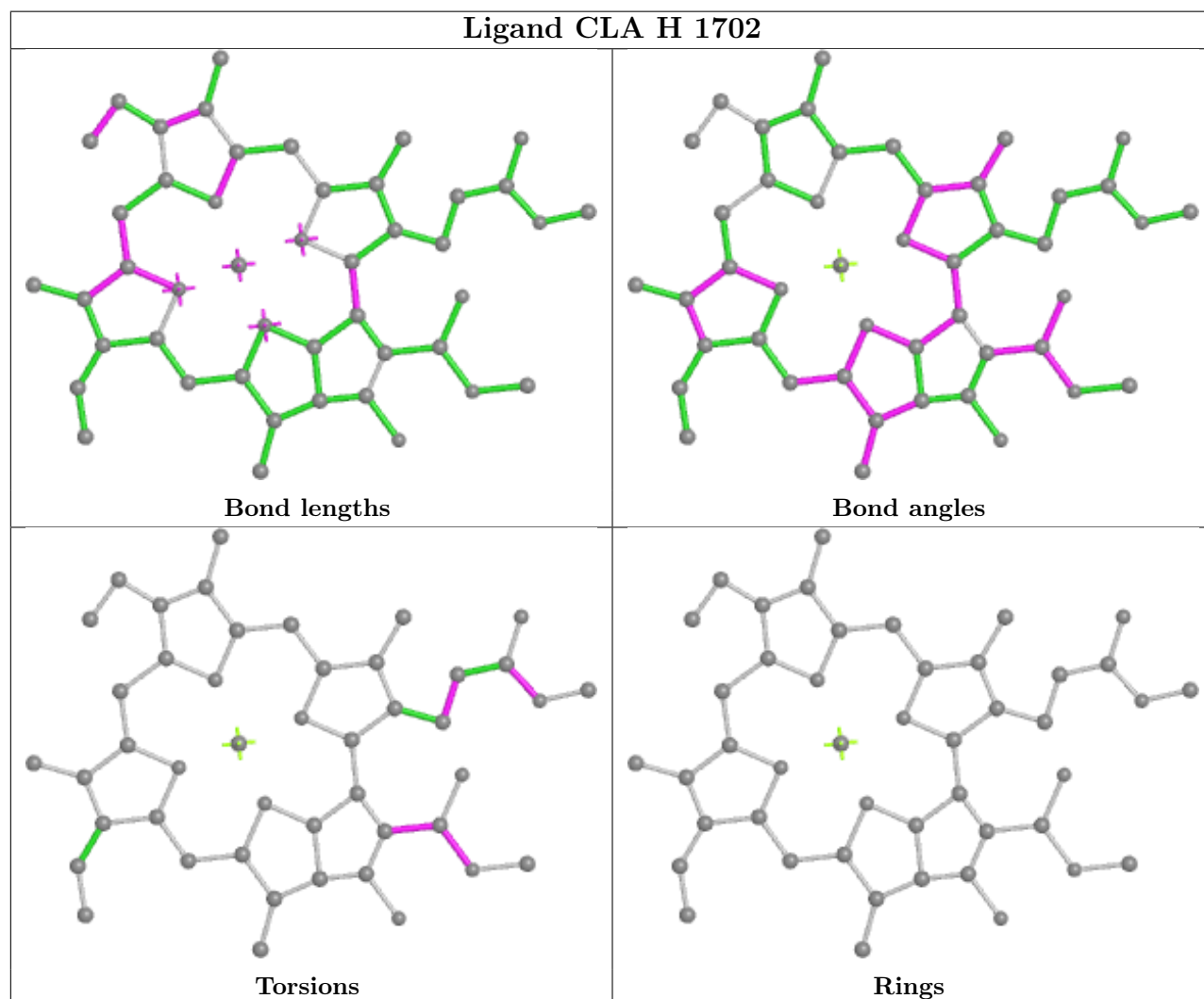
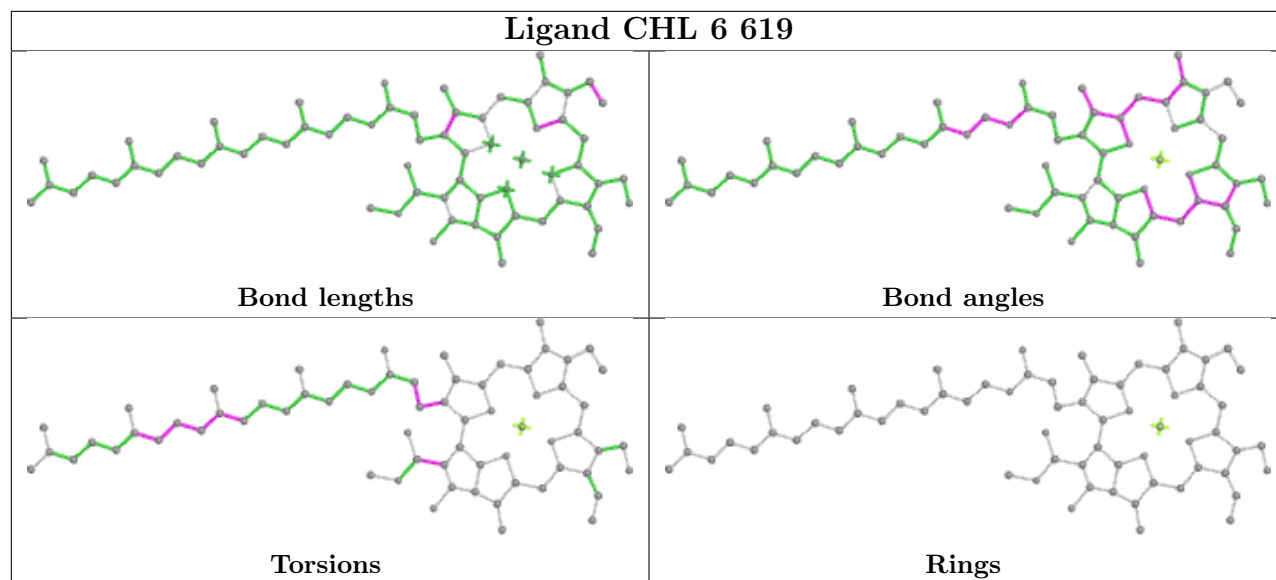


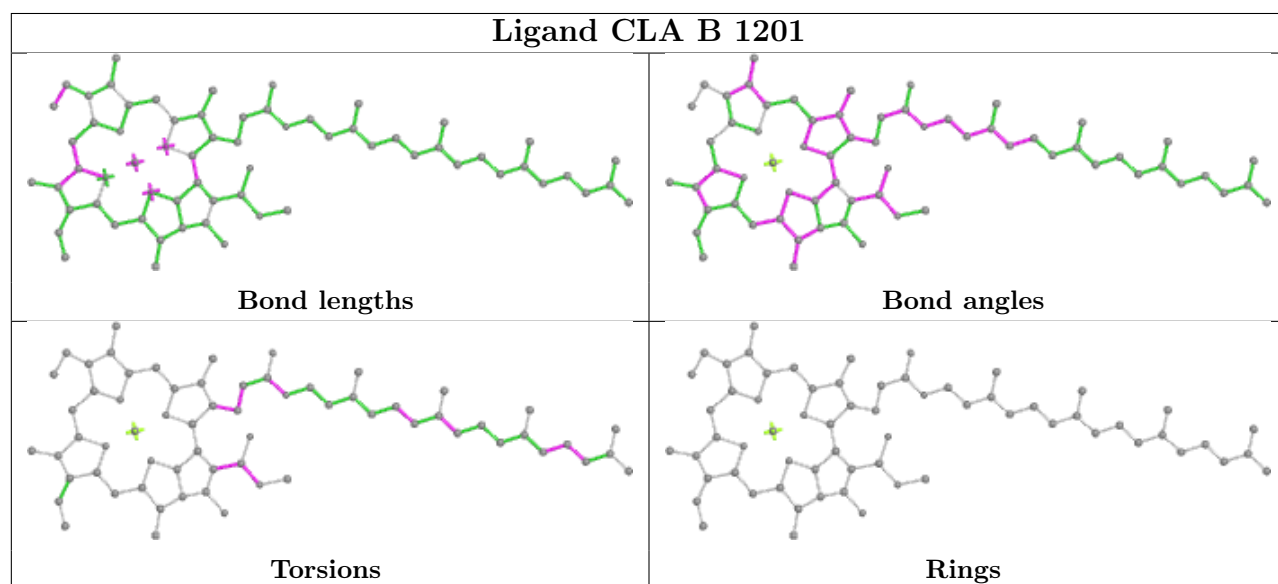
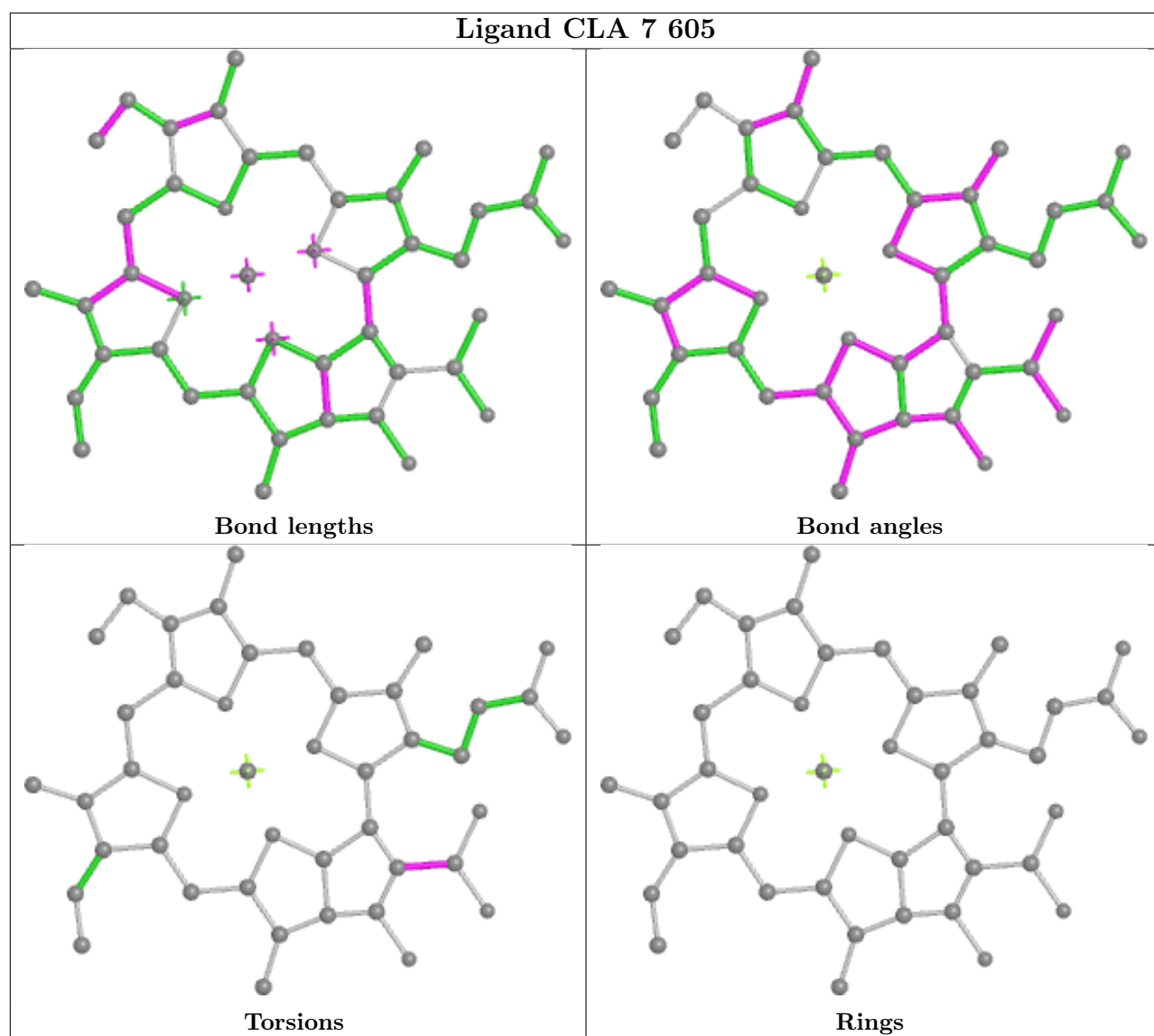


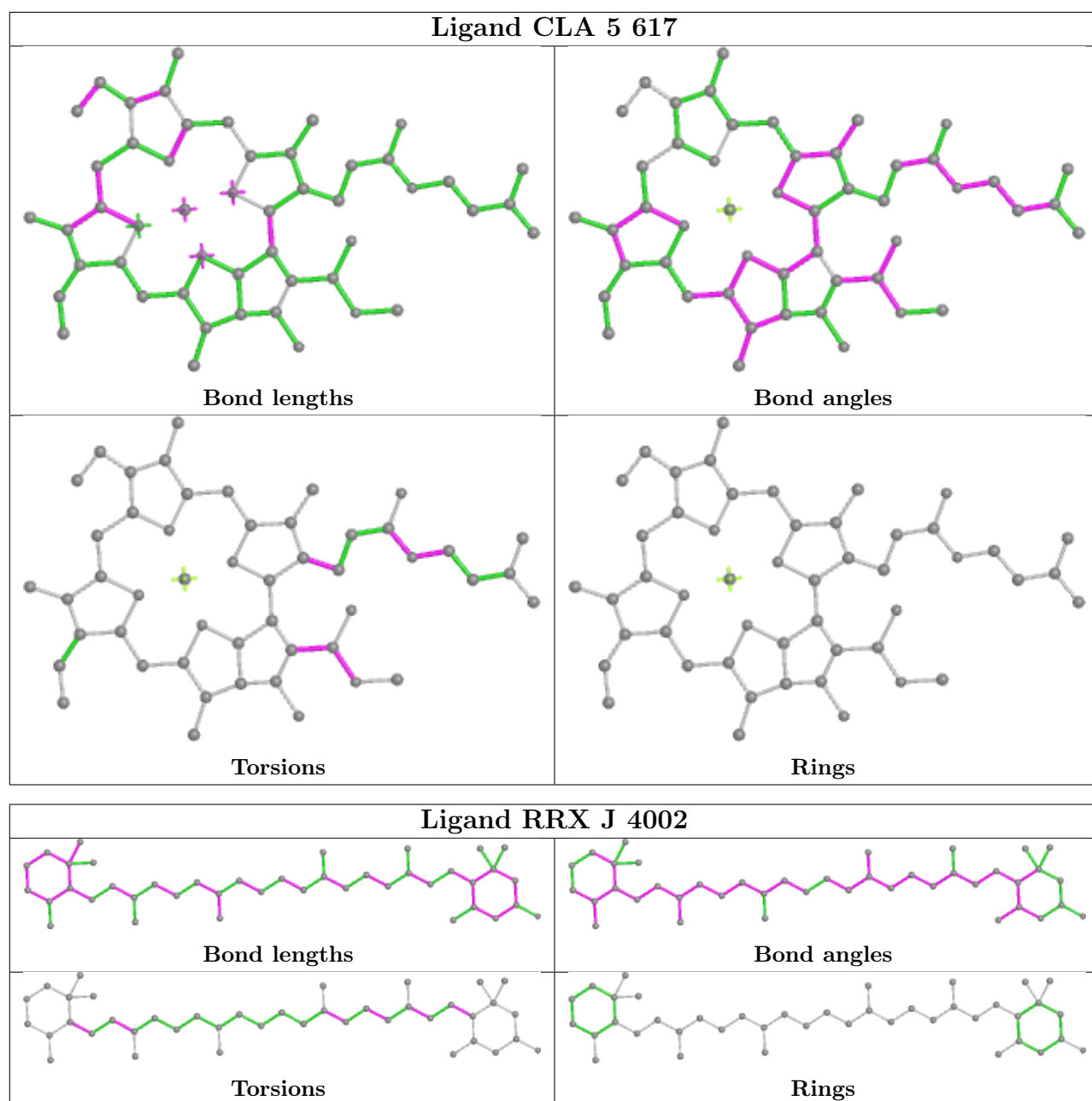


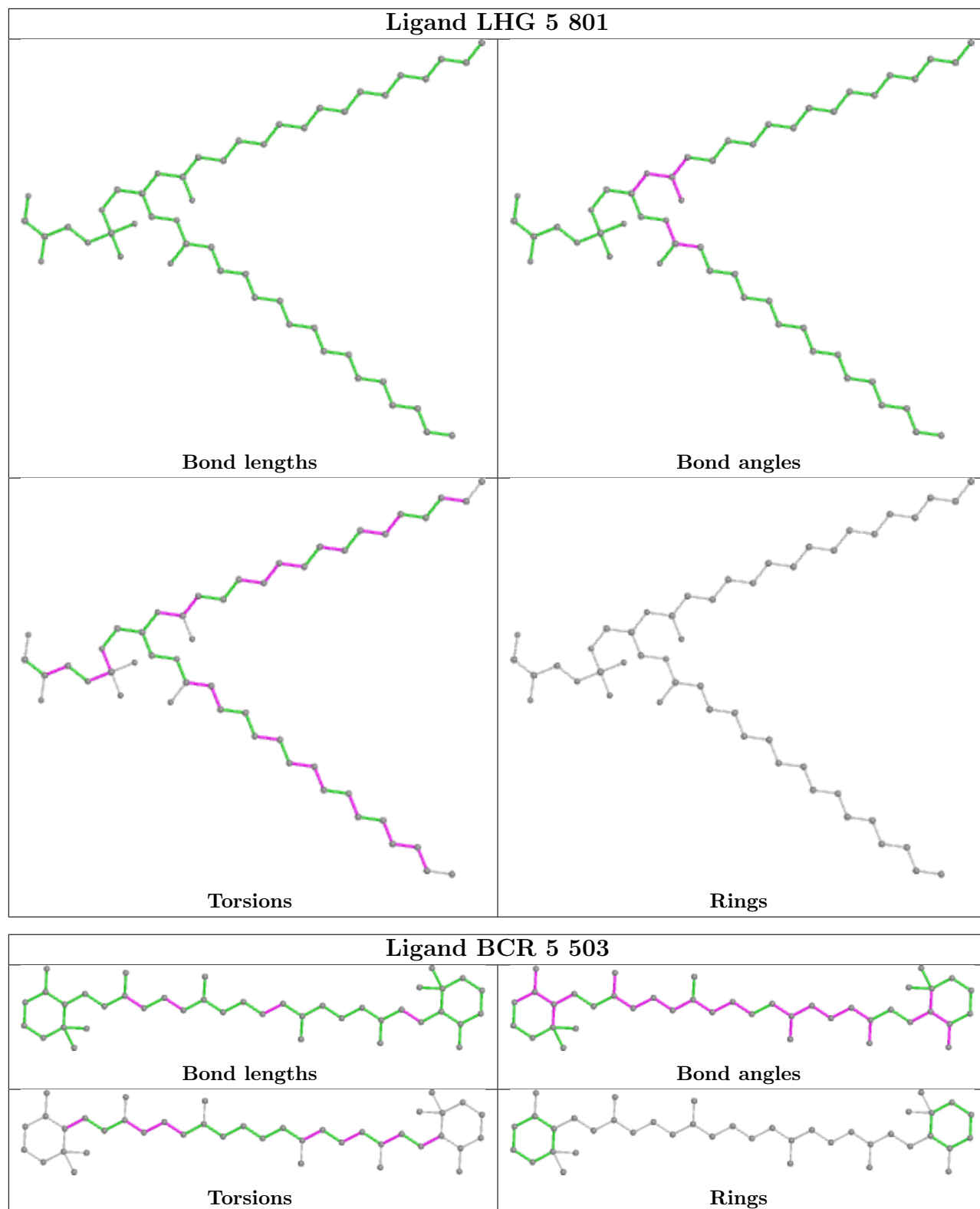


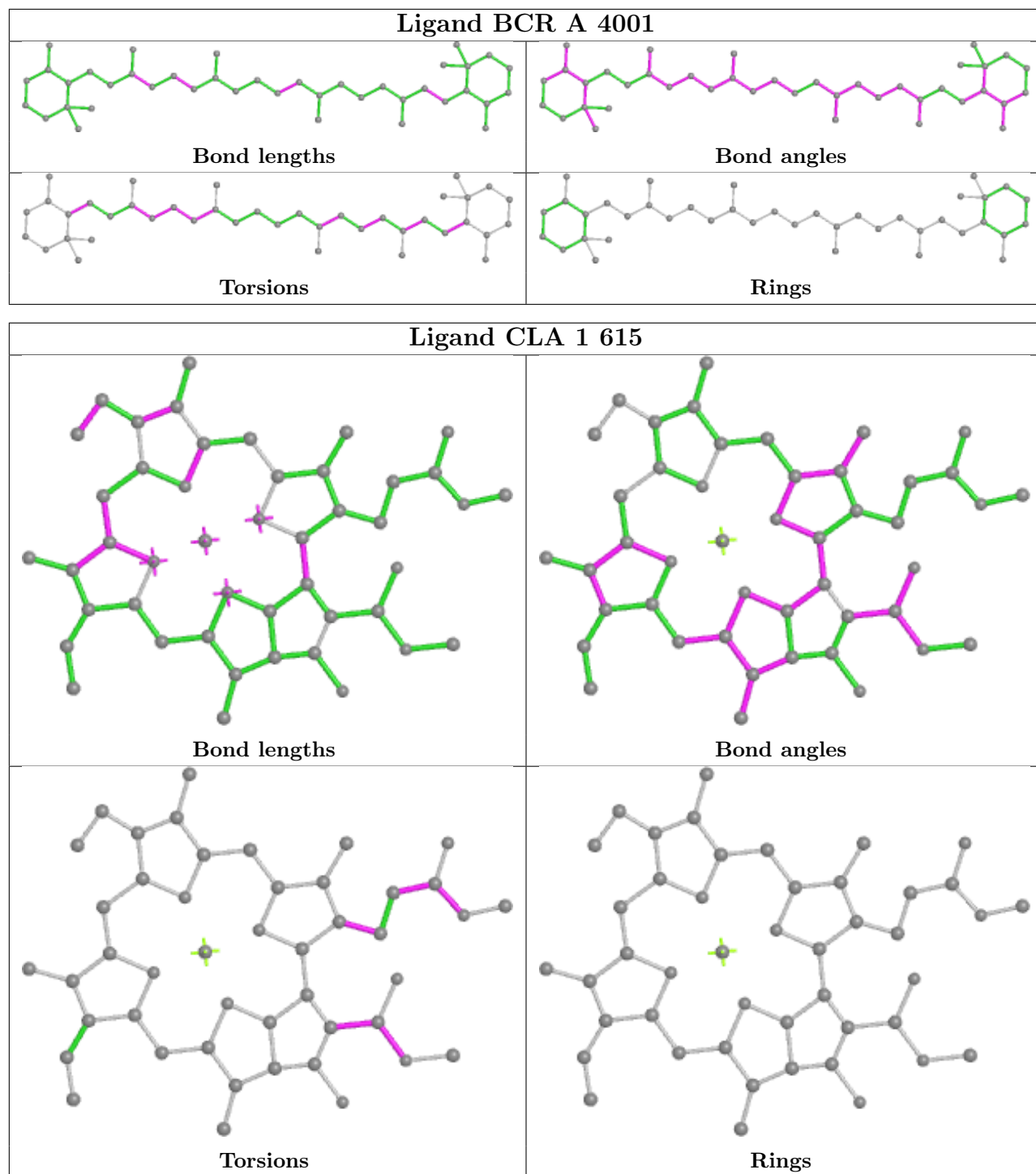


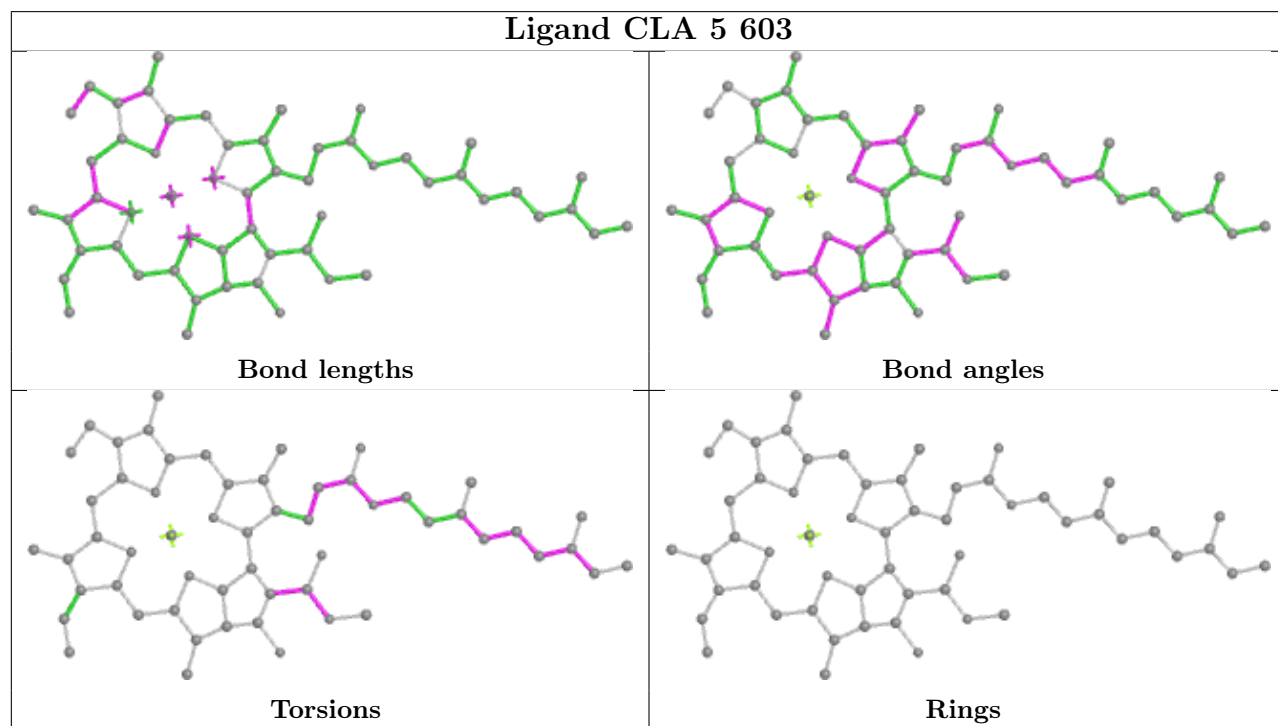
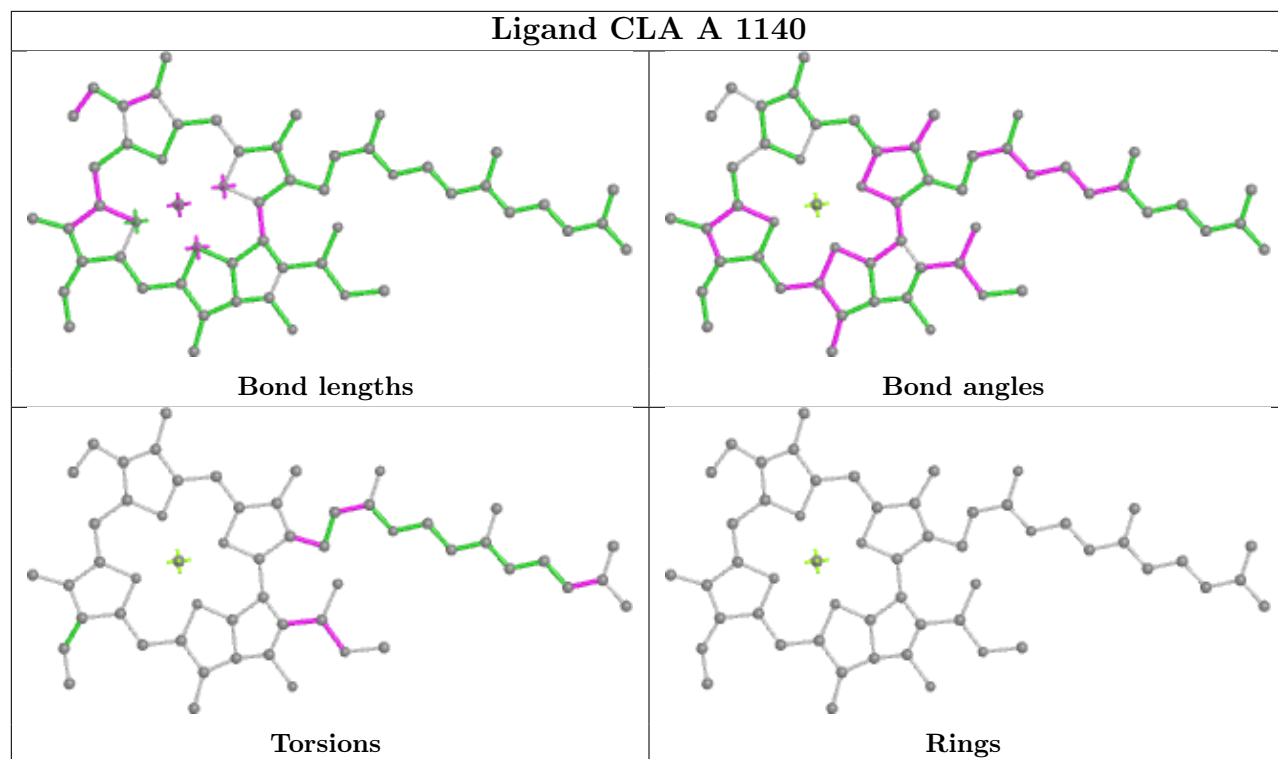


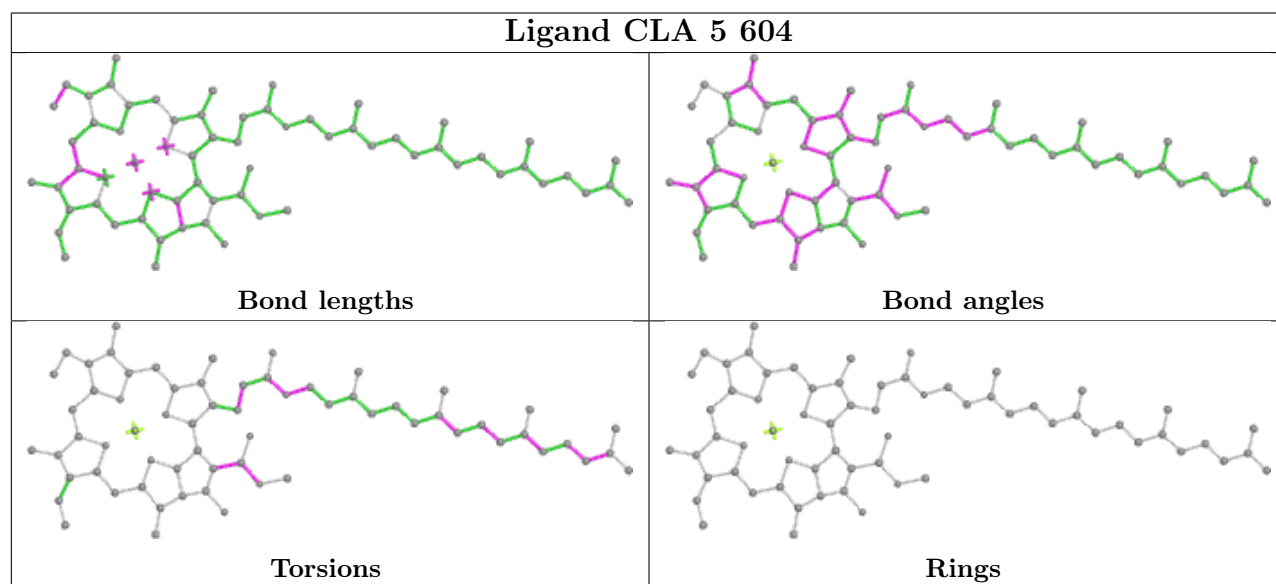
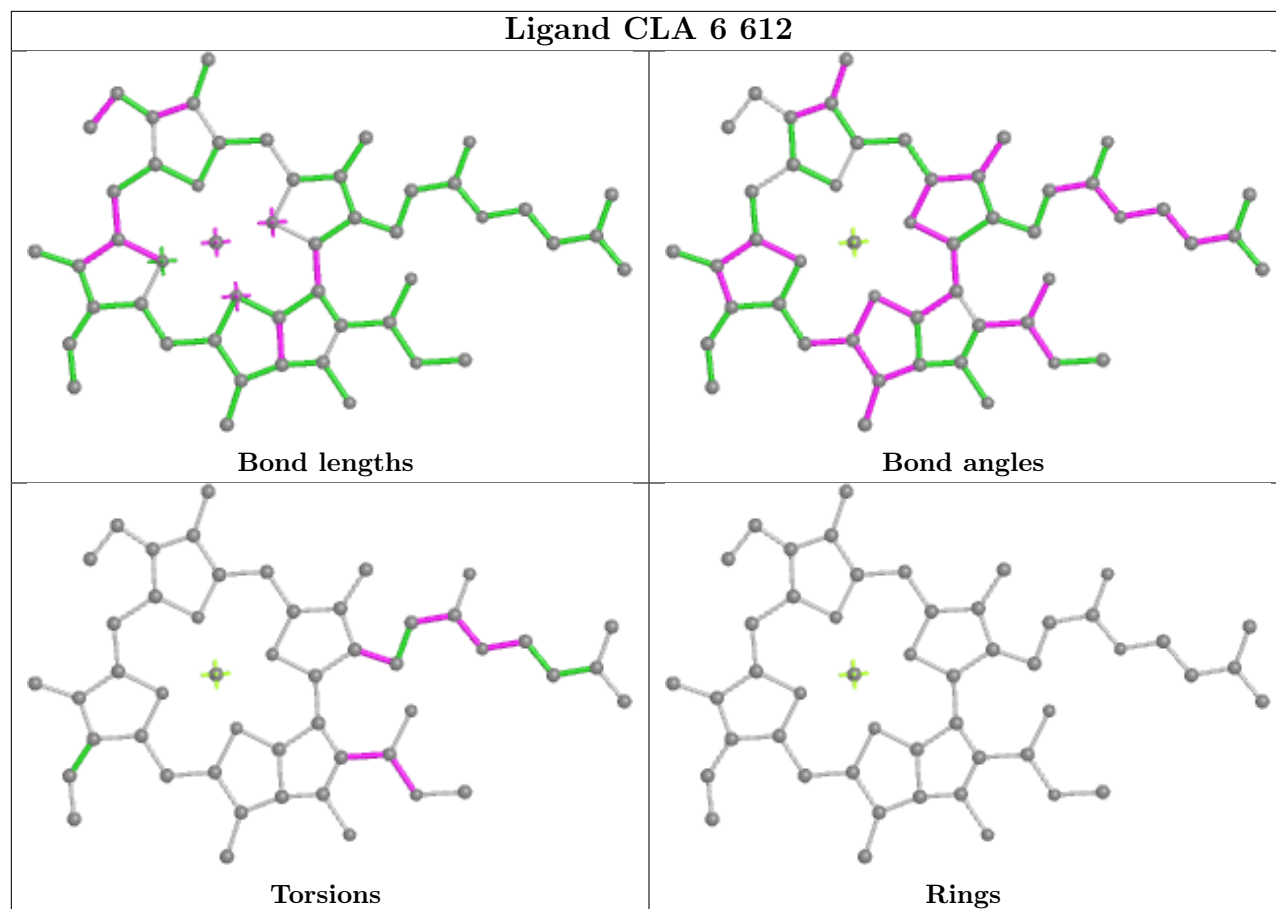


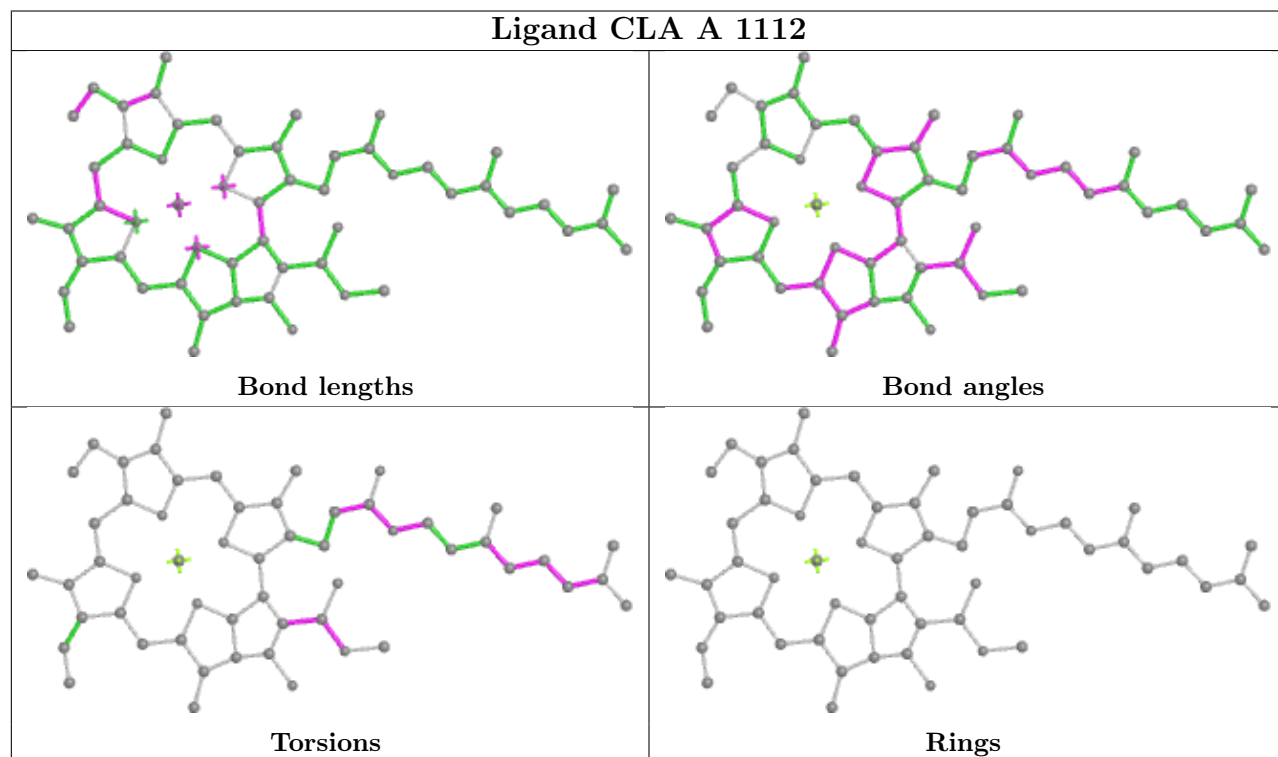
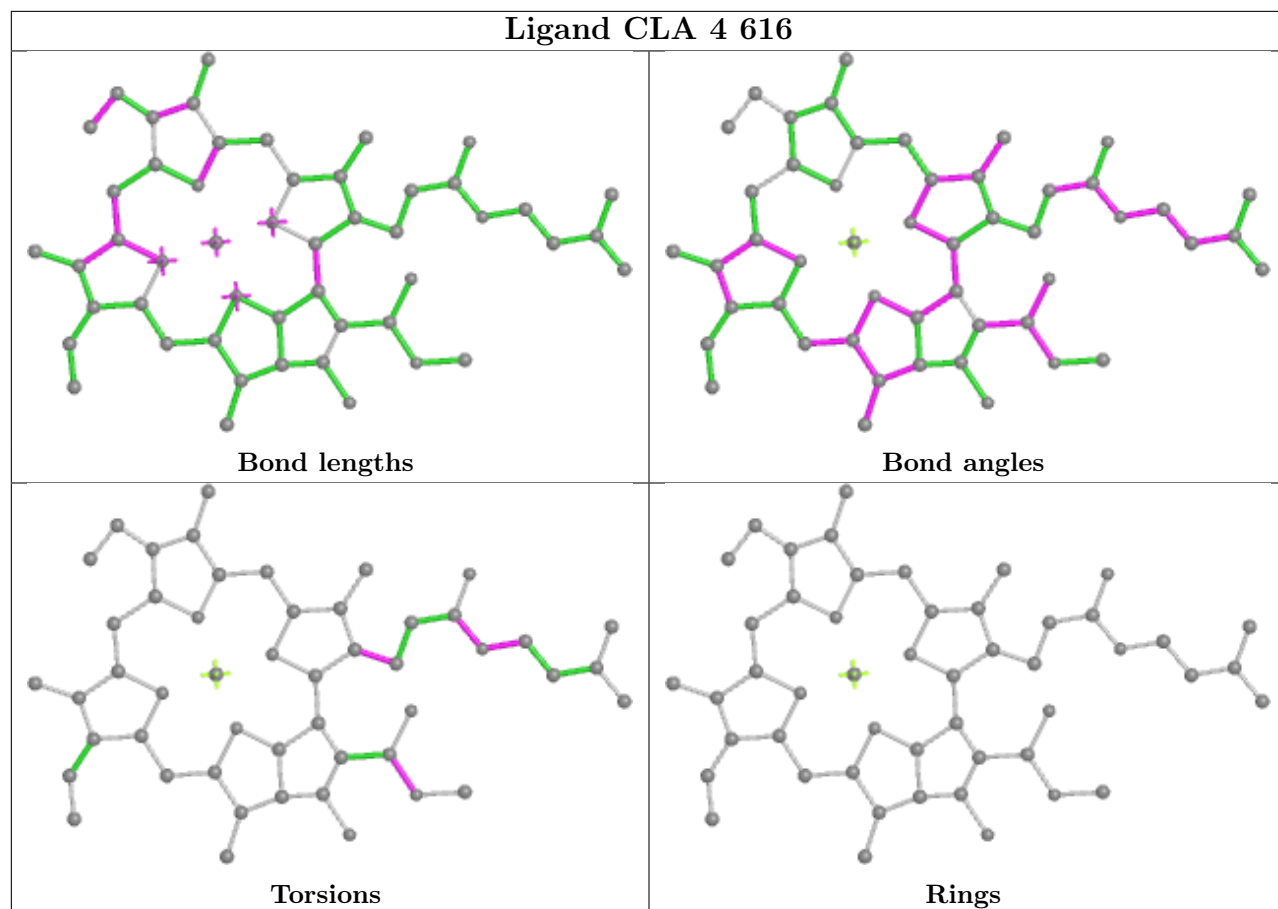


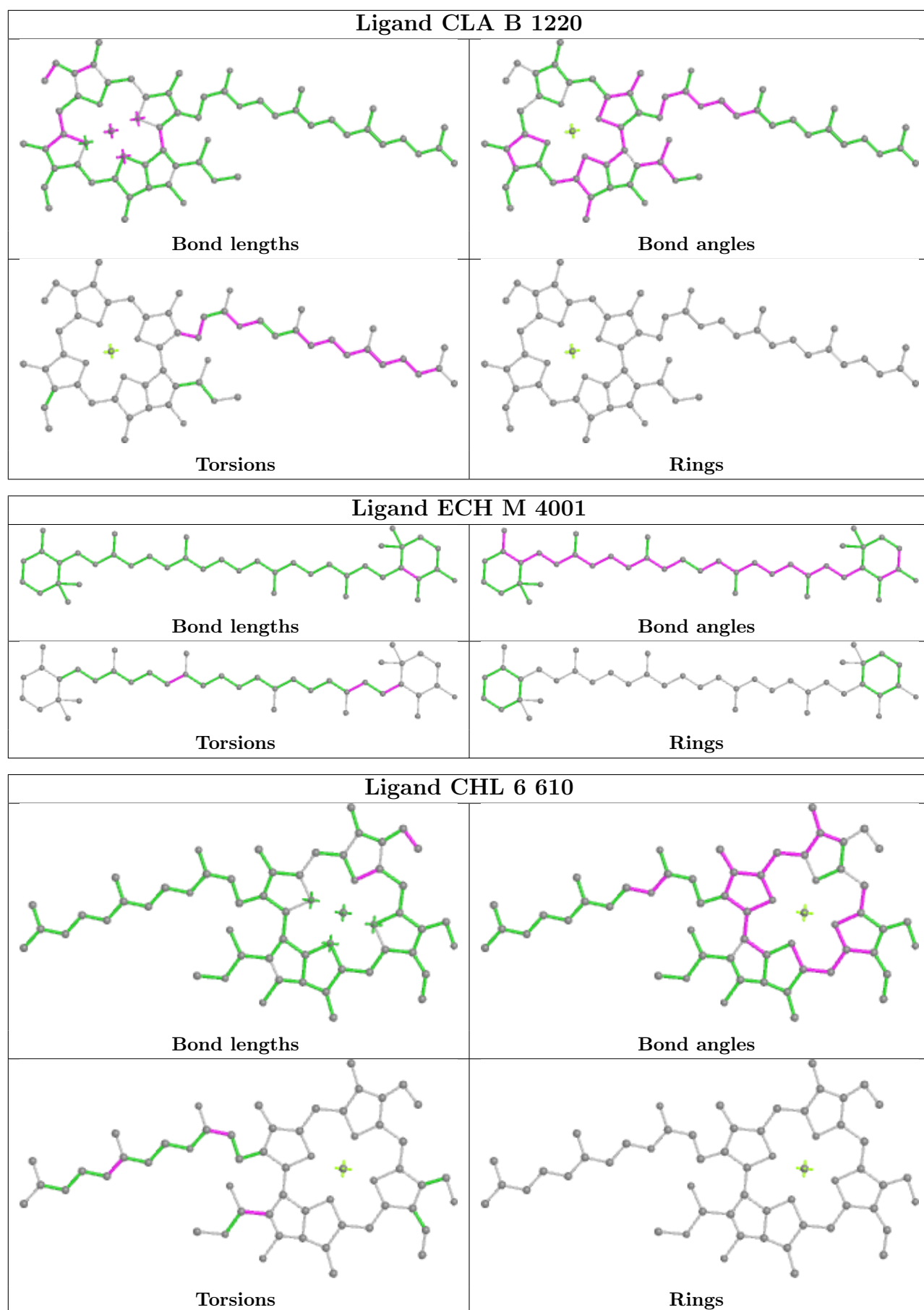


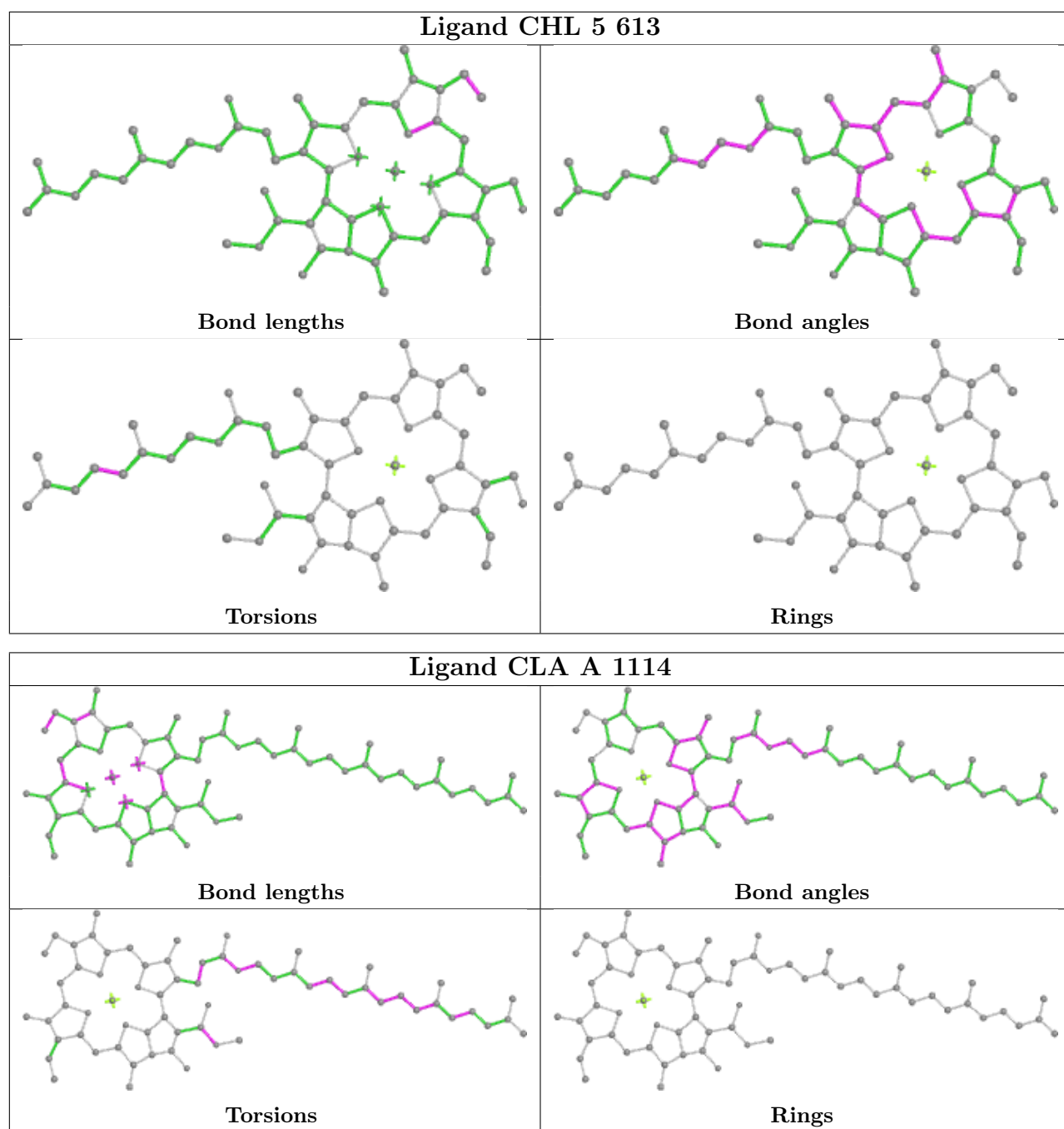


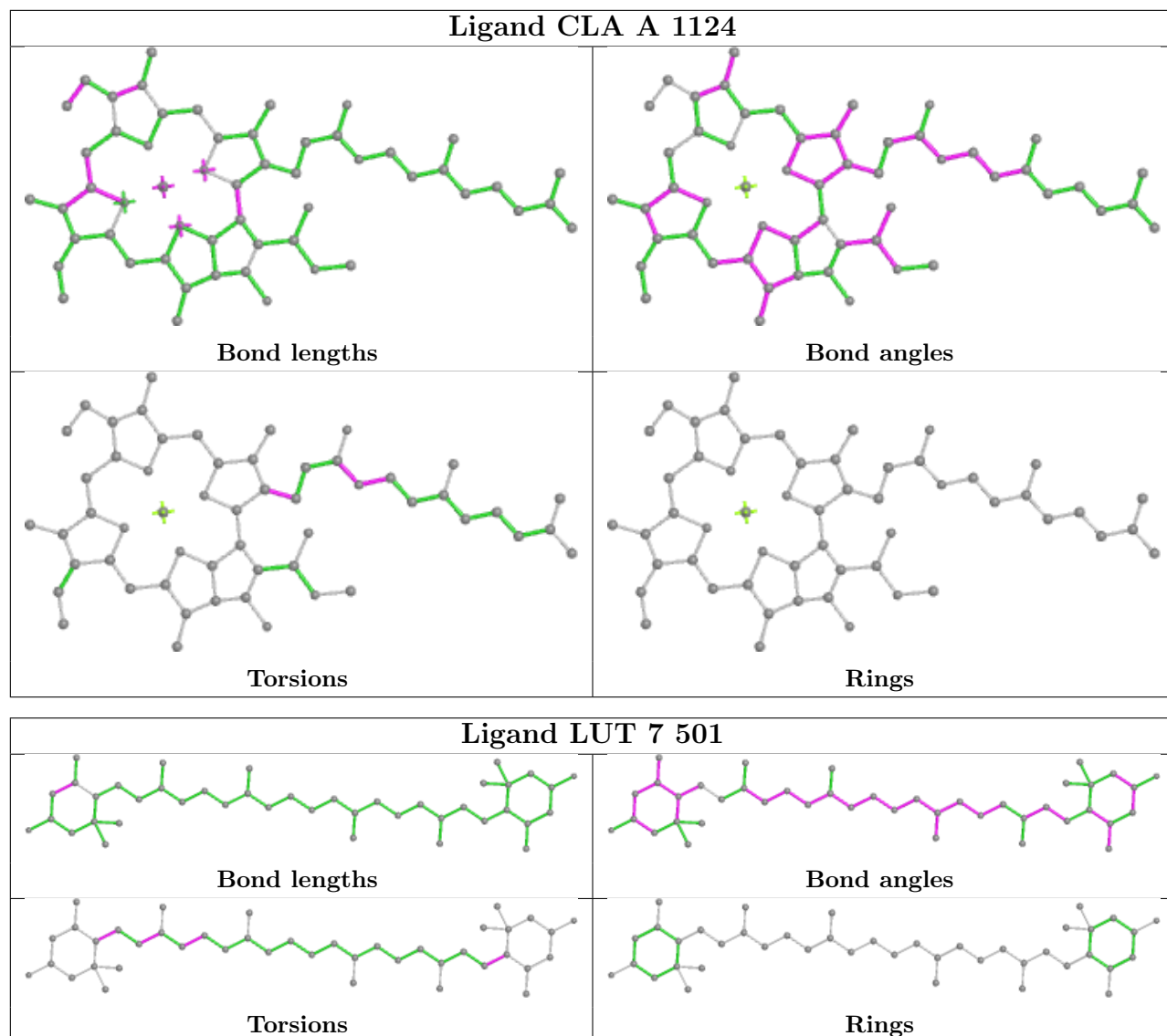


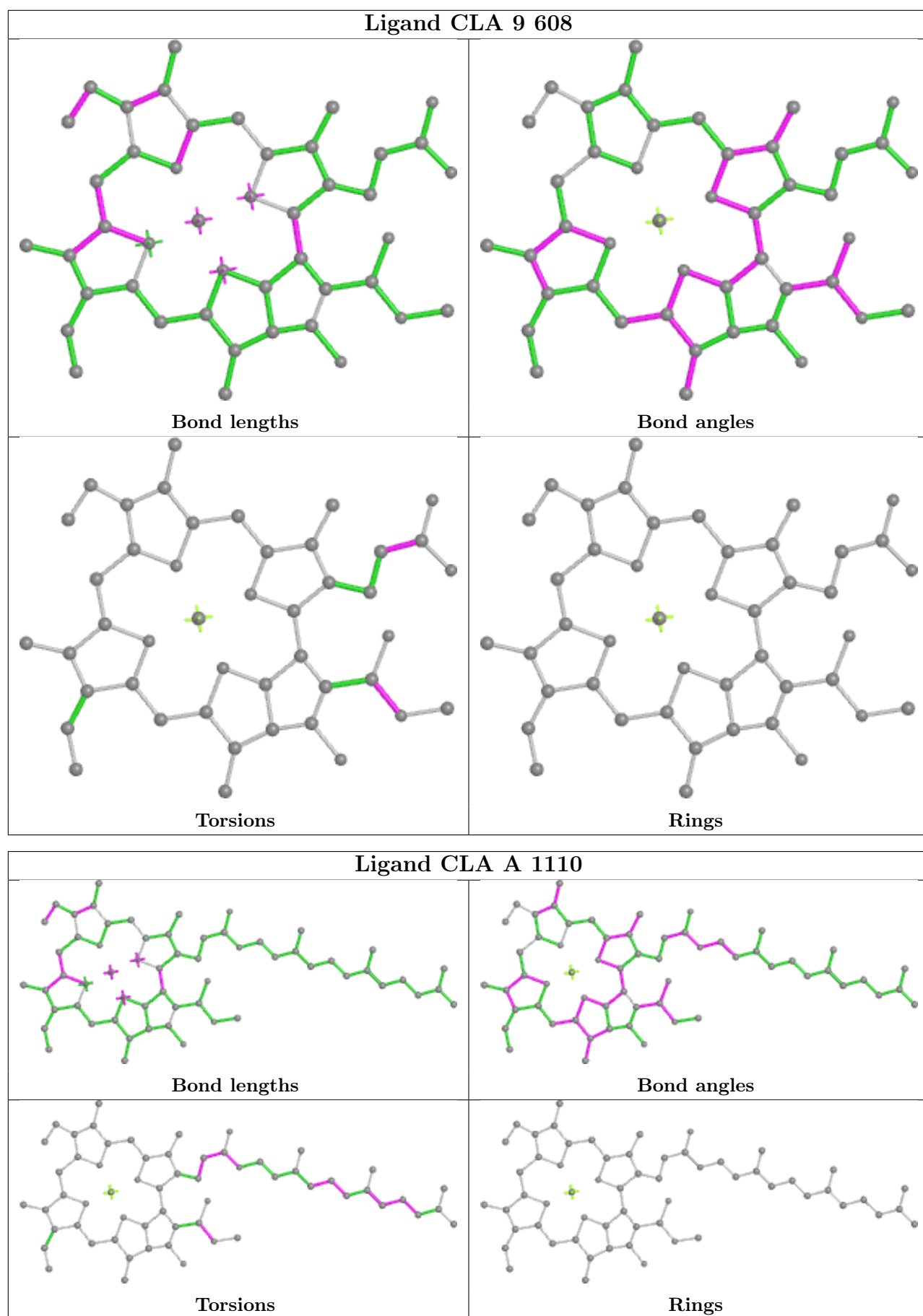


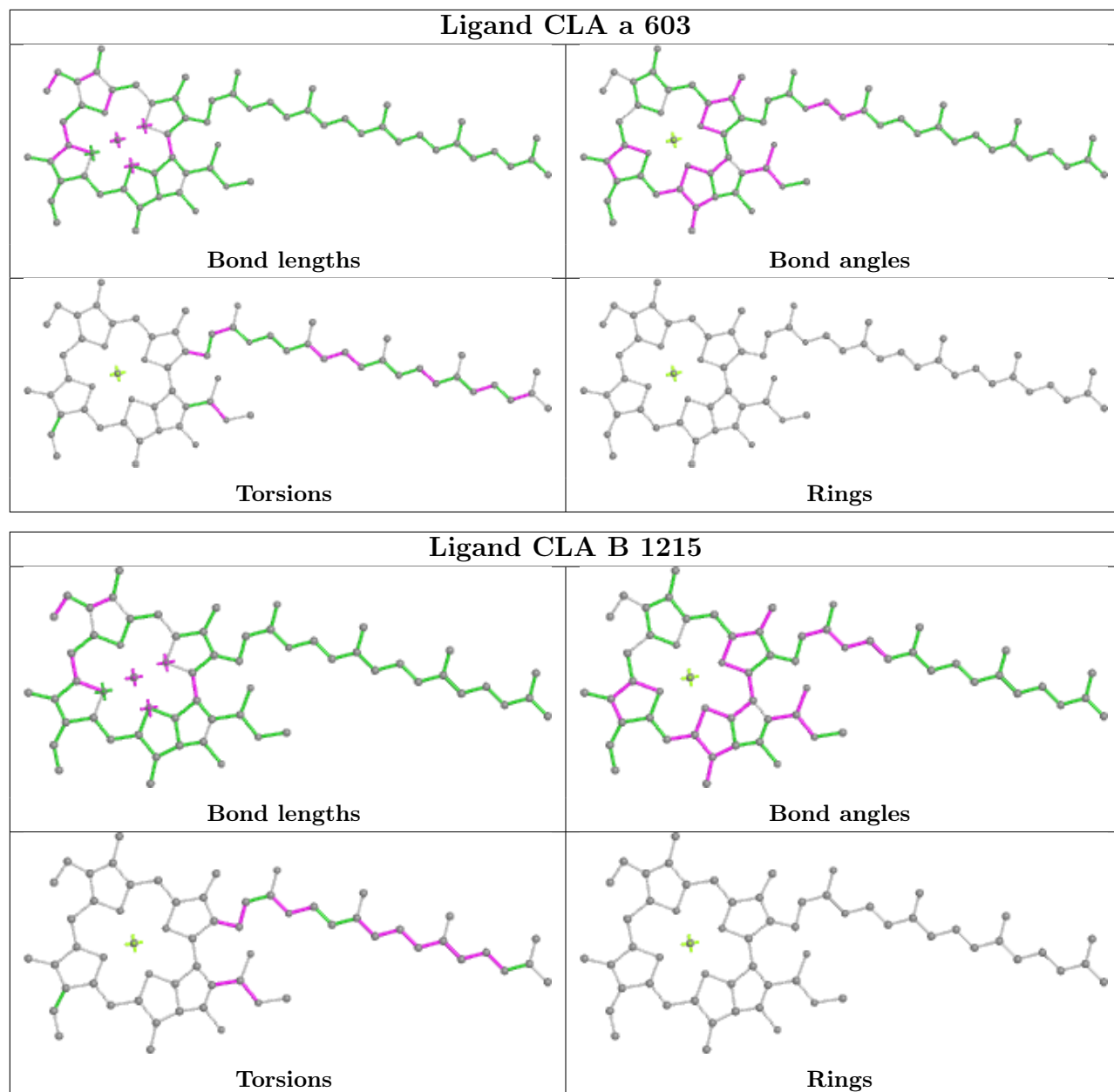


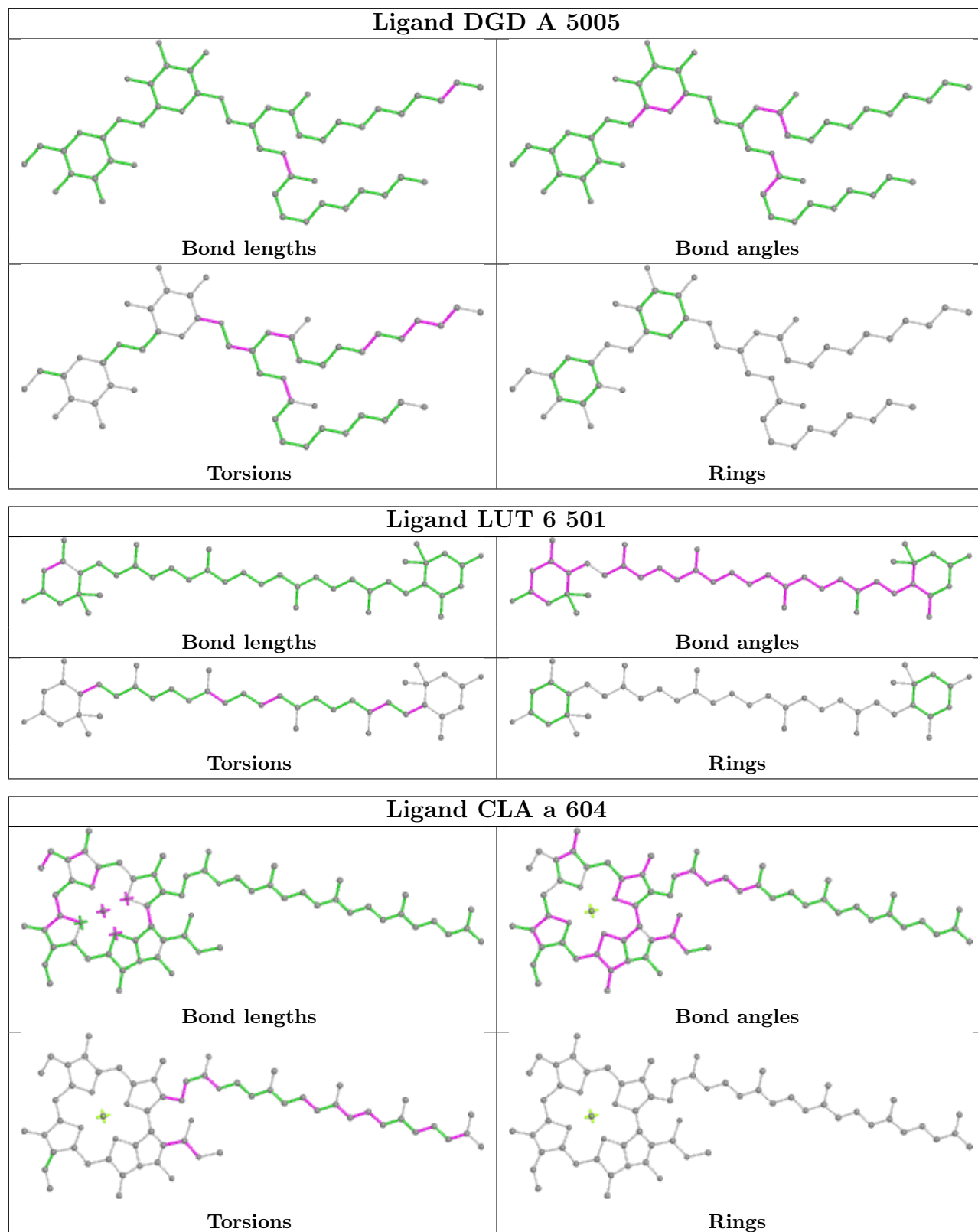


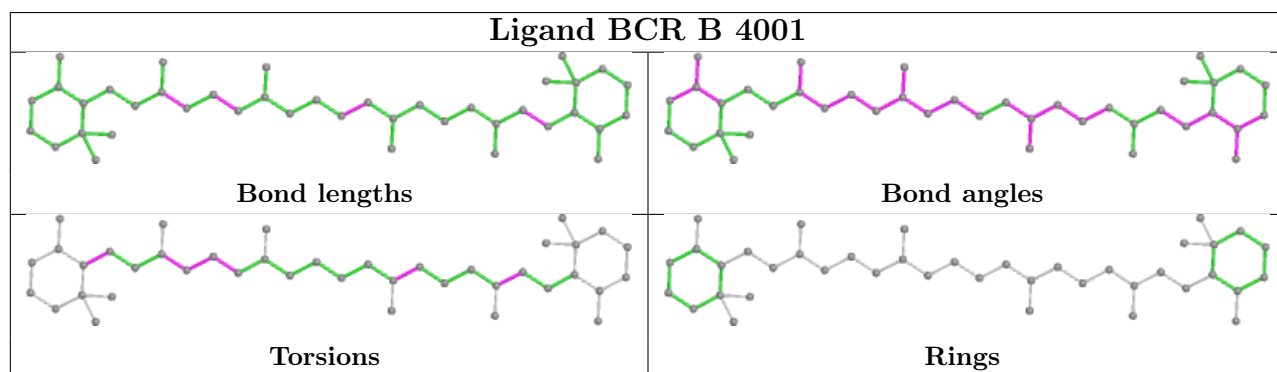
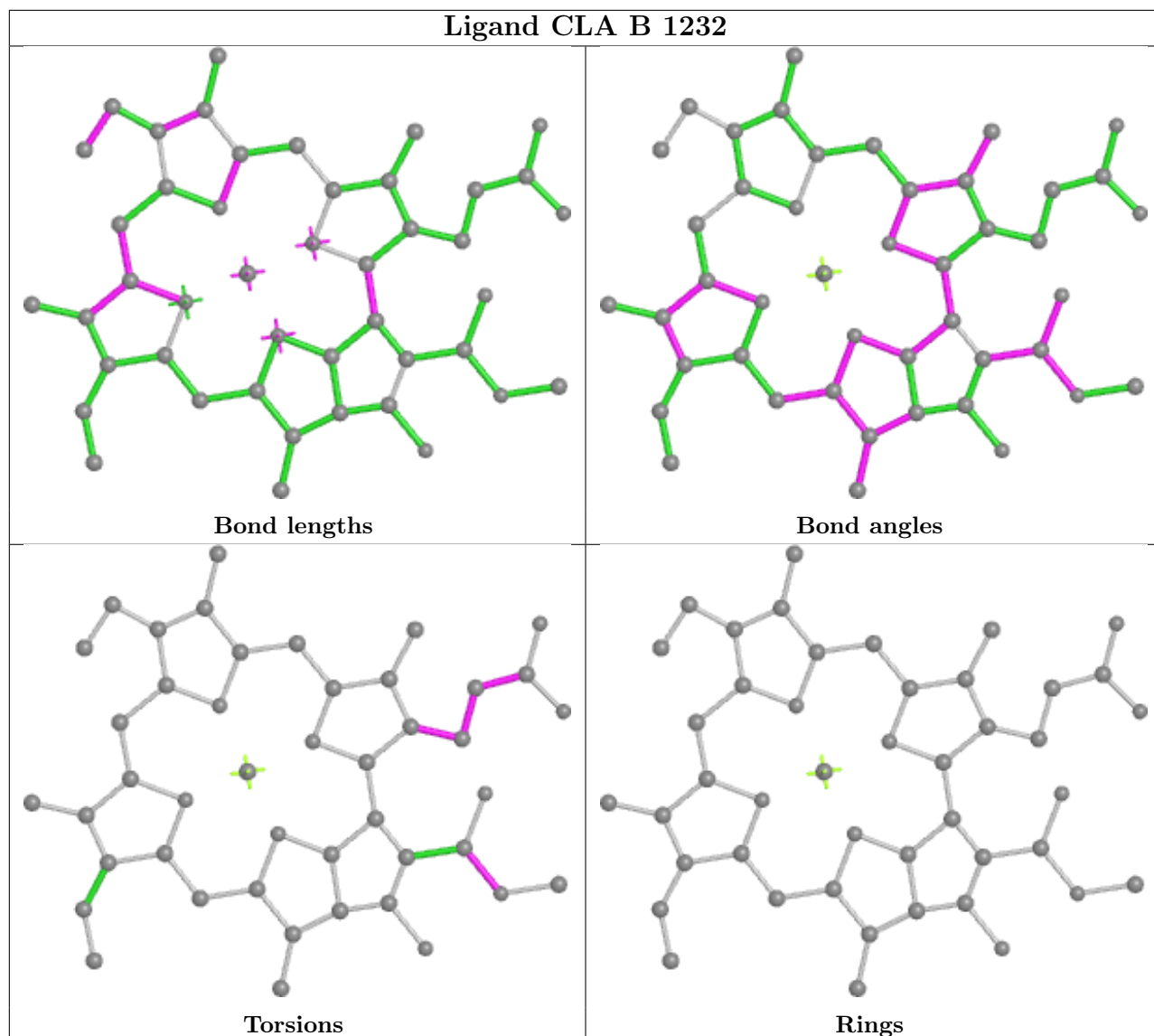


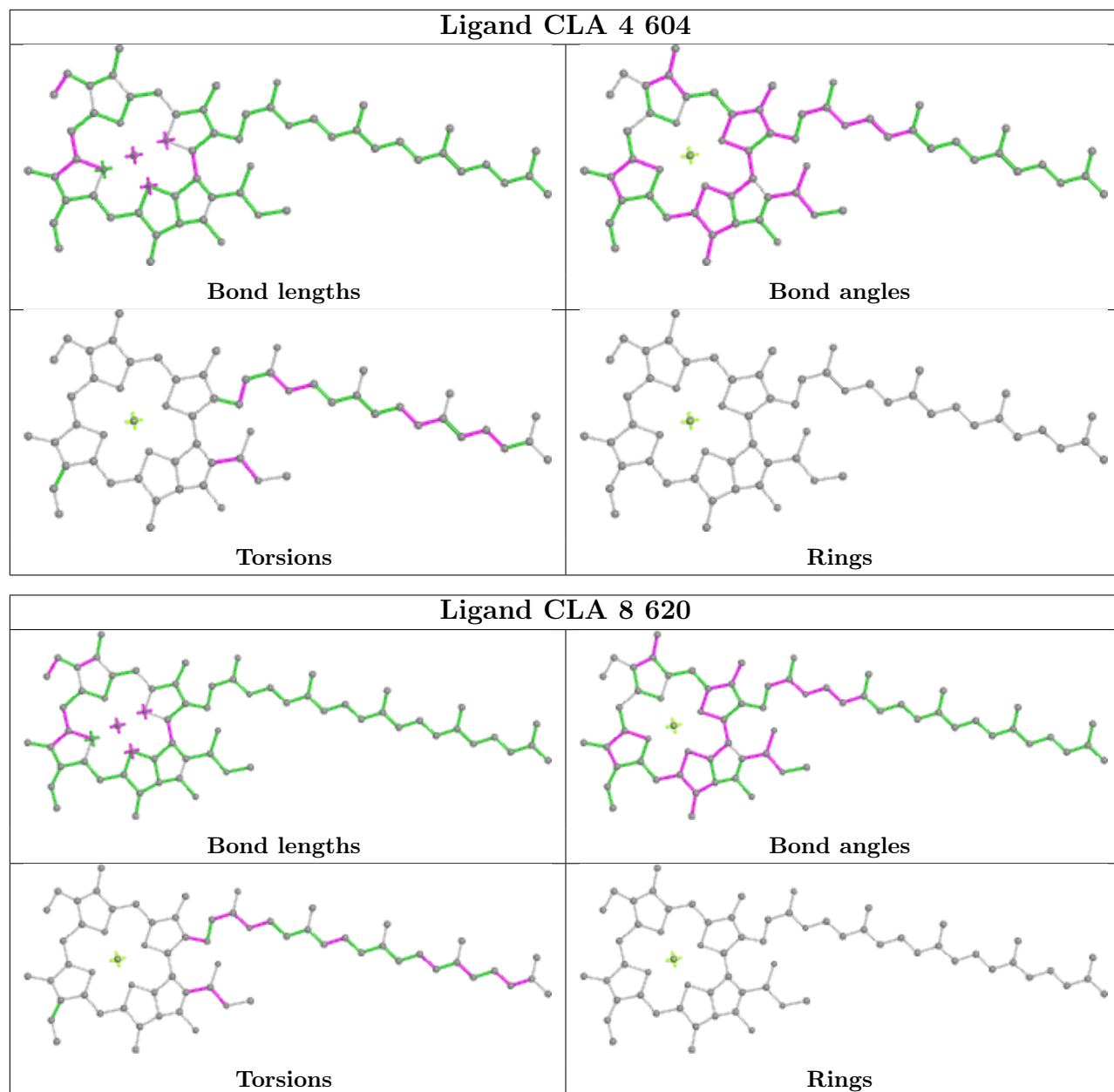


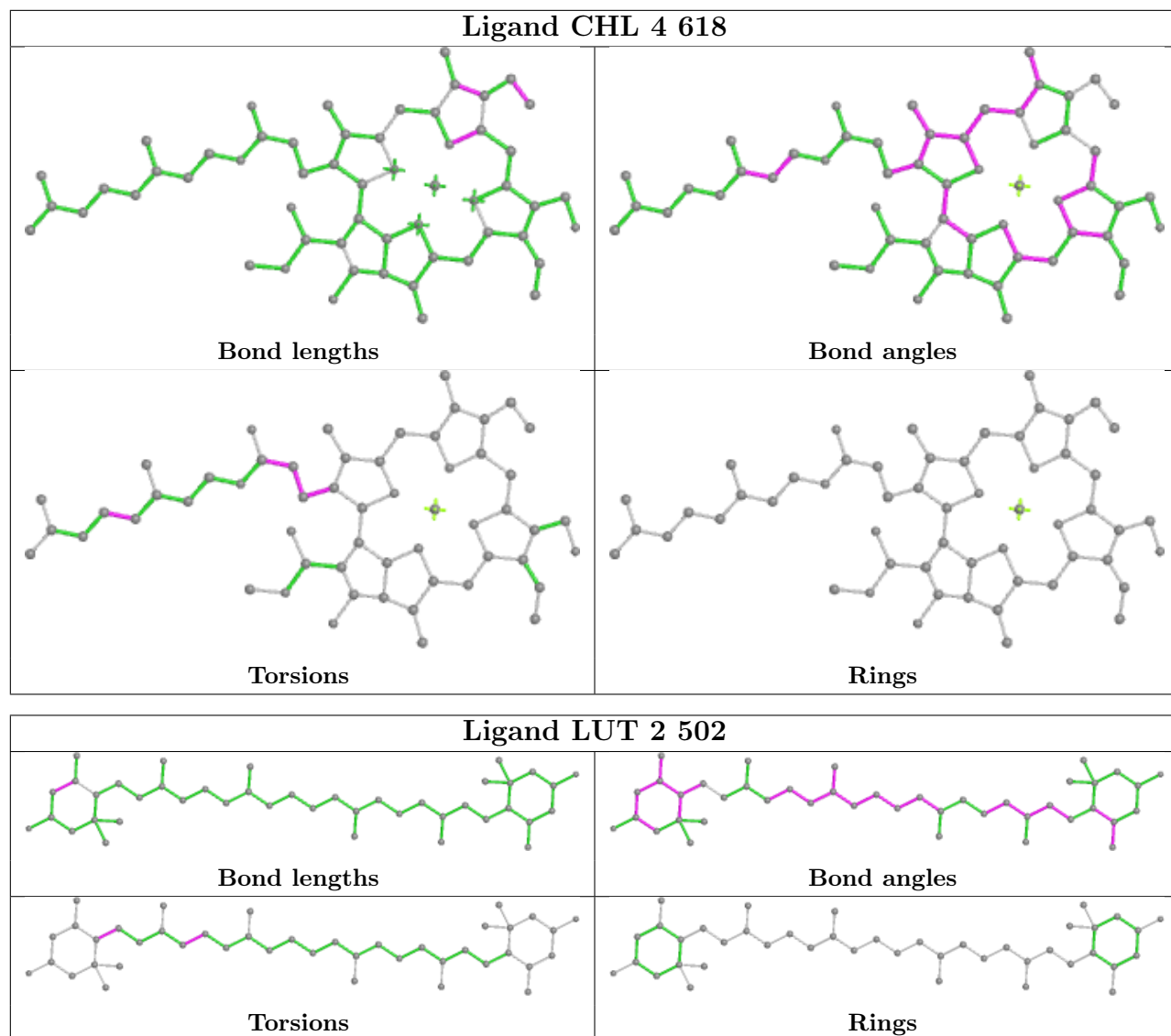


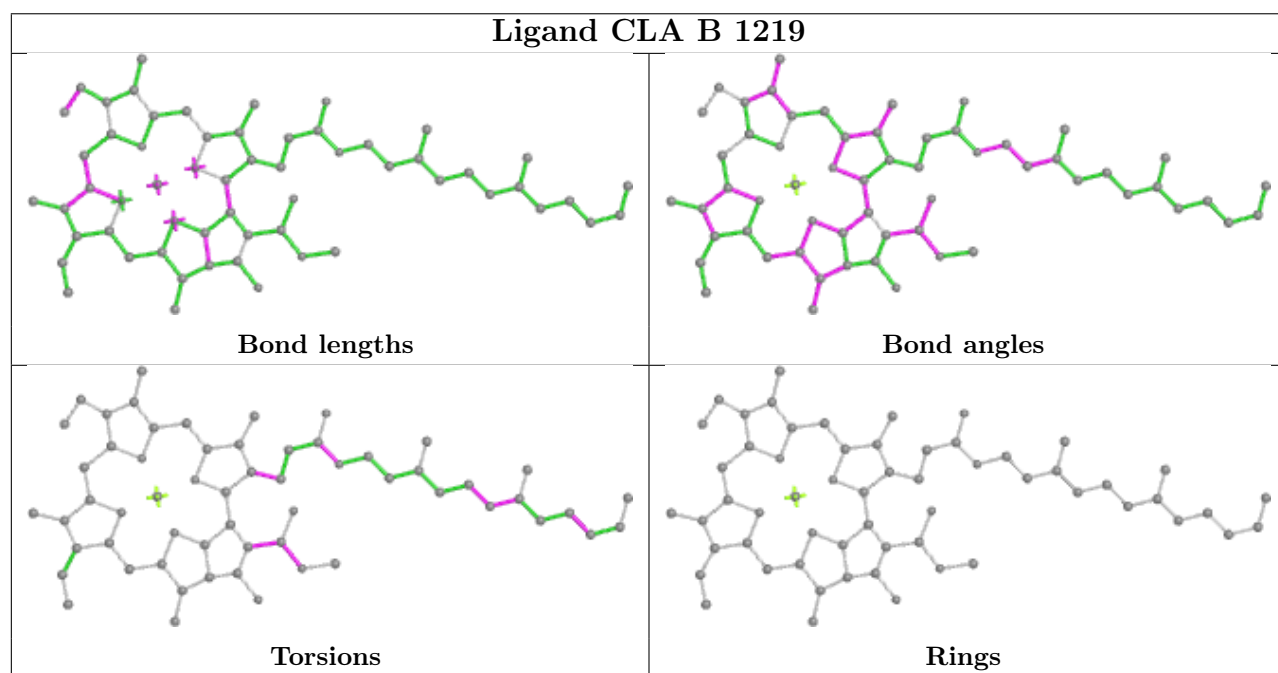
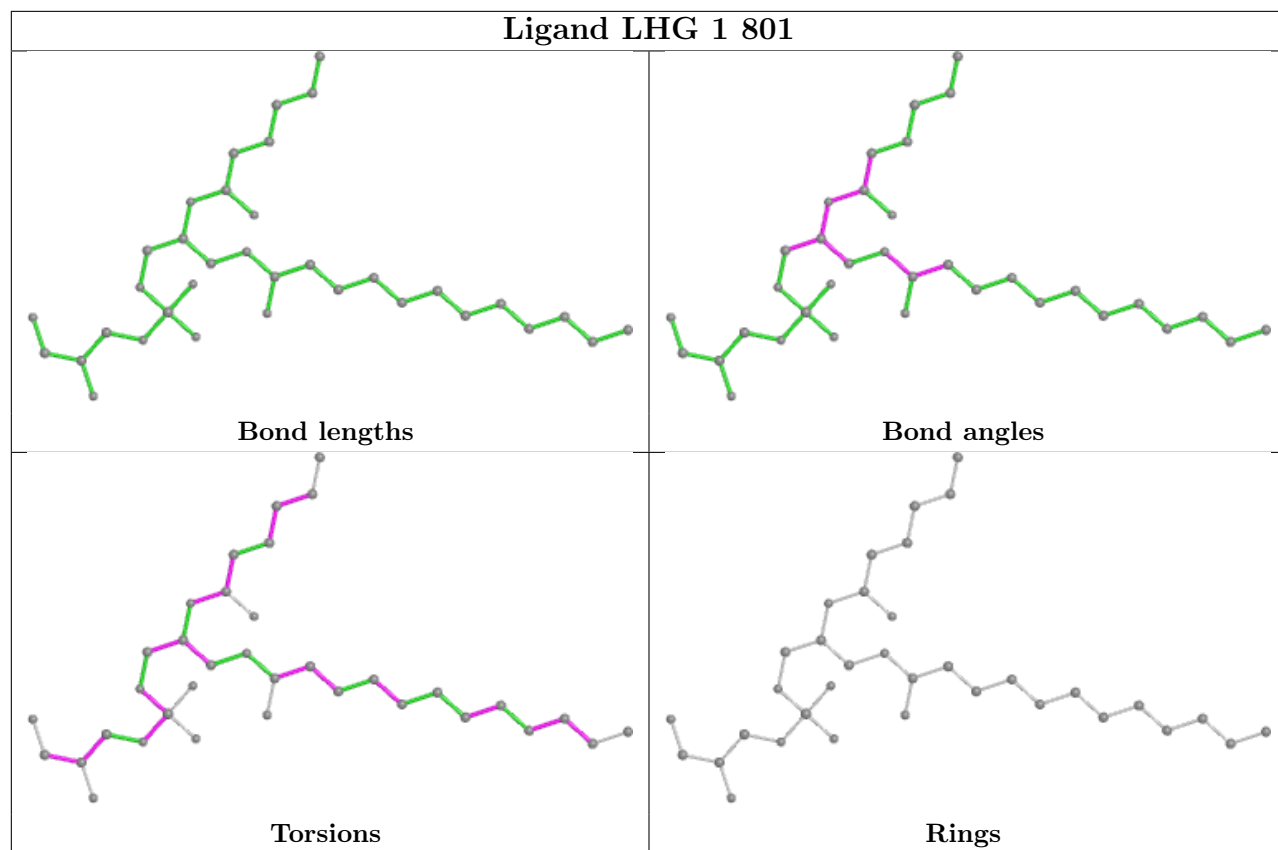


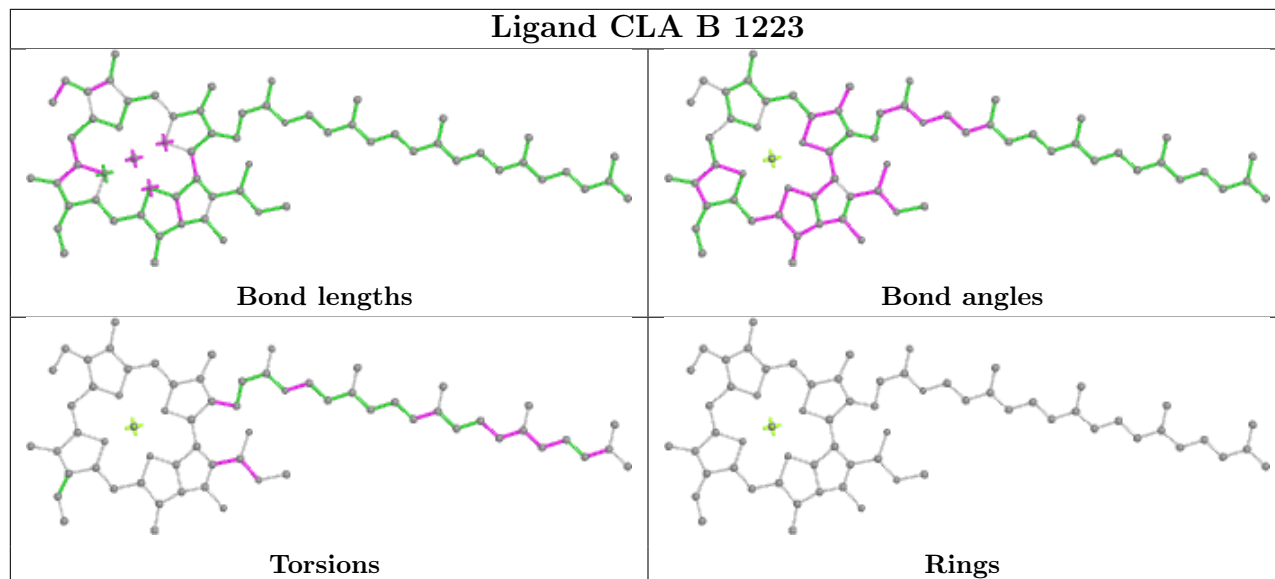
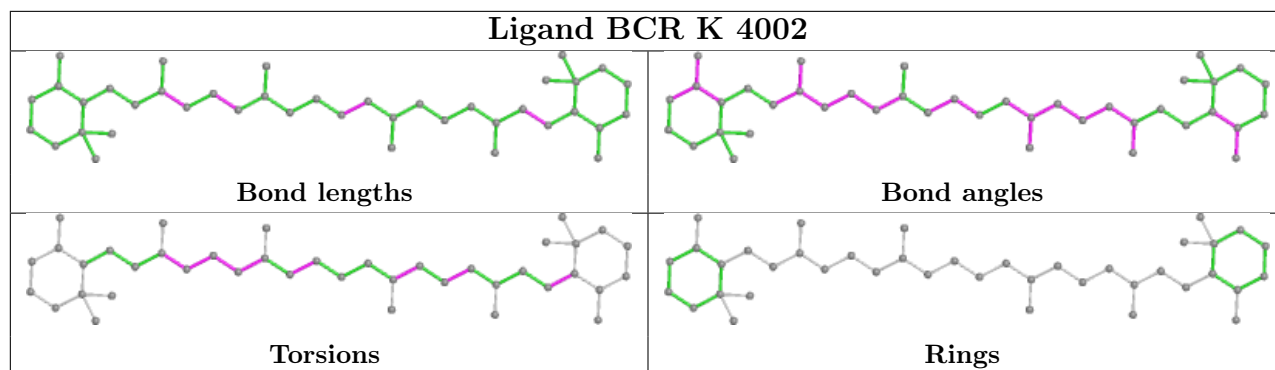


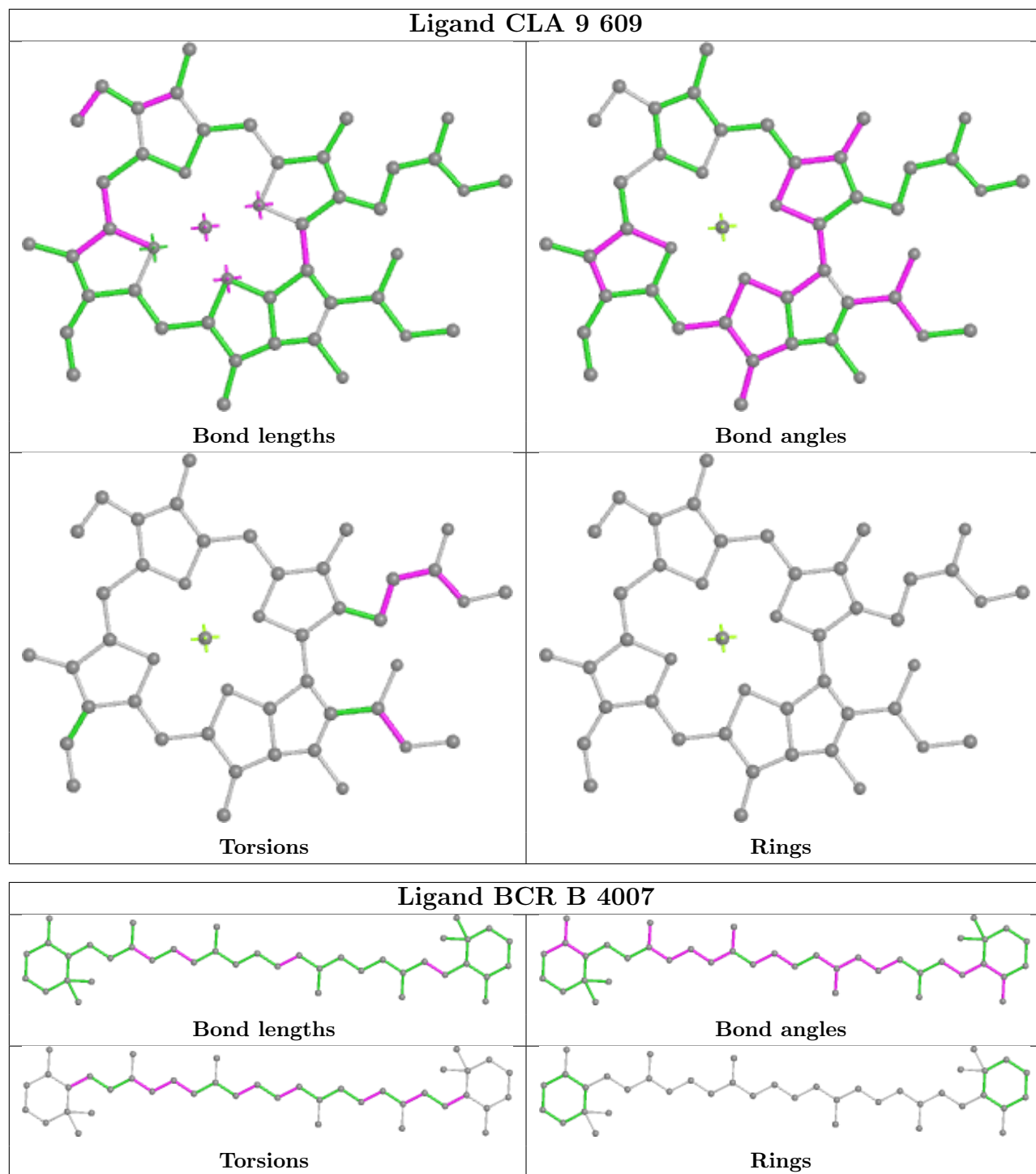


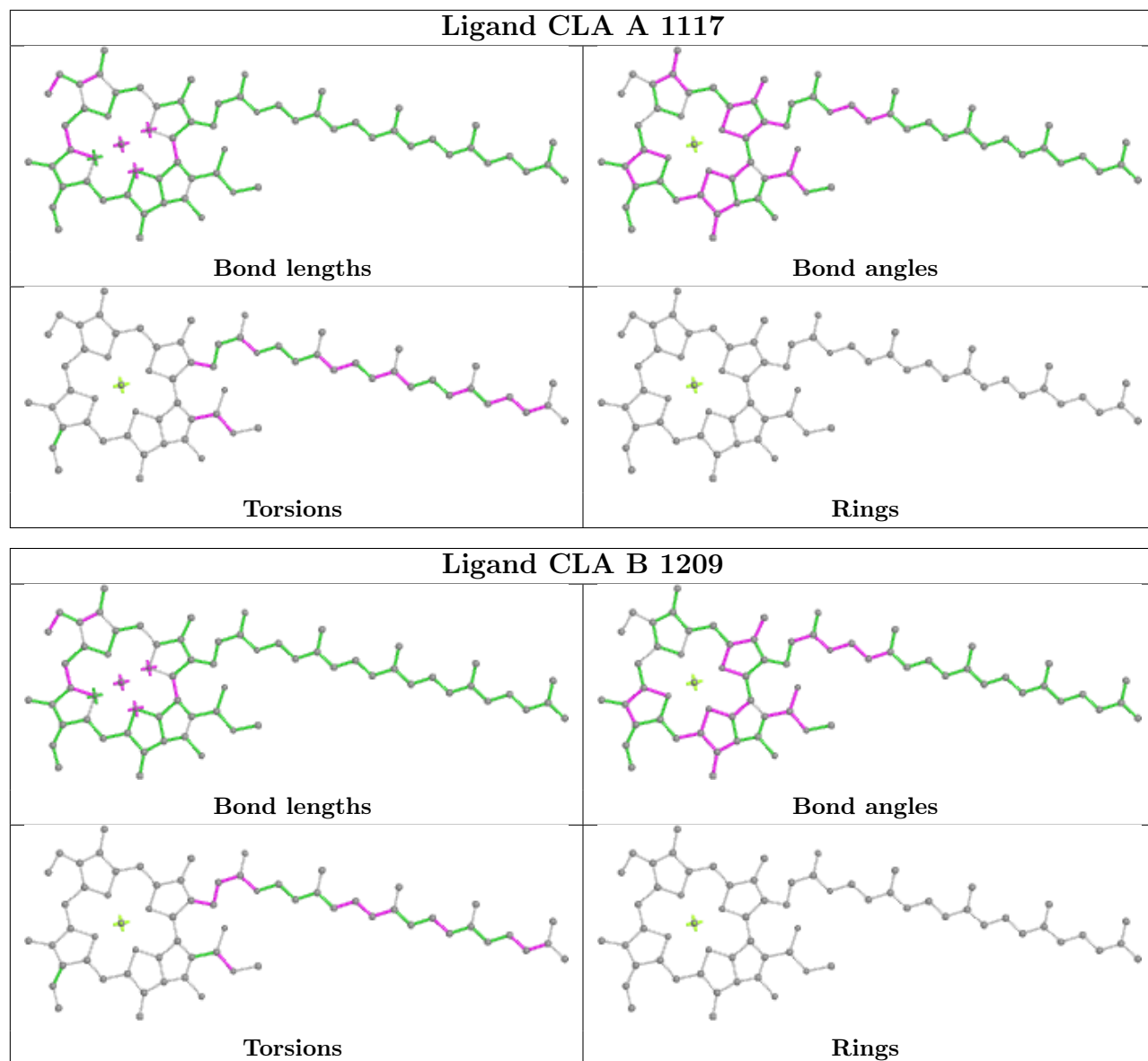


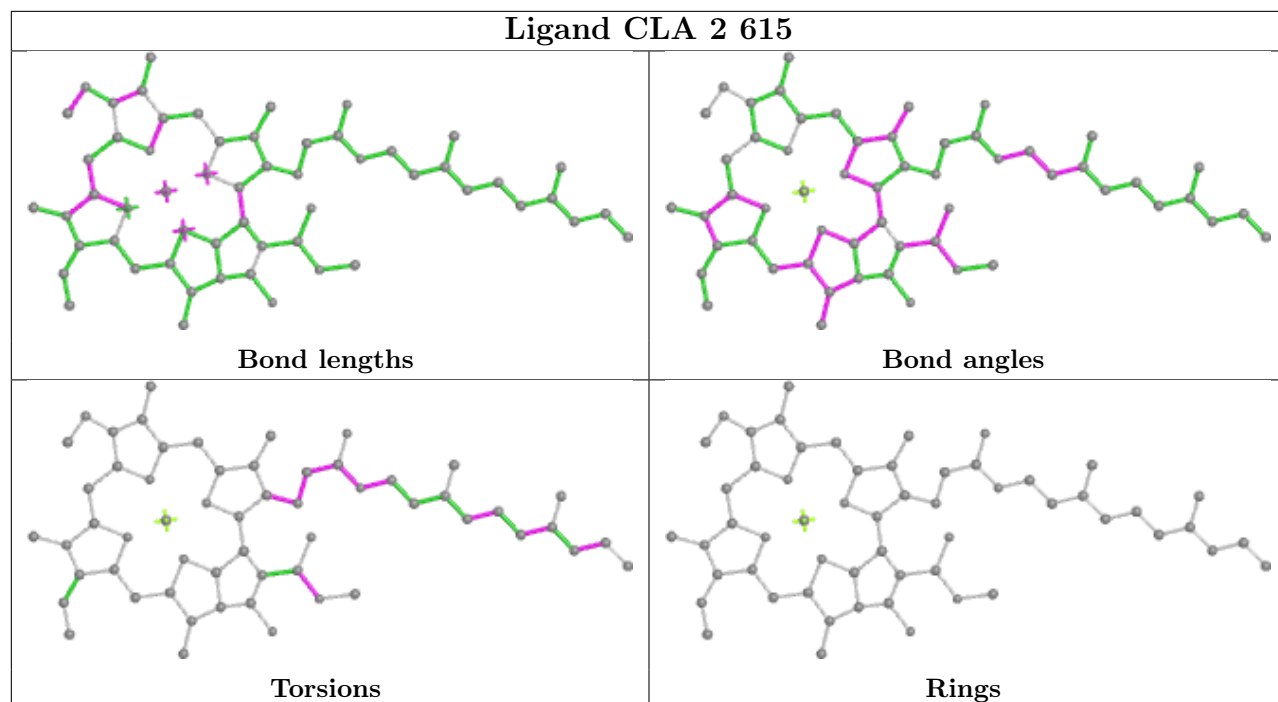


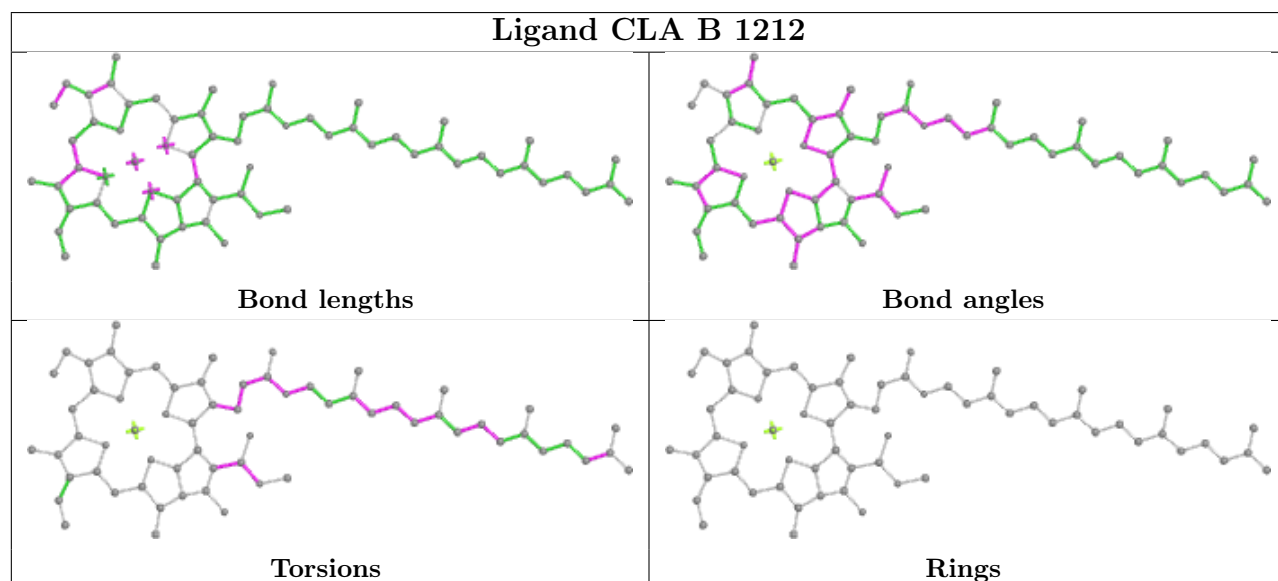
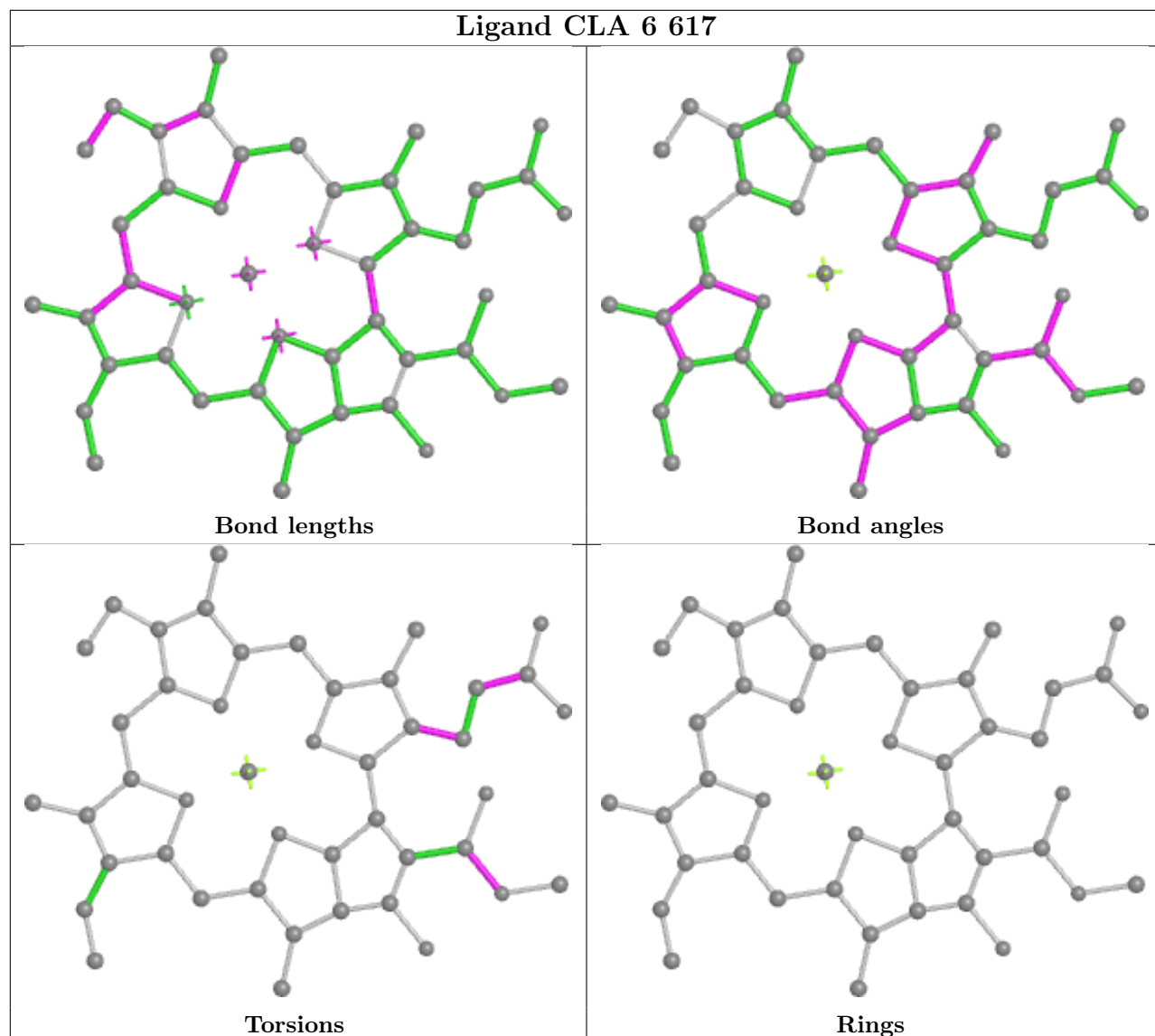


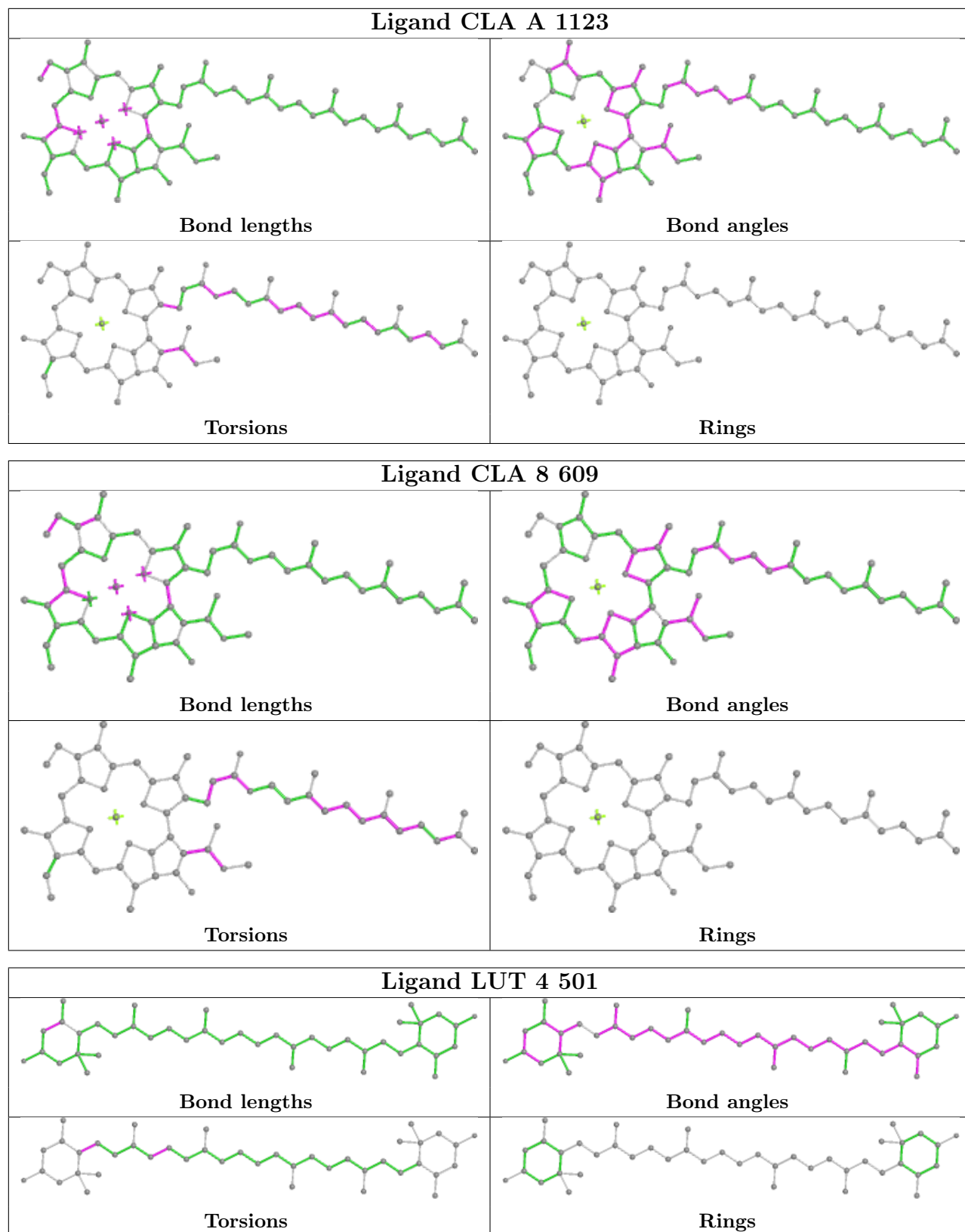


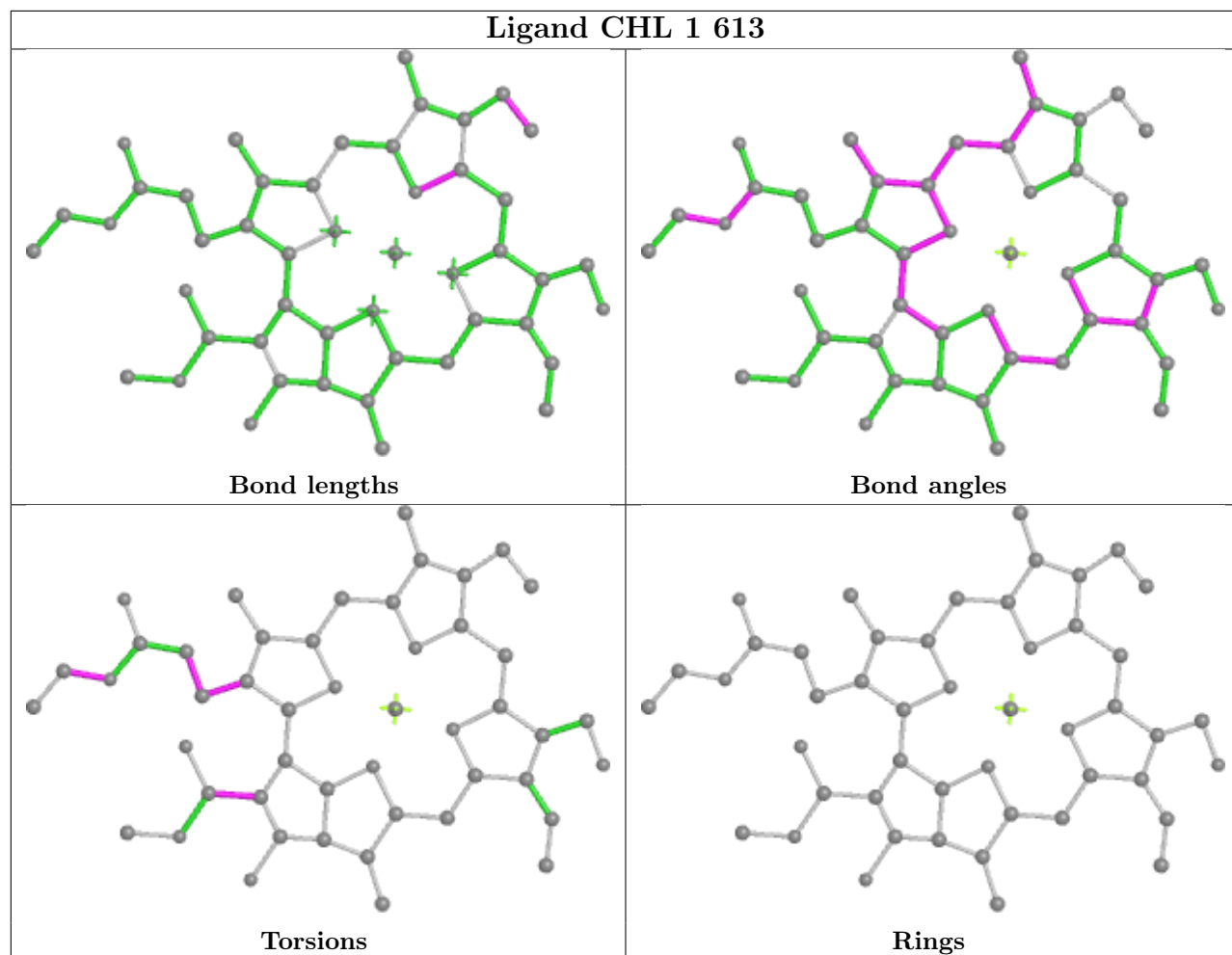


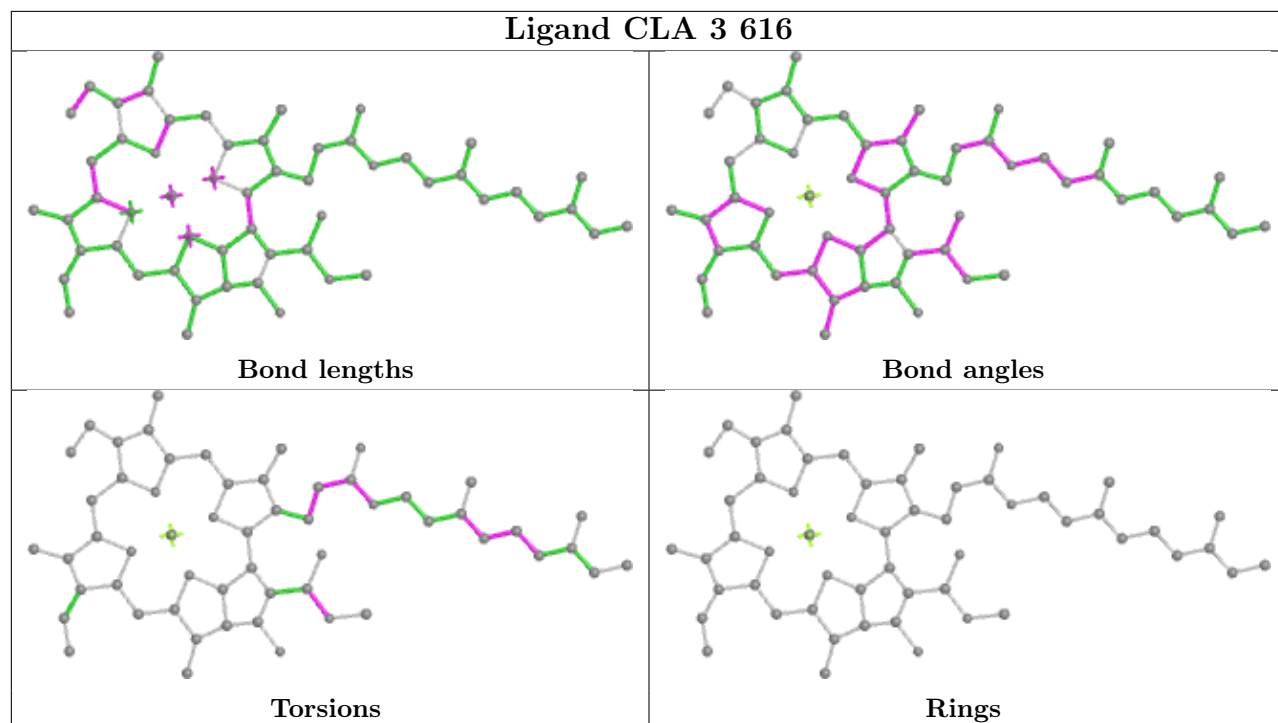
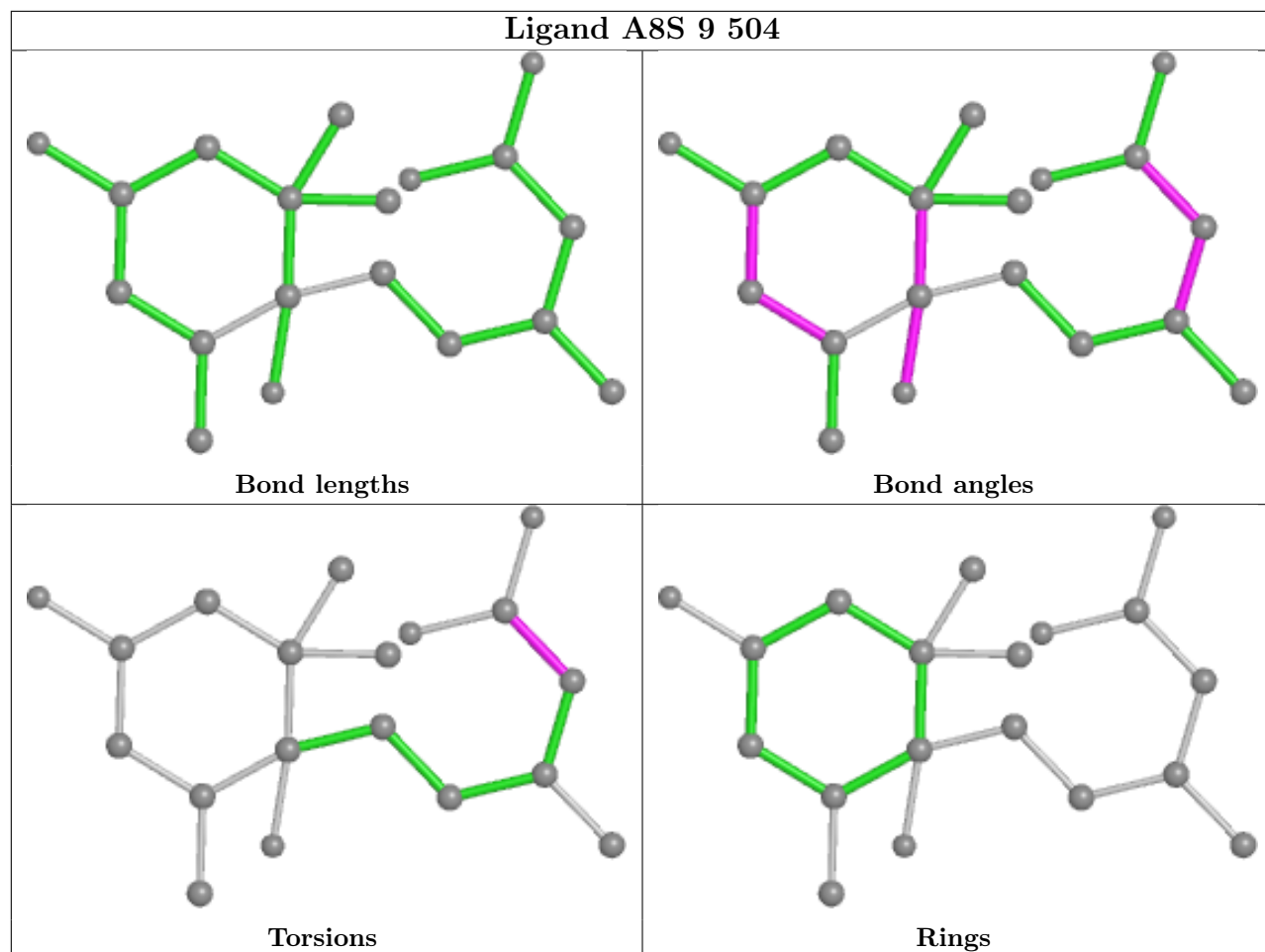


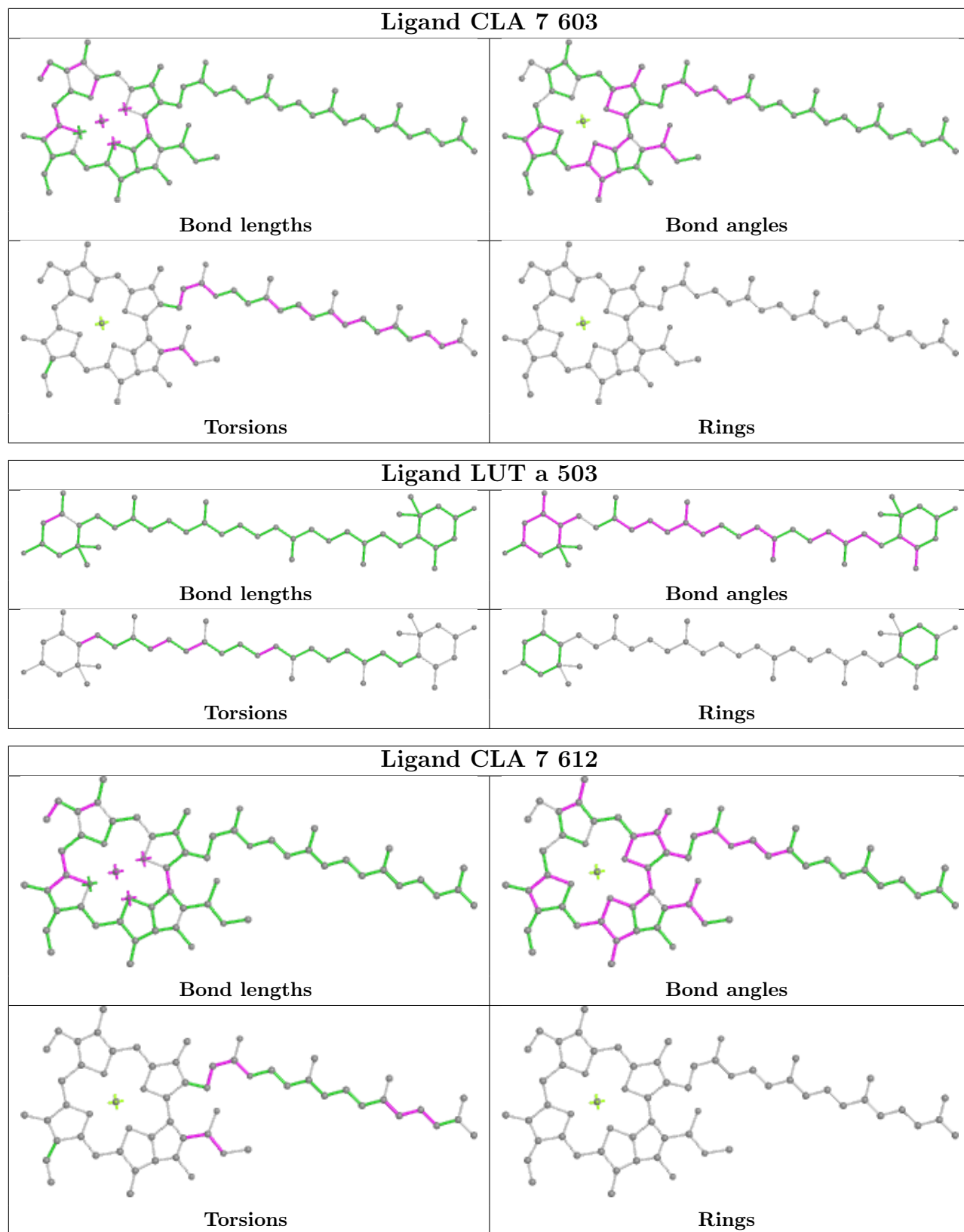


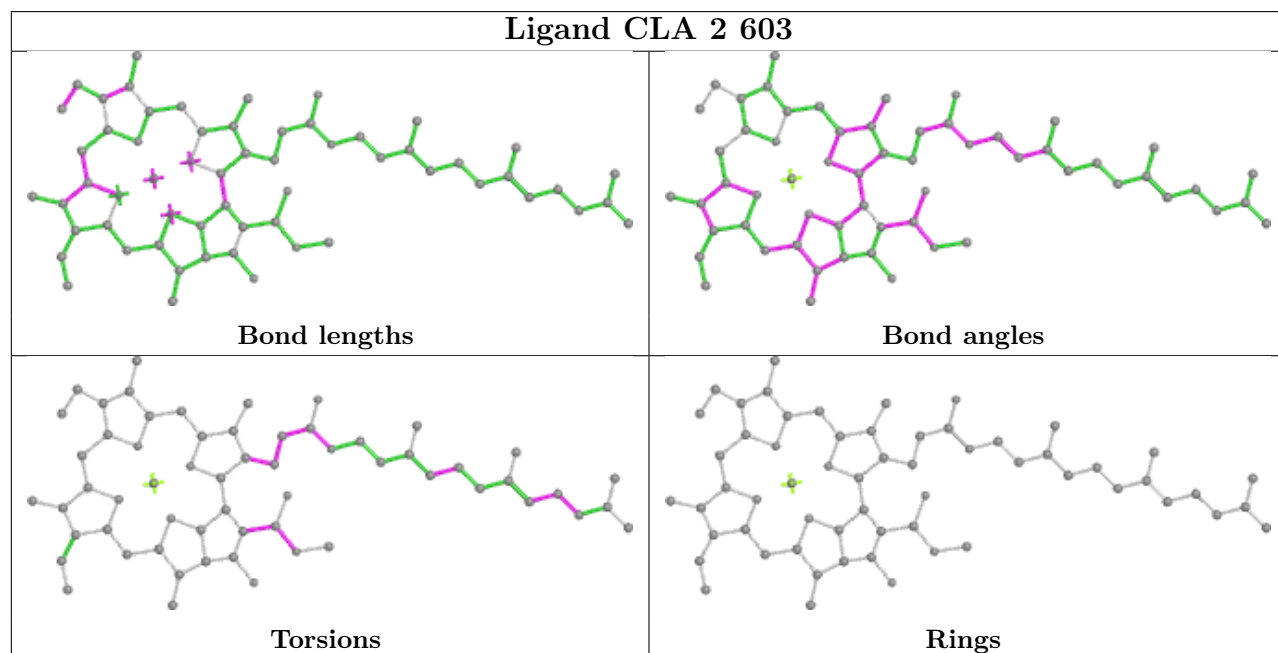
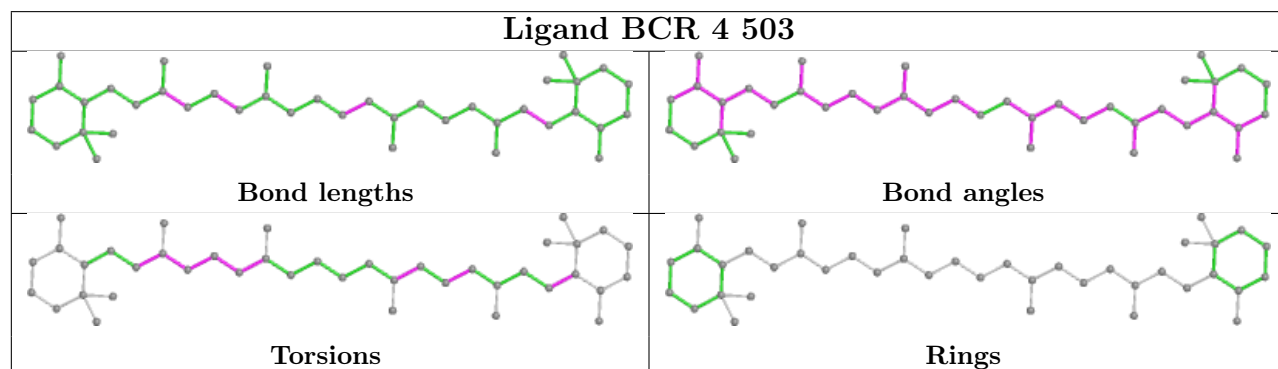
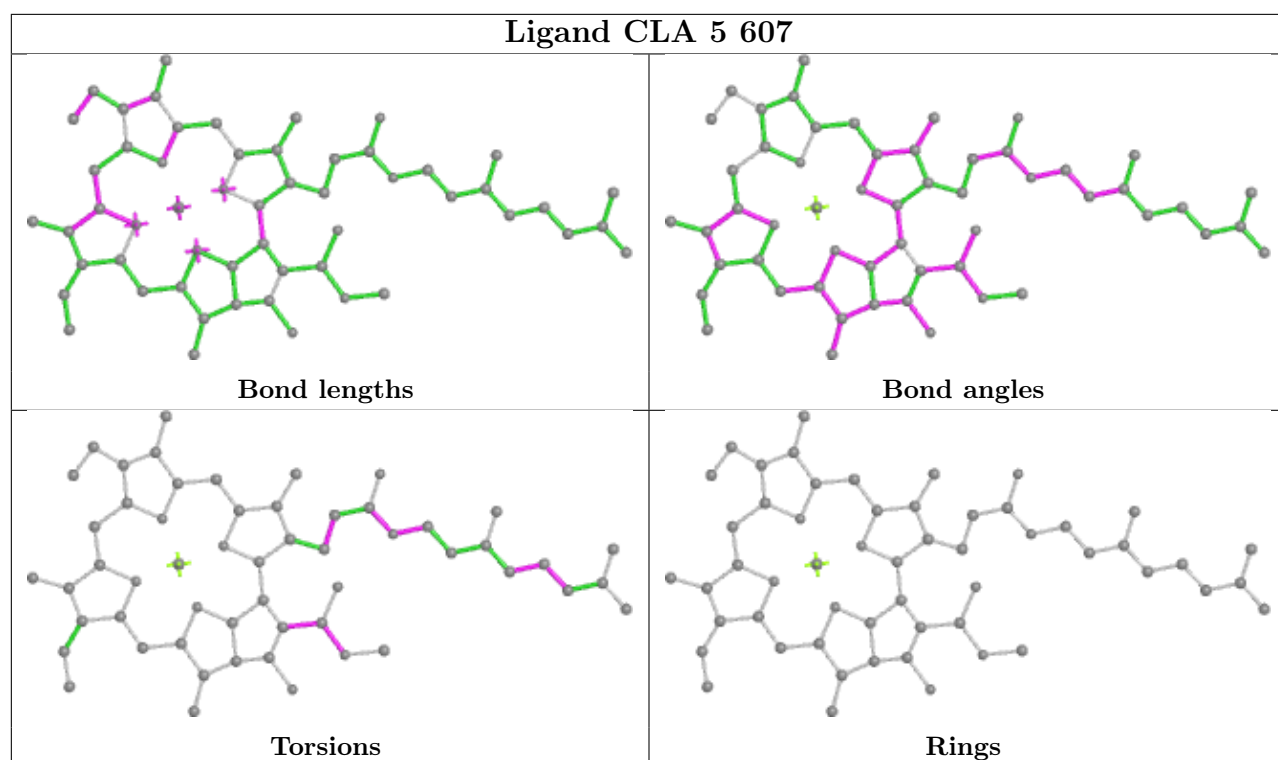


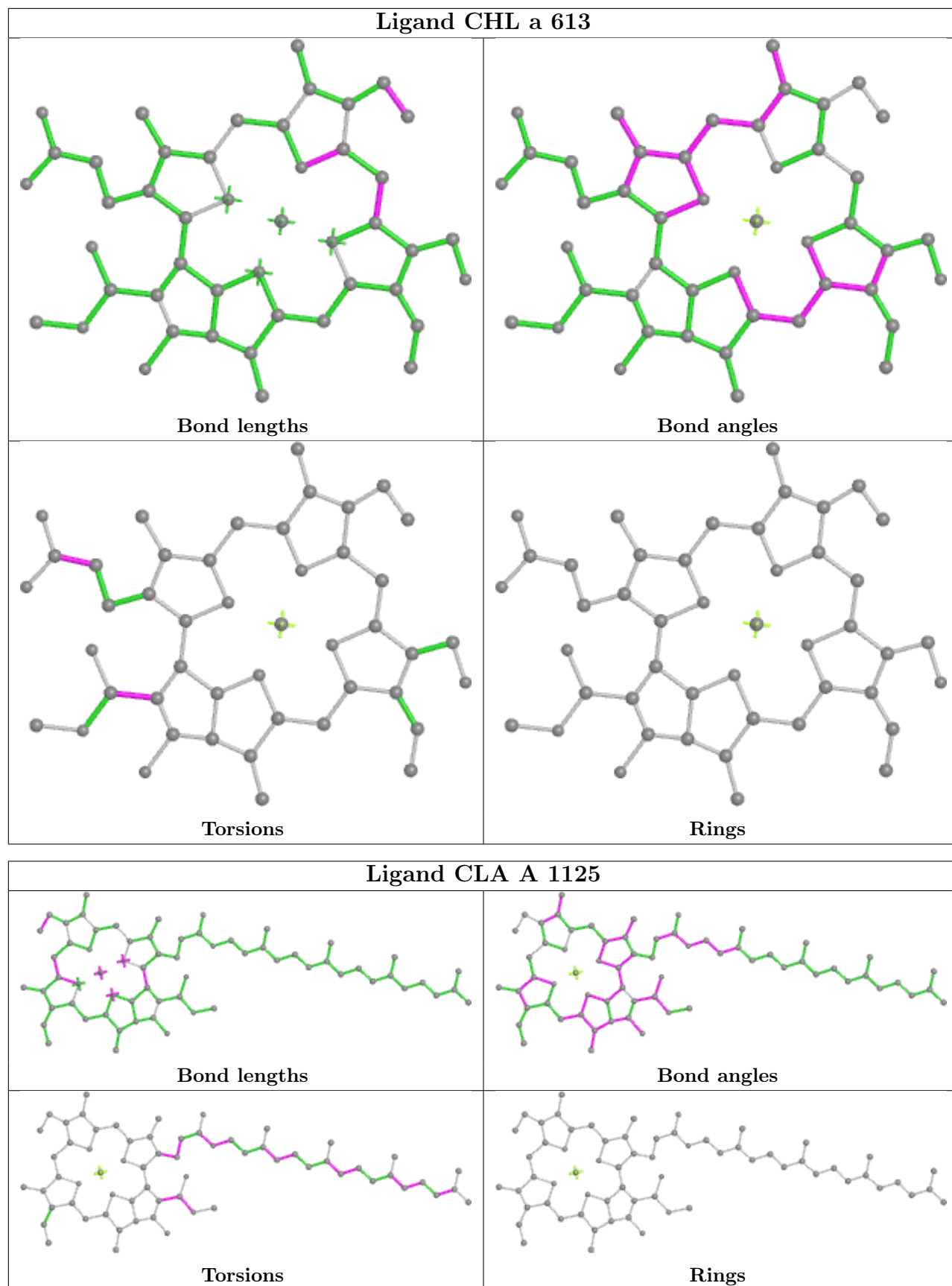


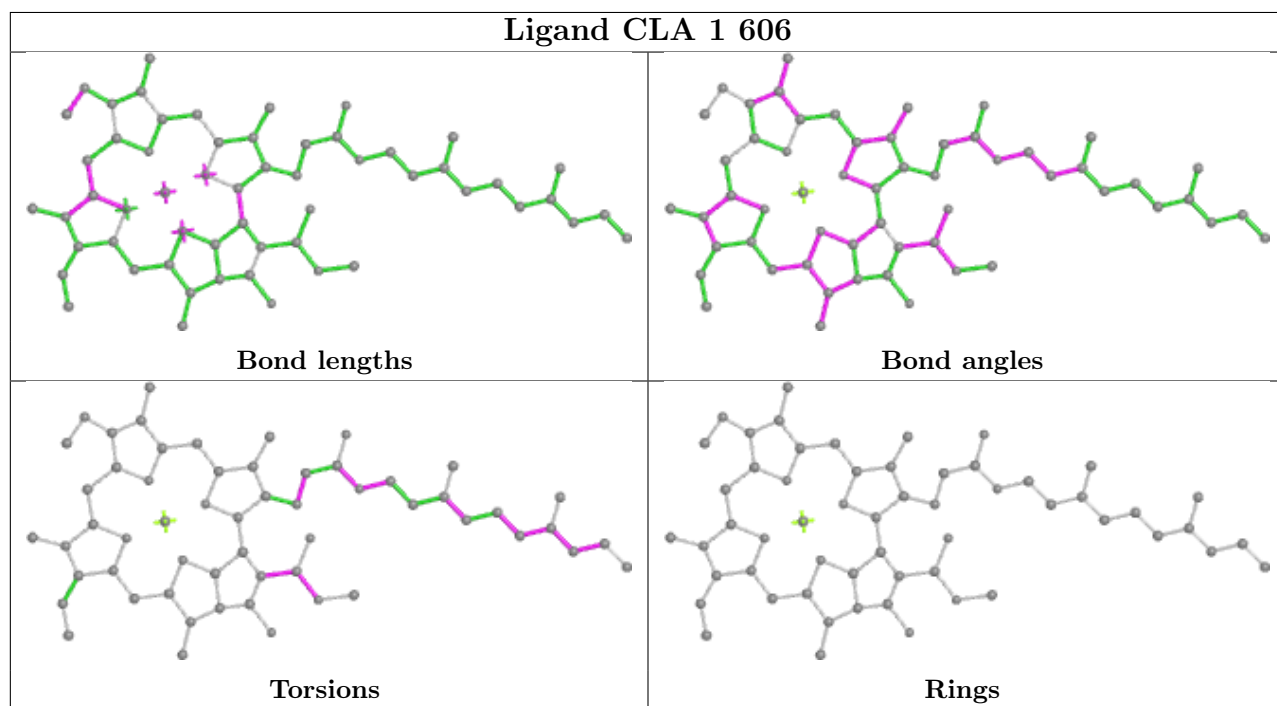
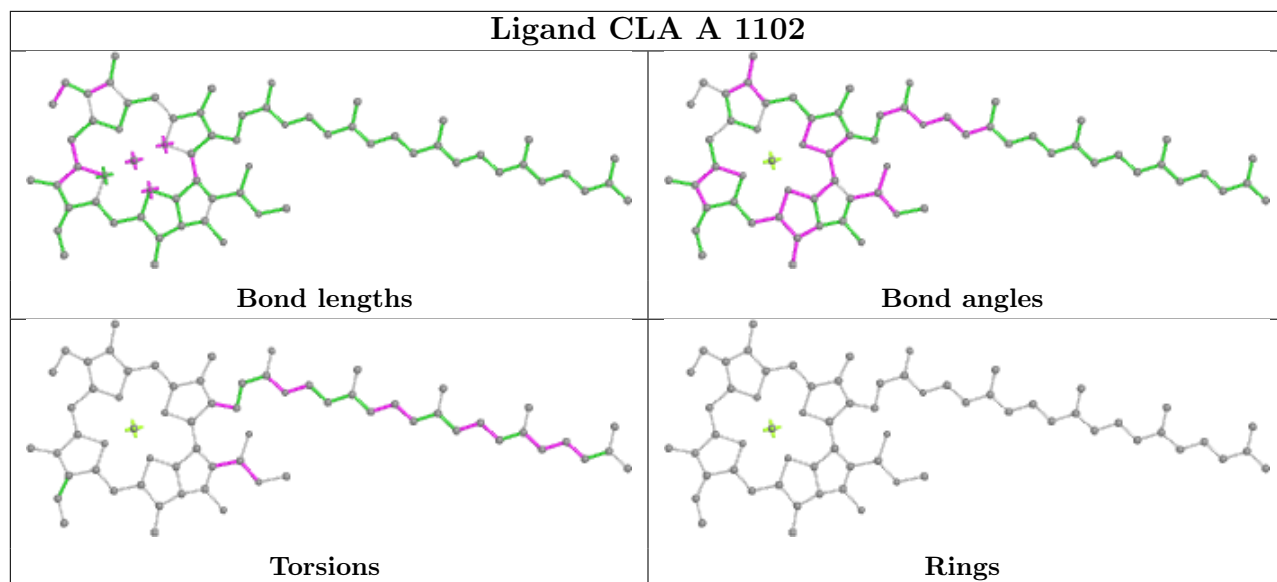


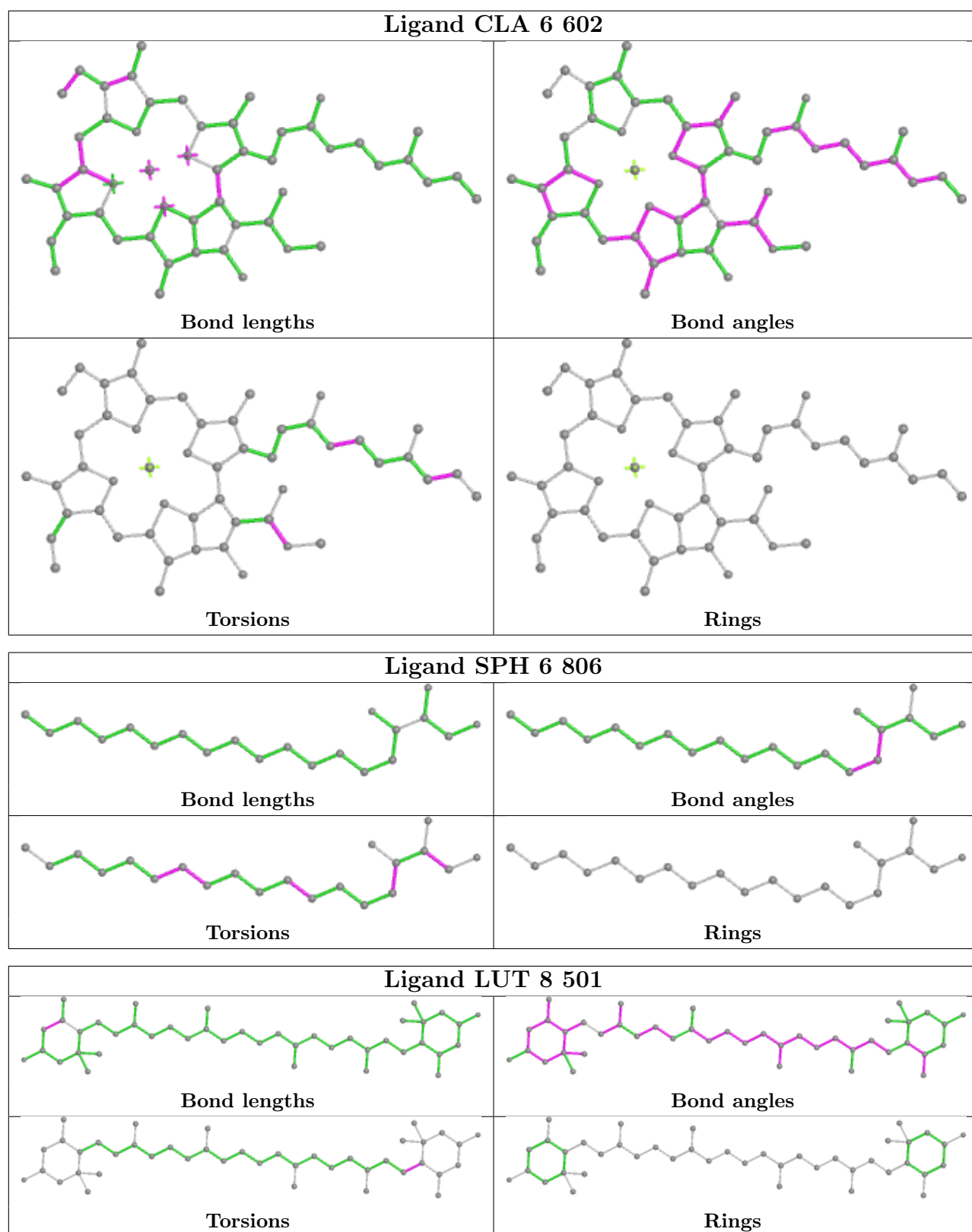


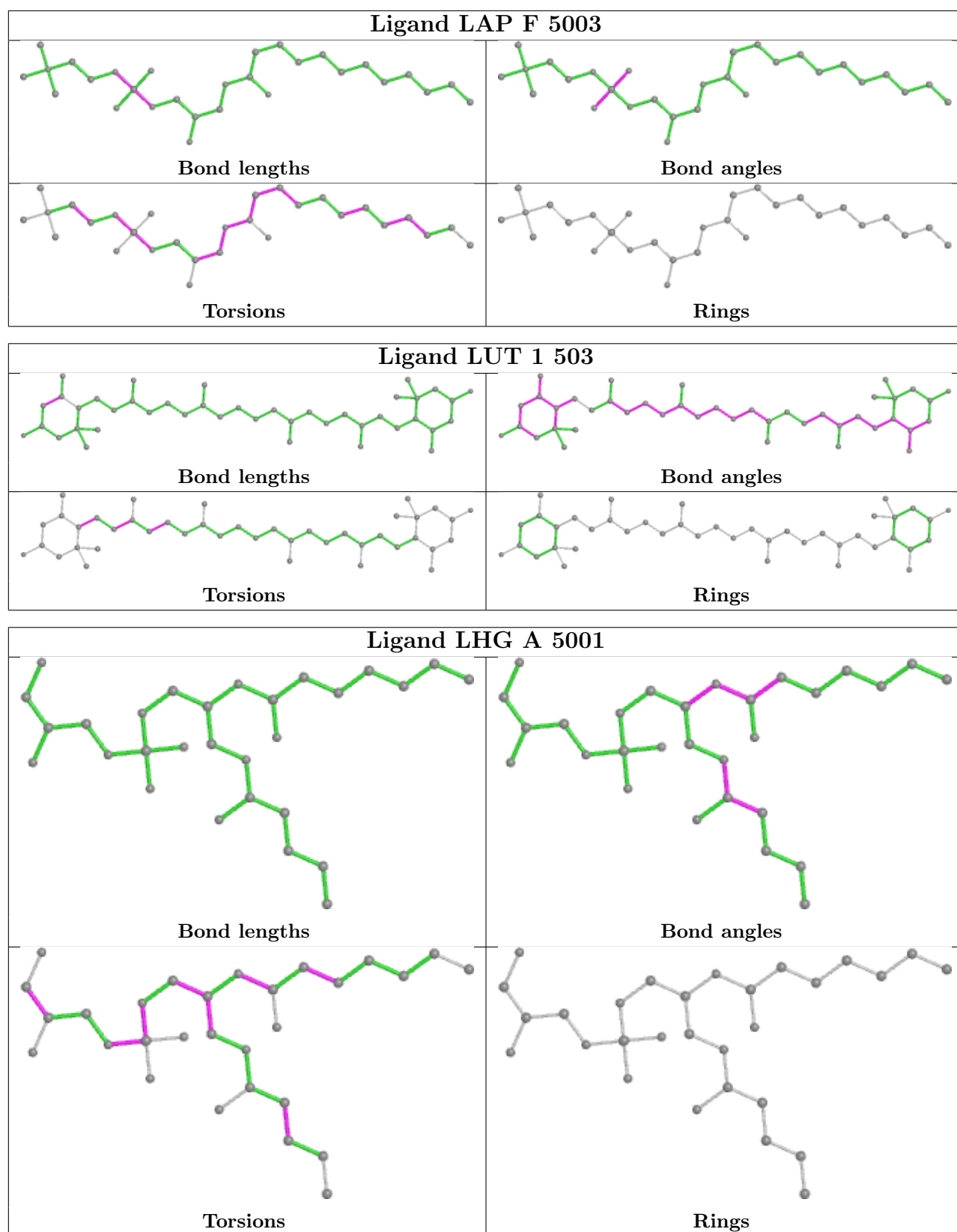


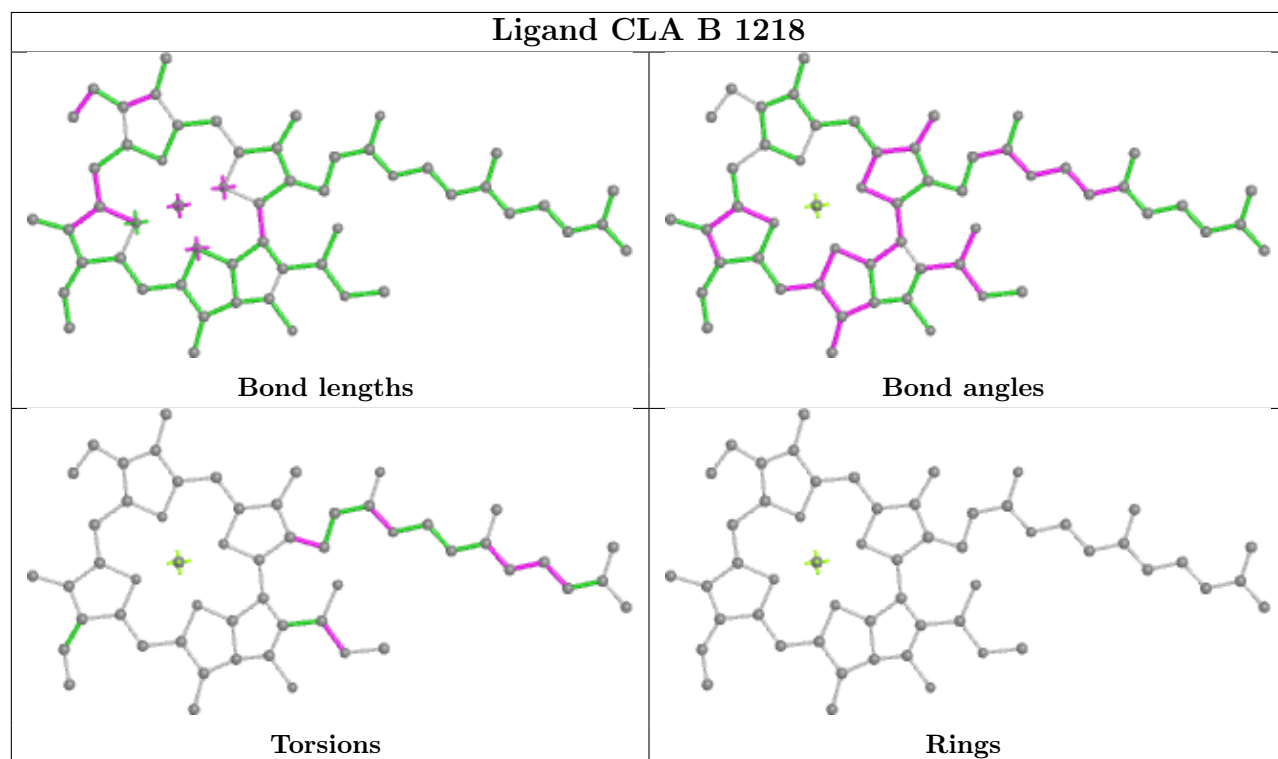
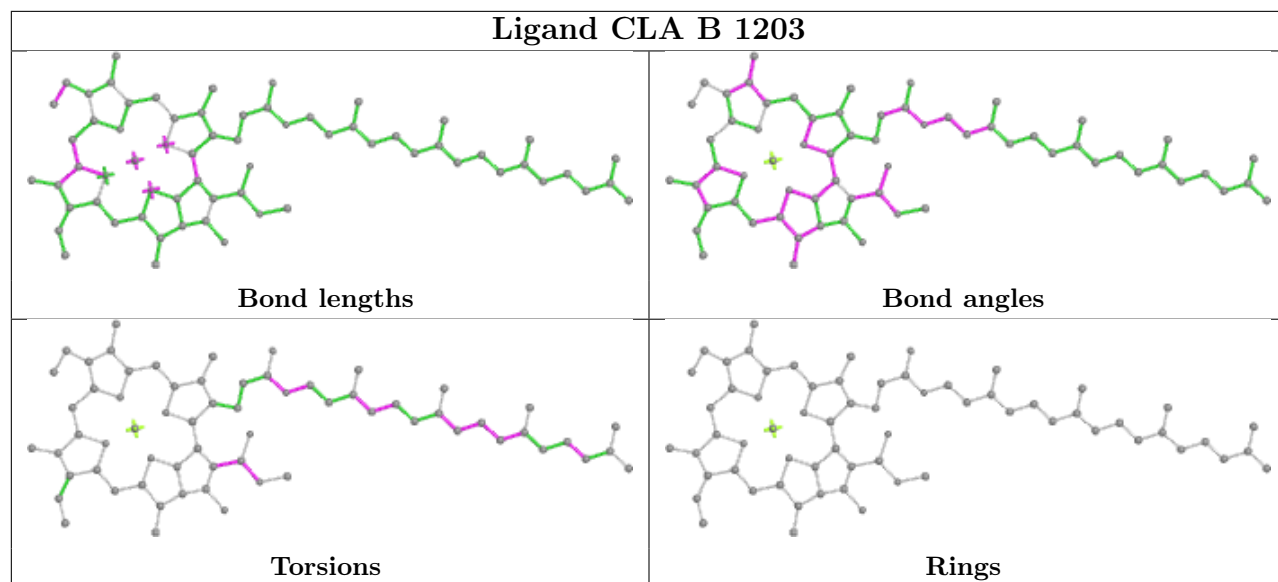


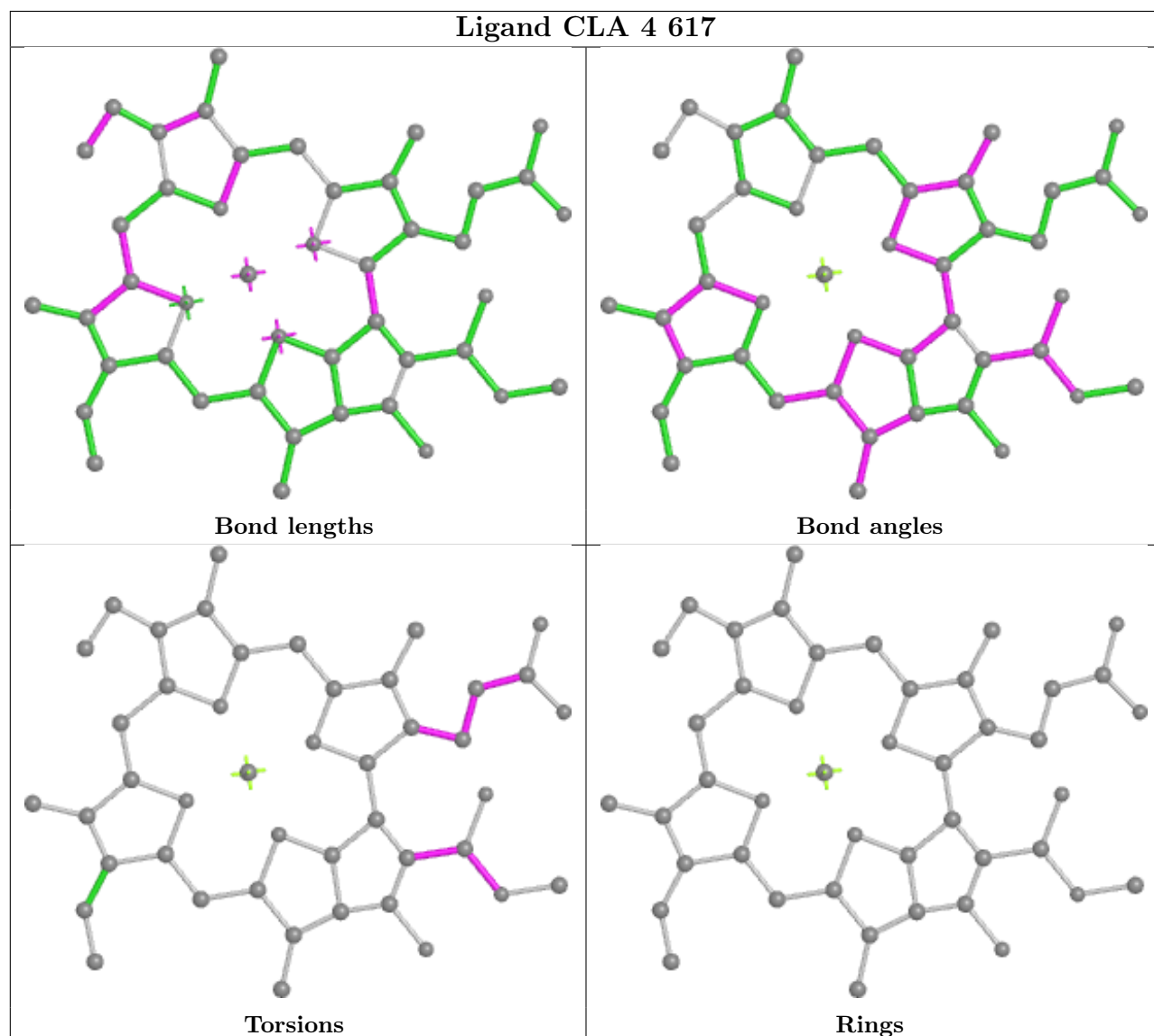
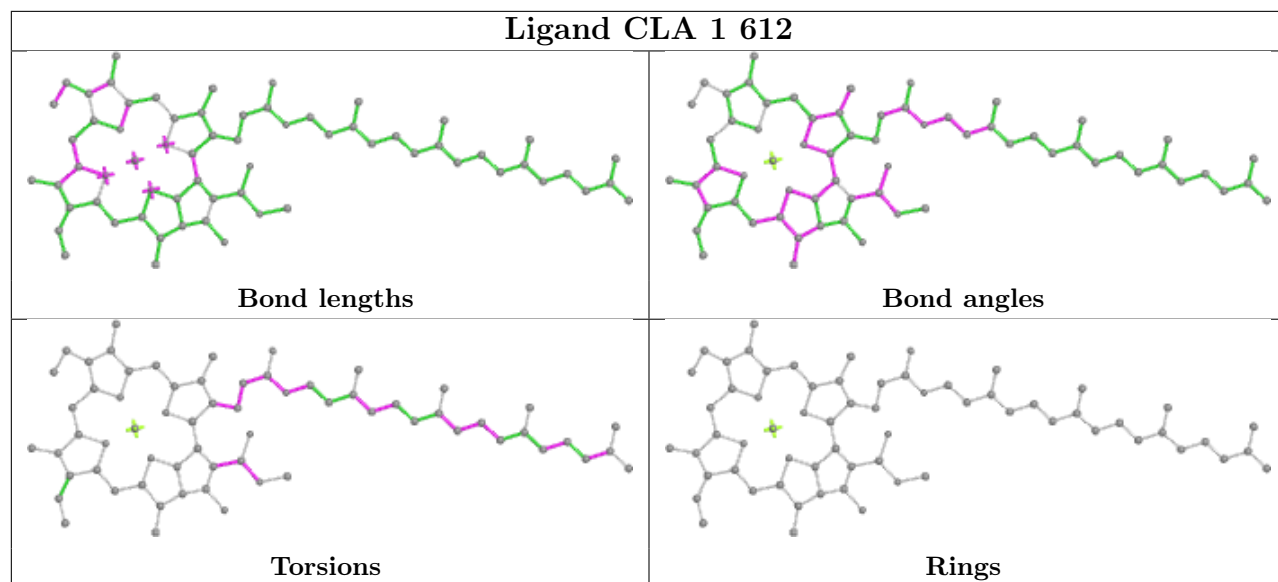


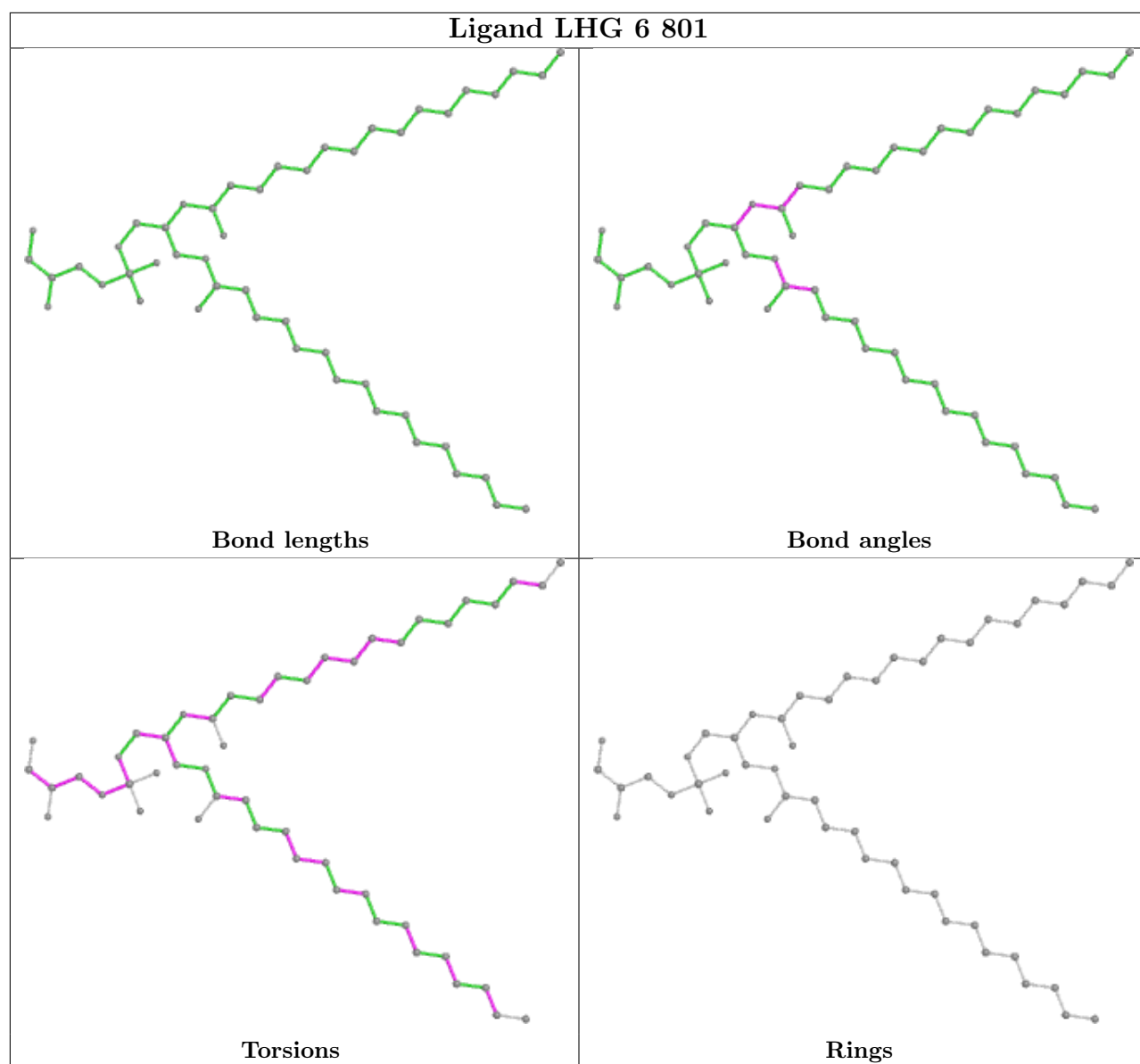


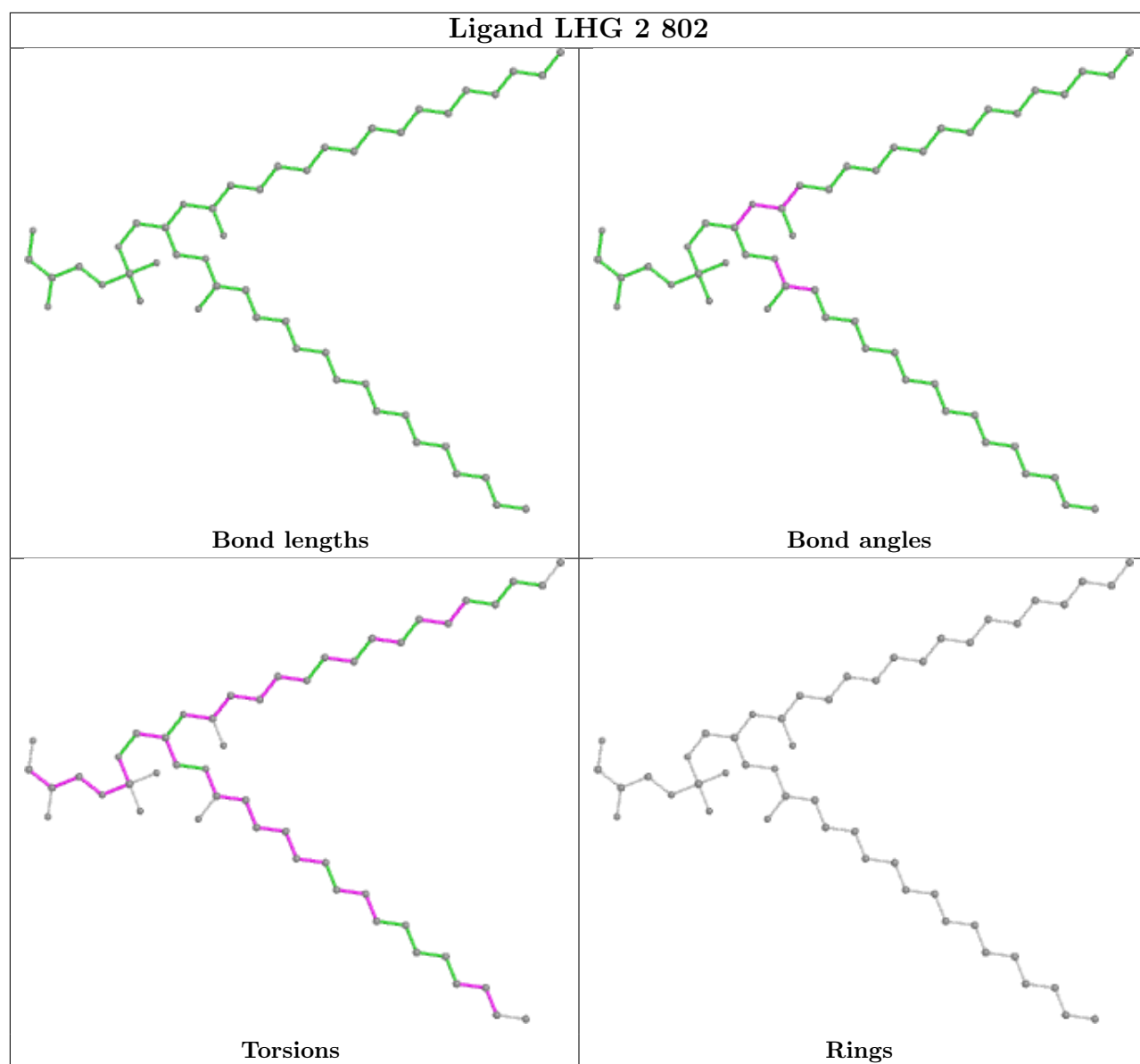


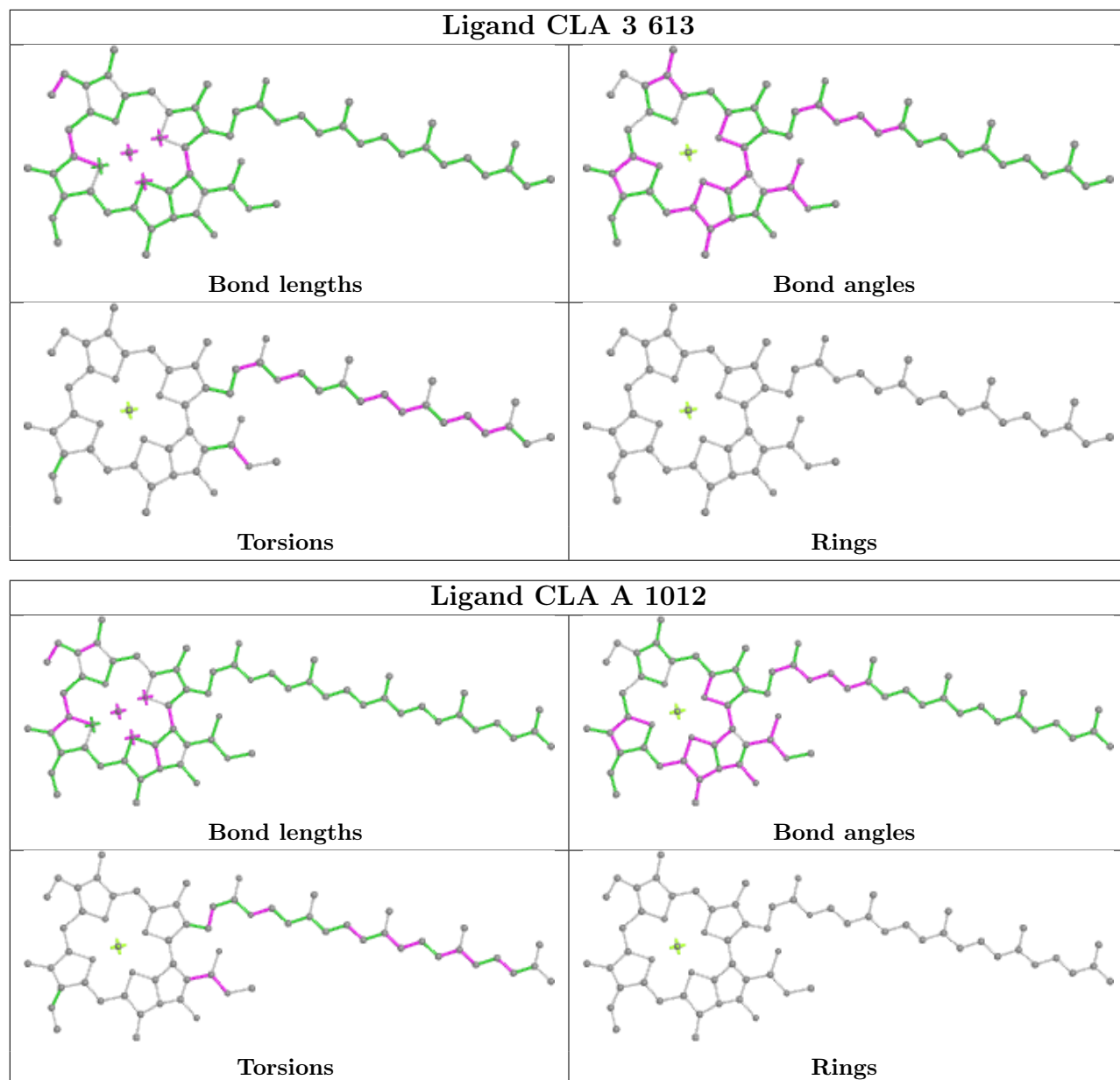


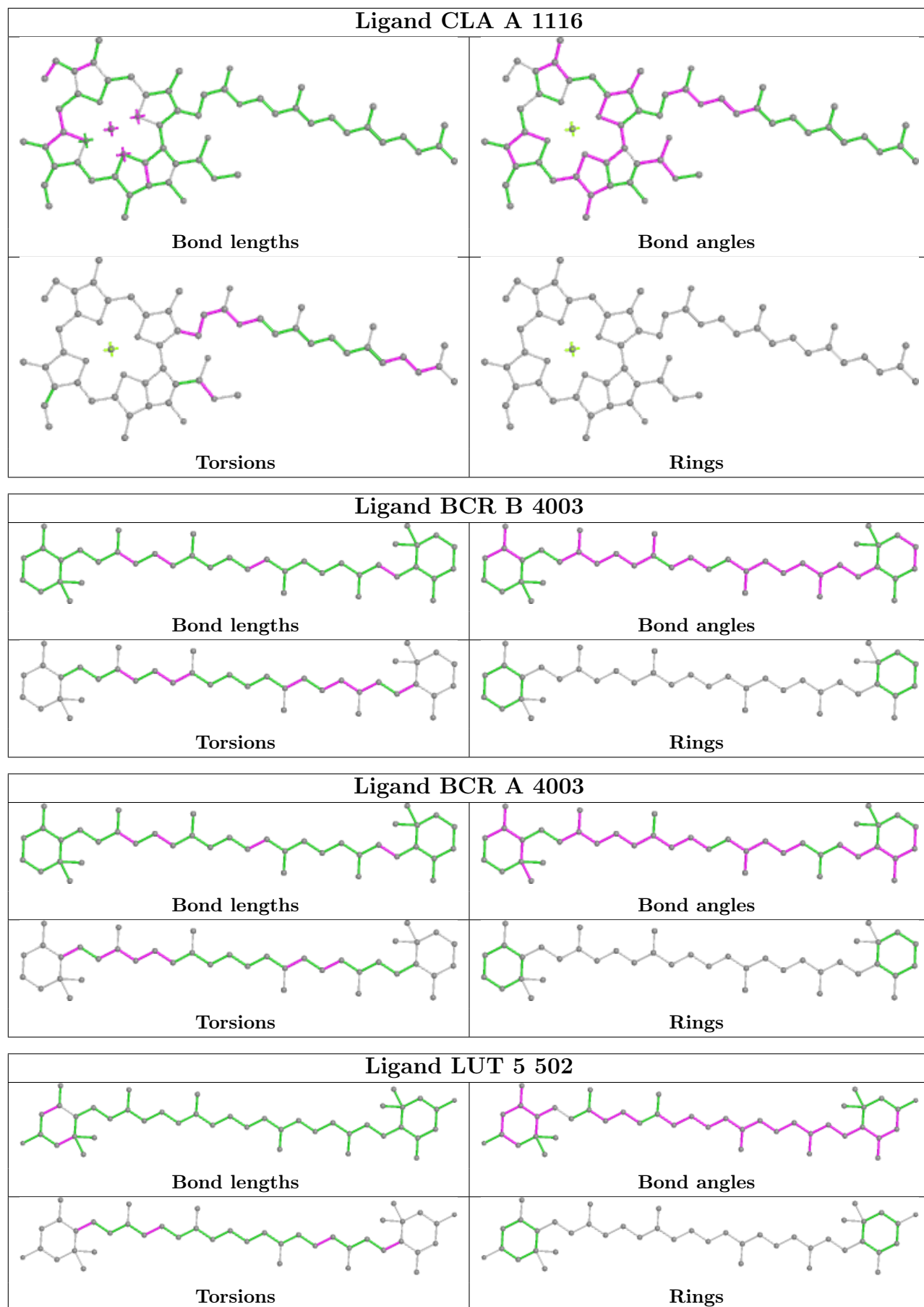


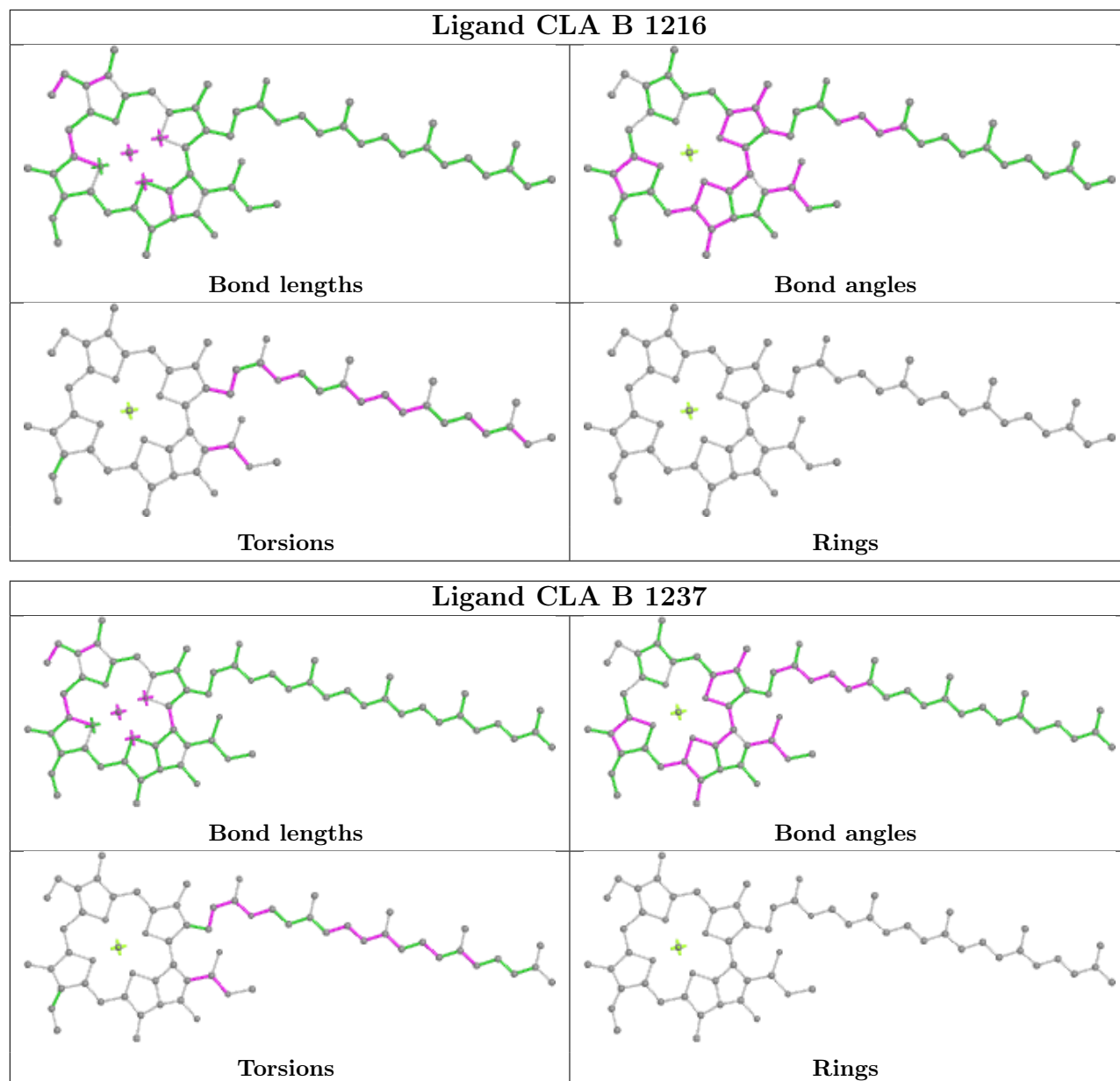


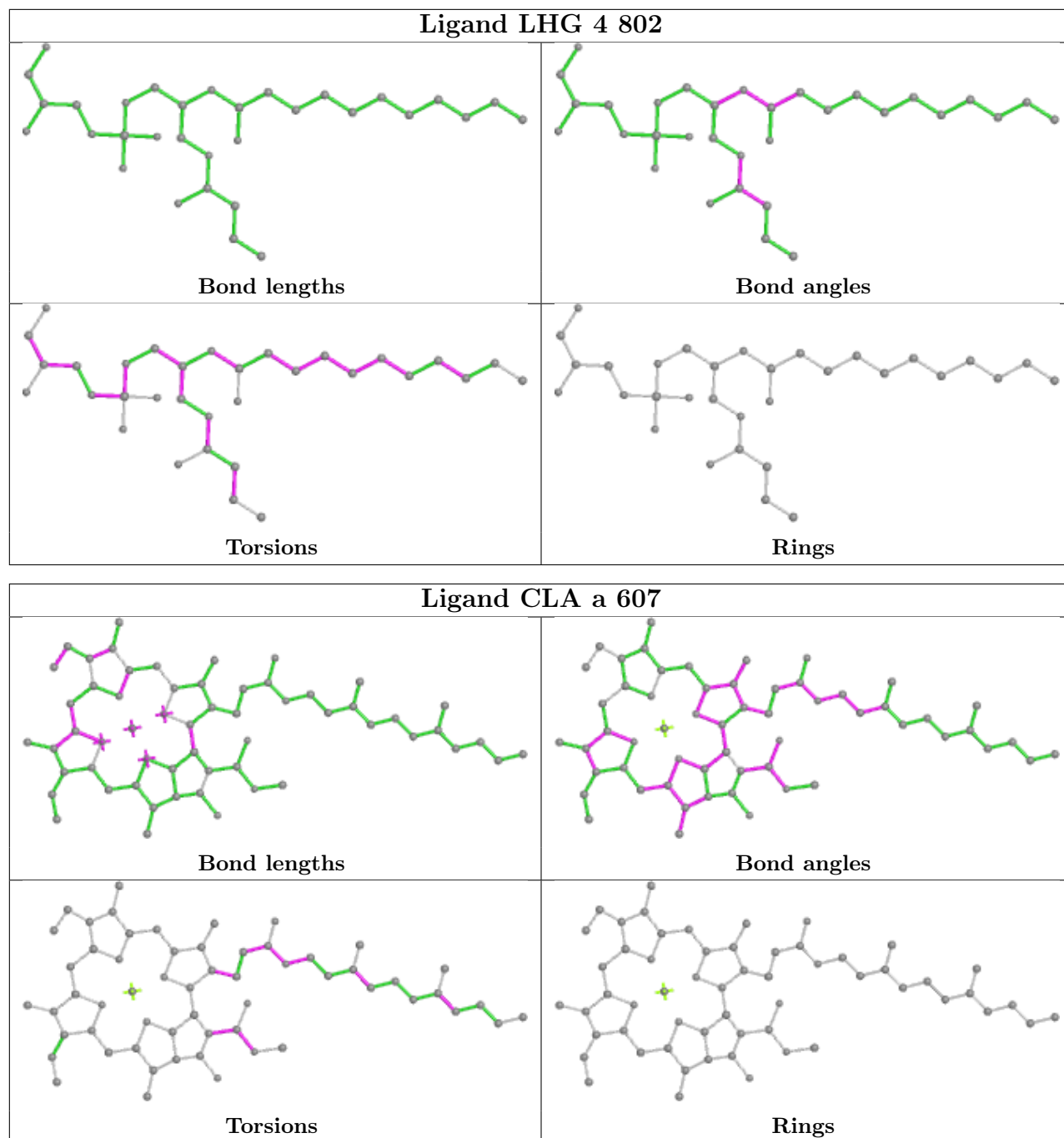


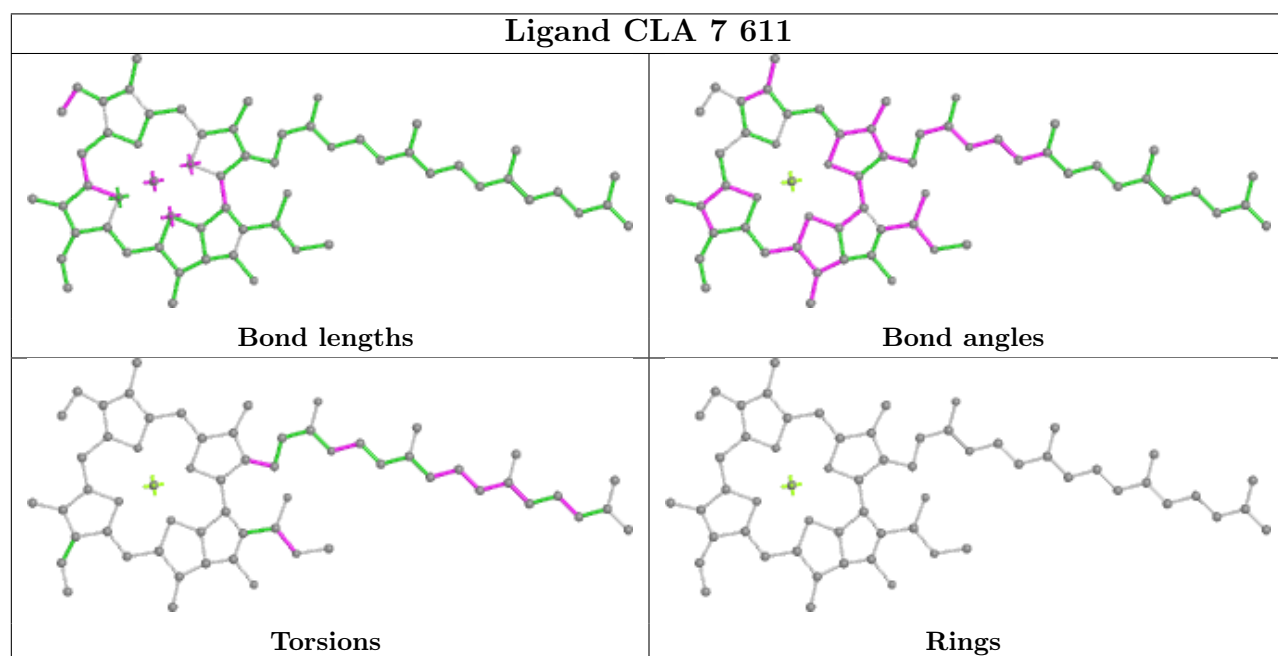
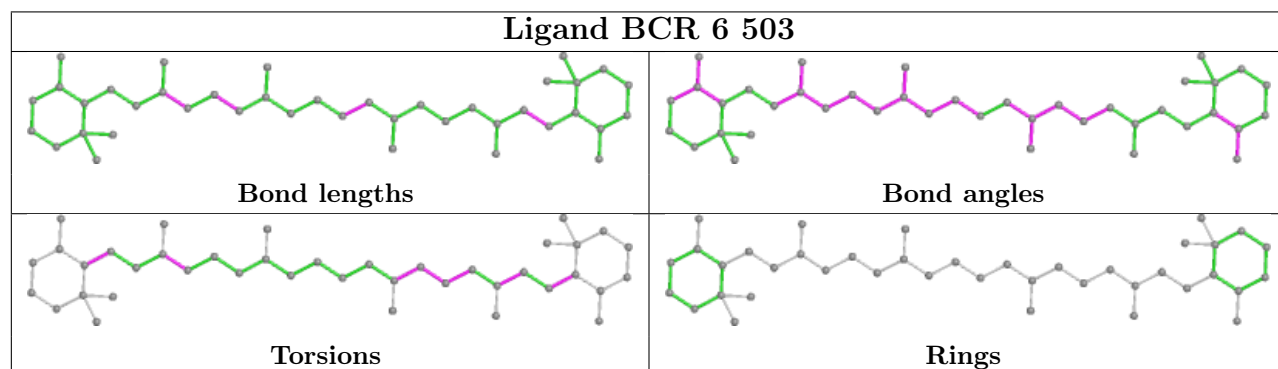
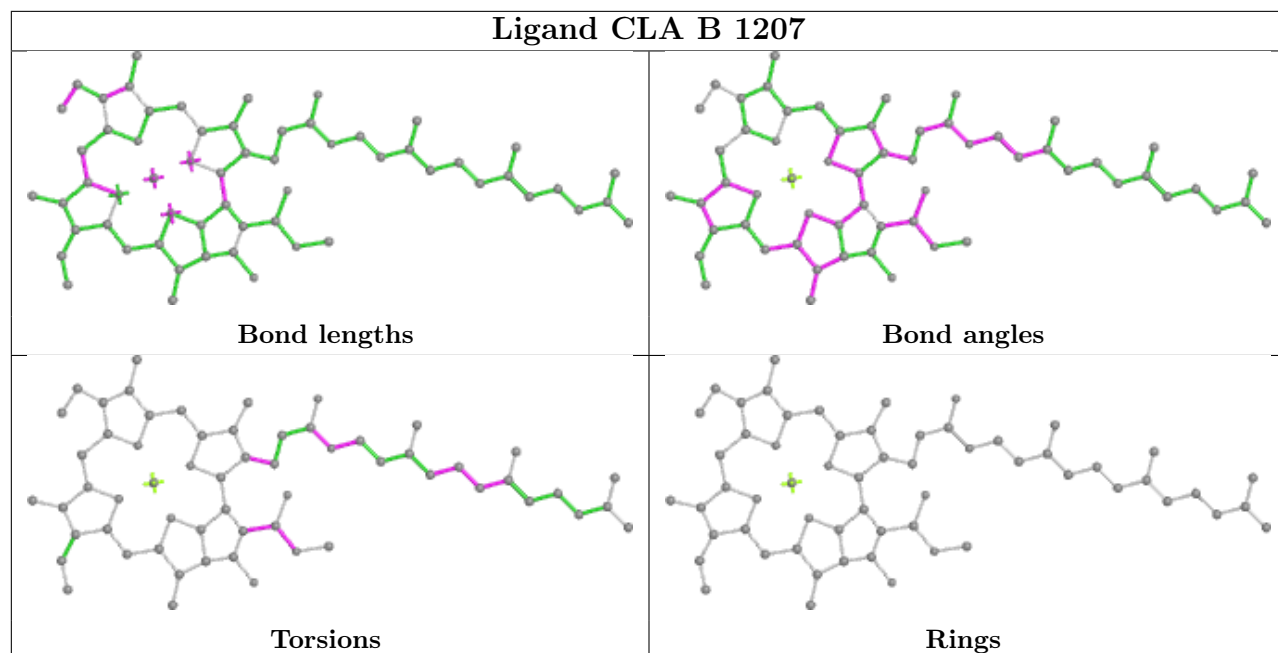


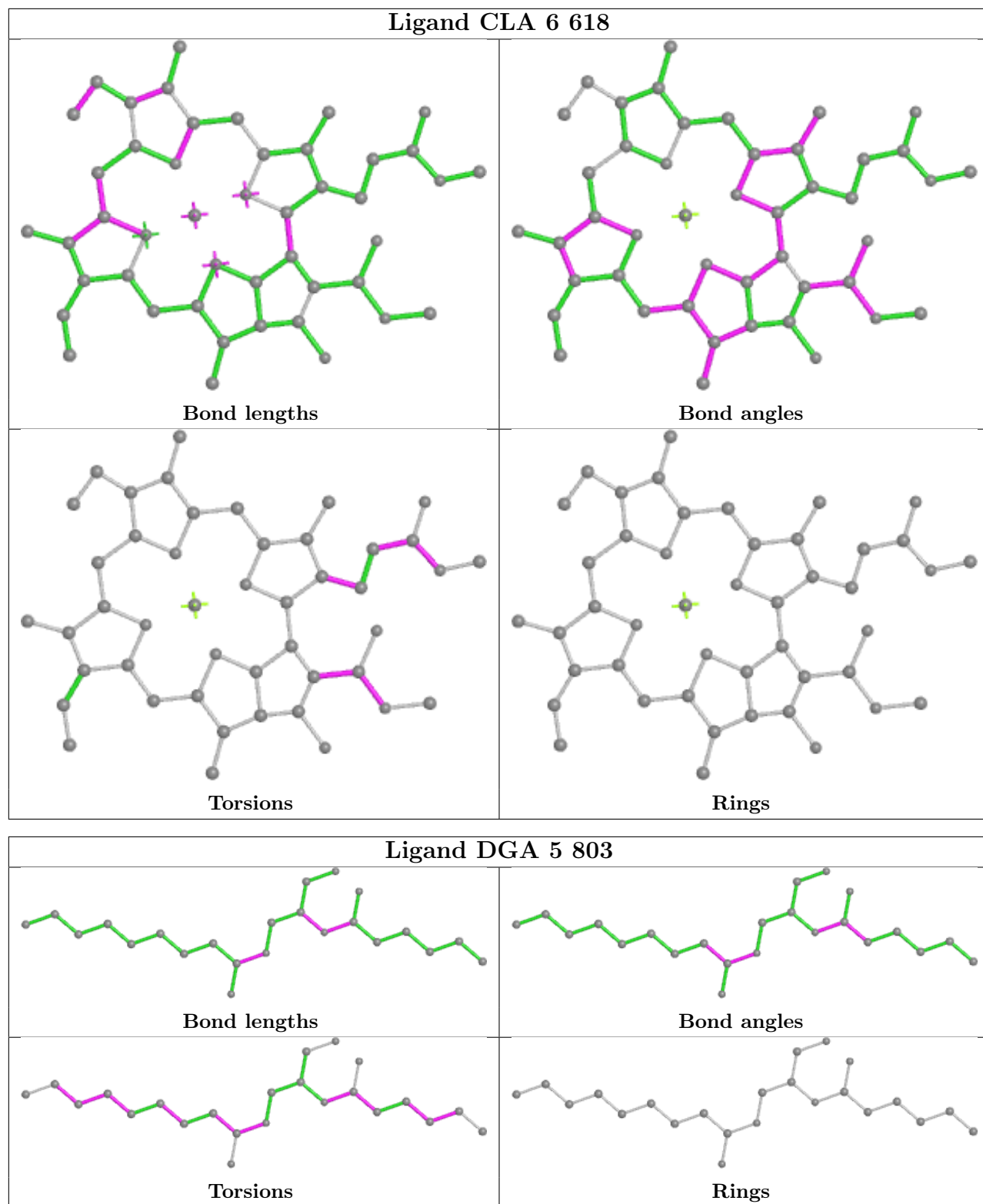


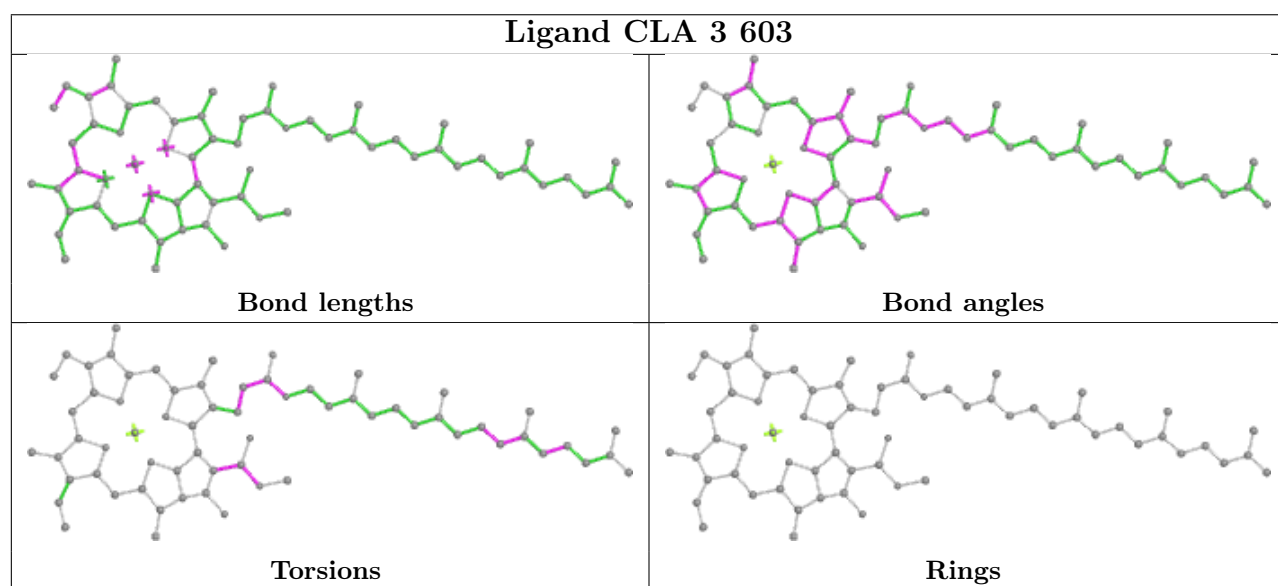
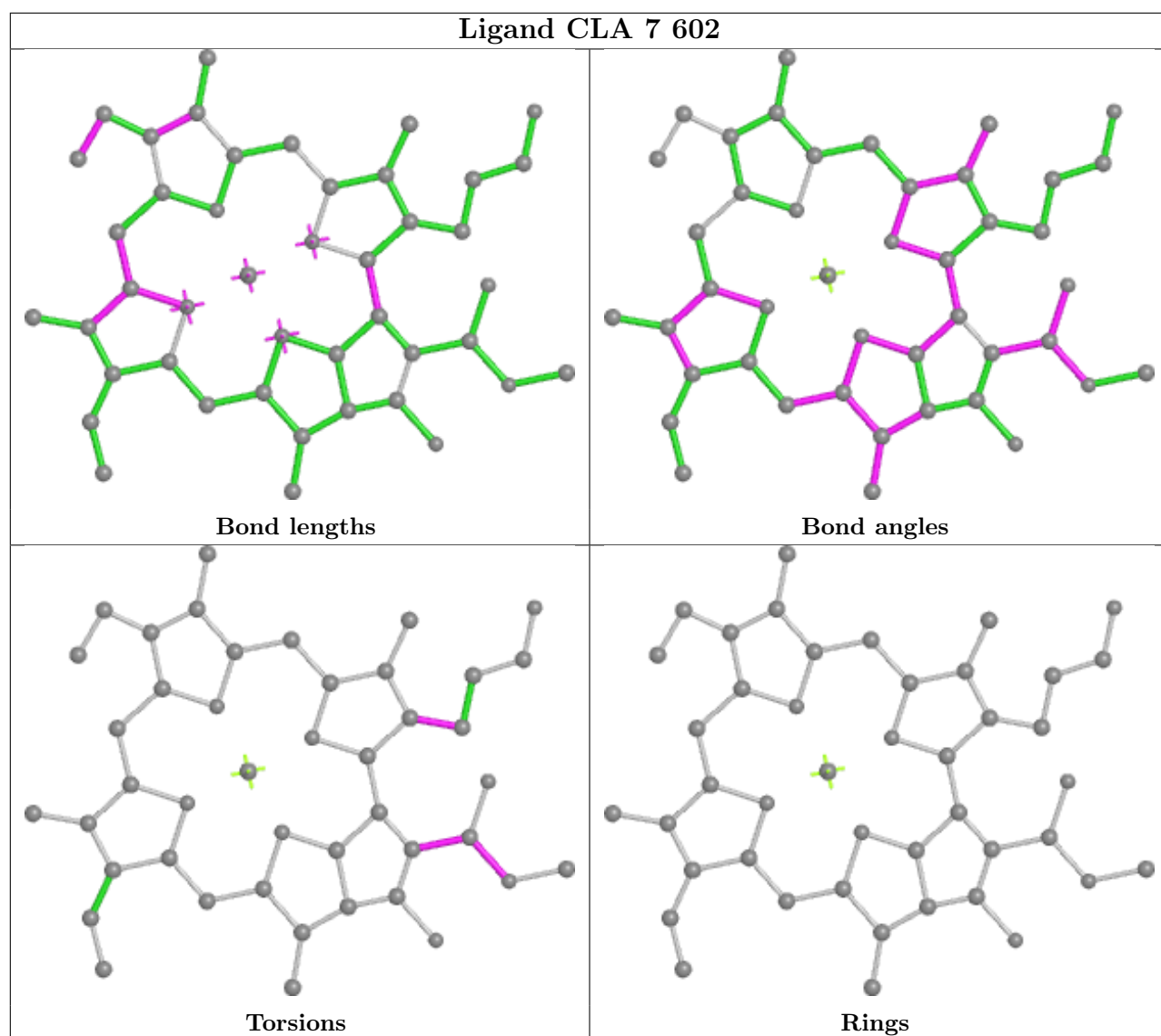


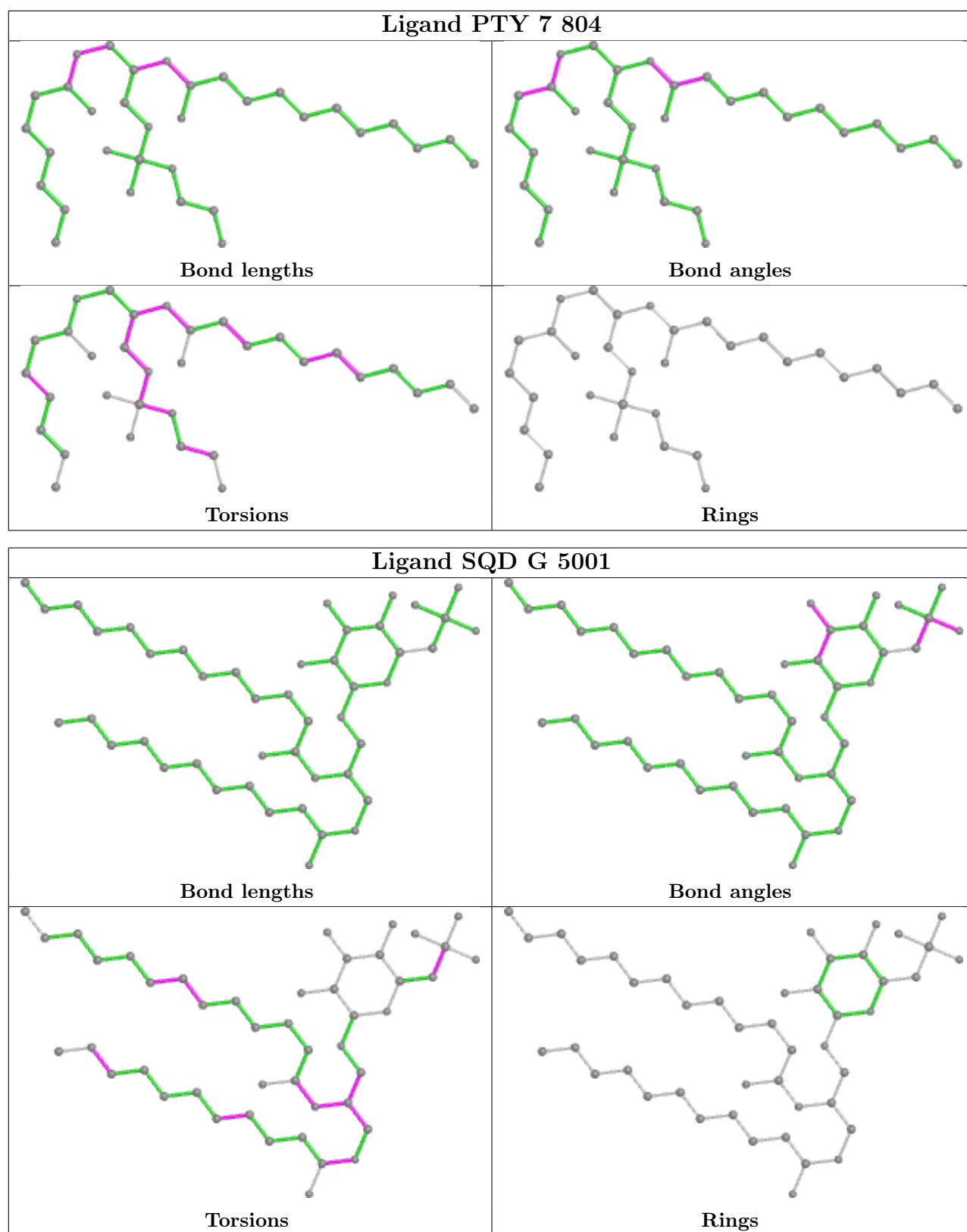


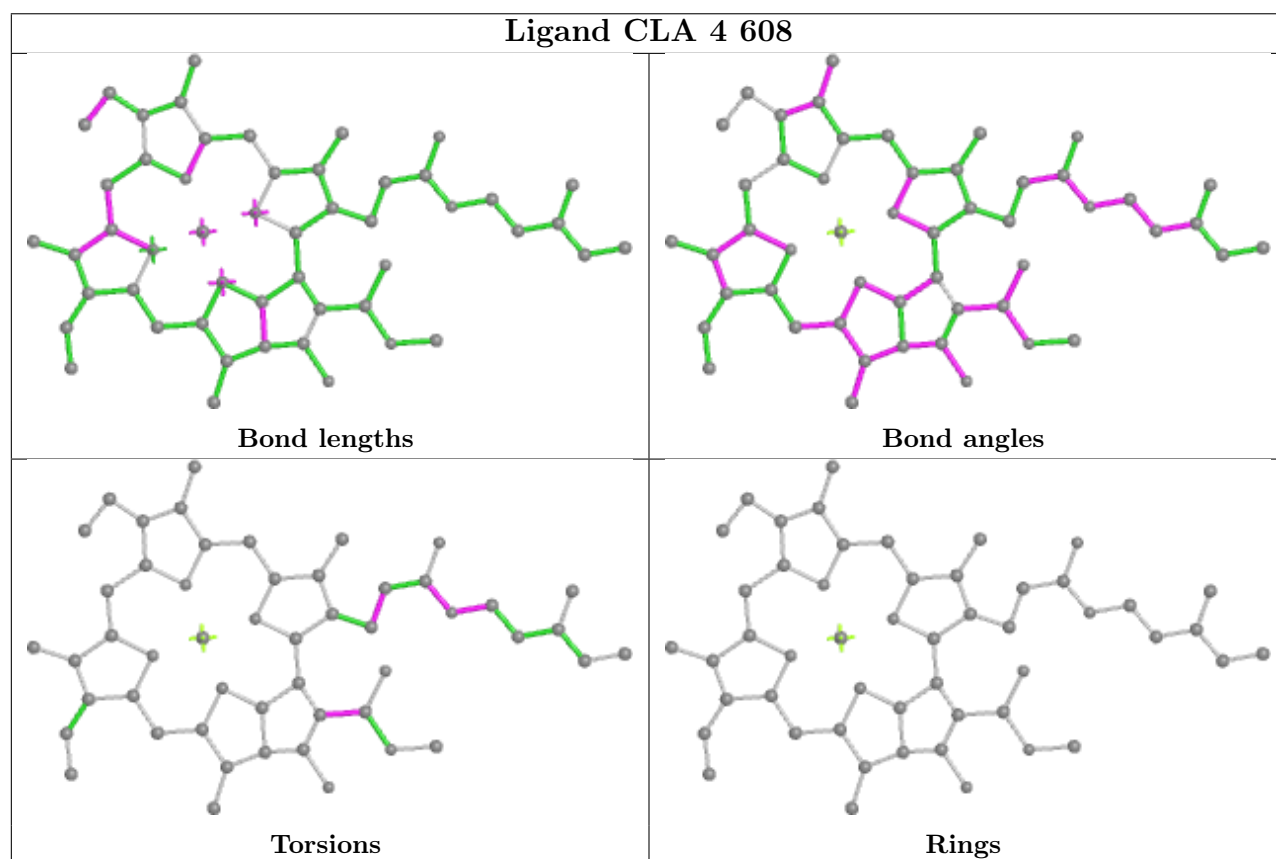
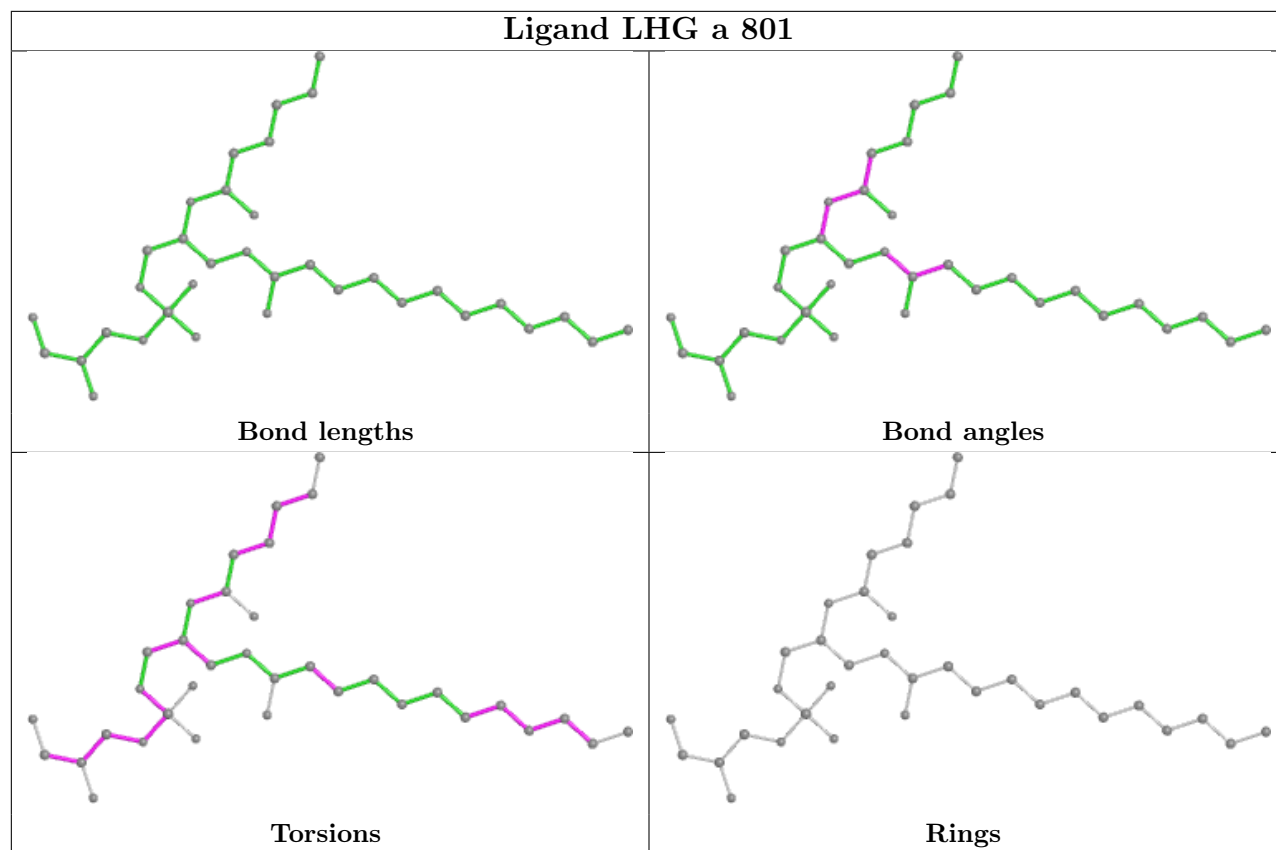


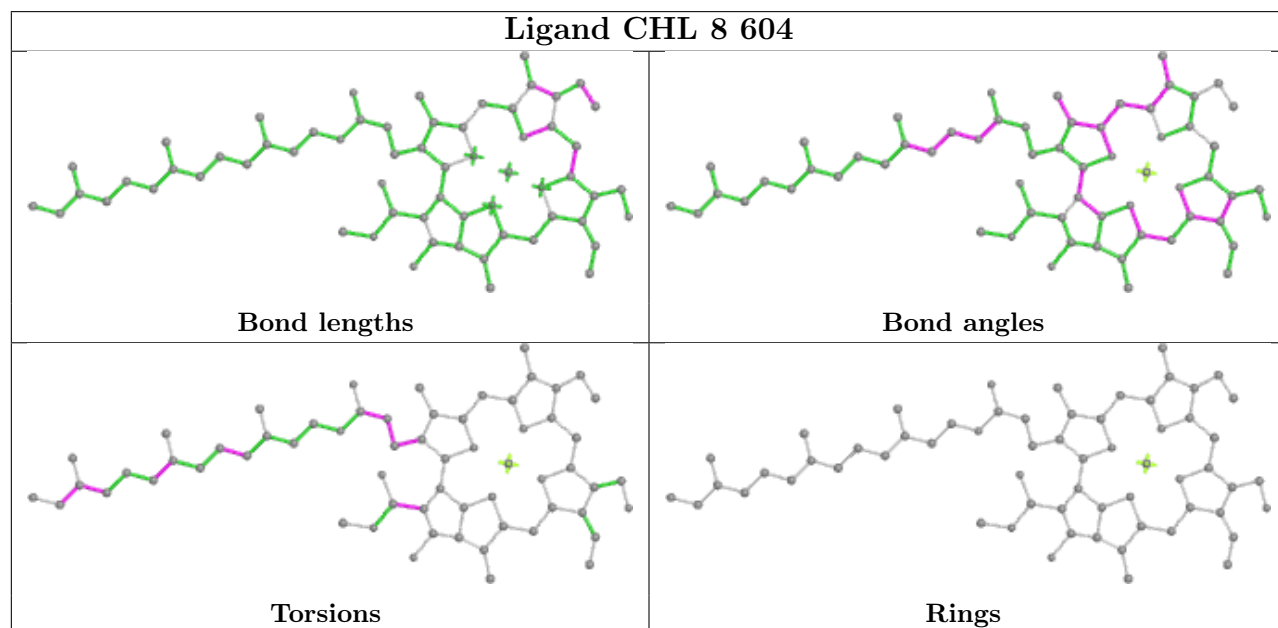
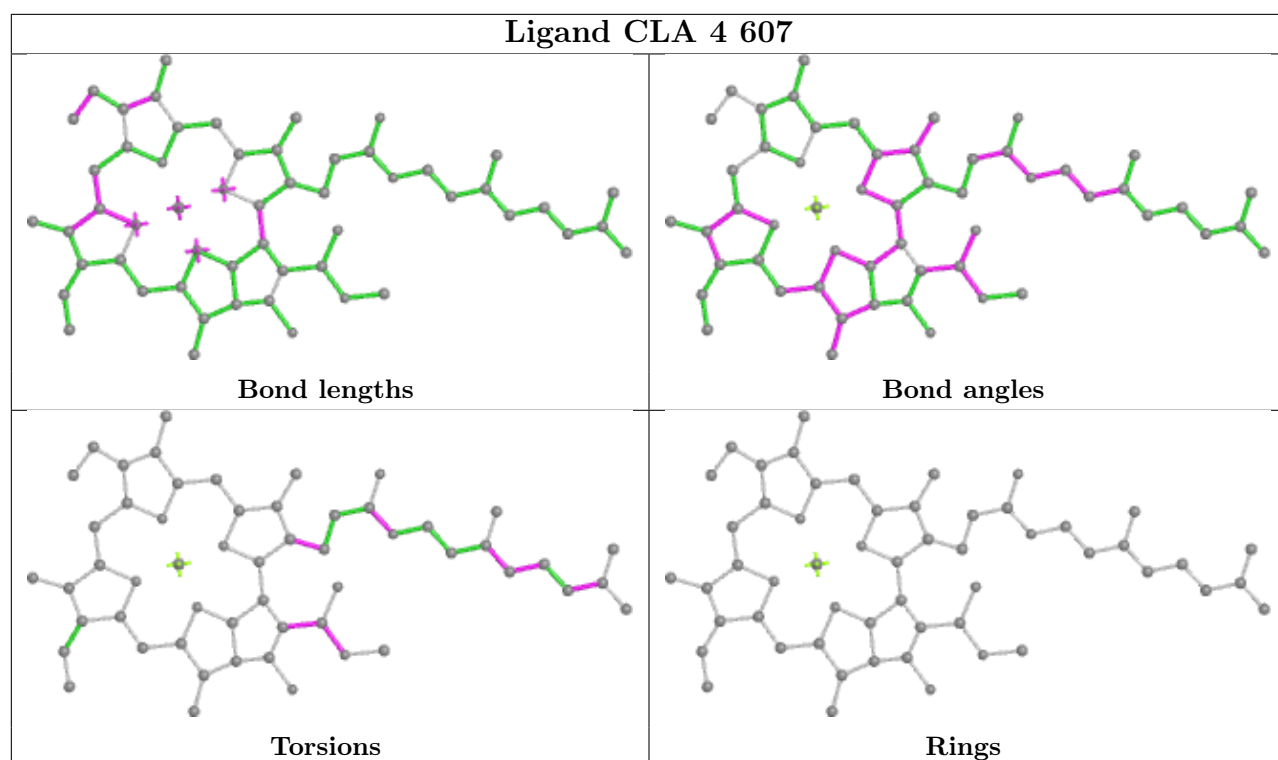


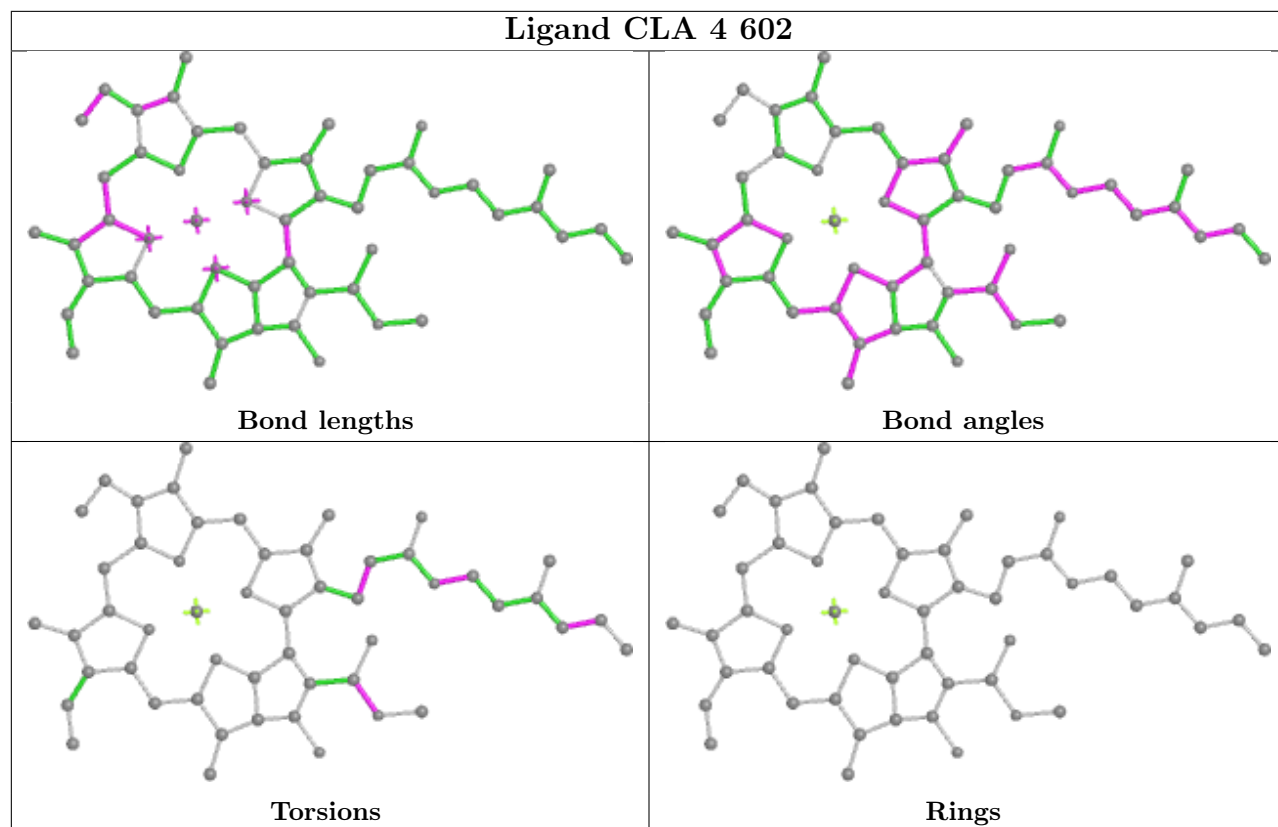


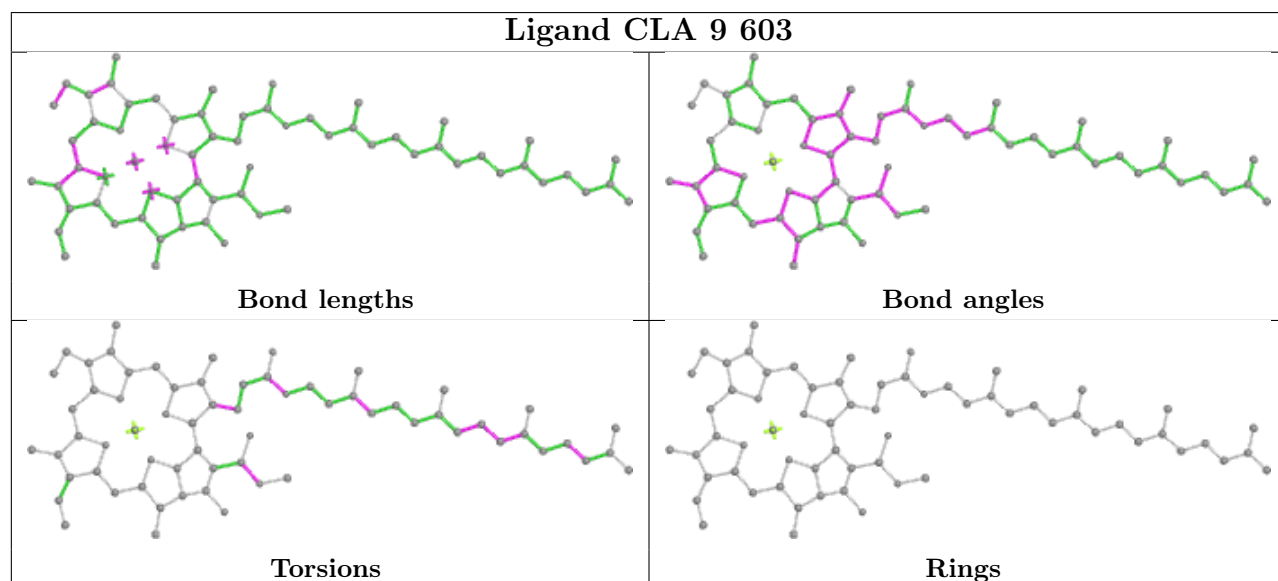
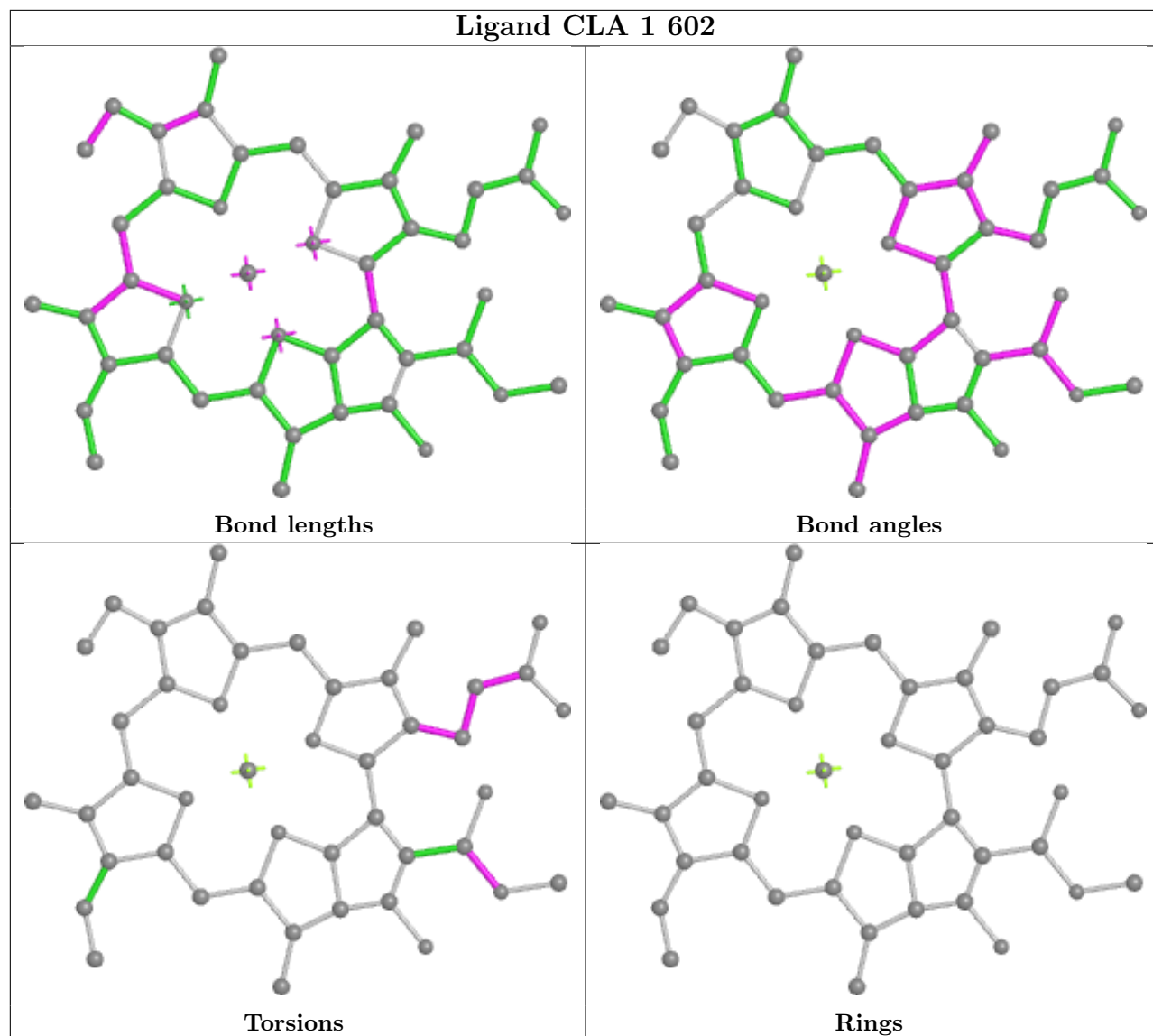


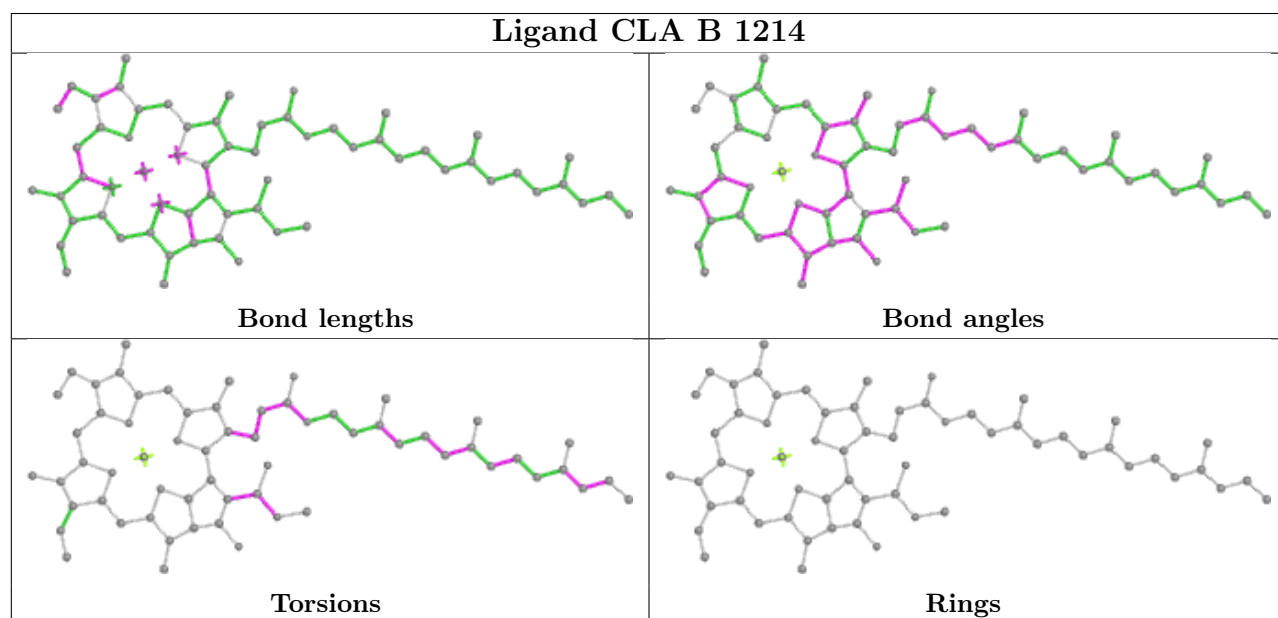
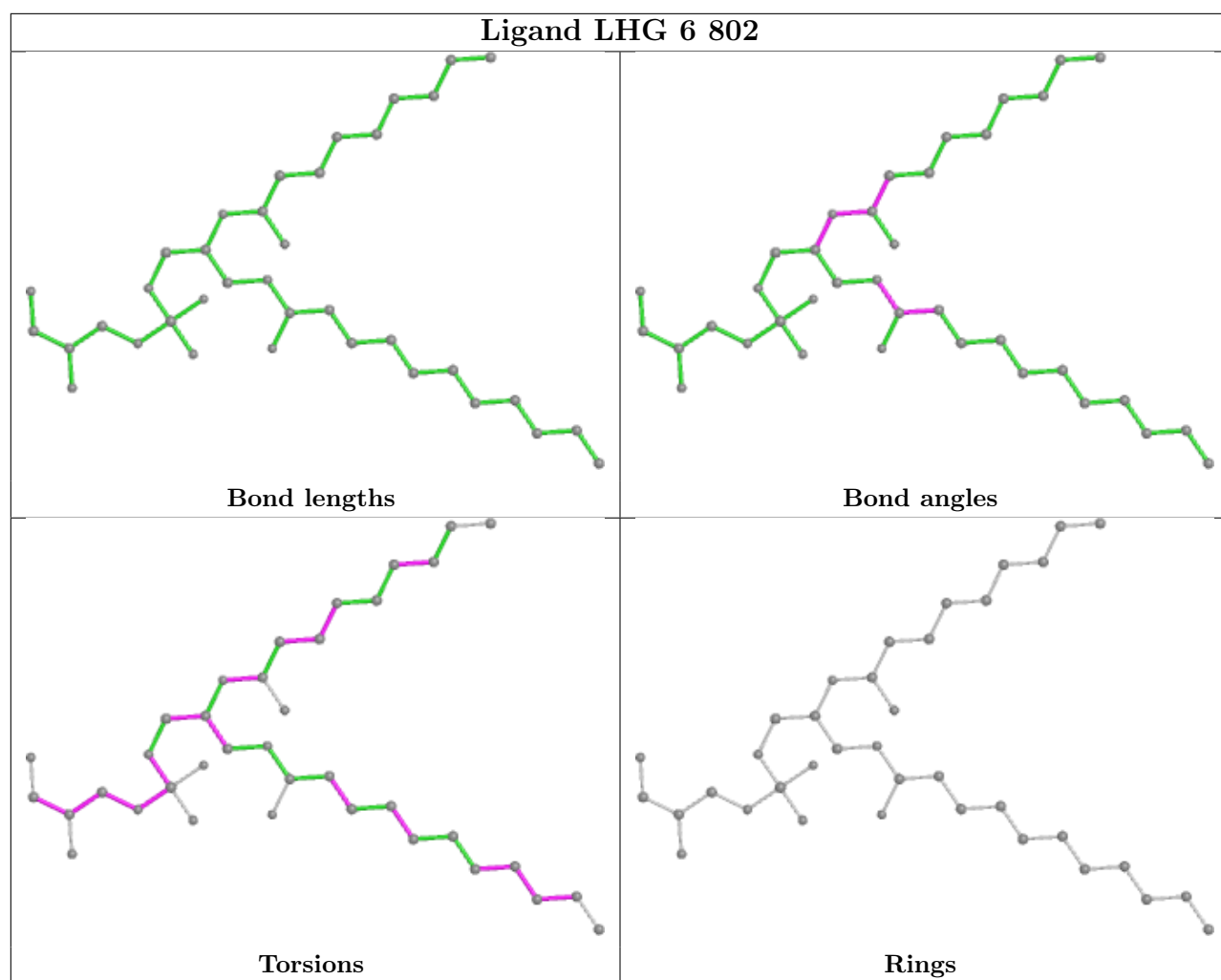


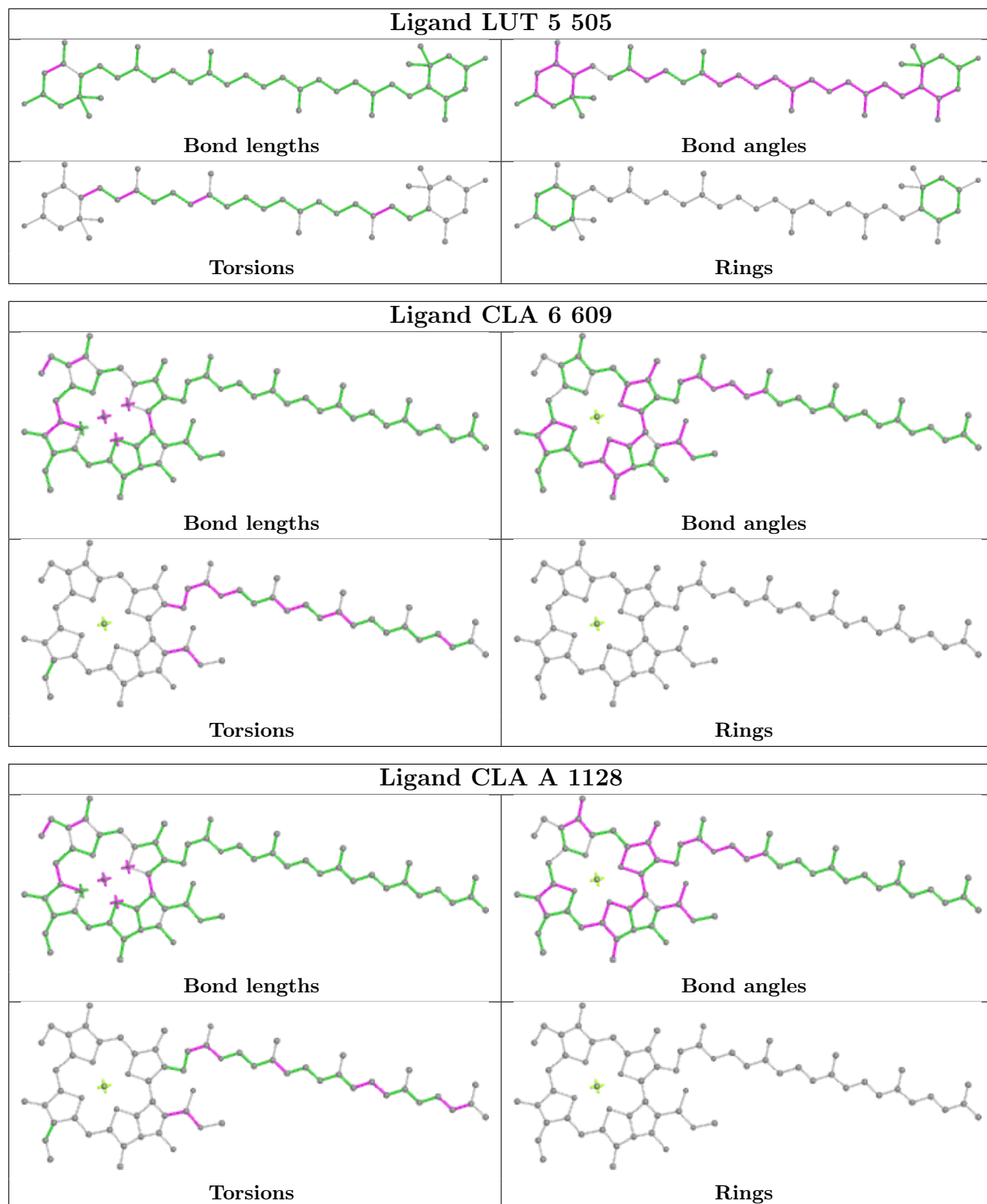


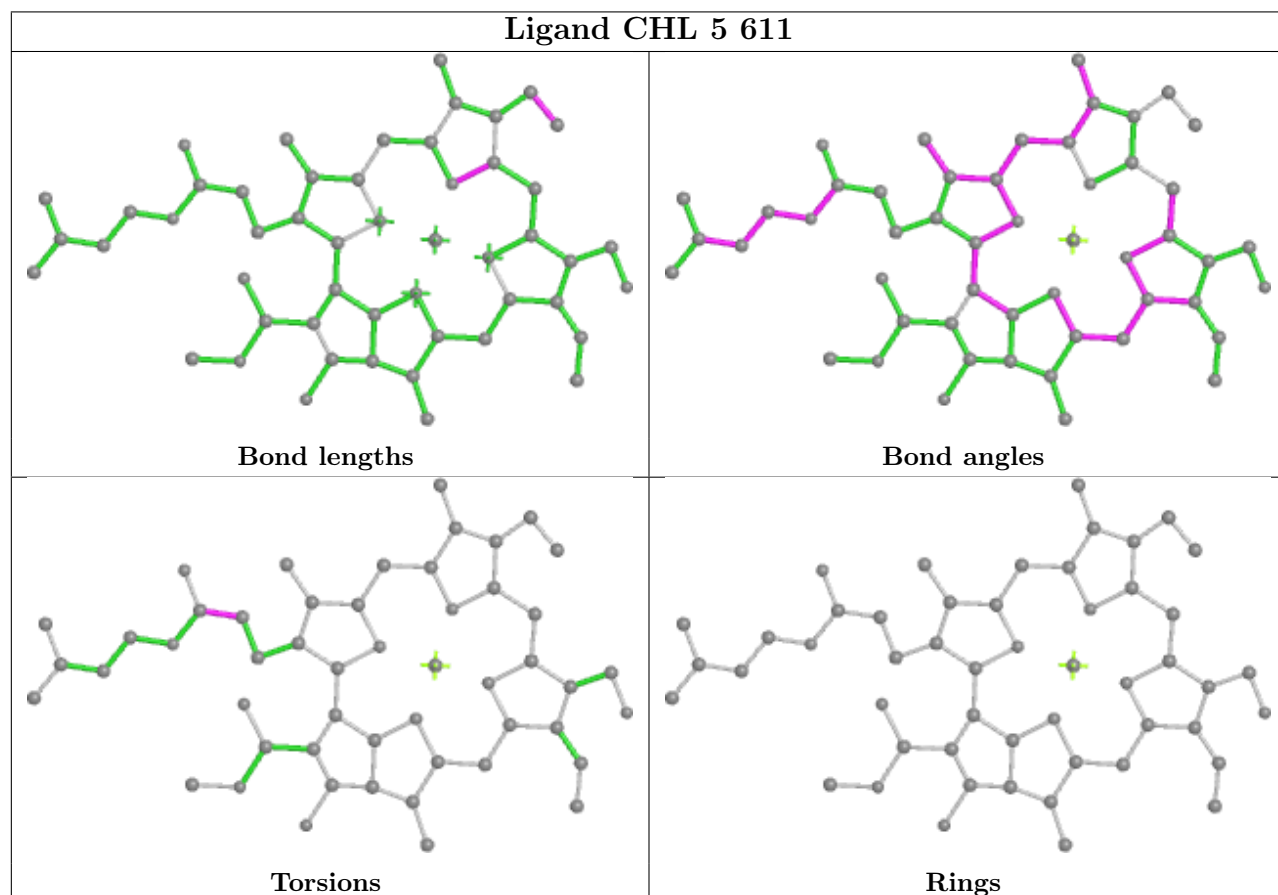
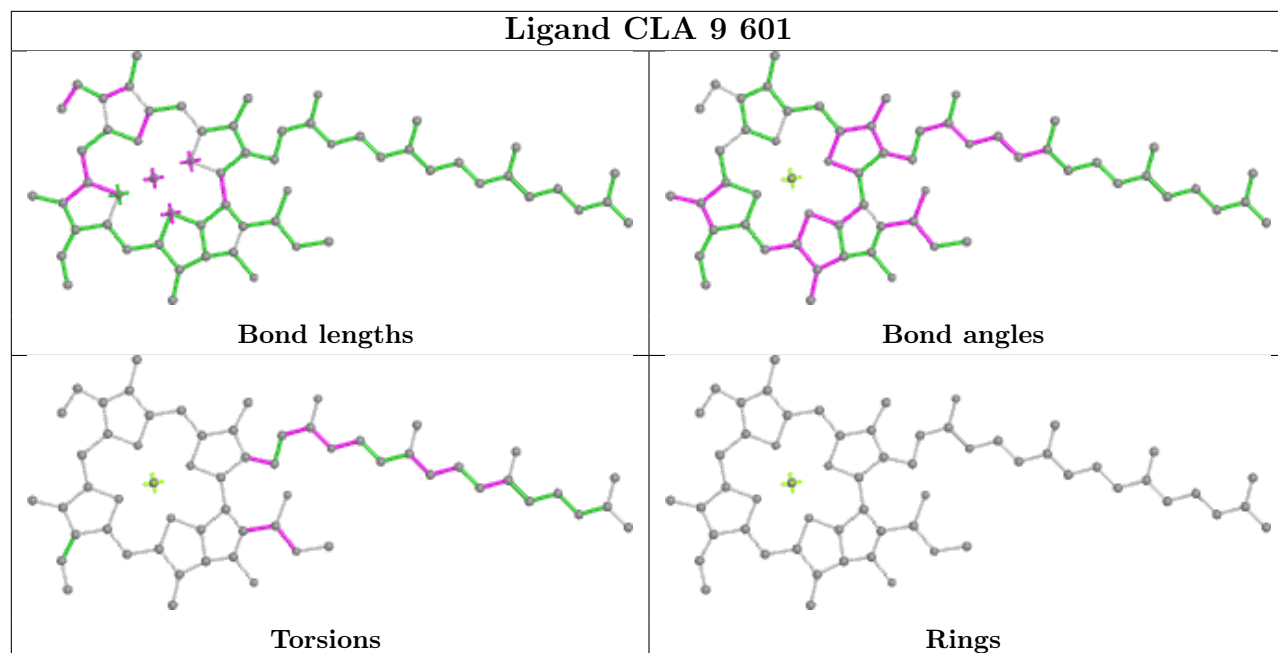


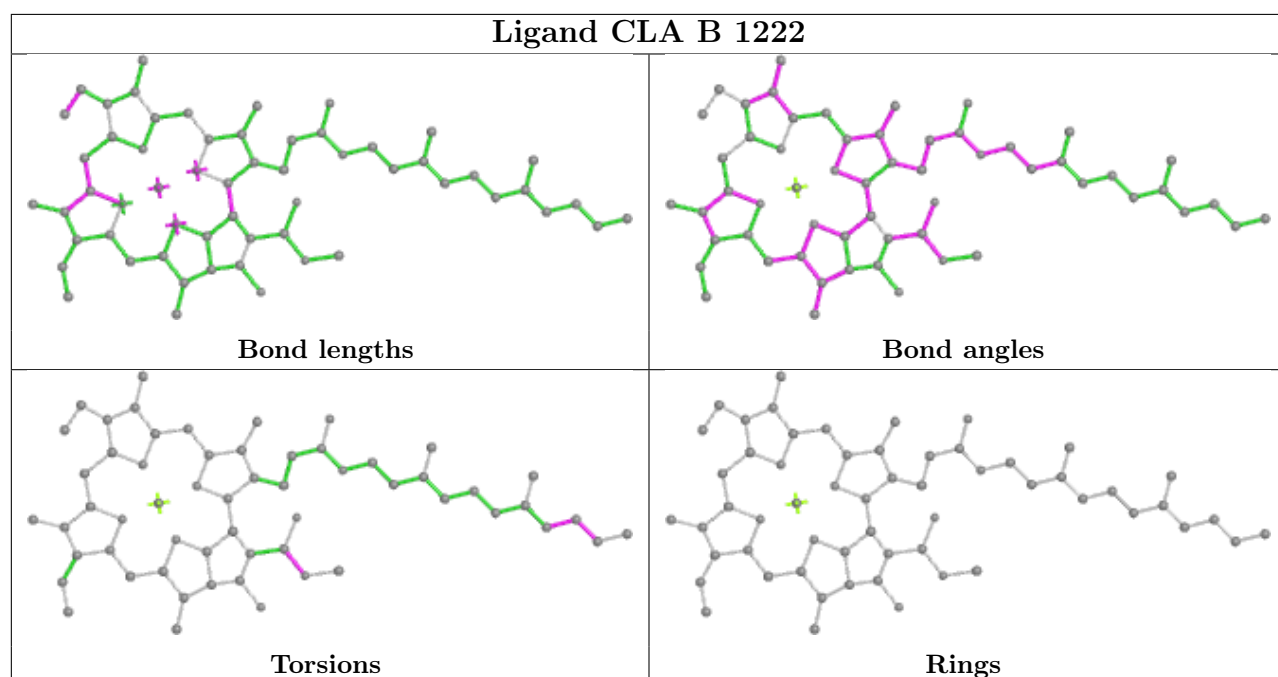
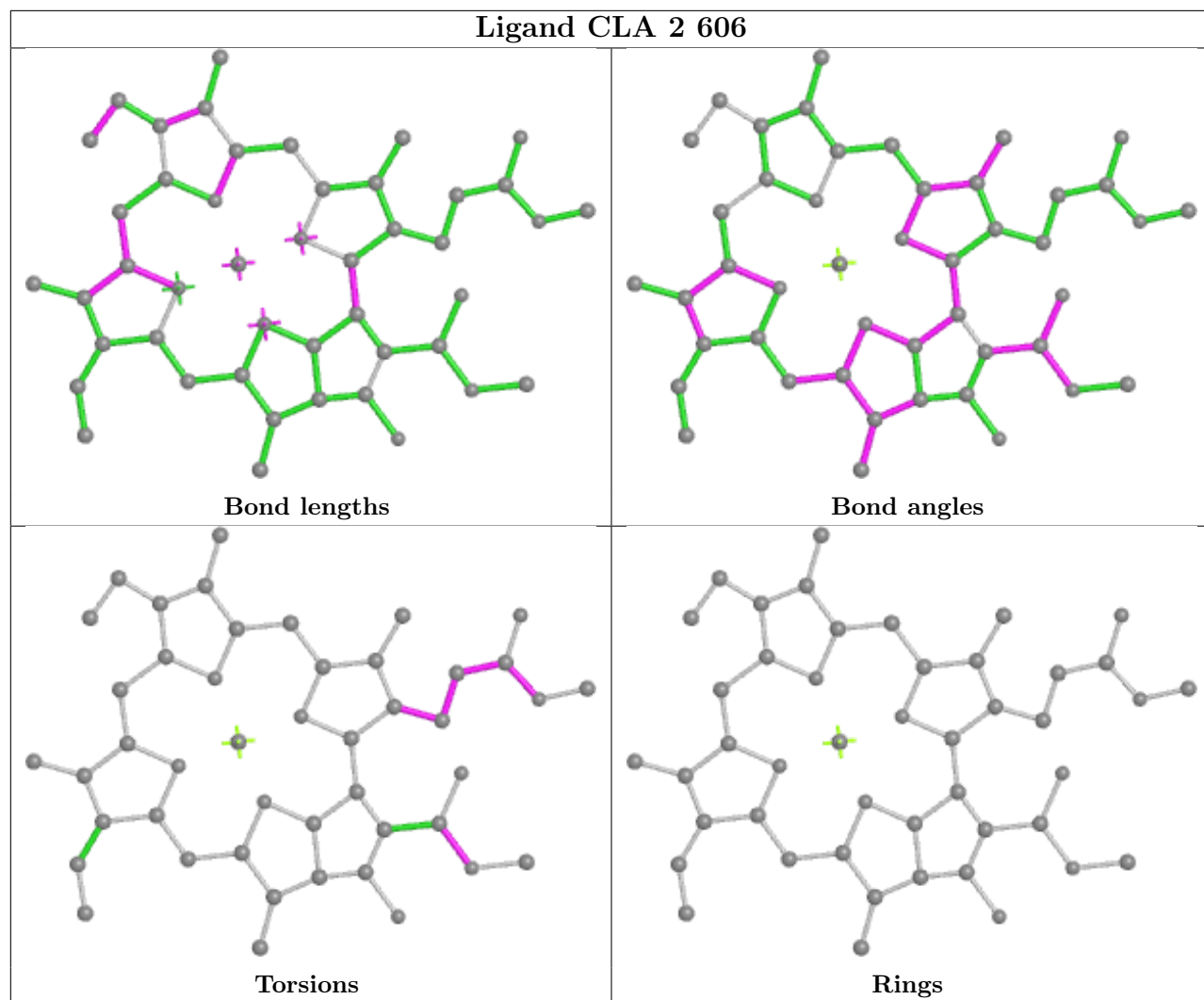


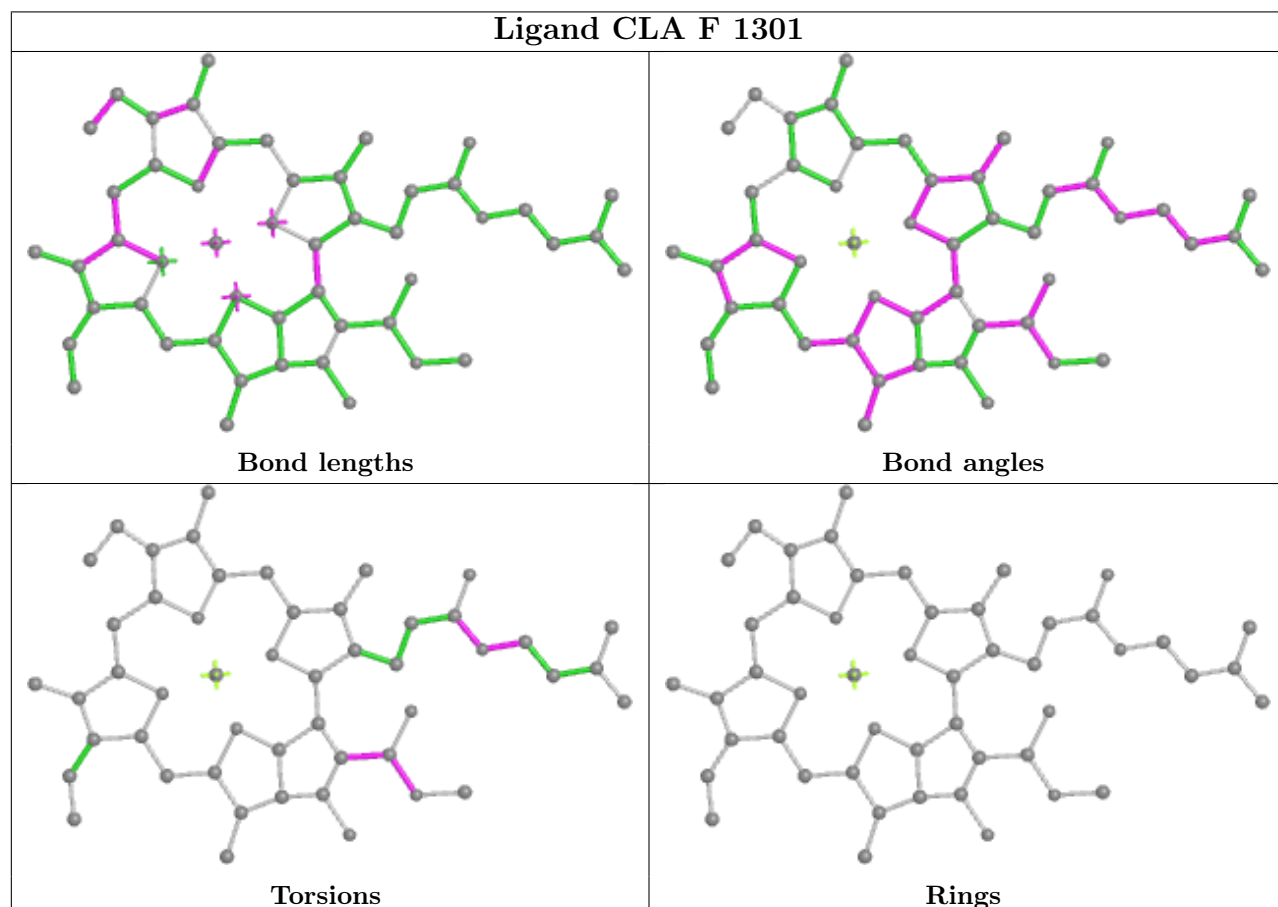
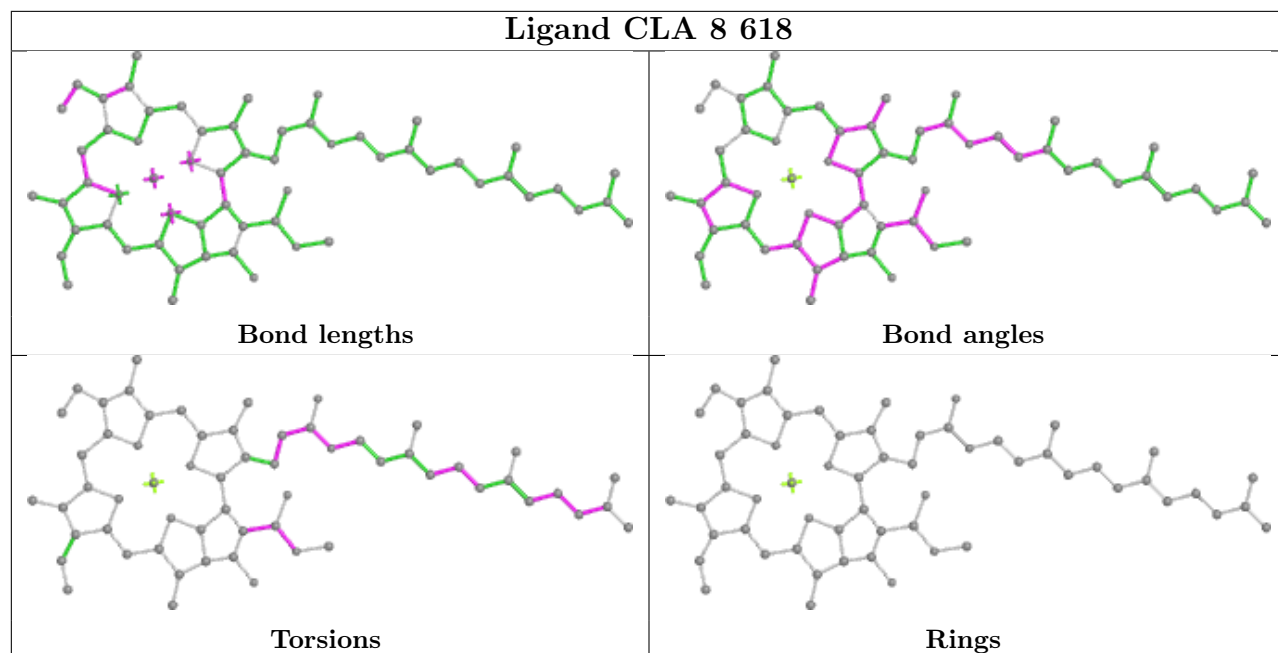


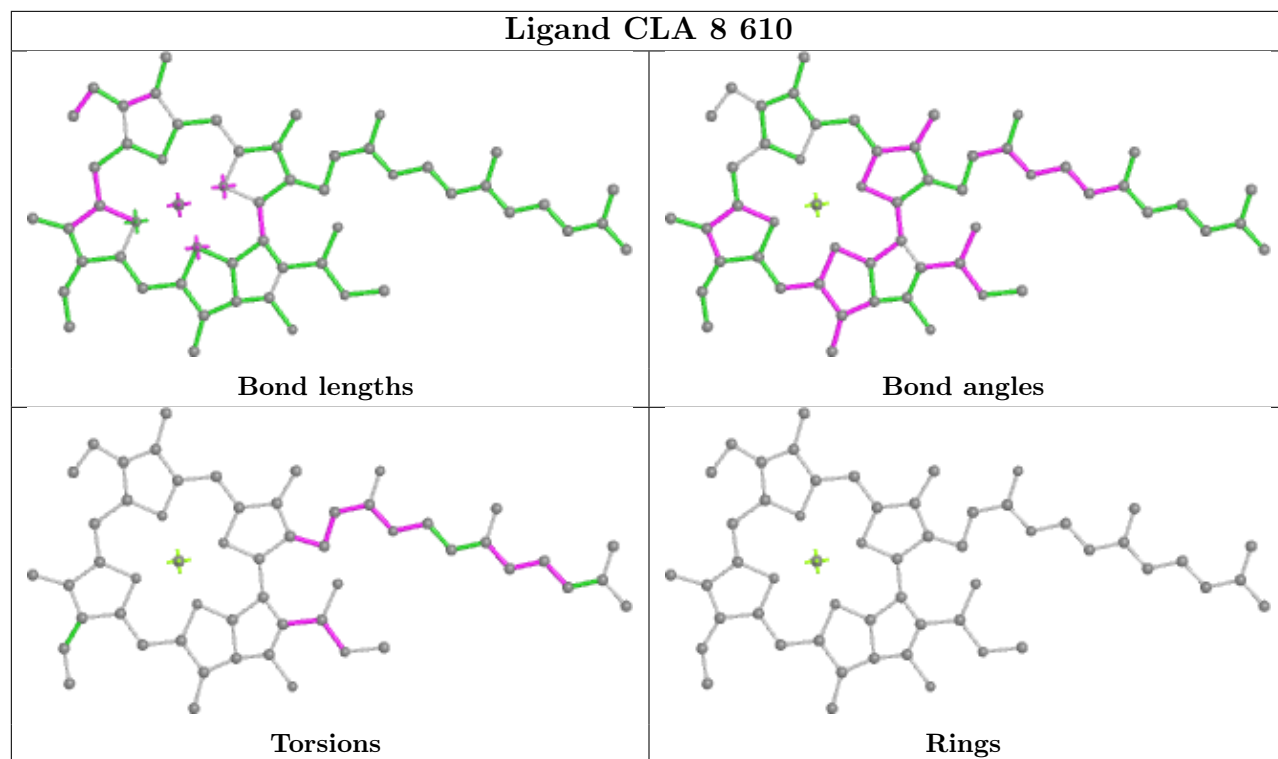


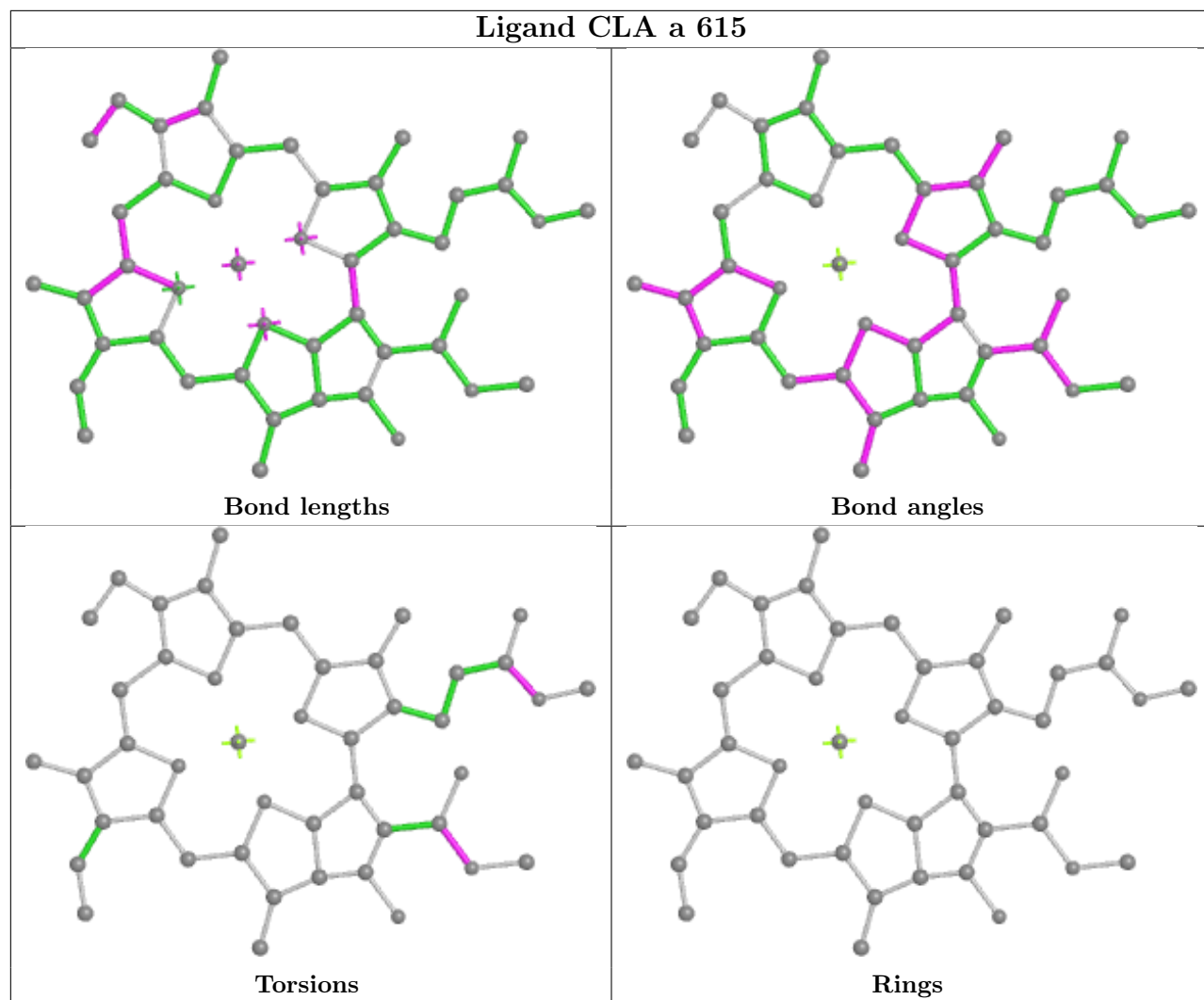


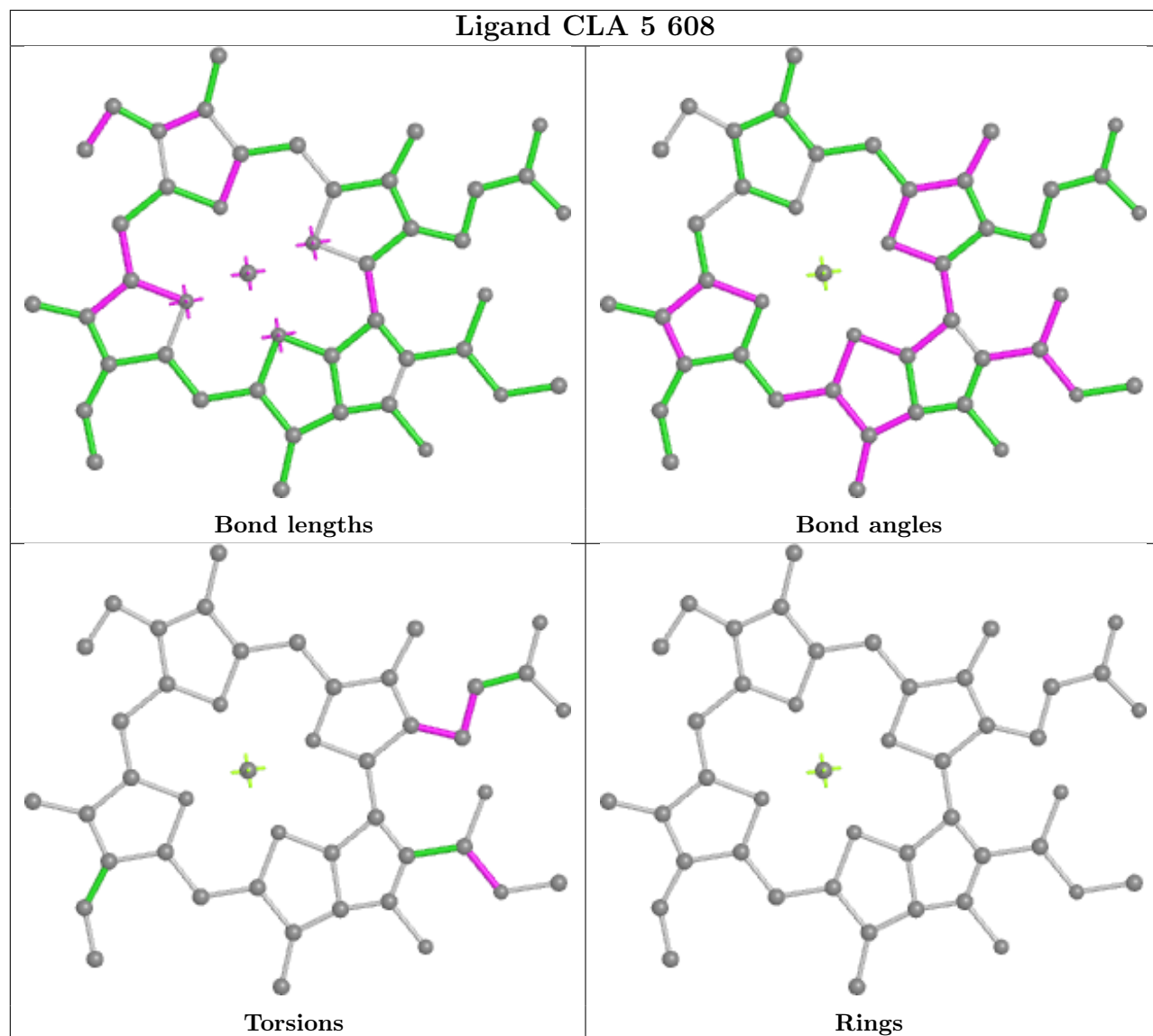


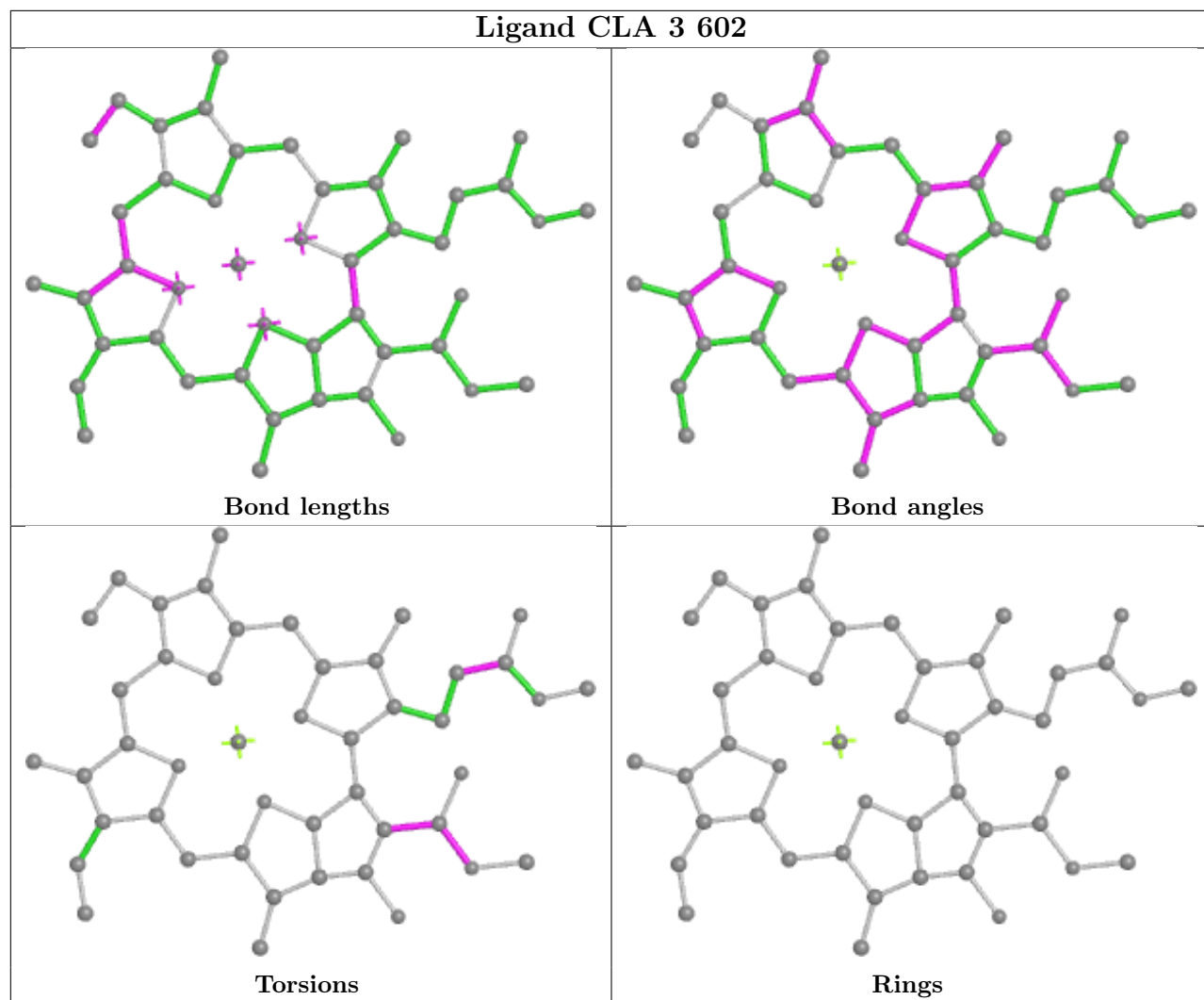


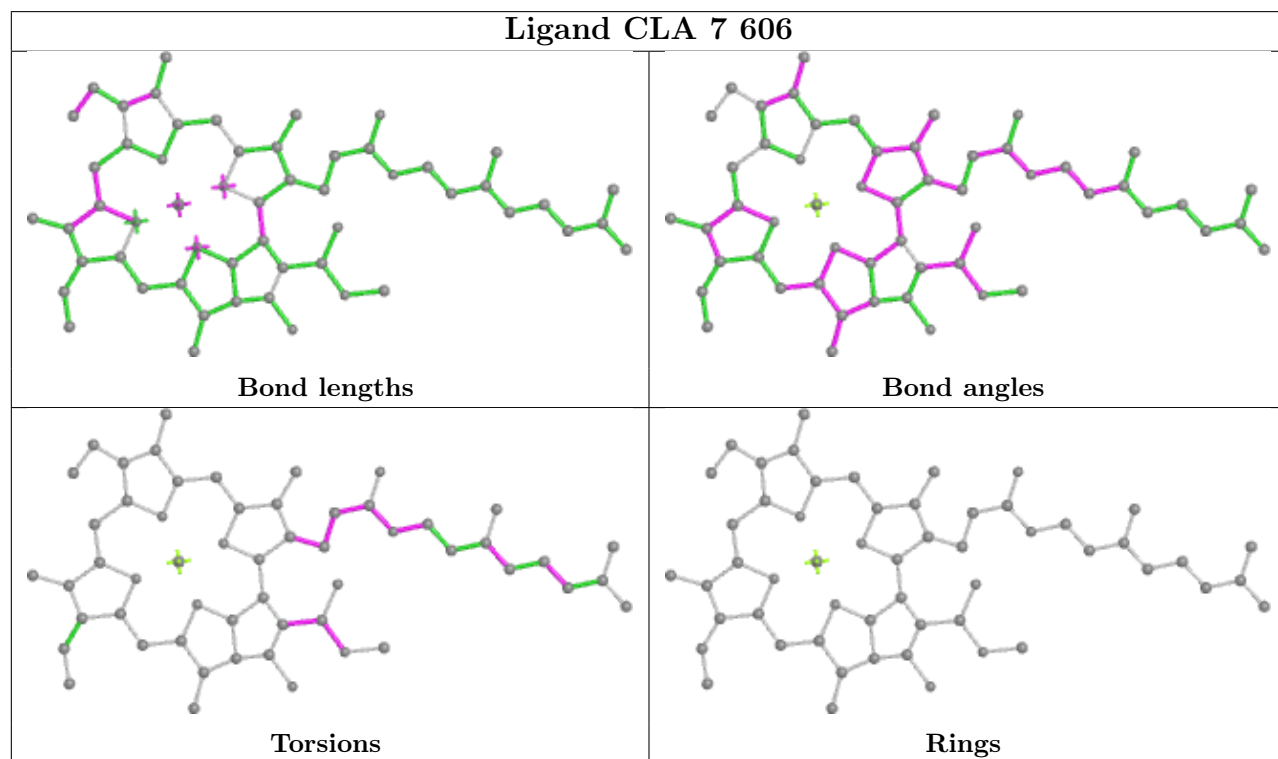
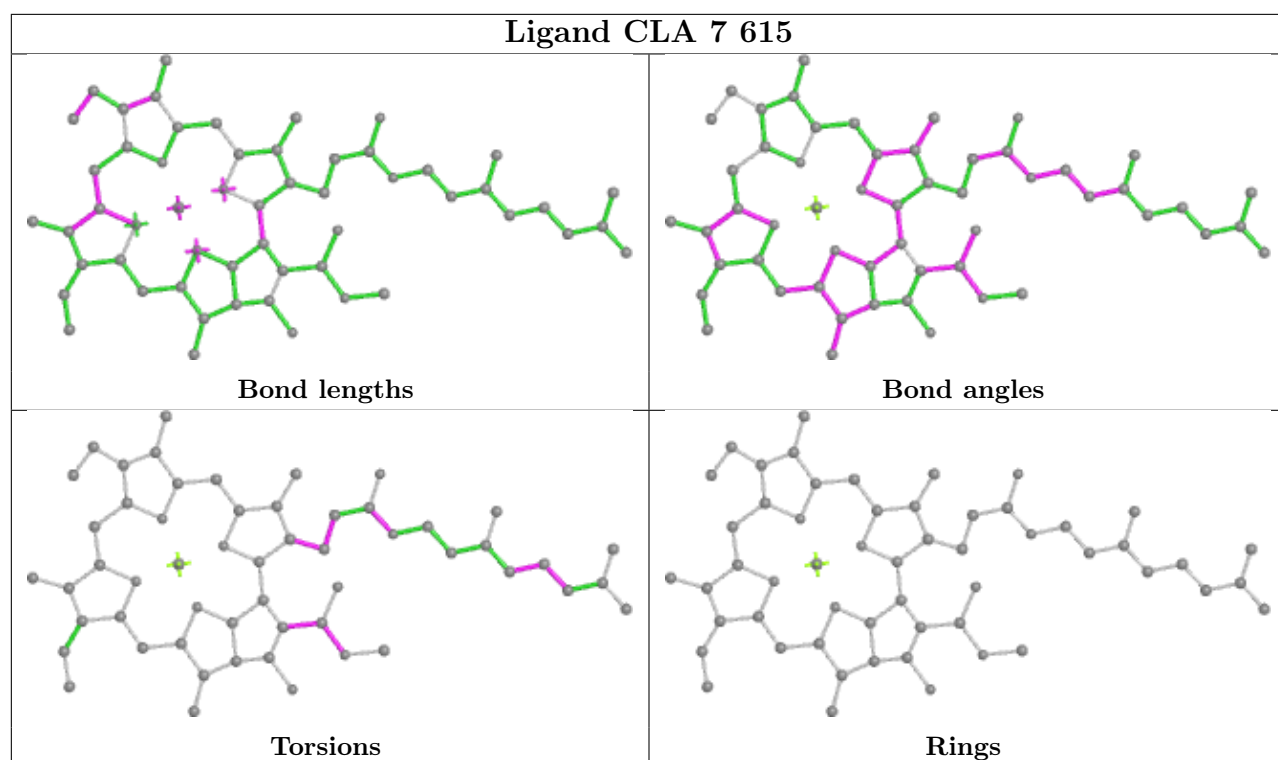


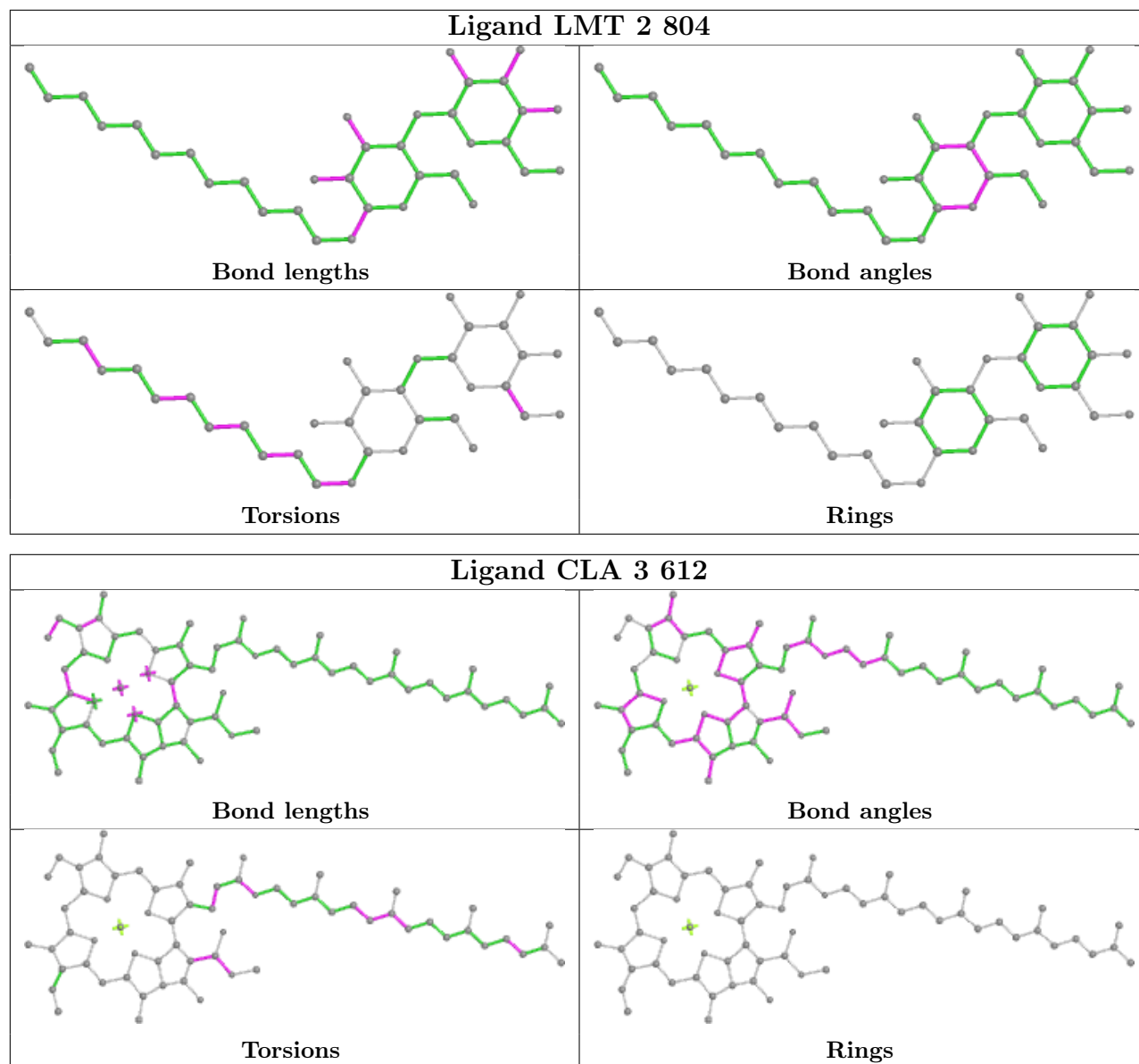


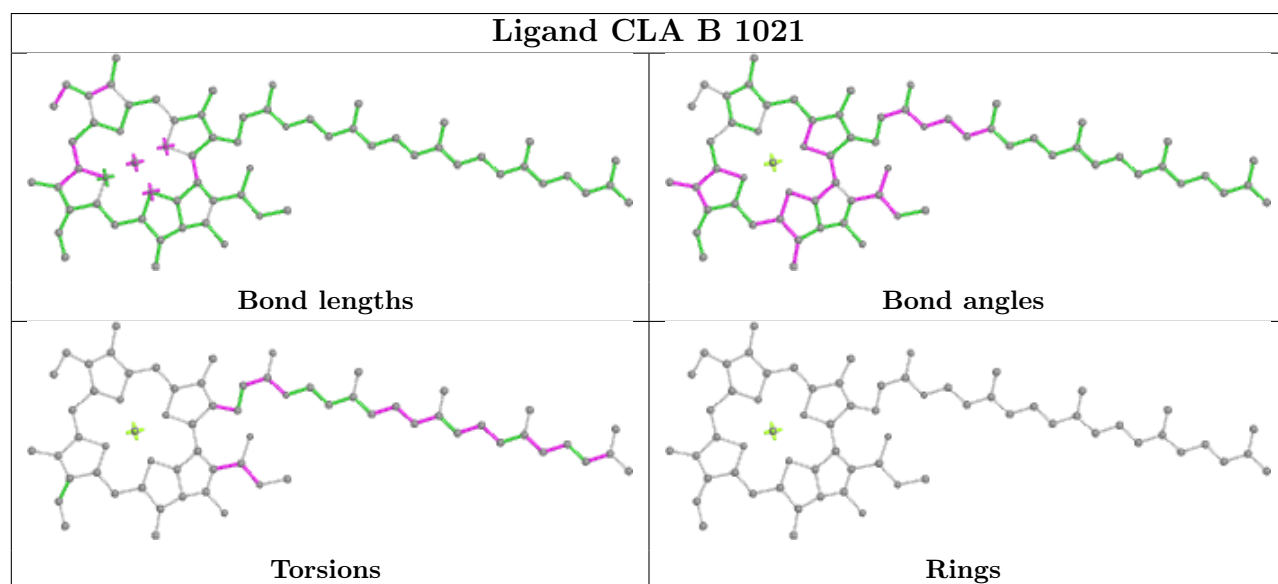
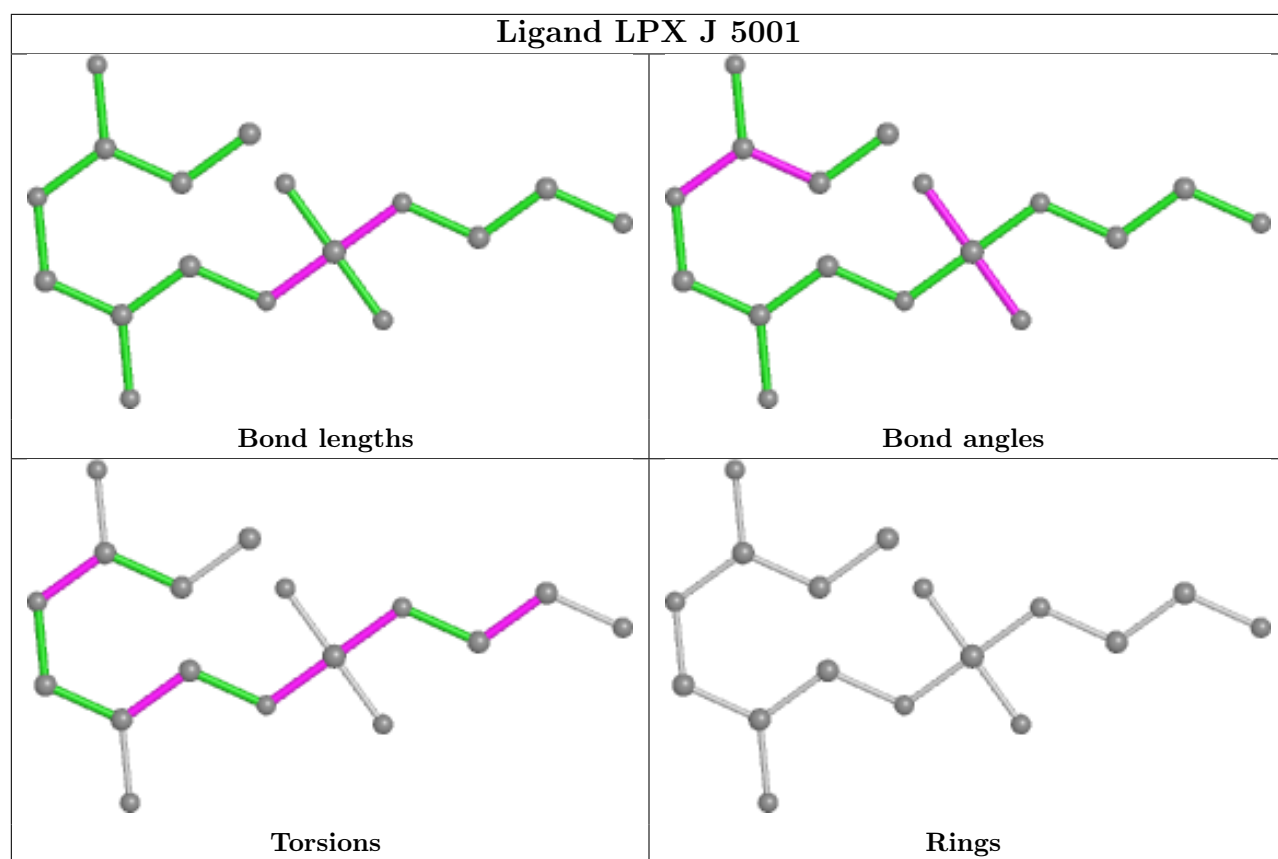


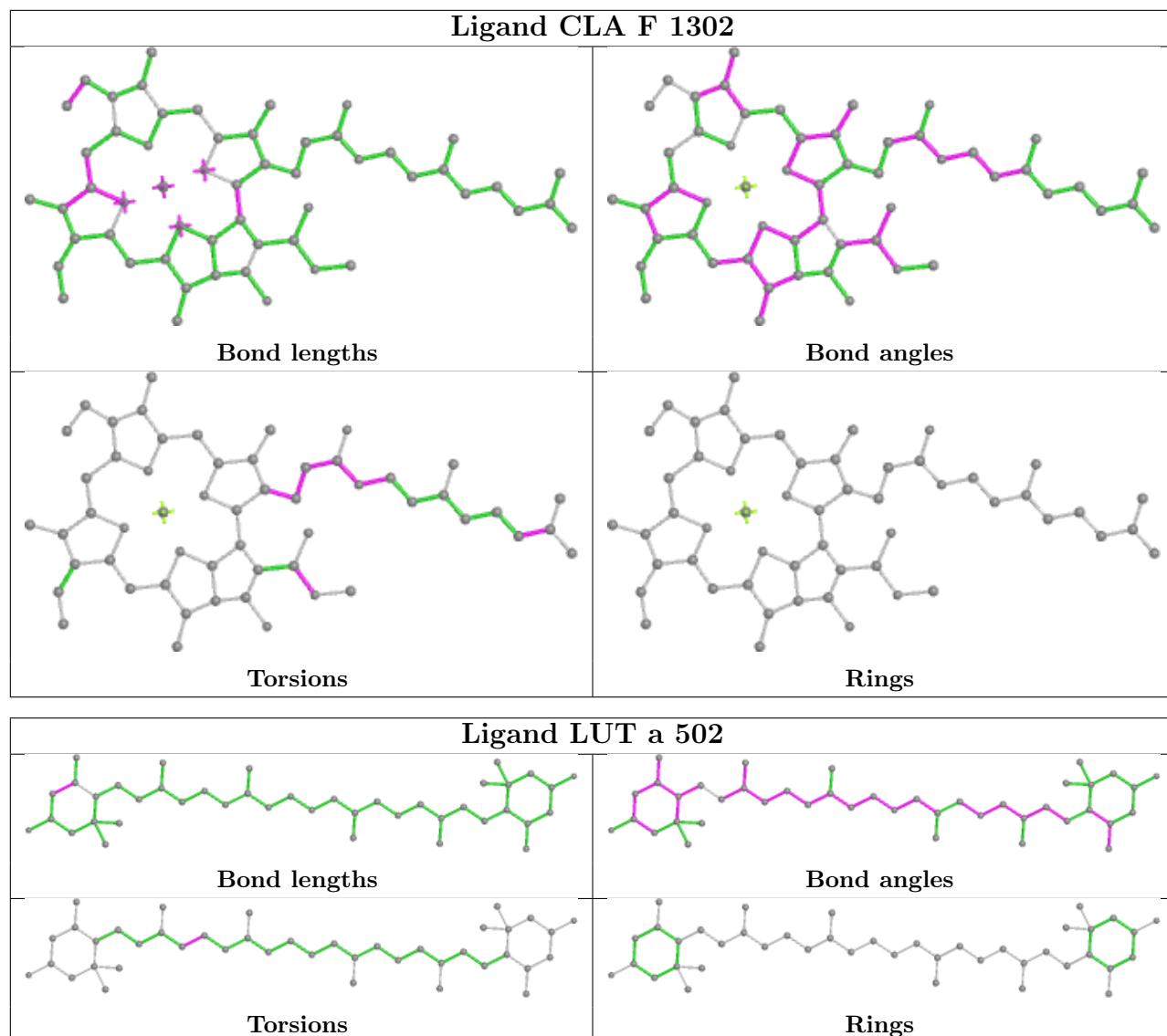


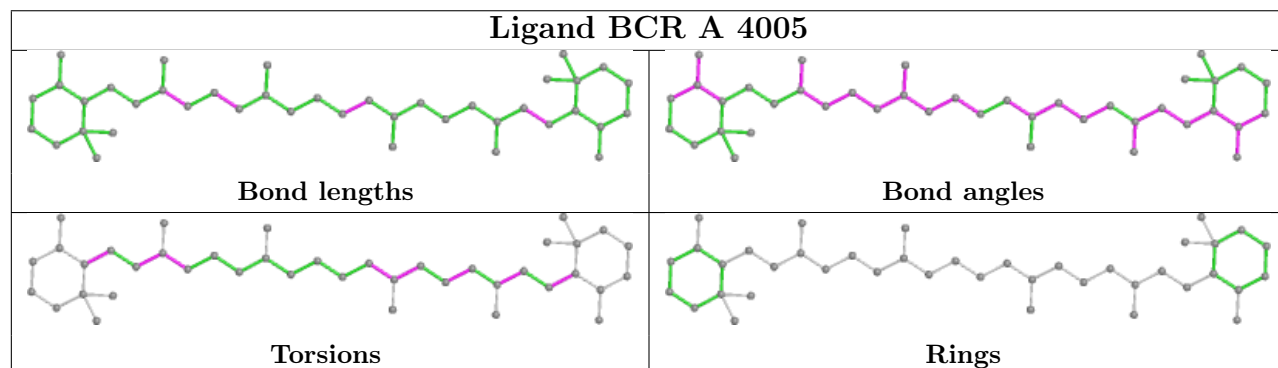
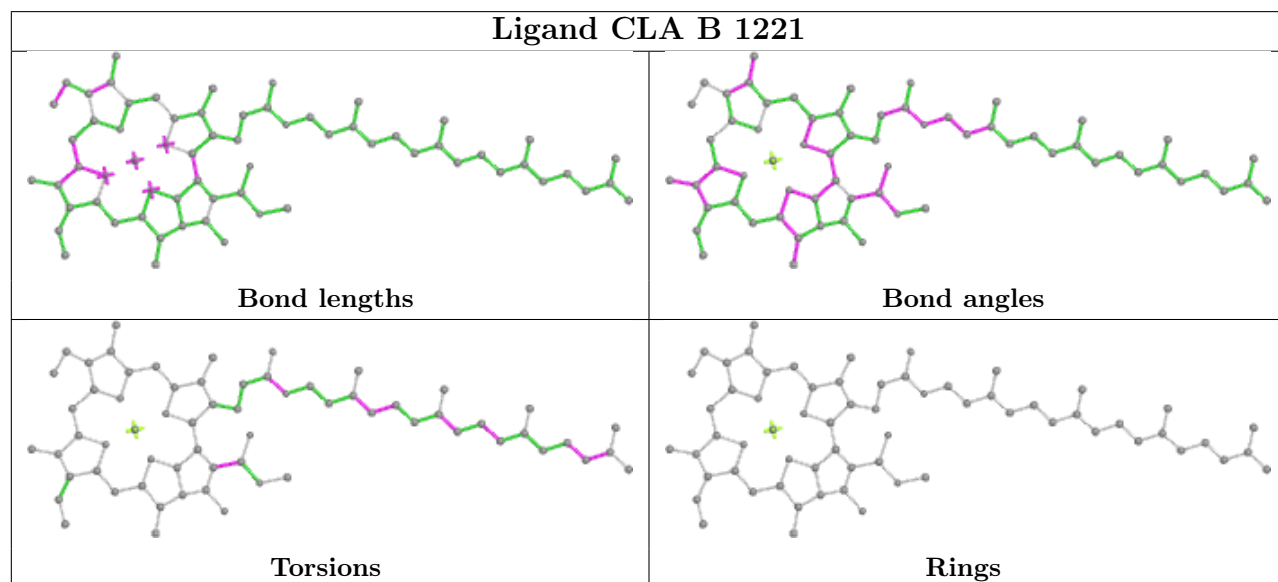
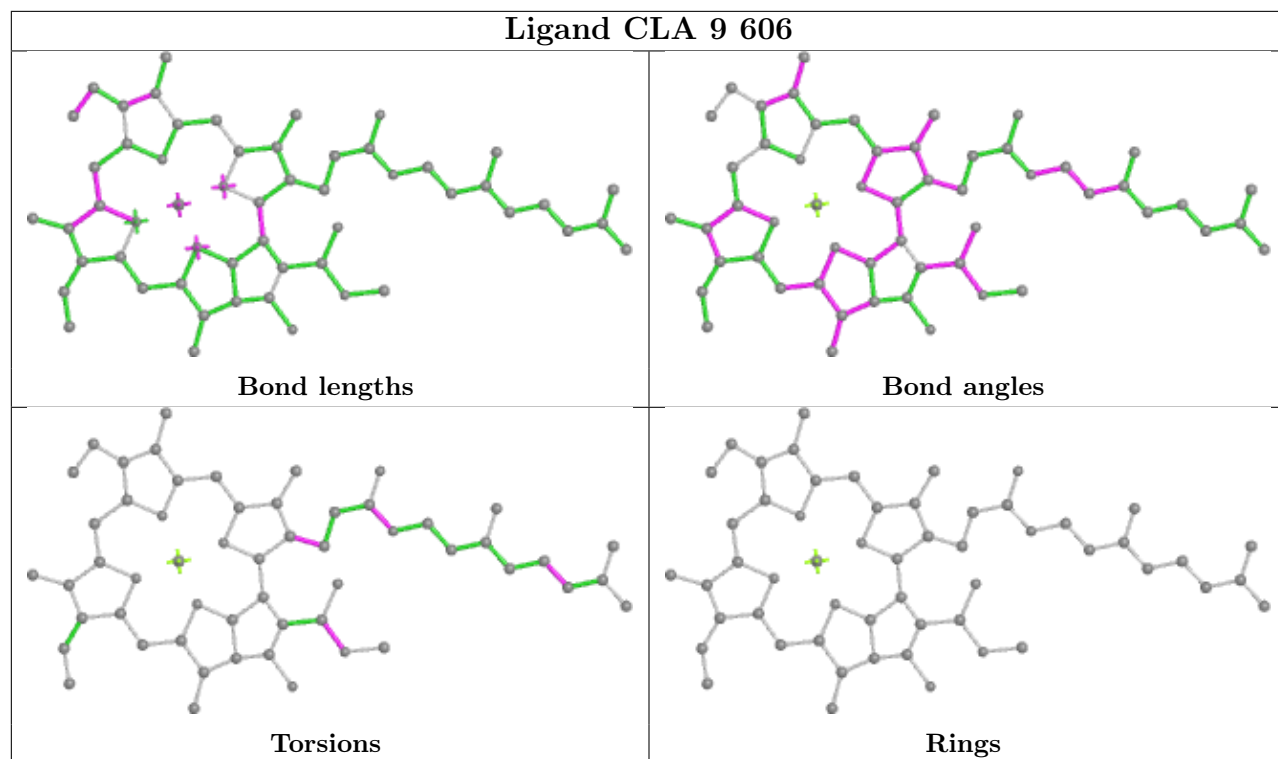


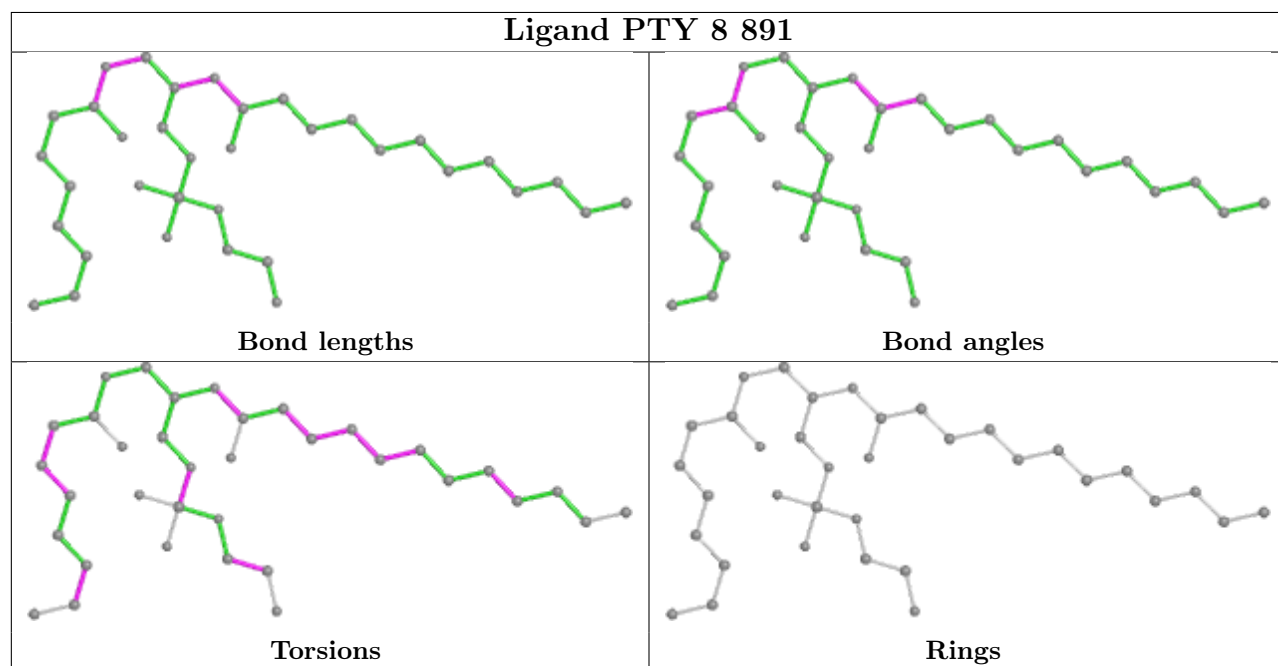
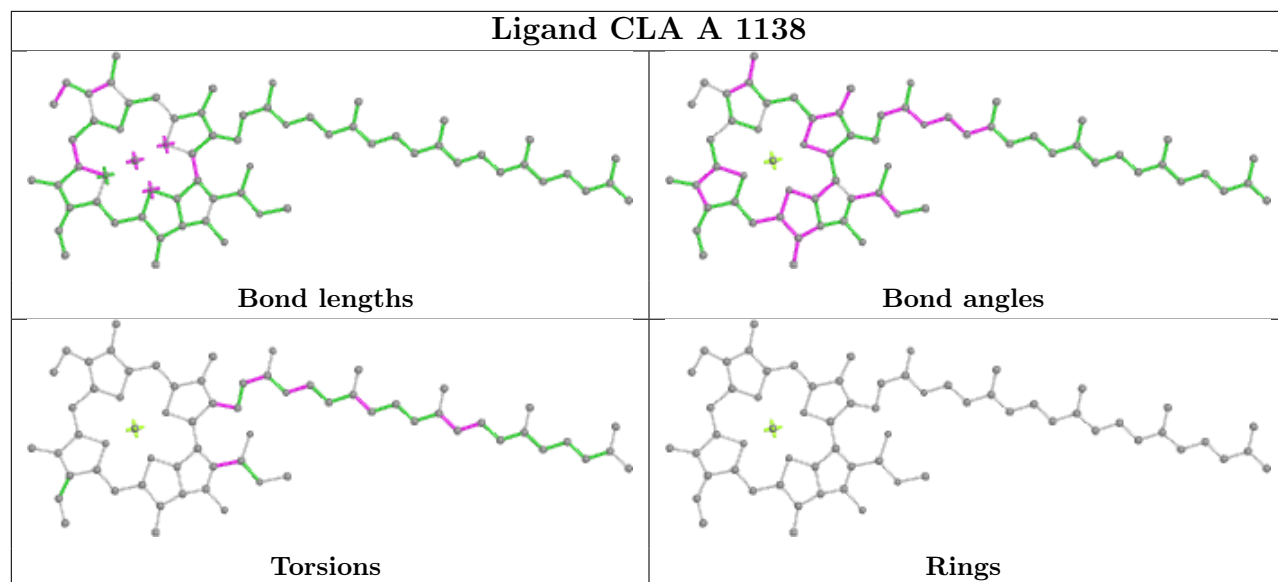


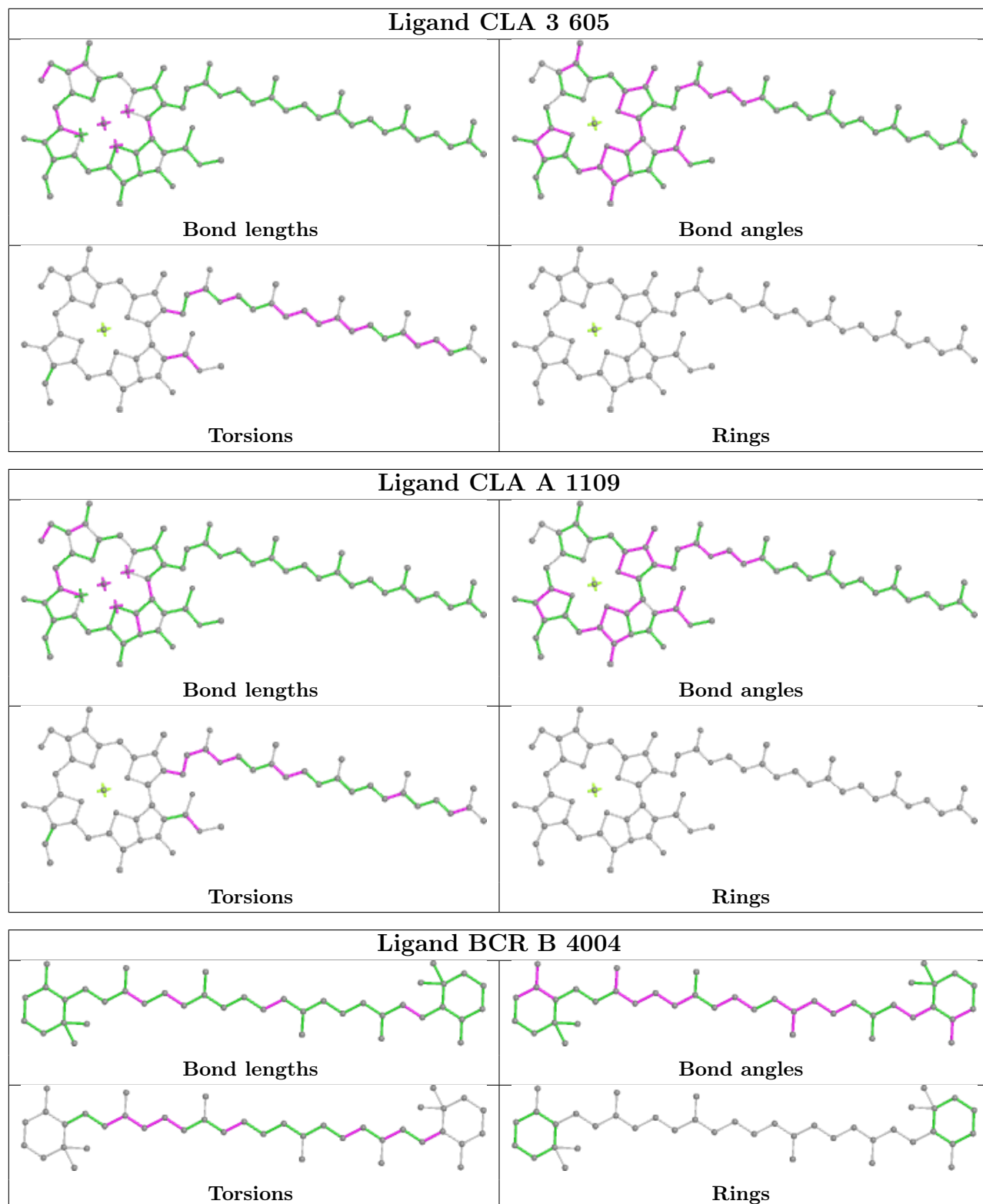


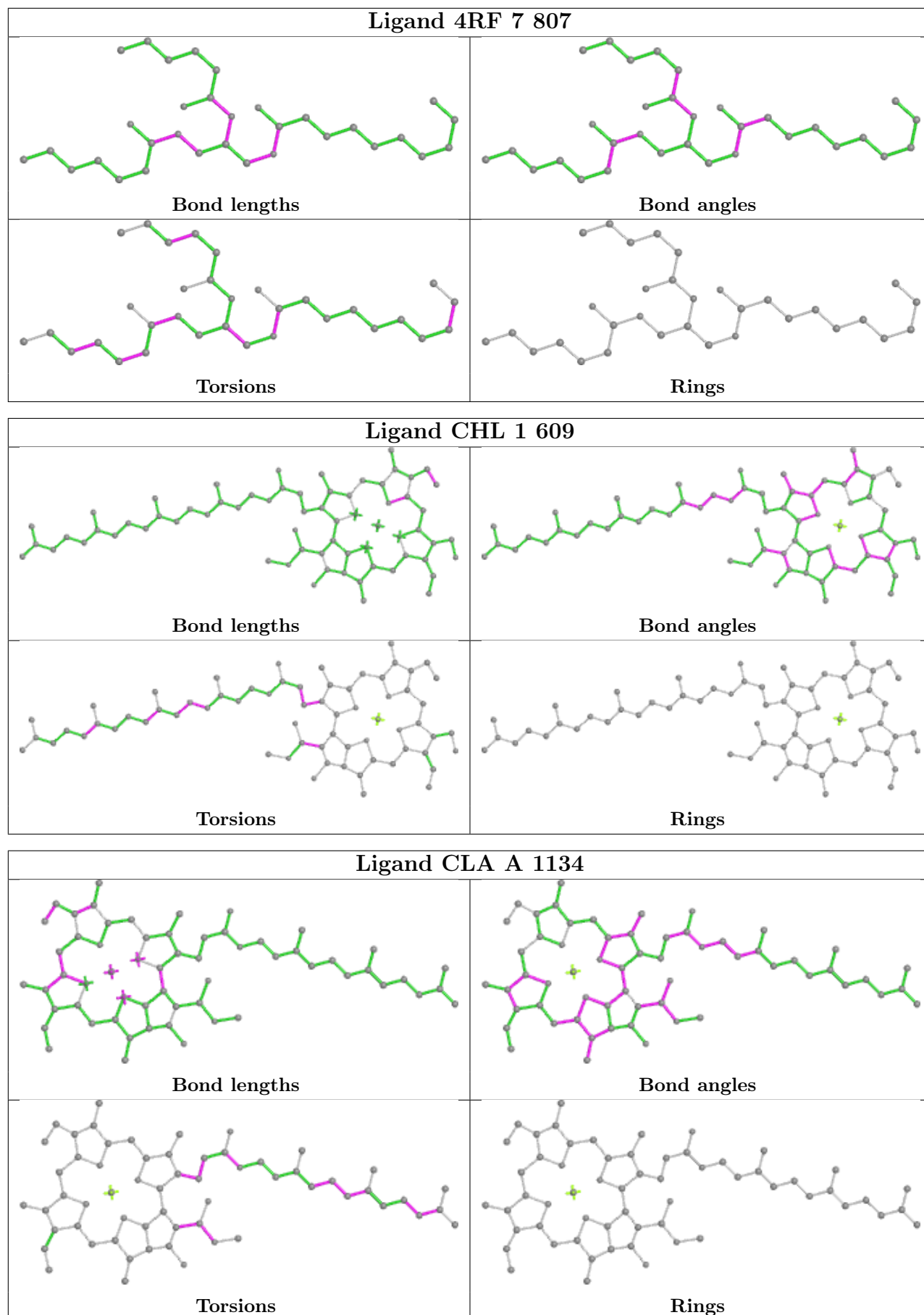


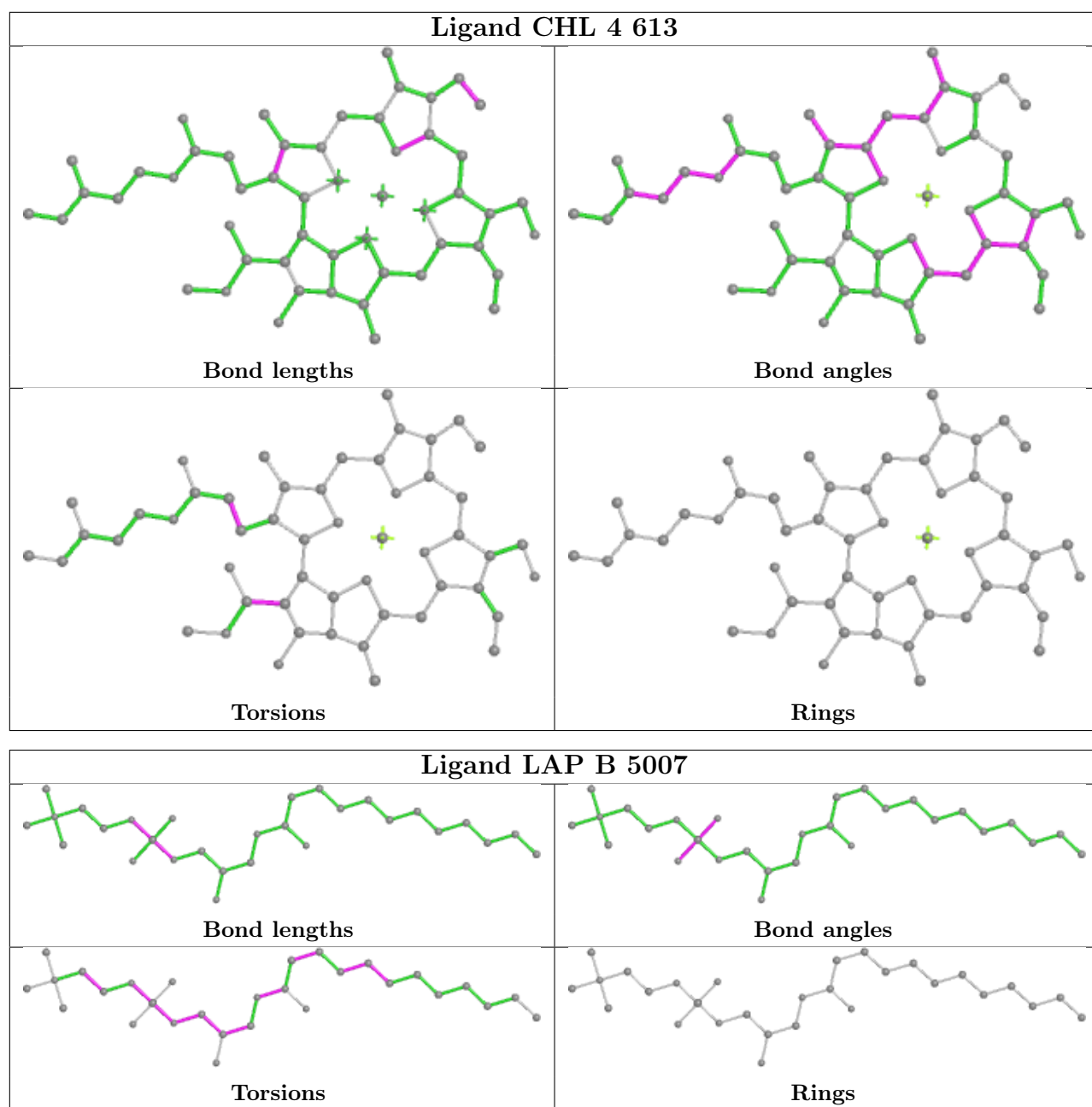


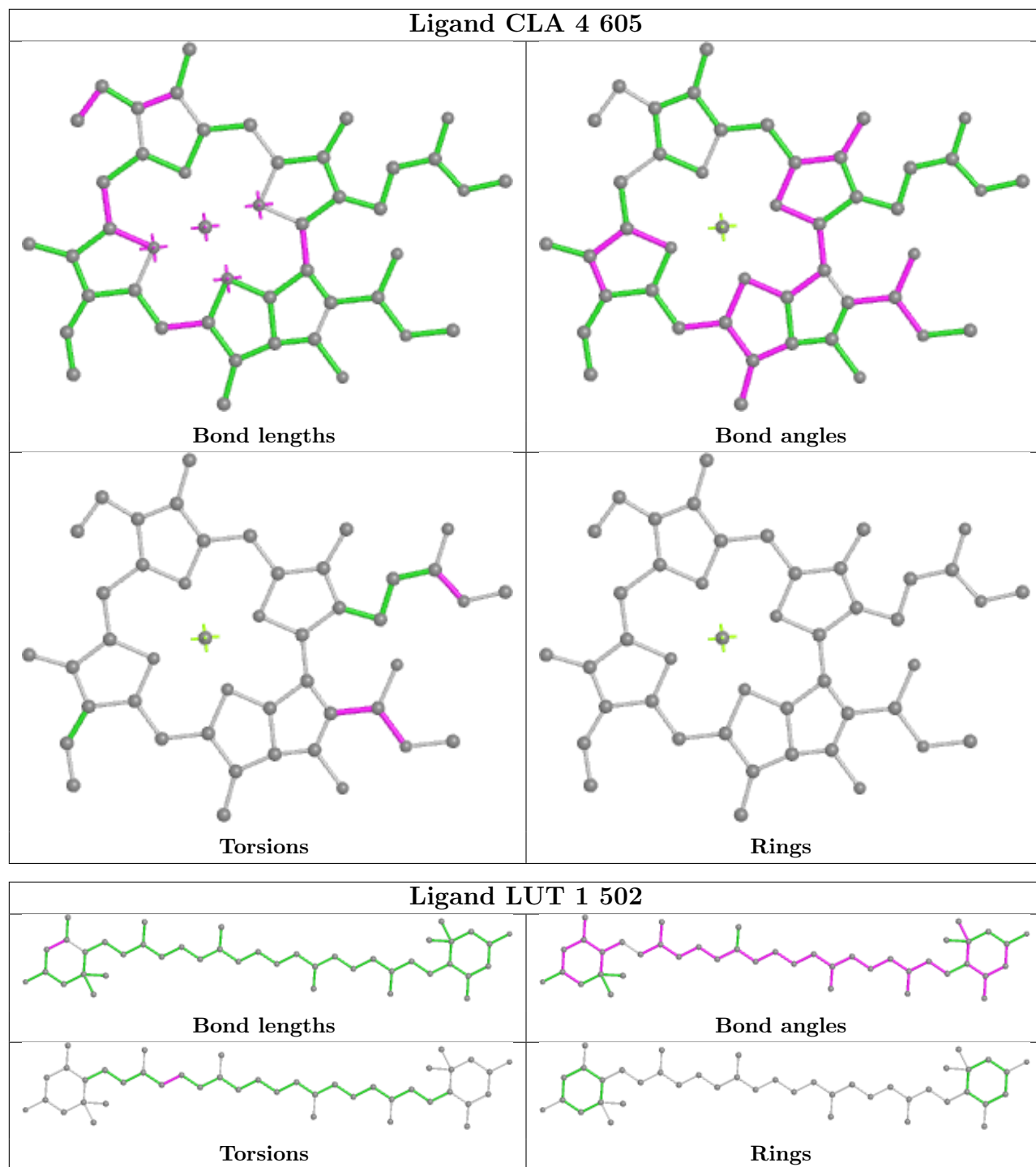


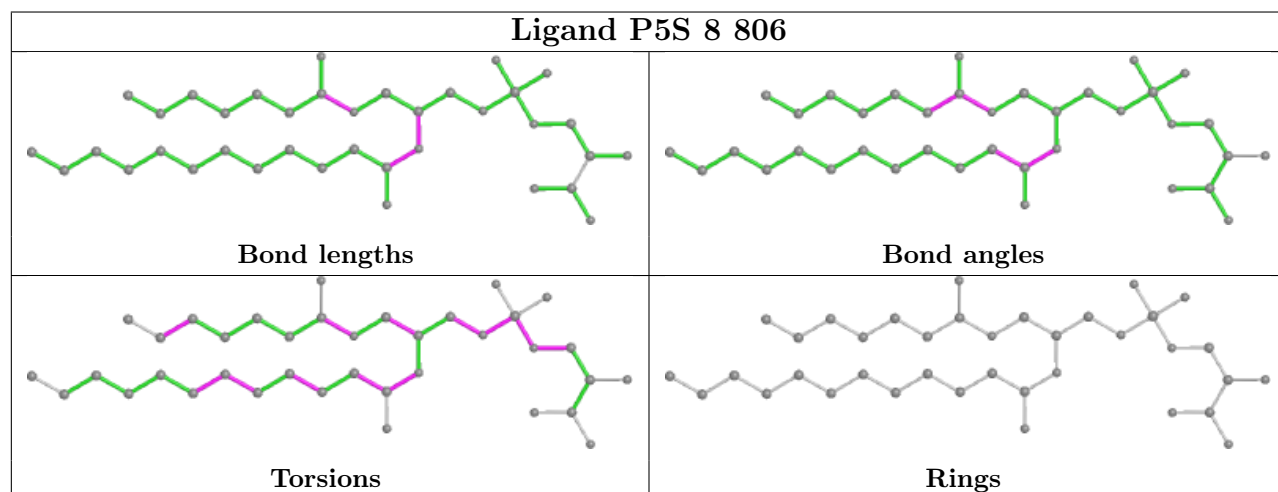
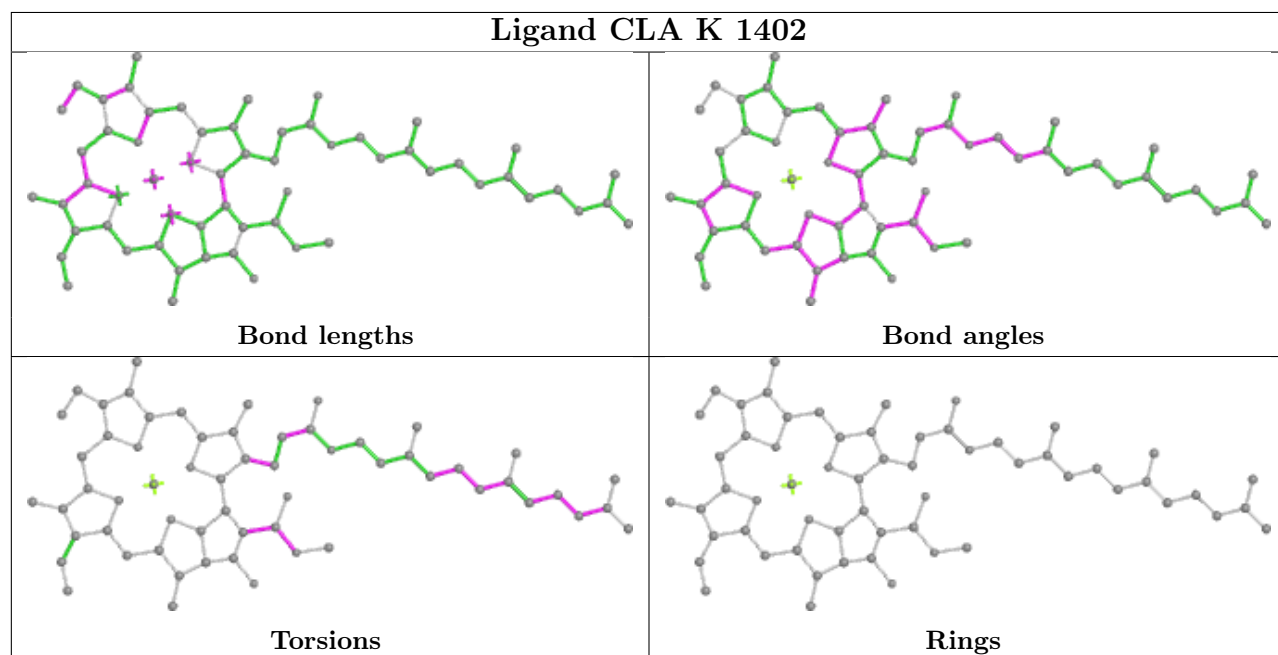
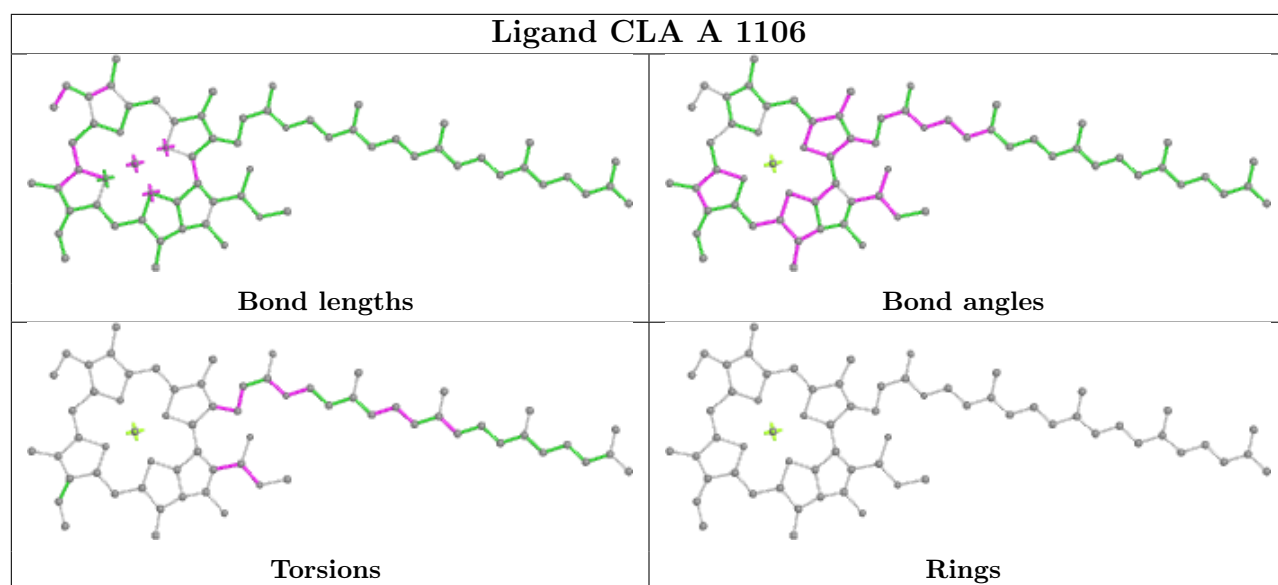


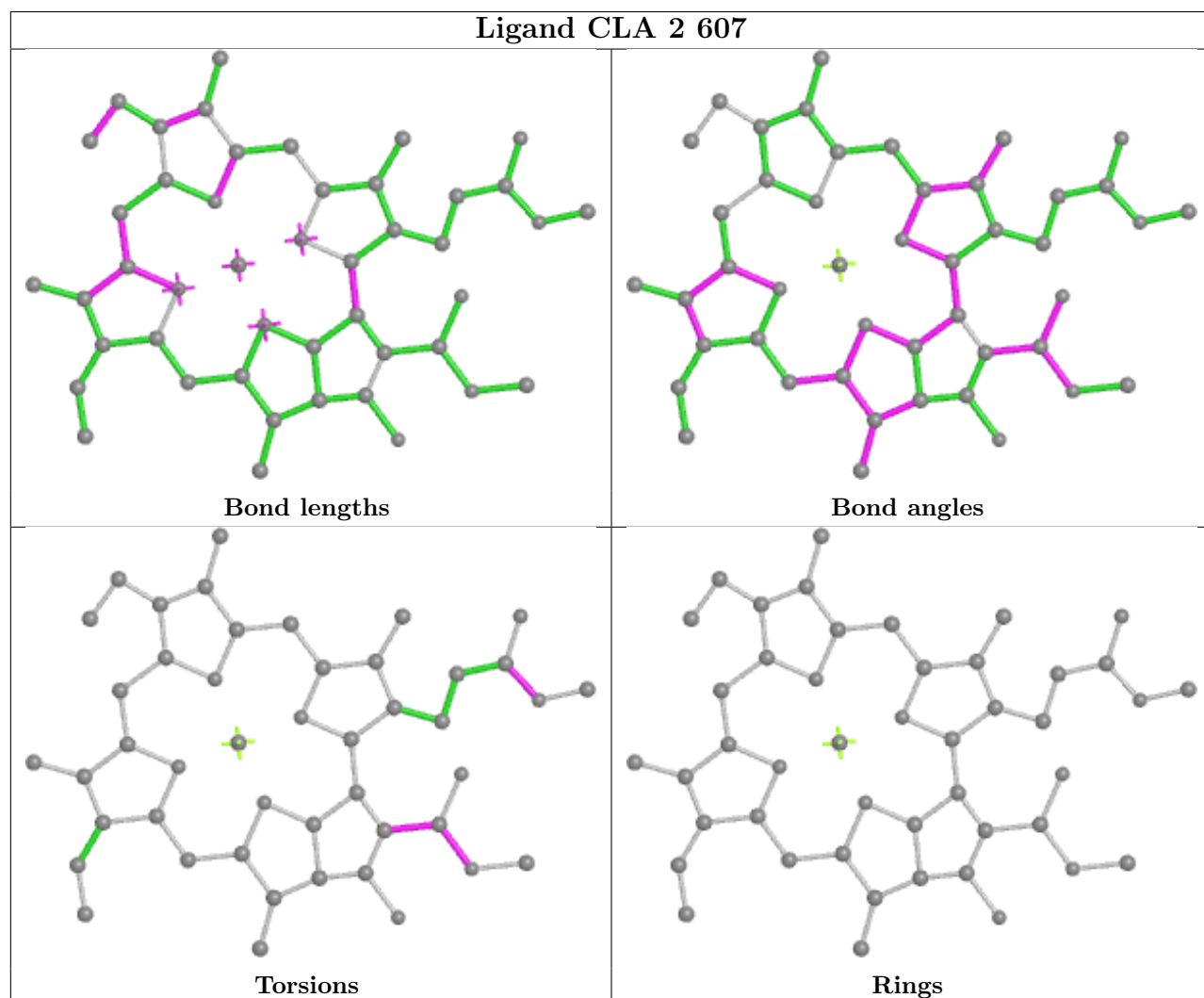
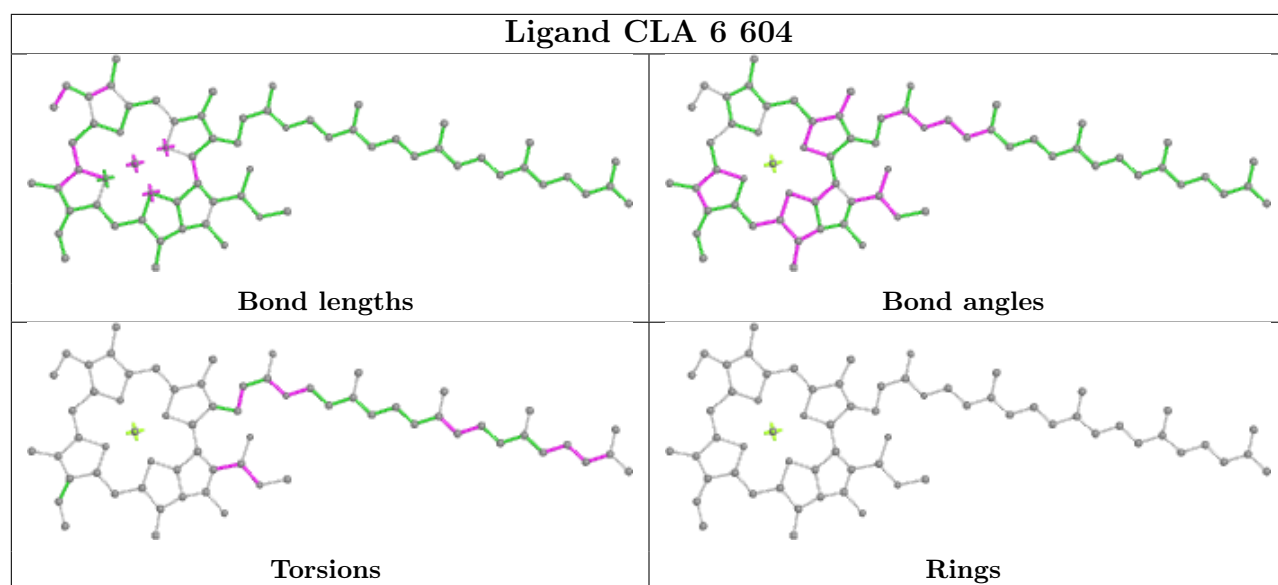


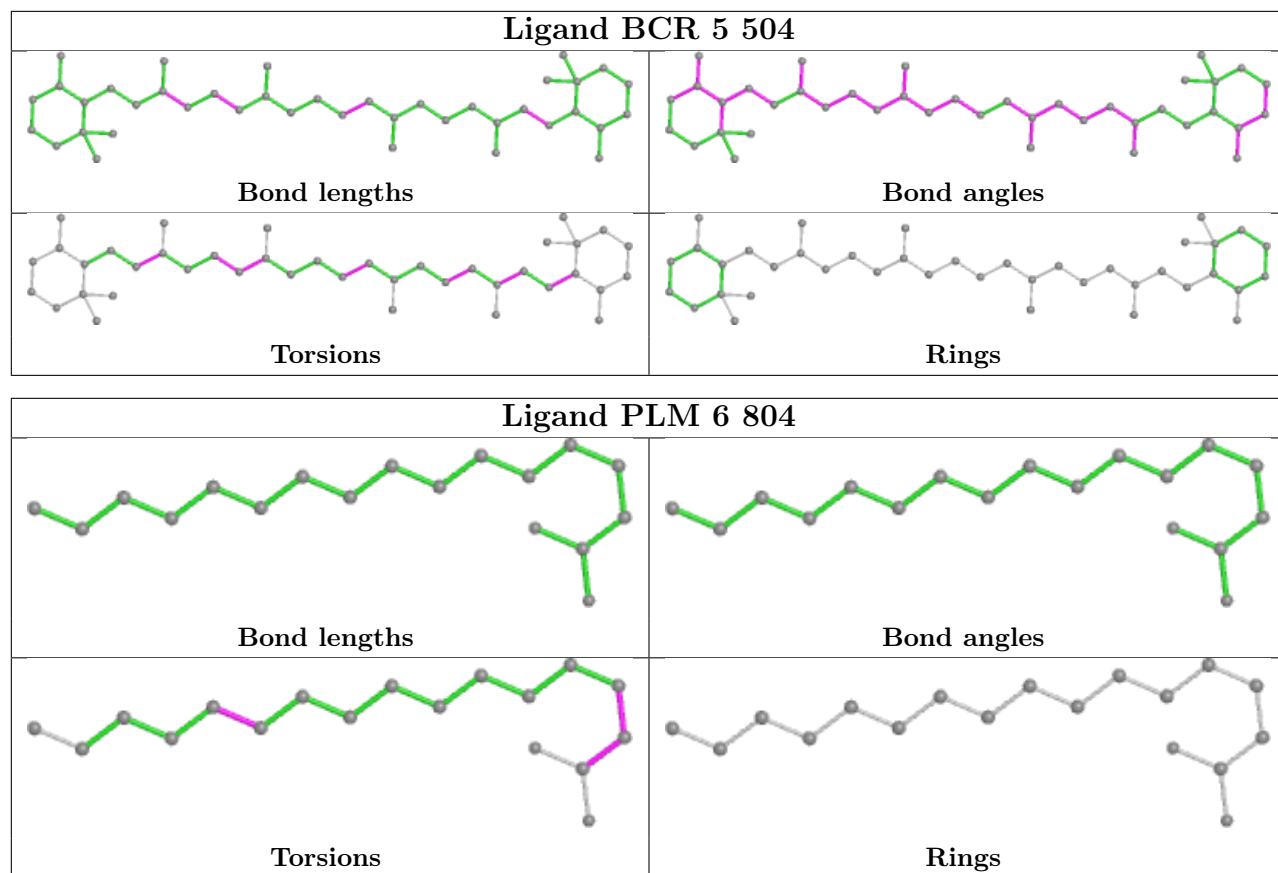


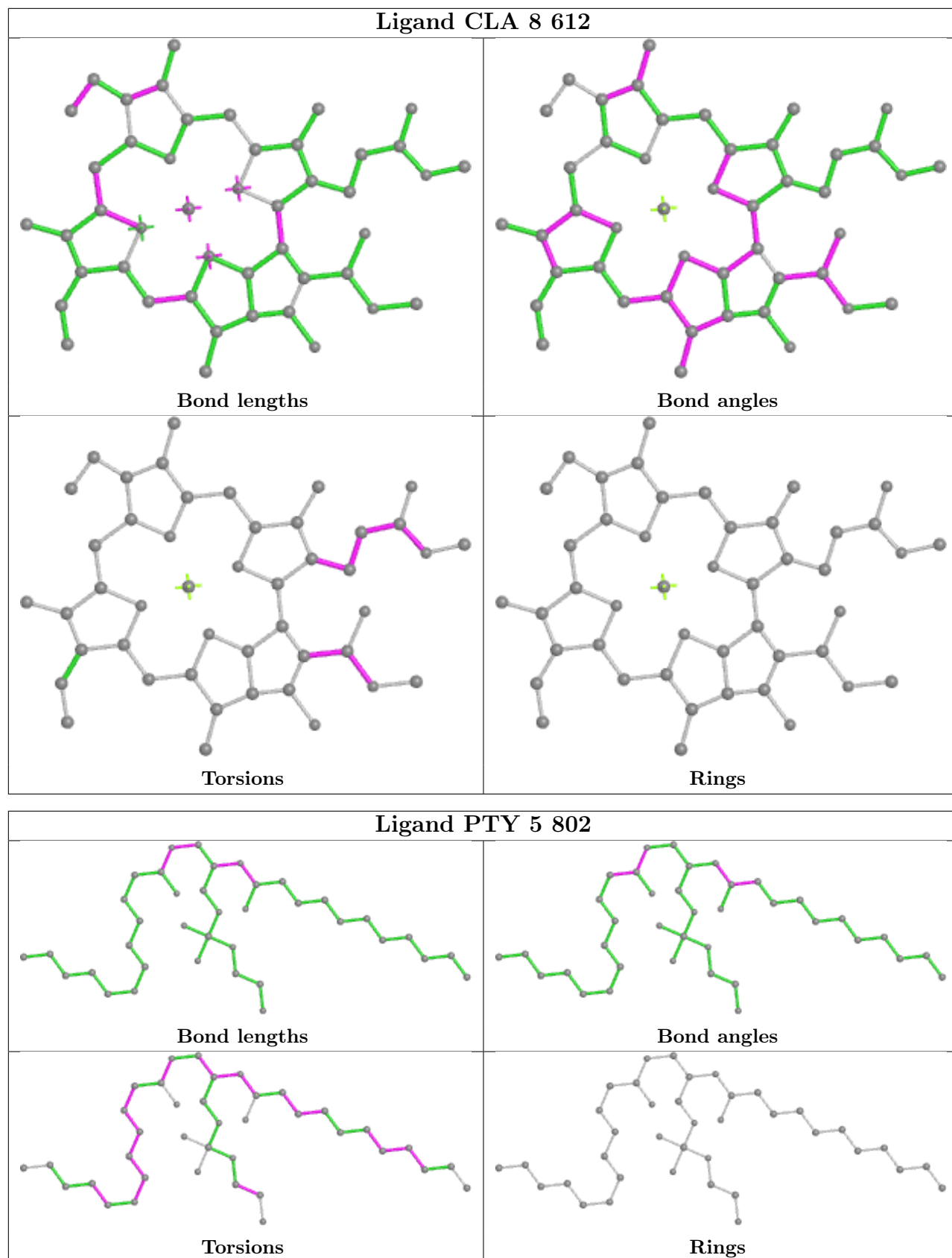


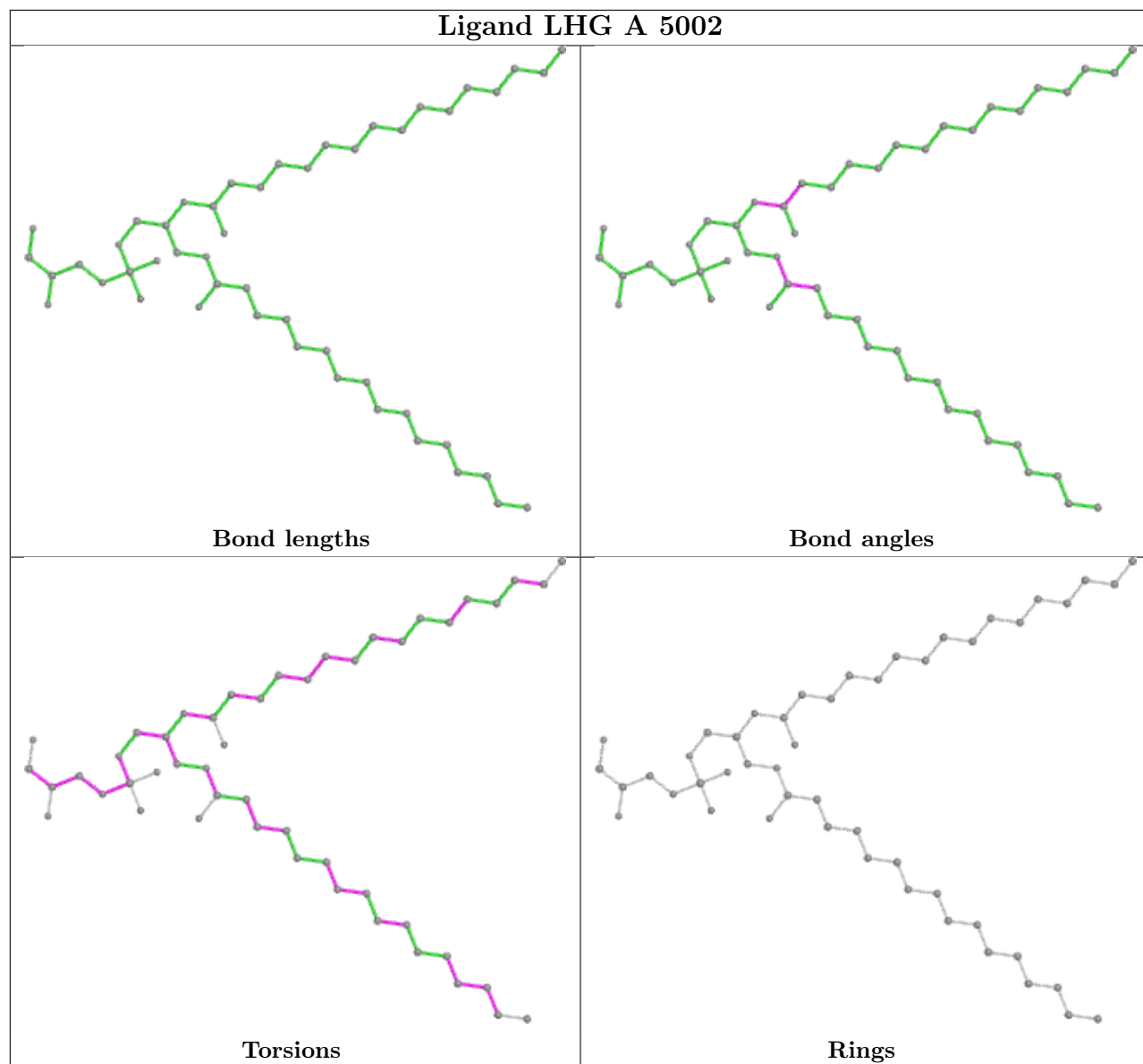


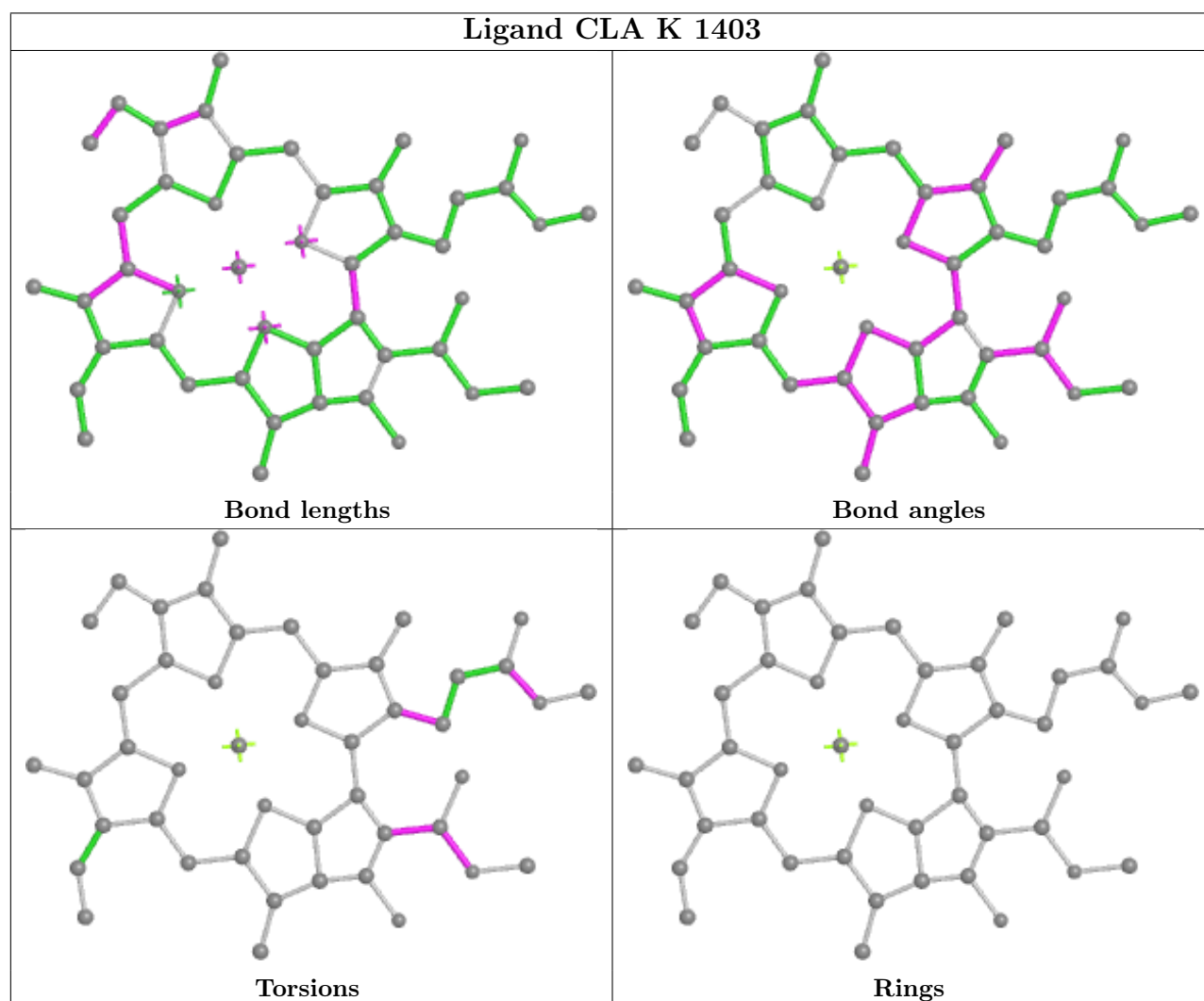
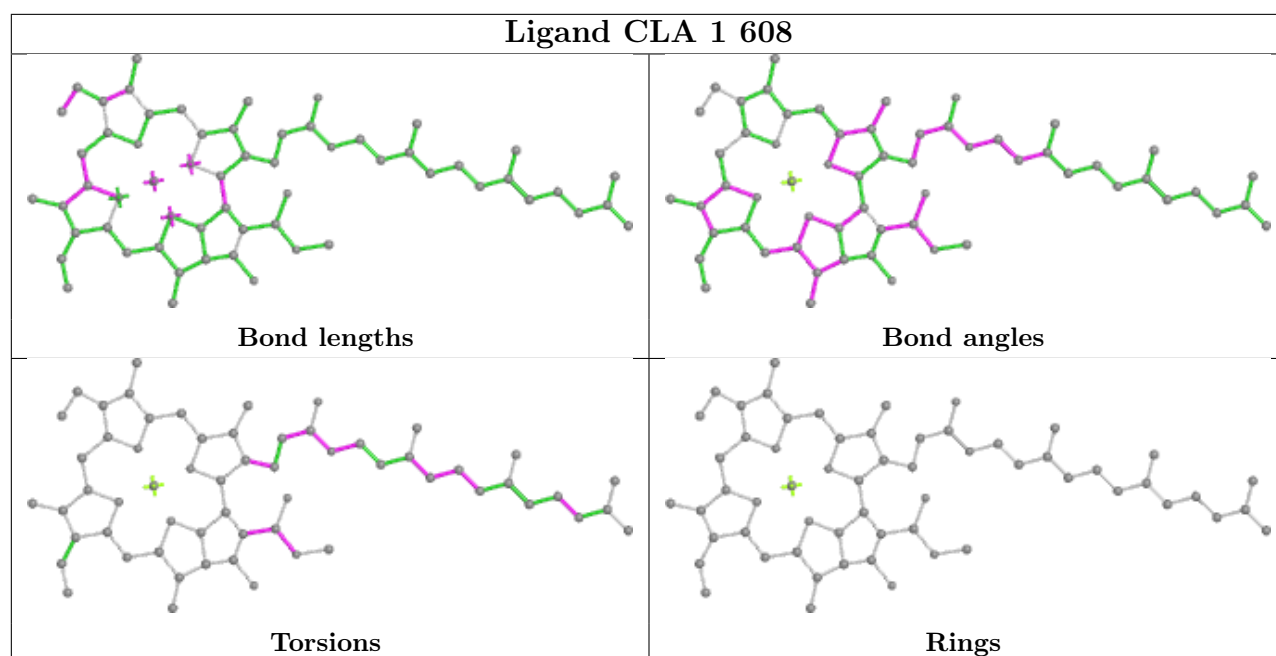


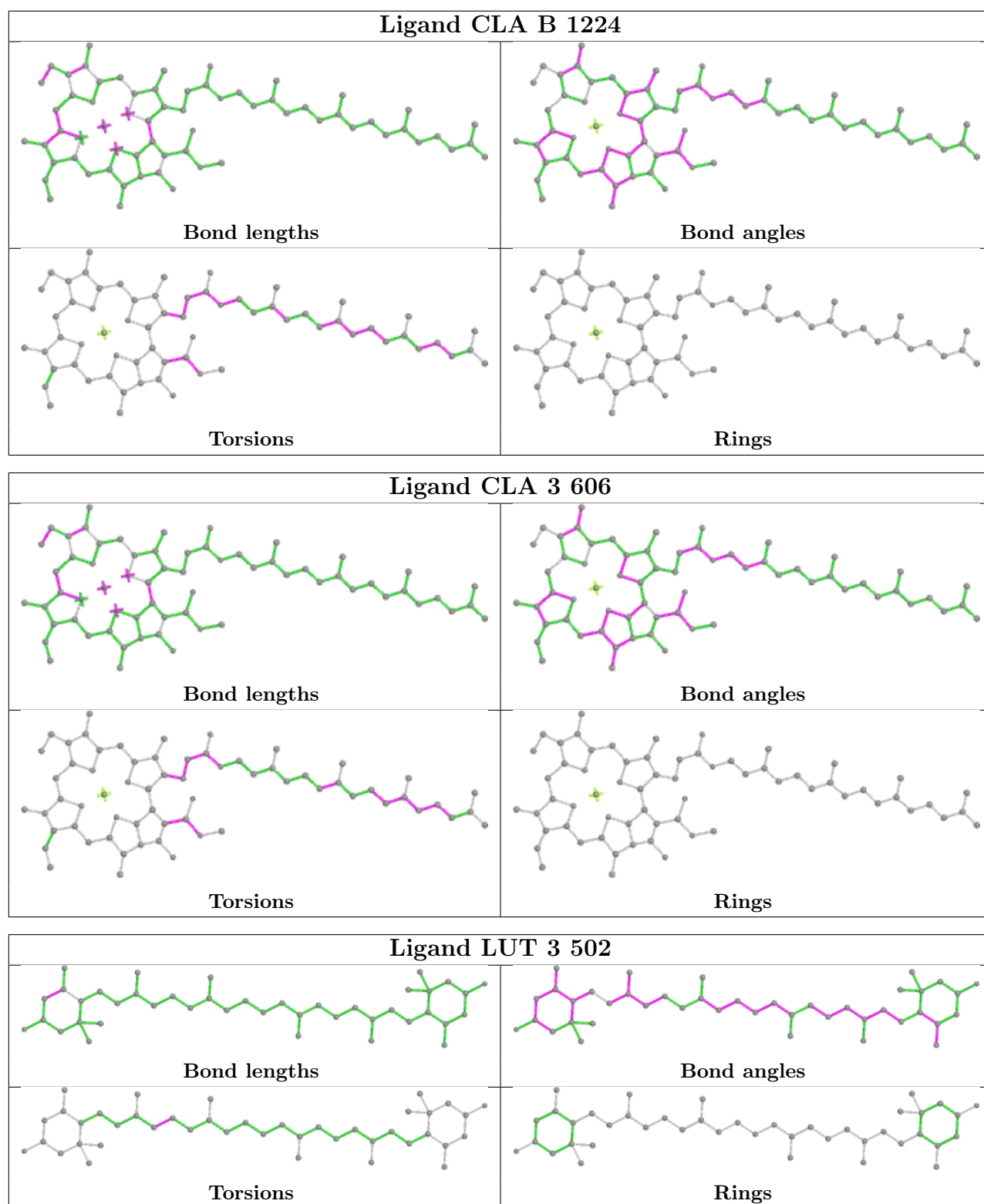


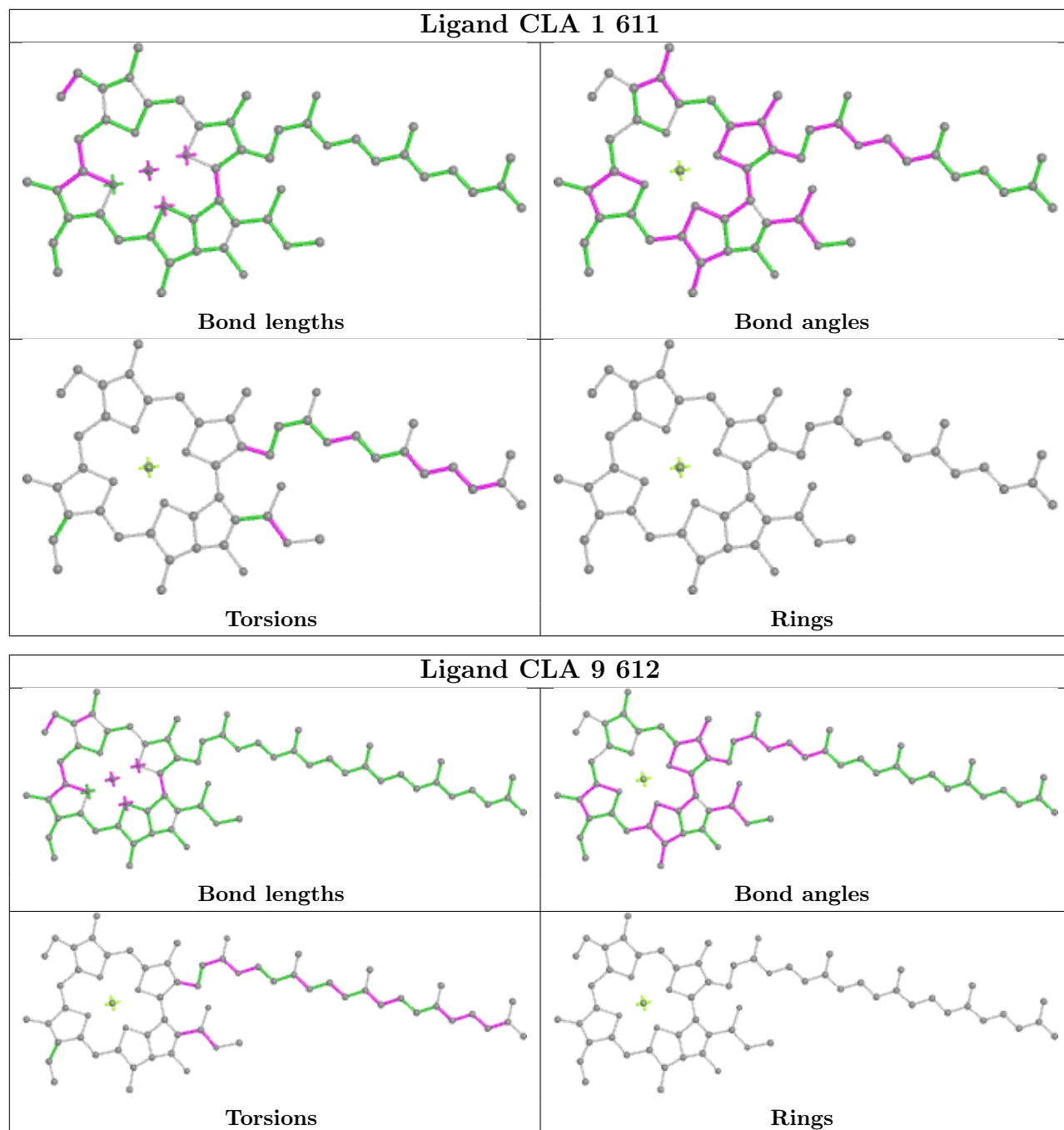


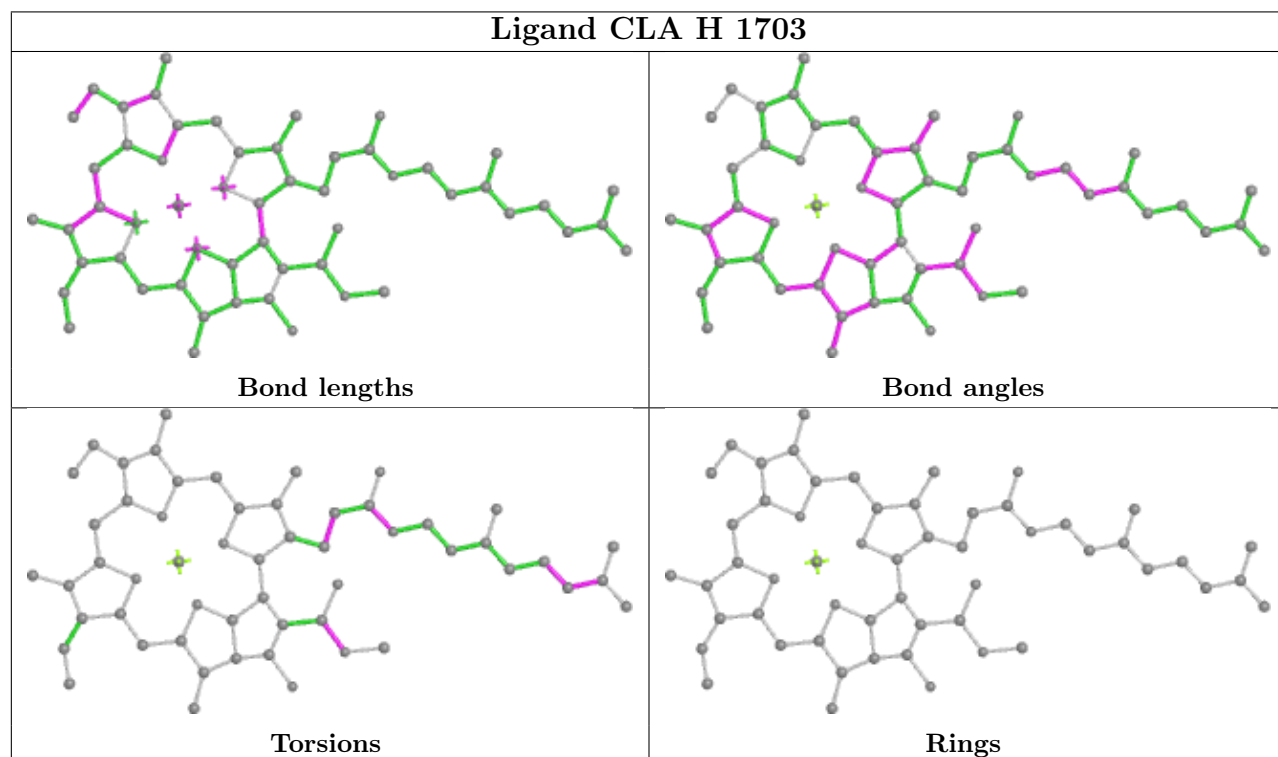
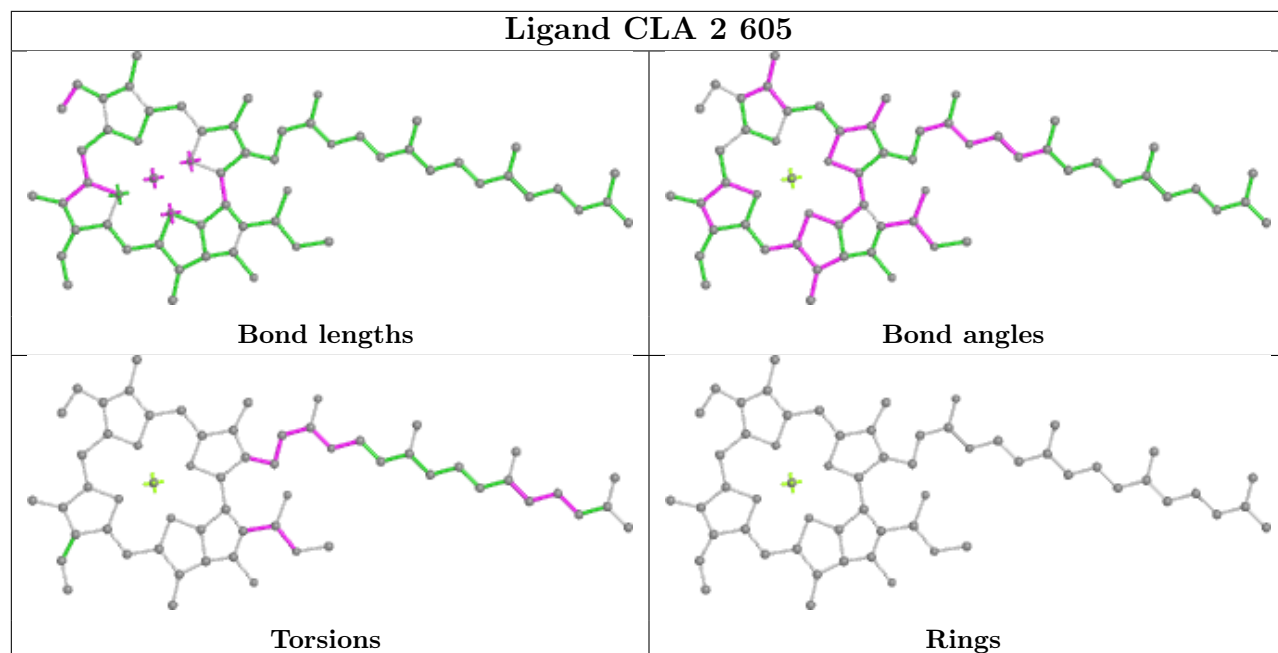


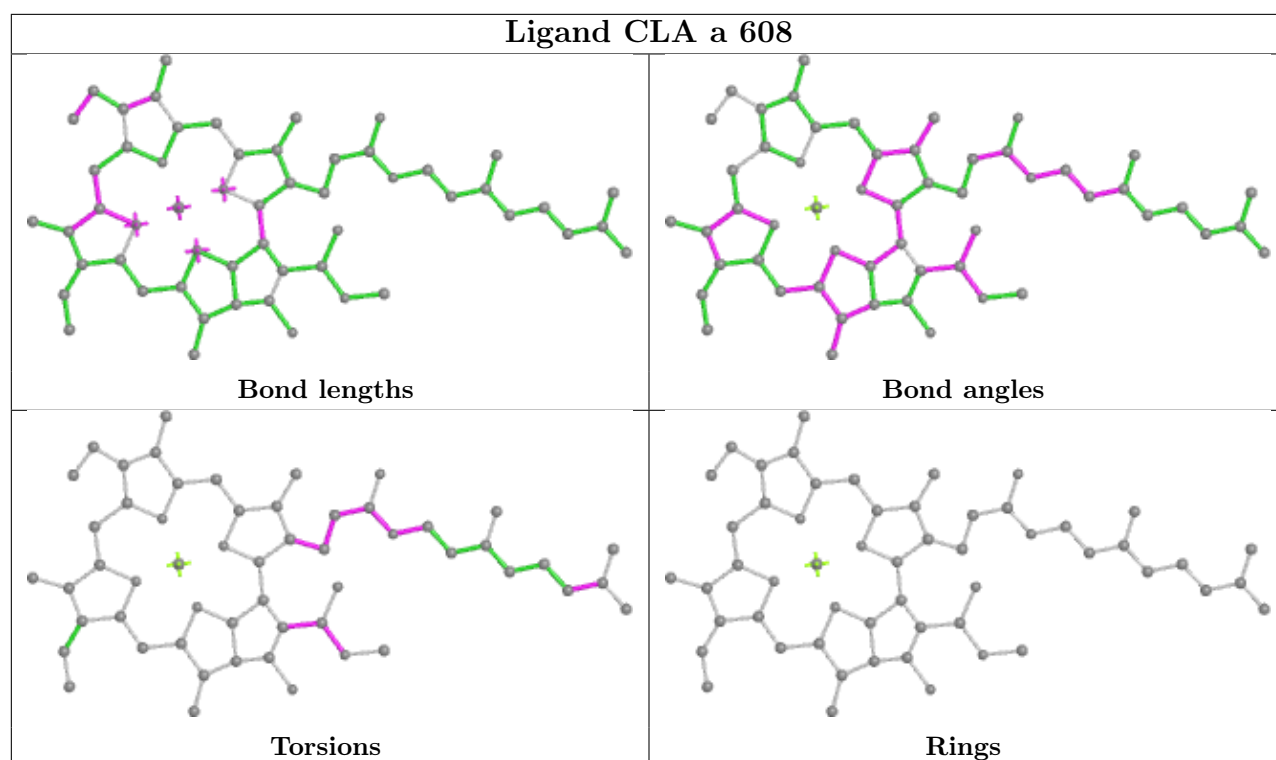












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

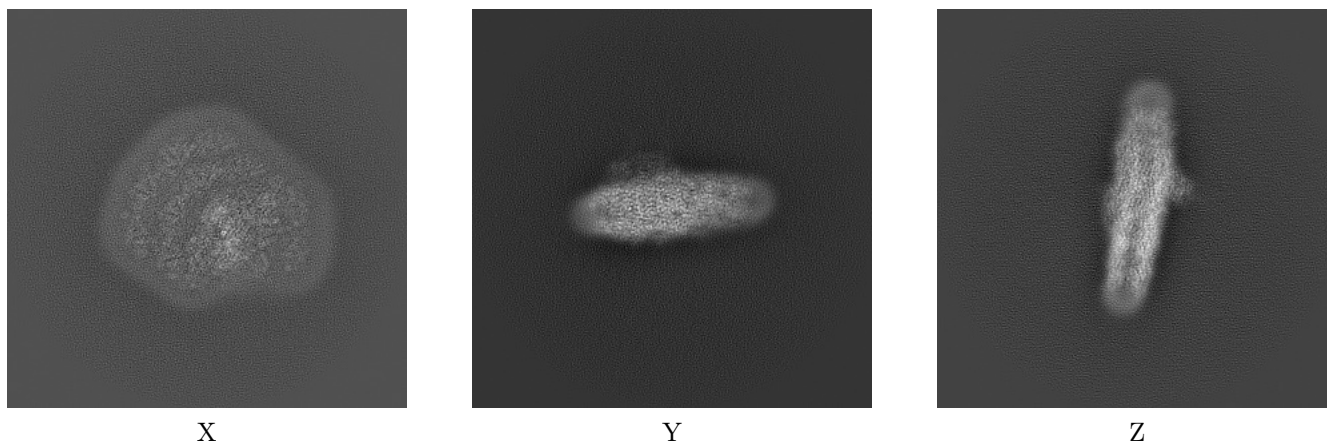
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11589. 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](#)

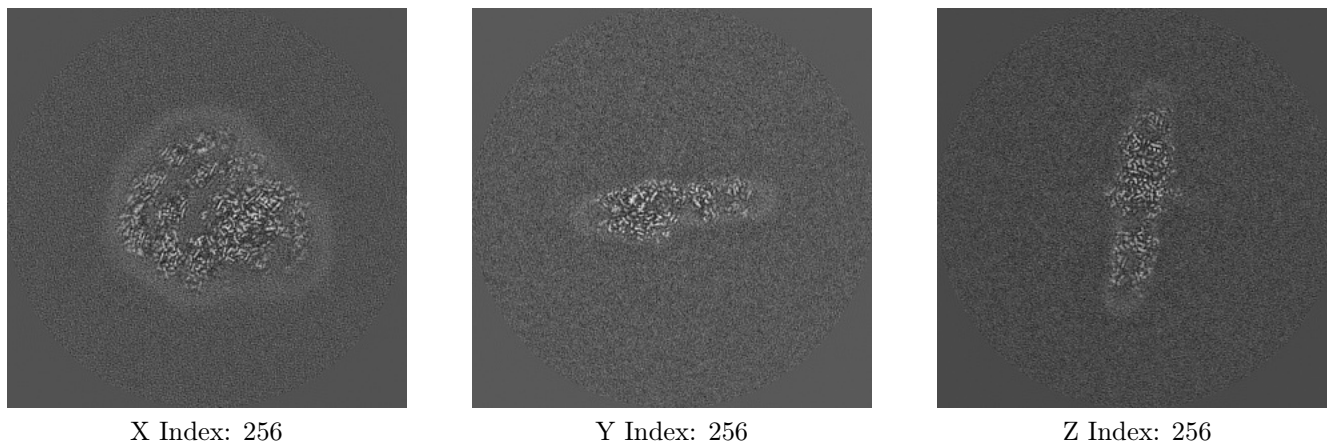
6.1.1 Primary map



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

6.2 Central slices [i](#)

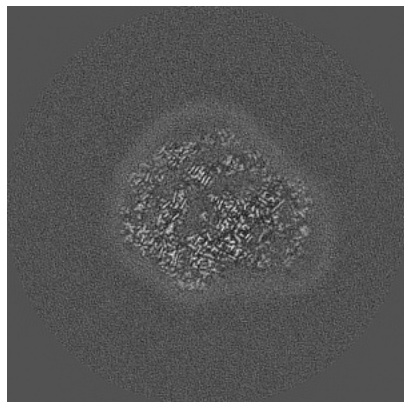
6.2.1 Primary map



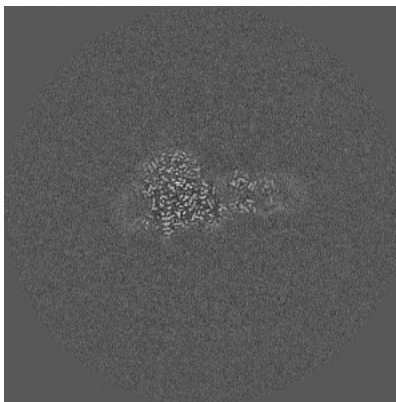
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

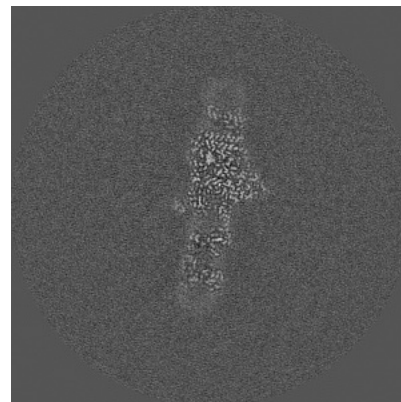
6.3.1 Primary map



X Index: 261



Y Index: 285



Z Index: 238

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 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

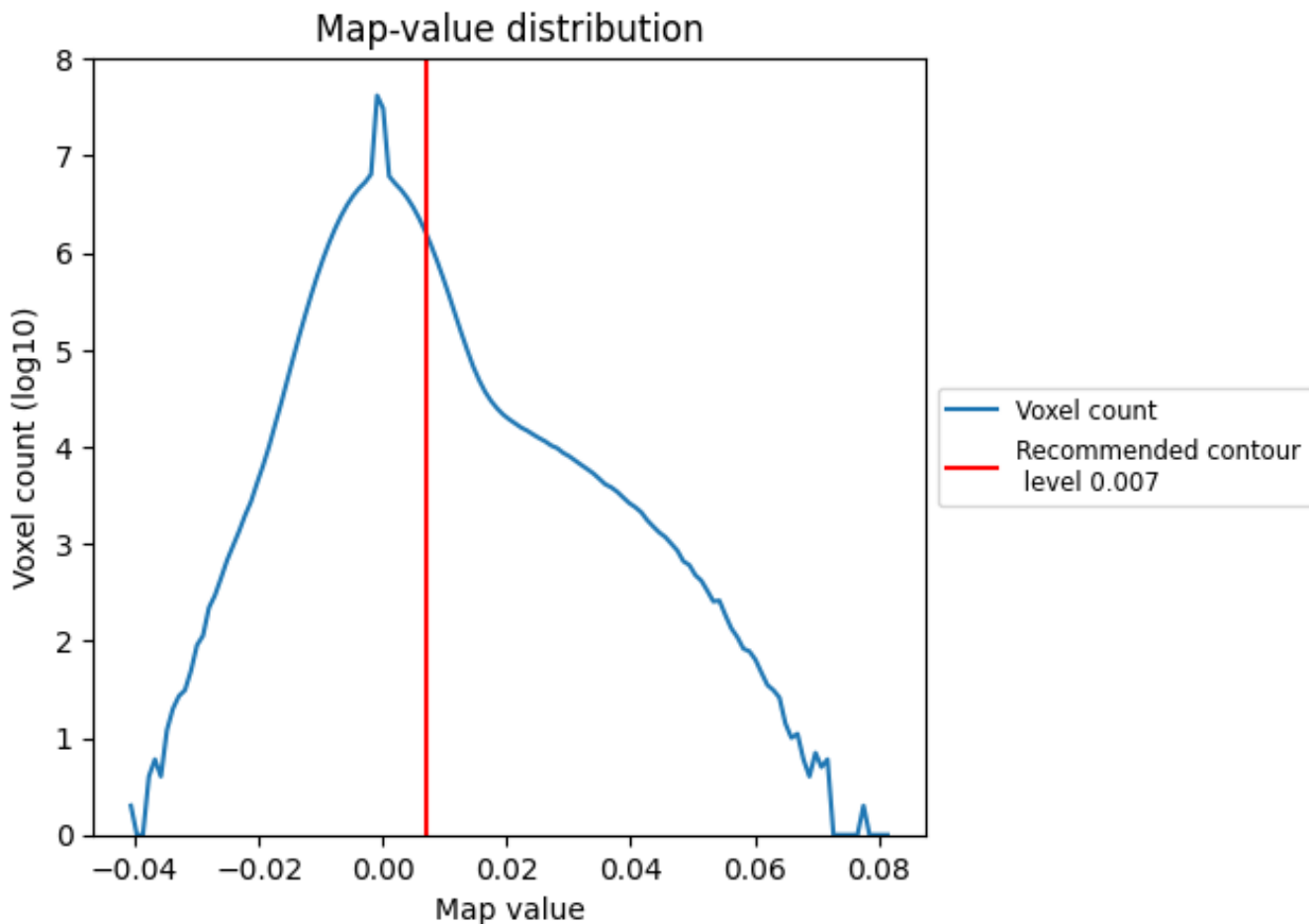
6.5 Mask visualisation

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

7 Map analysis [i](#)

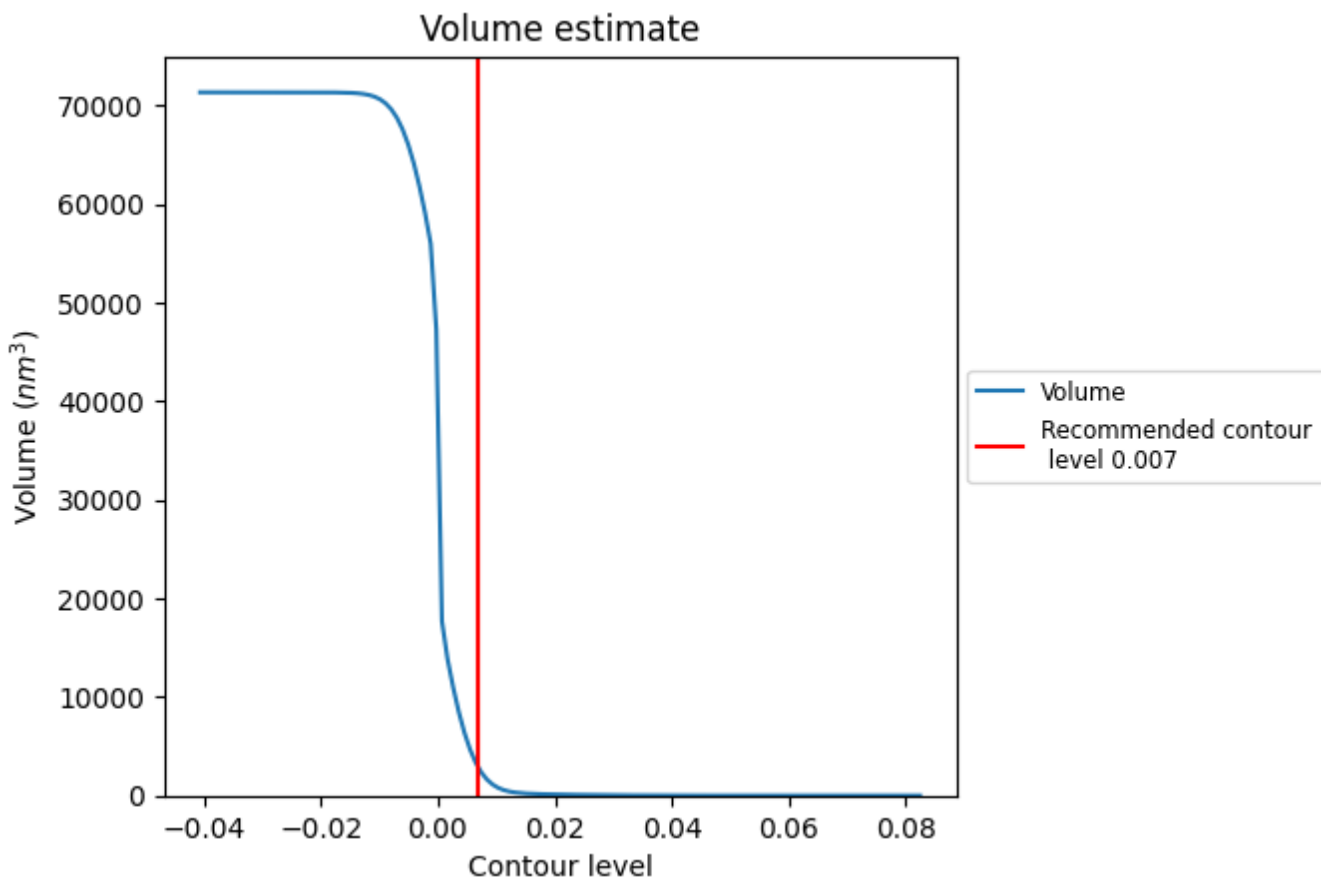
This section contains the results of statistical analysis of the map.

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.

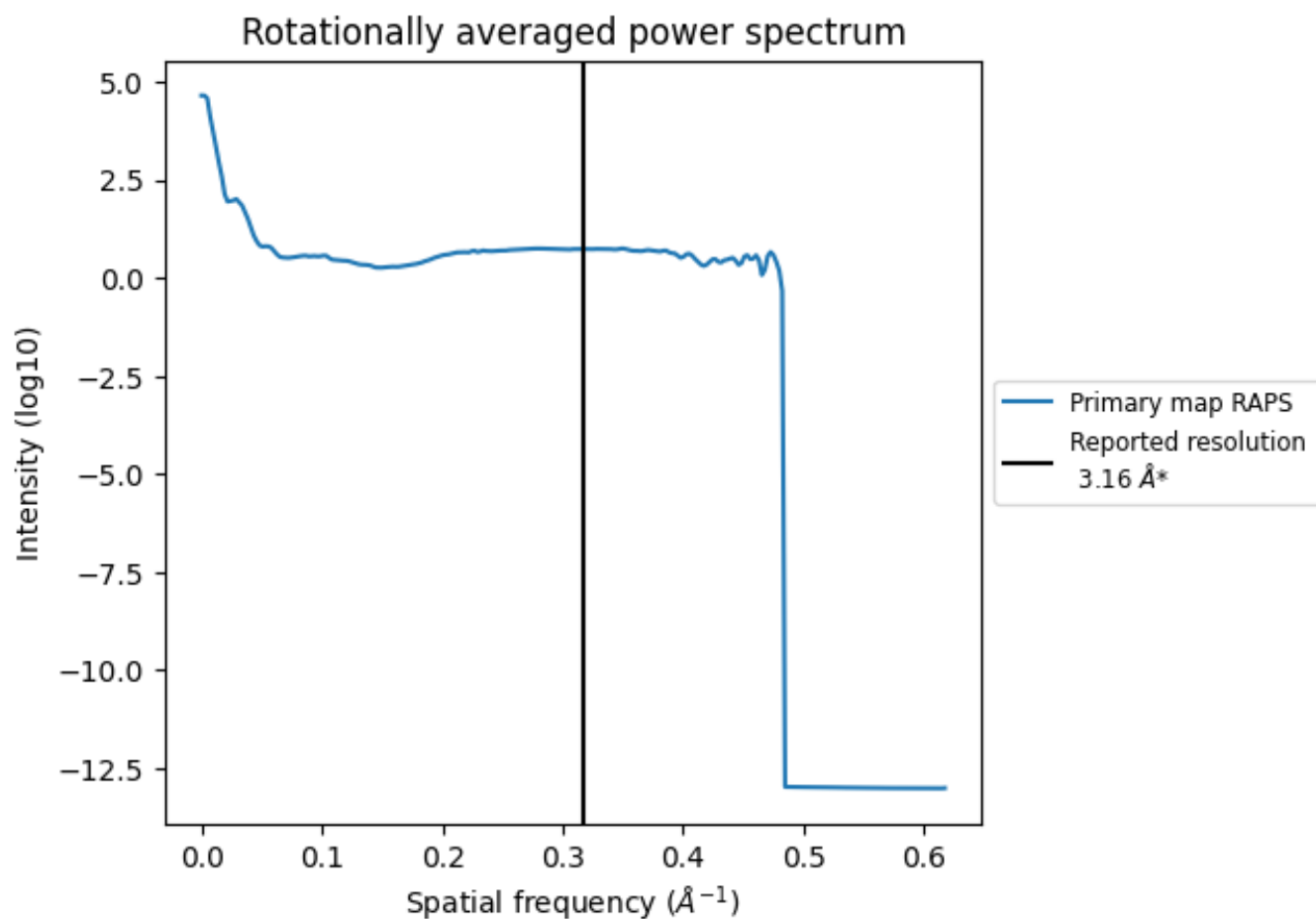
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2795 nm³; this corresponds to an approximate mass of 2525 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](#)

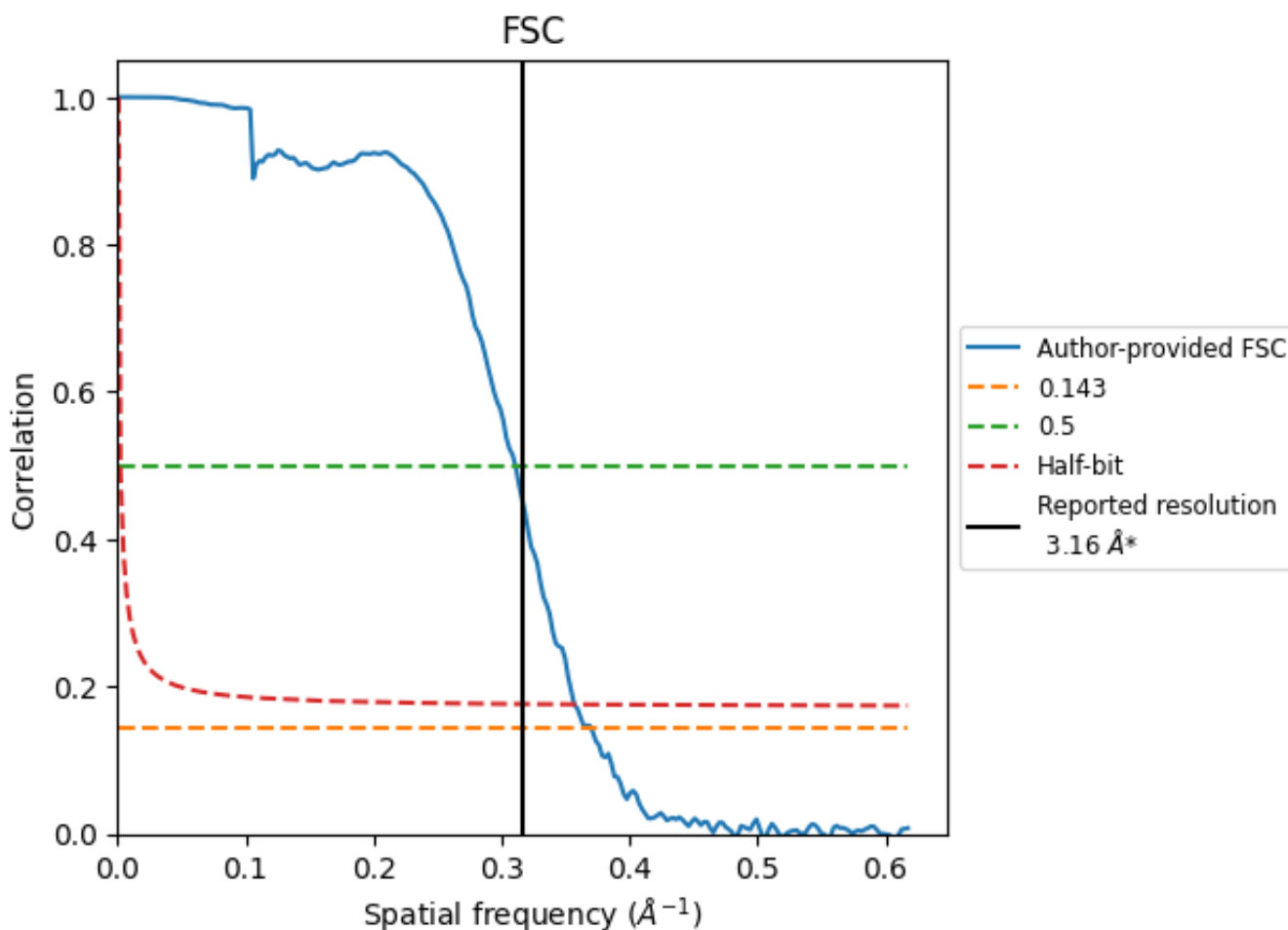


*Reported resolution corresponds to spatial frequency of 0.316\AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.316 Å⁻¹

8.2 Resolution estimates [i](#)

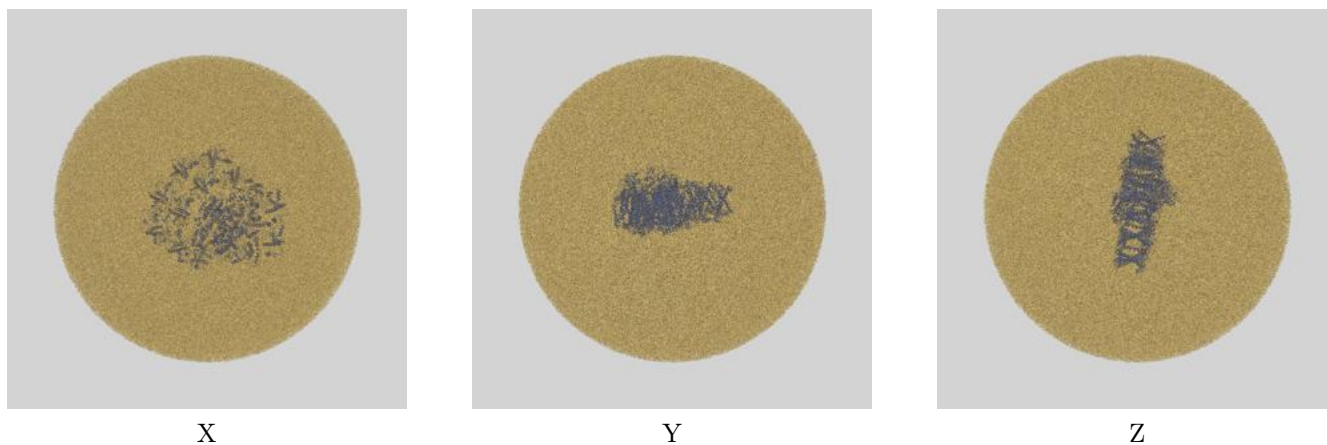
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	2.70	3.22	2.80
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.70 differs from the reported value 3.16 by more than 10 %

9 Map-model fit [i](#)

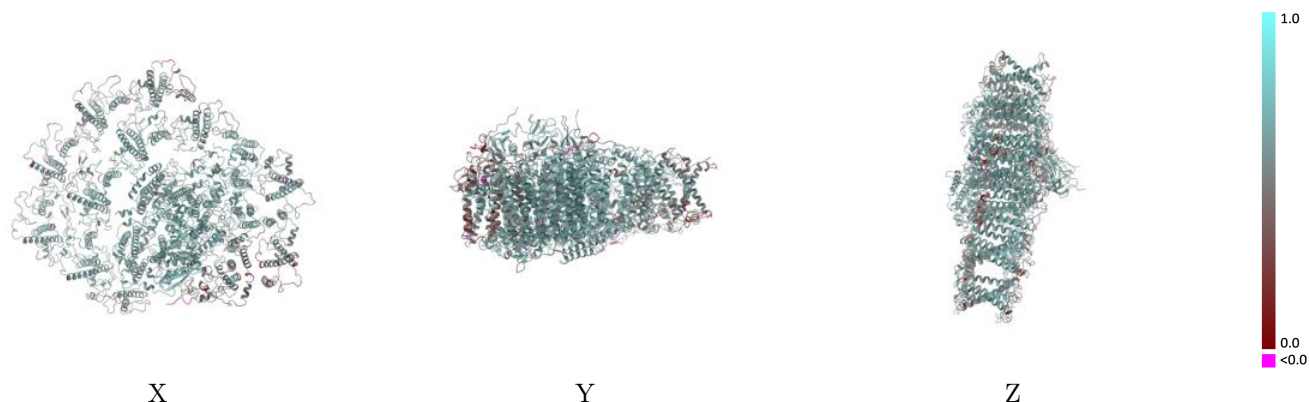
This section contains information regarding the fit between EMDB map EMD-11589 and PDB model 6ZZY. Per-residue inclusion information can be found in section 3 on page 51.

9.1 Map-model overlay [i](#)



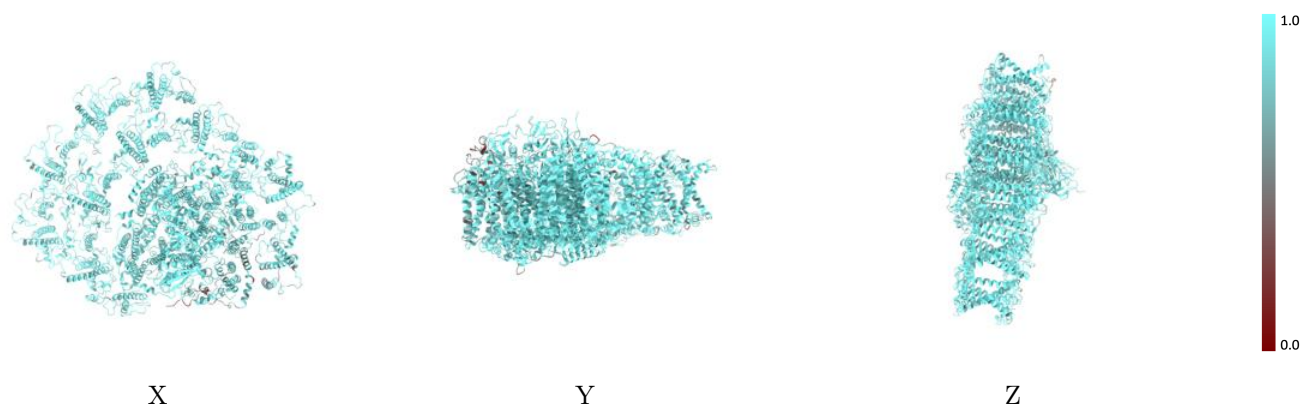
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



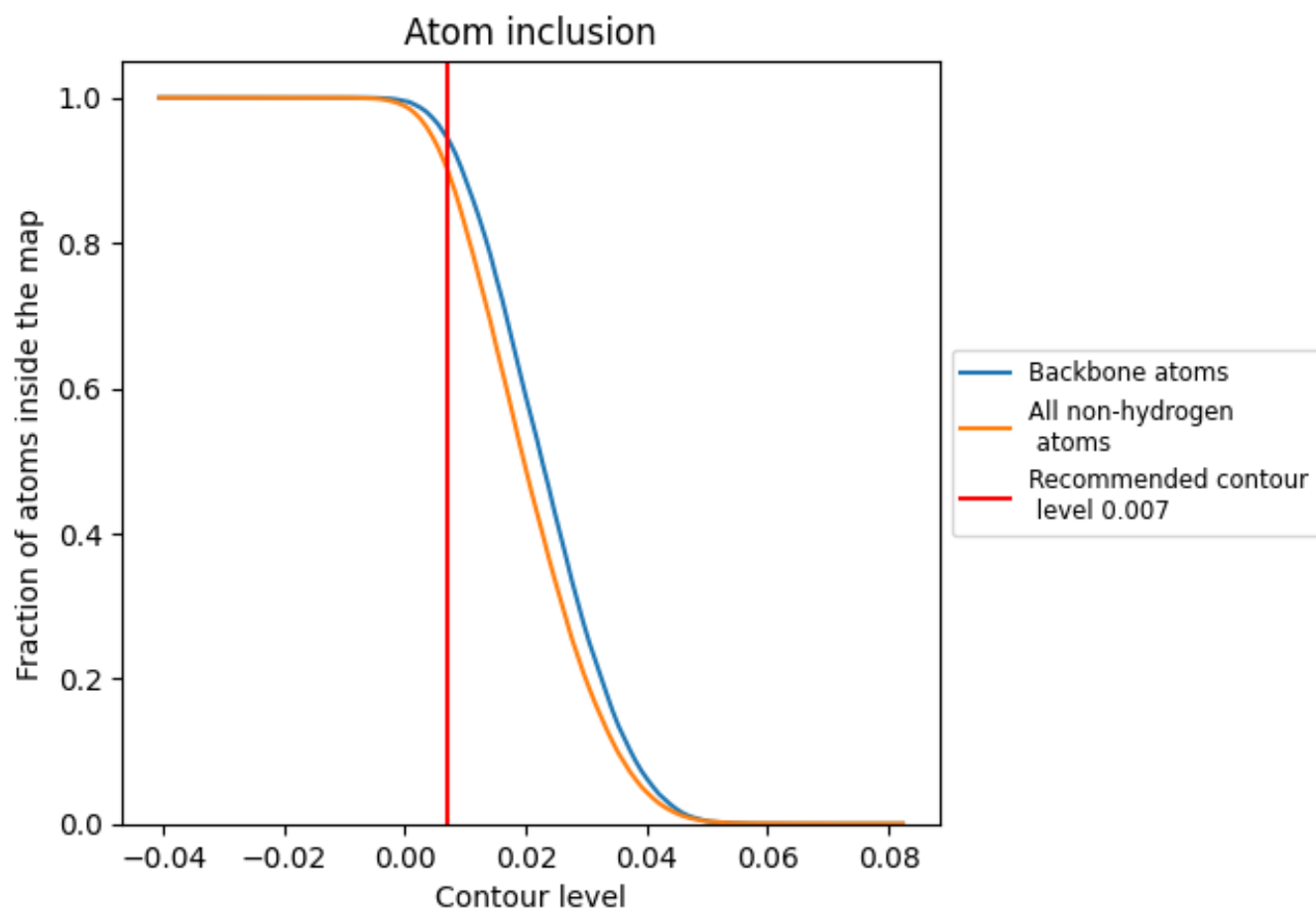
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

















































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9021	 0.5610
1	 0.8851	 0.5400
2	 0.8004	 0.4480
3	 0.9186	 0.5830
4	 0.8813	 0.5090
5	 0.8868	 0.5350
6	 0.8784	 0.5150
7	 0.9175	 0.5720
8	 0.9150	 0.5740
9	 0.8748	 0.5300
A	 0.9508	 0.6240
B	 0.9502	 0.6240
C	 0.9784	 0.6340
D	 0.9149	 0.5590
E	 0.9106	 0.5560
F	 0.9198	 0.5790
G	 0.8793	 0.5390
H	 0.6449	 0.3690
I	 0.8738	 0.5420
J	 0.9399	 0.5980
K	 0.8674	 0.5190
L	 0.8303	 0.4810
M	 0.9239	 0.5900
a	 0.8337	 0.4620

