



wwPDB EM Validation Summary Report ⓘ

Sep 11, 2026 – 06:41 am BST

PDB ID : 6ZOO / pdb_00006zoo
EMDB ID : EMD-11326
Title : Photosystem I reduced Plastocyanin Complex
Authors : Nelson, N.; Caspy, I.; Shkolnisky, Y.
Deposited on : 2020-07-07
Resolution : 2.74 Å(reported)
Based on initial model : 6YEZ

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:

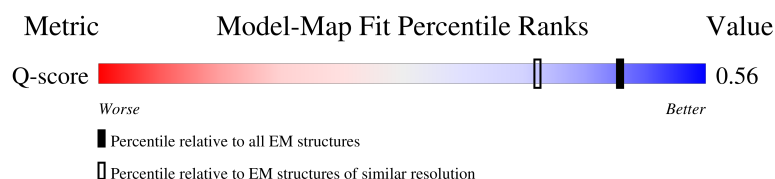
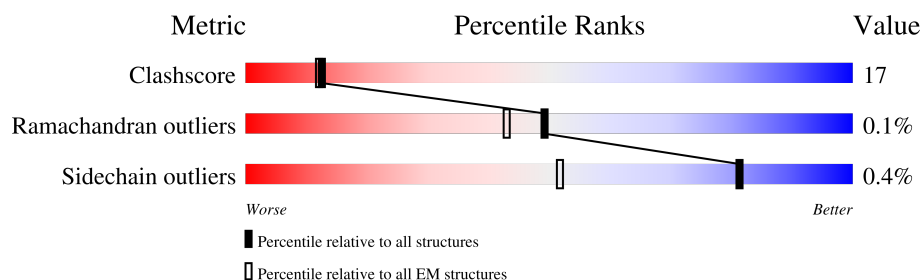
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.74 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.



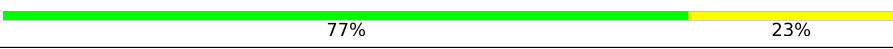
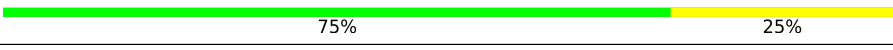
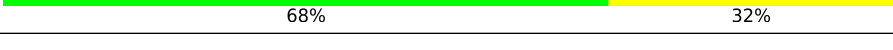
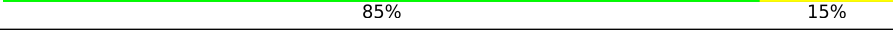
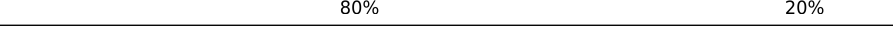
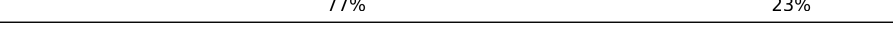
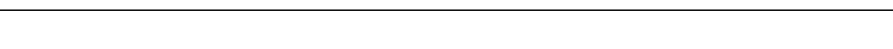
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10492 (2.24 - 3.24)

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	743	84% 16%
2	B	733	84% 16%
3	C	80	70% 30%
4	D	143	81% 18% .

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Mol	Chain	Length	Quality of chain
5	E	66	
6	F	154	
7	G	97	
8	H	93	
9	I	31	
10	J	42	
11	K	81	
12	L	159	
13	1	193	
14	2	208	
15	3	221	
16	4	198	
17	P	99	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	SNK	A	636	X	-	-	-
28	LUT	1	501	X	-	-	-
28	LUT	1	502	X	-	-	-
28	LUT	2	501	X	-	-	-
28	LUT	3	501	X	-	-	-
28	LUT	3	502	X	-	-	-
28	LUT	4	501	X	-	-	-
28	LUT	J	4013	X	-	-	-
29	CHL	1	609	X	-	-	-
29	CHL	1	612	X	-	-	-
29	CHL	2	609	X	-	-	-
29	CHL	2	610	X	-	-	-
29	CHL	2	615	X	-	-	-
29	CHL	3	604	X	-	-	-
29	CHL	4	613	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
29	CHL	4	615	X	-	-	-
30	XAT	2	502	X	-	-	-
30	XAT	4	502	X	-	-	-

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 38497 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
1	A	743	Total	C	N	O	S	0	0
			5866	3843	998	1005	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	733	Total	C	N	O	S	0	0
			5857	3848	998	997	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	80	Total	C	N	O	S	0	0
			612	379	107	115	11		

- Molecule 4 is a protein called PsaD.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	143	Total	C	N	O	S	0	0
			1132	731	194	204	3		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	69	GLY	-	insertion	UNP E1C9K8
D	70	PHE	-	insertion	UNP E1C9K8
D	71	THR	-	insertion	UNP E1C9K8
D	72	PRO	-	insertion	UNP E1C9K8
D	73	PRO	-	insertion	UNP E1C9K8
D	106	GLU	ASP	conflict	UNP E1C9K8
D	161	SER	ASN	conflict	UNP E1C9K8
D	180	PRO	ALA	conflict	UNP E1C9K8
D	187	VAL	GLN	conflict	UNP E1C9K8

- Molecule 5 is a protein called Putative uncharacterized protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	66	Total	C	N	O	0	0
			528	336	93	99		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	64	PRO	-	insertion	UNP E1C9K6
E	65	PRO	-	insertion	UNP E1C9K6
E	79	GLN	LYS	conflict	UNP E1C9K6
E	125	VAL	ILE	conflict	UNP E1C9K6
E	126	GLU	VAL	conflict	UNP E1C9K6
E	129	LYS	GLU	conflict	UNP E1C9K6

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	154	Total	C	N	O	S	0	0
			1206	782	207	215	2		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	80	ALA	SER	conflict	UNP A0A0M3KL12
F	87	ASP	GLU	conflict	UNP A0A0M3KL12
F	108	LEU	ILE	conflict	UNP A0A0M3KL12
F	111	PRO	ALA	conflict	UNP A0A0M3KL12
F	134	GLY	ALA	conflict	UNP A0A0M3KL12
F	188	ASP	GLU	conflict	UNP A0A0M3KL12
F	204	THR	SER	conflict	UNP A0A0M3KL12
F	205	GLY	ARG	conflict	UNP A0A0M3KL12

- Molecule 7 is a protein called photosystem I reaction center.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	97	Total	C	N	O	0	0
			757	492	125	140		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	106	THR	SER	conflict	UNP A0A0M3KL13

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Chain	Residue	Modelled	Actual	Comment	Reference
G	112	VAL	ALA	conflict	UNP A0A0M3KL13
G	113	SER	GLY	conflict	UNP A0A0M3KL13
G	114	LEU	VAL	conflict	UNP A0A0M3KL13
G	115	LEU	SER	conflict	UNP A0A0M3KL13
G	118	ASN	-	insertion	UNP A0A0M3KL13
G	119	ASP	-	insertion	UNP A0A0M3KL13
G	120	PRO	-	insertion	UNP A0A0M3KL13
G	121	VAL	-	insertion	UNP A0A0M3KL13
G	122	GLY	ALA	conflict	UNP A0A0M3KL13
G	123	PHE	ALA	conflict	UNP A0A0M3KL13
G	124	ASN	ALA	conflict	UNP A0A0M3KL13
G	125	ILE	LEU	conflict	UNP A0A0M3KL13

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	H	93	Total	C	N	O	0	0
			712	466	112	134		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	31	Total	C	N	O	S	0	0
			240	165	38	36	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	42	Total	C	N	O	S	0	0
			338	231	51	55	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	32	PHE	LEU	conflict	UNP D5MAL3

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	81	Total	C	N	O	S	0	0
			569	362	99	105	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	86	ALA	VAL	conflict	UNP E1C9L3

- Molecule 12 is a protein called PsaL domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	159	Total	C	N	O	S	0	0
			1197	788	191	217	1		

- Molecule 13 is a protein called Chlorophyll a-b binding protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	1	193	Total	C	N	O	S	0	0
			1508	982	252	269	5		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	40	ASP	HIS	conflict	UNP Q01667
1	45	GLN	GLU	conflict	UNP Q01667
1	49	SER	ALA	conflict	UNP Q01667
1	65	ARG	GLY	conflict	UNP Q01667
1	71	GLU	ALA	conflict	UNP Q01667
1	76	PHE	TYR	conflict	UNP Q01667
1	102	LEU	TYR	conflict	UNP Q01667
1	136	VAL	ALA	conflict	UNP Q01667
1	141	SER	ALA	conflict	UNP Q01667
1	177	PHE	LEU	conflict	UNP Q01667
1	178	HIS	GLU	conflict	UNP Q01667
1	180	TYR	LEU	conflict	UNP Q01667
1	182	ILE	VAL	conflict	UNP Q01667
1	185	VAL	ILE	conflict	UNP Q01667
1	198	ILE	PHE	conflict	UNP Q01667
1	225	THR	ASN	conflict	UNP Q01667
1	228	ASN	ASP	conflict	UNP Q01667
1	229	VAL	ILE	conflict	UNP Q01667
1	230	LEU	VAL	conflict	UNP Q01667

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2	208	Total	C	N	O	S	0	0
			1620	1059	265	292	4		

- Molecule 15 is a protein called Chlorophyll a-b binding protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	3	221	Total	C	N	O	S	0	0
			1706	1118	278	305	5		

- Molecule 16 is a protein called Chlorophyll a-b binding protein P4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	4	198	Total	C	N	O	S	0	0
			1559	1022	253	281	3		

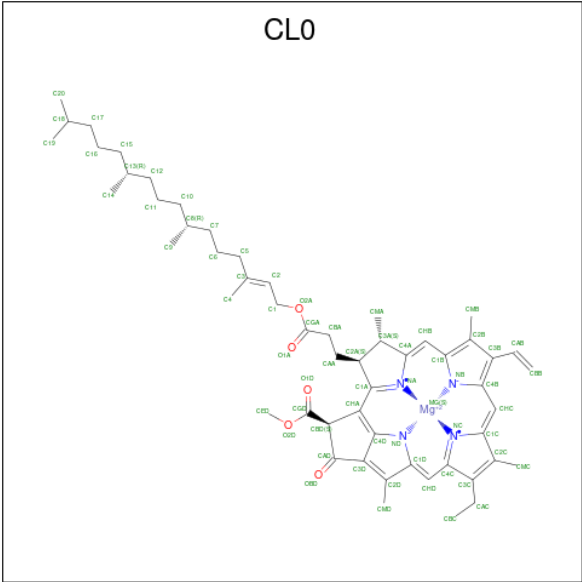
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	89	LYS	ARG	conflict	UNP Q9SQL2
4	128	ASP	ALA	conflict	UNP Q9SQL2
4	149	PHE	SER	conflict	UNP Q9SQL2

- Molecule 17 is a protein called Plastocyanin, chloroplastic.

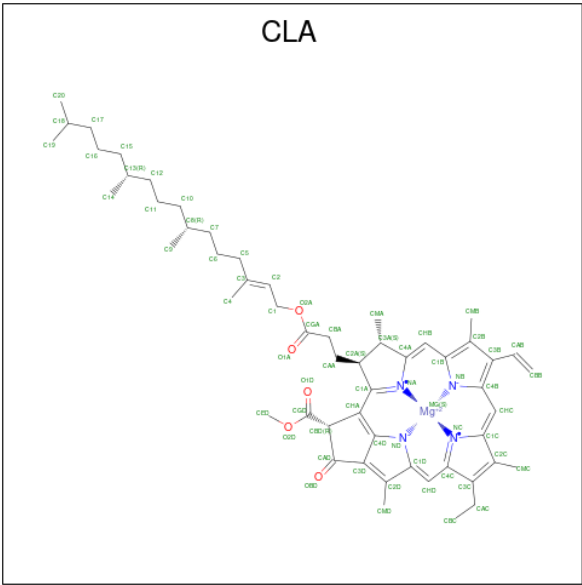
Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	99	Total	C	N	O	S	0	0
			728	460	115	150	3		

- Molecule 18 is CHLOROPHYLL A ISOMER (CCD ID: CL0) (formula: C₅₅H₇₂MgN₄O₅).



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

- Molecule 19 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅).



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

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Mol	Chain	Residues	Atoms					AltConf
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 56	C 46	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	A	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	A	1	Total 51	C 41	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	A	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	A	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	A	1	Total 45	C 35	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	B	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	B	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 55	C 45	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	B	1	Total 58	C 48	Mg 1	N 4	O 5	0
19	B	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	B	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	B	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	B	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	F	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	F	1	Total 65	C 55	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
19	G	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	G	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	G	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	H	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	J	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	K	1	Total 45	C 35	Mg 1	N 4	O 5	0
19	K	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	K	1	Total 48	C 38	Mg 1	N 4	O 5	0
19	K	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	L	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	L	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	L	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	1	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	1	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	1	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	1	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	1	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	1	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	1	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	1	1	Total 46	C 36	Mg 1	N 4	O 5	0
19	1	1	Total 65	C 55	Mg 1	N 4	O 5	0

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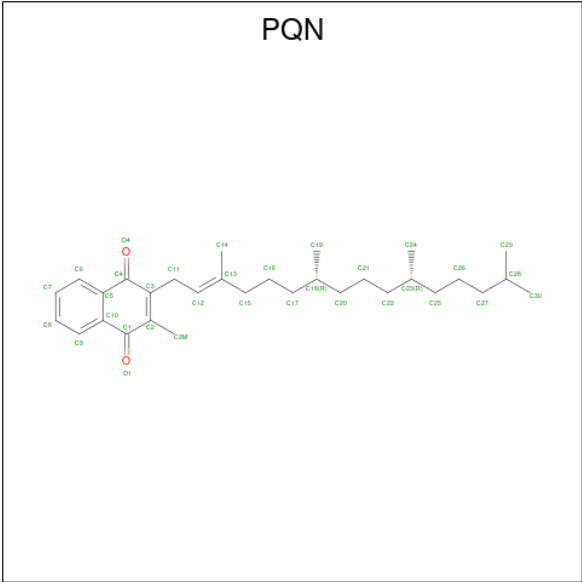
Mol	Chain	Residues	Atoms					AltConf
19	1	1	Total 45	C 35	Mg 1	N 4	O 5	0
19	1	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	2	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	2	1	Total 52	C 42	Mg 1	N 4	O 5	0
19	2	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	2	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	2	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	2	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	2	1	Total 60	C 50	Mg 1	N 4	O 5	0
19	2	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	2	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	3	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	3	1	Total 52	C 42	Mg 1	N 4	O 5	0
19	3	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	3	1	Total 55	C 45	Mg 1	N 4	O 5	0
19	3	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	3	1	Total 52	C 42	Mg 1	N 4	O 5	0
19	3	1	Total 48	C 38	Mg 1	N 4	O 5	0
19	3	1	Total 65	C 55	Mg 1	N 4	O 5	0
19	3	1	Total 50	C 40	Mg 1	N 4	O 5	0
19	3	1	Total 46	C 36	Mg 1	N 4	O 5	0

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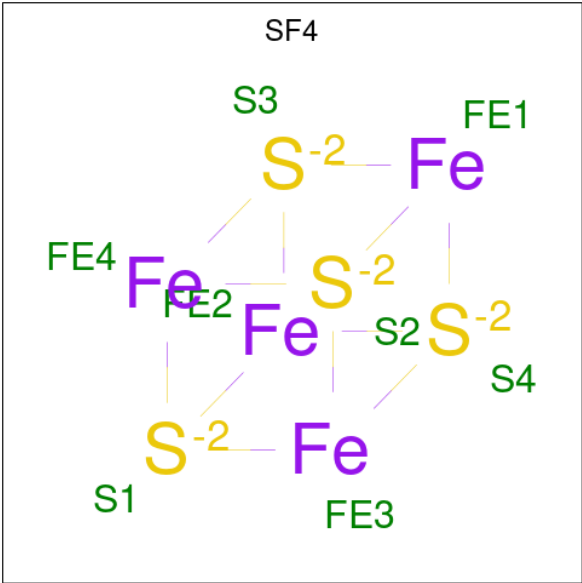
Mol	Chain	Residues	Atoms					AltConf
19	3	1	Total	C	Mg	N	O	0
			42	34	1	4	3	
19	3	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			46	36	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
19	4	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

- Molecule 20 is PHYLLOQUINONE (CCD ID: PQN) (formula: C₃₁H₄₆O₂).



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

- Molecule 21 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



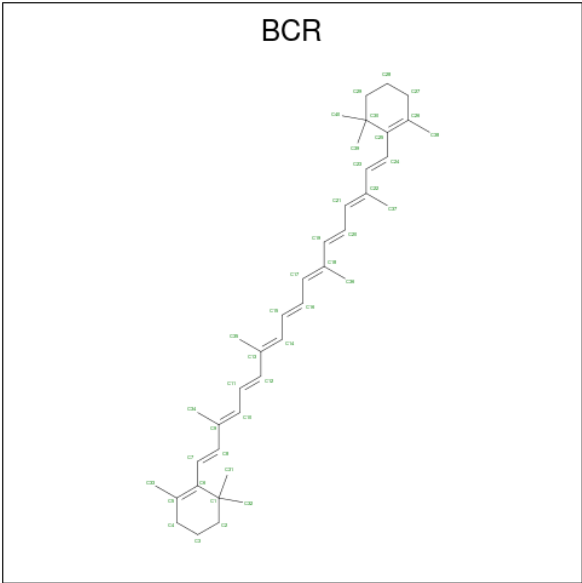
Mol	Chain	Residues	Atoms			AltConf
21	A	1	Total	Fe	S	0
			8	4	4	
21	C	1	Total	Fe	S	0
			8	4	4	

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Mol	Chain	Residues	Atoms			AltConf
21	C	1	Total	Fe	S	0
			8	4	4	

- Molecule 22 is BETA-CAROTENE (CCD ID: BCR) (formula: C₄₀H₅₆).



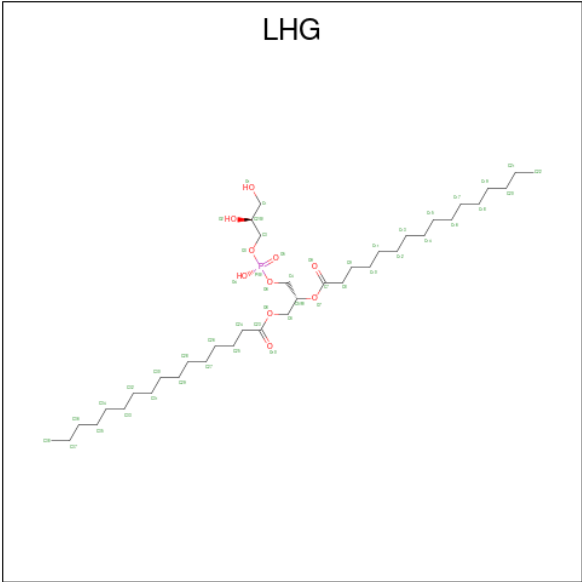
Mol	Chain	Residues	Atoms		AltConf
22	A	1	Total	C	0
			40	40	
22	A	1	Total	C	0
			40	40	
22	A	1	Total	C	0
			40	40	
22	A	1	Total	C	0
			40	40	
22	A	1	Total	C	0
			40	40	
22	A	1	Total	C	0
			40	40	
22	B	1	Total	C	0
			40	40	
22	B	1	Total	C	0
			40	40	
22	B	1	Total	C	0
			40	40	
22	B	1	Total	C	0
			40	40	

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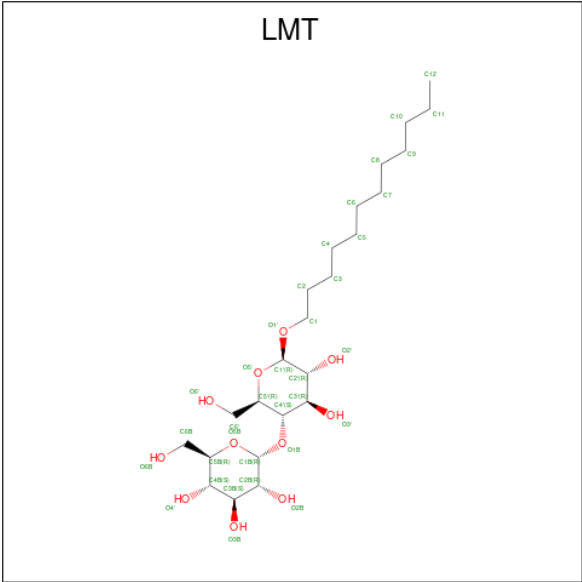
Mol	Chain	Residues	Atoms	AltConf
22	B	1	Total C 40 40	0
22	F	1	Total C 40 40	0
22	F	1	Total C 40 40	0
22	G	1	Total C 40 40	0
22	H	1	Total C 40 40	0
22	I	1	Total C 40 40	0
22	I	1	Total C 40 40	0
22	J	1	Total C 40 40	0
22	K	1	Total C 40 40	0
22	K	1	Total C 40 40	0
22	L	1	Total C 40 40	0
22	L	1	Total C 40 40	0
22	1	1	Total C 40 40	0
22	1	1	Total C 40 40	0
22	2	1	Total C 40 40	0
22	3	1	Total C 40 40	0
22	3	1	Total C 40 40	0

- Molecule 23 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: $C_{38}H_{75}O_{10}P$).



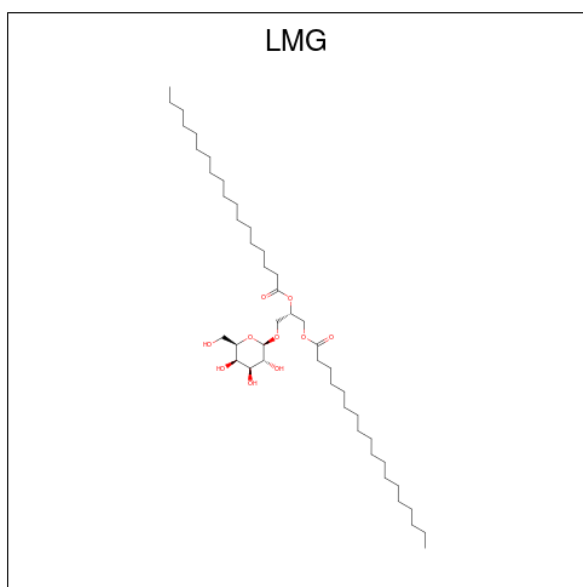
Mol	Chain	Residues	Atoms				AltConf
23	A	1	Total	C	O	P	0
			40	29	10	1	
23	A	1	Total	C	O	P	0
			49	38	10	1	
23	B	1	Total	C	O	P	0
			21	10	10	1	
23	B	1	Total	C	O	P	0
			49	38	10	1	
23	1	1	Total	C	O	P	0
			49	38	10	1	
23	2	1	Total	C	O	P	0
			35	24	10	1	
23	3	1	Total	C	O	P	0
			17	8	8	1	
23	4	1	Total	C	O	P	0
			35	24	10	1	

- Molecule 24 is DODECYL-BETA-D-MALTOSIDE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



Mol	Chain	Residues	Atoms			AltConf
24	A	1	Total	C	O	0
			35	24	11	
24	B	1	Total	C	O	0
			31	20	11	
24	B	1	Total	C	O	0
			32	21	11	
24	G	1	Total	C	O	0
			35	24	11	
24	G	1	Total	C	O	0
			31	20	11	
24	2	1	Total	C	O	0
			35	24	11	

- Molecule 25 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: C₄₅H₈₆O₁₀).



Mol	Chain	Residues	Atoms			AltConf
25	A	1	Total	C	O	0
			50	40	10	
25	B	1	Total	C	O	0
			35	25	10	
25	B	1	Total	C	O	0
			33	23	10	
25	B	1	Total	C	O	0
			34	24	10	
25	F	1	Total	C	O	0
			30	20	10	
25	F	1	Total	C	O	0
			47	37	10	
25	F	1	Total	C	O	0
			36	26	10	
25	F	1	Total	C	O	0
			34	24	10	
25	F	1	Total	C	O	0
			13	7	6	
25	G	1	Total	C	O	0
			25	15	10	
25	G	1	Total	C	O	0
			49	39	10	
25	G	1	Total	C	O	0
			50	40	10	
25	1	1	Total	C	O	0
			46	36	10	
25	2	1	Total	C	O	0
			25	15	10	

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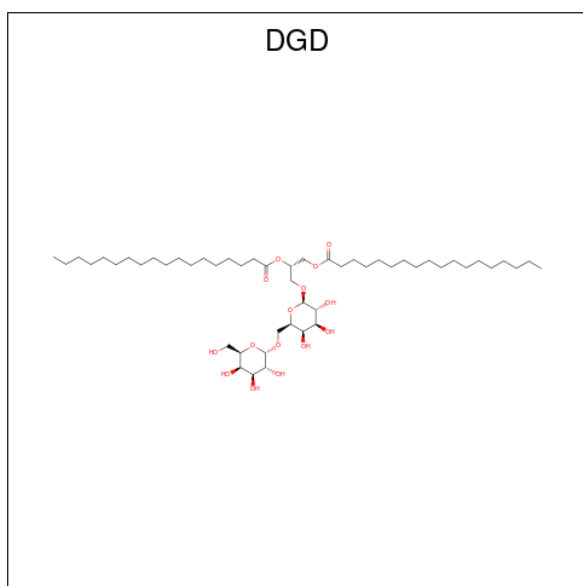
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Mol	Chain	Residues	Atoms			AltConf
25	2	1	Total	C	O	0
			36	26	10	
25	2	1	Total	C	O	0
			30	20	10	
25	2	1	Total	C	O	0
			30	20	10	
25	2	1	Total	C	O	0
			13	7	6	
25	3	1	Total	C	O	0
			30	20	10	

- Molecule 26 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
26	A	1	Total	Ca	0
			1	1	
26	B	1	Total	Ca	0
			1	1	

- Molecule 27 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (CCD ID: DGD) (formula: C₅₁H₉₆O₁₅).



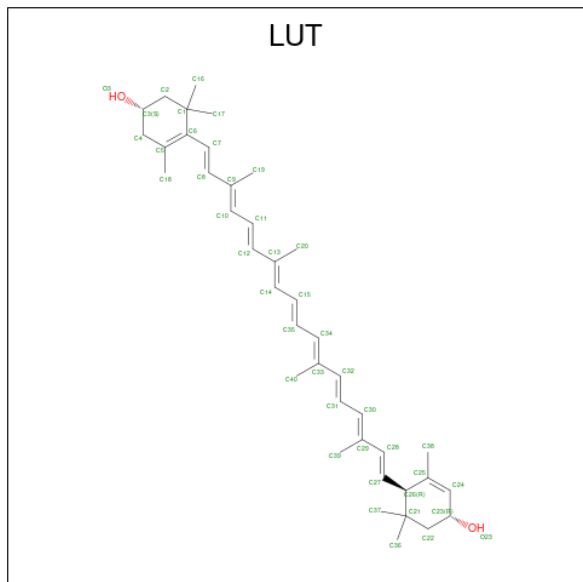
Mol	Chain	Residues	Atoms			AltConf
27	B	1	Total	C	O	0
			61	46	15	
27	F	1	Total	C	O	0
			57	42	15	

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Mol	Chain	Residues	Atoms			AltConf
27	G	1	Total	C	O	0
			47	32	15	
27	J	1	Total	C	O	0
			58	43	15	
27	1	1	Total	C	O	0
			41	26	15	
27	3	1	Total	C	O	0
			51	36	15	
27	4	1	Total	C	O	0
			50	35	15	

- Molecule 28 is (3R,3'R,6S)-4,5-DIDEHYDRO-5,6-DIHYDRO-BETA,BETA-CAROTENE-3,3'-DIOL (CCD ID: LUT) (formula: C₄₀H₅₆O₂).



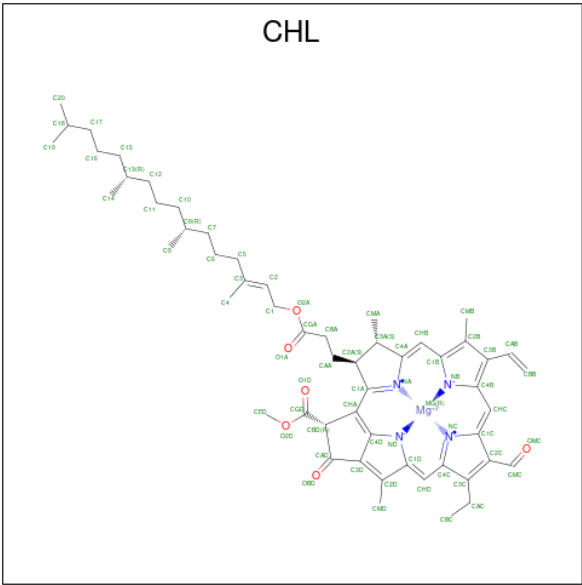
Mol	Chain	Residues	Atoms			AltConf
28	J	1	Total	C	O	0
			42	40	2	
28	1	1	Total	C	O	0
			42	40	2	
28	1	1	Total	C	O	0
			42	40	2	
28	2	1	Total	C	O	0
			42	40	2	
28	3	1	Total	C	O	0
			42	40	2	
28	3	1	Total	C	O	0
			42	40	2	

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Mol	Chain	Residues	Atoms			AltConf
28	4	1	Total	C	O	0
			42	40	2	
28	4	1	Total	C	O	0
			42	40	2	

- Molecule 29 is CHLOROPHYLL B (CCD ID: CHL) (formula: C₅₅H₇₀MgN₄O₆).



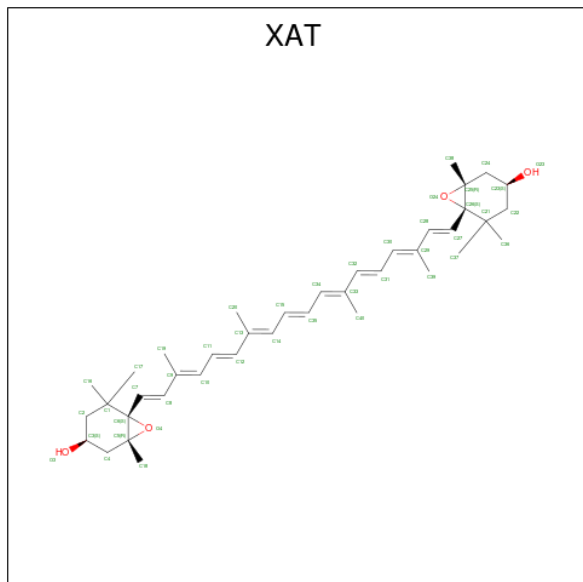
Mol	Chain	Residues	Atoms						AltConf
29	1	1	Total	C	Mg	N	O	0	
			56	45	1	4	6		
29	1	1	Total	C	Mg	N	O	0	
			47	36	1	4	6		
29	1	1	Total	C	Mg	N	O	0	
			61	50	1	4	6		
29	2	1	Total	C	Mg	N	O	0	
			56	45	1	4	6		
29	2	1	Total	C	Mg	N	O	0	
			48	37	1	4	6		
29	2	1	Total	C	Mg	N	O	0	
			46	35	1	4	6		
29	2	1	Total	C	Mg	N	O	0	
			56	45	1	4	6		
29	2	1	Total	C	Mg	N	O	0	
			66	55	1	4	6		
29	3	1	Total	C	Mg	N	O	0	
			66	55	1	4	6		

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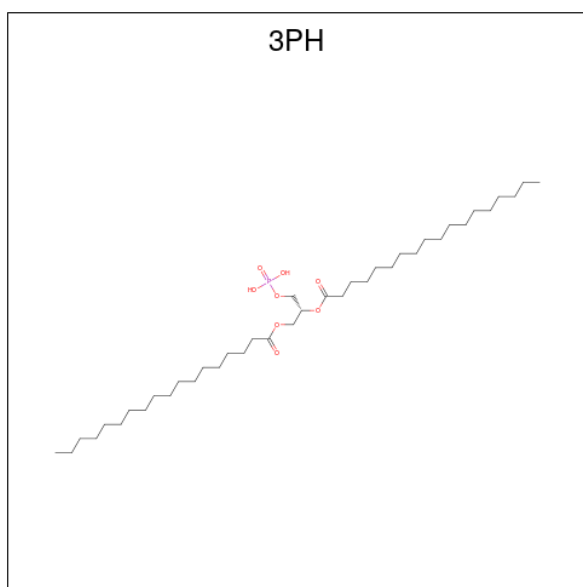
Mol	Chain	Residues	Atoms					AltConf
29	3	1	Total	C	Mg	N	O	0
			47	36	1	4	6	
29	4	1	Total	C	Mg	N	O	0
			47	36	1	4	6	
29	4	1	Total	C	Mg	N	O	0
			51	40	1	4	6	
29	4	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
29	4	1	Total	C	Mg	N	O	0
			43	34	1	4	4	

- Molecule 30 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 (CCD ID: XAT) (formula: C₄₀H₅₆O₄).



Mol	Chain	Residues	Atoms			AltConf
30	2	1	Total	C	O	0
			44	40	4	
30	4	1	Total	C	O	0
			44	40	4	

- Molecule 31 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (CCD ID: 3PH) (formula: C₃₉H₇₇O₈P).



Mol	Chain	Residues	Atoms				AltConf
31	2	1	Total	C	O	P	0
			33	24	8	1	

- Molecule 32 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
32	P	1	Total	Cu	0
			1	1	

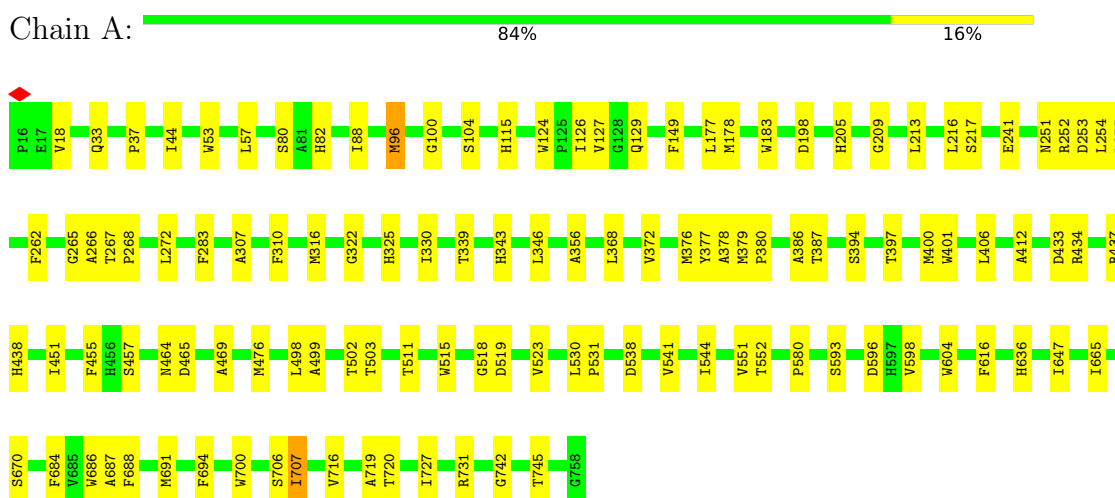
- Molecule 33 is water.

Mol	Chain	Residues	Atoms		AltConf
33	B	2	Total	O	0
			2	2	

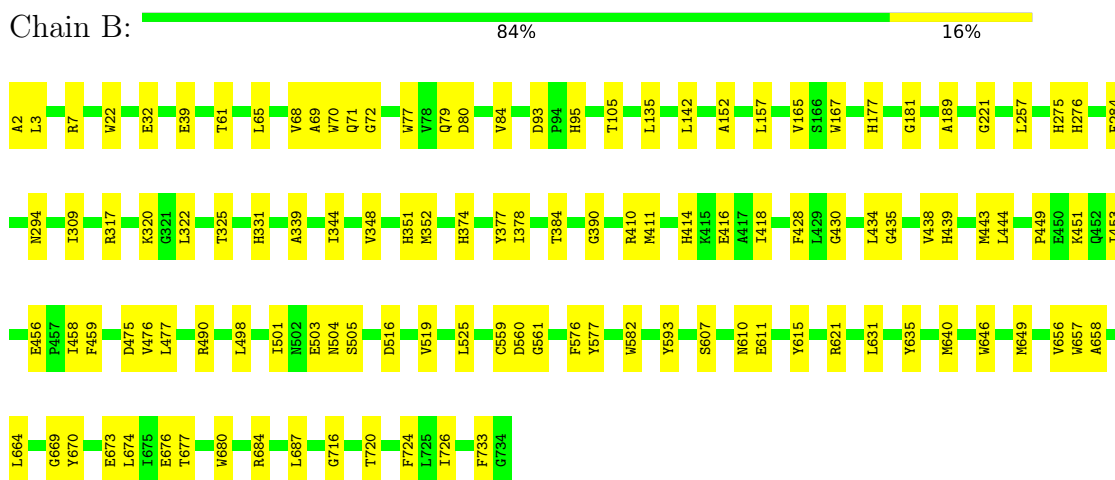
3 Residue-property plots

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

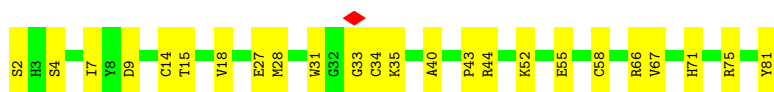


- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2

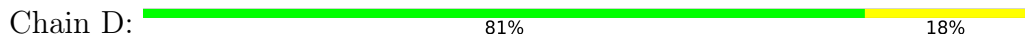


- Molecule 3: Photosystem I iron-sulfur center

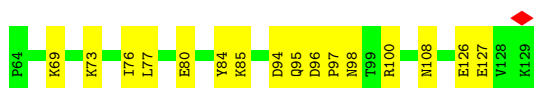




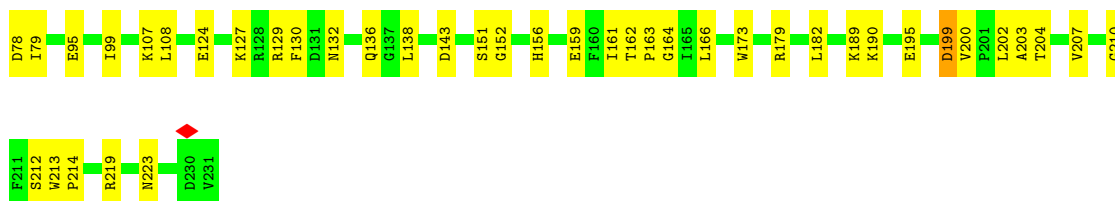
- Molecule 4: PsaD



- Molecule 5: Putative uncharacterized protein



- Molecule 6: Photosystem I reaction center subunit III



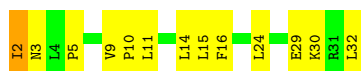
- Molecule 7: photosystem I reaction center



- Molecule 8: Photosystem I reaction center subunit VI,Photosystem I reaction center subunit VI



- Molecule 9: Photosystem I reaction center subunit VIII



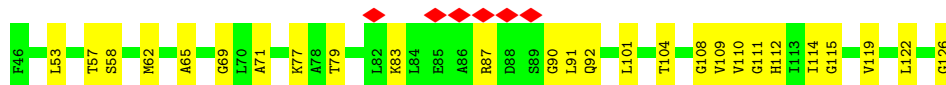
- Molecule 10: Photosystem I reaction center subunit IX

Chain J:  83% 17%



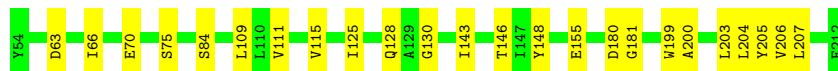
- Molecule 11: Photosystem I reaction center subunit X psaK

Chain K:  7% 68% 32%



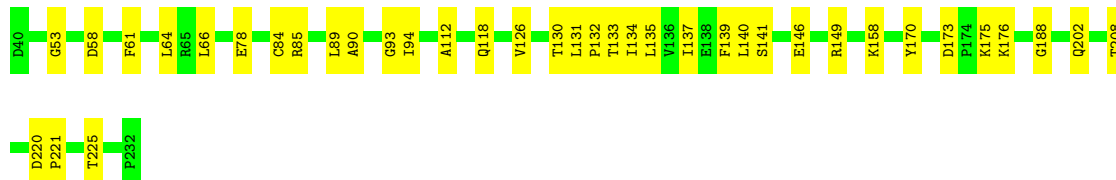
- Molecule 12: PsaL domain-containing protein

Chain L:  85% 15%



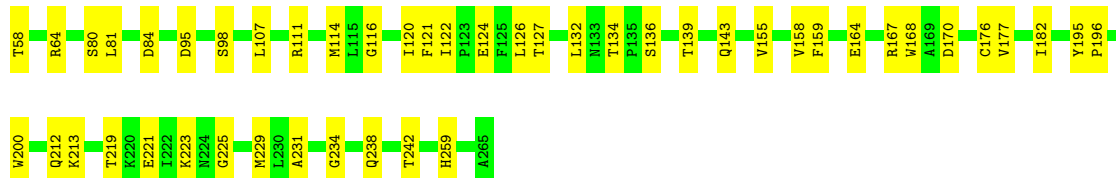
- Molecule 13: Chlorophyll a-b binding protein 6, chloroplastic

Chain 1:  80% 20%



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

Chain 2:  77% 23%



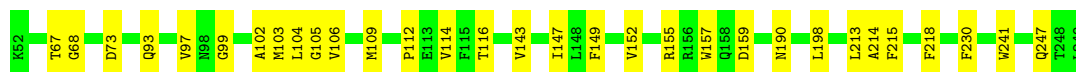
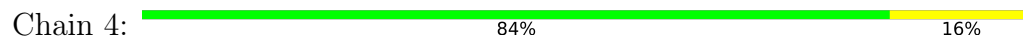
- Molecule 15: Chlorophyll a-b binding protein 3, chloroplastic

Chain 3:  67% 33%





- Molecule 16: Chlorophyll a-b binding protein P4, chloroplastic



- Molecule 17: Plastocyanin, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	104127	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 ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.176	Depositor
Minimum map value	-0.074	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0125	Depositor
Map size ($\text{\AA}$)	392.4, 392.4, 392.4	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.308, 1.308, 1.308	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SNK, LUT, SF4, CA, XAT, PQN, CHL, BCR, CL0, CU, CLA, LHG, LMT, DGD, 3PH, LMG

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	0.15	0/6033	0.31	0/8228
2	B	0.15	0/6069	0.32	0/8286
3	C	0.13	0/625	0.34	0/846
4	D	0.14	0/1163	0.31	0/1572
5	E	0.14	0/540	0.31	0/734
6	F	0.14	0/1234	0.35	0/1670
7	G	0.13	0/776	0.31	0/1054
8	H	0.13	0/733	0.32	0/995
9	I	0.17	0/246	0.39	0/335
10	J	0.15	0/349	0.27	0/476
11	K	0.14	0/576	0.30	0/779
12	L	0.12	0/1232	0.29	0/1684
13	1	0.16	0/1558	0.35	0/2125
14	2	0.15	0/1679	0.33	0/2302
15	3	0.19	0/1760	0.40	0/2390
16	4	0.14	0/1608	0.32	0/2191
17	P	0.87	3/743 (0.4%)	1.15	9/1009 (0.9%)
All	All	0.21	3/26924 (0.0%)	0.38	9/36676 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0
15	3	0	1
All	All	1	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	P	16	PRO	N-CA	12.99	1.69	1.47
17	P	15	VAL	C-N	5.79	1.45	1.34
17	P	15	VAL	N-CA	5.15	1.50	1.46

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	P	47	PRO	N-CA-C	8.25	124.32	110.95
17	P	16	PRO	CA-N-CD	-7.58	100.89	111.50
17	P	15	VAL	N-CA-C	7.55	115.62	108.15
17	P	47	PRO	CB-CA-C	-6.33	103.48	111.71
17	P	51	ASP	CA-C-N	-5.70	110.83	120.58

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	636	SNK	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	3	86	PRO	Peptide

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	5866	0	5705	125	0
2	B	5857	0	5653	121	0
3	C	612	0	591	27	0
4	D	1132	0	1141	43	0
5	E	528	0	528	18	0
6	F	1206	0	1231	36	0
7	G	757	0	743	31	0
8	H	712	0	701	35	0
9	I	240	0	264	26	0
10	J	338	0	345	12	0
11	K	569	0	596	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	1197	0	1197	36	0
13	1	1508	0	1489	38	0
14	2	1620	0	1557	70	0
15	3	1706	0	1661	102	0
16	4	1559	0	1527	32	0
17	P	728	0	699	61	0
18	A	65	0	72	2	0
19	1	608	0	564	28	0
19	2	522	0	501	38	0
19	3	630	0	539	42	0
19	4	631	0	600	40	0
19	A	2643	0	2752	137	0
19	B	2610	0	2750	146	0
19	F	130	0	144	2	0
19	G	166	0	152	8	0
19	H	60	0	59	3	0
19	J	50	0	38	2	0
19	K	199	0	159	9	0
19	L	160	0	137	11	0
20	A	33	0	46	2	0
20	B	33	0	46	1	0
21	A	8	0	0	0	0
21	C	16	0	0	2	0
22	1	80	0	103	9	0
22	2	40	0	51	8	0
22	3	80	0	105	25	0
22	A	240	0	311	41	0
22	B	200	0	261	44	0
22	F	80	0	104	13	0
22	G	40	0	52	8	0
22	H	40	0	52	10	0
22	I	80	0	104	10	0
22	J	40	0	52	9	0
22	K	80	0	104	25	0
22	L	80	0	104	17	0
23	1	49	0	74	0	0
23	2	35	0	40	0	0
23	3	17	0	12	1	0
23	4	35	0	40	0	0
23	A	89	0	127	1	0
23	B	70	0	86	0	0
24	2	35	0	45	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	A	35	0	45	0	0
24	B	63	0	70	2	0
24	G	66	0	79	3	0
25	1	46	0	65	0	0
25	2	134	0	133	0	0
25	3	30	0	30	0	0
25	A	50	0	73	2	0
25	B	102	0	114	0	0
25	F	160	0	188	1	0
25	G	124	0	161	2	0
26	A	1	0	0	0	0
26	B	1	0	0	0	0
27	1	41	0	40	0	0
27	3	51	0	60	0	0
27	4	50	0	58	1	0
27	B	61	0	83	0	0
27	F	57	0	75	1	0
27	G	47	0	52	1	0
27	J	58	0	77	0	0
28	1	84	0	110	17	0
28	2	42	0	55	11	0
28	3	84	0	110	24	0
28	4	84	0	110	23	0
28	J	42	0	55	12	0
29	1	164	0	135	5	0
29	2	272	0	225	19	0
29	3	113	0	99	6	0
29	4	202	0	152	6	0
30	2	44	0	56	4	0
30	4	44	0	56	2	0
31	2	33	0	39	0	0
32	P	1	0	0	0	0
33	B	2	0	0	0	0
All	All	38497	0	38619	1298	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 17.

The worst 5 of 1298 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)
1:A:377:TYR:OH	19:A:1135:CLA:HBC3	1.26	1.35
17:P:16:PRO:CA	17:P:16:PRO:N	1.69	1.32
1:A:178:MET:HE1	19:A:1108:CLA:CMC	1.69	1.22
12:L:204:LEU:HD21	19:L:1503:CLA:HED1	1.26	1.14
1:A:178:MET:HE2	1:A:178:MET:HA	1.29	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	739/743 (100%)	710 (96%)	29 (4%)	0	100	100
2	B	731/733 (100%)	698 (96%)	33 (4%)	0	100	100
3	C	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
4	D	141/143 (99%)	134 (95%)	6 (4%)	1 (1%)	18	32
5	E	64/66 (97%)	59 (92%)	5 (8%)	0	100	100
6	F	152/154 (99%)	149 (98%)	3 (2%)	0	100	100
7	G	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
8	H	91/93 (98%)	86 (94%)	5 (6%)	0	100	100
9	I	29/31 (94%)	26 (90%)	3 (10%)	0	100	100
10	J	40/42 (95%)	40 (100%)	0	0	100	100
11	K	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
12	L	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
13	1	191/193 (99%)	182 (95%)	9 (5%)	0	100	100
14	2	206/208 (99%)	194 (94%)	12 (6%)	0	100	100
15	3	219/221 (99%)	202 (92%)	15 (7%)	2 (1%)	14	26
16	4	196/198 (99%)	183 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	P	97/99 (98%)	87 (90%)	9 (9%)	1 (1%)	12	22
All	All	3305/3341 (99%)	3135 (95%)	166 (5%)	4 (0%)	49	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	3	86	PRO
15	3	87	GLU
4	D	107	SER
17	P	50	VAL

5.3.2 Protein sidechains ⓘ

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	602/602 (100%)	600 (100%)	2 (0%)	86	92
2	B	598/598 (100%)	598 (100%)	0	100	100
3	C	69/69 (100%)	68 (99%)	1 (1%)	59	74
4	D	122/122 (100%)	122 (100%)	0	100	100
5	E	58/58 (100%)	58 (100%)	0	100	100
6	F	125/126 (99%)	123 (98%)	2 (2%)	55	72
7	G	82/82 (100%)	82 (100%)	0	100	100
8	H	75/75 (100%)	75 (100%)	0	100	100
9	I	27/27 (100%)	26 (96%)	1 (4%)	30	52
10	J	35/35 (100%)	35 (100%)	0	100	100
11	K	59/59 (100%)	59 (100%)	0	100	100
12	L	126/126 (100%)	126 (100%)	0	100	100
13	1	158/158 (100%)	158 (100%)	0	100	100
14	2	167/167 (100%)	167 (100%)	0	100	100
15	3	171/172 (99%)	171 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	4	164/164 (100%)	164 (100%)	0	100	100
17	P	79/79 (100%)	75 (95%)	4 (5%)	21	39
All	All	2717/2719 (100%)	2707 (100%)	10 (0%)	81	90

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	P	15	VAL
17	P	27	ILE
17	P	28	VAL
6	F	132	ASN
6	F	199	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
13	1	223	HIS
14	2	249	ASN
15	3	199	ASN
15	3	185	GLN
2	B	89	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	SNK	A	115	1	11,14,15	1.33	2 (18%)	10,18,20	1.99	4 (40%)
1	SNK	A	636	1	11,14,15	1.22	2 (18%)	10,18,20	1.95	4 (40%)

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
1	SNK	A	115	1	-	4/8/10/12	0/1/1/1
1	SNK	A	636	1	1/1/2/3	6/8/10/12	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	115	SNK	CE1-ND1	2.57	1.39	1.35
1	A	636	SNK	CE1-ND1	2.36	1.39	1.35
1	A	636	SNK	C02-S04	2.28	1.85	1.77
1	A	115	SNK	C02-S04	2.25	1.85	1.77

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	115	SNK	CE1-NE2-CD2	3.41	106.04	103.47
1	A	636	SNK	CE1-NE2-CD2	3.29	105.96	103.47
1	A	115	SNK	C01-C02-S04	2.87	122.95	112.40
1	A	636	SNK	C01-C02-S04	2.85	122.85	112.40
1	A	115	SNK	ND1-CE1-NE2	-2.80	109.91	112.99

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	636	SNK	CA

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	115	SNK	CG-CD2-S04-C02
1	A	115	SNK	C01-C02-S04-CD2
1	A	115	SNK	O03-C02-S04-CD2
1	A	636	SNK	O-C-CA-CB

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Mol	Chain	Res	Type	Atoms
1	A	636	SNK	CG-CD2-S04-C02

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 243 ligands modelled in this entry, 3 are monoatomic - leaving 240 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
28	LUT	2	501	-	42,43,43	2.29	1 (2%)	51,60,60	2.24	17 (33%)
19	CLA	K	1404	-	50,54,73	1.58	7 (14%)	60,90,113	2.00	14 (23%)
19	CLA	A	1139	-	69,73,73	1.37	7 (10%)	83,113,113	1.89	18 (21%)
19	CLA	B	1239	2	69,73,73	1.35	7 (10%)	83,113,113	1.90	17 (20%)
29	CHL	4	611	-	55,59,74	0.88	1 (1%)	62,96,114	1.45	12 (19%)
22	BCR	A	4008	-	41,41,41	1.79	4 (9%)	56,56,56	4.42	25 (44%)
19	CLA	A	1125	1	69,73,73	1.36	6 (8%)	83,113,113	1.89	16 (19%)
19	CLA	A	1122	-	69,73,73	1.35	7 (10%)	83,113,113	1.91	17 (20%)
23	LHG	4	801	-	34,34,48	0.47	0	37,40,54	1.18	3 (8%)
29	CHL	1	612	13	65,69,74	0.83	1 (1%)	74,108,114	1.25	10 (13%)
29	CHL	2	610	-	60,64,74	0.83	1 (1%)	68,102,114	1.30	11 (16%)
19	CLA	A	1121	1	64,68,73	1.40	7 (10%)	77,107,113	1.98	16 (20%)
19	CLA	B	1209	2	50,54,73	1.58	7 (14%)	60,90,113	2.02	14 (23%)
25	LMG	1	802	-	46,46,55	0.94	3 (6%)	54,54,63	1.01	2 (3%)
22	BCR	1	504	-	41,41,41	1.85	4 (9%)	56,56,56	4.65	21 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	CLA	4	606	-	54,58,73	1.53	6 (11%)	65,95,113	2.04	16 (24%)
29	CHL	4	615	16	47,51,74	0.93	1 (2%)	52,86,114	1.51	10 (19%)
19	CLA	3	617	15	64,68,73	1.40	7 (10%)	77,107,113	1.94	18 (23%)
19	CLA	A	1113	-	49,53,73	1.60	6 (12%)	59,89,113	2.01	14 (23%)
27	DGD	G	5003	-	48,48,67	0.86	2 (4%)	62,62,81	0.97	3 (4%)
28	LUT	4	505	-	42,43,43	2.28	1 (2%)	51,60,60	2.38	20 (39%)
19	CLA	A	1117	1	69,73,73	1.35	6 (8%)	83,113,113	1.85	17 (20%)
19	CLA	B	1201	2	69,73,73	1.35	6 (8%)	83,113,113	1.82	16 (19%)
22	BCR	A	4007	-	41,41,41	1.85	4 (9%)	56,56,56	4.59	21 (37%)
19	CLA	A	1129	1	69,73,73	1.36	7 (10%)	83,113,113	1.96	18 (21%)
19	CLA	A	1109	1	69,73,73	1.35	8 (11%)	83,113,113	1.94	18 (21%)
19	CLA	G	1603	-	69,73,73	1.36	6 (8%)	83,113,113	1.85	16 (19%)
19	CLA	A	1104	-	69,73,73	1.34	7 (10%)	83,113,113	1.87	17 (20%)
19	CLA	A	1112	-	69,73,73	1.36	6 (8%)	83,113,113	1.87	16 (19%)
19	CLA	B	1206	2	69,73,73	1.35	6 (8%)	83,113,113	1.86	15 (18%)
19	CLA	B	1022	-	69,73,73	1.35	7 (10%)	83,113,113	1.86	17 (20%)
19	CLA	B	1236	2	54,58,73	1.52	6 (11%)	65,95,113	2.11	18 (27%)
19	CLA	3	606	-	54,58,73	1.52	6 (11%)	65,95,113	2.07	16 (24%)
23	LHG	2	801	-	34,34,48	0.46	0	37,40,54	1.09	3 (8%)
19	CLA	K	1402	-	64,68,73	1.40	6 (9%)	77,107,113	1.94	16 (20%)
19	CLA	3	612	15	54,58,73	1.53	7 (12%)	65,95,113	2.07	15 (23%)
19	CLA	3	602	-	56,60,73	1.50	6 (10%)	67,97,113	2.07	18 (26%)
19	CLA	A	1137	1	69,73,73	1.35	7 (10%)	83,113,113	1.87	16 (19%)
25	LMG	2	804	-	30,30,55	0.53	0	38,38,63	1.08	2 (5%)
22	BCR	B	4004	-	41,41,41	1.87	4 (9%)	56,56,56	4.79	18 (32%)
19	CLA	A	1123	-	69,73,73	1.36	7 (10%)	83,113,113	1.87	15 (18%)
27	DGD	B	5005	-	62,62,67	1.11	5 (8%)	76,76,81	0.99	3 (3%)
25	LMG	B	5004	-	33,33,55	0.52	0	41,41,63	1.21	4 (9%)
19	CLA	A	1103	1	69,73,73	1.33	6 (8%)	83,113,113	1.87	15 (18%)
19	CLA	B	1240	23	69,73,73	1.36	6 (8%)	83,113,113	1.85	18 (21%)
19	CLA	A	1127	-	69,73,73	1.36	7 (10%)	83,113,113	1.76	14 (16%)
19	CLA	A	1115	-	69,73,73	1.36	7 (10%)	83,113,113	1.84	17 (20%)
22	BCR	F	4016	-	41,41,41	1.80	4 (9%)	56,56,56	4.31	16 (28%)
23	LHG	3	801	-	16,16,48	0.87	1 (6%)	17,20,54	0.67	0
19	CLA	1	604	13	69,73,73	1.36	7 (10%)	83,113,113	1.84	15 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	CLA	A	1116	-	60,64,73	1.46	8 (13%)	72,102,113	2.06	18 (25%)
19	CLA	B	1238	33	69,73,73	1.35	6 (8%)	83,113,113	1.88	15 (18%)
22	BCR	A	4002	-	41,41,41	1.85	4 (9%)	56,56,56	4.30	22 (39%)
19	CLA	H	1701	8	64,68,73	1.40	6 (9%)	77,107,113	1.86	15 (19%)
19	CLA	B	1205	-	69,73,73	1.35	6 (8%)	83,113,113	1.90	16 (19%)
19	CLA	4	617	16	69,73,73	1.33	6 (8%)	83,113,113	1.91	18 (21%)
22	BCR	B	4005	-	41,41,41	1.79	4 (9%)	56,56,56	4.39	17 (30%)
19	CLA	3	614	-	46,50,73	1.66	6 (13%)	55,85,113	2.14	13 (23%)
29	CHL	2	615	-	60,64,74	0.84	1 (1%)	68,102,114	1.40	12 (17%)
19	CLA	A	1140	-	69,73,73	1.34	6 (8%)	83,113,113	1.86	15 (18%)
19	CLA	B	1204	2	69,73,73	1.36	7 (10%)	83,113,113	1.87	16 (19%)
22	BCR	I	4020	-	41,41,41	1.86	4 (9%)	56,56,56	4.42	20 (35%)
19	CLA	1	607	-	50,54,73	1.58	6 (12%)	60,90,113	2.05	13 (21%)
25	LMG	B	5007	-	34,34,55	0.51	0	42,42,63	1.07	2 (4%)
19	CLA	A	1013	-	69,73,73	1.35	7 (10%)	83,113,113	1.81	15 (18%)
19	CLA	B	1219	2	69,73,73	1.35	7 (10%)	83,113,113	1.90	16 (19%)
19	CLA	B	1227	-	69,73,73	1.35	6 (8%)	83,113,113	1.90	18 (21%)
24	LMT	2	808	-	36,36,36	1.15	5 (13%)	47,47,47	0.96	2 (4%)
25	LMG	A	5006	-	50,50,55	1.05	5 (10%)	58,58,63	1.05	3 (5%)
19	CLA	B	1232	-	59,63,73	1.47	7 (11%)	71,101,113	1.98	16 (22%)
22	BCR	G	4011	-	41,41,41	1.86	4 (9%)	56,56,56	4.46	23 (41%)
25	LMG	F	5004	-	34,34,55	0.49	0	42,42,63	1.09	3 (7%)
19	CLA	A	1101	1	69,73,73	1.36	7 (10%)	83,113,113	1.87	17 (20%)
29	CHL	2	609	14	70,74,74	0.80	1 (1%)	80,114,114	1.21	10 (12%)
19	CLA	B	1216	-	69,73,73	1.36	7 (10%)	83,113,113	1.81	16 (19%)
22	BCR	1	503	-	41,41,41	1.83	4 (9%)	56,56,56	4.66	22 (39%)
25	LMG	G	5002	-	50,50,55	1.05	5 (10%)	58,58,63	1.16	4 (6%)
19	CLA	K	1403	-	52,56,73	1.56	7 (13%)	62,92,113	2.16	16 (25%)
28	LUT	3	501	-	42,43,43	2.33	1 (2%)	51,60,60	2.20	17 (33%)
19	CLA	3	608	-	52,56,73	1.56	6 (11%)	62,92,113	2.07	14 (22%)
19	CLA	B	1207	2	69,73,73	1.34	7 (10%)	83,113,113	1.82	16 (19%)
23	LHG	B	5002	-	48,48,48	0.40	0	51,54,54	1.04	4 (7%)
29	CHL	4	610	-	51,55,74	0.96	1 (1%)	57,91,114	1.47	11 (19%)
19	CLA	B	1223	2	69,73,73	1.36	8 (11%)	83,113,113	1.90	20 (24%)
19	CLA	4	612	16	69,73,73	1.36	8 (11%)	83,113,113	1.82	15 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	CLA	B	1021	-	69,73,73	1.35	7 (10%)	83,113,113	1.91	18 (21%)
19	CLA	4	601	16	64,68,73	1.42	7 (10%)	77,107,113	1.96	18 (23%)
22	BCR	3	503	-	41,41,41	1.82	5 (12%)	56,56,56	4.29	19 (33%)
19	CLA	A	1105	1	64,68,73	1.41	7 (10%)	77,107,113	1.90	15 (19%)
19	CLA	K	1401	-	49,53,73	1.61	6 (12%)	59,89,113	2.09	13 (22%)
19	CLA	1	611	-	69,73,73	1.36	6 (8%)	83,113,113	1.82	14 (16%)
19	CLA	A	1119	-	69,73,73	1.37	7 (10%)	83,113,113	1.90	19 (22%)
22	BCR	L	4019	-	41,41,41	1.84	4 (9%)	56,56,56	4.58	19 (33%)
19	CLA	A	1141	-	64,68,73	1.41	7 (10%)	77,107,113	1.92	17 (22%)
19	CLA	B	1211	-	69,73,73	1.34	6 (8%)	83,113,113	1.82	14 (16%)
19	CLA	1	602	13	50,54,73	1.58	6 (12%)	60,90,113	1.97	13 (21%)
27	DGD	F	5005	-	58,58,67	1.06	6 (10%)	72,72,81	1.03	4 (5%)
19	CLA	A	1136	-	69,73,73	1.35	7 (10%)	83,113,113	1.85	16 (19%)
19	CLA	B	1208	-	64,68,73	1.40	6 (9%)	77,107,113	1.87	14 (18%)
22	BCR	J	4012	-	41,41,41	1.82	4 (9%)	56,56,56	4.54	17 (30%)
24	LMT	G	5005	-	32,32,36	1.21	5 (15%)	43,43,47	0.96	2 (4%)
19	CLA	F	1302	6	69,73,73	1.36	6 (8%)	83,113,113	1.87	18 (21%)
21	SF4	C	3003	3	0,12,12	-	-	-	-	-
30	XAT	4	502	-	39,47,47	0.66	1 (2%)	54,74,74	1.71	13 (24%)
19	CLA	A	1128	-	69,73,73	1.35	8 (11%)	83,113,113	1.84	16 (19%)
19	CLA	2	601	14	64,68,73	1.43	7 (10%)	77,107,113	1.97	19 (24%)
19	CLA	A	1114	-	50,54,73	1.57	7 (14%)	60,90,113	2.12	13 (21%)
22	BCR	B	4010	-	41,41,41	1.81	4 (9%)	56,56,56	4.47	21 (37%)
24	LMT	B	5008	-	32,32,36	1.23	5 (15%)	43,43,47	0.99	3 (6%)
24	LMT	G	5004	-	36,36,36	1.15	6 (16%)	47,47,47	0.97	2 (4%)
19	CLA	B	1231	2	64,68,73	1.41	7 (10%)	77,107,113	1.92	16 (20%)
19	CLA	B	1237	-	69,73,73	1.36	7 (10%)	83,113,113	1.81	15 (18%)
29	CHL	2	611	-	52,56,74	0.92	2 (3%)	58,92,114	1.45	11 (18%)
19	CLA	A	1102	1	69,73,73	1.36	7 (10%)	83,113,113	1.96	17 (20%)
19	CLA	A	1118	1	54,58,73	1.53	7 (12%)	65,95,113	2.08	16 (24%)
19	CLA	A	1107	1	69,73,73	1.36	6 (8%)	83,113,113	1.85	17 (20%)
29	CHL	2	613	-	50,54,74	0.91	1 (2%)	56,90,114	1.34	10 (17%)
19	CLA	A	1012	-	69,73,73	1.37	7 (10%)	83,113,113	1.84	18 (21%)
19	CLA	A	1138	1	69,73,73	1.35	7 (10%)	83,113,113	1.81	15 (18%)
19	CLA	B	1210	-	69,73,73	1.36	8 (11%)	83,113,113	1.89	19 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	CLA	B	1203	2	69,73,73	1.35	7 (10%)	83,113,113	1.82	16 (19%)
19	CLA	1	613	-	49,53,73	1.62	8 (16%)	59,89,113	2.04	14 (23%)
28	LUT	J	4013	-	42,43,43	2.30	1 (2%)	51,60,60	2.02	13 (25%)
19	CLA	B	1023	-	69,73,73	1.37	5 (7%)	83,113,113	1.75	14 (16%)
25	LMG	G	5001	-	49,49,55	1.02	4 (8%)	57,57,63	1.20	4 (7%)
20	PQN	B	2002	-	34,34,34	0.40	0	42,45,45	1.15	3 (7%)
25	LMG	F	5001	-	30,30,55	0.52	0	38,38,63	1.09	2 (5%)
19	CLA	2	602	-	56,60,73	1.50	6 (10%)	67,97,113	2.04	19 (28%)
19	CLA	4	608	-	50,54,73	1.58	7 (14%)	60,90,113	2.05	13 (21%)
19	CLA	4	604	16	64,68,73	1.40	6 (9%)	77,107,113	1.96	17 (22%)
19	CLA	3	613	-	50,54,73	1.60	7 (14%)	60,90,113	2.07	14 (23%)
22	BCR	A	4011	-	41,41,41	1.79	4 (9%)	56,56,56	4.43	22 (39%)
28	LUT	3	502	-	42,43,43	2.24	1 (2%)	51,60,60	1.93	17 (33%)
27	DGD	J	5001	-	59,59,67	1.08	6 (10%)	73,73,81	1.00	2 (2%)
19	CLA	3	601	15	59,63,73	1.48	7 (11%)	71,101,113	1.96	18 (25%)
19	CLA	2	605	14	69,73,73	1.35	8 (11%)	83,113,113	1.86	17 (20%)
19	CLA	B	1234	2	59,63,73	1.47	5 (8%)	71,101,113	1.99	16 (22%)
22	BCR	I	4018	-	41,41,41	1.78	5 (12%)	56,56,56	4.44	25 (44%)
22	BCR	3	506	-	41,41,41	1.84	4 (9%)	56,56,56	4.49	21 (37%)
29	CHL	1	610	13	51,55,74	0.92	1 (1%)	57,91,114	1.44	12 (21%)
19	CLA	F	1301	-	69,73,73	1.36	7 (10%)	83,113,113	1.82	16 (19%)
19	CLA	A	1126	-	69,73,73	1.38	7 (10%)	83,113,113	1.89	18 (21%)
19	CLA	B	1226	2	69,73,73	1.36	6 (8%)	83,113,113	1.88	17 (20%)
22	BCR	L	4020	-	41,41,41	1.80	4 (9%)	56,56,56	4.44	18 (32%)
29	CHL	1	609	13	60,64,74	0.87	1 (1%)	68,102,114	1.39	11 (16%)
19	CLA	A	1134	1	59,63,73	1.45	7 (11%)	71,101,113	1.96	13 (18%)
23	LHG	1	801	-	48,48,48	0.39	0	51,54,54	0.96	2 (3%)
24	LMT	B	5006	-	33,33,36	1.20	5 (15%)	44,44,47	0.93	2 (4%)
27	DGD	1	803	-	42,42,67	0.87	1 (2%)	56,56,81	0.99	2 (3%)
19	CLA	2	608	-	54,58,73	1.53	6 (11%)	65,95,113	2.13	17 (26%)
19	CLA	A	1132	1	69,73,73	1.35	7 (10%)	83,113,113	1.88	16 (19%)
19	CLA	4	607	-	64,68,73	1.40	6 (9%)	77,107,113	1.92	17 (22%)
22	BCR	K	4002	-	41,41,41	1.80	4 (9%)	56,56,56	4.41	21 (37%)
19	CLA	L	1501	12	54,58,73	1.52	7 (12%)	65,95,113	2.12	18 (27%)
25	LMG	B	5003	-	35,35,55	0.74	1 (2%)	43,43,63	1.15	4 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	SF4	C	3002	3	0,12,12	-	-	-		
29	CHL	4	613	-	65,69,74	0.84	3 (4%)	74,108,114	1.21	9 (12%)
19	CLA	B	1225	-	69,73,73	1.35	6 (8%)	83,113,113	1.83	16 (19%)
31	3PH	2	807	-	32,32,47	1.03	4 (12%)	36,37,52	1.17	2 (5%)
19	CLA	B	1217	2	50,54,73	1.57	6 (12%)	60,90,113	2.01	13 (21%)
27	DGD	3	803	-	52,52,67	0.90	3 (5%)	66,66,81	1.07	3 (4%)
25	LMG	F	5003	-	36,36,55	0.72	1 (2%)	44,44,63	1.02	2 (4%)
19	CLA	4	605	-	64,68,73	1.42	8 (12%)	77,107,113	1.94	18 (23%)
19	CLA	A	1111	-	69,73,73	1.35	7 (10%)	83,113,113	1.81	13 (15%)
19	CLA	J	1901	10	54,58,73	1.53	7 (12%)	65,95,113	2.03	15 (23%)
19	CLA	1	601	13	69,73,73	1.39	6 (8%)	83,113,113	1.82	16 (19%)
19	CLA	3	610	15	69,73,73	1.35	6 (8%)	83,113,113	1.85	17 (20%)
19	CLA	4	602	-	54,58,73	1.52	7 (12%)	65,95,113	2.06	17 (26%)
19	CLA	4	603	16	69,73,73	1.35	7 (10%)	83,113,113	1.93	17 (20%)
22	BCR	B	4006	-	41,41,41	1.81	4 (9%)	56,56,56	4.40	28 (50%)
25	LMG	G	5006	-	25,25,55	0.58	0	33,33,63	1.17	3 (9%)
19	CLA	2	604	14	69,73,73	1.36	6 (8%)	83,113,113	1.88	15 (18%)
25	LMG	2	805	-	30,30,55	0.55	0	38,38,63	1.08	2 (5%)
25	LMG	2	806	-	13,13,55	0.55	0	18,18,63	0.56	0
29	CHL	3	604	15	70,74,74	0.78	1 (1%)	80,114,114	1.28	9 (11%)
19	CLA	B	1214	-	69,73,73	1.36	8 (11%)	83,113,113	1.88	18 (21%)
19	CLA	B	1213	2	64,68,73	1.40	7 (10%)	77,107,113	1.90	16 (20%)
19	CLA	A	1124	-	59,63,73	1.49	7 (11%)	71,101,113	1.93	16 (22%)
19	CLA	B	1228	2	64,68,73	1.42	7 (10%)	77,107,113	1.91	16 (20%)
25	LMG	2	802	-	25,25,55	0.56	0	33,33,63	1.37	3 (9%)
28	LUT	1	501	-	42,43,43	2.29	1 (2%)	51,60,60	2.23	20 (39%)
22	BCR	A	4017	-	41,41,41	1.80	4 (9%)	56,56,56	4.93	20 (35%)
19	CLA	G	1602	7	50,54,73	1.59	6 (12%)	60,90,113	2.07	16 (26%)
19	CLA	G	1601	-	59,63,73	1.47	6 (10%)	71,101,113	2.00	17 (23%)
19	CLA	2	606	-	54,58,73	1.54	7 (12%)	65,95,113	2.04	16 (24%)
19	CLA	L	1503	-	54,58,73	1.53	7 (12%)	65,95,113	2.11	20 (30%)
19	CLA	B	1218	-	69,73,73	1.35	7 (10%)	83,113,113	1.87	16 (19%)
19	CLA	B	1215	2	69,73,73	1.34	6 (8%)	83,113,113	1.91	15 (18%)
19	CLA	B	1202	2	69,73,73	1.32	6 (8%)	83,113,113	1.96	17 (20%)
22	BCR	A	4003	-	41,41,41	1.81	4 (9%)	56,56,56	4.41	22 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	LMT	A	5004	-	36,36,36	1.16	6 (16%)	47,47,47	1.01	2 (4%)
25	LMG	2	803	-	36,36,55	0.69	2 (5%)	44,44,63	1.06	2 (4%)
22	BCR	K	4001	-	41,41,41	1.80	5 (12%)	56,56,56	4.56	15 (26%)
25	LMG	F	5006	-	13,13,55	0.57	0	18,18,63	0.71	0
30	XAT	2	502	-	39,47,47	0.68	1 (2%)	54,74,74	2.05	12 (22%)
19	CLA	B	1220	2	59,63,73	1.46	7 (11%)	71,101,113	1.94	16 (22%)
29	CHL	3	611	-	51,55,74	0.93	1 (1%)	57,91,114	1.47	12 (21%)
19	CLA	A	1130	1	59,63,73	1.47	7 (11%)	71,101,113	1.96	14 (19%)
19	CLA	1	614	13	64,68,73	1.40	6 (9%)	77,107,113	1.88	15 (19%)
22	BCR	B	4009	-	41,41,41	1.81	4 (9%)	56,56,56	4.20	19 (33%)
22	BCR	2	503	-	41,41,41	1.89	5 (12%)	56,56,56	5.43	26 (46%)
23	LHG	A	5001	-	39,39,48	0.43	0	42,45,54	1.02	2 (4%)
22	BCR	H	4021	-	41,41,41	1.84	4 (9%)	56,56,56	4.55	19 (33%)
25	LMG	3	802	-	30,30,55	0.55	0	38,38,63	1.08	3 (7%)
27	DGD	4	802	-	51,51,67	0.92	2 (3%)	65,65,81	0.98	3 (4%)
19	CLA	B	1235	2	69,73,73	1.35	8 (11%)	83,113,113	1.87	16 (19%)
19	CLA	2	607	-	64,68,73	1.41	7 (10%)	77,107,113	2.03	18 (23%)
21	SF4	A	3001	1,2	0,12,12	-	-	-	-	-
23	LHG	B	5001	19	20,20,48	0.58	0	23,26,54	1.48	2 (8%)
19	CLA	A	1110	1	59,63,73	1.45	5 (8%)	71,101,113	2.05	17 (23%)
19	CLA	B	1221	-	69,73,73	1.36	7 (10%)	83,113,113	1.90	16 (19%)
25	LMG	F	5002	-	47,47,55	0.97	4 (8%)	55,55,63	1.10	3 (5%)
22	BCR	F	4014	-	41,41,41	1.83	4 (9%)	56,56,56	4.45	20 (35%)
19	CLA	B	1224	-	69,73,73	1.37	7 (10%)	83,113,113	1.88	15 (18%)
19	CLA	1	603	-	59,63,73	1.46	7 (11%)	71,101,113	2.03	17 (23%)
19	CLA	A	1133	1	69,73,73	1.36	7 (10%)	83,113,113	1.79	14 (16%)
18	CL0	A	1011	1	69,73,73	2.36	21 (30%)	83,113,113	2.49	21 (25%)
19	CLA	B	1222	33	69,73,73	1.34	7 (10%)	83,113,113	1.88	16 (19%)
19	CLA	B	1230	-	62,66,73	1.43	7 (11%)	74,104,113	2.00	19 (25%)
28	LUT	4	501	-	42,43,43	2.25	1 (2%)	51,60,60	2.26	17 (33%)
23	LHG	A	5002	-	48,48,48	0.40	0	51,54,54	1.10	4 (7%)
19	CLA	2	603	14	69,73,73	1.34	6 (8%)	83,113,113	1.86	15 (18%)
19	CLA	3	603	15	59,63,73	1.45	7 (11%)	71,101,113	2.12	18 (25%)
19	CLA	B	1212	-	59,63,73	1.47	8 (13%)	71,101,113	2.04	17 (23%)
19	CLA	A	1106	1	69,73,73	1.34	7 (10%)	83,113,113	1.91	18 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	CLA	A	1108	-	54,58,73	1.53	6 (11%)	65,95,113	2.06	16 (24%)
19	CLA	1	605	13	69,73,73	1.36	6 (8%)	83,113,113	1.93	16 (19%)
19	CLA	1	608	13	50,54,73	1.58	6 (12%)	60,90,113	2.07	13 (21%)
19	CLA	A	1120	1	64,68,73	1.41	7 (10%)	77,107,113	1.89	15 (19%)
19	CLA	3	605	-	59,63,73	1.48	8 (13%)	71,101,113	2.03	19 (26%)
19	CLA	2	612	-	59,63,73	1.45	7 (11%)	71,101,113	1.94	14 (19%)
19	CLA	4	609	16	54,58,73	1.53	7 (12%)	65,95,113	2.04	16 (24%)
19	CLA	B	1229	2	69,73,73	1.35	5 (7%)	83,113,113	1.87	18 (21%)
19	CLA	3	607	-	56,60,73	1.50	6 (10%)	67,97,113	2.08	17 (25%)
19	CLA	1	606	-	54,58,73	1.52	6 (11%)	65,95,113	2.06	17 (26%)
19	CLA	L	1502	-	64,68,73	1.40	7 (10%)	77,107,113	2.00	19 (24%)
19	CLA	A	1131	1	69,73,73	1.35	6 (8%)	83,113,113	1.81	16 (19%)
28	LUT	1	502	-	42,43,43	2.31	1 (2%)	51,60,60	2.18	15 (29%)
20	PQN	A	2001	-	34,34,34	0.36	0	42,45,45	1.14	3 (7%)
19	CLA	A	1135	1	55,59,73	1.51	6 (10%)	66,96,113	2.08	15 (22%)

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
28	LUT	2	501	-	1/1/12/27	6/29/67/67	0/2/2/2
19	CLA	K	1404	-	-	7/17/93/115	-
19	CLA	A	1139	-	-	15/39/115/115	-
19	CLA	B	1239	2	-	10/39/115/115	-
29	CHL	4	611	-	-	1/23/99/117	-
22	BCR	A	4008	-	-	10/29/63/63	0/2/2/2
19	CLA	A	1125	1	-	15/39/115/115	-
19	CLA	A	1122	-	-	18/39/115/115	-
23	LHG	4	801	-	-	21/39/39/53	-
29	CHL	1	612	13	1/1/14/21	4/35/111/117	-
29	CHL	2	610	-	1/1/13/21	3/29/105/117	-
19	CLA	A	1121	1	-	15/33/109/115	-
19	CLA	B	1209	2	-	4/17/93/115	-
25	LMG	1	802	-	-	4/41/61/70	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	BCR	1	504	-	-	9/29/63/63	0/2/2/2
29	CHL	4	615	16	1/1/10/21	0/14/90/117	-
19	CLA	4	606	-	-	7/21/97/115	-
19	CLA	3	617	15	-	20/33/109/115	-
19	CLA	A	1113	-	-	8/15/91/115	-
27	DGD	G	5003	-	-	11/36/76/95	0/2/2/2
28	LUT	4	505	-	-	3/29/67/67	0/2/2/2
19	CLA	A	1117	1	-	15/39/115/115	-
19	CLA	B	1201	2	-	17/39/115/115	-
22	BCR	A	4007	-	-	10/29/63/63	0/2/2/2
19	CLA	A	1129	1	-	11/39/115/115	-
19	CLA	A	1109	1	-	18/39/115/115	-
19	CLA	G	1603	-	-	9/39/115/115	-
19	CLA	A	1104	-	-	17/39/115/115	-
19	CLA	A	1112	-	-	21/39/115/115	-
19	CLA	B	1206	2	-	16/39/115/115	-
19	CLA	B	1022	-	-	9/39/115/115	-
19	CLA	B	1236	2	-	8/21/97/115	-
19	CLA	3	606	-	-	11/21/97/115	-
23	LHG	2	801	-	-	18/39/39/53	-
19	CLA	K	1402	-	-	18/33/109/115	-
19	CLA	3	612	15	-	7/21/97/115	-
19	CLA	3	602	-	-	8/24/100/115	-
19	CLA	A	1137	1	-	19/39/115/115	-
25	LMG	2	804	-	-	5/25/45/70	0/1/1/1
22	BCR	B	4004	-	-	10/29/63/63	0/2/2/2
19	CLA	A	1123	-	-	15/39/115/115	-
27	DGD	B	5005	-	-	19/50/90/95	0/2/2/2
25	LMG	B	5004	-	-	10/28/48/70	0/1/1/1
19	CLA	A	1103	1	-	18/39/115/115	-
19	CLA	B	1240	23	-	19/39/115/115	-
19	CLA	A	1127	-	-	16/39/115/115	-
19	CLA	A	1115	-	-	12/39/115/115	-
22	BCR	F	4016	-	-	10/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	LHG	3	801	-	-	15/19/19/53	-
19	CLA	1	604	13	-	15/39/115/115	-
19	CLA	A	1116	-	-	12/29/105/115	-
19	CLA	B	1238	33	-	12/39/115/115	-
22	BCR	A	4002	-	-	8/29/63/63	0/2/2/2
19	CLA	H	1701	8	-	12/33/109/115	-
19	CLA	B	1205	-	-	13/39/115/115	-
29	CHL	2	615	-	1/1/13/21	7/29/105/117	-
19	CLA	4	617	16	-	18/39/115/115	-
19	CLA	3	614	-	-	3/12/88/115	-
22	BCR	B	4005	-	-	10/29/63/63	0/2/2/2
19	CLA	A	1140	-	-	7/39/115/115	-
19	CLA	B	1204	2	-	18/39/115/115	-
22	BCR	I	4020	-	-	14/29/63/63	0/2/2/2
19	CLA	1	607	-	-	9/17/93/115	-
25	LMG	B	5007	-	-	10/29/49/70	0/1/1/1
19	CLA	A	1013	-	-	14/39/115/115	-
19	CLA	B	1219	2	-	16/39/115/115	-
19	CLA	B	1227	-	-	14/39/115/115	-
24	LMT	2	808	-	-	4/21/61/61	0/2/2/2
25	LMG	A	5006	-	-	10/45/65/70	0/1/1/1
19	CLA	B	1232	-	-	13/27/103/115	-
22	BCR	G	4011	-	-	7/29/63/63	0/2/2/2
25	LMG	F	5004	-	-	8/29/49/70	0/1/1/1
19	CLA	A	1101	1	-	16/39/115/115	-
29	CHL	2	609	14	1/1/15/21	7/41/117/117	-
19	CLA	B	1216	-	-	12/39/115/115	-
22	BCR	1	503	-	-	6/29/63/63	0/2/2/2
25	LMG	G	5002	-	-	18/45/65/70	0/1/1/1
28	LUT	3	501	-	1/1/12/27	6/29/67/67	0/2/2/2
19	CLA	K	1403	-	-	8/19/95/115	-
19	CLA	3	608	-	-	6/19/95/115	-
19	CLA	B	1207	2	-	15/39/115/115	-
23	LHG	B	5002	-	-	29/53/53/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	CHL	4	610	-	-	3/19/95/117	-
19	CLA	B	1223	2	-	12/39/115/115	-
19	CLA	4	612	16	-	14/39/115/115	-
19	CLA	B	1021	-	-	8/39/115/115	-
19	CLA	4	601	16	-	16/33/109/115	-
22	BCR	3	503	-	-	10/29/63/63	0/2/2/2
19	CLA	A	1105	1	-	13/33/109/115	-
19	CLA	K	1401	-	-	8/15/91/115	-
19	CLA	1	611	-	-	17/39/115/115	-
19	CLA	A	1119	-	-	21/39/115/115	-
22	BCR	L	4019	-	-	6/29/63/63	0/2/2/2
19	CLA	A	1141	-	-	17/33/109/115	-
19	CLA	B	1211	-	-	18/39/115/115	-
19	CLA	1	602	13	-	6/17/93/115	-
27	DGD	F	5005	-	-	15/46/86/95	0/2/2/2
19	CLA	A	1136	-	-	20/39/115/115	-
19	CLA	B	1208	-	-	14/33/109/115	-
22	BCR	J	4012	-	-	6/29/63/63	0/2/2/2
24	LMT	G	5005	-	-	5/17/57/61	0/2/2/2
19	CLA	F	1302	6	-	13/39/115/115	-
21	SF4	C	3003	3	-	-	0/6/5/5
30	XAT	4	502	-	2/2/12/26	2/31/93/93	0/4/4/4
19	CLA	A	1128	-	-	16/39/115/115	-
19	CLA	2	601	14	-	9/33/109/115	-
19	CLA	A	1114	-	-	9/17/93/115	-
22	BCR	B	4010	-	-	8/29/63/63	0/2/2/2
24	LMT	B	5008	-	-	8/17/57/61	0/2/2/2
24	LMT	G	5004	-	-	10/21/61/61	0/2/2/2
19	CLA	B	1237	-	-	20/39/115/115	-
19	CLA	B	1231	2	-	6/33/109/115	-
29	CHL	2	611	-	-	3/20/96/117	-
19	CLA	A	1107	1	-	15/39/115/115	-
19	CLA	A	1118	1	-	7/21/97/115	-
19	CLA	A	1102	1	-	22/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	CHL	2	613	-	-	4/17/93/117	-
19	CLA	A	1012	-	-	10/39/115/115	-
19	CLA	A	1138	1	-	18/39/115/115	-
19	CLA	B	1210	-	-	11/39/115/115	-
19	CLA	B	1203	2	-	11/39/115/115	-
19	CLA	1	613	-	-	6/15/91/115	-
28	LUT	J	4013	-	1/1/12/27	5/29/67/67	0/2/2/2
19	CLA	B	1023	-	-	17/39/115/115	-
25	LMG	G	5001	-	-	16/44/64/70	0/1/1/1
20	PQN	B	2002	-	-	6/23/43/43	0/2/2/2
25	LMG	F	5001	-	-	4/25/45/70	0/1/1/1
19	CLA	2	602	-	-	7/24/100/115	-
19	CLA	4	608	-	-	7/17/93/115	-
19	CLA	4	604	16	-	7/33/109/115	-
19	CLA	3	613	-	-	6/17/93/115	-
22	BCR	A	4011	-	-	8/29/63/63	0/2/2/2
28	LUT	3	502	-	1/1/12/27	1/29/67/67	0/2/2/2
27	DGD	J	5001	-	-	11/47/87/95	0/2/2/2
19	CLA	3	601	15	-	12/27/103/115	-
19	CLA	2	605	14	-	17/39/115/115	-
19	CLA	B	1234	2	-	8/27/103/115	-
22	BCR	I	4018	-	-	7/29/63/63	0/2/2/2
22	BCR	3	506	-	-	5/29/63/63	0/2/2/2
29	CHL	1	610	13	-	5/19/95/117	-
19	CLA	F	1301	-	-	17/39/115/115	-
19	CLA	A	1126	-	-	16/39/115/115	-
19	CLA	B	1226	2	-	16/39/115/115	-
22	BCR	L	4020	-	-	7/29/63/63	0/2/2/2
29	CHL	1	609	13	1/1/13/21	3/29/105/117	-
19	CLA	A	1134	1	-	10/27/103/115	-
23	LHG	1	801	-	-	30/53/53/53	-
24	LMT	B	5006	-	-	4/18/58/61	0/2/2/2
27	DGD	1	803	-	-	14/30/70/95	0/2/2/2
19	CLA	2	608	-	-	8/21/97/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	CLA	A	1132	1	-	17/39/115/115	-
19	CLA	4	607	-	-	14/33/109/115	-
22	BCR	K	4002	-	-	5/29/63/63	0/2/2/2
29	CHL	4	613	-	1/1/14/21	6/35/111/117	-
19	CLA	L	1501	12	-	11/21/97/115	-
25	LMG	B	5003	-	-	9/30/50/70	0/1/1/1
21	SF4	C	3002	3	-	-	0/6/5/5
19	CLA	B	1225	-	-	15/39/115/115	-
31	3PH	2	807	-	-	16/34/34/49	-
19	CLA	B	1217	2	-	7/17/93/115	-
27	DGD	3	803	-	-	8/40/80/95	0/2/2/2
25	LMG	F	5003	-	-	13/31/51/70	0/1/1/1
19	CLA	4	605	-	-	10/33/109/115	-
19	CLA	A	1111	-	-	17/39/115/115	-
19	CLA	J	1901	10	-	7/21/97/115	-
19	CLA	1	601	13	-	16/39/115/115	-
19	CLA	3	610	15	-	19/39/115/115	-
19	CLA	4	602	-	-	7/21/97/115	-
19	CLA	4	603	16	-	13/39/115/115	-
22	BCR	B	4006	-	-	3/29/63/63	0/2/2/2
25	LMG	G	5006	-	-	10/20/40/70	0/1/1/1
29	CHL	3	604	15	1/1/15/21	10/41/117/117	-
19	CLA	2	604	14	-	18/39/115/115	-
25	LMG	2	805	-	-	6/25/45/70	0/1/1/1
25	LMG	2	806	-	-	1/4/24/70	0/1/1/1
19	CLA	B	1214	-	-	14/39/115/115	-
19	CLA	B	1213	2	-	8/33/109/115	-
19	CLA	A	1124	-	-	8/27/103/115	-
19	CLA	B	1228	2	-	14/33/109/115	-
25	LMG	2	802	-	-	4/20/40/70	0/1/1/1
28	LUT	1	501	-	1/1/12/27	4/29/67/67	0/2/2/2
22	BCR	A	4017	-	-	9/29/63/63	0/2/2/2
19	CLA	G	1602	7	-	9/17/93/115	-
19	CLA	G	1601	-	-	10/27/103/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	CLA	2	606	-	-	8/21/97/115	-
19	CLA	L	1503	-	-	8/21/97/115	-
19	CLA	B	1218	-	-	11/39/115/115	-
19	CLA	B	1215	2	-	12/39/115/115	-
30	XAT	2	502	-	2/2/12/26	7/31/93/93	0/4/4/4
19	CLA	B	1202	2	-	19/39/115/115	-
22	BCR	A	4003	-	-	6/29/63/63	0/2/2/2
24	LMT	A	5004	-	-	7/21/61/61	0/2/2/2
22	BCR	K	4001	-	-	6/29/63/63	0/2/2/2
25	LMG	F	5006	-	-	1/4/24/70	0/1/1/1
25	LMG	2	803	-	-	12/31/51/70	0/1/1/1
19	CLA	B	1220	2	-	9/27/103/115	-
29	CHL	3	611	-	-	0/19/95/117	-
19	CLA	A	1130	1	-	6/27/103/115	-
19	CLA	1	614	13	-	16/33/109/115	-
22	BCR	B	4009	-	-	8/29/63/63	0/2/2/2
22	BCR	2	503	-	-	14/29/63/63	0/2/2/2
23	LHG	A	5001	-	-	26/44/44/53	-
22	BCR	H	4021	-	-	8/29/63/63	0/2/2/2
25	LMG	3	802	-	-	6/25/45/70	0/1/1/1
27	DGD	4	802	-	-	17/39/79/95	0/2/2/2
19	CLA	B	1235	2	-	13/39/115/115	-
19	CLA	2	607	-	-	15/33/109/115	-
21	SF4	A	3001	1,2	-	-	0/6/5/5
23	LHG	B	5001	19	-	9/23/23/53	-
19	CLA	A	1110	1	-	8/27/103/115	-
19	CLA	B	1221	-	-	18/39/115/115	-
25	LMG	F	5002	-	-	11/42/62/70	0/1/1/1
22	BCR	F	4014	-	-	8/29/63/63	0/2/2/2
19	CLA	B	1224	-	-	19/39/115/115	-
19	CLA	1	603	-	-	10/27/103/115	-
19	CLA	A	1133	1	-	21/39/115/115	-
18	CL0	A	1011	1	-	10/39/115/115	-
19	CLA	B	1222	33	-	19/39/115/115	-
19	CLA	B	1230	-	-	15/31/107/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	LUT	4	501	-	1/1/12/27	7/29/67/67	0/2/2/2
23	LHG	A	5002	-	-	28/53/53/53	-
19	CLA	2	603	14	-	16/39/115/115	-
19	CLA	3	603	15	-	12/27/103/115	-
19	CLA	B	1212	-	-	12/27/103/115	-
19	CLA	A	1106	1	-	15/39/115/115	-
19	CLA	A	1108	-	-	8/21/97/115	-
19	CLA	1	605	13	-	16/39/115/115	-
19	CLA	1	608	13	-	7/17/93/115	-
19	CLA	A	1120	1	-	16/33/109/115	-
19	CLA	3	605	-	-	11/27/103/115	-
19	CLA	2	612	-	-	8/27/103/115	-
19	CLA	4	609	16	-	11/21/97/115	-
19	CLA	B	1229	2	-	13/39/115/115	-
19	CLA	3	607	-	-	9/24/100/115	-
19	CLA	1	606	-	-	5/21/97/115	-
19	CLA	L	1502	-	-	15/33/109/115	-
19	CLA	A	1131	1	-	19/39/115/115	-
28	LUT	1	502	-	1/1/12/27	5/29/67/67	0/2/2/2
20	PQN	A	2001	-	-	6/23/43/43	0/2/2/2
19	CLA	A	1135	1	-	11/23/99/115	-

The worst 5 of 1193 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	3	501	LUT	C24-C25	14.33	1.51	1.33
28	1	502	LUT	C24-C25	14.27	1.50	1.33
28	2	501	LUT	C24-C25	14.15	1.50	1.33
28	J	4013	LUT	C24-C25	14.13	1.50	1.33
28	1	501	LUT	C24-C25	14.08	1.50	1.33

The worst 5 of 3291 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	K	4001	BCR	C10-C11-C12	18.19	180.00	123.22
22	I	4018	BCR	C10-C11-C12	18.11	179.74	123.22
22	A	4017	BCR	C16-C15-C14	18.06	160.47	123.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	B	4005	BCR	C10-C11-C12	18.03	179.47	123.22
22	A	4017	BCR	C10-C11-C12	17.99	179.37	123.22

5 of 19 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
28	J	4013	LUT	C26
28	1	501	LUT	C26
28	1	502	LUT	C26
28	2	501	LUT	C26
28	3	501	LUT	C26

5 of 2631 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	A	1011	CL0	C1A-C2A-CAA-CBA
18	A	1011	CL0	C3A-C2A-CAA-CBA
19	A	1012	CLA	CBD-CGD-O2D-CED
19	A	1013	CLA	C2-C1-O2A-CGA
19	A	1013	CLA	CBD-CGD-O2D-CED

There are no ring outliers.

198 monomers are involved in 753 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	2	501	LUT	11	0
19	A	1139	CLA	3	0
19	B	1239	CLA	5	0
29	4	611	CHL	2	0
22	A	4008	BCR	4	0
19	A	1125	CLA	9	0
19	A	1122	CLA	5	0
29	1	612	CHL	1	0
29	2	610	CHL	1	0
19	A	1121	CLA	4	0
19	B	1209	CLA	2	0
22	1	504	BCR	3	0
19	4	606	CLA	6	0
29	4	615	CHL	1	0
19	3	617	CLA	1	0
19	A	1113	CLA	4	0
27	G	5003	DGD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	4	505	LUT	5	0
19	A	1117	CLA	3	0
19	B	1201	CLA	1	0
22	A	4007	BCR	5	0
19	A	1109	CLA	7	0
19	G	1603	CLA	6	0
19	A	1104	CLA	7	0
19	A	1112	CLA	4	0
19	B	1206	CLA	7	0
19	B	1022	CLA	5	0
19	B	1236	CLA	6	0
19	3	606	CLA	3	0
19	K	1402	CLA	3	0
19	3	612	CLA	8	0
19	3	602	CLA	3	0
19	A	1137	CLA	2	0
22	B	4004	BCR	8	0
19	A	1123	CLA	1	0
19	B	1240	CLA	1	0
19	A	1127	CLA	5	0
19	A	1115	CLA	1	0
22	F	4016	BCR	6	0
23	3	801	LHG	1	0
19	1	604	CLA	1	0
19	A	1116	CLA	3	0
19	B	1238	CLA	3	0
22	A	4002	BCR	8	0
19	H	1701	CLA	3	0
19	B	1205	CLA	5	0
19	4	617	CLA	3	0
22	B	4005	BCR	6	0
19	3	614	CLA	1	0
29	2	615	CHL	9	0
19	A	1140	CLA	4	0
19	B	1204	CLA	2	0
22	I	4020	BCR	4	0
19	1	607	CLA	1	0
19	A	1013	CLA	7	0
19	B	1219	CLA	4	0
19	B	1227	CLA	4	0
25	A	5006	LMG	2	0
19	B	1232	CLA	6	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	G	4011	BCR	8	0
19	A	1101	CLA	6	0
29	2	609	CHL	3	0
19	B	1216	CLA	4	0
22	1	503	BCR	6	0
25	G	5002	LMG	2	0
19	K	1403	CLA	2	0
28	3	501	LUT	12	0
19	3	608	CLA	2	0
19	B	1207	CLA	6	0
29	4	610	CHL	2	0
19	B	1223	CLA	4	0
19	4	612	CLA	1	0
19	B	1021	CLA	4	0
19	4	601	CLA	10	0
22	3	503	BCR	17	0
19	K	1401	CLA	4	0
19	1	611	CLA	5	0
19	A	1119	CLA	4	0
22	L	4019	BCR	9	0
19	A	1141	CLA	2	0
19	B	1211	CLA	7	0
27	F	5005	DGD	1	0
19	A	1136	CLA	2	0
19	B	1208	CLA	4	0
22	J	4012	BCR	9	0
19	F	1302	CLA	1	0
21	C	3003	SF4	1	0
30	4	502	XAT	2	0
19	A	1128	CLA	6	0
19	2	601	CLA	10	0
19	A	1114	CLA	2	0
22	B	4010	BCR	10	0
24	B	5008	LMT	2	0
24	G	5004	LMT	3	0
19	B	1231	CLA	6	0
19	B	1237	CLA	1	0
29	2	611	CHL	6	0
19	A	1102	CLA	3	0
19	A	1107	CLA	2	0
19	A	1012	CLA	3	0
19	A	1138	CLA	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	B	1210	CLA	3	0
19	B	1203	CLA	4	0
19	1	613	CLA	4	0
28	J	4013	LUT	12	0
19	B	1023	CLA	5	0
20	B	2002	PQN	1	0
19	2	602	CLA	2	0
19	4	608	CLA	3	0
19	4	604	CLA	5	0
19	3	613	CLA	5	0
22	A	4011	BCR	10	0
28	3	502	LUT	12	0
19	3	601	CLA	6	0
19	2	605	CLA	1	0
19	B	1234	CLA	5	0
22	I	4018	BCR	8	0
22	3	506	BCR	9	0
29	1	610	CHL	3	0
19	F	1301	CLA	1	0
19	A	1126	CLA	4	0
19	B	1226	CLA	4	0
22	L	4020	BCR	8	0
29	1	609	CHL	1	0
19	A	1134	CLA	2	0
19	2	608	CLA	3	0
19	A	1132	CLA	3	0
19	4	607	CLA	5	0
22	K	4002	BCR	9	0
19	L	1501	CLA	2	0
21	C	3002	SF4	1	0
29	4	613	CHL	3	0
19	B	1225	CLA	7	0
19	B	1217	CLA	2	0
19	A	1111	CLA	4	0
19	J	1901	CLA	2	0
19	1	601	CLA	6	0
19	3	610	CLA	4	0
19	4	602	CLA	5	0
19	4	603	CLA	4	0
22	B	4006	BCR	11	0
19	2	604	CLA	6	0
29	3	604	CHL	5	0

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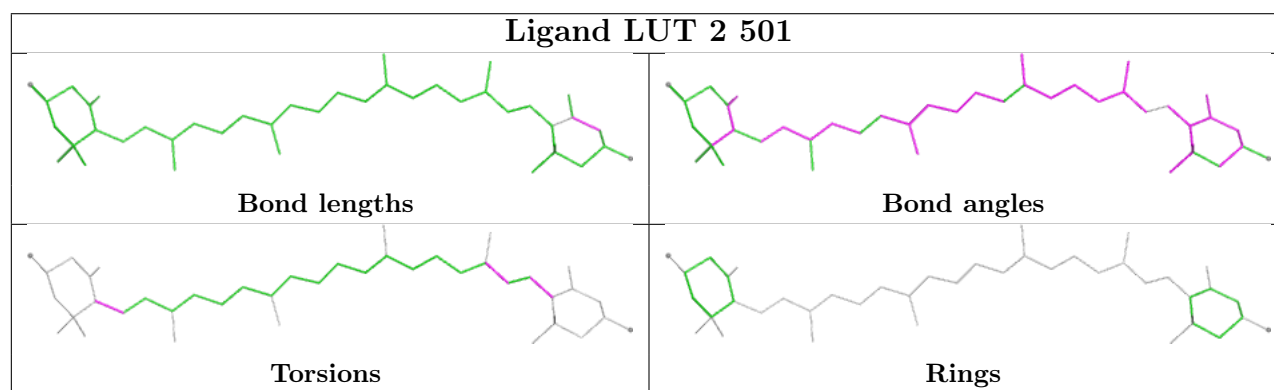
Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	B	1214	CLA	5	0
19	B	1213	CLA	4	0
19	A	1124	CLA	2	0
19	B	1228	CLA	2	0
28	1	501	LUT	10	0
22	A	4017	BCR	8	0
19	G	1602	CLA	1	0
19	G	1601	CLA	1	0
19	2	606	CLA	3	0
19	L	1503	CLA	6	0
19	B	1218	CLA	4	0
19	B	1215	CLA	4	0
19	B	1202	CLA	3	0
22	A	4003	BCR	6	0
22	K	4001	BCR	16	0
30	2	502	XAT	4	0
19	B	1220	CLA	4	0
29	3	611	CHL	1	0
19	A	1130	CLA	2	0
19	1	614	CLA	2	0
22	B	4009	BCR	10	0
22	2	503	BCR	8	0
23	A	5001	LHG	1	0
22	H	4021	BCR	10	0
27	4	802	DGD	1	0
19	B	1235	CLA	3	0
19	2	607	CLA	8	0
19	A	1110	CLA	4	0
19	B	1221	CLA	4	0
25	F	5002	LMG	1	0
22	F	4014	BCR	7	0
19	B	1224	CLA	2	0
19	1	603	CLA	3	0
19	A	1133	CLA	2	0
18	A	1011	CL0	2	0
19	B	1222	CLA	3	0
19	B	1230	CLA	2	0
28	4	501	LUT	18	0
19	2	603	CLA	4	0
19	3	603	CLA	4	0
19	A	1106	CLA	5	0
19	A	1108	CLA	7	0

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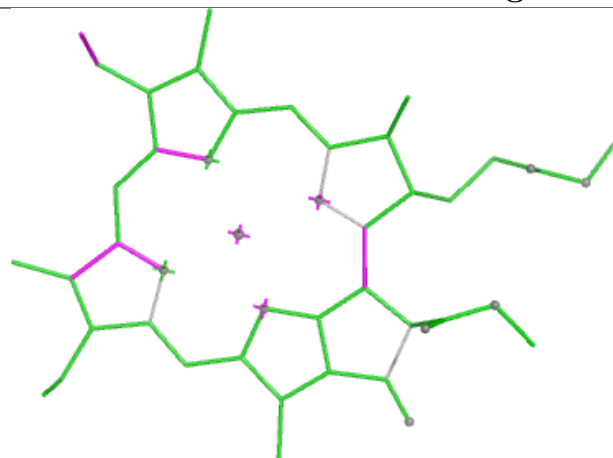
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	1	605	CLA	2	0
19	1	608	CLA	2	0
19	A	1120	CLA	2	0
19	3	605	CLA	2	0
19	2	612	CLA	1	0
19	B	1229	CLA	8	0
19	3	607	CLA	6	0
19	1	606	CLA	3	0
19	L	1502	CLA	3	0
19	A	1131	CLA	1	0
28	1	502	LUT	7	0
20	A	2001	PQN	2	0
19	A	1135	CLA	8	0

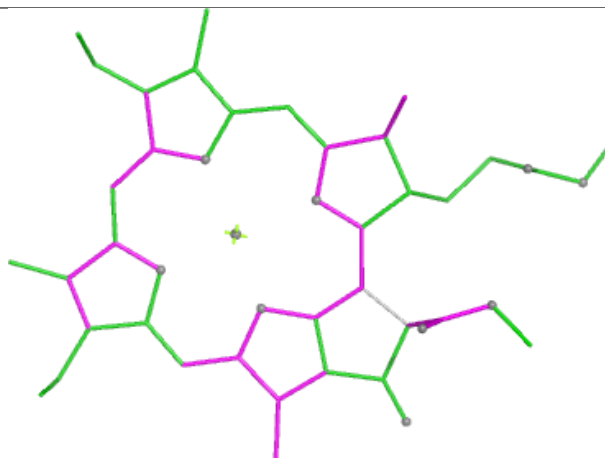
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



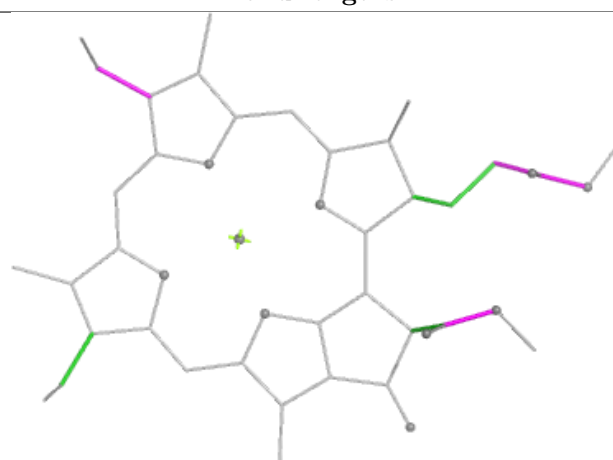
Ligand CLA K 1404



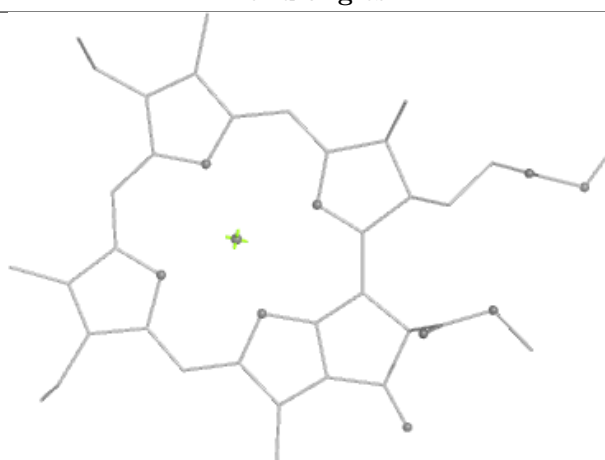
Bond lengths



Bond angles

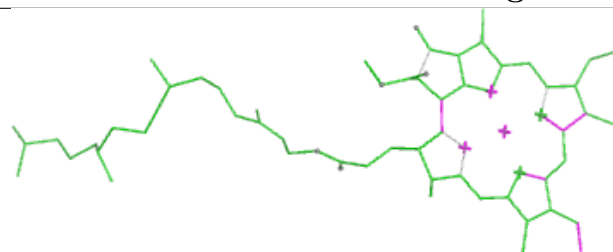


Torsions

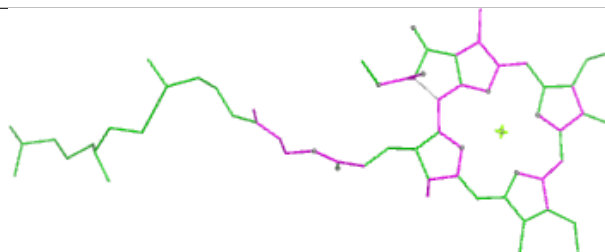


Rings

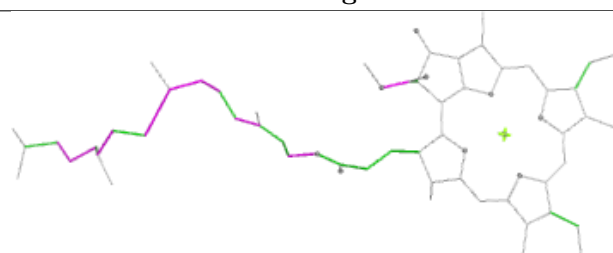
Ligand CLA A 1139



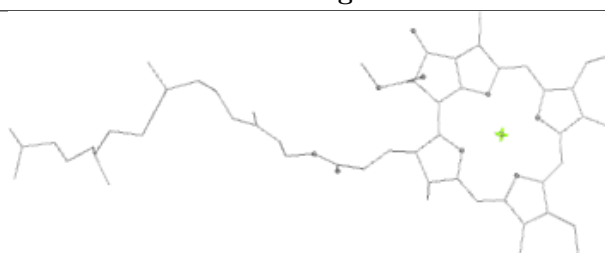
Bond lengths



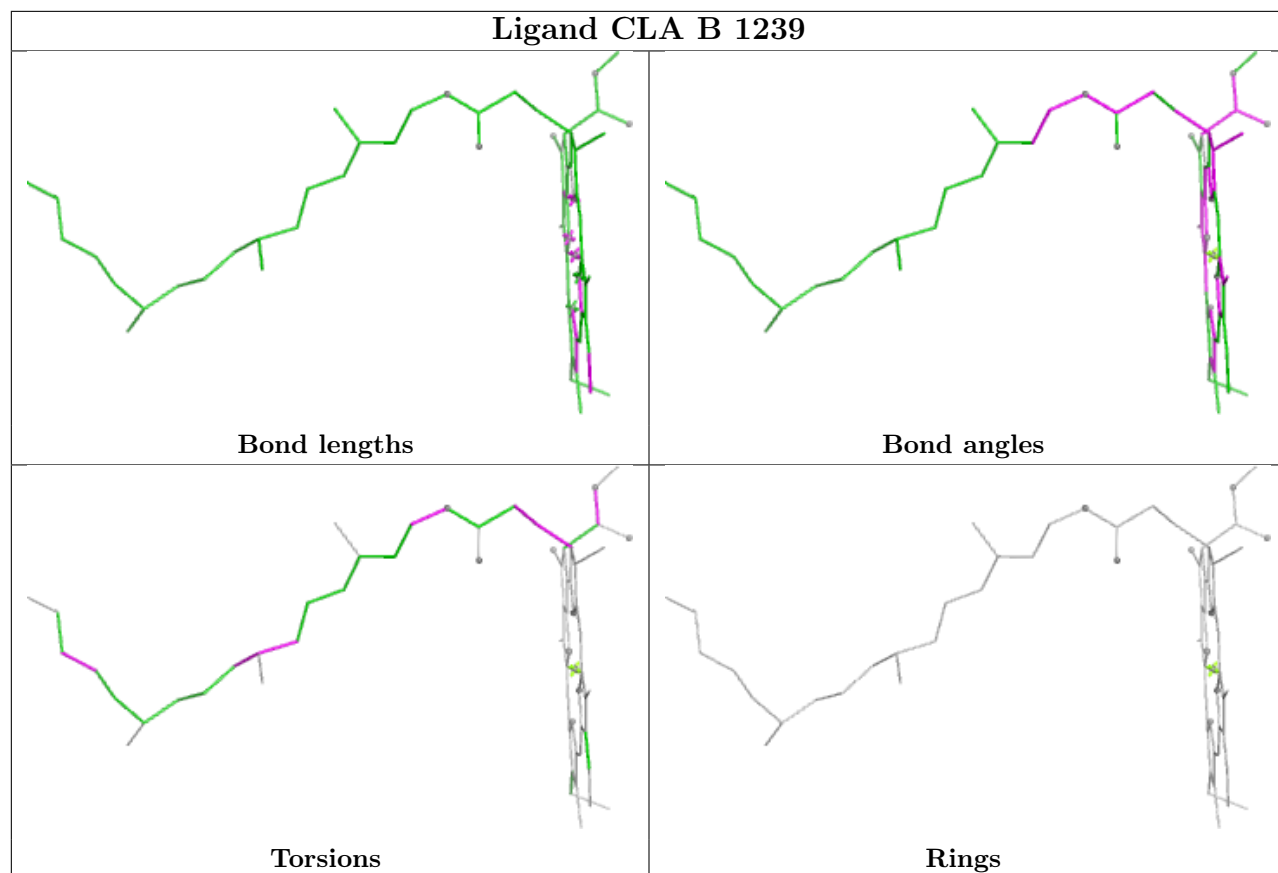
Bond angles

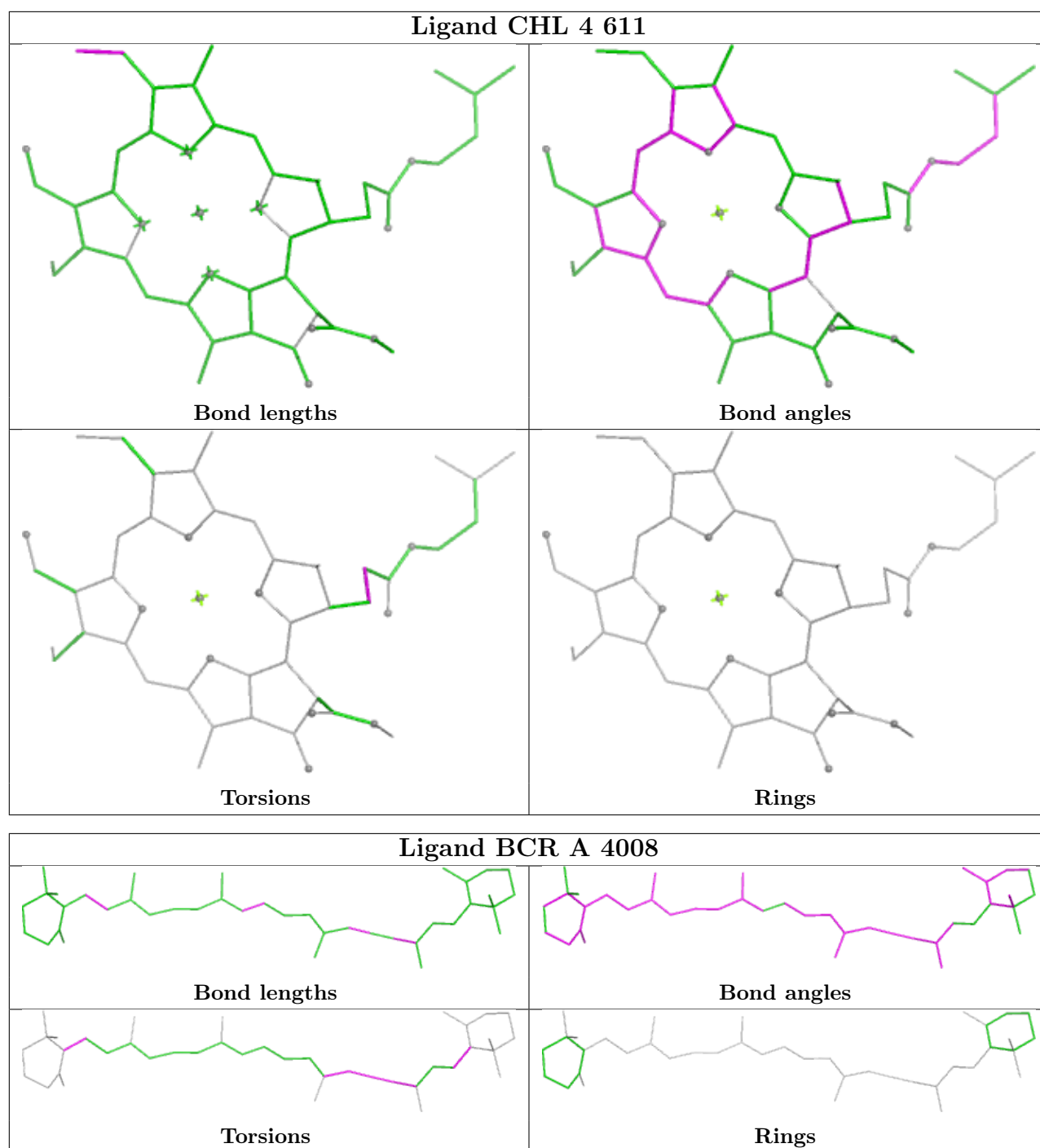


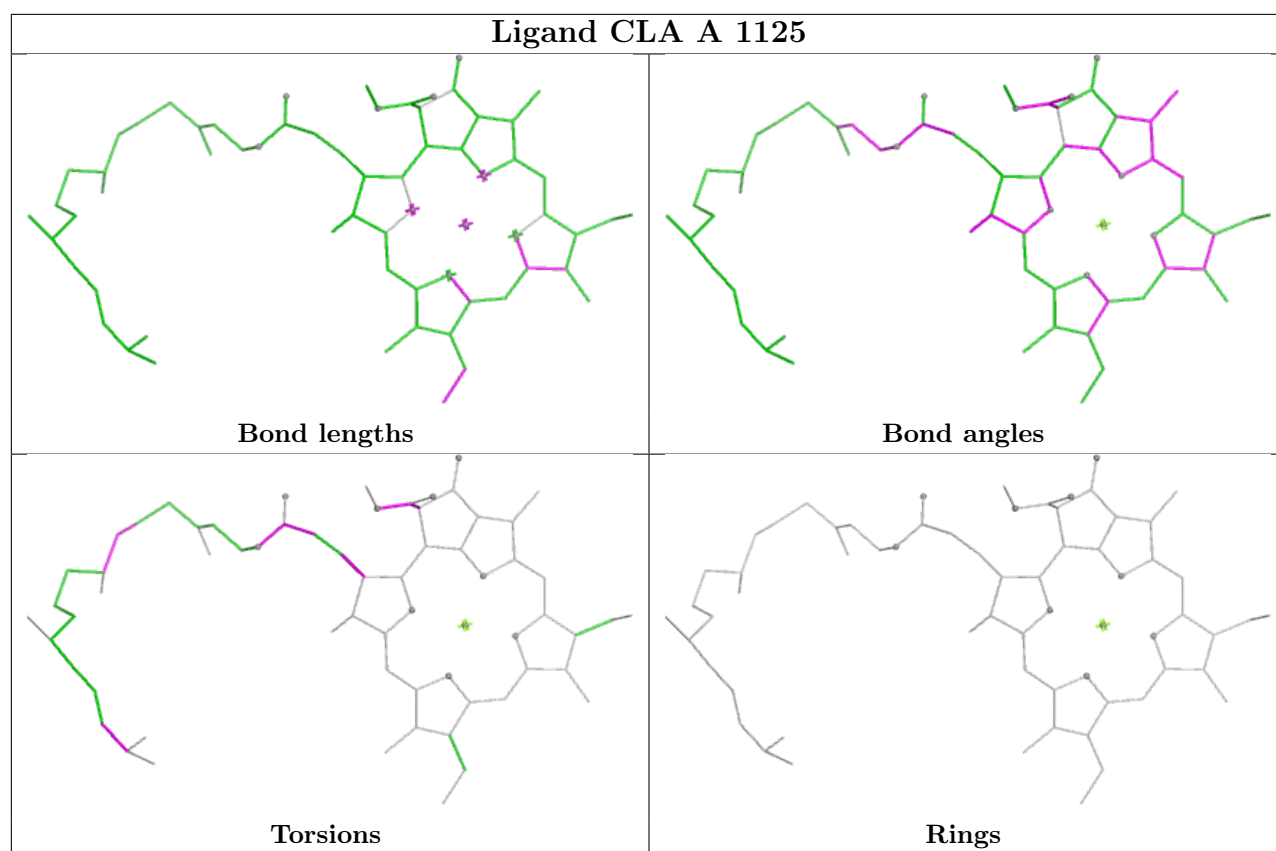
Torsions

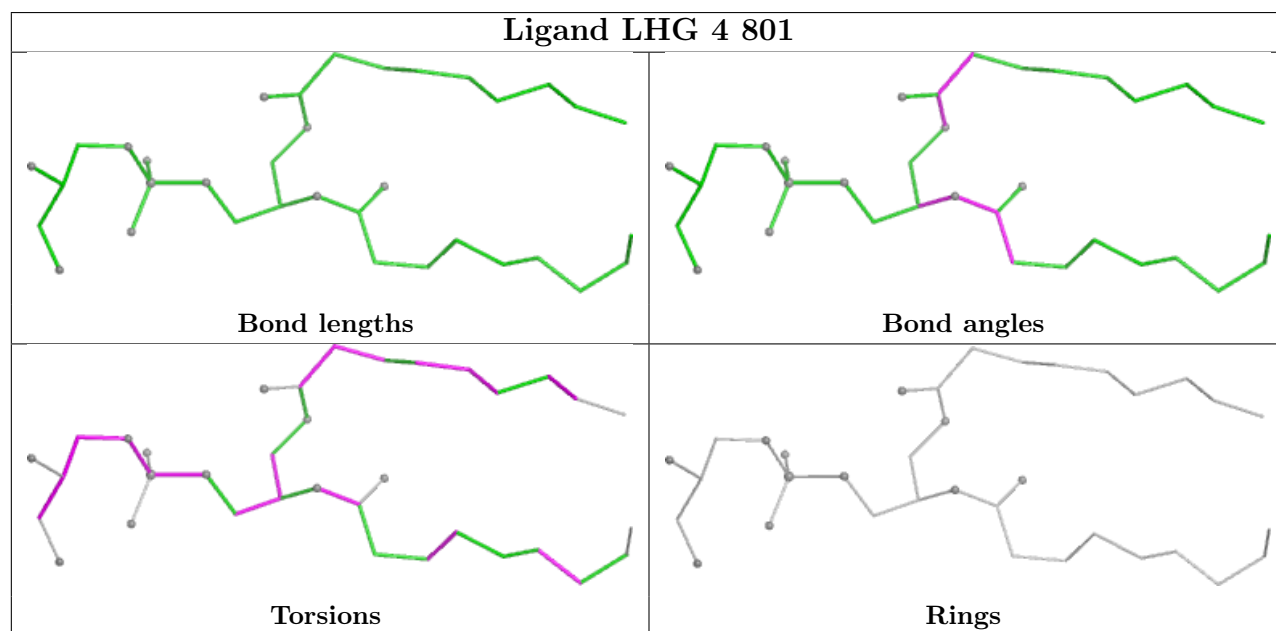
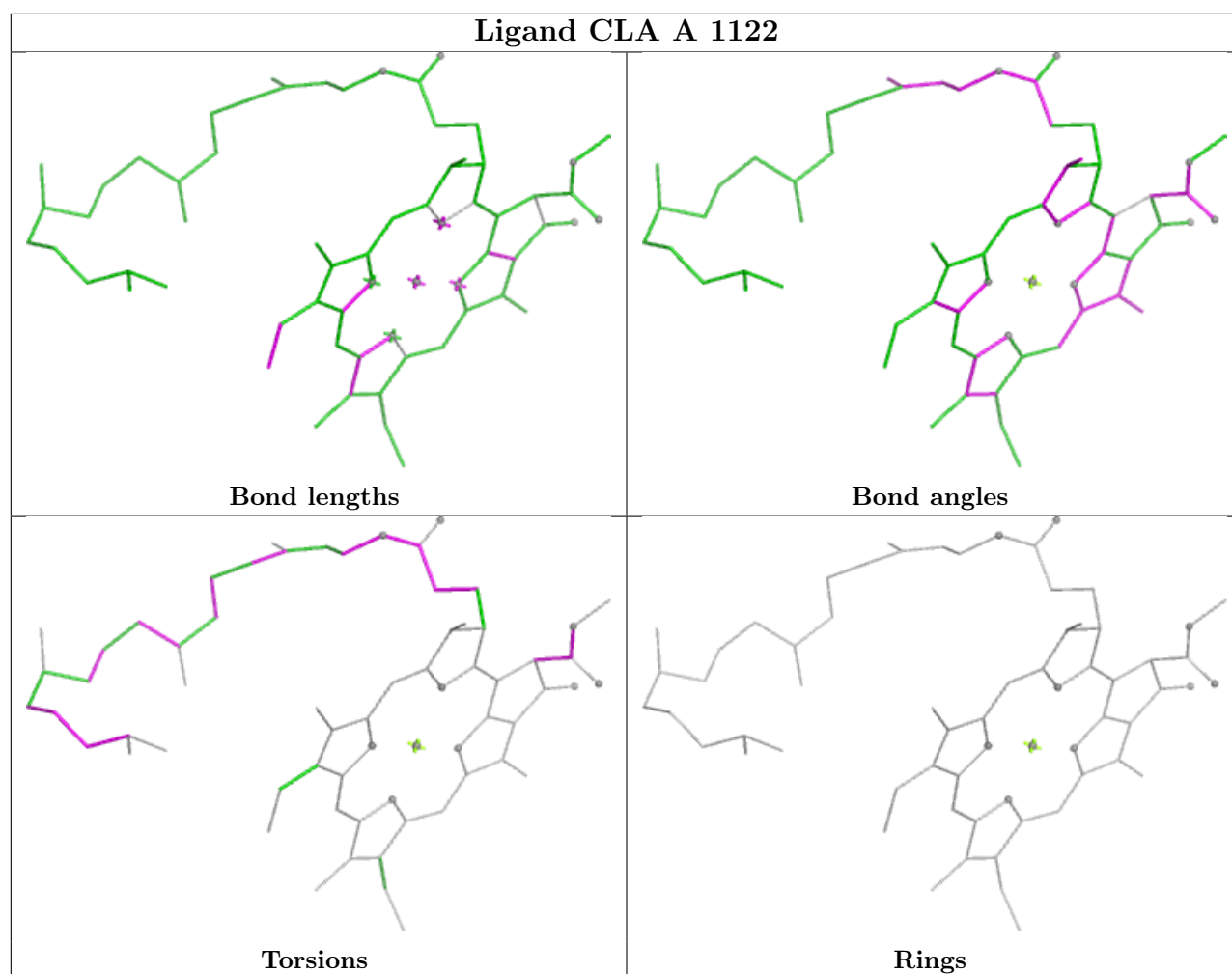


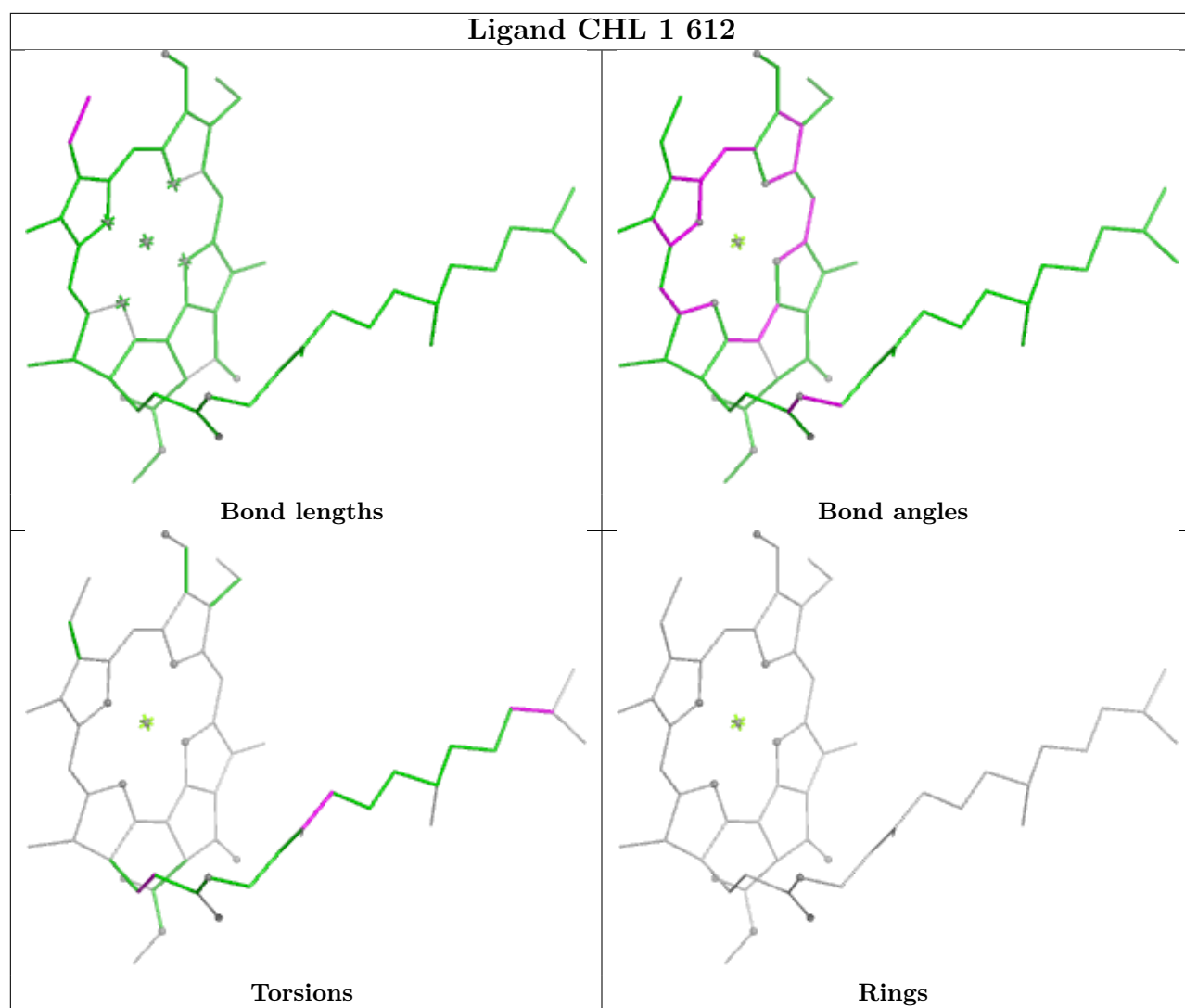
Rings



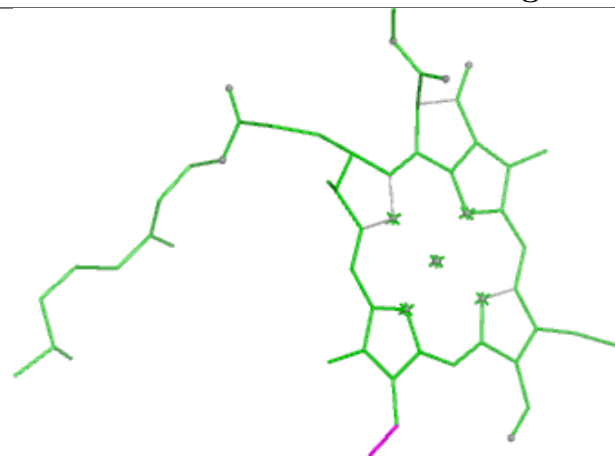




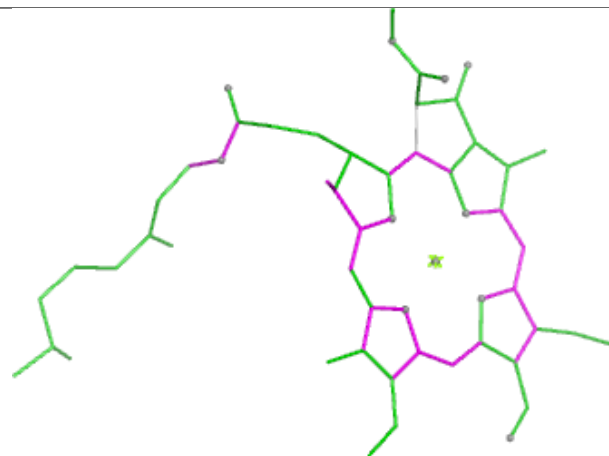




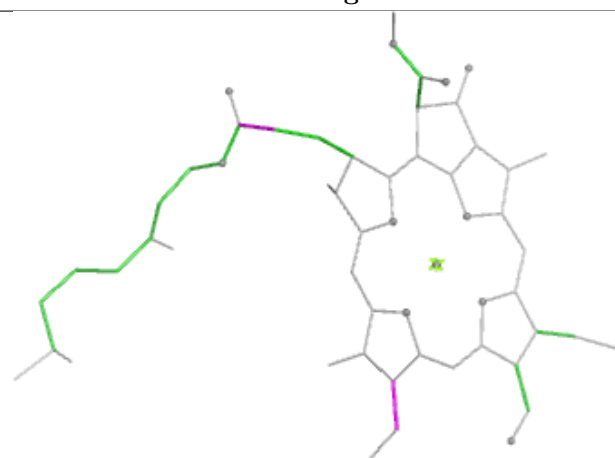
Ligand CHL 2 610



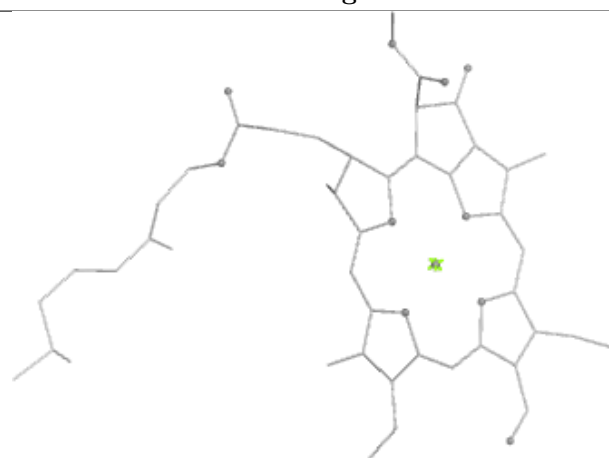
Bond lengths



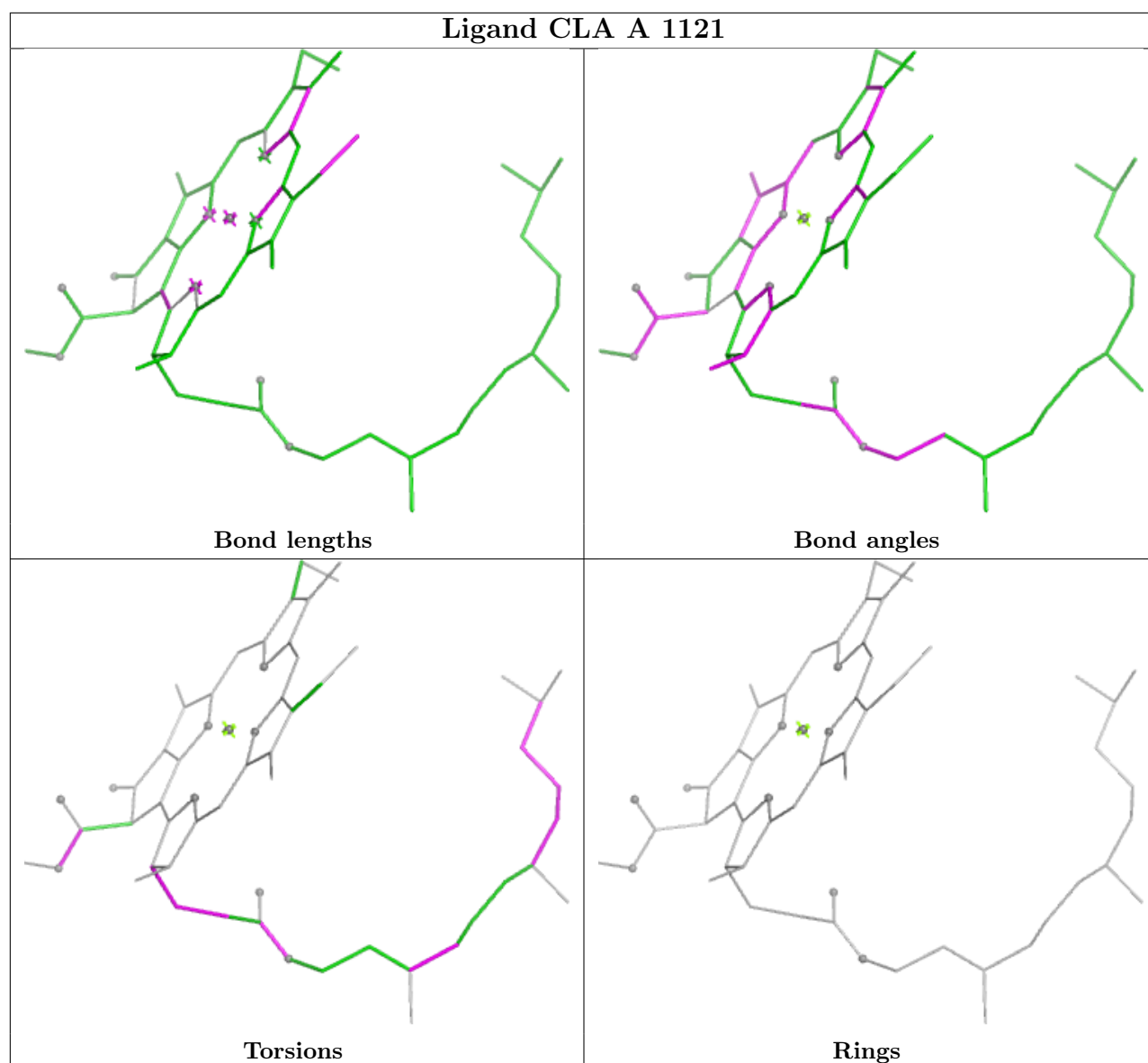
Bond angles

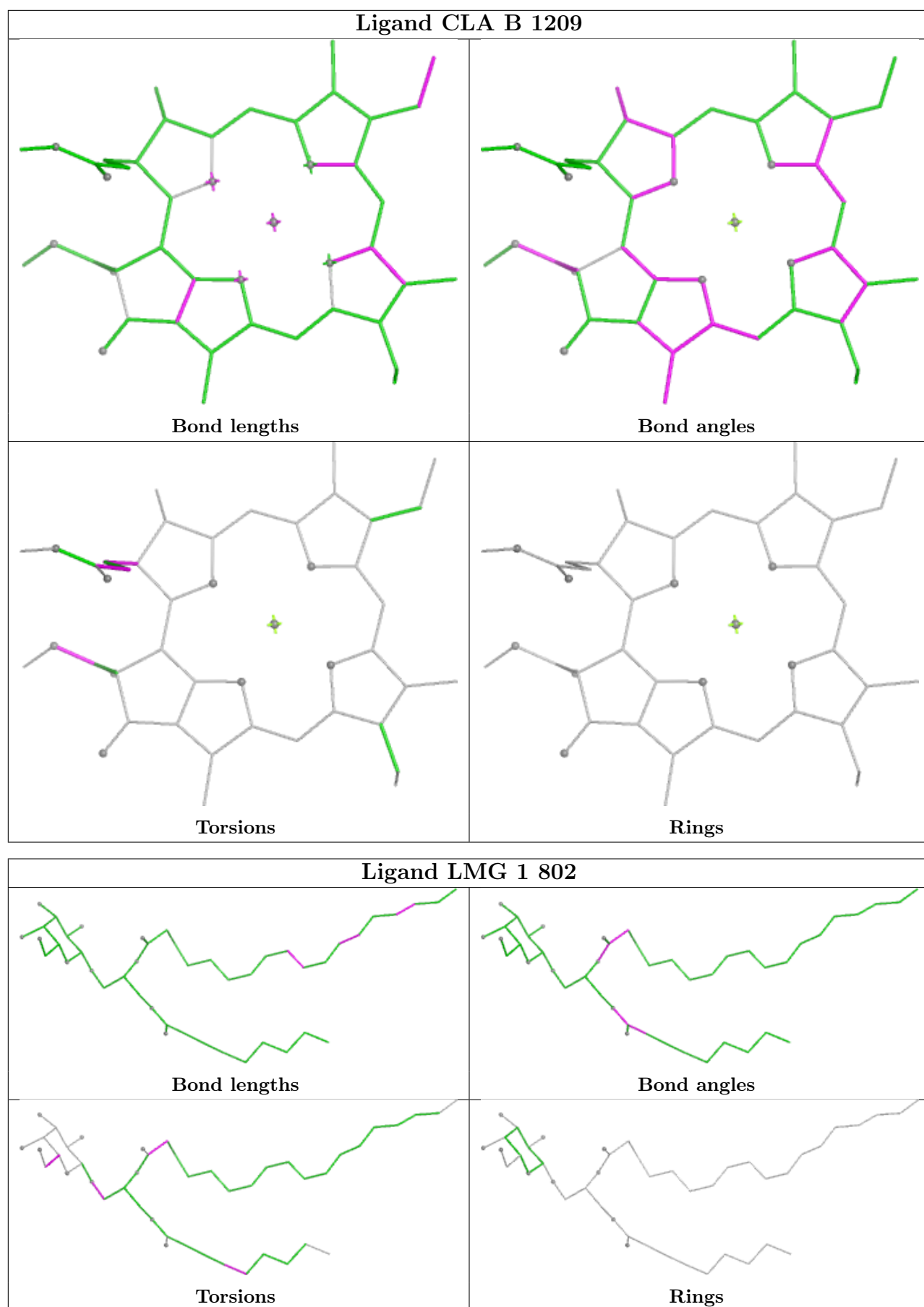


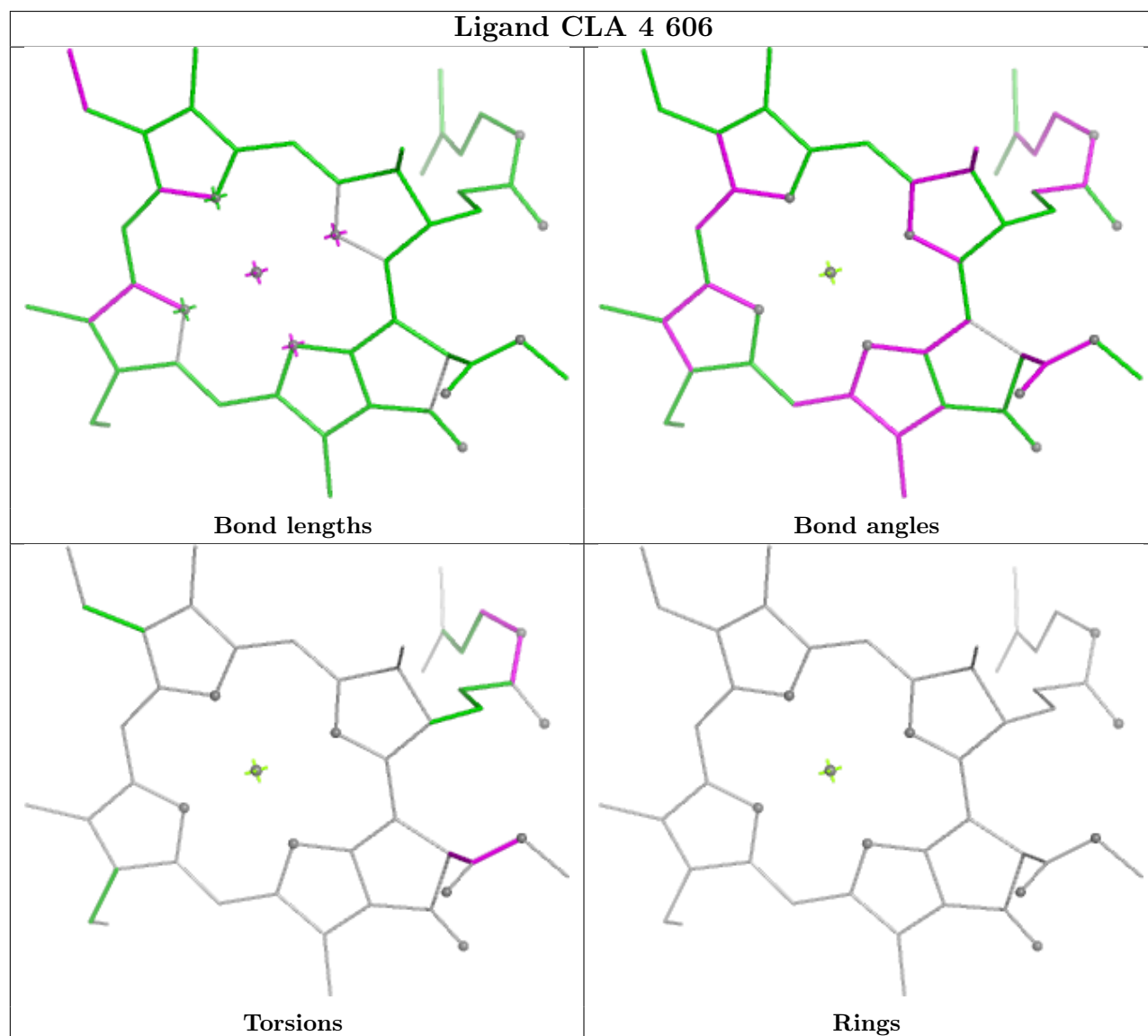
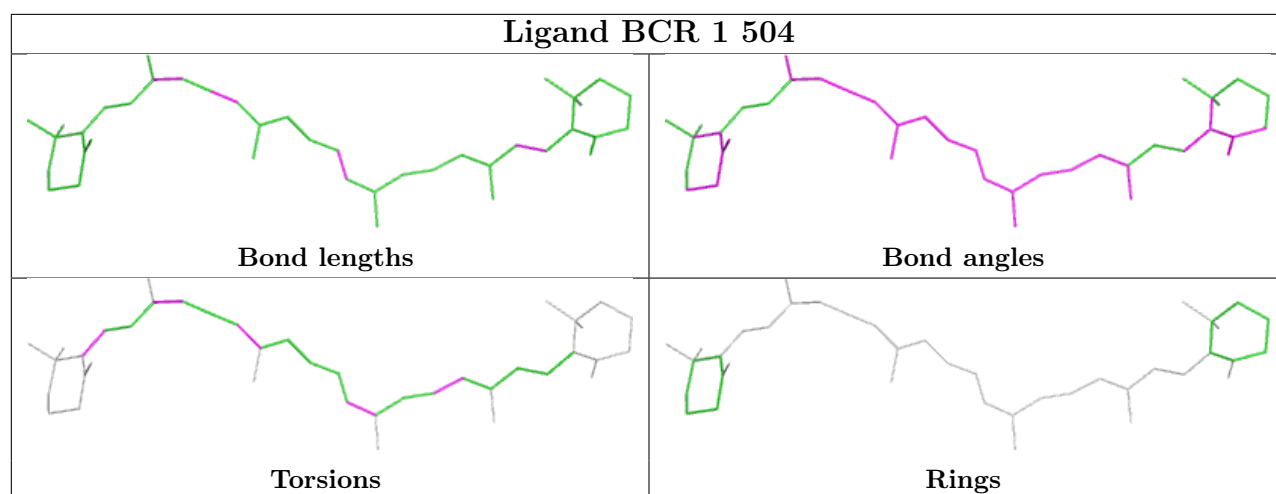
Torsions



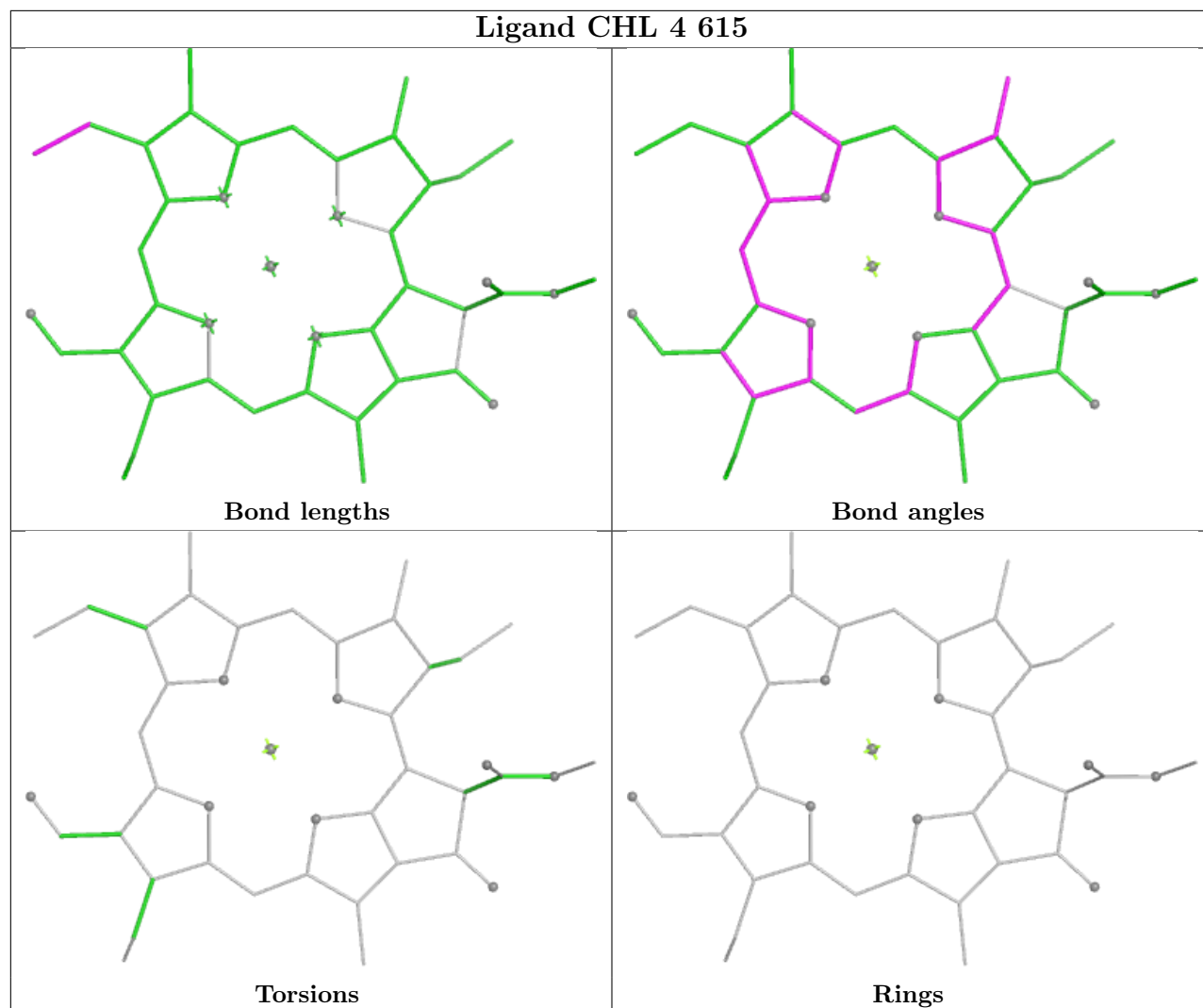
Rings

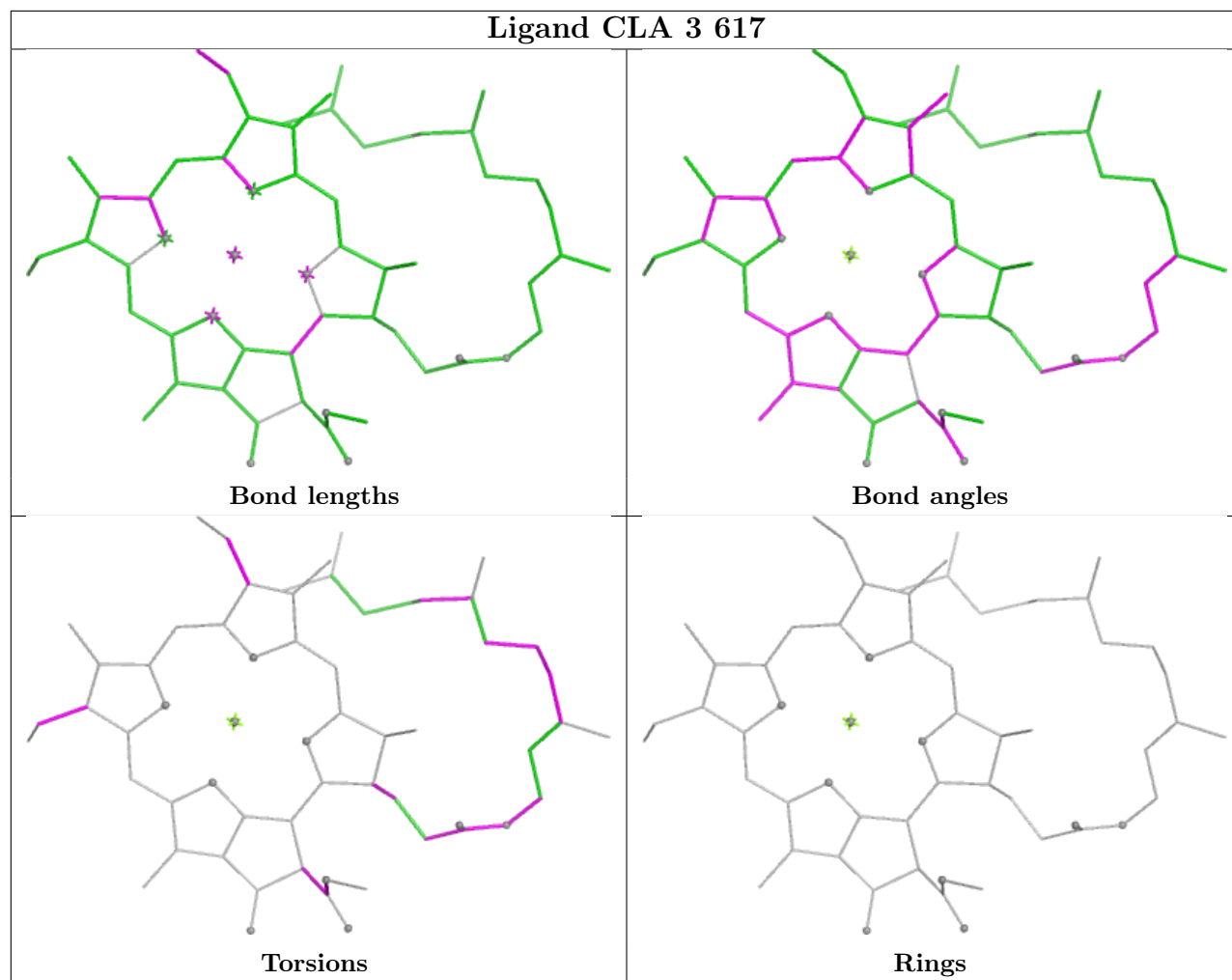




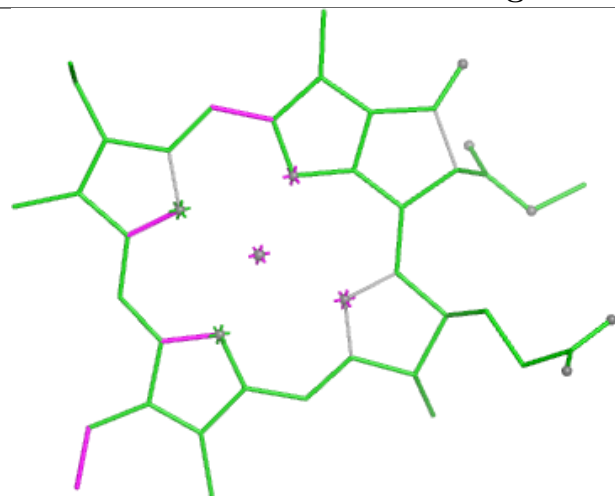


Ligand CHL 4 615

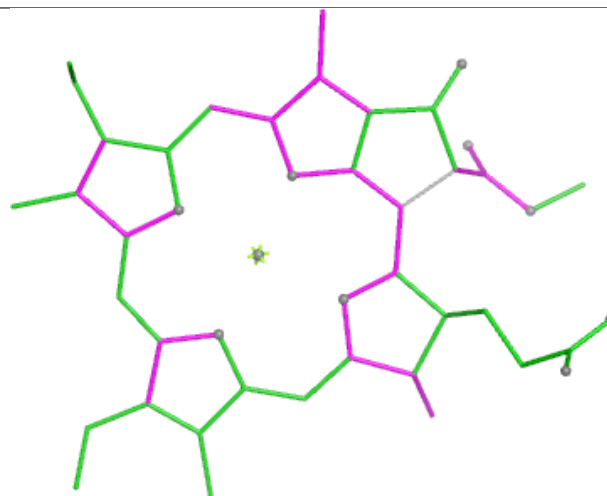




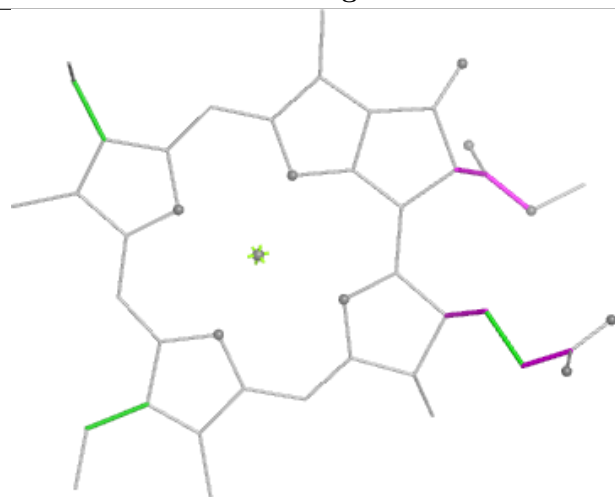
Ligand CLA A 1113



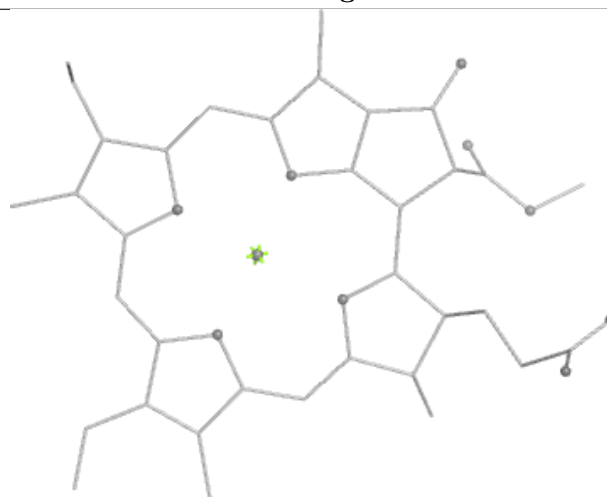
Bond lengths



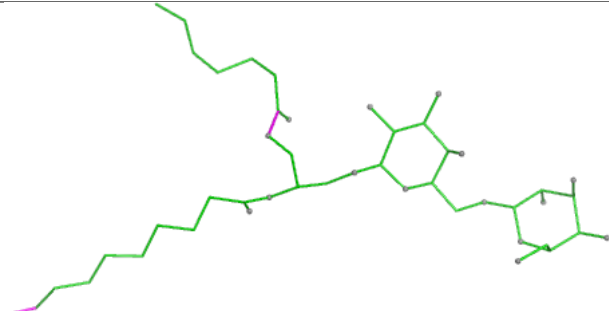
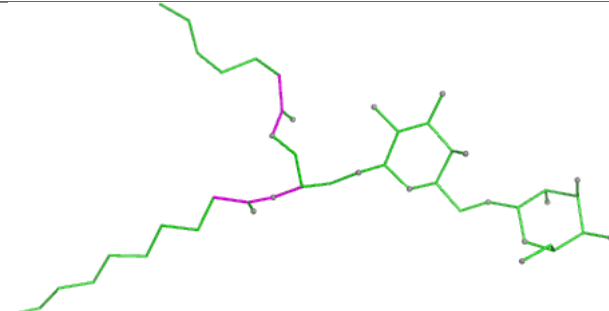
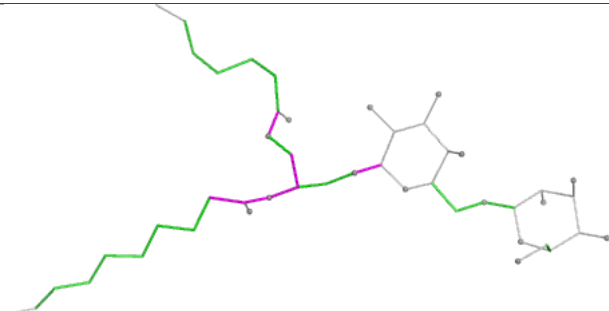
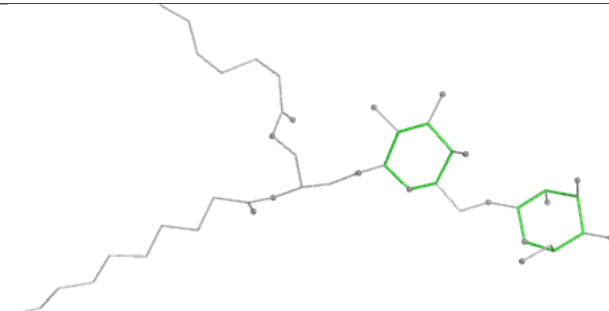
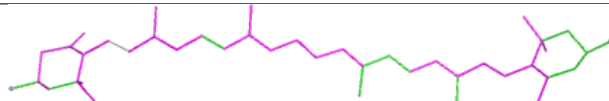
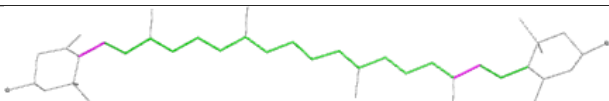
Bond angles

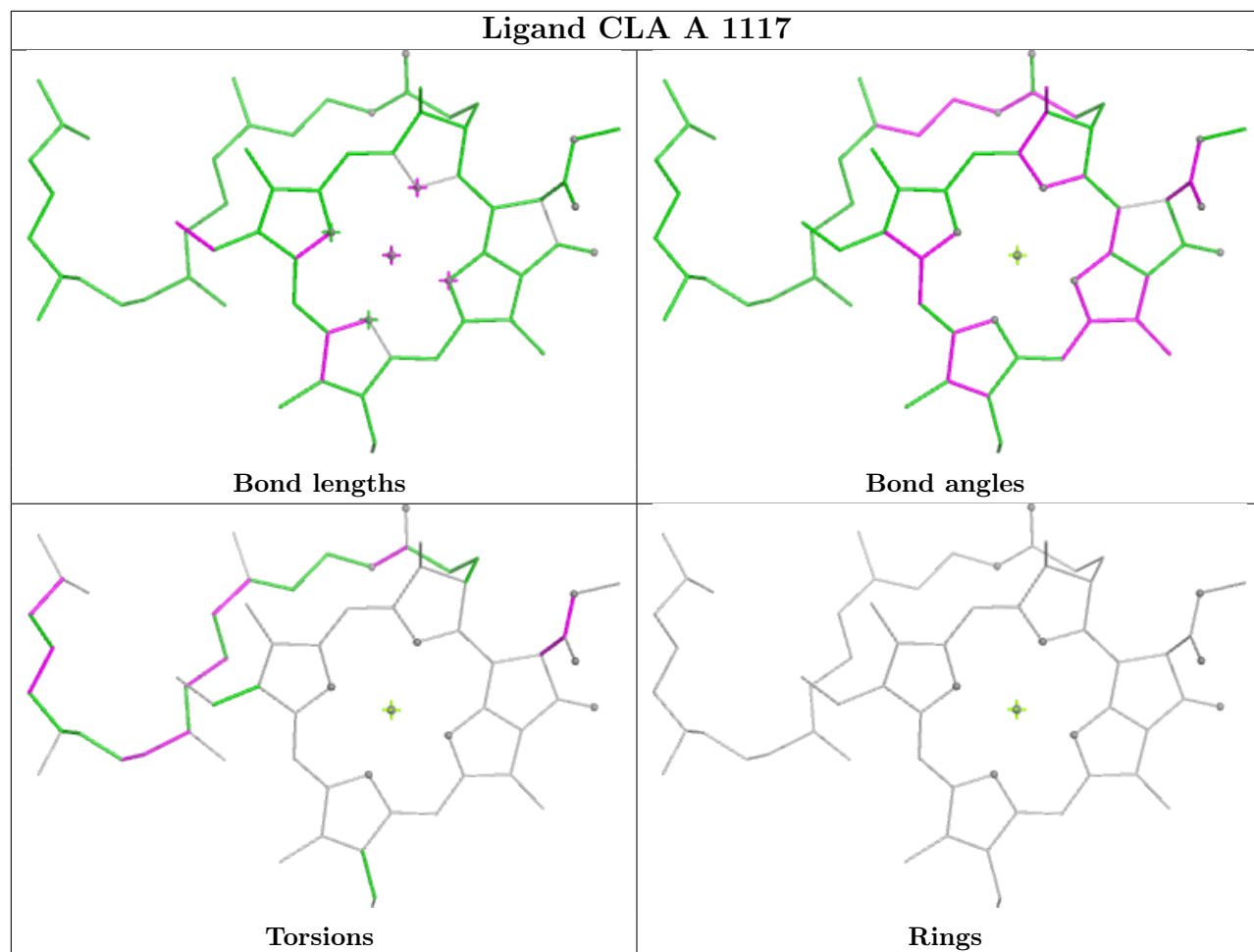


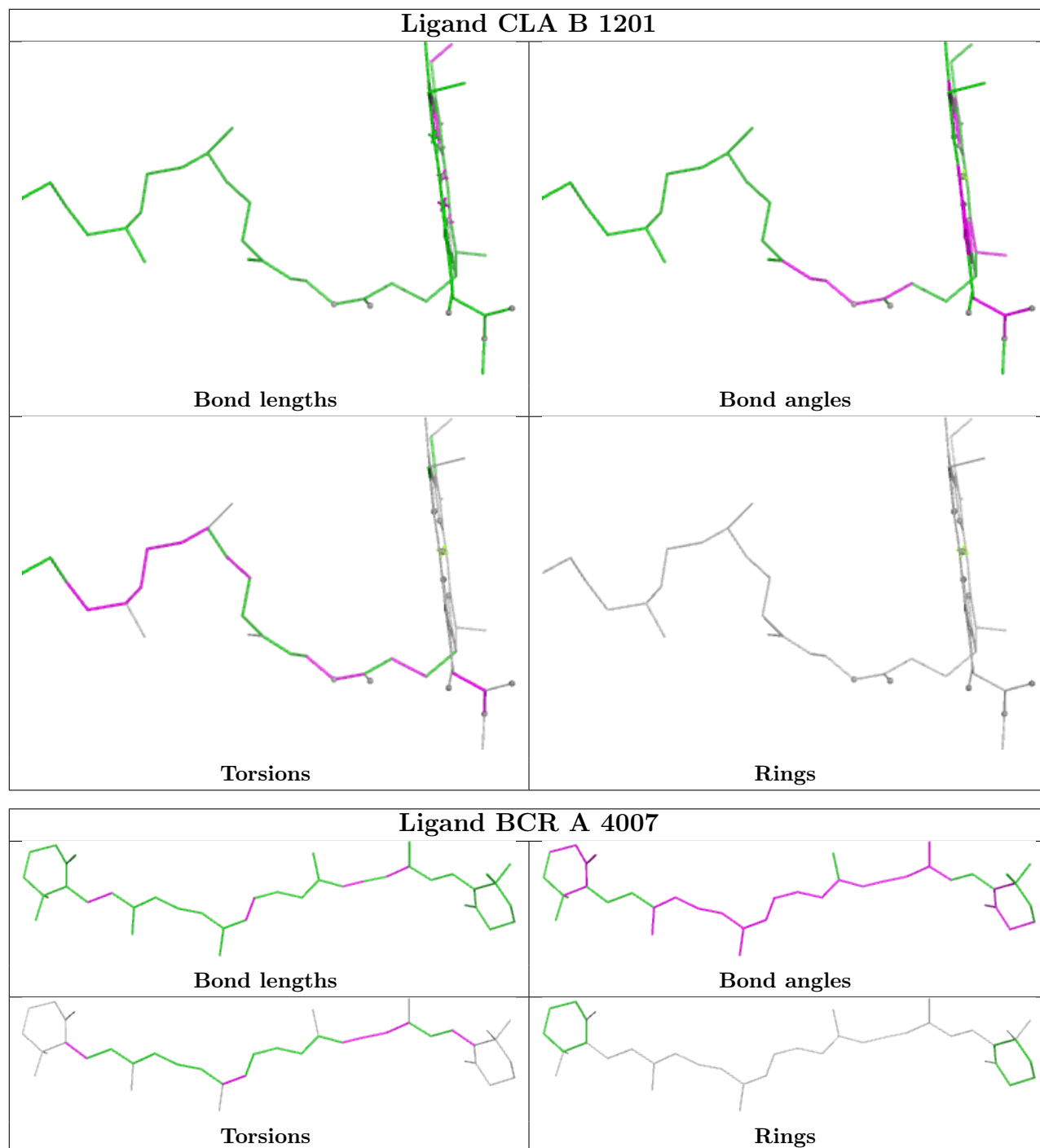
Torsions

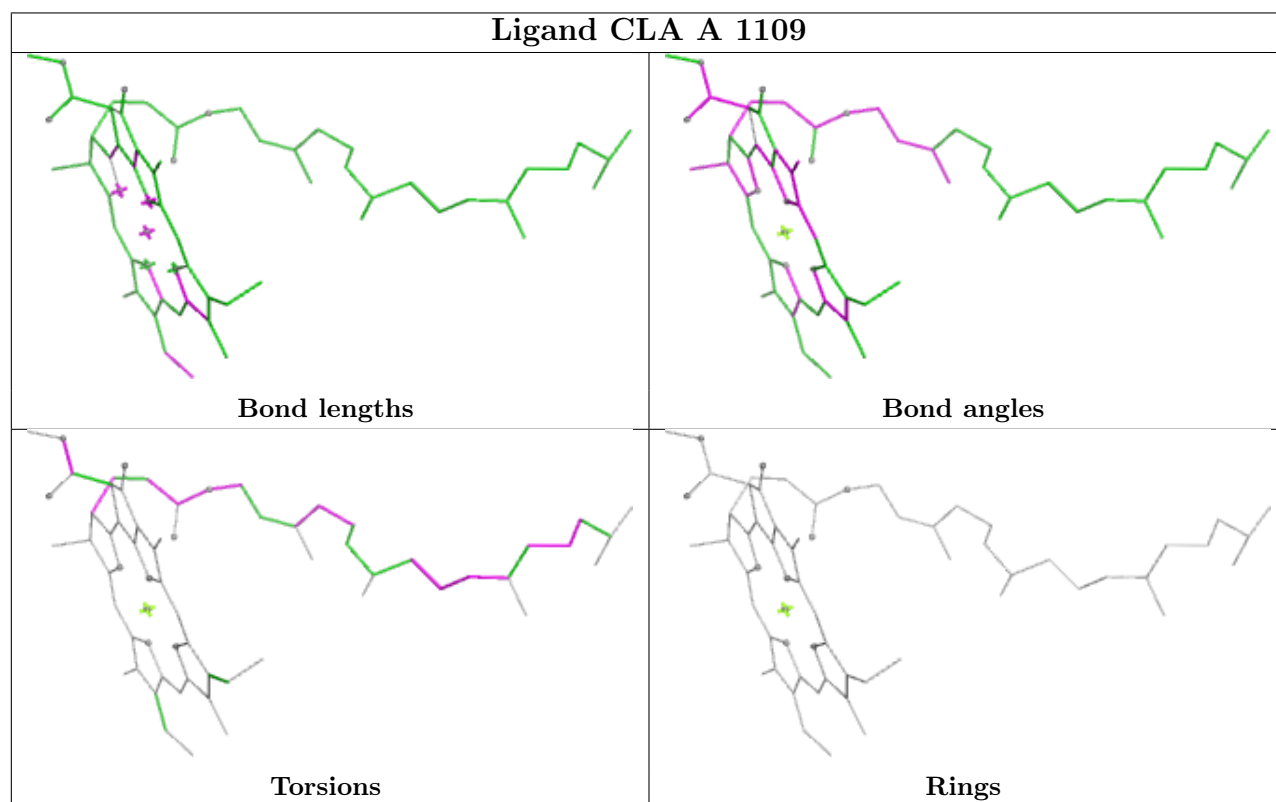
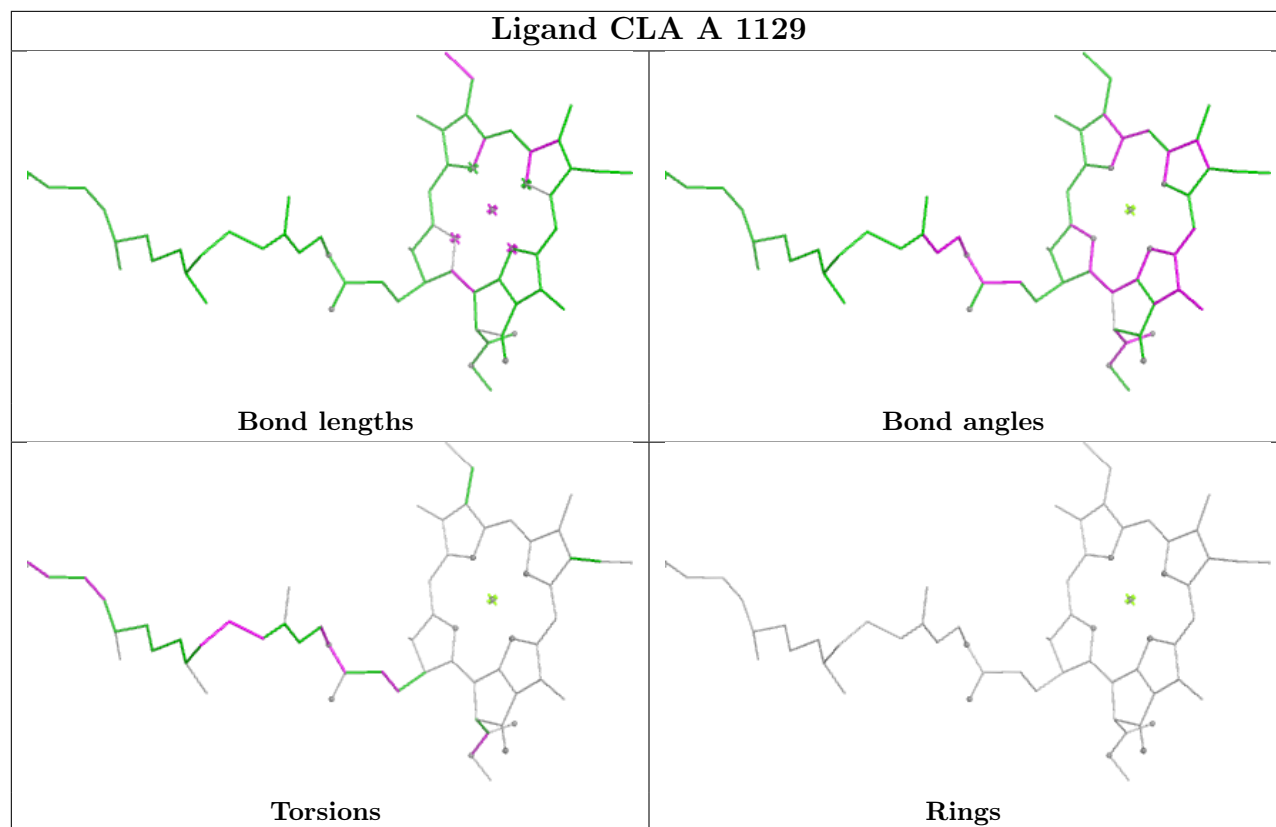


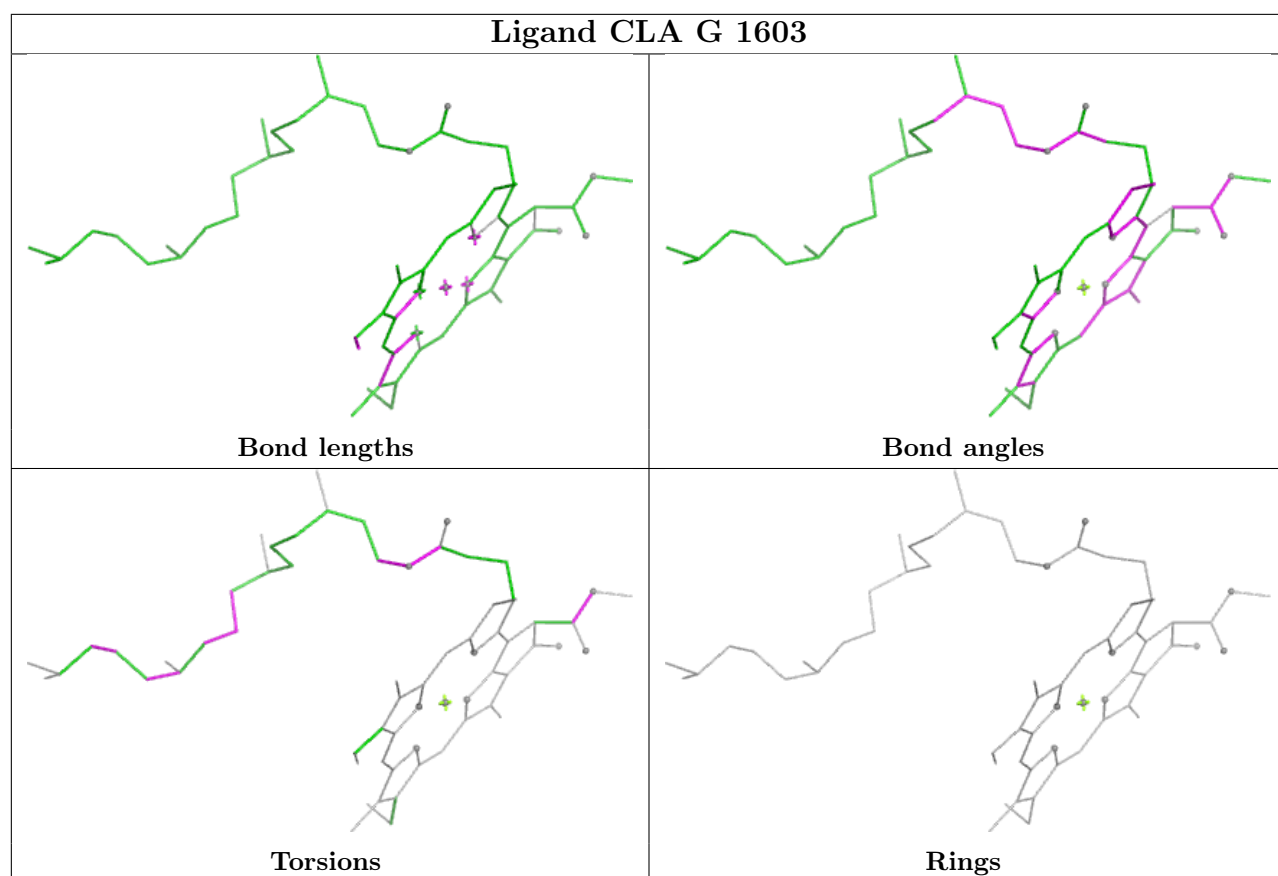
Rings

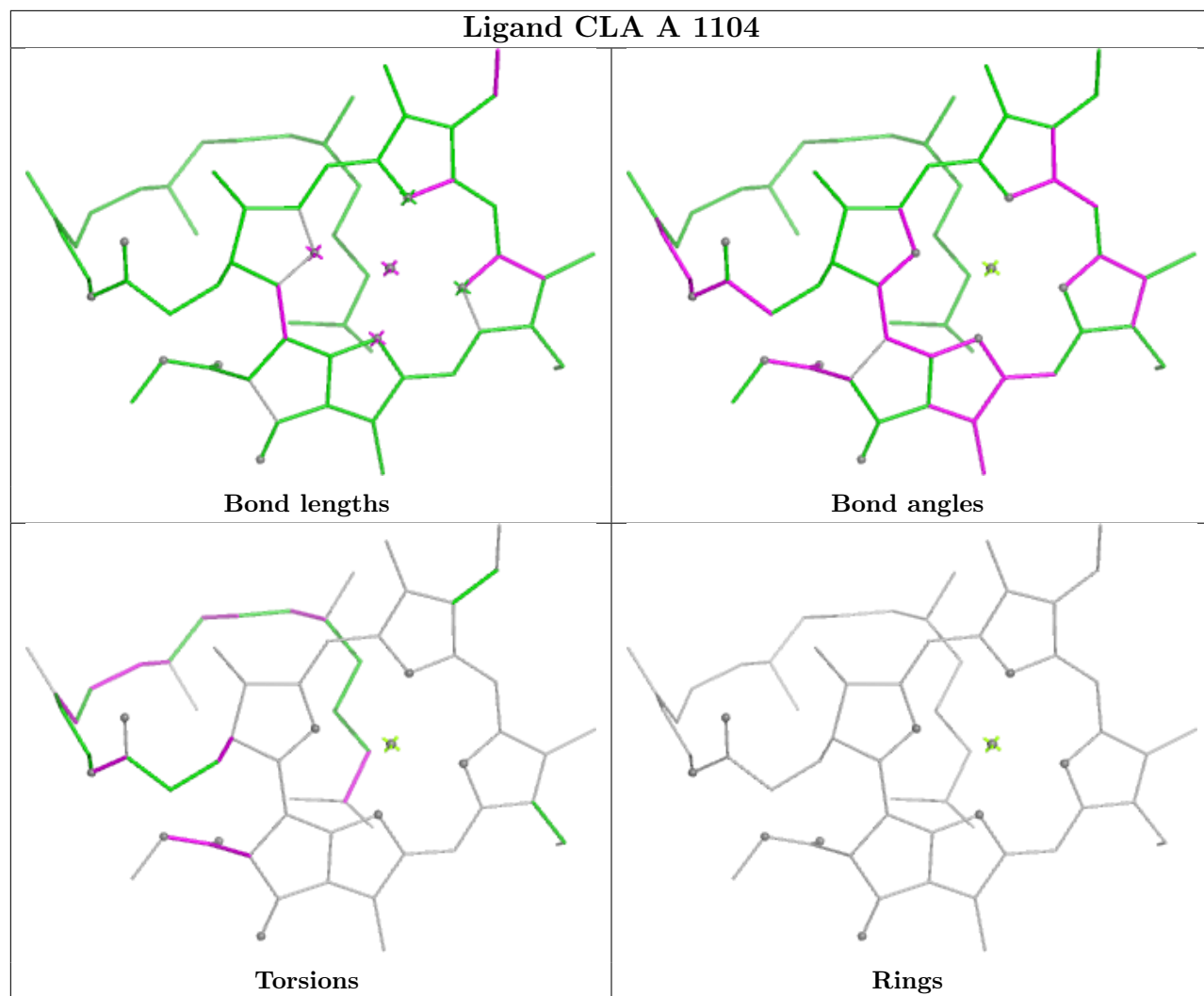
Ligand DGD G 5003	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand LUT 4 505	
 Bond lengths	 Bond angles
 Torsions	 Rings

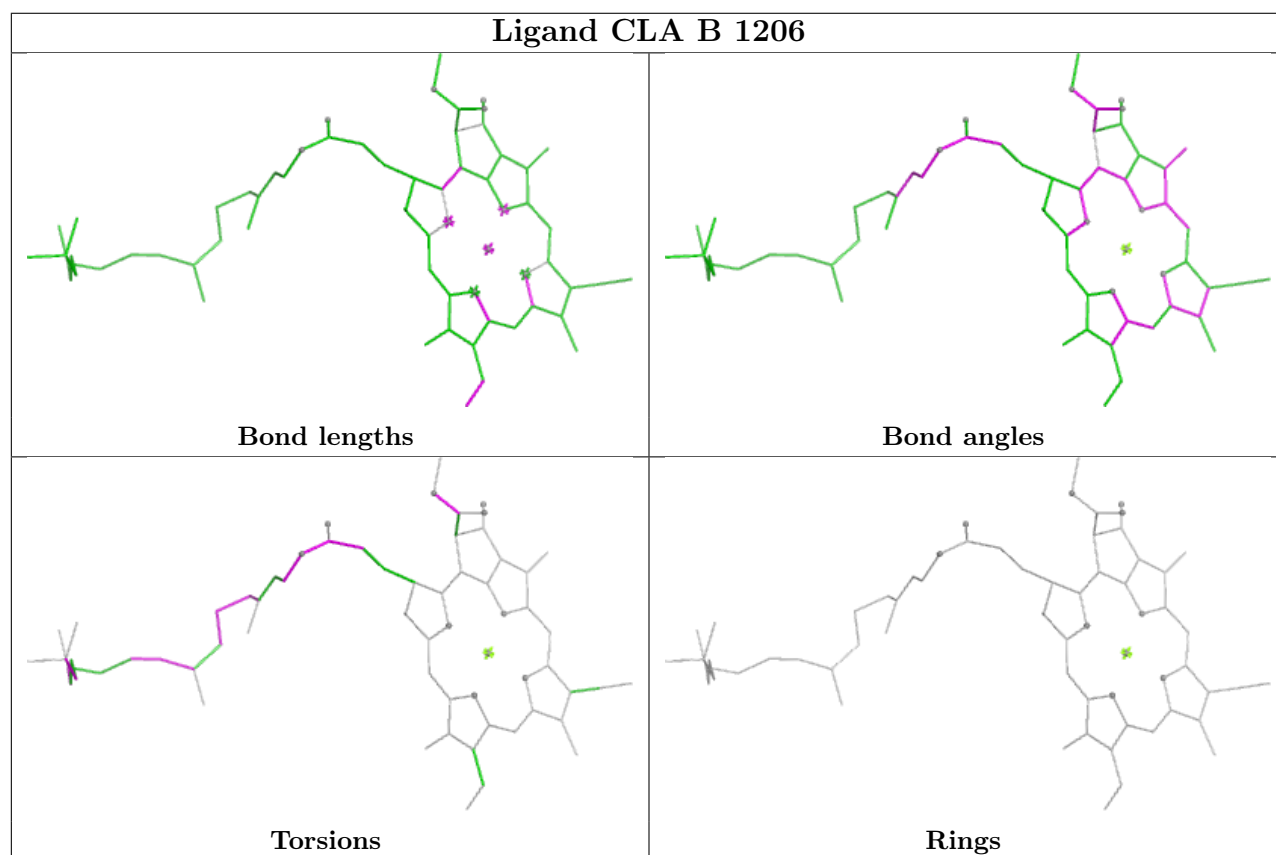
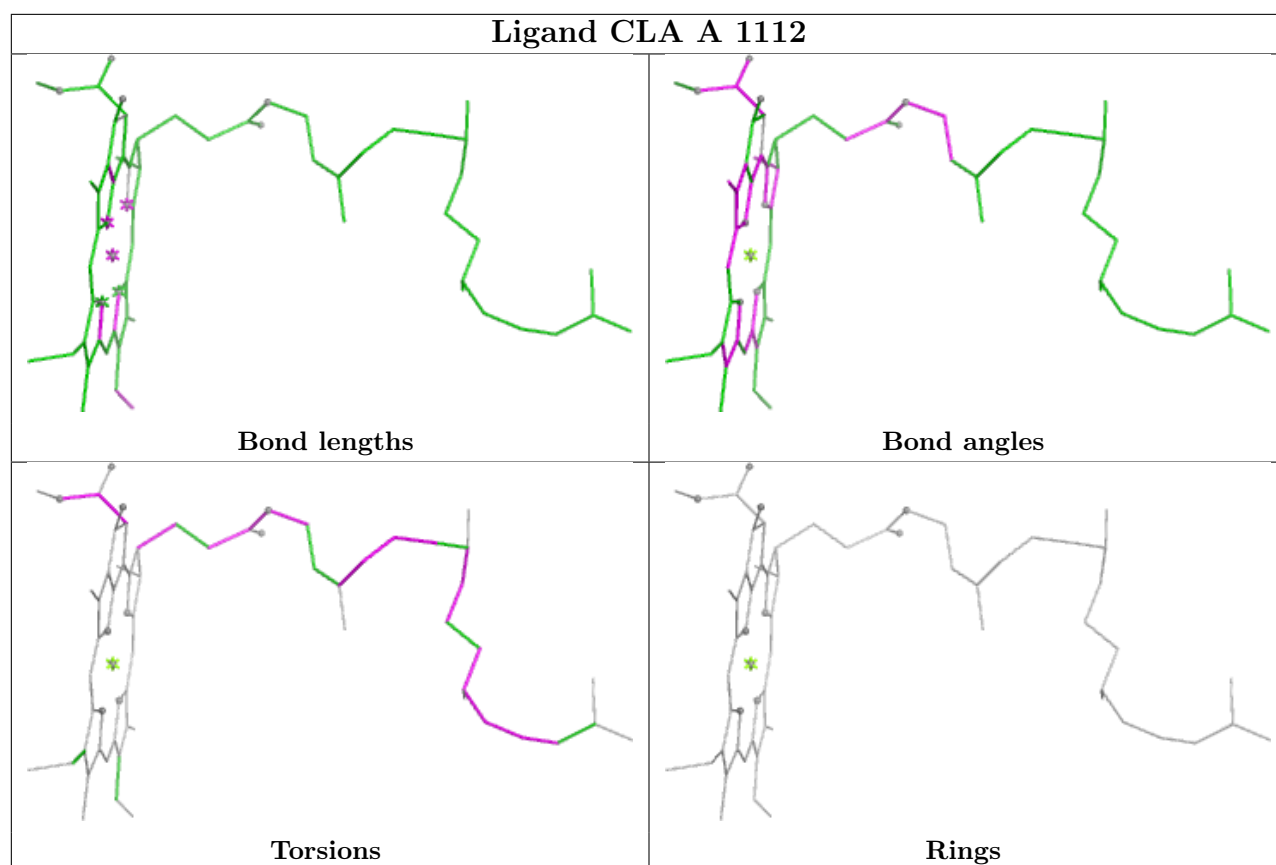


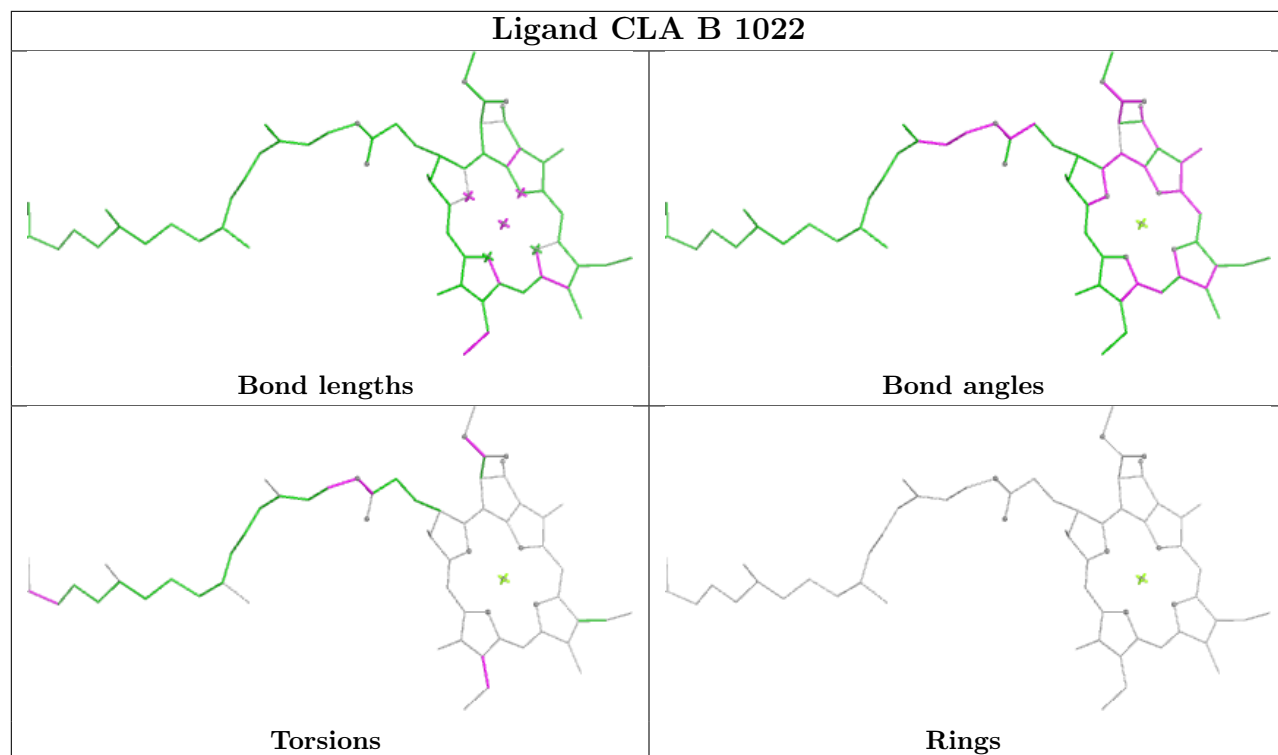




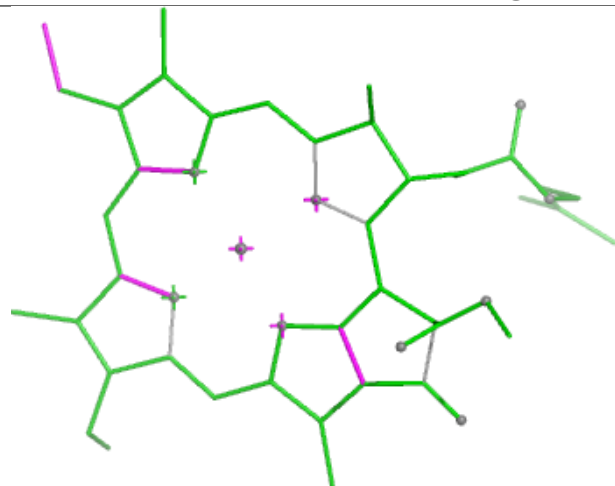




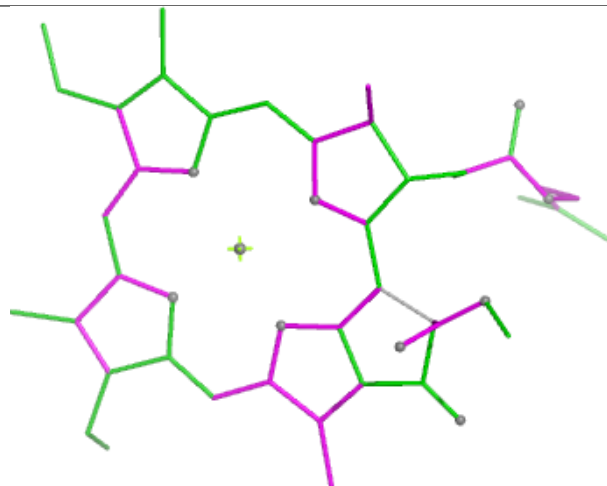




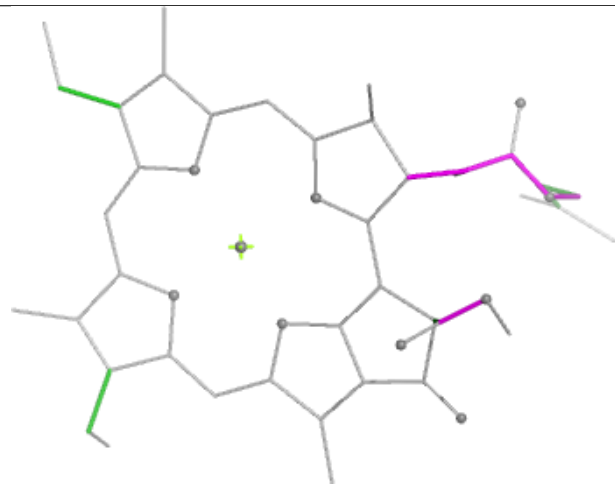
Ligand CLA B 1236



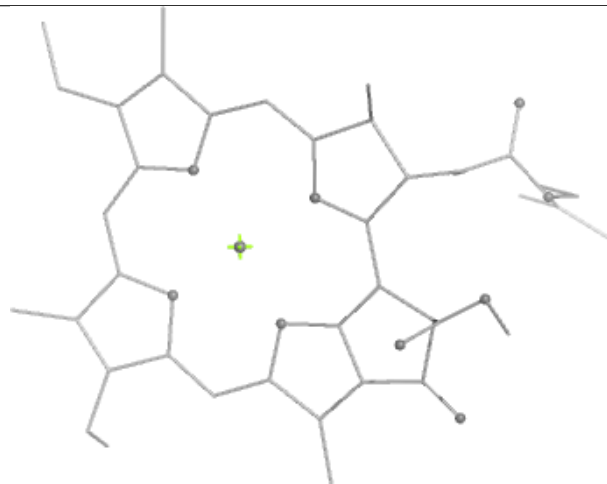
Bond lengths



Bond angles

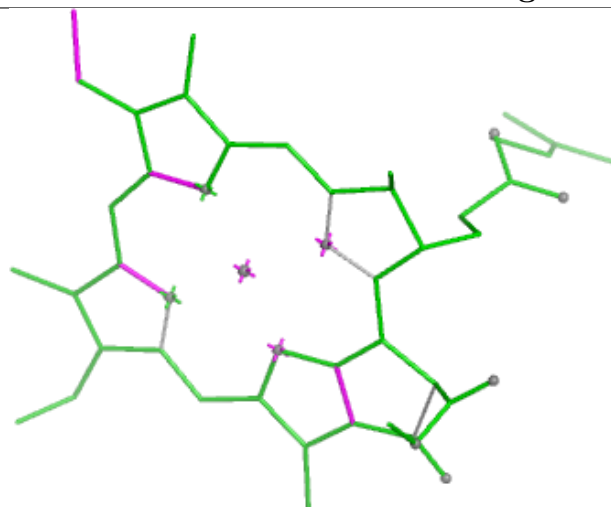


Torsions

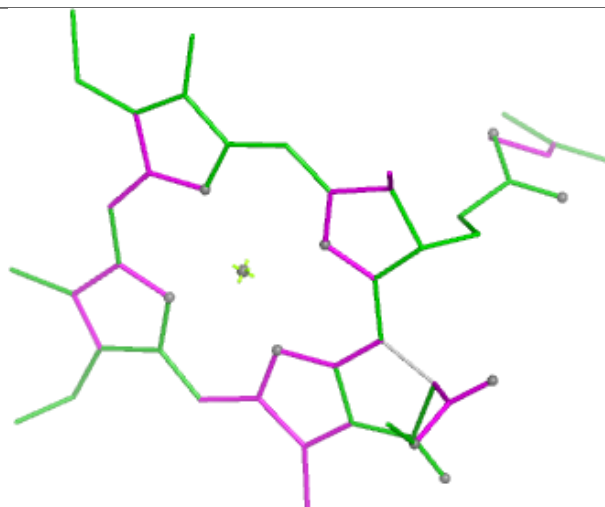


Rings

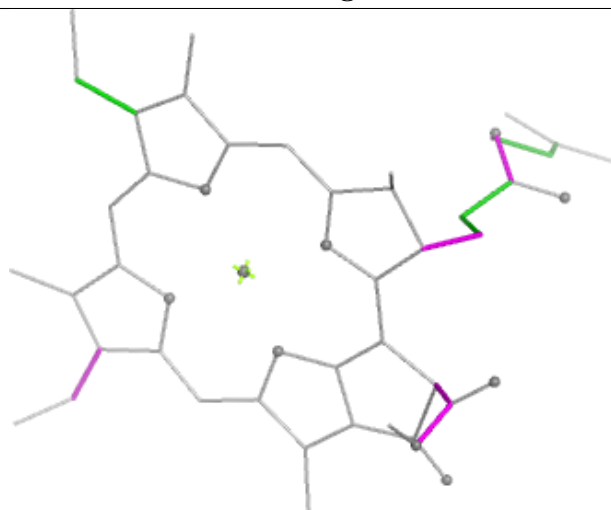
Ligand CLA 3 606



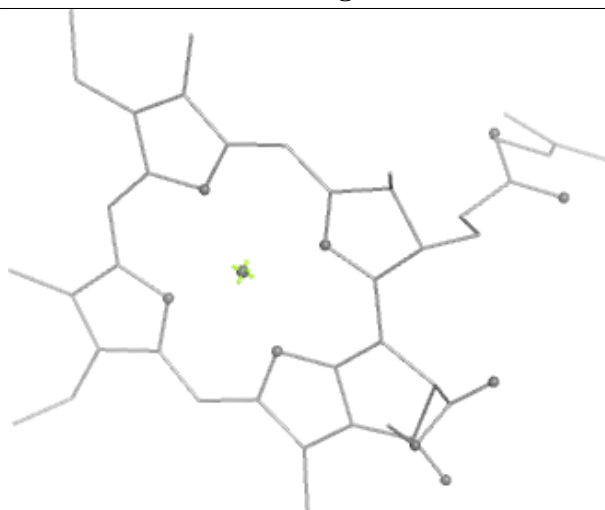
Bond lengths



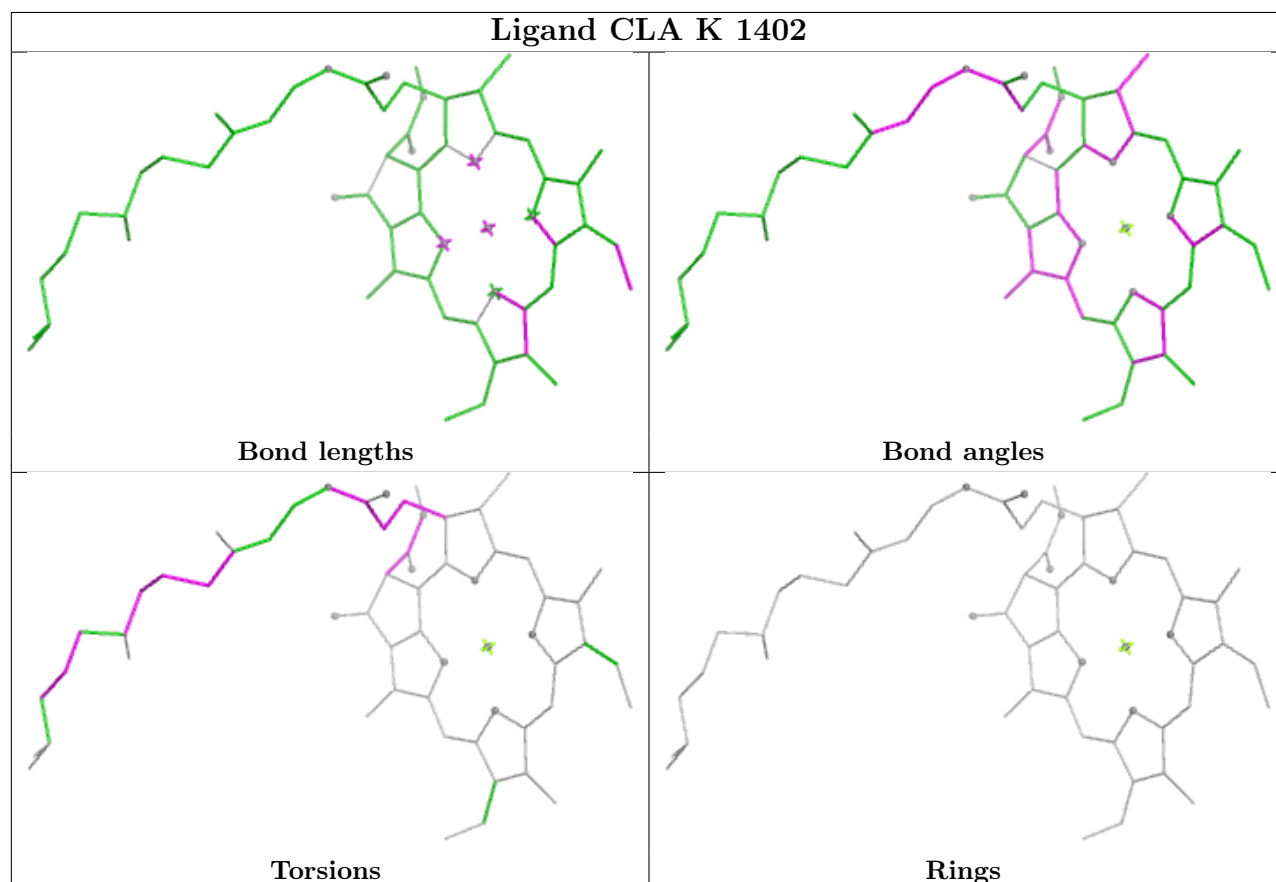
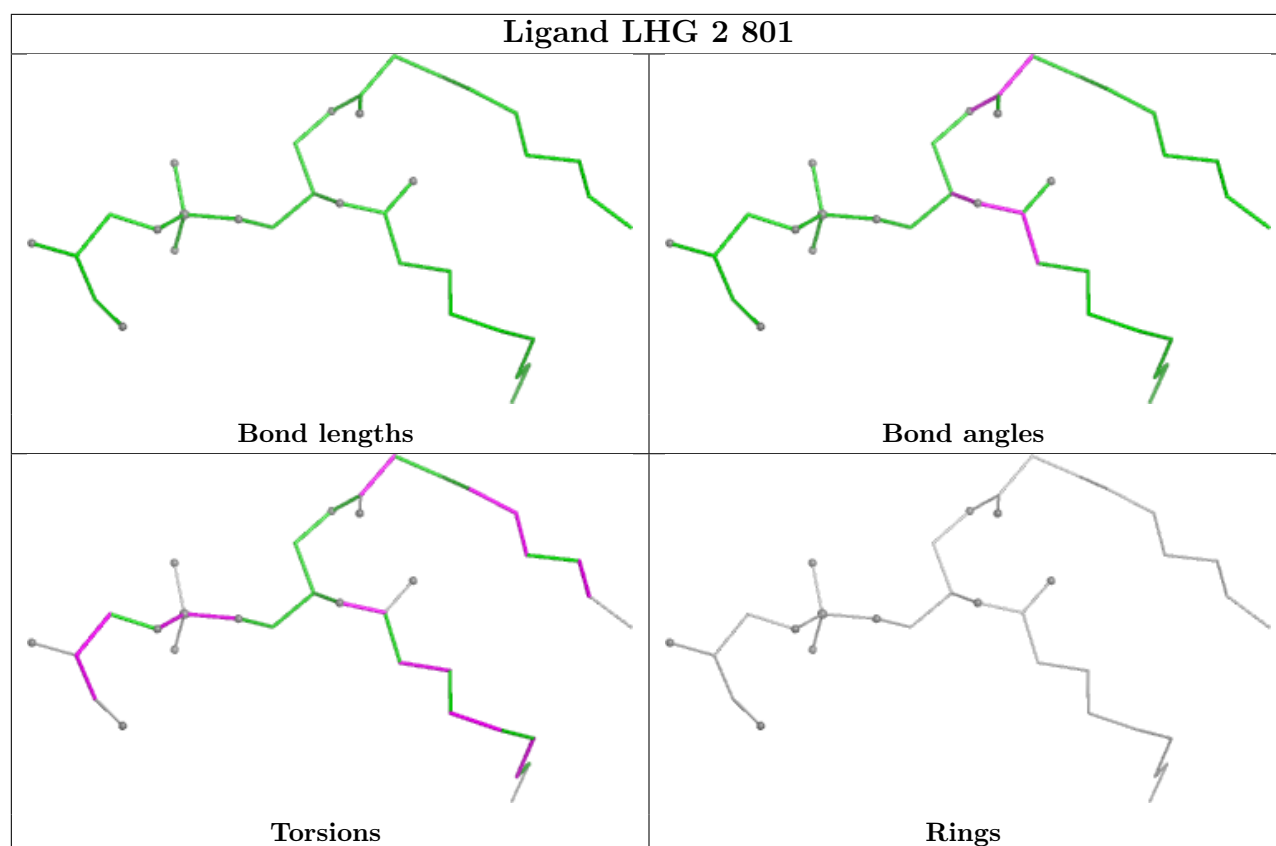
Bond angles

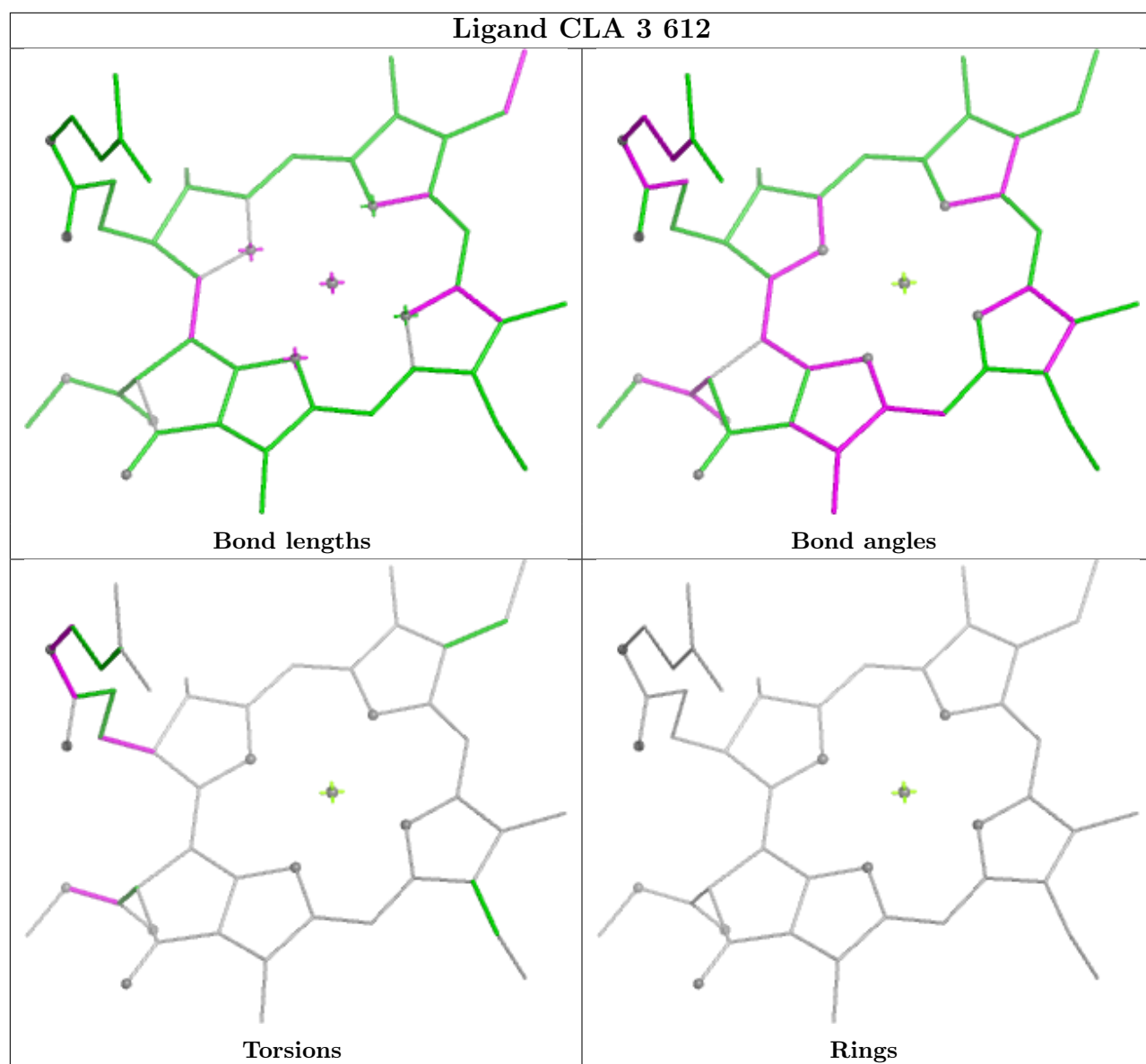


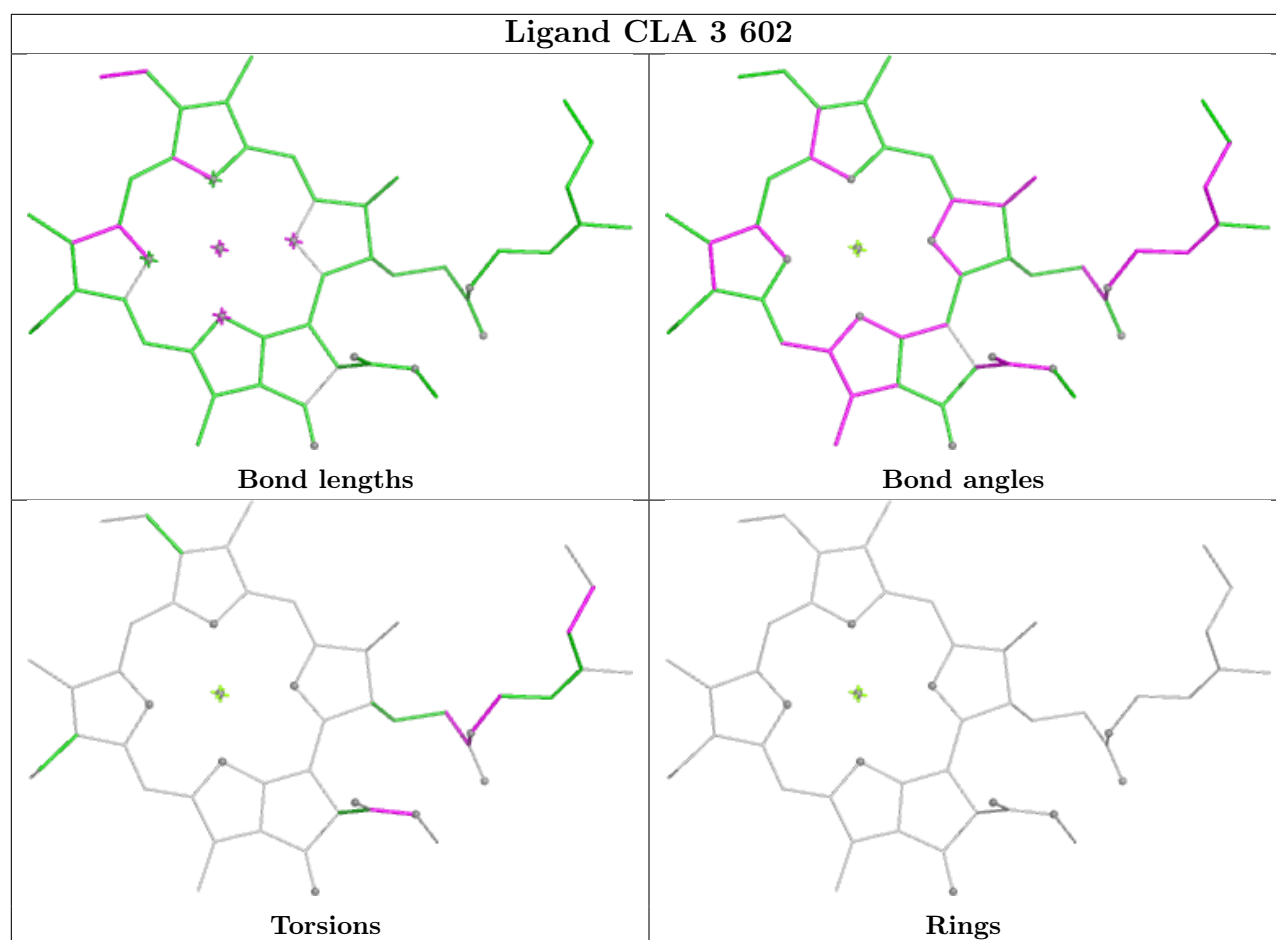
Torsions

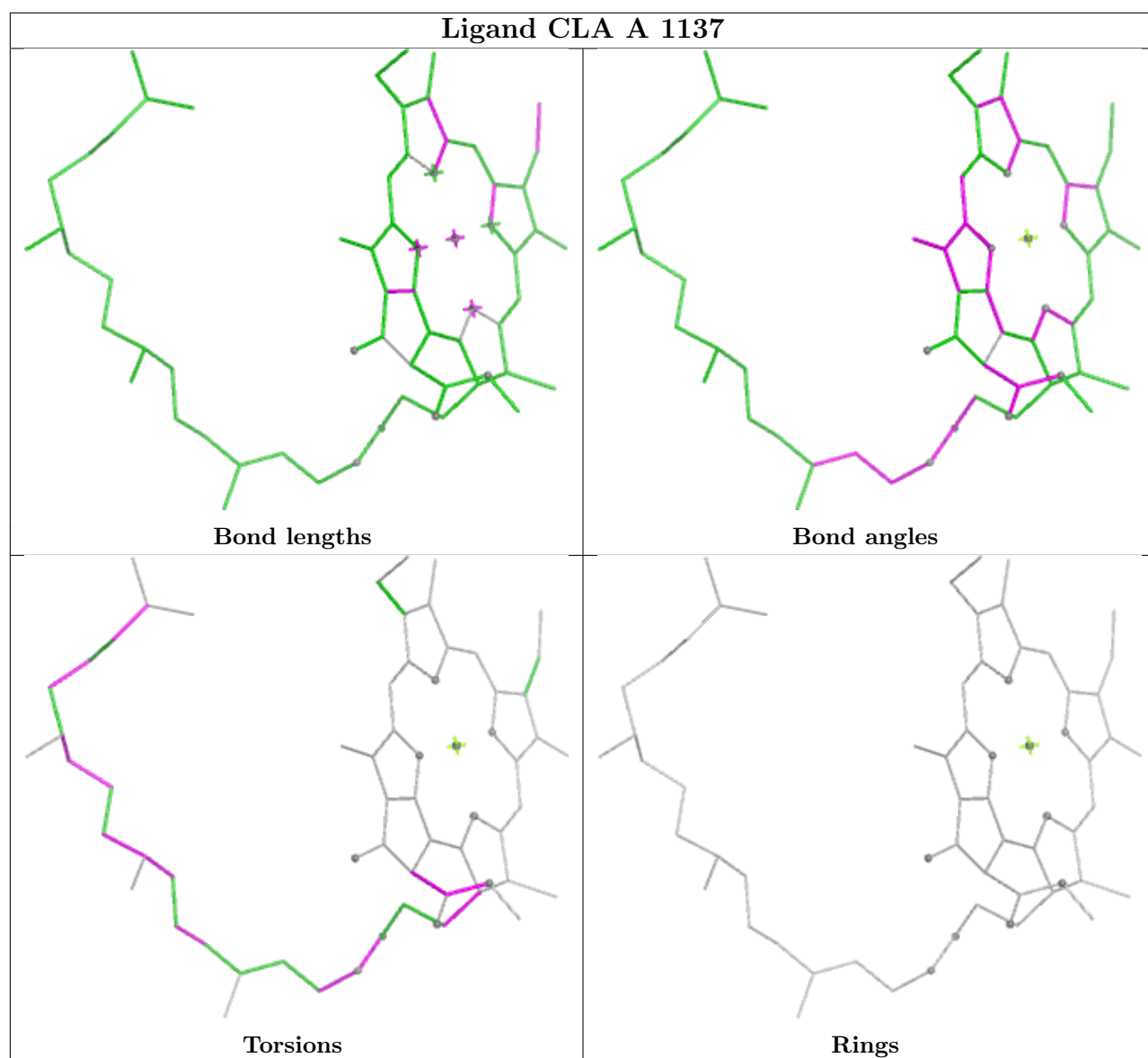


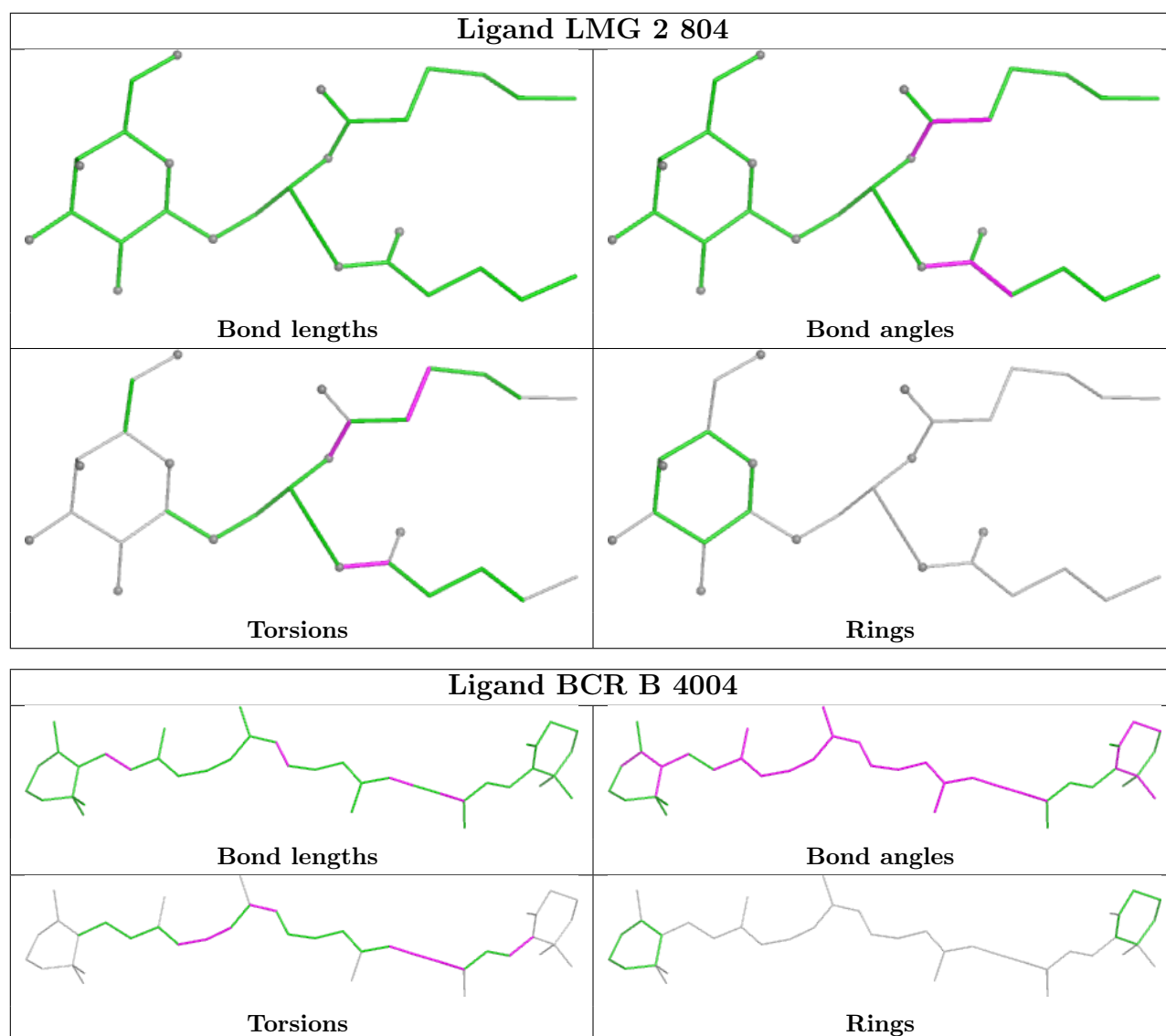
Rings

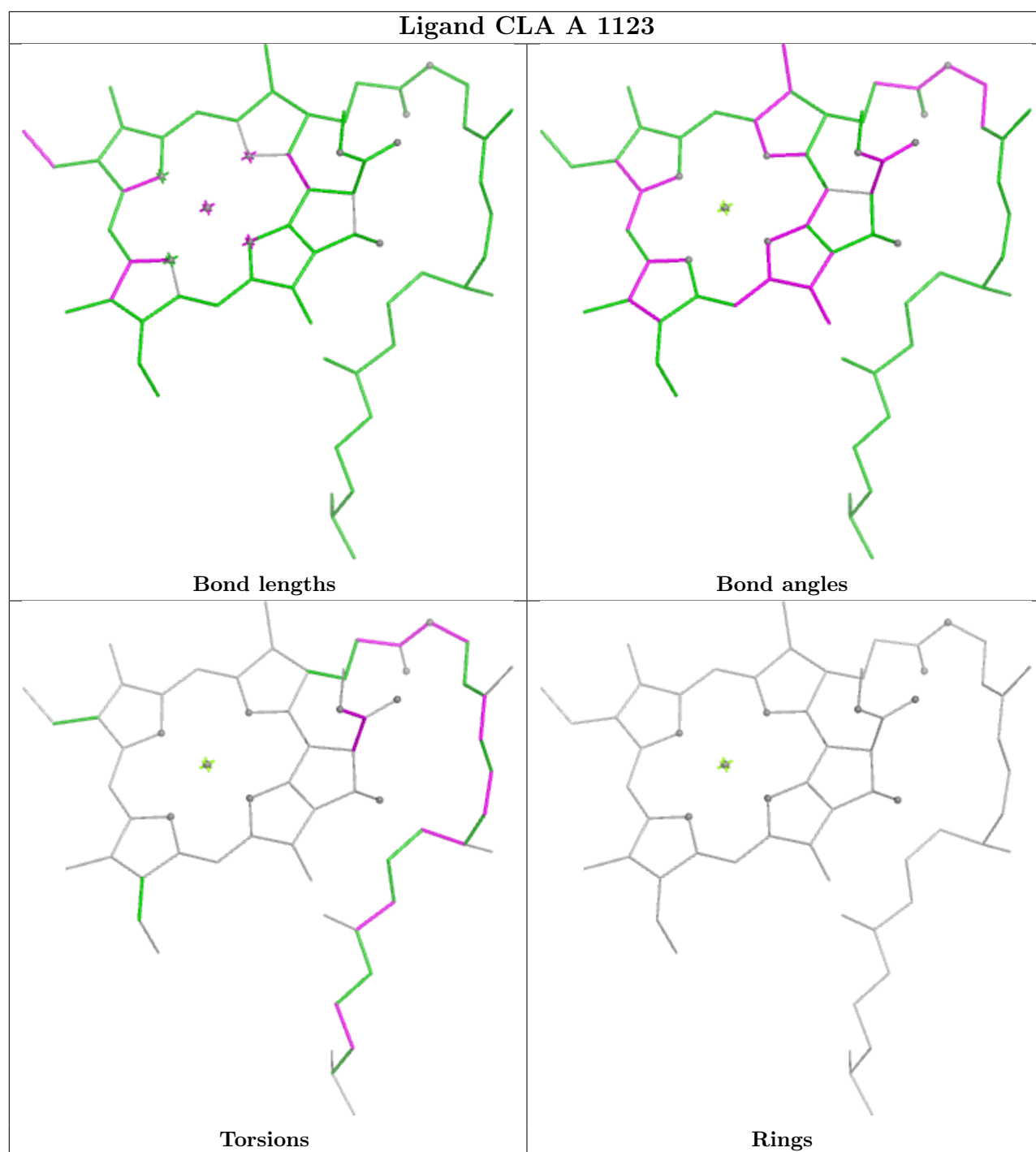


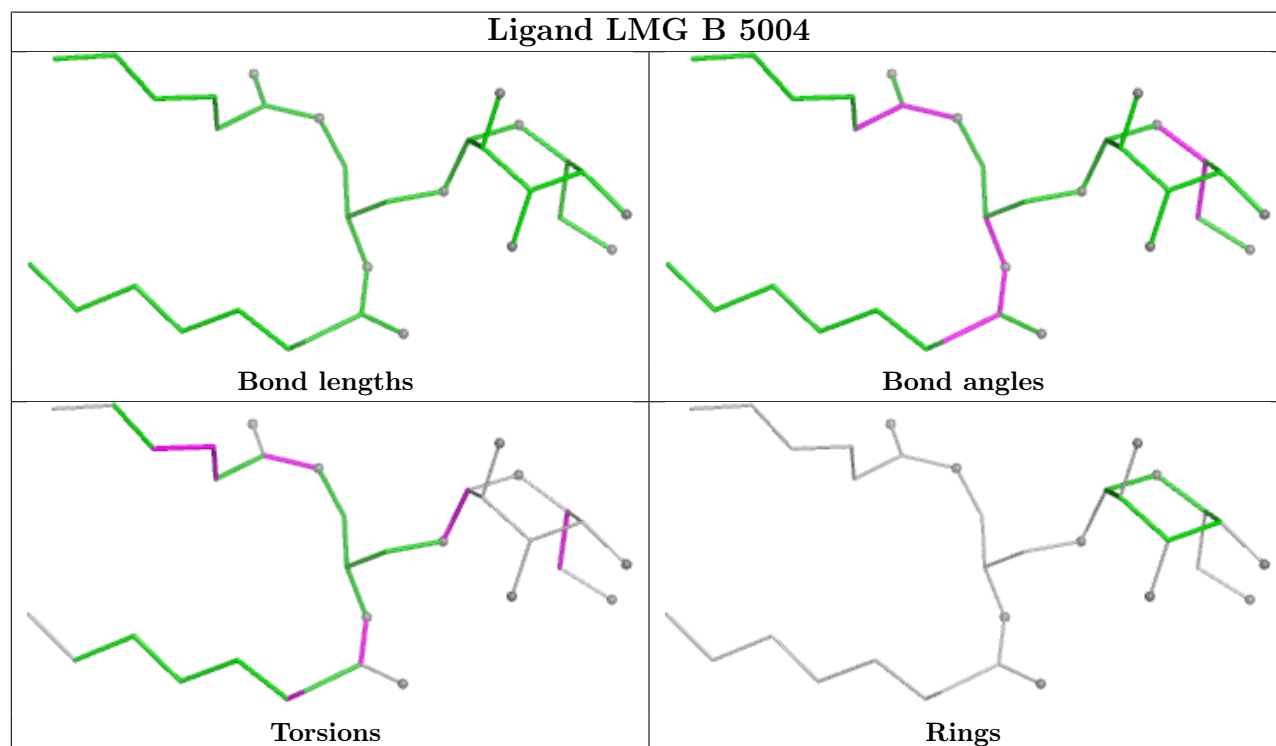
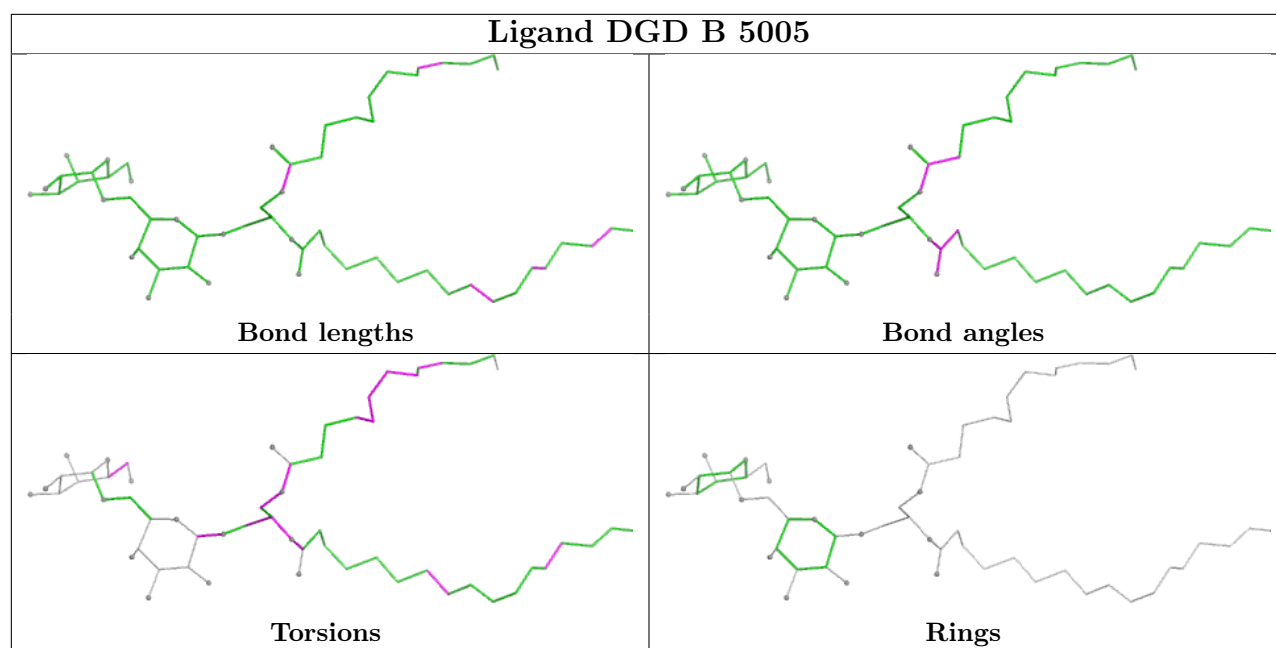


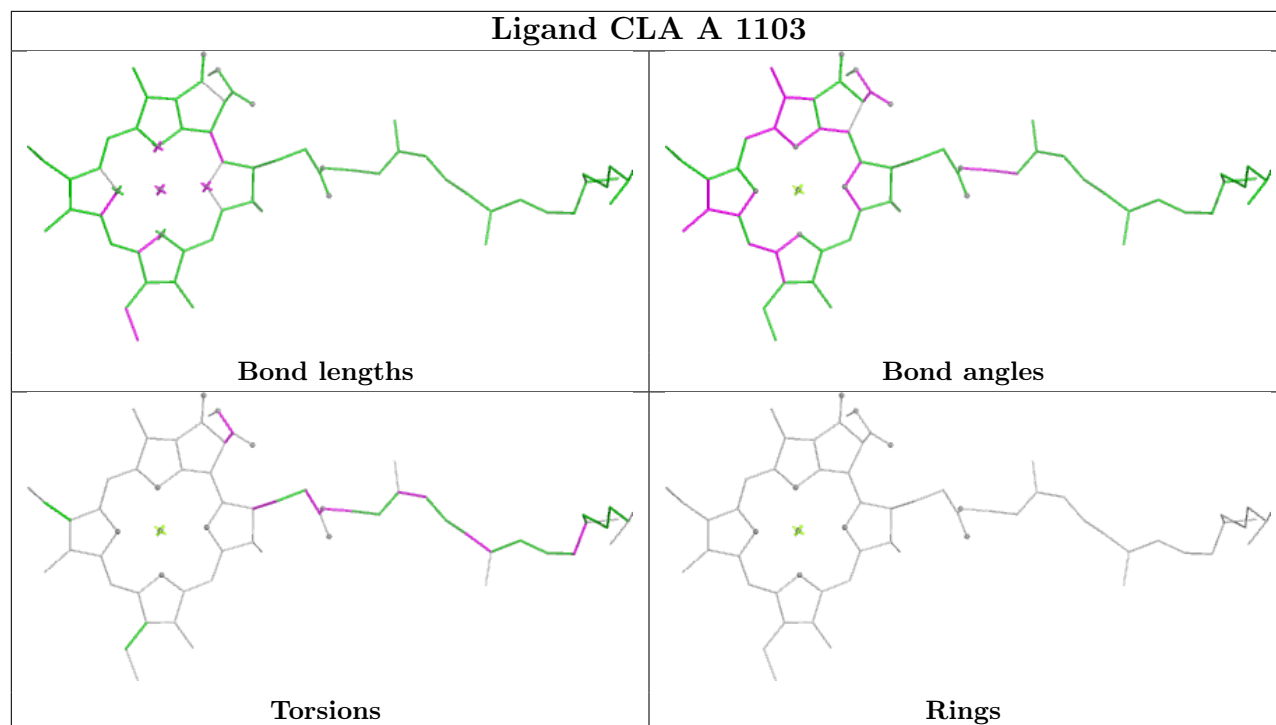
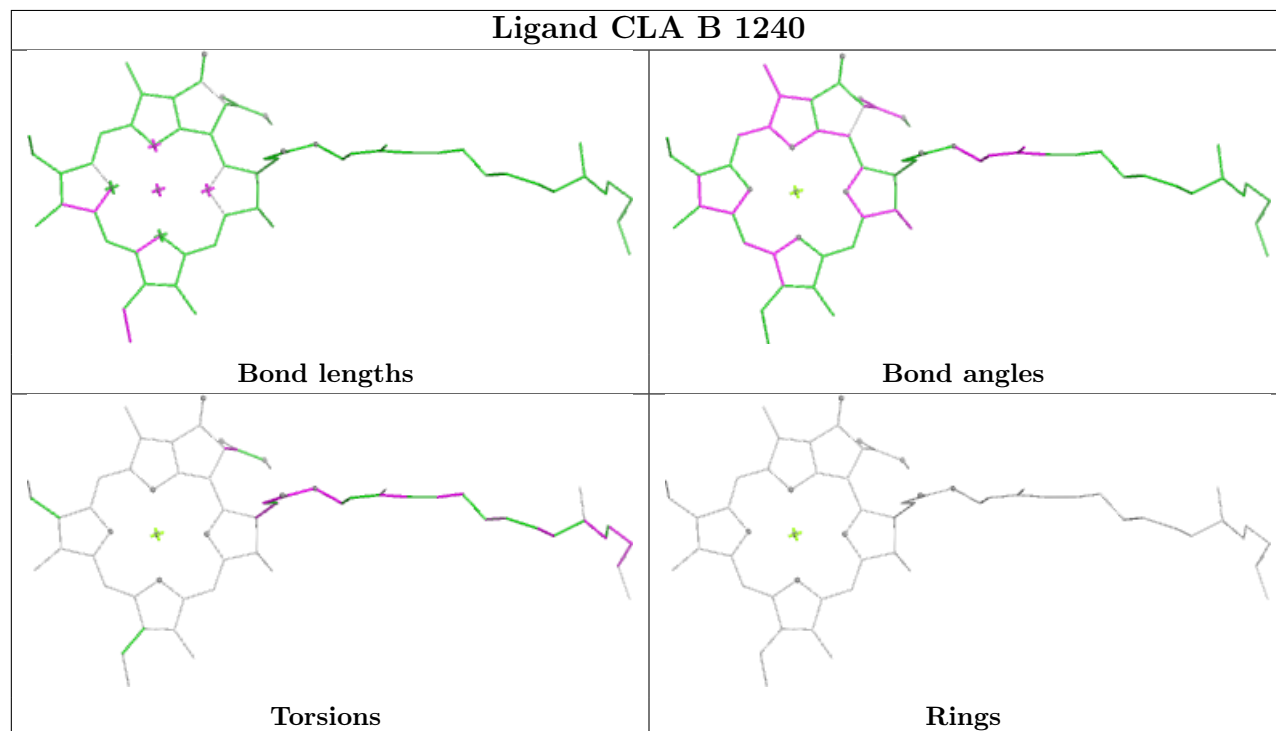


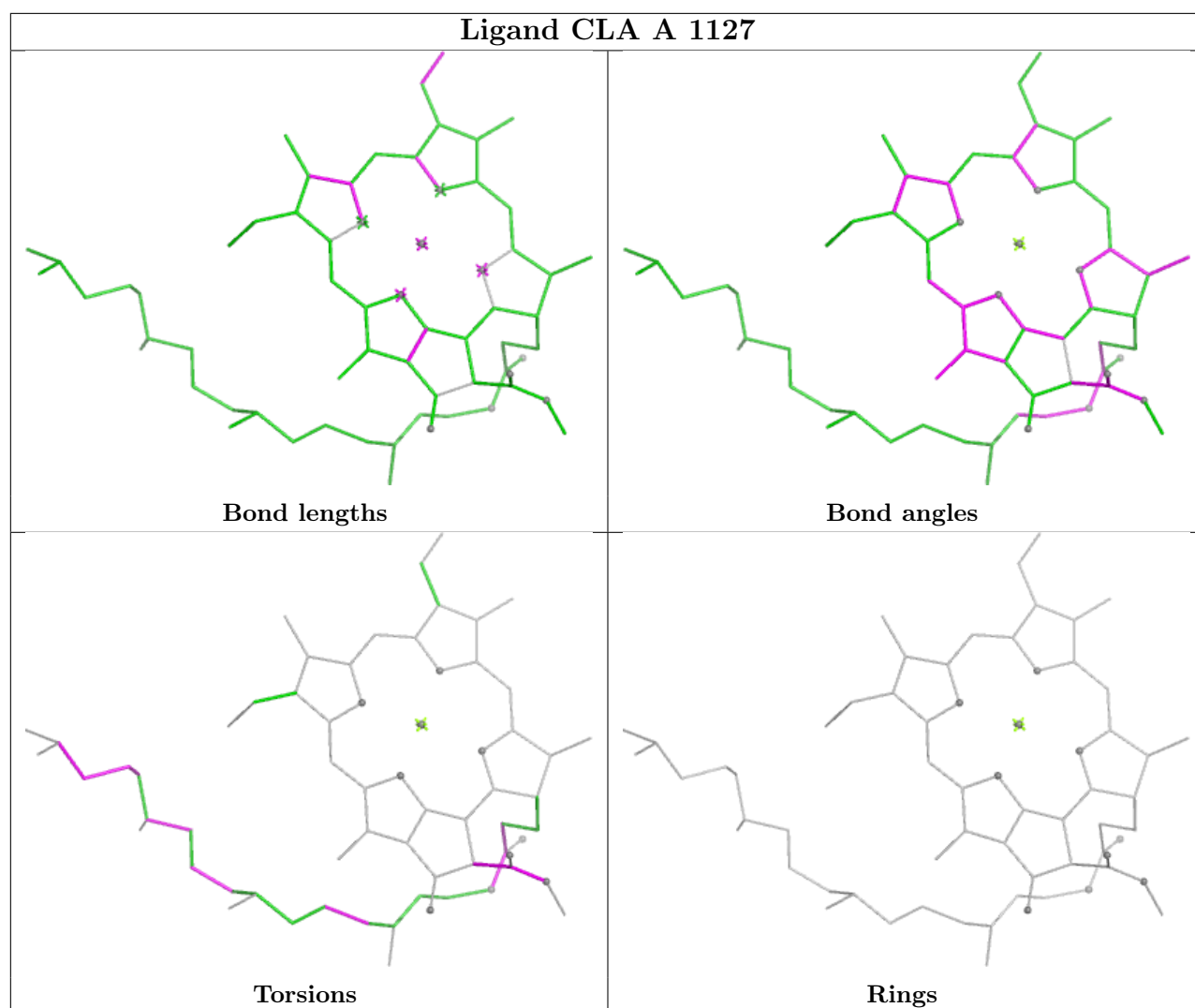


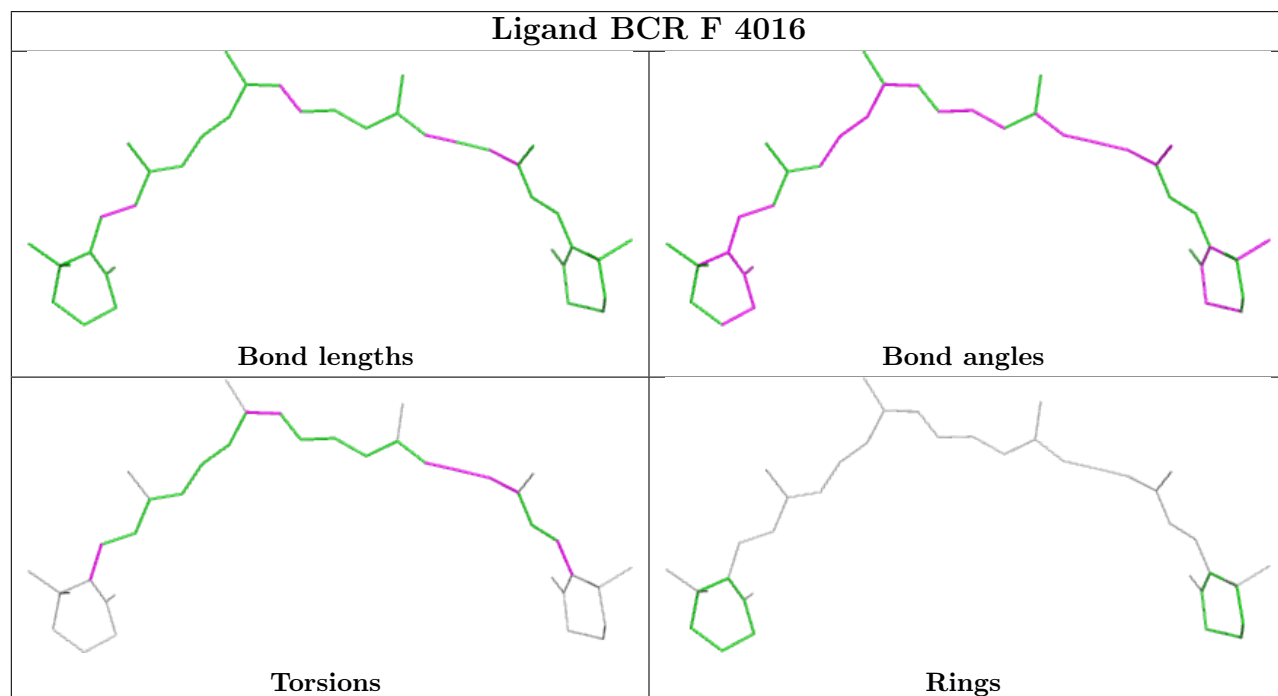
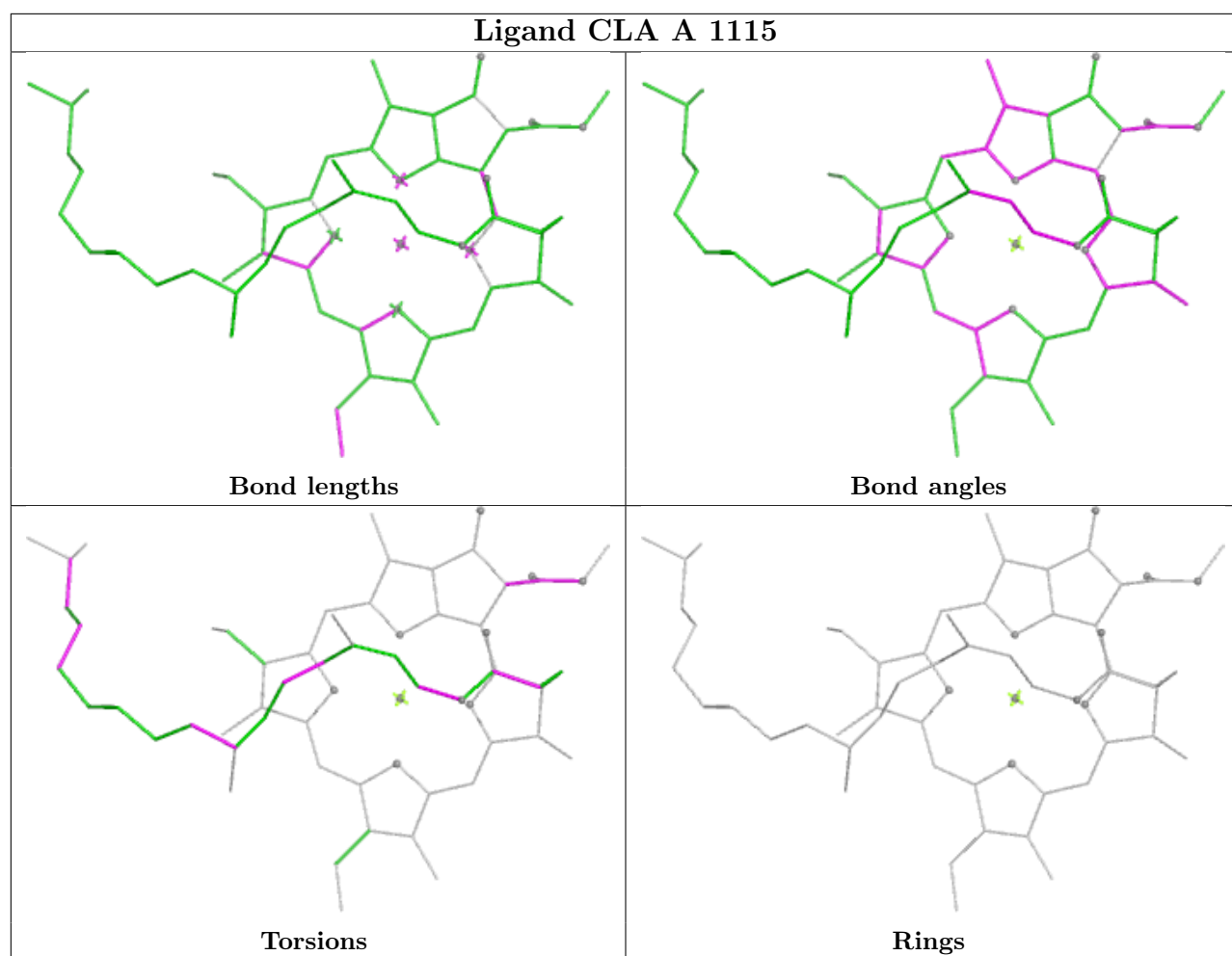


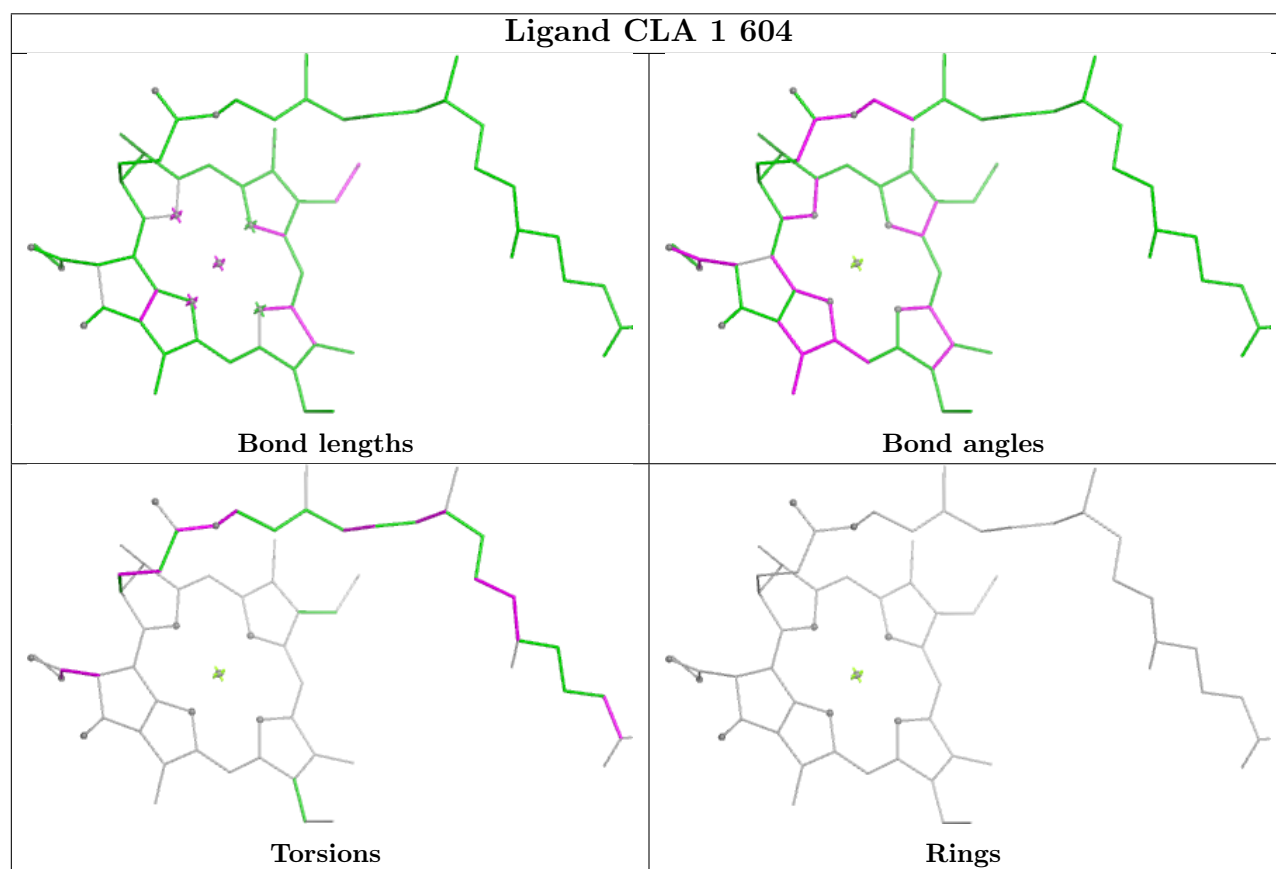
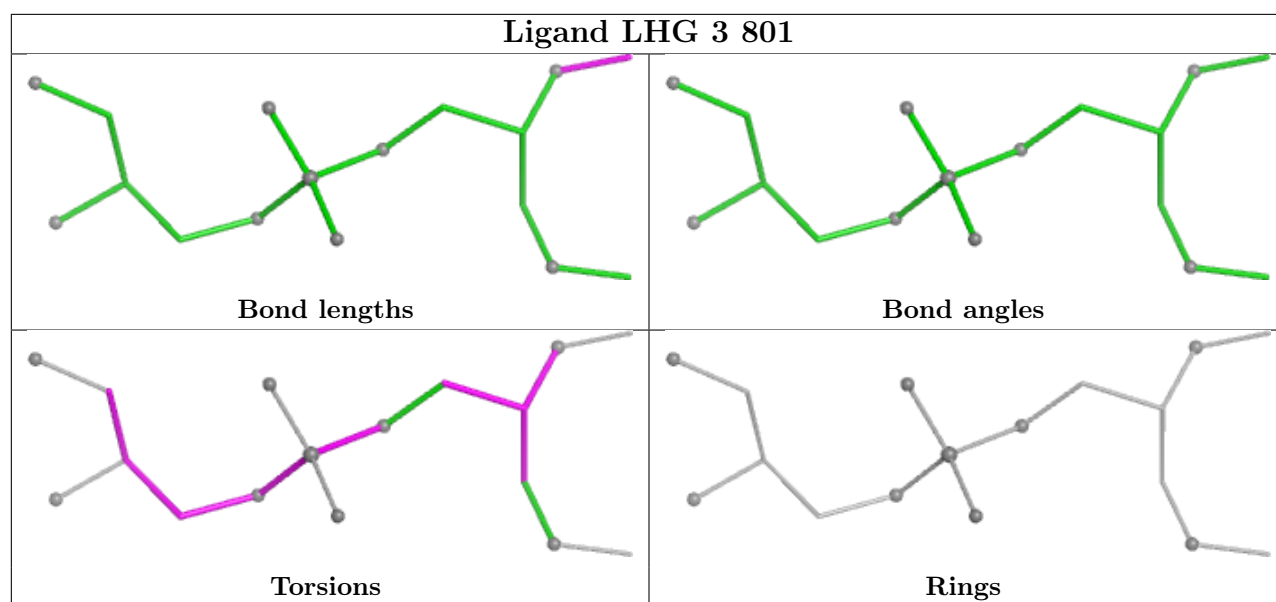


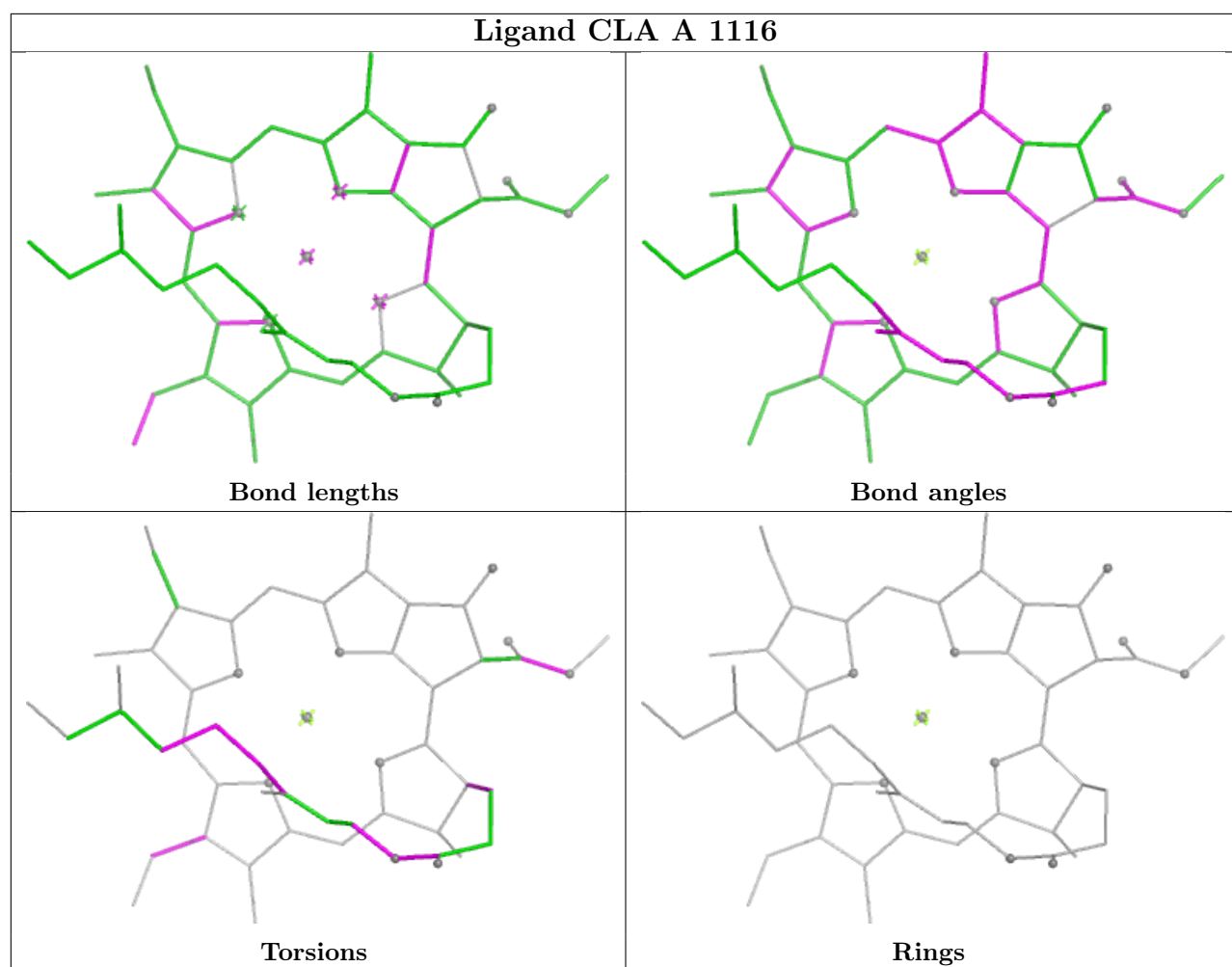


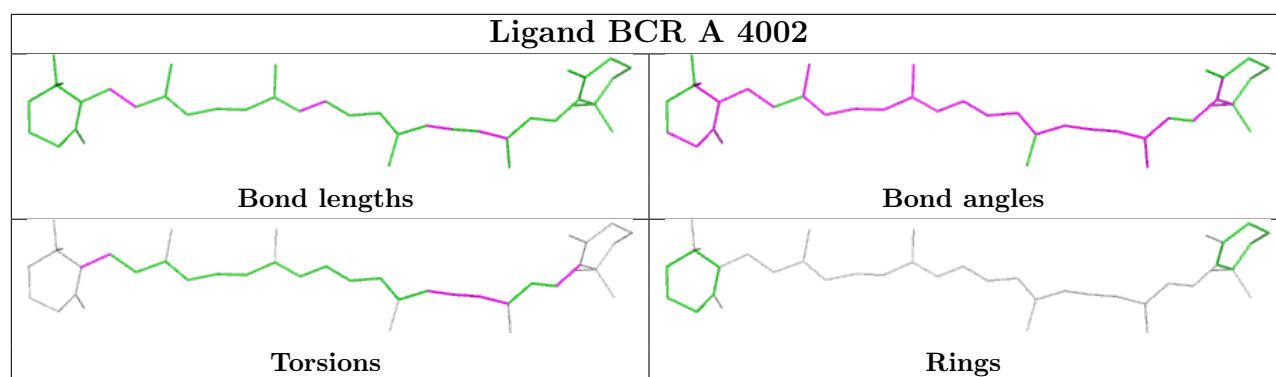
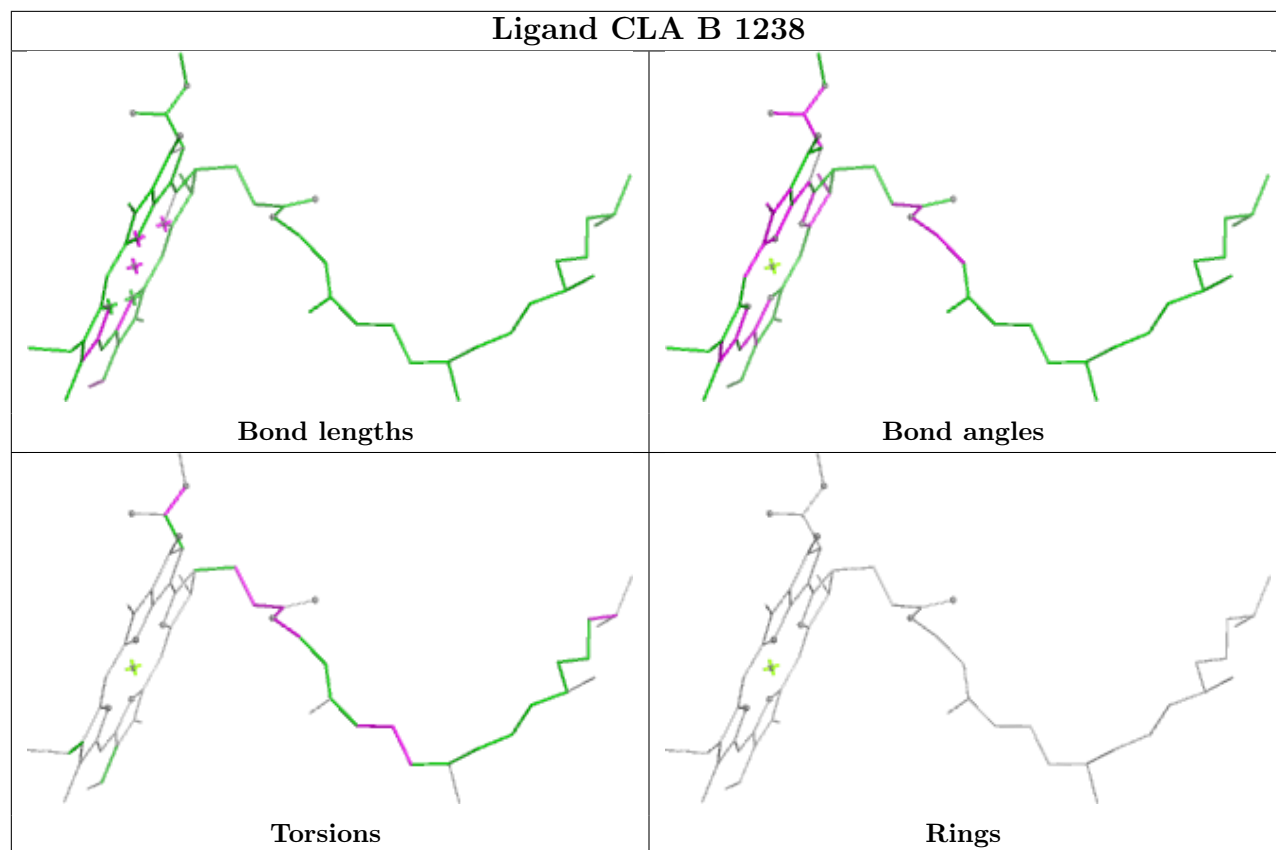
Ligand CLA A 1103**Ligand CLA B 1240**

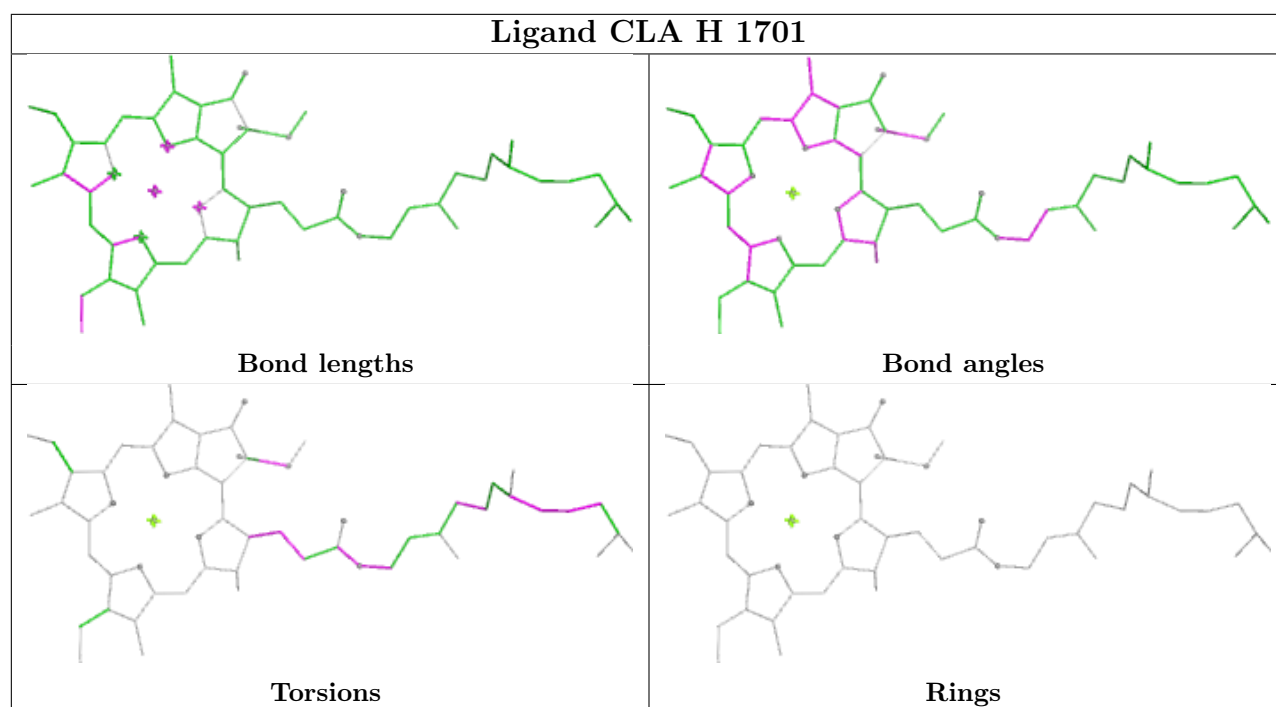


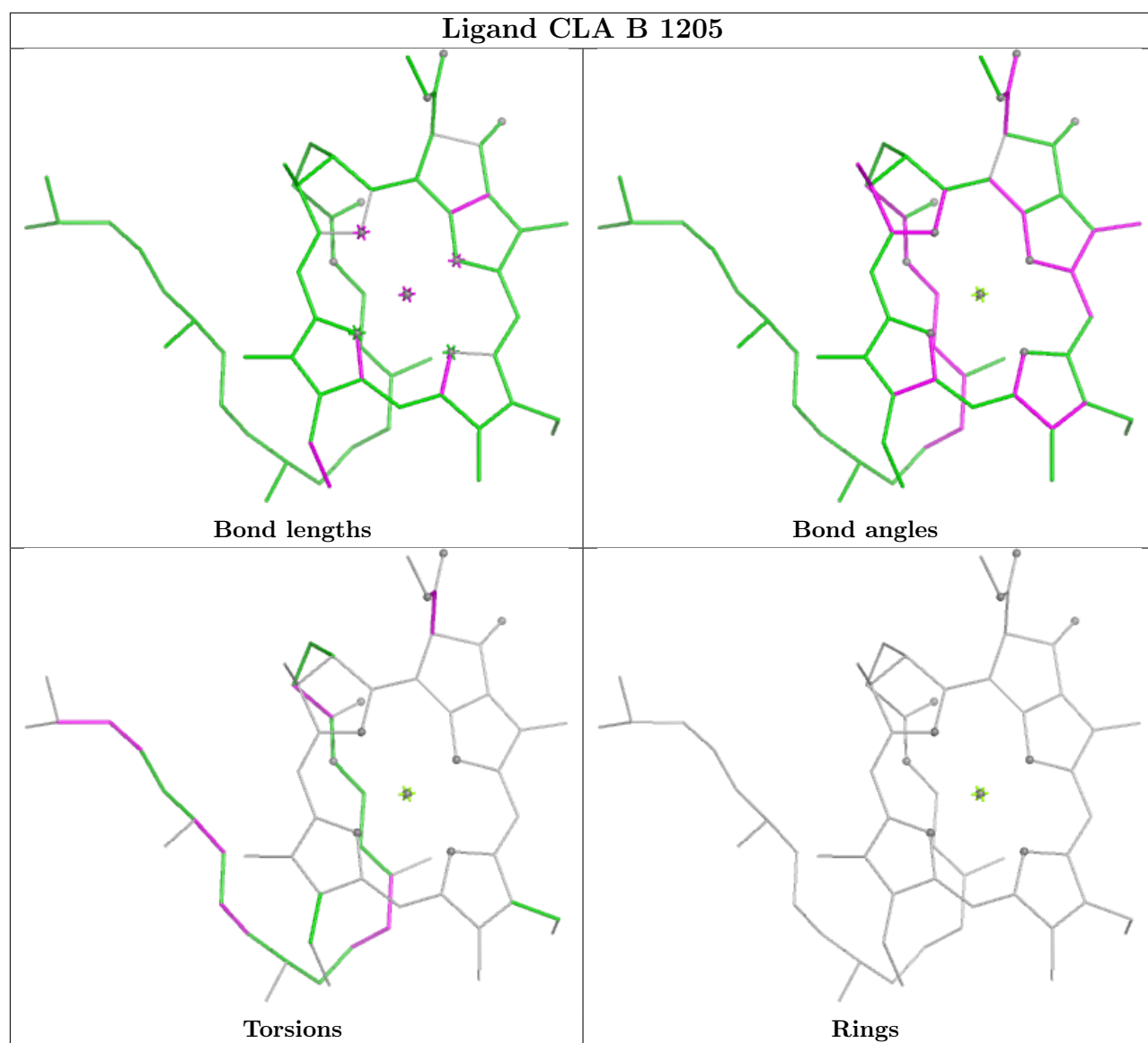


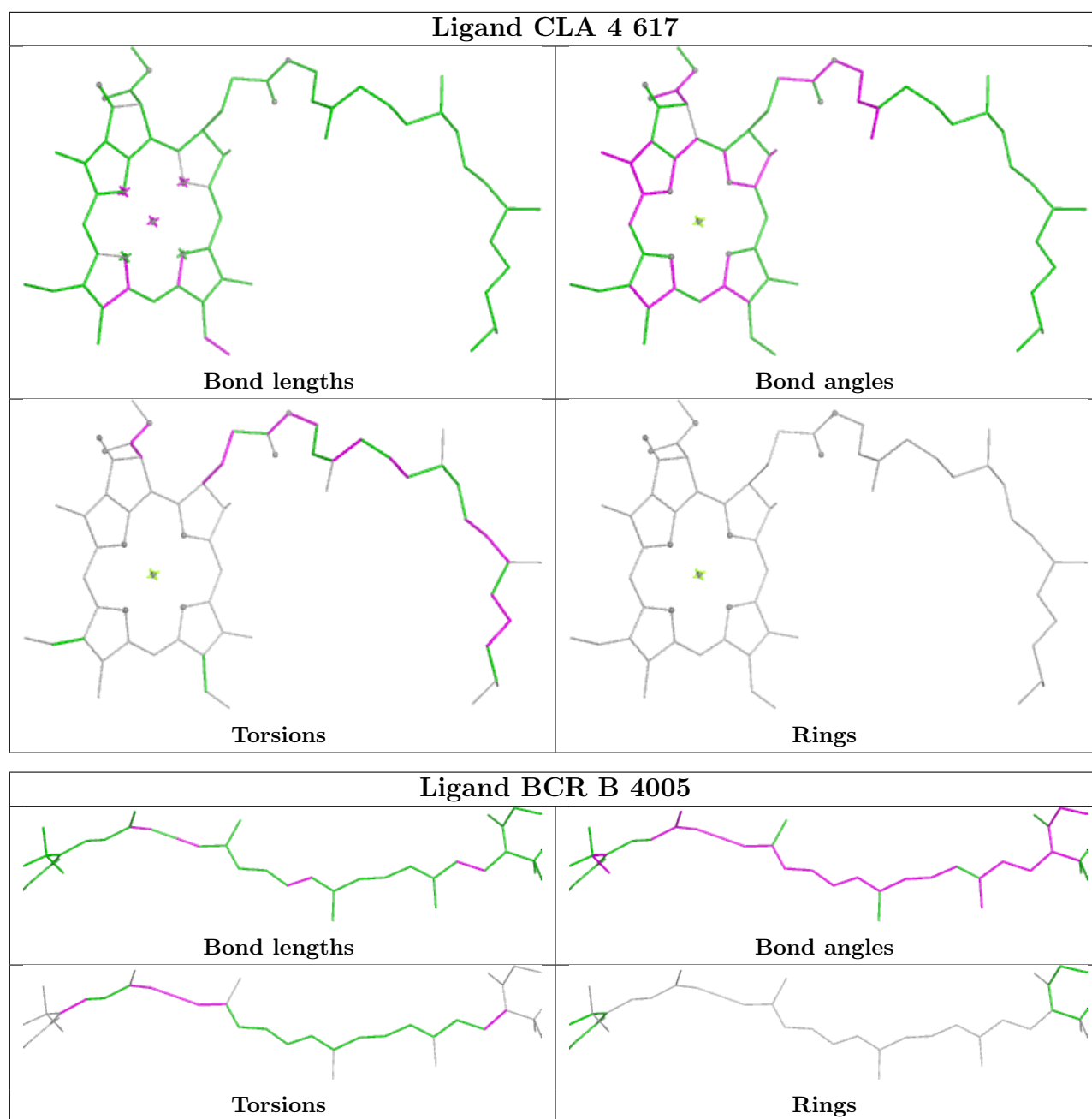




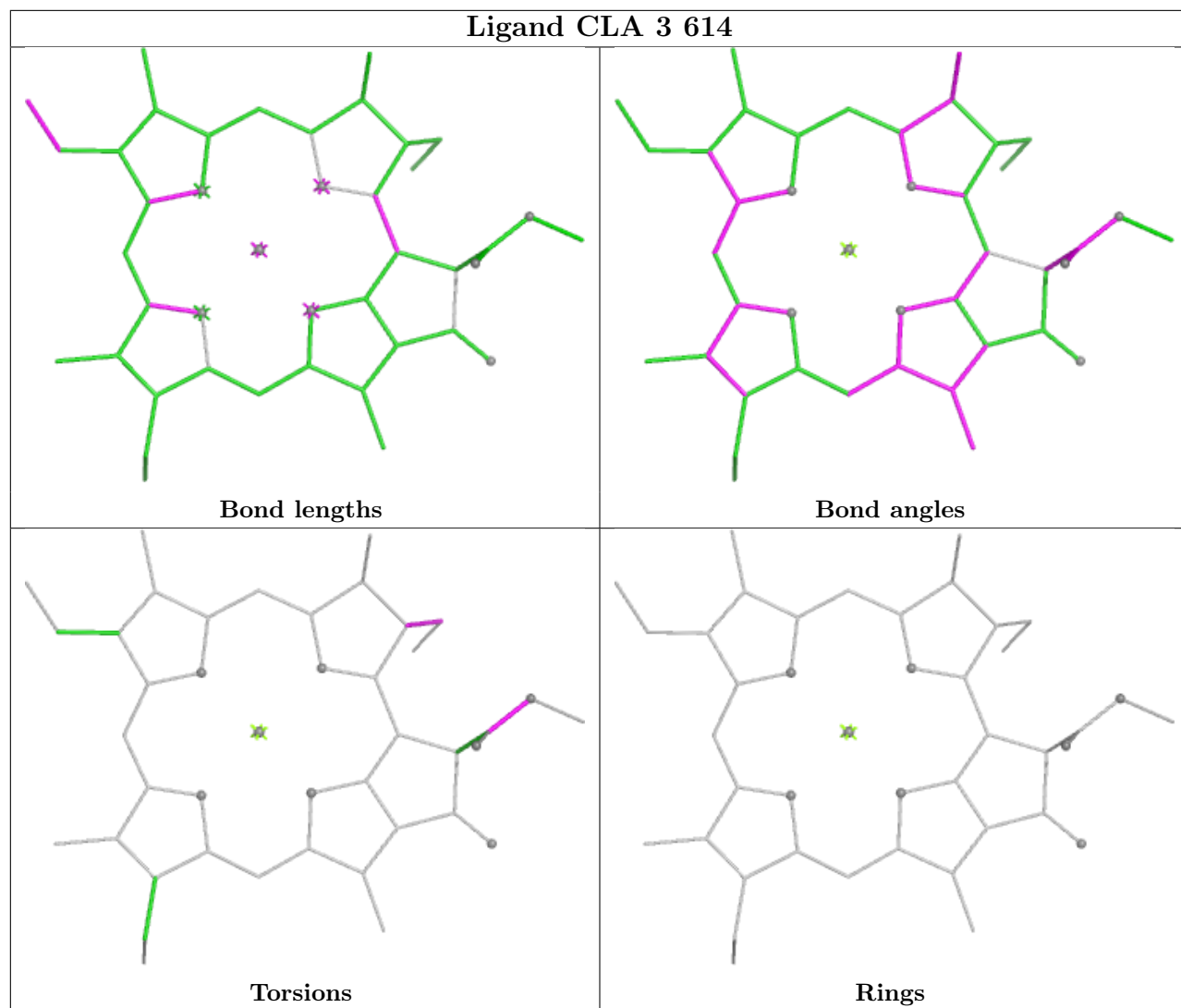




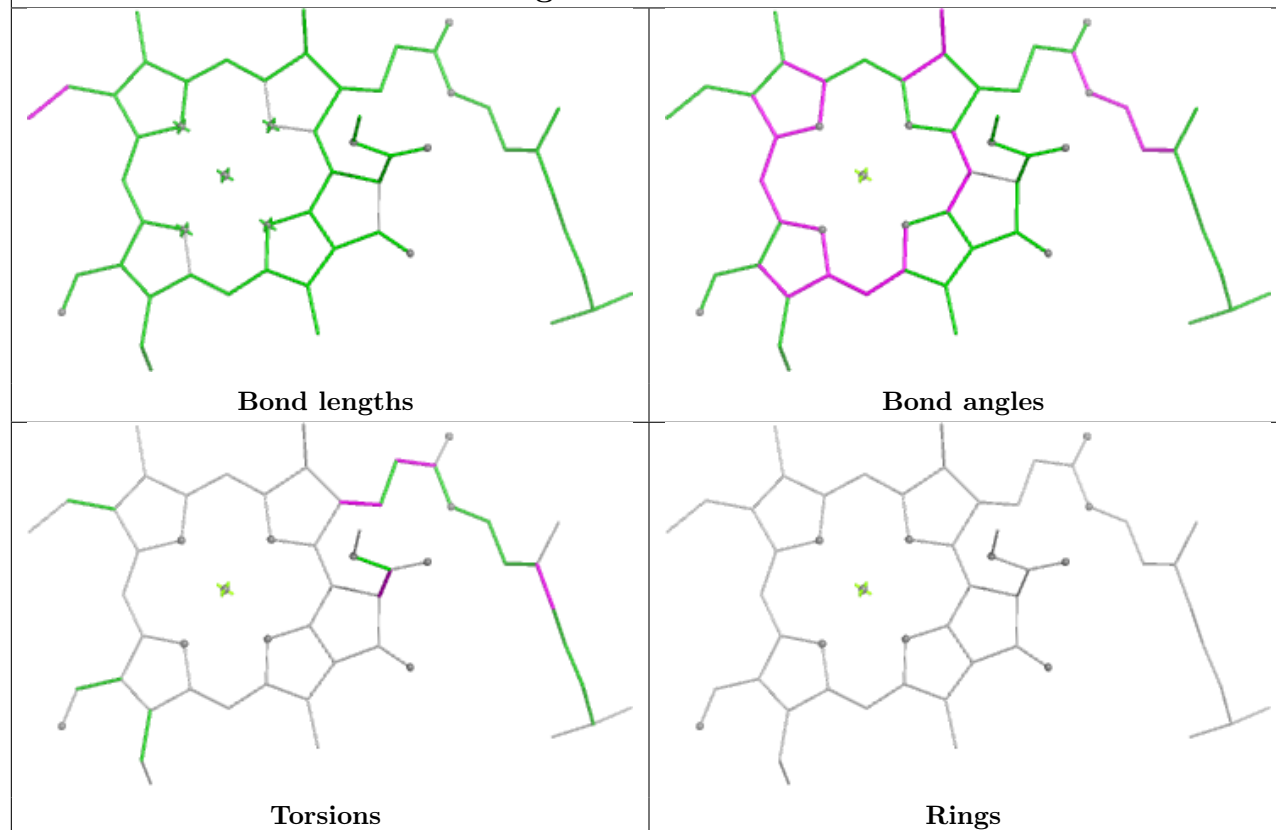




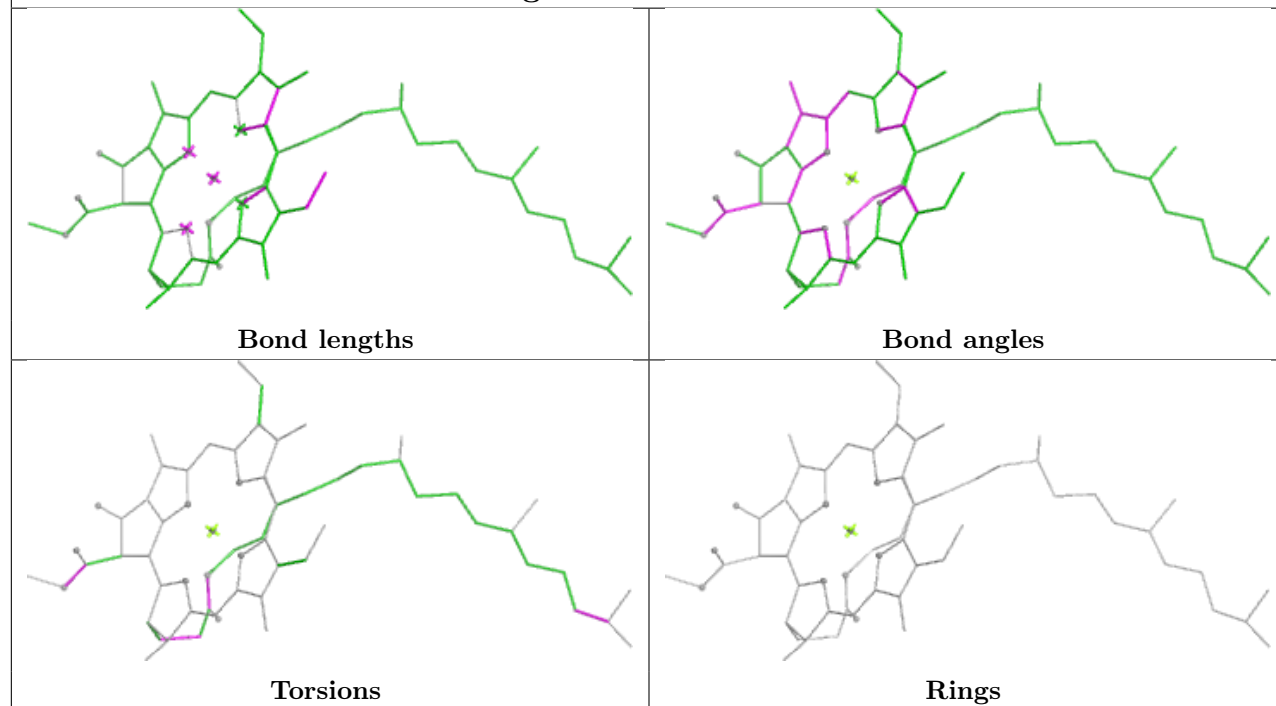
Ligand CLA 3 614

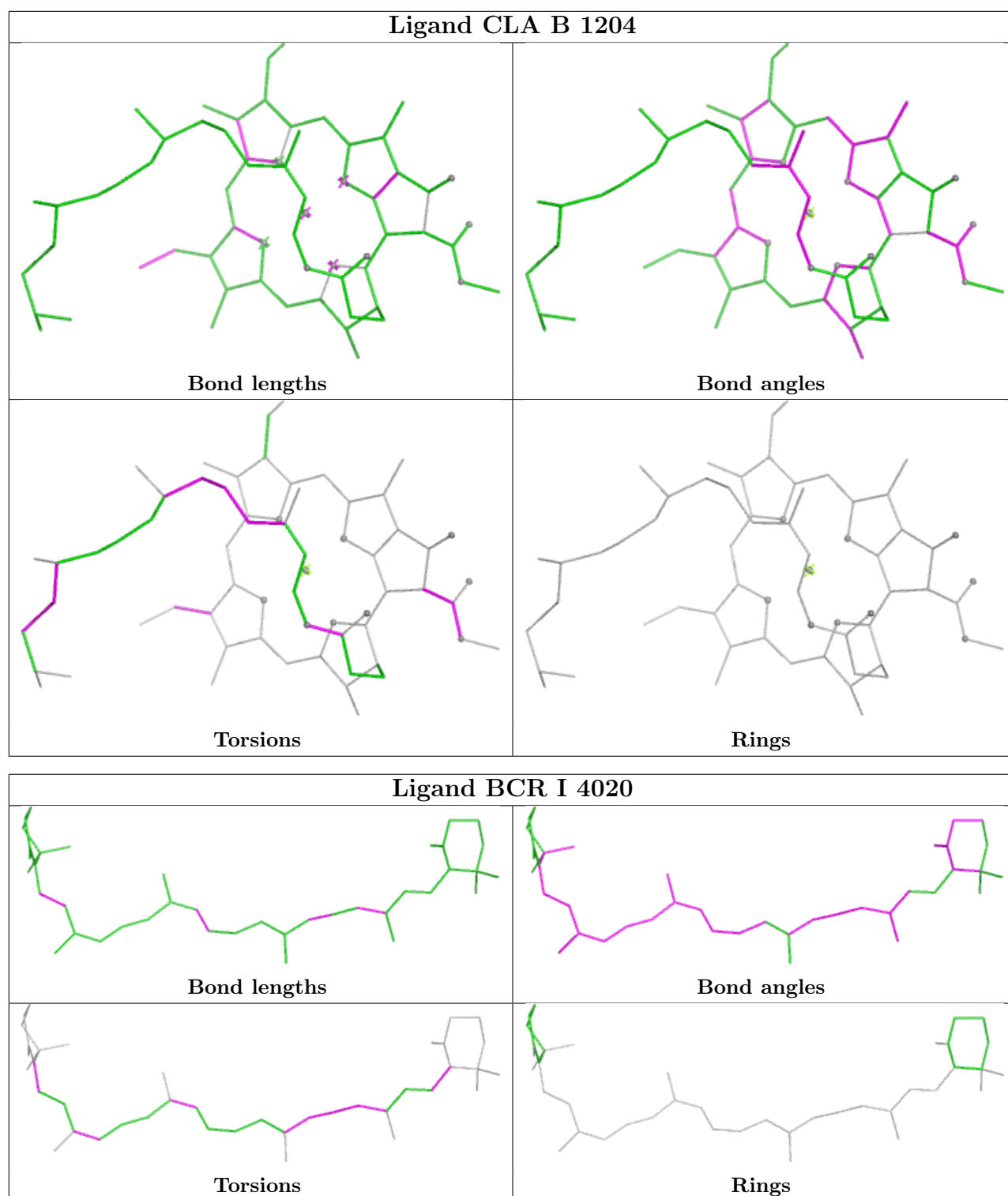


Ligand CHL 2 615

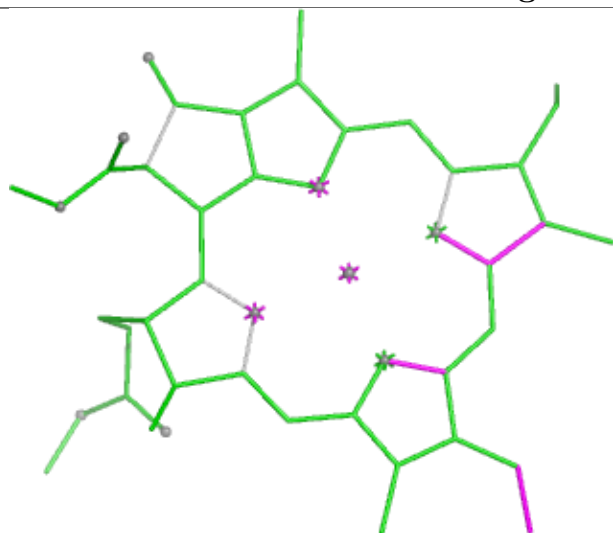


Ligand CLA A 1140

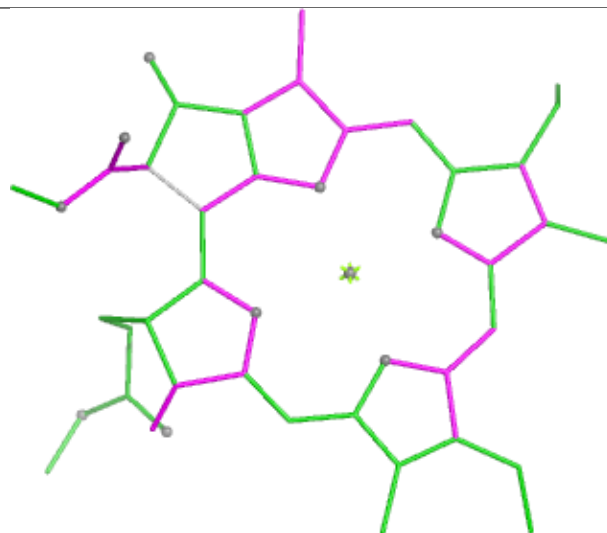




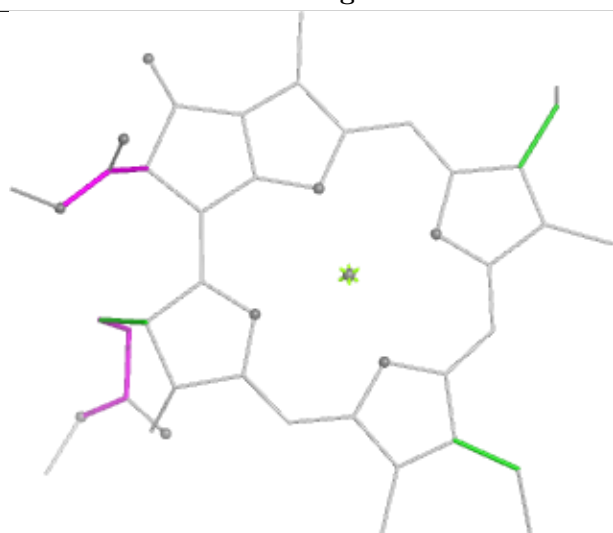
Ligand CLA 1 607



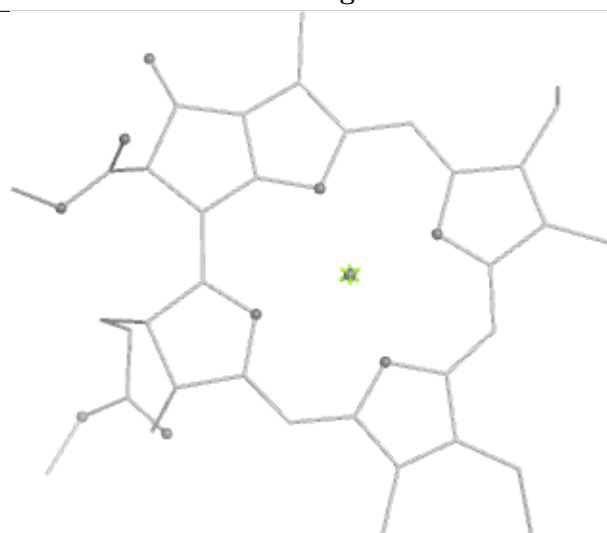
Bond lengths



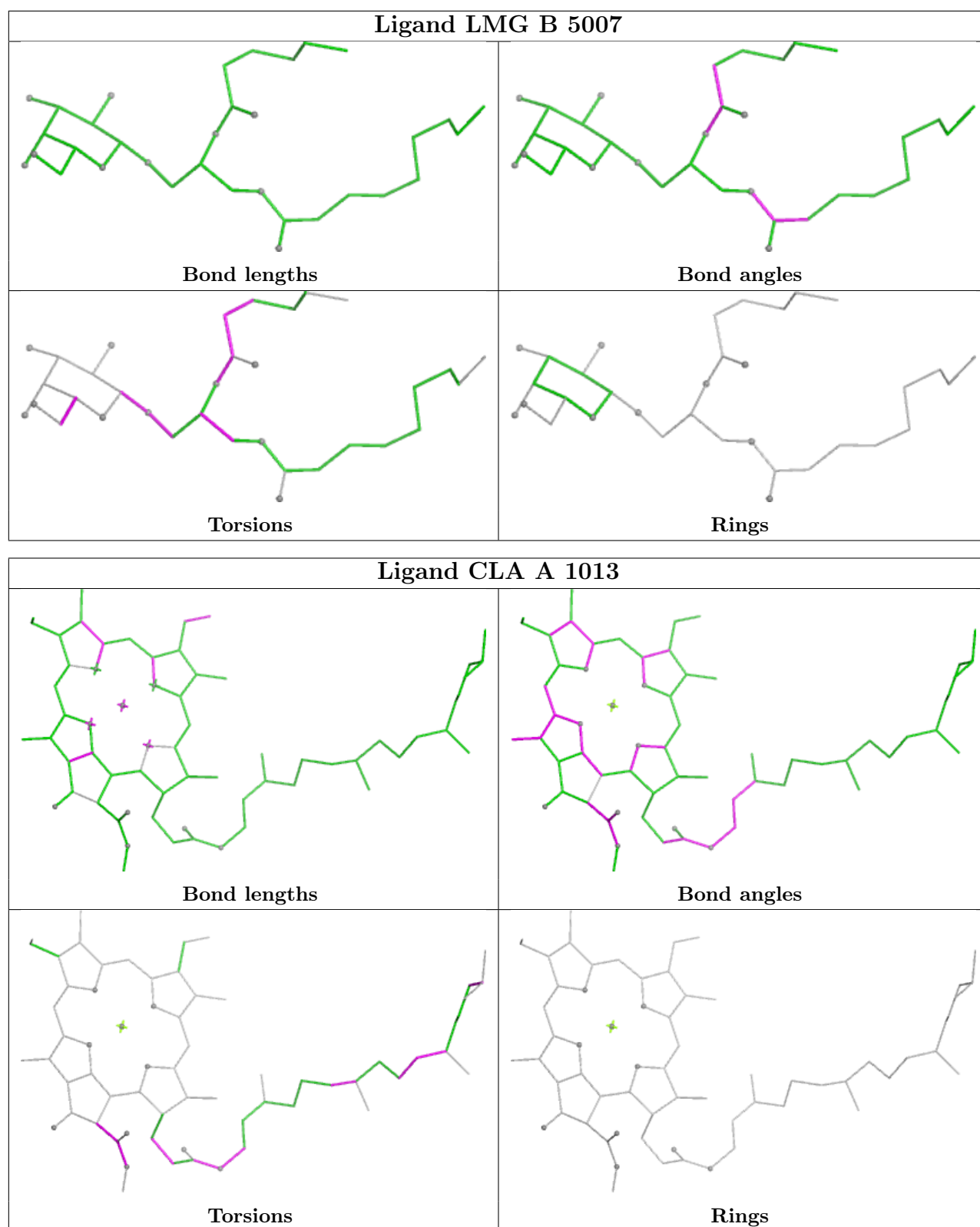
Bond angles

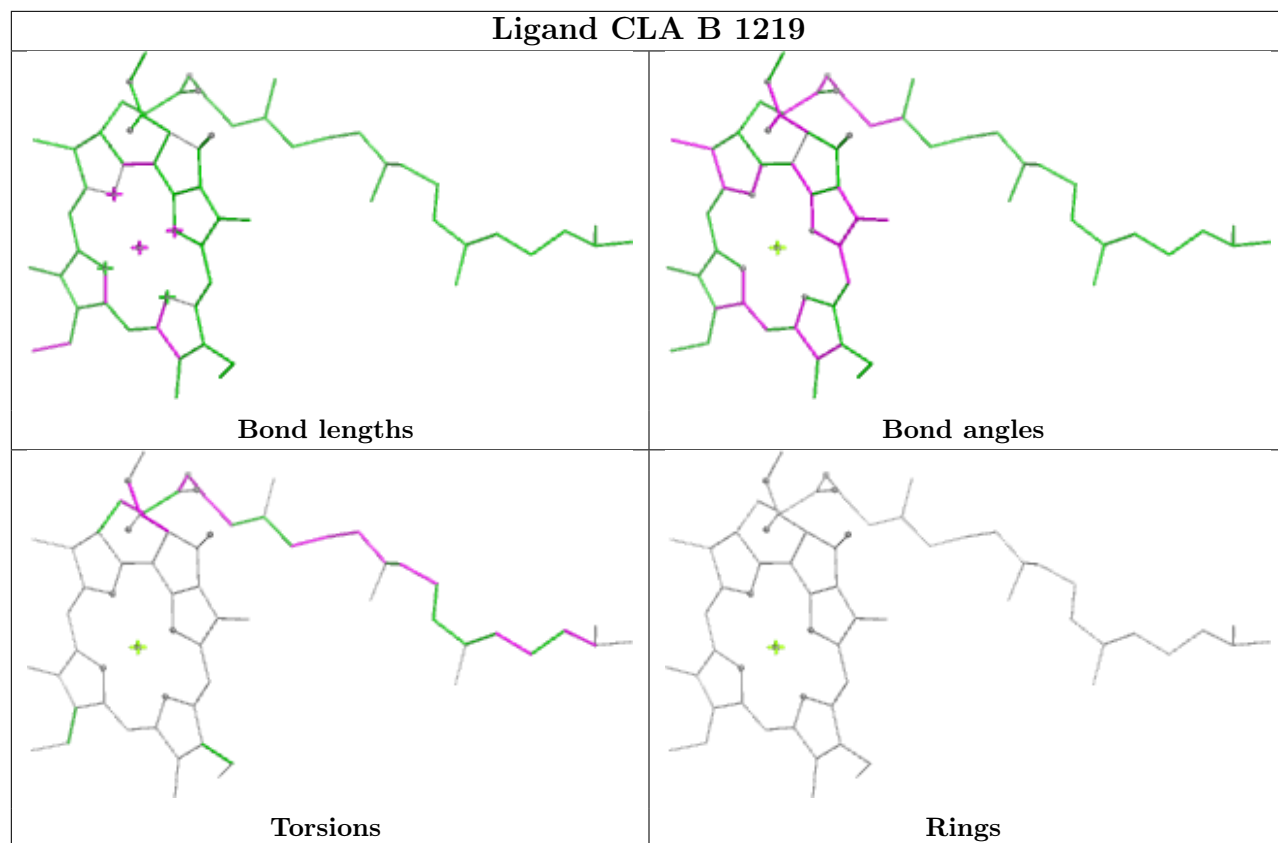


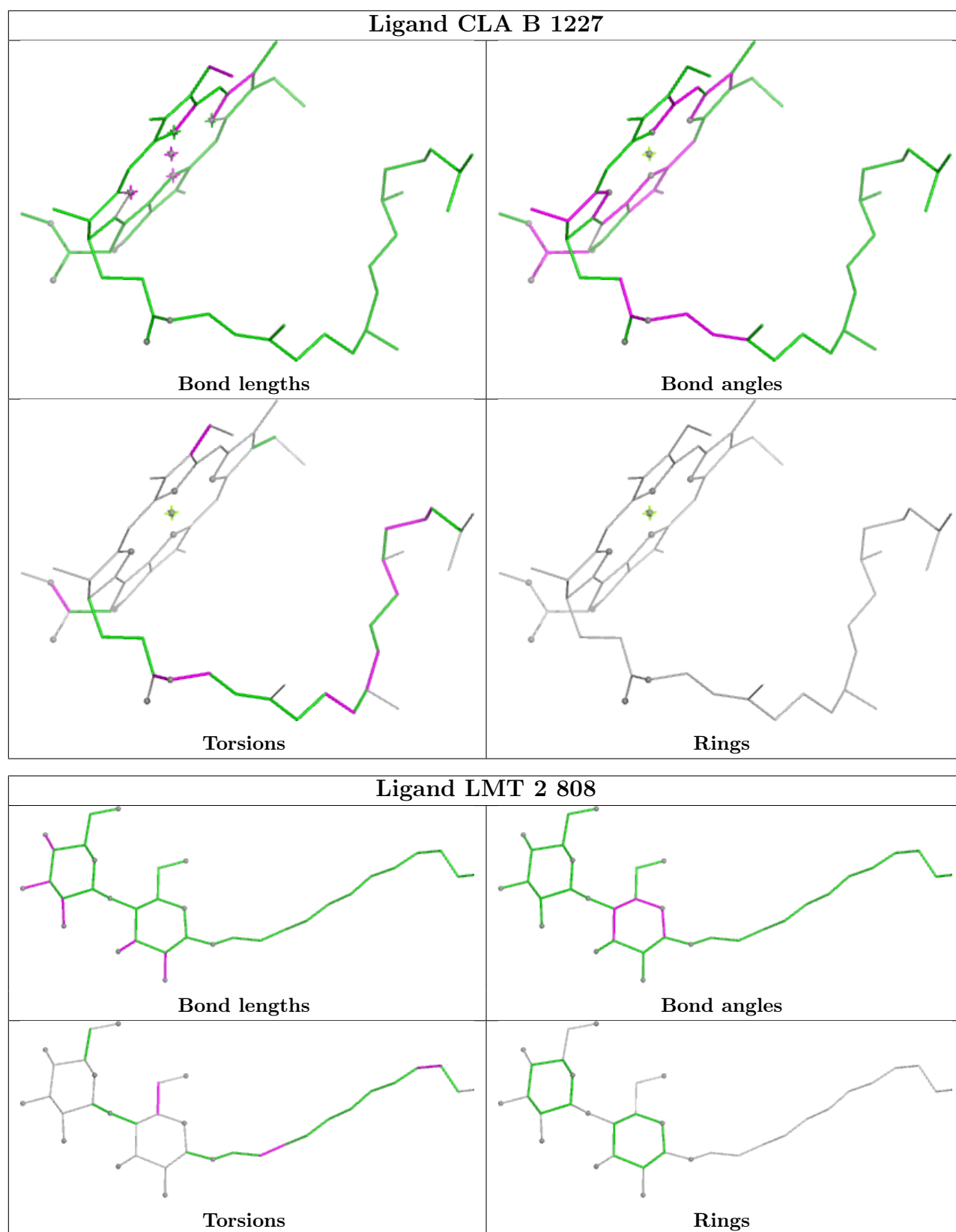
Torsions

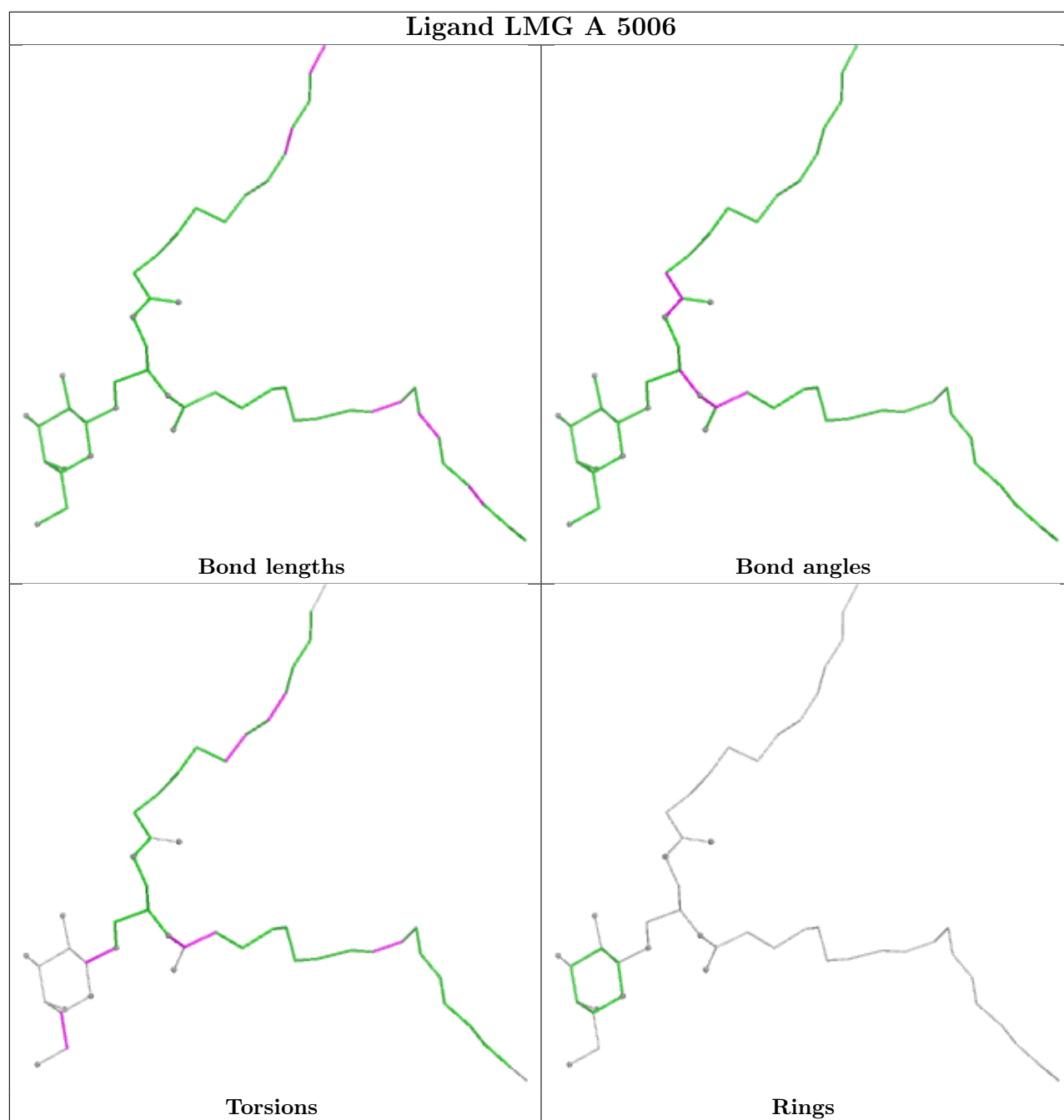


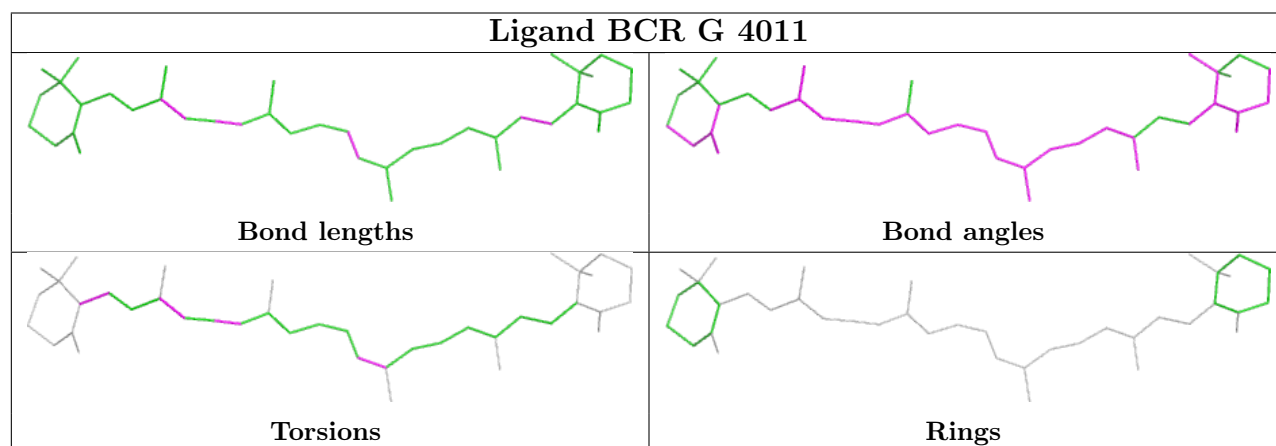
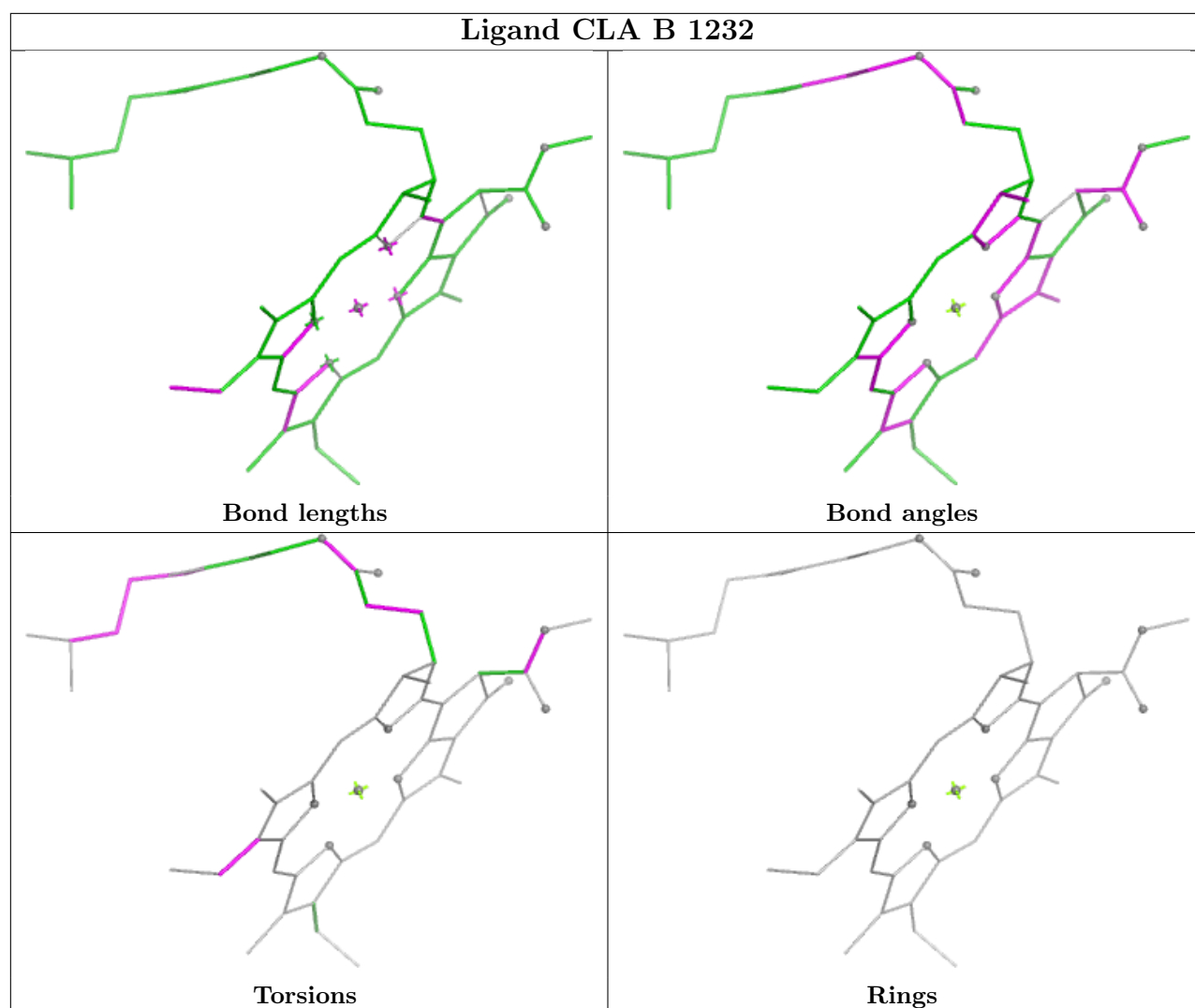
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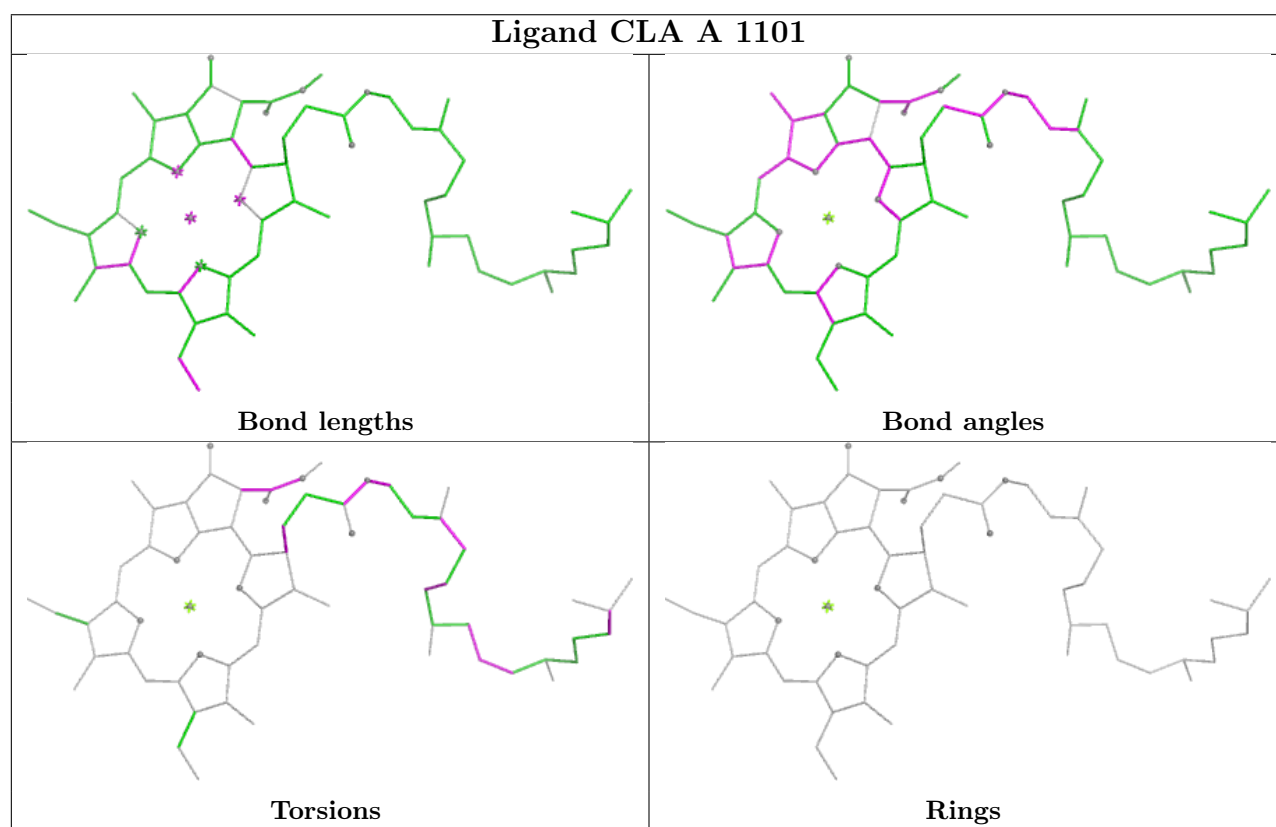
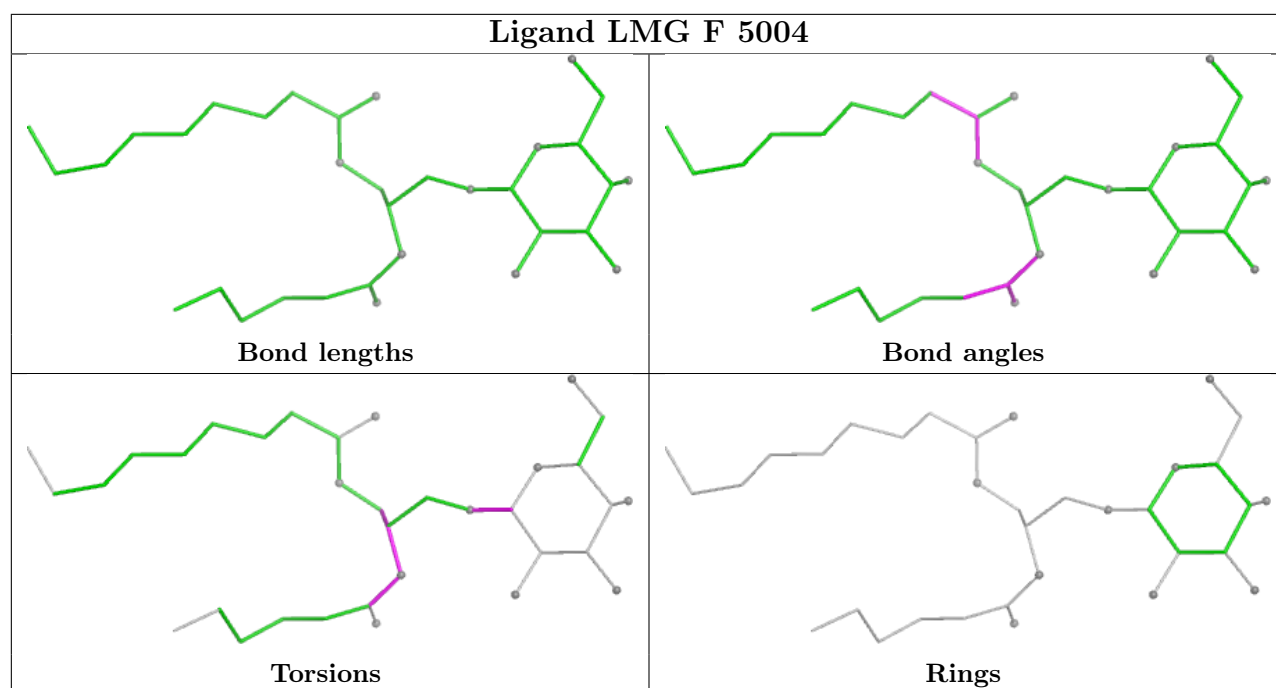


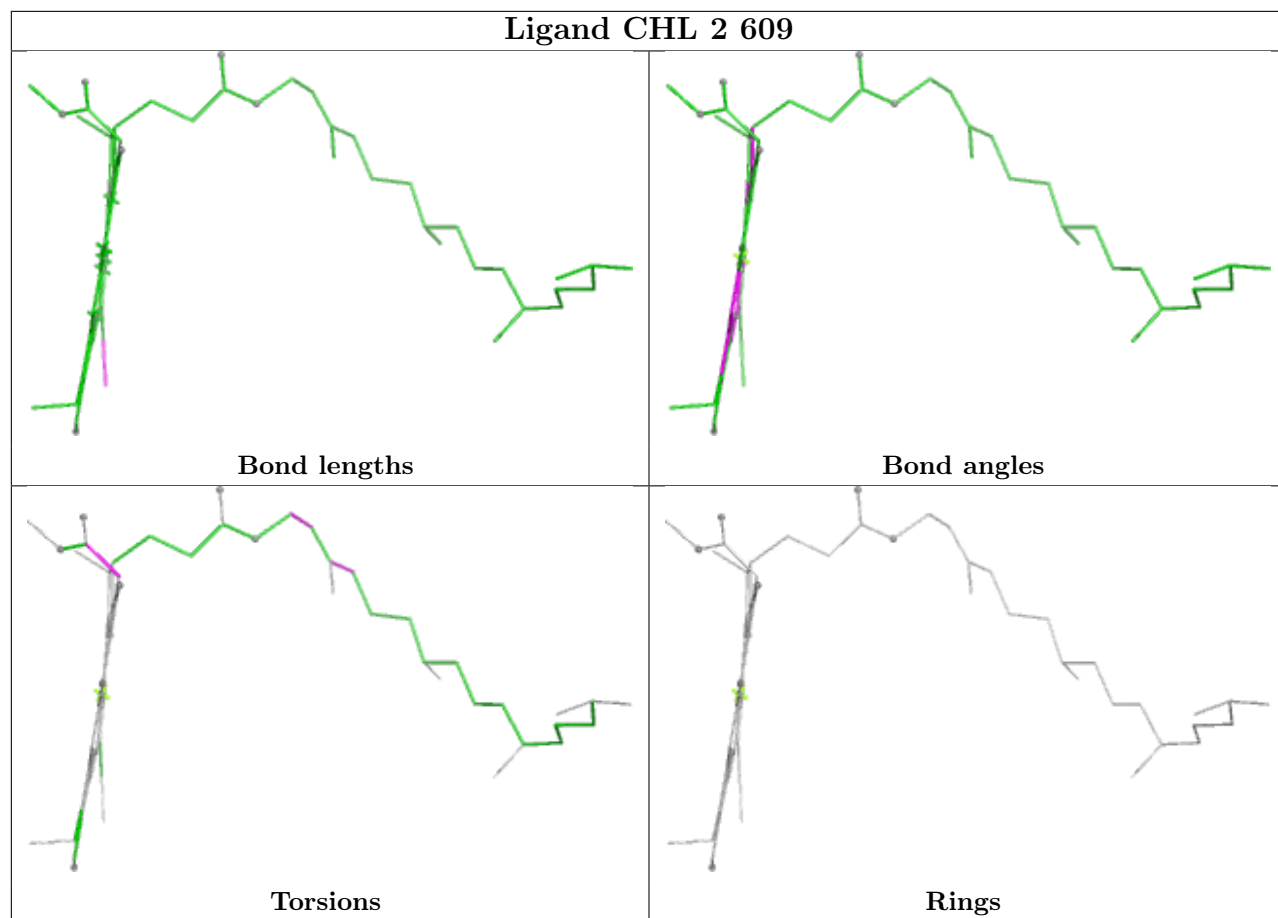


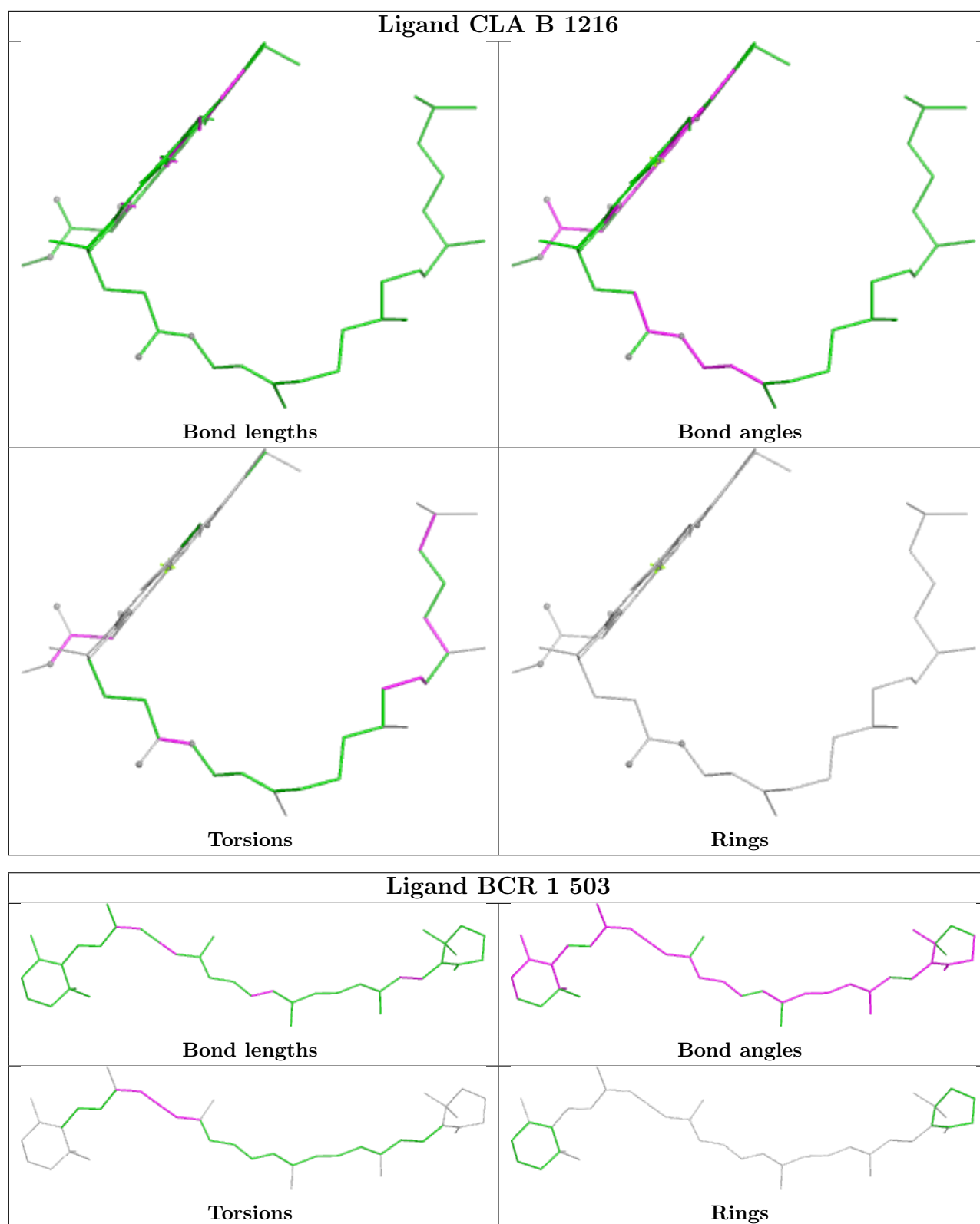


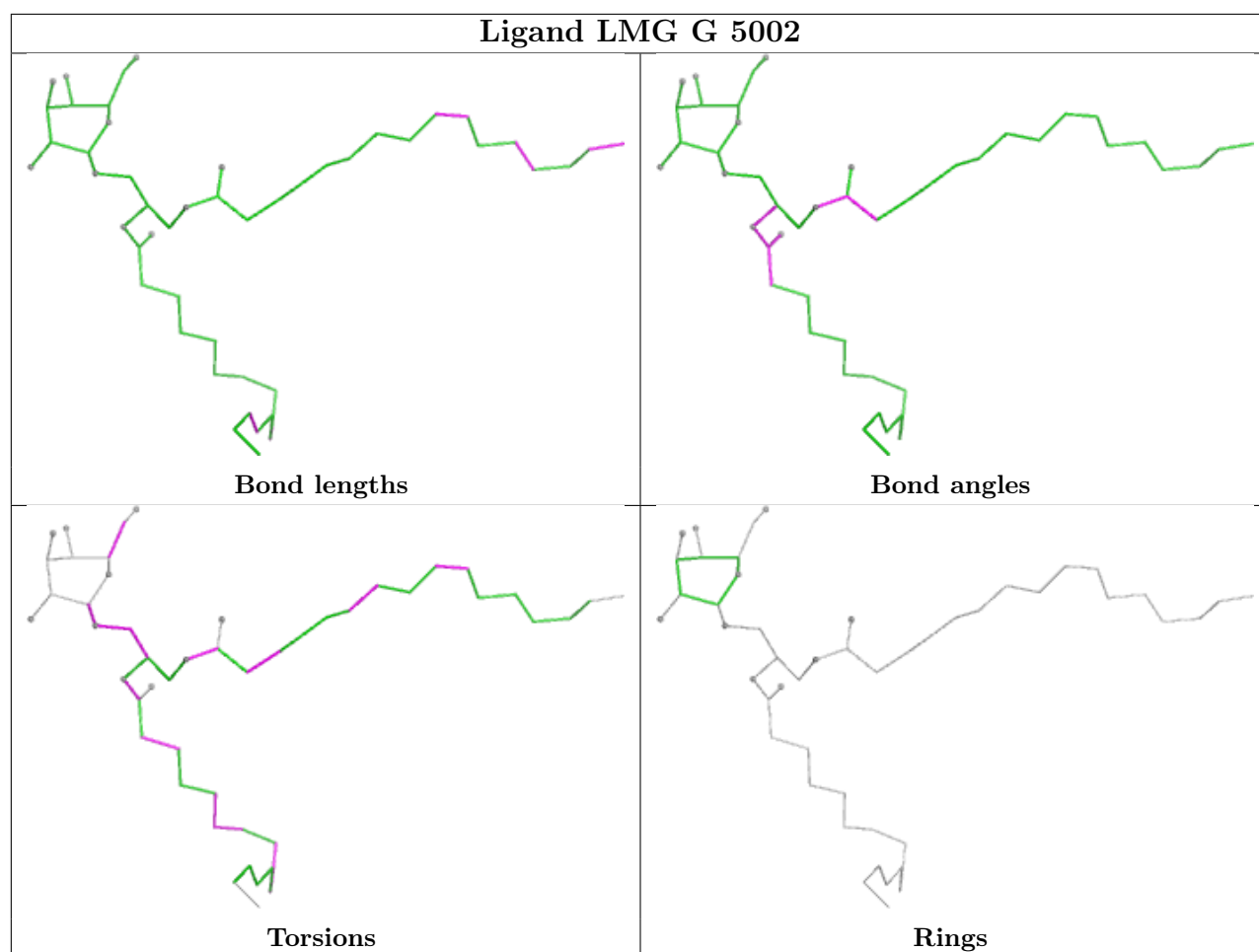


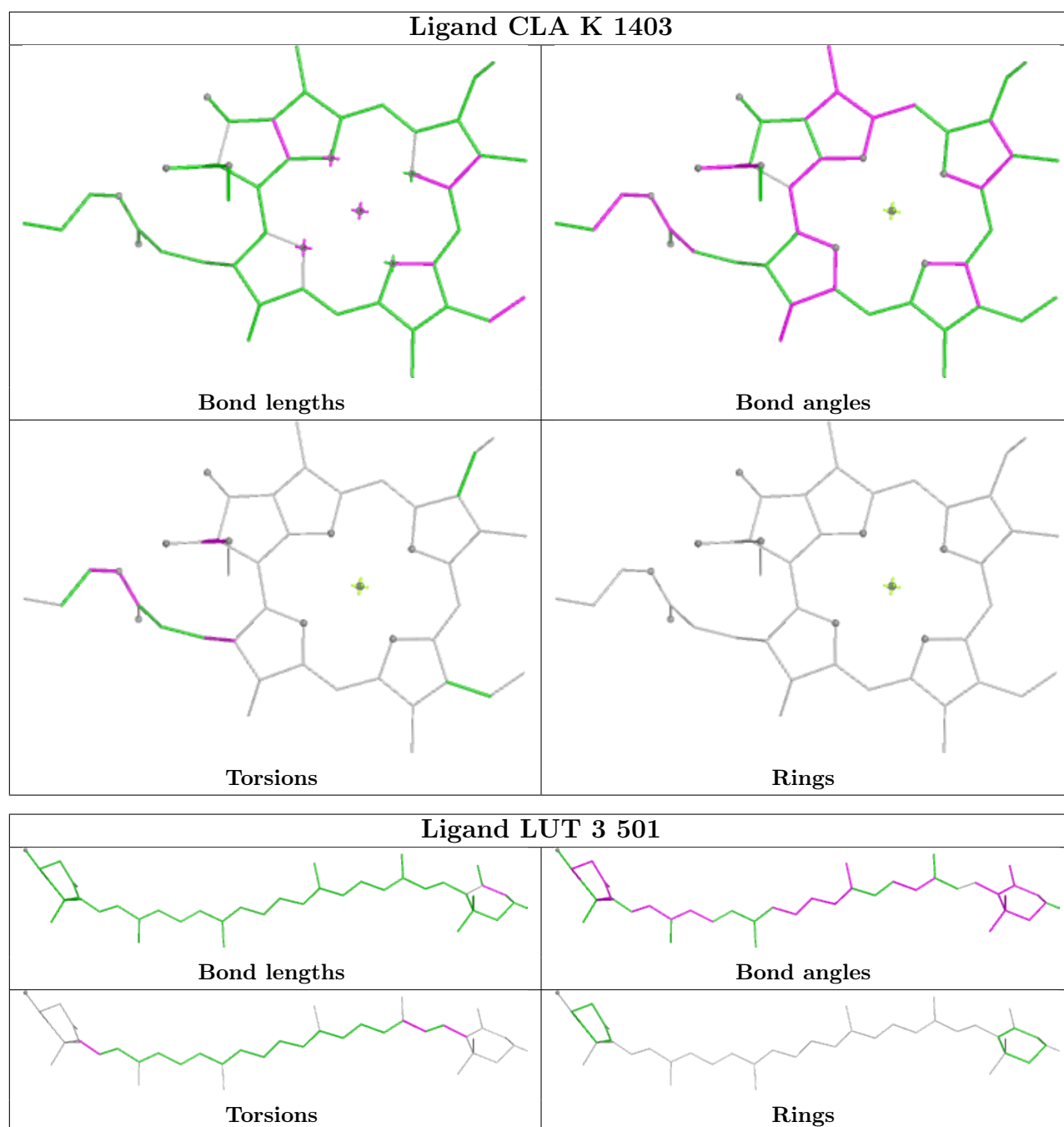




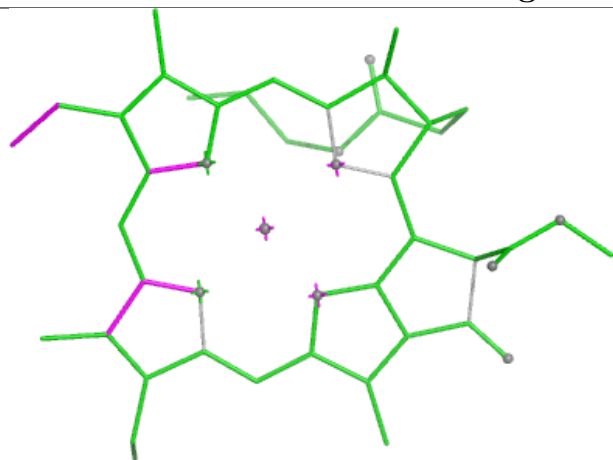




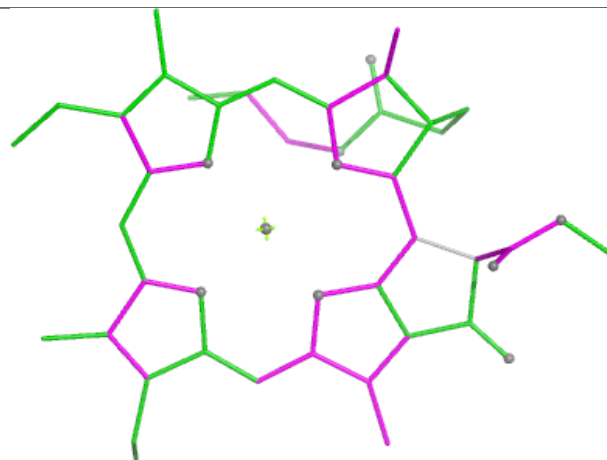




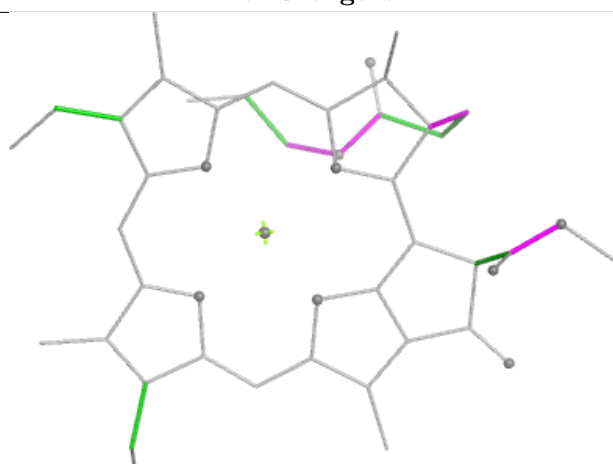
Ligand CLA 3 608



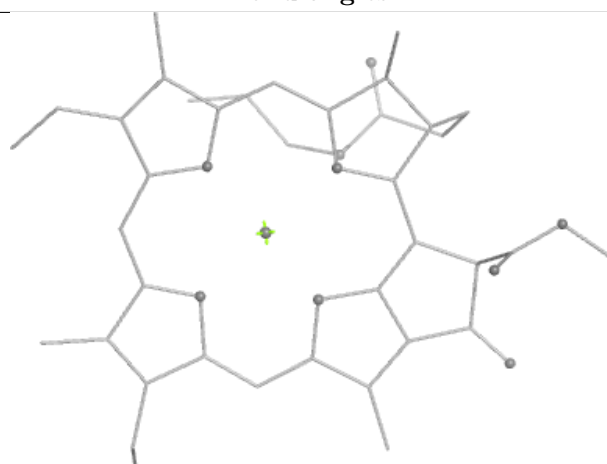
Bond lengths



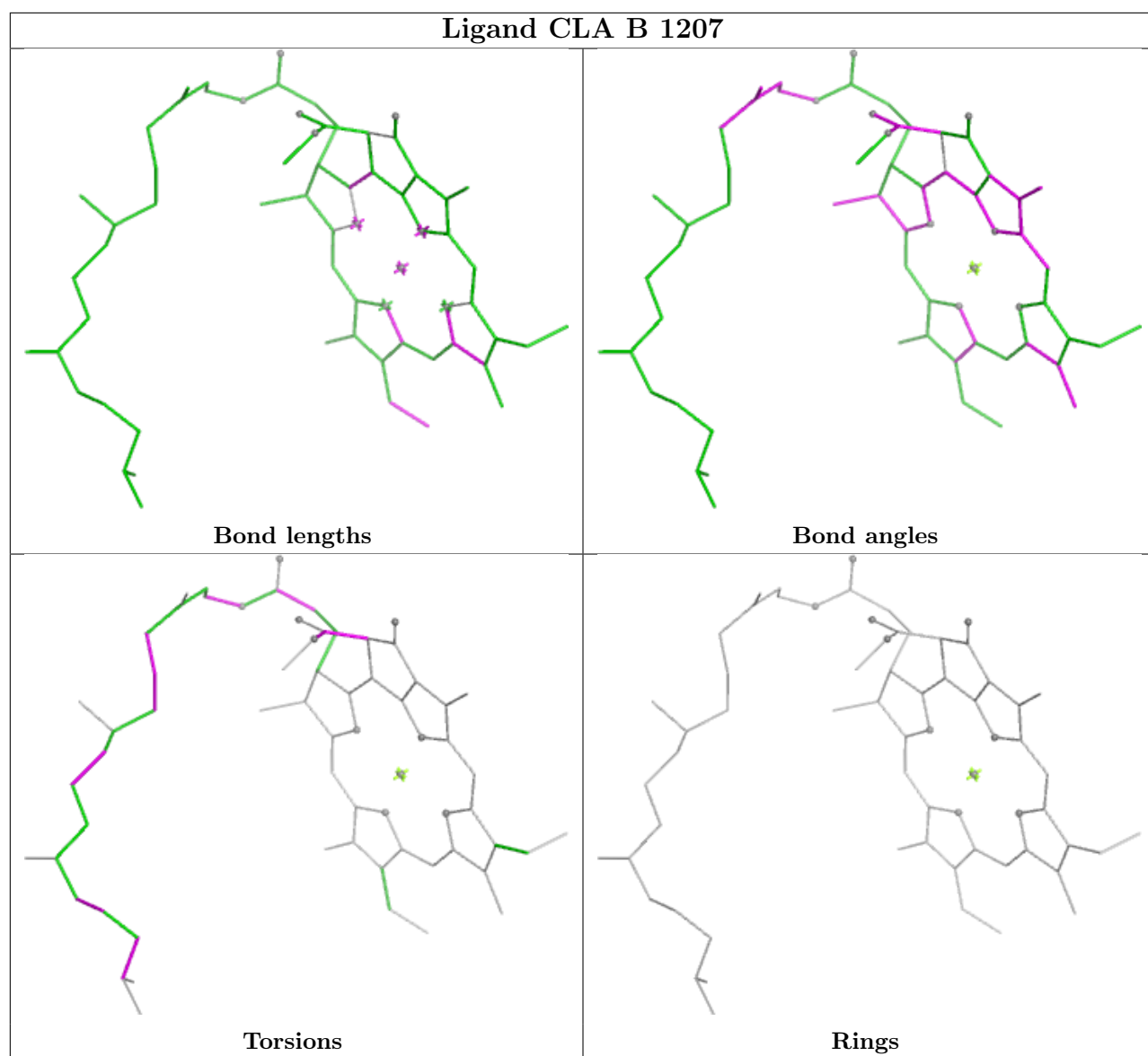
Bond angles

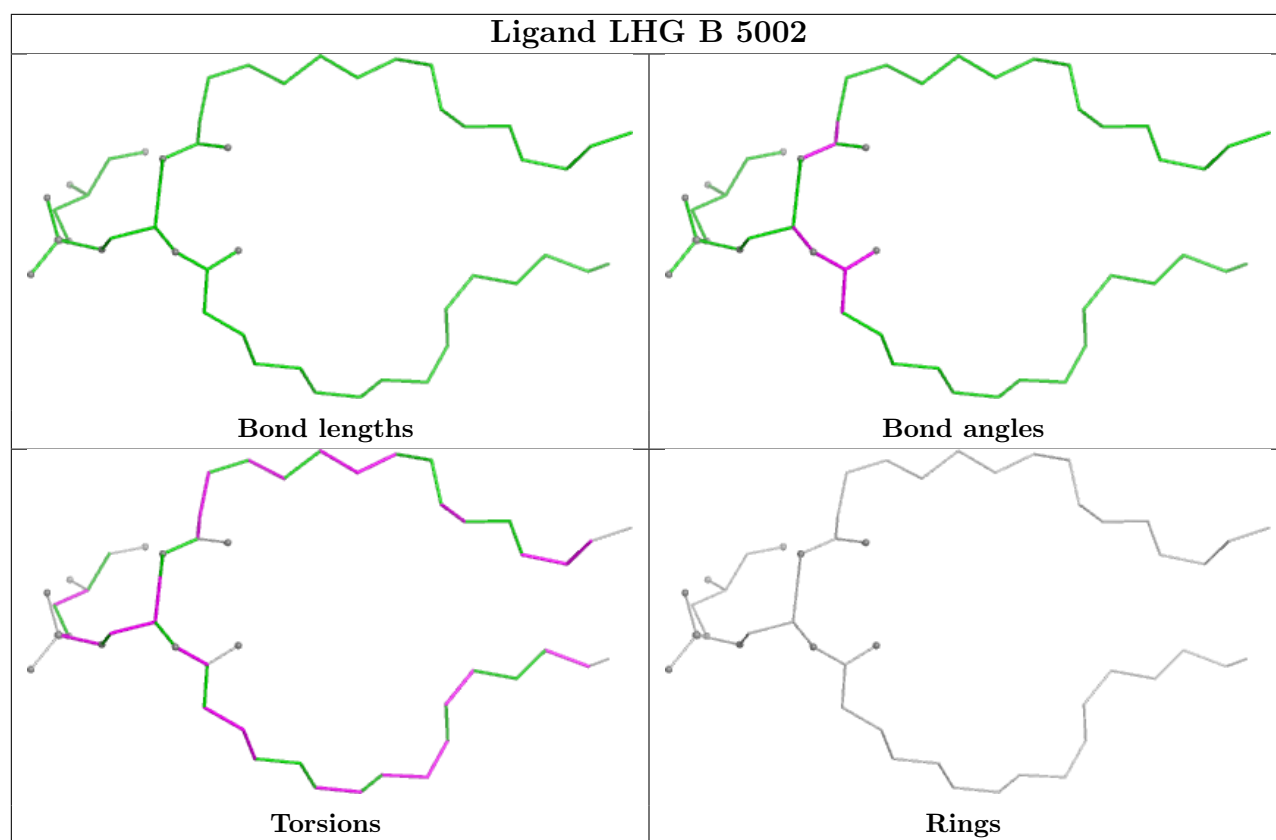


Torsions

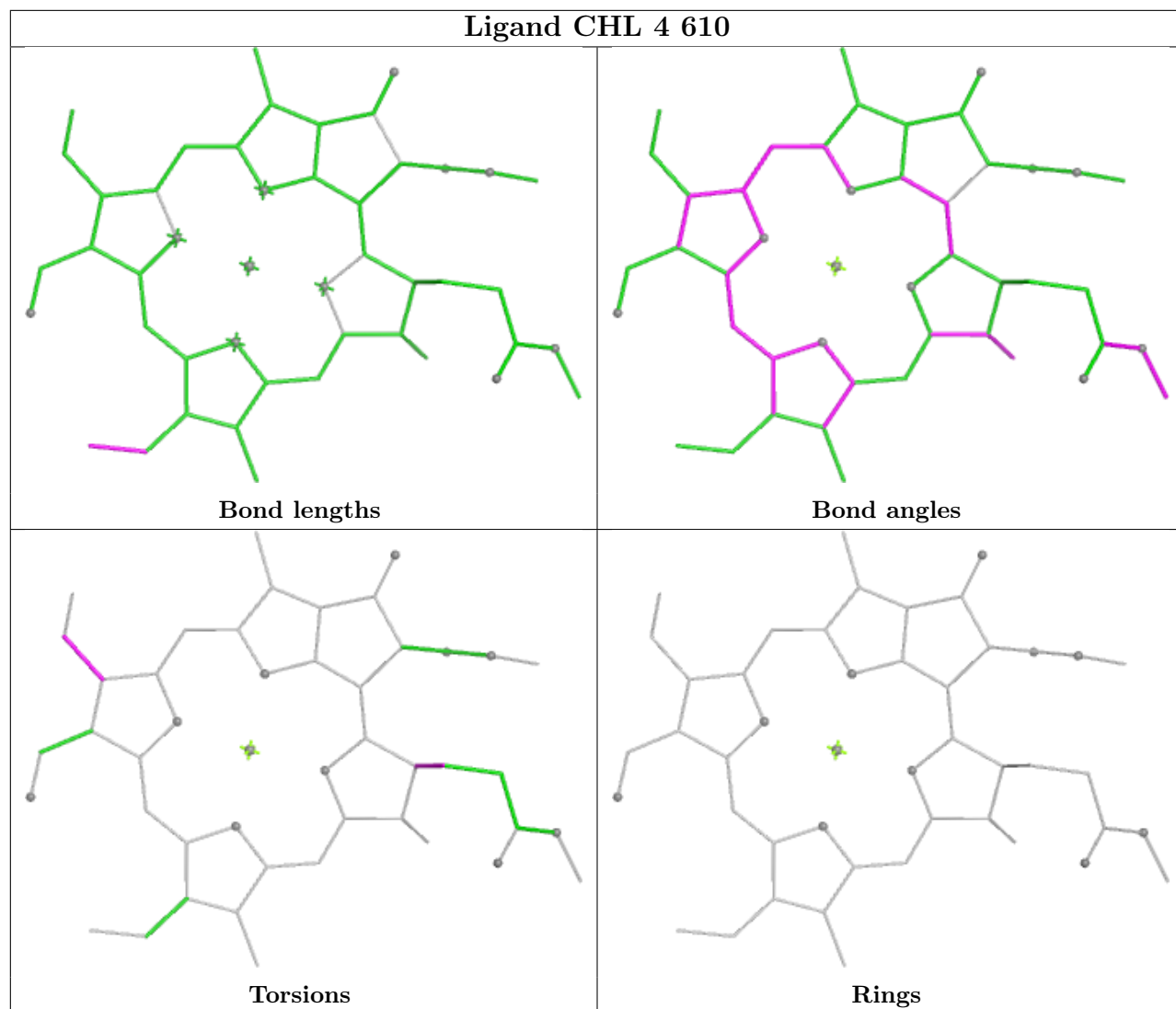


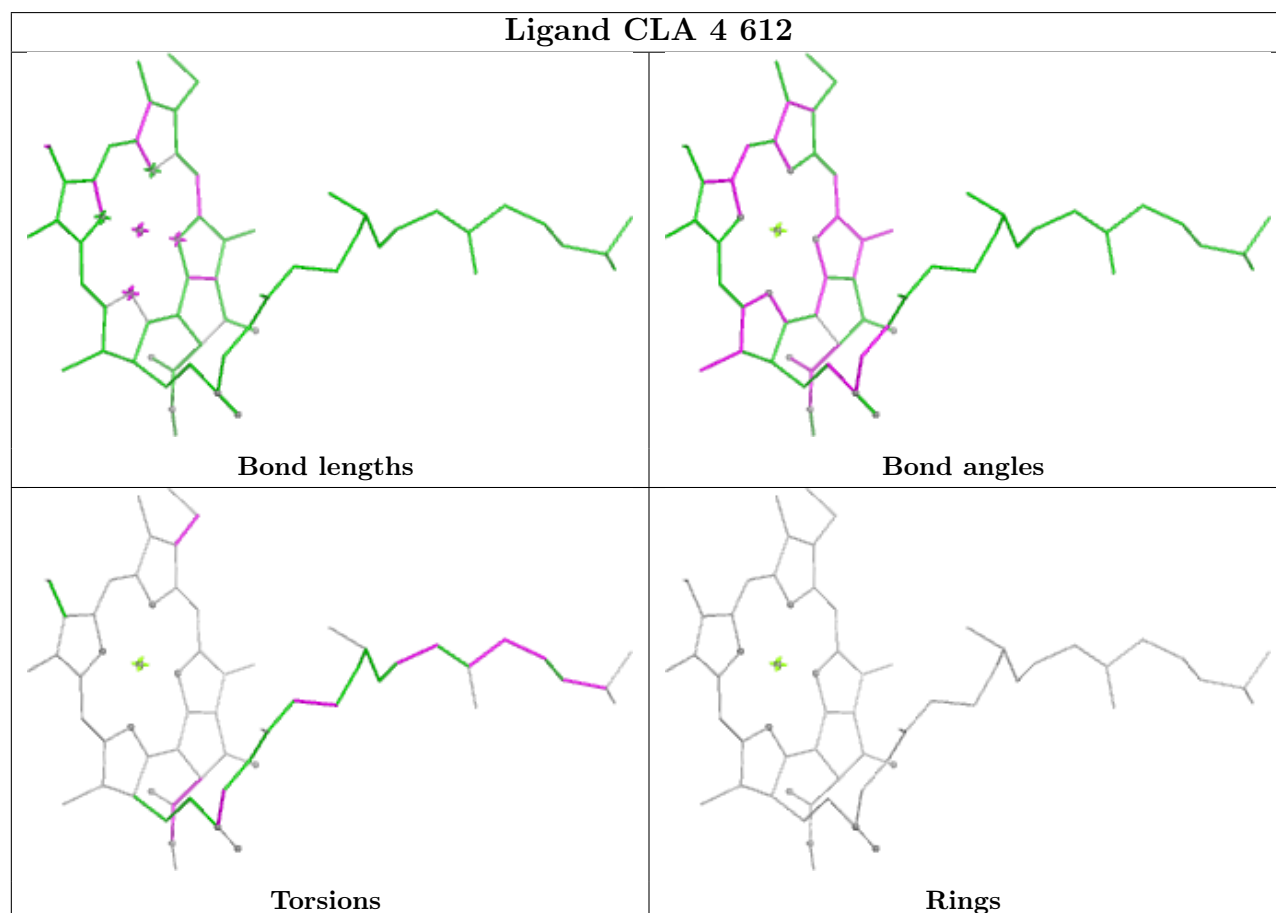
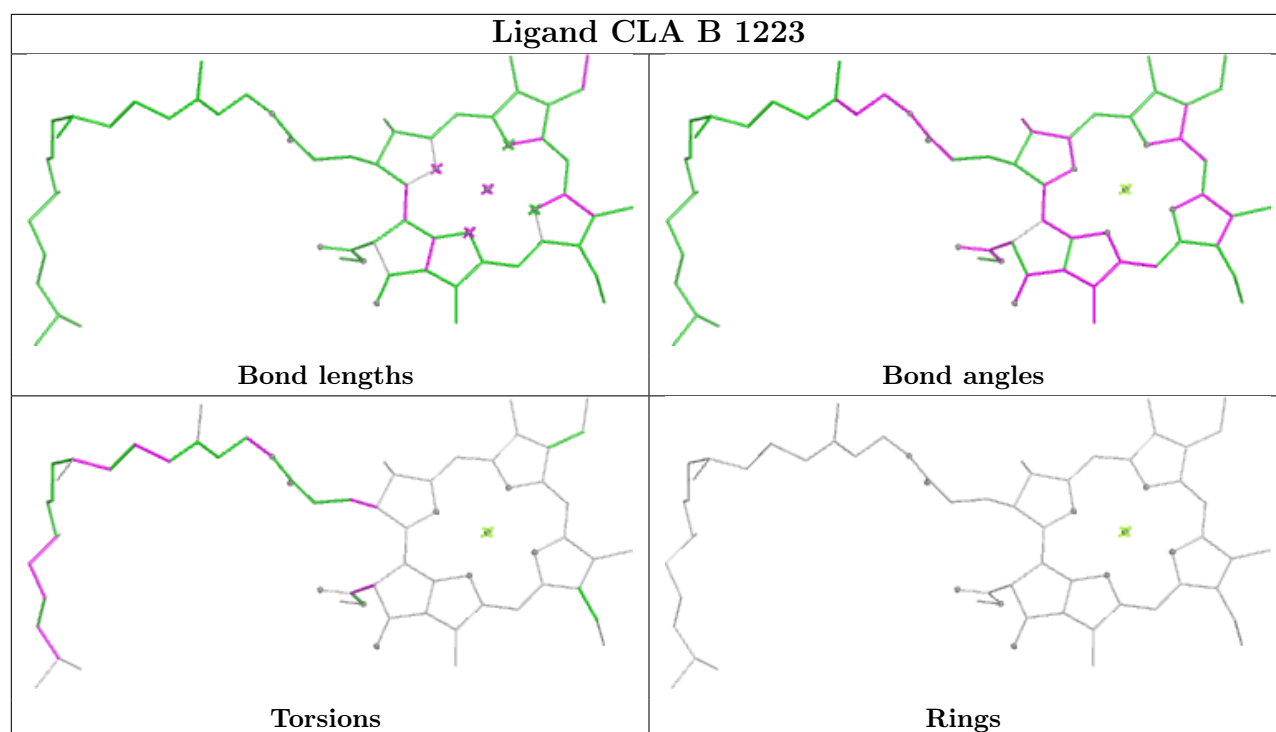
Rings

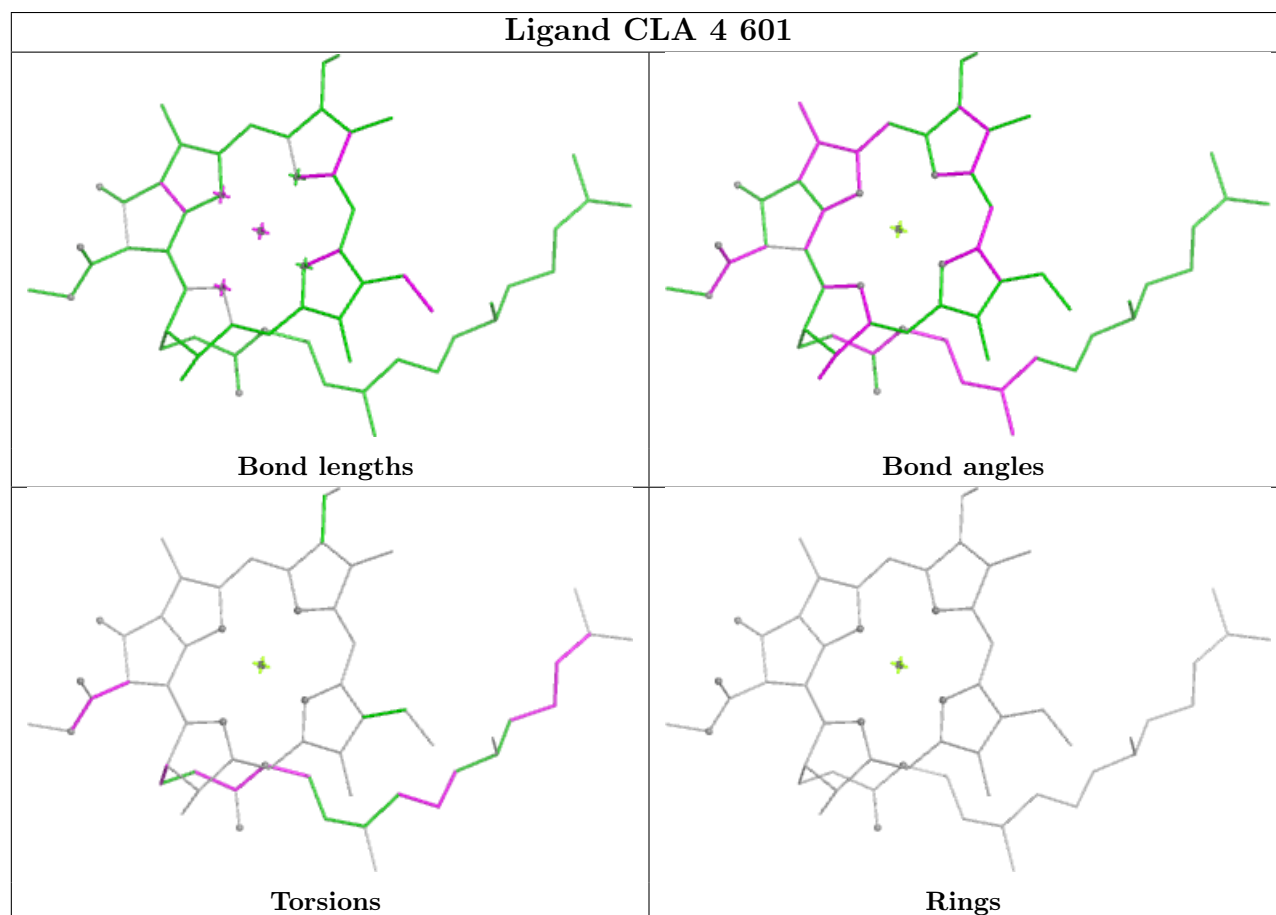
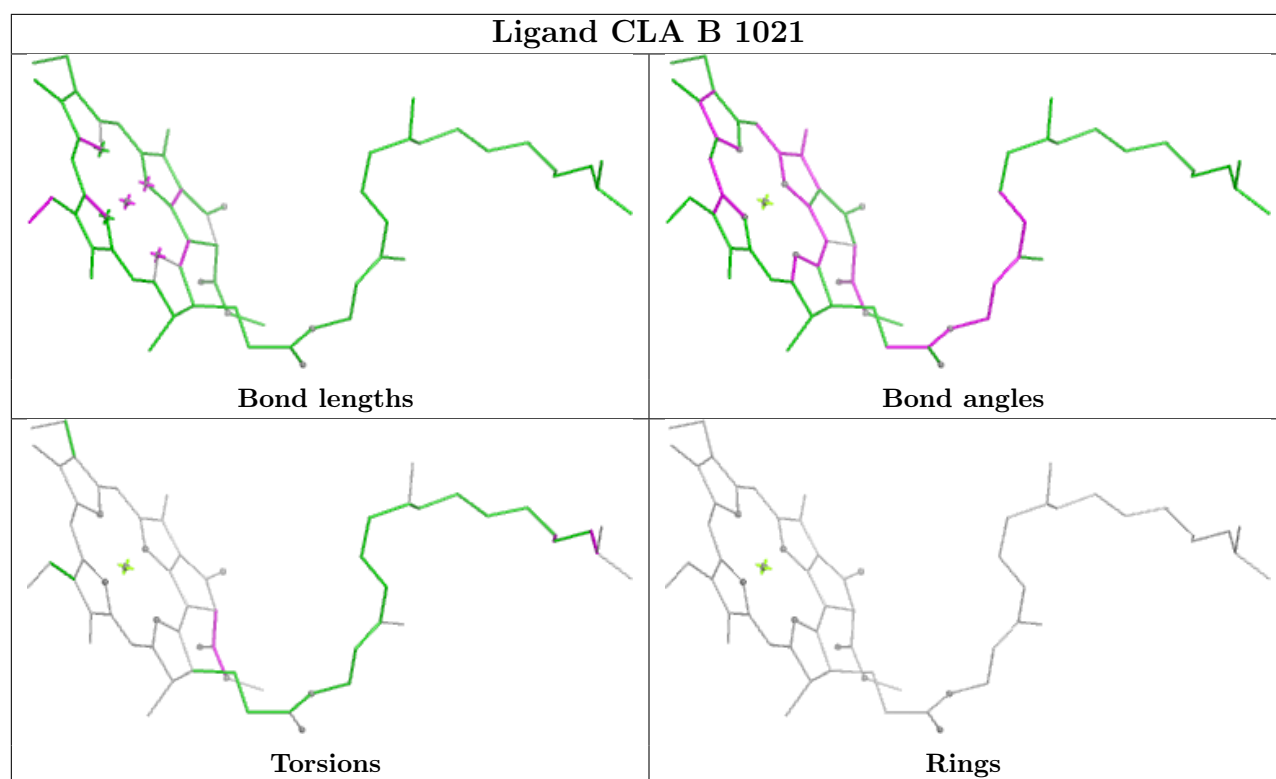


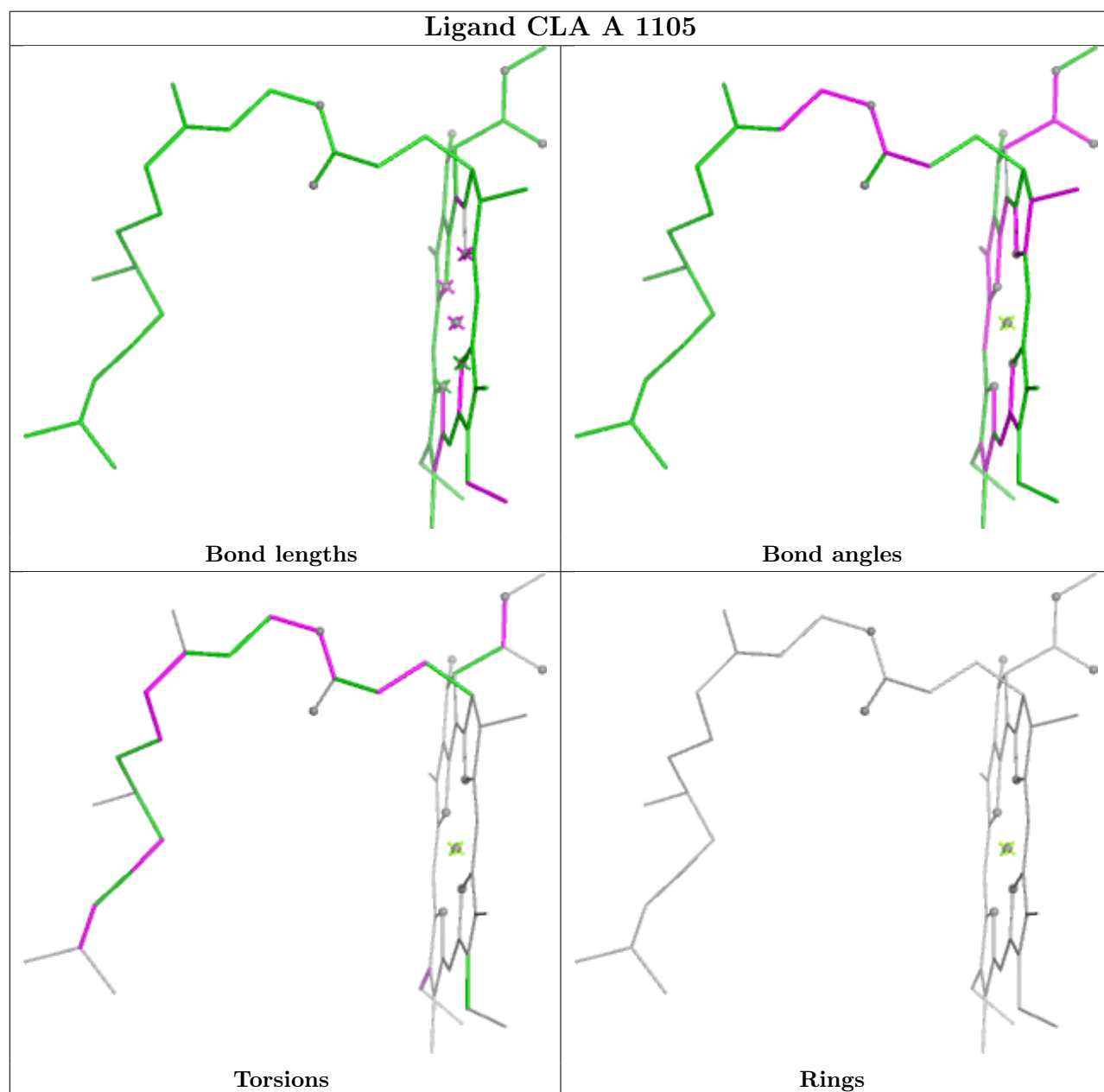
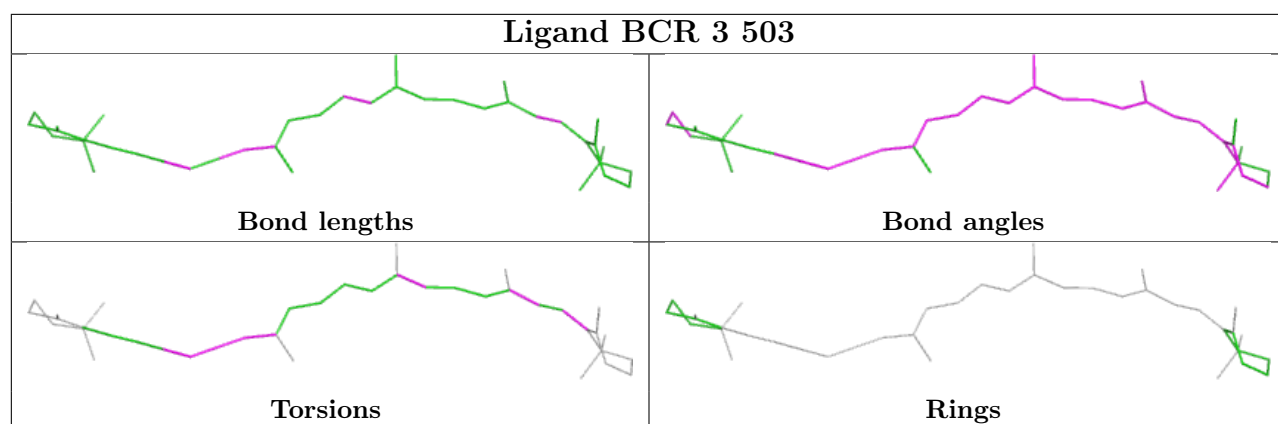


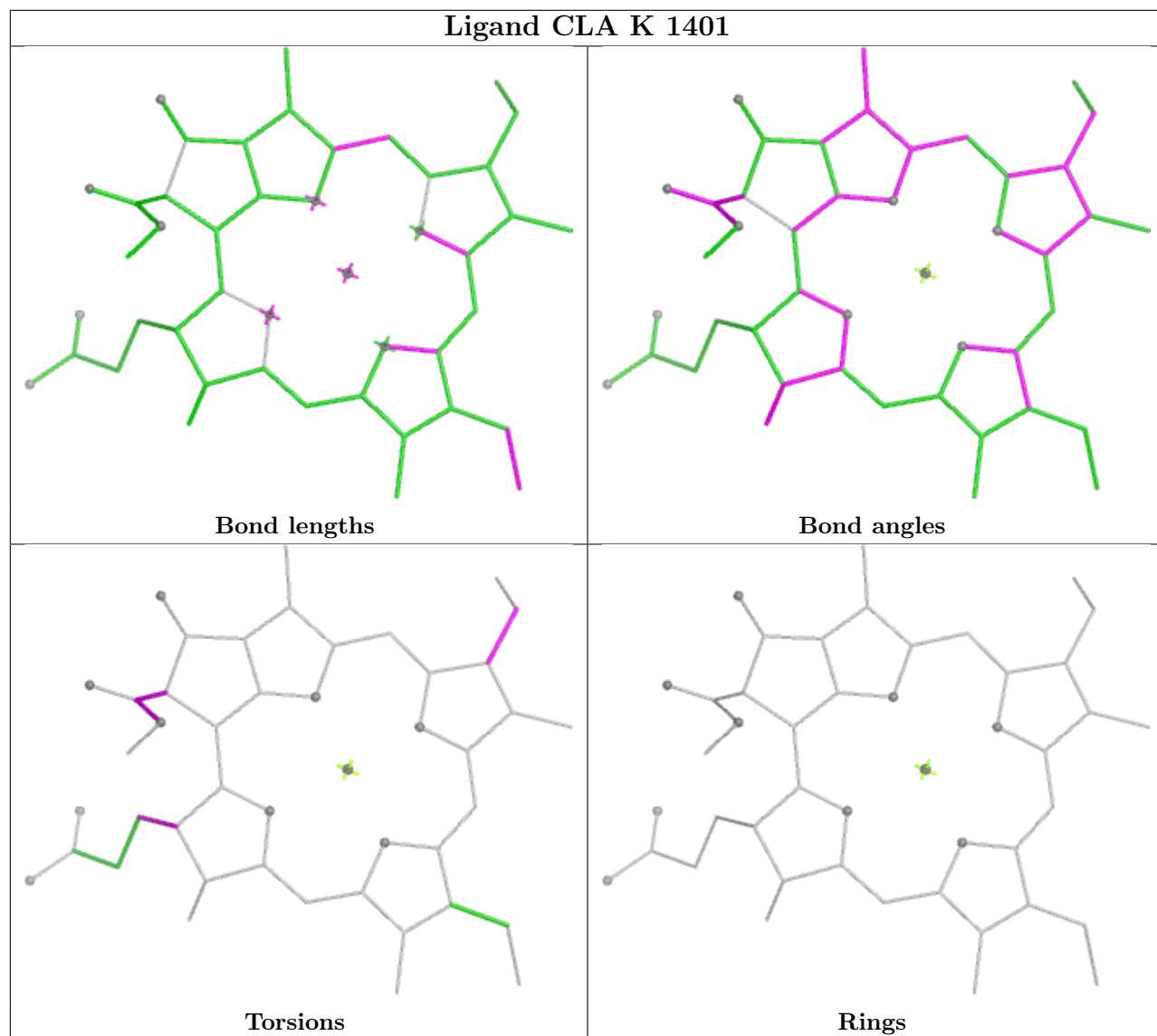
Ligand CHL 4 610

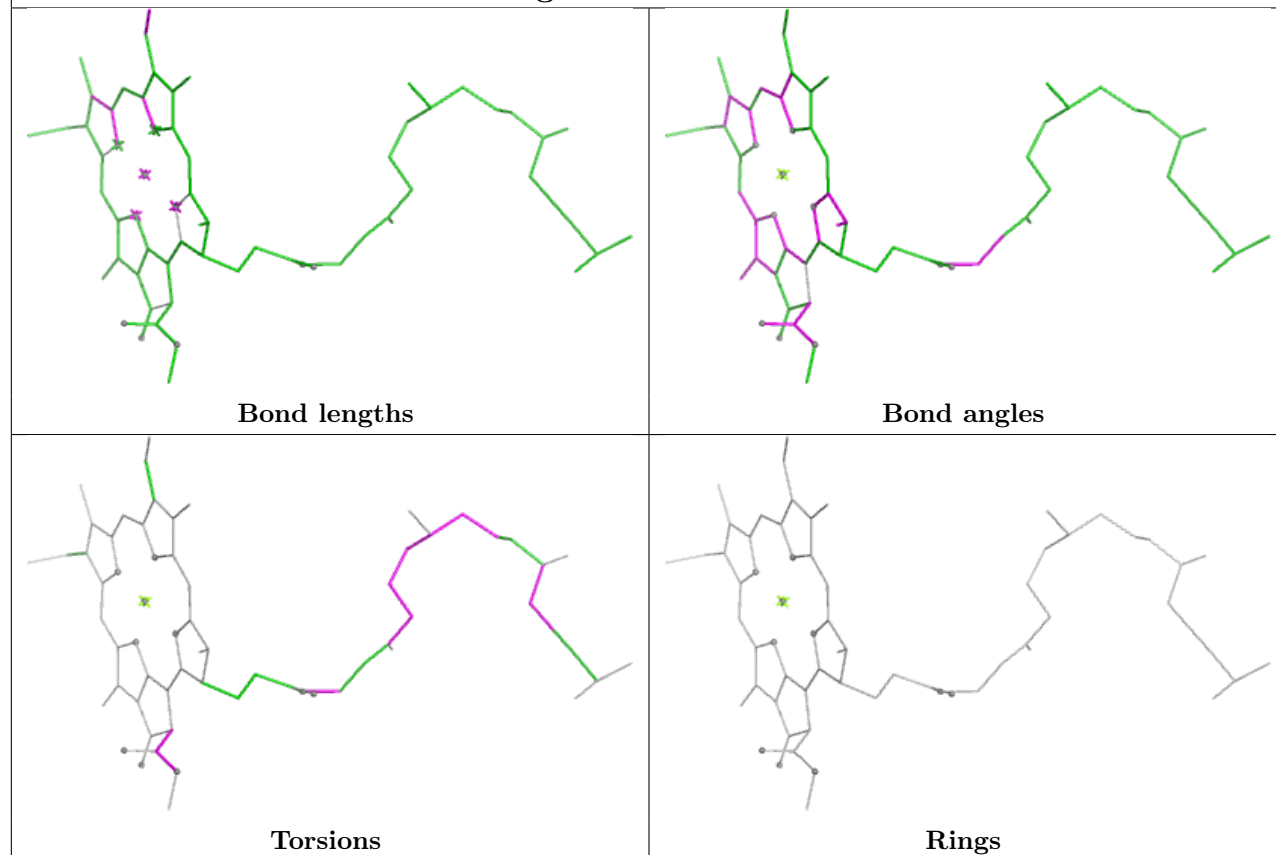
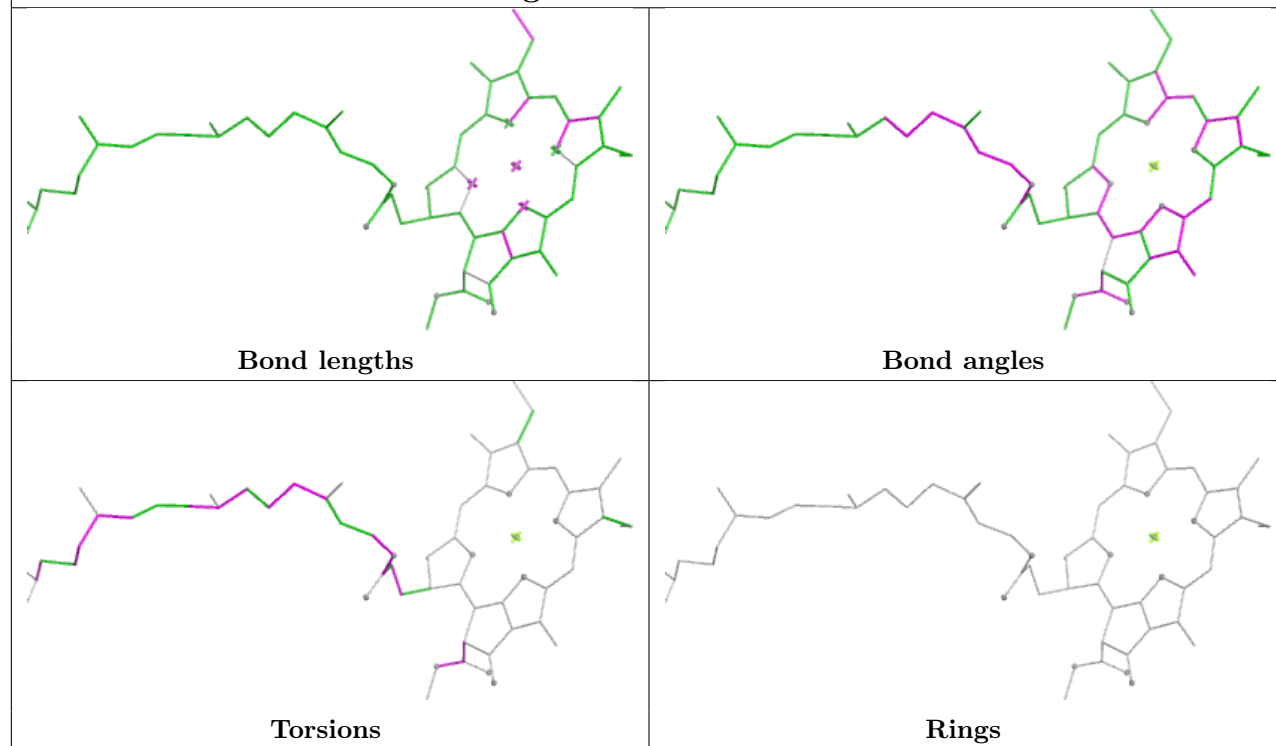


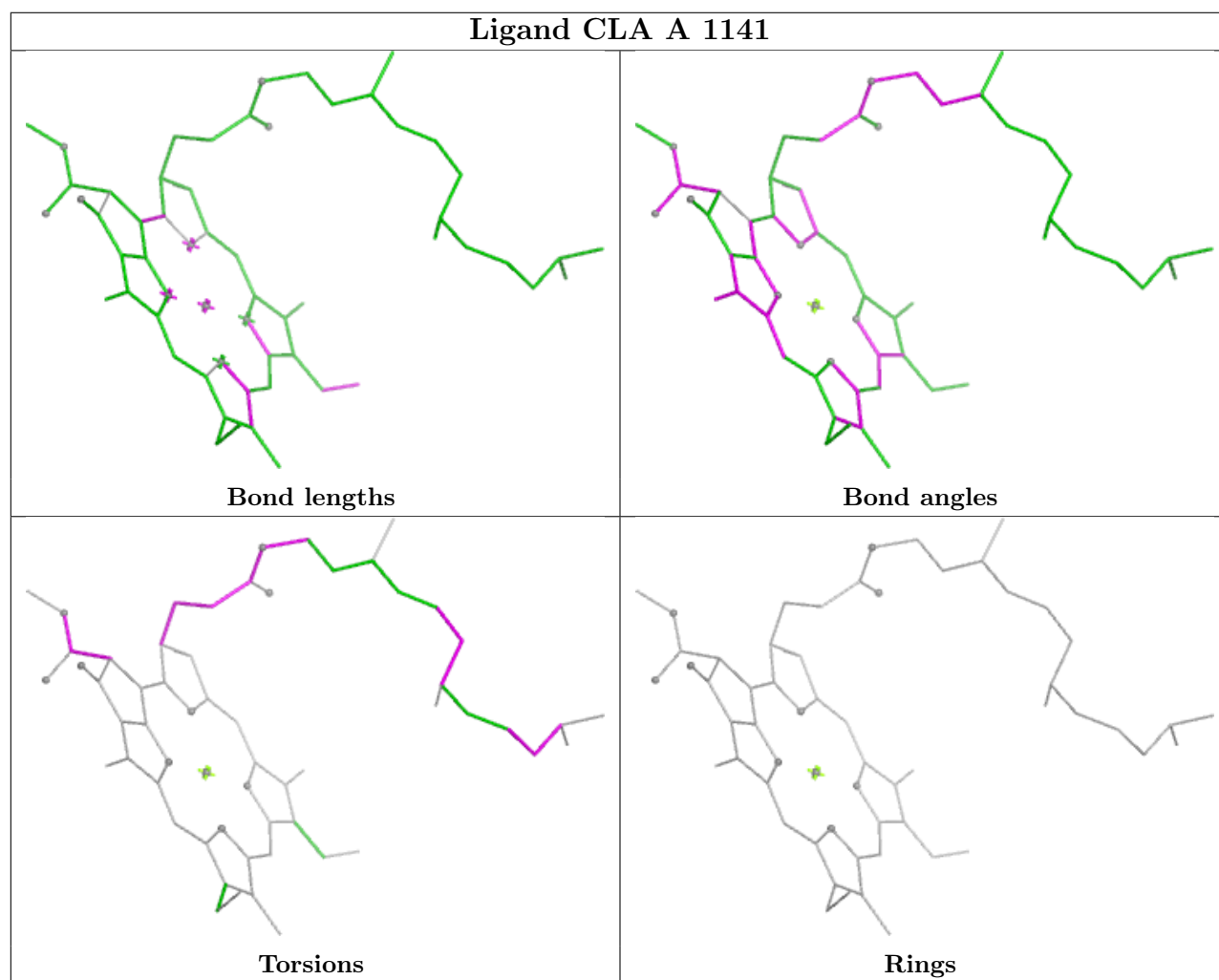
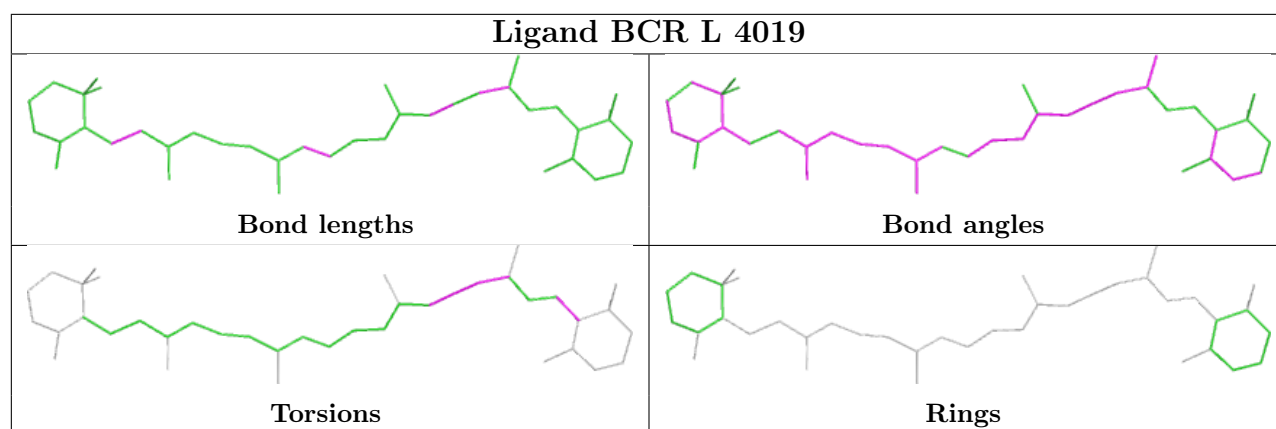


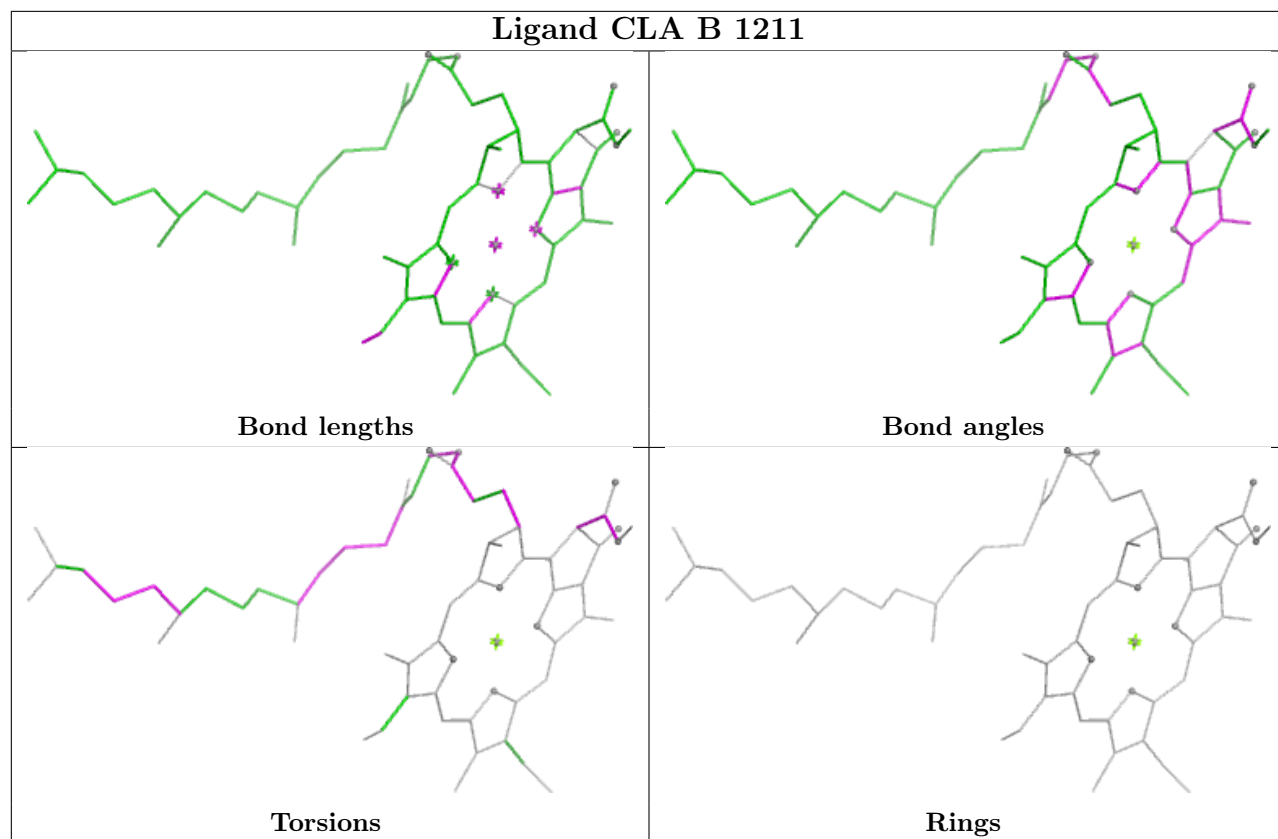


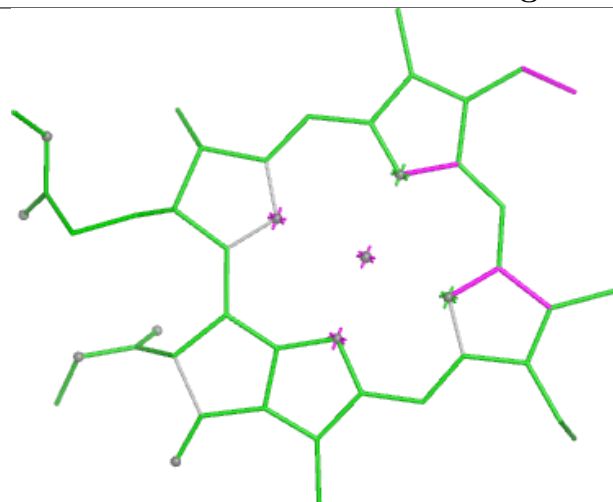
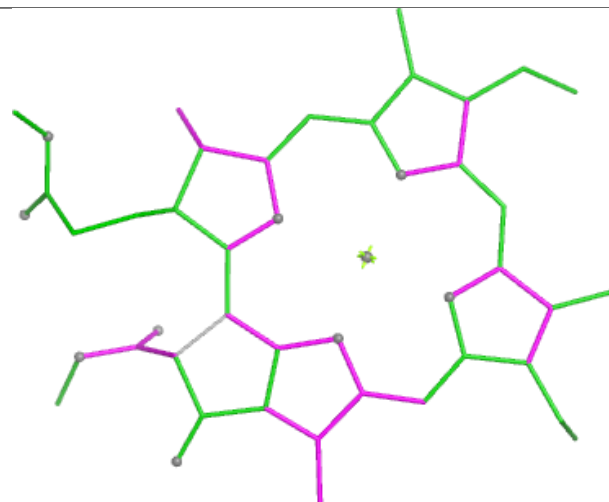
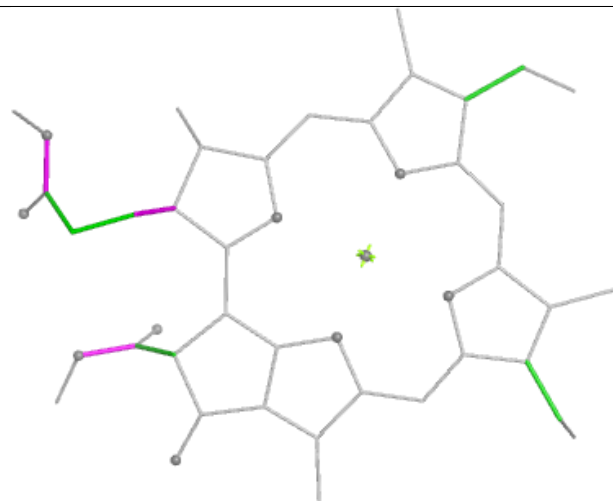
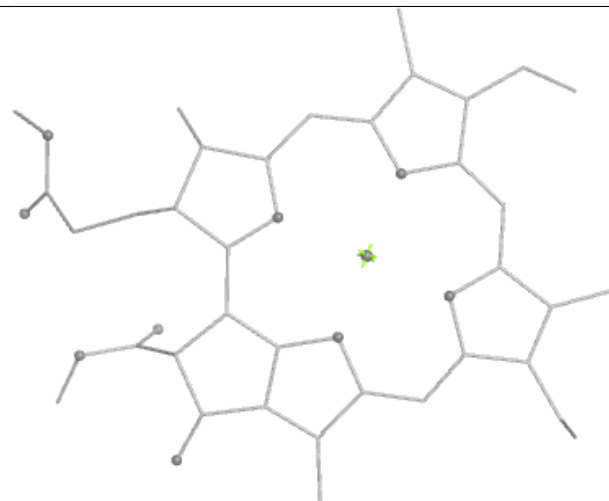
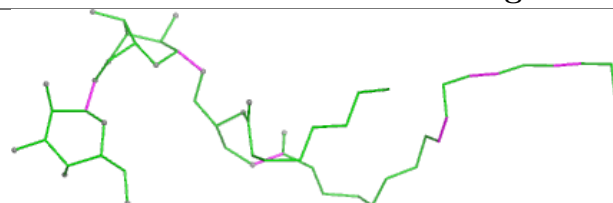
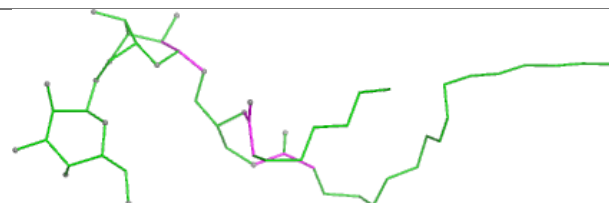
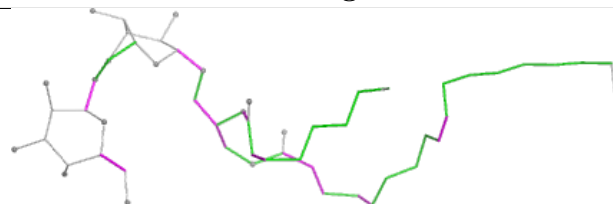
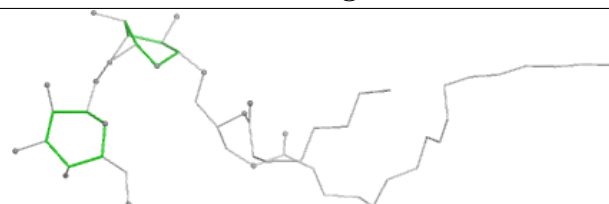


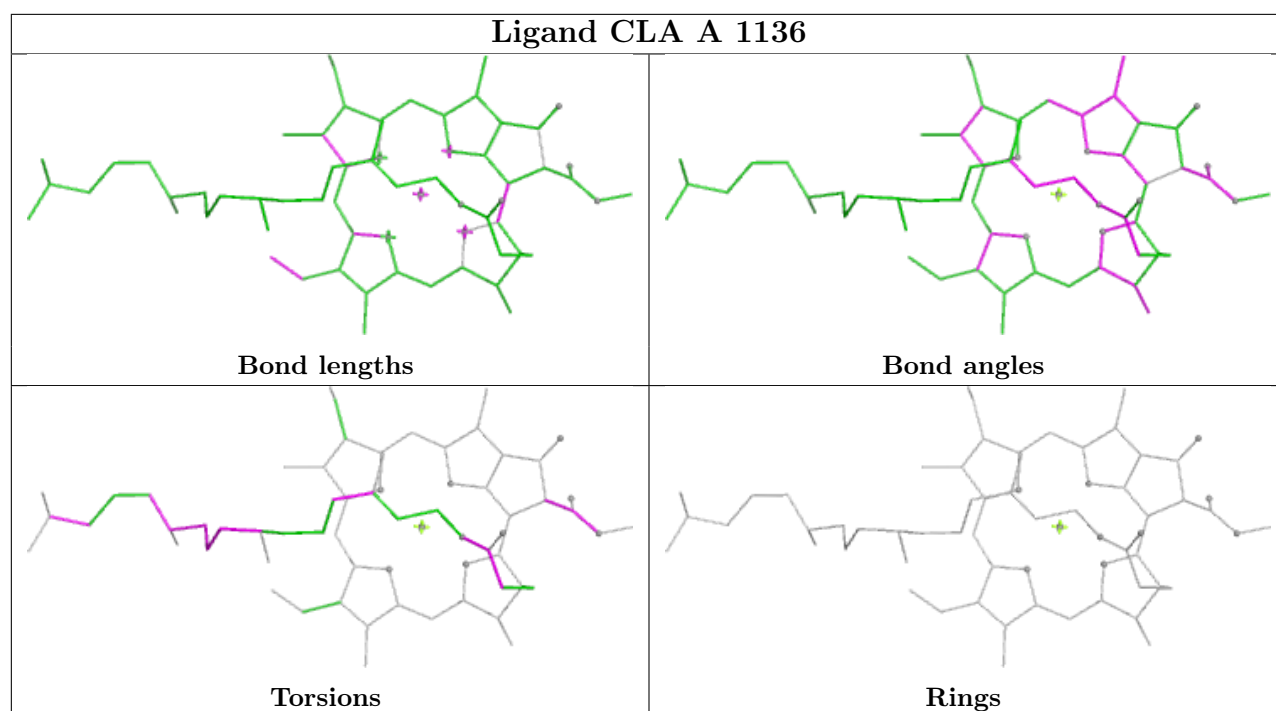


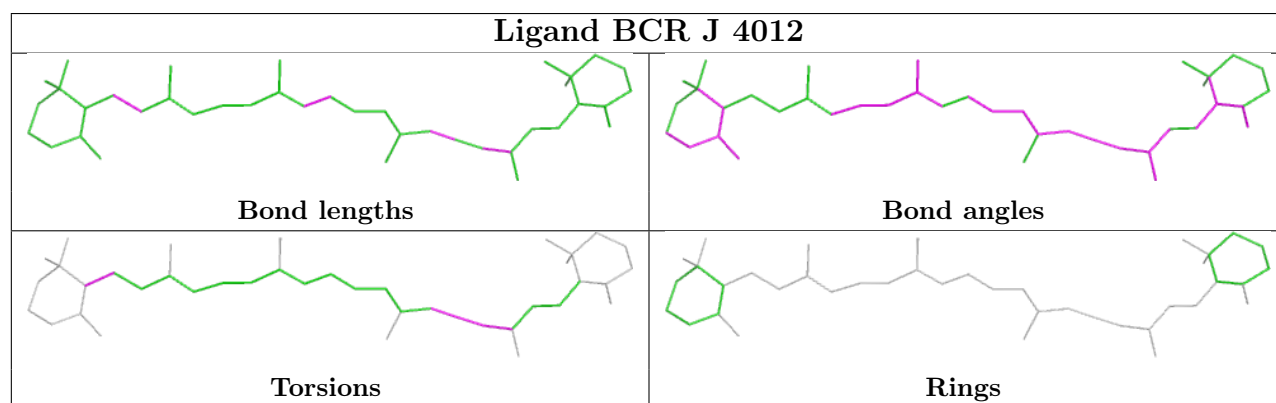
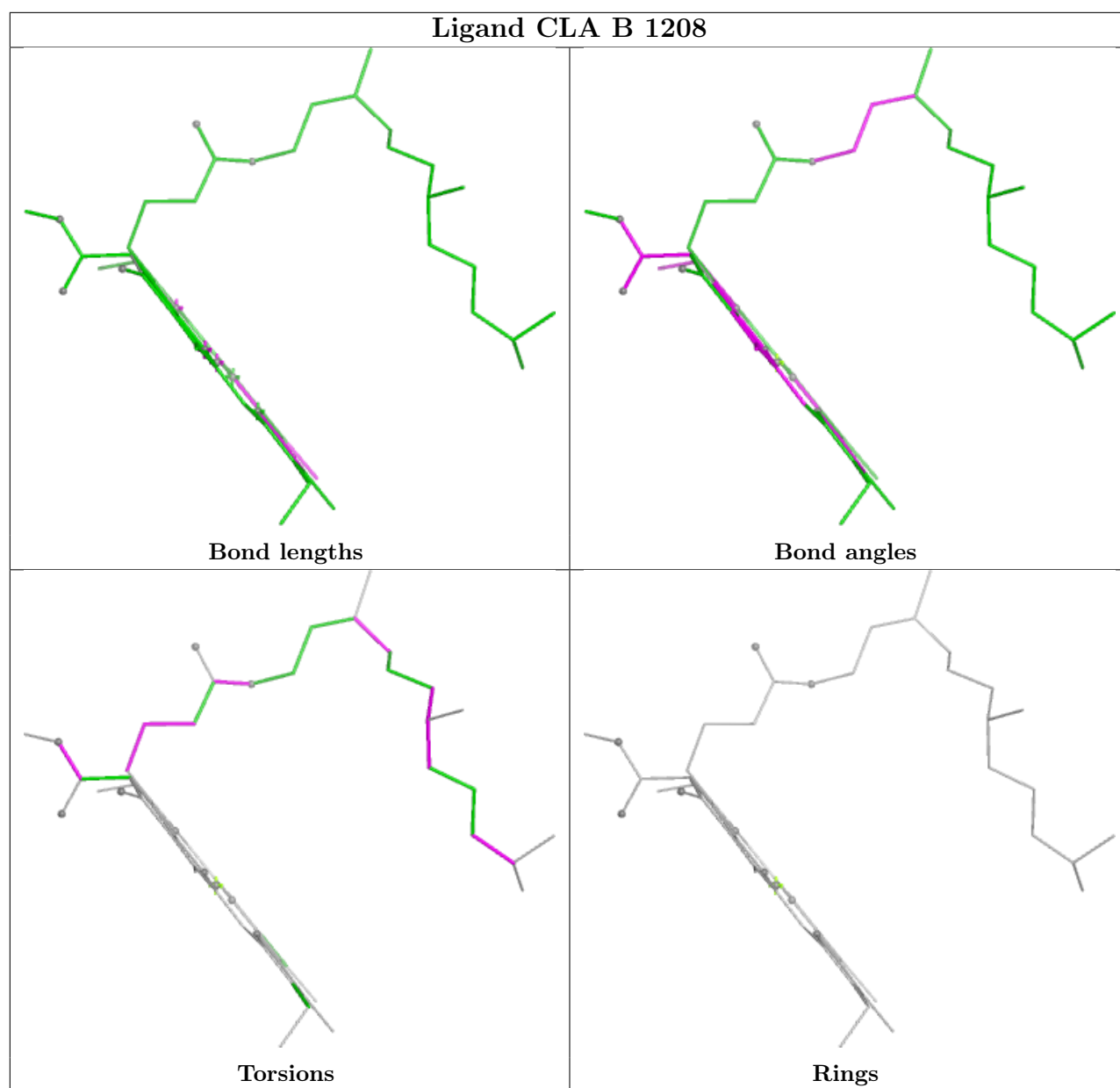
Ligand CLA 1 611**Ligand CLA A 1119**

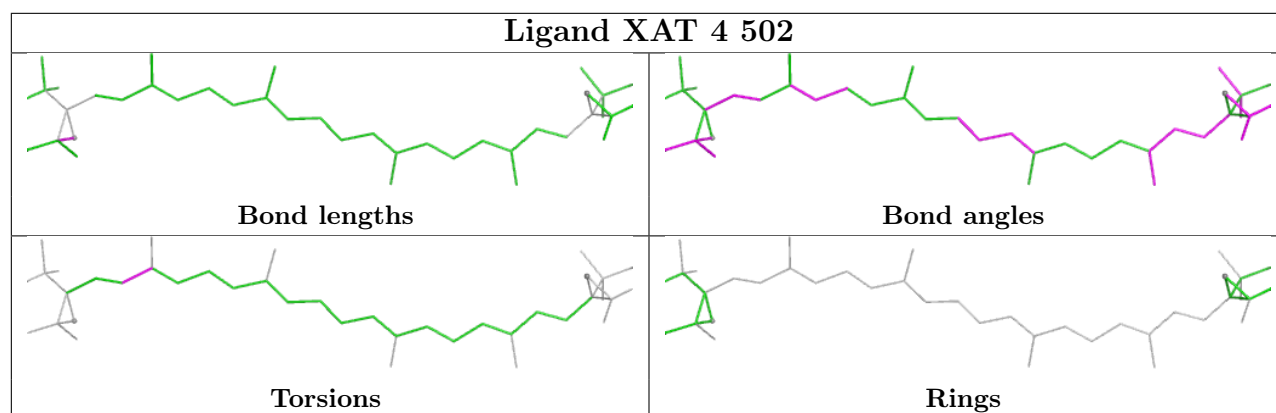
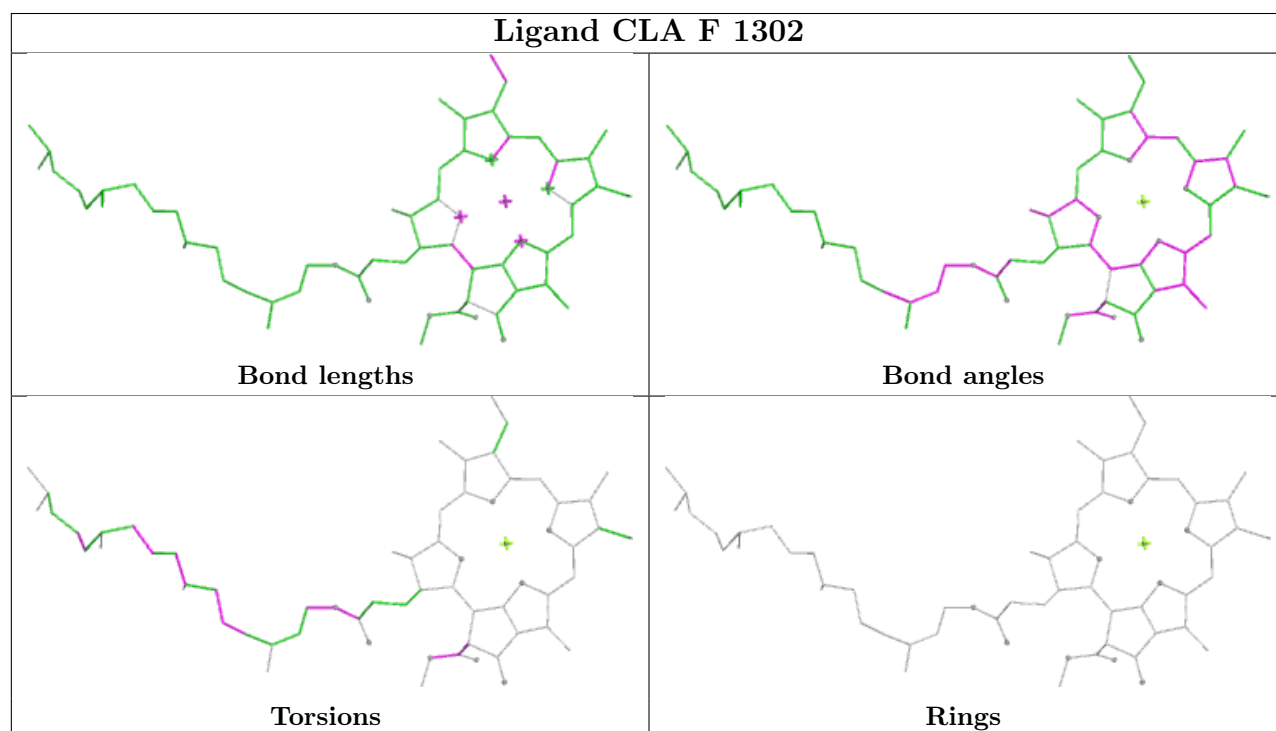
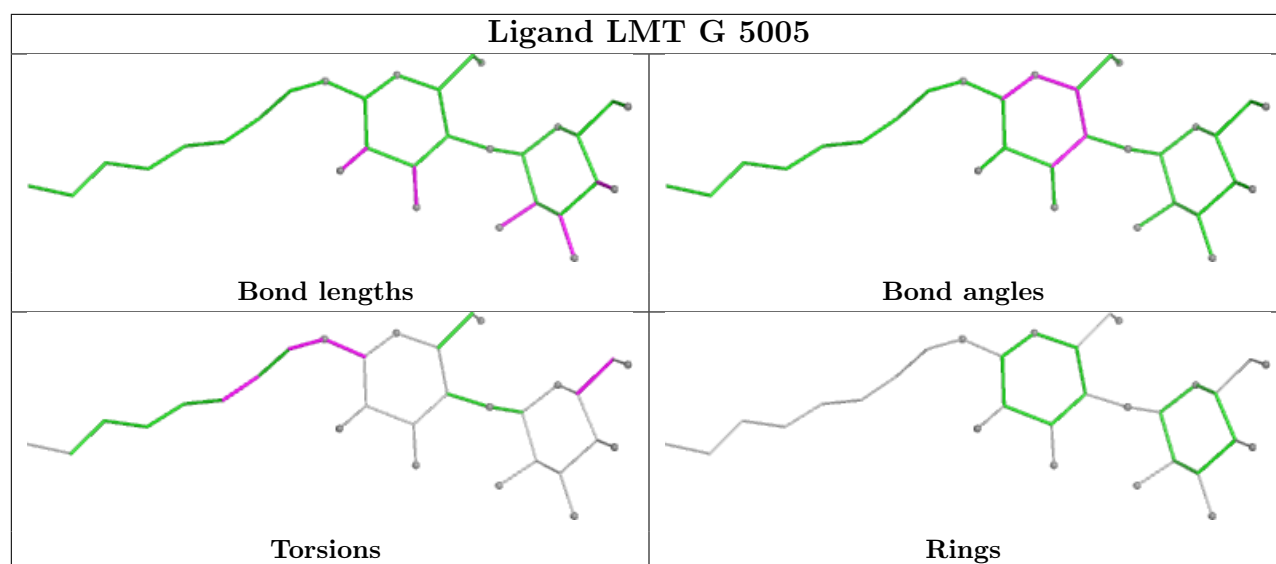


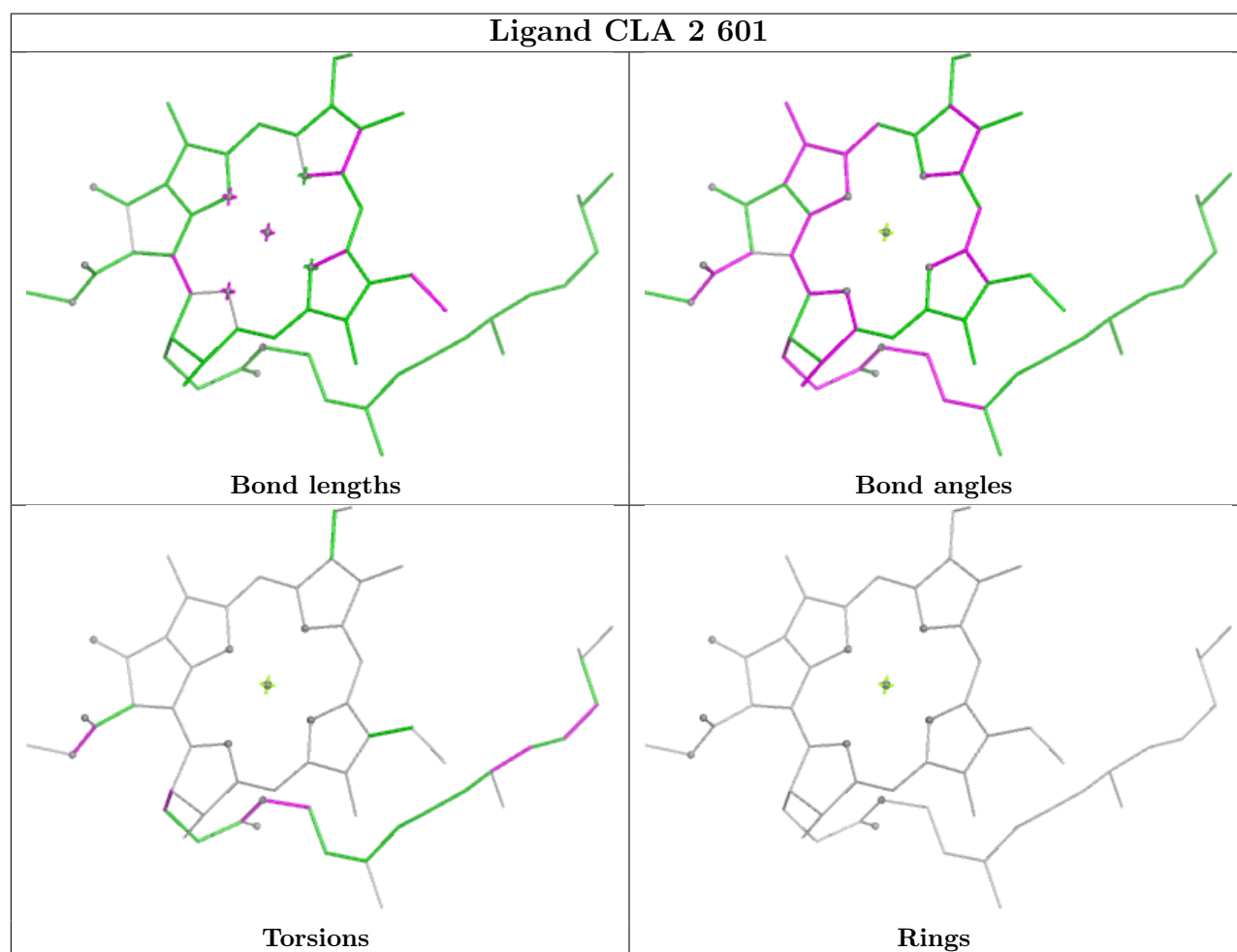
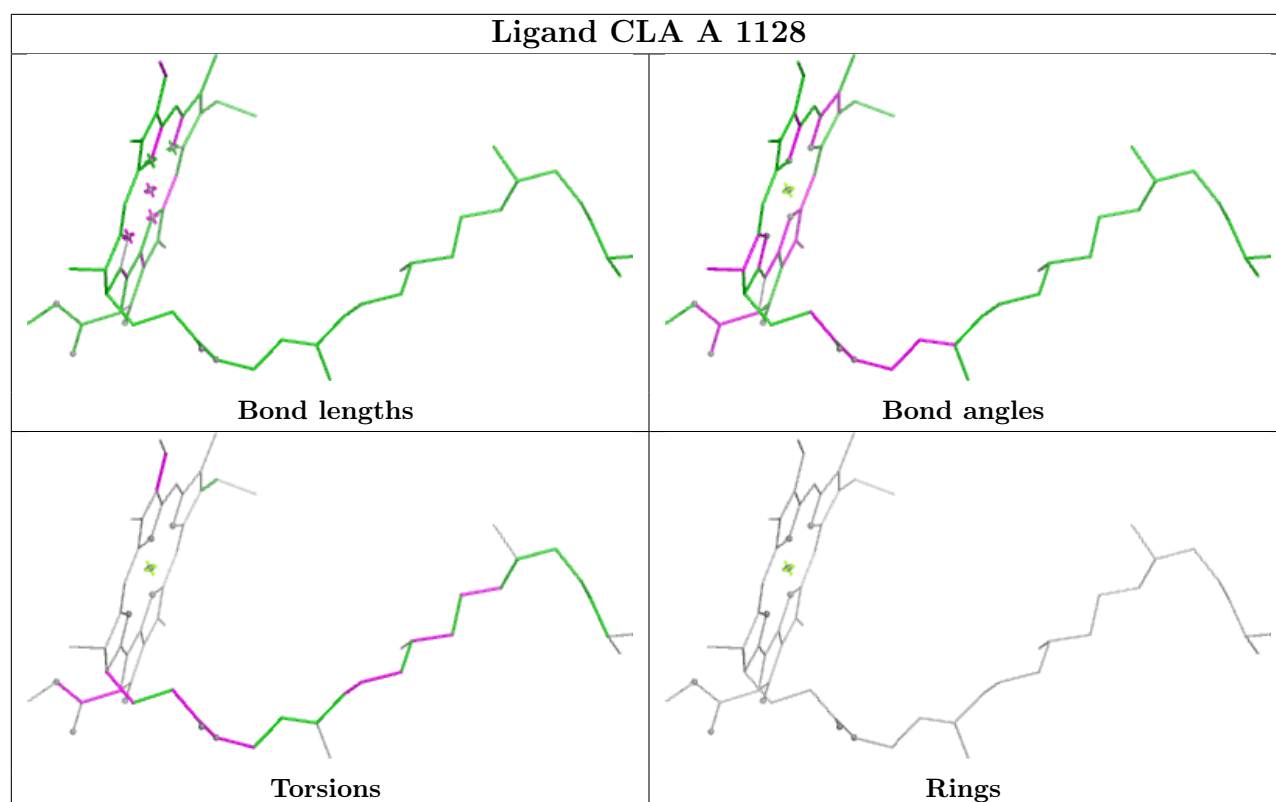


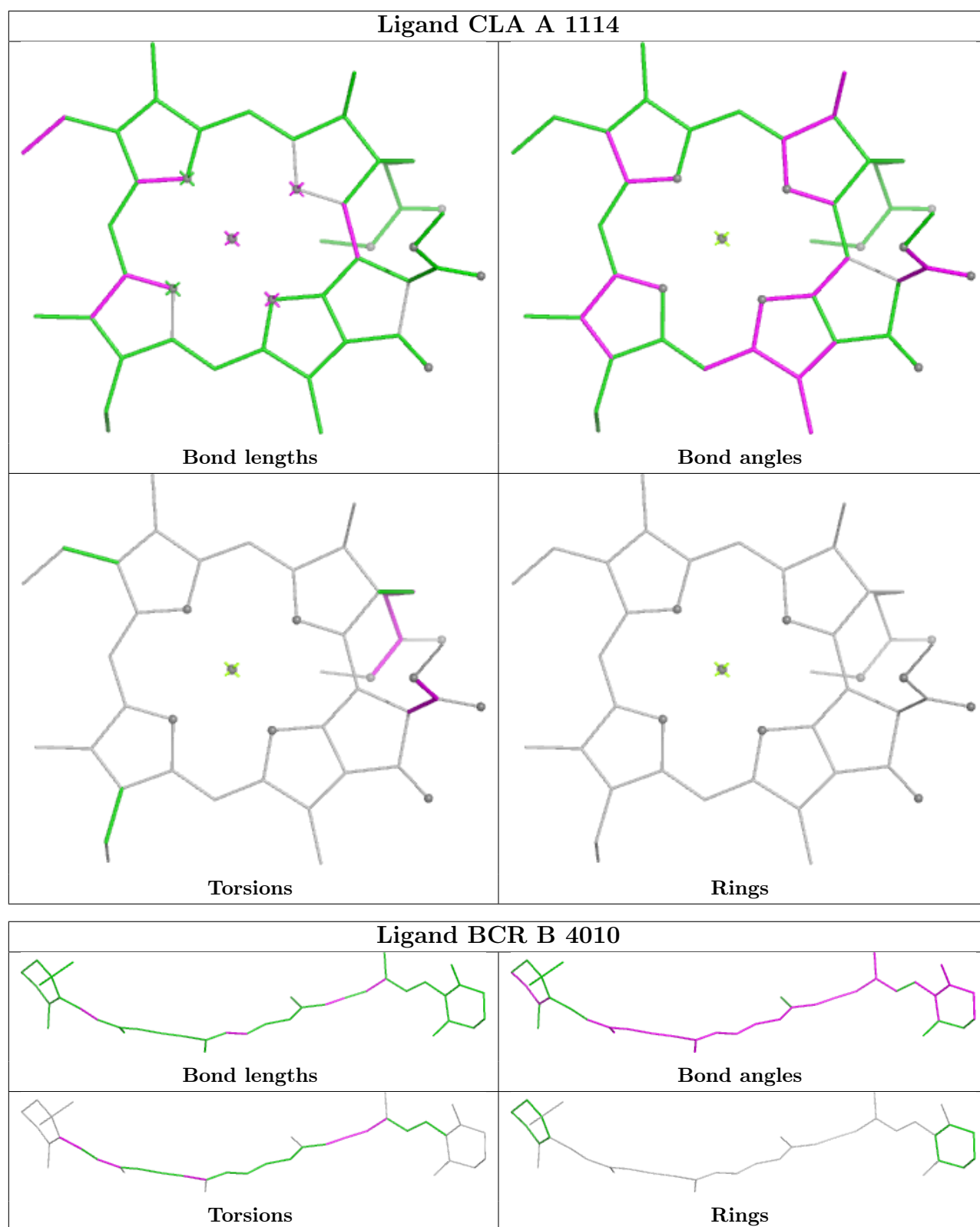
Ligand CLA 1 602**Bond lengths****Bond angles****Torsions****Rings****Ligand DGD F 5005****Bond lengths****Bond angles****Torsions****Rings**

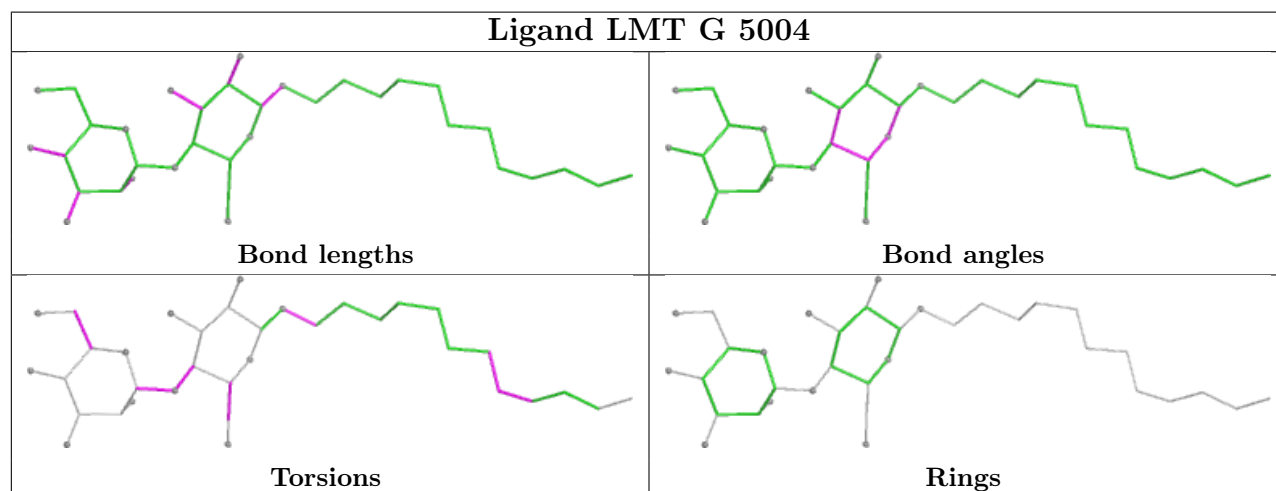
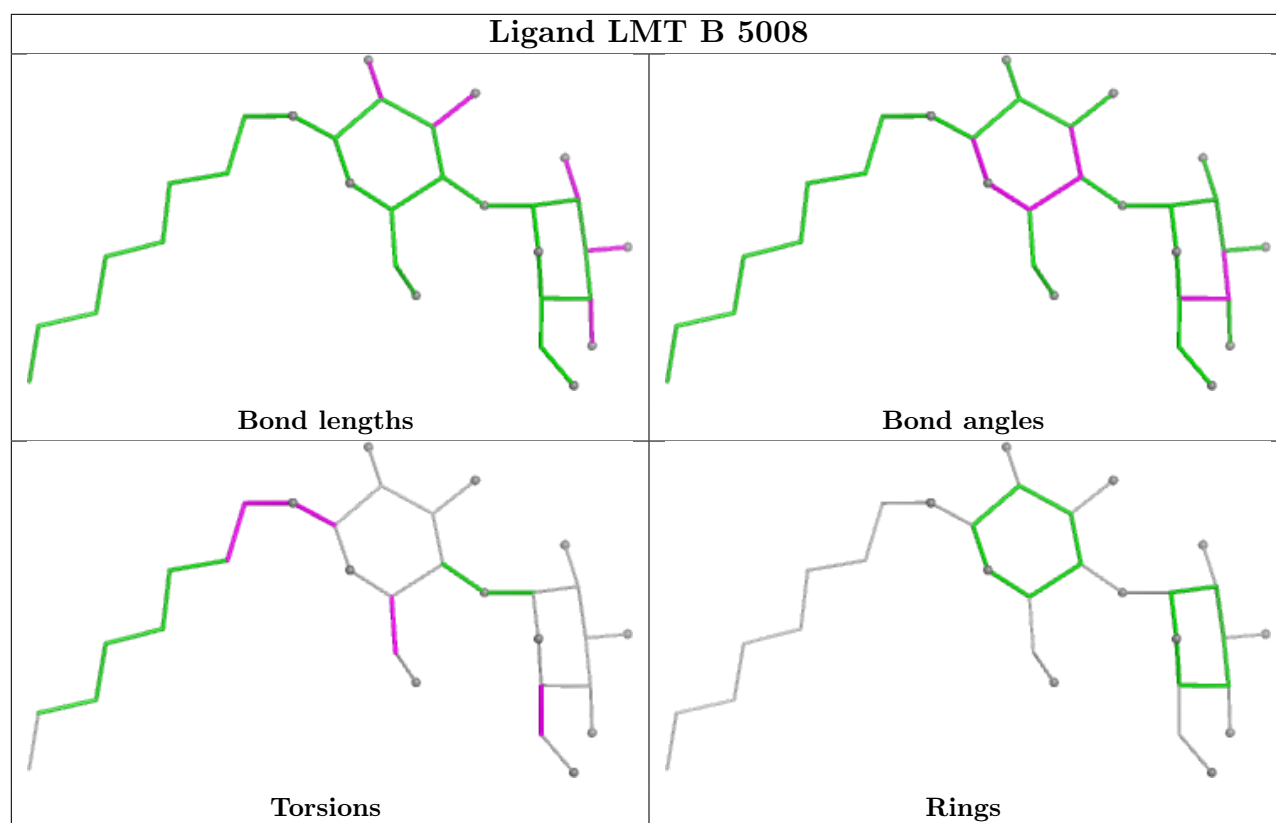


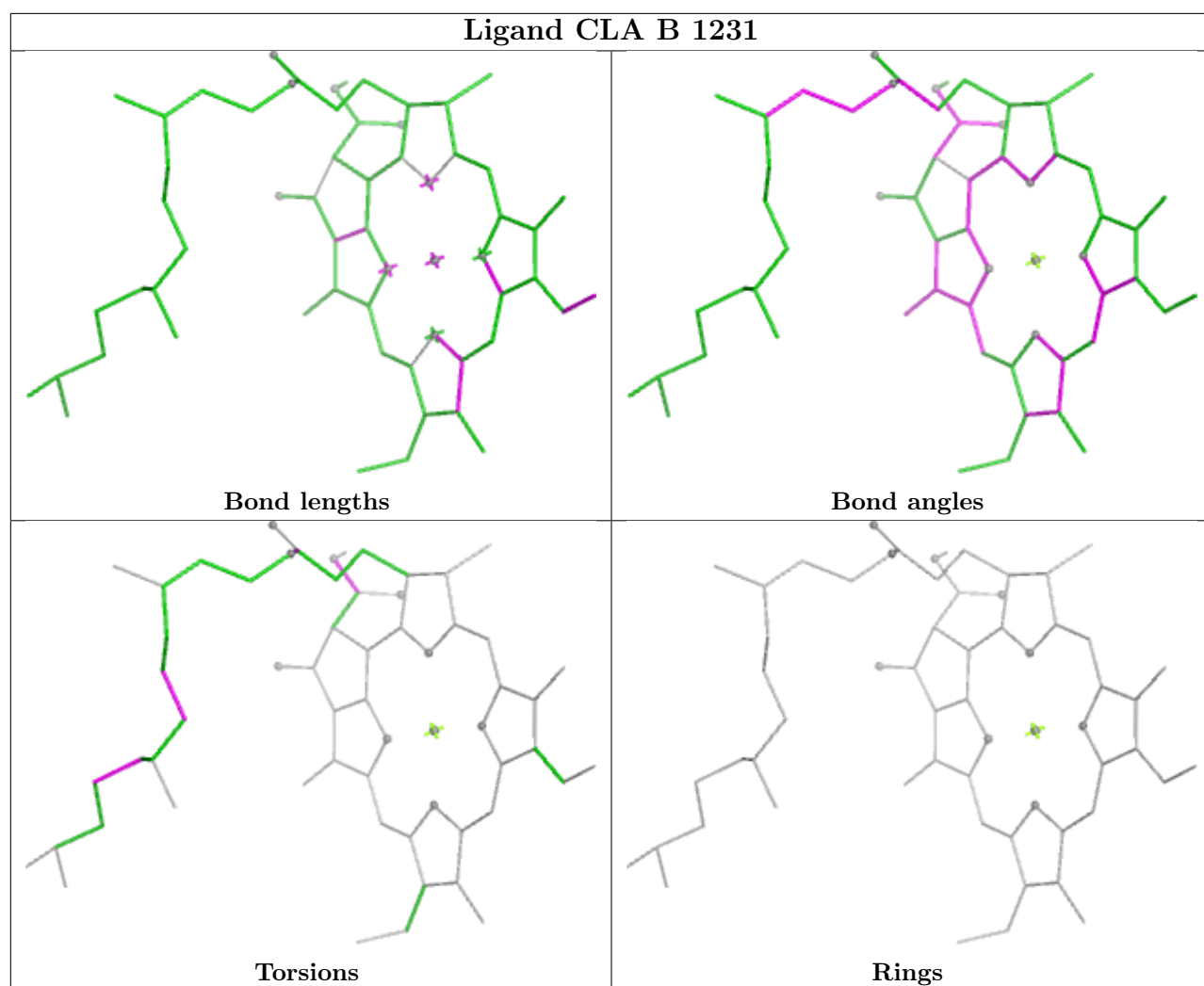


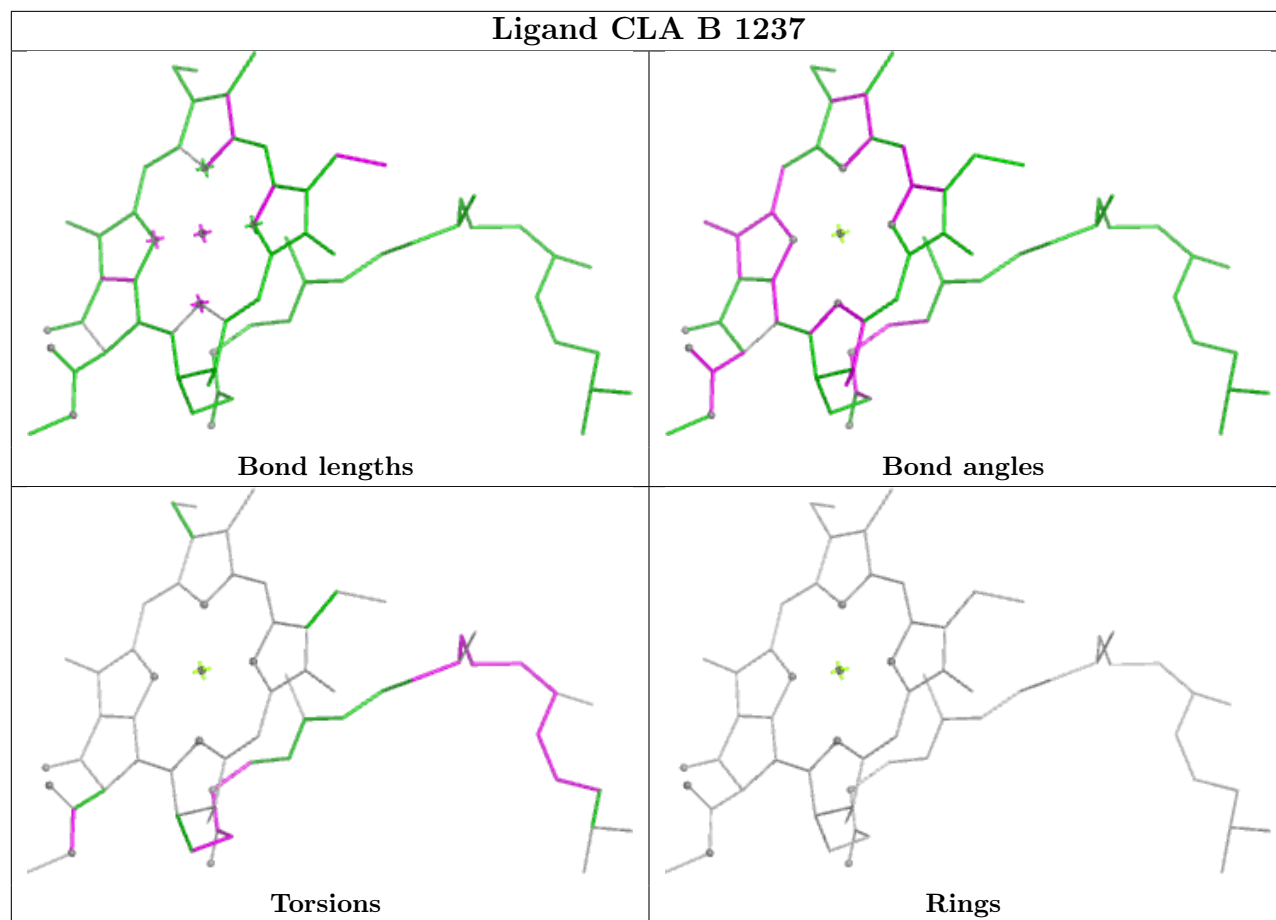




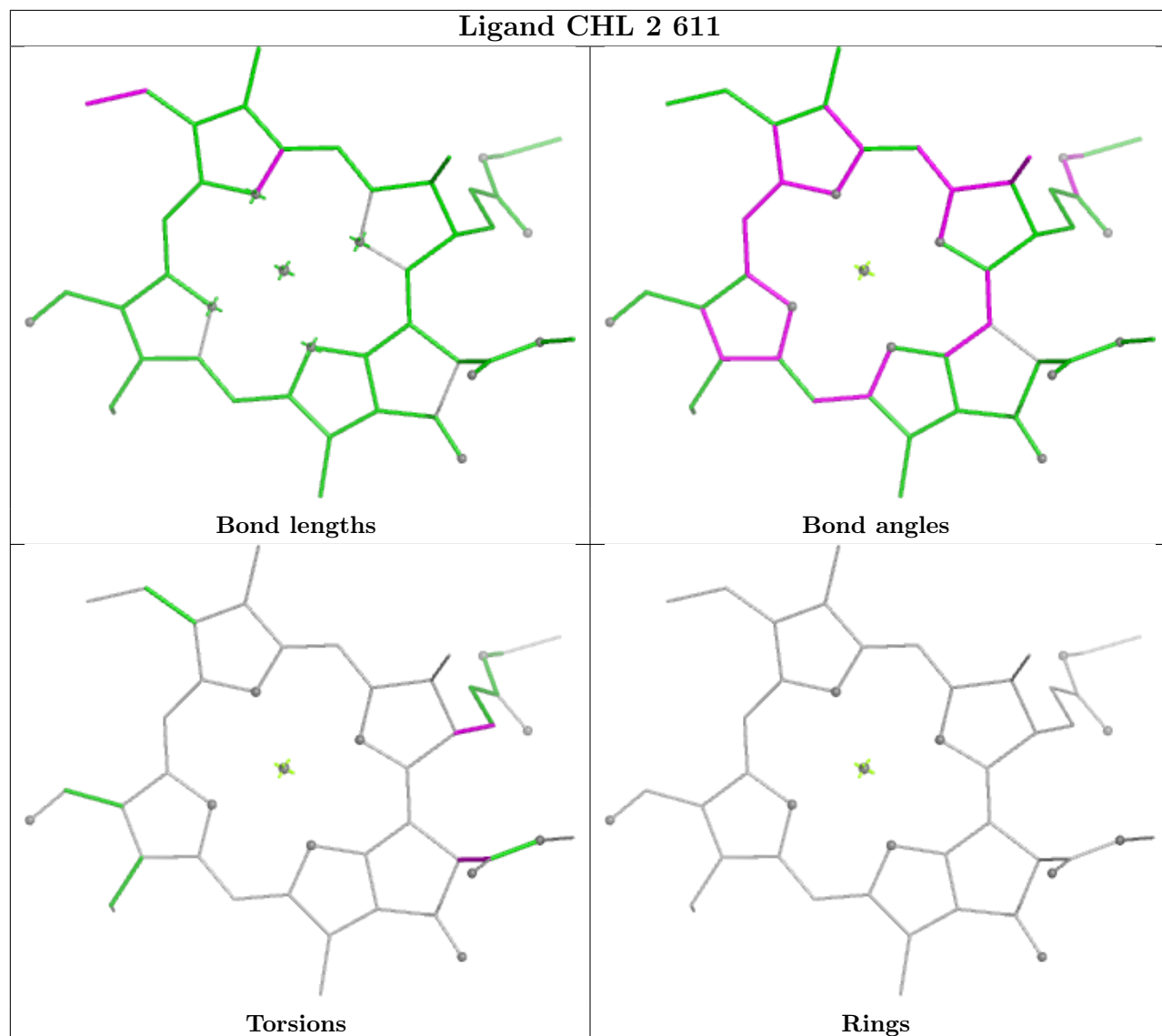


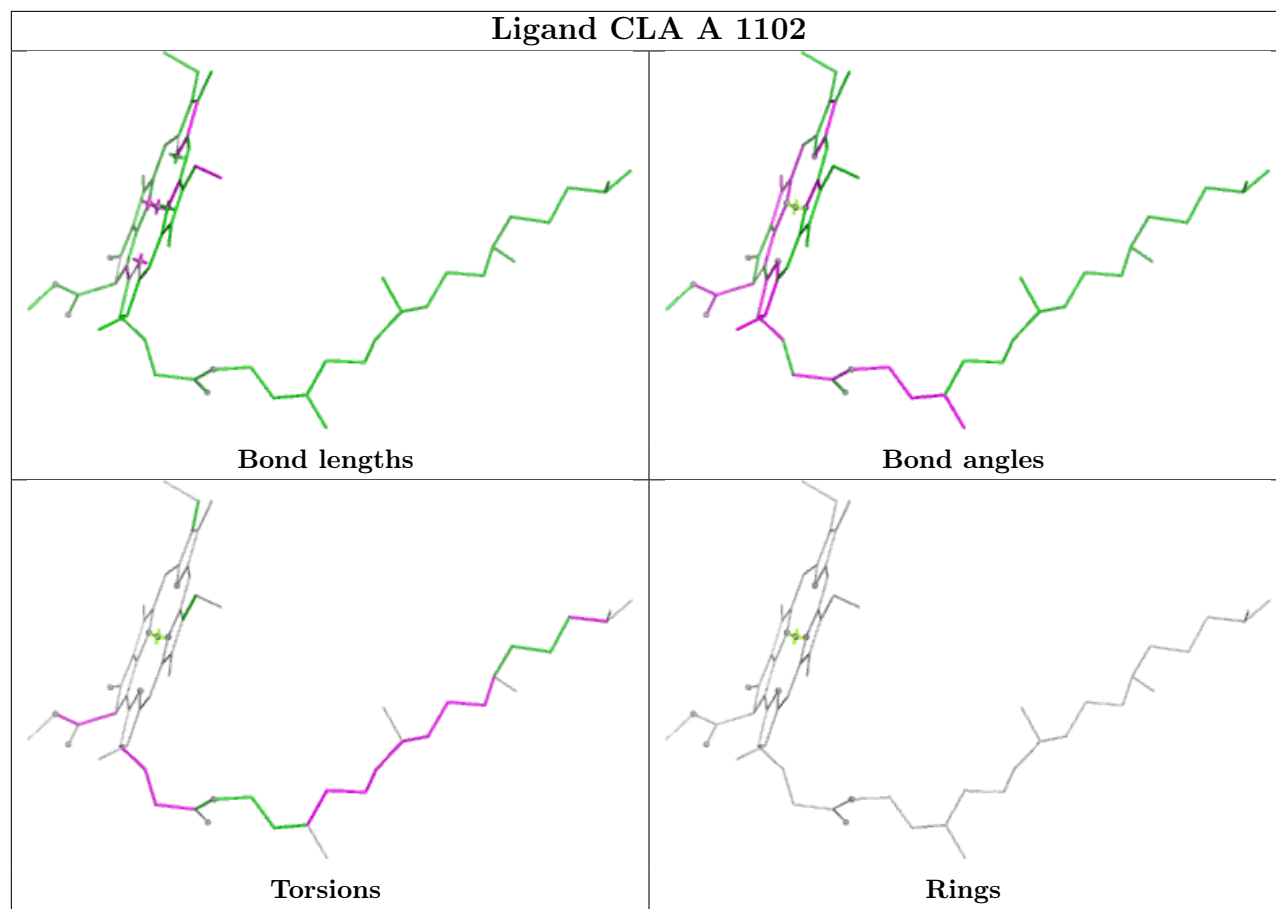


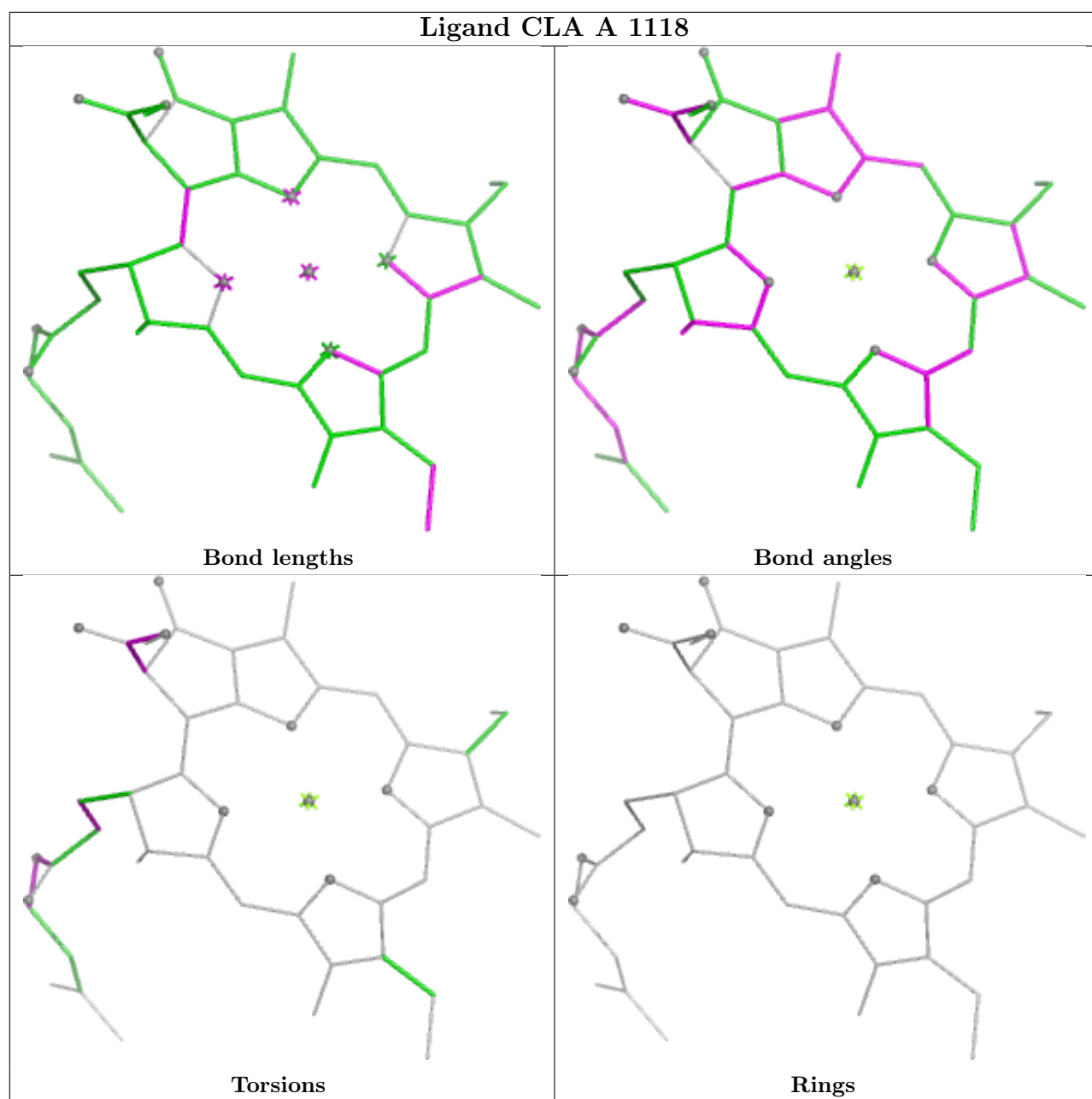


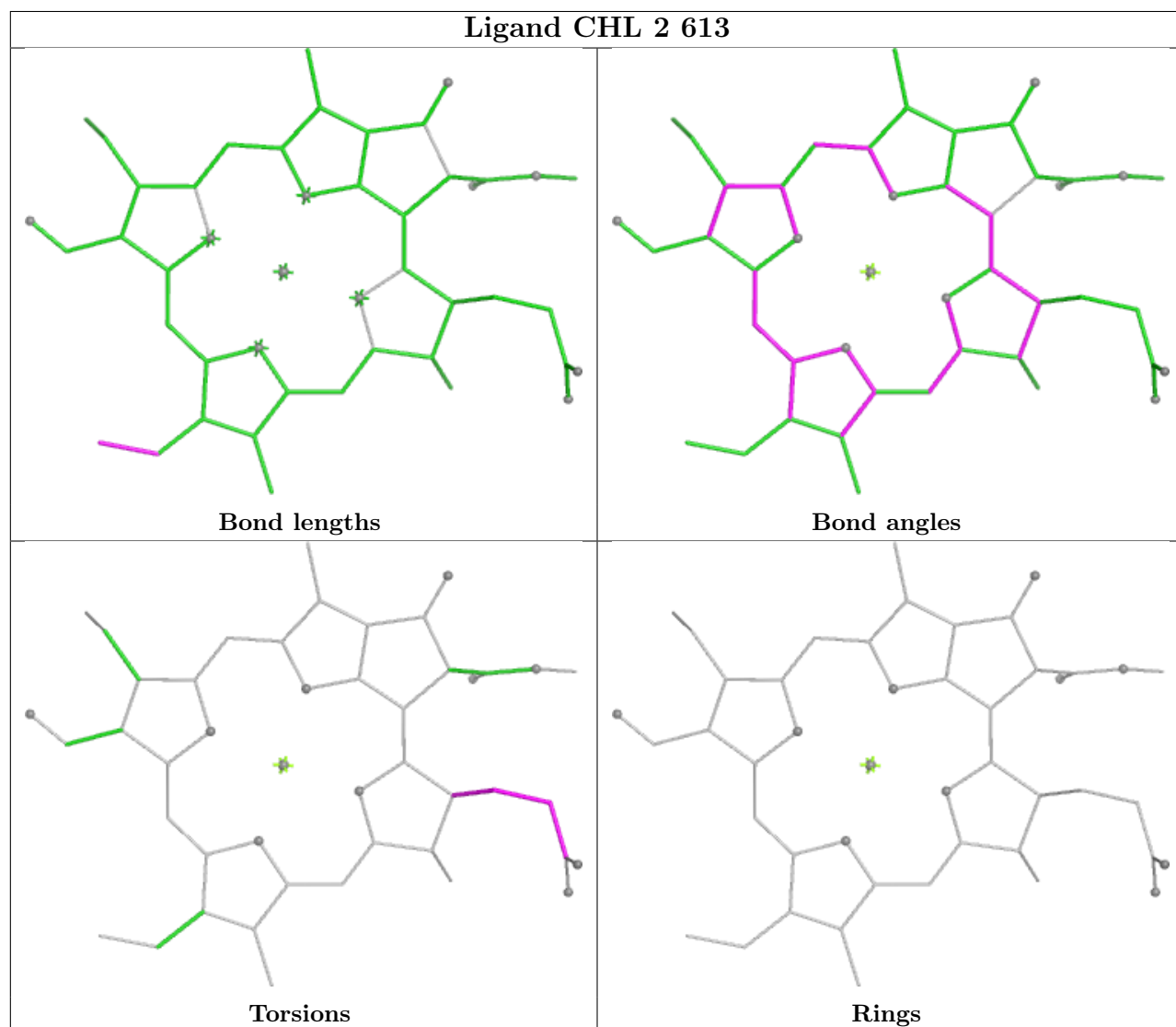
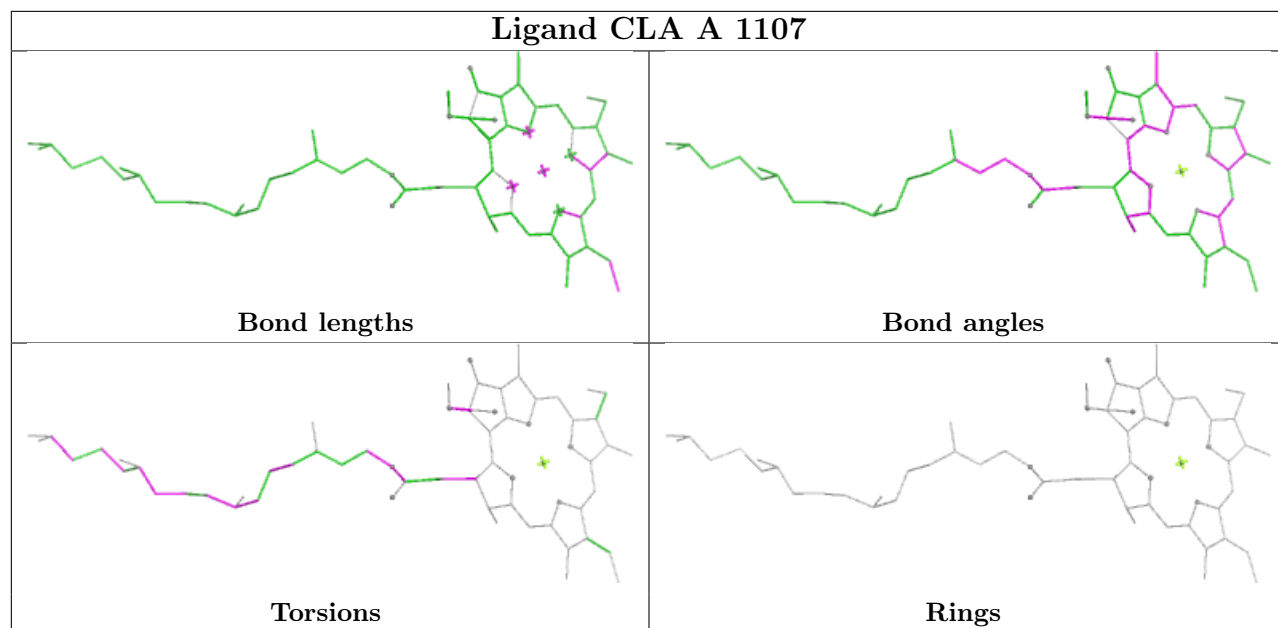


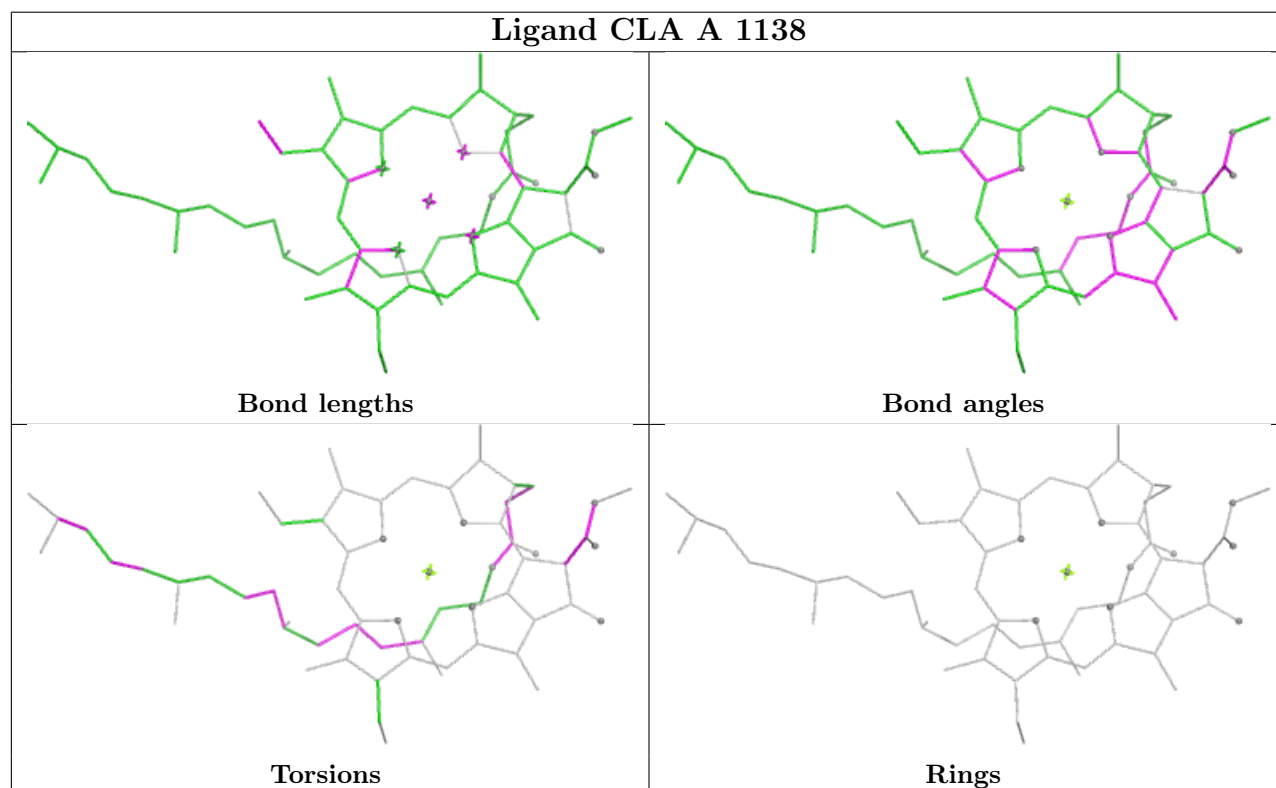
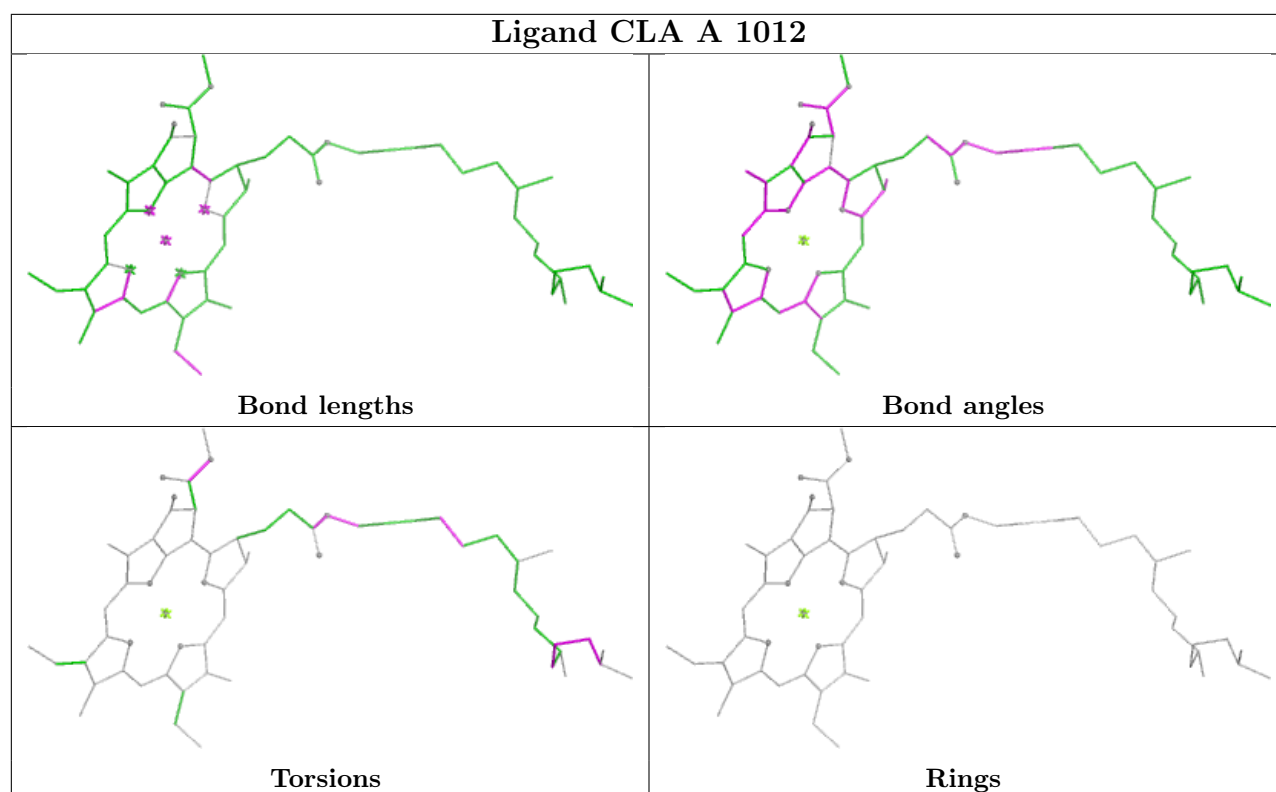
Ligand CHL 2 611

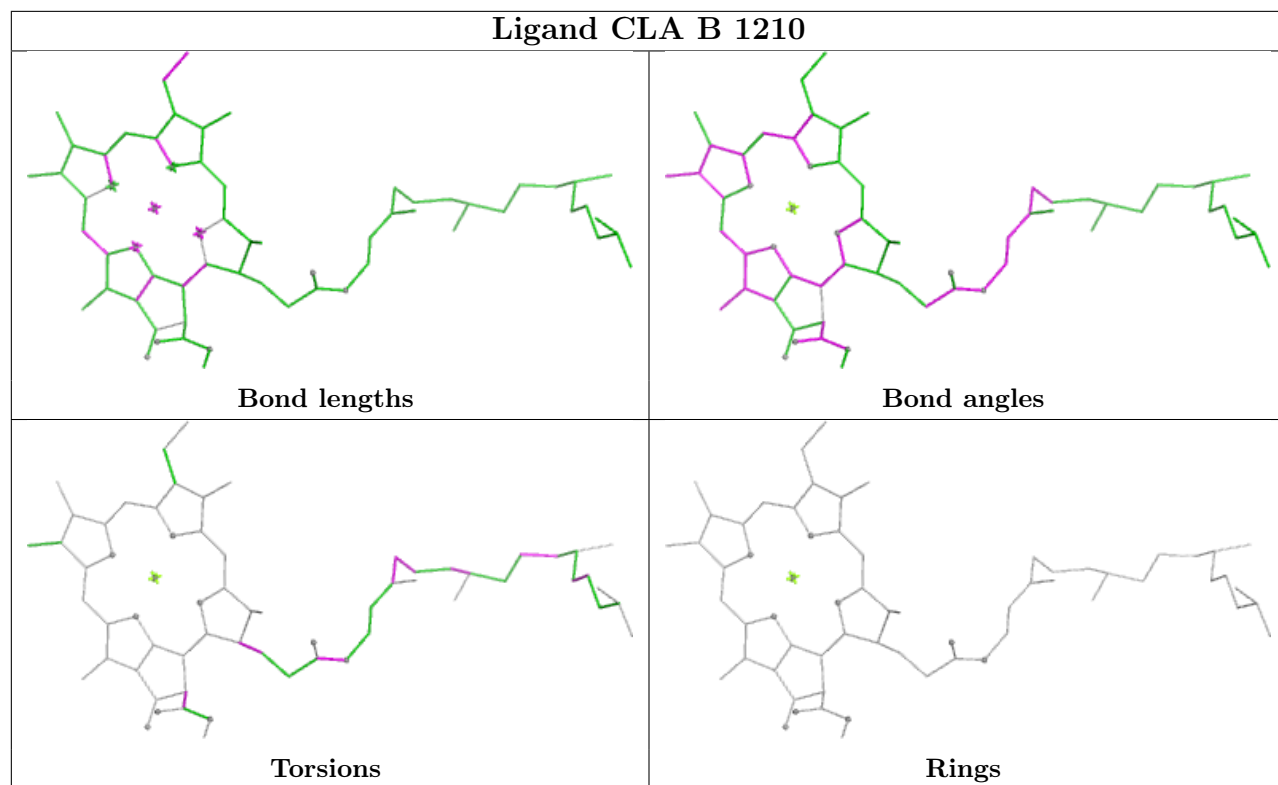


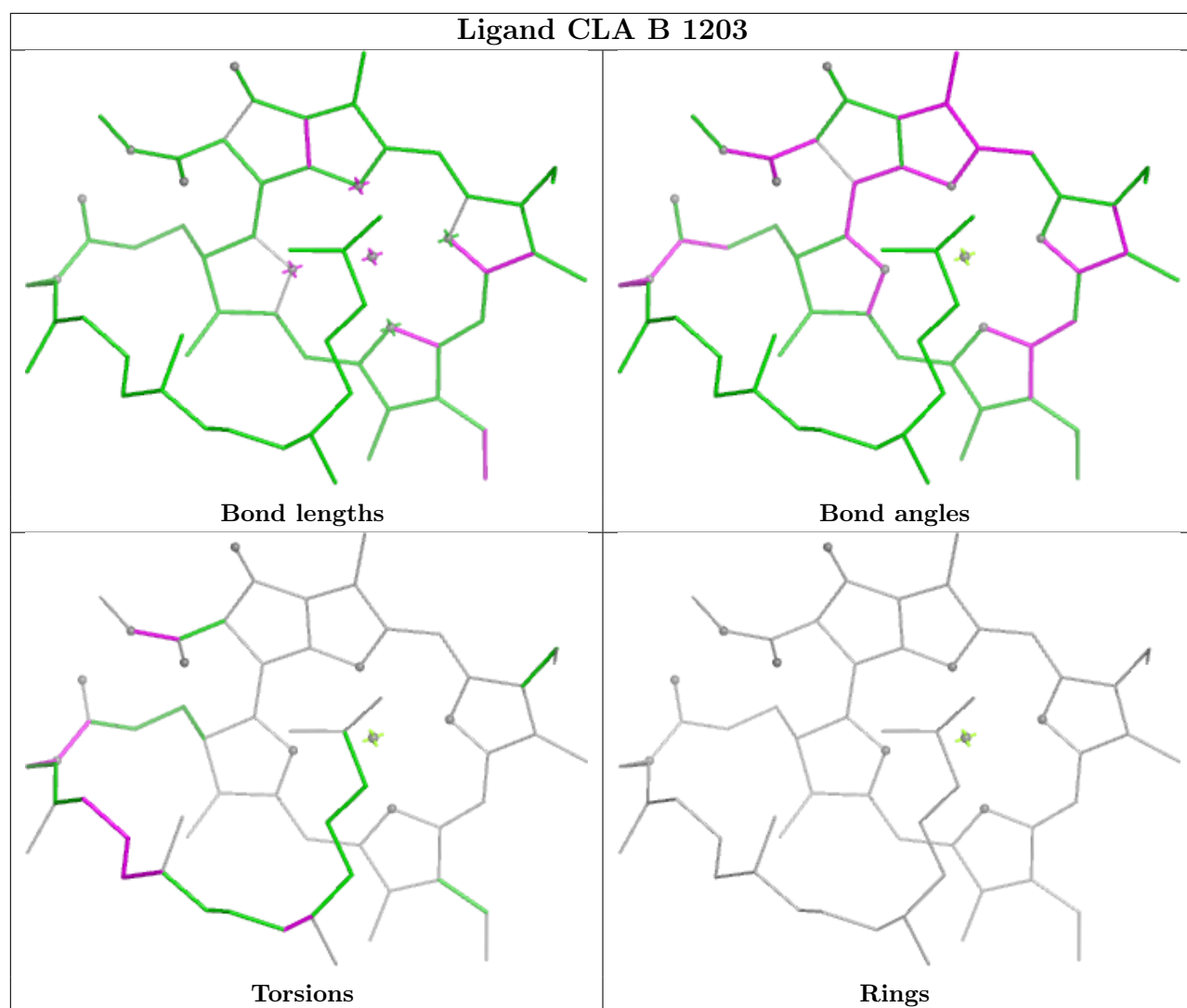




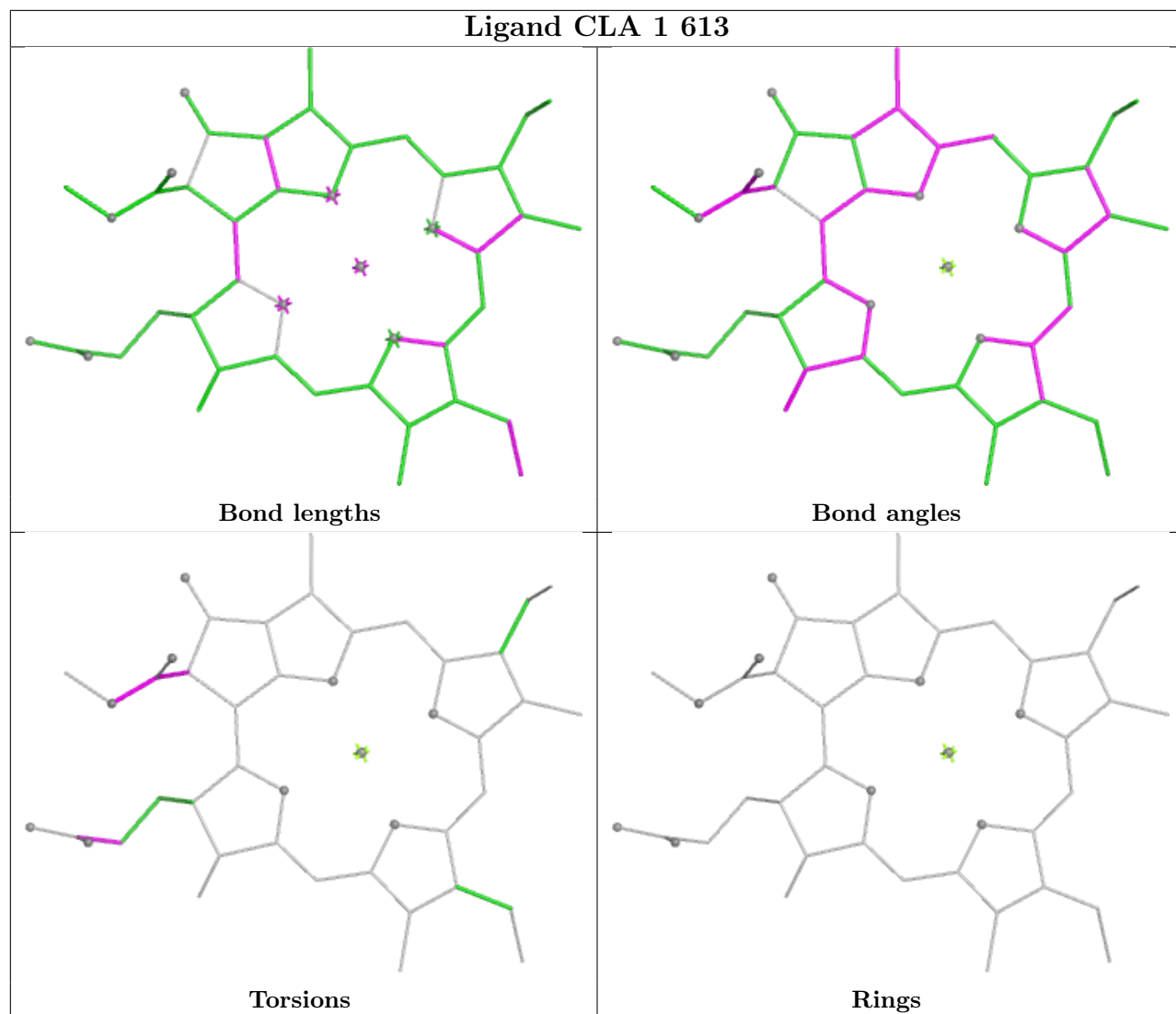




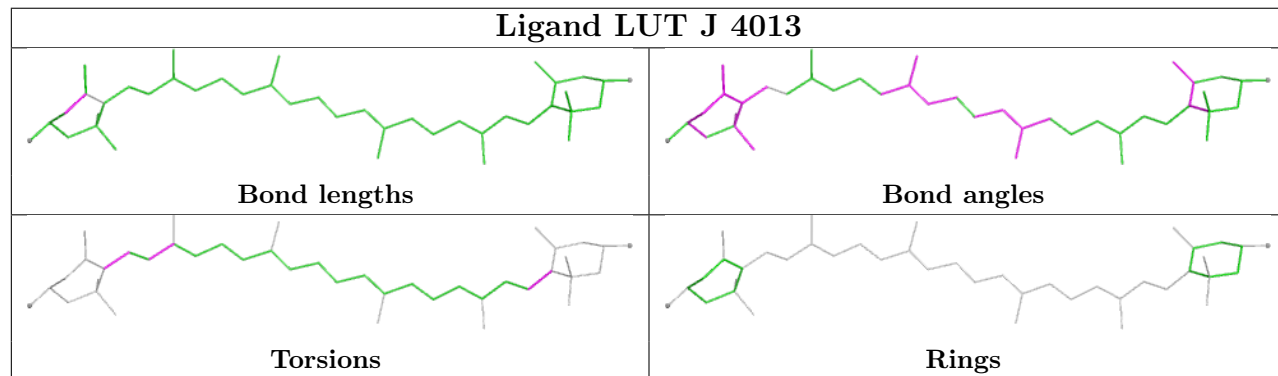


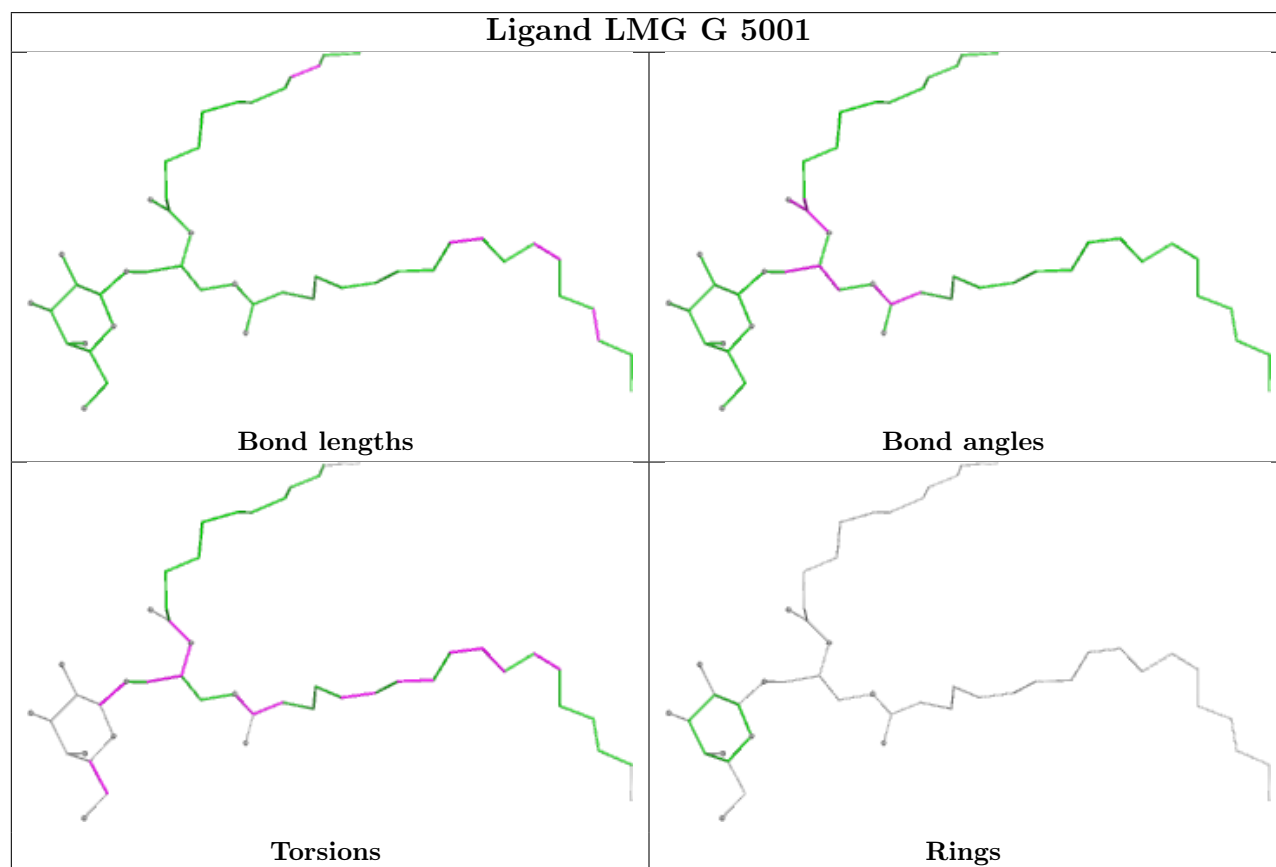
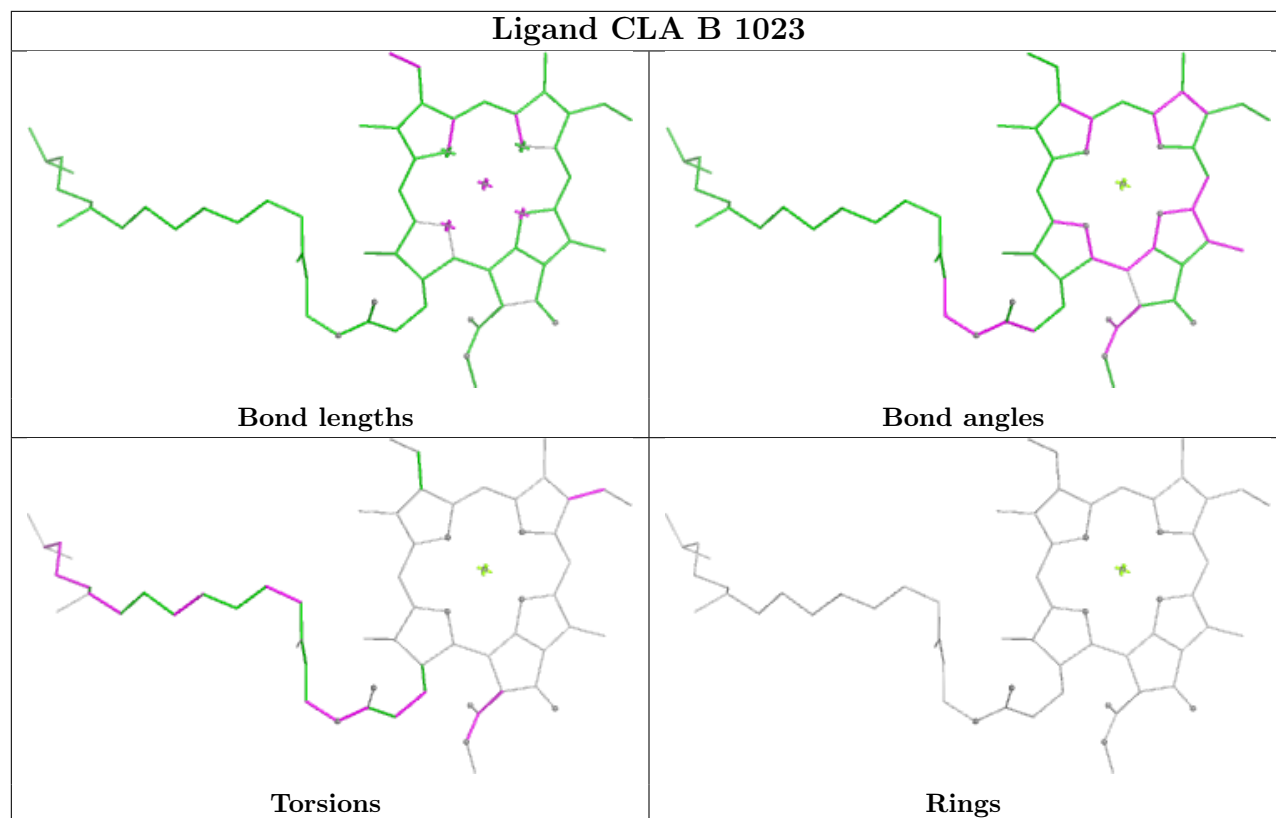


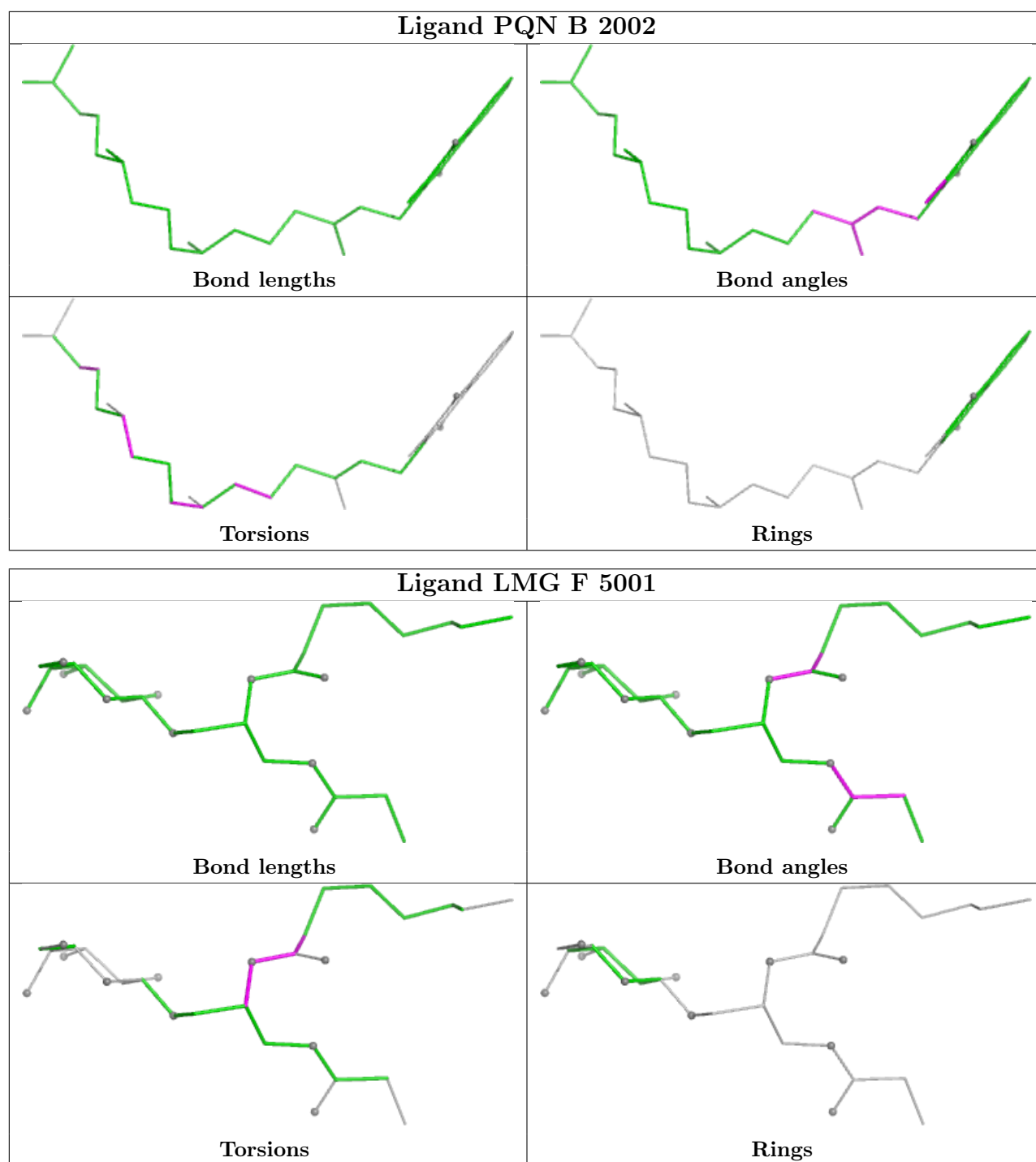
Ligand CLA 1 613



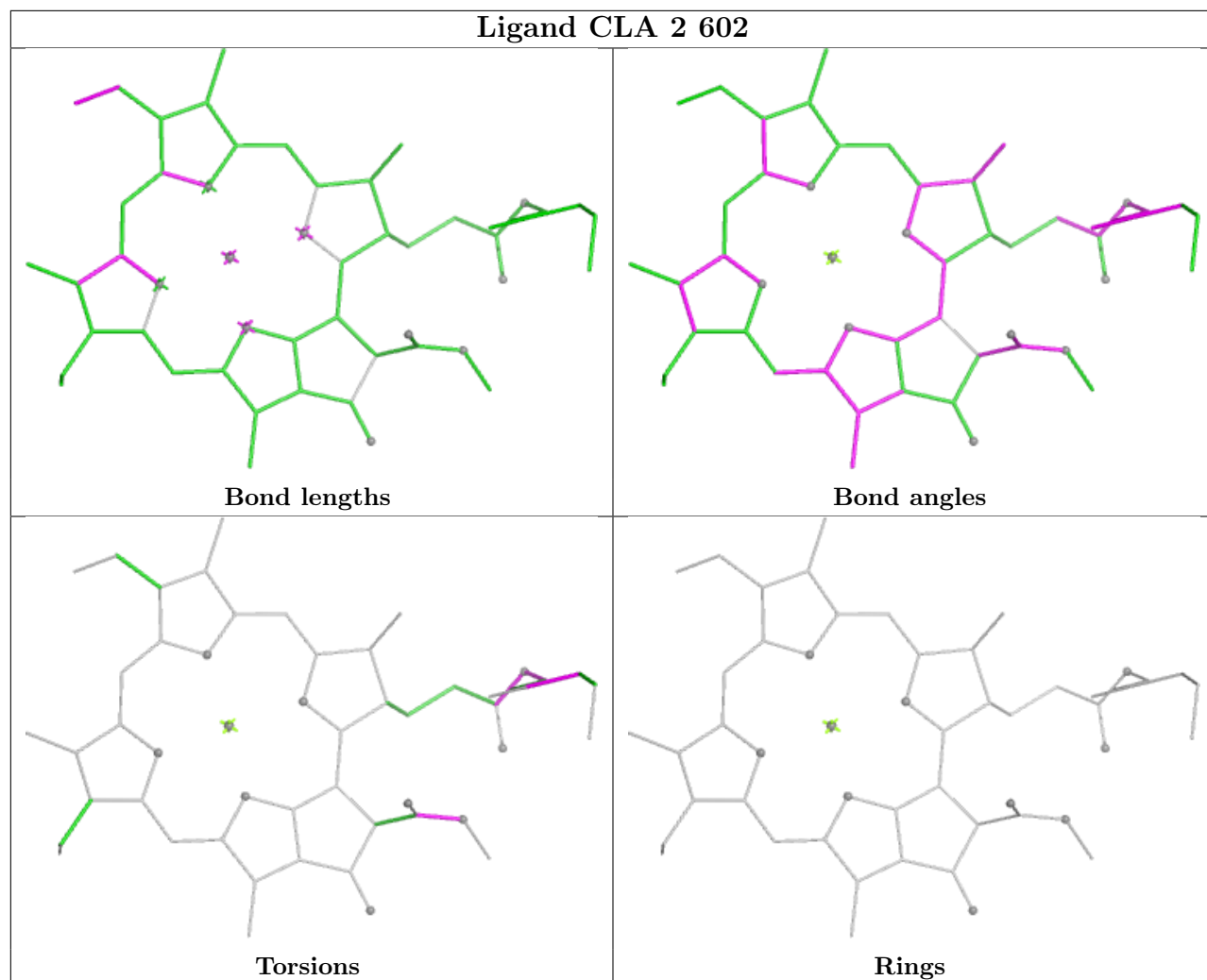
Ligand LUT J 4013



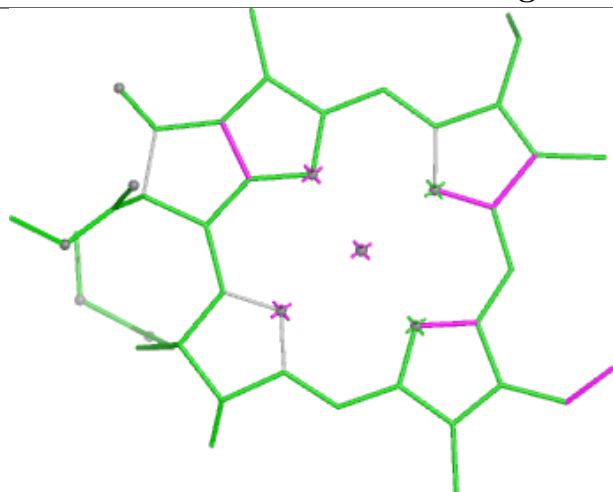




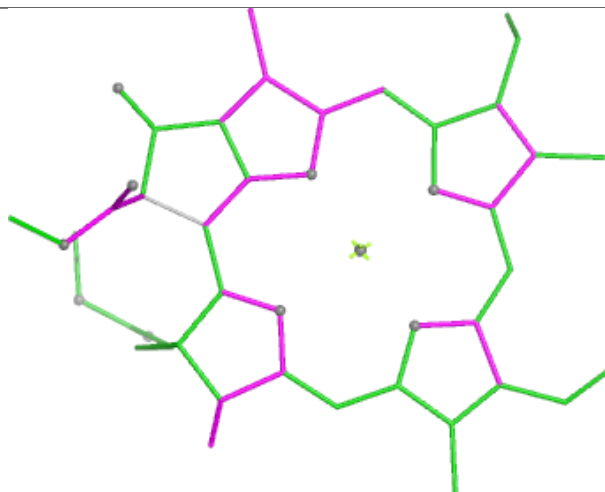
Ligand CLA 2 602



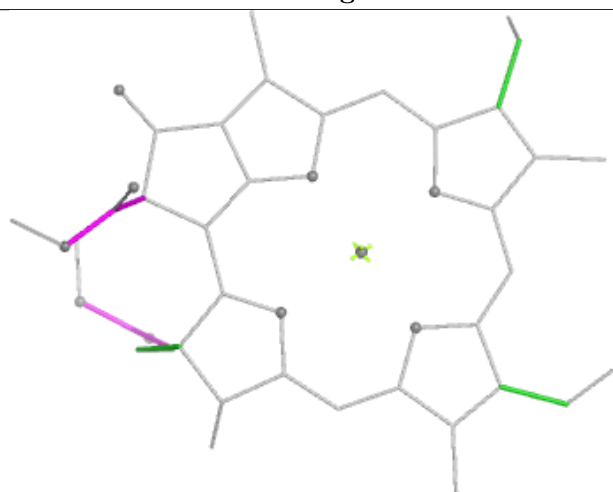
Ligand CLA 4 608



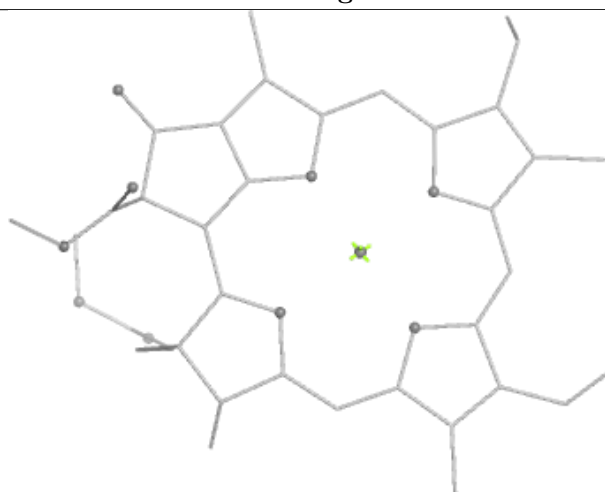
Bond lengths



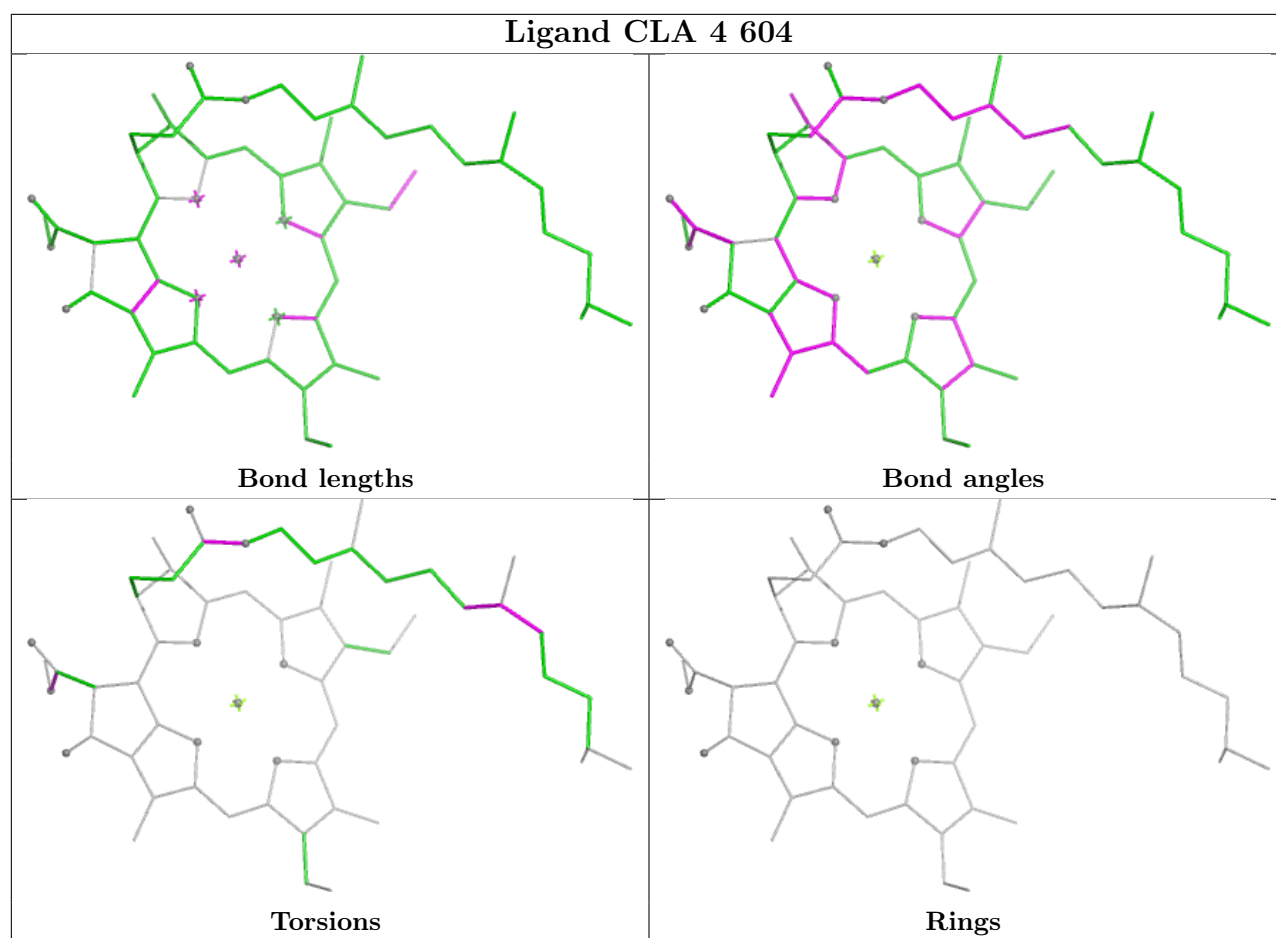
Bond angles



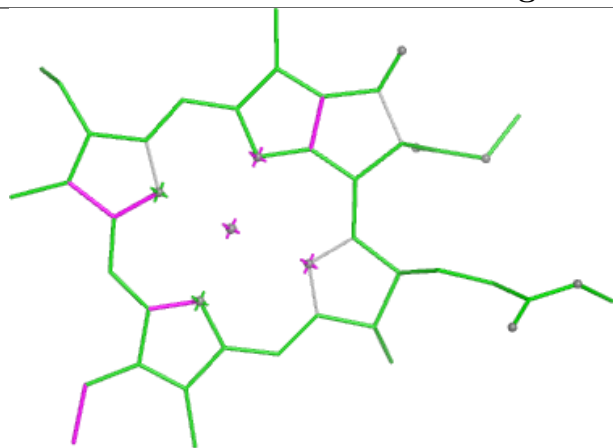
Torsions



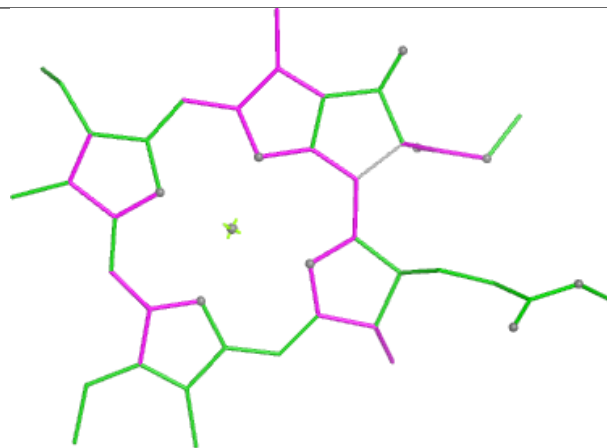
Rings



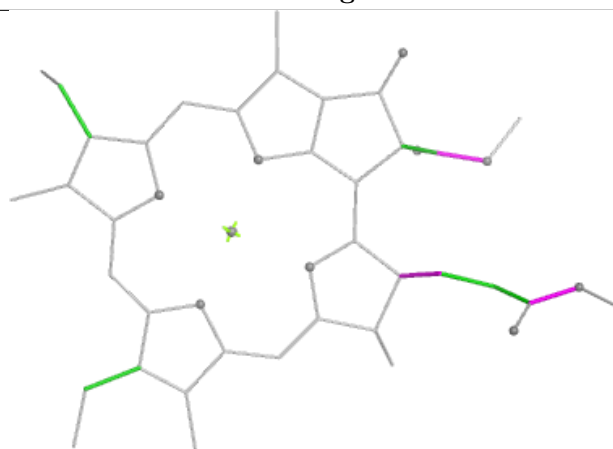
Ligand CLA 3 613



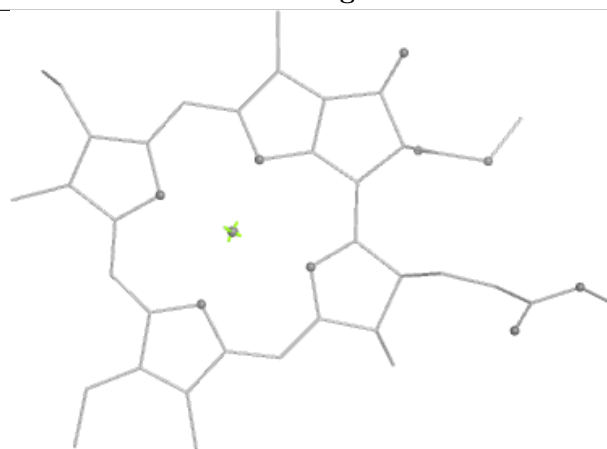
Bond lengths



Bond angles



Torsions

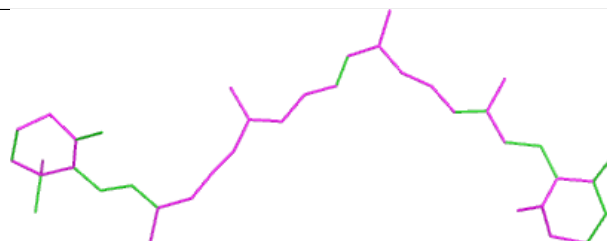


Rings

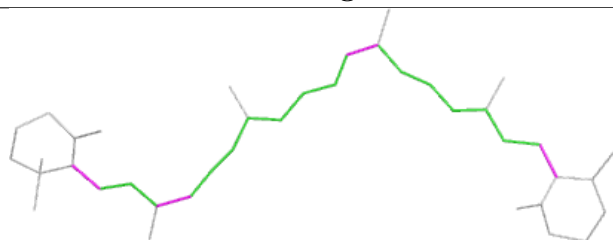
Ligand BCR A 4011



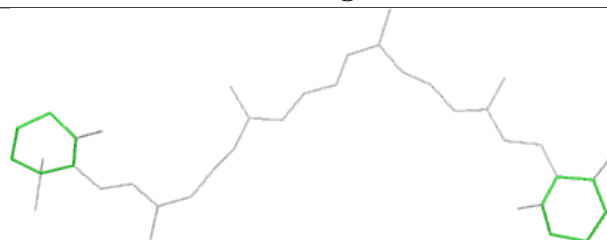
Bond lengths



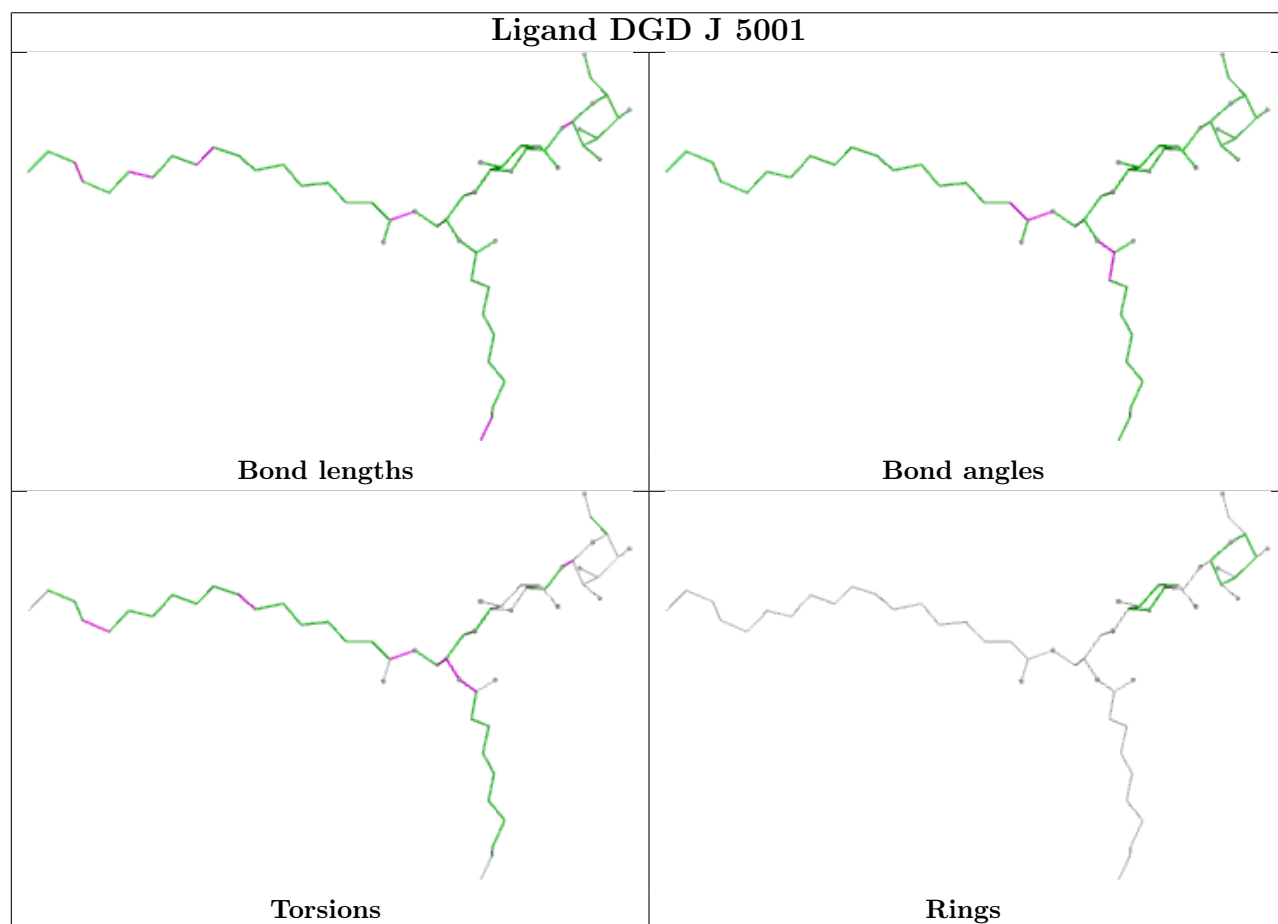
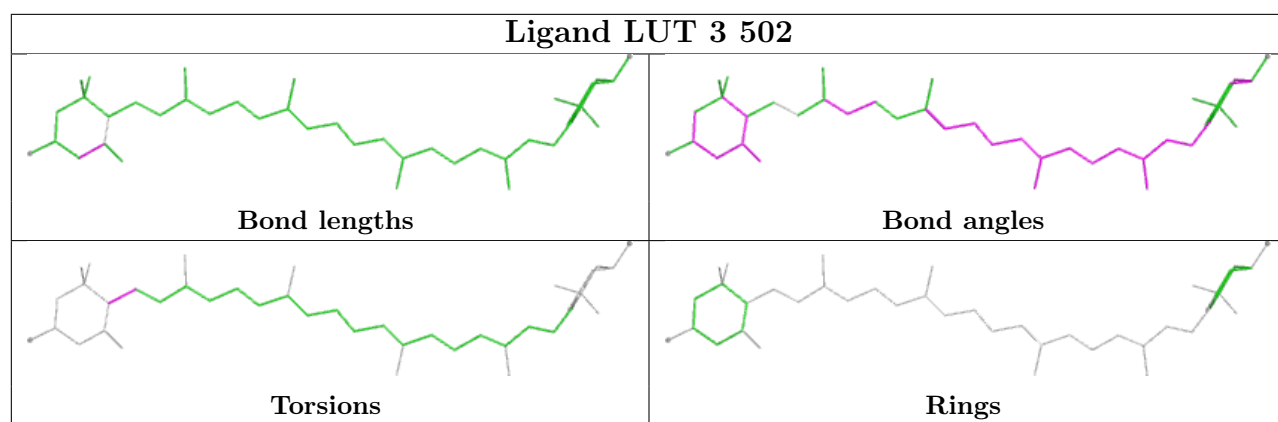
Bond angles



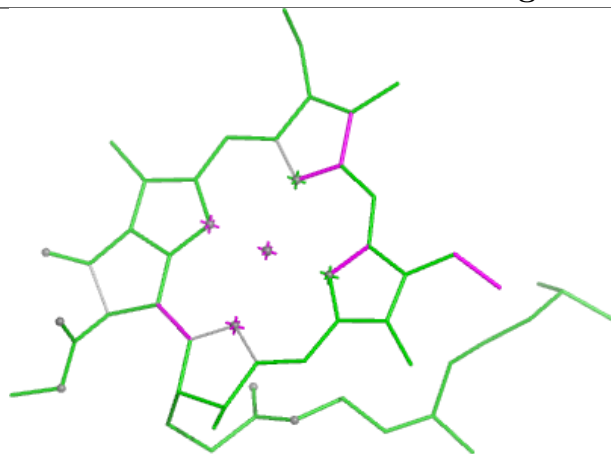
Torsions



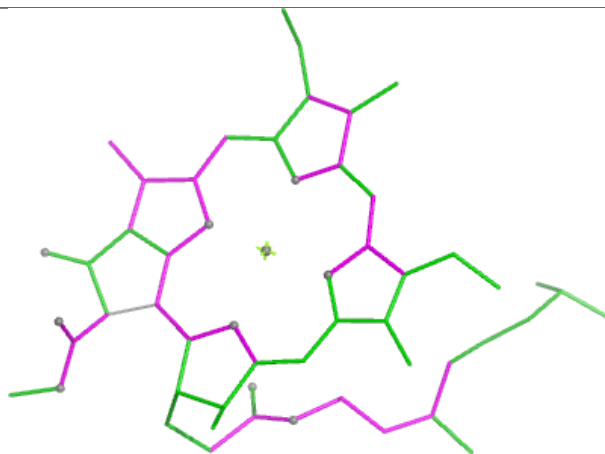
Rings



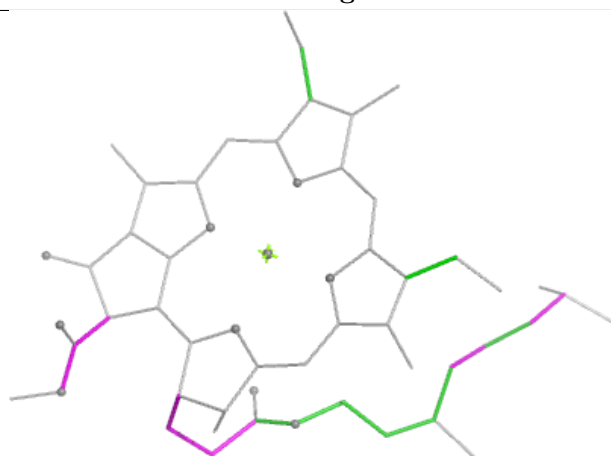
Ligand CLA 3 601



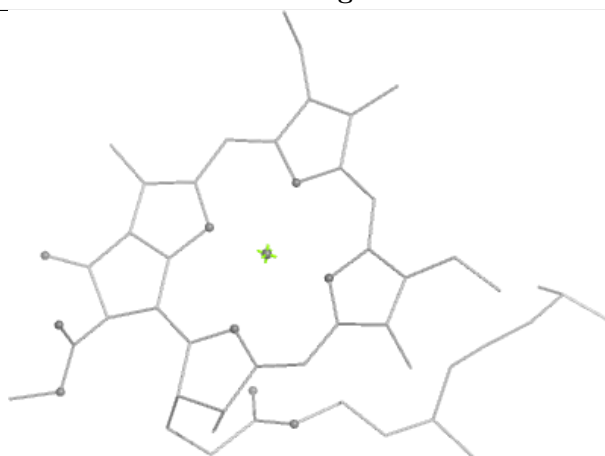
Bond lengths



Bond angles

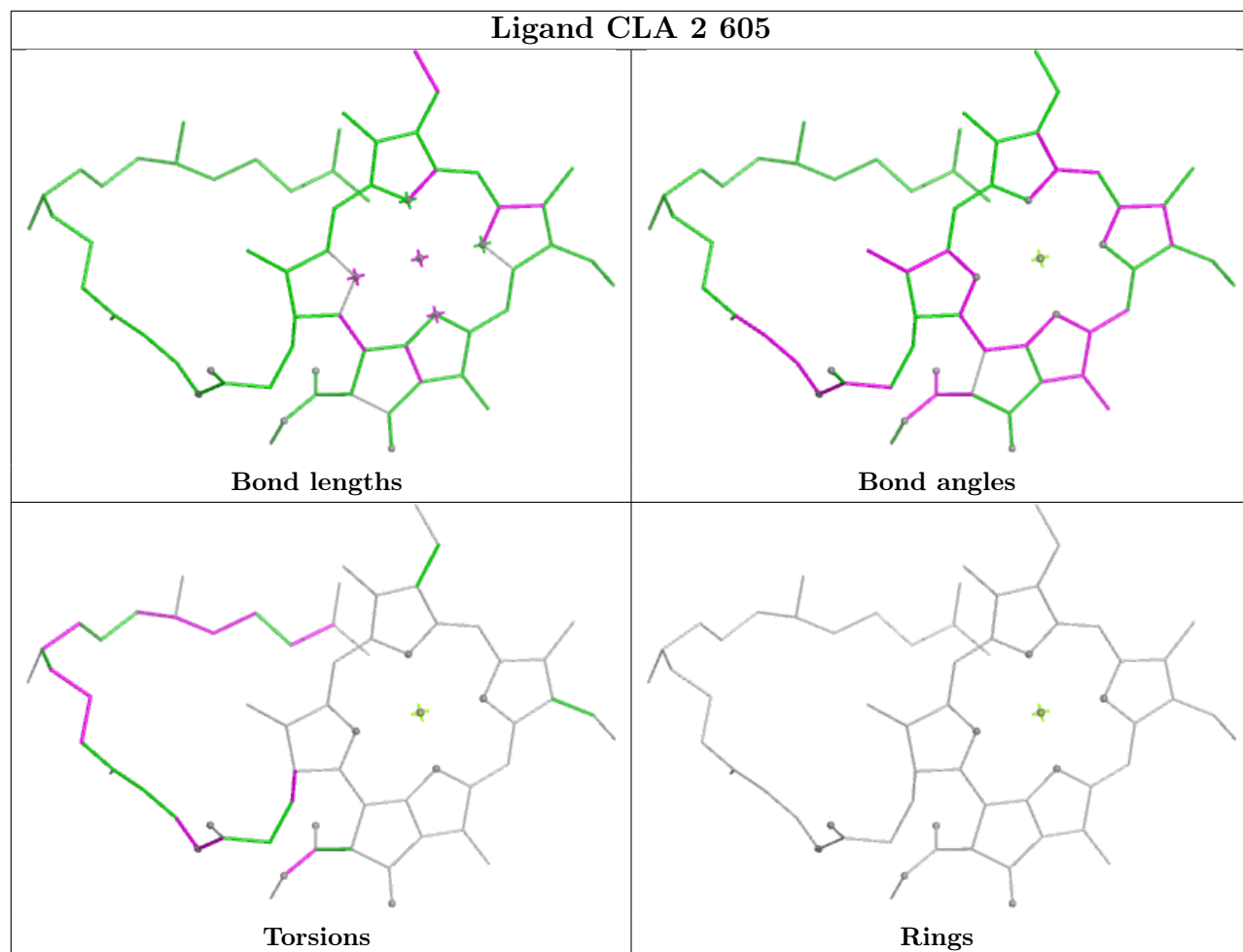


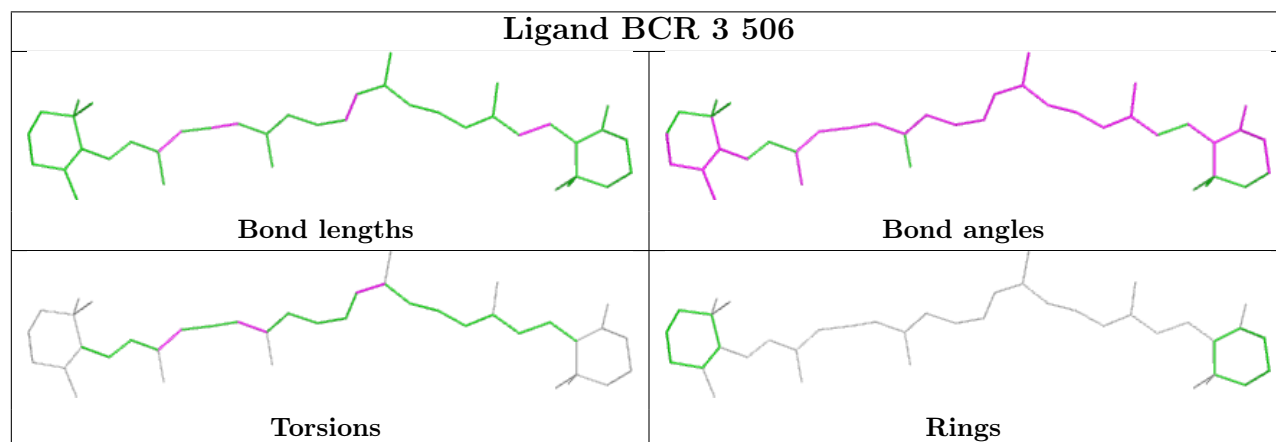
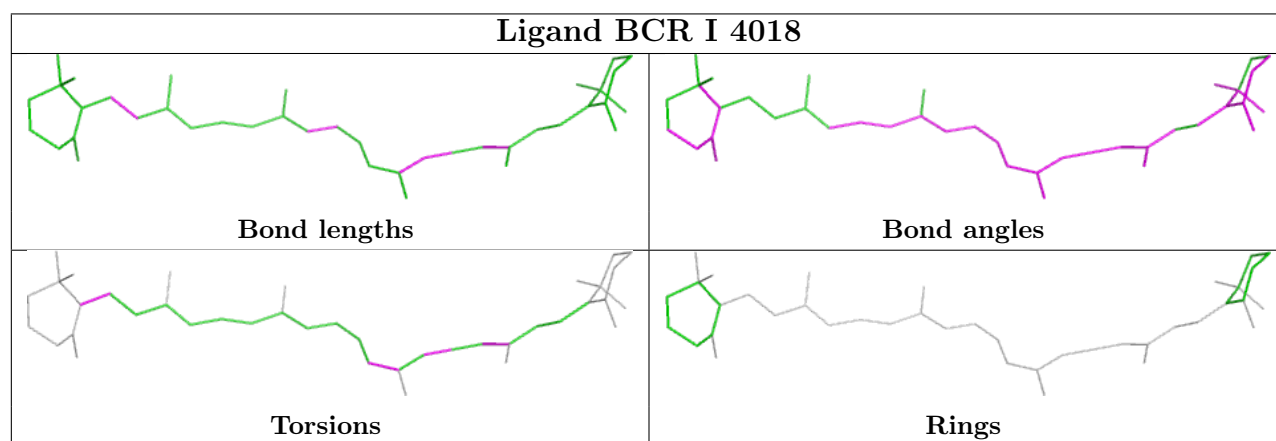
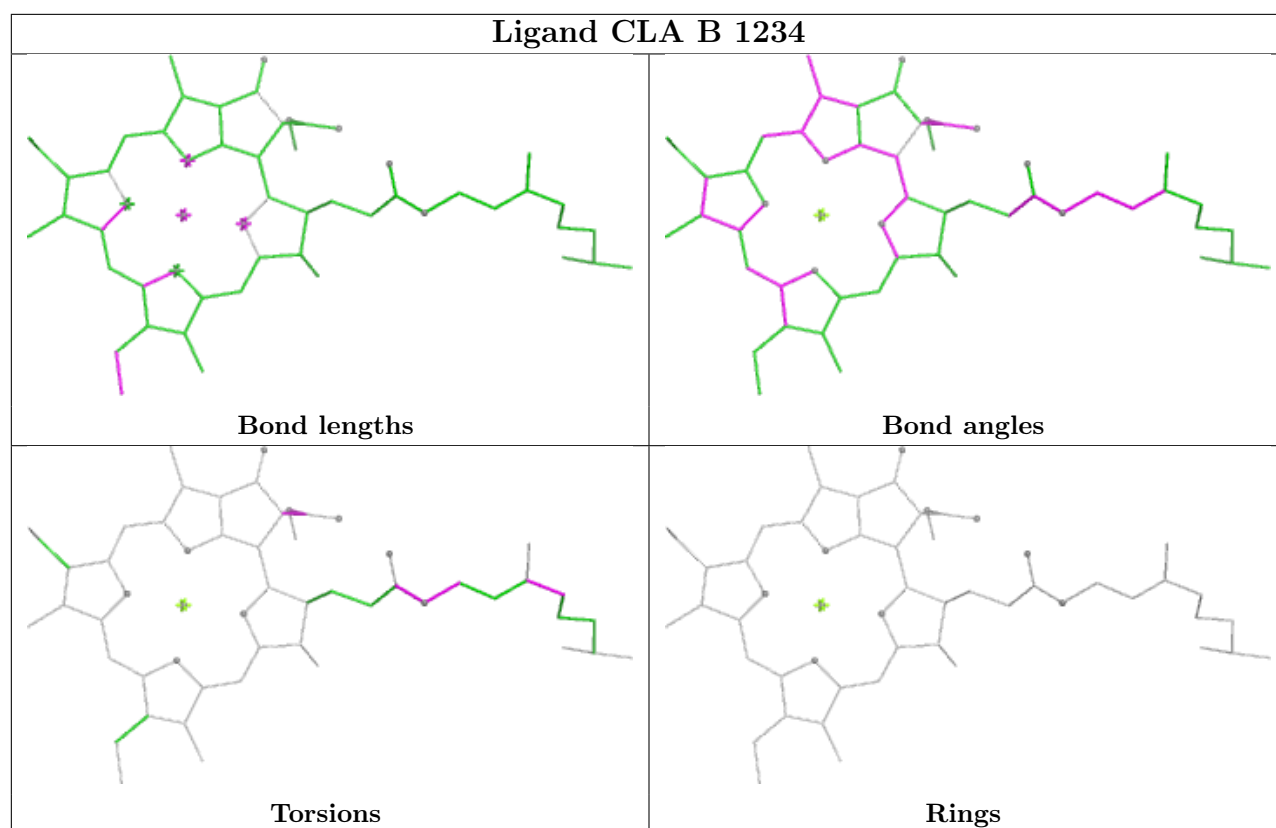
Torsions



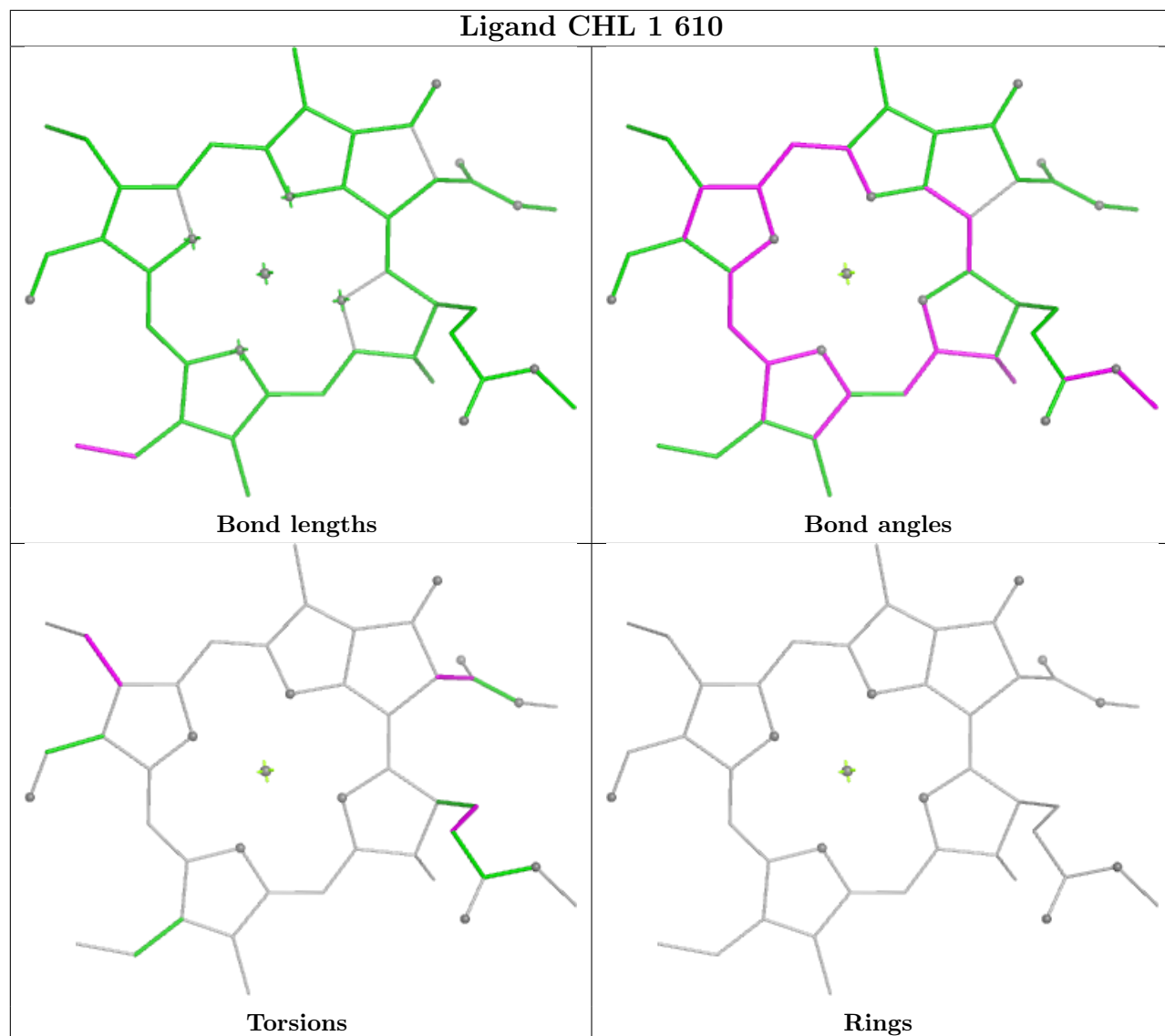
Rings

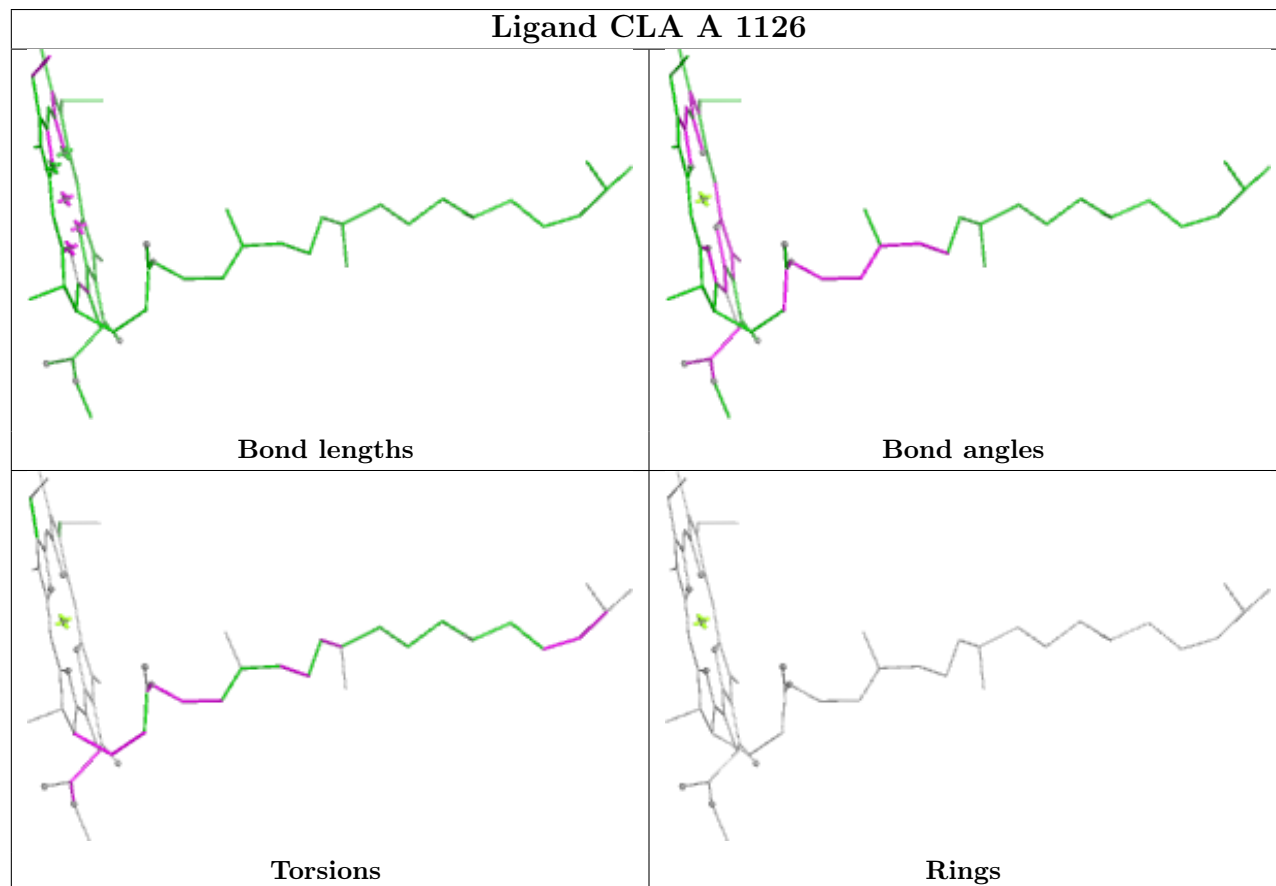
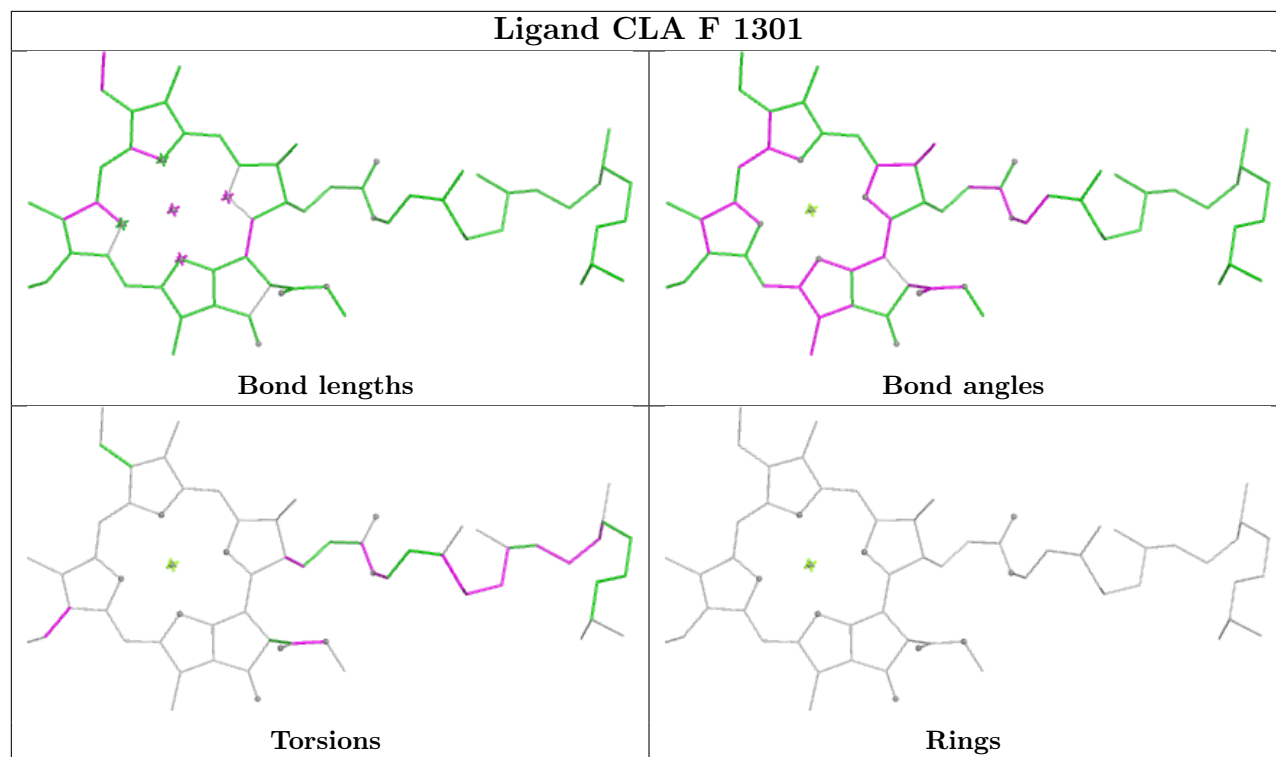
Ligand CLA 2 605

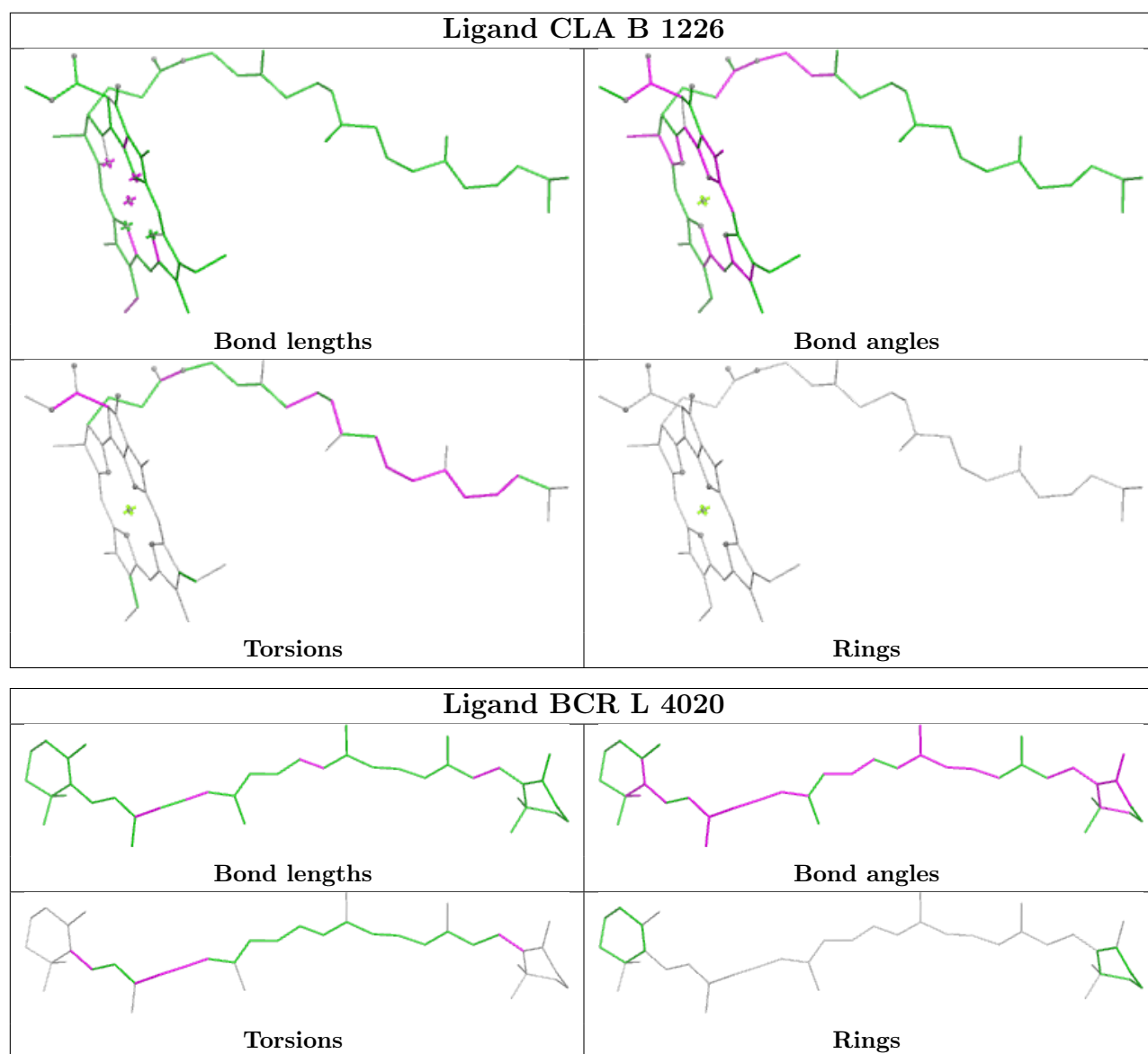


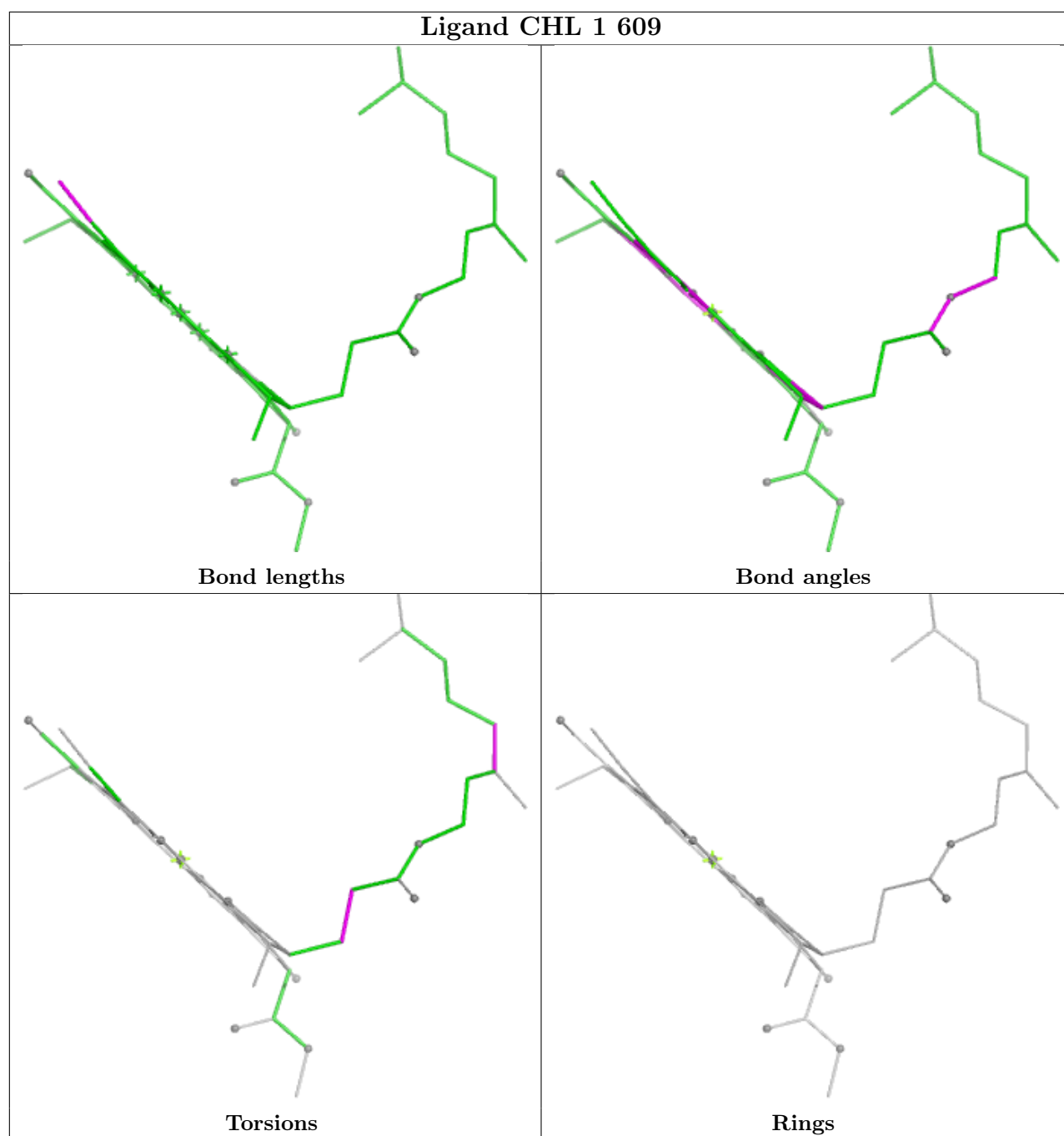


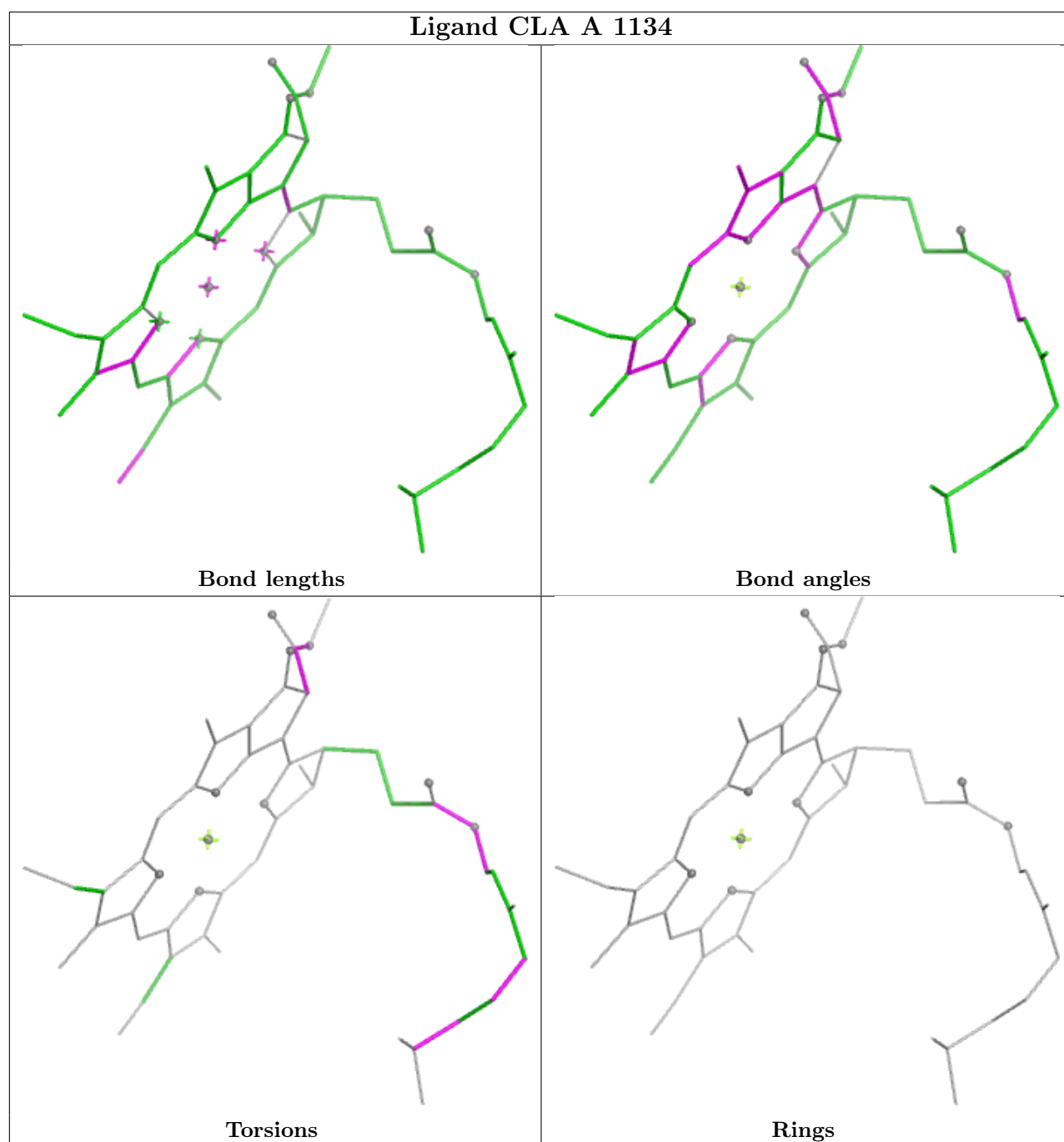
Ligand CHL 1 610

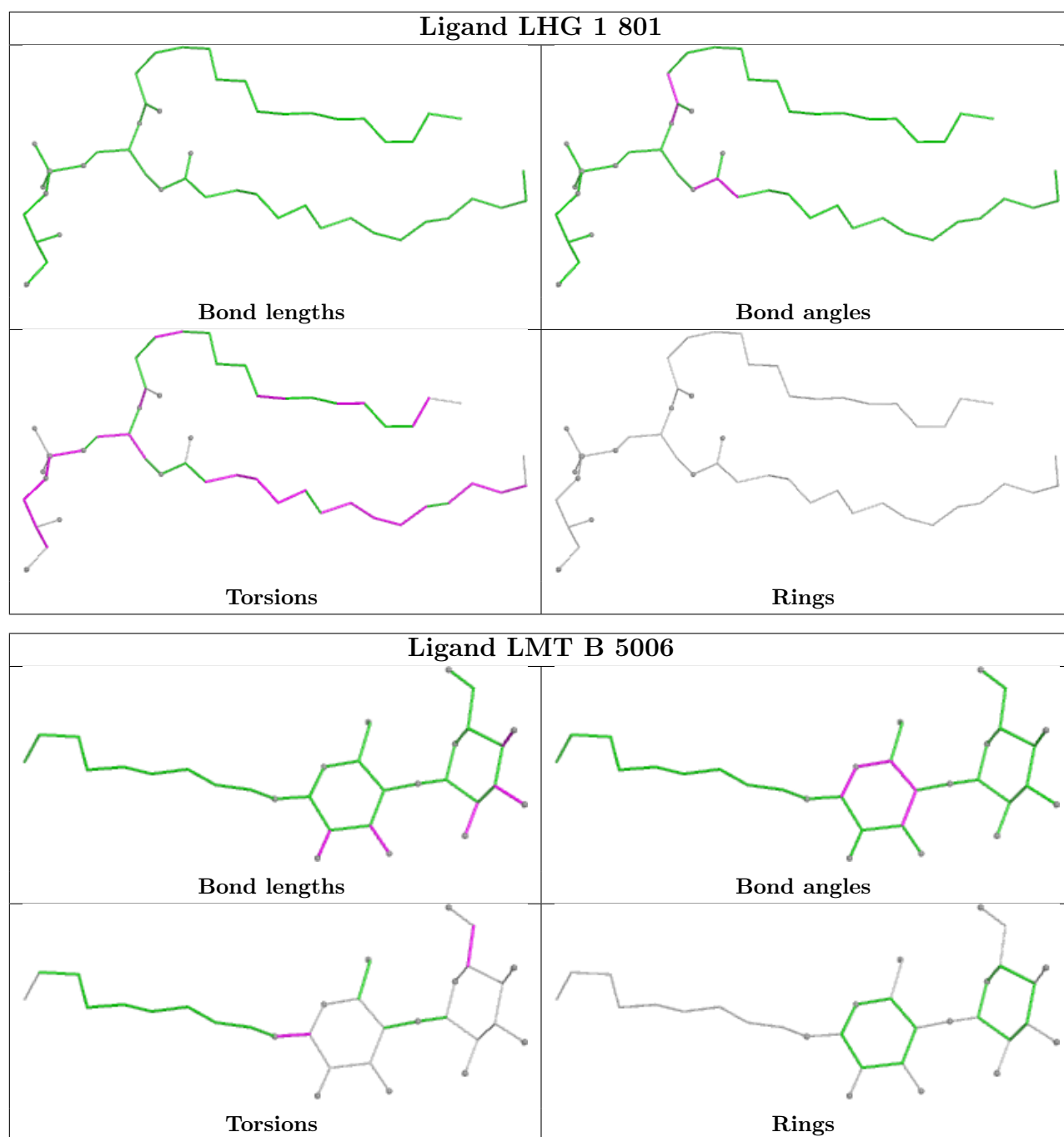


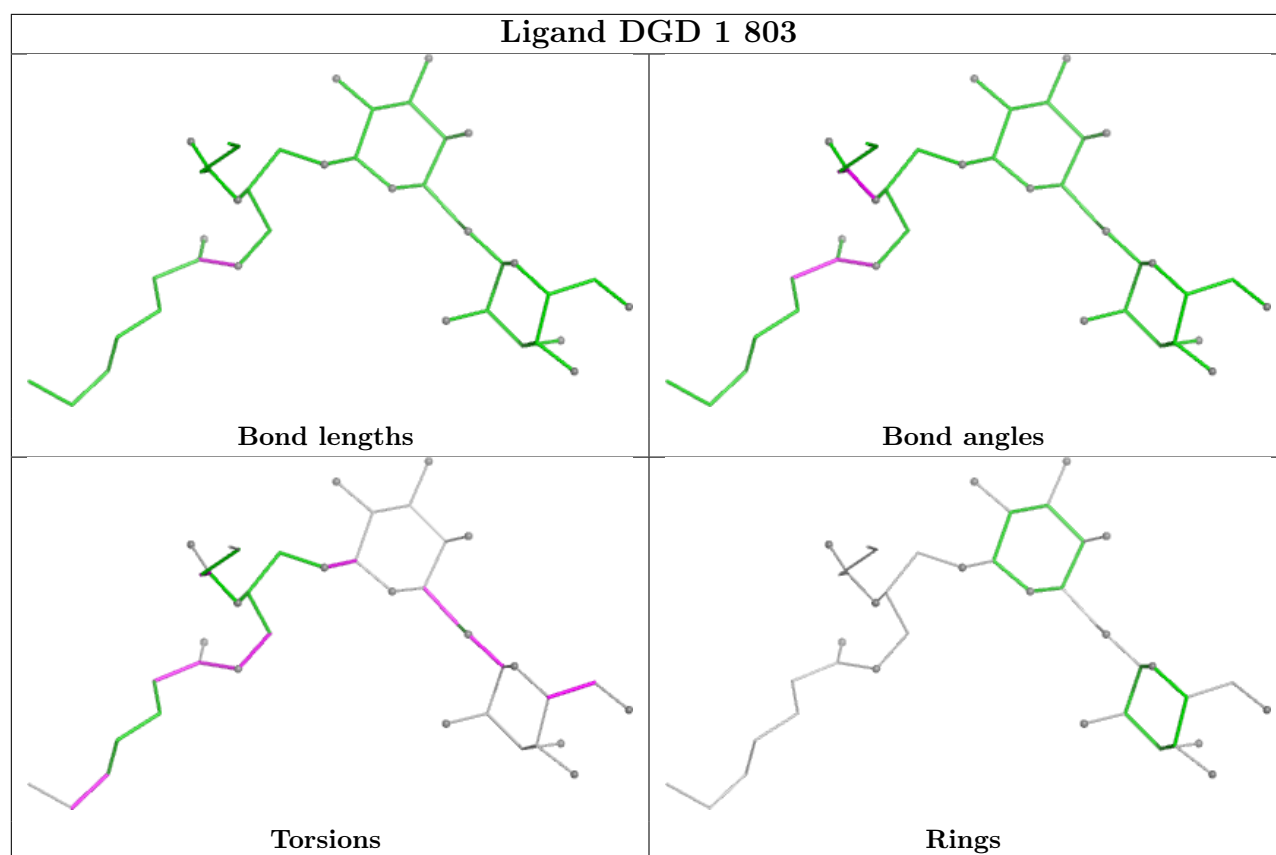




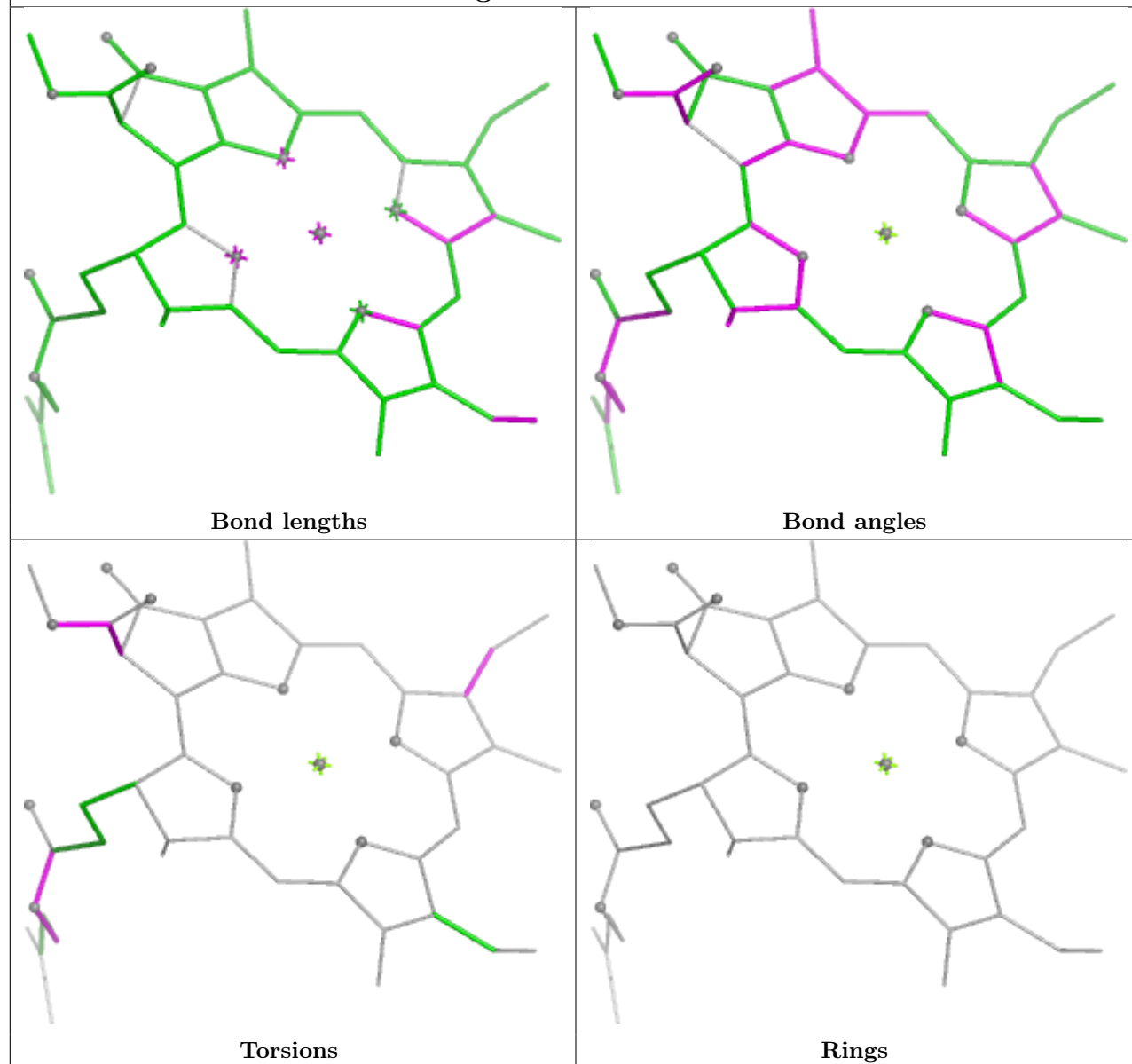


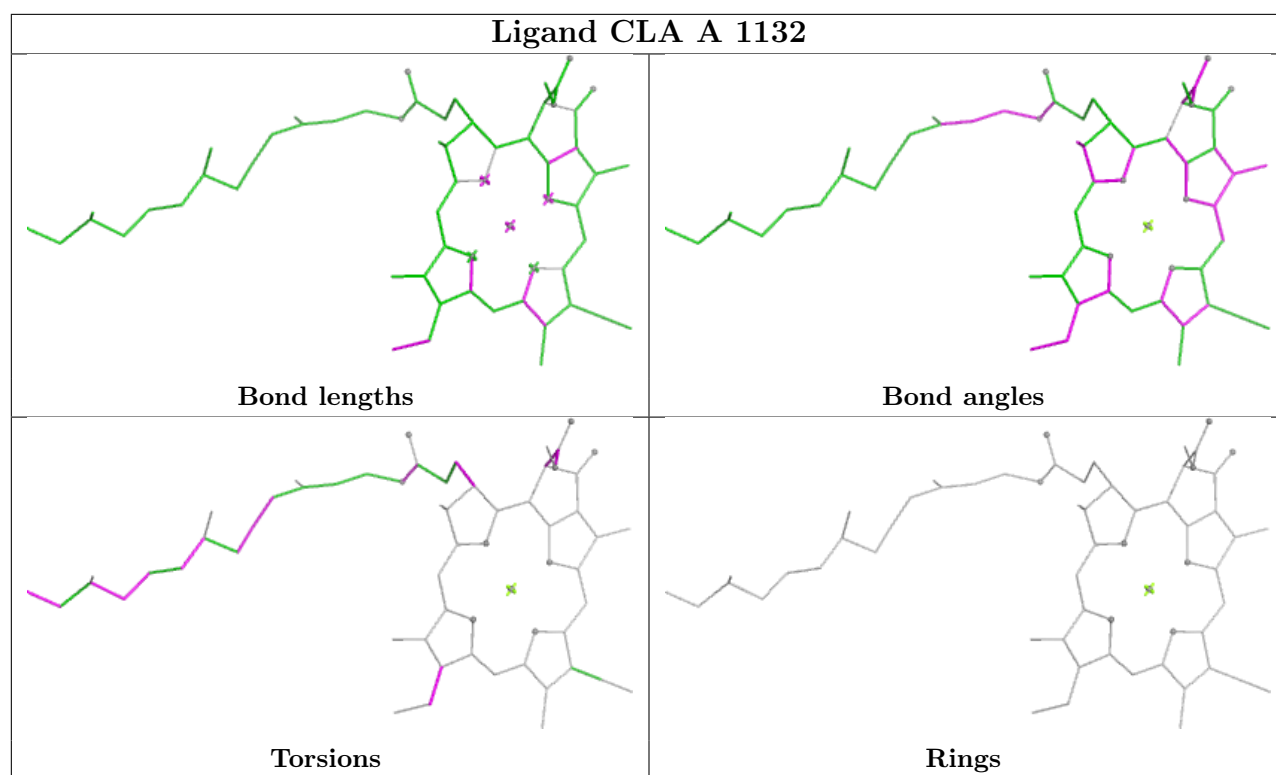


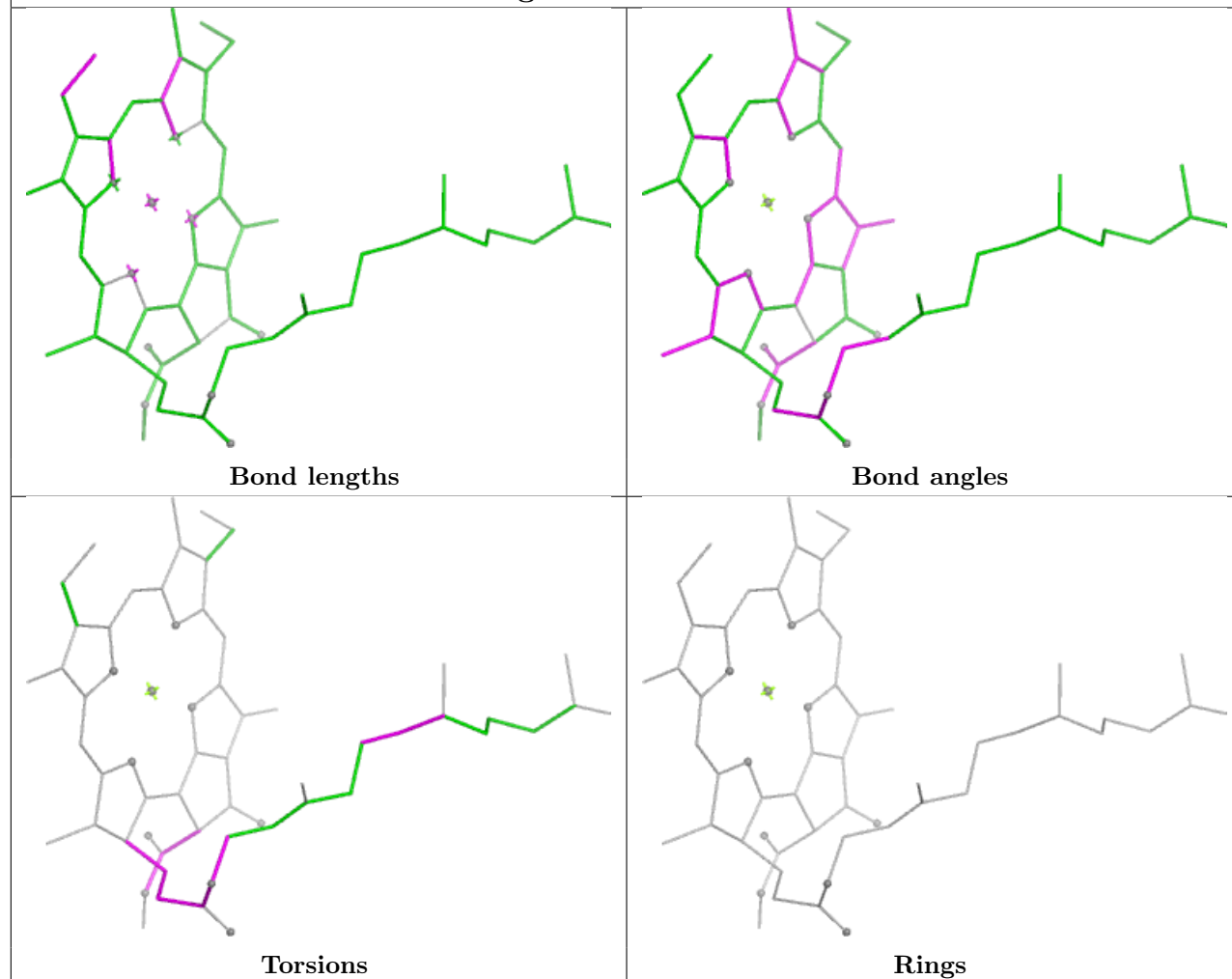
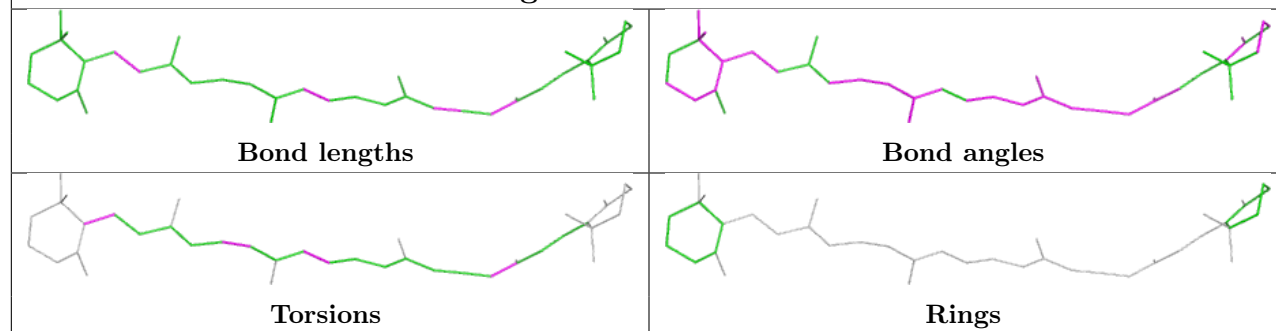


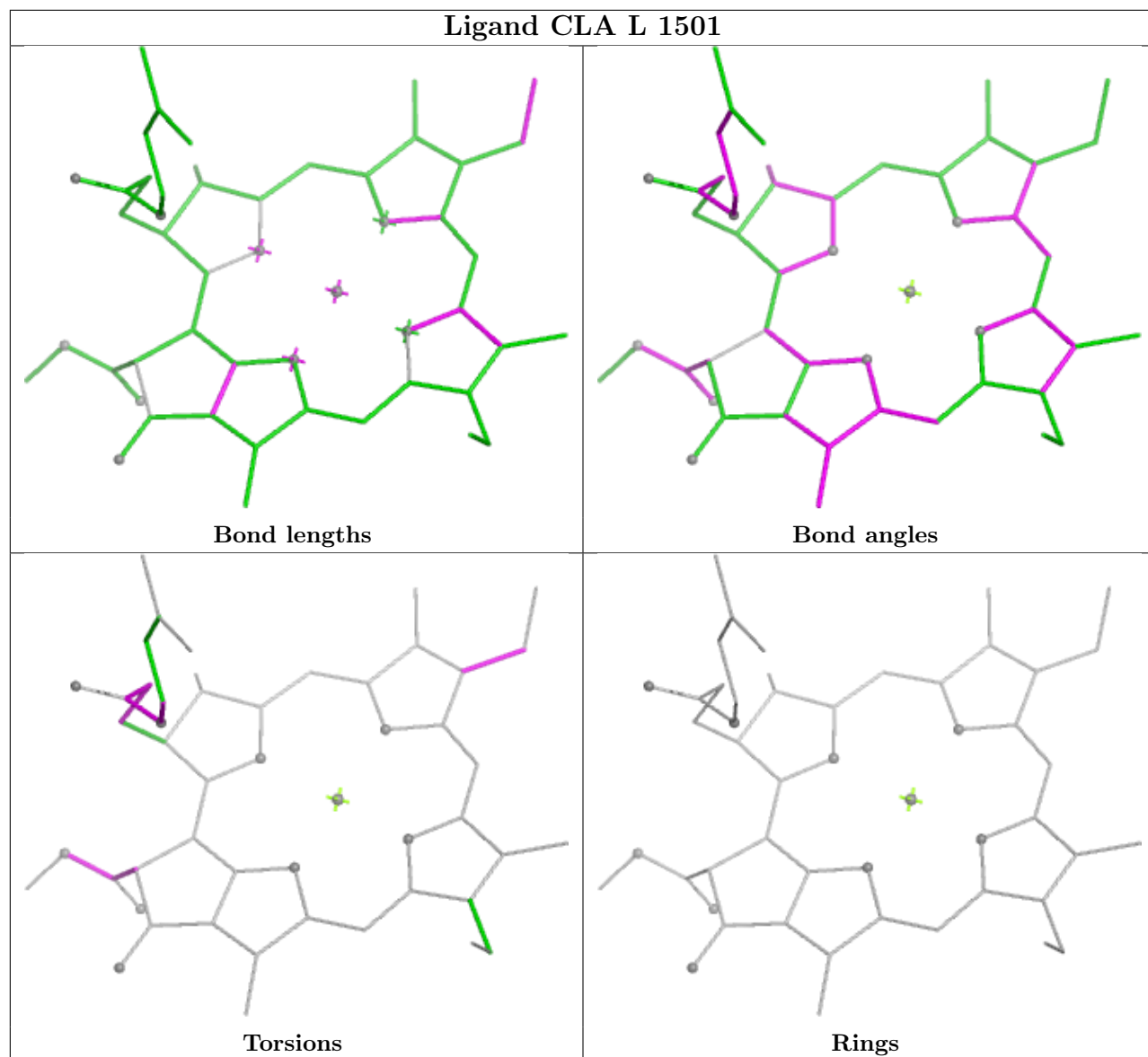


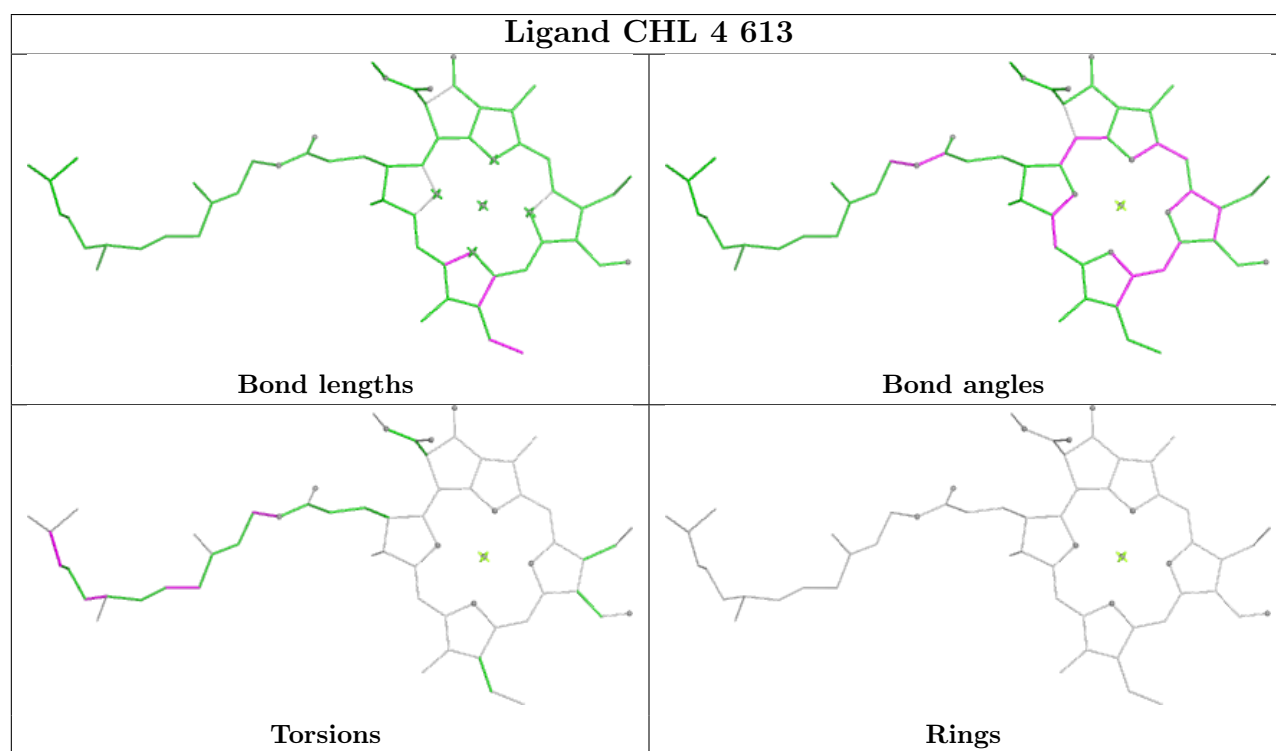
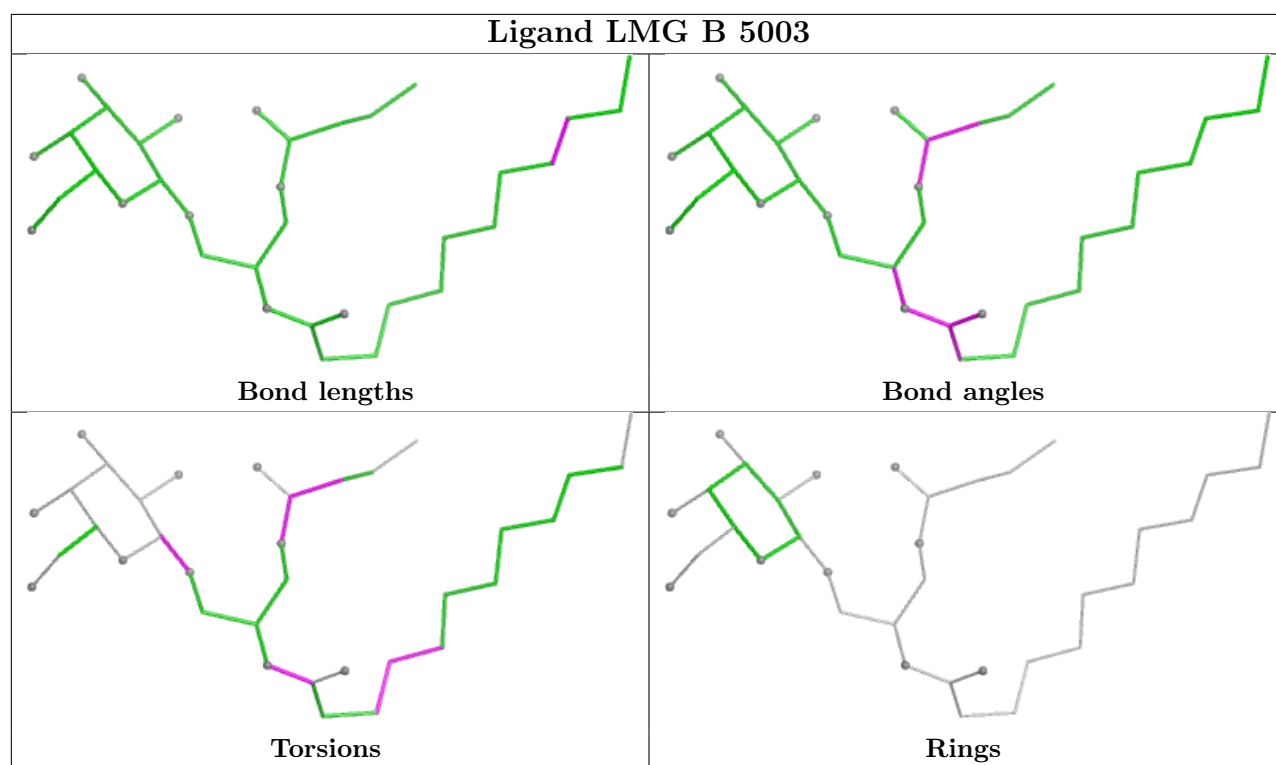
Ligand CLA 2 608

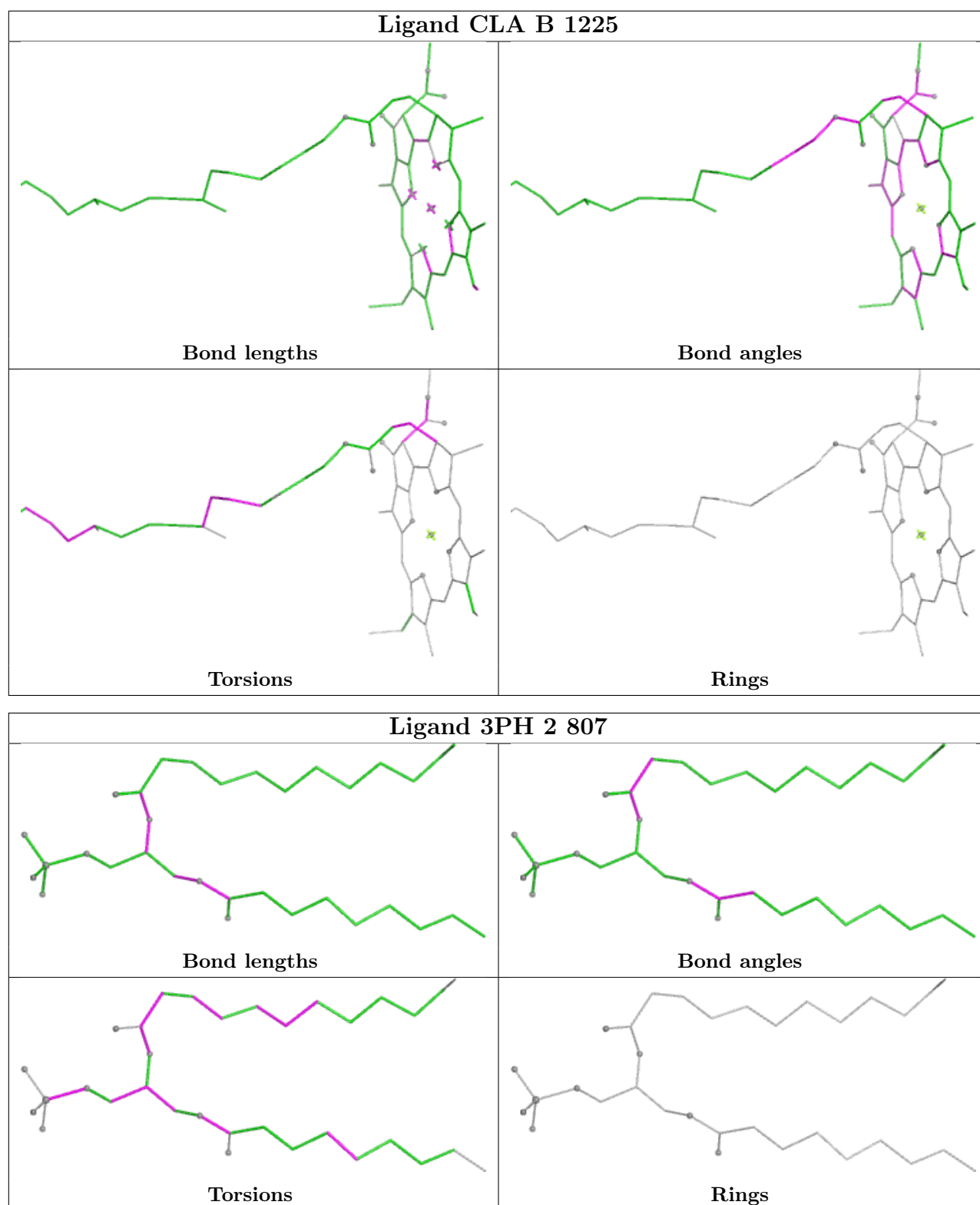


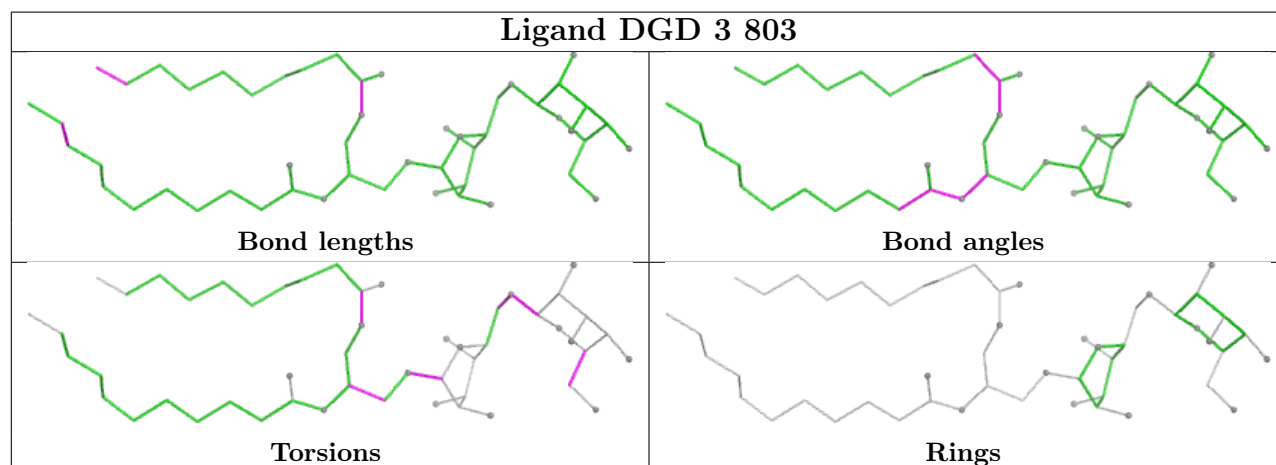
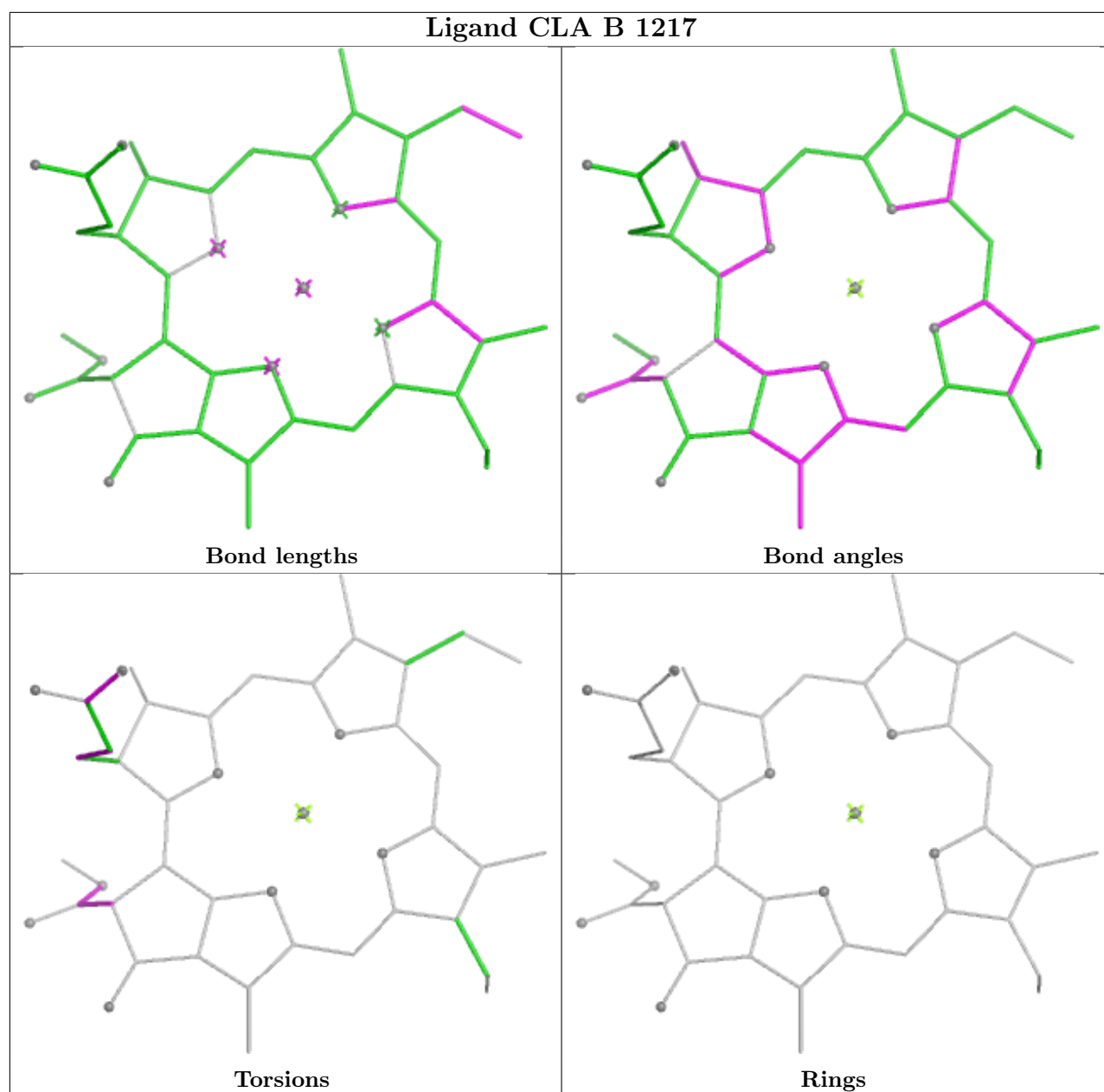


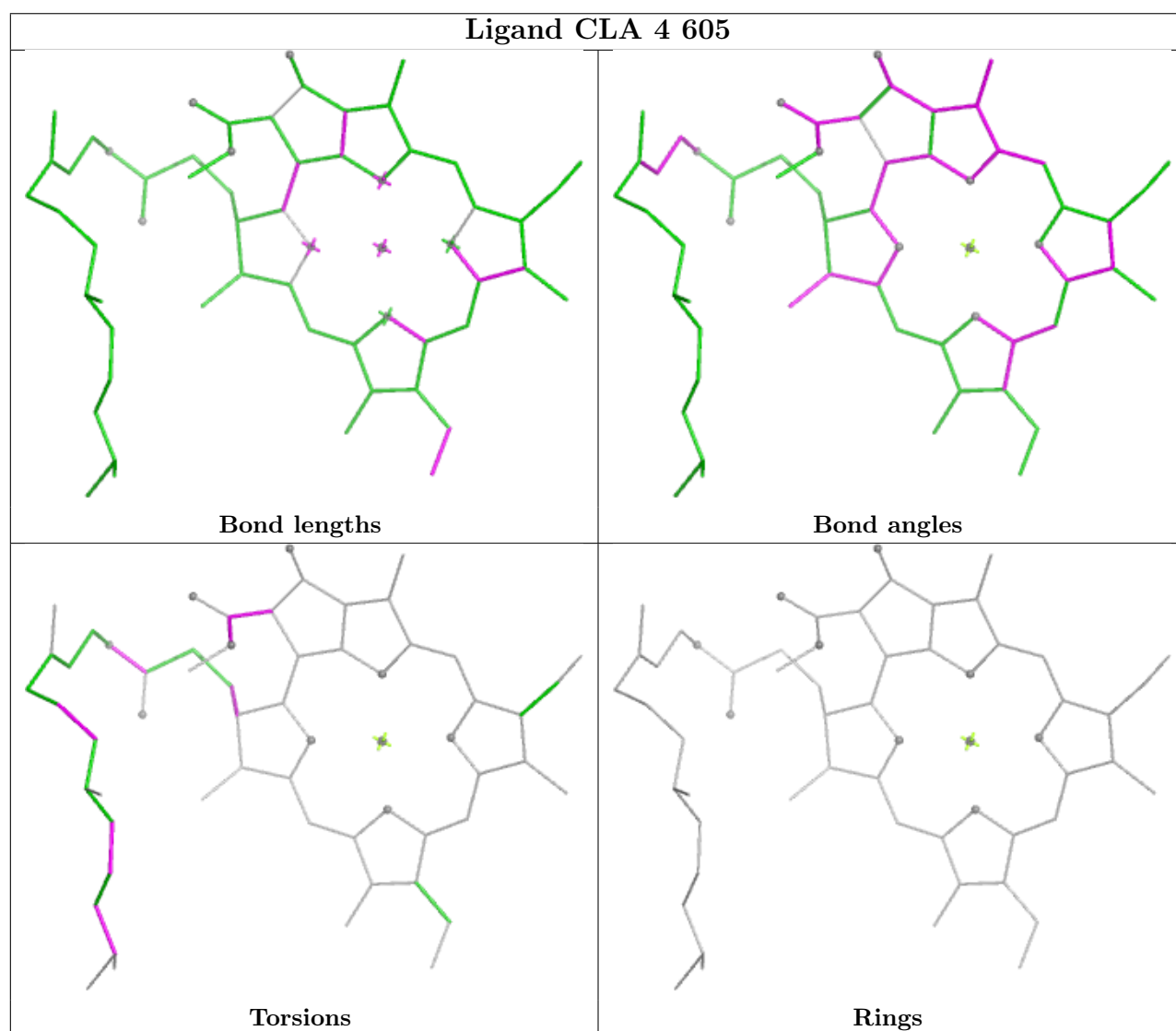
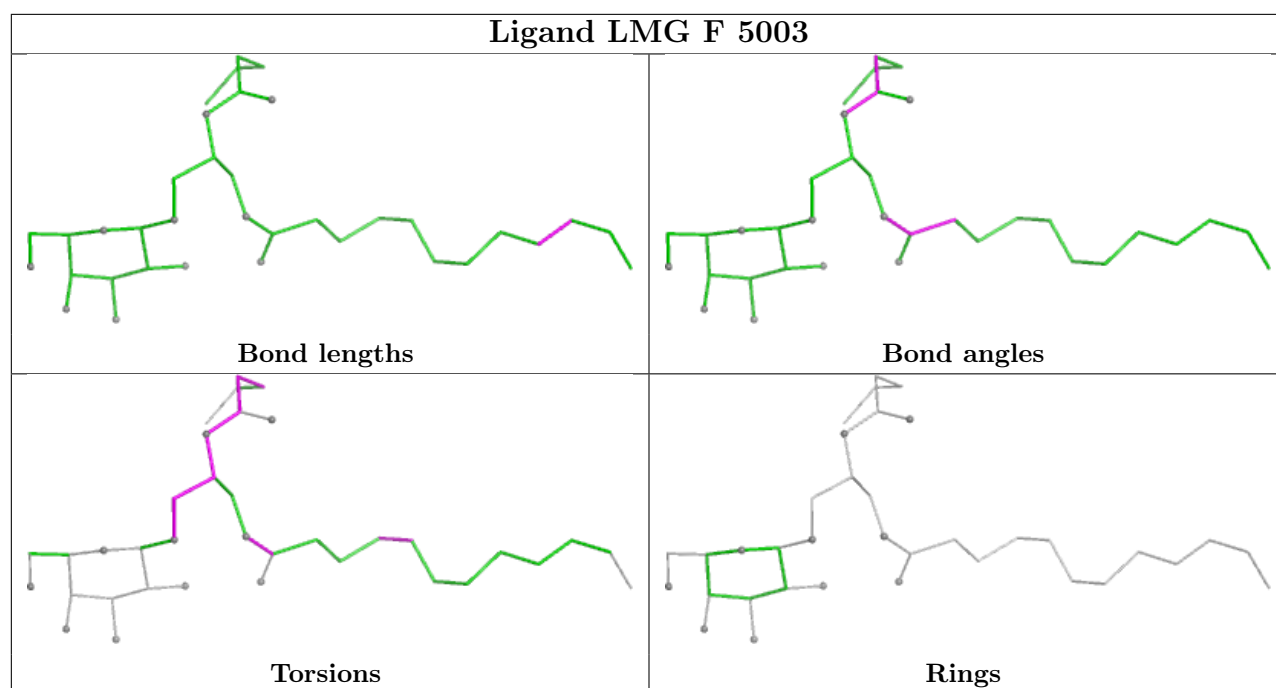
Ligand CLA 4 607**Ligand BCR K 4002**

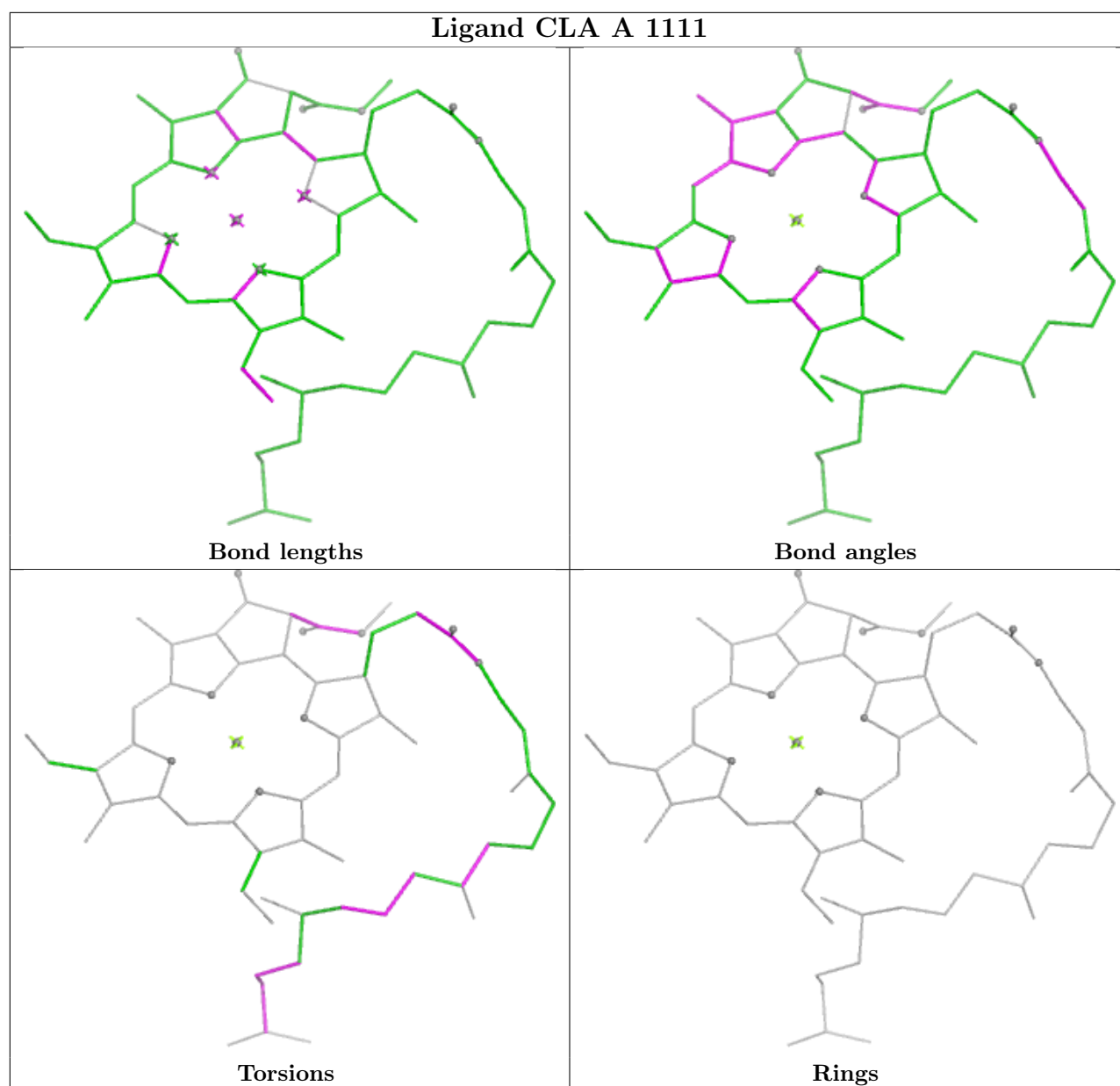


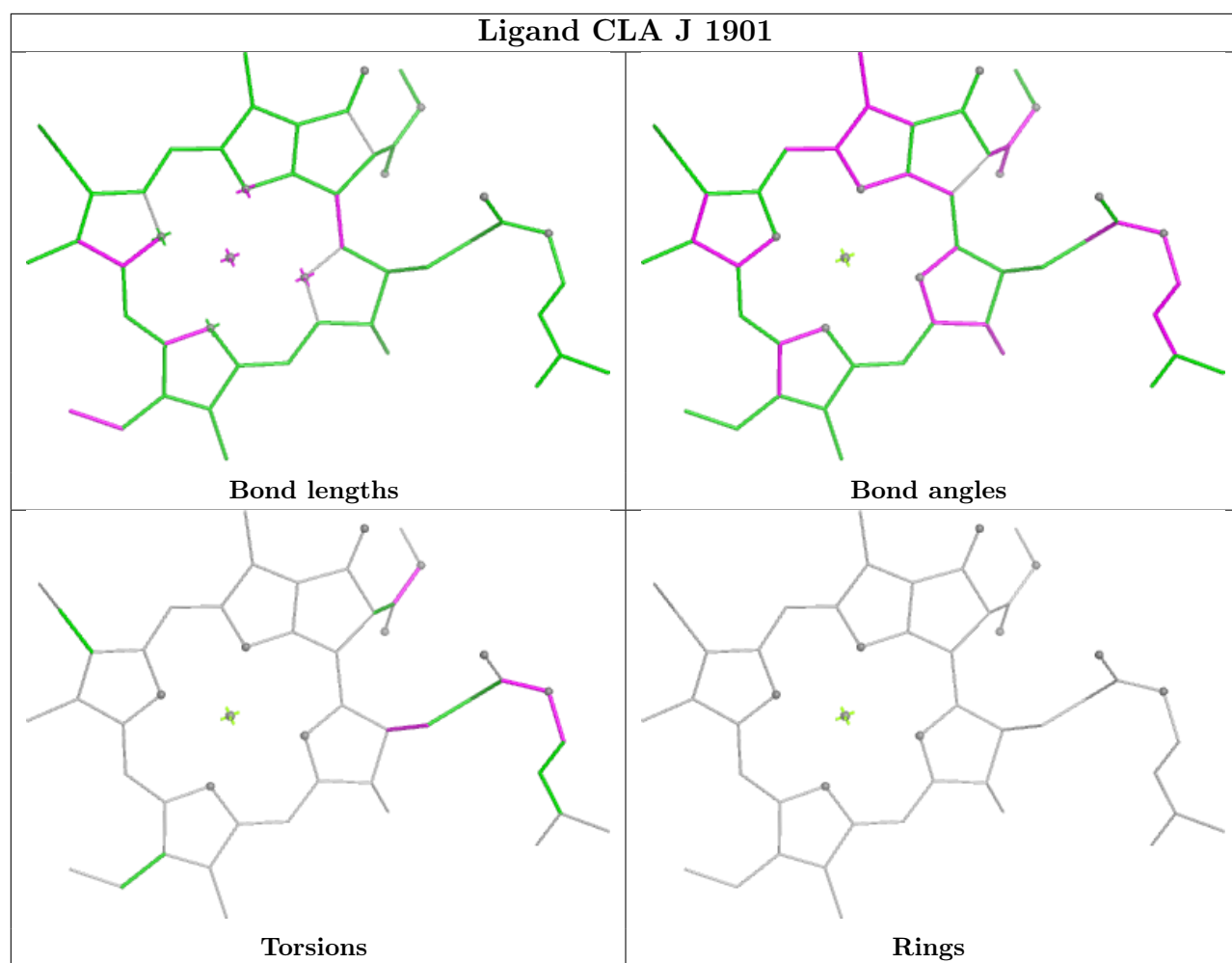


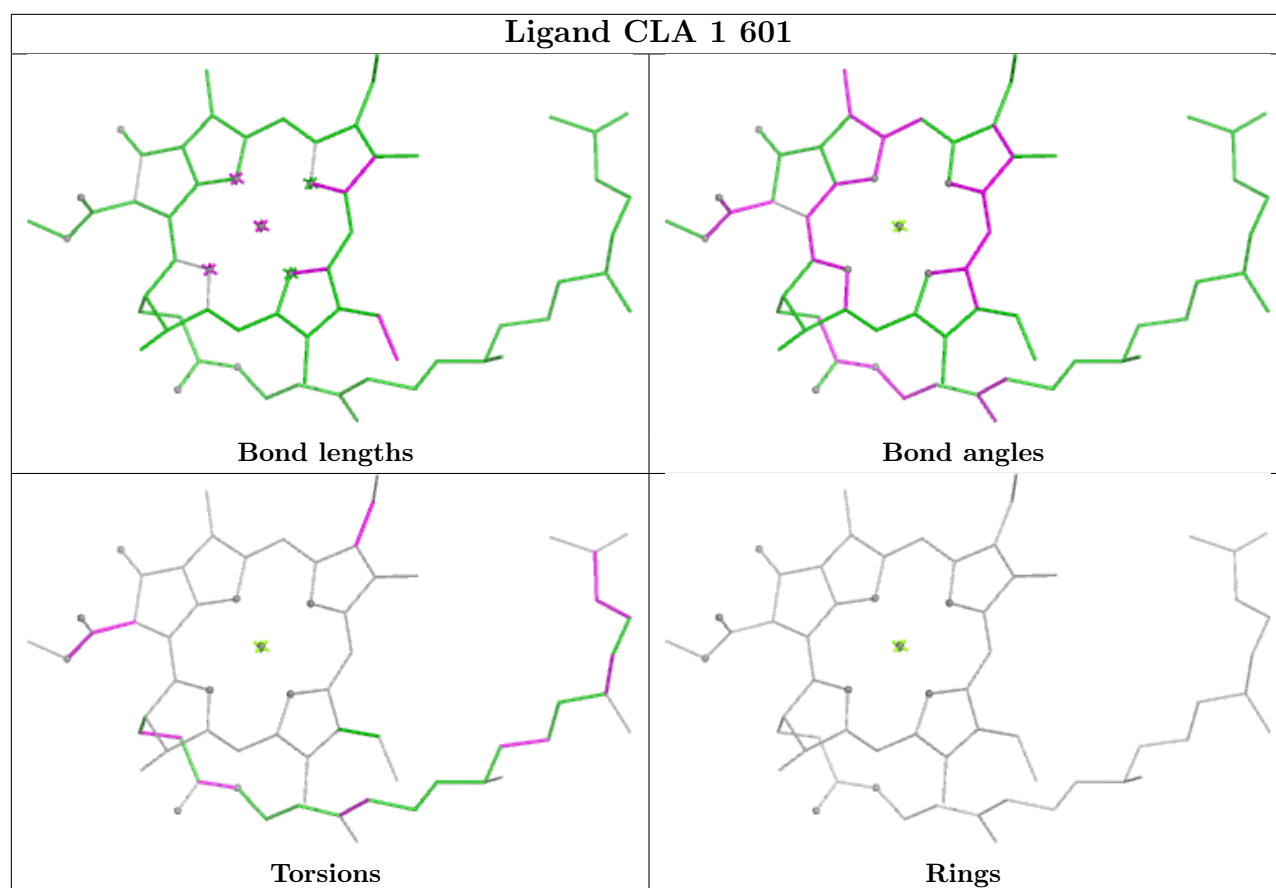




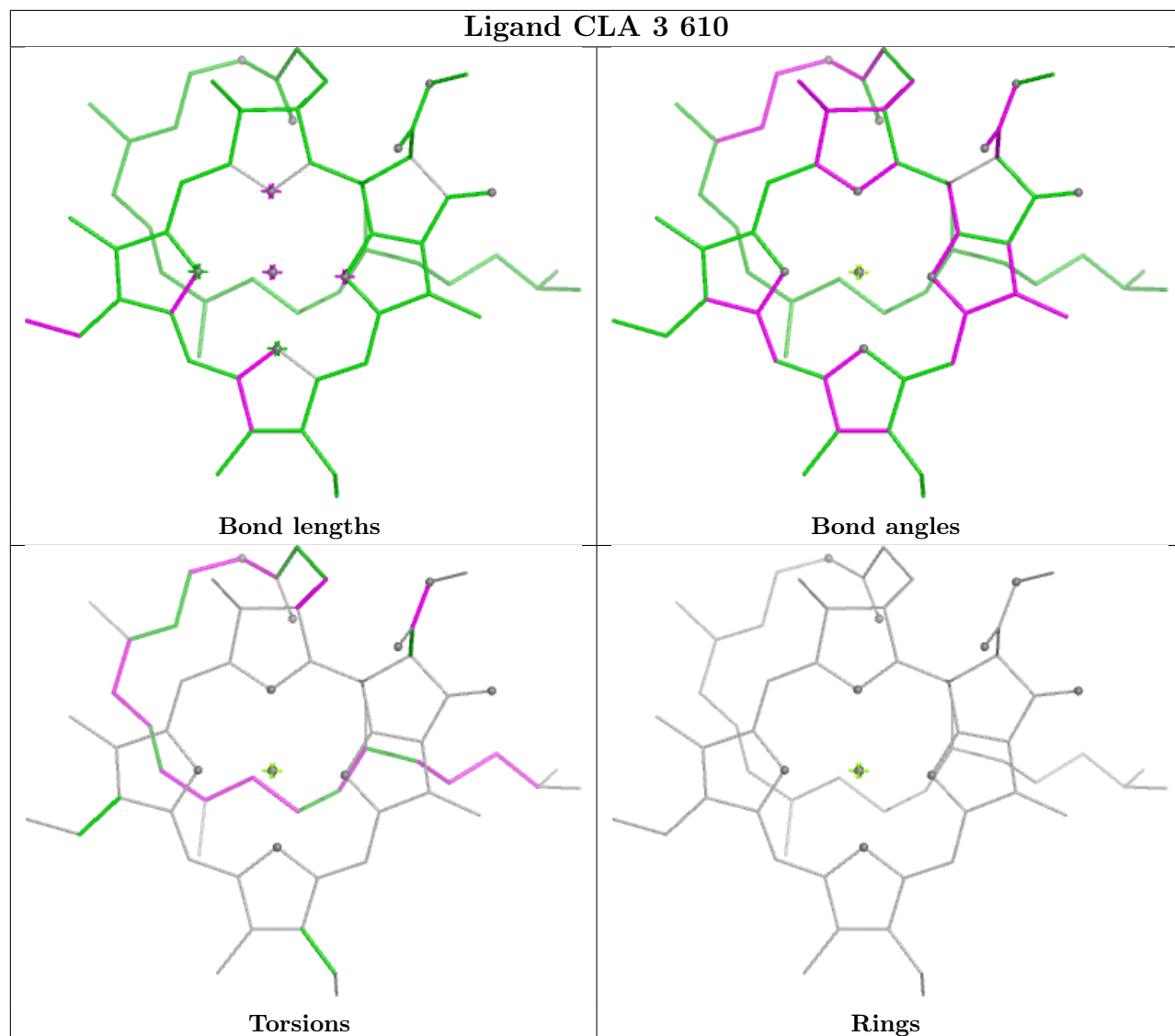


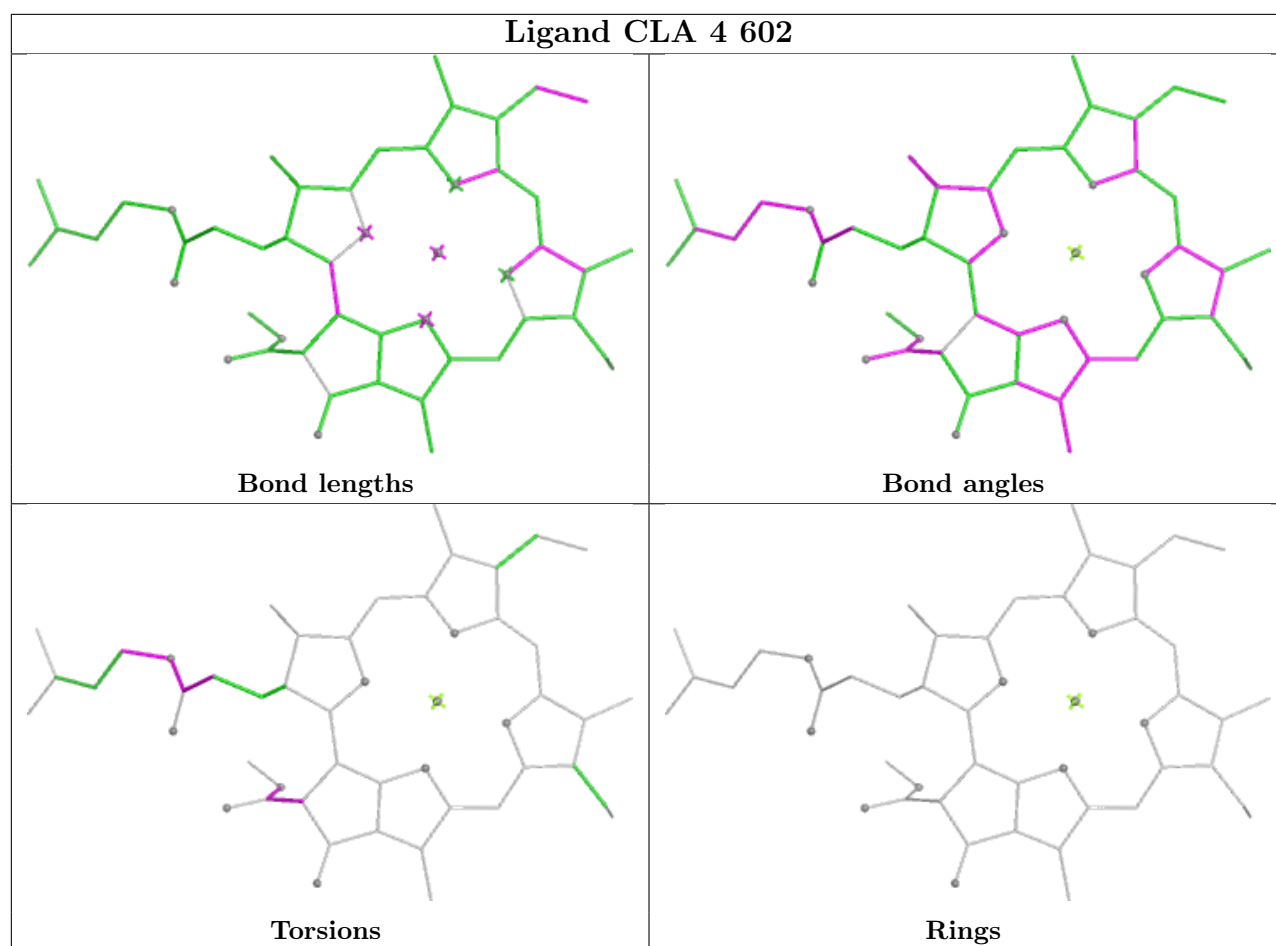


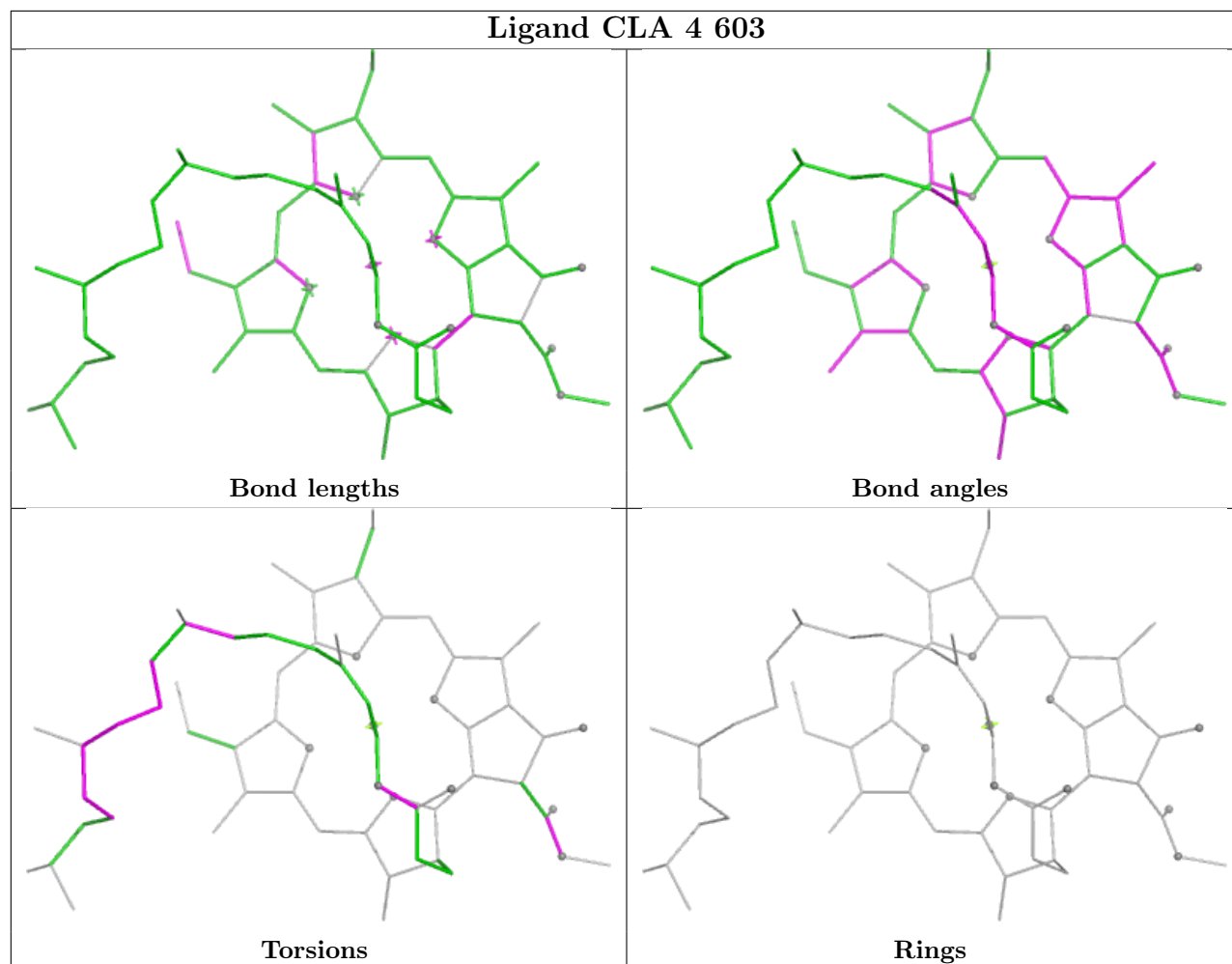
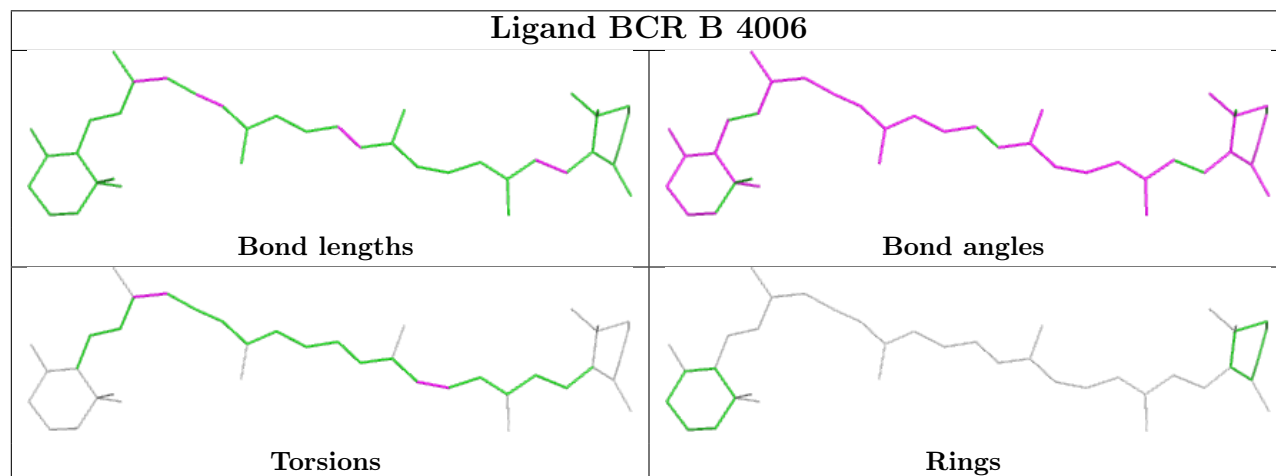


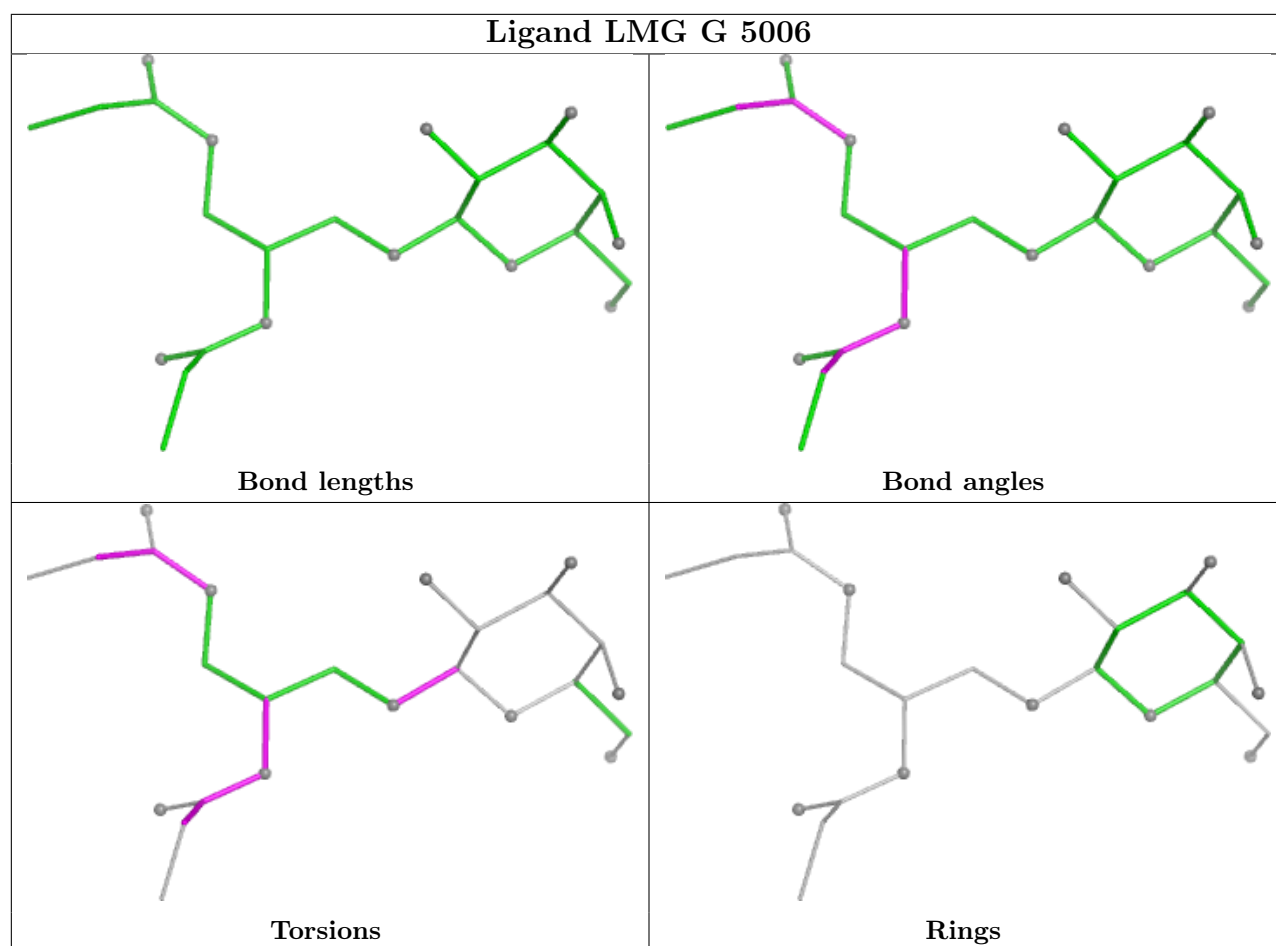


Ligand CLA 3 610

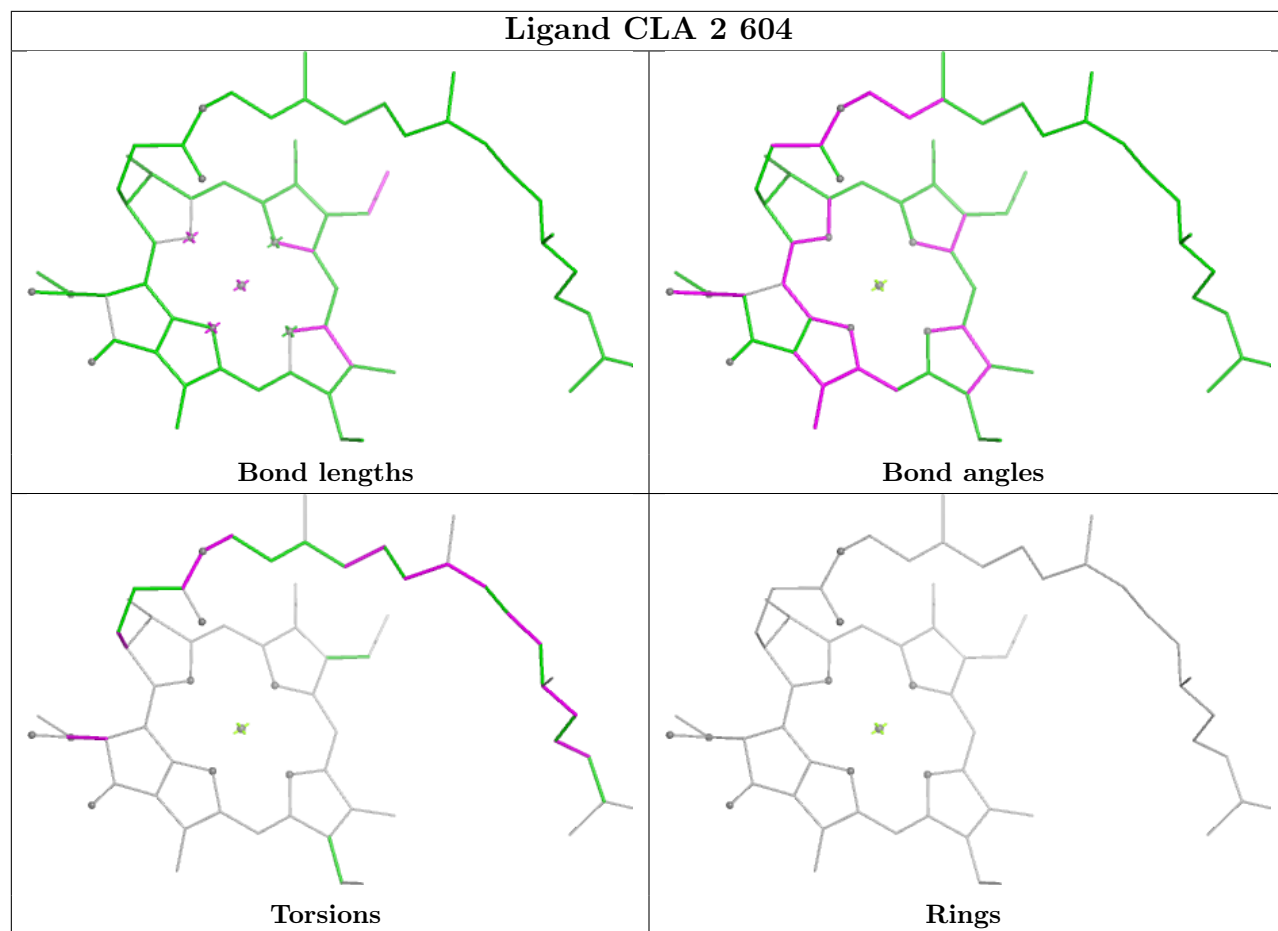


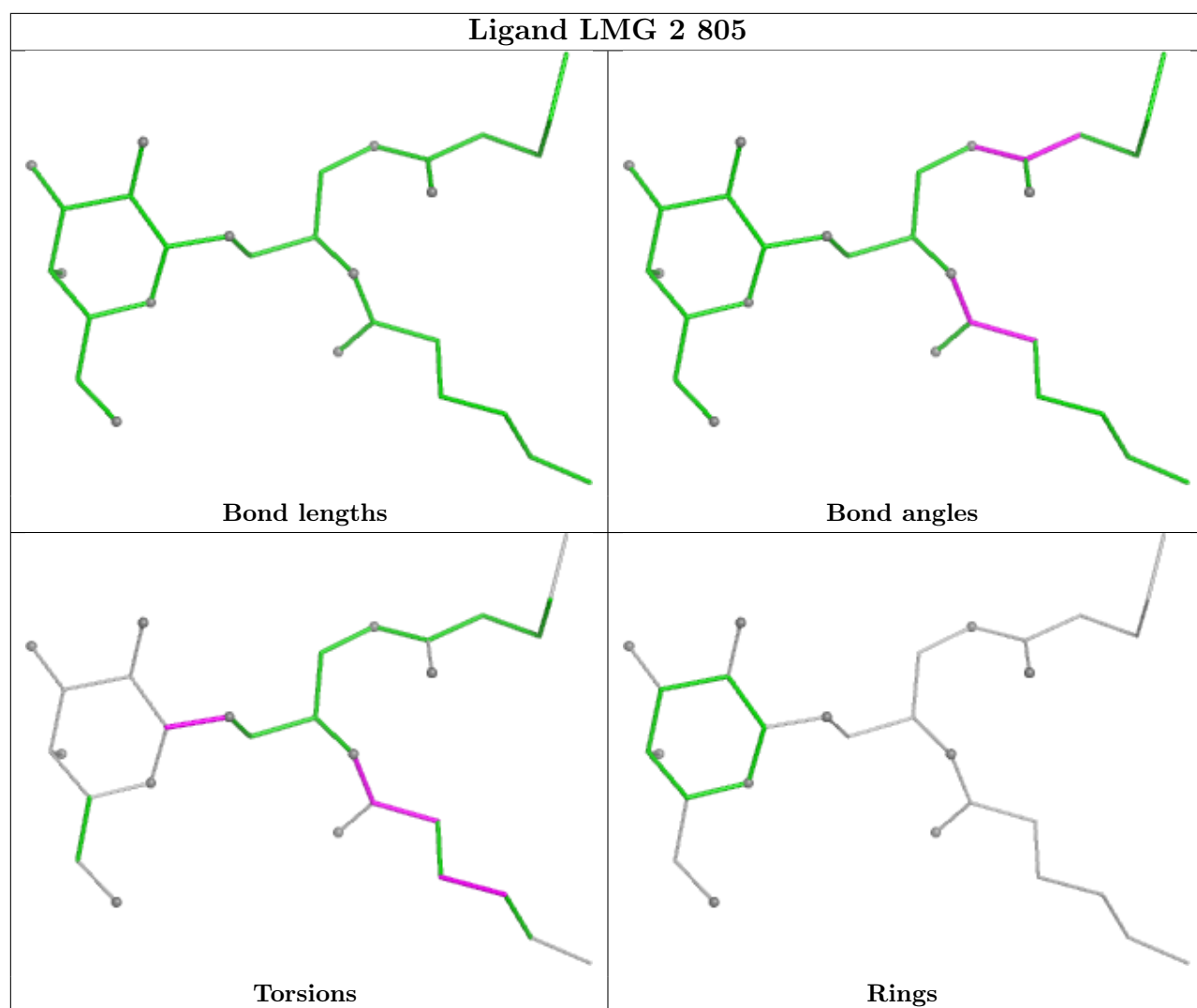


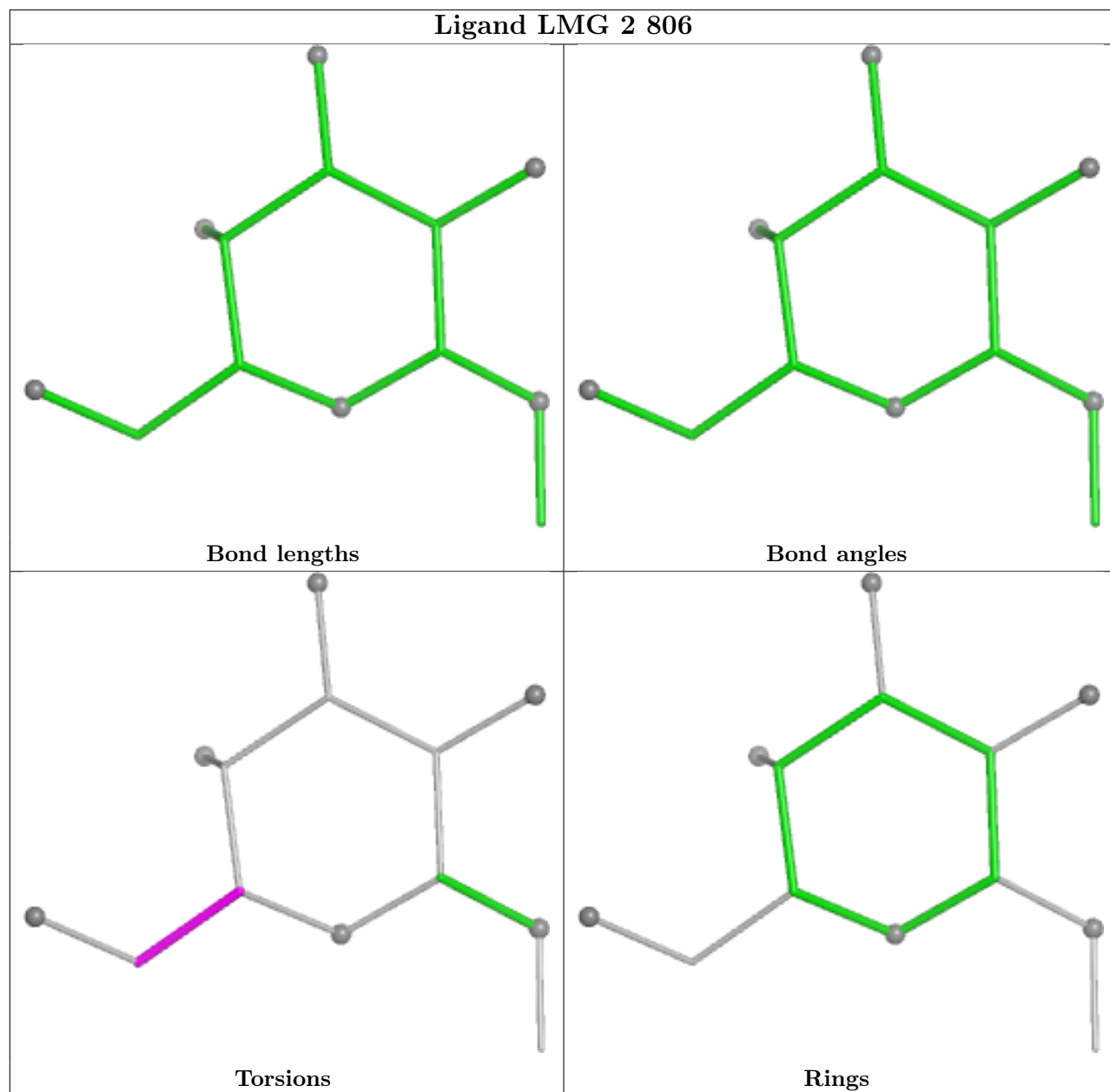
Ligand CLA 4 603**Ligand BCR B 4006**

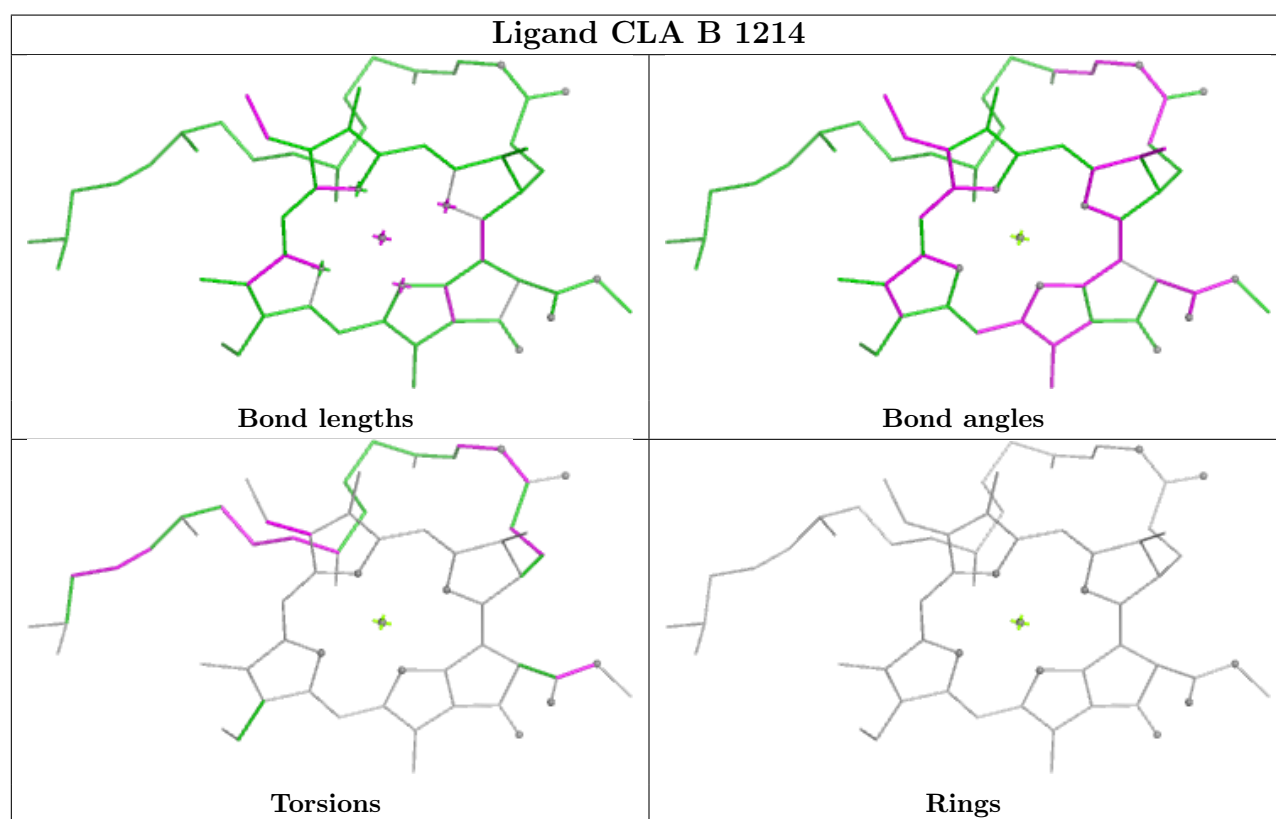
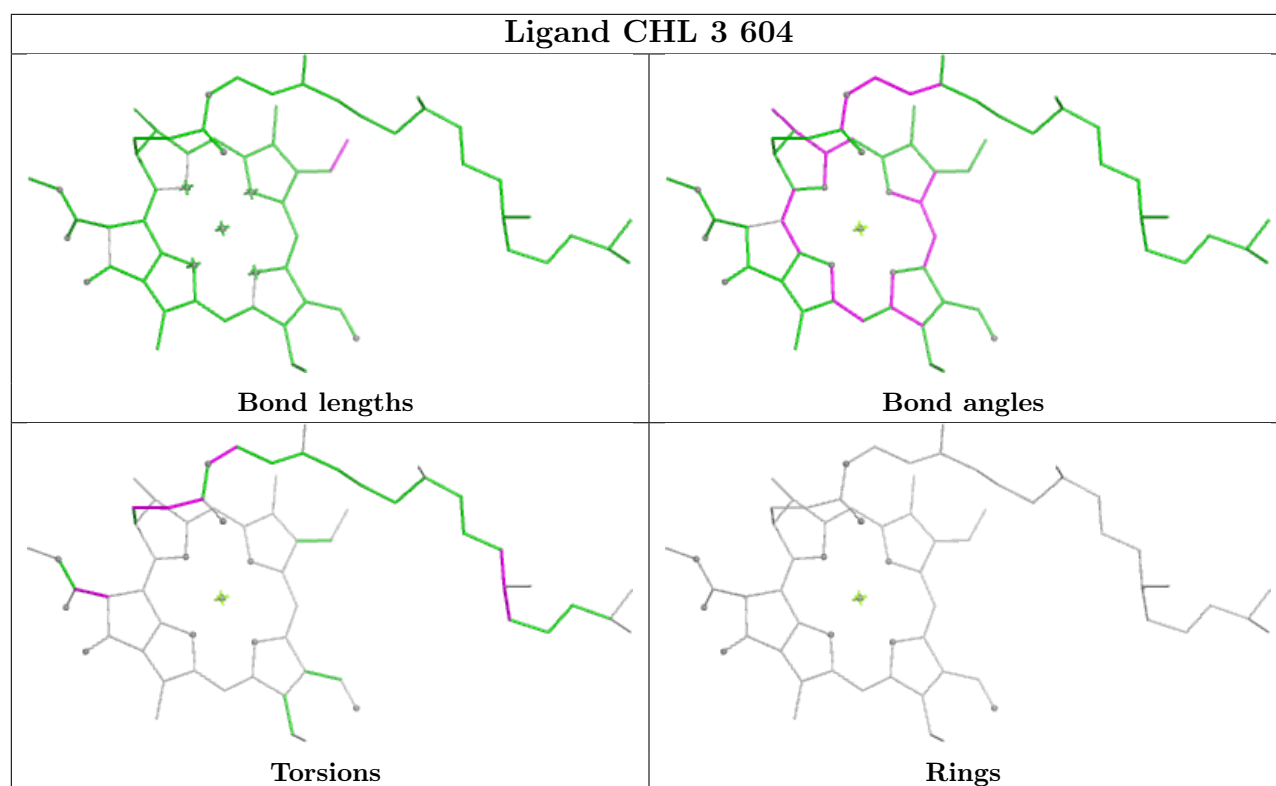


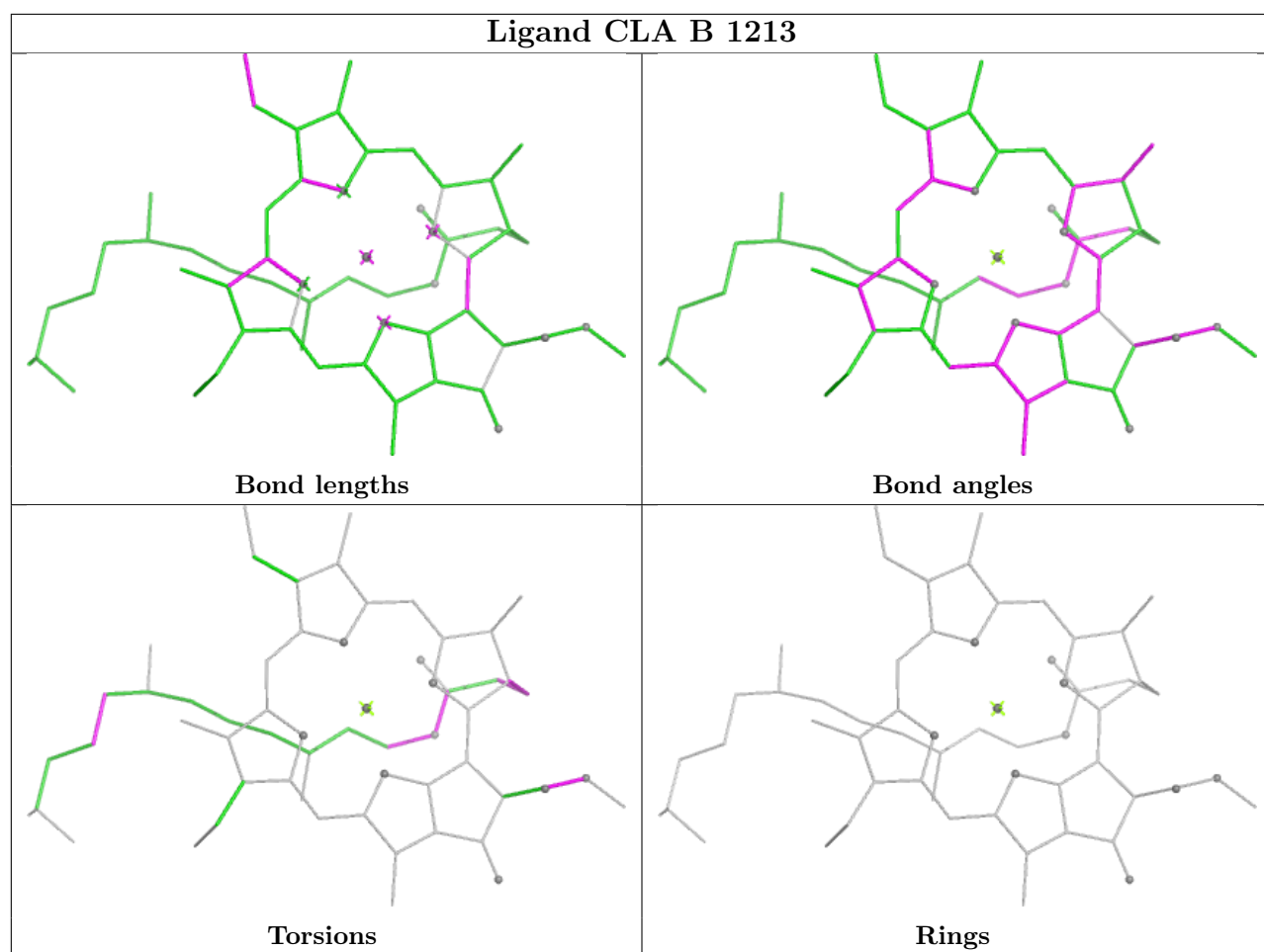
Ligand CLA 2 604

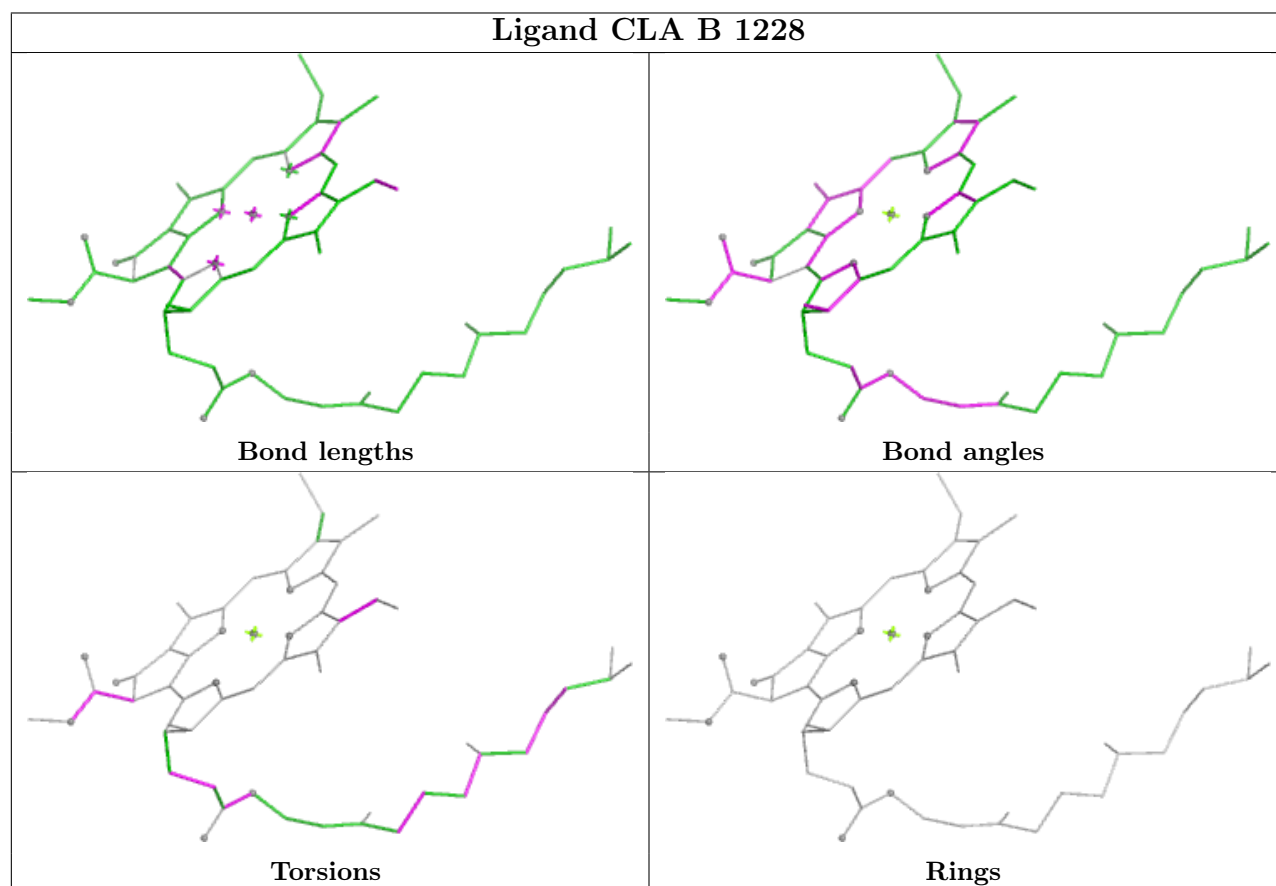
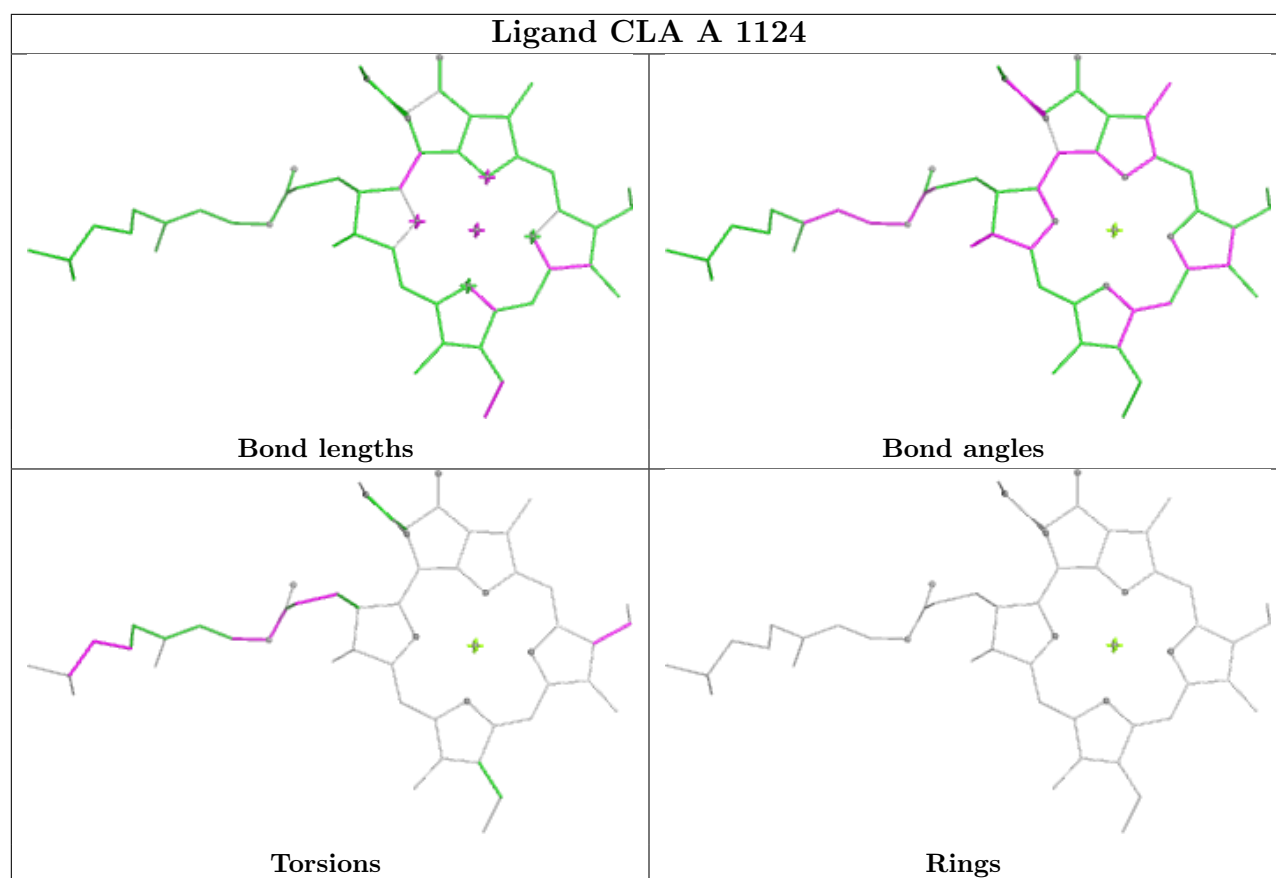


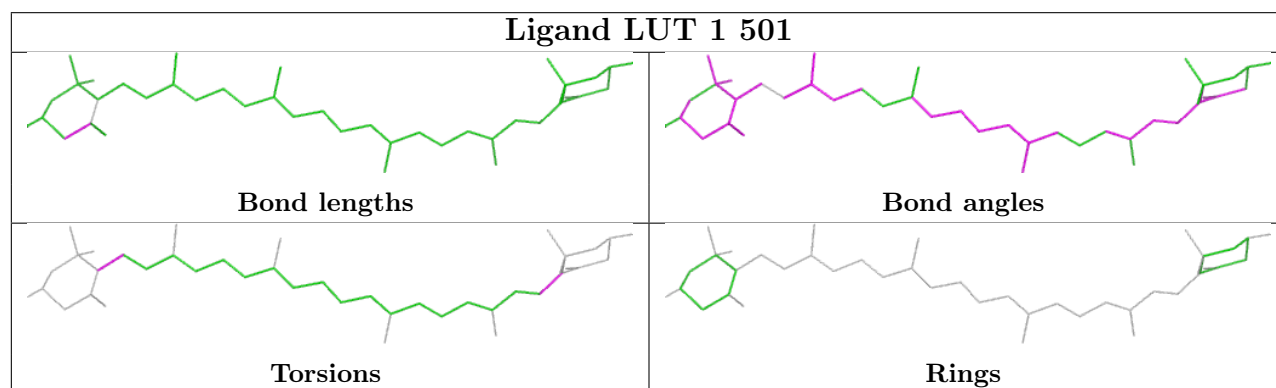
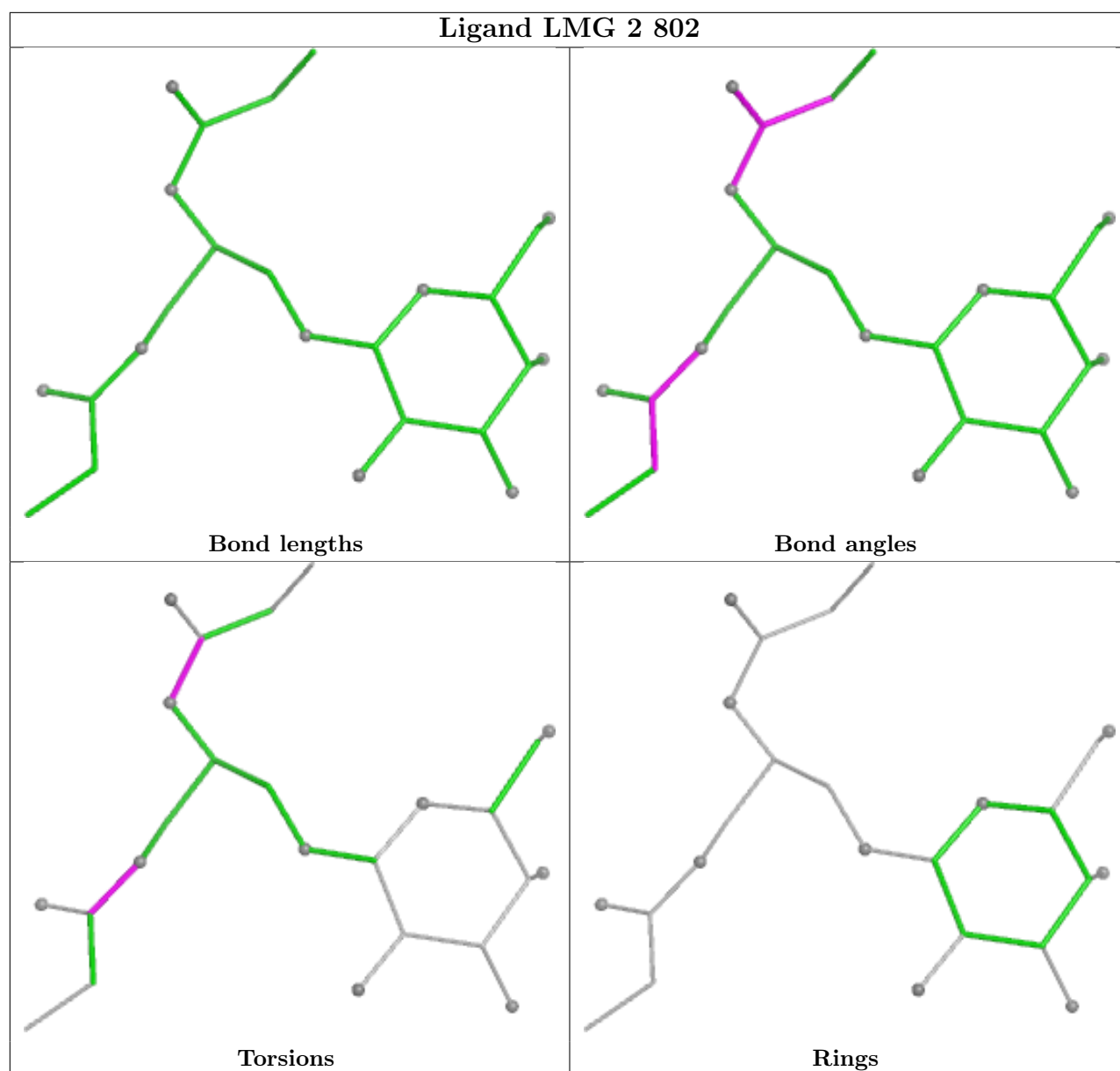


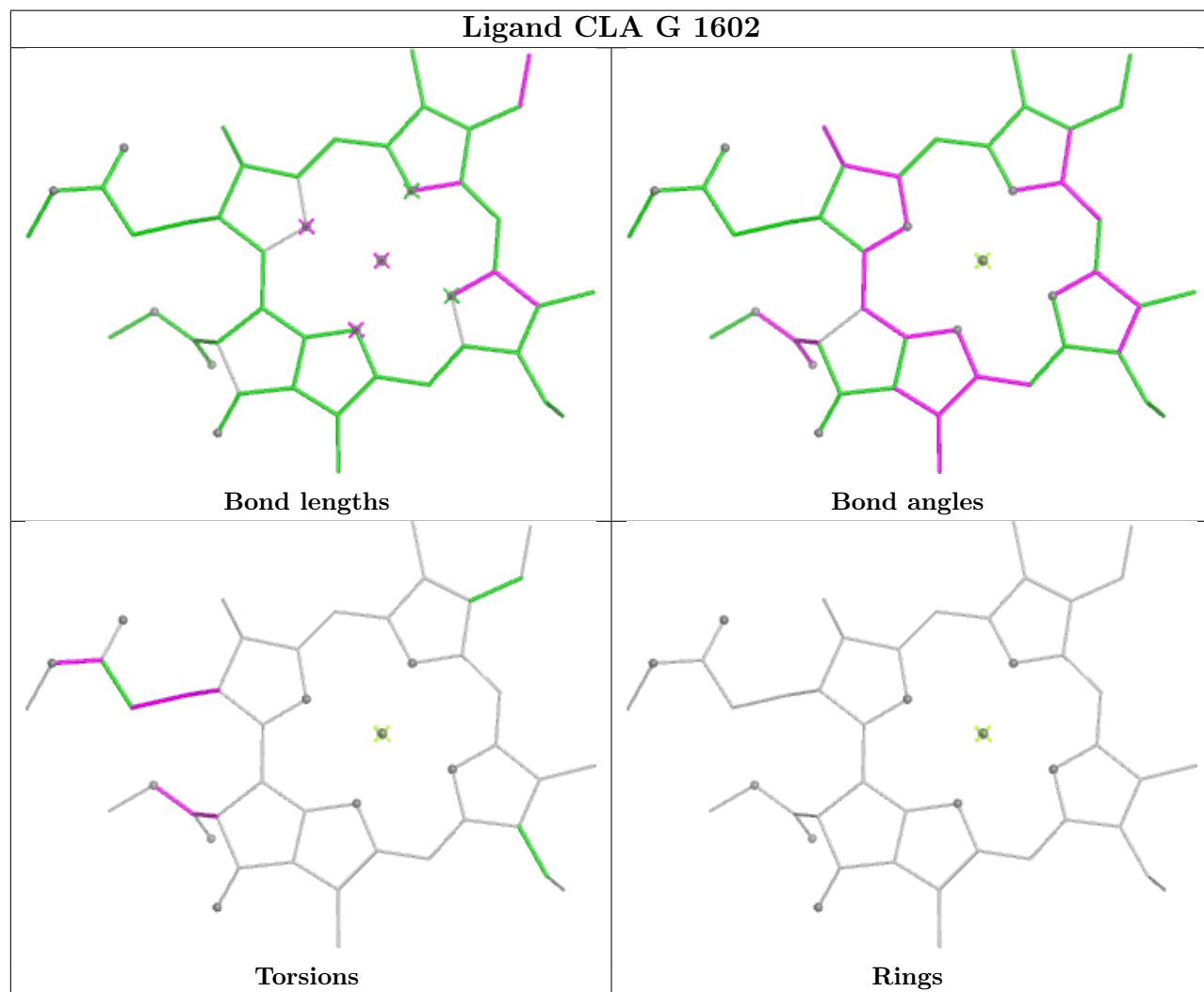
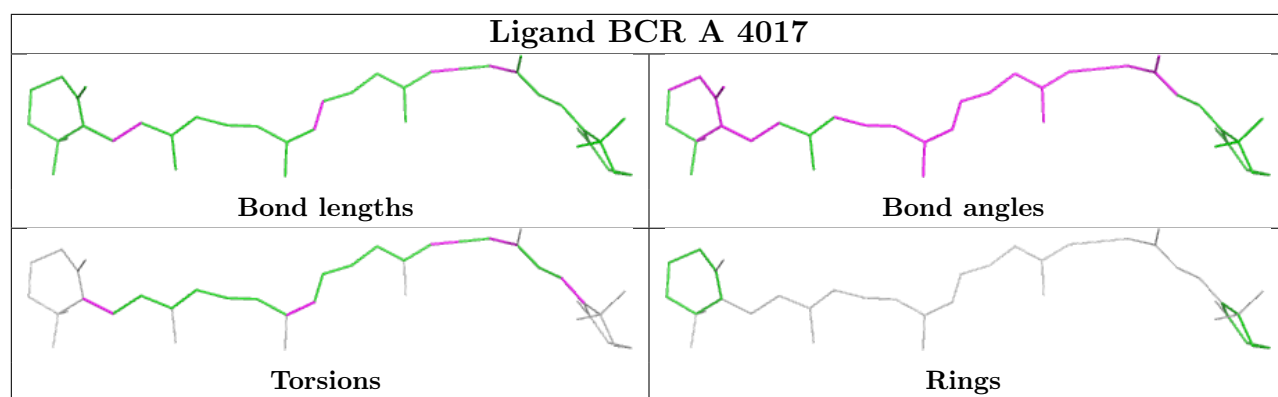


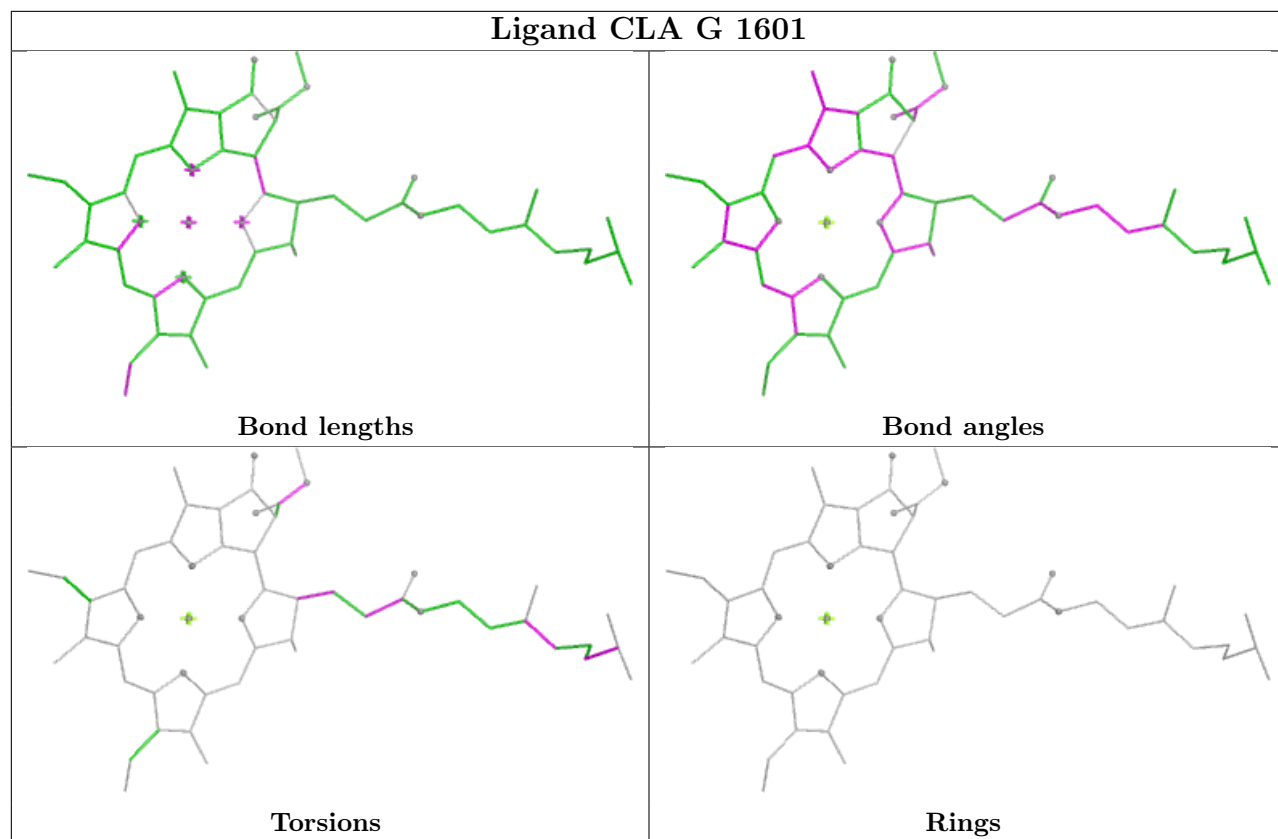




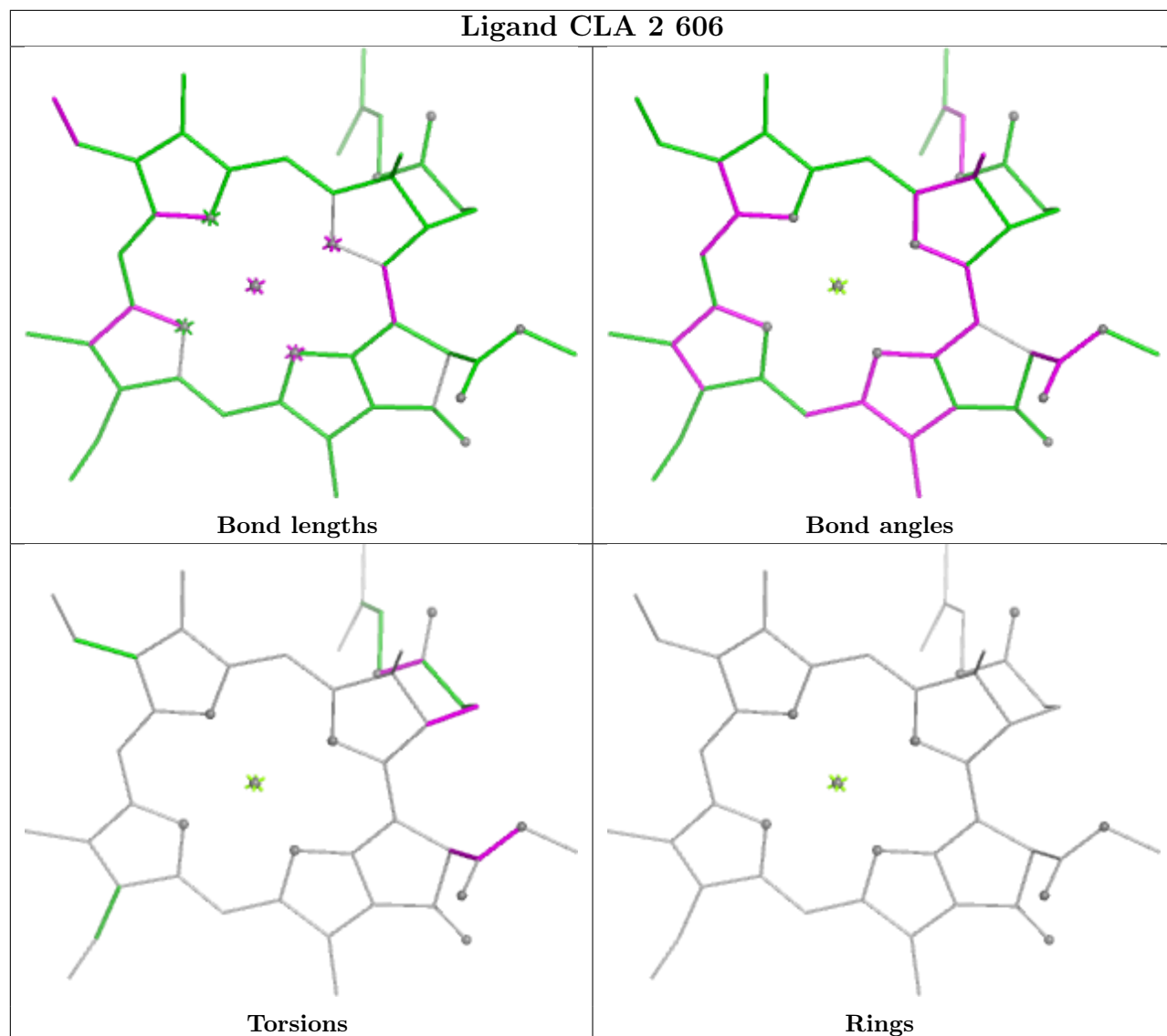


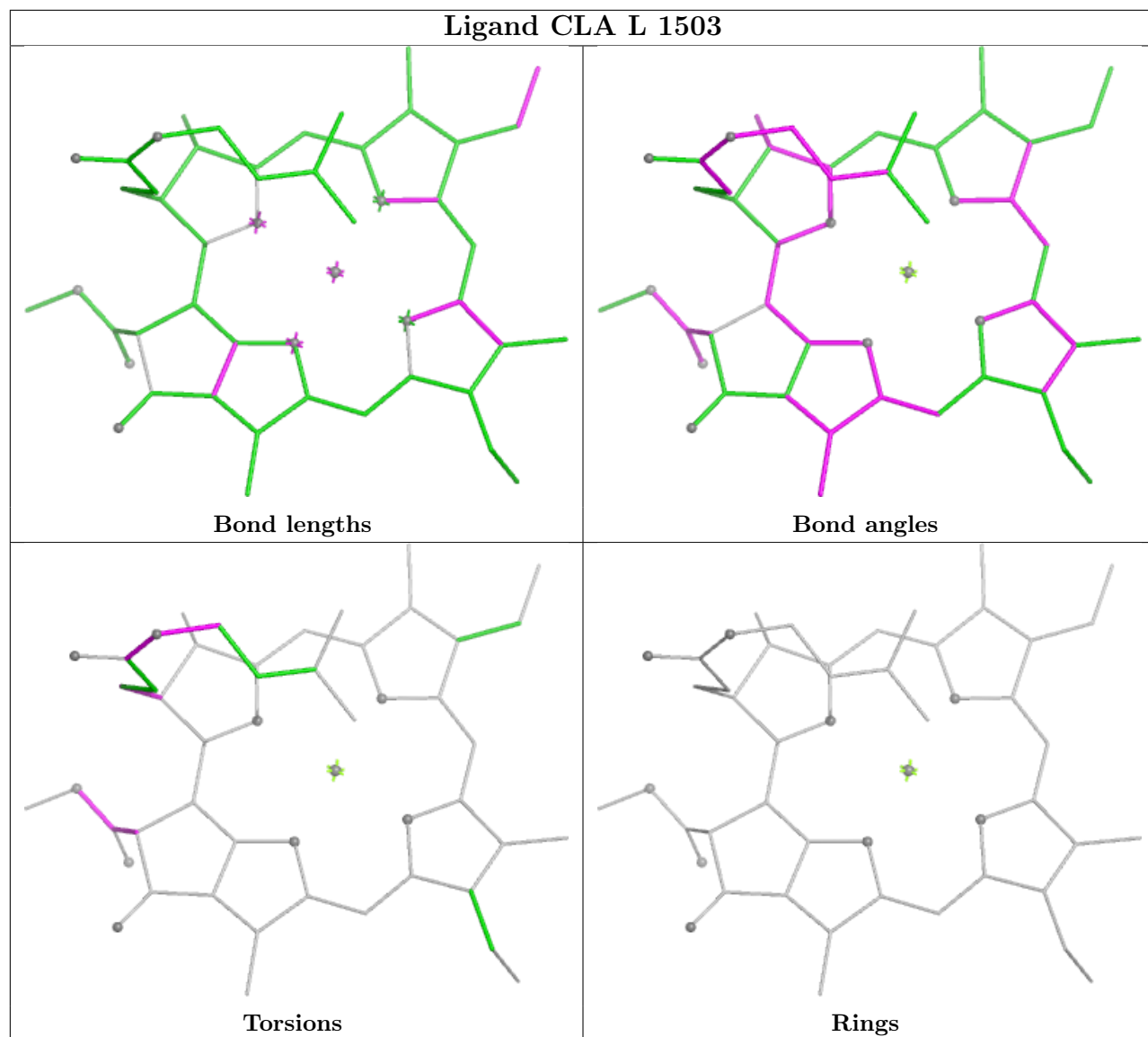


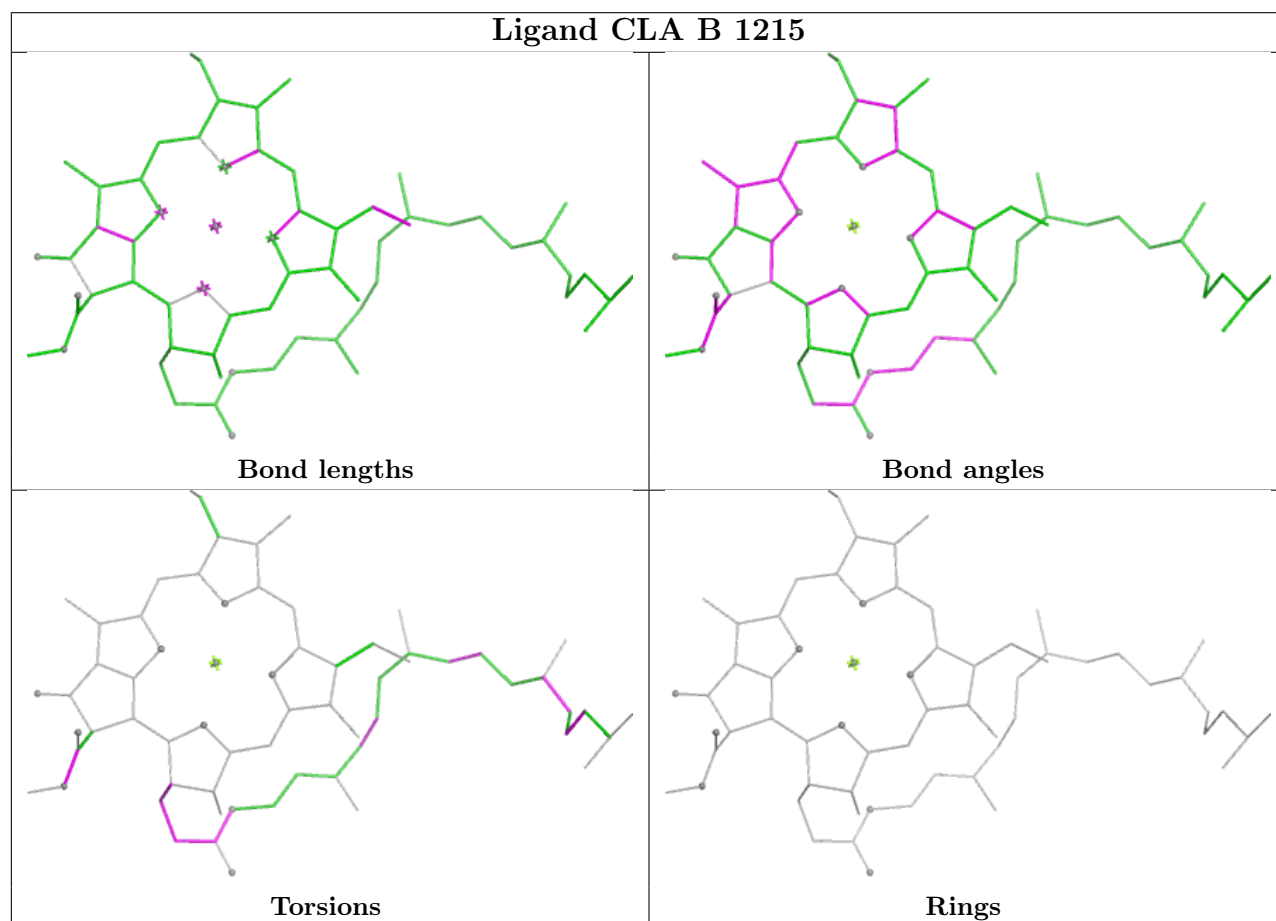
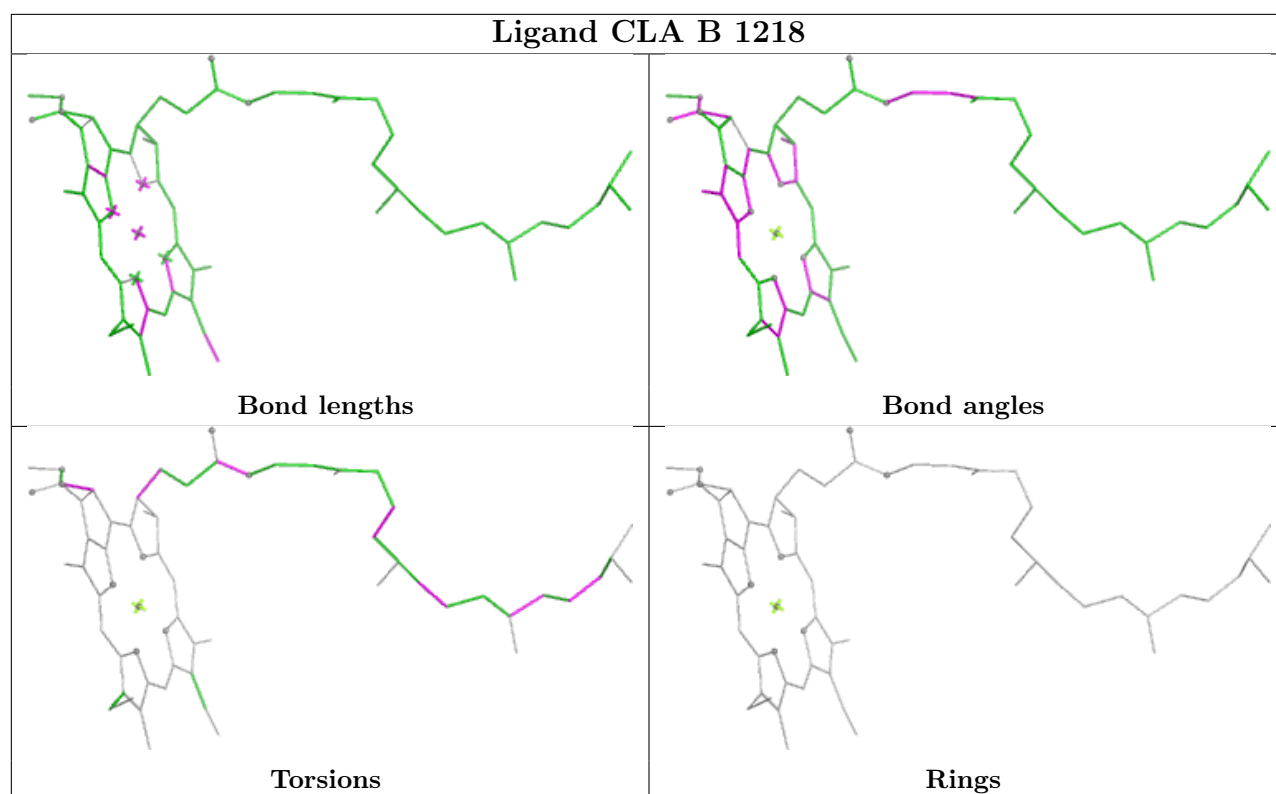


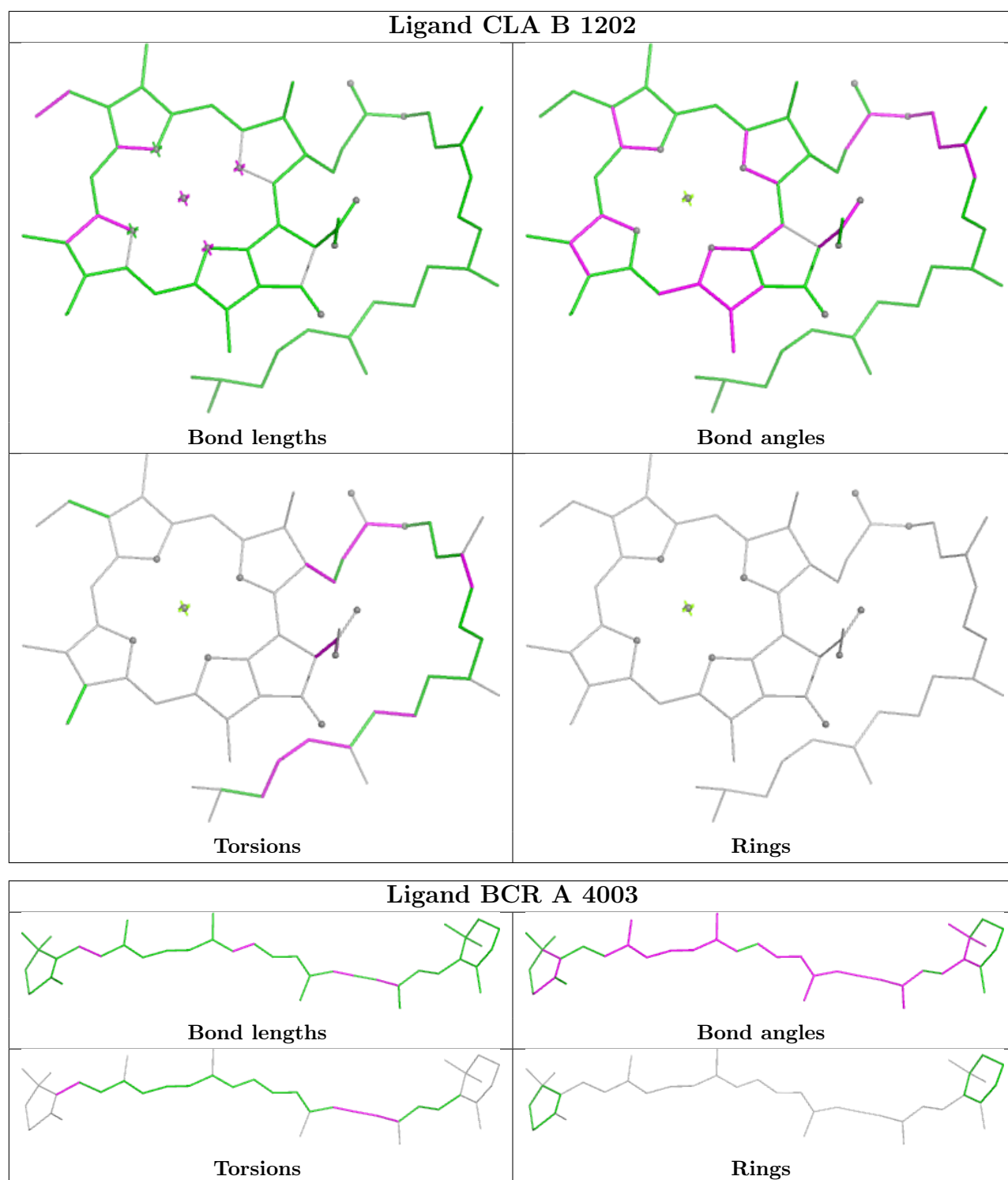


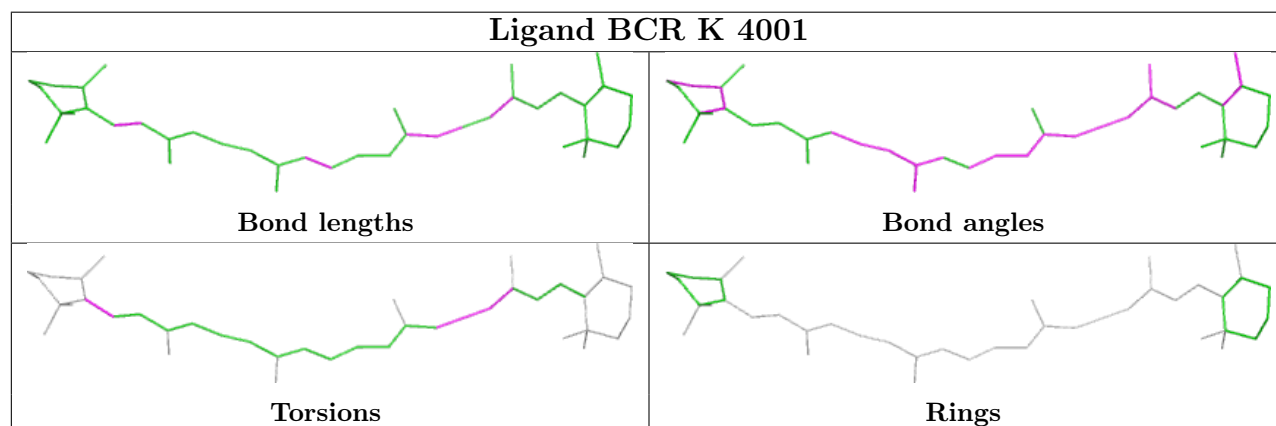
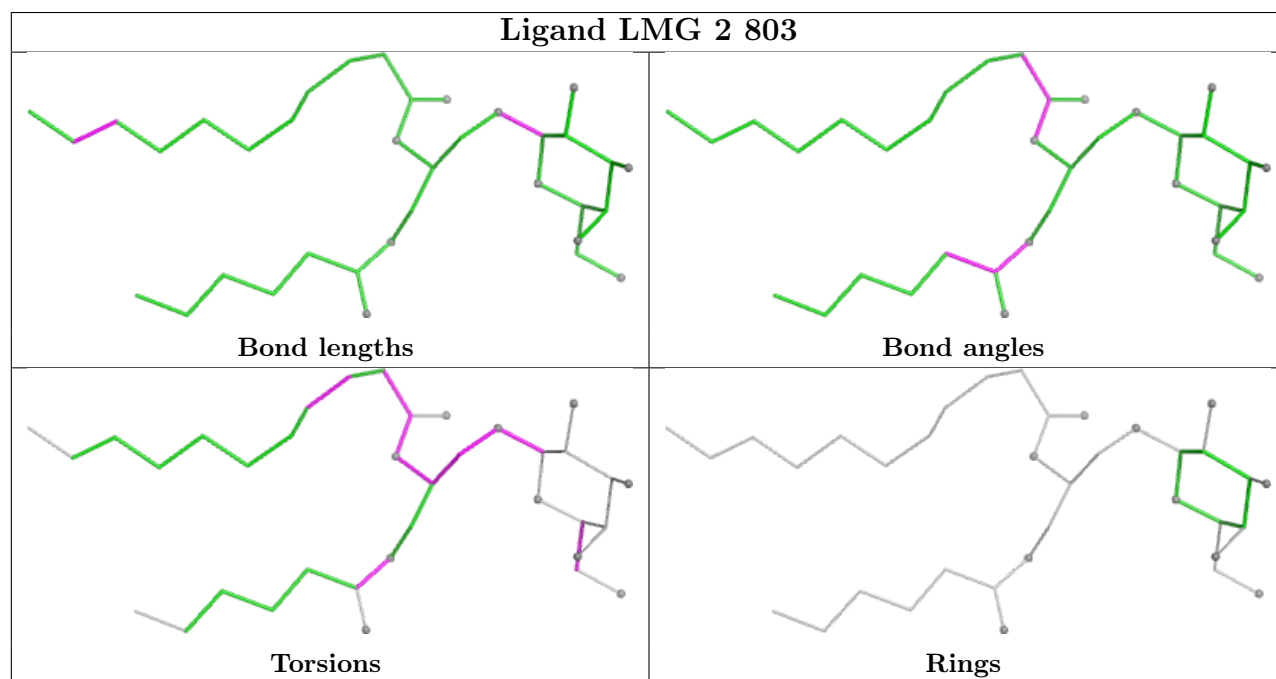
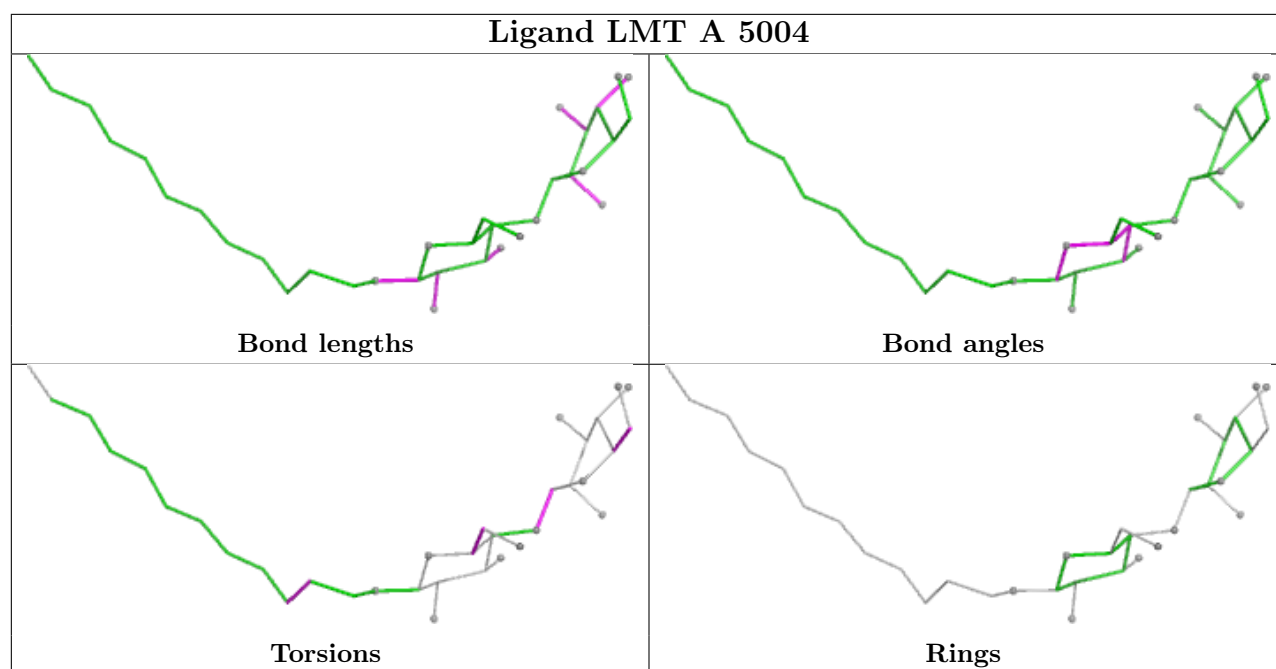
Ligand CLA 2 606

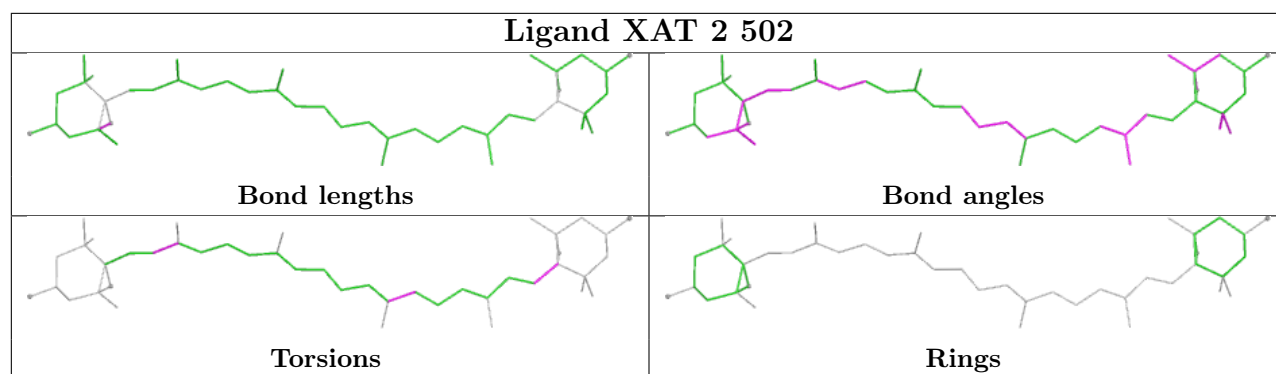
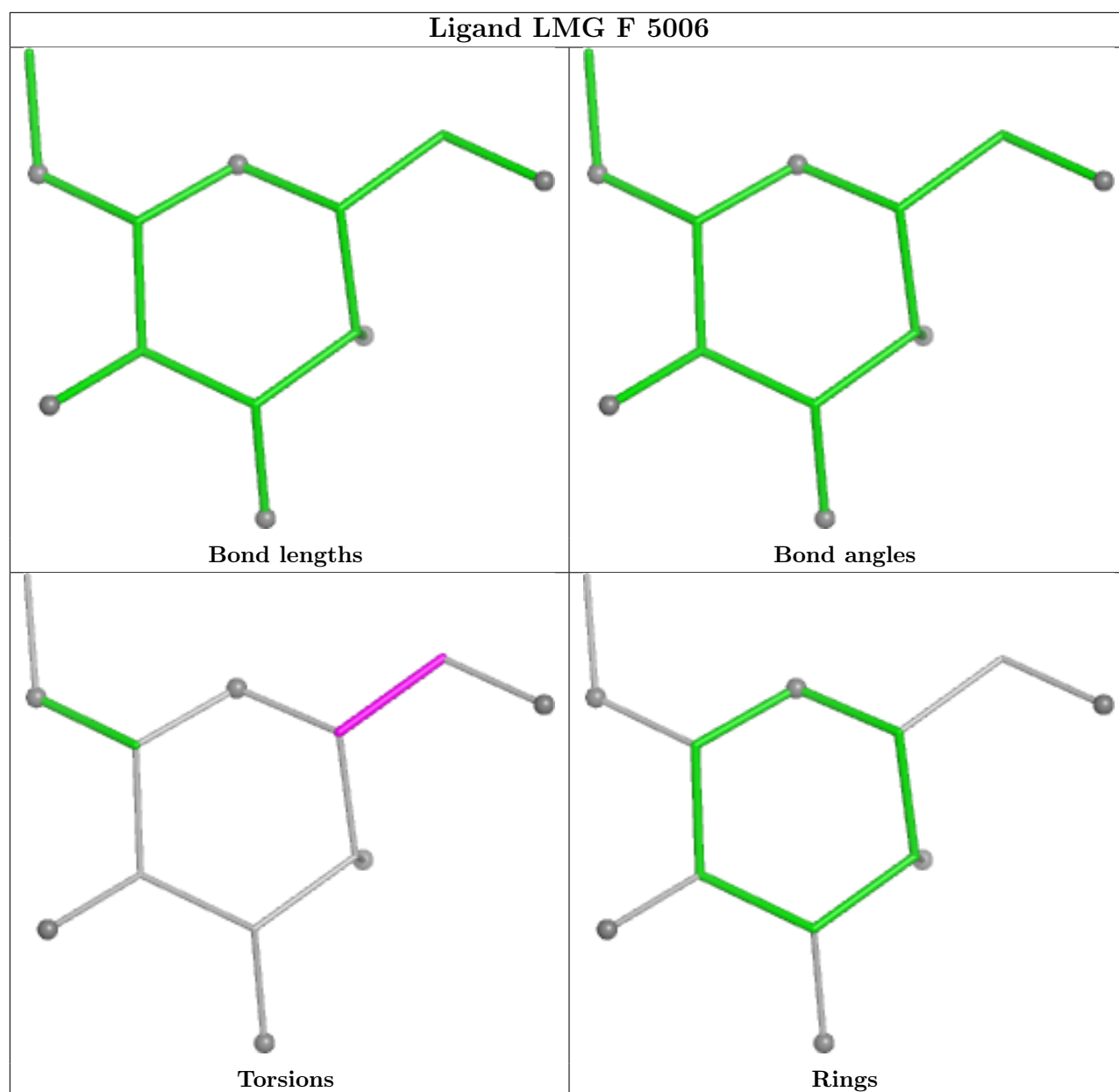


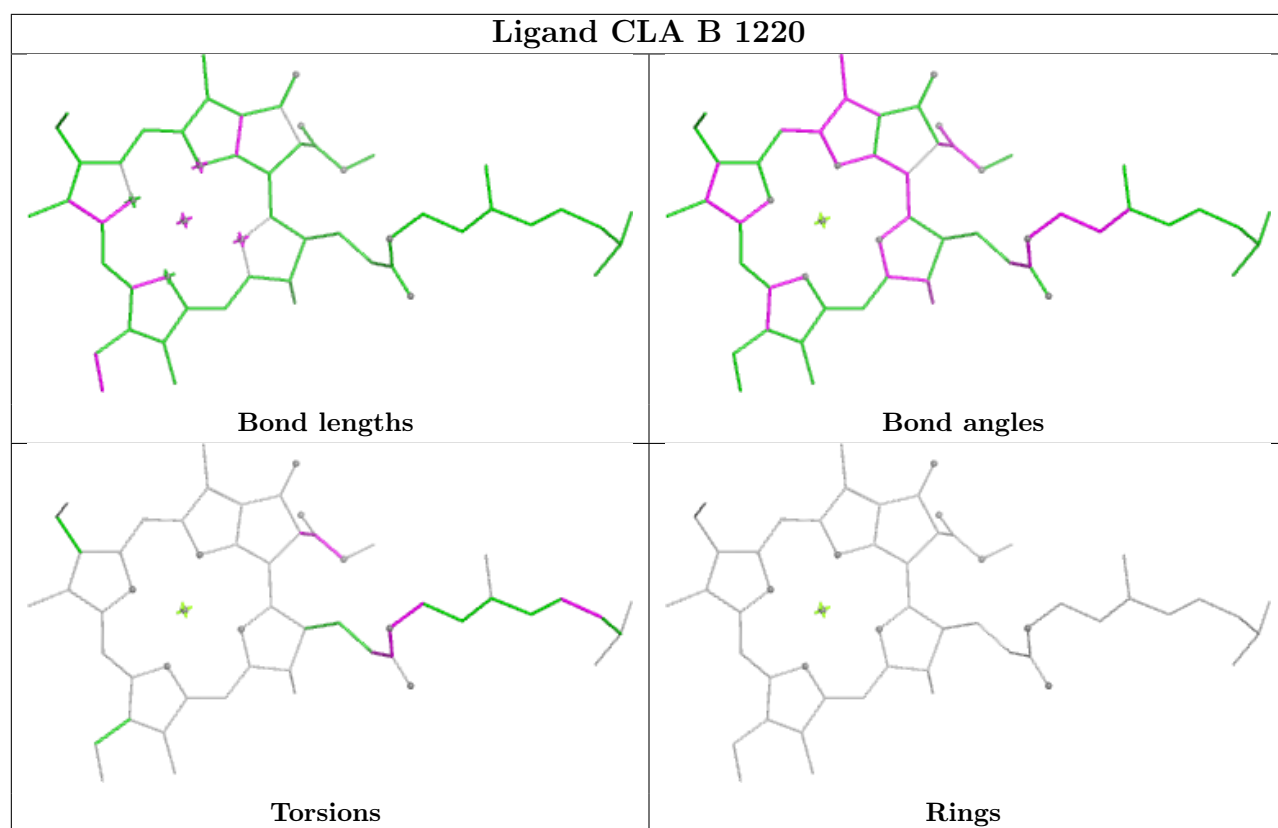




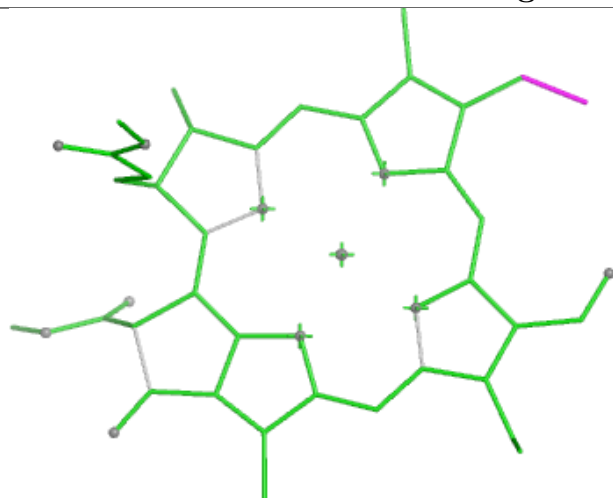




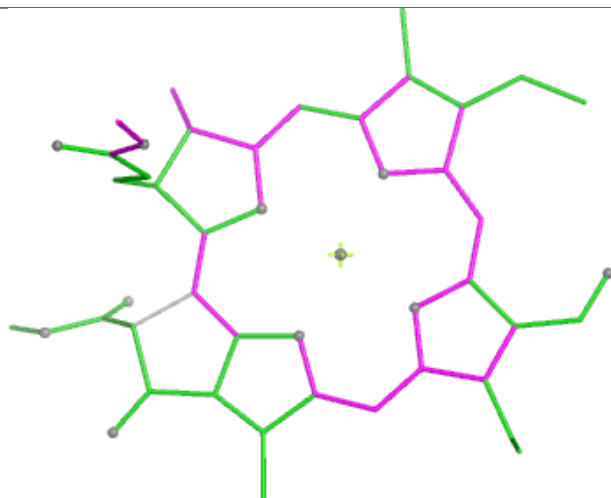




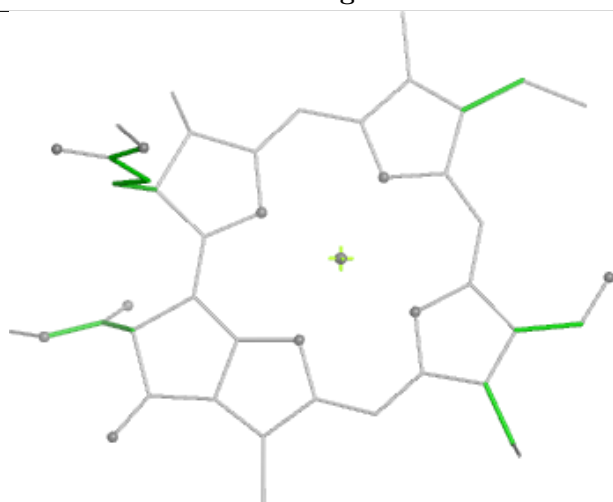
Ligand CHL 3 611



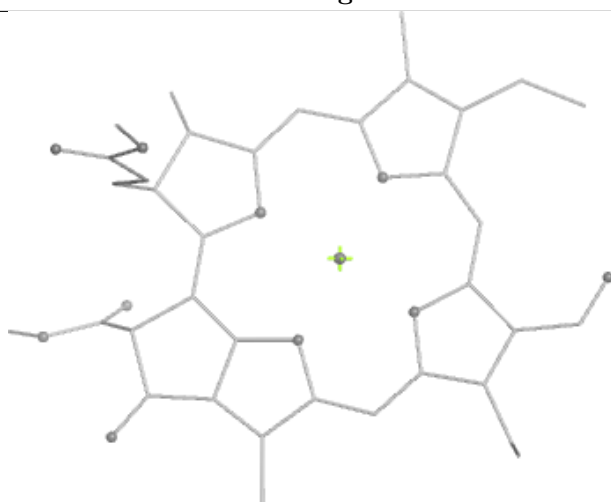
Bond lengths



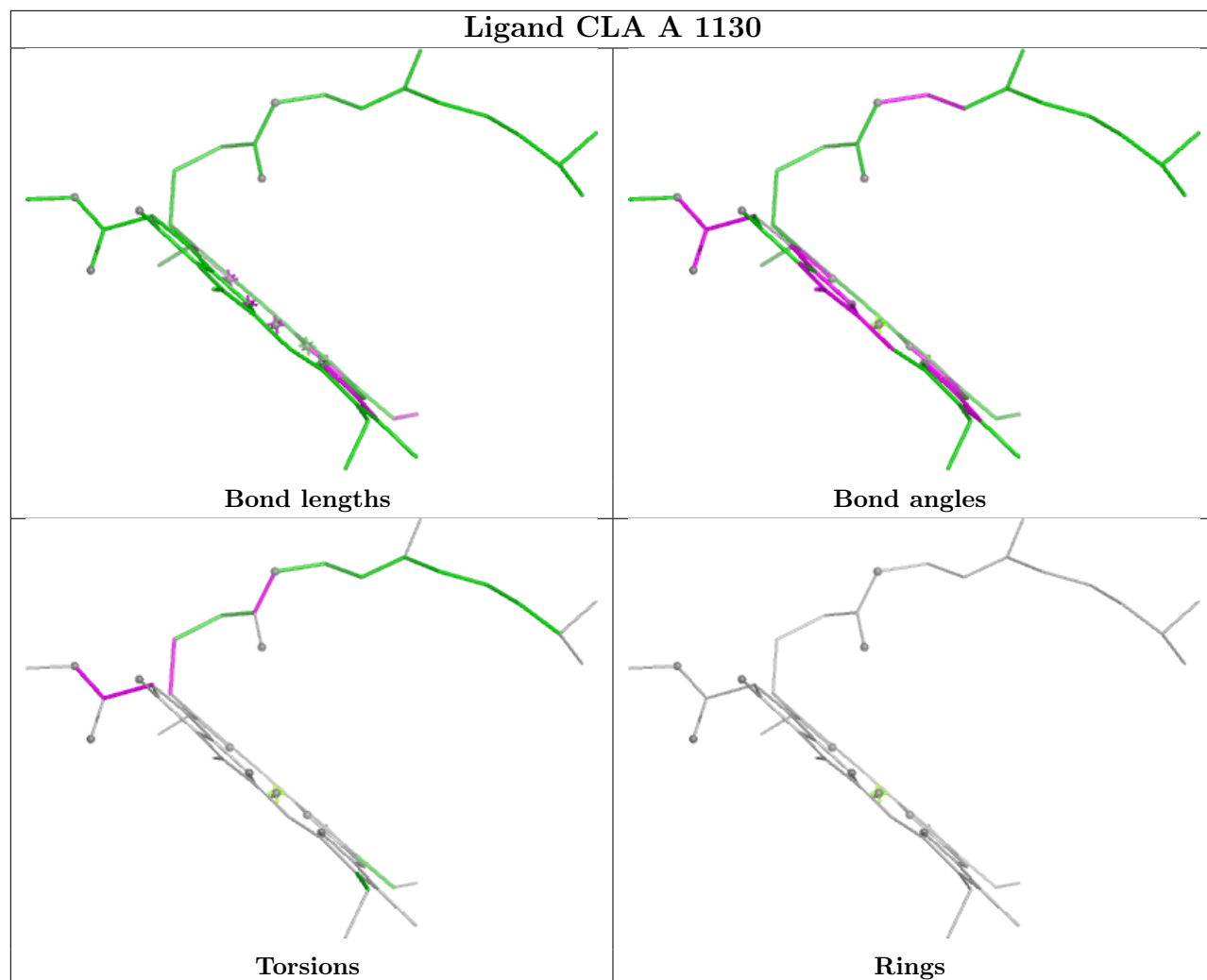
Bond angles

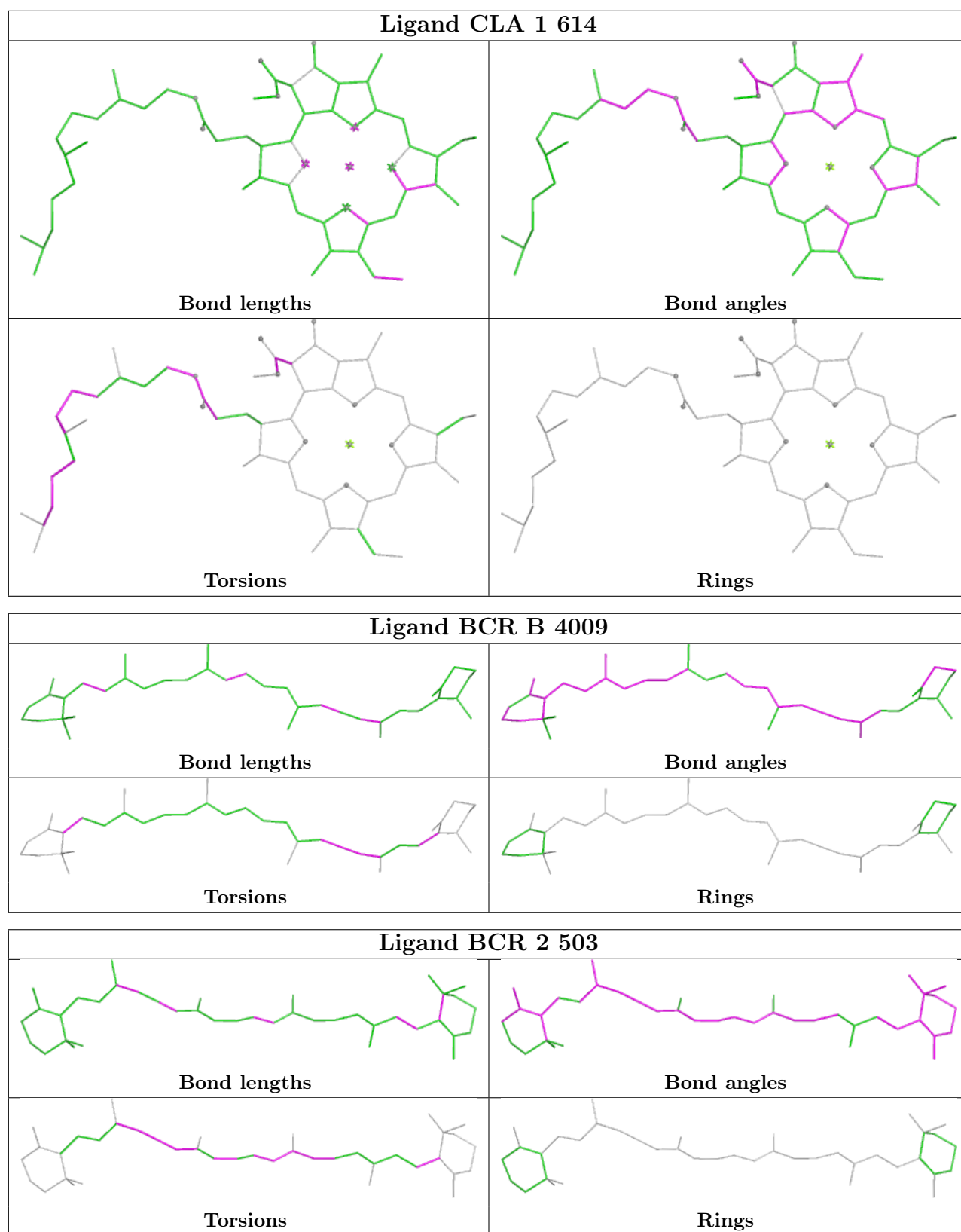


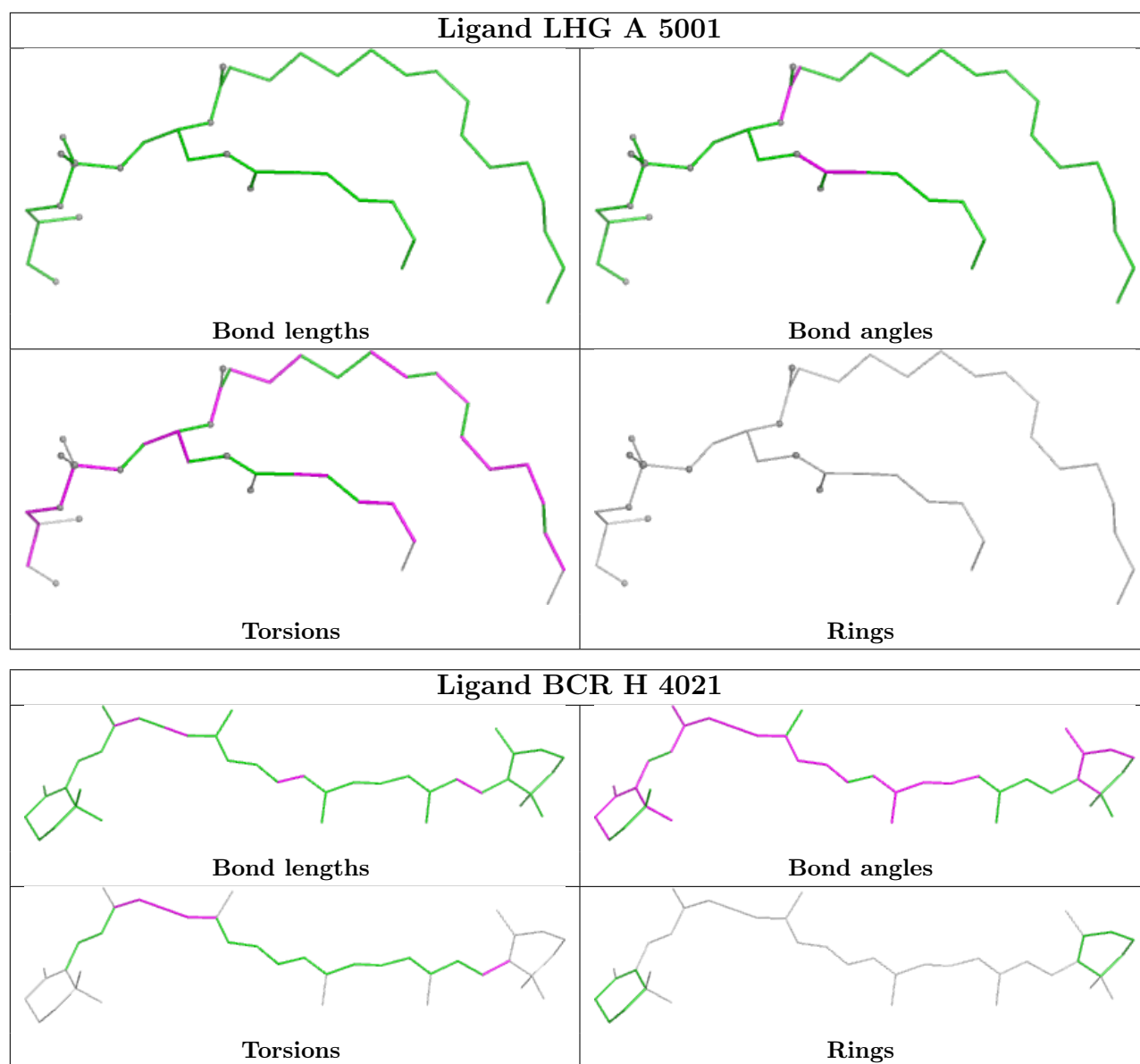
Torsions

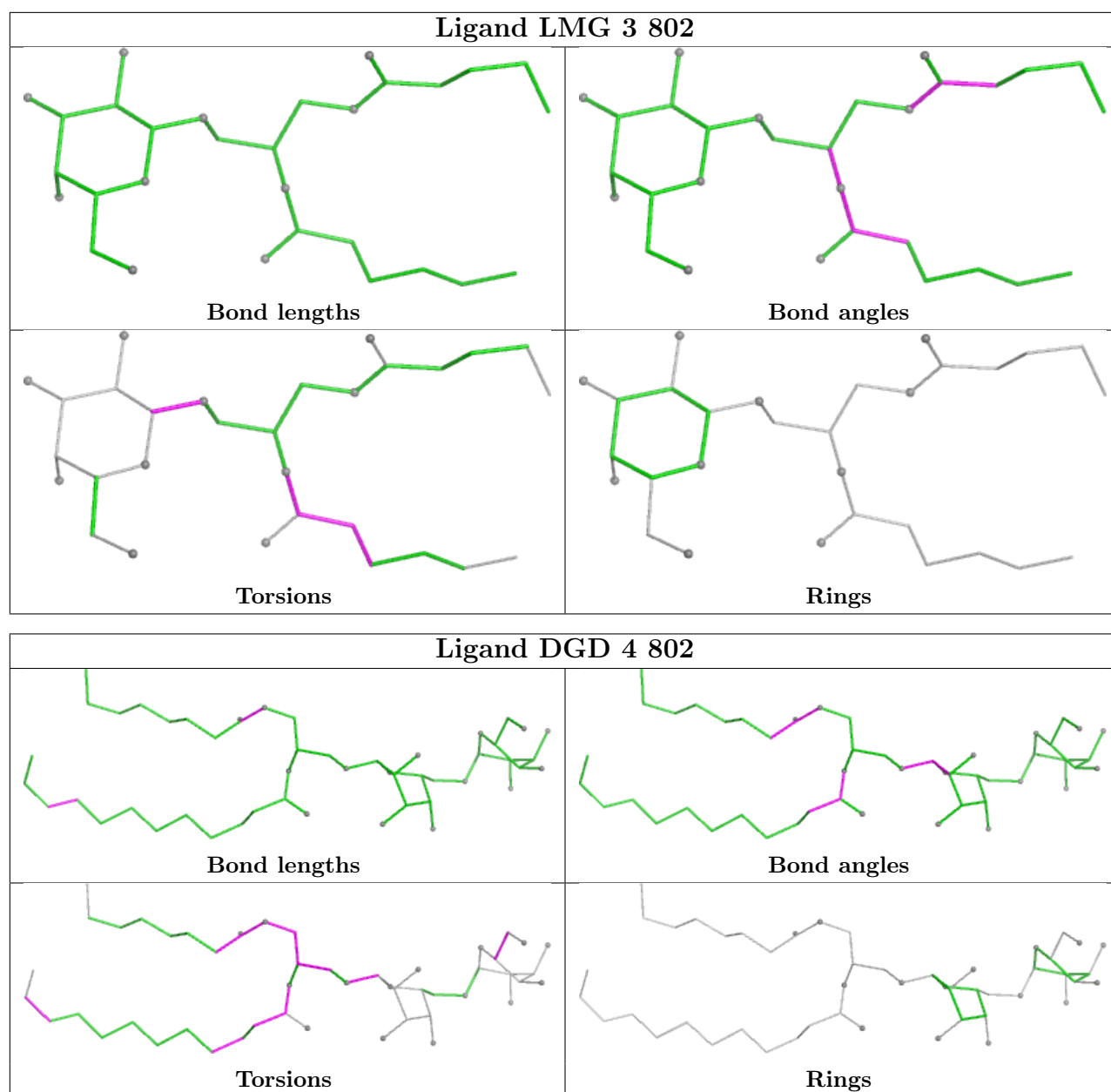


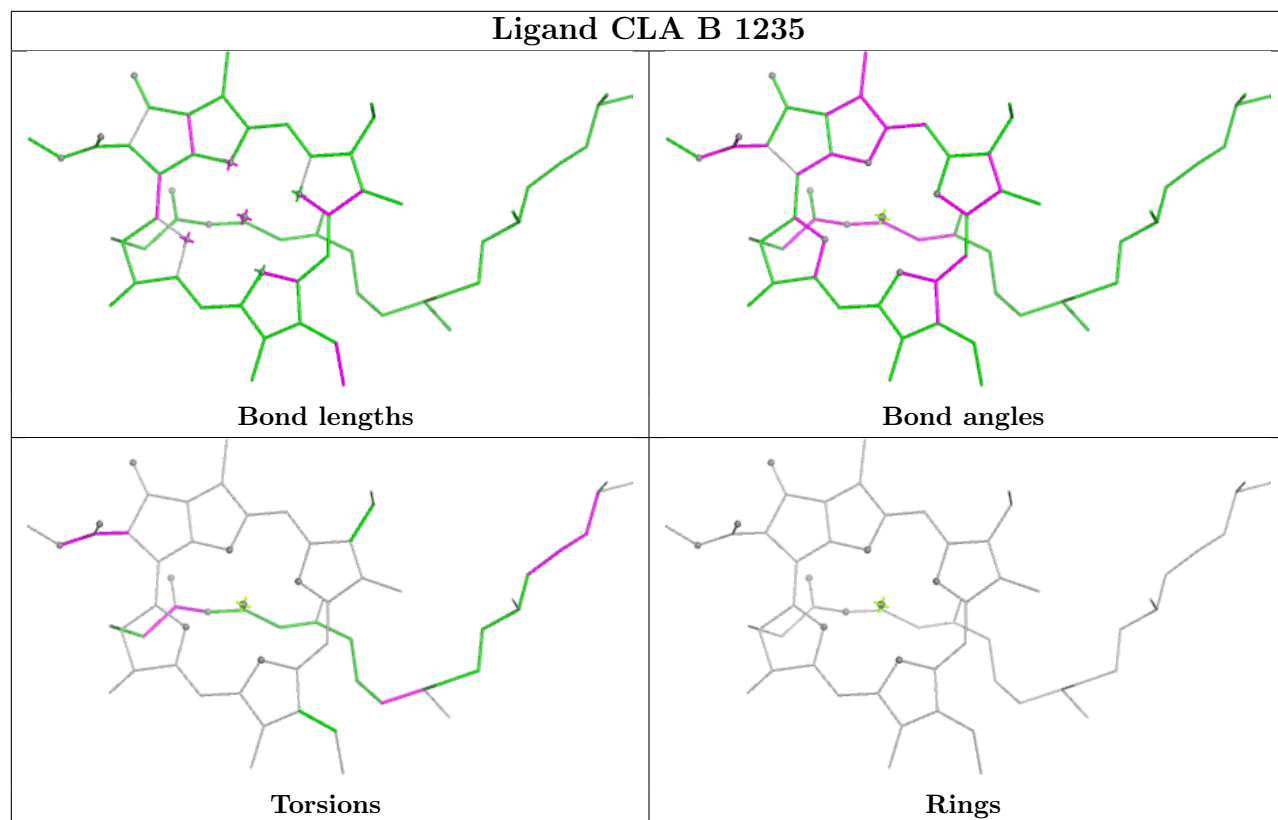
Rings



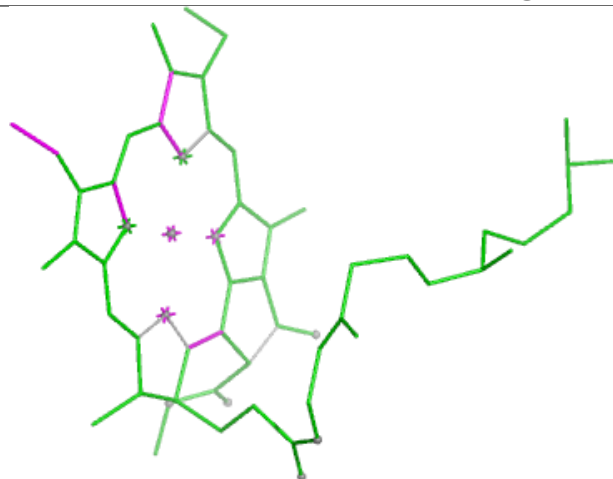




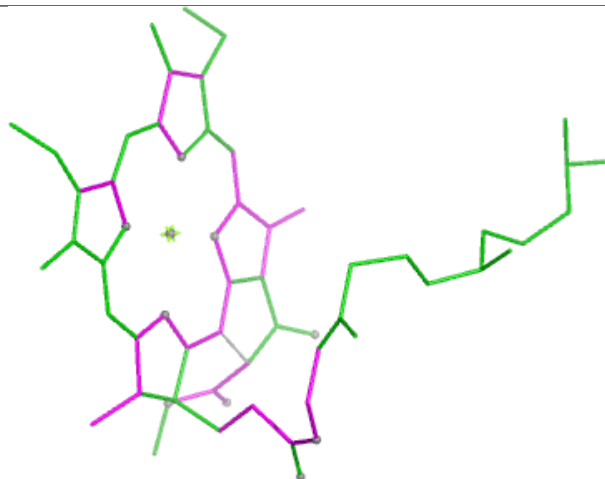




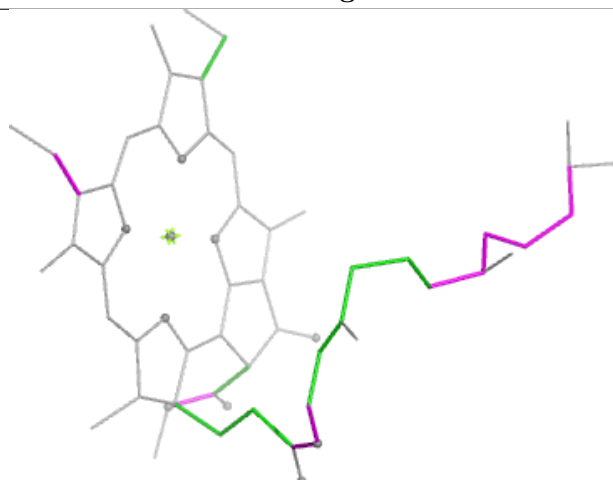
Ligand CLA 2 607



Bond lengths



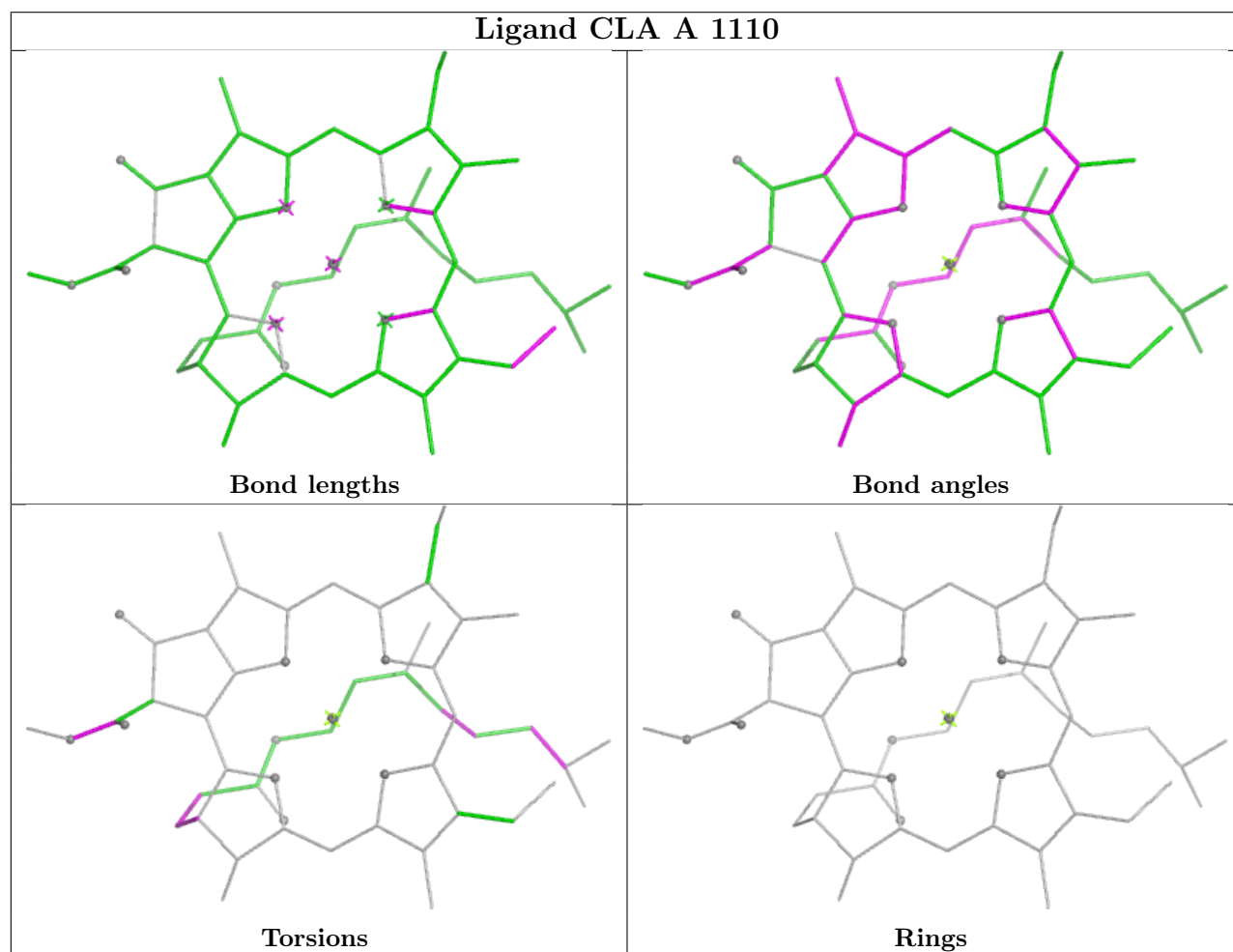
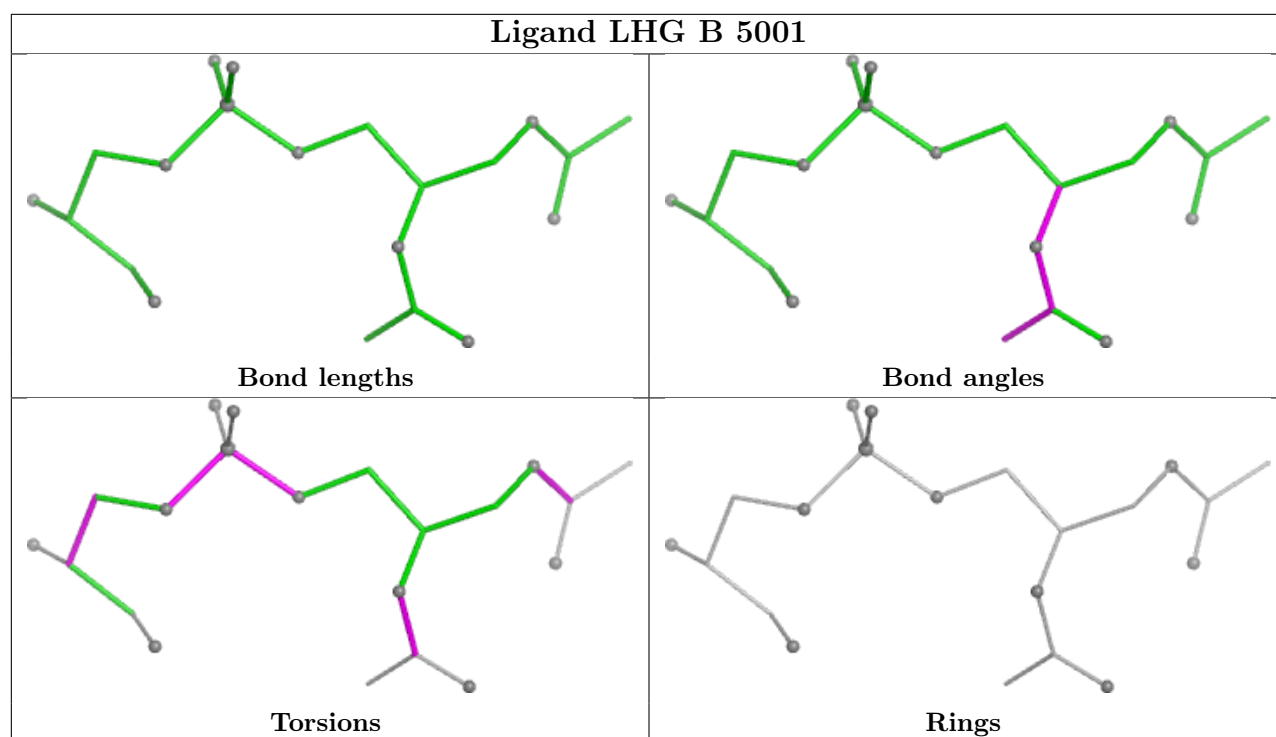
Bond angles

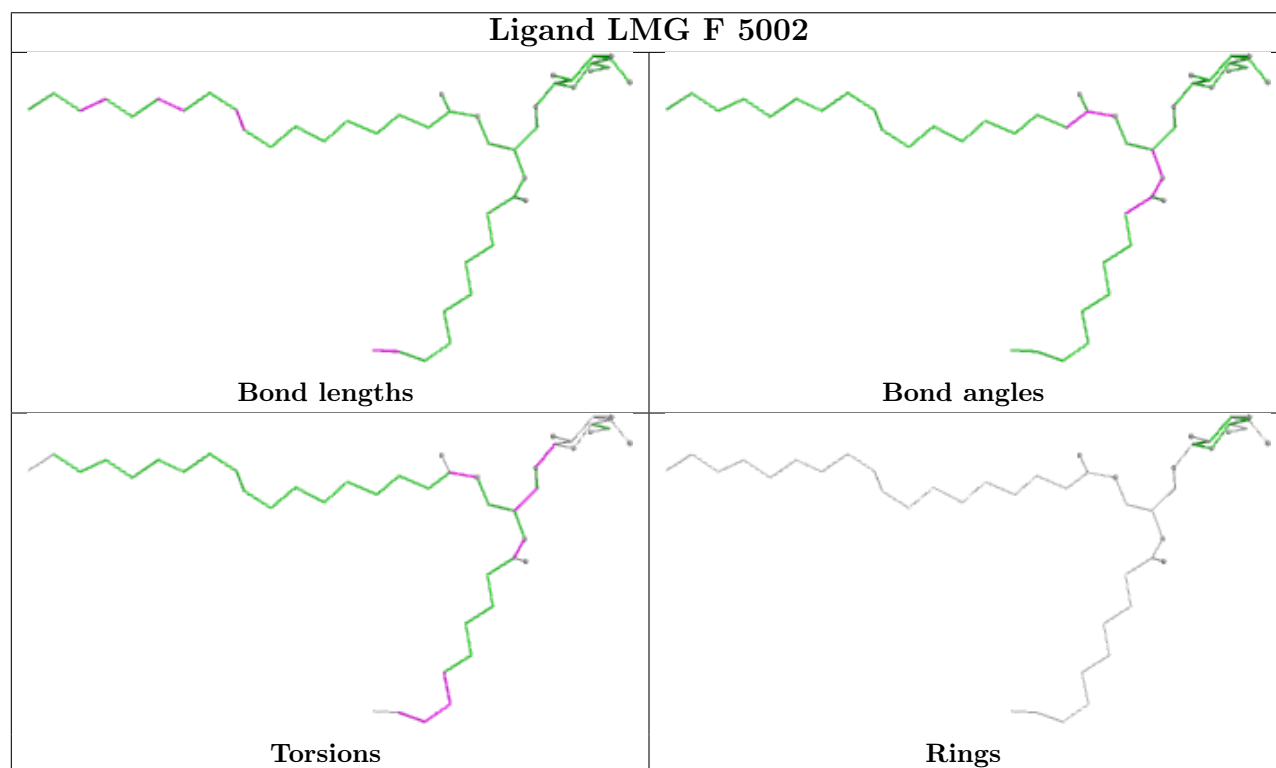
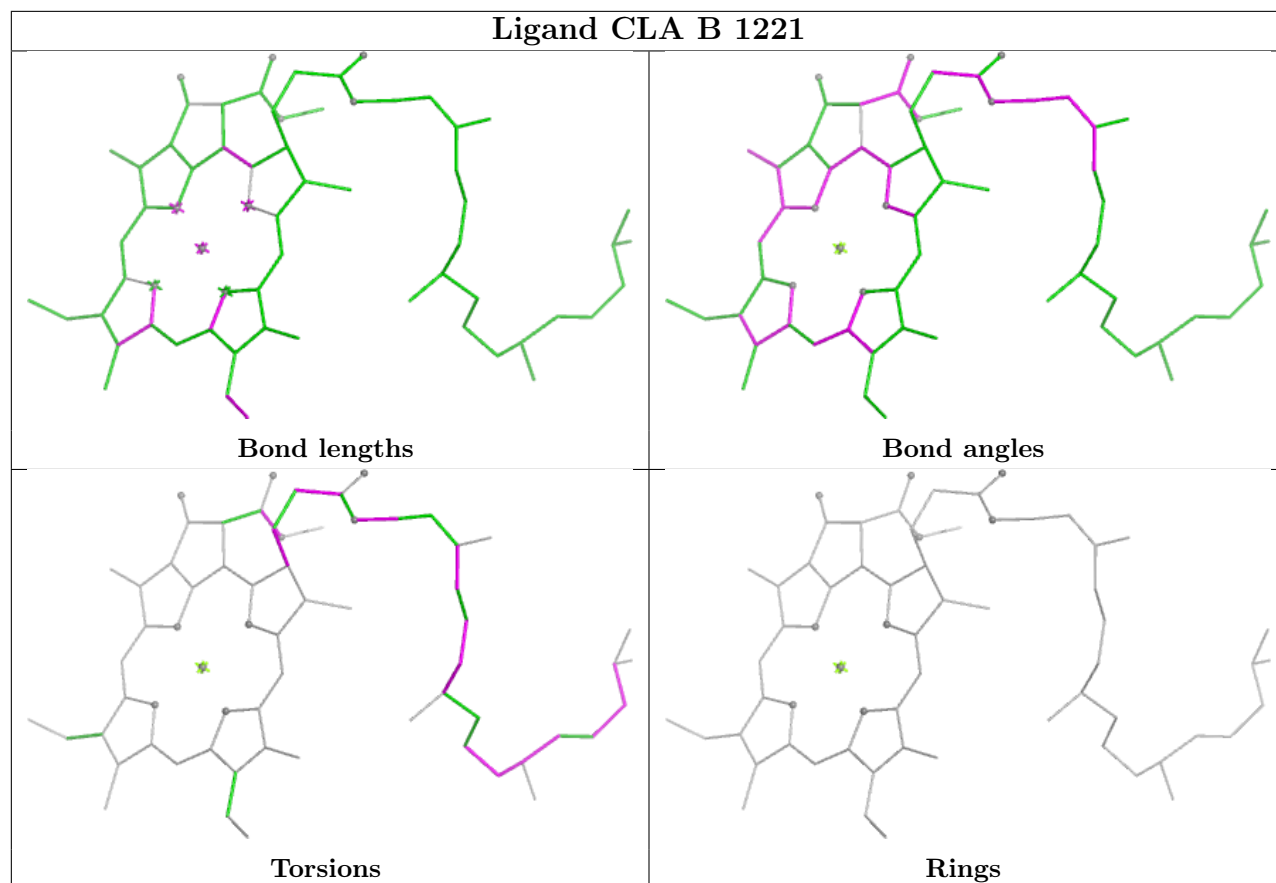


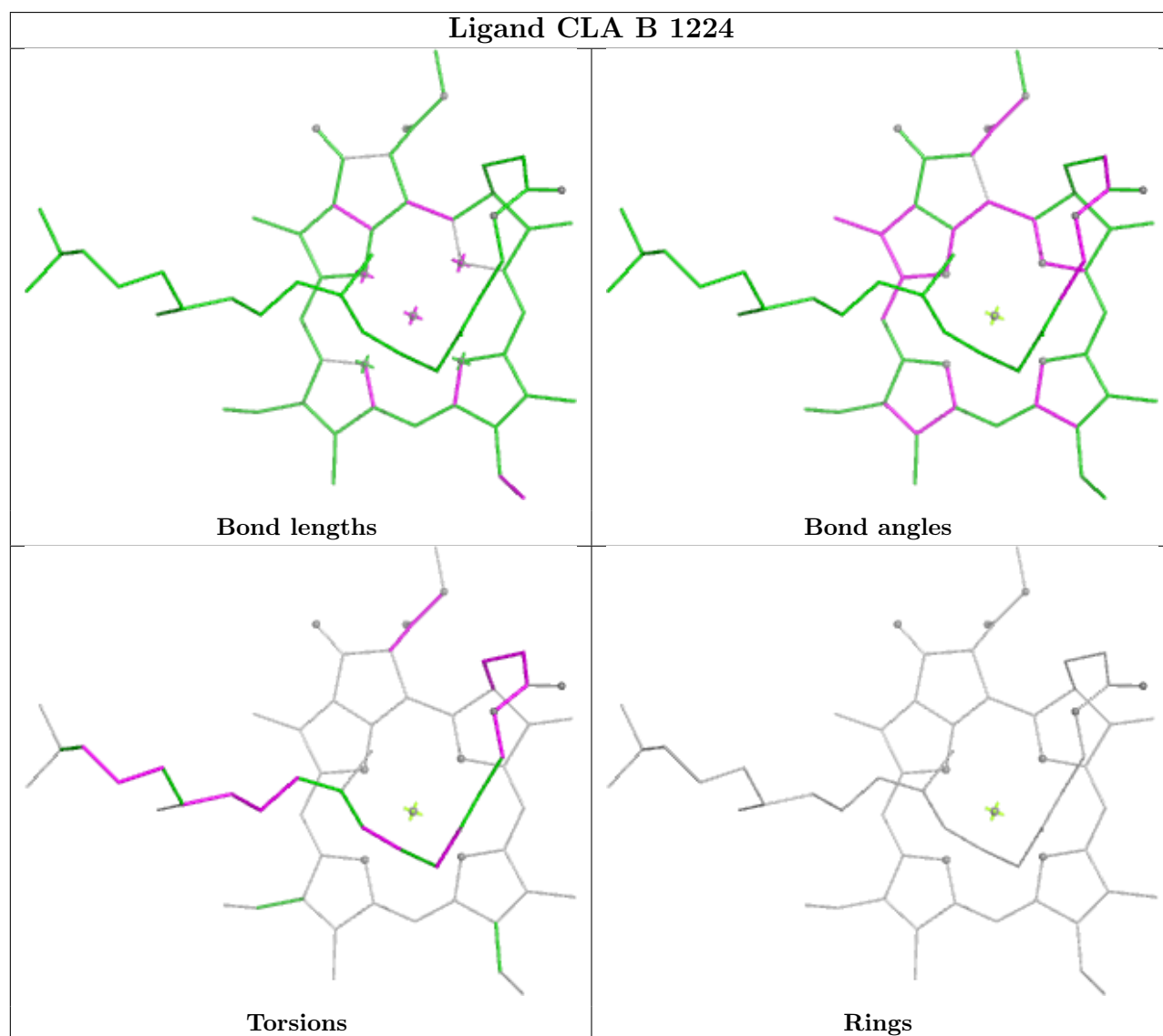
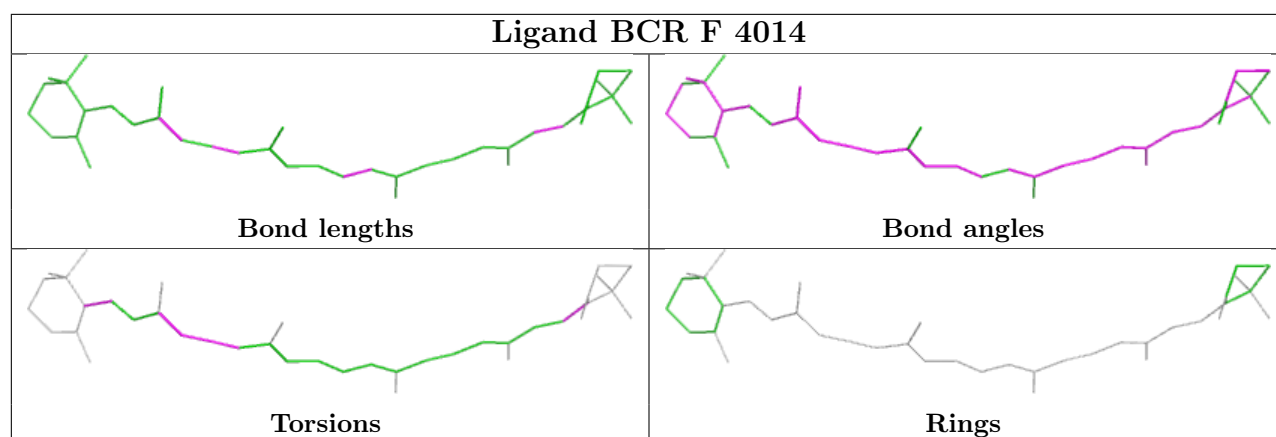
Torsions



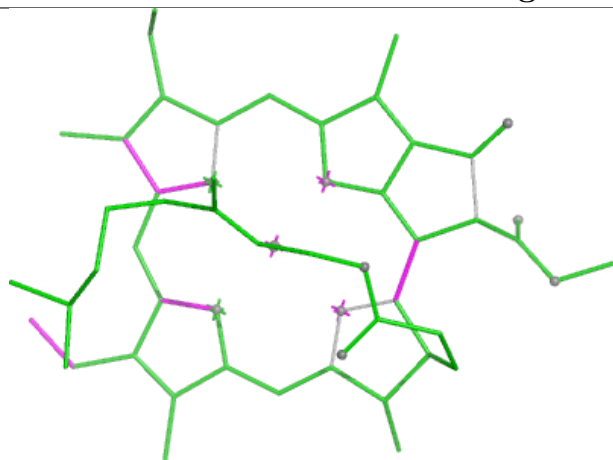
Rings



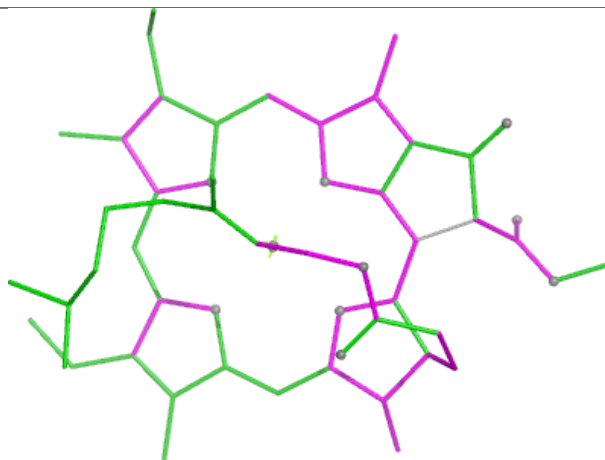




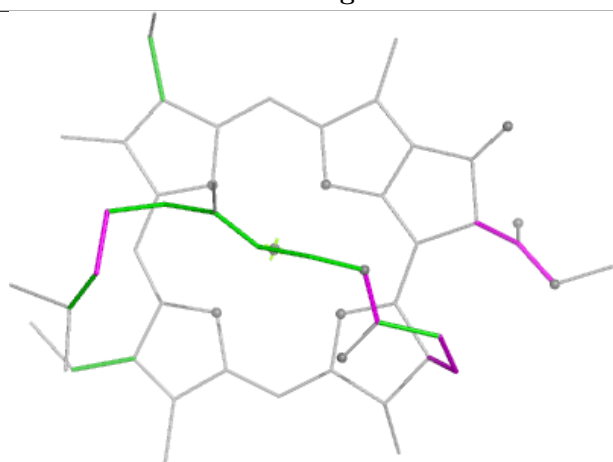
Ligand CLA 1 603



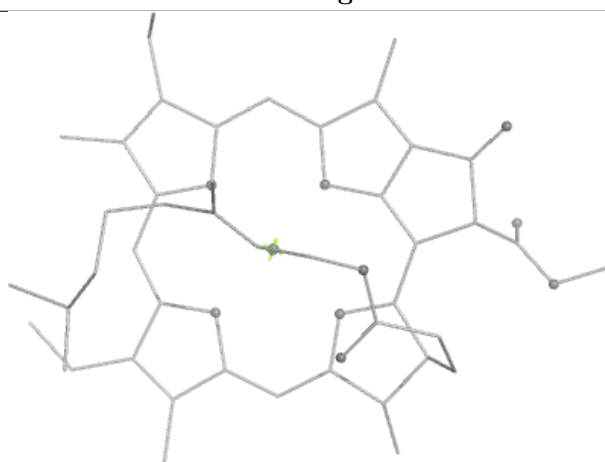
Bond lengths



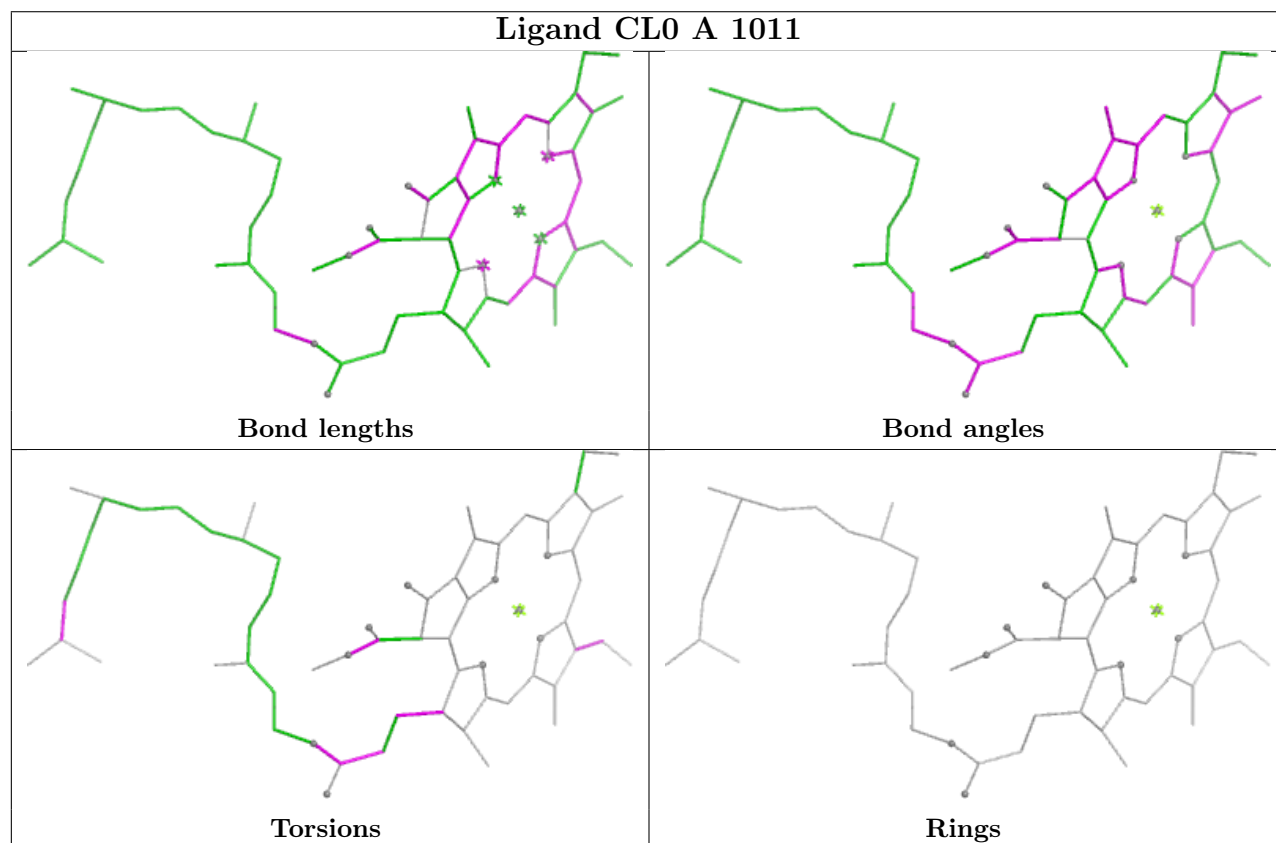
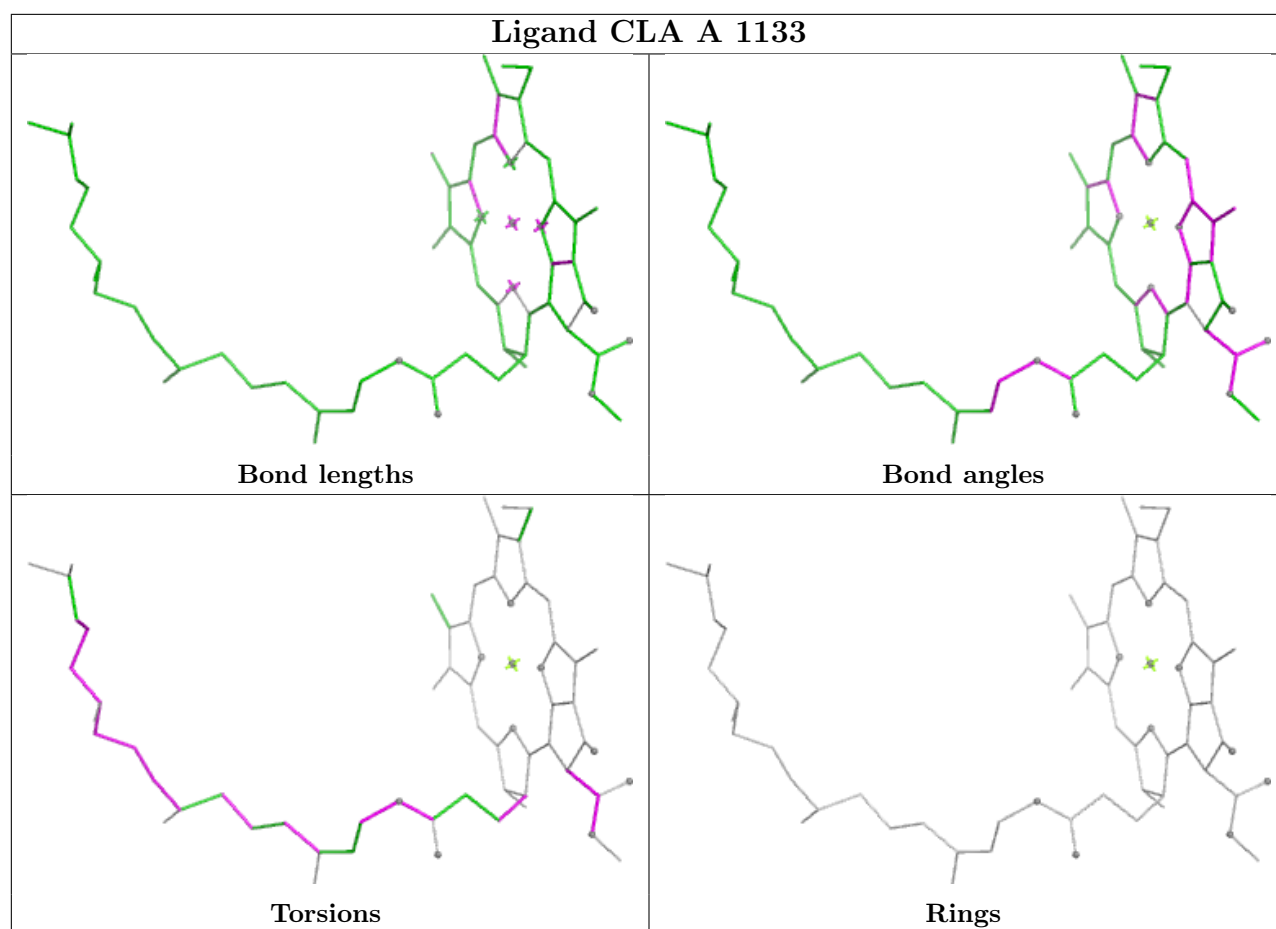
Bond angles

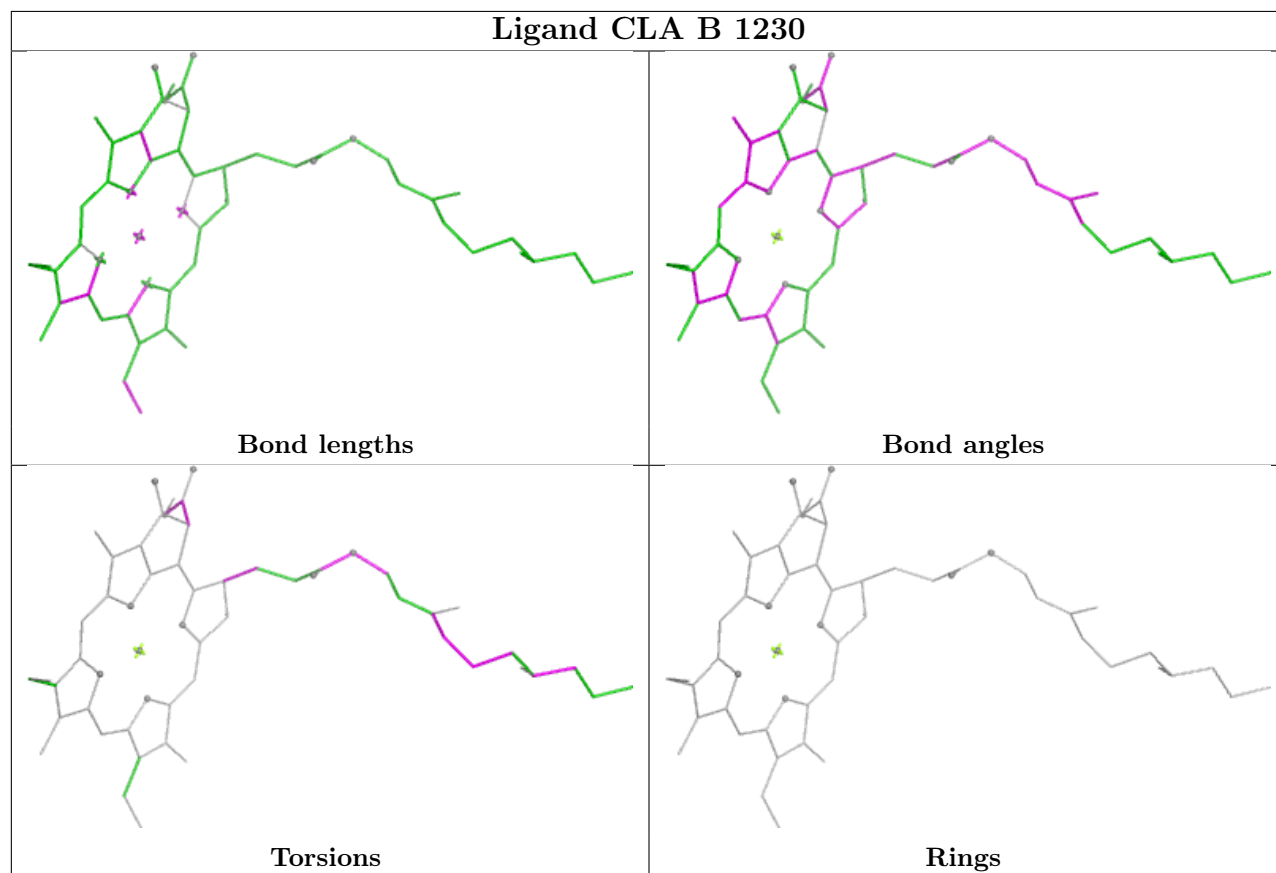
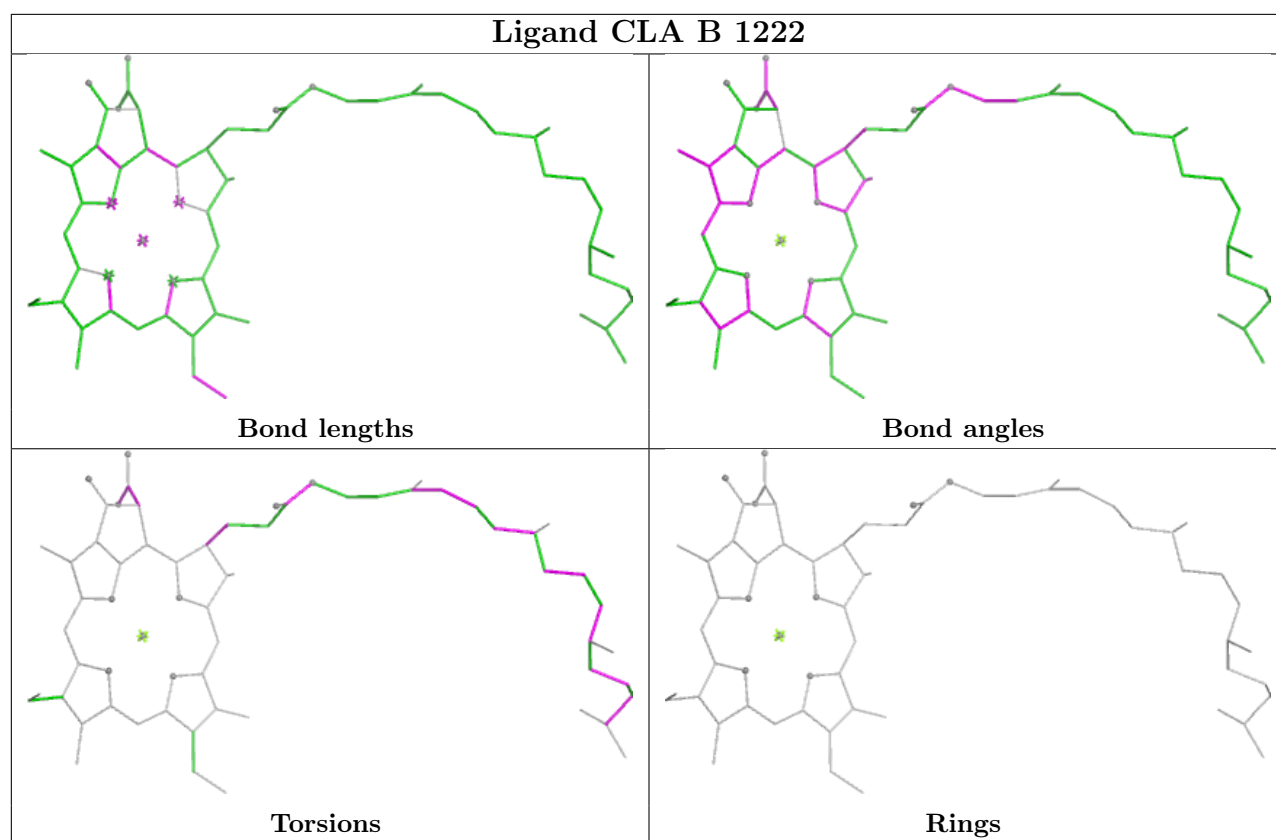


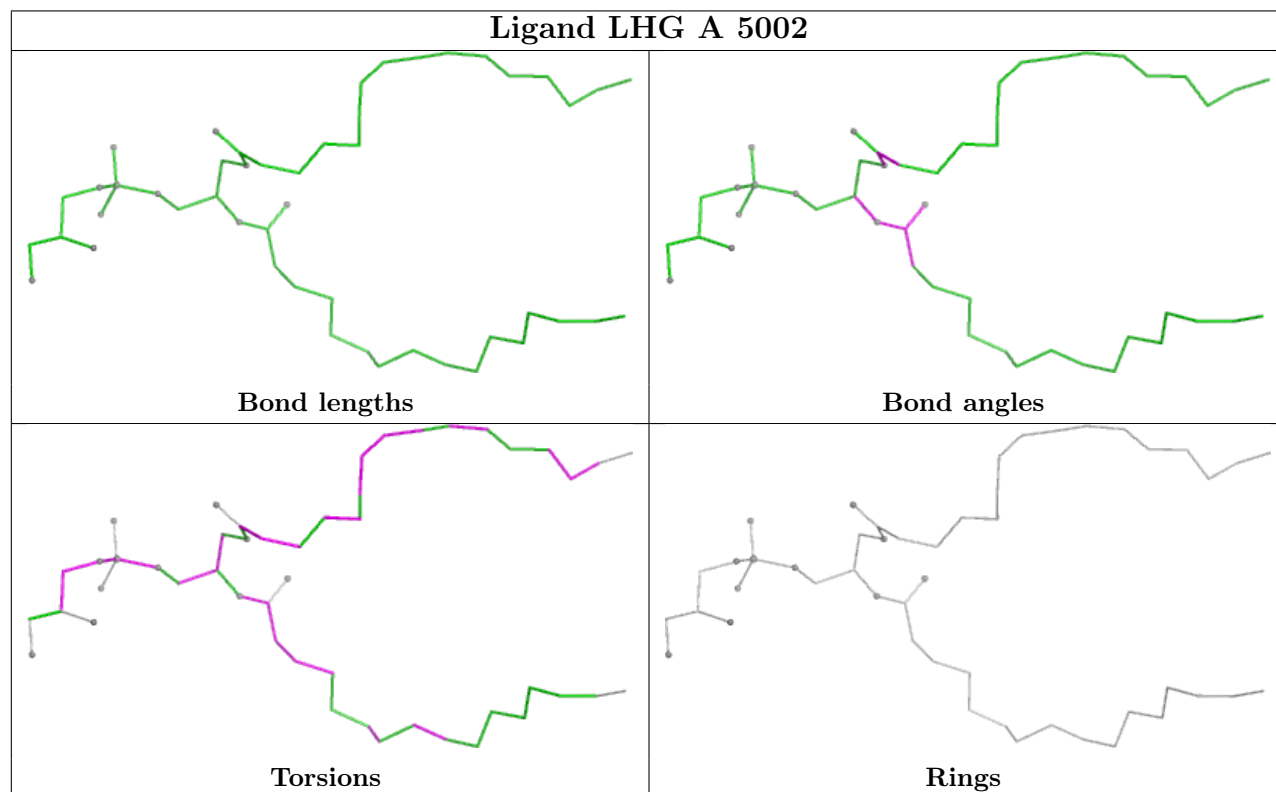
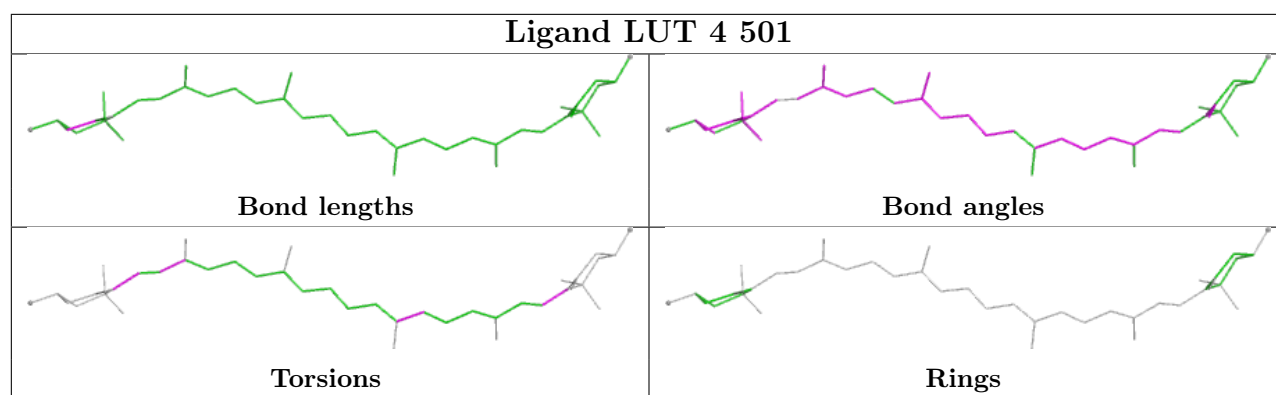
Torsions

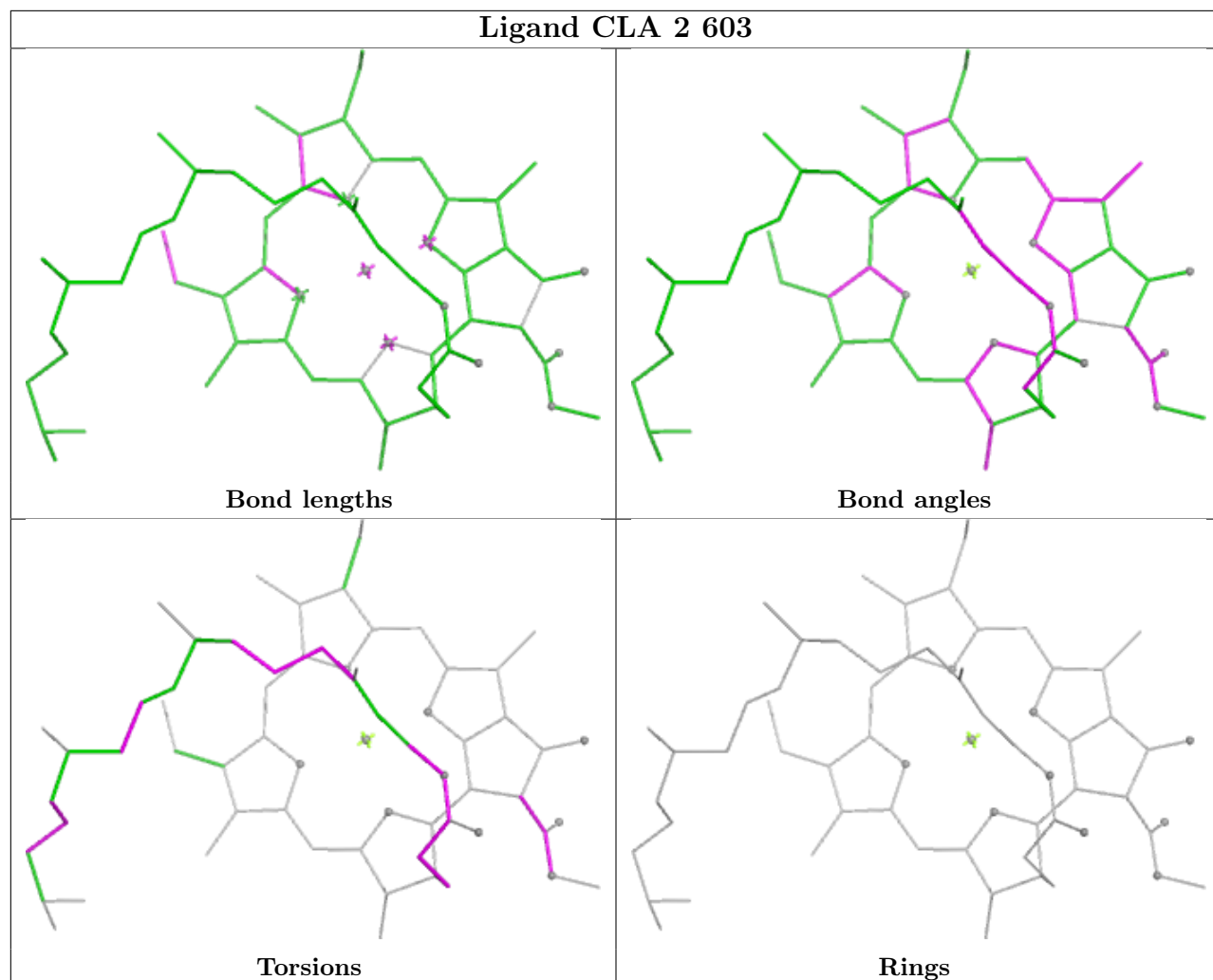


Rings

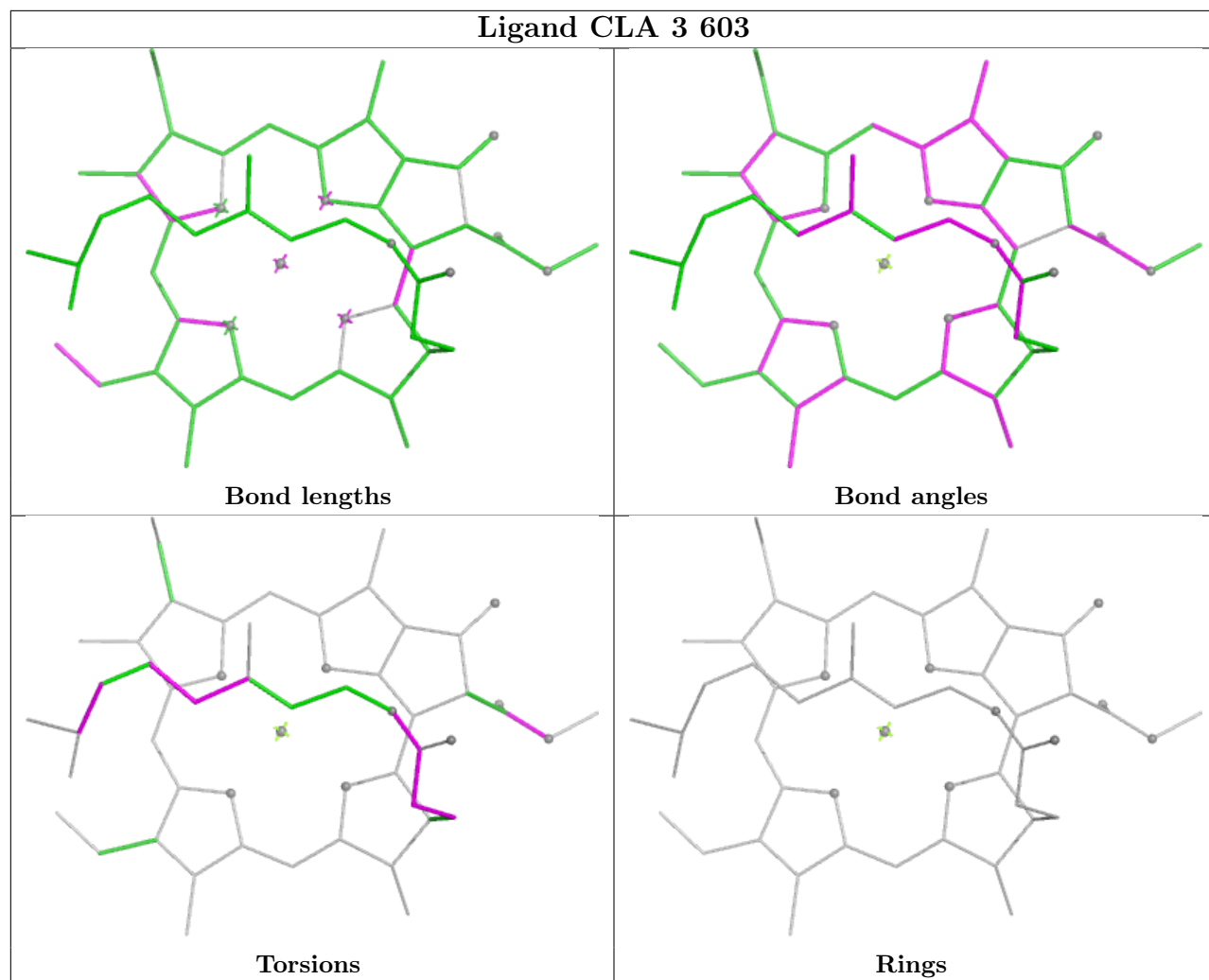


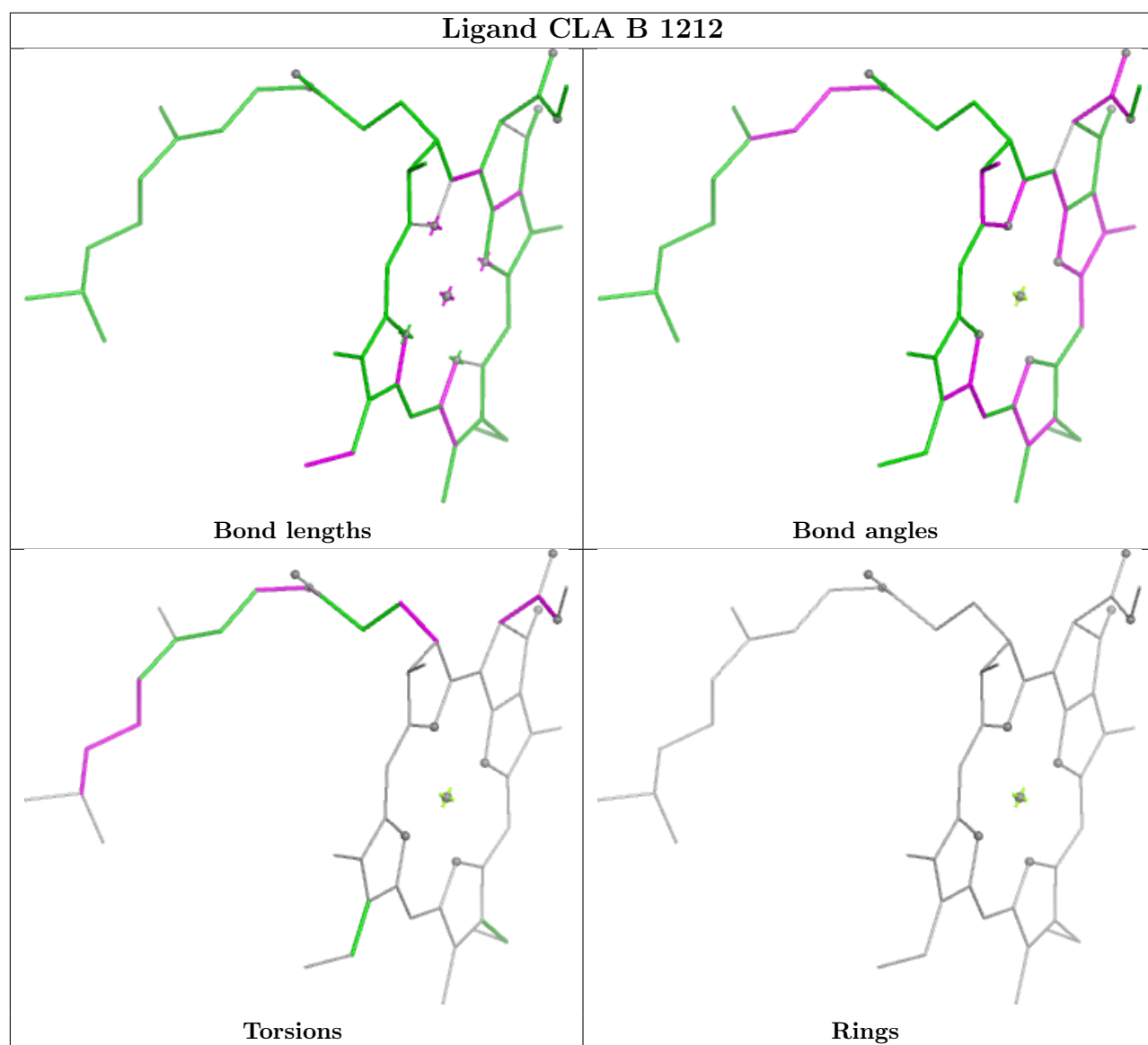


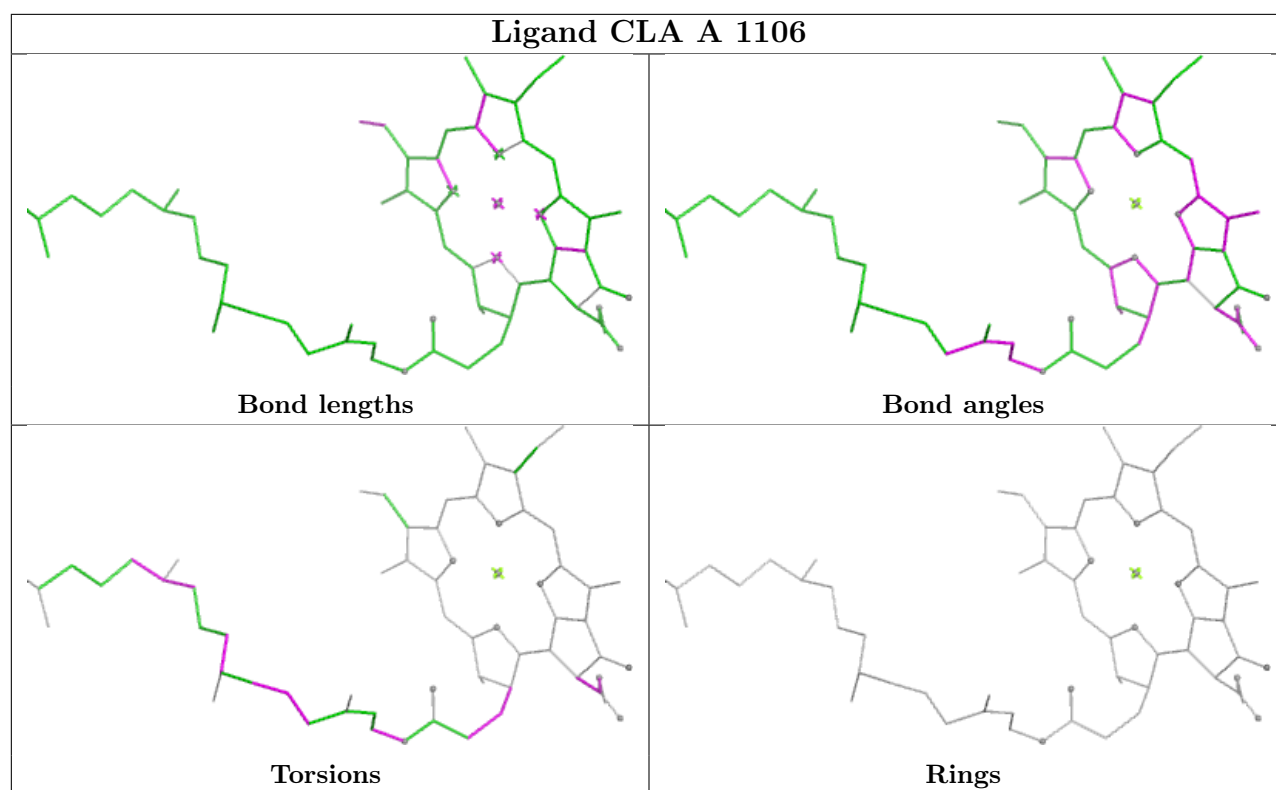


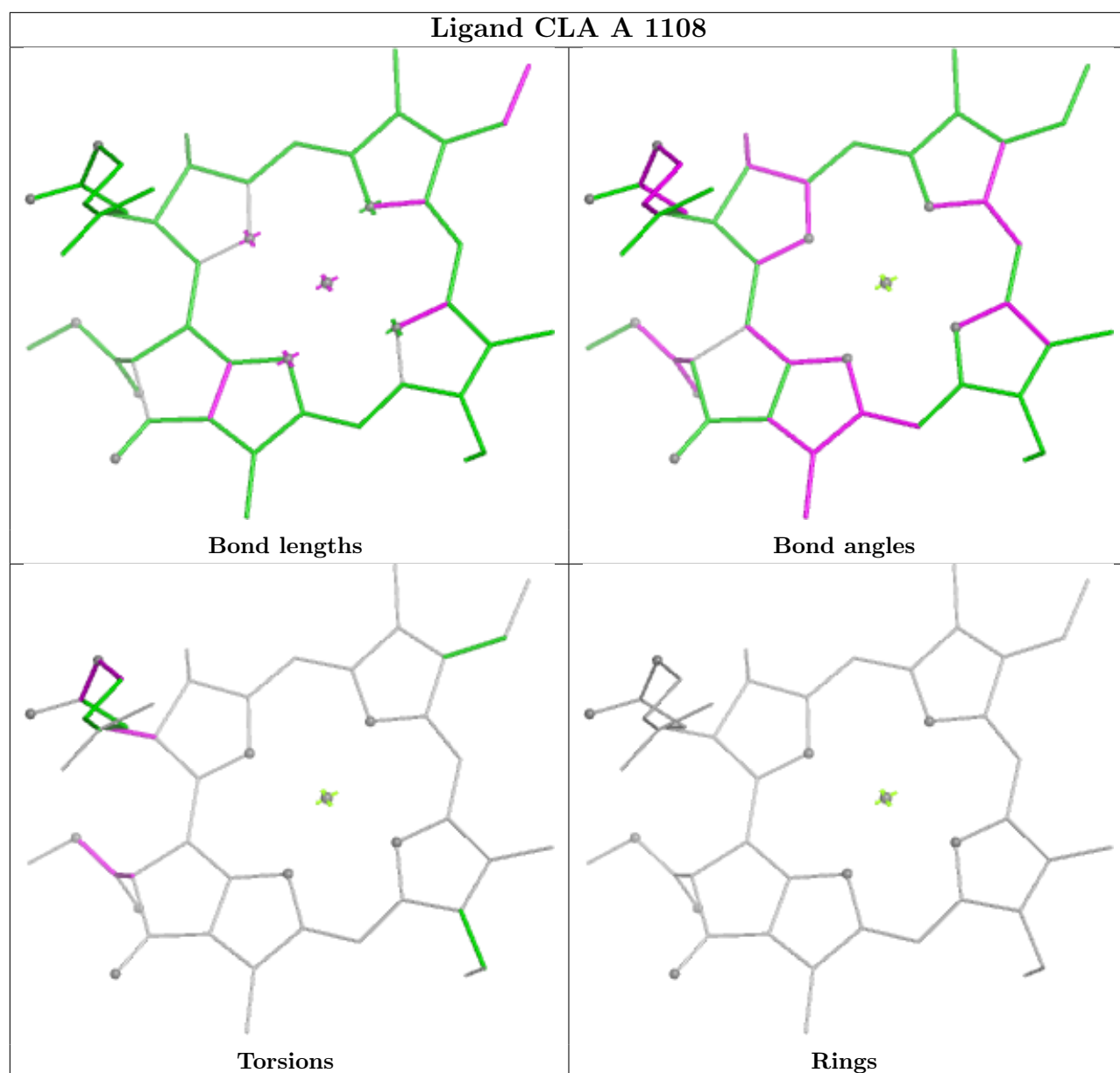
Ligand CLA 2 603

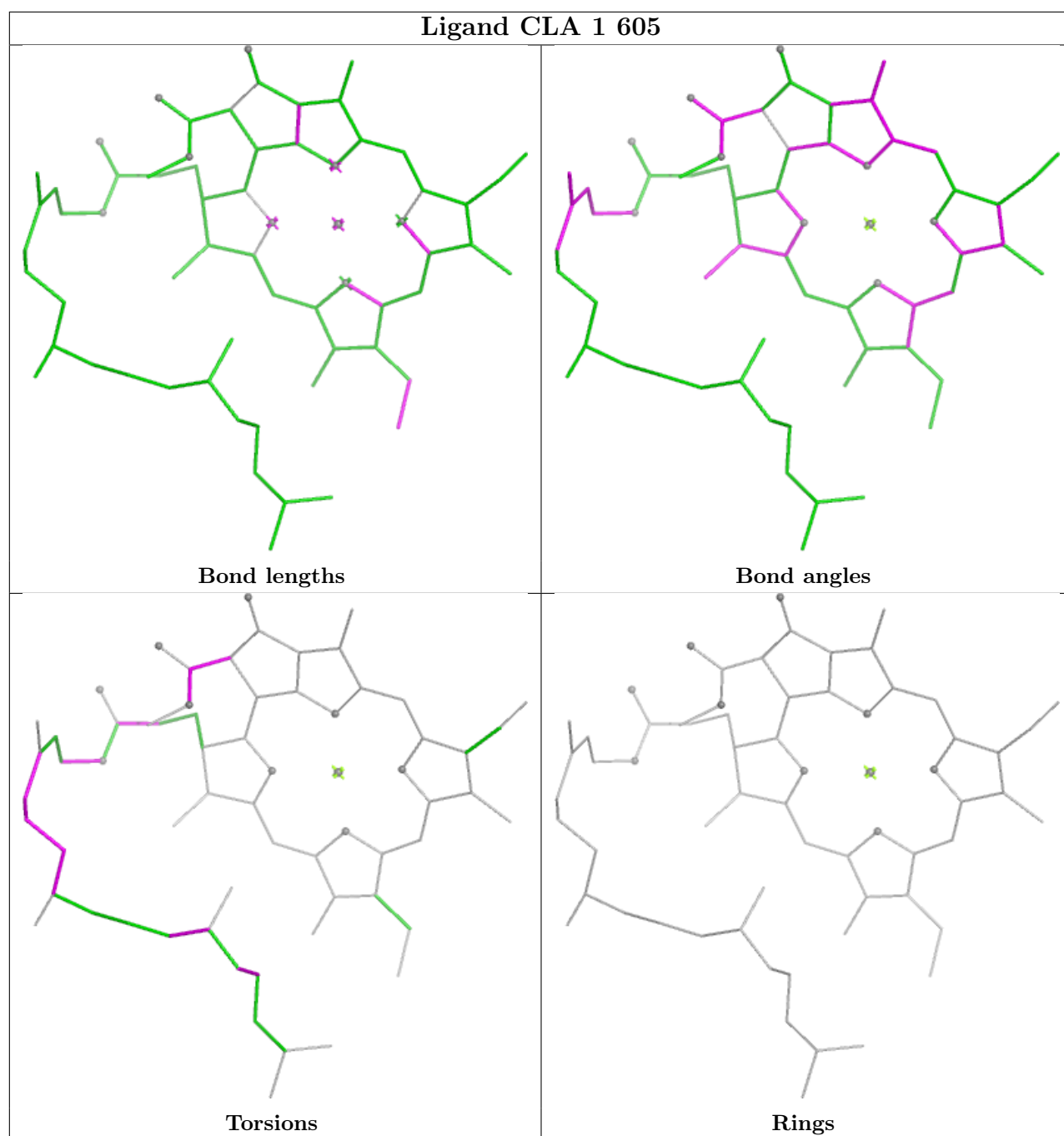
Ligand CLA 3 603



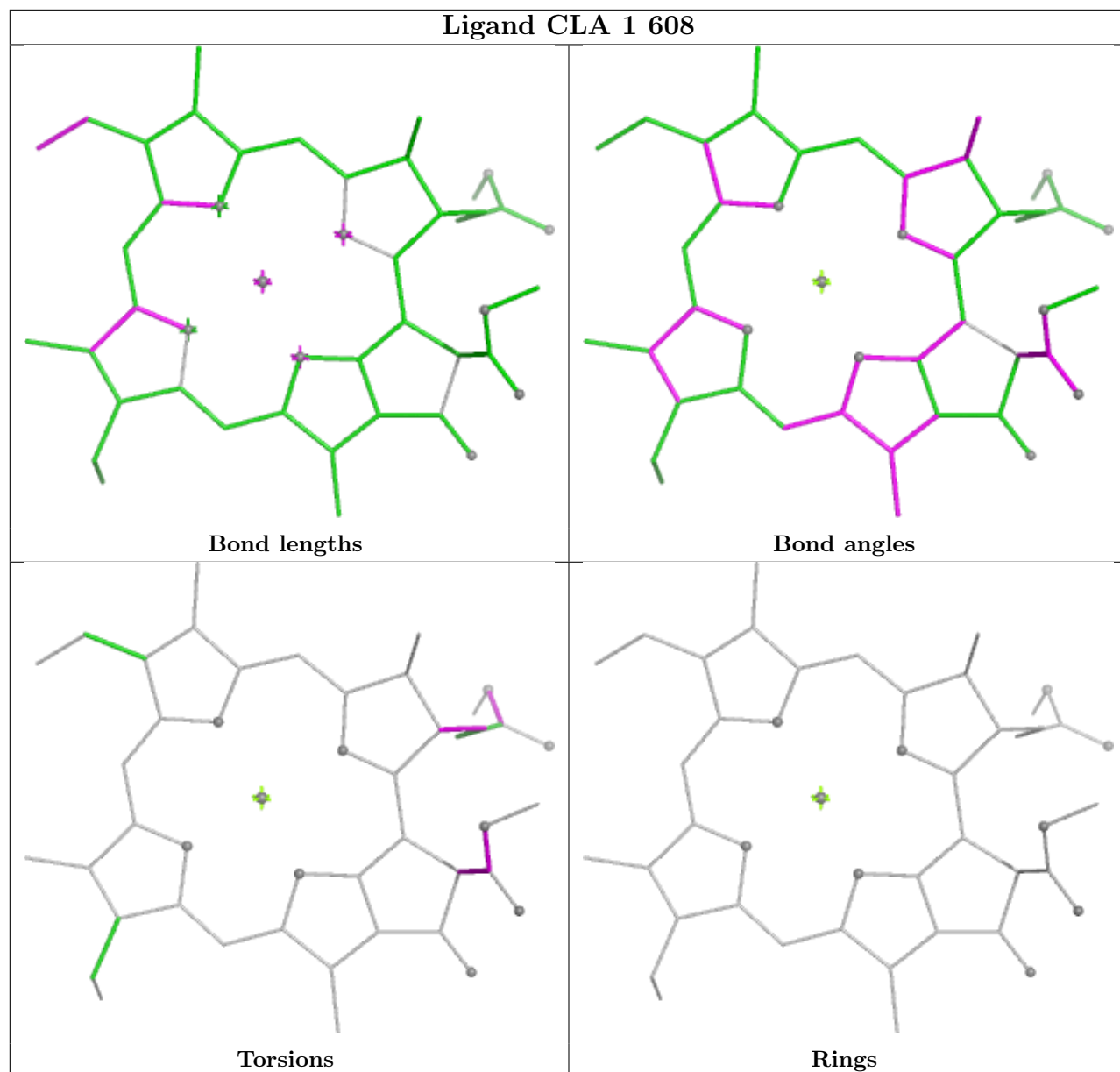


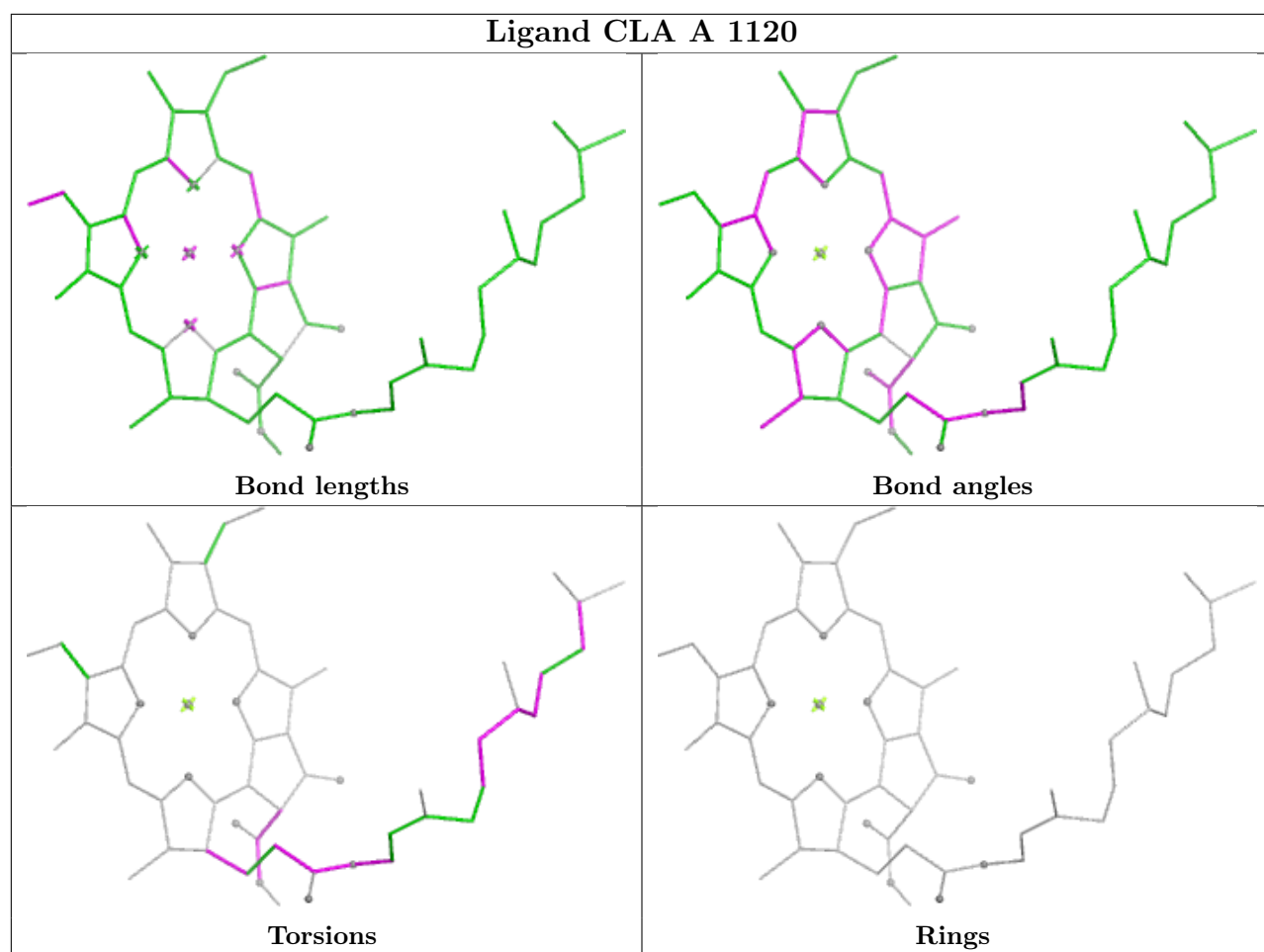




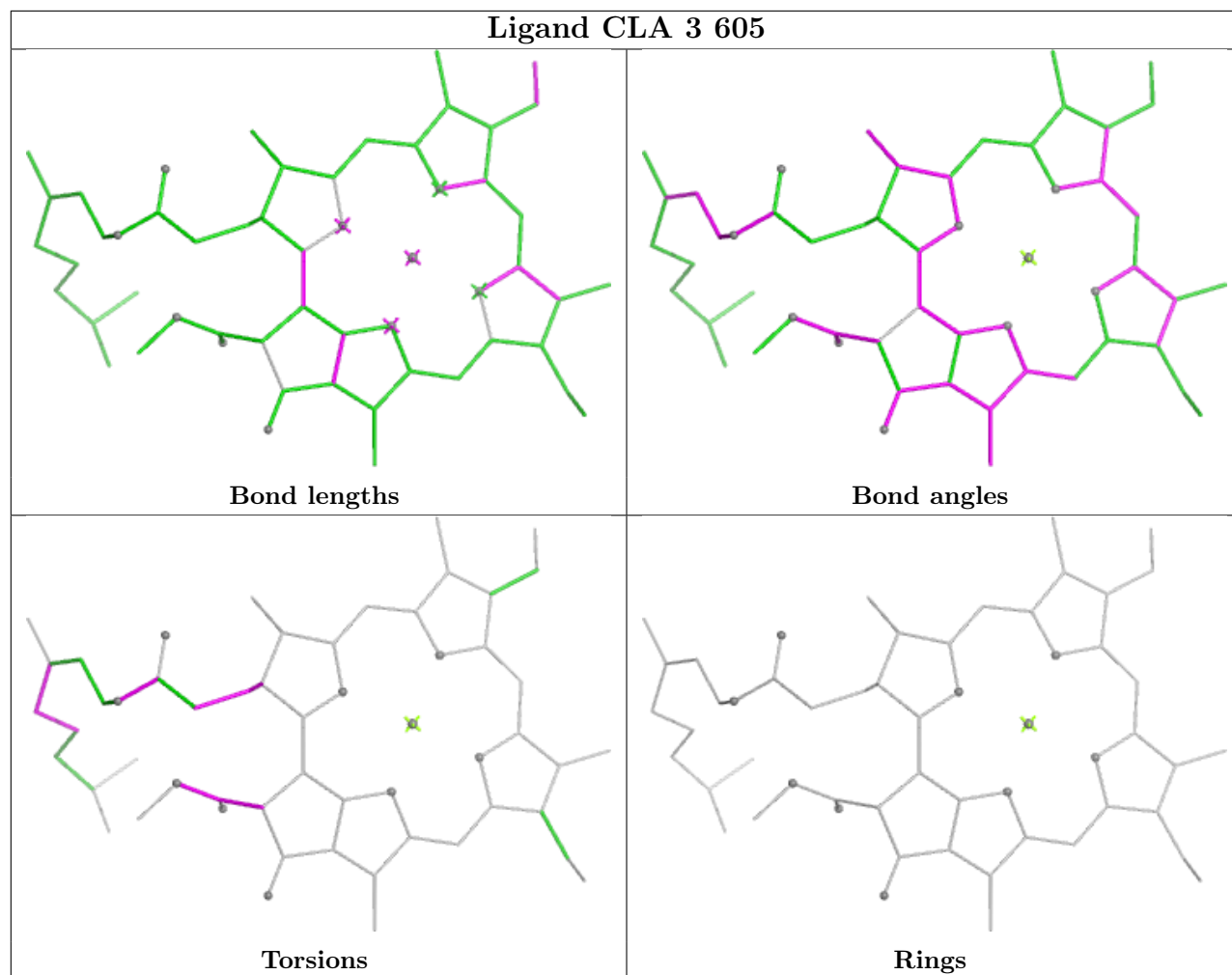


Ligand CLA 1 608

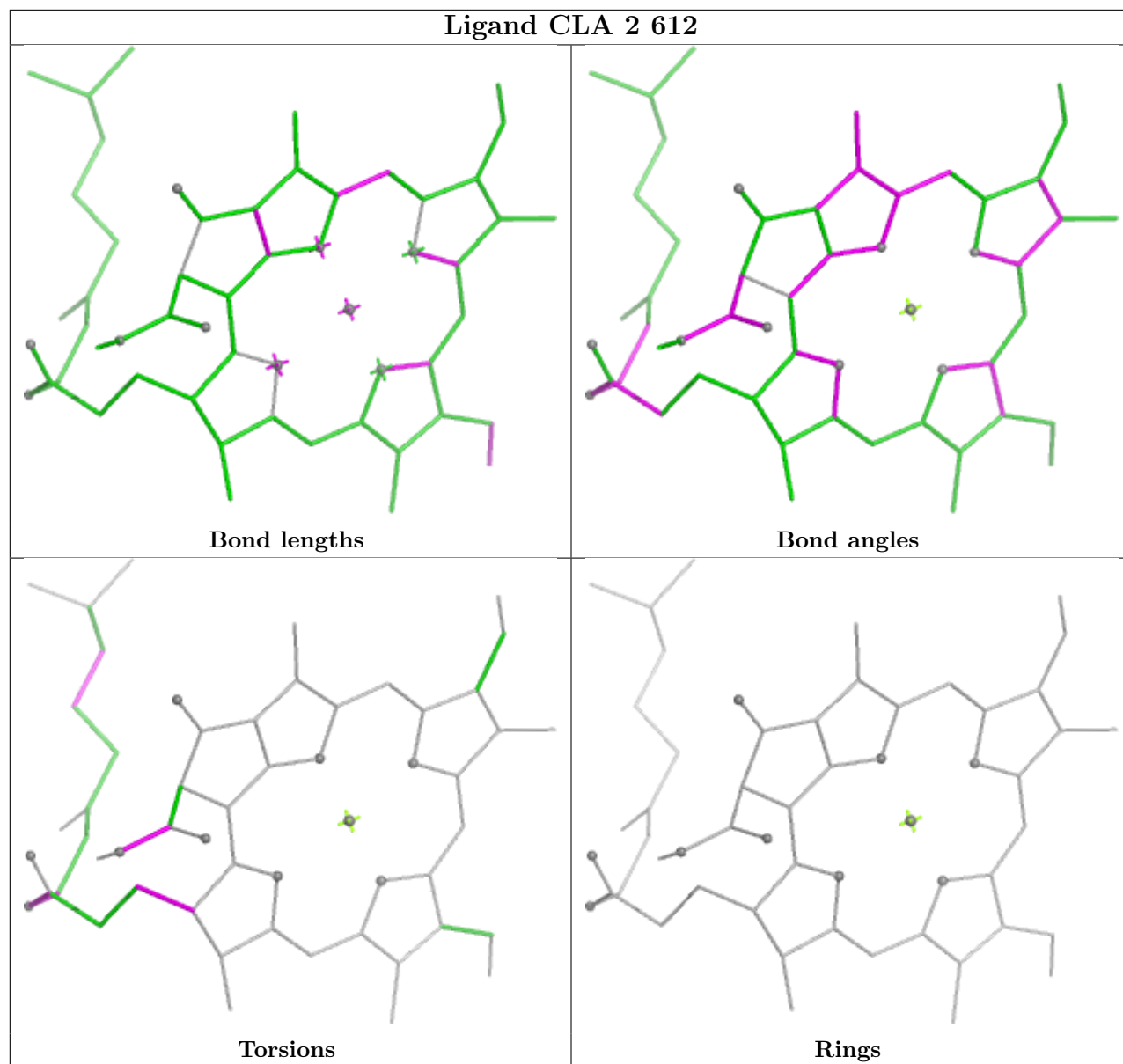


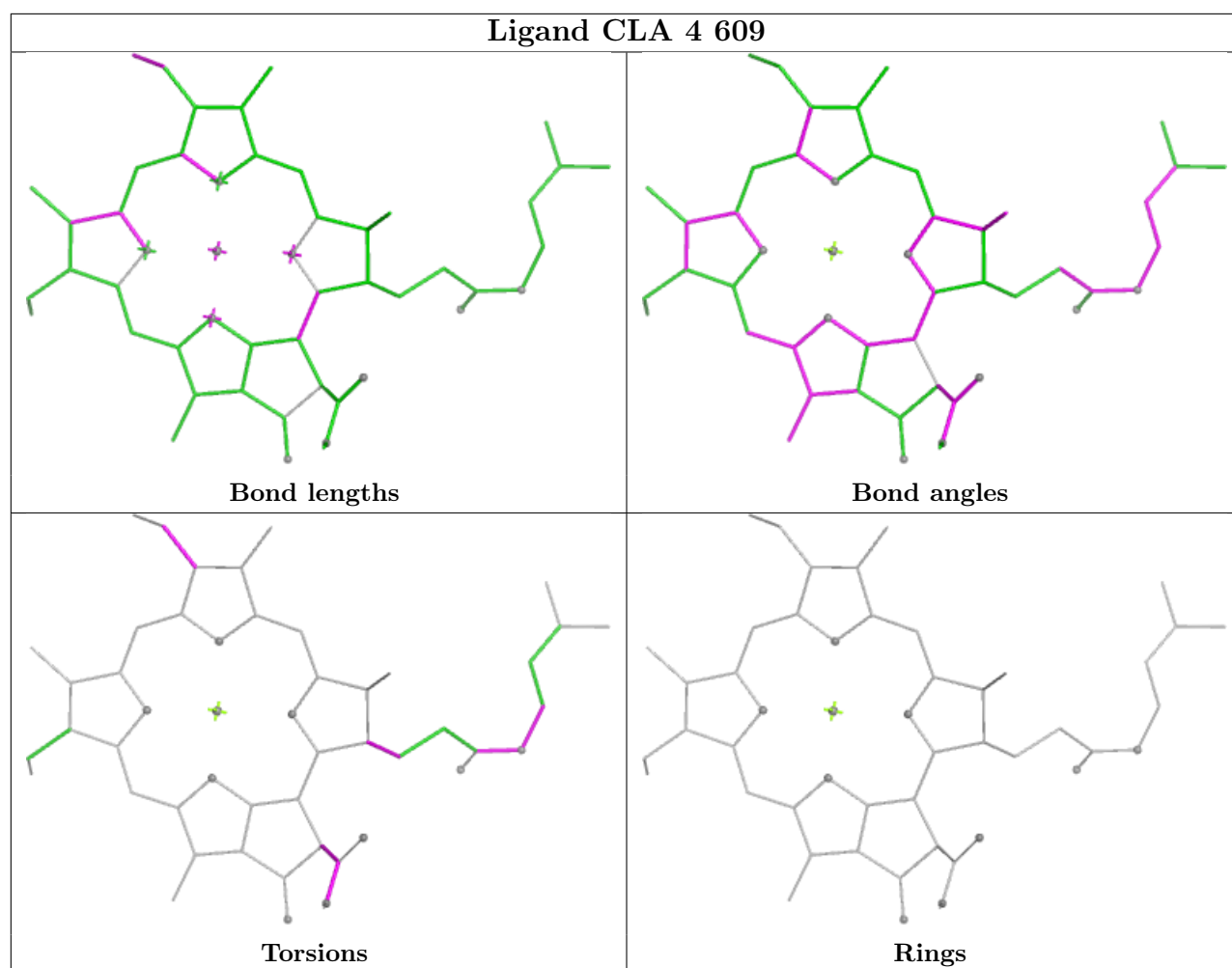


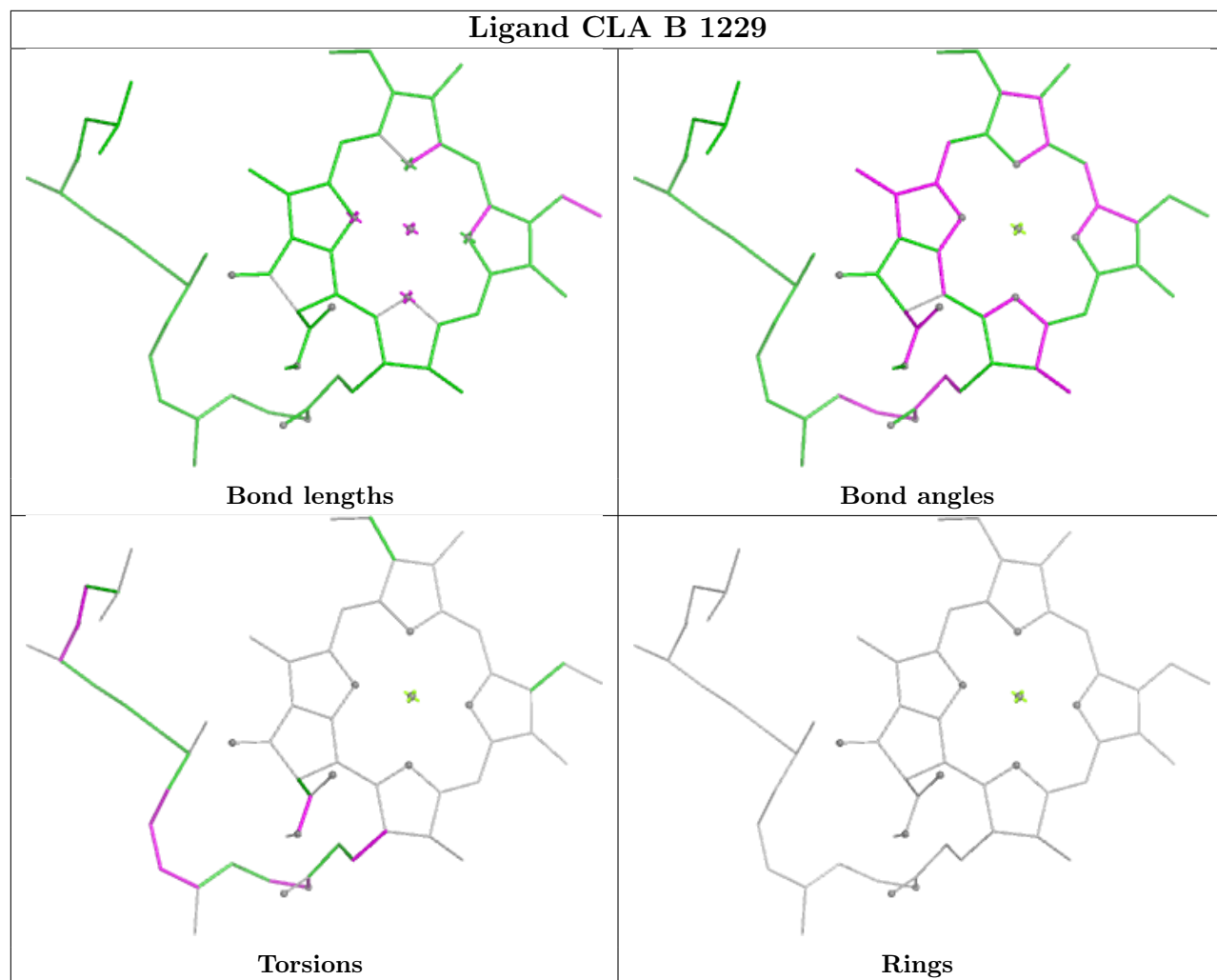
Ligand CLA 3 605

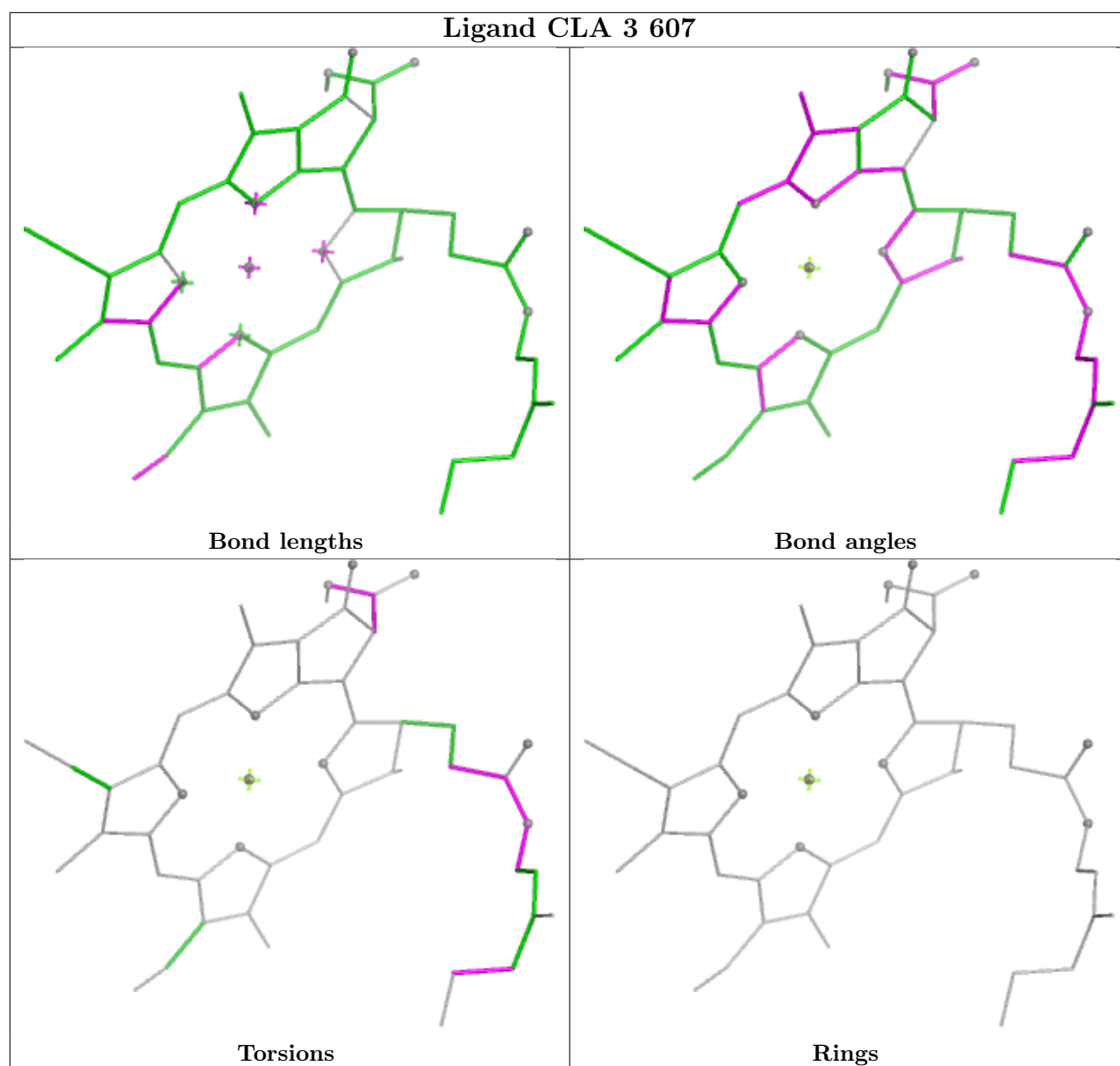


Ligand CLA 2 612

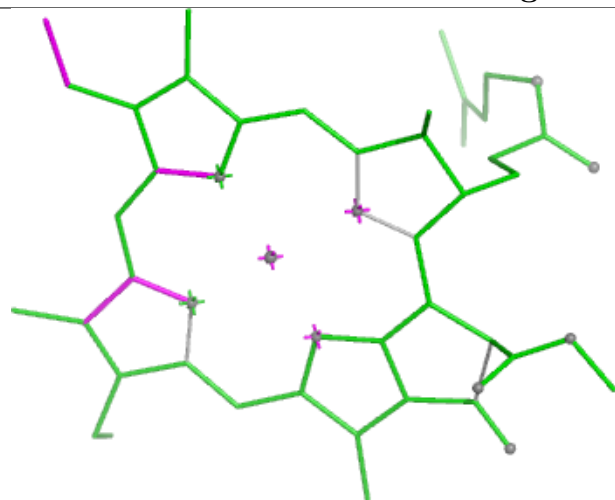




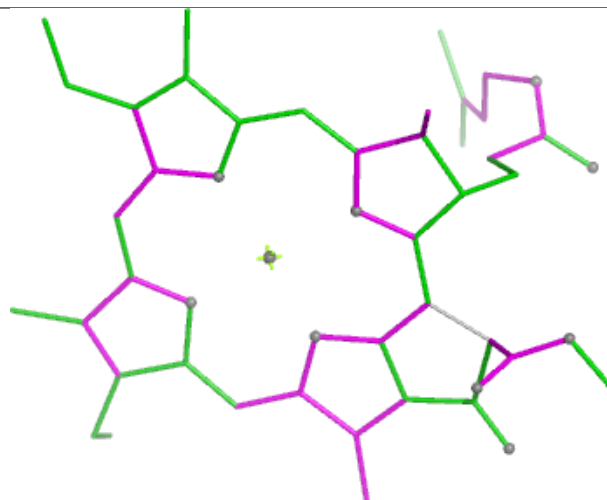




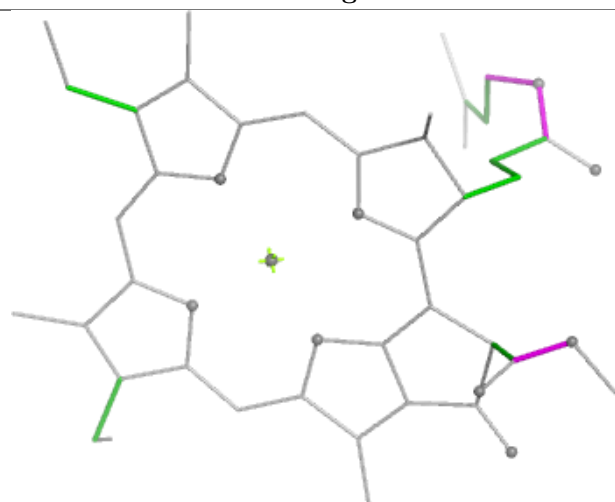
Ligand CLA 1 606



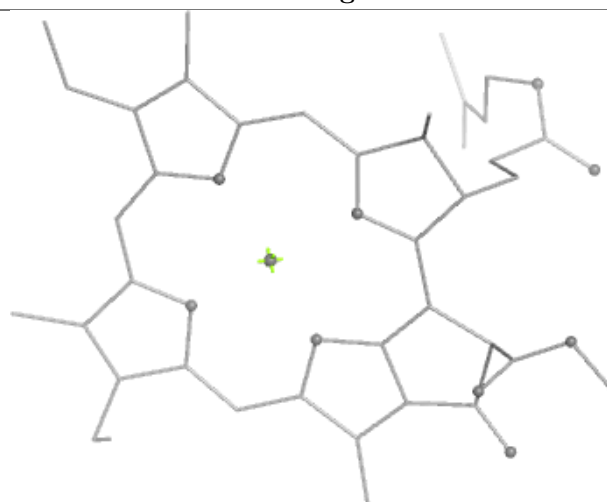
Bond lengths



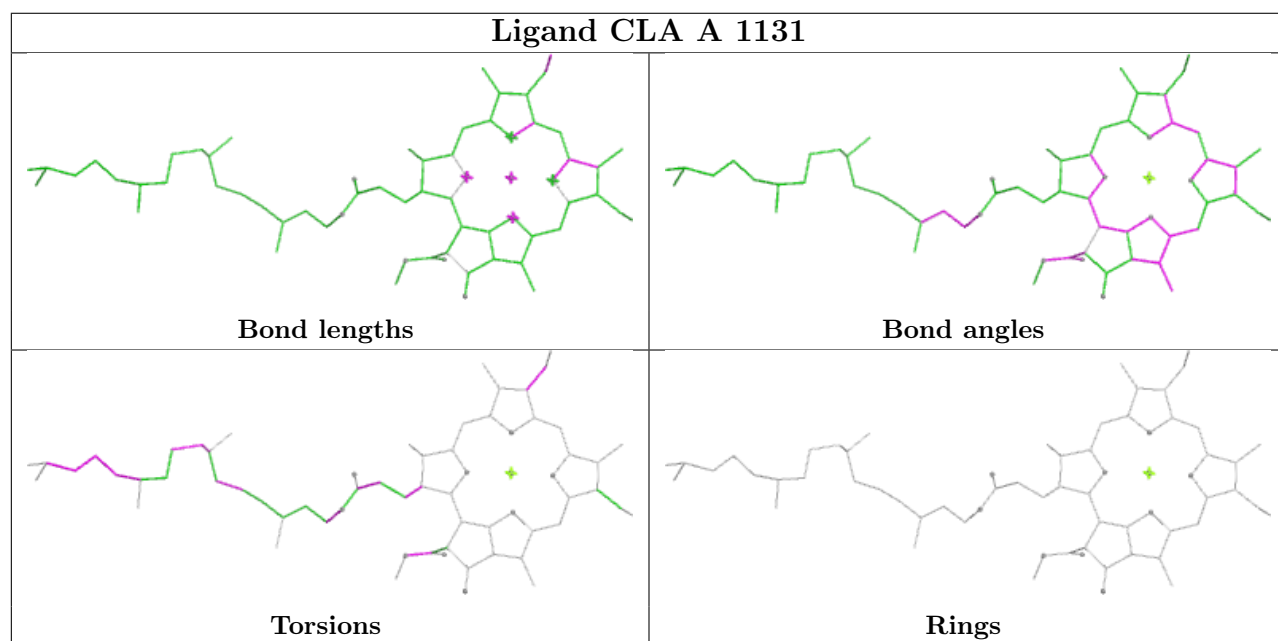
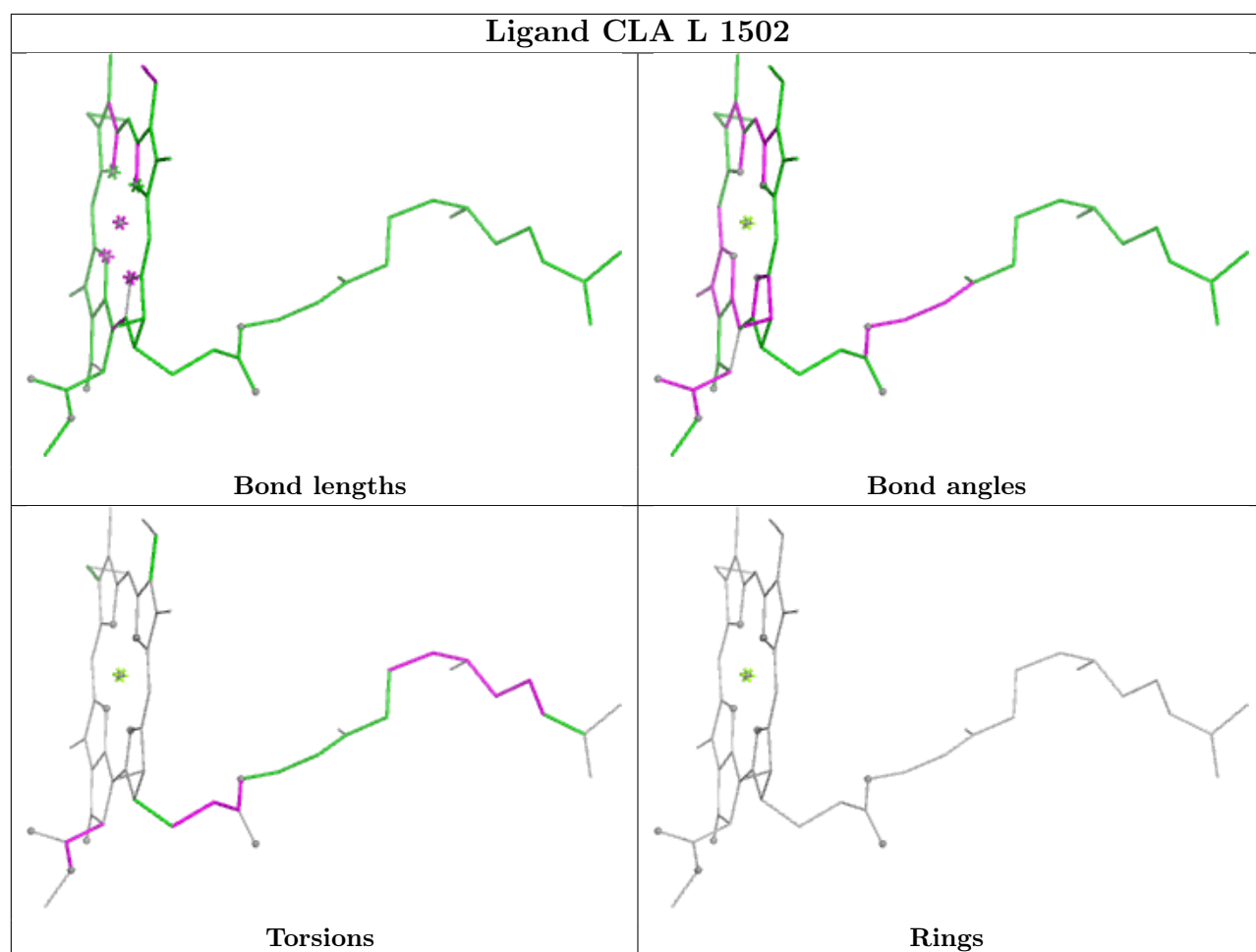
Bond angles

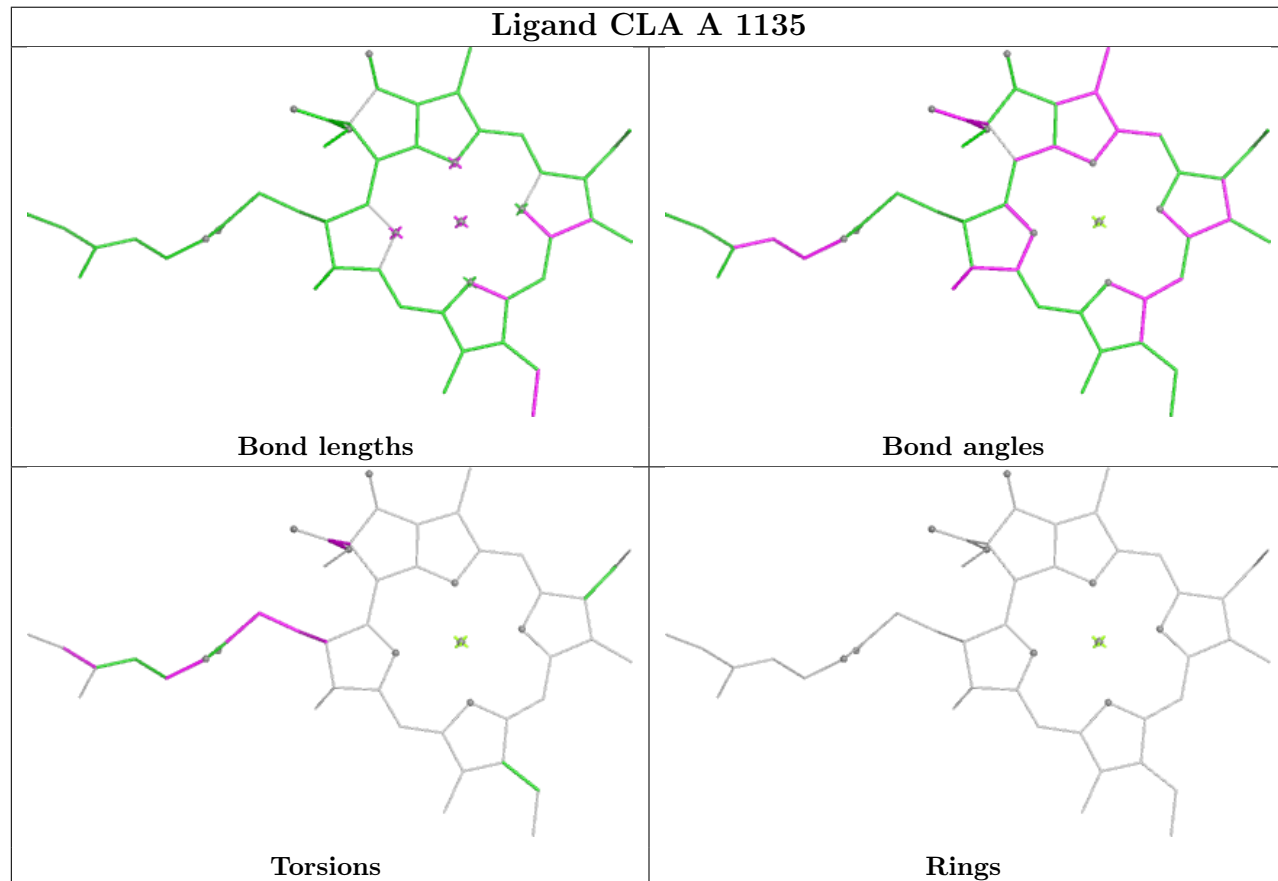
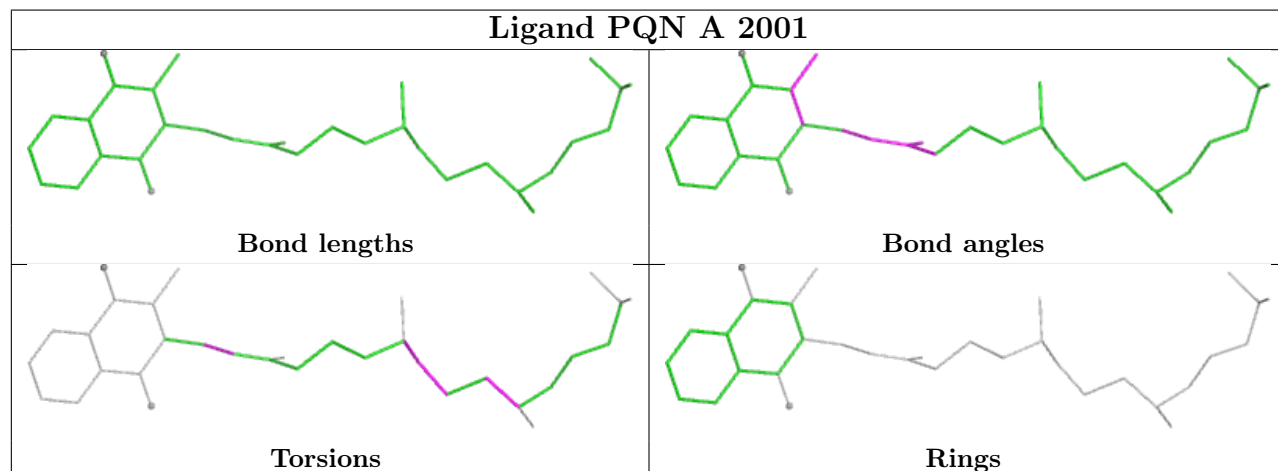
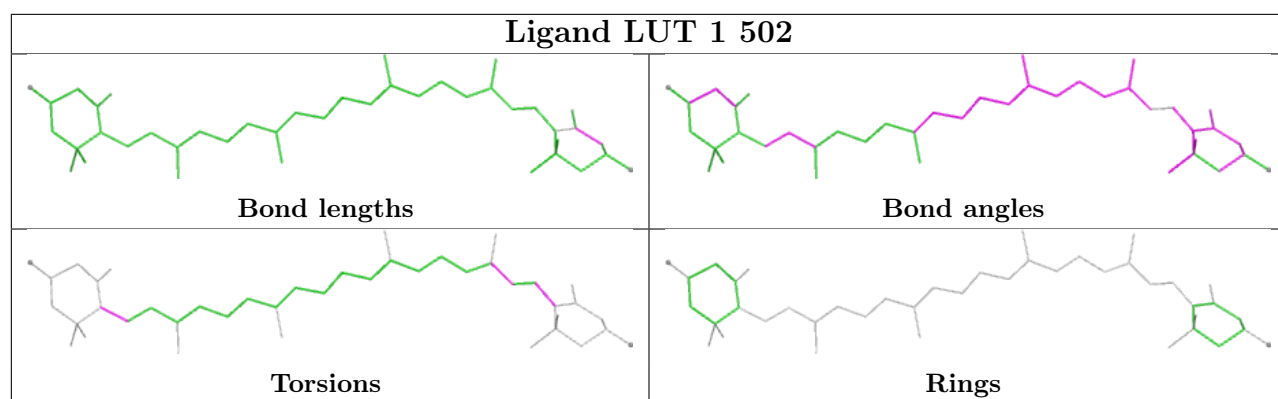


Torsions



Rings





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.

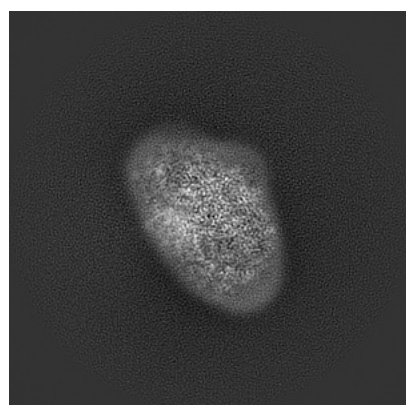
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11326. These allow visual inspection of the internal detail of the map and identification of artifacts.

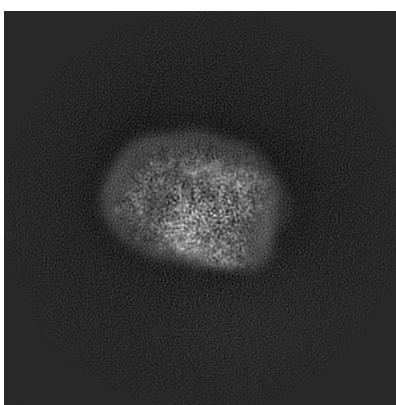
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

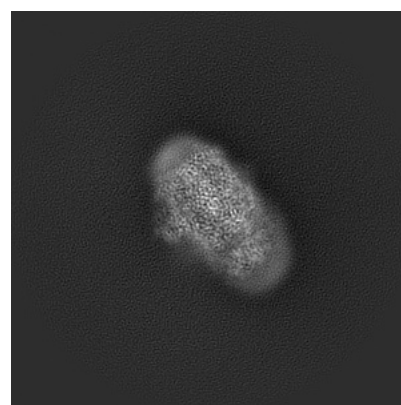
6.1.1 Primary map



X



Y

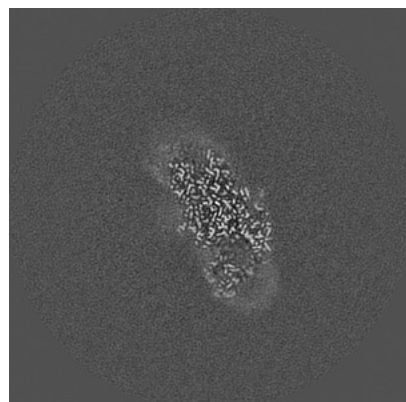


Z

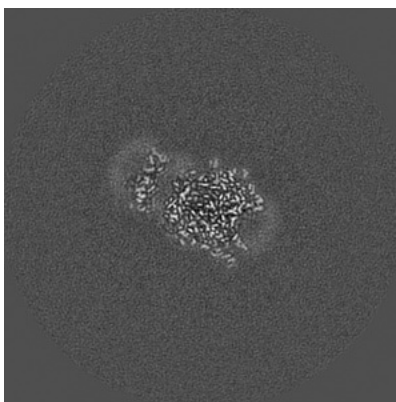
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

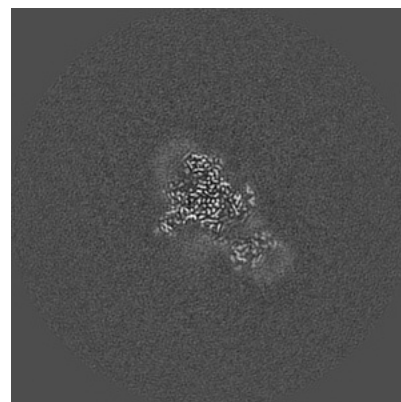
6.2.1 Primary map



X Index: 150



Y Index: 150

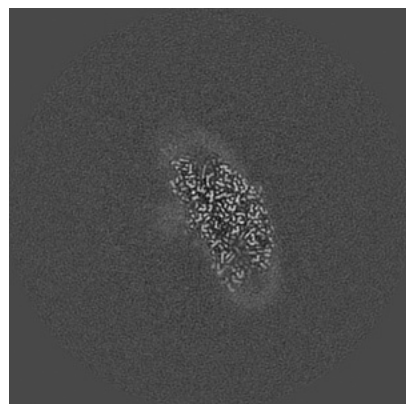


Z Index: 150

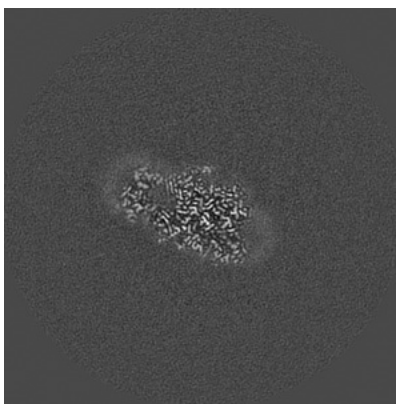
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

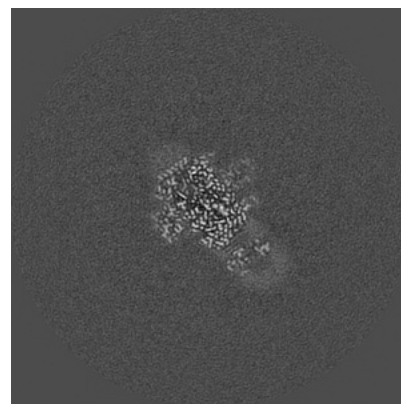
6.3.1 Primary map



X Index: 145



Y Index: 162

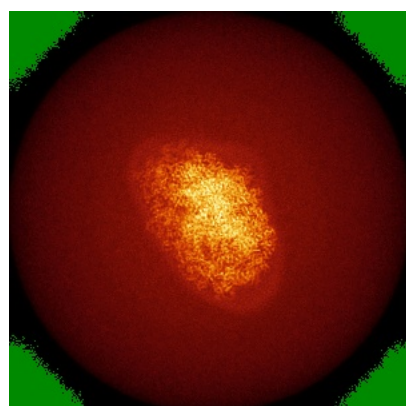


Z Index: 162

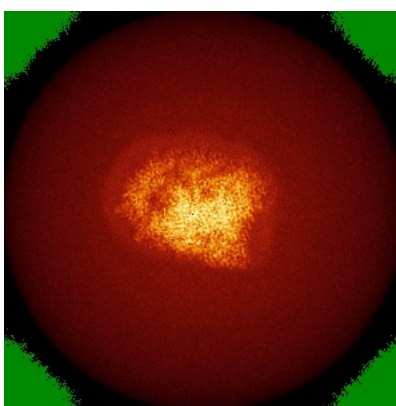
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

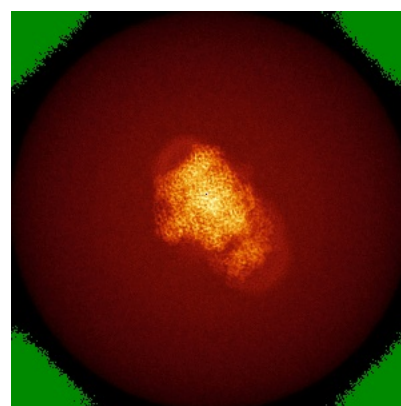
6.4.1 Primary map



X



Y

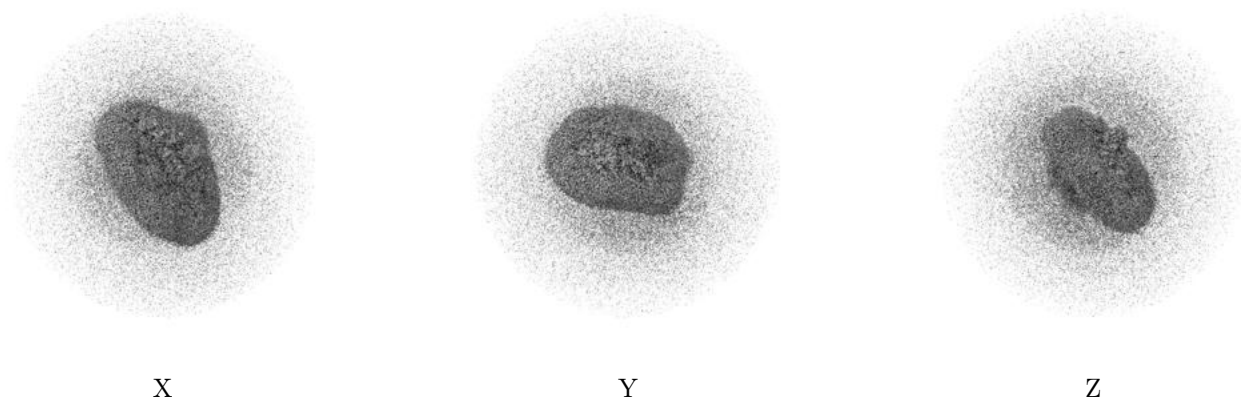


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

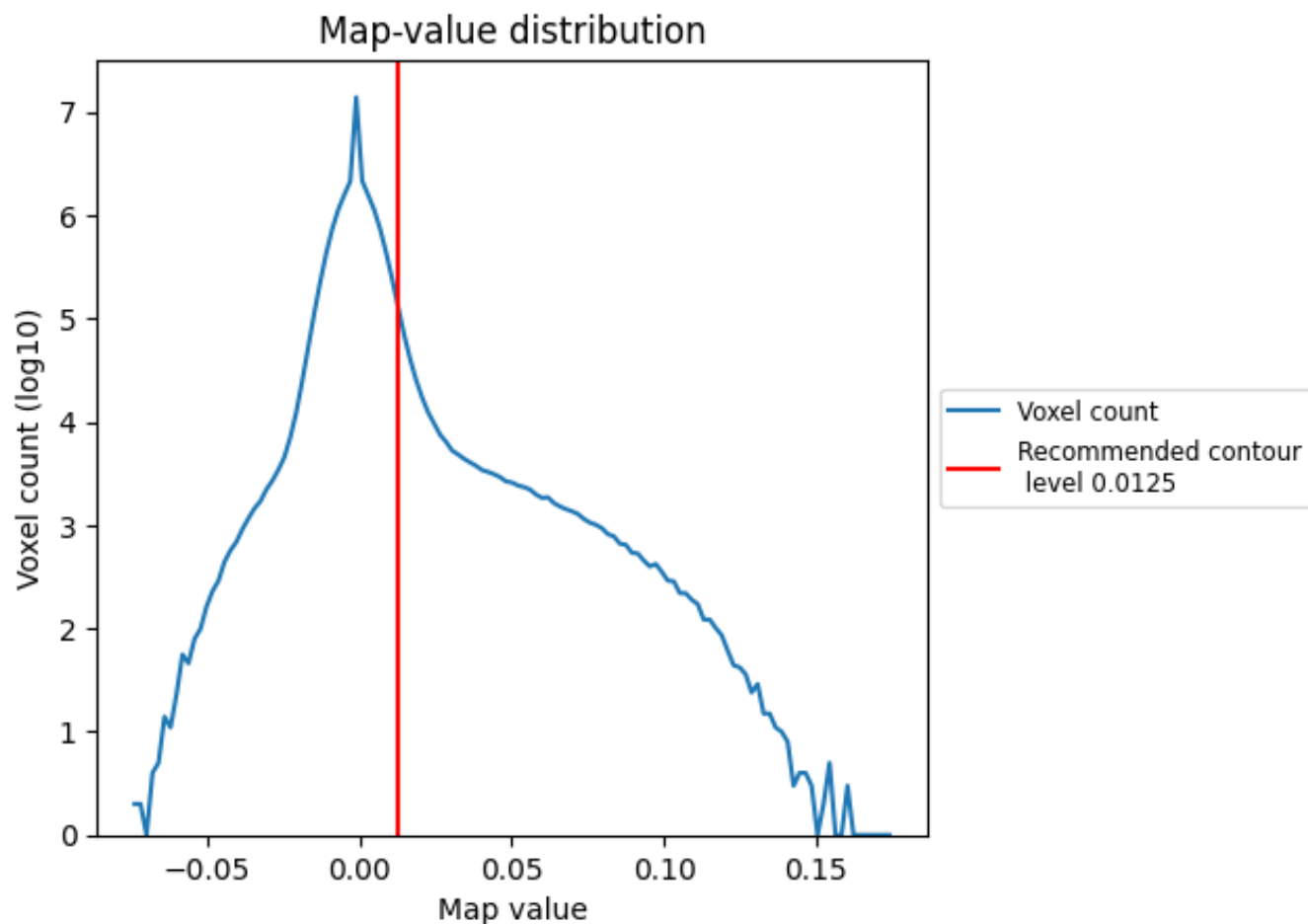
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

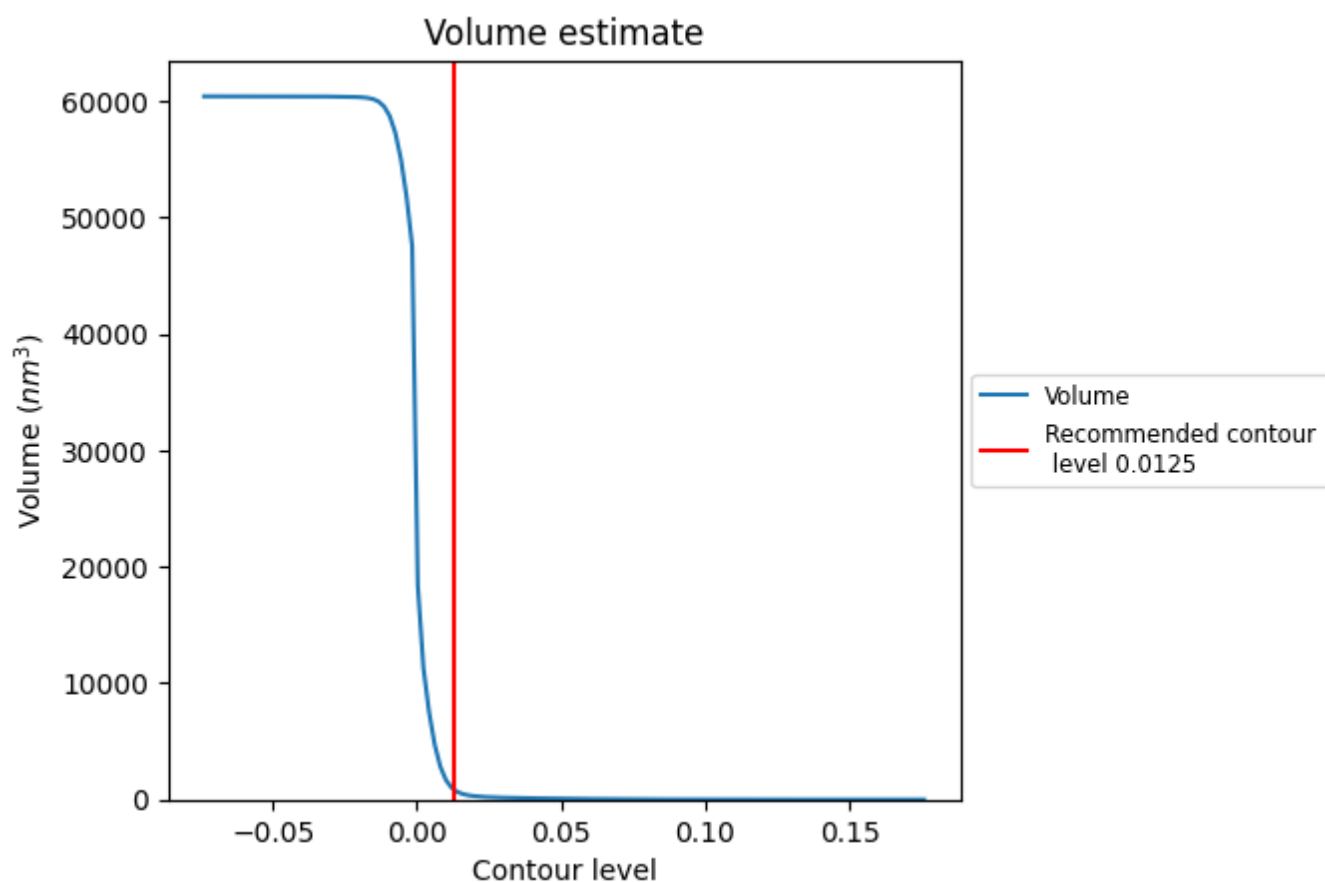
This section contains the results of statistical analysis of the map.

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.

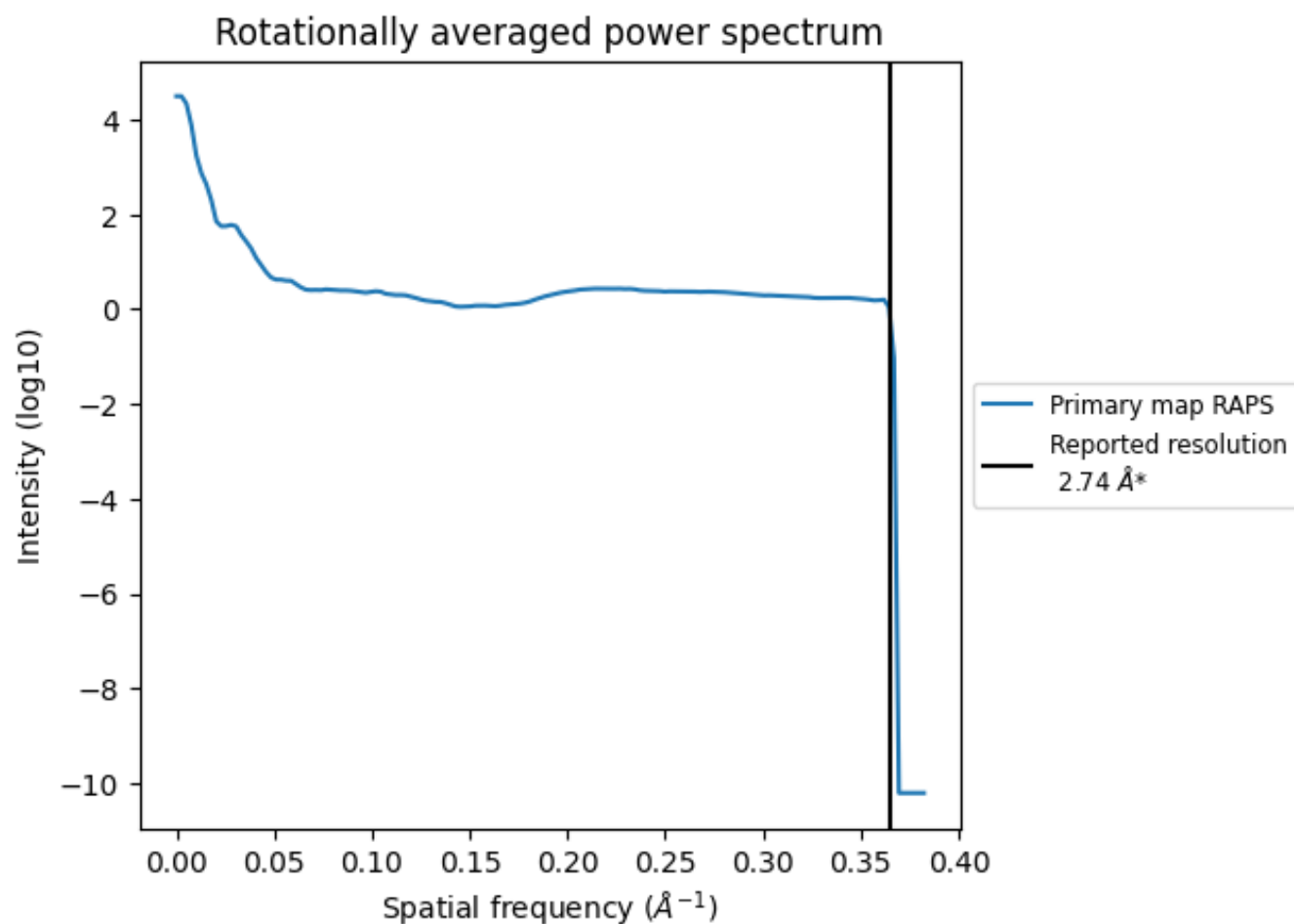
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 925 nm³; this corresponds to an approximate mass of 835 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 ⓘ

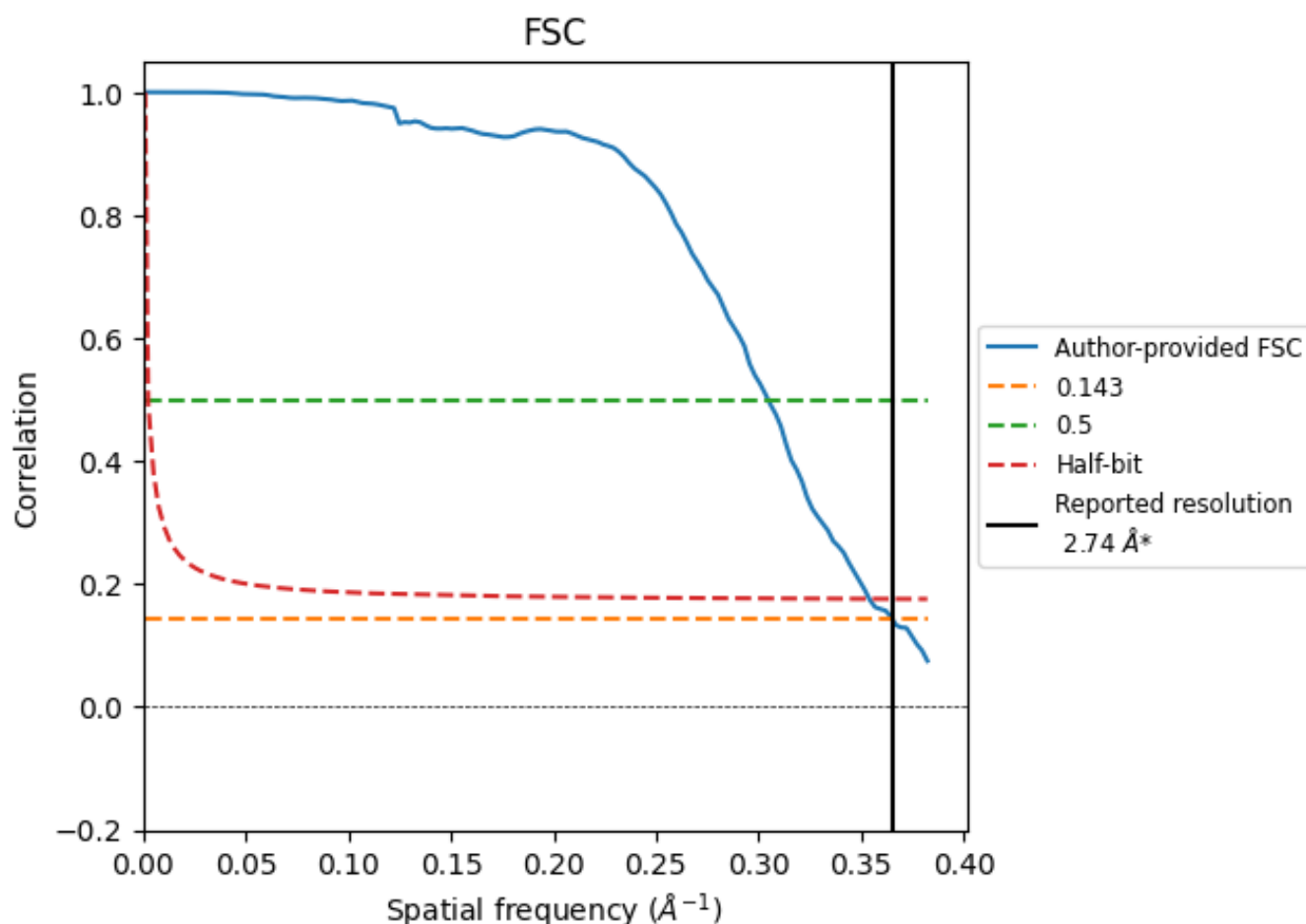


*Reported resolution corresponds to spatial frequency of 0.365 Å⁻¹

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 0.365 Å⁻¹

8.2 Resolution estimates [i](#)

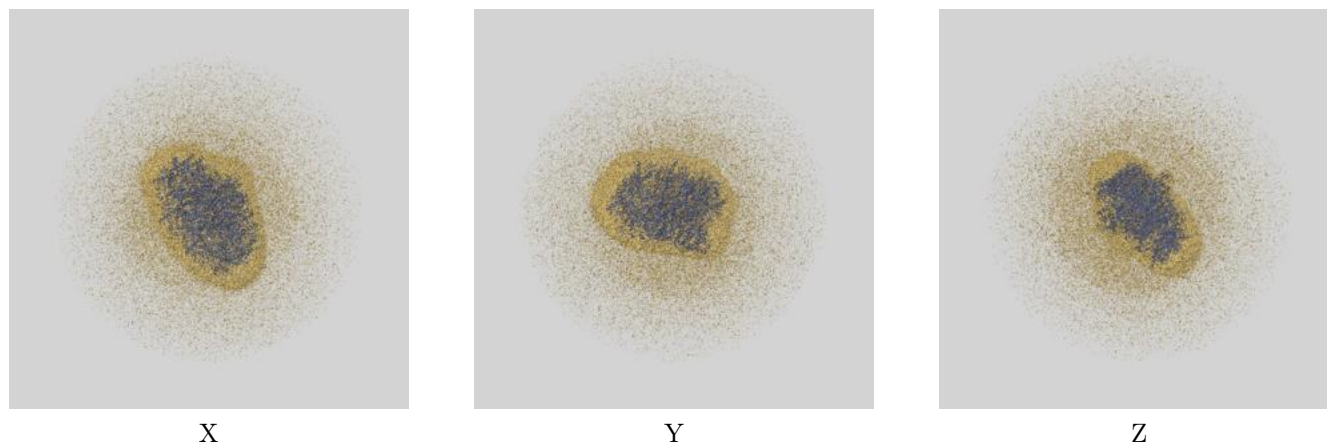
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.74	-	-
Author-provided FSC curve	2.74	3.28	2.82
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

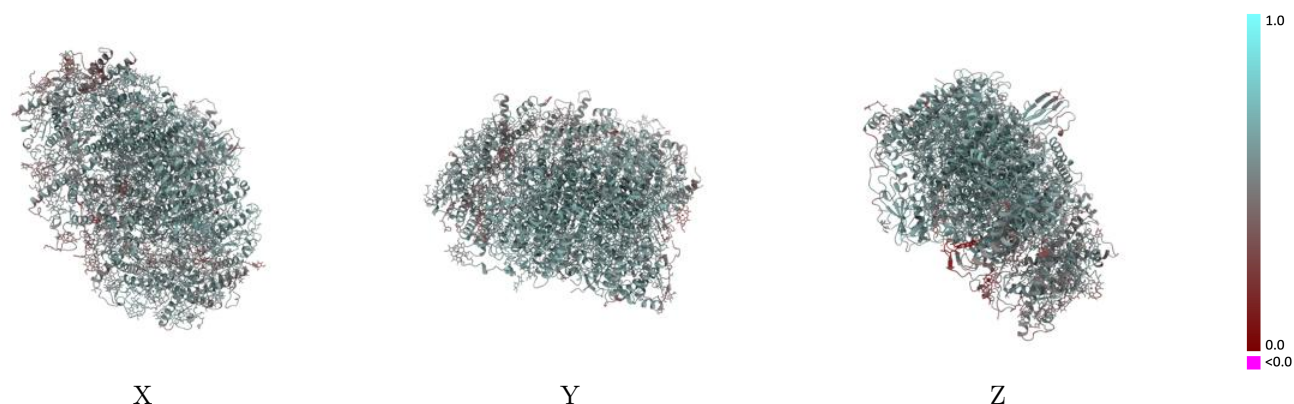
This section contains information regarding the fit between EMDB map EMD-11326 and PDB model 6ZOO. Per-residue inclusion information can be found in section 3 on page 29.

9.1 Map-model overlay [i](#)



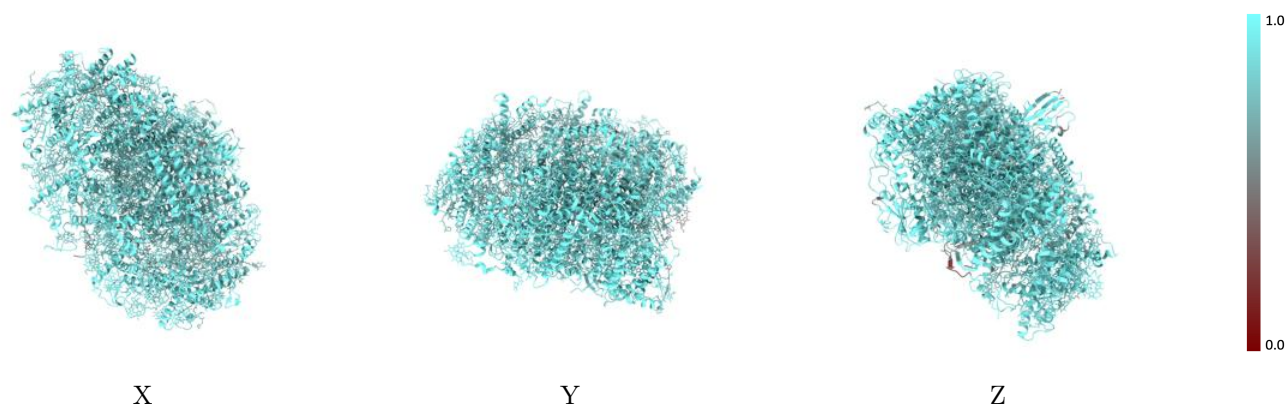
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



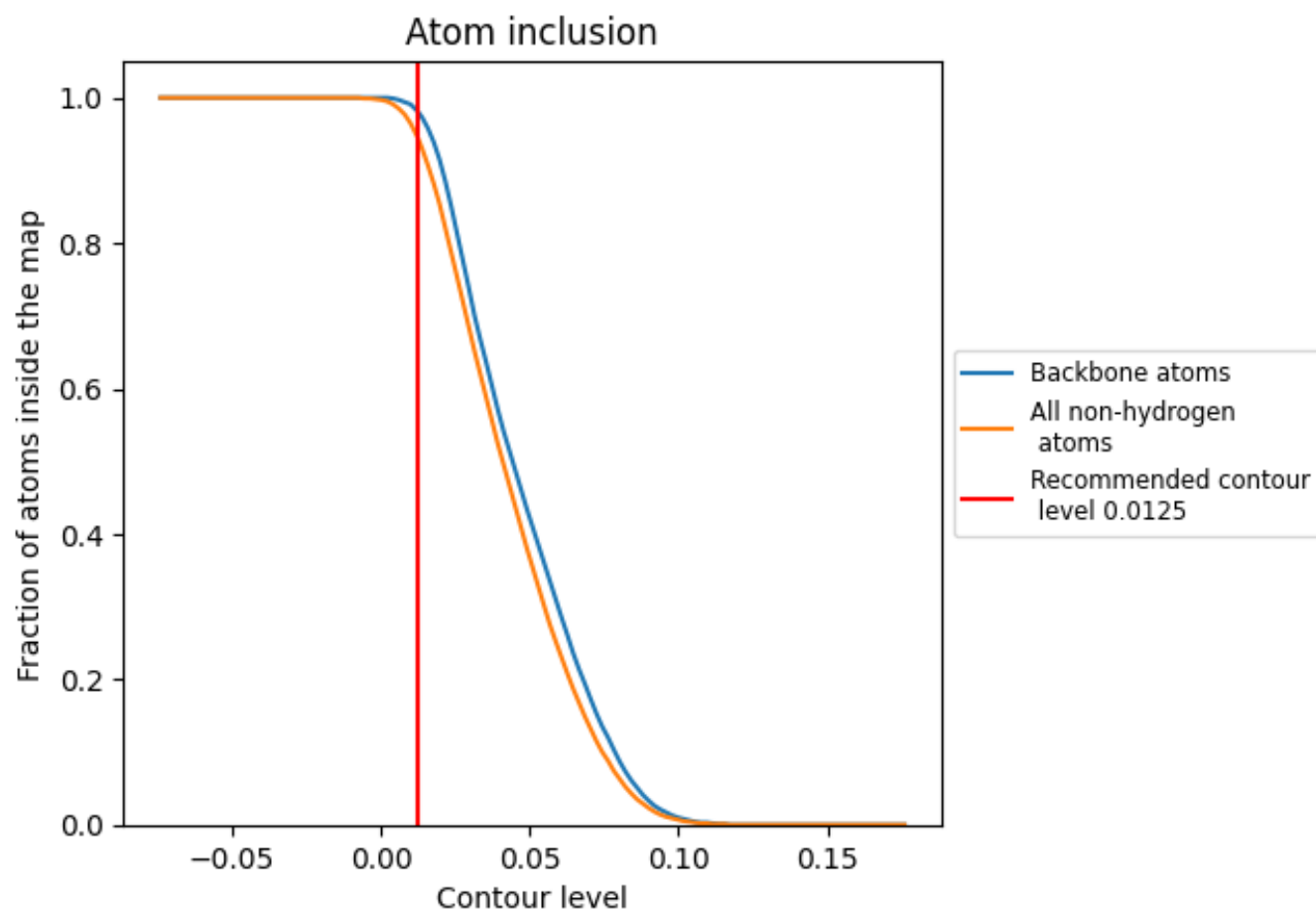
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0125).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 94% 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 (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9450	0.5600
1	0.9360	0.5350
2	0.9140	0.5030
3	0.9260	0.4950
4	0.9290	0.5310
A	0.9590	0.5920
B	0.9720	0.6050
C	0.9870	0.5950
D	0.9830	0.5900
E	0.9690	0.5560
F	0.9370	0.5620
G	0.9130	0.5220
H	0.9110	0.5050
I	0.9750	0.5800
J	0.9170	0.5090
K	0.8040	0.3930
L	0.9690	0.5600
P	0.8760	0.5280

