



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 09:08 AM JST

PDB ID : 7F4V / pdb_00007f4v
EMDB ID : EMD-31455
Title : Cryo-EM structure of a primordial cyanobacterial photosystem I
Authors : Kato, K.; Hamaguchi, T.; Nagao, R.; Kawakami, K.; Yonekura, K.; Shen, J.R.
Deposited on : 2021-06-21
Resolution : 2.04 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

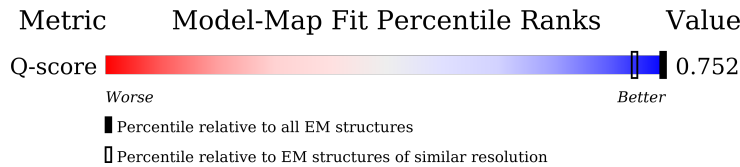
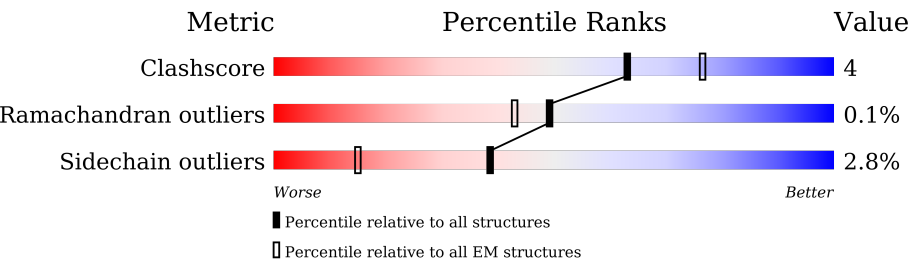
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using 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 i

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

The reported resolution of this entry is 2.04 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.



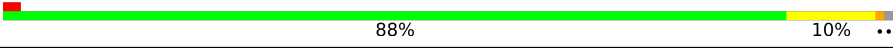
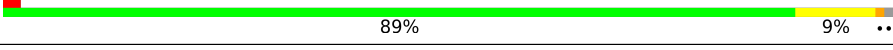
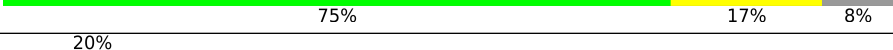
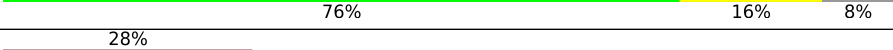
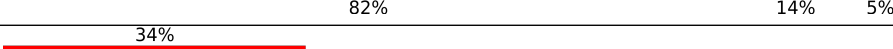
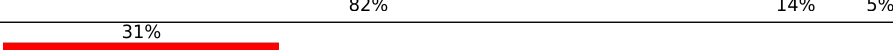
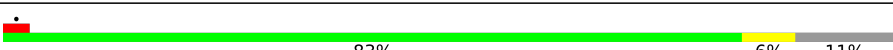
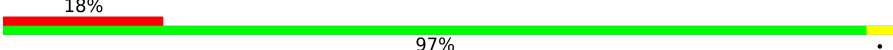
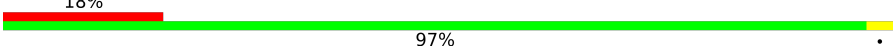
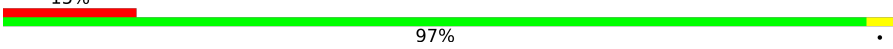
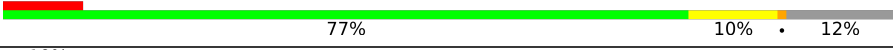
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1810 (1.55 - 2.54)

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	aA	783	7% 90% 8% .
1	bA	783	7% 90% 8% .
1	cA	783	7% 90% 8% .
2	aB	872	. 77% 6% 17%

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Mol	Chain	Length	Quality of chain
2	bB	872	
2	cB	872	
3	aC	81	
3	bC	81	
3	cC	81	
4	aD	144	
4	bD	144	
4	cD	144	
5	aE	65	
5	bE	65	
5	cE	65	
6	aF	181	
6	bF	181	
6	cF	181	
7	aI	35	
7	bI	35	
7	cI	35	
8	aJ	33	
8	bJ	33	
8	cJ	33	
9	aL	147	
9	bL	147	
9	cL	147	
10	aM	34	
10	bM	34	

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Mol	Chain	Length	Quality of chain
10	cM	34	 A horizontal bar chart showing the quality of the chain. The bar is divided into three segments: a green segment representing 82%, a yellow segment representing 15%, and a grey segment representing the remaining 3%. The green segment is the largest, followed by the yellow segment, and the grey segment is the smallest. The percentages are labeled at the end of each segment: 82%, 15%, and 3%.

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 67641 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	aA	772	Total	C	N	O	S	0	0
			6038	3957	1031	1025	25		
1	bA	772	Total	C	N	O	S	0	0
			6038	3957	1031	1025	25		
1	cA	772	Total	C	N	O	S	0	0
			6038	3957	1031	1025	25		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	aB	725	Total	C	N	O	S	0	0
			5701	3761	954	968	18		
2	bB	725	Total	C	N	O	S	0	0
			5701	3761	954	968	18		
2	cB	725	Total	C	N	O	S	0	0
			5701	3761	954	968	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	aC	80	Total	C	N	O	S	0	0
			599	368	103	118	10		
3	bC	80	Total	C	N	O	S	0	0
			599	368	103	118	10		
3	cC	80	Total	C	N	O	S	0	0
			599	368	103	118	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	aD	133	Total	C	N	O	S	0	0
			1038	660	180	194	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	bD	133	Total	C	N	O	S	0	0
			1038	660	180	194	4		
4	cD	133	Total	C	N	O	S	0	0
			1038	660	180	194	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	aE	62	Total	C	N	O		0	0
			507	321	87	99			
5	bE	62	Total	C	N	O		0	0
			507	321	87	99			
5	cE	62	Total	C	N	O		0	0
			507	321	87	99			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	aF	151	Total	C	N	O	S	0	0
			1182	761	200	218	3		
6	bF	151	Total	C	N	O	S	0	0
			1182	761	200	218	3		
6	cF	151	Total	C	N	O	S	0	0
			1182	761	200	218	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	aI	31	Total	C	N	O	S	0	0
			240	164	35	40	1		
7	bI	31	Total	C	N	O	S	0	0
			240	164	35	40	1		
7	cI	31	Total	C	N	O	S	0	0
			240	164	35	40	1		

- Molecule 8 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	aJ	33	Total	C	N	O	0	0
			164	98	33	33		
8	bJ	33	Total	C	N	O	0	0
			164	98	33	33		

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Mol	Chain	Residues	Atoms				AltConf	Trace
8	cJ	33	Total	C	N	O	0	0
			164	98	33	33		

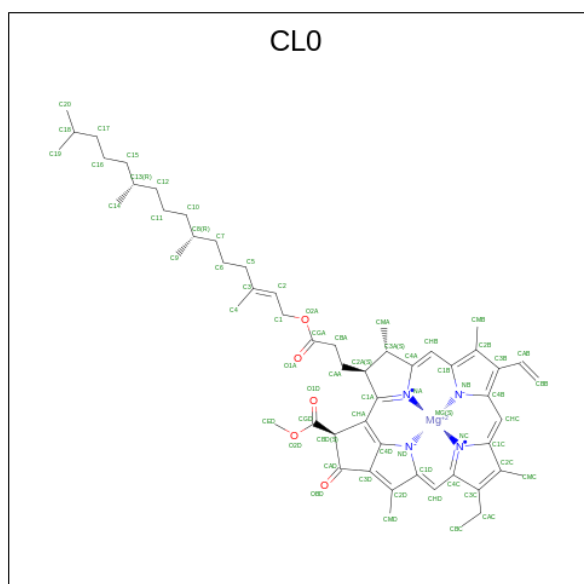
- Molecule 9 is a protein called Photosystem I reaction center subunit XI.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	aL	129	Total	C	N	O	S	0	0
			974	641	162	169	2		
9	bL	129	Total	C	N	O	S	0	0
			974	641	162	169	2		
9	cL	129	Total	C	N	O	S	0	0
			974	641	162	169	2		

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

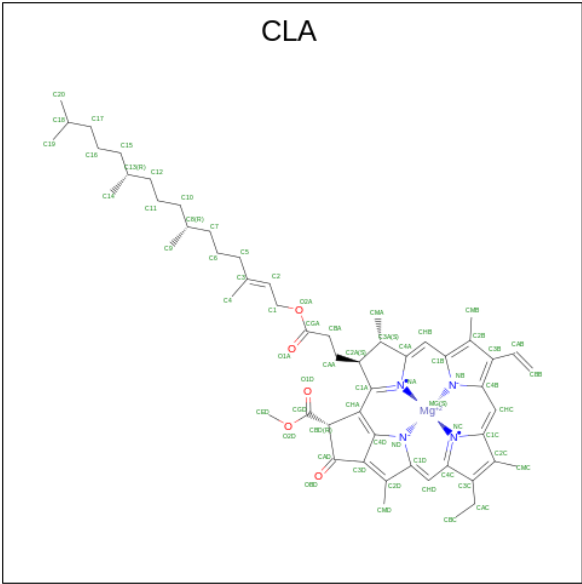
Mol	Chain	Residues	Atoms				AltConf	Trace
10	aM	29	Total	C	N	O	0	0
			190	127	30	33		
10	bM	29	Total	C	N	O	0	0
			190	127	30	33		
10	cM	29	Total	C	N	O	0	0
			190	127	30	33		

- Molecule 11 is CHLOROPHYLL A ISOMER (CCD ID: CL0) (formula: $C_{55}H_{72}MgN_4O_5$).



Mol	Chain	Residues	Atoms					AltConf
11	aA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
11	bA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
11	cA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

- Molecule 12 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅).



Mol	Chain	Residues	Atoms					AltConf
12	aA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			56	46	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			53	43	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			51	41	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	aA	1	Total	C	Mg	N	O	0
			45	35	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	aA	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	aA	1	Total 60	C 50	Mg 1	N 4	O 5	0
12	aA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	aA	1	Total 50	C 40	Mg 1	N 4	O 5	0
12	aA	1	Total 49	C 39	Mg 1	N 4	O 5	0
12	aA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	aA	1	Total 47	C 37	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	aA	1	Total 46	C 36	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 60	C 50	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 50	C 40	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	aA	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	aA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	aB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aB	1	Total 61	C 51	Mg 1	N 4	O 5	0
12	aB	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	aB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	aB	1	Total 52	C 42	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	aB	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			56	46	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			52	42	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			59	49	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			46	36	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			47	37	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			54	44	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			46	36	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	aB	1	Total	C	Mg	N	O	0
			50	40	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
12	aB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aB	1	Total 49	C 39	Mg 1	N 4	O 5	0
12	aB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	aB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aB	1	Total 50	C 40	Mg 1	N 4	O 5	0
12	aB	1	Total 59	C 49	Mg 1	N 4	O 5	0
12	aB	1	Total 47	C 37	Mg 1	N 4	O 5	0
12	aB	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	aB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aB	1	Total 41	C 33	Mg 1	N 4	O 3	0
12	aB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aF	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aL	1	Total 53	C 43	Mg 1	N 4	O 5	0
12	aL	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	aL	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	bA	1	Total 53	C 43	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	bA	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	bA	1	Total 60	C 50	Mg 1	N 4	O 5	0
12	bA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	bA	1	Total 50	C 40	Mg 1	N 4	O 5	0
12	bA	1	Total 49	C 39	Mg 1	N 4	O 5	0
12	bA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	bA	1	Total 47	C 37	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 55	C 45	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	bA	1	Total 46	C 36	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 60	C 50	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 50	C 40	Mg 1	N 4	O 5	0
12	bA	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	bA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	bB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bB	1	Total 61	C 51	Mg 1	N 4	O 5	0
12	bB	1	Total 51	C 41	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	bB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	bB	1	Total 52	C 42	Mg 1	N 4	O 5	0
12	bB	1	Total 48	C 38	Mg 1	N 4	O 5	0
12	bB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	bB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	bB	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	bB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bB	1	Total 52	C 42	Mg 1	N 4	O 5	0
12	bB	1	Total 59	C 49	Mg 1	N 4	O 5	0
12	bB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	bB	1	Total 46	C 36	Mg 1	N 4	O 5	0
12	bB	1	Total 47	C 37	Mg 1	N 4	O 5	0
12	bB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	bB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	bB	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	bB	1	Total 46	C 36	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	bB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			59	49	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			47	37	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			51	41	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bB	1	Total	C	Mg	N	O	0
			41	33	1	4	3	
12	bB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bF	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bL	1	Total	C	Mg	N	O	0
			53	43	1	4	5	
12	bL	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	bL	1	Total	C	Mg	N	O	0
			45	35	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	cA	1	Total 53	C 43	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	cA	1	Total 54	C 44	Mg 1	N 4	O 5	0
12	cA	1	Total 60	C 50	Mg 1	N 4	O 5	0
12	cA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	cA	1	Total 50	C 40	Mg 1	N 4	O 5	0
12	cA	1	Total 49	C 39	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	cA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	cA	1	Total 47	C 37	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	cA	1	Total 46	C 36	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 60	C 50	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 50	C 40	Mg 1	N 4	O 5	0
12	cA	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	cA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cA	1	Total 65	C 55	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
12	cA	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	cB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cB	1	Total 61	C 51	Mg 1	N 4	O 5	0
12	cB	1	Total 51	C 41	Mg 1	N 4	O 5	0
12	cB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	cB	1	Total 52	C 42	Mg 1	N 4	O 5	0
12	cB	1	Total 48	C 38	Mg 1	N 4	O 5	0
12	cB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	cB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cB	1	Total 65	C 55	Mg 1	N 4	O 5	0
12	cB	1	Total 56	C 46	Mg 1	N 4	O 5	0
12	cB	1	Total 45	C 35	Mg 1	N 4	O 5	0
12	cB	1	Total 52	C 42	Mg 1	N 4	O 5	0
12	cB	1	Total 59	C 49	Mg 1	N 4	O 5	0
12	cB	1	Total 55	C 45	Mg 1	N 4	O 5	0
12	cB	1	Total 46	C 36	Mg 1	N 4	O 5	0
12	cB	1	Total 47	C 37	Mg 1	N 4	O 5	0
12	cB	1	Total 45	C 35	Mg 1	N 4	O 5	0

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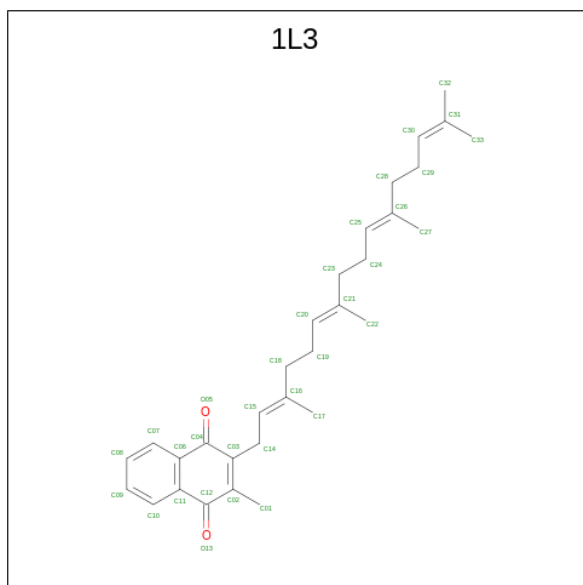
Mol	Chain	Residues	Atoms					AltConf
12	cB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			54	44	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			46	36	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			59	49	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			47	37	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			51	41	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cB	1	Total	C	Mg	N	O	0
			41	33	1	4	3	
12	cF	1	Total	C	Mg	N	O	0
			45	35	1	4	5	

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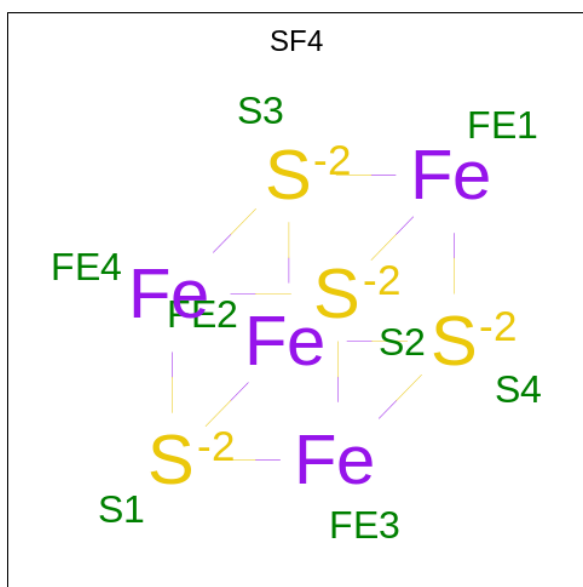
Mol	Chain	Residues	Atoms					AltConf
12	cL	1	Total	C	Mg	N	O	0
			53	43	1	4	5	
12	cL	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
12	cL	1	Total	C	Mg	N	O	0
			45	35	1	4	5	

- Molecule 13 is Menaquinone-4 (CCD ID: 1L3) (formula: $C_{31}H_{40}O_2$).



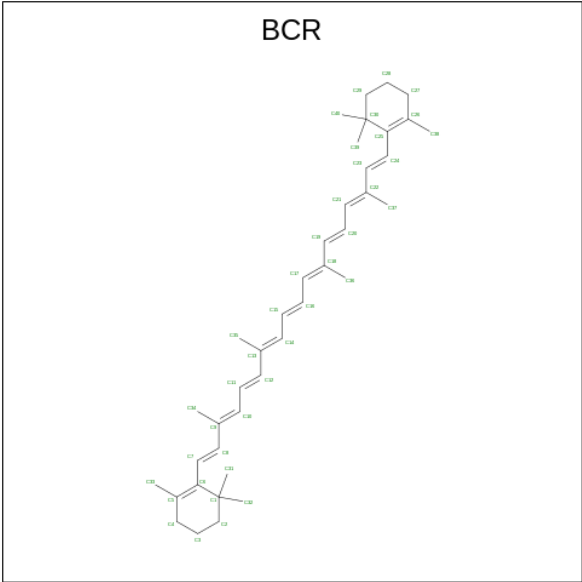
Mol	Chain	Residues	Atoms			AltConf
13	aA	1	Total	C	O	0
			33	31	2	
13	aB	1	Total	C	O	0
			33	31	2	
13	bA	1	Total	C	O	0
			33	31	2	
13	bB	1	Total	C	O	0
			33	31	2	
13	cA	1	Total	C	O	0
			33	31	2	
13	cB	1	Total	C	O	0
			33	31	2	

- Molecule 14 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			AltConf
14	aA	1	Total	Fe	S	0
			8	4	4	
14	aC	1	Total	Fe	S	0
			8	4	4	
14	aC	1	Total	Fe	S	0
			8	4	4	
14	bA	1	Total	Fe	S	0
			8	4	4	
14	bC	1	Total	Fe	S	0
			8	4	4	
14	bC	1	Total	Fe	S	0
			8	4	4	
14	cA	1	Total	Fe	S	0
			8	4	4	
14	cC	1	Total	Fe	S	0
			8	4	4	
14	cC	1	Total	Fe	S	0
			8	4	4	

- Molecule 15 is BETA-CAROTENE (CCD ID: BCR) (formula: C₄₀H₅₆).



Mol	Chain	Residues	Atoms		AltConf
15	aA	1	Total	C	0
			40	40	
15	aA	1	Total	C	0
			40	40	
15	aA	1	Total	C	0
			40	40	
15	aA	1	Total	C	0
			40	40	
15	aA	1	Total	C	0
			40	40	
15	aB	1	Total	C	0
			40	40	
15	aB	1	Total	C	0
			40	40	
15	aB	1	Total	C	0
			40	40	
15	aB	1	Total	C	0
			40	40	
15	aB	1	Total	C	0
			40	40	
15	aF	1	Total	C	0
			40	40	
15	aF	1	Total	C	0
			40	40	
15	aF	1	Total	C	0
			40	40	

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Mol	Chain	Residues	Atoms	AltConf
15	aI	1	Total C 40 40	0
15	aJ	1	Total C 40 40	0
15	aL	1	Total C 40 40	0
15	aL	1	Total C 40 40	0
15	aL	1	Total C 40 40	0
15	aM	1	Total C 40 40	0
15	bA	1	Total C 40 40	0
15	bA	1	Total C 40 40	0
15	bA	1	Total C 40 40	0
15	bA	1	Total C 40 40	0
15	bA	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bB	1	Total C 40 40	0
15	bF	1	Total C 40 40	0
15	bF	1	Total C 40 40	0
15	bF	1	Total C 40 40	0
15	bI	1	Total C 40 40	0

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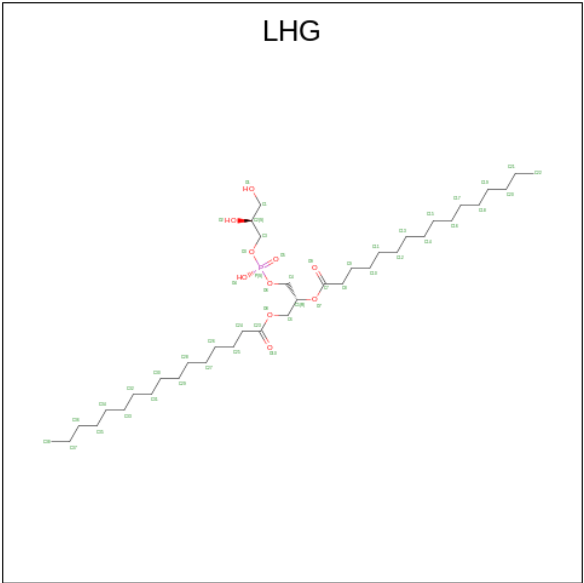
Mol	Chain	Residues	Atoms	AltConf
15	bJ	1	Total C 40 40	0
15	bL	1	Total C 40 40	0
15	bL	1	Total C 40 40	0
15	bL	1	Total C 40 40	0
15	bM	1	Total C 40 40	0
15	cA	1	Total C 40 40	0
15	cA	1	Total C 40 40	0
15	cA	1	Total C 40 40	0
15	cA	1	Total C 40 40	0
15	cA	1	Total C 40 40	0
15	cB	1	Total C 40 40	0
15	cB	1	Total C 40 40	0
15	cB	1	Total C 40 40	0
15	cB	1	Total C 40 40	0
15	cB	1	Total C 40 40	0
15	cB	1	Total C 40 40	0
15	cF	1	Total C 40 40	0
15	cF	1	Total C 40 40	0
15	cF	1	Total C 40 40	0
15	cI	1	Total C 40 40	0
15	cJ	1	Total C 40 40	0

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Mol	Chain	Residues	Atoms		AltConf
15	cL	1	Total	C	0
			40	40	
15	cL	1	Total	C	0
			40	40	
15	cL	1	Total	C	0
			40	40	
15	cM	1	Total	C	0
			40	40	

- Molecule 16 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C₃₈H₇₅O₁₀P).



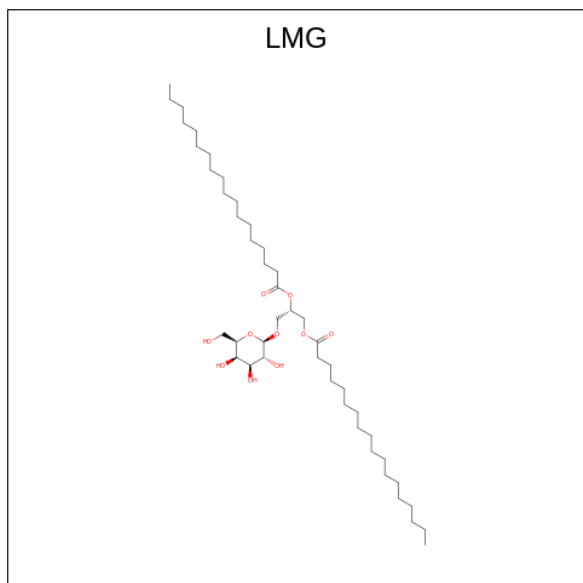
Mol	Chain	Residues	Atoms				AltConf
16	aA	1	Total	C	O	P	0
			49	38	10	1	
16	aA	1	Total	C	O	P	0
			27	16	10	1	
16	aB	1	Total	C	O	P	0
			23	12	10	1	
16	bA	1	Total	C	O	P	0
			49	38	10	1	
16	bA	1	Total	C	O	P	0
			27	16	10	1	
16	bB	1	Total	C	O	P	0
			23	12	10	1	
16	cA	1	Total	C	O	P	0
			49	38	10	1	

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Mol	Chain	Residues	Atoms				AltConf
16	cA	1	Total	C	O	P	0
			27	16	10	1	
16	cB	1	Total	C	O	P	0
			23	12	10	1	

- Molecule 17 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: $C_{45}H_{86}O_{10}$).



Mol	Chain	Residues	Atoms			AltConf
17	aB	1	Total	C	O	0
			43	33	10	
17	bB	1	Total	C	O	0
			43	33	10	
17	cB	1	Total	C	O	0
			43	33	10	

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		AltConf
18	aA	45	Total	O	0
			45	45	
18	aB	67	Total	O	0
			67	67	
18	aC	14	Total	O	0
			14	14	
18	aD	2	Total	O	0
			2	2	

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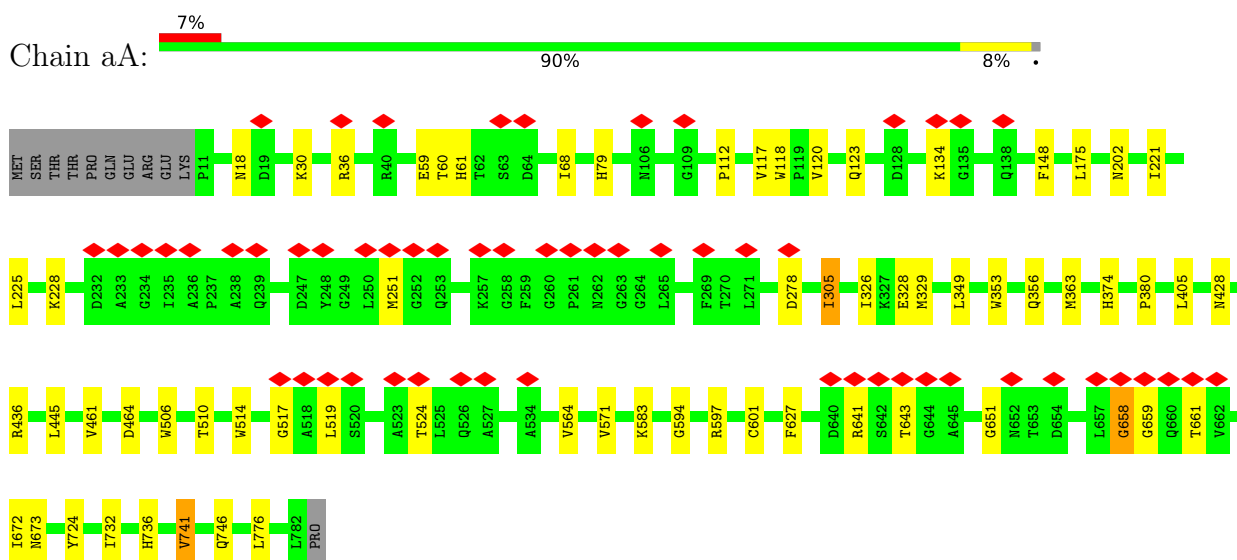
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Mol	Chain	Residues	Atoms		AltConf
18	aE	3	Total 3	O 3	0
18	aF	1	Total 1	O 1	0
18	aJ	1	Total 1	O 1	0
18	aL	1	Total 1	O 1	0
18	bA	45	Total 45	O 45	0
18	bB	67	Total 67	O 67	0
18	bC	14	Total 14	O 14	0
18	bD	2	Total 2	O 2	0
18	bE	3	Total 3	O 3	0
18	bF	1	Total 1	O 1	0
18	bJ	1	Total 1	O 1	0
18	bL	1	Total 1	O 1	0
18	cA	45	Total 45	O 45	0
18	cB	67	Total 67	O 67	0
18	cC	14	Total 14	O 14	0
18	cD	2	Total 2	O 2	0
18	cE	3	Total 3	O 3	0
18	cF	1	Total 1	O 1	0
18	cJ	1	Total 1	O 1	0
18	cL	1	Total 1	O 1	0

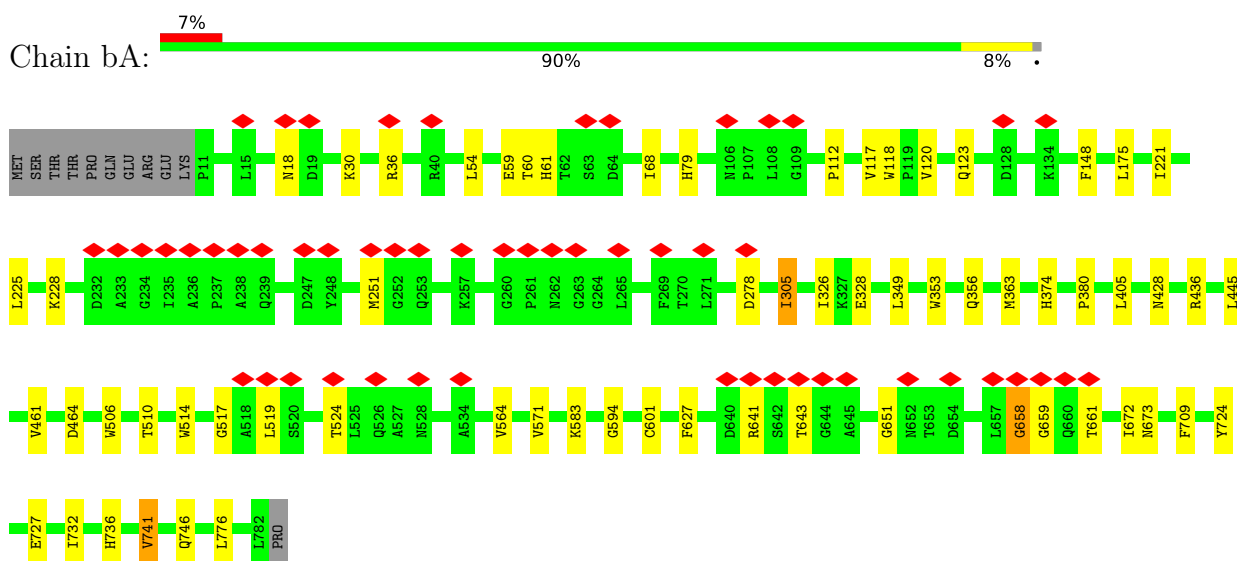
3 Residue-property plots

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

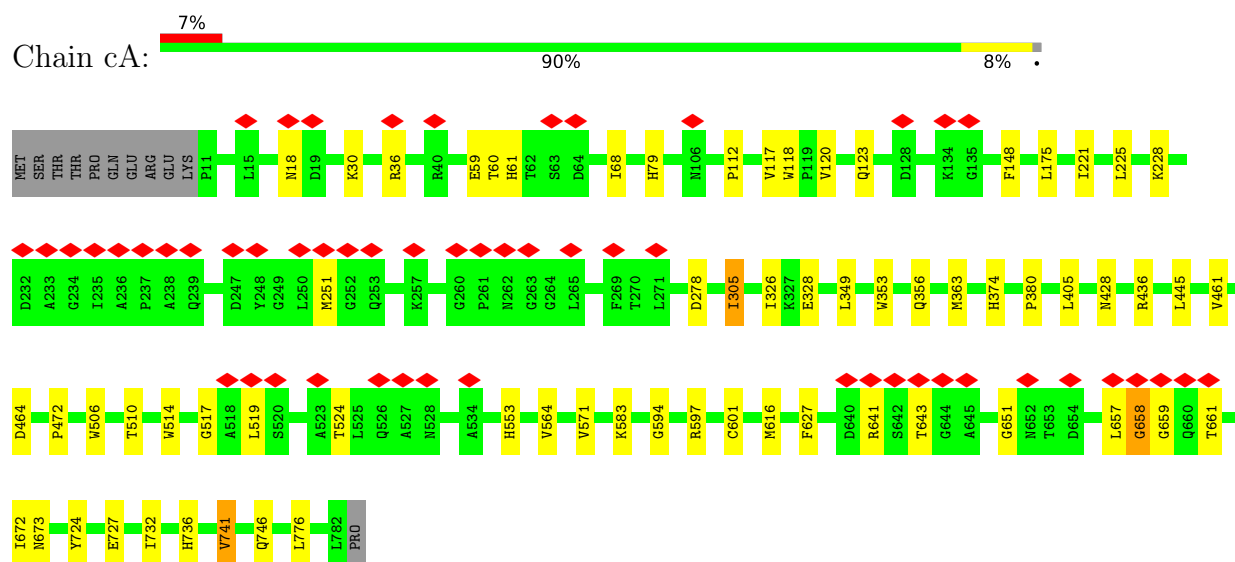
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



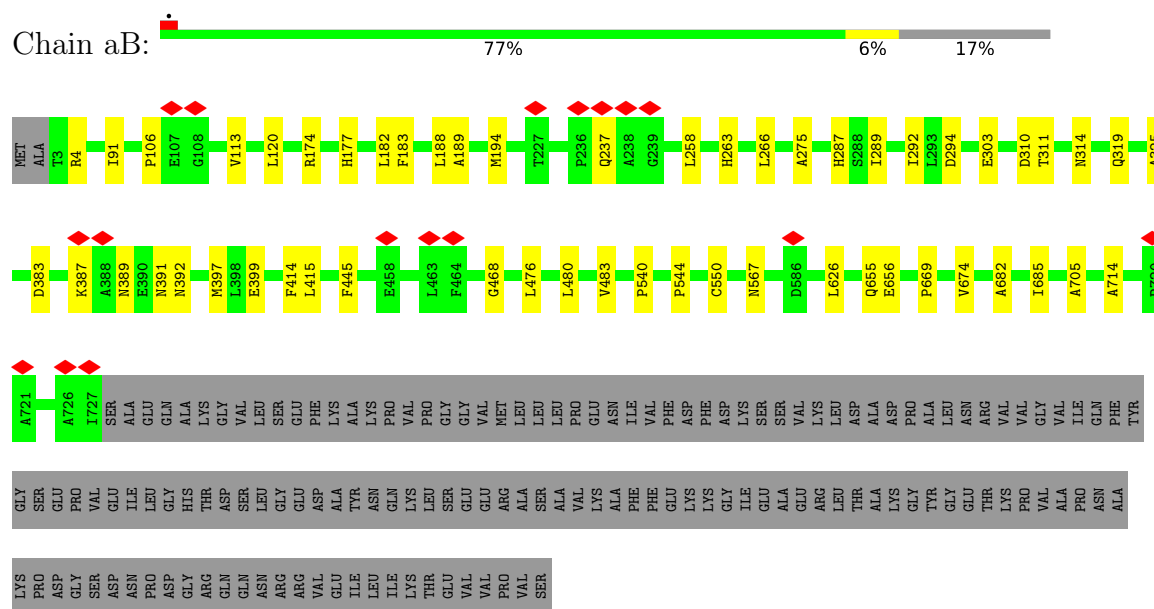
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



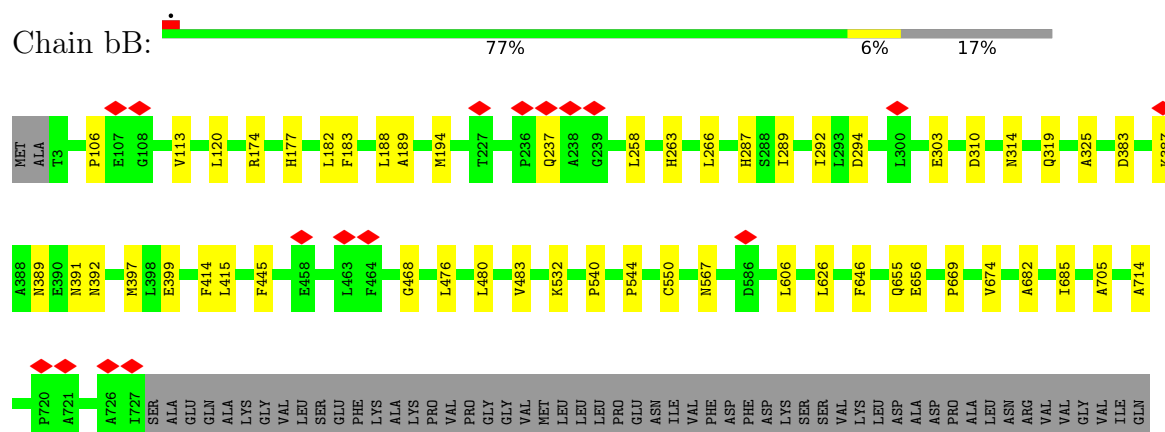
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1

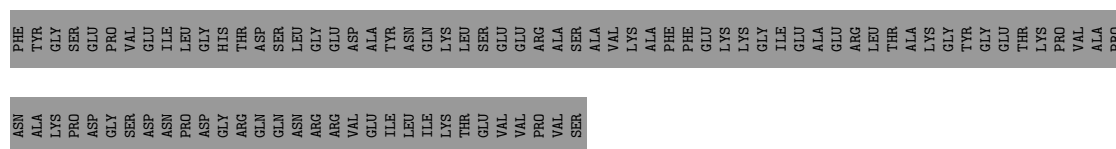


• Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2

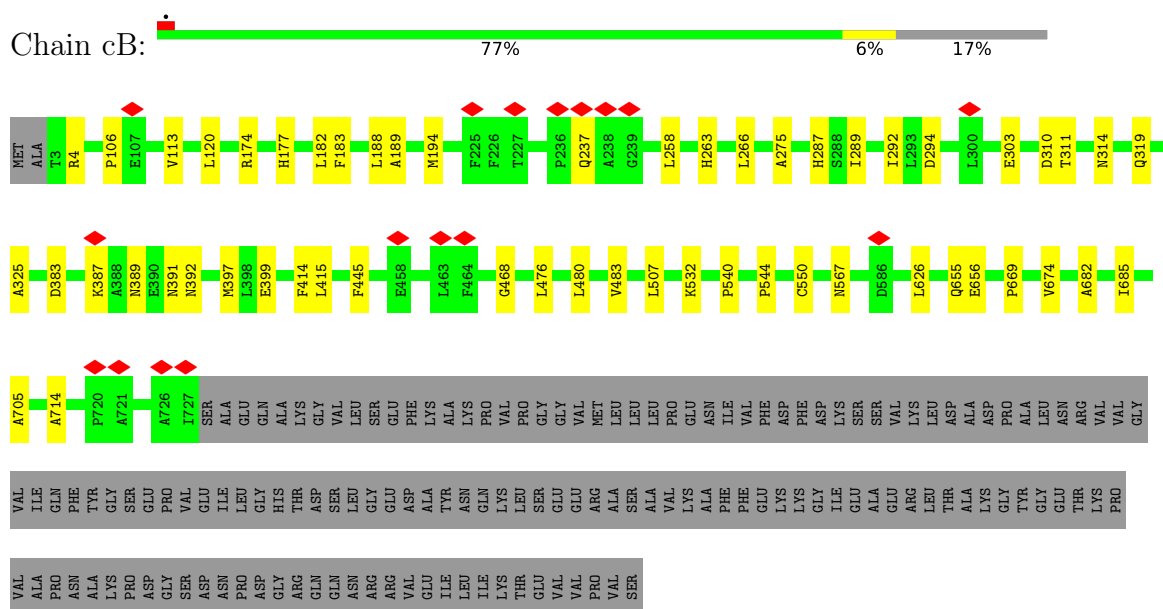


• Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2

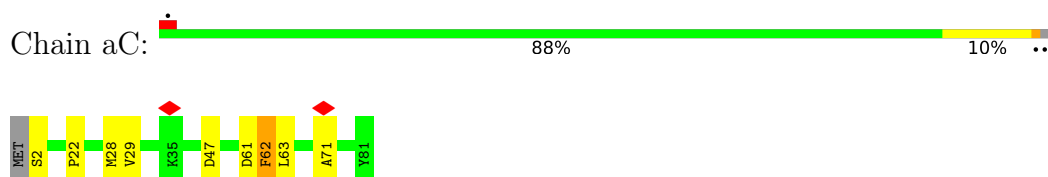




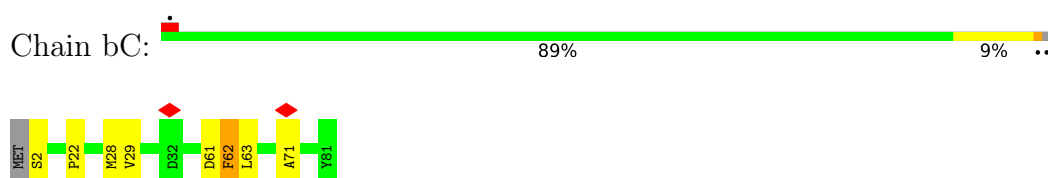
• Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2



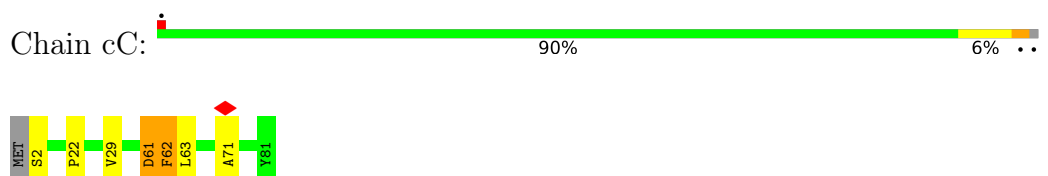
• Molecule 3: Photosystem I iron-sulfur center



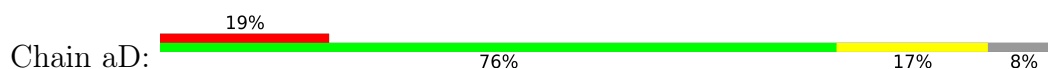
• Molecule 3: Photosystem I iron-sulfur center

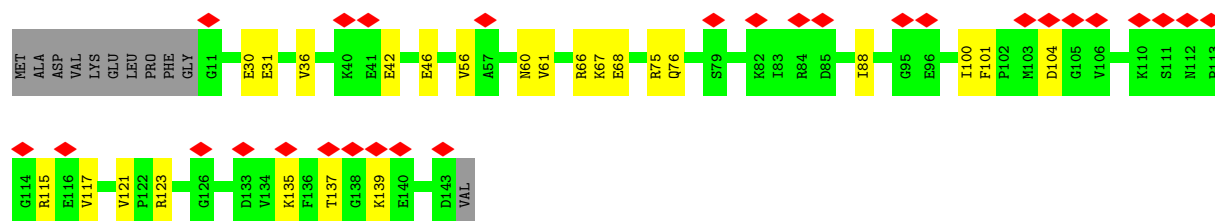


• Molecule 3: Photosystem I iron-sulfur center

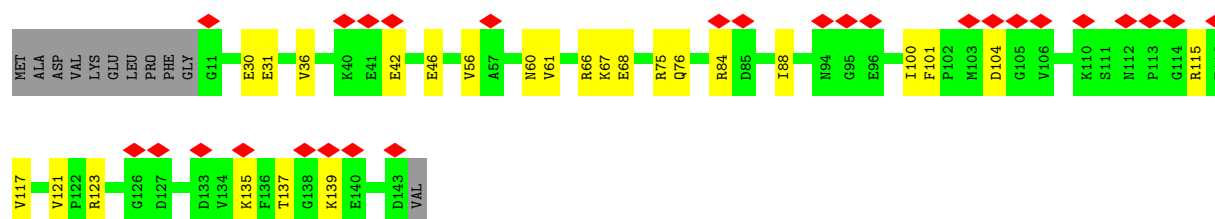
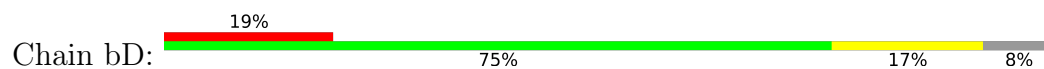


• Molecule 4: Photosystem I reaction center subunit II

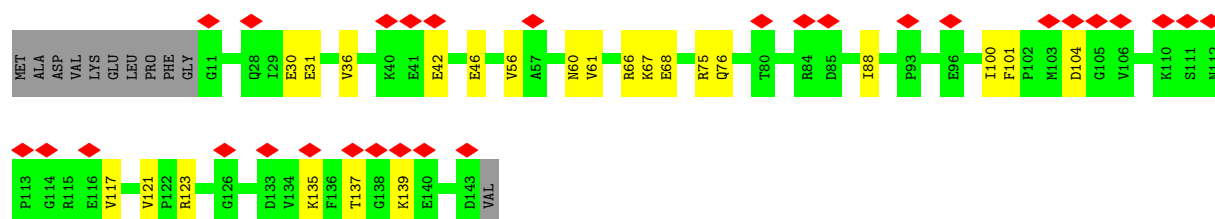
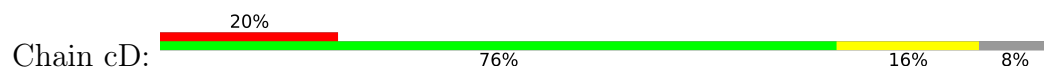




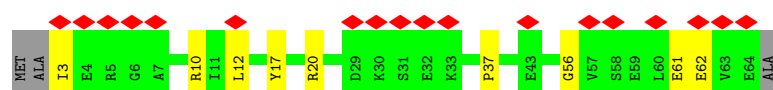
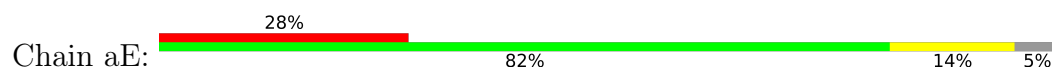
• Molecule 4: Photosystem I reaction center subunit II



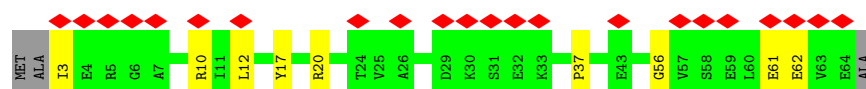
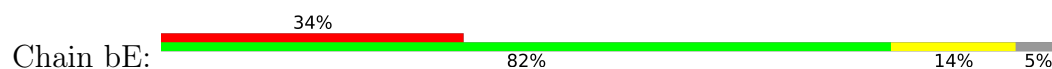
• Molecule 4: Photosystem I reaction center subunit II



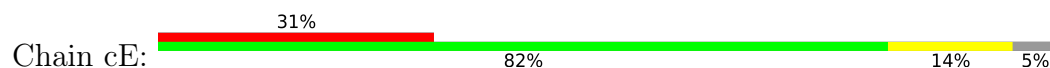
• Molecule 5: Photosystem I reaction center subunit IV

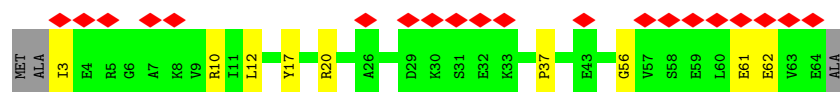


• Molecule 5: Photosystem I reaction center subunit IV

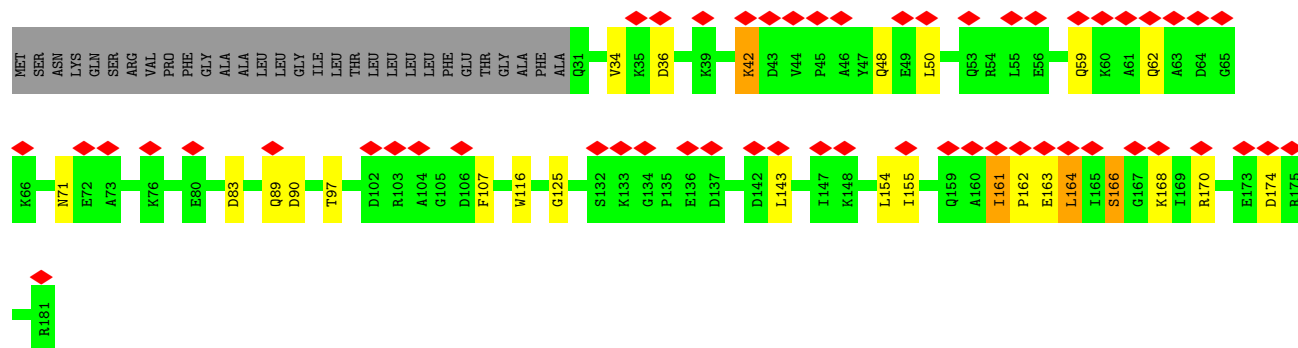


• Molecule 5: Photosystem I reaction center subunit IV

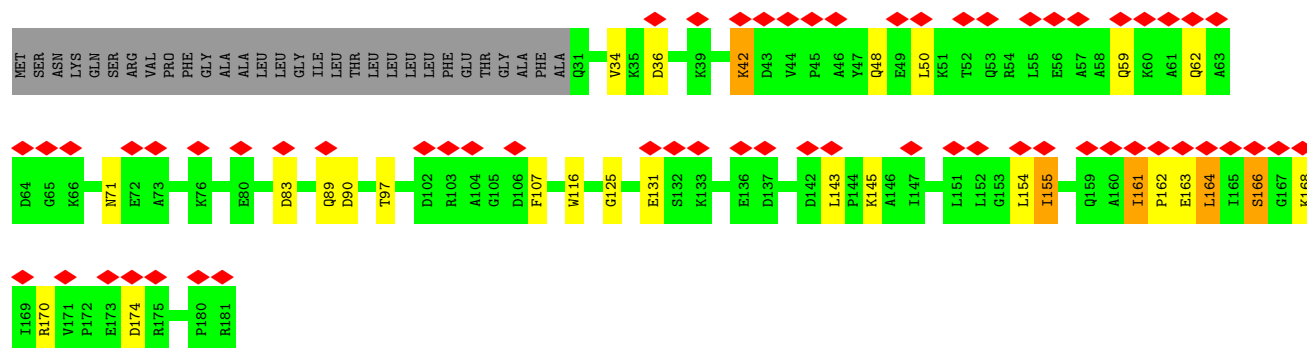




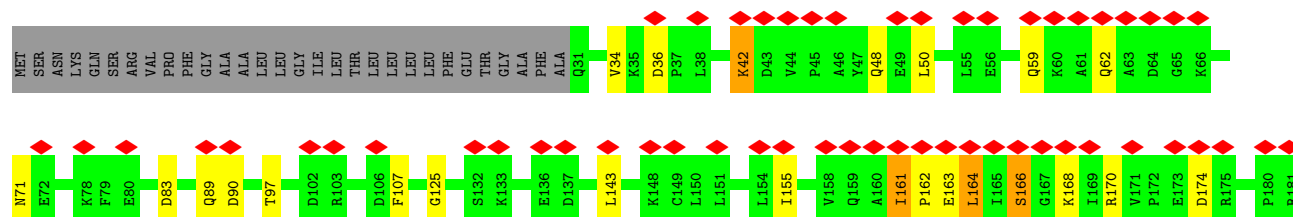
• Molecule 6: Photosystem I reaction center subunit III



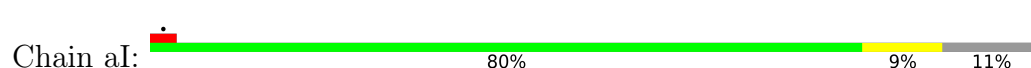
• Molecule 6: Photosystem I reaction center subunit III



• Molecule 6: Photosystem I reaction center subunit III

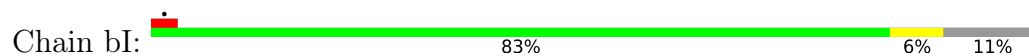


• Molecule 7: Photosystem I reaction center subunit Z

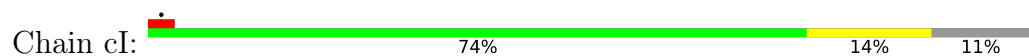




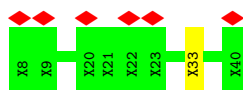
- Molecule 7: Photosystem I reaction center subunit Z



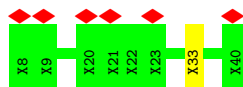
- Molecule 7: Photosystem I reaction center subunit Z



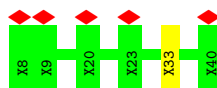
- Molecule 8: Unknown protein



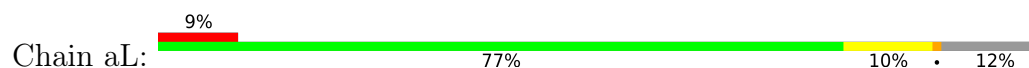
- Molecule 8: Unknown protein



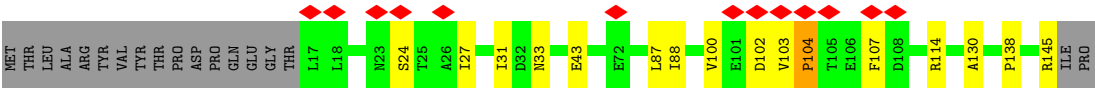
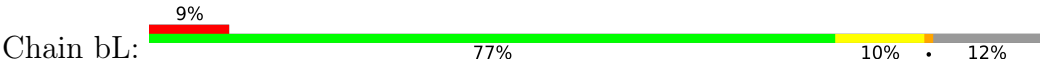
- Molecule 8: Unknown protein



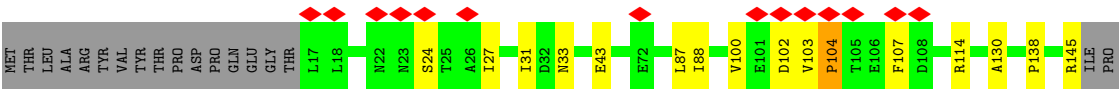
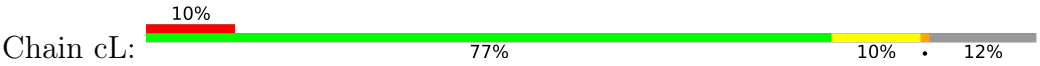
- Molecule 9: Photosystem I reaction center subunit XI



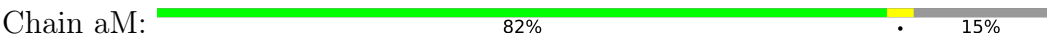
- Molecule 9: Photosystem I reaction center subunit XI



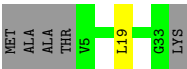
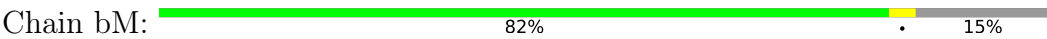
• Molecule 9: Photosystem I reaction center subunit XI



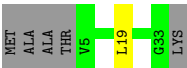
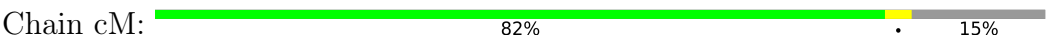
• Molecule 10: Photosystem I reaction center subunit XII



• Molecule 10: Photosystem I reaction center subunit XII



• Molecule 10: Photosystem I reaction center subunit XII



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	261743	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70.22	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.465	Depositor
Minimum map value	-0.239	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.045	Depositor
Map size (Å)	329.2, 329.2, 329.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.823, 0.823, 0.823	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LHG, LMG, 1L3, BCR, CL0, SF4, CLA

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	aA	0.31	0/6244	0.54	4/8520 (0.0%)
1	bA	0.31	0/6244	0.54	4/8520 (0.0%)
1	cA	0.31	0/6244	0.54	4/8520 (0.0%)
2	aB	0.32	0/5911	0.51	2/8084 (0.0%)
2	bB	0.32	0/5911	0.51	2/8084 (0.0%)
2	cB	0.32	0/5911	0.51	2/8084 (0.0%)
3	aC	0.30	0/609	0.61	2/825 (0.2%)
3	bC	0.31	0/609	0.61	2/825 (0.2%)
3	cC	0.30	0/609	0.61	2/825 (0.2%)
4	aD	0.26	0/1061	0.46	0/1434
4	bD	0.26	0/1061	0.46	0/1434
4	cD	0.26	0/1061	0.46	0/1434
5	aE	0.25	0/515	0.53	0/694
5	bE	0.26	0/515	0.53	0/694
5	cE	0.25	0/515	0.53	0/694
6	aF	0.26	0/1208	0.54	0/1638
6	bF	0.26	0/1208	0.53	0/1638
6	cF	0.26	0/1208	0.54	0/1638
7	aI	0.31	0/245	0.58	0/336
7	bI	0.32	0/245	0.58	0/336
7	cI	0.32	0/245	0.58	0/336
9	aL	0.32	0/997	0.63	0/1357
9	bL	0.32	0/997	0.63	0/1357
9	cL	0.32	0/997	0.63	0/1357
10	aM	0.29	0/190	0.43	0/260
10	bM	0.29	0/190	0.43	0/260
10	cM	0.28	0/190	0.44	0/260
All	All	0.31	0/50940	0.53	24/69444 (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
3	aC	0	1
3	bC	0	1
3	cC	0	1
8	aJ	0	1
8	bJ	0	1
8	cJ	0	1
9	aL	0	1
9	bL	0	1
9	cL	0	1
All	All	0	9

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	aA	517	GLY	CA-C-N	9.84	139.41	121.70
1	aA	517	GLY	C-N-CA	9.84	139.41	121.70
1	cA	517	GLY	CA-C-N	9.83	139.39	121.70
1	cA	517	GLY	C-N-CA	9.83	139.39	121.70
1	bA	517	GLY	CA-C-N	9.82	139.38	121.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	aC	61	ASP	Peptide
8	aJ	33	UNK	Peptide
9	aL	104	PRO	Peptide
3	bC	61	ASP	Peptide
8	bJ	33	UNK	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	aA	6038	0	5897	35	0
1	bA	6038	0	5897	34	0
1	cA	6038	0	5897	36	0
2	aB	5701	0	5519	38	0
2	bB	5701	0	5519	37	0
2	cB	5701	0	5519	39	0
3	aC	599	0	579	5	0
3	bC	599	0	579	4	0
3	cC	599	0	579	4	0
4	aD	1038	0	1039	15	0
4	bD	1038	0	1039	14	0
4	cD	1038	0	1039	14	0
5	aE	507	0	504	4	0
5	bE	507	0	504	4	0
5	cE	507	0	504	5	0
6	aF	1182	0	1207	11	0
6	bF	1182	0	1207	13	0
6	cF	1182	0	1207	10	0
7	aI	240	0	255	3	0
7	bI	240	0	255	2	0
7	cI	240	0	255	4	0
8	aJ	164	0	35	0	0
8	bJ	164	0	35	0	0
8	cJ	164	0	35	0	0
9	aL	974	0	998	9	0
9	bL	974	0	998	9	0
9	cL	974	0	998	9	0
10	aM	190	0	215	0	0
10	bM	190	0	215	0	0
10	cM	190	0	215	0	0
11	aA	65	0	72	0	0
11	bA	65	0	72	0	0
11	cA	65	0	72	0	0
12	aA	2396	0	2199	54	0
12	aB	2144	0	1874	46	0
12	aF	45	0	33	0	0
12	aL	143	0	111	3	0
12	bA	2351	0	2166	55	0
12	bB	2144	0	1874	44	0
12	bF	45	0	33	0	0
12	bL	143	0	111	3	0
12	cA	2351	0	2166	61	0
12	cB	2099	0	1841	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	cF	45	0	33	0	0
12	cL	143	0	111	3	0
13	aA	33	0	0	0	0
13	aB	33	0	0	0	0
13	bA	33	0	0	0	0
13	bB	33	0	0	1	0
13	cA	33	0	0	0	0
13	cB	33	0	0	0	0
14	aA	8	0	0	0	0
14	aC	16	0	0	0	0
14	bA	8	0	0	0	0
14	bC	16	0	0	0	0
14	cA	8	0	0	0	0
14	cC	16	0	0	0	0
15	aA	200	0	280	8	0
15	aB	240	0	336	11	0
15	aF	120	0	168	7	0
15	aI	40	0	56	2	0
15	aJ	40	0	56	1	0
15	aL	120	0	168	4	0
15	aM	40	0	55	0	0
15	bA	200	0	280	10	0
15	bB	240	0	336	12	0
15	bF	120	0	168	5	0
15	bI	40	0	56	2	0
15	bJ	40	0	56	1	0
15	bL	120	0	168	4	0
15	bM	40	0	55	0	0
15	cA	200	0	280	12	0
15	cB	240	0	336	9	0
15	cF	120	0	168	7	0
15	cI	40	0	56	1	0
15	cJ	40	0	56	0	0
15	cL	120	0	168	6	0
15	cM	40	0	55	0	0
16	aA	76	0	98	1	0
16	aB	23	0	16	0	0
16	bA	76	0	98	2	0
16	bB	23	0	16	0	0
16	cA	76	0	98	2	0
16	cB	23	0	16	0	0
17	aB	43	0	56	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	bB	43	0	56	0	0
17	cB	43	0	56	0	0
18	aA	45	0	0	1	0
18	aB	67	0	0	1	0
18	aC	14	0	0	0	0
18	aD	2	0	0	0	0
18	aE	3	0	0	0	0
18	aF	1	0	0	0	0
18	aJ	1	0	0	0	0
18	aL	1	0	0	0	0
18	bA	45	0	0	1	0
18	bB	67	0	0	1	0
18	bC	14	0	0	0	0
18	bD	2	0	0	0	0
18	bE	3	0	0	0	0
18	bF	1	0	0	0	0
18	bJ	1	0	0	0	0
18	bL	1	0	0	0	0
18	cA	45	0	0	1	0
18	cB	67	0	0	1	0
18	cC	14	0	0	0	0
18	cD	2	0	0	0	0
18	cE	3	0	0	0	0
18	cF	1	0	0	0	0
18	cJ	1	0	0	0	0
18	cL	1	0	0	0	0
All	All	67641	0	65379	561	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 4.

The worst 5 of 561 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)
12:cA:809:CLA:HBB2	12:cA:828:CLA:H171	1.71	0.72
12:bA:809:CLA:HBB2	12:bA:828:CLA:H171	1.71	0.72
12:aA:809:CLA:HBB2	12:aA:828:CLA:H171	1.71	0.71
12:bA:818:CLA:HBA2	12:bA:827:CLA:HBB2	1.73	0.71
12:aA:818:CLA:HBA2	12:aA:827:CLA:HBB2	1.73	0.69

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	aA	770/783 (98%)	742 (96%)	28 (4%)	0	100	100
1	bA	770/783 (98%)	742 (96%)	28 (4%)	0	100	100
1	cA	770/783 (98%)	742 (96%)	28 (4%)	0	100	100
2	aB	723/872 (83%)	708 (98%)	15 (2%)	0	100	100
2	bB	723/872 (83%)	708 (98%)	15 (2%)	0	100	100
2	cB	723/872 (83%)	708 (98%)	15 (2%)	0	100	100
3	aC	78/81 (96%)	75 (96%)	2 (3%)	1 (1%)	9	3
3	bC	78/81 (96%)	75 (96%)	2 (3%)	1 (1%)	9	3
3	cC	78/81 (96%)	75 (96%)	2 (3%)	1 (1%)	9	3
4	aD	131/144 (91%)	126 (96%)	5 (4%)	0	100	100
4	bD	131/144 (91%)	126 (96%)	5 (4%)	0	100	100
4	cD	131/144 (91%)	126 (96%)	5 (4%)	0	100	100
5	aE	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
5	bE	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
5	cE	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
6	aF	149/181 (82%)	144 (97%)	5 (3%)	0	100	100
6	bF	149/181 (82%)	144 (97%)	5 (3%)	0	100	100
6	cF	149/181 (82%)	144 (97%)	5 (3%)	0	100	100
7	aI	29/35 (83%)	28 (97%)	1 (3%)	0	100	100
7	bI	29/35 (83%)	28 (97%)	1 (3%)	0	100	100
7	cI	29/35 (83%)	28 (97%)	1 (3%)	0	100	100
9	aL	127/147 (86%)	122 (96%)	4 (3%)	1 (1%)	16	9
9	bL	127/147 (86%)	122 (96%)	4 (3%)	1 (1%)	16	9
9	cL	127/147 (86%)	122 (96%)	4 (3%)	1 (1%)	16	9
10	aM	27/34 (79%)	27 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	bM	27/34 (79%)	27 (100%)	0	0	100	100
10	cM	27/34 (79%)	27 (100%)	0	0	100	100
All	All	6282/7026 (89%)	6087 (97%)	189 (3%)	6 (0%)	49	43

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	aL	104	PRO
9	bL	104	PRO
9	cL	104	PRO
3	aC	62	PHE
3	bC	62	PHE

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	aA	612/623 (98%)	592 (97%)	20 (3%)	33	28
1	bA	612/623 (98%)	592 (97%)	20 (3%)	33	28
1	cA	612/623 (98%)	592 (97%)	20 (3%)	33	28
2	aB	573/694 (83%)	569 (99%)	4 (1%)	76	80
2	bB	573/694 (83%)	569 (99%)	4 (1%)	76	80
2	cB	573/694 (83%)	569 (99%)	4 (1%)	76	80
3	aC	68/69 (99%)	67 (98%)	1 (2%)	57	58
3	bC	68/69 (99%)	67 (98%)	1 (2%)	57	58
3	cC	68/69 (99%)	67 (98%)	1 (2%)	57	58
4	aD	113/122 (93%)	110 (97%)	3 (3%)	39	36
4	bD	113/122 (93%)	110 (97%)	3 (3%)	39	36
4	cD	113/122 (93%)	110 (97%)	3 (3%)	39	36
5	aE	56/57 (98%)	53 (95%)	3 (5%)	20	12
5	bE	56/57 (98%)	53 (95%)	3 (5%)	20	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	cE	56/57 (98%)	53 (95%)	3 (5%)	20	12
6	aF	125/148 (84%)	113 (90%)	12 (10%)	8	3
6	bF	125/148 (84%)	113 (90%)	12 (10%)	8	3
6	cF	125/148 (84%)	113 (90%)	12 (10%)	8	3
7	aI	26/30 (87%)	25 (96%)	1 (4%)	29	24
7	bI	26/30 (87%)	25 (96%)	1 (4%)	29	24
7	cI	26/30 (87%)	25 (96%)	1 (4%)	29	24
9	aL	100/116 (86%)	98 (98%)	2 (2%)	48	48
9	bL	100/116 (86%)	98 (98%)	2 (2%)	48	48
9	cL	100/116 (86%)	98 (98%)	2 (2%)	48	48
10	aM	18/21 (86%)	17 (94%)	1 (6%)	19	12
10	bM	18/21 (86%)	17 (94%)	1 (6%)	19	12
10	cM	18/21 (86%)	17 (94%)	1 (6%)	19	12
All	All	5073/5640 (90%)	4932 (97%)	141 (3%)	38	34

5 of 141 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	cB	294	ASP
4	cD	42	GLU
6	cF	83	ASP
1	bA	30	LYS
1	bA	18	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
2	bB	349	GLN
6	cF	62	GLN
6	bF	62	GLN
4	cD	76	GLN
2	cB	389	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

354 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
15	BCR	cA	849	-	41,41,41	1.18	2 (4%)	56,56,56	1.39	6 (10%)
15	BCR	aI	101	-	41,41,41	1.11	2 (4%)	56,56,56	1.39	9 (16%)
12	CLA	bB	930	2	53,57,73	2.27	20 (37%)	62,93,113	3.17	29 (46%)
12	CLA	bA	830	1	69,73,73	1.93	19 (27%)	83,113,113	2.66	28 (33%)
12	CLA	bB	929	2	49,53,73	2.33	20 (40%)	59,89,113	3.33	27 (45%)
15	BCR	aF	204	-	41,41,41	1.04	2 (4%)	56,56,56	1.29	9 (16%)
15	BCR	bL	205	-	41,41,41	1.05	2 (4%)	56,56,56	1.24	6 (10%)
12	CLA	cB	917	2	59,63,73	2.08	19 (32%)	71,101,113	2.92	30 (42%)
12	CLA	bL	204	18	49,53,73	2.36	21 (42%)	59,89,113	3.24	26 (44%)
12	CLA	bA	805	1	57,61,73	2.18	22 (38%)	68,98,113	3.13	28 (41%)
15	BCR	bA	846	-	41,41,41	1.07	2 (4%)	56,56,56	1.27	7 (12%)
12	CLA	cA	808	1	55,59,73	2.25	21 (38%)	66,96,113	3.07	31 (46%)
12	CLA	cB	910	2	49,53,73	2.36	18 (36%)	59,89,113	3.14	28 (47%)
12	CLA	aA	836	1	49,53,73	2.38	19 (38%)	59,89,113	3.08	29 (49%)
12	CLA	aB	930	2	53,57,73	2.27	20 (37%)	62,93,113	3.18	29 (46%)
15	BCR	bF	203	-	41,41,41	1.09	2 (4%)	56,56,56	1.32	7 (12%)
12	CLA	aA	844	16	49,53,73	2.33	20 (40%)	59,89,113	3.02	23 (38%)
12	CLA	cB	902	-	65,69,73	1.95	19 (29%)	78,108,113	2.82	26 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	cA	814	1	49,53,73	2.32	20 (40%)	59,89,113	3.10	27 (45%)
12	CLA	cB	931	2	69,73,73	1.94	19 (27%)	83,113,113	2.97	32 (38%)
15	BCR	bL	206	-	41,41,41	1.03	1 (2%)	56,56,56	1.19	5 (8%)
12	CLA	bB	934	2	49,53,73	2.46	19 (38%)	59,89,113	3.04	25 (42%)
13	1L3	aA	845	-	34,34,34	2.31	9 (26%)	42,45,45	1.61	10 (23%)
12	CLA	bL	202	9	57,61,73	2.17	21 (36%)	68,98,113	3.10	29 (42%)
12	CLA	bB	908	2	52,56,73	2.22	17 (32%)	62,92,113	2.80	27 (43%)
12	CLA	aA	840	1	69,73,73	1.99	19 (27%)	83,113,113	2.67	30 (36%)
12	CLA	cB	934	2	49,53,73	2.46	19 (38%)	59,89,113	3.04	25 (42%)
12	CLA	aB	950	16	49,53,73	2.33	20 (40%)	59,89,113	3.01	23 (38%)
15	BCR	aL	205	-	41,41,41	1.05	2 (4%)	56,56,56	1.23	6 (10%)
12	CLA	cB	922	2	49,53,73	2.31	19 (38%)	59,89,113	3.09	29 (49%)
12	CLA	bA	842	1	69,73,73	1.95	19 (27%)	83,113,113	2.79	30 (36%)
12	CLA	bB	933	18	49,53,73	2.28	19 (38%)	59,89,113	3.07	27 (45%)
12	CLA	cA	831	1	54,58,73	2.20	19 (35%)	65,95,113	3.03	34 (52%)
12	CLA	bA	838	1	69,73,73	1.93	19 (27%)	83,113,113	2.80	28 (33%)
15	BCR	cL	205	-	41,41,41	1.05	2 (4%)	56,56,56	1.23	6 (10%)
12	CLA	cB	914	2	49,53,73	2.32	20 (40%)	59,89,113	3.34	26 (44%)
12	CLA	bB	914	2	49,53,73	2.32	20 (40%)	59,89,113	3.35	26 (44%)
12	CLA	aA	813	1	49,53,73	2.41	21 (42%)	59,89,113	3.10	26 (44%)
15	BCR	cB	941	-	41,41,41	1.09	3 (7%)	56,56,56	1.27	5 (8%)
16	LHG	aA	853	12	26,26,48	0.94	1 (3%)	29,32,54	1.32	3 (10%)
12	CLA	aA	814	1	49,53,73	2.32	19 (38%)	59,89,113	3.11	27 (45%)
12	CLA	aB	907	2	56,60,73	2.13	19 (33%)	67,97,113	3.00	31 (46%)
12	CLA	bA	828	1	69,73,73	1.97	20 (28%)	83,113,113	2.80	30 (36%)
11	CL0	bA	801	1	69,73,73	1.93	20 (28%)	83,113,113	2.65	34 (40%)
12	CLA	bA	835	1	49,53,73	2.34	20 (40%)	59,89,113	3.01	27 (45%)
12	CLA	cL	203	9	49,53,73	2.32	22 (44%)	59,89,113	3.27	25 (42%)
15	BCR	cB	946	-	41,41,41	1.09	3 (7%)	56,56,56	1.23	6 (10%)
12	CLA	cA	803	-	69,73,73	1.93	20 (28%)	83,113,113	2.78	33 (39%)
12	CLA	aB	931	2	69,73,73	1.94	19 (27%)	83,113,113	2.98	32 (38%)
12	CLA	aA	854	18	60,64,73	2.04	20 (33%)	72,102,113	3.05	29 (40%)
16	LHG	bA	851	-	48,48,48	0.65	1 (2%)	51,54,54	1.27	6 (11%)
12	CLA	aB	914	2	49,53,73	2.32	20 (40%)	59,89,113	3.33	26 (44%)
12	CLA	bA	812	1	69,73,73	1.95	21 (30%)	83,113,113	2.77	32 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	bA	810	1	49,53,73	2.35	19 (38%)	59,89,113	3.31	28 (47%)
12	CLA	cB	926	2	69,73,73	1.91	20 (28%)	83,113,113	2.71	32 (38%)
12	CLA	cB	928	2	54,58,73	2.22	20 (37%)	65,95,113	2.91	30 (46%)
15	BCR	cF	201	-	41,41,41	1.08	2 (4%)	56,56,56	1.23	6 (10%)
12	CLA	cA	832	1	59,63,73	2.14	20 (33%)	71,101,113	3.00	31 (43%)
12	CLA	aF	202	6	49,53,73	2.37	20 (40%)	59,89,113	3.22	28 (47%)
15	BCR	aA	848	-	41,41,41	1.13	2 (4%)	56,56,56	1.51	13 (23%)
12	CLA	cB	949	16	45,49,73	2.50	18 (40%)	54,84,113	3.48	29 (53%)
12	CLA	bA	832	1	59,63,73	2.13	20 (33%)	71,101,113	3.00	32 (45%)
12	CLA	aB	924	18	50,54,73	2.28	21 (42%)	60,90,113	3.23	27 (45%)
12	CLA	cA	809	1	49,53,73	2.32	20 (40%)	59,89,113	3.28	29 (49%)
12	CLA	aA	802	18	69,73,73	1.93	19 (27%)	83,113,113	2.76	28 (33%)
15	BCR	cL	201	-	41,41,41	1.18	3 (7%)	56,56,56	1.23	4 (7%)
13	1L3	cA	844	-	34,34,34	2.31	9 (26%)	42,45,45	1.62	9 (21%)
12	CLA	aA	807	1	69,73,73	1.98	20 (28%)	83,113,113	2.82	34 (40%)
15	BCR	cB	944	-	41,41,41	1.08	2 (4%)	56,56,56	1.18	7 (12%)
12	CLA	cB	909	2	59,63,73	2.09	20 (33%)	71,101,113	2.83	32 (45%)
12	CLA	cA	823	1	55,59,73	2.19	20 (36%)	66,96,113	3.11	30 (45%)
12	CLA	cA	817	1	58,62,73	2.19	19 (32%)	69,99,113	3.12	27 (39%)
12	CLA	aA	843	18	69,73,73	1.93	20 (28%)	83,113,113	2.82	34 (40%)
12	CLA	bB	907	2	56,60,73	2.13	19 (33%)	67,97,113	3.01	31 (46%)
12	CLA	bB	910	2	49,53,73	2.36	19 (38%)	59,89,113	3.15	28 (47%)
12	CLA	bA	843	18	69,73,73	1.93	20 (28%)	83,113,113	2.81	34 (40%)
12	CLA	bB	902	-	65,69,73	1.95	20 (30%)	78,108,113	2.82	26 (33%)
12	CLA	aB	923	18	58,62,73	2.07	19 (32%)	69,99,113	2.97	27 (39%)
12	CLA	bA	819	1	64,68,73	2.03	19 (29%)	77,107,113	3.02	34 (44%)
12	CLA	bB	931	2	69,73,73	1.94	19 (27%)	83,113,113	2.97	32 (38%)
15	BCR	bF	201	-	41,41,41	1.07	2 (4%)	56,56,56	1.24	6 (10%)
12	CLA	bA	825	18	69,73,73	2.01	20 (28%)	83,113,113	2.78	31 (37%)
16	LHG	cA	852	12	26,26,48	0.94	1 (3%)	29,32,54	1.32	3 (10%)
12	CLA	aL	202	9	57,61,73	2.17	21 (36%)	68,98,113	3.11	29 (42%)
12	CLA	aB	933	18	49,53,73	2.27	19 (38%)	59,89,113	3.06	27 (45%)
12	CLA	aA	833	1	55,59,73	2.14	18 (32%)	66,96,113	3.06	33 (50%)
15	BCR	cB	943	-	41,41,41	1.06	2 (4%)	56,56,56	1.16	4 (7%)
15	BCR	bB	944	-	41,41,41	1.08	2 (4%)	56,56,56	1.18	7 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	BCR	cA	847	-	41,41,41	1.13	2 (4%)	56,56,56	1.51	13 (23%)
12	CLA	cF	202	6	49,53,73	2.37	21 (42%)	59,89,113	3.22	28 (47%)
12	CLA	bA	821	18	54,58,73	2.22	18 (33%)	65,95,113	2.91	28 (43%)
12	CLA	cB	908	2	52,56,73	2.22	17 (32%)	62,92,113	2.80	27 (43%)
15	BCR	aA	849	-	41,41,41	1.10	3 (7%)	56,56,56	1.18	4 (7%)
12	CLA	cA	807	1	69,73,73	1.97	20 (28%)	83,113,113	2.82	34 (40%)
15	BCR	aL	206	-	41,41,41	1.04	2 (4%)	56,56,56	1.19	4 (7%)
12	CLA	aA	812	1	69,73,73	1.94	21 (30%)	83,113,113	2.78	32 (38%)
12	CLA	cL	202	9	57,61,73	2.18	21 (36%)	68,98,113	3.11	29 (42%)
12	CLA	cA	835	1	49,53,73	2.34	20 (40%)	59,89,113	3.01	27 (45%)
12	CLA	aA	842	1	69,73,73	1.96	19 (27%)	83,113,113	2.79	30 (36%)
14	SF4	bA	845	2,1	0,12,12	-	-	-	-	-
12	CLA	cA	827	1	50,54,73	2.26	20 (40%)	60,90,113	3.24	27 (45%)
12	CLA	aA	809	1	49,53,73	2.32	20 (40%)	59,89,113	3.28	29 (49%)
12	CLA	aA	818	1	58,62,73	2.11	19 (32%)	69,99,113	3.01	29 (42%)
12	CLA	bB	903	2	55,59,73	2.19	20 (36%)	66,96,113	3.08	30 (45%)
15	BCR	aB	943	-	41,41,41	1.07	2 (4%)	56,56,56	1.17	4 (7%)
12	CLA	cA	837	1	55,59,73	2.18	20 (36%)	66,96,113	3.08	29 (43%)
12	CLA	bA	815	1	49,53,73	2.39	19 (38%)	59,89,113	3.20	26 (44%)
12	CLA	bA	803	-	69,73,73	1.93	20 (28%)	83,113,113	2.78	33 (39%)
12	CLA	aA	822	1	53,57,73	2.29	20 (37%)	62,93,113	3.31	27 (43%)
12	CLA	aB	927	2	69,73,73	1.97	19 (27%)	83,113,113	2.46	25 (30%)
15	BCR	cB	942	-	41,41,41	1.06	2 (4%)	56,56,56	1.19	4 (7%)
12	CLA	bA	811	1	49,53,73	2.37	19 (38%)	59,89,113	3.17	27 (45%)
12	CLA	aA	819	1	64,68,73	2.04	19 (29%)	77,107,113	3.01	35 (45%)
15	BCR	bB	941	-	41,41,41	1.10	3 (7%)	56,56,56	1.27	5 (8%)
12	CLA	cB	916	2	63,67,73	2.04	18 (28%)	75,105,113	2.97	30 (40%)
12	CLA	bB	936	2	63,67,73	2.05	21 (33%)	75,105,113	2.93	31 (41%)
15	BCR	aB	945	-	41,41,41	1.08	2 (4%)	56,56,56	1.35	7 (12%)
16	LHG	aB	948	12	22,22,48	1.05	1 (4%)	25,28,54	1.10	1 (4%)
12	CLA	aB	939	2	49,53,73	2.26	18 (36%)	59,89,113	3.28	27 (45%)
12	CLA	aL	203	9	49,53,73	2.32	21 (42%)	59,89,113	3.27	25 (42%)
12	CLA	bB	918	18	50,54,73	2.32	19 (38%)	60,90,113	2.98	27 (45%)
12	CLA	cA	843	18	69,73,73	1.93	20 (28%)	83,113,113	2.82	34 (40%)
12	CLA	cA	819	1	64,68,73	2.04	19 (29%)	77,107,113	3.01	35 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	bF	202	6	49,53,73	2.37	20 (40%)	59,89,113	3.22	28 (47%)
15	BCR	cF	204	-	41,41,41	1.05	2 (4%)	56,56,56	1.30	9 (16%)
12	CLA	cA	818	1	58,62,73	2.10	19 (32%)	69,99,113	3.02	30 (43%)
12	CLA	aA	805	1	57,61,73	2.18	22 (38%)	68,98,113	3.13	29 (42%)
15	BCR	cA	850	-	41,41,41	1.05	2 (4%)	56,56,56	1.30	8 (14%)
12	CLA	bA	839	1	49,53,73	2.28	20 (40%)	59,89,113	3.25	27 (45%)
15	BCR	bB	943	-	41,41,41	1.07	2 (4%)	56,56,56	1.16	4 (7%)
12	CLA	aB	918	18	50,54,73	2.33	19 (38%)	60,90,113	2.99	26 (43%)
12	CLA	cB	929	2	49,53,73	2.34	20 (40%)	59,89,113	3.33	28 (47%)
12	CLA	bA	802	18	69,73,73	1.92	18 (26%)	83,113,113	2.75	28 (33%)
12	CLA	aB	906	2	59,63,73	2.13	20 (33%)	71,101,113	2.95	30 (42%)
12	CLA	aB	917	2	59,63,73	2.09	19 (32%)	71,101,113	2.92	30 (42%)
12	CLA	aB	903	2	55,59,73	2.18	20 (36%)	66,96,113	3.09	30 (45%)
12	CLA	bB	927	2	69,73,73	1.97	20 (28%)	83,113,113	2.46	25 (30%)
12	CLA	cB	932	2	49,53,73	2.33	18 (36%)	59,89,113	3.30	29 (49%)
12	CLA	cB	925	2	59,63,73	2.08	19 (32%)	71,101,113	3.11	32 (45%)
12	CLA	cA	820	1	60,64,73	2.13	21 (35%)	72,102,113	2.93	31 (43%)
12	CLA	cA	828	1	69,73,73	1.97	20 (28%)	83,113,113	2.80	30 (36%)
12	CLA	bA	827	1	50,54,73	2.26	20 (40%)	60,90,113	3.22	27 (45%)
12	CLA	aB	913	2	60,64,73	2.08	20 (33%)	72,102,113	2.95	31 (43%)
14	SF4	aC	102	3	0,12,12	-	-	-	-	-
12	CLA	cB	907	2	56,60,73	2.14	19 (33%)	67,97,113	3.01	31 (46%)
12	CLA	cB	920	2	49,53,73	2.35	19 (38%)	59,89,113	3.32	25 (42%)
12	CLA	bA	837	1	55,59,73	2.18	20 (36%)	66,96,113	3.07	29 (43%)
12	CLA	aB	904	2	69,73,73	1.96	21 (30%)	83,113,113	2.92	33 (39%)
12	CLA	cA	841	18	55,59,73	2.22	21 (38%)	66,96,113	3.07	26 (39%)
12	CLA	aB	929	2	49,53,73	2.34	20 (40%)	59,89,113	3.33	27 (45%)
12	CLA	aA	826	18	59,63,73	2.10	20 (33%)	71,101,113	3.07	28 (39%)
12	CLA	aB	936	2	63,67,73	2.05	21 (33%)	75,105,113	2.93	32 (42%)
15	BCR	aF	201	-	41,41,41	1.07	2 (4%)	56,56,56	1.23	7 (12%)
16	LHG	bB	948	12	22,22,48	1.06	1 (4%)	25,28,54	1.10	1 (4%)
12	CLA	cA	833	1	55,59,73	2.14	18 (32%)	66,96,113	3.05	33 (50%)
12	CLA	cA	811	1	49,53,73	2.37	19 (38%)	59,89,113	3.17	27 (45%)
15	BCR	bB	942	-	41,41,41	1.06	2 (4%)	56,56,56	1.19	3 (5%)
12	CLA	aA	803	-	69,73,73	1.92	20 (28%)	83,113,113	2.77	33 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	CL0	aA	801	1	69,73,73	1.93	20 (28%)	83,113,113	2.65	35 (42%)
12	CLA	aB	910	2	49,53,73	2.35	19 (38%)	59,89,113	3.13	28 (47%)
12	CLA	aB	934	2	49,53,73	2.46	19 (38%)	59,89,113	3.05	25 (42%)
12	CLA	bA	824	1	51,55,73	2.30	21 (41%)	61,91,113	3.09	28 (45%)
12	CLA	bA	813	1	49,53,73	2.42	21 (42%)	59,89,113	3.09	26 (44%)
12	CLA	aB	920	2	49,53,73	2.35	19 (38%)	59,89,113	3.33	25 (42%)
12	CLA	cB	901	2	69,73,73	1.88	18 (26%)	83,113,113	2.80	31 (37%)
15	BCR	bB	945	-	41,41,41	1.07	2 (4%)	56,56,56	1.36	7 (12%)
12	CLA	bB	905	2	69,73,73	1.94	20 (28%)	83,113,113	2.75	29 (34%)
12	CLA	bA	826	18	59,63,73	2.09	20 (33%)	71,101,113	3.07	28 (39%)
12	CLA	cA	825	18	69,73,73	2.01	20 (28%)	83,113,113	2.77	31 (37%)
12	CLA	cA	839	1	49,53,73	2.28	20 (40%)	59,89,113	3.26	27 (45%)
12	CLA	cA	805	1	57,61,73	2.18	22 (38%)	68,98,113	3.13	28 (41%)
12	CLA	aA	810	1	49,53,73	2.35	20 (40%)	59,89,113	3.31	28 (47%)
14	SF4	cC	102	3	0,12,12	-	-	-	-	-
12	CLA	aB	949	16	45,49,73	2.50	18 (40%)	54,84,113	3.48	29 (53%)
12	CLA	cA	842	1	69,73,73	1.96	19 (27%)	83,113,113	2.80	30 (36%)
12	CLA	aA	806	1	69,73,73	1.93	20 (28%)	83,113,113	2.90	28 (33%)
12	CLA	bA	806	1	69,73,73	1.93	20 (28%)	83,113,113	2.89	28 (33%)
12	CLA	cA	834	1	69,73,73	1.96	20 (28%)	83,113,113	2.89	30 (36%)
12	CLA	aA	835	1	49,53,73	2.33	19 (38%)	59,89,113	3.01	27 (45%)
15	BCR	bI	101	-	41,41,41	1.12	2 (4%)	56,56,56	1.38	9 (16%)
14	SF4	cC	101	3	0,12,12	-	-	-	-	-
17	LMG	cB	947	-	43,43,55	0.95	2 (4%)	51,51,63	1.25	6 (11%)
12	CLA	bB	912	2	69,73,73	1.90	21 (30%)	83,113,113	2.68	29 (34%)
15	BCR	bJ	101	-	41,41,41	1.05	2 (4%)	56,56,56	1.35	6 (10%)
12	CLA	bL	203	9	49,53,73	2.32	20 (40%)	59,89,113	3.26	24 (40%)
17	LMG	bB	947	-	43,43,55	0.95	1 (2%)	51,51,63	1.25	6 (11%)
12	CLA	aB	921	2	59,63,73	2.17	20 (33%)	71,101,113	3.04	27 (38%)
14	SF4	bC	102	3	0,12,12	-	-	-	-	-
12	CLA	cA	830	1	69,73,73	1.93	19 (27%)	83,113,113	2.66	28 (33%)
15	BCR	aJ	101	-	41,41,41	1.05	2 (4%)	56,56,56	1.35	6 (10%)
12	CLA	bB	913	2	60,64,73	2.08	20 (33%)	72,102,113	2.94	31 (43%)
12	CLA	bB	924	18	50,54,73	2.29	21 (42%)	60,90,113	3.23	27 (45%)
16	LHG	bA	852	12	26,26,48	0.94	1 (3%)	29,32,54	1.32	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	cB	937	2	51,55,73	2.27	22 (43%)	61,91,113	3.25	27 (44%)
15	BCR	bA	850	-	41,41,41	1.05	2 (4%)	56,56,56	1.30	8 (14%)
12	CLA	bB	906	2	59,63,73	2.13	21 (35%)	71,101,113	2.96	30 (42%)
12	CLA	cB	924	18	50,54,73	2.29	21 (42%)	60,90,113	3.24	27 (45%)
12	CLA	aB	909	2	59,63,73	2.09	20 (33%)	71,101,113	2.83	32 (45%)
12	CLA	aB	916	2	63,67,73	2.05	18 (28%)	75,105,113	2.97	30 (40%)
12	CLA	cB	906	2	59,63,73	2.13	21 (35%)	71,101,113	2.95	30 (42%)
15	BCR	cA	848	-	41,41,41	1.10	3 (7%)	56,56,56	1.18	4 (7%)
12	CLA	aB	902	-	65,69,73	1.96	19 (29%)	78,108,113	2.82	26 (33%)
12	CLA	bA	820	1	60,64,73	2.13	21 (35%)	72,102,113	2.93	31 (43%)
12	CLA	aA	837	1	55,59,73	2.19	20 (36%)	66,96,113	3.08	28 (42%)
15	BCR	aB	941	-	41,41,41	1.09	3 (7%)	56,56,56	1.28	5 (8%)
15	BCR	bA	847	-	41,41,41	1.13	2 (4%)	56,56,56	1.51	13 (23%)
14	SF4	cA	845	2,1	0,12,12	-	-	-	-	-
12	CLA	cB	938	18	55,59,73	2.20	19 (34%)	66,96,113	2.94	30 (45%)
12	CLA	bA	822	1	53,57,73	2.29	20 (37%)	62,93,113	3.30	26 (41%)
15	BCR	bM	101	10	41,41,41	1.07	2 (4%)	56,56,56	1.17	6 (10%)
12	CLA	cB	912	2	69,73,73	1.91	21 (30%)	83,113,113	2.68	29 (34%)
12	CLA	bB	935	2	54,58,73	2.21	20 (37%)	65,95,113	3.14	31 (47%)
12	CLA	bA	804	1	60,64,73	2.09	19 (31%)	72,102,113	2.94	29 (40%)
15	BCR	aA	850	-	41,41,41	1.17	2 (4%)	56,56,56	1.39	6 (10%)
12	CLA	bB	921	2	59,63,73	2.17	20 (33%)	71,101,113	3.04	27 (38%)
15	BCR	cF	203	-	41,41,41	1.09	2 (4%)	56,56,56	1.33	8 (14%)
12	CLA	aB	922	2	49,53,73	2.31	19 (38%)	59,89,113	3.10	28 (47%)
16	LHG	cB	948	12	22,22,48	1.05	1 (4%)	25,28,54	1.10	1 (4%)
12	CLA	bB	904	2	69,73,73	1.96	21 (30%)	83,113,113	2.92	33 (39%)
12	CLA	aB	926	2	69,73,73	1.91	20 (28%)	83,113,113	2.71	31 (37%)
12	CLA	cB	903	2	55,59,73	2.19	20 (36%)	66,96,113	3.08	30 (45%)
15	BCR	aB	944	-	41,41,41	1.08	2 (4%)	56,56,56	1.18	7 (12%)
12	CLA	bB	920	2	49,53,73	2.35	19 (38%)	59,89,113	3.33	25 (42%)
12	CLA	cB	935	2	54,58,73	2.21	20 (37%)	65,95,113	3.15	31 (47%)
12	CLA	aA	829	1	64,68,73	2.00	19 (29%)	77,107,113	2.77	30 (38%)
14	SF4	aC	101	3	0,12,12	-	-	-	-	-
12	CLA	aA	823	1	55,59,73	2.19	19 (34%)	66,96,113	3.12	31 (46%)
12	CLA	cA	810	1	49,53,73	2.35	20 (40%)	59,89,113	3.30	28 (47%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	bA	833	1	55,59,73	2.14	18 (32%)	66,96,113	3.06	33 (50%)
12	CLA	bB	919	2	51,55,73	2.26	19 (37%)	61,91,113	3.16	28 (45%)
12	CLA	bB	937	2	51,55,73	2.28	22 (43%)	61,91,113	3.25	27 (44%)
12	CLA	cA	829	1	64,68,73	2.00	19 (29%)	77,107,113	2.77	31 (40%)
12	CLA	aL	204	18	49,53,73	2.35	21 (42%)	59,89,113	3.23	26 (44%)
13	1L3	aB	940	-	34,34,34	2.31	9 (26%)	42,45,45	1.43	6 (14%)
12	CLA	bB	932	2	49,53,73	2.33	18 (36%)	59,89,113	3.29	29 (49%)
12	CLA	bA	807	1	69,73,73	1.98	20 (28%)	83,113,113	2.82	34 (40%)
13	1L3	bB	940	-	34,34,34	2.31	9 (26%)	42,45,45	1.43	7 (16%)
12	CLA	aA	816	1	49,53,73	2.36	21 (42%)	59,89,113	3.17	25 (42%)
12	CLA	aB	912	2	69,73,73	1.91	21 (30%)	83,113,113	2.68	29 (34%)
12	CLA	bA	831	1	54,58,73	2.21	19 (35%)	65,95,113	3.04	34 (52%)
12	CLA	bB	916	2	63,67,73	2.05	18 (28%)	75,105,113	2.97	30 (40%)
15	BCR	cM	101	10	41,41,41	1.07	2 (4%)	56,56,56	1.17	6 (10%)
12	CLA	bB	928	2	54,58,73	2.22	20 (37%)	65,95,113	2.91	30 (46%)
12	CLA	aA	830	1	69,73,73	1.92	19 (27%)	83,113,113	2.66	28 (33%)
12	CLA	aB	915	2	56,60,73	2.20	19 (33%)	67,97,113	3.17	27 (40%)
12	CLA	bA	841	18	55,59,73	2.23	21 (38%)	66,96,113	3.07	26 (39%)
13	1L3	cB	940	-	34,34,34	2.30	9 (26%)	42,45,45	1.44	7 (16%)
12	CLA	aB	919	2	51,55,73	2.26	19 (37%)	61,91,113	3.16	28 (45%)
12	CLA	aA	839	1	49,53,73	2.28	20 (40%)	59,89,113	3.25	27 (45%)
12	CLA	cA	836	1	49,53,73	2.39	19 (38%)	59,89,113	3.09	29 (49%)
12	CLA	bB	915	2	56,60,73	2.20	19 (33%)	67,97,113	3.16	27 (40%)
15	BCR	aB	942	-	41,41,41	1.06	2 (4%)	56,56,56	1.19	3 (5%)
12	CLA	bB	950	16	49,53,73	2.33	20 (40%)	59,89,113	3.02	23 (38%)
12	CLA	cB	915	2	56,60,73	2.19	19 (33%)	67,97,113	3.16	27 (40%)
15	BCR	cJ	101	-	41,41,41	1.06	2 (4%)	56,56,56	1.35	6 (10%)
12	CLA	cB	913	2	60,64,73	2.09	20 (33%)	72,102,113	2.95	32 (44%)
12	CLA	bA	816	1	49,53,73	2.36	21 (42%)	59,89,113	3.17	25 (42%)
12	CLA	aB	905	2	69,73,73	1.94	20 (28%)	83,113,113	2.75	29 (34%)
15	BCR	bF	204	-	41,41,41	1.04	2 (4%)	56,56,56	1.30	9 (16%)
13	1L3	bA	844	-	34,34,34	2.31	9 (26%)	42,45,45	1.61	9 (21%)
16	LHG	cA	851	-	48,48,48	0.65	1 (2%)	51,54,54	1.27	6 (11%)
12	CLA	aB	925	2	59,63,73	2.08	18 (30%)	71,101,113	3.12	32 (45%)
12	CLA	bB	938	18	55,59,73	2.20	19 (34%)	66,96,113	2.95	30 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	BCR	cB	945	-	41,41,41	1.07	2 (4%)	56,56,56	1.36	7 (12%)
12	CLA	cA	812	1	69,73,73	1.94	20 (28%)	83,113,113	2.77	32 (38%)
14	SF4	aA	846	2,1	0,12,12	-	-	-	-	-
12	CLA	cA	821	18	54,58,73	2.23	18 (33%)	65,95,113	2.92	28 (43%)
12	CLA	bA	817	1	58,62,73	2.19	19 (32%)	69,99,113	3.10	27 (39%)
12	CLA	bA	853	18	60,64,73	2.04	20 (33%)	72,102,113	3.05	29 (40%)
14	SF4	bC	101	3	0,12,12	-	-	-	-	-
12	CLA	cB	923	18	58,62,73	2.07	19 (32%)	69,99,113	2.97	27 (39%)
12	CLA	aA	828	1	69,73,73	1.98	20 (28%)	83,113,113	2.80	30 (36%)
12	CLA	bA	808	1	55,59,73	2.25	21 (38%)	66,96,113	3.07	31 (46%)
12	CLA	bA	823	1	55,59,73	2.20	20 (36%)	66,96,113	3.11	30 (45%)
12	CLA	aA	831	1	54,58,73	2.20	19 (35%)	65,95,113	3.04	34 (52%)
15	BCR	aA	847	-	41,41,41	1.07	2 (4%)	56,56,56	1.27	7 (12%)
15	BCR	cA	846	-	41,41,41	1.06	2 (4%)	56,56,56	1.28	7 (12%)
12	CLA	aA	808	1	55,59,73	2.25	21 (38%)	66,96,113	3.06	31 (46%)
12	CLA	cA	840	1	69,73,73	1.98	19 (27%)	83,113,113	2.67	28 (33%)
12	CLA	aA	841	18	55,59,73	2.22	21 (38%)	66,96,113	3.07	26 (39%)
12	CLA	cA	802	18	69,73,73	1.93	19 (27%)	83,113,113	2.76	28 (33%)
12	CLA	aA	824	1	51,55,73	2.29	21 (41%)	61,91,113	3.09	30 (49%)
15	BCR	aL	201	-	41,41,41	1.19	3 (7%)	56,56,56	1.23	4 (7%)
12	CLA	cB	936	2	63,67,73	2.05	21 (33%)	75,105,113	2.94	32 (42%)
12	CLA	cL	204	18	49,53,73	2.36	21 (42%)	59,89,113	3.24	26 (44%)
12	CLA	cB	930	2	53,57,73	2.27	20 (37%)	62,93,113	3.18	29 (46%)
12	CLA	bB	925	2	59,63,73	2.09	18 (30%)	71,101,113	3.11	32 (45%)
12	CLA	cB	905	2	69,73,73	1.94	20 (28%)	83,113,113	2.75	29 (34%)
12	CLA	bB	926	2	69,73,73	1.90	20 (28%)	83,113,113	2.71	32 (38%)
12	CLA	cA	815	1	49,53,73	2.38	20 (40%)	59,89,113	3.19	26 (44%)
12	CLA	bB	923	18	58,62,73	2.07	19 (32%)	69,99,113	2.97	27 (39%)
12	CLA	aA	832	1	59,63,73	2.14	20 (33%)	71,101,113	3.00	32 (45%)
12	CLA	cA	813	1	49,53,73	2.41	21 (42%)	59,89,113	3.10	26 (44%)
15	BCR	aB	946	-	41,41,41	1.09	3 (7%)	56,56,56	1.23	6 (10%)
12	CLA	bA	829	1	64,68,73	2.00	19 (29%)	77,107,113	2.77	30 (38%)
12	CLA	cA	826	18	59,63,73	2.09	20 (33%)	71,101,113	3.07	28 (39%)
12	CLA	bB	922	2	49,53,73	2.30	20 (40%)	59,89,113	3.09	28 (47%)
12	CLA	bA	834	1	69,73,73	1.95	20 (28%)	83,113,113	2.89	32 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	aA	811	1	49,53,73	2.37	19 (38%)	59,89,113	3.16	27 (45%)
12	CLA	bB	909	2	59,63,73	2.09	21 (35%)	71,101,113	2.83	32 (45%)
12	CLA	aB	901	2	69,73,73	1.89	18 (26%)	83,113,113	2.79	31 (37%)
12	CLA	aA	825	18	69,73,73	2.01	20 (28%)	83,113,113	2.77	31 (37%)
12	CLA	aA	817	1	58,62,73	2.19	19 (32%)	69,99,113	3.10	27 (39%)
12	CLA	aB	935	2	54,58,73	2.21	20 (37%)	65,95,113	3.15	31 (47%)
12	CLA	bB	901	2	69,73,73	1.88	18 (26%)	83,113,113	2.80	31 (37%)
12	CLA	cA	853	18	60,64,73	2.04	20 (33%)	72,102,113	3.04	29 (40%)
12	CLA	bB	911	2	49,53,73	2.34	19 (38%)	59,89,113	3.16	29 (49%)
12	CLA	bB	939	2	49,53,73	2.26	18 (36%)	59,89,113	3.27	27 (45%)
12	CLA	aA	834	1	69,73,73	1.96	20 (28%)	83,113,113	2.89	31 (37%)
16	LHG	aA	852	-	48,48,48	0.65	1 (2%)	51,54,54	1.27	6 (11%)
12	CLA	bA	809	1	49,53,73	2.32	20 (40%)	59,89,113	3.28	29 (49%)
12	CLA	bA	836	1	49,53,73	2.38	19 (38%)	59,89,113	3.08	29 (49%)
12	CLA	bB	949	16	45,49,73	2.50	19 (42%)	54,84,113	3.50	29 (53%)
12	CLA	aB	932	2	49,53,73	2.33	18 (36%)	59,89,113	3.31	29 (49%)
15	BCR	bB	946	-	41,41,41	1.09	3 (7%)	56,56,56	1.23	6 (10%)
12	CLA	cB	904	2	69,73,73	1.96	21 (30%)	83,113,113	2.92	33 (39%)
12	CLA	aA	838	1	69,73,73	1.94	19 (27%)	83,113,113	2.80	28 (33%)
12	CLA	aA	820	1	60,64,73	2.13	21 (35%)	72,102,113	2.94	31 (43%)
12	CLA	cA	824	1	51,55,73	2.29	21 (41%)	61,91,113	3.10	30 (49%)
15	BCR	aM	101	10	41,41,41	1.07	2 (4%)	56,56,56	1.16	6 (10%)
12	CLA	aB	911	2	49,53,73	2.34	19 (38%)	59,89,113	3.16	29 (49%)
12	CLA	bA	840	1	69,73,73	1.99	19 (27%)	83,113,113	2.68	29 (34%)
17	LMG	aB	947	-	43,43,55	0.95	1 (2%)	51,51,63	1.25	6 (11%)
12	CLA	cA	822	1	53,57,73	2.29	20 (37%)	62,93,113	3.29	27 (43%)
12	CLA	cA	838	1	69,73,73	1.94	19 (27%)	83,113,113	2.80	28 (33%)
15	BCR	bL	201	-	41,41,41	1.19	3 (7%)	56,56,56	1.23	4 (7%)
12	CLA	cB	927	2	69,73,73	1.97	20 (28%)	83,113,113	2.46	25 (30%)
12	CLA	aB	928	2	54,58,73	2.22	20 (37%)	65,95,113	2.91	29 (44%)
12	CLA	cB	939	2	49,53,73	2.26	18 (36%)	59,89,113	3.26	27 (45%)
12	CLA	cA	804	1	60,64,73	2.10	20 (33%)	72,102,113	2.94	29 (40%)
12	CLA	aB	937	2	51,55,73	2.27	22 (43%)	61,91,113	3.24	27 (44%)
12	CLA	aB	908	2	52,56,73	2.23	17 (32%)	62,92,113	2.80	27 (43%)
15	BCR	bA	849	-	41,41,41	1.17	2 (4%)	56,56,56	1.40	6 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	CLA	aA	821	18	54,58,73	2.22	19 (35%)	65,95,113	2.92	28 (43%)
12	CLA	bA	814	1	49,53,73	2.32	19 (38%)	59,89,113	3.10	27 (45%)
12	CLA	aA	815	1	49,53,73	2.39	19 (38%)	59,89,113	3.20	26 (44%)
11	CL0	cA	801	1	69,73,73	1.92	20 (28%)	83,113,113	2.64	35 (42%)
12	CLA	cB	911	2	49,53,73	2.34	19 (38%)	59,89,113	3.16	29 (49%)
12	CLA	aA	827	1	50,54,73	2.26	19 (38%)	60,90,113	3.23	27 (45%)
15	BCR	cI	101	-	41,41,41	1.12	2 (4%)	56,56,56	1.39	9 (16%)
12	CLA	bB	917	2	59,63,73	2.09	19 (32%)	71,101,113	2.92	30 (42%)
12	CLA	cB	933	18	49,53,73	2.27	20 (40%)	59,89,113	3.05	27 (45%)
12	CLA	cB	919	2	51,55,73	2.26	18 (35%)	61,91,113	3.17	28 (45%)
12	CLA	cB	921	2	59,63,73	2.17	20 (33%)	71,101,113	3.04	27 (38%)
12	CLA	aB	938	18	55,59,73	2.20	19 (34%)	66,96,113	2.96	30 (45%)
12	CLA	bA	818	1	58,62,73	2.10	19 (32%)	69,99,113	3.01	30 (43%)
15	BCR	aA	851	-	41,41,41	1.06	2 (4%)	56,56,56	1.30	8 (14%)
12	CLA	cB	918	18	50,54,73	2.33	19 (38%)	60,90,113	2.99	26 (43%)
15	BCR	aF	203	-	41,41,41	1.08	2 (4%)	56,56,56	1.33	8 (14%)
15	BCR	bA	848	-	41,41,41	1.10	3 (7%)	56,56,56	1.18	4 (7%)
12	CLA	aA	804	1	60,64,73	2.09	19 (31%)	72,102,113	2.94	29 (40%)
12	CLA	cA	806	1	69,73,73	1.93	20 (28%)	83,113,113	2.89	28 (33%)
15	BCR	cL	206	-	41,41,41	1.03	2 (4%)	56,56,56	1.20	5 (8%)
12	CLA	cA	816	1	49,53,73	2.35	21 (42%)	59,89,113	3.17	25 (42%)

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
15	BCR	cA	849	-	-	10/29/63/63	0/2/2/2
15	BCR	aI	101	-	-	10/29/63/63	0/2/2/2
12	CLA	bB	930	2	-	4/20/96/115	-
12	CLA	bA	830	1	-	11/39/115/115	-
12	CLA	bB	929	2	-	7/15/91/115	-
15	BCR	aF	204	-	-	6/29/63/63	0/2/2/2
15	BCR	bL	205	-	-	10/29/63/63	0/2/2/2
12	CLA	cB	917	2	-	10/27/103/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	bL	204	18	-	0/15/91/115	-
12	CLA	bA	805	1	-	6/25/101/115	-
15	BCR	bA	846	-	-	11/29/63/63	0/2/2/2
12	CLA	cA	808	1	-	7/23/99/115	-
12	CLA	cB	910	2	-	4/15/91/115	-
12	CLA	aA	836	1	-	5/15/91/115	-
12	CLA	aB	930	2	-	4/20/96/115	-
15	BCR	bF	203	-	-	15/29/63/63	0/2/2/2
12	CLA	aA	844	16	-	6/15/91/115	-
12	CLA	cB	902	-	-	9/35/111/115	-
12	CLA	cA	814	1	-	8/15/91/115	-
12	CLA	cB	931	2	-	12/39/115/115	-
15	BCR	bL	206	-	-	6/29/63/63	0/2/2/2
12	CLA	bB	934	2	-	3/15/91/115	-
13	1L3	aA	845	-	-	3/23/43/43	0/2/2/2
12	CLA	bL	202	9	-	2/25/101/115	-
12	CLA	bB	908	2	-	10/19/95/115	-
12	CLA	aA	840	1	-	11/39/115/115	-
12	CLA	cB	934	2	-	4/15/91/115	-
12	CLA	aB	950	16	-	7/15/91/115	-
15	BCR	aL	205	-	-	10/29/63/63	0/2/2/2
12	CLA	cB	922	2	-	7/15/91/115	-
12	CLA	bA	842	1	-	14/39/115/115	-
12	CLA	bB	933	18	-	3/15/91/115	-
12	CLA	cA	831	1	-	6/21/97/115	-
12	CLA	bA	838	1	-	8/39/115/115	-
15	BCR	cL	205	-	-	10/29/63/63	0/2/2/2
12	CLA	cB	914	2	-	7/15/91/115	-
12	CLA	bB	914	2	-	7/15/91/115	-
12	CLA	aA	813	1	-	3/15/91/115	-
15	BCR	cB	941	-	-	10/29/63/63	0/2/2/2
16	LHG	aA	853	12	-	11/31/31/53	-
12	CLA	aA	814	1	-	8/15/91/115	-
12	CLA	aB	907	2	-	7/24/100/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	bA	828	1	-	3/39/115/115	-
11	CL0	bA	801	1	-	7/39/115/115	-
12	CLA	bA	835	1	-	2/15/91/115	-
12	CLA	cL	203	9	-	6/15/91/115	-
15	BCR	cB	946	-	-	4/29/63/63	0/2/2/2
12	CLA	cA	803	-	-	7/39/115/115	-
12	CLA	aB	931	2	-	12/39/115/115	-
12	CLA	aA	854	18	-	6/29/105/115	-
16	LHG	bA	851	-	-	23/53/53/53	-
12	CLA	aB	914	2	-	7/15/91/115	-
12	CLA	bA	812	1	-	10/39/115/115	-
12	CLA	bA	810	1	-	7/15/91/115	-
12	CLA	cB	926	2	-	23/39/115/115	-
12	CLA	cB	928	2	-	4/21/97/115	-
15	BCR	cF	201	-	-	9/29/63/63	0/2/2/2
12	CLA	cA	832	1	-	10/27/103/115	-
12	CLA	aF	202	6	-	9/15/91/115	-
15	BCR	aA	848	-	-	7/29/63/63	0/2/2/2
12	CLA	cB	949	16	-	3/10/86/115	-
12	CLA	bA	832	1	-	10/27/103/115	-
12	CLA	aB	924	18	-	2/17/93/115	-
12	CLA	cA	809	1	-	7/15/91/115	-
12	CLA	aA	802	18	-	5/39/115/115	-
15	BCR	cL	201	-	-	7/29/63/63	0/2/2/2
13	1L3	cA	844	-	-	3/23/43/43	0/2/2/2
12	CLA	aA	807	1	-	13/39/115/115	-
15	BCR	cB	944	-	-	16/29/63/63	0/2/2/2
12	CLA	cB	909	2	-	9/27/103/115	-
12	CLA	cA	823	1	-	8/23/99/115	-
12	CLA	cA	817	1	-	9/26/102/115	-
12	CLA	aA	843	18	-	11/39/115/115	-
12	CLA	bB	907	2	-	8/24/100/115	-
12	CLA	bB	910	2	-	4/15/91/115	-
12	CLA	bA	843	18	-	11/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	bB	902	-	-	9/35/111/115	-
12	CLA	aB	923	18	-	12/26/102/115	-
12	CLA	bA	819	1	-	6/33/109/115	-
12	CLA	bB	931	2	-	12/39/115/115	-
15	BCR	bF	201	-	-	9/29/63/63	0/2/2/2
12	CLA	bA	825	18	-	12/39/115/115	-
16	LHG	cA	852	12	-	11/31/31/53	-
12	CLA	aL	202	9	-	2/25/101/115	-
12	CLA	aB	933	18	-	3/15/91/115	-
12	CLA	aA	833	1	-	5/23/99/115	-
15	BCR	cB	943	-	-	9/29/63/63	0/2/2/2
15	BCR	bB	944	-	-	16/29/63/63	0/2/2/2
15	BCR	cA	847	-	-	7/29/63/63	0/2/2/2
12	CLA	cF	202	6	-	9/15/91/115	-
12	CLA	bA	821	18	-	4/21/97/115	-
12	CLA	cB	908	2	-	10/19/95/115	-
15	BCR	aA	849	-	-	10/29/63/63	0/2/2/2
12	CLA	cA	807	1	-	13/39/115/115	-
15	BCR	aL	206	-	-	6/29/63/63	0/2/2/2
12	CLA	aA	812	1	-	10/39/115/115	-
12	CLA	cL	202	9	-	2/25/101/115	-
12	CLA	cA	835	1	-	2/15/91/115	-
12	CLA	aA	842	1	-	14/39/115/115	-
14	SF4	bA	845	2,1	-	-	0/6/5/5
12	CLA	cA	827	1	-	6/17/93/115	-
12	CLA	aA	809	1	-	7/15/91/115	-
12	CLA	aA	818	1	-	12/26/102/115	-
12	CLA	bB	903	2	-	5/23/99/115	-
15	BCR	aB	943	-	-	9/29/63/63	0/2/2/2
12	CLA	cA	837	1	-	7/23/99/115	-
12	CLA	bA	815	1	-	6/15/91/115	-
12	CLA	bA	803	-	-	7/39/115/115	-
12	CLA	aA	822	1	-	8/20/96/115	-
12	CLA	aB	927	2	-	12/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BCR	cB	942	-	-	9/29/63/63	0/2/2/2
12	CLA	bA	811	1	-	6/15/91/115	-
12	CLA	aA	819	1	-	6/33/109/115	-
15	BCR	bB	941	-	-	10/29/63/63	0/2/2/2
12	CLA	cB	916	2	-	9/32/108/115	-
12	CLA	bB	936	2	-	9/32/108/115	-
15	BCR	aB	945	-	-	9/29/63/63	0/2/2/2
16	LHG	aB	948	12	-	8/26/26/53	-
12	CLA	aB	939	2	-	5/15/91/115	-
12	CLA	aL	203	9	-	6/15/91/115	-
12	CLA	bB	918	18	-	3/17/93/115	-
12	CLA	cA	843	18	-	11/39/115/115	-
12	CLA	cA	819	1	-	6/33/109/115	-
12	CLA	bF	202	6	-	9/15/91/115	-
15	BCR	cF	204	-	-	6/29/63/63	0/2/2/2
12	CLA	cA	818	1	-	12/26/102/115	-
12	CLA	aA	805	1	-	6/25/101/115	-
15	BCR	cA	850	-	-	10/29/63/63	0/2/2/2
12	CLA	bA	839	1	-	7/15/91/115	-
15	BCR	bB	943	-	-	9/29/63/63	0/2/2/2
12	CLA	aB	918	18	-	3/17/93/115	-
12	CLA	cB	929	2	-	7/15/91/115	-
12	CLA	bA	802	18	-	5/39/115/115	-
12	CLA	aB	906	2	-	2/27/103/115	-
12	CLA	aB	917	2	-	10/27/103/115	-
12	CLA	aB	903	2	-	5/23/99/115	-
12	CLA	bB	927	2	-	12/39/115/115	-
12	CLA	cB	932	2	-	4/15/91/115	-
12	CLA	cB	925	2	-	5/27/103/115	-
12	CLA	cA	820	1	-	13/29/105/115	-
12	CLA	cA	828	1	-	3/39/115/115	-
12	CLA	bA	827	1	-	6/17/93/115	-
12	CLA	aB	913	2	-	6/29/105/115	-
14	SF4	aC	102	3	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	cB	907	2	-	7/24/100/115	-
12	CLA	cB	920	2	-	3/15/91/115	-
12	CLA	bA	837	1	-	7/23/99/115	-
12	CLA	aB	904	2	-	12/39/115/115	-
12	CLA	cA	841	18	-	5/23/99/115	-
12	CLA	aB	929	2	-	7/15/91/115	-
12	CLA	aA	826	18	-	8/27/103/115	-
12	CLA	aB	936	2	-	9/32/108/115	-
15	BCR	aF	201	-	-	9/29/63/63	0/2/2/2
16	LHG	bB	948	12	-	8/26/26/53	-
12	CLA	cA	833	1	-	5/23/99/115	-
12	CLA	cA	811	1	-	6/15/91/115	-
15	BCR	bB	942	-	-	9/29/63/63	0/2/2/2
12	CLA	aA	803	-	-	7/39/115/115	-
11	CL0	aA	801	1	-	7/39/115/115	-
12	CLA	aB	910	2	-	4/15/91/115	-
12	CLA	aB	934	2	-	4/15/91/115	-
12	CLA	bA	824	1	-	7/18/94/115	-
12	CLA	bA	813	1	-	3/15/91/115	-
12	CLA	aB	920	2	-	3/15/91/115	-
12	CLA	cB	901	2	-	8/39/115/115	-
15	BCR	bB	945	-	-	10/29/63/63	0/2/2/2
12	CLA	bB	905	2	-	15/39/115/115	-
12	CLA	bA	826	18	-	8/27/103/115	-
12	CLA	cA	825	18	-	12/39/115/115	-
12	CLA	cA	839	1	-	7/15/91/115	-
12	CLA	cA	805	1	-	6/25/101/115	-
12	CLA	aA	810	1	-	7/15/91/115	-
14	SF4	cC	102	3	-	-	0/6/5/5
12	CLA	aB	949	16	-	3/10/86/115	-
12	CLA	cA	842	1	-	14/39/115/115	-
12	CLA	aA	806	1	-	11/39/115/115	-
12	CLA	bA	806	1	-	11/39/115/115	-
12	CLA	cA	834	1	-	14/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	aA	835	1	-	2/15/91/115	-
15	BCR	bI	101	-	-	10/29/63/63	0/2/2/2
14	SF4	cC	101	3	-	-	0/6/5/5
17	LMG	cB	947	-	-	12/38/58/70	0/1/1/1
12	CLA	bB	912	2	-	17/39/115/115	-
15	BCR	bJ	101	-	-	13/29/63/63	0/2/2/2
12	CLA	bL	203	9	-	6/15/91/115	-
17	LMG	bB	947	-	-	12/38/58/70	0/1/1/1
12	CLA	aB	921	2	-	8/27/103/115	-
14	SF4	bC	102	3	-	-	0/6/5/5
12	CLA	cA	830	1	-	11/39/115/115	-
15	BCR	aJ	101	-	-	13/29/63/63	0/2/2/2
12	CLA	bB	913	2	-	6/29/105/115	-
12	CLA	bB	924	18	-	2/17/93/115	-
16	LHG	bA	852	12	-	11/31/31/53	-
12	CLA	cB	937	2	-	2/18/94/115	-
15	BCR	bA	850	-	-	9/29/63/63	0/2/2/2
12	CLA	bB	906	2	-	2/27/103/115	-
12	CLA	cB	924	18	-	2/17/93/115	-
12	CLA	aB	909	2	-	9/27/103/115	-
12	CLA	aB	916	2	-	9/32/108/115	-
12	CLA	cB	906	2	-	2/27/103/115	-
15	BCR	cA	848	-	-	10/29/63/63	0/2/2/2
12	CLA	aB	902	-	-	9/35/111/115	-
12	CLA	bA	820	1	-	13/29/105/115	-
12	CLA	aA	837	1	-	7/23/99/115	-
15	BCR	aB	941	-	-	10/29/63/63	0/2/2/2
15	BCR	bA	847	-	-	7/29/63/63	0/2/2/2
14	SF4	cA	845	2,1	-	-	0/6/5/5
12	CLA	cB	938	18	-	1/23/99/115	-
12	CLA	bA	822	1	-	8/20/96/115	-
15	BCR	bM	101	10	-	18/29/63/63	0/2/2/2
12	CLA	cB	912	2	-	17/39/115/115	-
12	CLA	bB	935	2	-	7/21/97/115	-
12	CLA	bA	804	1	-	7/29/105/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BCR	aA	850	-	-	10/29/63/63	0/2/2/2
12	CLA	bB	921	2	-	8/27/103/115	-
15	BCR	cF	203	-	-	15/29/63/63	0/2/2/2
12	CLA	aB	922	2	-	7/15/91/115	-
16	LHG	cB	948	12	-	8/26/26/53	-
12	CLA	bB	904	2	-	12/39/115/115	-
12	CLA	aB	926	2	-	23/39/115/115	-
12	CLA	cB	903	2	-	5/23/99/115	-
15	BCR	aB	944	-	-	16/29/63/63	0/2/2/2
12	CLA	bB	920	2	-	3/15/91/115	-
12	CLA	cB	935	2	-	7/21/97/115	-
12	CLA	aA	829	1	-	6/33/109/115	-
14	SF4	aC	101	3	-	-	0/6/5/5
12	CLA	aA	823	1	-	8/23/99/115	-
12	CLA	cA	810	1	-	7/15/91/115	-
12	CLA	bA	833	1	-	5/23/99/115	-
12	CLA	bB	919	2	-	7/18/94/115	-
12	CLA	bB	937	2	-	3/18/94/115	-
12	CLA	cA	829	1	-	6/33/109/115	-
12	CLA	aL	204	18	-	0/15/91/115	-
13	1L3	aB	940	-	-	1/23/43/43	0/2/2/2
12	CLA	bB	932	2	-	4/15/91/115	-
12	CLA	bA	807	1	-	13/39/115/115	-
13	1L3	bB	940	-	-	1/23/43/43	0/2/2/2
12	CLA	aA	816	1	-	6/15/91/115	-
12	CLA	aB	912	2	-	17/39/115/115	-
12	CLA	bA	831	1	-	6/21/97/115	-
12	CLA	bB	916	2	-	9/32/108/115	-
15	BCR	cM	101	10	-	18/29/63/63	0/2/2/2
12	CLA	bB	928	2	-	4/21/97/115	-
12	CLA	aA	830	1	-	11/39/115/115	-
12	CLA	aB	915	2	-	11/24/100/115	-
12	CLA	bA	841	18	-	5/23/99/115	-
13	1L3	cB	940	-	-	1/23/43/43	0/2/2/2
12	CLA	aB	919	2	-	7/18/94/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	aA	839	1	-	7/15/91/115	-
12	CLA	cA	836	1	-	5/15/91/115	-
12	CLA	bB	915	2	-	11/24/100/115	-
15	BCR	aB	942	-	-	9/29/63/63	0/2/2/2
12	CLA	bB	950	16	-	6/15/91/115	-
12	CLA	cB	915	2	-	11/24/100/115	-
15	BCR	cJ	101	-	-	13/29/63/63	0/2/2/2
12	CLA	cB	913	2	-	6/29/105/115	-
12	CLA	bA	816	1	-	7/15/91/115	-
12	CLA	aB	905	2	-	15/39/115/115	-
15	BCR	bF	204	-	-	6/29/63/63	0/2/2/2
13	1L3	bA	844	-	-	3/23/43/43	0/2/2/2
16	LHG	cA	851	-	-	22/53/53/53	-
12	CLA	aB	925	2	-	5/27/103/115	-
12	CLA	bB	938	18	-	1/23/99/115	-
15	BCR	cB	945	-	-	9/29/63/63	0/2/2/2
12	CLA	cA	812	1	-	10/39/115/115	-
14	SF4	aA	846	2,1	-	-	0/6/5/5
12	CLA	cA	821	18	-	4/21/97/115	-
12	CLA	bA	817	1	-	9/26/102/115	-
12	CLA	bA	853	18	-	6/29/105/115	-
14	SF4	bC	101	3	-	-	0/6/5/5
12	CLA	cB	923	18	-	12/26/102/115	-
12	CLA	aA	828	1	-	3/39/115/115	-
12	CLA	bA	808	1	-	7/23/99/115	-
12	CLA	bA	823	1	-	8/23/99/115	-
12	CLA	aA	831	1	-	6/21/97/115	-
15	BCR	aA	847	-	-	11/29/63/63	0/2/2/2
15	BCR	cA	846	-	-	11/29/63/63	0/2/2/2
12	CLA	aA	808	1	-	7/23/99/115	-
12	CLA	cA	840	1	-	11/39/115/115	-
12	CLA	aA	841	18	-	5/23/99/115	-
12	CLA	cA	802	18	-	5/39/115/115	-
12	CLA	aA	824	1	-	7/18/94/115	-
15	BCR	aL	201	-	-	7/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	cB	936	2	-	9/32/108/115	-
12	CLA	cL	204	18	-	0/15/91/115	-
12	CLA	cB	930	2	-	4/20/96/115	-
12	CLA	bB	925	2	-	5/27/103/115	-
12	CLA	cB	905	2	-	15/39/115/115	-
12	CLA	bB	926	2	-	23/39/115/115	-
12	CLA	cA	815	1	-	6/15/91/115	-
12	CLA	bB	923	18	-	12/26/102/115	-
12	CLA	aA	832	1	-	10/27/103/115	-
12	CLA	cA	813	1	-	3/15/91/115	-
15	BCR	aB	946	-	-	4/29/63/63	0/2/2/2
12	CLA	bA	829	1	-	6/33/109/115	-
12	CLA	cA	826	18	-	8/27/103/115	-
12	CLA	bB	922	2	-	7/15/91/115	-
12	CLA	bA	834	1	-	14/39/115/115	-
12	CLA	aA	811	1	-	6/15/91/115	-
12	CLA	bB	909	2	-	9/27/103/115	-
12	CLA	aB	901	2	-	8/39/115/115	-
12	CLA	aA	825	18	-	12/39/115/115	-
12	CLA	aA	817	1	-	9/26/102/115	-
12	CLA	aB	935	2	-	7/21/97/115	-
12	CLA	bB	901	2	-	8/39/115/115	-
12	CLA	cA	853	18	-	6/29/105/115	-
12	CLA	bB	911	2	-	0/15/91/115	-
12	CLA	bB	939	2	-	5/15/91/115	-
12	CLA	aA	834	1	-	14/39/115/115	-
16	LHG	aA	852	-	-	22/53/53/53	-
12	CLA	bA	809	1	-	7/15/91/115	-
12	CLA	bA	836	1	-	5/15/91/115	-
12	CLA	bB	949	16	-	3/10/86/115	-
12	CLA	aB	932	2	-	4/15/91/115	-
15	BCR	bB	946	-	-	4/29/63/63	0/2/2/2
12	CLA	cB	904	2	-	12/39/115/115	-
12	CLA	aA	838	1	-	8/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	CLA	aA	820	1	-	13/29/105/115	-
12	CLA	cA	824	1	-	7/18/94/115	-
15	BCR	aM	101	10	-	18/29/63/63	0/2/2/2
12	CLA	aB	911	2	-	0/15/91/115	-
12	CLA	bA	840	1	-	11/39/115/115	-
17	LMG	aB	947	-	-	12/38/58/70	0/1/1/1
12	CLA	cA	822	1	-	8/20/96/115	-
12	CLA	cA	838	1	-	8/39/115/115	-
15	BCR	bL	201	-	-	7/29/63/63	0/2/2/2
12	CLA	cB	927	2	-	12/39/115/115	-
12	CLA	aB	928	2	-	4/21/97/115	-
12	CLA	cB	939	2	-	5/15/91/115	-
12	CLA	cA	804	1	-	7/29/105/115	-
12	CLA	aB	937	2	-	3/18/94/115	-
12	CLA	aB	908	2	-	10/19/95/115	-
15	BCR	bA	849	-	-	11/29/63/63	0/2/2/2
12	CLA	aA	821	18	-	4/21/97/115	-
12	CLA	bA	814	1	-	8/15/91/115	-
12	CLA	aA	815	1	-	6/15/91/115	-
11	CL0	cA	801	1	-	7/39/115/115	-
12	CLA	cB	911	2	-	0/15/91/115	-
12	CLA	aA	827	1	-	6/17/93/115	-
15	BCR	cI	101	-	-	10/29/63/63	0/2/2/2
12	CLA	bB	917	2	-	10/27/103/115	-
12	CLA	cB	933	18	-	3/15/91/115	-
12	CLA	cB	919	2	-	7/18/94/115	-
12	CLA	cB	921	2	-	8/27/103/115	-
12	CLA	aB	938	18	-	1/23/99/115	-
12	CLA	bA	818	1	-	12/26/102/115	-
15	BCR	aA	851	-	-	10/29/63/63	0/2/2/2
12	CLA	cB	918	18	-	3/17/93/115	-
15	BCR	aF	203	-	-	15/29/63/63	0/2/2/2
15	BCR	bA	848	-	-	10/29/63/63	0/2/2/2
12	CLA	aA	804	1	-	7/29/105/115	-
12	CLA	cA	806	1	-	11/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BCR	cL	206	-	-	6/29/63/63	0/2/2/2
12	CLA	cA	816	1	-	6/15/91/115	-

The worst 5 of 5449 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	bB	940	1L3	C03-C02	7.88	1.49	1.35
13	aB	940	1L3	C03-C02	7.85	1.49	1.35
13	cB	940	1L3	C03-C02	7.83	1.49	1.35
13	bA	844	1L3	C03-C02	7.76	1.49	1.35
13	cA	844	1L3	C03-C02	7.74	1.49	1.35

The worst 5 of 8212 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	aB	931	CLA	C1D-ND-C4D	-10.64	98.77	106.33
12	cB	931	CLA	C1D-ND-C4D	-10.60	98.81	106.33
12	bB	931	CLA	C1D-ND-C4D	-10.58	98.82	106.33
12	aB	931	CLA	C2D-C1D-ND	10.15	117.58	110.10
12	cB	931	CLA	C2D-C1D-ND	10.10	117.55	110.10

There are no chirality outliers.

5 of 2727 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	aA	804	CLA	C1A-C2A-CAA-CBA
12	aA	804	CLA	C3A-C2A-CAA-CBA
12	aA	807	CLA	C1A-C2A-CAA-CBA
12	aA	808	CLA	C2A-CAA-CBA-CGA
12	aA	808	CLA	C2-C3-C5-C6

There are no ring outliers.

235 monomers are involved in 370 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	cA	849	BCR	4	0
15	aI	101	BCR	2	0
12	bB	930	CLA	1	0
12	bA	830	CLA	2	0
12	bB	929	CLA	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	aF	204	BCR	3	0
15	bL	205	BCR	2	0
12	cB	917	CLA	1	0
12	bL	204	CLA	1	0
12	cA	808	CLA	1	0
12	aA	836	CLA	1	0
12	aB	930	CLA	1	0
15	bF	203	BCR	1	0
12	cA	814	CLA	1	0
12	cB	931	CLA	4	0
12	bL	202	CLA	2	0
12	aA	840	CLA	4	0
15	aL	205	BCR	2	0
12	cB	922	CLA	2	0
12	bA	842	CLA	4	0
12	bB	933	CLA	1	0
12	bA	838	CLA	1	0
15	cL	205	BCR	2	0
12	cB	914	CLA	1	0
12	bB	914	CLA	1	0
15	cB	941	BCR	1	0
16	aA	853	LHG	1	0
12	aA	814	CLA	1	0
12	bA	828	CLA	1	0
15	cB	946	BCR	1	0
12	cA	803	CLA	1	0
12	aB	931	CLA	6	0
12	aA	854	CLA	2	0
16	bA	851	LHG	1	0
12	aB	914	CLA	1	0
12	bA	812	CLA	1	0
12	bA	810	CLA	2	0
12	cB	926	CLA	3	0
15	cF	201	BCR	2	0
12	cA	832	CLA	2	0
15	aA	848	BCR	2	0
12	bA	832	CLA	2	0
12	cA	809	CLA	3	0
12	aA	802	CLA	2	0
15	cL	201	BCR	3	0
12	aA	807	CLA	1	0
15	cB	944	BCR	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	cB	909	CLA	1	0
12	cA	817	CLA	1	0
12	aA	843	CLA	4	0
12	bA	843	CLA	3	0
12	bB	902	CLA	1	0
12	aB	923	CLA	3	0
12	bA	819	CLA	3	0
12	bB	931	CLA	5	0
15	bF	201	BCR	1	0
12	bA	825	CLA	6	0
16	cA	852	LHG	1	0
12	aL	202	CLA	2	0
12	aB	933	CLA	1	0
12	aA	833	CLA	1	0
15	cB	943	BCR	2	0
15	bB	944	BCR	3	0
15	cA	847	BCR	3	0
12	bA	821	CLA	2	0
15	aA	849	BCR	1	0
12	cA	807	CLA	2	0
15	aL	206	BCR	1	0
12	aA	812	CLA	1	0
12	cL	202	CLA	2	0
12	aA	842	CLA	3	0
12	cA	827	CLA	2	0
12	aA	809	CLA	4	0
12	aA	818	CLA	2	0
15	aB	943	BCR	3	0
12	cA	837	CLA	1	0
12	bA	803	CLA	1	0
12	aB	927	CLA	3	0
12	aA	819	CLA	3	0
15	bB	941	BCR	1	0
12	cB	916	CLA	2	0
12	bB	936	CLA	2	0
15	aB	945	BCR	1	0
12	cA	843	CLA	4	0
12	cA	819	CLA	3	0
15	cF	204	BCR	3	0
12	cA	818	CLA	3	0
15	cA	850	BCR	2	0
15	bB	943	BCR	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	aB	918	CLA	1	0
12	cB	929	CLA	2	0
12	bA	802	CLA	2	0
12	aB	906	CLA	1	0
12	aB	917	CLA	1	0
12	bB	927	CLA	2	0
12	cB	925	CLA	3	0
12	cA	820	CLA	1	0
12	cA	828	CLA	1	0
12	bA	827	CLA	2	0
12	bA	837	CLA	1	0
12	aB	904	CLA	1	0
12	cA	841	CLA	2	0
12	aB	929	CLA	2	0
12	aA	826	CLA	1	0
12	aB	936	CLA	2	0
15	aF	201	BCR	2	0
15	bB	942	BCR	1	0
12	aA	803	CLA	1	0
15	bB	945	BCR	2	0
12	bB	905	CLA	1	0
12	bA	826	CLA	1	0
12	cA	825	CLA	6	0
12	cA	805	CLA	1	0
12	aA	810	CLA	2	0
12	aB	949	CLA	1	0
12	cA	842	CLA	4	0
12	aA	806	CLA	3	0
12	bA	806	CLA	4	0
12	cA	834	CLA	3	0
15	bI	101	BCR	2	0
12	bB	912	CLA	4	0
15	bJ	101	BCR	1	0
12	cA	830	CLA	2	0
15	aJ	101	BCR	1	0
16	bA	852	LHG	1	0
15	bA	850	BCR	3	0
12	bB	906	CLA	1	0
12	cB	924	CLA	1	0
12	aB	909	CLA	2	0
12	aB	916	CLA	2	0
12	cB	906	CLA	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	cA	848	BCR	2	0
12	aB	902	CLA	1	0
12	bA	820	CLA	1	0
12	aA	837	CLA	2	0
15	aB	941	BCR	2	0
15	bA	847	BCR	3	0
12	bA	822	CLA	1	0
12	cB	912	CLA	5	0
12	bB	935	CLA	1	0
12	bA	804	CLA	2	0
15	aA	850	BCR	3	0
12	bB	921	CLA	1	0
15	cF	203	BCR	2	0
12	aB	922	CLA	2	0
12	bB	904	CLA	2	0
12	aB	926	CLA	2	0
15	aB	944	BCR	3	0
12	cB	935	CLA	1	0
12	aA	829	CLA	1	0
12	cA	810	CLA	2	0
12	bB	919	CLA	1	0
12	cA	829	CLA	1	0
12	aL	204	CLA	1	0
12	bA	807	CLA	1	0
13	bB	940	1L3	1	0
12	aB	912	CLA	5	0
12	bB	916	CLA	2	0
12	aA	830	CLA	2	0
12	aB	915	CLA	2	0
12	bA	841	CLA	2	0
12	aB	919	CLA	1	0
12	cA	836	CLA	1	0
12	bB	915	CLA	2	0
12	cB	915	CLA	2	0
12	cB	913	CLA	1	0
12	aB	905	CLA	2	0
15	bF	204	BCR	3	0
16	cA	851	LHG	1	0
12	aB	925	CLA	2	0
15	cB	945	BCR	3	0
12	cA	812	CLA	1	0
12	cA	821	CLA	2	0

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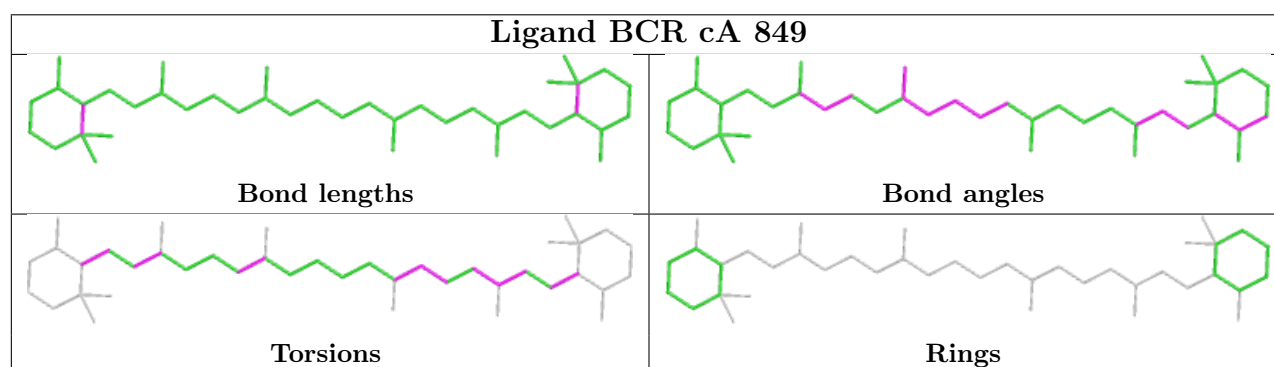
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12	bA	817	CLA	1	0
12	bA	853	CLA	2	0
12	cB	923	CLA	3	0
12	aA	828	CLA	1	0
12	bA	808	CLA	1	0
15	cA	846	BCR	1	0
12	aA	808	CLA	1	0
12	cA	840	CLA	4	0
12	aA	841	CLA	2	0
12	cA	802	CLA	1	0
15	aL	201	BCR	1	0
12	cB	936	CLA	2	0
12	cL	204	CLA	1	0
12	cB	930	CLA	1	0
12	bB	925	CLA	2	0
12	cB	905	CLA	2	0
12	bB	926	CLA	3	0
12	bB	923	CLA	2	0
12	aA	832	CLA	2	0
15	aB	946	BCR	2	0
12	bA	829	CLA	1	0
12	cA	826	CLA	1	0
12	bB	922	CLA	1	0
12	bA	834	CLA	2	0
12	bB	909	CLA	2	0
12	aA	825	CLA	5	0
12	aA	817	CLA	1	0
12	aB	935	CLA	1	0
12	bB	901	CLA	1	0
12	cA	853	CLA	3	0
12	bB	911	CLA	1	0
12	aA	834	CLA	2	0
12	bA	809	CLA	3	0
12	bA	836	CLA	1	0
12	bB	949	CLA	1	0
15	bB	946	BCR	2	0
12	aA	838	CLA	1	0
12	aA	820	CLA	1	0
12	aB	911	CLA	1	0
12	bA	840	CLA	4	0
12	cA	822	CLA	1	0
12	cA	838	CLA	2	0

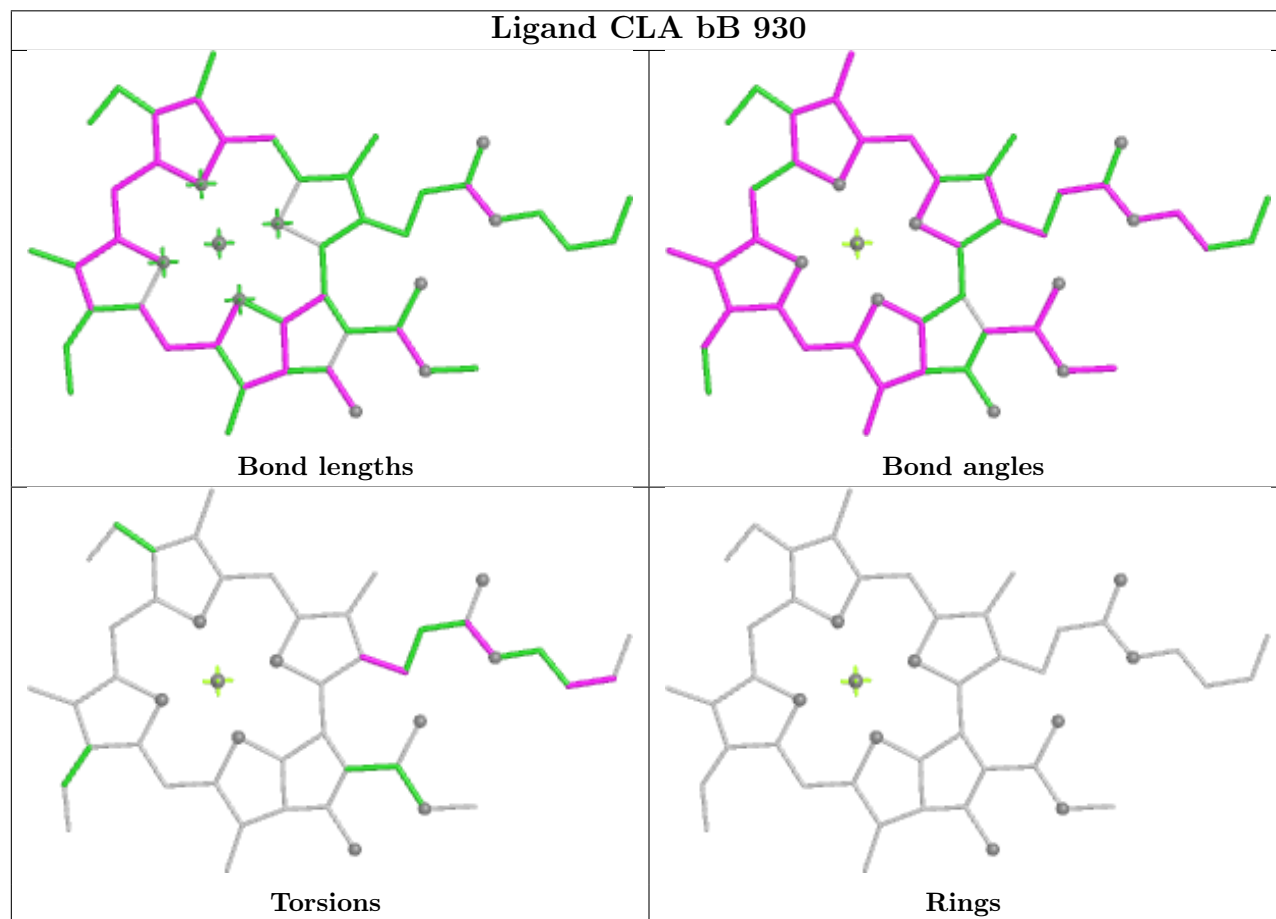
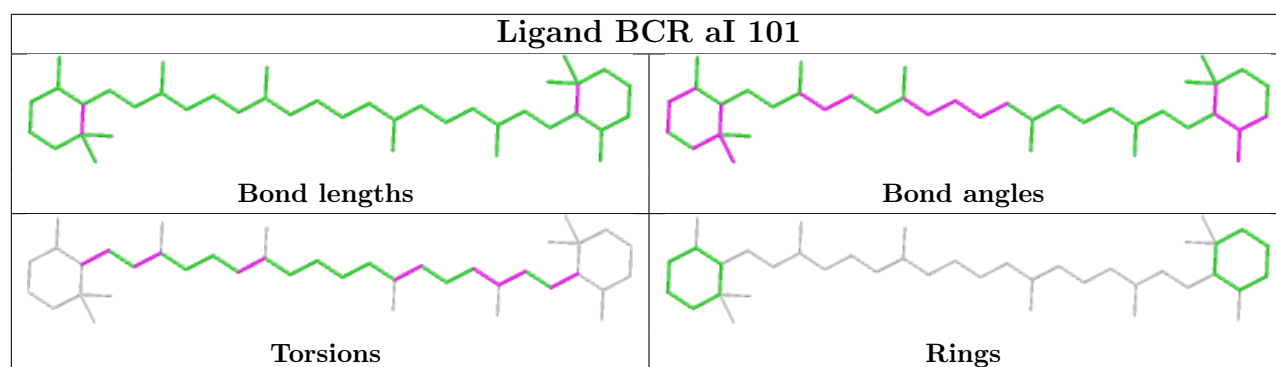
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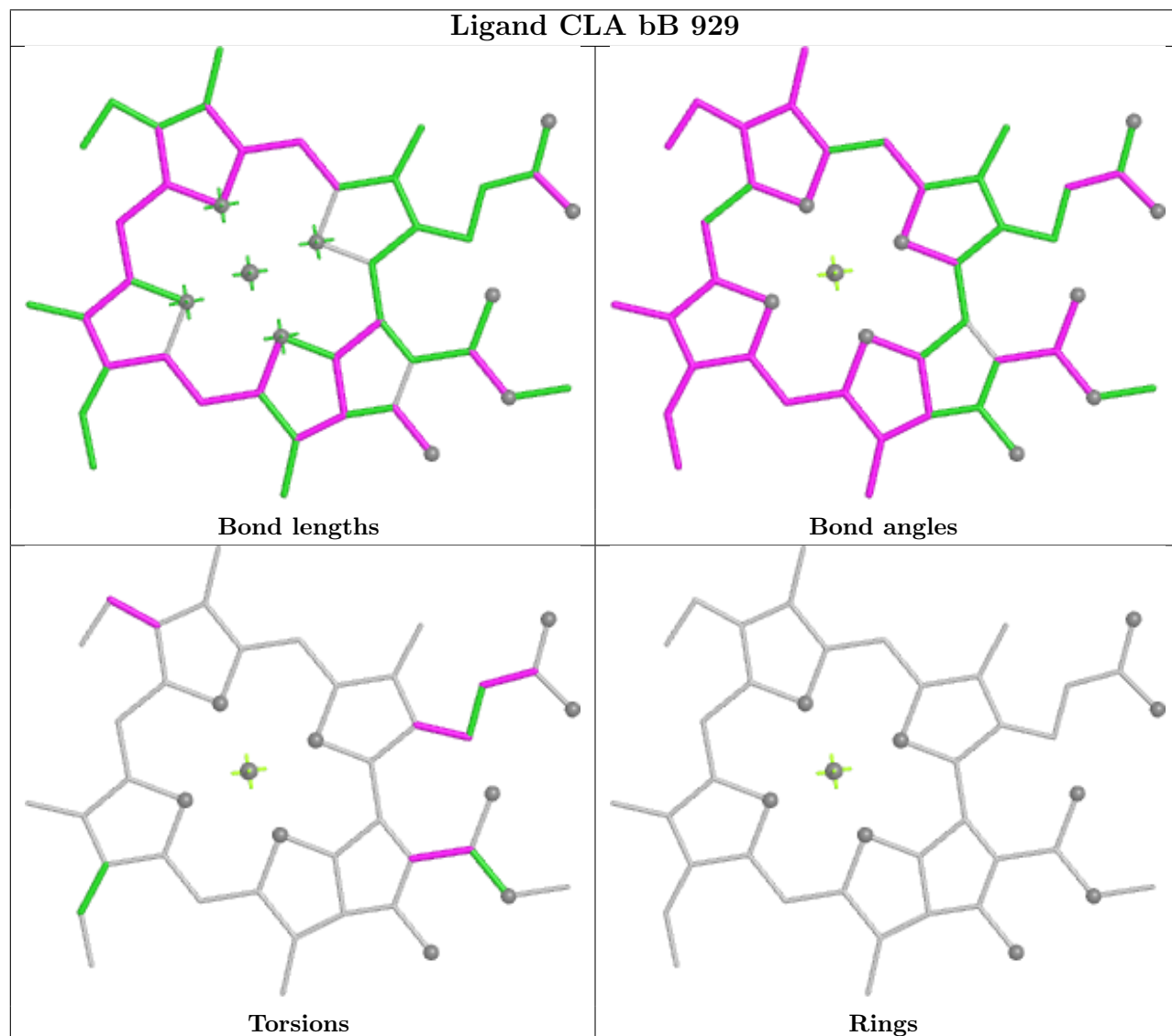
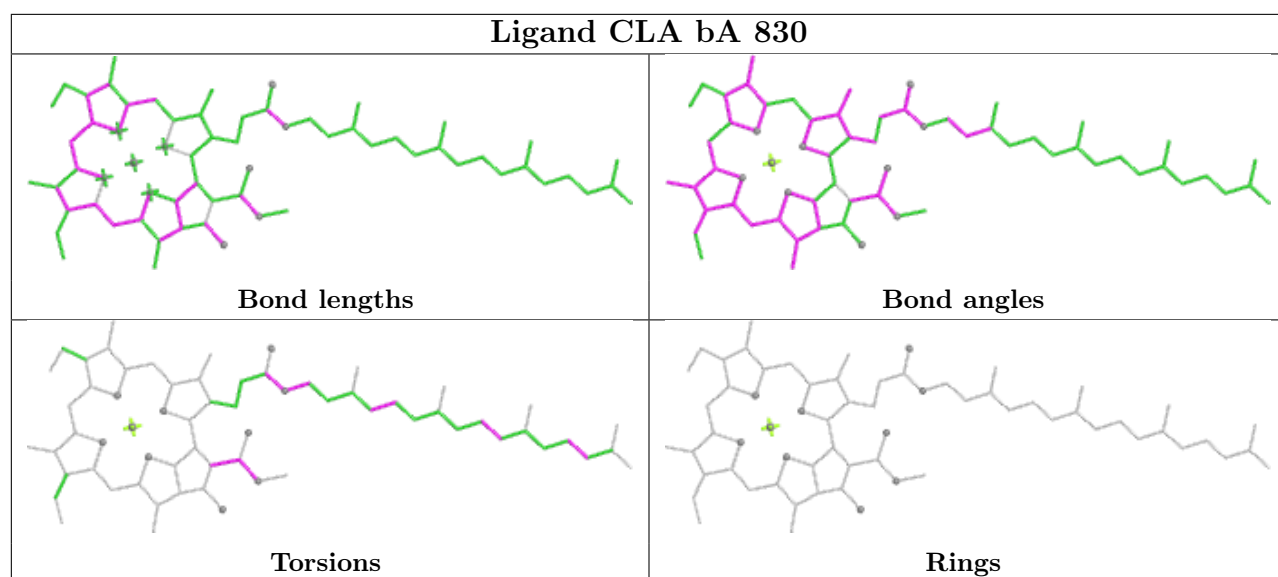
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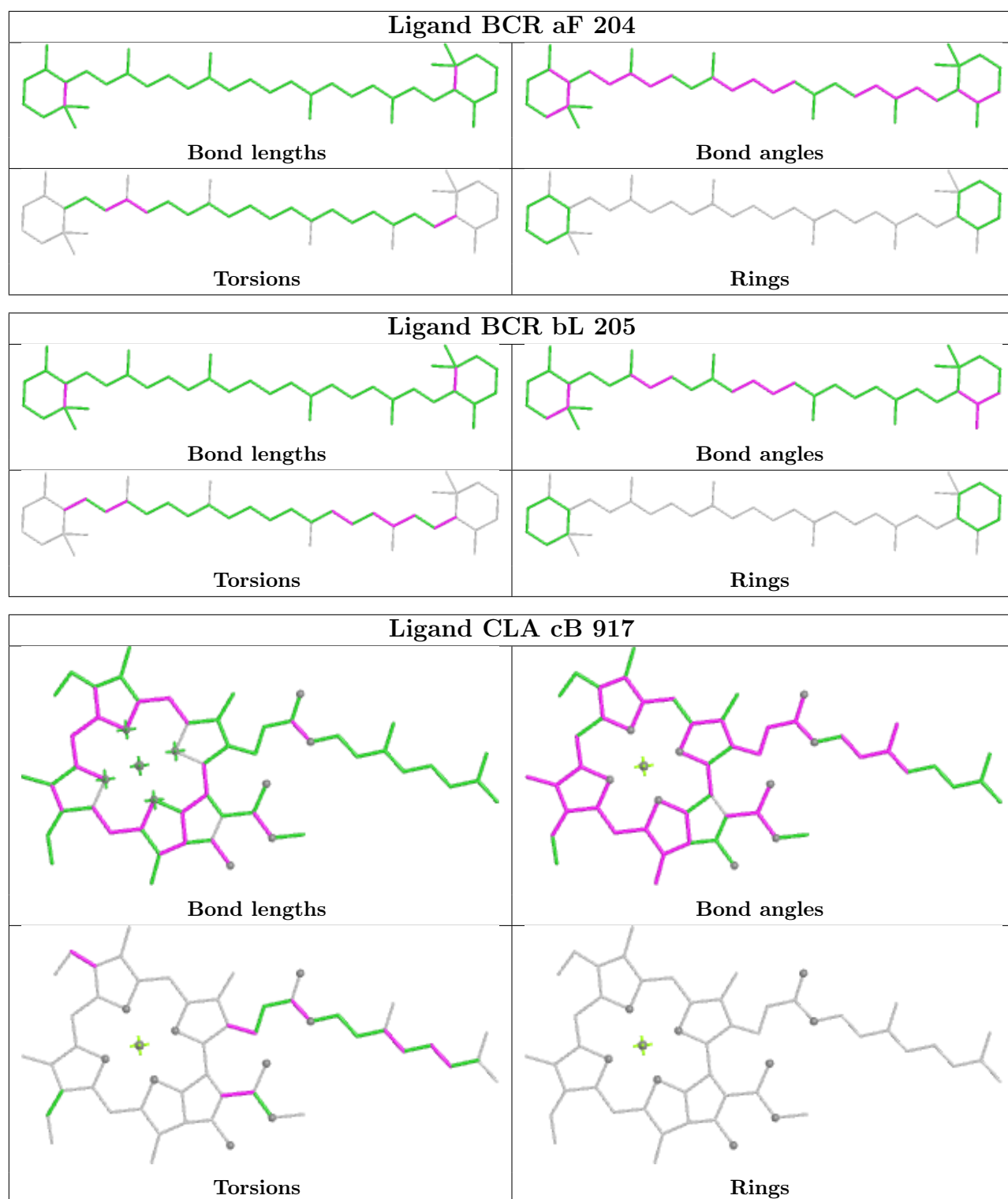
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	bL	201	BCR	2	0
12	cB	927	CLA	3	0
12	cA	804	CLA	2	0
15	bA	849	BCR	2	0
12	aA	821	CLA	2	0
12	bA	814	CLA	1	0
12	cB	911	CLA	1	0
12	aA	827	CLA	2	0
15	cI	101	BCR	1	0
12	bB	917	CLA	1	0
12	cB	933	CLA	1	0
12	cB	919	CLA	1	0
12	bA	818	CLA	3	0
15	aA	851	BCR	2	0
12	cB	918	CLA	1	0
15	aF	203	BCR	2	0
15	bA	848	BCR	2	0
12	aA	804	CLA	2	0
12	cA	806	CLA	5	0
15	cL	206	BCR	1	0

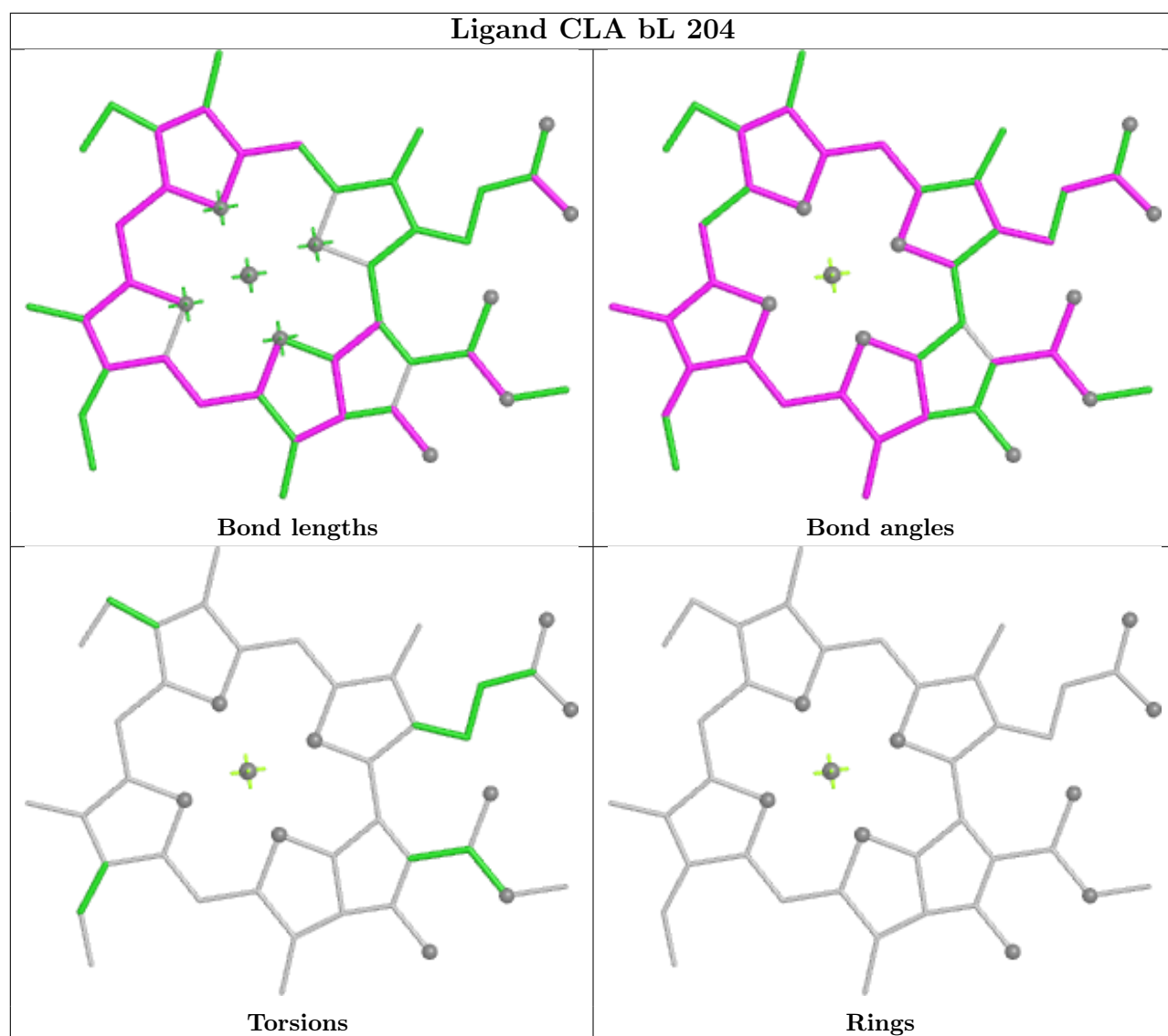
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

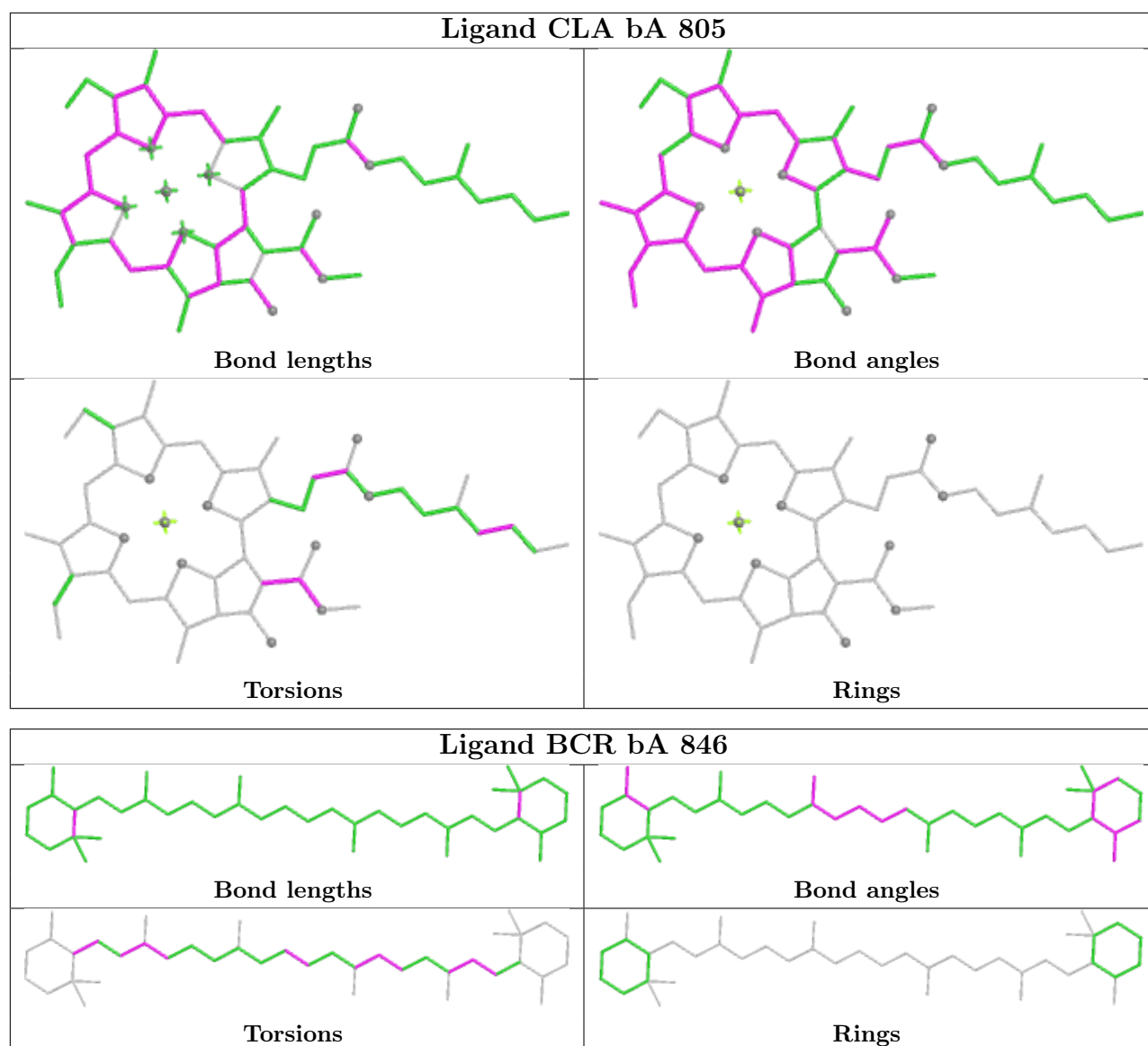


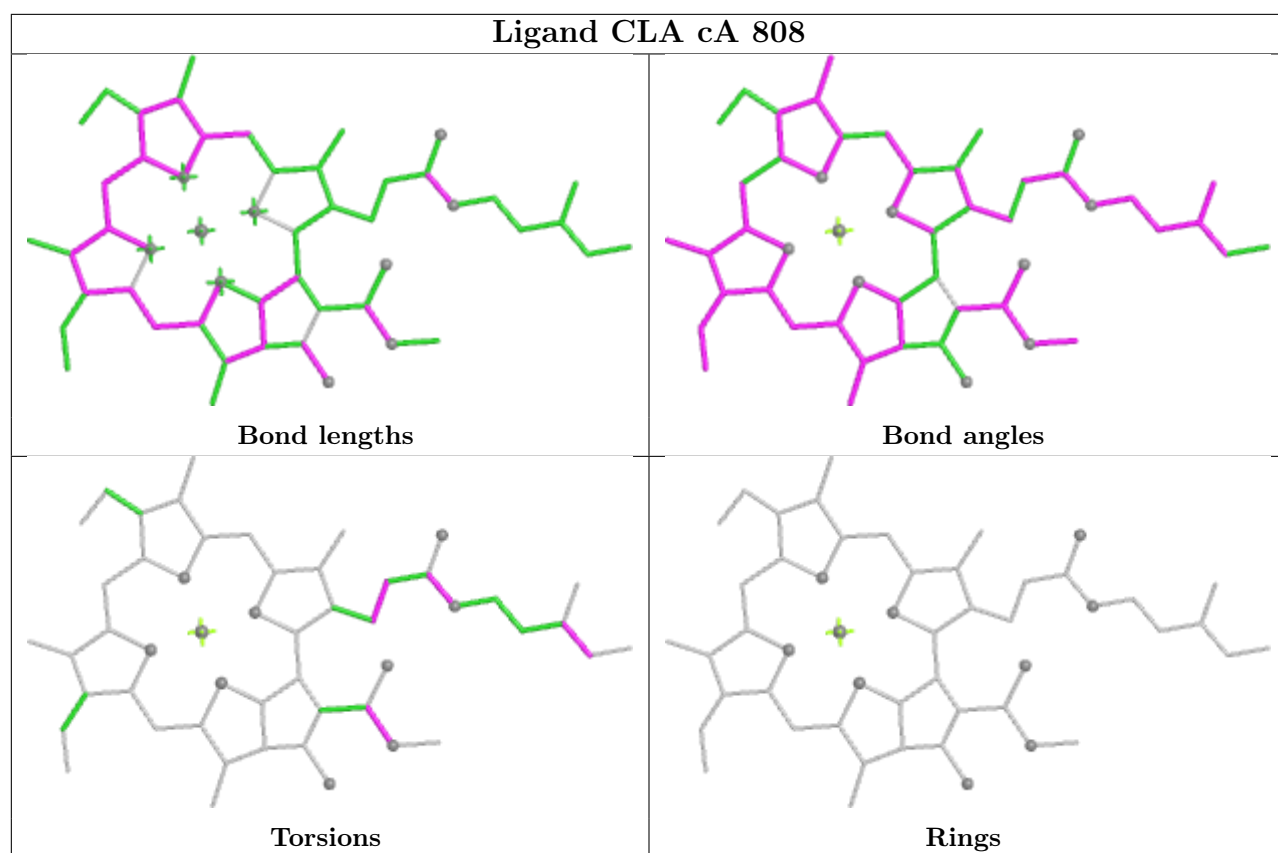


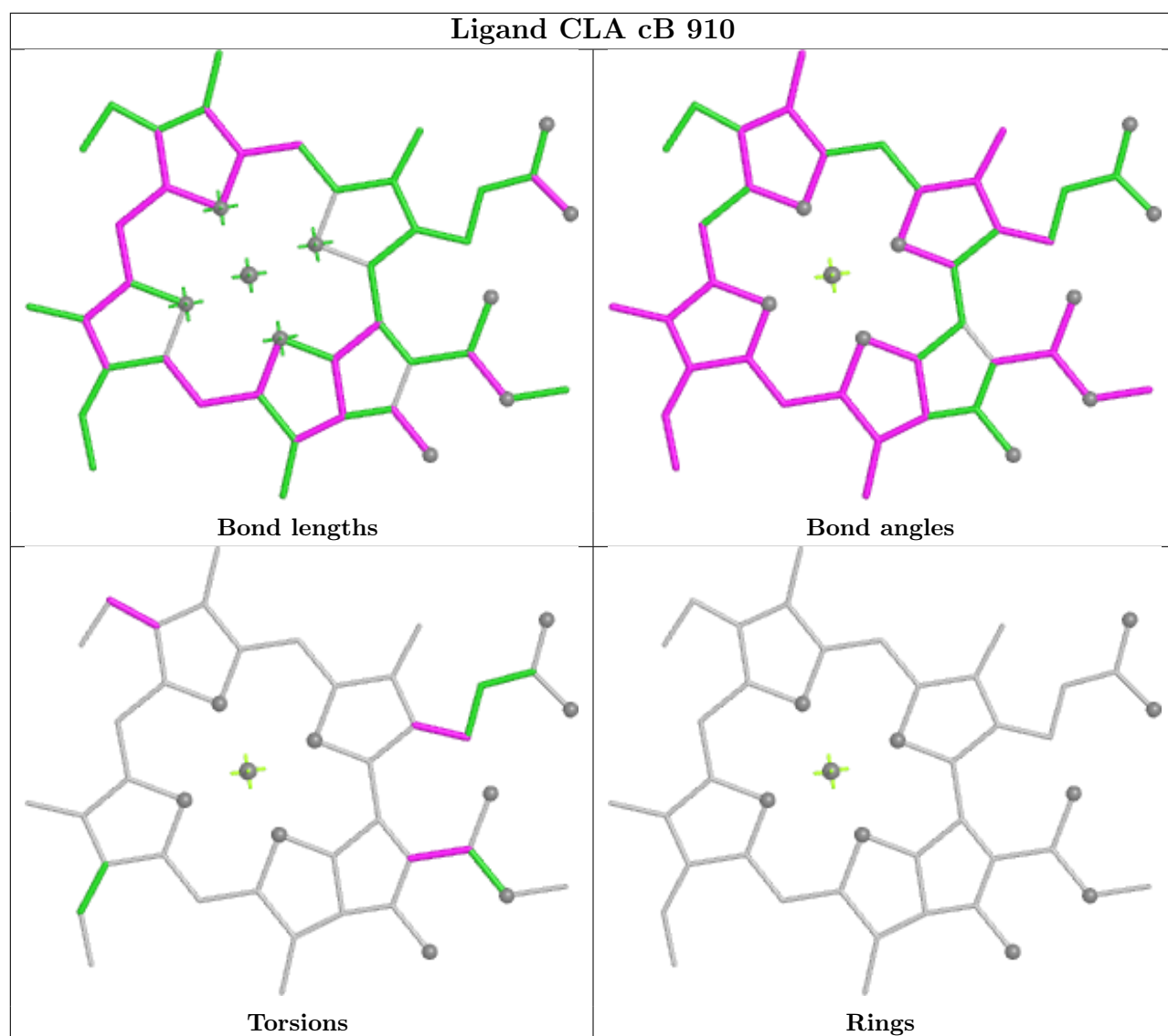


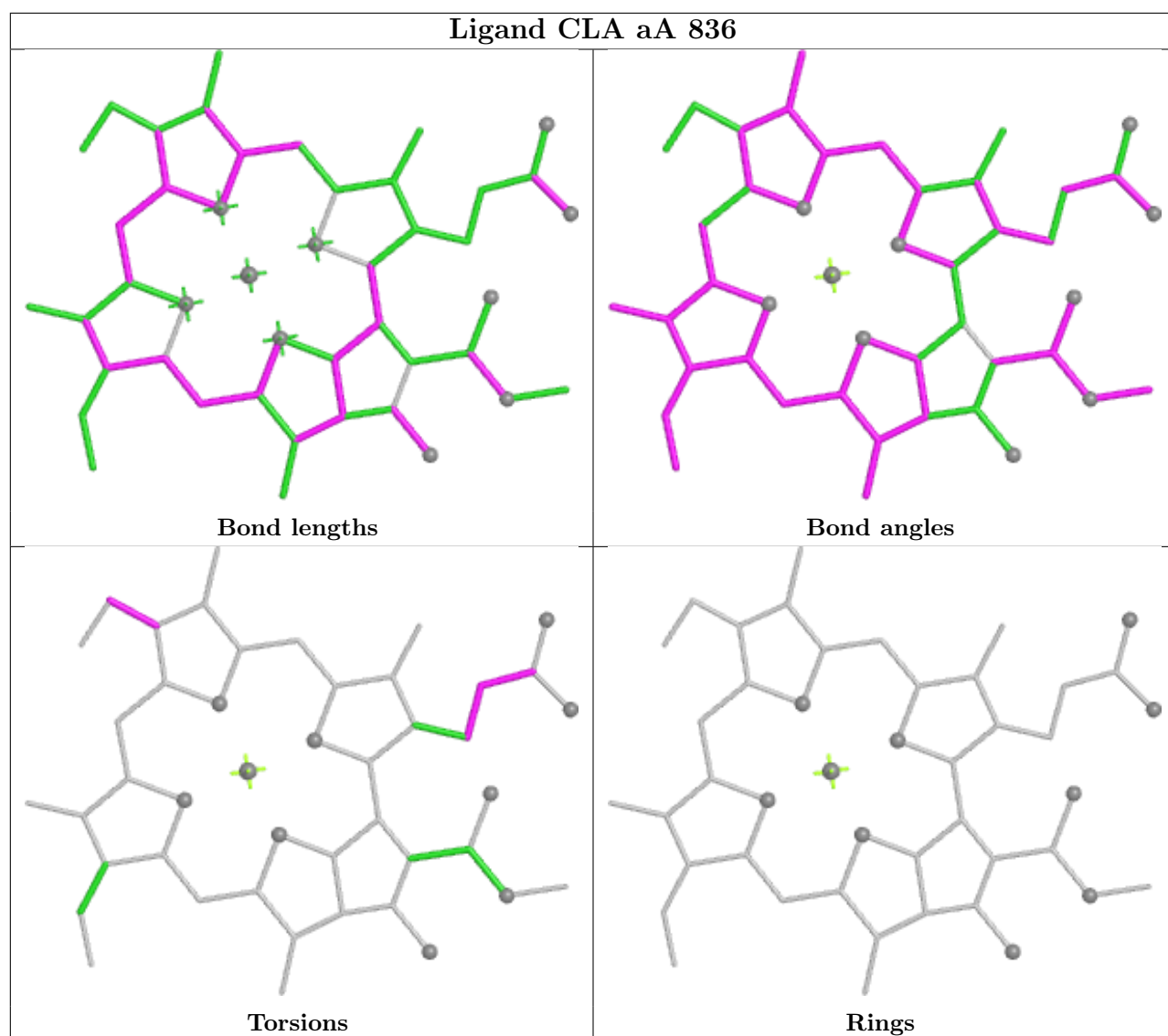


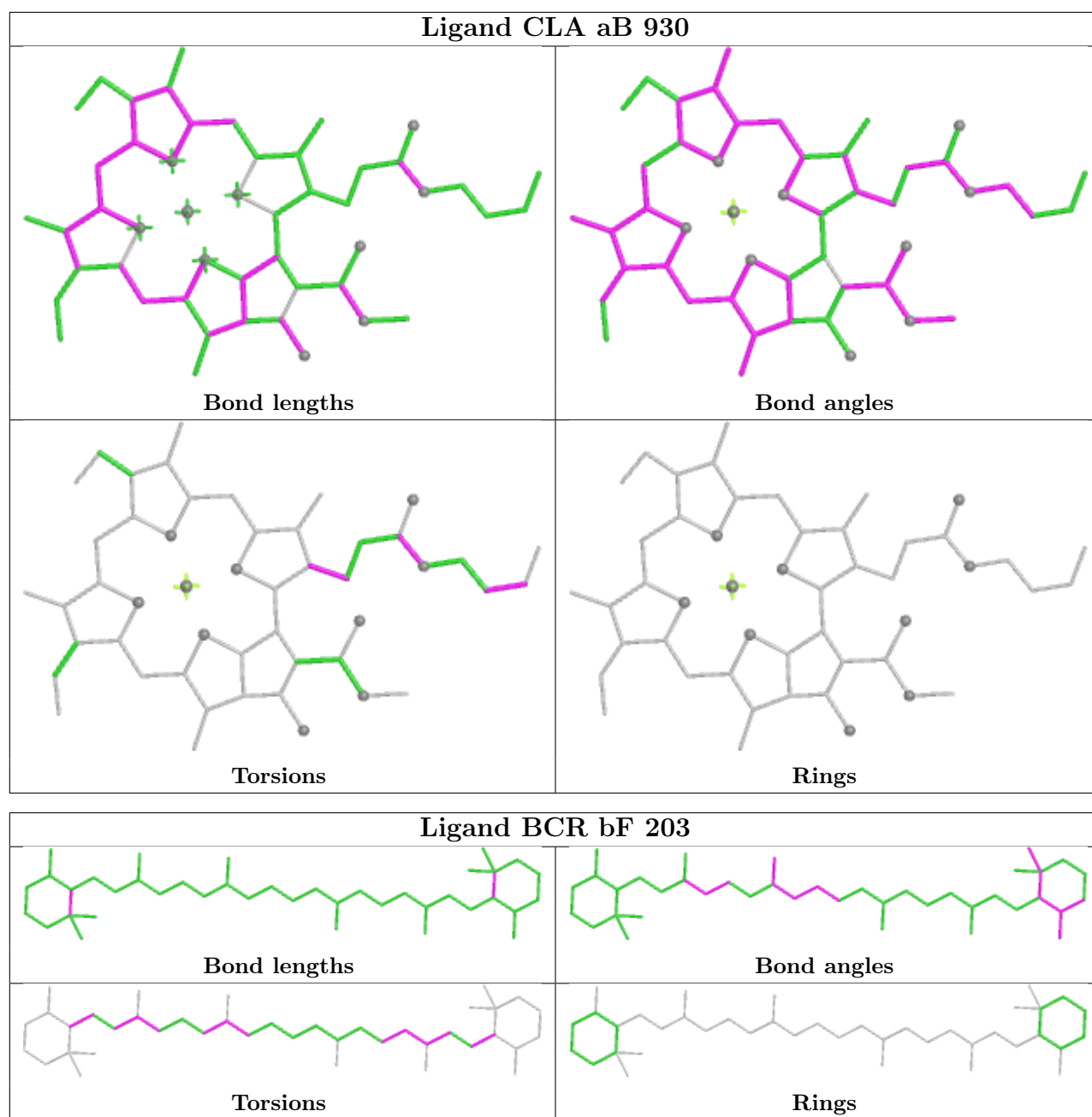




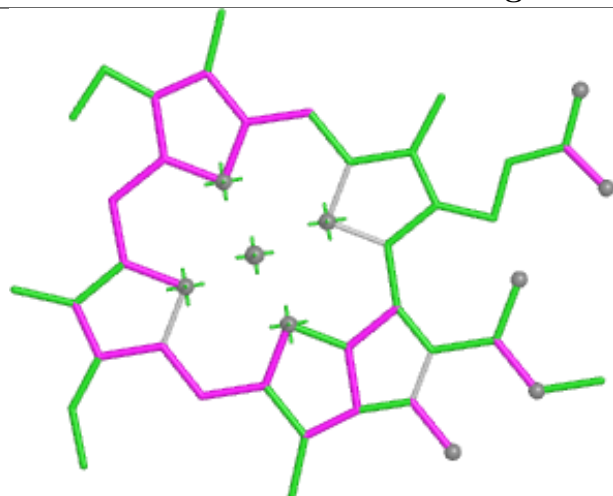




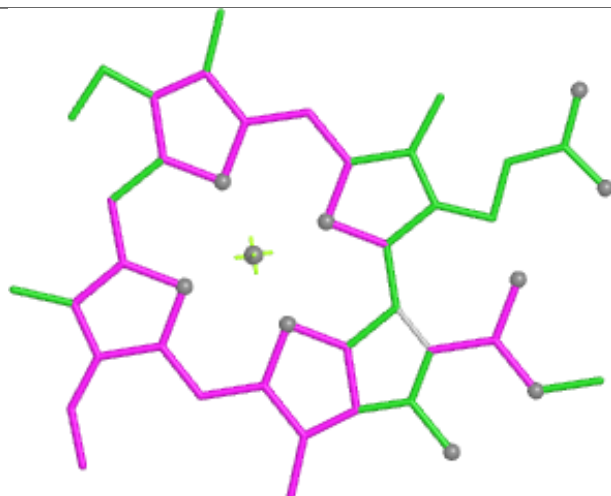




Ligand CLA aA 844



Bond lengths



Bond angles

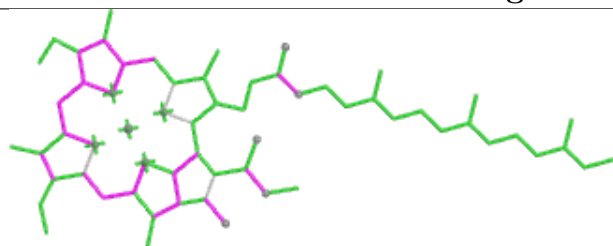


Torsions

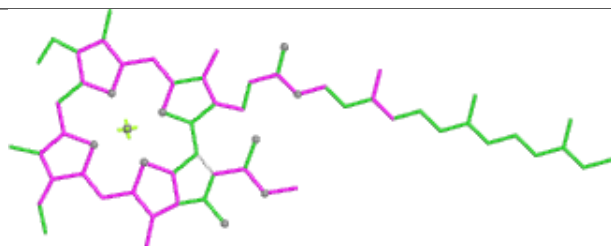


Rings

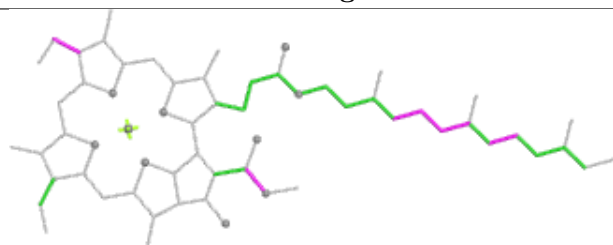
Ligand CLA cB 902



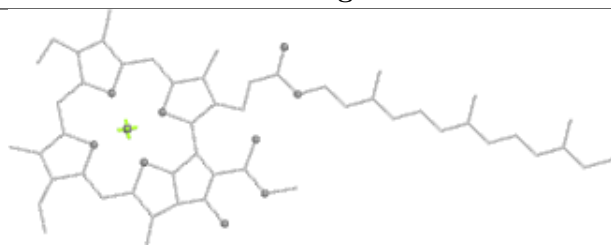
Bond lengths



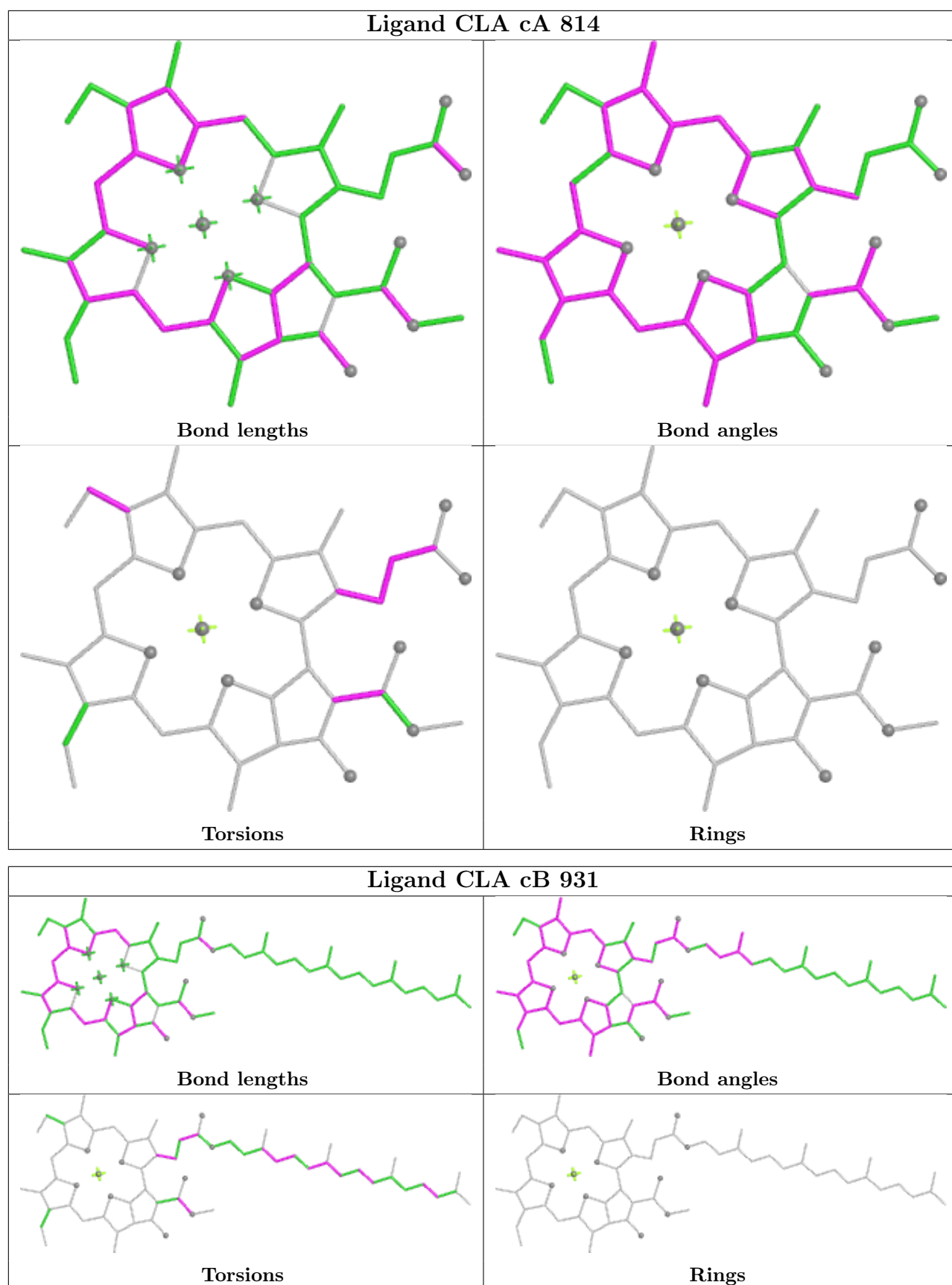
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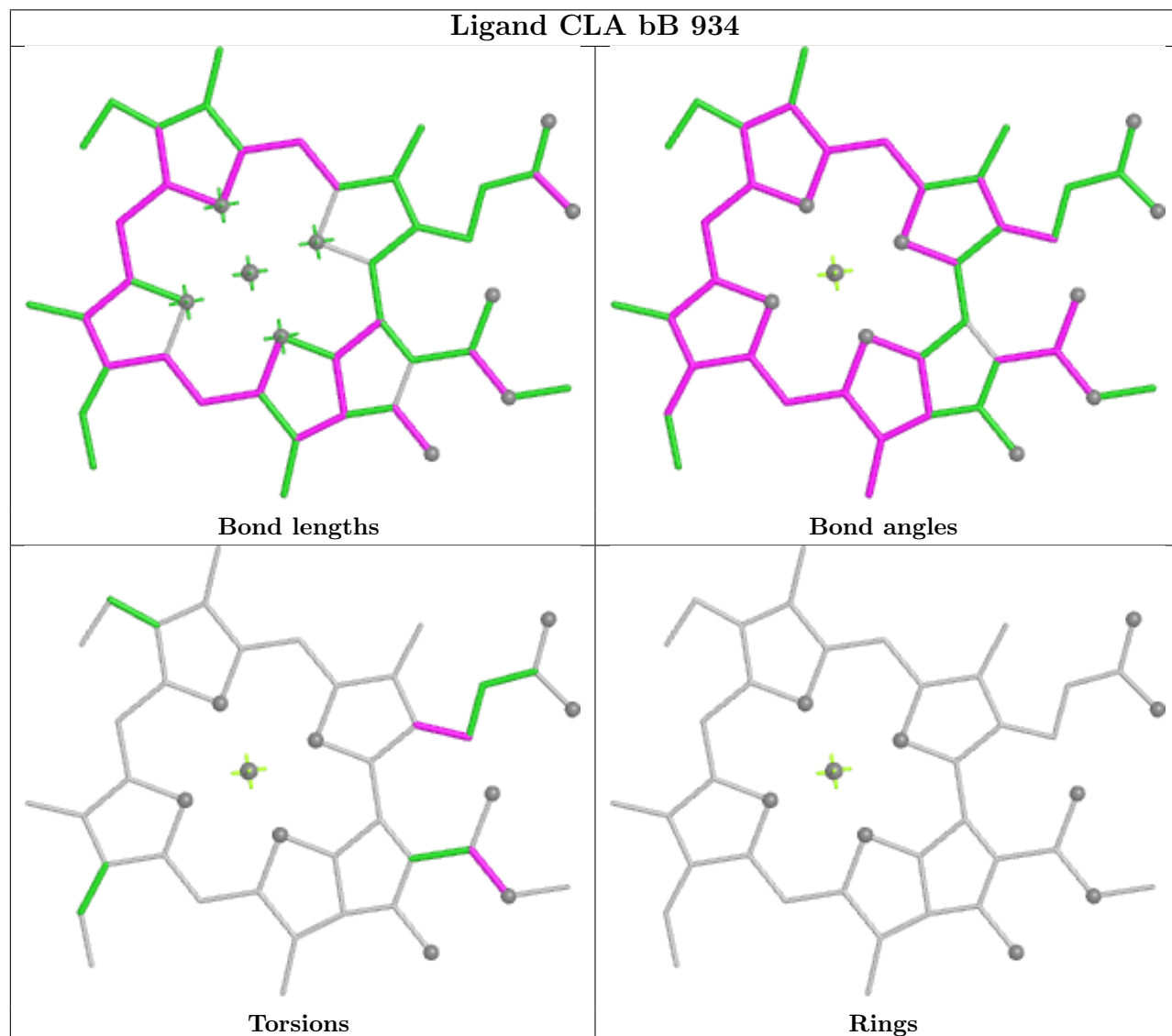
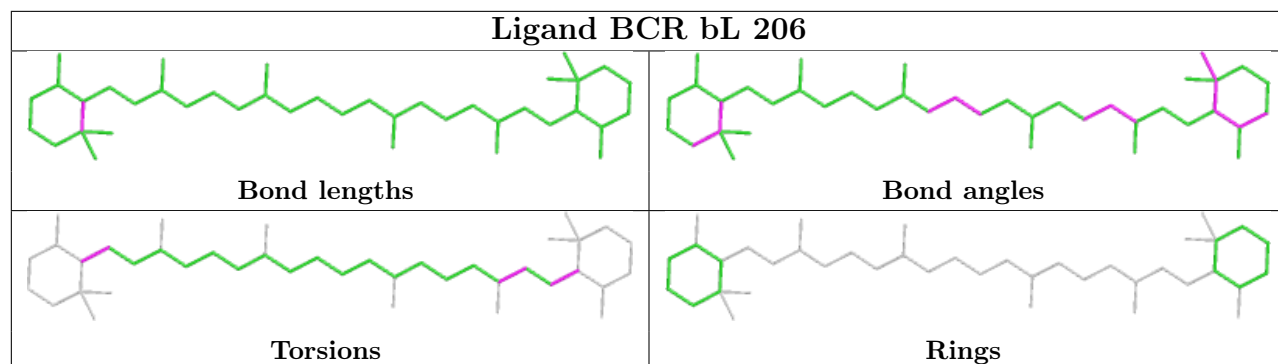


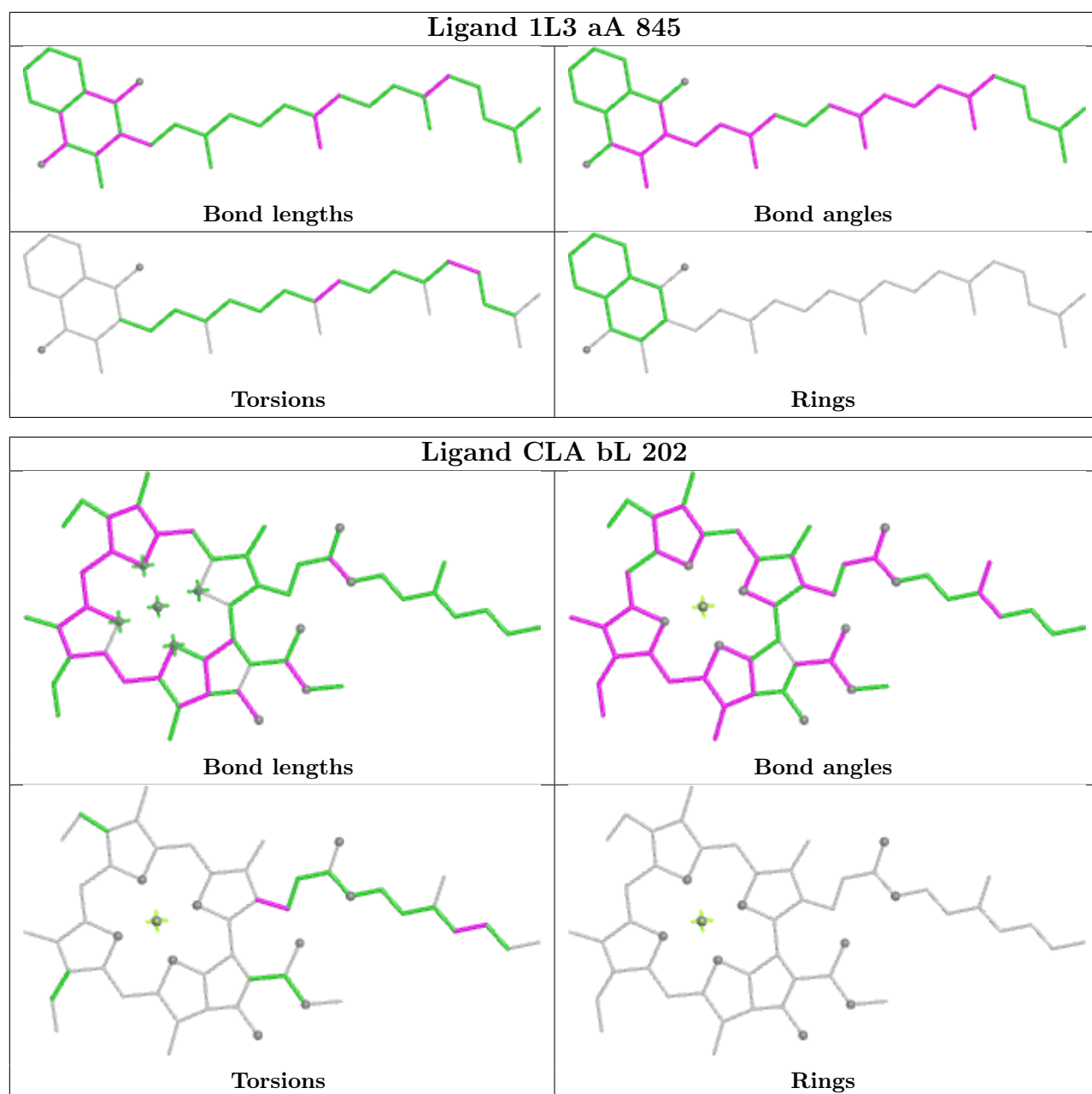
Torsions

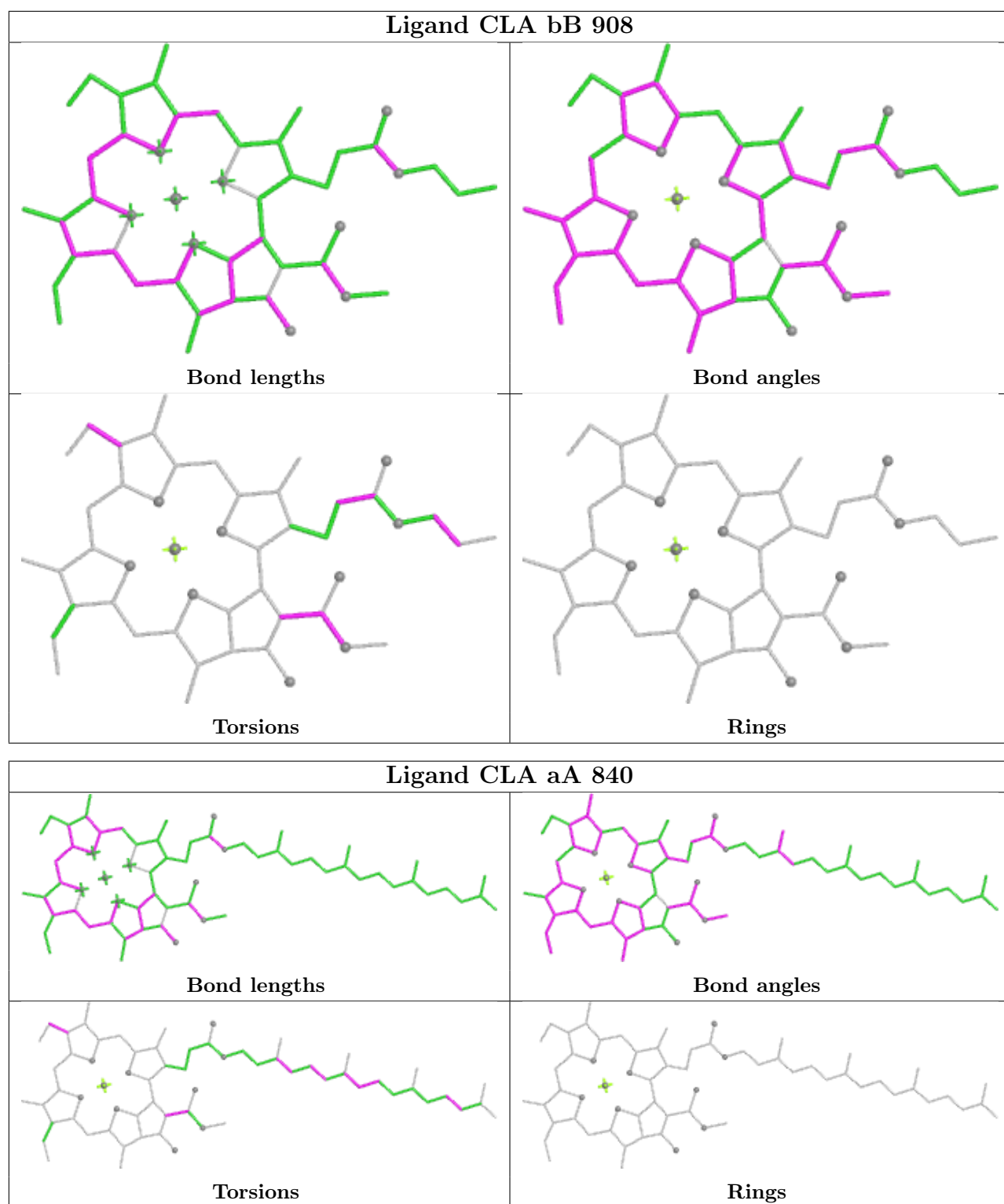


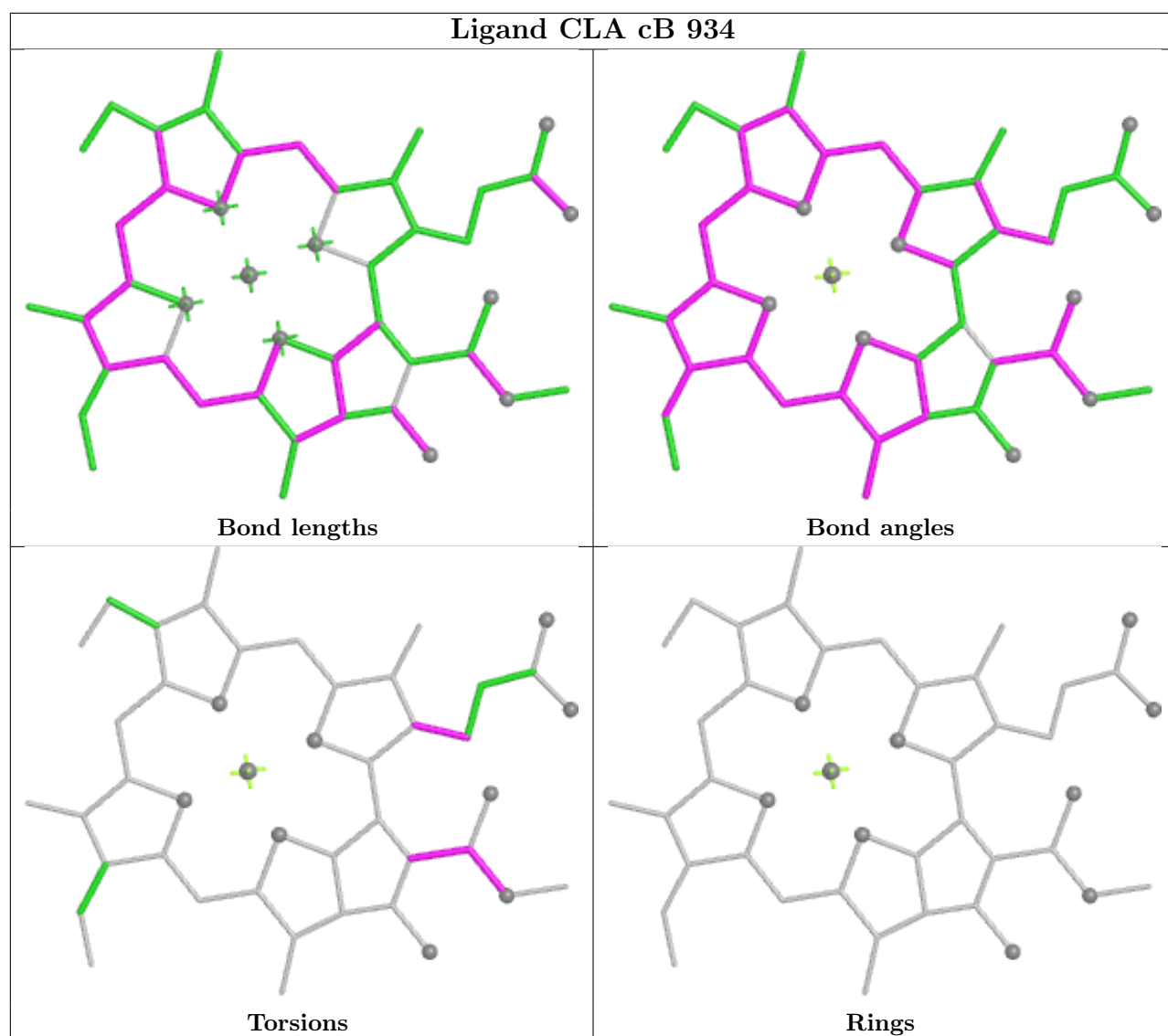
Rings

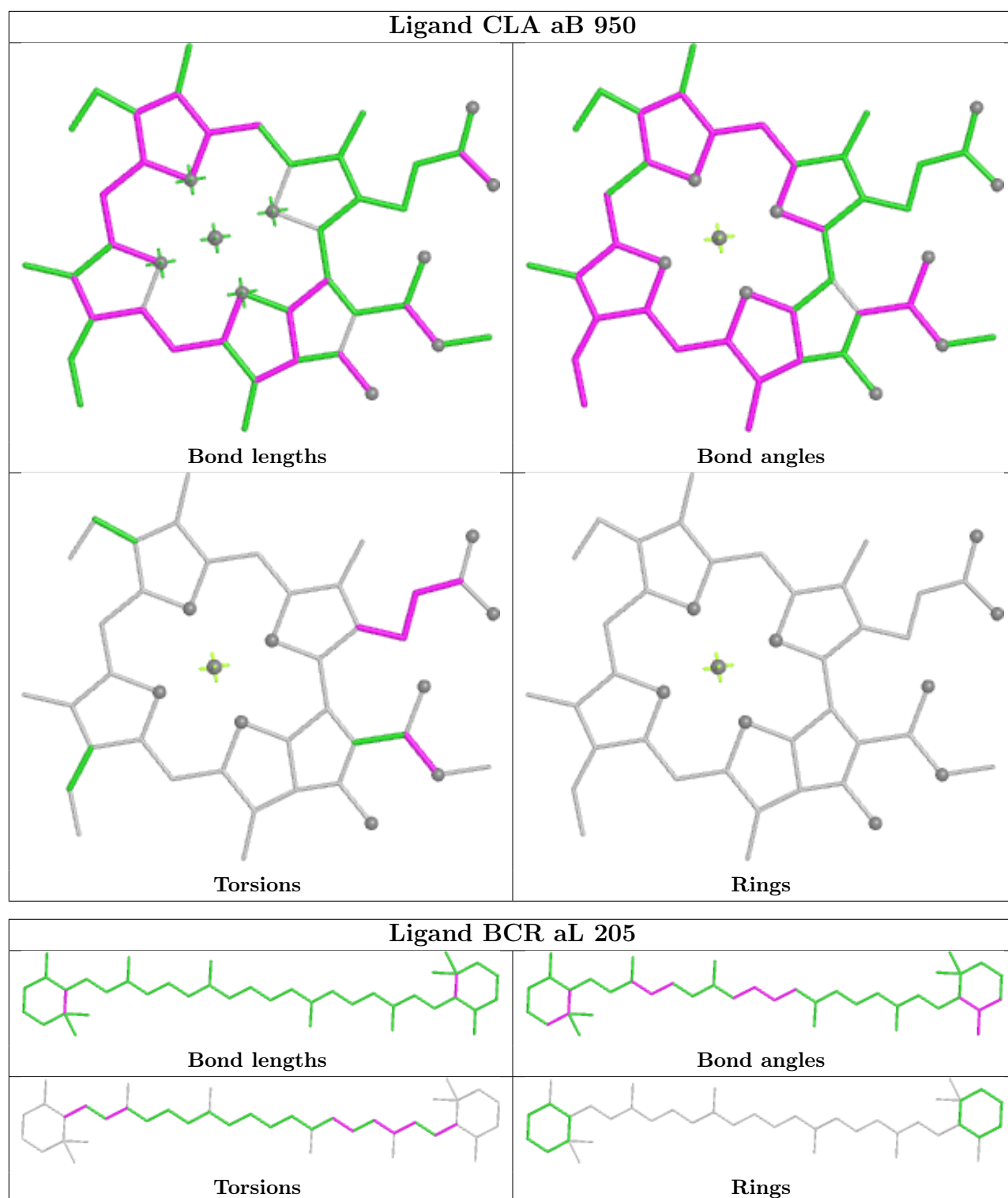


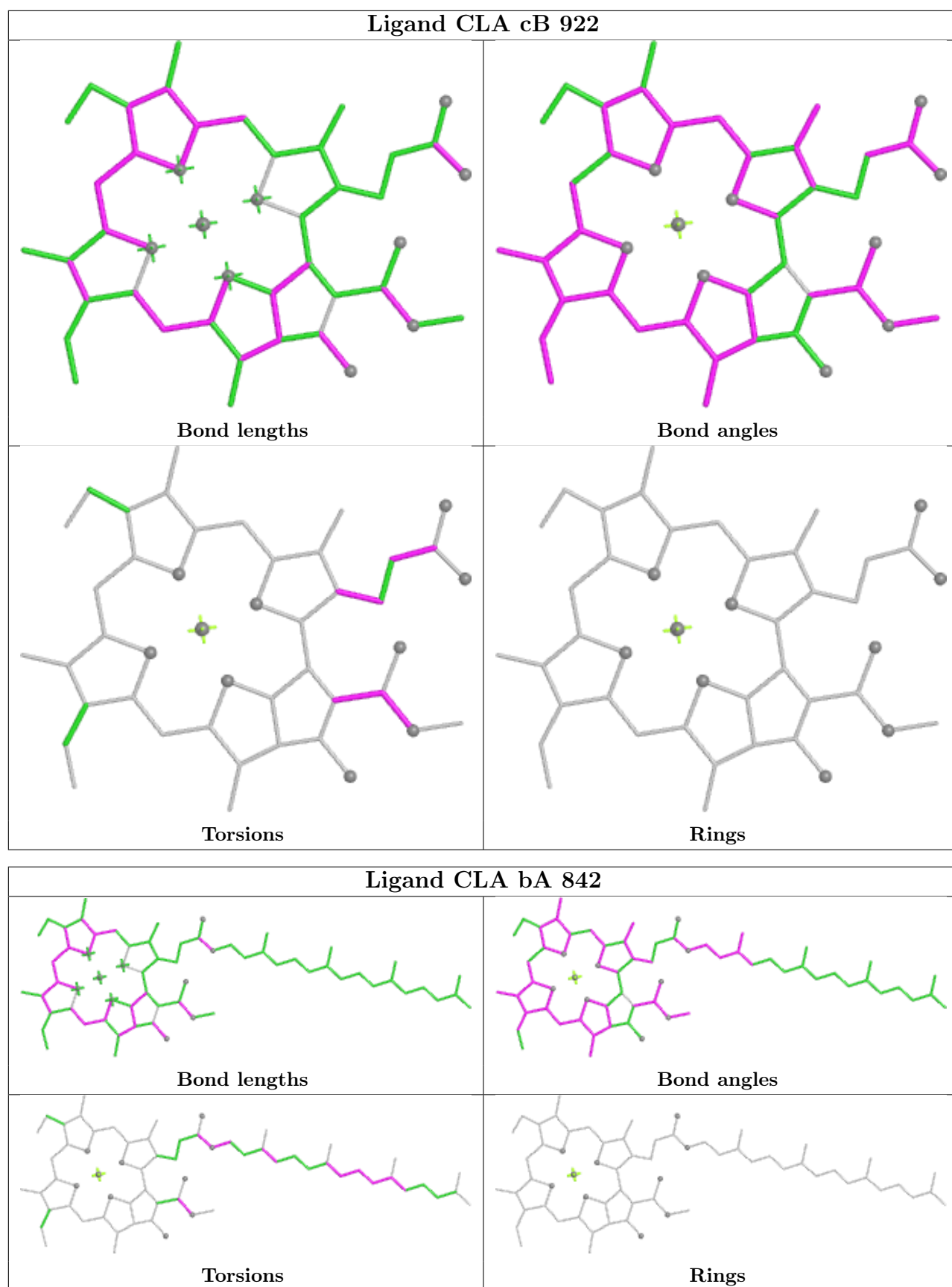


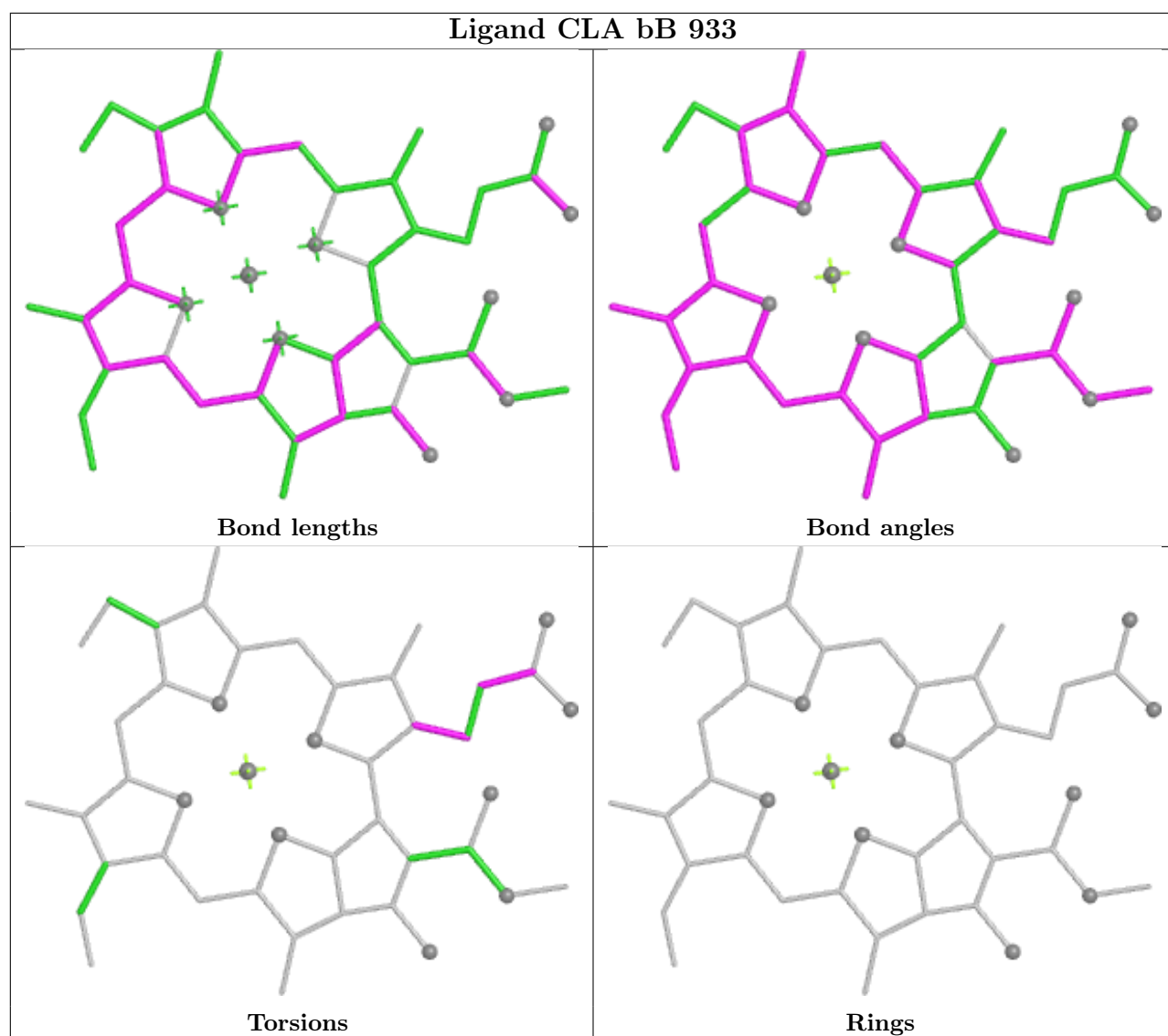


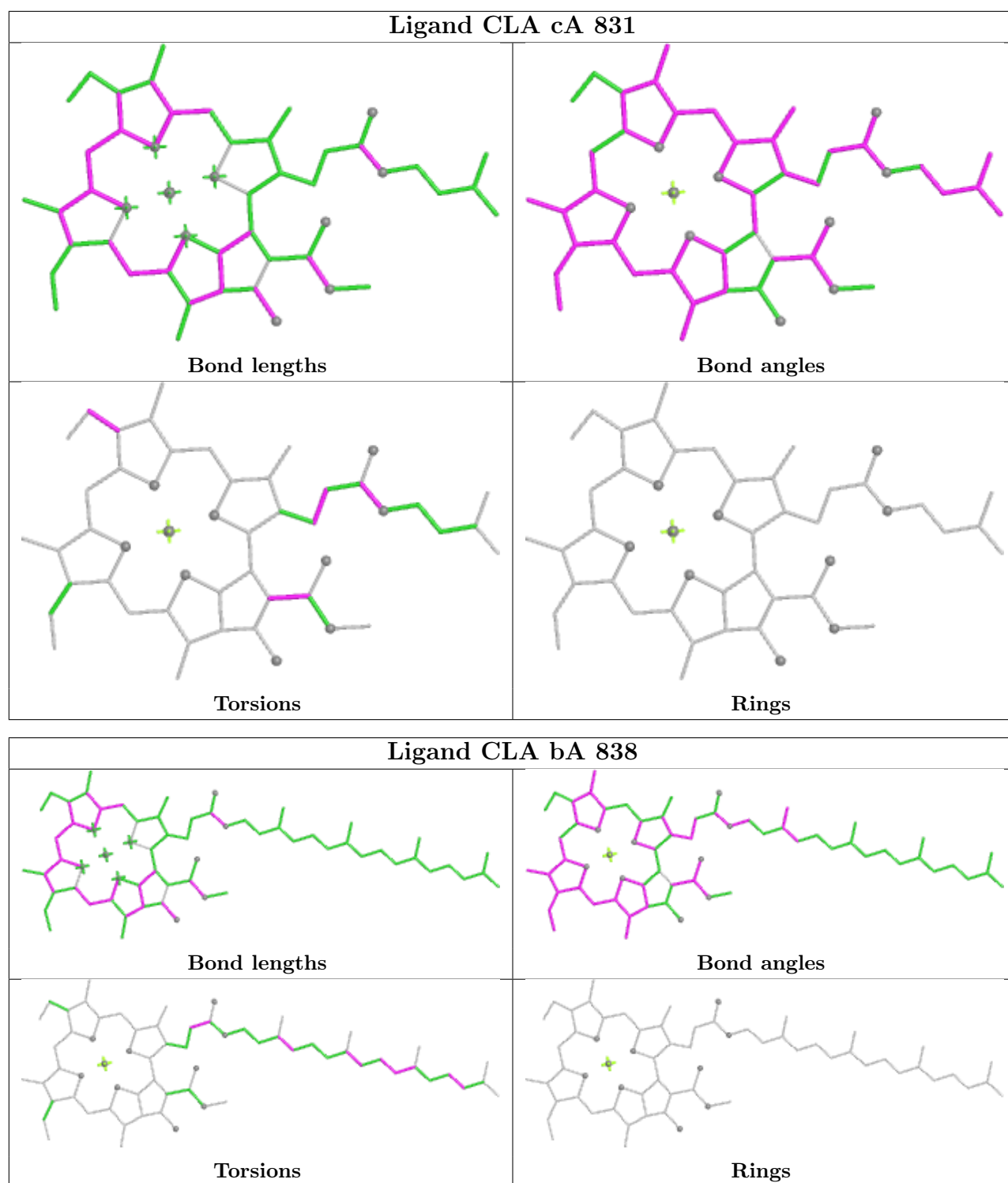


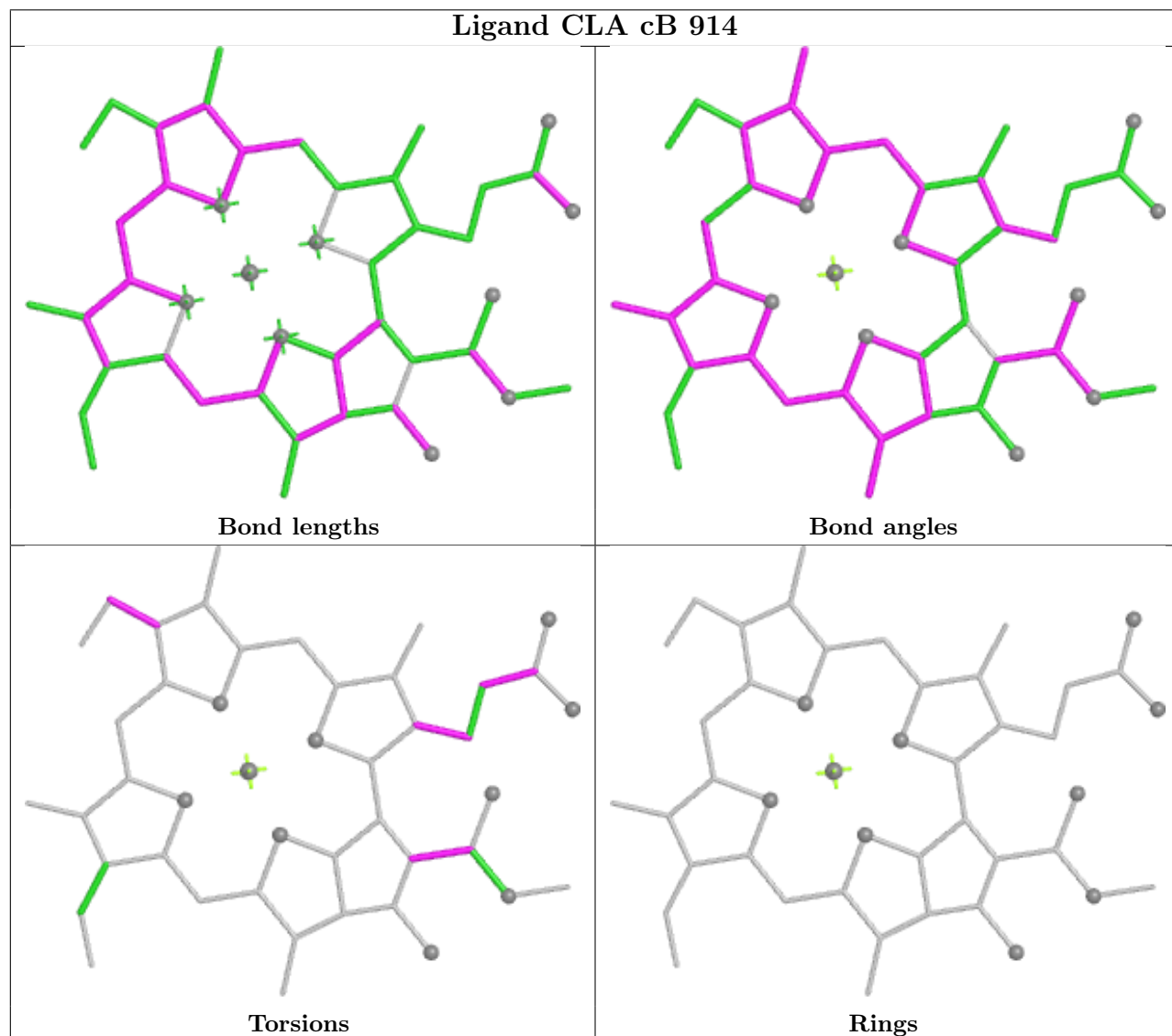
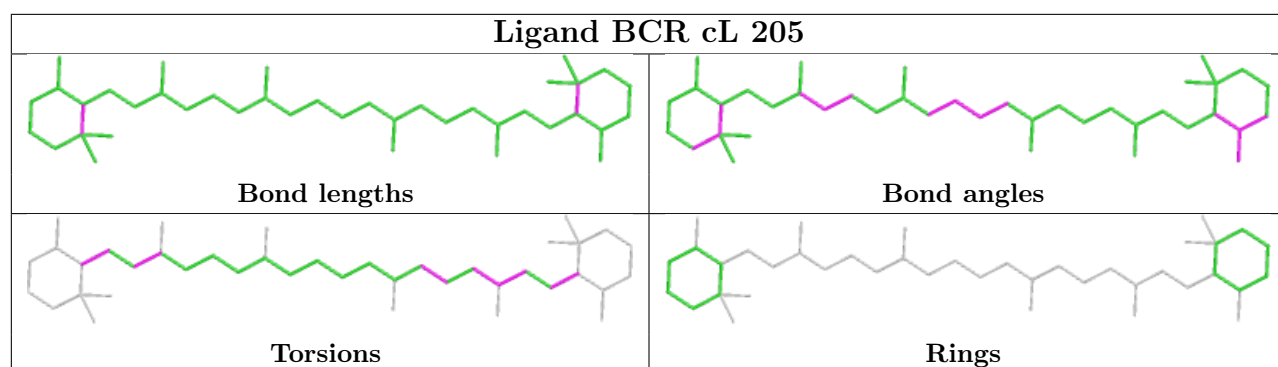


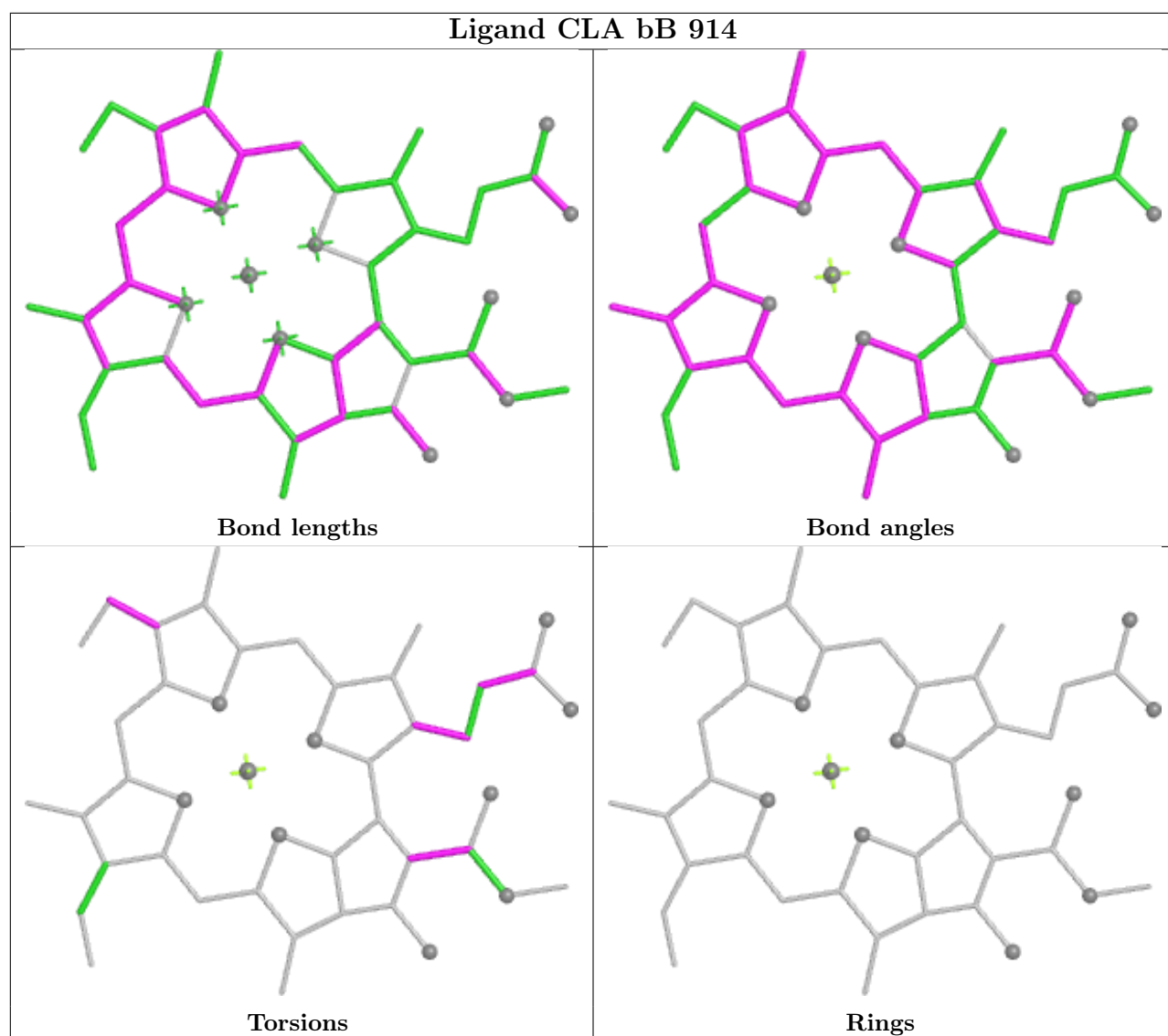


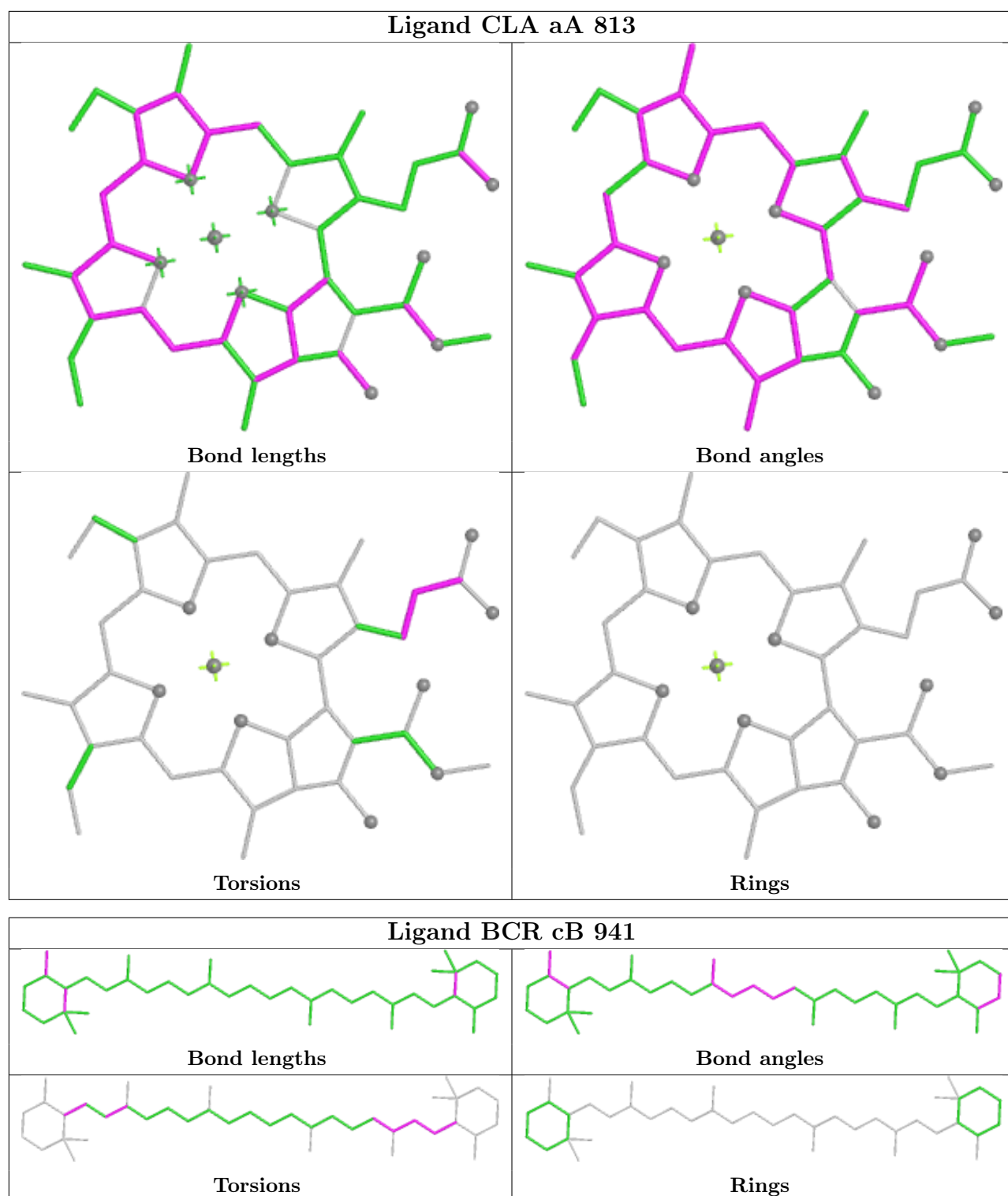


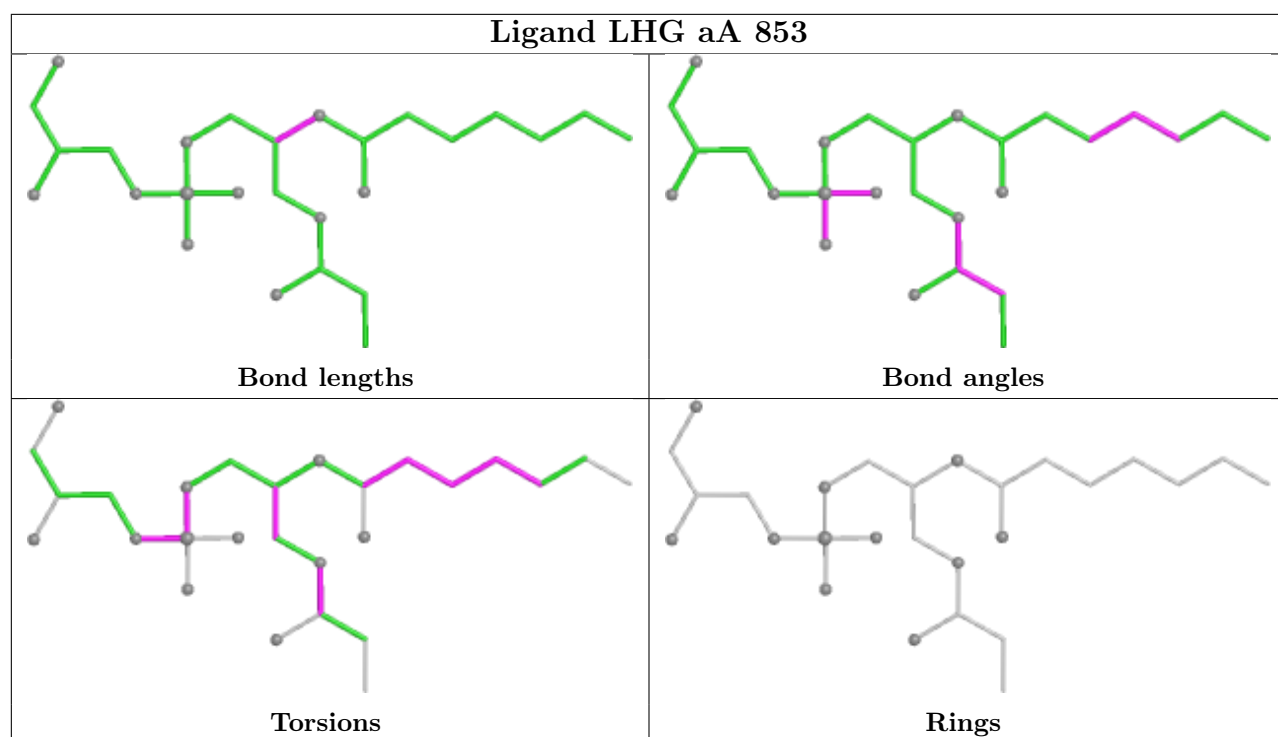


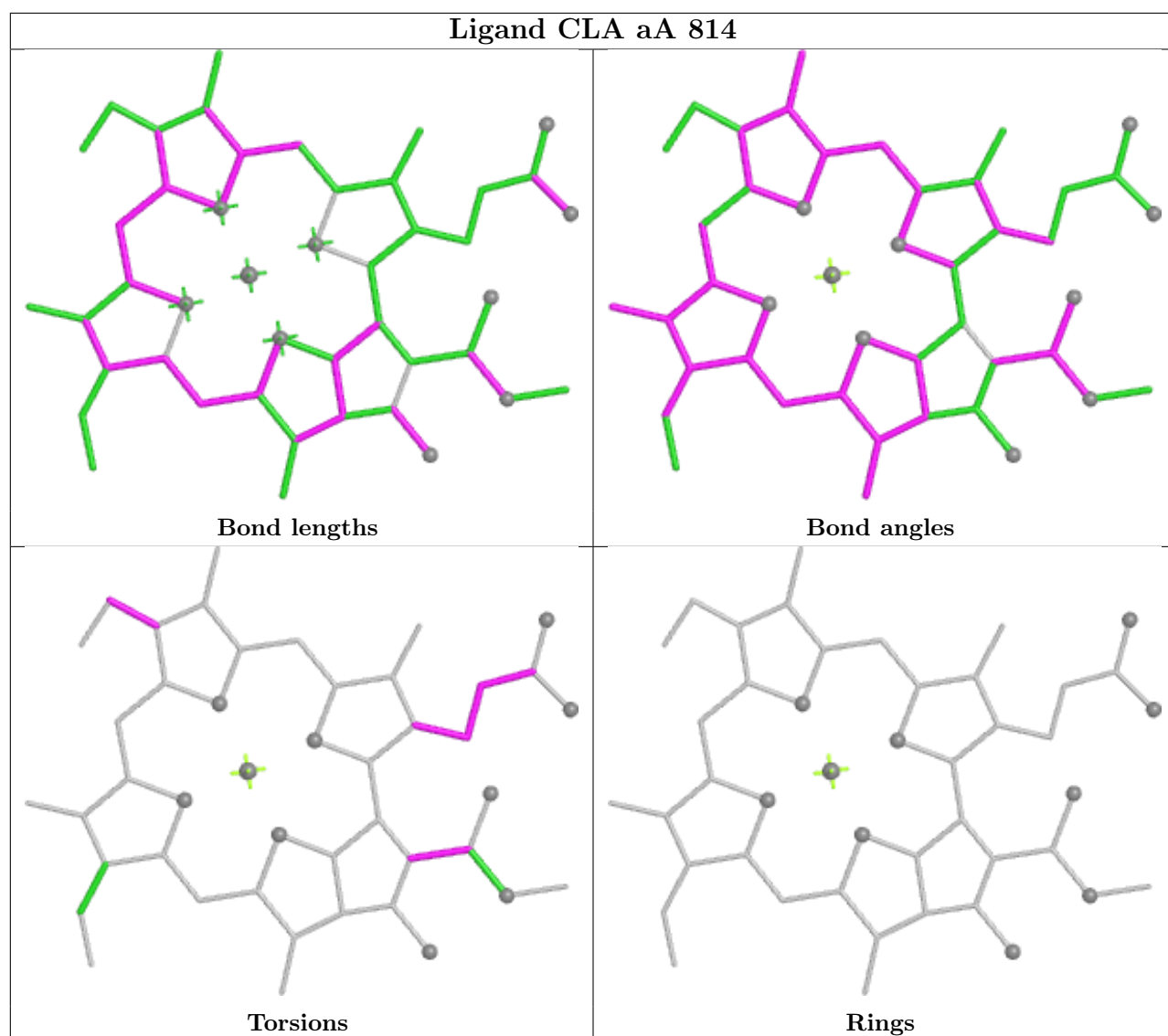


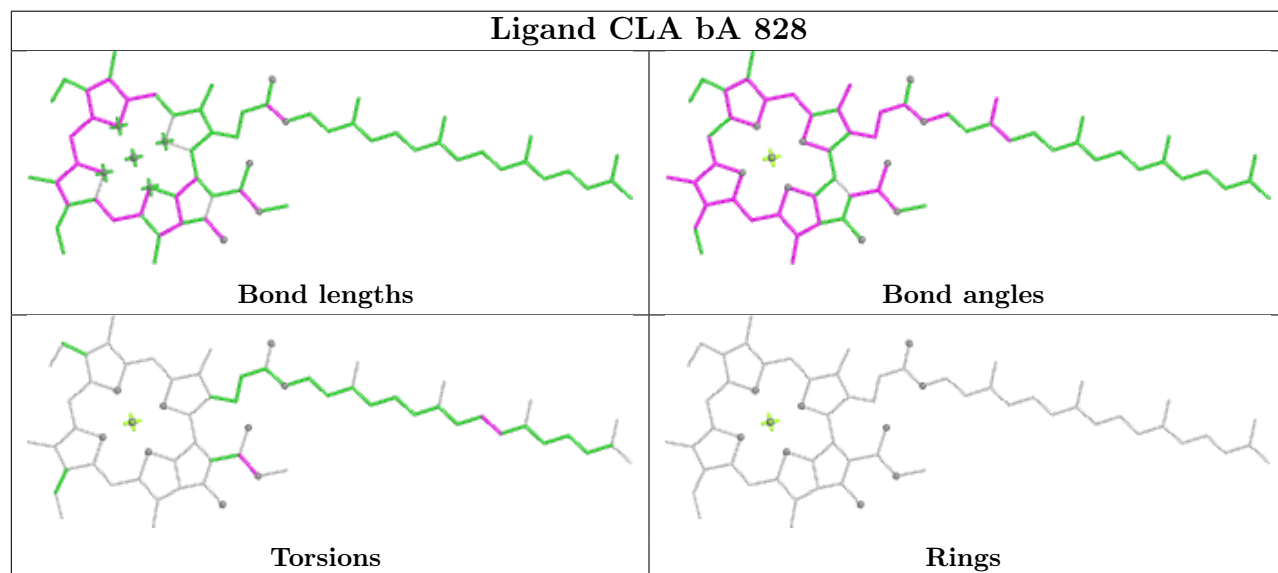
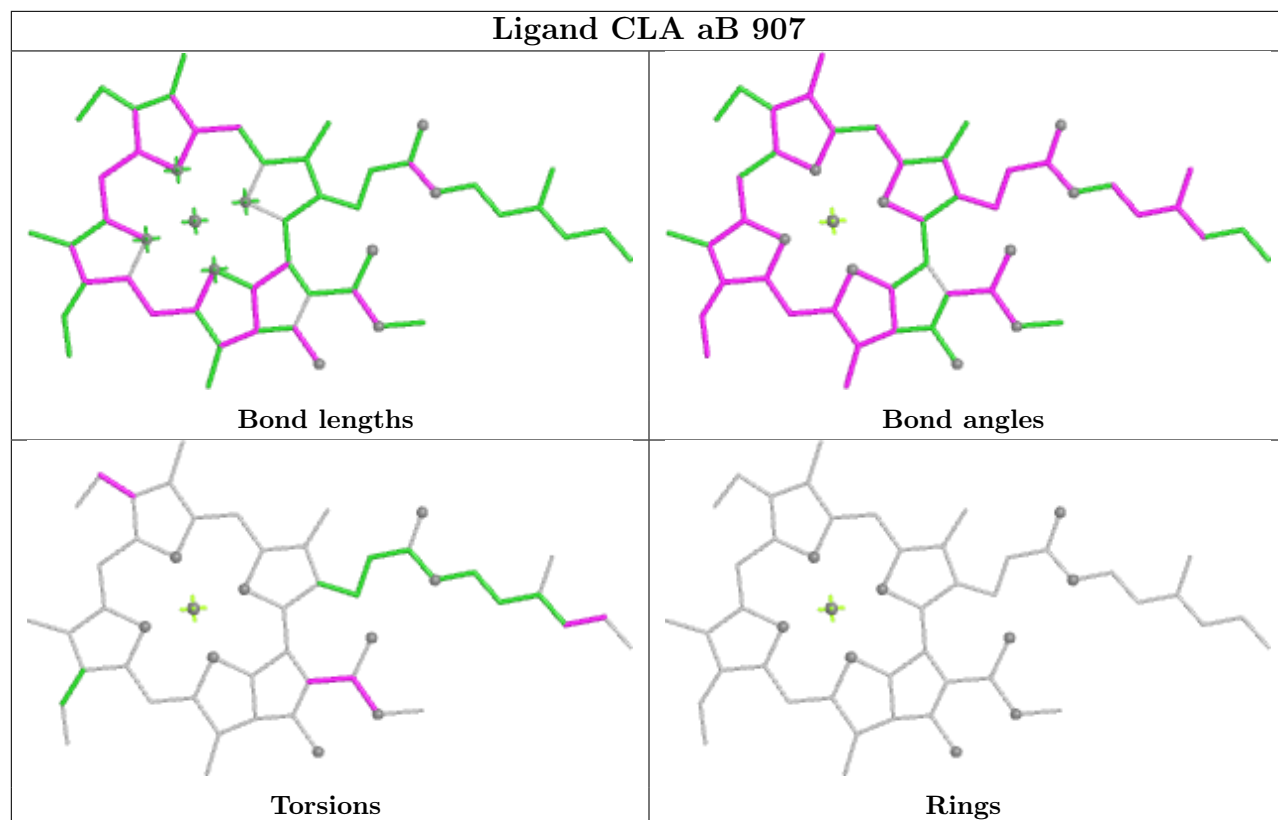


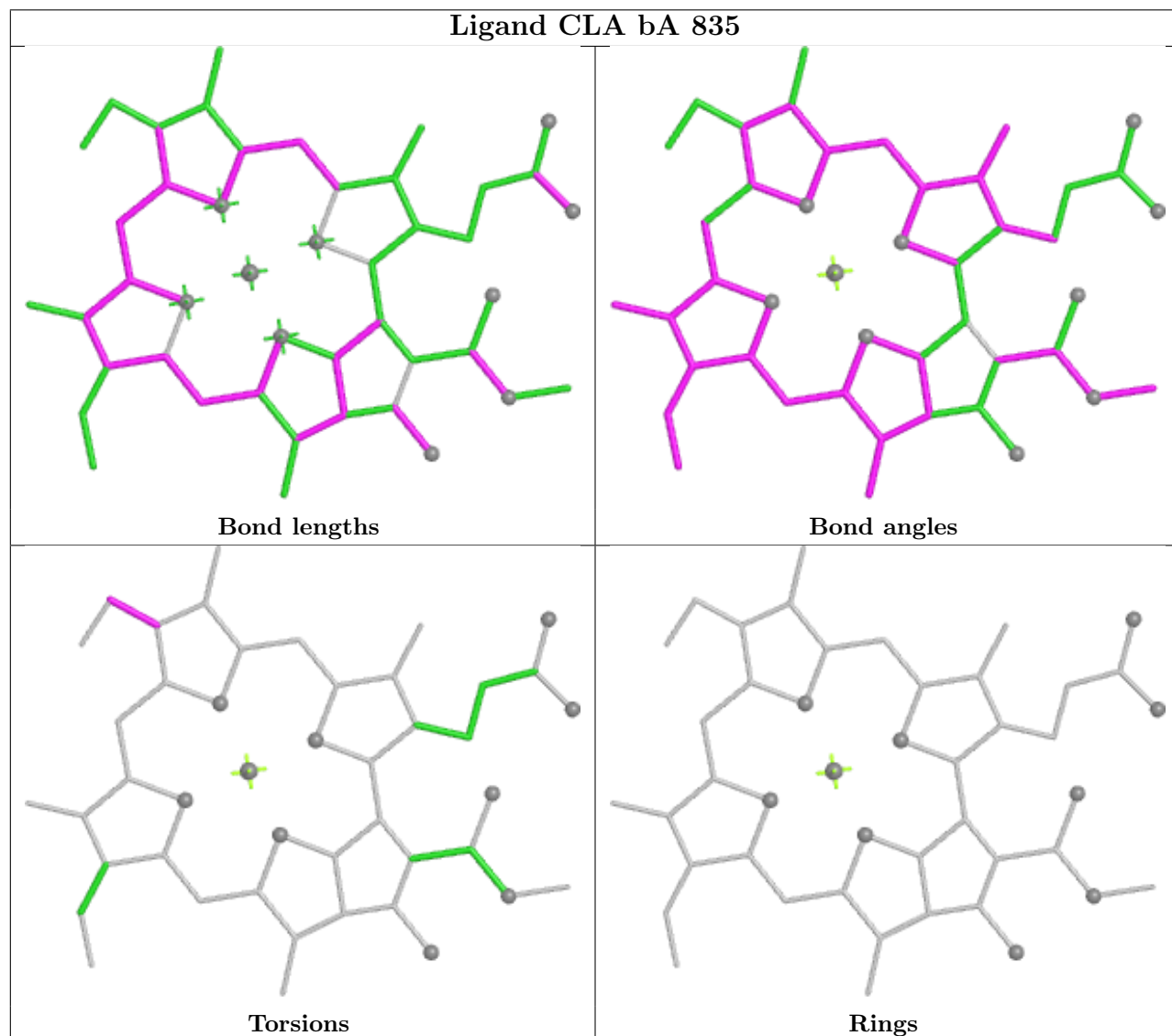
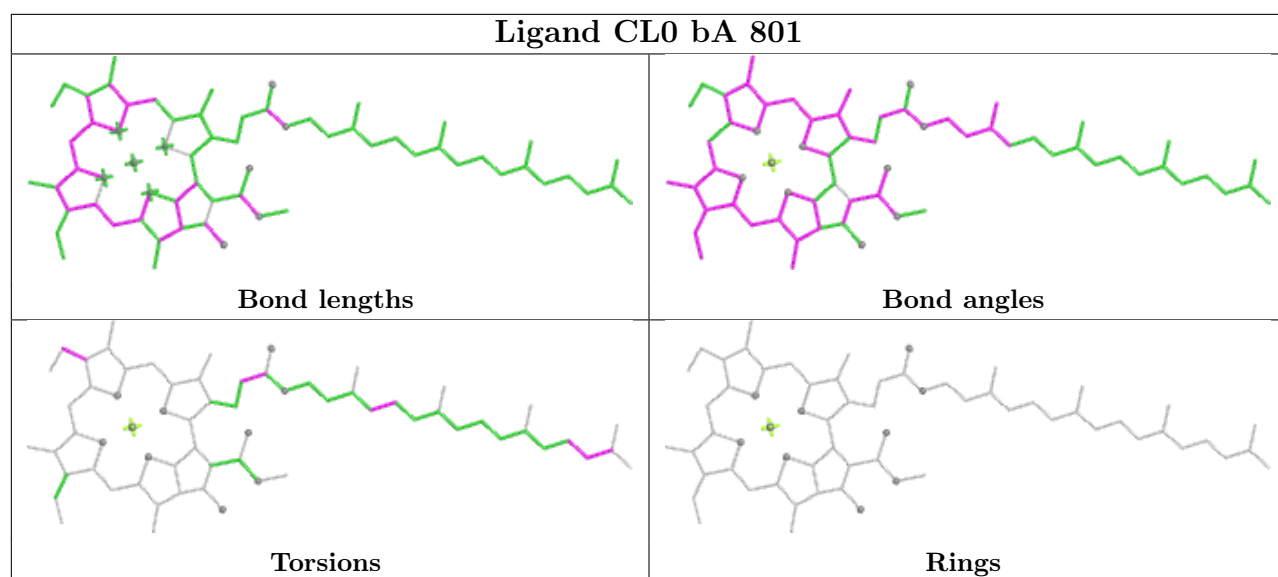


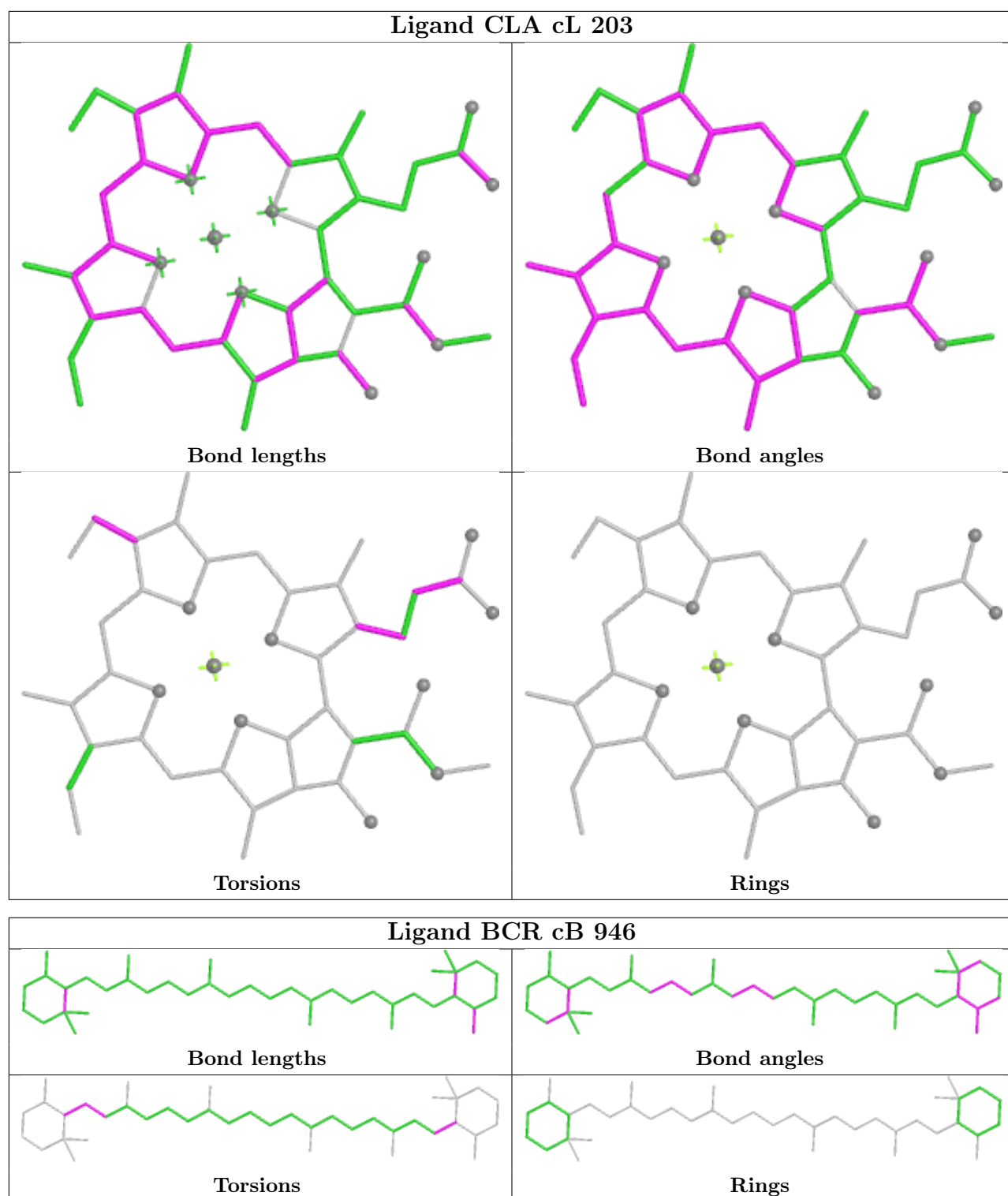


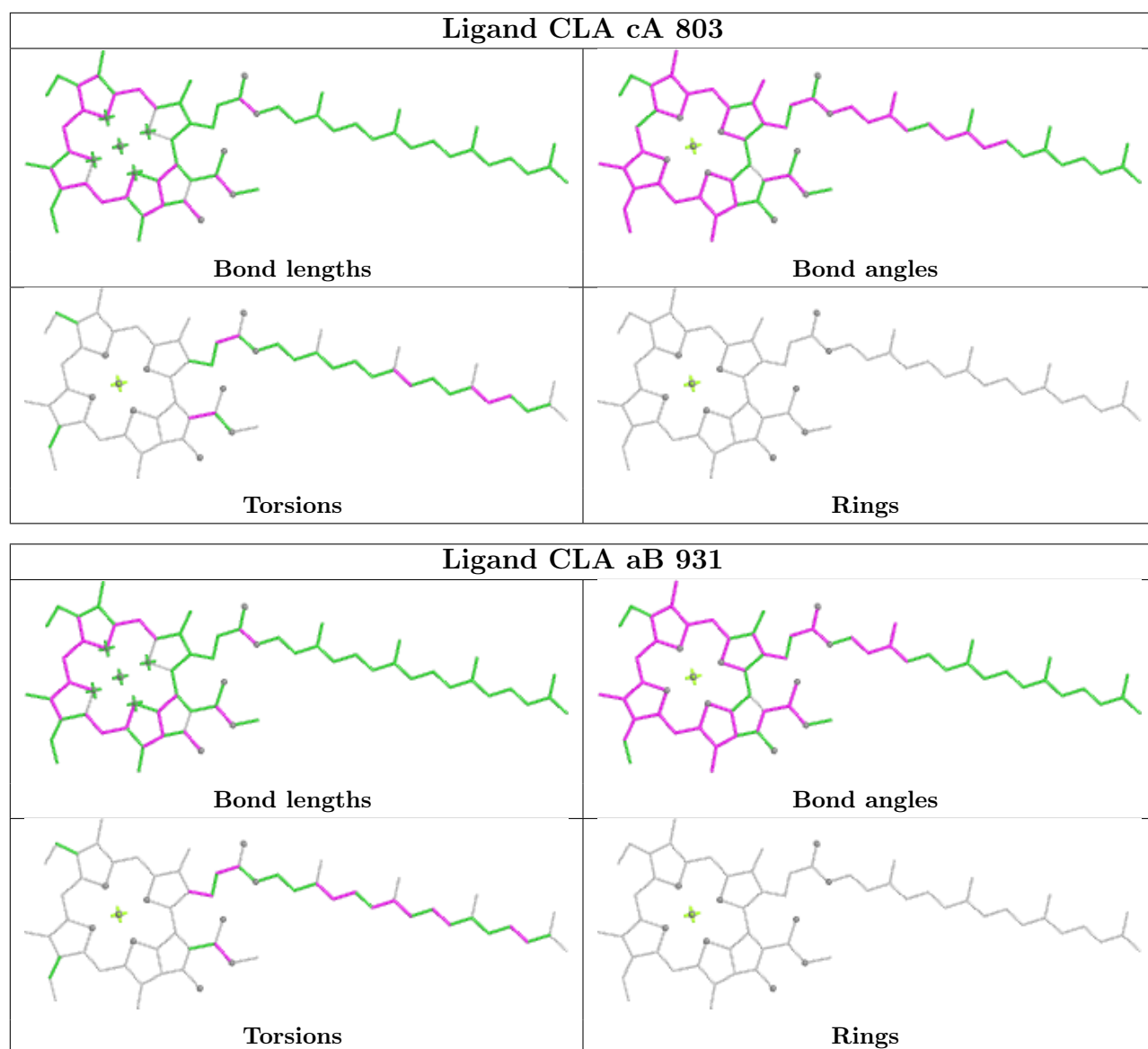


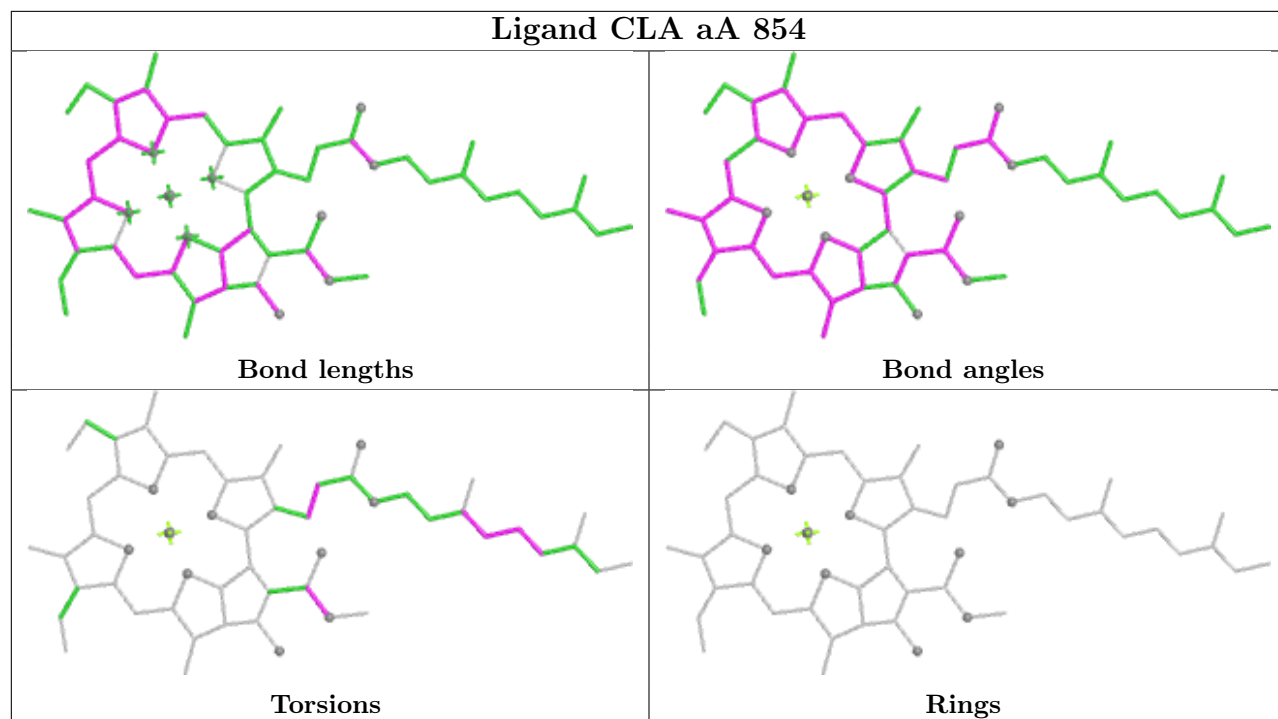


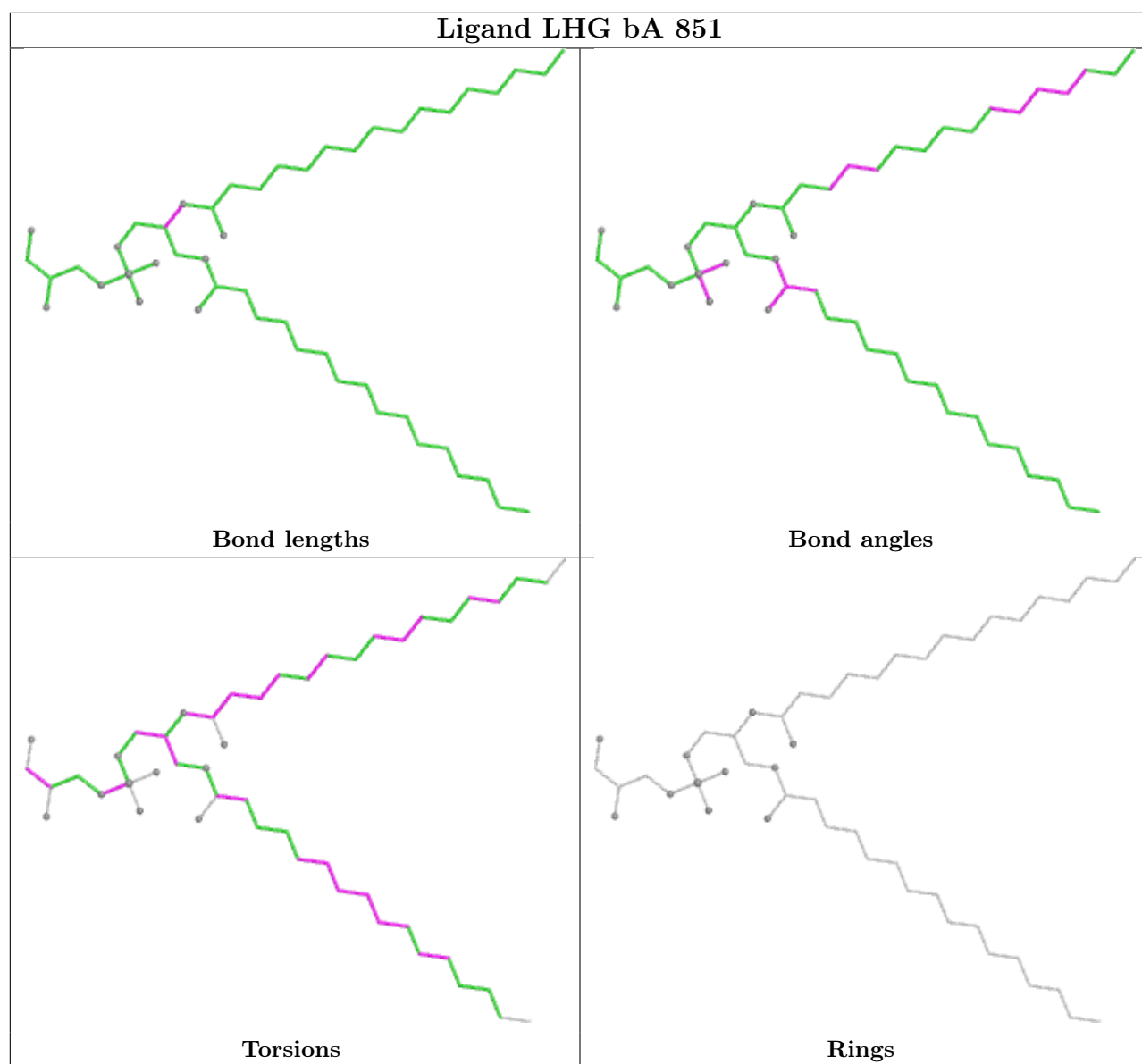


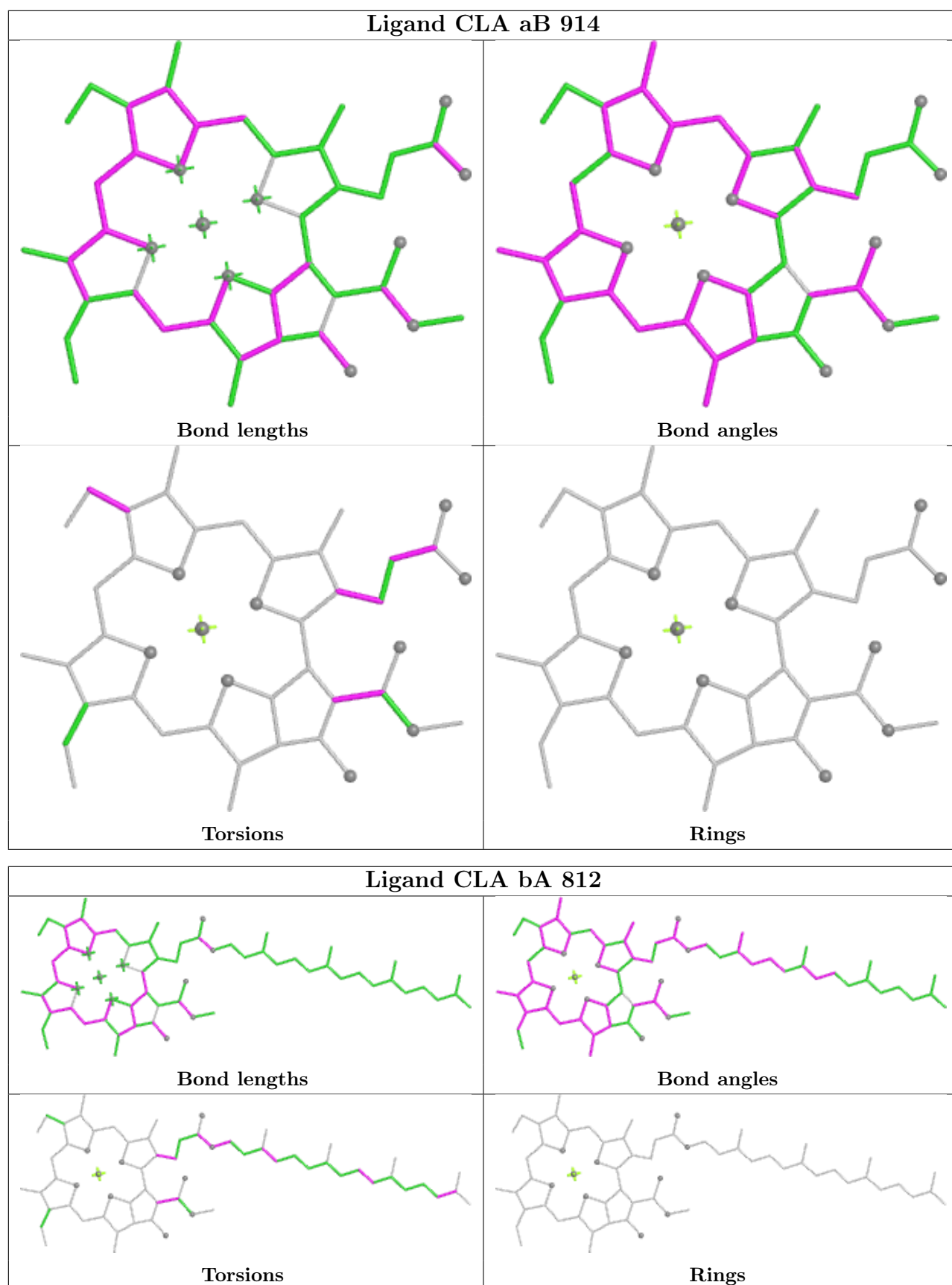


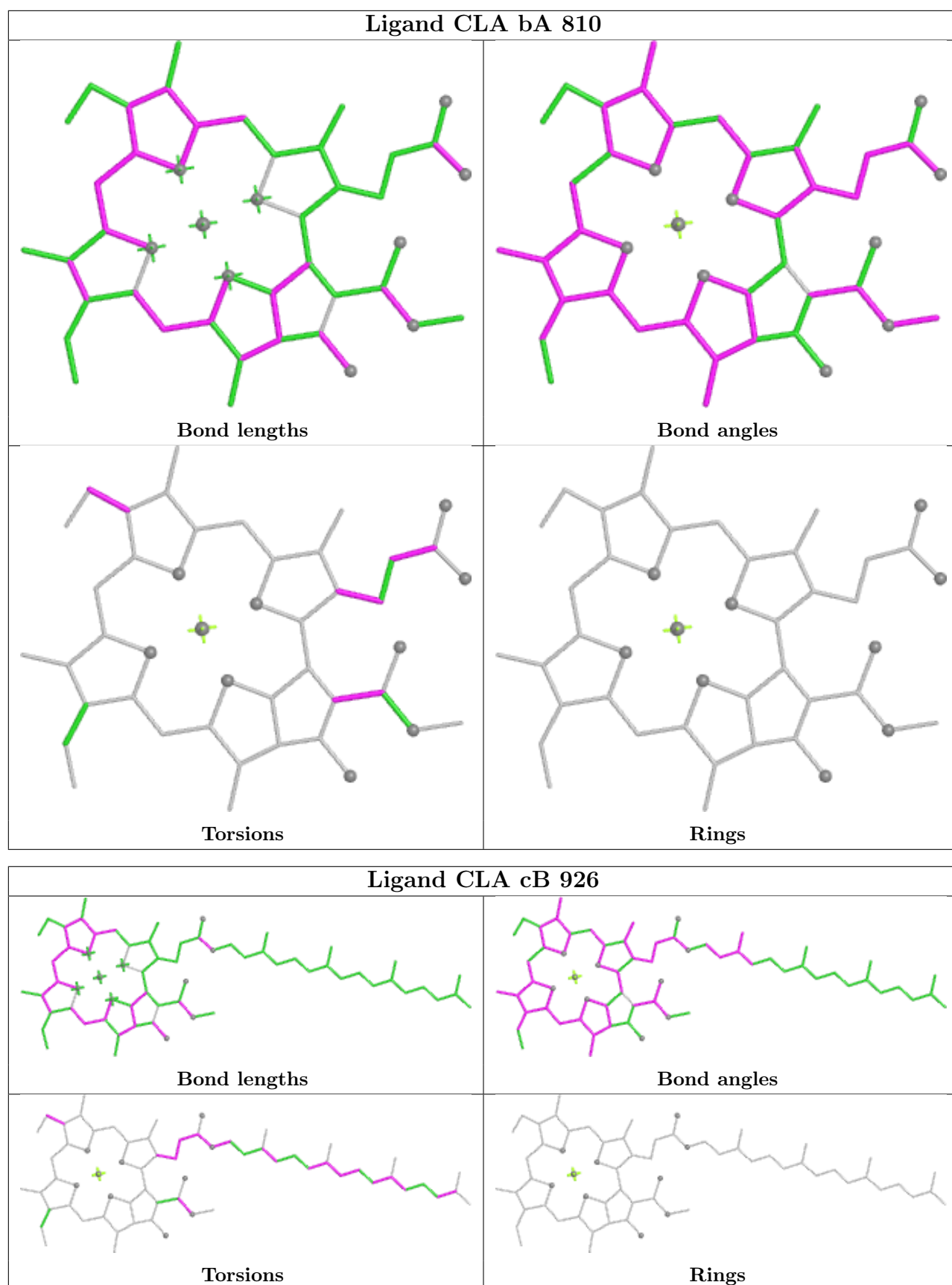


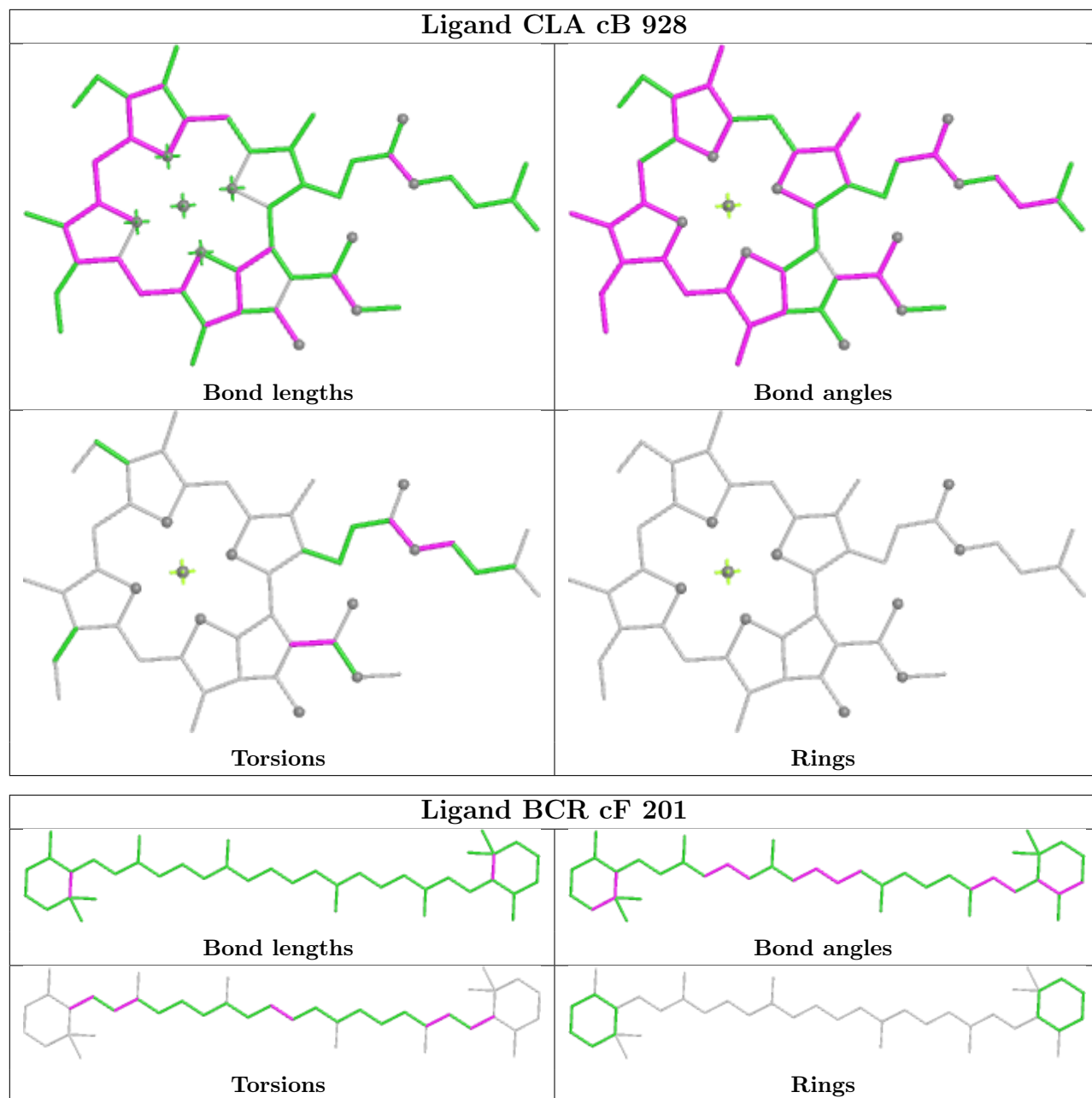


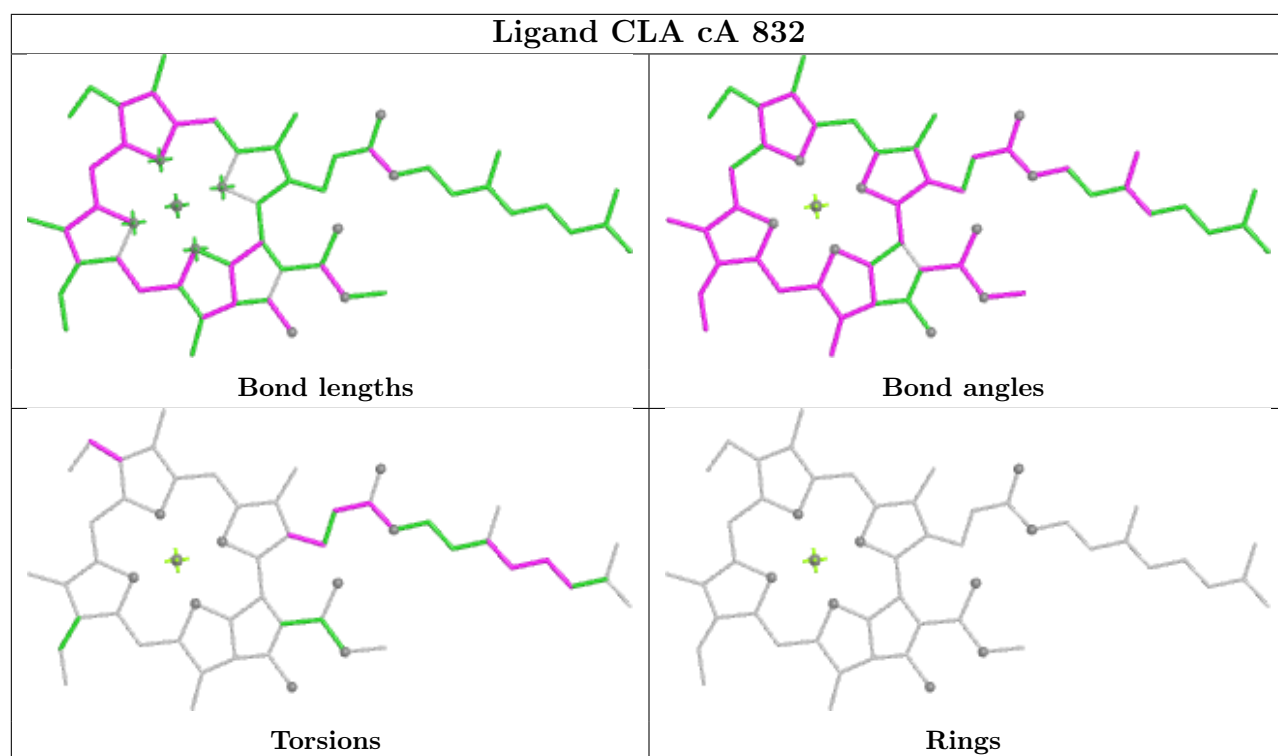


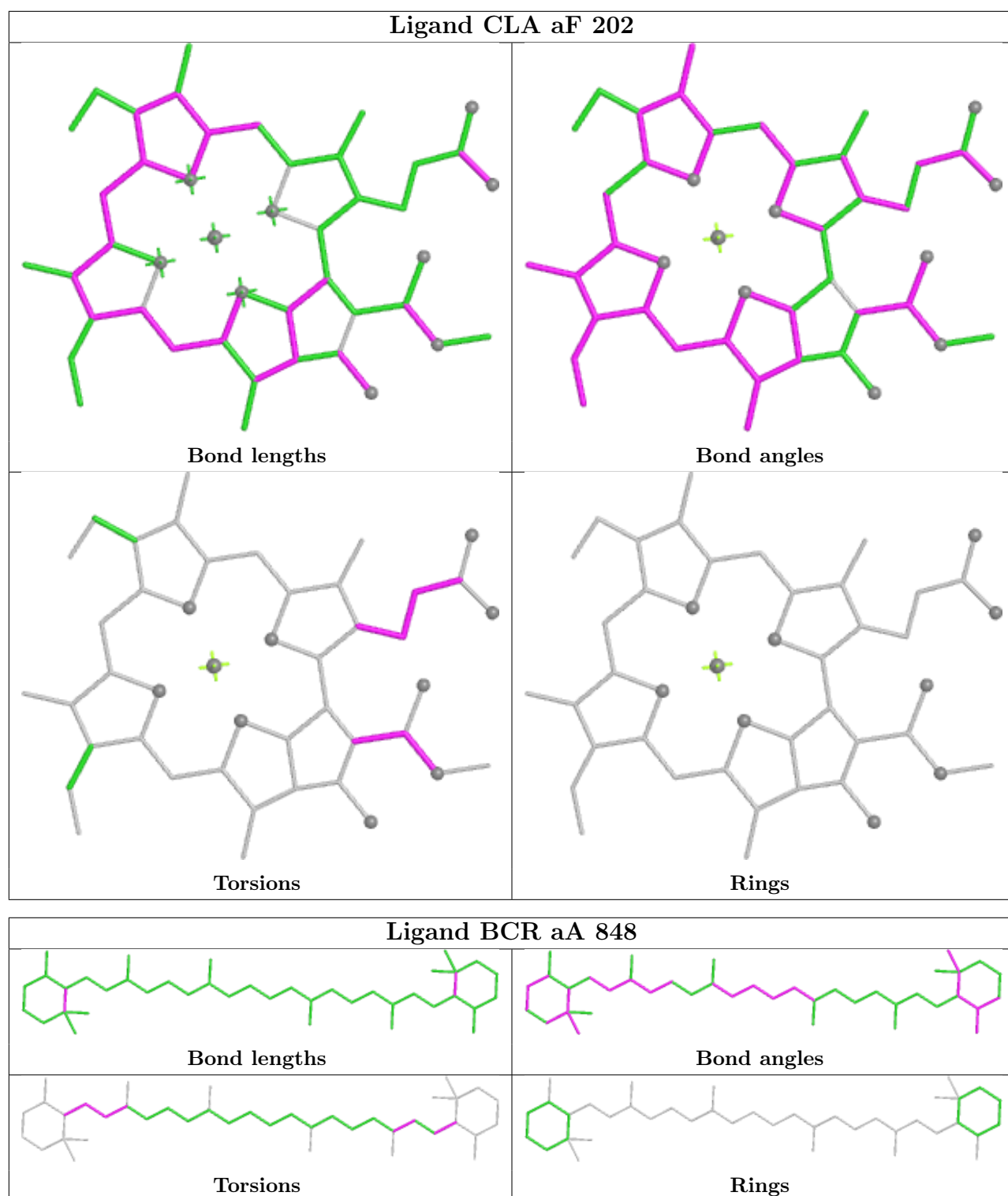


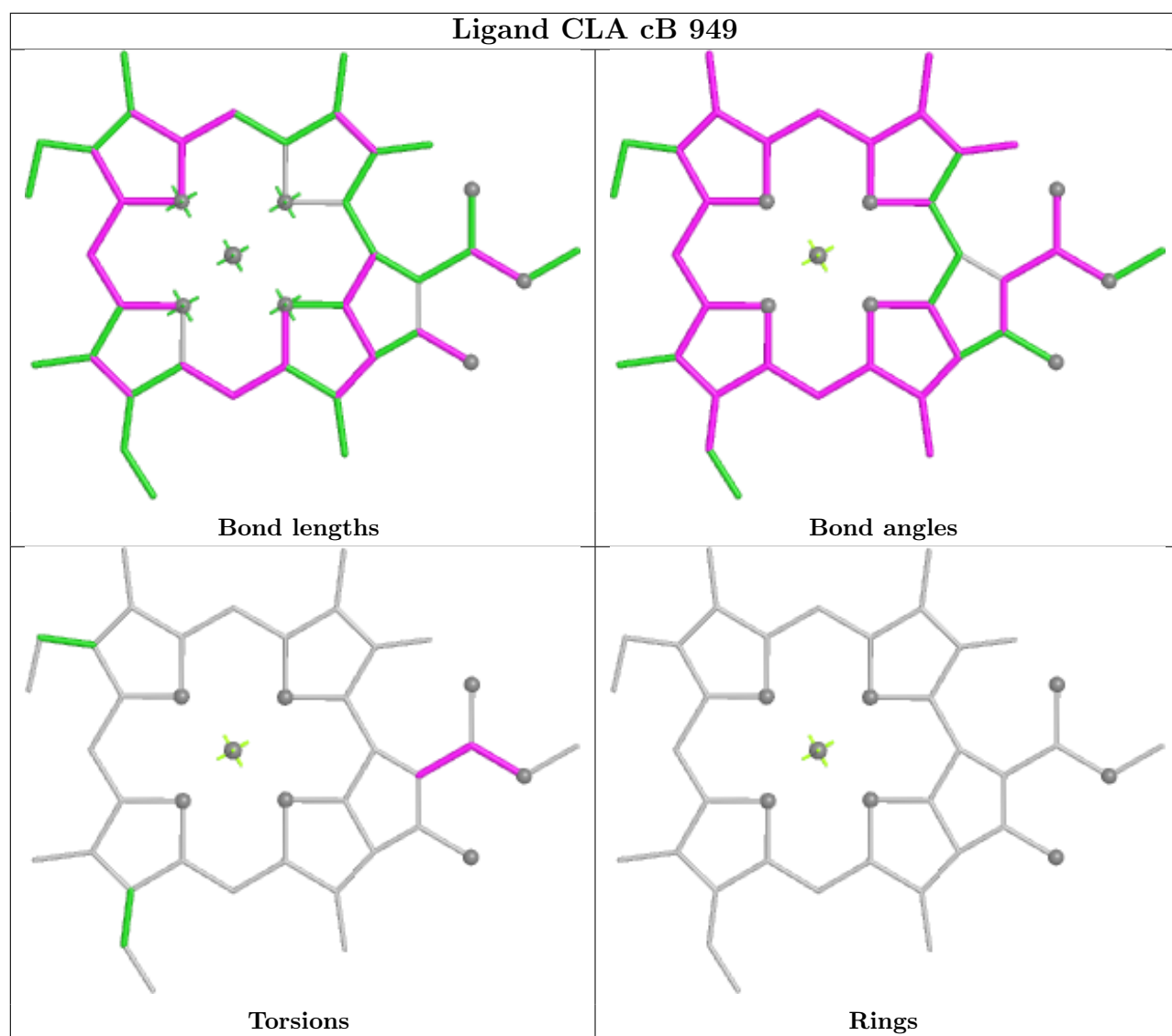


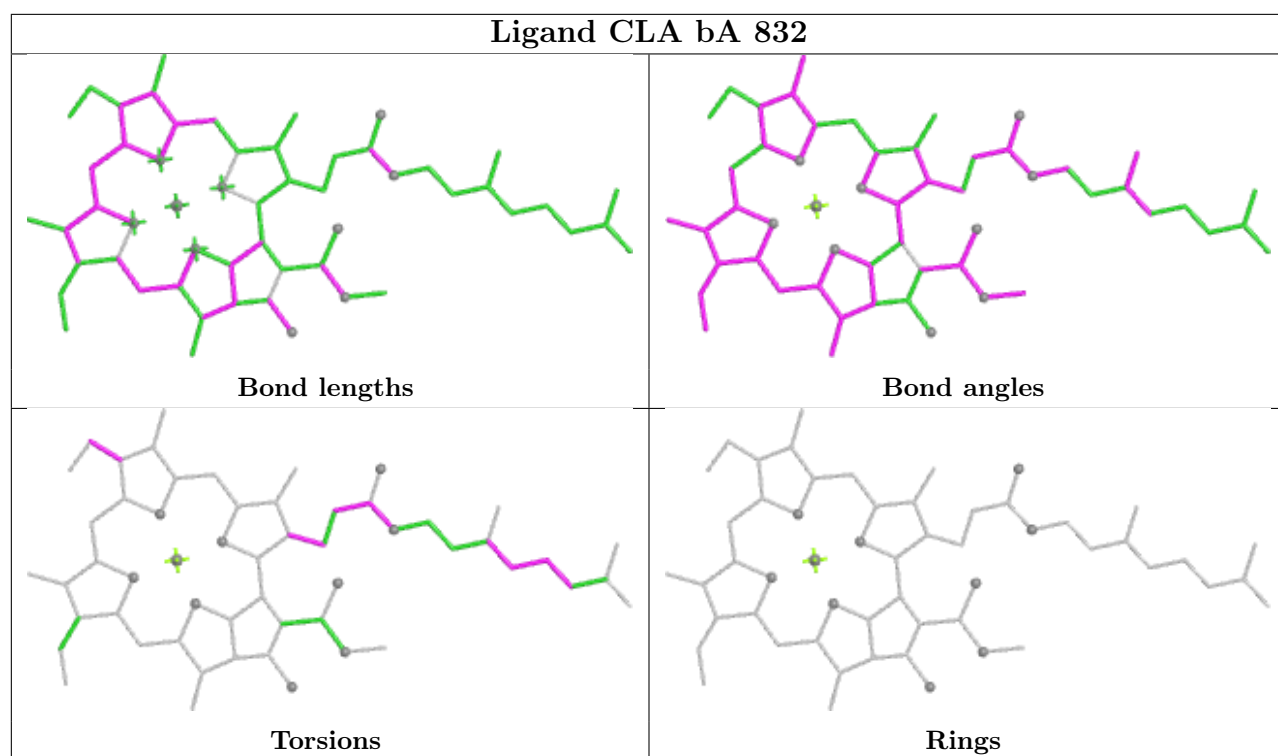


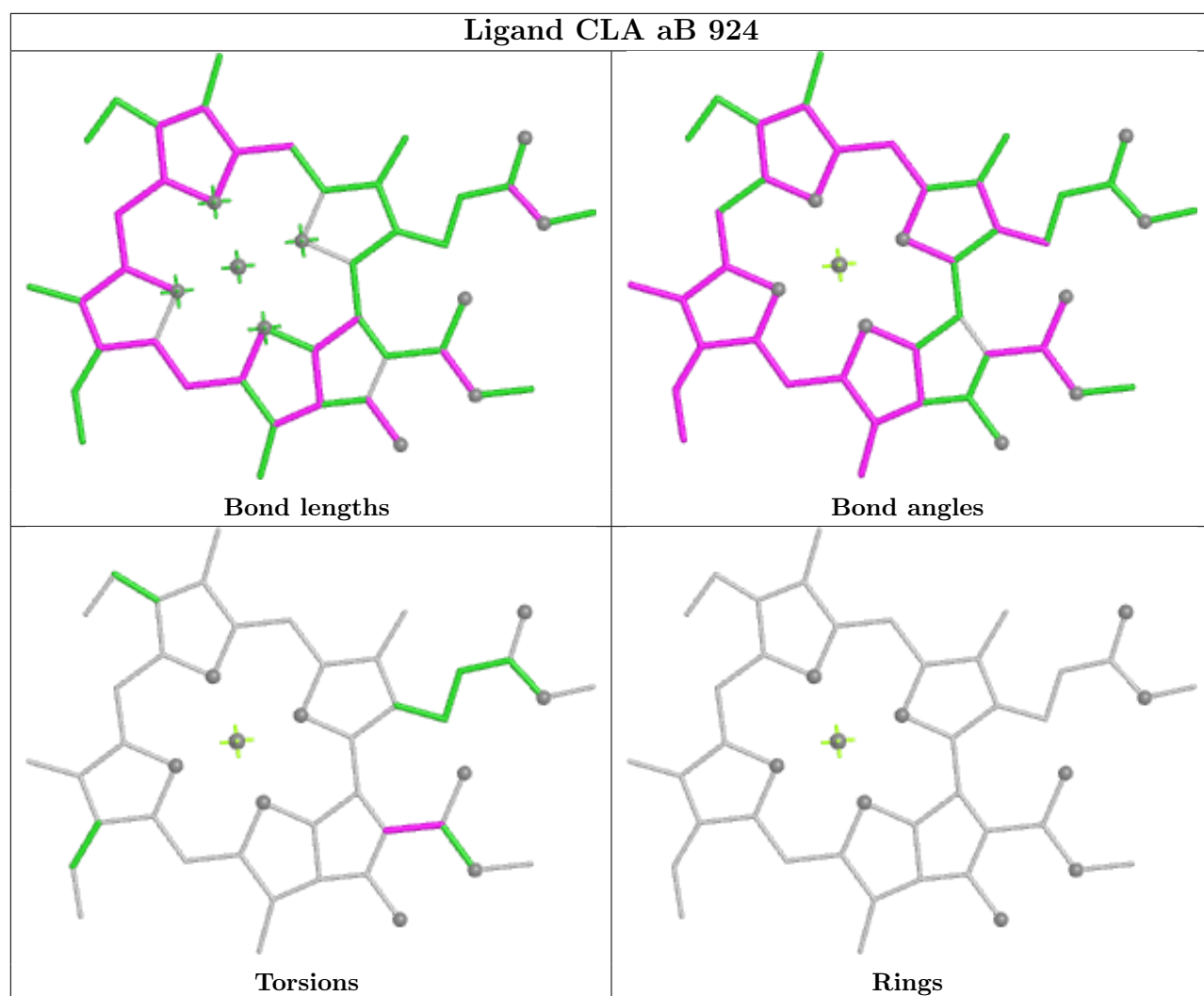


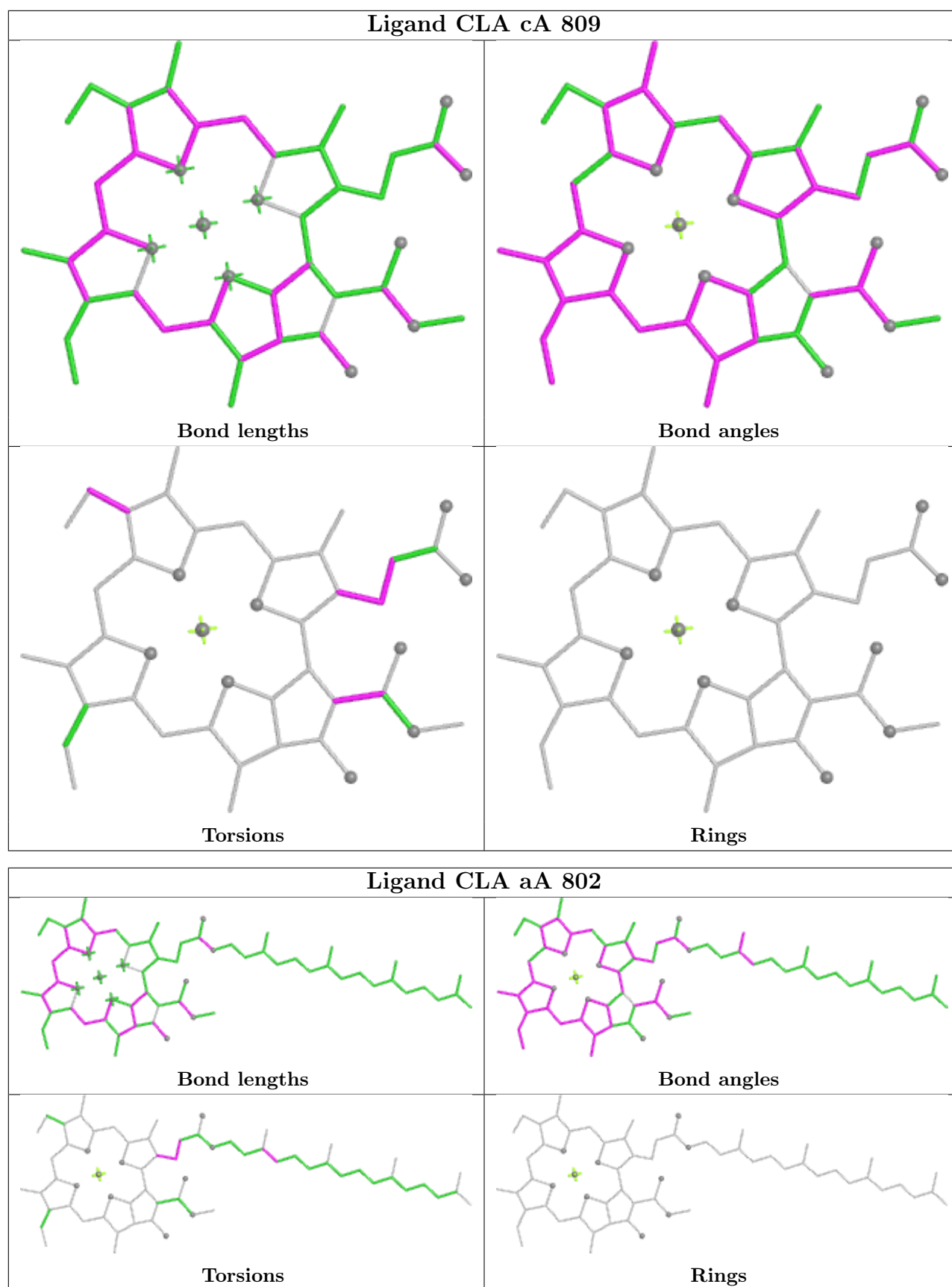


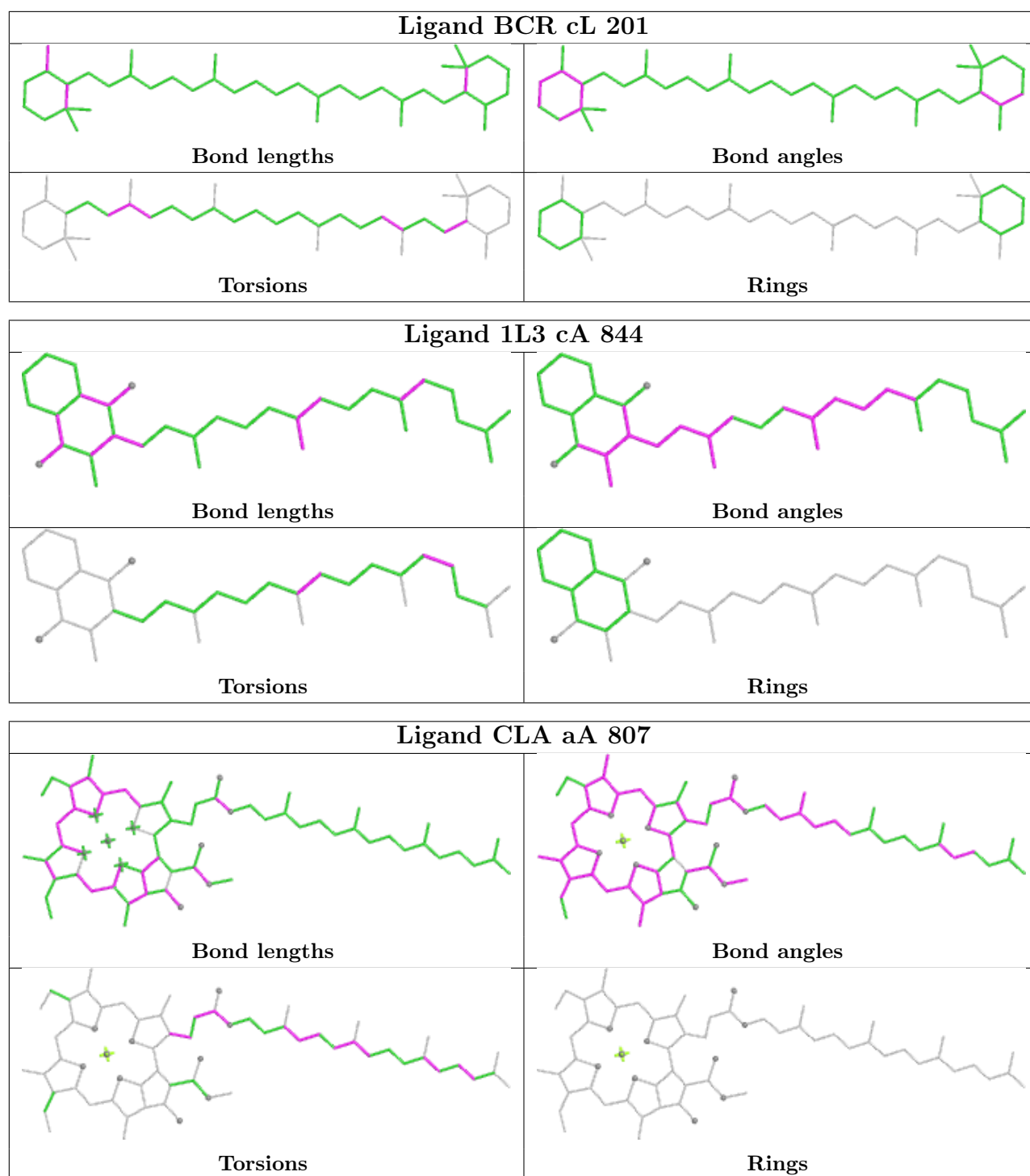


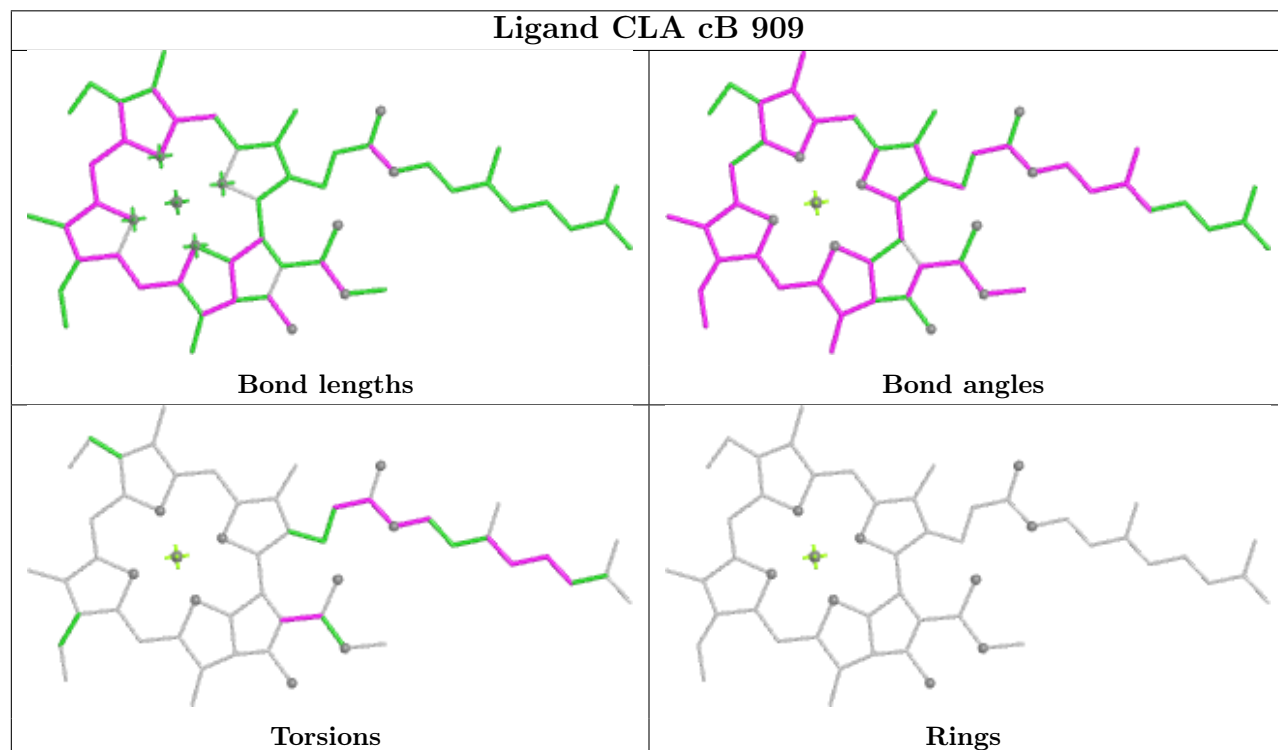
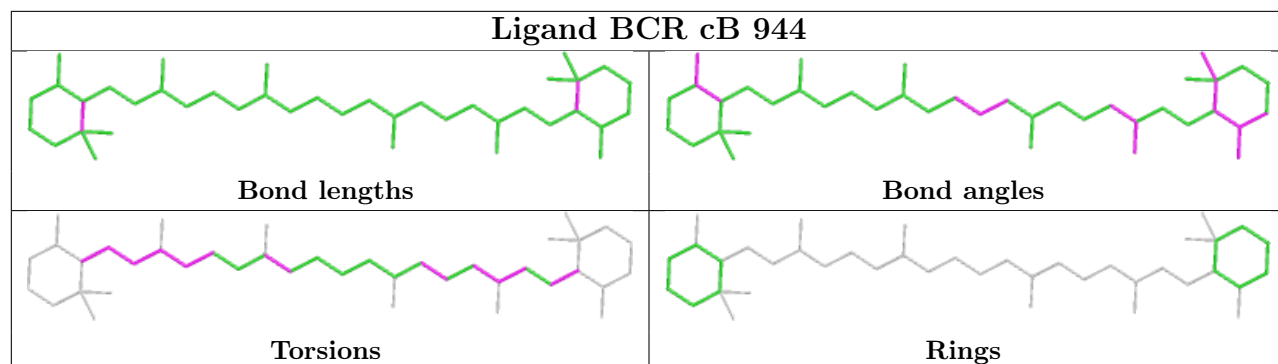




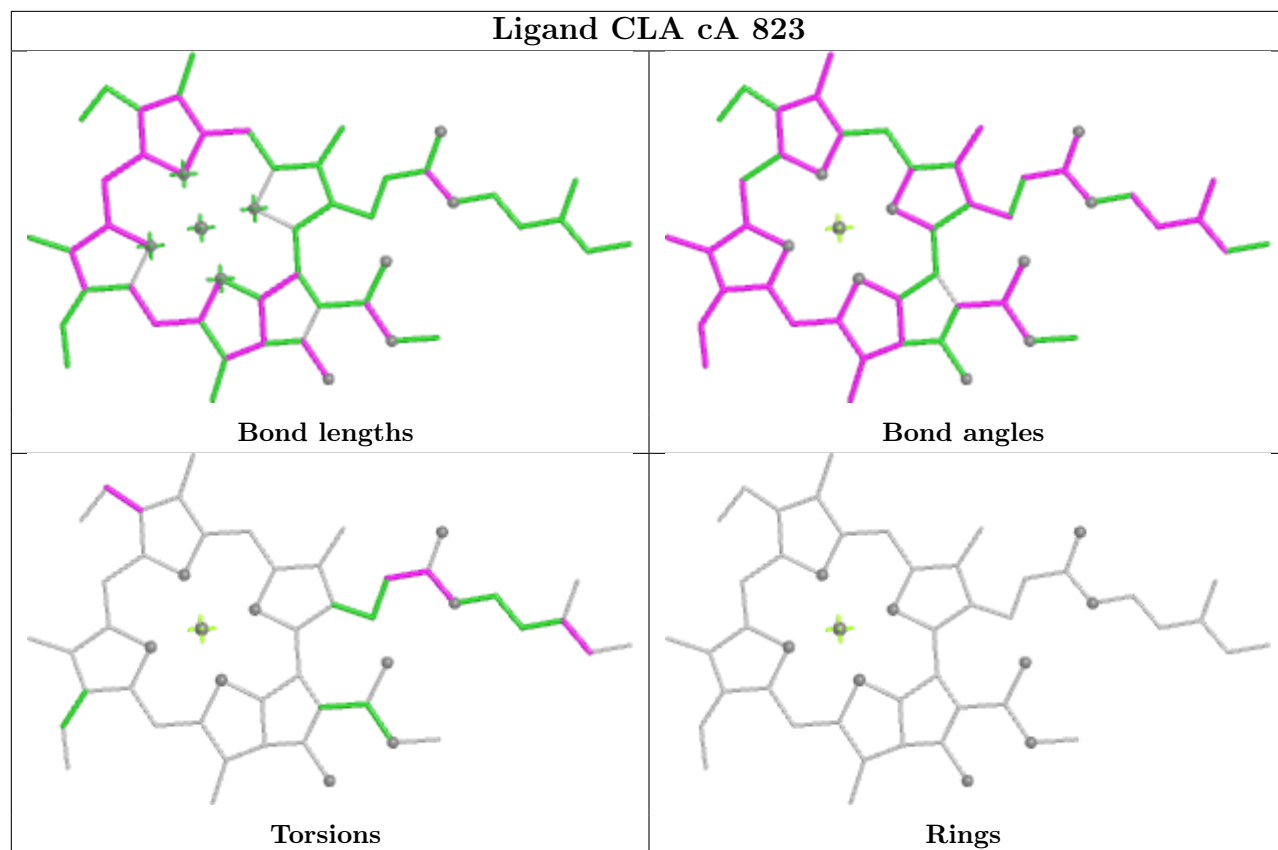




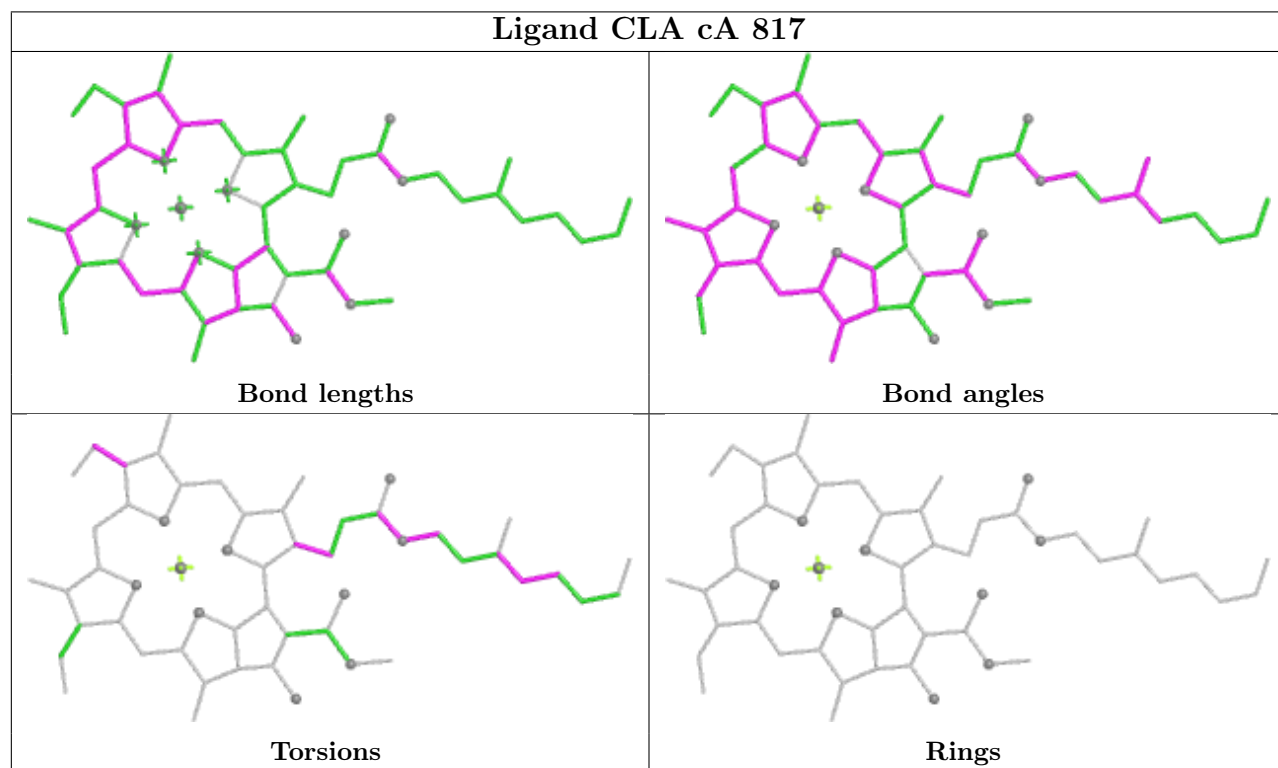


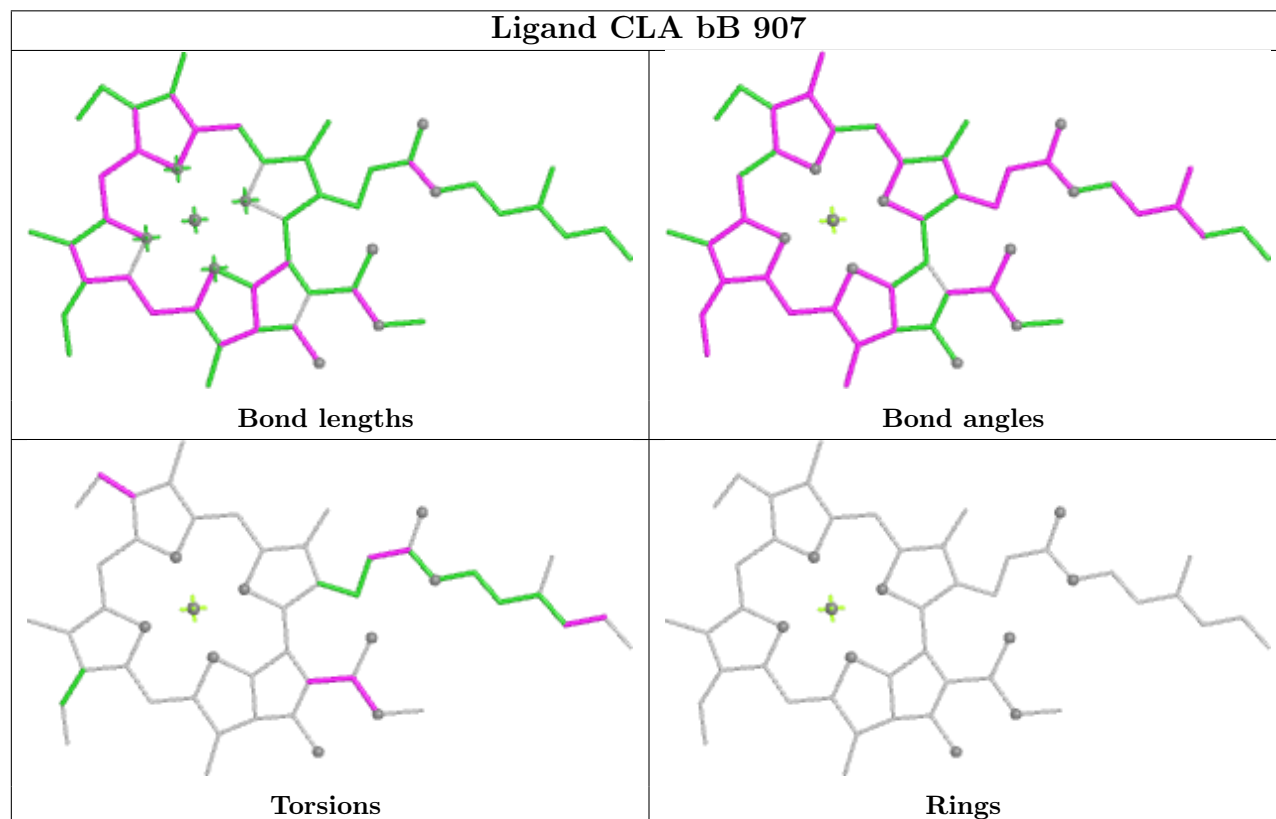
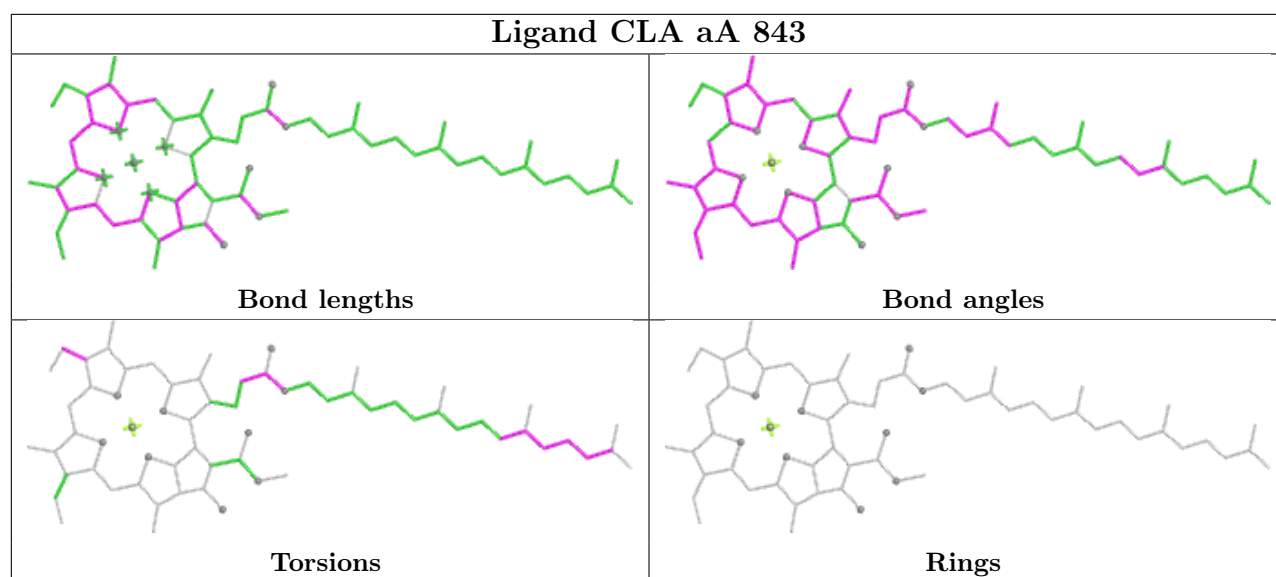


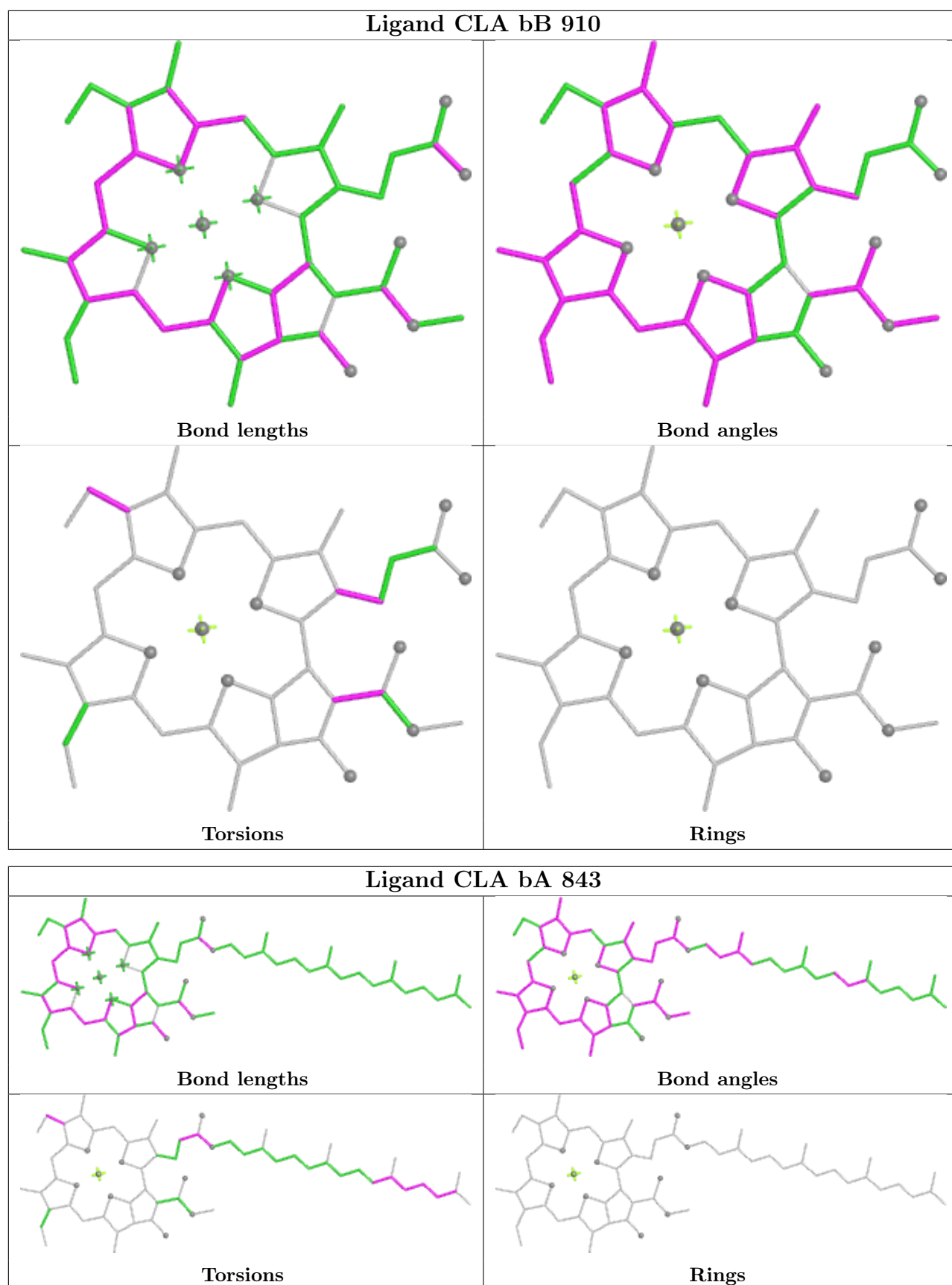
Ligand CLA cA 823

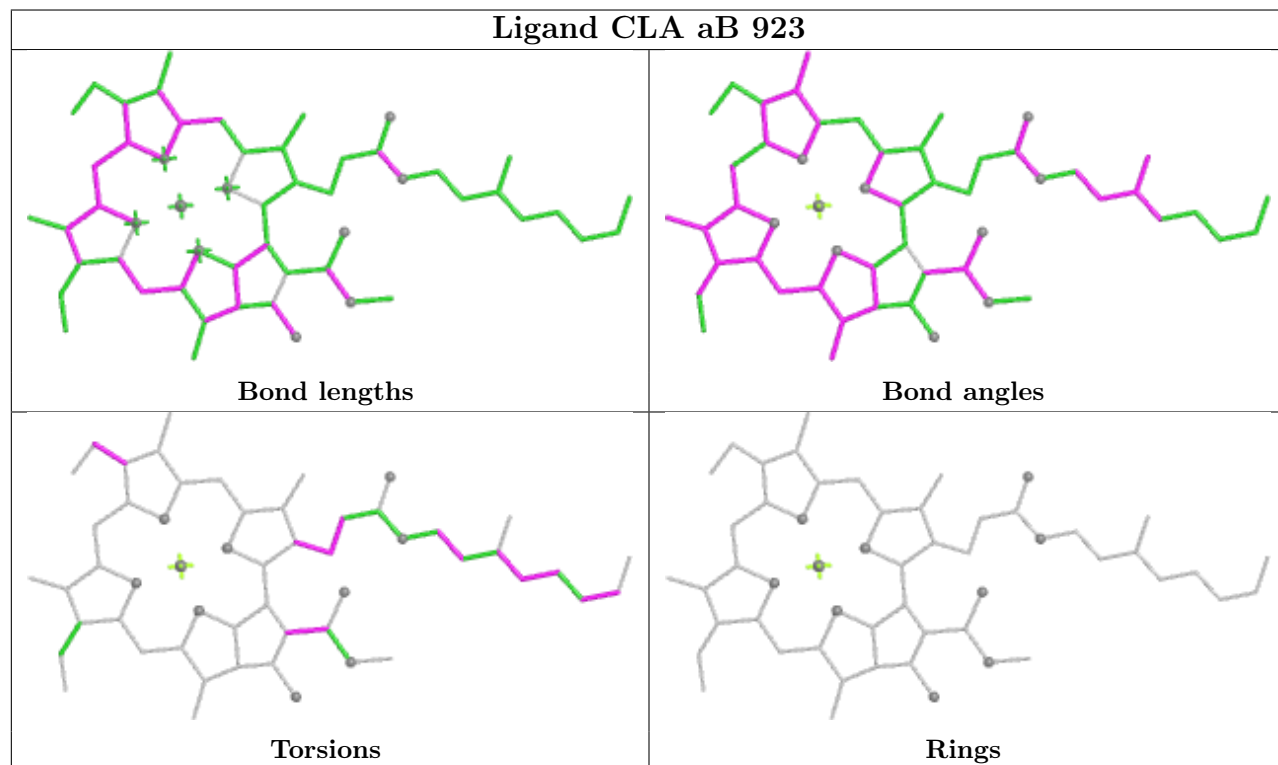
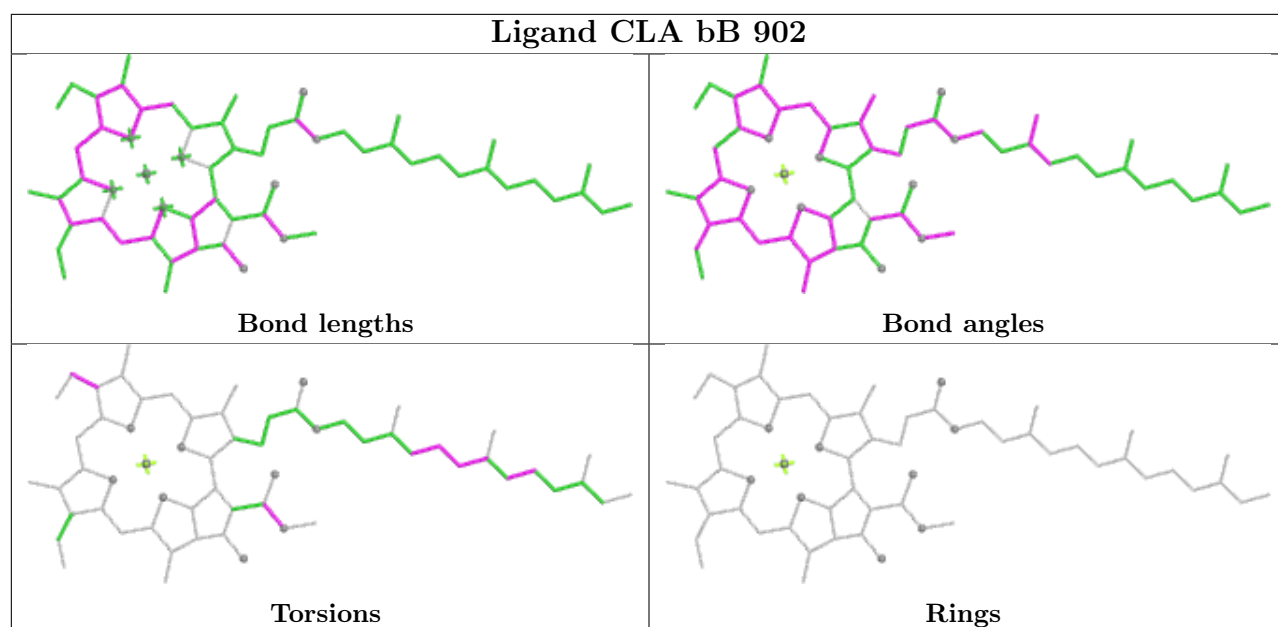


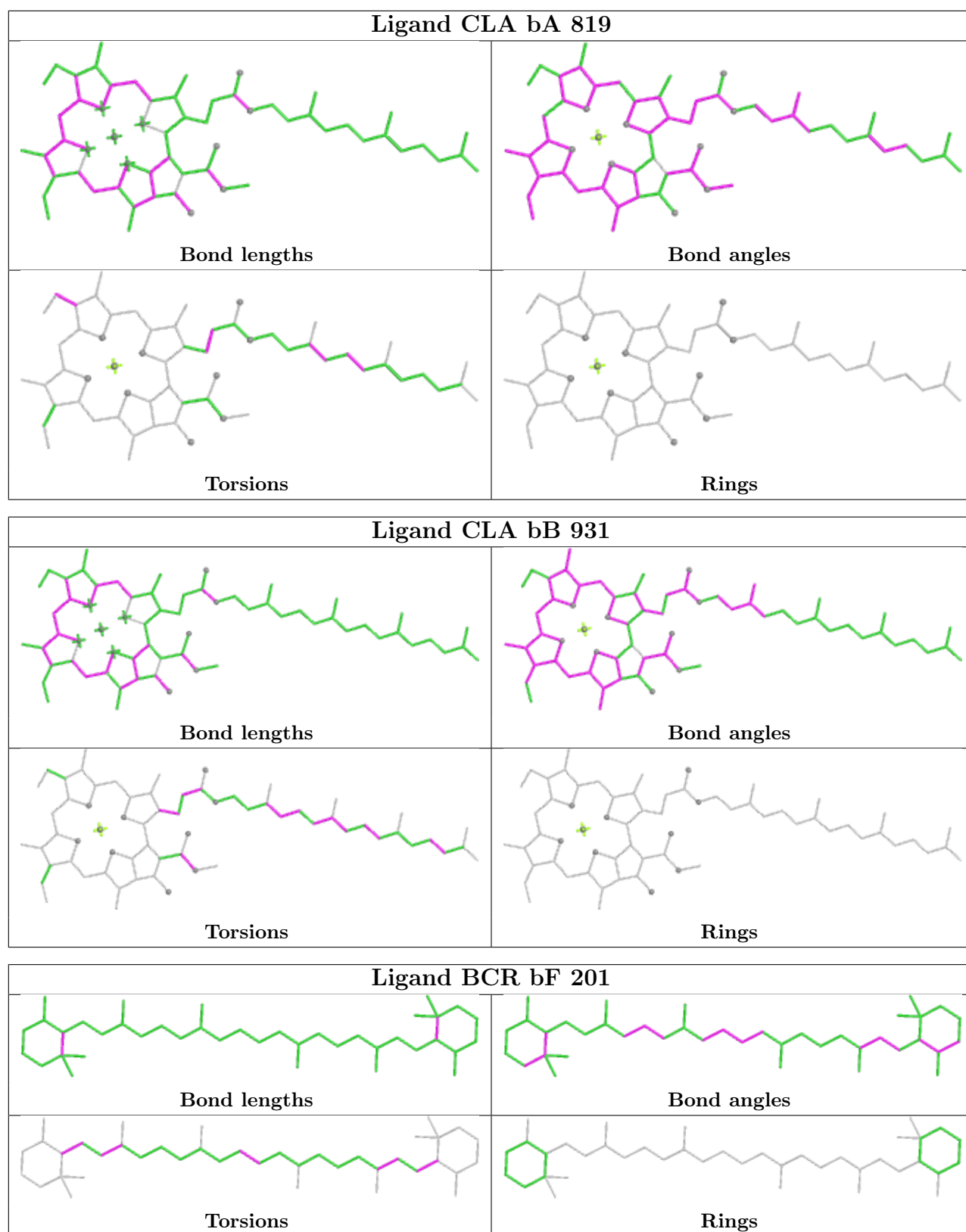
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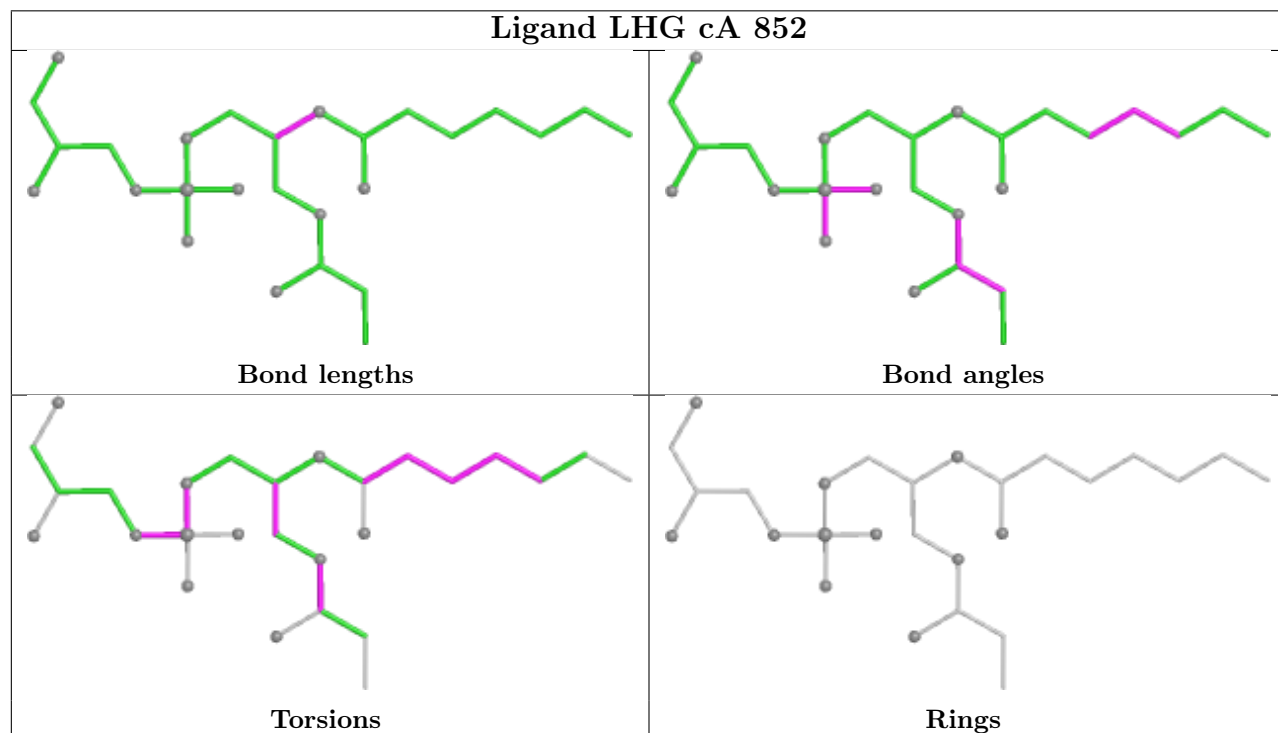
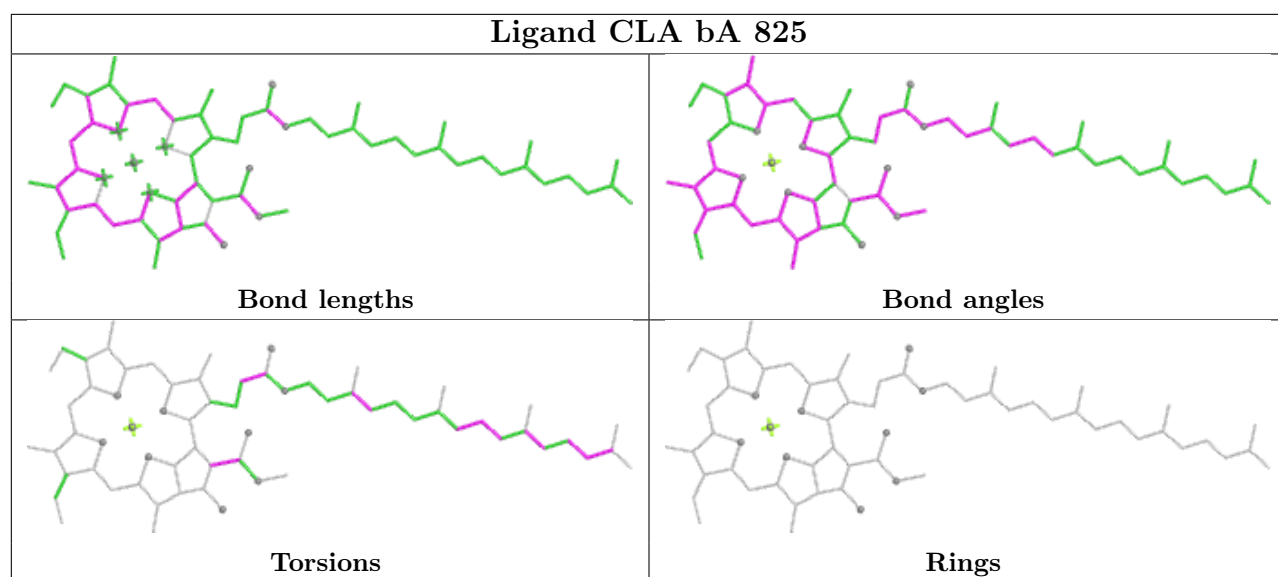


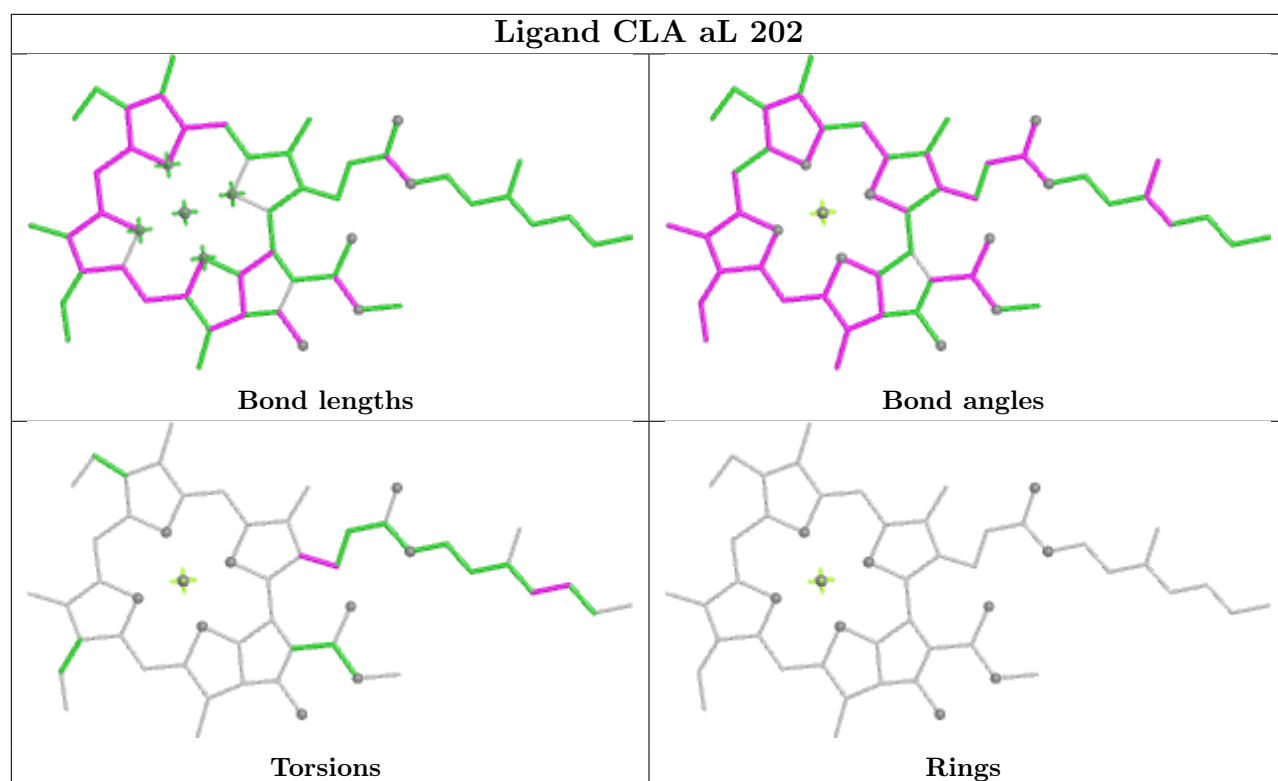


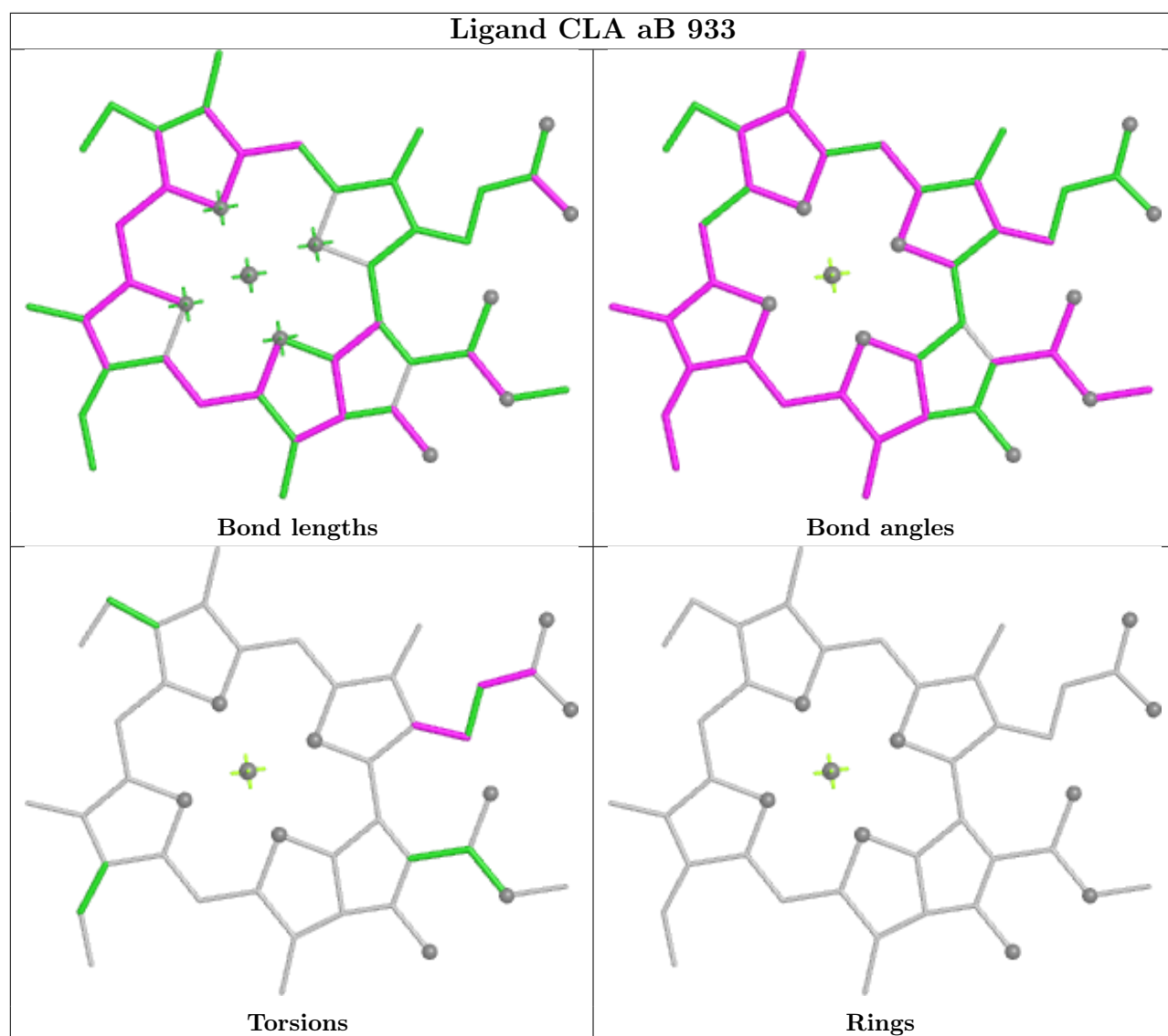


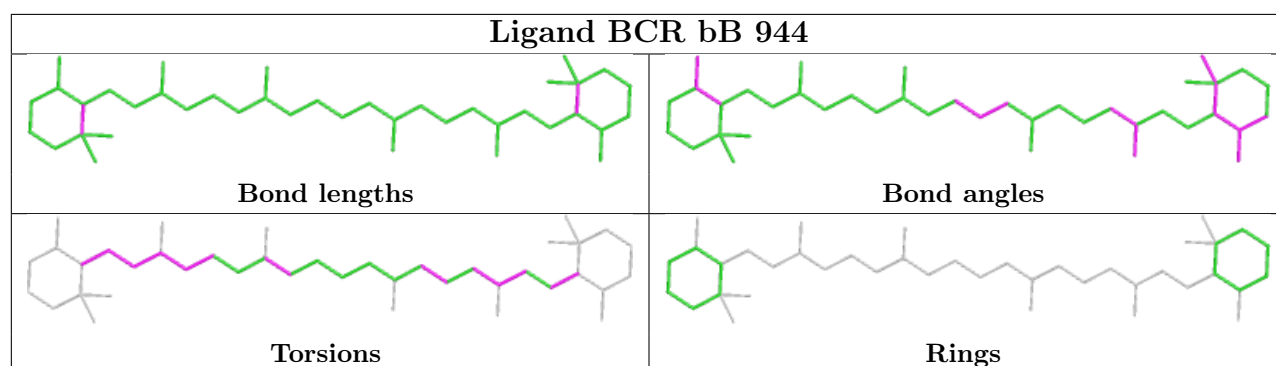
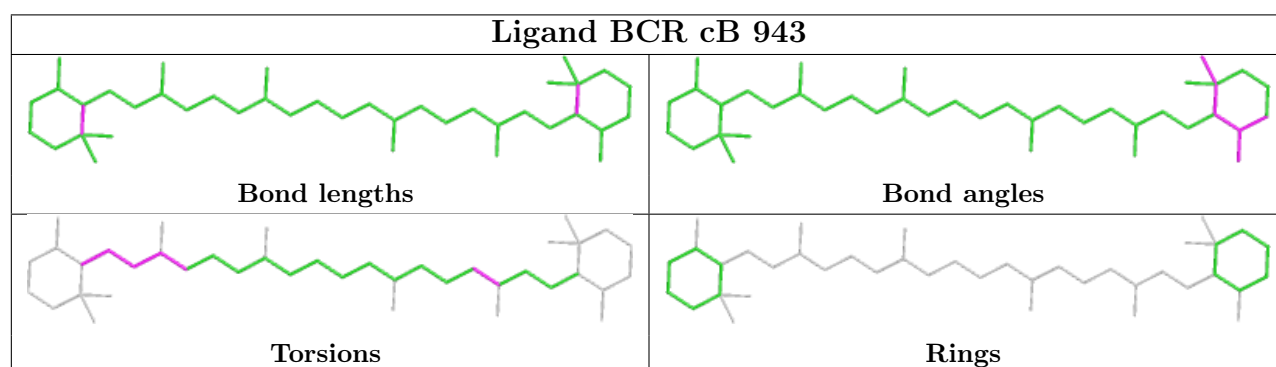
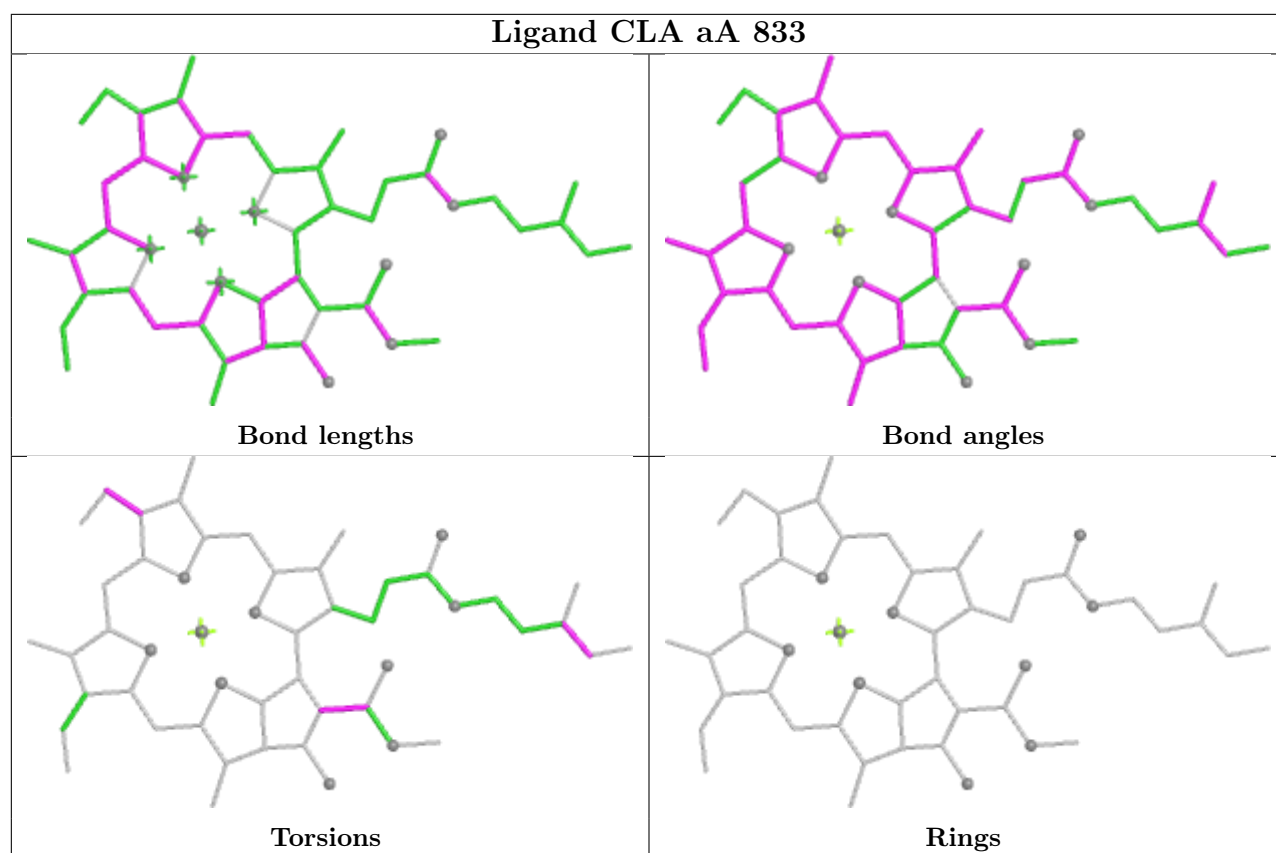


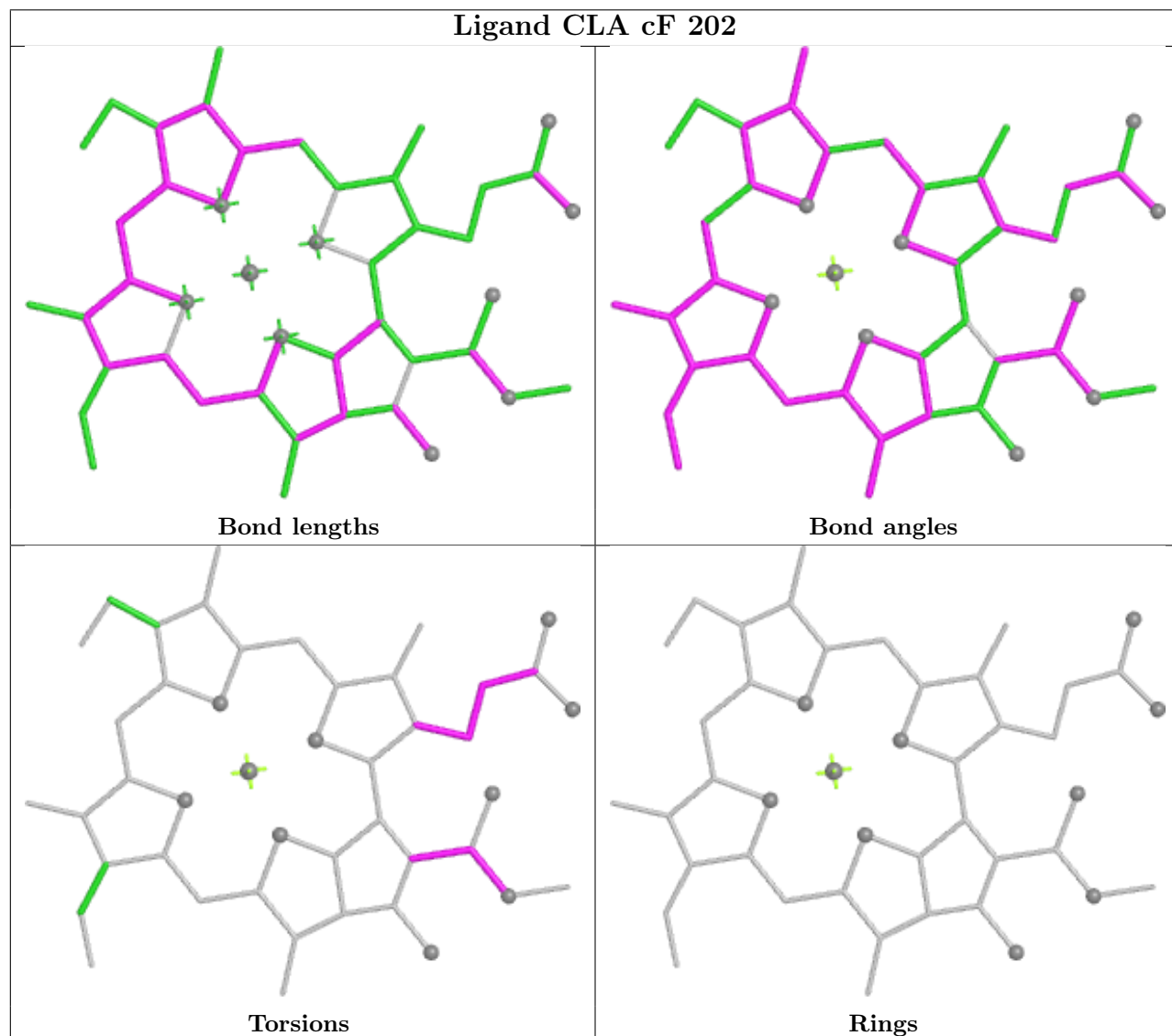
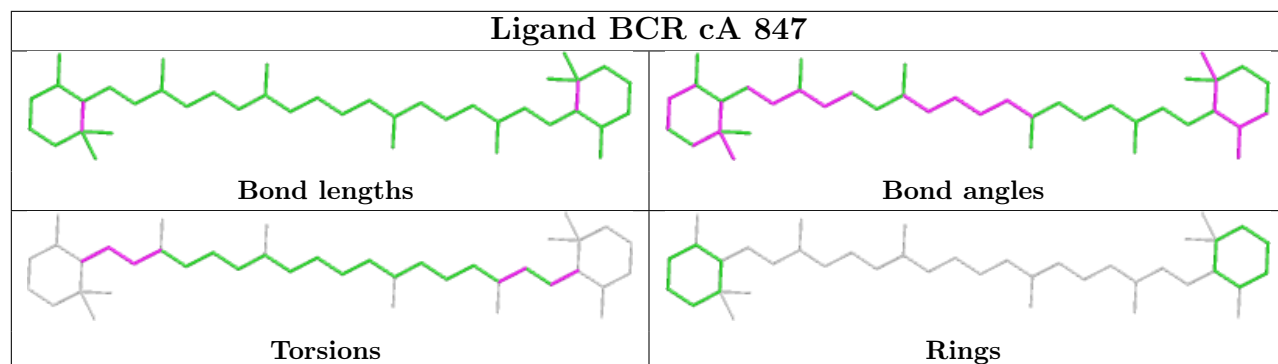


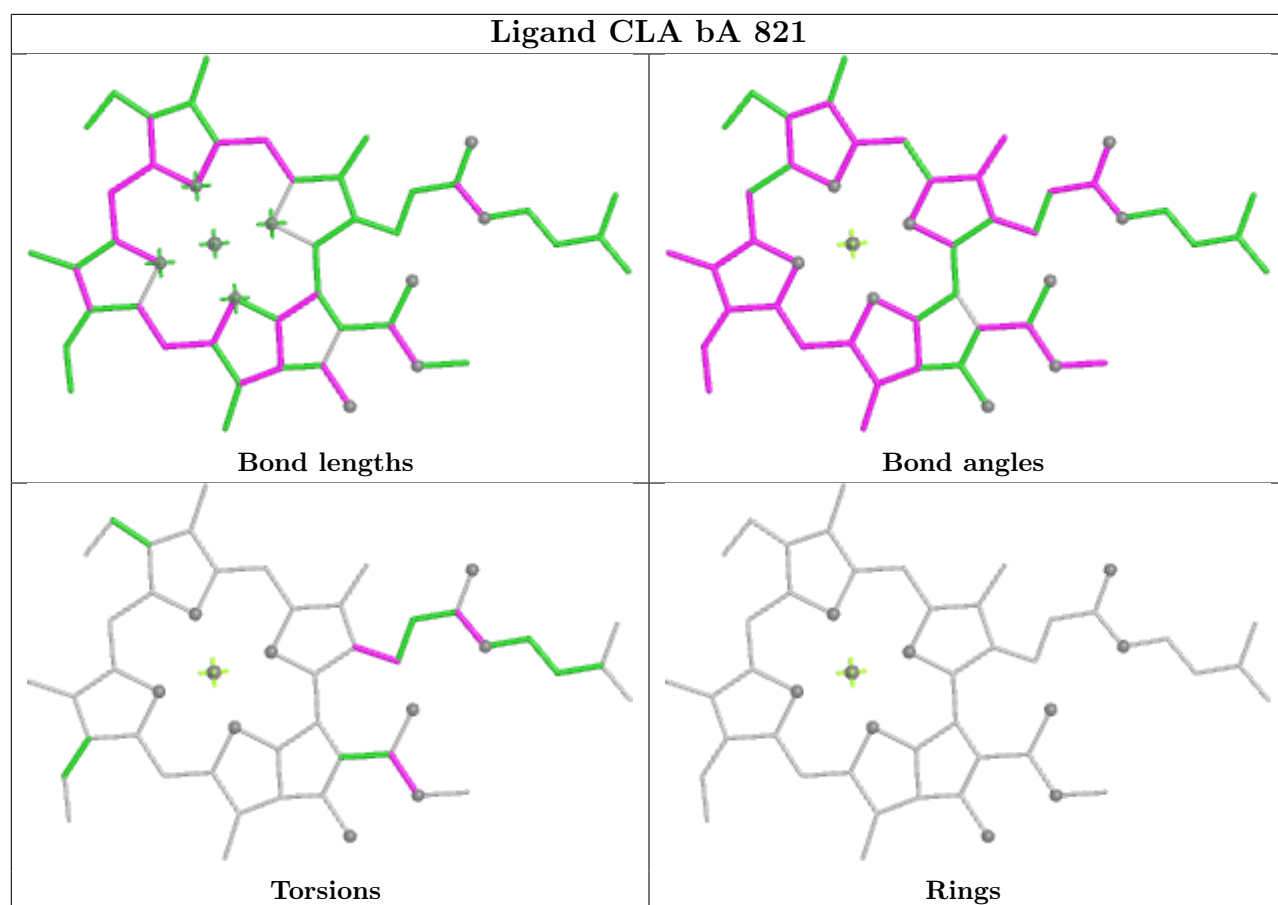


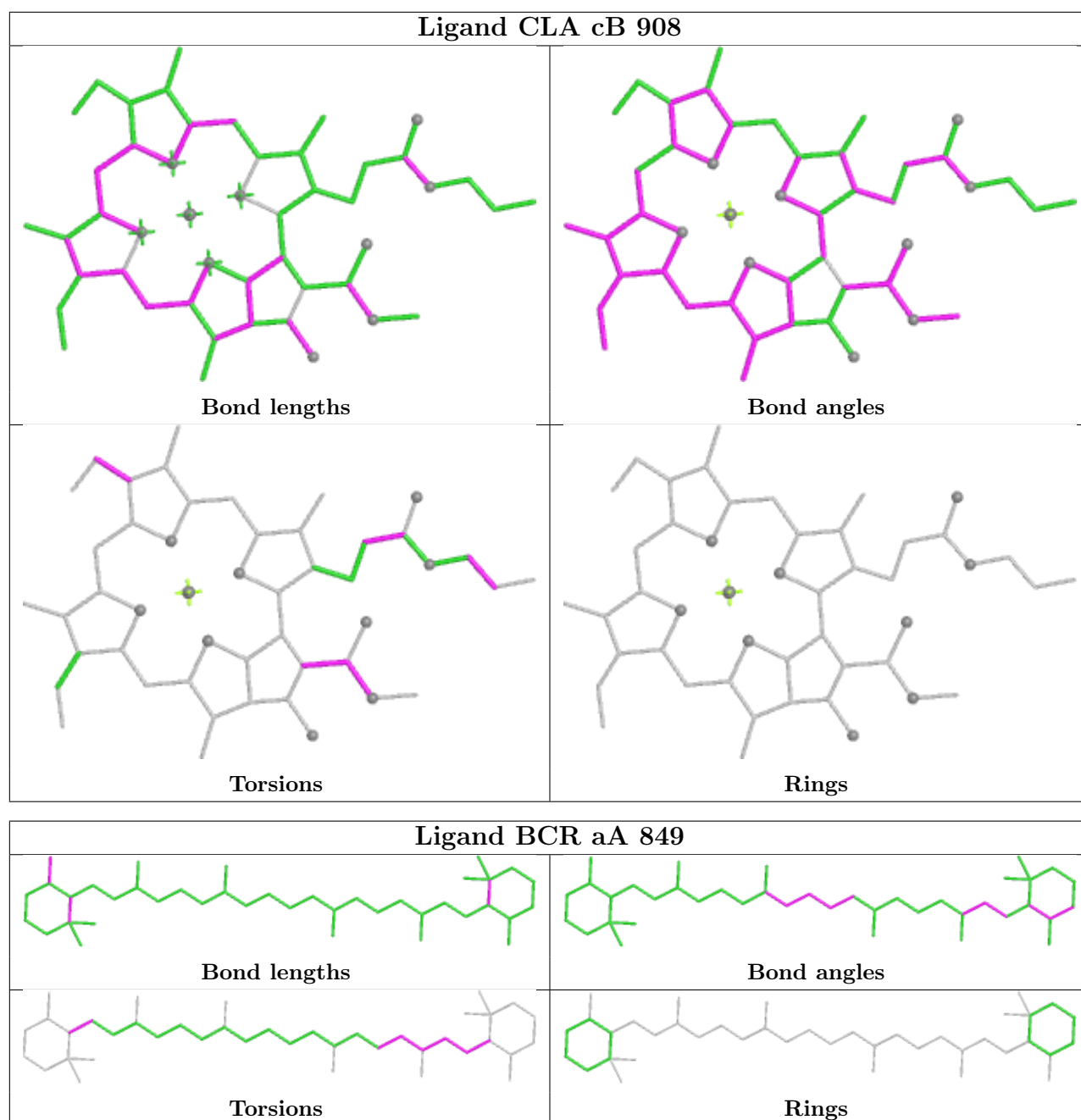


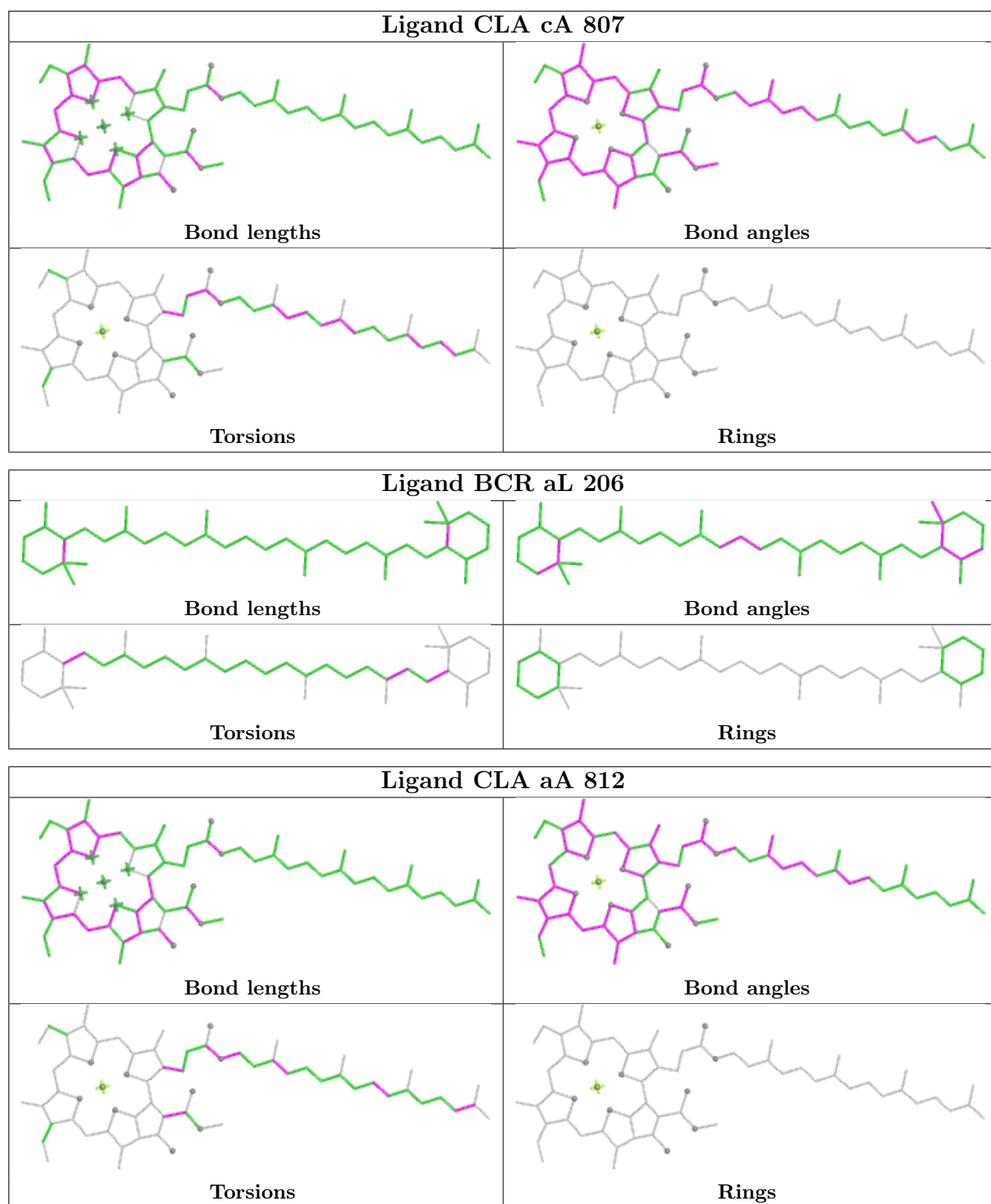


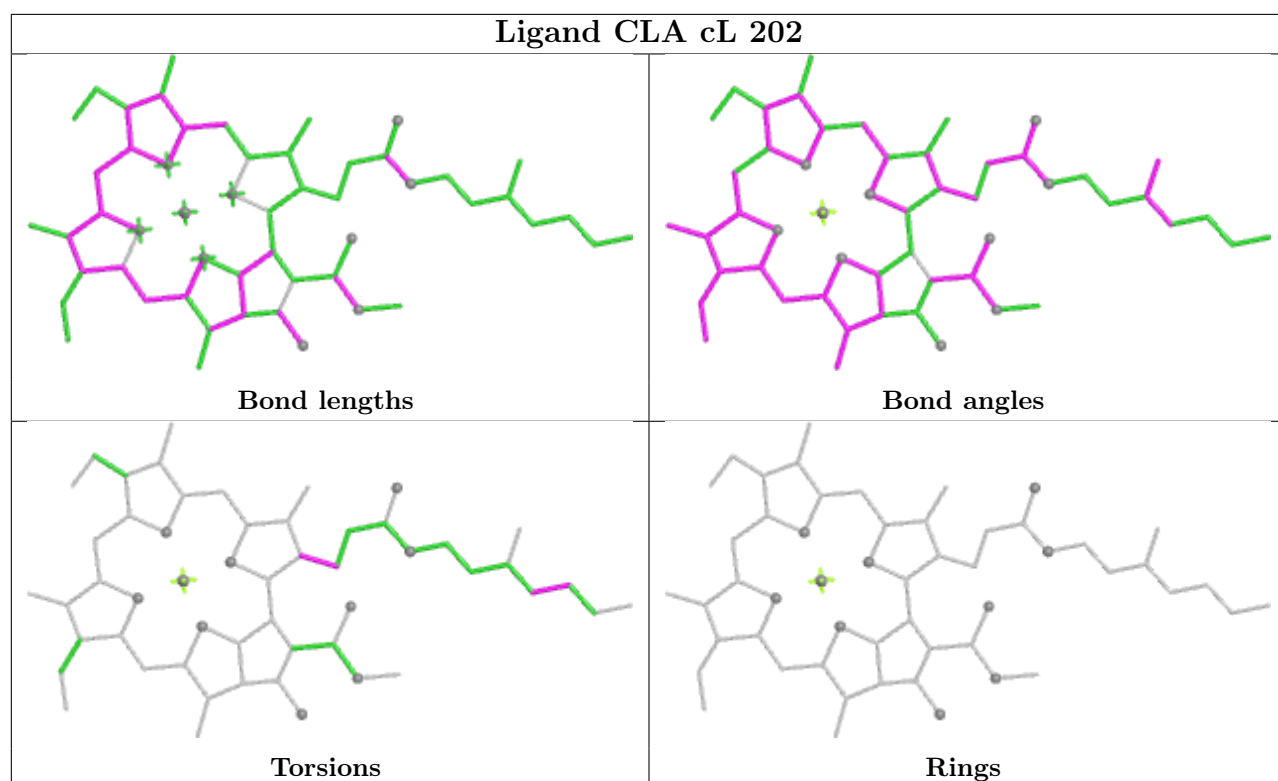


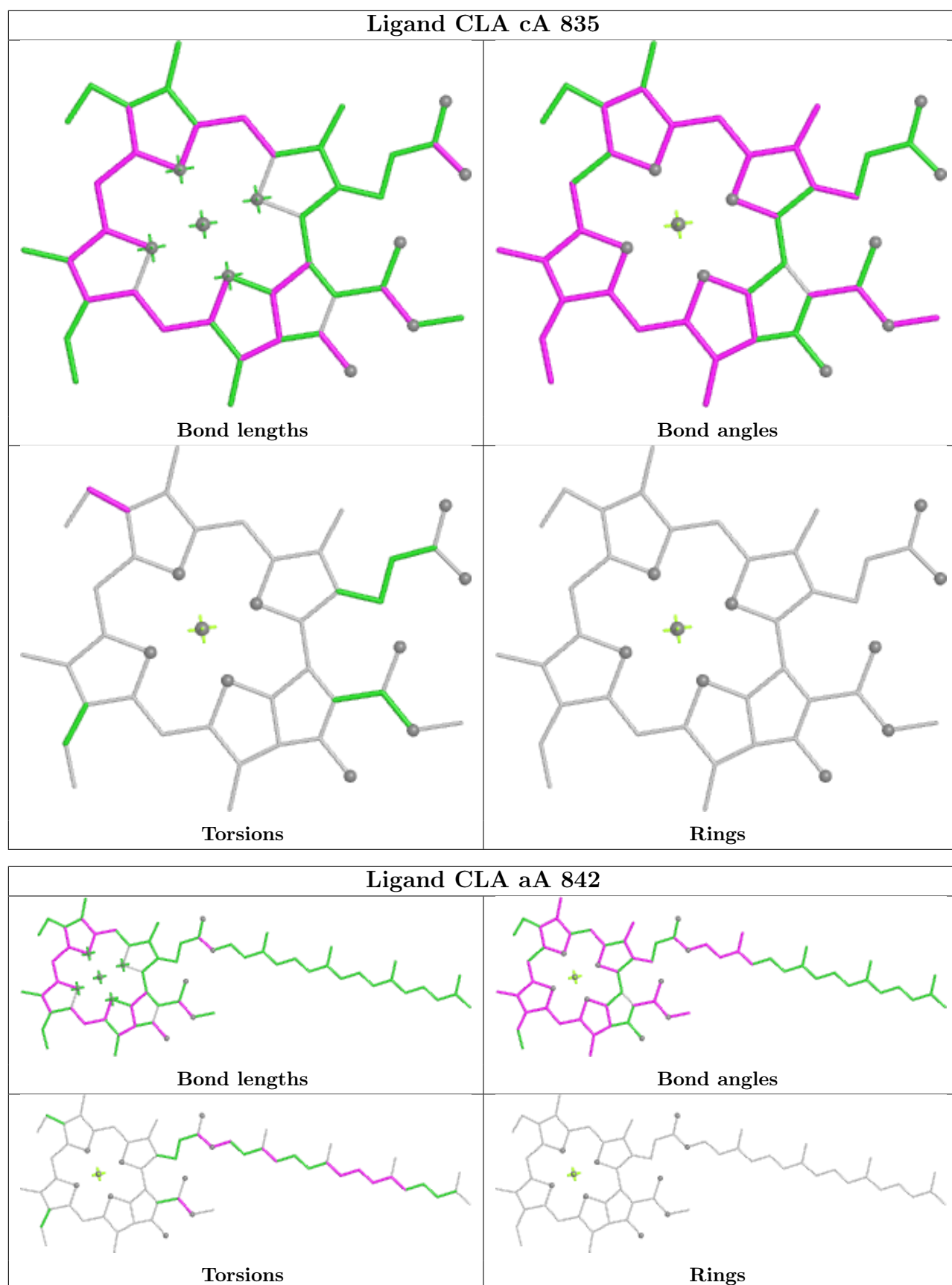


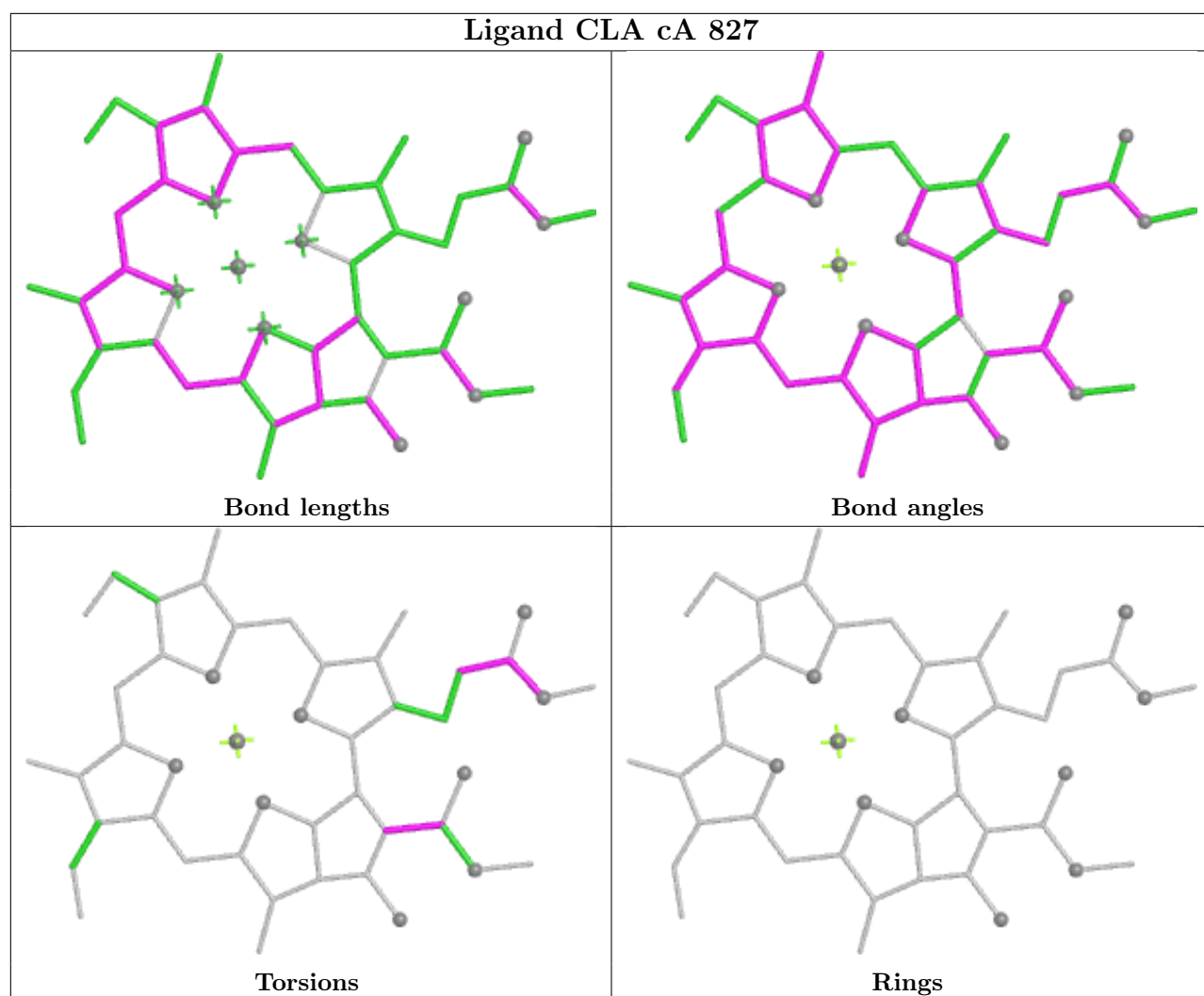


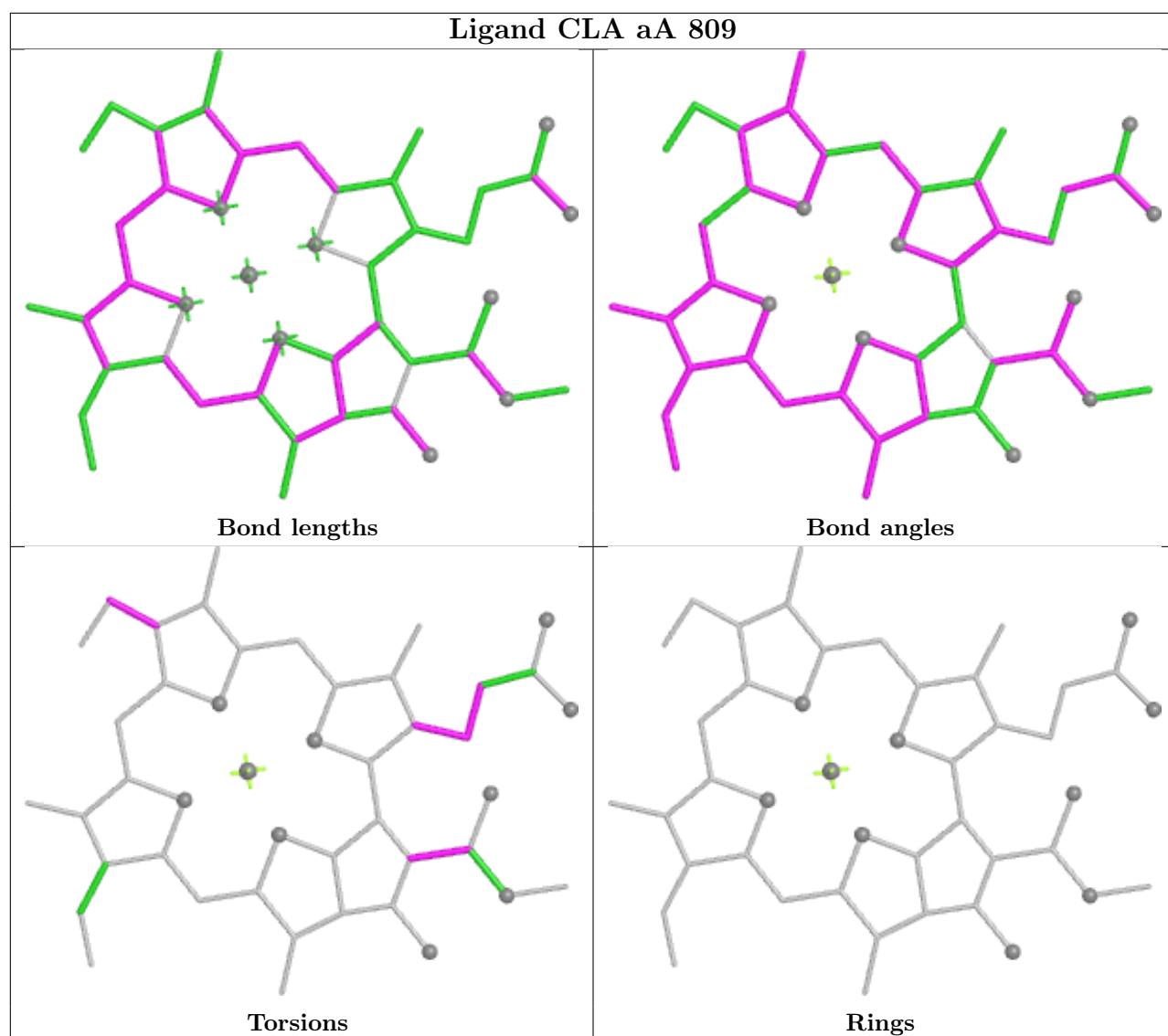


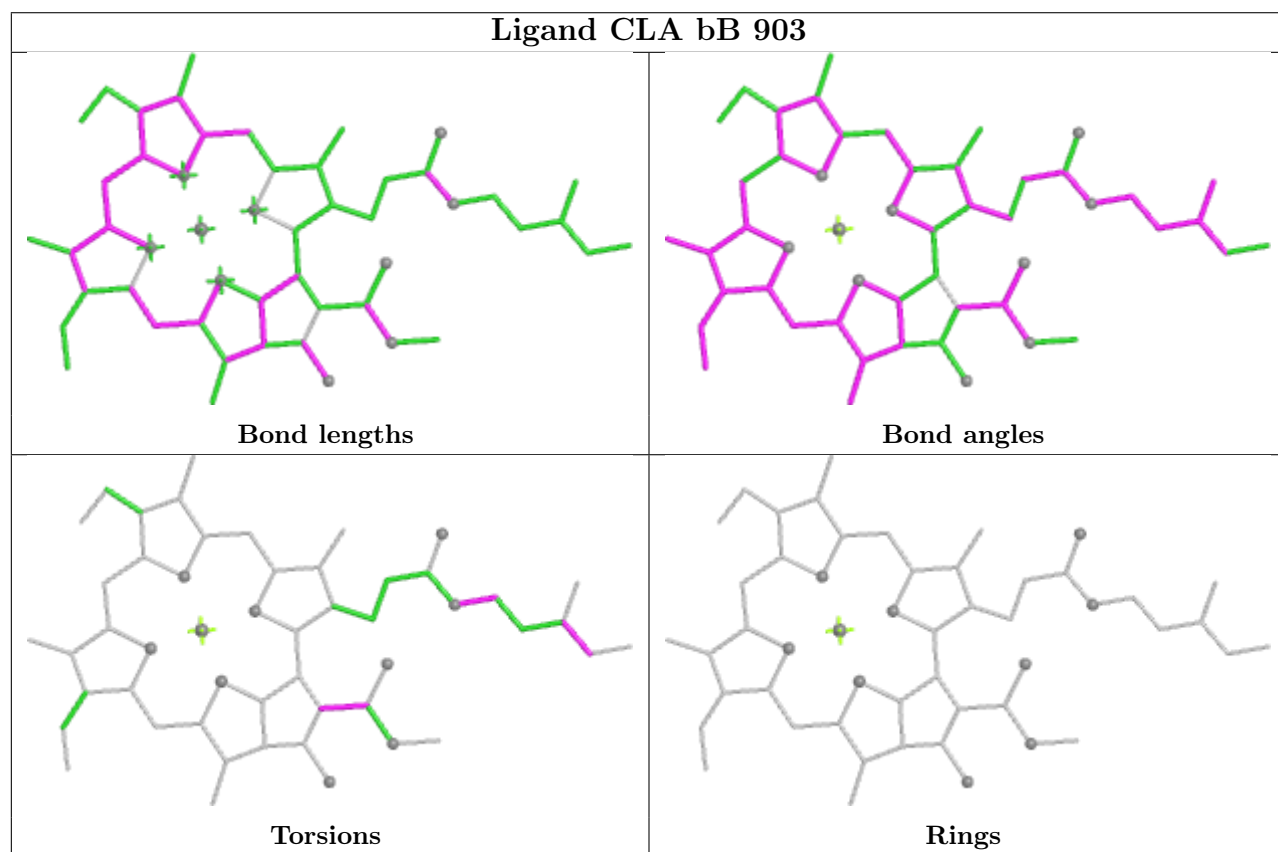
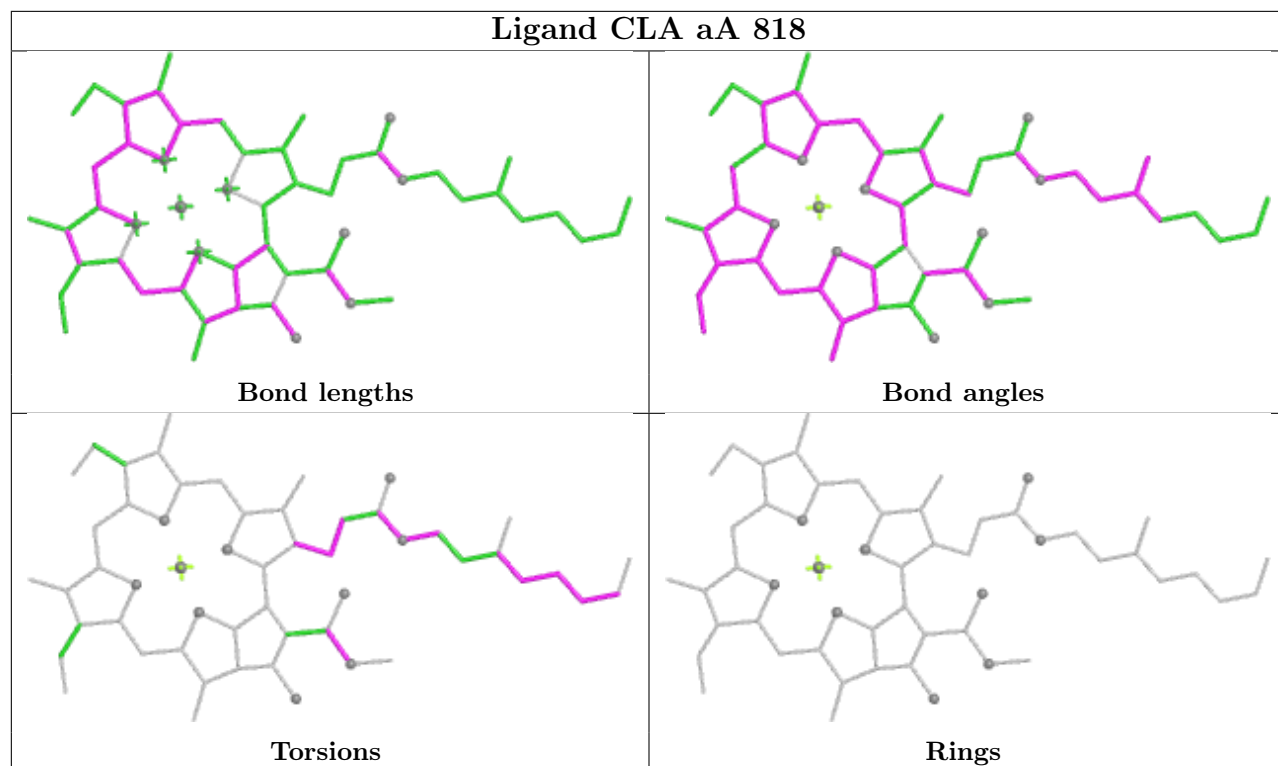


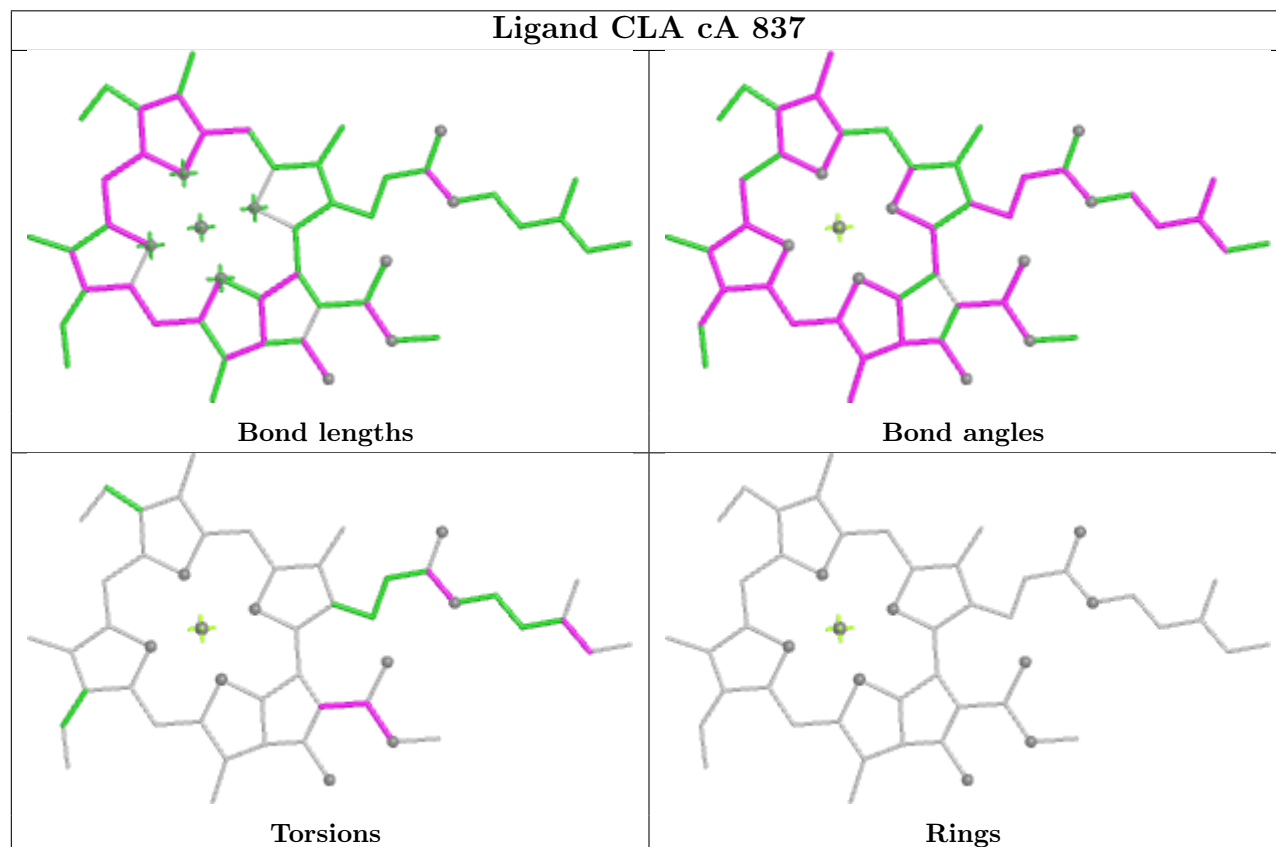
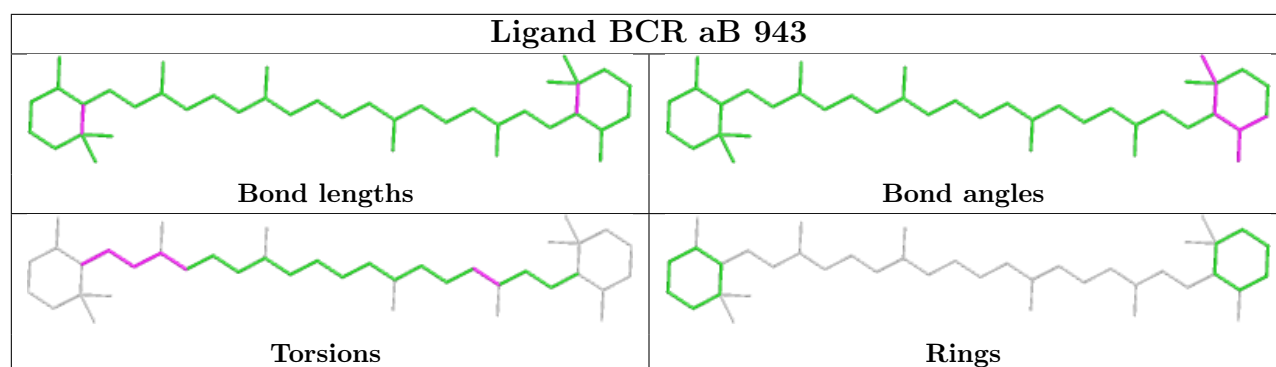




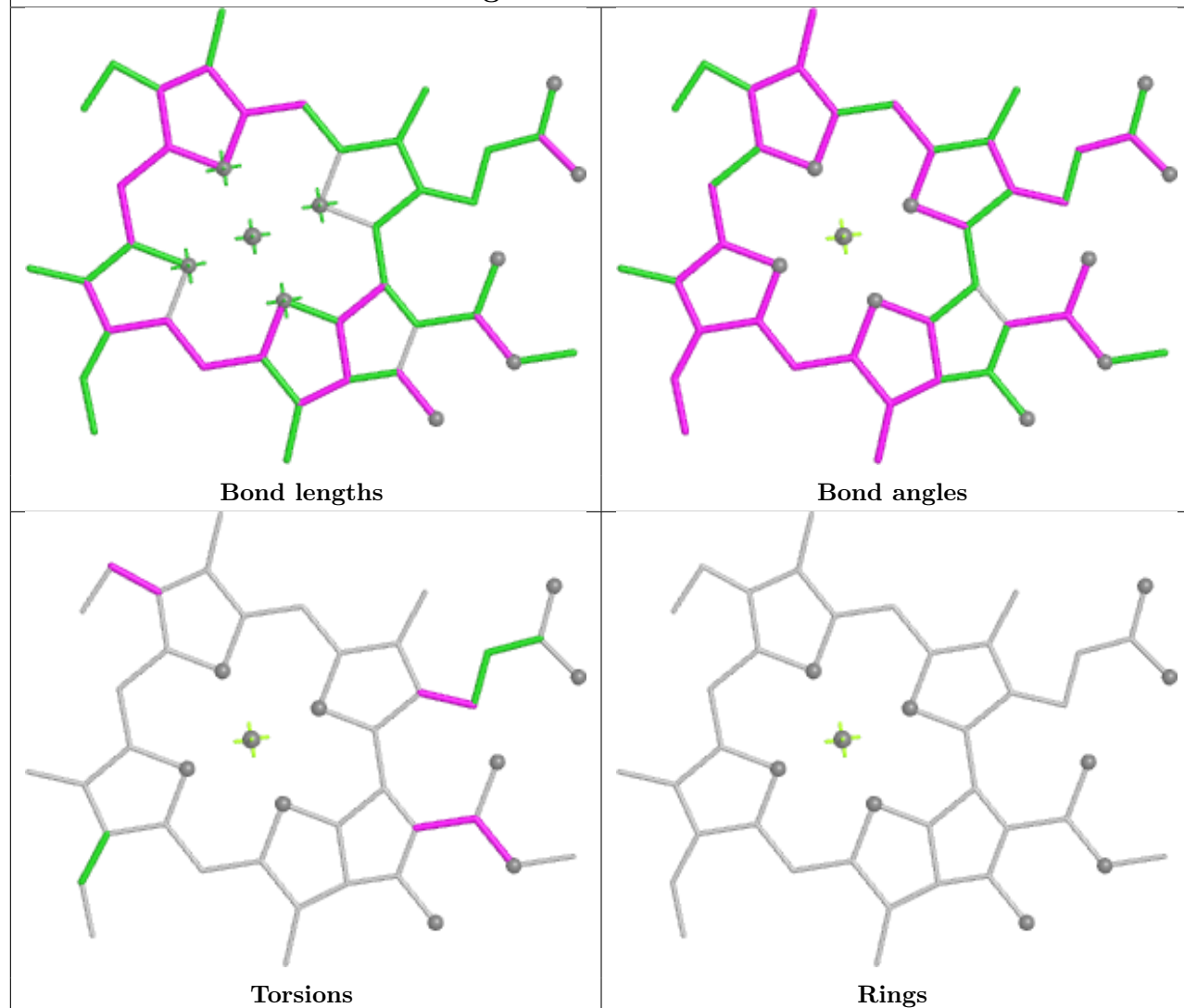




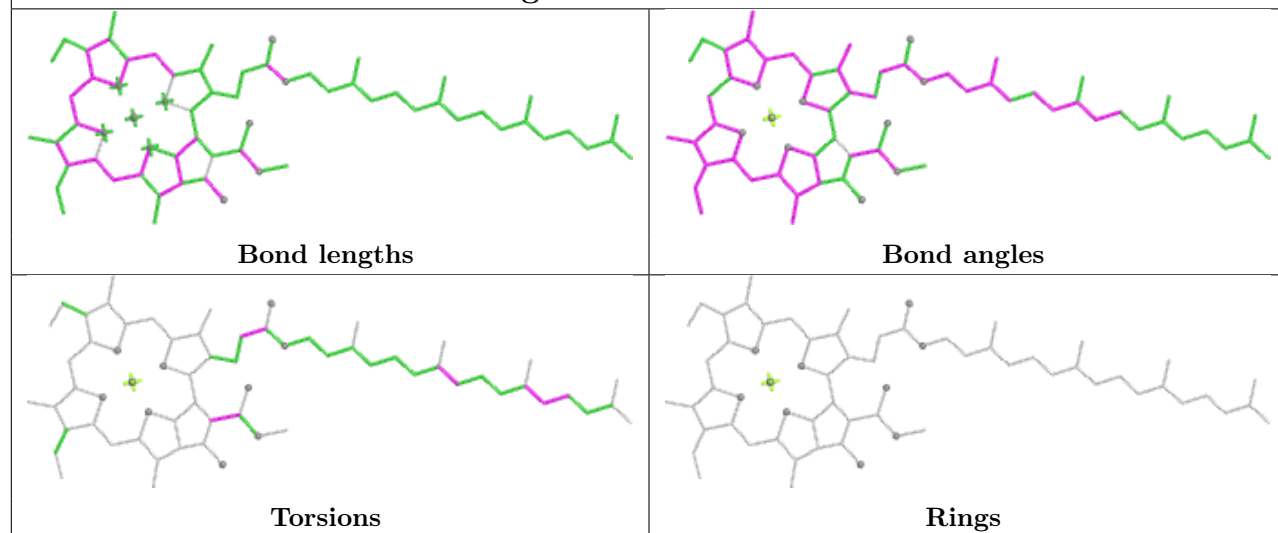




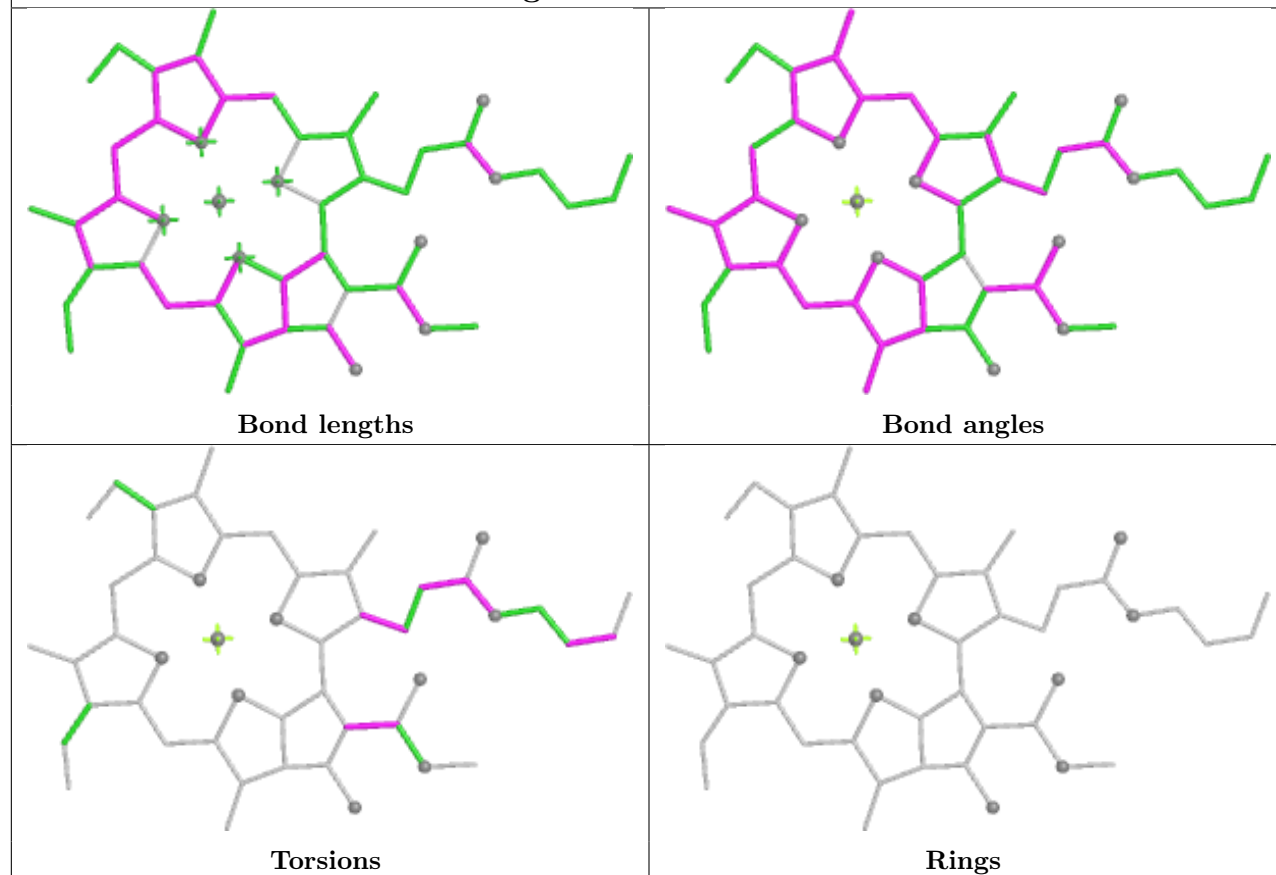
Ligand CLA bA 815



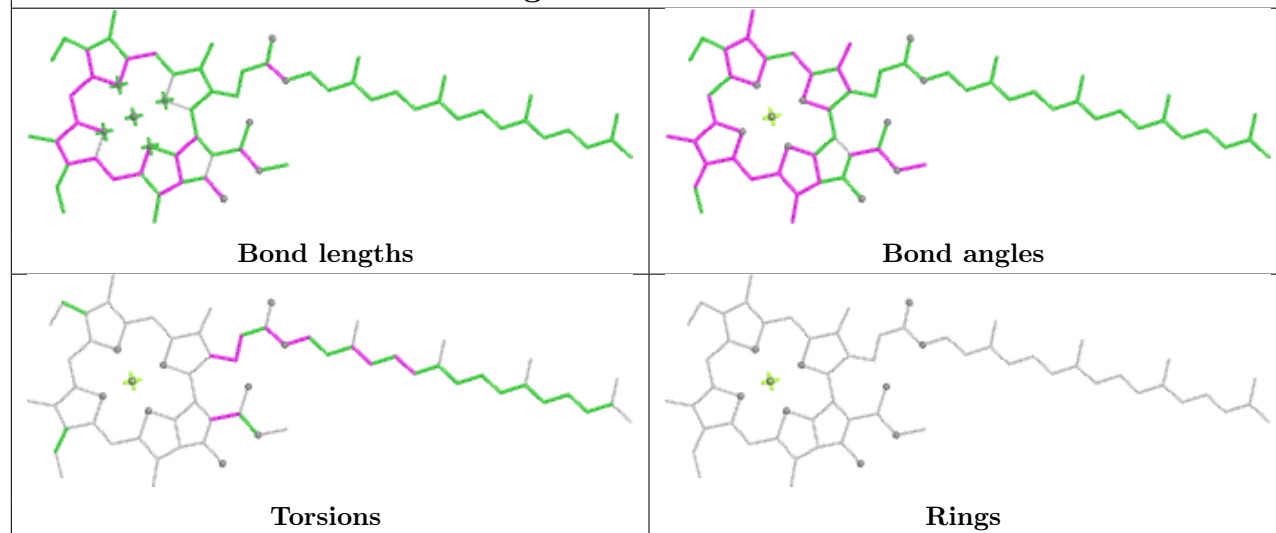
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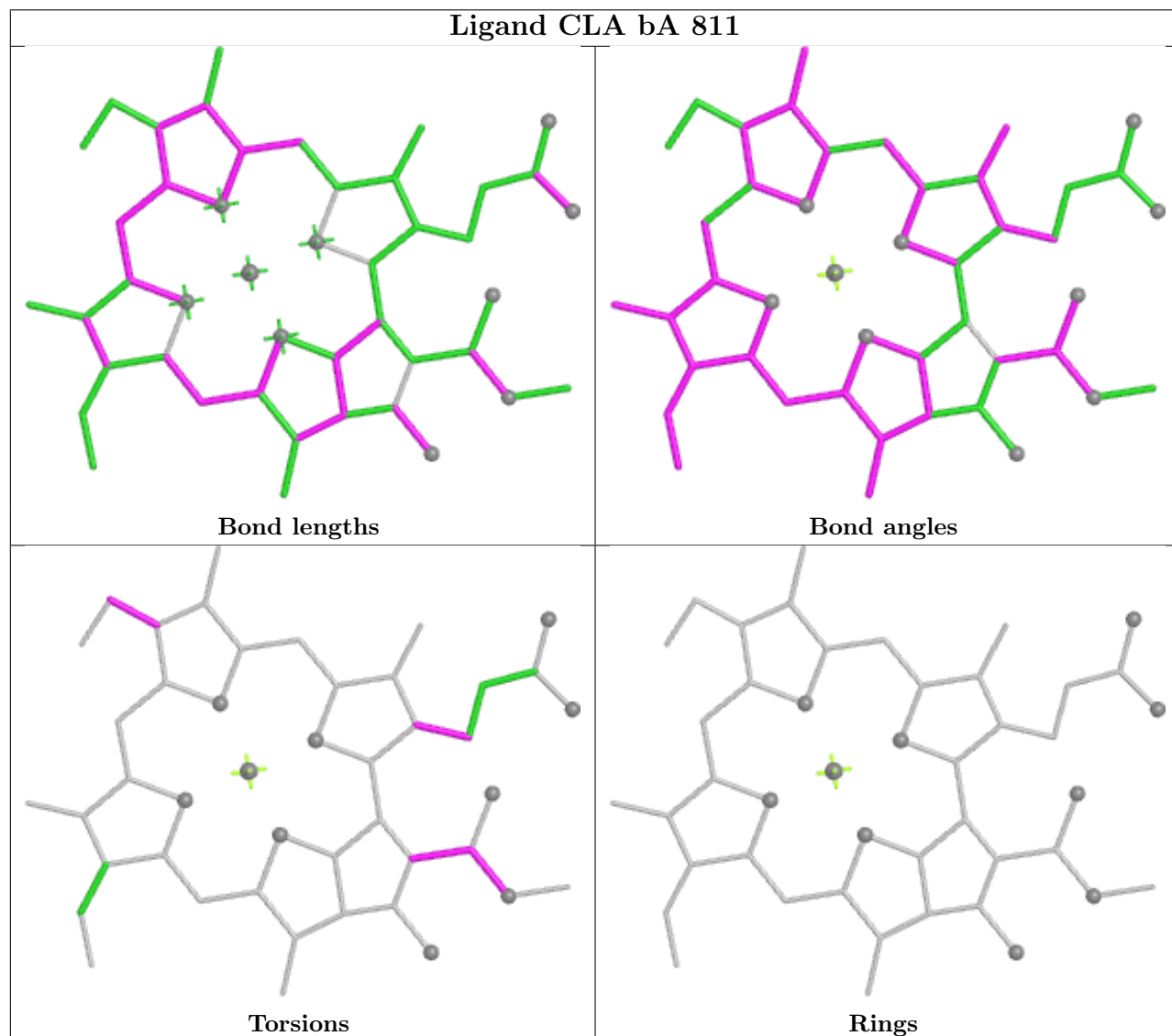
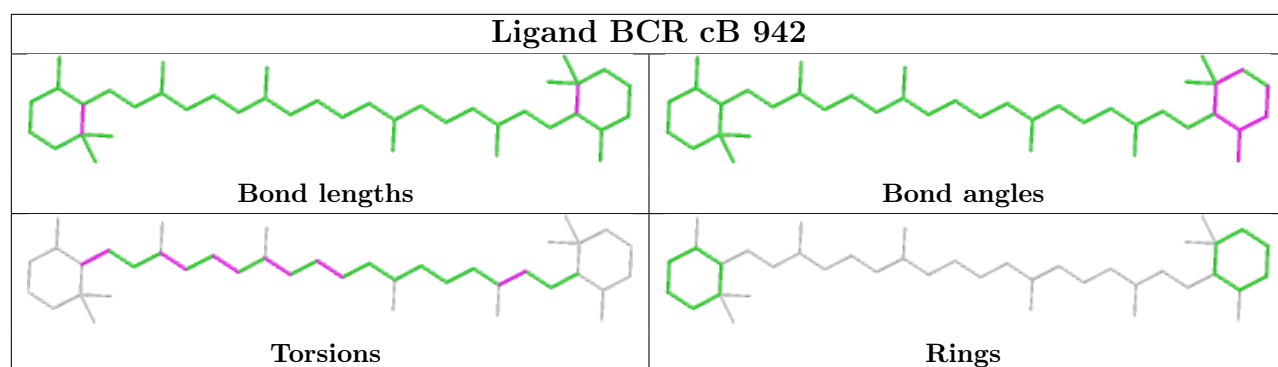


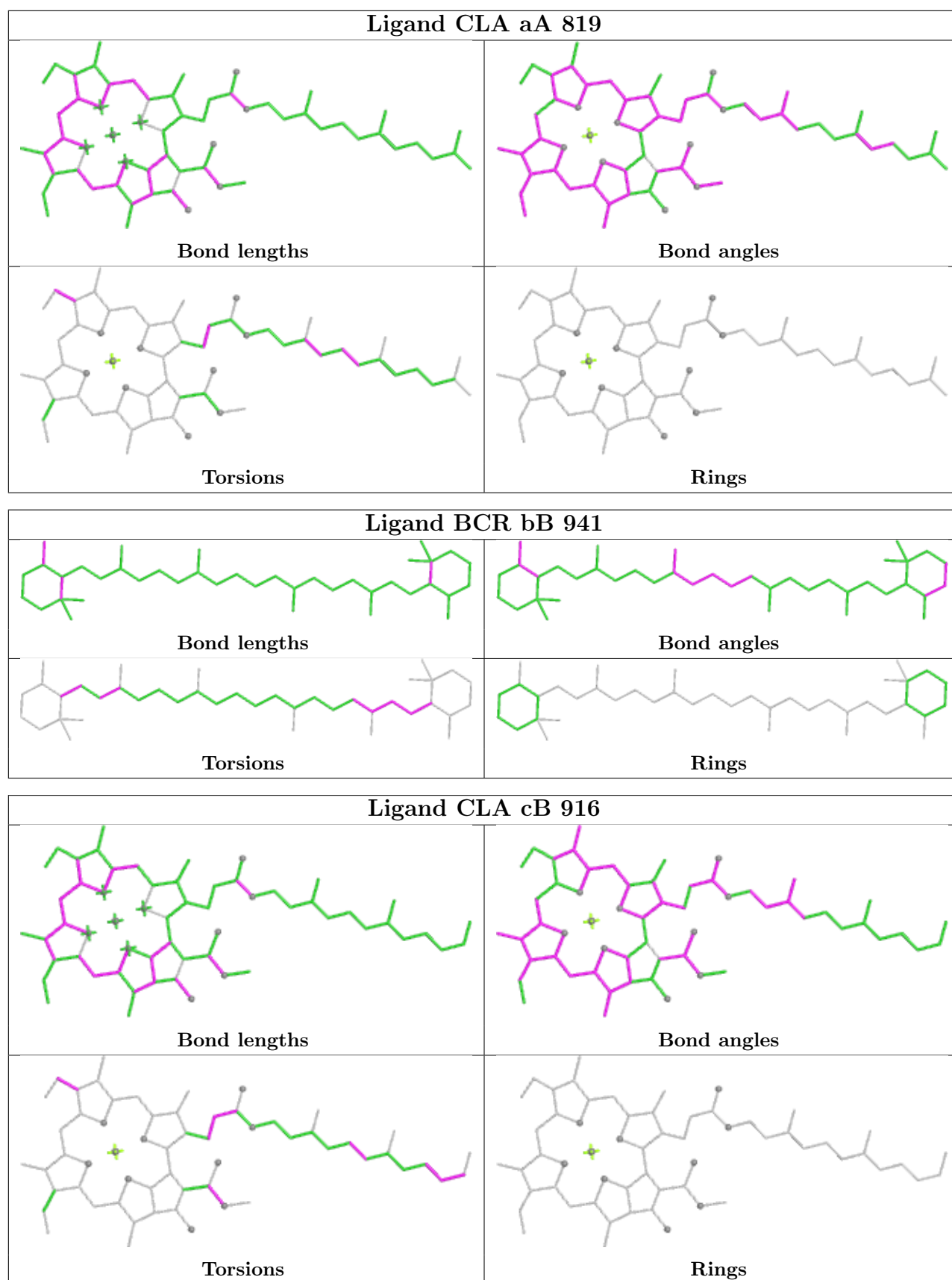
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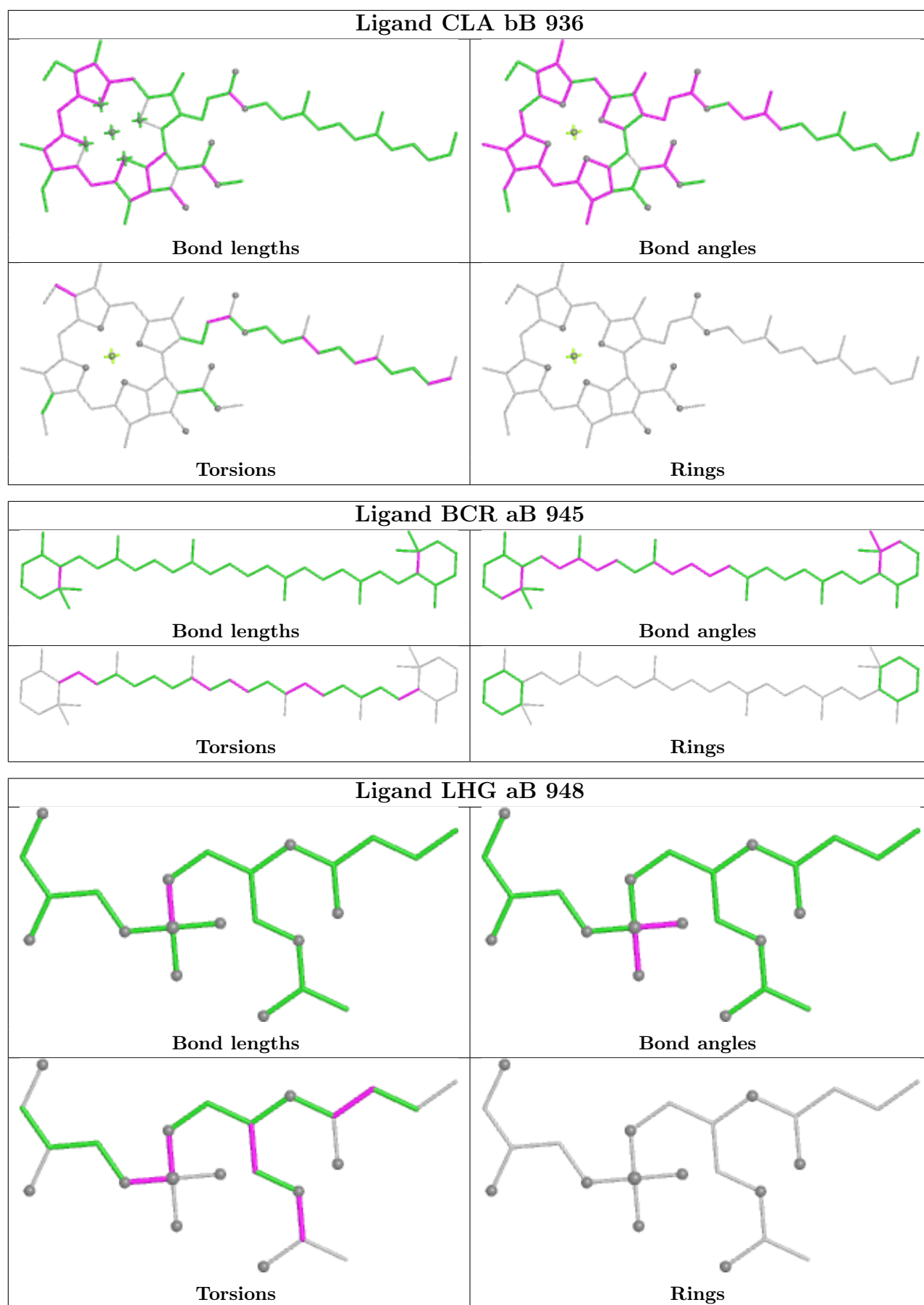


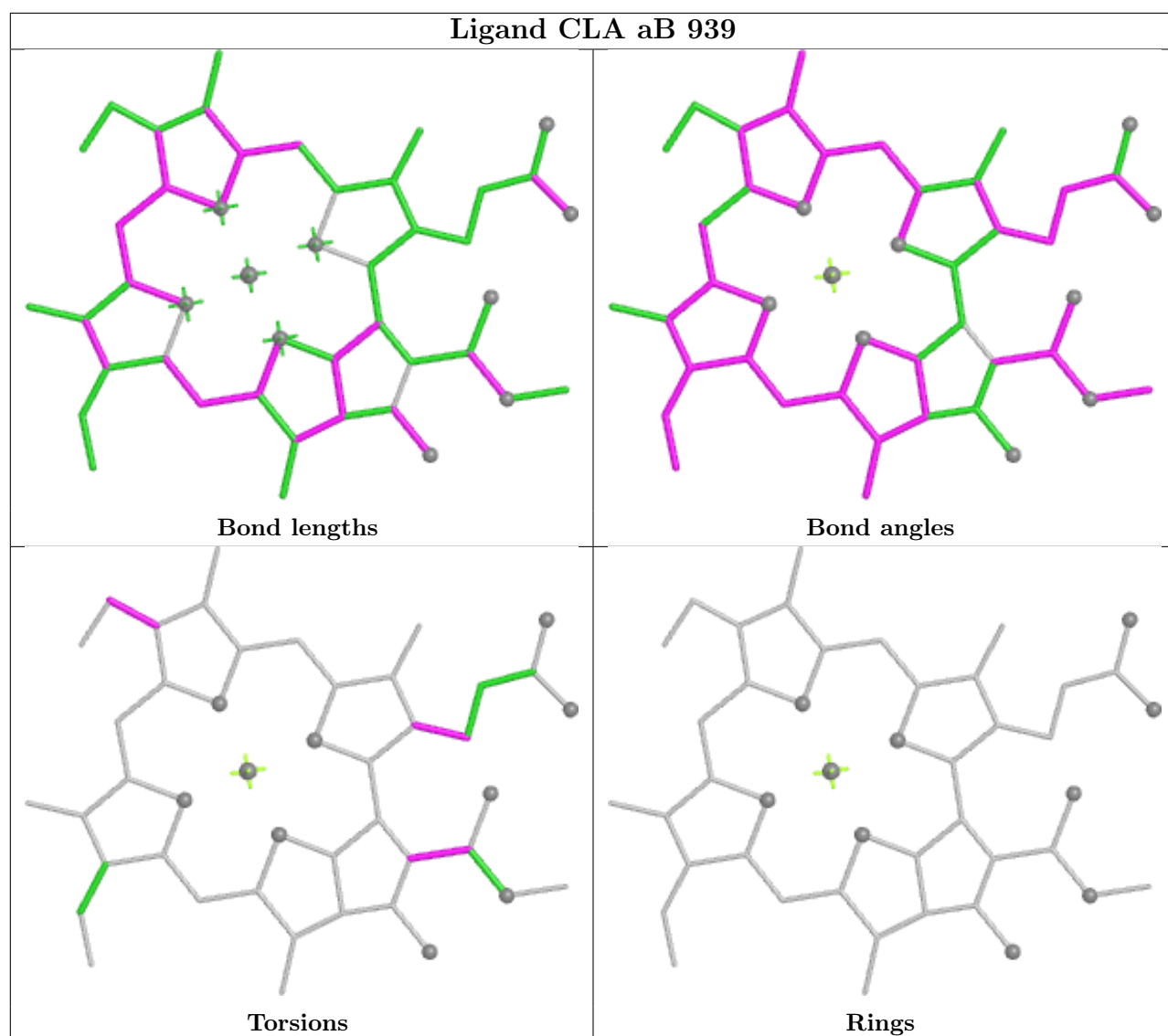
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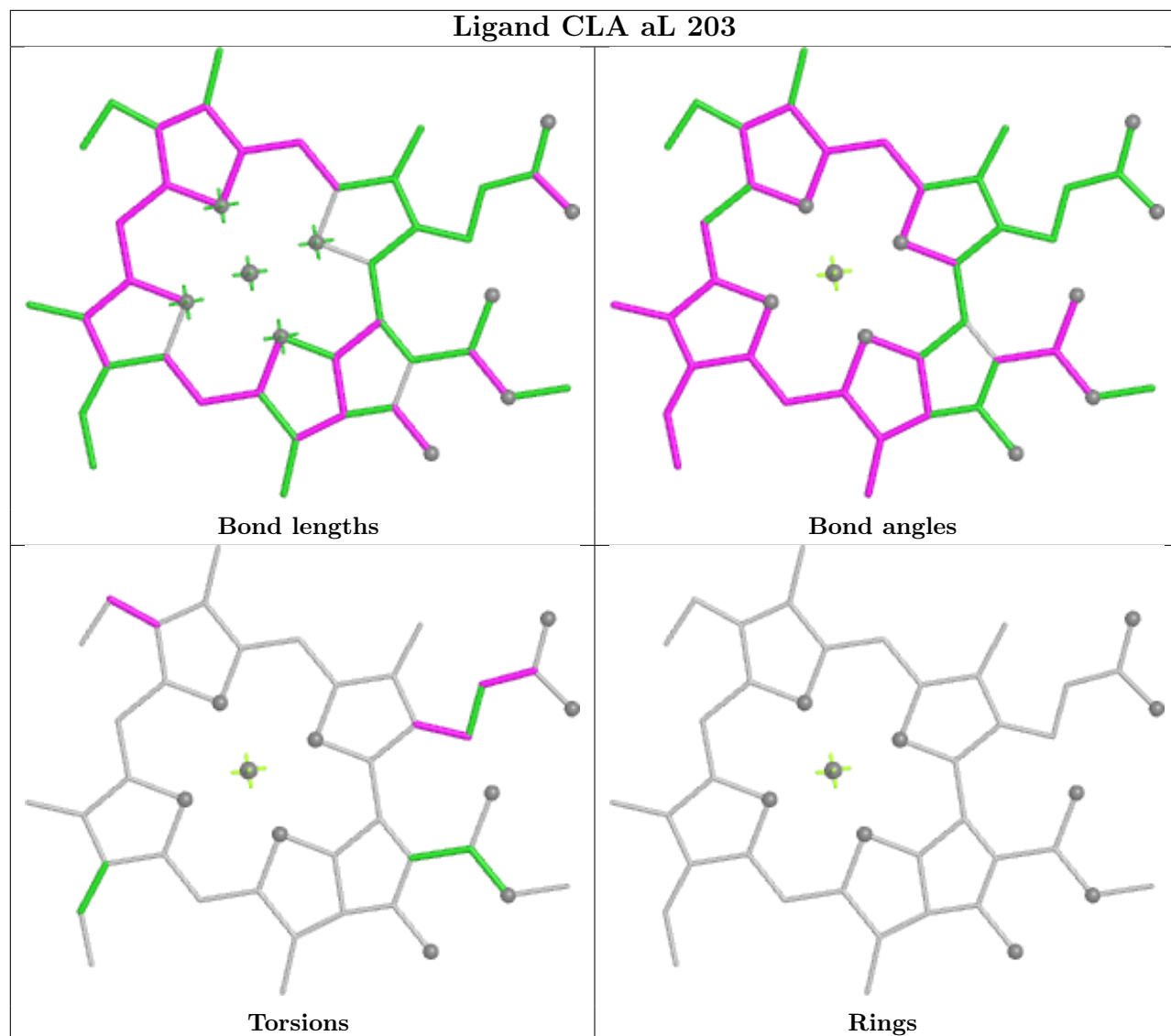




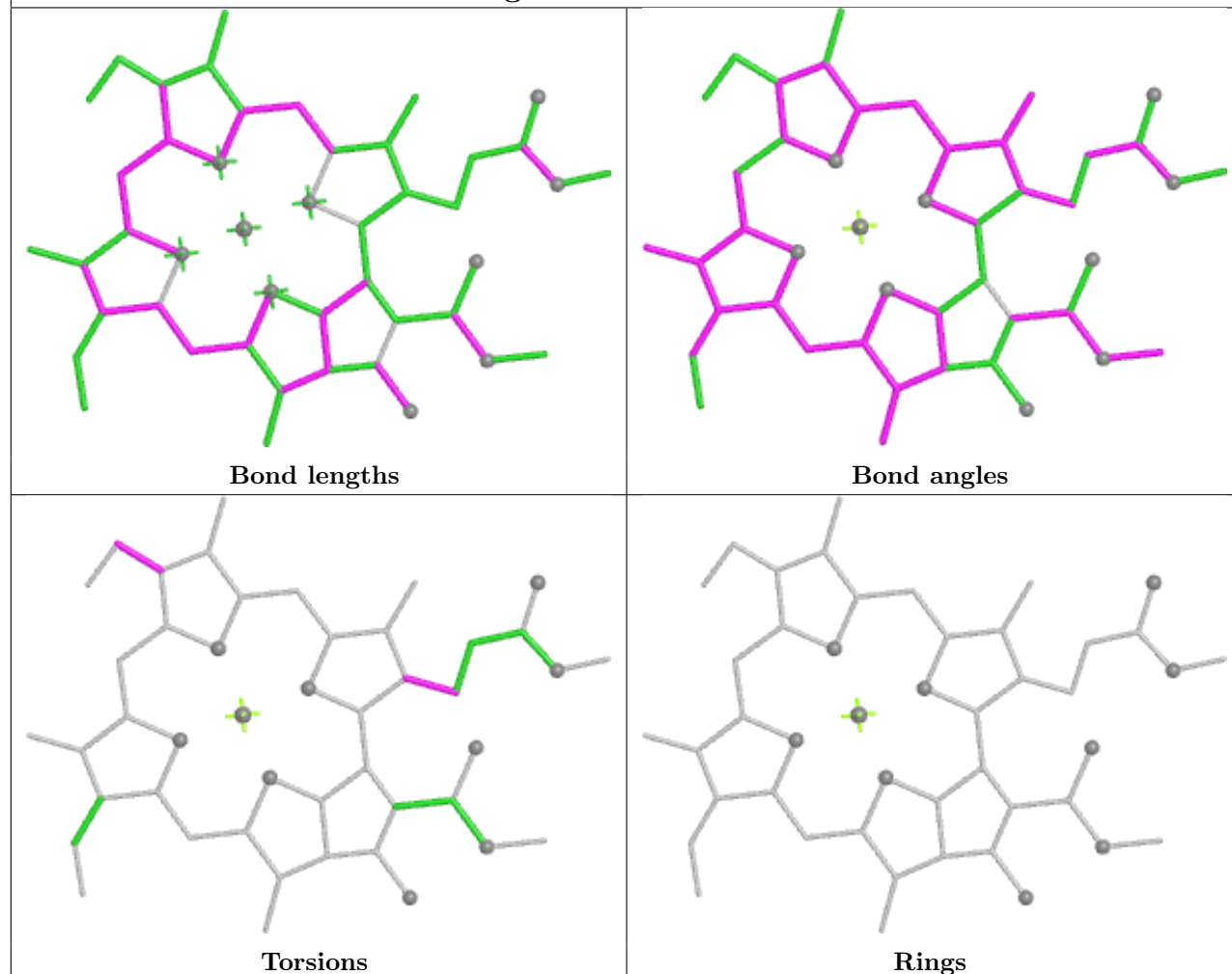




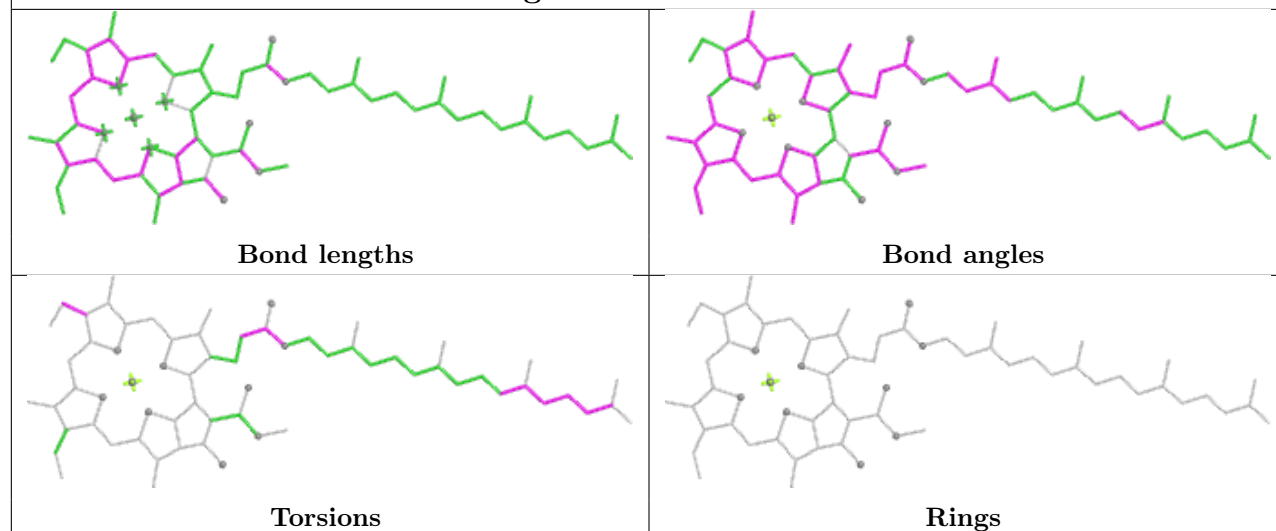


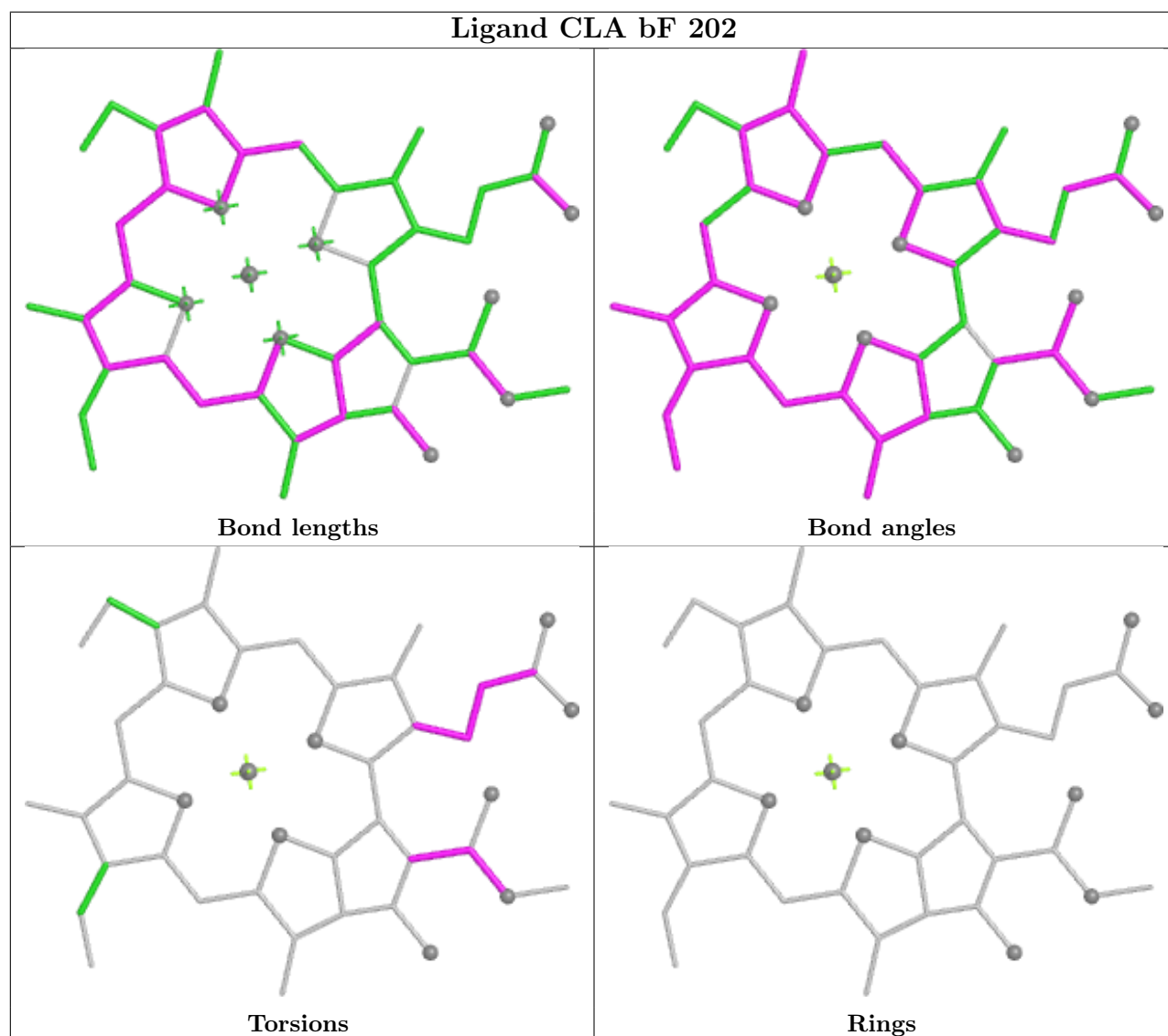
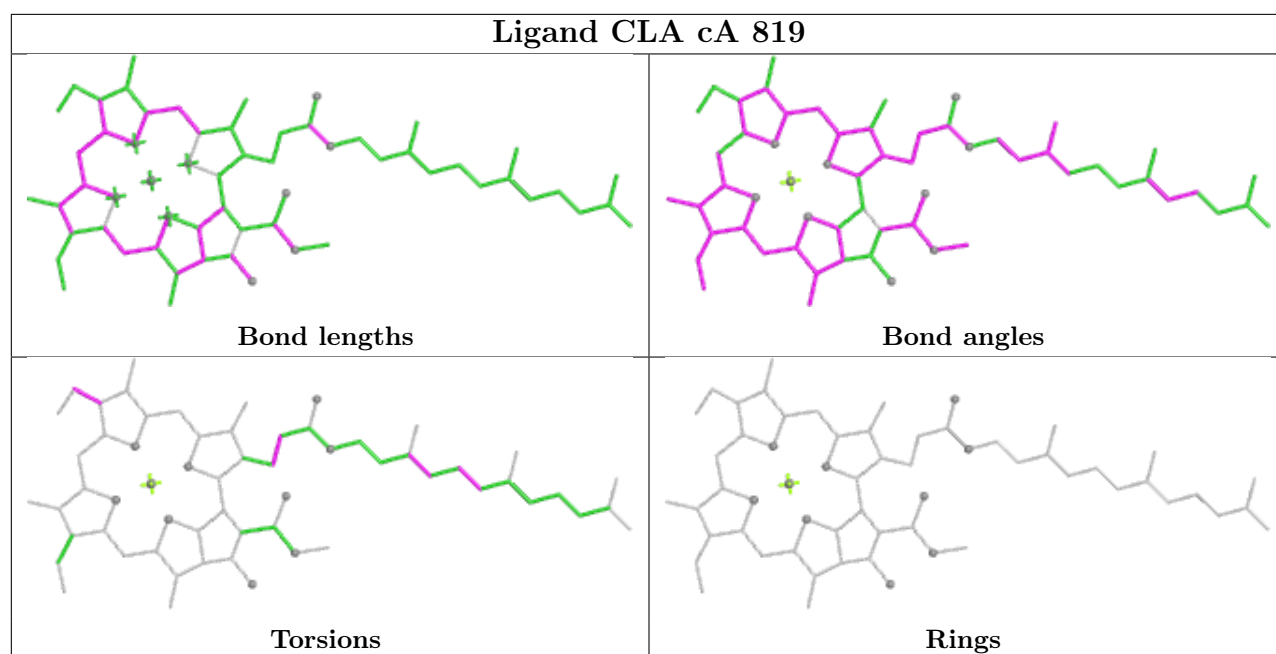


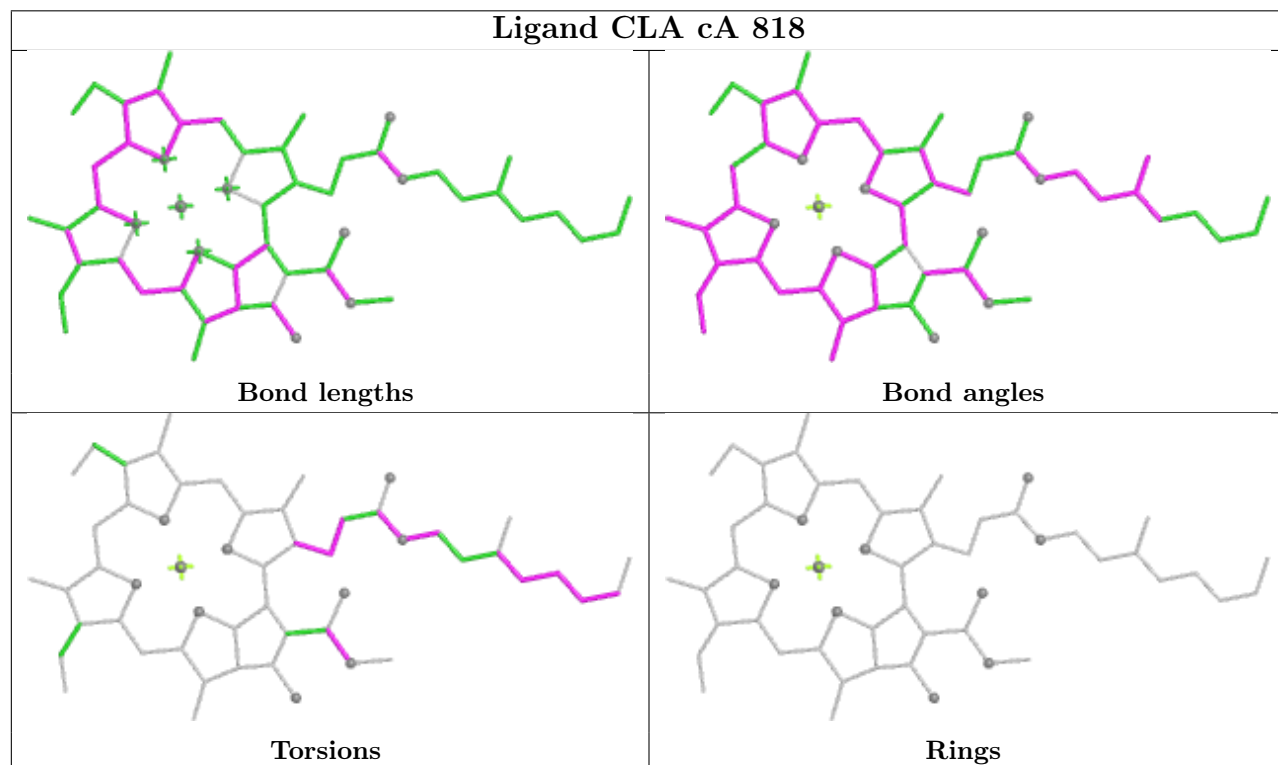
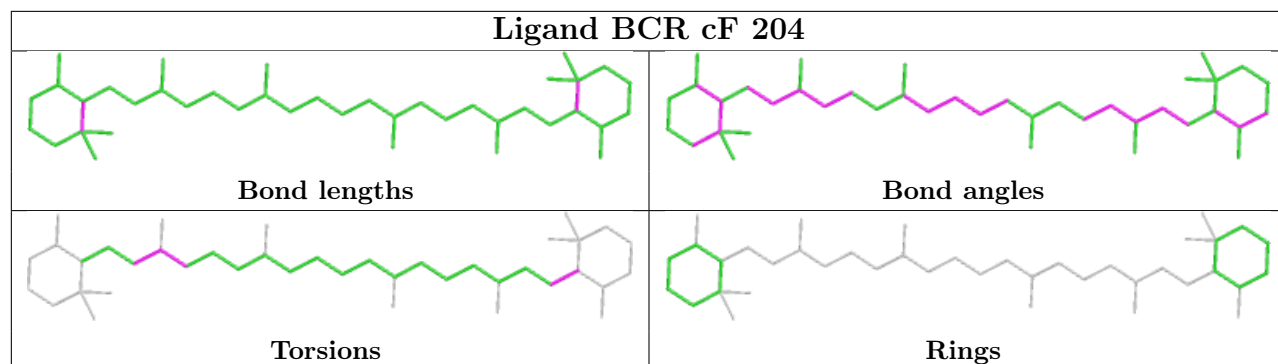
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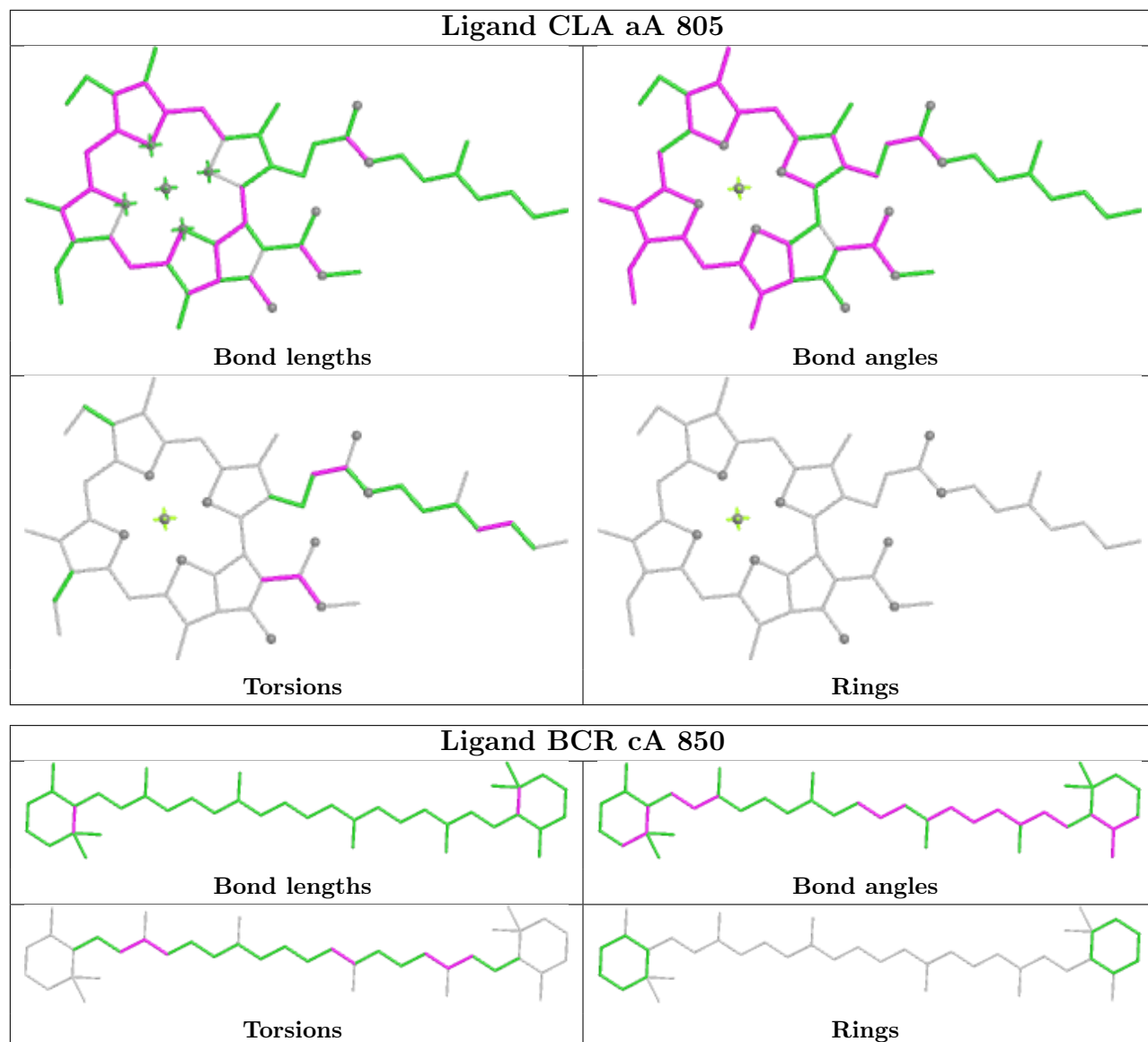


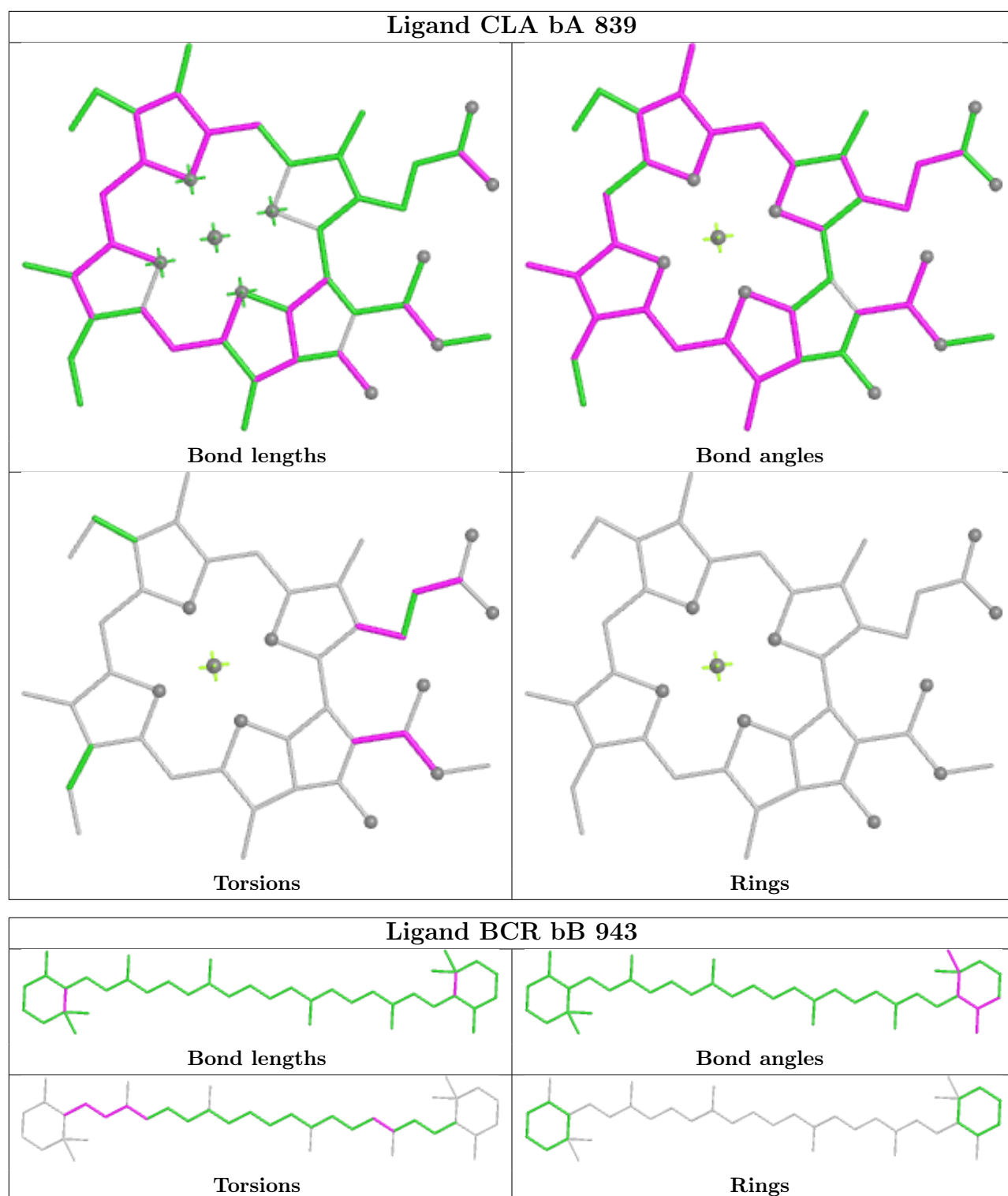
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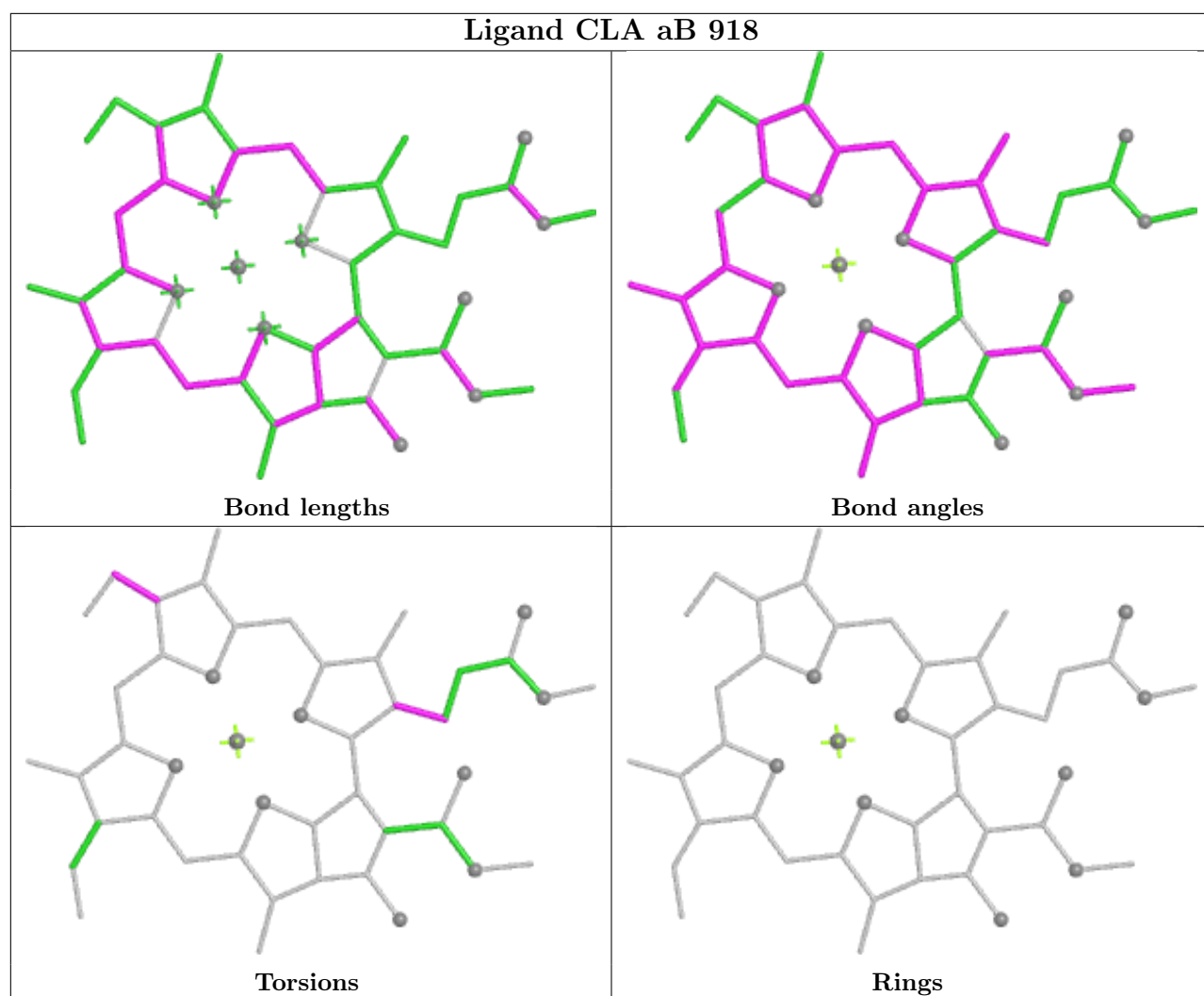


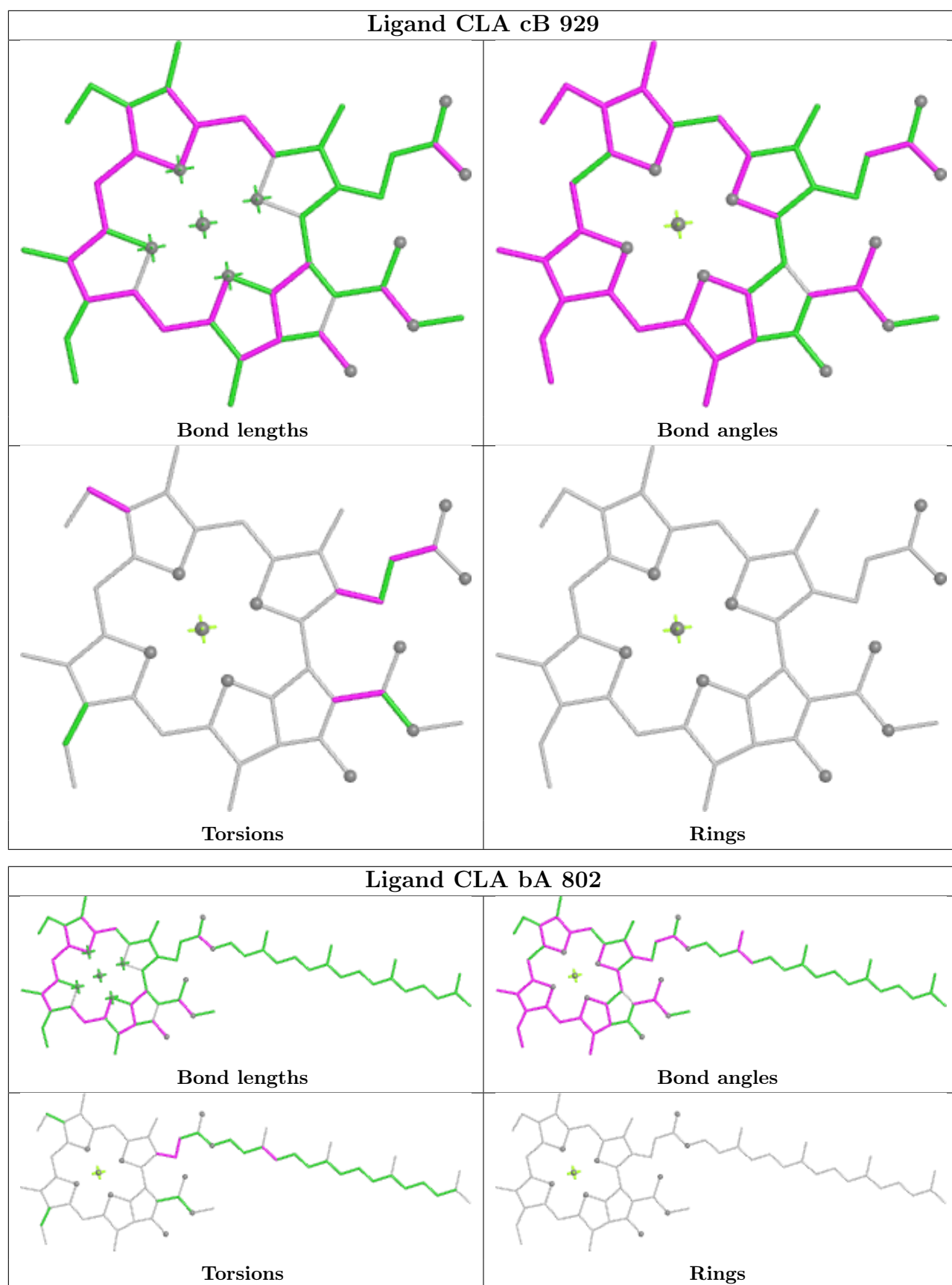


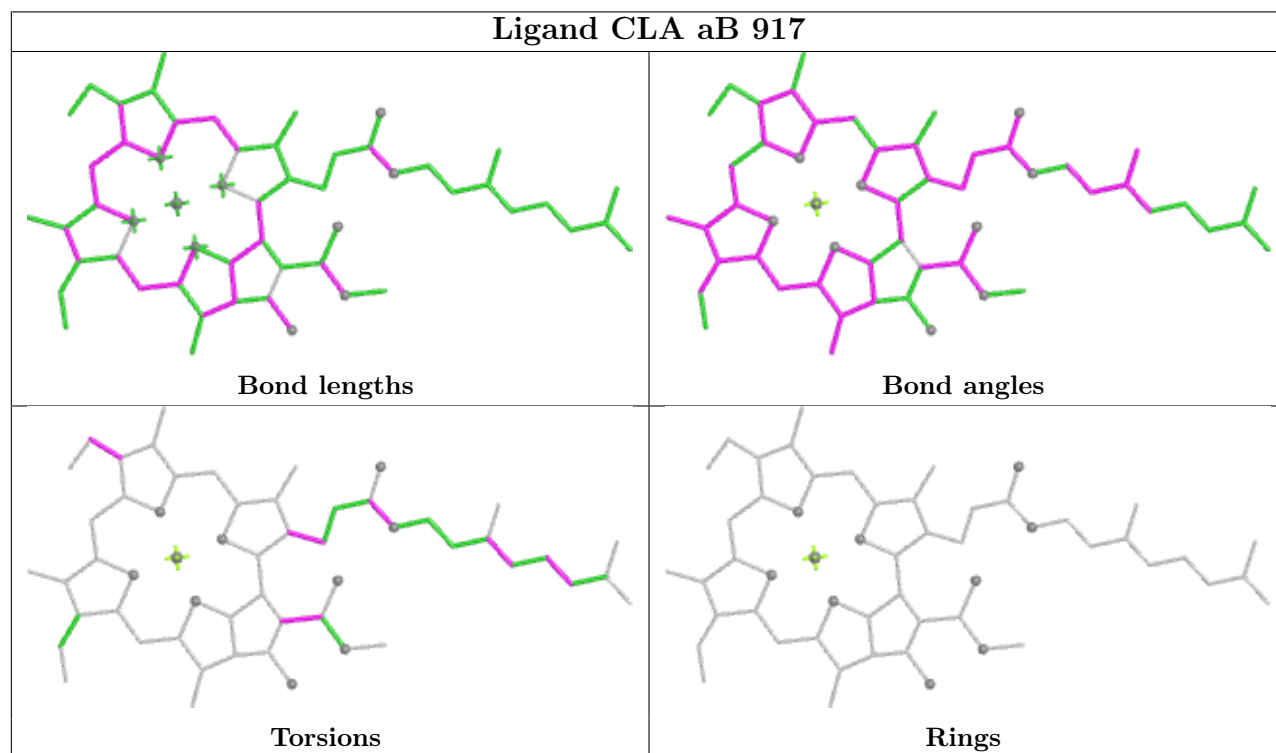
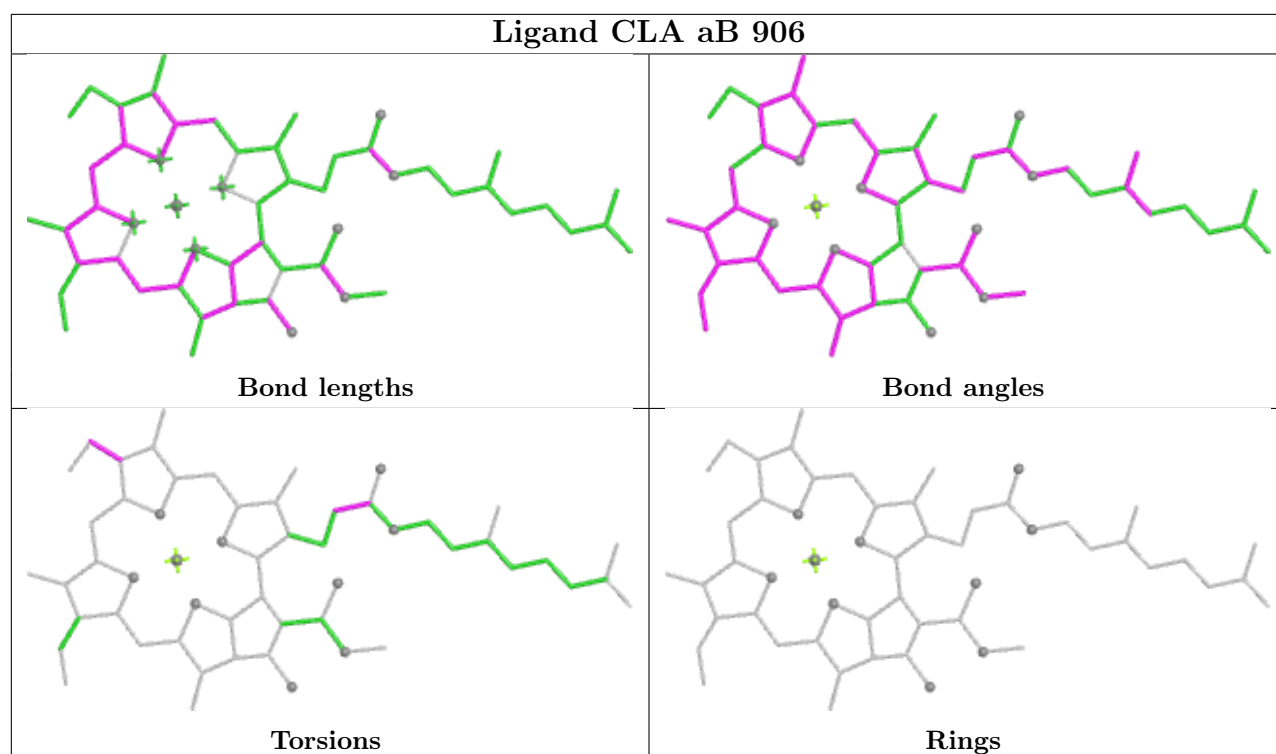


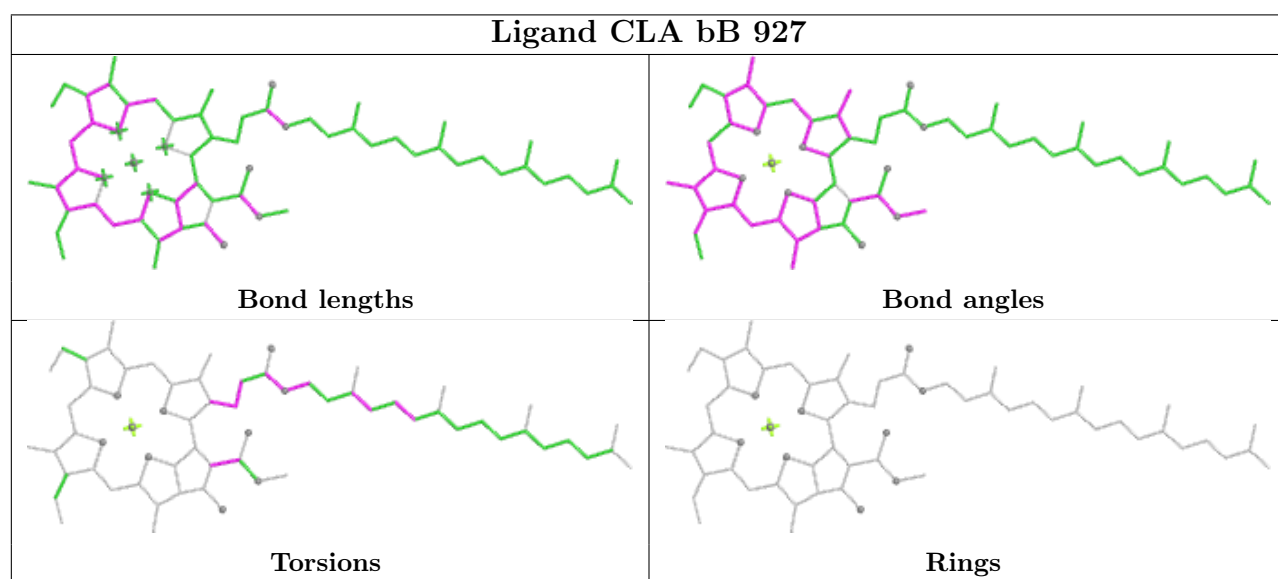
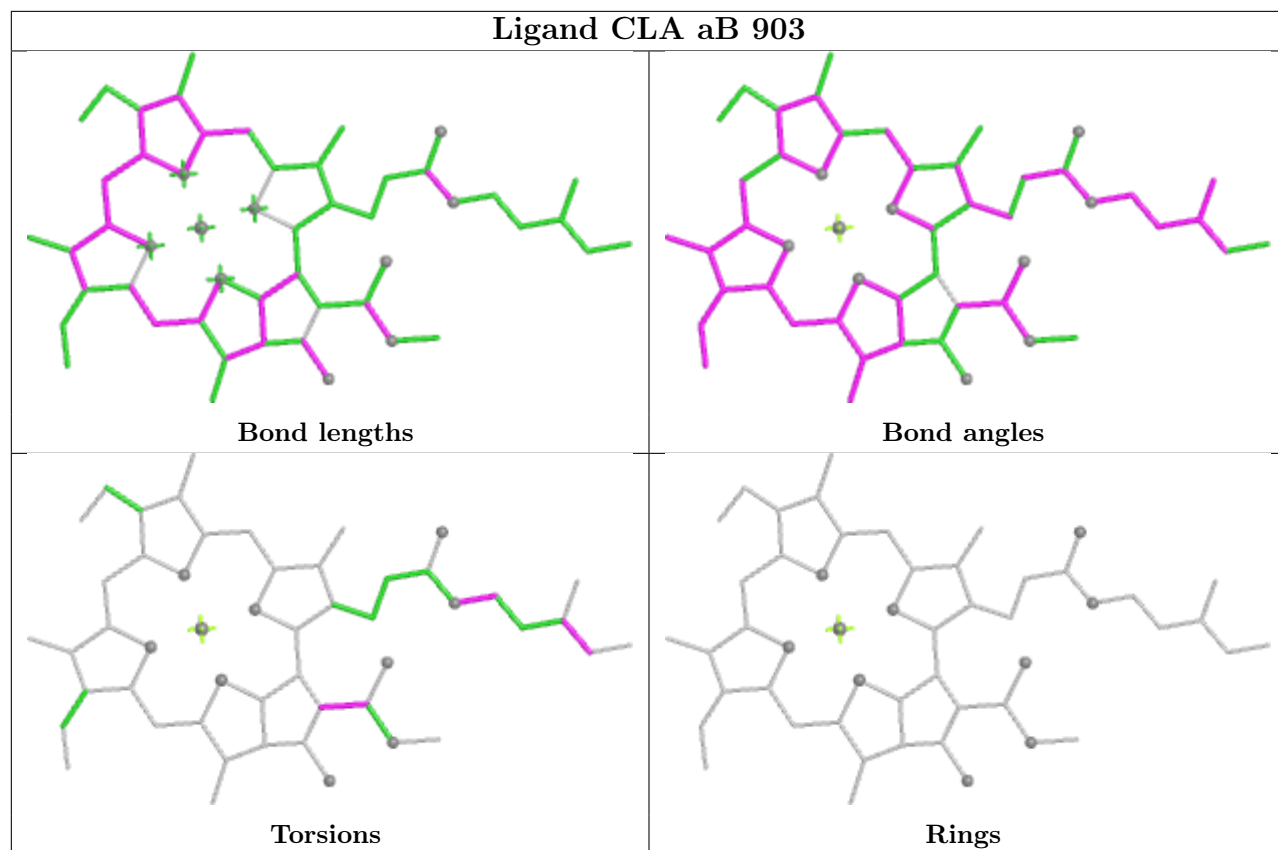


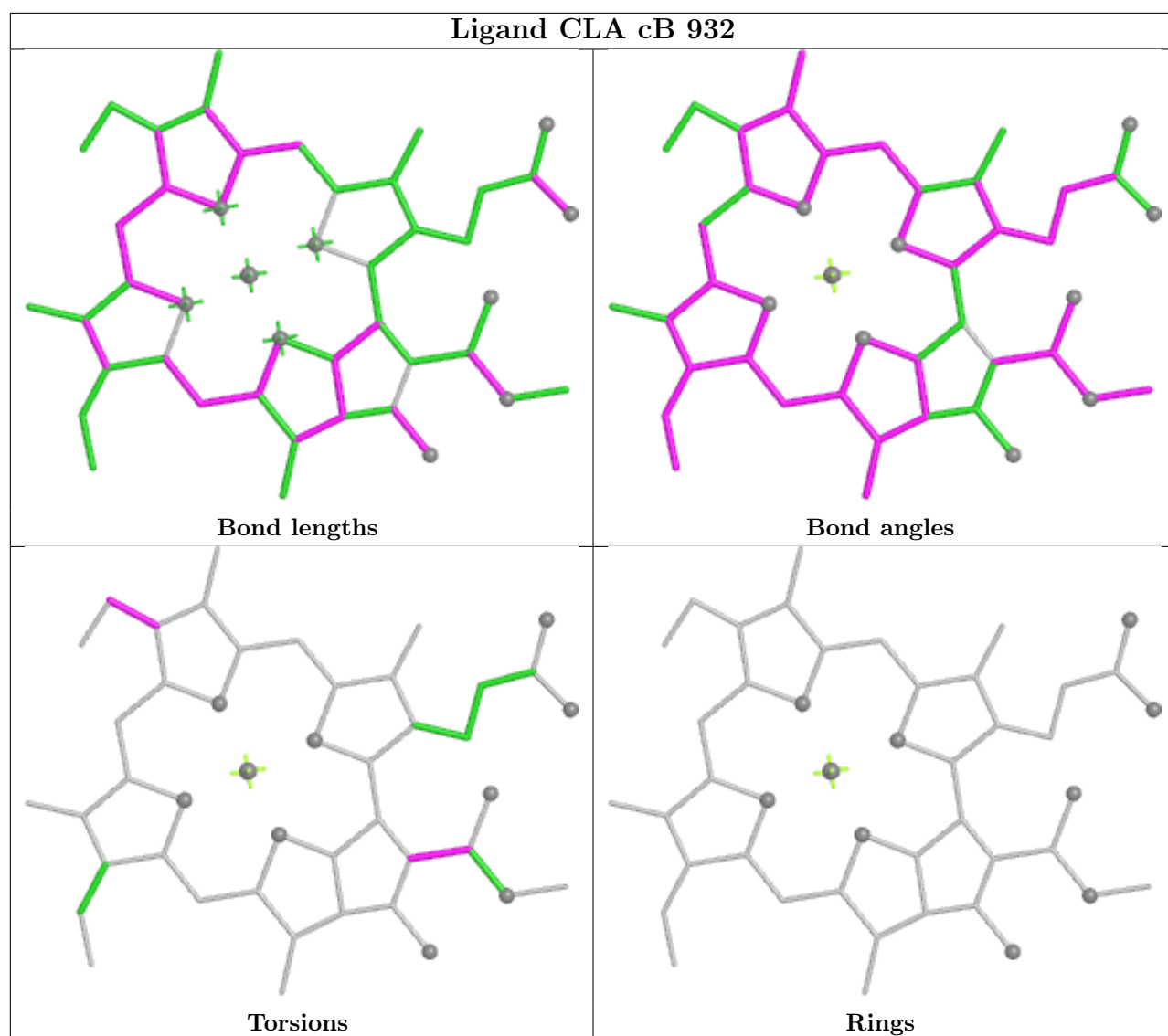


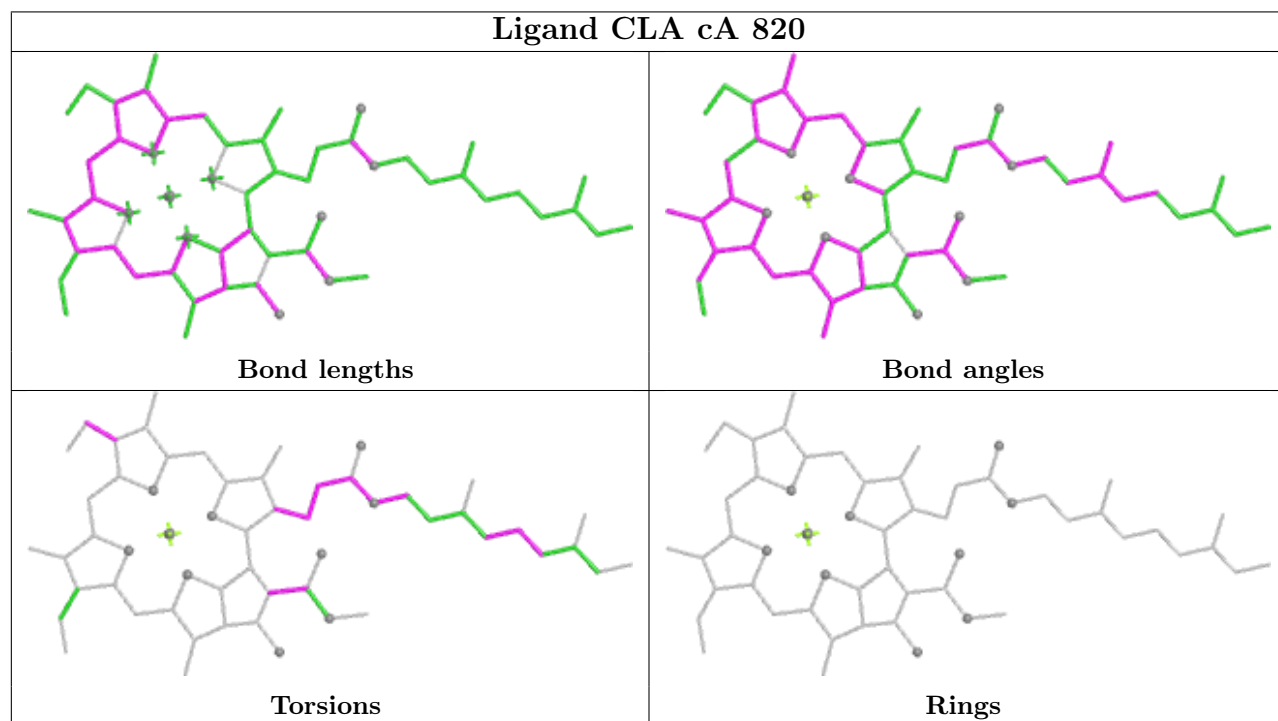
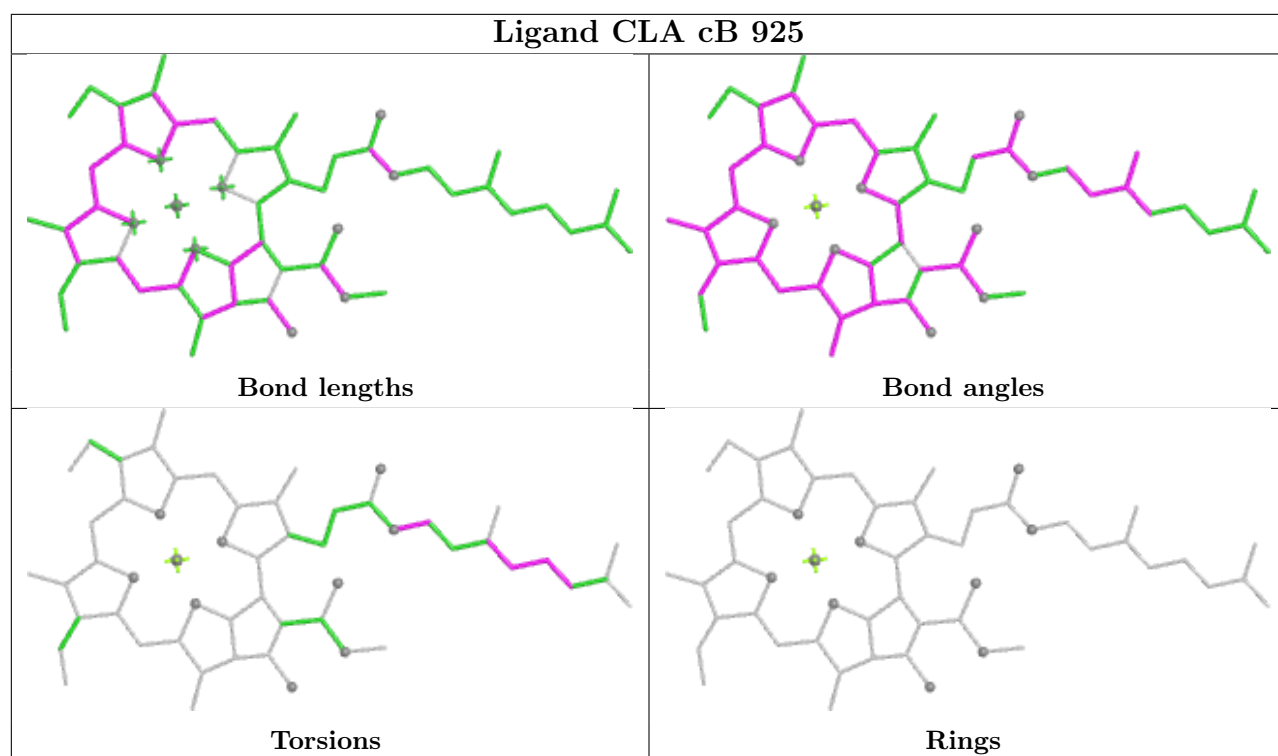


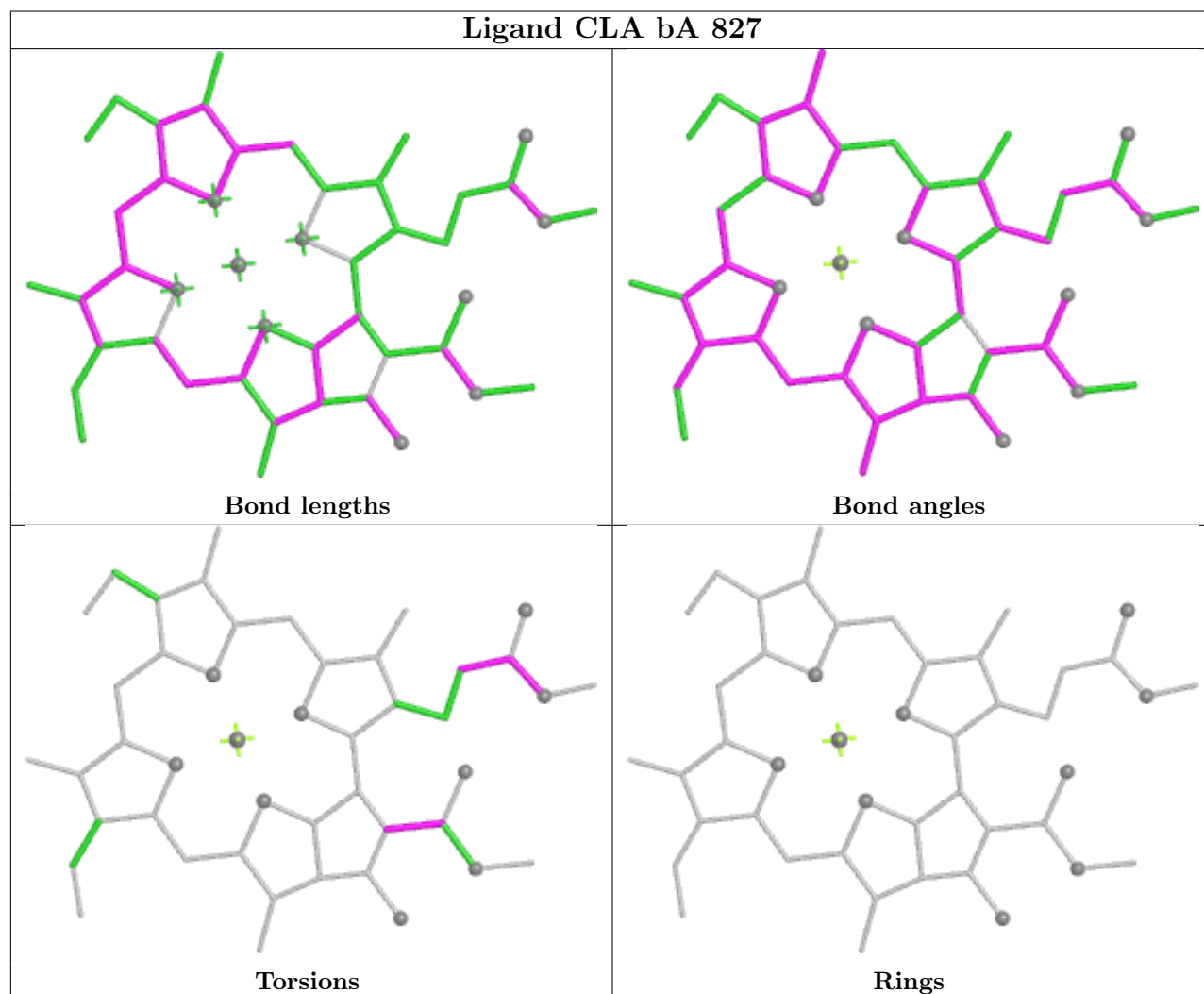
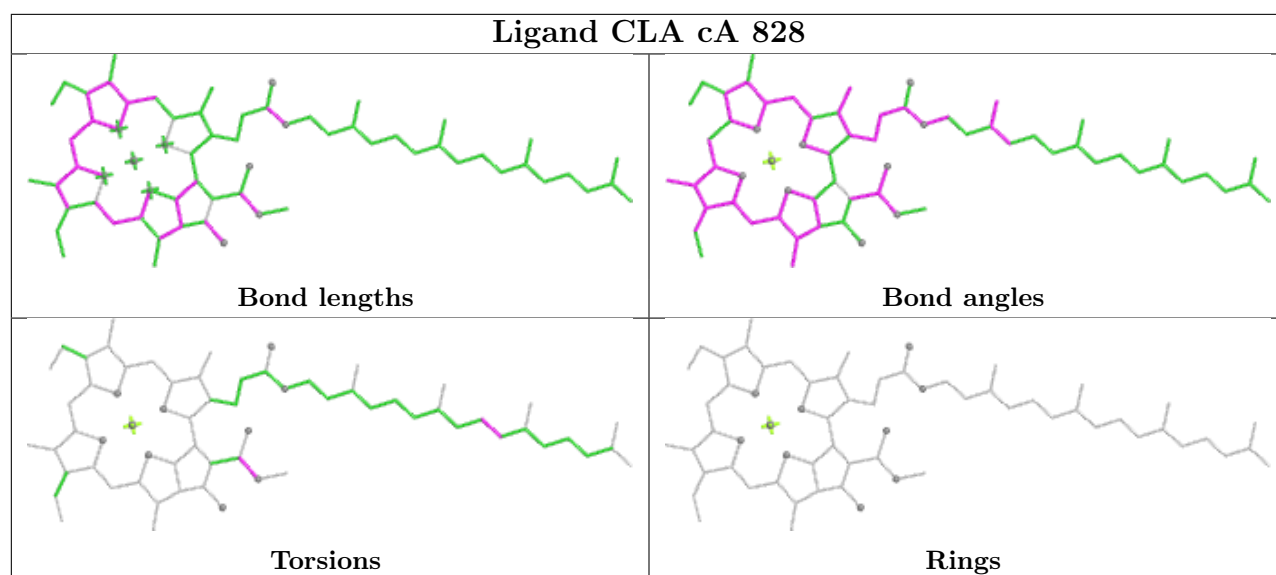


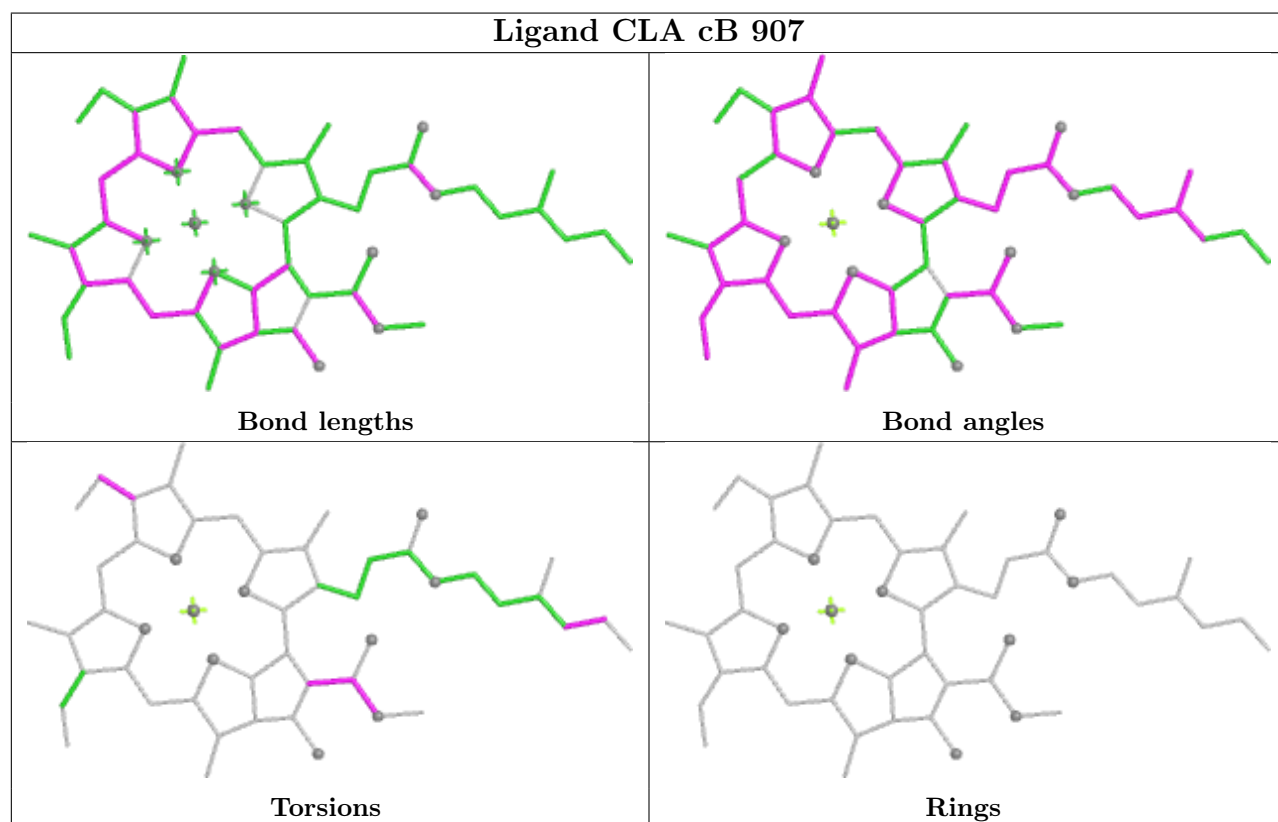
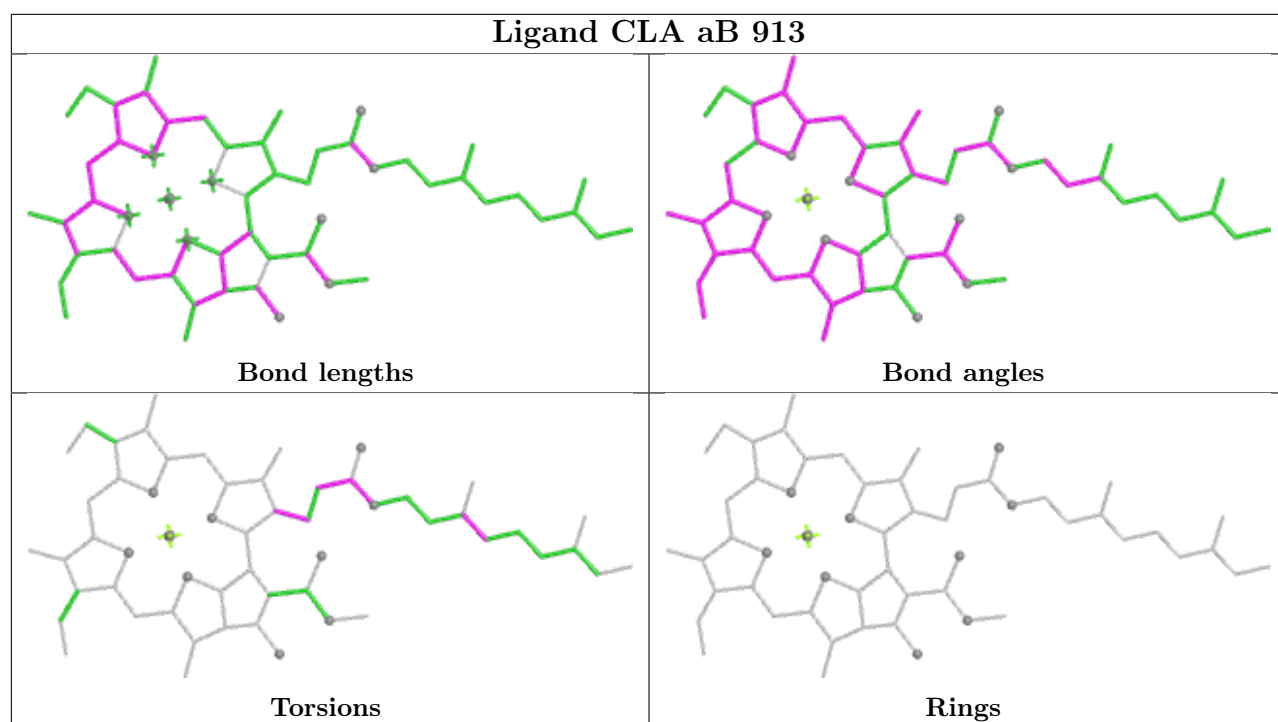


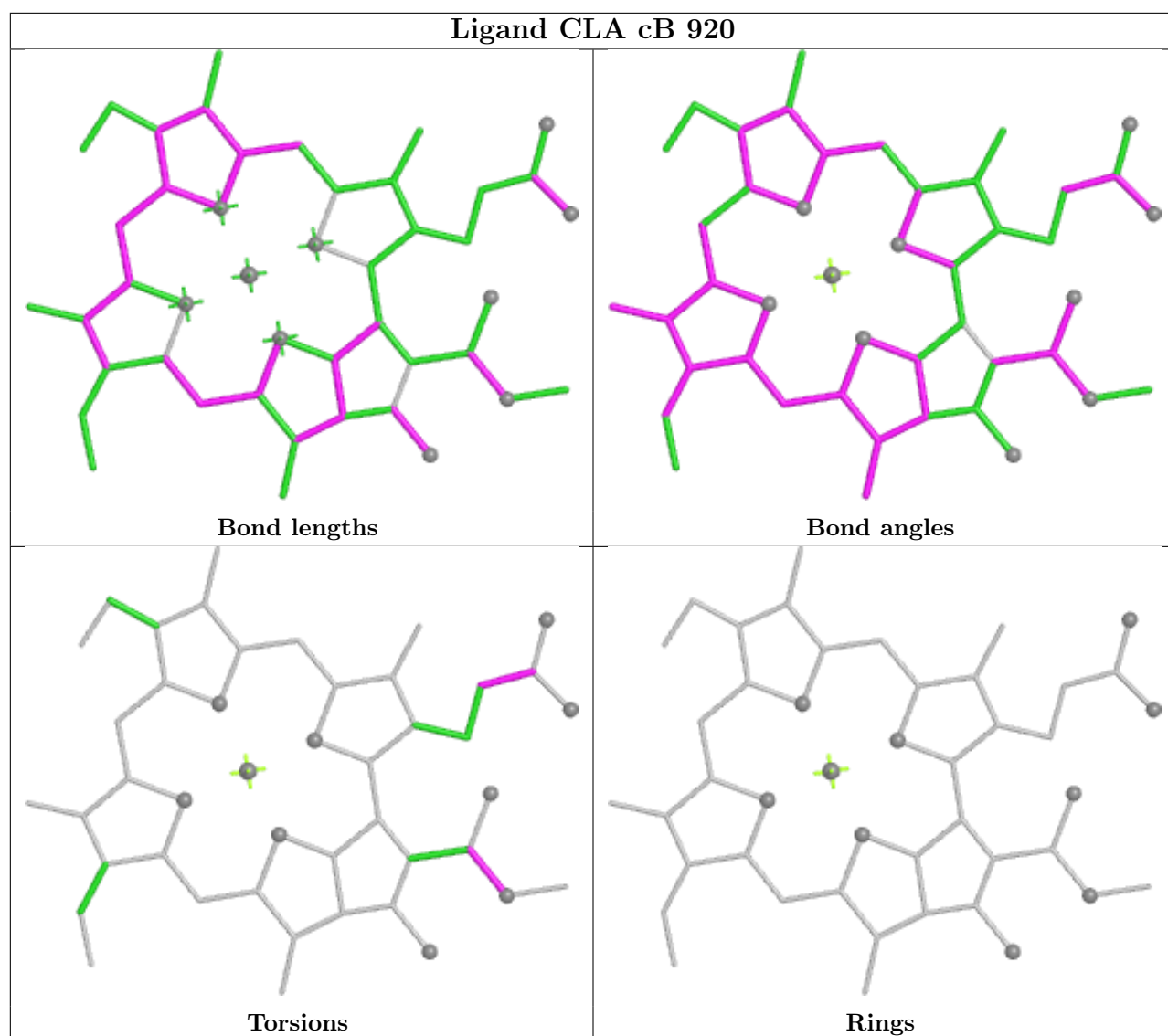


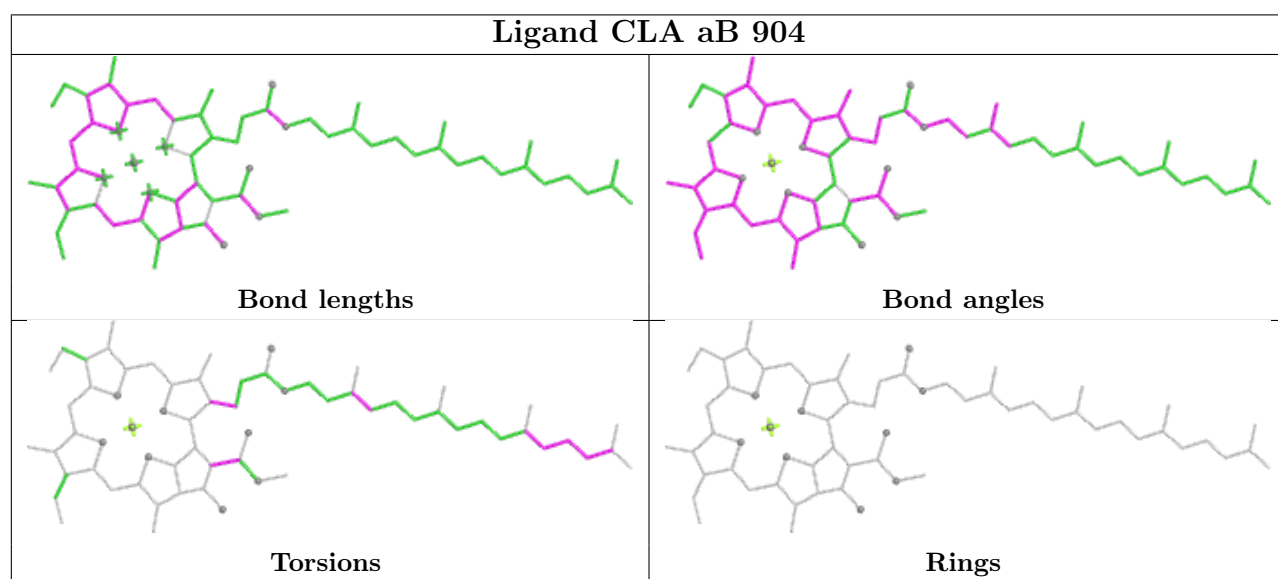
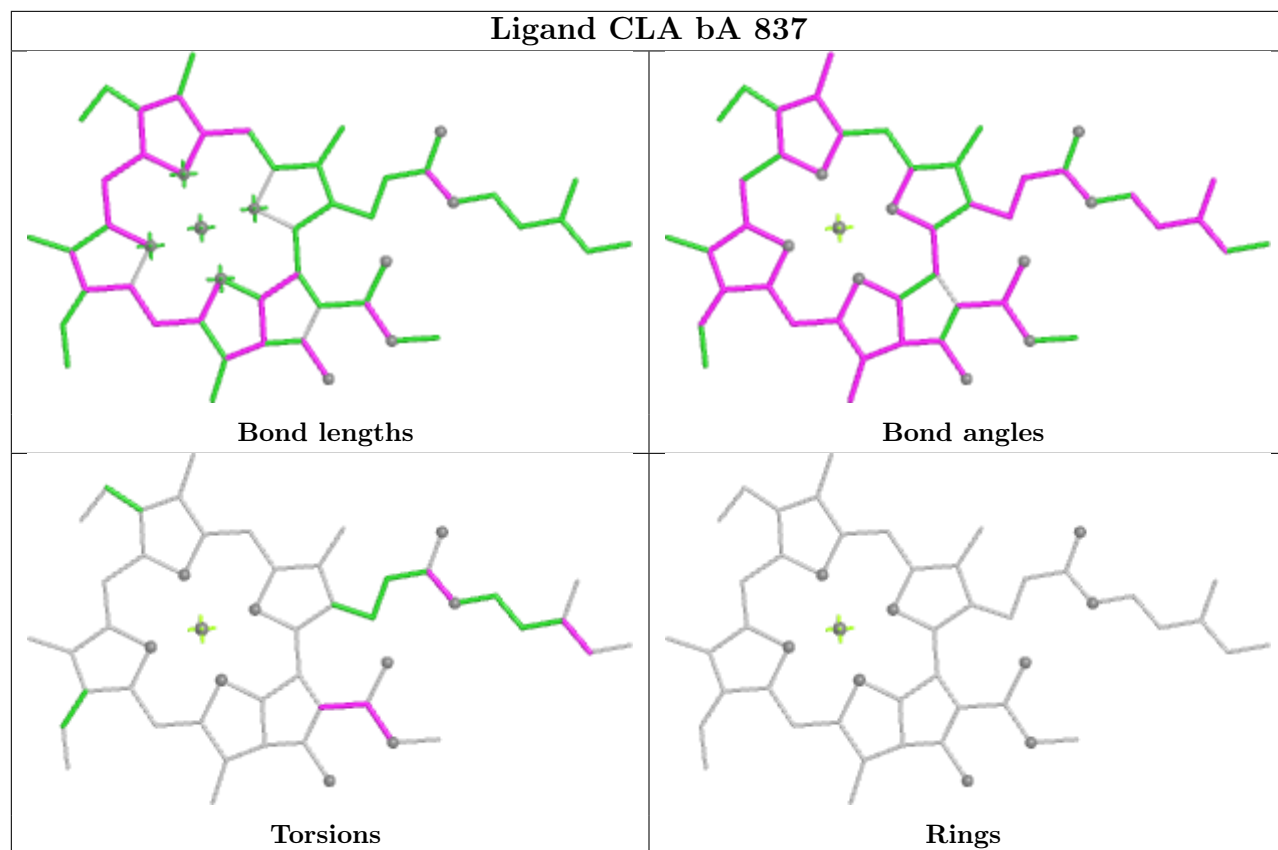


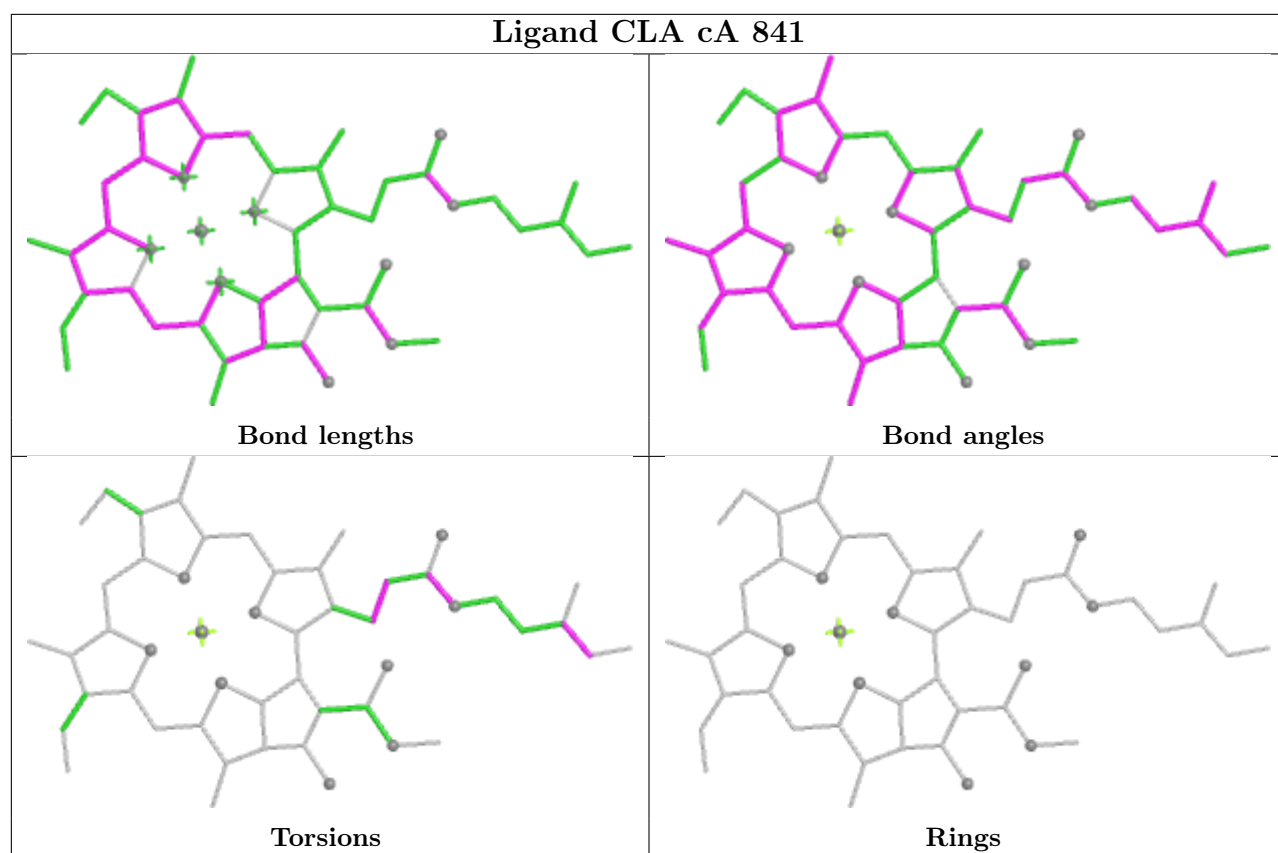


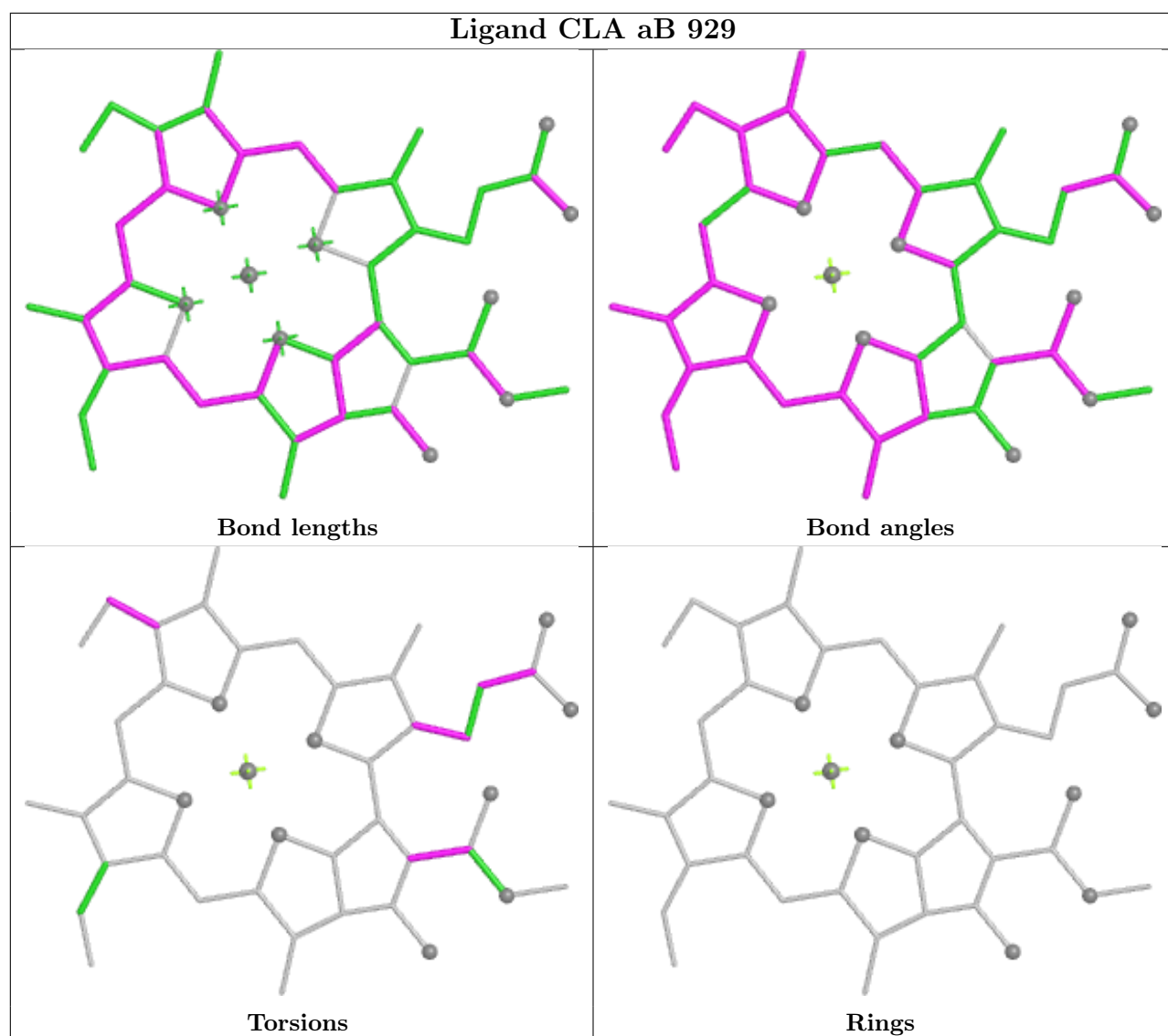


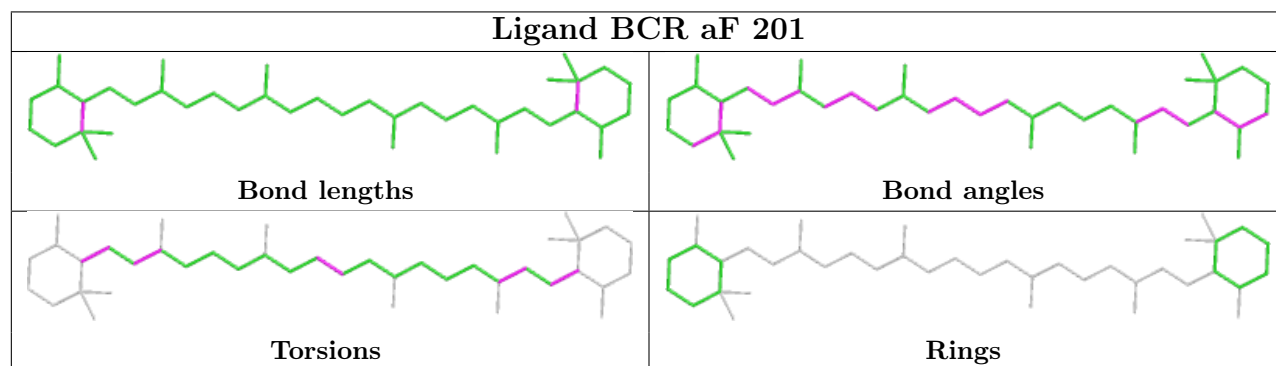
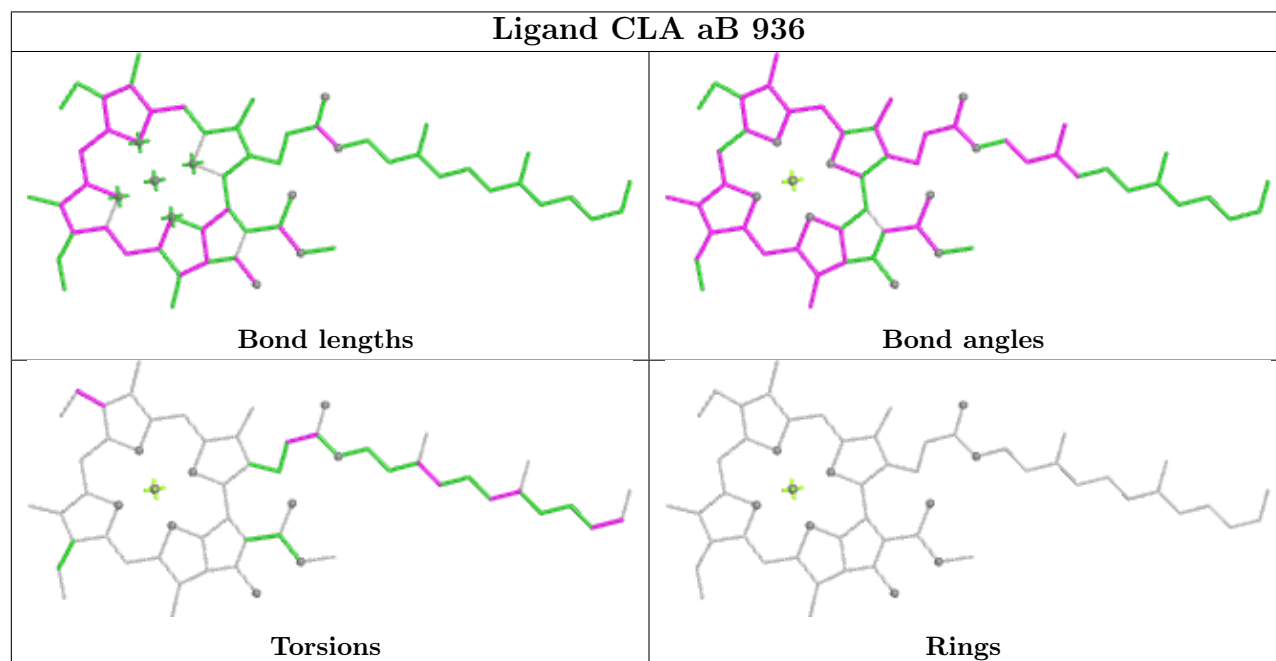
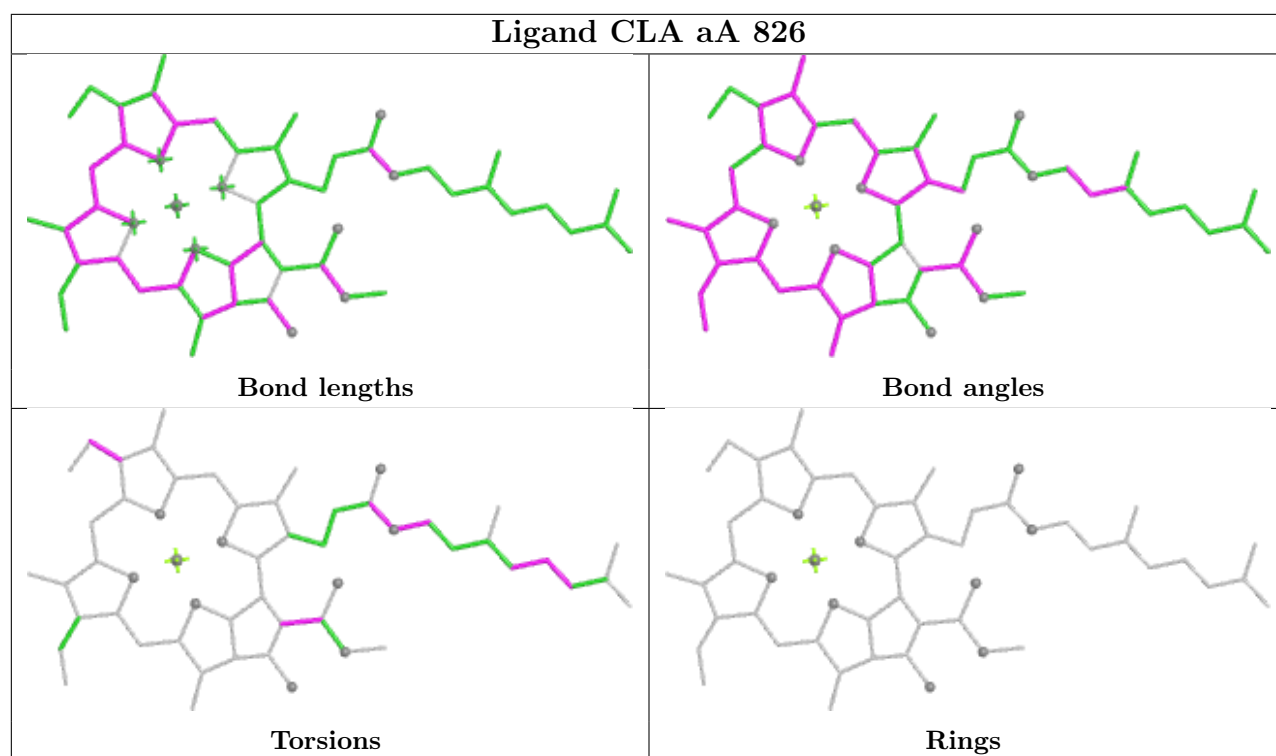


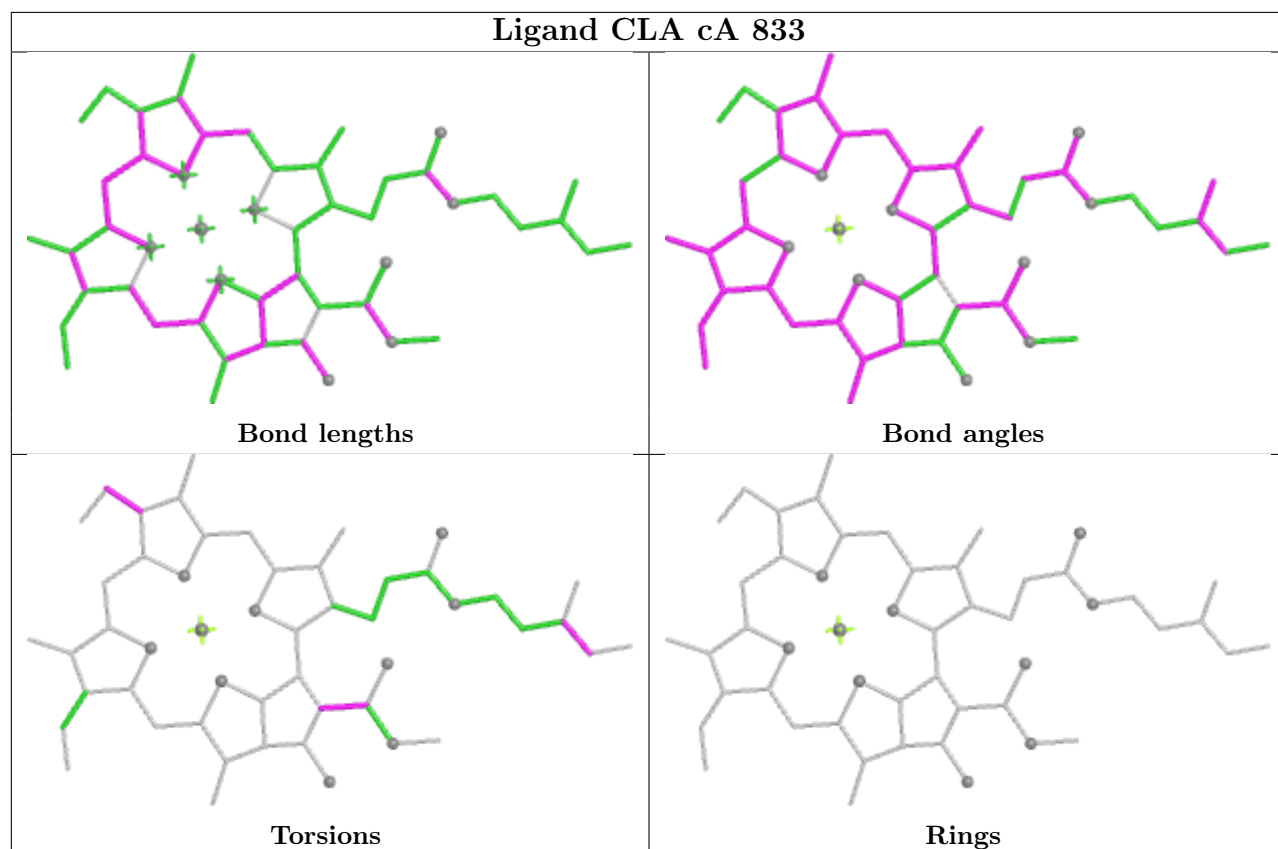
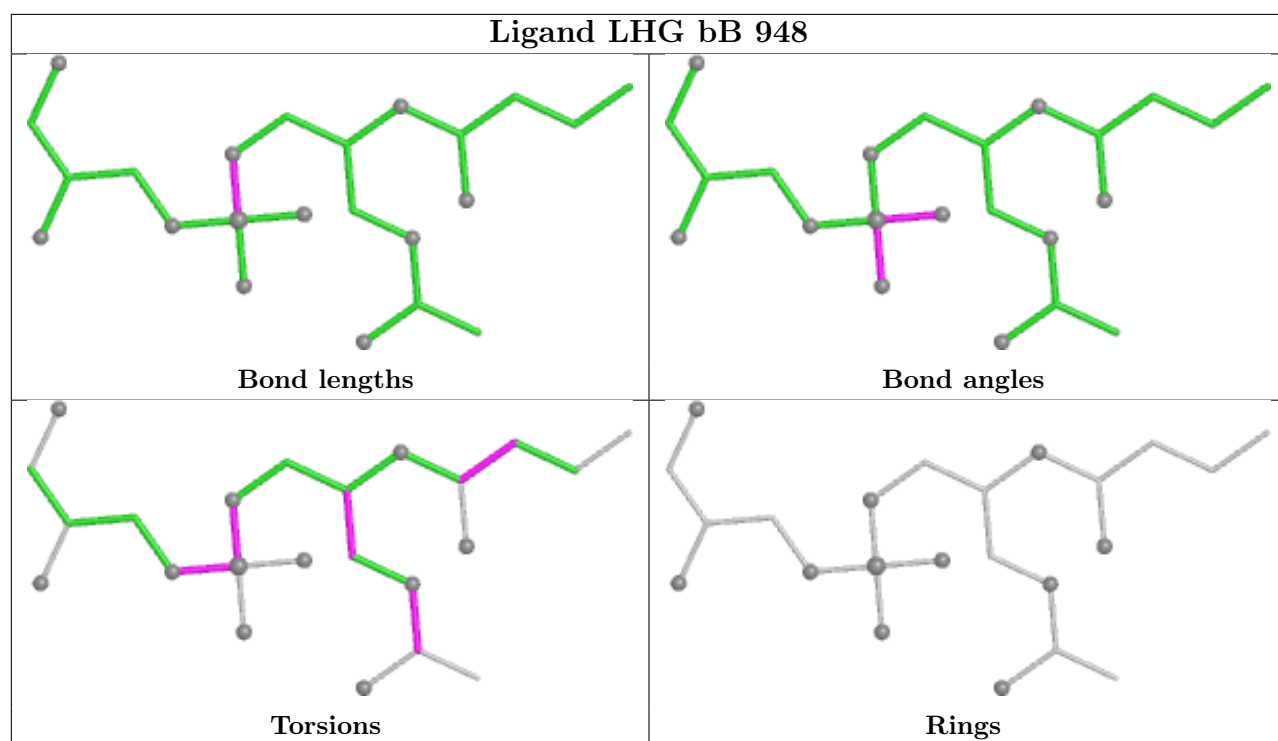


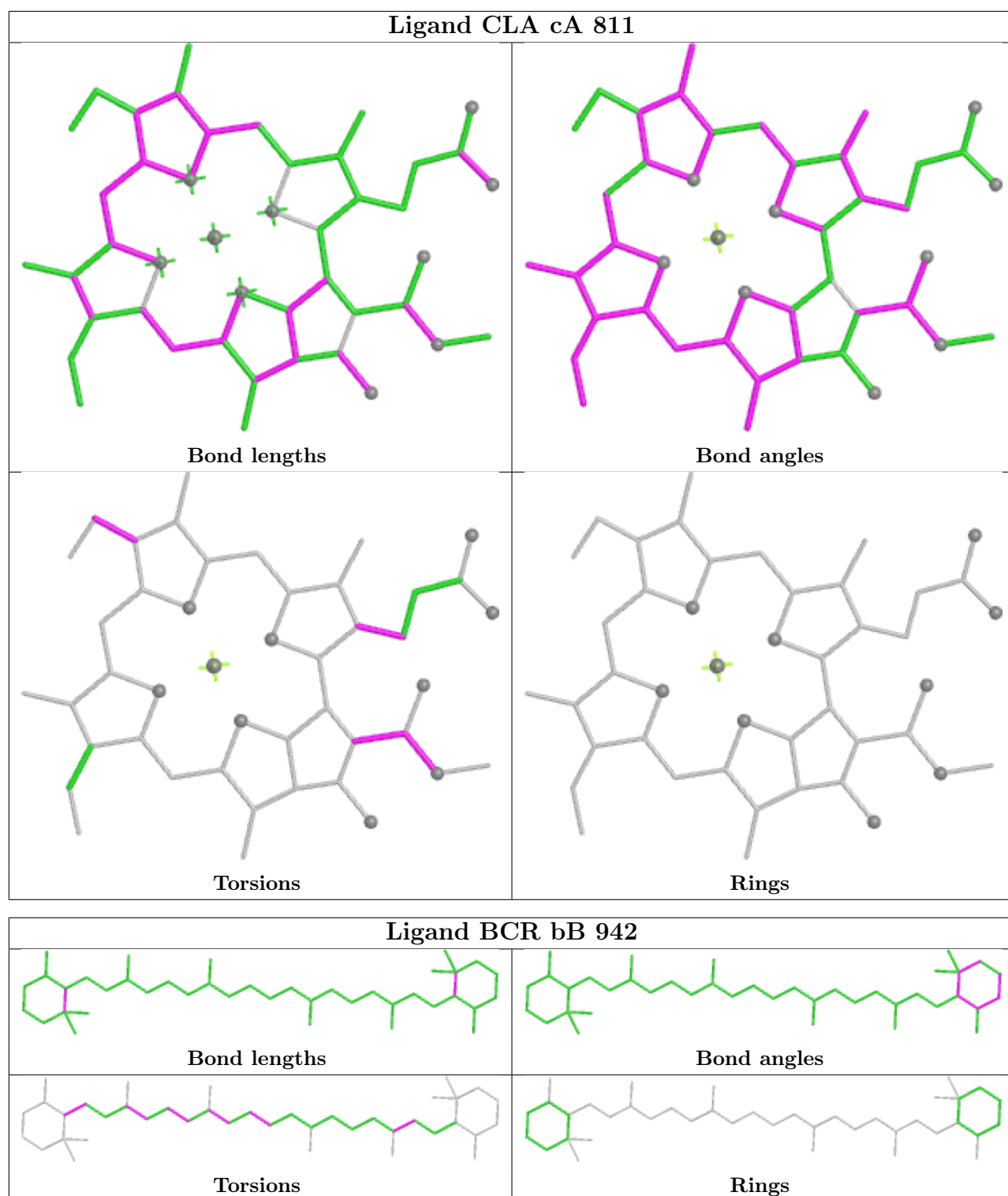


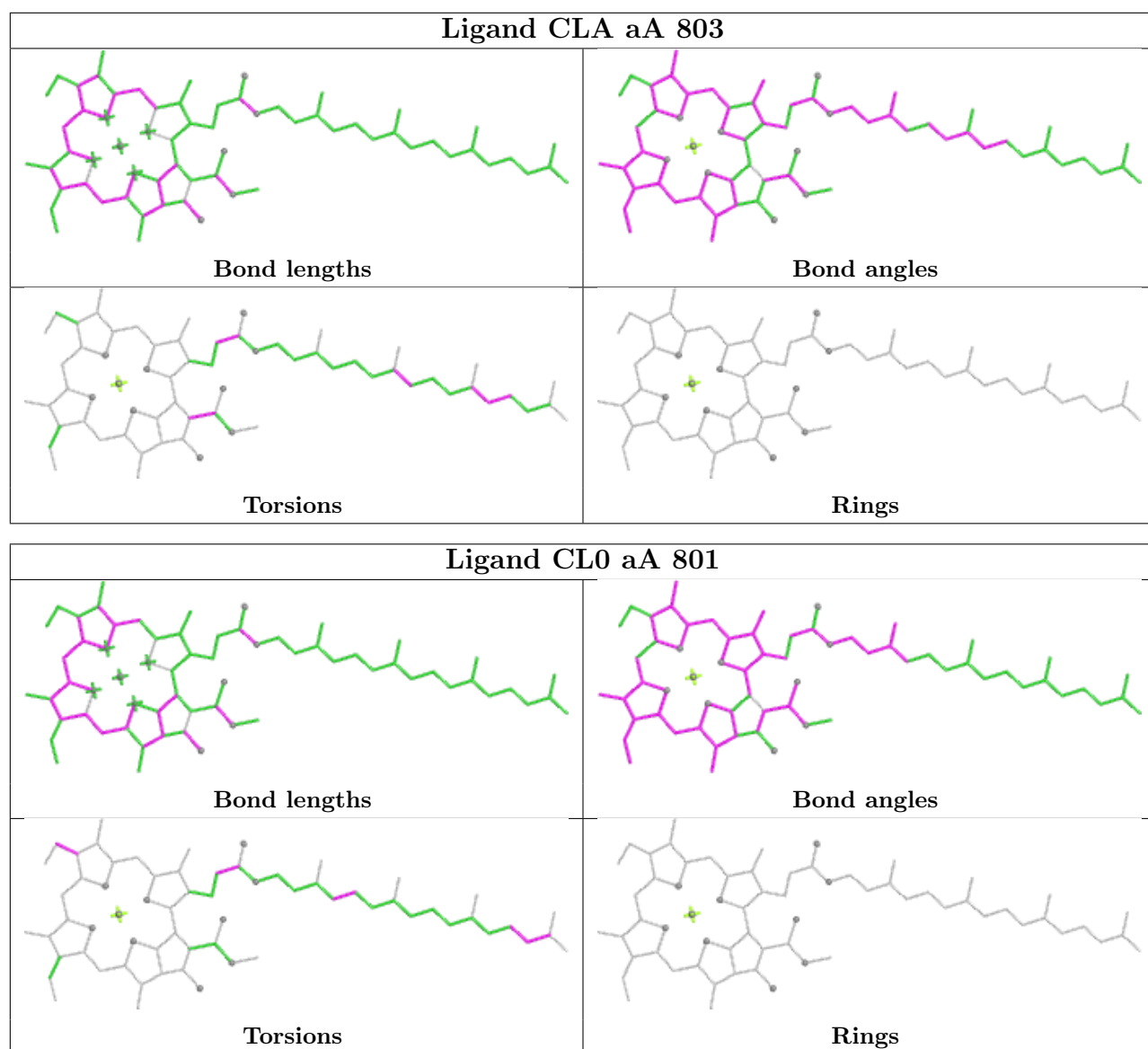


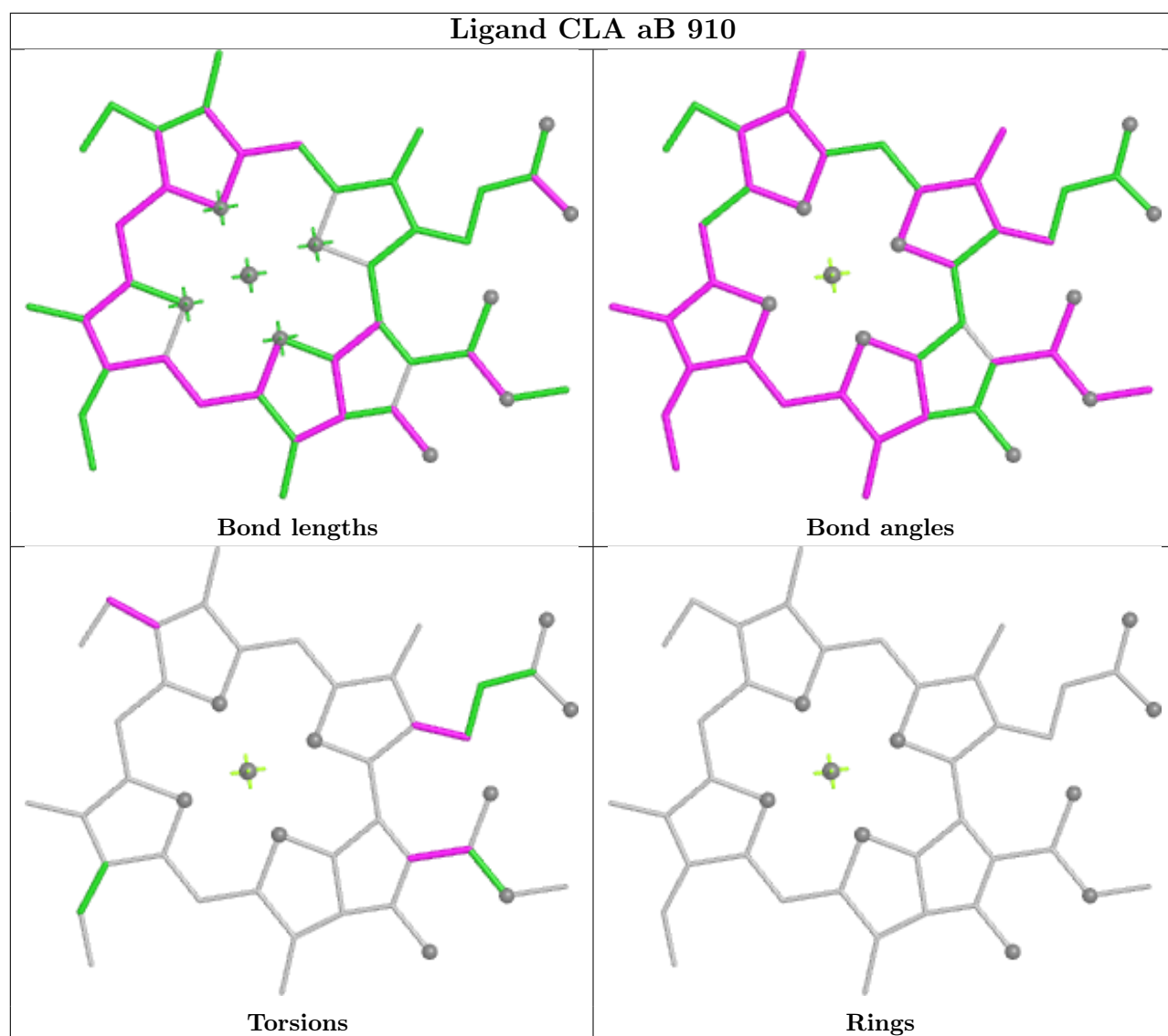


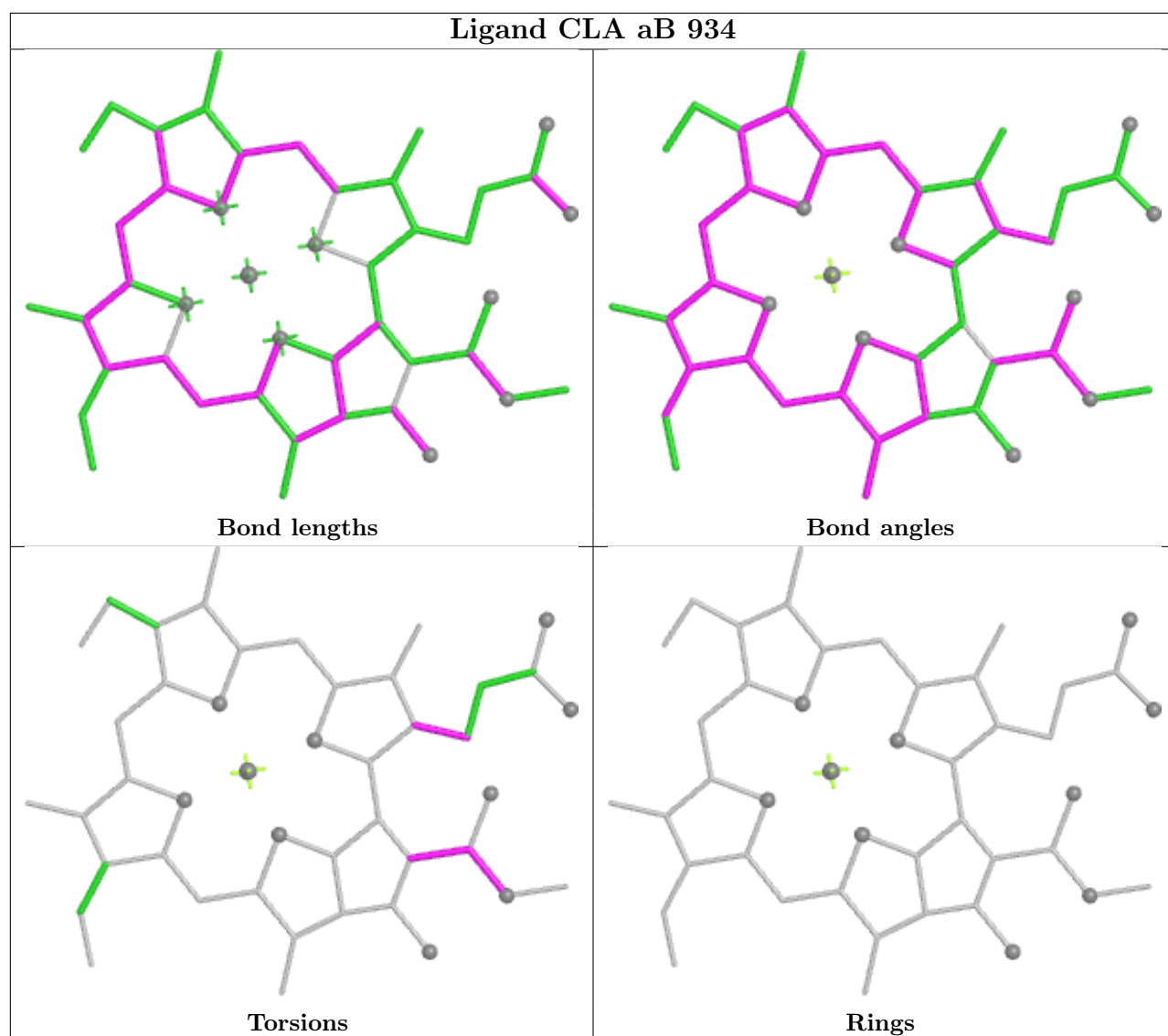




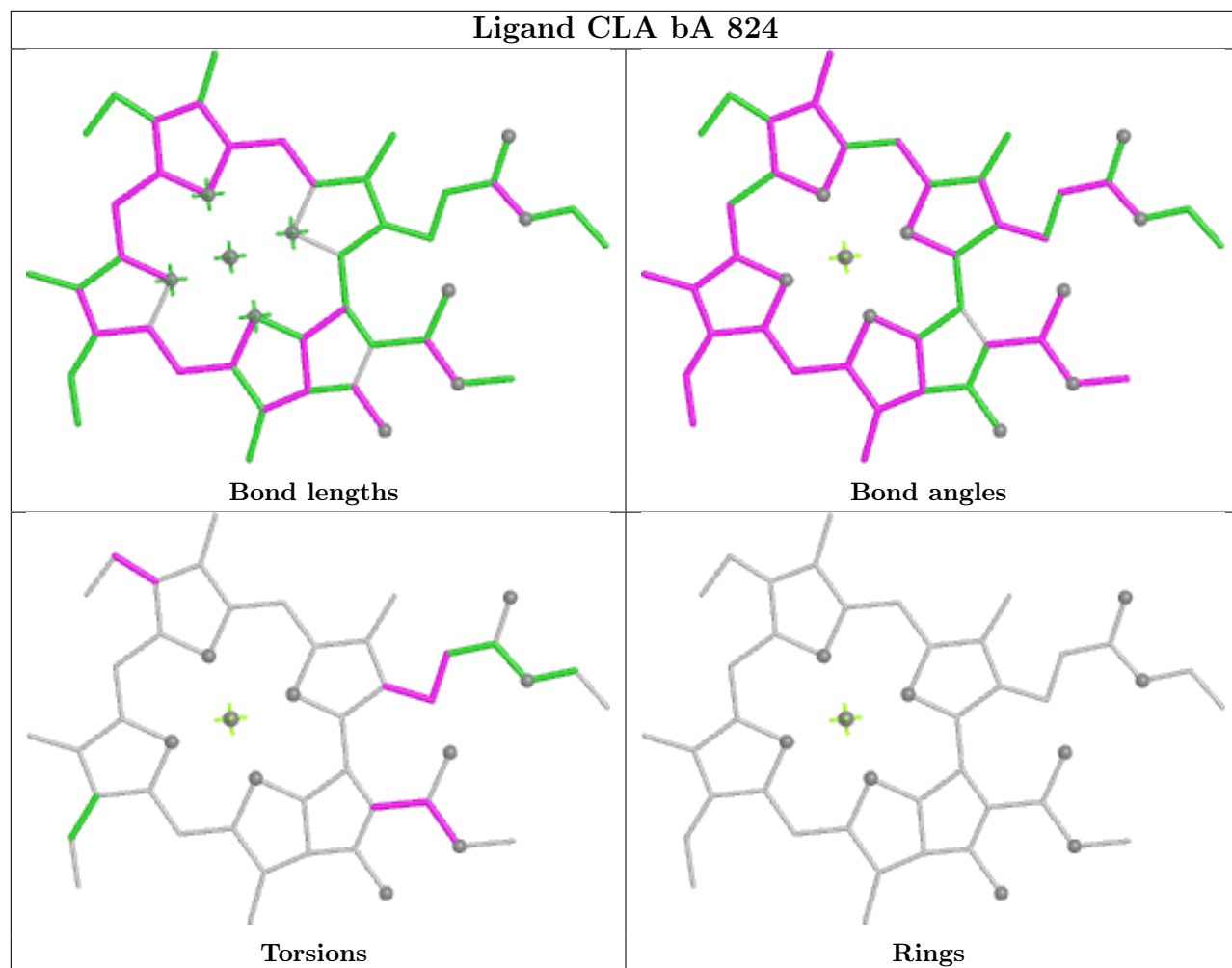


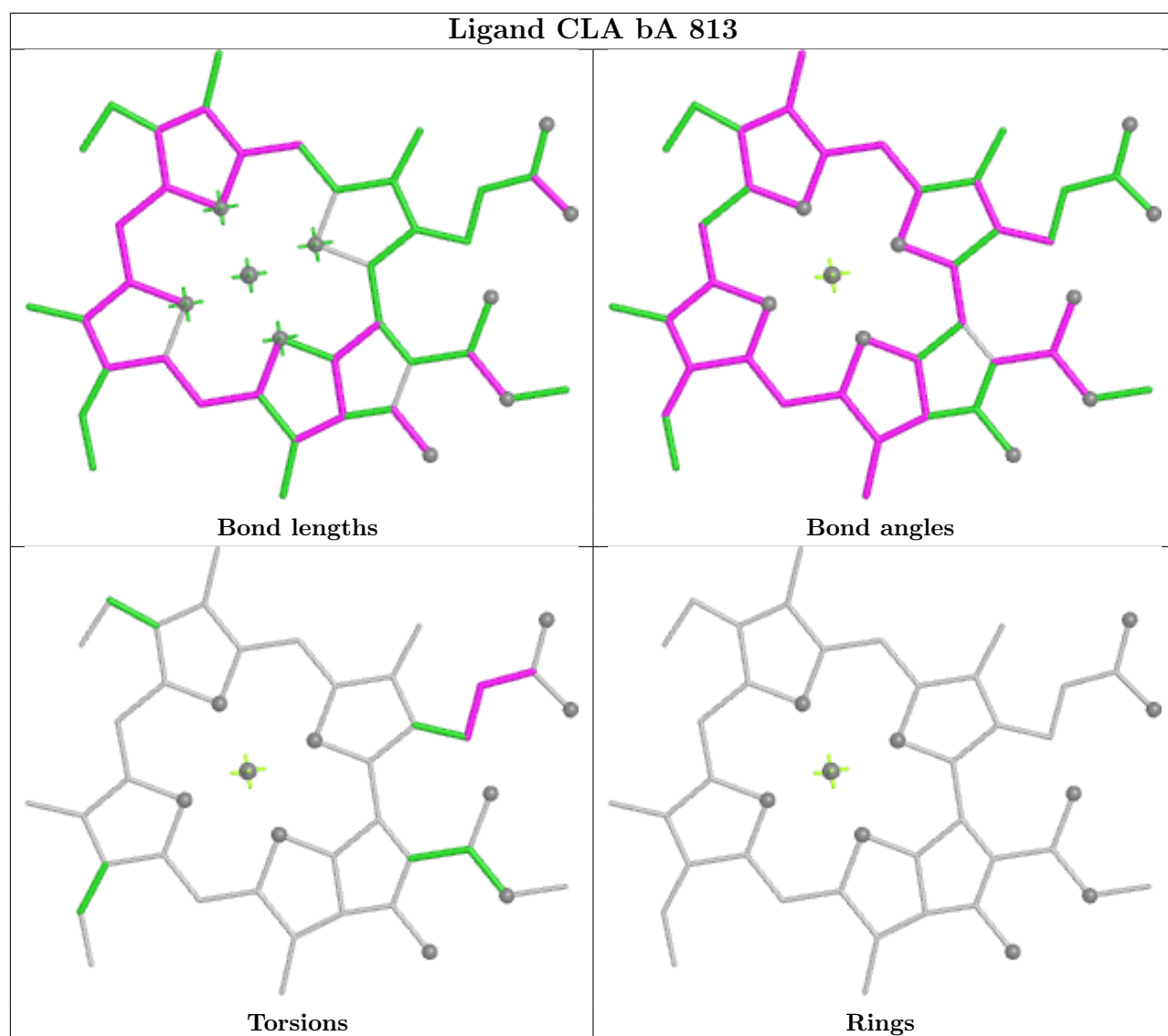


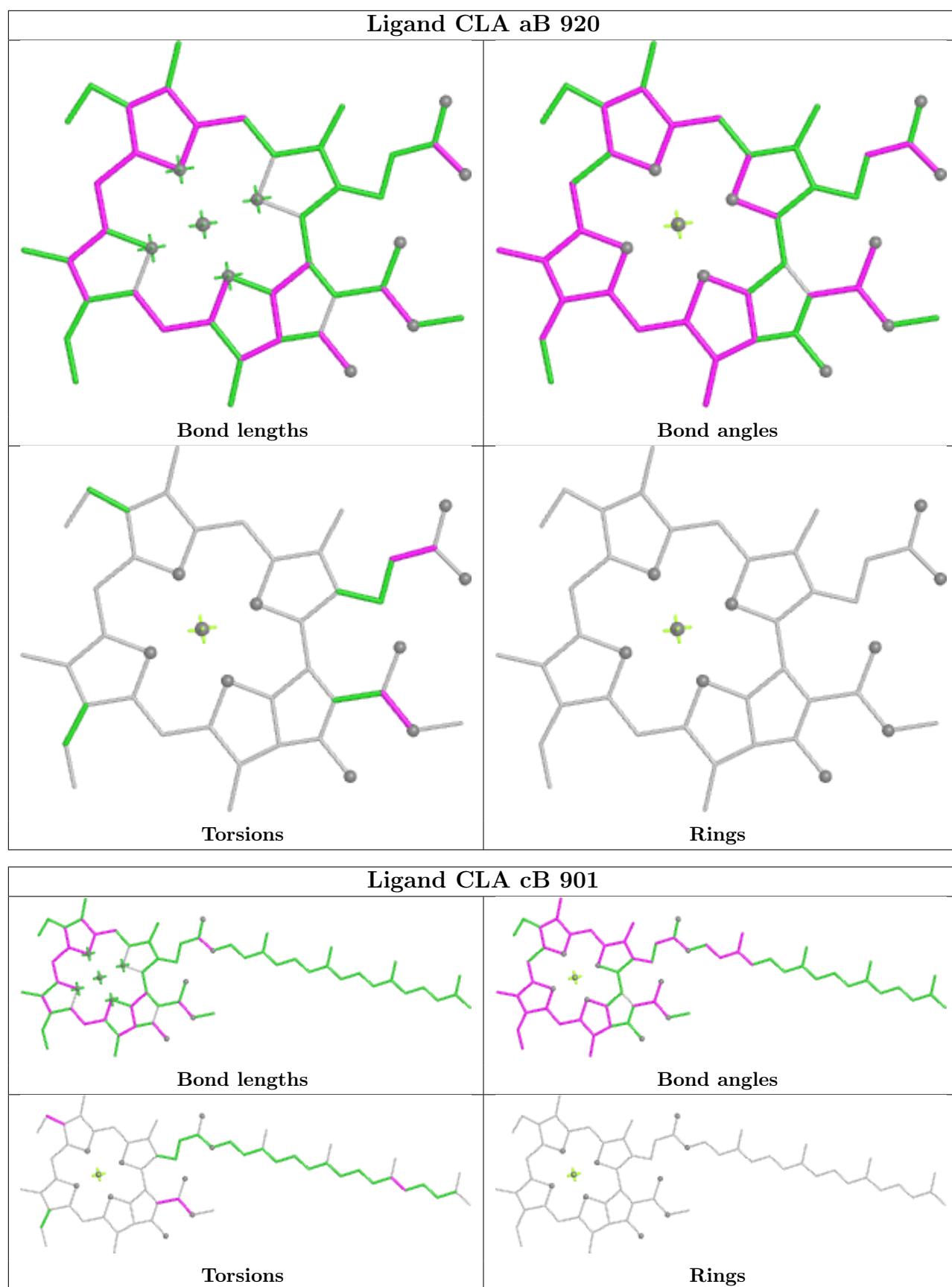


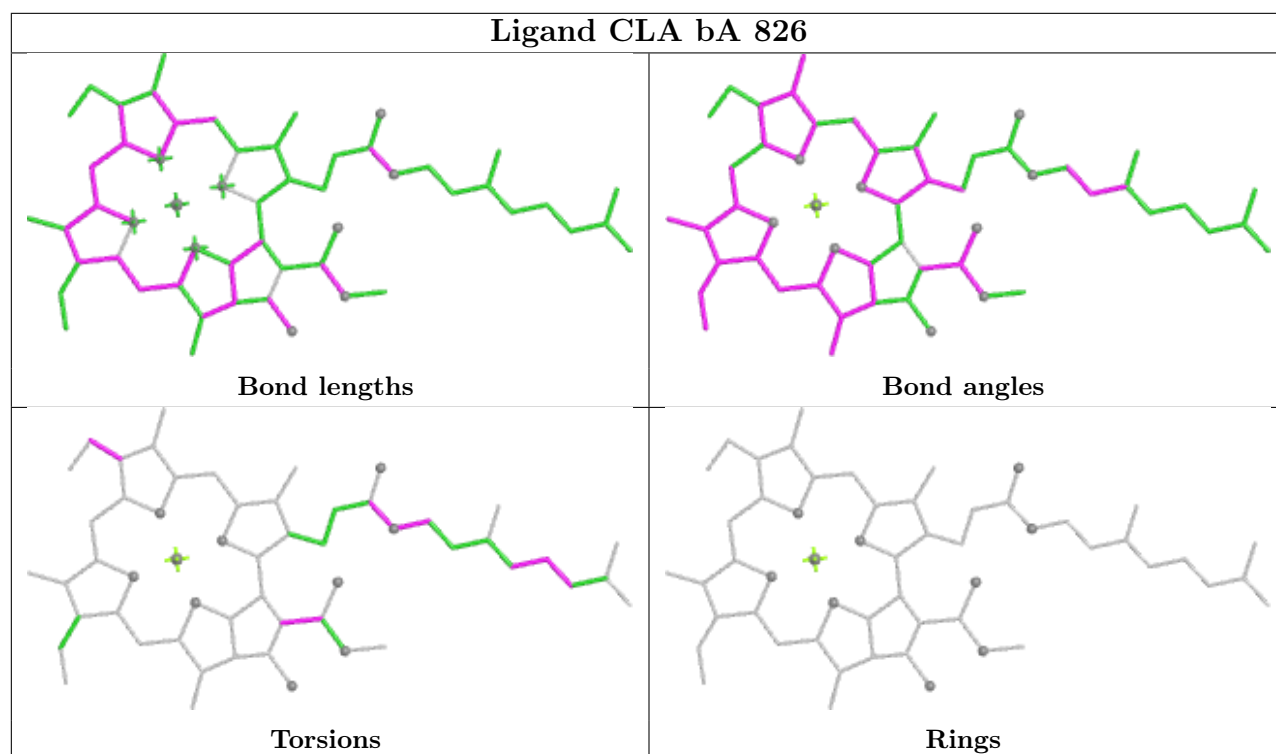
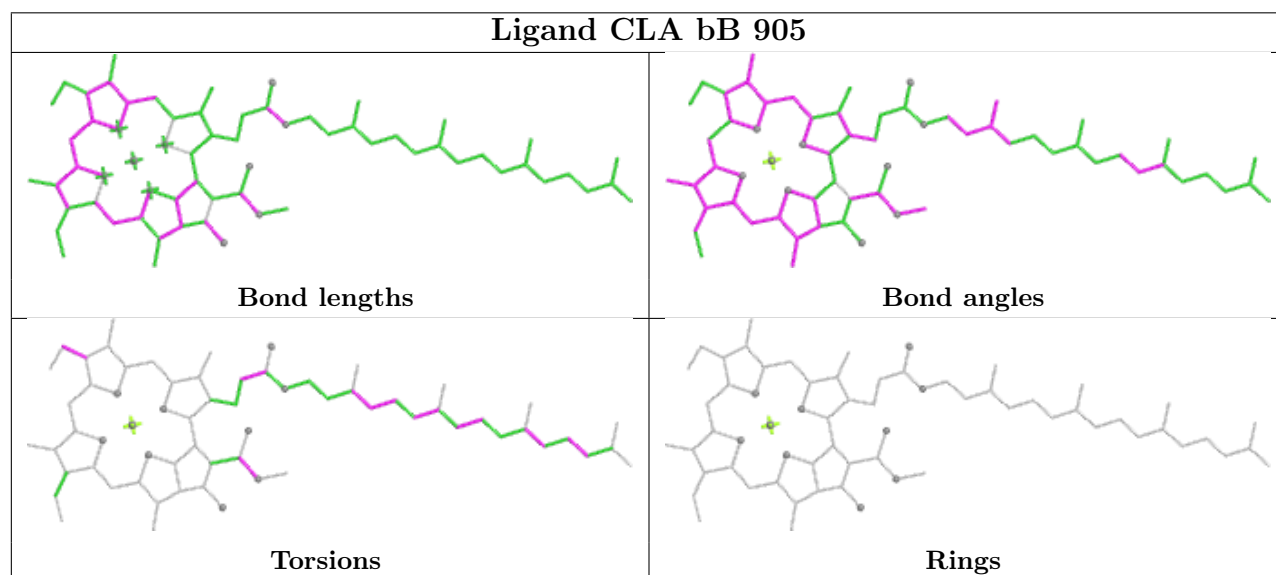
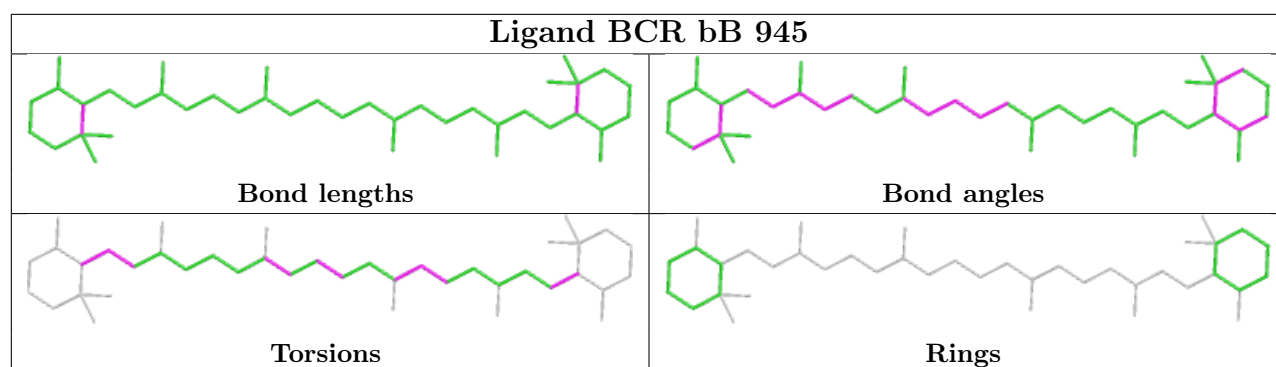


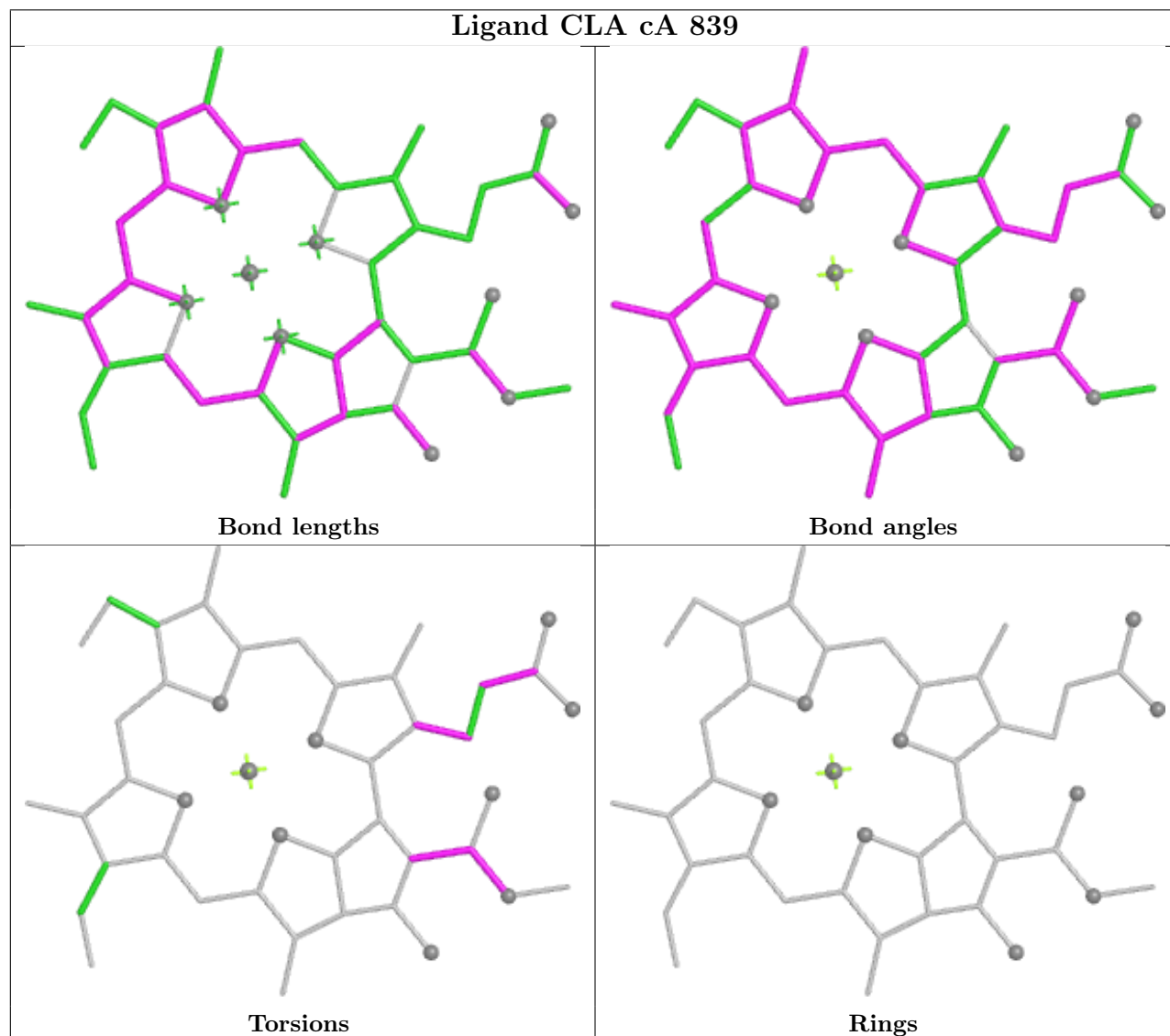
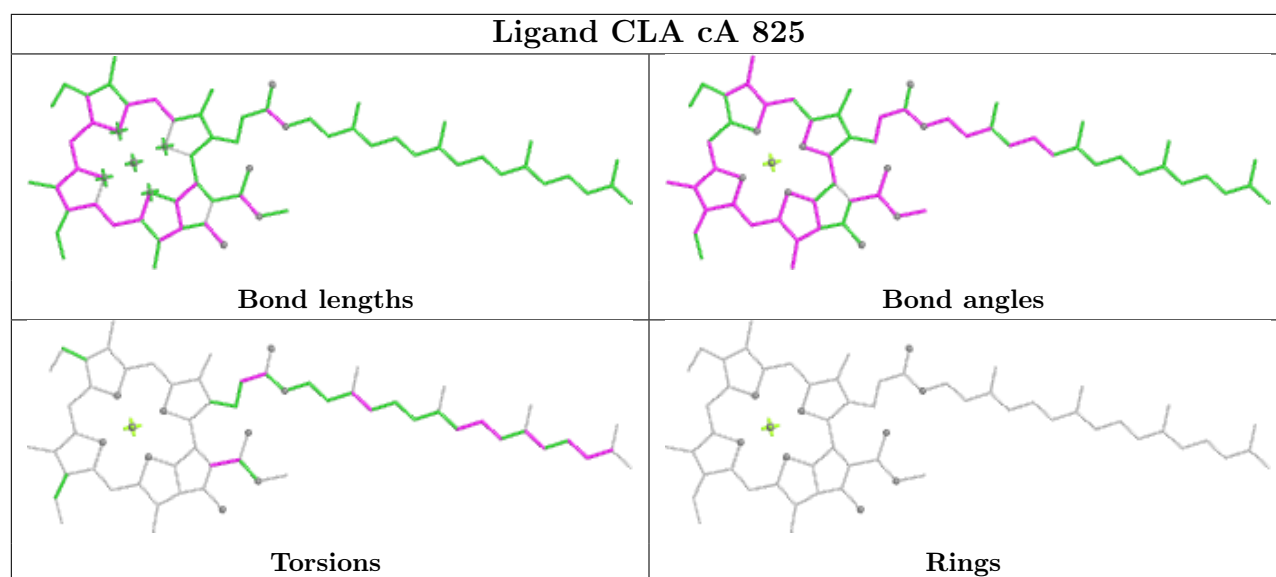
Ligand CLA bA 824

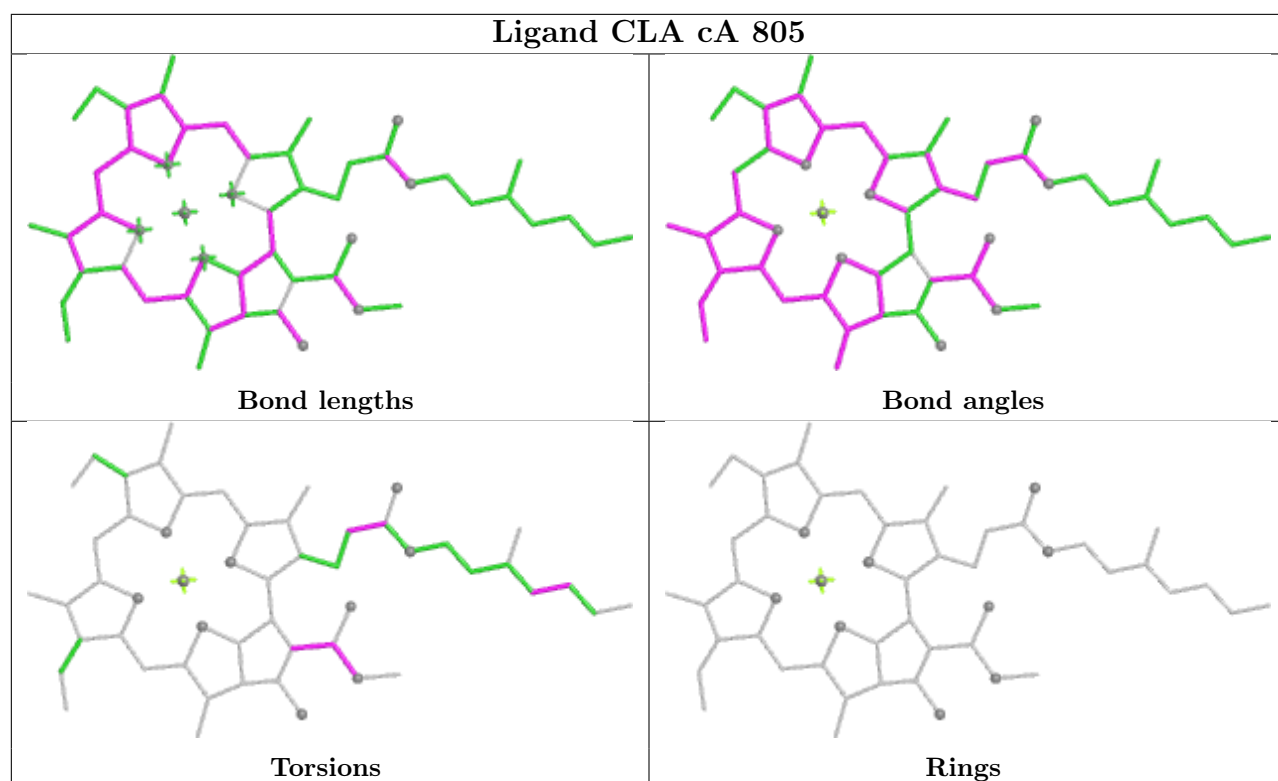




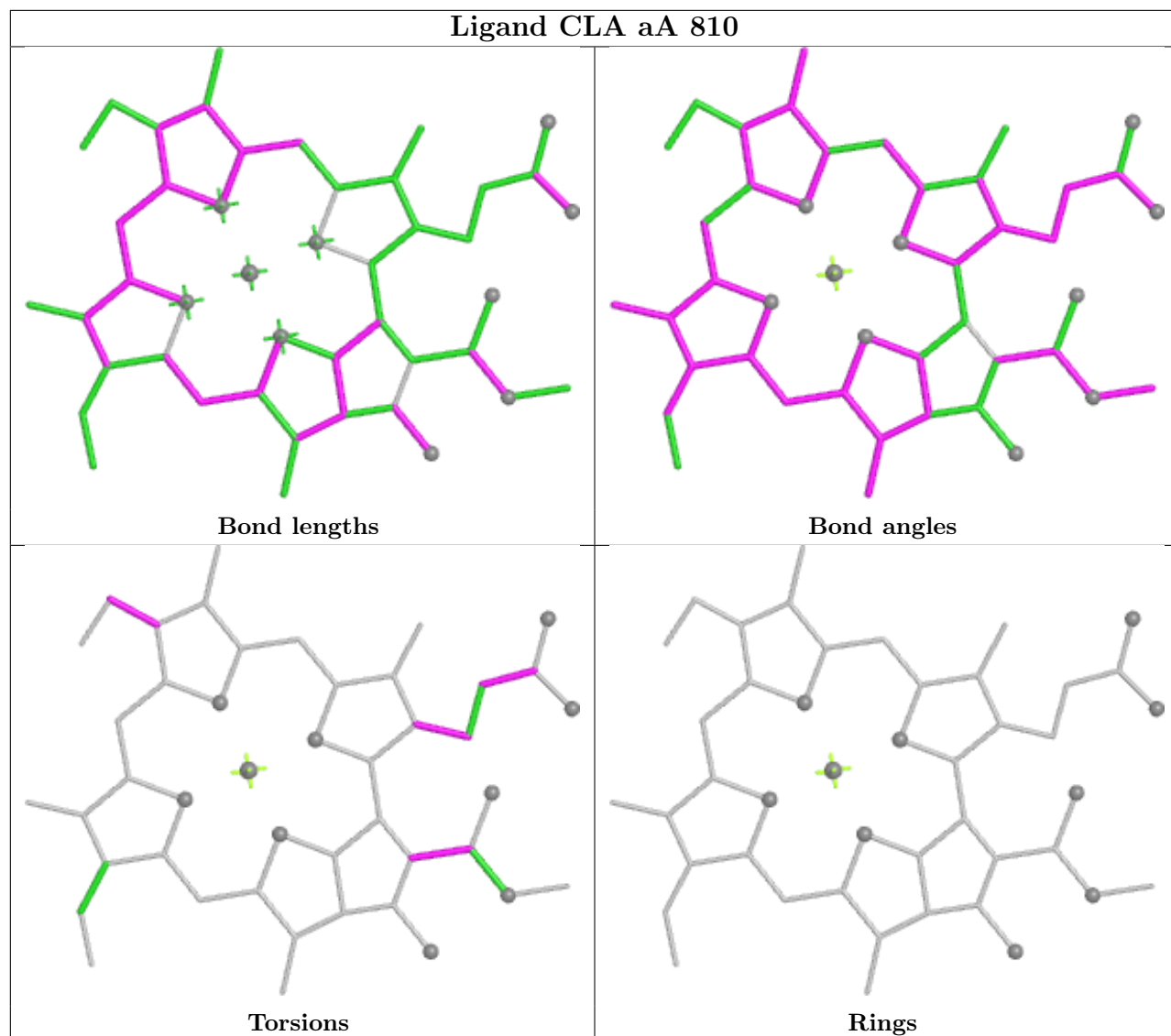




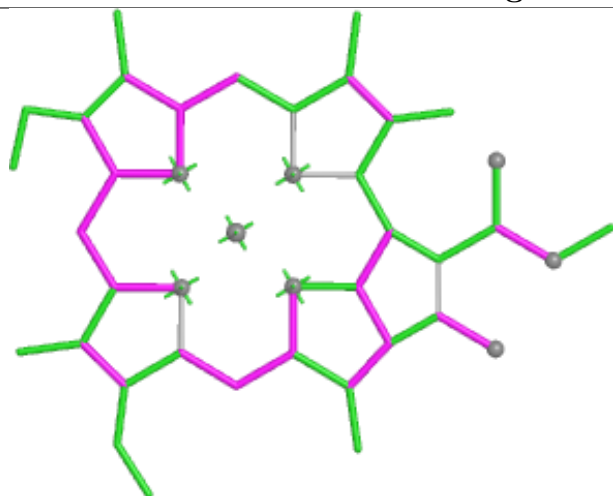




Ligand CLA aA 810



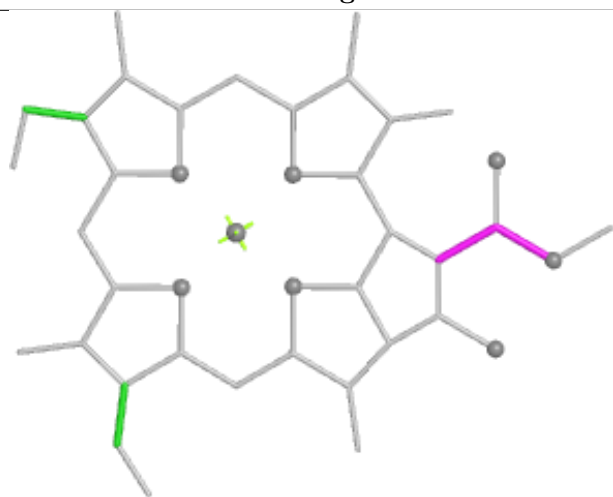
Ligand CLA aB 949



Bond lengths



Bond angles

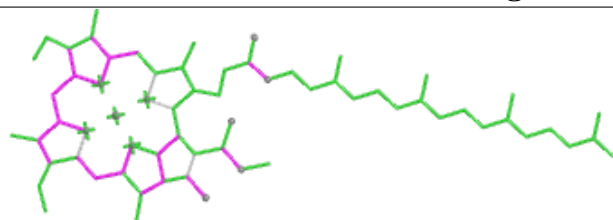


Torsions

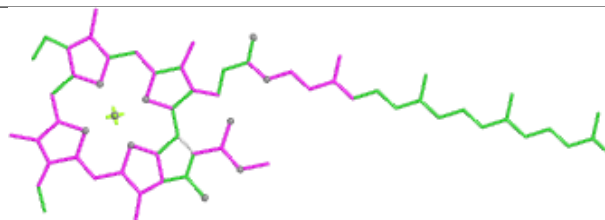


Rings

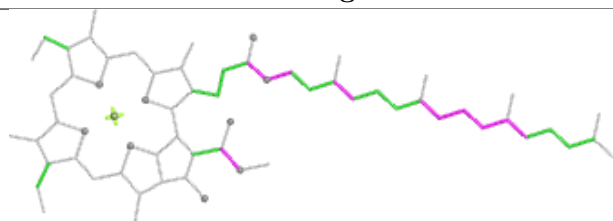
Ligand CLA cA 842



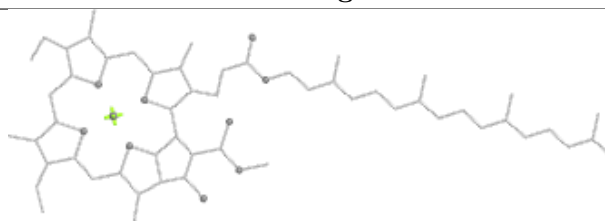
Bond lengths



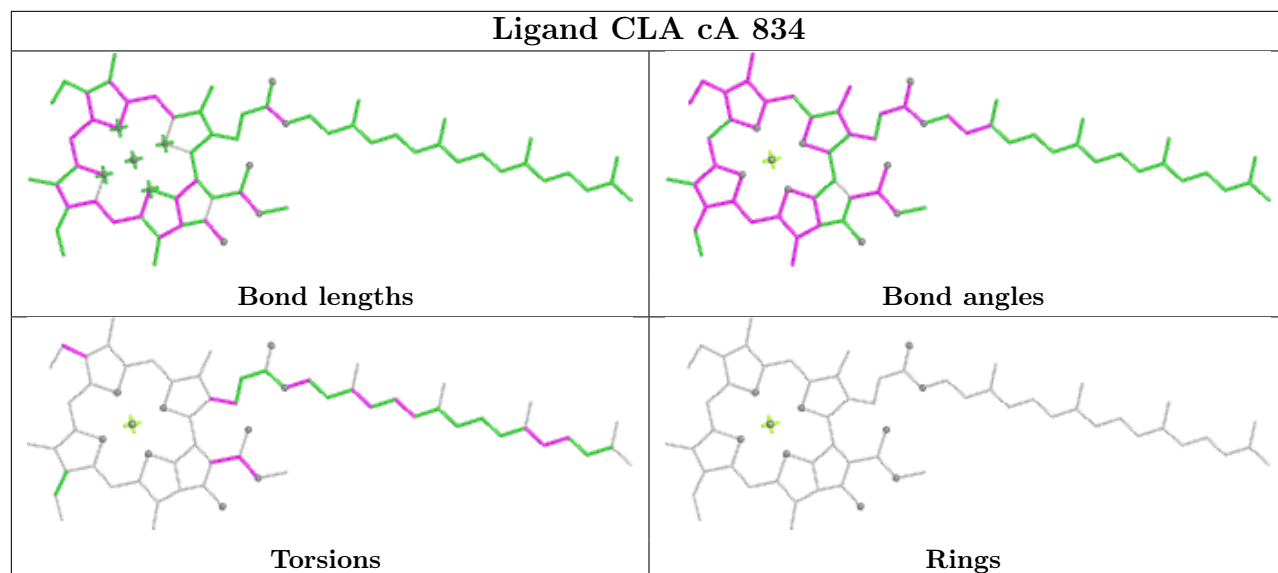
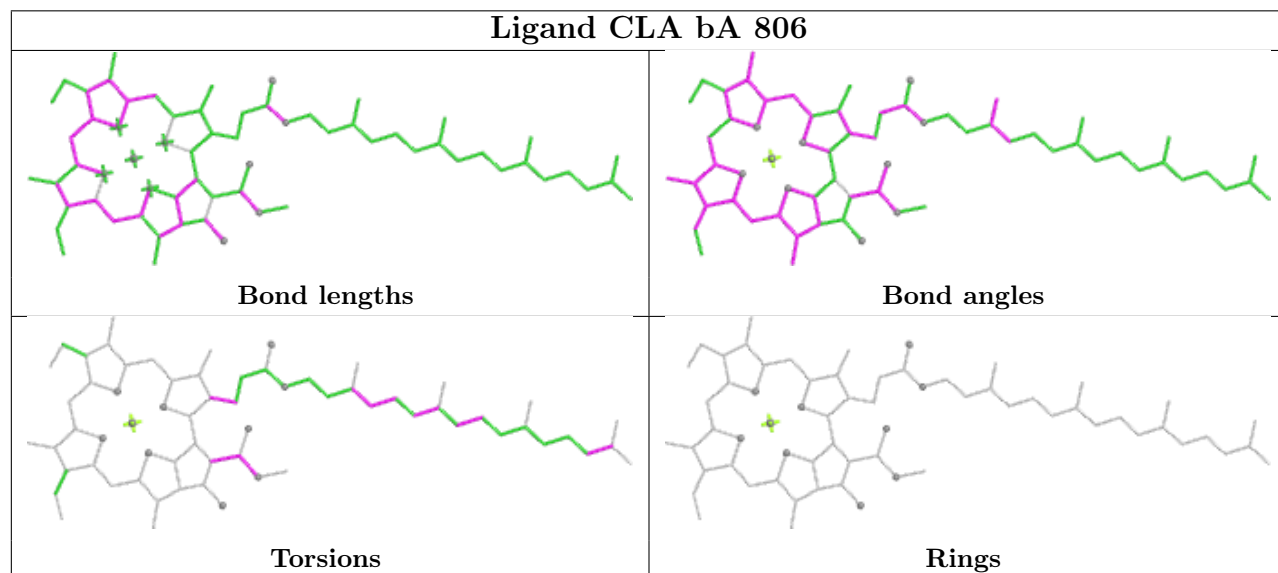
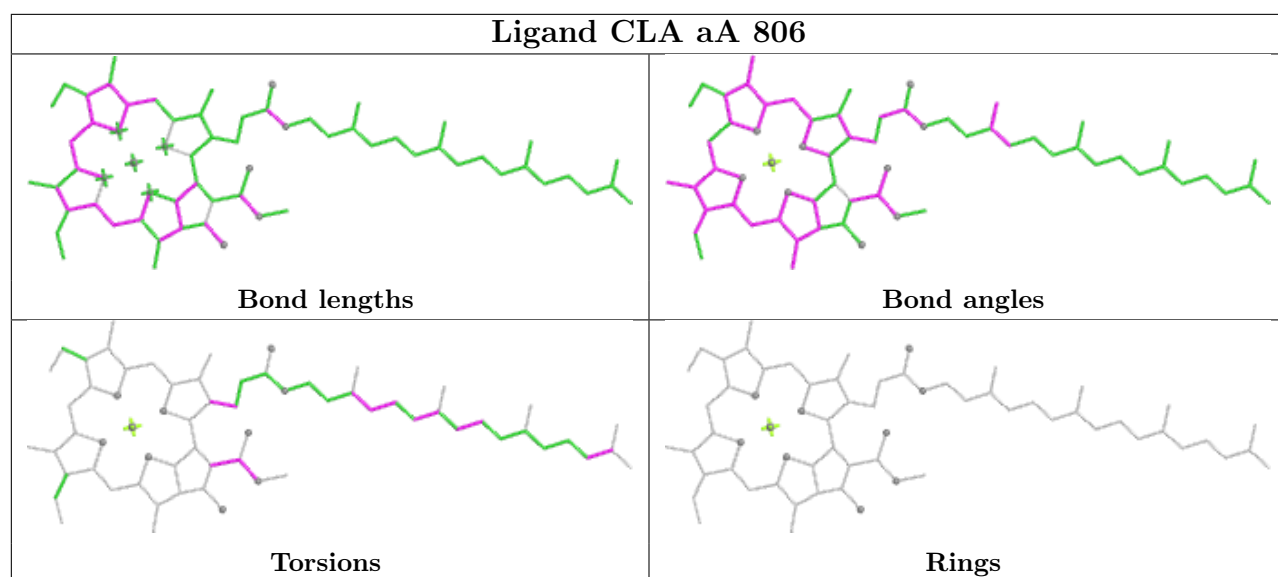
Bond angles

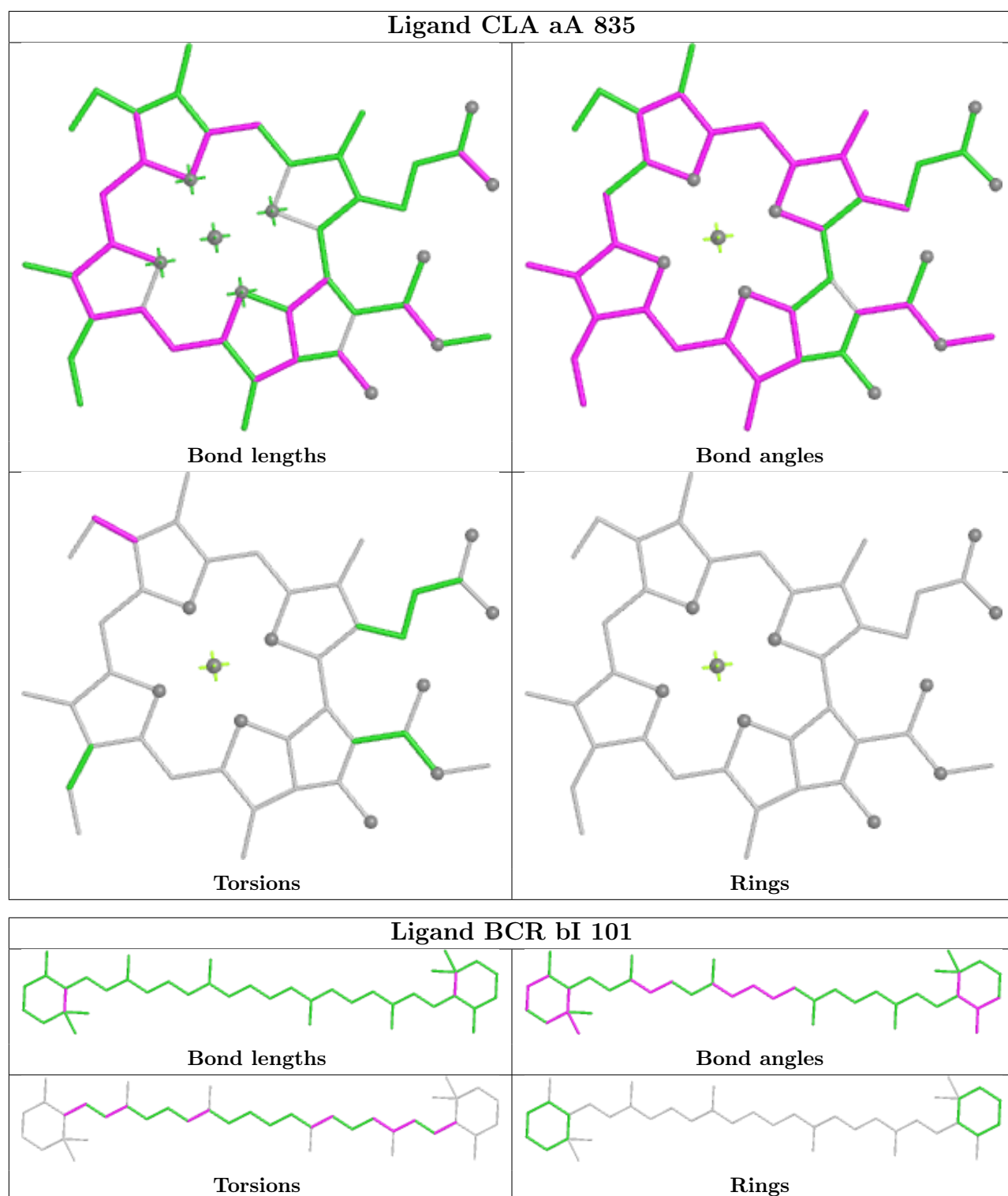


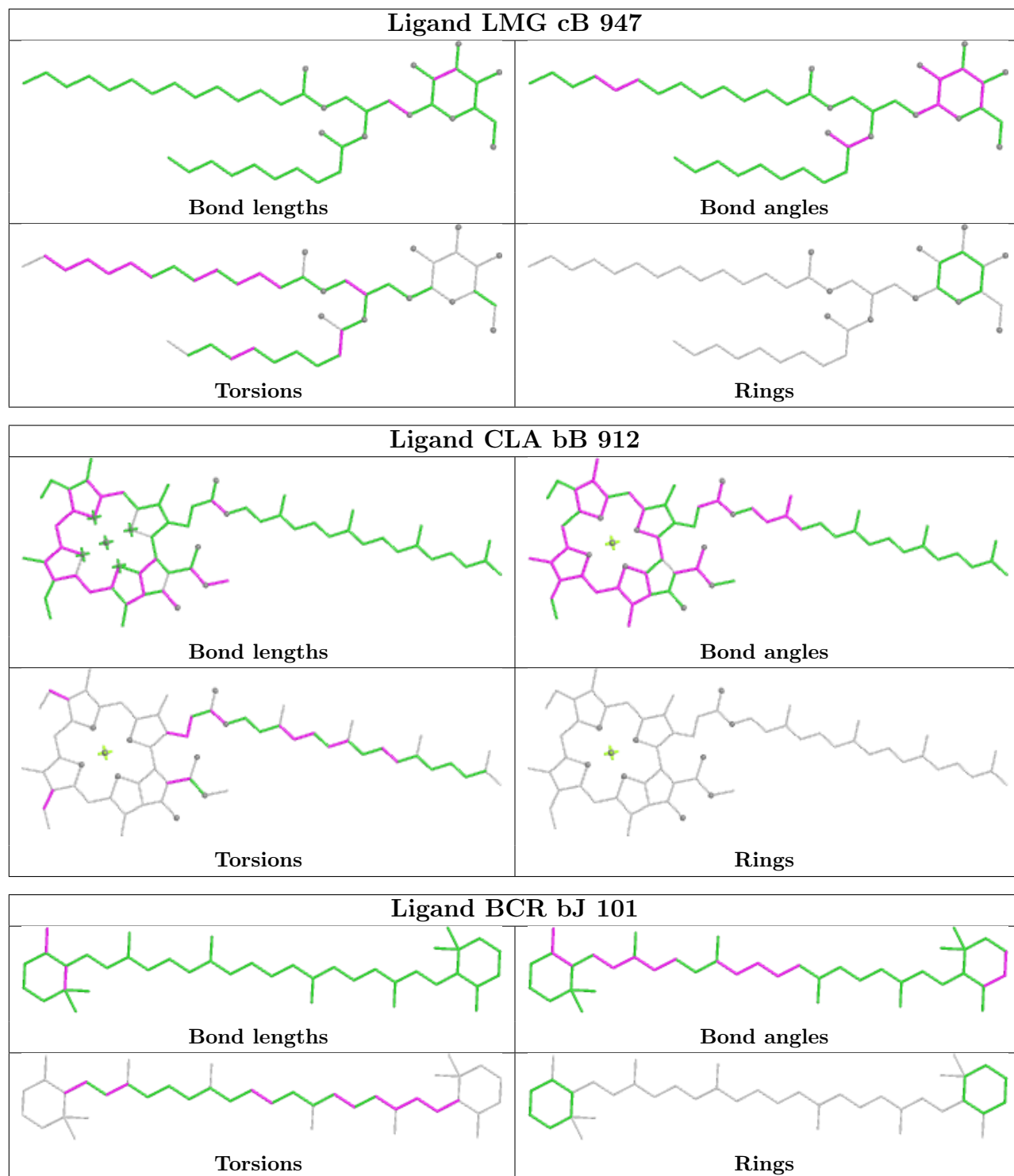
Torsions

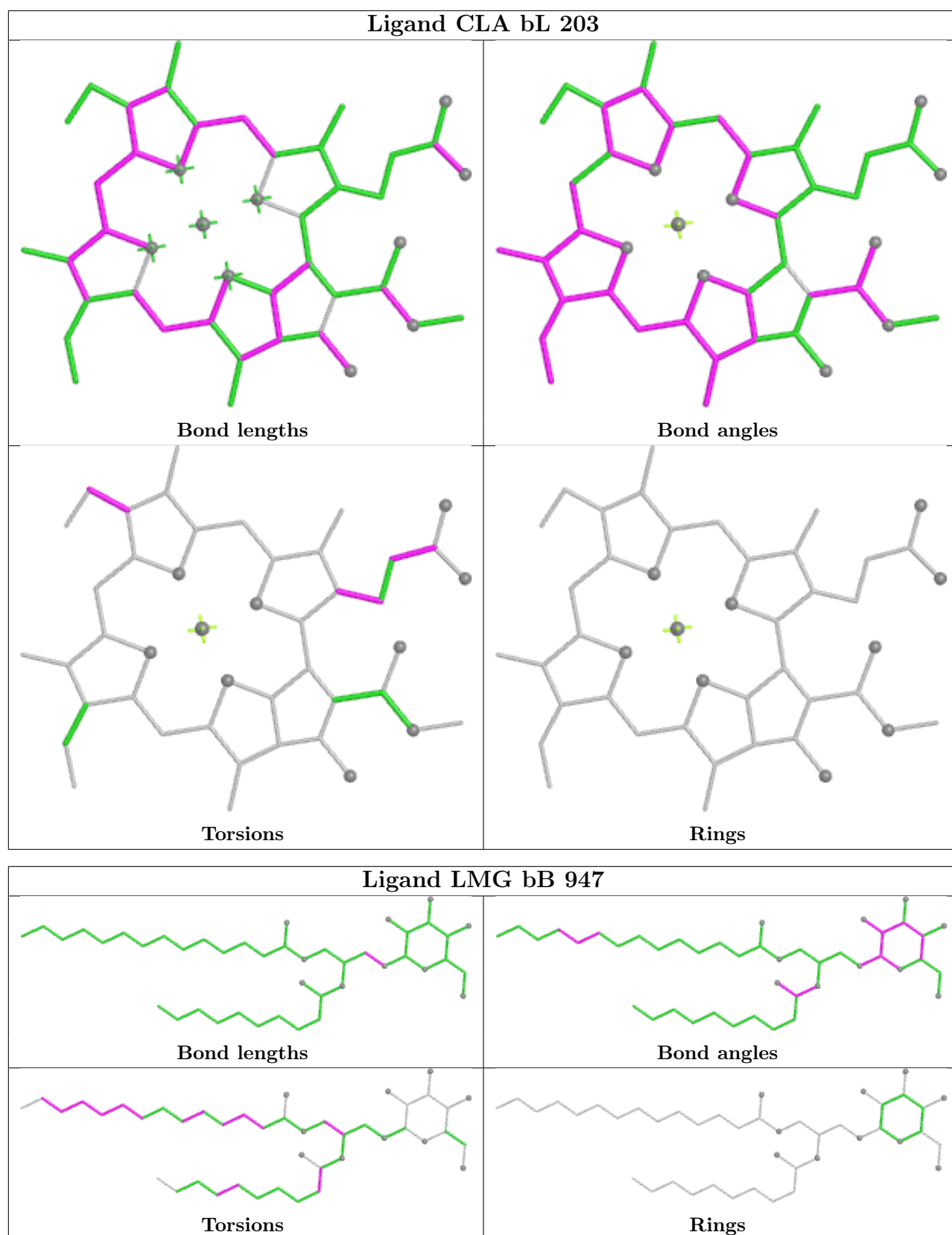


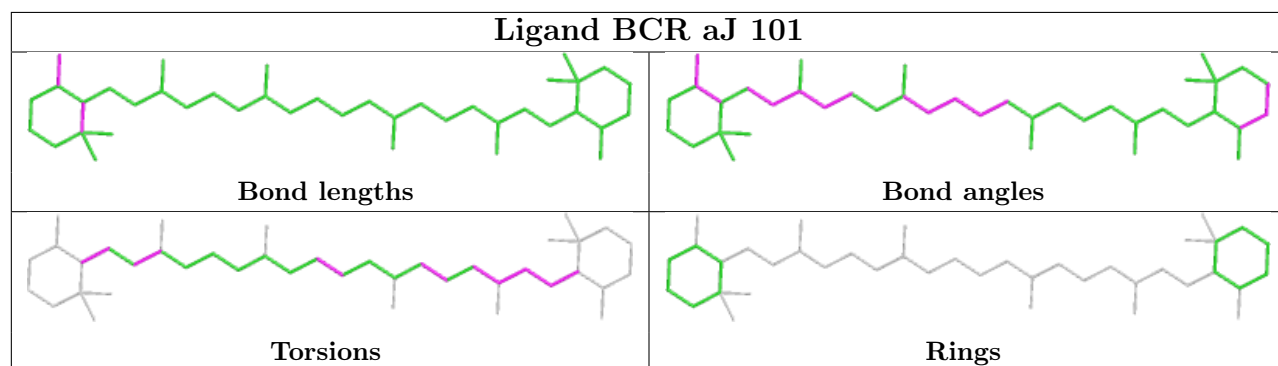
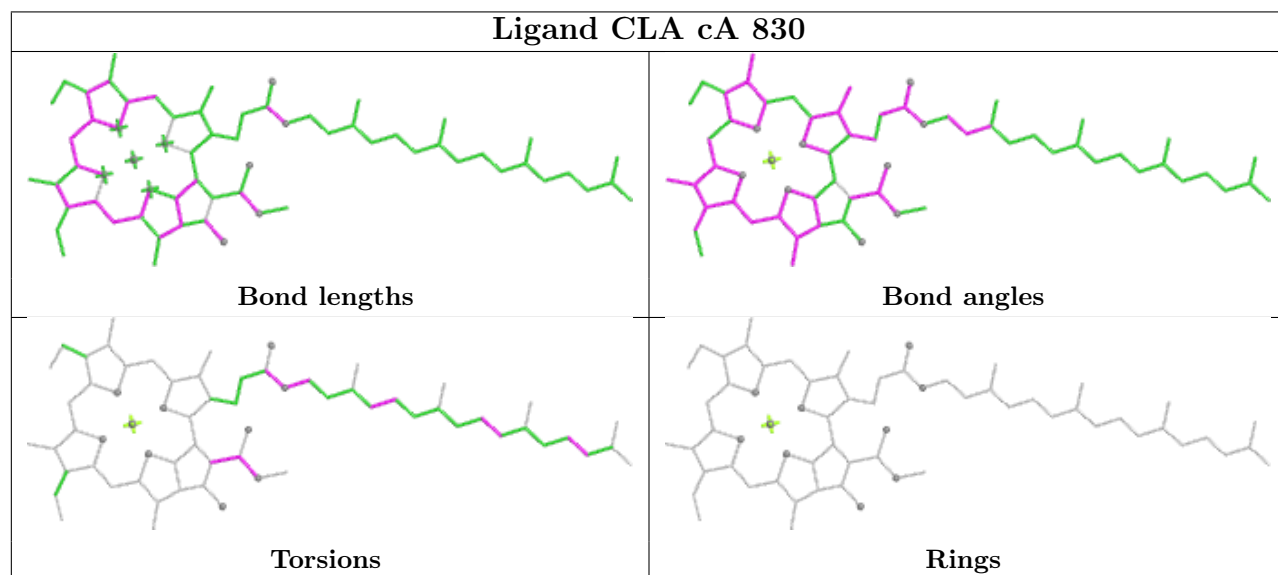
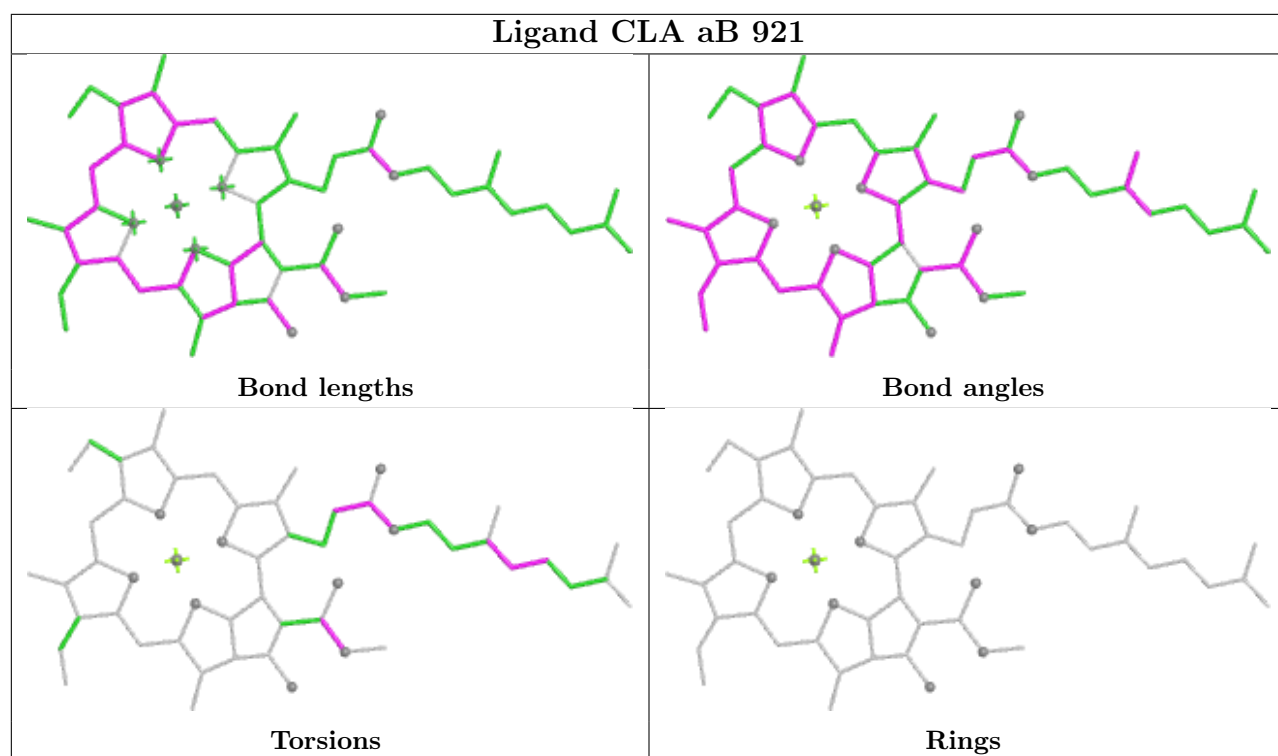
Rings



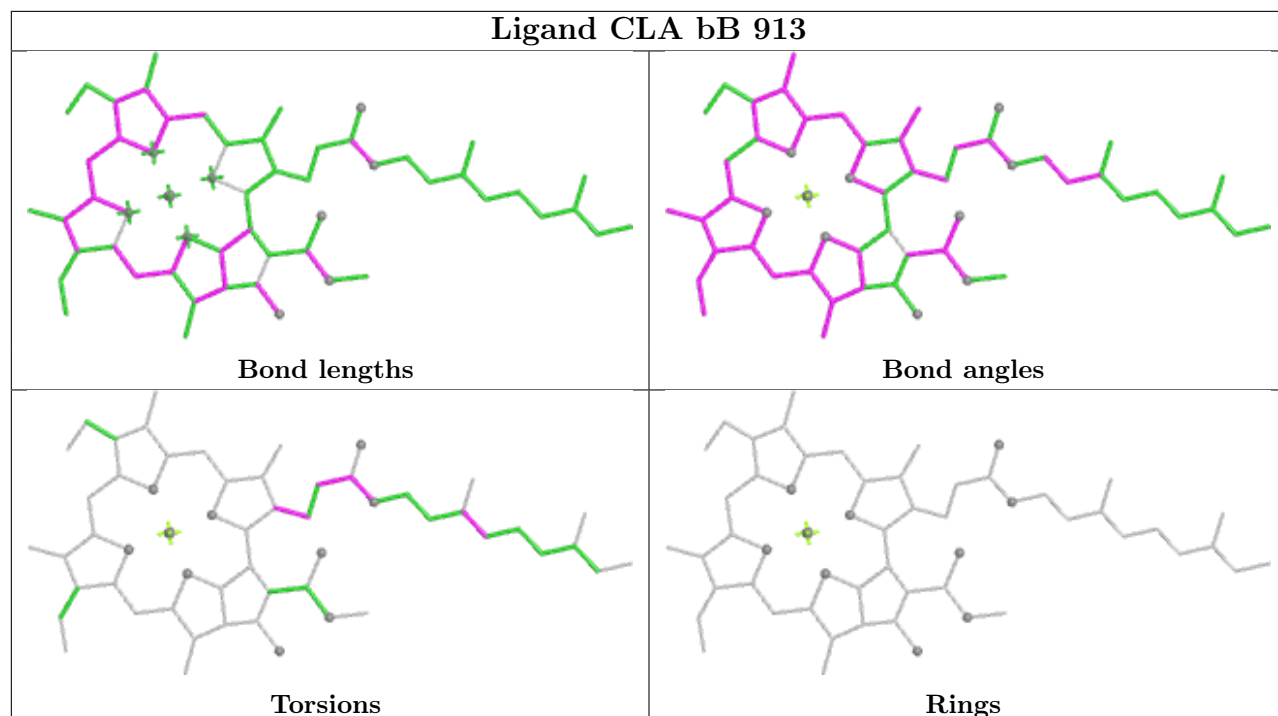




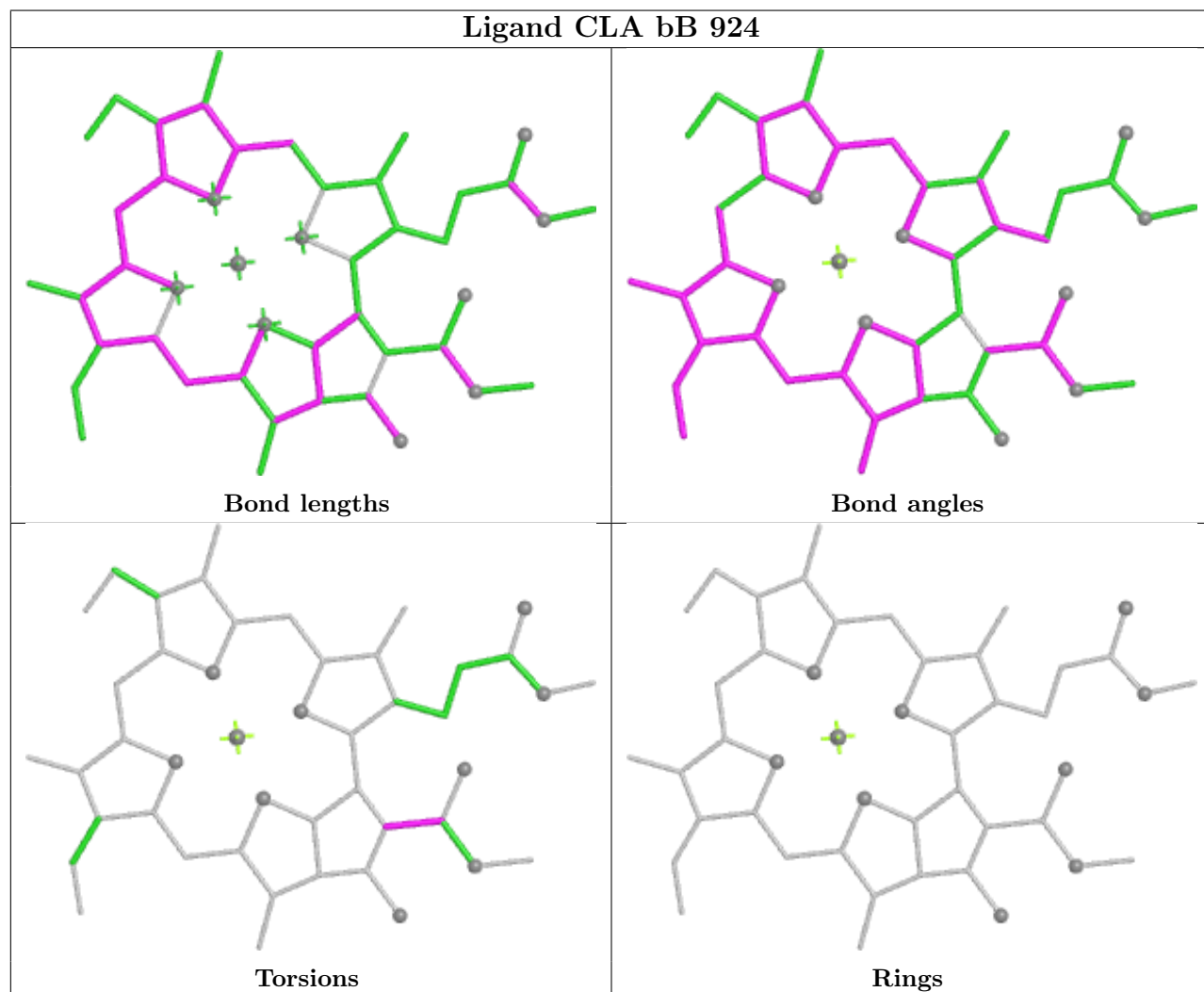


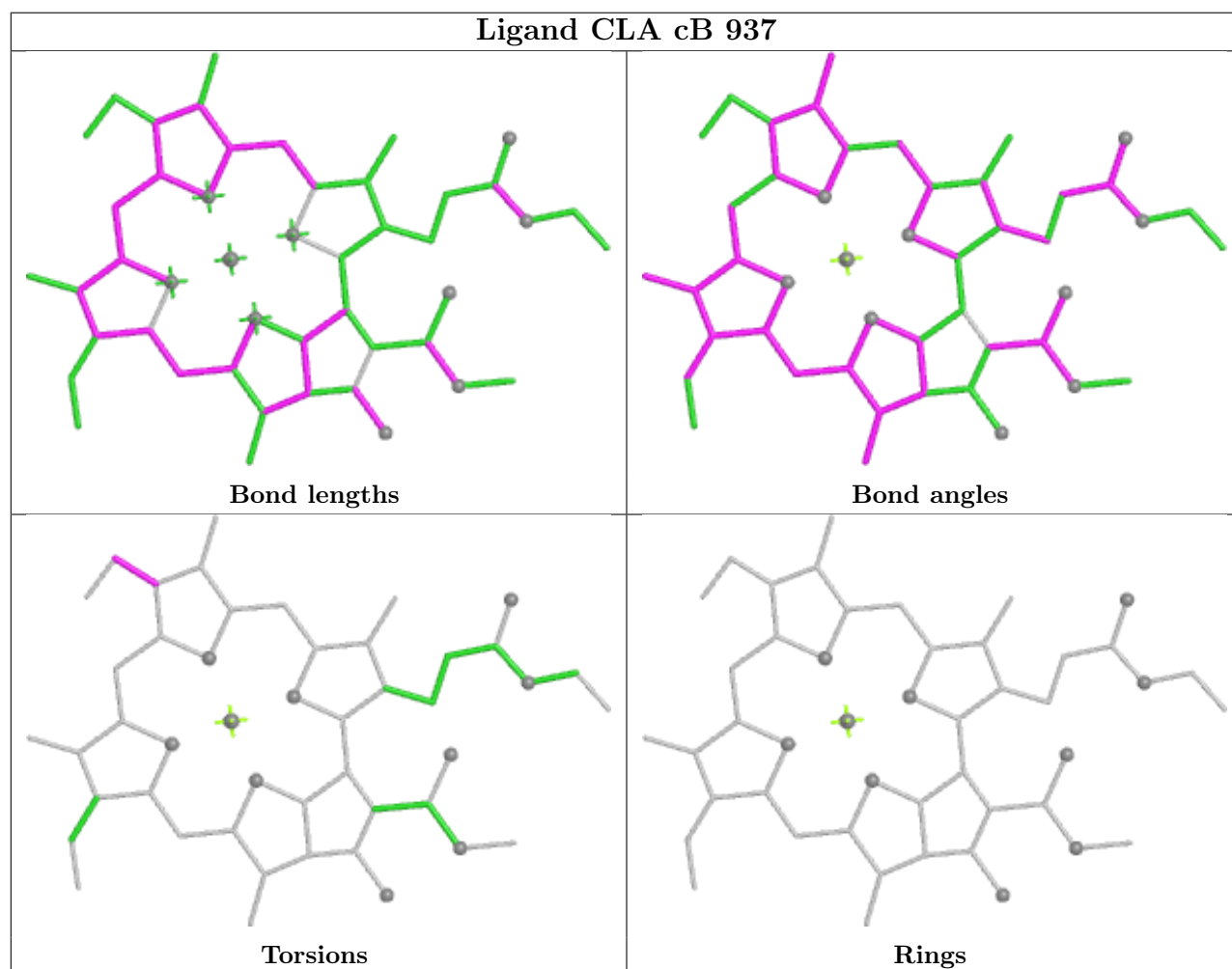
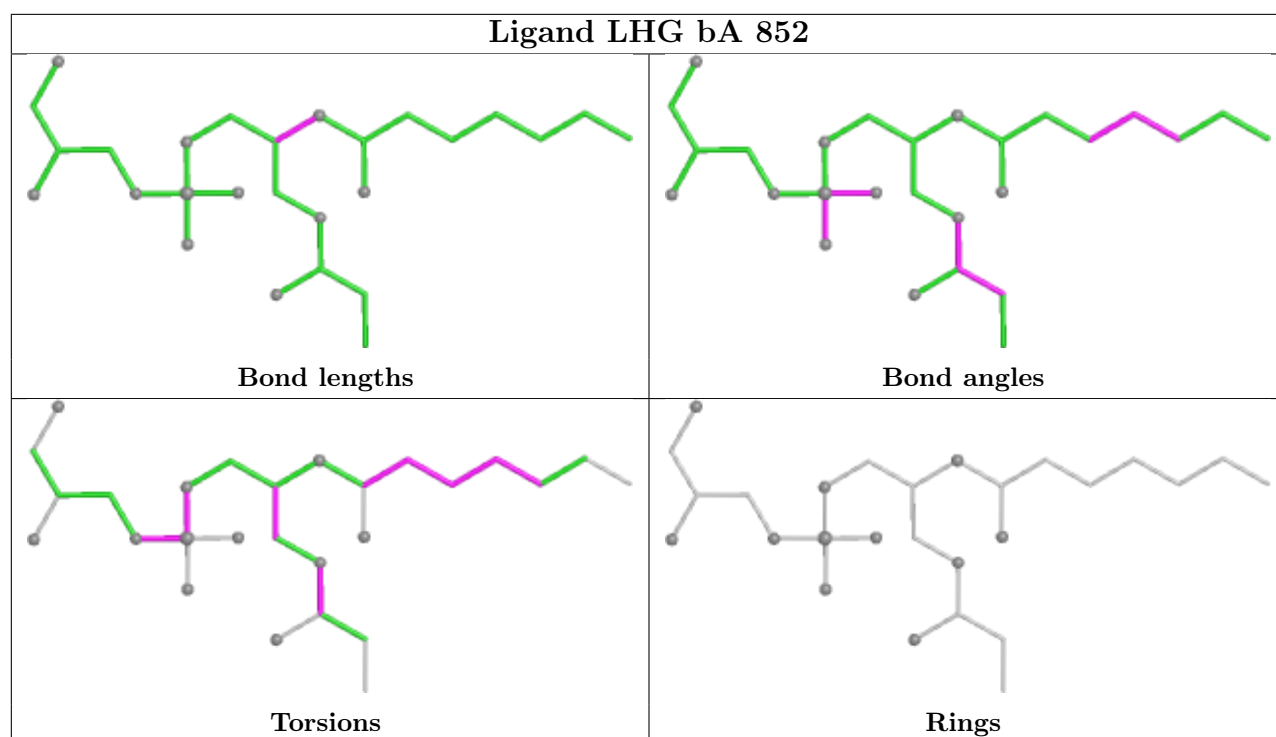


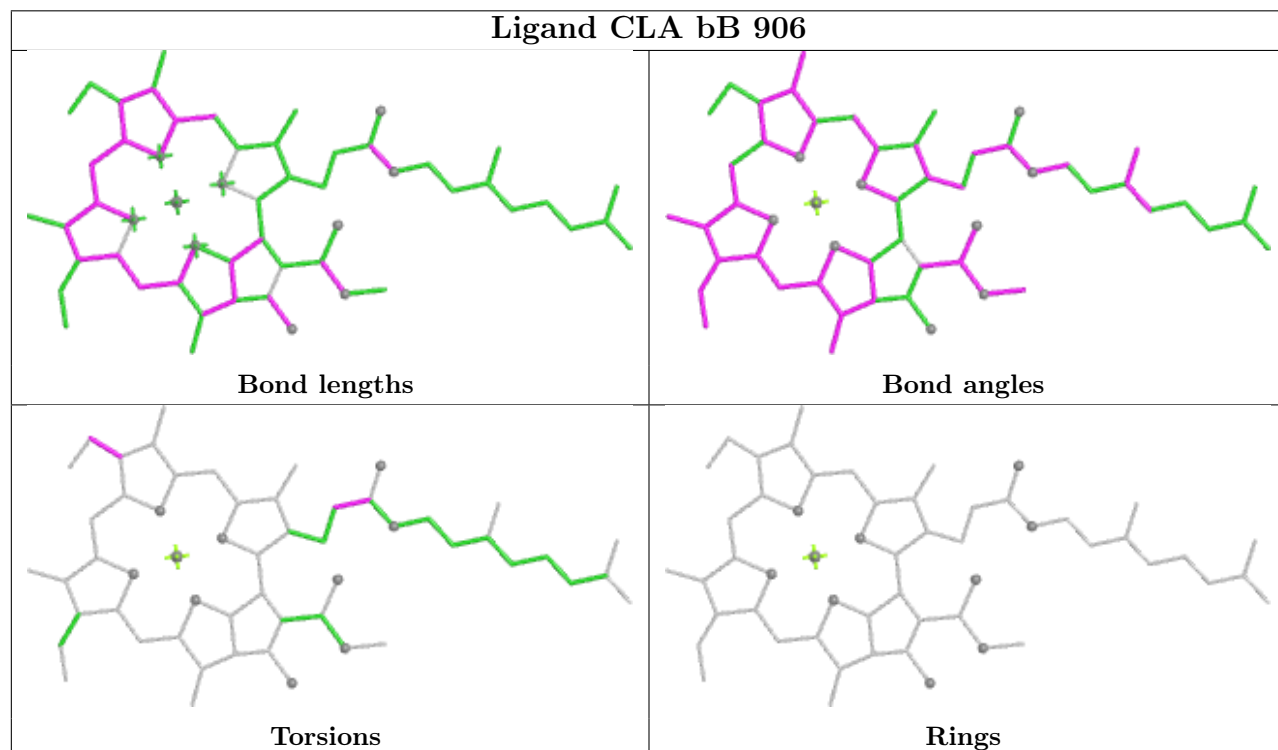
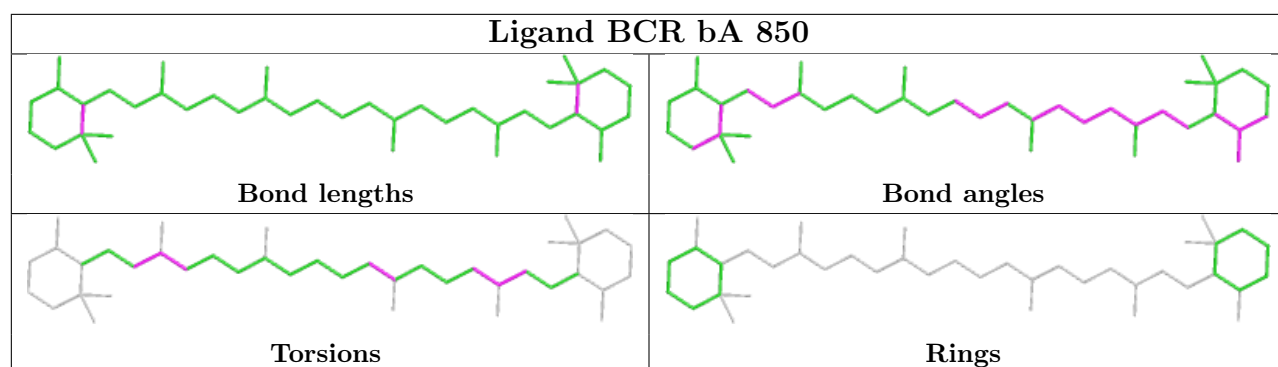
Ligand CLA bB 913

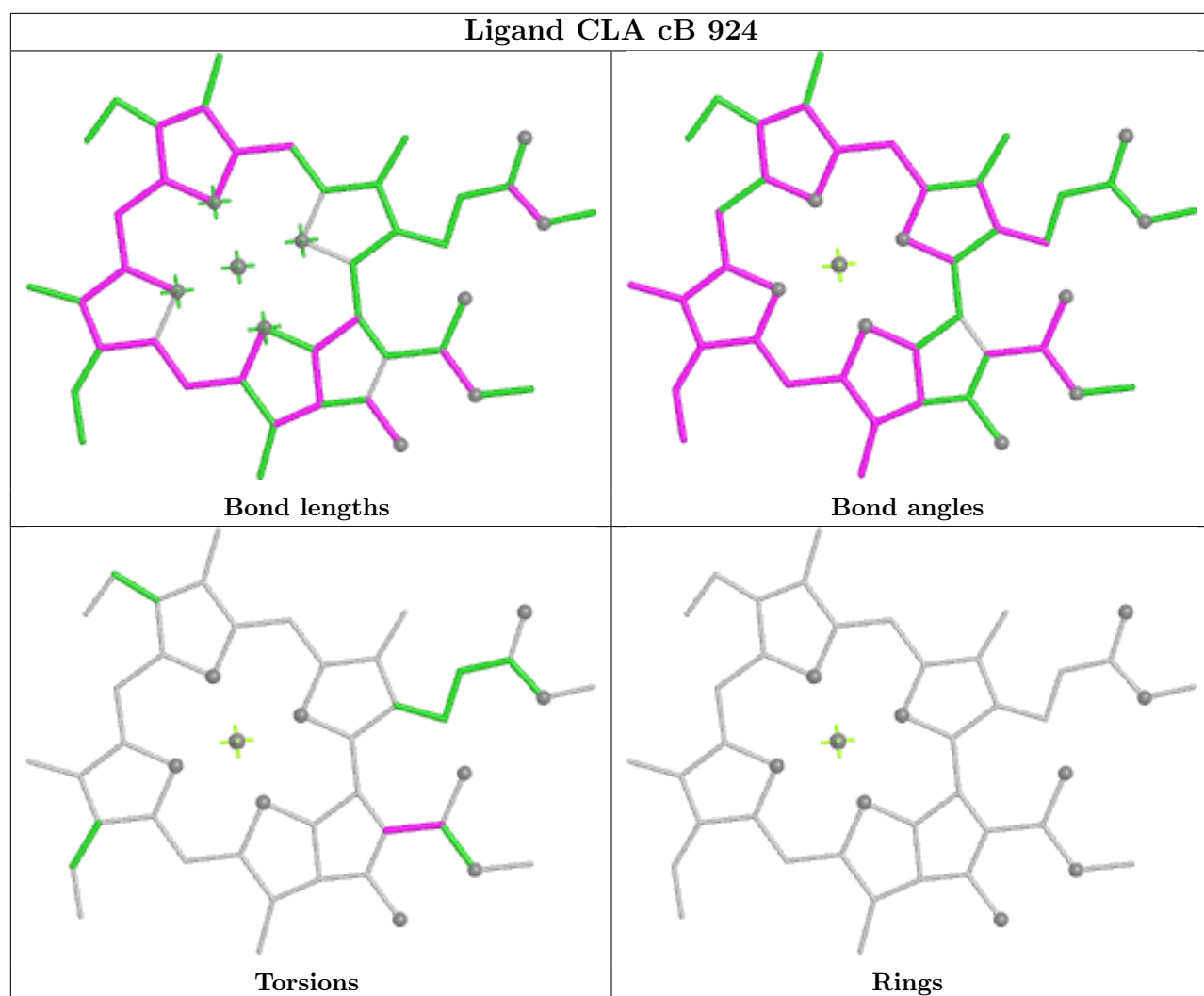


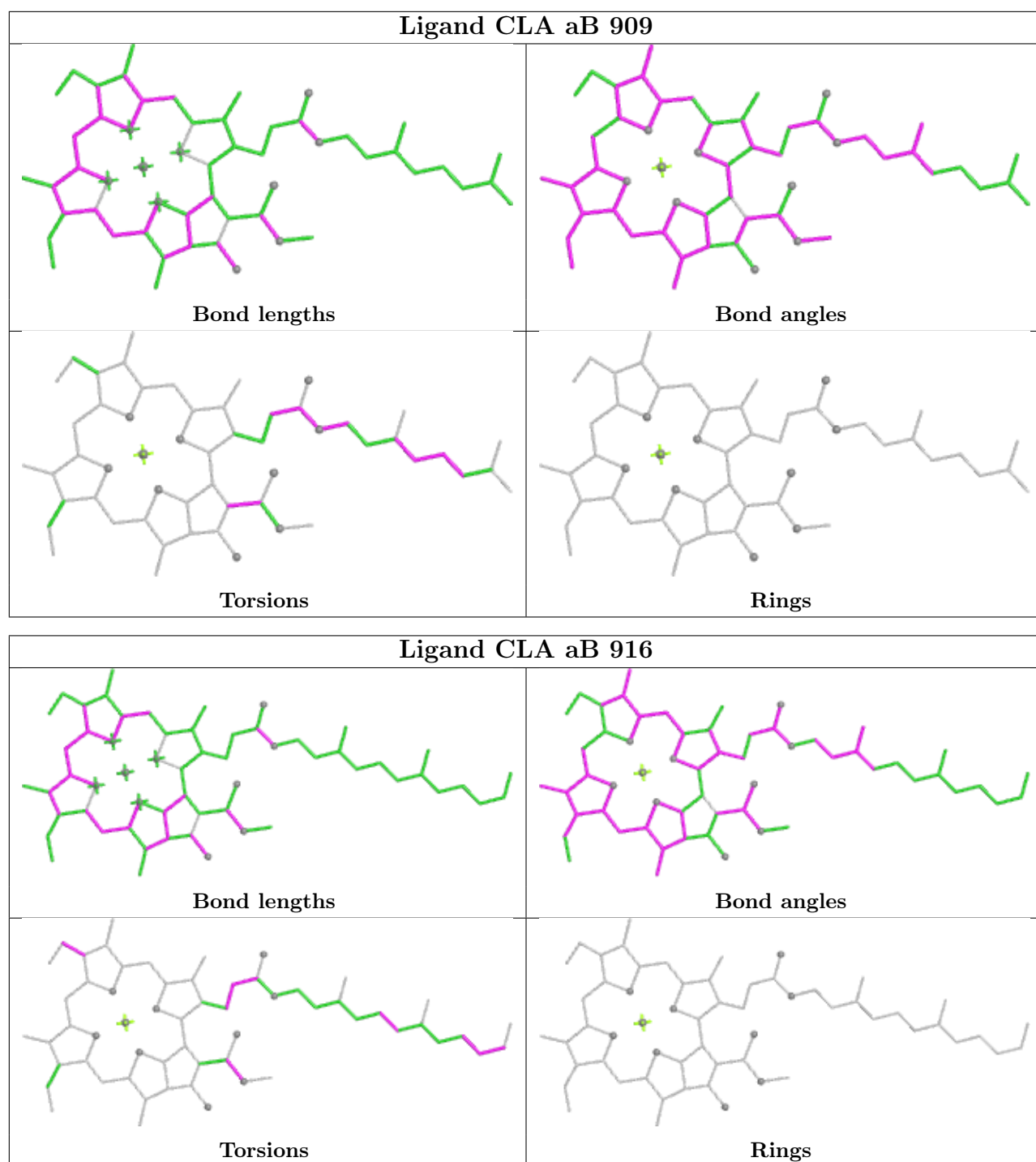
Ligand CLA bB 924

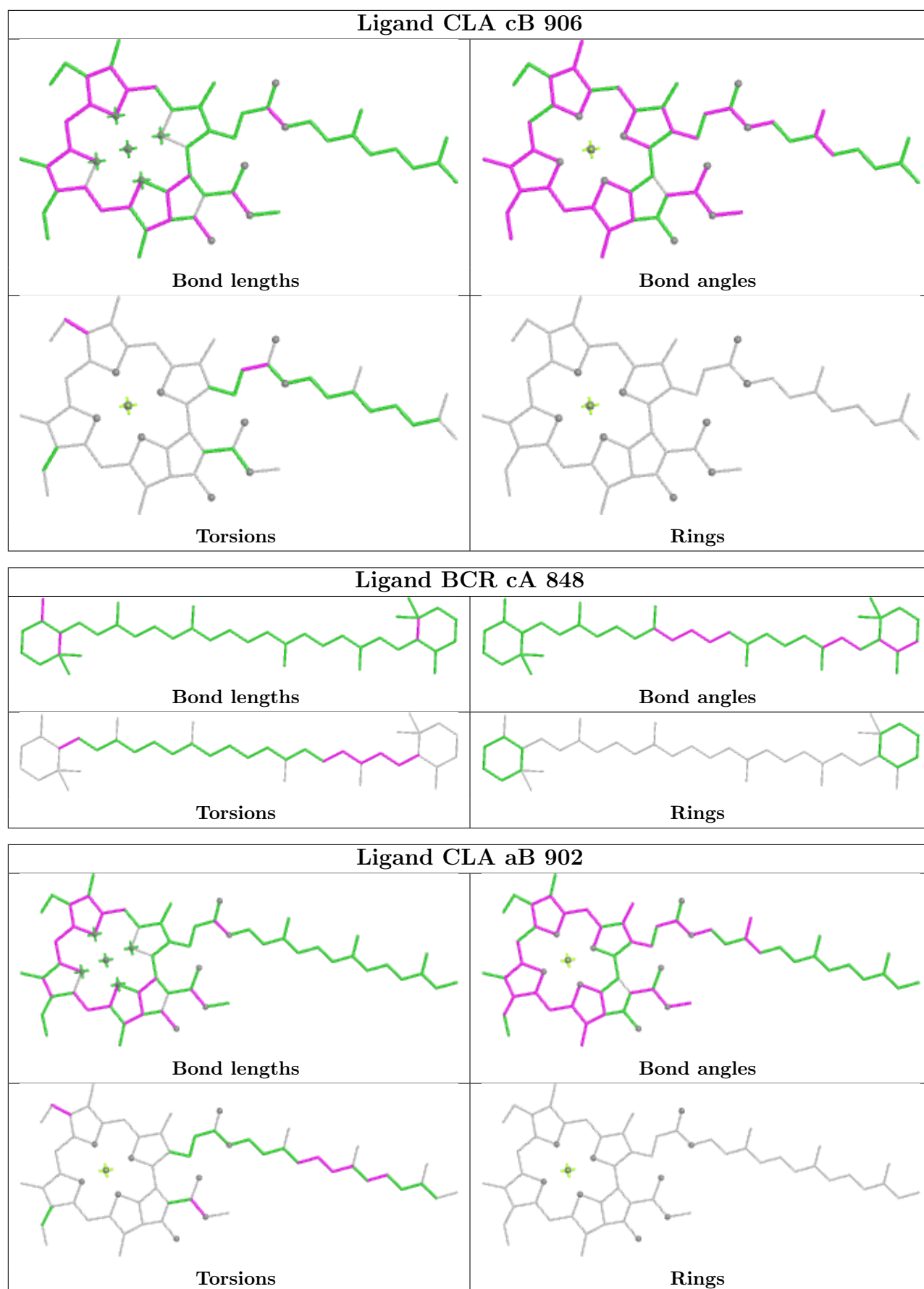


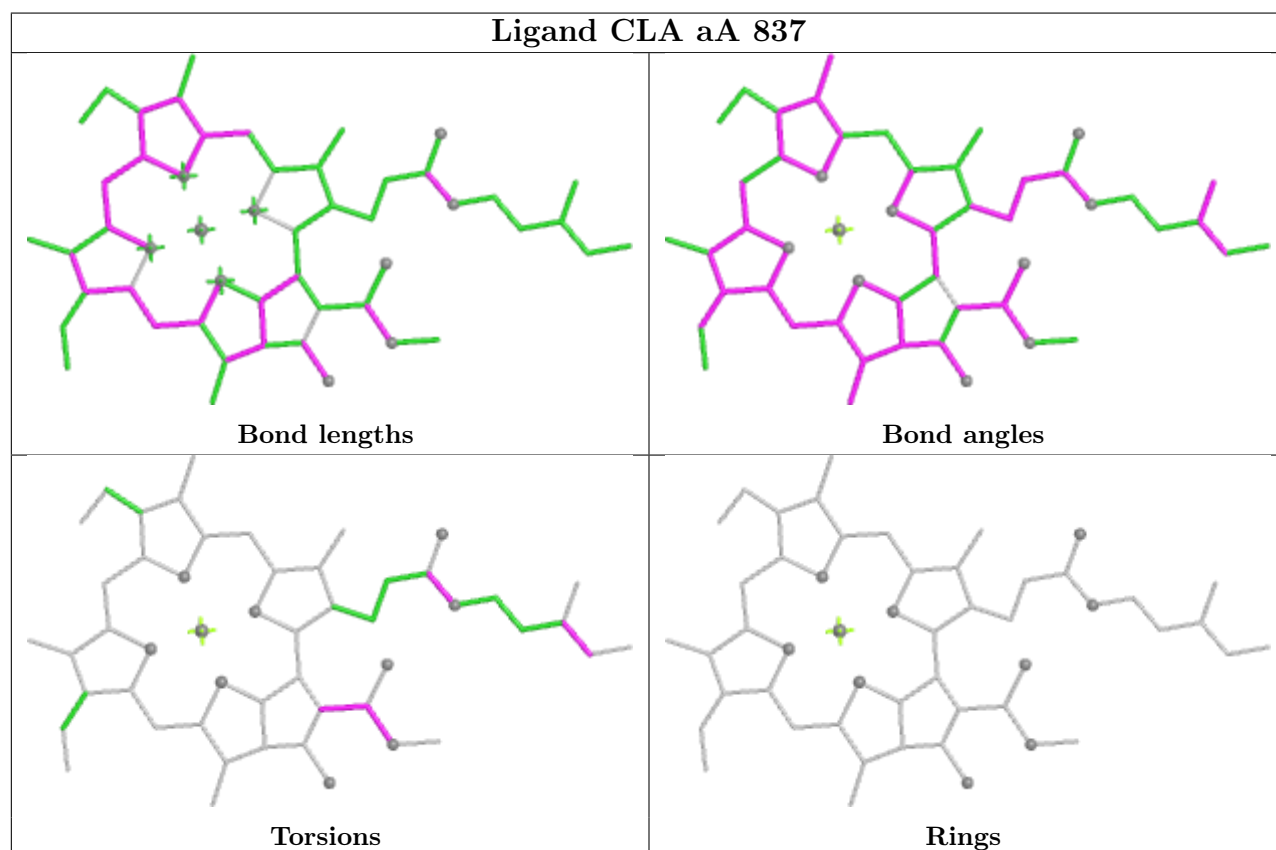
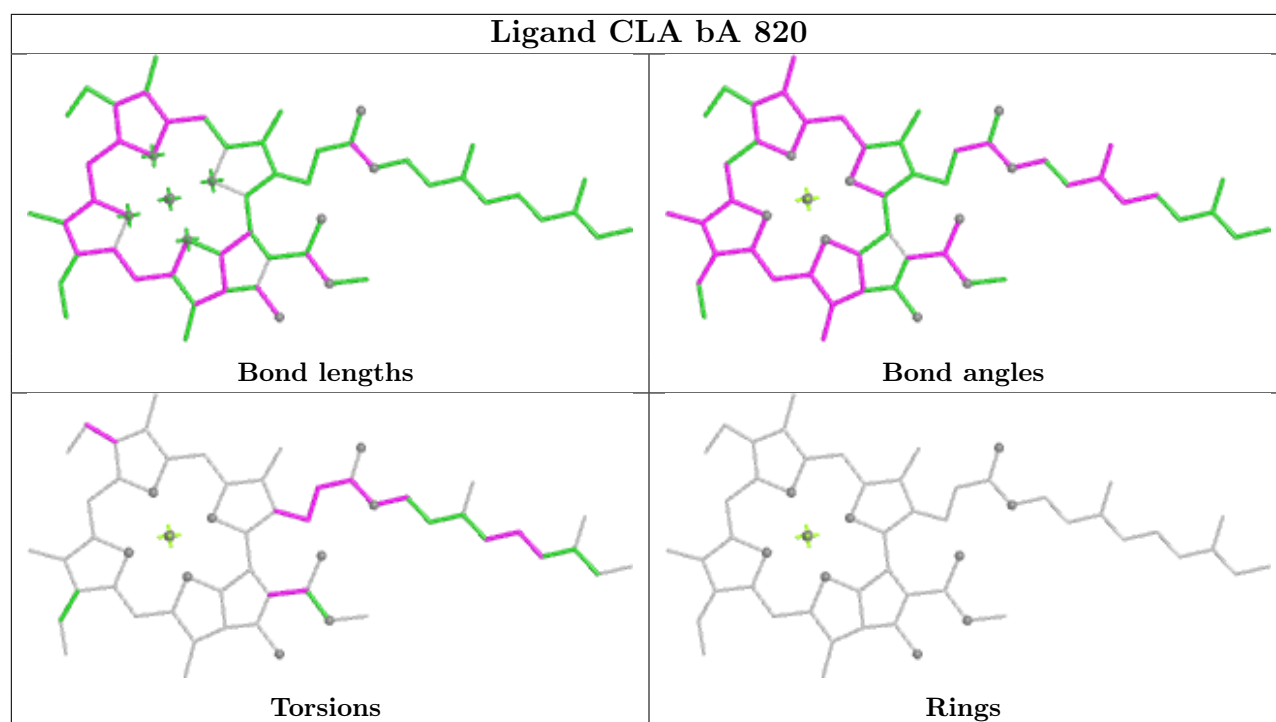


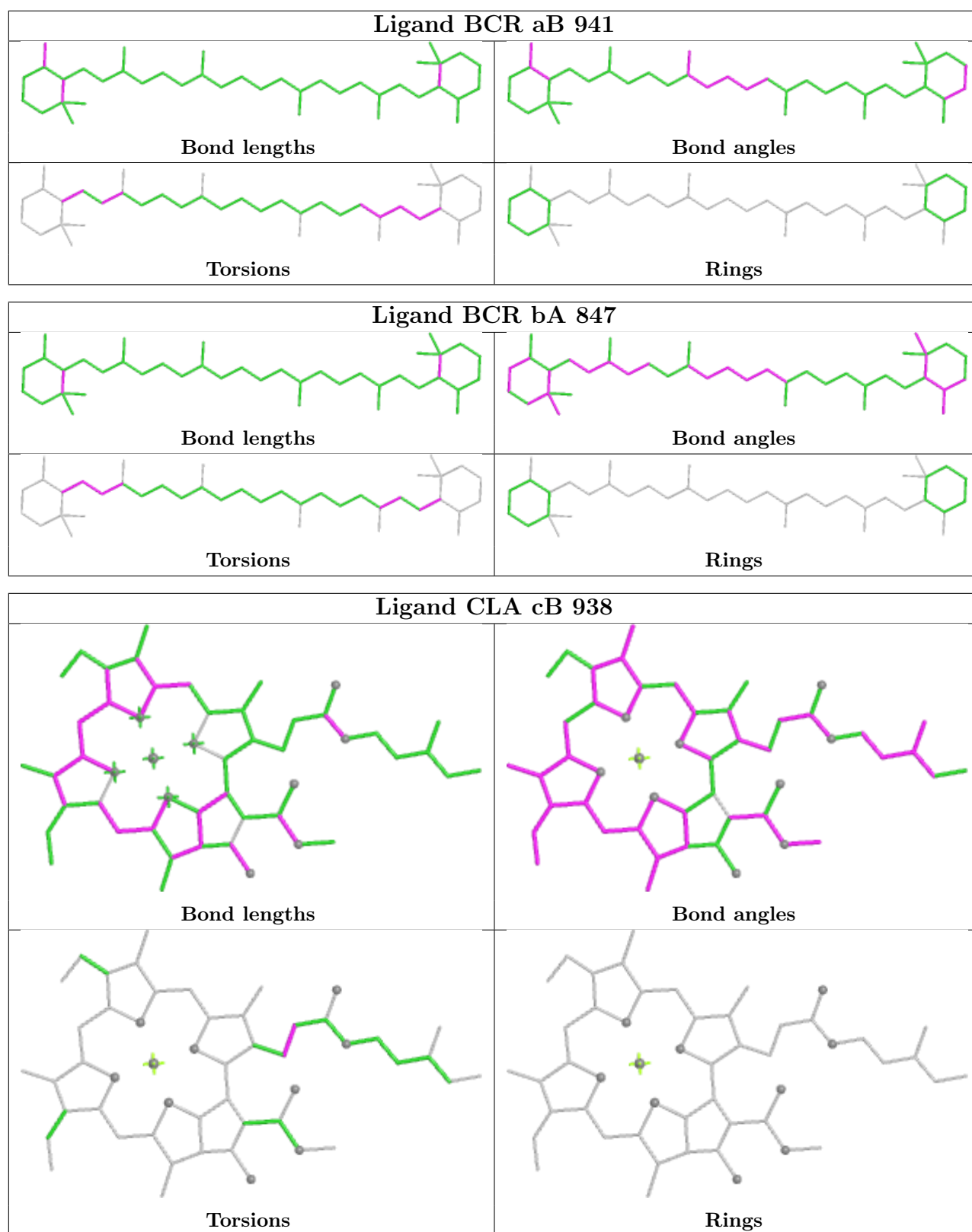


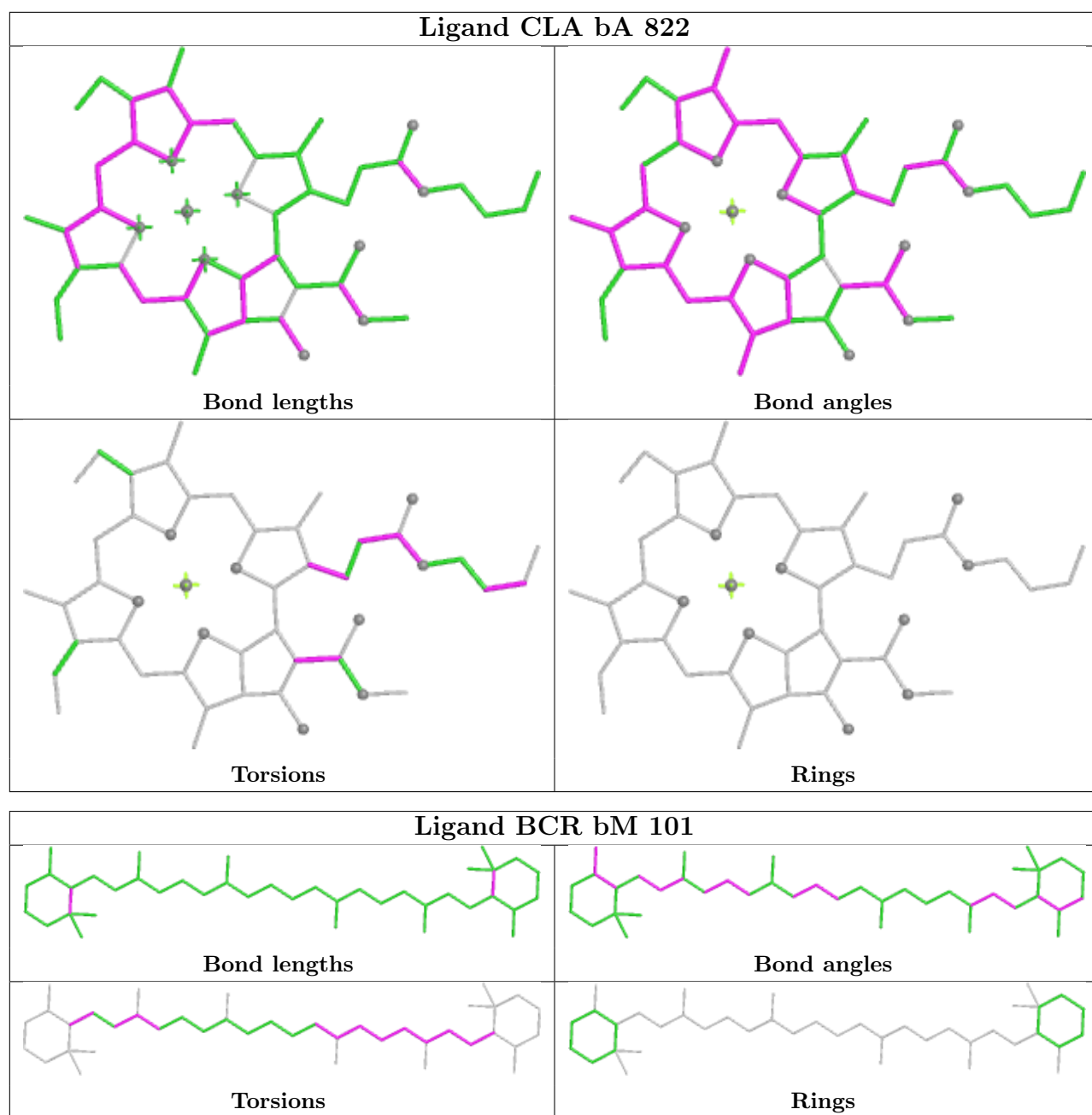


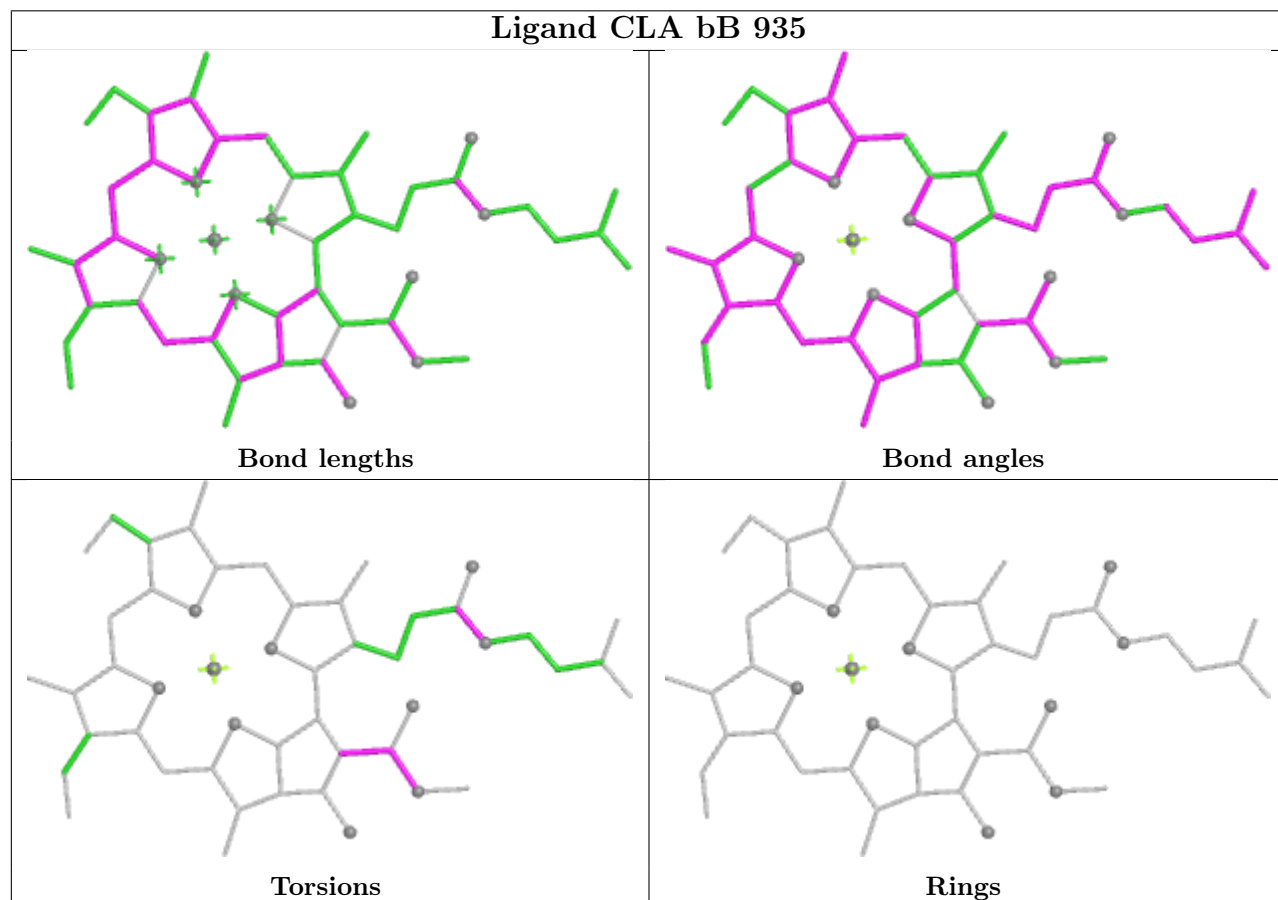
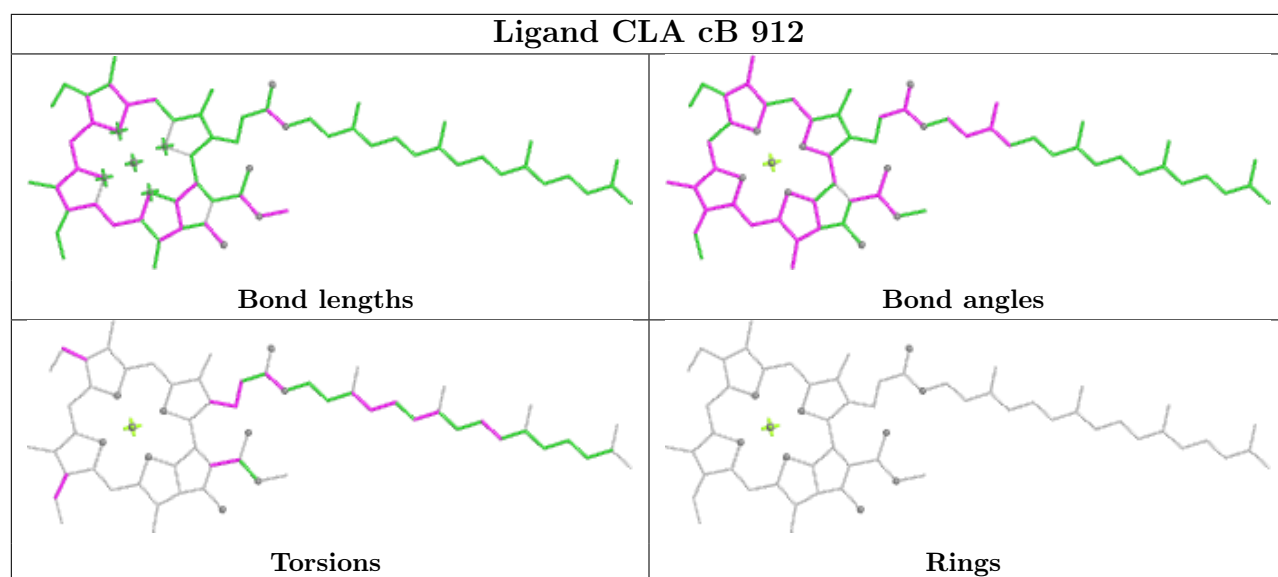


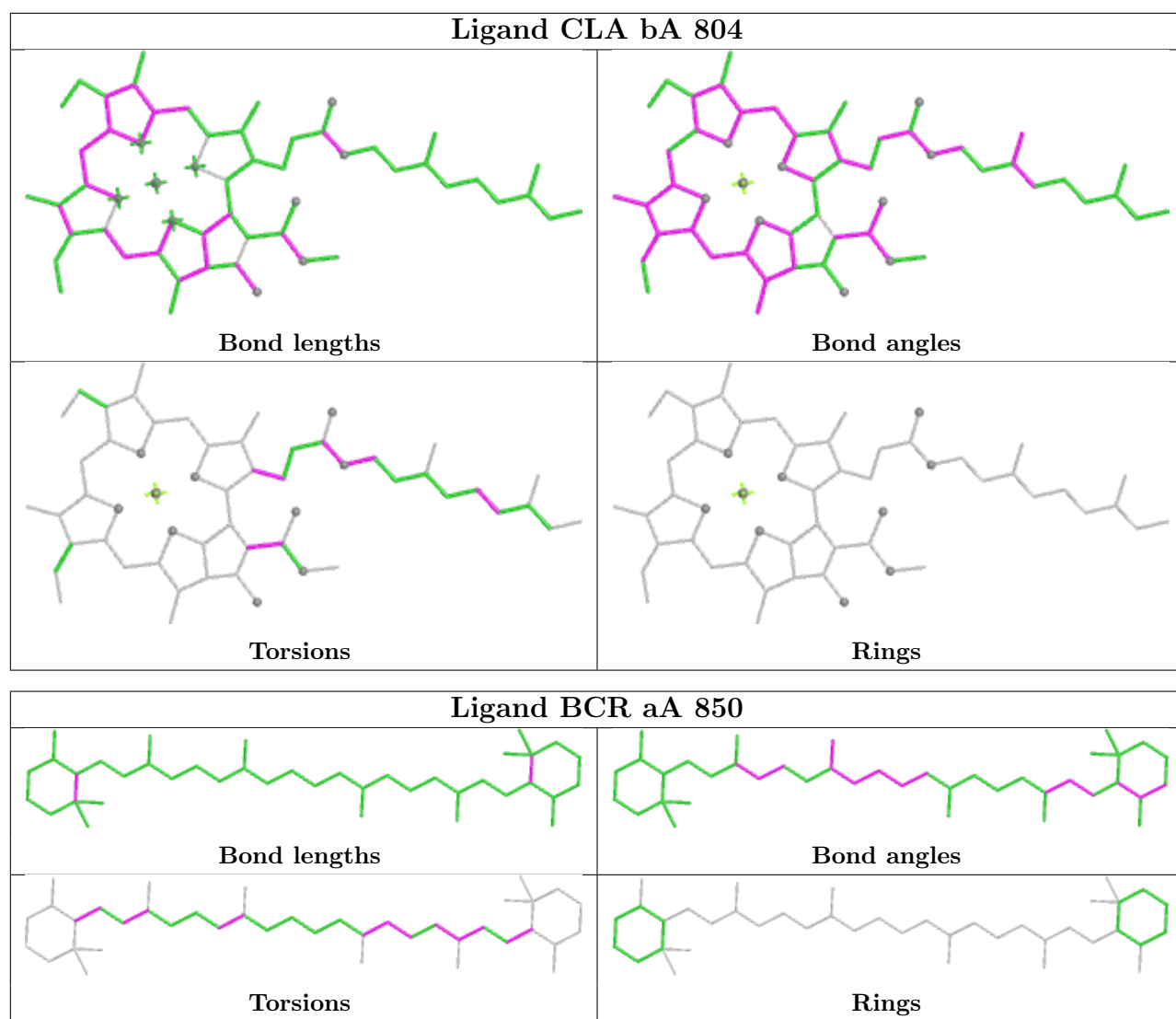


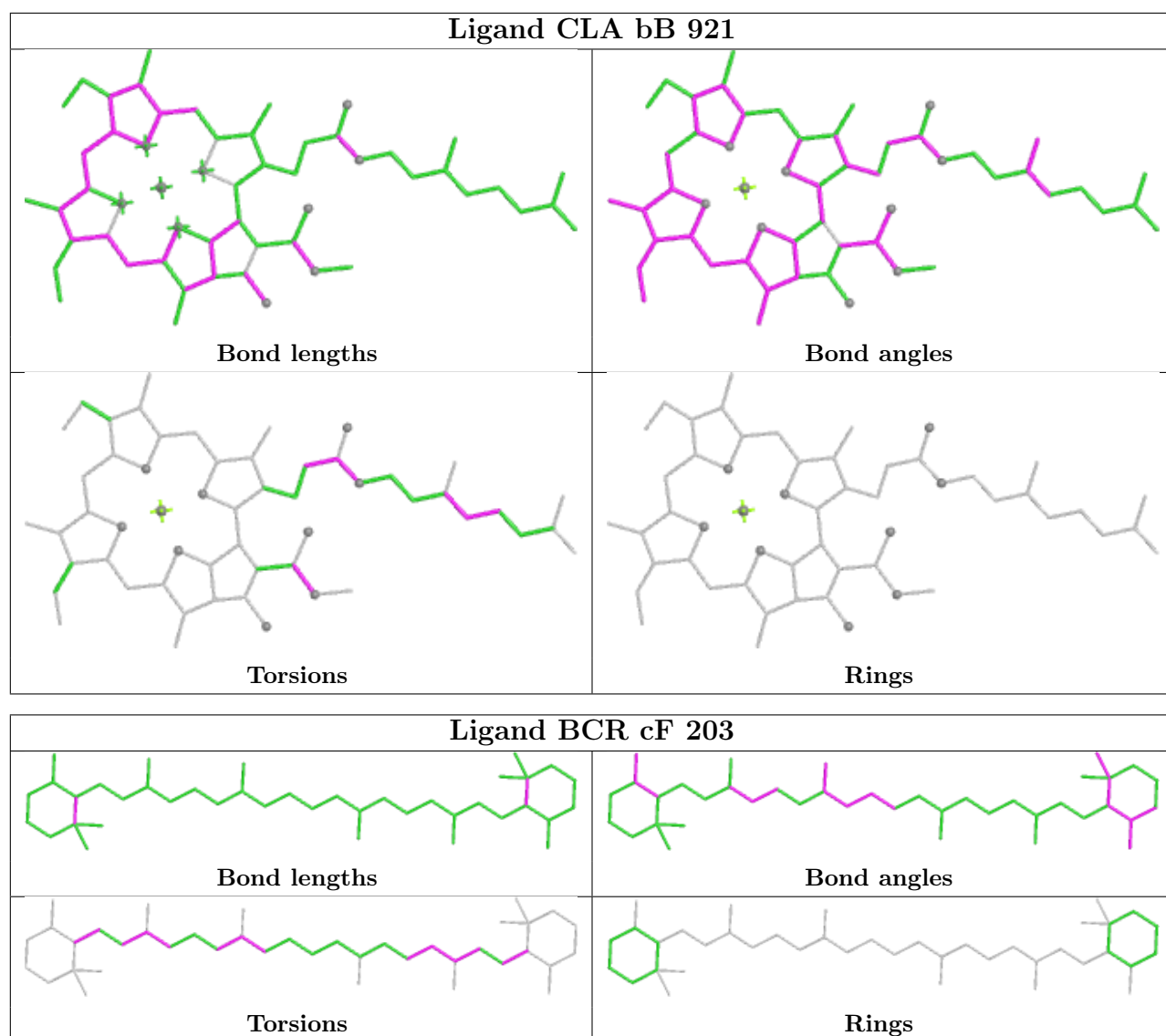


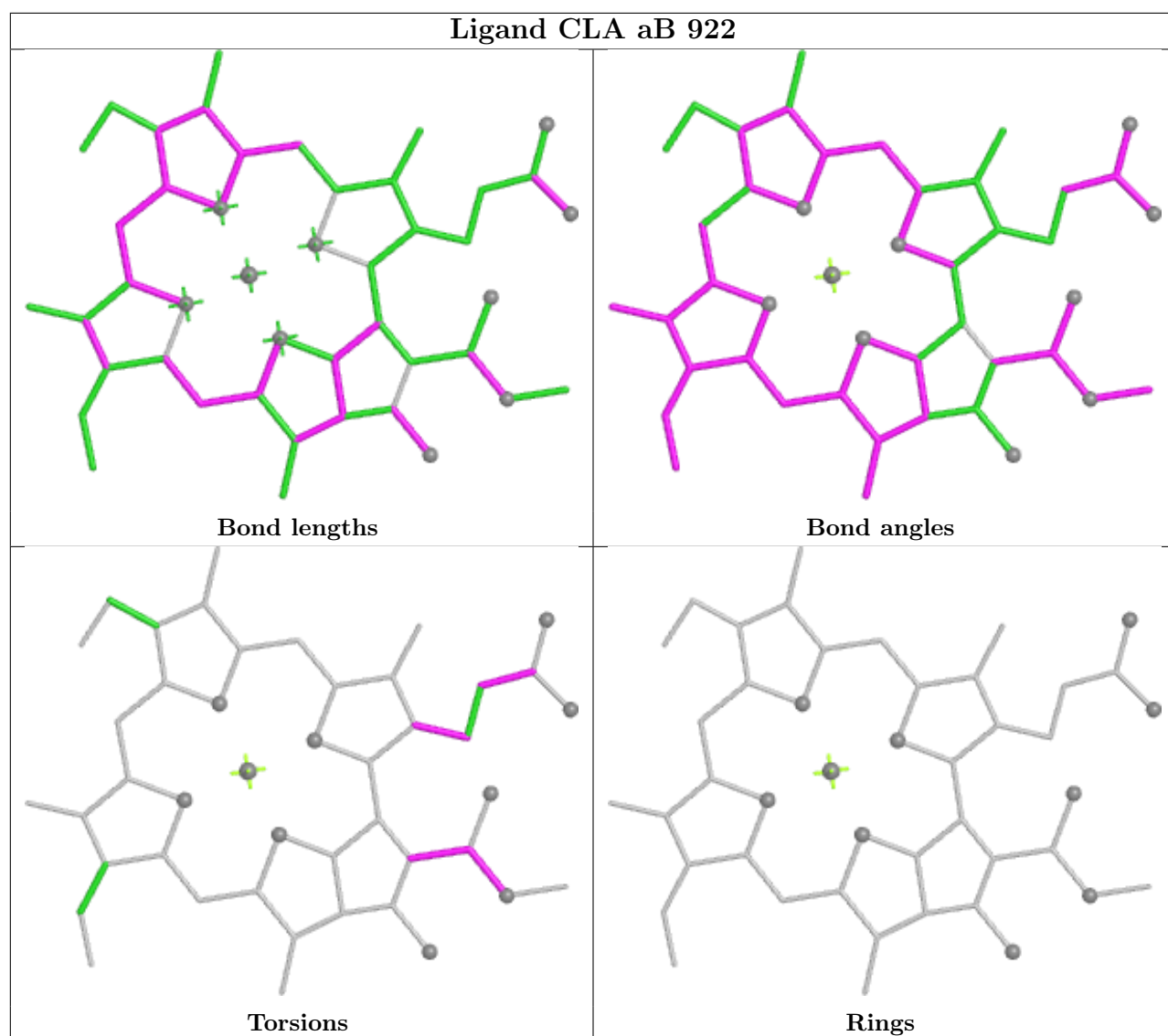


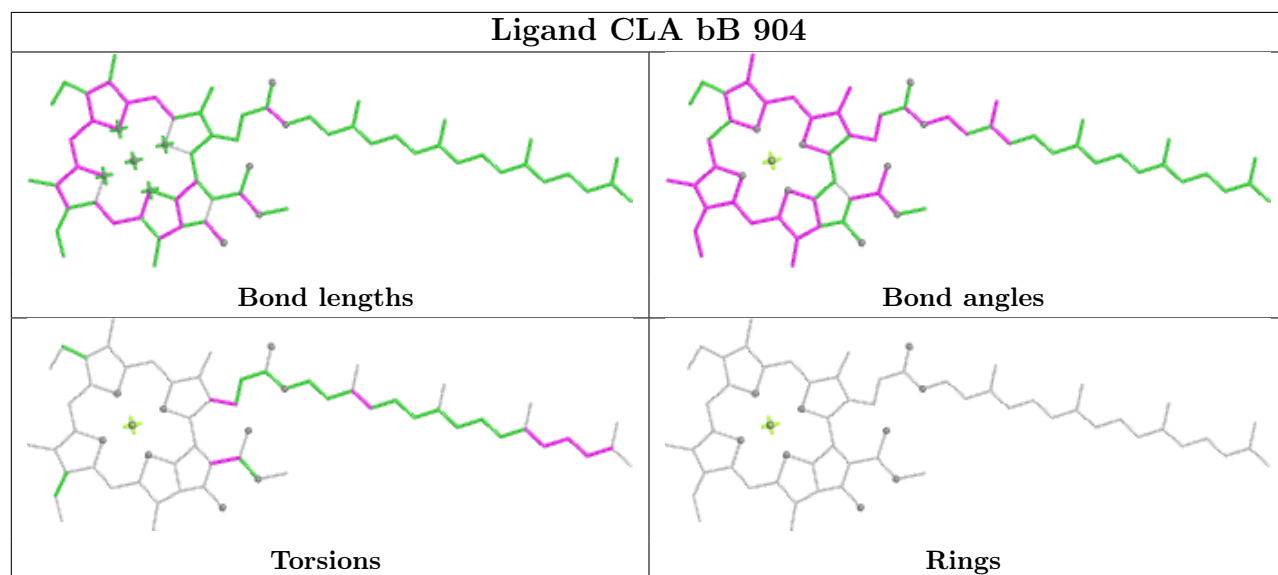
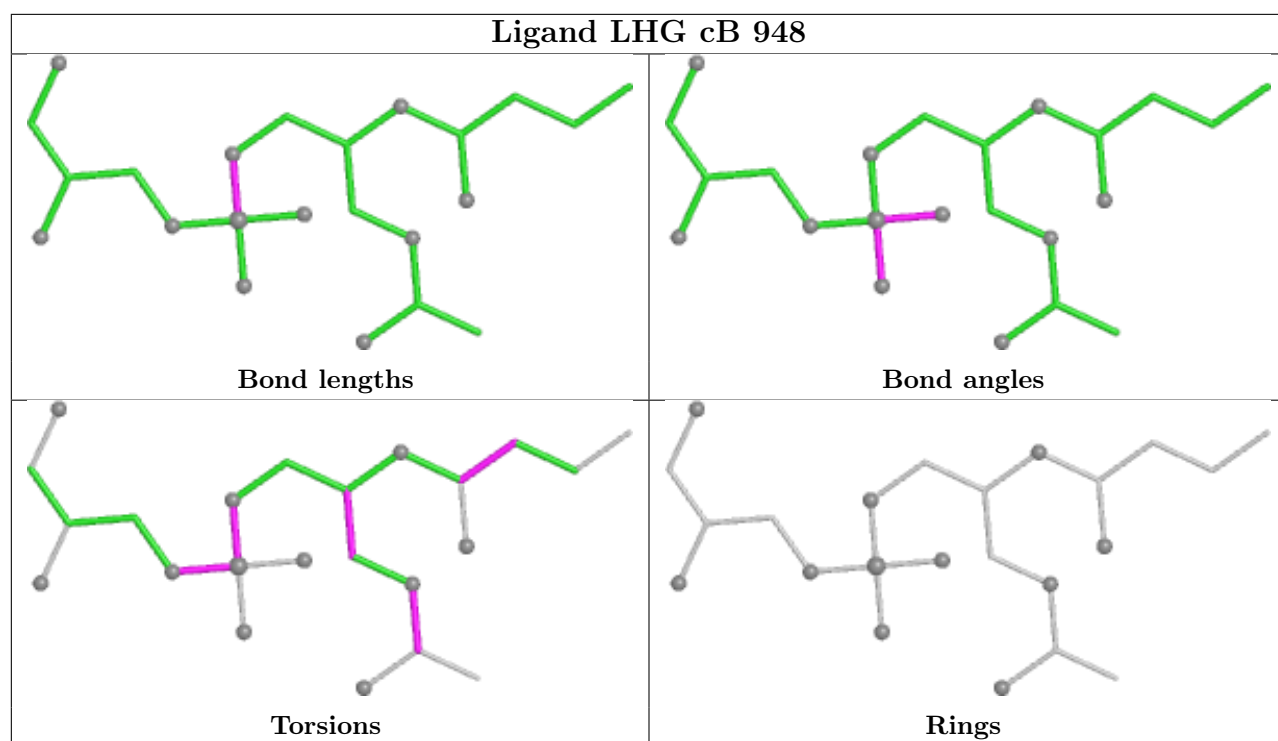


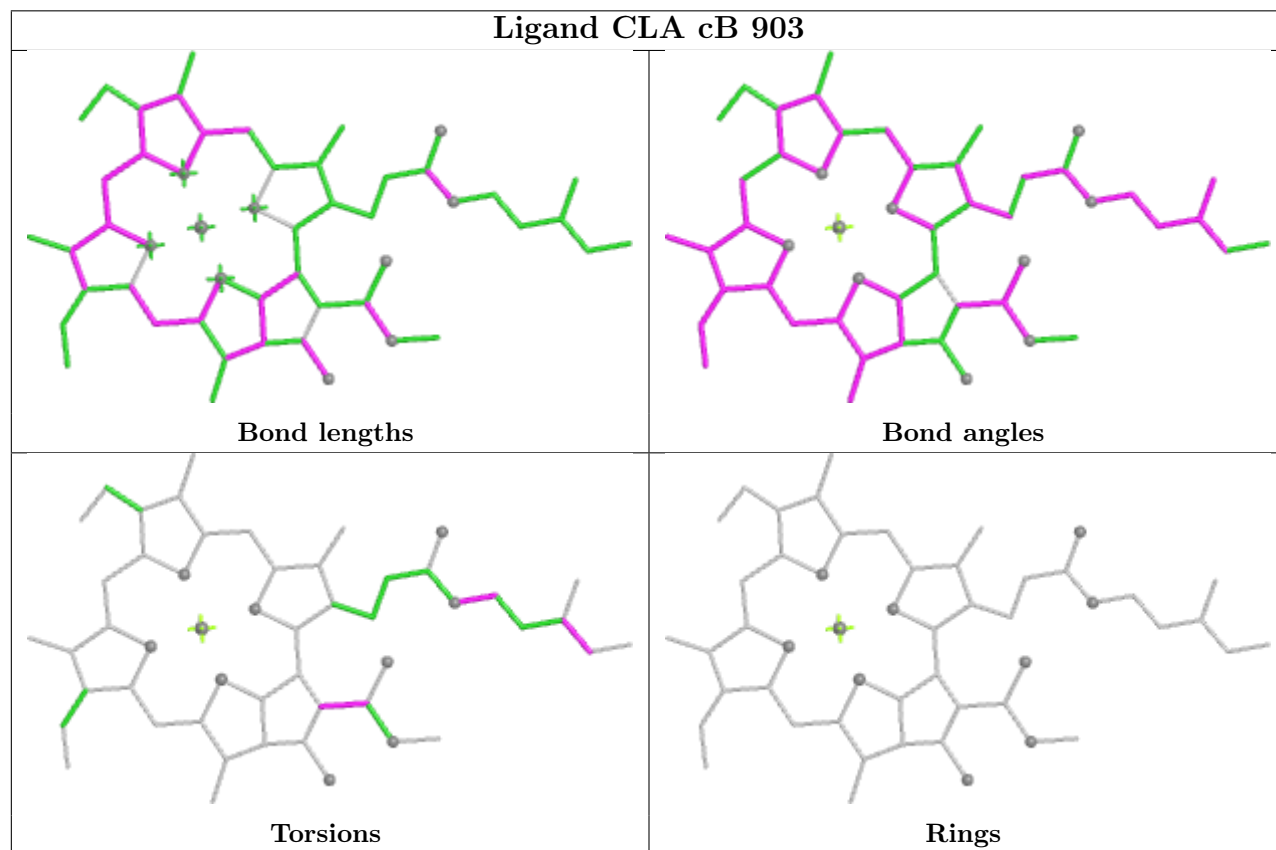
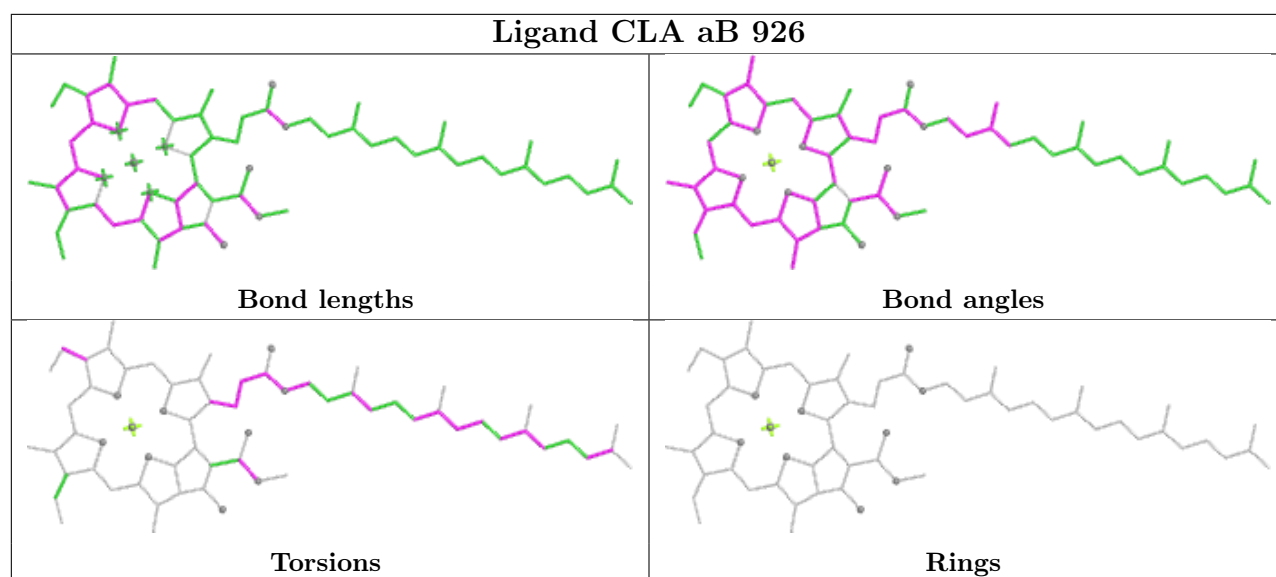


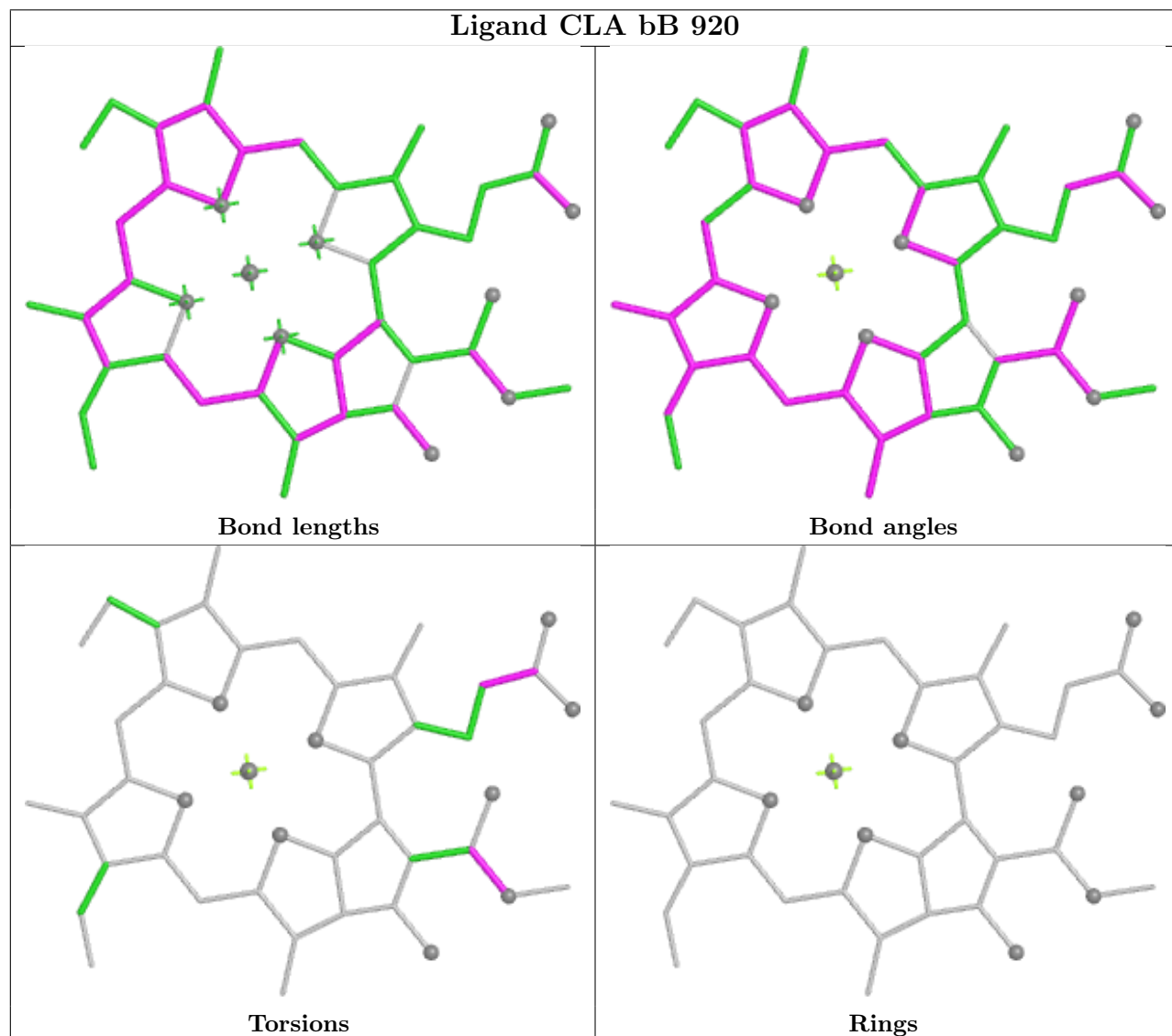
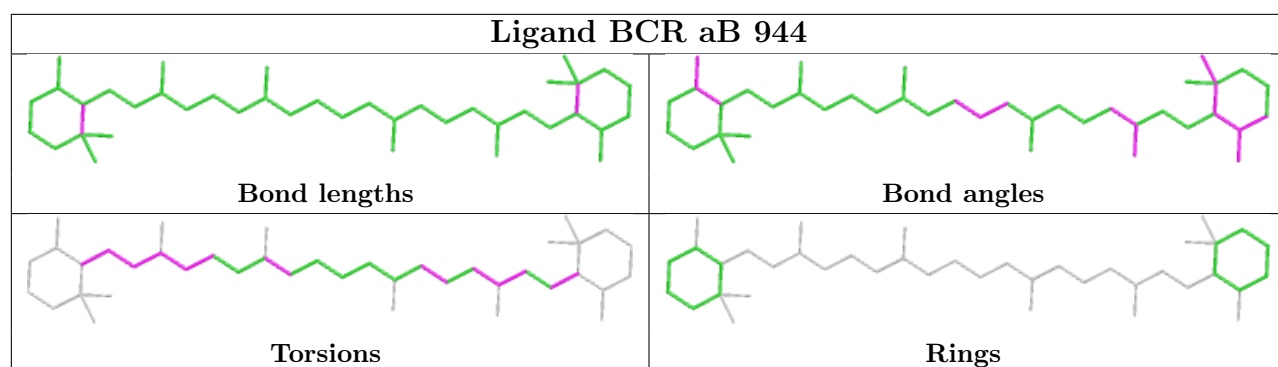


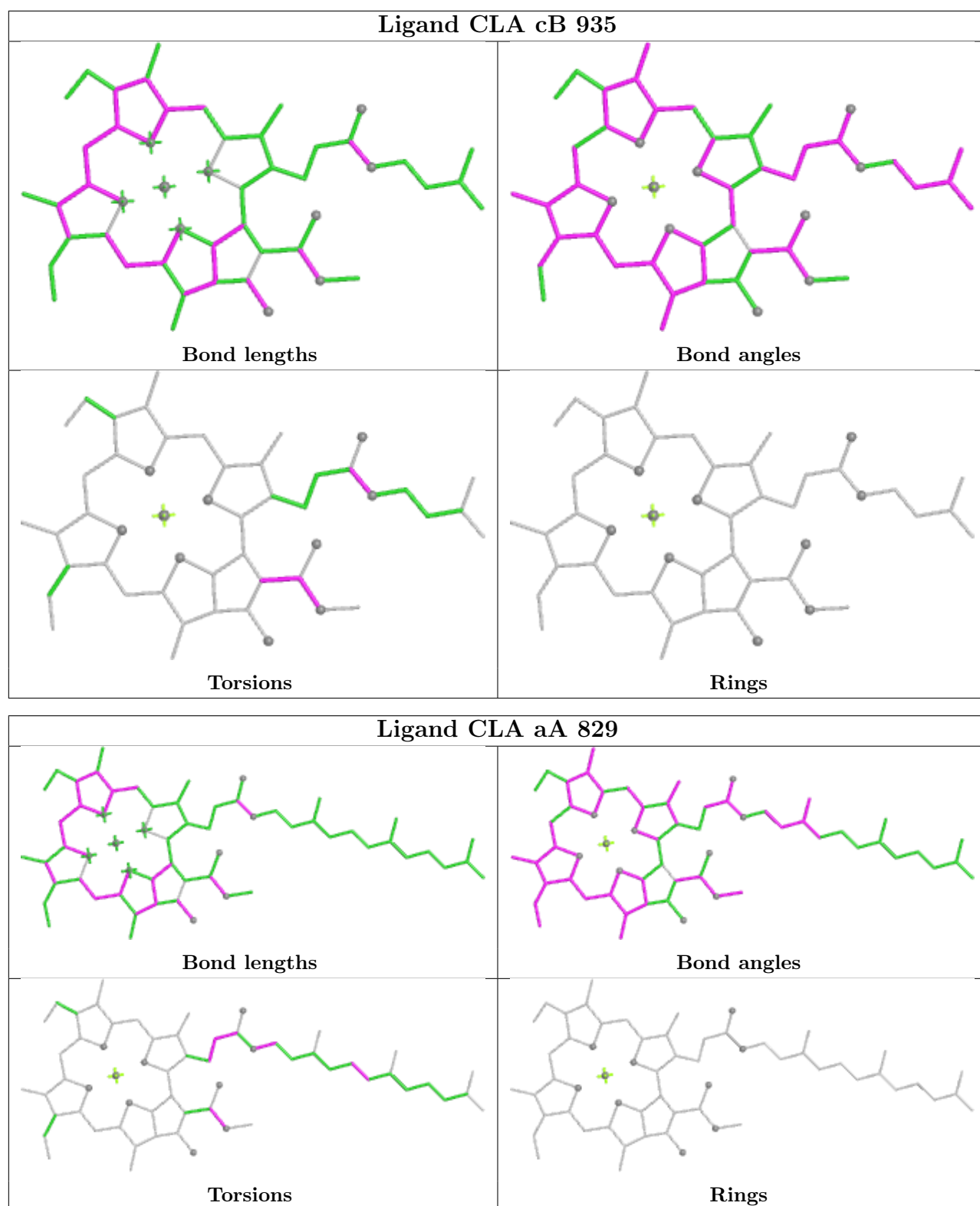


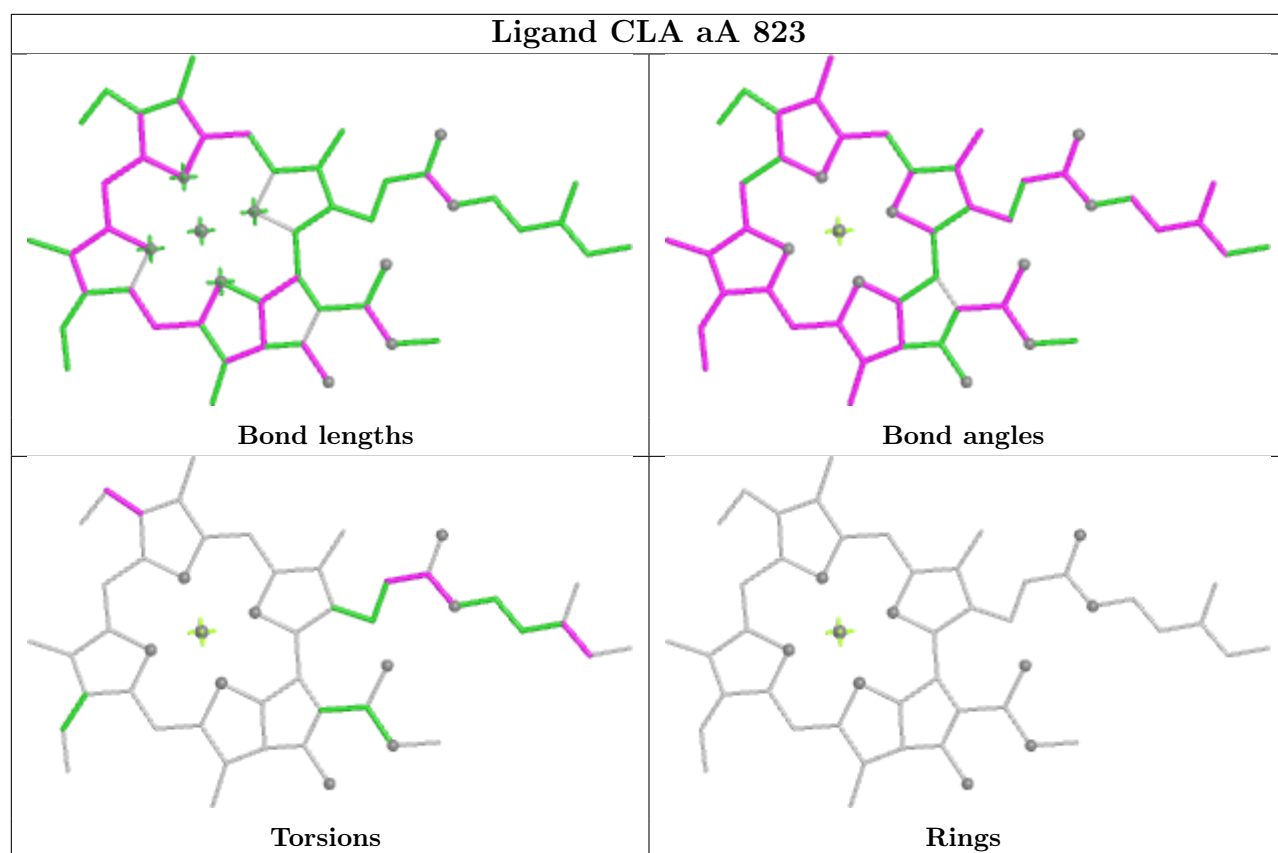


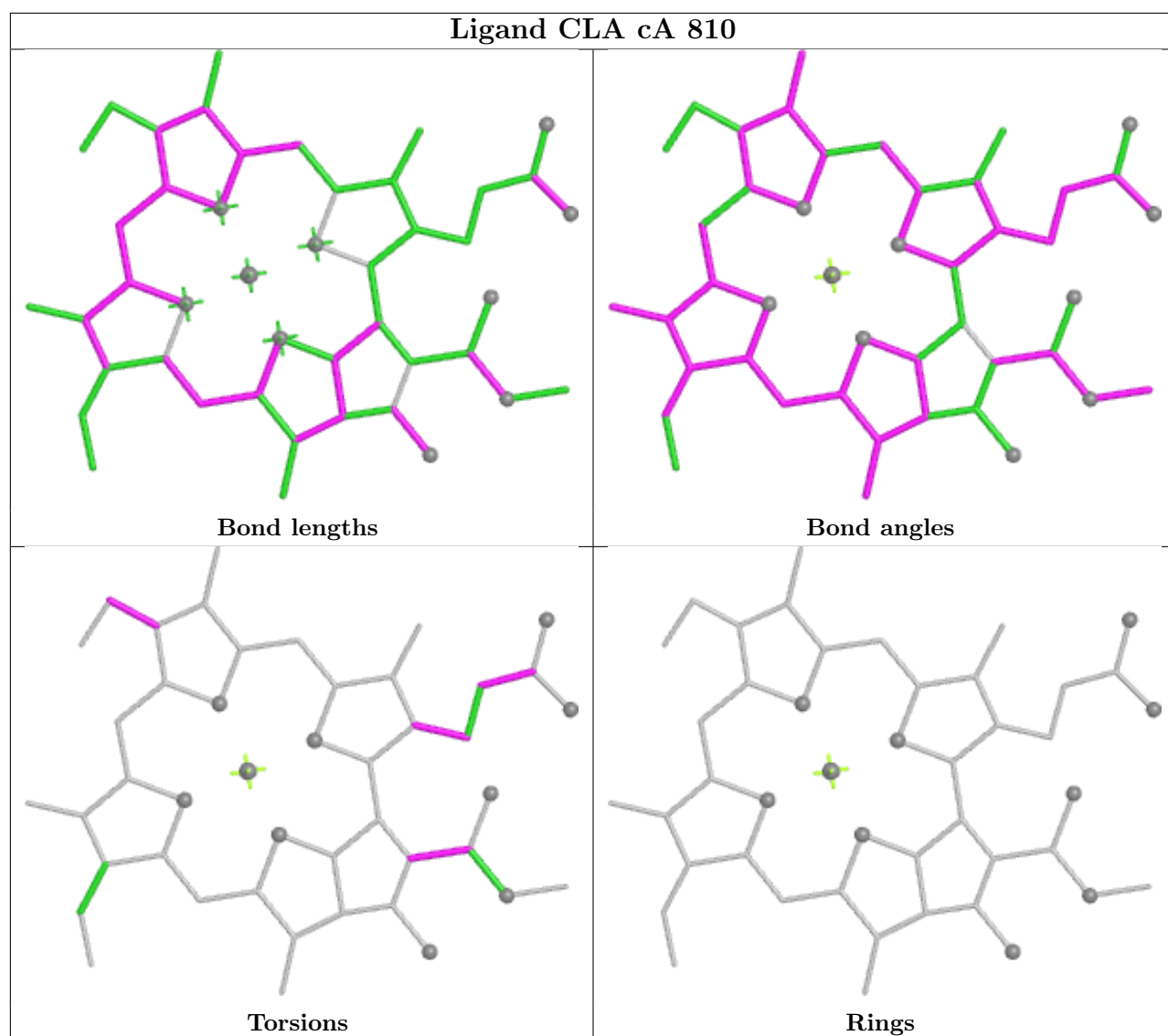


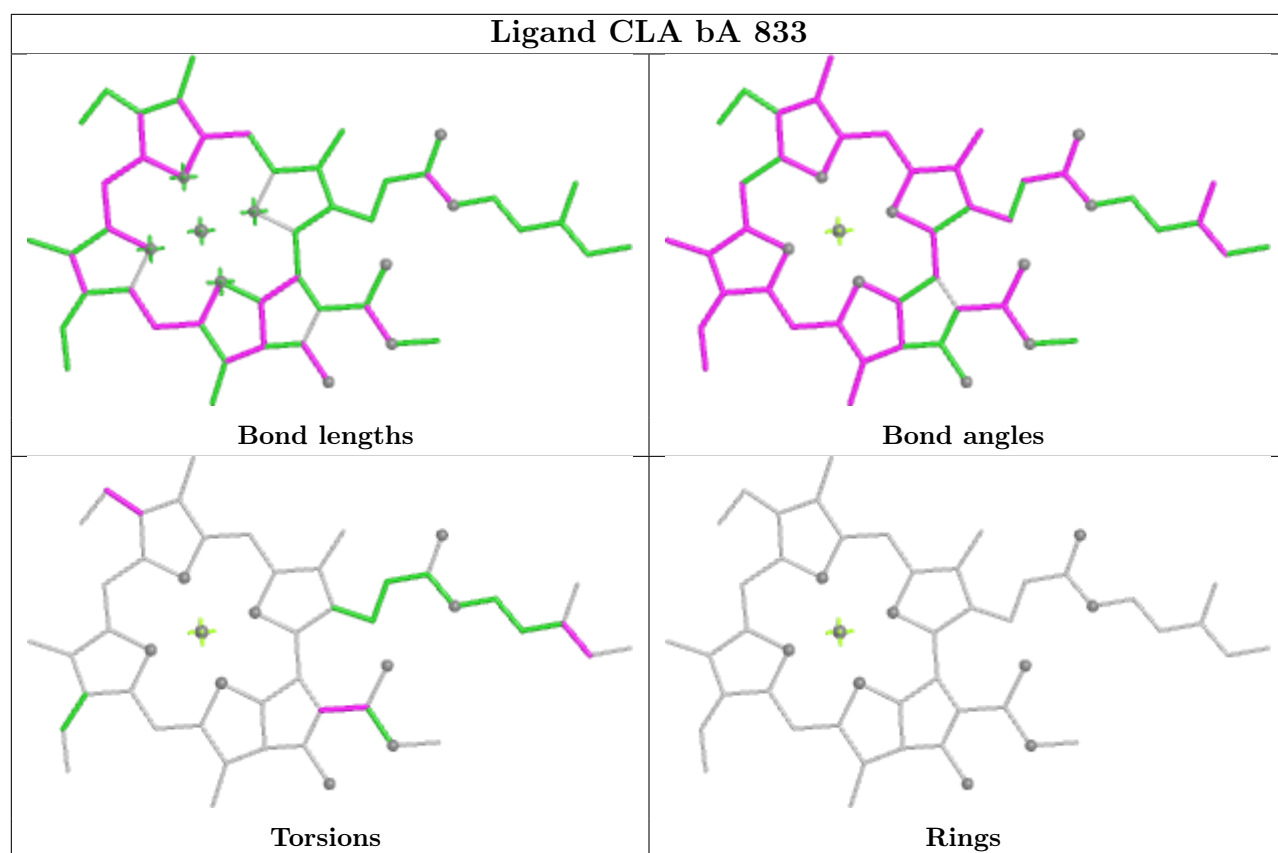


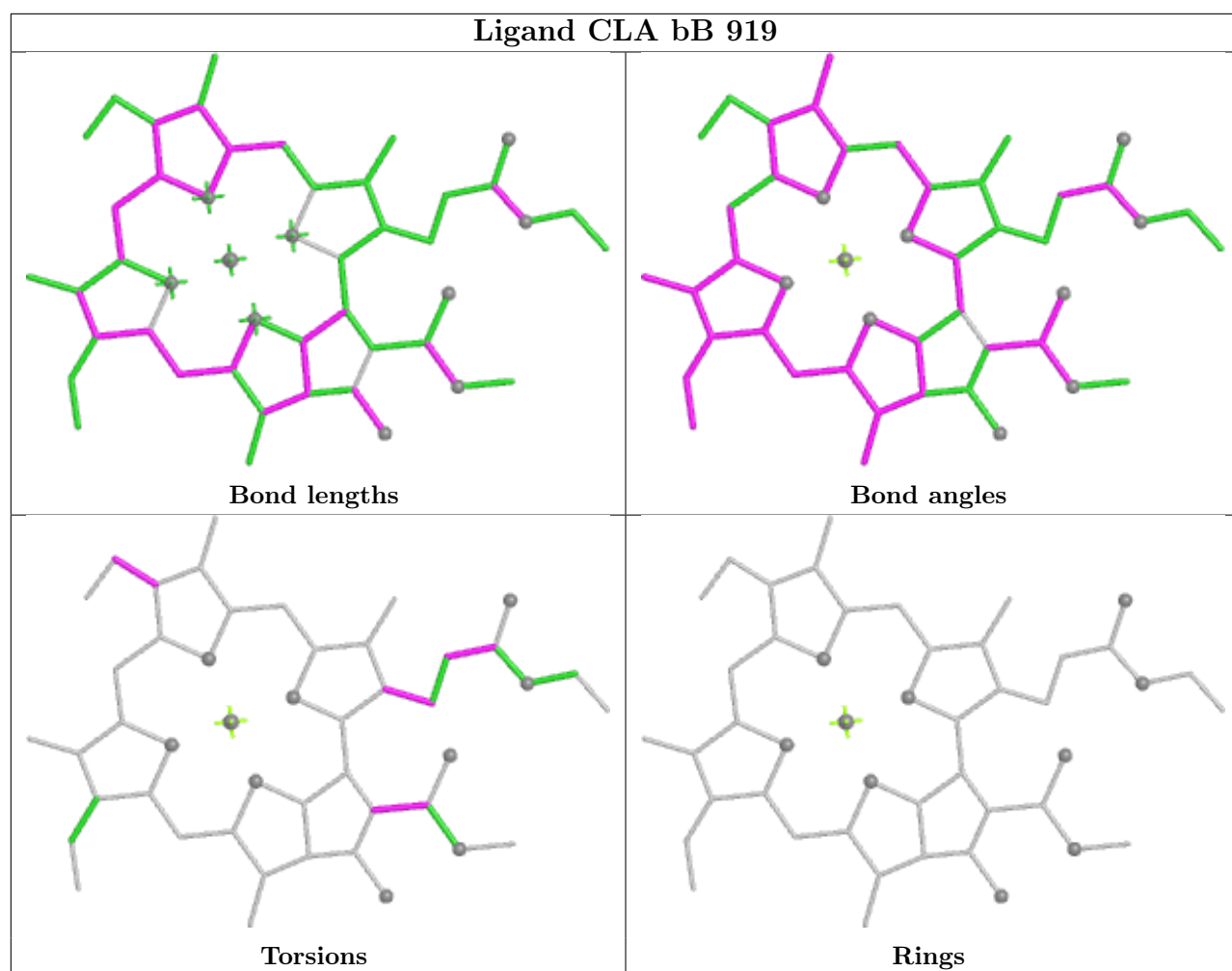




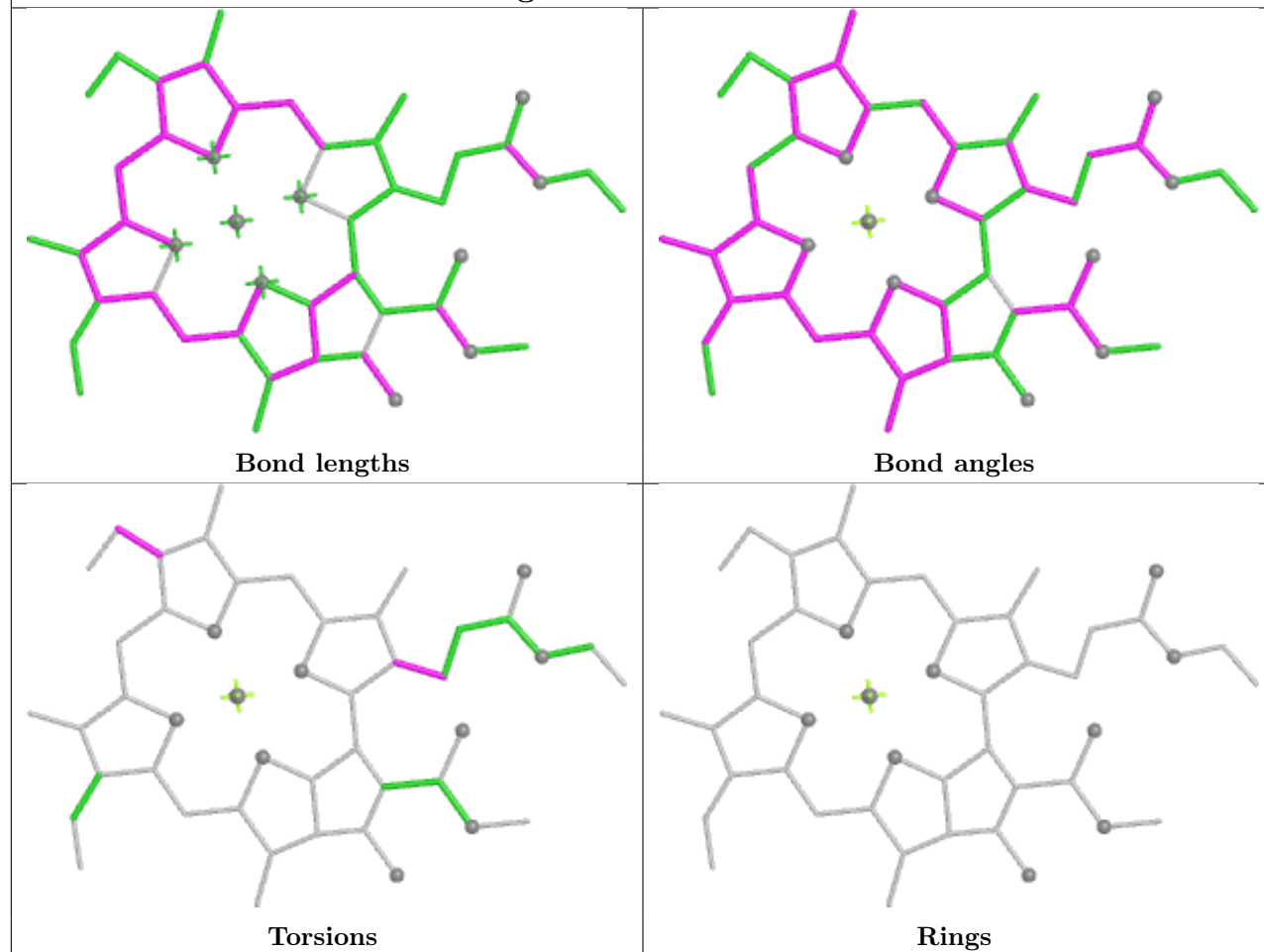




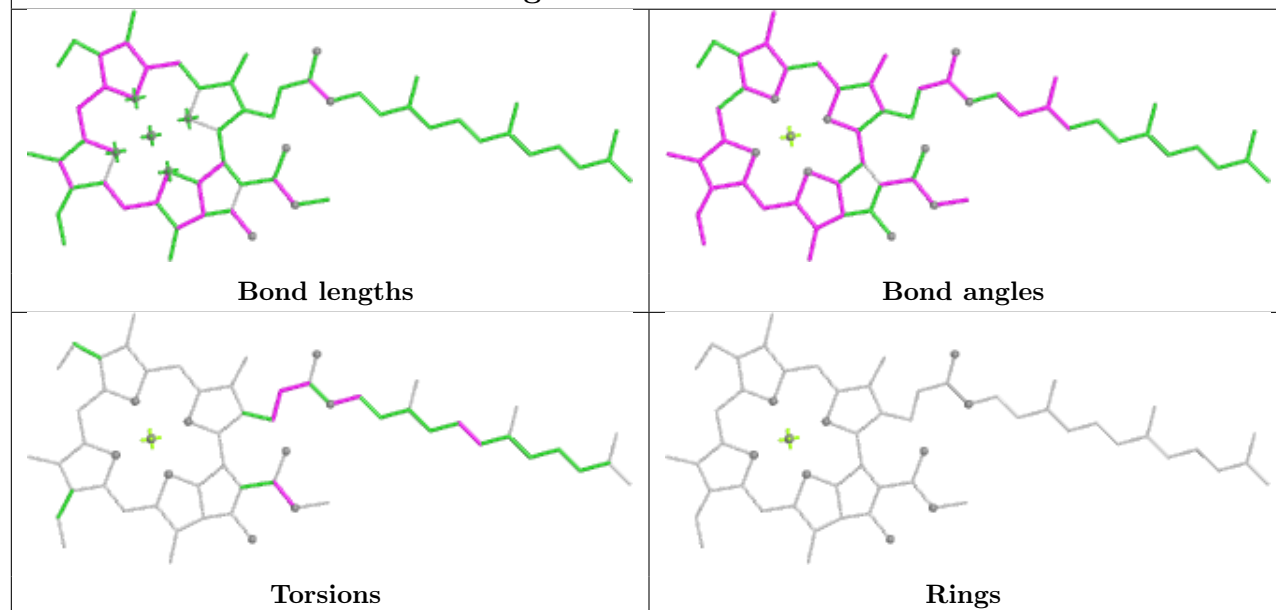


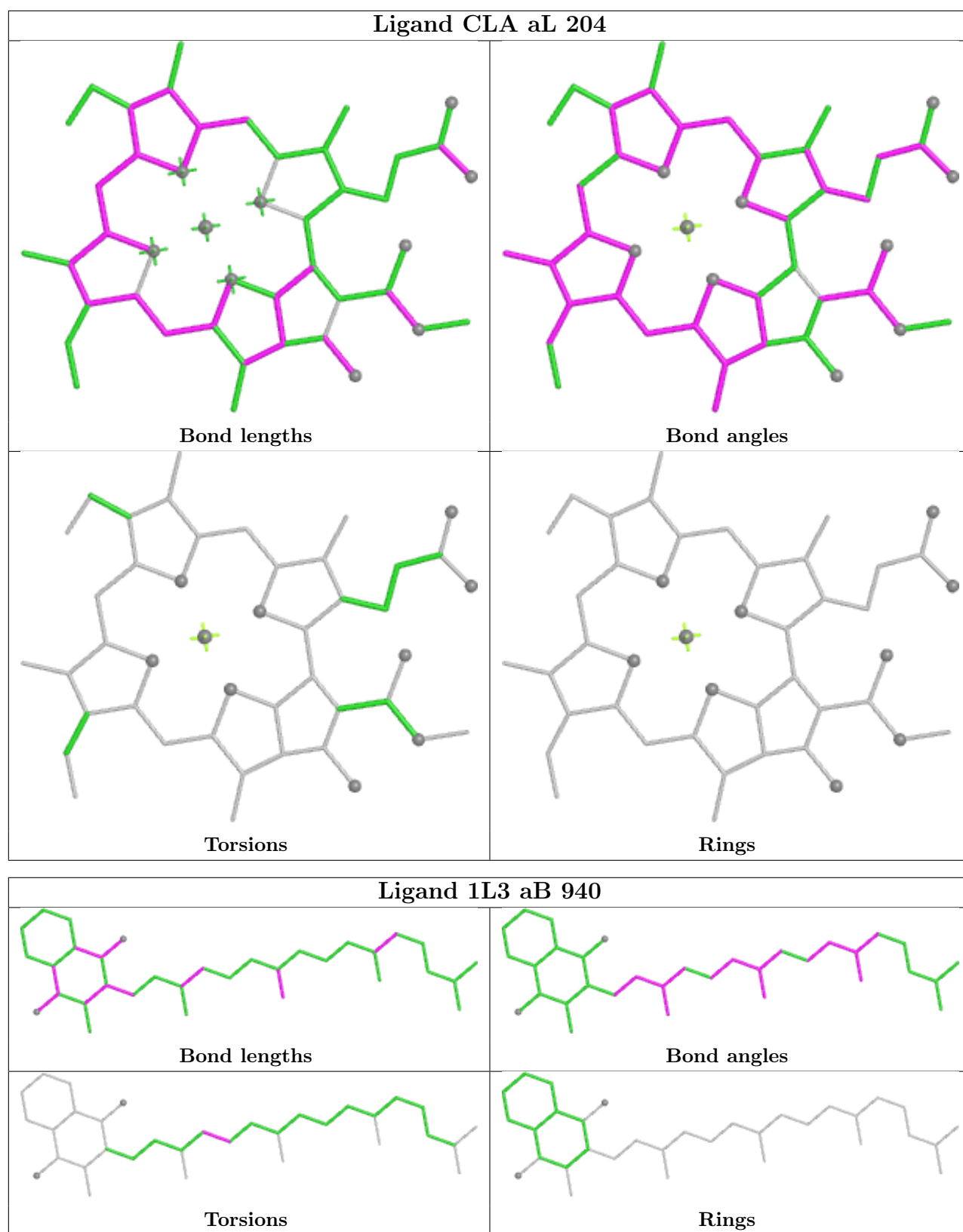


Ligand CLA bB 937

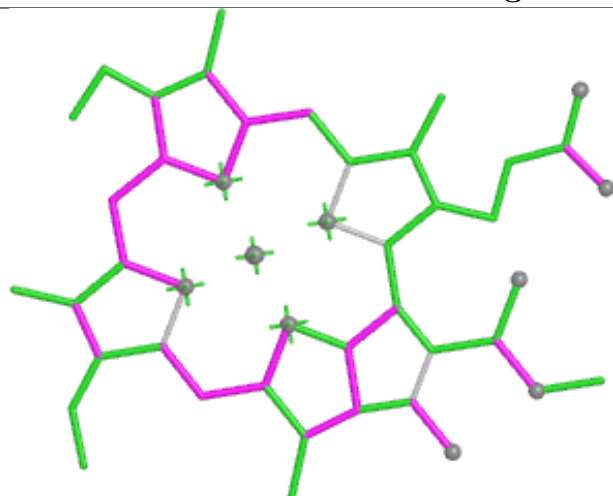


Ligand CLA cA 829

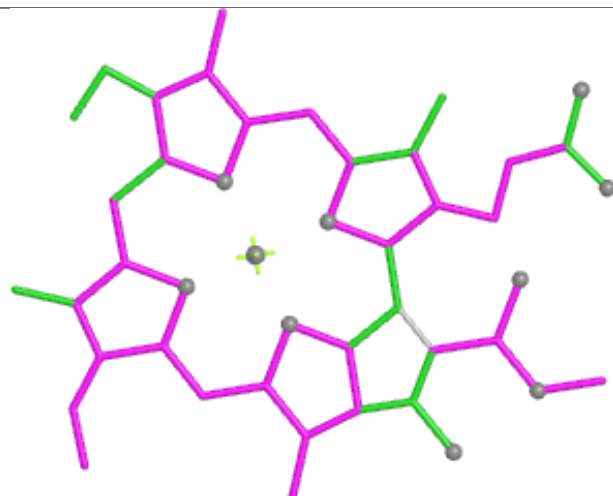




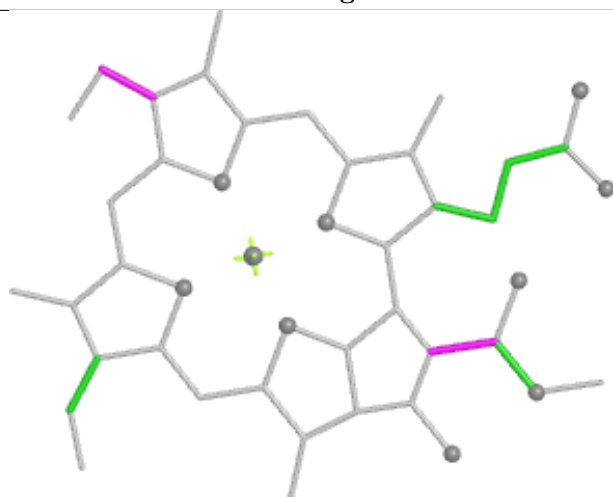
Ligand CLA bB 932



Bond lengths



Bond angles

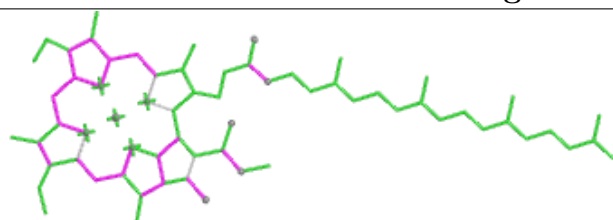


Torsions

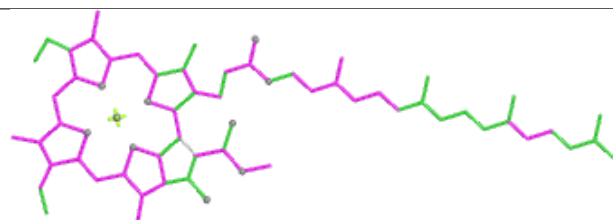


Rings

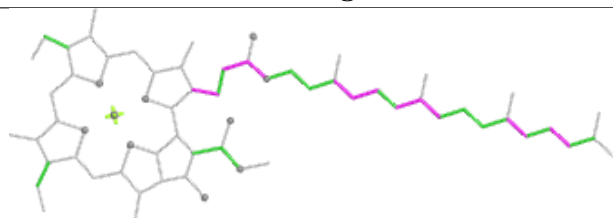
Ligand CLA bA 807



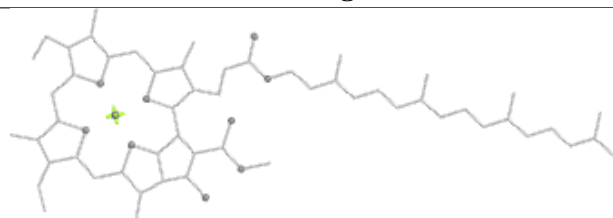
Bond lengths



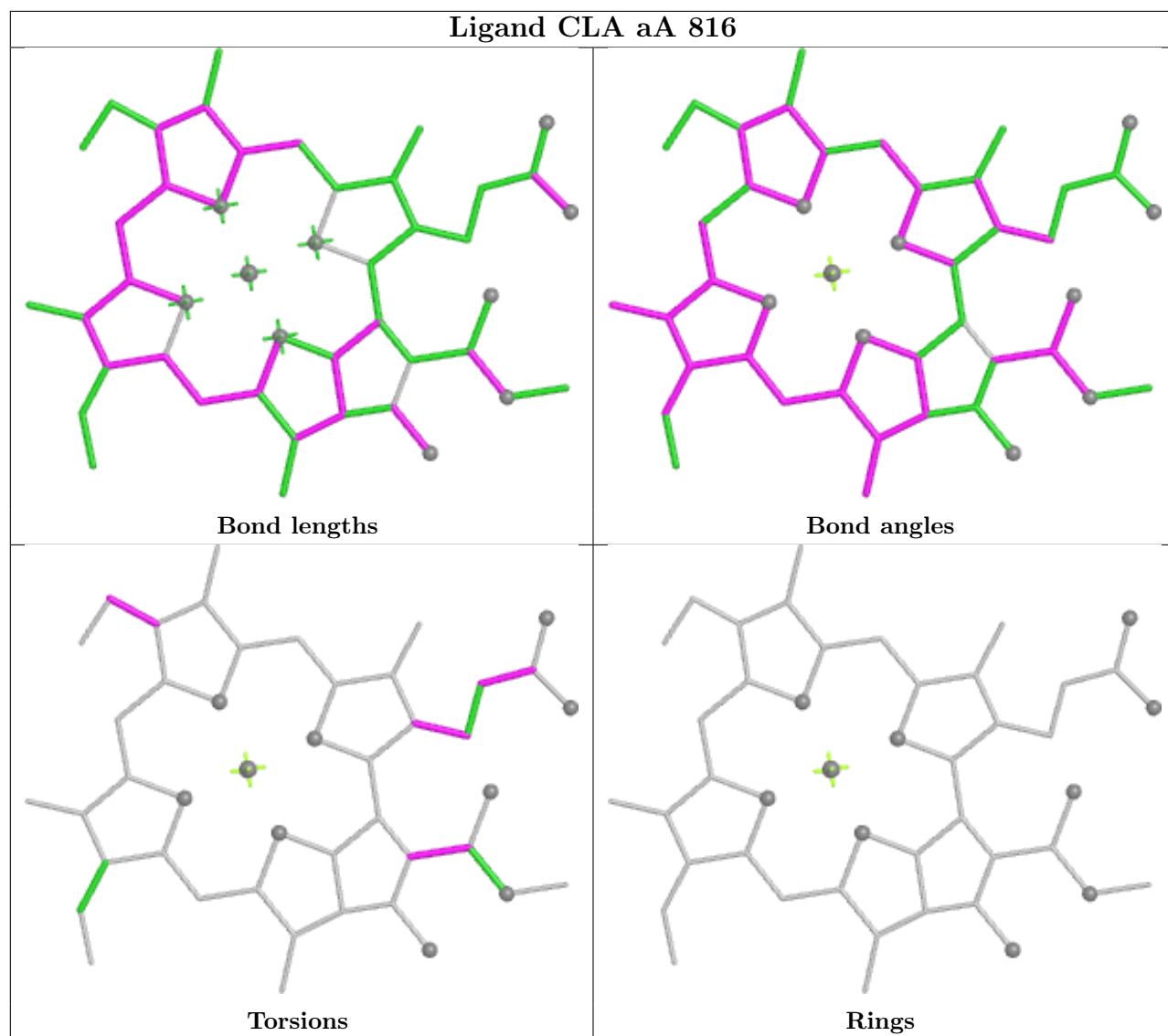
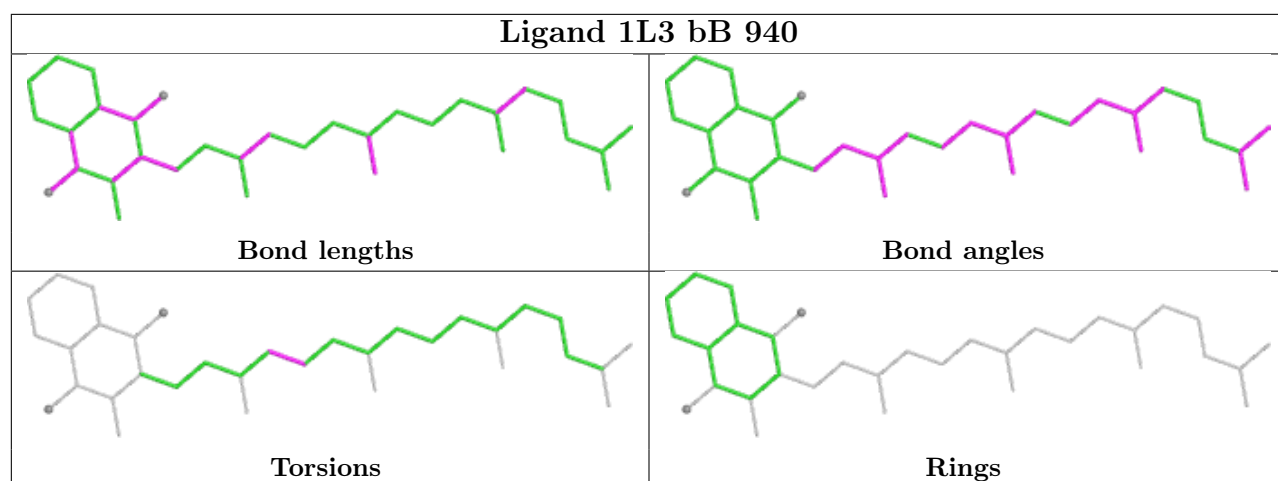
Bond angles

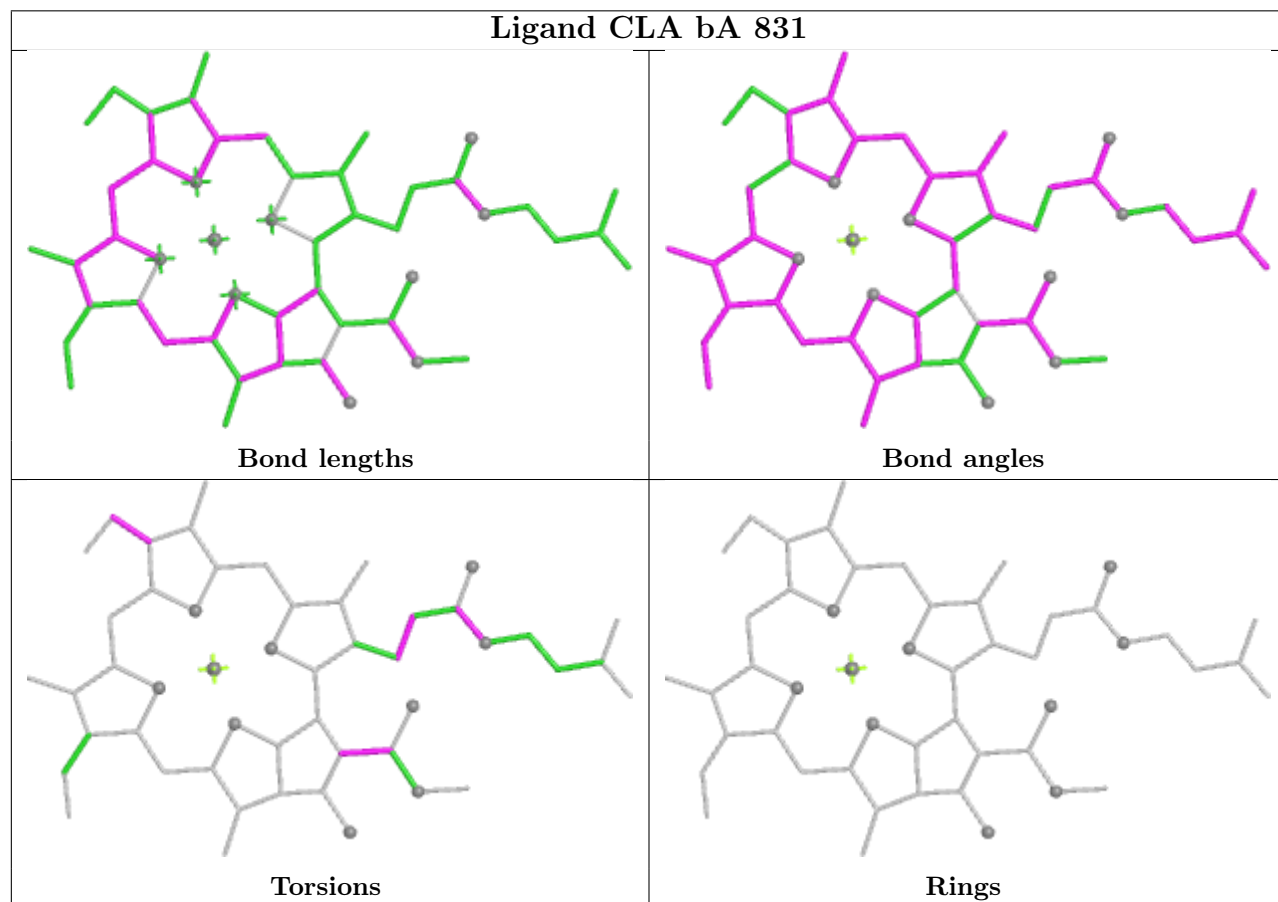
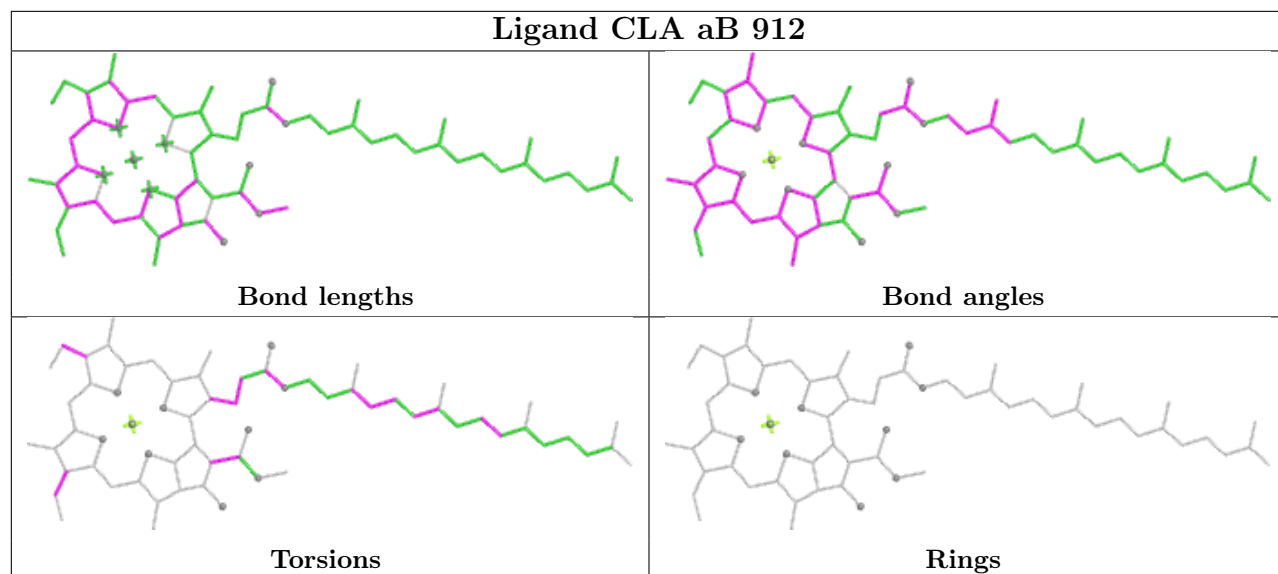


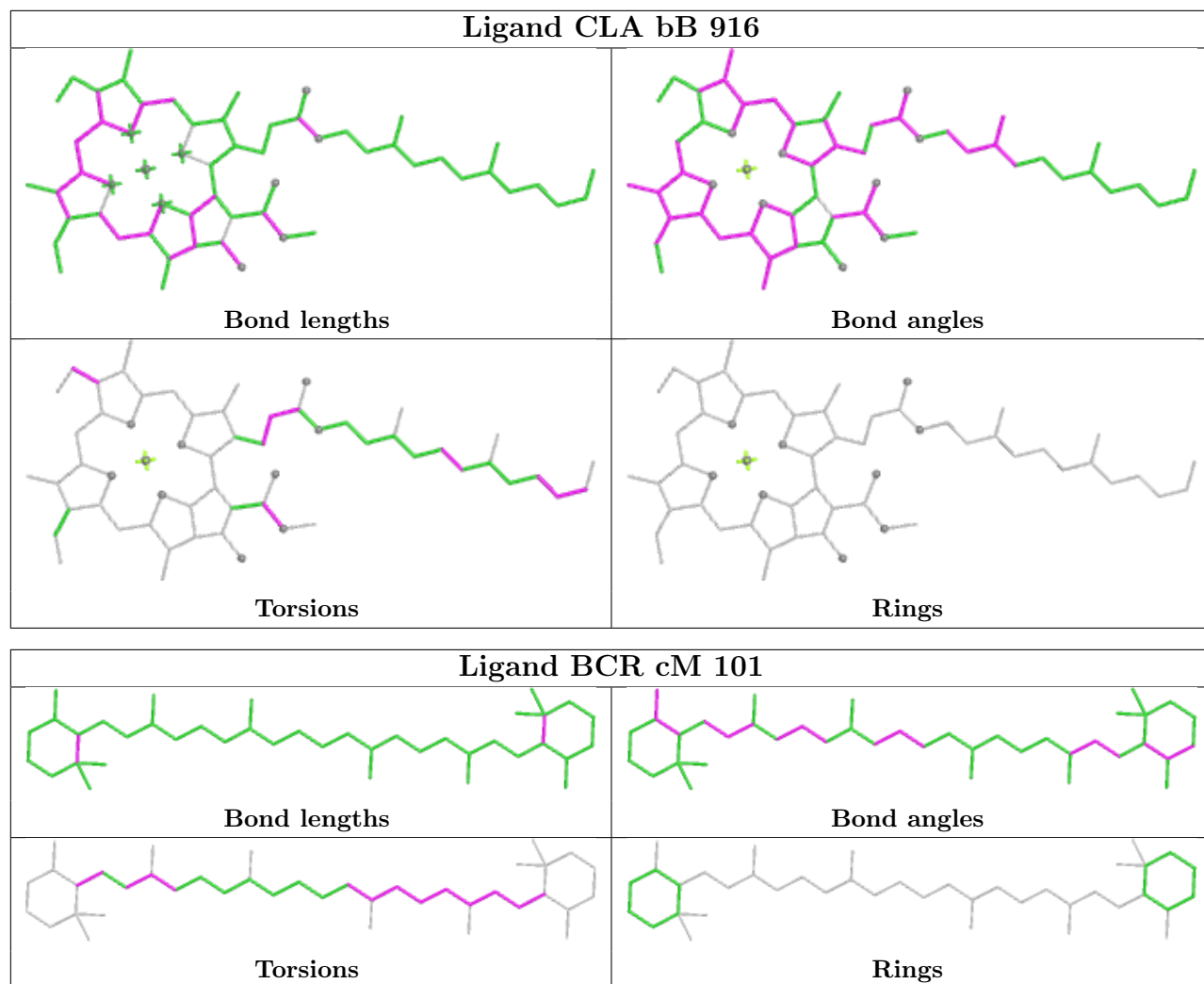
Torsions

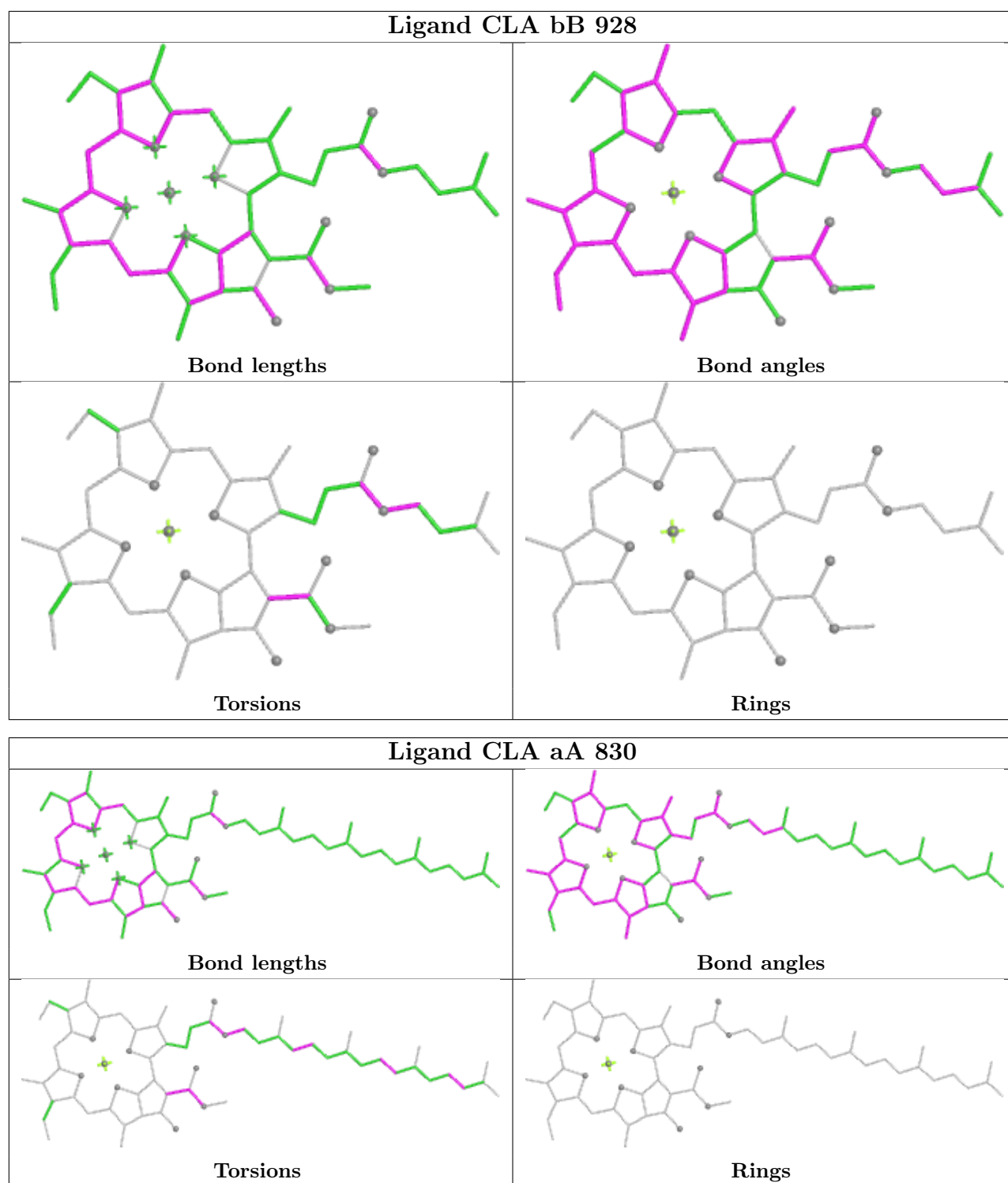


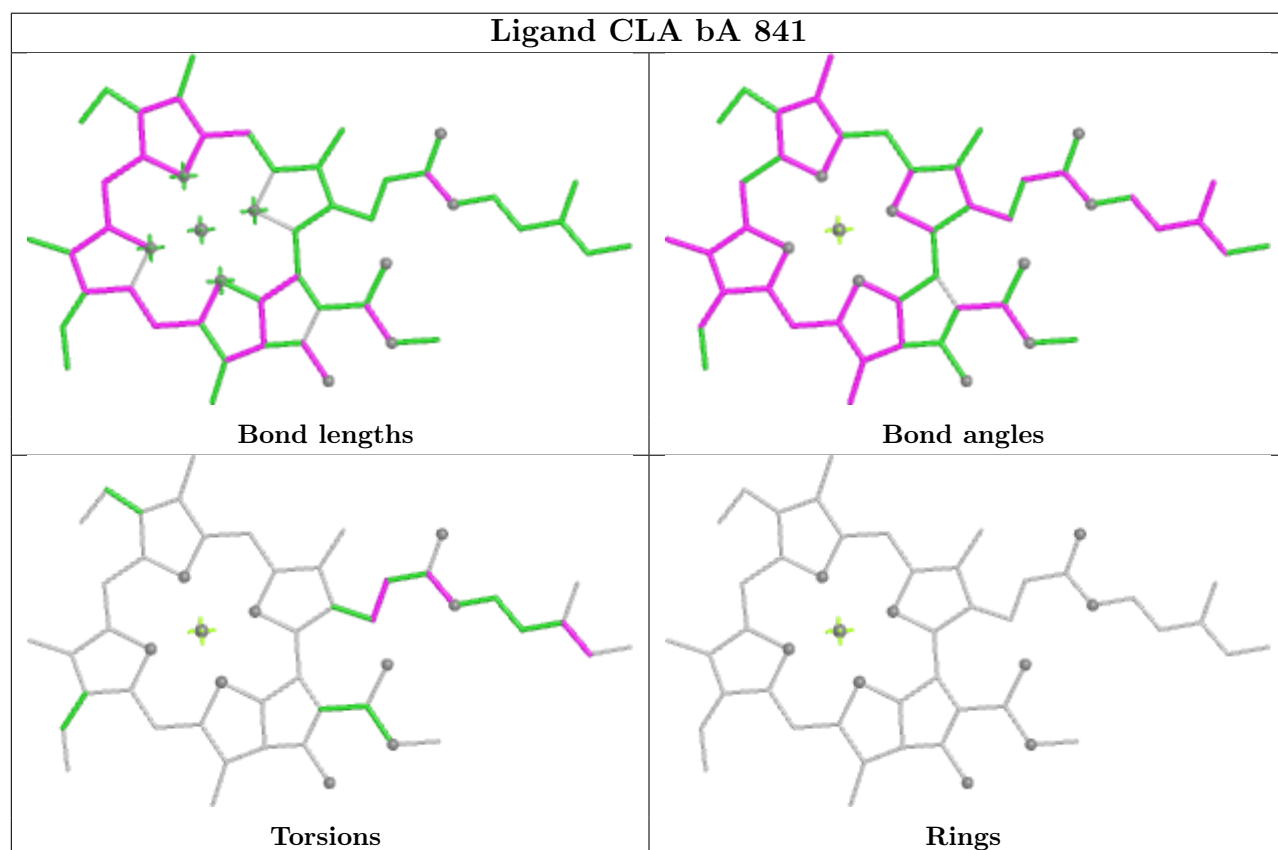
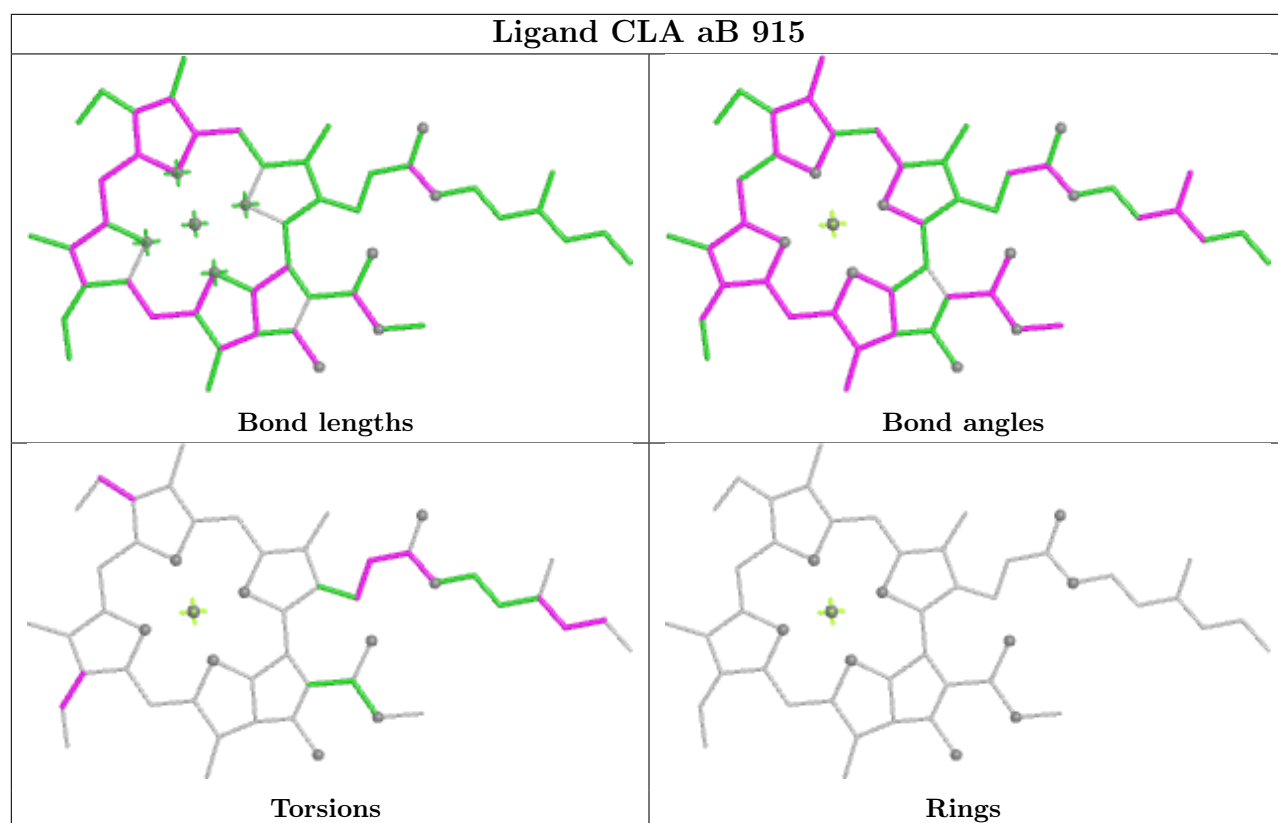
Rings

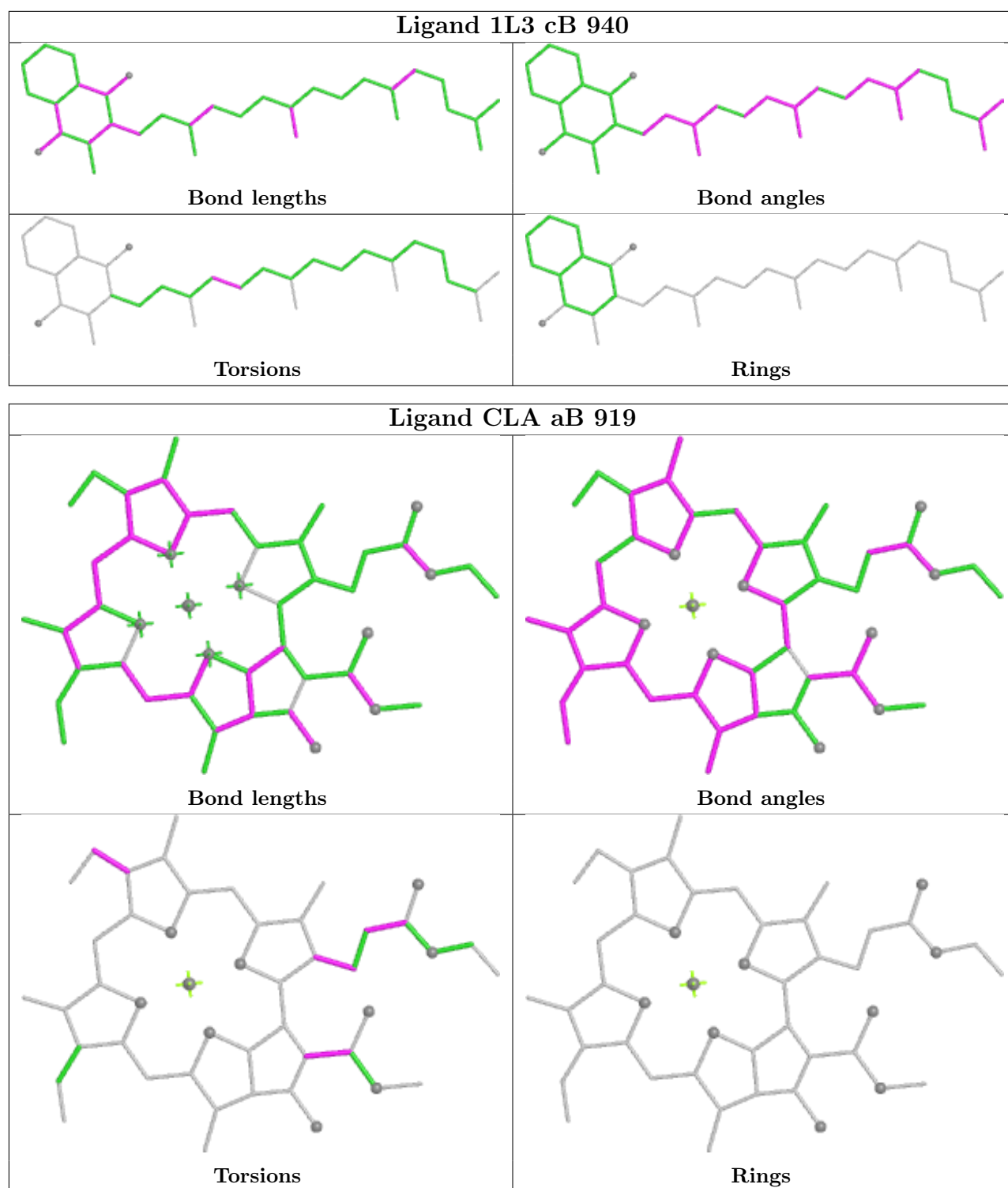


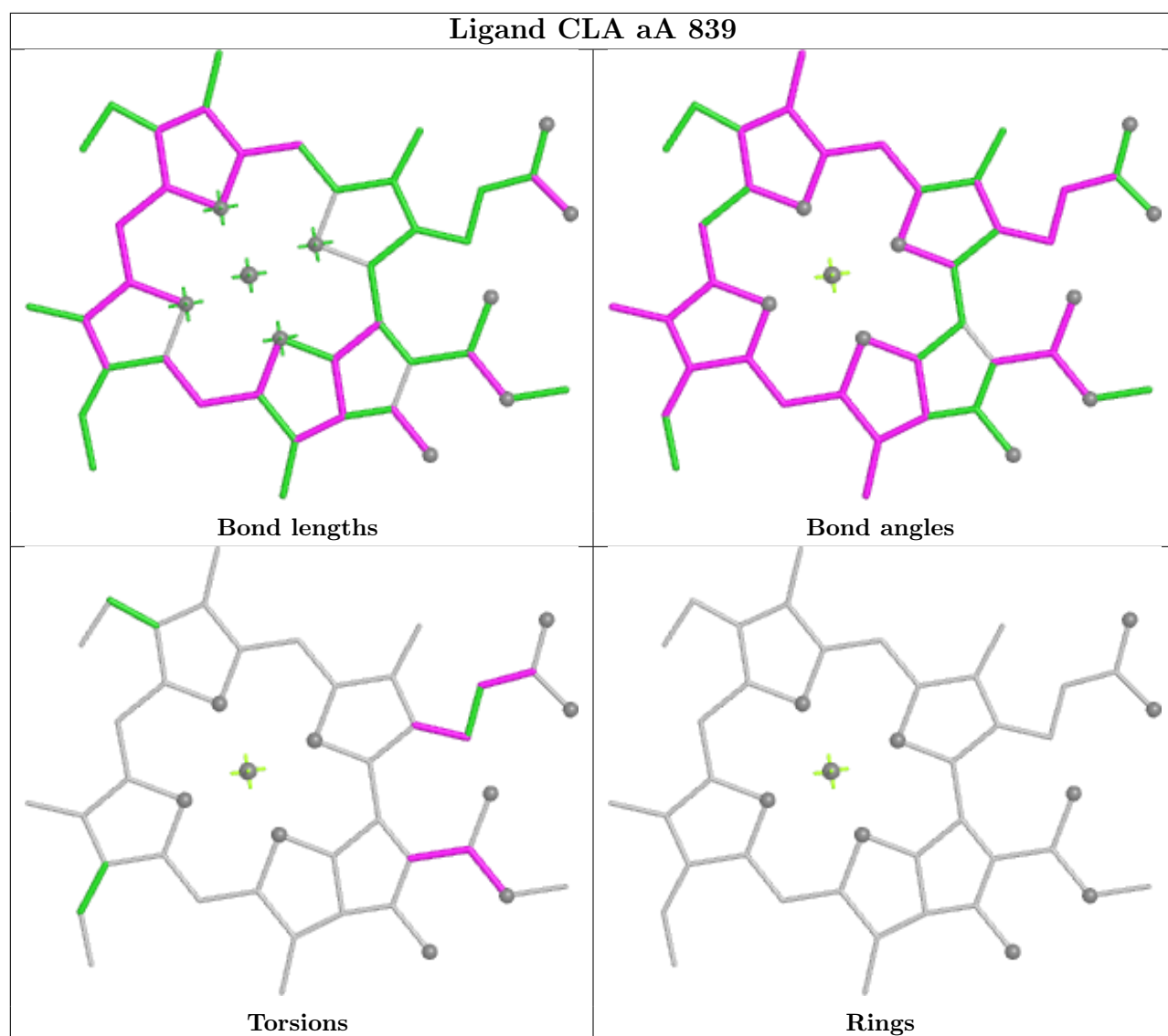


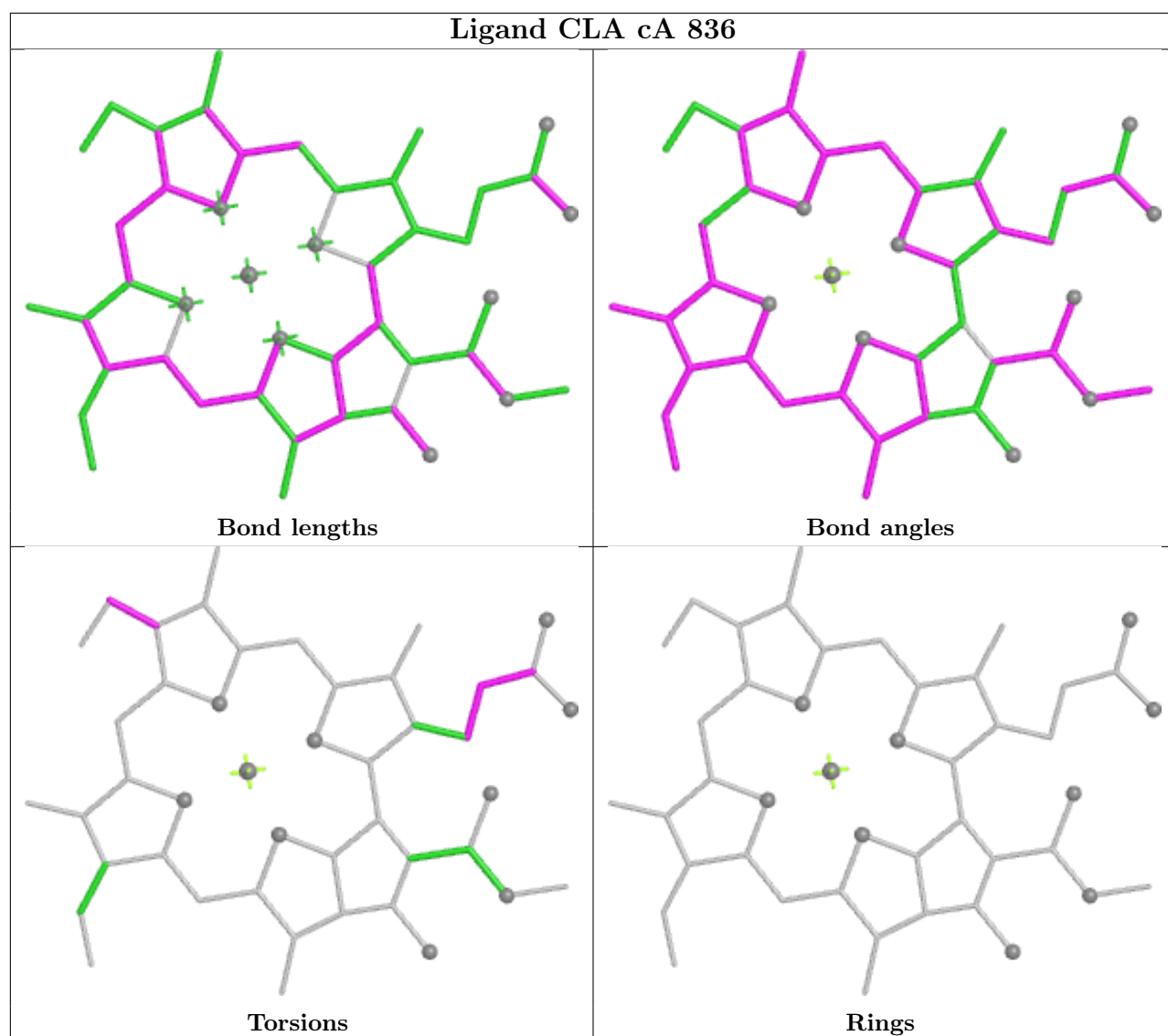


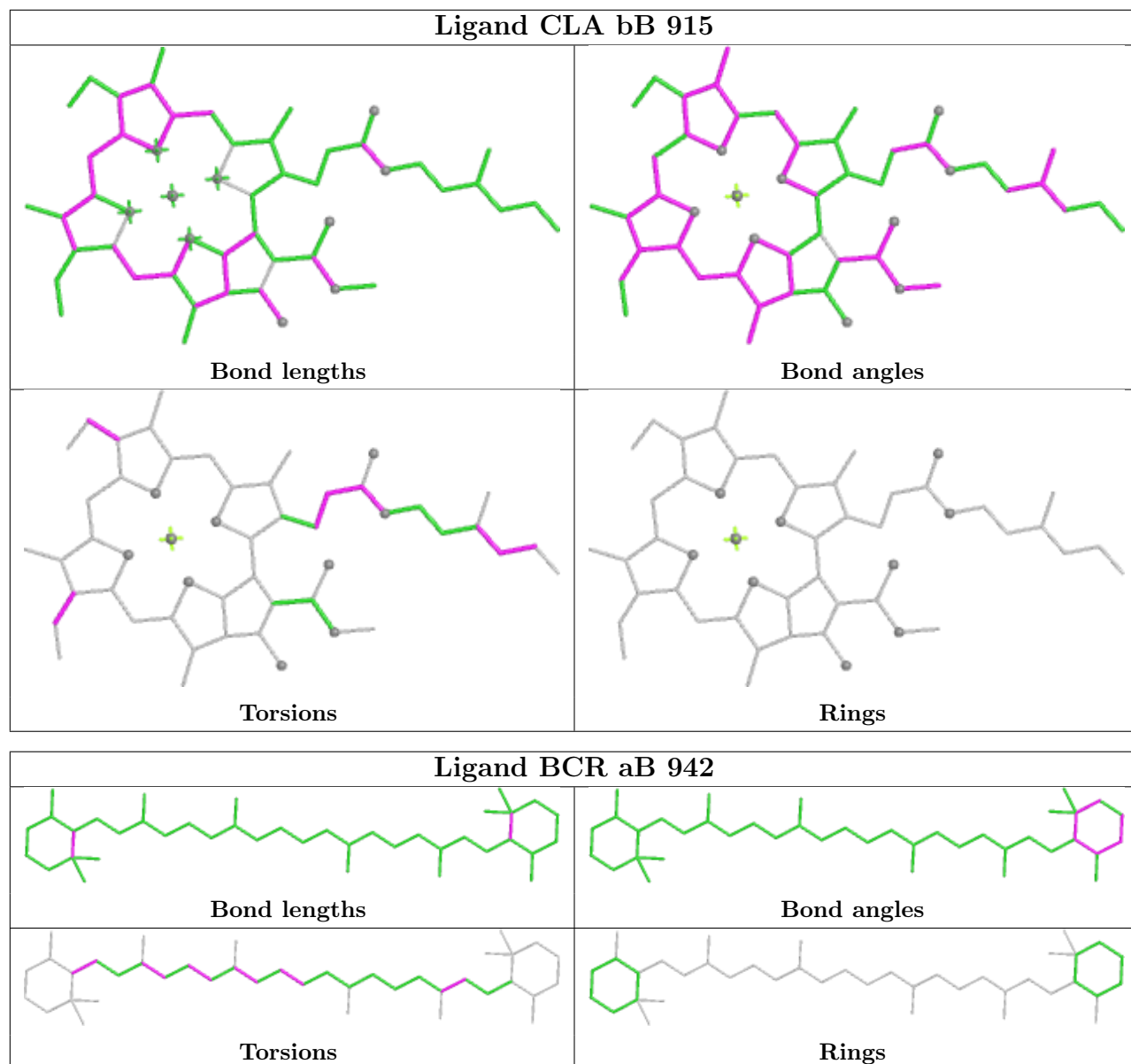


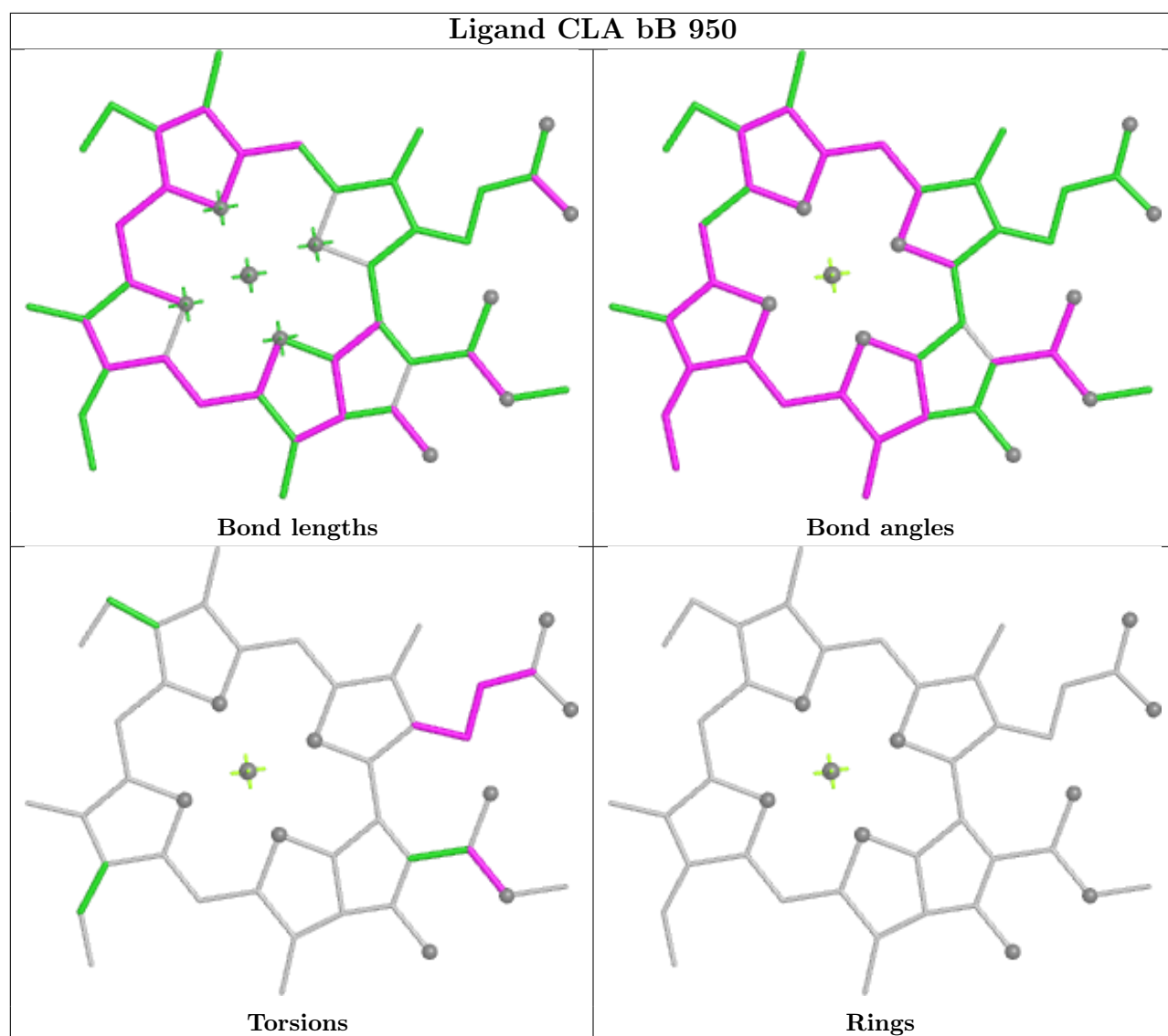


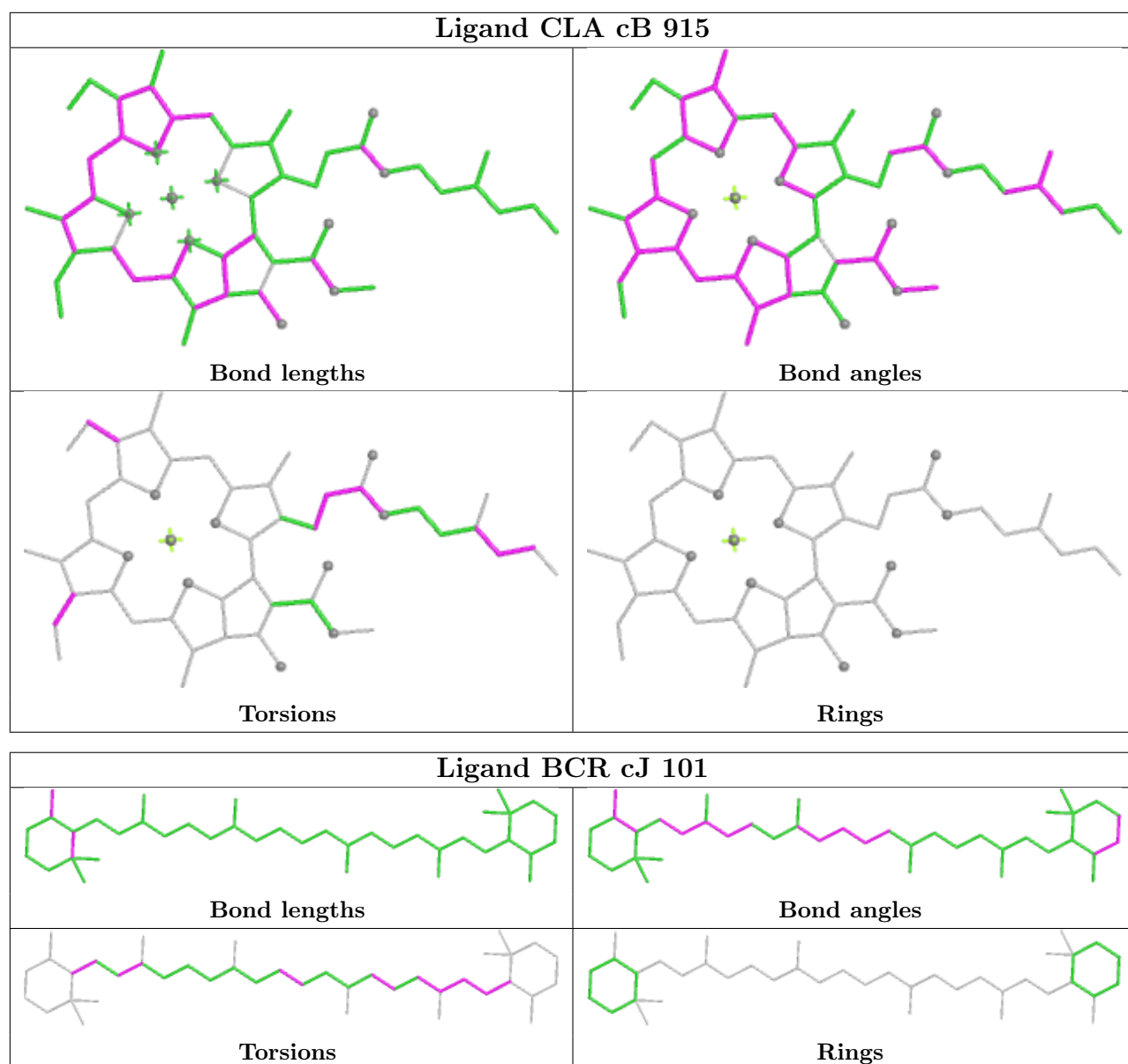


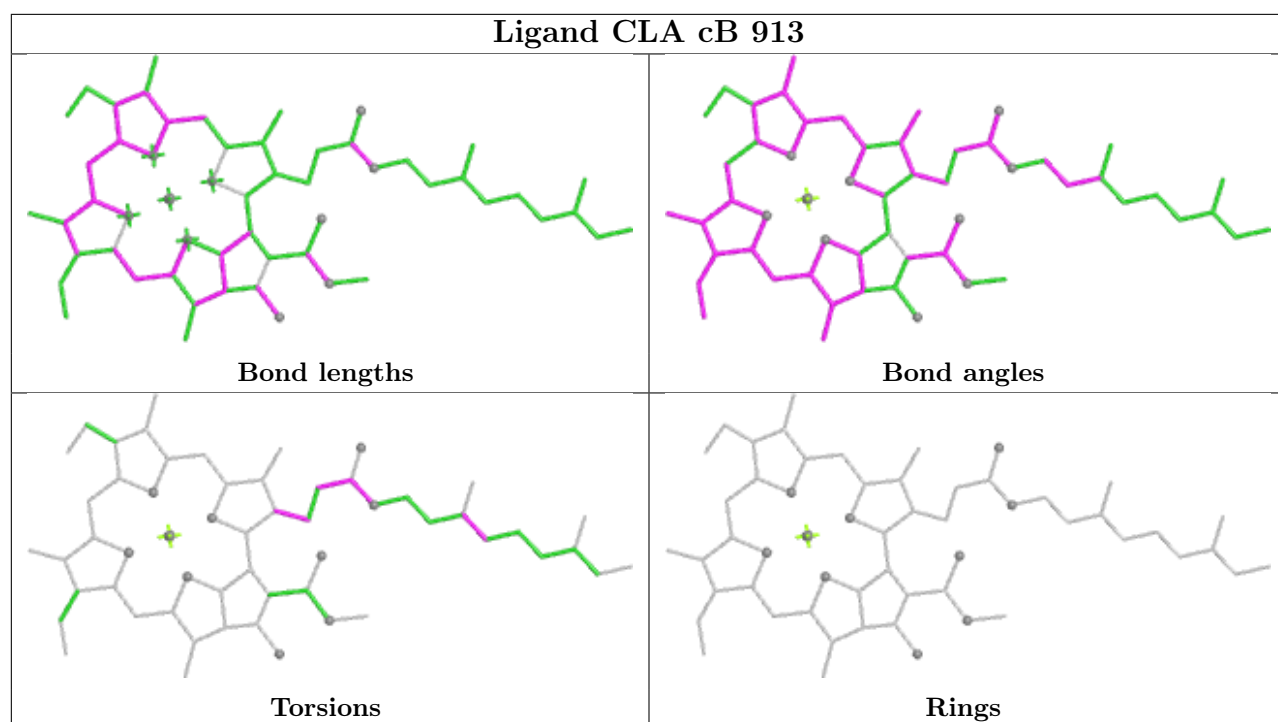


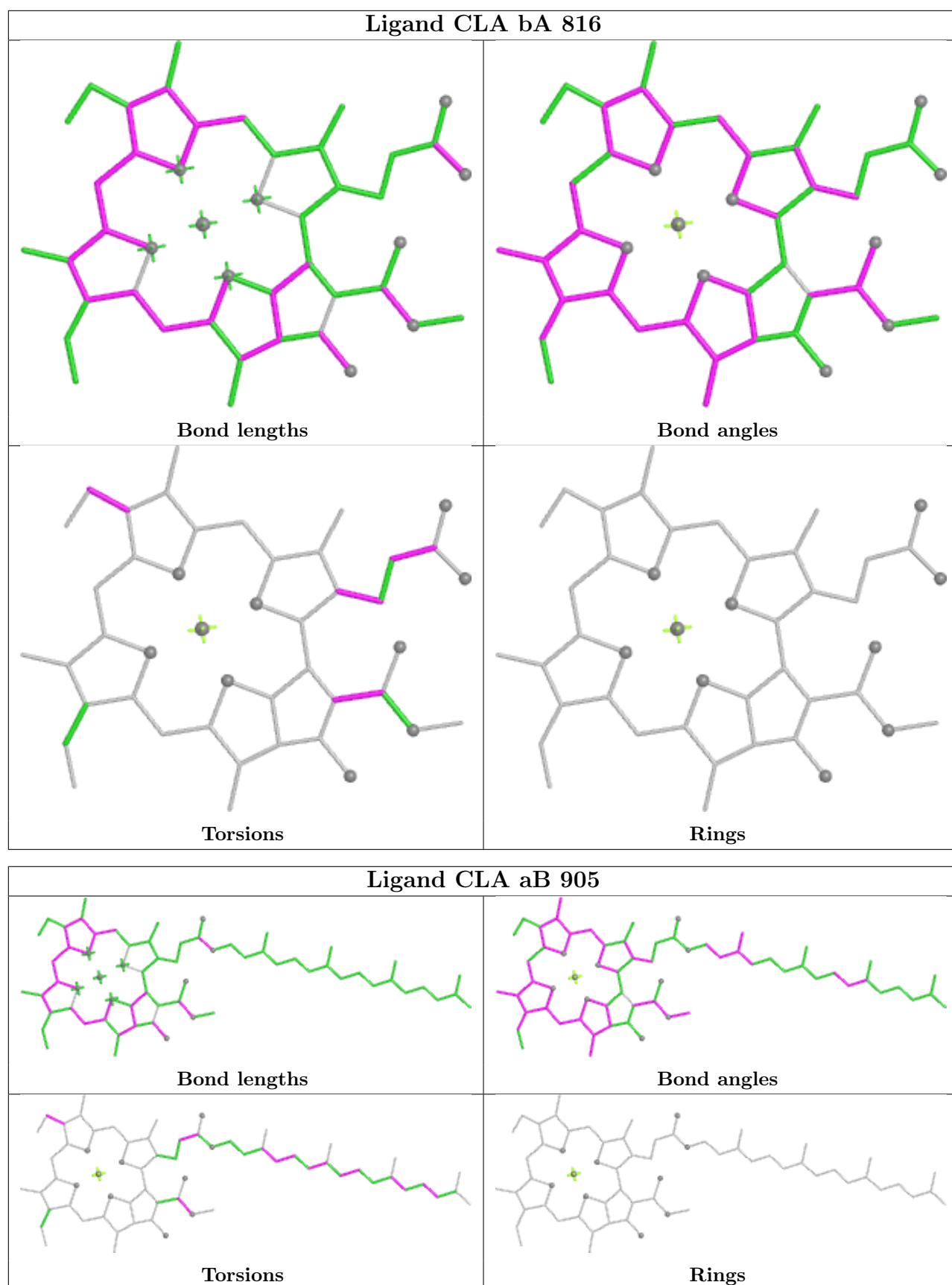


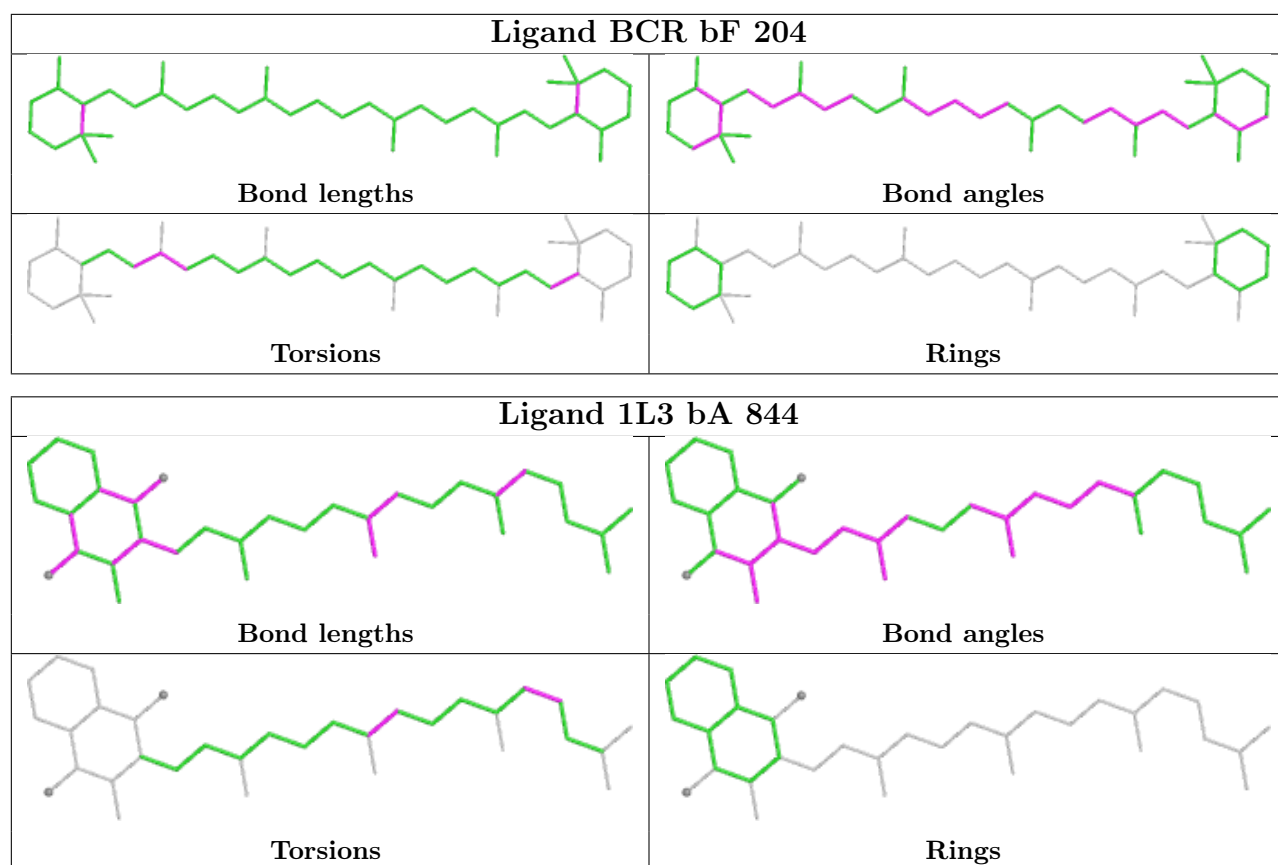


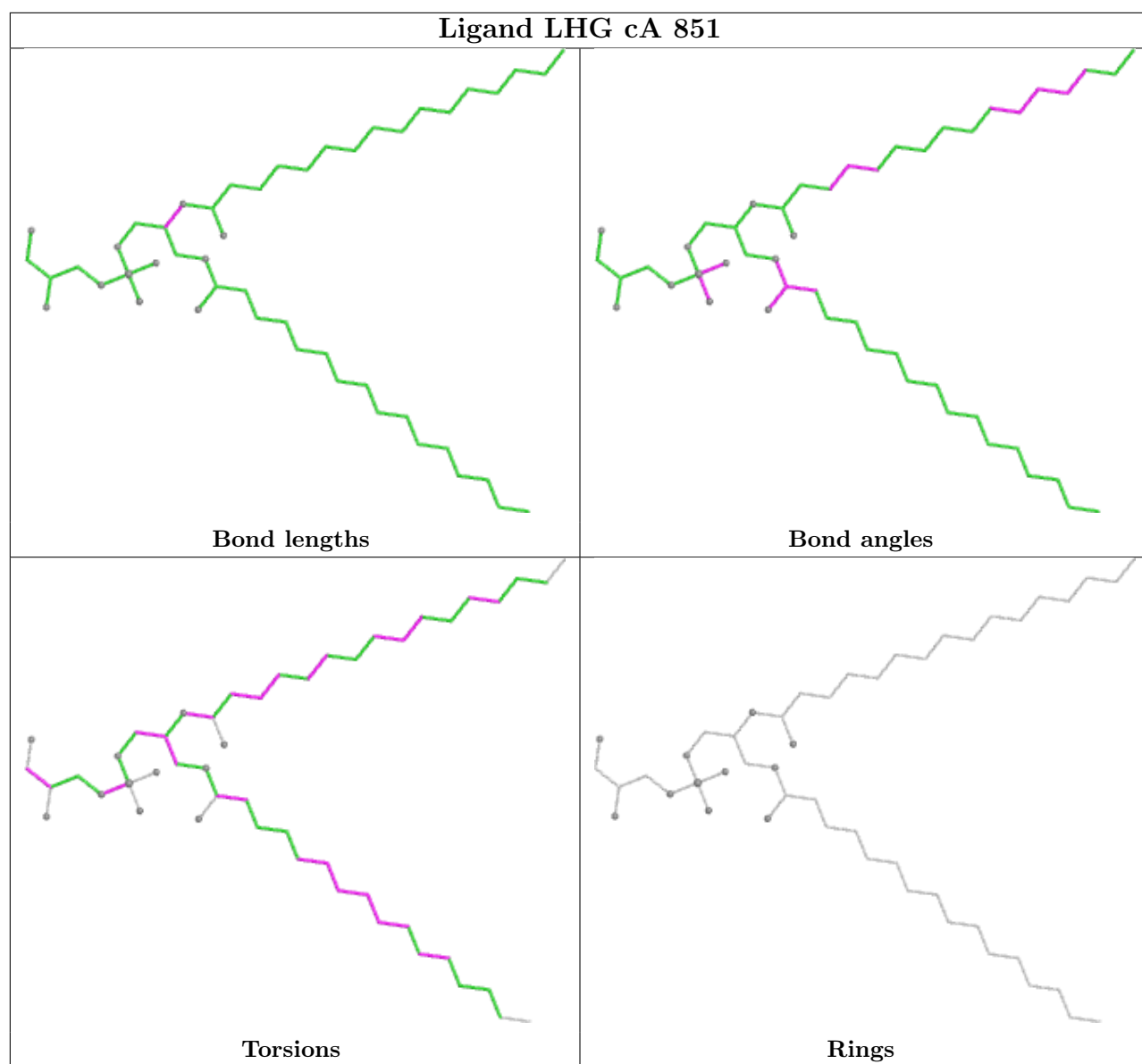


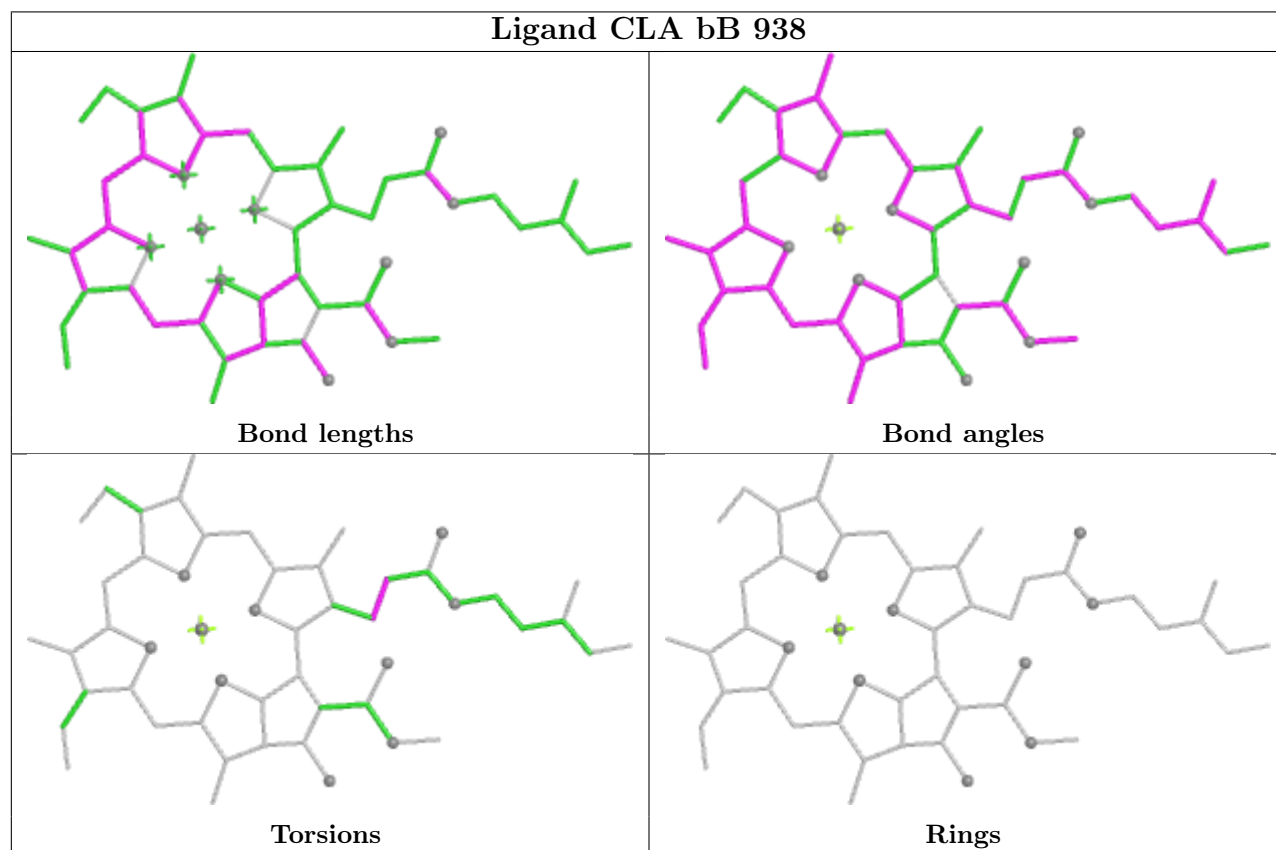
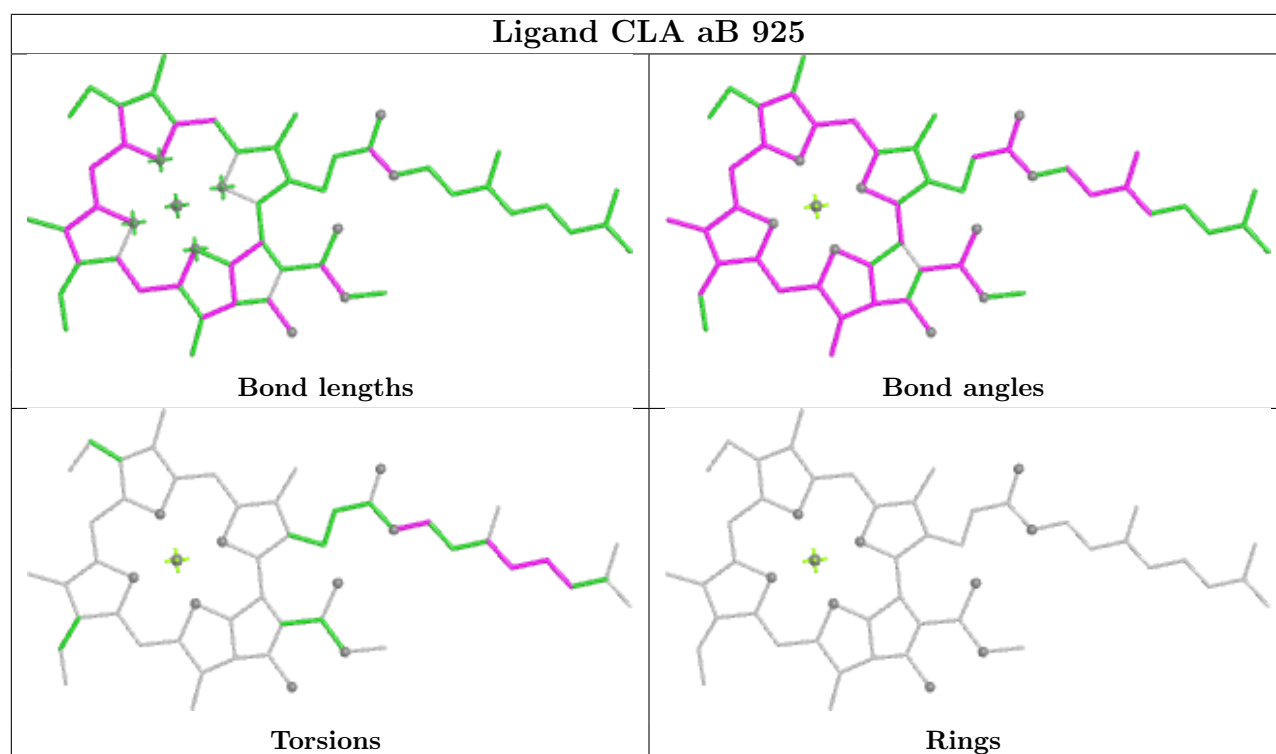


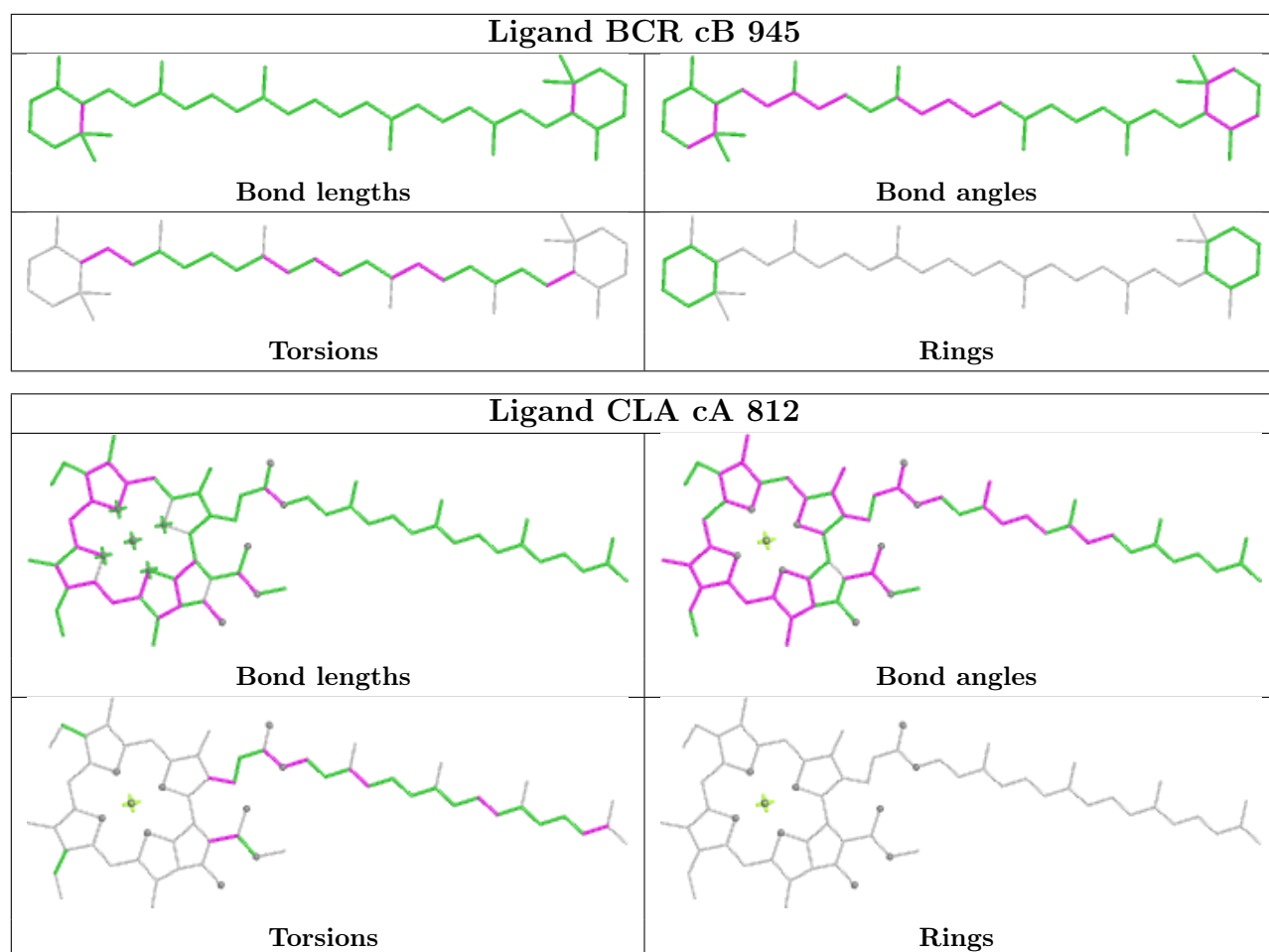




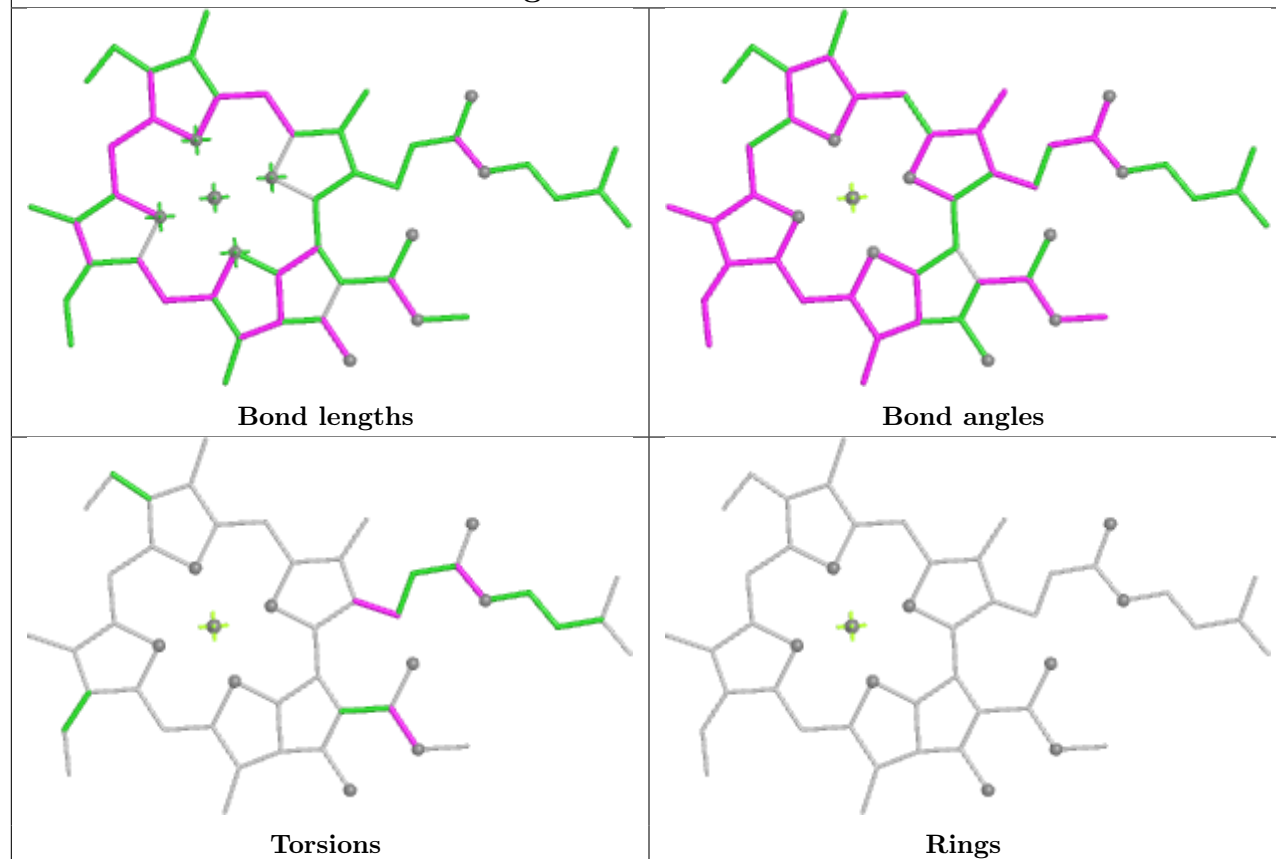




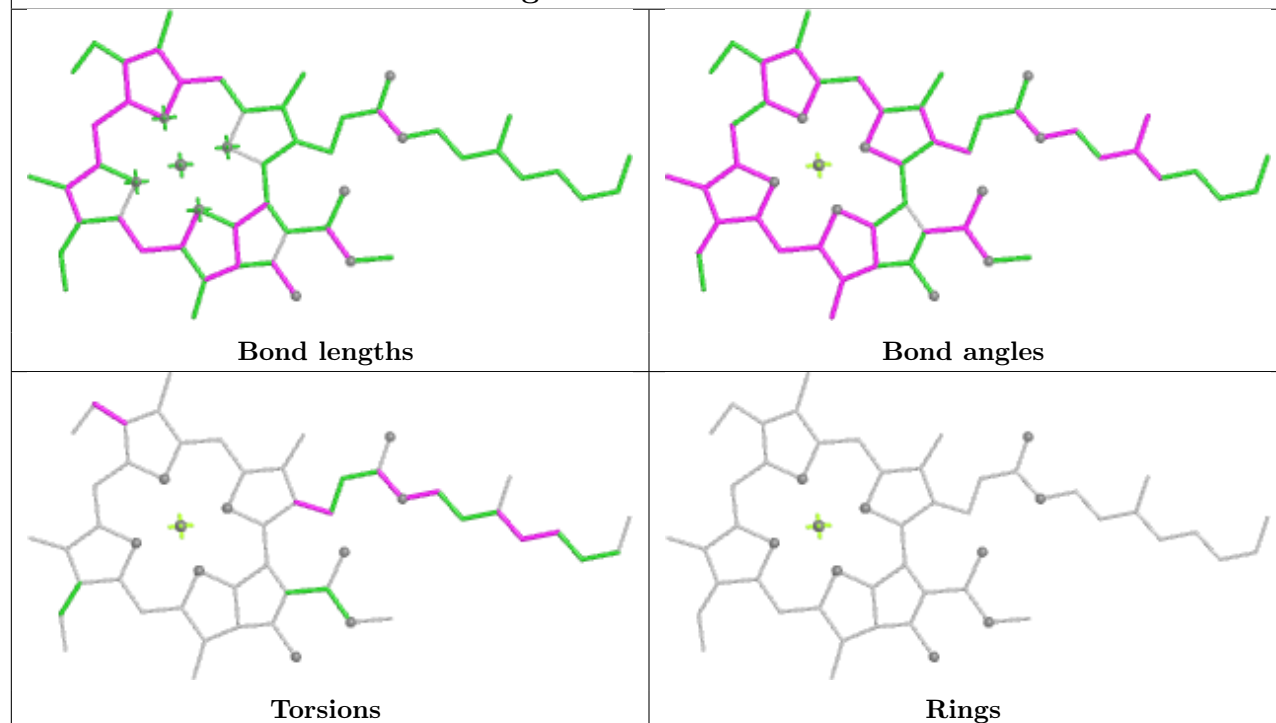




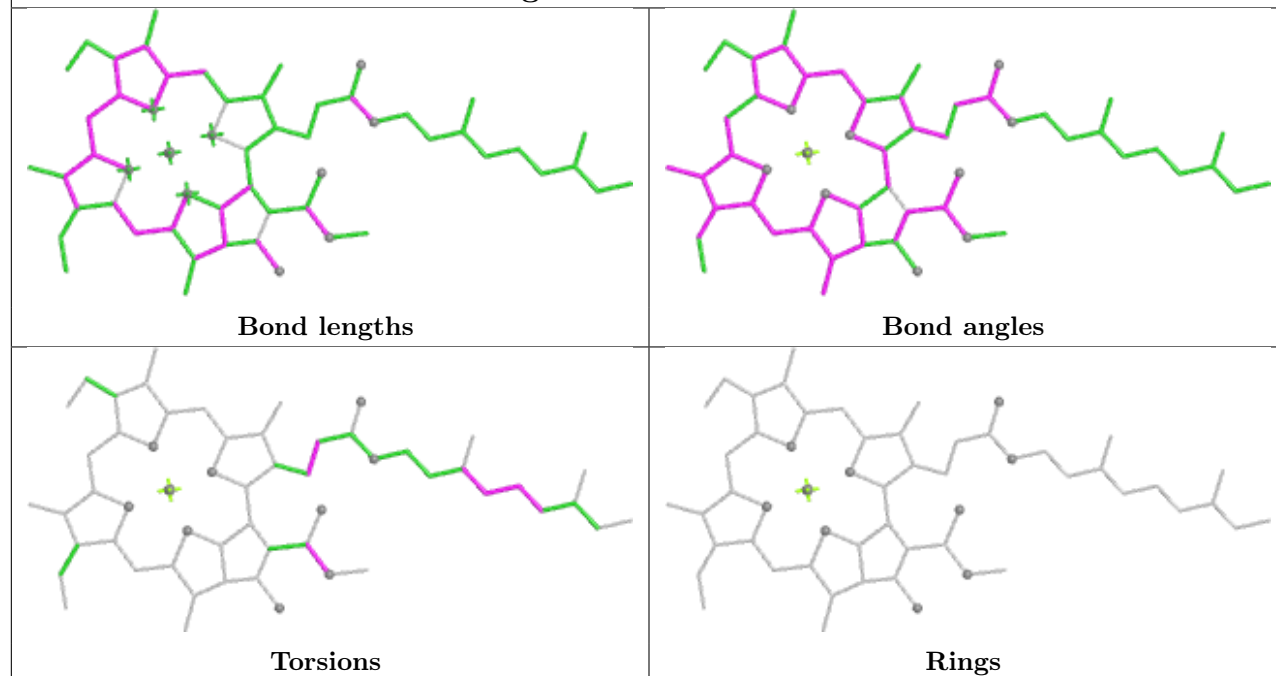
Ligand CLA cA 821



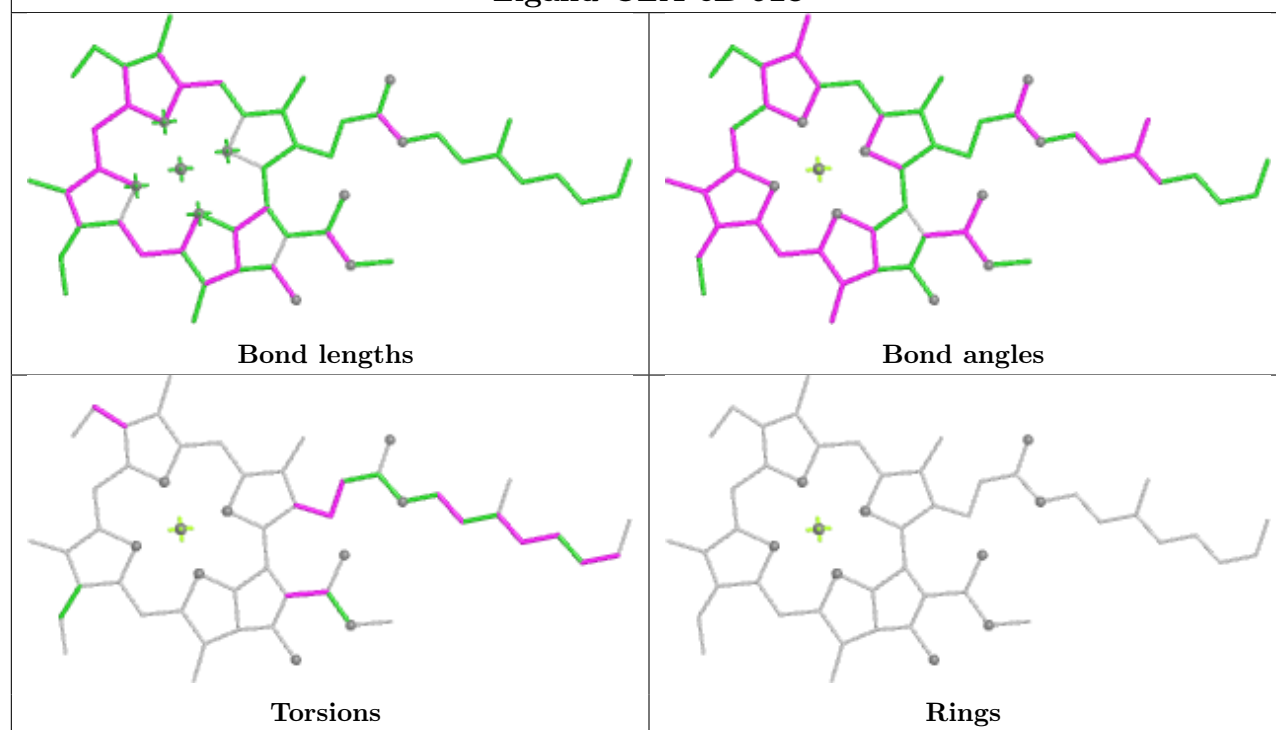
Ligand CLA bA 817

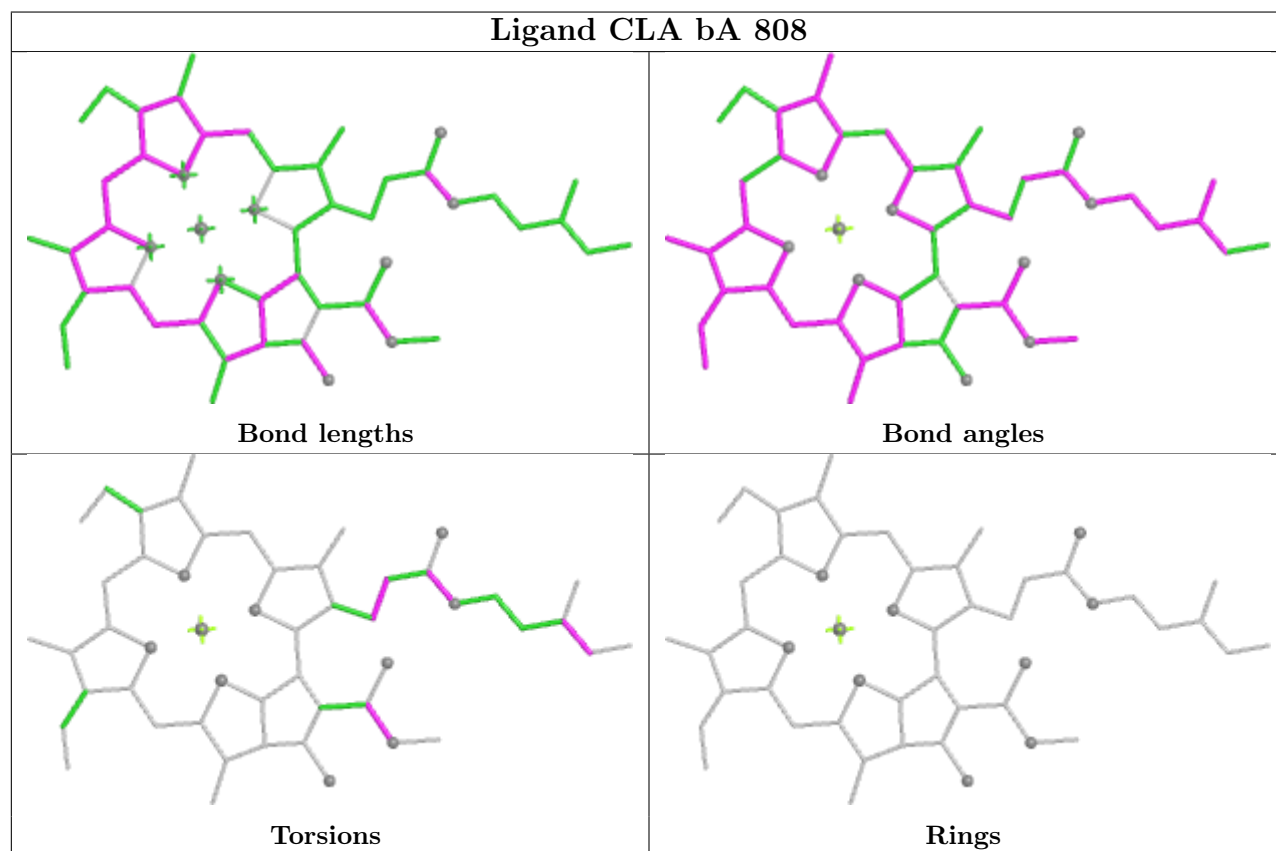
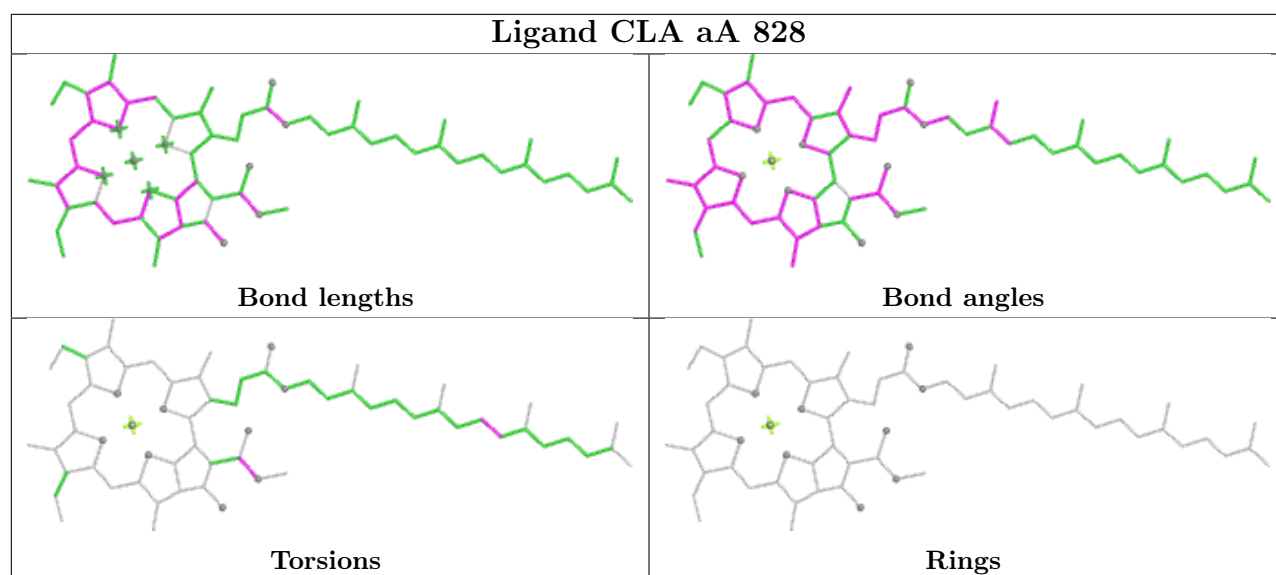


Ligand CLA bA 853

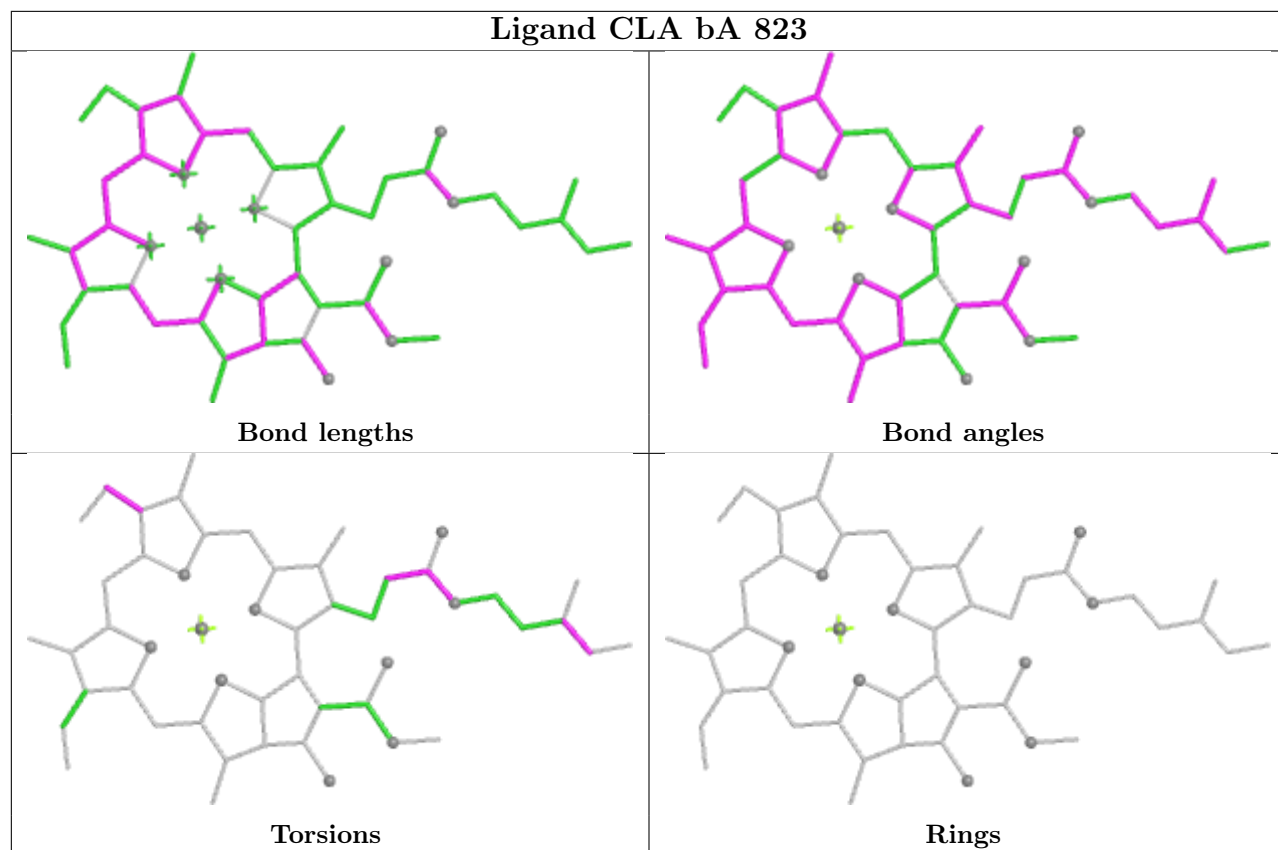


Ligand CLA cB 923

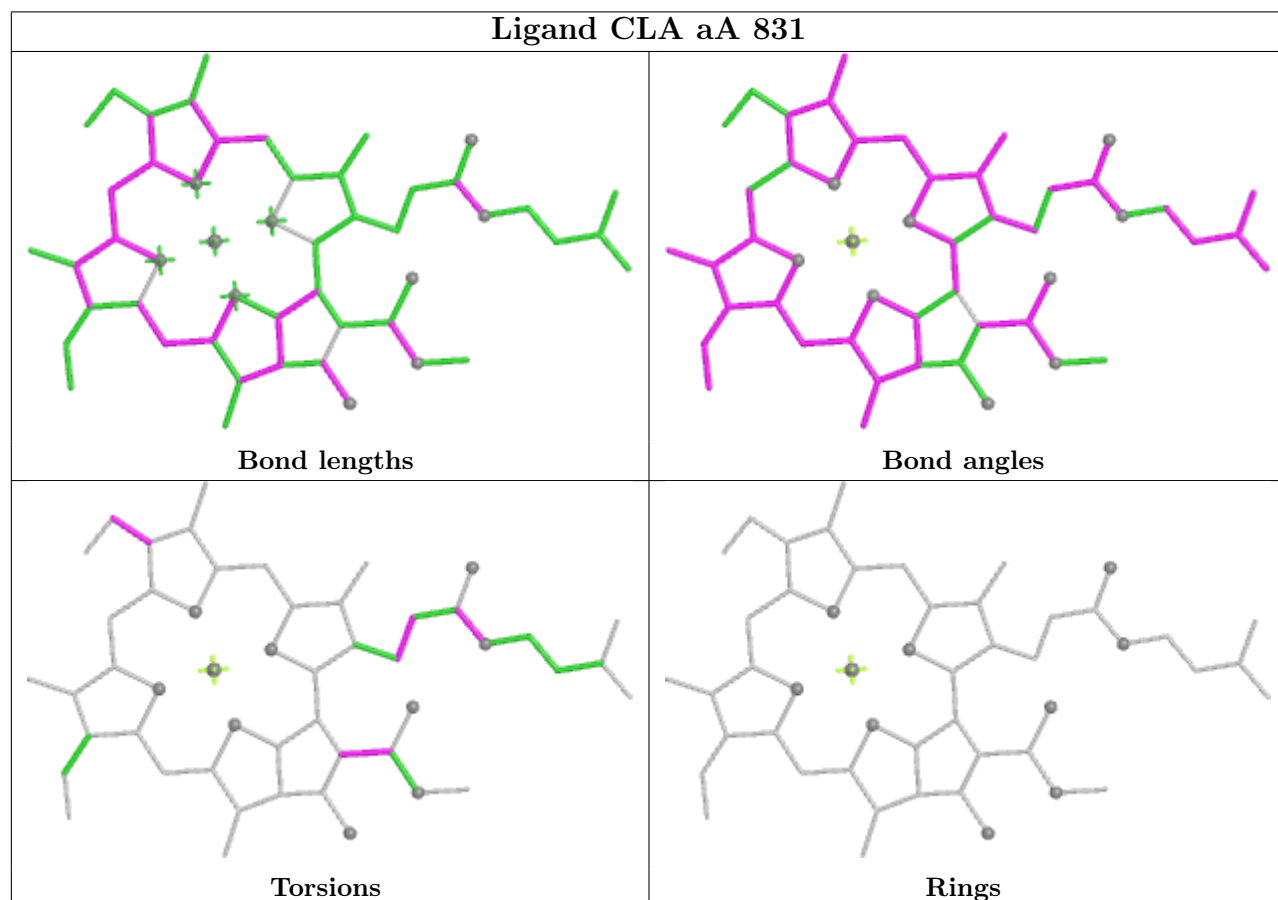


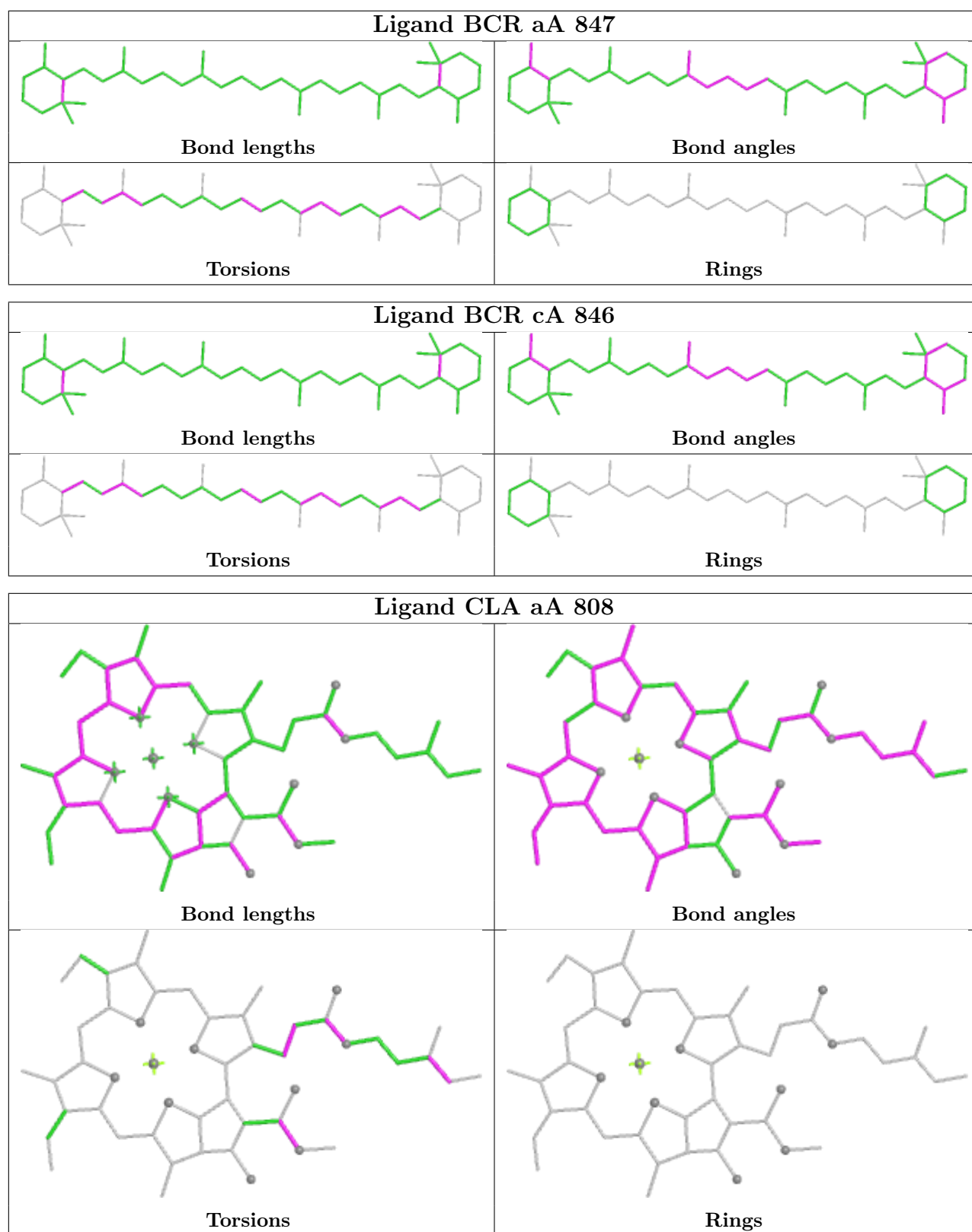


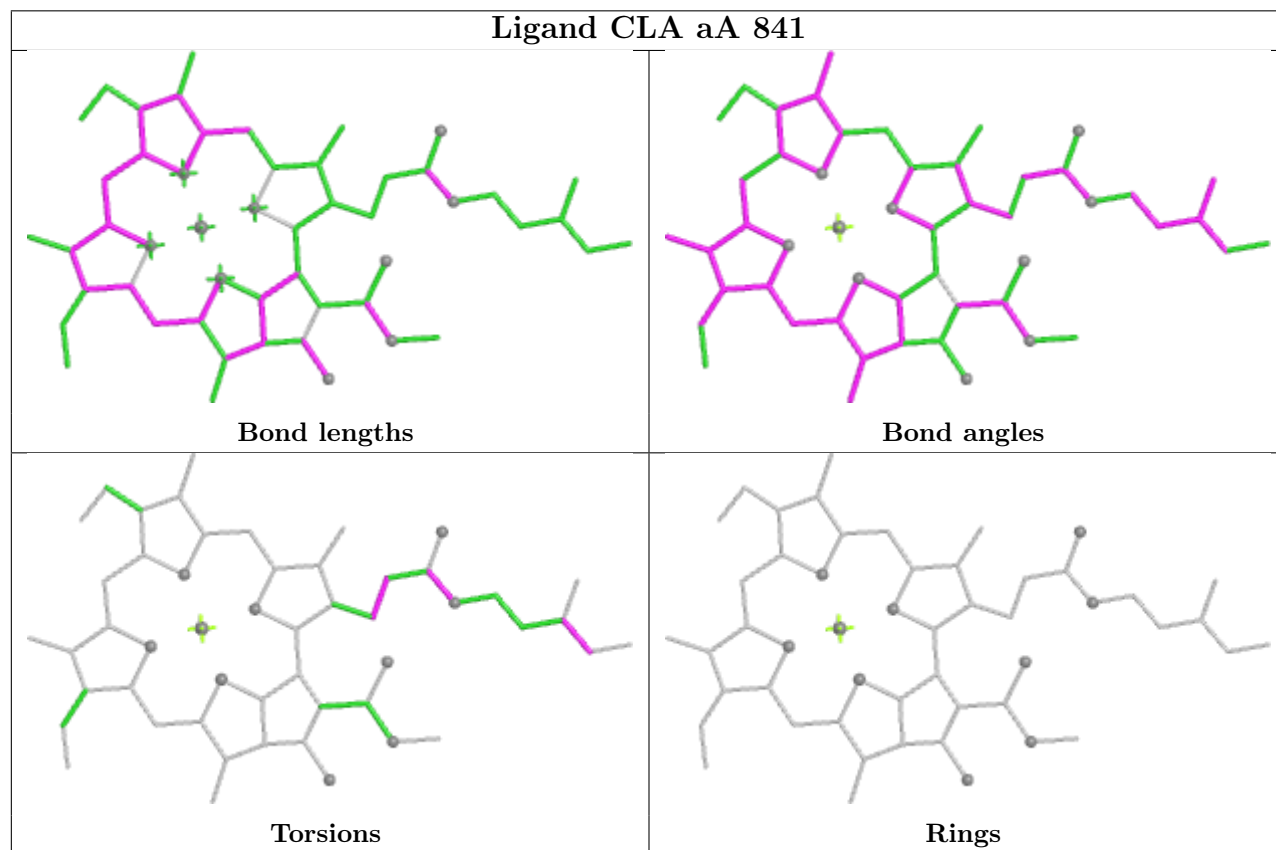
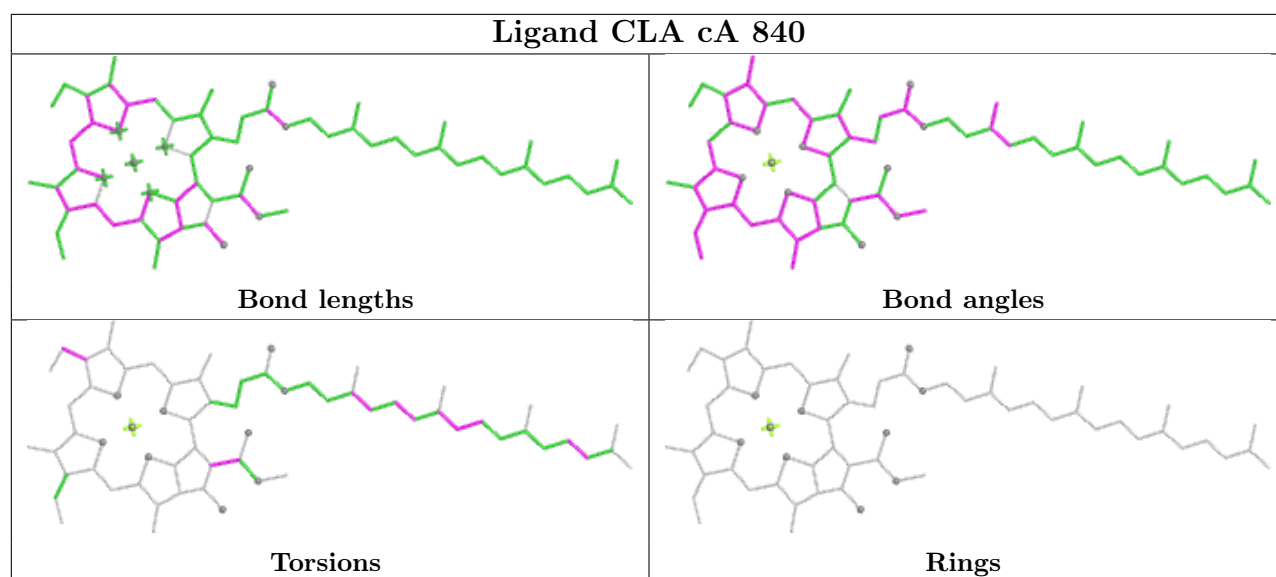
Ligand CLA bA 823

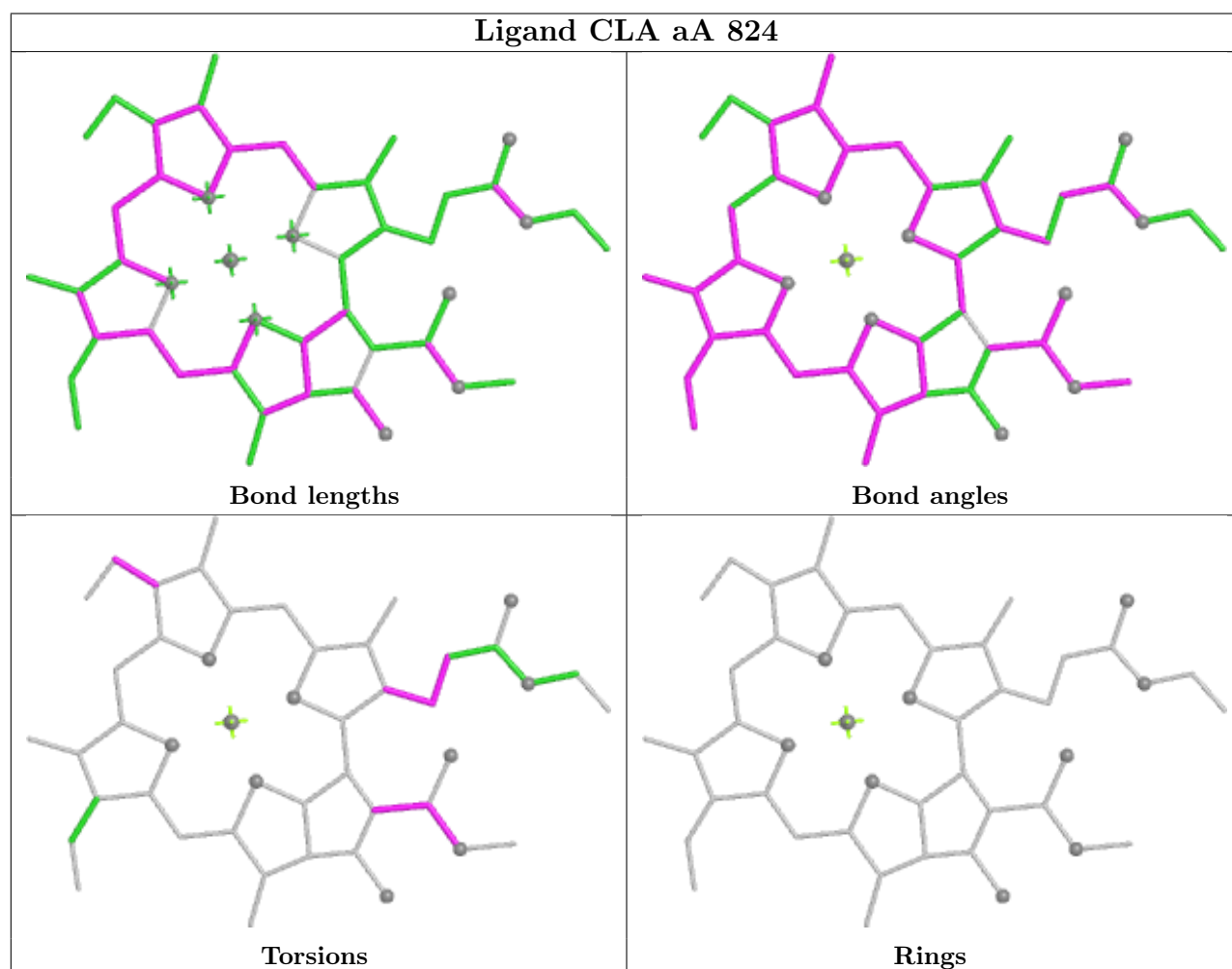
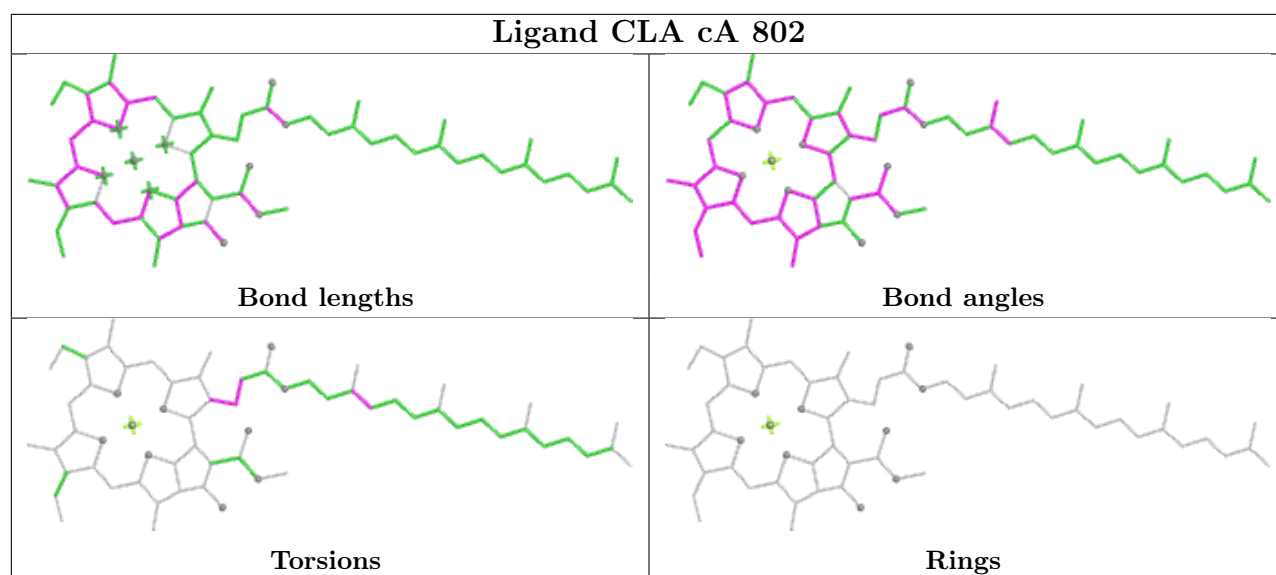


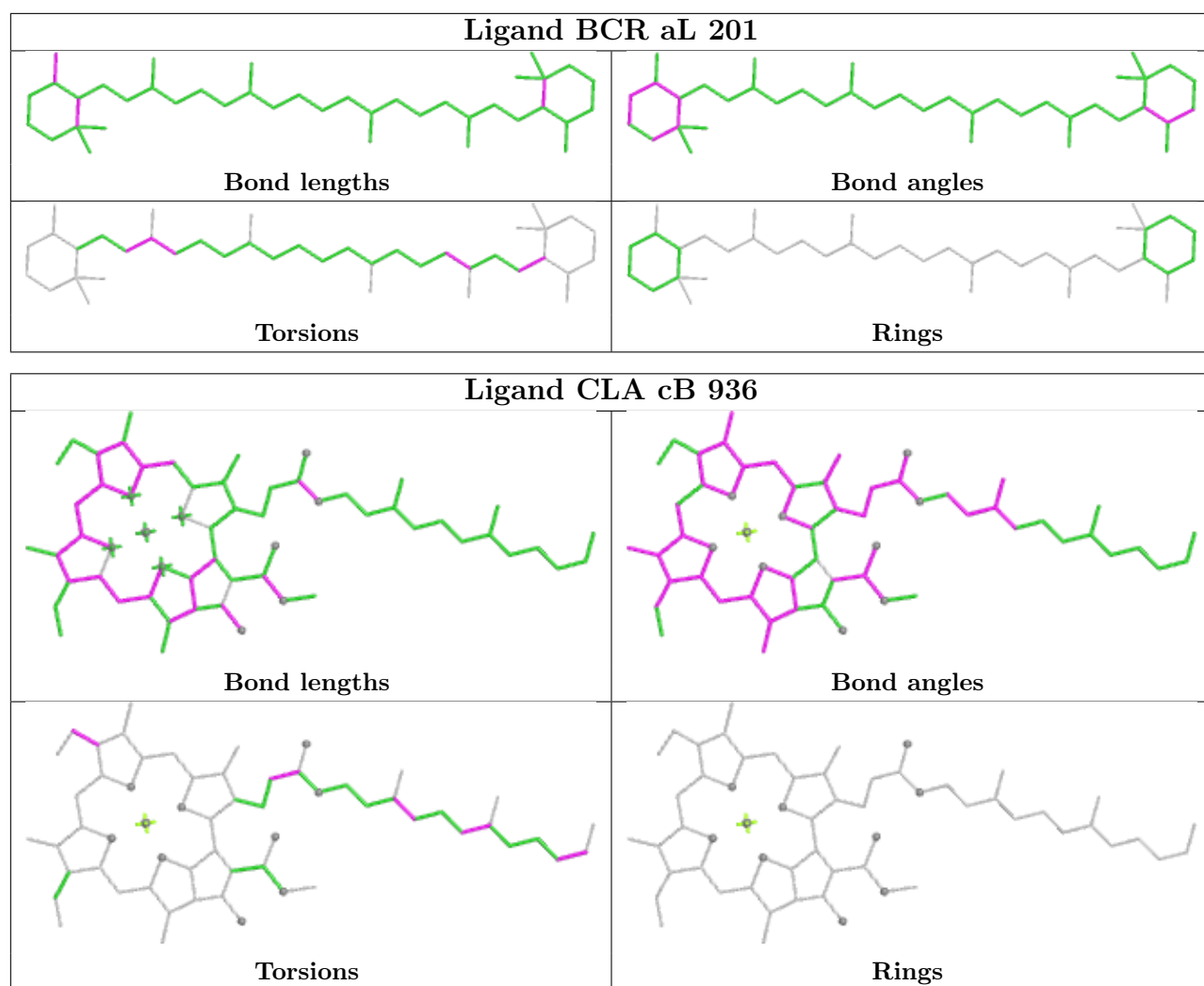
Ligand CLA aA 831

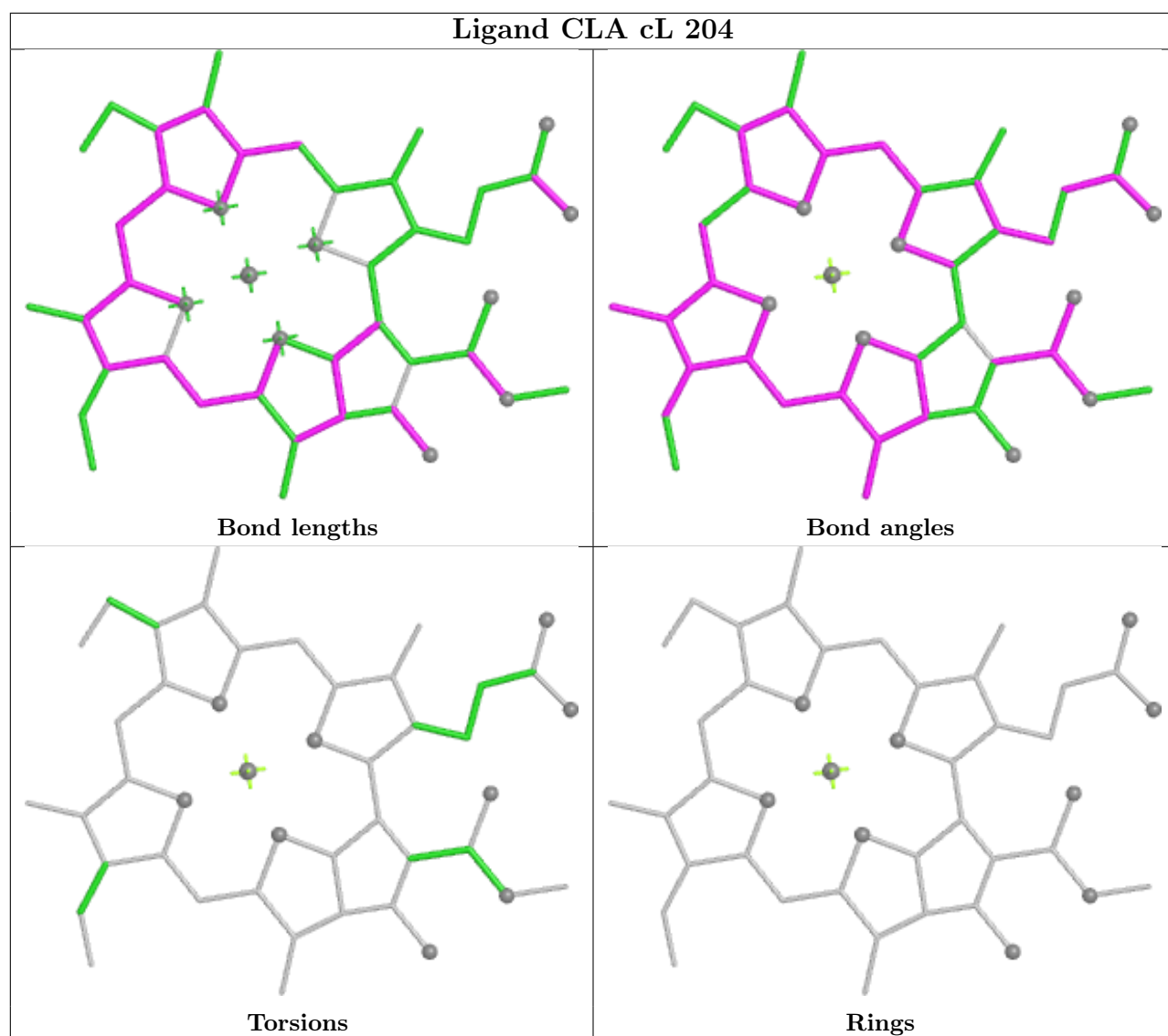




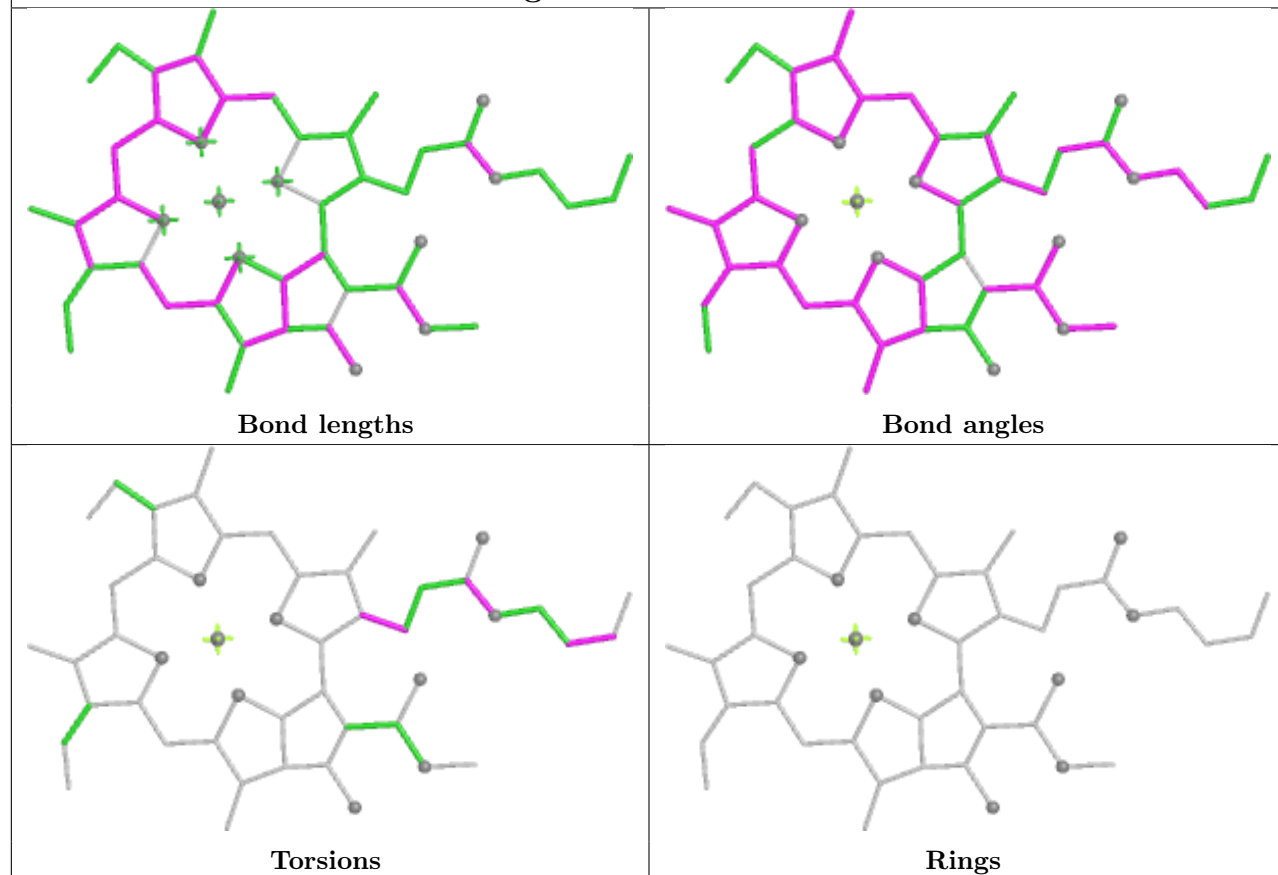




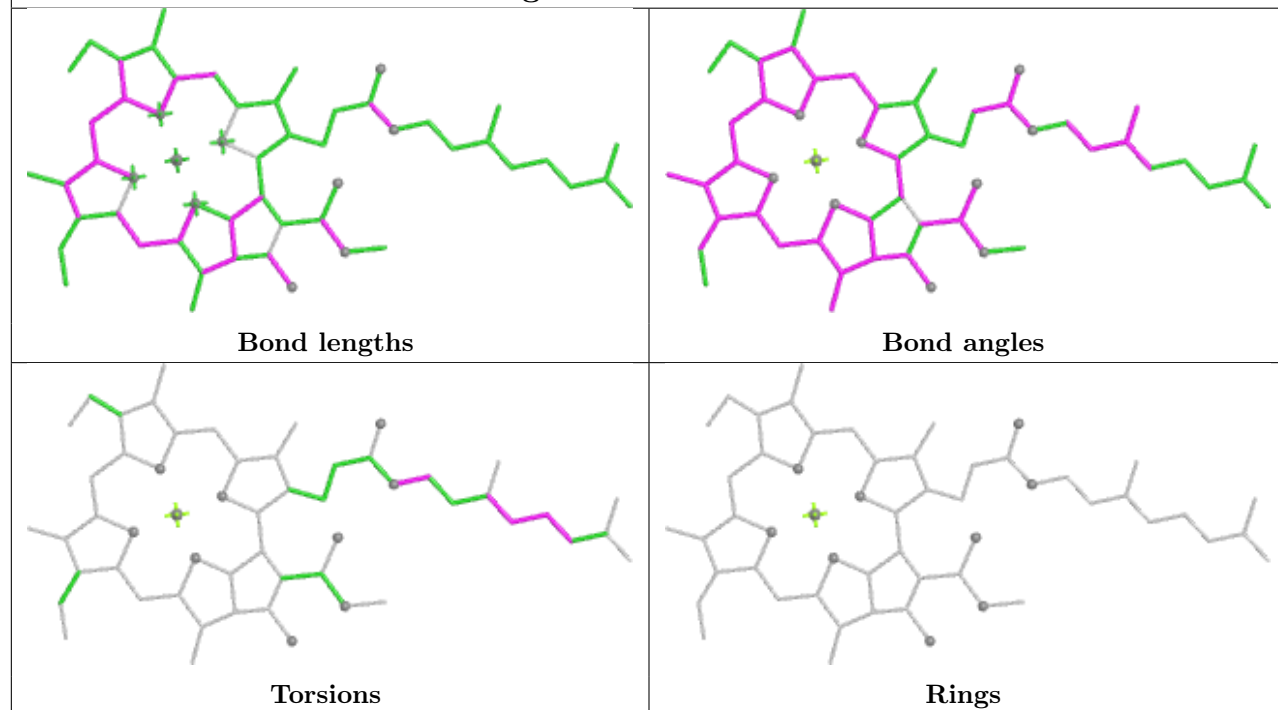


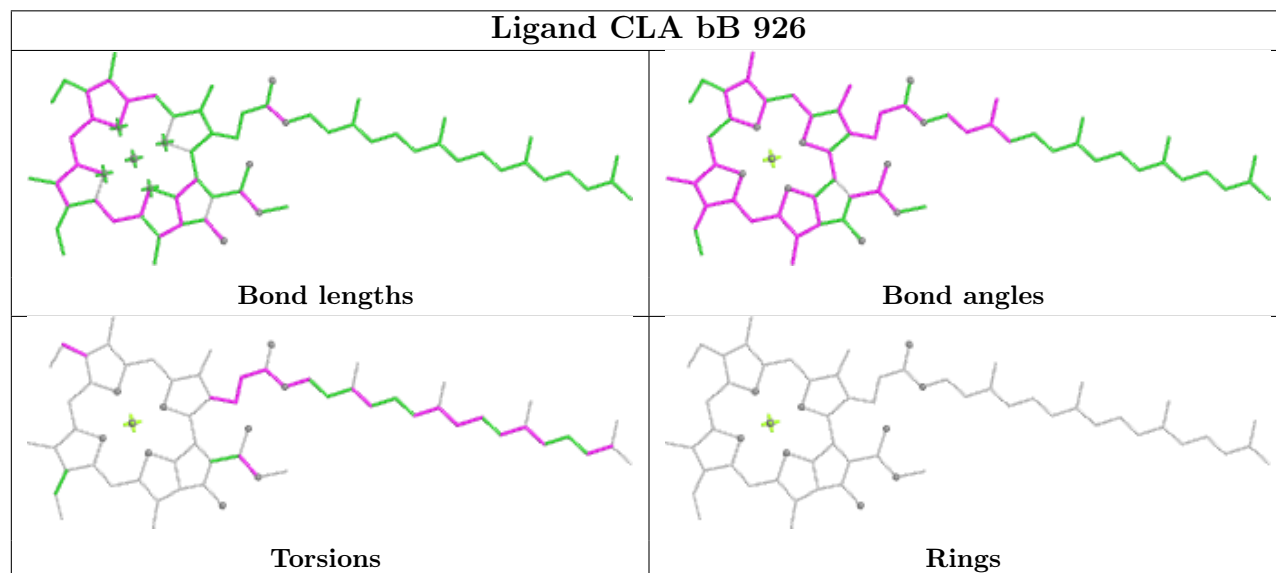
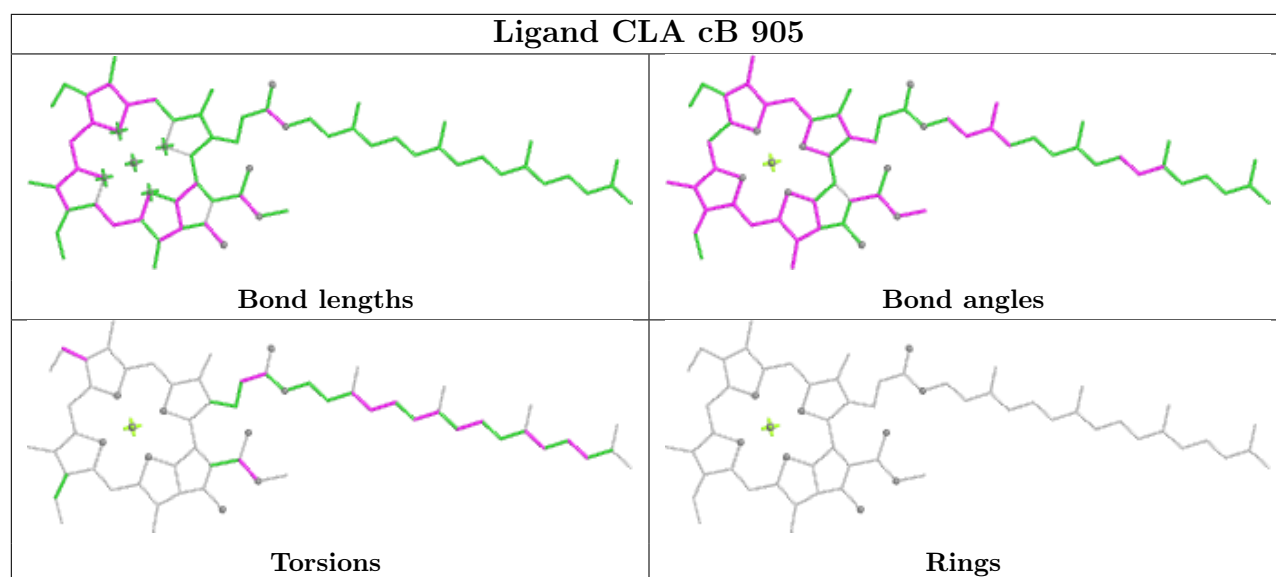


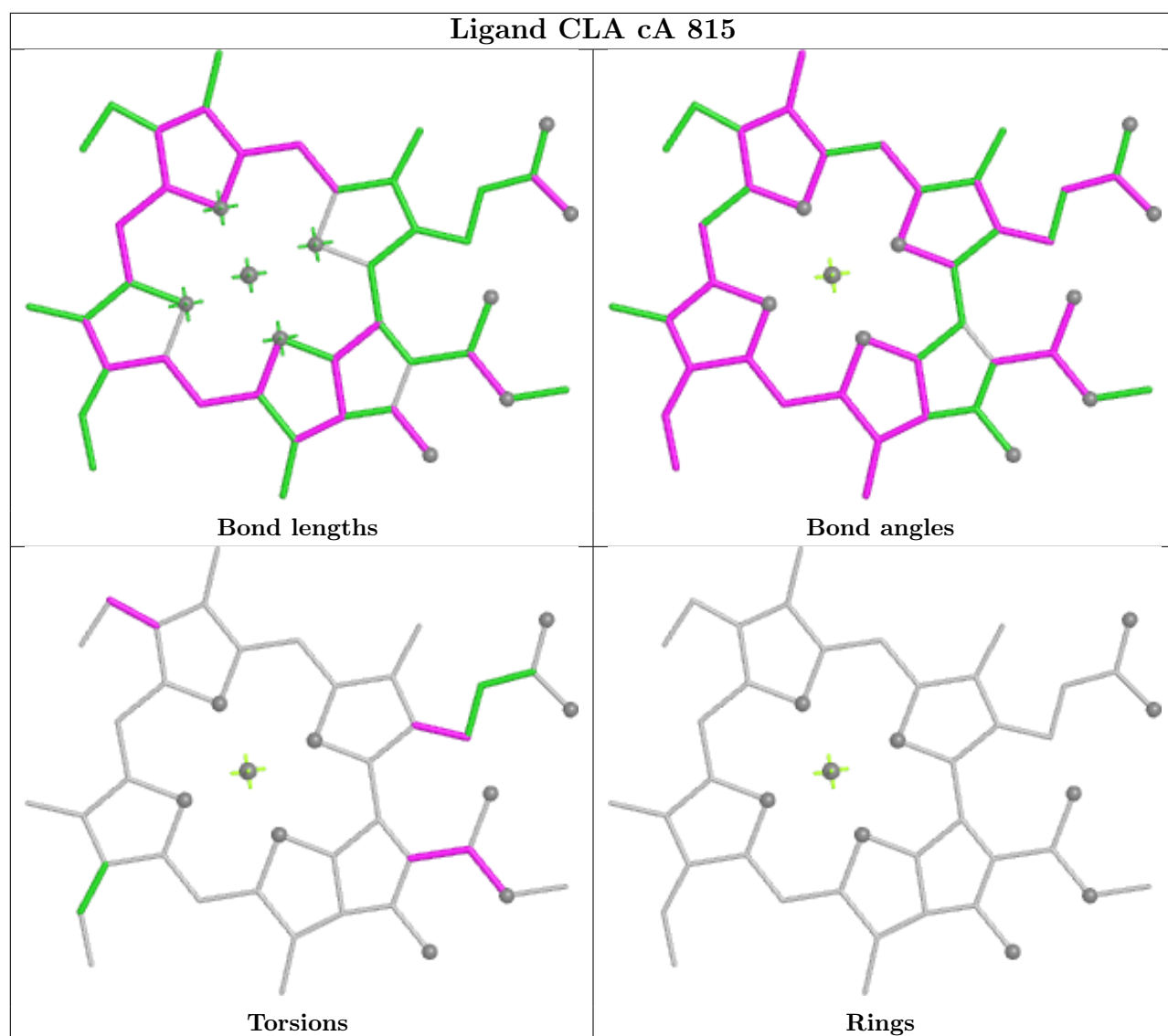
Ligand CLA cB 930



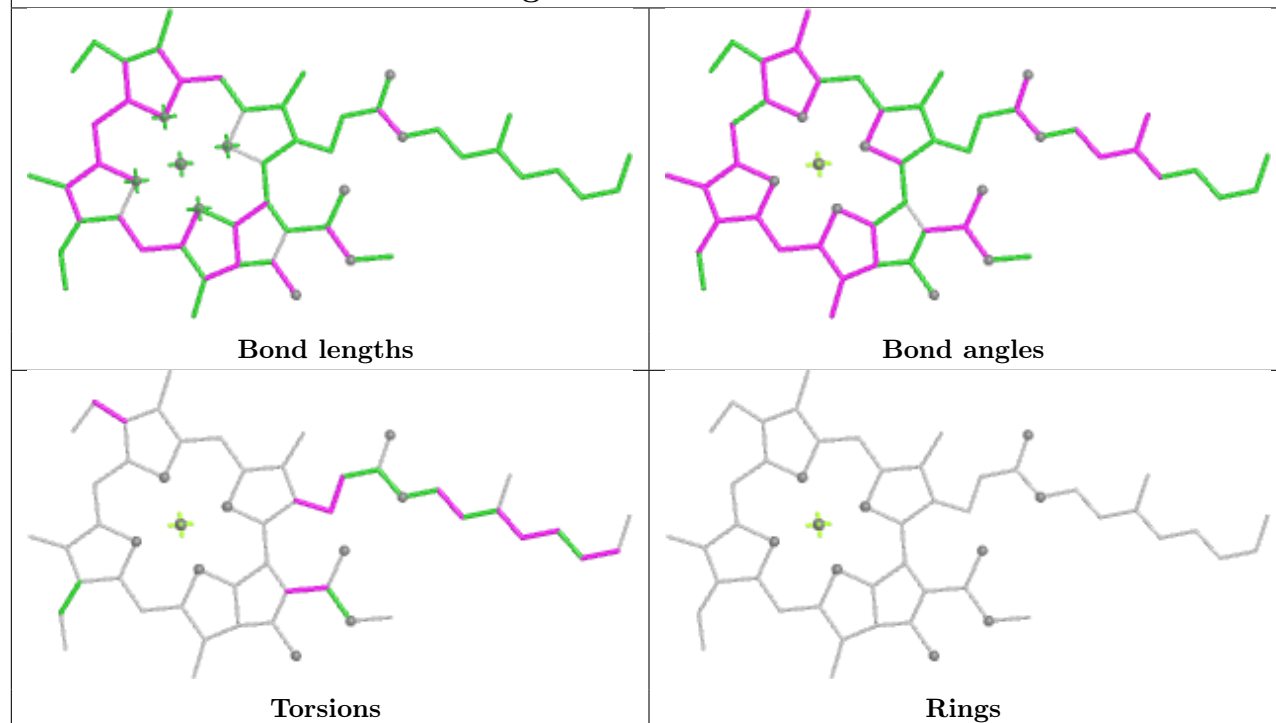
Ligand CLA bB 925



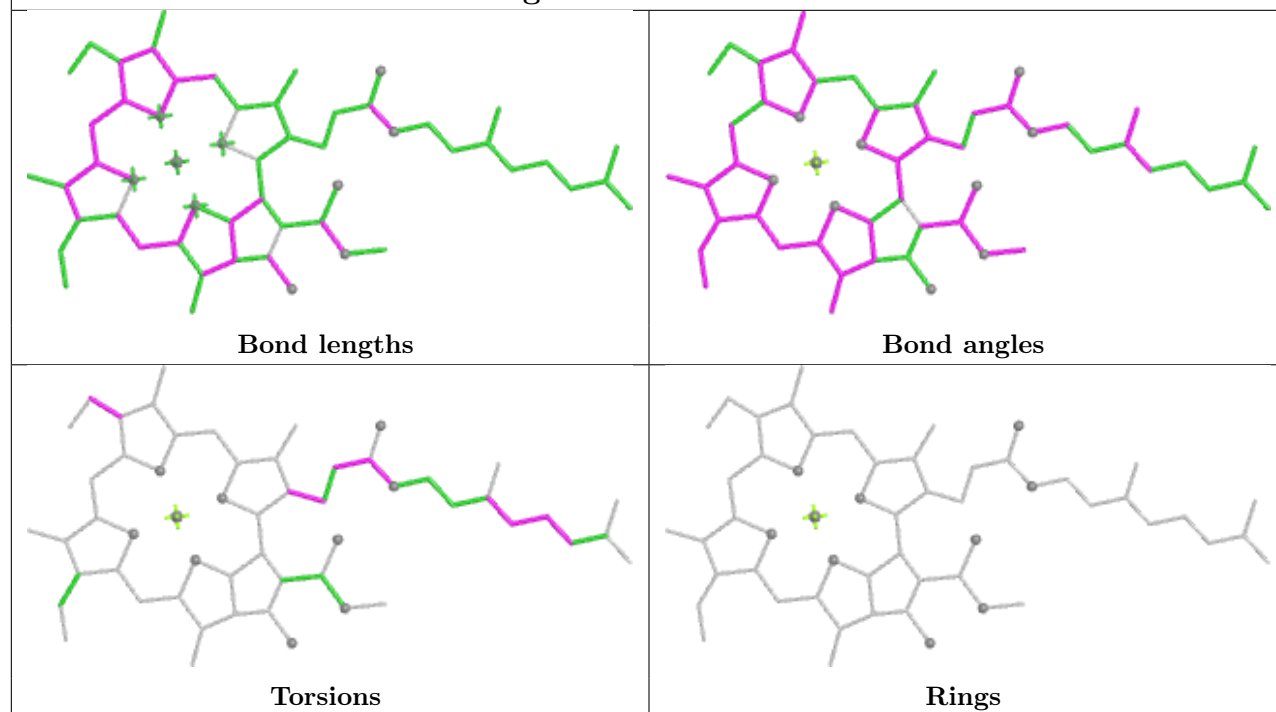


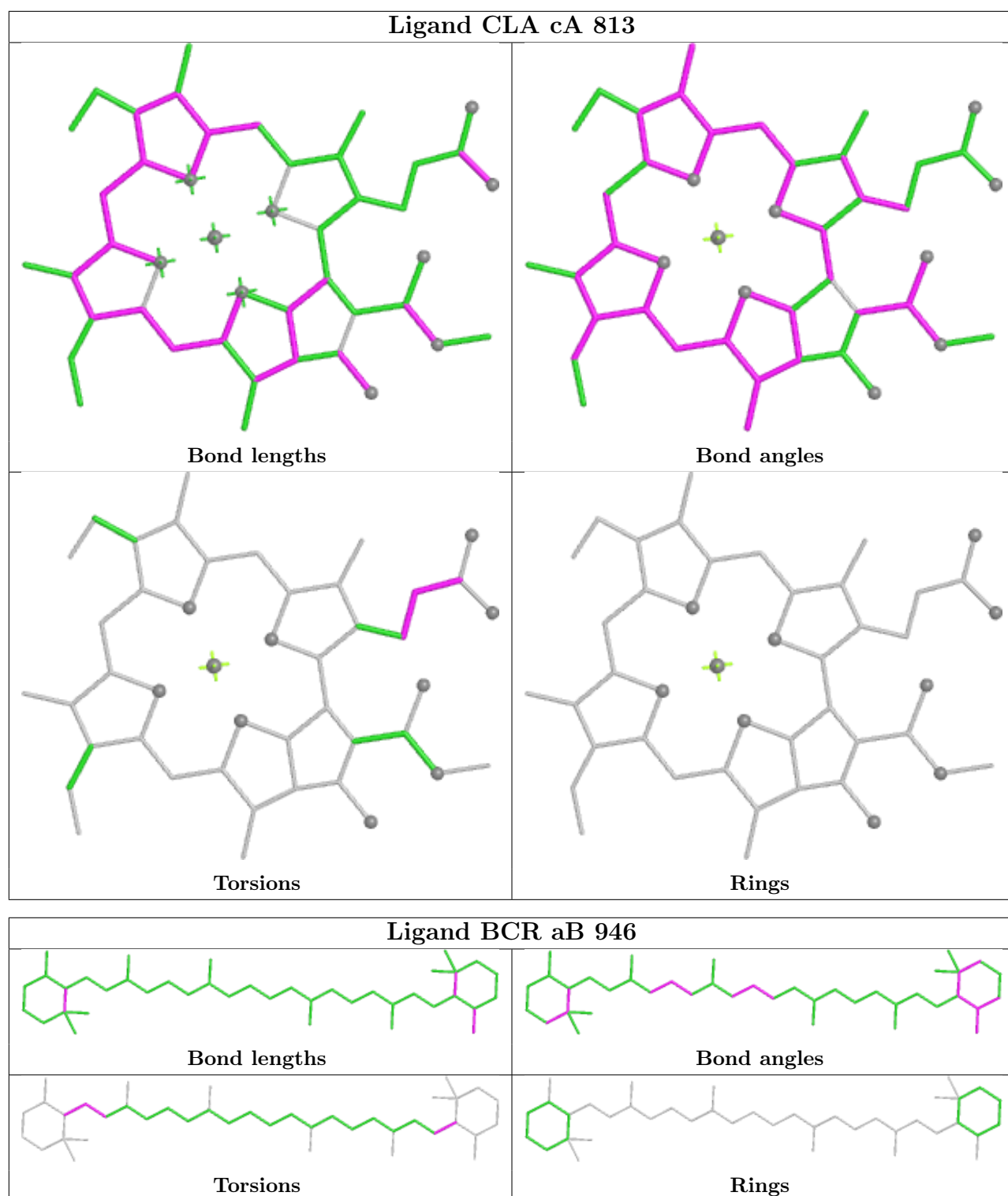


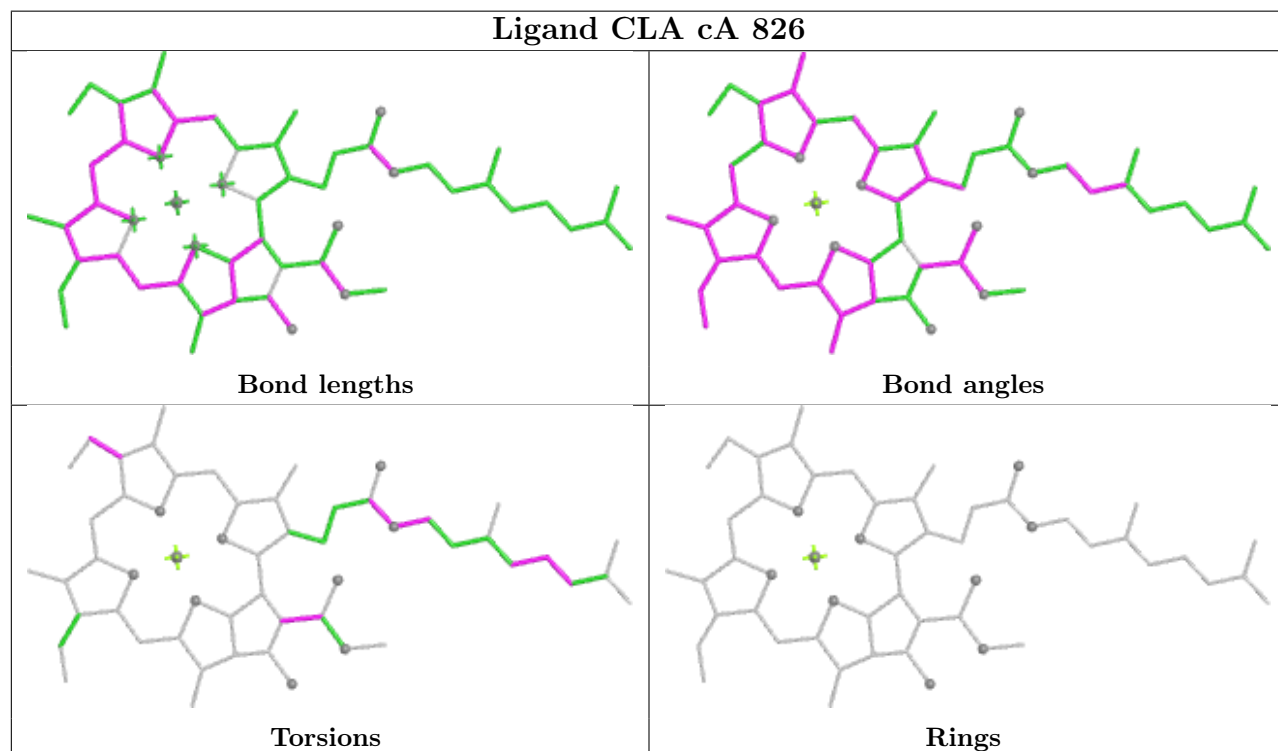
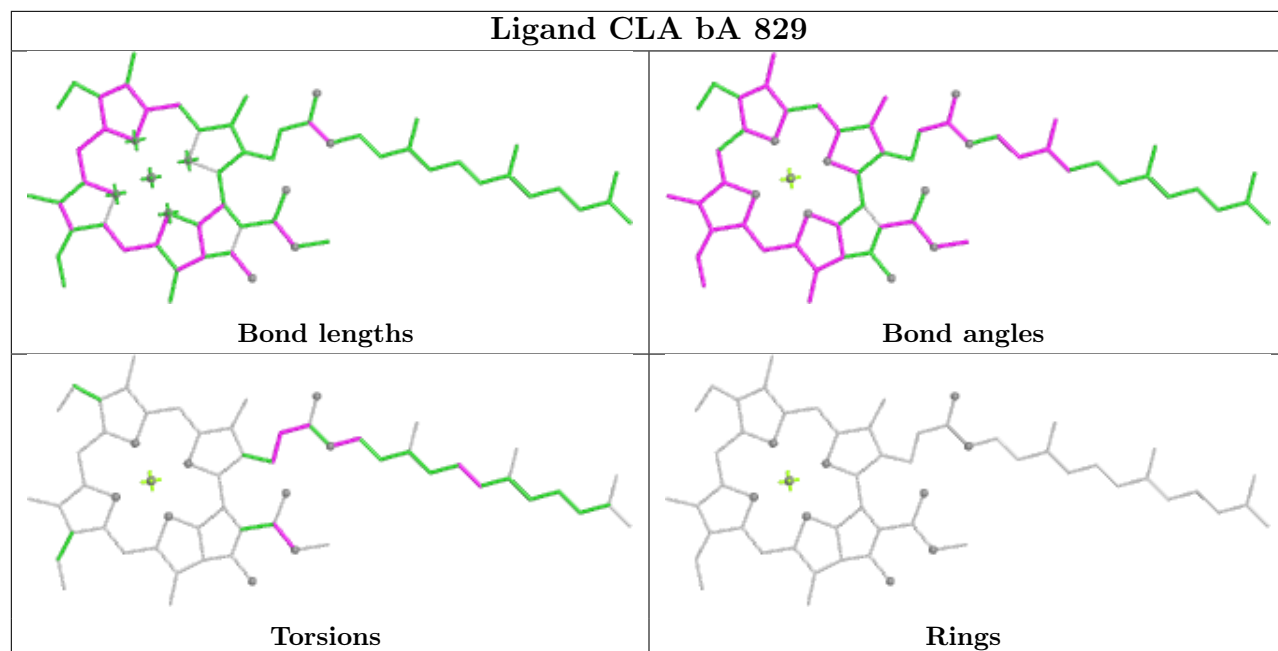
Ligand CLA bB 923

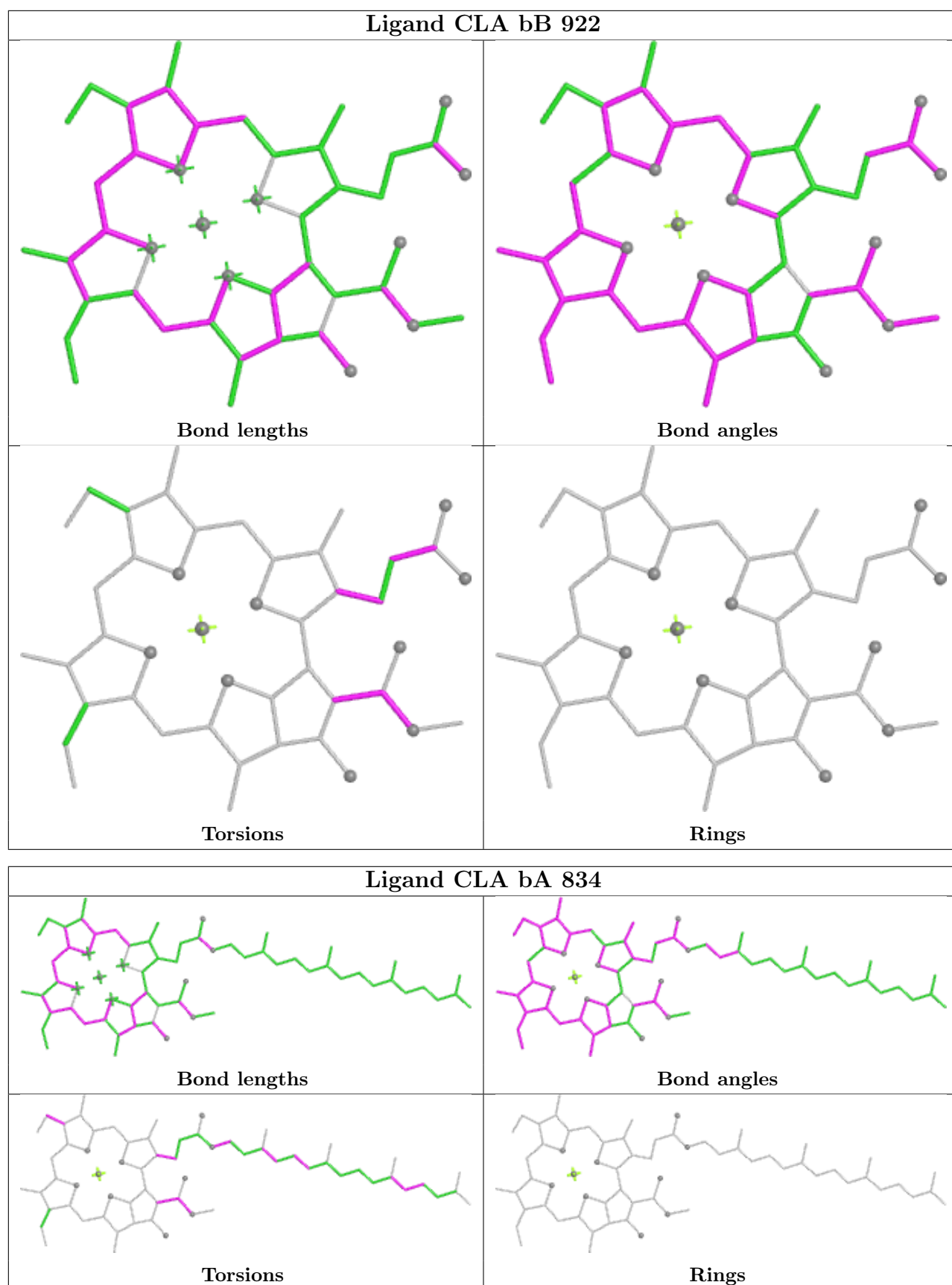


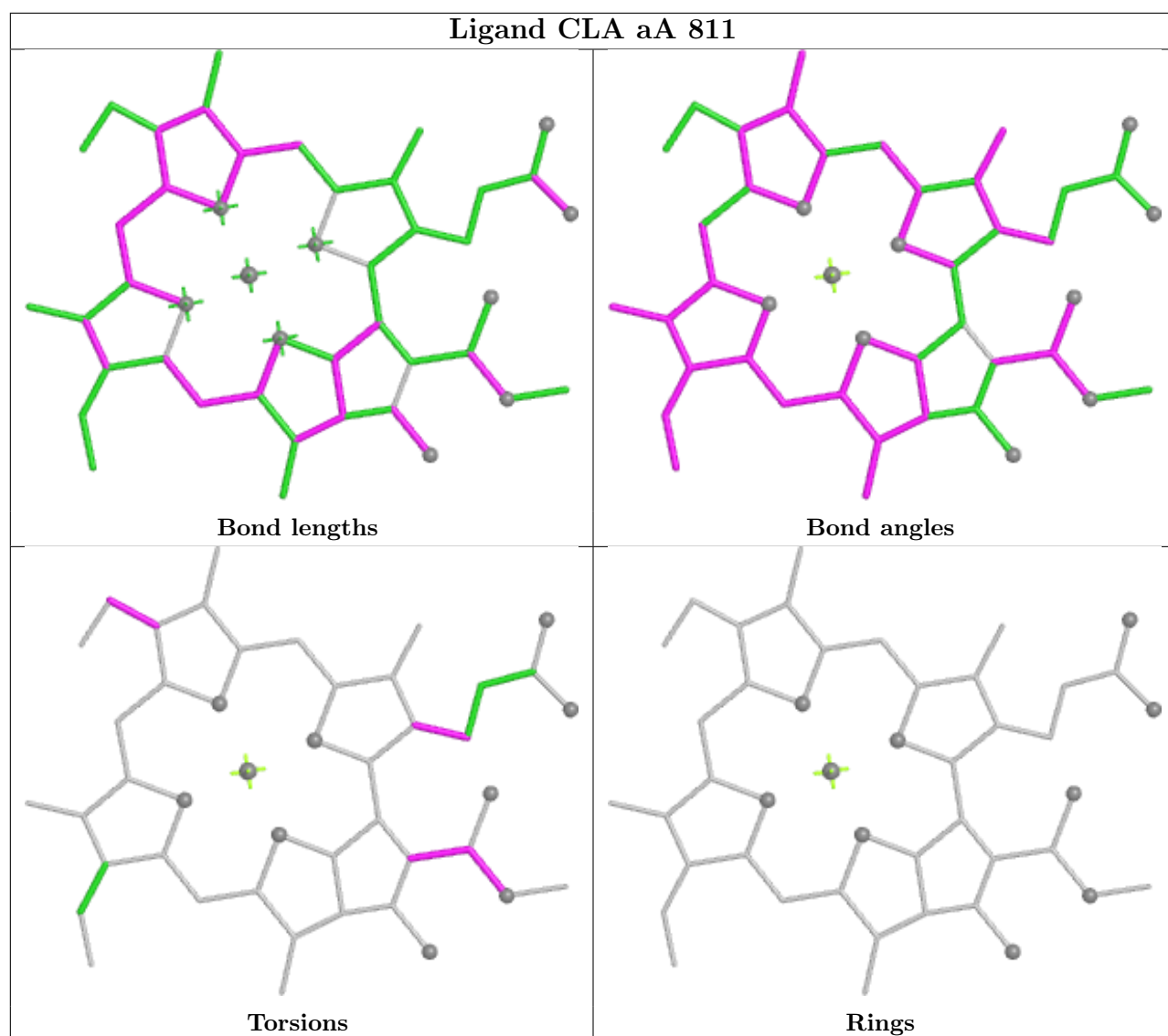
Ligand CLA aA 832

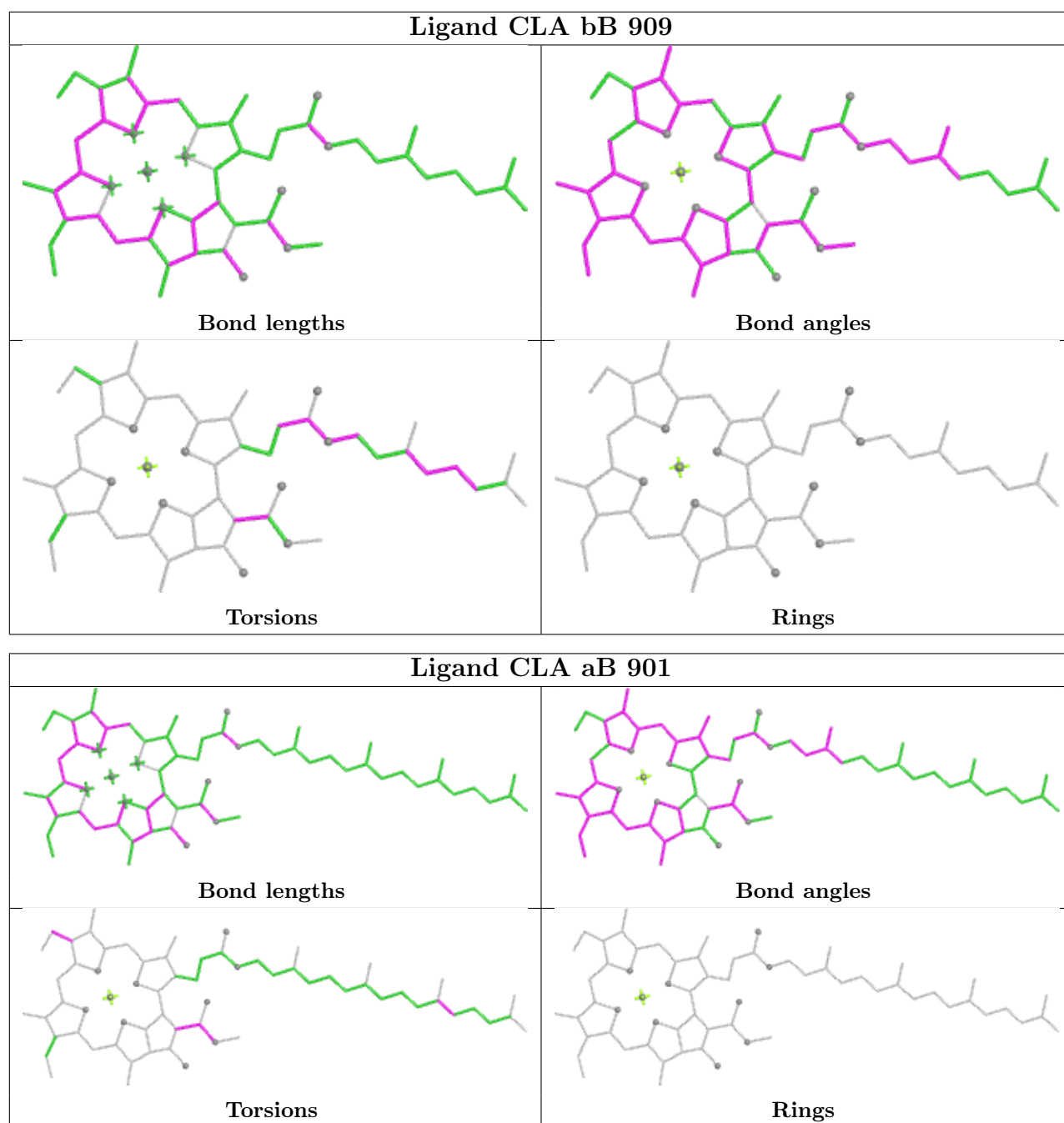


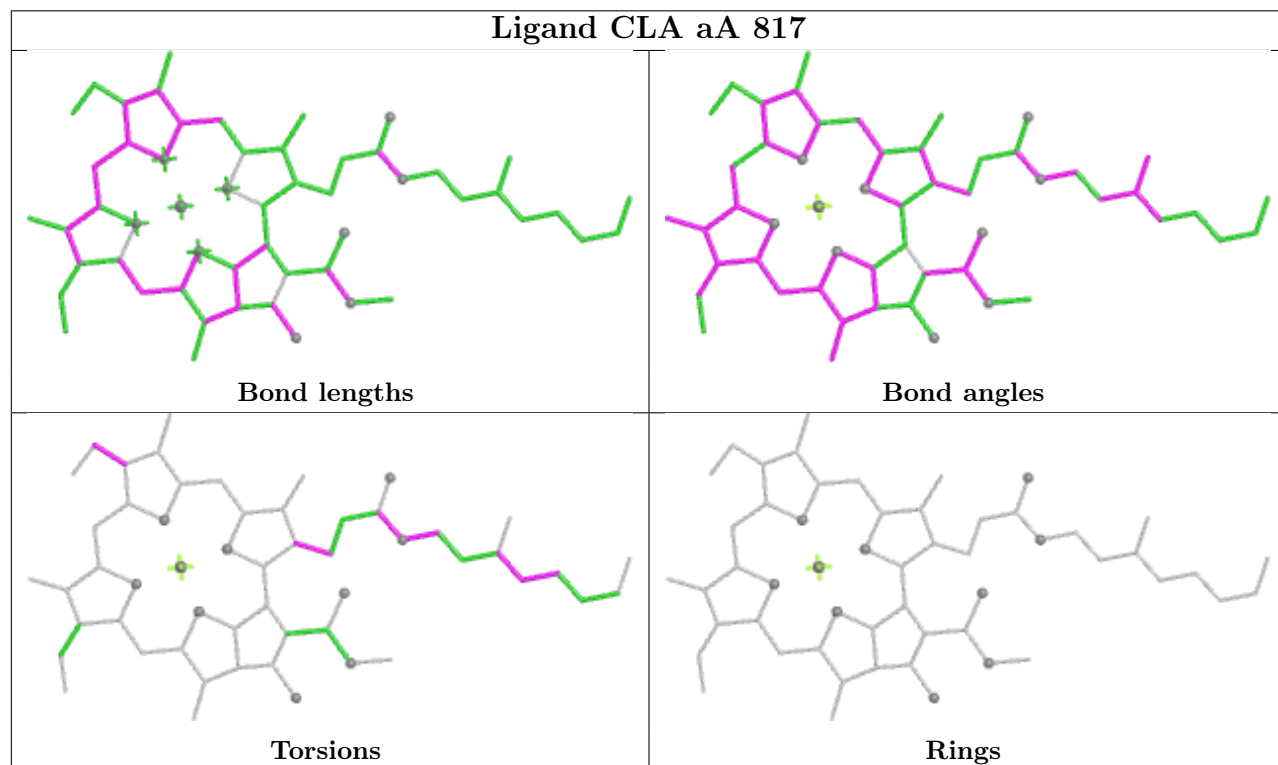
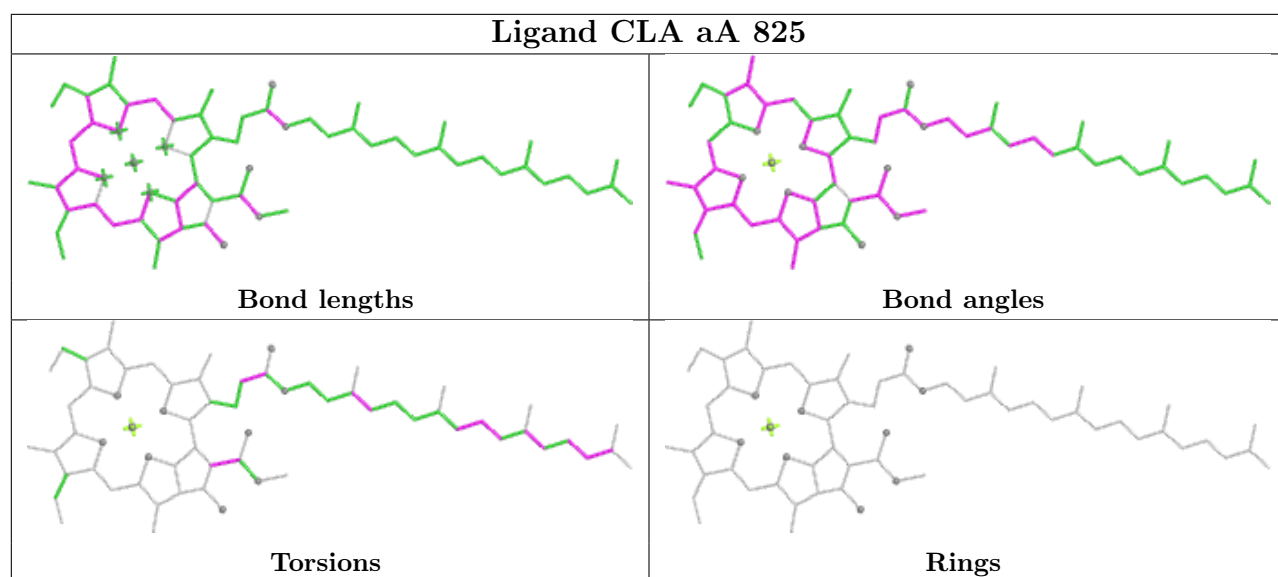


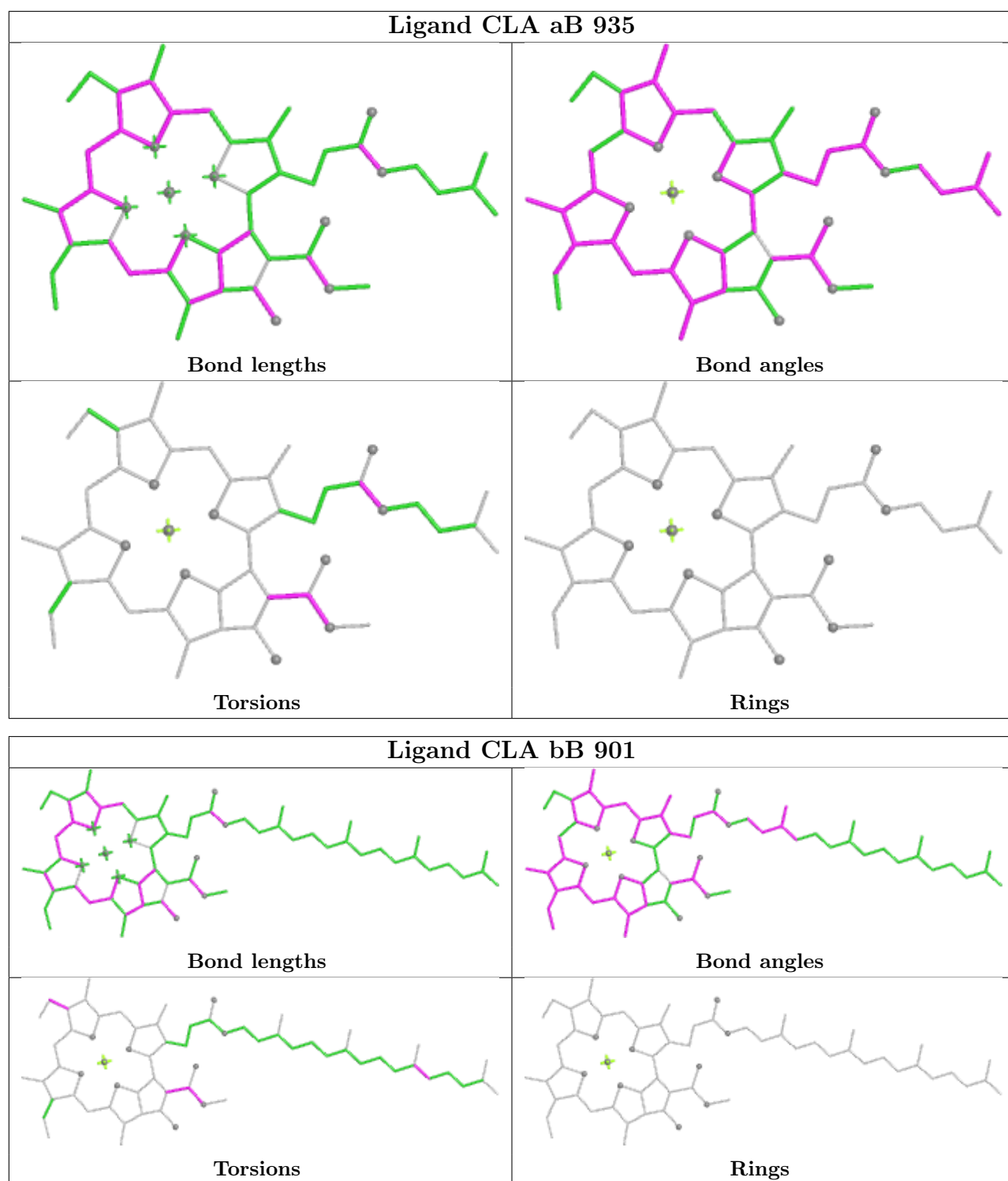


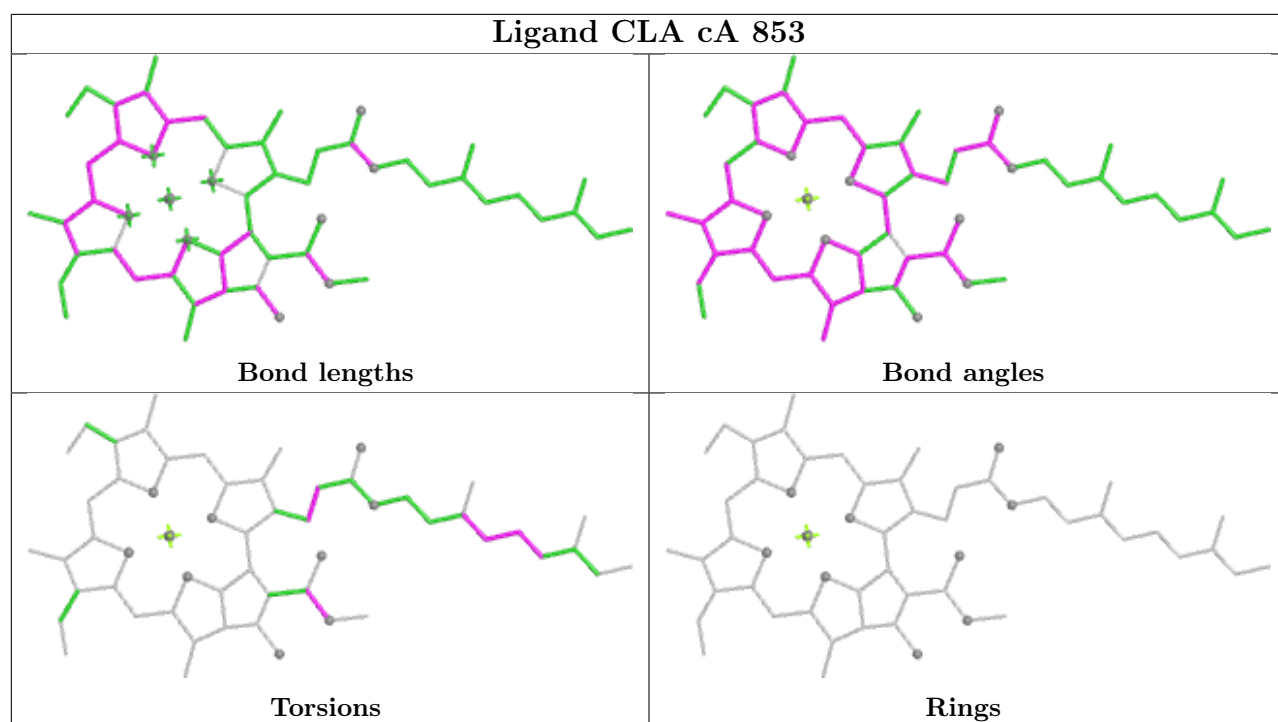




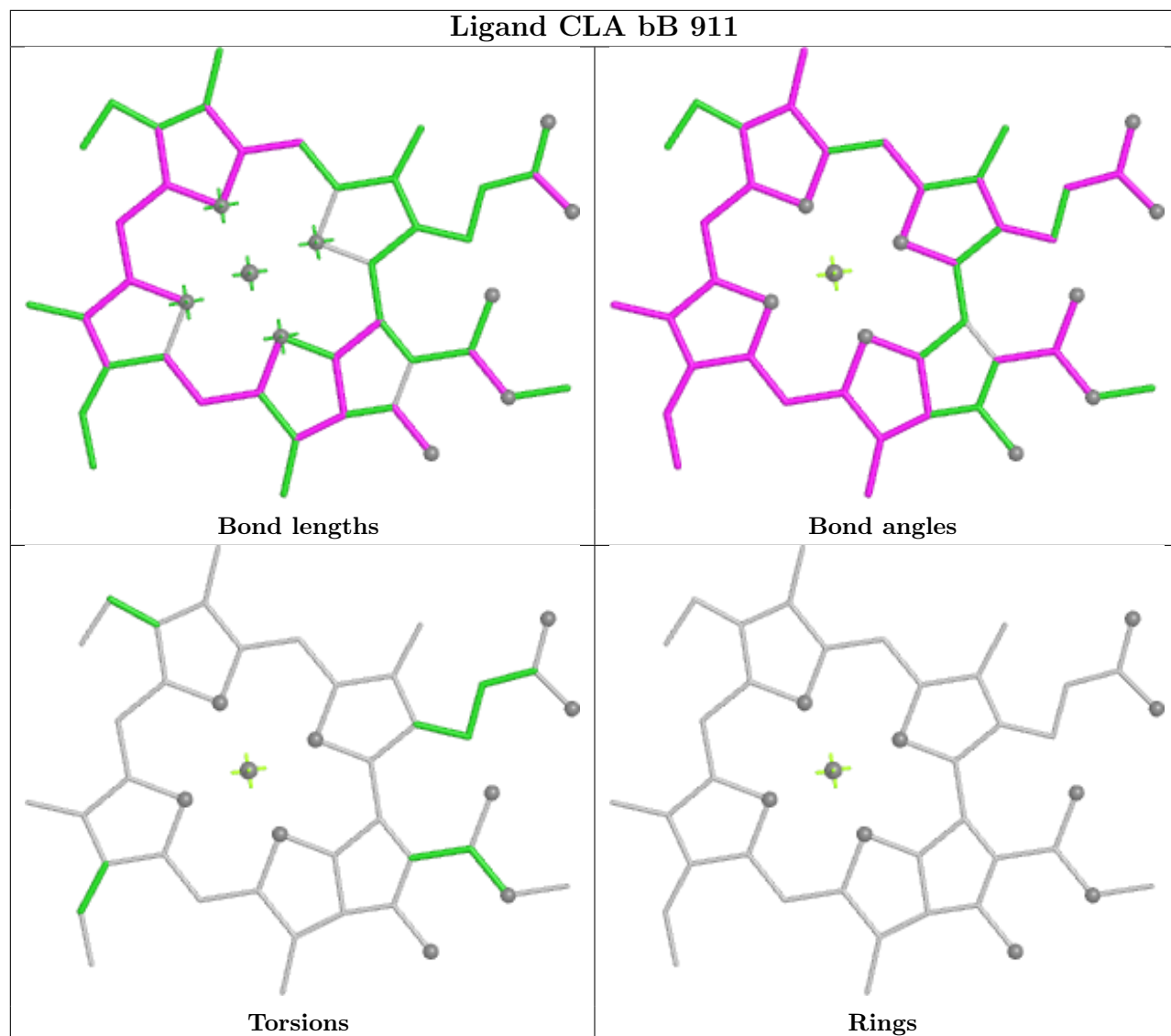




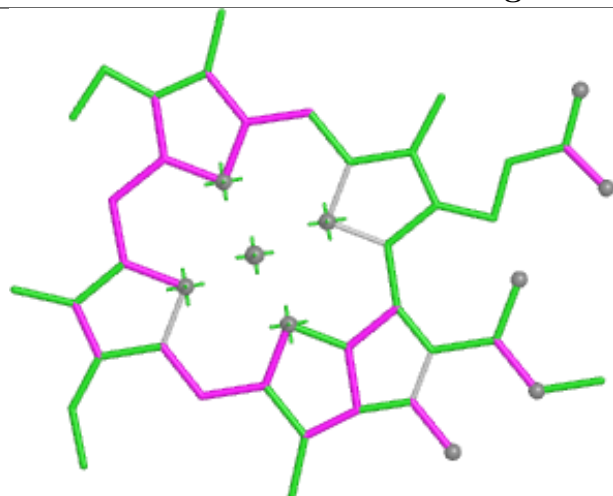




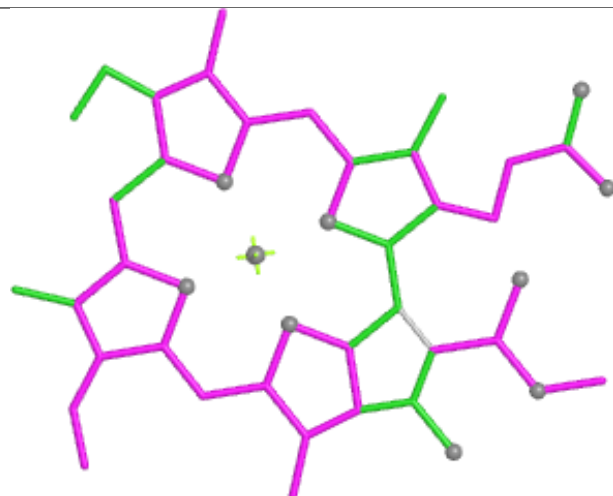
Ligand CLA bB 911



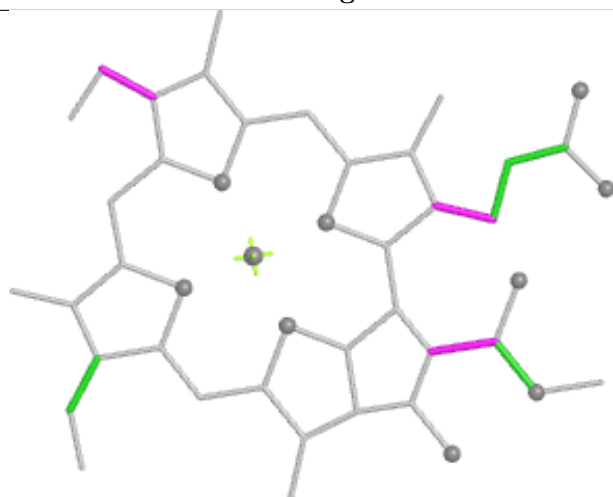
Ligand CLA bB 939



Bond lengths



Bond angles

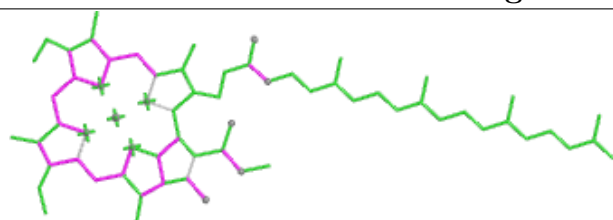


Torsions

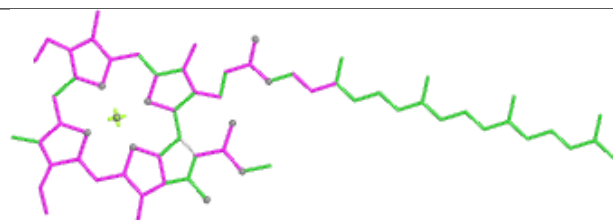


Rings

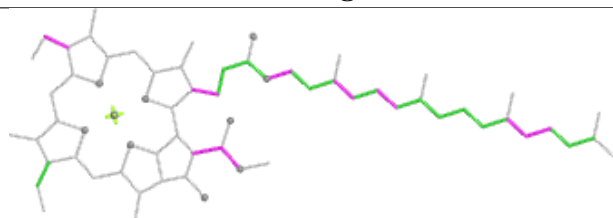
Ligand CLA aA 834



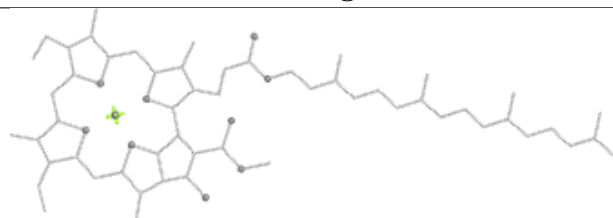
Bond lengths



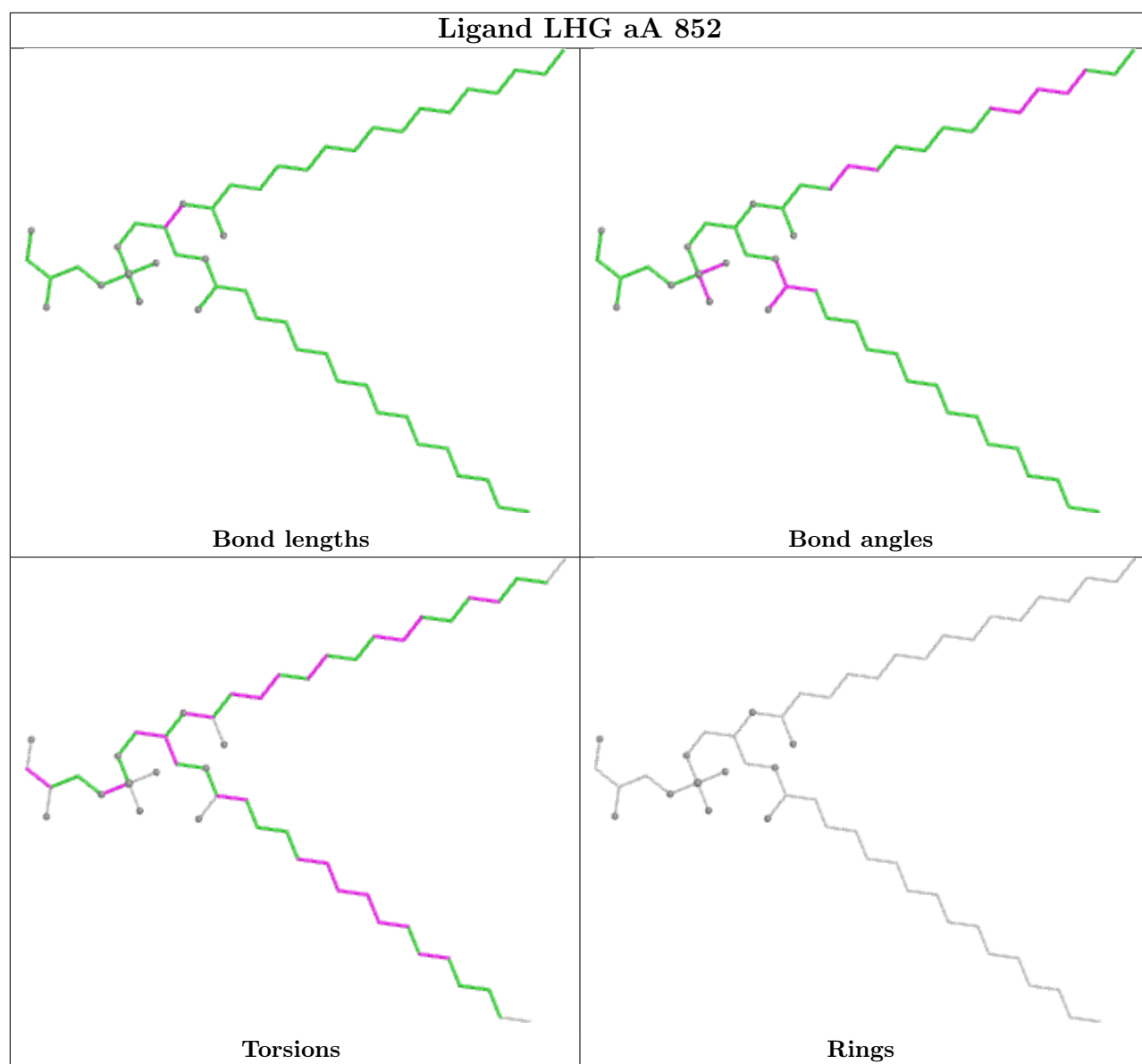
Bond angles

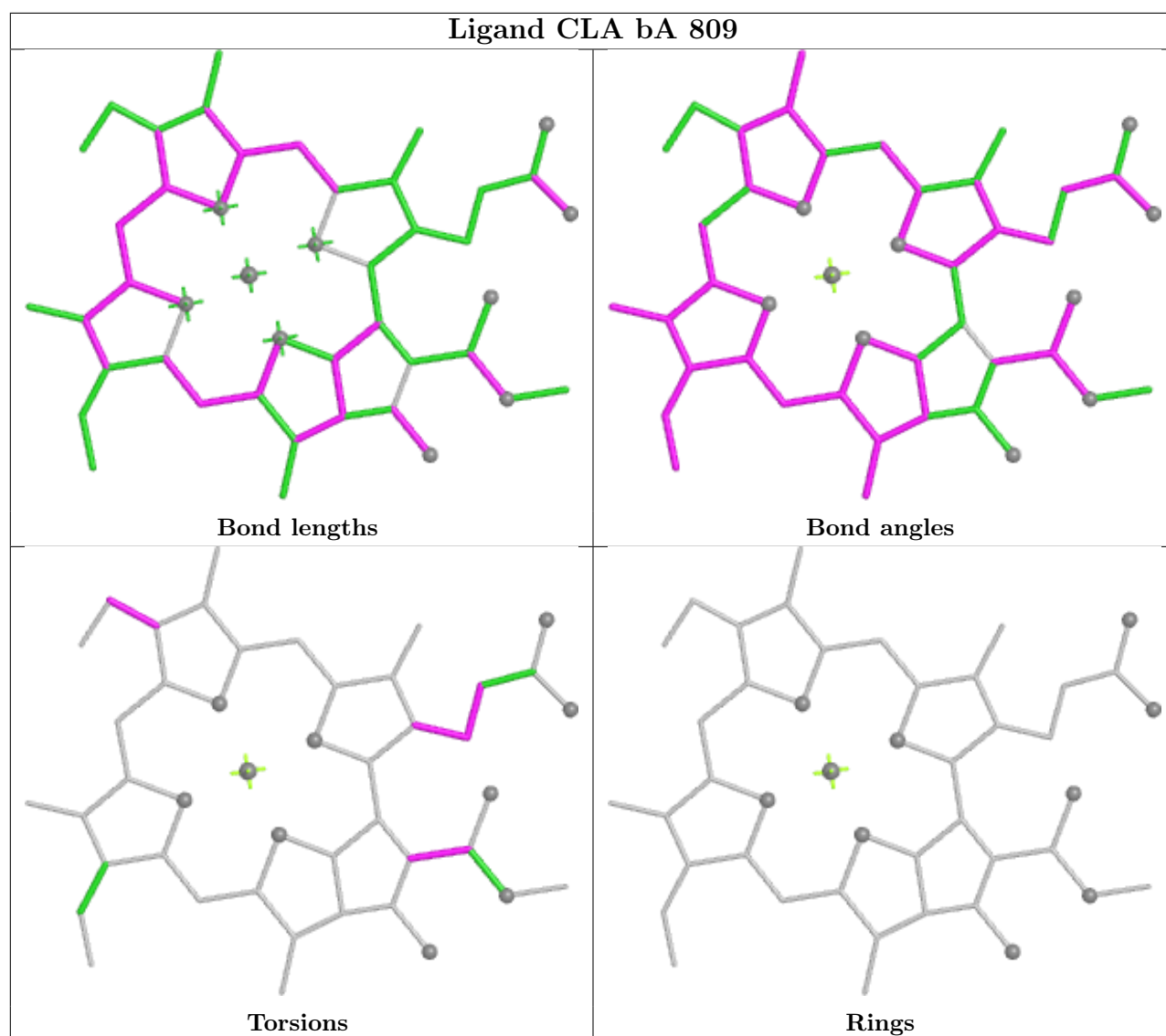


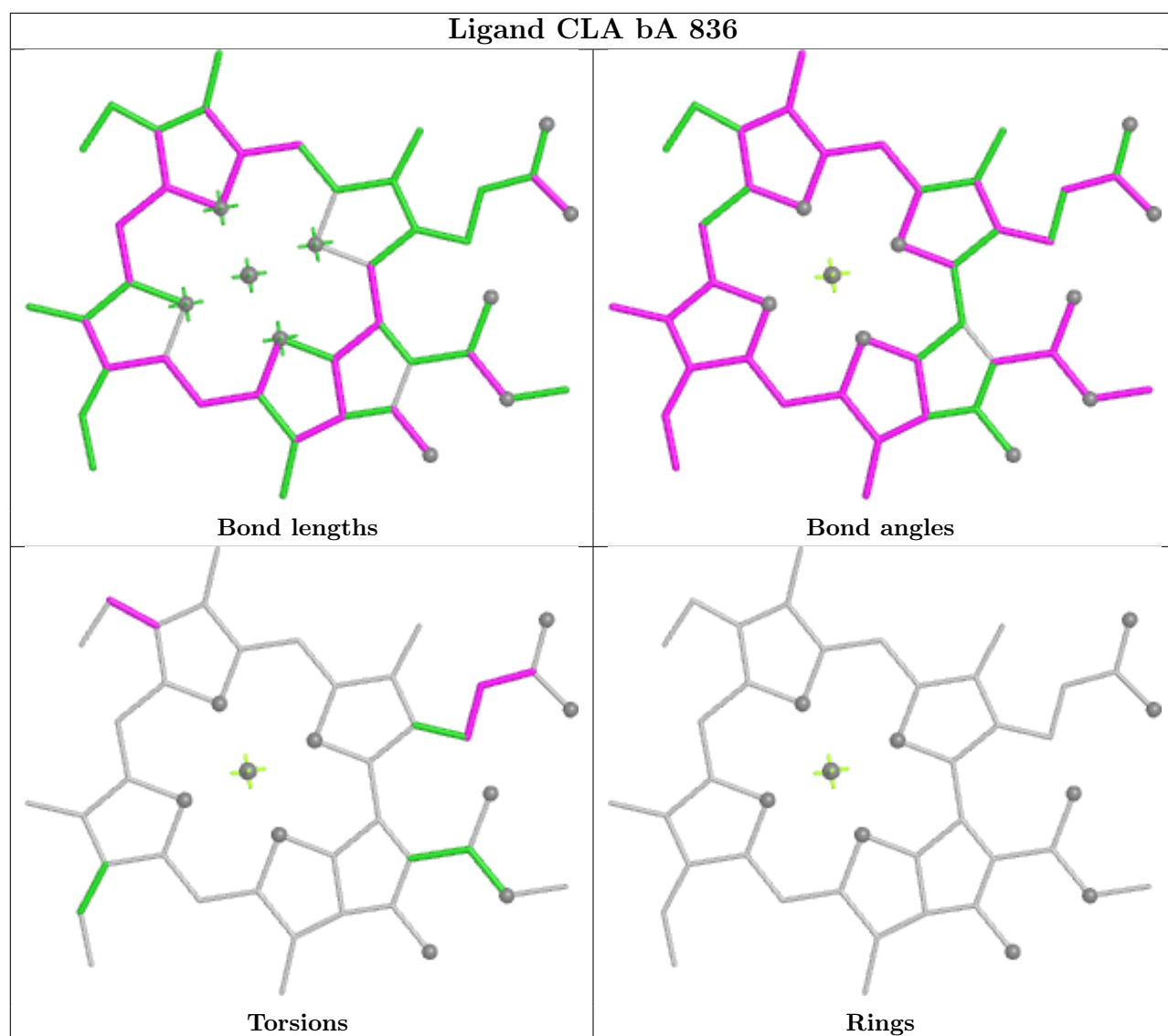
Torsions

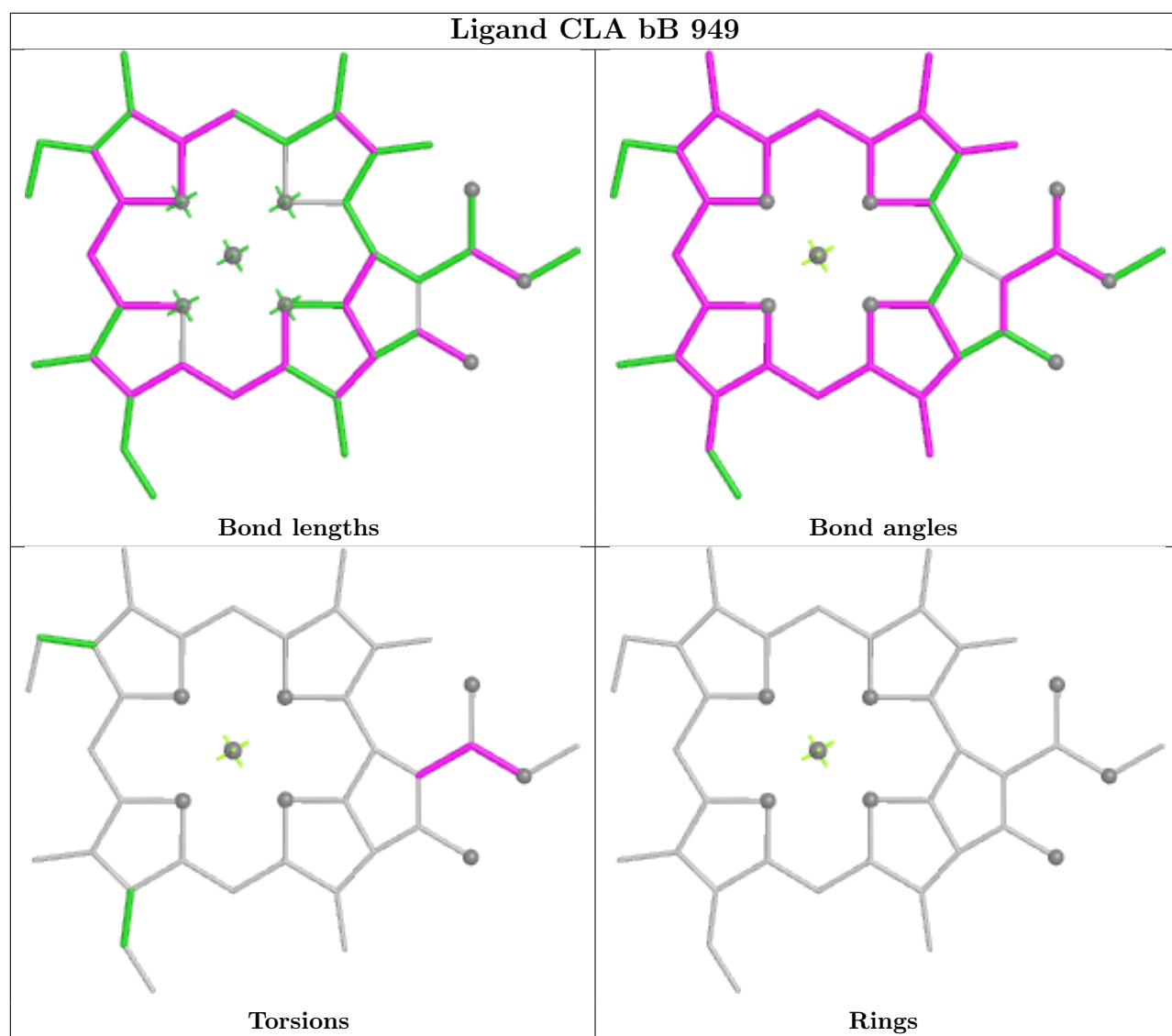


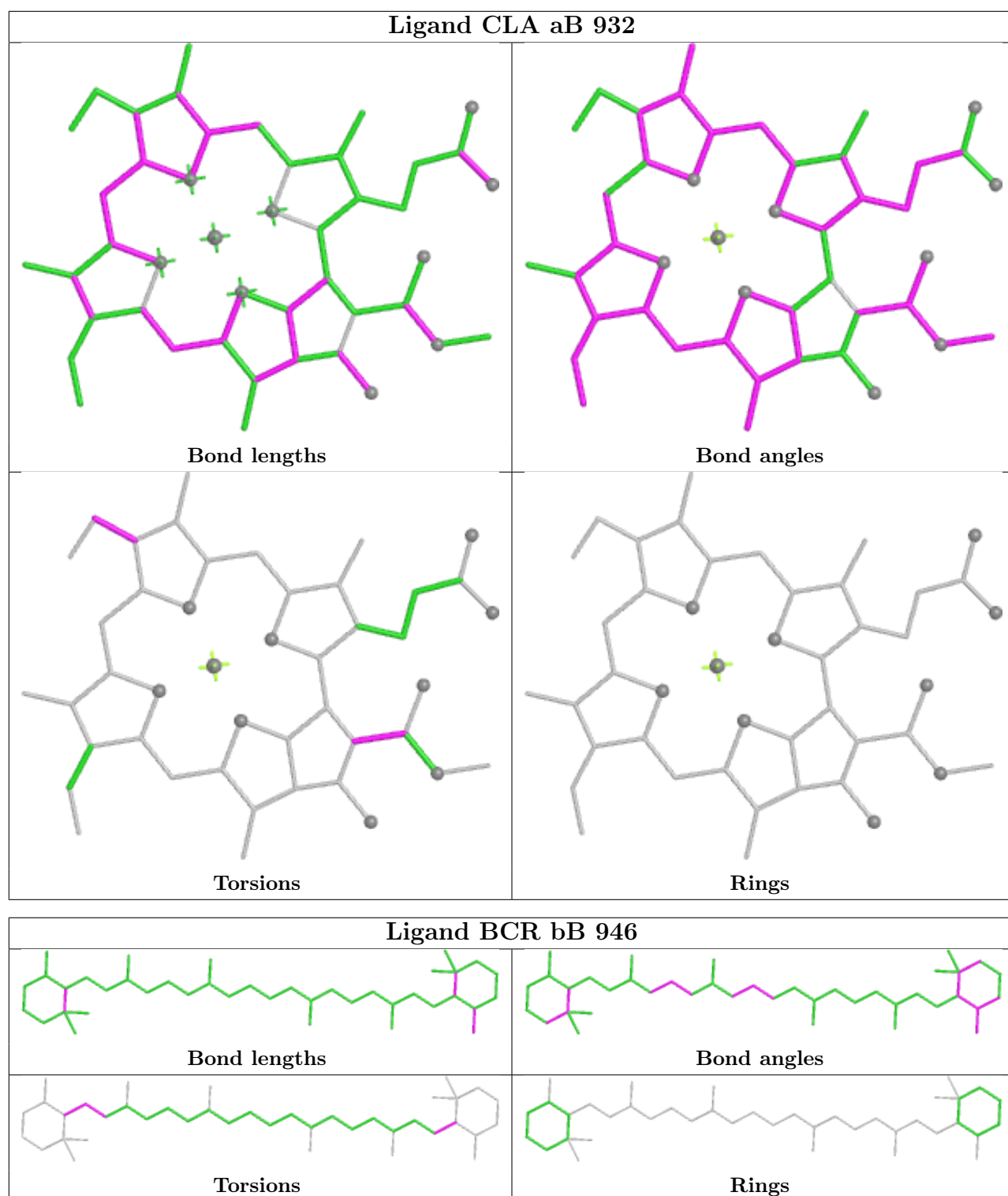
Rings

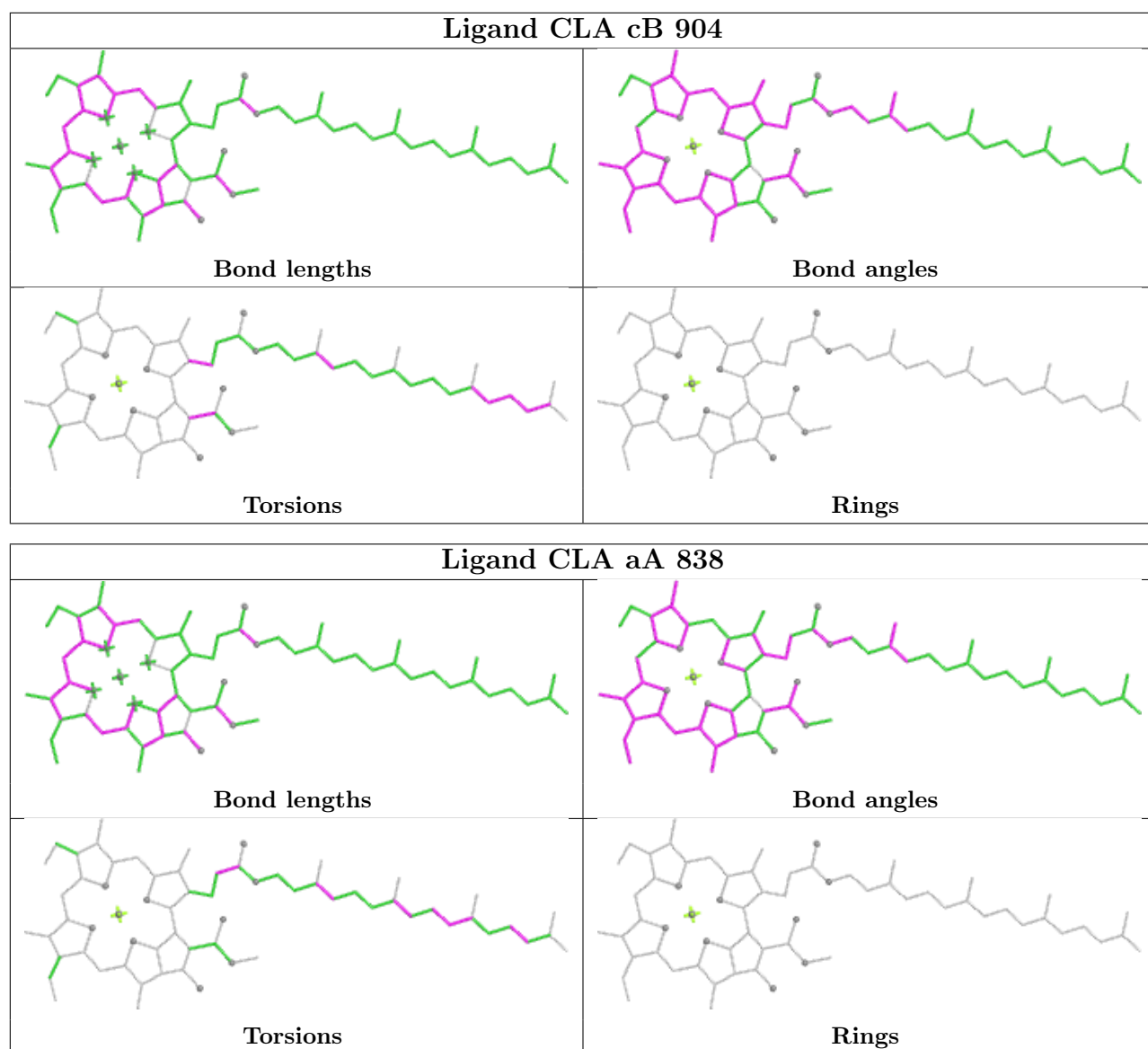


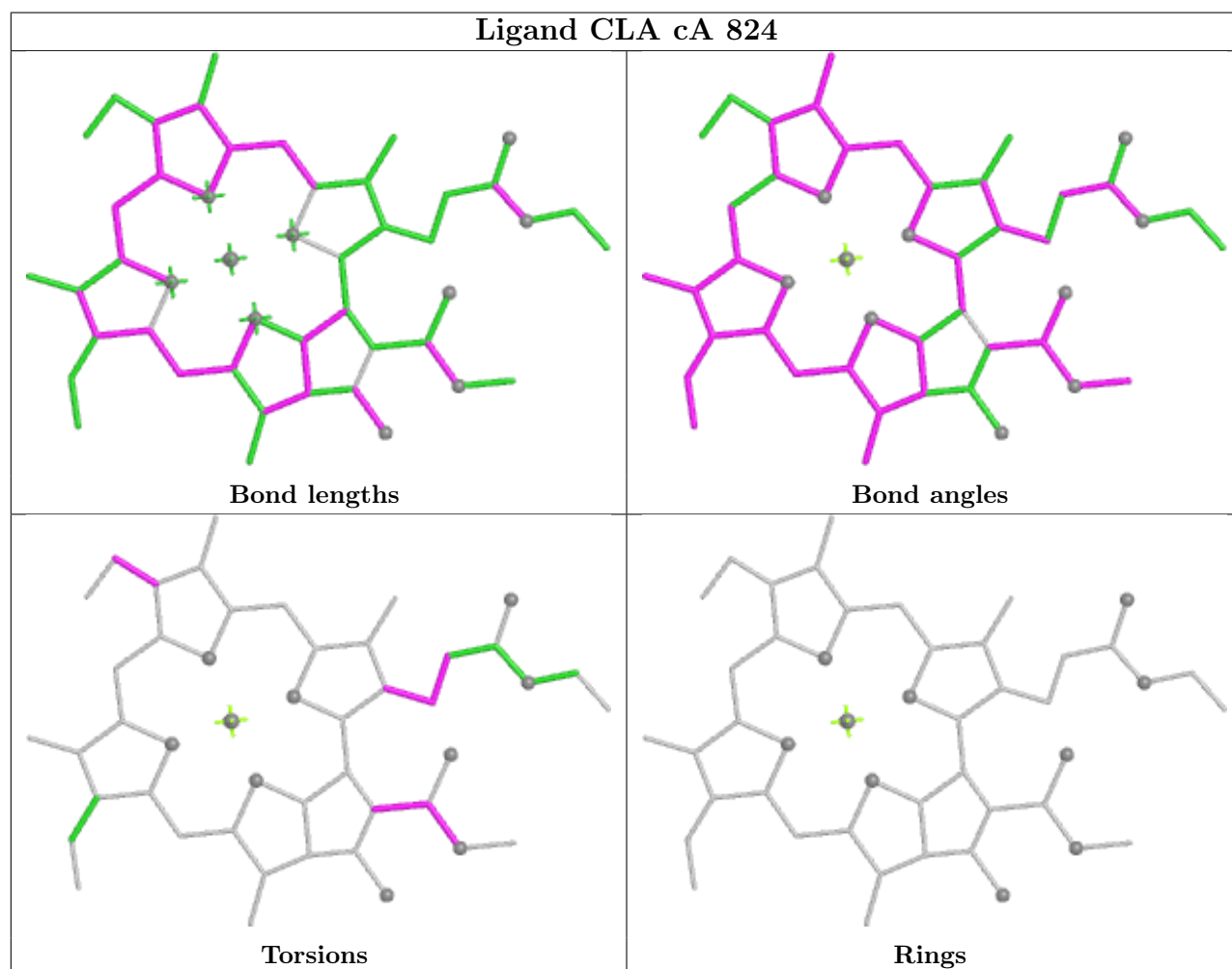
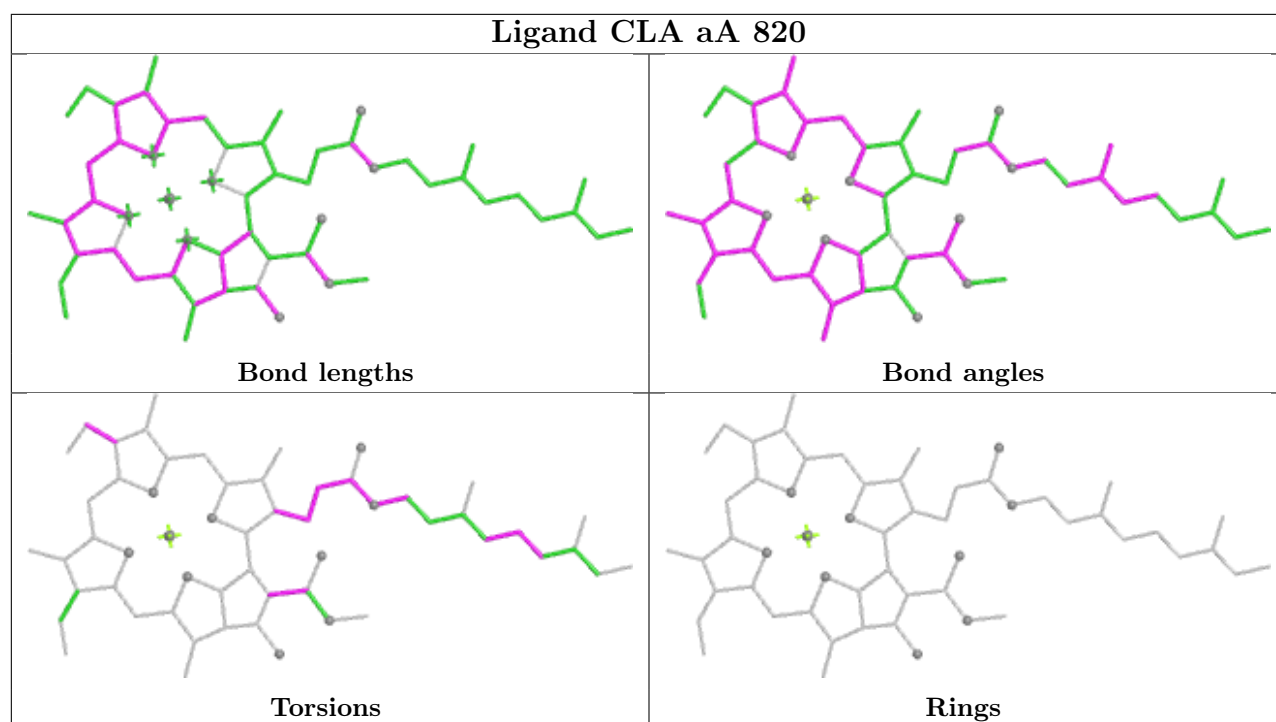


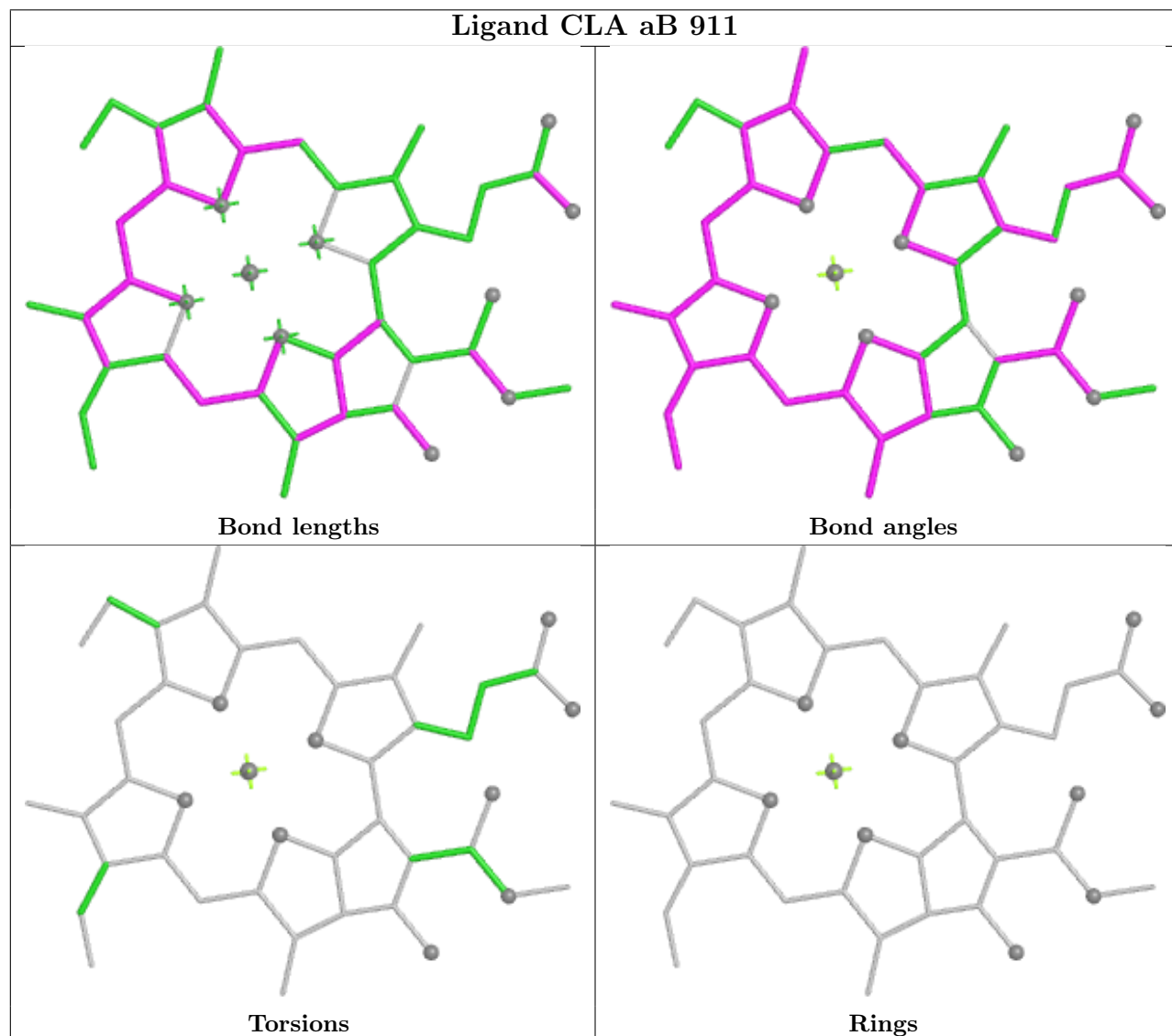
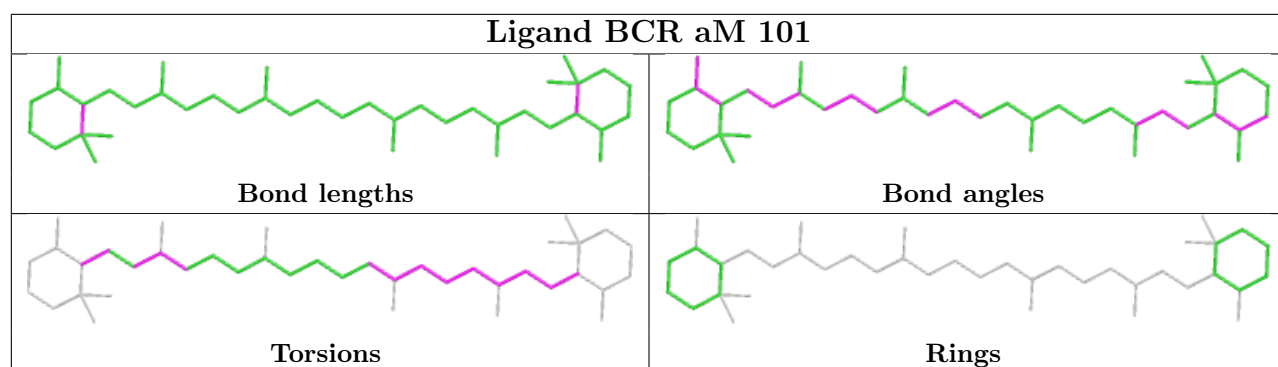


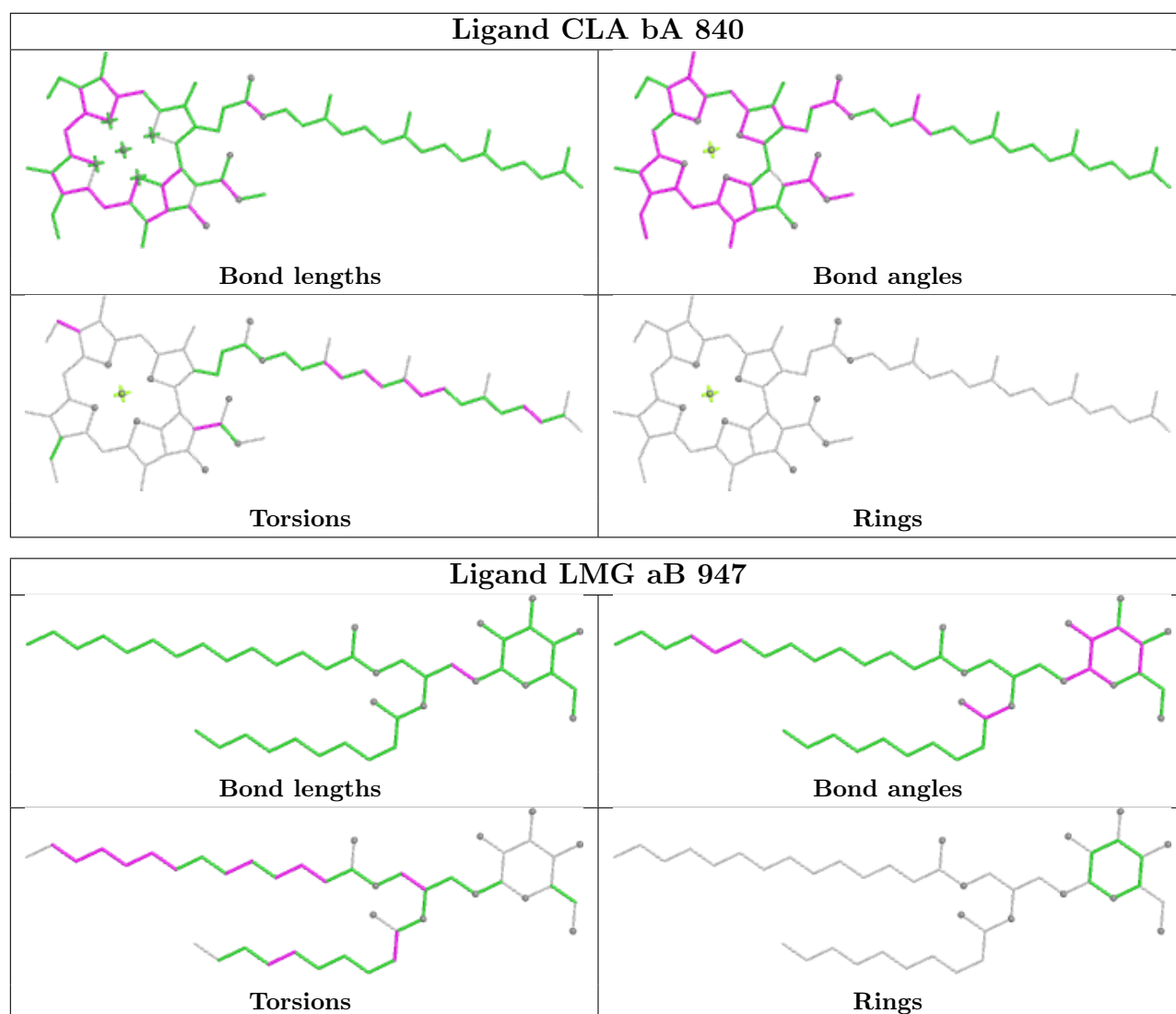




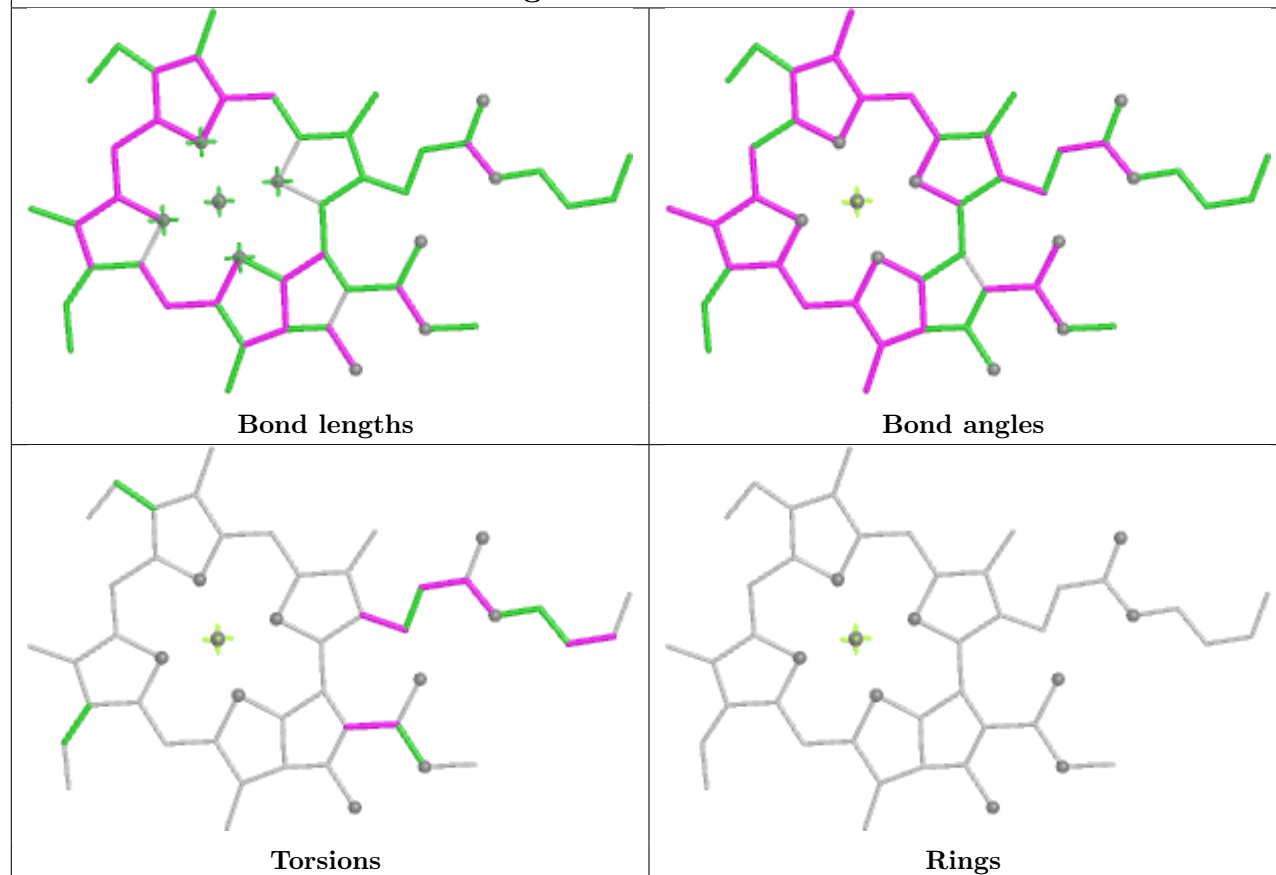




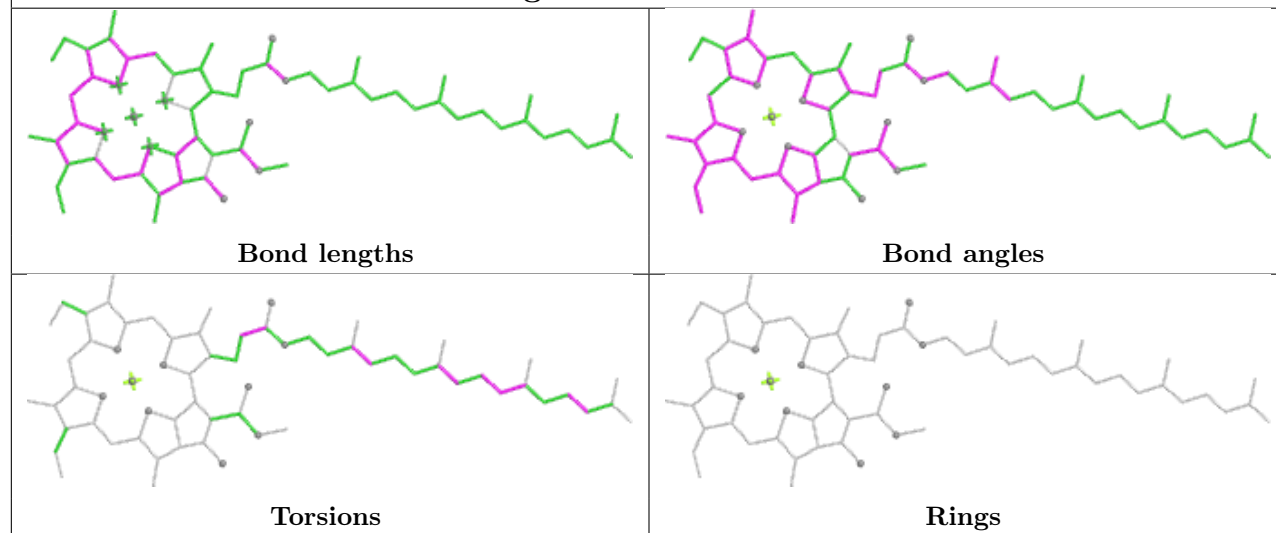


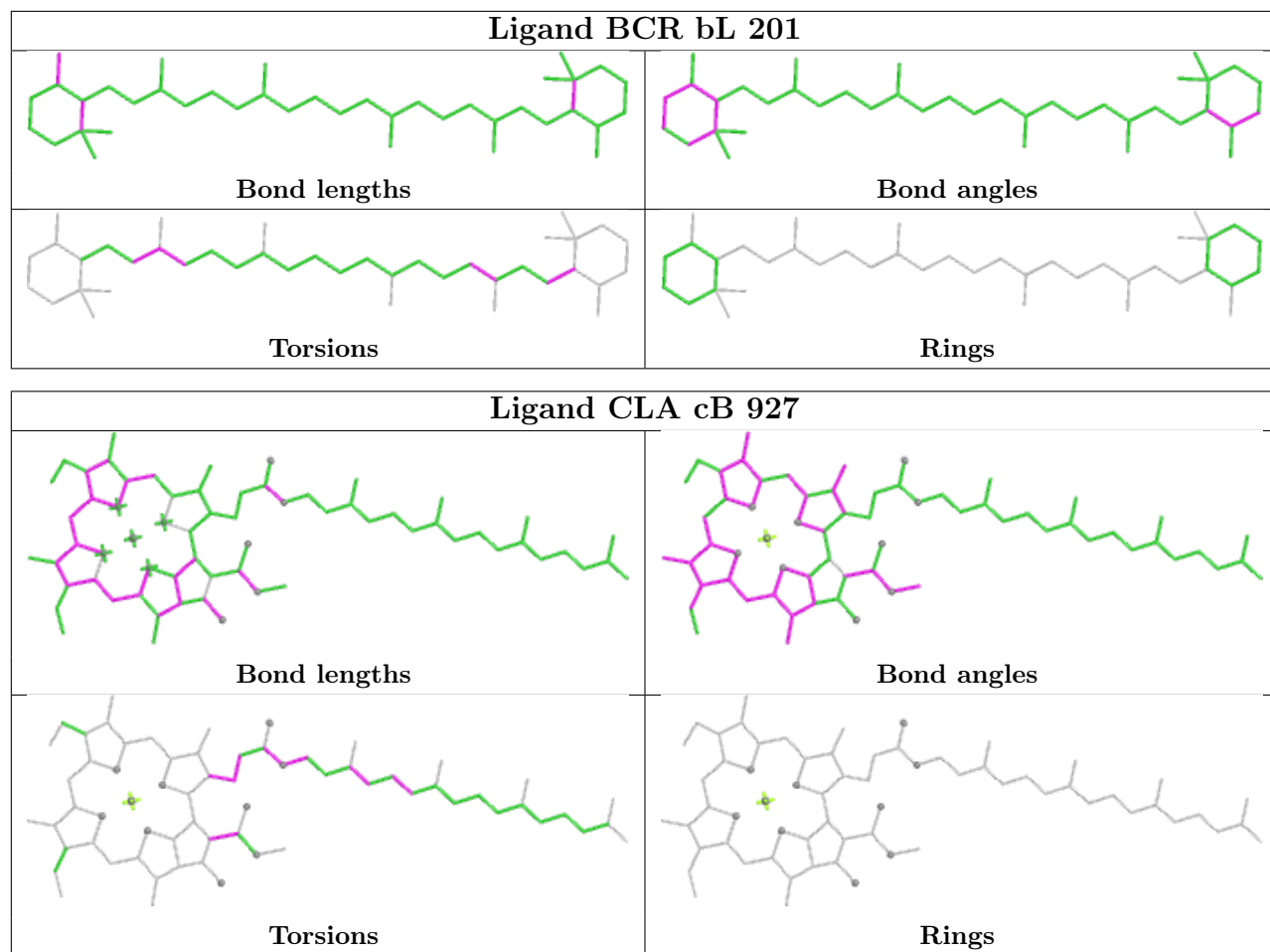


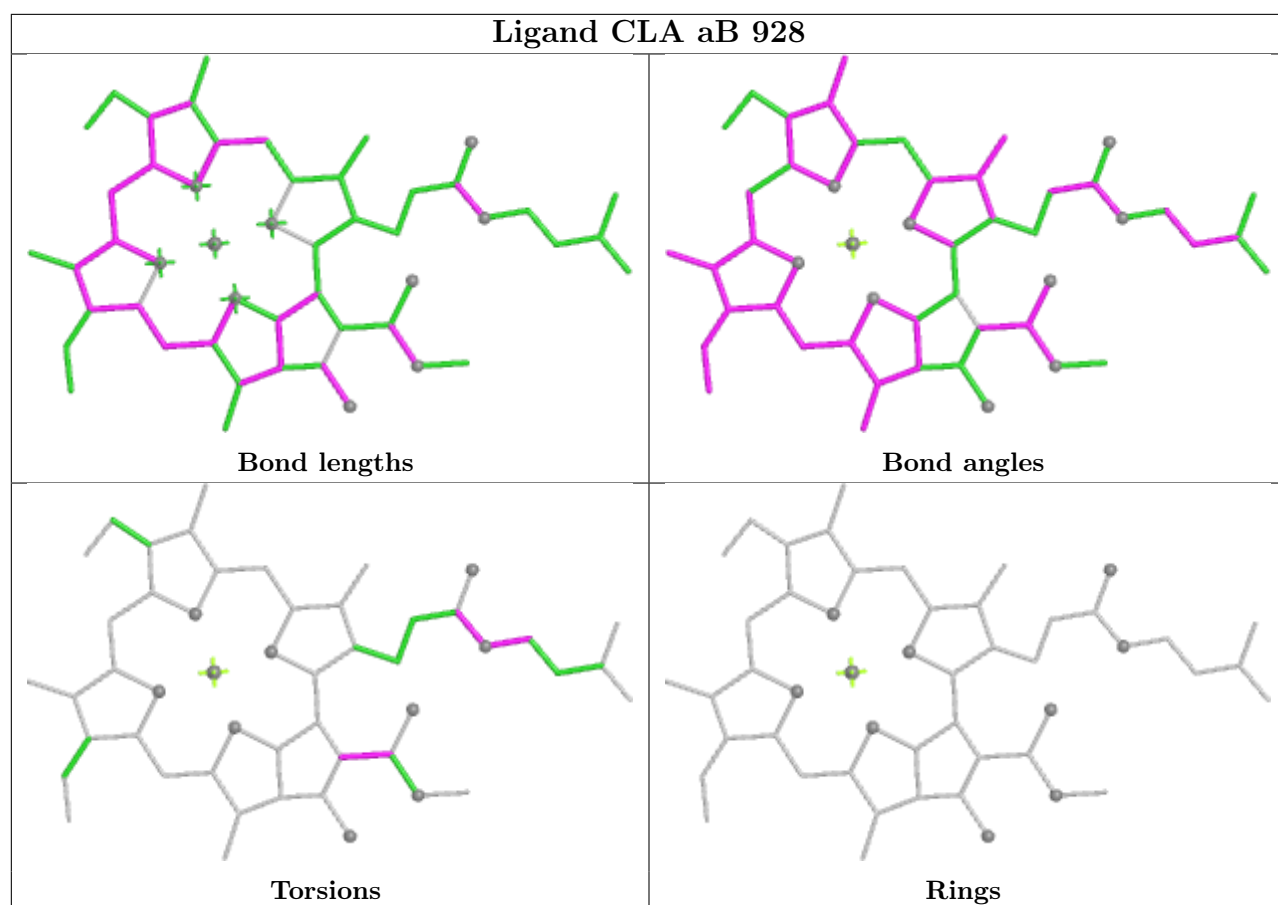
Ligand CLA cA 822

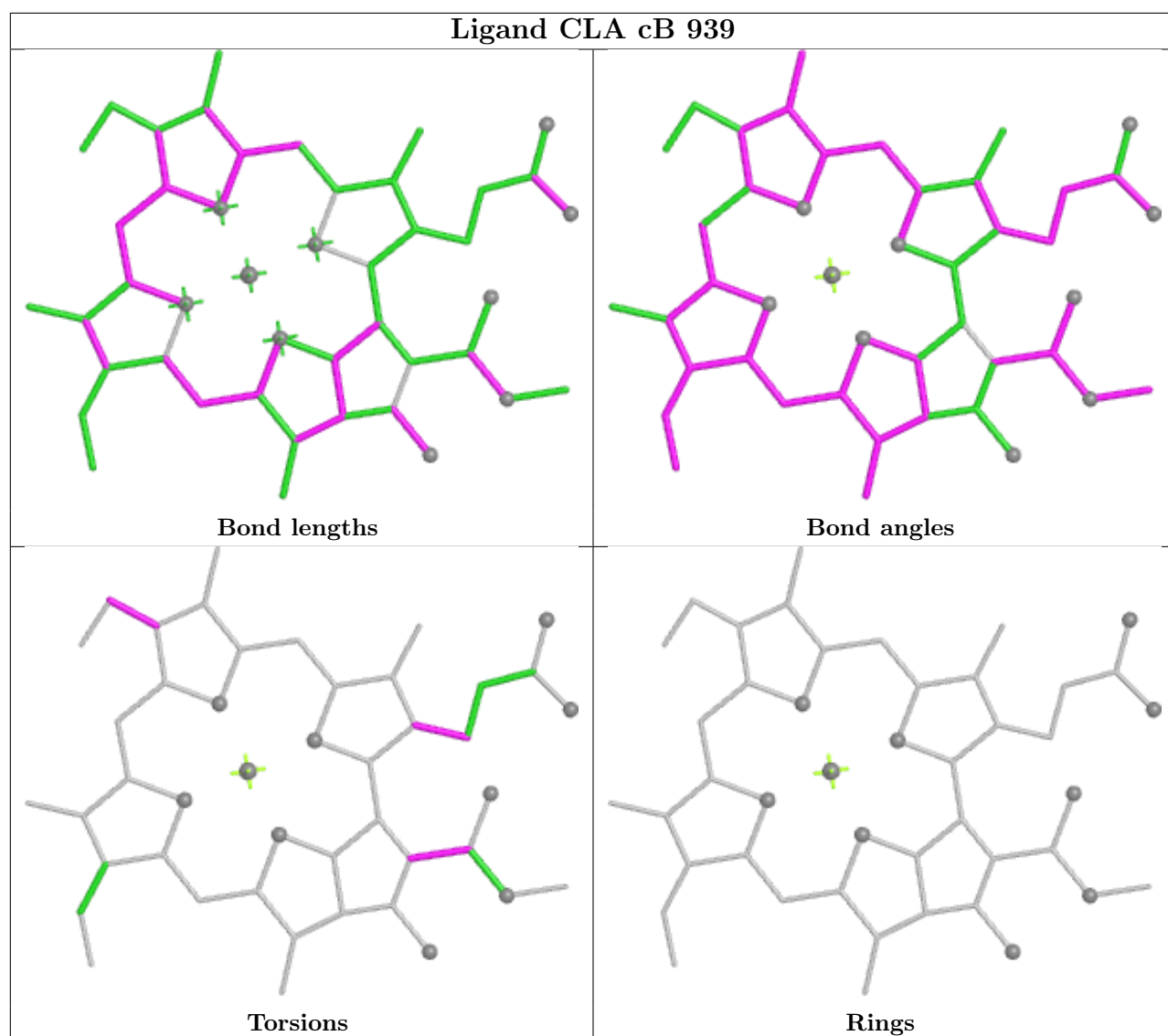


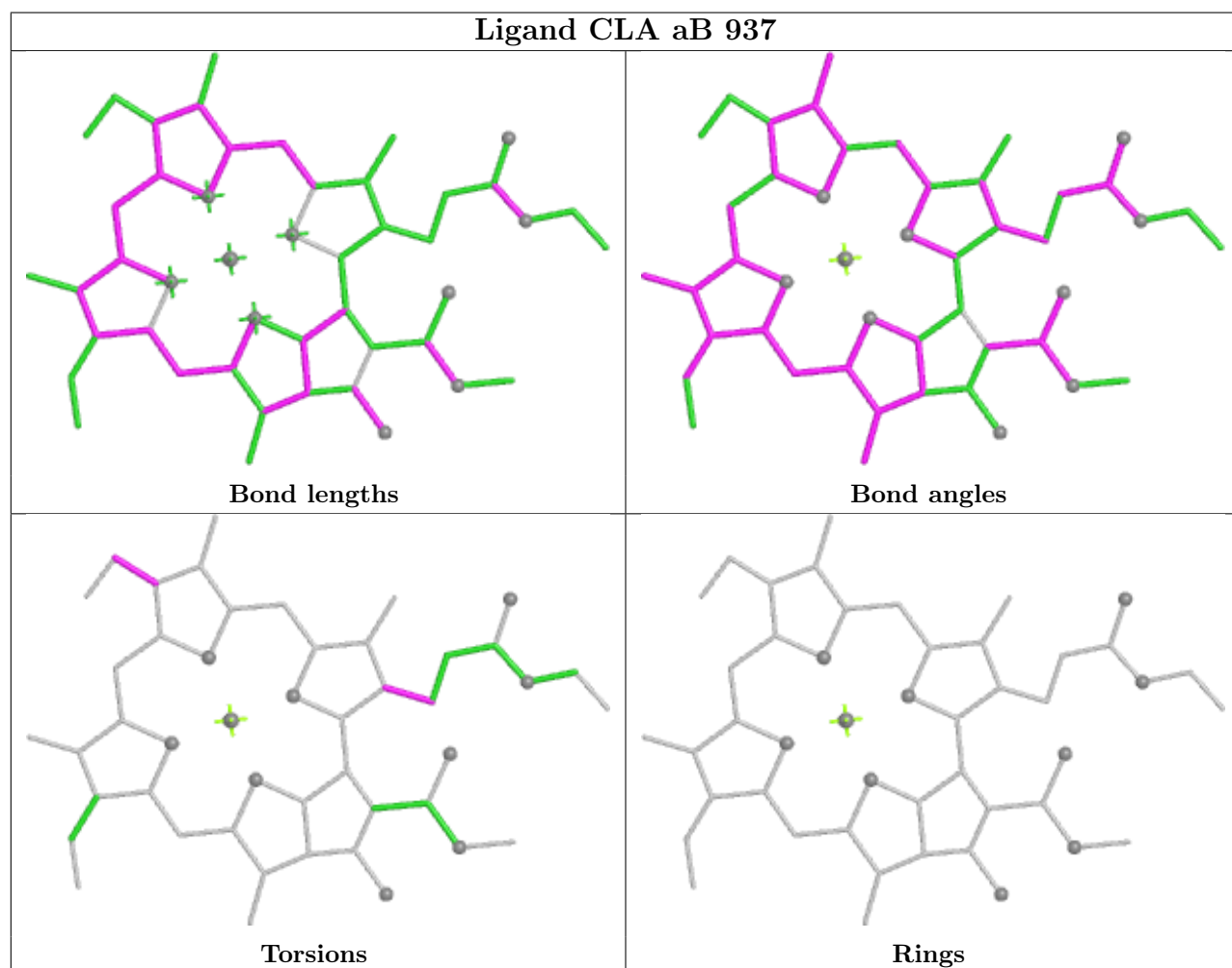
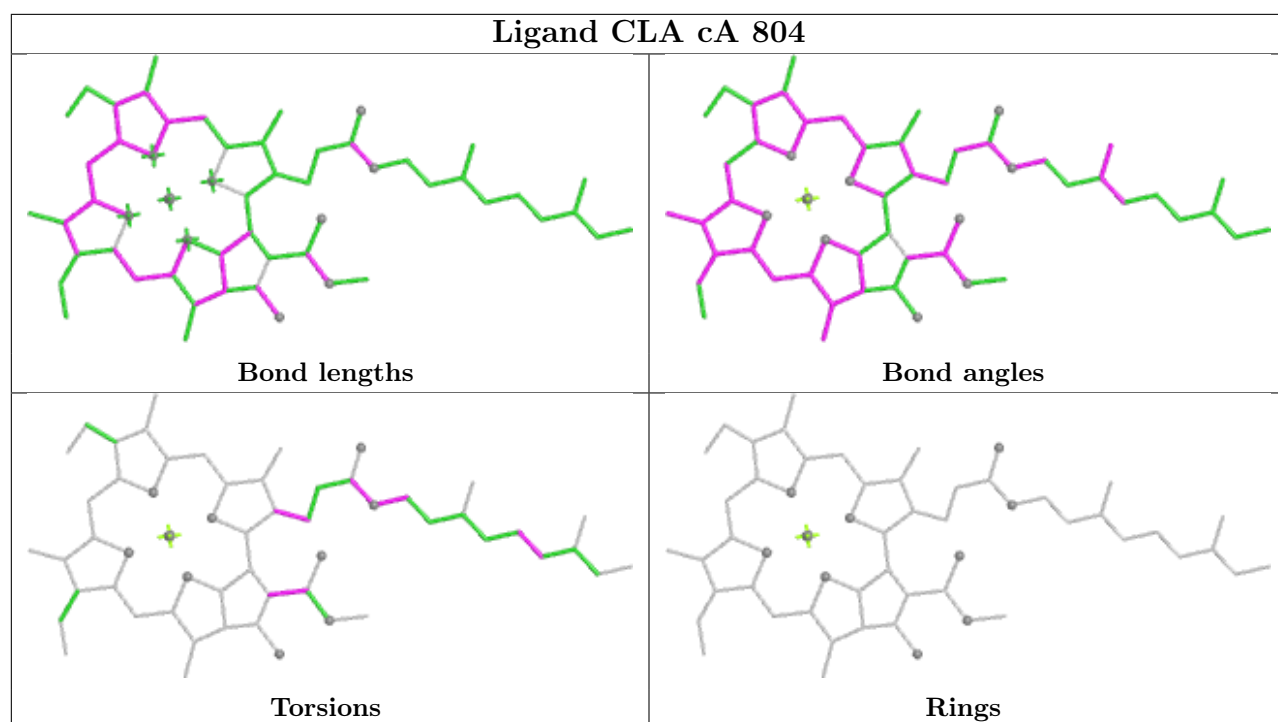
Ligand CLA cA 838

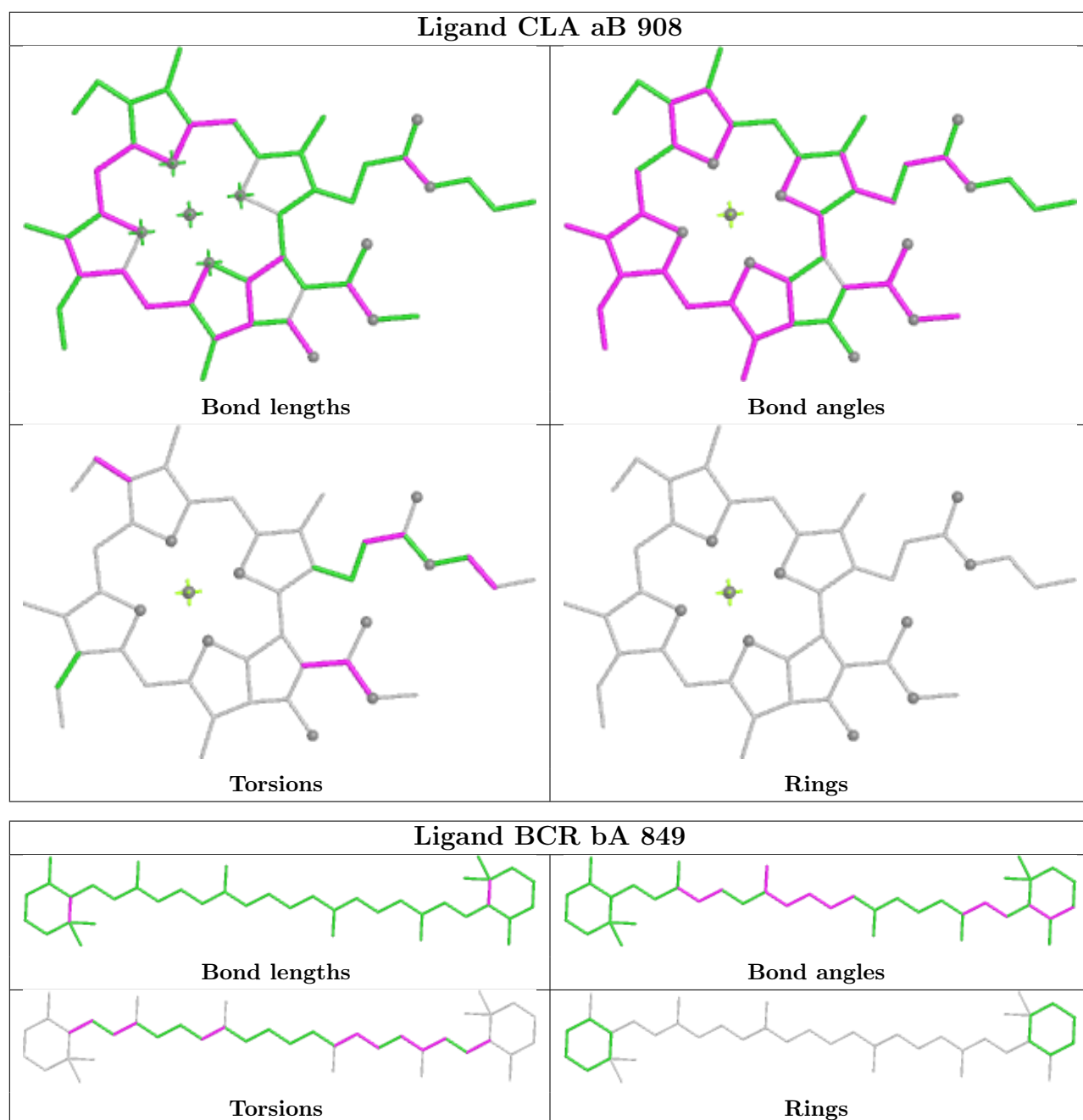


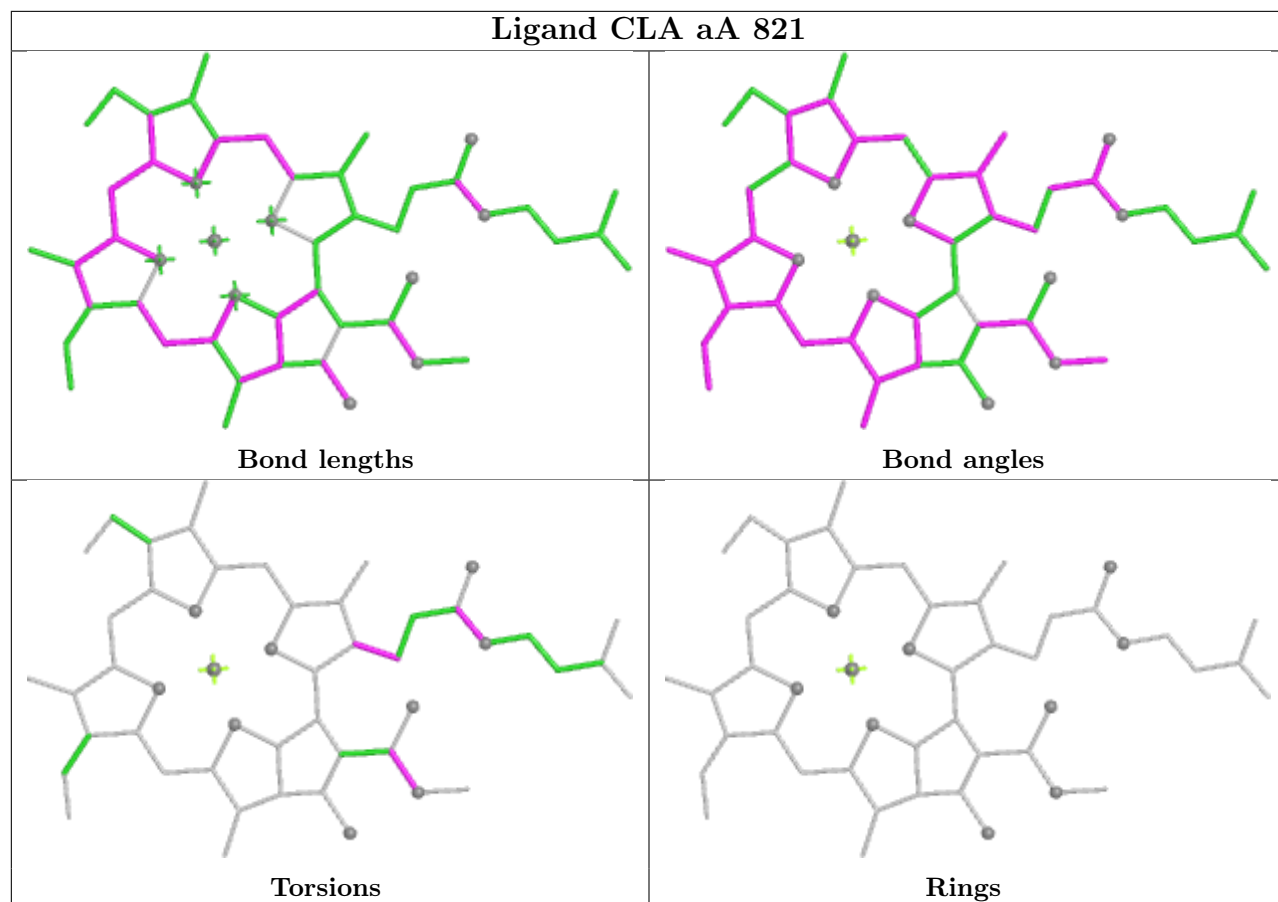


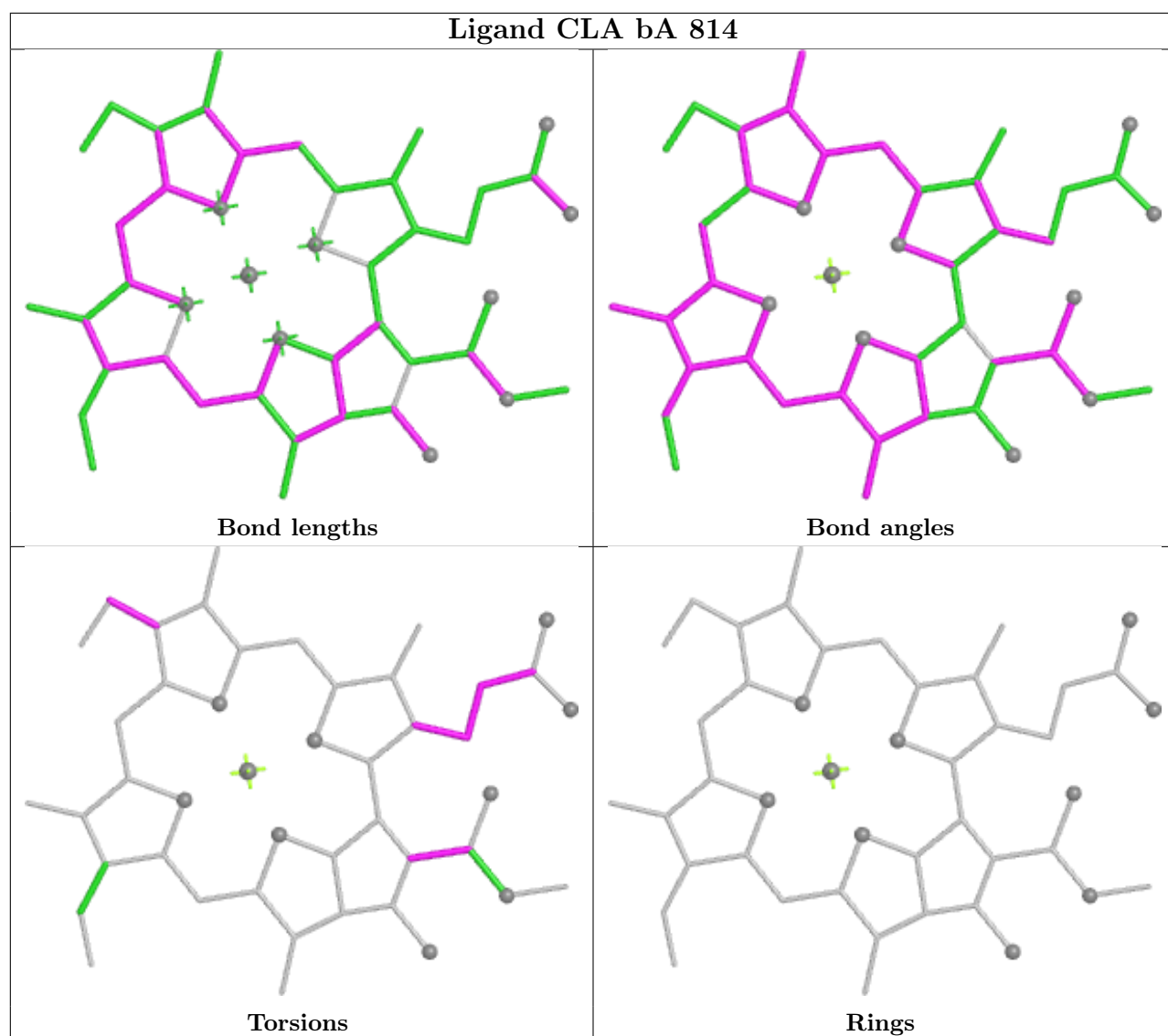




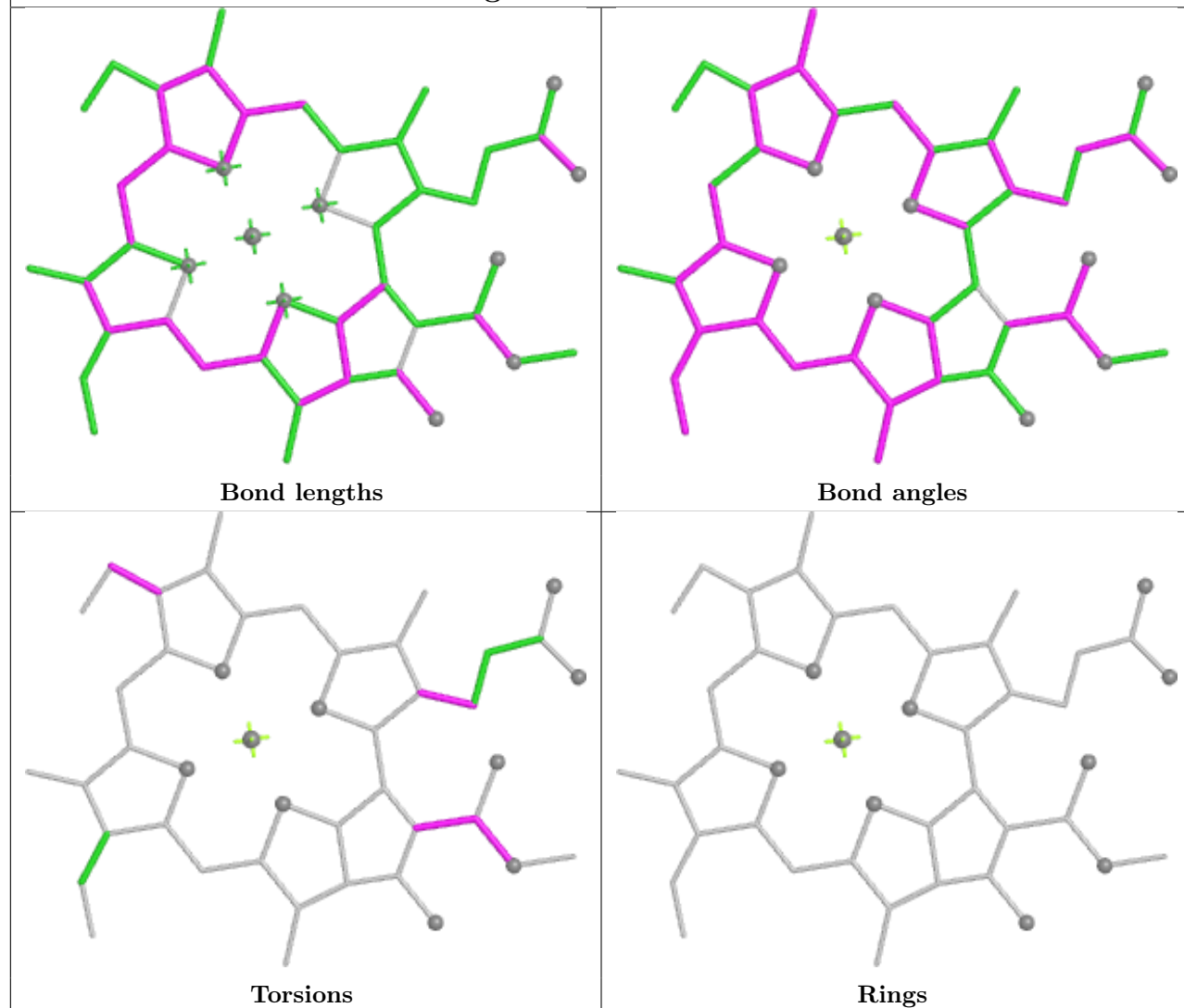




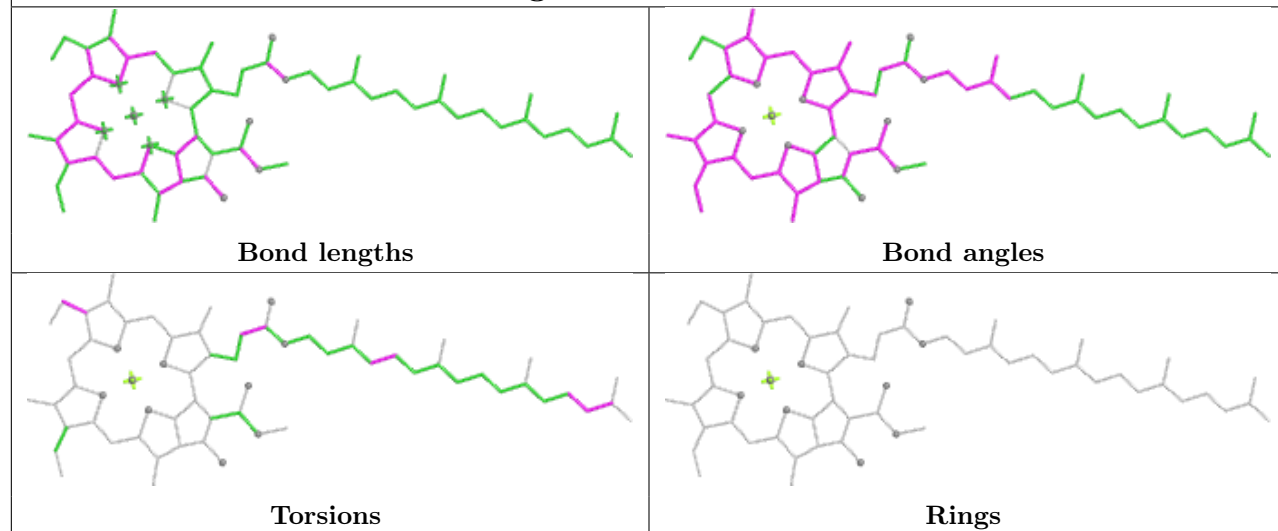


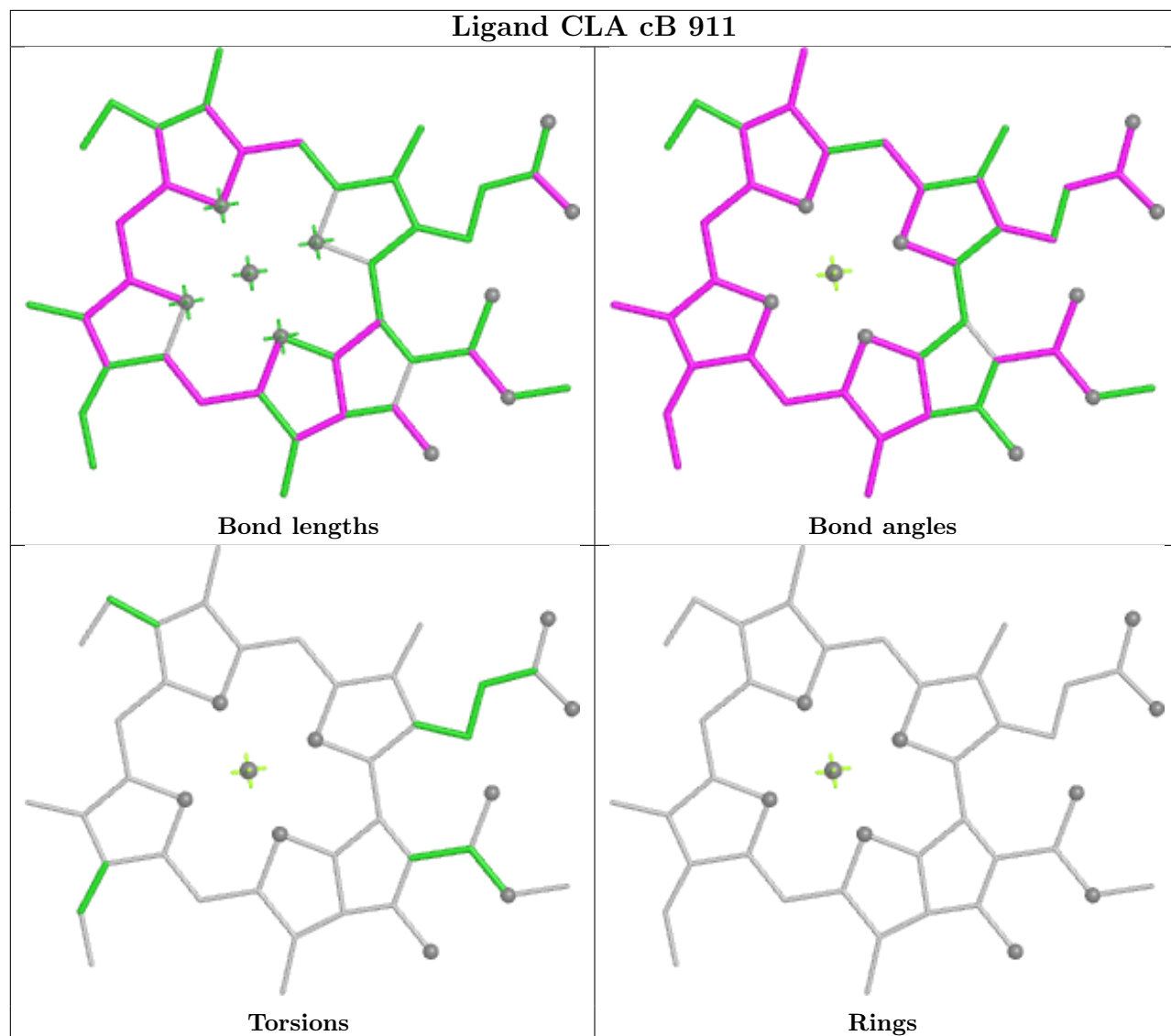


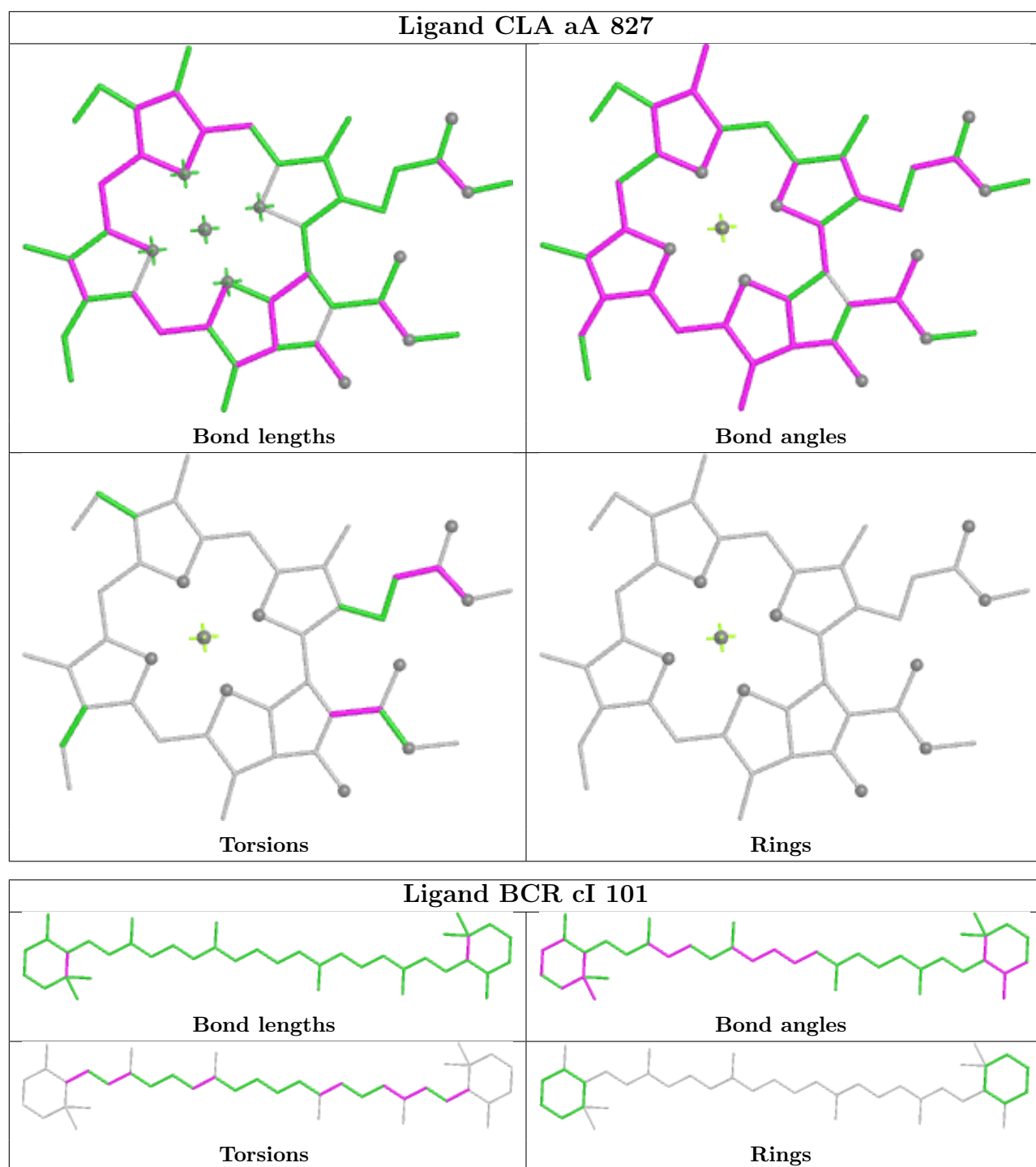
Ligand CLA aA 815

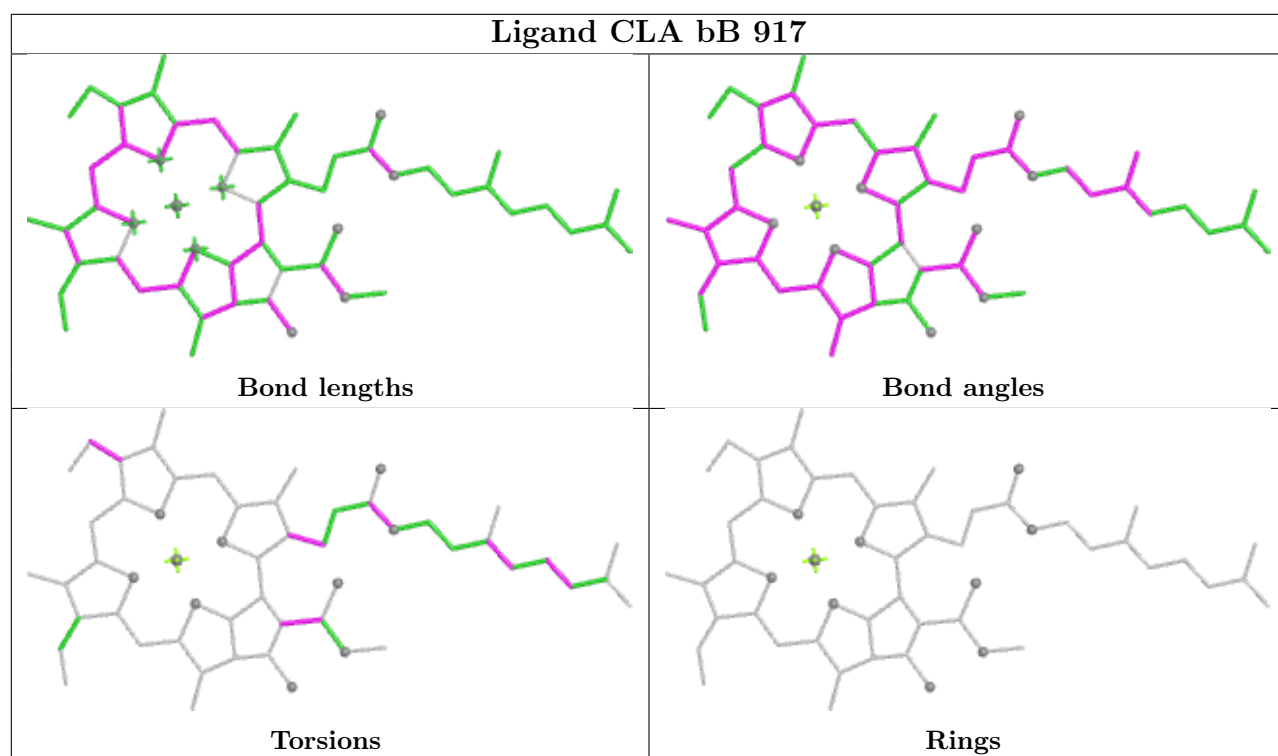


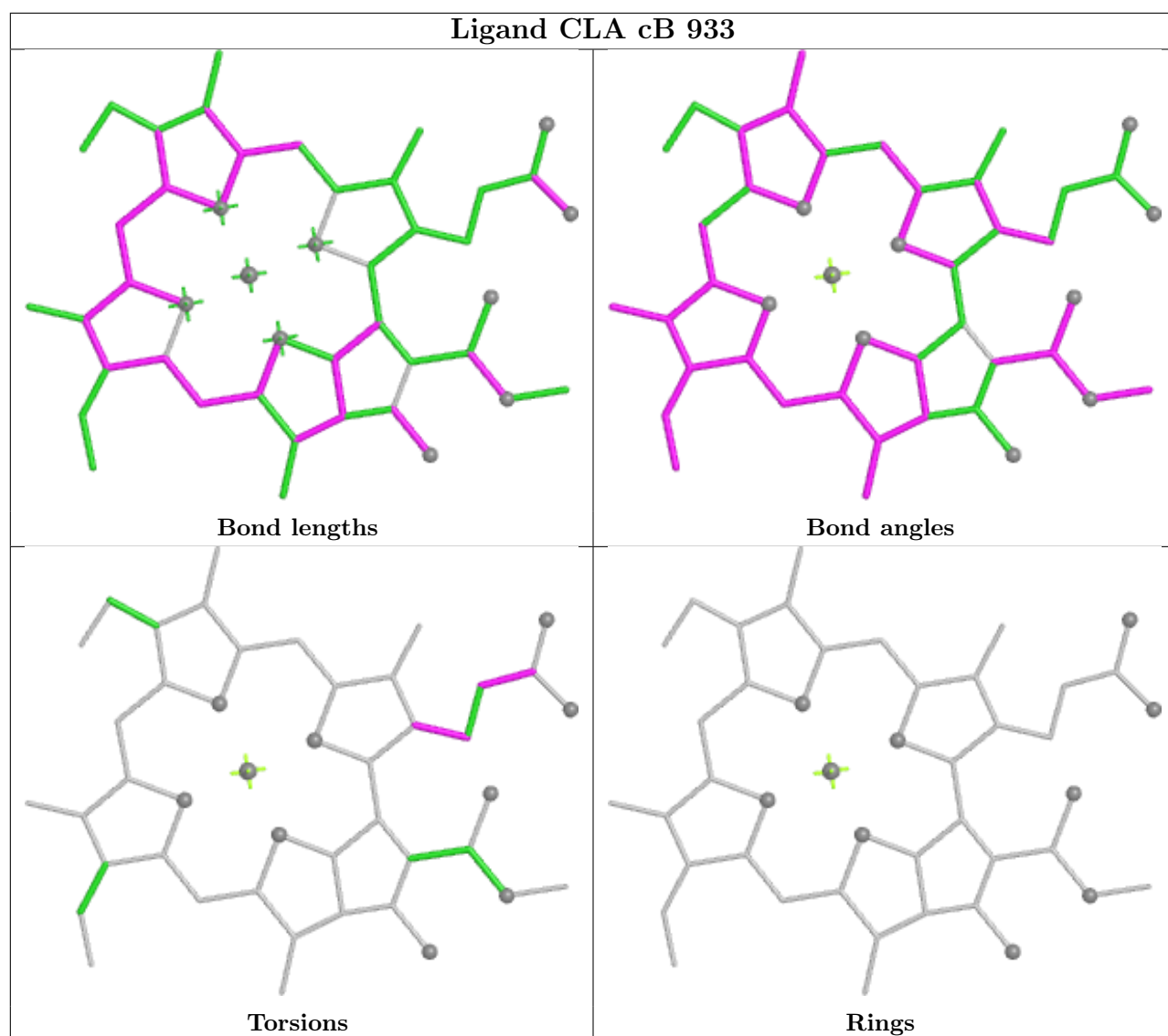
Ligand CL0 cA 801

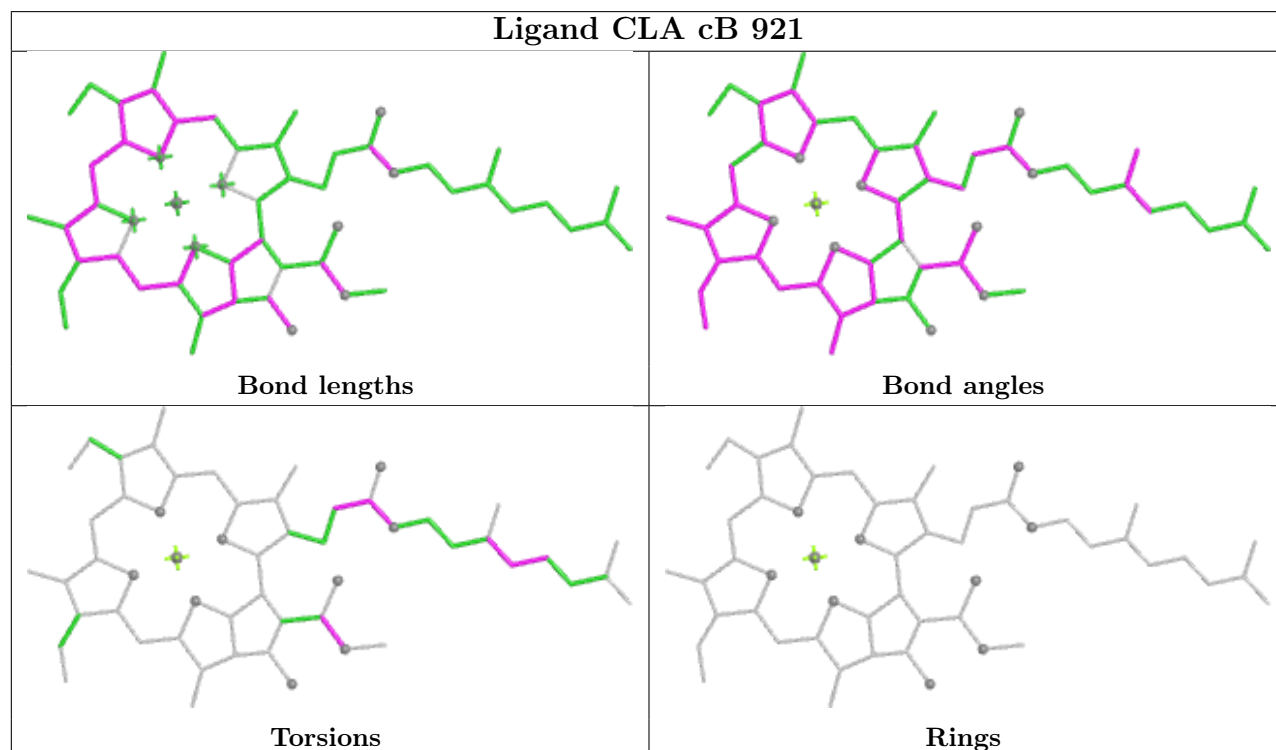
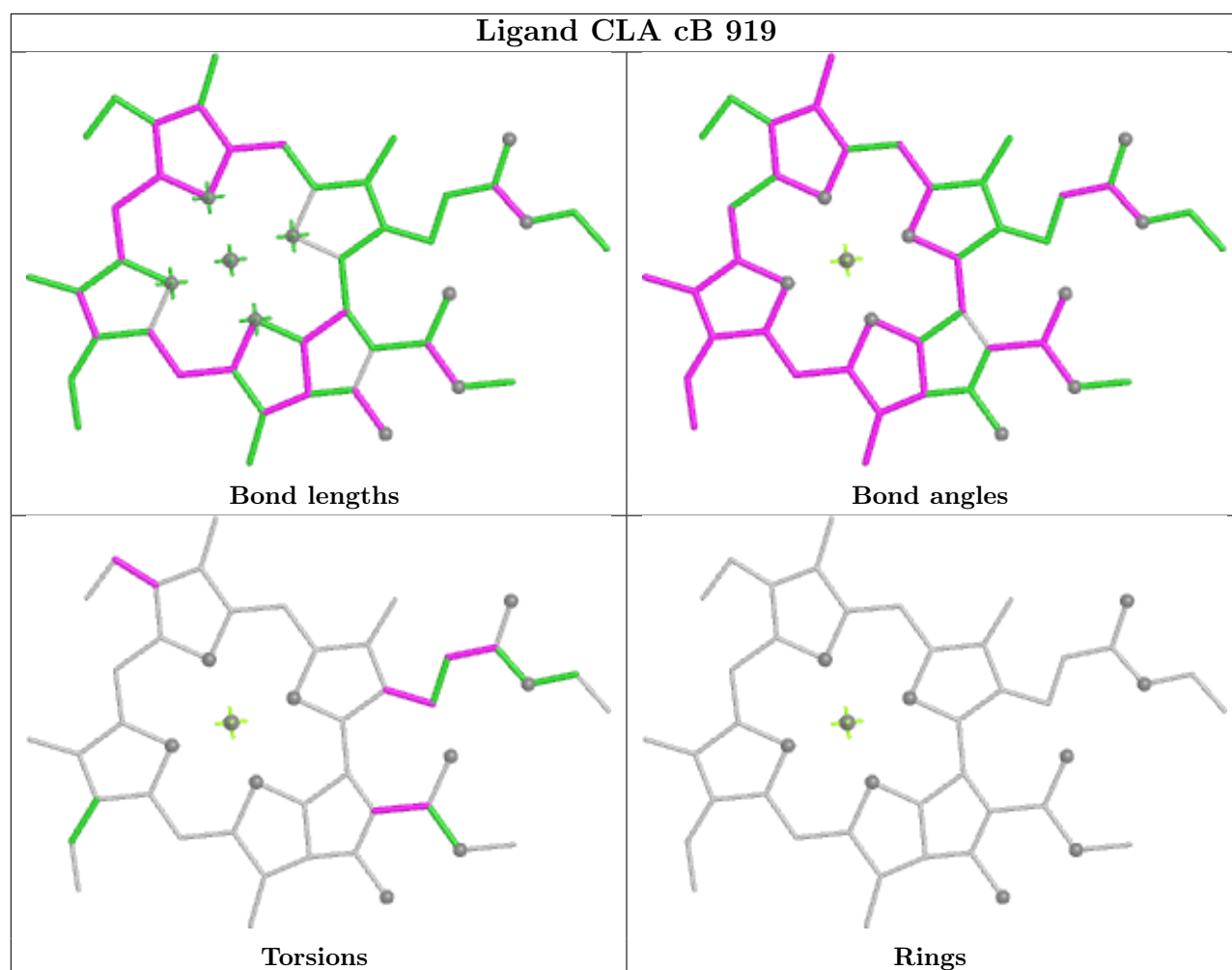




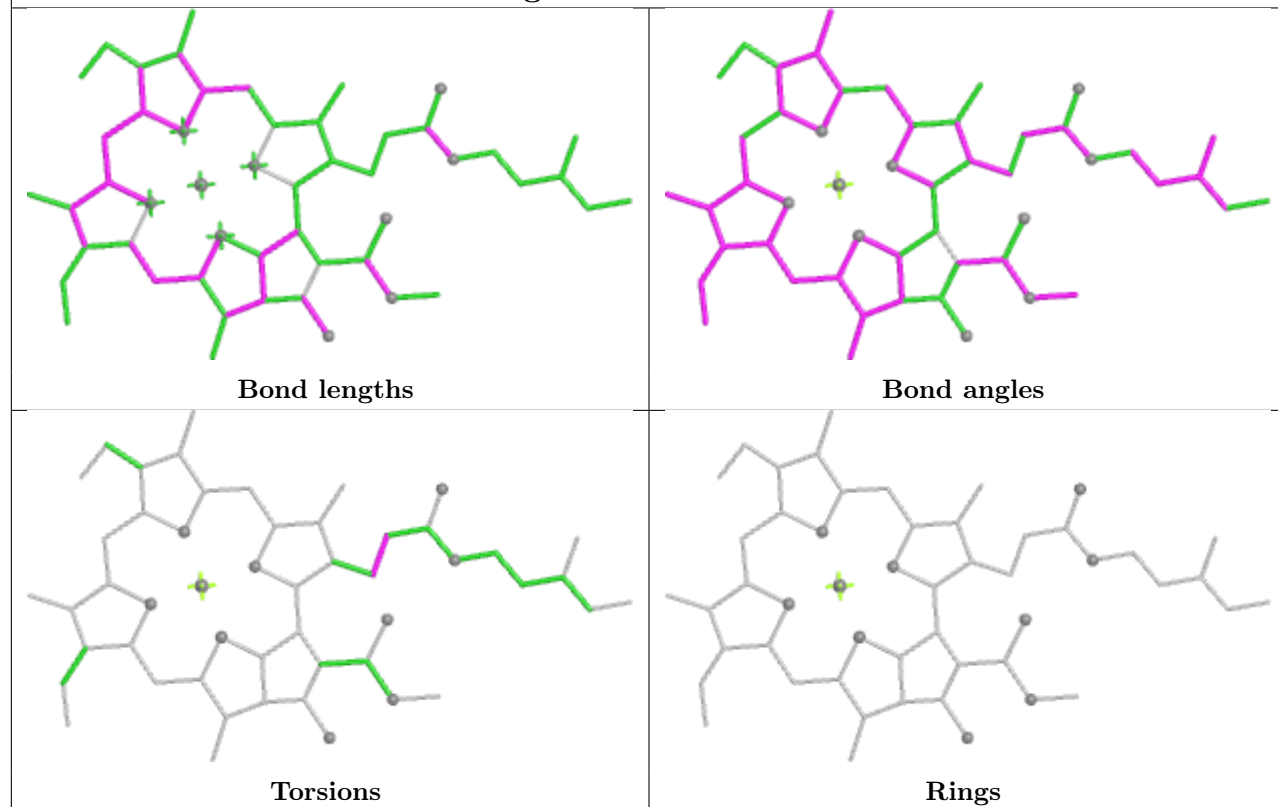




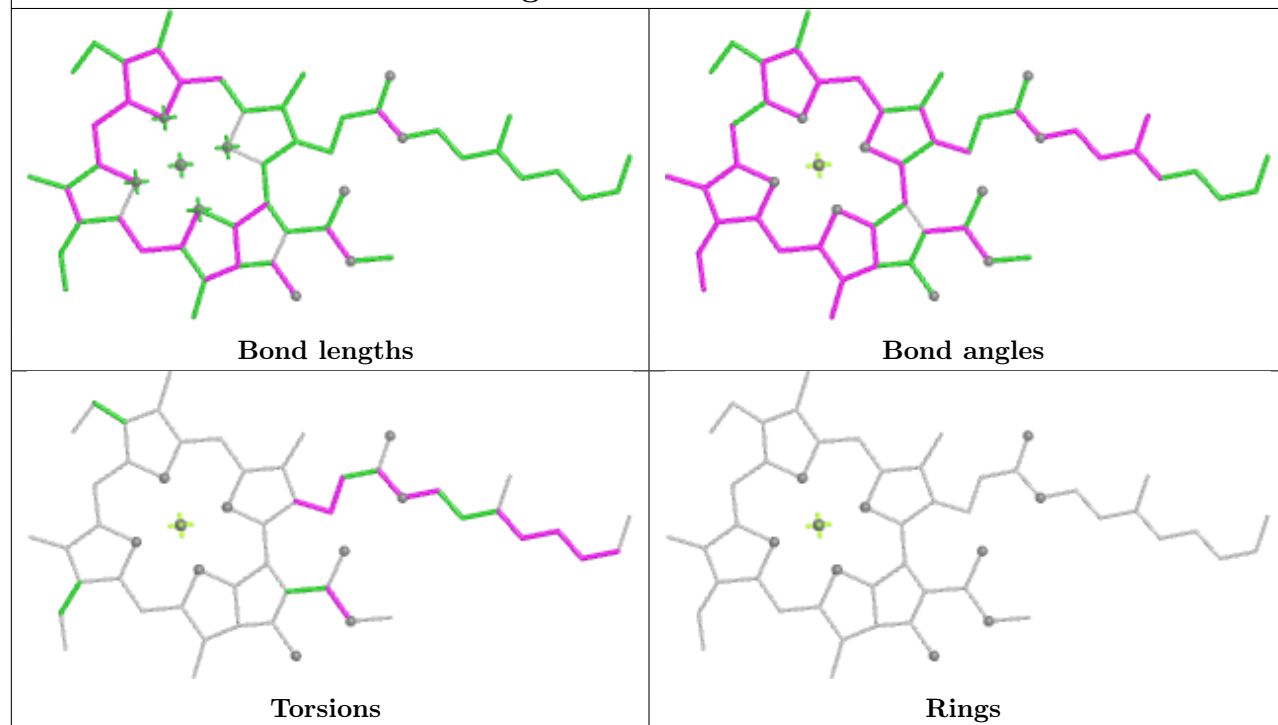


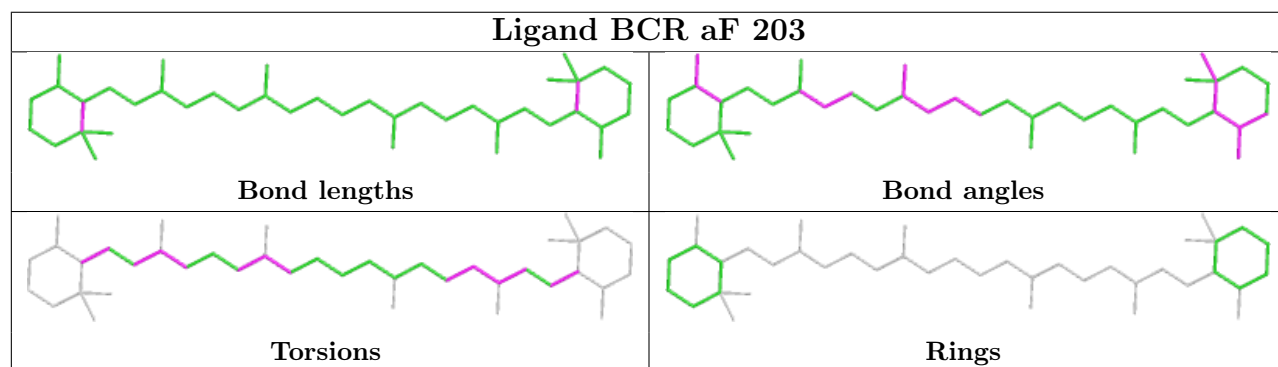
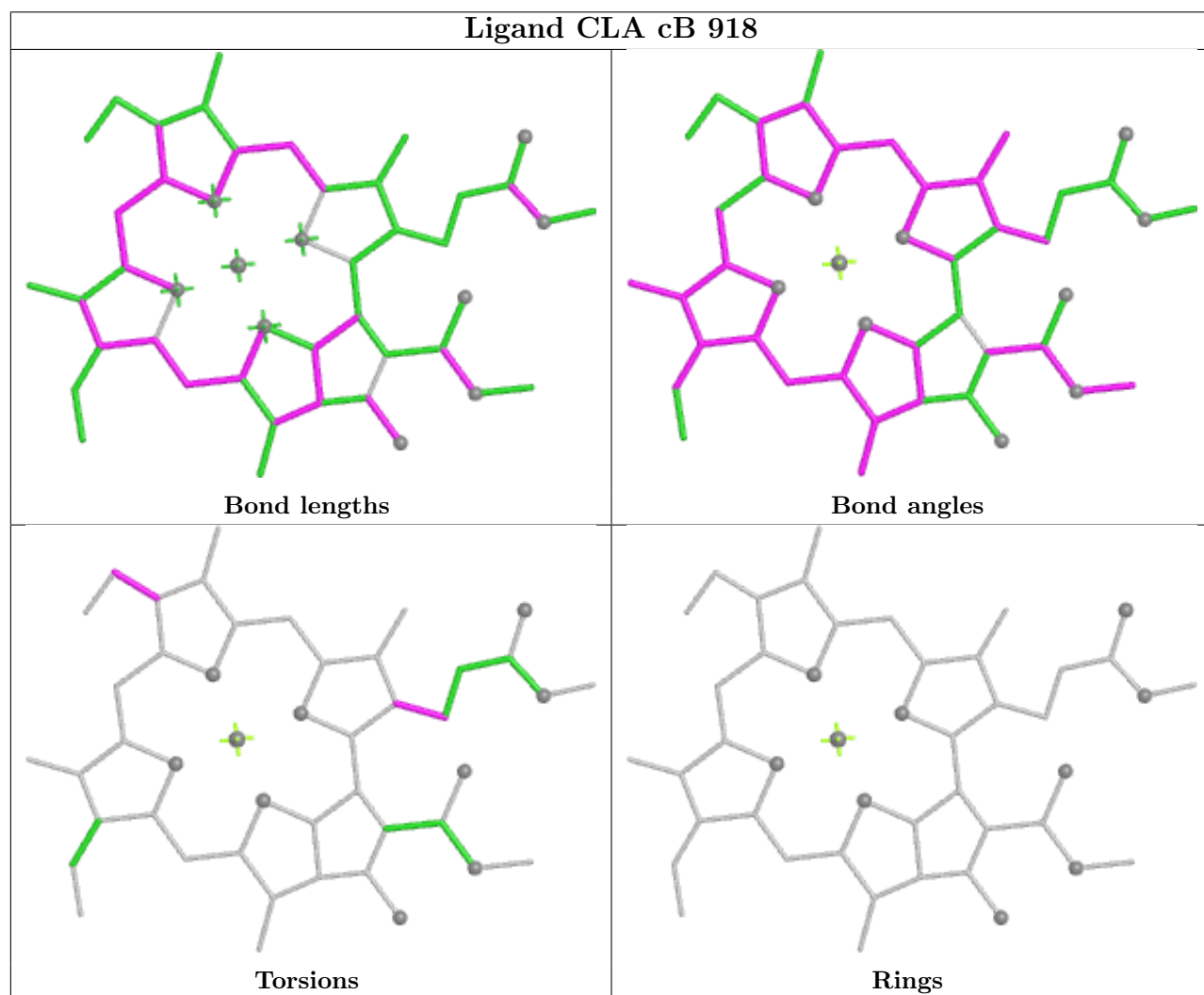
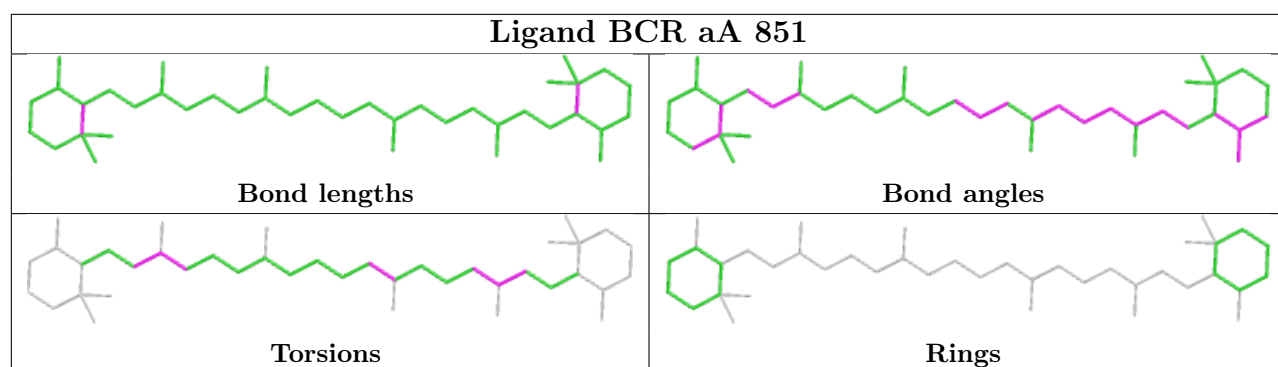


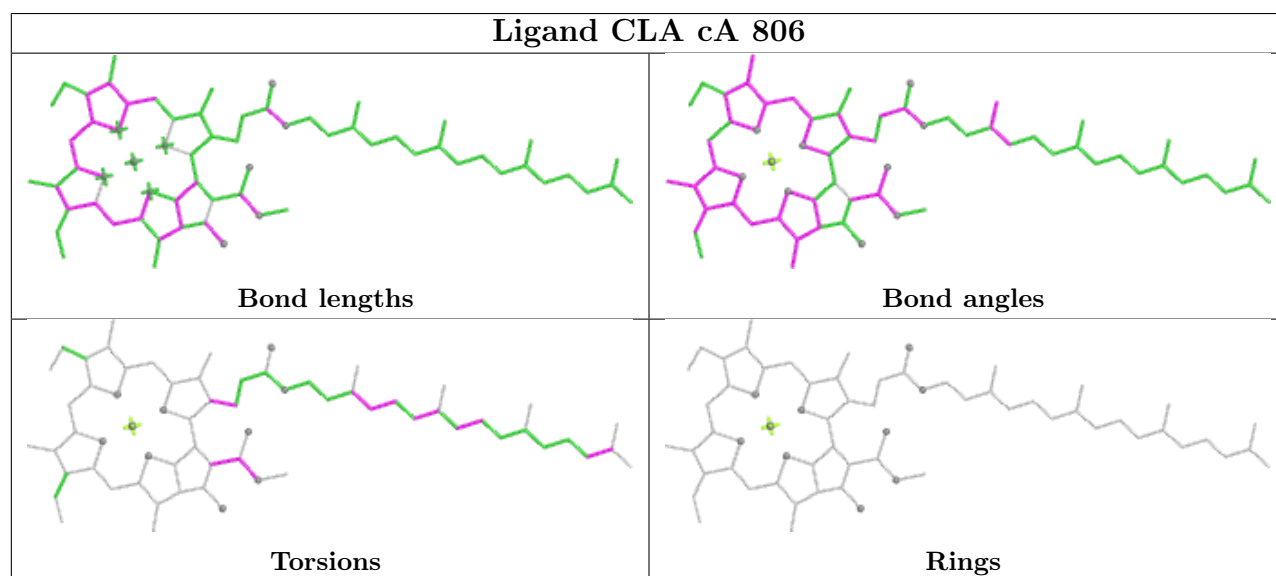
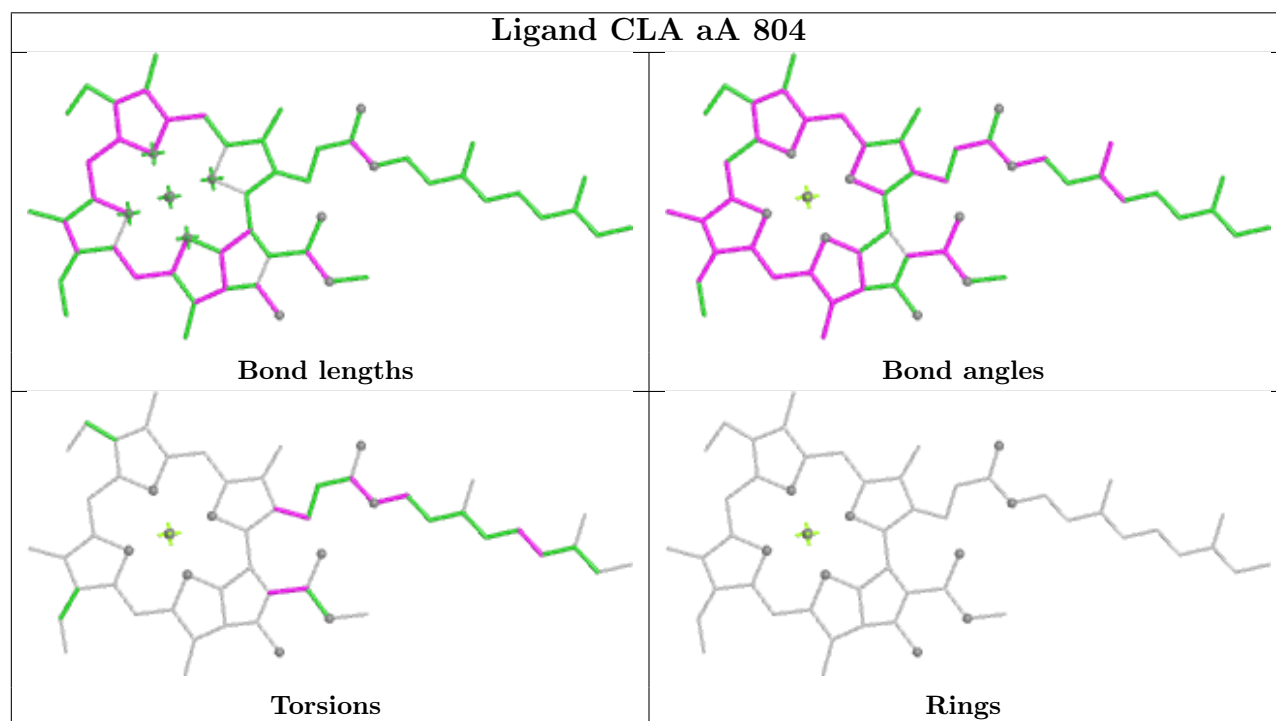
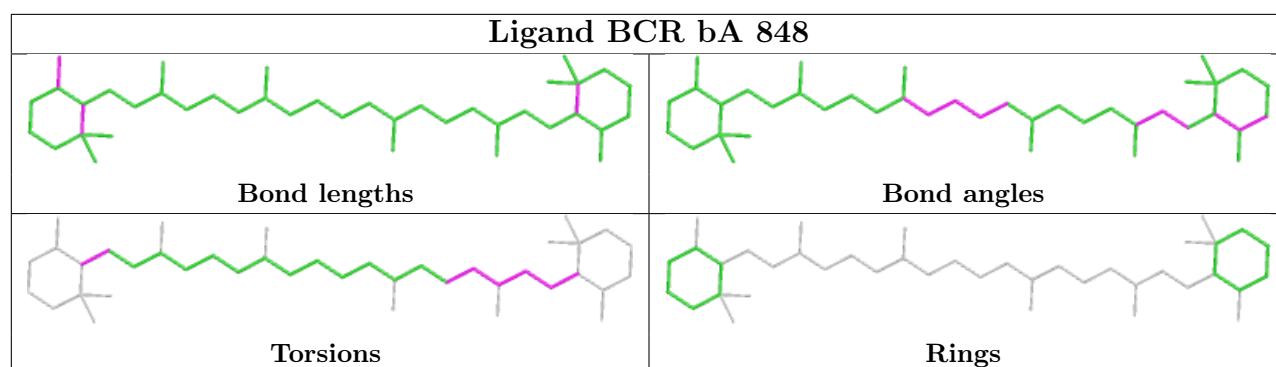
Ligand CLA aB 938

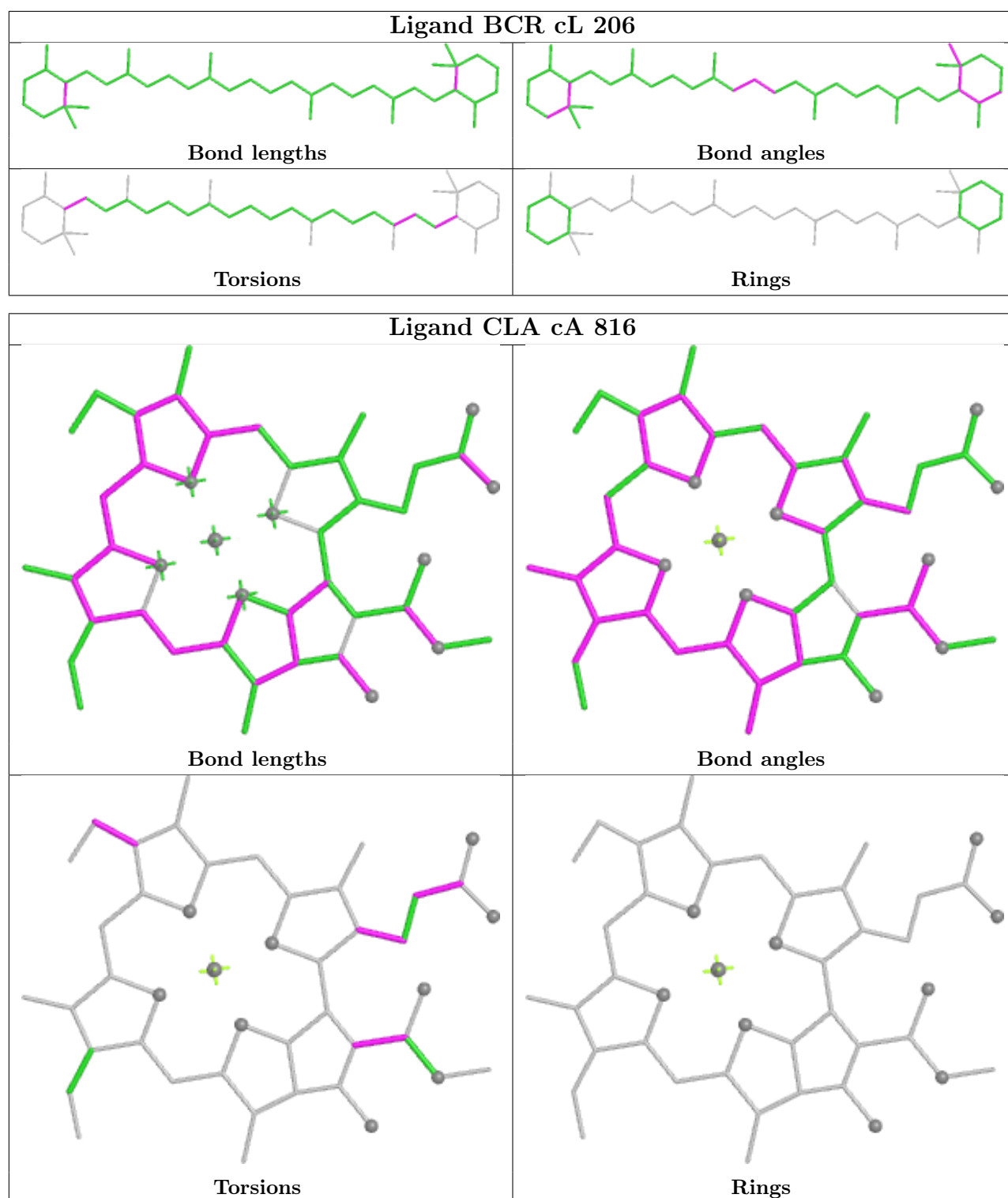


Ligand CLA bA 818









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

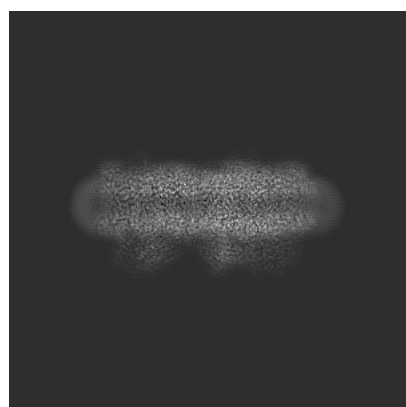
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31455. These allow visual inspection of the internal detail of the map and identification of artifacts.

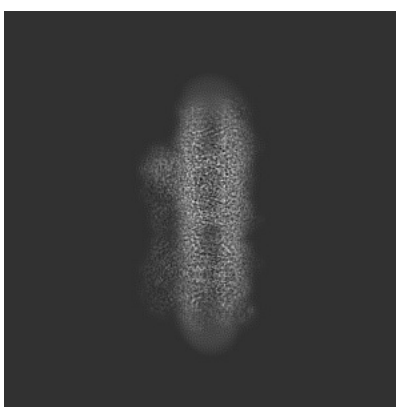
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

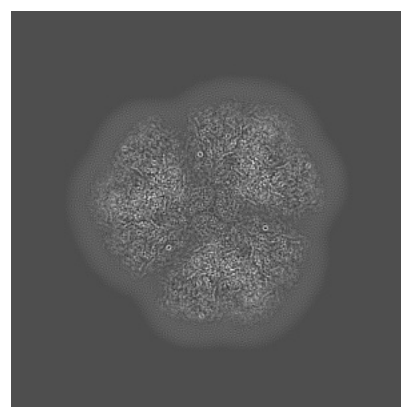
6.1.1 Primary map



X



Y

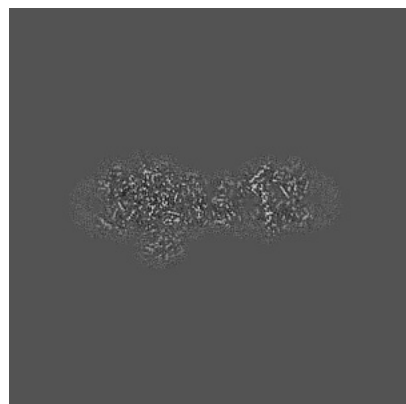


Z

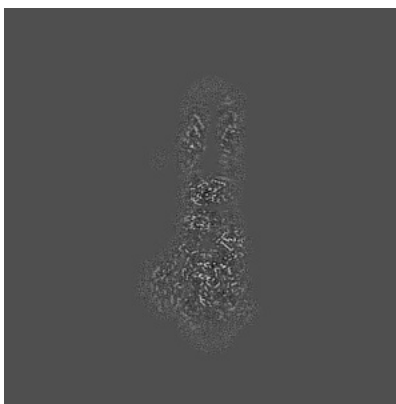
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

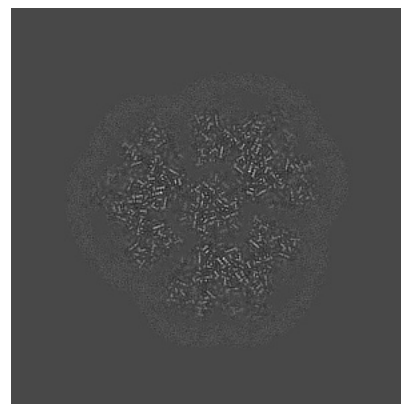
6.2.1 Primary map



X Index: 200



Y Index: 200

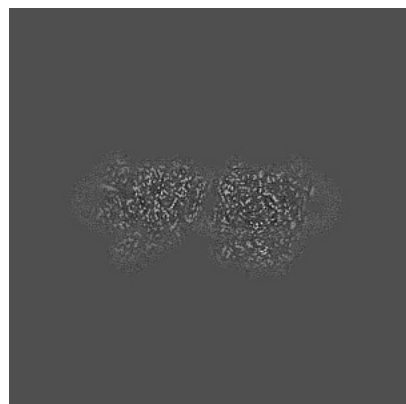


Z Index: 200

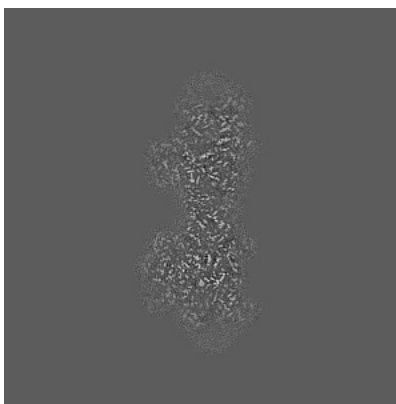
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

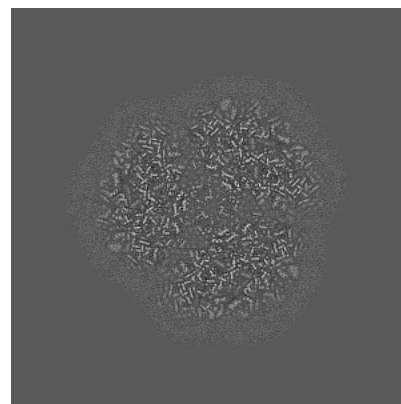
6.3.1 Primary map



X Index: 245



Y Index: 216

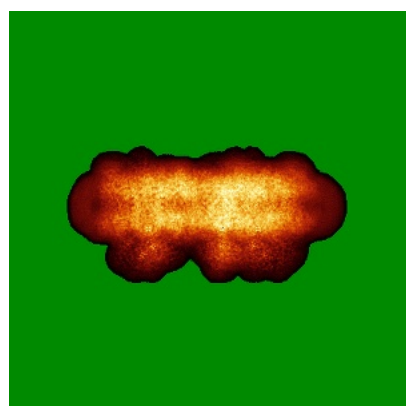


Z Index: 219

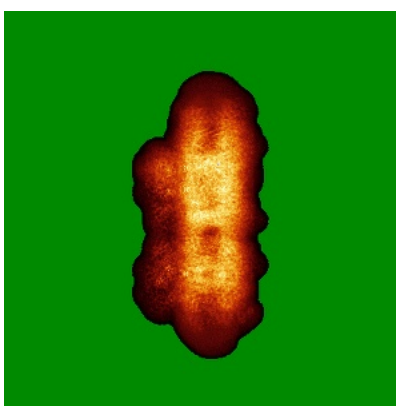
The images above show the largest variance slices of the map in three orthogonal directions.

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

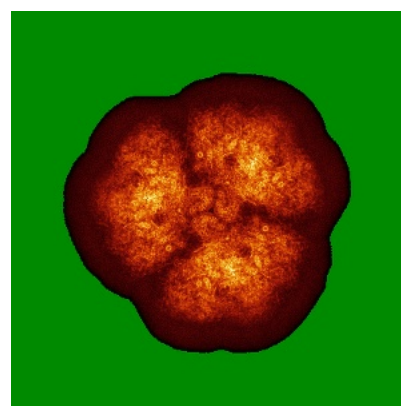
6.4.1 Primary map



X



Y

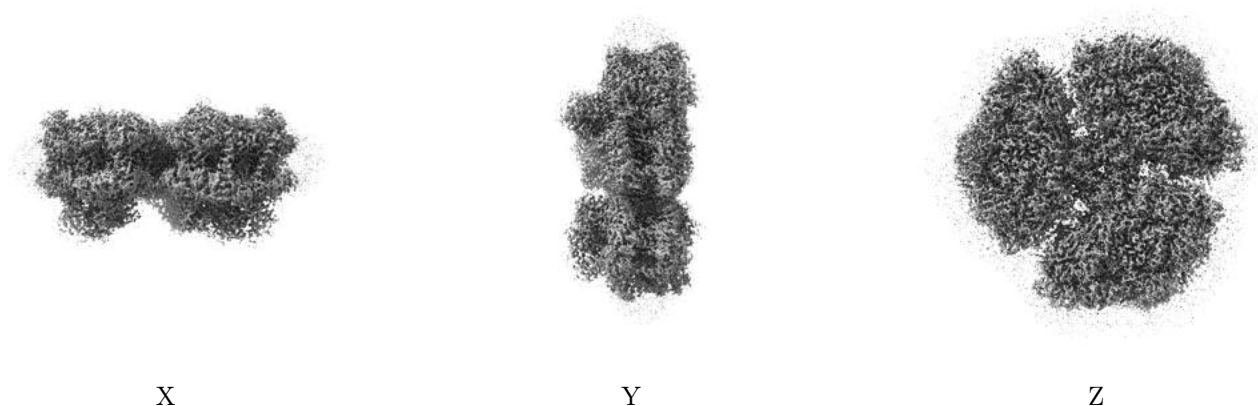


Z

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

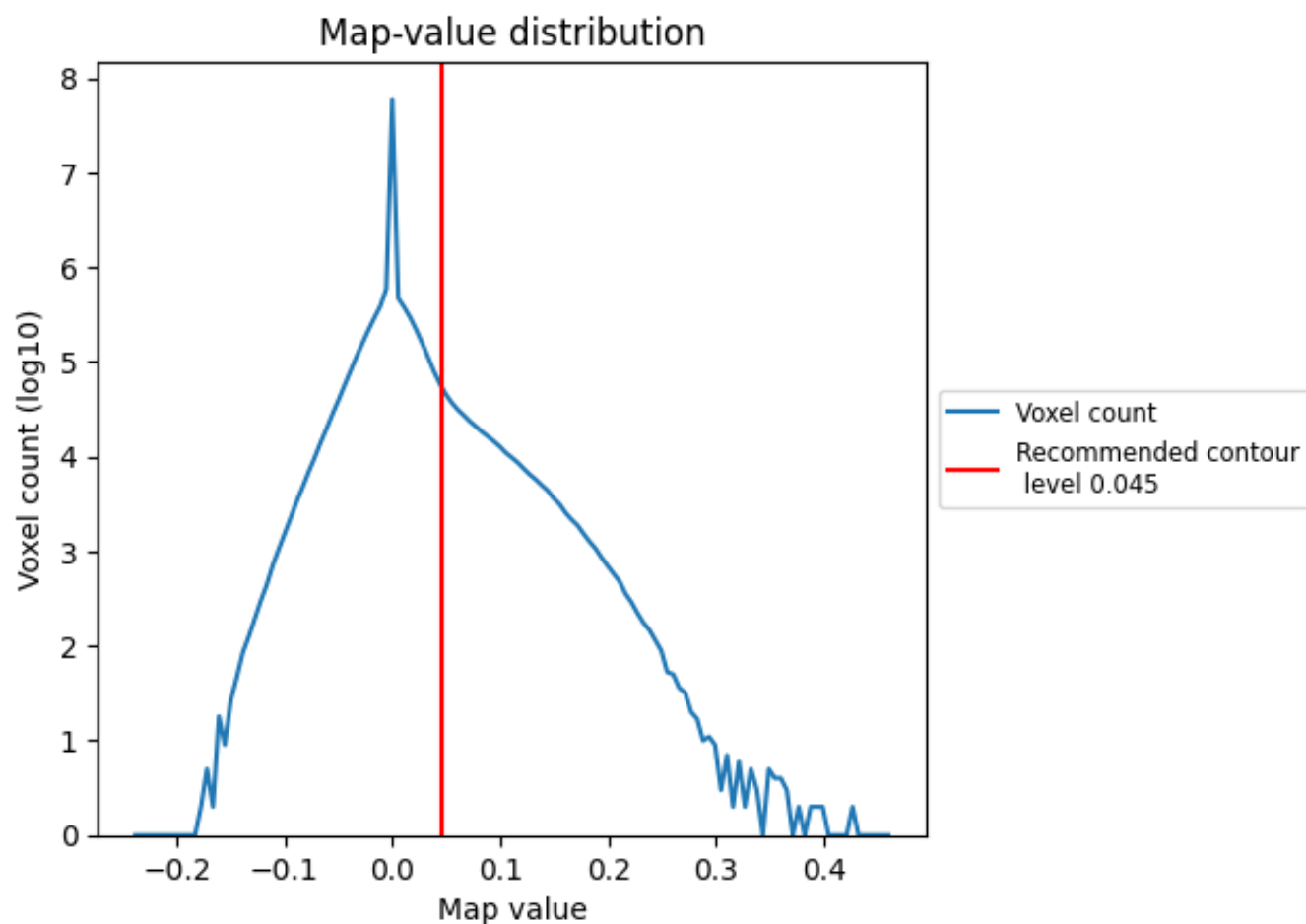
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

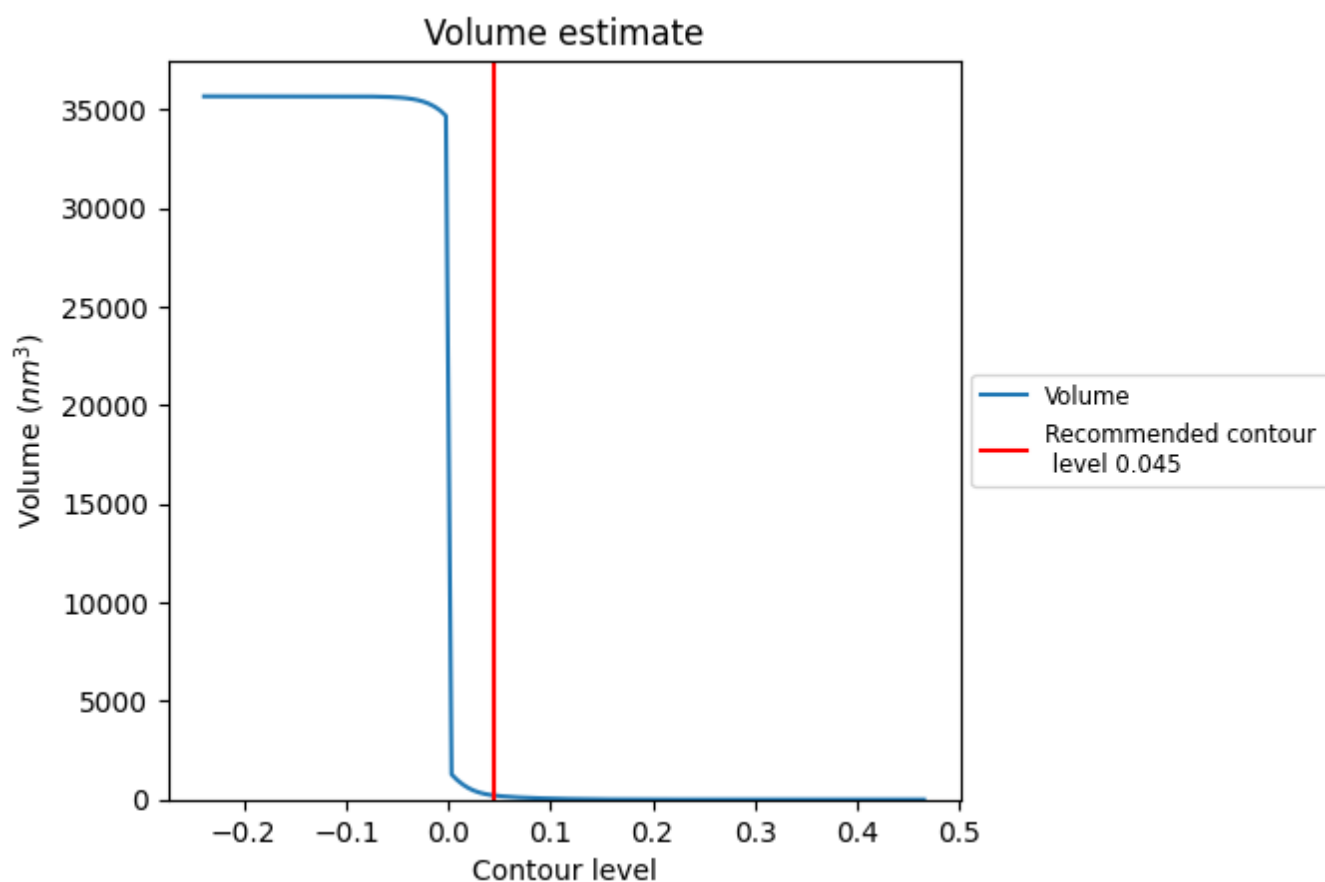
This section contains the results of statistical analysis of the map.

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.

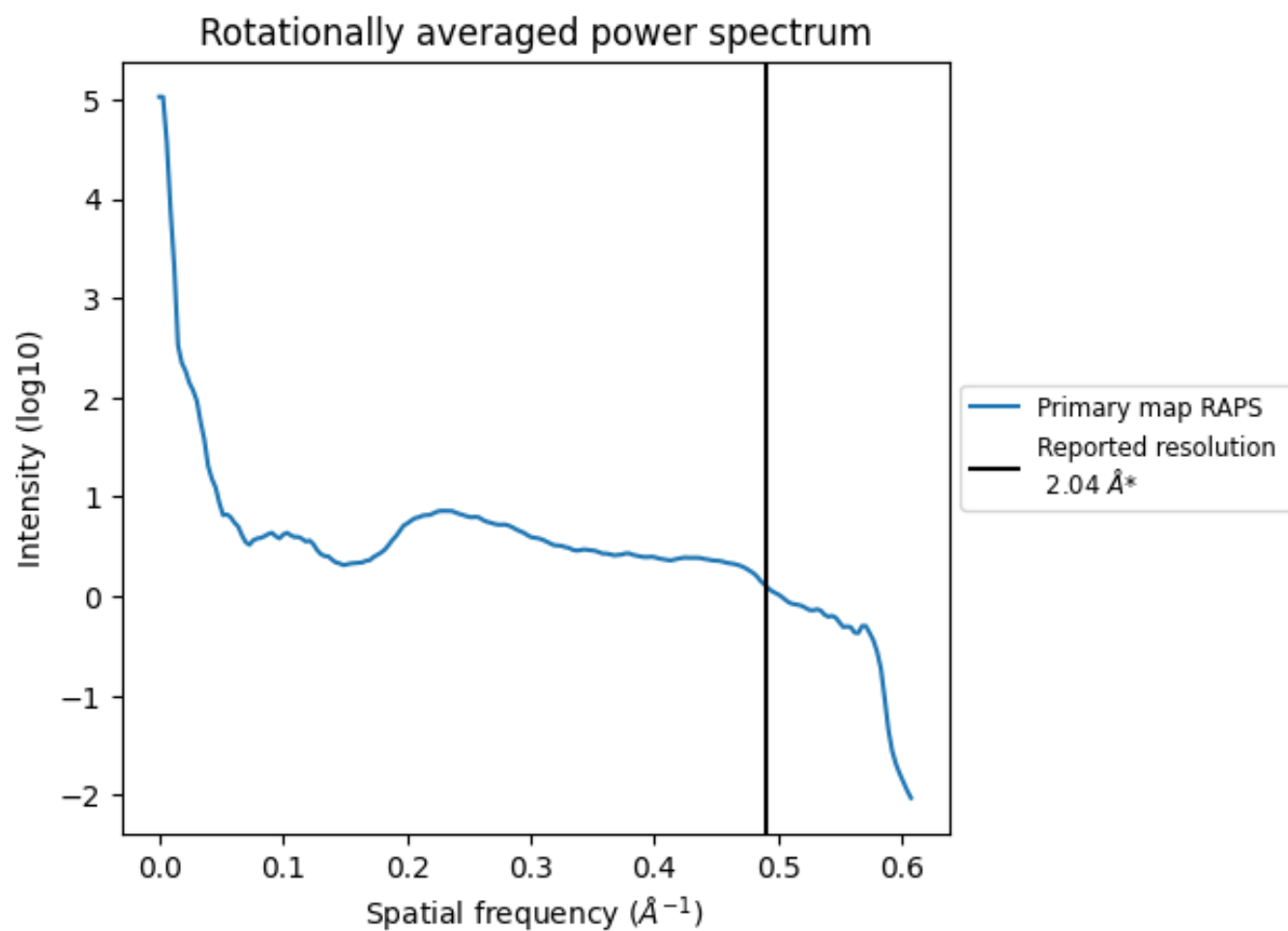
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 209 nm³; this corresponds to an approximate mass of 189 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

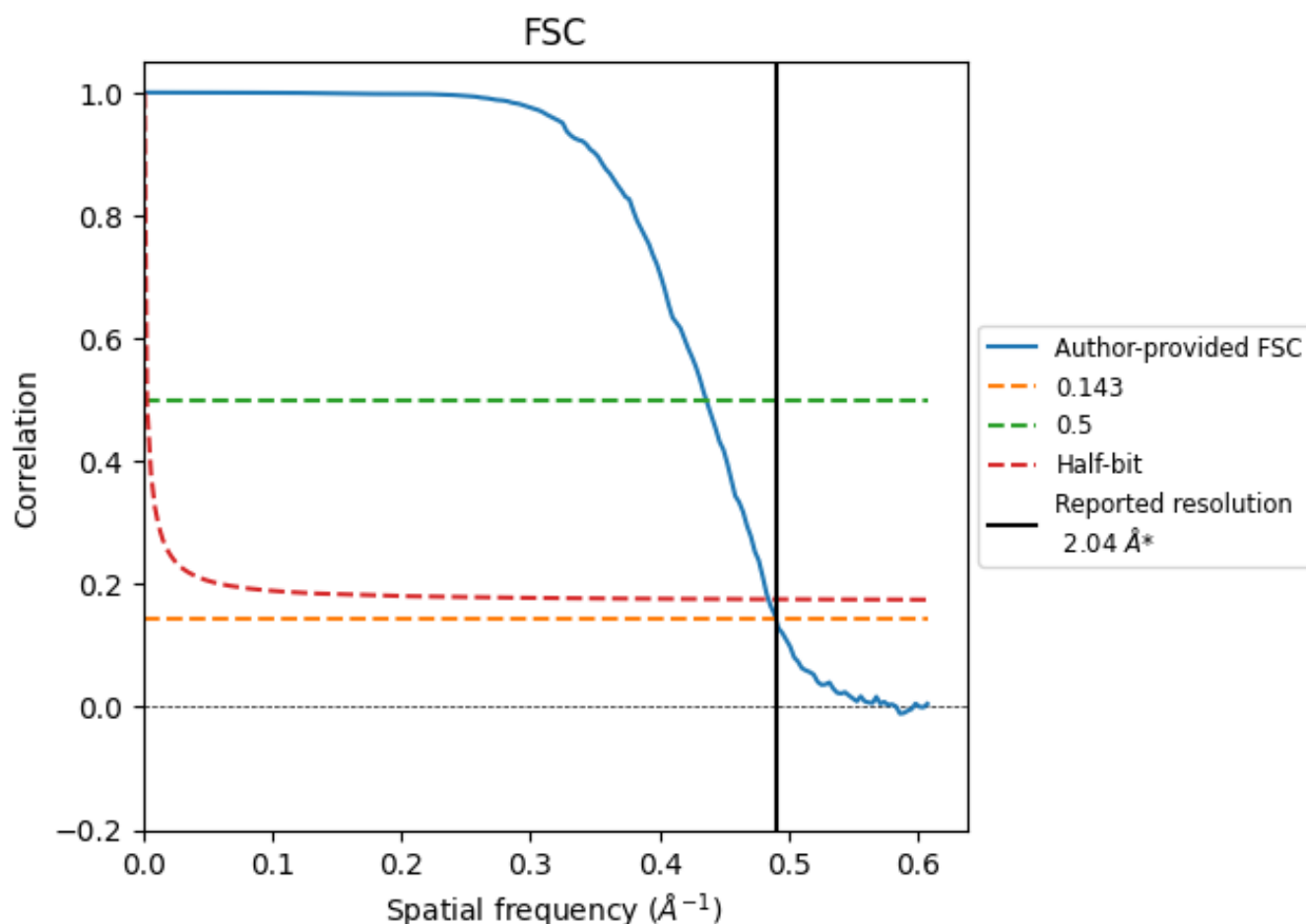


*Reported resolution corresponds to spatial frequency of 0.490 Å⁻¹

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 0.490 Å⁻¹

8.2 Resolution estimates [i](#)

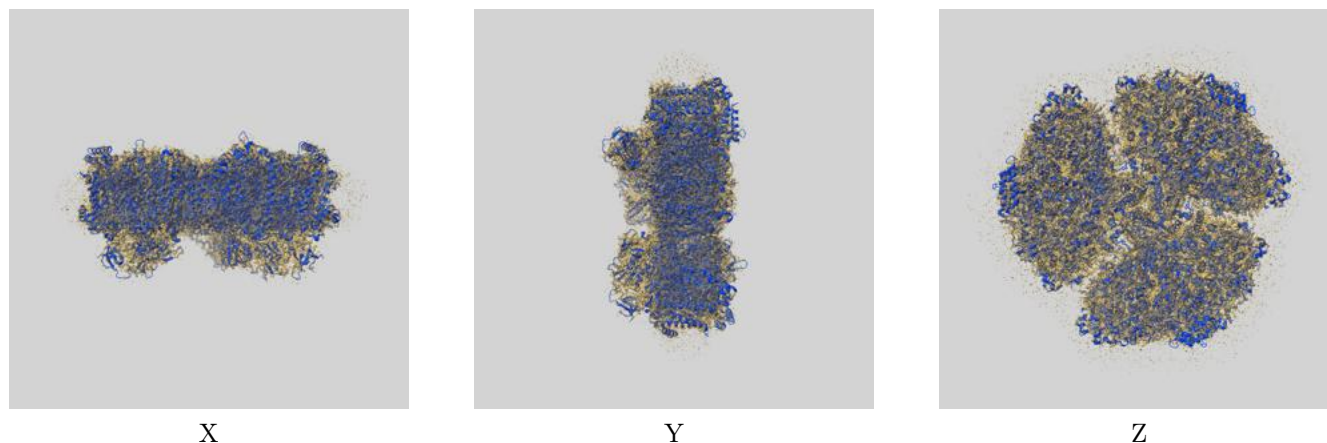
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.04	-	-
Author-provided FSC curve	2.04	2.29	2.06
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

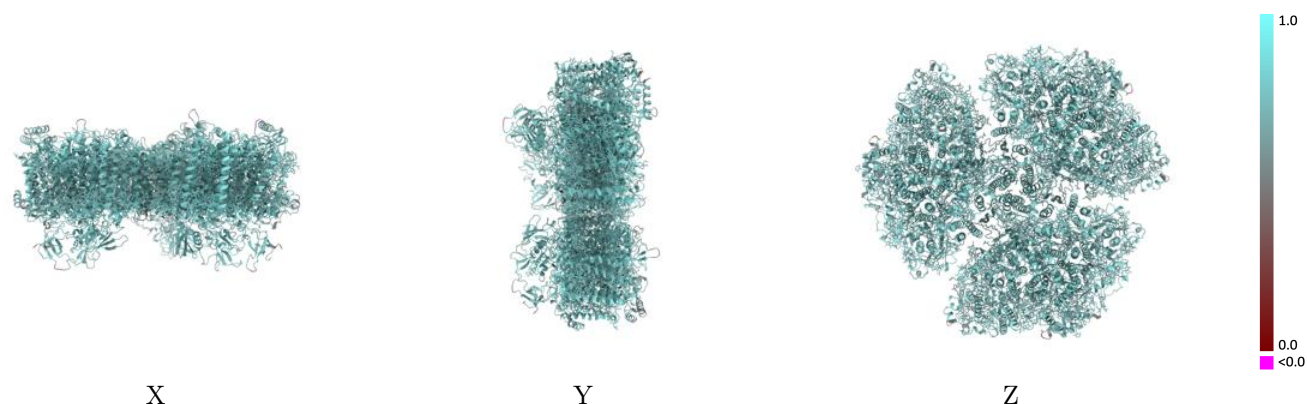
This section contains information regarding the fit between EMDB map EMD-31455 and PDB model 7F4V. Per-residue inclusion information can be found in section [3](#) on page [29](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



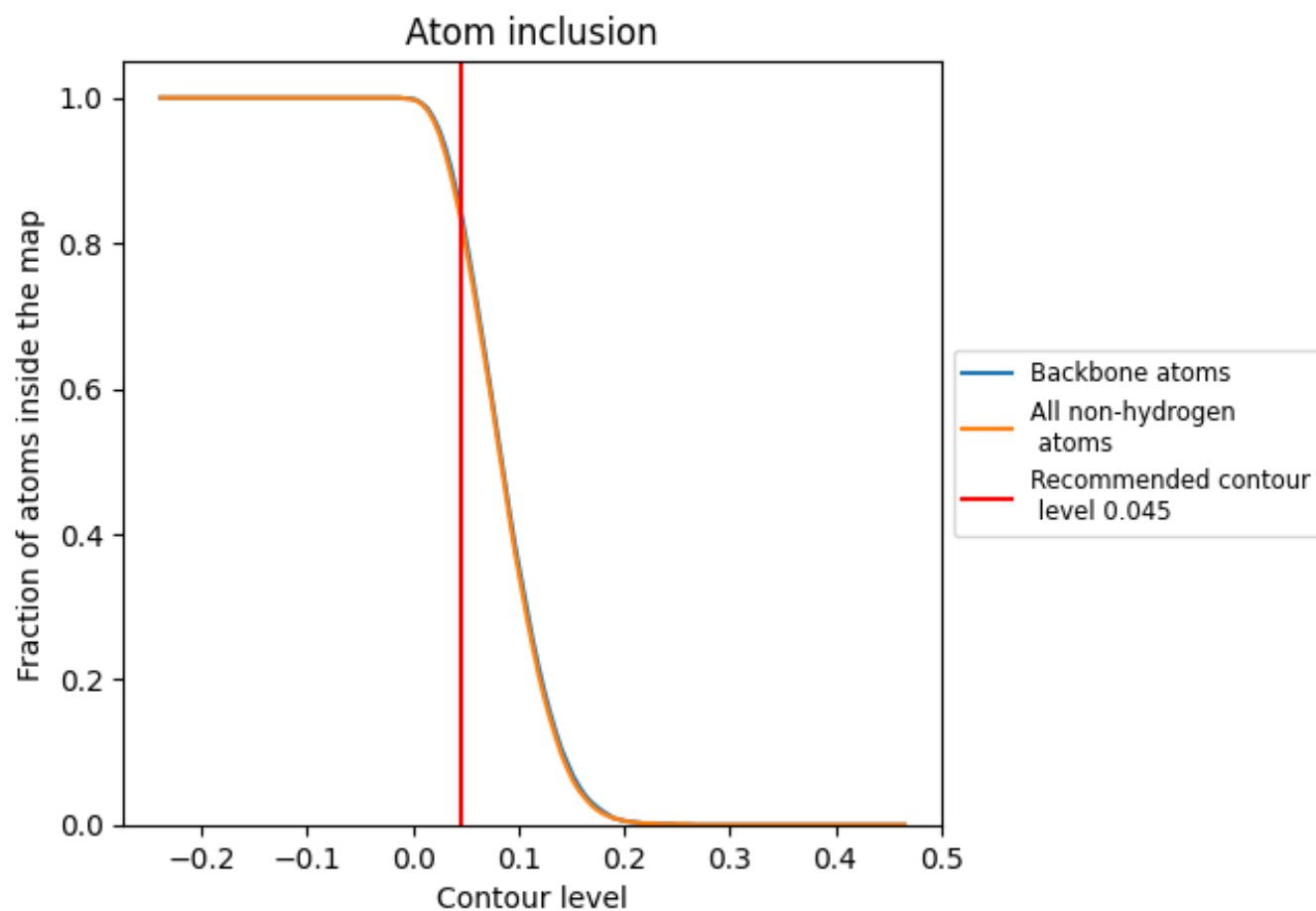
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 84% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8360	 0.7520
aA	 0.8580	 0.7580
aB	 0.8960	 0.7710
aC	 0.9170	 0.7710
aD	 0.6990	 0.7180
aE	 0.6140	 0.6720
aF	 0.5440	 0.6770
aI	 0.8340	 0.7470
aJ	 0.7450	 0.7110
aL	 0.8460	 0.7570
aM	 0.8480	 0.7480
bA	 0.8530	 0.7560
bB	 0.8940	 0.7690
bC	 0.9180	 0.7680
bD	 0.6930	 0.7150
bE	 0.5960	 0.6670
bF	 0.5280	 0.6720
bI	 0.8340	 0.7450
bJ	 0.7500	 0.7120
bL	 0.8400	 0.7540
bM	 0.8390	 0.7460
cA	 0.8500	 0.7550
cB	 0.8920	 0.7690
cC	 0.9320	 0.7690
cD	 0.6880	 0.7150
cE	 0.6020	 0.6650
cF	 0.5300	 0.6720
cI	 0.8300	 0.7480
cJ	 0.7450	 0.7060
cL	 0.8380	 0.7500
cM	 0.8480	 0.7470

