



## wwPDB EM Validation Summary Report ⓘ

Aug 5, 2026 – 07:11 AM EDT

PDB ID : 9E0J / pdb\_00009e0j  
EMDB ID : EMD-47359  
Title : Structure and evolution of Photosystem I in the early-branching cyanobacterium *Anthocerotibacter panamensis*  
Authors : Gisriel, C.J.; Ho, M.  
Deposited on : 2024-10-18  
Resolution : 2.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev133  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.50

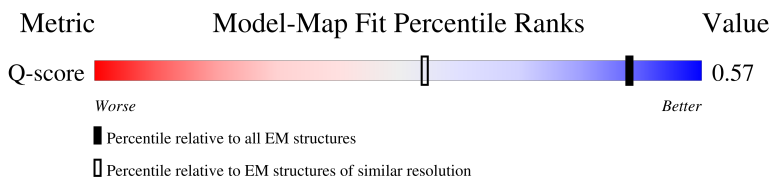
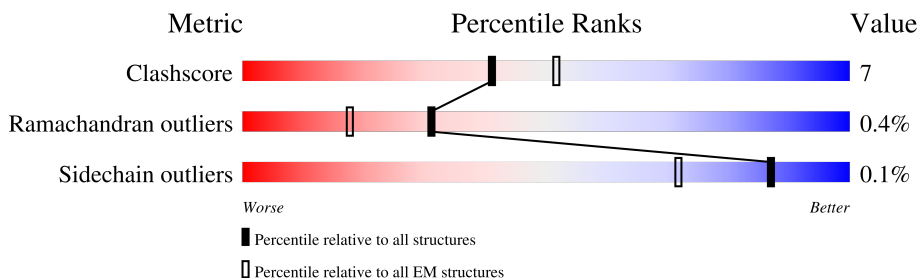
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.40 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.



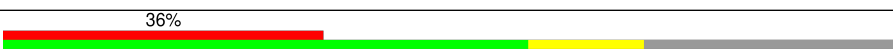
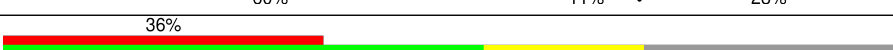
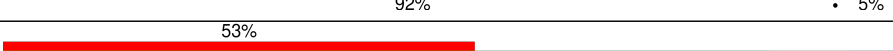
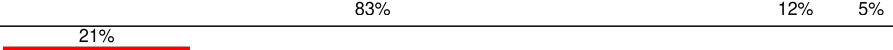
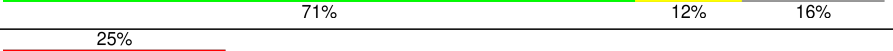
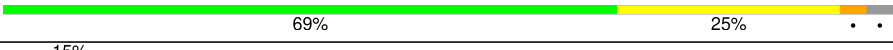
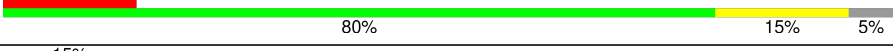
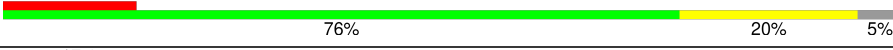
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| Q-score               | -                           | 25397                       | 5628 ( 1.90 - 2.90 )                                     |

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

| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | A     | 785    |  |
| 1   | G     | 785    |  |
| 1   | a     | 785    |  |
| 2   | M     | 32     |  |

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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 2   | T     | 32     |    |
| 2   | m     | 32     |    |
| 3   | B     | 749    |    |
| 3   | H     | 749    |    |
| 3   | b     | 749    |    |
| 4   | C     | 81     |    |
| 4   | K     | 81     |    |
| 4   | c     | 81     |    |
| 5   | D     | 143    |    |
| 5   | N     | 143    |    |
| 5   | d     | 143    |    |
| 6   | E     | 64     |    |
| 6   | O     | 64     |  |
| 6   | e     | 64     |  |
| 7   | F     | 177    |  |
| 7   | P     | 177    |  |
| 7   | f     | 177    |  |
| 8   | I     | 32     |  |
| 8   | Q     | 32     |  |
| 8   | i     | 32     |  |
| 9   | J     | 41     |  |
| 9   | R     | 41     |  |
| 9   | j     | 41     |  |
| 10  | L     | 160    |  |
| 10  | S     | 160    |  |

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| Mol | Chain | Length | Quality of chain                                                             |
|-----|-------|--------|------------------------------------------------------------------------------|
| 10  | 1     | 160    | <div><div></div><div>9%</div><div>81%</div><div>14%</div><div>..</div></div> |

## 2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 69921 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   | G     | 773      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 5997  | 3925 | 1024 | 1023 | 25 |         |       |
| 1   | a     | 773      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 5997  | 3925 | 1024 | 1023 | 25 |         |       |
| 1   | A     | 773      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 5997  | 3925 | 1024 | 1023 | 25 |         |       |

- Molecule 2 is a protein called Photosystem I reaction center subunit XII.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 2   | T     | 31       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 226   | 152 | 34 | 38 | 2 |         |       |
| 2   | m     | 31       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 226   | 152 | 34 | 38 | 2 |         |       |
| 2   | M     | 31       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 226   | 152 | 34 | 38 | 2 |         |       |

- Molecule 3 is a protein called Photosystem I P700 chlorophyll a apoprotein A2.

| Mol | Chain | Residues | Atoms |      |     |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|----|---------|-------|
| 3   | H     | 746      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5866  | 3864 | 981 | 1001 | 20 |         |       |
| 3   | b     | 746      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5866  | 3864 | 981 | 1001 | 20 |         |       |
| 3   | B     | 746      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5866  | 3864 | 981 | 1001 | 20 |         |       |

- Molecule 4 is a protein called Photosystem I iron-sulfur center.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 4   | K     | 80       | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 599   | 367 | 105 | 117 | 10 |         |       |

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| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 4   | c     | 80       | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 599   | 367 | 105 | 117 | 10 |         |       |
| 4   | C     | 80       | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 599   | 367 | 105 | 117 | 10 |         |       |

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

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 5   | N     | 103      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 784   | 500 | 138 | 143 | 3 |         |       |
| 5   | d     | 103      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 784   | 500 | 138 | 143 | 3 |         |       |
| 5   | D     | 103      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 784   | 500 | 138 | 143 | 3 |         |       |

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

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 6   | O     | 61       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 489   | 308 | 84 | 97 |         |       |
| 6   | e     | 61       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 489   | 308 | 84 | 97 |         |       |
| 6   | E     | 61       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 489   | 308 | 84 | 97 |         |       |

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

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 7   | P     | 148      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1148  | 738 | 191 | 215 | 4 |         |       |
| 7   | f     | 148      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1148  | 738 | 191 | 215 | 4 |         |       |
| 7   | F     | 148      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1148  | 738 | 191 | 215 | 4 |         |       |

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

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 8   | Q     | 31       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 254   | 175 | 36 | 42 | 1 |         |       |
| 8   | i     | 31       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 254   | 175 | 36 | 42 | 1 |         |       |

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| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 8   | I     | 31       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 254   | 175 | 36 | 42 | 1 |         |       |

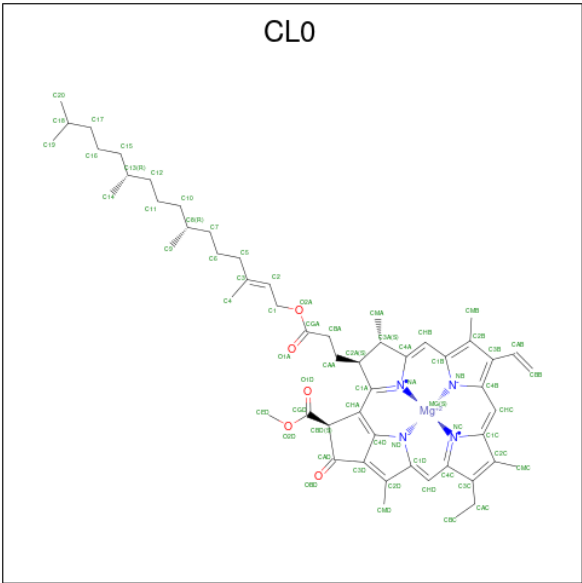
- Molecule 9 is a protein called Photosystem I reaction center subunit IX.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 9   | R     | 39       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 293   | 204 | 44 | 45 |  |         |       |
| 9   | j     | 39       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 293   | 204 | 44 | 45 |  |         |       |
| 9   | J     | 39       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 293   | 204 | 44 | 45 |  |         |       |

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

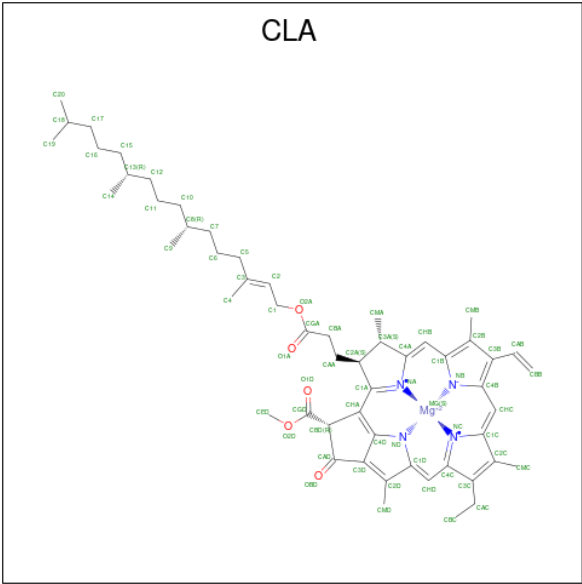
| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | S     | 154      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1159  | 772 | 186 | 198 | 3 |         |       |
| 10  | l     | 154      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1159  | 772 | 186 | 198 | 3 |         |       |
| 10  | L     | 154      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1159  | 772 | 186 | 198 | 3 |         |       |

- Molecule 11 is CHLOROPHYLL A ISOMER (CCD ID: CL0) (formula: C<sub>55</sub>H<sub>72</sub>MgN<sub>4</sub>O<sub>5</sub>).



| Mol | Chain | Residues | Atoms |    |    |   |   | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 11  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 11  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 11  | A     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |

- Molecule 12 is CHLOROPHYLL A (CCD ID: CLA) (formula: C<sub>55</sub>H<sub>72</sub>MgN<sub>4</sub>O<sub>5</sub>).



| Mol | Chain | Residues | Atoms |    |    |   |   | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 60    | 50 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |

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| Mol | Chain | Residues | Atoms |    |    |   |   | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 60    | 50 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | G     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | G     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | H     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | P     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | P     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | R     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | S     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | S     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | S     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms |    |    |   |   | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 45    | 35 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 50    | 40 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | a     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | a     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | a     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | b     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | f     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | f     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | j     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | j     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | l     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | l     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | l     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | l     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | A     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>50 | C<br>40 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | A     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | B     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>55 | C<br>45 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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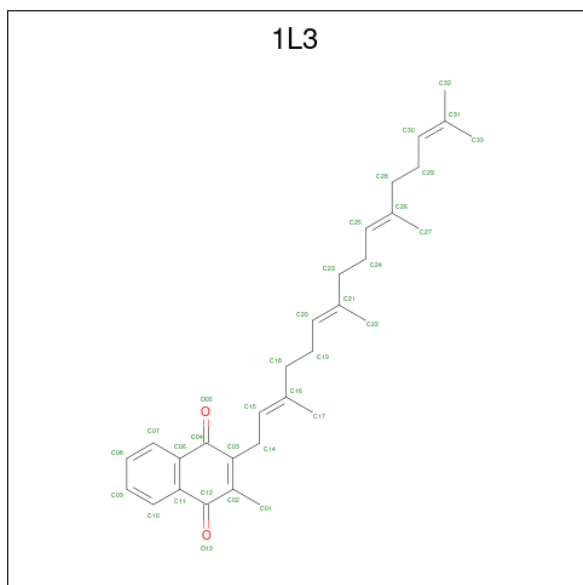
| Mol | Chain | Residues | Atoms       |         |         |        |        | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>60 | C<br>50 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | B     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | F     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | F     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | J     | 1        | Total<br>45 | C<br>35 | Mg<br>1 | N<br>4 | O<br>5 | 0       |
| 12  | L     | 1        | Total<br>65 | C<br>55 | Mg<br>1 | N<br>4 | O<br>5 | 0       |

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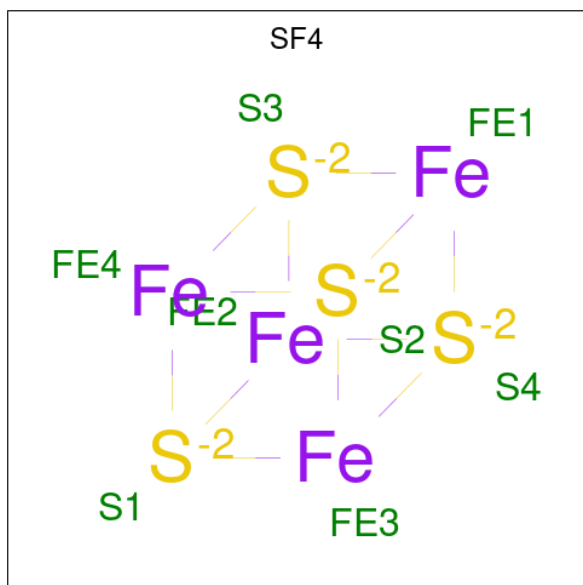
| Mol | Chain | Residues | Atoms |    |    |   |   | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 12  | L     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 55    | 45 | 1  | 4 | 5 |         |
| 12  | L     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |
| 12  | L     | 1        | Total | C  | Mg | N | O | 0       |
|     |       |          | 65    | 55 | 1  | 4 | 5 |         |

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



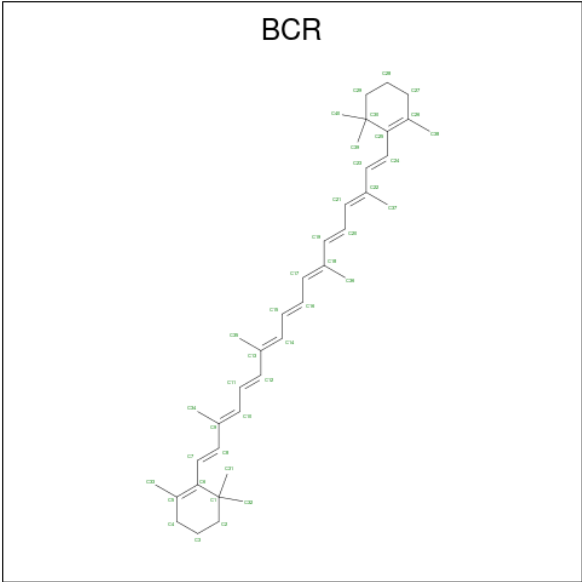
| Mol | Chain | Residues | Atoms |    |   | AltConf |
|-----|-------|----------|-------|----|---|---------|
| 13  | G     | 1        | Total | C  | O | 0       |
|     |       |          | 33    | 31 | 2 |         |
| 13  | H     | 1        | Total | C  | O | 0       |
|     |       |          | 33    | 31 | 2 |         |
| 13  | a     | 1        | Total | C  | O | 0       |
|     |       |          | 33    | 31 | 2 |         |
| 13  | b     | 1        | Total | C  | O | 0       |
|     |       |          | 33    | 31 | 2 |         |
| 13  | A     | 1        | Total | C  | O | 0       |
|     |       |          | 33    | 31 | 2 |         |
| 13  | B     | 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  | G     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | K     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | K     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | a     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | c     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | c     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | A     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | C     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |
| 14  | C     | 1        | Total | Fe | S | 0       |
|     |       |          | 8     | 4  | 4 |         |

- Molecule 15 is BETA-CAROTENE (CCD ID: BCR) (formula: C<sub>40</sub>H<sub>56</sub>).



| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 15  | G     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | G     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | G     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | G     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | G     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | G     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 25    | 25 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | H     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |

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| Mol | Chain | Residues | Atoms            | AltConf |
|-----|-------|----------|------------------|---------|
| 15  | P     | 1        | Total C<br>40 40 | 0       |
| 15  | P     | 1        | Total C<br>40 40 | 0       |
| 15  | Q     | 1        | Total C<br>40 40 | 0       |
| 15  | Q     | 1        | Total C<br>40 40 | 0       |
| 15  | R     | 1        | Total C<br>40 40 | 0       |
| 15  | R     | 1        | Total C<br>40 40 | 0       |
| 15  | S     | 1        | Total C<br>40 40 | 0       |
| 15  | S     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | a     | 1        | Total C<br>40 40 | 0       |
| 15  | b     | 1        | Total C<br>40 40 | 0       |
| 15  | b     | 1        | Total C<br>40 40 | 0       |
| 15  | b     | 1        | Total C<br>40 40 | 0       |
| 15  | b     | 1        | Total C<br>25 25 | 0       |
| 15  | b     | 1        | Total C<br>40 40 | 0       |
| 15  | b     | 1        | Total C<br>40 40 | 0       |

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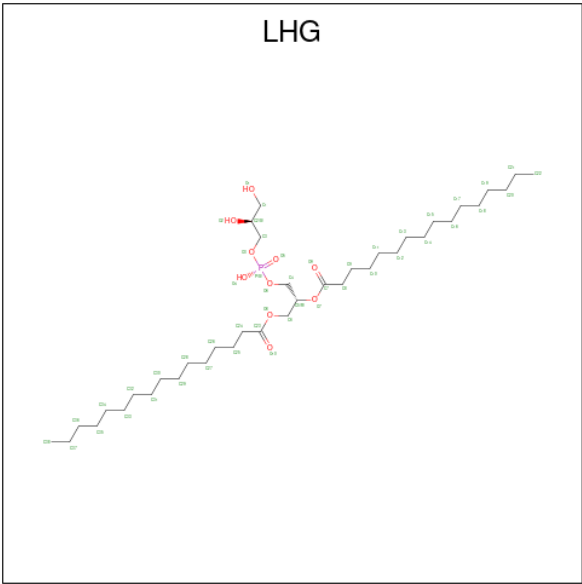
| Mol | Chain | Residues | Atoms            | AltConf |
|-----|-------|----------|------------------|---------|
| 15  | b     | 1        | Total C<br>40 40 | 0       |
| 15  | f     | 1        | Total C<br>40 40 | 0       |
| 15  | f     | 1        | Total C<br>40 40 | 0       |
| 15  | i     | 1        | Total C<br>40 40 | 0       |
| 15  | i     | 1        | Total C<br>40 40 | 0       |
| 15  | j     | 1        | Total C<br>40 40 | 0       |
| 15  | j     | 1        | Total C<br>40 40 | 0       |
| 15  | l     | 1        | Total C<br>40 40 | 0       |
| 15  | l     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | A     | 1        | Total C<br>40 40 | 0       |
| 15  | B     | 1        | Total C<br>40 40 | 0       |
| 15  | B     | 1        | Total C<br>40 40 | 0       |
| 15  | B     | 1        | Total C<br>40 40 | 0       |
| 15  | B     | 1        | Total C<br>25 25 | 0       |
| 15  | B     | 1        | Total C<br>40 40 | 0       |

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| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 15  | B     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | F     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | F     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | I     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | J     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | J     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | J     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | L     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | L     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |
| 15  | L     | 1        | Total | C  | 0       |
|     |       |          | 40    | 40 |         |

- Molecule 16 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C<sub>38</sub>H<sub>75</sub>O<sub>10</sub>P).



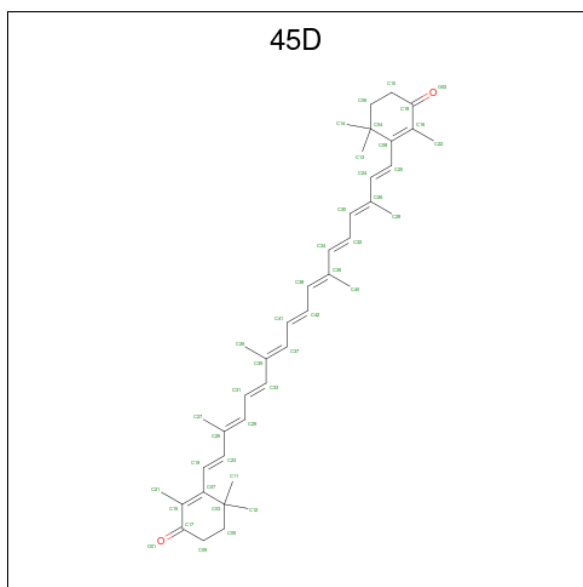
| Mol | Chain | Residues | Atoms |    |    |   | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 16  | G     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 49    | 38 | 10 | 1 |         |

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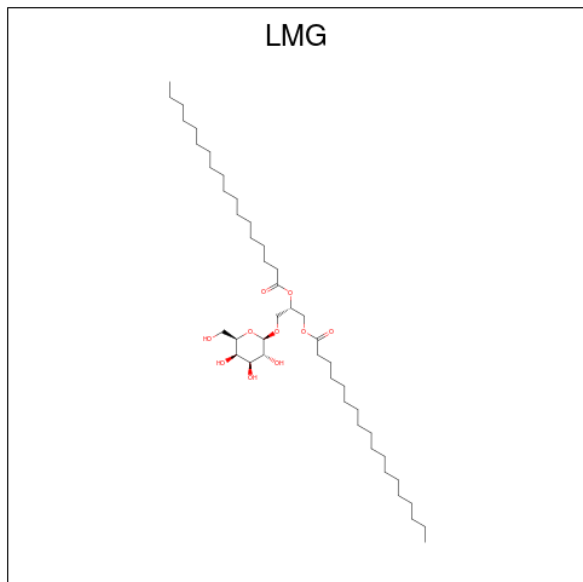
| Mol | Chain | Residues | Atoms |    |    |   | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 16  | G     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 27    | 16 | 10 | 1 |         |
| 16  | G     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 49    | 38 | 10 | 1 |         |
| 16  | a     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 49    | 38 | 10 | 1 |         |
| 16  | a     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 27    | 16 | 10 | 1 |         |
| 16  | a     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 49    | 38 | 10 | 1 |         |
| 16  | A     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 49    | 38 | 10 | 1 |         |
| 16  | A     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 27    | 16 | 10 | 1 |         |
| 16  | A     | 1        | Total | C  | O  | P | 0       |
|     |       |          | 49    | 38 | 10 | 1 |         |

- Molecule 17 is beta,beta-carotene-4,4'-dione (CCD ID: 45D) (formula: C<sub>40</sub>H<sub>52</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



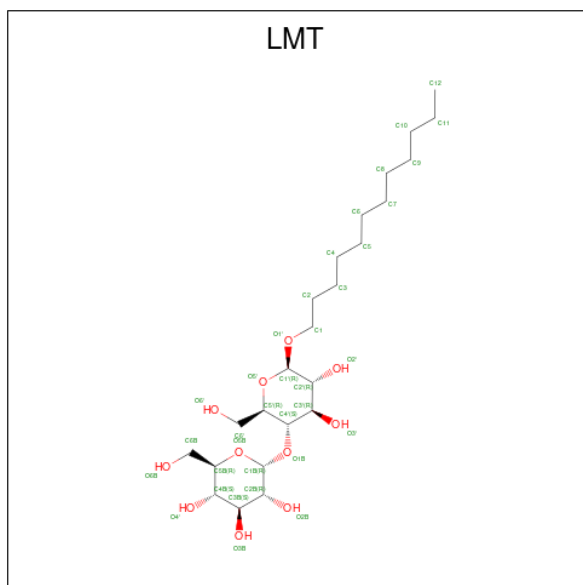
| Mol | Chain | Residues | Atoms |    |   | AltConf |
|-----|-------|----------|-------|----|---|---------|
| 17  | T     | 1        | Total | C  | O | 0       |
|     |       |          | 42    | 40 | 2 |         |
| 17  | m     | 1        | Total | C  | O | 0       |
|     |       |          | 42    | 40 | 2 |         |
| 17  | M     | 1        | Total | C  | O | 0       |
|     |       |          | 42    | 40 | 2 |         |

- Molecule 18 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula:  $C_{45}H_{86}O_{10}$ ).



| Mol | Chain | Residues | Atoms |    |    | AltConf |
|-----|-------|----------|-------|----|----|---------|
| 18  | H     | 1        | Total | C  | O  | 0       |
|     |       |          | 55    | 45 | 10 |         |
| 18  | b     | 1        | Total | C  | O  | 0       |
|     |       |          | 55    | 45 | 10 |         |
| 18  | B     | 1        | Total | C  | O  | 0       |
|     |       |          | 55    | 45 | 10 |         |

- Molecule 19 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula:  $C_{24}H_{46}O_{11}$ ).



| Mol | Chain | Residues | Atoms |    |    | AltConf |
|-----|-------|----------|-------|----|----|---------|
| 19  | H     | 1        | Total | C  | O  | 0       |
|     |       |          | 35    | 24 | 11 |         |
| 19  | b     | 1        | Total | C  | O  | 0       |
|     |       |          | 35    | 24 | 11 |         |
| 19  | B     | 1        | Total | C  | O  | 0       |
|     |       |          | 35    | 24 | 11 |         |

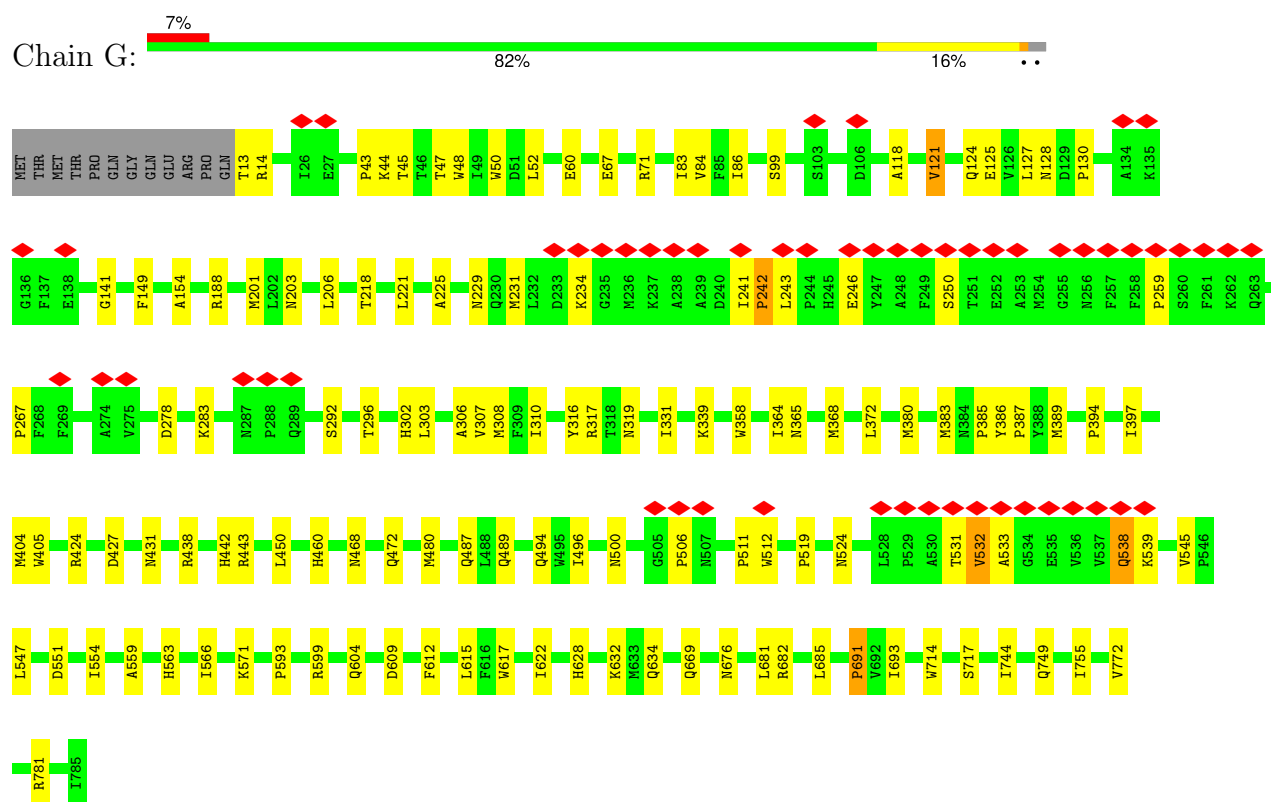
- Molecule 20 is water.

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 20  | G     | 58       | Total | O  | 0       |
|     |       |          | 58    | 58 |         |
| 20  | H     | 80       | Total | O  | 0       |
|     |       |          | 80    | 80 |         |
| 20  | K     | 26       | Total | O  | 0       |
|     |       |          | 26    | 26 |         |
| 20  | N     | 15       | Total | O  | 0       |
|     |       |          | 15    | 15 |         |
| 20  | O     | 1        | Total | O  | 0       |
|     |       |          | 1     | 1  |         |
| 20  | S     | 5        | Total | O  | 0       |
|     |       |          | 5     | 5  |         |
| 20  | a     | 57       | Total | O  | 0       |
|     |       |          | 57    | 57 |         |
| 20  | b     | 82       | Total | O  | 0       |
|     |       |          | 82    | 82 |         |
| 20  | c     | 22       | Total | O  | 0       |
|     |       |          | 22    | 22 |         |
| 20  | d     | 17       | Total | O  | 0       |
|     |       |          | 17    | 17 |         |
| 20  | e     | 1        | Total | O  | 0       |
|     |       |          | 1     | 1  |         |
| 20  | l     | 6        | Total | O  | 0       |
|     |       |          | 6     | 6  |         |
| 20  | A     | 56       | Total | O  | 0       |
|     |       |          | 56    | 56 |         |
| 20  | B     | 82       | Total | O  | 0       |
|     |       |          | 82    | 82 |         |
| 20  | C     | 24       | Total | O  | 0       |
|     |       |          | 24    | 24 |         |
| 20  | D     | 16       | Total | O  | 0       |
|     |       |          | 16    | 16 |         |
| 20  | L     | 7        | Total | O  | 0       |
|     |       |          | 7     | 7  |         |

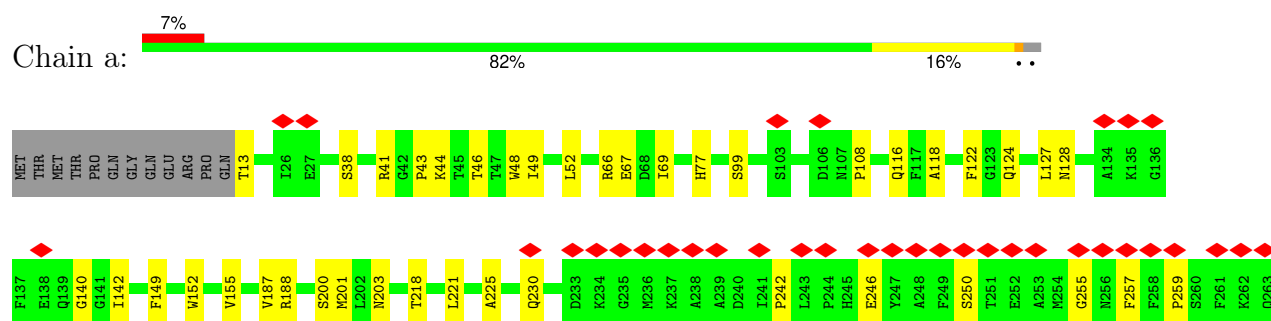
### 3 Residue-property plots

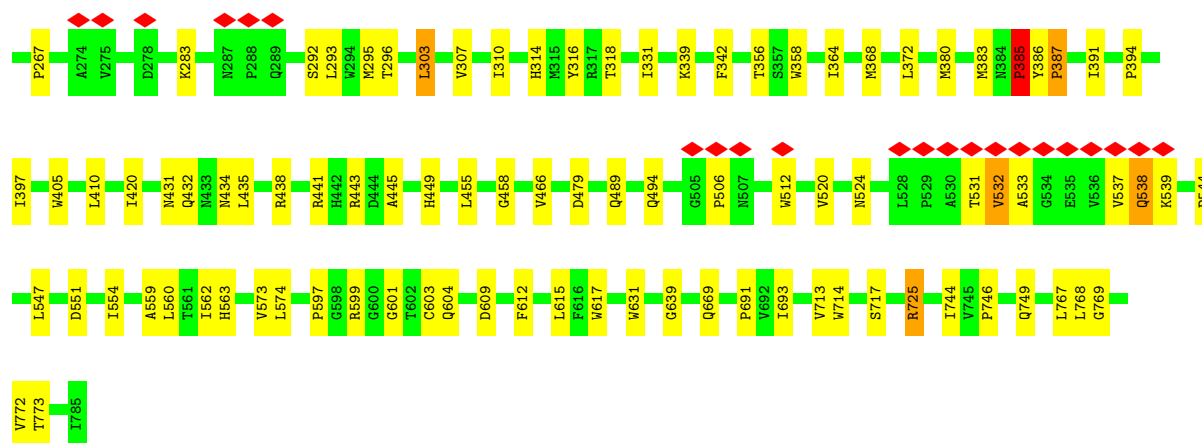
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

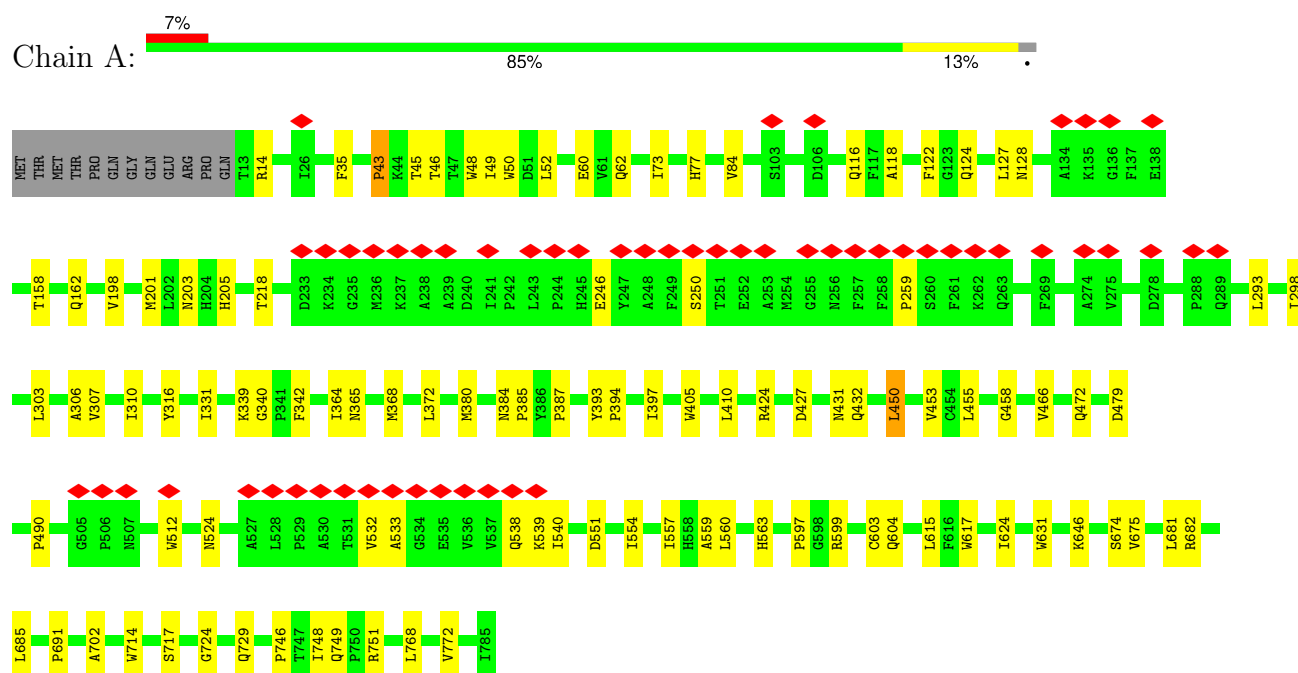


- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1

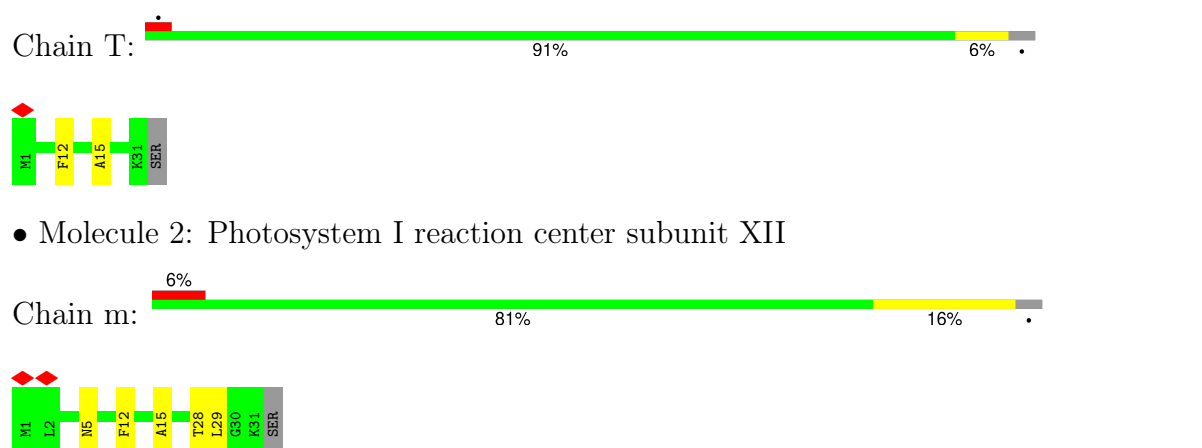




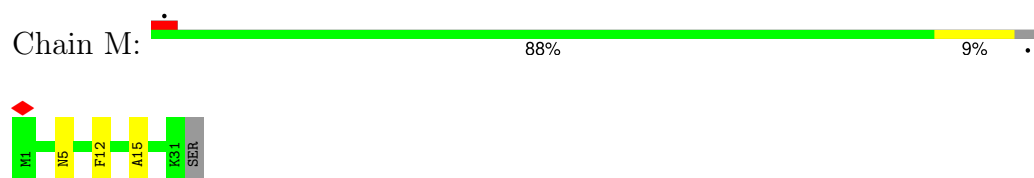
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



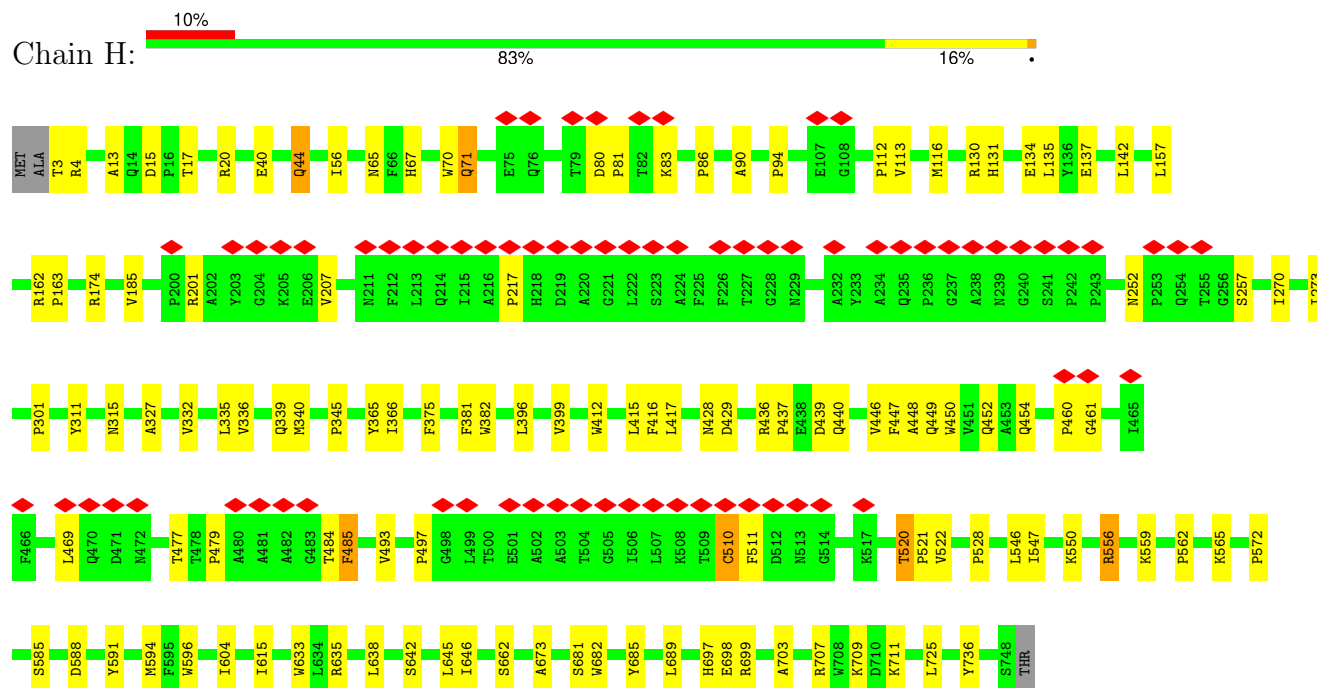
- Molecule 2: Photosystem I reaction center subunit XII



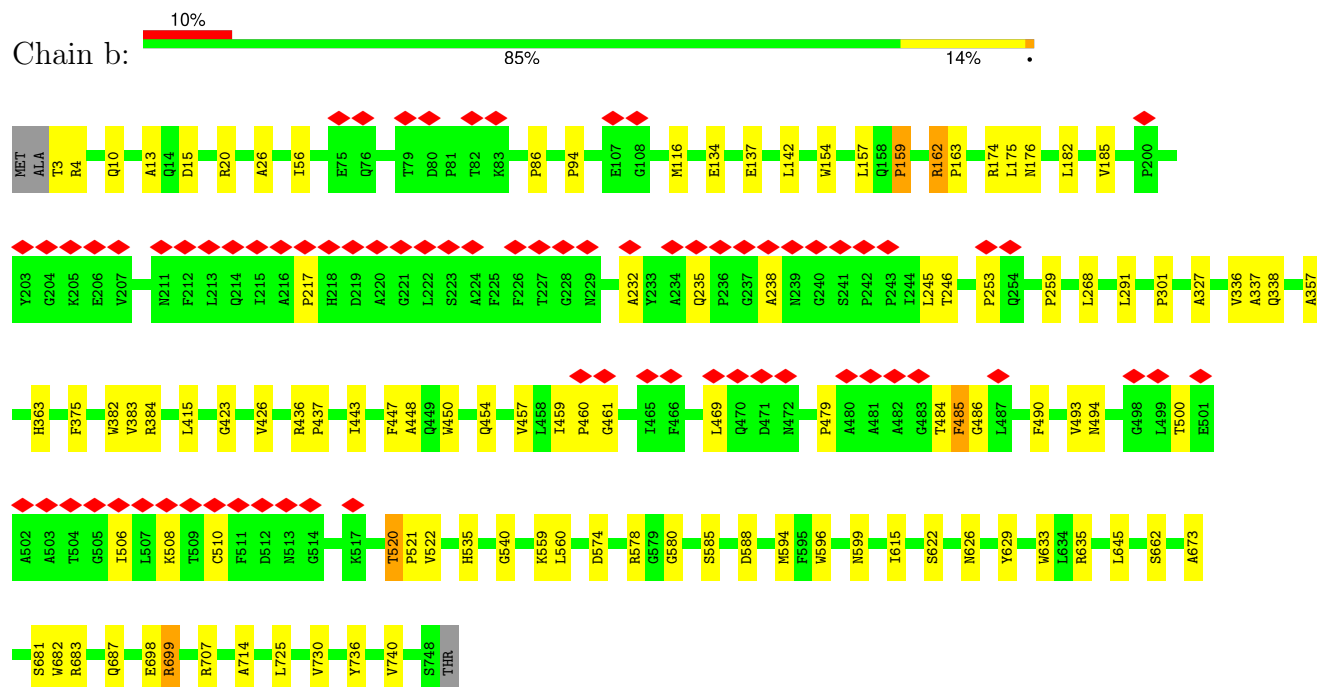
- Molecule 2: Photosystem I reaction center subunit XII



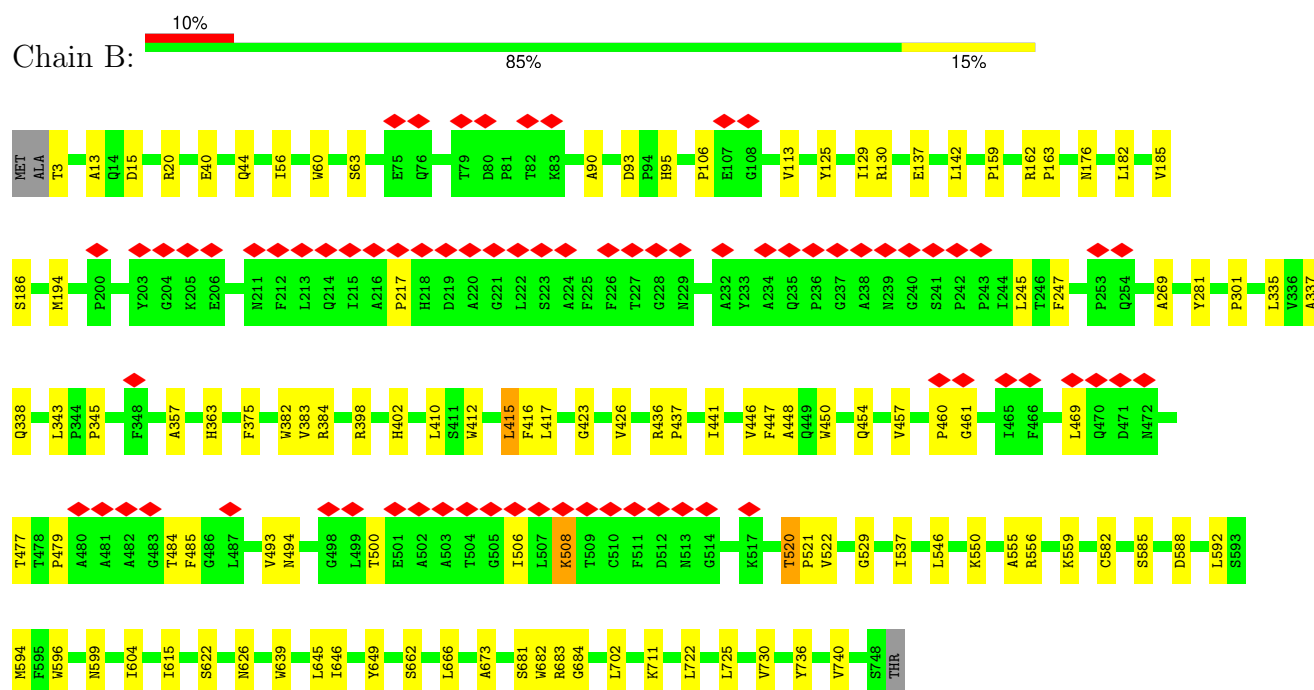
- Molecule 3: Photosystem I P700 chlorophyll a apoprotein A2



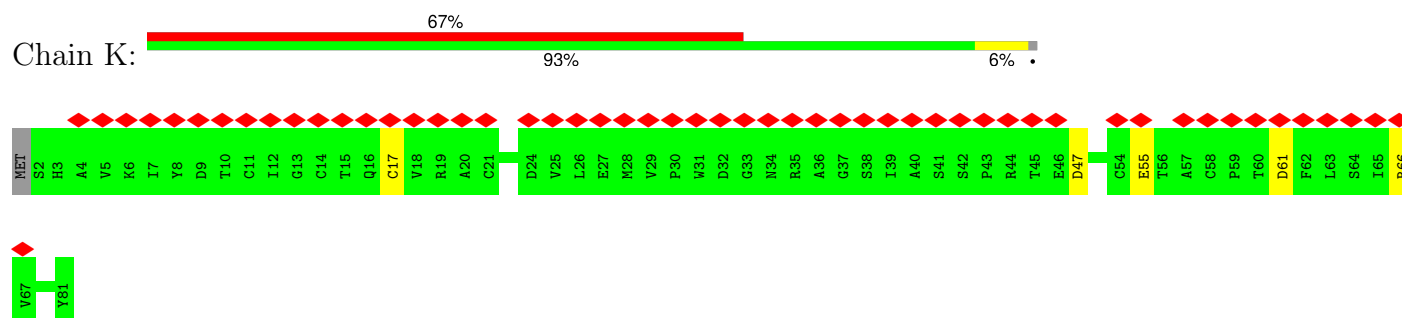
- Molecule 3: Photosystem I P700 chlorophyll a apoprotein A2



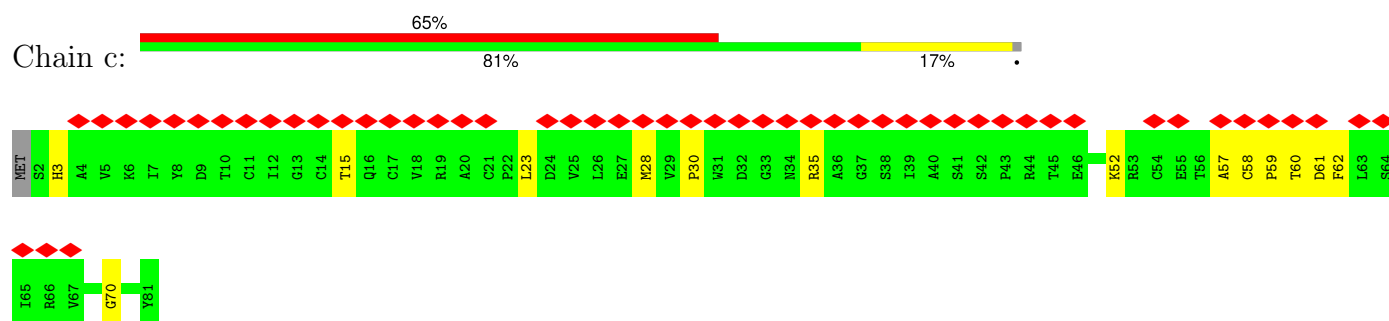
- Molecule 3: Photosystem I P700 chlorophyll a apoprotein A2



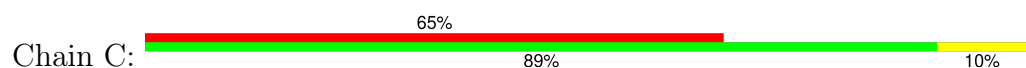
- Molecule 4: Photosystem I iron-sulfur center

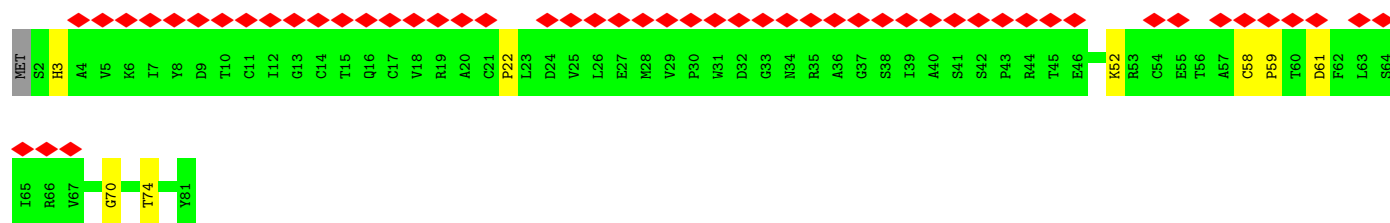


- Molecule 4: Photosystem I iron-sulfur center

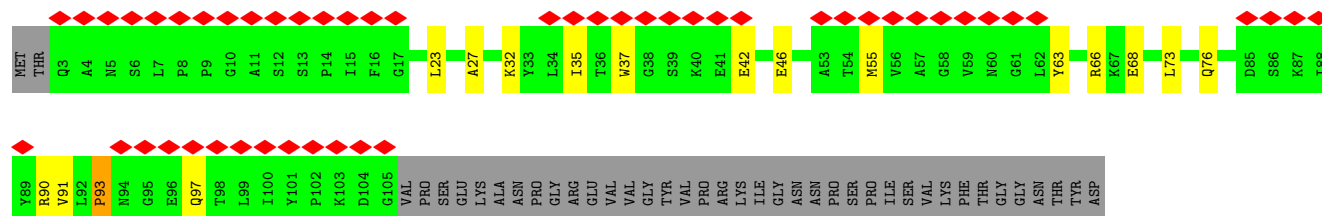


- Molecule 4: Photosystem I iron-sulfur center

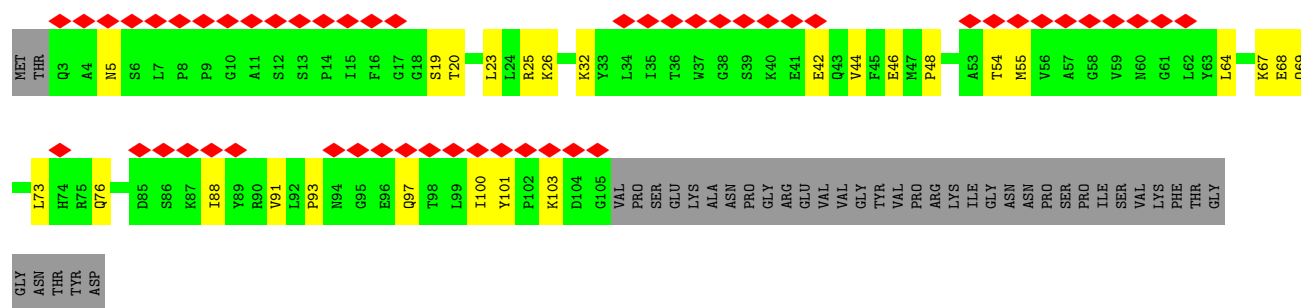




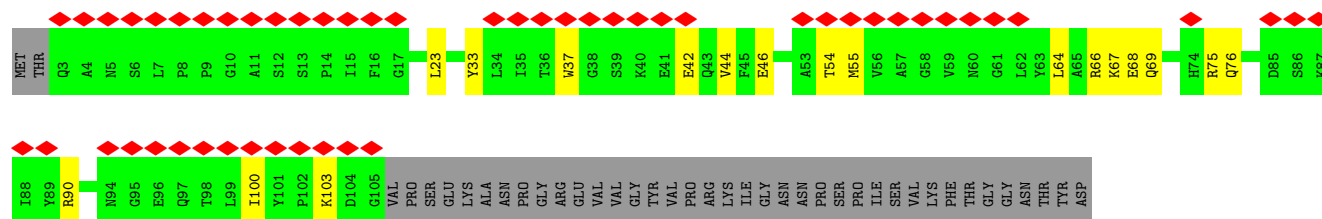
- Molecule 5: Photosystem I reaction center subunit II



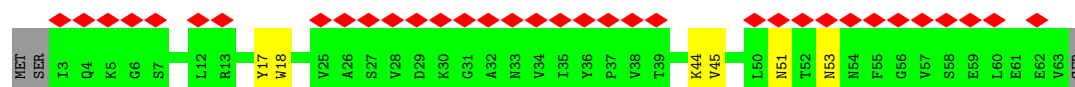
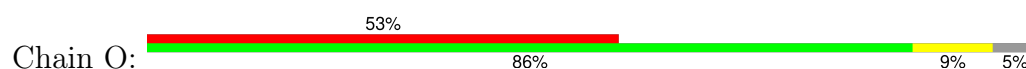
- Molecule 5: Photosystem I reaction center subunit II



- Molecule 5: Photosystem I reaction center subunit II

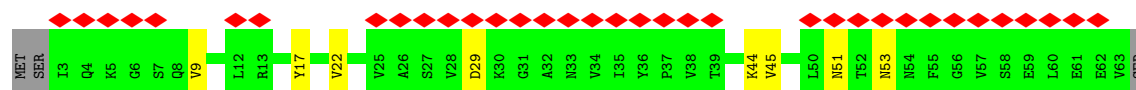


- Molecule 6: Photosystem I reaction center subunit IV

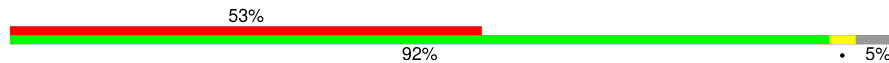


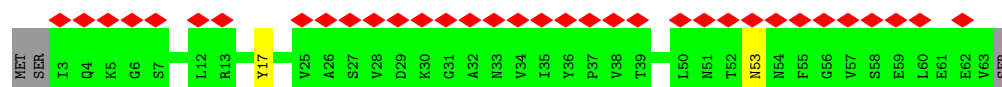
- Molecule 6: Photosystem I reaction center subunit IV

Chain e: 



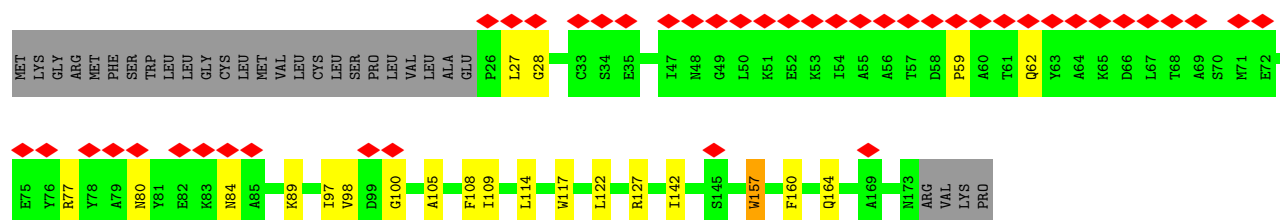
- Molecule 6: Photosystem I reaction center subunit IV

Chain E: 



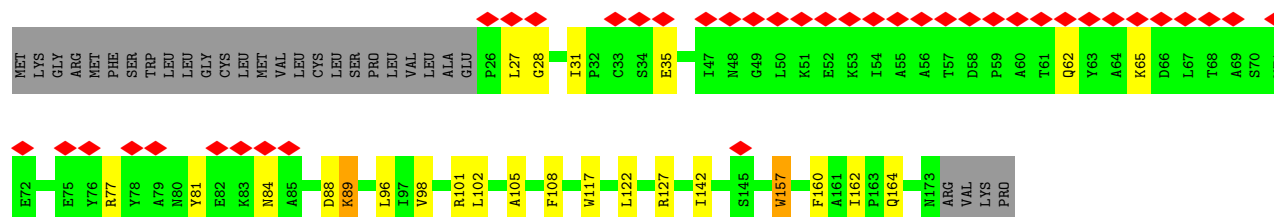
- Molecule 7: Photosystem I reaction center subunit III

Chain P: 



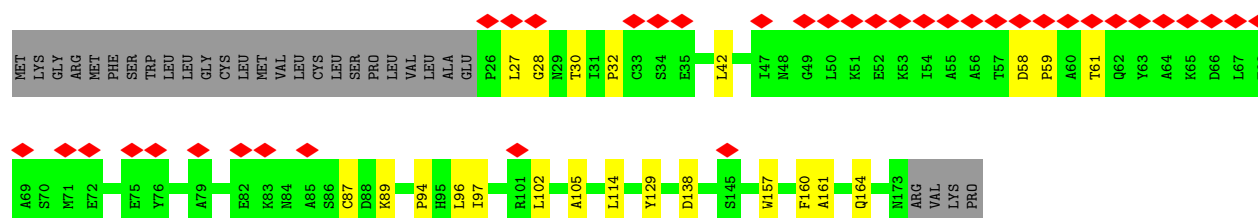
- Molecule 7: Photosystem I reaction center subunit III

Chain f: 



- Molecule 7: Photosystem I reaction center subunit III

Chain F: 



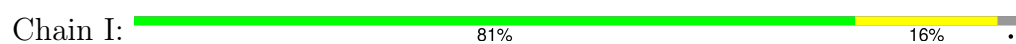
- Molecule 8: Photosystem I reaction center subunit VIII



- Molecule 8: Photosystem I reaction center subunit VIII



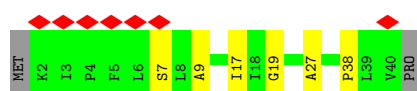
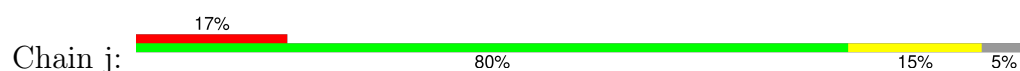
- Molecule 8: Photosystem I reaction center subunit VIII



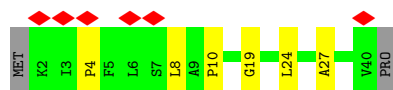
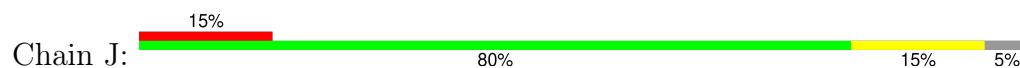
- Molecule 9: Photosystem I reaction center subunit IX



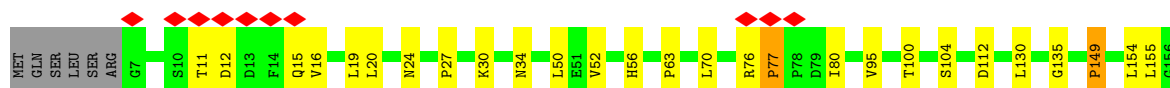
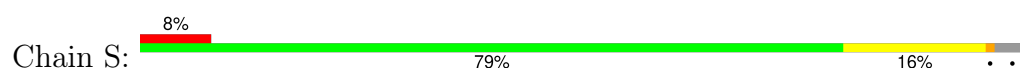
- Molecule 9: Photosystem I reaction center subunit IX



- Molecule 9: Photosystem I reaction center subunit IX



- Molecule 10: Photosystem I reaction center subunit XI





## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 403080                                  | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | TFS KRIOS                               | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 50                                      | Depositor |
| Minimum defocus (nm)                 | 800                                     | Depositor |
| Maximum defocus (nm)                 | 2200                                    | Depositor |
| Magnification                        | Not provided                            |           |
| Image detector                       | GATAN K3 (6k x 4k)                      | Depositor |
| Maximum map value                    | 0.066                                   | Depositor |
| Minimum map value                    | -0.039                                  | Depositor |
| Average map value                    | 0.000                                   | Depositor |
| Map value standard deviation         | 0.002                                   | Depositor |
| Recommended contour level            | 0.00112                                 | Depositor |
| Map size (Å)                         | 264.0, 264.0, 264.0                     | wwPDB     |
| Map dimensions                       | 320, 320, 320                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 0.825, 0.825, 0.825                     | Depositor |

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LMG, SF4, 1L3, LHG, BCR, CLA, 45D, LMT, CL0

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

| Mol | Chain | Bond lengths |                 | Bond angles |                  |
|-----|-------|--------------|-----------------|-------------|------------------|
|     |       | RMSZ         | $\# Z  > 5$     | RMSZ        | $\# Z  > 5$      |
| 1   | A     | 0.57         | 3/6200 (0.0%)   | 1.03        | 16/8468 (0.2%)   |
| 1   | G     | 0.60         | 6/6200 (0.1%)   | 1.07        | 25/8468 (0.3%)   |
| 1   | a     | 0.62         | 9/6200 (0.1%)   | 1.14        | 29/8468 (0.3%)   |
| 2   | M     | 0.37         | 0/229           | 0.79        | 0/308            |
| 2   | T     | 0.40         | 0/229           | 0.69        | 0/308            |
| 2   | m     | 0.42         | 0/229           | 0.75        | 0/308            |
| 3   | B     | 0.62         | 7/6079 (0.1%)   | 1.16        | 32/8310 (0.4%)   |
| 3   | H     | 0.62         | 7/6079 (0.1%)   | 1.13        | 33/8310 (0.4%)   |
| 3   | b     | 0.68         | 9/6079 (0.1%)   | 1.17        | 36/8310 (0.4%)   |
| 4   | C     | 0.39         | 0/609           | 0.81        | 3/825 (0.4%)     |
| 4   | K     | 0.34         | 0/609           | 0.74        | 0/825            |
| 4   | c     | 0.41         | 0/609           | 0.95        | 4/825 (0.5%)     |
| 5   | D     | 0.40         | 0/800           | 0.72        | 0/1079           |
| 5   | N     | 0.40         | 1/800 (0.1%)    | 0.76        | 3/1079 (0.3%)    |
| 5   | d     | 0.40         | 1/800 (0.1%)    | 0.76        | 3/1079 (0.3%)    |
| 6   | E     | 0.25         | 0/497           | 0.54        | 0/675            |
| 6   | O     | 0.32         | 0/497           | 0.70        | 0/675            |
| 6   | e     | 0.29         | 0/497           | 0.59        | 0/675            |
| 7   | F     | 0.55         | 2/1175 (0.2%)   | 1.11        | 10/1596 (0.6%)   |
| 7   | P     | 0.52         | 1/1175 (0.1%)   | 1.06        | 4/1596 (0.3%)    |
| 7   | f     | 0.57         | 2/1175 (0.2%)   | 1.03        | 2/1596 (0.1%)    |
| 8   | I     | 0.43         | 0/261           | 0.82        | 0/360            |
| 8   | Q     | 0.45         | 0/261           | 0.91        | 0/360            |
| 8   | i     | 0.52         | 0/261           | 0.95        | 0/360            |
| 9   | J     | 0.56         | 0/301           | 1.21        | 2/413 (0.5%)     |
| 9   | R     | 1.38         | 3/301 (1.0%)    | 1.89        | 7/413 (1.7%)     |
| 9   | j     | 0.58         | 1/301 (0.3%)    | 1.02        | 0/413            |
| 10  | L     | 0.59         | 2/1193 (0.2%)   | 1.09        | 6/1628 (0.4%)    |
| 10  | S     | 0.56         | 1/1193 (0.1%)   | 1.10        | 7/1628 (0.4%)    |
| 10  | l     | 0.72         | 2/1193 (0.2%)   | 1.22        | 14/1628 (0.9%)   |
| All | All   | 0.59         | 57/52032 (0.1%) | 1.08        | 236/70986 (0.3%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | a     | 0                   | 1                   |
| 3   | B     | 0                   | 3                   |
| 3   | H     | 0                   | 5                   |
| 3   | b     | 0                   | 5                   |
| 5   | D     | 0                   | 1                   |
| 8   | i     | 0                   | 1                   |
| 10  | S     | 0                   | 1                   |
| 10  | l     | 0                   | 3                   |
| All | All   | 0                   | 20                  |

The worst 5 of 57 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z      | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|--------|-------------|----------|
| 3   | b     | 163 | PRO  | CG-CD | -24.62 | 0.67        | 1.50     |
| 1   | a     | 387 | PRO  | CG-CD | -19.52 | 0.84        | 1.50     |
| 1   | A     | 746 | PRO  | CG-CD | -17.89 | 0.90        | 1.50     |
| 9   | R     | 38  | PRO  | CG-CD | -17.11 | 0.92        | 1.50     |
| 3   | H     | 528 | PRO  | CG-CD | -16.43 | 0.94        | 1.50     |

The worst 5 of 236 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|--------|-------------|----------|
| 3   | b     | 163 | PRO  | N-CD-CG  | -28.03 | 61.15       | 103.20   |
| 1   | G     | 242 | PRO  | CB-CG-CD | -25.47 | 24.60       | 106.10   |
| 3   | B     | 163 | PRO  | N-CD-CG  | -25.10 | 65.55       | 103.20   |
| 1   | a     | 387 | PRO  | N-CD-CG  | -25.02 | 65.67       | 103.20   |
| 1   | A     | 746 | PRO  | N-CD-CG  | -23.74 | 67.59       | 103.20   |

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group     |
|-----|-------|-----|------|-----------|
| 3   | H     | 485 | PHE  | Peptide   |
| 3   | H     | 510 | CYS  | Peptide   |
| 3   | H     | 556 | ARG  | Sidechain |
| 3   | H     | 682 | TRP  | Peptide   |
| 3   | H     | 70  | TRP  | Peptide   |

## 5.2 Too-close contacts ⓘ

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | A     | 5997  | 0        | 5811     | 69      | 0            |
| 1   | G     | 5997  | 0        | 5811     | 81      | 0            |
| 1   | a     | 5997  | 0        | 5811     | 87      | 0            |
| 2   | M     | 226   | 0        | 240      | 3       | 0            |
| 2   | T     | 226   | 0        | 240      | 2       | 0            |
| 2   | m     | 226   | 0        | 240      | 5       | 0            |
| 3   | B     | 5866  | 0        | 5675     | 75      | 0            |
| 3   | H     | 5866  | 0        | 5675     | 86      | 0            |
| 3   | b     | 5866  | 0        | 5675     | 73      | 0            |
| 4   | C     | 599   | 0        | 577      | 5       | 0            |
| 4   | K     | 599   | 0        | 577      | 4       | 0            |
| 4   | c     | 599   | 0        | 577      | 8       | 0            |
| 5   | D     | 784   | 0        | 798      | 12      | 0            |
| 5   | N     | 784   | 0        | 798      | 12      | 0            |
| 5   | d     | 784   | 0        | 798      | 16      | 0            |
| 6   | E     | 489   | 0        | 474      | 2       | 0            |
| 6   | O     | 489   | 0        | 474      | 6       | 0            |
| 6   | e     | 489   | 0        | 474      | 7       | 0            |
| 7   | F     | 1148  | 0        | 1143     | 10      | 0            |
| 7   | P     | 1148  | 0        | 1143     | 16      | 0            |
| 7   | f     | 1148  | 0        | 1143     | 15      | 0            |
| 8   | I     | 254   | 0        | 269      | 5       | 0            |
| 8   | Q     | 254   | 0        | 269      | 10      | 0            |
| 8   | i     | 254   | 0        | 269      | 9       | 0            |
| 9   | J     | 293   | 0        | 327      | 5       | 0            |
| 9   | R     | 293   | 0        | 327      | 8       | 0            |
| 9   | j     | 293   | 0        | 327      | 5       | 0            |
| 10  | L     | 1159  | 0        | 1179     | 21      | 0            |
| 10  | S     | 1159  | 0        | 1179     | 16      | 0            |
| 10  | l     | 1159  | 0        | 1179     | 15      | 0            |
| 11  | A     | 65    | 0        | 72       | 4       | 0            |
| 11  | G     | 65    | 0        | 72       | 1       | 0            |
| 11  | a     | 65    | 0        | 72       | 0       | 0            |
| 12  | A     | 2375  | 0        | 2267     | 65      | 0            |
| 12  | B     | 2190  | 0        | 2162     | 57      | 0            |
| 12  | F     | 110   | 0        | 104      | 4       | 0            |
| 12  | G     | 2440  | 0        | 2339     | 67      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 12  | H     | 2310  | 0        | 2282     | 68      | 0            |
| 12  | J     | 45    | 0        | 32       | 1       | 0            |
| 12  | L     | 250   | 0        | 265      | 11      | 0            |
| 12  | P     | 110   | 0        | 104      | 5       | 0            |
| 12  | R     | 45    | 0        | 32       | 1       | 0            |
| 12  | S     | 185   | 0        | 193      | 7       | 0            |
| 12  | a     | 2375  | 0        | 2270     | 75      | 0            |
| 12  | b     | 2185  | 0        | 2148     | 66      | 0            |
| 12  | f     | 110   | 0        | 104      | 5       | 0            |
| 12  | j     | 110   | 0        | 104      | 2       | 0            |
| 12  | l     | 250   | 0        | 265      | 12      | 0            |
| 13  | A     | 33    | 0        | 0        | 0       | 0            |
| 13  | B     | 33    | 0        | 0        | 0       | 0            |
| 13  | G     | 33    | 0        | 0        | 0       | 0            |
| 13  | H     | 33    | 0        | 0        | 0       | 0            |
| 13  | a     | 33    | 0        | 0        | 0       | 0            |
| 13  | b     | 33    | 0        | 0        | 0       | 0            |
| 14  | A     | 8     | 0        | 0        | 0       | 0            |
| 14  | C     | 16    | 0        | 0        | 0       | 0            |
| 14  | G     | 8     | 0        | 0        | 0       | 0            |
| 14  | K     | 16    | 0        | 0        | 1       | 0            |
| 14  | a     | 8     | 0        | 0        | 0       | 0            |
| 14  | c     | 16    | 0        | 0        | 0       | 0            |
| 15  | A     | 280   | 0        | 341      | 15      | 0            |
| 15  | B     | 225   | 0        | 273      | 13      | 0            |
| 15  | F     | 80    | 0        | 98       | 5       | 0            |
| 15  | G     | 280   | 0        | 341      | 14      | 0            |
| 15  | H     | 265   | 0        | 322      | 21      | 0            |
| 15  | I     | 40    | 0        | 49       | 4       | 0            |
| 15  | J     | 120   | 0        | 145      | 6       | 0            |
| 15  | L     | 120   | 0        | 147      | 5       | 0            |
| 15  | P     | 80    | 0        | 98       | 5       | 0            |
| 15  | Q     | 80    | 0        | 98       | 5       | 0            |
| 15  | R     | 80    | 0        | 96       | 5       | 0            |
| 15  | S     | 80    | 0        | 98       | 5       | 0            |
| 15  | a     | 280   | 0        | 341      | 15      | 0            |
| 15  | b     | 265   | 0        | 322      | 21      | 0            |
| 15  | f     | 80    | 0        | 98       | 4       | 0            |
| 15  | i     | 80    | 0        | 98       | 3       | 0            |
| 15  | j     | 80    | 0        | 96       | 5       | 0            |
| 15  | l     | 80    | 0        | 98       | 4       | 0            |
| 16  | A     | 125   | 0        | 172      | 3       | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 16  | G     | 125   | 0        | 172      | 5       | 0            |
| 16  | a     | 125   | 0        | 172      | 4       | 0            |
| 17  | M     | 42    | 0        | 52       | 3       | 0            |
| 17  | T     | 42    | 0        | 52       | 3       | 0            |
| 17  | m     | 42    | 0        | 52       | 4       | 0            |
| 18  | B     | 55    | 0        | 86       | 4       | 0            |
| 18  | H     | 55    | 0        | 86       | 5       | 0            |
| 18  | b     | 55    | 0        | 86       | 3       | 0            |
| 19  | B     | 35    | 0        | 44       | 2       | 0            |
| 19  | H     | 35    | 0        | 45       | 1       | 0            |
| 19  | b     | 35    | 0        | 46       | 1       | 0            |
| 20  | A     | 56    | 0        | 0        | 1       | 0            |
| 20  | B     | 82    | 0        | 0        | 0       | 0            |
| 20  | C     | 24    | 0        | 0        | 0       | 0            |
| 20  | D     | 16    | 0        | 0        | 0       | 0            |
| 20  | G     | 58    | 0        | 0        | 2       | 0            |
| 20  | H     | 80    | 0        | 0        | 0       | 0            |
| 20  | K     | 26    | 0        | 0        | 0       | 0            |
| 20  | L     | 7     | 0        | 0        | 0       | 0            |
| 20  | N     | 15    | 0        | 0        | 0       | 0            |
| 20  | O     | 1     | 0        | 0        | 0       | 0            |
| 20  | S     | 5     | 0        | 0        | 0       | 0            |
| 20  | a     | 57    | 0        | 0        | 2       | 0            |
| 20  | b     | 82    | 0        | 0        | 0       | 0            |
| 20  | c     | 22    | 0        | 0        | 0       | 0            |
| 20  | d     | 17    | 0        | 0        | 1       | 0            |
| 20  | e     | 1     | 0        | 0        | 0       | 0            |
| 20  | l     | 6     | 0        | 0        | 0       | 0            |
| All | All   | 69921 | 0        | 68590    | 949     | 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 7.

The worst 5 of 949 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) |
|-------------------|-------------------|--------------------------|-------------------|
| 3:H:67:HIS:O      | 3:H:71:GLN:HB3    | 1.71                     | 0.88              |
| 5:d:42:GLU:HA     | 5:d:55:MET:O      | 1.78                     | 0.83              |
| 12:a:839:CLA:HAB  | 12:a:839:CLA:H111 | 1.66                     | 0.78              |
| 5:N:42:GLU:HA     | 5:N:55:MET:O      | 1.84                     | 0.77              |
| 12:A:839:CLA:H111 | 12:A:839:CLA:HAB  | 1.69                     | 0.74              |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1   | A     | 771/785 (98%) | 720 (93%) | 46 (6%) | 5 (1%)   | 21          | 32  |
| 1   | G     | 771/785 (98%) | 725 (94%) | 40 (5%) | 6 (1%)   | 16          | 25  |
| 1   | a     | 771/785 (98%) | 722 (94%) | 45 (6%) | 4 (0%)   | 24          | 37  |
| 2   | M     | 29/32 (91%)   | 29 (100%) | 0       | 0        | 100         | 100 |
| 2   | T     | 29/32 (91%)   | 29 (100%) | 0       | 0        | 100         | 100 |
| 2   | m     | 29/32 (91%)   | 29 (100%) | 0       | 0        | 100         | 100 |
| 3   | B     | 744/749 (99%) | 707 (95%) | 36 (5%) | 1 (0%)   | 48          | 64  |
| 3   | H     | 744/749 (99%) | 702 (94%) | 41 (6%) | 1 (0%)   | 48          | 64  |
| 3   | b     | 744/749 (99%) | 700 (94%) | 43 (6%) | 1 (0%)   | 48          | 64  |
| 4   | C     | 78/81 (96%)   | 74 (95%)  | 4 (5%)  | 0        | 100         | 100 |
| 4   | K     | 78/81 (96%)   | 73 (94%)  | 5 (6%)  | 0        | 100         | 100 |
| 4   | c     | 78/81 (96%)   | 75 (96%)  | 3 (4%)  | 0        | 100         | 100 |
| 5   | D     | 101/143 (71%) | 98 (97%)  | 3 (3%)  | 0        | 100         | 100 |
| 5   | N     | 101/143 (71%) | 97 (96%)  | 4 (4%)  | 0        | 100         | 100 |
| 5   | d     | 101/143 (71%) | 95 (94%)  | 6 (6%)  | 0        | 100         | 100 |
| 6   | E     | 59/64 (92%)   | 57 (97%)  | 2 (3%)  | 0        | 100         | 100 |
| 6   | O     | 59/64 (92%)   | 56 (95%)  | 3 (5%)  | 0        | 100         | 100 |
| 6   | e     | 59/64 (92%)   | 56 (95%)  | 3 (5%)  | 0        | 100         | 100 |
| 7   | F     | 146/177 (82%) | 132 (90%) | 13 (9%) | 1 (1%)   | 18          | 28  |
| 7   | P     | 146/177 (82%) | 134 (92%) | 11 (8%) | 1 (1%)   | 18          | 28  |
| 7   | f     | 146/177 (82%) | 135 (92%) | 10 (7%) | 1 (1%)   | 18          | 28  |
| 8   | I     | 29/32 (91%)   | 27 (93%)  | 2 (7%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 8   | Q     | 29/32 (91%)     | 29 (100%)  | 0        | 0        | 100         | 100 |
| 8   | i     | 29/32 (91%)     | 28 (97%)   | 1 (3%)   | 0        | 100         | 100 |
| 9   | J     | 37/41 (90%)     | 35 (95%)   | 2 (5%)   | 0        | 100         | 100 |
| 9   | R     | 37/41 (90%)     | 35 (95%)   | 2 (5%)   | 0        | 100         | 100 |
| 9   | j     | 37/41 (90%)     | 35 (95%)   | 2 (5%)   | 0        | 100         | 100 |
| 10  | L     | 152/160 (95%)   | 143 (94%)  | 7 (5%)   | 2 (1%)   | 9           | 14  |
| 10  | S     | 152/160 (95%)   | 145 (95%)  | 5 (3%)   | 2 (1%)   | 9           | 14  |
| 10  | l     | 152/160 (95%)   | 143 (94%)  | 7 (5%)   | 2 (1%)   | 9           | 14  |
| All | All   | 6438/6792 (95%) | 6065 (94%) | 346 (5%) | 27 (0%)  | 31          | 43  |

5 of 27 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | G     | 259 | PRO  |
| 7   | P     | 89  | LYS  |
| 10  | S     | 12  | ASP  |
| 10  | S     | 77  | PRO  |
| 7   | f     | 89  | LYS  |

### 5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 1   | A     | 603/628 (96%)  | 603 (100%) | 0        | 100         | 100 |
| 1   | G     | 603/628 (96%)  | 602 (100%) | 1 (0%)   | 87          | 94  |
| 1   | a     | 603/628 (96%)  | 601 (100%) | 2 (0%)   | 86          | 93  |
| 2   | M     | 22/23 (96%)    | 22 (100%)  | 0        | 100         | 100 |
| 2   | T     | 22/23 (96%)    | 22 (100%)  | 0        | 100         | 100 |
| 2   | m     | 22/23 (96%)    | 22 (100%)  | 0        | 100         | 100 |
| 3   | B     | 591/593 (100%) | 591 (100%) | 0        | 100         | 100 |
| 3   | H     | 591/593 (100%) | 591 (100%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Rotameric   | Outliers | Percentiles |     |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 3   | b     | 591/593 (100%)  | 591 (100%)  | 0        | 100         | 100 |
| 4   | C     | 67/68 (98%)     | 67 (100%)   | 0        | 100         | 100 |
| 4   | K     | 67/68 (98%)     | 67 (100%)   | 0        | 100         | 100 |
| 4   | c     | 67/68 (98%)     | 67 (100%)   | 0        | 100         | 100 |
| 5   | D     | 81/116 (70%)    | 81 (100%)   | 0        | 100         | 100 |
| 5   | N     | 81/116 (70%)    | 80 (99%)    | 1 (1%)   | 63          | 81  |
| 5   | d     | 81/116 (70%)    | 81 (100%)   | 0        | 100         | 100 |
| 6   | E     | 55/58 (95%)     | 55 (100%)   | 0        | 100         | 100 |
| 6   | O     | 55/58 (95%)     | 55 (100%)   | 0        | 100         | 100 |
| 6   | e     | 55/58 (95%)     | 55 (100%)   | 0        | 100         | 100 |
| 7   | F     | 120/146 (82%)   | 120 (100%)  | 0        | 100         | 100 |
| 7   | P     | 120/146 (82%)   | 120 (100%)  | 0        | 100         | 100 |
| 7   | f     | 120/146 (82%)   | 120 (100%)  | 0        | 100         | 100 |
| 8   | I     | 29/30 (97%)     | 29 (100%)   | 0        | 100         | 100 |
| 8   | Q     | 29/30 (97%)     | 29 (100%)   | 0        | 100         | 100 |
| 8   | i     | 29/30 (97%)     | 29 (100%)   | 0        | 100         | 100 |
| 9   | J     | 32/34 (94%)     | 32 (100%)   | 0        | 100         | 100 |
| 9   | R     | 32/34 (94%)     | 32 (100%)   | 0        | 100         | 100 |
| 9   | j     | 32/34 (94%)     | 32 (100%)   | 0        | 100         | 100 |
| 10  | L     | 119/125 (95%)   | 119 (100%)  | 0        | 100         | 100 |
| 10  | S     | 119/125 (95%)   | 119 (100%)  | 0        | 100         | 100 |
| 10  | l     | 119/125 (95%)   | 119 (100%)  | 0        | 100         | 100 |
| All | All   | 5157/5463 (94%) | 5153 (100%) | 4 (0%)   | 87          | 95  |

All (4) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | G     | 691 | PRO  |
| 5   | N     | 93  | PRO  |
| 1   | a     | 385 | PRO  |
| 1   | a     | 387 | PRO  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 145 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3   | B     | 158 | GLN  |
| 10  | L     | 34  | ASN  |
| 3   | B     | 298 | GLN  |
| 5   | D     | 5   | ASN  |
| 1   | a     | 489 | GLN  |

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

366 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$ |
| 12  | CLA  | A     | 803 | 1    | 69,73,73     | 2.26 | 23 (33%)    | 82,113,113  | 2.53 | 30 (36%)    |
| 12  | CLA  | G     | 802 | -    | 64,68,73     | 2.33 | 22 (34%)    | 76,107,113  | 2.64 | 30 (39%)    |
| 12  | CLA  | B     | 810 | 3    | 69,73,73     | 2.21 | 22 (31%)    | 82,113,113  | 2.71 | 29 (35%)    |
| 15  | BCR  | b     | 847 | -    | 41,41,41     | 2.63 | 6 (14%)     | 56,56,56    | 6.61 | 22 (39%)    |
| 12  | CLA  | G     | 842 | 16   | 64,68,73     | 2.29 | 22 (34%)    | 76,107,113  | 2.55 | 26 (34%)    |
| 12  | CLA  | A     | 841 | 20   | 69,73,73     | 2.21 | 21 (30%)    | 82,113,113  | 2.41 | 27 (32%)    |
| 12  | CLA  | B     | 814 | -    | 59,63,73     | 2.36 | 22 (37%)    | 70,101,113  | 2.64 | 25 (35%)    |
| 12  | CLA  | a     | 804 | 12   | 59,63,73     | 2.41 | 23 (38%)    | 70,101,113  | 2.80 | 30 (42%)    |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | A     | 810 | 12,1 | 54,58,73     | 2.48 | 23 (42%) | 64,95,113   | 2.93 | 27 (42%) |
| 12  | CLA  | A     | 812 | -    | 54,58,73     | 2.53 | 24 (44%) | 64,95,113   | 2.90 | 28 (43%) |
| 12  | CLA  | A     | 826 | 1    | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.57 | 29 (35%) |
| 12  | CLA  | b     | 802 | -    | 69,73,73     | 2.15 | 21 (30%) | 82,113,113  | 2.85 | 33 (40%) |
| 12  | CLA  | a     | 810 | 12,1 | 54,58,73     | 2.49 | 23 (42%) | 64,95,113   | 2.88 | 28 (43%) |
| 12  | CLA  | B     | 819 | -    | 49,53,73     | 2.54 | 22 (44%) | 58,89,113   | 2.84 | 26 (44%) |
| 12  | CLA  | H     | 816 | -    | 64,68,73     | 2.36 | 22 (34%) | 76,107,113  | 2.90 | 28 (36%) |
| 12  | CLA  | S     | 204 | 20   | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.46 | 25 (30%) |
| 12  | CLA  | G     | 827 | -    | 69,73,73     | 2.23 | 23 (33%) | 82,113,113  | 2.54 | 31 (37%) |
| 12  | CLA  | A     | 825 | 20   | 59,63,73     | 2.40 | 23 (38%) | 70,101,113  | 2.68 | 28 (40%) |
| 12  | CLA  | B     | 835 | 3    | 49,53,73     | 2.49 | 21 (42%) | 58,89,113   | 2.93 | 25 (43%) |
| 12  | CLA  | b     | 824 | 3    | 69,73,73     | 2.18 | 23 (33%) | 82,113,113  | 2.53 | 32 (39%) |
| 12  | CLA  | a     | 855 | -    | 69,73,73     | 2.15 | 22 (31%) | 82,113,113  | 2.72 | 29 (35%) |
| 12  | CLA  | a     | 811 | -    | 49,53,73     | 2.56 | 22 (44%) | 58,89,113   | 2.74 | 23 (39%) |
| 12  | CLA  | B     | 825 | -    | 69,73,73     | 2.27 | 22 (31%) | 82,113,113  | 2.12 | 26 (31%) |
| 15  | BCR  | b     | 840 | -    | 41,41,41     | 2.62 | 6 (14%)  | 56,56,56    | 6.59 | 25 (44%) |
| 13  | 1L3  | B     | 839 | -    | 34,34,34     | 2.67 | 12 (35%) | 43,45,45    | 1.54 | 9 (20%)  |
| 12  | CLA  | L     | 206 | 20   | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.44 | 24 (29%) |
| 12  | CLA  | B     | 809 | 3    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 2.81 | 25 (43%) |
| 16  | LHG  | a     | 850 | -    | 48,48,48     | 0.92 | 2 (4%)   | 51,54,54    | 0.93 | 2 (3%)   |
| 12  | CLA  | H     | 806 | -    | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.72 | 28 (34%) |
| 12  | CLA  | A     | 819 | 1    | 49,53,73     | 2.55 | 23 (46%) | 58,89,113   | 2.84 | 25 (43%) |
| 12  | CLA  | B     | 833 | 3    | 64,68,73     | 2.28 | 22 (34%) | 76,107,113  | 2.68 | 26 (34%) |
| 12  | CLA  | A     | 836 | 1    | 54,58,73     | 2.63 | 23 (42%) | 64,95,113   | 3.26 | 32 (50%) |
| 12  | CLA  | B     | 828 | 3    | 49,53,73     | 2.55 | 23 (46%) | 58,89,113   | 2.81 | 26 (44%) |
| 12  | CLA  | H     | 829 | 3    | 49,53,73     | 2.55 | 23 (46%) | 58,89,113   | 2.79 | 26 (44%) |
| 12  | CLA  | b     | 811 | -    | 64,68,73     | 2.33 | 23 (35%) | 76,107,113  | 2.59 | 27 (35%) |
| 12  | CLA  | J     | 103 | -    | 49,53,73     | 2.58 | 24 (48%) | 58,89,113   | 2.78 | 23 (39%) |
| 15  | BCR  | H     | 849 | -    | 41,41,41     | 2.57 | 6 (14%)  | 56,56,56    | 6.50 | 20 (35%) |
| 12  | CLA  | B     | 805 | 3    | 69,73,73     | 2.22 | 23 (33%) | 82,113,113  | 2.56 | 28 (34%) |
| 12  | CLA  | B     | 836 | 20   | 69,73,73     | 2.28 | 23 (33%) | 82,113,113  | 2.52 | 29 (35%) |
| 15  | BCR  | L     | 207 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.75 | 18 (32%) |
| 12  | CLA  | b     | 806 | -    | 69,73,73     | 2.19 | 21 (30%) | 82,113,113  | 2.75 | 29 (35%) |
| 12  | CLA  | b     | 813 | 3    | 59,63,73     | 2.42 | 25 (42%) | 70,101,113  | 2.70 | 26 (37%) |
| 12  | CLA  | A     | 832 | 1    | 69,73,73     | 2.25 | 22 (31%) | 82,113,113  | 2.35 | 25 (30%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 15  | BCR  | G     | 849 | -    | 41,41,41     | 2.75 | 6 (14%)  | 56,56,56    | 6.76 | 21 (37%) |
| 12  | CLA  | A     | 818 | -    | 69,73,73     | 2.19 | 23 (33%) | 82,113,113  | 2.60 | 27 (32%) |
| 12  | CLA  | b     | 831 | 3    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 2.85 | 25 (43%) |
| 12  | CLA  | a     | 803 | 1    | 69,73,73     | 2.25 | 23 (33%) | 82,113,113  | 2.53 | 32 (39%) |
| 16  | LHG  | A     | 851 | 12   | 26,26,48     | 1.25 | 2 (7%)   | 29,32,54    | 1.24 | 3 (10%)  |
| 12  | CLA  | B     | 832 | 3    | 49,53,73     | 2.56 | 22 (44%) | 58,89,113   | 2.82 | 25 (43%) |
| 12  | CLA  | B     | 818 | -    | 49,53,73     | 2.57 | 23 (46%) | 58,89,113   | 2.87 | 23 (39%) |
| 12  | CLA  | H     | 831 | -    | 69,73,73     | 2.22 | 20 (28%) | 82,113,113  | 2.48 | 28 (34%) |
| 15  | BCR  | L     | 203 | -    | 41,41,41     | 2.78 | 6 (14%)  | 56,56,56    | 6.44 | 21 (37%) |
| 18  | LMG  | H     | 847 | -    | 55,55,55     | 1.49 | 8 (14%)  | 63,63,63    | 1.10 | 4 (6%)   |
| 12  | CLA  | G     | 812 | -    | 49,53,73     | 2.54 | 22 (44%) | 58,89,113   | 2.75 | 22 (37%) |
| 12  | CLA  | G     | 839 | 1    | 69,73,73     | 2.27 | 24 (34%) | 82,113,113  | 2.47 | 26 (31%) |
| 12  | CLA  | A     | 831 | 1    | 59,63,73     | 2.42 | 23 (38%) | 70,101,113  | 2.62 | 29 (41%) |
| 12  | CLA  | A     | 809 | 1    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 2.88 | 25 (43%) |
| 19  | LMT  | b     | 846 | -    | 36,36,36     | 1.17 | 4 (11%)  | 47,47,47    | 1.01 | 2 (4%)   |
| 12  | CLA  | B     | 813 | 3    | 59,63,73     | 2.43 | 24 (40%) | 70,101,113  | 2.67 | 25 (35%) |
| 12  | CLA  | H     | 809 | 3    | 49,53,73     | 2.55 | 22 (44%) | 58,89,113   | 2.83 | 27 (46%) |
| 12  | CLA  | A     | 823 | -    | 59,63,73     | 2.38 | 22 (37%) | 70,101,113  | 2.68 | 25 (35%) |
| 12  | CLA  | b     | 809 | 3    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 2.82 | 25 (43%) |
| 12  | CLA  | G     | 820 | 1    | 49,53,73     | 2.51 | 22 (44%) | 58,89,113   | 2.83 | 26 (44%) |
| 12  | CLA  | a     | 823 | -    | 59,63,73     | 2.38 | 22 (37%) | 70,101,113  | 2.70 | 26 (37%) |
| 12  | CLA  | G     | 819 | -    | 69,73,73     | 2.20 | 24 (34%) | 82,113,113  | 2.56 | 30 (36%) |
| 15  | BCR  | G     | 848 | -    | 41,41,41     | 2.65 | 6 (14%)  | 56,56,56    | 6.74 | 25 (44%) |
| 12  | CLA  | H     | 814 | 3    | 59,63,73     | 2.42 | 24 (40%) | 70,101,113  | 2.64 | 24 (34%) |
| 12  | CLA  | a     | 807 | -    | 69,73,73     | 2.22 | 22 (31%) | 82,113,113  | 2.61 | 29 (35%) |
| 12  | CLA  | A     | 835 | -    | 49,53,73     | 2.53 | 21 (42%) | 58,89,113   | 2.85 | 25 (43%) |
| 12  | CLA  | H     | 817 | -    | 69,73,73     | 2.26 | 24 (34%) | 82,113,113  | 2.33 | 27 (32%) |
| 12  | CLA  | G     | 809 | 1    | 54,58,73     | 2.56 | 23 (42%) | 64,95,113   | 2.87 | 27 (42%) |
| 12  | CLA  | F     | 201 | 20   | 69,73,73     | 2.27 | 23 (33%) | 82,113,113  | 2.30 | 27 (32%) |
| 15  | BCR  | B     | 842 | -    | 41,41,41     | 2.58 | 6 (14%)  | 56,56,56    | 6.62 | 21 (37%) |
| 12  | CLA  | a     | 822 | -    | 54,58,73     | 2.56 | 23 (42%) | 64,95,113   | 2.77 | 25 (39%) |
| 12  | CLA  | b     | 821 | 20   | 69,73,73     | 2.18 | 22 (31%) | 82,113,113  | 2.53 | 33 (40%) |
| 12  | CLA  | H     | 838 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.65 | 32 (39%) |
| 15  | BCR  | H     | 845 | -    | 41,41,41     | 2.64 | 6 (14%)  | 56,56,56    | 6.83 | 25 (44%) |
| 12  | CLA  | G     | 814 | 1    | 49,53,73     | 2.52 | 22 (44%) | 58,89,113   | 3.00 | 24 (41%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 19  | LMT  | B     | 847 | -    | 36,36,36     | 1.26 | 5 (13%)  | 47,47,47    | 1.11 | 3 (6%)   |
| 12  | CLA  | A     | 816 | 1    | 54,58,73     | 2.51 | 22 (40%) | 64,95,113   | 2.78 | 30 (46%) |
| 12  | CLA  | b     | 814 | 3    | 59,63,73     | 2.39 | 21 (35%) | 70,101,113  | 2.61 | 26 (37%) |
| 12  | CLA  | B     | 817 | 3    | 49,53,73     | 2.53 | 21 (42%) | 58,89,113   | 2.95 | 23 (39%) |
| 12  | CLA  | a     | 838 | 1    | 49,53,73     | 2.55 | 22 (44%) | 58,89,113   | 2.89 | 27 (46%) |
| 12  | CLA  | b     | 817 | 3    | 49,53,73     | 2.53 | 21 (42%) | 58,89,113   | 2.85 | 24 (41%) |
| 17  | 45D  | M     | 101 | -    | 43,43,43     | 3.99 | 19 (44%) | 54,60,60    | 7.88 | 31 (57%) |
| 17  | 45D  | m     | 101 | -    | 43,43,43     | 4.00 | 19 (44%) | 54,60,60    | 7.90 | 31 (57%) |
| 12  | CLA  | B     | 812 | -    | 49,53,73     | 2.55 | 24 (48%) | 58,89,113   | 2.84 | 24 (41%) |
| 12  | CLA  | a     | 831 | 1    | 59,63,73     | 2.44 | 23 (38%) | 70,101,113  | 2.59 | 27 (38%) |
| 15  | BCR  | j     | 101 | -    | 41,41,41     | 2.69 | 6 (14%)  | 56,56,56    | 6.57 | 21 (37%) |
| 12  | CLA  | B     | 816 | -    | 69,73,73     | 2.25 | 24 (34%) | 82,113,113  | 2.35 | 29 (35%) |
| 15  | BCR  | B     | 843 | -    | 25,25,41     | 2.18 | 2 (8%)   | 33,33,56    | 7.57 | 17 (51%) |
| 12  | CLA  | H     | 830 | 3    | 69,73,73     | 2.22 | 23 (33%) | 82,113,113  | 2.59 | 25 (30%) |
| 13  | 1L3  | a     | 842 | -    | 34,34,34     | 2.65 | 14 (41%) | 43,45,45    | 1.51 | 11 (25%) |
| 15  | BCR  | G     | 847 | -    | 41,41,41     | 2.70 | 6 (14%)  | 56,56,56    | 6.50 | 21 (37%) |
| 15  | BCR  | a     | 848 | -    | 41,41,41     | 2.72 | 6 (14%)  | 56,56,56    | 6.78 | 21 (37%) |
| 15  | BCR  | b     | 844 | -    | 41,41,41     | 2.57 | 6 (14%)  | 56,56,56    | 6.69 | 22 (39%) |
| 13  | 1L3  | b     | 838 | -    | 34,34,34     | 2.67 | 12 (35%) | 43,45,45    | 1.51 | 8 (18%)  |
| 12  | CLA  | G     | 841 | 20   | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.39 | 26 (31%) |
| 15  | BCR  | G     | 850 | -    | 41,41,41     | 2.65 | 6 (14%)  | 56,56,56    | 6.77 | 25 (44%) |
| 15  | BCR  | L     | 201 | -    | 41,41,41     | 2.67 | 6 (14%)  | 56,56,56    | 6.55 | 26 (46%) |
| 12  | CLA  | H     | 801 | 1    | 59,63,73     | 2.43 | 24 (40%) | 70,101,113  | 2.61 | 28 (40%) |
| 12  | CLA  | A     | 824 | 20   | 69,73,73     | 2.26 | 23 (33%) | 82,113,113  | 2.39 | 26 (31%) |
| 14  | SF4  | K     | 102 | 4    | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | b     | 804 | -    | 69,73,73     | 2.18 | 21 (30%) | 82,113,113  | 2.63 | 26 (31%) |
| 12  | CLA  | H     | 802 | -    | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.80 | 34 (41%) |
| 12  | CLA  | a     | 808 | 1    | 54,58,73     | 2.56 | 22 (40%) | 64,95,113   | 2.82 | 27 (42%) |
| 15  | BCR  | a     | 844 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.65 | 21 (37%) |
| 12  | CLA  | P     | 203 | -    | 49,53,73     | 2.55 | 22 (44%) | 58,89,113   | 4.47 | 25 (43%) |
| 12  | CLA  | b     | 830 | -    | 49,53,73     | 2.54 | 21 (42%) | 58,89,113   | 2.71 | 24 (41%) |
| 16  | LHG  | G     | 852 | 12   | 26,26,48     | 1.24 | 2 (7%)   | 29,32,54    | 1.25 | 4 (13%)  |
| 12  | CLA  | H     | 822 | 20   | 69,73,73     | 2.22 | 21 (30%) | 82,113,113  | 2.41 | 30 (36%) |
| 12  | CLA  | A     | 839 | 1    | 69,73,73     | 2.27 | 24 (34%) | 82,113,113  | 2.46 | 29 (35%) |
| 12  | CLA  | A     | 829 | 1    | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.37 | 28 (34%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | G     | 803 | 20   | 69,73,73     | 2.24 | 20 (28%) | 82,113,113  | 2.23 | 26 (31%) |
| 12  | CLA  | S     | 202 | 10   | 59,63,73     | 2.41 | 21 (35%) | 70,101,113  | 2.63 | 27 (38%) |
| 12  | CLA  | f     | 203 | -    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 4.46 | 25 (43%) |
| 12  | CLA  | a     | 839 | 1    | 69,73,73     | 2.27 | 24 (34%) | 82,113,113  | 2.49 | 24 (29%) |
| 15  | BCR  | B     | 840 | -    | 41,41,41     | 2.62 | 6 (14%)  | 56,56,56    | 6.68 | 20 (35%) |
| 12  | CLA  | a     | 827 | -    | 64,68,73     | 2.29 | 21 (32%) | 76,107,113  | 2.61 | 28 (36%) |
| 12  | CLA  | H     | 807 | 3    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.45 | 30 (36%) |
| 12  | CLA  | a     | 830 | 1    | 54,58,73     | 2.54 | 22 (40%) | 64,95,113   | 2.77 | 29 (45%) |
| 12  | CLA  | a     | 834 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.39 | 29 (35%) |
| 12  | CLA  | b     | 810 | 3    | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.71 | 32 (39%) |
| 12  | CLA  | A     | 811 | -    | 49,53,73     | 2.56 | 22 (44%) | 58,89,113   | 2.71 | 22 (37%) |
| 12  | CLA  | A     | 822 | -    | 54,58,73     | 2.57 | 23 (42%) | 64,95,113   | 2.72 | 27 (42%) |
| 13  | 1L3  | G     | 843 | -    | 34,34,34     | 2.68 | 15 (44%) | 43,45,45    | 1.48 | 10 (23%) |
| 15  | BCR  | S     | 205 | -    | 41,41,41     | 2.67 | 6 (14%)  | 56,56,56    | 6.46 | 25 (44%) |
| 12  | CLA  | G     | 828 | -    | 64,68,73     | 2.30 | 21 (32%) | 76,107,113  | 2.59 | 28 (36%) |
| 12  | CLA  | G     | 856 | -    | 69,73,73     | 2.18 | 23 (33%) | 82,113,113  | 2.55 | 28 (34%) |
| 12  | CLA  | G     | 818 | -    | 59,63,73     | 2.50 | 23 (38%) | 70,101,113  | 2.72 | 33 (47%) |
| 12  | CLA  | b     | 808 | 3    | 49,53,73     | 2.53 | 22 (44%) | 58,89,113   | 2.87 | 28 (48%) |
| 12  | CLA  | b     | 822 | 20   | 69,73,73     | 2.24 | 24 (34%) | 82,113,113  | 2.61 | 28 (34%) |
| 12  | CLA  | B     | 811 | -    | 64,68,73     | 2.32 | 23 (35%) | 76,107,113  | 2.55 | 26 (34%) |
| 16  | LHG  | A     | 850 | -    | 48,48,48     | 0.90 | 2 (4%)   | 51,54,54    | 1.00 | 4 (7%)   |
| 12  | CLA  | B     | 802 | -    | 69,73,73     | 2.18 | 22 (31%) | 82,113,113  | 2.71 | 31 (37%) |
| 12  | CLA  | b     | 803 | -    | 69,73,73     | 2.27 | 22 (31%) | 82,113,113  | 2.56 | 27 (32%) |
| 12  | CLA  | a     | 841 | 20   | 69,73,73     | 2.18 | 21 (30%) | 82,113,113  | 2.42 | 28 (34%) |
| 15  | BCR  | P     | 204 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.51 | 23 (41%) |
| 12  | CLA  | G     | 816 | -    | 49,53,73     | 2.55 | 23 (46%) | 58,89,113   | 2.85 | 25 (43%) |
| 12  | CLA  | S     | 203 | 10   | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.60 | 27 (32%) |
| 12  | CLA  | H     | 837 | 20   | 69,73,73     | 2.29 | 23 (33%) | 82,113,113  | 2.54 | 26 (31%) |
| 12  | CLA  | G     | 815 | -    | 49,53,73     | 2.53 | 22 (44%) | 58,89,113   | 2.85 | 25 (43%) |
| 15  | BCR  | J     | 101 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.56 | 22 (39%) |
| 12  | CLA  | a     | 840 | 1    | 54,58,73     | 2.54 | 22 (40%) | 64,95,113   | 2.72 | 27 (42%) |
| 12  | CLA  | a     | 819 | 1    | 49,53,73     | 2.49 | 22 (44%) | 58,89,113   | 2.86 | 26 (44%) |
| 15  | BCR  | f     | 204 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.44 | 22 (39%) |
| 12  | CLA  | G     | 838 | 1    | 49,53,73     | 2.55 | 22 (44%) | 58,89,113   | 2.90 | 26 (44%) |
| 12  | CLA  | b     | 805 | 3    | 69,73,73     | 2.21 | 22 (31%) | 82,113,113  | 2.57 | 29 (35%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | A     | 820 | -    | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.66 | 30 (36%) |
| 12  | CLA  | b     | 815 | -    | 64,68,73     | 2.25 | 22 (34%) | 76,107,113  | 2.73 | 27 (35%) |
| 15  | BCR  | J     | 104 | -    | 41,41,41     | 2.54 | 6 (14%)  | 56,56,56    | 6.56 | 23 (41%) |
| 15  | BCR  | H     | 841 | -    | 41,41,41     | 2.62 | 6 (14%)  | 56,56,56    | 6.61 | 20 (35%) |
| 12  | CLA  | B     | 831 | -    | 49,53,73     | 2.59 | 22 (44%) | 58,89,113   | 2.71 | 24 (41%) |
| 12  | CLA  | G     | 806 | -    | 69,73,73     | 2.17 | 21 (30%) | 82,113,113  | 2.61 | 26 (31%) |
| 12  | CLA  | a     | 820 | -    | 69,73,73     | 2.27 | 23 (33%) | 82,113,113  | 2.37 | 26 (31%) |
| 15  | BCR  | B     | 841 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.61 | 25 (44%) |
| 17  | 45D  | T     | 101 | -    | 43,43,43     | 4.00 | 19 (44%) | 54,60,60    | 7.84 | 31 (57%) |
| 12  | CLA  | H     | 810 | 3    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 2.82 | 24 (41%) |
| 15  | BCR  | H     | 844 | -    | 25,25,41     | 2.21 | 2 (8%)   | 33,33,56    | 7.59 | 18 (54%) |
| 12  | CLA  | G     | 813 | 1    | 54,58,73     | 2.51 | 23 (42%) | 64,95,113   | 2.91 | 28 (43%) |
| 12  | CLA  | b     | 819 | -    | 49,53,73     | 2.55 | 22 (44%) | 58,89,113   | 2.81 | 23 (39%) |
| 15  | BCR  | A     | 849 | -    | 41,41,41     | 2.63 | 6 (14%)  | 56,56,56    | 6.81 | 25 (44%) |
| 16  | LHG  | G     | 854 | -    | 48,48,48     | 0.94 | 2 (4%)   | 51,54,54    | 3.78 | 6 (11%)  |
| 12  | CLA  | A     | 830 | 1    | 54,58,73     | 2.52 | 22 (40%) | 64,95,113   | 2.83 | 30 (46%) |
| 12  | CLA  | H     | 825 | -    | 69,73,73     | 2.18 | 21 (30%) | 82,113,113  | 2.44 | 28 (34%) |
| 12  | CLA  | H     | 808 | 3    | 69,73,73     | 2.26 | 21 (30%) | 82,113,113  | 2.41 | 27 (32%) |
| 12  | CLA  | B     | 804 | -    | 69,73,73     | 2.17 | 21 (30%) | 82,113,113  | 2.60 | 26 (31%) |
| 14  | SF4  | K     | 101 | 4    | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | G     | 804 | 1    | 69,73,73     | 2.25 | 23 (33%) | 82,113,113  | 2.50 | 29 (35%) |
| 15  | BCR  | J     | 102 | -    | 41,41,41     | 2.65 | 6 (14%)  | 56,56,56    | 6.86 | 19 (33%) |
| 12  | CLA  | l     | 204 | 10   | 59,63,73     | 2.41 | 21 (35%) | 70,101,113  | 2.65 | 25 (35%) |
| 12  | CLA  | H     | 813 | -    | 49,53,73     | 2.48 | 22 (44%) | 58,89,113   | 3.02 | 26 (44%) |
| 12  | CLA  | B     | 803 | -    | 69,73,73     | 2.23 | 24 (34%) | 82,113,113  | 2.68 | 28 (34%) |
| 12  | CLA  | A     | 837 | 1    | 69,73,73     | 2.21 | 23 (33%) | 82,113,113  | 2.58 | 30 (36%) |
| 15  | BCR  | a     | 845 | -    | 41,41,41     | 2.65 | 6 (14%)  | 56,56,56    | 6.65 | 23 (41%) |
| 12  | CLA  | G     | 826 | 20   | 59,63,73     | 2.41 | 21 (35%) | 70,101,113  | 2.68 | 32 (45%) |
| 12  | CLA  | b     | 832 | 3    | 64,68,73     | 2.31 | 22 (34%) | 76,107,113  | 2.58 | 28 (36%) |
| 15  | BCR  | b     | 841 | -    | 41,41,41     | 2.55 | 6 (14%)  | 56,56,56    | 6.66 | 26 (46%) |
| 12  | CLA  | G     | 810 | 1    | 49,53,73     | 2.54 | 22 (44%) | 58,89,113   | 2.86 | 25 (43%) |
| 15  | BCR  | A     | 847 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.75 | 27 (48%) |
| 12  | CLA  | G     | 833 | 1    | 69,73,73     | 2.22 | 21 (30%) | 82,113,113  | 2.42 | 27 (32%) |
| 12  | CLA  | a     | 837 | 1    | 69,73,73     | 2.21 | 23 (33%) | 82,113,113  | 2.61 | 30 (36%) |
| 15  | BCR  | I     | 101 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.86 | 21 (37%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | G     | 831 | 1    | 54,58,73     | 2.54 | 22 (40%) | 64,95,113   | 2.70 | 30 (46%) |
| 12  | CLA  | b     | 826 | 3    | 69,73,73     | 2.36 | 21 (30%) | 82,113,113  | 2.55 | 30 (36%) |
| 12  | CLA  | A     | 828 | -    | 69,73,73     | 2.28 | 22 (31%) | 82,113,113  | 2.28 | 27 (32%) |
| 12  | CLA  | G     | 855 | 20   | 69,73,73     | 2.27 | 23 (33%) | 82,113,113  | 2.57 | 28 (34%) |
| 12  | CLA  | H     | 819 | -    | 49,53,73     | 2.59 | 23 (46%) | 58,89,113   | 2.83 | 24 (41%) |
| 12  | CLA  | H     | 805 | 3    | 69,73,73     | 2.24 | 24 (34%) | 82,113,113  | 2.59 | 29 (35%) |
| 12  | CLA  | A     | 802 | 20   | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.26 | 26 (31%) |
| 12  | CLA  | A     | 827 | 1    | 64,68,73     | 2.28 | 21 (32%) | 76,107,113  | 2.59 | 29 (38%) |
| 15  | BCR  | G     | 846 | -    | 41,41,41     | 2.63 | 6 (14%)  | 56,56,56    | 6.69 | 22 (39%) |
| 13  | 1L3  | H     | 840 | -    | 34,34,34     | 2.70 | 13 (38%) | 43,45,45    | 1.46 | 8 (18%)  |
| 12  | CLA  | A     | 833 | -    | 69,73,73     | 2.20 | 22 (31%) | 82,113,113  | 2.49 | 28 (34%) |
| 12  | CLA  | b     | 834 | 3    | 49,53,73     | 2.50 | 22 (44%) | 58,89,113   | 2.95 | 23 (39%) |
| 12  | CLA  | H     | 821 | -    | 49,53,73     | 2.50 | 21 (42%) | 58,89,113   | 2.83 | 26 (44%) |
| 12  | CLA  | A     | 855 | -    | 69,73,73     | 2.15 | 23 (33%) | 82,113,113  | 2.70 | 30 (36%) |
| 12  | CLA  | b     | 825 | -    | 69,73,73     | 2.29 | 22 (31%) | 82,113,113  | 2.17 | 25 (30%) |
| 12  | CLA  | H     | 839 | -    | 69,73,73     | 2.21 | 23 (33%) | 82,113,113  | 2.59 | 31 (37%) |
| 12  | CLA  | G     | 805 | 12,1 | 59,63,73     | 2.40 | 24 (40%) | 70,101,113  | 2.80 | 31 (44%) |
| 12  | CLA  | G     | 836 | 1    | 54,58,73     | 2.61 | 24 (44%) | 64,95,113   | 2.89 | 27 (42%) |
| 12  | CLA  | H     | 834 | 20   | 64,68,73     | 2.30 | 22 (34%) | 76,107,113  | 2.56 | 25 (32%) |
| 15  | BCR  | H     | 846 | -    | 41,41,41     | 2.59 | 6 (14%)  | 56,56,56    | 6.68 | 19 (33%) |
| 12  | CLA  | A     | 806 | 1    | 69,73,73     | 2.17 | 21 (30%) | 82,113,113  | 2.64 | 25 (30%) |
| 12  | CLA  | A     | 821 | 1    | 49,53,73     | 2.55 | 23 (46%) | 58,89,113   | 2.91 | 23 (39%) |
| 12  | CLA  | a     | 821 | -    | 49,53,73     | 2.55 | 23 (46%) | 58,89,113   | 2.91 | 24 (41%) |
| 12  | CLA  | H     | 832 | -    | 49,53,73     | 2.52 | 22 (44%) | 58,89,113   | 2.71 | 24 (41%) |
| 12  | CLA  | A     | 813 | -    | 49,53,73     | 2.60 | 22 (44%) | 58,89,113   | 2.96 | 26 (44%) |
| 15  | BCR  | a     | 847 | -    | 41,41,41     | 2.66 | 6 (14%)  | 56,56,56    | 6.76 | 26 (46%) |
| 16  | LHG  | G     | 851 | -    | 48,48,48     | 0.91 | 2 (4%)   | 51,54,54    | 1.05 | 3 (5%)   |
| 12  | CLA  | L     | 205 | 10   | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.61 | 27 (32%) |
| 12  | CLA  | B     | 806 | 3    | 69,73,73     | 2.19 | 21 (30%) | 82,113,113  | 2.75 | 29 (35%) |
| 12  | CLA  | B     | 838 | -    | 69,73,73     | 2.22 | 23 (33%) | 82,113,113  | 2.59 | 31 (37%) |
| 12  | CLA  | G     | 840 | 1    | 54,58,73     | 2.54 | 22 (40%) | 64,95,113   | 2.70 | 26 (40%) |
| 12  | CLA  | b     | 807 | -    | 69,73,73     | 2.18 | 22 (31%) | 82,113,113  | 2.52 | 27 (32%) |
| 15  | BCR  | a     | 852 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.46 | 20 (35%) |
| 13  | 1L3  | A     | 842 | -    | 34,34,34     | 2.63 | 14 (41%) | 43,45,45    | 1.50 | 11 (25%) |
| 14  | SF4  | a     | 843 | 3,1  | 0,12,12      | -    | -        | -           | -    | -        |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | a     | 854 | 20   | 69,73,73     | 2.26 | 24 (34%) | 82,113,113  | 2.55 | 30 (36%) |
| 15  | BCR  | b     | 839 | -    | 41,41,41     | 2.68 | 6 (14%)  | 56,56,56    | 6.58 | 20 (35%) |
| 12  | CLA  | H     | 820 | -    | 49,53,73     | 2.54 | 22 (44%) | 58,89,113   | 2.85 | 25 (43%) |
| 14  | SF4  | C     | 102 | 4    | 0,12,12      | -    | -        | -           |      |          |
| 15  | BCR  | b     | 843 | -    | 41,41,41     | 2.63 | 6 (14%)  | 56,56,56    | 6.84 | 24 (42%) |
| 12  | CLA  | H     | 803 | -    | 69,73,73     | 2.26 | 22 (31%) | 82,113,113  | 2.53 | 26 (31%) |
| 12  | CLA  | G     | 817 | 1    | 54,58,73     | 2.51 | 23 (42%) | 64,95,113   | 2.79 | 32 (50%) |
| 12  | CLA  | A     | 838 | 1    | 49,53,73     | 2.55 | 22 (44%) | 58,89,113   | 2.92 | 27 (46%) |
| 11  | CL0  | a     | 801 | 1    | 69,73,73     | 2.32 | 20 (28%) | 82,113,113  | 2.49 | 33 (40%) |
| 12  | CLA  | b     | 848 | 16   | 64,68,73     | 2.29 | 21 (32%) | 76,107,113  | 2.57 | 25 (32%) |
| 12  | CLA  | a     | 813 | -    | 49,53,73     | 2.52 | 23 (46%) | 58,89,113   | 2.83 | 26 (44%) |
| 12  | CLA  | L     | 202 | 3    | 69,73,73     | 2.25 | 21 (30%) | 82,113,113  | 2.40 | 27 (32%) |
| 15  | BCR  | B     | 845 | -    | 41,41,41     | 2.58 | 6 (14%)  | 56,56,56    | 6.68 | 18 (32%) |
| 12  | CLA  | G     | 835 | 1    | 49,53,73     | 2.52 | 23 (46%) | 58,89,113   | 2.84 | 25 (43%) |
| 12  | CLA  | G     | 823 | 1    | 54,58,73     | 2.56 | 24 (44%) | 64,95,113   | 2.76 | 24 (37%) |
| 15  | BCR  | A     | 852 | -    | 41,41,41     | 2.70 | 6 (14%)  | 56,56,56    | 6.43 | 20 (35%) |
| 12  | CLA  | a     | 814 | -    | 49,53,73     | 2.53 | 21 (42%) | 58,89,113   | 2.82 | 24 (41%) |
| 15  | BCR  | F     | 202 | -    | 41,41,41     | 2.79 | 6 (14%)  | 56,56,56    | 6.76 | 23 (41%) |
| 12  | CLA  | B     | 823 | 3    | 69,73,73     | 2.22 | 21 (30%) | 82,113,113  | 2.50 | 32 (39%) |
| 15  | BCR  | l     | 201 | -    | 41,41,41     | 2.67 | 6 (14%)  | 56,56,56    | 6.52 | 24 (42%) |
| 12  | CLA  | H     | 835 | 3    | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.43 | 26 (31%) |
| 12  | CLA  | H     | 824 | 3    | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.51 | 32 (39%) |
| 12  | CLA  | H     | 827 | 3    | 69,73,73     | 2.31 | 22 (31%) | 82,113,113  | 2.74 | 34 (41%) |
| 12  | CLA  | l     | 205 | 10   | 69,73,73     | 2.19 | 21 (30%) | 82,113,113  | 2.63 | 27 (32%) |
| 12  | CLA  | G     | 811 | 12,1 | 54,58,73     | 2.49 | 24 (44%) | 64,95,113   | 2.97 | 28 (43%) |
| 12  | CLA  | G     | 824 | -    | 59,63,73     | 2.39 | 23 (38%) | 70,101,113  | 2.65 | 25 (35%) |
| 12  | CLA  | a     | 824 | 20   | 69,73,73     | 2.26 | 23 (33%) | 82,113,113  | 2.48 | 32 (39%) |
| 12  | CLA  | B     | 827 | 3    | 49,53,73     | 2.58 | 21 (42%) | 58,89,113   | 2.70 | 24 (41%) |
| 12  | CLA  | a     | 812 | -    | 54,58,73     | 2.53 | 23 (42%) | 64,95,113   | 2.87 | 29 (45%) |
| 12  | CLA  | B     | 830 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.36 | 27 (32%) |
| 12  | CLA  | B     | 834 | 3    | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.48 | 28 (34%) |
| 12  | CLA  | a     | 826 | 1    | 69,73,73     | 2.23 | 23 (33%) | 82,113,113  | 2.57 | 28 (34%) |
| 12  | CLA  | b     | 823 | 3    | 69,73,73     | 2.22 | 21 (30%) | 82,113,113  | 2.49 | 30 (36%) |
| 12  | CLA  | R     | 103 | -    | 49,53,73     | 2.58 | 23 (46%) | 58,89,113   | 2.78 | 23 (39%) |
| 15  | BCR  | A     | 844 | -    | 41,41,41     | 2.60 | 6 (14%)  | 56,56,56    | 6.59 | 21 (37%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | H     | 828 | 3    | 49,53,73     | 2.56 | 21 (42%) | 58,89,113   | 2.87 | 24 (41%) |
| 12  | CLA  | H     | 811 | 3    | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.61 | 32 (39%) |
| 12  | CLA  | G     | 807 | 1    | 69,73,73     | 2.16 | 22 (31%) | 82,113,113  | 2.63 | 24 (29%) |
| 12  | CLA  | G     | 825 | 20   | 69,73,73     | 2.28 | 23 (33%) | 82,113,113  | 2.37 | 30 (36%) |
| 12  | CLA  | a     | 825 | 20   | 59,63,73     | 2.42 | 23 (38%) | 70,101,113  | 2.68 | 28 (40%) |
| 12  | CLA  | A     | 808 | 1    | 54,58,73     | 2.54 | 23 (42%) | 64,95,113   | 2.88 | 25 (39%) |
| 12  | CLA  | B     | 824 | -    | 69,73,73     | 2.18 | 21 (30%) | 82,113,113  | 2.41 | 29 (35%) |
| 12  | CLA  | l     | 206 | 20   | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.46 | 24 (29%) |
| 15  | BCR  | R     | 101 | -    | 41,41,41     | 2.67 | 6 (14%)  | 56,56,56    | 6.58 | 23 (41%) |
| 12  | CLA  | H     | 818 | -    | 49,53,73     | 2.54 | 22 (44%) | 58,89,113   | 2.84 | 23 (39%) |
| 12  | CLA  | a     | 832 | 1    | 69,73,73     | 2.25 | 22 (31%) | 82,113,113  | 2.33 | 26 (31%) |
| 12  | CLA  | a     | 828 | -    | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.31 | 30 (36%) |
| 15  | BCR  | j     | 103 | -    | 41,41,41     | 2.65 | 6 (14%)  | 56,56,56    | 6.80 | 16 (28%) |
| 12  | CLA  | a     | 818 | -    | 69,73,73     | 2.22 | 24 (34%) | 82,113,113  | 2.54 | 28 (34%) |
| 12  | CLA  | A     | 834 | -    | 69,73,73     | 2.24 | 23 (33%) | 82,113,113  | 2.43 | 27 (32%) |
| 12  | CLA  | b     | 835 | 20   | 69,73,73     | 2.28 | 23 (33%) | 82,113,113  | 2.49 | 29 (35%) |
| 12  | CLA  | B     | 808 | 3    | 49,53,73     | 2.56 | 23 (46%) | 58,89,113   | 2.84 | 27 (46%) |
| 12  | CLA  | B     | 822 | 20   | 69,73,73     | 2.26 | 23 (33%) | 82,113,113  | 2.44 | 27 (32%) |
| 12  | CLA  | a     | 802 | 20   | 69,73,73     | 2.23 | 20 (28%) | 82,113,113  | 2.26 | 27 (32%) |
| 12  | CLA  | A     | 817 | -    | 59,63,73     | 2.52 | 22 (37%) | 70,101,113  | 2.66 | 32 (45%) |
| 12  | CLA  | A     | 805 | -    | 69,73,73     | 2.19 | 23 (33%) | 82,113,113  | 2.64 | 28 (34%) |
| 12  | CLA  | G     | 822 | 1    | 49,53,73     | 2.56 | 23 (46%) | 58,89,113   | 2.90 | 24 (41%) |
| 15  | BCR  | A     | 848 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.77 | 20 (35%) |
| 12  | CLA  | a     | 805 | 1    | 69,73,73     | 2.19 | 23 (33%) | 82,113,113  | 2.55 | 27 (32%) |
| 18  | LMG  | B     | 846 | -    | 55,55,55     | 1.48 | 8 (14%)  | 63,63,63    | 1.12 | 3 (4%)   |
| 15  | BCR  | G     | 853 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.40 | 20 (35%) |
| 12  | CLA  | b     | 829 | 3    | 69,73,73     | 2.26 | 23 (33%) | 82,113,113  | 2.57 | 27 (32%) |
| 12  | CLA  | b     | 833 | 3    | 69,73,73     | 2.21 | 23 (33%) | 82,113,113  | 2.48 | 30 (36%) |
| 15  | BCR  | i     | 101 | -    | 41,41,41     | 2.60 | 6 (14%)  | 56,56,56    | 6.97 | 21 (37%) |
| 15  | BCR  | H     | 843 | -    | 41,41,41     | 2.57 | 6 (14%)  | 56,56,56    | 6.64 | 24 (42%) |
| 12  | CLA  | H     | 804 | -    | 69,73,73     | 2.18 | 21 (30%) | 82,113,113  | 2.65 | 25 (30%) |
| 12  | CLA  | b     | 828 | 3    | 49,53,73     | 2.55 | 24 (48%) | 58,89,113   | 2.83 | 26 (44%) |
| 15  | BCR  | A     | 846 | -    | 41,41,41     | 2.63 | 6 (14%)  | 56,56,56    | 6.91 | 19 (33%) |
| 12  | CLA  | G     | 808 | 1    | 69,73,73     | 2.17 | 22 (31%) | 82,113,113  | 2.60 | 27 (32%) |
| 12  | CLA  | a     | 809 | 1    | 49,53,73     | 2.49 | 21 (42%) | 58,89,113   | 2.89 | 25 (43%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | H     | 826 | -    | 69,73,73     | 2.29 | 22 (31%) | 82,113,113  | 2.09 | 26 (31%) |
| 12  | CLA  | b     | 836 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.67 | 32 (39%) |
| 12  | CLA  | b     | 816 | -    | 69,73,73     | 2.23 | 24 (34%) | 82,113,113  | 2.33 | 28 (34%) |
| 16  | LHG  | a     | 851 | 12   | 26,26,48     | 1.25 | 2 (7%)   | 29,32,54    | 1.25 | 3 (10%)  |
| 12  | CLA  | a     | 833 | -    | 69,73,73     | 2.21 | 22 (31%) | 82,113,113  | 2.49 | 28 (34%) |
| 12  | CLA  | G     | 829 | 1    | 69,73,73     | 2.28 | 23 (33%) | 82,113,113  | 2.27 | 26 (31%) |
| 12  | CLA  | A     | 814 | -    | 49,53,73     | 2.54 | 22 (44%) | 58,89,113   | 2.78 | 25 (43%) |
| 15  | BCR  | a     | 849 | -    | 41,41,41     | 2.64 | 6 (14%)  | 56,56,56    | 6.77 | 26 (46%) |
| 12  | CLA  | a     | 829 | 1    | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.38 | 26 (31%) |
| 15  | BCR  | Q     | 102 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.73 | 17 (30%) |
| 12  | CLA  | H     | 836 | 3    | 49,53,73     | 2.49 | 22 (44%) | 58,89,113   | 2.95 | 23 (39%) |
| 12  | CLA  | H     | 815 | 3    | 59,63,73     | 2.39 | 21 (35%) | 70,101,113  | 2.69 | 28 (40%) |
| 12  | CLA  | a     | 836 | 1    | 54,58,73     | 2.64 | 24 (44%) | 64,95,113   | 2.95 | 31 (48%) |
| 15  | BCR  | P     | 202 | -    | 41,41,41     | 2.72 | 6 (14%)  | 56,56,56    | 6.71 | 23 (41%) |
| 12  | CLA  | B     | 837 | 3    | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.68 | 31 (37%) |
| 15  | BCR  | i     | 102 | -    | 41,41,41     | 2.71 | 6 (14%)  | 56,56,56    | 6.73 | 19 (33%) |
| 15  | BCR  | A     | 845 | -    | 41,41,41     | 2.62 | 6 (14%)  | 56,56,56    | 6.64 | 22 (39%) |
| 12  | CLA  | B     | 829 | 3    | 69,73,73     | 2.26 | 25 (36%) | 82,113,113  | 2.54 | 26 (31%) |
| 12  | CLA  | H     | 823 | 20   | 69,73,73     | 2.25 | 23 (33%) | 82,113,113  | 2.47 | 27 (32%) |
| 12  | CLA  | b     | 818 | -    | 49,53,73     | 2.57 | 23 (46%) | 58,89,113   | 2.85 | 24 (41%) |
| 12  | CLA  | A     | 840 | 1    | 54,58,73     | 2.54 | 21 (38%) | 64,95,113   | 2.66 | 26 (40%) |
| 12  | CLA  | b     | 812 | -    | 49,53,73     | 2.54 | 21 (42%) | 58,89,113   | 3.01 | 25 (43%) |
| 11  | CL0  | G     | 801 | 1    | 69,73,73     | 2.25 | 21 (30%) | 82,113,113  | 2.35 | 28 (34%) |
| 12  | CLA  | H     | 812 | 3    | 64,68,73     | 2.33 | 24 (37%) | 76,107,113  | 2.57 | 26 (34%) |
| 14  | SF4  | G     | 844 | 3,1  | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | P     | 201 | 20   | 69,73,73     | 2.27 | 21 (30%) | 82,113,113  | 2.34 | 25 (30%) |
| 18  | LMG  | b     | 845 | -    | 55,55,55     | 1.49 | 8 (14%)  | 63,63,63    | 1.11 | 3 (4%)   |
| 14  | SF4  | c     | 101 | 4    | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | B     | 821 | 20   | 69,73,73     | 2.19 | 22 (31%) | 82,113,113  | 2.54 | 31 (37%) |
| 15  | BCR  | R     | 102 | -    | 41,41,41     | 2.63 | 6 (14%)  | 56,56,56    | 6.83 | 17 (30%) |
| 12  | CLA  | b     | 837 | -    | 69,73,73     | 2.20 | 23 (33%) | 82,113,113  | 2.60 | 30 (36%) |
| 12  | CLA  | G     | 834 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.45 | 28 (34%) |
| 14  | SF4  | C     | 101 | 4    | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | H     | 833 | -    | 49,53,73     | 2.57 | 22 (44%) | 58,89,113   | 2.82 | 24 (41%) |
| 12  | CLA  | A     | 815 | -    | 49,53,73     | 2.52 | 23 (46%) | 58,89,113   | 2.90 | 25 (43%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 16  | LHG  | A     | 853 | -    | 48,48,48     | 0.93 | 2 (4%)   | 51,54,54    | 3.77 | 6 (11%)  |
| 12  | CLA  | a     | 835 | 1    | 49,53,73     | 2.51 | 23 (46%) | 58,89,113   | 2.85 | 24 (41%) |
| 12  | CLA  | j     | 104 | -    | 49,53,73     | 2.60 | 23 (46%) | 58,89,113   | 2.74 | 24 (41%) |
| 15  | BCR  | Q     | 101 | -    | 41,41,41     | 2.62 | 6 (14%)  | 56,56,56    | 6.90 | 22 (39%) |
| 15  | BCR  | H     | 842 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.63 | 25 (44%) |
| 12  | CLA  | B     | 815 | -    | 64,68,73     | 2.30 | 24 (37%) | 76,107,113  | 2.67 | 26 (34%) |
| 12  | CLA  | B     | 807 | 3    | 69,73,73     | 2.19 | 21 (30%) | 82,113,113  | 2.44 | 30 (36%) |
| 14  | SF4  | c     | 102 | 4    | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | f     | 201 | 20   | 69,73,73     | 2.27 | 22 (31%) | 82,113,113  | 2.29 | 26 (31%) |
| 15  | BCR  | a     | 846 | -    | 41,41,41     | 2.68 | 6 (14%)  | 56,56,56    | 6.62 | 22 (39%) |
| 12  | CLA  | j     | 102 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.34 | 29 (35%) |
| 12  | CLA  | b     | 827 | 3    | 49,53,73     | 2.58 | 22 (44%) | 58,89,113   | 2.79 | 24 (41%) |
| 14  | SF4  | A     | 843 | 3,1  | 0,12,12      | -    | -        | -           | -    | -        |
| 12  | CLA  | F     | 203 | -    | 49,53,73     | 2.57 | 23 (46%) | 58,89,113   | 4.48 | 26 (44%) |
| 12  | CLA  | B     | 820 | 3    | 49,53,73     | 2.53 | 22 (44%) | 58,89,113   | 2.79 | 25 (43%) |
| 12  | CLA  | b     | 820 | -    | 49,53,73     | 2.51 | 22 (44%) | 58,89,113   | 2.83 | 23 (39%) |
| 12  | CLA  | a     | 817 | -    | 59,63,73     | 2.45 | 25 (42%) | 70,101,113  | 2.75 | 28 (40%) |
| 12  | CLA  | G     | 832 | 1    | 69,73,73     | 2.26 | 24 (34%) | 82,113,113  | 2.33 | 27 (32%) |
| 15  | BCR  | b     | 842 | -    | 25,25,41     | 2.19 | 2 (8%)   | 33,33,56    | 7.60 | 18 (54%) |
| 19  | LMT  | H     | 848 | -    | 36,36,36     | 1.18 | 4 (11%)  | 47,47,47    | 0.96 | 1 (2%)   |
| 12  | CLA  | A     | 854 | 20   | 69,73,73     | 2.31 | 24 (34%) | 82,113,113  | 2.57 | 33 (40%) |
| 12  | CLA  | A     | 807 | 1    | 69,73,73     | 2.20 | 21 (30%) | 82,113,113  | 2.63 | 28 (34%) |
| 12  | CLA  | H     | 850 | 16   | 64,68,73     | 2.30 | 22 (34%) | 76,107,113  | 2.53 | 28 (36%) |
| 12  | CLA  | a     | 816 | 1    | 54,58,73     | 2.52 | 20 (37%) | 64,95,113   | 2.72 | 31 (48%) |
| 12  | CLA  | a     | 815 | -    | 49,53,73     | 2.56 | 22 (44%) | 58,89,113   | 2.82 | 23 (39%) |
| 16  | LHG  | a     | 853 | -    | 48,48,48     | 0.94 | 2 (4%)   | 51,54,54    | 1.09 | 3 (5%)   |
| 15  | BCR  | G     | 845 | -    | 41,41,41     | 2.61 | 6 (14%)  | 56,56,56    | 6.63 | 21 (37%) |
| 11  | CL0  | A     | 801 | 1    | 69,73,73     | 2.23 | 21 (30%) | 82,113,113  | 2.44 | 29 (35%) |
| 12  | CLA  | l     | 202 | 3    | 69,73,73     | 2.26 | 23 (33%) | 82,113,113  | 2.41 | 25 (30%) |
| 12  | CLA  | L     | 204 | 10   | 59,63,73     | 2.41 | 21 (35%) | 70,101,113  | 2.68 | 24 (34%) |
| 12  | CLA  | a     | 806 | -    | 69,73,73     | 2.16 | 20 (28%) | 82,113,113  | 2.63 | 27 (32%) |
| 12  | CLA  | G     | 830 | -    | 69,73,73     | 2.23 | 22 (31%) | 82,113,113  | 2.40 | 25 (30%) |
| 15  | BCR  | f     | 202 | -    | 41,41,41     | 2.80 | 6 (14%)  | 56,56,56    | 6.66 | 24 (42%) |
| 15  | BCR  | B     | 844 | -    | 41,41,41     | 2.64 | 6 (14%)  | 56,56,56    | 6.82 | 25 (44%) |
| 15  | BCR  | S     | 201 | -    | 41,41,41     | 2.80 | 6 (14%)  | 56,56,56    | 6.51 | 23 (41%) |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 12  | CLA  | A     | 804 | 12   | 59,63,73     | 2.42 | 23 (38%) | 70,101,113  | 2.81 | 30 (42%) |
| 12  | CLA  | G     | 821 | -    | 69,73,73     | 2.26 | 23 (33%) | 82,113,113  | 2.41 | 30 (36%) |
| 15  | BCR  | l     | 203 | -    | 41,41,41     | 2.79 | 6 (14%)  | 56,56,56    | 6.50 | 22 (39%) |
| 12  | CLA  | B     | 826 | 3    | 69,73,73     | 2.33 | 22 (31%) | 82,113,113  | 2.57 | 31 (37%) |
| 12  | CLA  | G     | 837 | 1    | 69,73,73     | 2.20 | 23 (33%) | 82,113,113  | 2.59 | 31 (37%) |
| 12  | CLA  | B     | 801 | -    | 64,68,73     | 2.30 | 21 (32%) | 76,107,113  | 2.60 | 27 (35%) |
| 15  | BCR  | F     | 204 | -    | 41,41,41     | 2.63 | 6 (14%)  | 56,56,56    | 6.47 | 22 (39%) |
| 12  | CLA  | b     | 801 | -    | 64,68,73     | 2.30 | 22 (34%) | 76,107,113  | 2.58 | 27 (35%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | A     | 803 | 1    | -       | 14/39/115/115 | -       |
| 12  | CLA  | G     | 802 | -    | -       | 7/33/109/115  | -       |
| 12  | CLA  | B     | 810 | 3    | -       | 27/39/115/115 | -       |
| 15  | BCR  | b     | 847 | -    | -       | 7/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 842 | 16   | -       | 13/33/109/115 | -       |
| 12  | CLA  | A     | 841 | 20   | -       | 17/39/115/115 | -       |
| 12  | CLA  | B     | 814 | -    | -       | 9/27/103/115  | -       |
| 12  | CLA  | a     | 804 | 12   | -       | 13/27/103/115 | -       |
| 12  | CLA  | A     | 810 | 12,1 | -       | 7/21/97/115   | -       |
| 12  | CLA  | A     | 812 | -    | -       | 10/21/97/115  | -       |
| 12  | CLA  | A     | 826 | 1    | -       | 15/39/115/115 | -       |
| 12  | CLA  | b     | 802 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | a     | 810 | 12,1 | -       | 9/21/97/115   | -       |
| 12  | CLA  | B     | 819 | -    | -       | 7/15/91/115   | -       |
| 12  | CLA  | H     | 816 | -    | -       | 10/33/109/115 | -       |
| 12  | CLA  | S     | 204 | 20   | -       | 10/39/115/115 | -       |
| 12  | CLA  | G     | 827 | -    | -       | 16/39/115/115 | -       |
| 12  | CLA  | A     | 825 | 20   | -       | 5/27/103/115  | -       |
| 12  | CLA  | B     | 835 | 3    | -       | 7/15/91/115   | -       |
| 12  | CLA  | b     | 824 | 3    | -       | 22/39/115/115 | -       |
| 12  | CLA  | a     | 855 | -    | -       | 13/39/115/115 | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | a     | 811 | -    | -       | 6/15/91/115   | -       |
| 12  | CLA  | B     | 825 | -    | -       | 11/39/115/115 | -       |
| 15  | BCR  | b     | 840 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 13  | 1L3  | B     | 839 | -    | -       | 5/23/43/43    | 0/2/2/2 |
| 12  | CLA  | L     | 206 | 20   | -       | 10/39/115/115 | -       |
| 12  | CLA  | B     | 809 | 3    | -       | 5/15/91/115   | -       |
| 16  | LHG  | a     | 850 | -    | -       | 26/53/53/53   | -       |
| 12  | CLA  | H     | 806 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | A     | 819 | 1    | -       | 9/15/91/115   | -       |
| 12  | CLA  | B     | 833 | 3    | -       | 15/33/109/115 | -       |
| 12  | CLA  | A     | 836 | 1    | -       | 7/21/97/115   | -       |
| 12  | CLA  | B     | 828 | 3    | -       | 4/15/91/115   | -       |
| 12  | CLA  | H     | 829 | 3    | -       | 4/15/91/115   | -       |
| 12  | CLA  | b     | 811 | -    | -       | 10/33/109/115 | -       |
| 12  | CLA  | J     | 103 | -    | -       | 8/15/91/115   | -       |
| 15  | BCR  | H     | 849 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | B     | 805 | 3    | -       | 17/39/115/115 | -       |
| 12  | CLA  | B     | 836 | 20   | -       | 13/39/115/115 | -       |
| 15  | BCR  | L     | 207 | -    | -       | 10/29/63/63   | 0/2/2/2 |
| 12  | CLA  | b     | 806 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | b     | 813 | 3    | -       | 9/27/103/115  | -       |
| 12  | CLA  | A     | 832 | 1    | -       | 15/39/115/115 | -       |
| 15  | BCR  | G     | 849 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 12  | CLA  | A     | 818 | -    | -       | 15/39/115/115 | -       |
| 12  | CLA  | b     | 831 | 3    | -       | 5/15/91/115   | -       |
| 12  | CLA  | a     | 803 | 1    | -       | 14/39/115/115 | -       |
| 16  | LHG  | A     | 851 | 12   | -       | 14/31/31/53   | -       |
| 12  | CLA  | B     | 832 | 3    | -       | 5/15/91/115   | -       |
| 12  | CLA  | B     | 818 | -    | -       | 3/15/91/115   | -       |
| 12  | CLA  | H     | 831 | -    | -       | 13/39/115/115 | -       |
| 15  | BCR  | L     | 203 | -    | -       | 14/29/63/63   | 0/2/2/2 |
| 18  | LMG  | H     | 847 | -    | -       | 16/50/70/70   | 0/1/1/1 |
| 12  | CLA  | G     | 812 | -    | -       | 6/15/91/115   | -       |
| 12  | CLA  | G     | 839 | 1    | -       | 7/39/115/115  | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | A     | 831 | 1    | -       | 11/27/103/115 | -       |
| 12  | CLA  | A     | 809 | 1    | -       | 7/15/91/115   | -       |
| 19  | LMT  | b     | 846 | -    | -       | 10/21/61/61   | 0/2/2/2 |
| 12  | CLA  | B     | 813 | 3    | -       | 7/27/103/115  | -       |
| 12  | CLA  | H     | 809 | 3    | -       | 3/15/91/115   | -       |
| 12  | CLA  | A     | 823 | -    | -       | 13/27/103/115 | -       |
| 12  | CLA  | b     | 809 | 3    | -       | 2/15/91/115   | -       |
| 12  | CLA  | G     | 820 | 1    | -       | 8/15/91/115   | -       |
| 12  | CLA  | a     | 823 | -    | -       | 11/27/103/115 | -       |
| 12  | CLA  | G     | 819 | -    | -       | 15/39/115/115 | -       |
| 15  | BCR  | G     | 848 | -    | -       | 4/29/63/63    | 0/2/2/2 |
| 12  | CLA  | H     | 814 | 3    | -       | 6/27/103/115  | -       |
| 12  | CLA  | a     | 807 | -    | -       | 22/39/115/115 | -       |
| 12  | CLA  | A     | 835 | -    | -       | 9/15/91/115   | -       |
| 12  | CLA  | H     | 817 | -    | -       | 15/39/115/115 | -       |
| 12  | CLA  | G     | 809 | 1    | -       | 7/21/97/115   | -       |
| 12  | CLA  | F     | 201 | 20   | -       | 13/39/115/115 | -       |
| 15  | BCR  | B     | 842 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | a     | 822 | -    | -       | 6/21/97/115   | -       |
| 12  | CLA  | b     | 821 | 20   | -       | 15/39/115/115 | -       |
| 12  | CLA  | H     | 838 | -    | -       | 20/39/115/115 | -       |
| 15  | BCR  | H     | 845 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 814 | 1    | -       | 4/15/91/115   | -       |
| 19  | LMT  | B     | 847 | -    | -       | 10/21/61/61   | 0/2/2/2 |
| 12  | CLA  | A     | 816 | 1    | -       | 6/21/97/115   | -       |
| 12  | CLA  | b     | 814 | 3    | -       | 8/27/103/115  | -       |
| 12  | CLA  | B     | 817 | 3    | -       | 10/15/91/115  | -       |
| 12  | CLA  | a     | 838 | 1    | -       | 3/15/91/115   | -       |
| 12  | CLA  | b     | 817 | 3    | -       | 10/15/91/115  | -       |
| 17  | 45D  | M     | 101 | -    | -       | 13/29/69/69   | 0/2/2/2 |
| 17  | 45D  | m     | 101 | -    | -       | 13/29/69/69   | 0/2/2/2 |
| 12  | CLA  | B     | 812 | -    | -       | 9/15/91/115   | -       |
| 12  | CLA  | a     | 831 | 1    | -       | 11/27/103/115 | -       |
| 15  | BCR  | j     | 101 | -    | -       | 12/29/63/63   | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | B     | 816 | -    | -       | 15/39/115/115 | -       |
| 15  | BCR  | B     | 843 | -    | -       | 3/18/35/63    | 0/1/1/2 |
| 12  | CLA  | H     | 830 | 3    | -       | 18/39/115/115 | -       |
| 13  | 1L3  | a     | 842 | -    | -       | 5/23/43/43    | 0/2/2/2 |
| 15  | BCR  | G     | 847 | -    | -       | 6/29/63/63    | 0/2/2/2 |
| 15  | BCR  | a     | 848 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 15  | BCR  | b     | 844 | -    | -       | 6/29/63/63    | 0/2/2/2 |
| 13  | 1L3  | b     | 838 | -    | -       | 5/23/43/43    | 0/2/2/2 |
| 12  | CLA  | G     | 841 | 20   | -       | 15/39/115/115 | -       |
| 15  | BCR  | G     | 850 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 15  | BCR  | L     | 201 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | H     | 801 | 1    | -       | 11/27/103/115 | -       |
| 12  | CLA  | A     | 824 | 20   | -       | 18/39/115/115 | -       |
| 14  | SF4  | K     | 102 | 4    | -       | -             | 0/6/5/5 |
| 12  | CLA  | b     | 804 | -    | -       | 18/39/115/115 | -       |
| 12  | CLA  | H     | 802 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | a     | 808 | 1    | -       | 7/21/97/115   | -       |
| 15  | BCR  | a     | 844 | -    | -       | 11/29/63/63   | 0/2/2/2 |
| 12  | CLA  | P     | 203 | -    | -       | 8/15/91/115   | -       |
| 12  | CLA  | b     | 830 | -    | -       | 6/15/91/115   | -       |
| 16  | LHG  | G     | 852 | 12   | -       | 16/31/31/53   | -       |
| 12  | CLA  | H     | 822 | 20   | -       | 16/39/115/115 | -       |
| 12  | CLA  | A     | 839 | 1    | -       | 7/39/115/115  | -       |
| 12  | CLA  | A     | 829 | 1    | -       | 10/39/115/115 | -       |
| 12  | CLA  | G     | 803 | 20   | -       | 8/39/115/115  | -       |
| 12  | CLA  | S     | 202 | 10   | -       | 9/27/103/115  | -       |
| 12  | CLA  | f     | 203 | -    | -       | 8/15/91/115   | -       |
| 12  | CLA  | a     | 839 | 1    | -       | 11/39/115/115 | -       |
| 15  | BCR  | B     | 840 | -    | -       | 10/29/63/63   | 0/2/2/2 |
| 12  | CLA  | a     | 827 | -    | -       | 12/33/109/115 | -       |
| 12  | CLA  | H     | 807 | 3    | -       | 9/39/115/115  | -       |
| 12  | CLA  | a     | 830 | 1    | -       | 10/21/97/115  | -       |
| 12  | CLA  | a     | 834 | -    | -       | 20/39/115/115 | -       |
| 12  | CLA  | b     | 810 | 3    | -       | 25/39/115/115 | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | A     | 811 | -    | -       | 6/15/91/115   | -       |
| 12  | CLA  | A     | 822 | -    | -       | 6/21/97/115   | -       |
| 13  | 1L3  | G     | 843 | -    | -       | 5/23/43/43    | 0/2/2/2 |
| 15  | BCR  | S     | 205 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 828 | -    | -       | 13/33/109/115 | -       |
| 12  | CLA  | G     | 856 | -    | -       | 12/39/115/115 | -       |
| 12  | CLA  | G     | 818 | -    | -       | 15/27/103/115 | -       |
| 12  | CLA  | b     | 808 | 3    | -       | 3/15/91/115   | -       |
| 12  | CLA  | b     | 822 | 20   | -       | 16/39/115/115 | -       |
| 12  | CLA  | B     | 811 | -    | -       | 11/33/109/115 | -       |
| 16  | LHG  | A     | 850 | -    | -       | 30/53/53/53   | -       |
| 12  | CLA  | B     | 802 | -    | -       | 15/39/115/115 | -       |
| 12  | CLA  | b     | 803 | -    | -       | 16/39/115/115 | -       |
| 12  | CLA  | a     | 841 | 20   | -       | 15/39/115/115 | -       |
| 15  | BCR  | P     | 204 | -    | -       | 7/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 816 | -    | -       | 5/15/91/115   | -       |
| 12  | CLA  | S     | 203 | 10   | -       | 14/39/115/115 | -       |
| 12  | CLA  | H     | 837 | 20   | -       | 14/39/115/115 | -       |
| 12  | CLA  | G     | 815 | -    | -       | 7/15/91/115   | -       |
| 15  | BCR  | J     | 101 | -    | -       | 10/29/63/63   | 0/2/2/2 |
| 12  | CLA  | a     | 840 | 1    | -       | 9/21/97/115   | -       |
| 12  | CLA  | a     | 819 | 1    | -       | 8/15/91/115   | -       |
| 15  | BCR  | f     | 204 | -    | -       | 7/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 838 | 1    | -       | 3/15/91/115   | -       |
| 12  | CLA  | b     | 805 | 3    | -       | 20/39/115/115 | -       |
| 12  | CLA  | A     | 820 | -    | -       | 17/39/115/115 | -       |
| 12  | CLA  | b     | 815 | -    | -       | 8/33/109/115  | -       |
| 15  | BCR  | J     | 104 | -    | -       | 5/29/63/63    | 0/2/2/2 |
| 15  | BCR  | H     | 841 | -    | -       | 14/29/63/63   | 0/2/2/2 |
| 12  | CLA  | B     | 831 | -    | -       | 6/15/91/115   | -       |
| 12  | CLA  | G     | 806 | -    | -       | 10/39/115/115 | -       |
| 12  | CLA  | a     | 820 | -    | -       | 15/39/115/115 | -       |
| 15  | BCR  | B     | 841 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 17  | 45D  | T     | 101 | -    | -       | 13/29/69/69   | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | H     | 810 | 3    | -       | 2/15/91/115   | -       |
| 15  | BCR  | H     | 844 | -    | -       | 3/18/35/63    | 0/1/1/2 |
| 12  | CLA  | G     | 813 | 1    | -       | 10/21/97/115  | -       |
| 12  | CLA  | b     | 819 | -    | -       | 7/15/91/115   | -       |
| 15  | BCR  | A     | 849 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 16  | LHG  | G     | 854 | -    | -       | 37/53/53/53   | -       |
| 12  | CLA  | A     | 830 | 1    | -       | 7/21/97/115   | -       |
| 12  | CLA  | H     | 825 | -    | -       | 22/39/115/115 | -       |
| 12  | CLA  | H     | 808 | 3    | -       | 13/39/115/115 | -       |
| 12  | CLA  | B     | 804 | -    | -       | 18/39/115/115 | -       |
| 14  | SF4  | K     | 101 | 4    | -       | -             | 0/6/5/5 |
| 12  | CLA  | G     | 804 | 1    | -       | 15/39/115/115 | -       |
| 15  | BCR  | J     | 102 | -    | -       | 18/29/63/63   | 0/2/2/2 |
| 12  | CLA  | l     | 204 | 10   | -       | 6/27/103/115  | -       |
| 12  | CLA  | H     | 813 | -    | -       | 9/15/91/115   | -       |
| 12  | CLA  | B     | 803 | -    | -       | 17/39/115/115 | -       |
| 12  | CLA  | A     | 837 | 1    | -       | 17/39/115/115 | -       |
| 15  | BCR  | a     | 845 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 826 | 20   | -       | 7/27/103/115  | -       |
| 12  | CLA  | b     | 832 | 3    | -       | 15/33/109/115 | -       |
| 15  | BCR  | b     | 841 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 810 | 1    | -       | 7/15/91/115   | -       |
| 15  | BCR  | A     | 847 | -    | -       | 4/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 833 | 1    | -       | 15/39/115/115 | -       |
| 12  | CLA  | a     | 837 | 1    | -       | 14/39/115/115 | -       |
| 15  | BCR  | I     | 101 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 831 | 1    | -       | 8/21/97/115   | -       |
| 12  | CLA  | b     | 826 | 3    | -       | 10/39/115/115 | -       |
| 12  | CLA  | A     | 828 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | G     | 855 | 20   | -       | 18/39/115/115 | -       |
| 12  | CLA  | H     | 819 | -    | -       | 3/15/91/115   | -       |
| 12  | CLA  | H     | 805 | 3    | -       | 16/39/115/115 | -       |
| 12  | CLA  | A     | 802 | 20   | -       | 8/39/115/115  | -       |
| 12  | CLA  | A     | 827 | 1    | -       | 14/33/109/115 | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 15  | BCR  | G     | 846 | -    | -       | 3/29/63/63    | 0/2/2/2 |
| 13  | 1L3  | H     | 840 | -    | -       | 5/23/43/43    | 0/2/2/2 |
| 12  | CLA  | A     | 833 | -    | -       | 15/39/115/115 | -       |
| 12  | CLA  | b     | 834 | 3    | -       | 7/15/91/115   | -       |
| 12  | CLA  | H     | 821 | -    | -       | 2/15/91/115   | -       |
| 12  | CLA  | A     | 855 | -    | -       | 11/39/115/115 | -       |
| 12  | CLA  | b     | 825 | -    | -       | 12/39/115/115 | -       |
| 12  | CLA  | H     | 839 | -    | -       | 14/39/115/115 | -       |
| 12  | CLA  | G     | 805 | 12,1 | -       | 13/27/103/115 | -       |
| 12  | CLA  | G     | 836 | 1    | -       | 5/21/97/115   | -       |
| 12  | CLA  | H     | 834 | 20   | -       | 15/33/109/115 | -       |
| 15  | BCR  | H     | 846 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | A     | 806 | 1    | -       | 13/39/115/115 | -       |
| 12  | CLA  | A     | 821 | 1    | -       | 9/15/91/115   | -       |
| 12  | CLA  | a     | 821 | -    | -       | 9/15/91/115   | -       |
| 12  | CLA  | H     | 832 | -    | -       | 6/15/91/115   | -       |
| 12  | CLA  | A     | 813 | -    | -       | 2/15/91/115   | -       |
| 15  | BCR  | a     | 847 | -    | -       | 4/29/63/63    | 0/2/2/2 |
| 16  | LHG  | G     | 851 | -    | -       | 31/53/53/53   | -       |
| 12  | CLA  | L     | 205 | 10   | -       | 14/39/115/115 | -       |
| 12  | CLA  | B     | 806 | 3    | -       | 13/39/115/115 | -       |
| 12  | CLA  | B     | 838 | -    | -       | 19/39/115/115 | -       |
| 12  | CLA  | G     | 840 | 1    | -       | 7/21/97/115   | -       |
| 12  | CLA  | b     | 807 | -    | -       | 10/39/115/115 | -       |
| 15  | BCR  | a     | 852 | -    | -       | 13/29/63/63   | 0/2/2/2 |
| 13  | 1L3  | A     | 842 | -    | -       | 5/23/43/43    | 0/2/2/2 |
| 14  | SF4  | a     | 843 | 3,1  | -       | -             | 0/6/5/5 |
| 12  | CLA  | a     | 854 | 20   | -       | 19/39/115/115 | -       |
| 15  | BCR  | b     | 839 | -    | -       | 13/29/63/63   | 0/2/2/2 |
| 12  | CLA  | H     | 820 | -    | -       | 7/15/91/115   | -       |
| 14  | SF4  | C     | 102 | 4    | -       | -             | 0/6/5/5 |
| 15  | BCR  | b     | 843 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | H     | 803 | -    | -       | 17/39/115/115 | -       |
| 12  | CLA  | G     | 817 | 1    | -       | 6/21/97/115   | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | A     | 838 | 1    | -       | 3/15/91/115   | -       |
| 11  | CL0  | a     | 801 | 1    | -       | 8/39/115/115  | -       |
| 12  | CLA  | b     | 848 | 16   | -       | 15/33/109/115 | -       |
| 12  | CLA  | a     | 813 | -    | -       | 2/15/91/115   | -       |
| 12  | CLA  | L     | 202 | 3    | -       | 13/39/115/115 | -       |
| 15  | BCR  | B     | 845 | -    | -       | 6/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 835 | 1    | -       | 9/15/91/115   | -       |
| 12  | CLA  | G     | 823 | 1    | -       | 7/21/97/115   | -       |
| 15  | BCR  | A     | 852 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 12  | CLA  | a     | 814 | -    | -       | 7/15/91/115   | -       |
| 15  | BCR  | F     | 202 | -    | -       | 13/29/63/63   | 0/2/2/2 |
| 12  | CLA  | B     | 823 | 3    | -       | 17/39/115/115 | -       |
| 15  | BCR  | l     | 201 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | H     | 835 | 3    | -       | 12/39/115/115 | -       |
| 12  | CLA  | H     | 824 | 3    | -       | 18/39/115/115 | -       |
| 12  | CLA  | H     | 827 | 3    | -       | 12/39/115/115 | -       |
| 12  | CLA  | l     | 205 | 10   | -       | 13/39/115/115 | -       |
| 12  | CLA  | G     | 811 | 12,1 | -       | 8/21/97/115   | -       |
| 12  | CLA  | G     | 824 | -    | -       | 9/27/103/115  | -       |
| 12  | CLA  | a     | 824 | 20   | -       | 16/39/115/115 | -       |
| 12  | CLA  | B     | 827 | 3    | -       | 6/15/91/115   | -       |
| 12  | CLA  | a     | 812 | -    | -       | 10/21/97/115  | -       |
| 12  | CLA  | B     | 830 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | B     | 834 | 3    | -       | 9/39/115/115  | -       |
| 12  | CLA  | a     | 826 | 1    | -       | 15/39/115/115 | -       |
| 12  | CLA  | b     | 823 | 3    | -       | 16/39/115/115 | -       |
| 12  | CLA  | R     | 103 | -    | -       | 7/15/91/115   | -       |
| 15  | BCR  | A     | 844 | -    | -       | 10/29/63/63   | 0/2/2/2 |
| 12  | CLA  | H     | 828 | 3    | -       | 5/15/91/115   | -       |
| 12  | CLA  | H     | 811 | 3    | -       | 23/39/115/115 | -       |
| 12  | CLA  | G     | 807 | 1    | -       | 13/39/115/115 | -       |
| 12  | CLA  | G     | 825 | 20   | -       | 16/39/115/115 | -       |
| 12  | CLA  | a     | 825 | 20   | -       | 5/27/103/115  | -       |
| 12  | CLA  | A     | 808 | 1    | -       | 7/21/97/115   | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | B     | 824 | -    | -       | 24/39/115/115 | -       |
| 12  | CLA  | l     | 206 | 20   | -       | 11/39/115/115 | -       |
| 15  | BCR  | R     | 101 | -    | -       | 11/29/63/63   | 0/2/2/2 |
| 12  | CLA  | H     | 818 | -    | -       | 10/15/91/115  | -       |
| 12  | CLA  | a     | 832 | 1    | -       | 15/39/115/115 | -       |
| 12  | CLA  | a     | 828 | -    | -       | 11/39/115/115 | -       |
| 15  | BCR  | j     | 103 | -    | -       | 17/29/63/63   | 0/2/2/2 |
| 12  | CLA  | a     | 818 | -    | -       | 17/39/115/115 | -       |
| 12  | CLA  | A     | 834 | -    | -       | 18/39/115/115 | -       |
| 12  | CLA  | b     | 835 | 20   | -       | 13/39/115/115 | -       |
| 12  | CLA  | B     | 808 | 3    | -       | 3/15/91/115   | -       |
| 12  | CLA  | B     | 822 | 20   | -       | 18/39/115/115 | -       |
| 12  | CLA  | a     | 802 | 20   | -       | 10/39/115/115 | -       |
| 12  | CLA  | A     | 817 | -    | -       | 15/27/103/115 | -       |
| 12  | CLA  | A     | 805 | -    | -       | 12/39/115/115 | -       |
| 12  | CLA  | G     | 822 | 1    | -       | 9/15/91/115   | -       |
| 15  | BCR  | A     | 848 | -    | -       | 13/29/63/63   | 0/2/2/2 |
| 12  | CLA  | a     | 805 | 1    | -       | 14/39/115/115 | -       |
| 18  | LMG  | B     | 846 | -    | -       | 18/50/70/70   | 0/1/1/1 |
| 15  | BCR  | G     | 853 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 12  | CLA  | b     | 829 | 3    | -       | 18/39/115/115 | -       |
| 12  | CLA  | b     | 833 | 3    | -       | 11/39/115/115 | -       |
| 15  | BCR  | i     | 101 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 15  | BCR  | H     | 843 | -    | -       | 9/29/63/63    | 0/2/2/2 |
| 12  | CLA  | H     | 804 | -    | -       | 18/39/115/115 | -       |
| 12  | CLA  | b     | 828 | 3    | -       | 4/15/91/115   | -       |
| 15  | BCR  | A     | 846 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | G     | 808 | 1    | -       | 21/39/115/115 | -       |
| 12  | CLA  | a     | 809 | 1    | -       | 7/15/91/115   | -       |
| 12  | CLA  | H     | 826 | -    | -       | 12/39/115/115 | -       |
| 12  | CLA  | b     | 836 | -    | -       | 18/39/115/115 | -       |
| 12  | CLA  | b     | 816 | -    | -       | 15/39/115/115 | -       |
| 16  | LHG  | a     | 851 | 12   | -       | 18/31/31/53   | -       |
| 12  | CLA  | a     | 833 | -    | -       | 15/39/115/115 | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | G     | 829 | 1    | -       | 14/39/115/115 | -       |
| 12  | CLA  | A     | 814 | -    | -       | 7/15/91/115   | -       |
| 15  | BCR  | a     | 849 | -    | -       | 12/29/63/63   | 0/2/2/2 |
| 12  | CLA  | a     | 829 | 1    | -       | 10/39/115/115 | -       |
| 15  | BCR  | Q     | 102 | -    | -       | 11/29/63/63   | 0/2/2/2 |
| 12  | CLA  | H     | 836 | 3    | -       | 5/15/91/115   | -       |
| 12  | CLA  | H     | 815 | 3    | -       | 8/27/103/115  | -       |
| 12  | CLA  | a     | 836 | 1    | -       | 5/21/97/115   | -       |
| 15  | BCR  | P     | 202 | -    | -       | 13/29/63/63   | 0/2/2/2 |
| 12  | CLA  | B     | 837 | 3    | -       | 18/39/115/115 | -       |
| 15  | BCR  | i     | 102 | -    | -       | 11/29/63/63   | 0/2/2/2 |
| 15  | BCR  | A     | 845 | -    | -       | 7/29/63/63    | 0/2/2/2 |
| 12  | CLA  | B     | 829 | 3    | -       | 18/39/115/115 | -       |
| 12  | CLA  | H     | 823 | 20   | -       | 19/39/115/115 | -       |
| 12  | CLA  | b     | 818 | -    | -       | 4/15/91/115   | -       |
| 12  | CLA  | A     | 840 | 1    | -       | 9/21/97/115   | -       |
| 12  | CLA  | b     | 812 | -    | -       | 9/15/91/115   | -       |
| 11  | CL0  | G     | 801 | 1    | -       | 10/39/115/115 | -       |
| 12  | CLA  | H     | 812 | 3    | -       | 11/33/109/115 | -       |
| 14  | SF4  | G     | 844 | 3,1  | -       | -             | 0/6/5/5 |
| 12  | CLA  | P     | 201 | 20   | -       | 16/39/115/115 | -       |
| 18  | LMG  | b     | 845 | -    | -       | 18/50/70/70   | 0/1/1/1 |
| 14  | SF4  | c     | 101 | 4    | -       | -             | 0/6/5/5 |
| 12  | CLA  | B     | 821 | 20   | -       | 17/39/115/115 | -       |
| 15  | BCR  | R     | 102 | -    | -       | 19/29/63/63   | 0/2/2/2 |
| 12  | CLA  | b     | 837 | -    | -       | 14/39/115/115 | -       |
| 12  | CLA  | G     | 834 | -    | -       | 21/39/115/115 | -       |
| 14  | SF4  | C     | 101 | 4    | -       | -             | 0/6/5/5 |
| 12  | CLA  | H     | 833 | -    | -       | 7/15/91/115   | -       |
| 12  | CLA  | A     | 815 | -    | -       | 5/15/91/115   | -       |
| 16  | LHG  | A     | 853 | -    | -       | 39/53/53/53   | -       |
| 12  | CLA  | a     | 835 | 1    | -       | 7/15/91/115   | -       |
| 12  | CLA  | j     | 104 | -    | -       | 7/15/91/115   | -       |
| 15  | BCR  | Q     | 101 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 15  | BCR  | H     | 842 | -    | -       | 8/29/63/63    | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | B     | 815 | -    | -       | 11/33/109/115 | -       |
| 12  | CLA  | B     | 807 | 3    | -       | 8/39/115/115  | -       |
| 14  | SF4  | c     | 102 | 4    | -       | -             | 0/6/5/5 |
| 12  | CLA  | f     | 201 | 20   | -       | 16/39/115/115 | -       |
| 15  | BCR  | a     | 846 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 12  | CLA  | j     | 102 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | b     | 827 | 3    | -       | 5/15/91/115   | -       |
| 14  | SF4  | A     | 843 | 3,1  | -       | -             | 0/6/5/5 |
| 12  | CLA  | F     | 203 | -    | -       | 8/15/91/115   | -       |
| 12  | CLA  | B     | 820 | 3    | -       | 4/15/91/115   | -       |
| 12  | CLA  | b     | 820 | -    | -       | 2/15/91/115   | -       |
| 12  | CLA  | a     | 817 | -    | -       | 15/27/103/115 | -       |
| 12  | CLA  | G     | 832 | 1    | -       | 14/39/115/115 | -       |
| 15  | BCR  | b     | 842 | -    | -       | 3/18/35/63    | 0/1/1/2 |
| 19  | LMT  | H     | 848 | -    | -       | 11/21/61/61   | 0/2/2/2 |
| 12  | CLA  | A     | 854 | 20   | -       | 18/39/115/115 | -       |
| 12  | CLA  | A     | 807 | 1    | -       | 23/39/115/115 | -       |
| 12  | CLA  | H     | 850 | 16   | -       | 14/33/109/115 | -       |
| 12  | CLA  | a     | 816 | 1    | -       | 9/21/97/115   | -       |
| 12  | CLA  | a     | 815 | -    | -       | 5/15/91/115   | -       |
| 16  | LHG  | a     | 853 | -    | -       | 35/53/53/53   | -       |
| 15  | BCR  | G     | 845 | -    | -       | 10/29/63/63   | 0/2/2/2 |
| 11  | CL0  | A     | 801 | 1    | -       | 6/39/115/115  | -       |
| 12  | CLA  | l     | 202 | 3    | -       | 17/39/115/115 | -       |
| 12  | CLA  | L     | 204 | 10   | -       | 7/27/103/115  | -       |
| 12  | CLA  | a     | 806 | -    | -       | 13/39/115/115 | -       |
| 12  | CLA  | G     | 830 | -    | -       | 10/39/115/115 | -       |
| 15  | BCR  | f     | 202 | -    | -       | 14/29/63/63   | 0/2/2/2 |
| 15  | BCR  | B     | 844 | -    | -       | 8/29/63/63    | 0/2/2/2 |
| 15  | BCR  | S     | 201 | -    | -       | 16/29/63/63   | 0/2/2/2 |
| 12  | CLA  | A     | 804 | 12   | -       | 14/27/103/115 | -       |
| 12  | CLA  | G     | 821 | -    | -       | 11/39/115/115 | -       |
| 15  | BCR  | l     | 203 | -    | -       | 16/29/63/63   | 0/2/2/2 |
| 12  | CLA  | B     | 826 | 3    | -       | 12/39/115/115 | -       |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions      | Rings   |
|-----|------|-------|-----|------|---------|---------------|---------|
| 12  | CLA  | G     | 837 | 1    | -       | 14/39/115/115 | -       |
| 12  | CLA  | B     | 801 | -    | -       | 6/33/109/115  | -       |
| 15  | BCR  | F     | 204 | -    | -       | 7/29/63/63    | 0/2/2/2 |
| 12  | CLA  | b     | 801 | -    | -       | 7/33/109/115  | -       |

The worst 5 of 6515 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 17  | T     | 101 | 45D  | C07-C15 | 13.72 | 1.54        | 1.35     |
| 17  | m     | 101 | 45D  | C07-C15 | 13.70 | 1.54        | 1.35     |
| 17  | M     | 101 | 45D  | C07-C15 | 13.69 | 1.54        | 1.35     |
| 17  | m     | 101 | 45D  | C08-C16 | 13.67 | 1.54        | 1.35     |
| 17  | M     | 101 | 45D  | C08-C16 | 13.59 | 1.54        | 1.35     |

The worst 5 of 8897 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms       | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|-------|-------------|----------|
| 15  | i     | 101 | BCR  | C16-C17-C18 | 24.83 | 162.10      | 127.28   |
| 15  | A     | 846 | BCR  | C16-C17-C18 | 24.60 | 161.77      | 127.28   |
| 15  | R     | 102 | BCR  | C16-C17-C18 | 24.51 | 161.65      | 127.28   |
| 15  | j     | 103 | BCR  | C16-C17-C18 | 24.44 | 161.55      | 127.28   |
| 15  | G     | 849 | BCR  | C20-C21-C22 | 24.28 | 161.33      | 127.28   |

There are no chirality outliers.

5 of 4013 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms           |
|-----|-------|-----|------|-----------------|
| 12  | G     | 805 | CLA  | C1A-C2A-CAA-CBA |
| 12  | G     | 805 | CLA  | C3A-C2A-CAA-CBA |
| 12  | G     | 806 | CLA  | CAD-CBD-CGD-O1D |
| 12  | G     | 806 | CLA  | CAD-CBD-CGD-O2D |
| 12  | G     | 807 | CLA  | C1A-C2A-CAA-CBA |

There are no ring outliers.

278 monomers are involved in 560 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 12  | A     | 803 | CLA  | 3       | 0            |
| 12  | G     | 802 | CLA  | 5       | 0            |
| 12  | B     | 810 | CLA  | 1       | 0            |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 15  | b     | 847 | BCR  | 4       | 0            |
| 12  | G     | 842 | CLA  | 2       | 0            |
| 12  | A     | 841 | CLA  | 1       | 0            |
| 12  | B     | 814 | CLA  | 2       | 0            |
| 12  | A     | 812 | CLA  | 1       | 0            |
| 12  | A     | 826 | CLA  | 2       | 0            |
| 12  | b     | 802 | CLA  | 3       | 0            |
| 12  | H     | 816 | CLA  | 3       | 0            |
| 12  | S     | 204 | CLA  | 3       | 0            |
| 12  | G     | 827 | CLA  | 3       | 0            |
| 12  | A     | 825 | CLA  | 2       | 0            |
| 12  | B     | 835 | CLA  | 2       | 0            |
| 12  | b     | 824 | CLA  | 2       | 0            |
| 12  | a     | 855 | CLA  | 6       | 0            |
| 12  | B     | 825 | CLA  | 4       | 0            |
| 15  | b     | 840 | BCR  | 4       | 0            |
| 12  | L     | 206 | CLA  | 4       | 0            |
| 16  | a     | 850 | LHG  | 2       | 0            |
| 12  | H     | 806 | CLA  | 2       | 0            |
| 12  | B     | 833 | CLA  | 7       | 0            |
| 12  | B     | 828 | CLA  | 2       | 0            |
| 12  | H     | 829 | CLA  | 1       | 0            |
| 12  | J     | 103 | CLA  | 1       | 0            |
| 15  | H     | 849 | BCR  | 3       | 0            |
| 12  | B     | 805 | CLA  | 6       | 0            |
| 12  | B     | 836 | CLA  | 1       | 0            |
| 15  | L     | 207 | BCR  | 1       | 0            |
| 12  | b     | 806 | CLA  | 3       | 0            |
| 12  | b     | 813 | CLA  | 1       | 0            |
| 12  | A     | 832 | CLA  | 3       | 0            |
| 15  | G     | 849 | BCR  | 3       | 0            |
| 12  | A     | 818 | CLA  | 5       | 0            |
| 12  | a     | 803 | CLA  | 1       | 0            |
| 16  | A     | 851 | LHG  | 3       | 0            |
| 12  | H     | 831 | CLA  | 3       | 0            |
| 15  | L     | 203 | BCR  | 2       | 0            |
| 18  | H     | 847 | LMG  | 5       | 0            |
| 12  | G     | 839 | CLA  | 2       | 0            |
| 12  | A     | 831 | CLA  | 2       | 0            |
| 19  | b     | 846 | LMT  | 1       | 0            |
| 12  | A     | 823 | CLA  | 2       | 0            |
| 12  | a     | 823 | CLA  | 1       | 0            |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 12  | G     | 819 | CLA  | 4       | 0            |
| 15  | G     | 848 | BCR  | 2       | 0            |
| 12  | a     | 807 | CLA  | 5       | 0            |
| 12  | A     | 835 | CLA  | 1       | 0            |
| 12  | H     | 817 | CLA  | 2       | 0            |
| 12  | F     | 201 | CLA  | 3       | 0            |
| 15  | B     | 842 | BCR  | 1       | 0            |
| 12  | a     | 822 | CLA  | 1       | 0            |
| 12  | b     | 821 | CLA  | 3       | 0            |
| 12  | H     | 838 | CLA  | 4       | 0            |
| 15  | H     | 845 | BCR  | 6       | 0            |
| 19  | B     | 847 | LMT  | 2       | 0            |
| 12  | A     | 816 | CLA  | 1       | 0            |
| 12  | b     | 817 | CLA  | 1       | 0            |
| 17  | M     | 101 | 45D  | 3       | 0            |
| 17  | m     | 101 | 45D  | 4       | 0            |
| 12  | B     | 812 | CLA  | 1       | 0            |
| 12  | a     | 831 | CLA  | 2       | 0            |
| 15  | j     | 101 | BCR  | 2       | 0            |
| 15  | B     | 843 | BCR  | 3       | 0            |
| 15  | G     | 847 | BCR  | 3       | 0            |
| 15  | a     | 848 | BCR  | 2       | 0            |
| 15  | b     | 844 | BCR  | 3       | 0            |
| 12  | G     | 841 | CLA  | 1       | 0            |
| 15  | G     | 850 | BCR  | 3       | 0            |
| 15  | L     | 201 | BCR  | 2       | 0            |
| 12  | H     | 801 | CLA  | 1       | 0            |
| 12  | A     | 824 | CLA  | 7       | 0            |
| 14  | K     | 102 | SF4  | 1       | 0            |
| 12  | b     | 804 | CLA  | 3       | 0            |
| 12  | H     | 802 | CLA  | 3       | 0            |
| 12  | b     | 830 | CLA  | 1       | 0            |
| 16  | G     | 852 | LHG  | 1       | 0            |
| 12  | H     | 822 | CLA  | 2       | 0            |
| 12  | A     | 839 | CLA  | 1       | 0            |
| 12  | A     | 829 | CLA  | 4       | 0            |
| 12  | G     | 803 | CLA  | 2       | 0            |
| 12  | S     | 202 | CLA  | 1       | 0            |
| 12  | f     | 203 | CLA  | 2       | 0            |
| 12  | a     | 839 | CLA  | 2       | 0            |
| 12  | a     | 827 | CLA  | 2       | 0            |
| 12  | H     | 807 | CLA  | 3       | 0            |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 12  | a     | 834 | CLA  | 2       | 0            |
| 12  | b     | 810 | CLA  | 3       | 0            |
| 15  | S     | 205 | BCR  | 3       | 0            |
| 12  | G     | 828 | CLA  | 1       | 0            |
| 12  | G     | 856 | CLA  | 4       | 0            |
| 12  | G     | 818 | CLA  | 4       | 0            |
| 12  | b     | 822 | CLA  | 8       | 0            |
| 12  | B     | 802 | CLA  | 2       | 0            |
| 12  | b     | 803 | CLA  | 1       | 0            |
| 12  | a     | 841 | CLA  | 2       | 0            |
| 15  | P     | 204 | BCR  | 1       | 0            |
| 12  | S     | 203 | CLA  | 3       | 0            |
| 12  | H     | 837 | CLA  | 2       | 0            |
| 15  | J     | 101 | BCR  | 2       | 0            |
| 12  | a     | 840 | CLA  | 1       | 0            |
| 15  | f     | 204 | BCR  | 2       | 0            |
| 12  | b     | 805 | CLA  | 7       | 0            |
| 12  | A     | 820 | CLA  | 2       | 0            |
| 12  | b     | 815 | CLA  | 2       | 0            |
| 15  | J     | 104 | BCR  | 2       | 0            |
| 15  | H     | 841 | BCR  | 1       | 0            |
| 12  | B     | 831 | CLA  | 2       | 0            |
| 12  | G     | 806 | CLA  | 3       | 0            |
| 12  | a     | 820 | CLA  | 1       | 0            |
| 15  | B     | 841 | BCR  | 3       | 0            |
| 17  | T     | 101 | 45D  | 3       | 0            |
| 15  | H     | 844 | BCR  | 4       | 0            |
| 12  | G     | 813 | CLA  | 1       | 0            |
| 15  | A     | 849 | BCR  | 5       | 0            |
| 16  | G     | 854 | LHG  | 1       | 0            |
| 12  | H     | 825 | CLA  | 5       | 0            |
| 12  | H     | 808 | CLA  | 4       | 0            |
| 12  | B     | 804 | CLA  | 3       | 0            |
| 12  | G     | 804 | CLA  | 2       | 0            |
| 15  | J     | 102 | BCR  | 2       | 0            |
| 12  | l     | 204 | CLA  | 2       | 0            |
| 12  | B     | 803 | CLA  | 1       | 0            |
| 12  | A     | 837 | CLA  | 1       | 0            |
| 15  | a     | 845 | BCR  | 2       | 0            |
| 12  | G     | 826 | CLA  | 2       | 0            |
| 12  | b     | 832 | CLA  | 5       | 0            |
| 15  | b     | 841 | BCR  | 1       | 0            |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 12  | G     | 810 | CLA  | 1       | 0            |
| 15  | A     | 847 | BCR  | 1       | 0            |
| 12  | G     | 833 | CLA  | 2       | 0            |
| 15  | I     | 101 | BCR  | 4       | 0            |
| 12  | b     | 826 | CLA  | 2       | 0            |
| 12  | A     | 828 | CLA  | 2       | 0            |
| 12  | G     | 855 | CLA  | 3       | 0            |
| 12  | H     | 805 | CLA  | 5       | 0            |
| 12  | A     | 802 | CLA  | 3       | 0            |
| 12  | A     | 827 | CLA  | 3       | 0            |
| 15  | G     | 846 | BCR  | 1       | 0            |
| 12  | A     | 833 | CLA  | 3       | 0            |
| 12  | b     | 834 | CLA  | 2       | 0            |
| 12  | A     | 855 | CLA  | 3       | 0            |
| 12  | b     | 825 | CLA  | 4       | 0            |
| 12  | H     | 834 | CLA  | 4       | 0            |
| 15  | H     | 846 | BCR  | 2       | 0            |
| 12  | A     | 806 | CLA  | 2       | 0            |
| 12  | A     | 821 | CLA  | 1       | 0            |
| 12  | a     | 821 | CLA  | 1       | 0            |
| 12  | H     | 832 | CLA  | 2       | 0            |
| 15  | a     | 847 | BCR  | 3       | 0            |
| 16  | G     | 851 | LHG  | 3       | 0            |
| 12  | L     | 205 | CLA  | 3       | 0            |
| 12  | B     | 806 | CLA  | 3       | 0            |
| 12  | G     | 840 | CLA  | 1       | 0            |
| 12  | b     | 807 | CLA  | 2       | 0            |
| 15  | a     | 852 | BCR  | 1       | 0            |
| 12  | a     | 854 | CLA  | 5       | 0            |
| 15  | b     | 839 | BCR  | 1       | 0            |
| 15  | b     | 843 | BCR  | 6       | 0            |
| 12  | G     | 817 | CLA  | 1       | 0            |
| 12  | b     | 848 | CLA  | 2       | 0            |
| 12  | L     | 202 | CLA  | 2       | 0            |
| 15  | B     | 845 | BCR  | 3       | 0            |
| 12  | G     | 835 | CLA  | 2       | 0            |
| 12  | G     | 823 | CLA  | 1       | 0            |
| 15  | A     | 852 | BCR  | 2       | 0            |
| 12  | a     | 814 | CLA  | 1       | 0            |
| 15  | F     | 202 | BCR  | 3       | 0            |
| 12  | B     | 823 | CLA  | 2       | 0            |
| 15  | l     | 201 | BCR  | 2       | 0            |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 12  | H     | 835 | CLA  | 4       | 0            |
| 12  | H     | 824 | CLA  | 3       | 0            |
| 12  | H     | 827 | CLA  | 1       | 0            |
| 12  | l     | 205 | CLA  | 4       | 0            |
| 12  | G     | 824 | CLA  | 4       | 0            |
| 12  | a     | 824 | CLA  | 5       | 0            |
| 12  | B     | 827 | CLA  | 2       | 0            |
| 12  | a     | 812 | CLA  | 2       | 0            |
| 12  | B     | 830 | CLA  | 4       | 0            |
| 12  | B     | 834 | CLA  | 2       | 0            |
| 12  | a     | 826 | CLA  | 3       | 0            |
| 12  | b     | 823 | CLA  | 2       | 0            |
| 12  | R     | 103 | CLA  | 1       | 0            |
| 12  | H     | 828 | CLA  | 3       | 0            |
| 12  | H     | 811 | CLA  | 2       | 0            |
| 12  | G     | 807 | CLA  | 2       | 0            |
| 12  | G     | 825 | CLA  | 7       | 0            |
| 12  | a     | 825 | CLA  | 1       | 0            |
| 12  | A     | 808 | CLA  | 1       | 0            |
| 12  | B     | 824 | CLA  | 1       | 0            |
| 12  | l     | 206 | CLA  | 3       | 0            |
| 15  | R     | 101 | BCR  | 2       | 0            |
| 12  | a     | 832 | CLA  | 3       | 0            |
| 12  | a     | 828 | CLA  | 6       | 0            |
| 15  | j     | 103 | BCR  | 3       | 0            |
| 12  | a     | 818 | CLA  | 5       | 0            |
| 12  | A     | 834 | CLA  | 2       | 0            |
| 12  | b     | 835 | CLA  | 2       | 0            |
| 12  | B     | 822 | CLA  | 6       | 0            |
| 12  | a     | 802 | CLA  | 3       | 0            |
| 12  | A     | 817 | CLA  | 1       | 0            |
| 12  | A     | 805 | CLA  | 2       | 0            |
| 12  | G     | 822 | CLA  | 1       | 0            |
| 15  | A     | 848 | BCR  | 2       | 0            |
| 12  | a     | 805 | CLA  | 4       | 0            |
| 18  | B     | 846 | LMG  | 4       | 0            |
| 15  | G     | 853 | BCR  | 1       | 0            |
| 12  | b     | 829 | CLA  | 1       | 0            |
| 12  | b     | 833 | CLA  | 2       | 0            |
| 15  | i     | 101 | BCR  | 3       | 0            |
| 15  | H     | 843 | BCR  | 4       | 0            |
| 12  | H     | 804 | CLA  | 3       | 0            |

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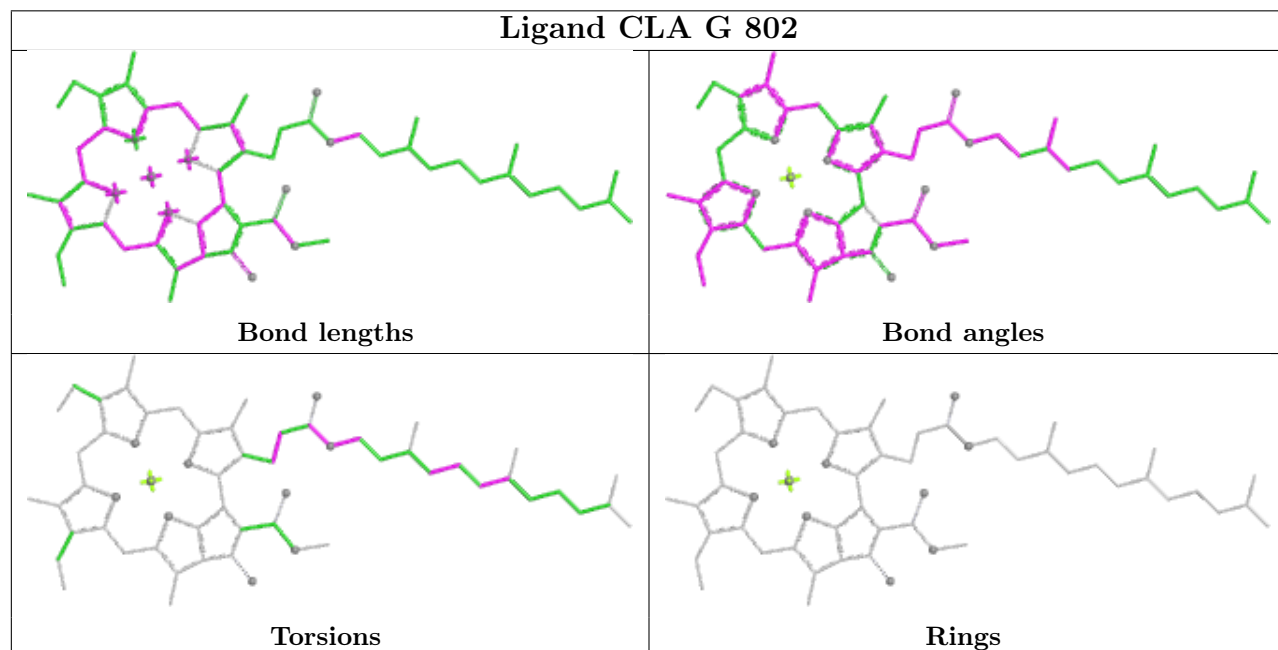
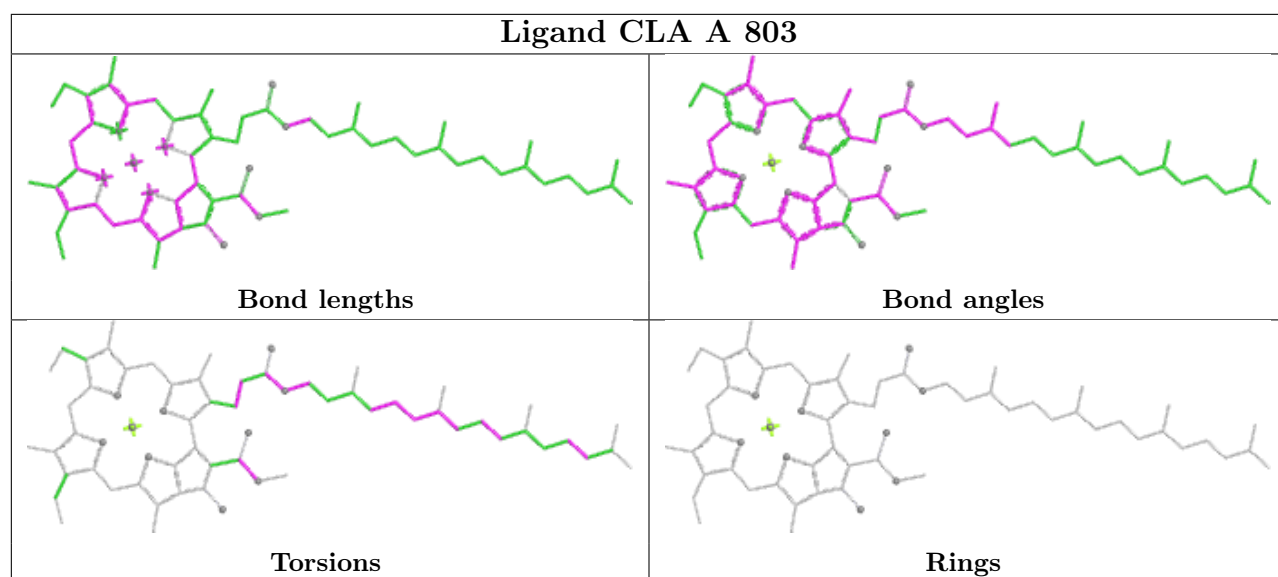
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 12  | b     | 828 | CLA  | 2       | 0            |
| 15  | A     | 846 | BCR  | 3       | 0            |
| 12  | G     | 808 | CLA  | 3       | 0            |
| 12  | a     | 809 | CLA  | 2       | 0            |
| 12  | H     | 826 | CLA  | 3       | 0            |
| 12  | b     | 836 | CLA  | 5       | 0            |
| 12  | b     | 816 | CLA  | 2       | 0            |
| 16  | a     | 851 | LHG  | 1       | 0            |
| 12  | a     | 833 | CLA  | 4       | 0            |
| 12  | G     | 829 | CLA  | 5       | 0            |
| 15  | a     | 849 | BCR  | 3       | 0            |
| 12  | a     | 829 | CLA  | 3       | 0            |
| 15  | Q     | 102 | BCR  | 1       | 0            |
| 12  | H     | 836 | CLA  | 3       | 0            |
| 12  | H     | 815 | CLA  | 2       | 0            |
| 12  | a     | 836 | CLA  | 1       | 0            |
| 15  | P     | 202 | BCR  | 4       | 0            |
| 12  | B     | 837 | CLA  | 3       | 0            |
| 15  | A     | 845 | BCR  | 3       | 0            |
| 12  | B     | 829 | CLA  | 1       | 0            |
| 12  | H     | 823 | CLA  | 6       | 0            |
| 12  | A     | 840 | CLA  | 4       | 0            |
| 12  | b     | 812 | CLA  | 2       | 0            |
| 11  | G     | 801 | CL0  | 1       | 0            |
| 12  | H     | 812 | CLA  | 1       | 0            |
| 12  | P     | 201 | CLA  | 5       | 0            |
| 18  | b     | 845 | LMG  | 3       | 0            |
| 15  | R     | 102 | BCR  | 3       | 0            |
| 12  | b     | 837 | CLA  | 1       | 0            |
| 12  | G     | 834 | CLA  | 3       | 0            |
| 12  | a     | 835 | CLA  | 2       | 0            |
| 15  | Q     | 101 | BCR  | 4       | 0            |
| 15  | H     | 842 | BCR  | 2       | 0            |
| 12  | B     | 815 | CLA  | 1       | 0            |
| 12  | B     | 807 | CLA  | 4       | 0            |
| 12  | f     | 201 | CLA  | 3       | 0            |
| 15  | a     | 846 | BCR  | 4       | 0            |
| 12  | j     | 102 | CLA  | 2       | 0            |
| 12  | b     | 827 | CLA  | 3       | 0            |
| 12  | F     | 203 | CLA  | 1       | 0            |
| 12  | a     | 817 | CLA  | 3       | 0            |
| 12  | G     | 832 | CLA  | 2       | 0            |

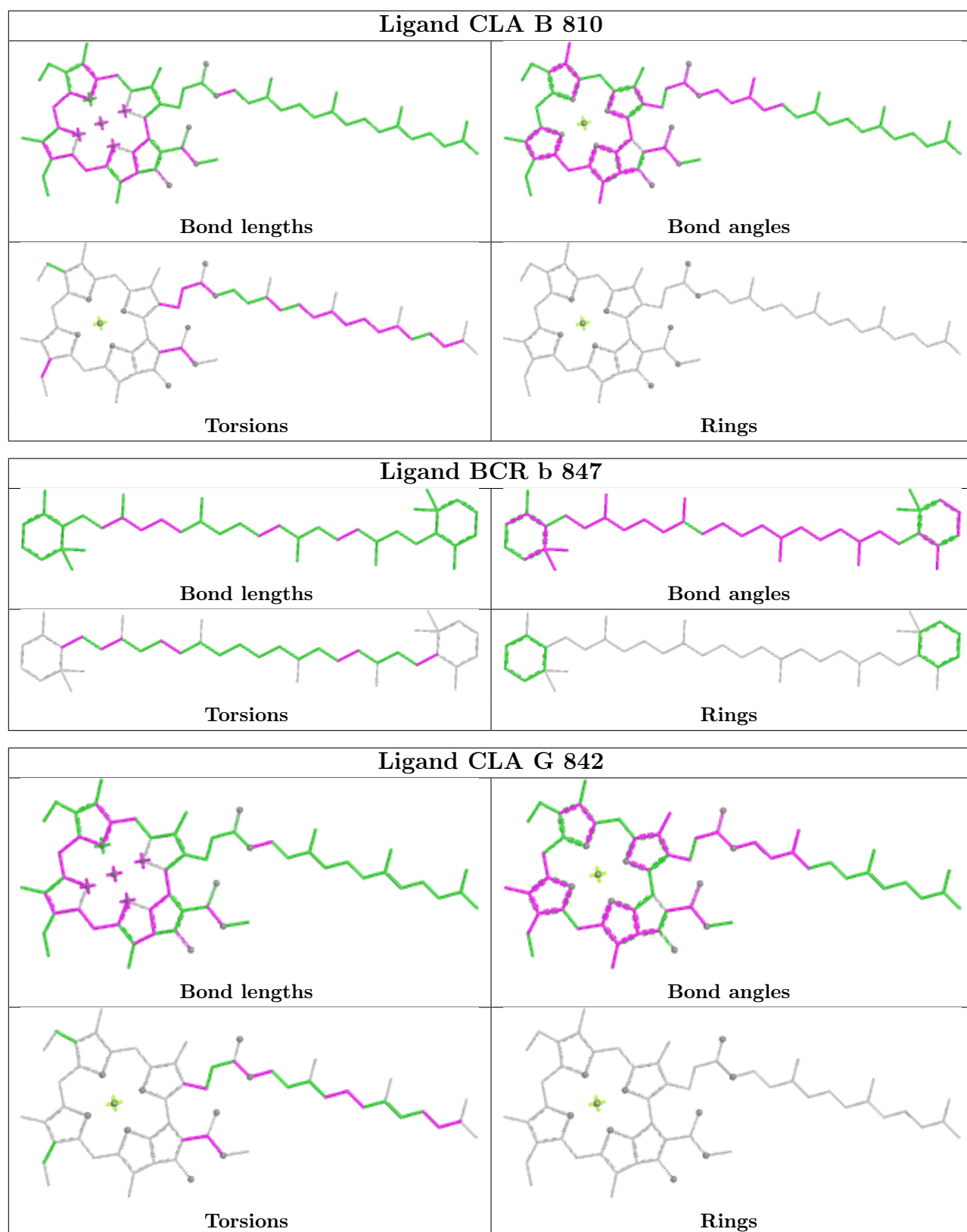
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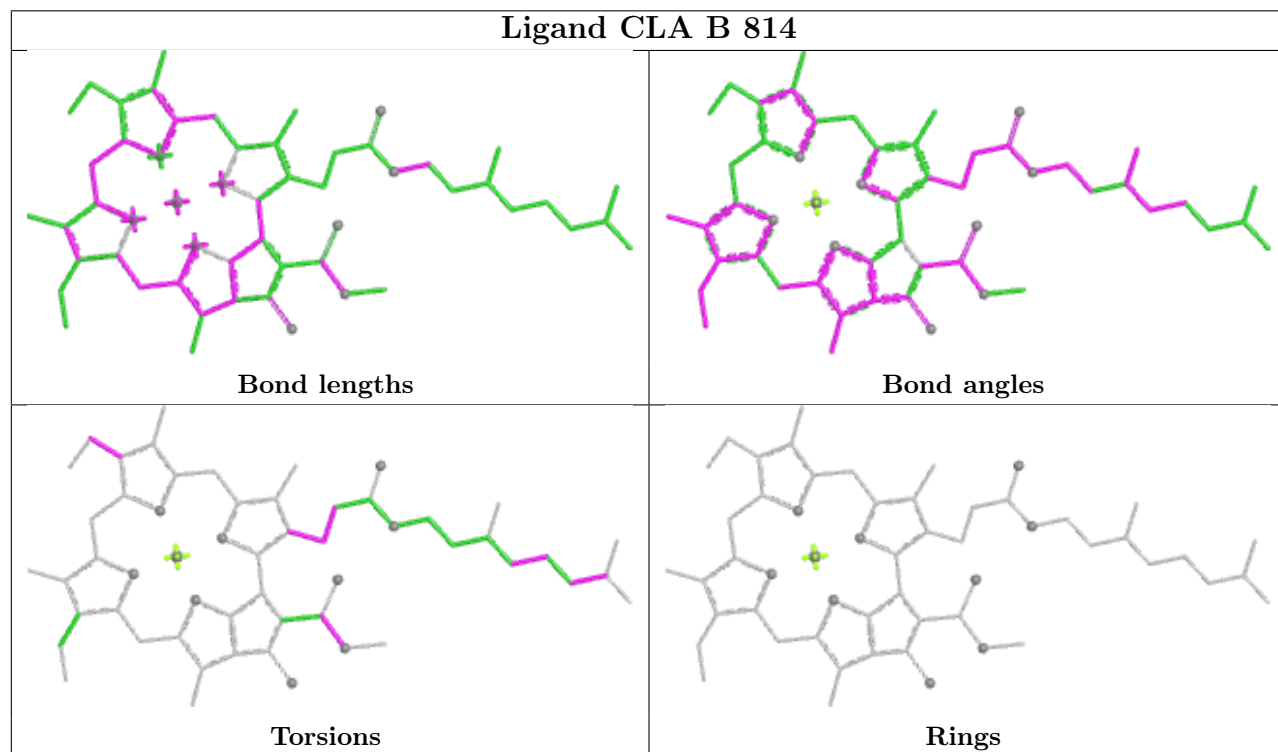
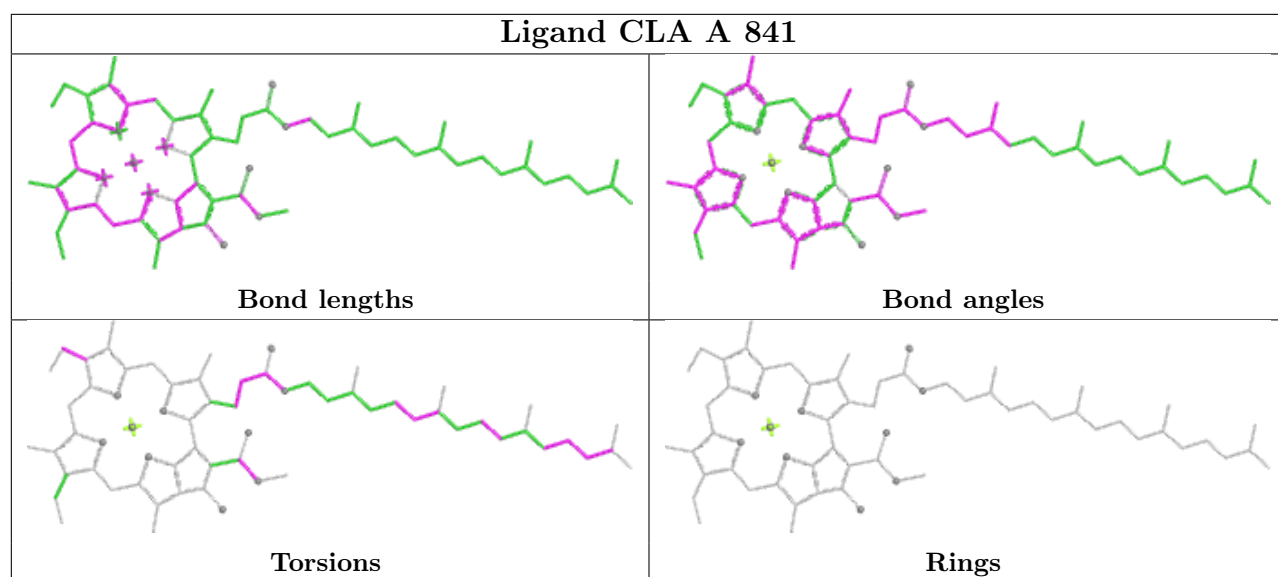
*Continued from previous page...*

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 15  | b     | 842 | BCR  | 4       | 0            |
| 19  | H     | 848 | LMT  | 1       | 0            |
| 12  | A     | 854 | CLA  | 4       | 0            |
| 12  | A     | 807 | CLA  | 3       | 0            |
| 12  | H     | 850 | CLA  | 3       | 0            |
| 12  | a     | 816 | CLA  | 1       | 0            |
| 16  | a     | 853 | LHG  | 1       | 0            |
| 15  | G     | 845 | BCR  | 1       | 0            |
| 11  | A     | 801 | CL0  | 4       | 0            |
| 12  | l     | 202 | CLA  | 5       | 0            |
| 12  | L     | 204 | CLA  | 2       | 0            |
| 12  | a     | 806 | CLA  | 3       | 0            |
| 12  | G     | 830 | CLA  | 3       | 0            |
| 15  | f     | 202 | BCR  | 2       | 0            |
| 15  | B     | 844 | BCR  | 4       | 0            |
| 15  | S     | 201 | BCR  | 2       | 0            |
| 12  | A     | 804 | CLA  | 2       | 0            |
| 12  | G     | 821 | CLA  | 3       | 0            |
| 15  | l     | 203 | BCR  | 2       | 0            |
| 12  | G     | 837 | CLA  | 1       | 0            |
| 12  | B     | 801 | CLA  | 5       | 0            |
| 15  | F     | 204 | BCR  | 2       | 0            |
| 12  | b     | 801 | CLA  | 1       | 0            |

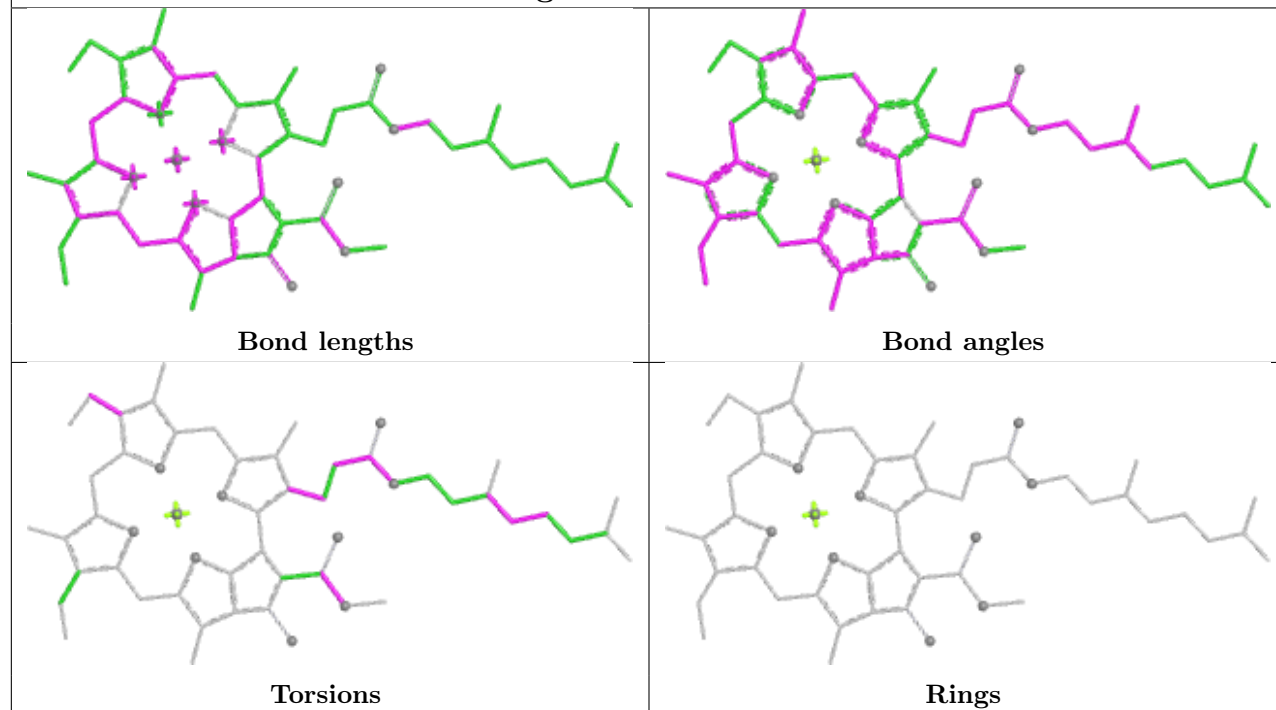
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



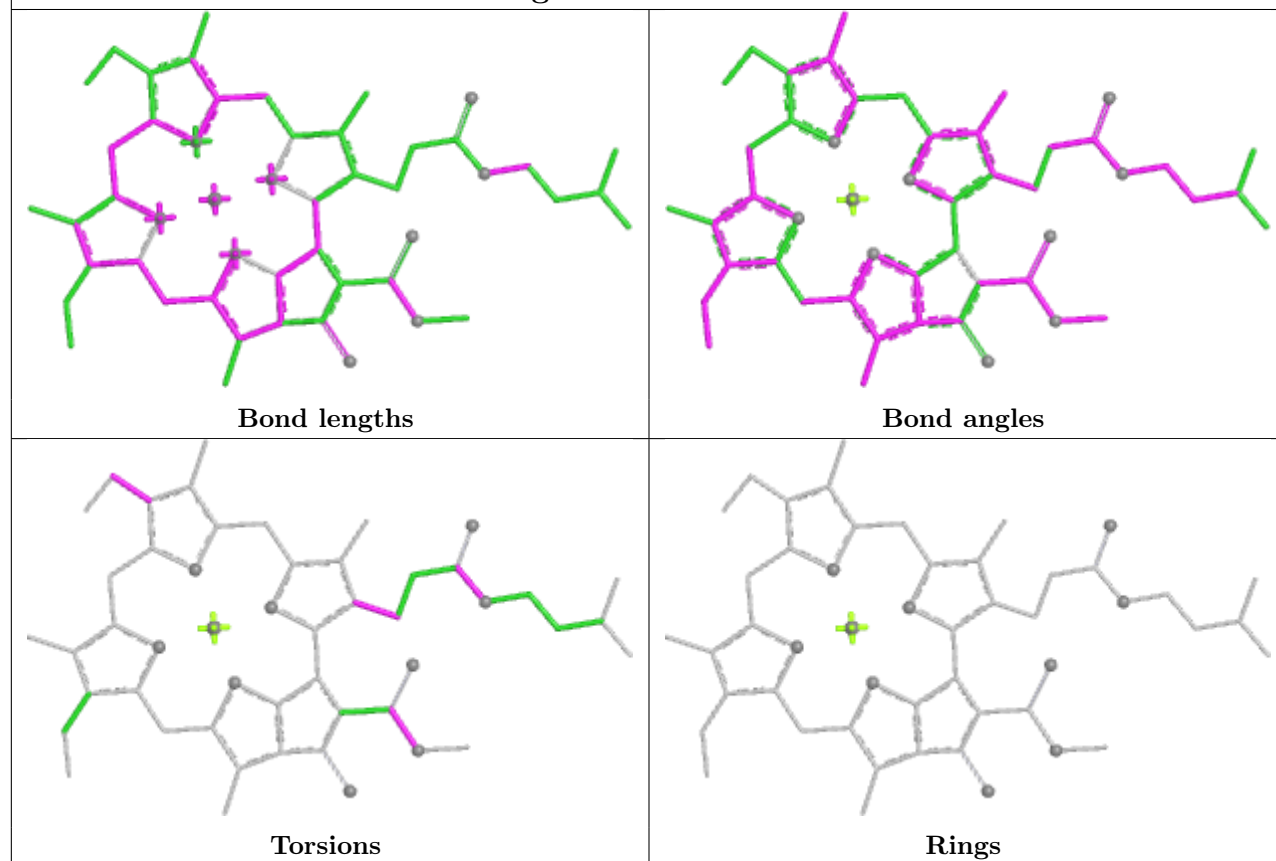




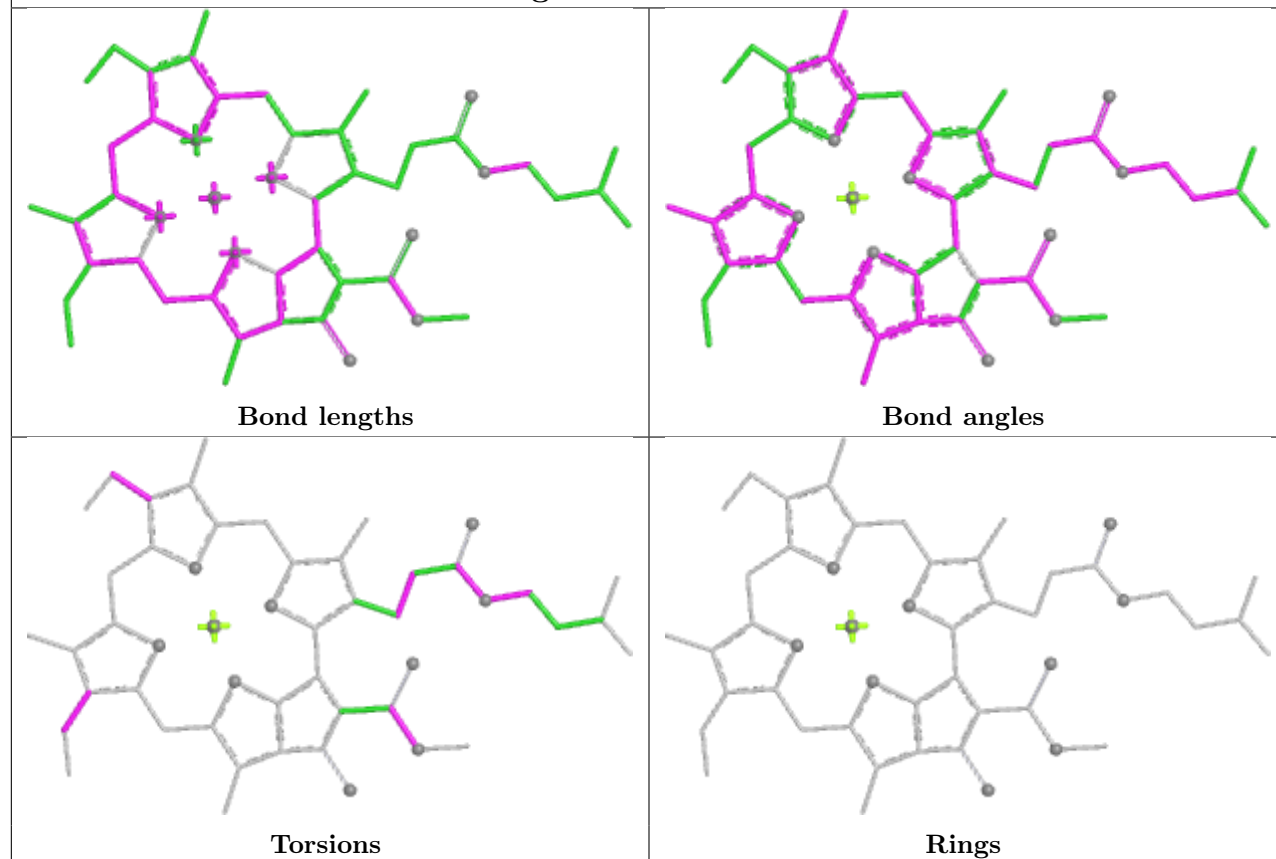
## Ligand CLA a 804



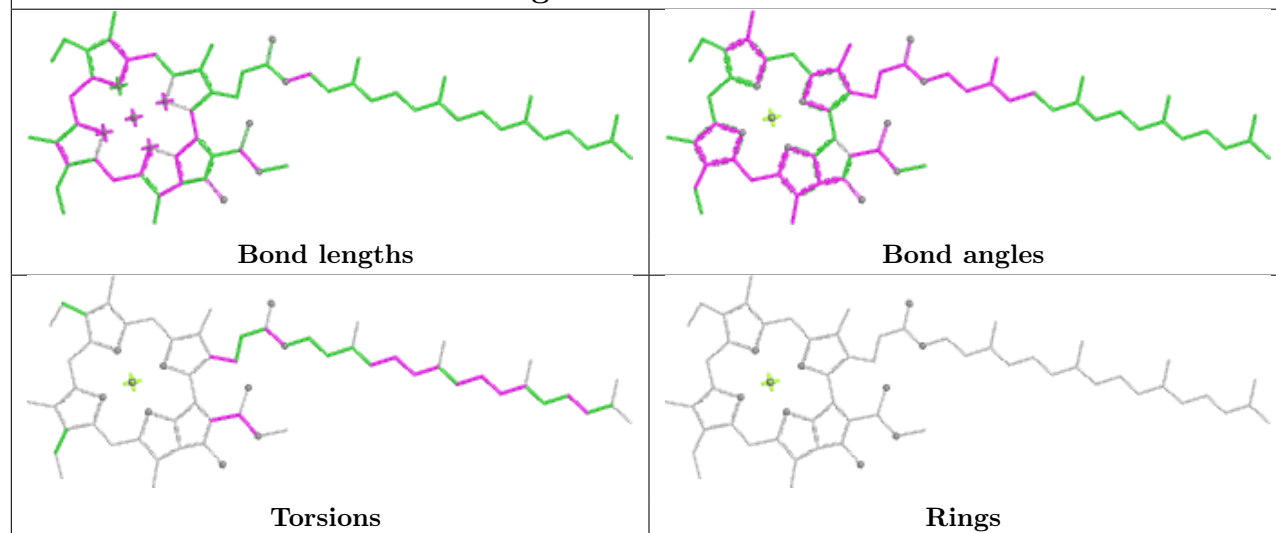
## Ligand CLA A 810

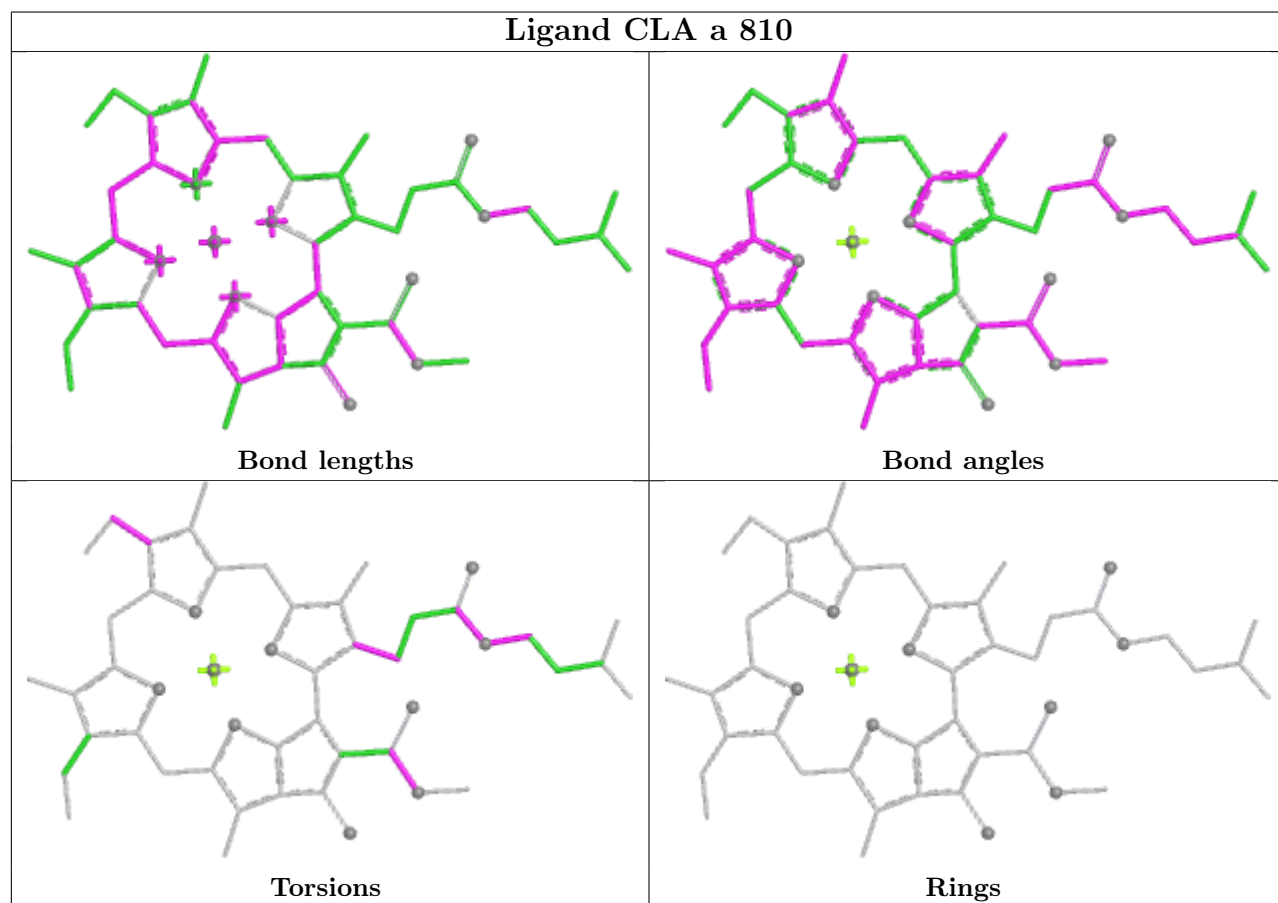
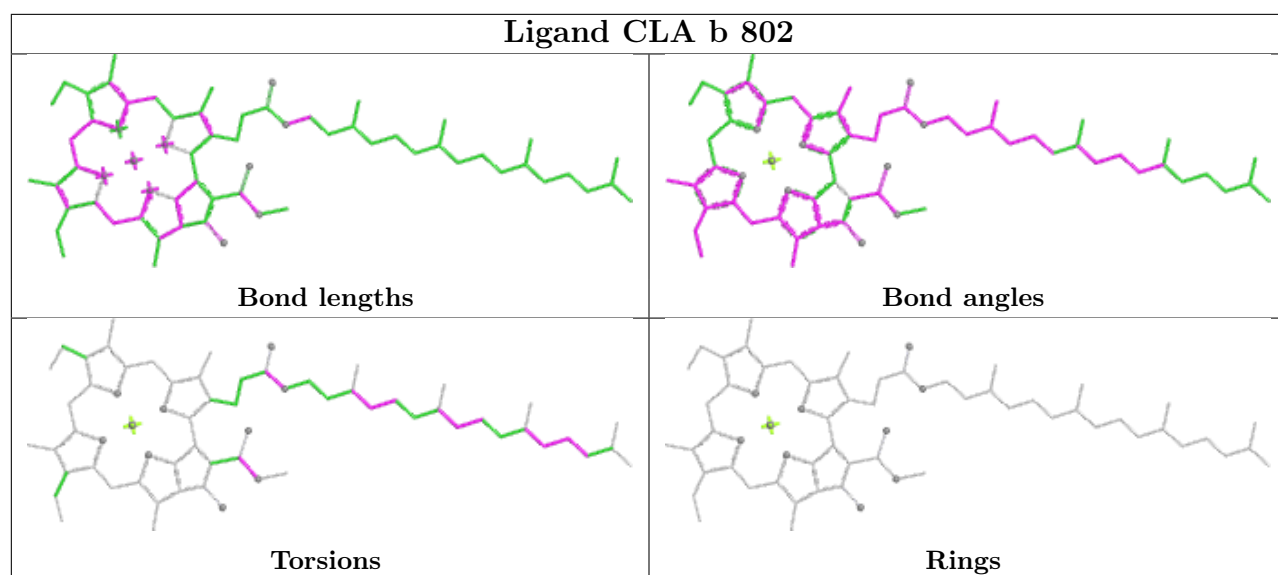


## Ligand CLA A 812

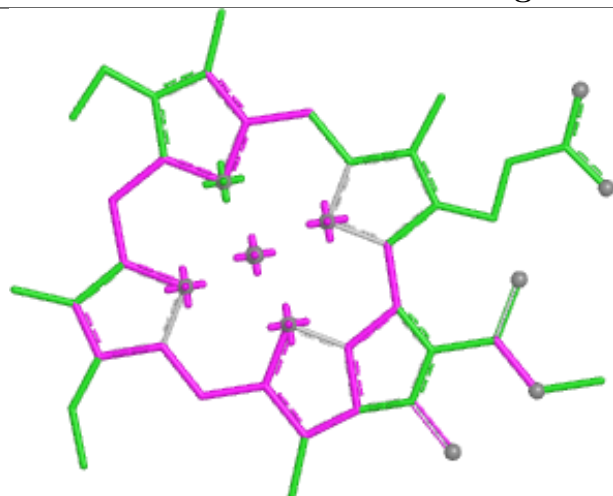


## Ligand CLA A 826

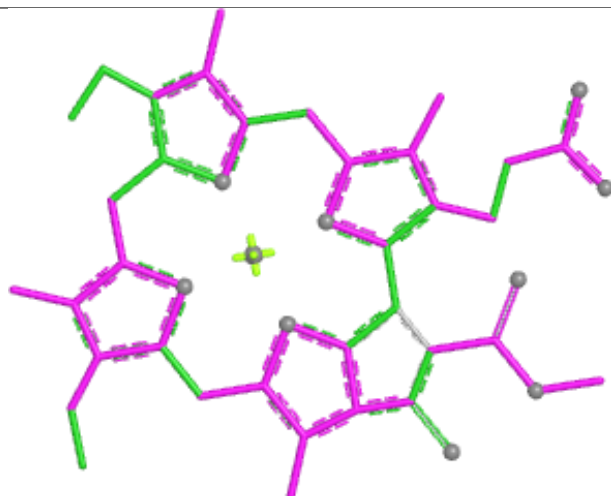




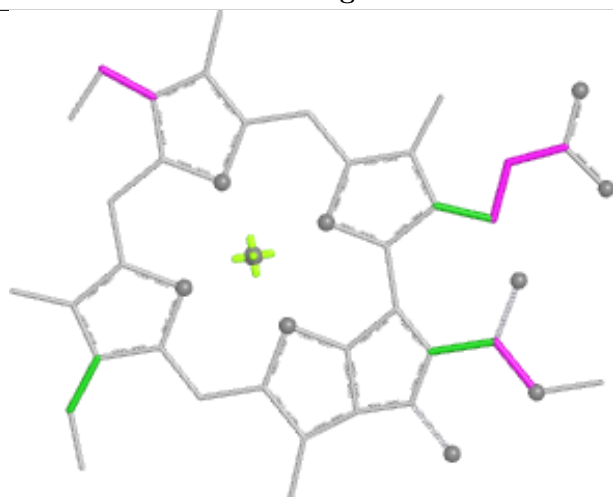
## Ligand CLA B 819



Bond lengths



Bond angles

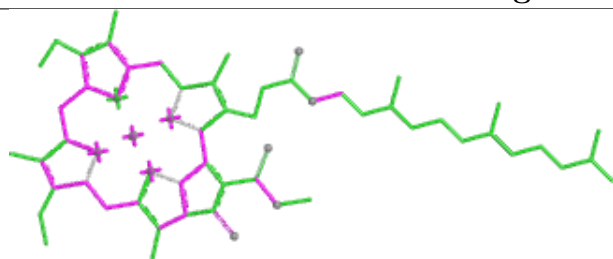


Torsions

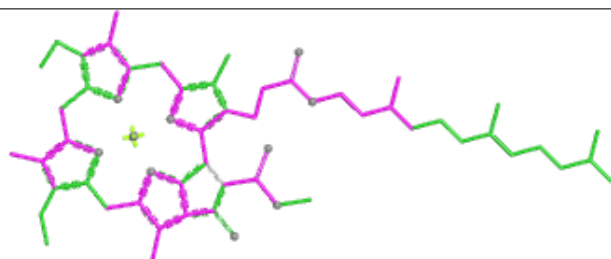


Rings

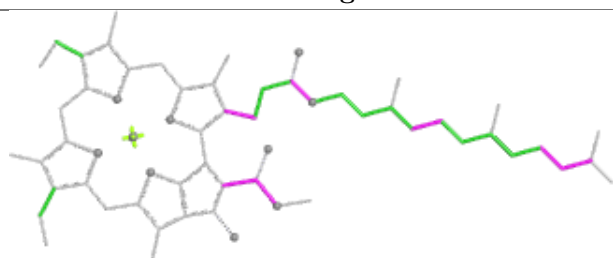
## Ligand CLA H 816



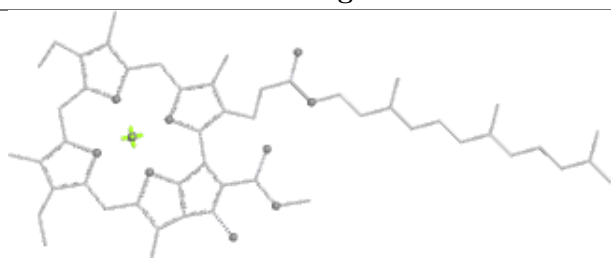
Bond lengths



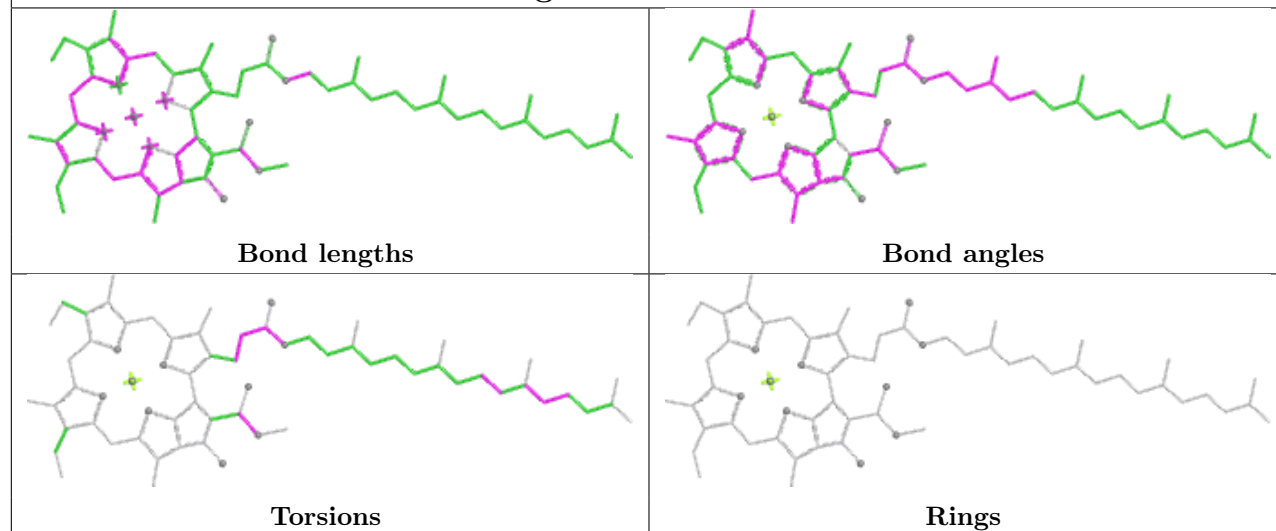
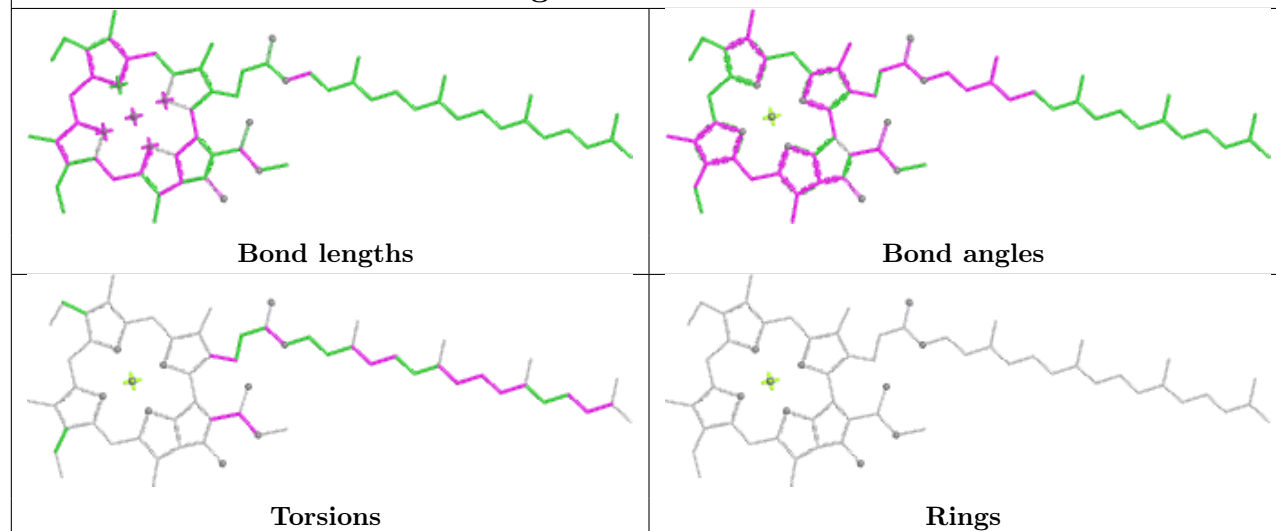
Bond angles

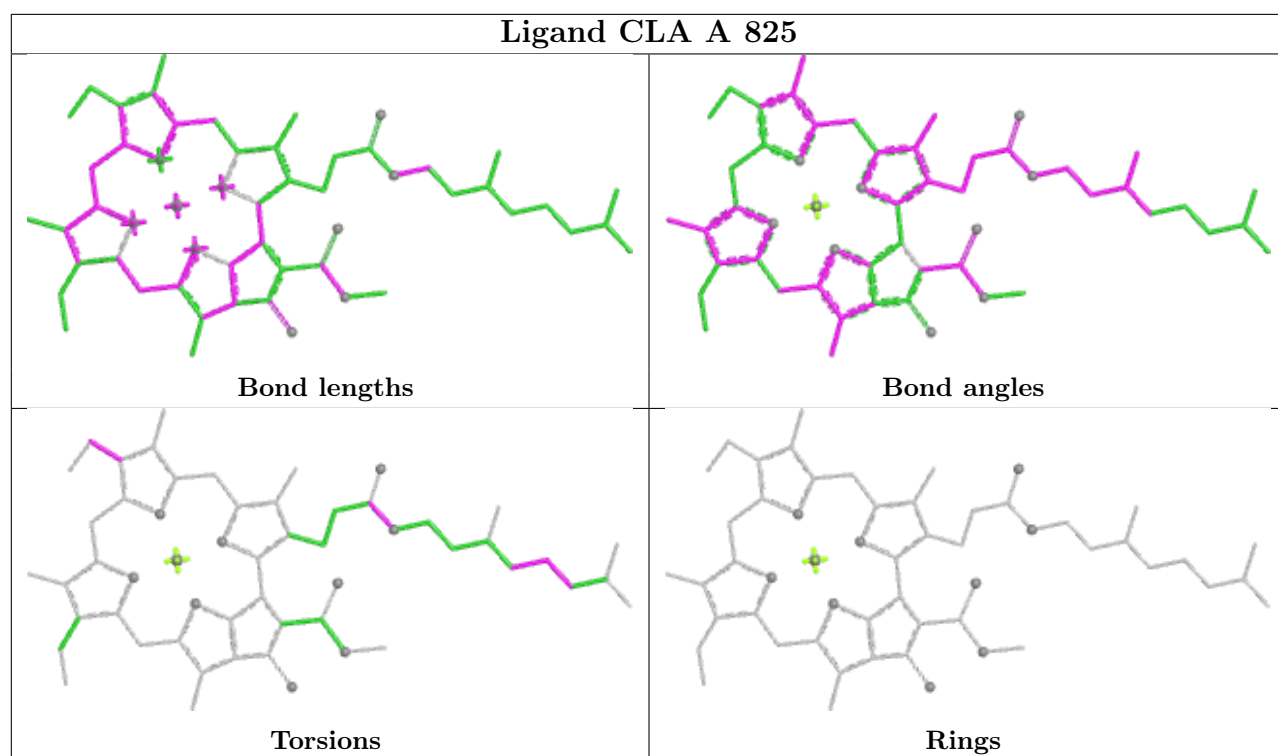


Torsions

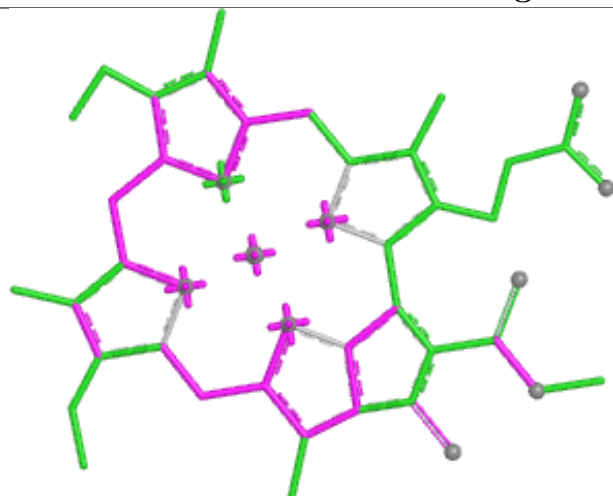


Rings

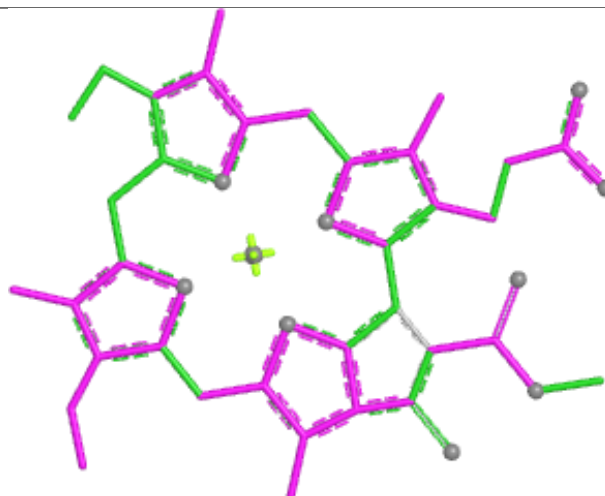
**Ligand CLA S 204****Ligand CLA G 827**



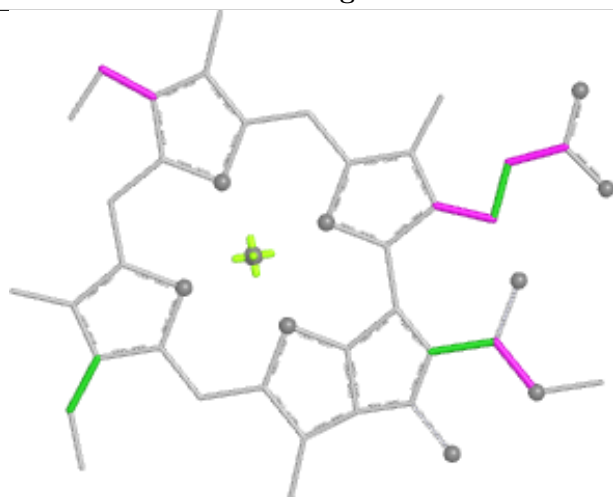
## Ligand CLA B 835



Bond lengths



Bond angles

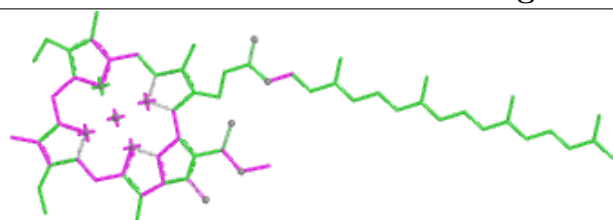


Torsions

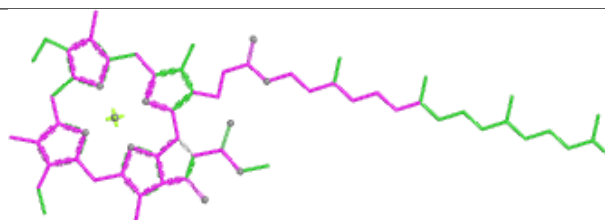


Rings

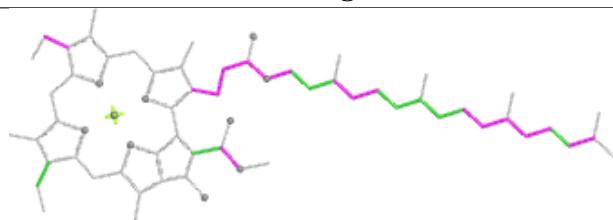
## Ligand CLA b 824



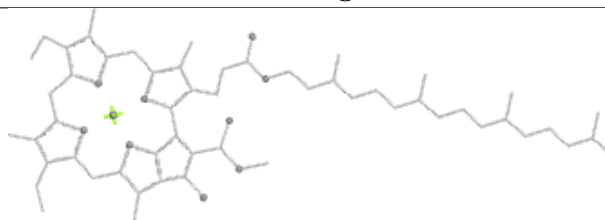
Bond lengths



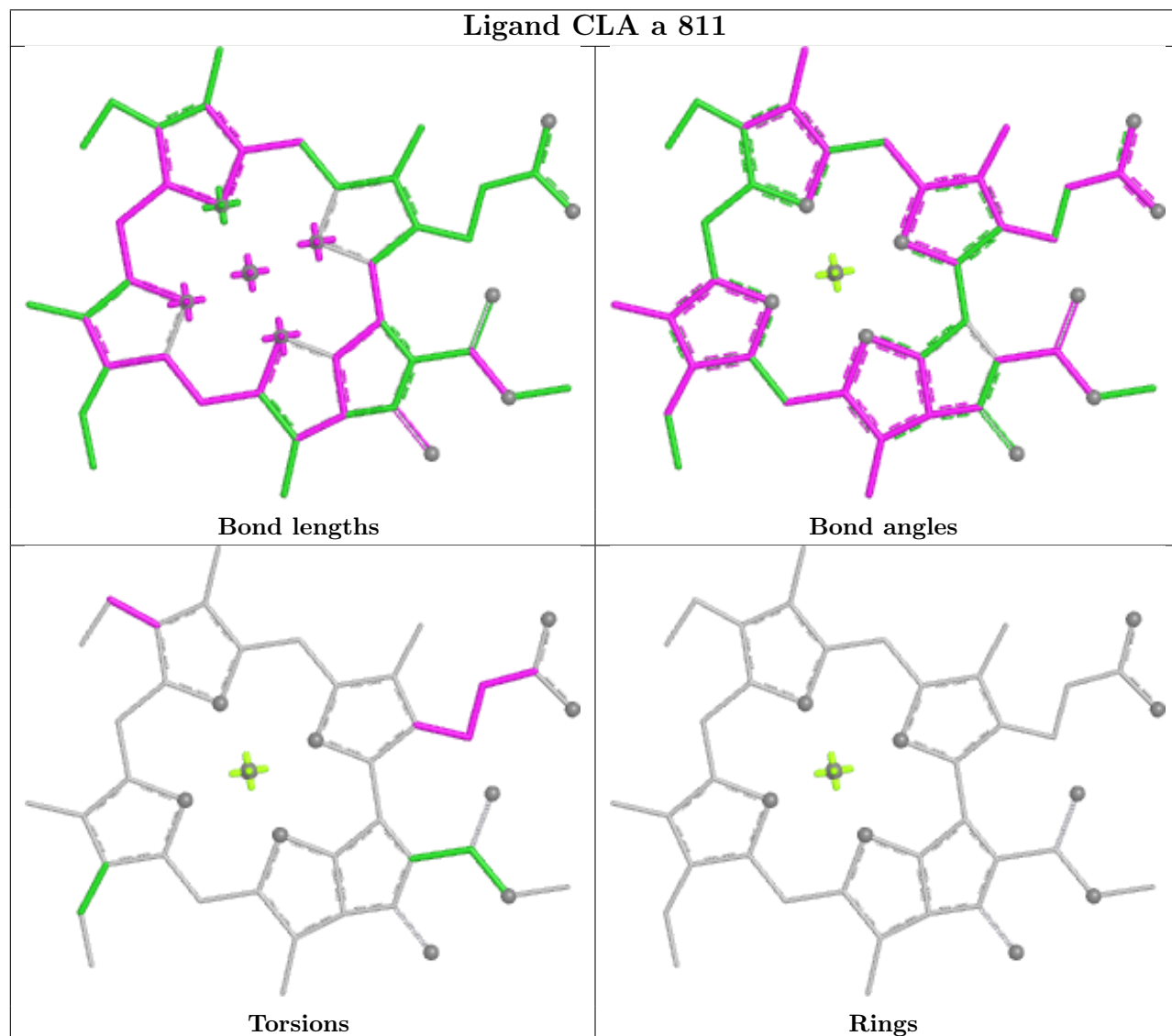
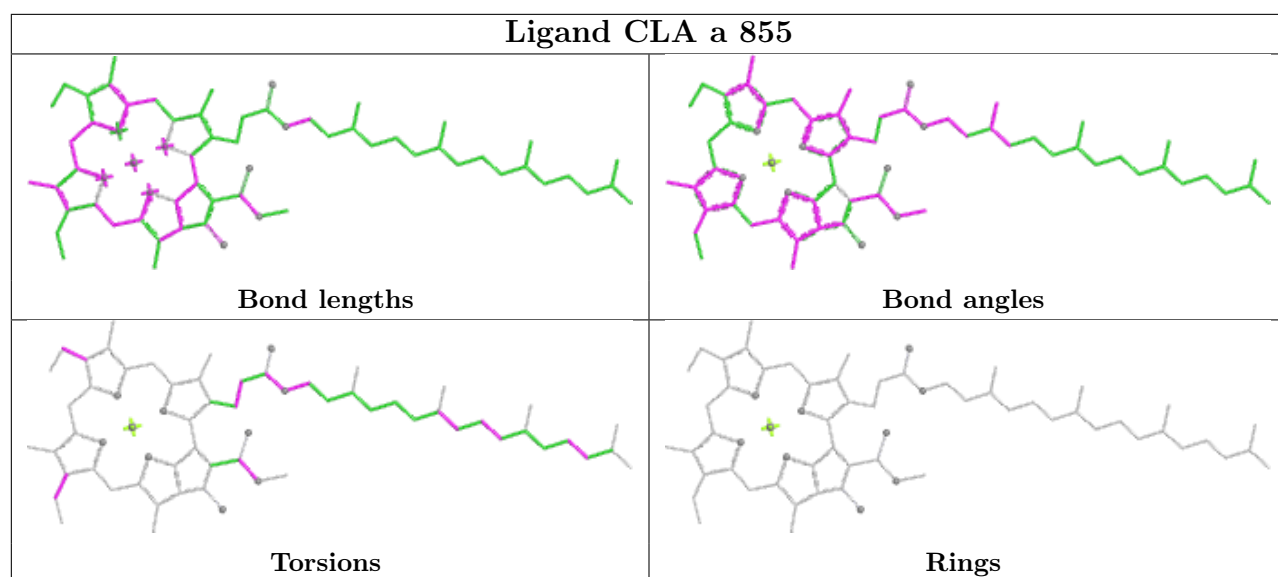
Bond angles

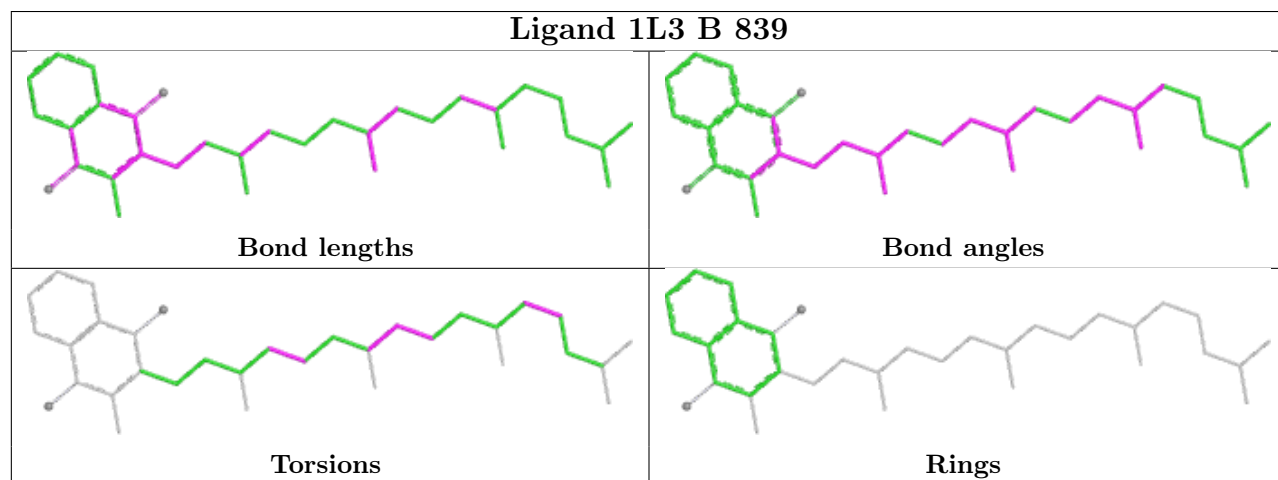
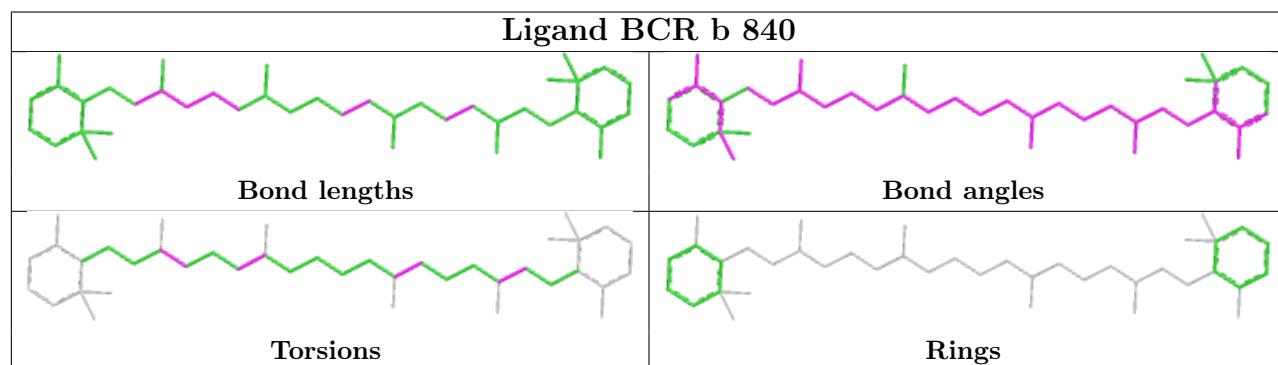
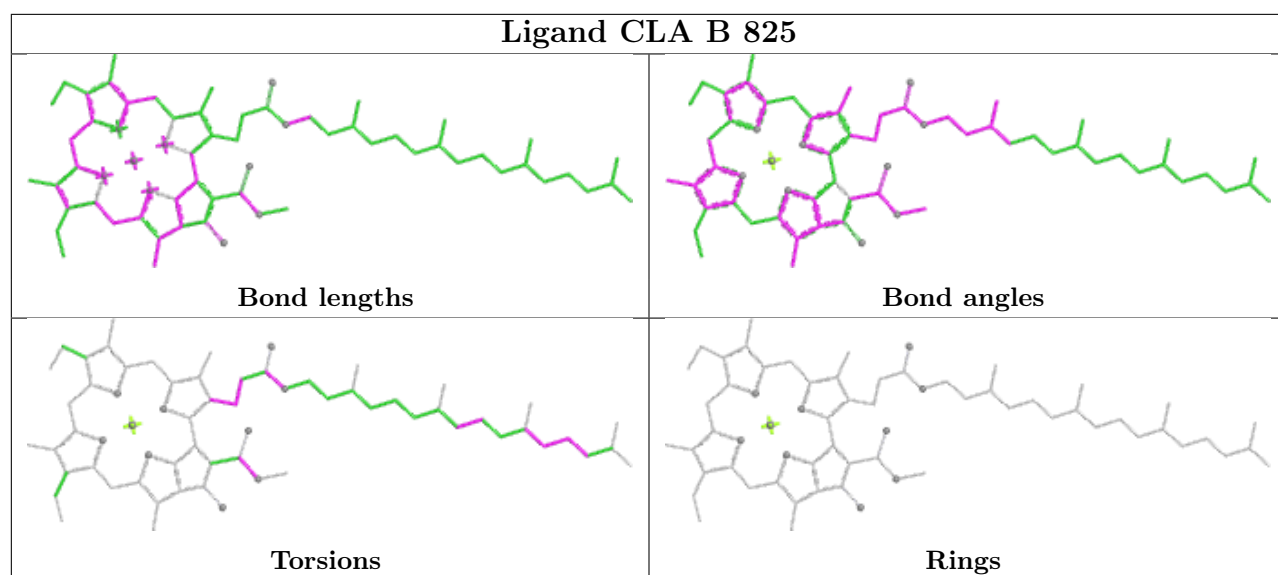


Torsions

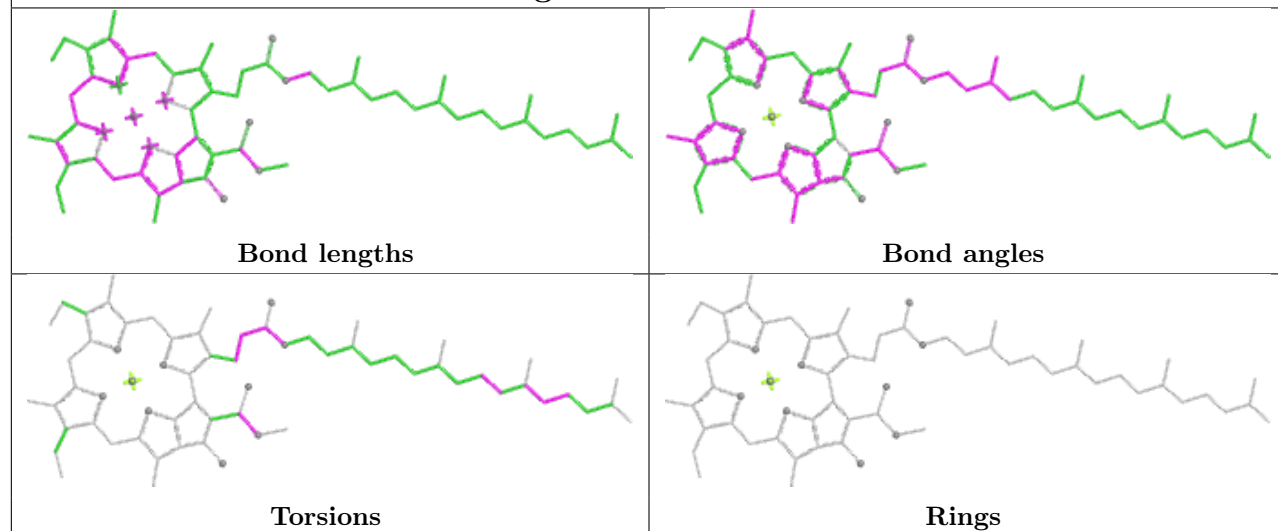


Rings

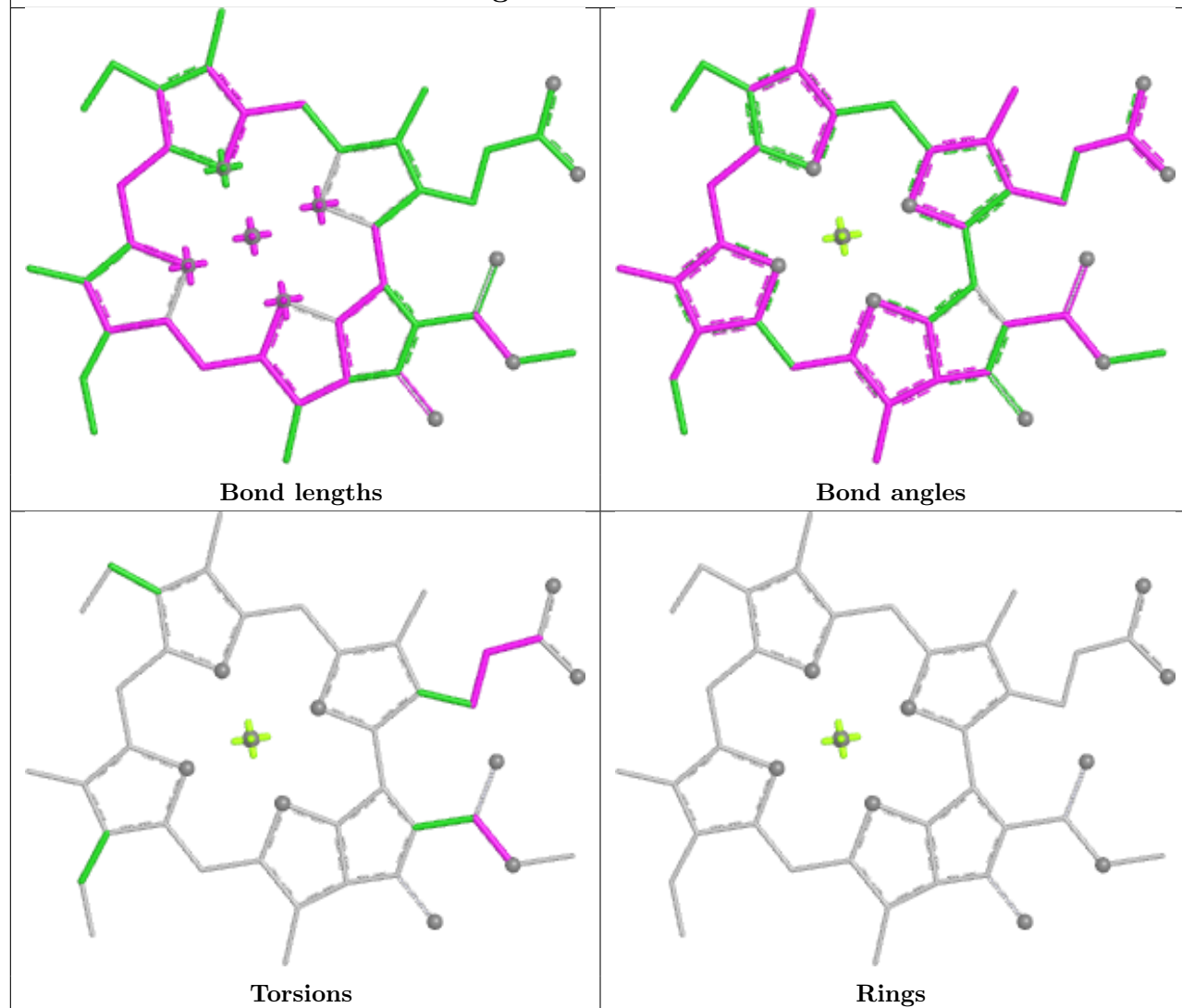


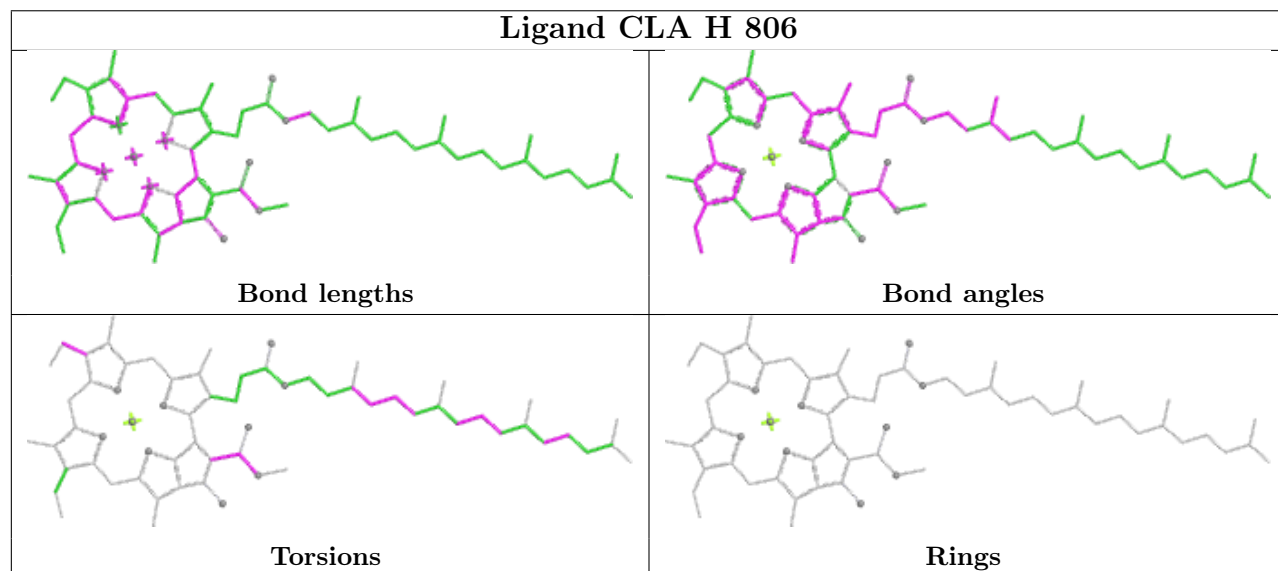
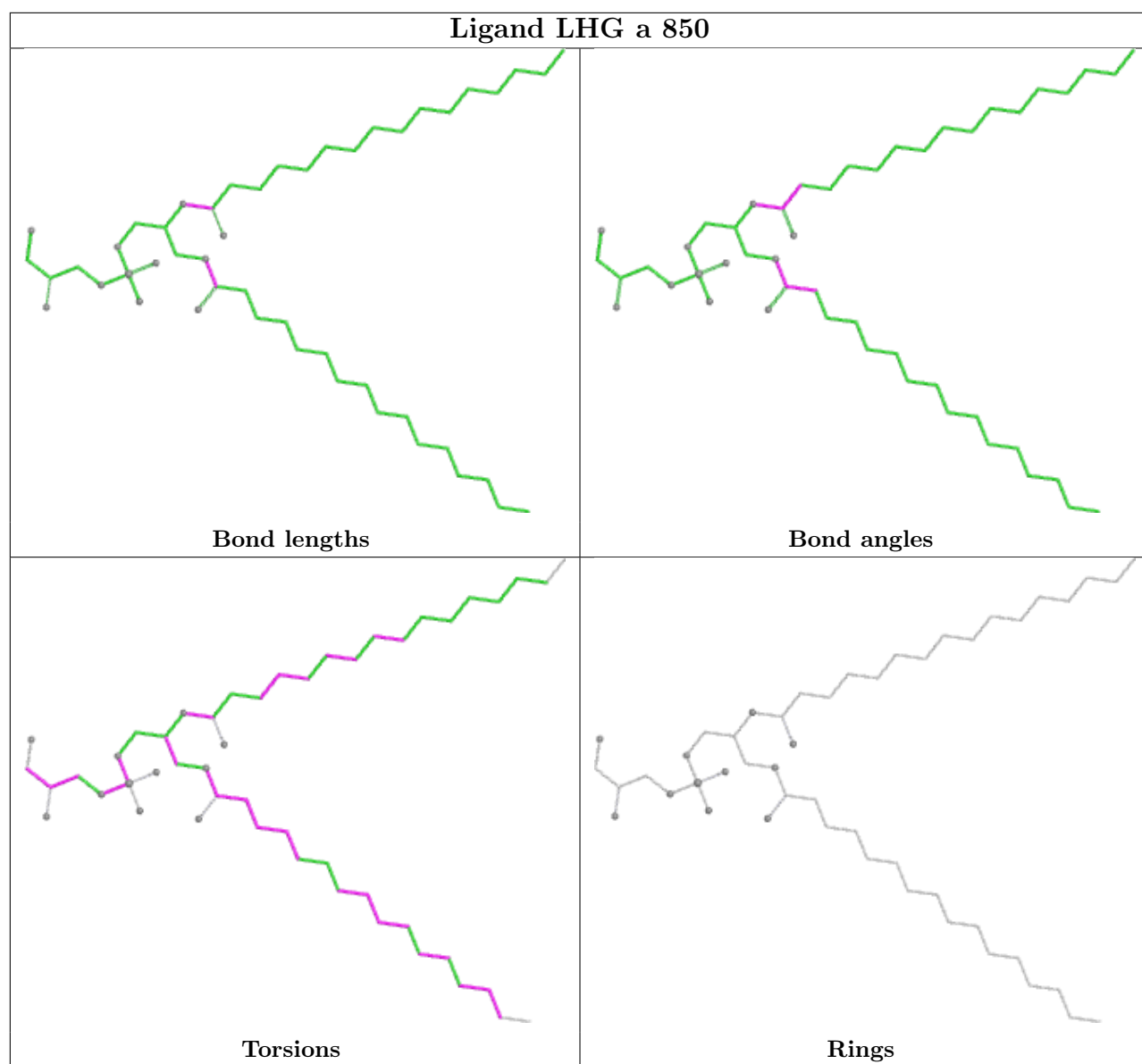


## Ligand CLA L 206

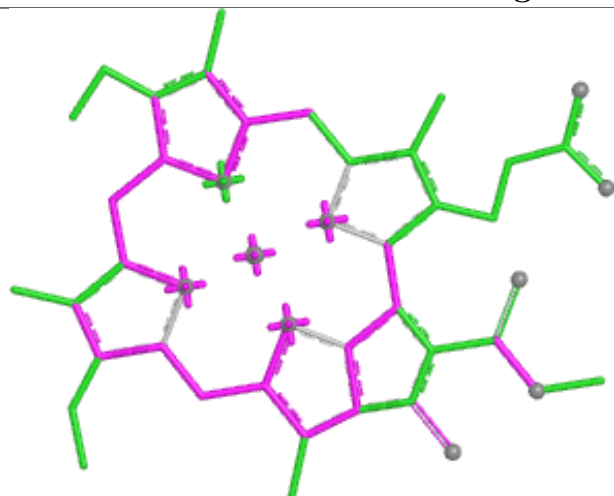


## Ligand CLA B 809

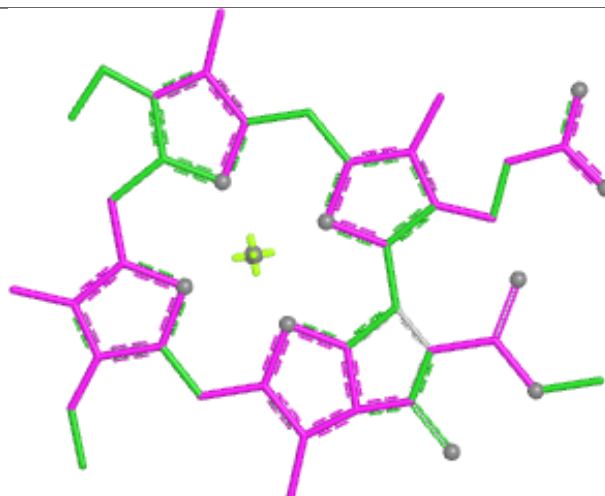




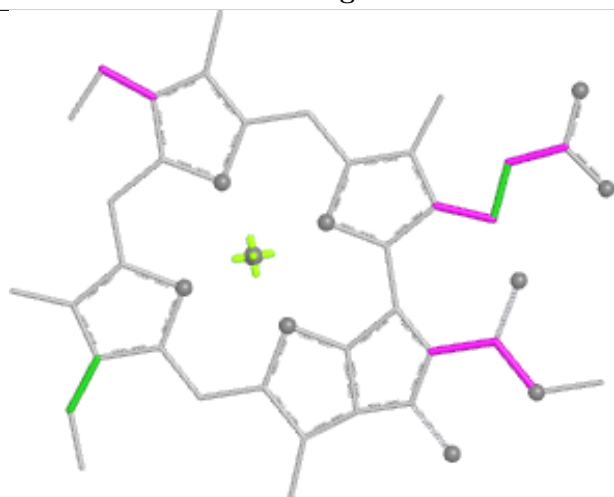
## Ligand CLA A 819



Bond lengths



Bond angles

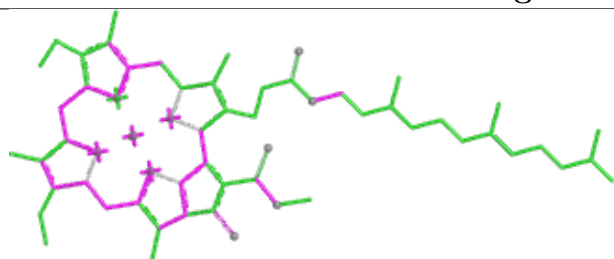


Torsions

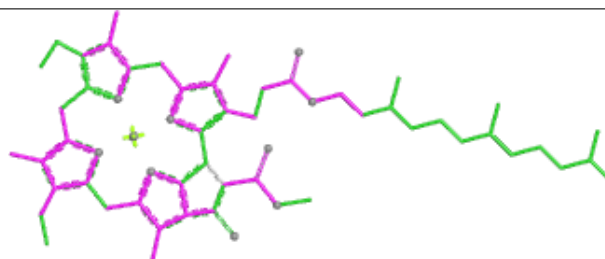


Rings

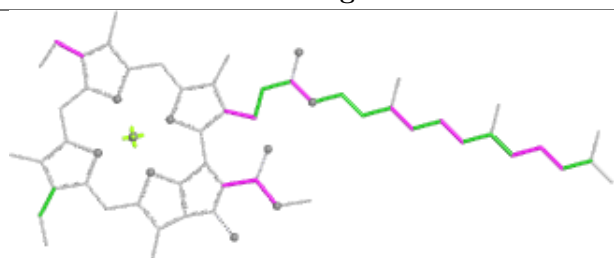
## Ligand CLA B 833



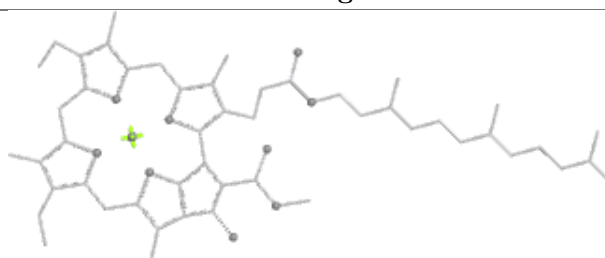
Bond lengths



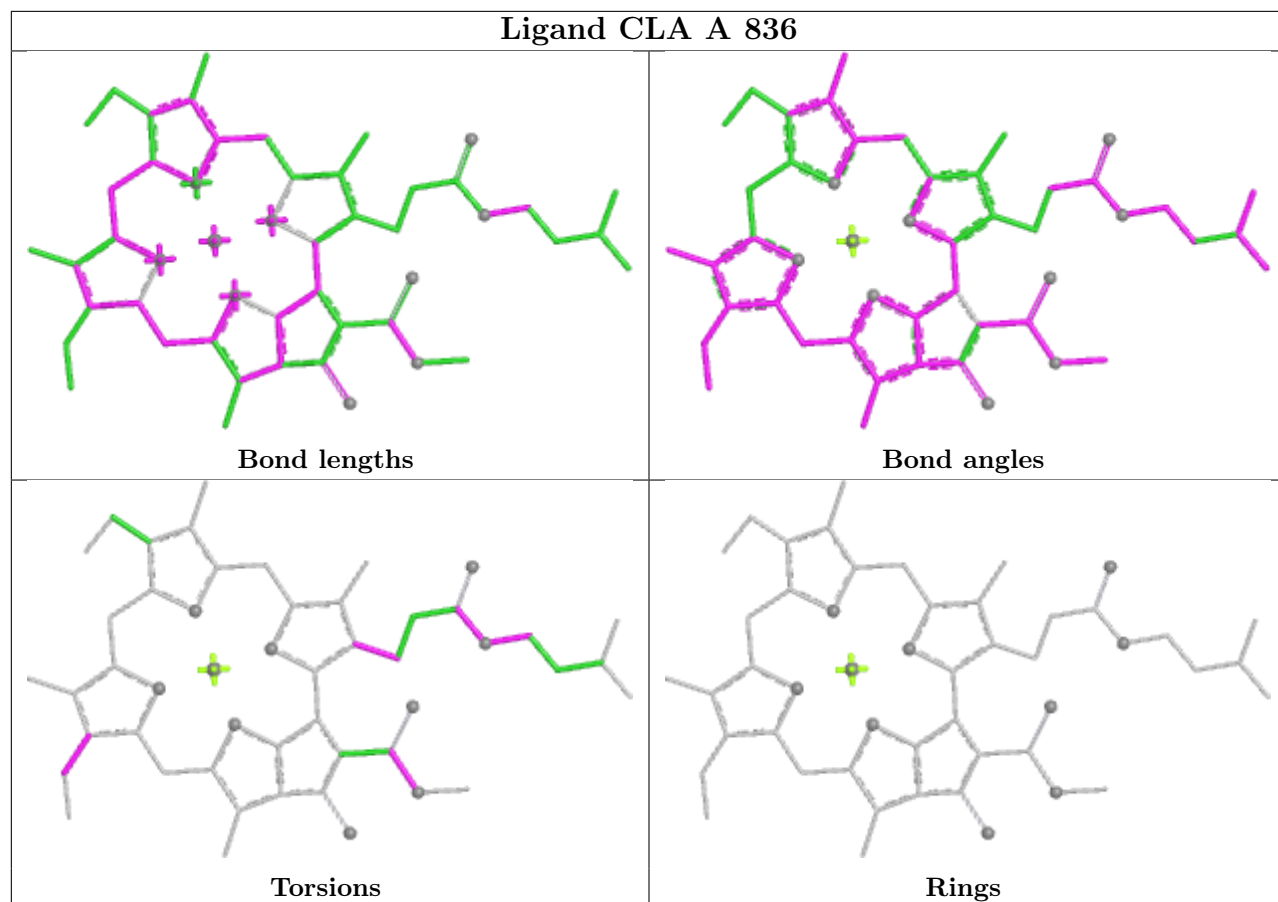
Bond angles



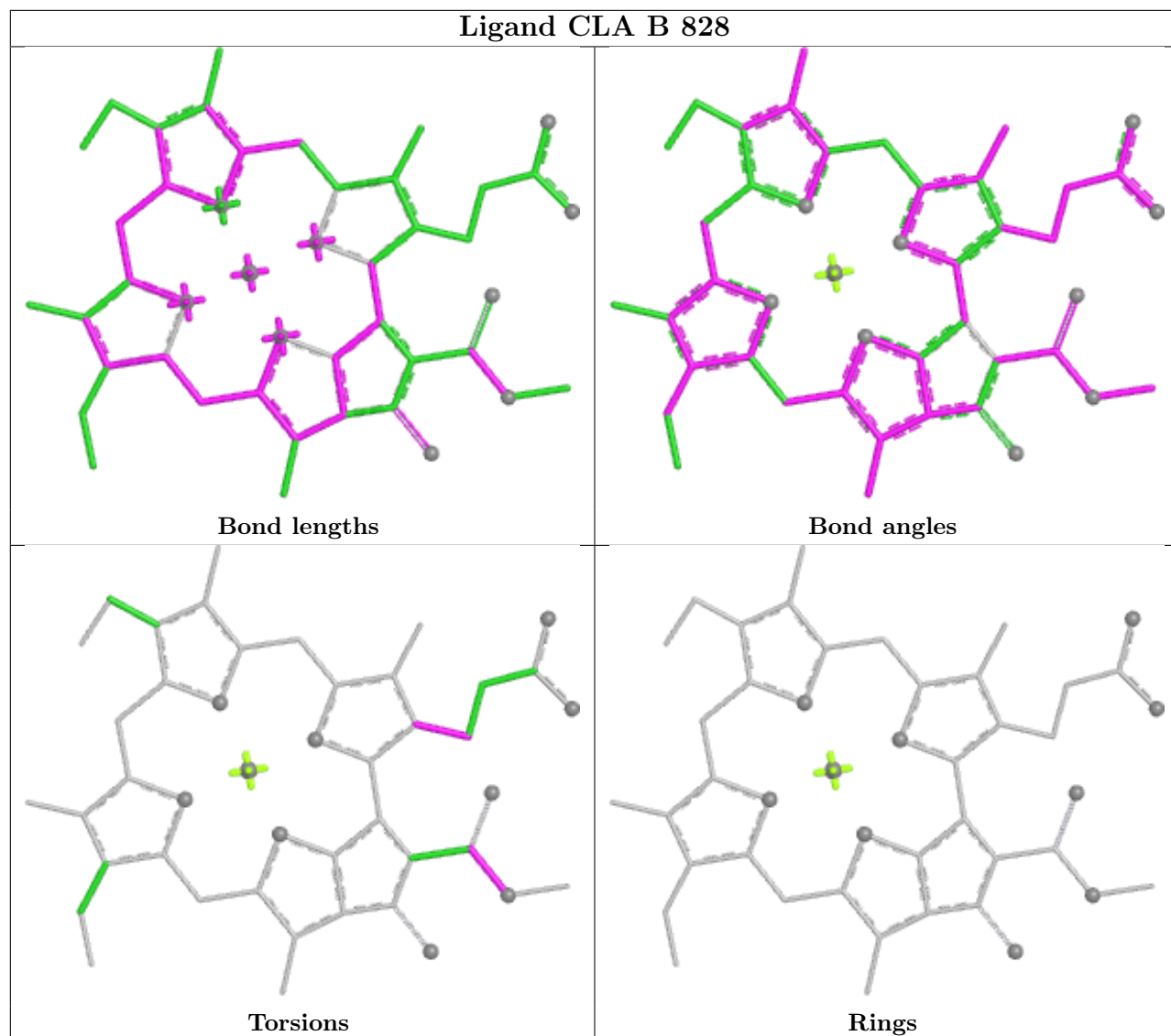
Torsions



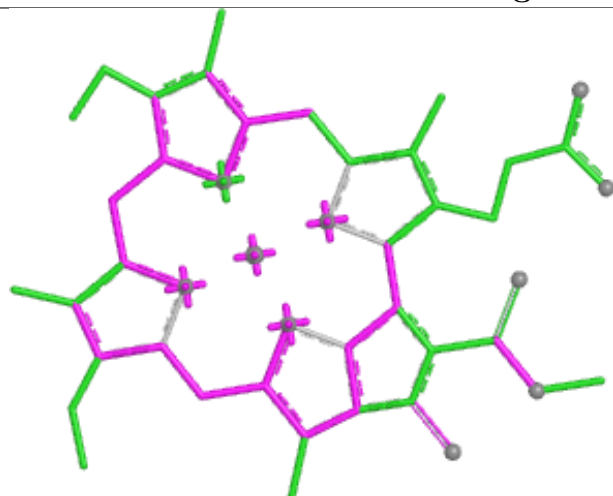
Rings



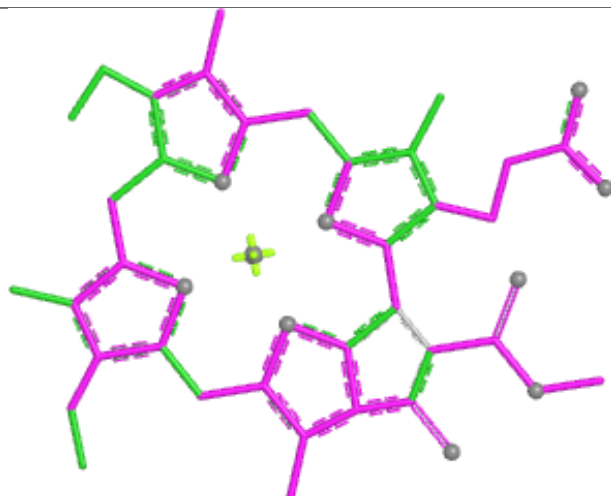
## Ligand CLA B 828



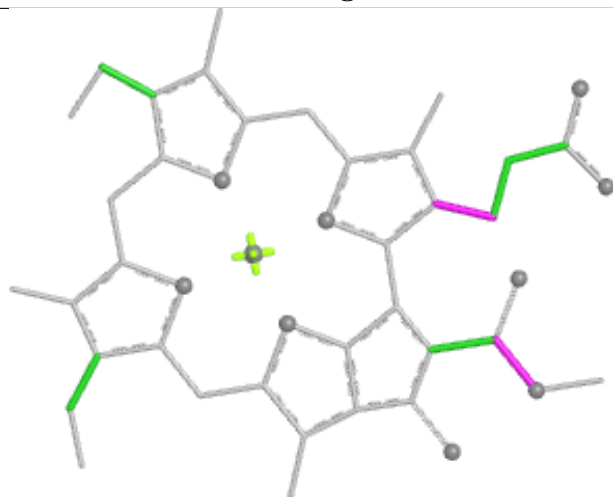
## Ligand CLA H 829



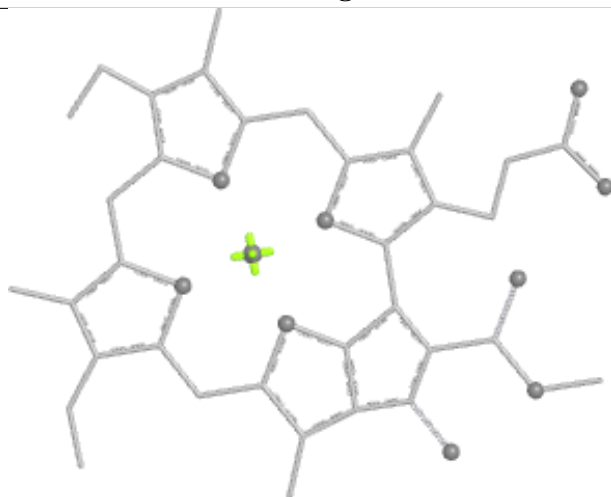
Bond lengths



Bond angles

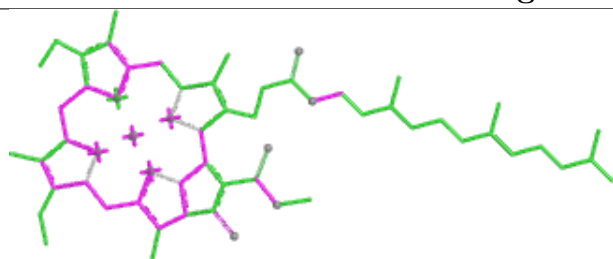


Torsions

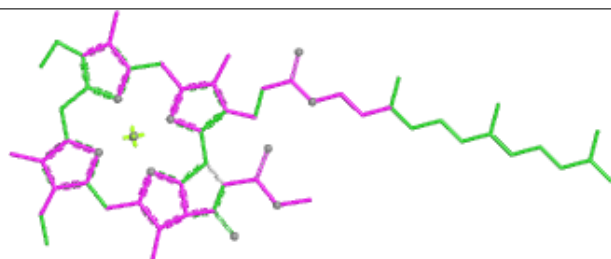


Rings

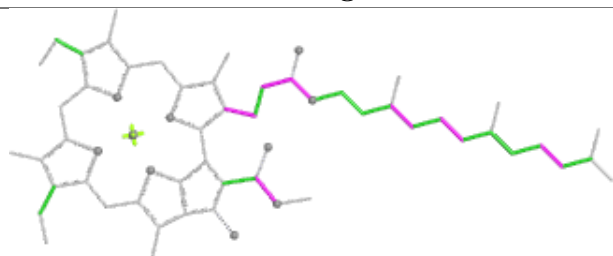
## Ligand CLA b 811



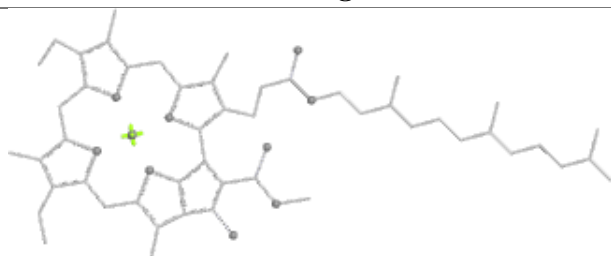
Bond lengths



Bond angles

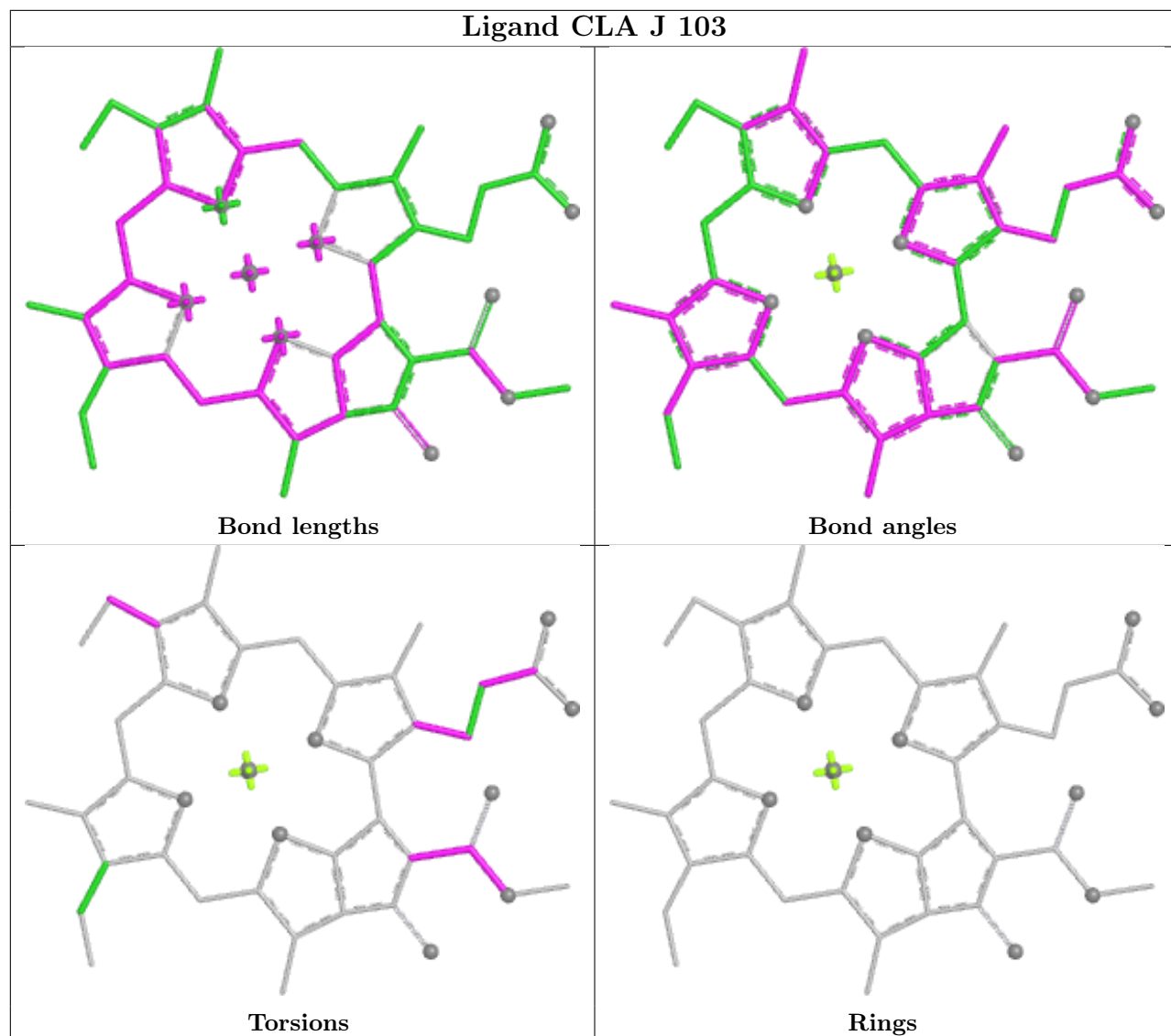


Torsions

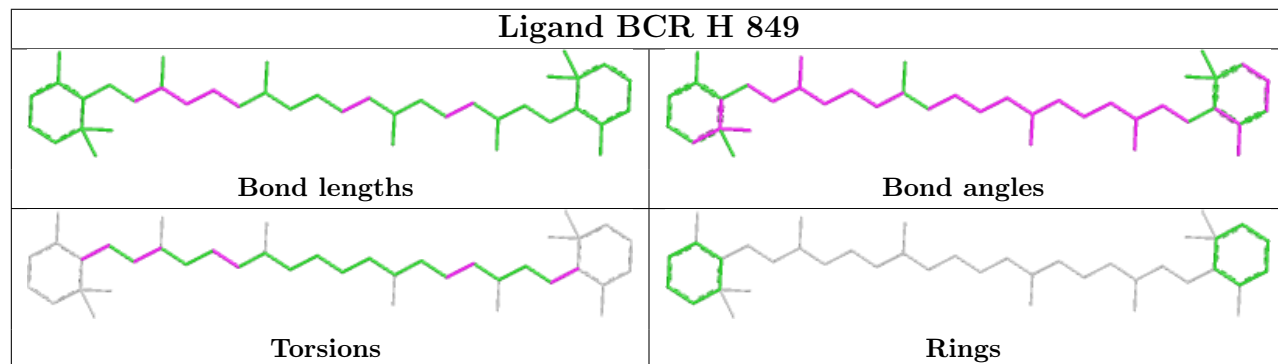


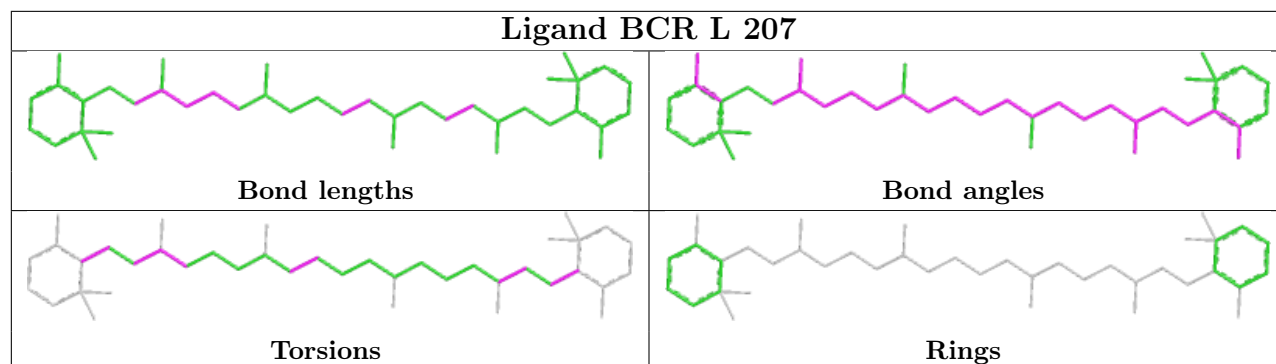
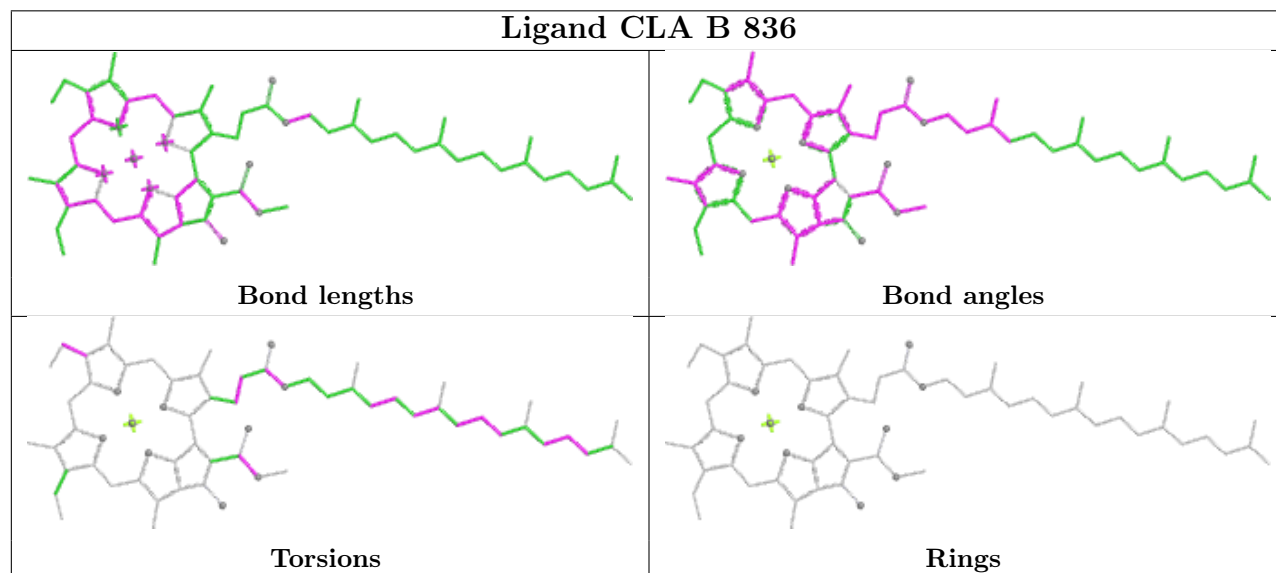
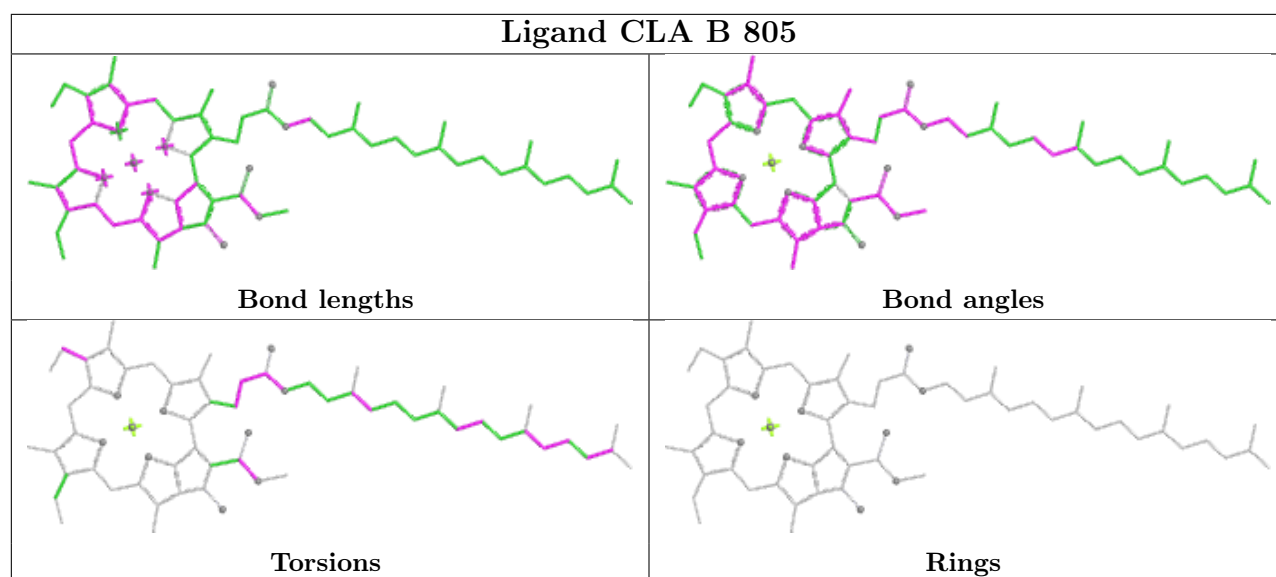
Rings

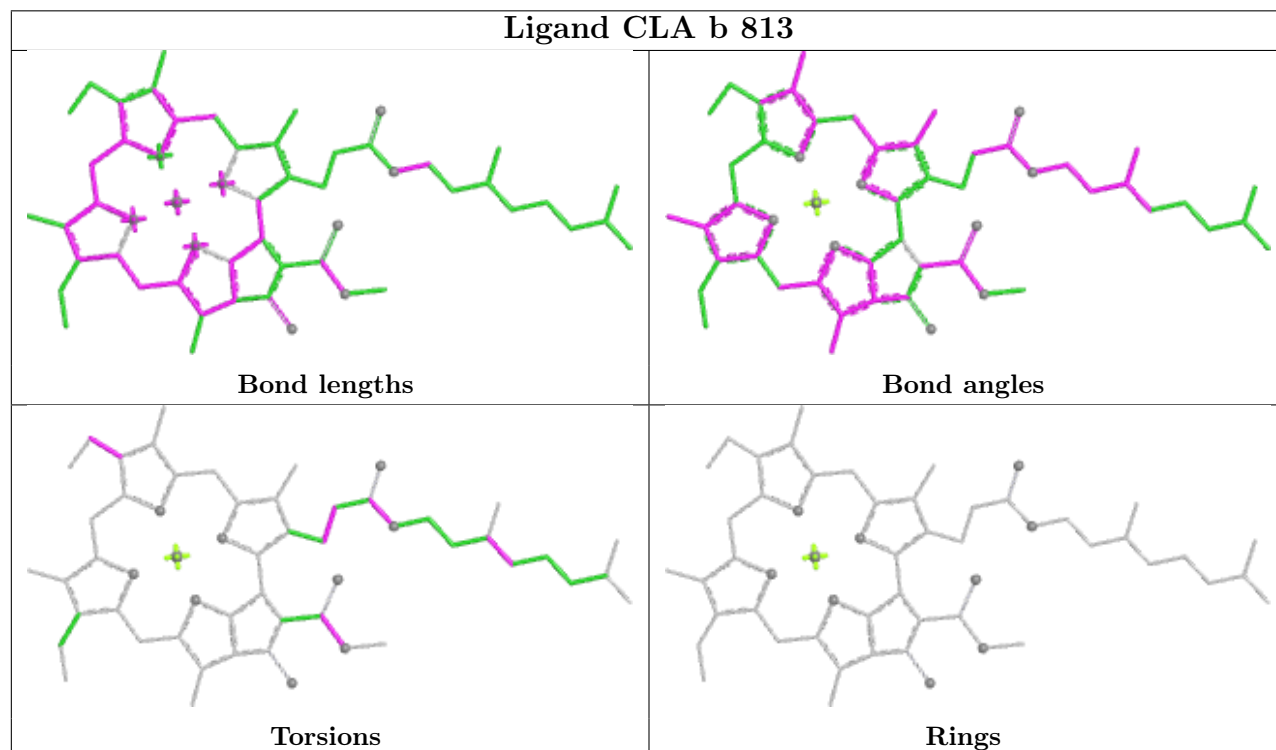
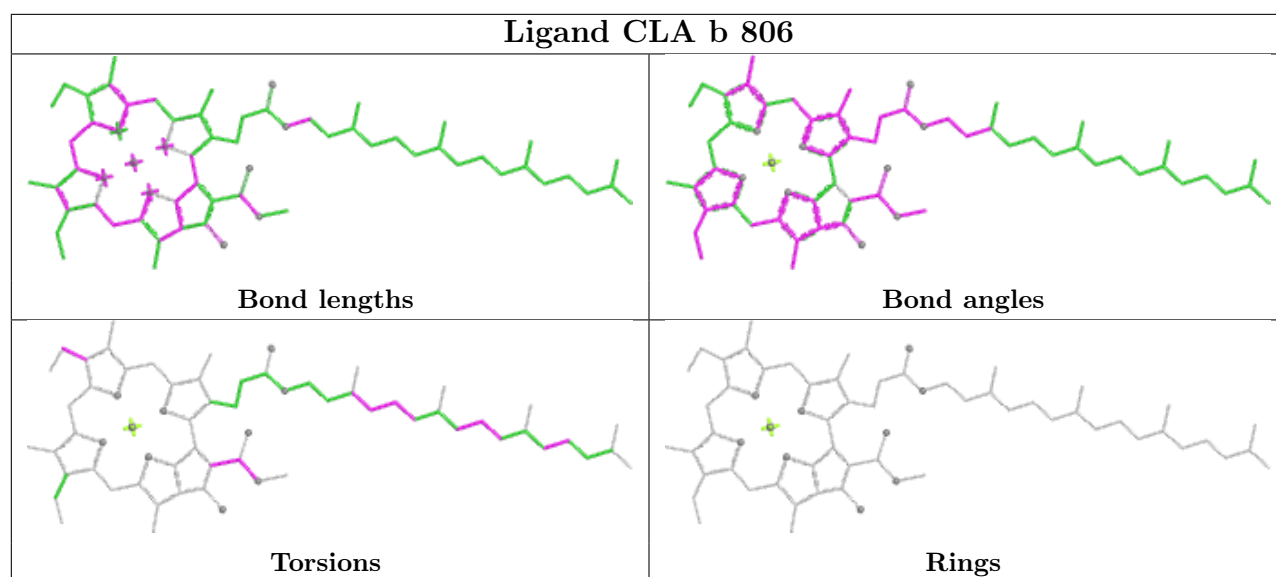
## Ligand CLA J 103

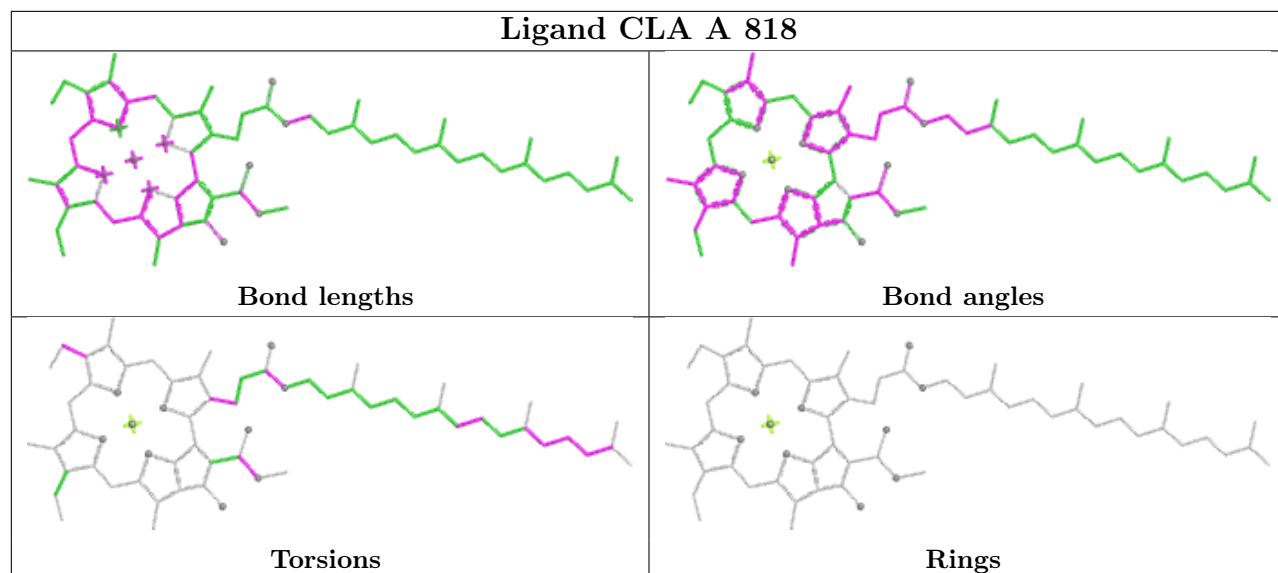
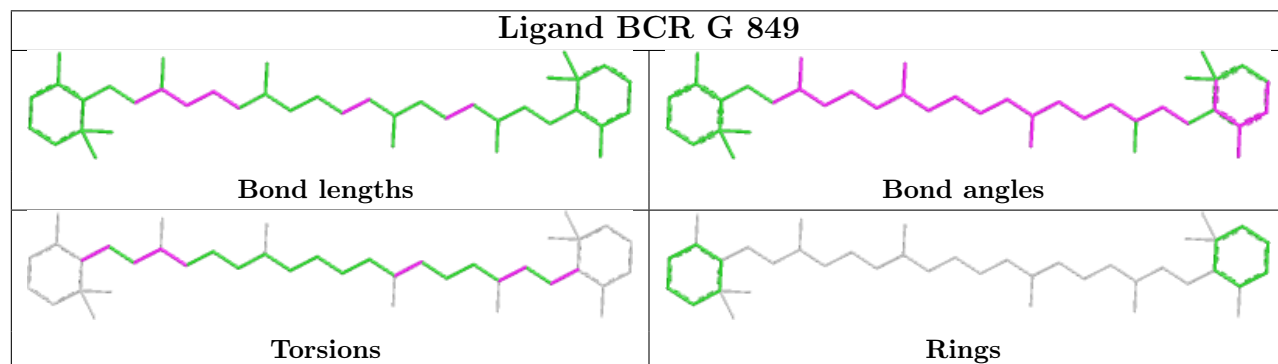
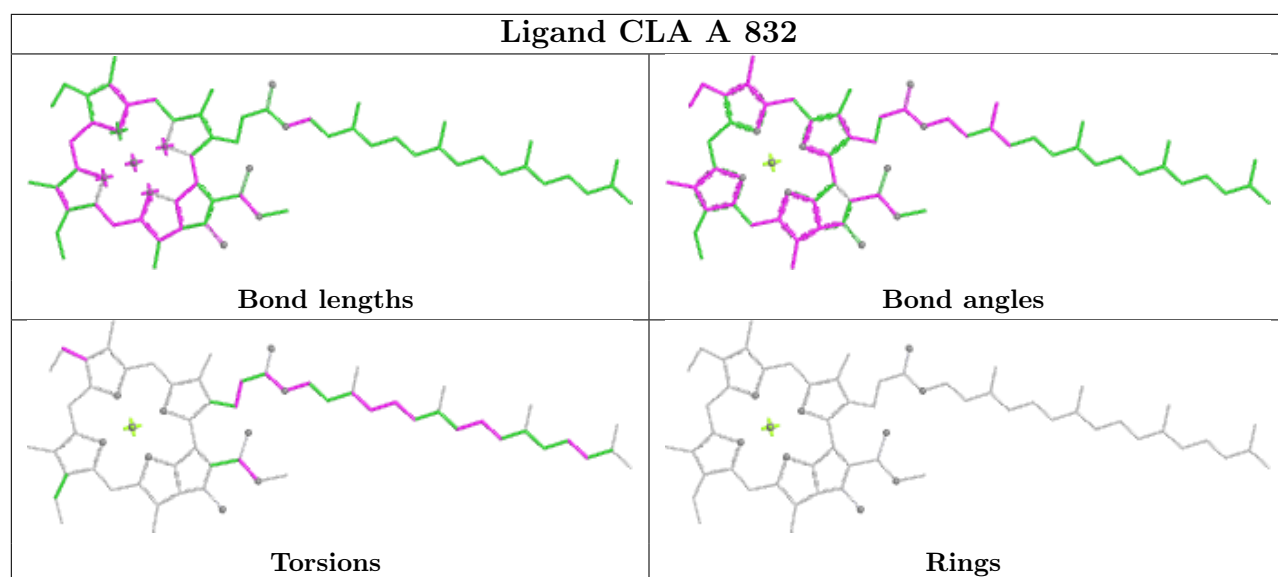


## Ligand BCR H 849

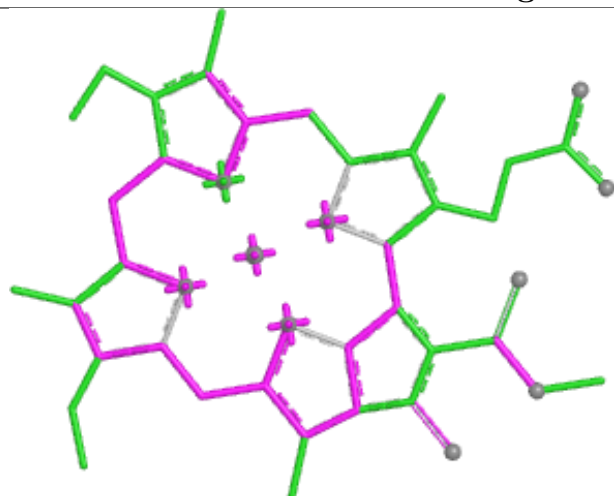




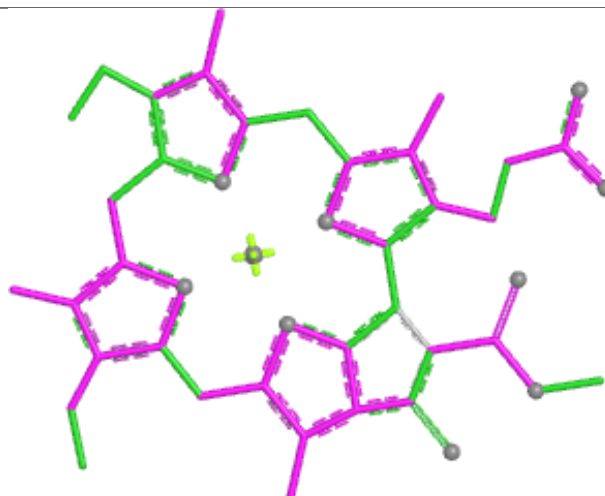




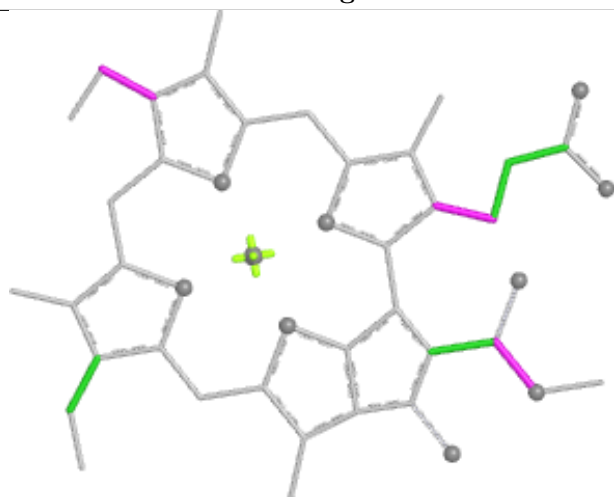
## Ligand CLA b 831



Bond lengths



Bond angles

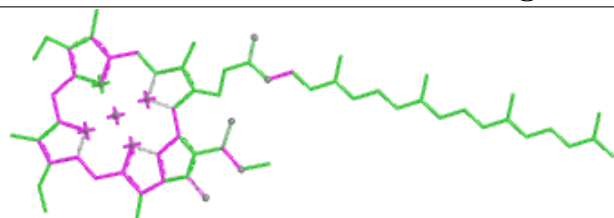


Torsions

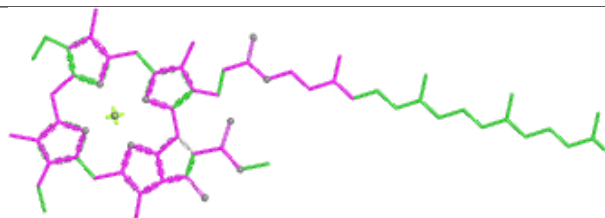


Rings

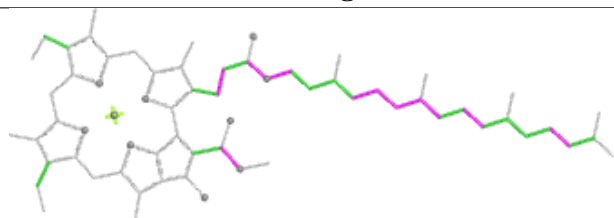
## Ligand CLA a 803



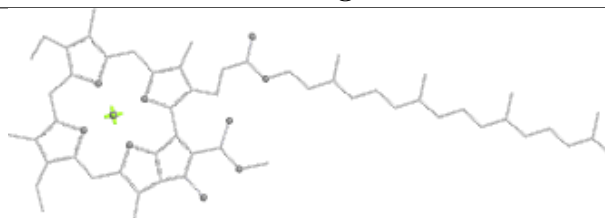
Bond lengths



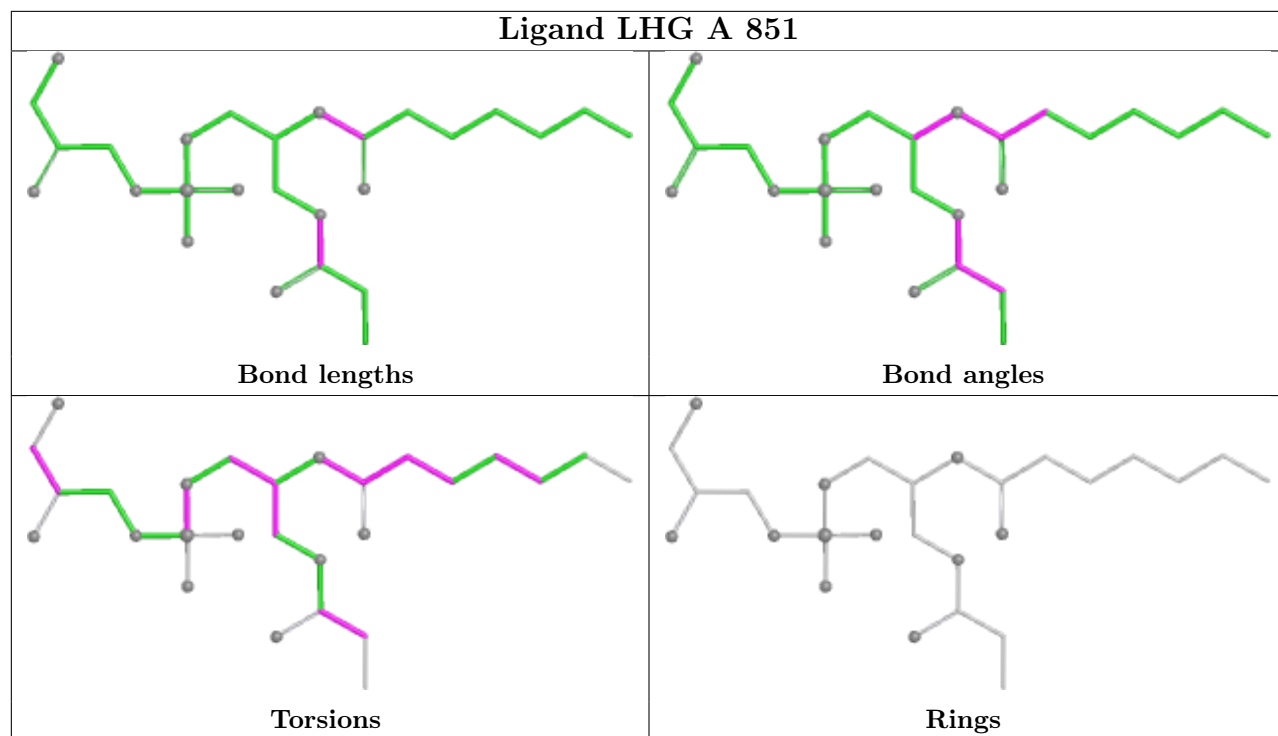
Bond angles



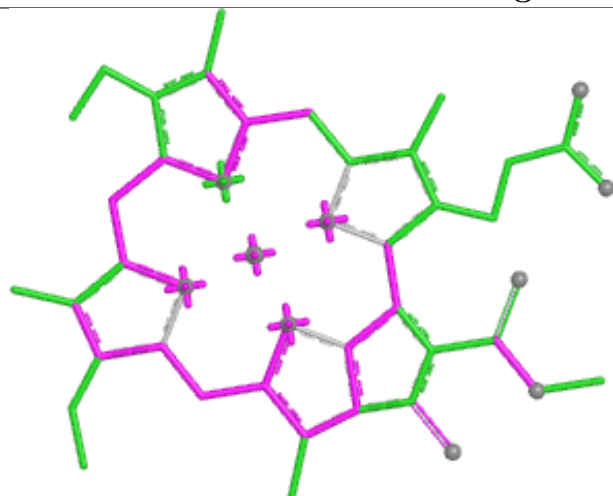
Torsions



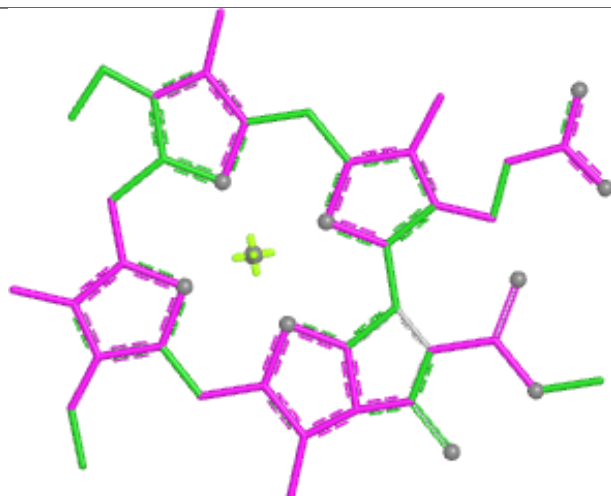
Rings



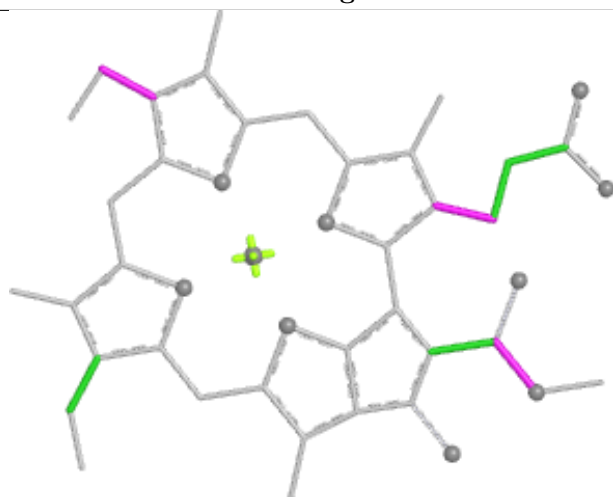
## Ligand CLA B 832



Bond lengths



Bond angles

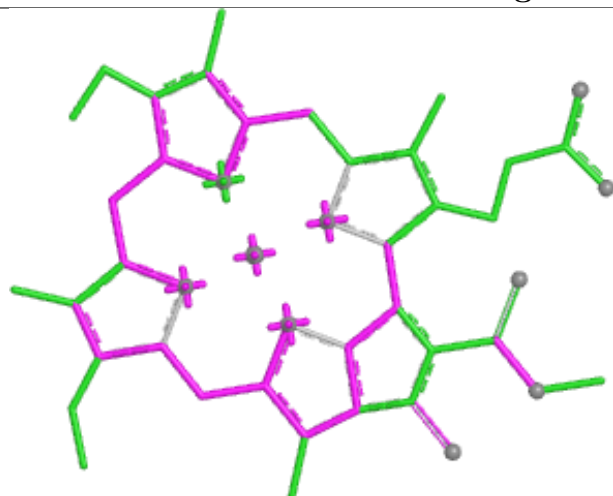


Torsions

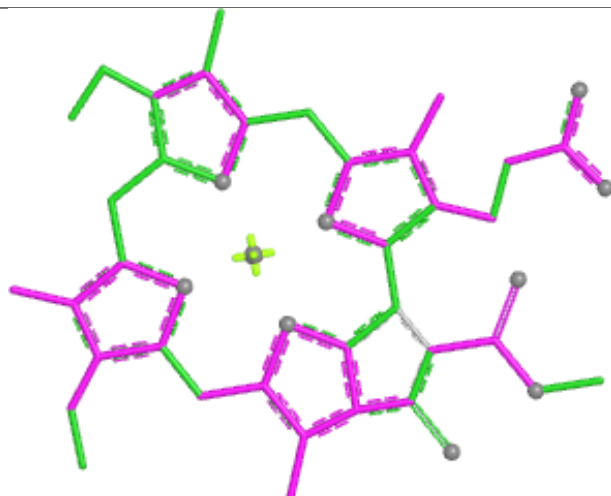


Rings

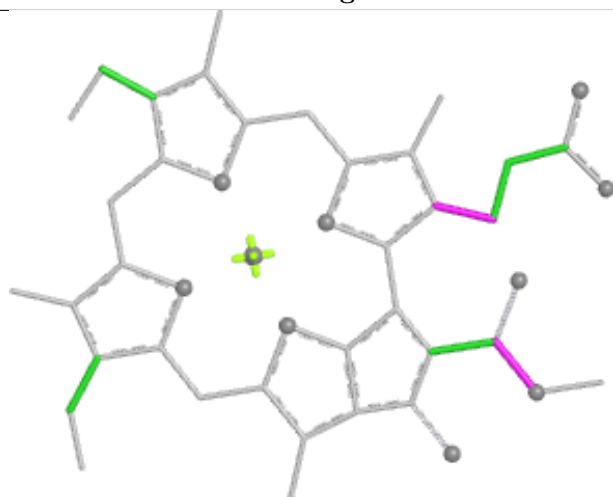
## Ligand CLA B 818



Bond lengths



Bond angles

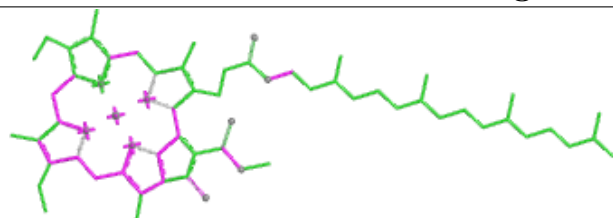


Torsions

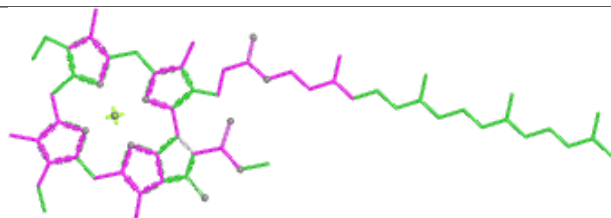


Rings

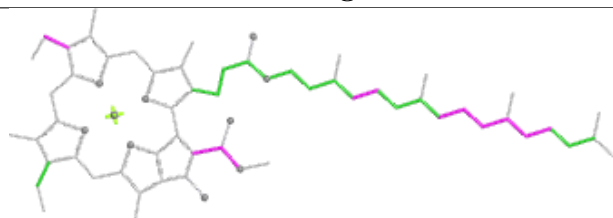
## Ligand CLA H 831



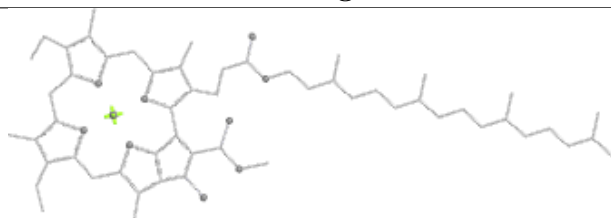
Bond lengths



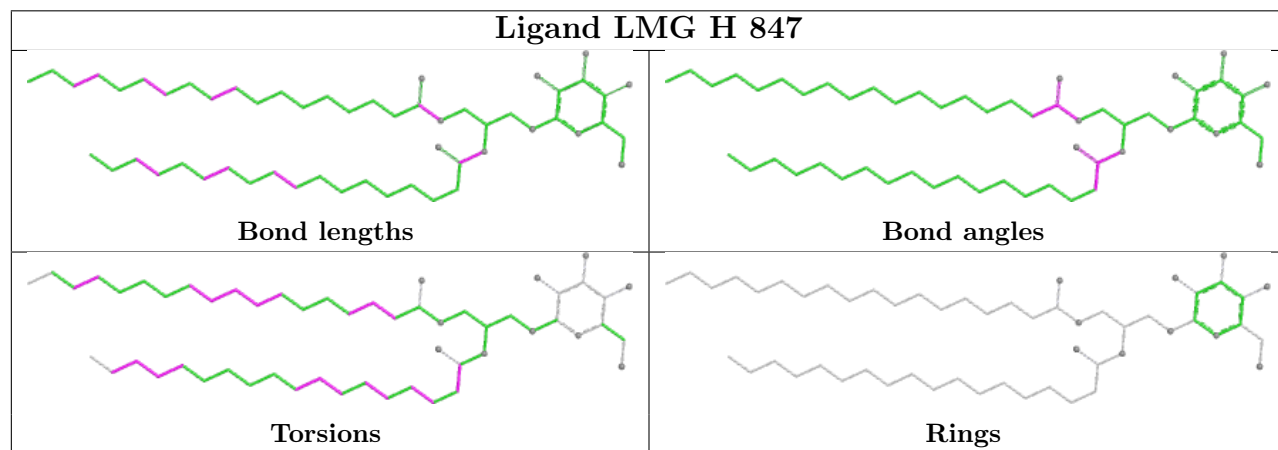
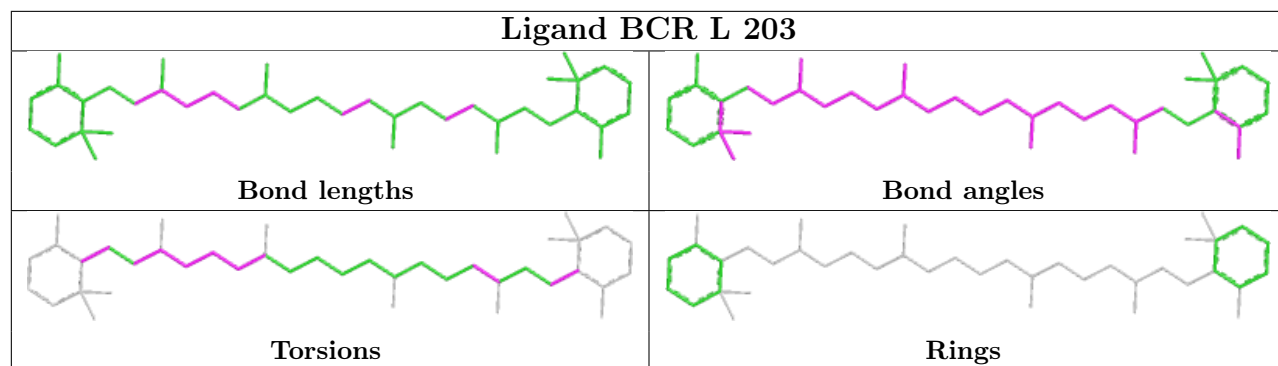
Bond angles

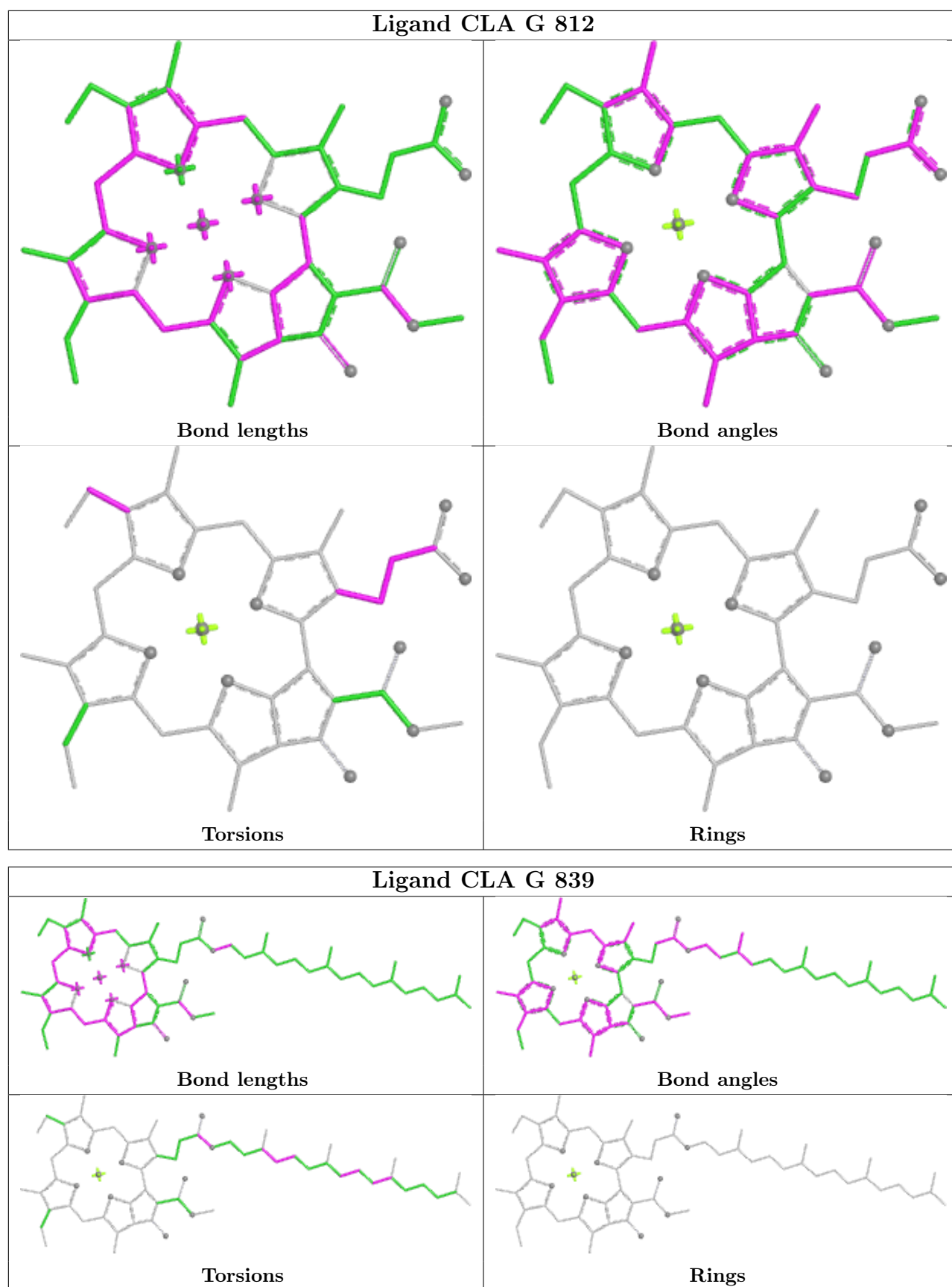


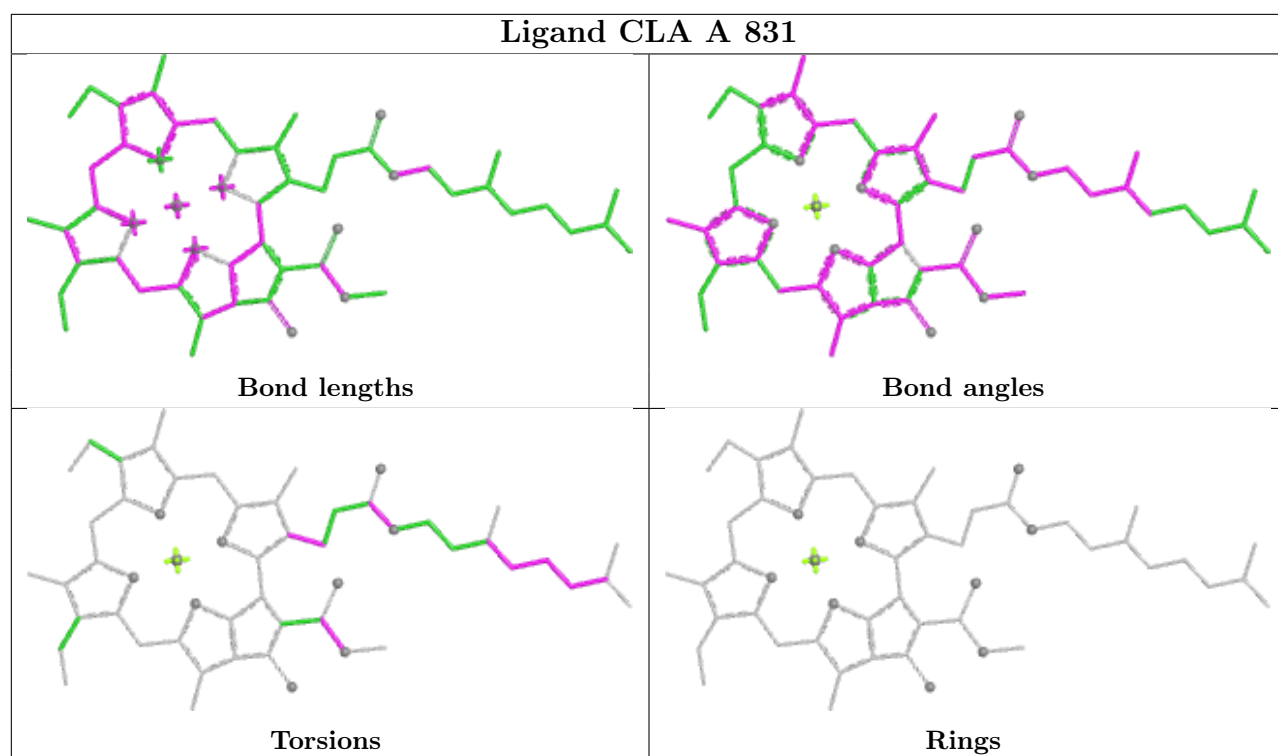
Torsions



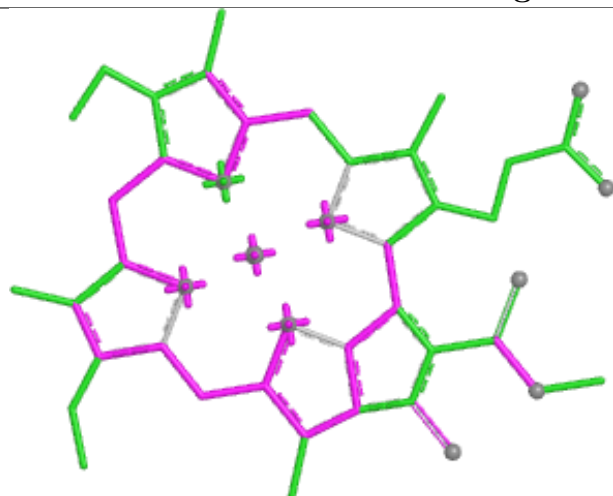
Rings



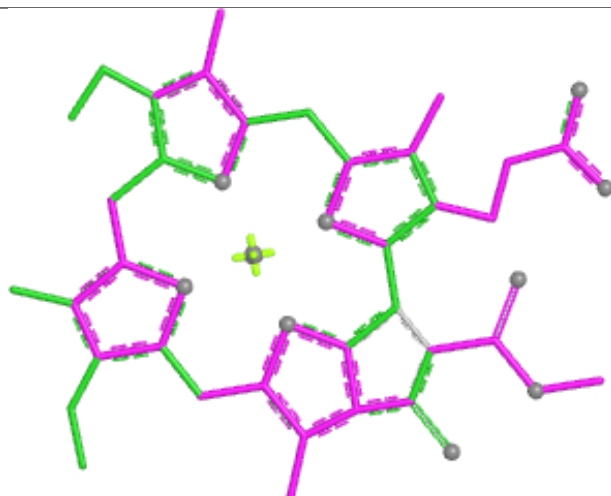




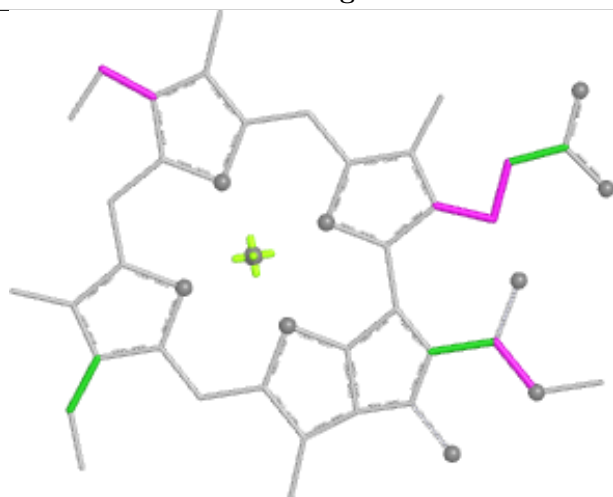
## Ligand CLA A 809



Bond lengths



Bond angles

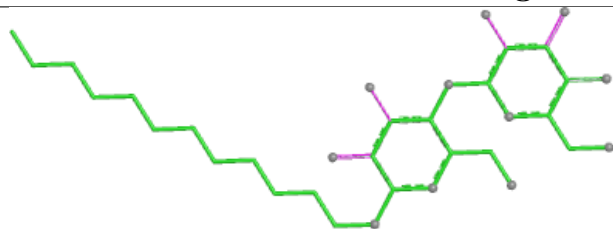


Torsions

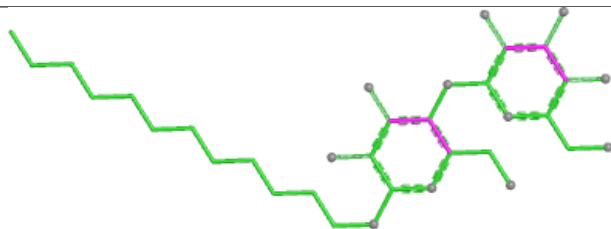


Rings

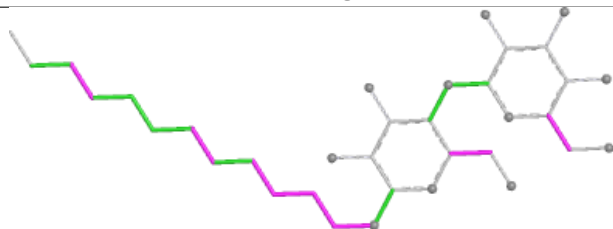
## Ligand LMT b 846



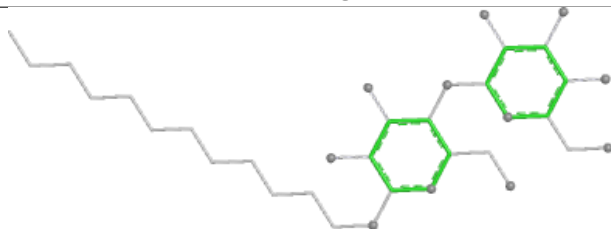
Bond lengths



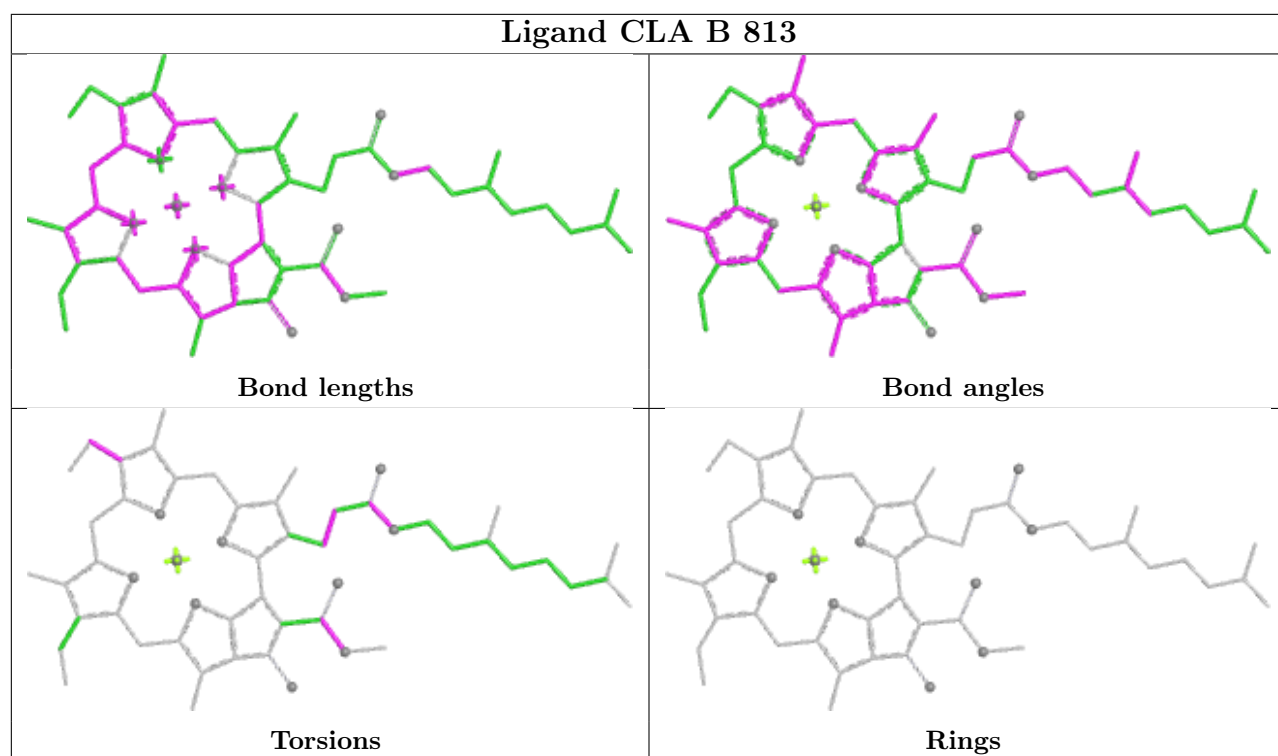
Bond angles



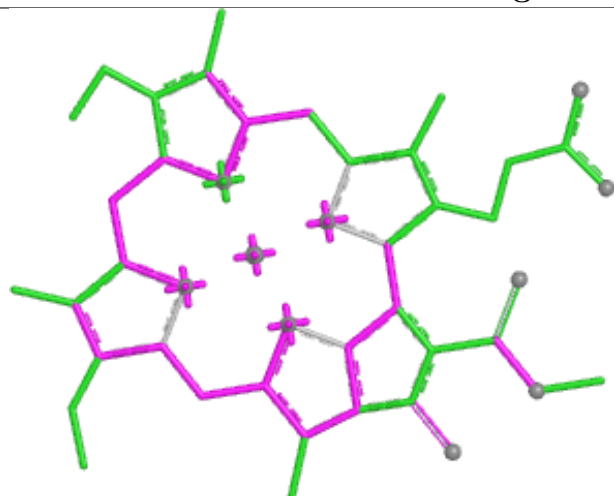
Torsions



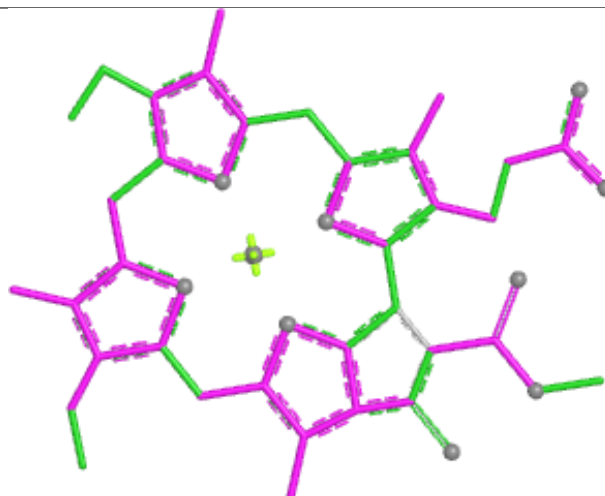
Rings



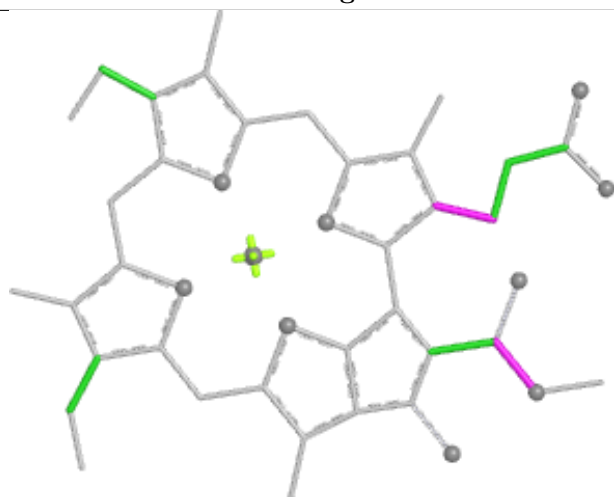
## Ligand CLA H 809



Bond lengths



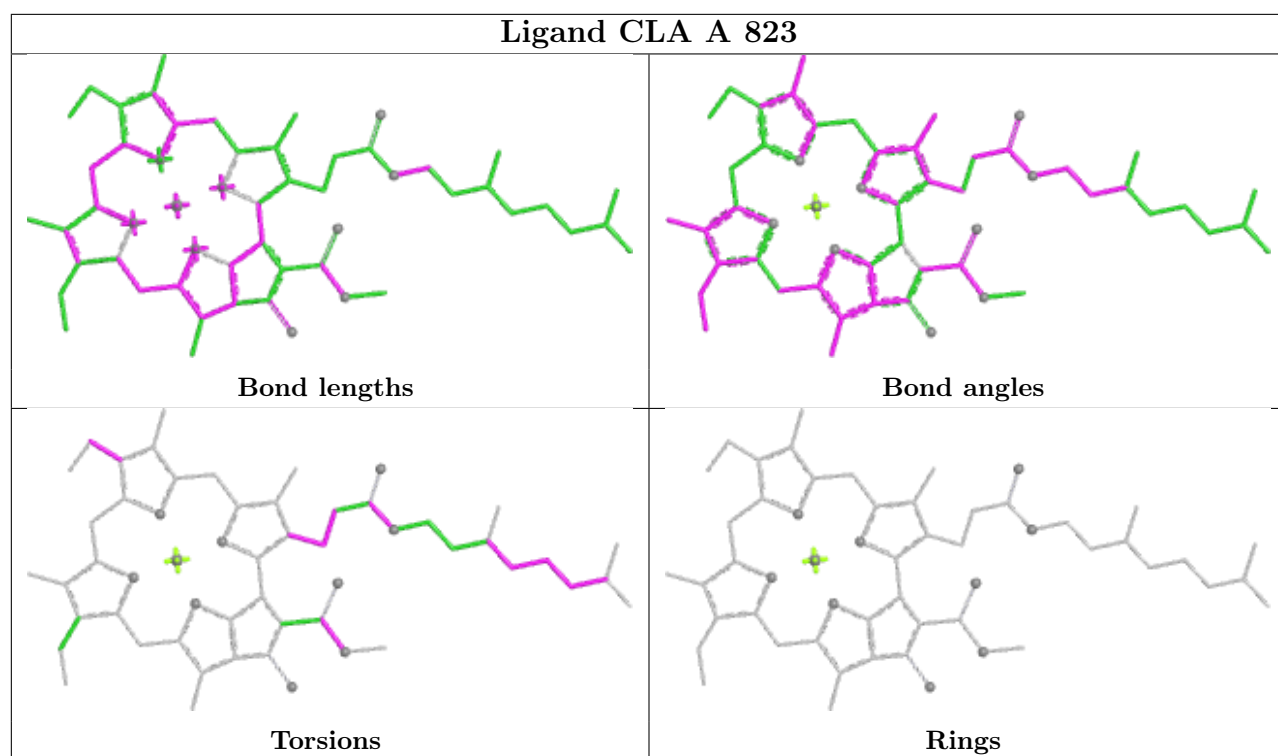
Bond angles



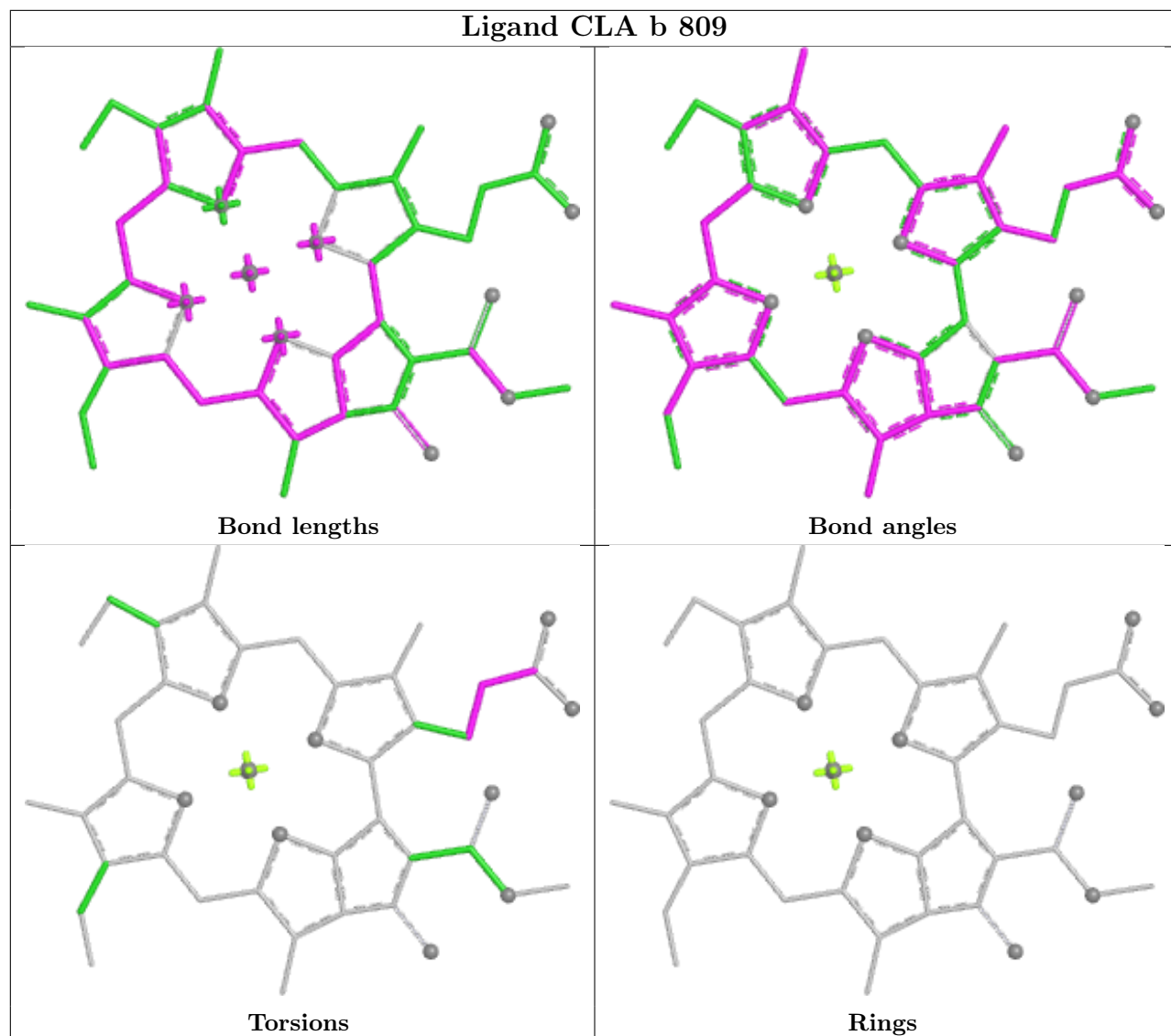
Torsions

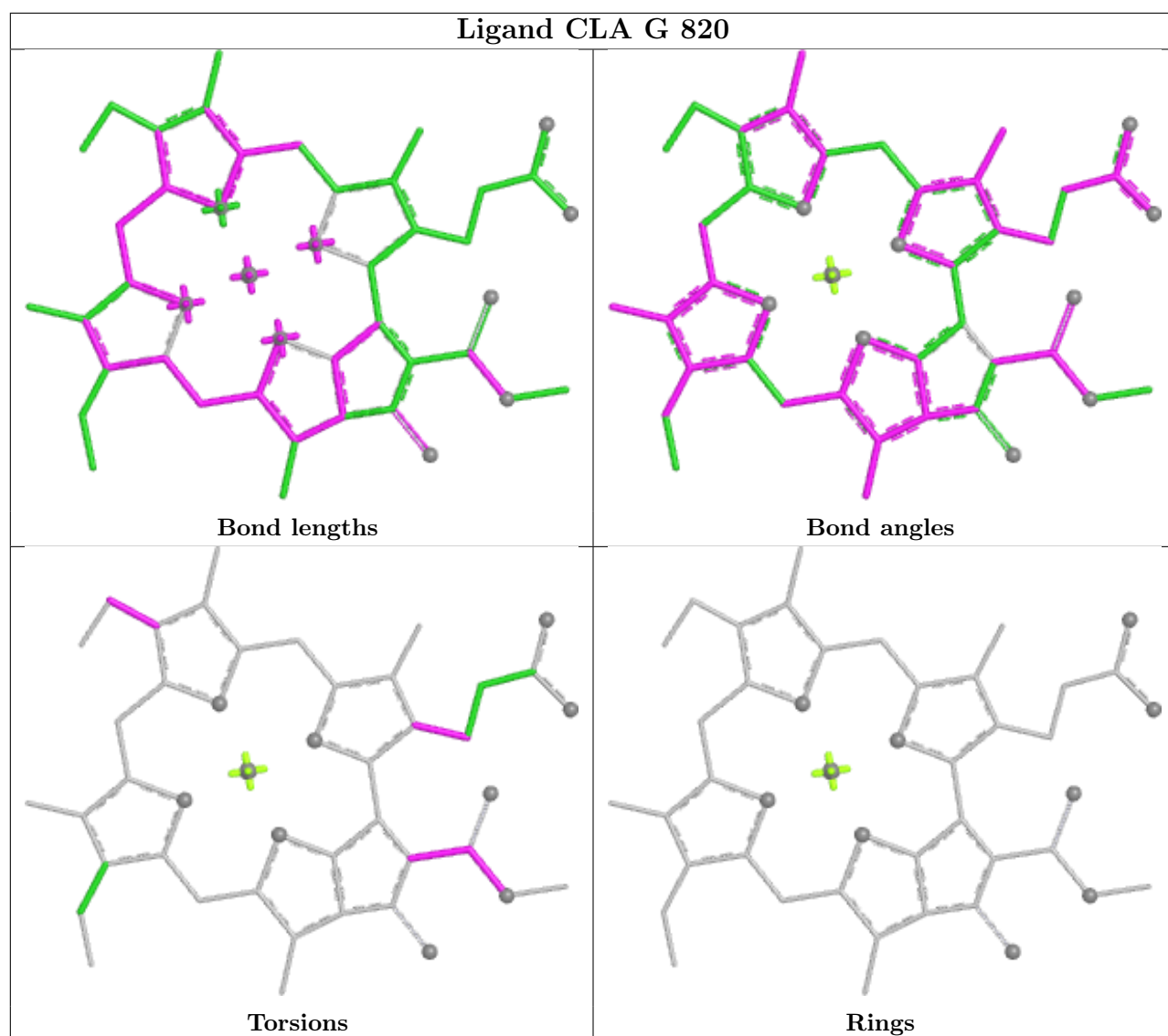


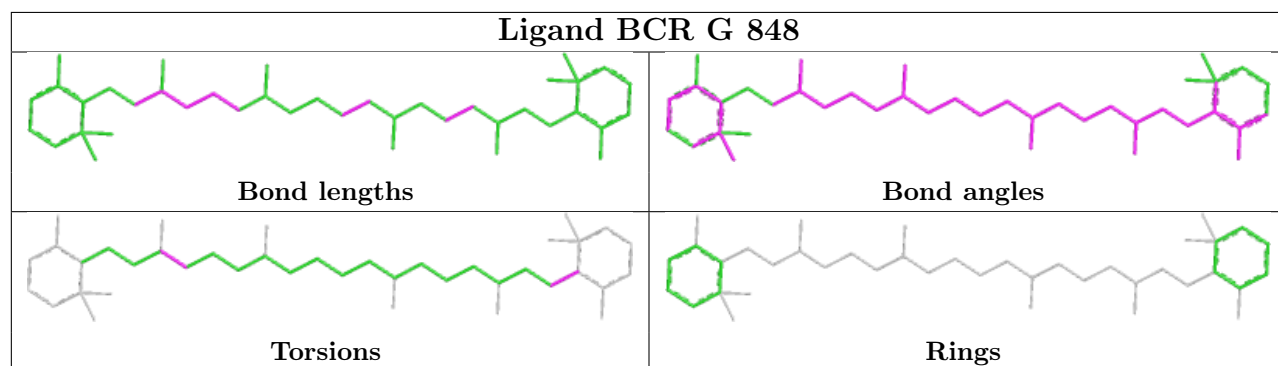
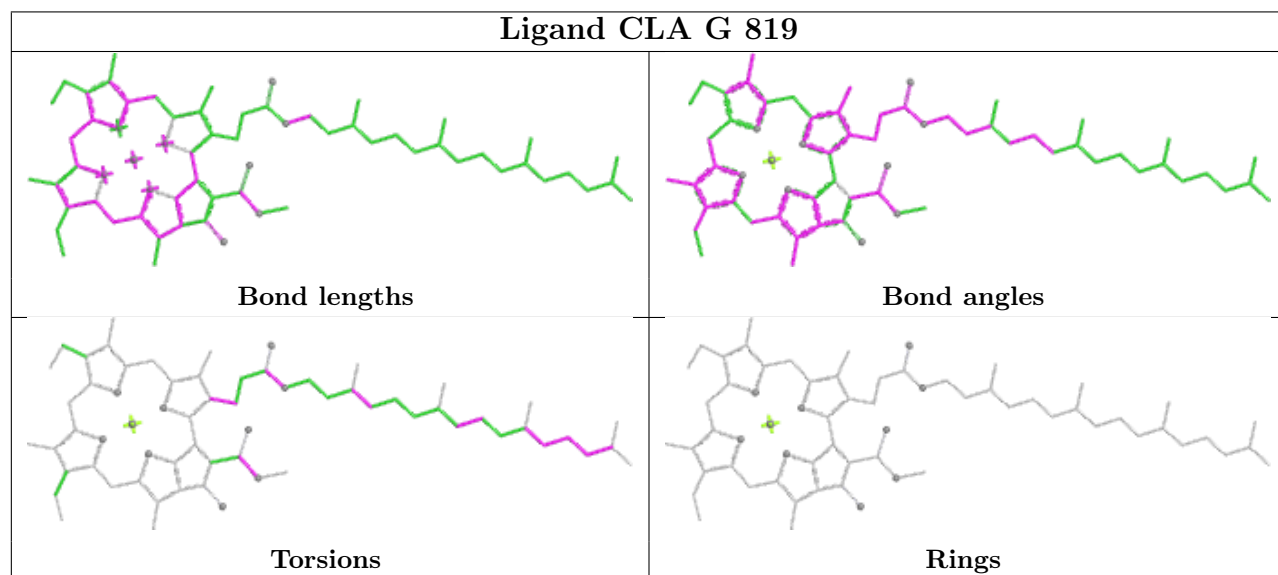
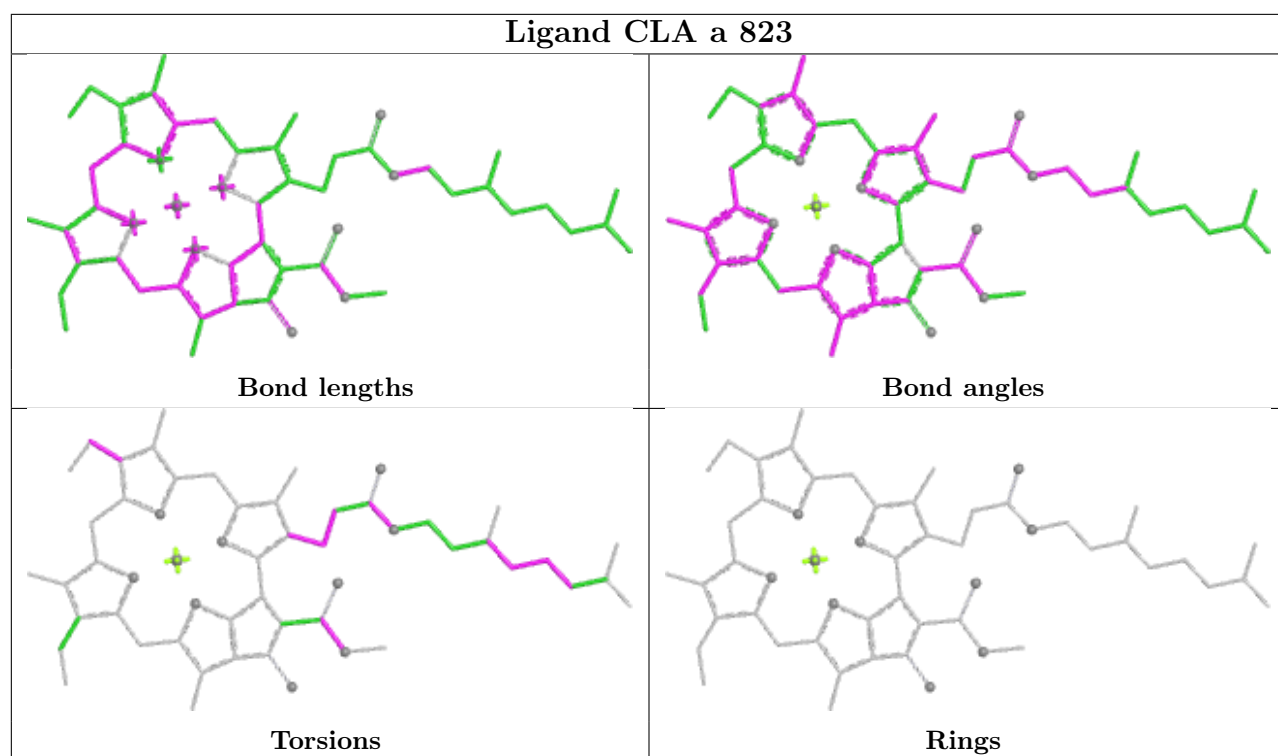
Rings



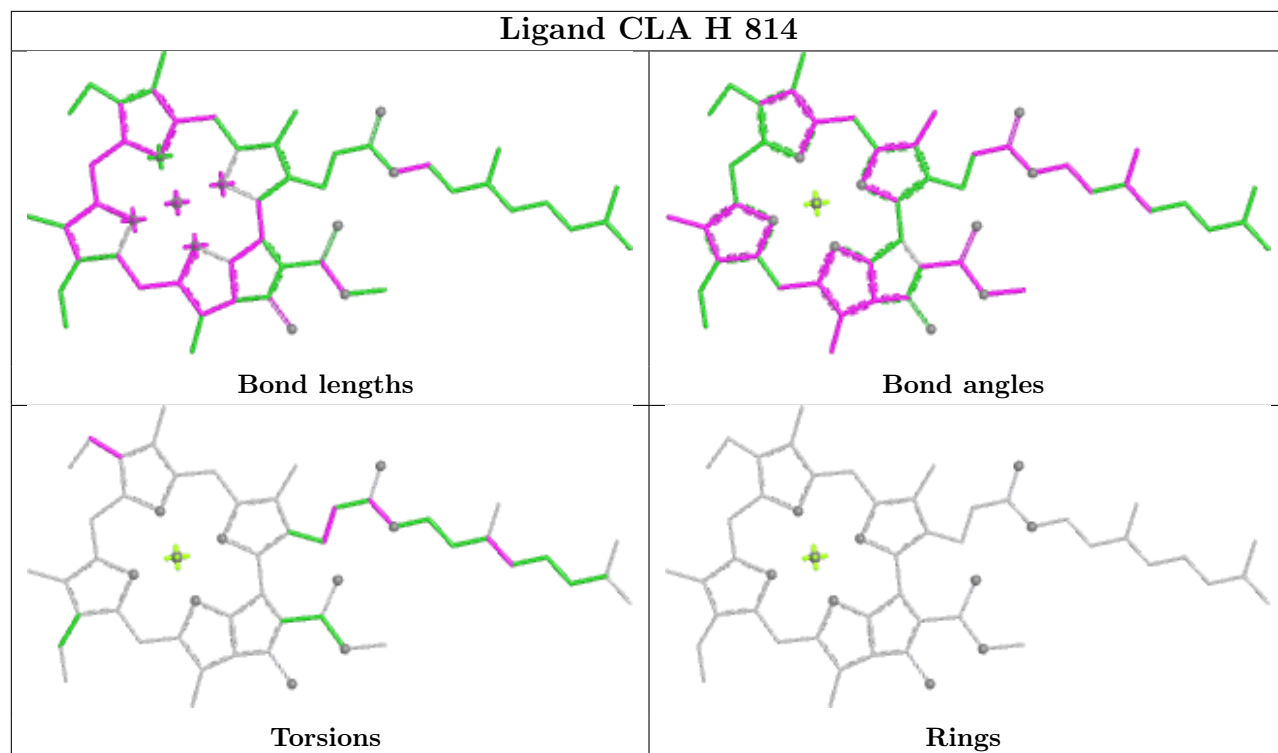
## Ligand CLA b 809



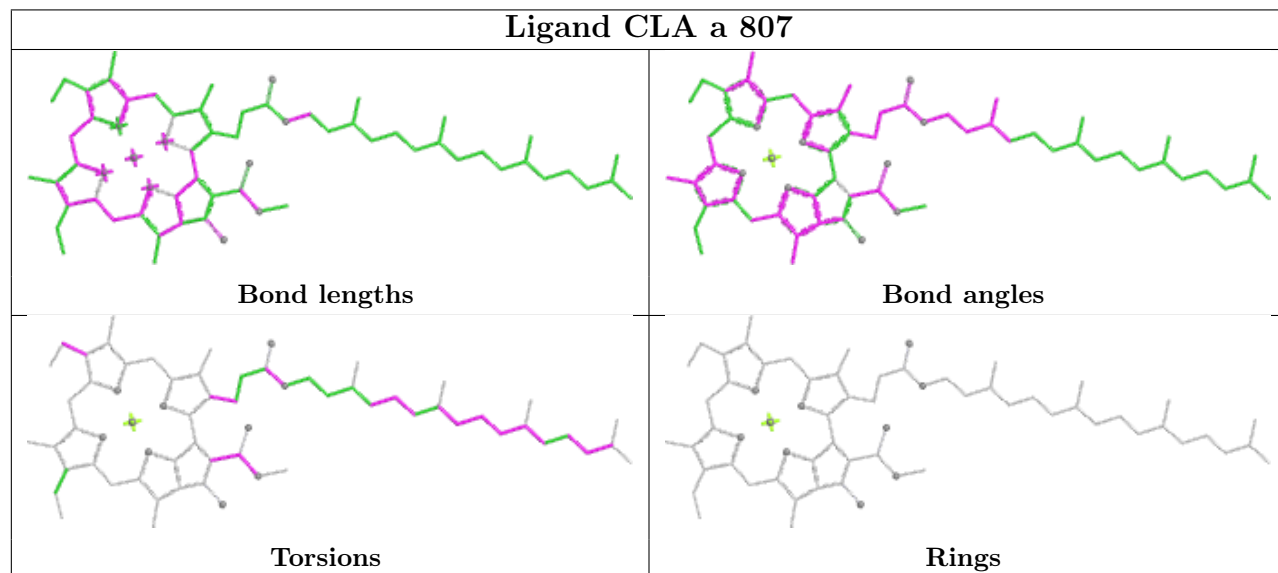




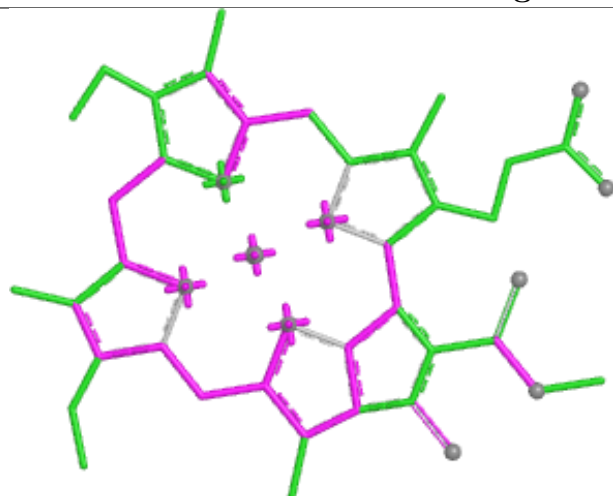
## Ligand CLA H 814



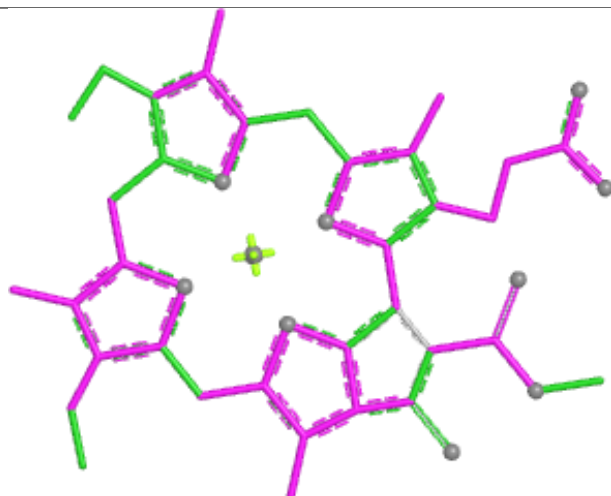
## Ligand CLA a 807



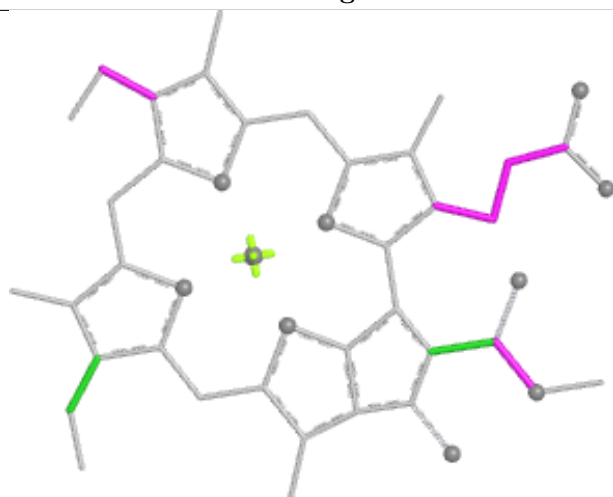
## Ligand CLA A 835



Bond lengths



Bond angles

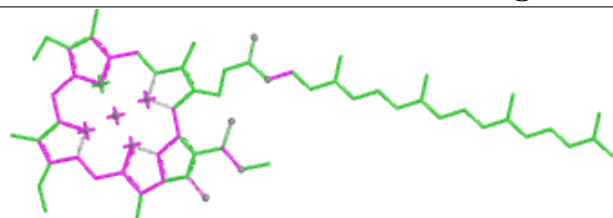


Torsions

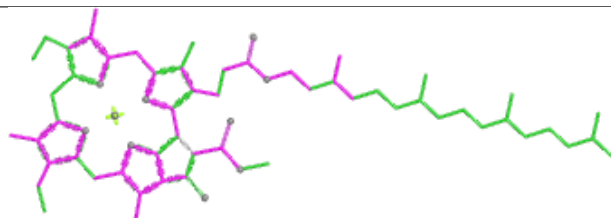


Rings

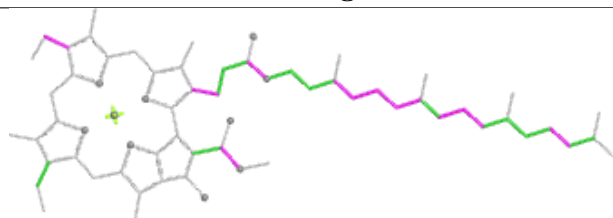
## Ligand CLA H 817



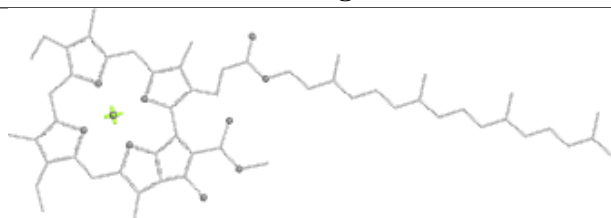
Bond lengths



Bond angles

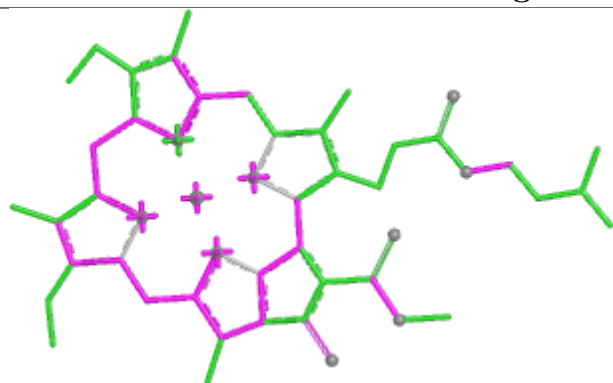


Torsions

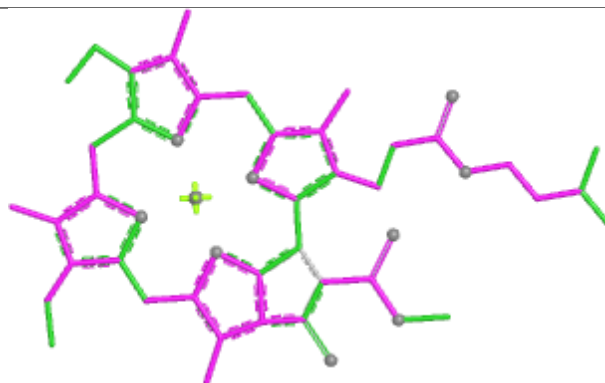


Rings

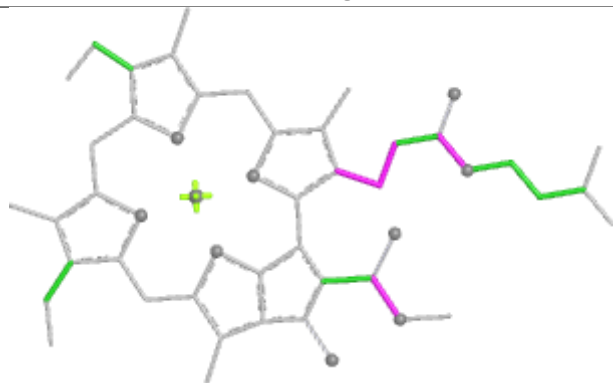
## Ligand CLA G 809



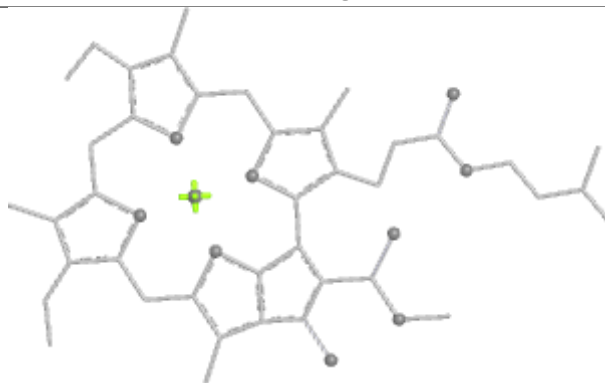
Bond lengths



Bond angles

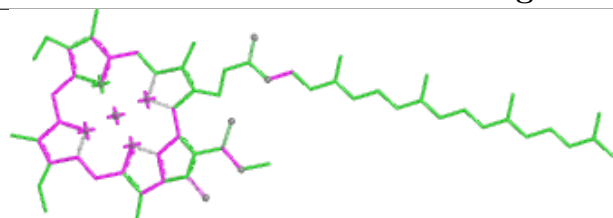


Torsions

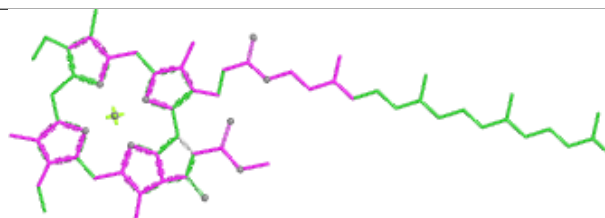


Rings

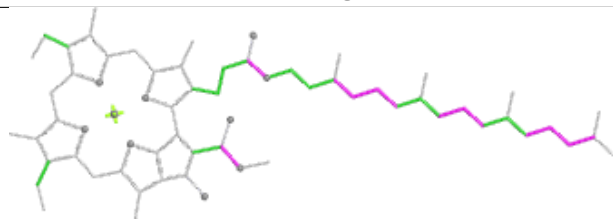
## Ligand CLA F 201



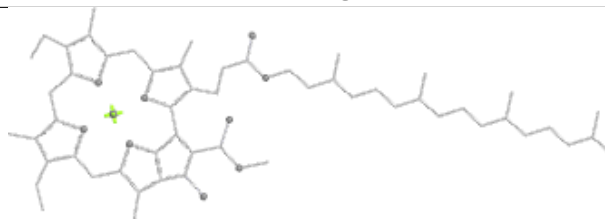
Bond lengths



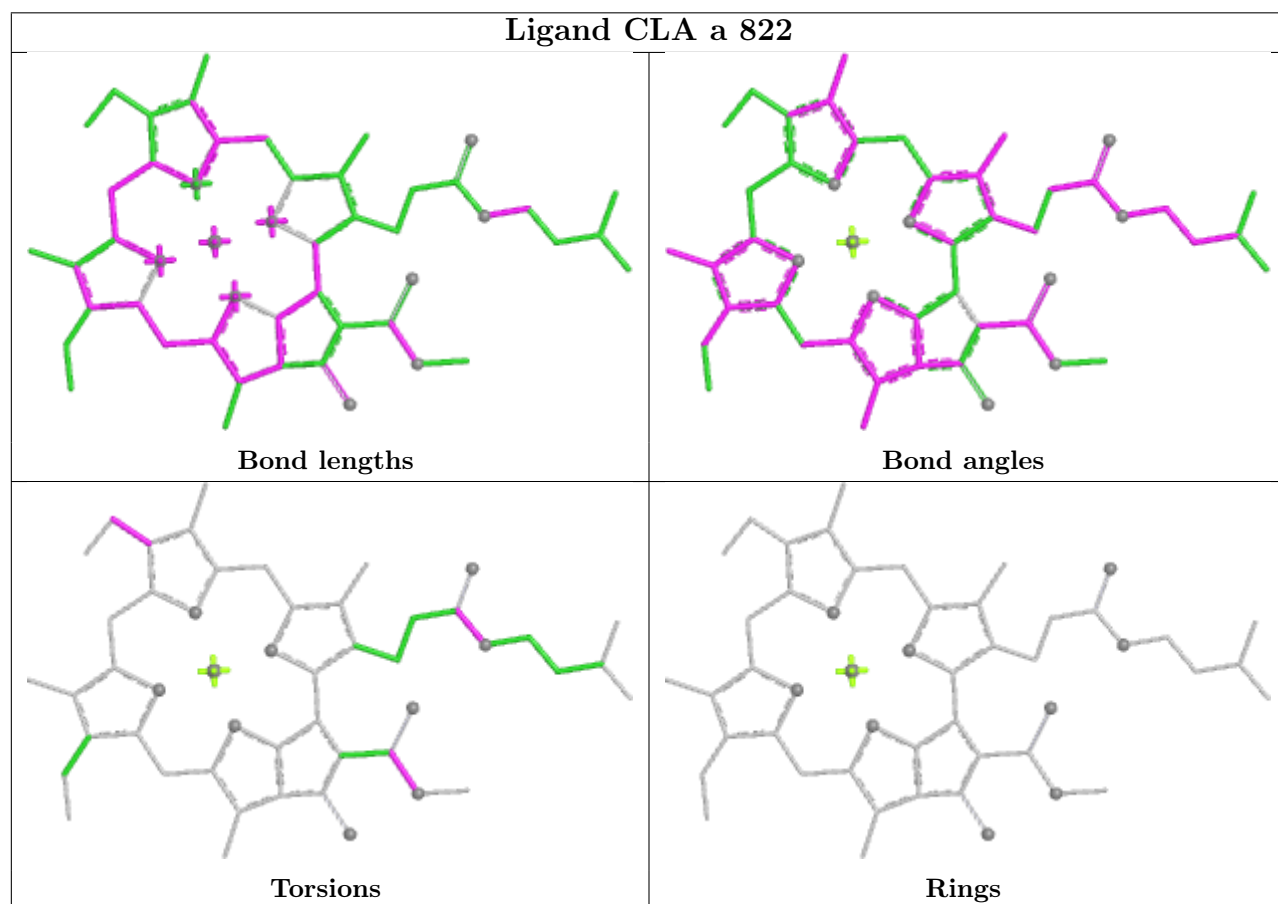
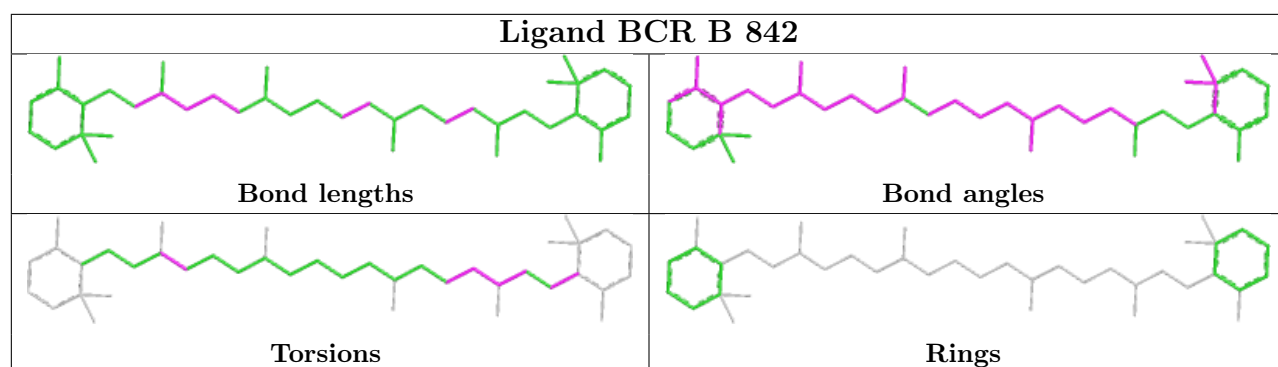
Bond angles

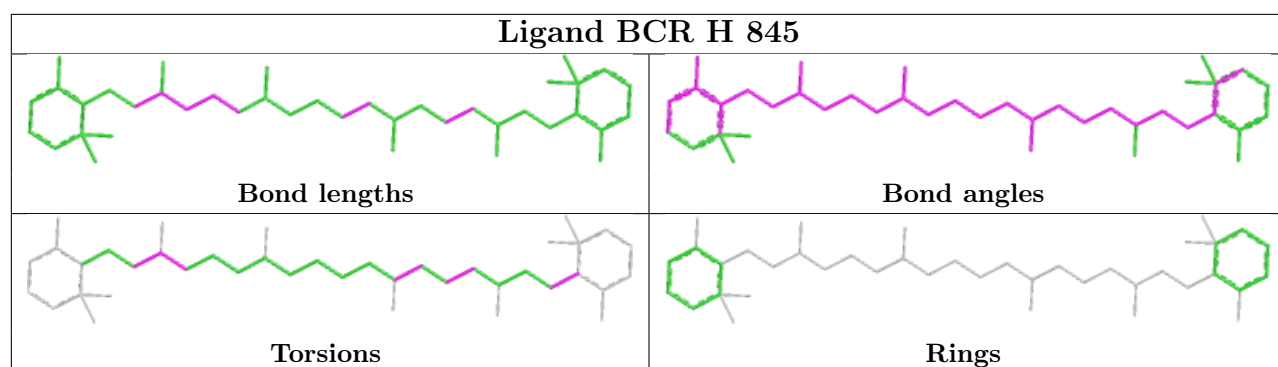
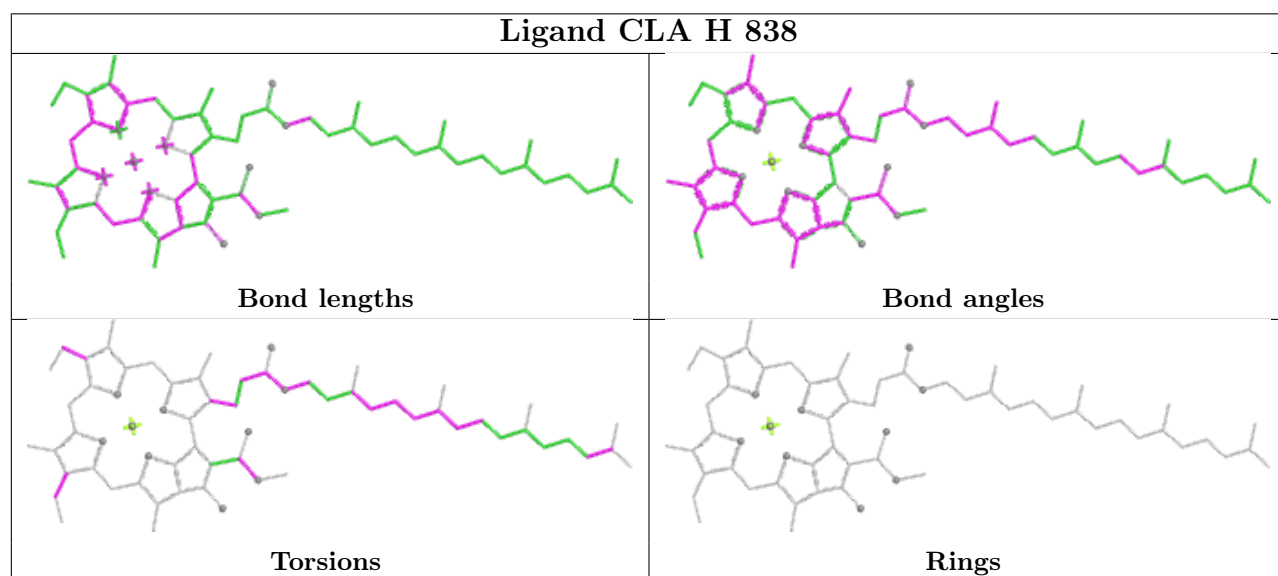
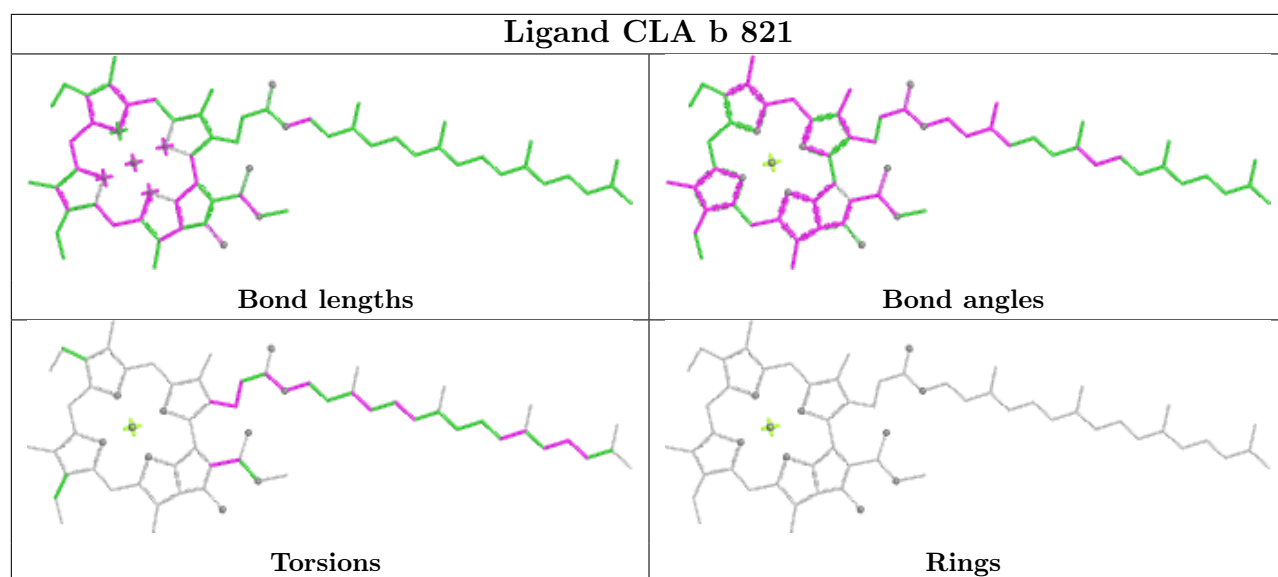


Torsions

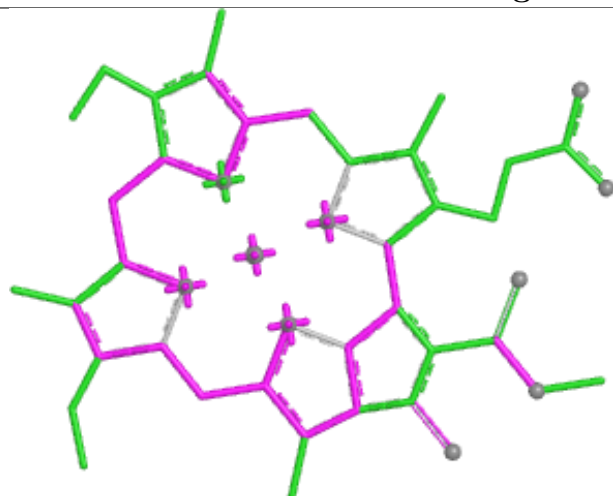


Rings

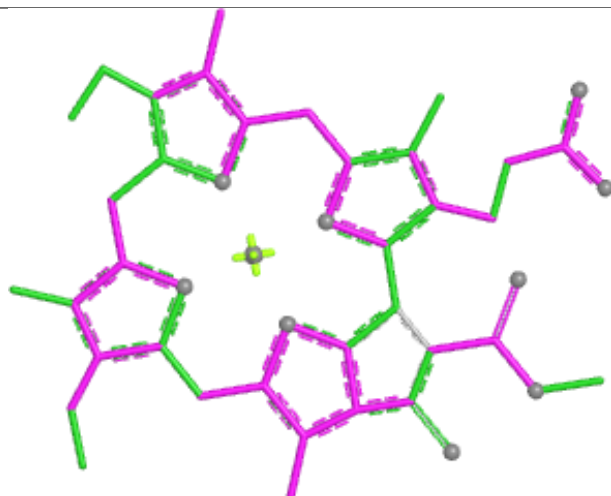




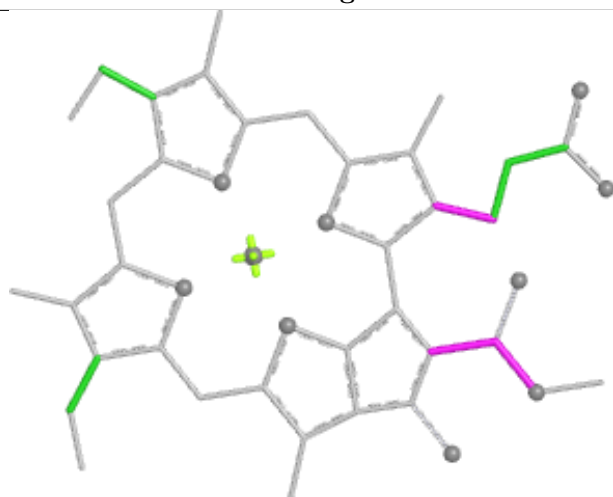
## Ligand CLA G 814



Bond lengths



Bond angles

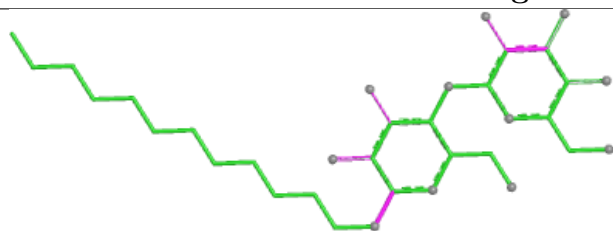


Torsions

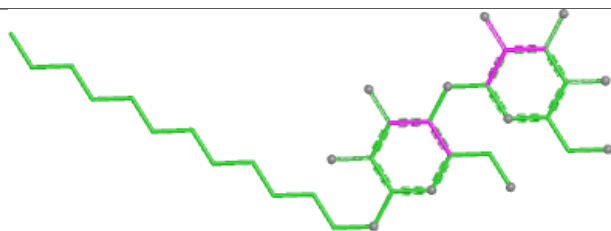


Rings

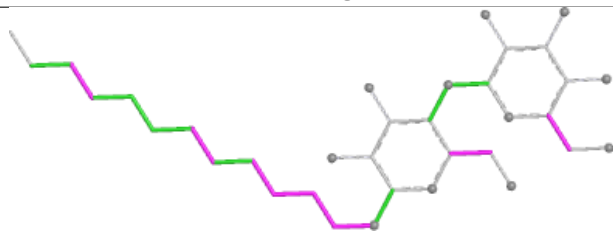
## Ligand LMT B 847



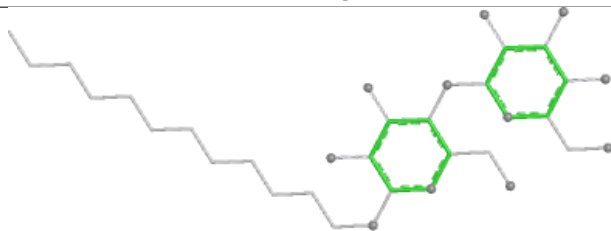
Bond lengths



Bond angles

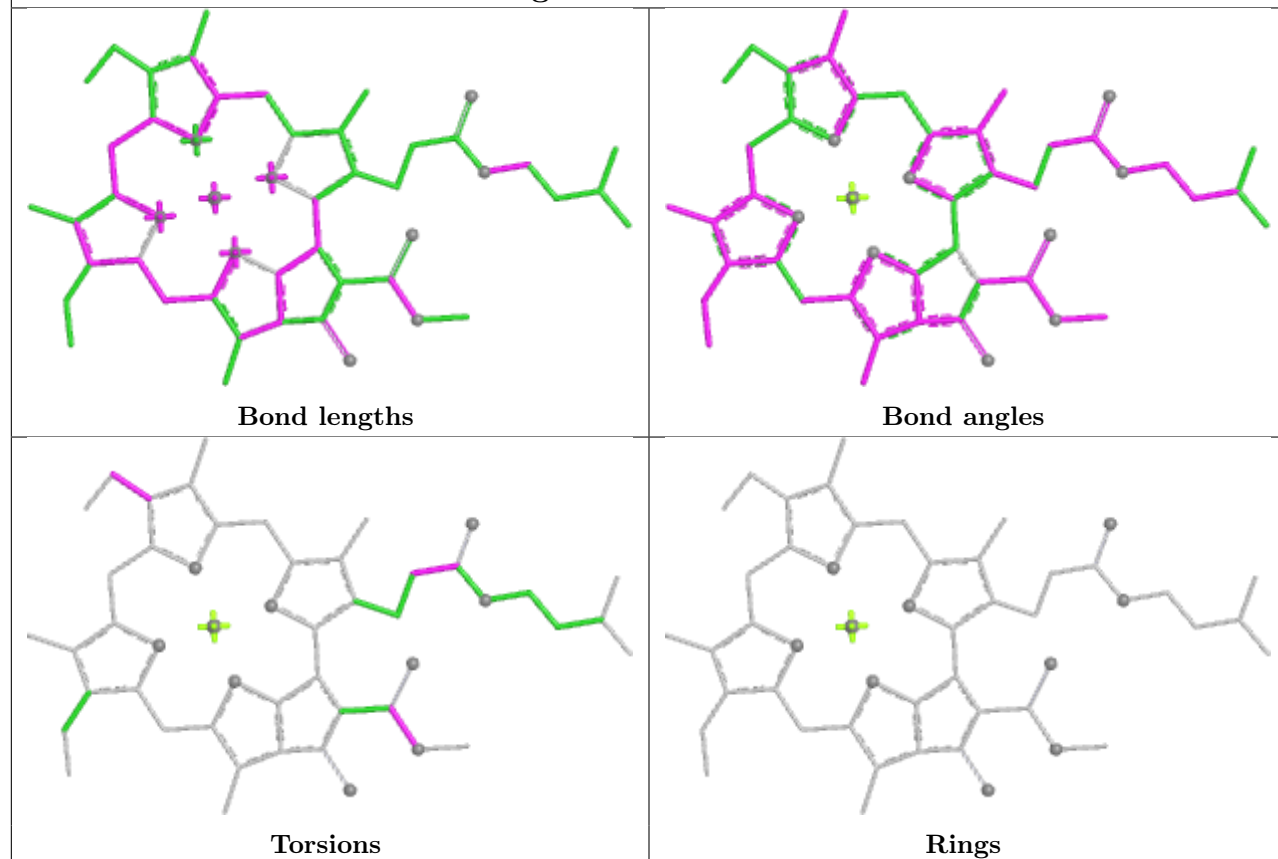


Torsions

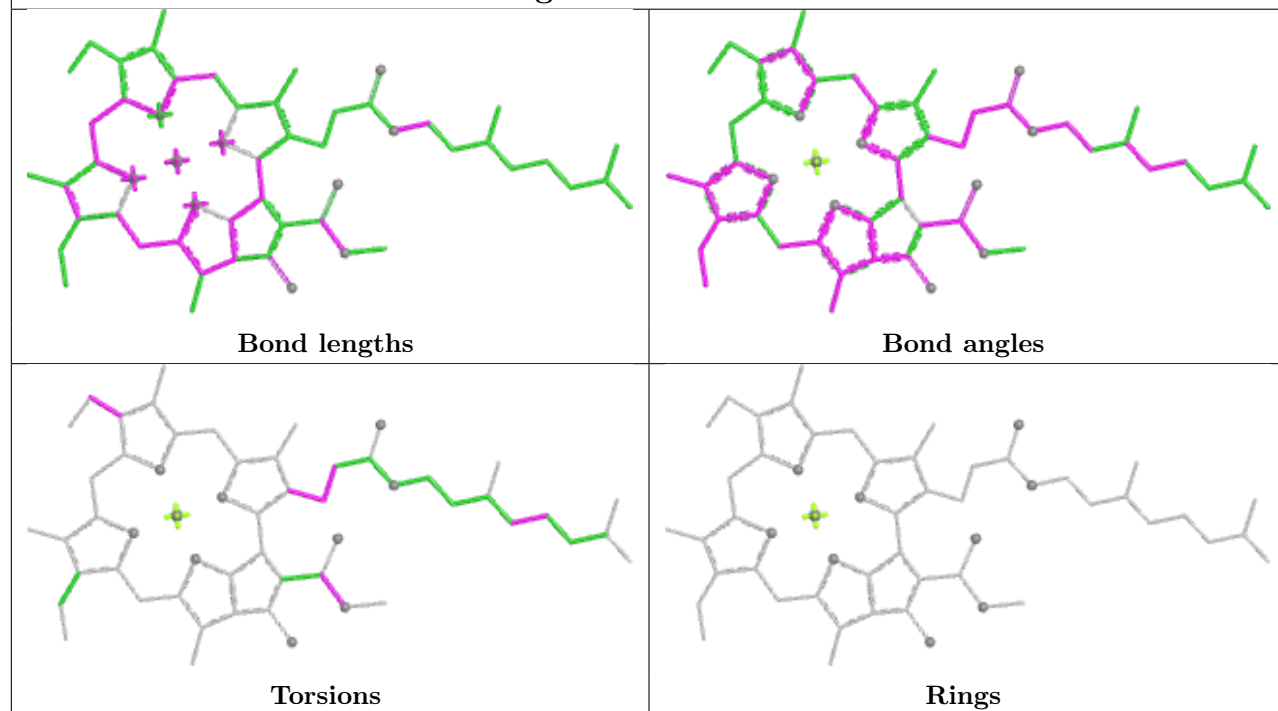


Rings

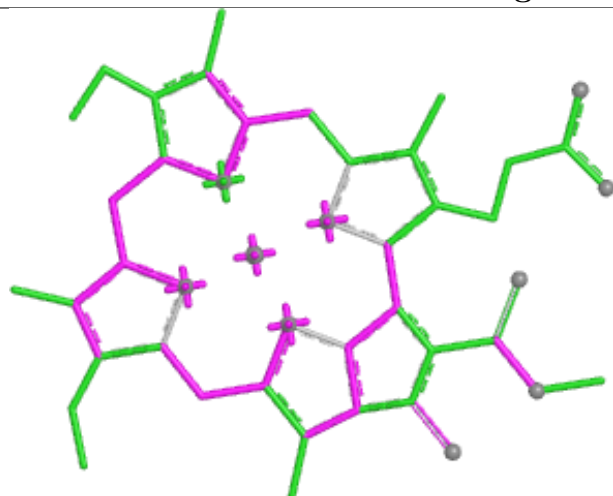
## Ligand CLA A 816



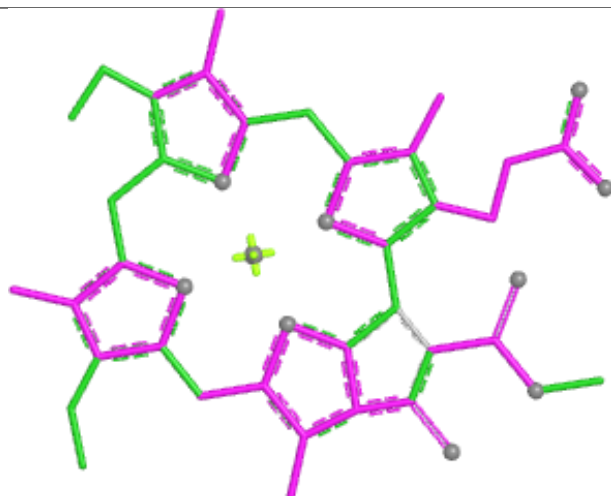
## Ligand CLA b 814



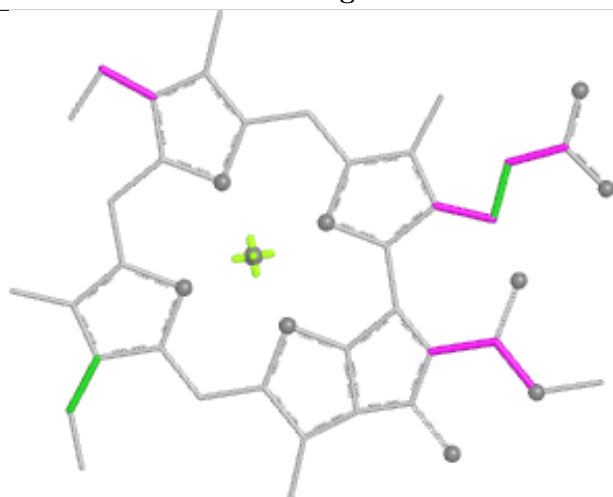
## Ligand CLA B 817



Bond lengths



Bond angles

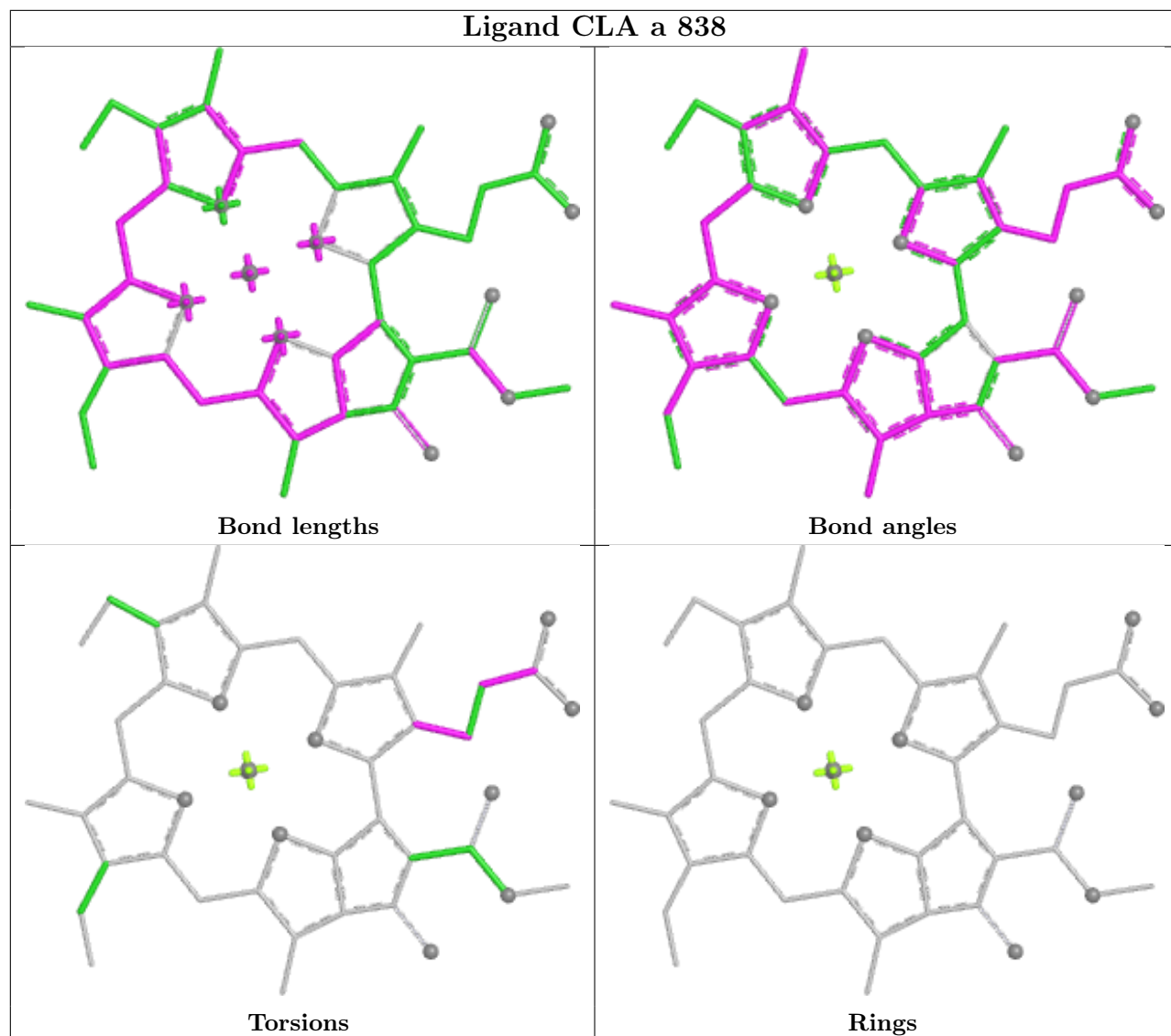


Torsions

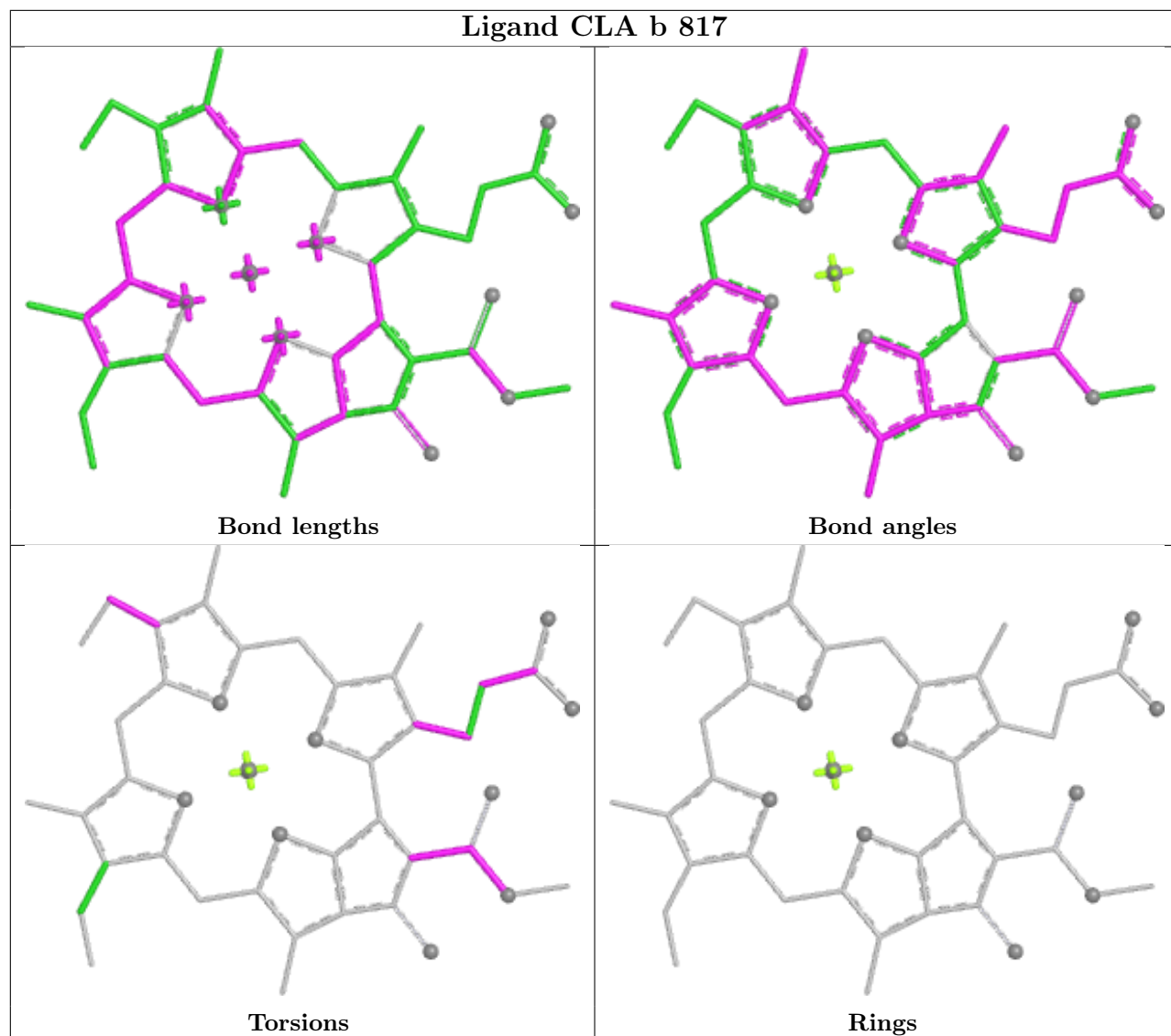


Rings

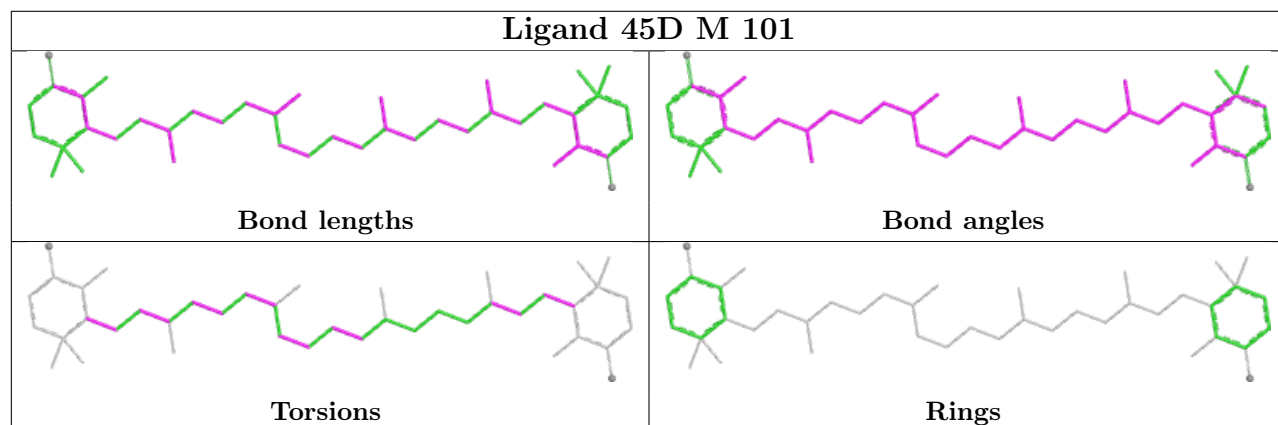
## Ligand CLA a 838

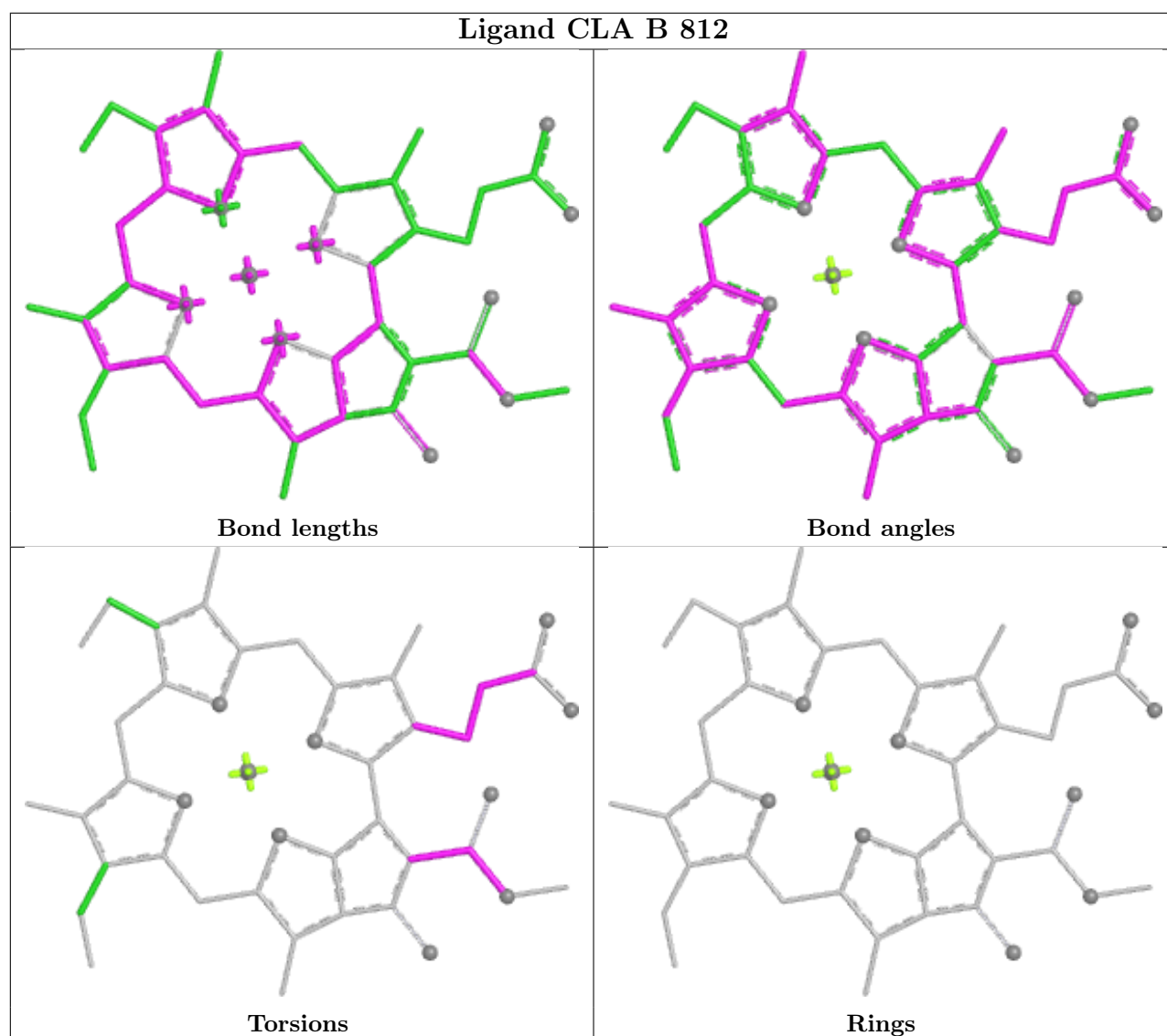
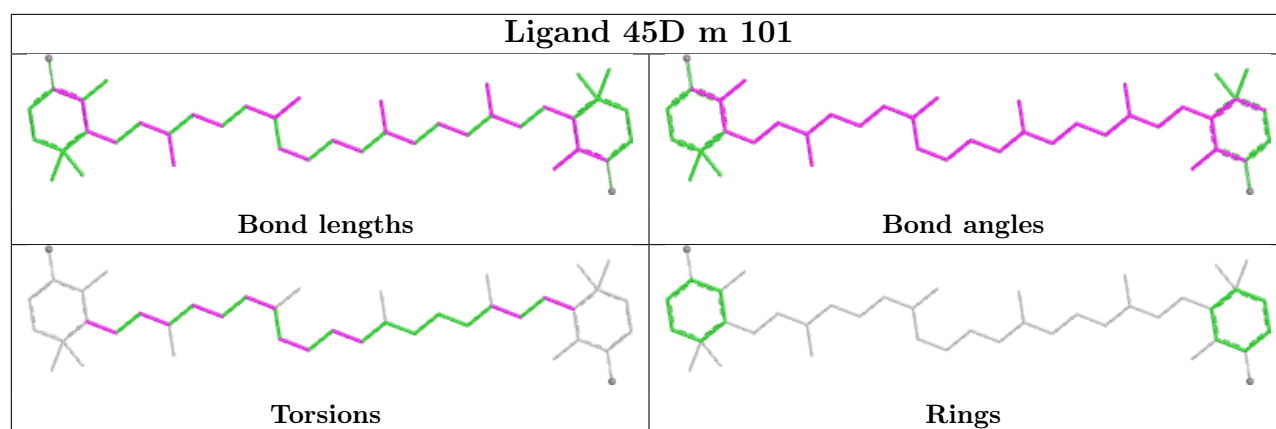


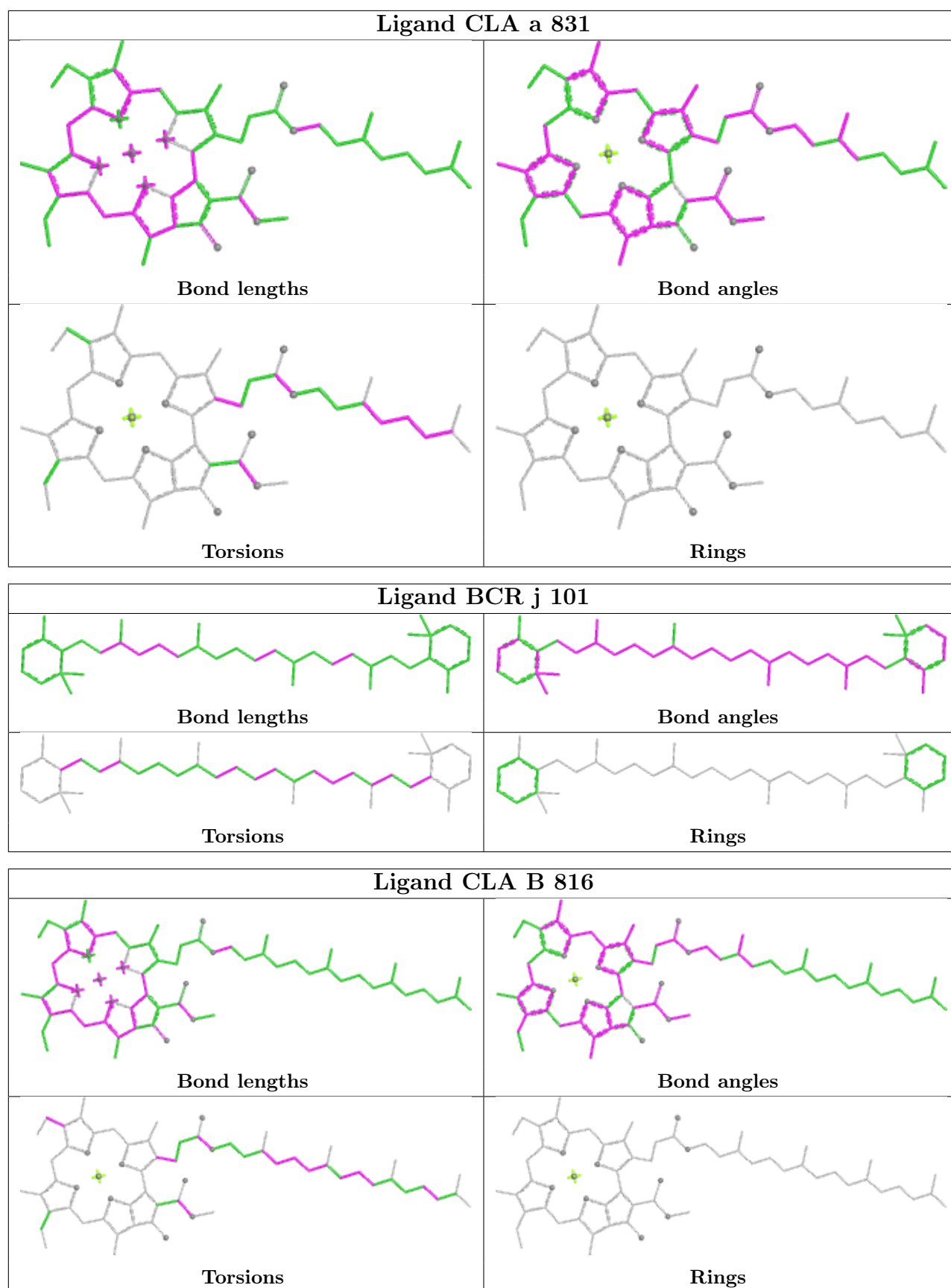
## Ligand CLA b 817

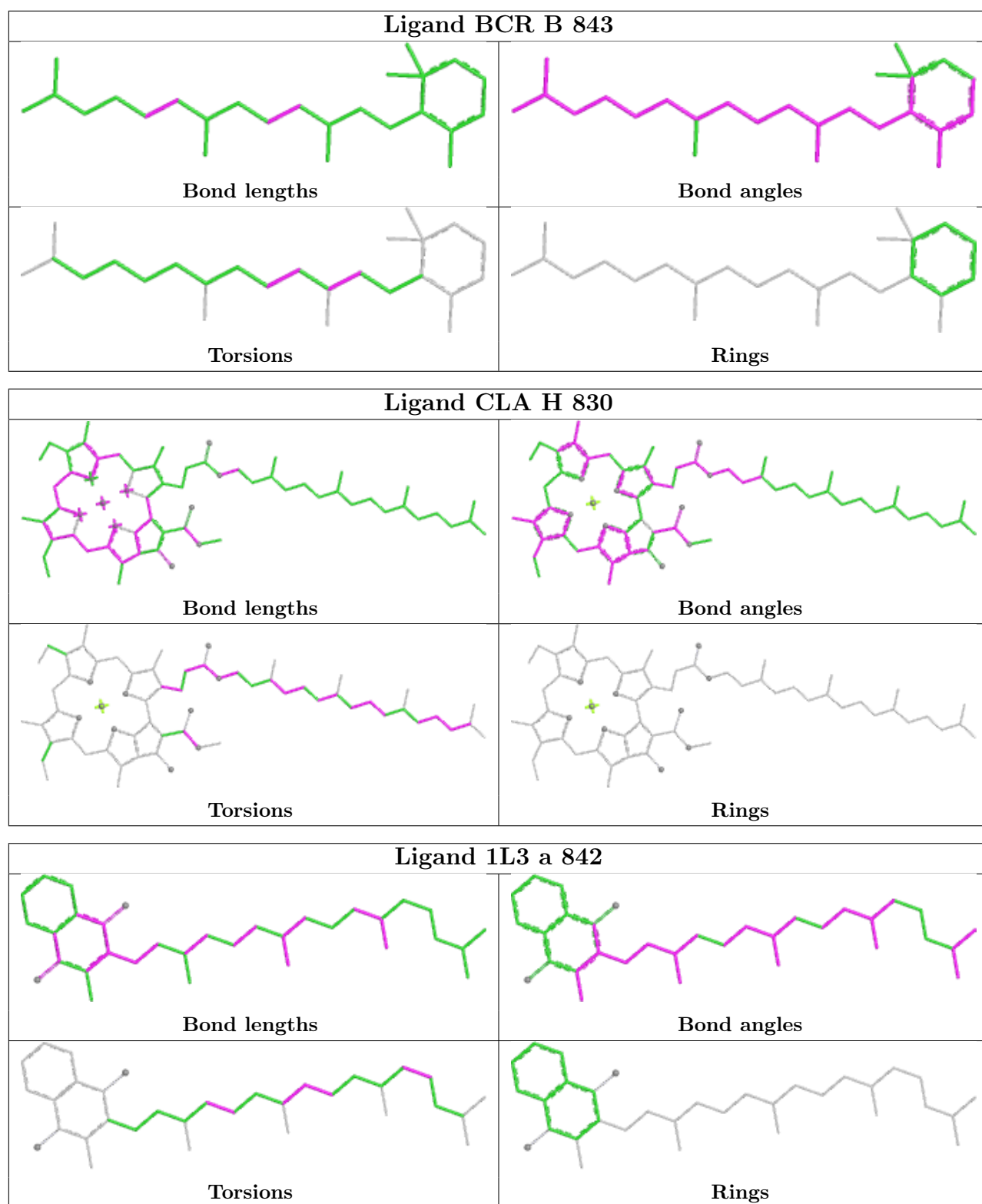


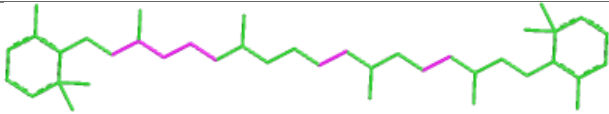
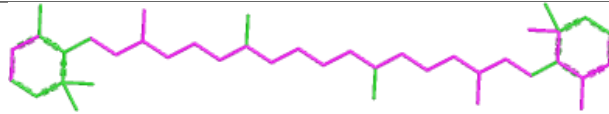
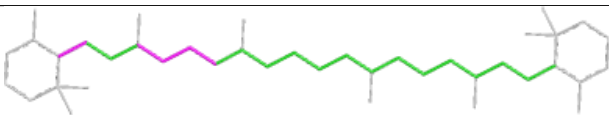
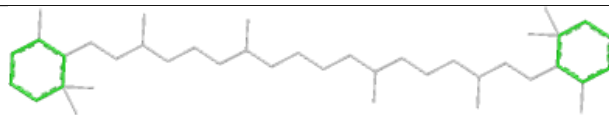
## Ligand 45D M 101

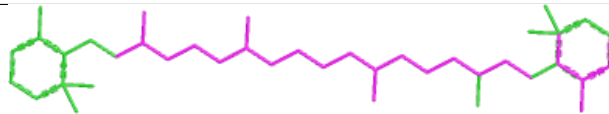
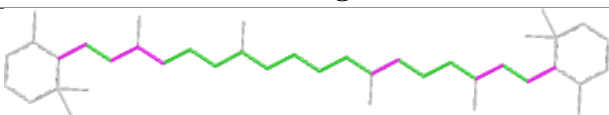
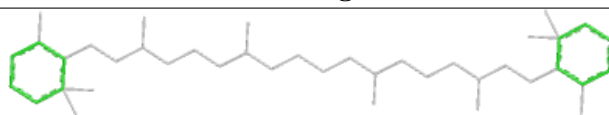


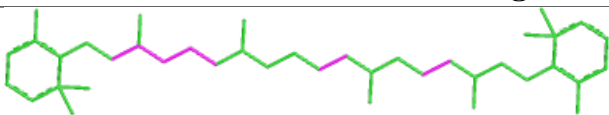
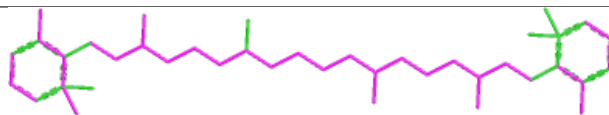
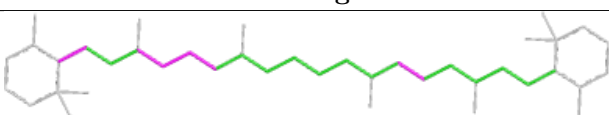
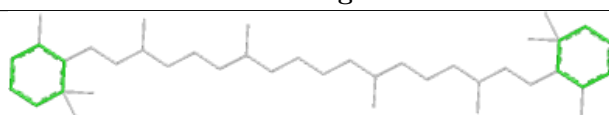


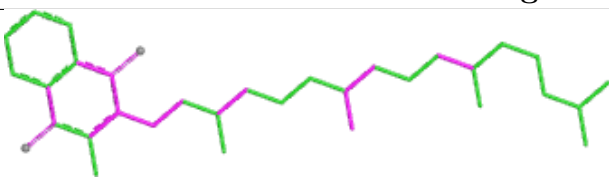
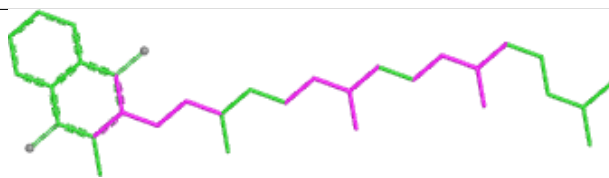
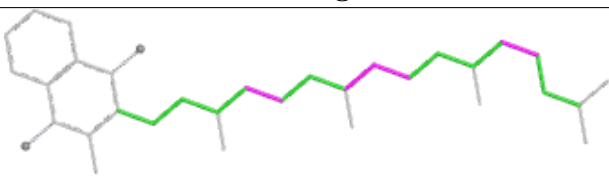
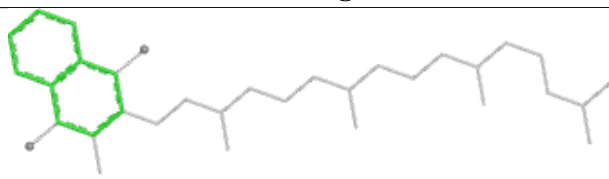


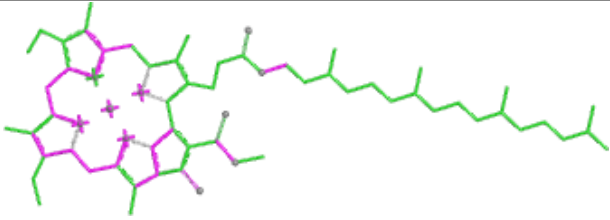
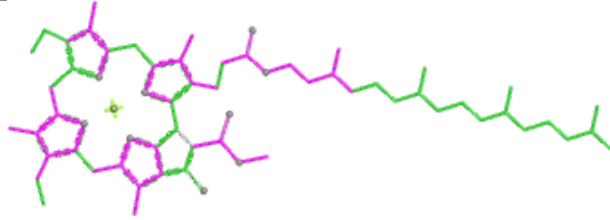
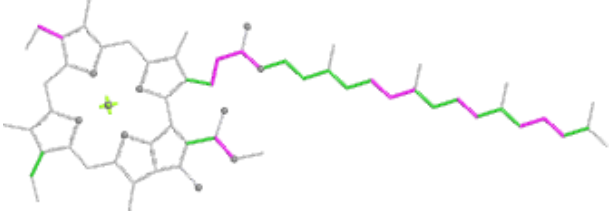
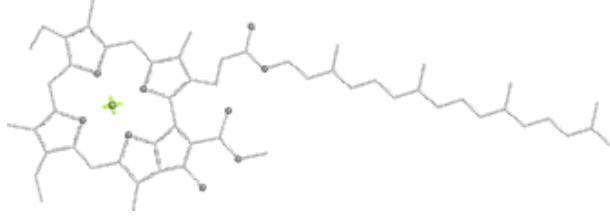
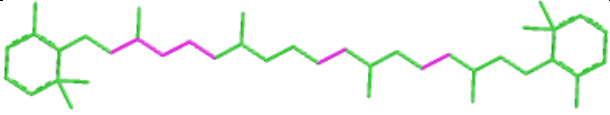
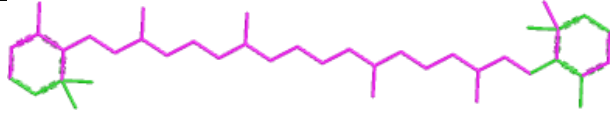
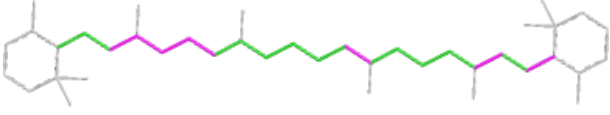
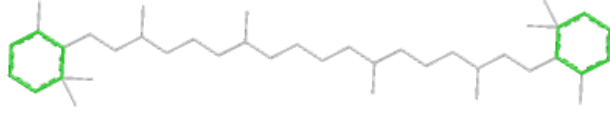
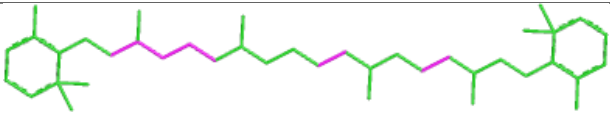
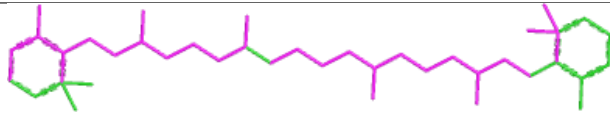
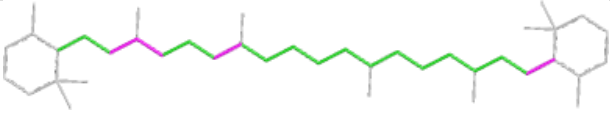
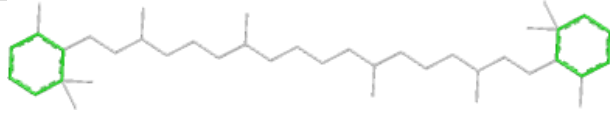


| Ligand BCR G 847                                                                  |                                                                                    |
|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                      | Bond angles                                                                        |
|  |  |
| Torsions                                                                          | Rings                                                                              |

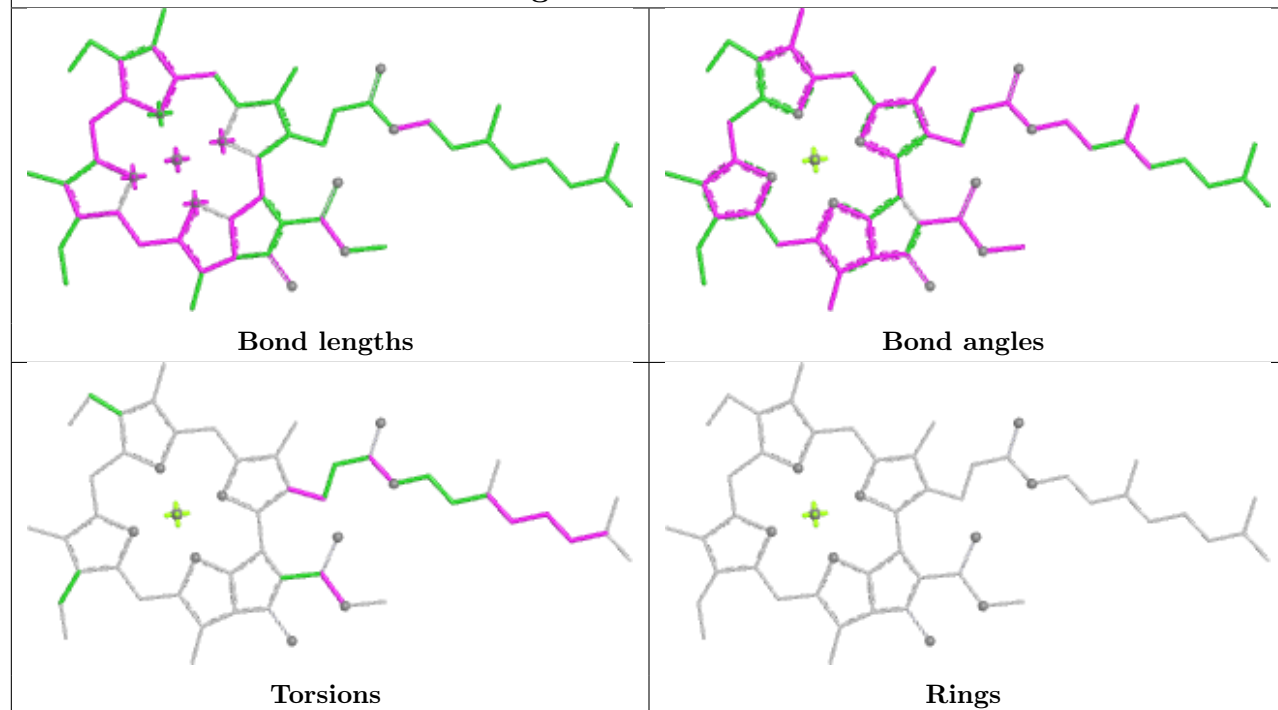
| Ligand BCR a 848                                                                  |                                                                                    |
|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                      | Bond angles                                                                        |
|  |  |
| Torsions                                                                          | Rings                                                                              |

| Ligand BCR b 844                                                                    |                                                                                      |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
|   |   |
| Bond lengths                                                                        | Bond angles                                                                          |
|  |  |
| Torsions                                                                            | Rings                                                                                |

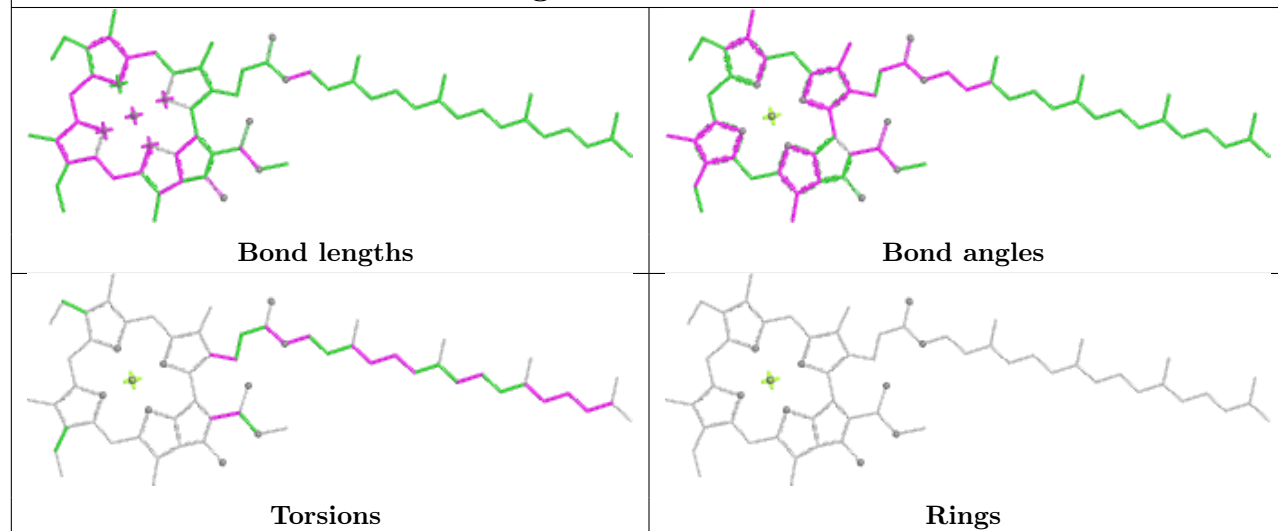
| Ligand 1L3 b 838                                                                    |                                                                                      |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                        | Bond angles                                                                          |
|  |  |
| Torsions                                                                            | Rings                                                                                |

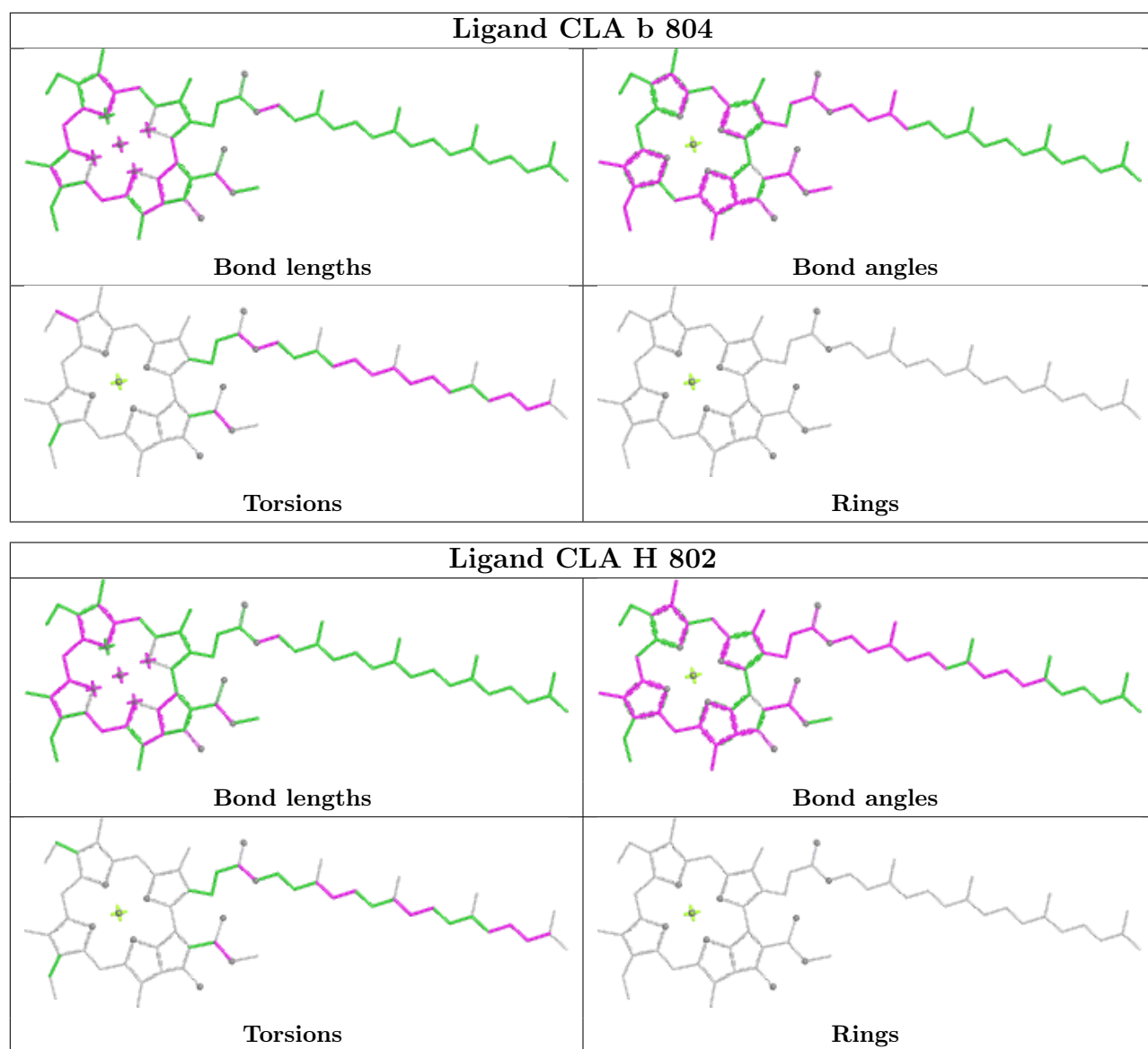
| Ligand CLA G 841                                                                                        |                                                                                                         |
|---------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|
|  <p>Bond lengths</p>   |  <p>Bond angles</p>   |
|  <p>Torsions</p>       |  <p>Rings</p>         |
| Ligand BCR G 850                                                                                        |                                                                                                         |
|  <p>Bond lengths</p>   |  <p>Bond angles</p>   |
|  <p>Torsions</p>      |  <p>Rings</p>        |
| Ligand BCR L 201                                                                                        |                                                                                                         |
|  <p>Bond lengths</p> |  <p>Bond angles</p> |
|  <p>Torsions</p>     |  <p>Rings</p>       |

## Ligand CLA H 801

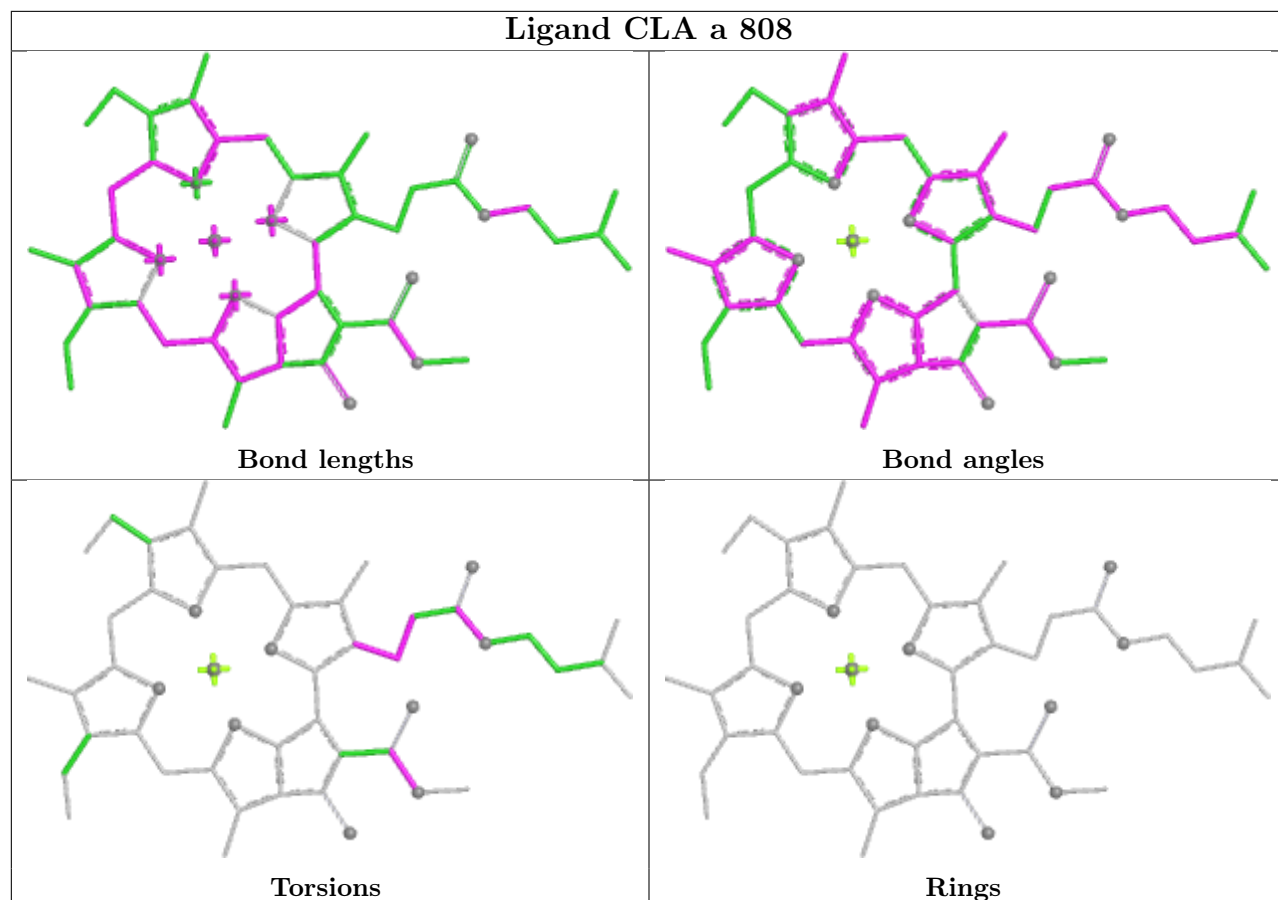


## Ligand CLA A 824

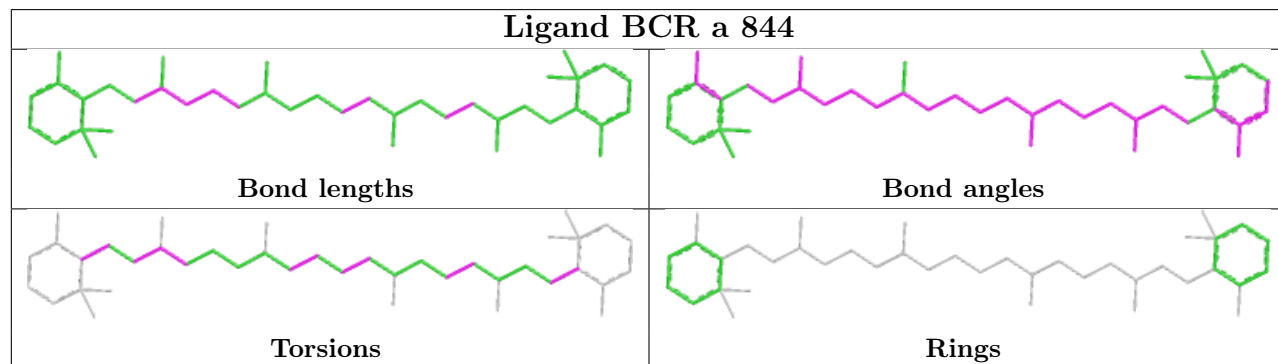




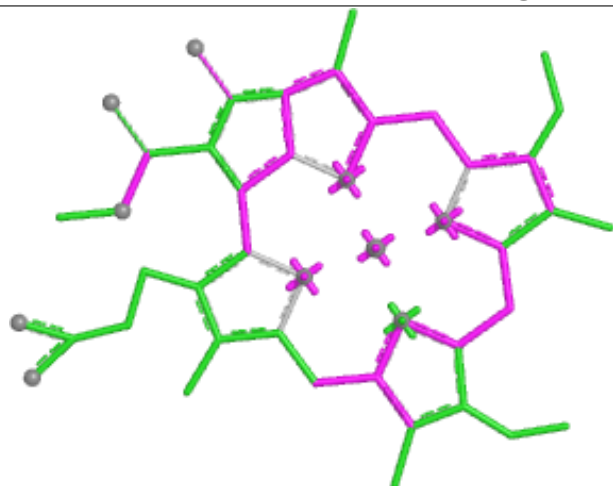
## Ligand CLA a 808



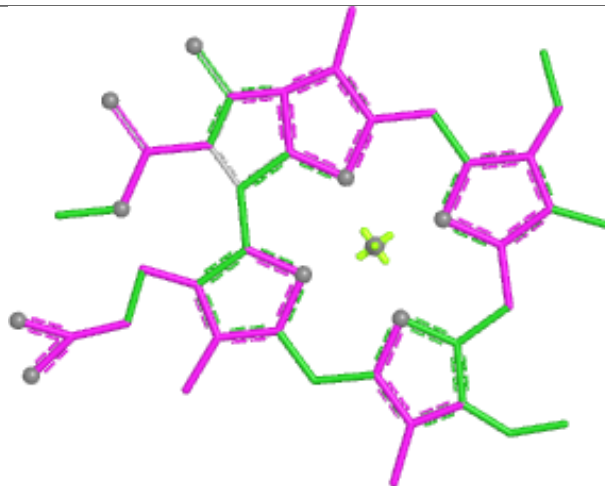
## Ligand BCR a 844



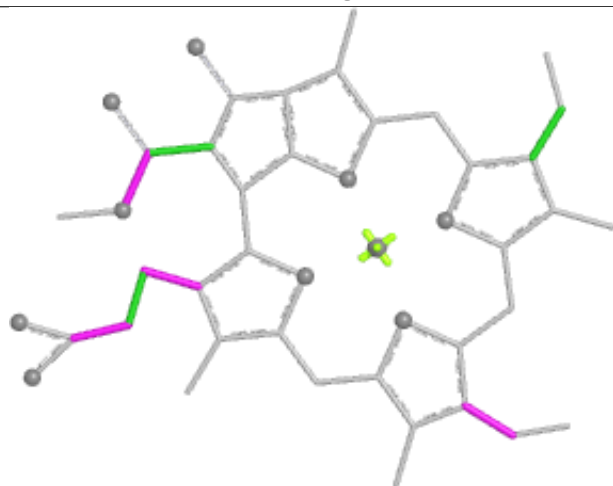
## Ligand CLA P 203



Bond lengths



Bond angles

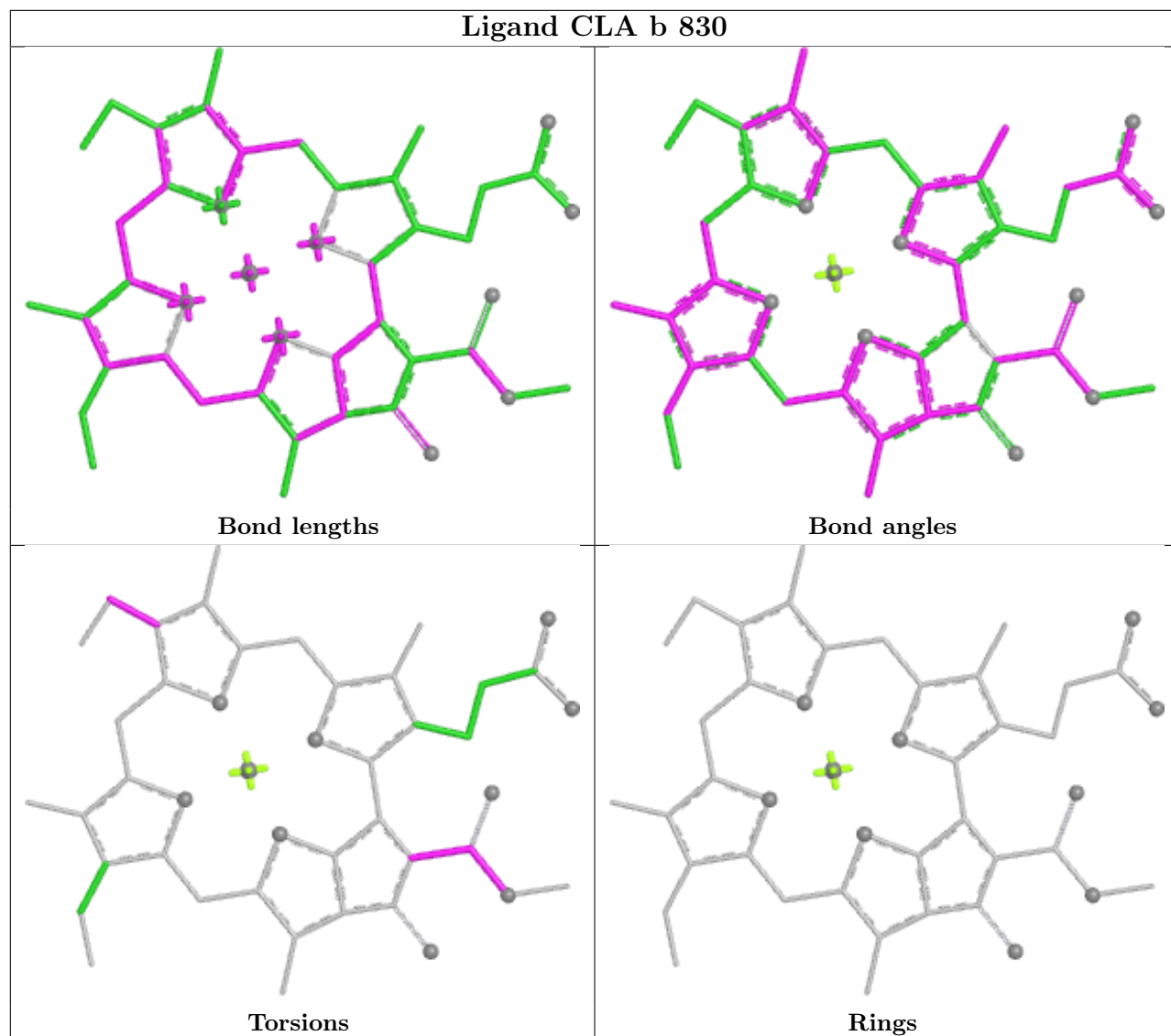


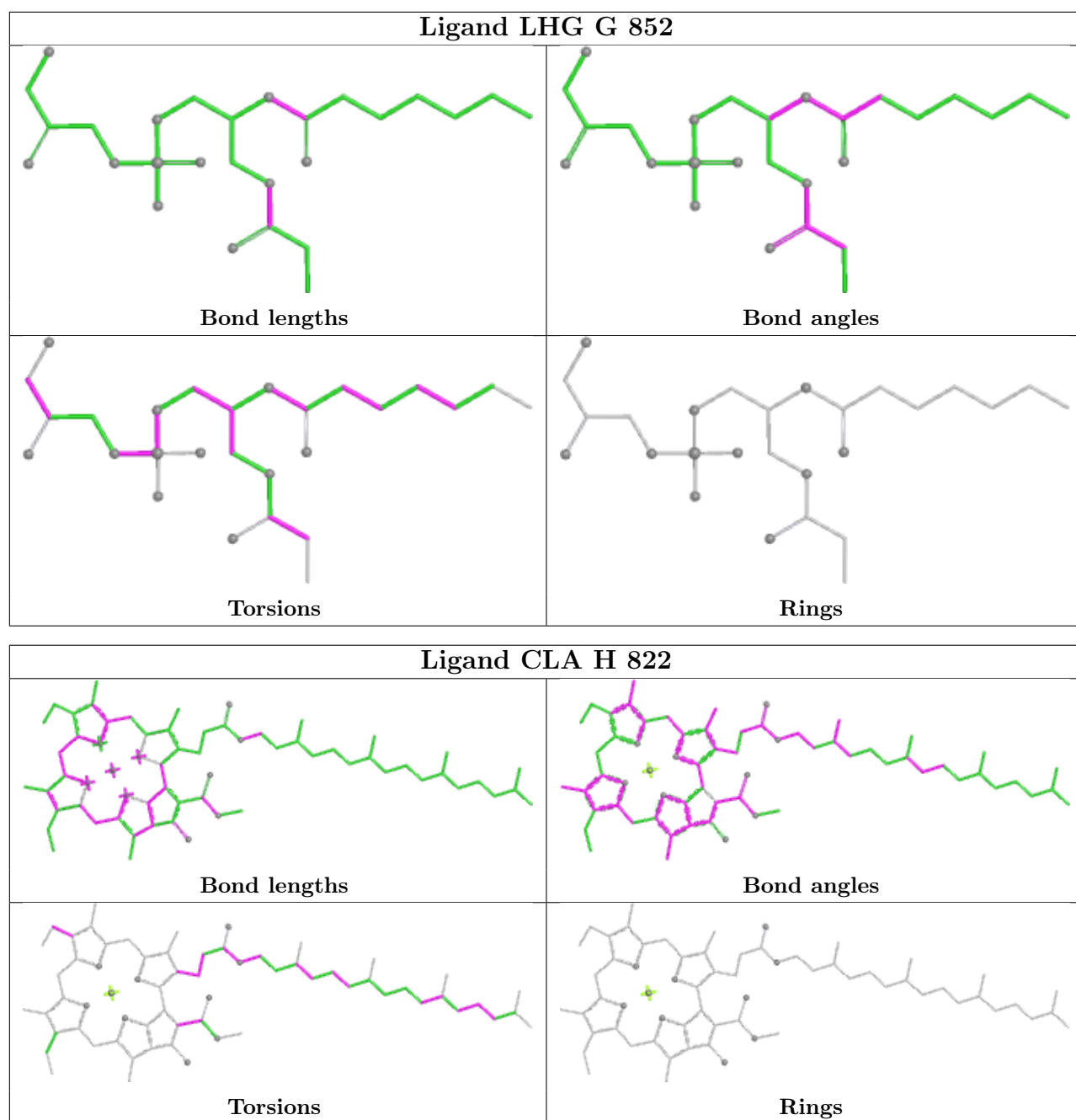
Torsions

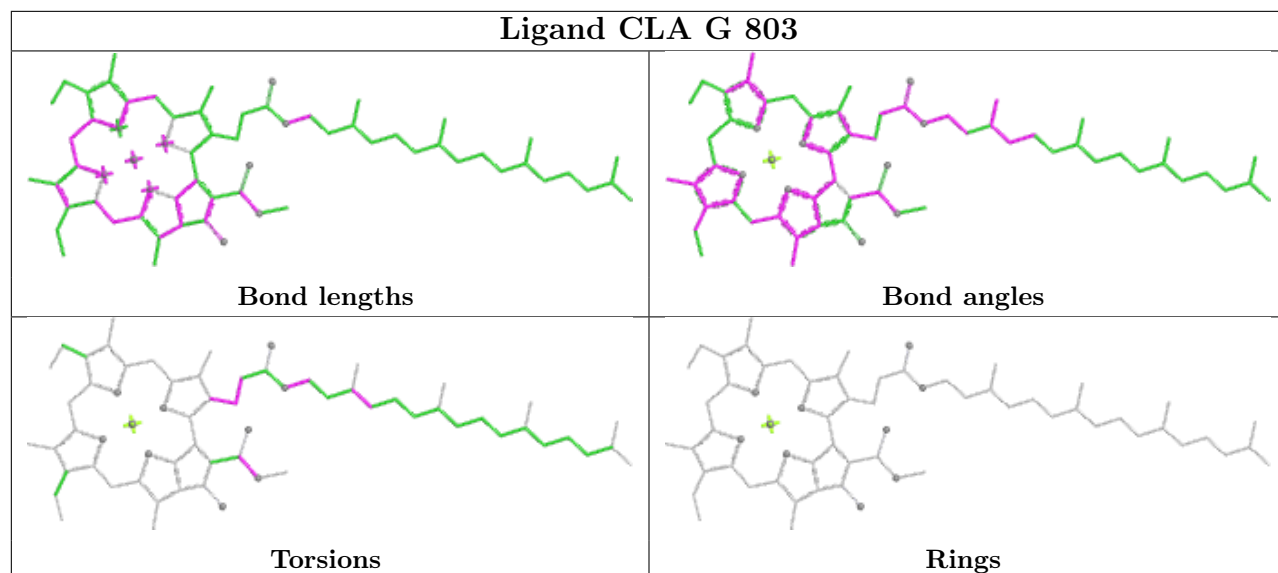
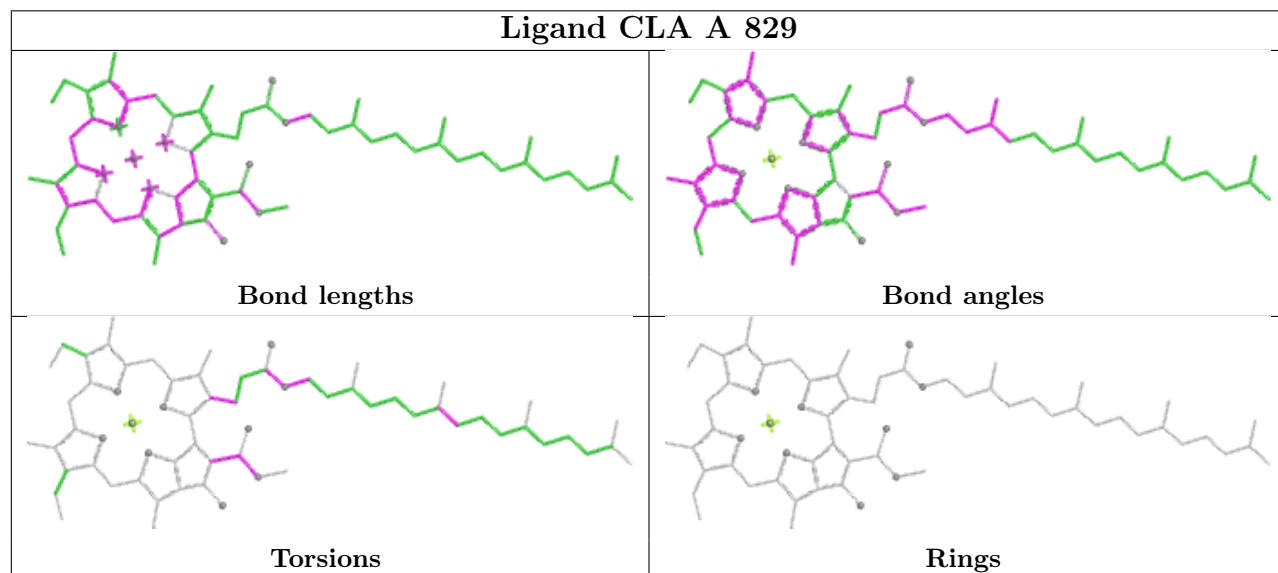
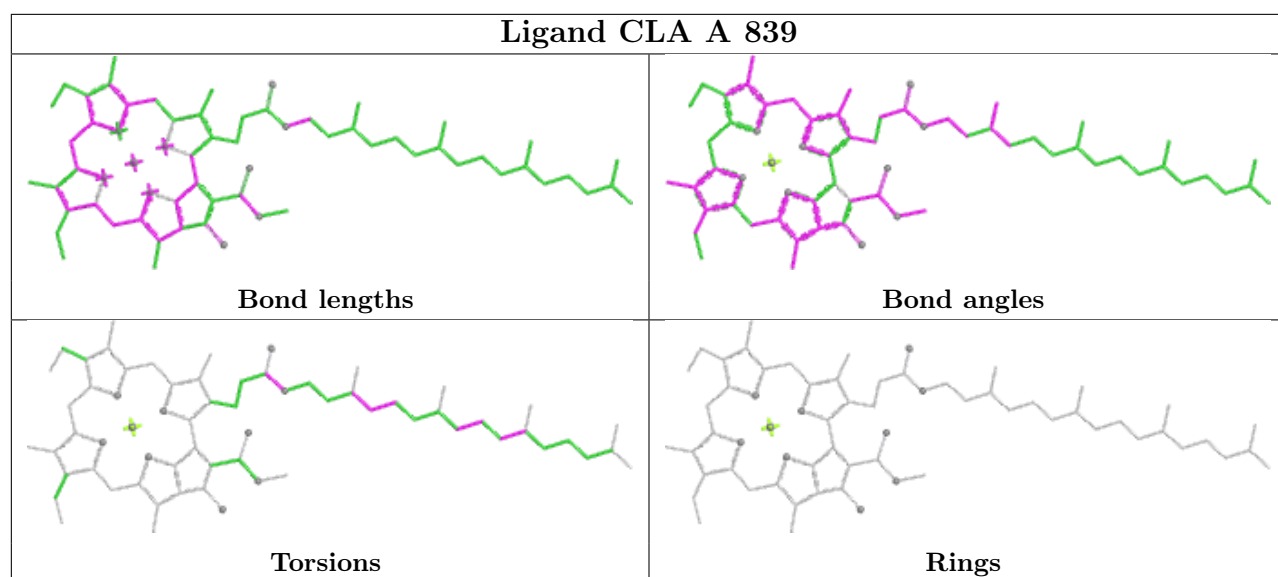


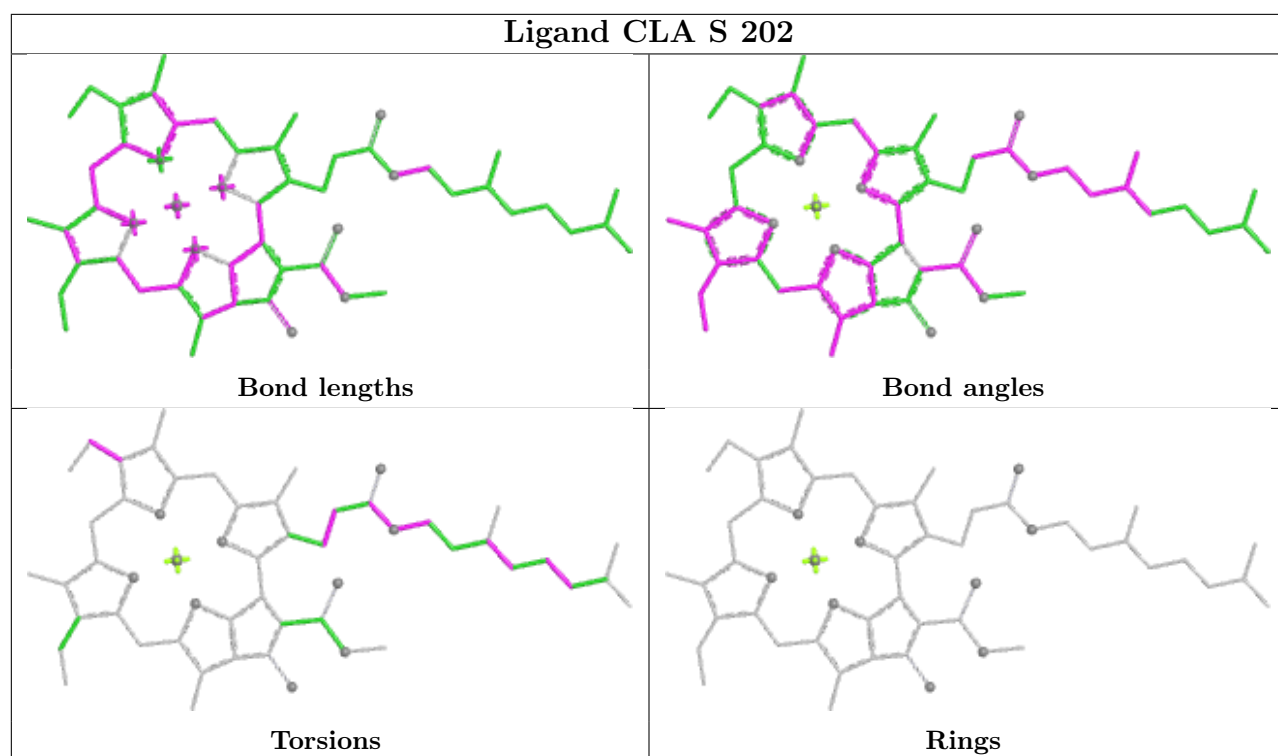
Rings

## Ligand CLA b 830

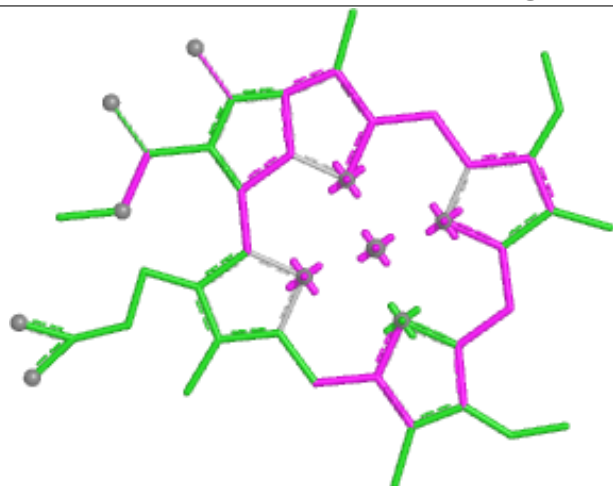




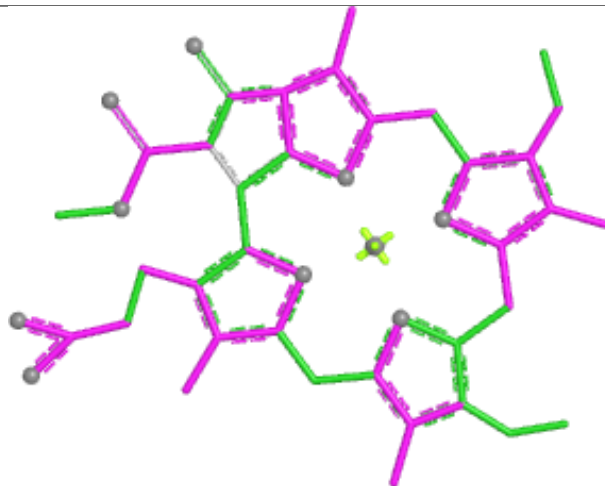




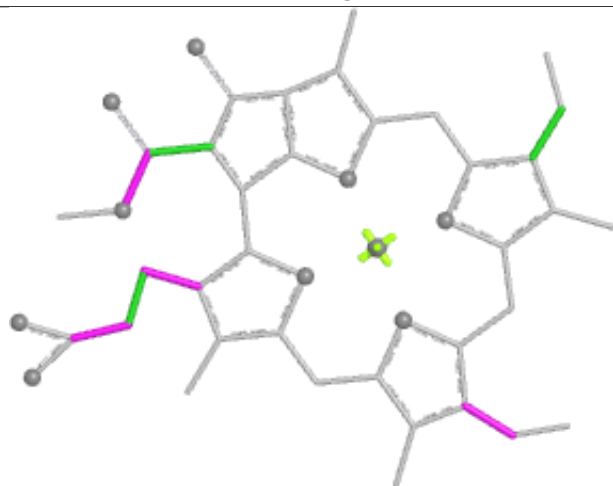
## Ligand CLA f 203



Bond lengths



Bond angles

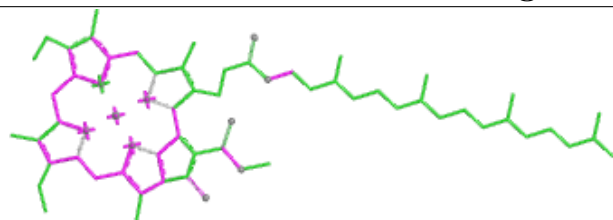


Torsions

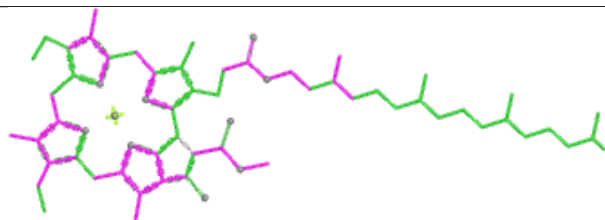


Rings

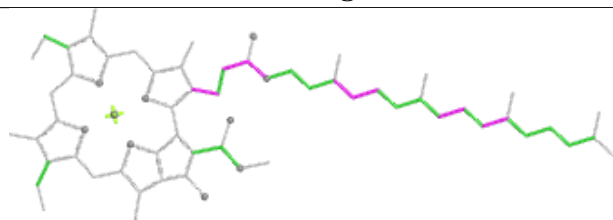
## Ligand CLA a 839



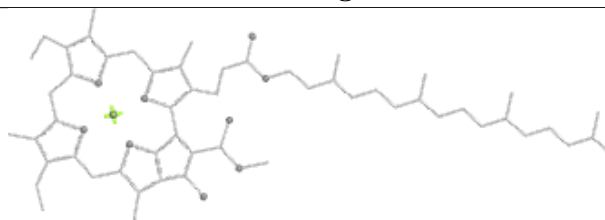
Bond lengths



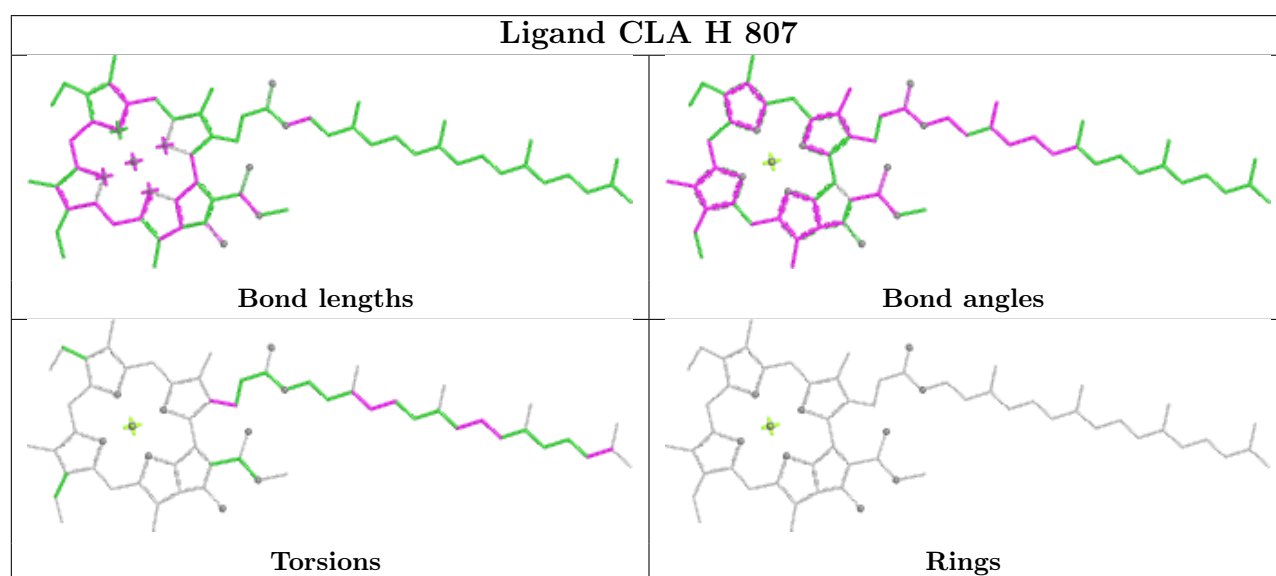
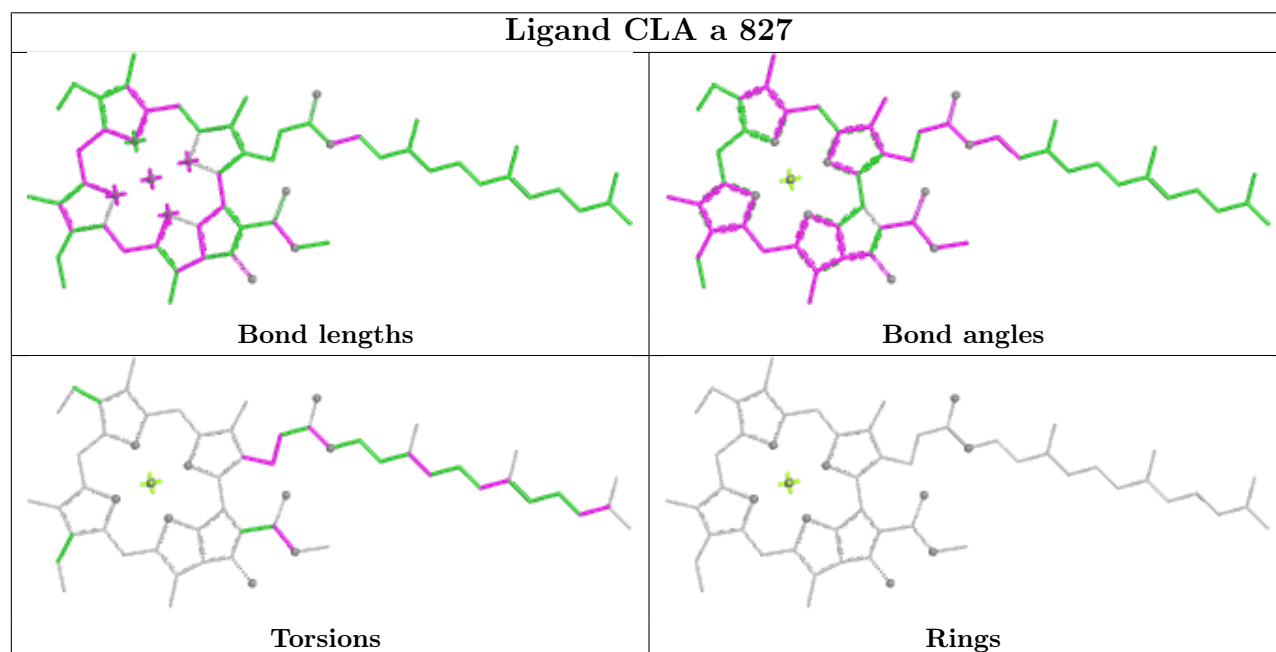
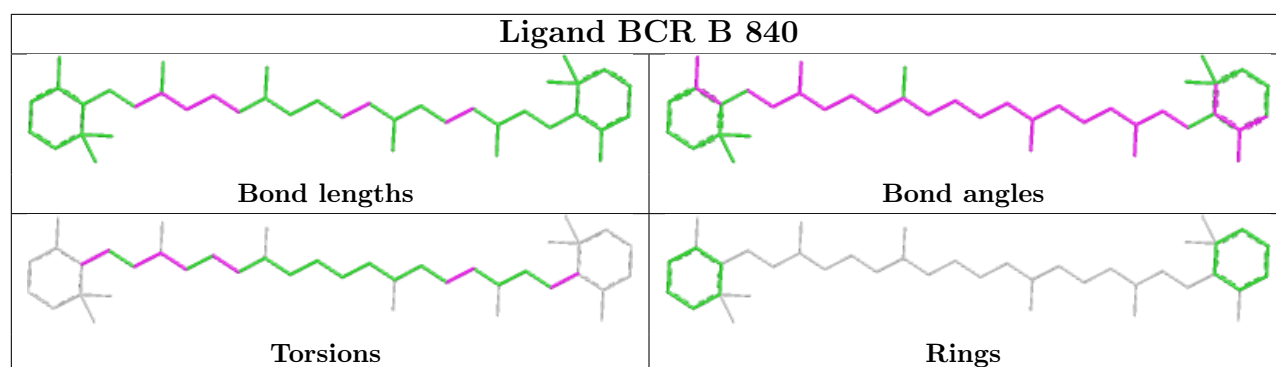
Bond angles



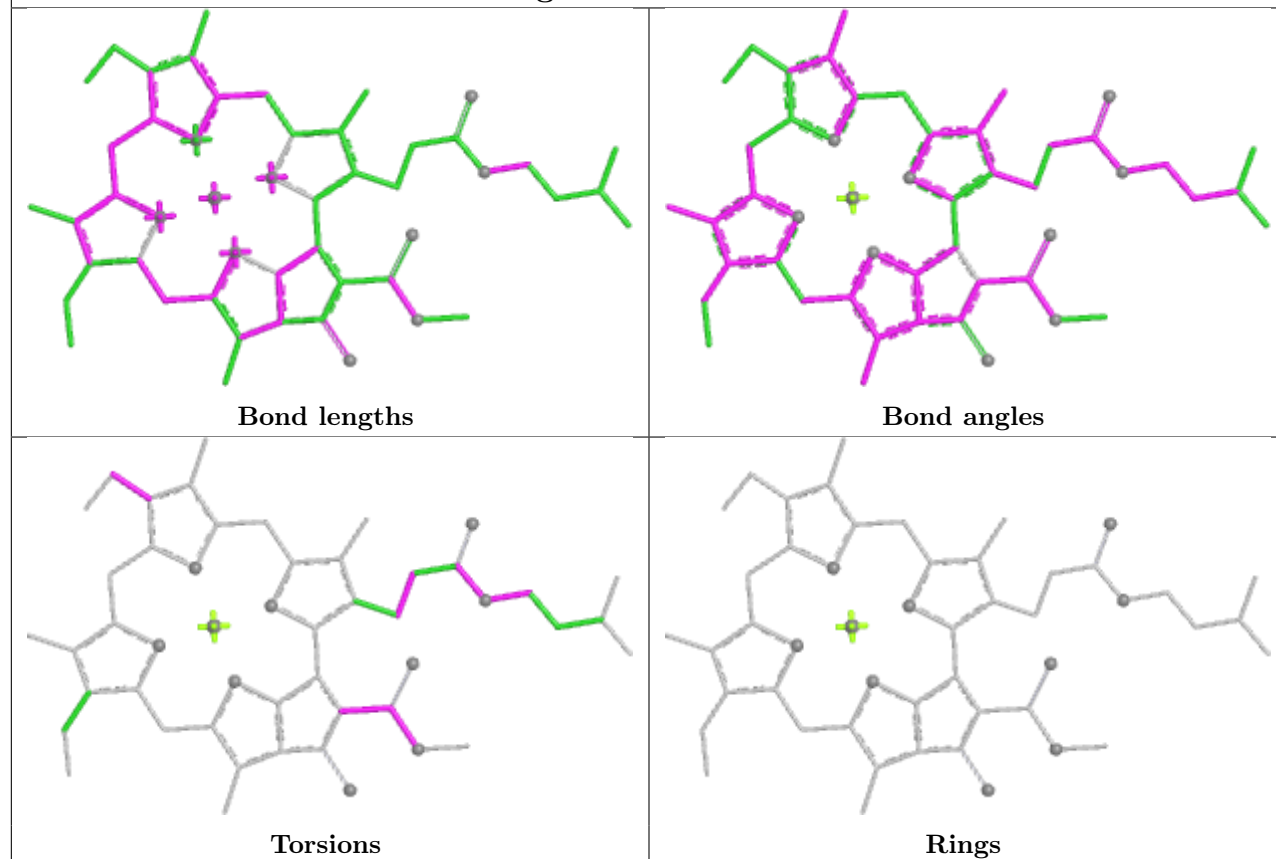
Torsions



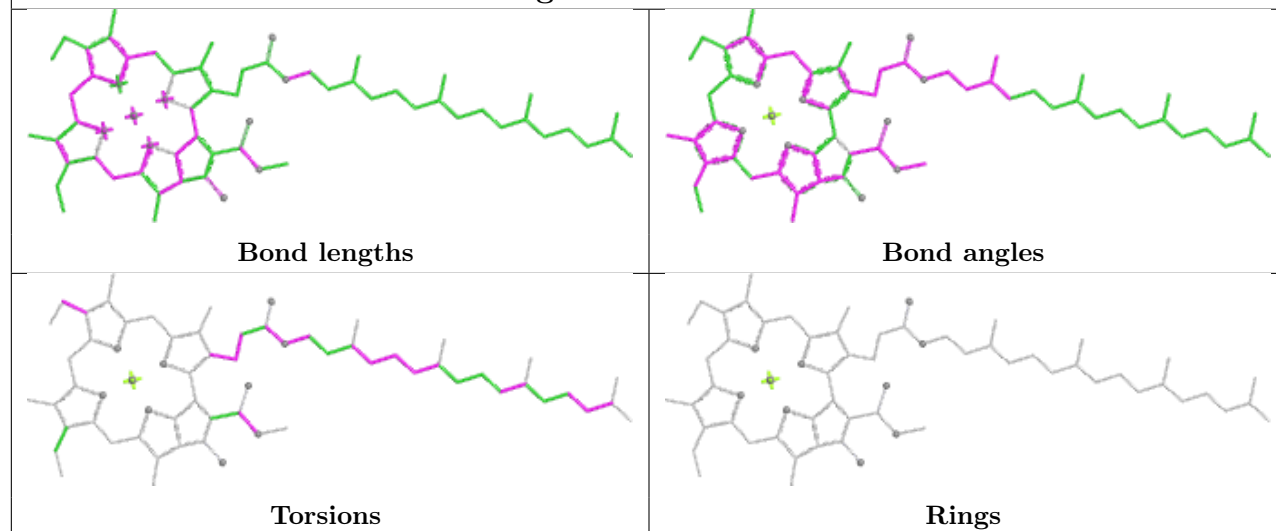
Rings



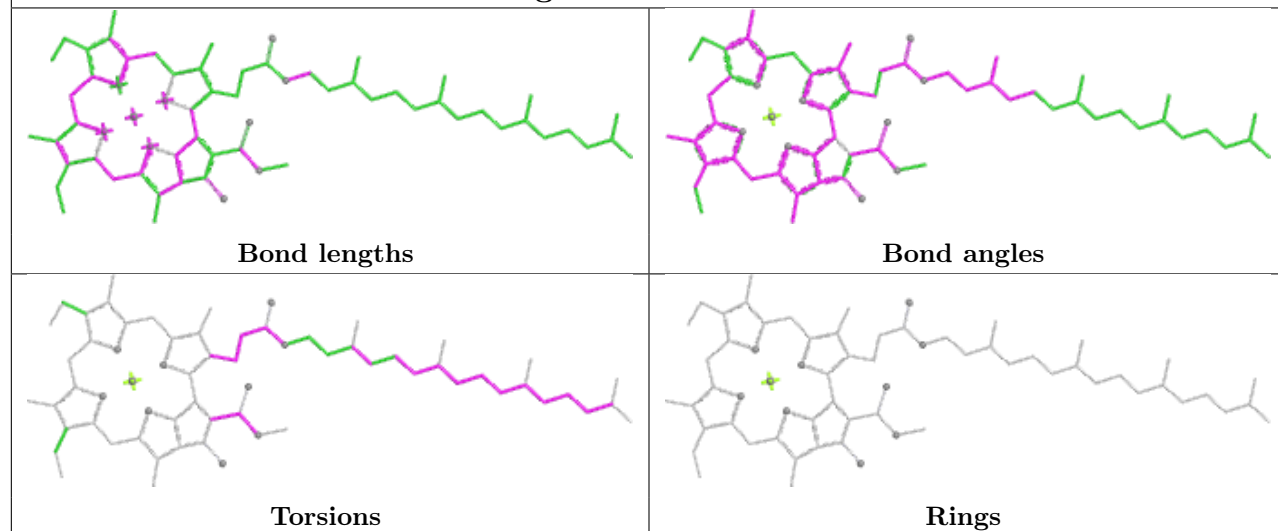
## Ligand CLA a 830



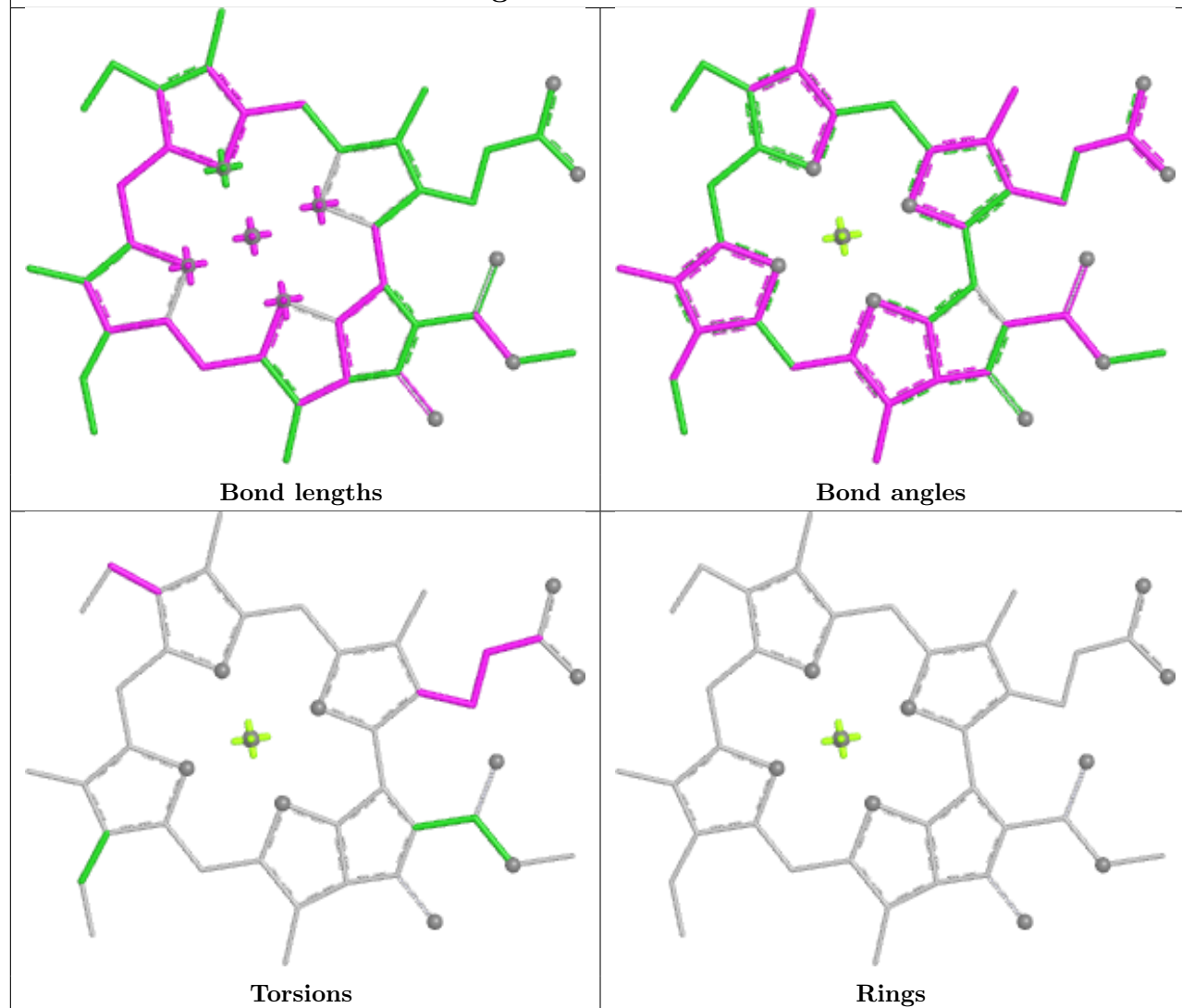
## Ligand CLA a 834



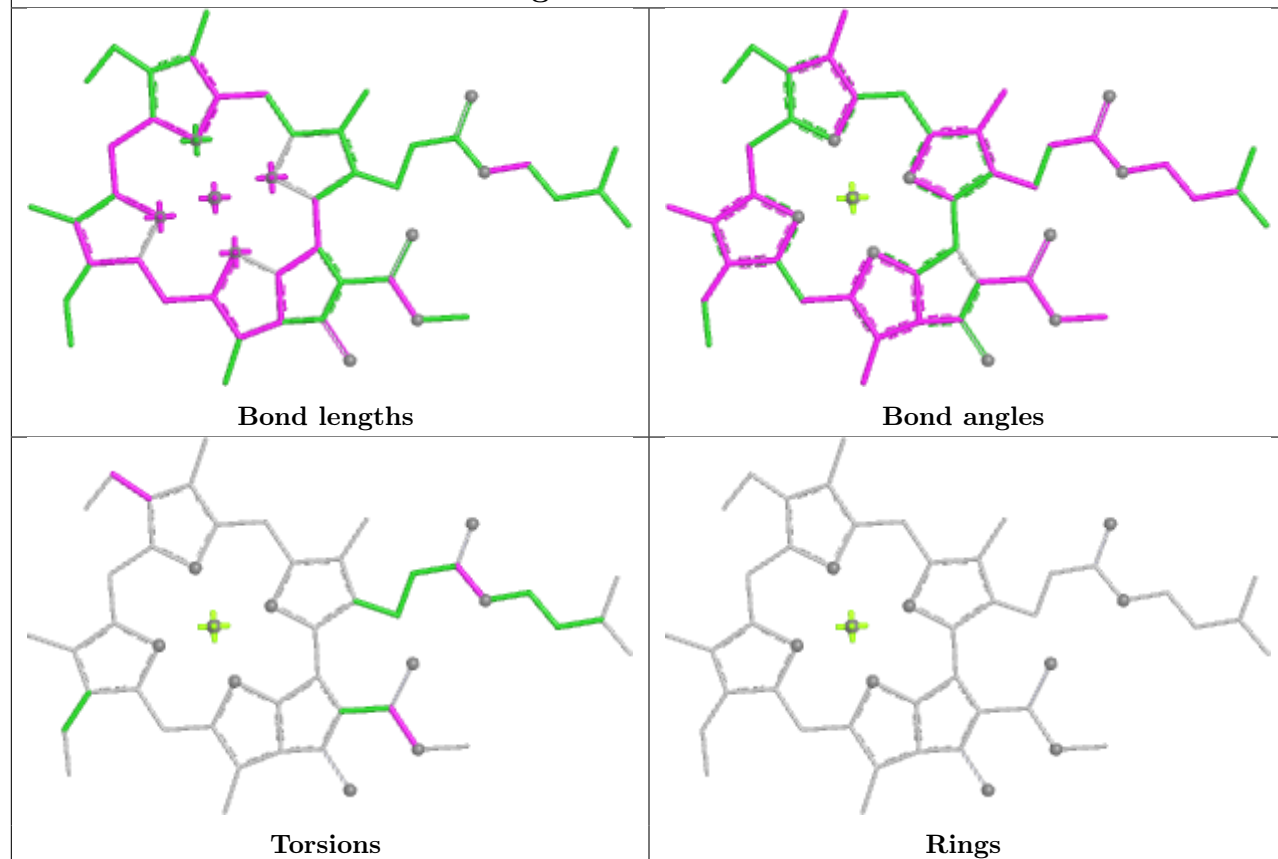
## Ligand CLA b 810



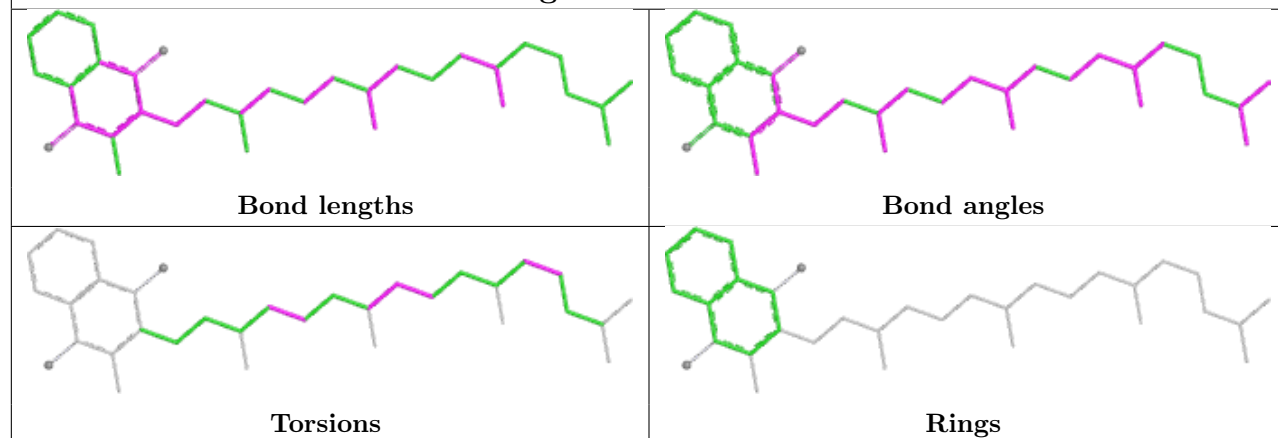
## Ligand CLA A 811



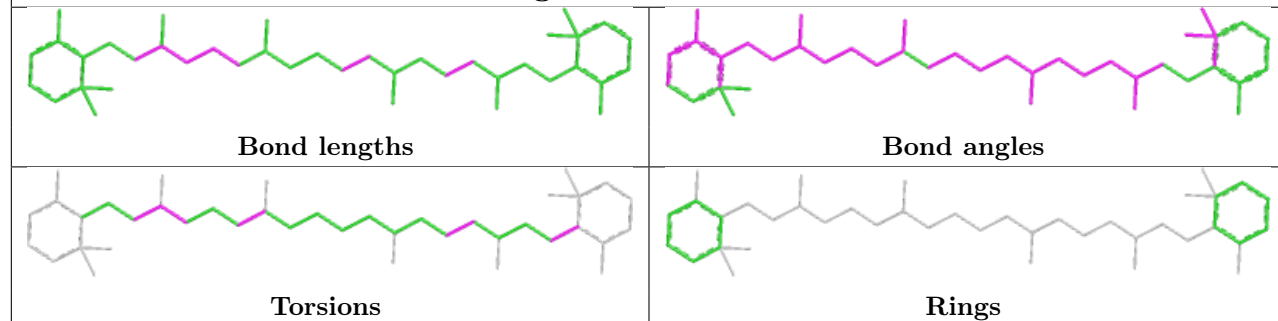
## Ligand CLA A 822

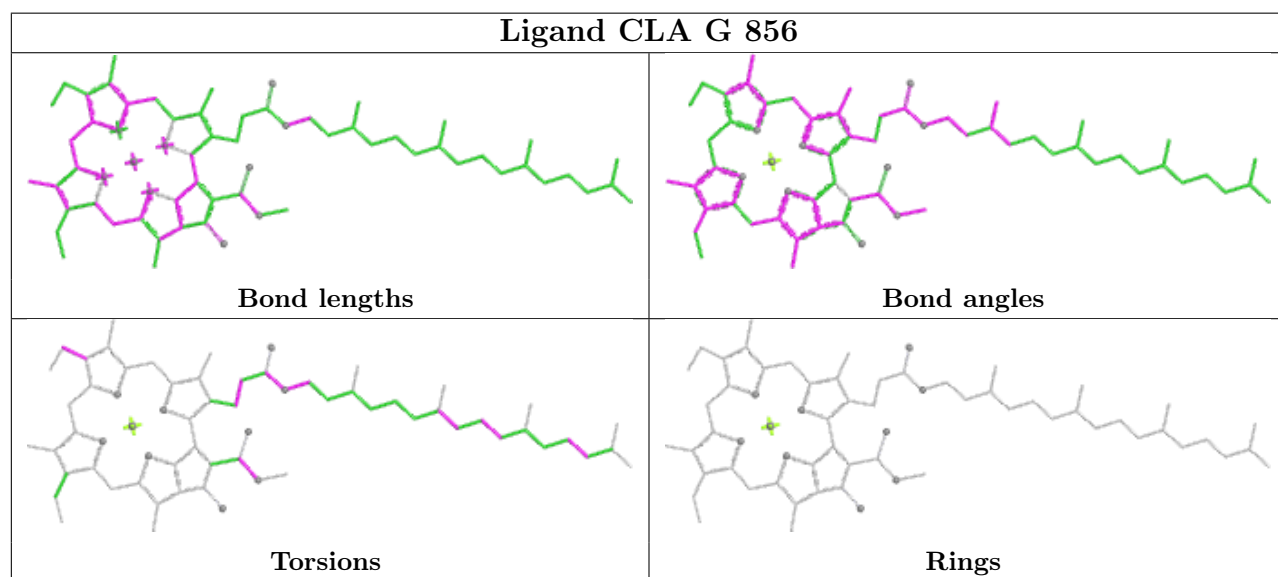
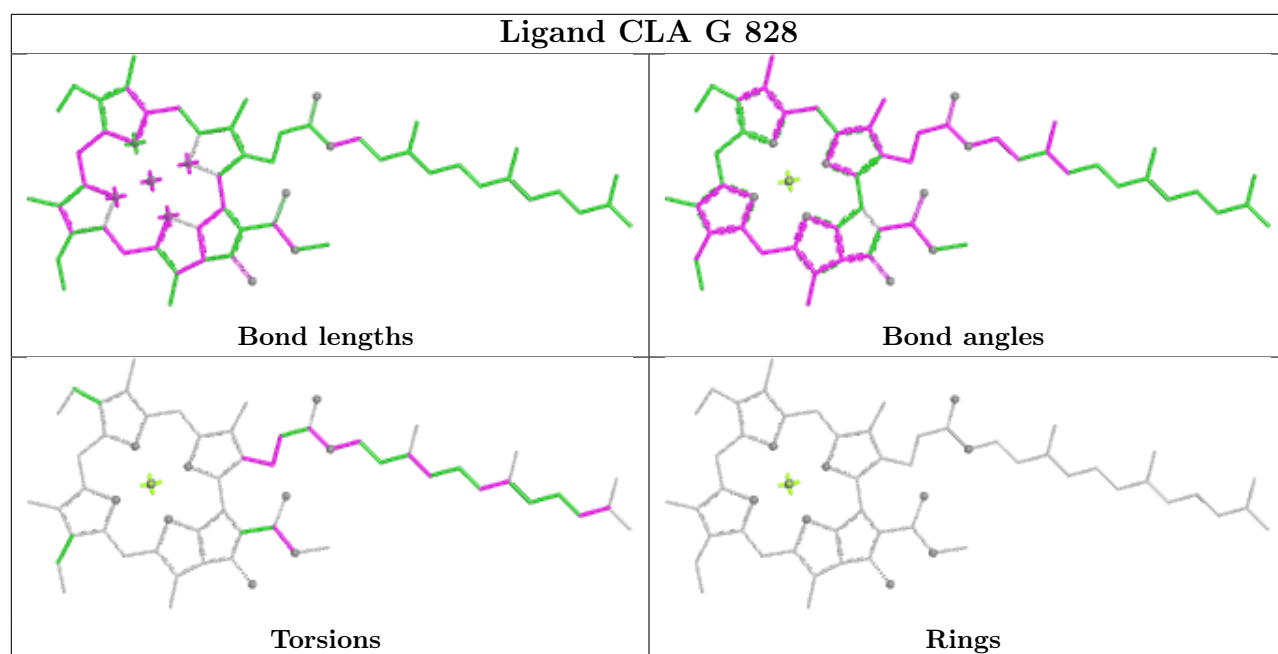


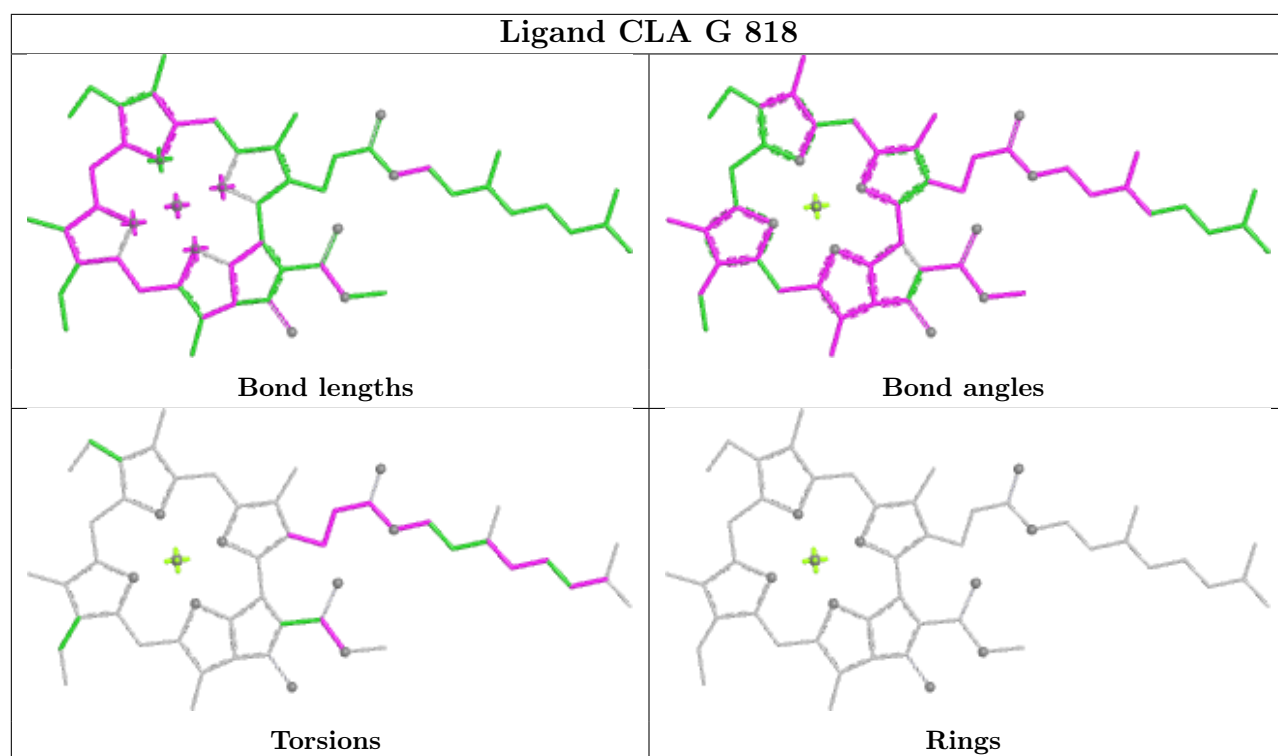
## Ligand 1L3 G 843



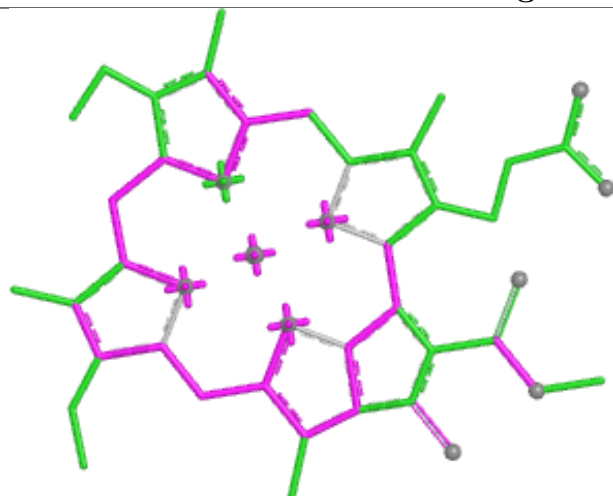
## Ligand BCR S 205



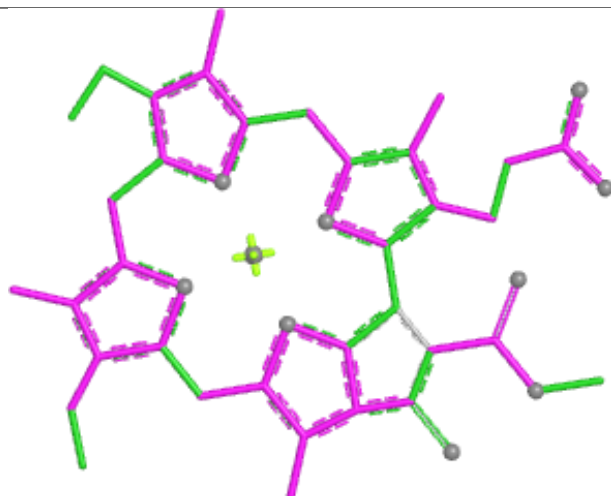




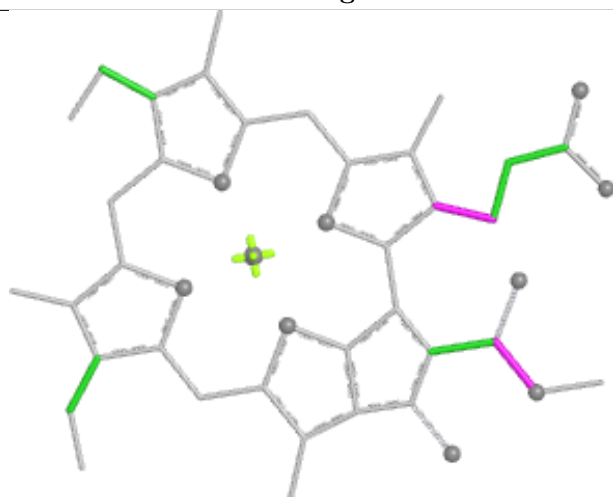
## Ligand CLA b 808



Bond lengths



Bond angles

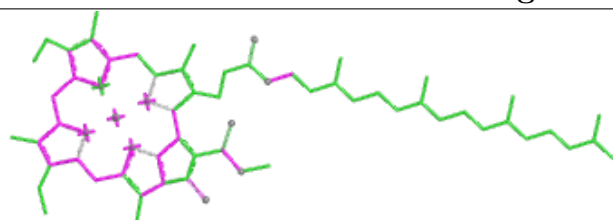


Torsions

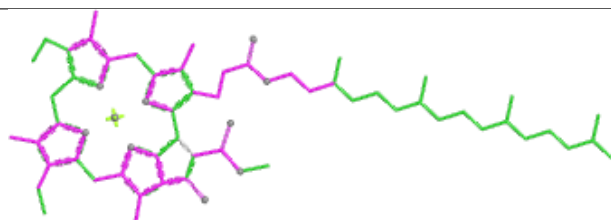


Rings

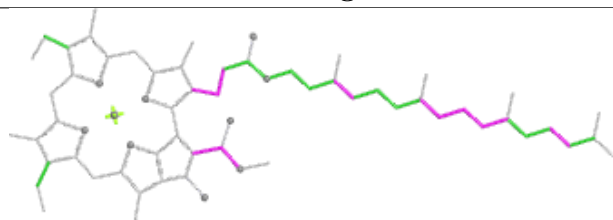
## Ligand CLA b 822



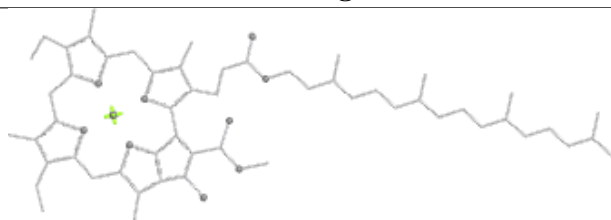
Bond lengths



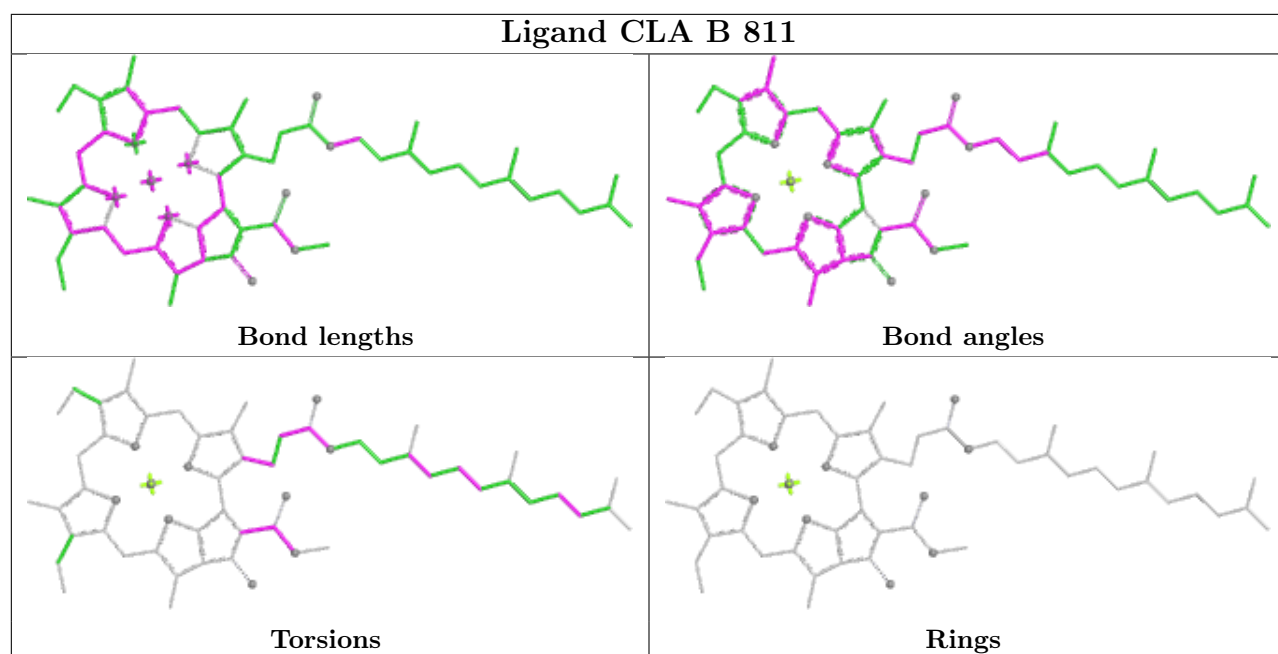
Bond angles

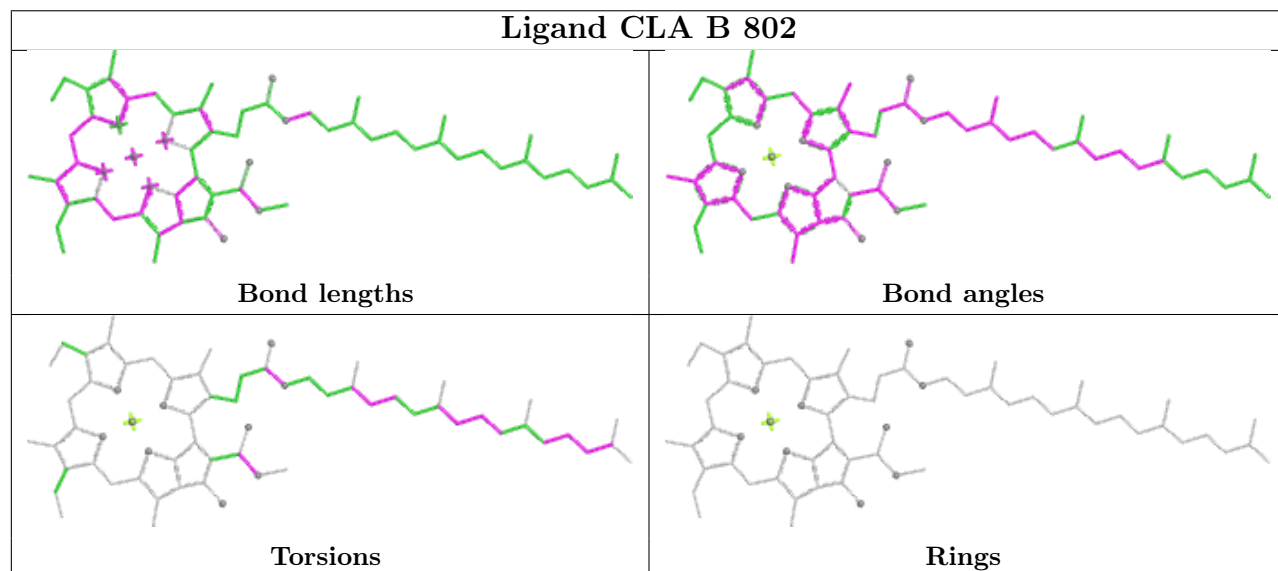
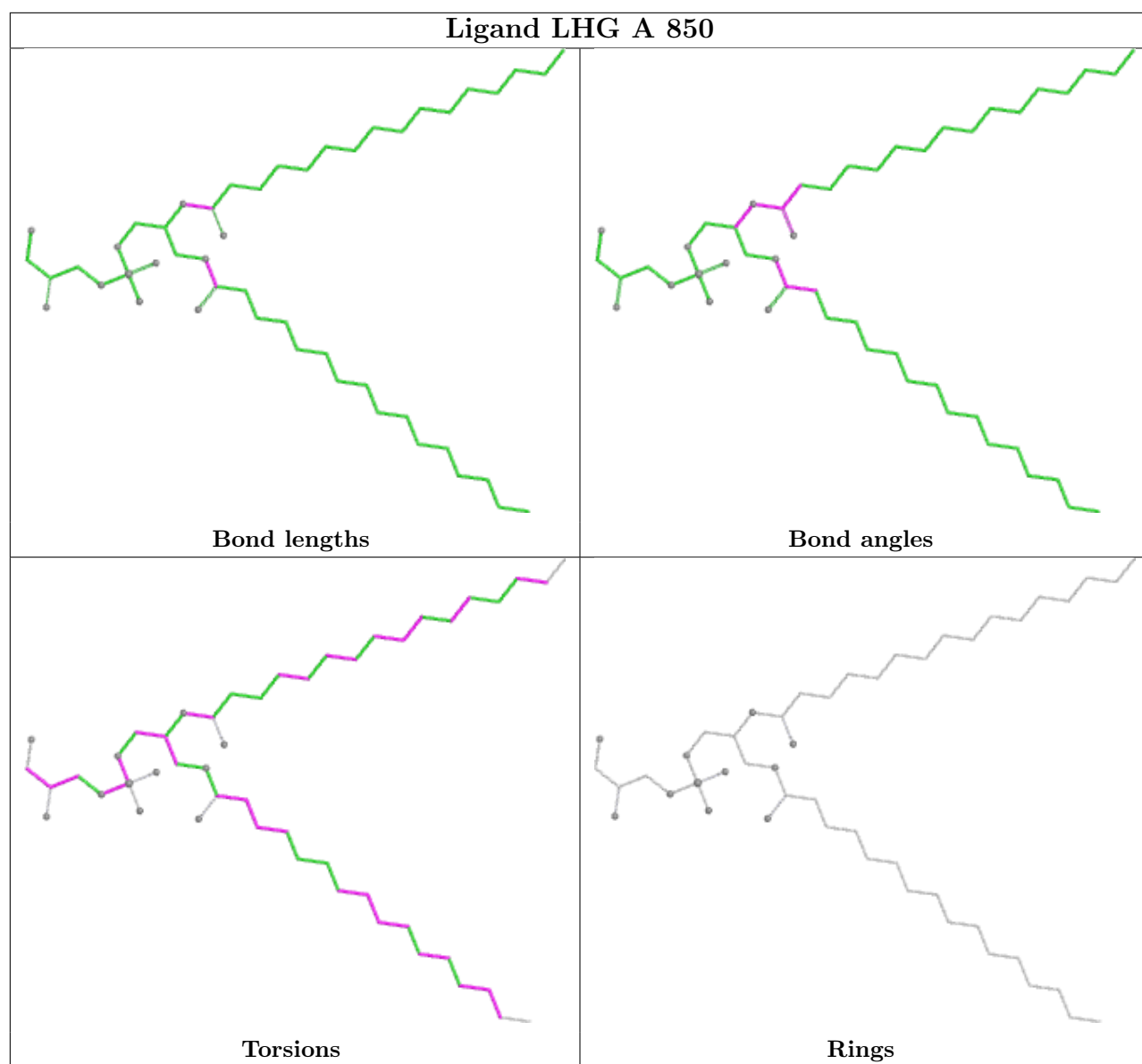


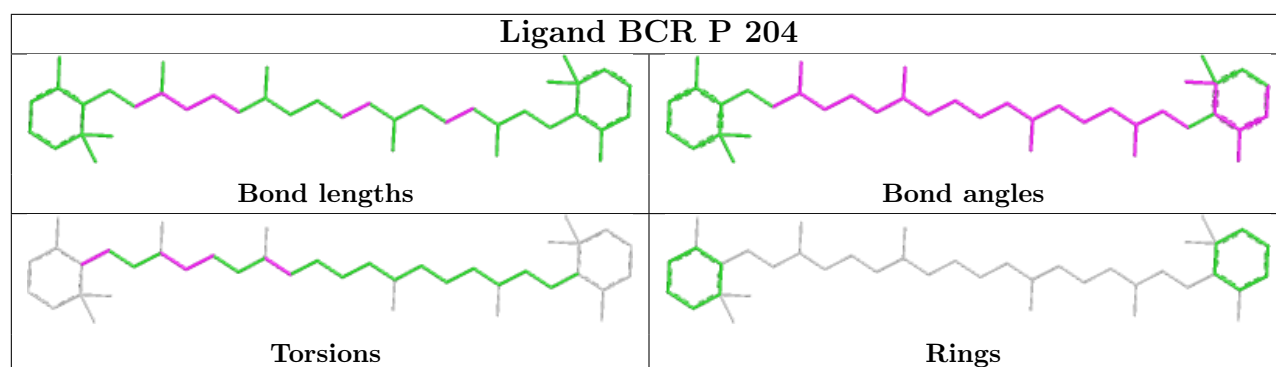
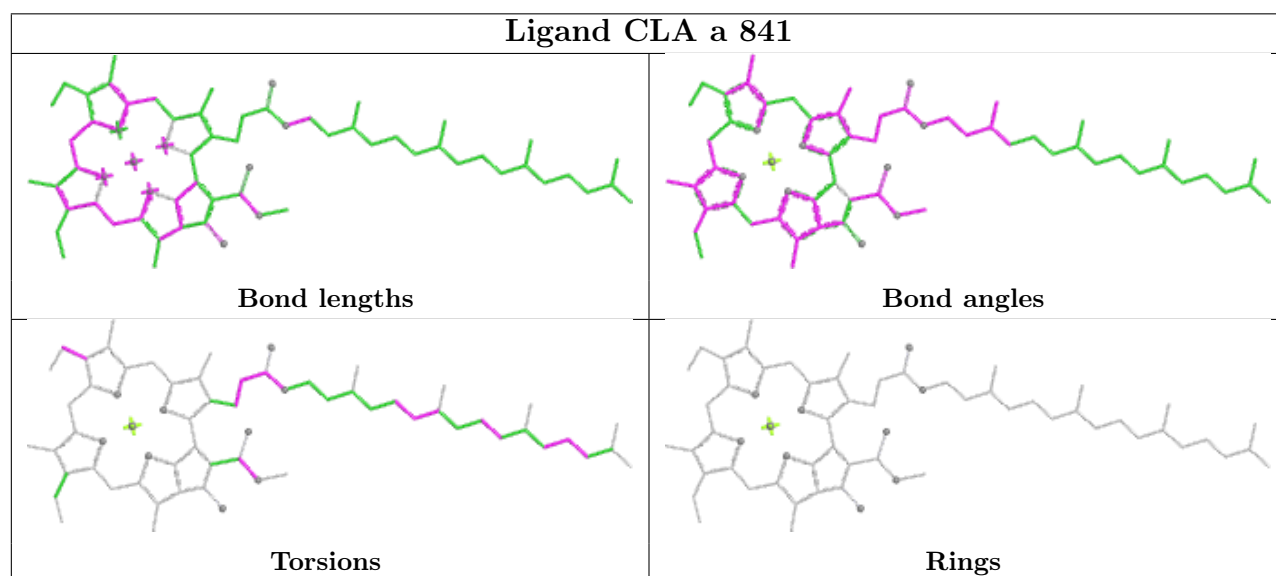
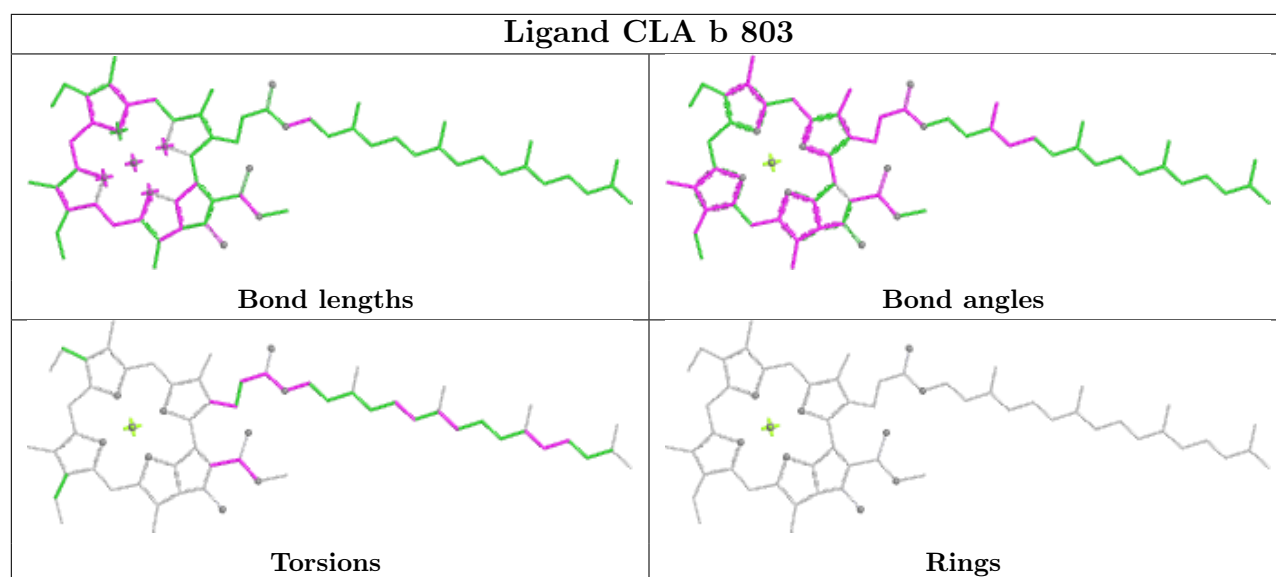
Torsions



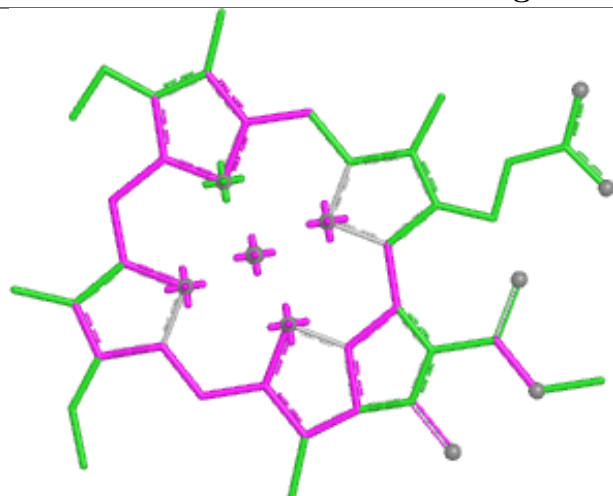
Rings



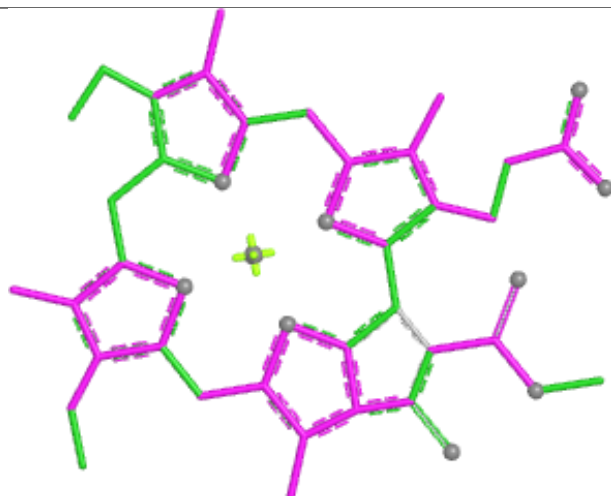




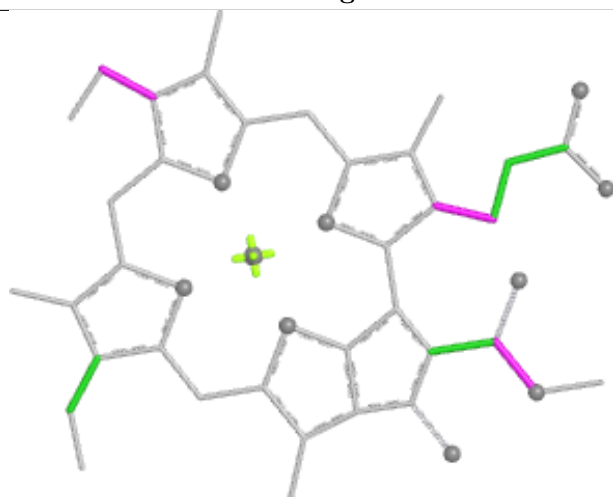
## Ligand CLA G 816



Bond lengths



Bond angles

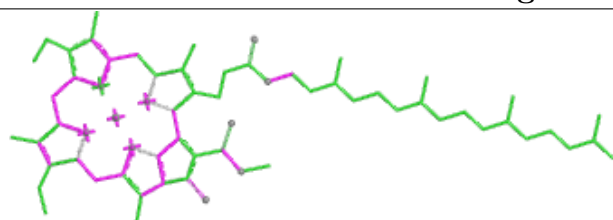


Torsions

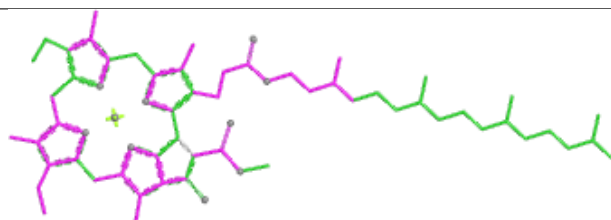


Rings

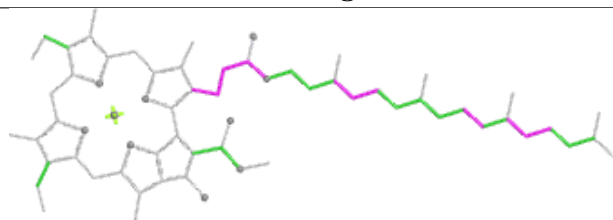
## Ligand CLA S 203



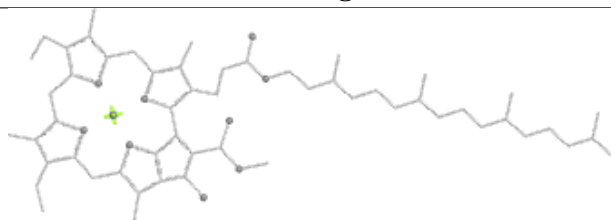
Bond lengths



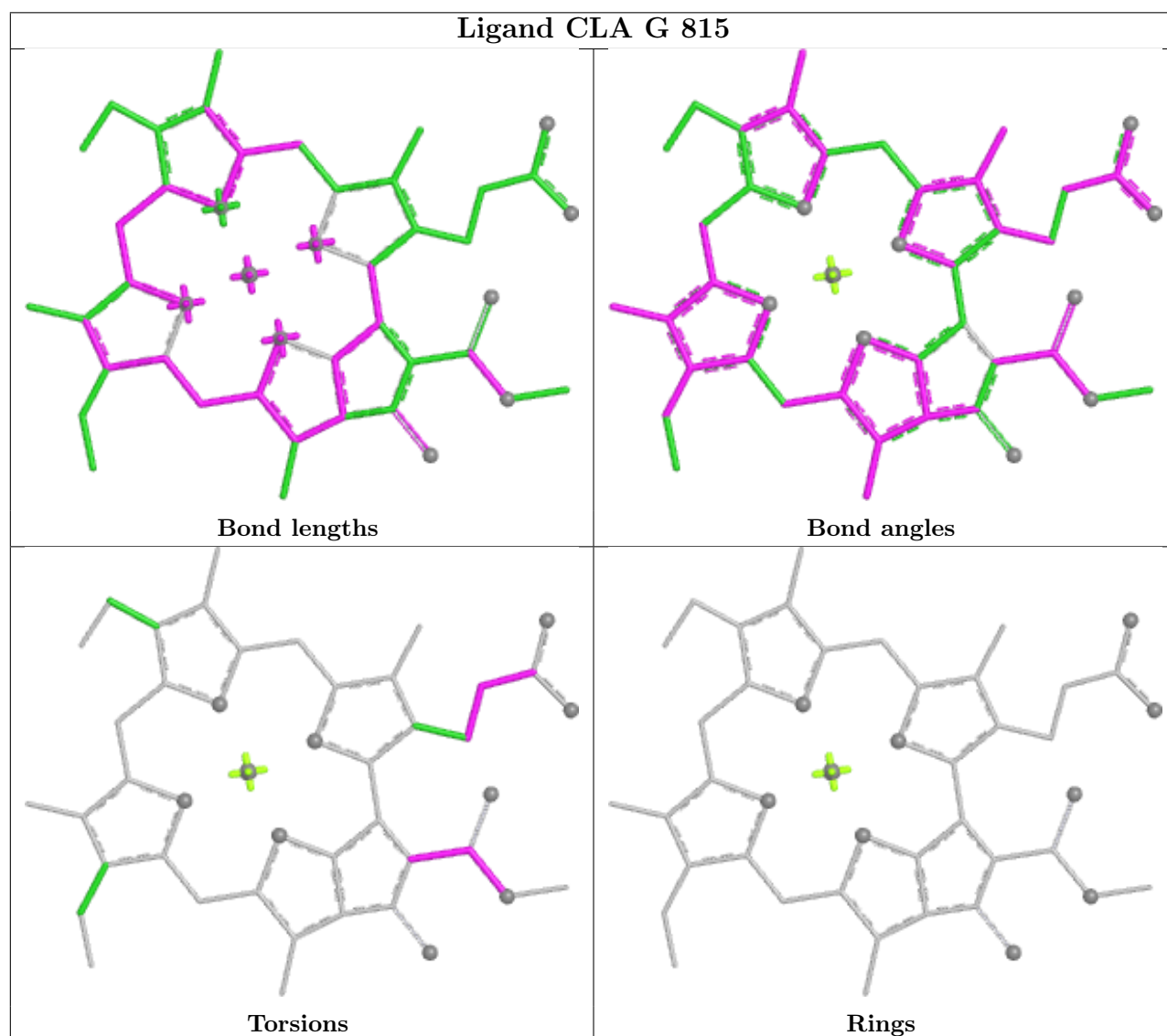
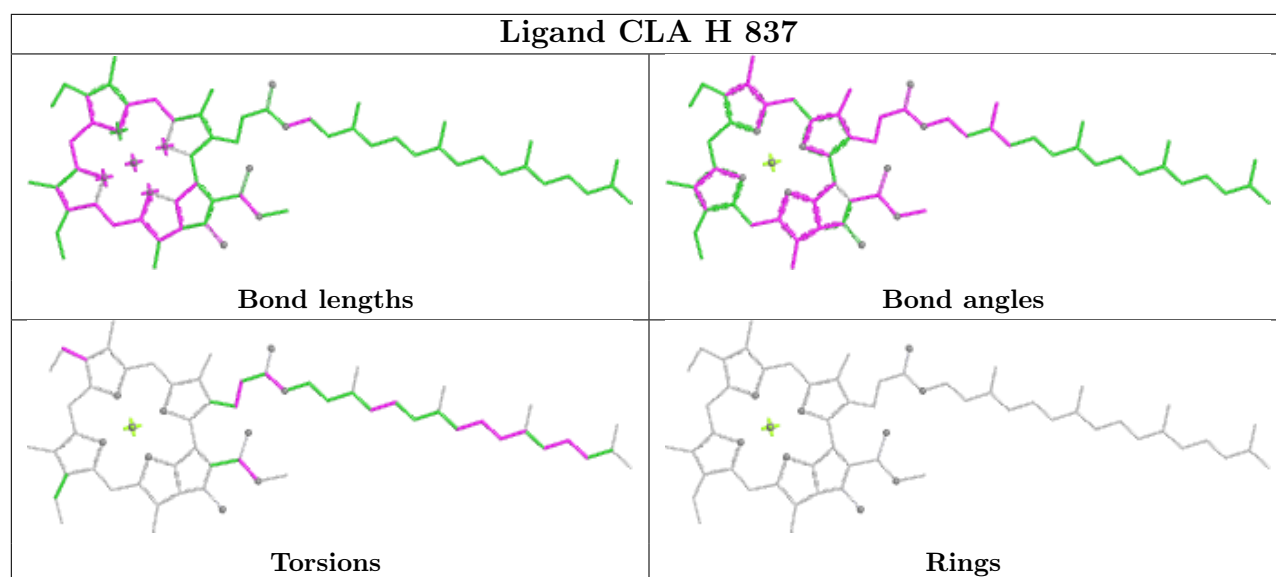
Bond angles

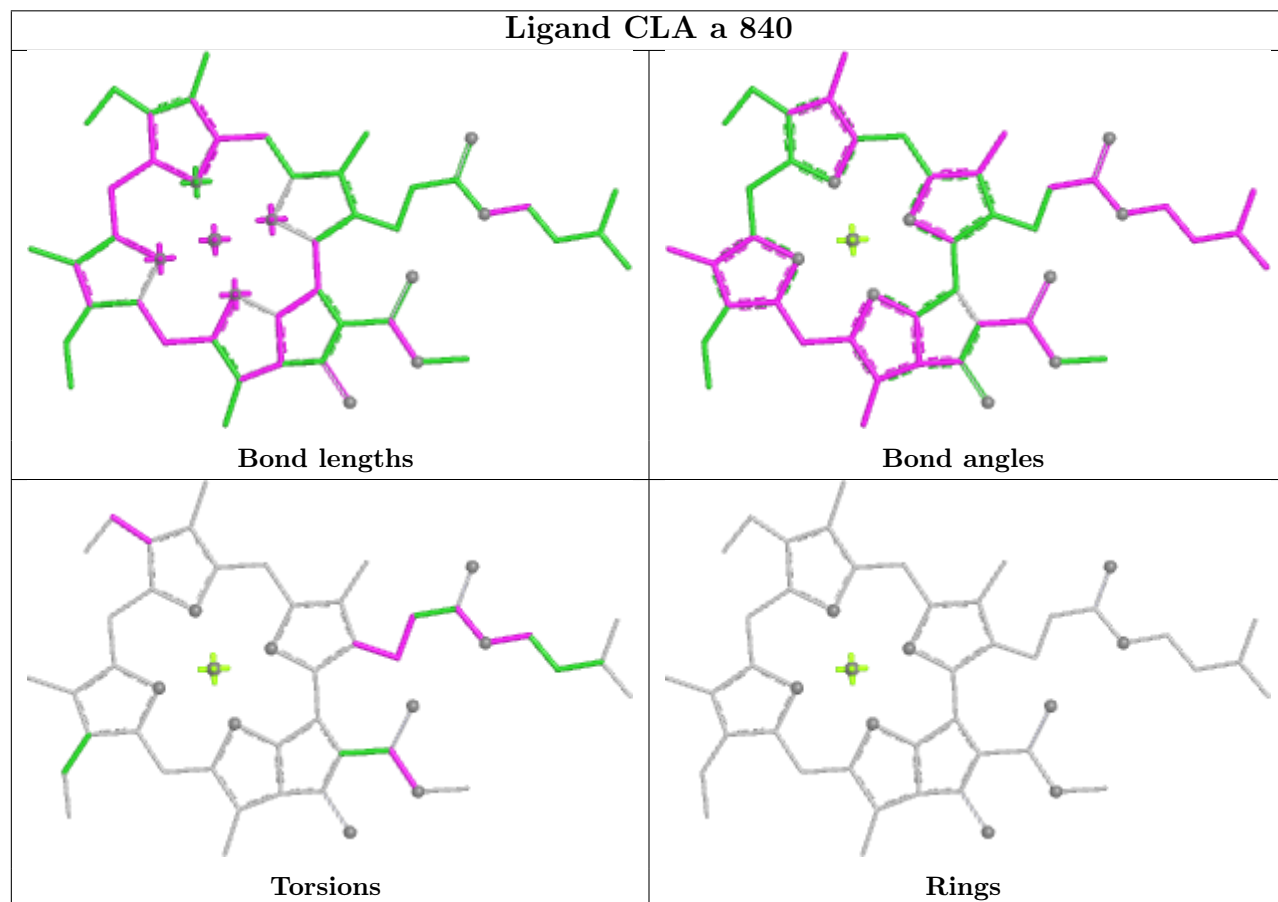
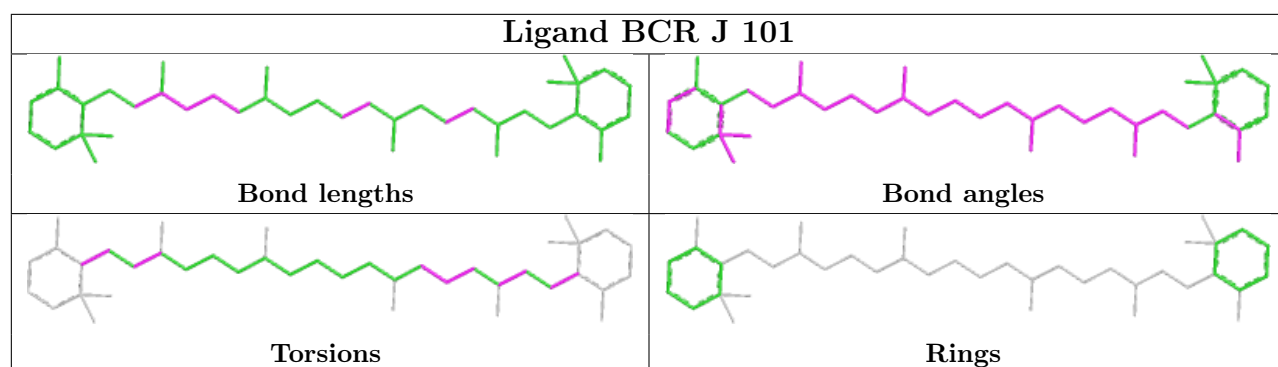


Torsions

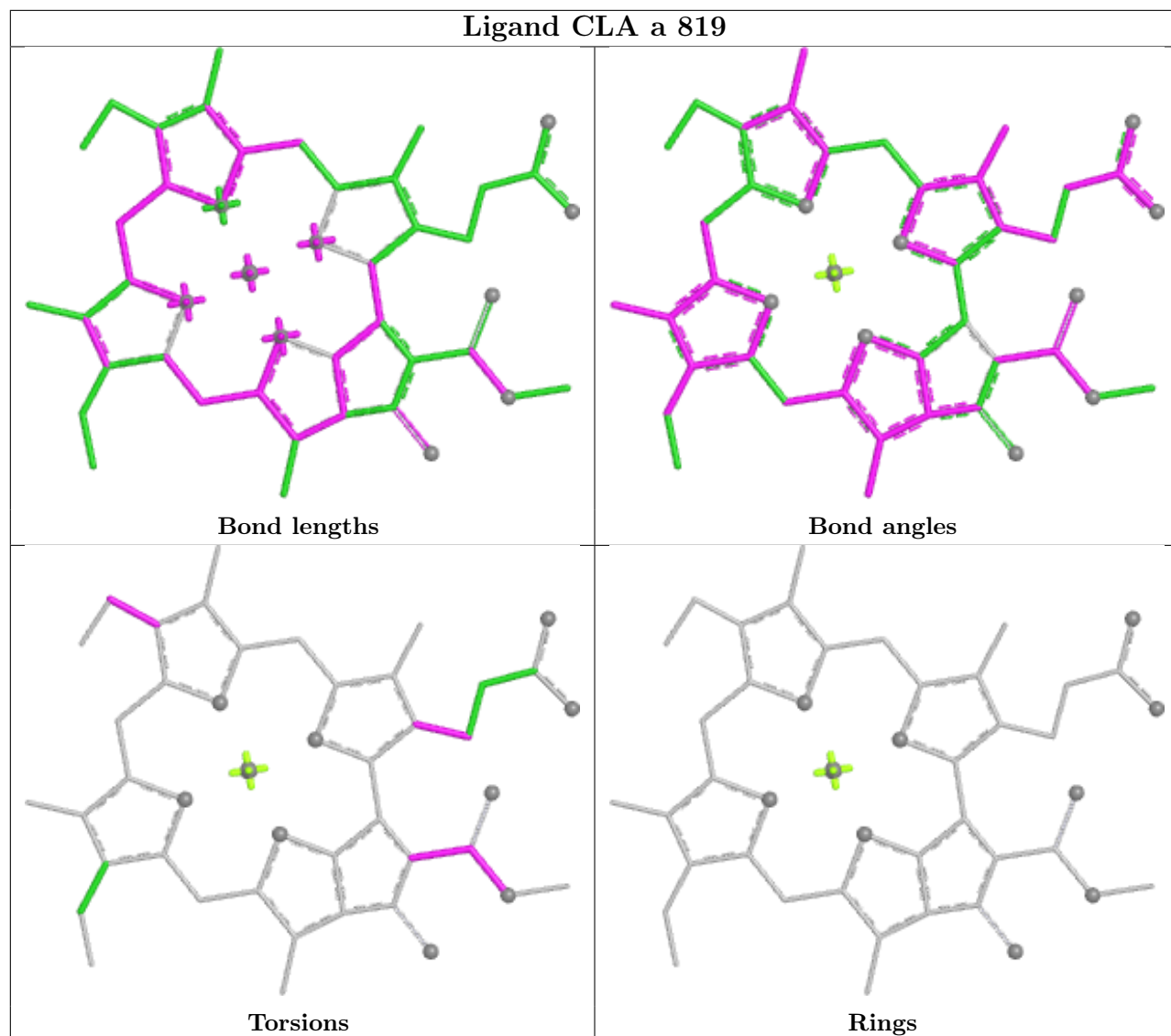


Rings

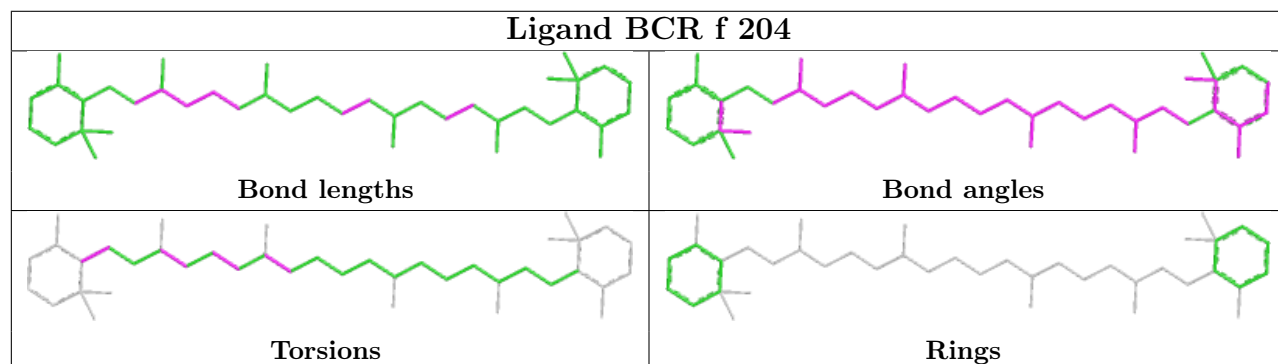




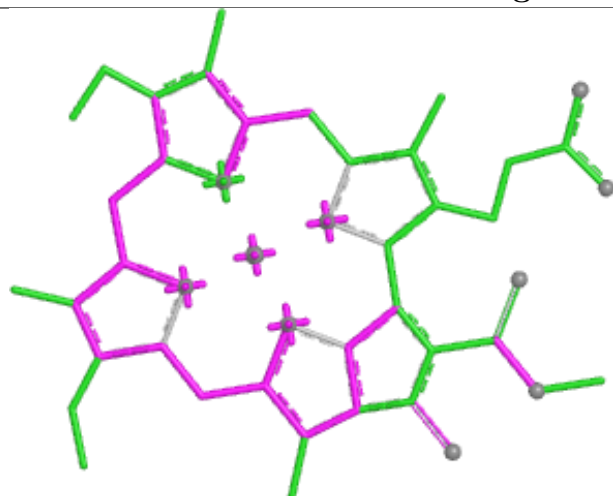
## Ligand CLA a 819



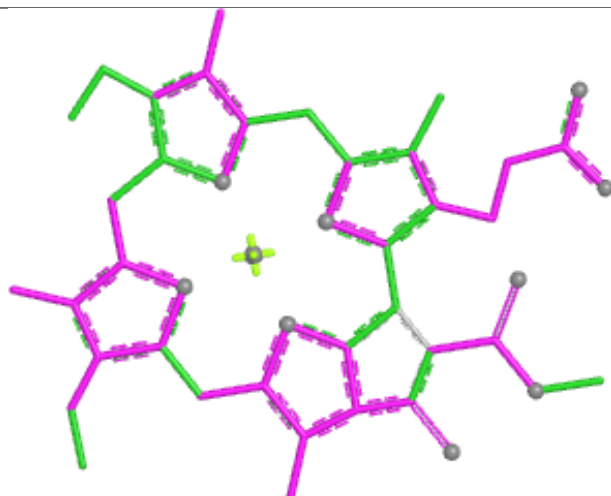
## Ligand BCR f 204



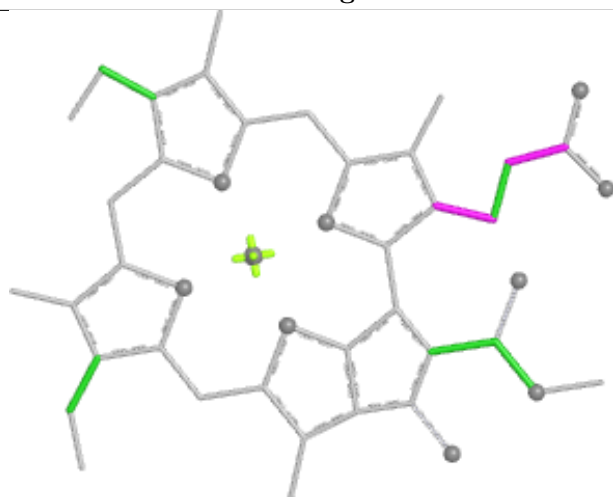
## Ligand CLA G 838



Bond lengths



Bond angles

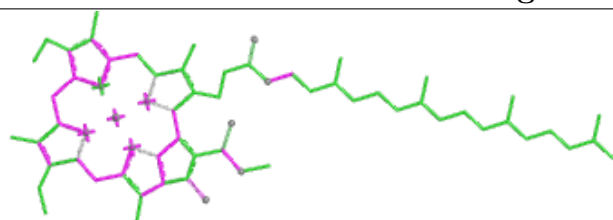


Torsions

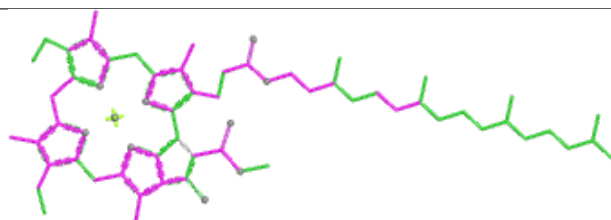


Rings

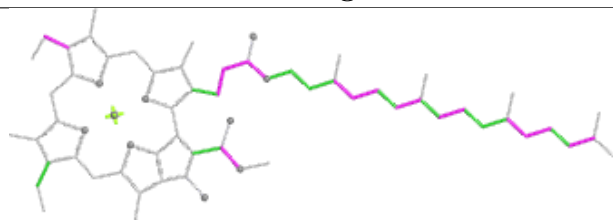
## Ligand CLA b 805



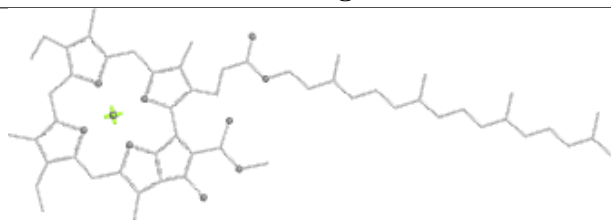
Bond lengths



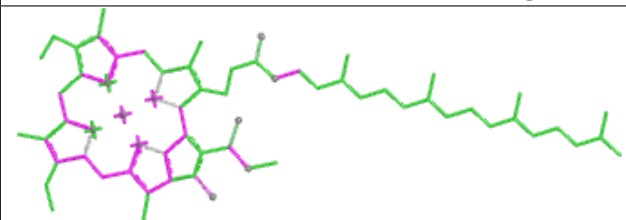
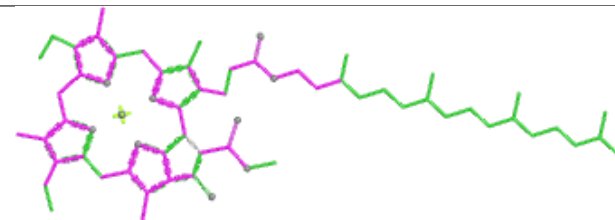
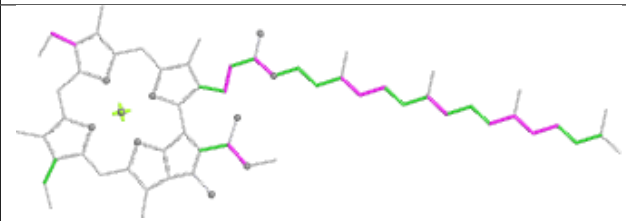
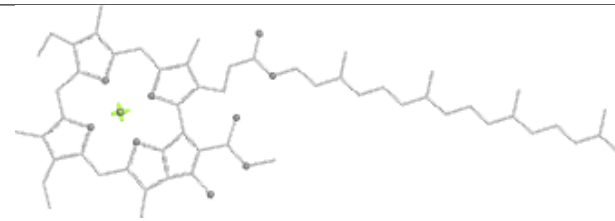
Bond angles

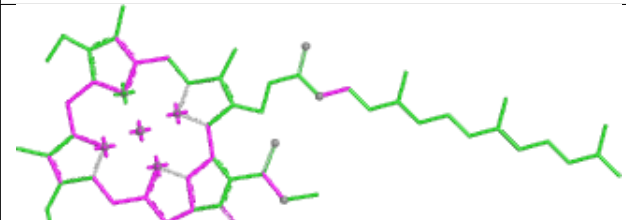
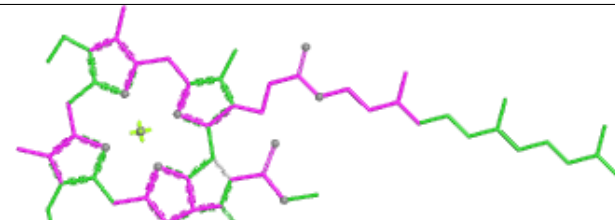
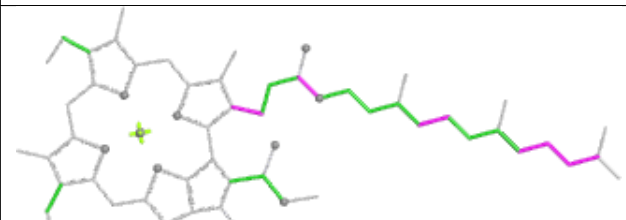
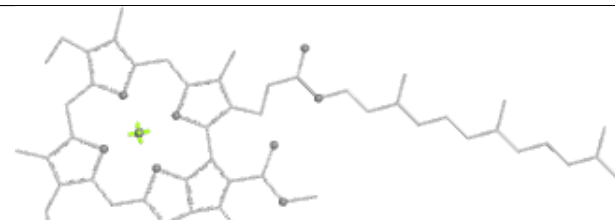


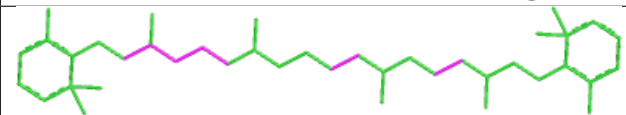
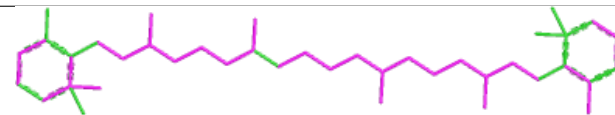
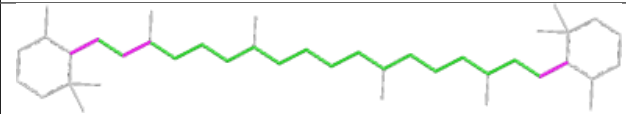
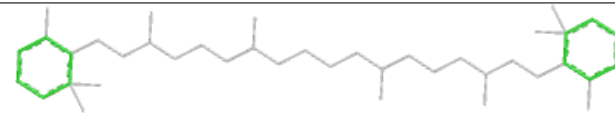
Torsions

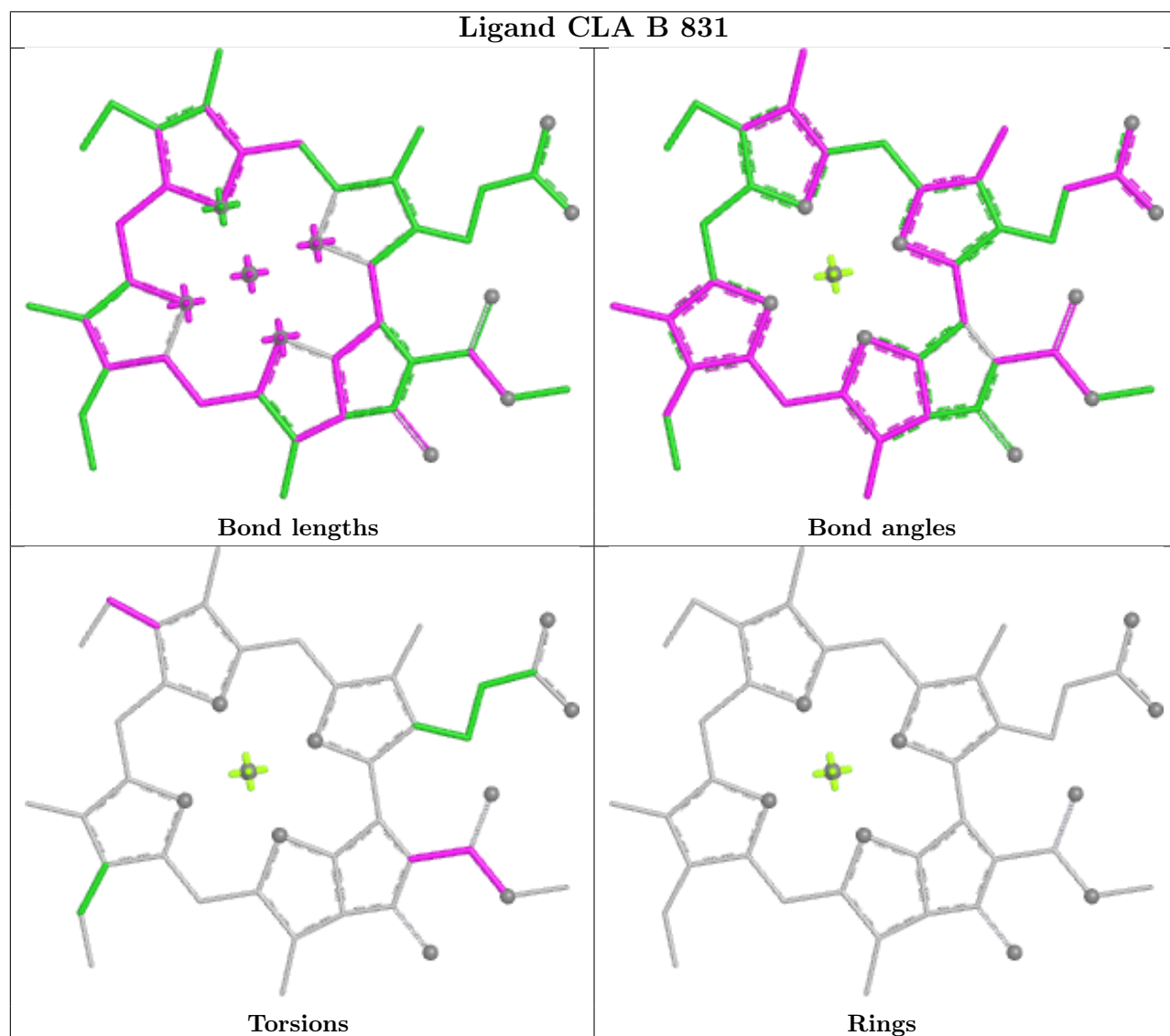
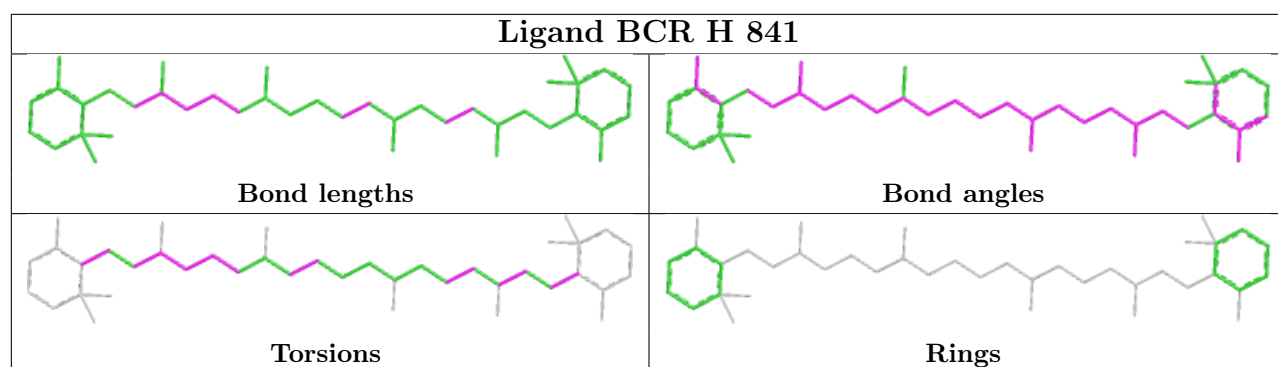


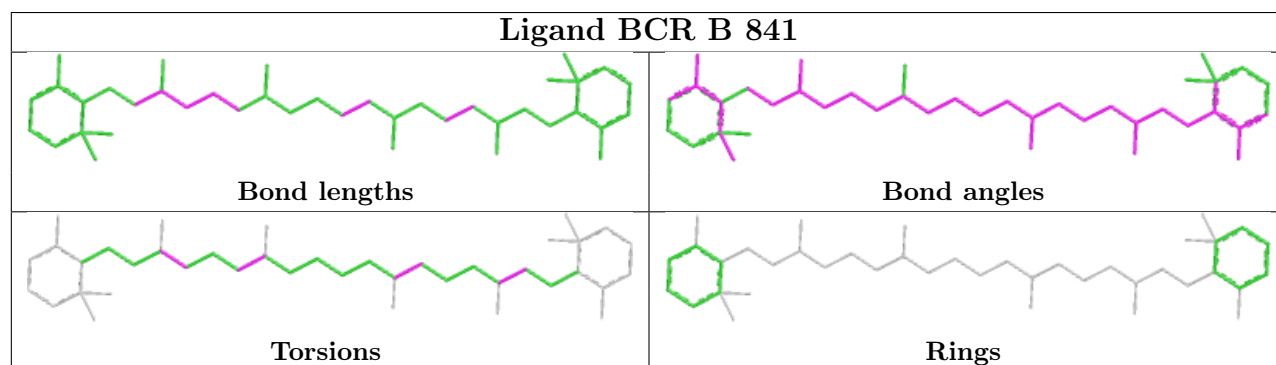
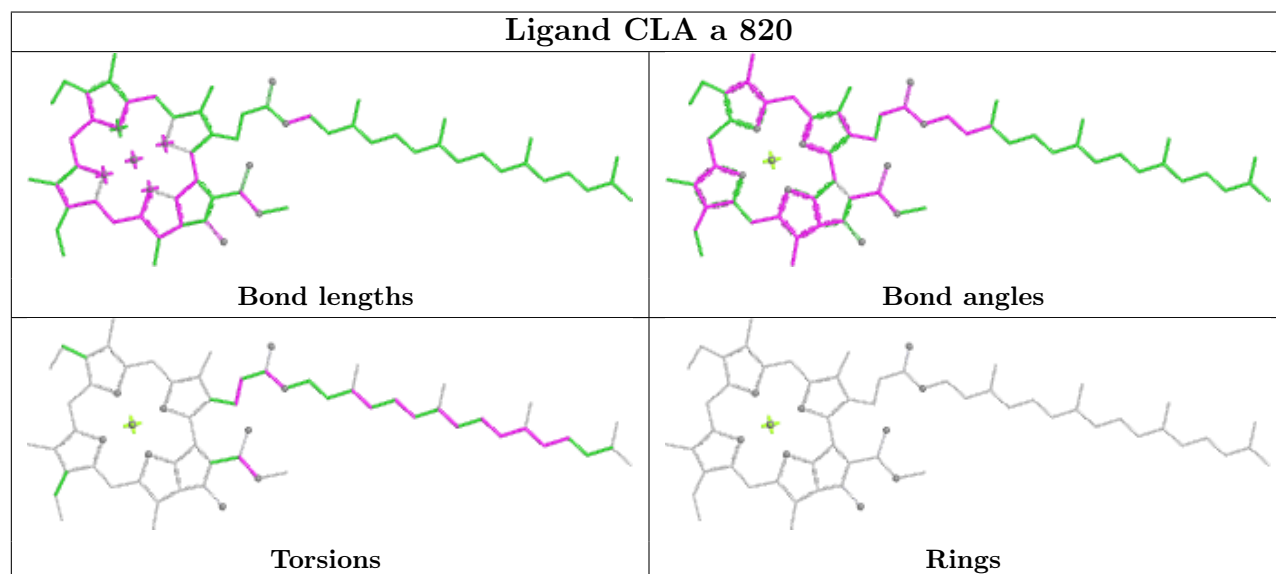
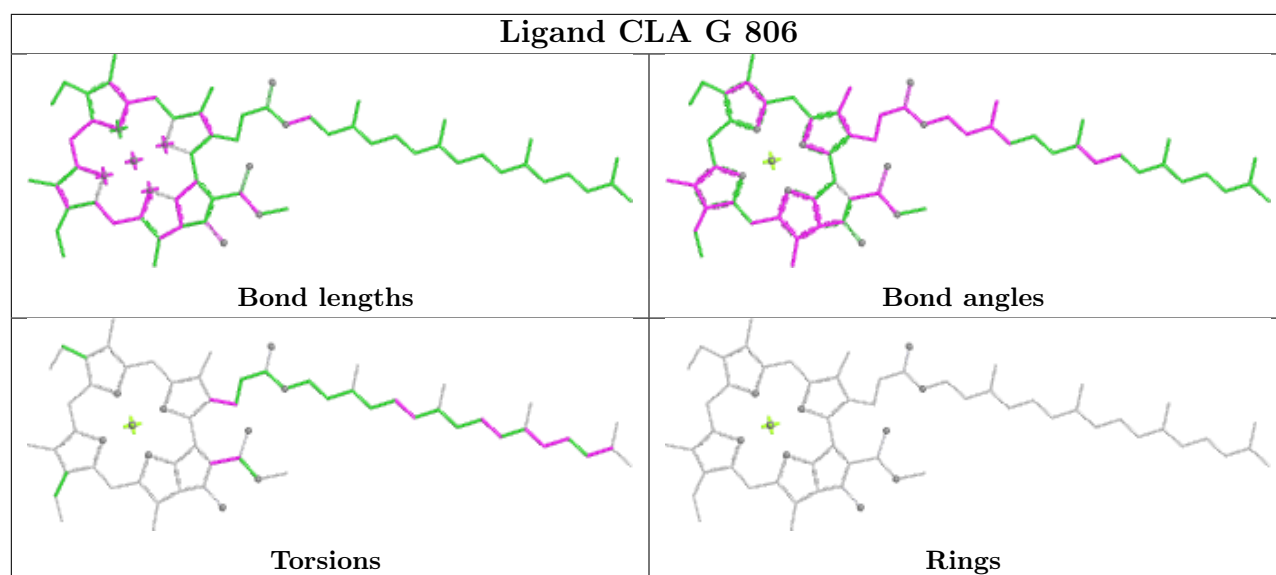
Rings

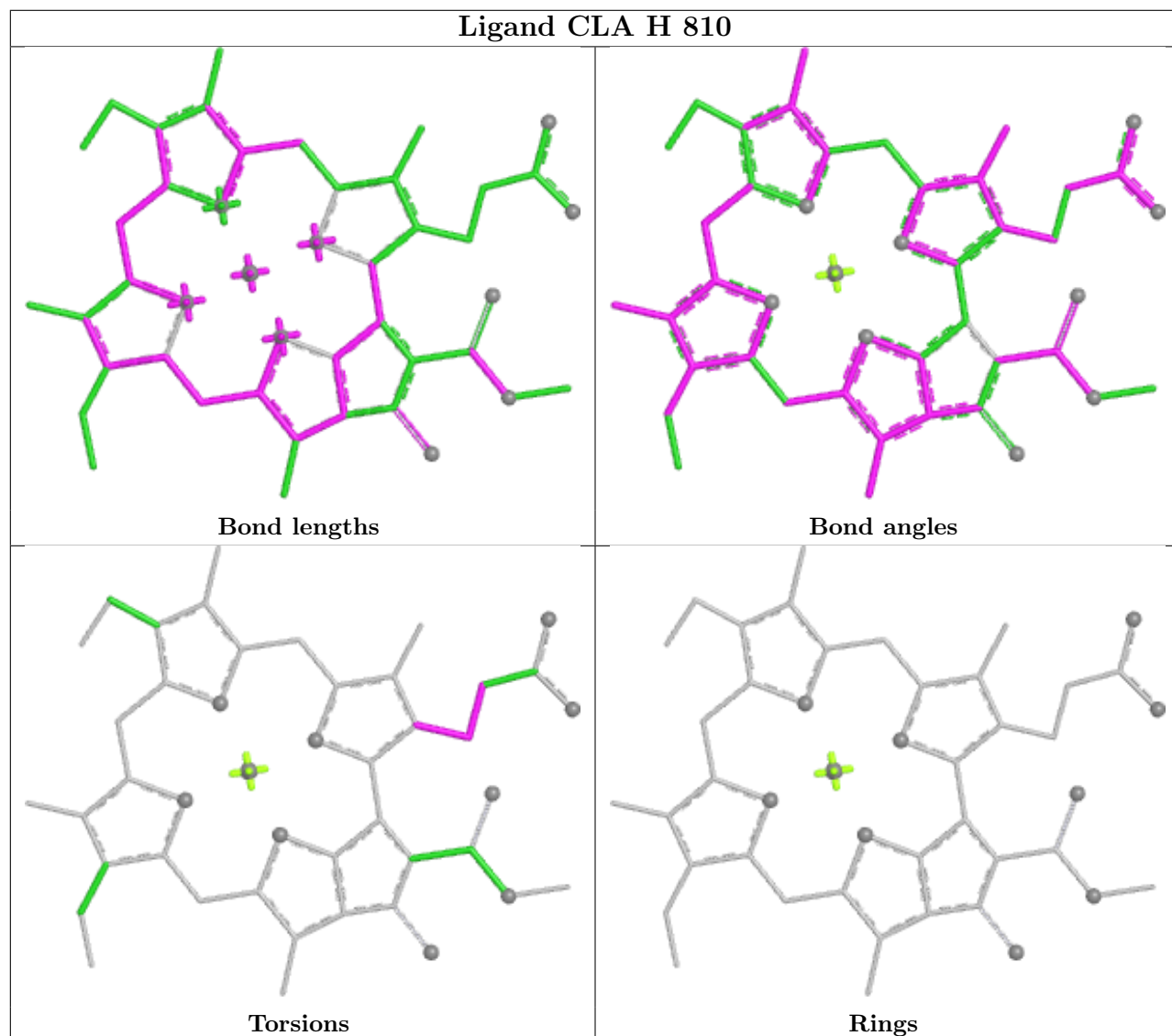
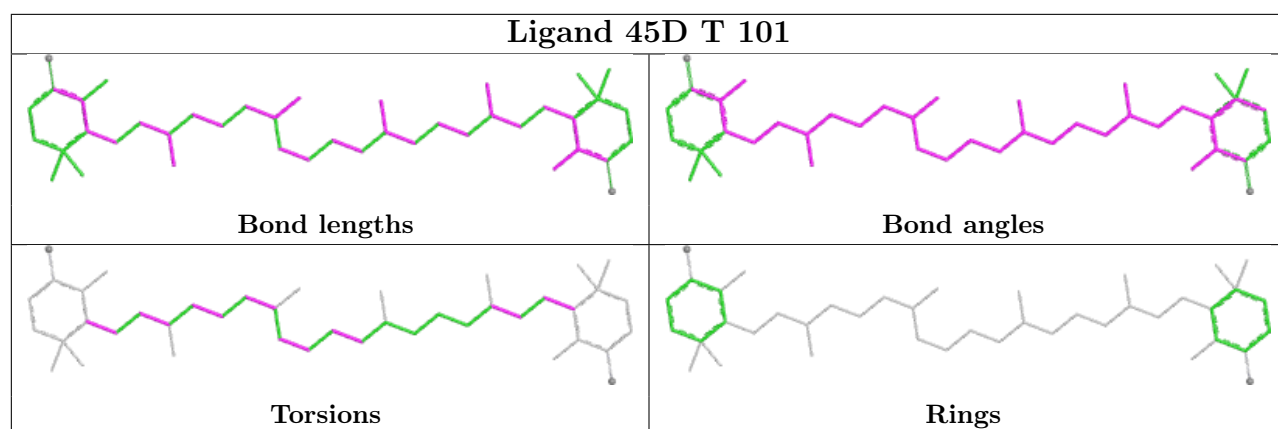
| Ligand CLA A 820                                                                  |                                                                                    |
|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                      | Bond angles                                                                        |
|  |  |
| Torsions                                                                          | Rings                                                                              |

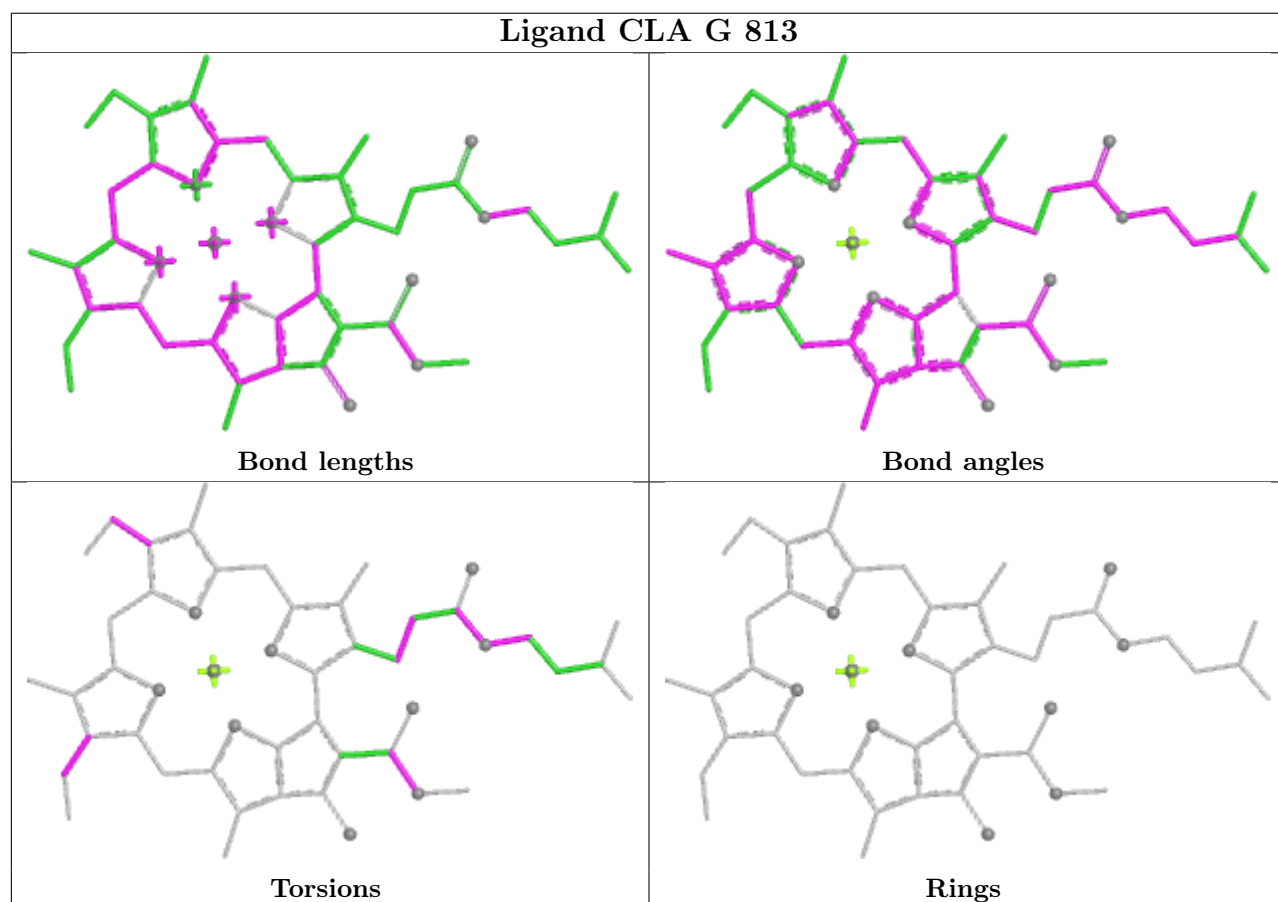
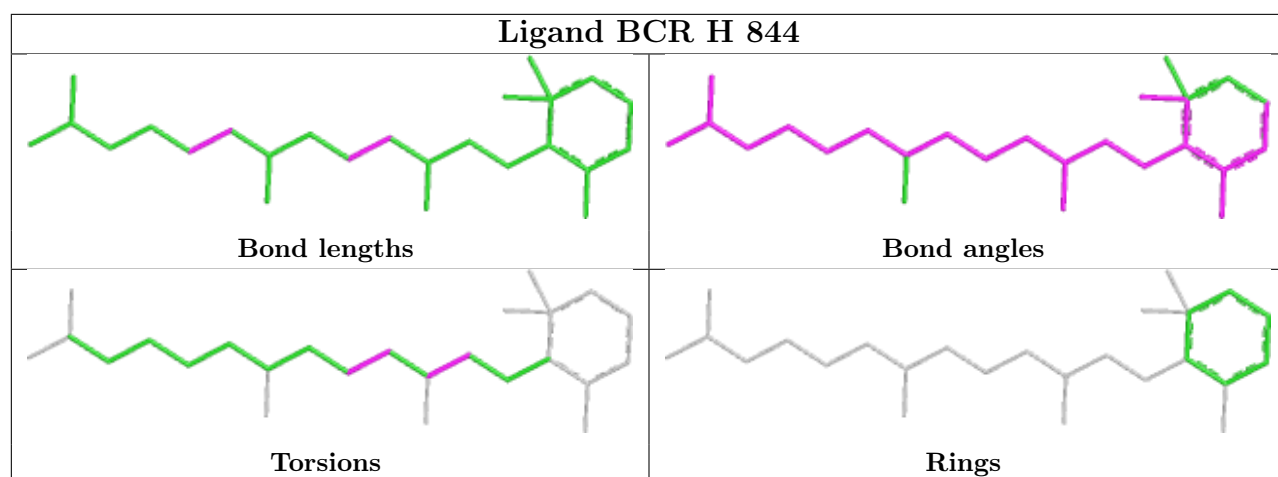
| Ligand CLA b 815                                                                    |                                                                                      |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
|    |    |
| Bond lengths                                                                        | Bond angles                                                                          |
|  |  |
| Torsions                                                                            | Rings                                                                                |

| Ligand BCR J 104                                                                    |                                                                                      |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                        | Bond angles                                                                          |
|  |  |
| Torsions                                                                            | Rings                                                                                |

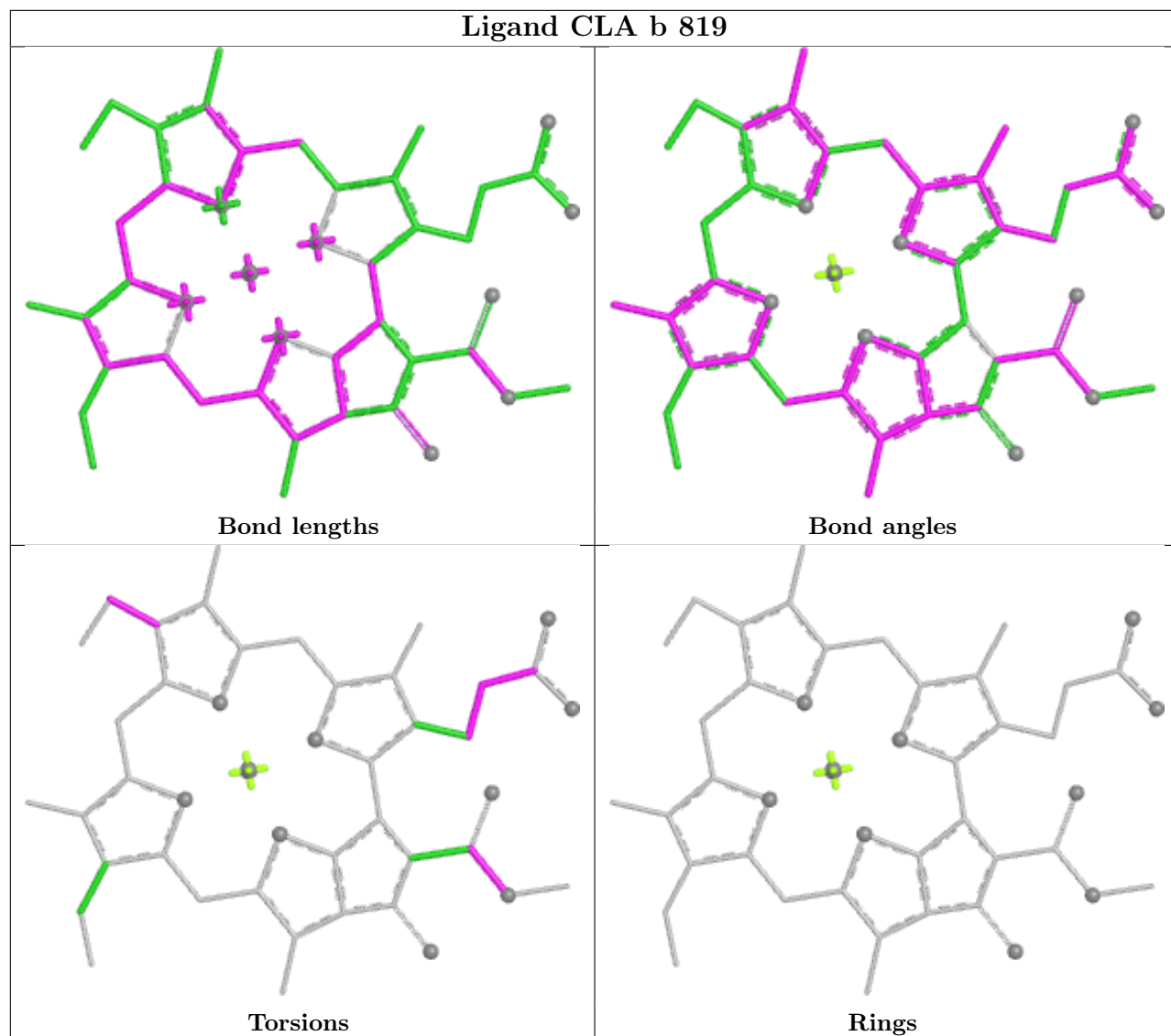




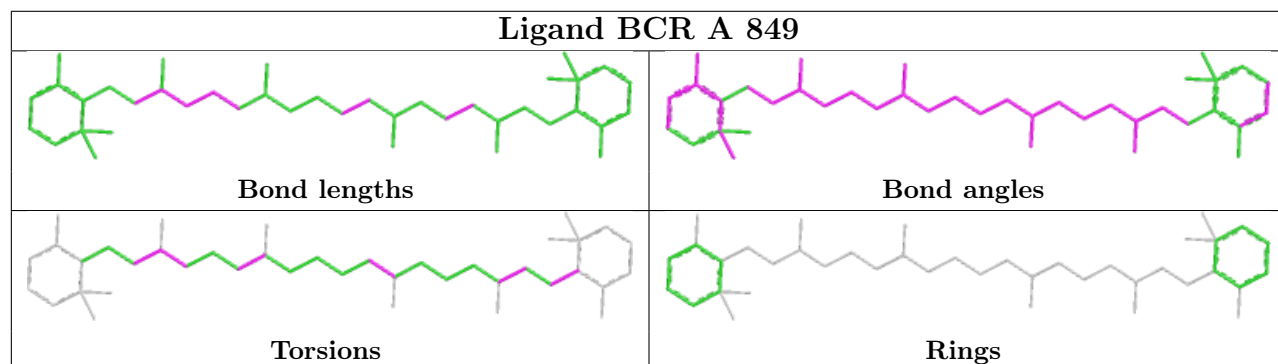


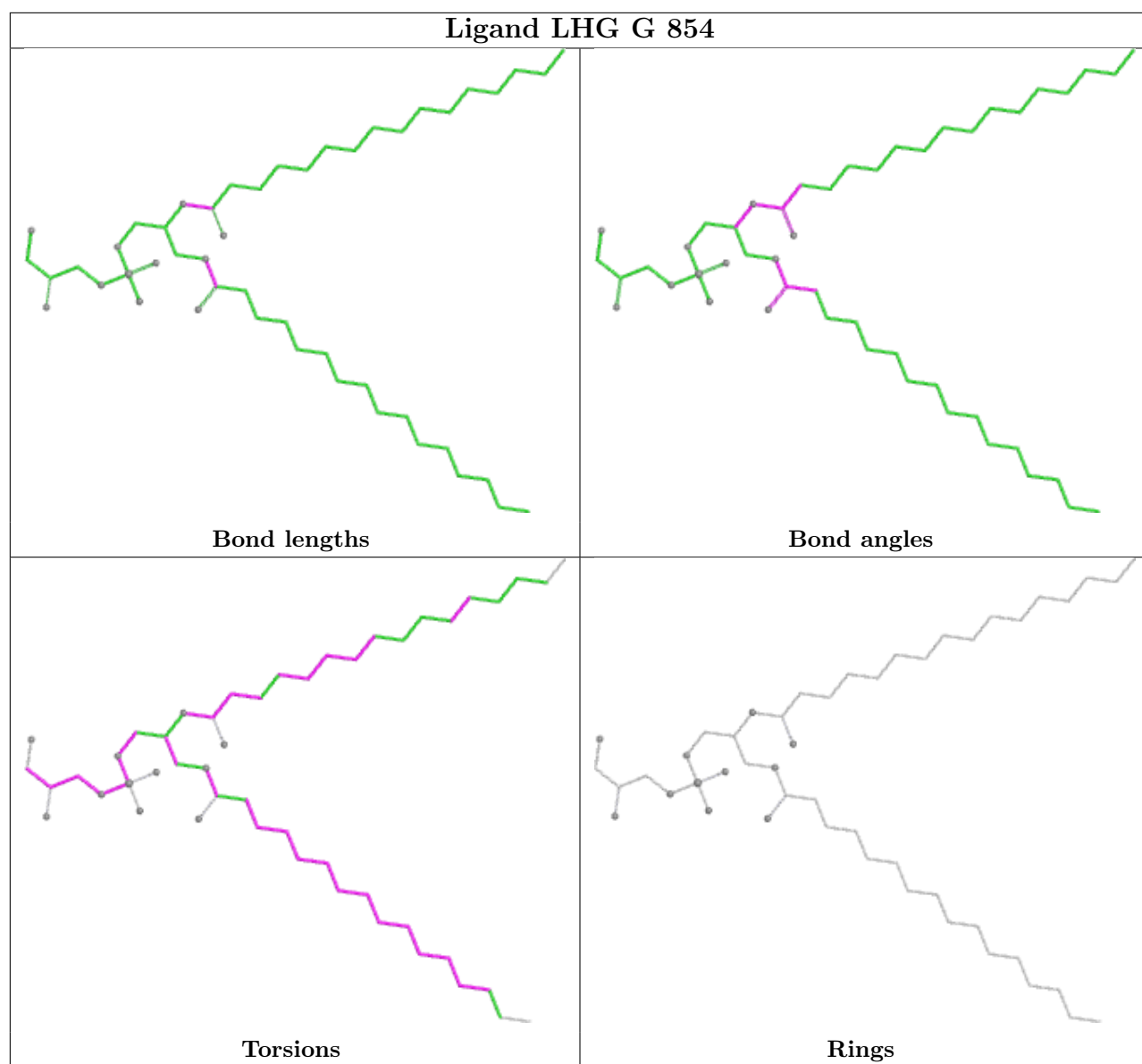


## Ligand CLA b 819

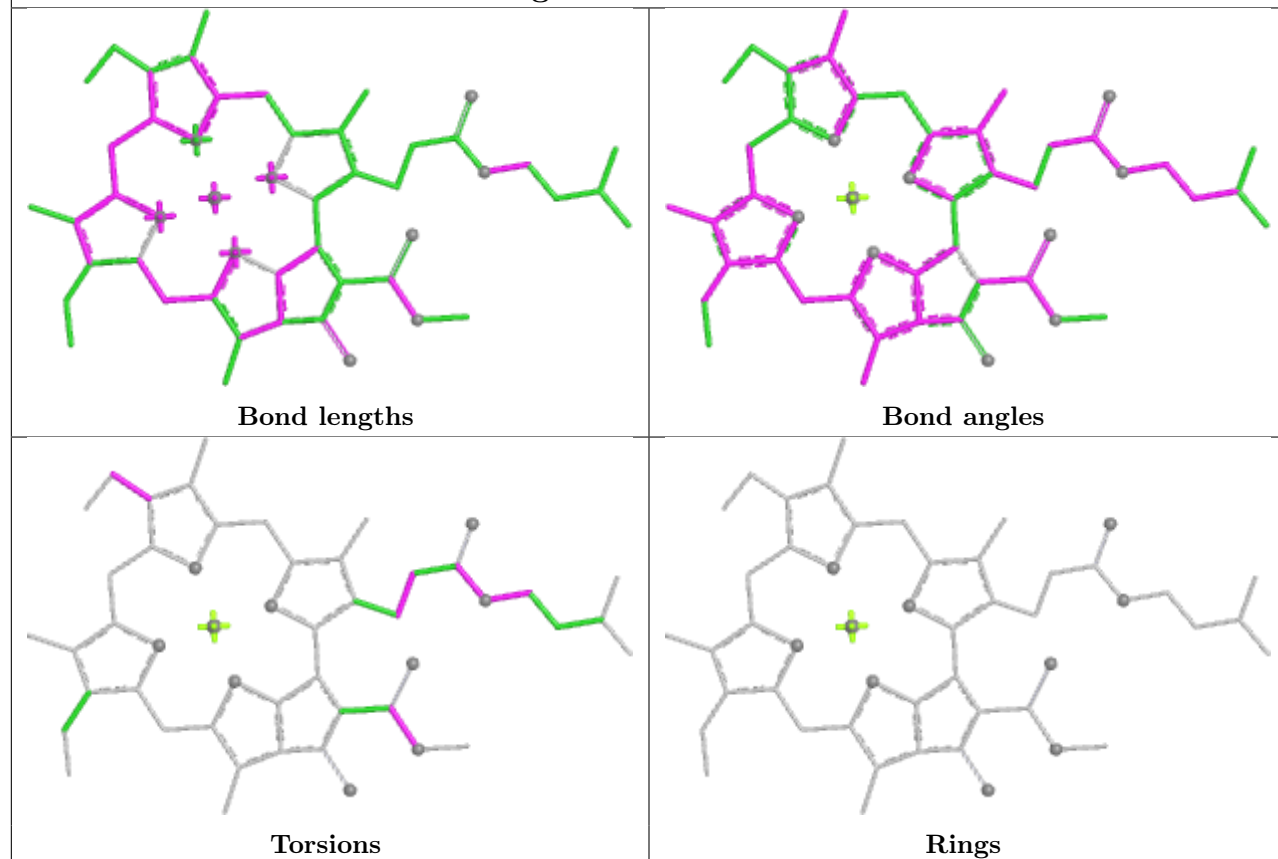


## Ligand BCR A 849

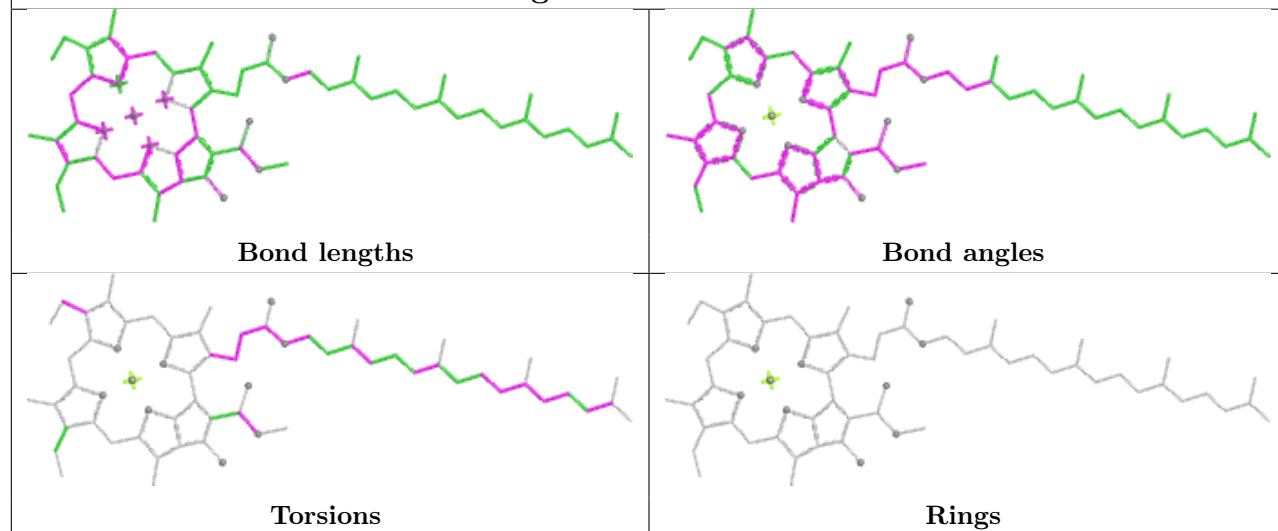


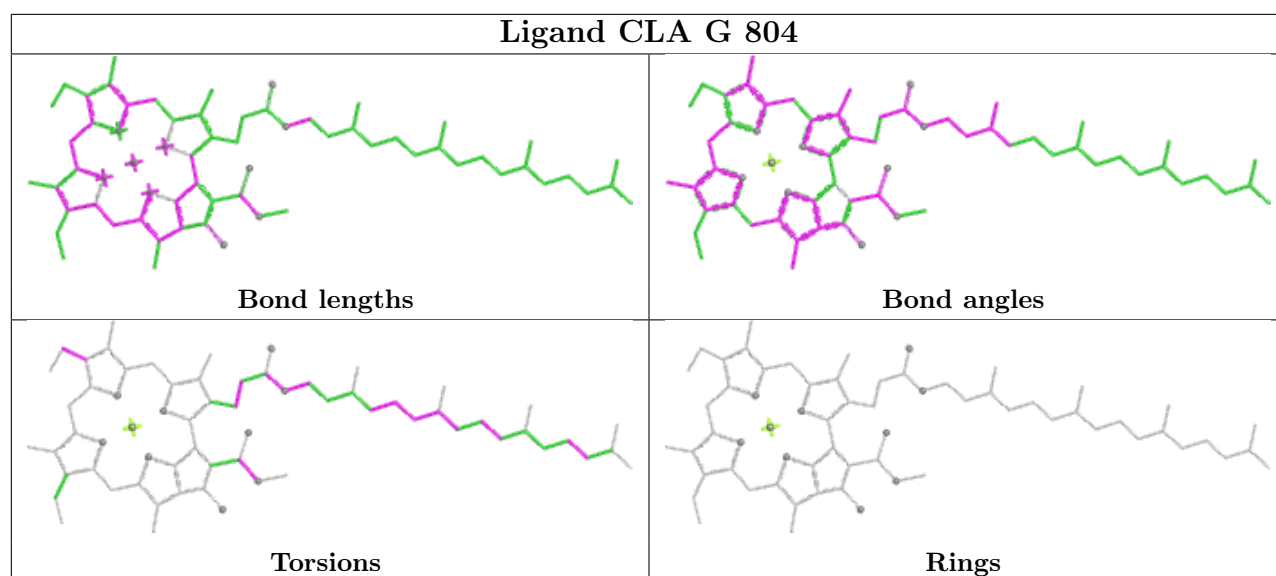
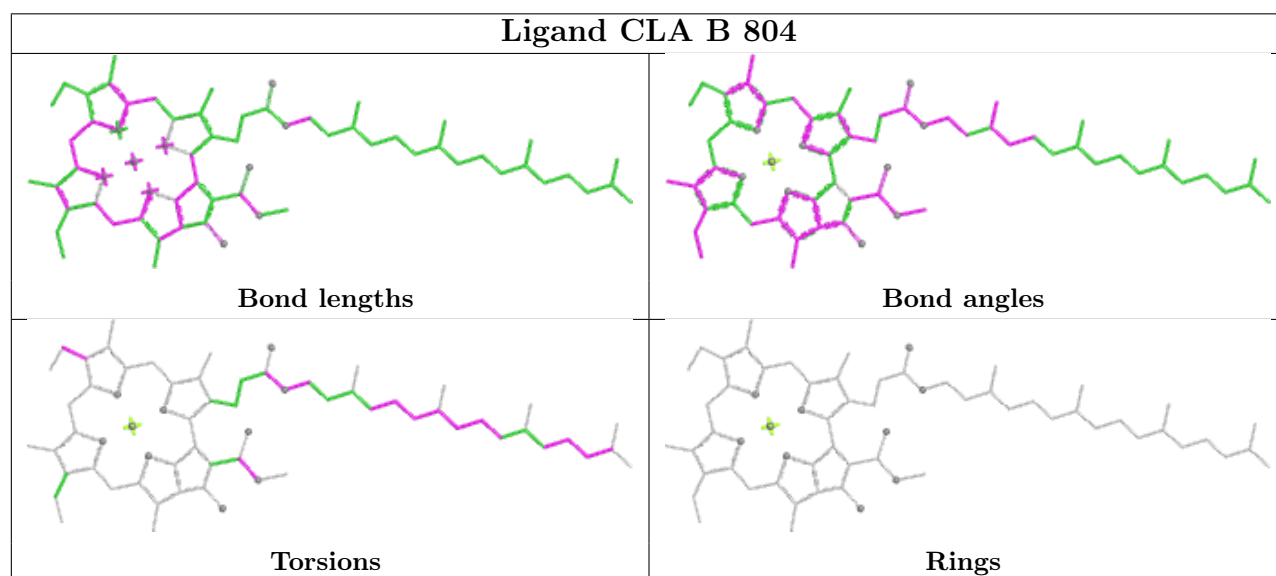
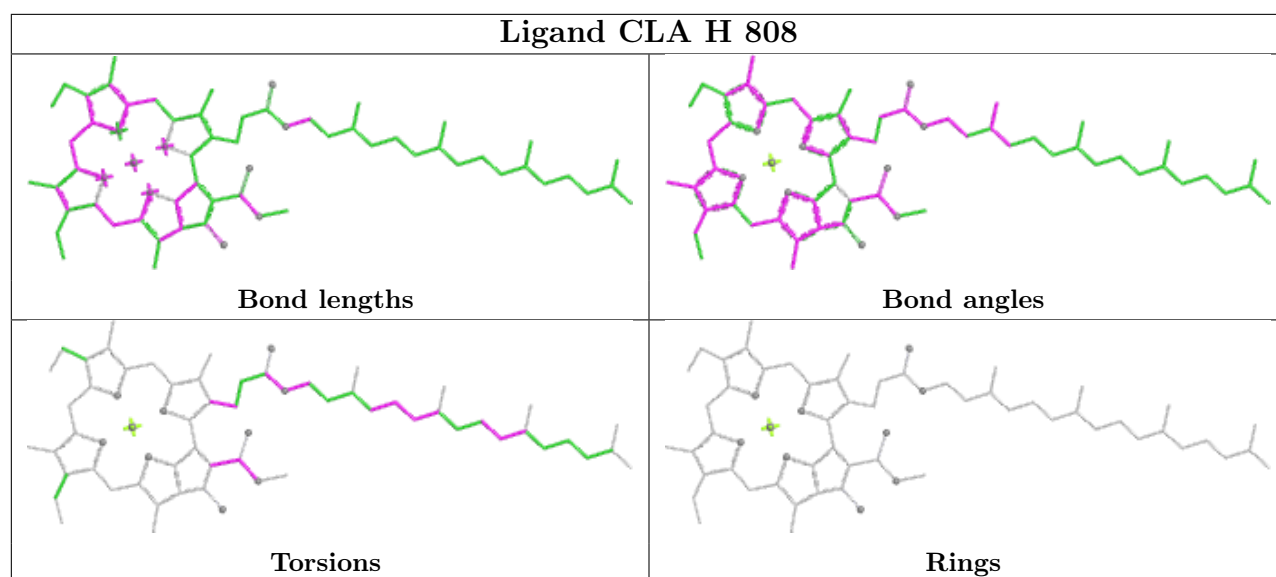


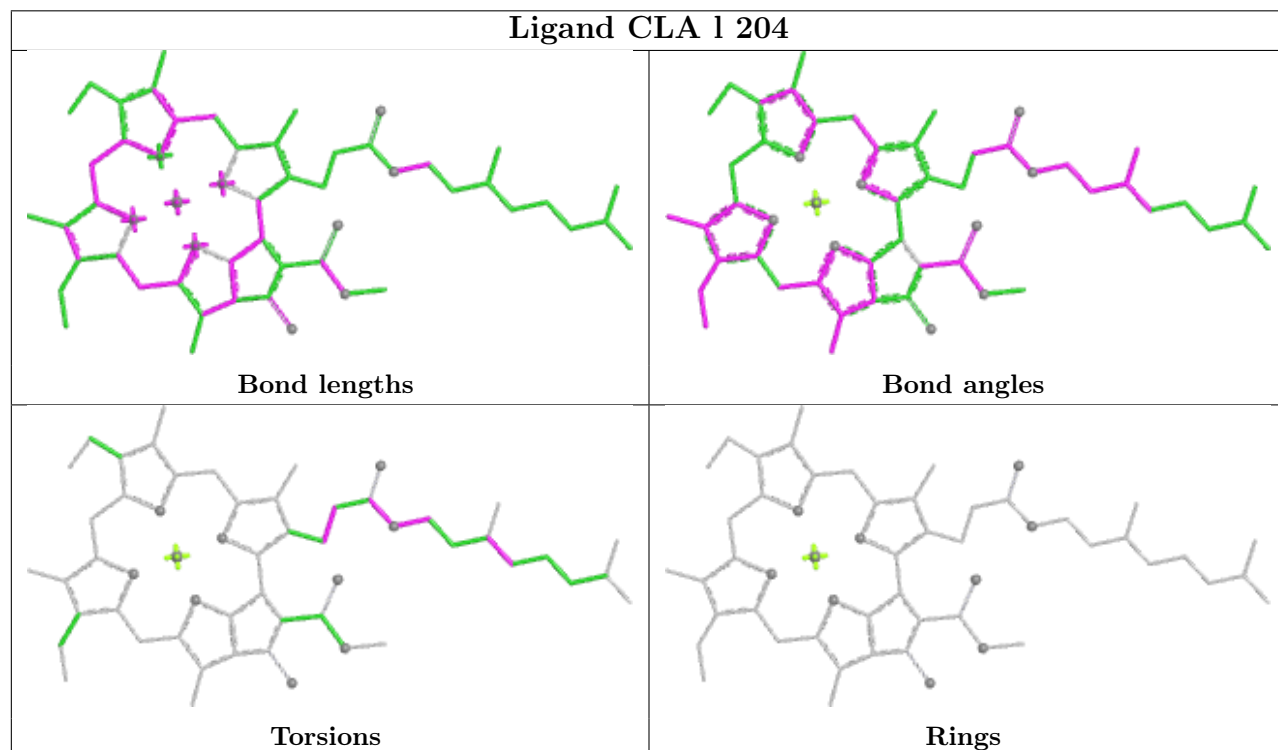
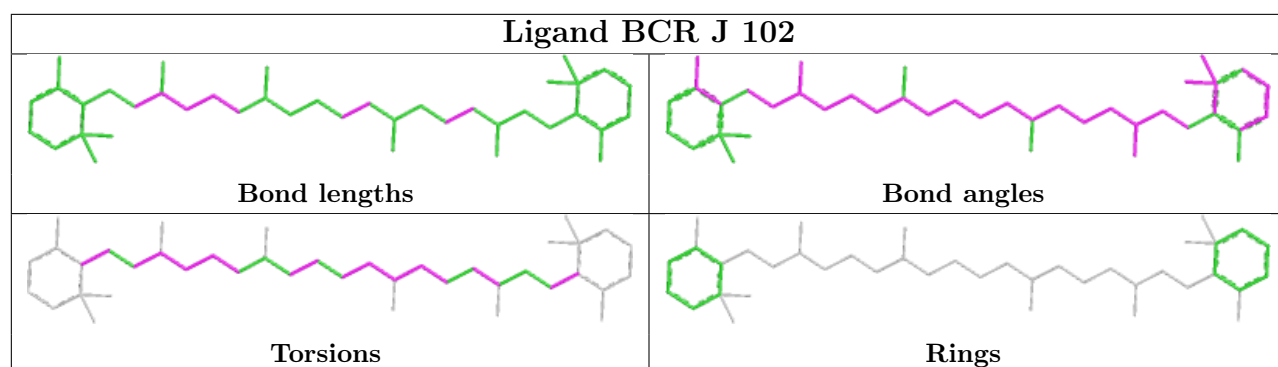
## Ligand CLA A 830

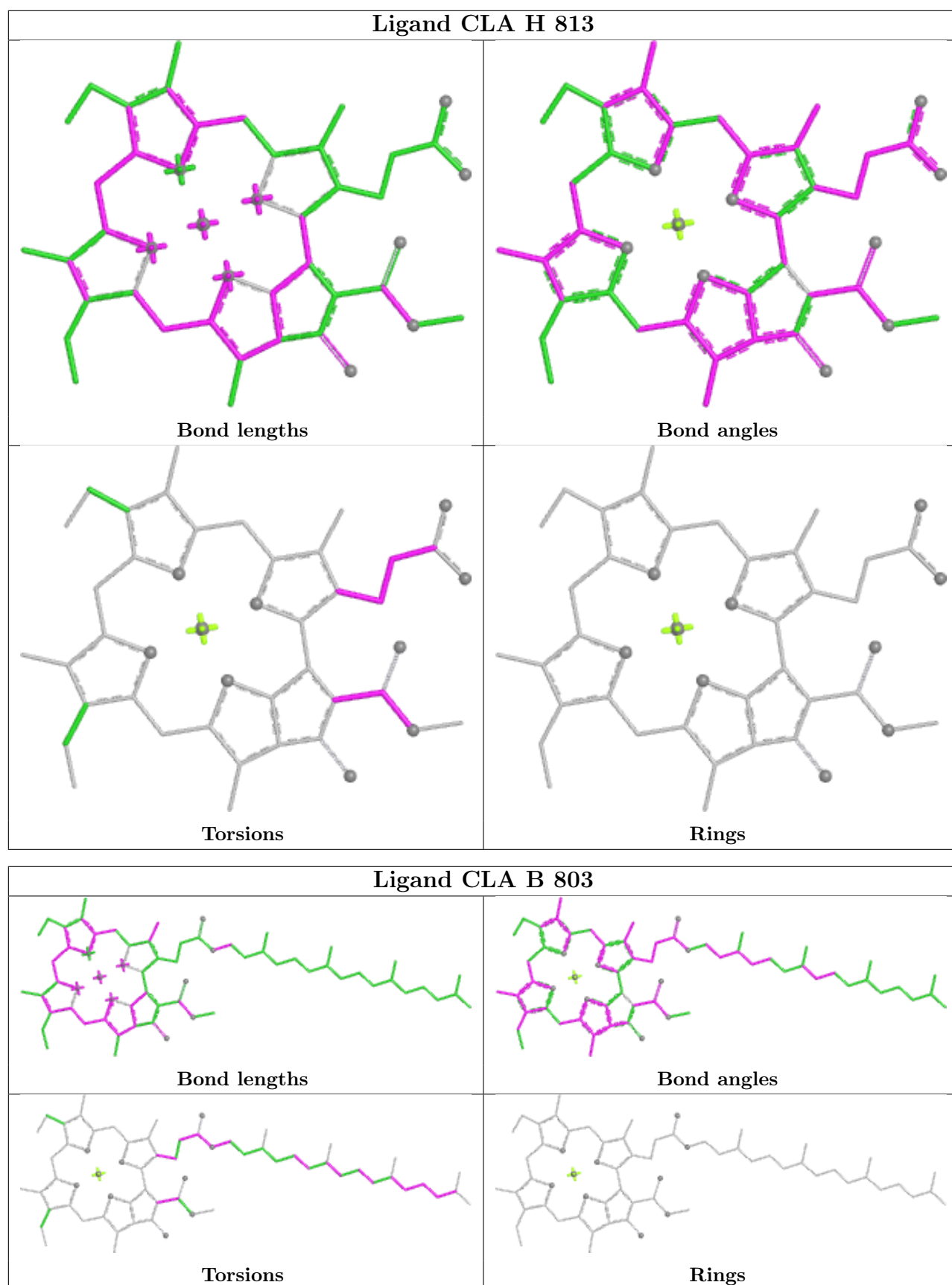


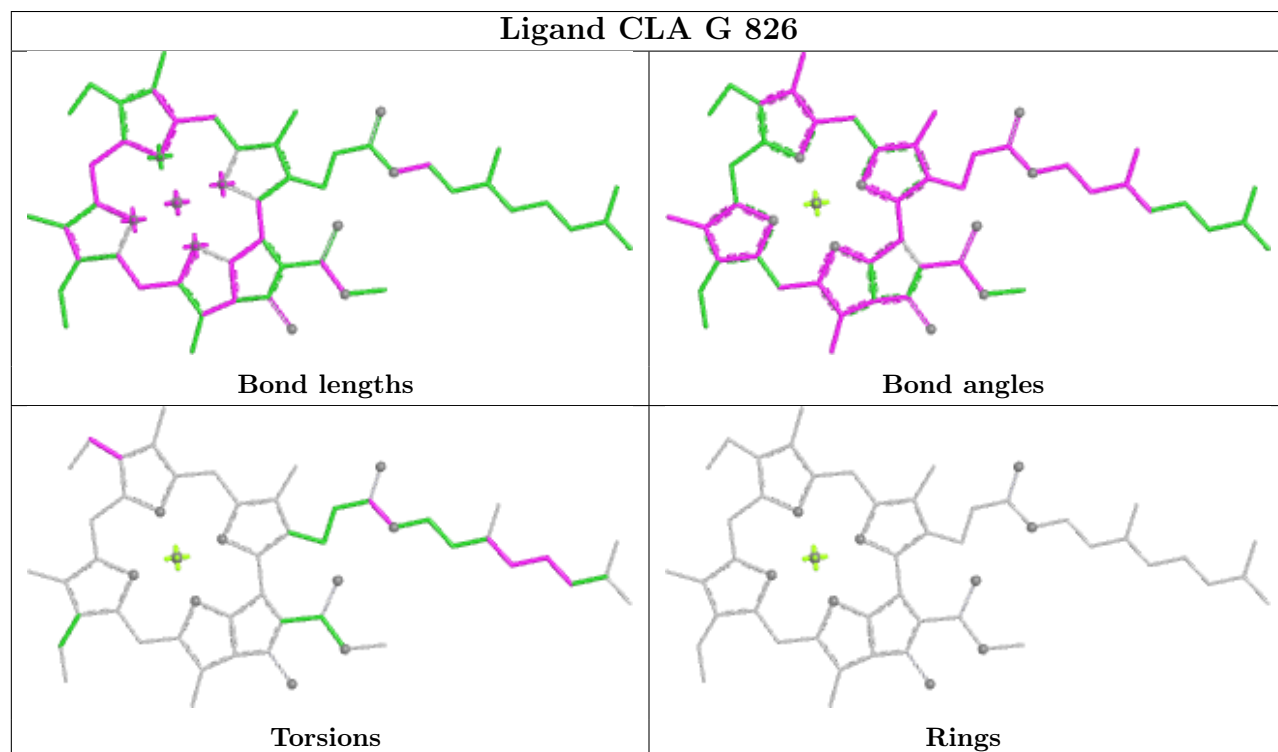
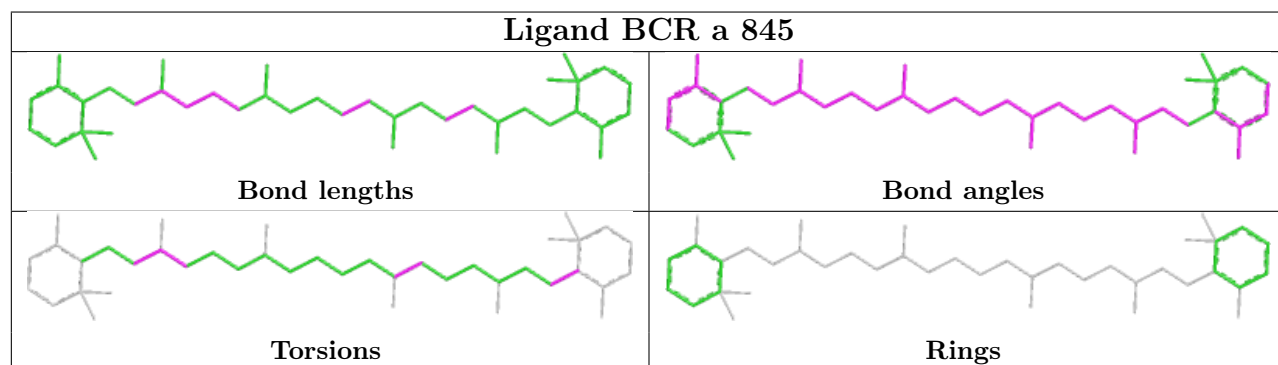
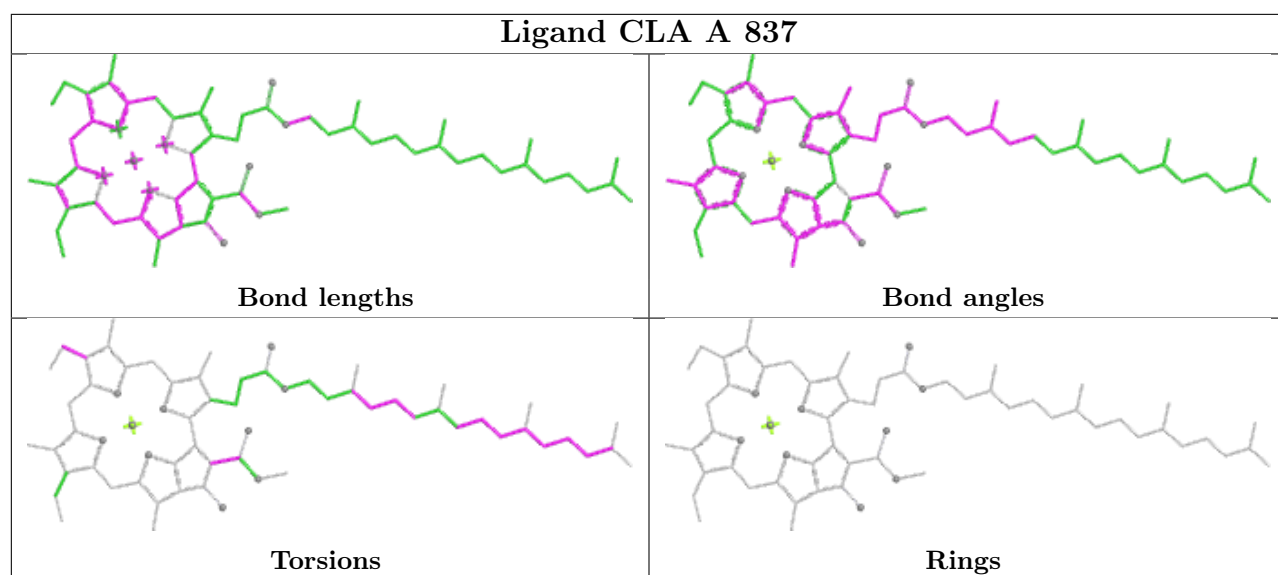
## Ligand CLA H 825

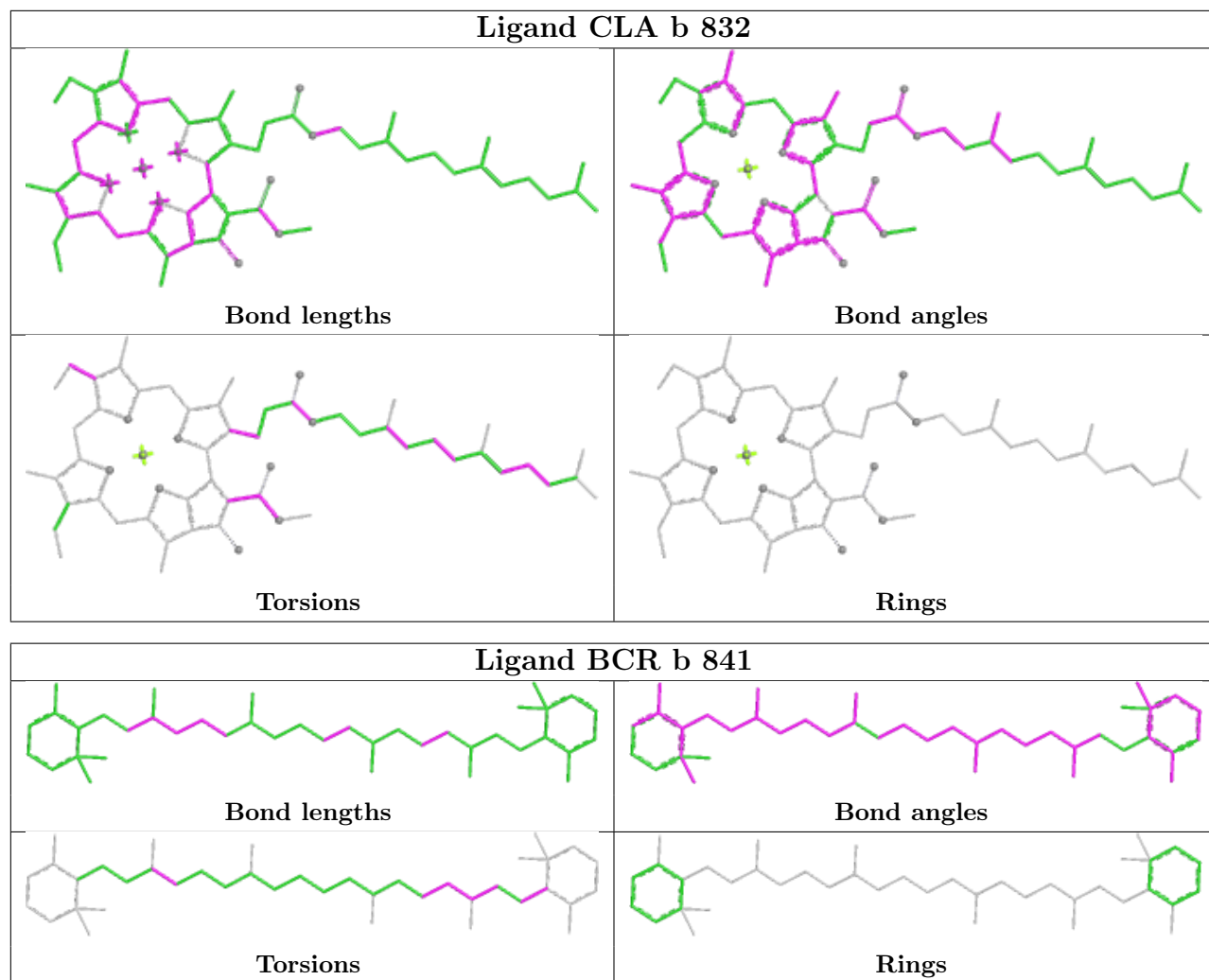


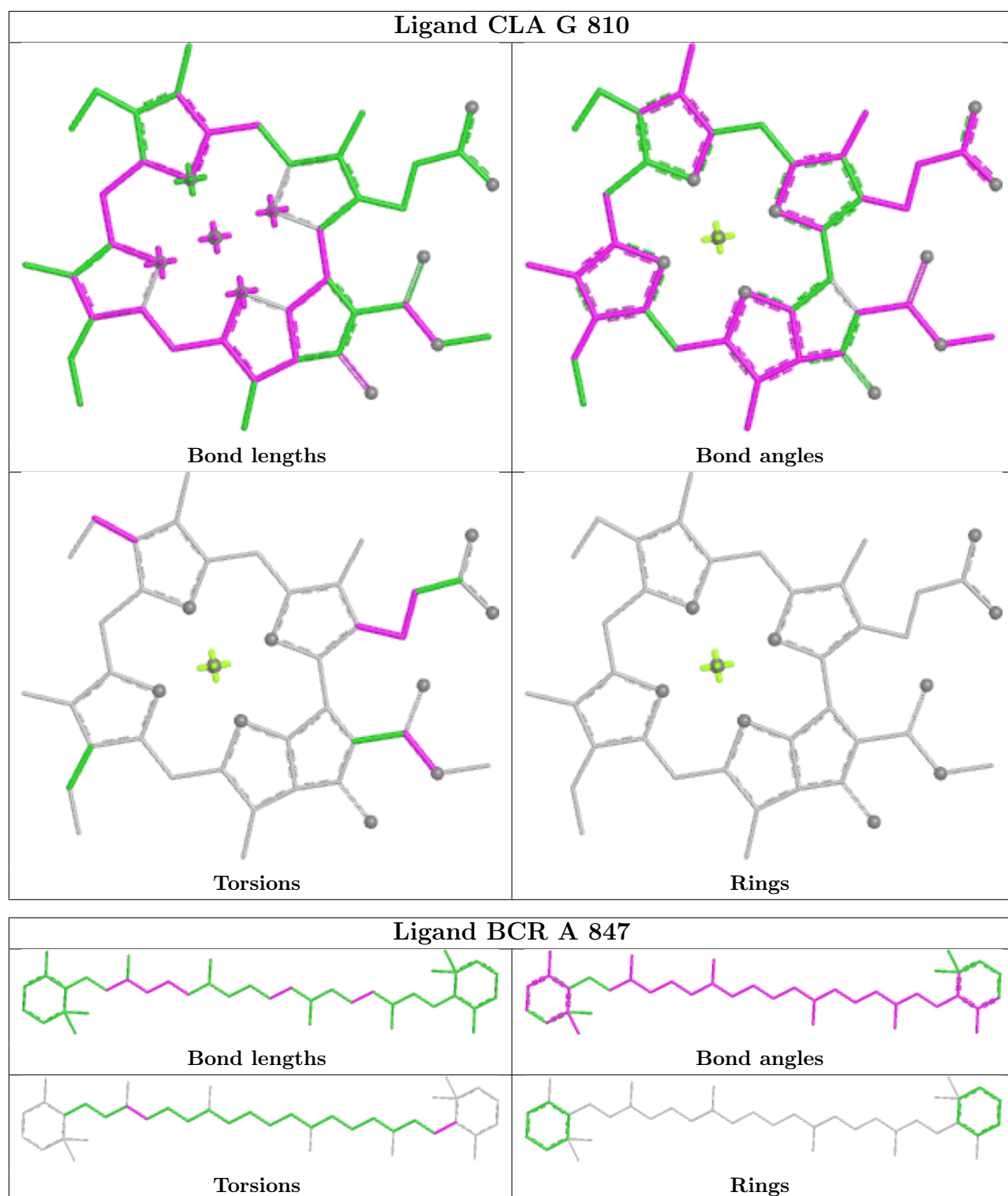


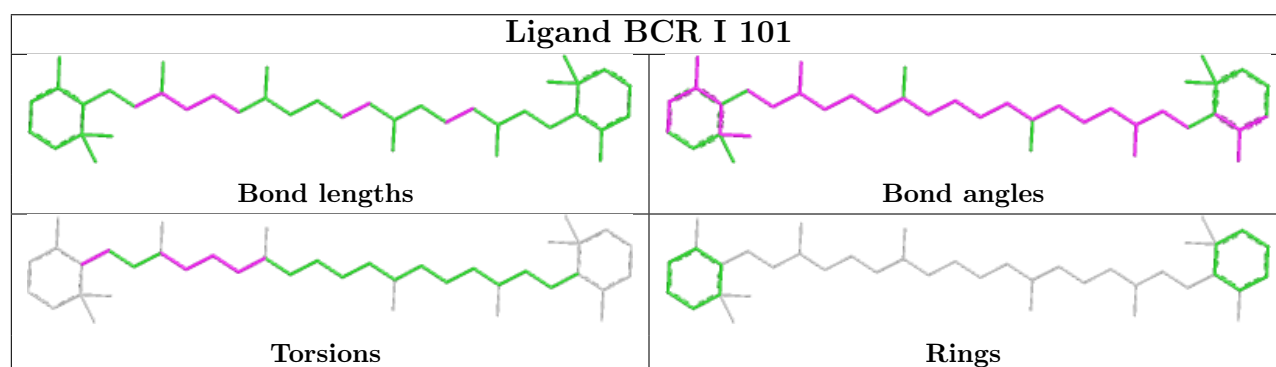
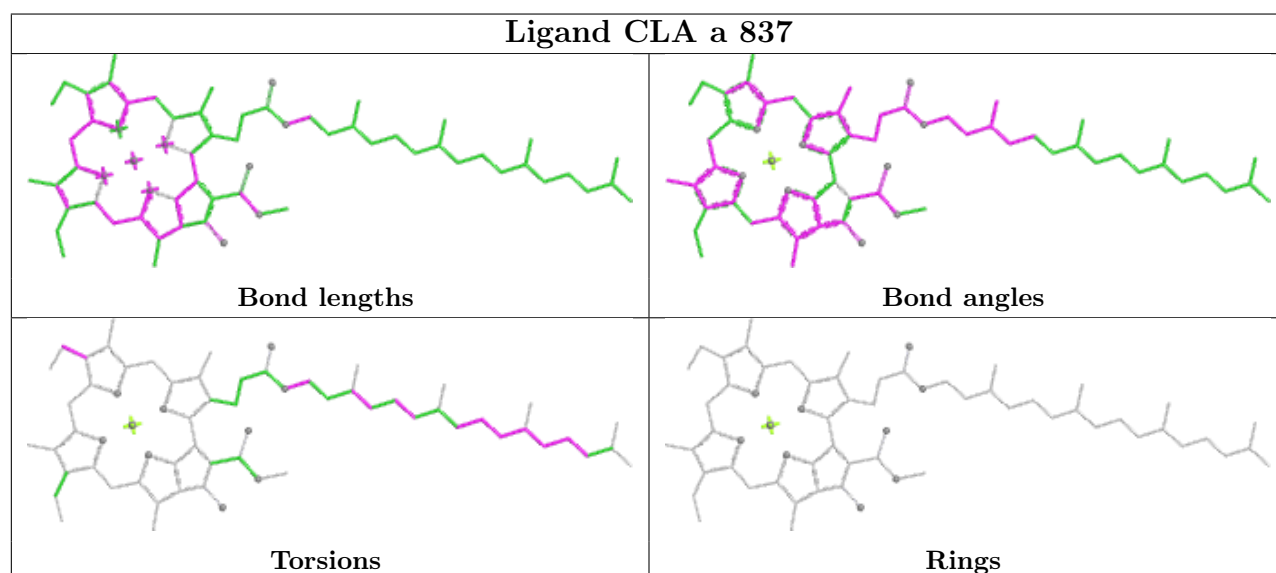
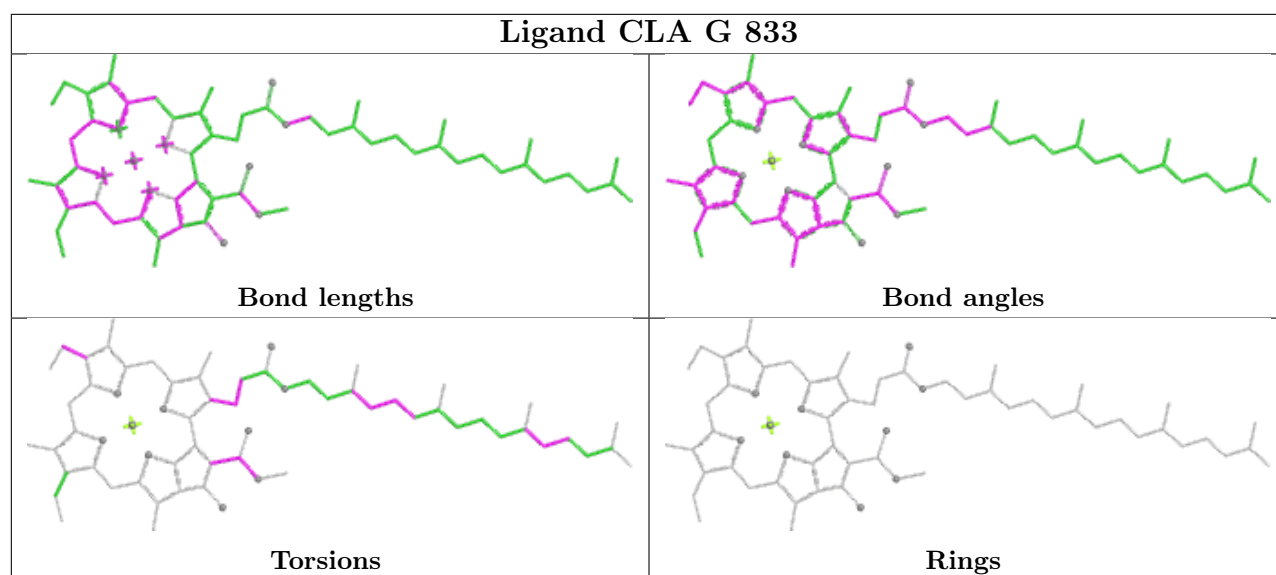




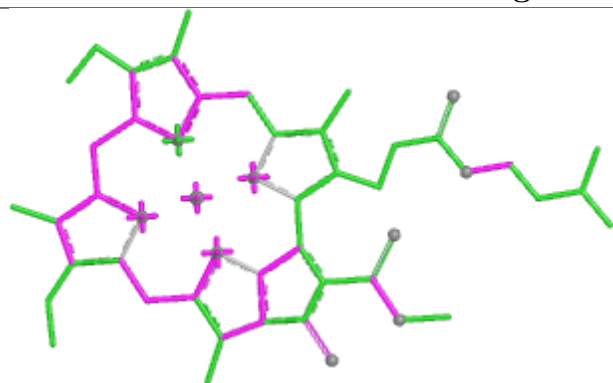




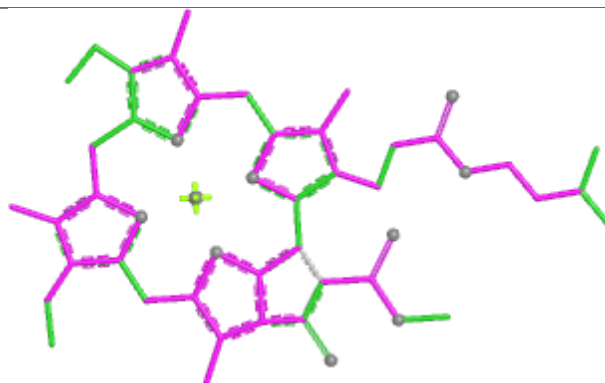




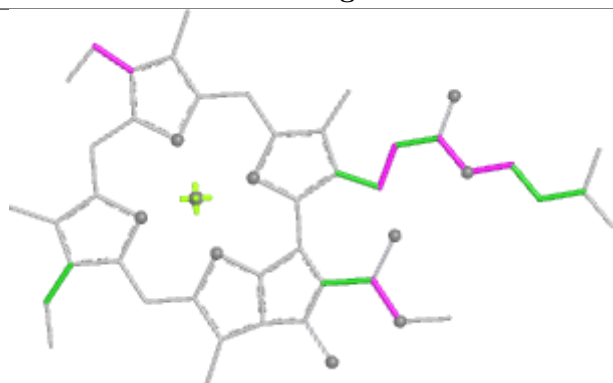
## Ligand CLA G 831



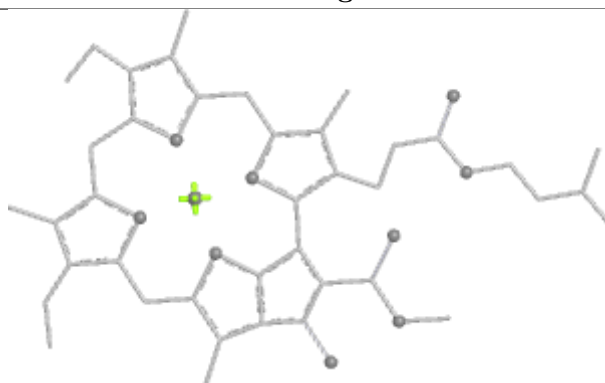
Bond lengths



Bond angles

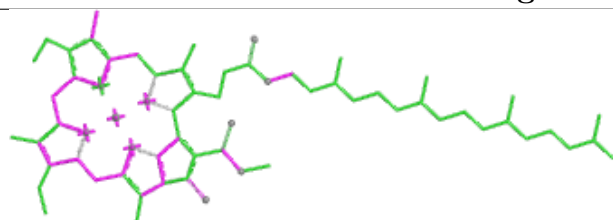


Torsions

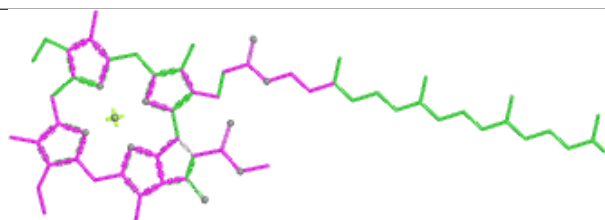


Rings

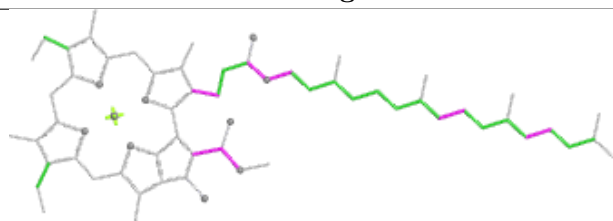
## Ligand CLA b 826



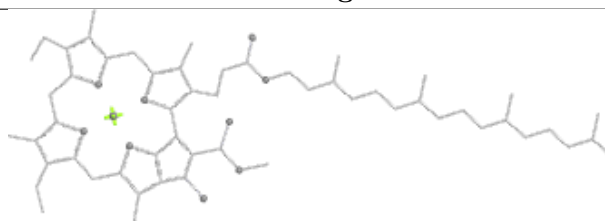
Bond lengths



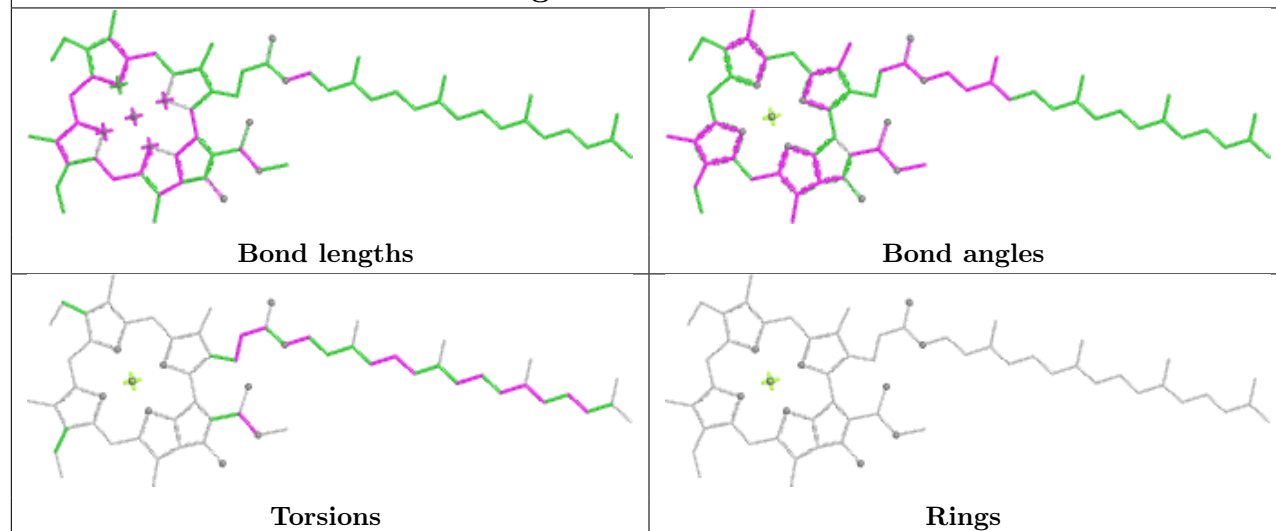
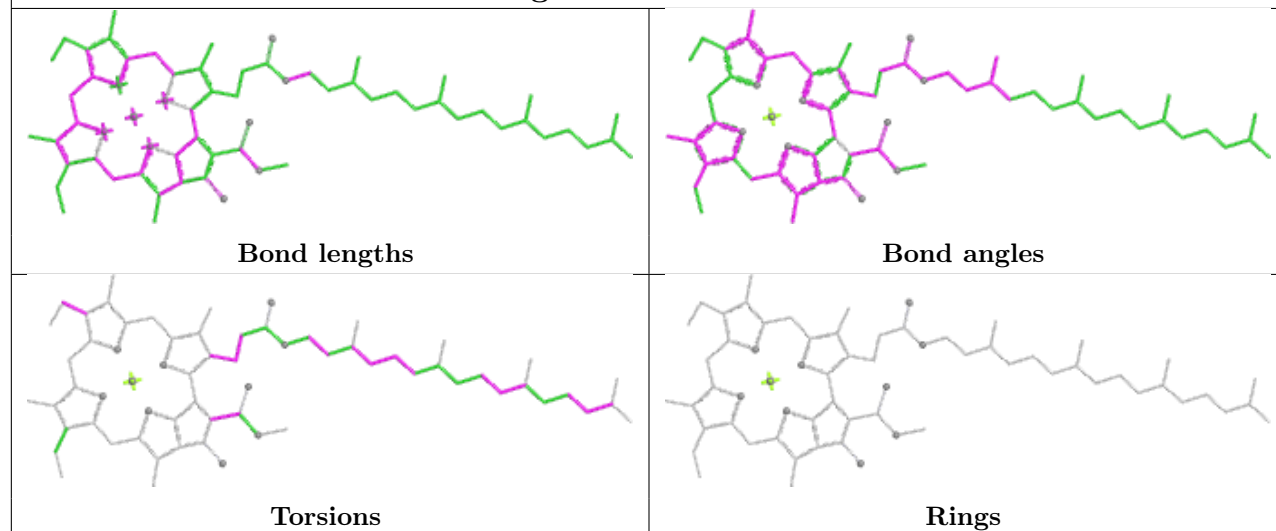
Bond angles



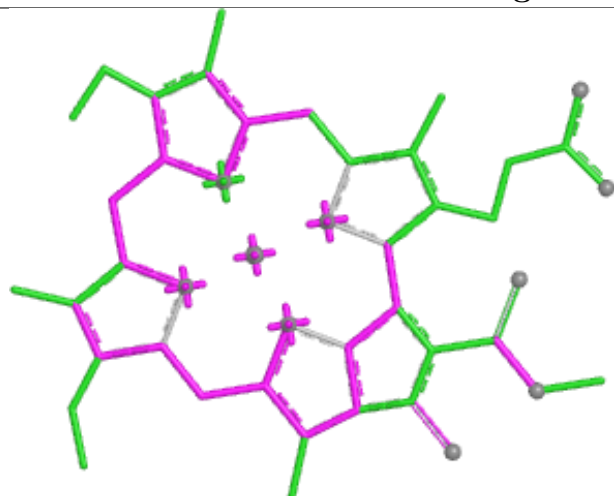
Torsions



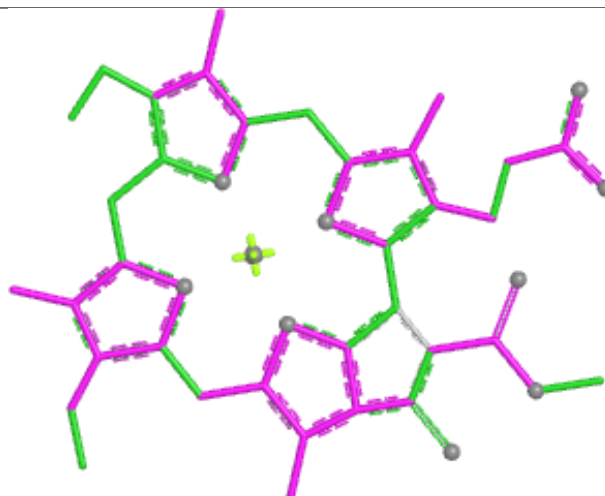
Rings

**Ligand CLA A 828****Ligand CLA G 855**

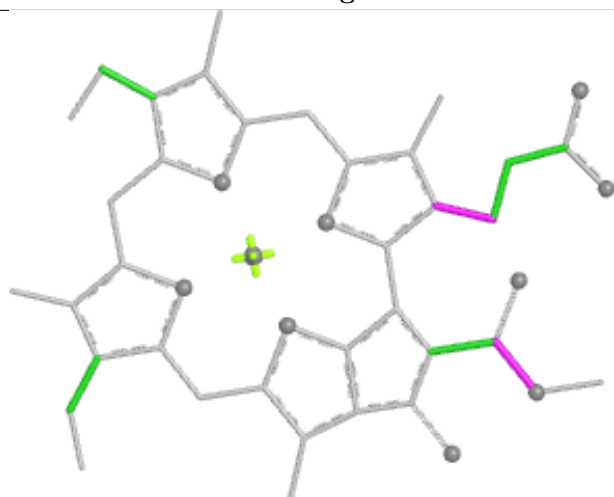
## Ligand CLA H 819



Bond lengths



Bond angles

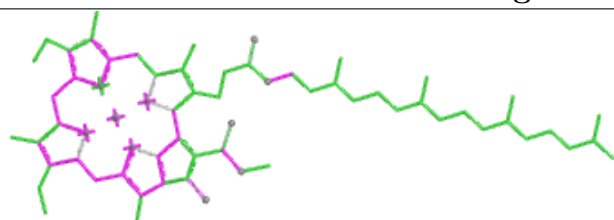


Torsions

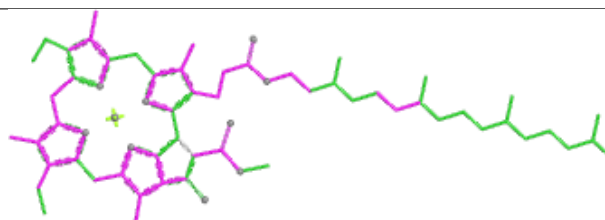


Rings

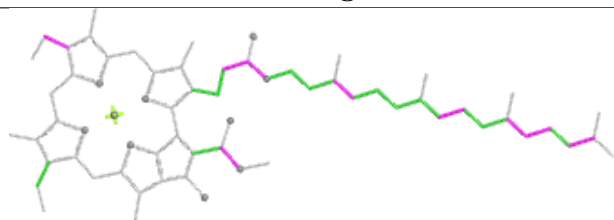
## Ligand CLA H 805



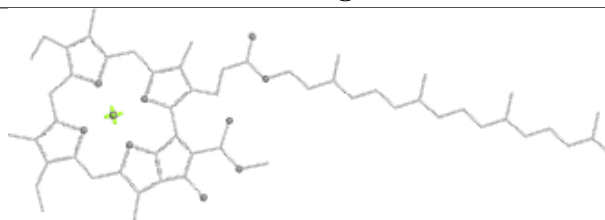
Bond lengths



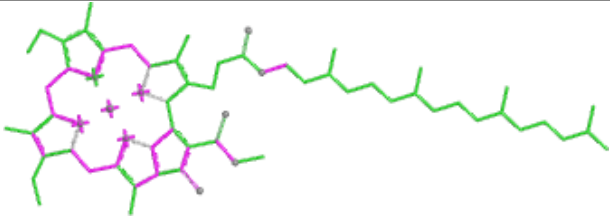
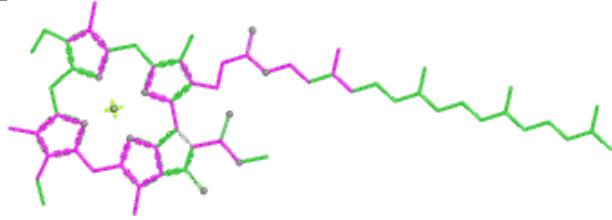
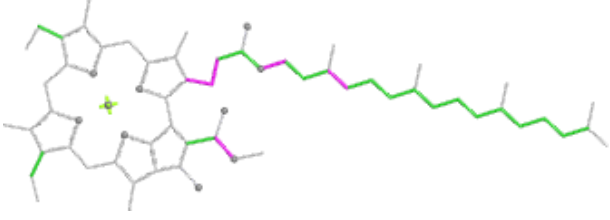
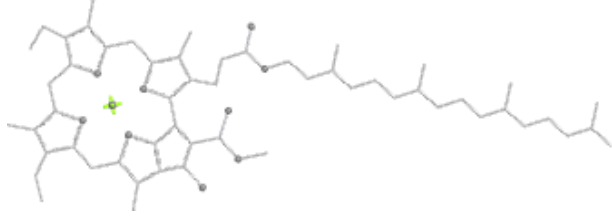
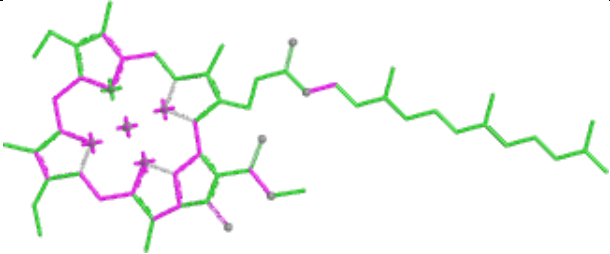
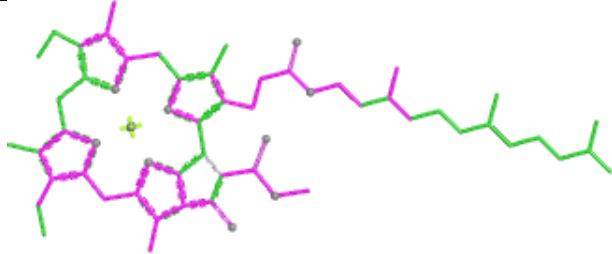
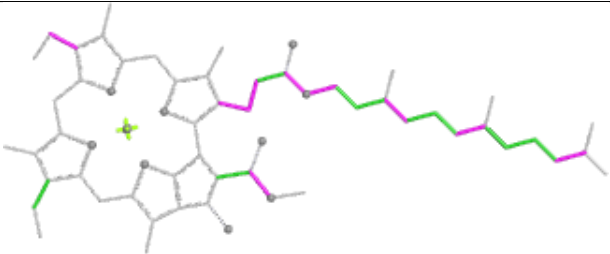
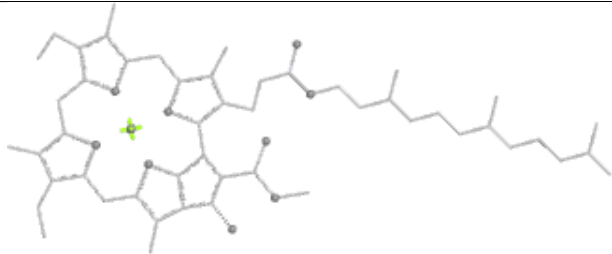
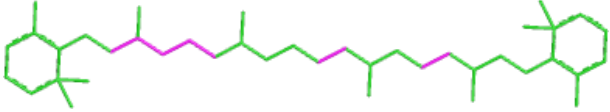
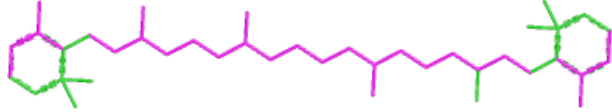
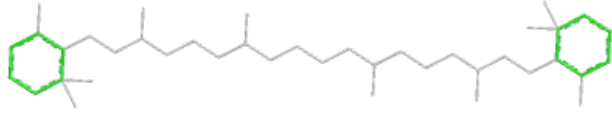
Bond angles

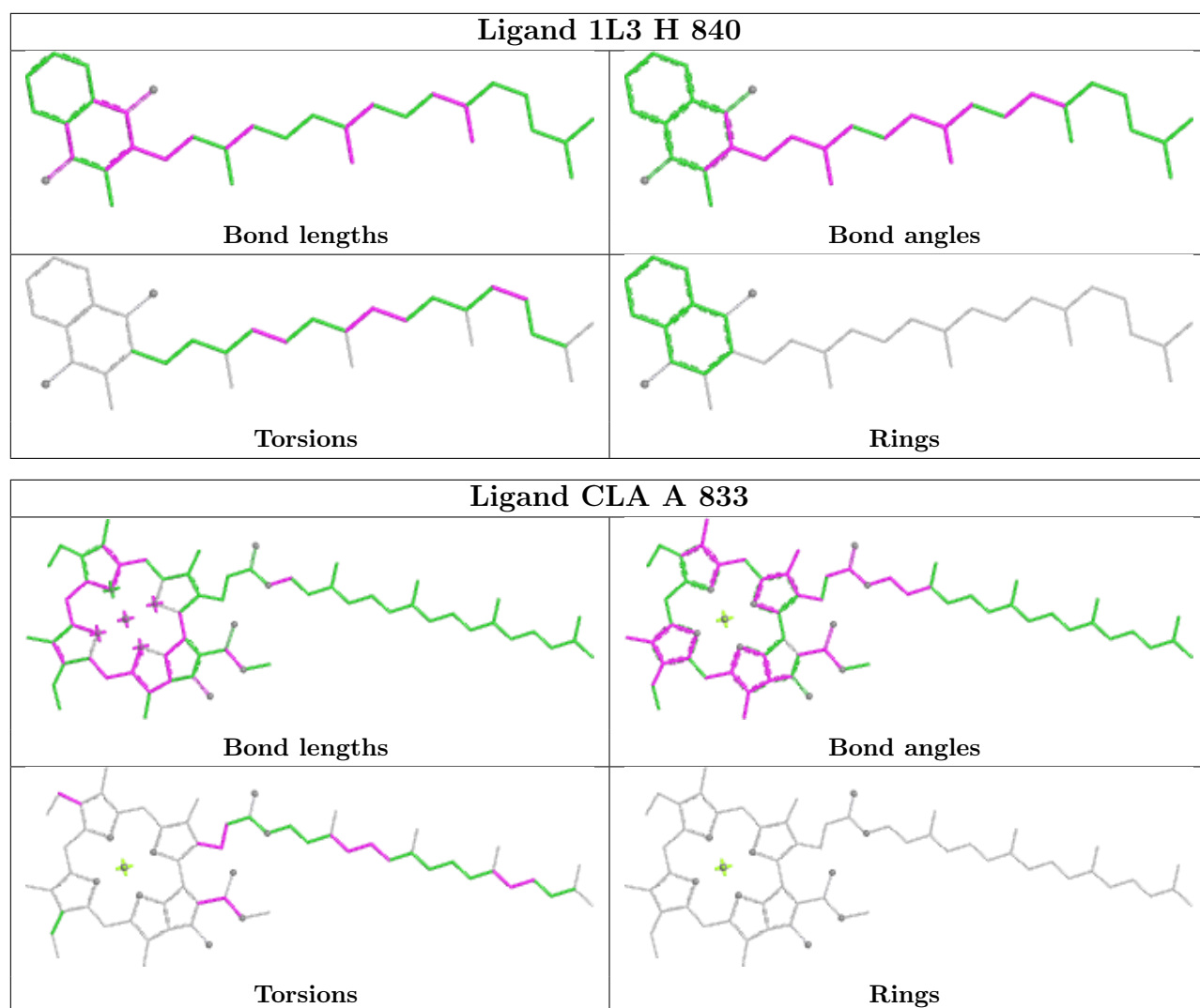


Torsions

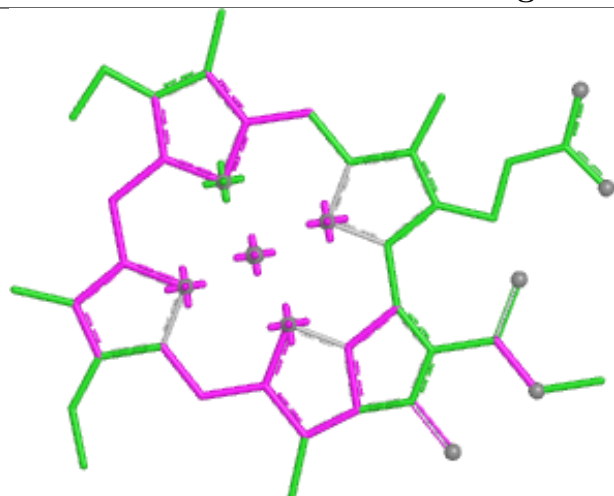


Rings

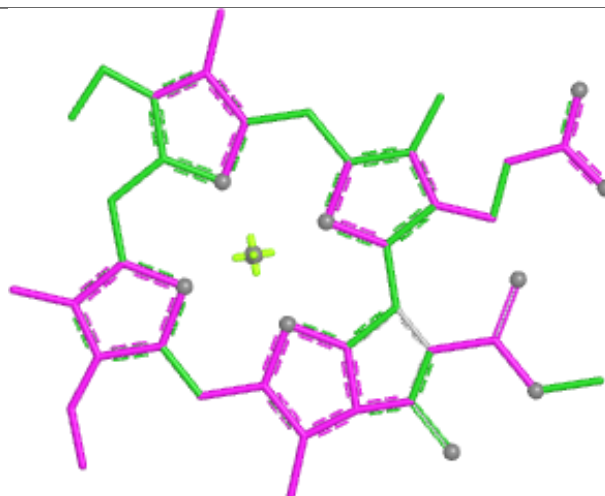
| Ligand CLA A 802                                                                                        |                                                                                                         |
|---------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|
|  <p>Bond lengths</p>   |  <p>Bond angles</p>   |
|  <p>Torsions</p>       |  <p>Rings</p>         |
| Ligand CLA A 827                                                                                        |                                                                                                         |
|  <p>Bond lengths</p>  |  <p>Bond angles</p>  |
|  <p>Torsions</p>     |  <p>Rings</p>       |
| Ligand BCR G 846                                                                                        |                                                                                                         |
|  <p>Bond lengths</p> |  <p>Bond angles</p> |
|  <p>Torsions</p>     |  <p>Rings</p>       |



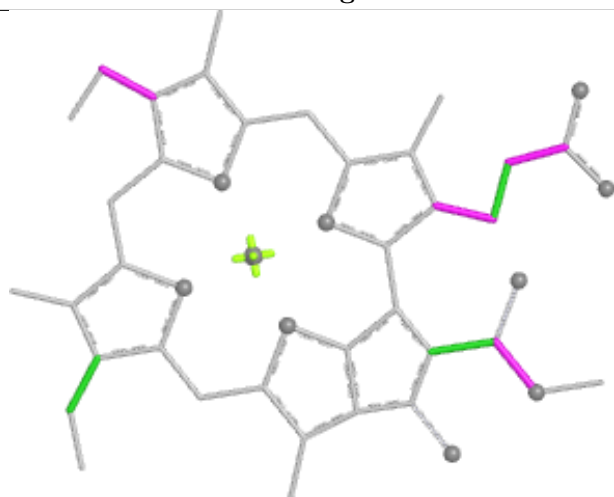
## Ligand CLA b 834



Bond lengths



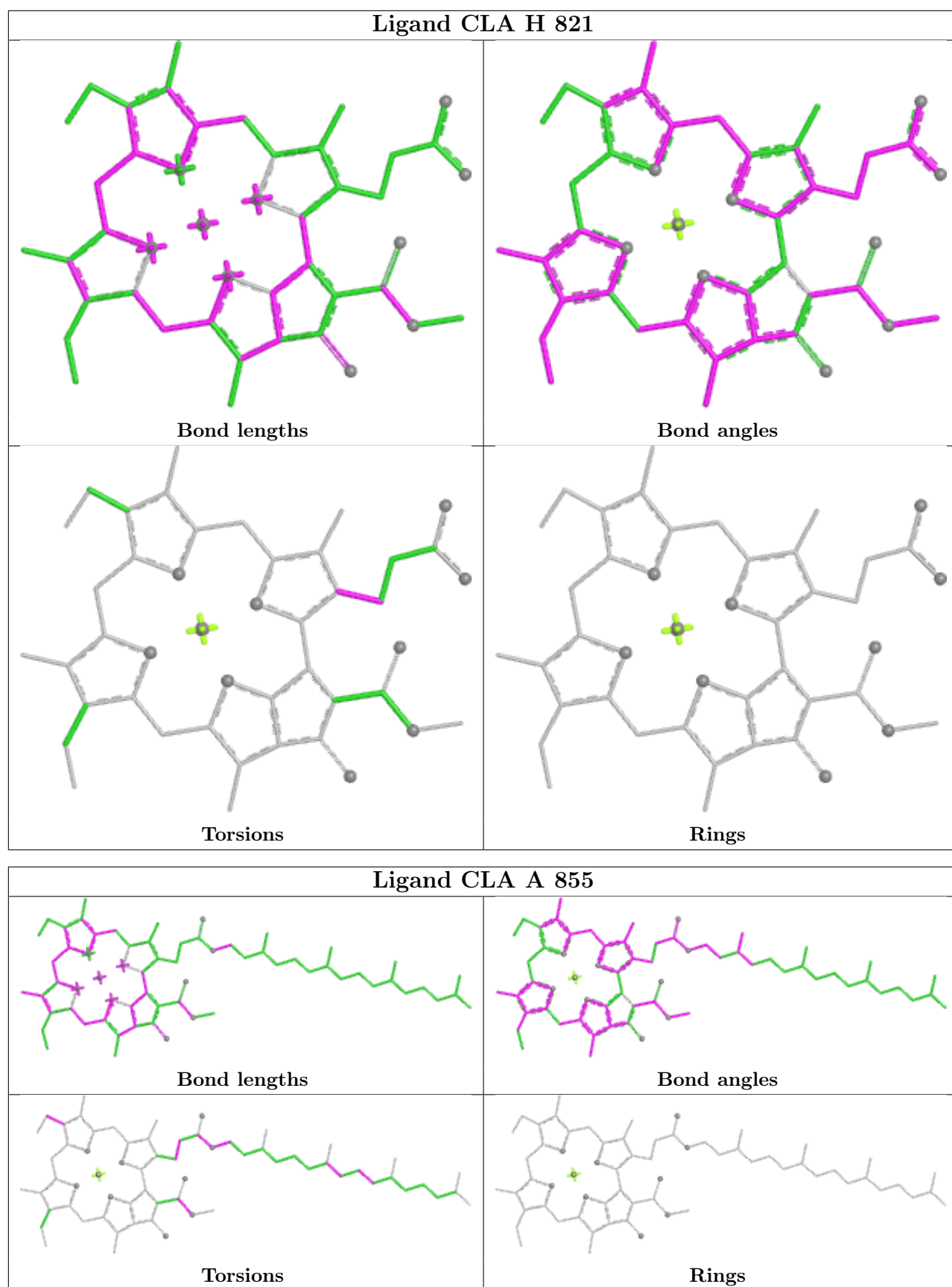
Bond angles

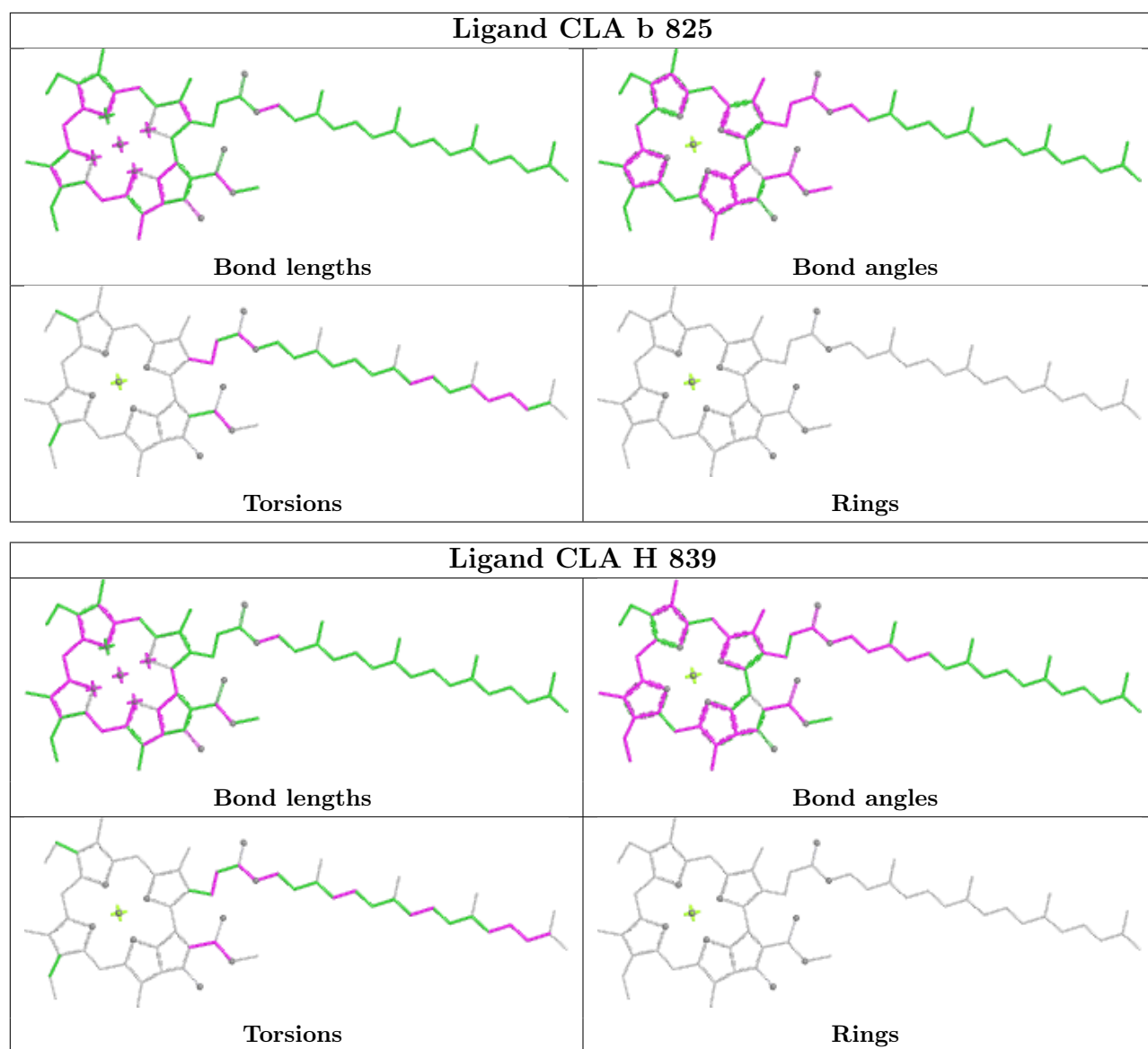


Torsions

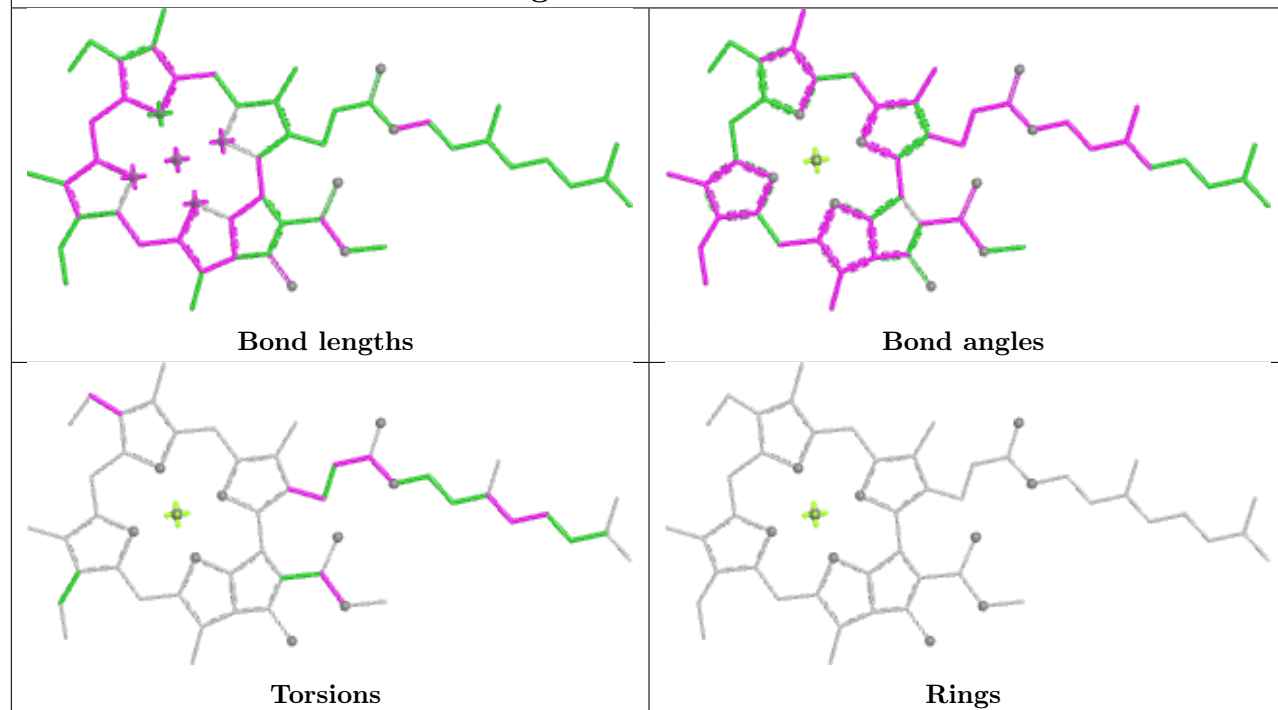


Rings

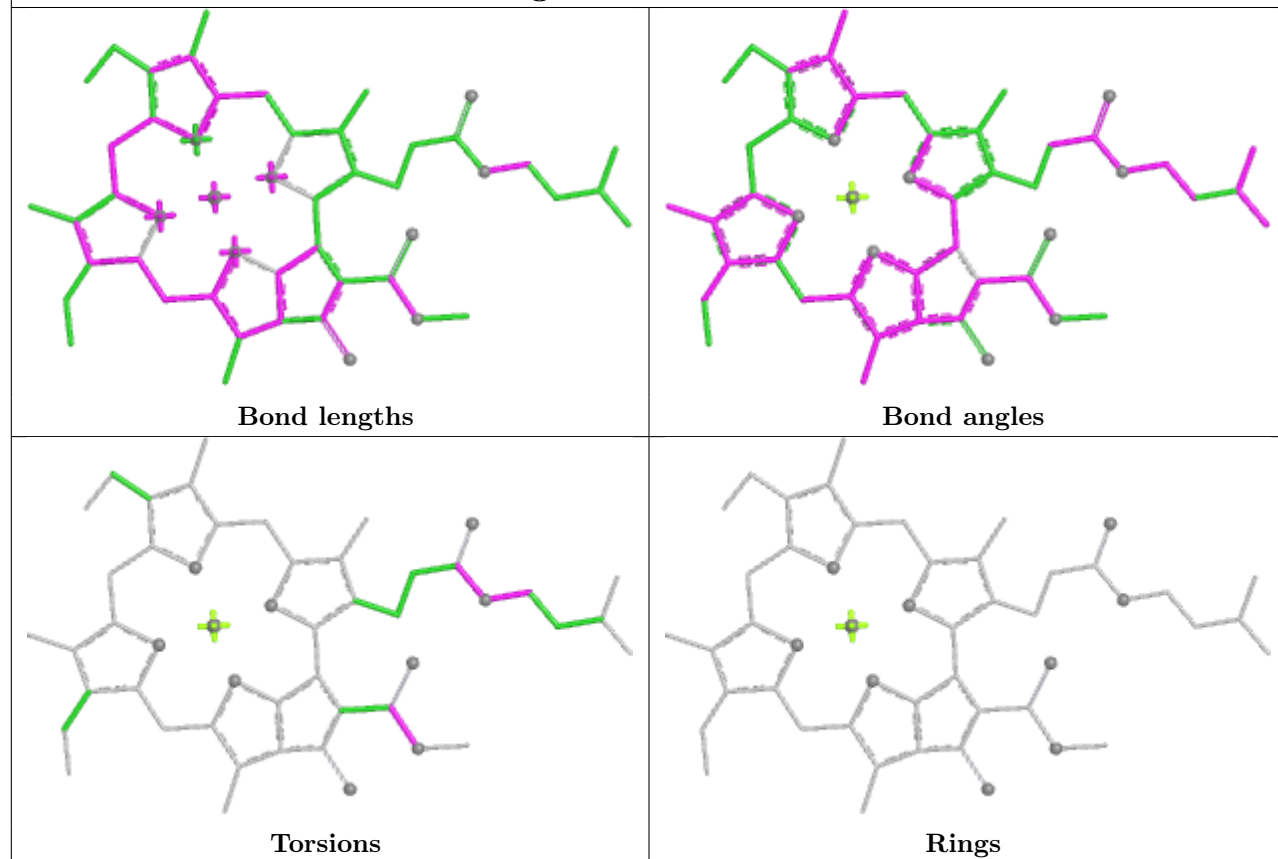


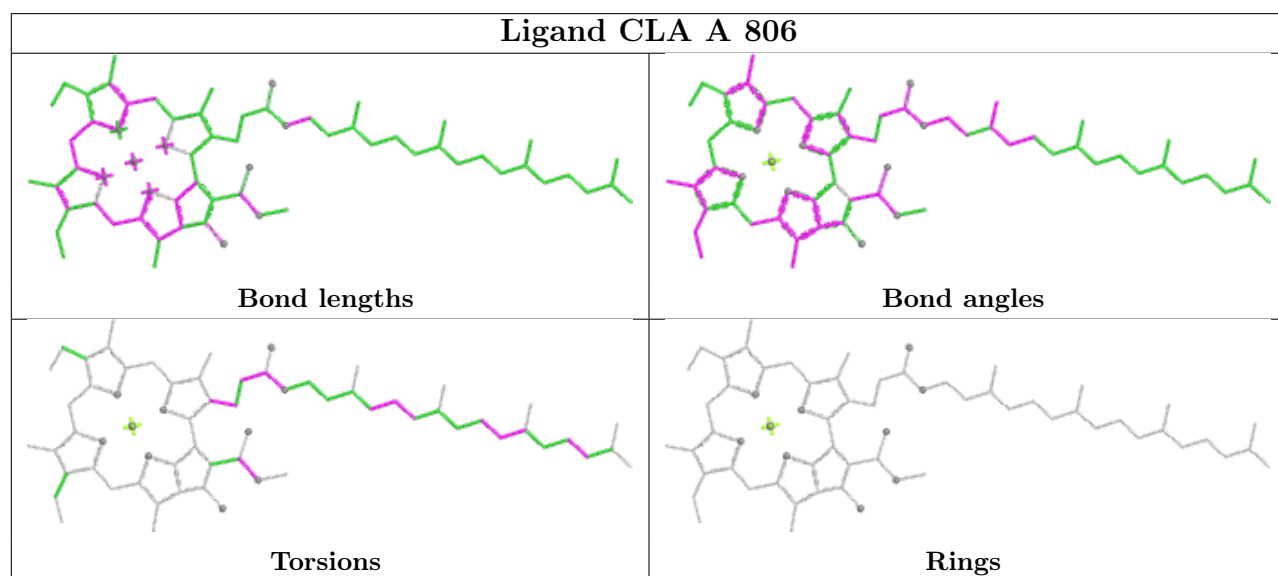
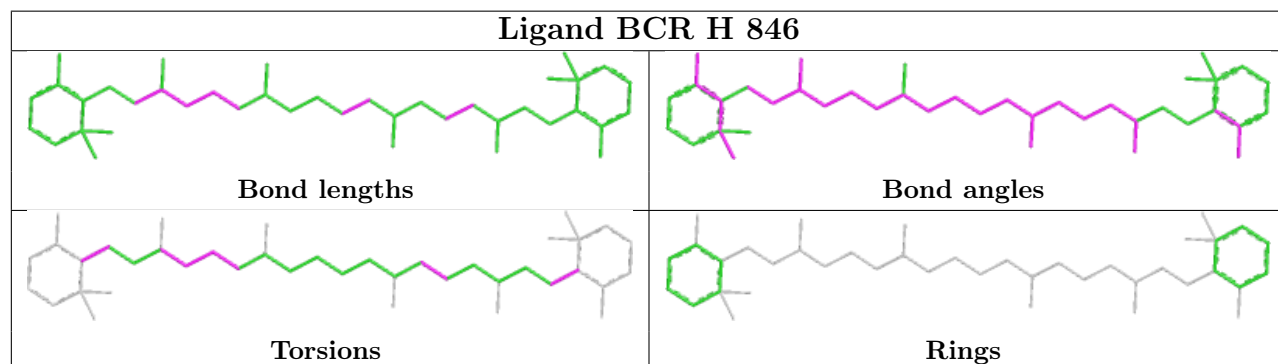
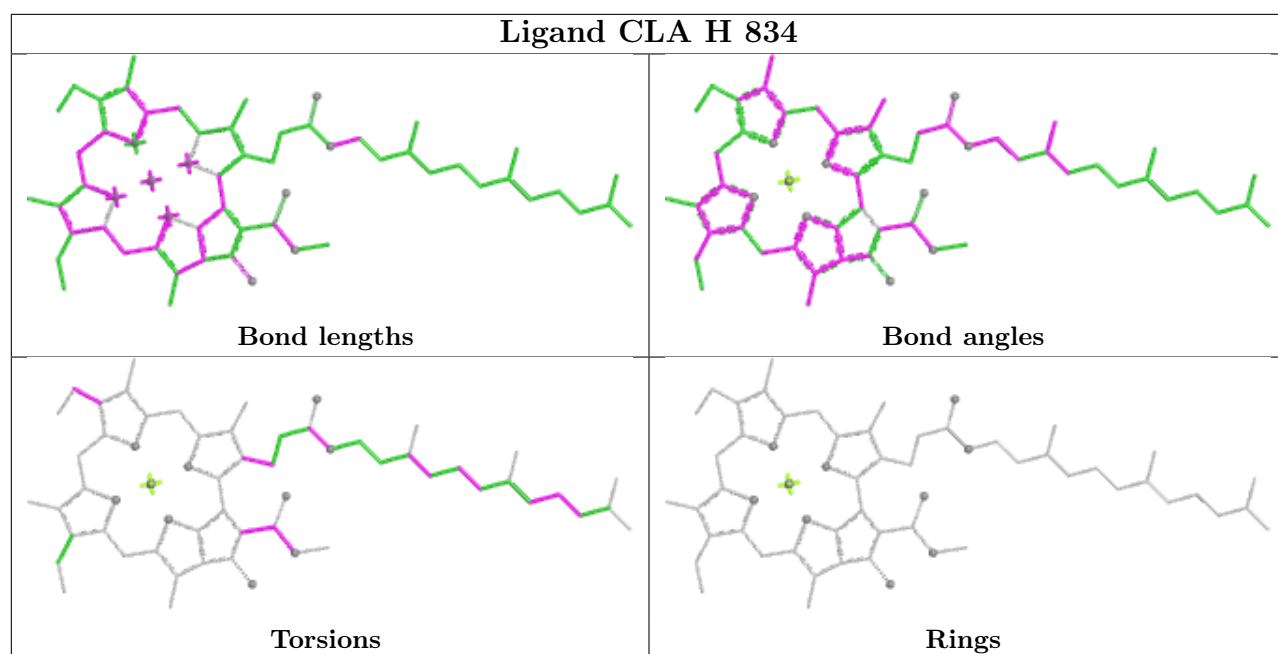


## Ligand CLA G 805

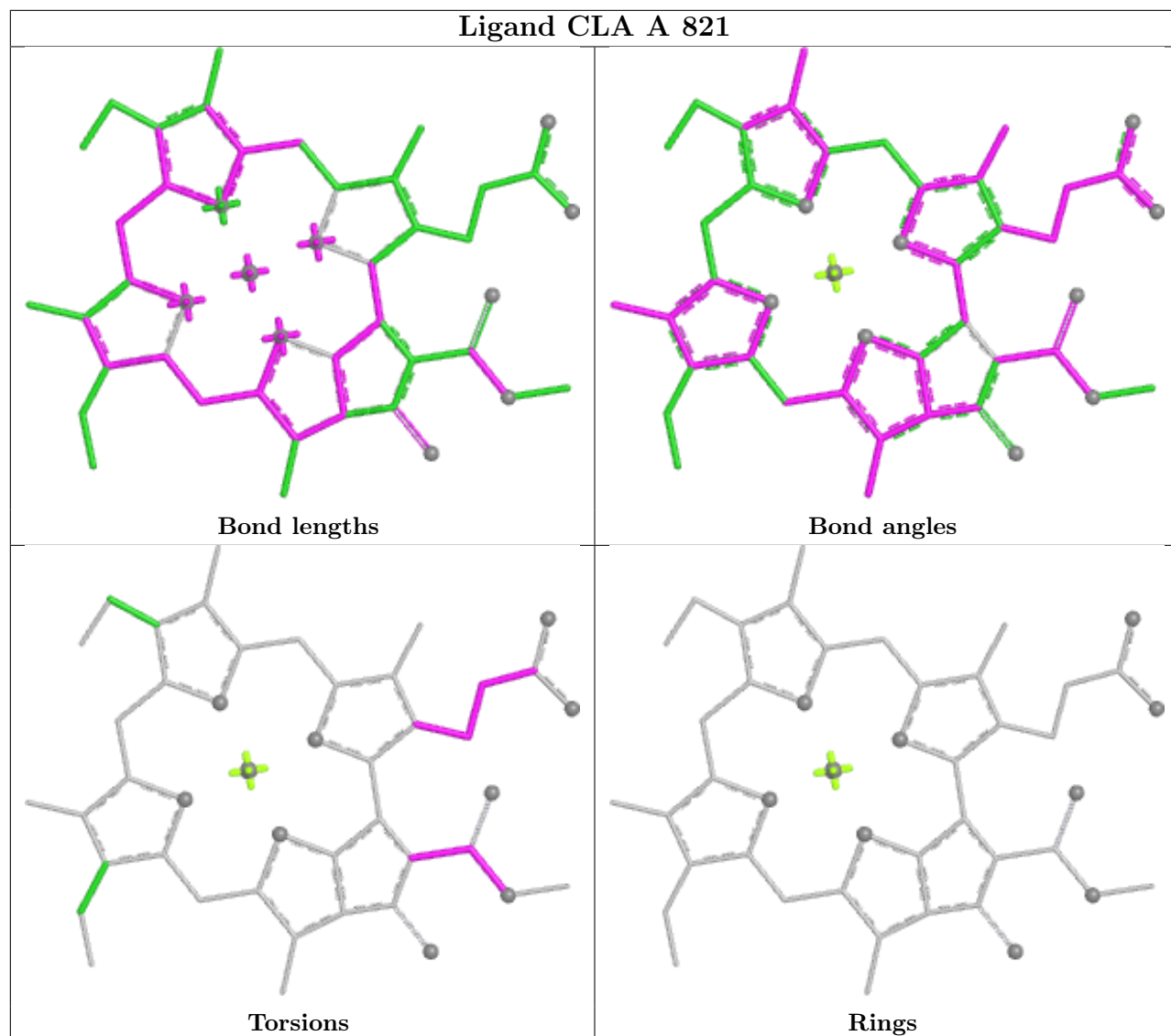


## Ligand CLA G 836

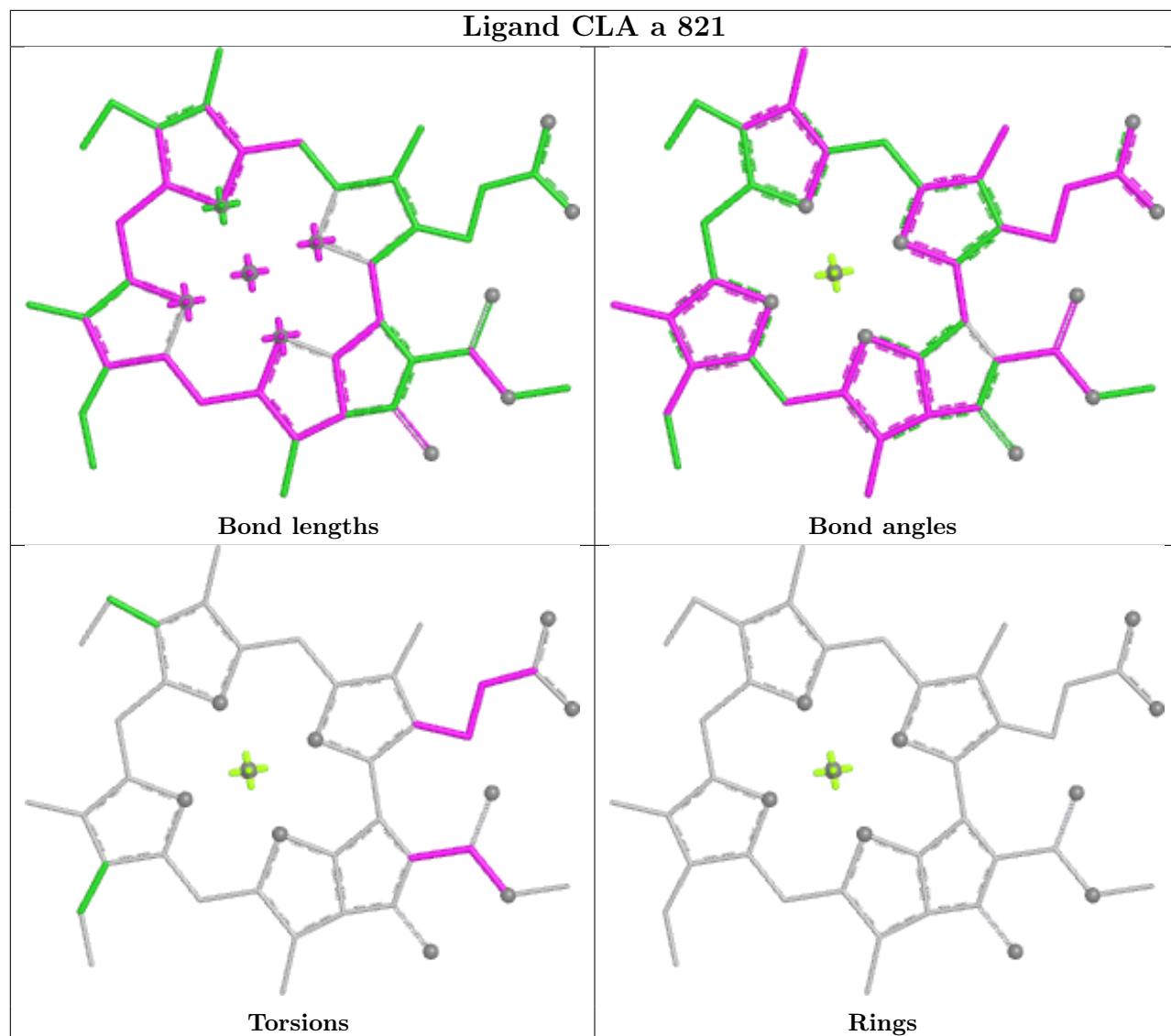




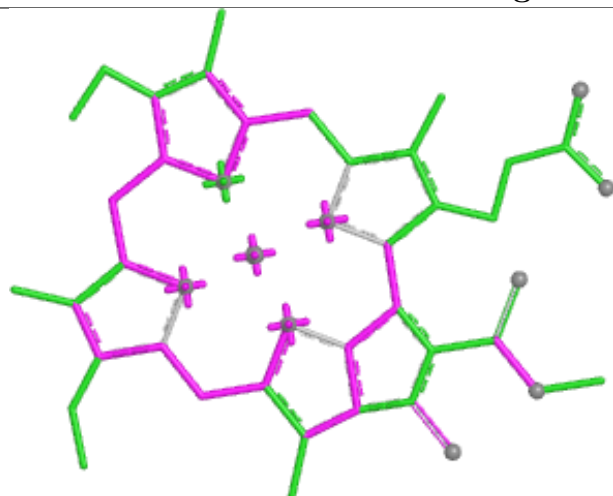
## Ligand CLA A 821



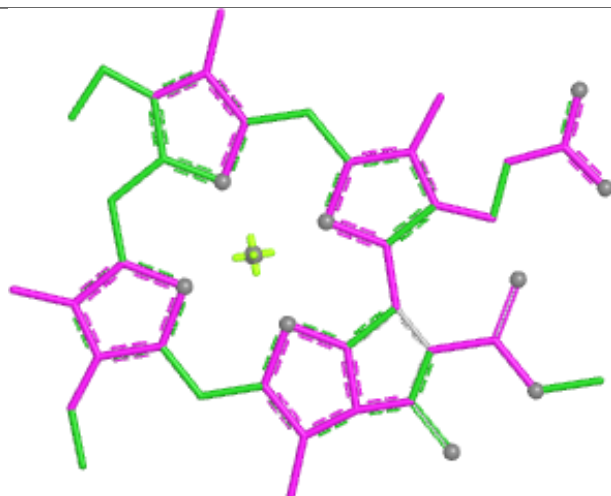
## Ligand CLA a 821



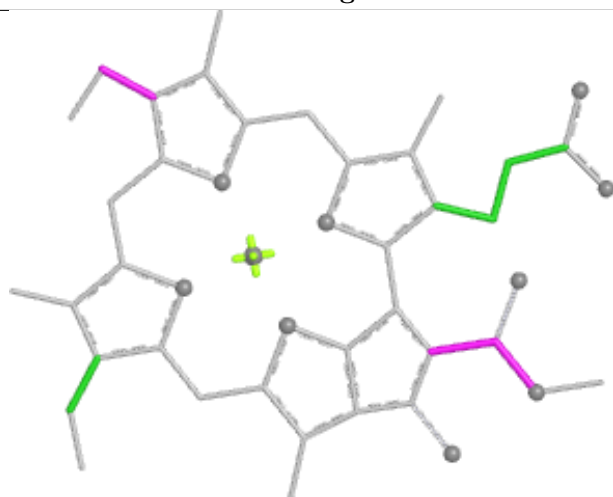
## Ligand CLA H 832



Bond lengths



Bond angles

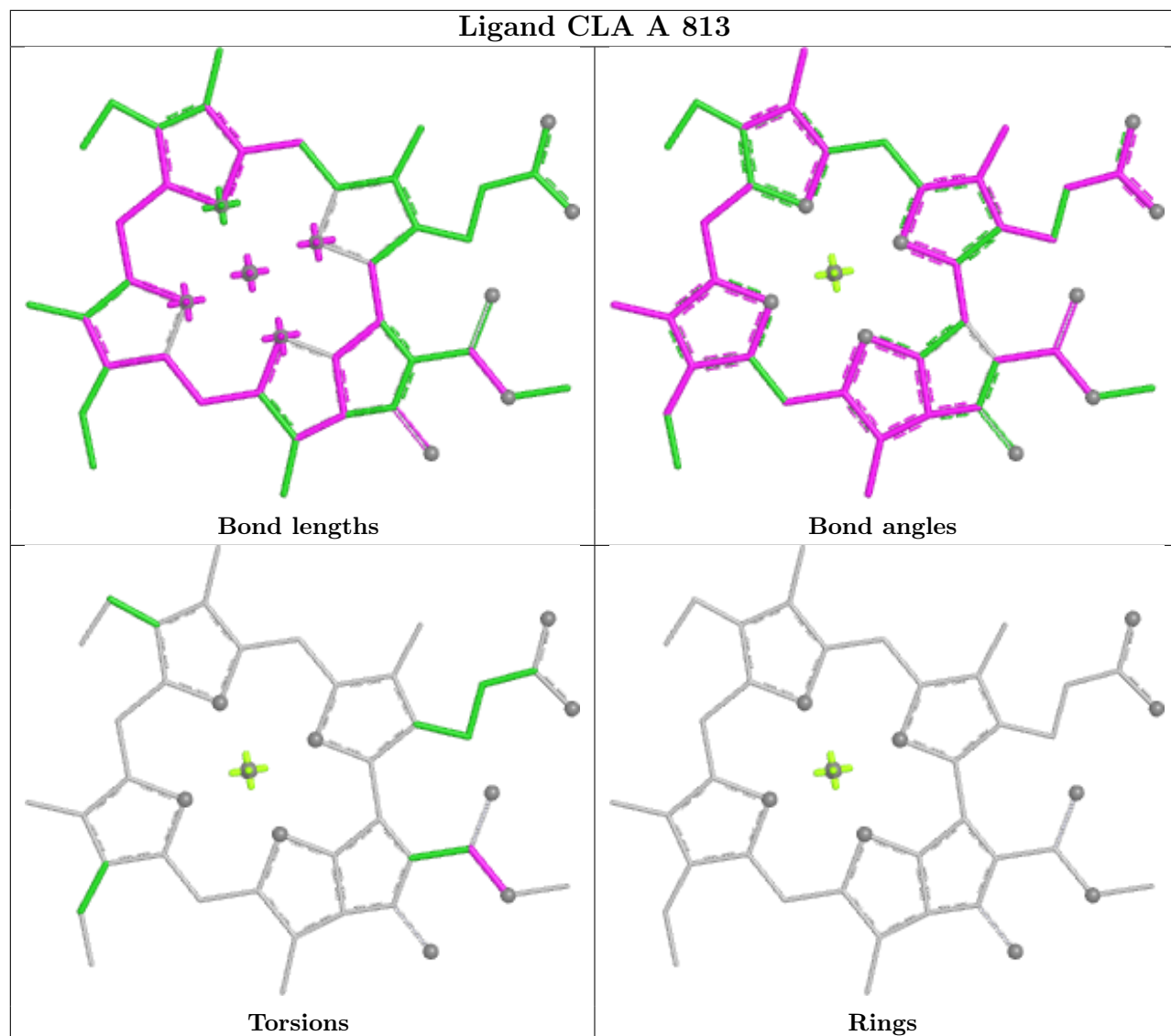


Torsions

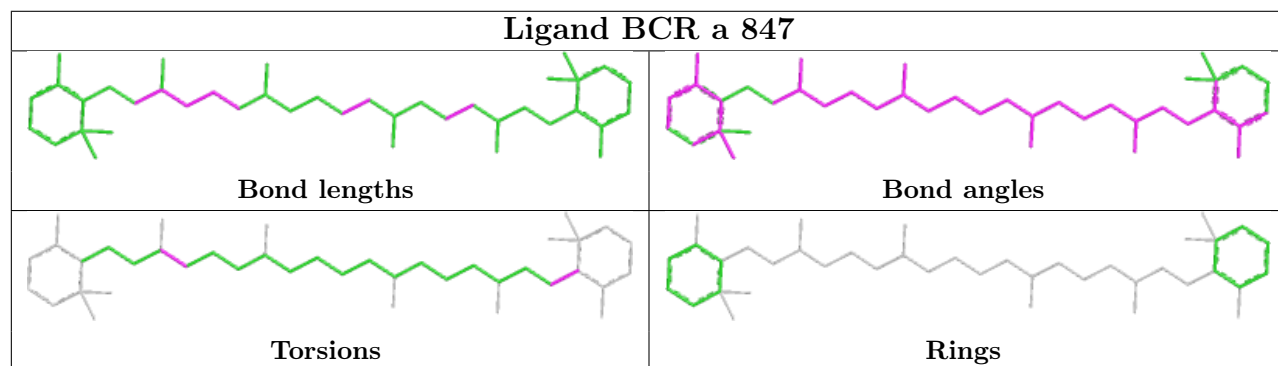


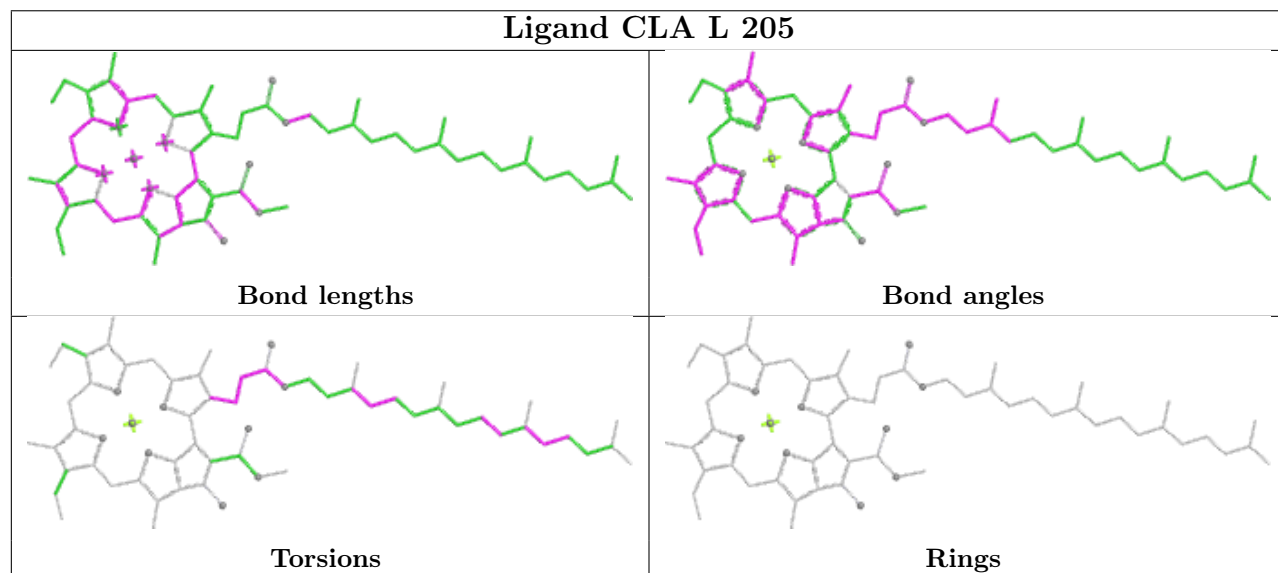
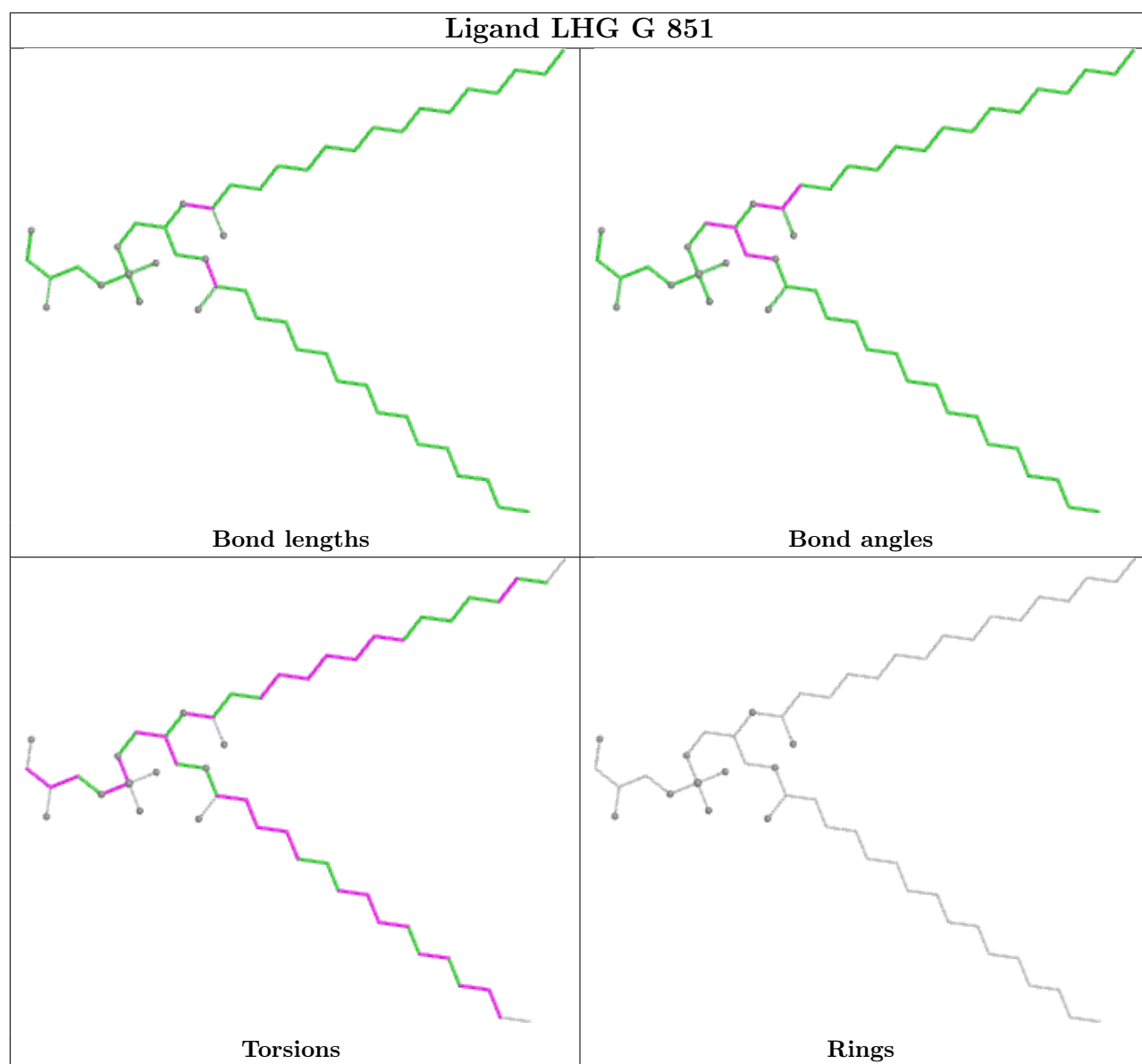
Rings

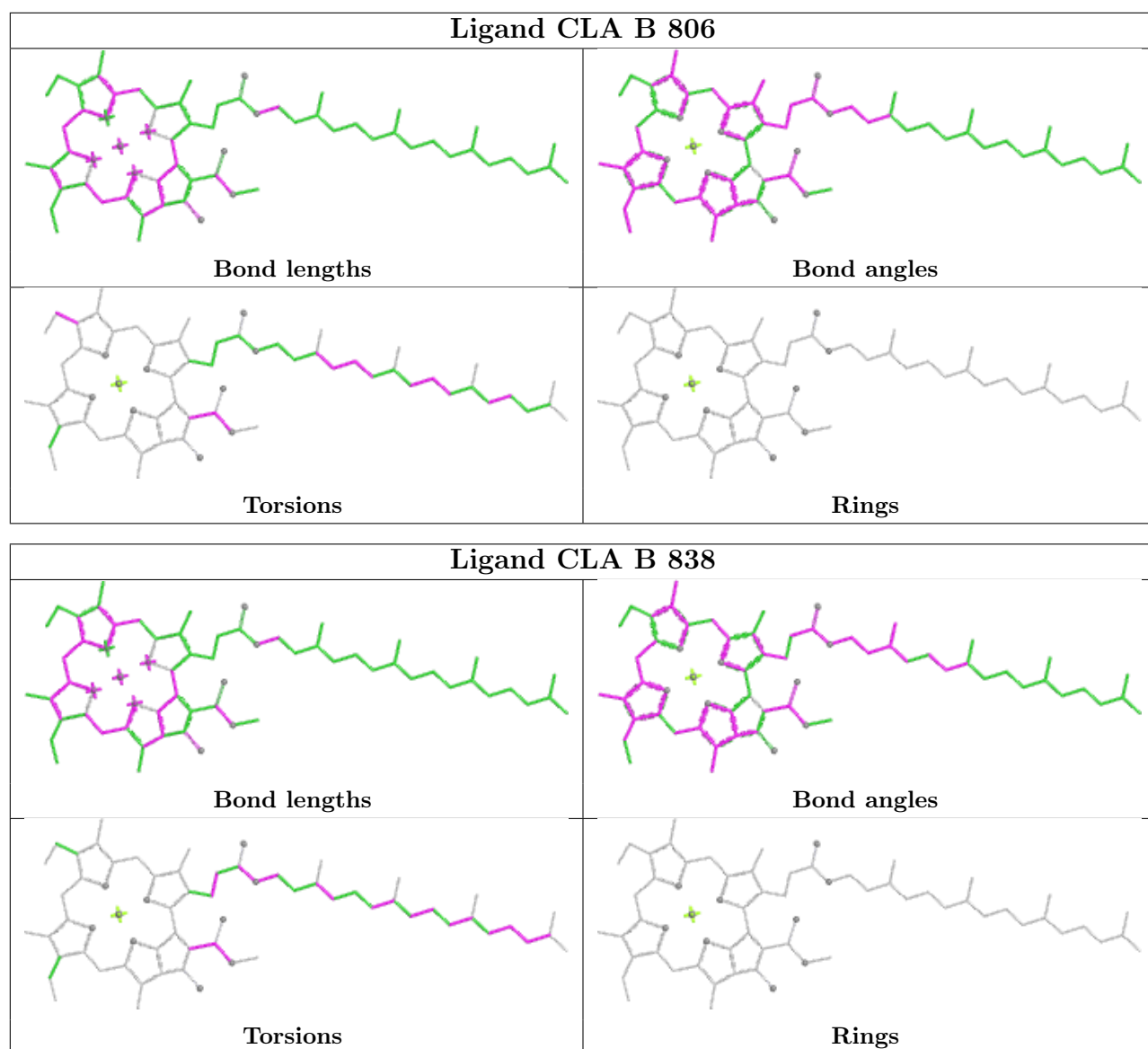
## Ligand CLA A 813

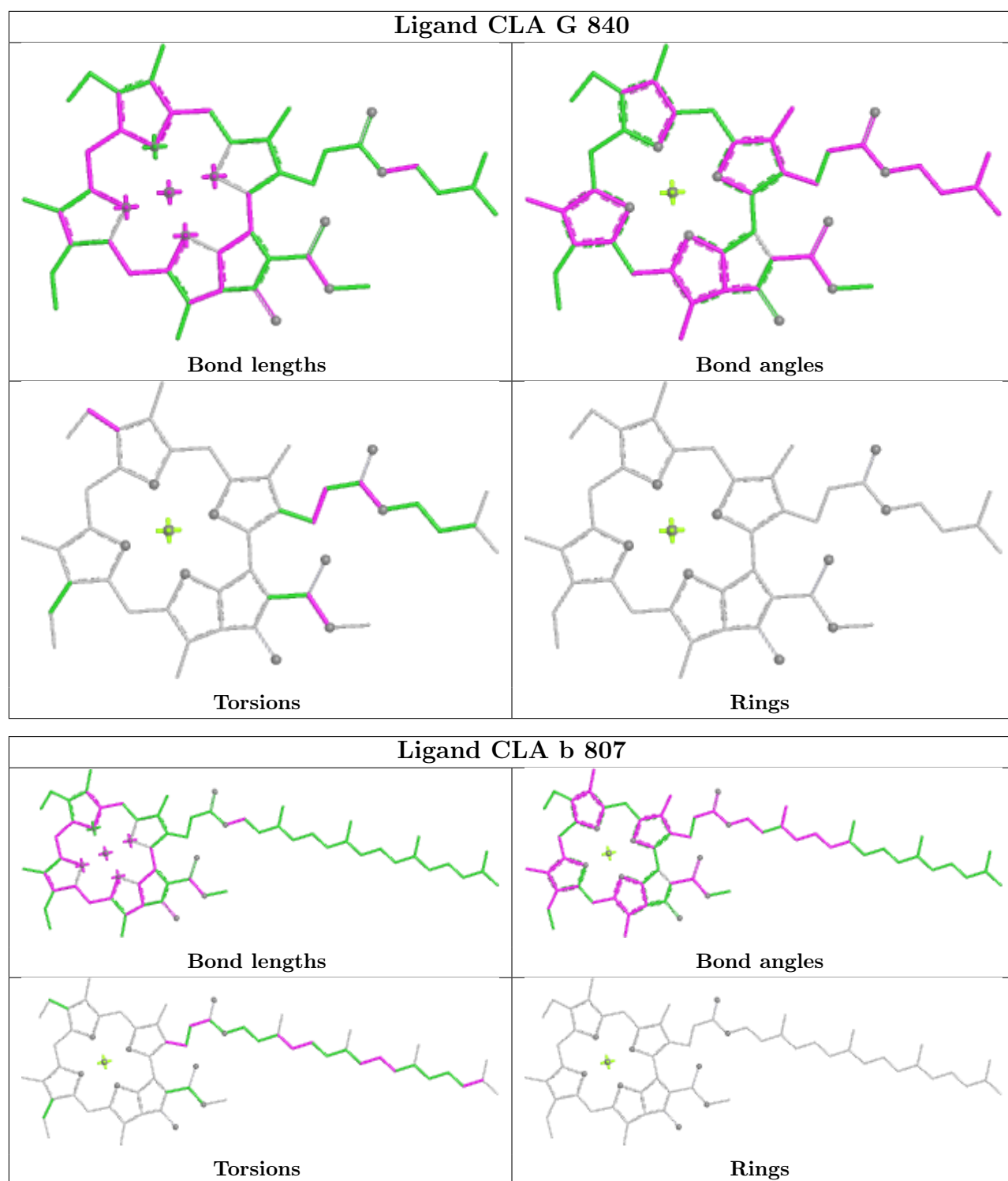


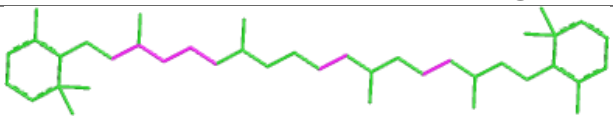
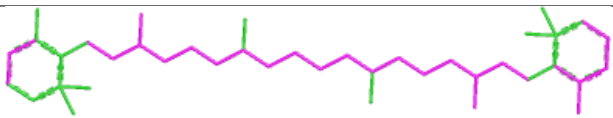
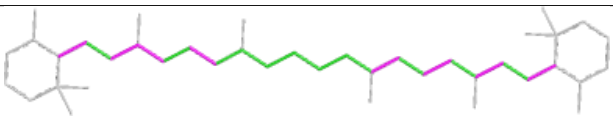
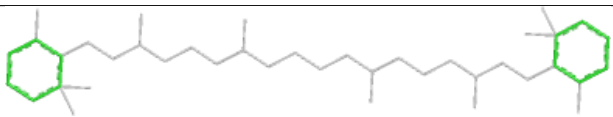
## Ligand BCR a 847

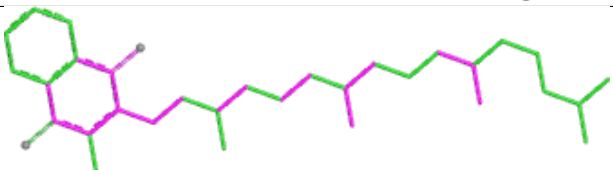
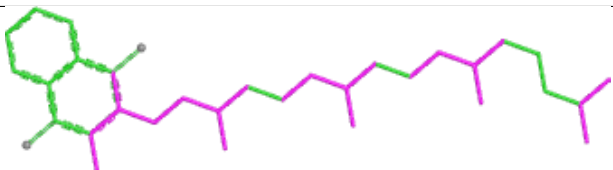
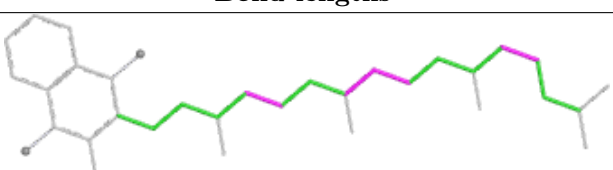
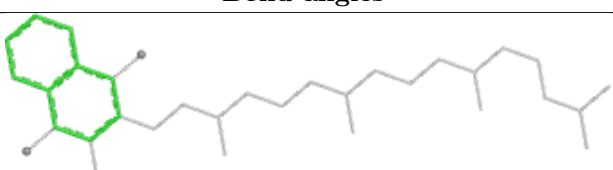


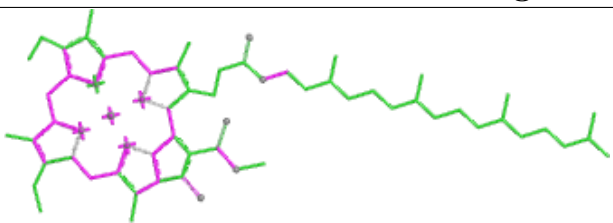
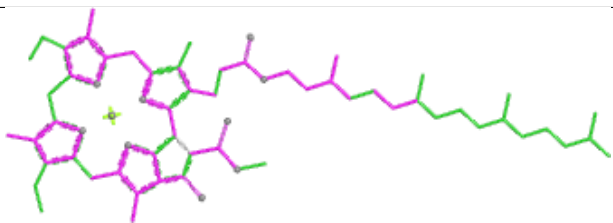
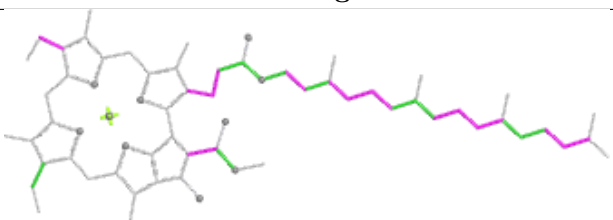
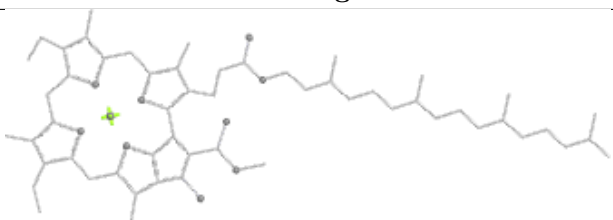


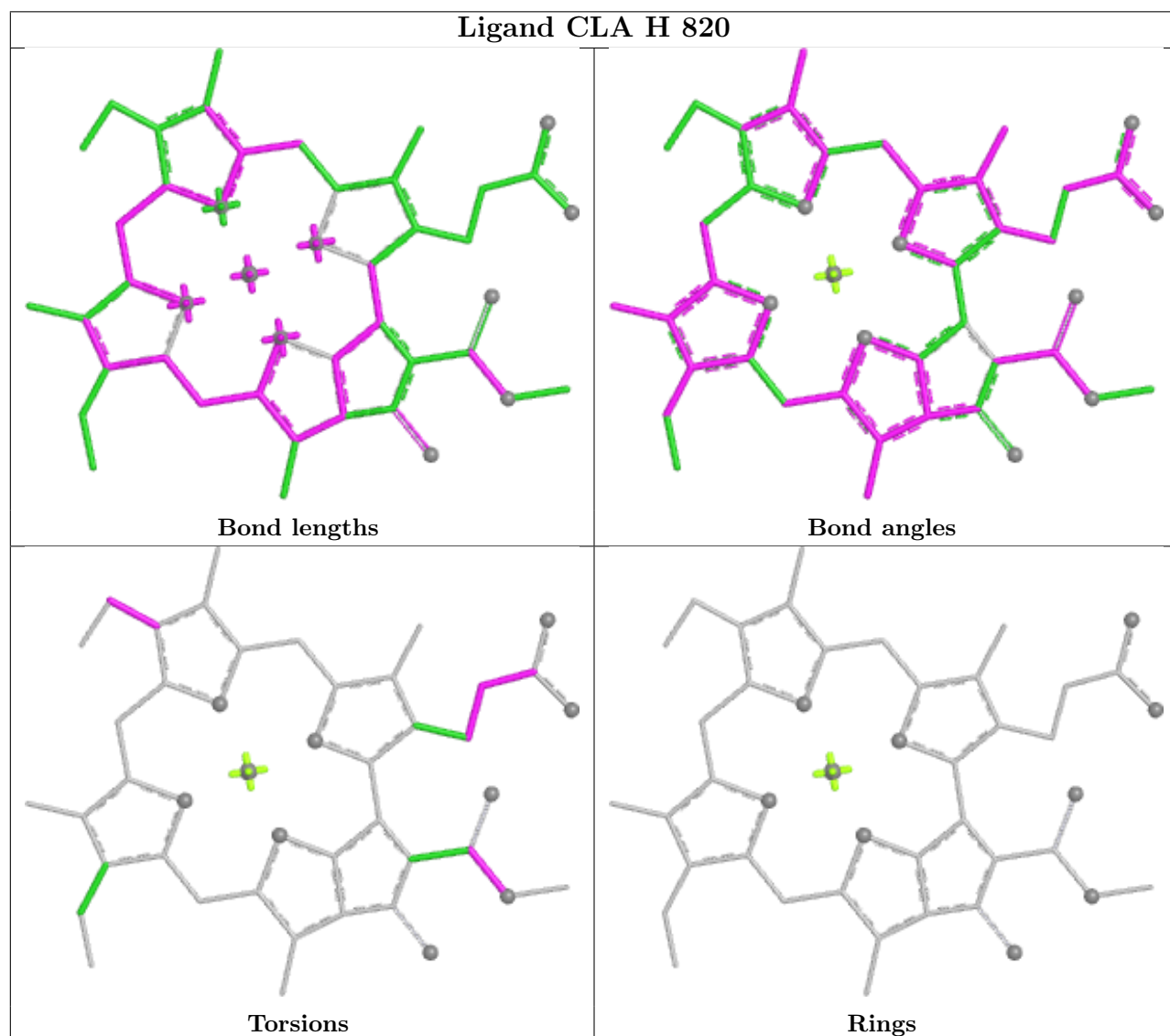
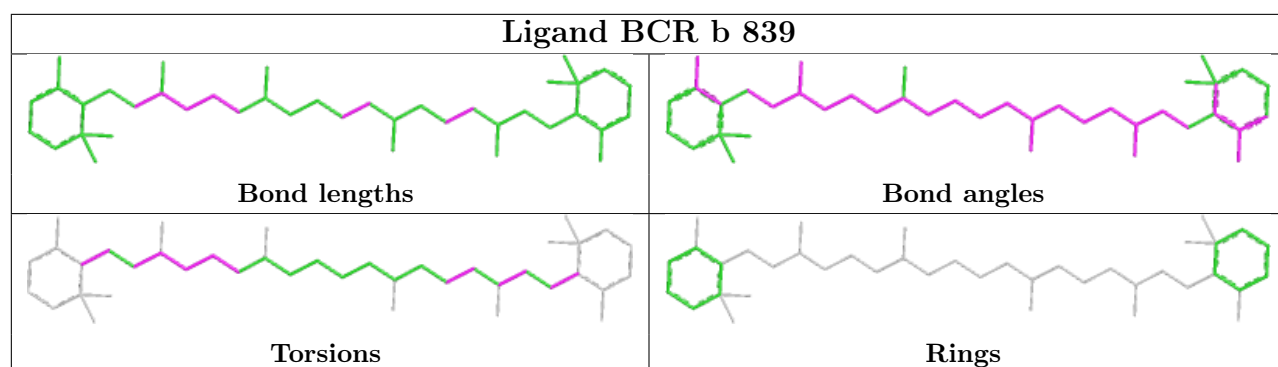


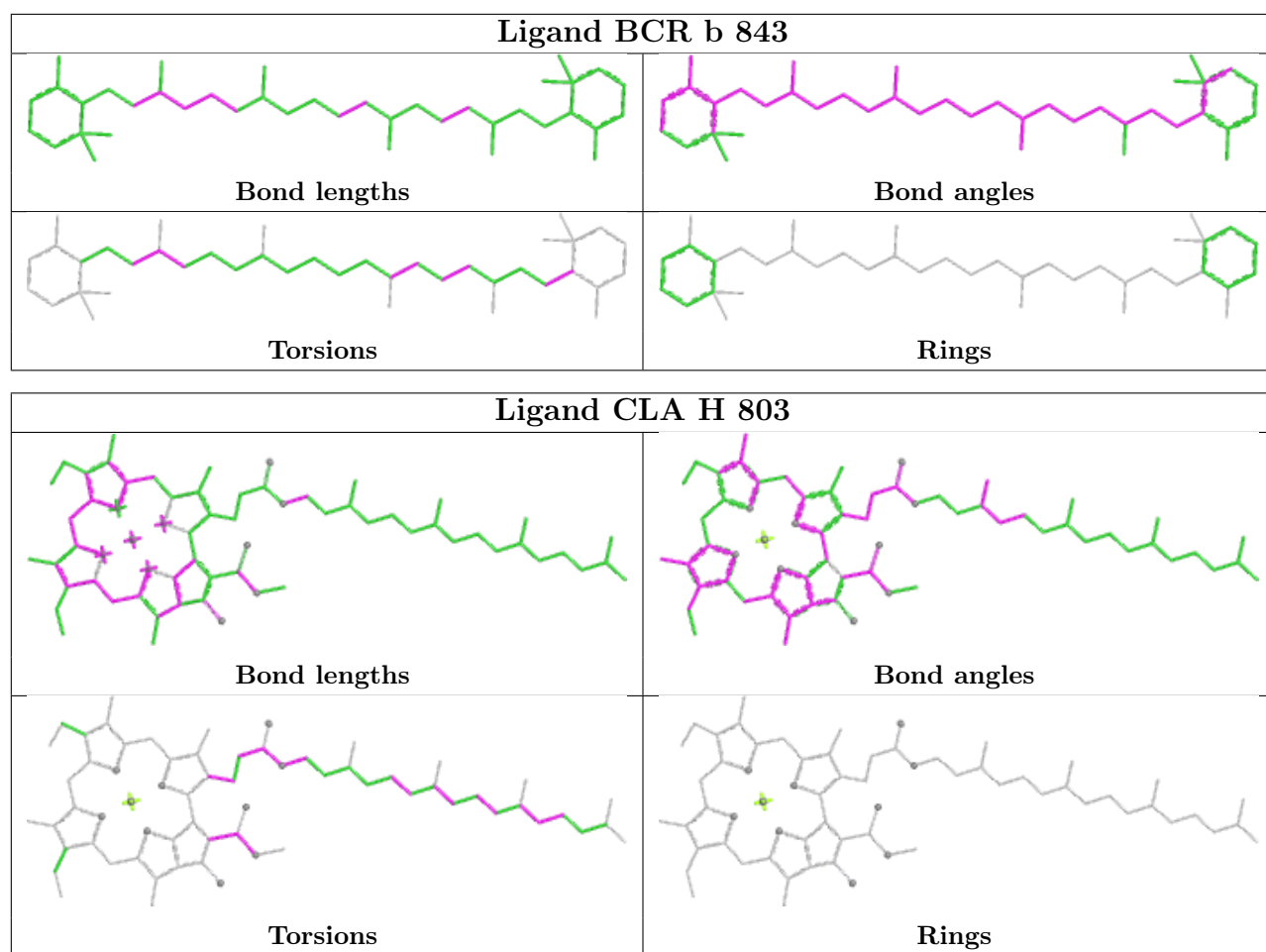


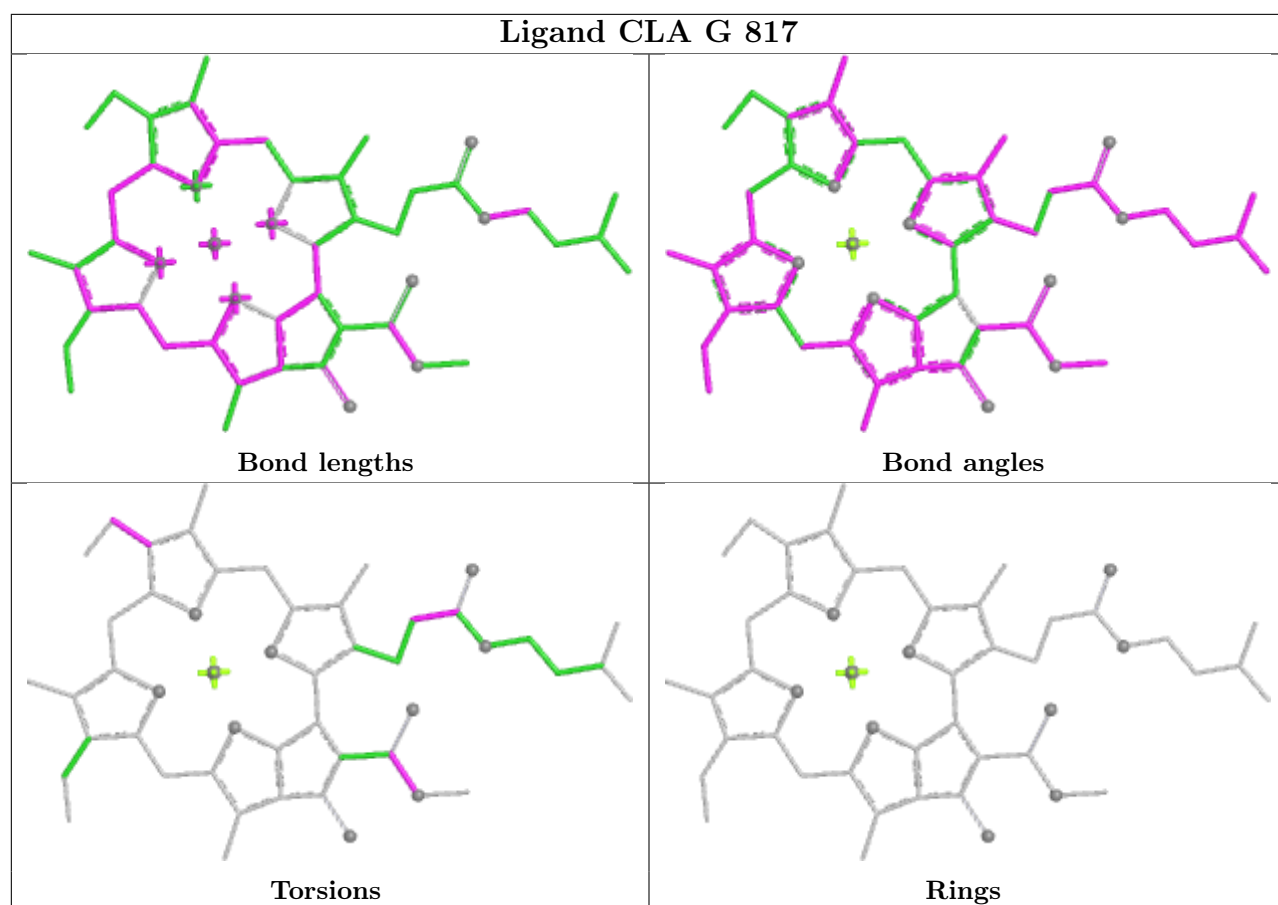
| Ligand BCR a 852                                                                  |                                                                                    |
|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                      | Bond angles                                                                        |
|  |  |
| Torsions                                                                          | Rings                                                                              |

| Ligand 1L3 A 842                                                                  |                                                                                    |
|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                      | Bond angles                                                                        |
|  |  |
| Torsions                                                                          | Rings                                                                              |

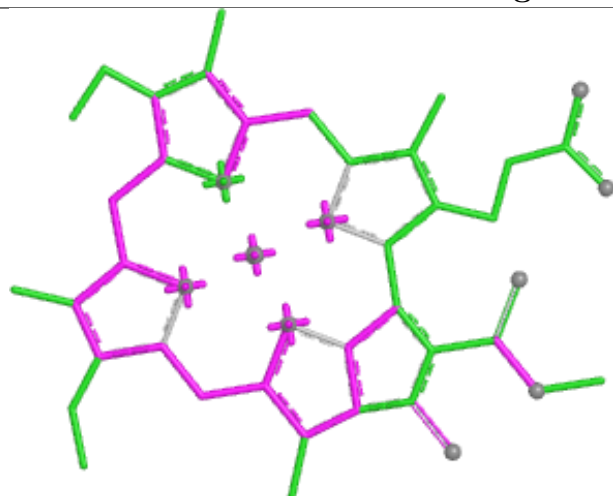
| Ligand CLA a 854                                                                    |                                                                                      |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                        | Bond angles                                                                          |
|  |  |
| Torsions                                                                            | Rings                                                                                |



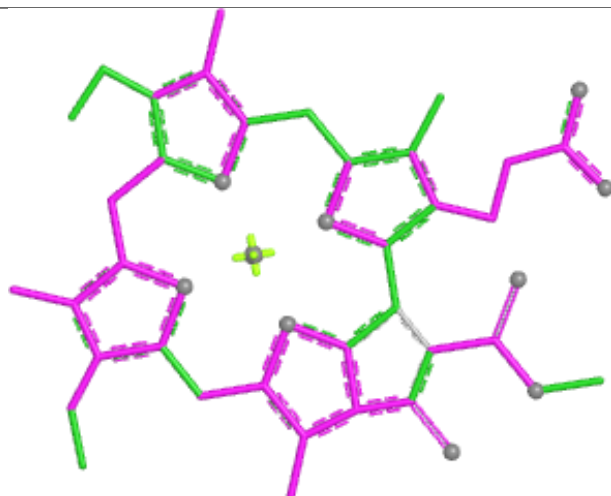




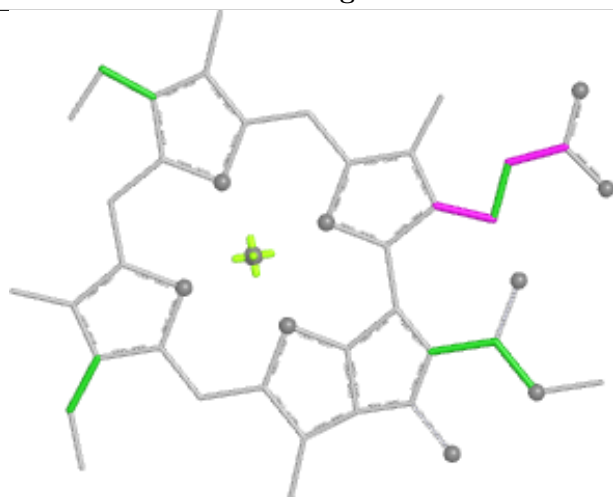
## Ligand CLA A 838



Bond lengths



Bond angles

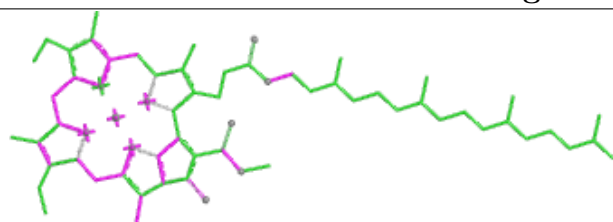


Torsions

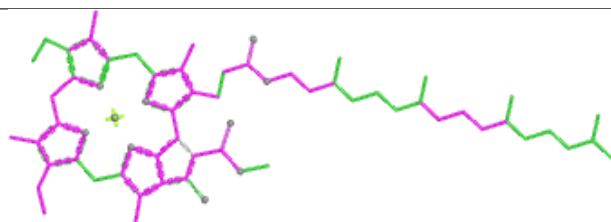


Rings

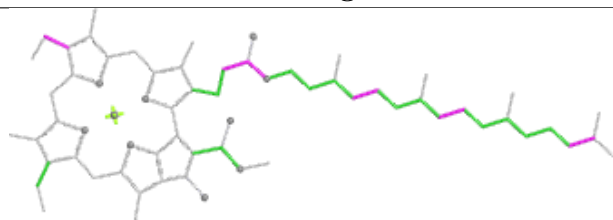
## Ligand CL0 a 801



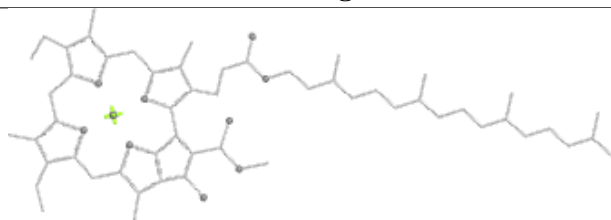
Bond lengths



Bond angles

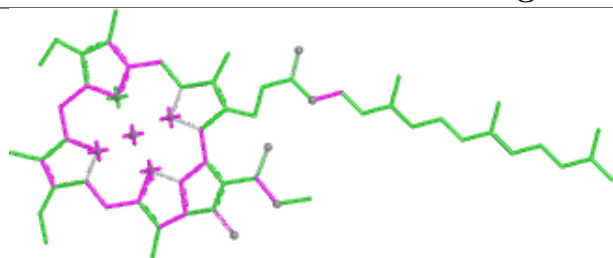


Torsions

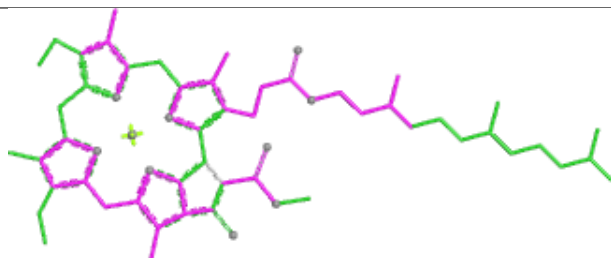


Rings

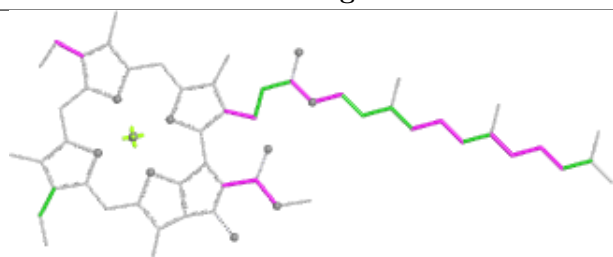
## Ligand CLA b 848



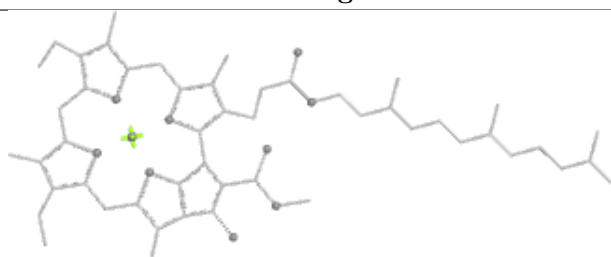
Bond lengths



Bond angles

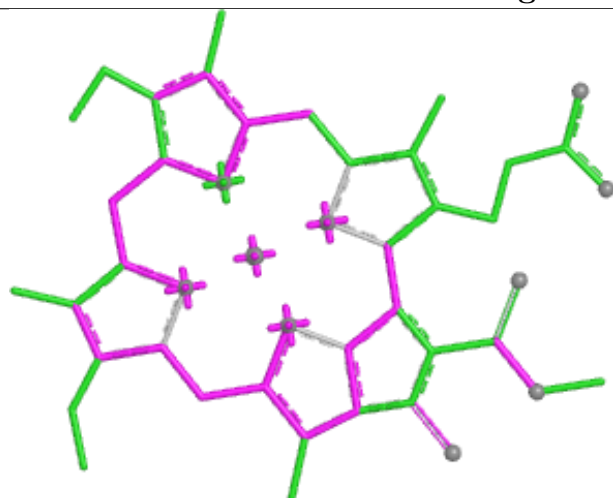


Torsions

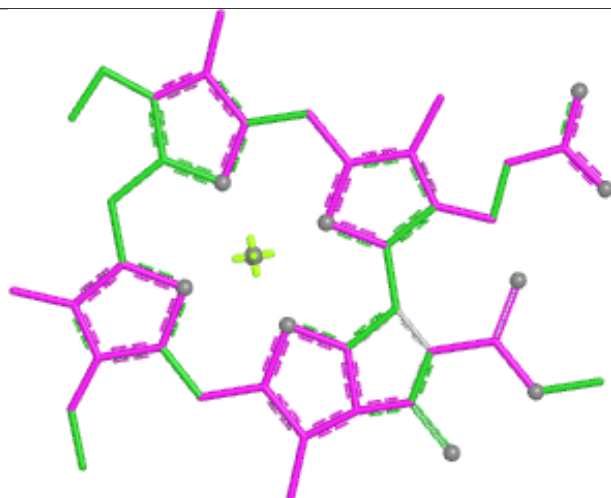


Rings

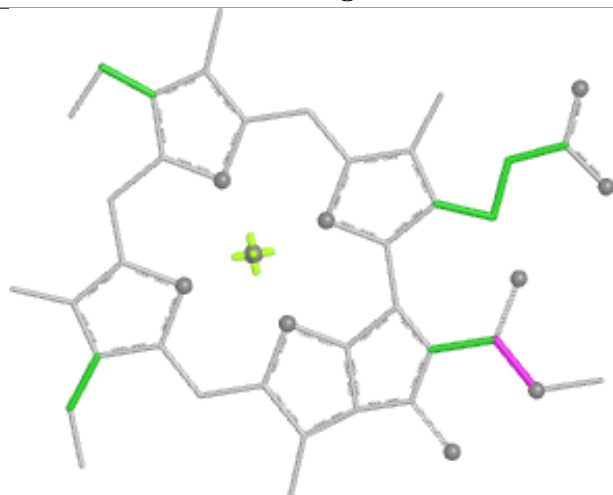
## Ligand CLA a 813



Bond lengths



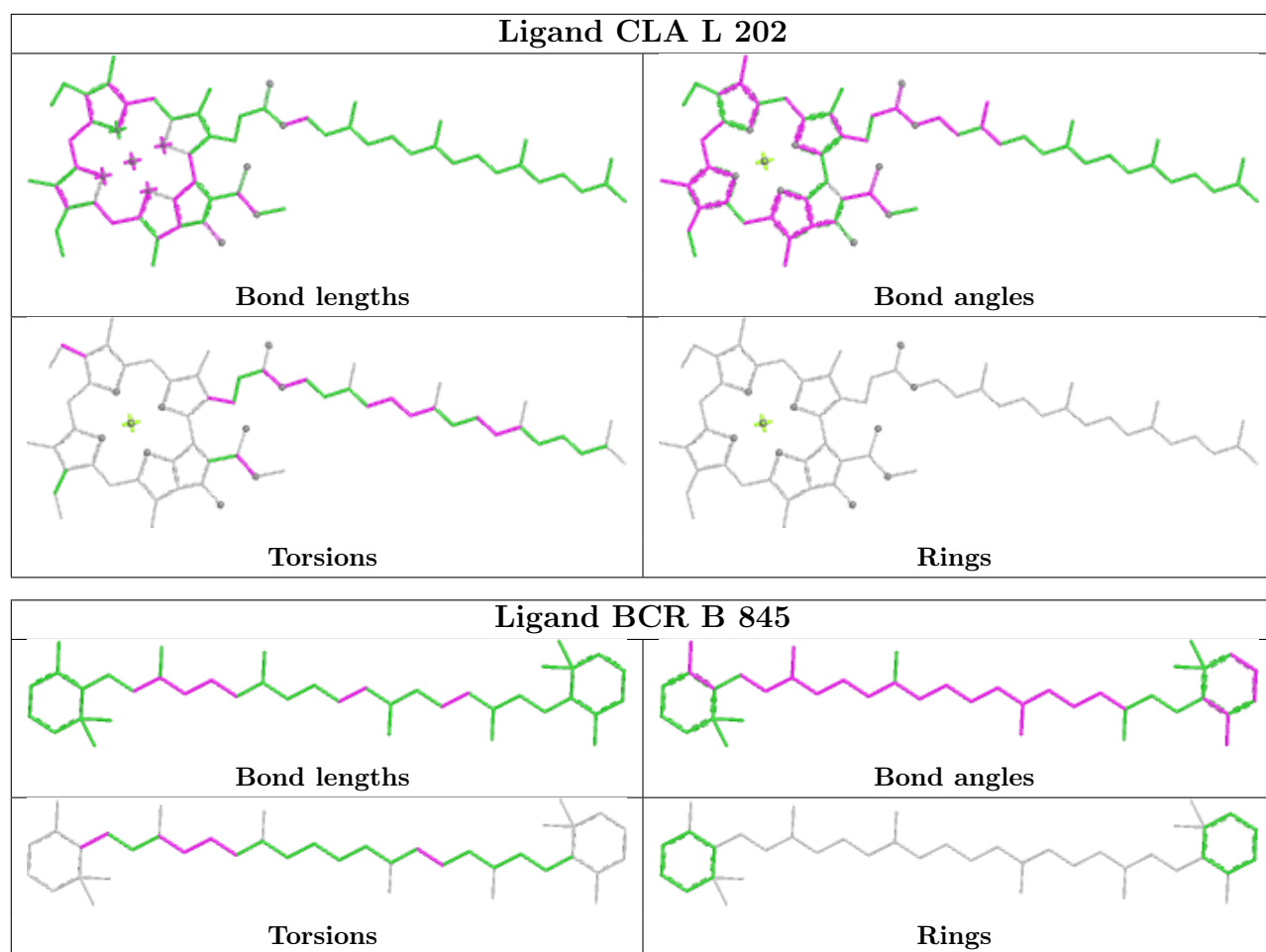
Bond angles

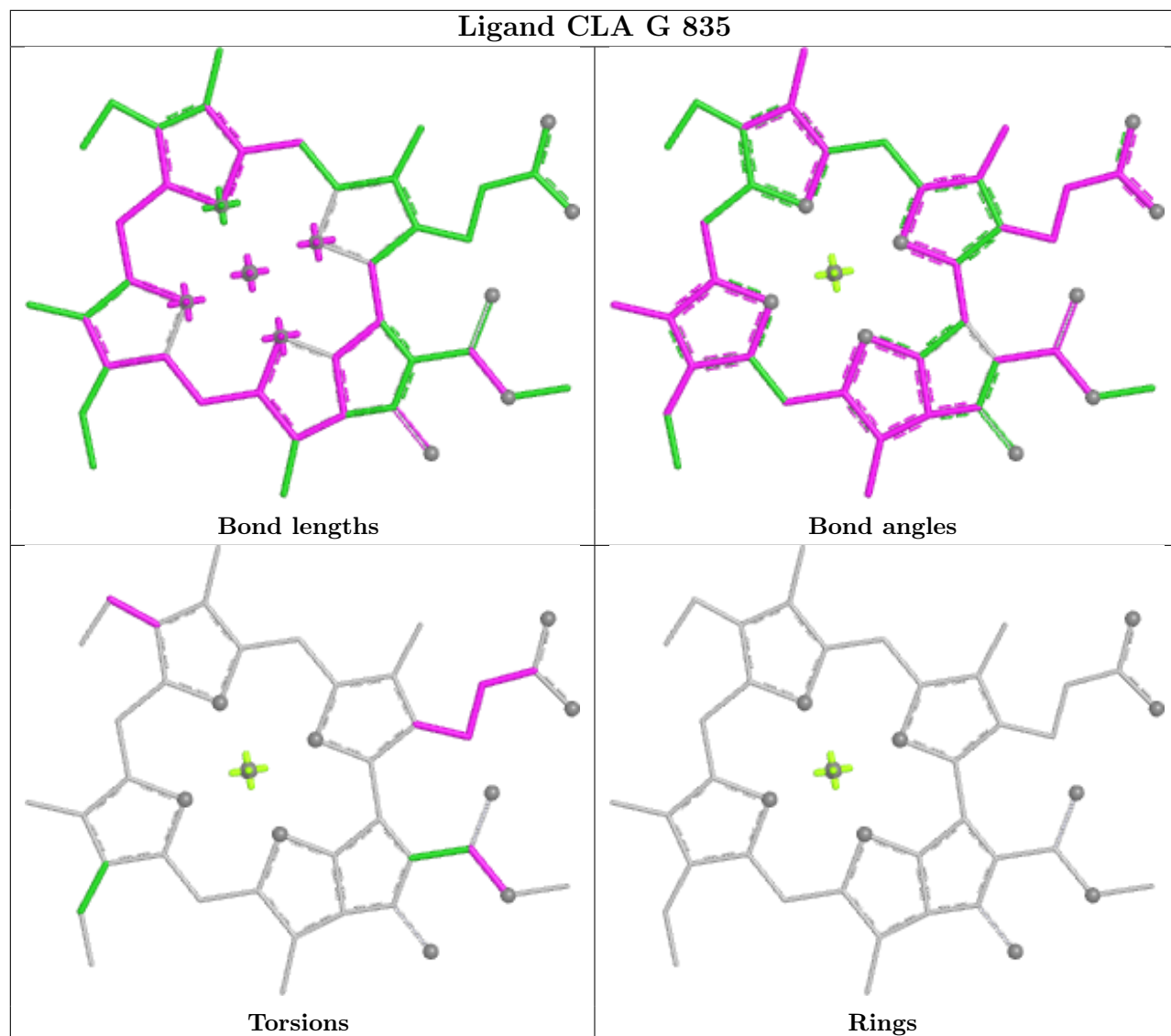


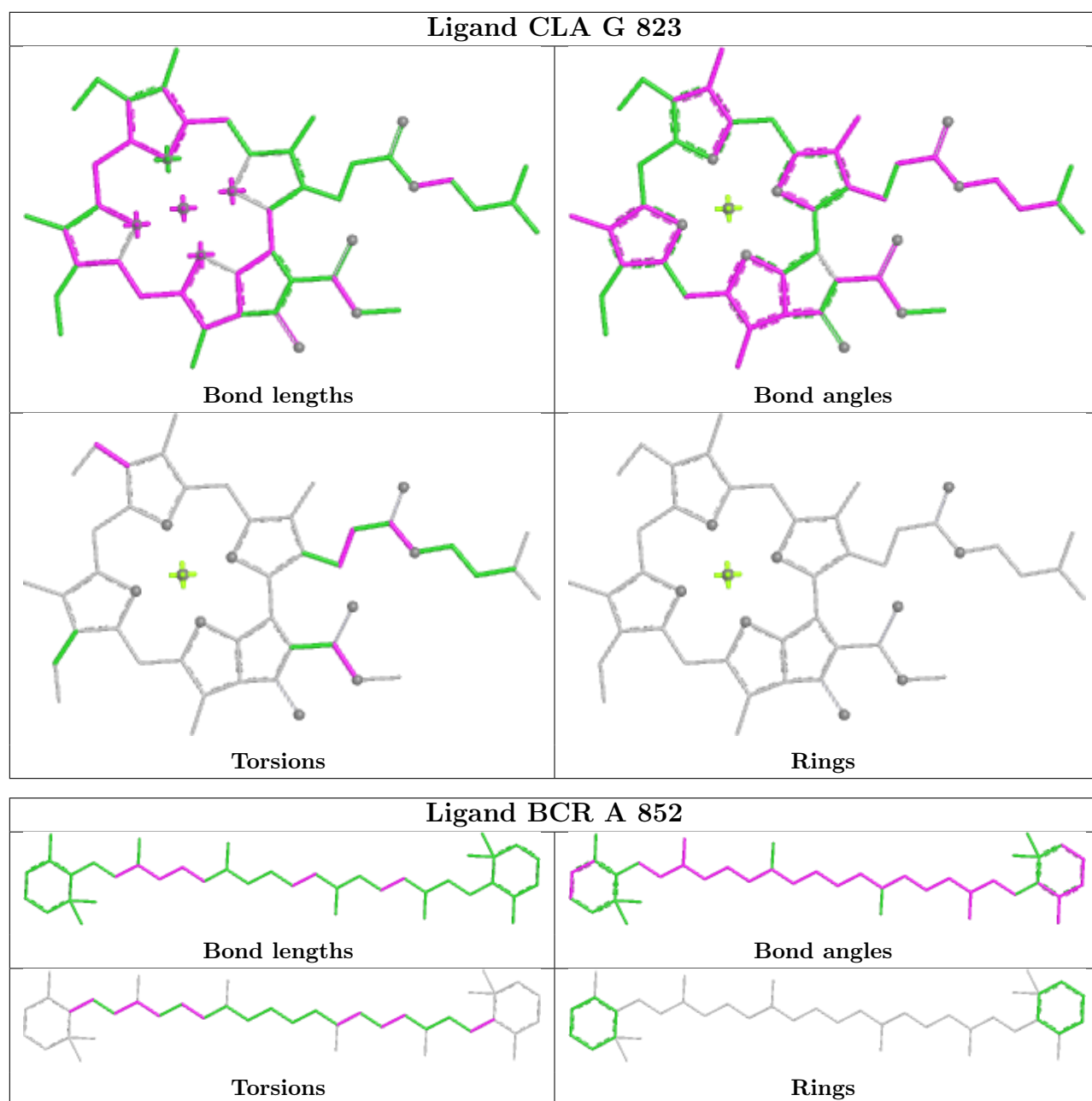
Torsions



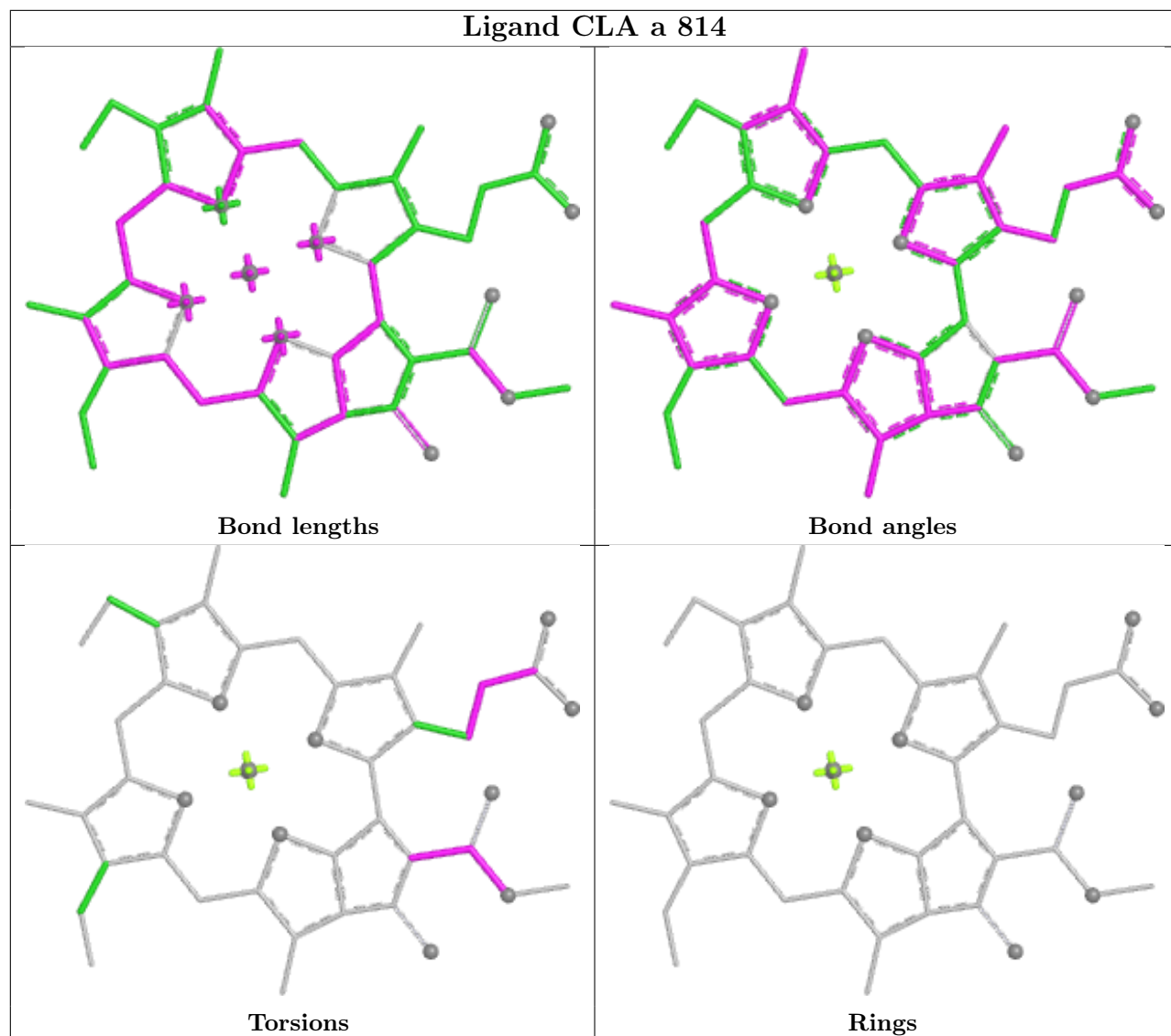
Rings



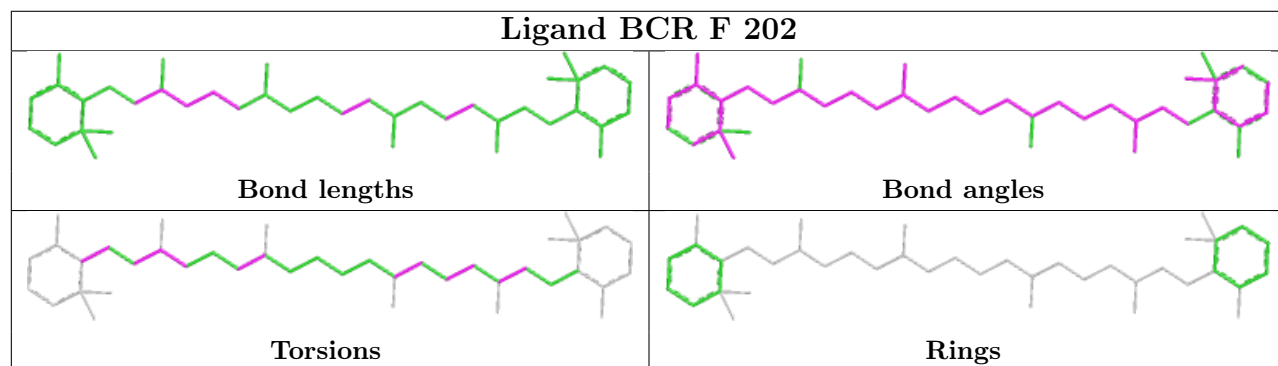


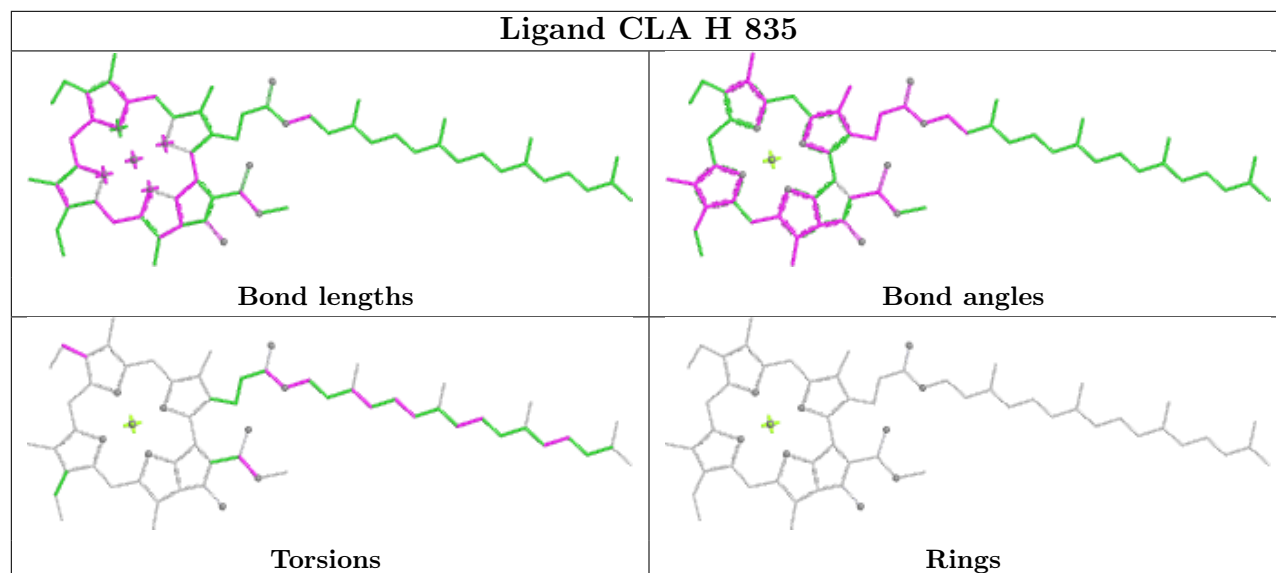
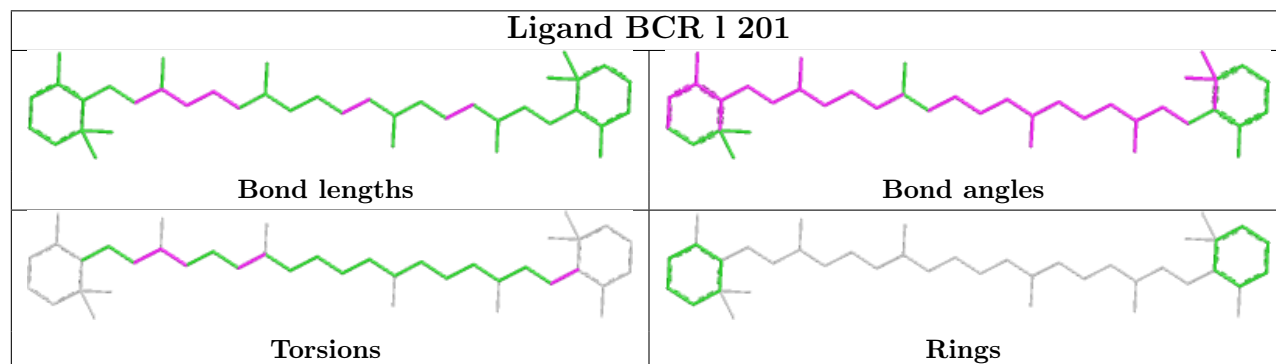
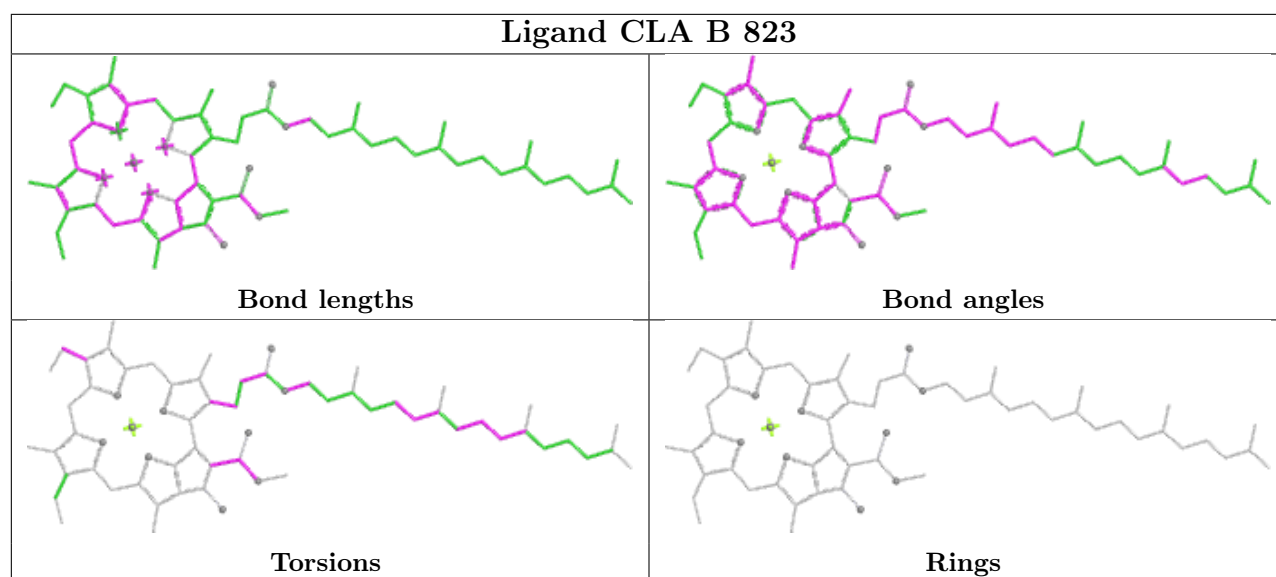


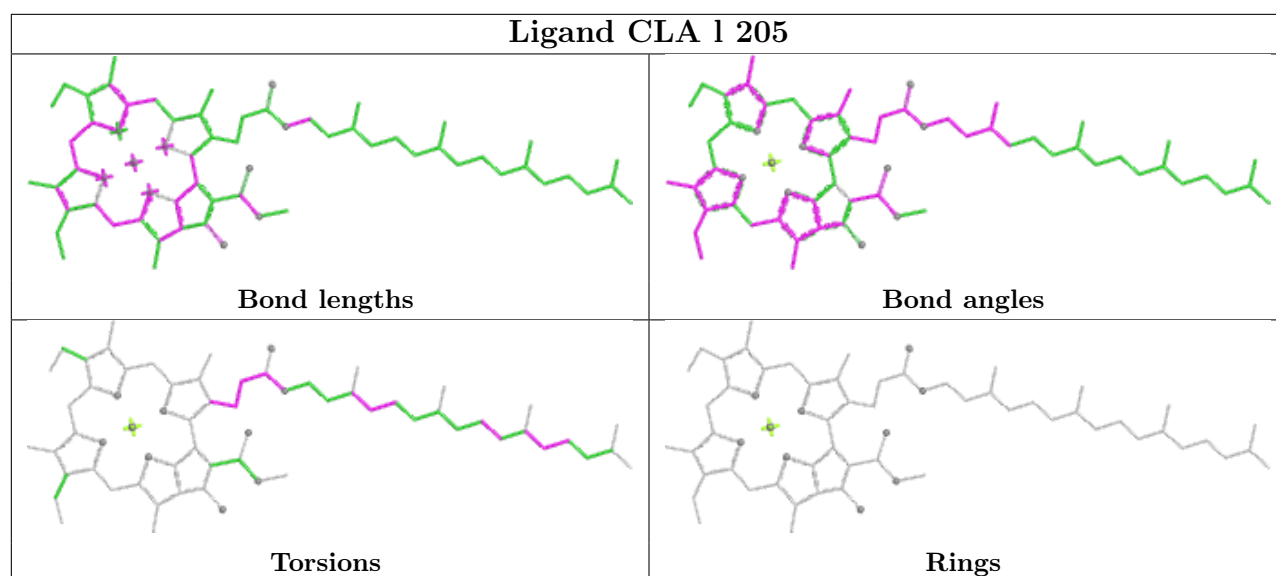
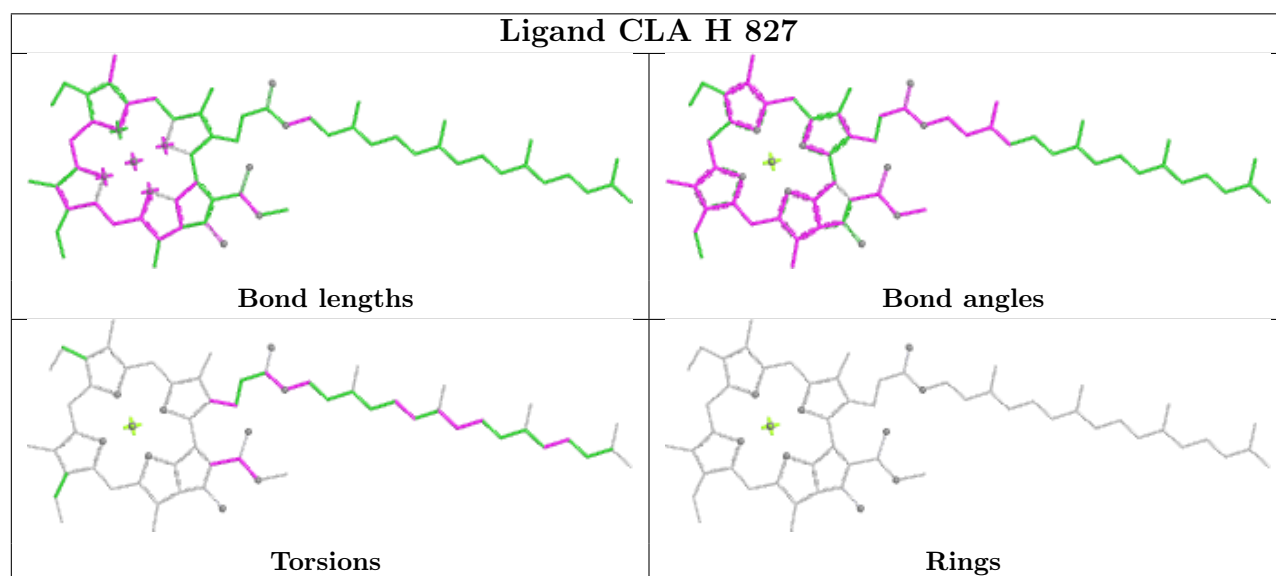
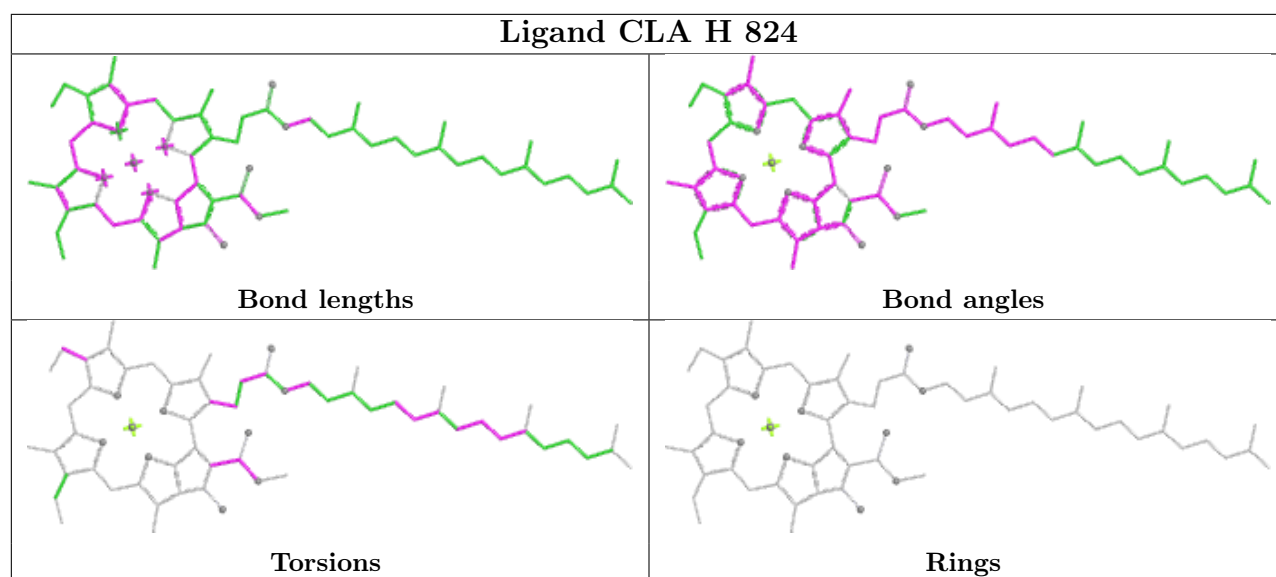
## Ligand CLA a 814



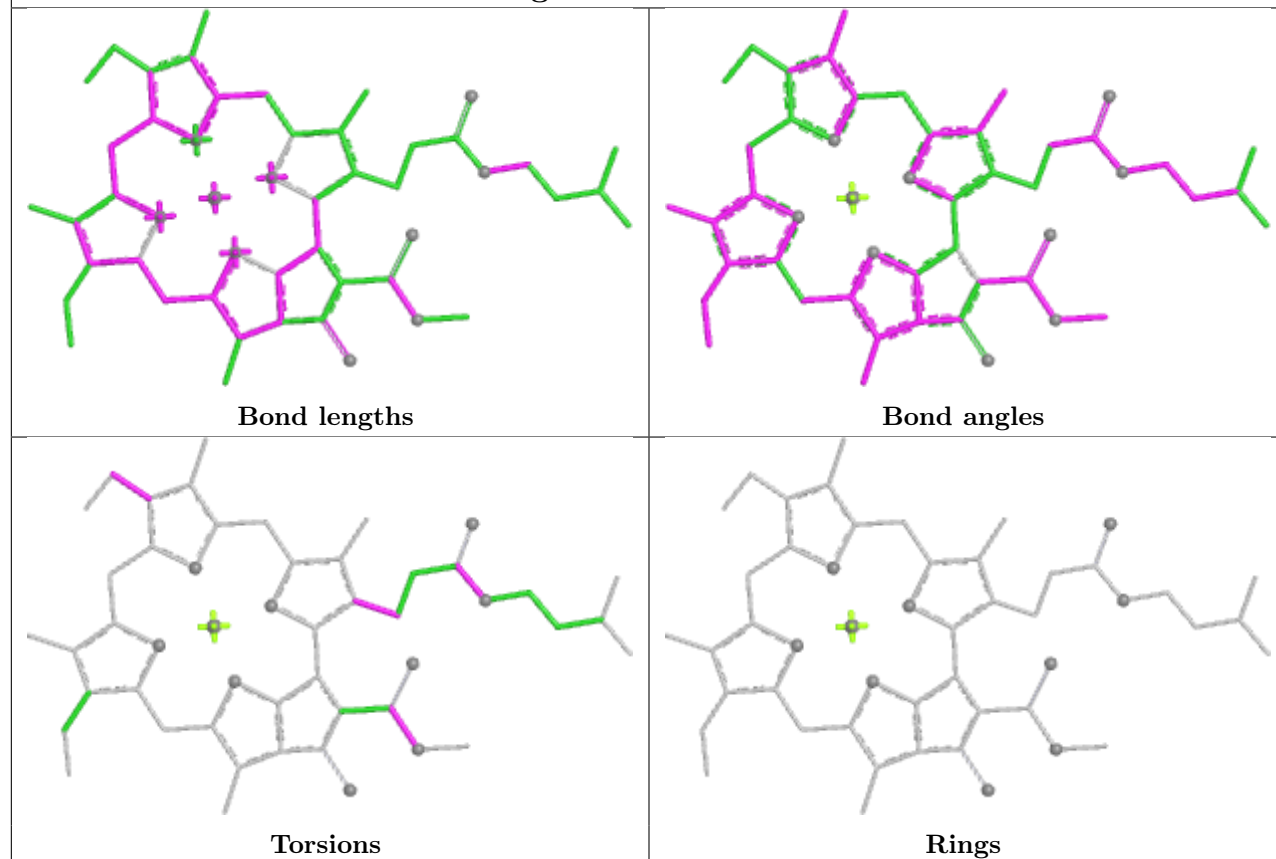
## Ligand BCR F 202



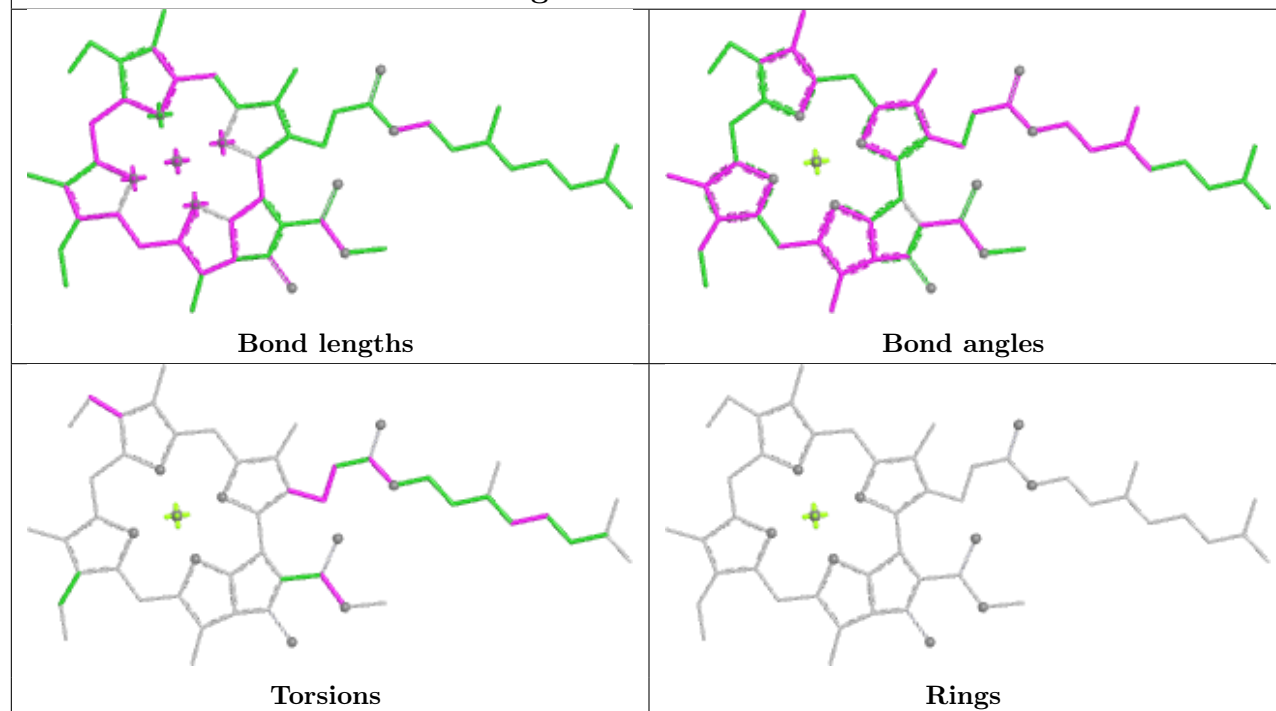


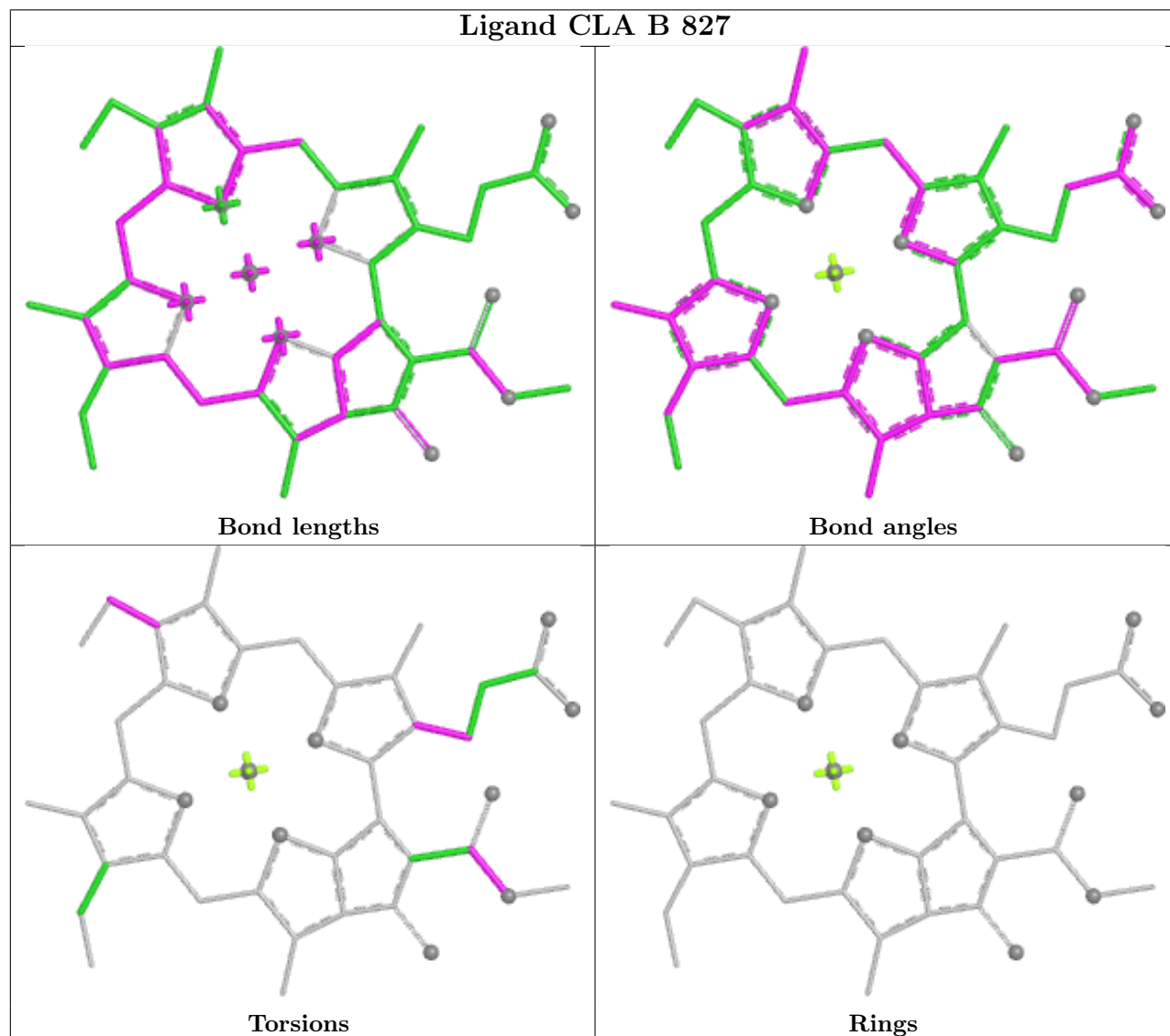
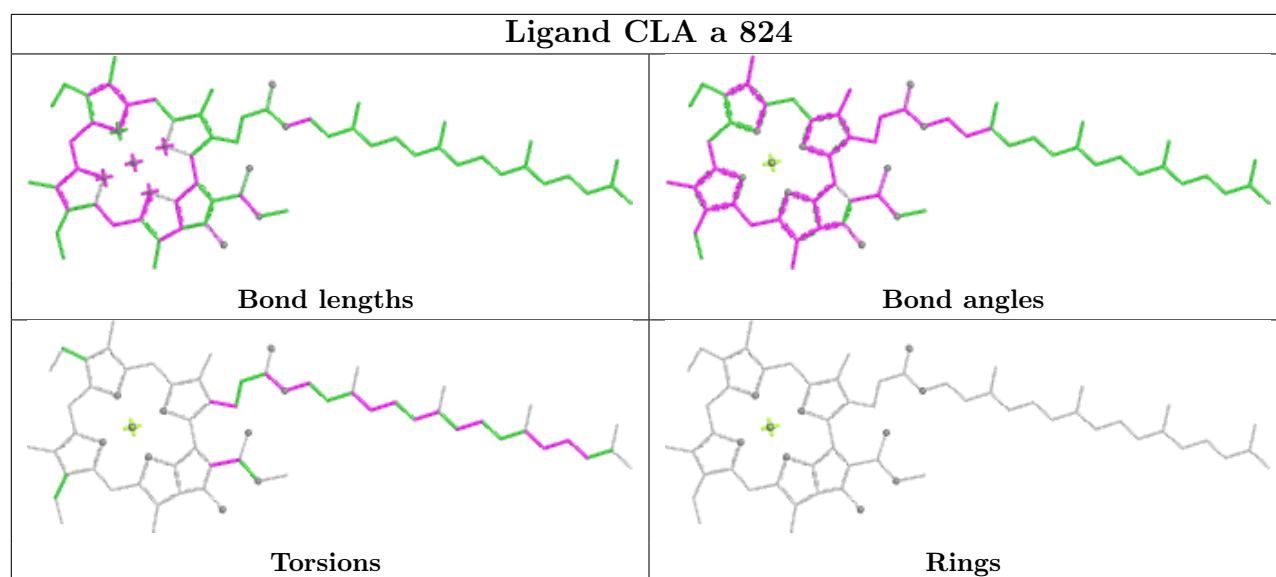


## Ligand CLA G 811

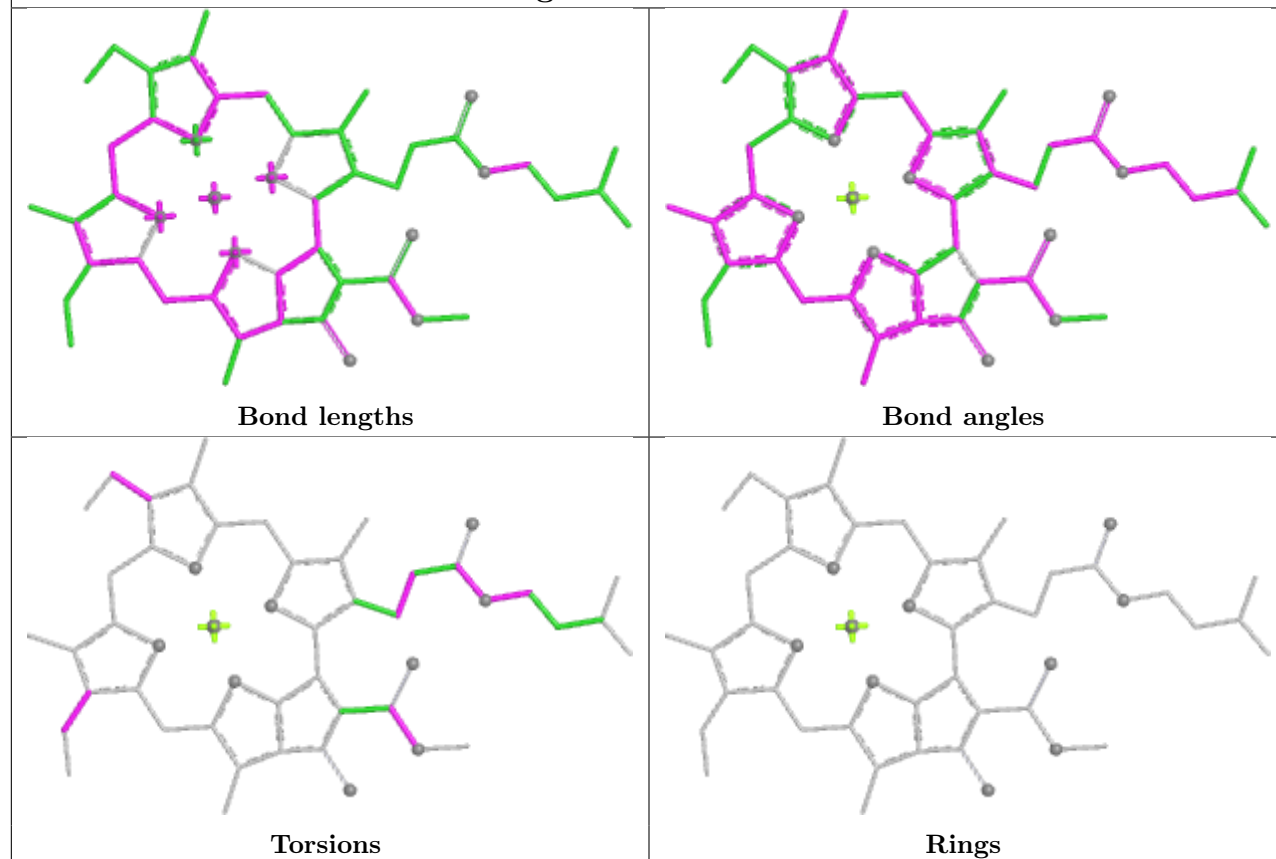


## Ligand CLA G 824

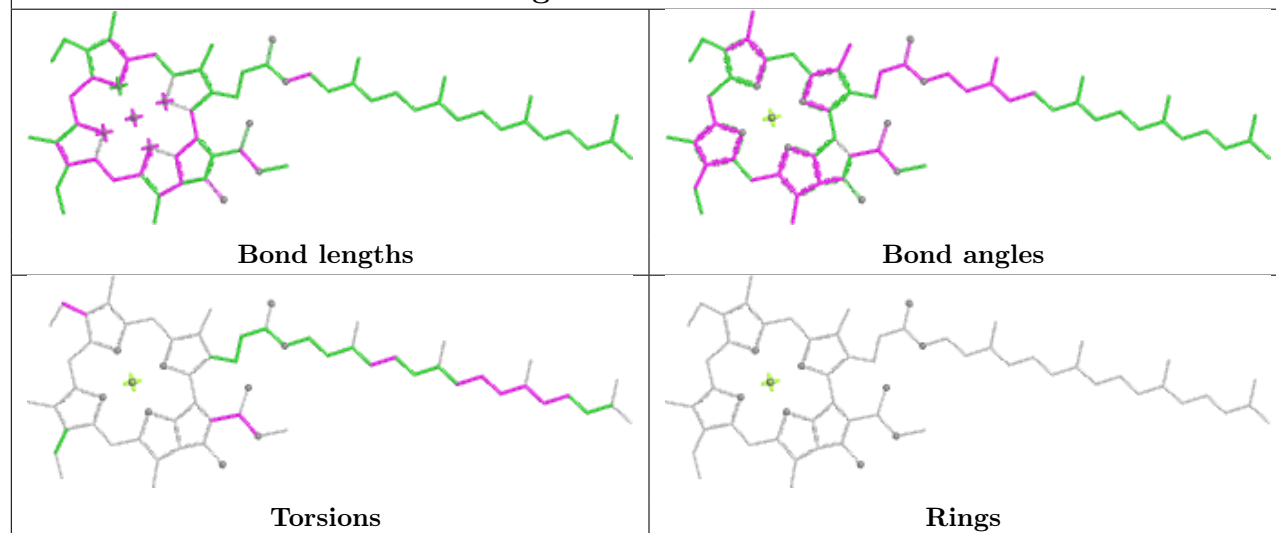


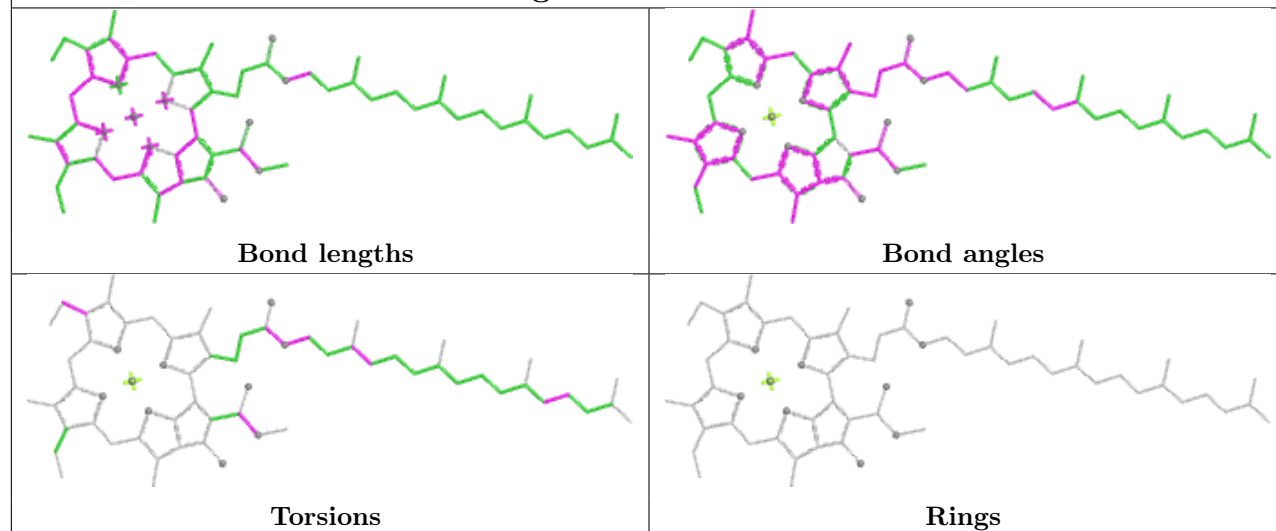
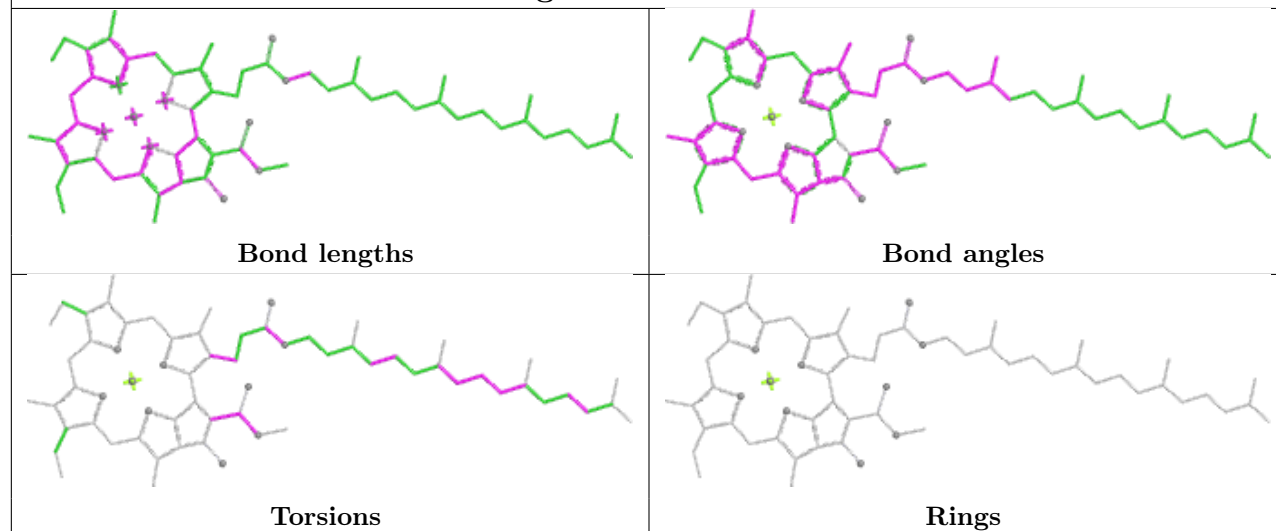
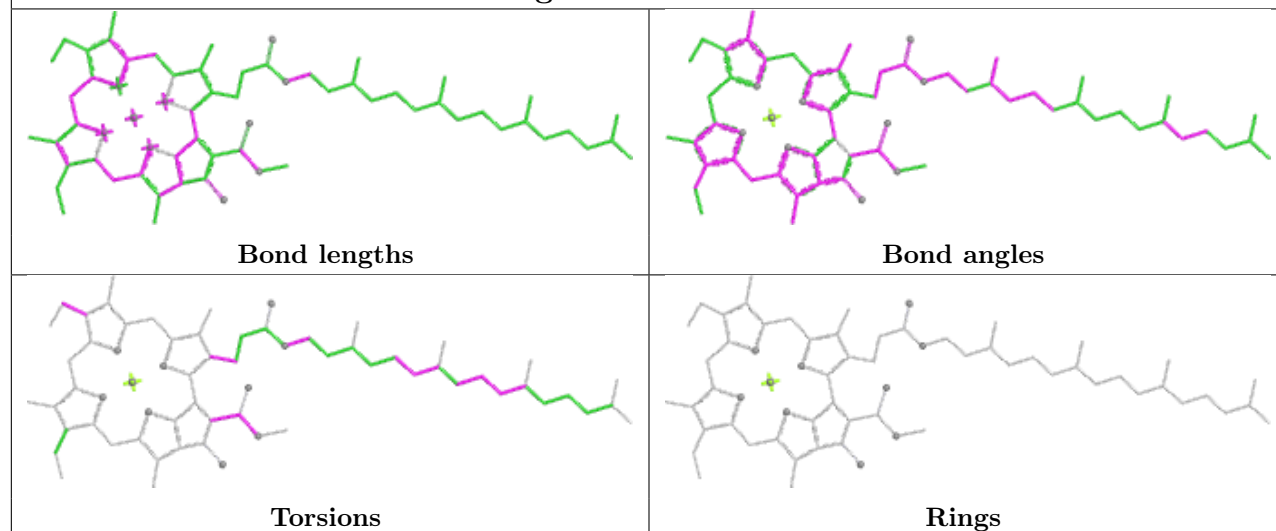


## Ligand CLA a 812

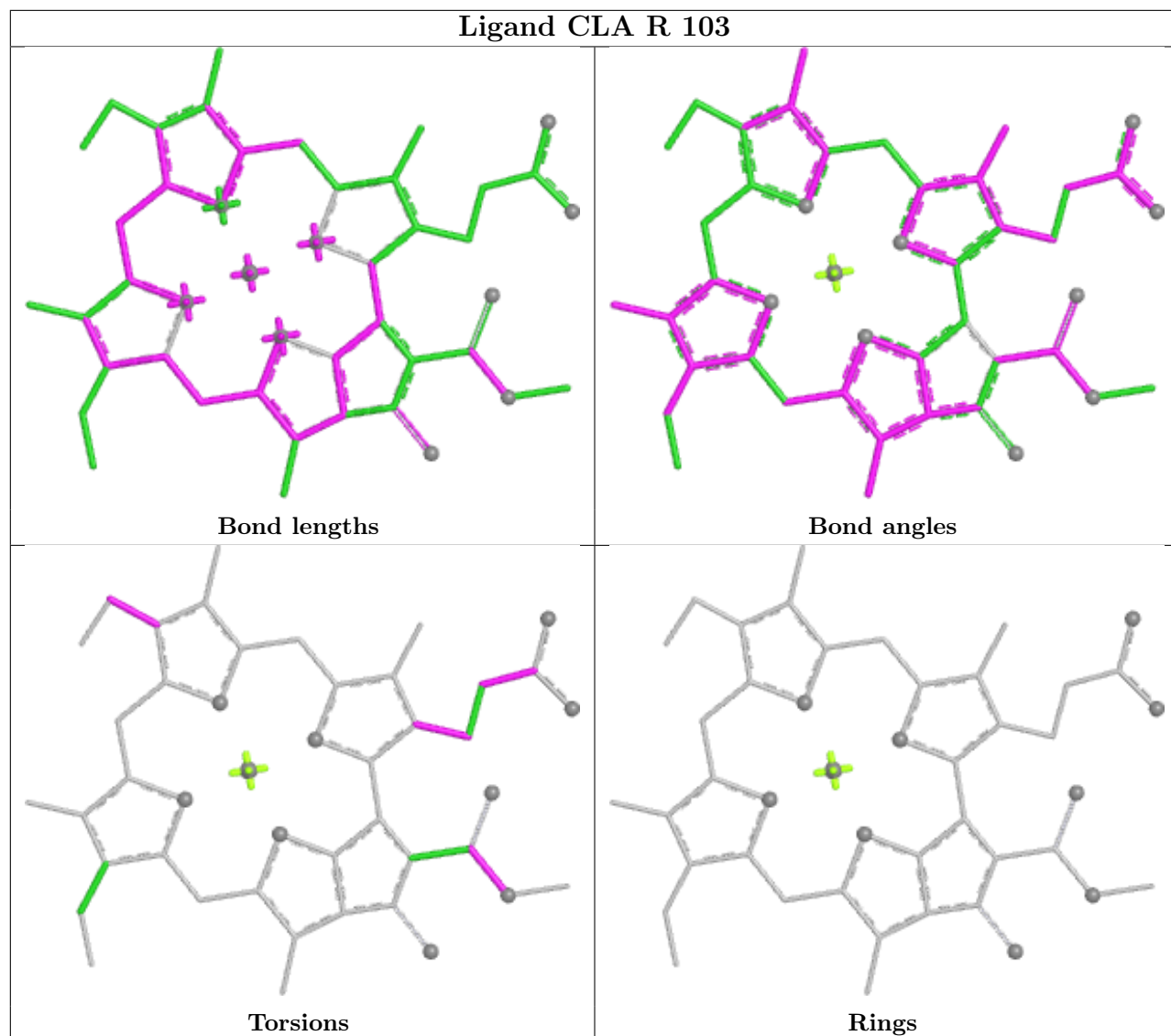


## Ligand CLA B 830

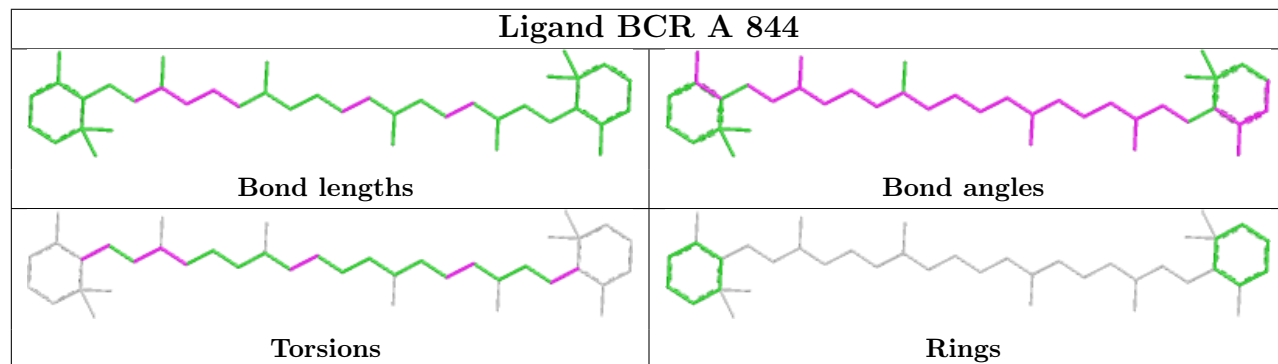


**Ligand CLA B 834****Ligand CLA a 826****Ligand CLA b 823**

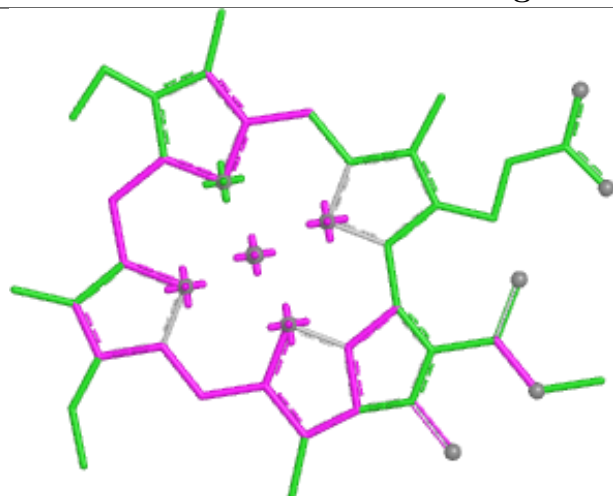
## Ligand CLA R 103



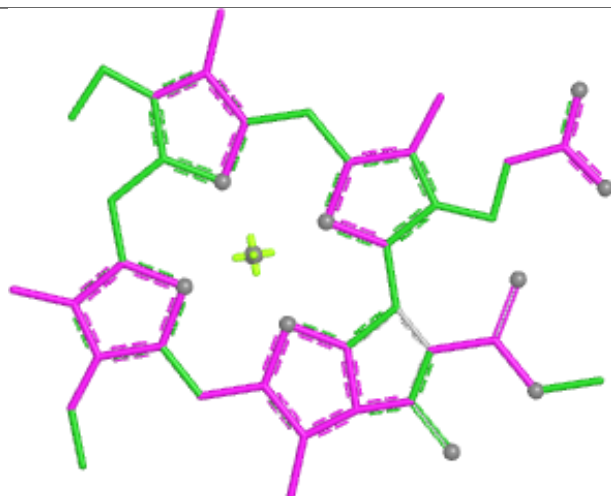
## Ligand BCR A 844



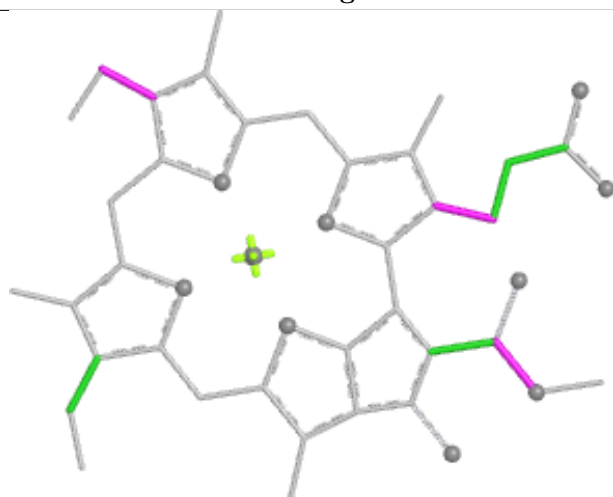
## Ligand CLA H 828



Bond lengths



Bond angles

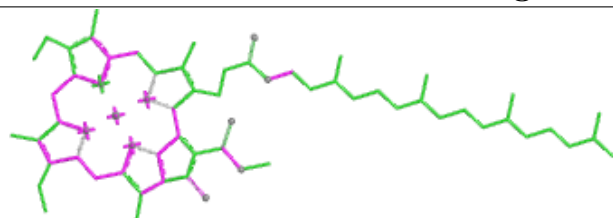


Torsions

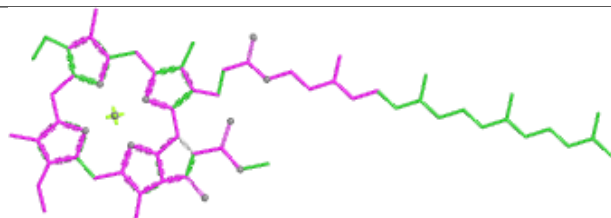


Rings

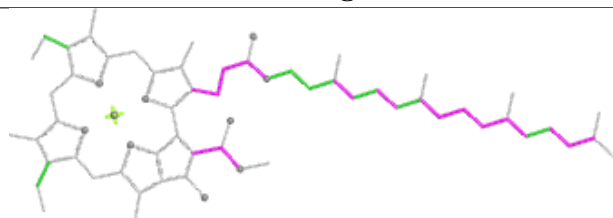
## Ligand CLA H 811



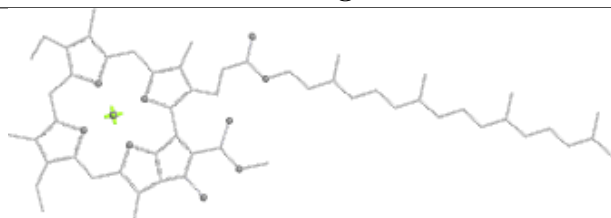
Bond lengths



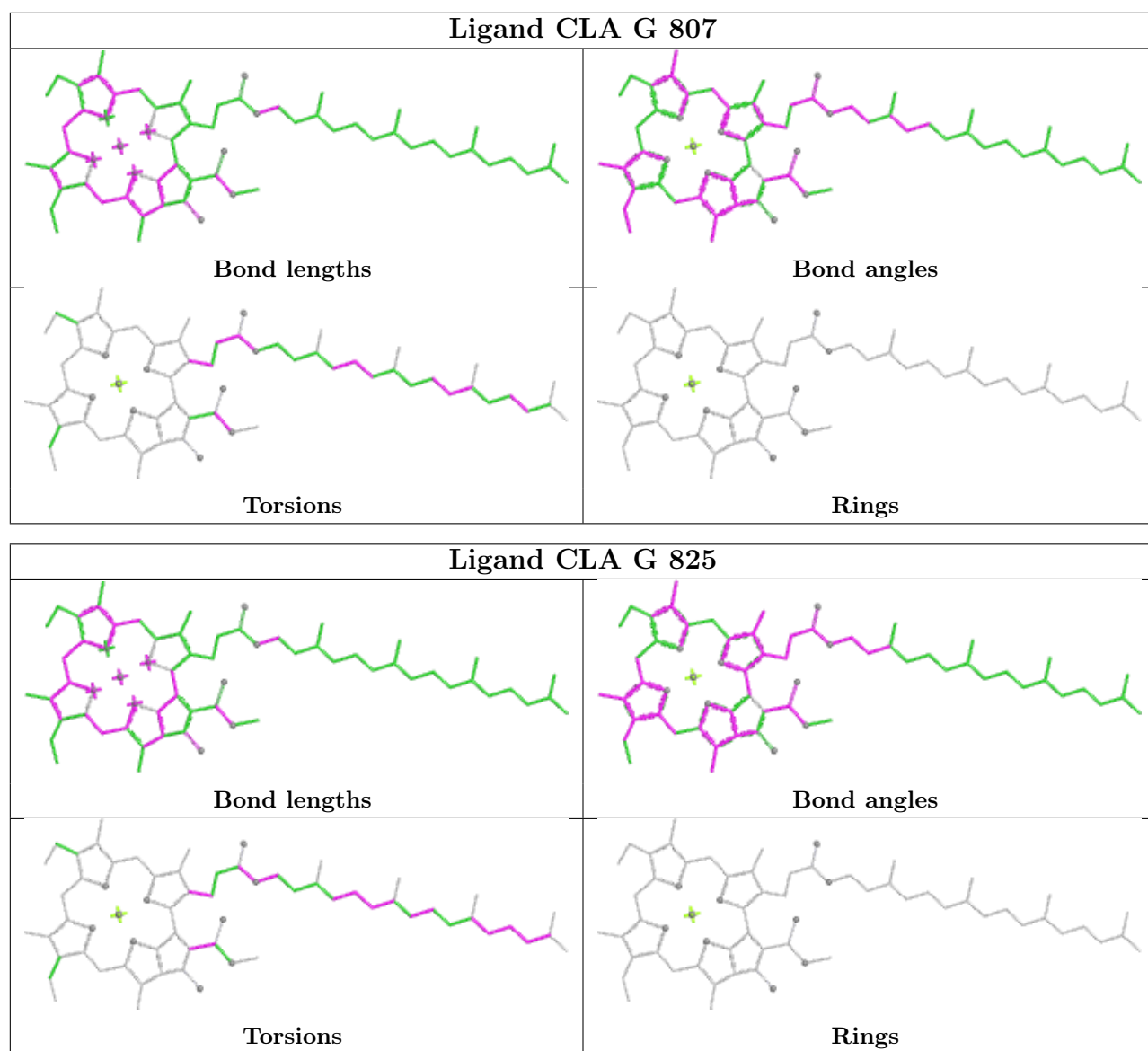
Bond angles



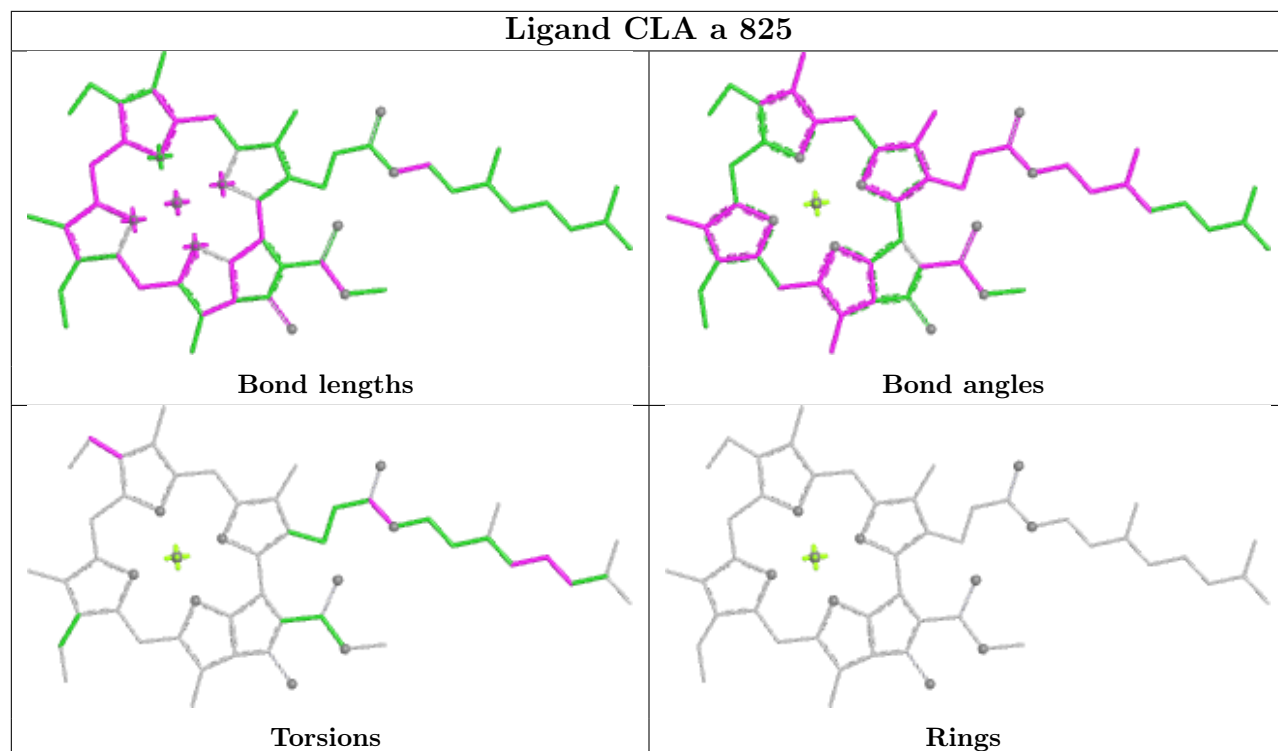
Torsions



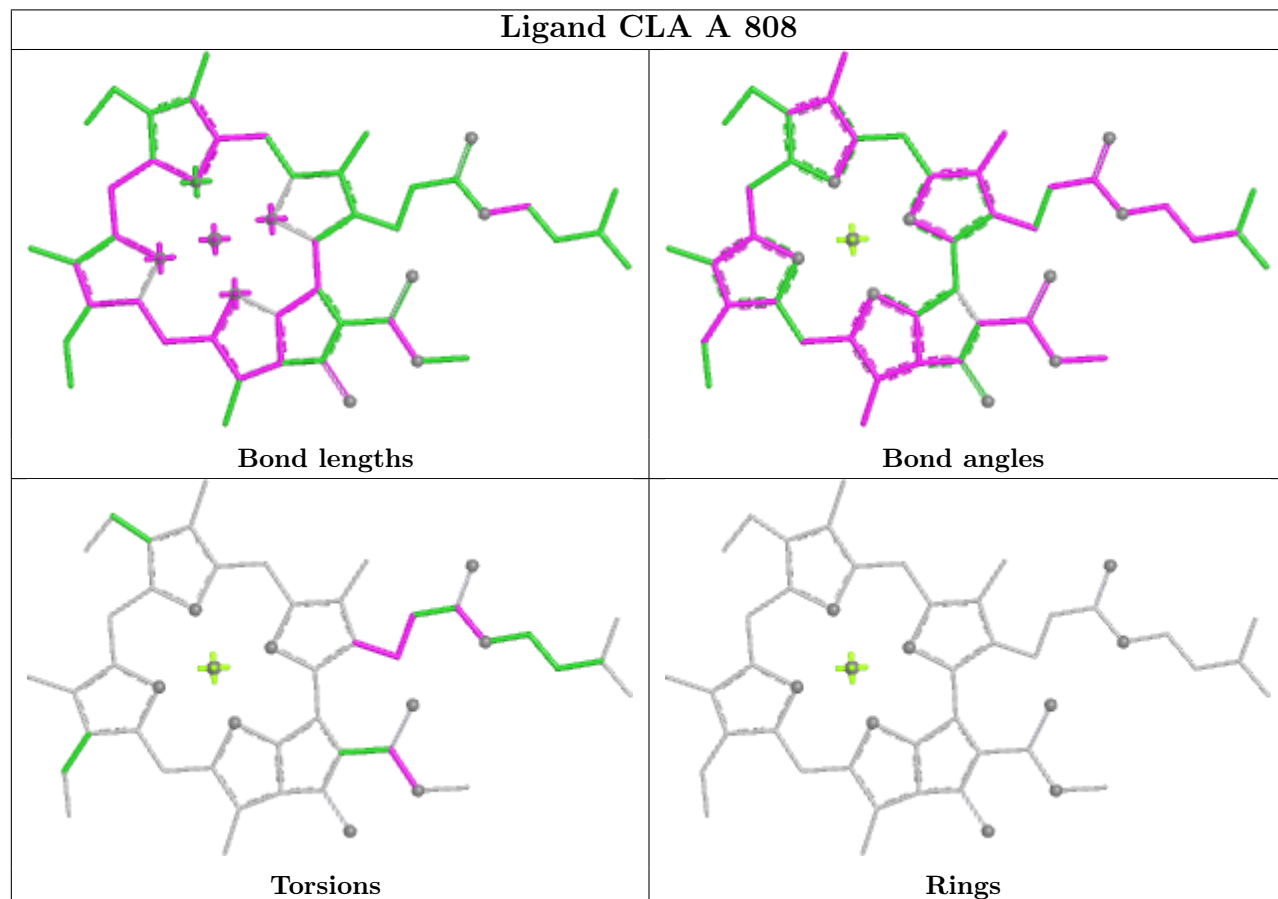
Rings

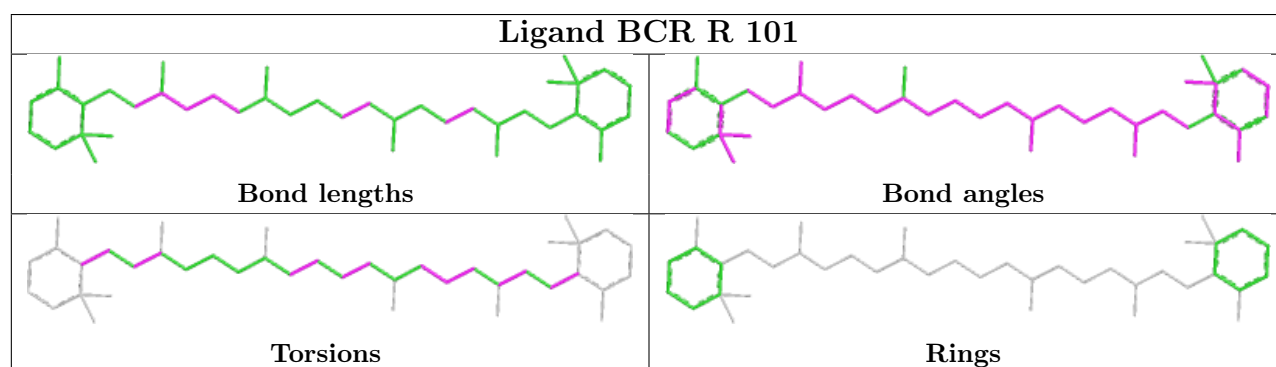
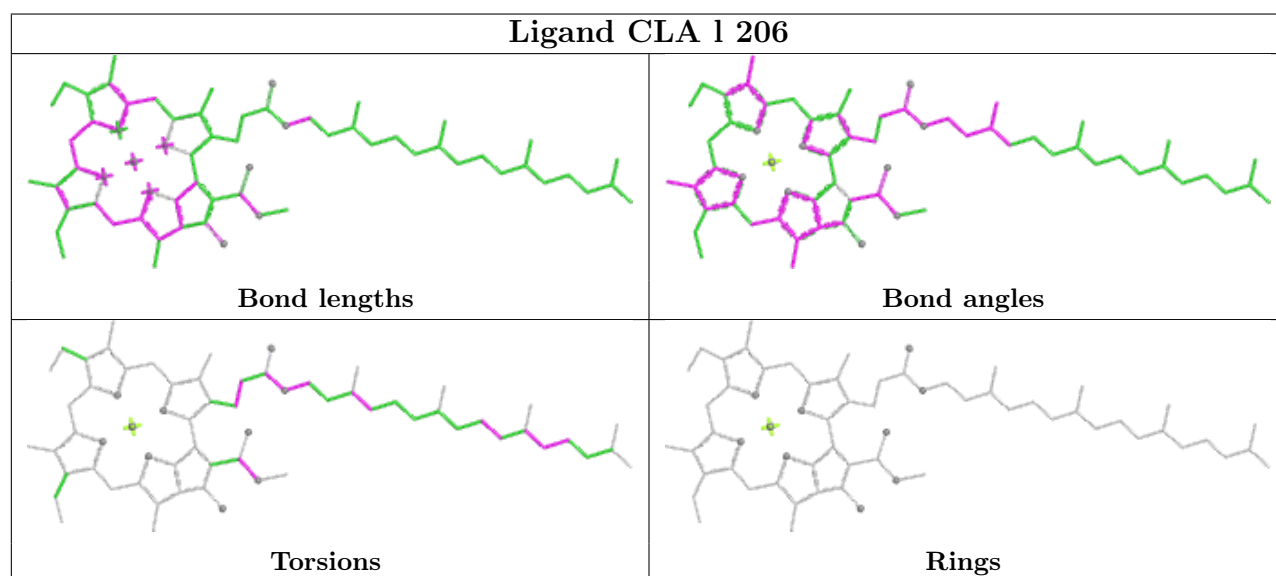
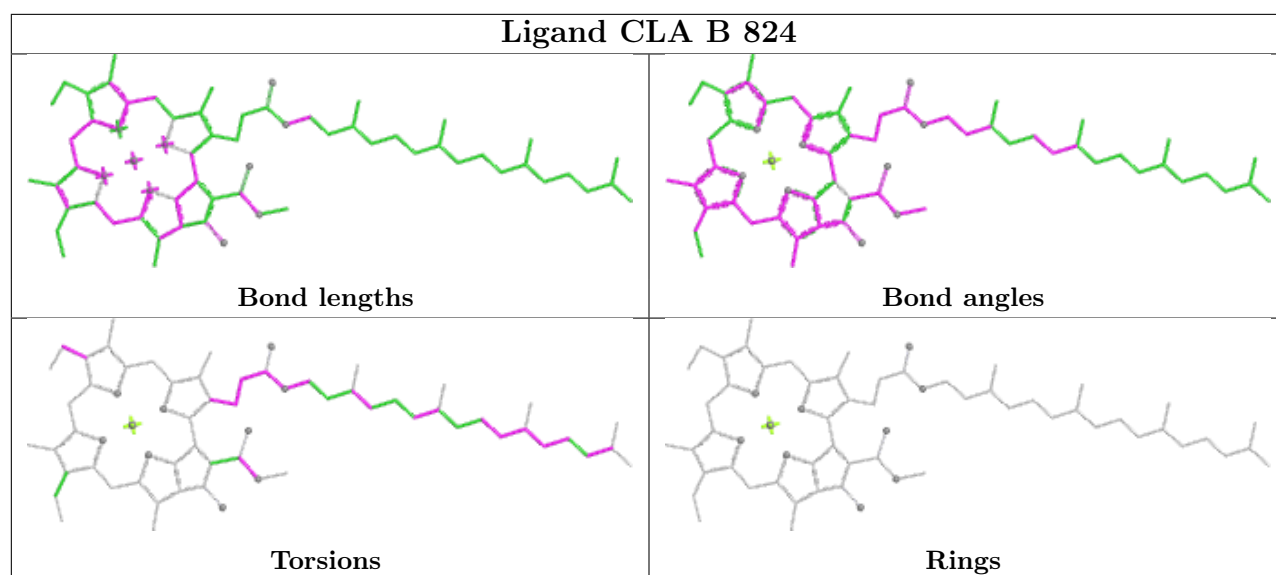


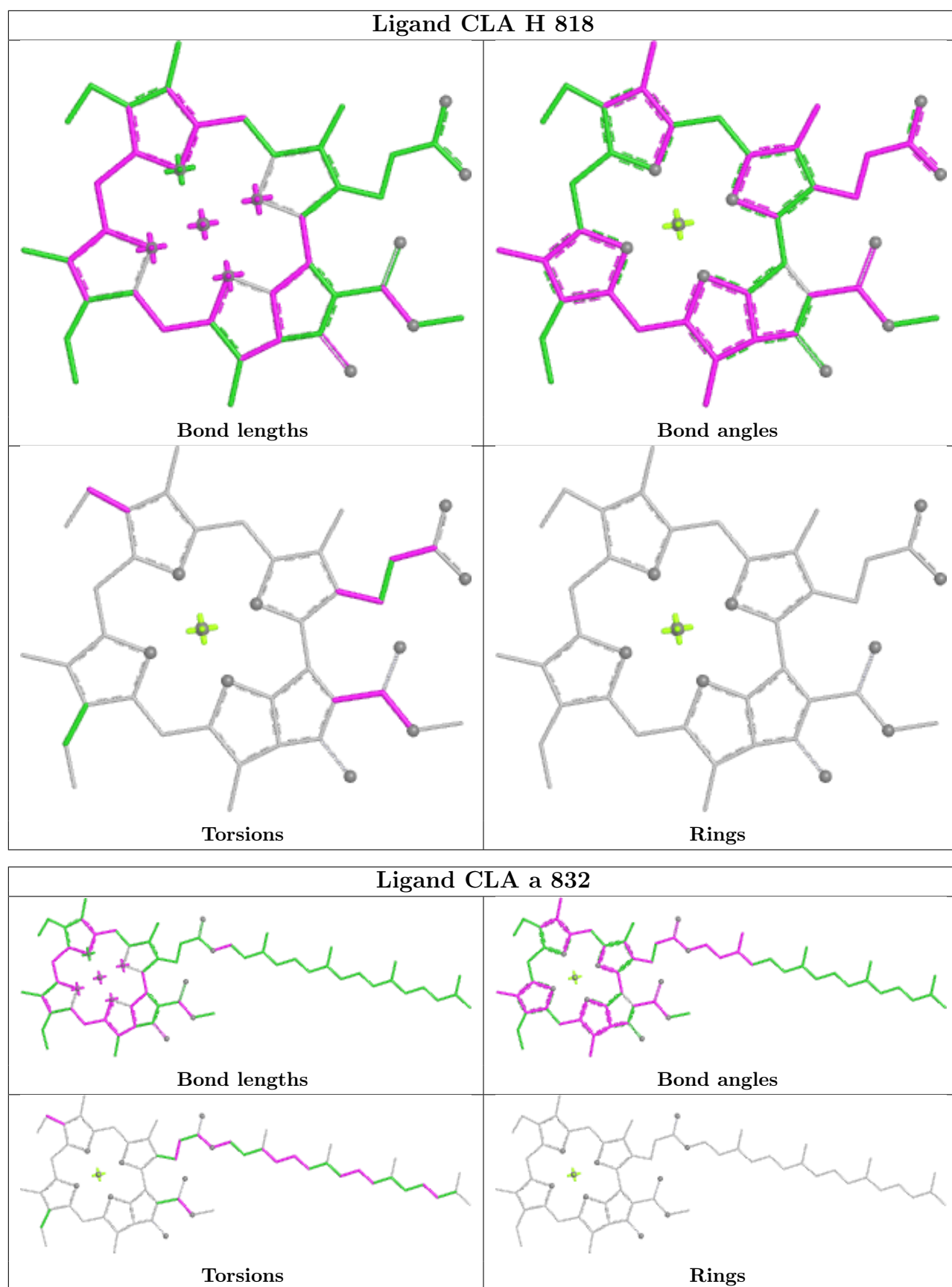
## Ligand CLA a 825

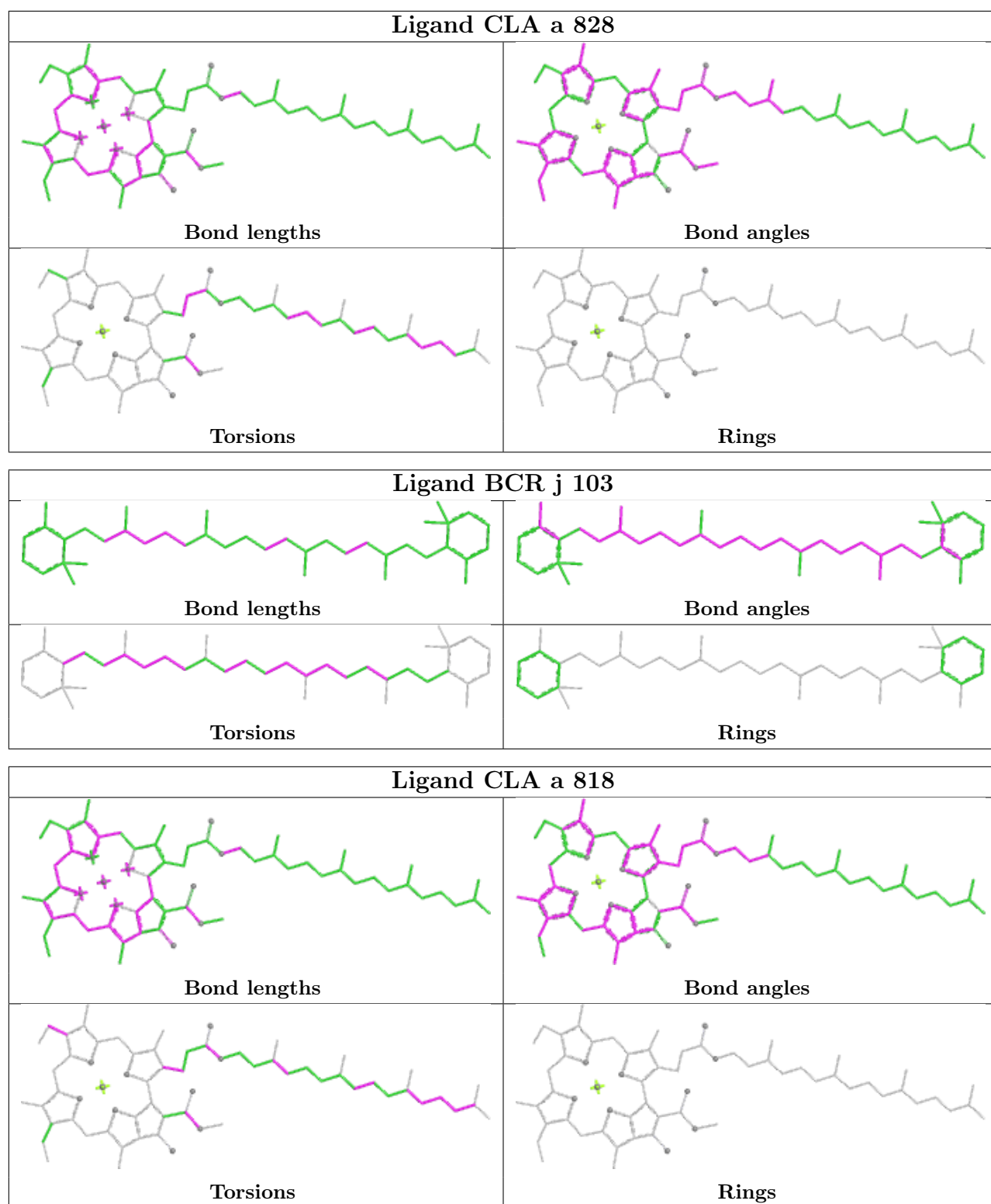


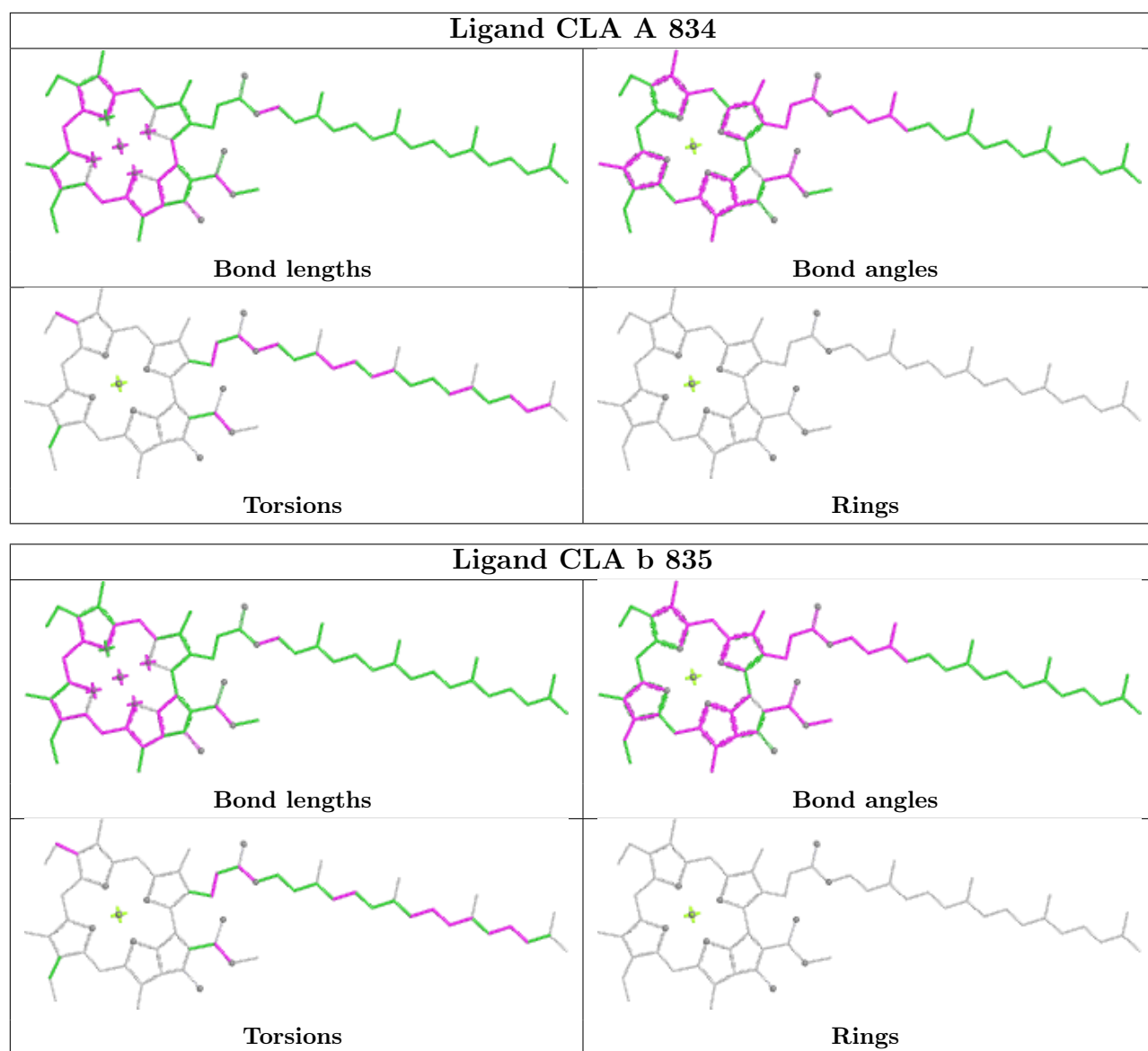
## Ligand CLA A 808



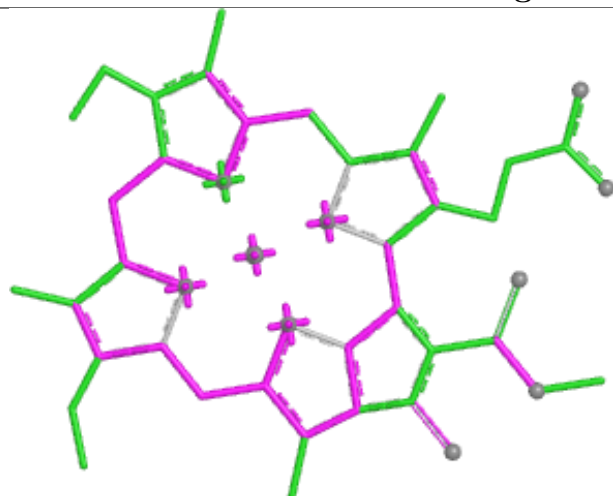




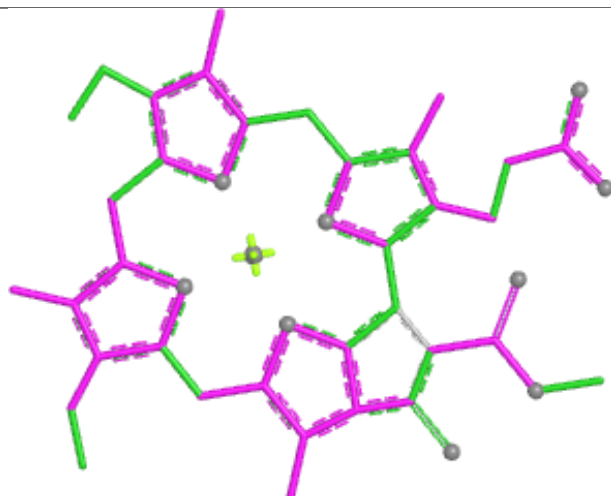




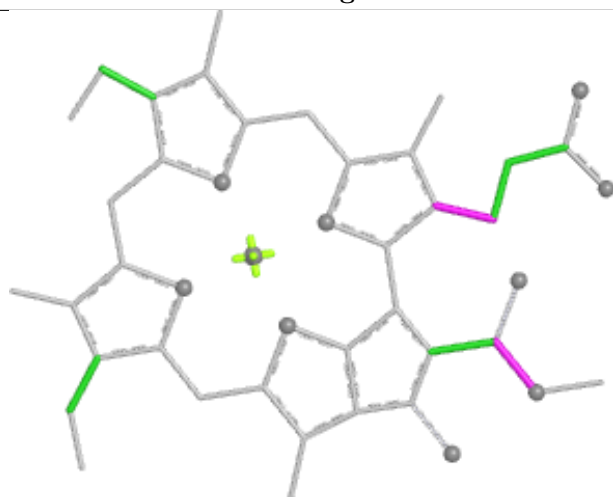
## Ligand CLA B 808



Bond lengths



Bond angles

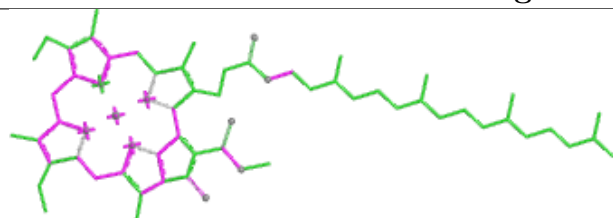


Torsions

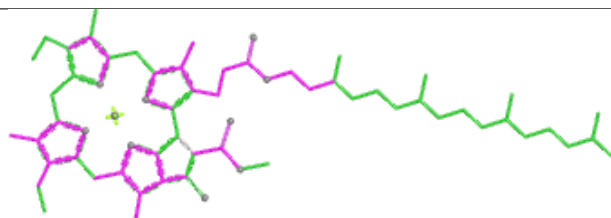


Rings

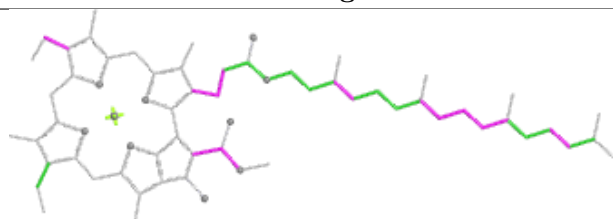
## Ligand CLA B 822



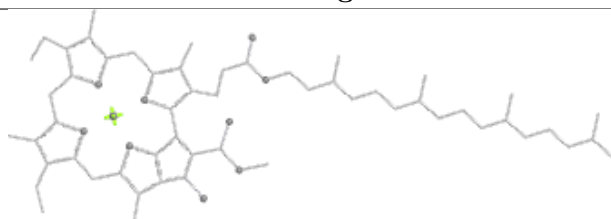
Bond lengths



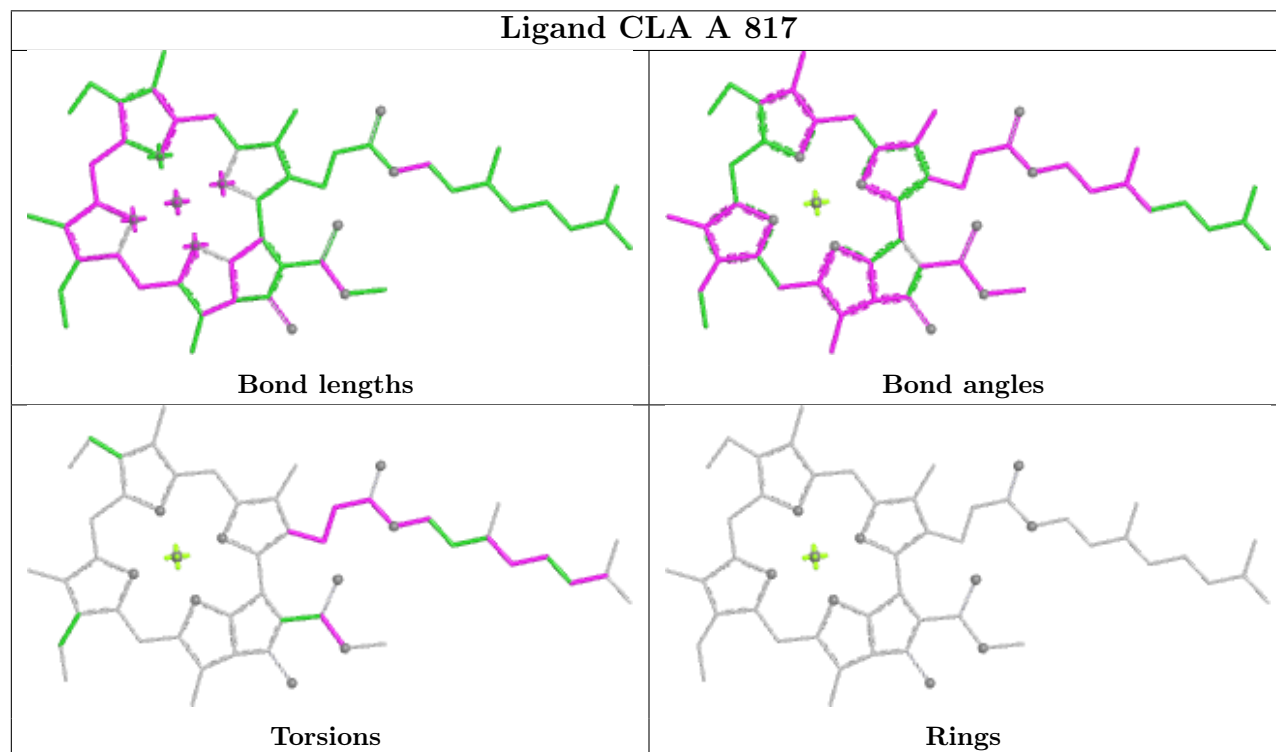
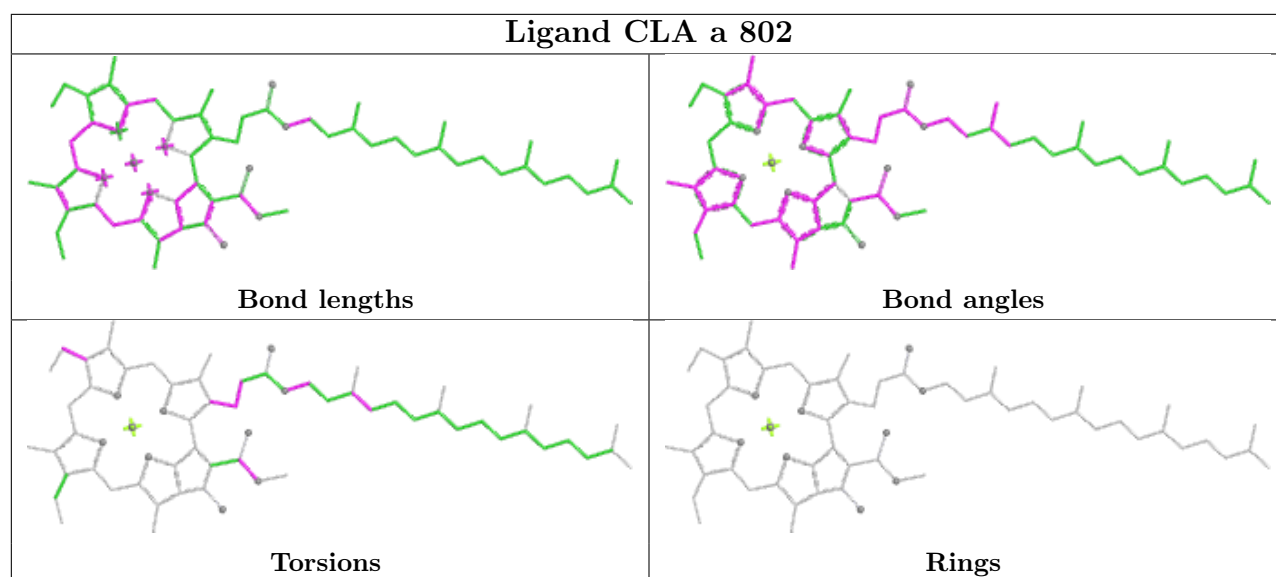
Bond angles

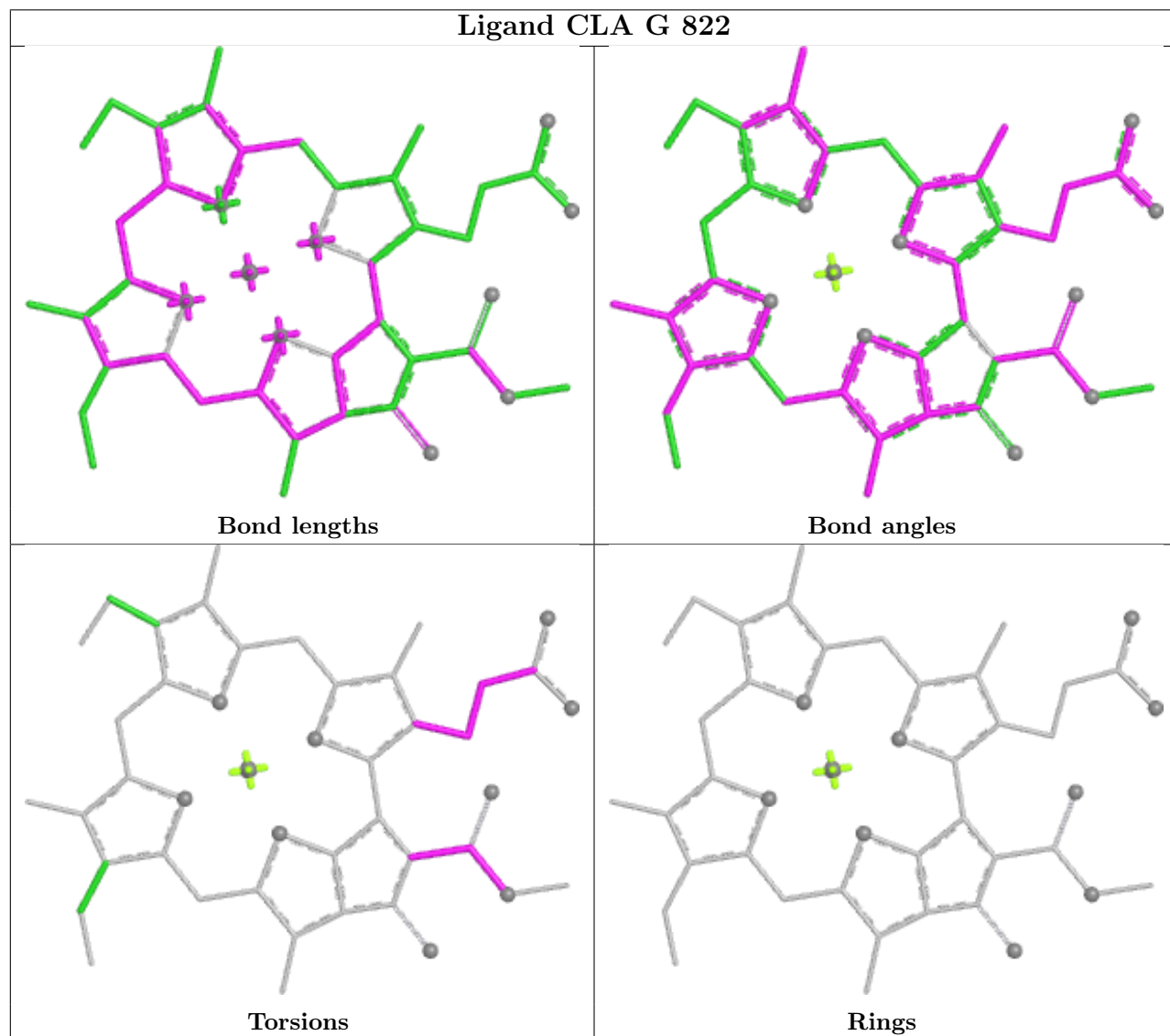
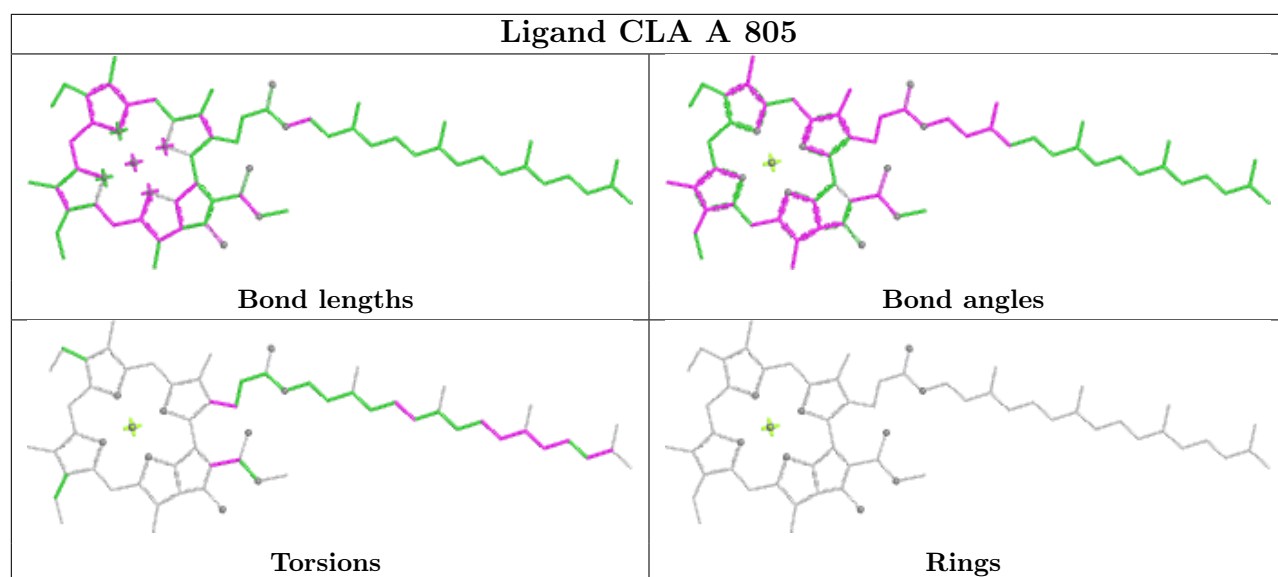


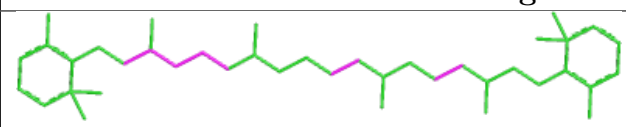
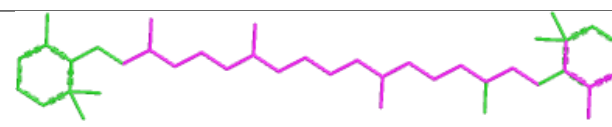
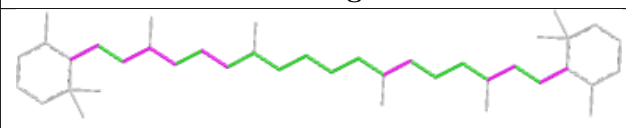
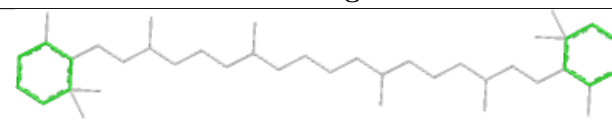
Torsions

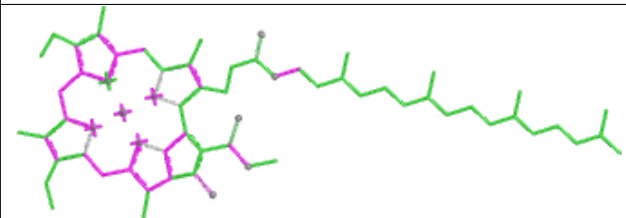
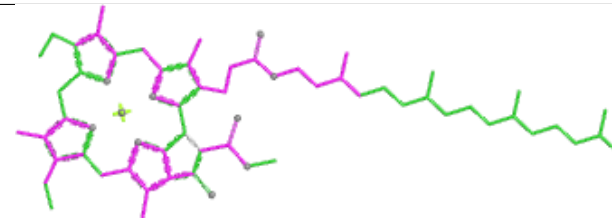
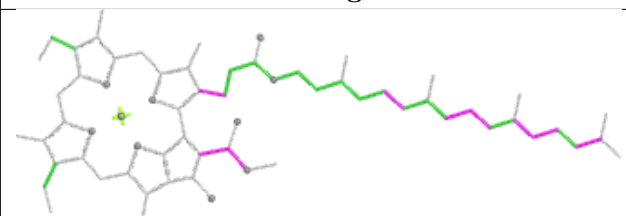
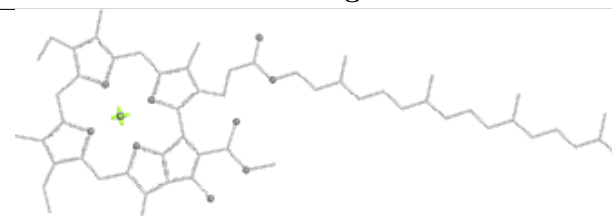


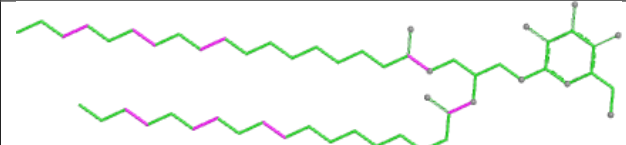
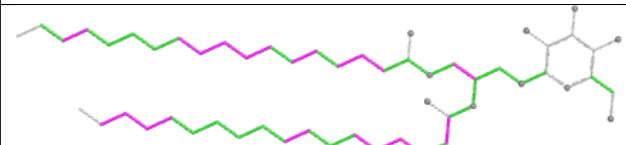
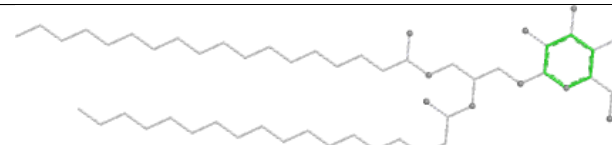
Rings

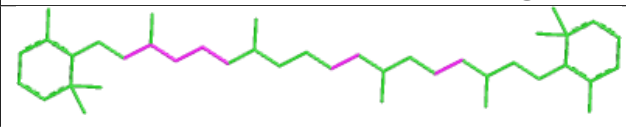
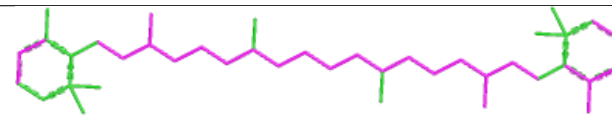
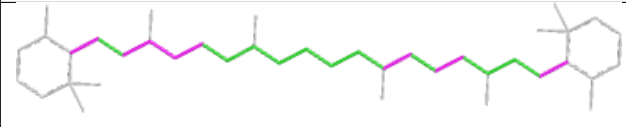
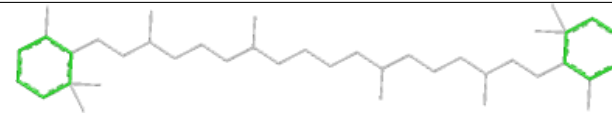


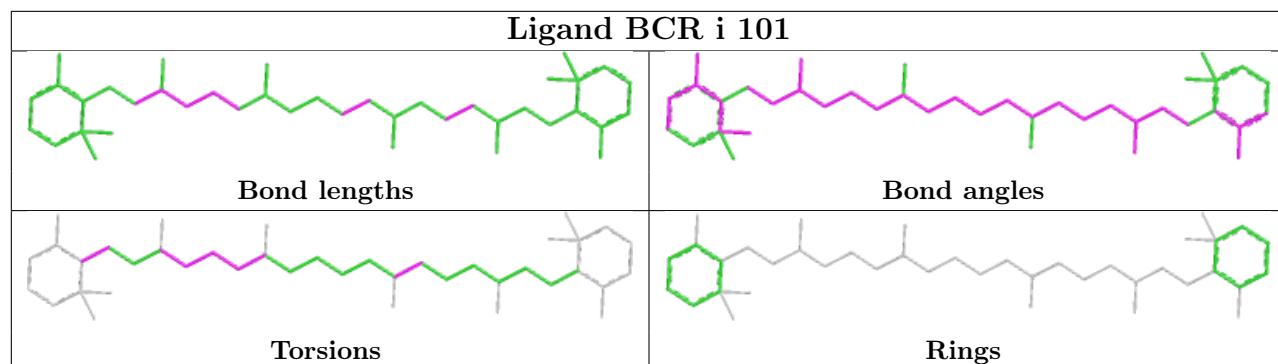
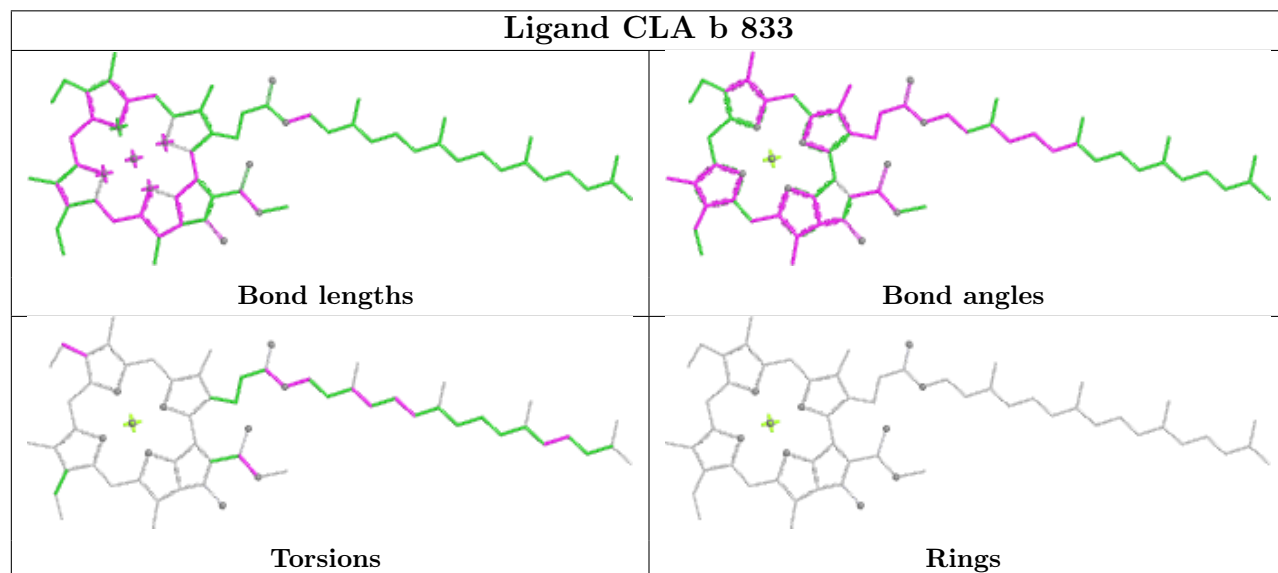
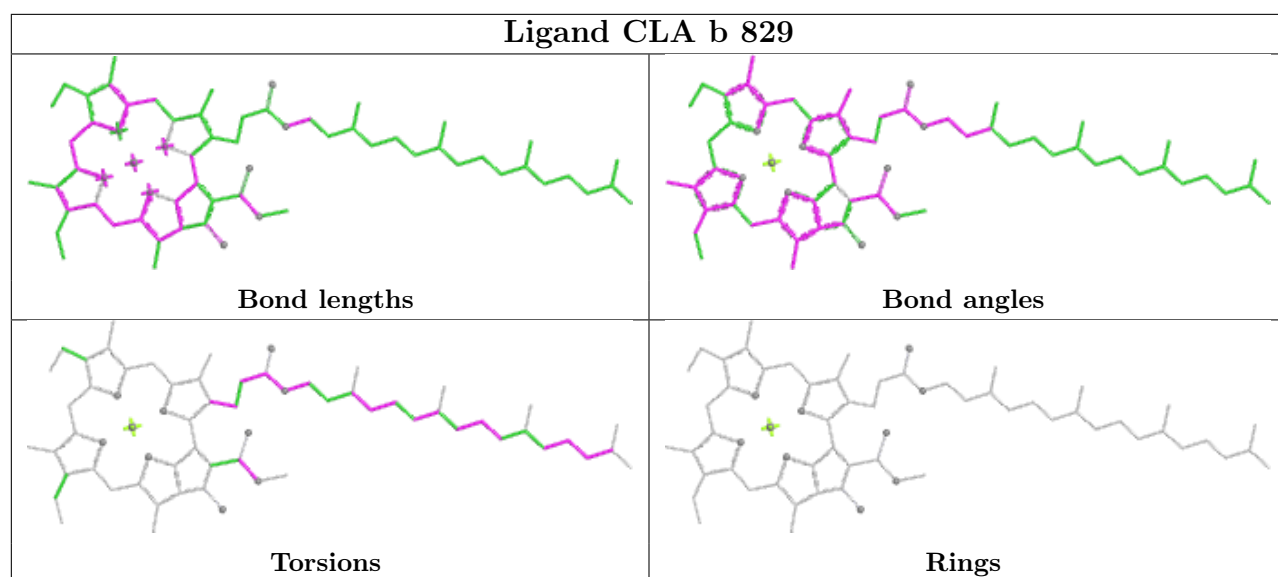


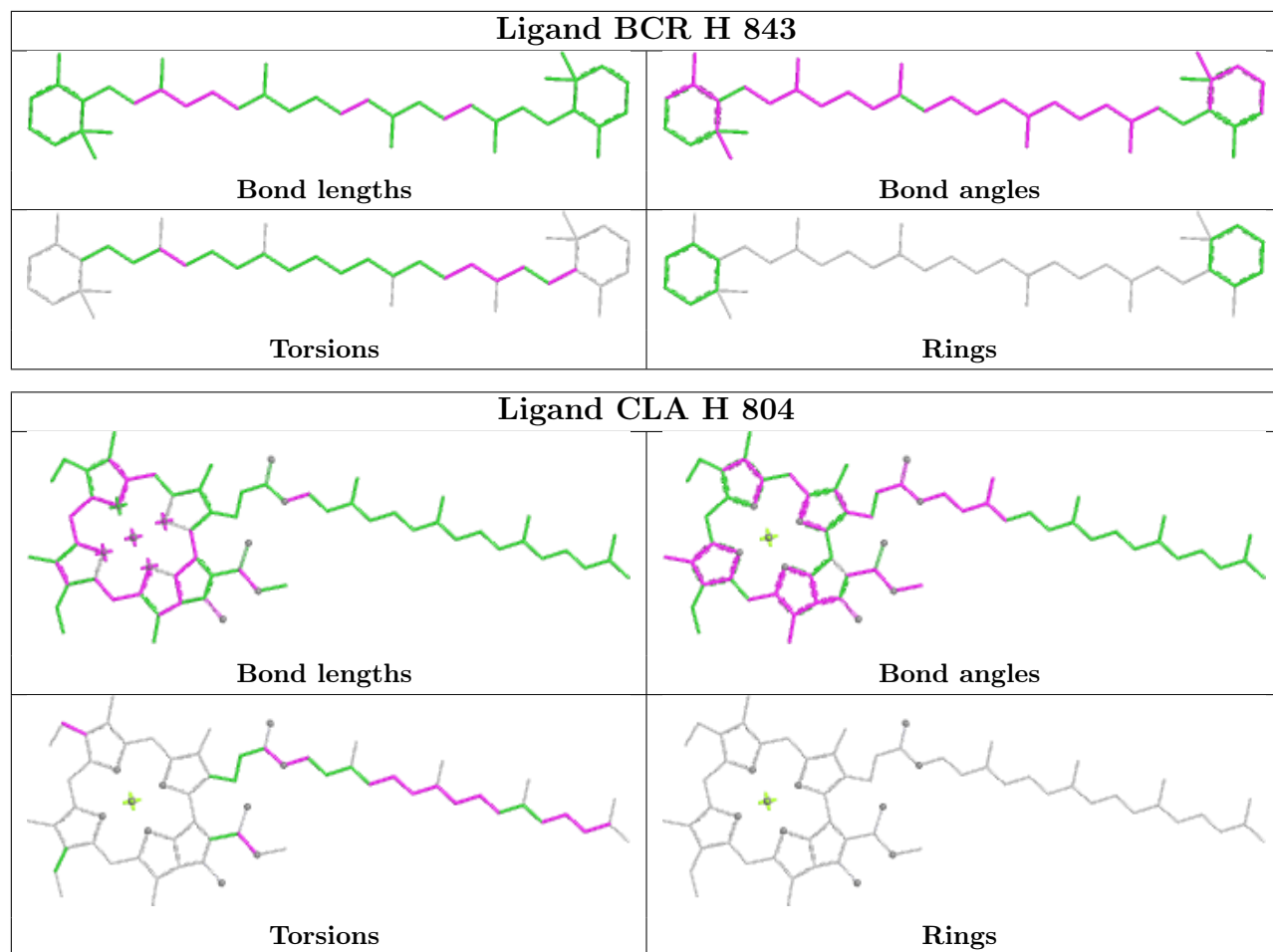
| Ligand BCR A 848                                                                                  |                                                                                                   |
|---------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|
| <br>Bond lengths | <br>Bond angles |
| <br>Torsions     | <br>Rings       |

| Ligand CLA a 805                                                                                  |                                                                                                   |
|---------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|
| <br>Bond lengths | <br>Bond angles |
| <br>Torsions    | <br>Rings      |

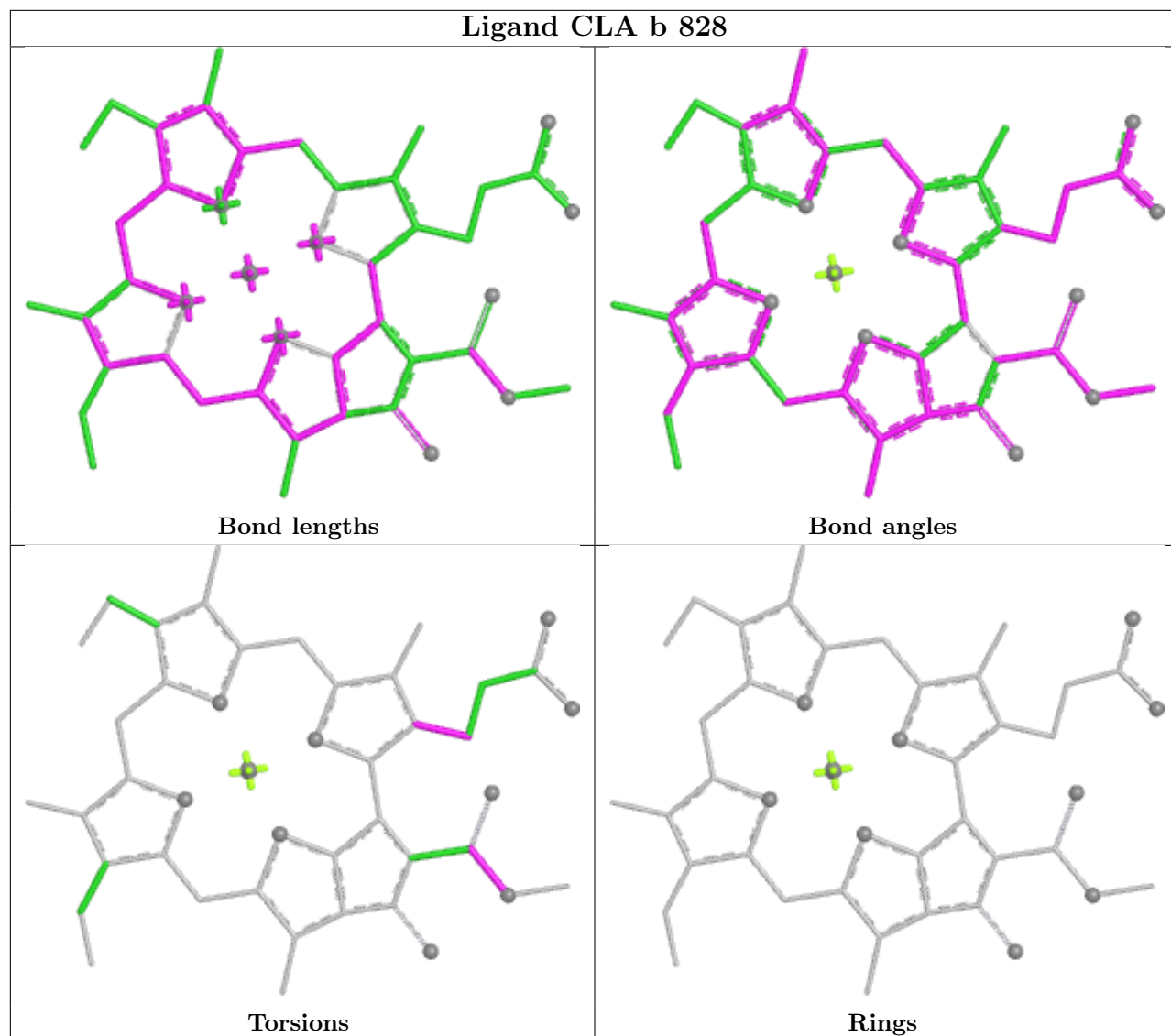
| Ligand LMG B 846                                                                                    |                                                                                                     |
|-----------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|
| <br>Bond lengths | <br>Bond angles |
| <br>Torsions     | <br>Rings       |

| Ligand BCR G 853                                                                                    |                                                                                                     |
|-----------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|
| <br>Bond lengths | <br>Bond angles |
| <br>Torsions     | <br>Rings       |

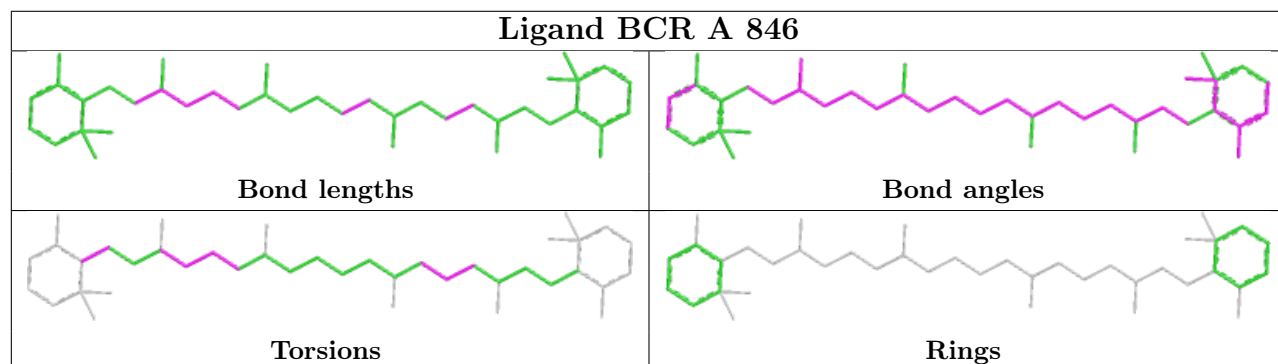


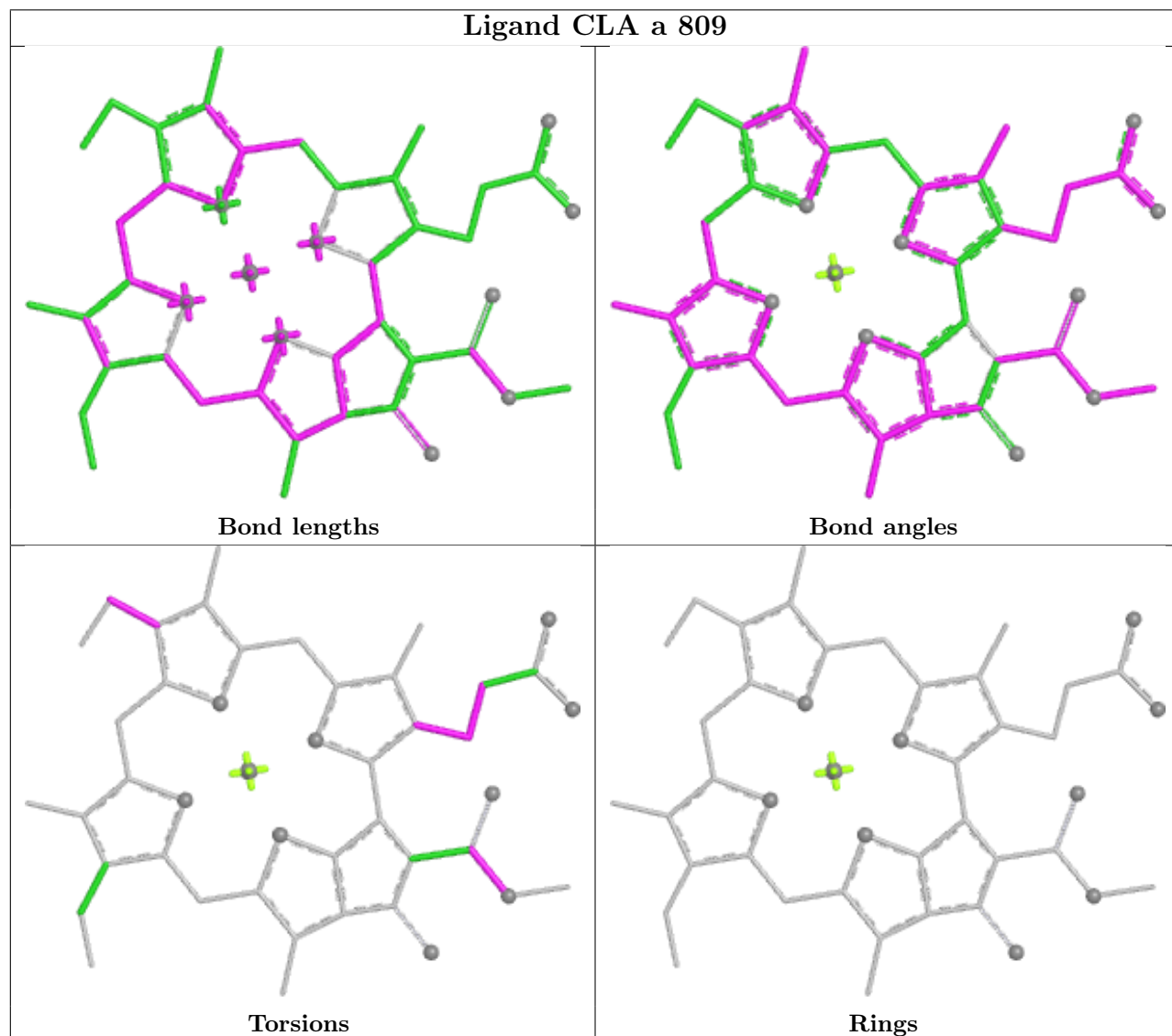
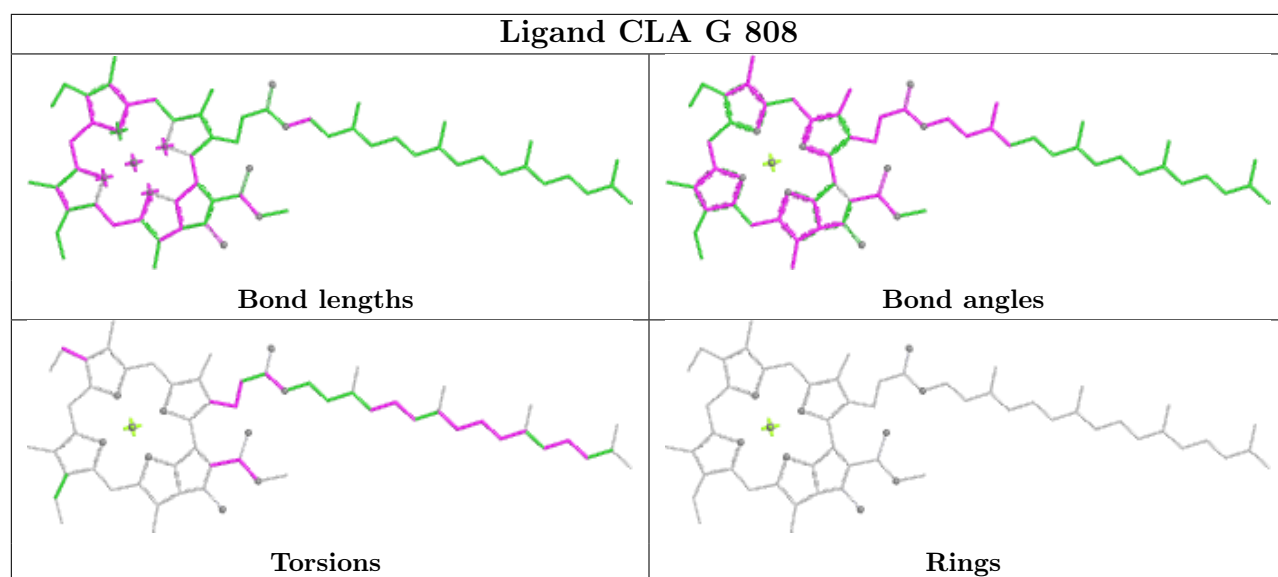


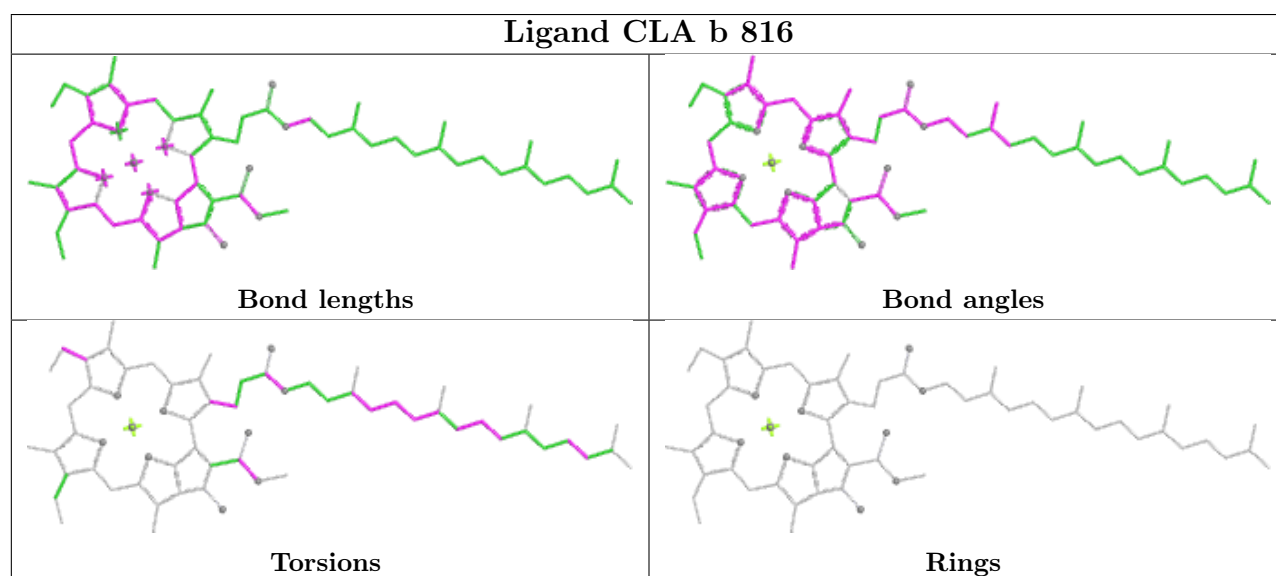
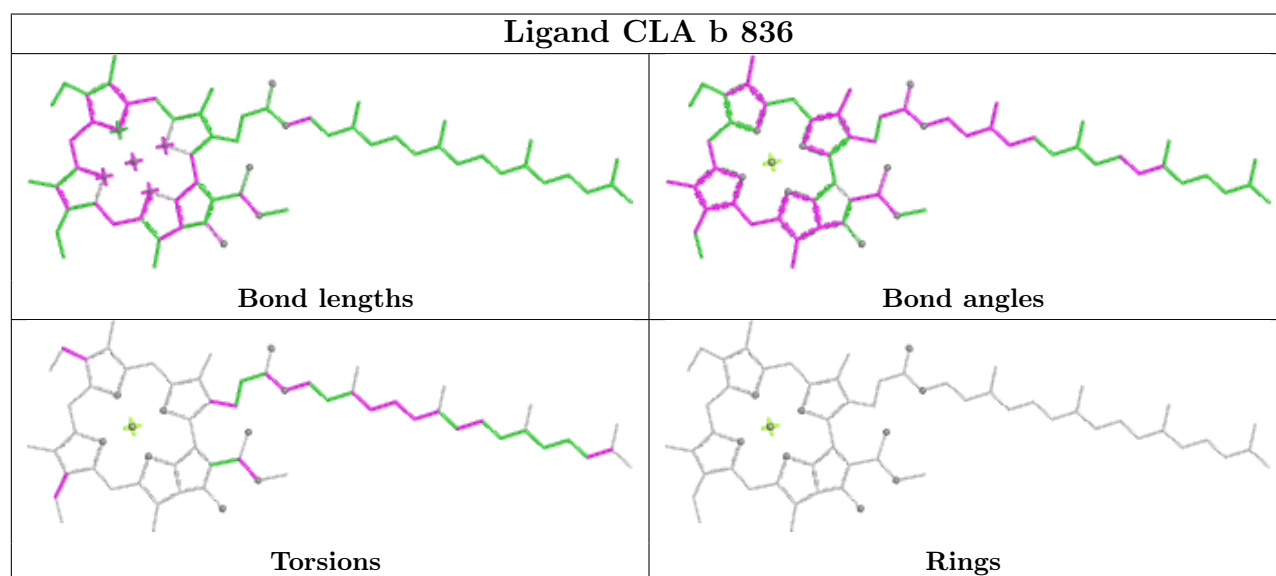
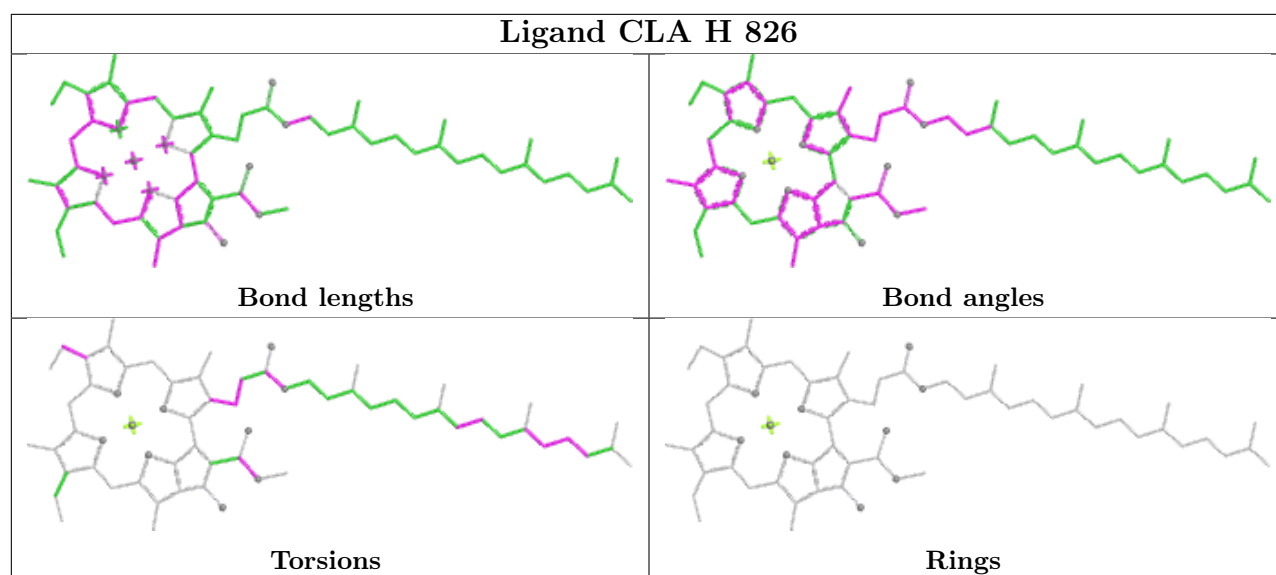
## Ligand CLA b 828

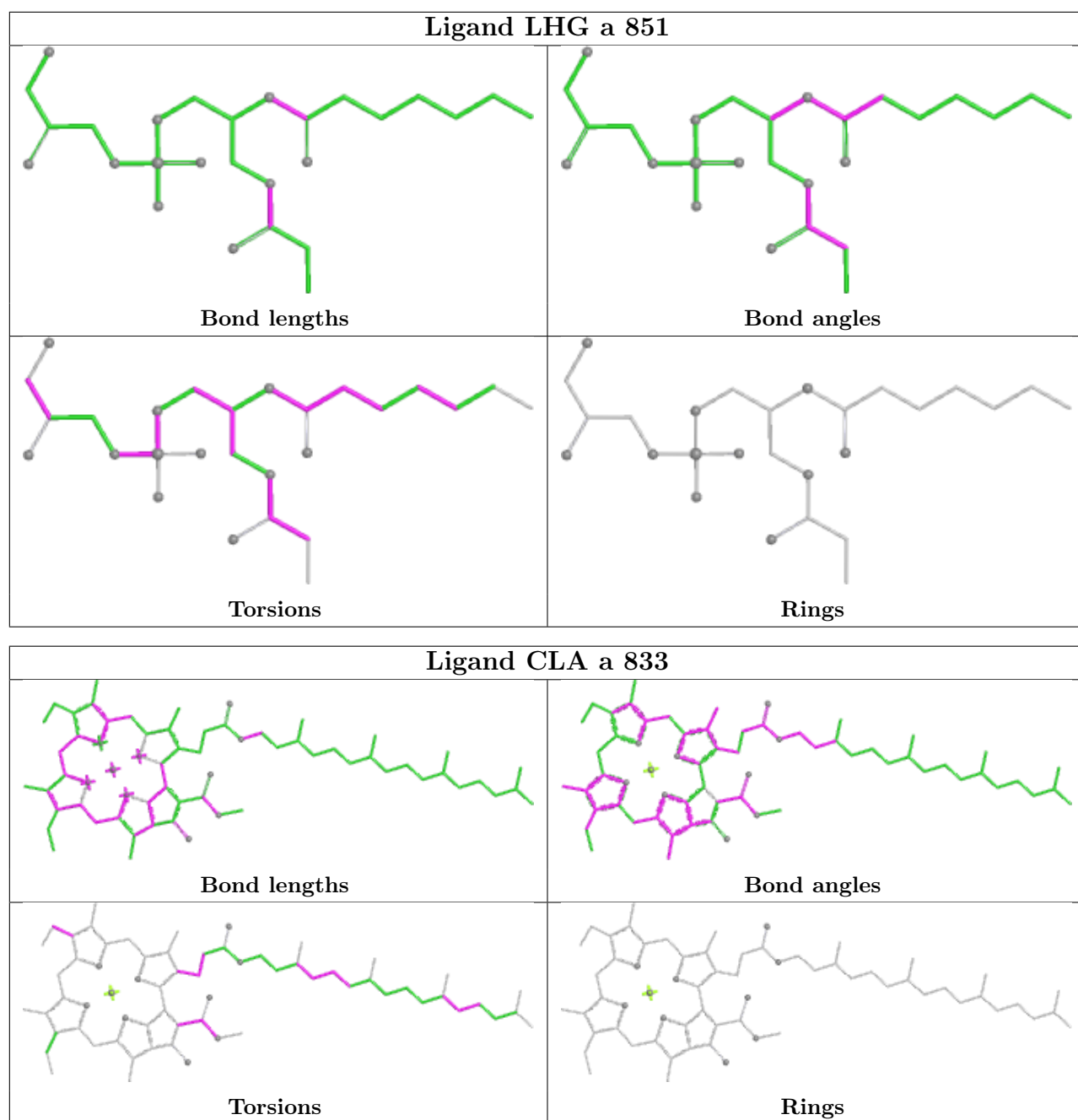


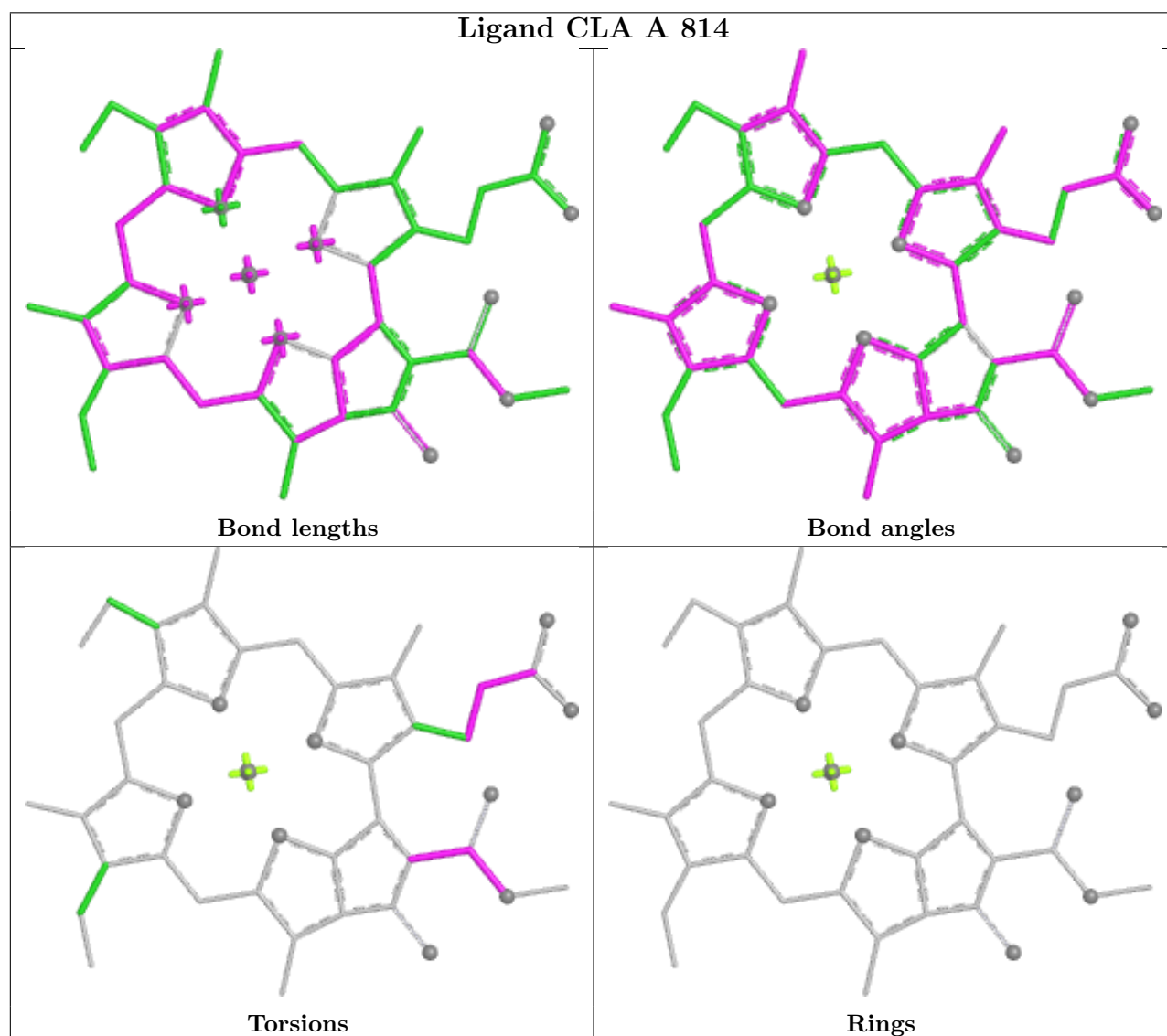
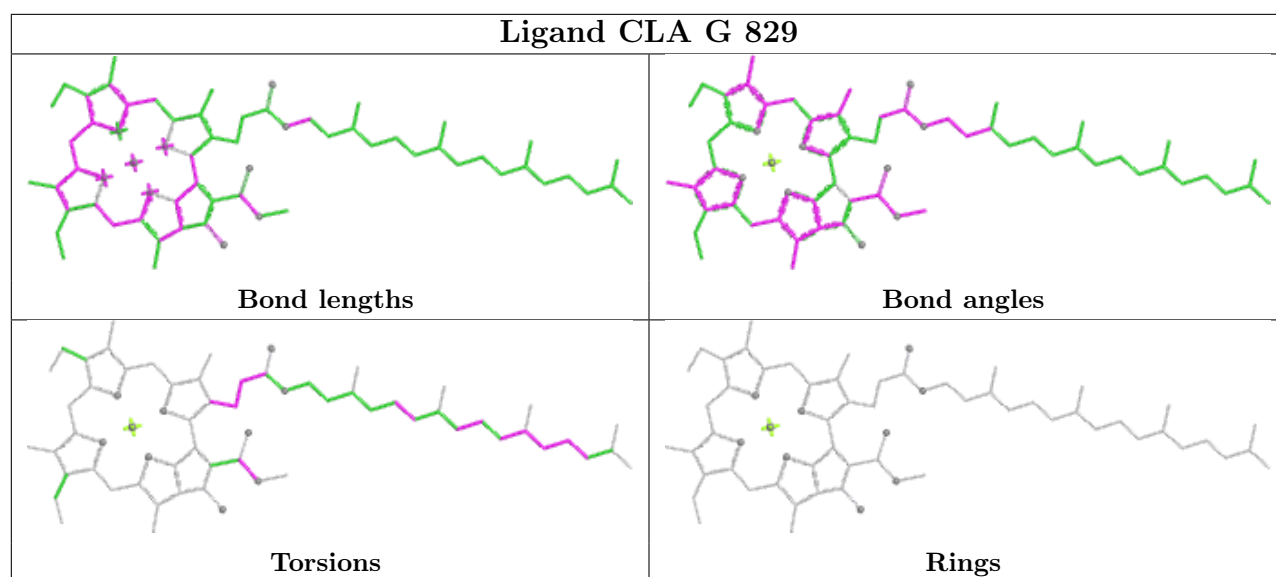
## Ligand BCR A 846

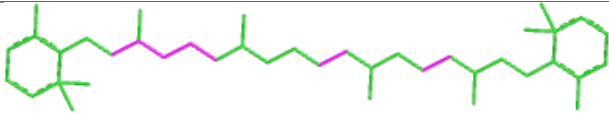
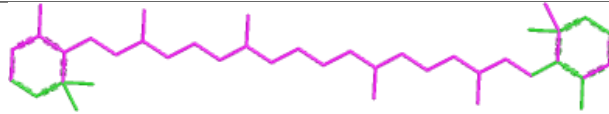
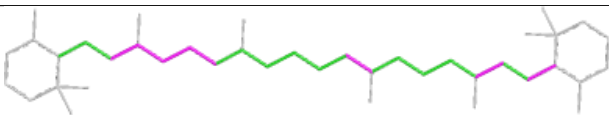
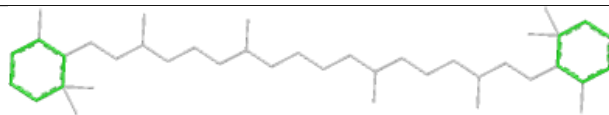


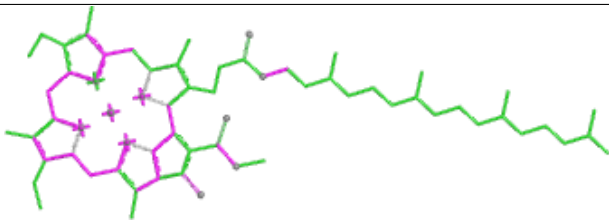
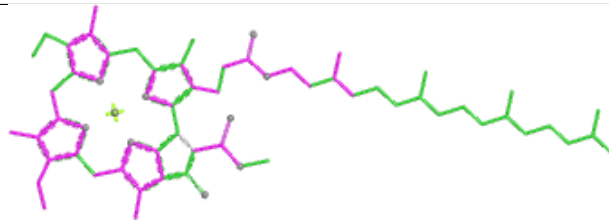
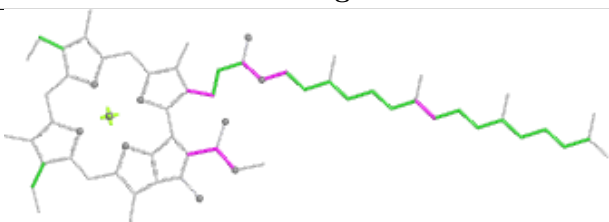
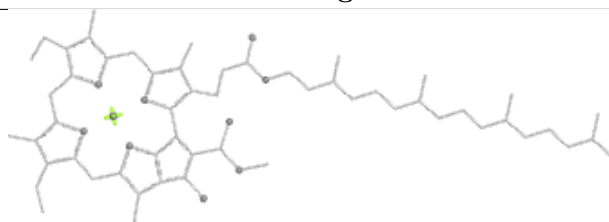


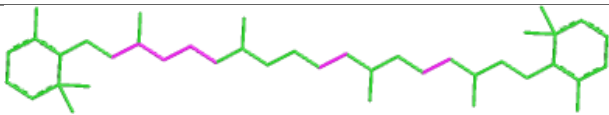
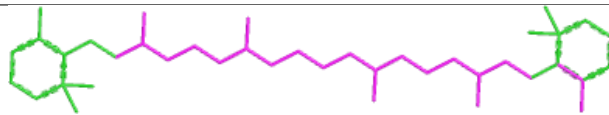
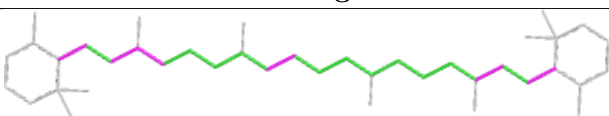
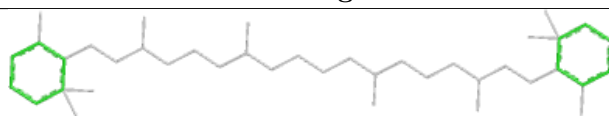




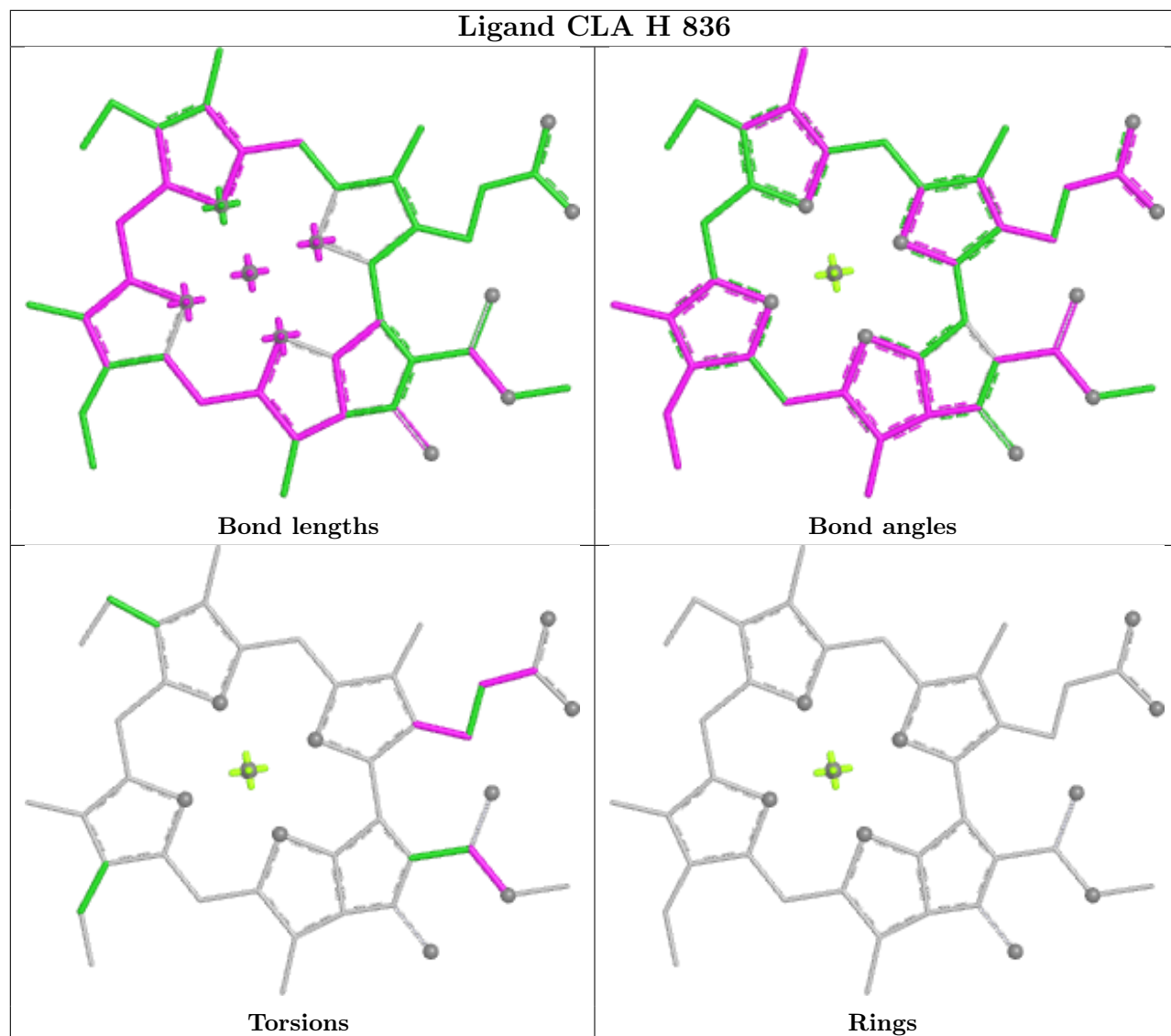


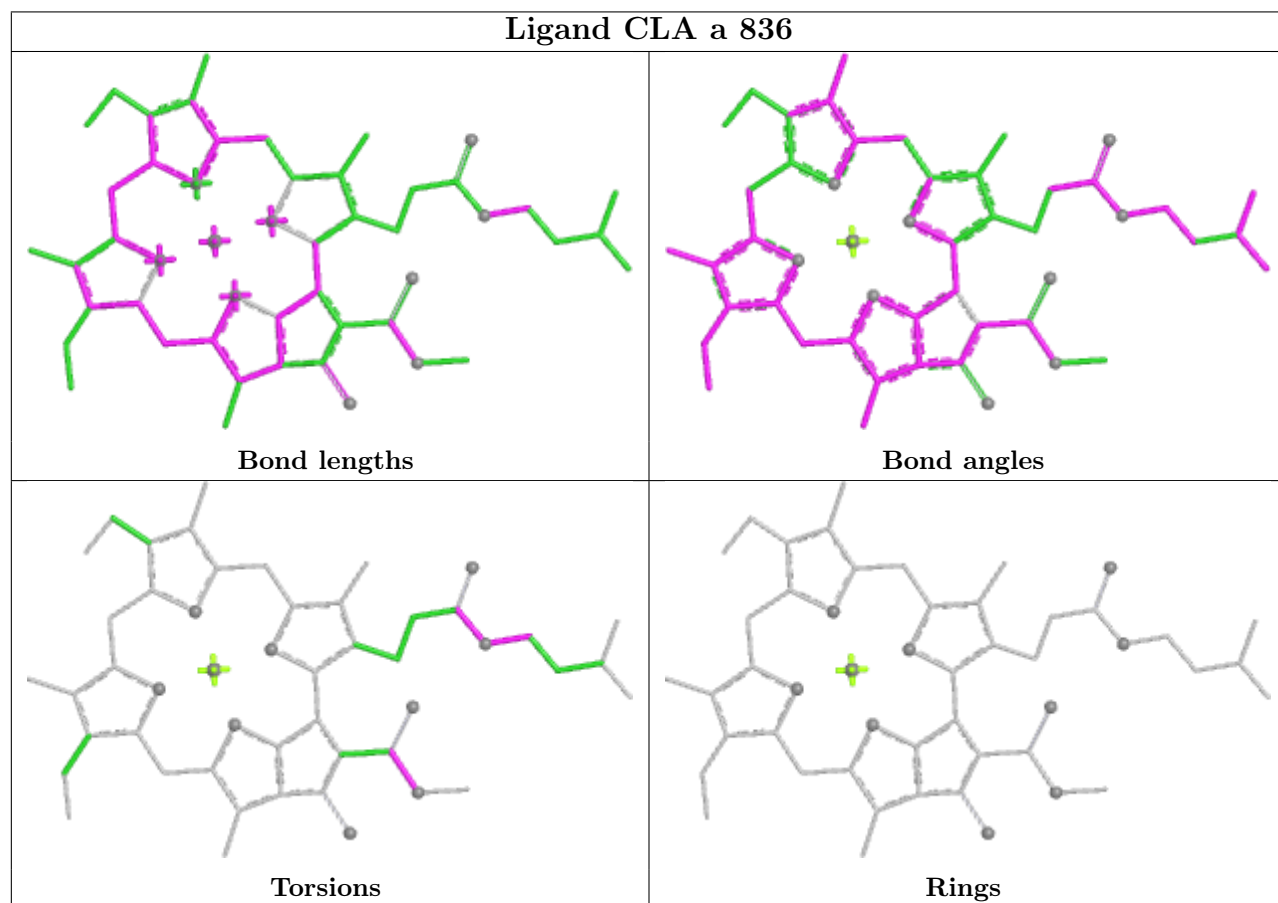
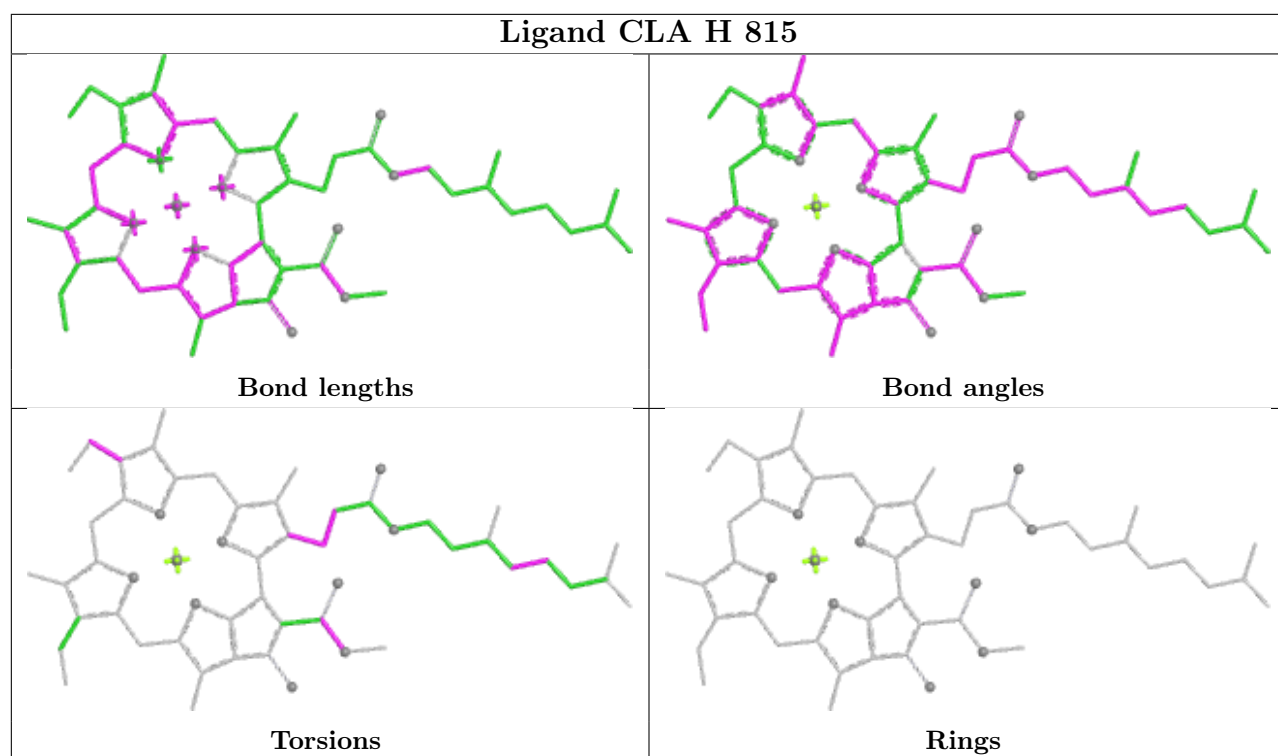
| Ligand BCR a 849                                                                  |                                                                                    |
|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                      | Bond angles                                                                        |
|  |  |
| Torsions                                                                          | Rings                                                                              |

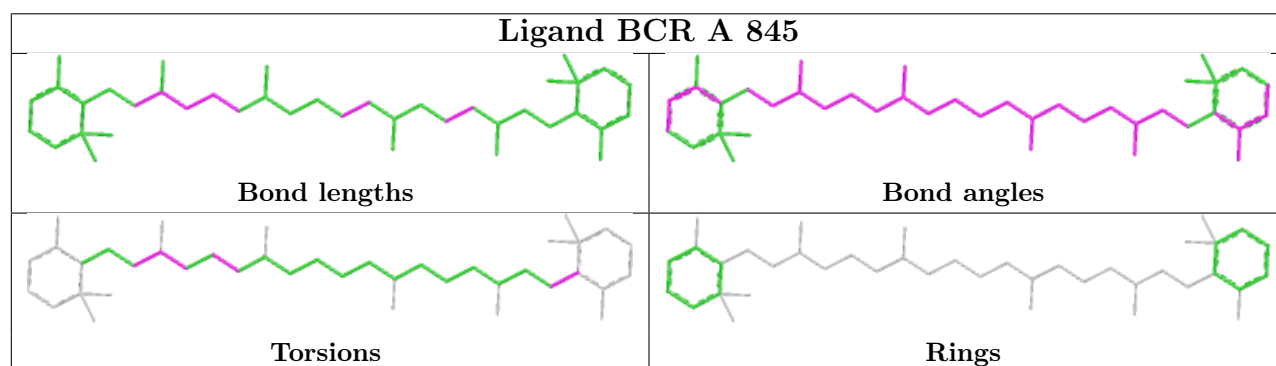
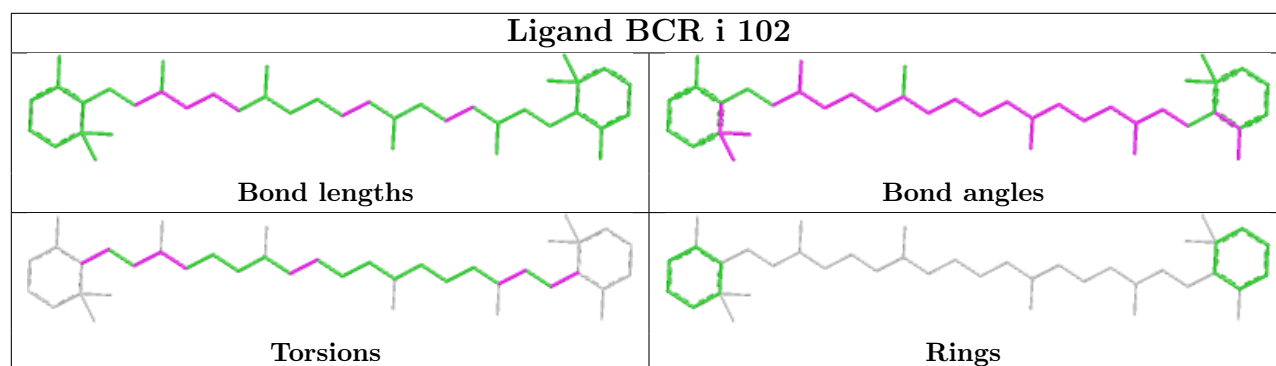
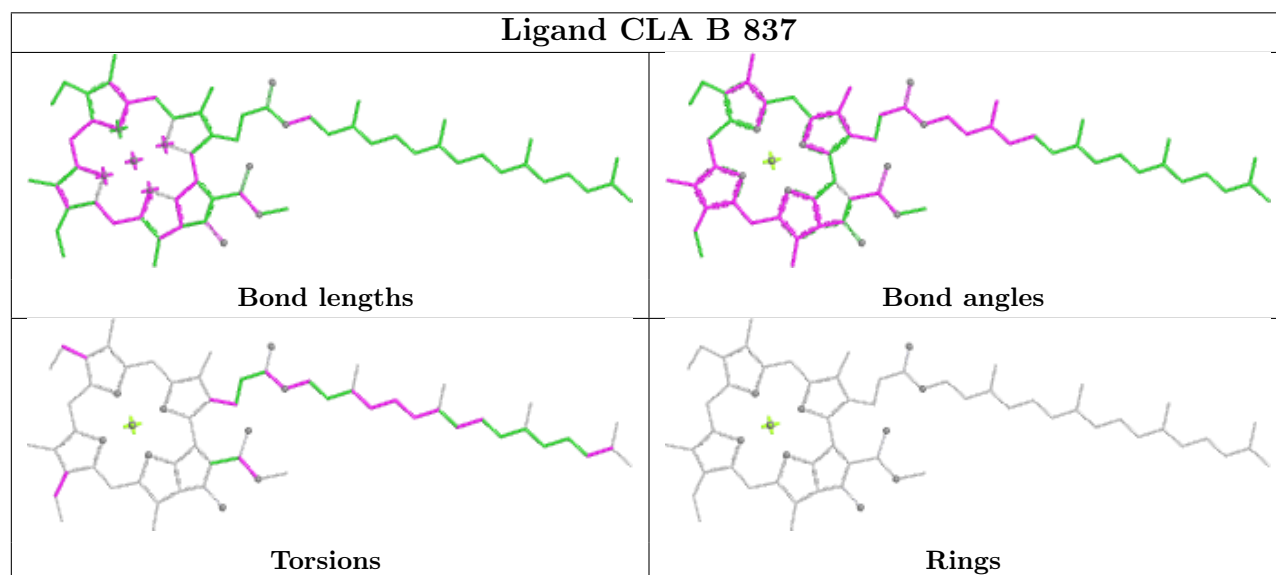
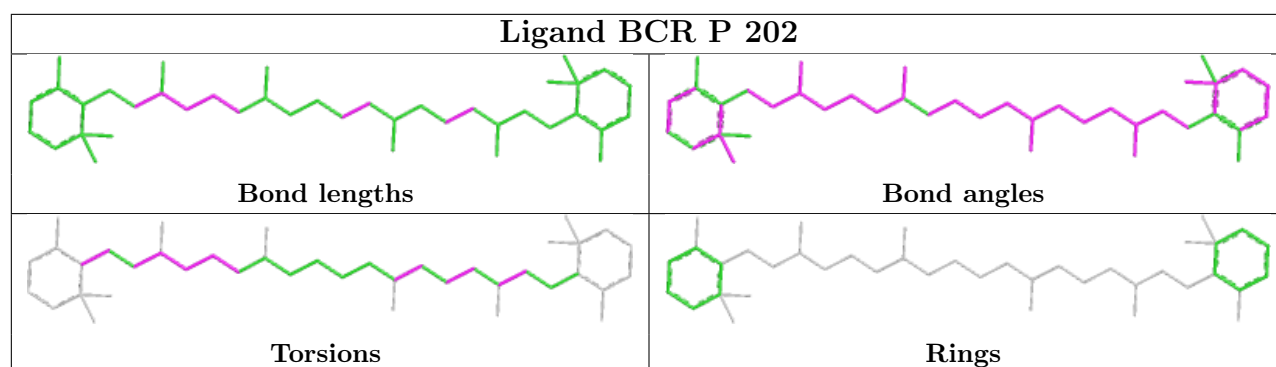
| Ligand CLA a 829                                                                   |                                                                                     |
|------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|
|   |   |
| Bond lengths                                                                       | Bond angles                                                                         |
|  |  |
| Torsions                                                                           | Rings                                                                               |

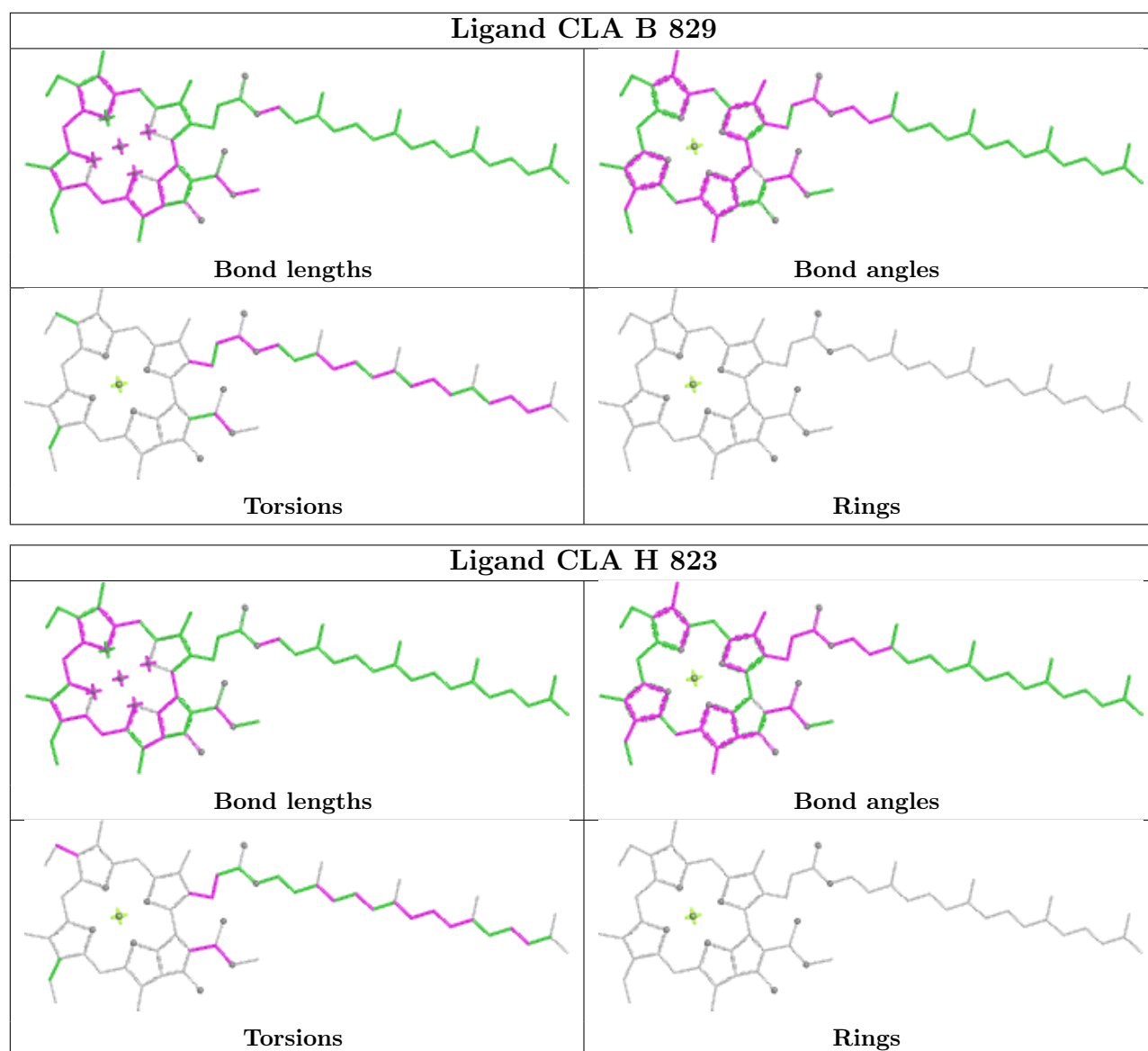
| Ligand BCR Q 102                                                                    |                                                                                      |
|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
|  |  |
| Bond lengths                                                                        | Bond angles                                                                          |
|  |  |
| Torsions                                                                            | Rings                                                                                |

## Ligand CLA H 836

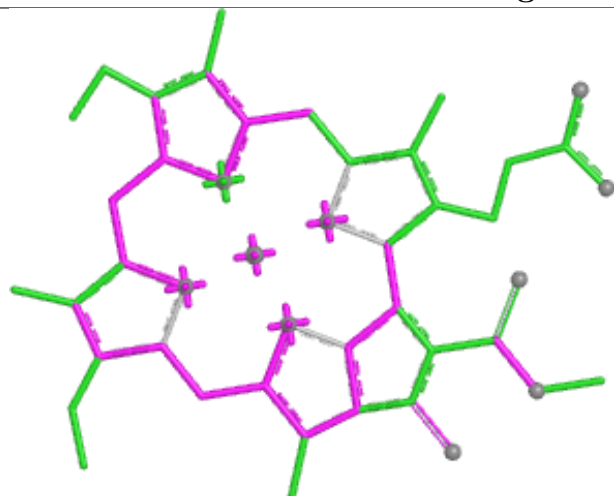




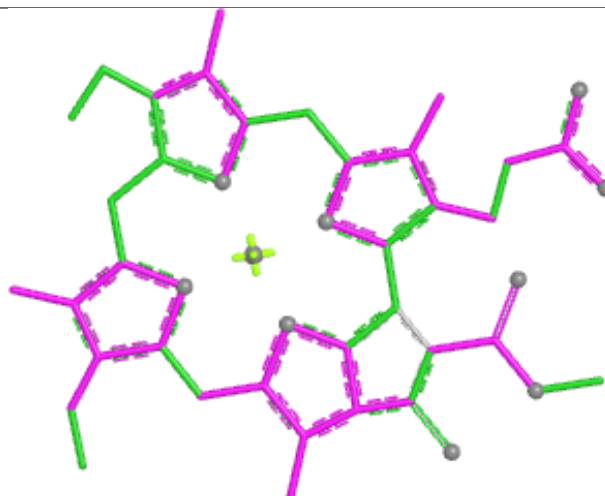




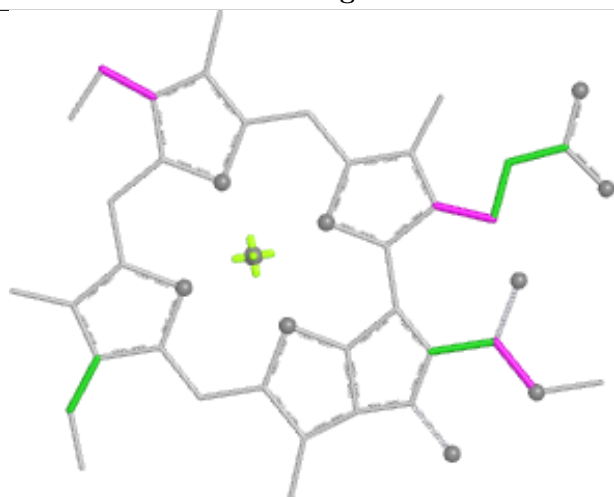
## Ligand CLA b 818



Bond lengths



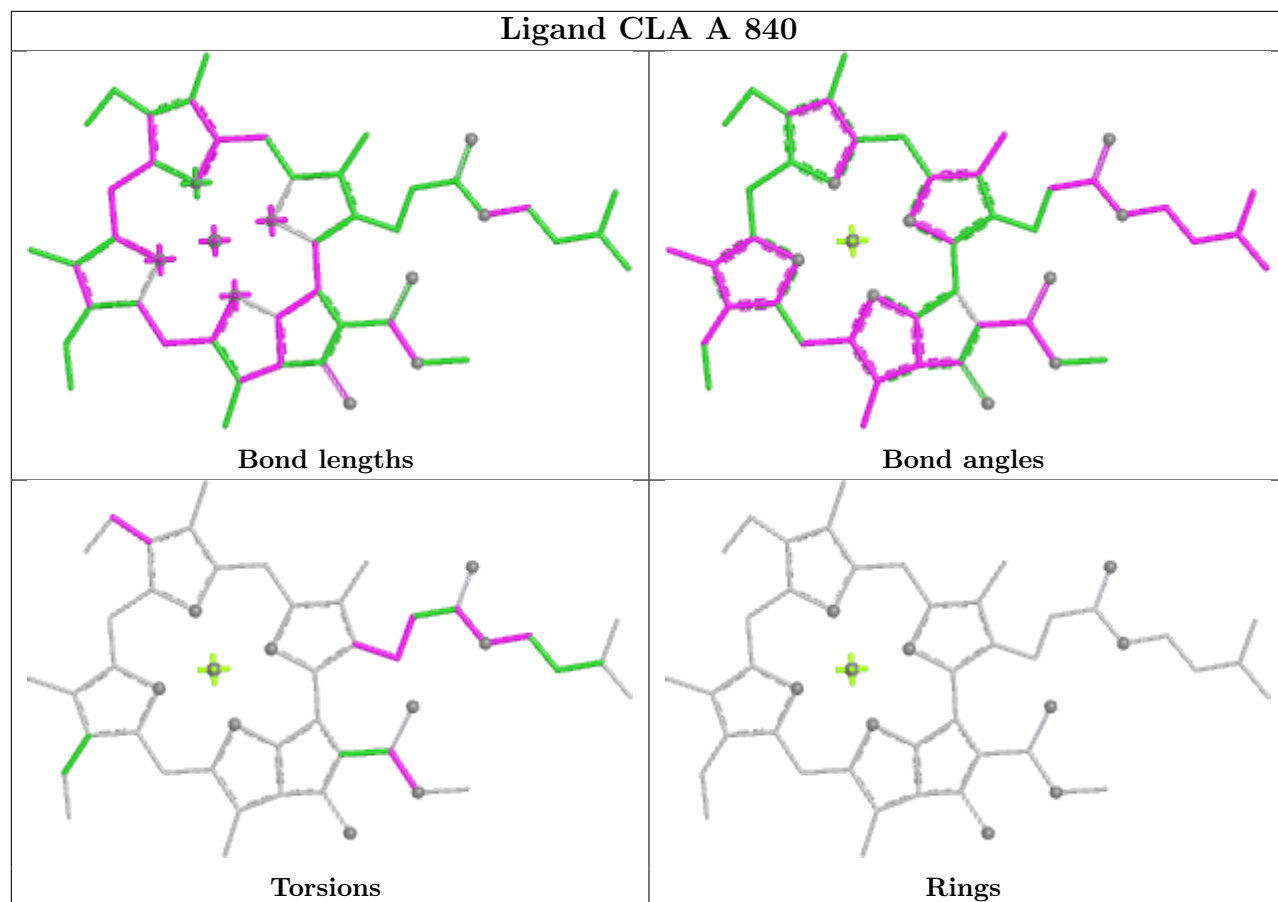
Bond angles



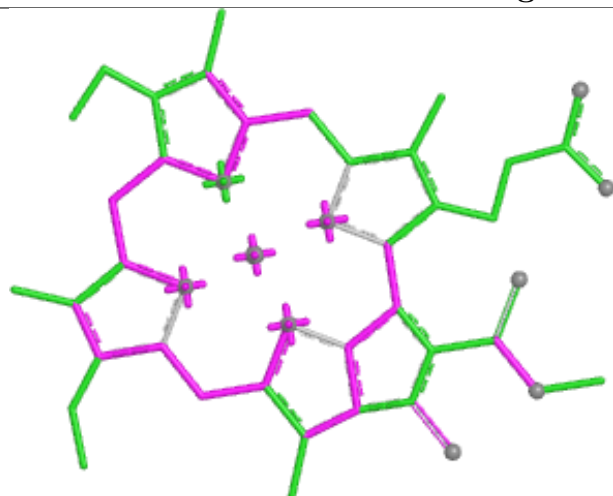
Torsions



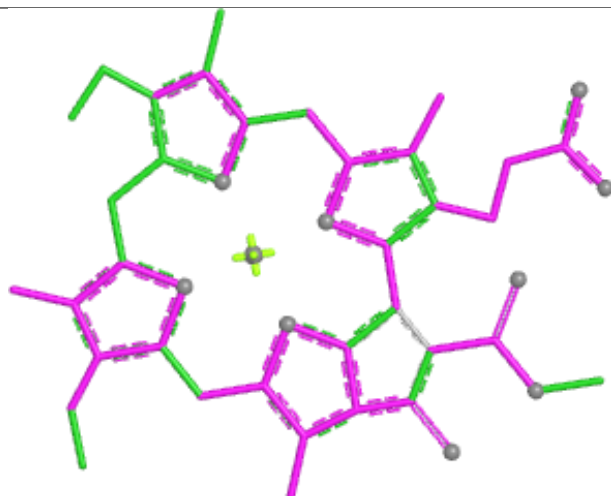
Rings



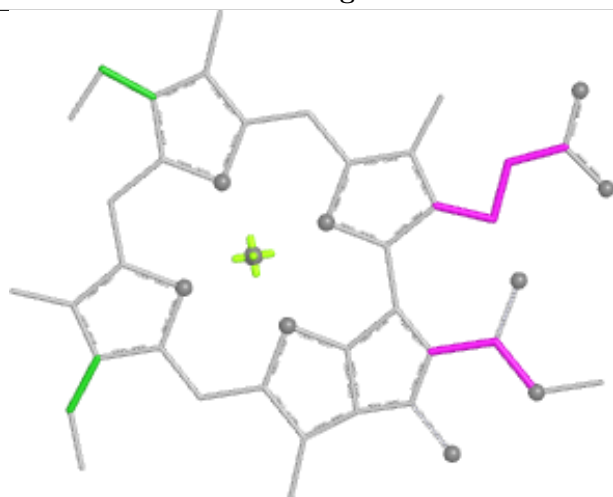
## Ligand CLA b 812



Bond lengths



Bond angles

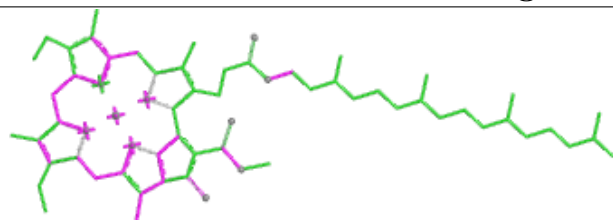


Torsions

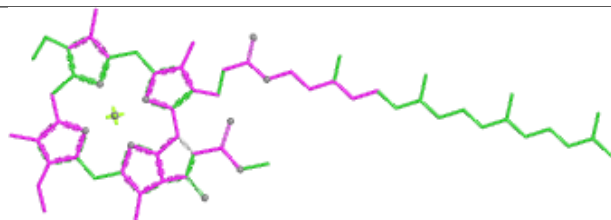


Rings

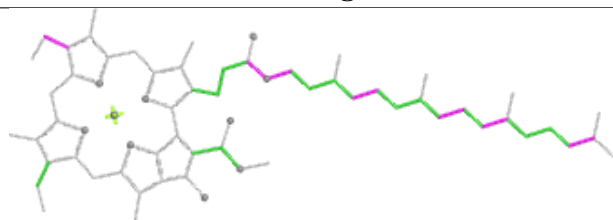
## Ligand CL0 G 801



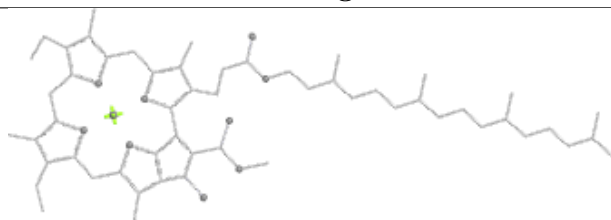
Bond lengths



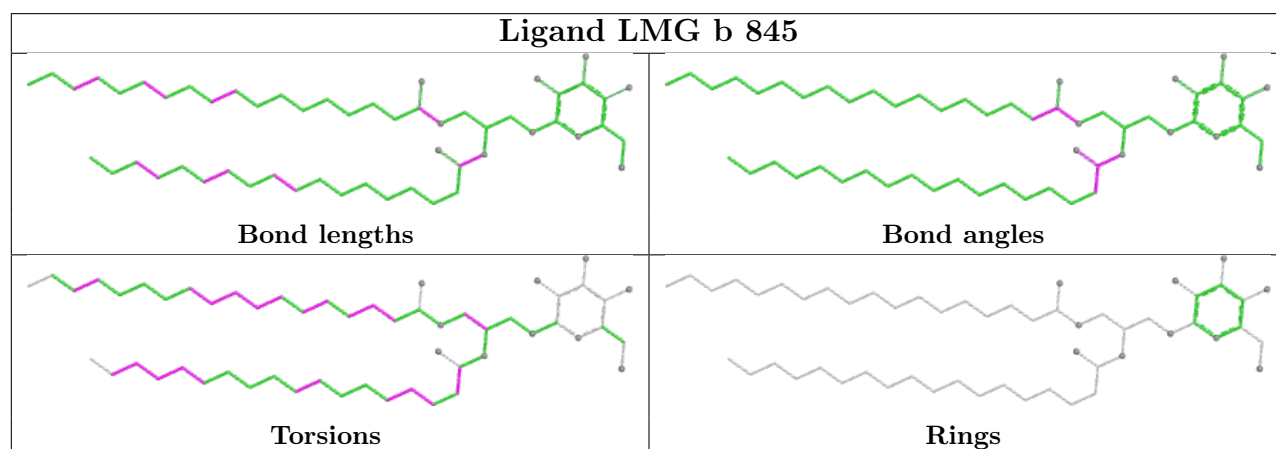
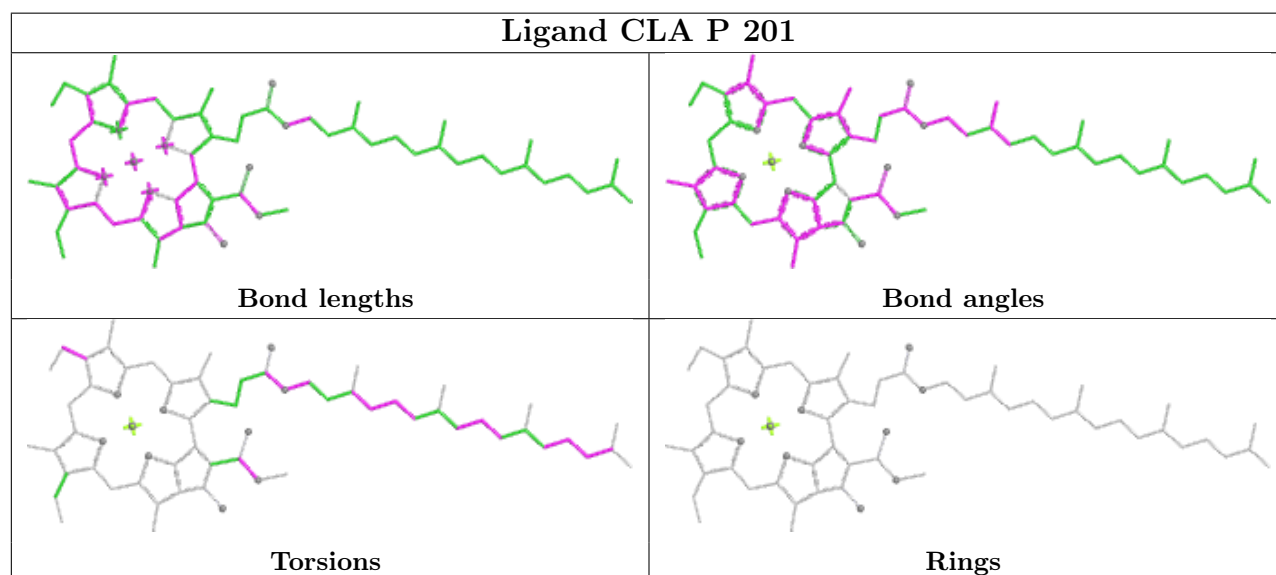
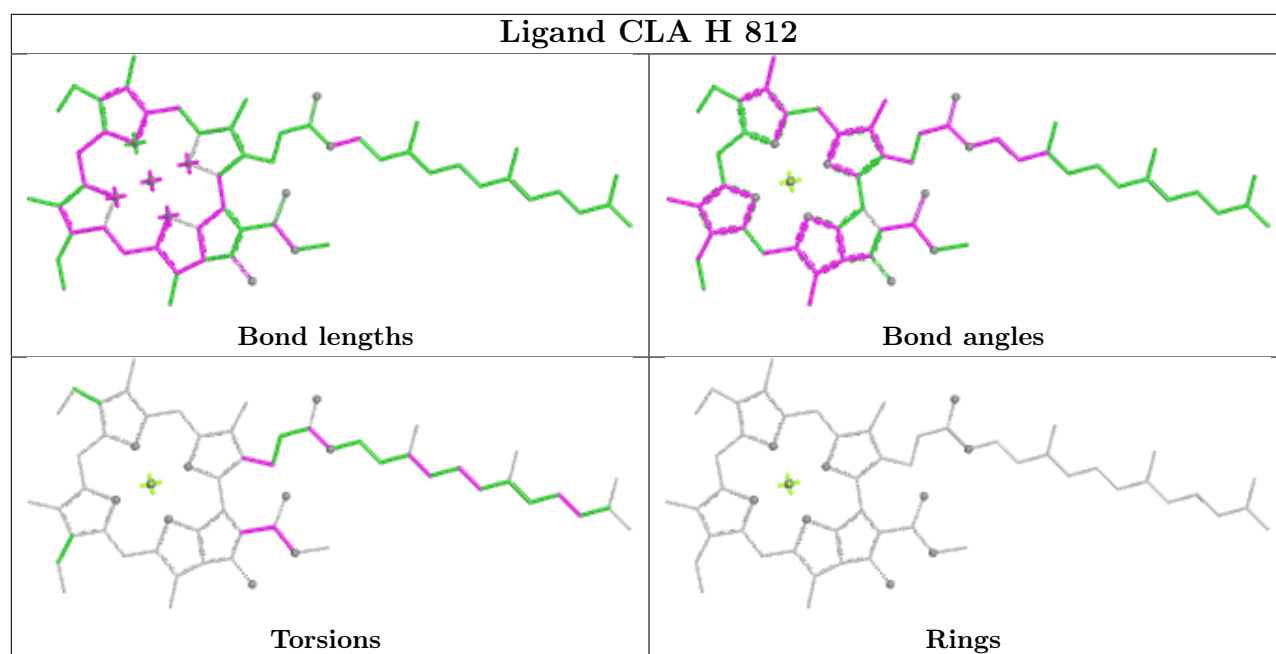
Bond angles

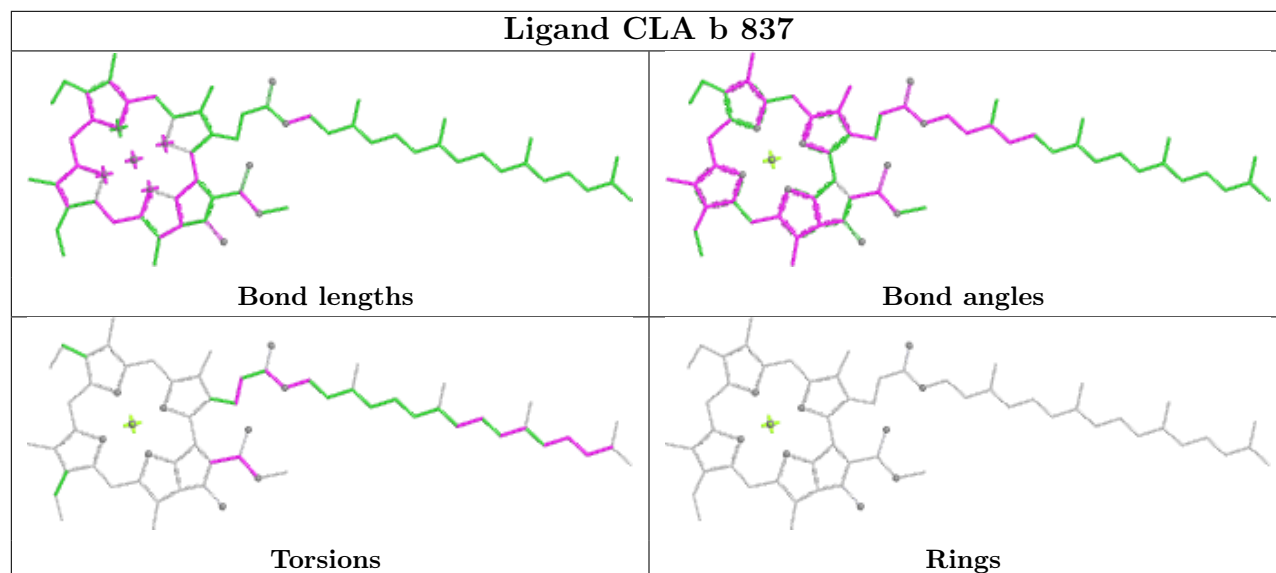
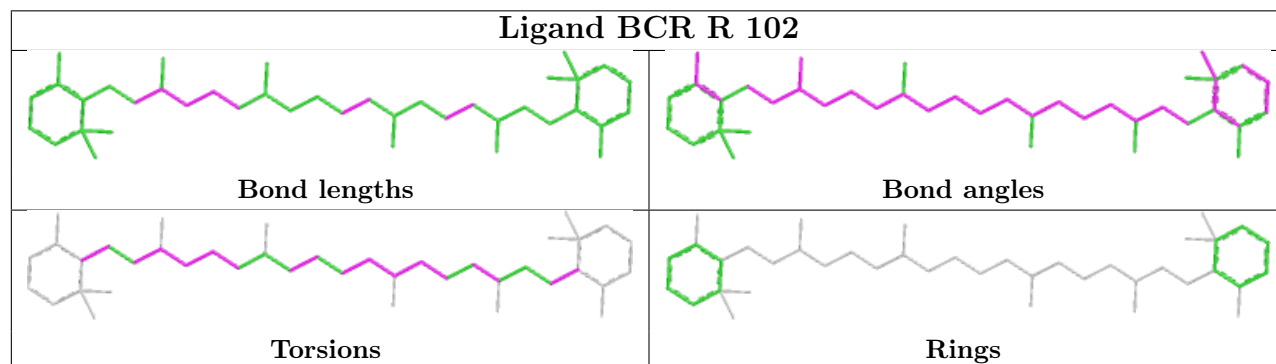
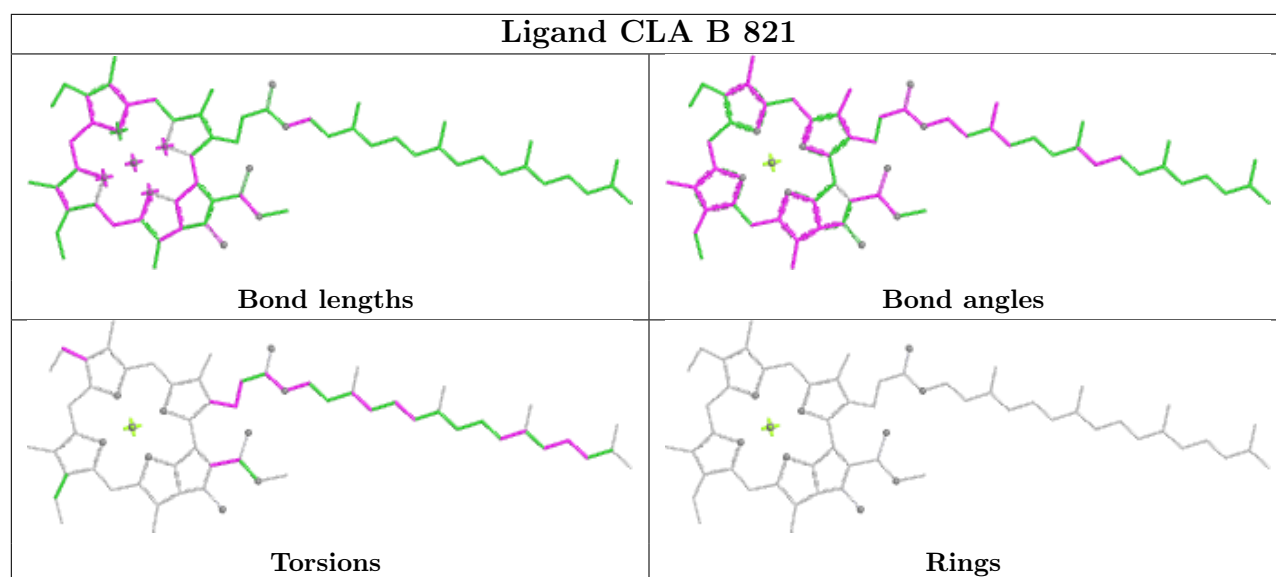


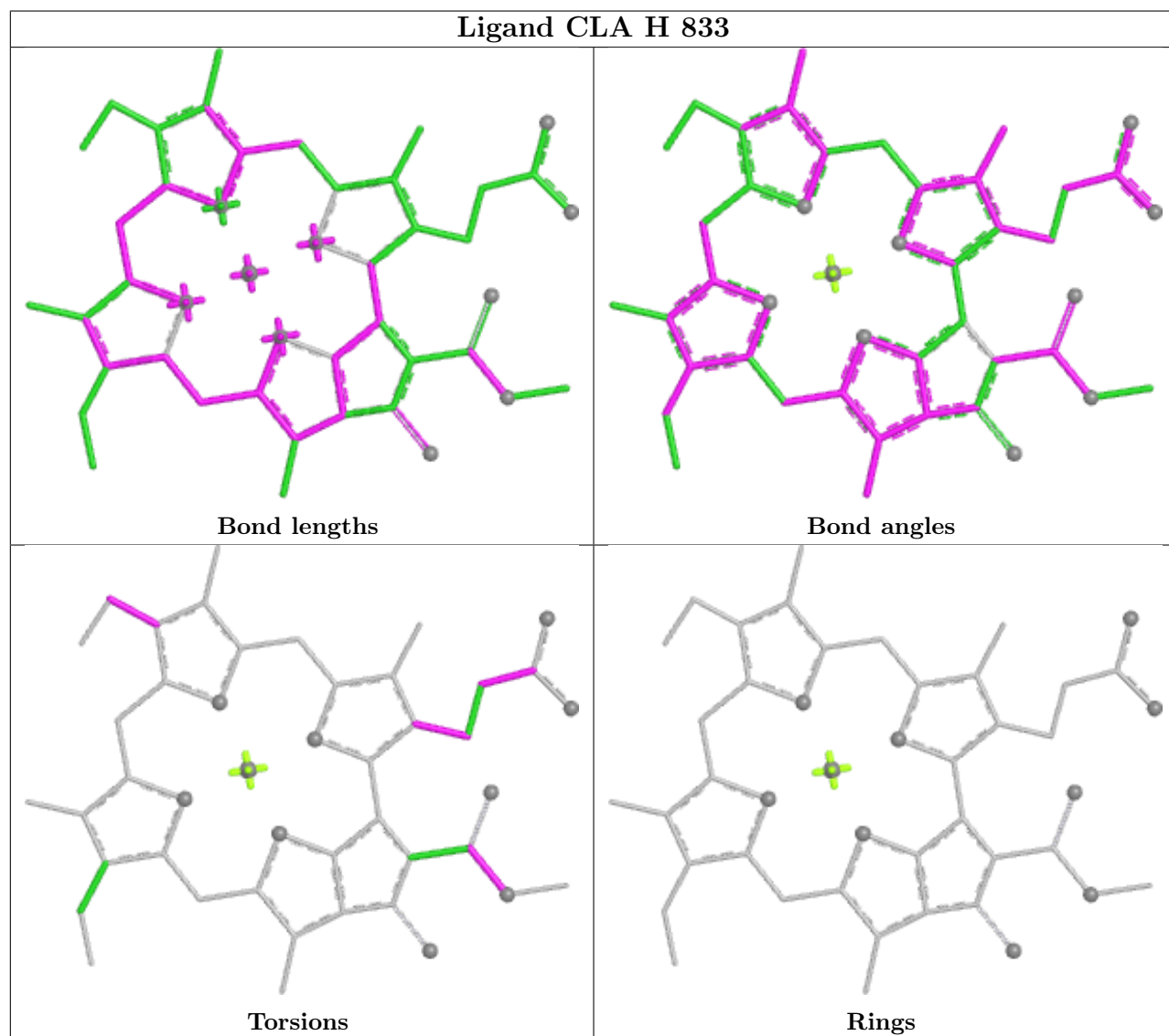
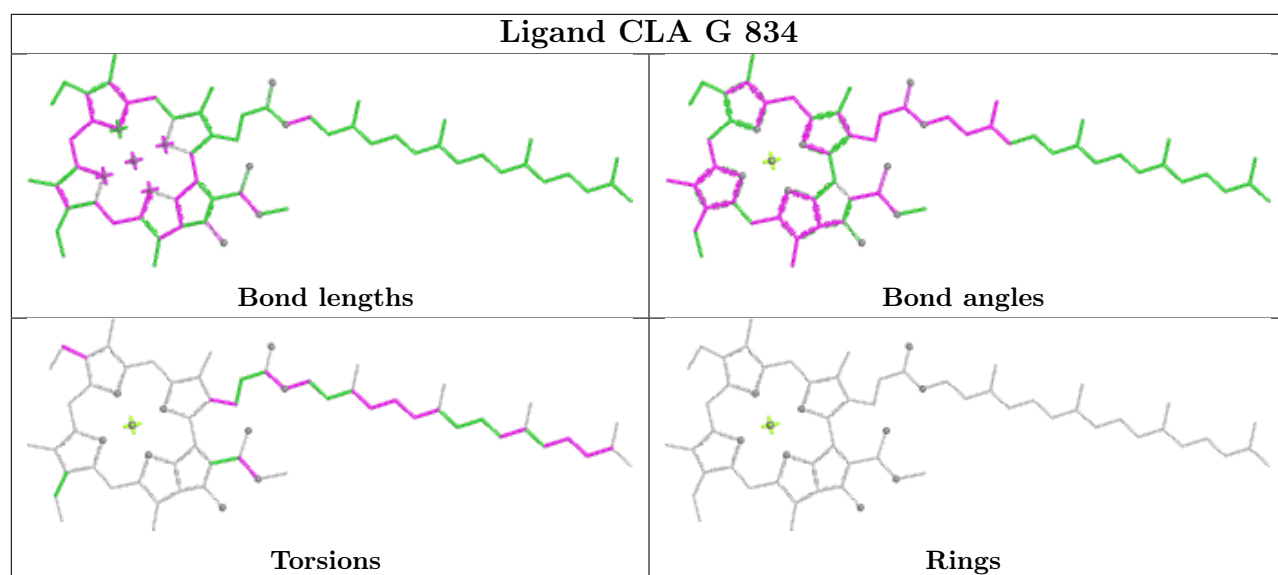
Torsions

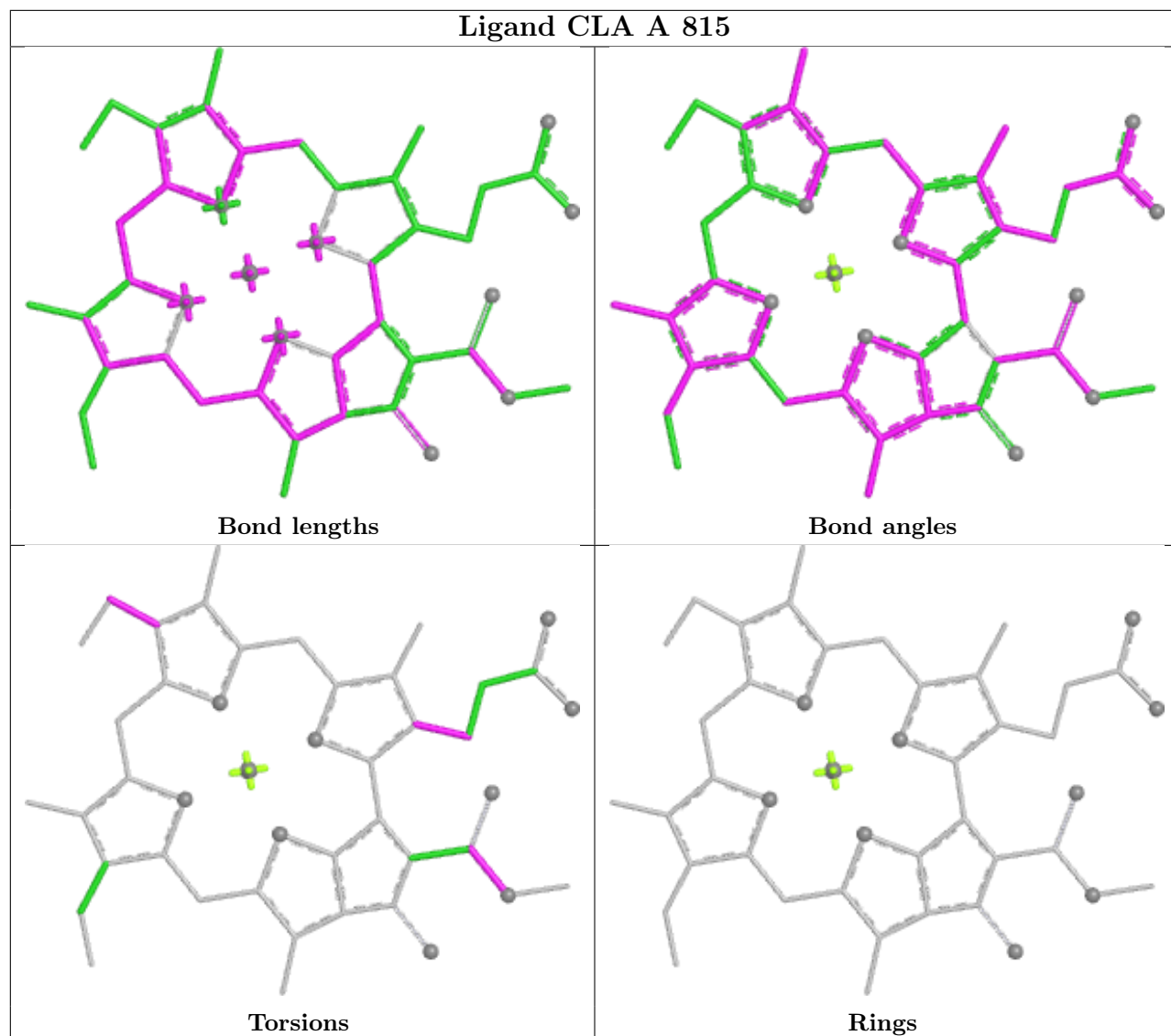


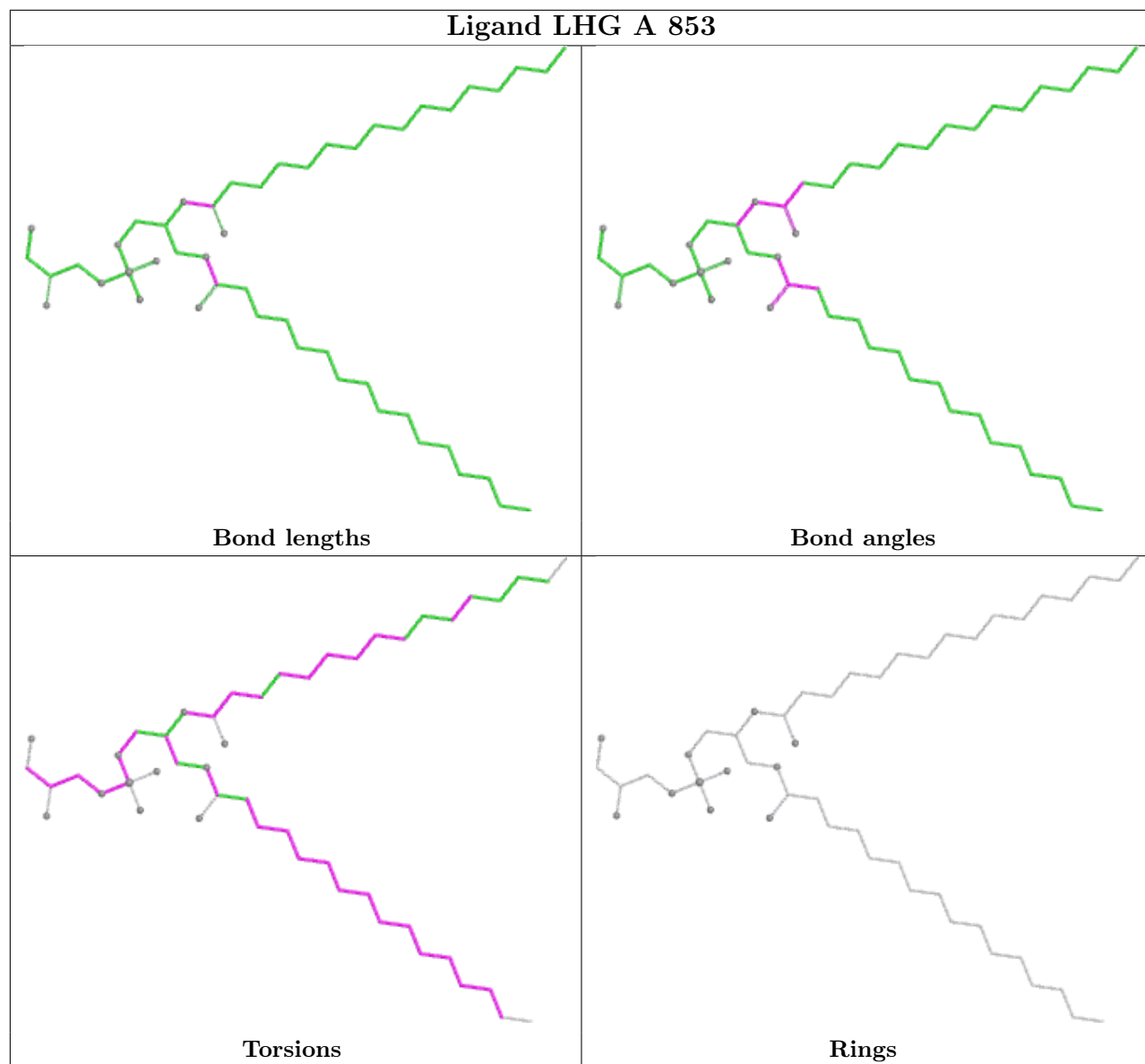
Rings



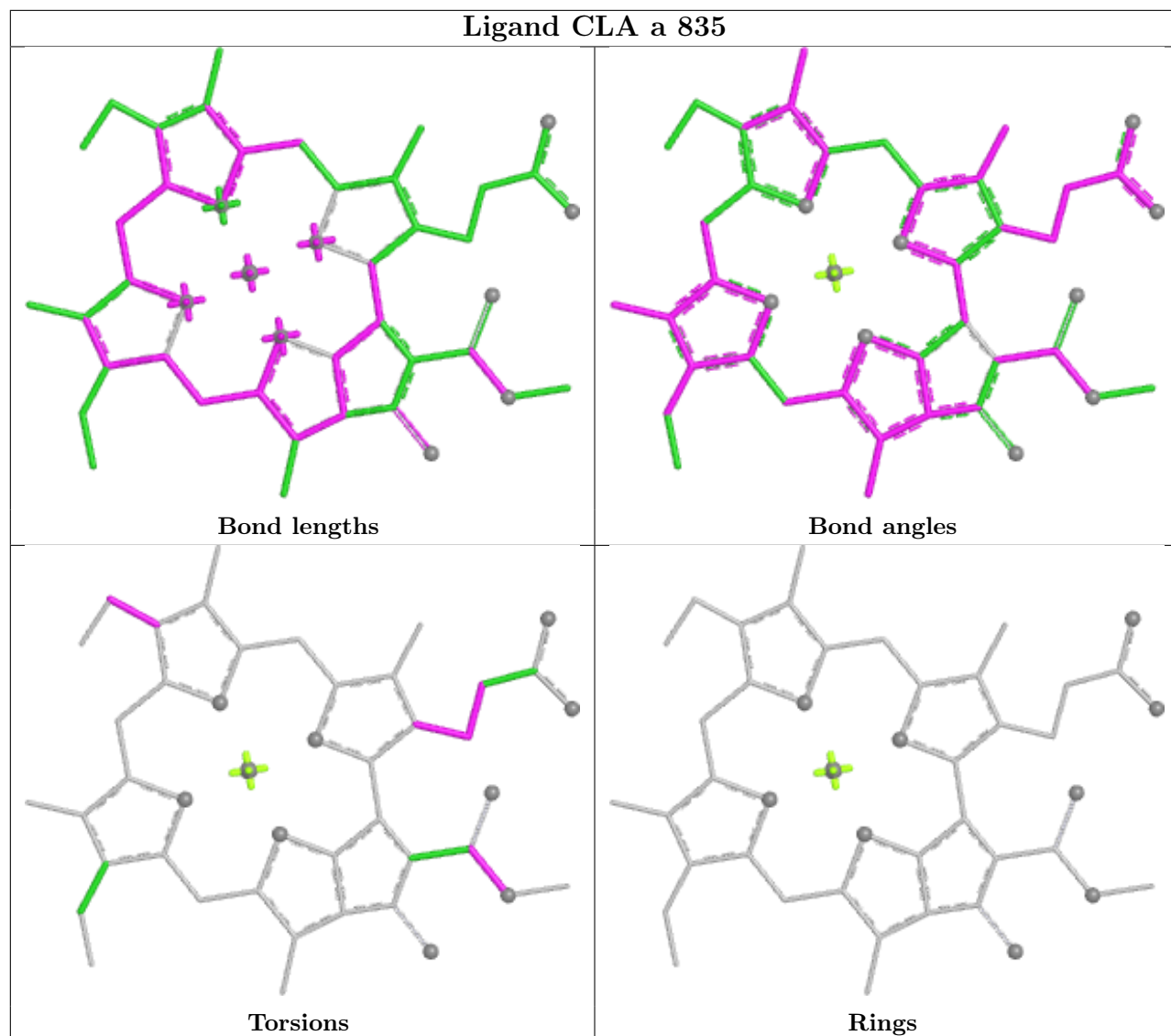




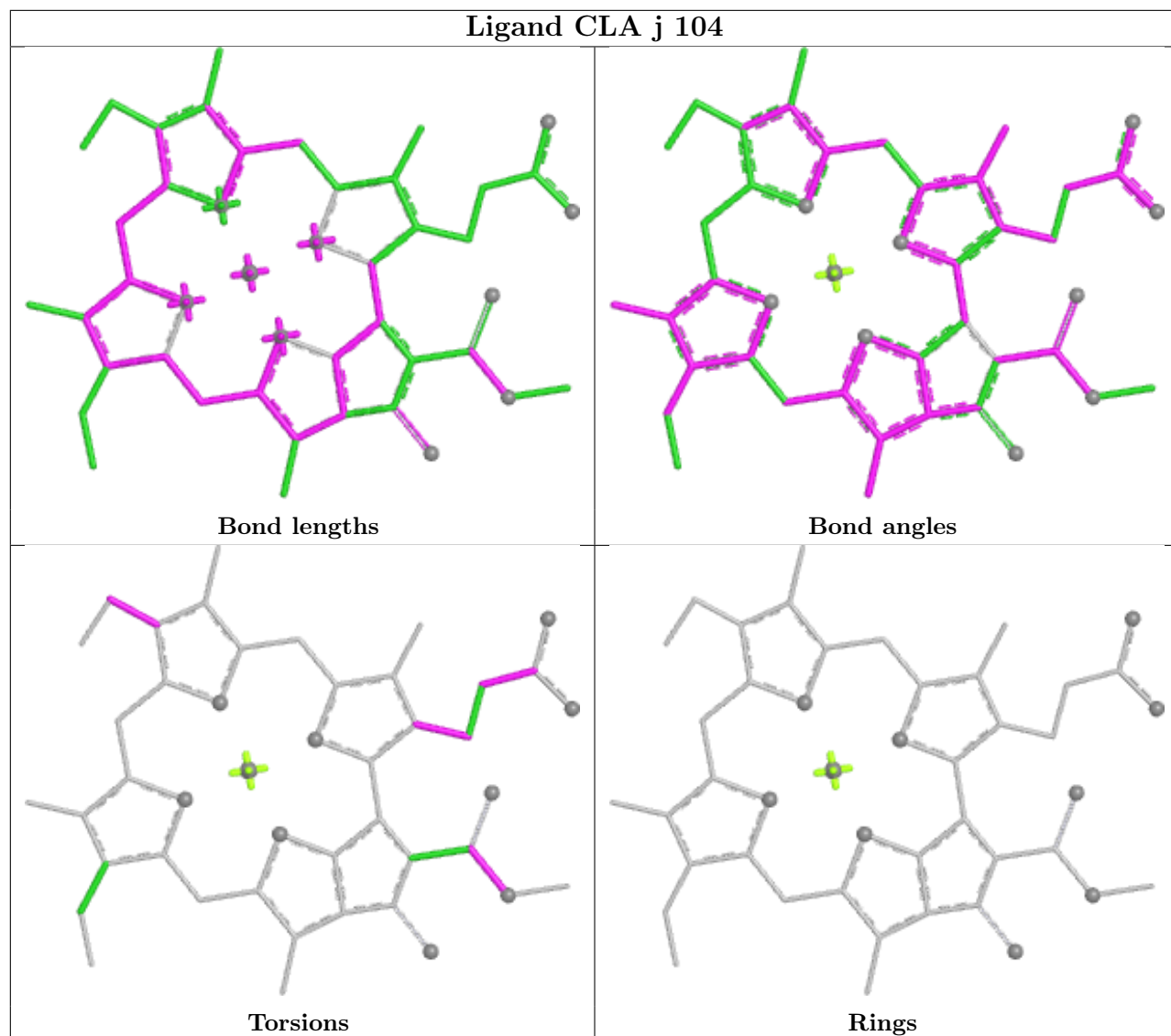




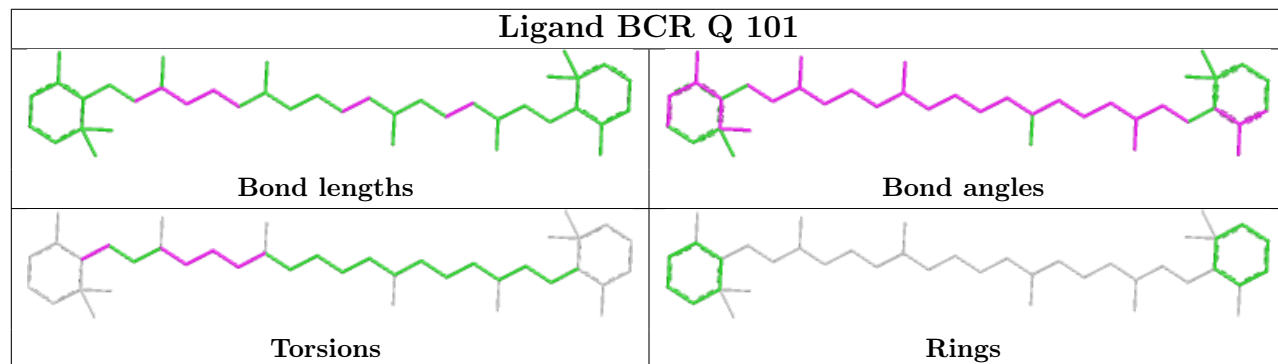
## Ligand CLA a 835

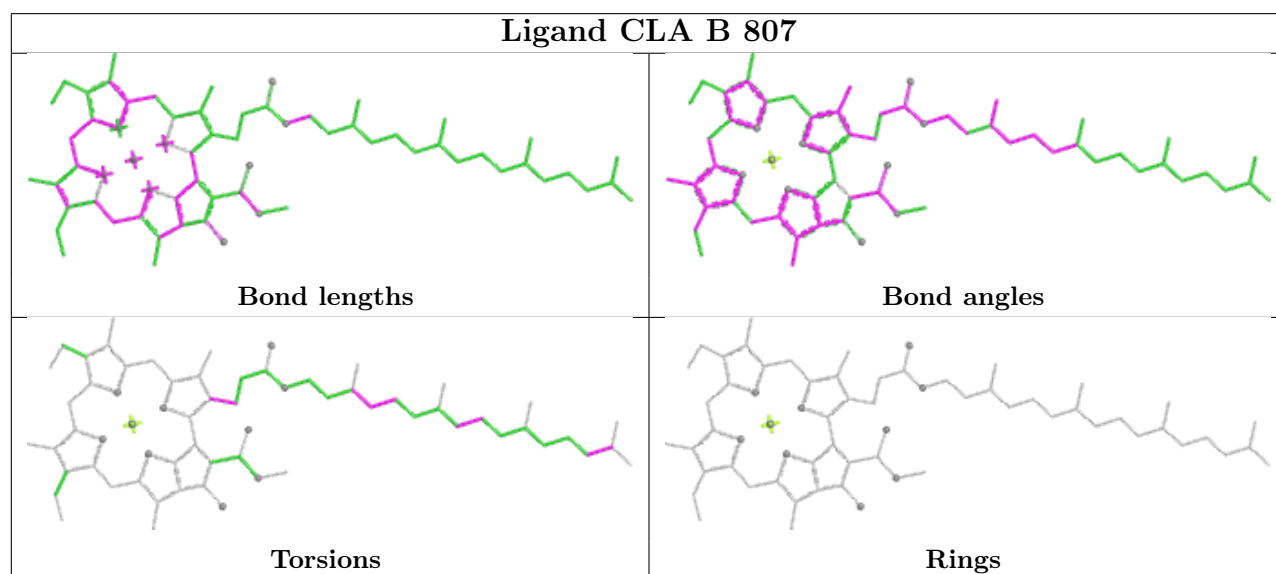
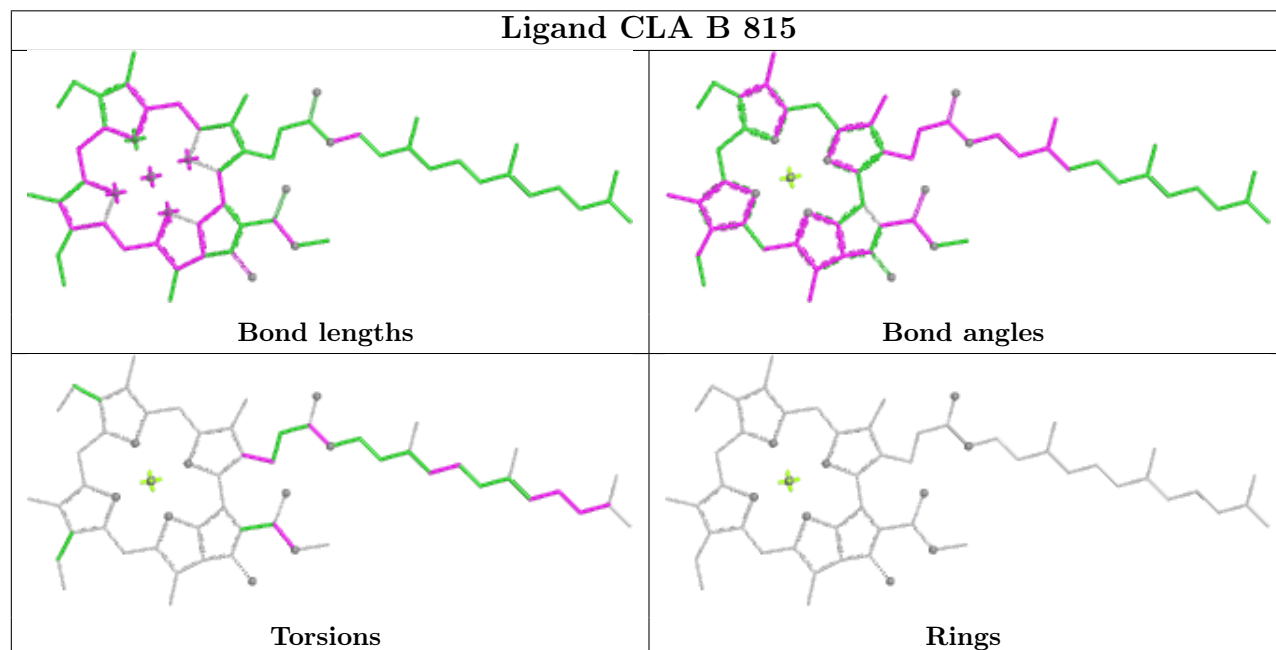
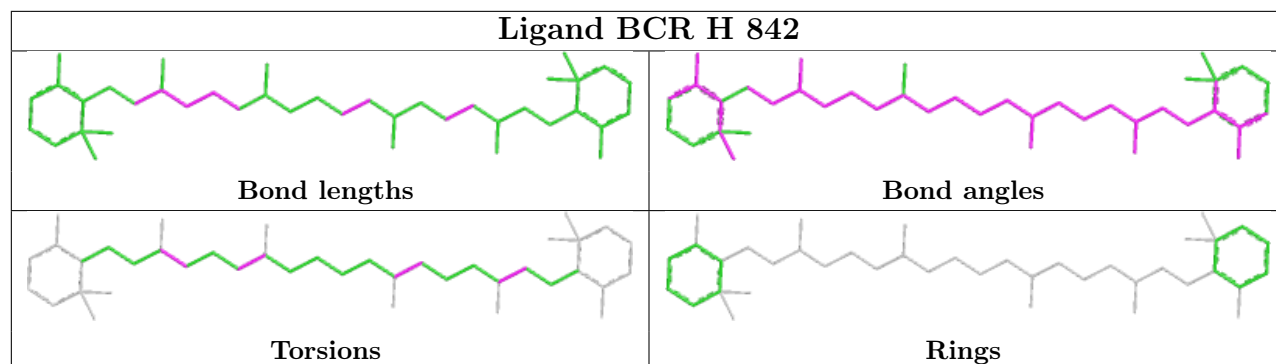


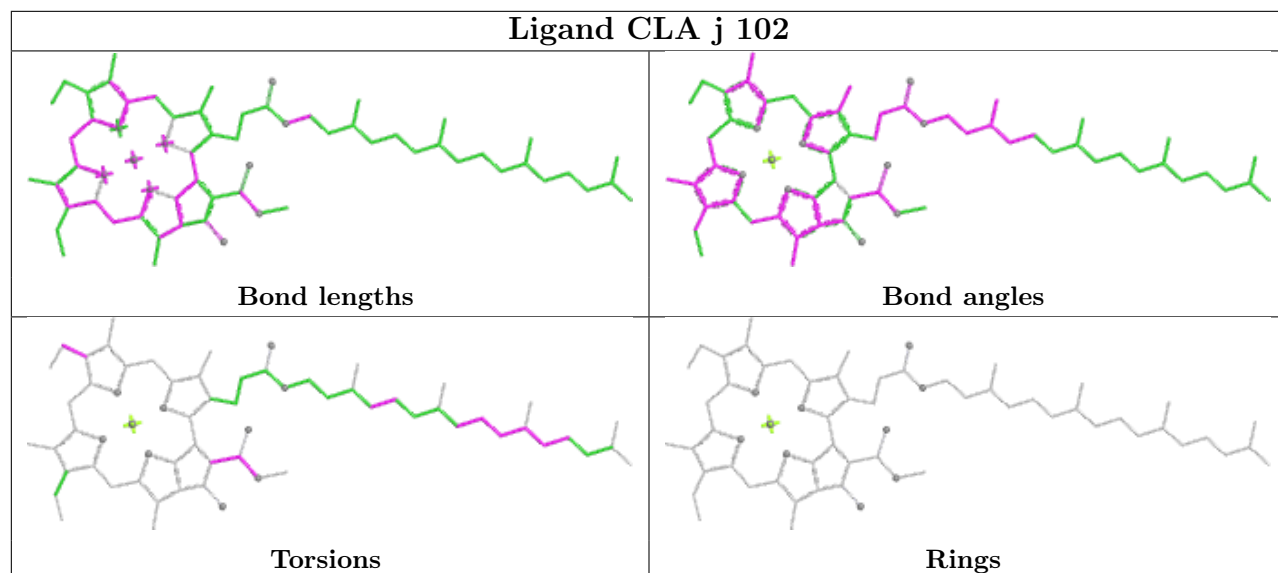
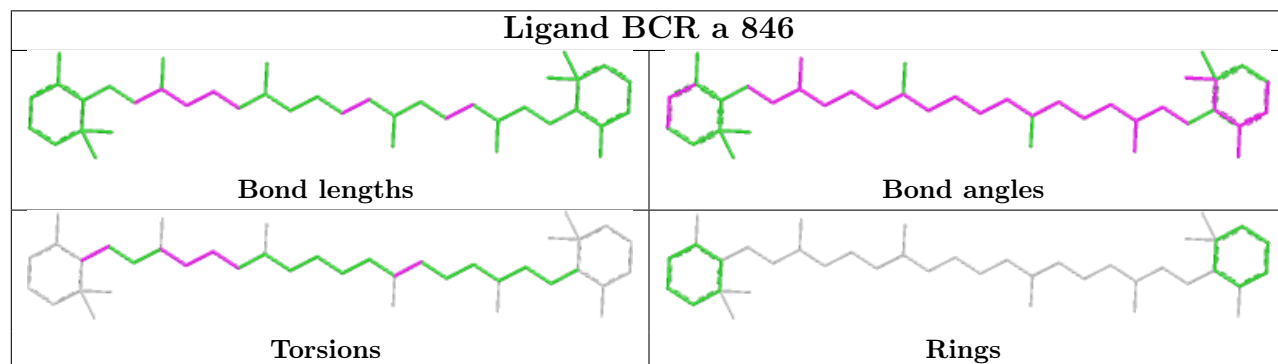
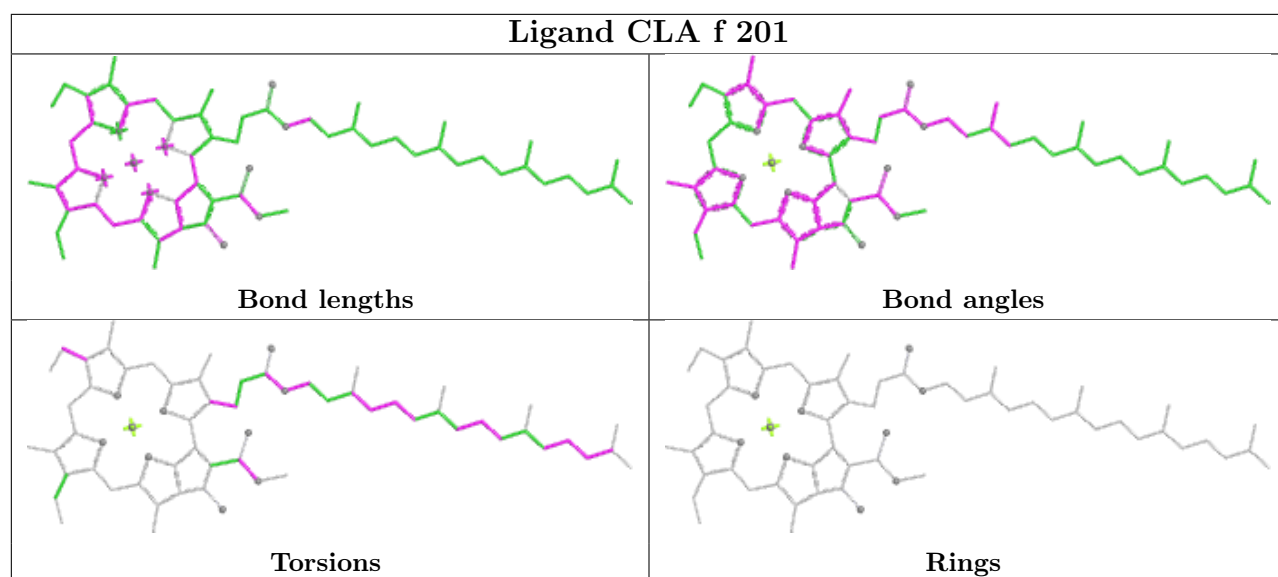
## Ligand CLA j 104



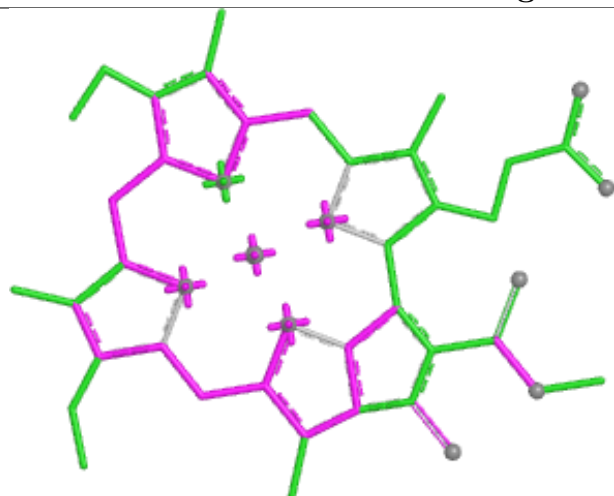
## Ligand BCR Q 101



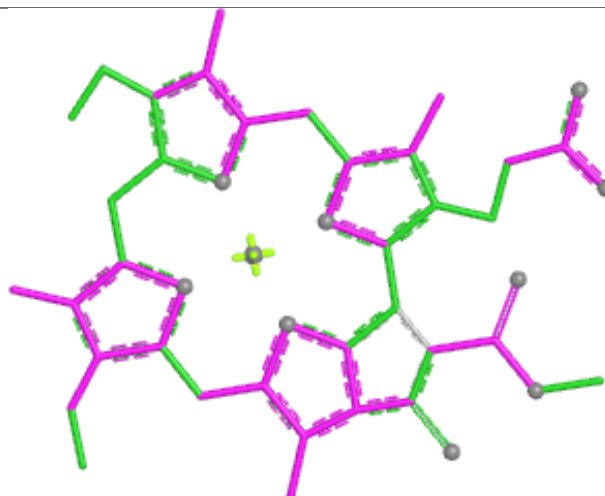




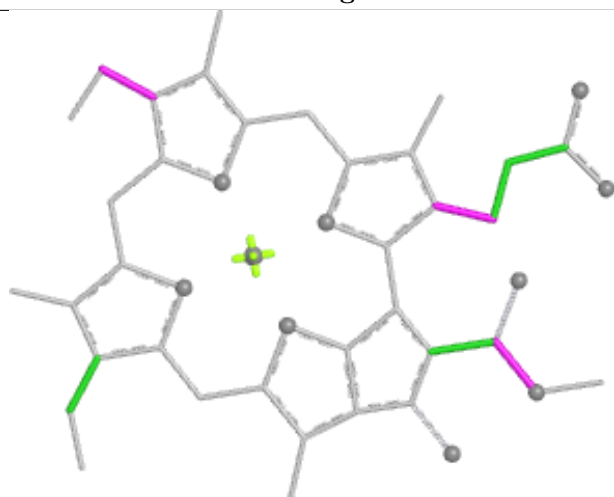
## Ligand CLA b 827



Bond lengths



Bond angles

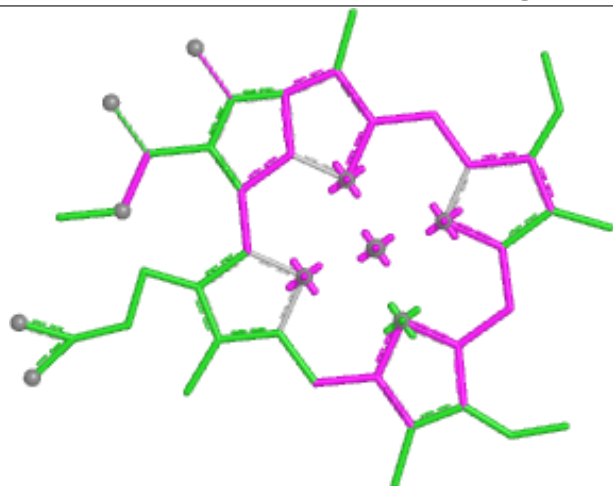


Torsions

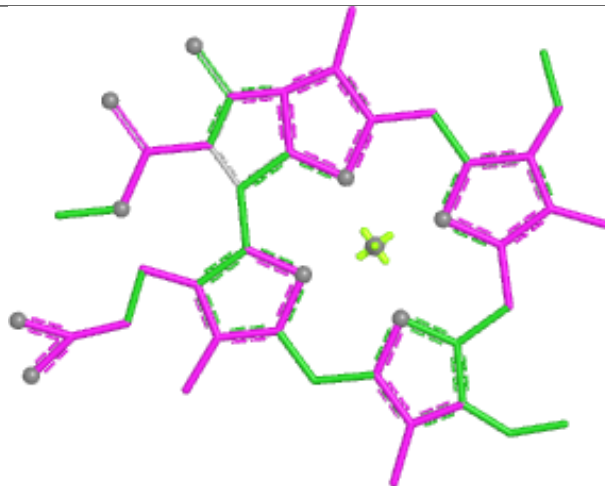


Rings

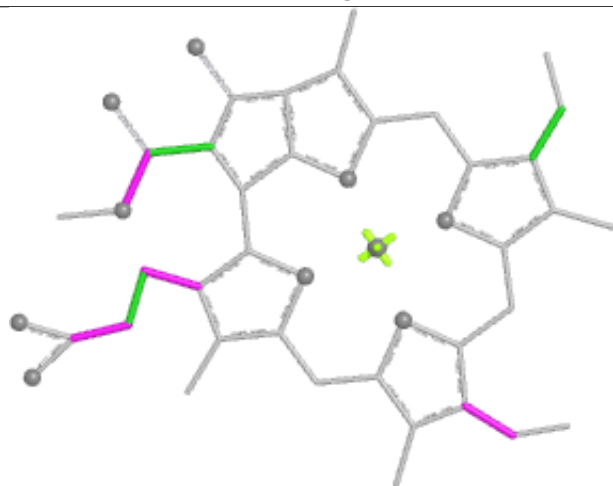
## Ligand CLA F 203



Bond lengths



Bond angles

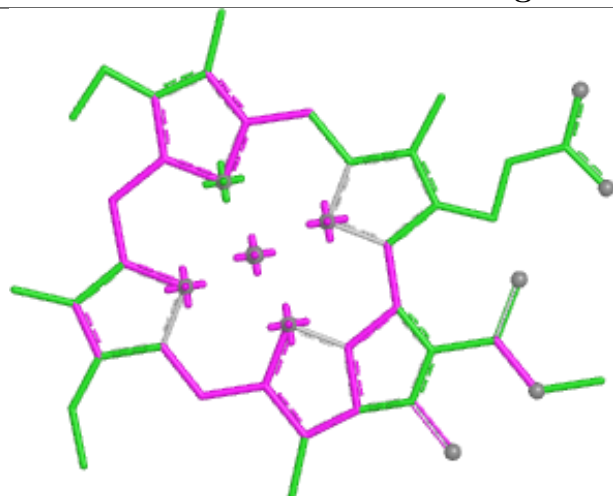


Torsions

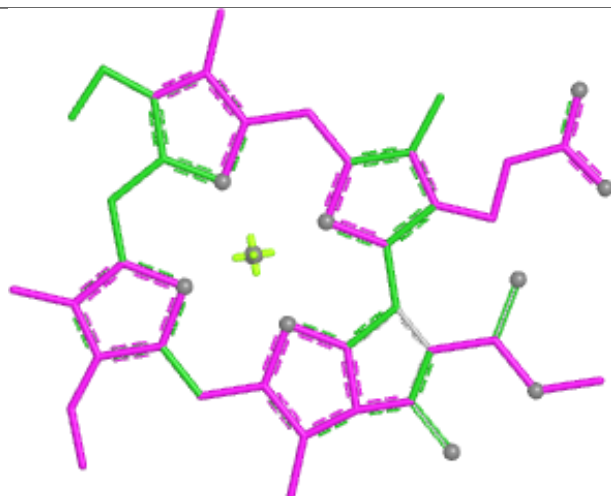


Rings

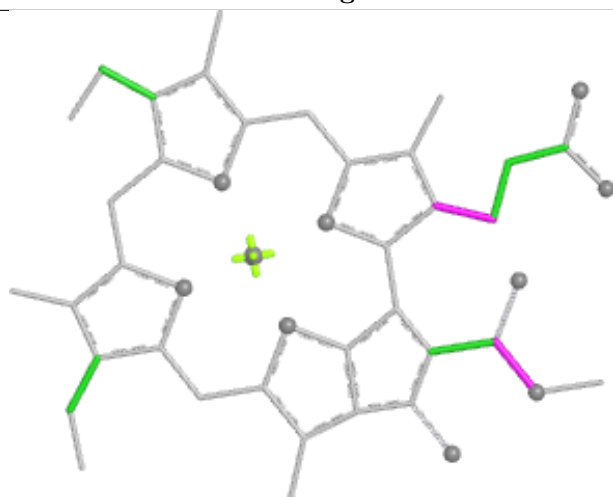
## Ligand CLA B 820



Bond lengths



Bond angles

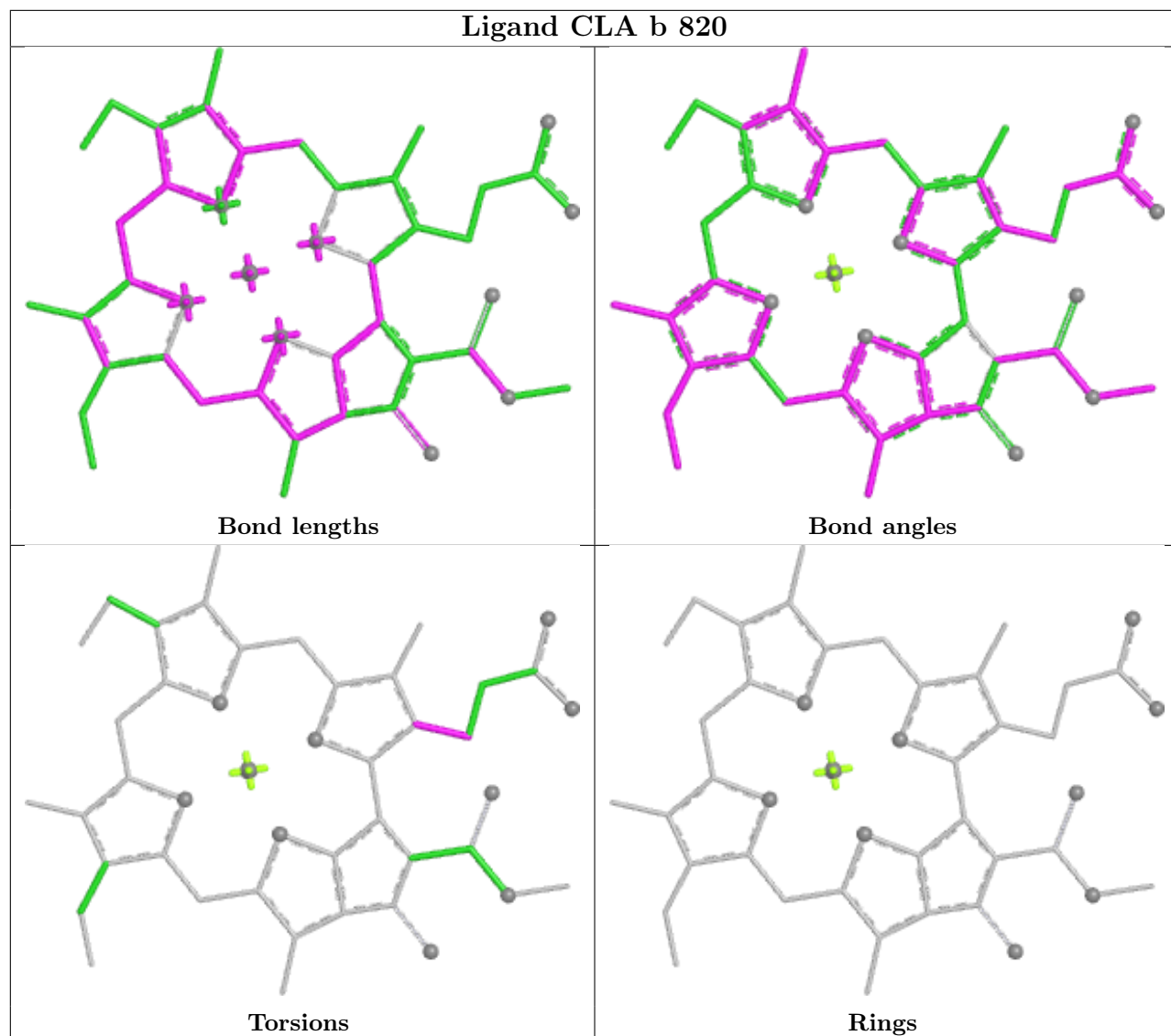


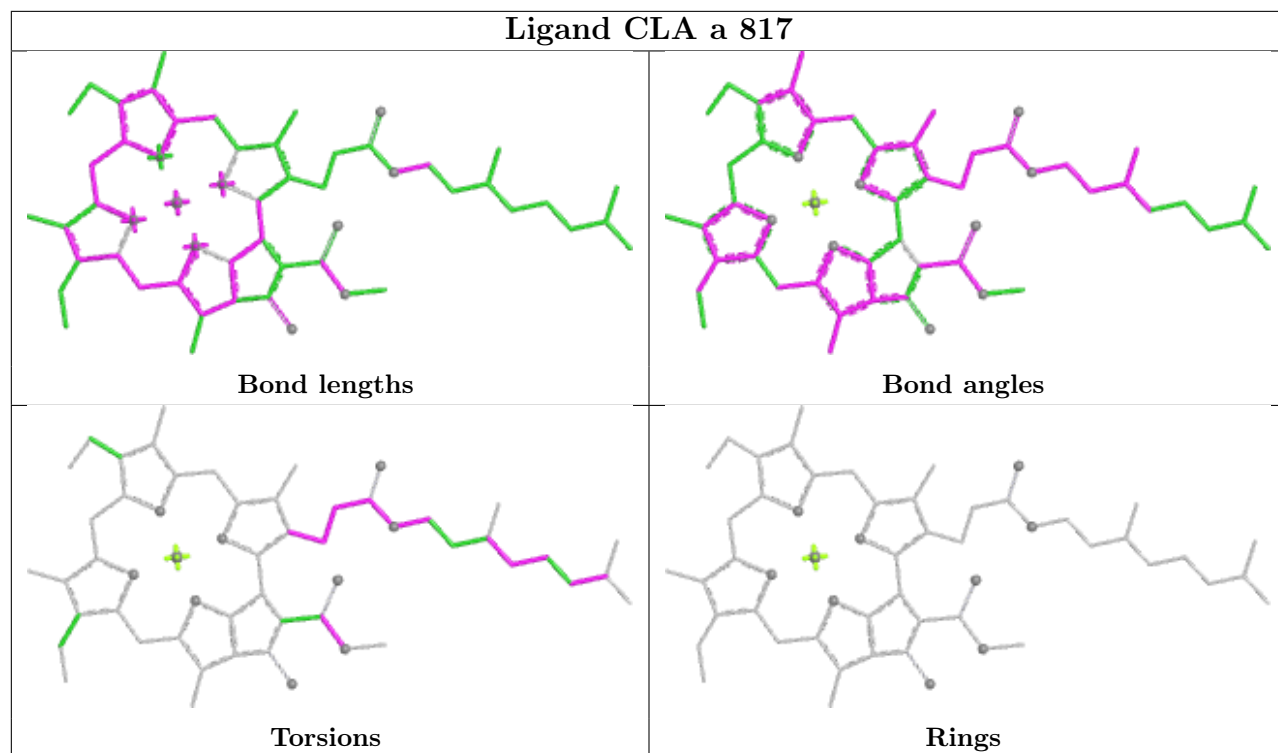
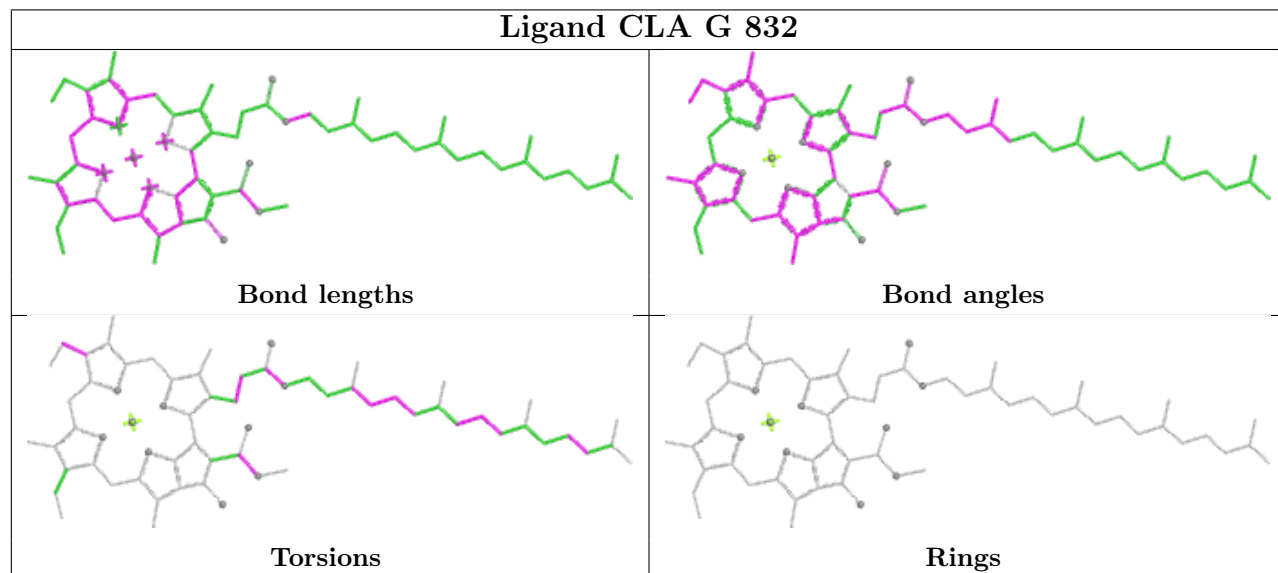
Torsions

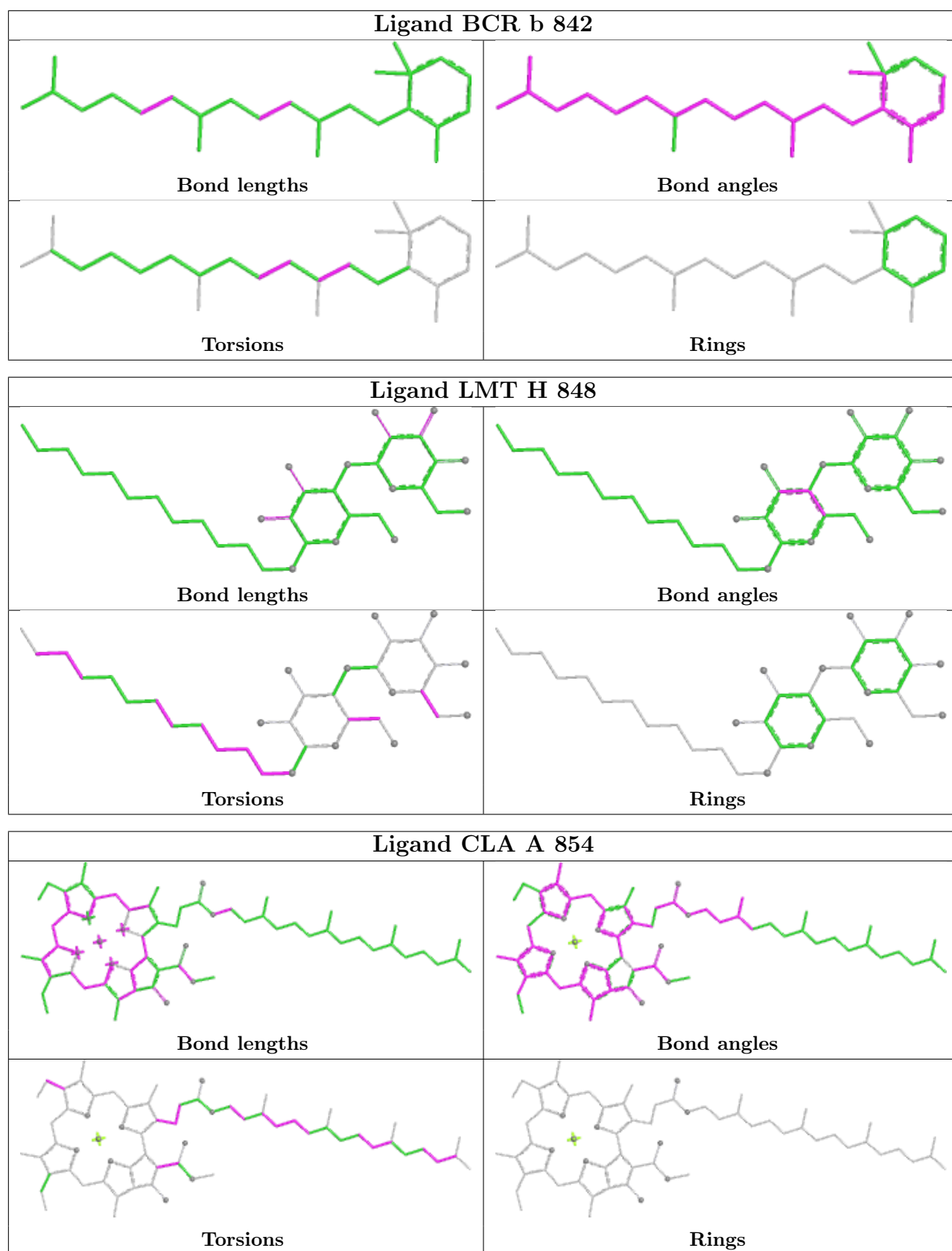


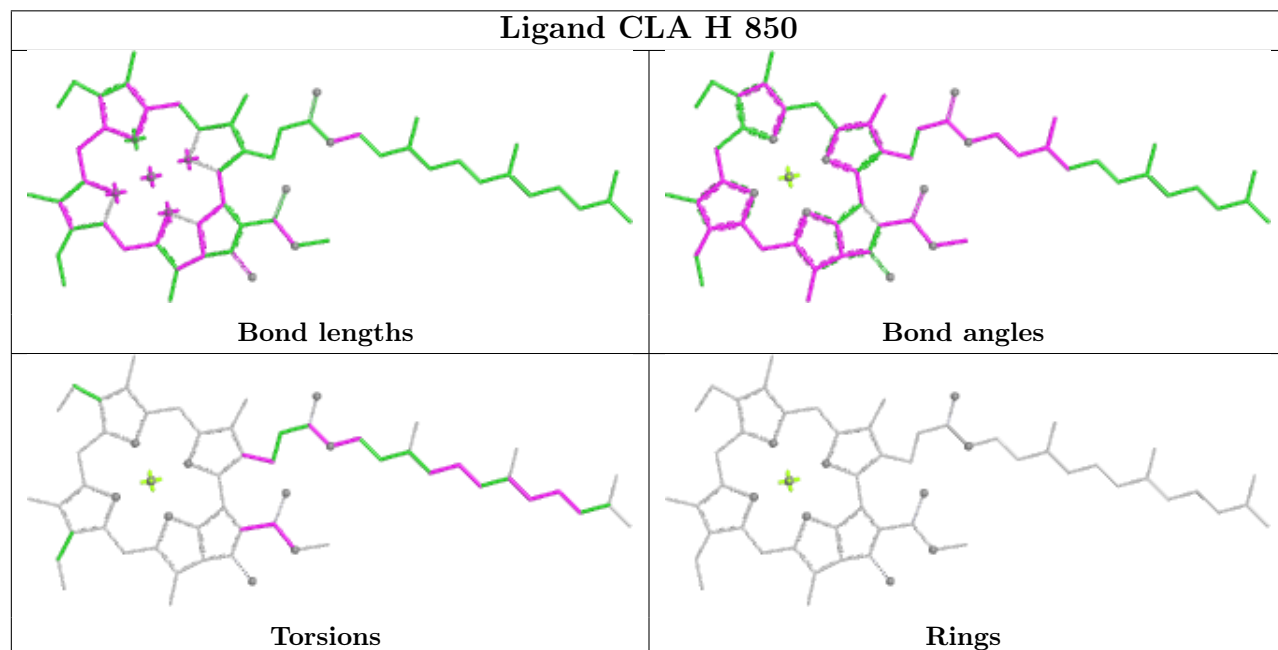
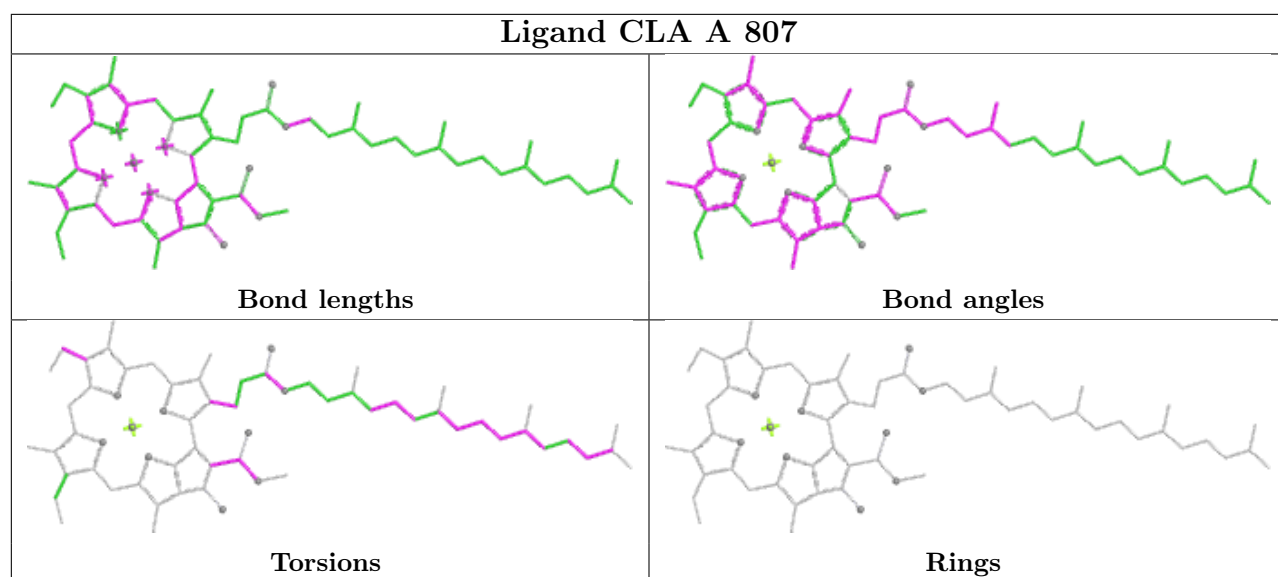
Rings

## Ligand CLA b 820

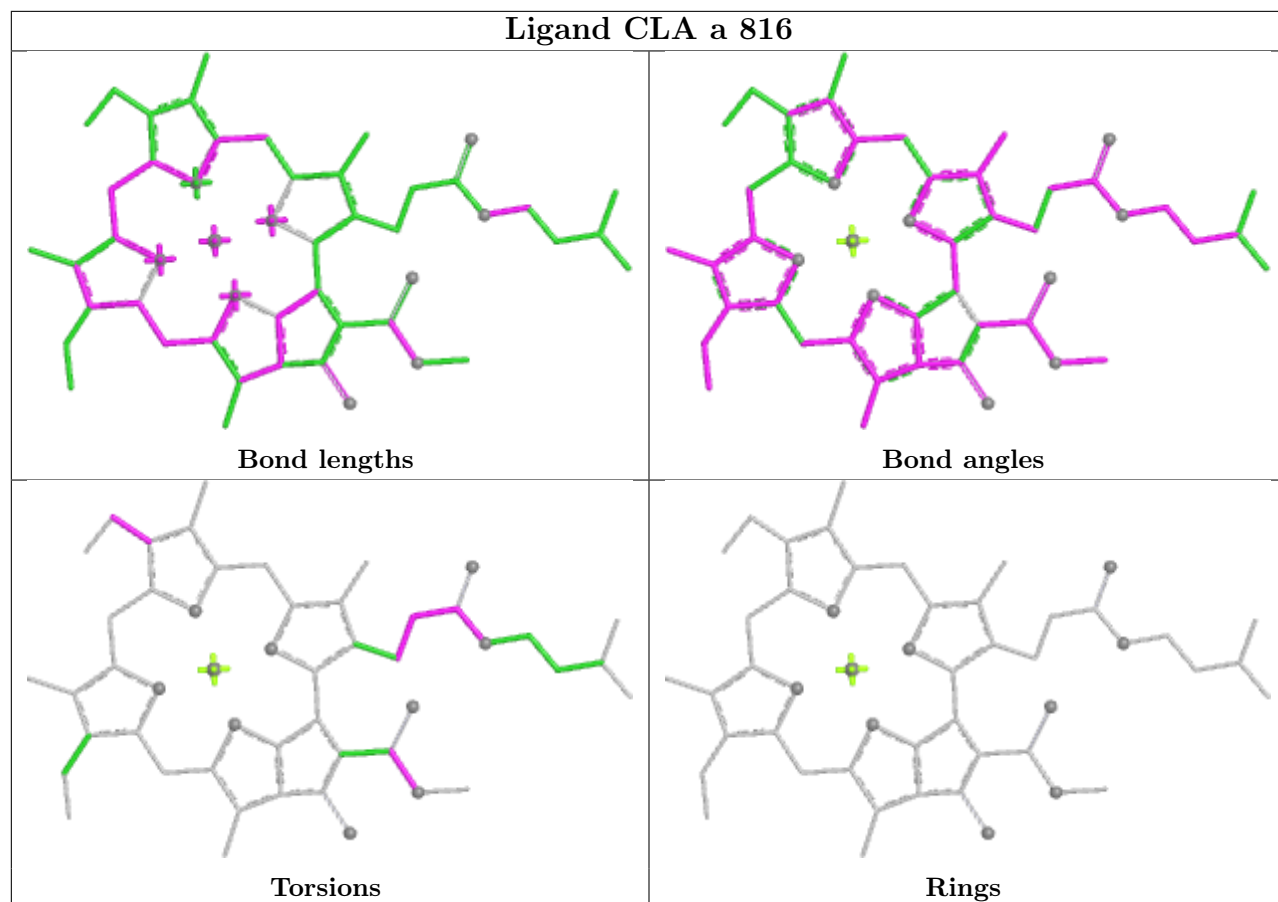


**Ligand CLA a 817****Ligand CLA G 832**

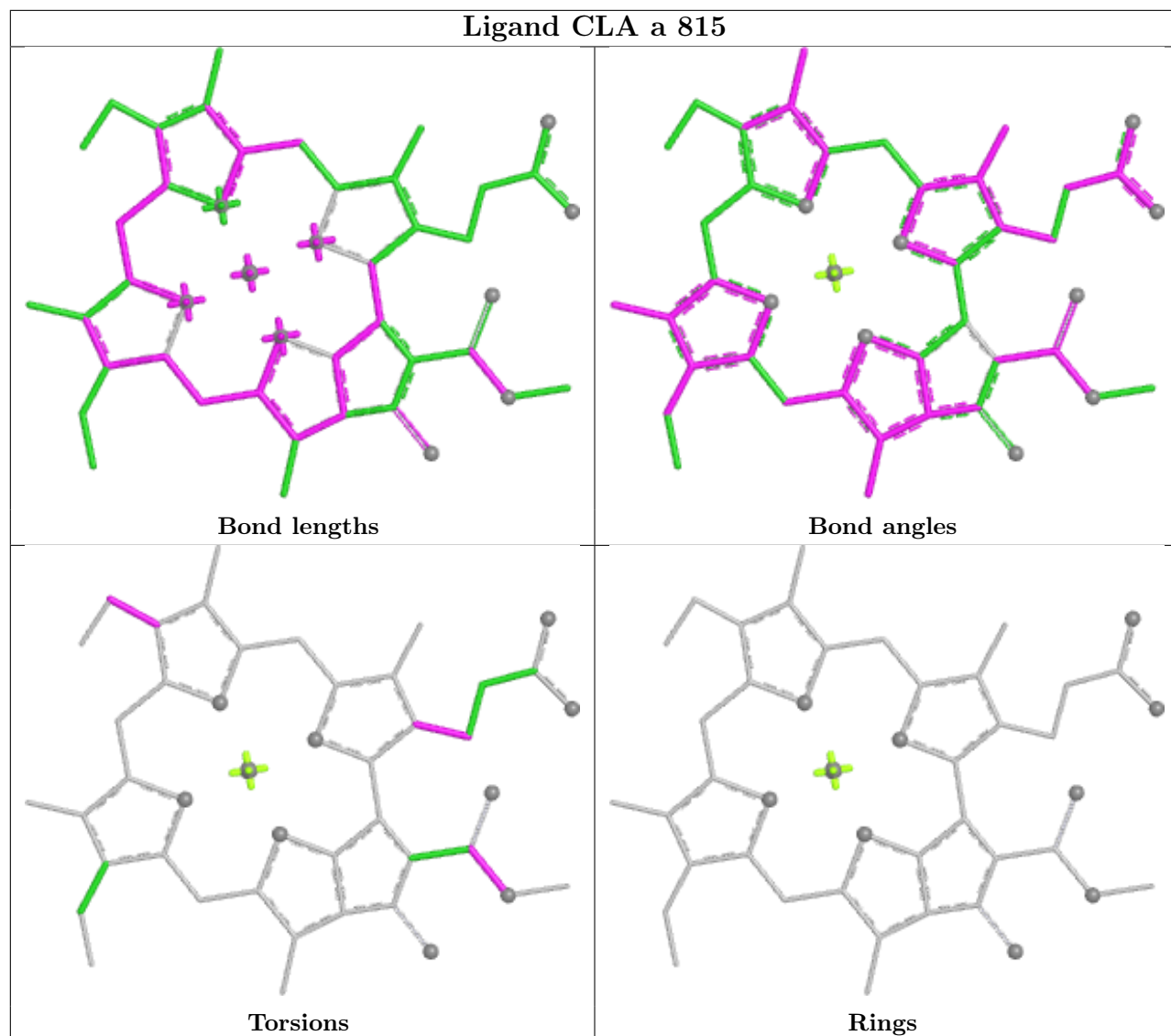




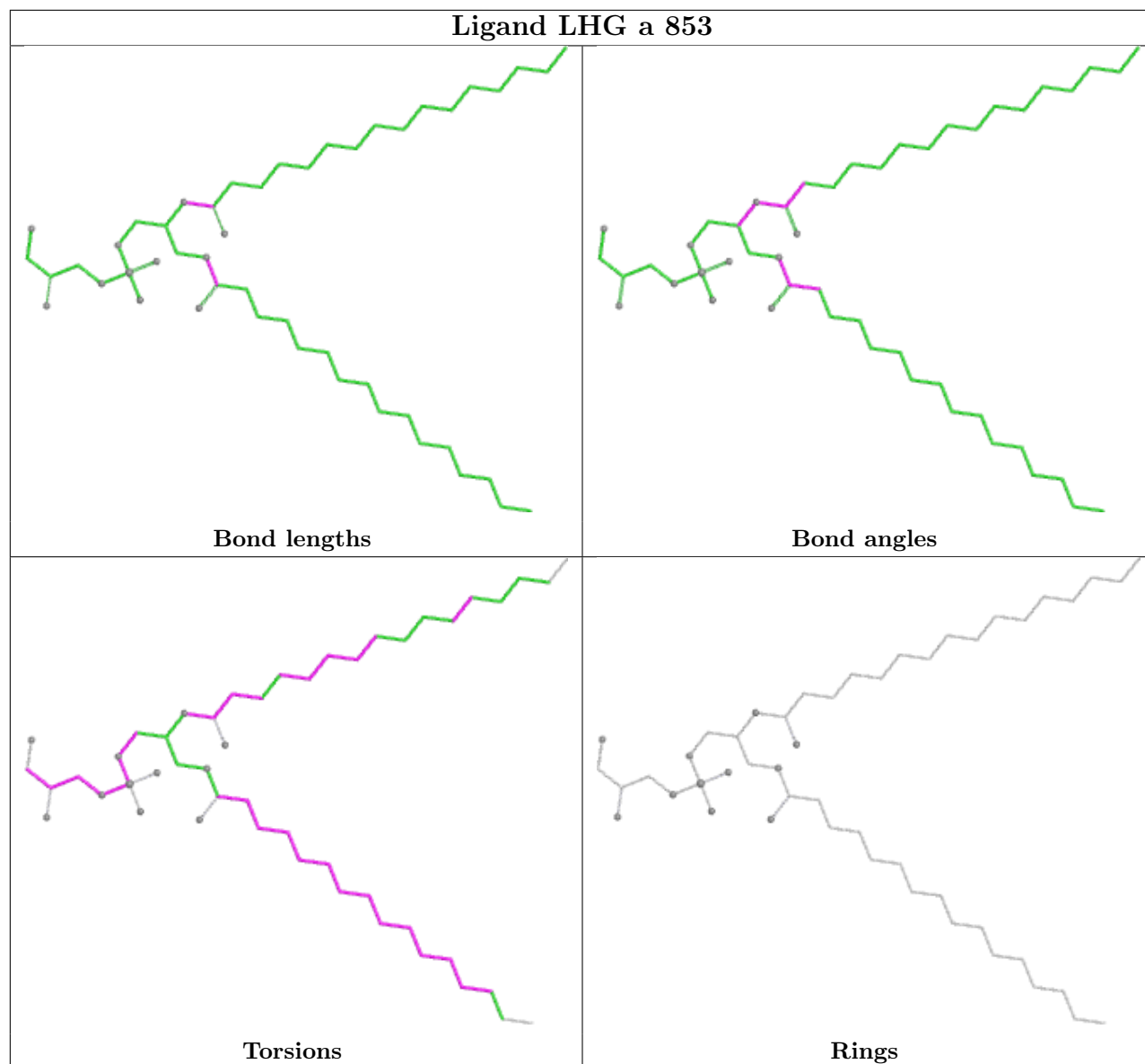
## Ligand CLA a 816



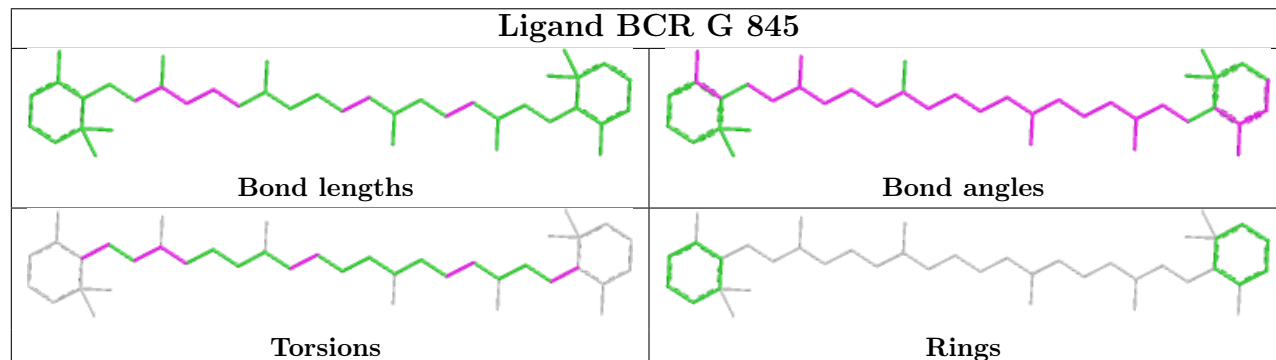
## Ligand CLA a 815

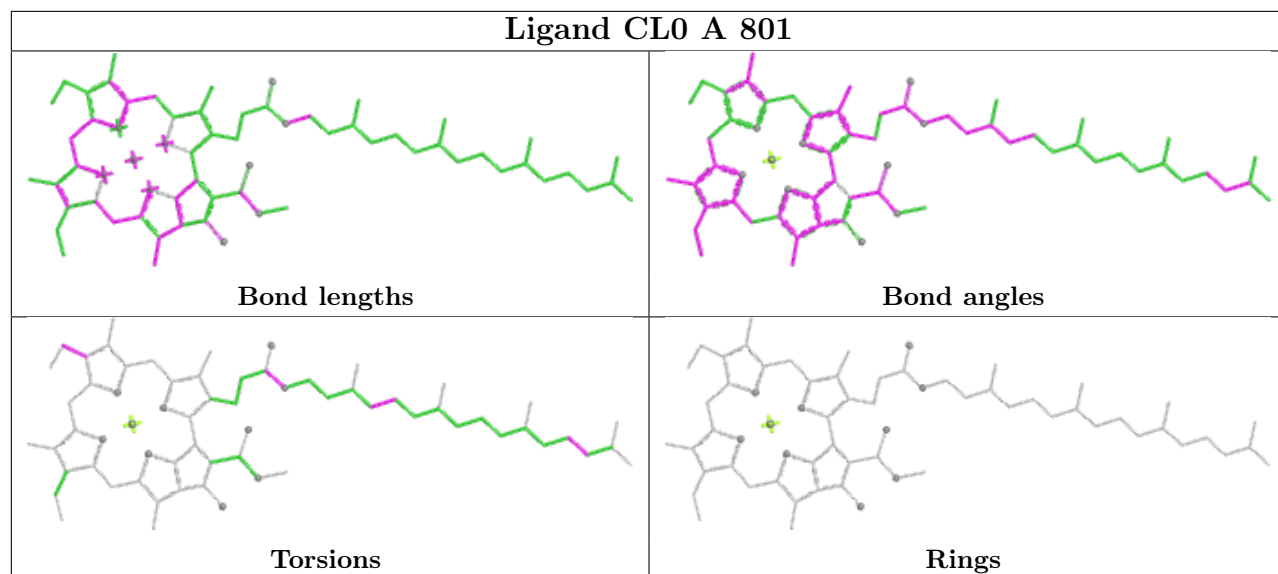
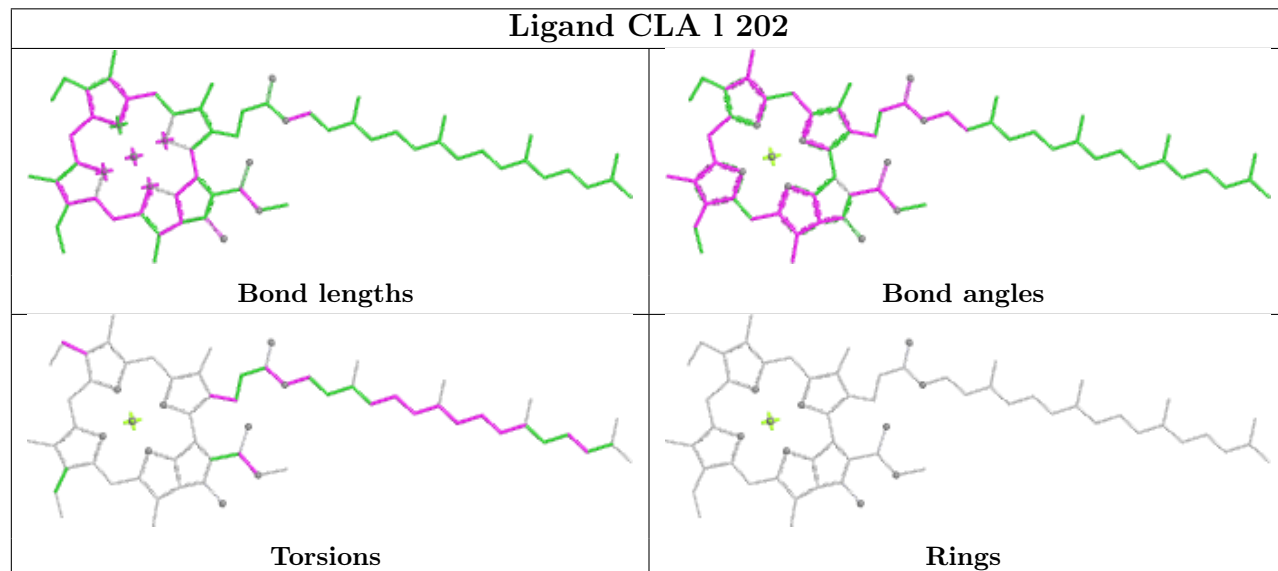


## Ligand LHG a 853

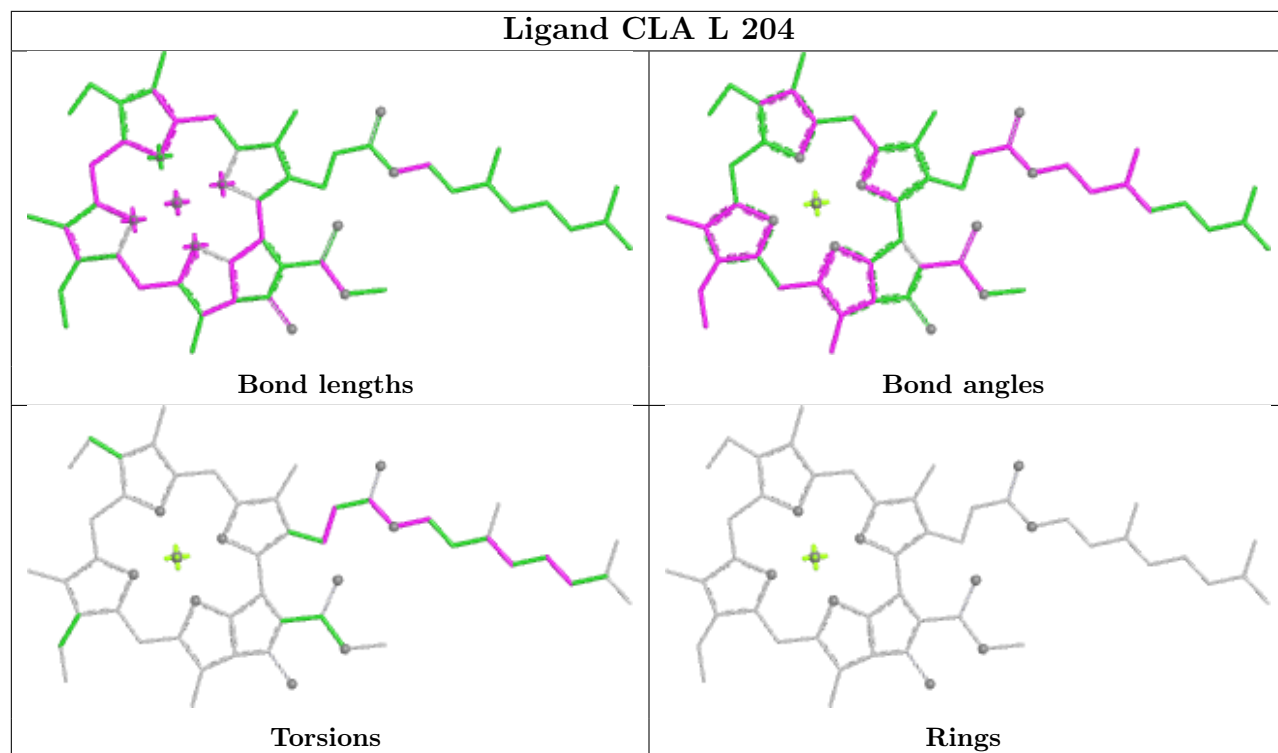


## Ligand BCR G 845

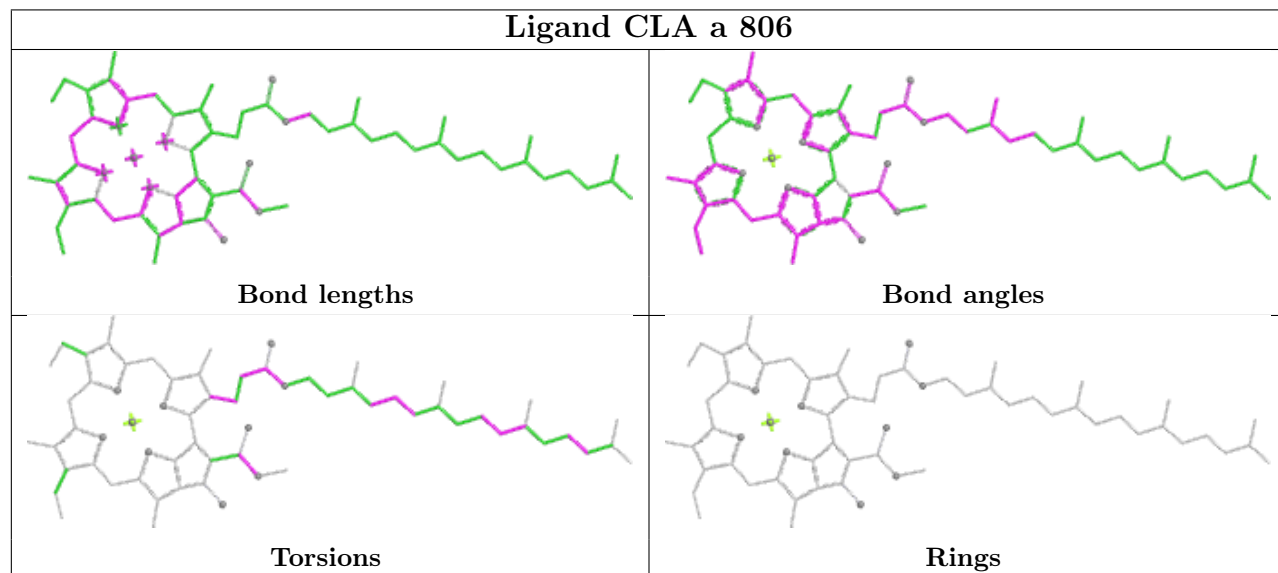


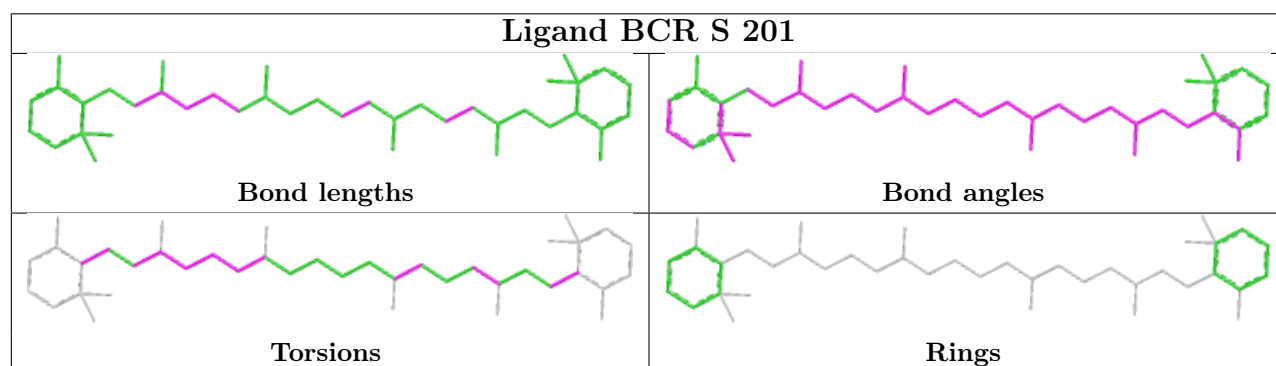
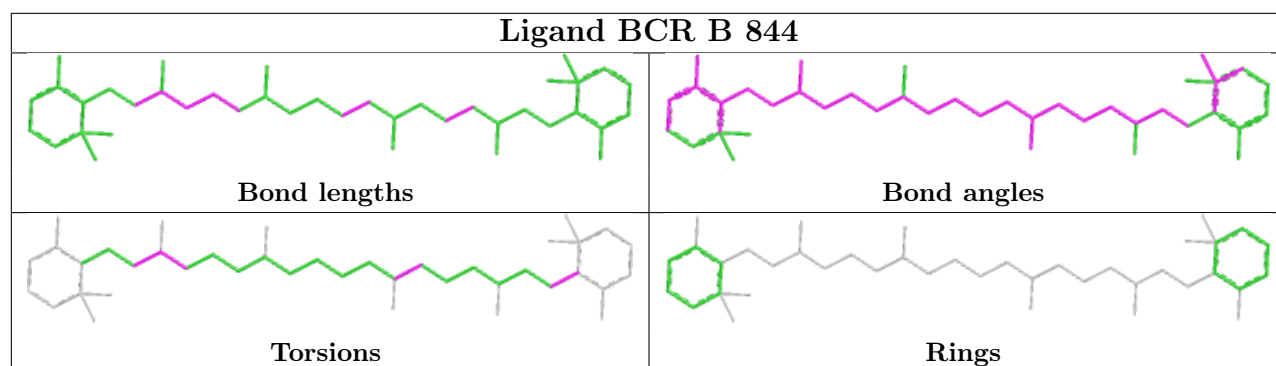
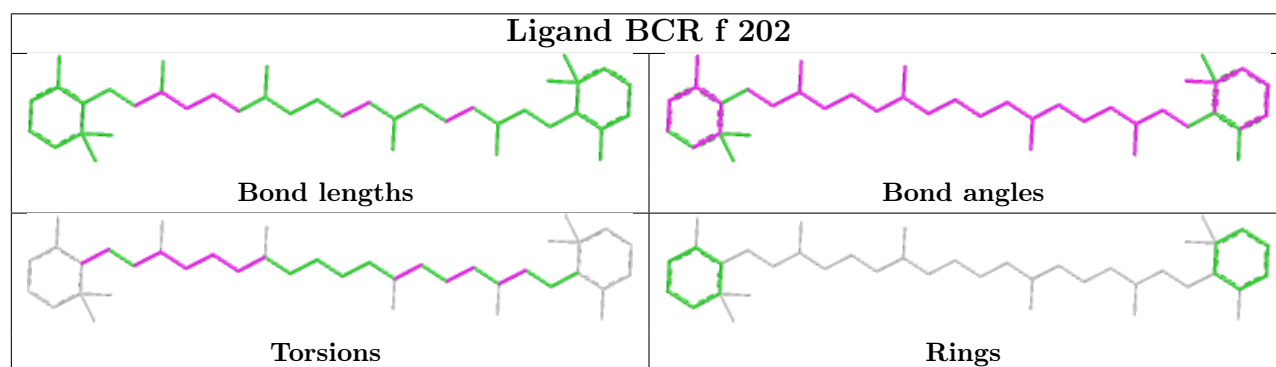
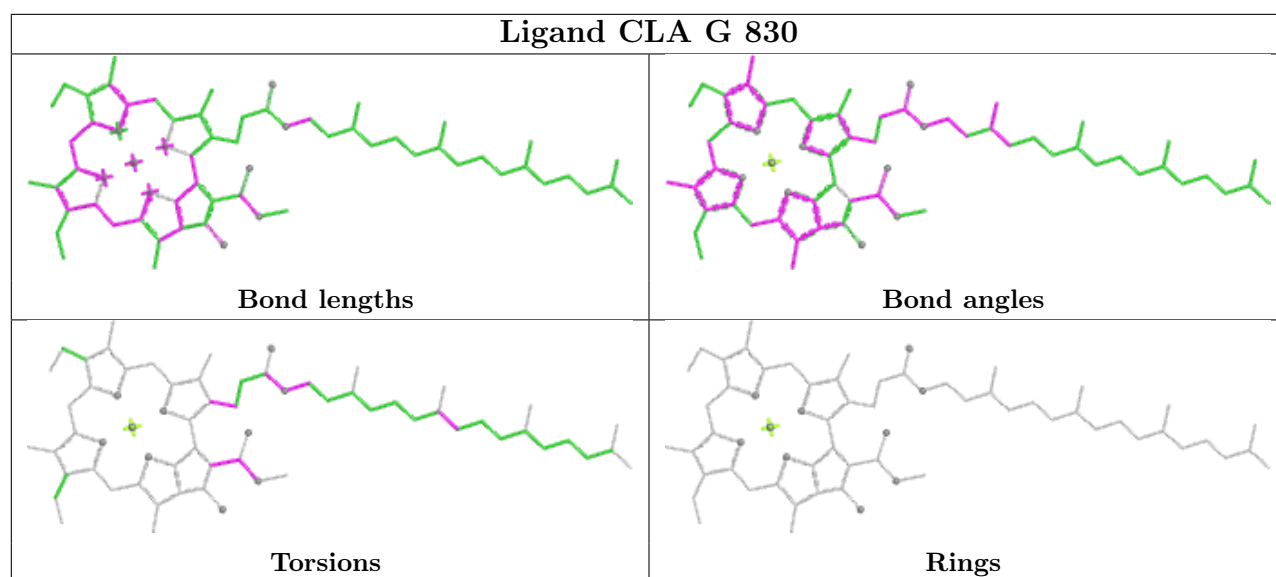
**Ligand CL0 A 801****Ligand CLA 1 202**

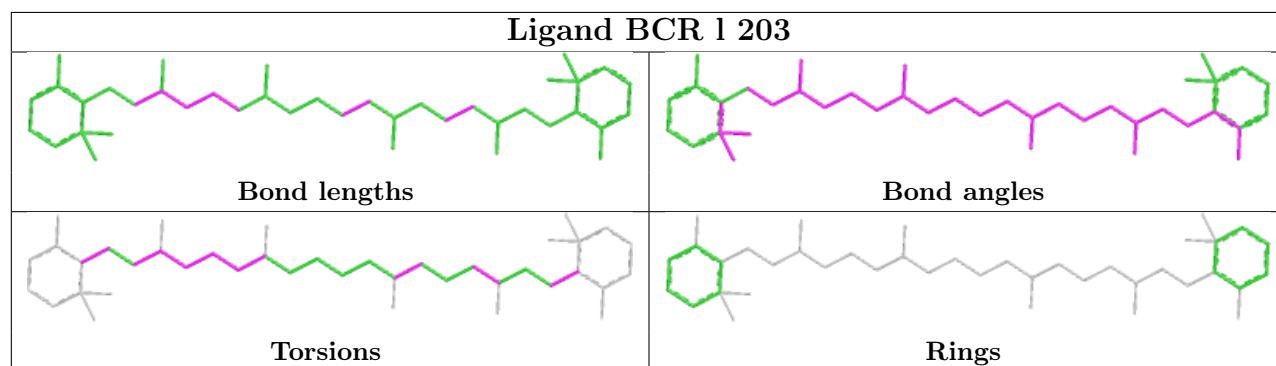
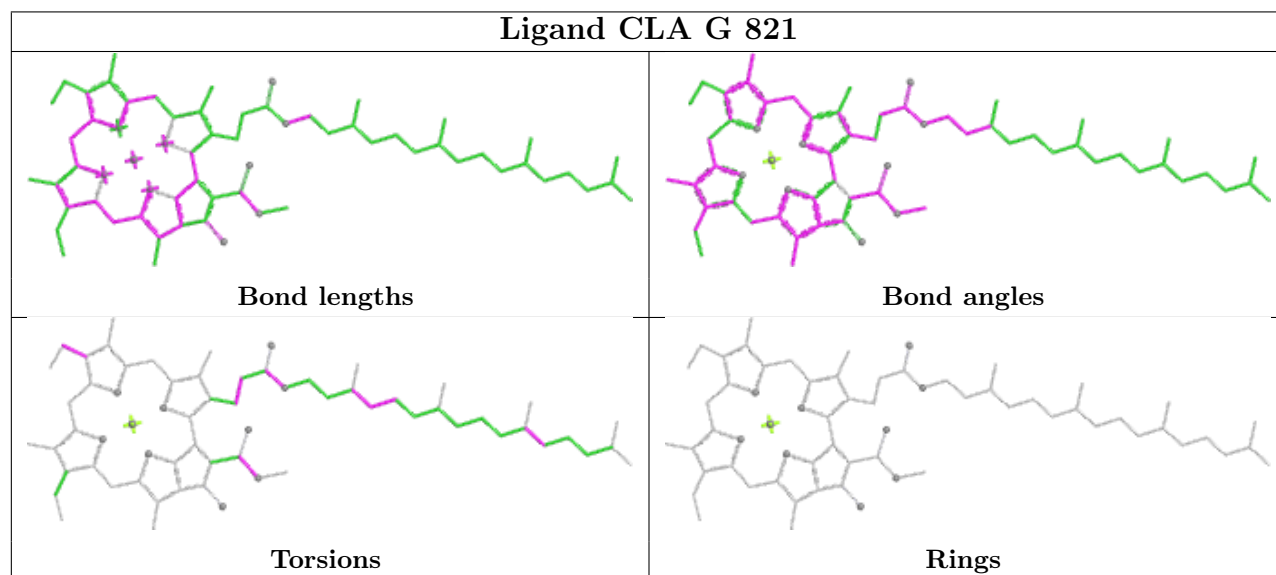
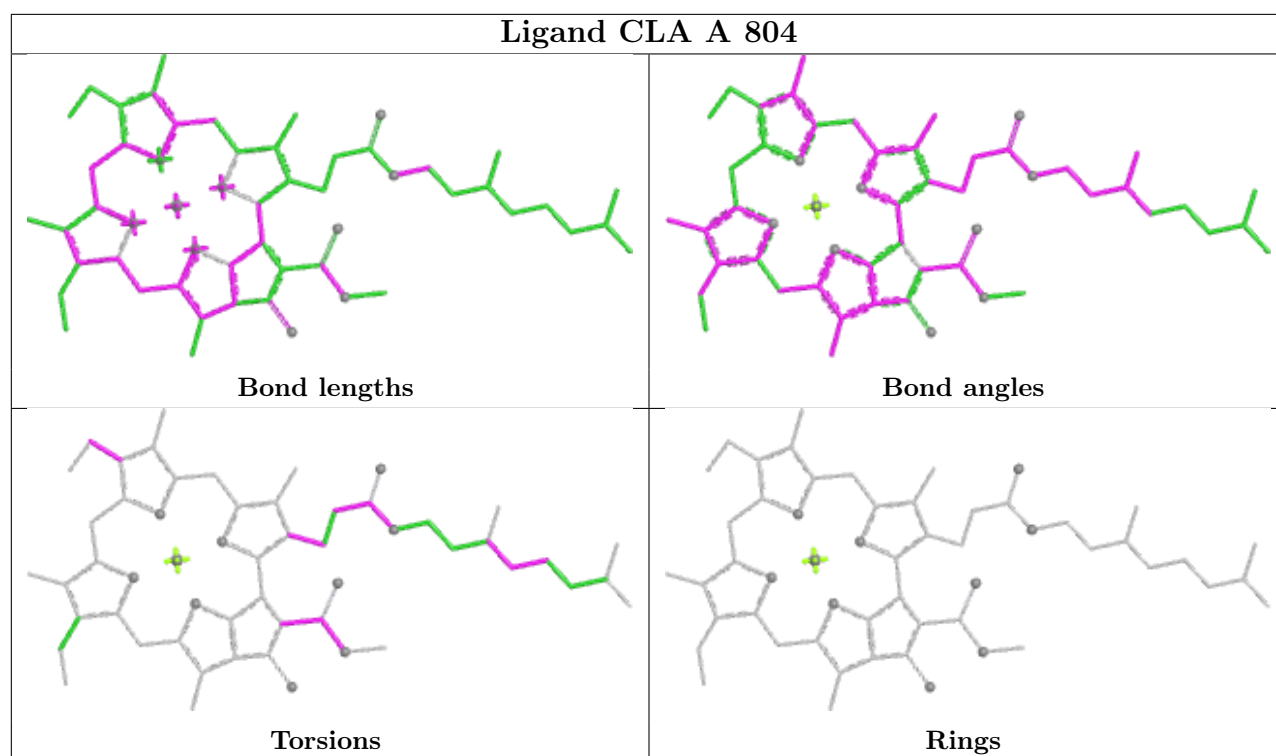
## Ligand CLA L 204

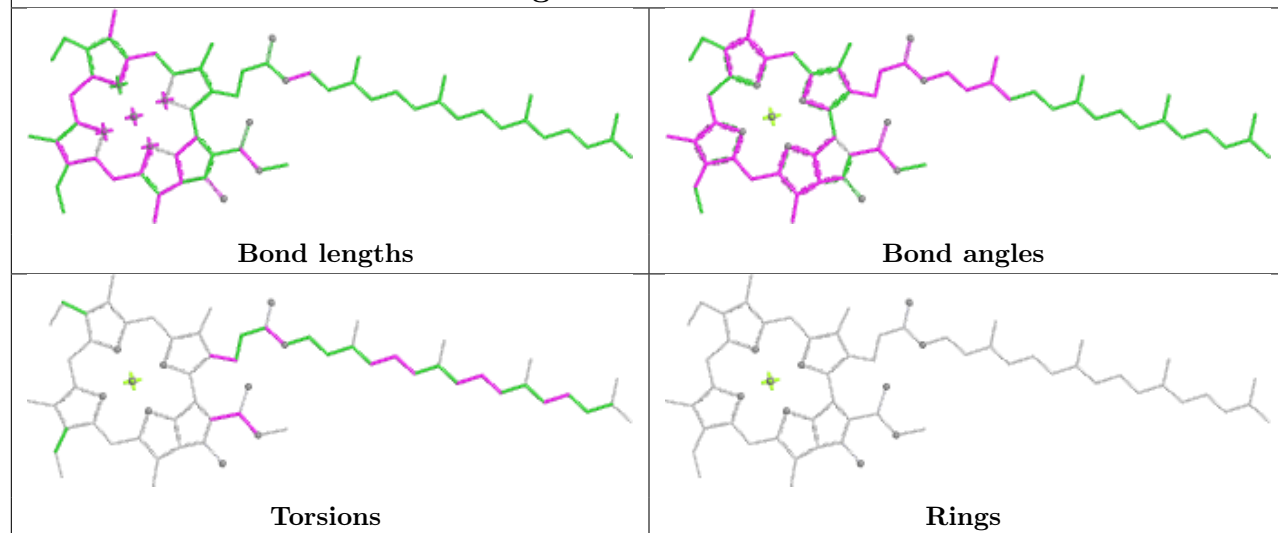
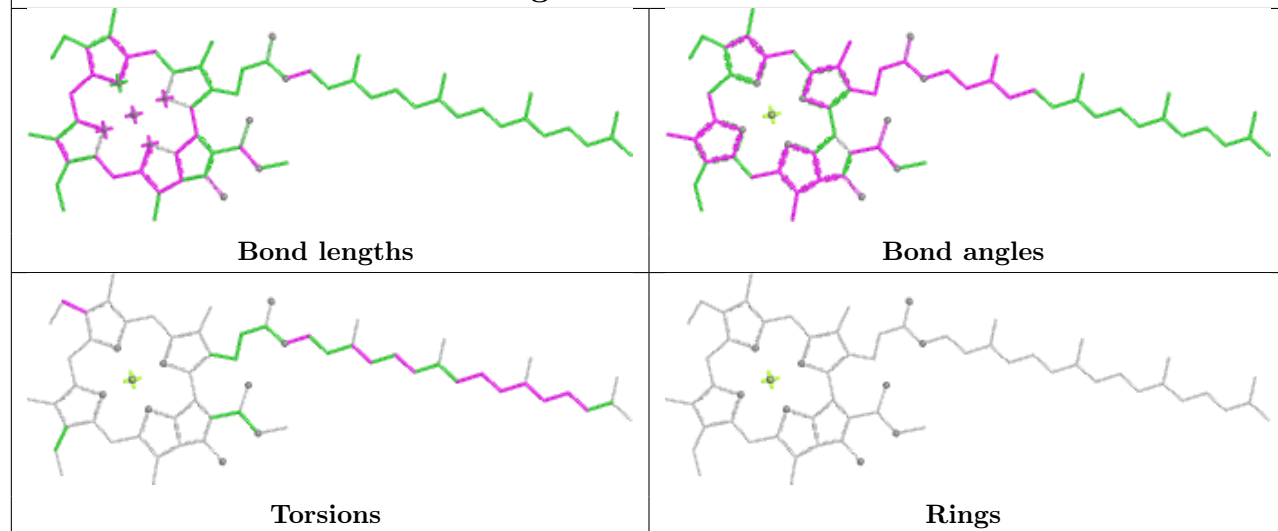


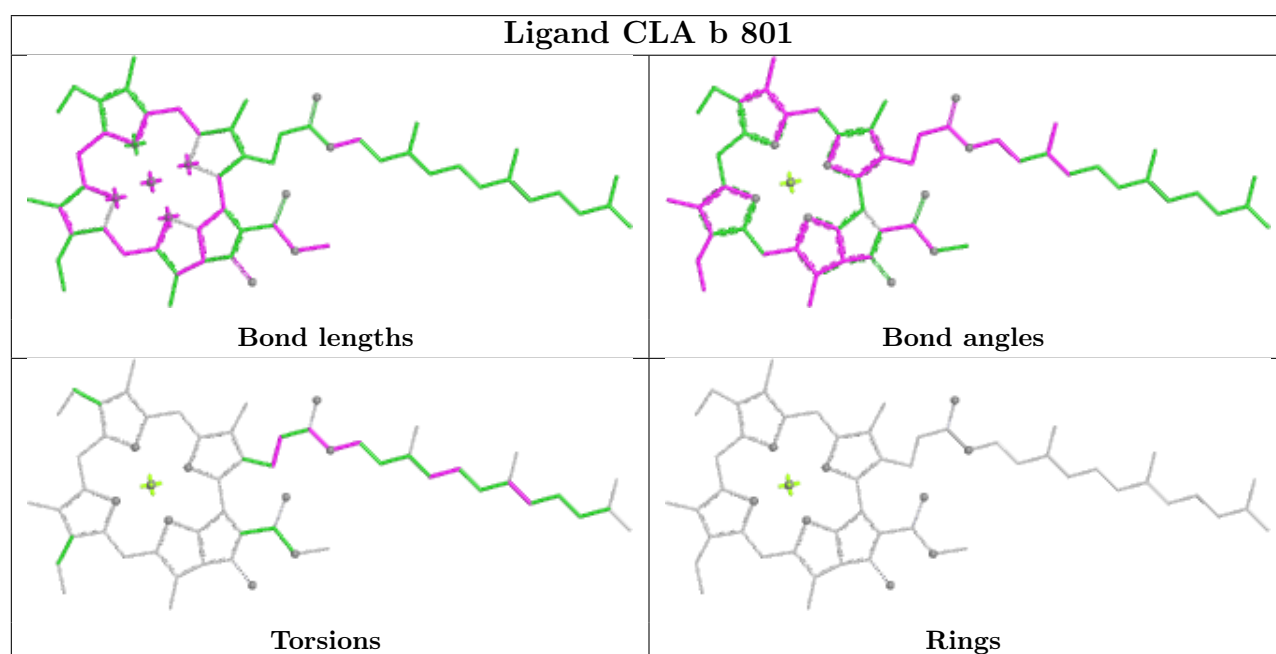
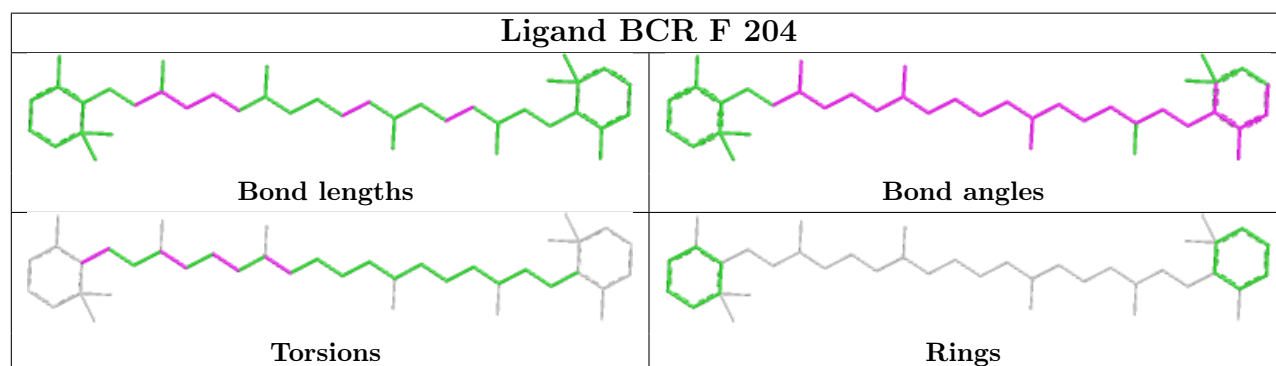
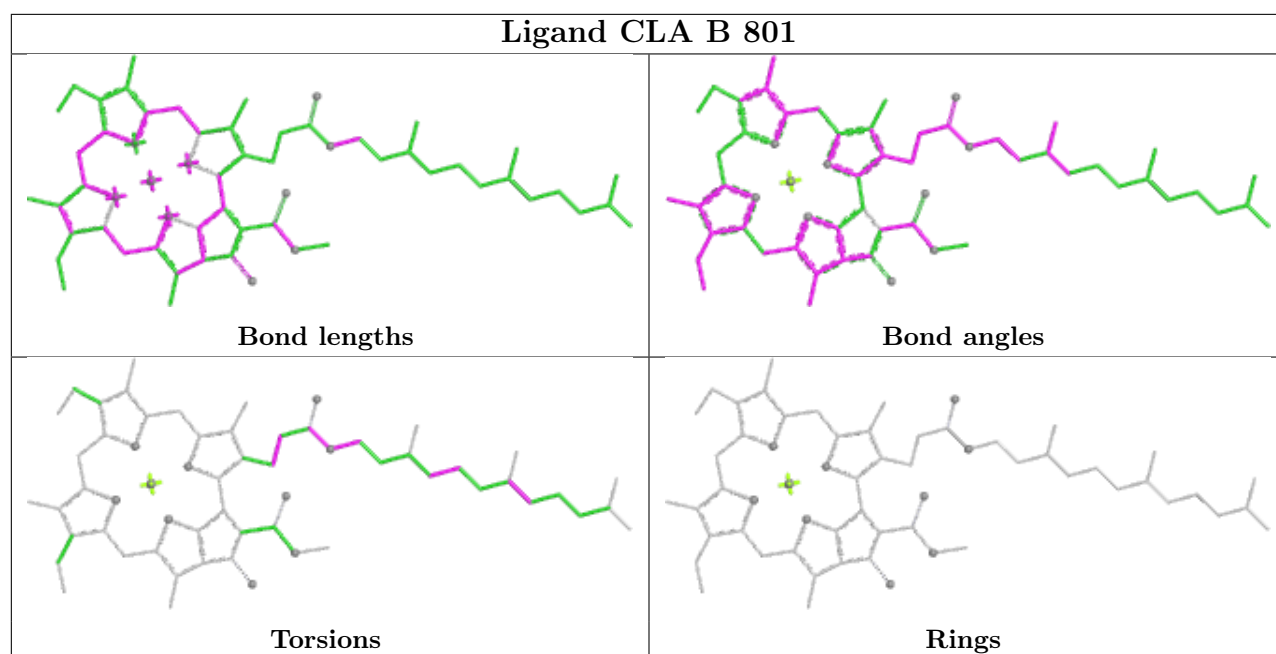
## Ligand CLA a 806







**Ligand CLA B 826****Ligand CLA G 837**



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

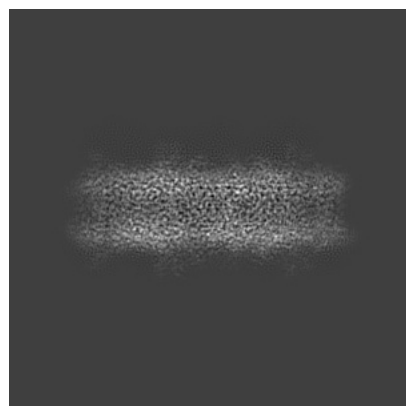
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47359. These allow visual inspection of the internal detail of the map and identification of artifacts.

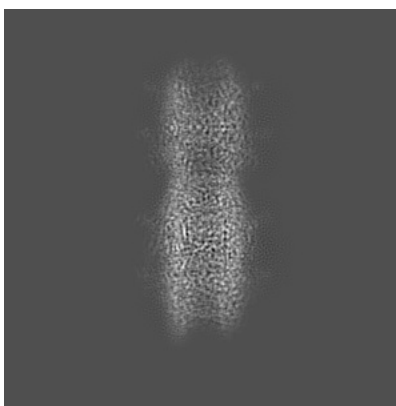
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

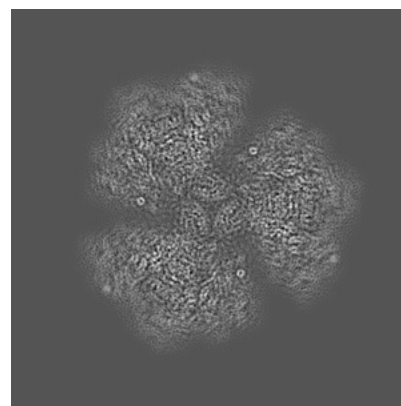
#### 6.1.1 Primary map



X

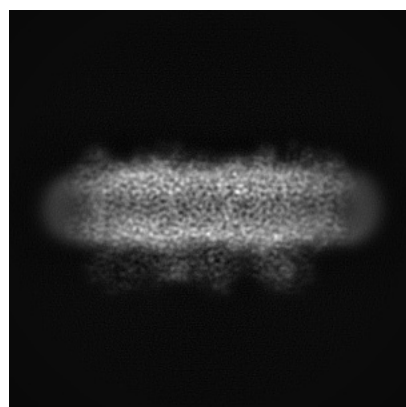


Y

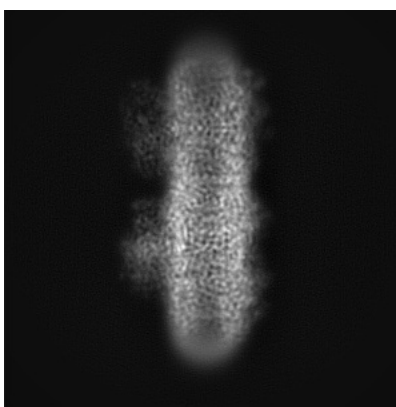


Z

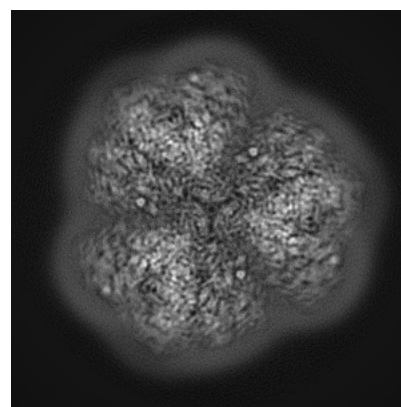
#### 6.1.2 Raw map



X



Y

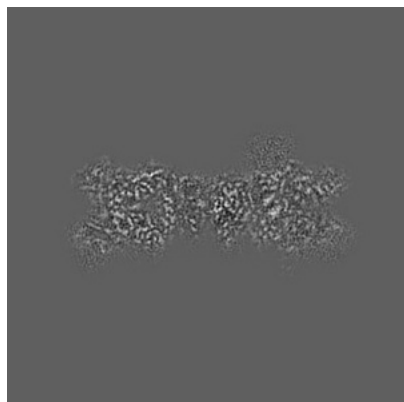


Z

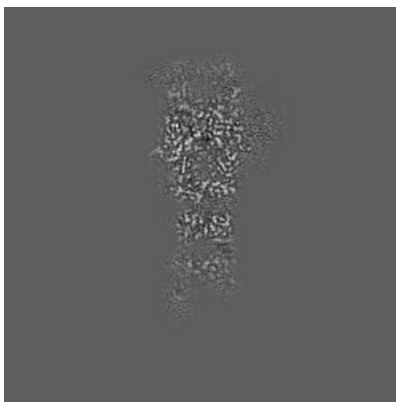
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

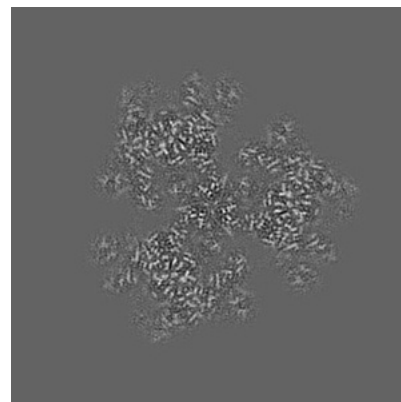
### 6.2.1 Primary map



X Index: 160

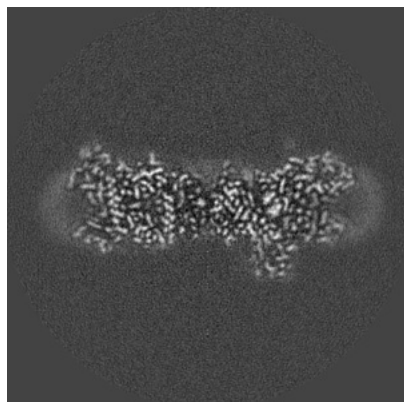


Y Index: 160

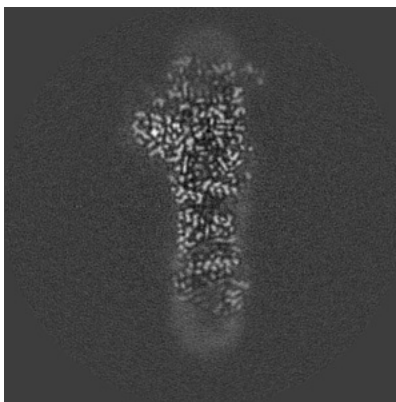


Z Index: 160

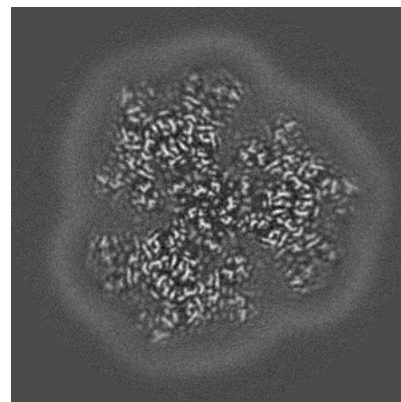
### 6.2.2 Raw map



X Index: 160



Y Index: 160

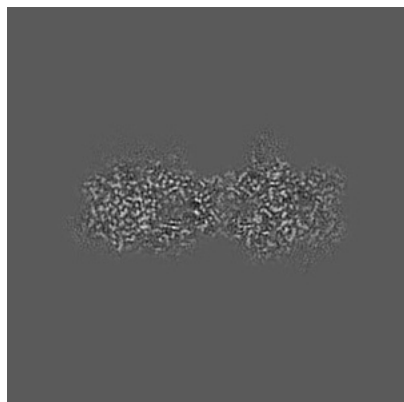


Z Index: 160

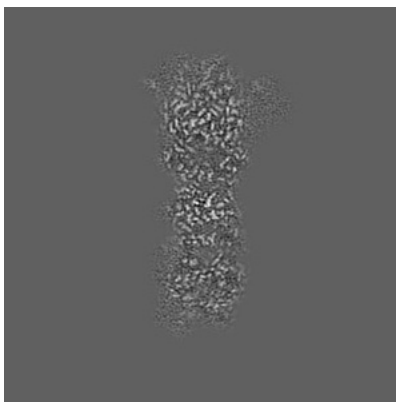
The images above show central slices of the map in three orthogonal directions.

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

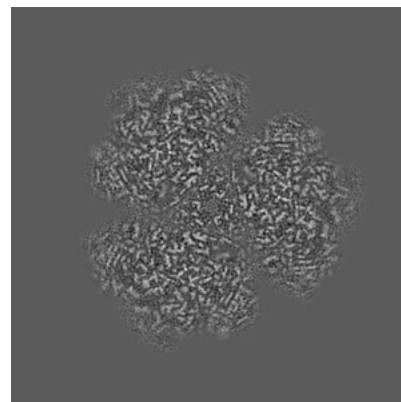
### 6.3.1 Primary map



X Index: 142

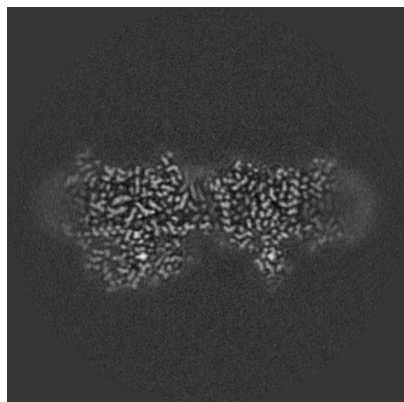


Y Index: 175

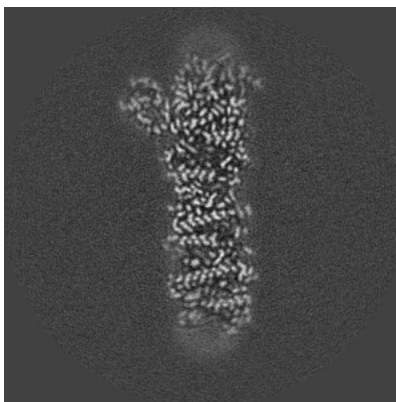


Z Index: 174

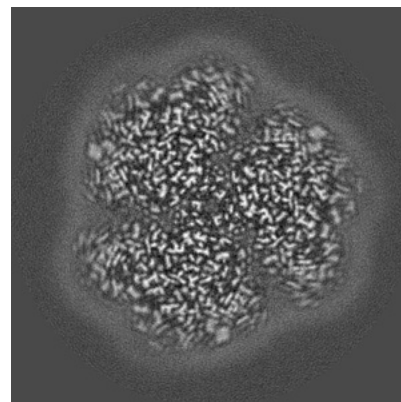
### 6.3.2 Raw map



X Index: 131



Y Index: 175

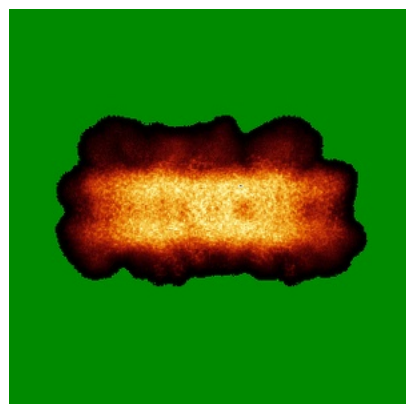


Z Index: 175

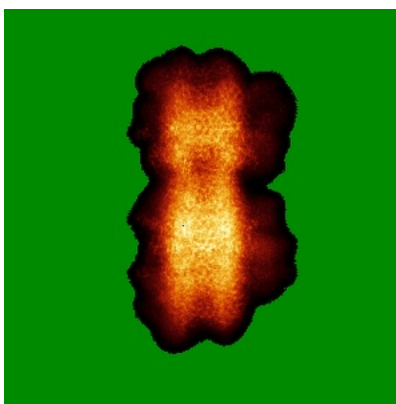
The images above show the largest variance slices of the map in three orthogonal directions.

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

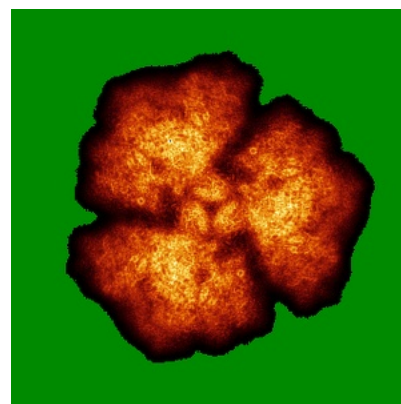
### 6.4.1 Primary map



X

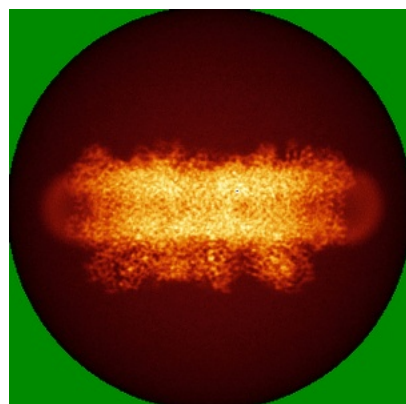


Y

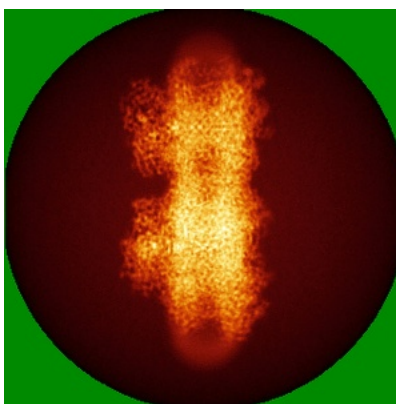


Z

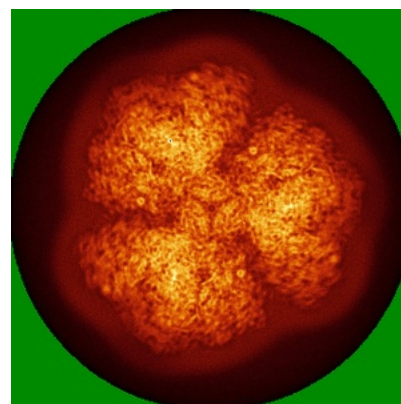
### 6.4.2 Raw map



X



Y

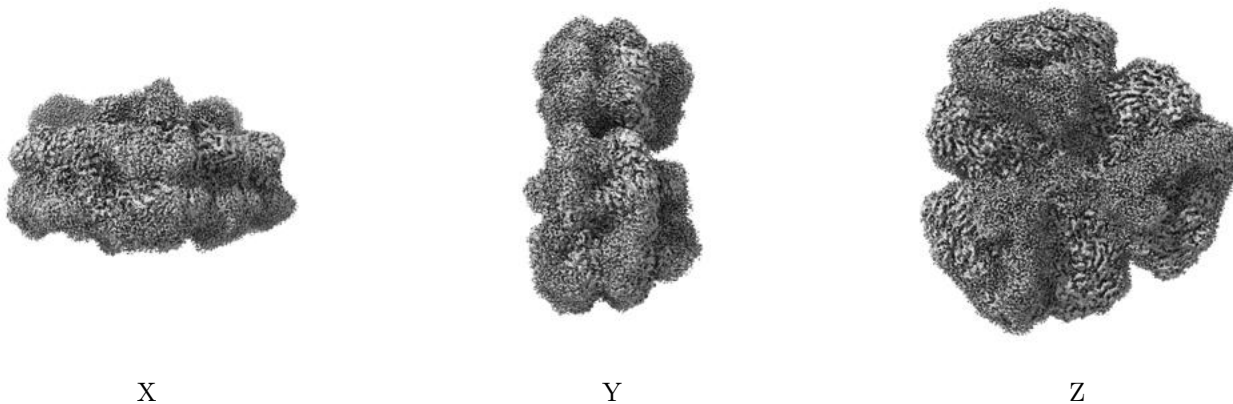


Z

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.

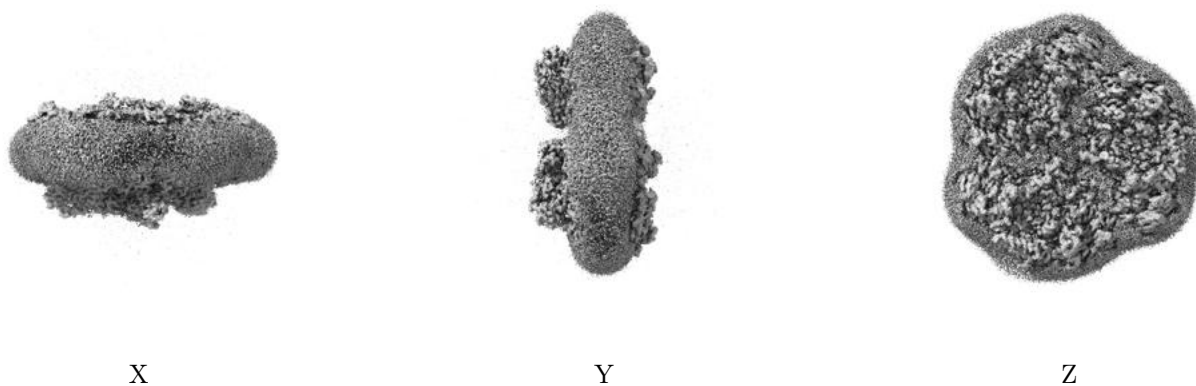
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00112. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

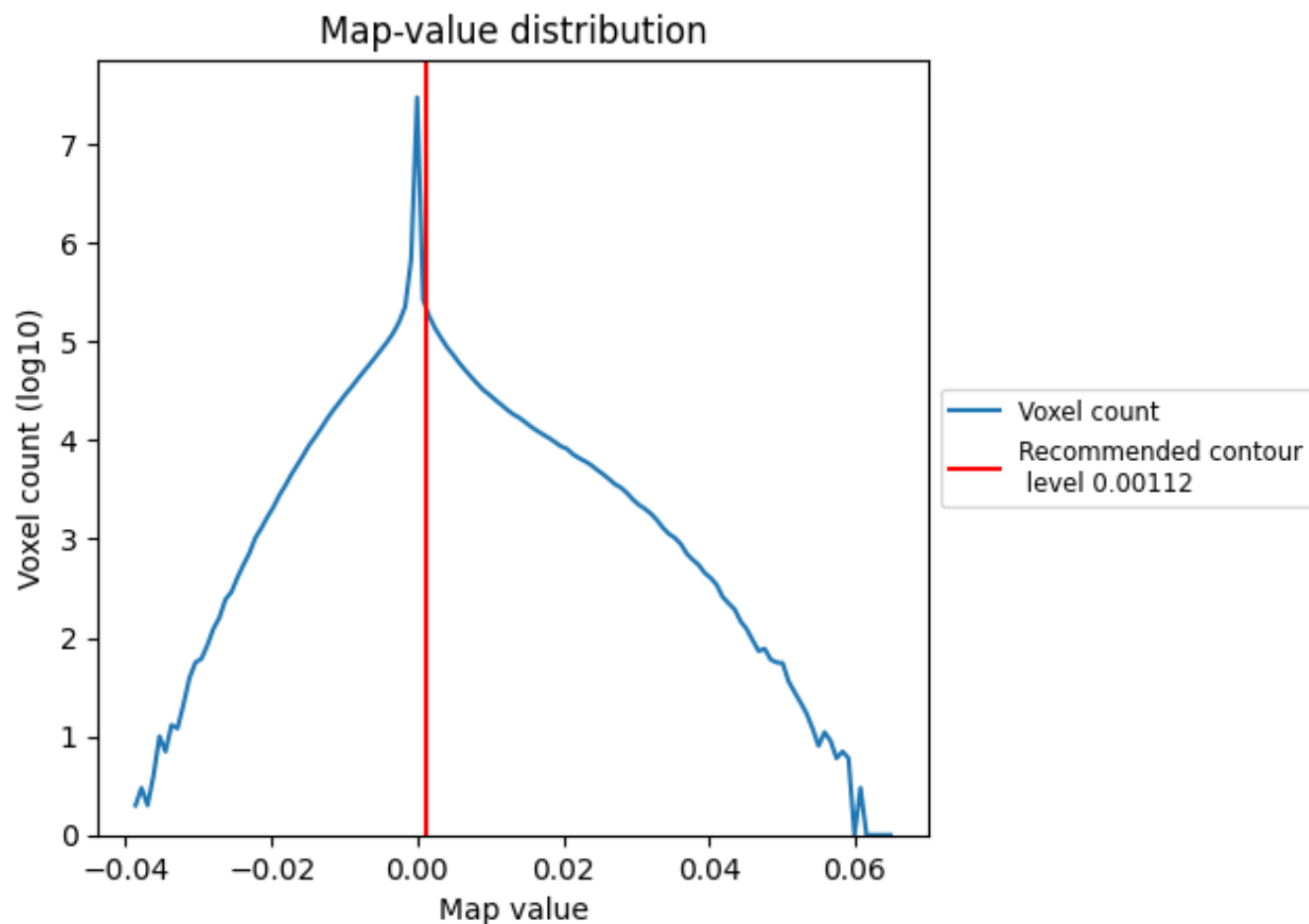
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

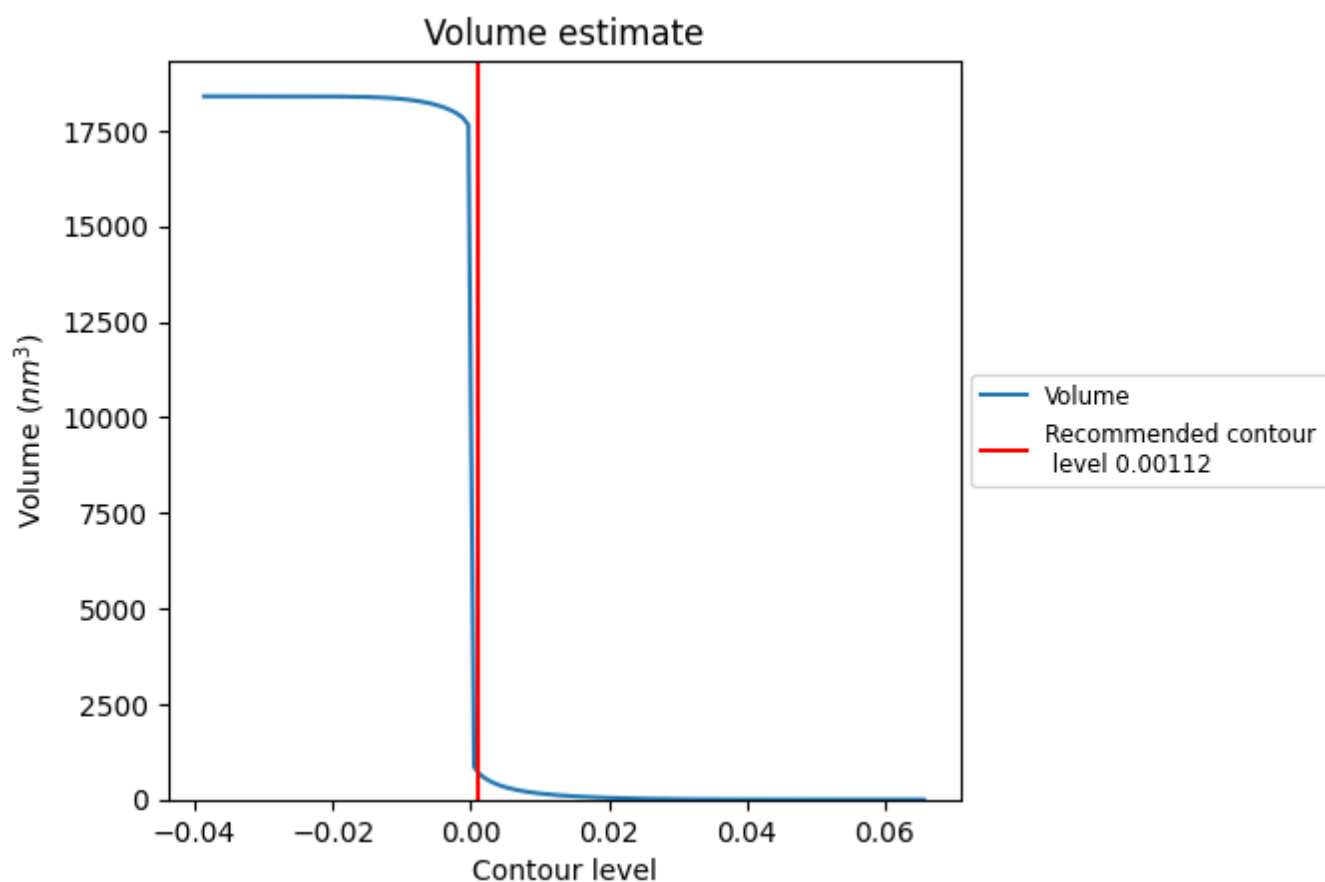
This section contains the results of statistical analysis of the map.

### 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.

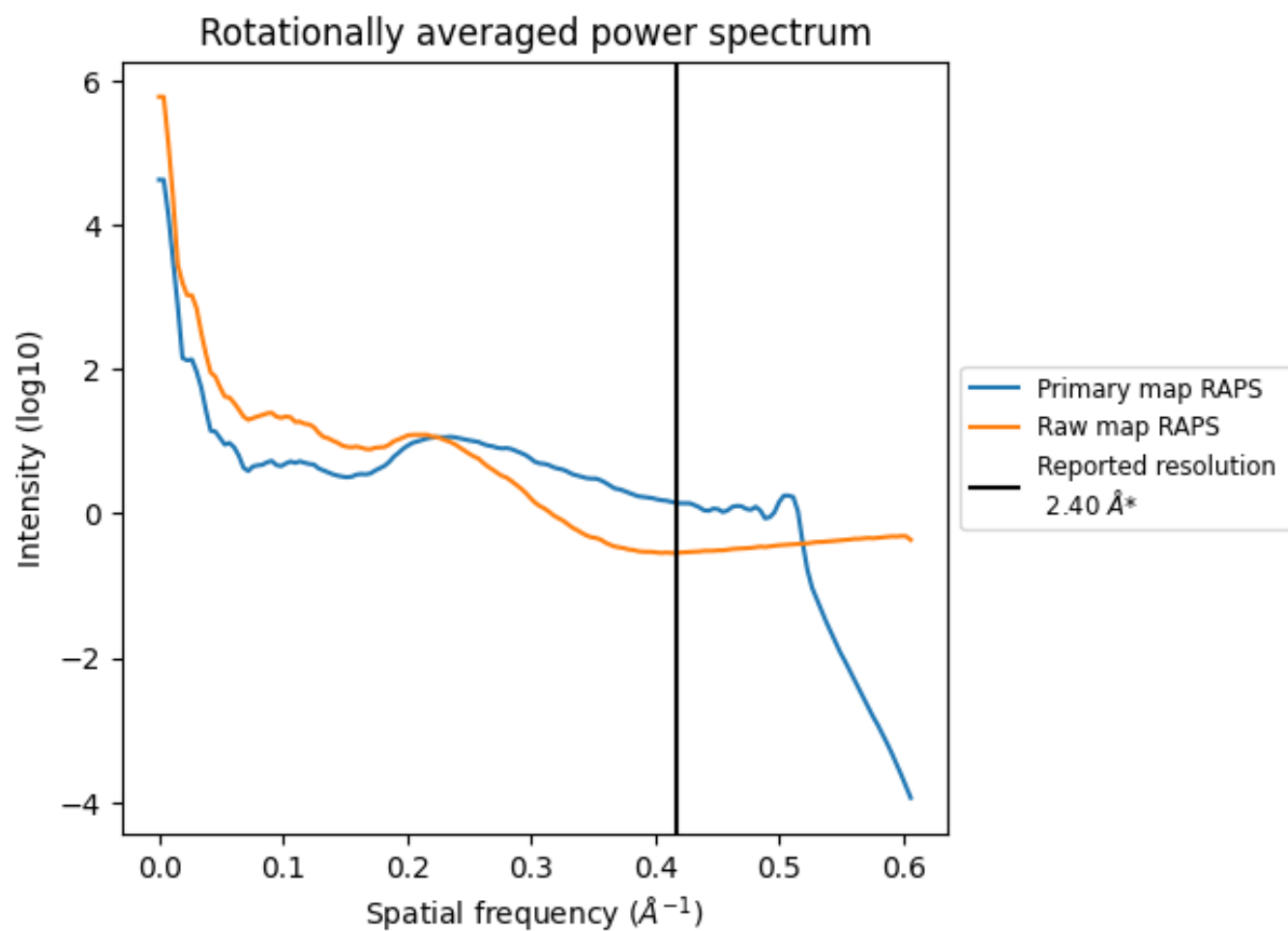
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 708 nm<sup>3</sup>; this corresponds to an approximate mass of 640 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

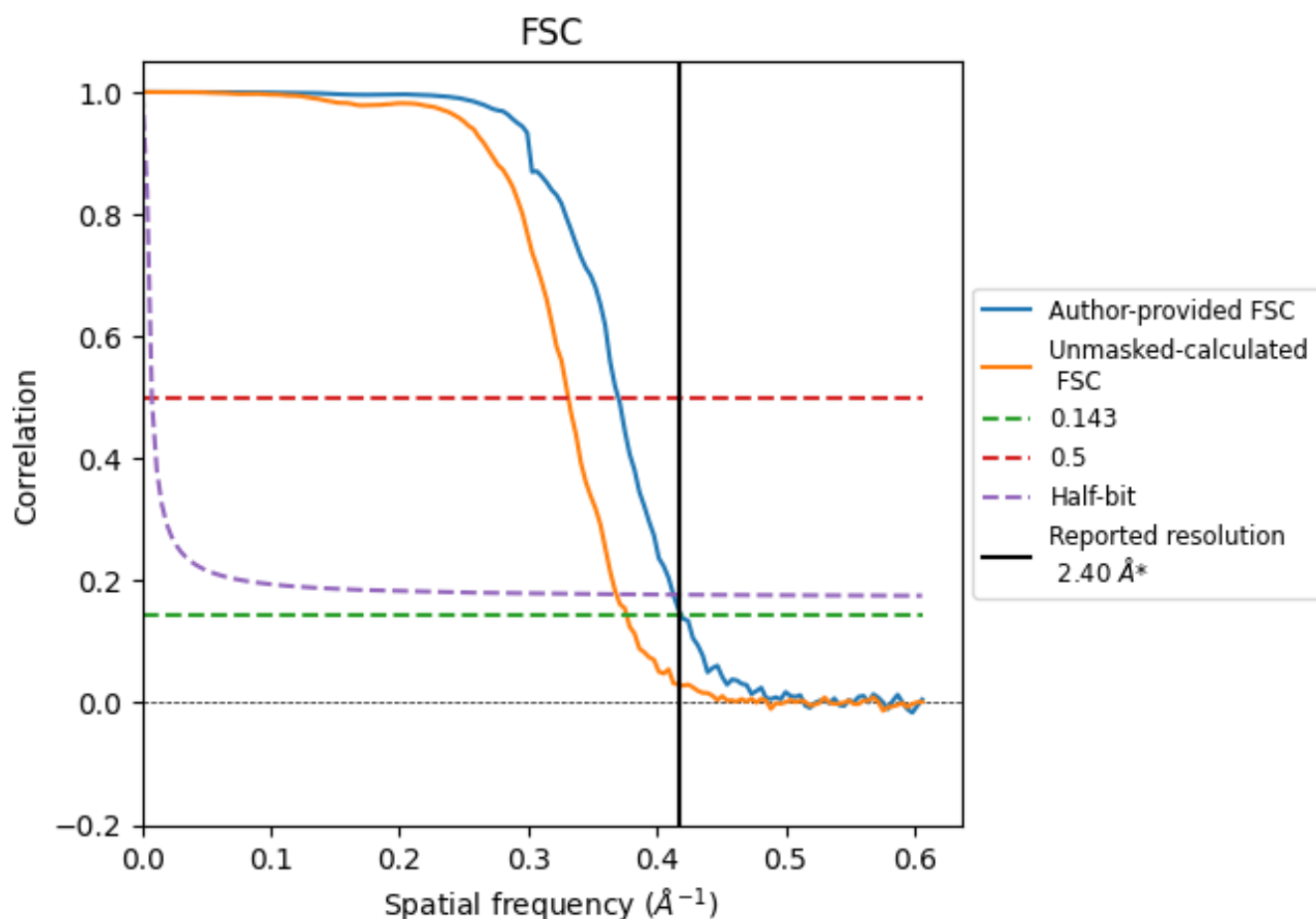


\*Reported resolution corresponds to spatial frequency of  $0.417 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.417 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

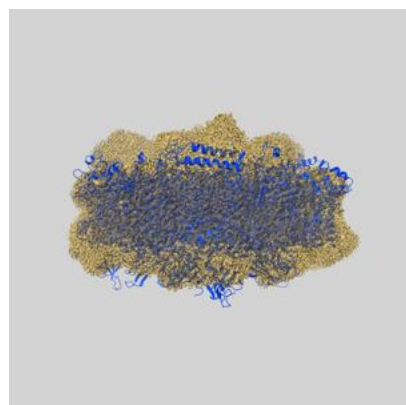
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.40                               | -    | -        |
| Author-provided FSC curve | 2.39                               | 2.70 | 2.42     |
| Unmasked-calculated*      | 2.66                               | 3.02 | 2.71     |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.66 differs from the reported value 2.4 by more than 10 %

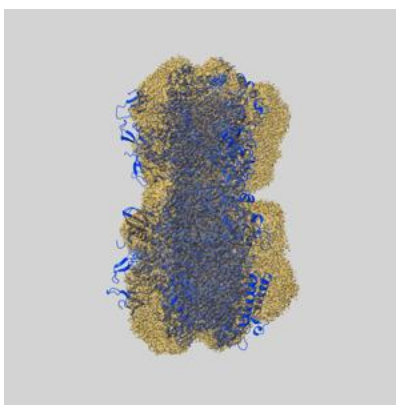
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47359 and PDB model 9E0J. Per-residue inclusion information can be found in section [3](#) on page [30](#).

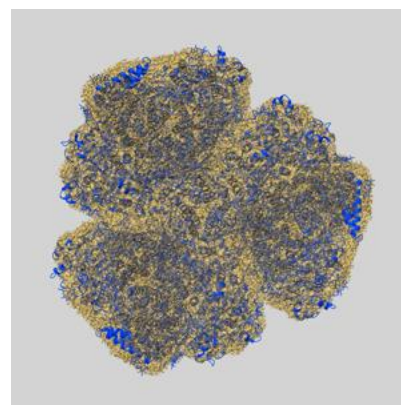
### 9.1 Map-model overlay [i](#)



X



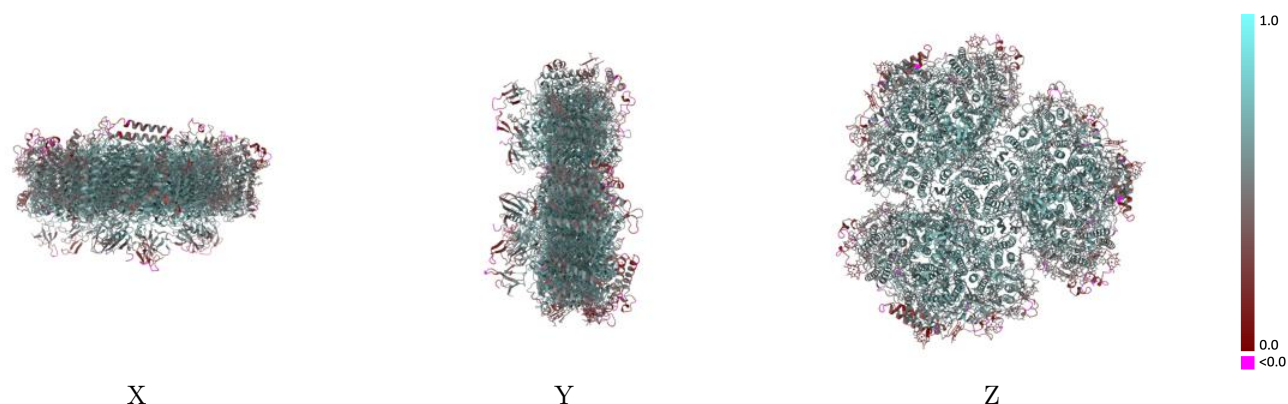
Y



Z

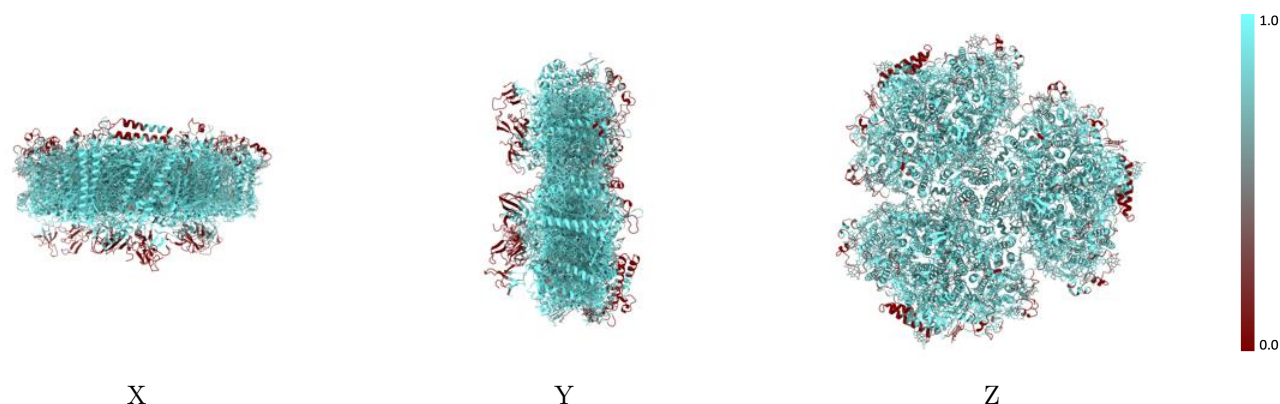
The images above show the 3D surface view of the map at the recommended contour level 0.00112 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



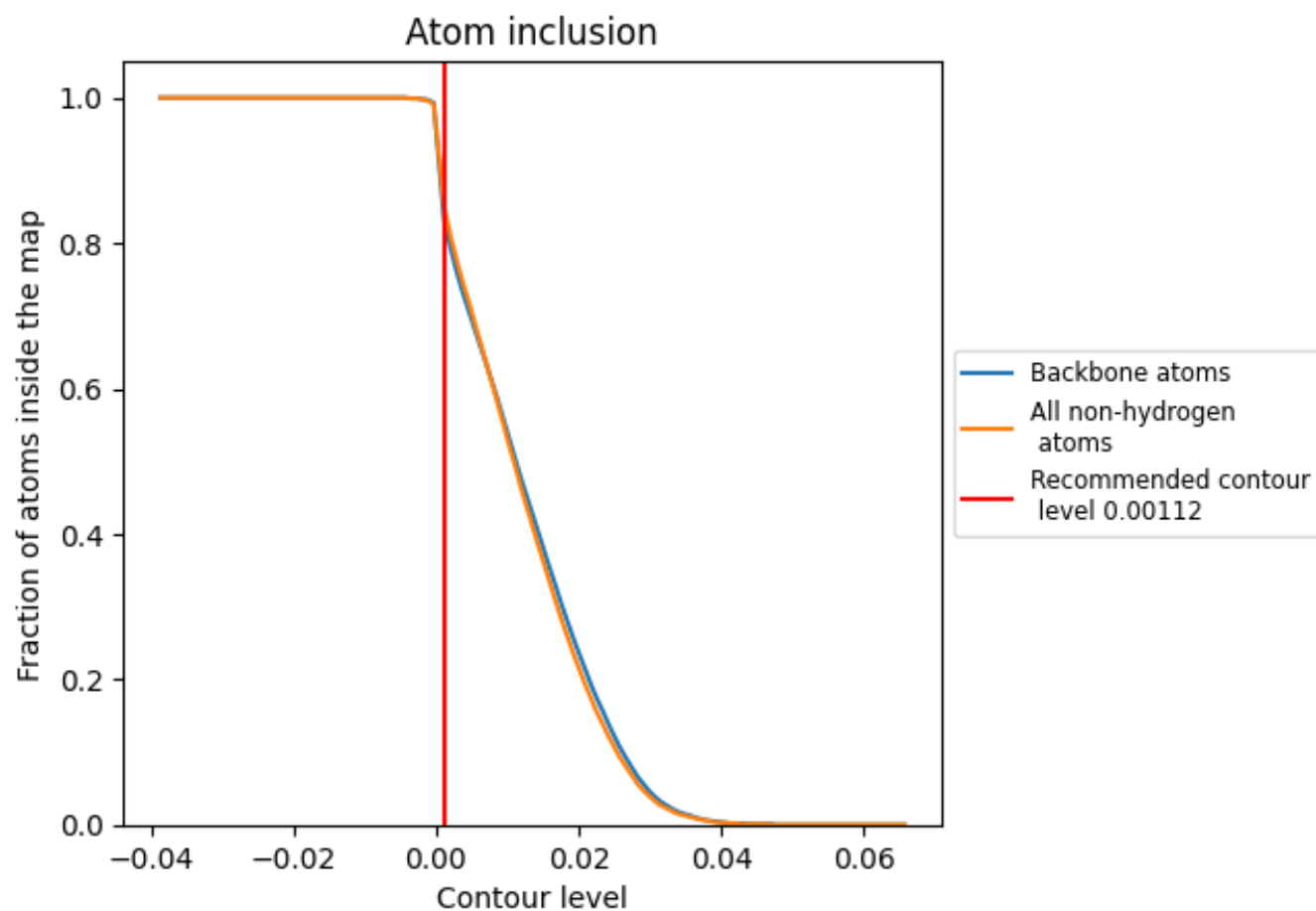
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00112).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 85% 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 (0.00112) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.8510   |  0.5700   |
| A     |  0.9120   |  0.5760   |
| B     |  0.9030   |  0.6090   |
| C     |  0.3140   |  0.4450   |
| D     |  0.4860   |  0.4910   |
| E     |  0.4120   |  0.3990   |
| F     |  0.6840   |  0.4230   |
| G     |  0.9130   |  0.5760   |
| H     |  0.8980   |  0.6030   |
| I     |  0.9590   |  0.6510   |
| J     |  0.7760   |  0.4280   |
| K     |  0.3120   |  0.4410   |
| L     |  0.9010   |  0.6240   |
| M     |  0.9370   |  0.6550   |
| N     |  0.4850  |  0.5060  |
| O     |  0.4290 |  0.4260 |
| P     |  0.6600 |  0.4140 |
| Q     |  0.9450 |  0.6480 |
| R     |  0.7480 |  0.3910 |
| S     |  0.8980 |  0.6210 |
| T     |  0.9400 |  0.6400 |
| a     |  0.9100 |  0.5760 |
| b     |  0.9000 |  0.6050 |
| c     |  0.3170 |  0.4490 |
| d     |  0.4840 |  0.4930 |
| e     |  0.4100 |  0.4110 |
| f     |  0.6690 |  0.4100 |
| i     |  0.9670 |  0.6570 |
| j     |  0.7930 |  0.4330 |
| l     |  0.9000 |  0.6200 |
| m     |  0.9370 |  0.6320 |

