



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:29 AM UTC

PDB ID : 4RKM / pdb_00004rkm
Title : Wolinella succinogenes octaheme sulfite reductase MccA, form I
Authors : Hermann, B.; Kern, M.; La Pietra, L.; Simon, J.; Einsle, O.
Deposited on : 2014-10-13
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

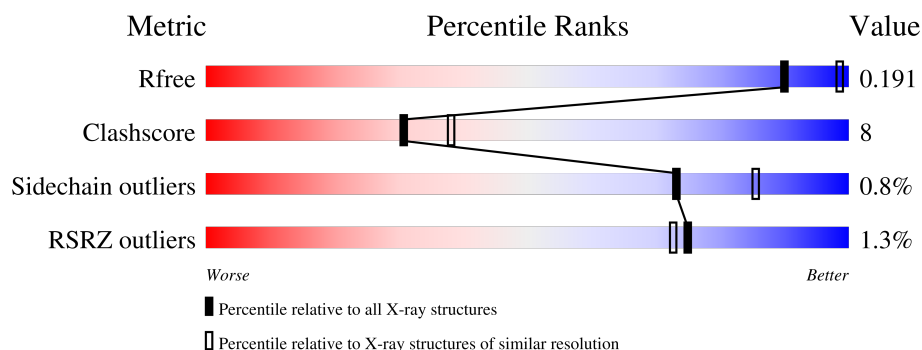
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	732	
1	B	732	
1	C	732	
1	D	732	
1	E	732	
1	F	732	

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Mol	Chain	Length	Quality of chain
1	G	732	% 84% 5% 10%
1	H	732	% 86% 10%
1	I	732	85% 10%
1	J	732	2% 84% 5% 10%
1	K	732	% 85% 5% 10%
1	L	732	2% 85% 5% 10%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 70014 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 MccA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	B	660	Total	C	N	O	S	0	0	0
			5232	3289	920	988	35			
1	C	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	D	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	E	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	F	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	H	660	Total	C	N	O	S	0	0	0
			5232	3289	920	988	35			
1	I	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	J	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	K	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	L	659	Total	C	N	O	S	0	0	0
			5224	3283	919	987	35			
1	G	658	Total	C	N	O	S	0	0	0
			5218	3280	918	985	35			

There are 360 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	691	SER	-	expression tag	UNP Q7MSJ8
A	692	ALA	-	expression tag	UNP Q7MSJ8
A	693	TRP	-	expression tag	UNP Q7MSJ8
A	694	SER	-	expression tag	UNP Q7MSJ8
A	695	HIS	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	696	PRO	-	expression tag	UNP Q7MSJ8
A	697	GLN	-	expression tag	UNP Q7MSJ8
A	698	PHE	-	expression tag	UNP Q7MSJ8
A	699	GLU	-	expression tag	UNP Q7MSJ8
A	700	LYS	-	expression tag	UNP Q7MSJ8
A	701	GLY	-	expression tag	UNP Q7MSJ8
A	702	GLY	-	expression tag	UNP Q7MSJ8
A	703	GLY	-	expression tag	UNP Q7MSJ8
A	704	SER	-	expression tag	UNP Q7MSJ8
A	705	GLY	-	expression tag	UNP Q7MSJ8
A	706	GLY	-	expression tag	UNP Q7MSJ8
A	707	GLY	-	expression tag	UNP Q7MSJ8
A	708	SER	-	expression tag	UNP Q7MSJ8
A	709	GLY	-	expression tag	UNP Q7MSJ8
A	710	GLY	-	expression tag	UNP Q7MSJ8
A	711	SER	-	expression tag	UNP Q7MSJ8
A	712	ALA	-	expression tag	UNP Q7MSJ8
A	713	TRP	-	expression tag	UNP Q7MSJ8
A	714	SER	-	expression tag	UNP Q7MSJ8
A	715	HIS	-	expression tag	UNP Q7MSJ8
A	716	PRO	-	expression tag	UNP Q7MSJ8
A	717	GLN	-	expression tag	UNP Q7MSJ8
A	718	PHE	-	expression tag	UNP Q7MSJ8
A	719	GLU	-	expression tag	UNP Q7MSJ8
A	720	LYS	-	expression tag	UNP Q7MSJ8
B	691	SER	-	expression tag	UNP Q7MSJ8
B	692	ALA	-	expression tag	UNP Q7MSJ8
B	693	TRP	-	expression tag	UNP Q7MSJ8
B	694	SER	-	expression tag	UNP Q7MSJ8
B	695	HIS	-	expression tag	UNP Q7MSJ8
B	696	PRO	-	expression tag	UNP Q7MSJ8
B	697	GLN	-	expression tag	UNP Q7MSJ8
B	698	PHE	-	expression tag	UNP Q7MSJ8
B	699	GLU	-	expression tag	UNP Q7MSJ8
B	700	LYS	-	expression tag	UNP Q7MSJ8
B	701	GLY	-	expression tag	UNP Q7MSJ8
B	702	GLY	-	expression tag	UNP Q7MSJ8
B	703	GLY	-	expression tag	UNP Q7MSJ8
B	704	SER	-	expression tag	UNP Q7MSJ8
B	705	GLY	-	expression tag	UNP Q7MSJ8
B	706	GLY	-	expression tag	UNP Q7MSJ8
B	707	GLY	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	708	SER	-	expression tag	UNP Q7MSJ8
B	709	GLY	-	expression tag	UNP Q7MSJ8
B	710	GLY	-	expression tag	UNP Q7MSJ8
B	711	SER	-	expression tag	UNP Q7MSJ8
B	712	ALA	-	expression tag	UNP Q7MSJ8
B	713	TRP	-	expression tag	UNP Q7MSJ8
B	714	SER	-	expression tag	UNP Q7MSJ8
B	715	HIS	-	expression tag	UNP Q7MSJ8
B	716	PRO	-	expression tag	UNP Q7MSJ8
B	717	GLN	-	expression tag	UNP Q7MSJ8
B	718	PHE	-	expression tag	UNP Q7MSJ8
B	719	GLU	-	expression tag	UNP Q7MSJ8
B	720	LYS	-	expression tag	UNP Q7MSJ8
C	691	SER	-	expression tag	UNP Q7MSJ8
C	692	ALA	-	expression tag	UNP Q7MSJ8
C	693	TRP	-	expression tag	UNP Q7MSJ8
C	694	SER	-	expression tag	UNP Q7MSJ8
C	695	HIS	-	expression tag	UNP Q7MSJ8
C	696	PRO	-	expression tag	UNP Q7MSJ8
C	697	GLN	-	expression tag	UNP Q7MSJ8
C	698	PHE	-	expression tag	UNP Q7MSJ8
C	699	GLU	-	expression tag	UNP Q7MSJ8
C	700	LYS	-	expression tag	UNP Q7MSJ8
C	701	GLY	-	expression tag	UNP Q7MSJ8
C	702	GLY	-	expression tag	UNP Q7MSJ8
C	703	GLY	-	expression tag	UNP Q7MSJ8
C	704	SER	-	expression tag	UNP Q7MSJ8
C	705	GLY	-	expression tag	UNP Q7MSJ8
C	706	GLY	-	expression tag	UNP Q7MSJ8
C	707	GLY	-	expression tag	UNP Q7MSJ8
C	708	SER	-	expression tag	UNP Q7MSJ8
C	709	GLY	-	expression tag	UNP Q7MSJ8
C	710	GLY	-	expression tag	UNP Q7MSJ8
C	711	SER	-	expression tag	UNP Q7MSJ8
C	712	ALA	-	expression tag	UNP Q7MSJ8
C	713	TRP	-	expression tag	UNP Q7MSJ8
C	714	SER	-	expression tag	UNP Q7MSJ8
C	715	HIS	-	expression tag	UNP Q7MSJ8
C	716	PRO	-	expression tag	UNP Q7MSJ8
C	717	GLN	-	expression tag	UNP Q7MSJ8
C	718	PHE	-	expression tag	UNP Q7MSJ8
C	719	GLU	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	720	LYS	-	expression tag	UNP Q7MSJ8
D	691	SER	-	expression tag	UNP Q7MSJ8
D	692	ALA	-	expression tag	UNP Q7MSJ8
D	693	TRP	-	expression tag	UNP Q7MSJ8
D	694	SER	-	expression tag	UNP Q7MSJ8
D	695	HIS	-	expression tag	UNP Q7MSJ8
D	696	PRO	-	expression tag	UNP Q7MSJ8
D	697	GLN	-	expression tag	UNP Q7MSJ8
D	698	PHE	-	expression tag	UNP Q7MSJ8
D	699	GLU	-	expression tag	UNP Q7MSJ8
D	700	LYS	-	expression tag	UNP Q7MSJ8
D	701	GLY	-	expression tag	UNP Q7MSJ8
D	702	GLY	-	expression tag	UNP Q7MSJ8
D	703	GLY	-	expression tag	UNP Q7MSJ8
D	704	SER	-	expression tag	UNP Q7MSJ8
D	705	GLY	-	expression tag	UNP Q7MSJ8
D	706	GLY	-	expression tag	UNP Q7MSJ8
D	707	GLY	-	expression tag	UNP Q7MSJ8
D	708	SER	-	expression tag	UNP Q7MSJ8
D	709	GLY	-	expression tag	UNP Q7MSJ8
D	710	GLY	-	expression tag	UNP Q7MSJ8
D	711	SER	-	expression tag	UNP Q7MSJ8
D	712	ALA	-	expression tag	UNP Q7MSJ8
D	713	TRP	-	expression tag	UNP Q7MSJ8
D	714	SER	-	expression tag	UNP Q7MSJ8
D	715	HIS	-	expression tag	UNP Q7MSJ8
D	716	PRO	-	expression tag	UNP Q7MSJ8
D	717	GLN	-	expression tag	UNP Q7MSJ8
D	718	PHE	-	expression tag	UNP Q7MSJ8
D	719	GLU	-	expression tag	UNP Q7MSJ8
D	720	LYS	-	expression tag	UNP Q7MSJ8
E	691	SER	-	expression tag	UNP Q7MSJ8
E	692	ALA	-	expression tag	UNP Q7MSJ8
E	693	TRP	-	expression tag	UNP Q7MSJ8
E	694	SER	-	expression tag	UNP Q7MSJ8
E	695	HIS	-	expression tag	UNP Q7MSJ8
E	696	PRO	-	expression tag	UNP Q7MSJ8
E	697	GLN	-	expression tag	UNP Q7MSJ8
E	698	PHE	-	expression tag	UNP Q7MSJ8
E	699	GLU	-	expression tag	UNP Q7MSJ8
E	700	LYS	-	expression tag	UNP Q7MSJ8
E	701	GLY	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	702	GLY	-	expression tag	UNP Q7MSJ8
E	703	GLY	-	expression tag	UNP Q7MSJ8
E	704	SER	-	expression tag	UNP Q7MSJ8
E	705	GLY	-	expression tag	UNP Q7MSJ8
E	706	GLY	-	expression tag	UNP Q7MSJ8
E	707	GLY	-	expression tag	UNP Q7MSJ8
E	708	SER	-	expression tag	UNP Q7MSJ8
E	709	GLY	-	expression tag	UNP Q7MSJ8
E	710	GLY	-	expression tag	UNP Q7MSJ8
E	711	SER	-	expression tag	UNP Q7MSJ8
E	712	ALA	-	expression tag	UNP Q7MSJ8
E	713	TRP	-	expression tag	UNP Q7MSJ8
E	714	SER	-	expression tag	UNP Q7MSJ8
E	715	HIS	-	expression tag	UNP Q7MSJ8
E	716	PRO	-	expression tag	UNP Q7MSJ8
E	717	GLN	-	expression tag	UNP Q7MSJ8
E	718	PHE	-	expression tag	UNP Q7MSJ8
E	719	GLU	-	expression tag	UNP Q7MSJ8
E	720	LYS	-	expression tag	UNP Q7MSJ8
F	691	SER	-	expression tag	UNP Q7MSJ8
F	692	ALA	-	expression tag	UNP Q7MSJ8
F	693	TRP	-	expression tag	UNP Q7MSJ8
F	694	SER	-	expression tag	UNP Q7MSJ8
F	695	HIS	-	expression tag	UNP Q7MSJ8
F	696	PRO	-	expression tag	UNP Q7MSJ8
F	697	GLN	-	expression tag	UNP Q7MSJ8
F	698	PHE	-	expression tag	UNP Q7MSJ8
F	699	GLU	-	expression tag	UNP Q7MSJ8
F	700	LYS	-	expression tag	UNP Q7MSJ8
F	701	GLY	-	expression tag	UNP Q7MSJ8
F	702	GLY	-	expression tag	UNP Q7MSJ8
F	703	GLY	-	expression tag	UNP Q7MSJ8
F	704	SER	-	expression tag	UNP Q7MSJ8
F	705	GLY	-	expression tag	UNP Q7MSJ8
F	706	GLY	-	expression tag	UNP Q7MSJ8
F	707	GLY	-	expression tag	UNP Q7MSJ8
F	708	SER	-	expression tag	UNP Q7MSJ8
F	709	GLY	-	expression tag	UNP Q7MSJ8
F	710	GLY	-	expression tag	UNP Q7MSJ8
F	711	SER	-	expression tag	UNP Q7MSJ8
F	712	ALA	-	expression tag	UNP Q7MSJ8
F	713	TRP	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	714	SER	-	expression tag	UNP Q7MSJ8
F	715	HIS	-	expression tag	UNP Q7MSJ8
F	716	PRO	-	expression tag	UNP Q7MSJ8
F	717	GLN	-	expression tag	UNP Q7MSJ8
F	718	PHE	-	expression tag	UNP Q7MSJ8
F	719	GLU	-	expression tag	UNP Q7MSJ8
F	720	LYS	-	expression tag	UNP Q7MSJ8
H	691	SER	-	expression tag	UNP Q7MSJ8
H	692	ALA	-	expression tag	UNP Q7MSJ8
H	693	TRP	-	expression tag	UNP Q7MSJ8
H	694	SER	-	expression tag	UNP Q7MSJ8
H	695	HIS	-	expression tag	UNP Q7MSJ8
H	696	PRO	-	expression tag	UNP Q7MSJ8
H	697	GLN	-	expression tag	UNP Q7MSJ8
H	698	PHE	-	expression tag	UNP Q7MSJ8
H	699	GLU	-	expression tag	UNP Q7MSJ8
H	700	LYS	-	expression tag	UNP Q7MSJ8
H	701	GLY	-	expression tag	UNP Q7MSJ8
H	702	GLY	-	expression tag	UNP Q7MSJ8
H	703	GLY	-	expression tag	UNP Q7MSJ8
H	704	SER	-	expression tag	UNP Q7MSJ8
H	705	GLY	-	expression tag	UNP Q7MSJ8
H	706	GLY	-	expression tag	UNP Q7MSJ8
H	707	GLY	-	expression tag	UNP Q7MSJ8
H	708	SER	-	expression tag	UNP Q7MSJ8
H	709	GLY	-	expression tag	UNP Q7MSJ8
H	710	GLY	-	expression tag	UNP Q7MSJ8
H	711	SER	-	expression tag	UNP Q7MSJ8
H	712	ALA	-	expression tag	UNP Q7MSJ8
H	713	TRP	-	expression tag	UNP Q7MSJ8
H	714	SER	-	expression tag	UNP Q7MSJ8
H	715	HIS	-	expression tag	UNP Q7MSJ8
H	716	PRO	-	expression tag	UNP Q7MSJ8
H	717	GLN	-	expression tag	UNP Q7MSJ8
H	718	PHE	-	expression tag	UNP Q7MSJ8
H	719	GLU	-	expression tag	UNP Q7MSJ8
H	720	LYS	-	expression tag	UNP Q7MSJ8
I	691	SER	-	expression tag	UNP Q7MSJ8
I	692	ALA	-	expression tag	UNP Q7MSJ8
I	693	TRP	-	expression tag	UNP Q7MSJ8
I	694	SER	-	expression tag	UNP Q7MSJ8
I	695	HIS	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
I	696	PRO	-	expression tag	UNP Q7MSJ8
I	697	GLN	-	expression tag	UNP Q7MSJ8
I	698	PHE	-	expression tag	UNP Q7MSJ8
I	699	GLU	-	expression tag	UNP Q7MSJ8
I	700	LYS	-	expression tag	UNP Q7MSJ8
I	701	GLY	-	expression tag	UNP Q7MSJ8
I	702	GLY	-	expression tag	UNP Q7MSJ8
I	703	GLY	-	expression tag	UNP Q7MSJ8
I	704	SER	-	expression tag	UNP Q7MSJ8
I	705	GLY	-	expression tag	UNP Q7MSJ8
I	706	GLY	-	expression tag	UNP Q7MSJ8
I	707	GLY	-	expression tag	UNP Q7MSJ8
I	708	SER	-	expression tag	UNP Q7MSJ8
I	709	GLY	-	expression tag	UNP Q7MSJ8
I	710	GLY	-	expression tag	UNP Q7MSJ8
I	711	SER	-	expression tag	UNP Q7MSJ8
I	712	ALA	-	expression tag	UNP Q7MSJ8
I	713	TRP	-	expression tag	UNP Q7MSJ8
I	714	SER	-	expression tag	UNP Q7MSJ8
I	715	HIS	-	expression tag	UNP Q7MSJ8
I	716	PRO	-	expression tag	UNP Q7MSJ8
I	717	GLN	-	expression tag	UNP Q7MSJ8
I	718	PHE	-	expression tag	UNP Q7MSJ8
I	719	GLU	-	expression tag	UNP Q7MSJ8
I	720	LYS	-	expression tag	UNP Q7MSJ8
J	691	SER	-	expression tag	UNP Q7MSJ8
J	692	ALA	-	expression tag	UNP Q7MSJ8
J	693	TRP	-	expression tag	UNP Q7MSJ8
J	694	SER	-	expression tag	UNP Q7MSJ8
J	695	HIS	-	expression tag	UNP Q7MSJ8
J	696	PRO	-	expression tag	UNP Q7MSJ8
J	697	GLN	-	expression tag	UNP Q7MSJ8
J	698	PHE	-	expression tag	UNP Q7MSJ8
J	699	GLU	-	expression tag	UNP Q7MSJ8
J	700	LYS	-	expression tag	UNP Q7MSJ8
J	701	GLY	-	expression tag	UNP Q7MSJ8
J	702	GLY	-	expression tag	UNP Q7MSJ8
J	703	GLY	-	expression tag	UNP Q7MSJ8
J	704	SER	-	expression tag	UNP Q7MSJ8
J	705	GLY	-	expression tag	UNP Q7MSJ8
J	706	GLY	-	expression tag	UNP Q7MSJ8
J	707	GLY	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
J	708	SER	-	expression tag	UNP Q7MSJ8
J	709	GLY	-	expression tag	UNP Q7MSJ8
J	710	GLY	-	expression tag	UNP Q7MSJ8
J	711	SER	-	expression tag	UNP Q7MSJ8
J	712	ALA	-	expression tag	UNP Q7MSJ8
J	713	TRP	-	expression tag	UNP Q7MSJ8
J	714	SER	-	expression tag	UNP Q7MSJ8
J	715	HIS	-	expression tag	UNP Q7MSJ8
J	716	PRO	-	expression tag	UNP Q7MSJ8
J	717	GLN	-	expression tag	UNP Q7MSJ8
J	718	PHE	-	expression tag	UNP Q7MSJ8
J	719	GLU	-	expression tag	UNP Q7MSJ8
J	720	LYS	-	expression tag	UNP Q7MSJ8
K	691	SER	-	expression tag	UNP Q7MSJ8
K	692	ALA	-	expression tag	UNP Q7MSJ8
K	693	TRP	-	expression tag	UNP Q7MSJ8
K	694	SER	-	expression tag	UNP Q7MSJ8
K	695	HIS	-	expression tag	UNP Q7MSJ8
K	696	PRO	-	expression tag	UNP Q7MSJ8
K	697	GLN	-	expression tag	UNP Q7MSJ8
K	698	PHE	-	expression tag	UNP Q7MSJ8
K	699	GLU	-	expression tag	UNP Q7MSJ8
K	700	LYS	-	expression tag	UNP Q7MSJ8
K	701	GLY	-	expression tag	UNP Q7MSJ8
K	702	GLY	-	expression tag	UNP Q7MSJ8
K	703	GLY	-	expression tag	UNP Q7MSJ8
K	704	SER	-	expression tag	UNP Q7MSJ8
K	705	GLY	-	expression tag	UNP Q7MSJ8
K	706	GLY	-	expression tag	UNP Q7MSJ8
K	707	GLY	-	expression tag	UNP Q7MSJ8
K	708	SER	-	expression tag	UNP Q7MSJ8
K	709	GLY	-	expression tag	UNP Q7MSJ8
K	710	GLY	-	expression tag	UNP Q7MSJ8
K	711	SER	-	expression tag	UNP Q7MSJ8
K	712	ALA	-	expression tag	UNP Q7MSJ8
K	713	TRP	-	expression tag	UNP Q7MSJ8
K	714	SER	-	expression tag	UNP Q7MSJ8
K	715	HIS	-	expression tag	UNP Q7MSJ8
K	716	PRO	-	expression tag	UNP Q7MSJ8
K	717	GLN	-	expression tag	UNP Q7MSJ8
K	718	PHE	-	expression tag	UNP Q7MSJ8
K	719	GLU	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
K	720	LYS	-	expression tag	UNP Q7MSJ8
L	691	SER	-	expression tag	UNP Q7MSJ8
L	692	ALA	-	expression tag	UNP Q7MSJ8
L	693	TRP	-	expression tag	UNP Q7MSJ8
L	694	SER	-	expression tag	UNP Q7MSJ8
L	695	HIS	-	expression tag	UNP Q7MSJ8
L	696	PRO	-	expression tag	UNP Q7MSJ8
L	697	GLN	-	expression tag	UNP Q7MSJ8
L	698	PHE	-	expression tag	UNP Q7MSJ8
L	699	GLU	-	expression tag	UNP Q7MSJ8
L	700	LYS	-	expression tag	UNP Q7MSJ8
L	701	GLY	-	expression tag	UNP Q7MSJ8
L	702	GLY	-	expression tag	UNP Q7MSJ8
L	703	GLY	-	expression tag	UNP Q7MSJ8
L	704	SER	-	expression tag	UNP Q7MSJ8
L	705	GLY	-	expression tag	UNP Q7MSJ8
L	706	GLY	-	expression tag	UNP Q7MSJ8
L	707	GLY	-	expression tag	UNP Q7MSJ8
L	708	SER	-	expression tag	UNP Q7MSJ8
L	709	GLY	-	expression tag	UNP Q7MSJ8
L	710	GLY	-	expression tag	UNP Q7MSJ8
L	711	SER	-	expression tag	UNP Q7MSJ8
L	712	ALA	-	expression tag	UNP Q7MSJ8
L	713	TRP	-	expression tag	UNP Q7MSJ8
L	714	SER	-	expression tag	UNP Q7MSJ8
L	715	HIS	-	expression tag	UNP Q7MSJ8
L	716	PRO	-	expression tag	UNP Q7MSJ8
L	717	GLN	-	expression tag	UNP Q7MSJ8
L	718	PHE	-	expression tag	UNP Q7MSJ8
L	719	GLU	-	expression tag	UNP Q7MSJ8
L	720	LYS	-	expression tag	UNP Q7MSJ8
G	691	SER	-	expression tag	UNP Q7MSJ8
G	692	ALA	-	expression tag	UNP Q7MSJ8
G	693	TRP	-	expression tag	UNP Q7MSJ8
G	694	SER	-	expression tag	UNP Q7MSJ8
G	695	HIS	-	expression tag	UNP Q7MSJ8
G	696	PRO	-	expression tag	UNP Q7MSJ8
G	697	GLN	-	expression tag	UNP Q7MSJ8
G	698	PHE	-	expression tag	UNP Q7MSJ8
G	699	GLU	-	expression tag	UNP Q7MSJ8
G	700	LYS	-	expression tag	UNP Q7MSJ8
G	701	GLY	-	expression tag	UNP Q7MSJ8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	702	GLY	-	expression tag	UNP Q7MSJ8
G	703	GLY	-	expression tag	UNP Q7MSJ8
G	704	SER	-	expression tag	UNP Q7MSJ8
G	705	GLY	-	expression tag	UNP Q7MSJ8
G	706	GLY	-	expression tag	UNP Q7MSJ8
G	707	GLY	-	expression tag	UNP Q7MSJ8
G	708	SER	-	expression tag	UNP Q7MSJ8
G	709	GLY	-	expression tag	UNP Q7MSJ8
G	710	GLY	-	expression tag	UNP Q7MSJ8
G	711	SER	-	expression tag	UNP Q7MSJ8
G	712	ALA	-	expression tag	UNP Q7MSJ8
G	713	TRP	-	expression tag	UNP Q7MSJ8
G	714	SER	-	expression tag	UNP Q7MSJ8
G	715	HIS	-	expression tag	UNP Q7MSJ8
G	716	PRO	-	expression tag	UNP Q7MSJ8
G	717	GLN	-	expression tag	UNP Q7MSJ8
G	718	PHE	-	expression tag	UNP Q7MSJ8
G	719	GLU	-	expression tag	UNP Q7MSJ8
G	720	LYS	-	expression tag	UNP Q7MSJ8

- Molecule 2 is COPPER (I) ION (CCD ID: CU1) (formula: Cu).

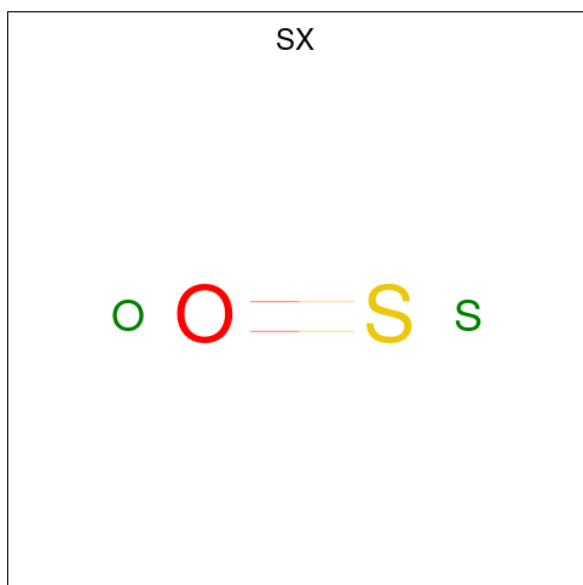
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cu 1 1	0	0
2	B	1	Total Cu 1 1	0	0
2	C	1	Total Cu 1 1	0	0
2	D	1	Total Cu 1 1	0	0
2	E	1	Total Cu 1 1	0	0
2	F	1	Total Cu 1 1	0	0
2	H	1	Total Cu 1 1	0	0
2	I	1	Total Cu 1 1	0	0
2	J	1	Total Cu 1 1	0	0
2	K	1	Total Cu 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	L	1	Total 1	Cu 1	0	0
2	G	1	Total 1	Cu 1	0	0

- Molecule 3 is SULFUR OXIDE (CCD ID: SX) (formula: OS).



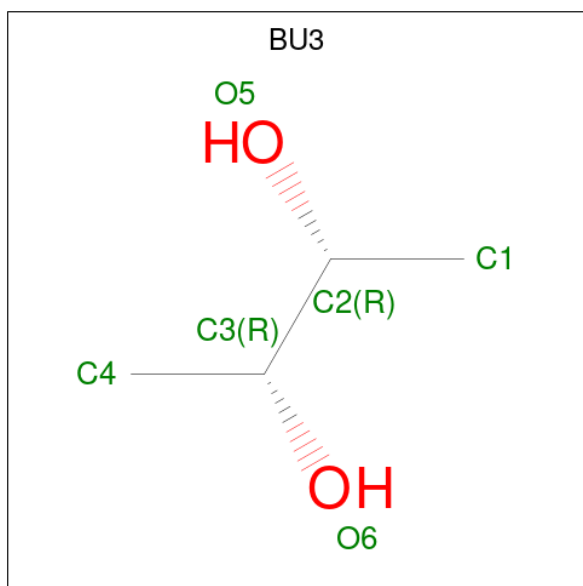
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 2	O 1	S 1	0	0
3	B	1	Total 2	O 1	S 1	0	0
3	C	1	Total 2	O 1	S 1	0	0
3	E	1	Total 2	O 1	S 1	0	0
3	F	1	Total 2	O 1	S 1	0	0
3	H	1	Total 2	O 1	S 1	0	0
3	J	1	Total 2	O 1	S 1	0	0
3	K	1	Total 2	O 1	S 1	0	0
3	L	1	Total 2	O 1	S 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	O	S	0	0
			2	1	1		

- Molecule 4 is (R,R)-2,3-BUTANEDIOL (CCD ID: BU3) (formula: C₄H₁₀O₂).



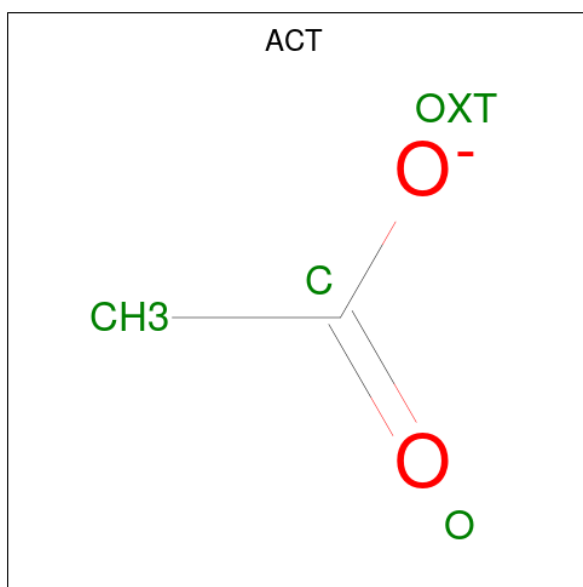
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	4	2		
4	A	1	Total	C	O	0	0
			6	4	2		
4	B	1	Total	C	O	0	0
			6	4	2		
4	B	1	Total	C	O	0	0
			6	4	2		
4	B	1	Total	C	O	0	0
			6	4	2		
4	C	1	Total	C	O	0	0
			6	4	2		
4	C	1	Total	C	O	0	0
			6	4	2		
4	D	1	Total	C	O	0	0
			6	4	2		
4	D	1	Total	C	O	0	0
			6	4	2		
4	E	1	Total	C	O	0	0
			6	4	2		

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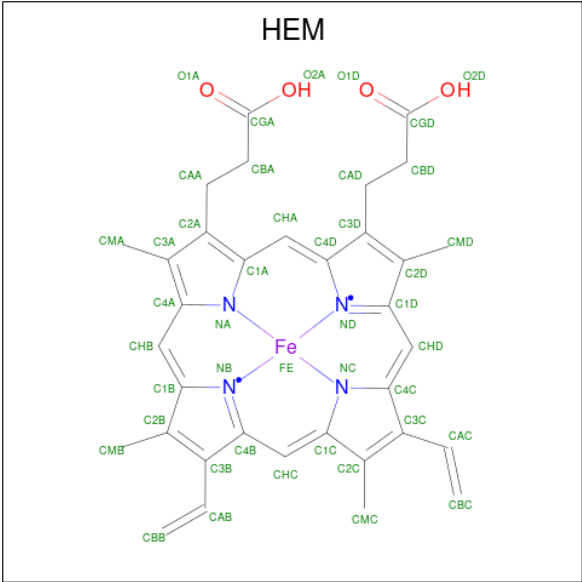
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total C O 6 4 2	0	0
4	F	1	Total C O 6 4 2	0	0
4	F	1	Total C O 6 4 2	0	0
4	F	1	Total C O 6 4 2	0	0
4	H	1	Total C O 6 4 2	0	0
4	H	1	Total C O 6 4 2	0	0
4	H	1	Total C O 6 4 2	0	0
4	I	1	Total C O 6 4 2	0	0
4	I	1	Total C O 6 4 2	0	0
4	J	1	Total C O 6 4 2	0	0
4	J	1	Total C O 6 4 2	0	0
4	K	1	Total C O 6 4 2	0	0
4	K	1	Total C O 6 4 2	0	0
4	L	1	Total C O 6 4 2	0	0
4	L	1	Total C O 6 4 2	0	0
4	G	1	Total C O 6 4 2	0	0
4	G	1	Total C O 6 4 2	0	0

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	H	1	Total	C	O	0	0
			4	2	2		
5	I	1	Total	C	O	0	0
			4	2	2		
5	J	1	Total	C	O	0	0
			4	2	2		
5	K	1	Total	C	O	0	0
			4	2	2		
5	L	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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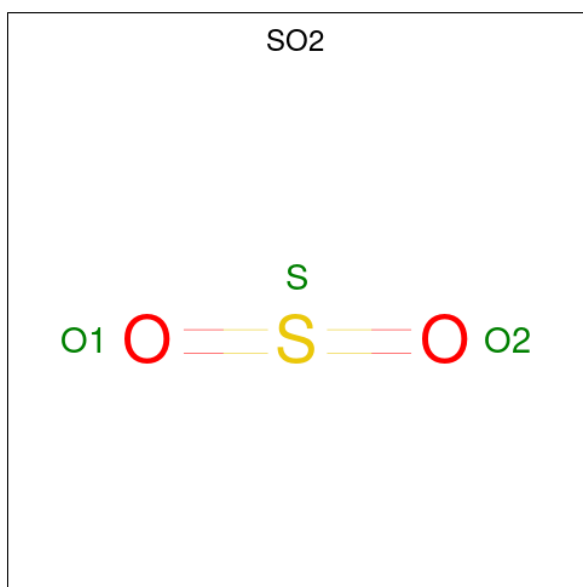
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 7 is SULFUR DIOXIDE (CCD ID: SO2) (formula: O₂S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			3	2	1		
7	D	1	Total	O	S	0	0
			3	2	1		
7	I	1	Total	O	S	0	0
			3	2	1		
7	G	1	Total	O	S	0	0
			3	2	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	416	Total	O	0	0
			416	416		
8	B	298	Total	O	0	0
			298	298		
8	C	285	Total	O	0	0
			285	285		
8	D	307	Total	O	0	0
			307	307		
8	E	219	Total	O	0	0
			219	219		
8	F	245	Total	O	0	0
			245	245		
8	H	250	Total	O	0	0
			250	250		
8	I	218	Total	O	0	0
			218	218		

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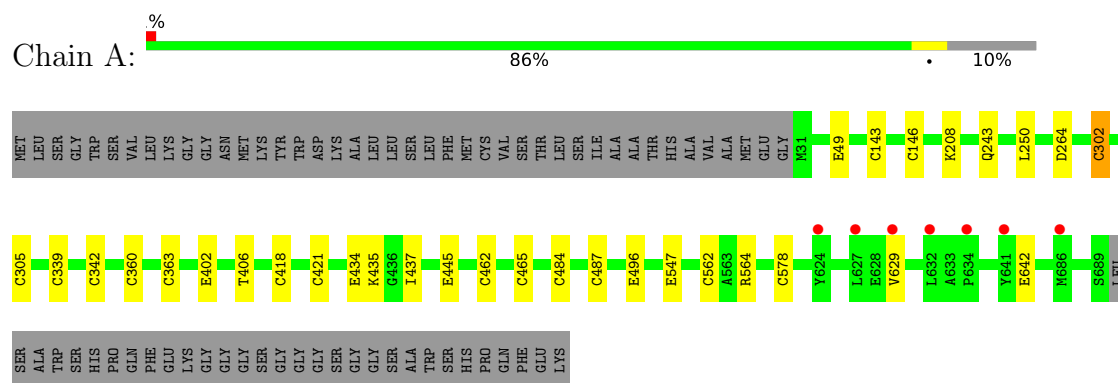
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	J	180	Total 180	O 180	0	0
8	K	158	Total 158	O 158	0	0
8	L	126	Total 126	O 126	0	0
8	G	232	Total 232	O 232	0	0

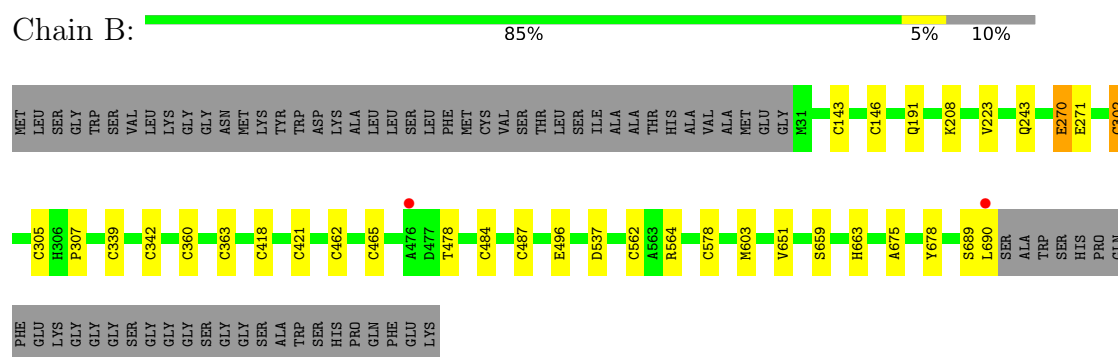
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

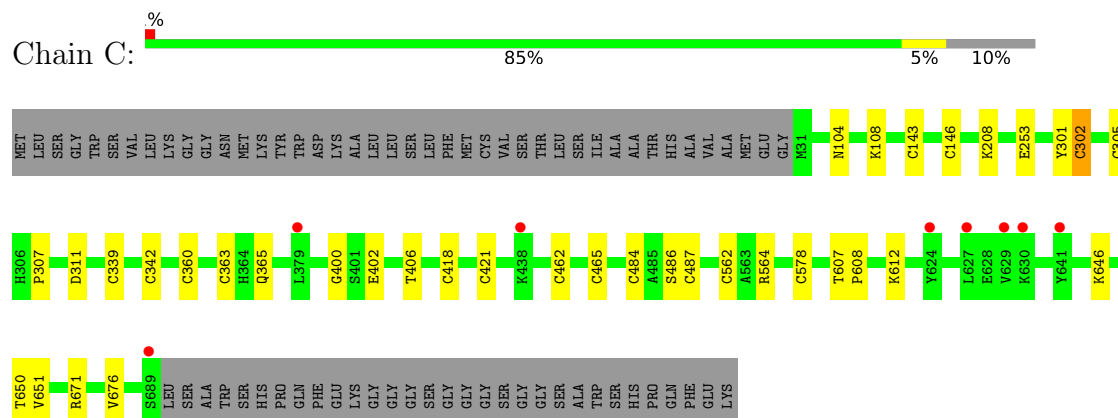
• Molecule 1: MccA



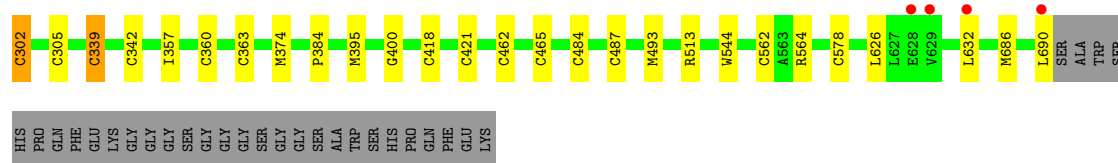
• Molecule 1: MccA



• Molecule 1: MccA

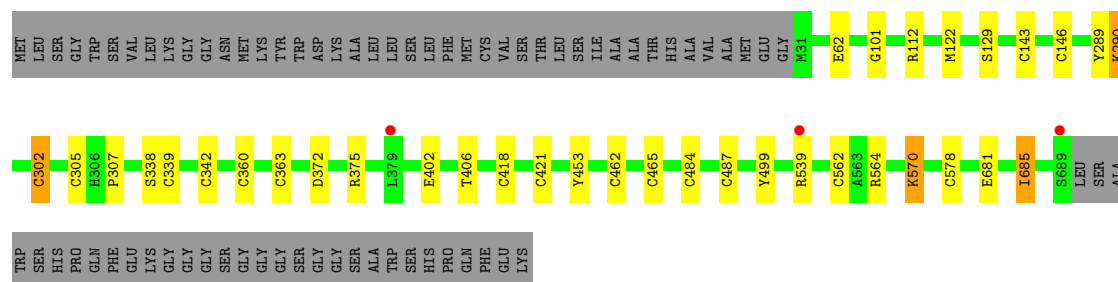


Residue	Position	Frequency	Frequency (%)
MET	1	1	0.0002
LEU	2	1	0.0002
SER	3	1	0.0002
GLY	4	1	0.0002
TRP	5	1	0.0002
SER	6	1	0.0002
VAL	7	1	0.0002
LEU	8	1	0.0002
LYS	9	1	0.0002
GLY	10	1	0.0002
GLY	11	1	0.0002
ASN	12	1	0.0002
MET	13	1	0.0002
LYS	14	1	0.0002
TVR	15	1	0.0002
TRP	16	1	0.0002
ASP	17	1	0.0002
LYS	18	1	0.0002
ALA	19	1	0.0002
LEU	20	1	0.0002
LEU	21	1	0.0002
SER	22	1	0.0002
LEU	23	1	0.0002
PHE	24	1	0.0002
MET	25	1	0.0002
CYS	26	1	0.0002
VAL	27	1	0.0002
SER	28	1	0.0002
THR	29	1	0.0002
LEU	30	1	0.0002
ILE	31	1	0.0002
ALA	32	1	0.0002
ALA	33	1	0.0002
THR	34	1	0.0002
HIS	35	1	0.0002
ALA	36	1	0.0002
VAL	37	1	0.0002
ALA	38	1	0.0002
VAL	39	1	0.0002
GLU	40	1	0.0002
GLY	41	1	0.0002
R31	42	1	0.0002
E39	43	1	0.0002
T84	44	1	0.0002
V85	45	1	0.0002
G86	46	1	0.0002
R112	47	1	0.0002
Y123	48	1	0.0002
C143	49	1	0.0002
C146	50	1	0.0002
G203	51	1	0.0002



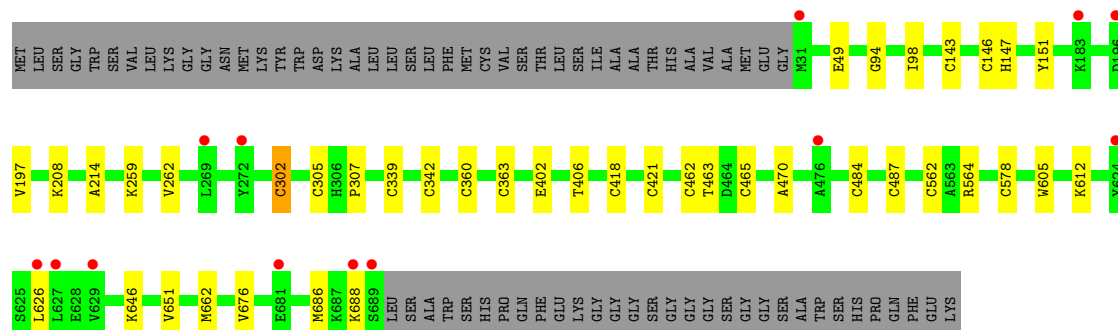
• Molecule 1: MccA

Chain I: 85% 10%



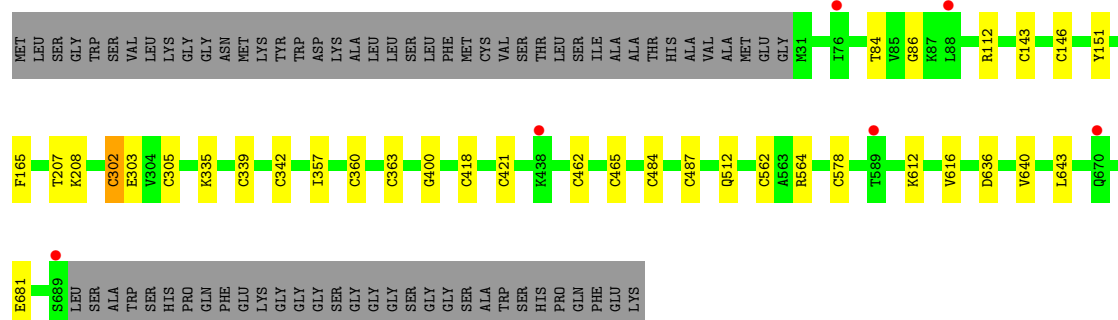
• Molecule 1: MccA

Chain J: 84% 5% 10%



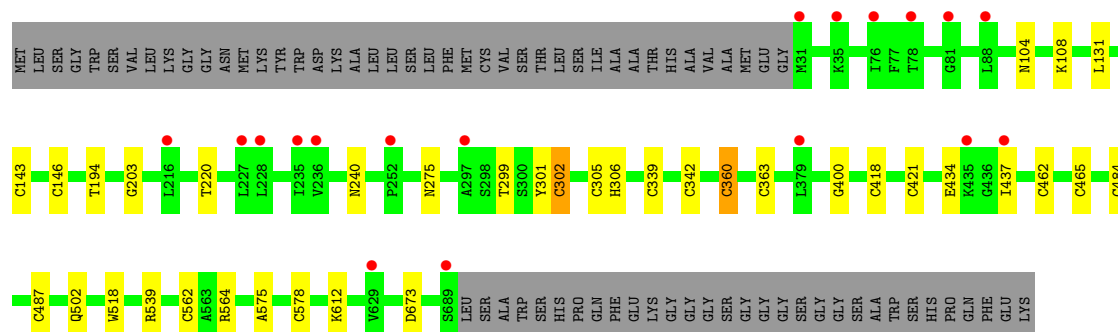
• Molecule 1: MccA

Chain K: 85% 5% 10%

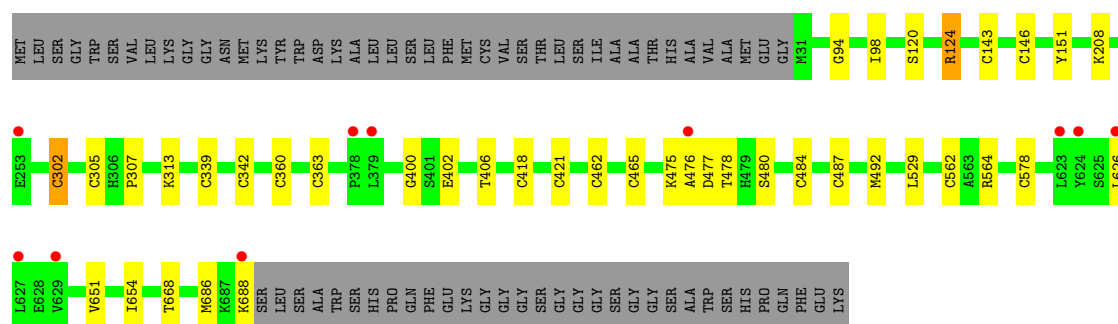
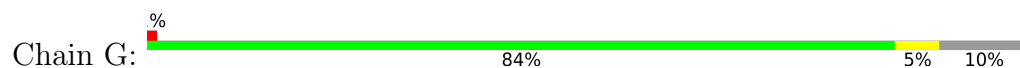


• Molecule 1: MccA

Chain L: 85% 5% 10%



- Molecule 1: MccA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	211.12Å 103.04Å 233.07Å 90.00° 98.46° 90.00°	Depositor
Resolution (Å)	49.37 – 2.20 49.37 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.37-2.20) 99.8 (49.37-2.20)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.184 , 0.220 (Not available) , 0.191	Depositor DCC
R_{free} test set	24857 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	34.3	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	70014	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CU1, SX, BU3, HEM, ACT, SO2

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	0.48	0/5354	0.72	0/7212
1	B	0.44	0/5362	0.72	0/7223
1	C	0.45	0/5354	0.72	0/7212
1	D	0.43	0/5354	0.72	0/7212
1	E	0.43	0/5354	0.71	1/7212 (0.0%)
1	F	0.44	0/5354	0.72	0/7212
1	G	0.44	0/5348	0.72	0/7204
1	H	0.43	0/5362	0.72	0/7223
1	I	0.44	0/5354	0.71	0/7212
1	J	0.42	0/5354	0.71	0/7212
1	K	0.42	0/5354	0.72	0/7212
1	L	0.43	0/5354	0.72	0/7212
All	All	0.44	0/64258	0.72	1/86558 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	98	ILE	CB-CA-C	-5.41	106.24	111.05

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5224	0	5051	72	0
1	B	5232	0	5063	68	0
1	C	5224	0	5052	74	0
1	D	5224	0	5054	72	0
1	E	5224	0	5052	77	0
1	F	5224	0	5052	72	0
1	G	5218	0	5048	73	0
1	H	5232	0	5064	70	0
1	I	5224	0	5053	68	0
1	J	5224	0	5054	71	0
1	K	5224	0	5053	68	0
1	L	5224	0	5054	72	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
3	J	2	0	0	0	0
3	K	2	0	0	0	0
3	L	2	0	0	0	0
4	A	12	0	20	0	0
4	B	18	0	30	0	0
4	C	12	0	20	0	0
4	D	12	0	20	0	0
4	E	12	0	20	2	0
4	F	18	0	30	0	0
4	G	12	0	20	0	0
4	H	18	0	30	1	0
4	I	12	0	20	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	J	12	0	20	0	0
4	K	12	0	20	1	0
4	L	12	0	20	0	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
5	C	4	0	3	1	0
5	D	4	0	3	0	0
5	E	4	0	3	0	0
5	F	4	0	3	1	0
5	G	4	0	3	0	0
5	H	4	0	3	0	0
5	I	4	0	3	0	0
5	J	4	0	3	0	0
5	K	4	0	3	0	0
5	L	4	0	3	0	0
6	A	344	0	240	64	0
6	B	344	0	240	65	0
6	C	344	0	240	70	0
6	D	344	0	240	67	0
6	E	344	0	240	65	0
6	F	344	0	240	61	0
6	G	344	0	240	65	0
6	H	344	0	240	67	0
6	I	344	0	240	58	0
6	J	344	0	240	64	0
6	K	344	0	240	63	0
6	L	344	0	240	75	0
7	A	3	0	0	0	0
7	D	3	0	0	0	0
7	G	3	0	0	0	0
7	I	3	0	0	0	0
8	A	416	0	0	2	0
8	B	298	0	0	0	0
8	C	285	0	0	0	0
8	D	307	0	0	1	0
8	E	219	0	0	1	0
8	F	245	0	0	0	0
8	G	232	0	0	0	0
8	H	250	0	0	0	0
8	I	218	0	0	0	0
8	J	180	0	0	0	0
8	K	158	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	126	0	0	0	0
All	All	70014	0	63836	897	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 8.

The worst 5 of 897 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:462:CYS:SG	6:A:811:HEM:HAB	1.41	1.55
1:A:339:CYS:SG	6:A:808:HEM:CAB	2.04	1.46
1:A:462:CYS:SG	6:A:811:HEM:CAB	2.02	1.46
1:F:462:CYS:SG	6:F:812:HEM:CAB	2.03	1.46
1:A:484:CYS:SG	6:A:812:HEM:CAB	2.05	1.45

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	559/613 (91%)	556 (100%)	3 (0%)	81	90
1	B	560/613 (91%)	555 (99%)	5 (1%)	70	84
1	C	559/613 (91%)	555 (99%)	4 (1%)	76	87
1	D	559/613 (91%)	554 (99%)	5 (1%)	70	84
1	E	559/613 (91%)	557 (100%)	2 (0%)	84	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	559/613 (91%)	552 (99%)	7 (1%)	61	76
1	G	558/613 (91%)	553 (99%)	5 (1%)	70	84
1	H	560/613 (91%)	555 (99%)	5 (1%)	70	84
1	I	559/613 (91%)	554 (99%)	5 (1%)	70	84
1	J	559/613 (91%)	554 (99%)	5 (1%)	70	84
1	K	559/613 (91%)	556 (100%)	3 (0%)	81	90
1	L	559/613 (91%)	554 (99%)	5 (1%)	70	84
All	All	6709/7356 (91%)	6655 (99%)	54 (1%)	73	85

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	564	ARG
1	I	685	ILE
1	G	124	ARG
1	H	632	LEU
1	I	302	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	621	GLN
1	L	104	ASN
1	L	670	GLN
1	E	380	ASN
1	E	64	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

Of 161 ligands modelled in this entry, 12 are monoatomic - leaving 149 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	D	805	-	3,3,3	0.88	0	3,3,3	0.52	0
6	HEM	K	806	1	50,50,50	2.46	12 (24%)	67,82,82	2.55	21 (31%)
6	HEM	G	809	1	50,50,50	2.44	11 (22%)	67,82,82	2.12	17 (25%)
6	HEM	F	813	1	50,50,50	2.40	9 (18%)	67,82,82	2.39	15 (22%)
6	HEM	F	814	1	50,50,50	2.44	11 (22%)	67,82,82	2.28	15 (22%)
4	BU3	E	804	-	4,5,5	0.31	0	6,6,6	0.29	0
6	HEM	K	808	1	50,50,50	2.41	9 (18%)	67,82,82	2.19	14 (20%)
4	BU3	K	804	-	4,5,5	0.50	0	6,6,6	0.27	0
4	BU3	L	804	-	4,5,5	0.43	0	6,6,6	0.35	0
4	BU3	G	803	-	4,5,5	0.45	0	6,6,6	0.27	0
6	HEM	A	812	1	50,50,50	2.39	10 (20%)	67,82,82	2.44	20 (29%)
6	HEM	J	809	1	50,50,50	2.49	10 (20%)	67,82,82	2.16	17 (25%)
6	HEM	I	808	1	50,50,50	2.40	10 (20%)	67,82,82	2.22	14 (20%)
7	SO2	G	814	6	2,2,2	1.72	0	1,1,1	1.58	0
4	BU3	H	803	-	4,5,5	0.32	0	6,6,6	0.24	0
5	ACT	B	806	-	3,3,3	0.78	0	3,3,3	0.97	0
6	HEM	B	814	1	50,50,50	2.46	10 (20%)	67,82,82	2.21	15 (22%)
6	HEM	I	806	1	50,50,50	2.46	9 (18%)	67,82,82	2.21	16 (23%)
6	HEM	G	811	1	50,50,50	2.45	12 (24%)	67,82,82	2.36	16 (23%)
6	HEM	F	808	1,3	50,50,50	2.48	10 (20%)	67,82,82	2.17	16 (23%)
6	HEM	G	808	1	50,50,50	2.44	10 (20%)	67,82,82	2.20	13 (19%)
6	HEM	C	813	1	50,50,50	2.42	10 (20%)	67,82,82	2.27	14 (20%)
6	HEM	E	808	1	50,50,50	2.39	12 (24%)	67,82,82	2.31	14 (20%)
4	BU3	B	804	-	4,5,5	0.40	0	6,6,6	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BU3	B	803	-	4,5,5	0.41	0	6,6,6	0.20	0
5	ACT	K	805	-	3,3,3	0.84	0	3,3,3	0.62	0
6	HEM	L	808	1	50,50,50	2.47	9 (18%)	67,82,82	2.19	14 (20%)
7	SO2	A	814	6	2,2,2	1.74	0	1,1,1	1.43	0
6	HEM	D	813	1	50,50,50	2.43	10 (20%)	67,82,82	2.27	14 (20%)
6	HEM	H	809	1	50,50,50	2.46	11 (22%)	67,82,82	2.16	14 (20%)
6	HEM	F	811	1	50,50,50	2.42	10 (20%)	67,82,82	2.32	18 (26%)
6	HEM	F	812	1	50,50,50	2.38	7 (14%)	67,82,82	2.40	13 (19%)
6	HEM	D	806	1	50,50,50	2.40	7 (14%)	67,82,82	2.31	16 (23%)
5	ACT	J	805	-	3,3,3	0.77	0	3,3,3	0.94	0
6	HEM	L	813	1	50,50,50	2.44	8 (16%)	67,82,82	2.26	19 (28%)
6	HEM	C	809	1	50,50,50	2.43	9 (18%)	67,82,82	2.22	15 (22%)
6	HEM	B	807	1	50,50,50	2.37	9 (18%)	67,82,82	2.27	16 (23%)
5	ACT	H	806	-	3,3,3	0.78	0	3,3,3	0.81	0
6	HEM	E	812	1	50,50,50	2.43	9 (18%)	67,82,82	2.25	17 (25%)
4	BU3	D	804	-	4,5,5	0.48	0	6,6,6	0.36	0
5	ACT	E	805	-	3,3,3	0.75	0	3,3,3	0.92	0
6	HEM	H	812	1	50,50,50	2.41	9 (18%)	67,82,82	2.24	15 (22%)
6	HEM	G	807	1,3,7	50,50,50	2.46	12 (24%)	67,82,82	2.22	14 (20%)
6	HEM	K	811	1	50,50,50	2.45	10 (20%)	67,82,82	2.24	13 (19%)
6	HEM	B	809	1	50,50,50	2.42	12 (24%)	67,82,82	2.38	15 (22%)
5	ACT	G	805	-	3,3,3	0.83	0	3,3,3	0.64	0
6	HEM	L	812	1	50,50,50	2.45	9 (18%)	67,82,82	2.15	15 (22%)
6	HEM	J	811	1	50,50,50	2.44	12 (24%)	67,82,82	2.36	15 (22%)
4	BU3	A	803	-	4,5,5	0.37	0	6,6,6	0.32	0
5	ACT	L	805	-	3,3,3	0.84	0	3,3,3	0.56	0
6	HEM	G	813	1	50,50,50	2.46	9 (18%)	67,82,82	2.20	18 (26%)
3	SX	J	802	6	0,1,1	-	-	-	-	-
6	HEM	E	806	1	50,50,50	2.43	11 (22%)	67,82,82	2.27	14 (20%)
6	HEM	A	811	1	50,50,50	2.42	12 (24%)	67,82,82	2.51	21 (31%)
6	HEM	C	811	1	50,50,50	2.40	9 (18%)	67,82,82	2.36	15 (22%)
6	HEM	I	811	1	50,50,50	2.39	8 (16%)	67,82,82	2.39	14 (20%)
6	HEM	K	807	1,3	50,50,50	2.47	11 (22%)	67,82,82	2.20	13 (19%)
6	HEM	H	810	1	50,50,50	2.48	9 (18%)	67,82,82	2.16	17 (25%)
6	HEM	C	806	1	50,50,50	2.36	11 (22%)	67,82,82	2.31	14 (20%)
4	BU3	L	803	-	4,5,5	0.46	0	6,6,6	0.18	0
6	HEM	B	811	1	50,50,50	2.43	9 (18%)	67,82,82	2.29	19 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	HEM	B	812	1	50,50,50	2.42	9 (18%)	67,82,82	2.26	15 (22%)
6	HEM	H	807	1	50,50,50	2.44	8 (16%)	67,82,82	2.28	15 (22%)
3	SX	B	802	6	0,1,1	-	-	-	-	-
6	HEM	J	810	1	50,50,50	2.44	10 (20%)	67,82,82	2.21	17 (25%)
4	BU3	B	805	-	4,5,5	0.33	0	6,6,6	0.26	0
6	HEM	A	813	1	50,50,50	2.49	12 (24%)	67,82,82	2.29	15 (22%)
6	HEM	L	807	1,3	50,50,50	2.48	10 (20%)	67,82,82	2.20	13 (19%)
6	HEM	K	812	1	50,50,50	2.45	11 (22%)	67,82,82	2.20	14 (20%)
4	BU3	I	804	-	4,5,5	0.52	0	6,6,6	0.31	0
6	HEM	C	810	1	50,50,50	2.45	11 (22%)	67,82,82	2.38	19 (28%)
3	SX	H	802	6	0,1,1	-	-	-	-	-
4	BU3	H	805	-	4,5,5	0.28	0	6,6,6	0.58	0
6	HEM	K	809	1	50,50,50	2.51	9 (18%)	67,82,82	2.04	14 (20%)
3	SX	A	802	6	0,1,1	-	-	-	-	-
3	SX	C	802	6	0,1,1	-	-	-	-	-
6	HEM	D	807	1,7	50,50,50	2.46	10 (20%)	67,82,82	2.16	13 (19%)
3	SX	G	802	6	0,1,1	-	-	-	-	-
6	HEM	D	811	1	50,50,50	2.40	8 (16%)	67,82,82	2.31	16 (23%)
6	HEM	D	812	1	50,50,50	2.40	10 (20%)	67,82,82	2.27	16 (23%)
6	HEM	E	810	1	50,50,50	2.42	10 (20%)	67,82,82	2.29	16 (23%)
6	HEM	I	810	1	50,50,50	2.38	10 (20%)	67,82,82	2.28	17 (25%)
6	HEM	L	809	1	50,50,50	2.51	11 (22%)	67,82,82	2.15	15 (22%)
6	HEM	D	809	1	50,50,50	2.44	11 (22%)	67,82,82	2.14	15 (22%)
6	HEM	H	811	1	50,50,50	2.38	9 (18%)	67,82,82	2.30	18 (26%)
4	BU3	C	804	-	4,5,5	0.33	0	6,6,6	0.29	0
6	HEM	H	808	1,3	50,50,50	2.49	10 (20%)	67,82,82	2.22	14 (20%)
6	HEM	L	811	1	50,50,50	2.45	8 (16%)	67,82,82	2.27	20 (29%)
6	HEM	A	810	1	50,50,50	2.37	10 (20%)	67,82,82	2.34	17 (25%)
6	HEM	I	809	1	50,50,50	2.43	9 (18%)	67,82,82	2.07	15 (22%)
4	BU3	F	804	-	4,5,5	0.45	0	6,6,6	0.31	0
4	BU3	E	803	-	4,5,5	0.32	0	6,6,6	0.27	0
4	BU3	G	804	-	4,5,5	0.41	0	6,6,6	0.26	0
6	HEM	J	806	1	50,50,50	2.45	11 (22%)	67,82,82	2.48	19 (28%)
6	HEM	B	808	1,3	50,50,50	2.45	10 (20%)	67,82,82	2.20	12 (17%)
3	SX	F	802	6	0,1,1	-	-	-	-	-
4	BU3	F	805	-	4,5,5	0.42	0	6,6,6	0.23	0
4	BU3	J	804	-	4,5,5	0.47	0	6,6,6	0.23	0
6	HEM	J	808	1	50,50,50	2.46	11 (22%)	67,82,82	2.21	15 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	HEM	F	807	1	50,50,50	2.45	12 (24%)	67,82,82	2.35	14 (20%)
6	HEM	D	808	1	50,50,50	2.45	12 (24%)	67,82,82	2.36	16 (23%)
6	HEM	G	810	1	50,50,50	2.38	8 (16%)	67,82,82	2.28	16 (23%)
6	HEM	C	808	1	50,50,50	2.38	12 (24%)	67,82,82	2.32	17 (25%)
6	HEM	J	807	1,3	50,50,50	2.50	11 (22%)	67,82,82	2.19	13 (19%)
6	HEM	E	809	1	50,50,50	2.48	11 (22%)	67,82,82	2.15	17 (25%)
6	HEM	J	813	1	50,50,50	2.49	10 (20%)	67,82,82	2.11	14 (20%)
7	SO2	D	802	6	2,2,2	1.81	0	1,1,1	1.52	0
5	ACT	F	806	-	3,3,3	0.80	0	3,3,3	0.87	0
3	SX	K	802	6	0,1,1	-	-	-	-	-
6	HEM	H	814	1	50,50,50	2.43	11 (22%)	67,82,82	2.21	15 (22%)
6	HEM	E	813	1	50,50,50	2.44	11 (22%)	67,82,82	2.25	15 (22%)
6	HEM	I	813	1	50,50,50	2.47	12 (24%)	67,82,82	2.27	16 (23%)
6	HEM	I	807	1,7	50,50,50	2.45	11 (22%)	67,82,82	2.22	14 (20%)
6	HEM	A	808	1	50,50,50	2.38	11 (22%)	67,82,82	2.25	14 (20%)
3	SX	L	802	6	0,1,1	-	-	-	-	-
6	HEM	A	806	1	50,50,50	2.39	11 (22%)	67,82,82	2.31	16 (23%)
6	HEM	J	812	1	50,50,50	2.44	10 (20%)	67,82,82	2.26	13 (19%)
6	HEM	F	809	1	50,50,50	2.46	10 (20%)	67,82,82	2.24	16 (23%)
6	HEM	K	813	1	50,50,50	2.48	11 (22%)	67,82,82	2.26	16 (23%)
4	BU3	F	803	-	4,5,5	0.39	0	6,6,6	0.41	0
7	SO2	I	802	6	2,2,2	1.83	0	1,1,1	1.49	0
6	HEM	B	813	1	50,50,50	2.43	11 (22%)	67,82,82	2.30	16 (23%)
4	BU3	H	804	-	4,5,5	0.40	0	6,6,6	0.30	0
6	HEM	C	812	1	50,50,50	2.46	10 (20%)	67,82,82	2.31	17 (25%)
6	HEM	I	812	1	50,50,50	2.39	10 (20%)	67,82,82	2.30	15 (22%)
5	ACT	A	805	-	3,3,3	0.72	0	3,3,3	0.98	0
5	ACT	C	805	-	3,3,3	0.79	0	3,3,3	0.89	0
6	HEM	E	811	1	50,50,50	2.40	9 (18%)	67,82,82	2.37	15 (22%)
6	HEM	K	810	1	50,50,50	2.42	8 (16%)	67,82,82	2.27	17 (25%)
5	ACT	I	805	-	3,3,3	0.82	0	3,3,3	0.71	0
4	BU3	A	804	-	4,5,5	0.38	0	6,6,6	0.38	0
6	HEM	G	812	1	50,50,50	2.42	8 (16%)	67,82,82	2.30	18 (26%)
4	BU3	C	803	-	4,5,5	0.35	0	6,6,6	0.33	0
6	HEM	B	810	1	50,50,50	2.41	11 (22%)	67,82,82	2.17	14 (20%)
4	BU3	J	803	-	4,5,5	0.34	0	6,6,6	0.30	0
4	BU3	D	803	-	4,5,5	0.38	0	6,6,6	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	HEM	D	810	1	50,50,50	2.38	9 (18%)	67,82,82	2.38	17 (25%)
6	HEM	G	806	1	50,50,50	2.42	9 (18%)	67,82,82	2.24	13 (19%)
6	HEM	E	807	1,3	50,50,50	2.43	8 (16%)	67,82,82	2.19	12 (17%)
4	BU3	K	803	-	4,5,5	0.36	0	6,6,6	0.39	0
6	HEM	L	806	1	50,50,50	2.47	10 (20%)	67,82,82	2.18	14 (20%)
6	HEM	A	809	1	50,50,50	2.39	9 (18%)	67,82,82	2.01	15 (22%)
4	BU3	I	803	-	4,5,5	0.40	0	6,6,6	0.18	0
6	HEM	A	807	1,3,7	50,50,50	2.43	9 (18%)	67,82,82	2.12	13 (19%)
6	HEM	C	807	1,3	50,50,50	2.44	8 (16%)	67,82,82	2.13	13 (19%)
6	HEM	H	813	1	50,50,50	2.40	11 (22%)	67,82,82	2.30	15 (22%)
6	HEM	L	810	1	50,50,50	2.43	10 (20%)	67,82,82	2.28	15 (22%)
6	HEM	F	810	1	50,50,50	2.48	11 (22%)	67,82,82	2.12	17 (25%)
3	SX	E	802	6	0,1,1	-	-	-	-	-

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
6	HEM	K	806	1	-	3/14/54/54	-
6	HEM	G	809	1	-	0/14/54/54	-
6	HEM	F	813	1	-	2/14/54/54	-
6	HEM	F	814	1	-	4/14/54/54	-
4	BU3	E	804	-	-	0/4/4/4	-
6	HEM	K	808	1	-	3/14/54/54	-
4	BU3	K	804	-	-	4/4/4/4	-
4	BU3	L	804	-	-	4/4/4/4	-
4	BU3	G	803	-	-	4/4/4/4	-
6	HEM	A	812	1	-	4/14/54/54	-
6	HEM	J	809	1	-	2/14/54/54	-
6	HEM	I	808	1	-	3/14/54/54	-
4	BU3	H	803	-	-	0/4/4/4	-
6	HEM	B	814	1	-	4/14/54/54	-
6	HEM	I	806	1	-	1/14/54/54	-
6	HEM	G	811	1	-	2/14/54/54	-
6	HEM	F	808	1,3	-	2/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEM	G	808	1	-	4/14/54/54	-
6	HEM	C	813	1	-	4/14/54/54	-
6	HEM	E	808	1	-	5/14/54/54	-
4	BU3	B	804	-	-	4/4/4/4	-
4	BU3	B	803	-	-	4/4/4/4	-
6	HEM	L	808	1	-	3/14/54/54	-
6	HEM	D	813	1	-	4/14/54/54	-
6	HEM	H	809	1	-	3/14/54/54	-
6	HEM	F	811	1	-	4/14/54/54	-
6	HEM	F	812	1	-	4/14/54/54	-
6	HEM	D	806	1	-	4/14/54/54	-
6	HEM	L	813	1	-	5/14/54/54	-
6	HEM	C	809	1	-	2/14/54/54	-
6	HEM	B	807	1	-	1/14/54/54	-
6	HEM	E	812	1	-	4/14/54/54	-
4	BU3	D	804	-	-	4/4/4/4	-
6	HEM	H	812	1	-	2/14/54/54	-
6	HEM	G	807	1,3,7	-	3/14/54/54	-
6	HEM	K	811	1	-	4/14/54/54	-
6	HEM	B	809	1	-	3/14/54/54	-
6	HEM	L	812	1	-	4/14/54/54	-
6	HEM	J	811	1	-	2/14/54/54	-
4	BU3	A	803	-	-	4/4/4/4	-
6	HEM	G	813	1	-	4/14/54/54	-
6	HEM	E	806	1	-	1/14/54/54	-
6	HEM	A	811	1	-	2/14/54/54	-
6	HEM	C	811	1	-	2/14/54/54	-
6	HEM	I	811	1	-	2/14/54/54	-
6	HEM	K	807	1,3	-	4/14/54/54	-
6	HEM	H	810	1	-	2/14/54/54	-
6	HEM	C	806	1	-	2/14/54/54	-
4	BU3	L	803	-	-	4/4/4/4	-
6	HEM	B	811	1	-	5/14/54/54	-
6	HEM	B	812	1	-	4/14/54/54	-
6	HEM	H	807	1	-	1/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEM	J	810	1	-	4/14/54/54	-
4	BU3	B	805	-	-	0/4/4/4	-
6	HEM	A	813	1	-	4/14/54/54	-
6	HEM	L	807	1,3	-	3/14/54/54	-
6	HEM	K	812	1	-	4/14/54/54	-
4	BU3	I	804	-	-	4/4/4/4	-
6	HEM	C	810	1	-	2/14/54/54	-
4	BU3	H	805	-	-	0/4/4/4	-
6	HEM	K	809	1	-	2/14/54/54	-
6	HEM	D	807	1,7	-	2/14/54/54	-
6	HEM	D	811	1	-	2/14/54/54	-
6	HEM	D	812	1	-	4/14/54/54	-
6	HEM	I	810	1	-	4/14/54/54	-
6	HEM	E	810	1	-	2/14/54/54	-
6	HEM	L	809	1	-	2/14/54/54	-
6	HEM	D	809	1	-	2/14/54/54	-
6	HEM	H	811	1	-	4/14/54/54	-
4	BU3	C	804	-	-	4/4/4/4	-
6	HEM	H	808	1,3	-	4/14/54/54	-
6	HEM	L	811	1	-	6/14/54/54	-
6	HEM	A	810	1	-	5/14/54/54	-
6	HEM	I	809	1	-	2/14/54/54	-
4	BU3	F	804	-	-	4/4/4/4	-
4	BU3	E	803	-	-	1/4/4/4	-
4	BU3	G	804	-	-	0/4/4/4	-
6	HEM	J	806	1	-	2/14/54/54	-
6	HEM	B	808	1,3	-	4/14/54/54	-
4	BU3	F	805	-	-	4/4/4/4	-
4	BU3	J	804	-	-	4/4/4/4	-
6	HEM	J	808	1	-	3/14/54/54	-
6	HEM	F	807	1	-	1/14/54/54	-
6	HEM	D	808	1	-	3/14/54/54	-
6	HEM	G	810	1	-	2/14/54/54	-
6	HEM	C	808	1	-	5/14/54/54	-
6	HEM	J	807	1,3	-	3/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEM	E	809	1	-	2/14/54/54	-
6	HEM	J	813	1	-	6/14/54/54	-
6	HEM	H	814	1	-	4/14/54/54	-
6	HEM	E	813	1	-	2/14/54/54	-
6	HEM	I	813	1	-	4/14/54/54	-
6	HEM	I	807	1,7	-	3/14/54/54	-
6	HEM	A	808	1	-	3/14/54/54	-
6	HEM	K	813	1	-	4/14/54/54	-
6	HEM	A	806	1	-	2/14/54/54	-
6	HEM	J	812	1	-	4/14/54/54	-
6	HEM	F	809	1	-	3/14/54/54	-
4	BU3	F	803	-	-	4/4/4/4	-
6	HEM	B	813	1	-	4/14/54/54	-
4	BU3	H	804	-	-	4/4/4/4	-
6	HEM	C	812	1	-	4/14/54/54	-
6	HEM	I	812	1	-	4/14/54/54	-
6	HEM	E	811	1	-	4/14/54/54	-
6	HEM	K	810	1	-	2/14/54/54	-
4	BU3	A	804	-	-	4/4/4/4	-
6	HEM	G	812	1	-	4/14/54/54	-
4	BU3	C	803	-	-	4/4/4/4	-
6	HEM	B	810	1	-	2/14/54/54	-
4	BU3	J	803	-	-	4/4/4/4	-
4	BU3	D	803	-	-	0/4/4/4	-
6	HEM	D	810	1	-	5/14/54/54	-
6	HEM	G	806	1	-	1/14/54/54	-
6	HEM	E	807	1,3	-	2/14/54/54	-
4	BU3	K	803	-	-	0/4/4/4	-
6	HEM	L	806	1	-	1/14/54/54	-
6	HEM	A	809	1	-	2/14/54/54	-
4	BU3	I	803	-	-	4/4/4/4	-
6	HEM	A	807	1,3,7	-	2/14/54/54	-
6	HEM	C	807	1,3	-	2/14/54/54	-
6	HEM	H	813	1	-	3/14/54/54	-
6	HEM	L	810	1	-	4/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEM	F	810	1	-	2/14/54/54	-

The worst 5 of 960 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	809	HEM	FE-NB	12.67	2.33	1.94
6	L	813	HEM	FE-NB	12.66	2.33	1.94
6	L	809	HEM	FE-NB	12.58	2.33	1.94
6	H	810	HEM	FE-NB	12.55	2.33	1.94
6	J	807	HEM	FE-NB	12.48	2.33	1.94

The worst 5 of 1483 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	K	806	HEM	C3B-C4B-NB	-10.94	101.61	109.47
6	A	811	HEM	C3B-C4B-NB	-10.71	101.77	109.47
6	J	806	HEM	C3B-C4B-NB	-10.70	101.79	109.47
6	F	812	HEM	C1B-NB-C4B	10.66	117.83	105.21
6	A	812	HEM	C1B-NB-C4B	10.66	117.83	105.21

There are no chirality outliers.

5 of 367 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	803	BU3	O5-C2-C3-O6
4	A	803	BU3	C1-C2-C3-O6
4	A	803	BU3	O5-C2-C3-C4
4	A	804	BU3	O5-C2-C3-O6
4	A	804	BU3	C1-C2-C3-O6

There are no ring outliers.

101 monomers are involved in 790 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	806	HEM	10	0
6	G	809	HEM	9	0
6	F	813	HEM	6	0
6	F	814	HEM	7	0
4	E	804	BU3	2	0
6	K	808	HEM	7	0
6	A	812	HEM	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	J	809	HEM	9	0
6	I	808	HEM	5	0
4	H	803	BU3	1	0
6	B	814	HEM	8	0
6	I	806	HEM	8	0
6	G	811	HEM	6	0
6	F	808	HEM	12	0
6	G	808	HEM	6	0
6	C	813	HEM	9	0
6	E	808	HEM	8	0
6	L	808	HEM	9	0
6	D	813	HEM	8	0
6	H	809	HEM	8	0
6	F	811	HEM	9	0
6	F	812	HEM	6	0
6	D	806	HEM	8	0
6	L	813	HEM	11	0
6	C	809	HEM	6	0
6	B	807	HEM	6	0
6	E	812	HEM	8	0
6	H	812	HEM	7	0
6	G	807	HEM	11	0
6	K	811	HEM	7	0
6	B	809	HEM	7	0
6	L	812	HEM	9	0
6	J	811	HEM	6	0
6	G	813	HEM	8	0
6	E	806	HEM	7	0
6	A	811	HEM	6	0
6	C	811	HEM	7	0
6	I	811	HEM	6	0
6	K	807	HEM	9	0
6	H	810	HEM	8	0
6	C	806	HEM	8	0
6	B	811	HEM	9	0
6	B	812	HEM	7	0
6	H	807	HEM	9	0
6	J	810	HEM	7	0
6	A	813	HEM	7	0
6	L	807	HEM	14	0
6	K	812	HEM	7	0
6	C	810	HEM	8	0

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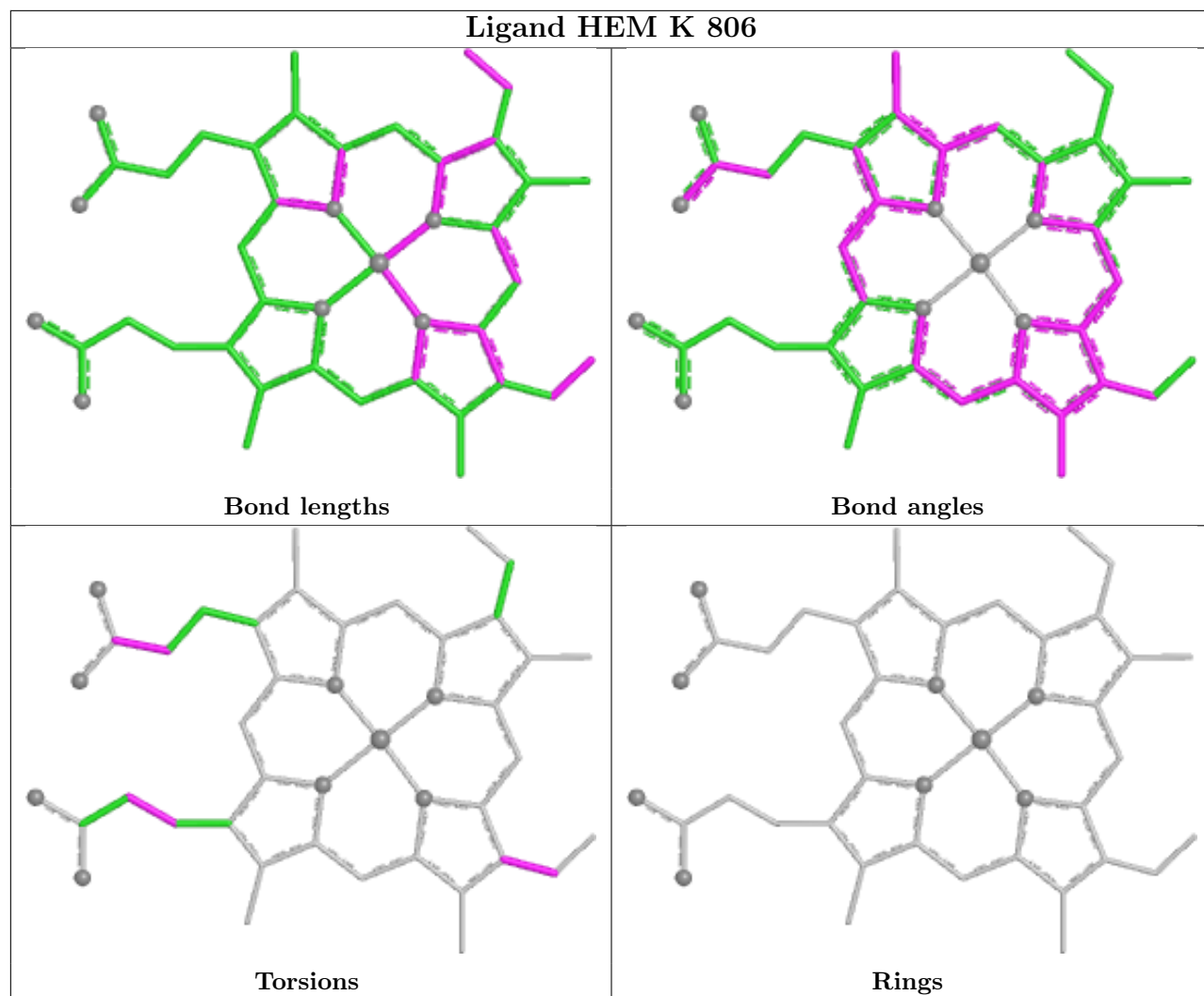
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	809	HEM	8	0
6	D	807	HEM	8	0
6	D	811	HEM	6	0
6	D	812	HEM	9	0
6	E	810	HEM	11	0
6	I	810	HEM	8	0
6	L	809	HEM	11	0
6	D	809	HEM	11	0
6	H	811	HEM	10	0
6	H	808	HEM	11	0
6	L	811	HEM	8	0
6	A	810	HEM	10	0
6	I	809	HEM	8	0
6	J	806	HEM	7	0
6	B	808	HEM	13	0
6	J	808	HEM	7	0
6	F	807	HEM	8	0
6	D	808	HEM	8	0
6	G	810	HEM	7	0
6	C	808	HEM	10	0
6	J	807	HEM	12	0
6	E	809	HEM	7	0
6	J	813	HEM	9	0
5	F	806	ACT	1	0
6	H	814	HEM	7	0
6	E	813	HEM	8	0
6	I	813	HEM	7	0
6	I	807	HEM	6	0
6	A	808	HEM	7	0
6	A	806	HEM	7	0
6	J	812	HEM	7	0
6	F	809	HEM	4	0
6	K	813	HEM	7	0
6	B	813	HEM	6	0
6	C	812	HEM	8	0
6	I	812	HEM	10	0
5	C	805	ACT	1	0
6	E	811	HEM	5	0
6	K	810	HEM	8	0
6	G	812	HEM	9	0
6	B	810	HEM	10	0
6	D	810	HEM	10	0

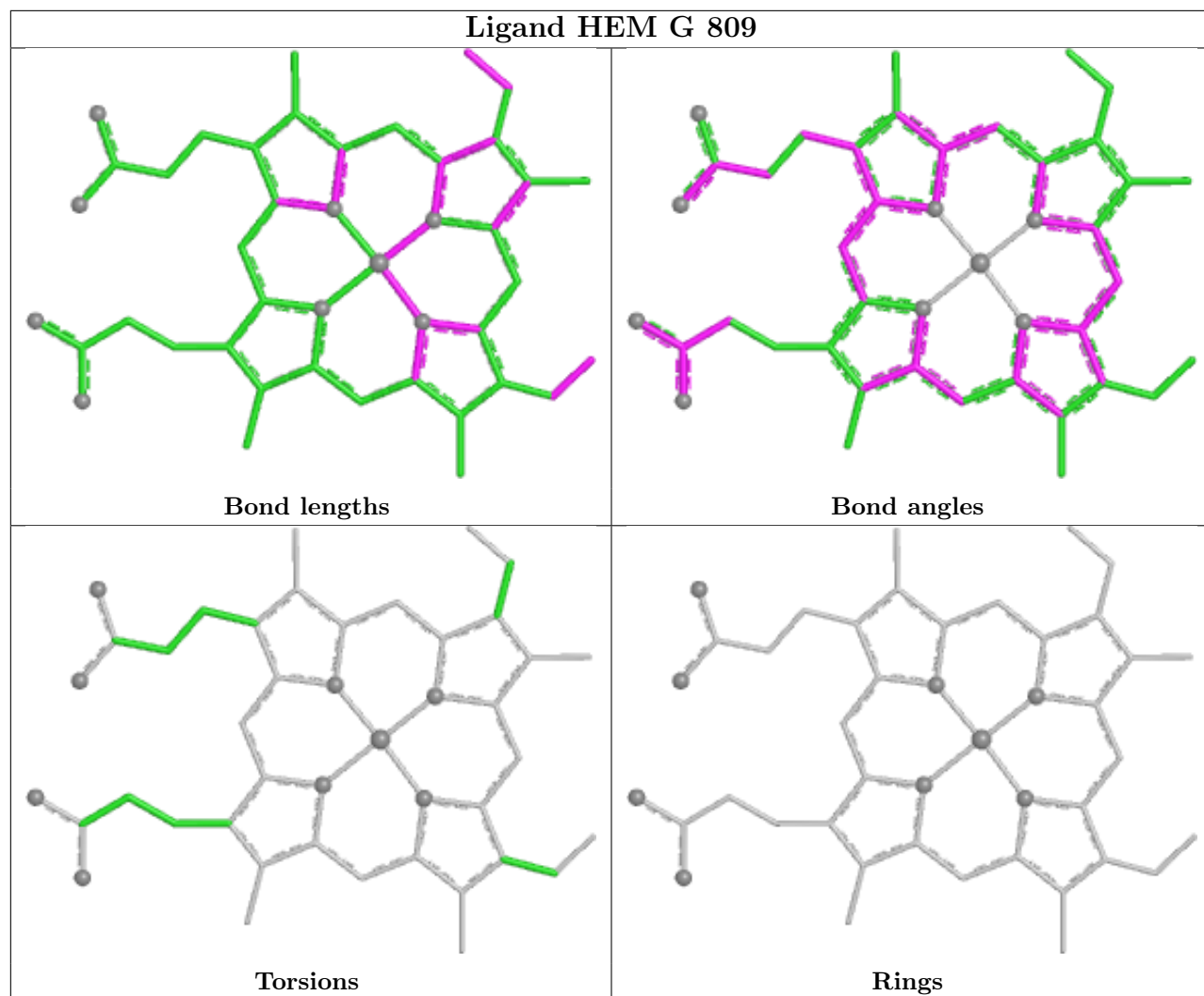
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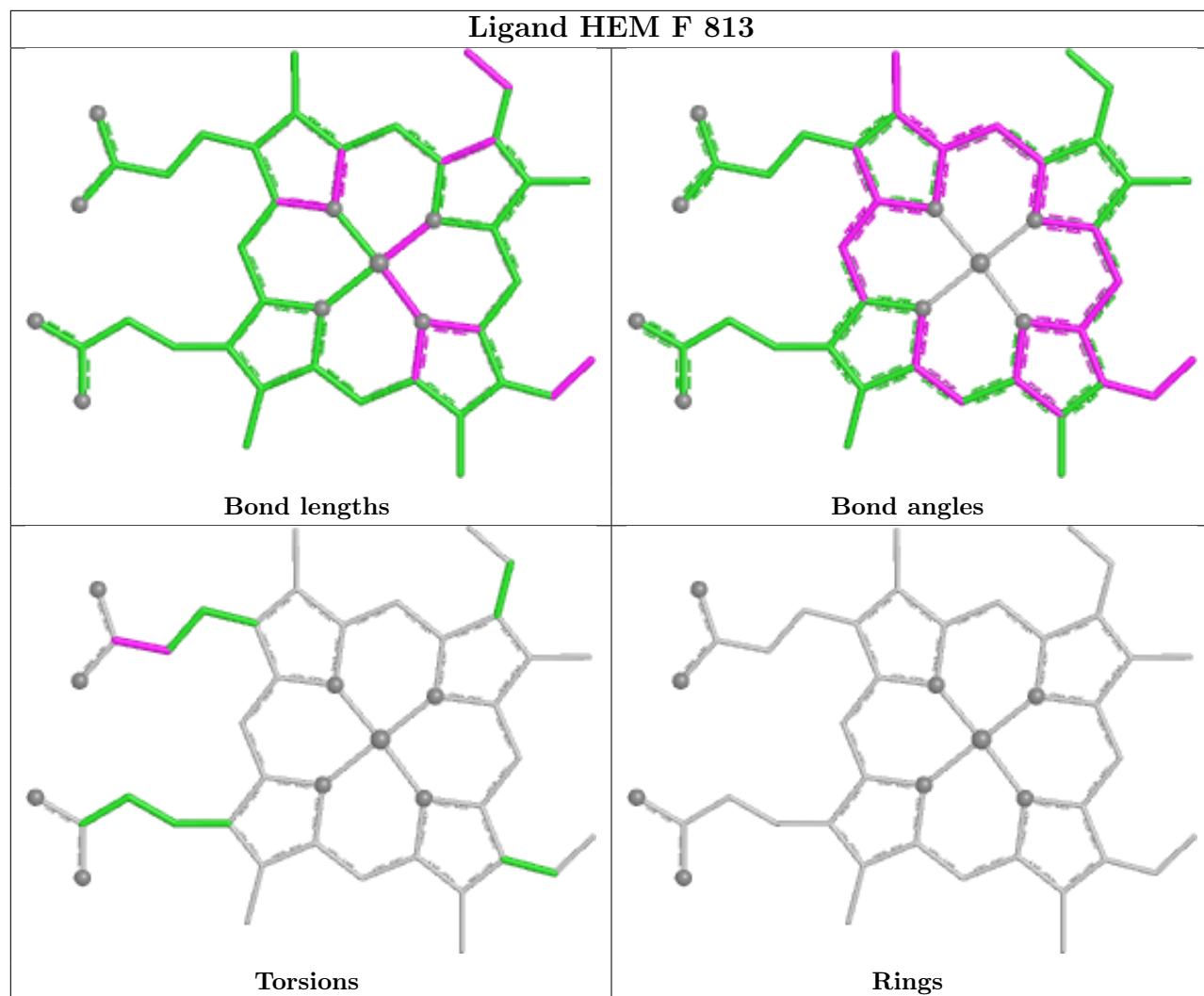
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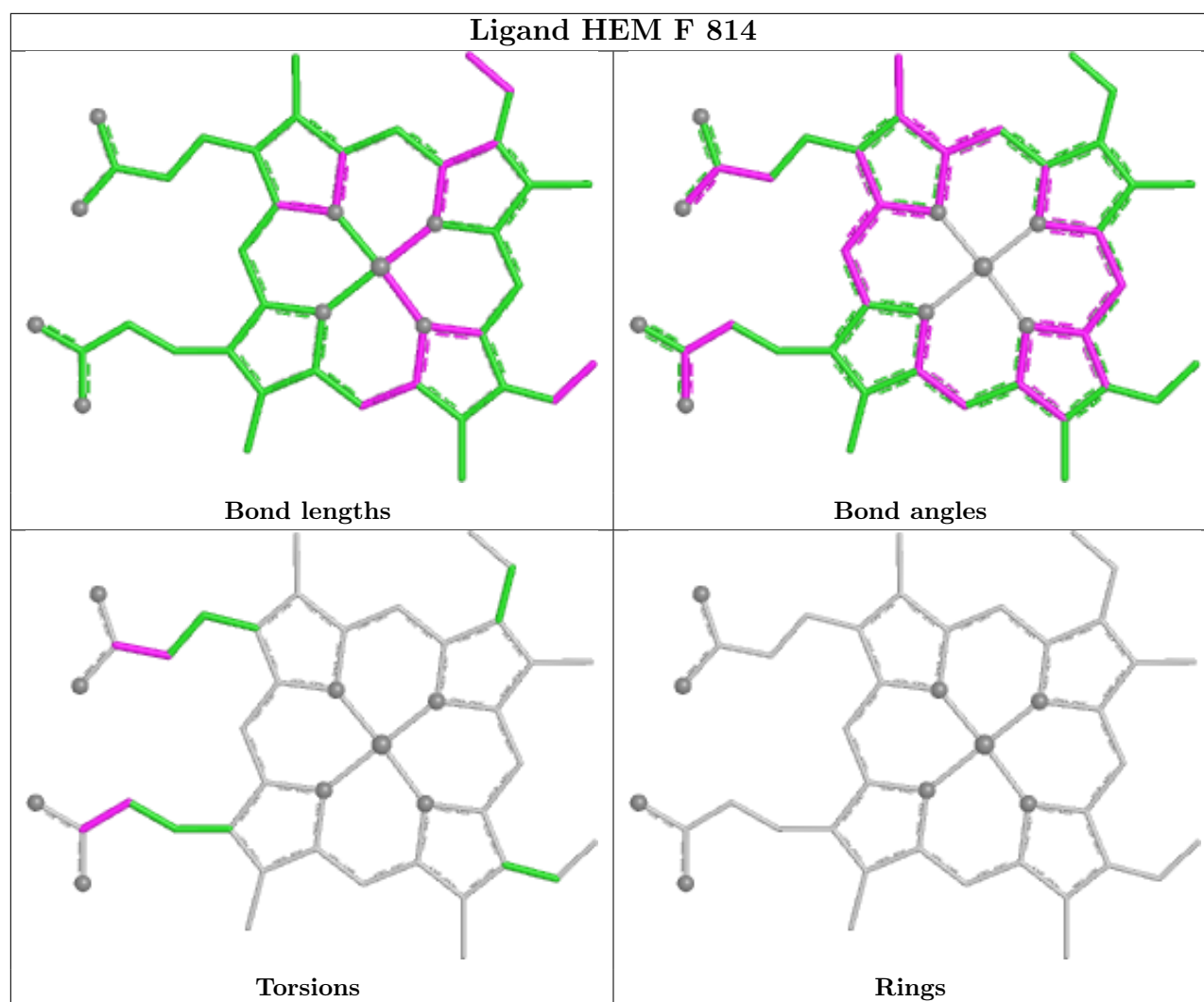
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	806	HEM	9	0
6	E	807	HEM	11	0
4	K	803	BU3	1	0
6	L	806	HEM	8	0
6	A	809	HEM	10	0
6	A	807	HEM	9	0
6	C	807	HEM	14	0
6	H	813	HEM	8	0
6	L	810	HEM	6	0
6	F	810	HEM	9	0

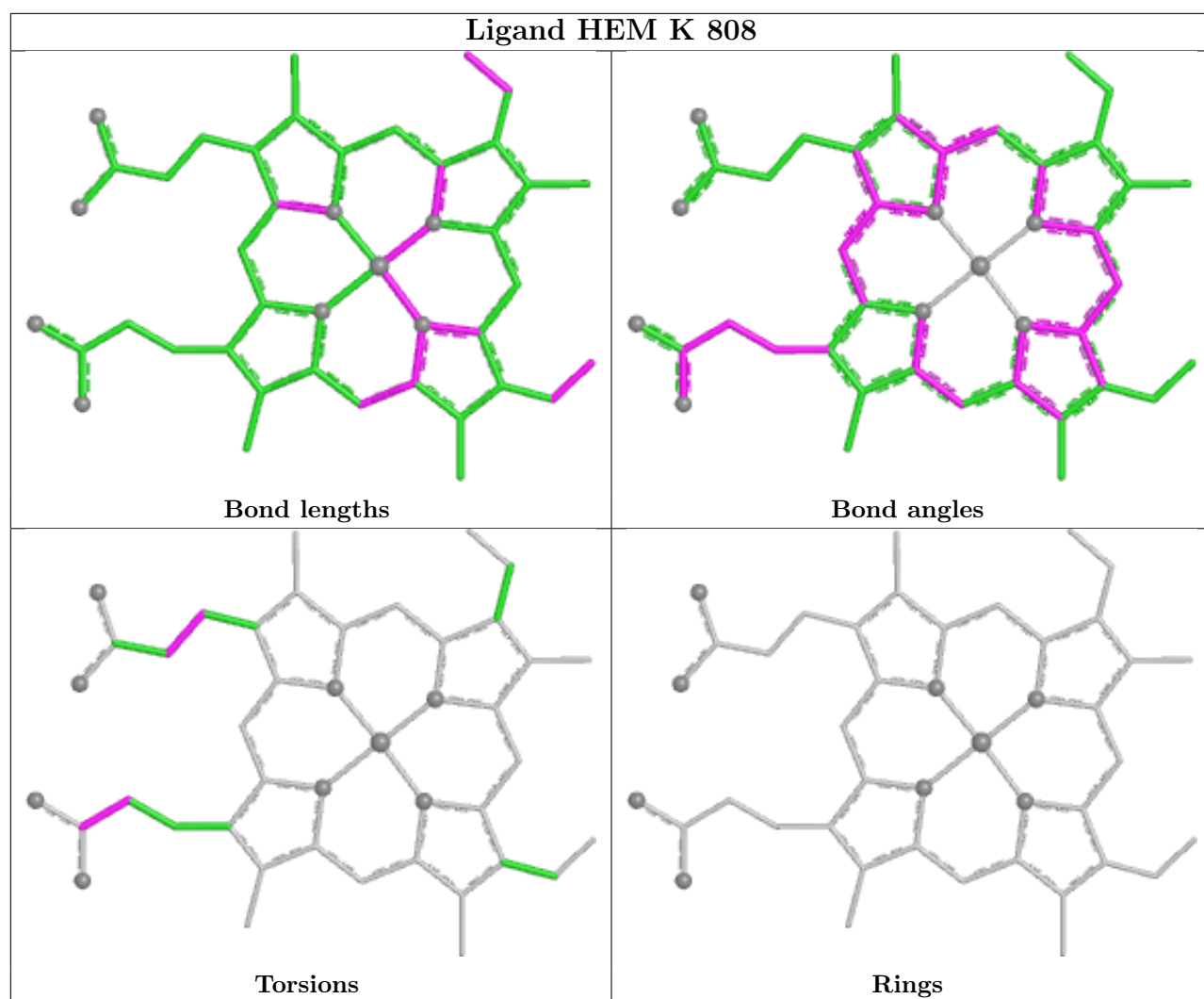
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

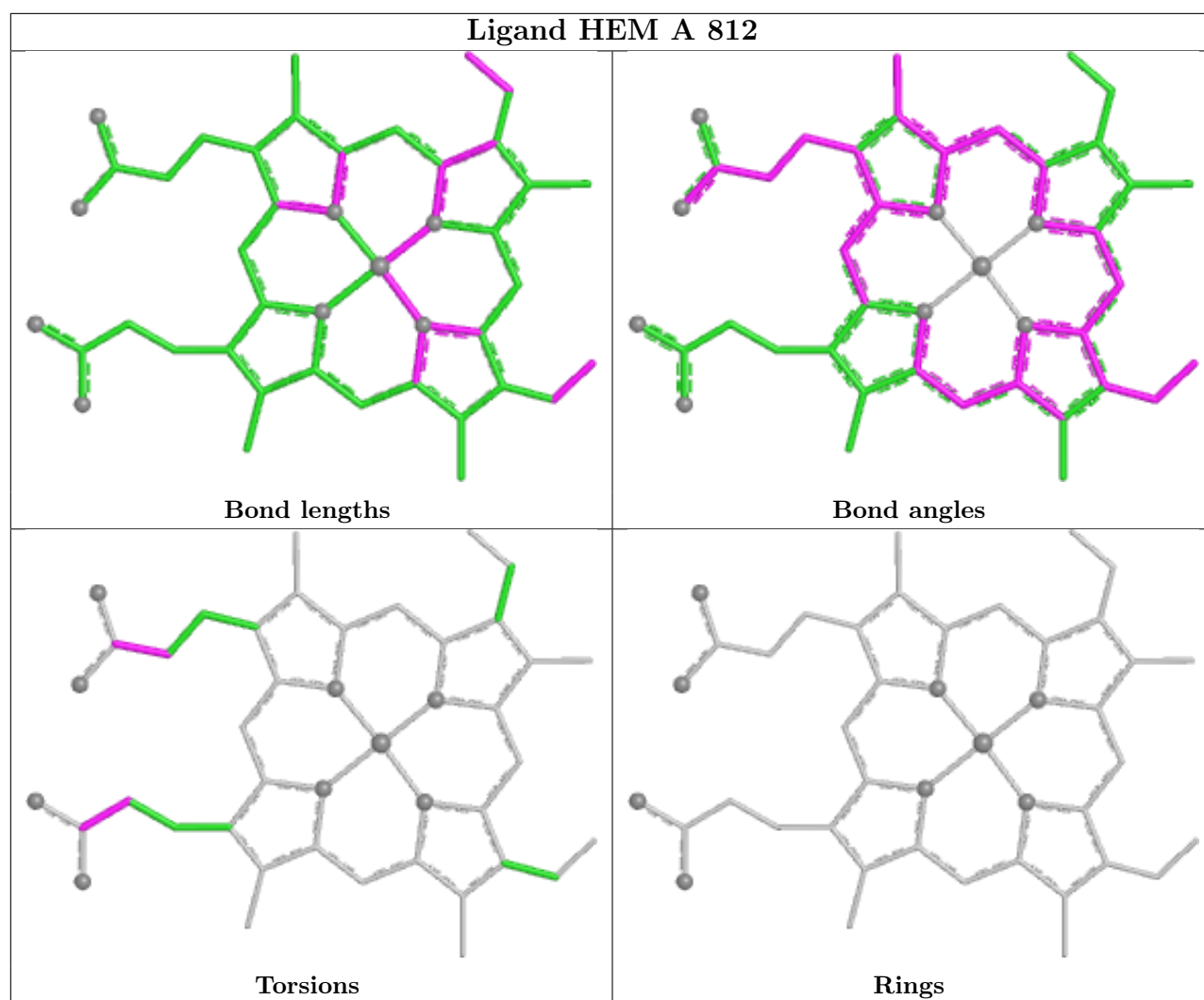


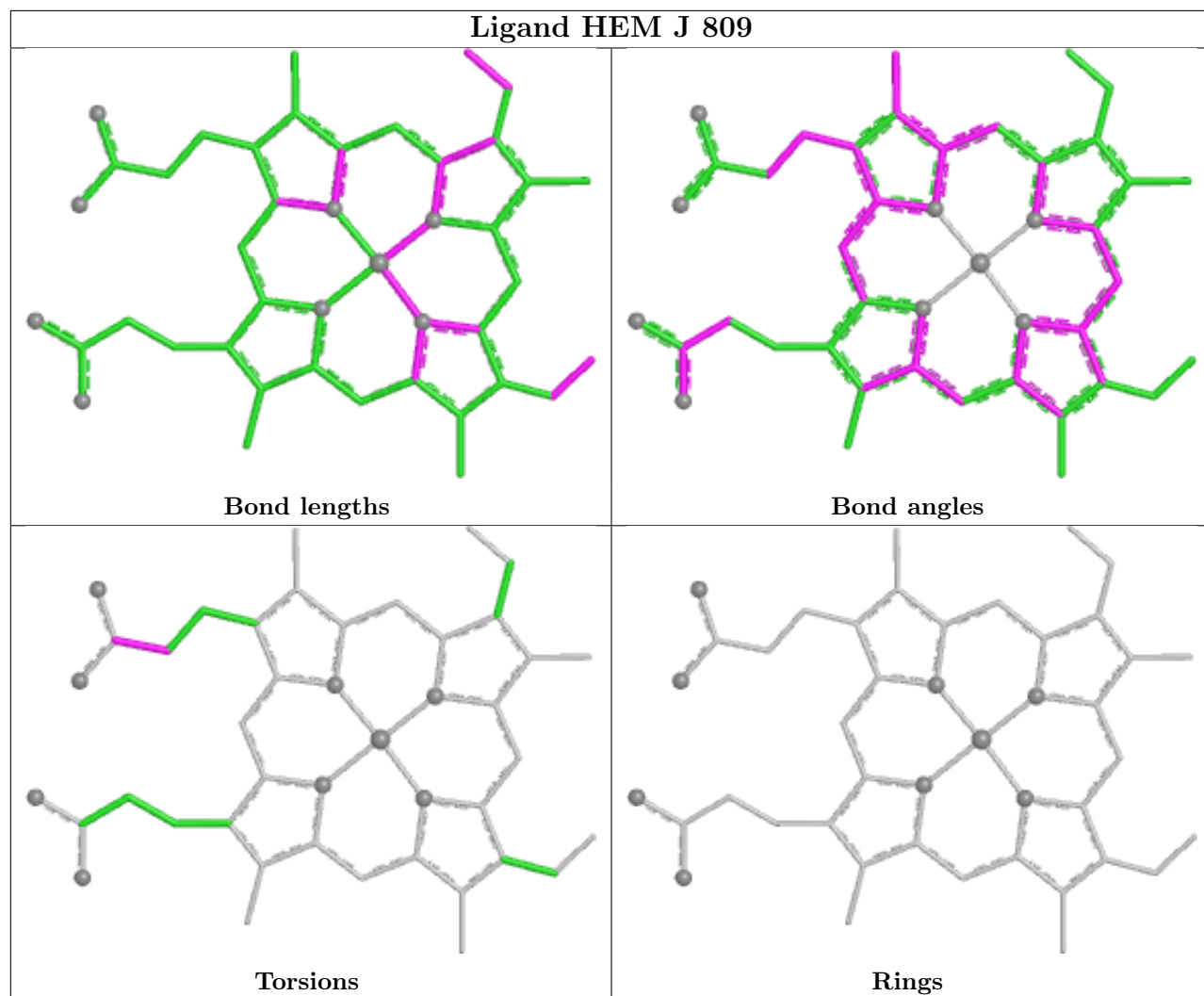




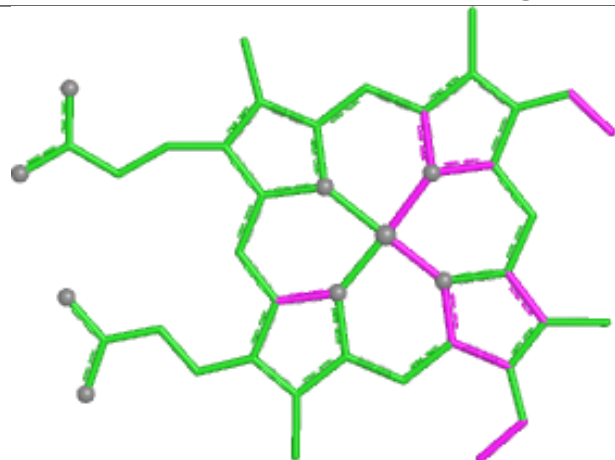




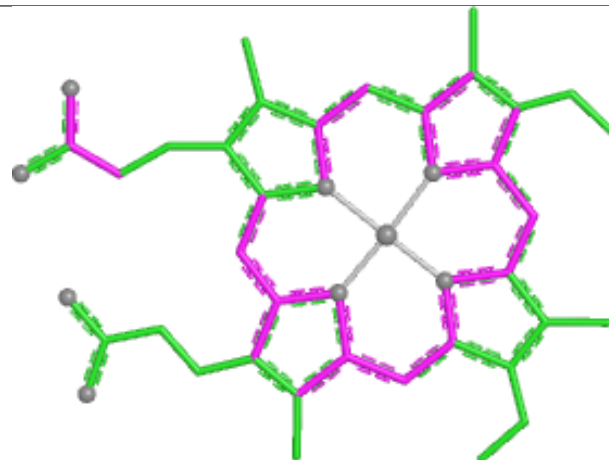




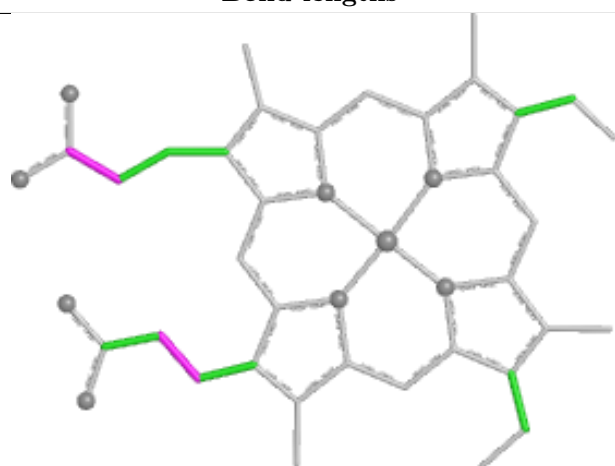
Ligand HEM I 808



Bond lengths



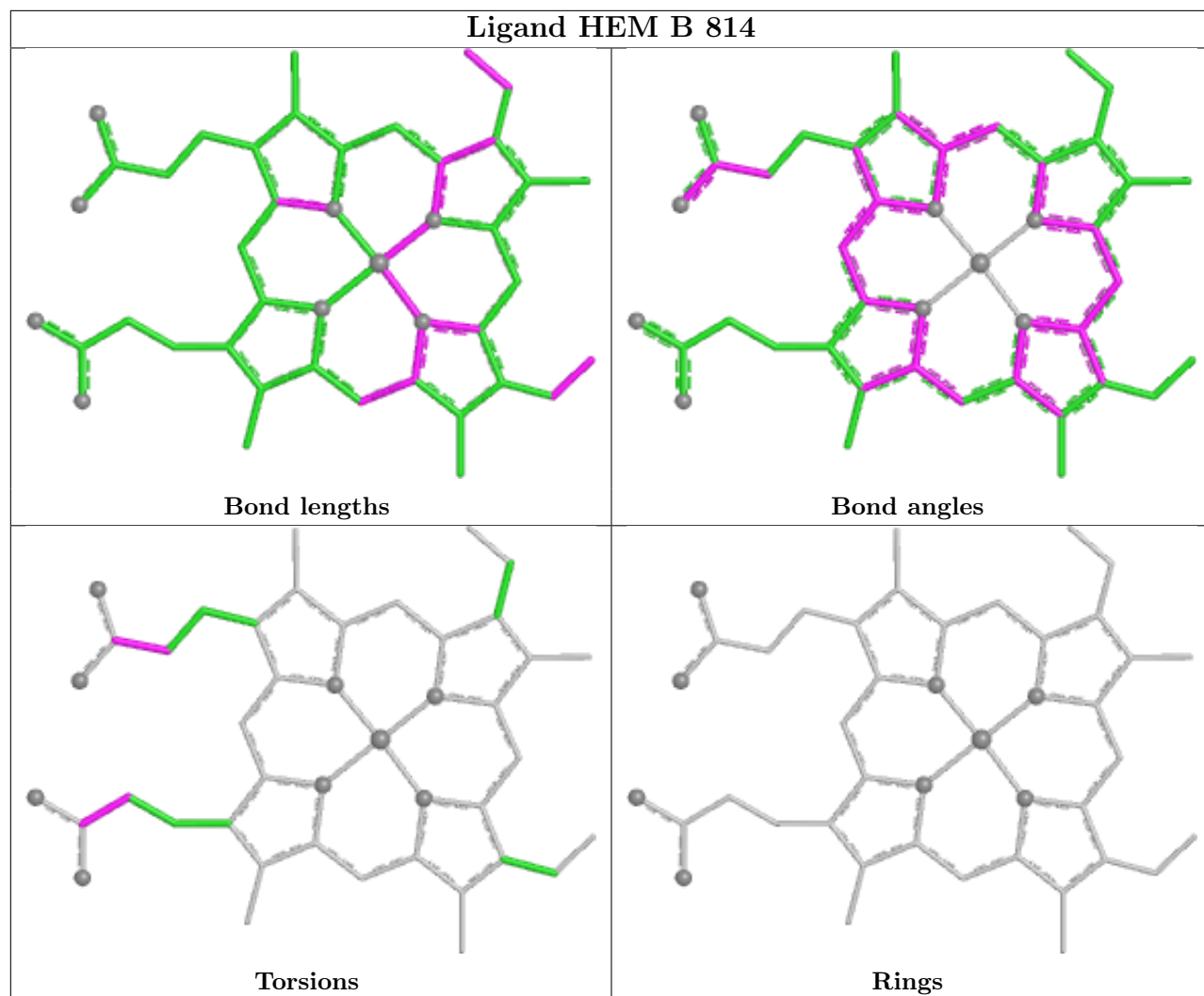
Bond angles



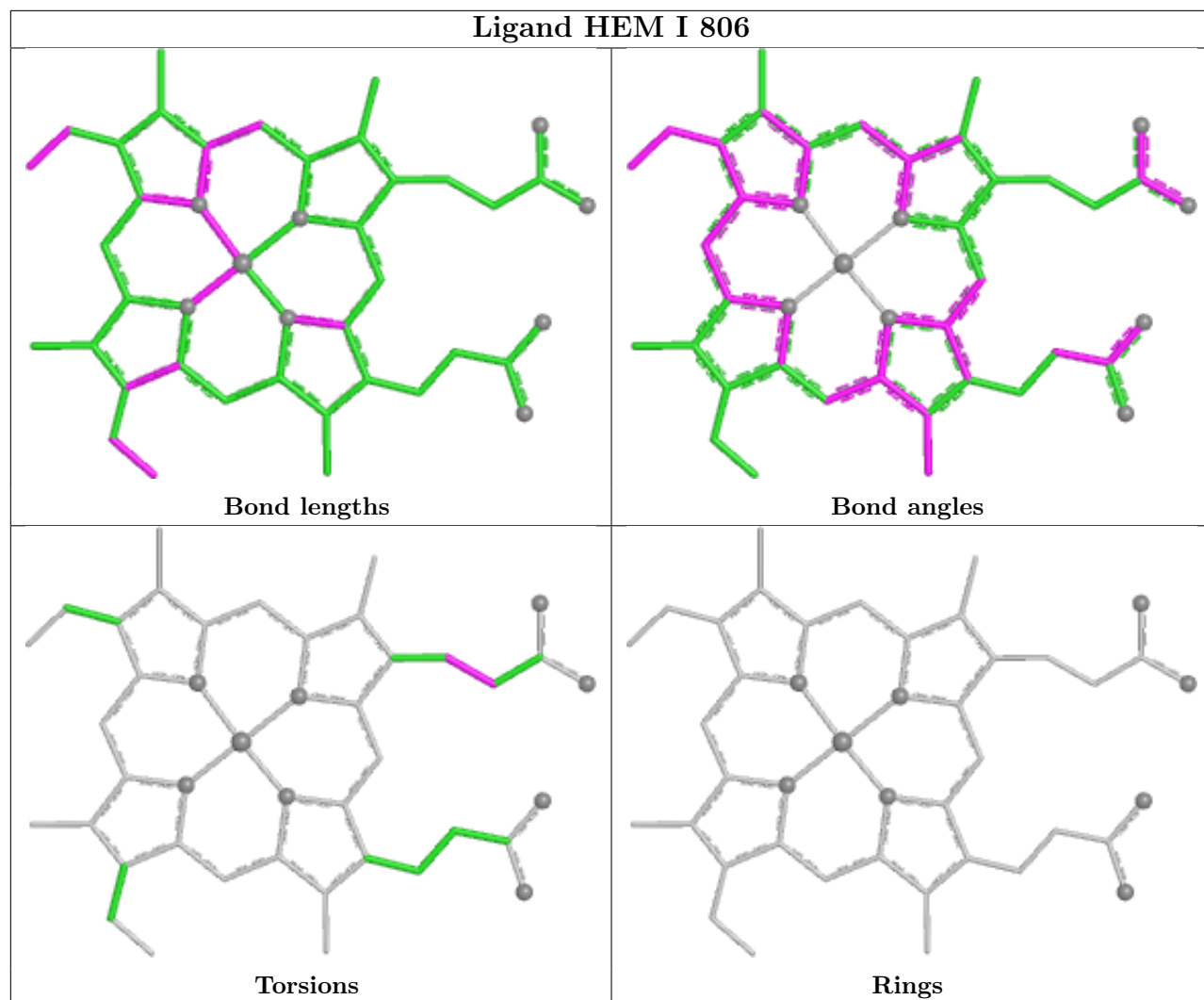
Torsions

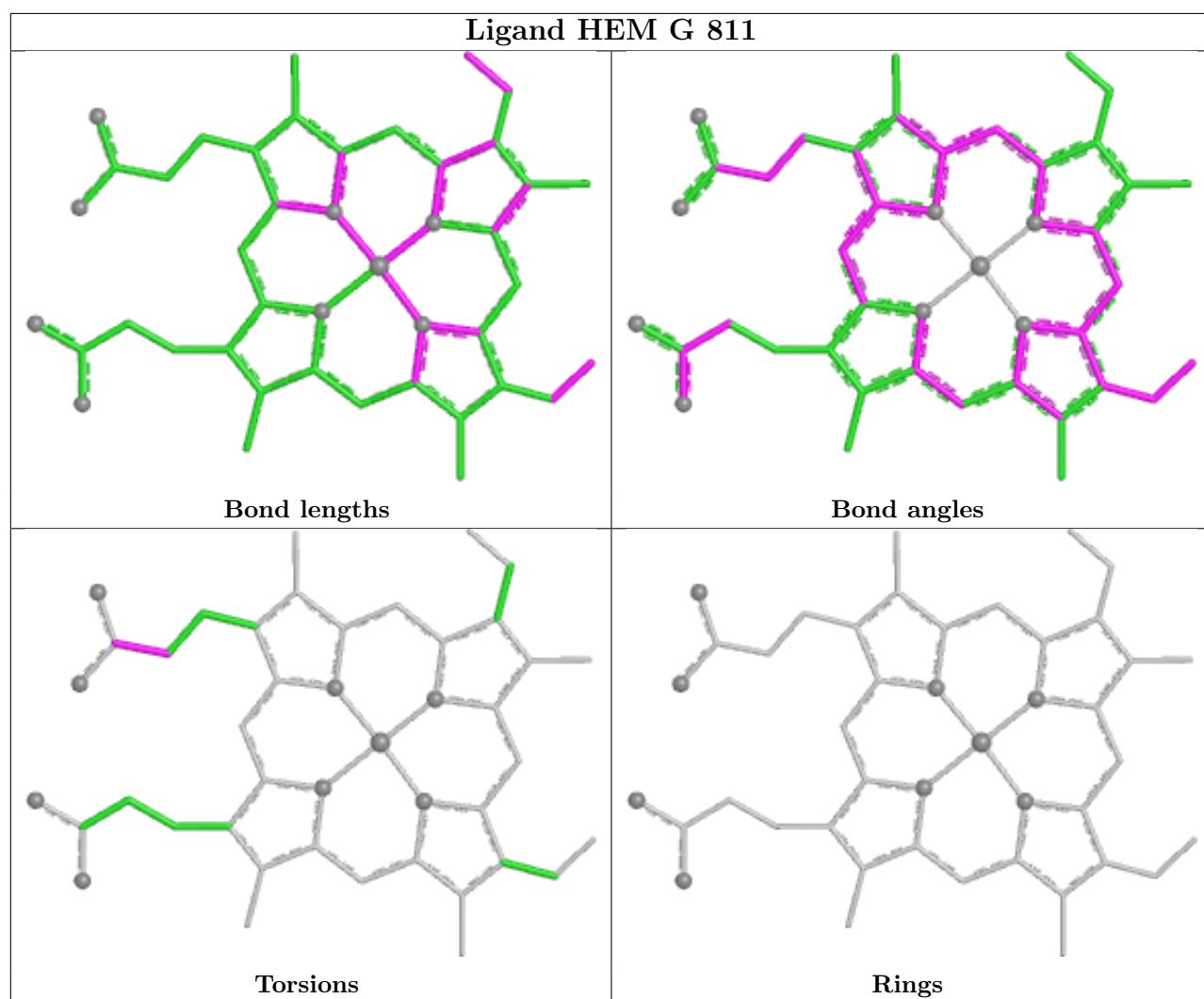


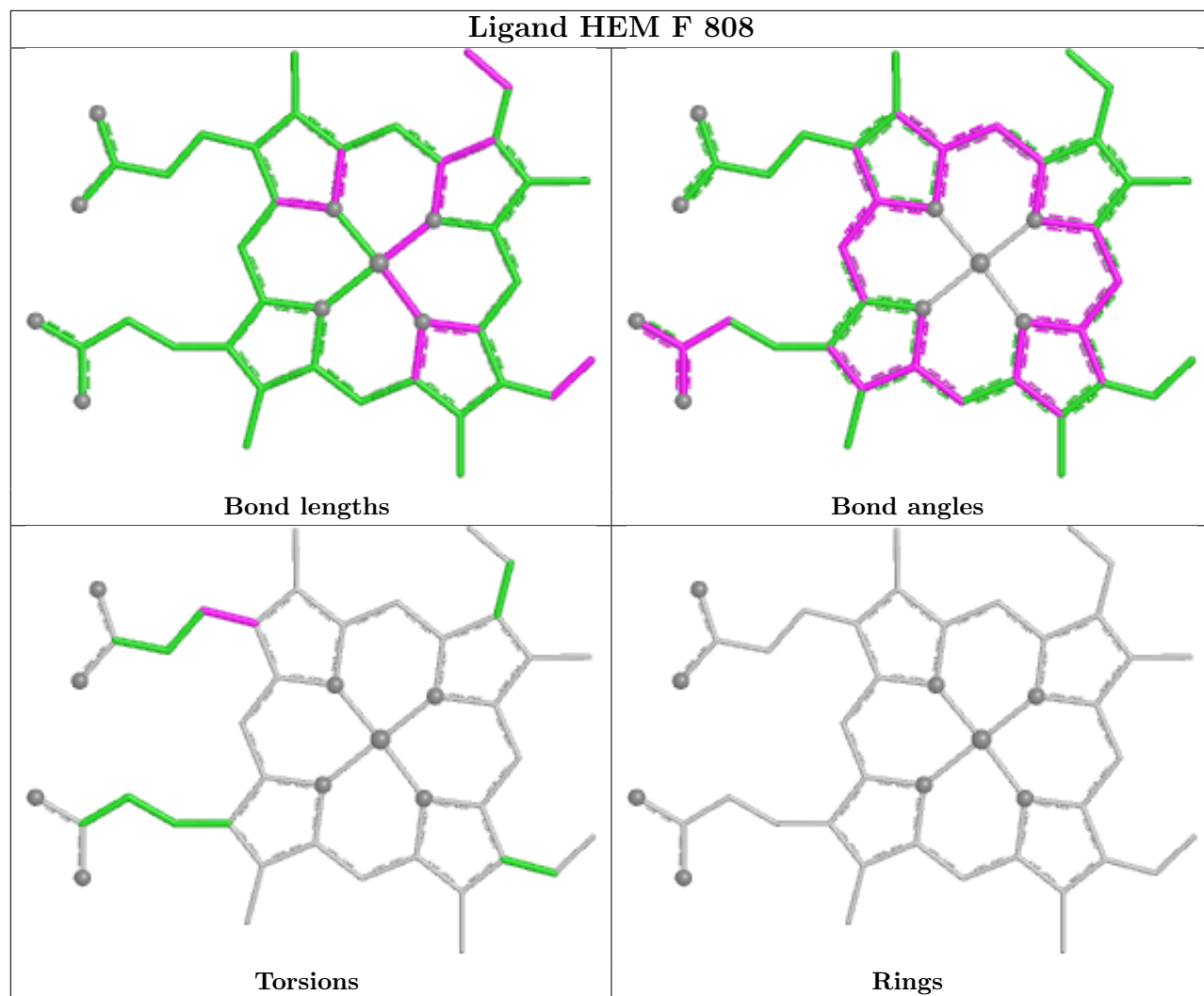
Rings



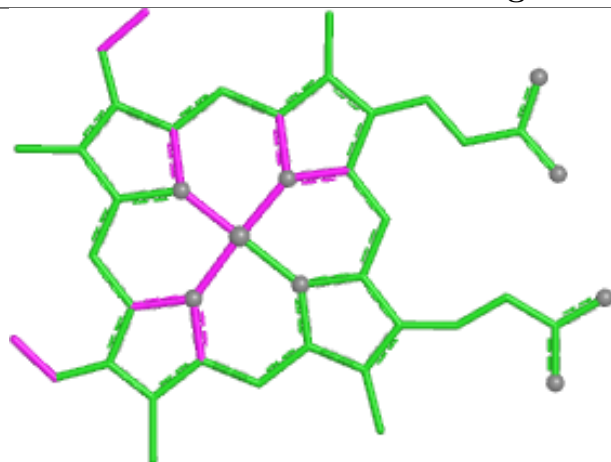
Ligand HEM I 806



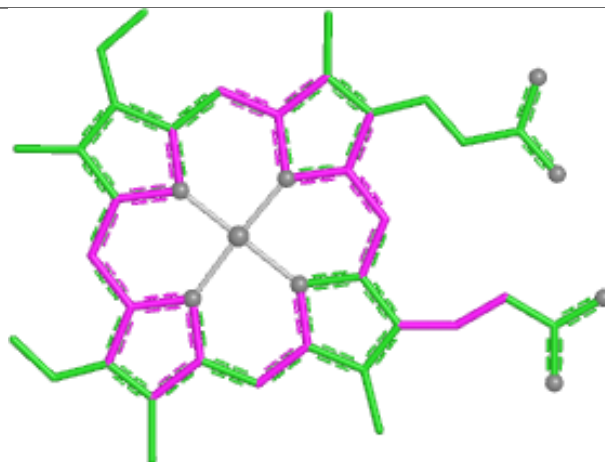




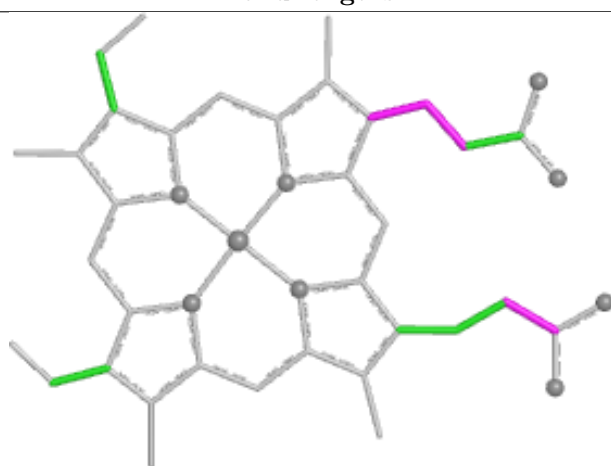
Ligand HEM G 808



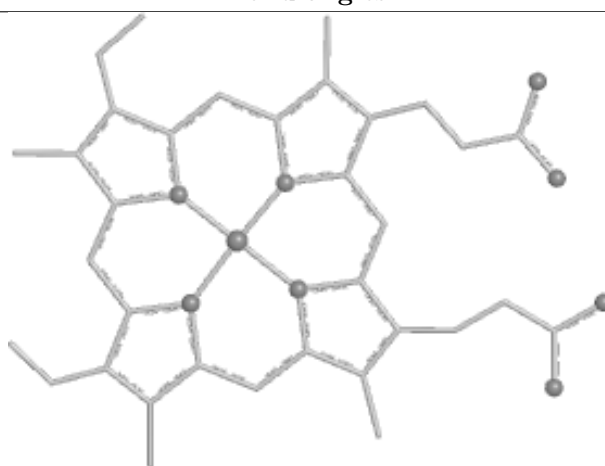
Bond lengths



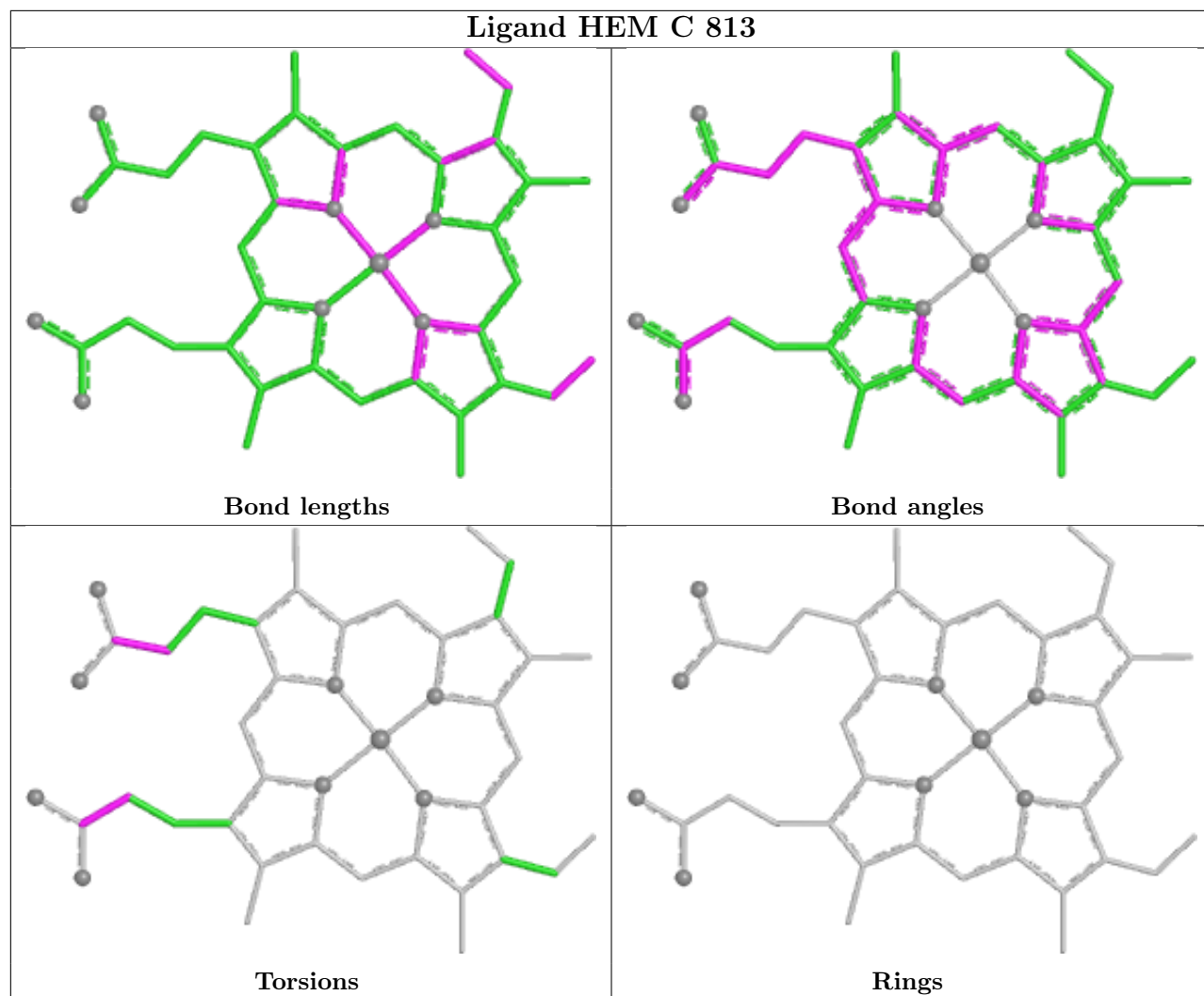
Bond angles

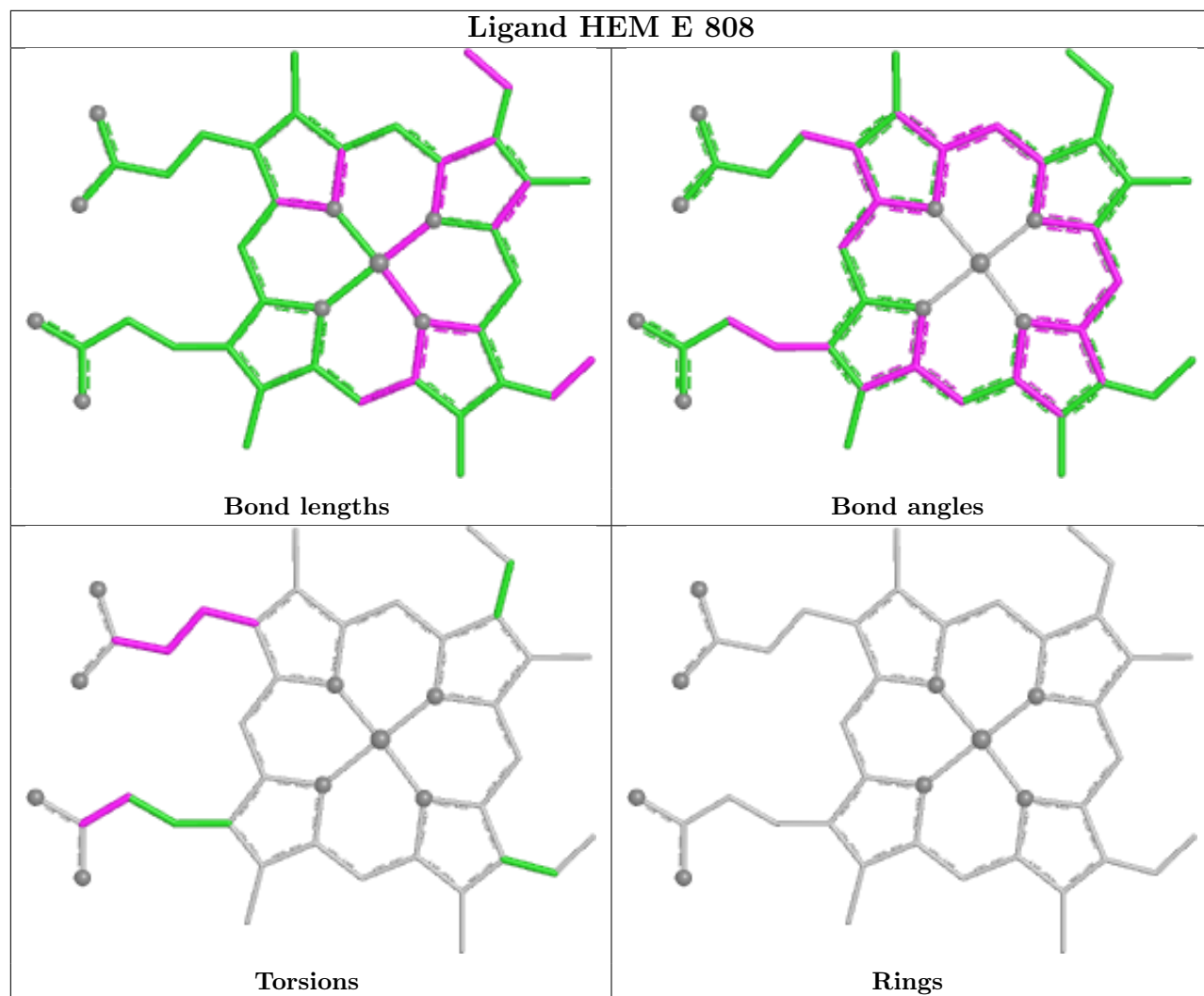


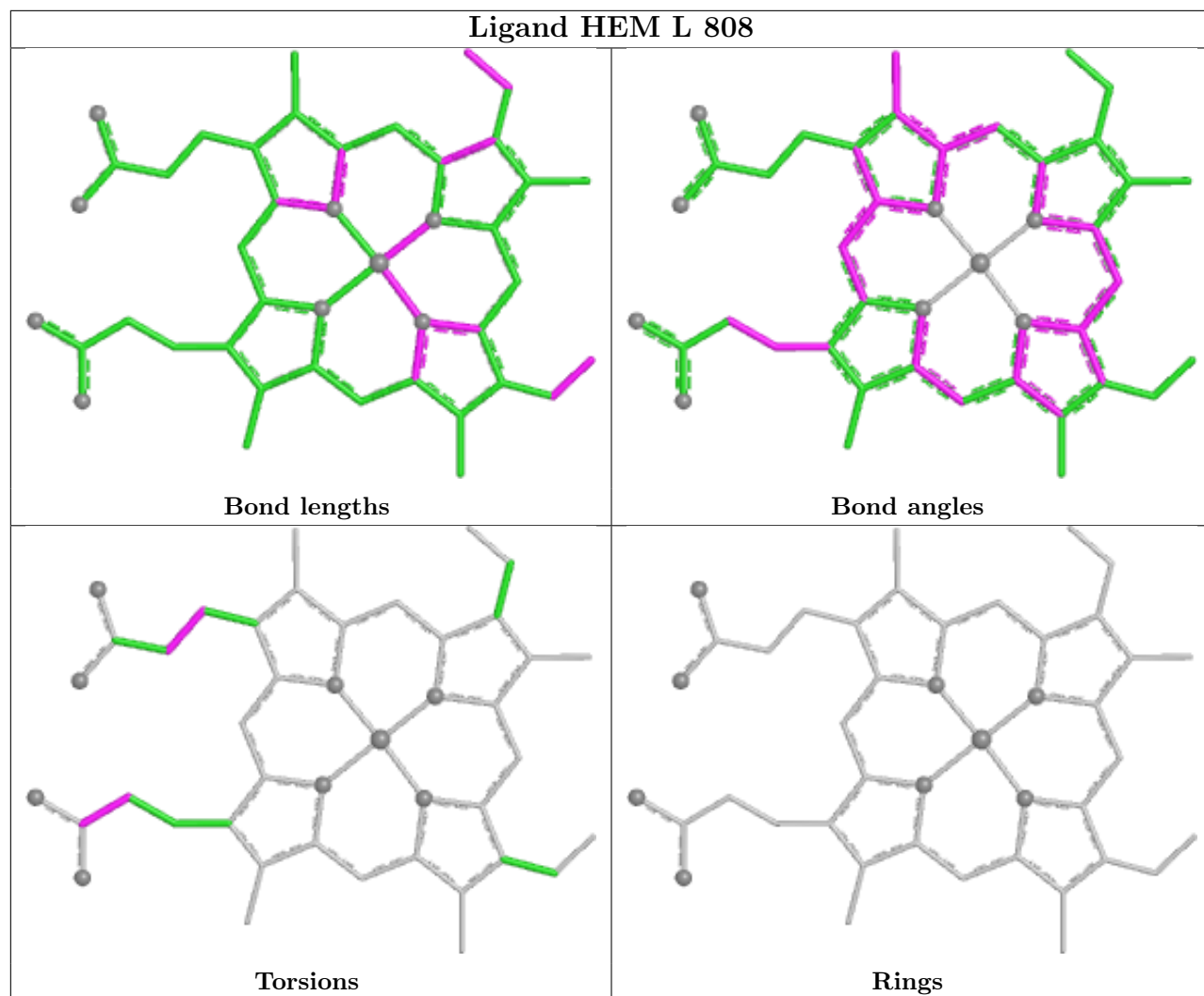
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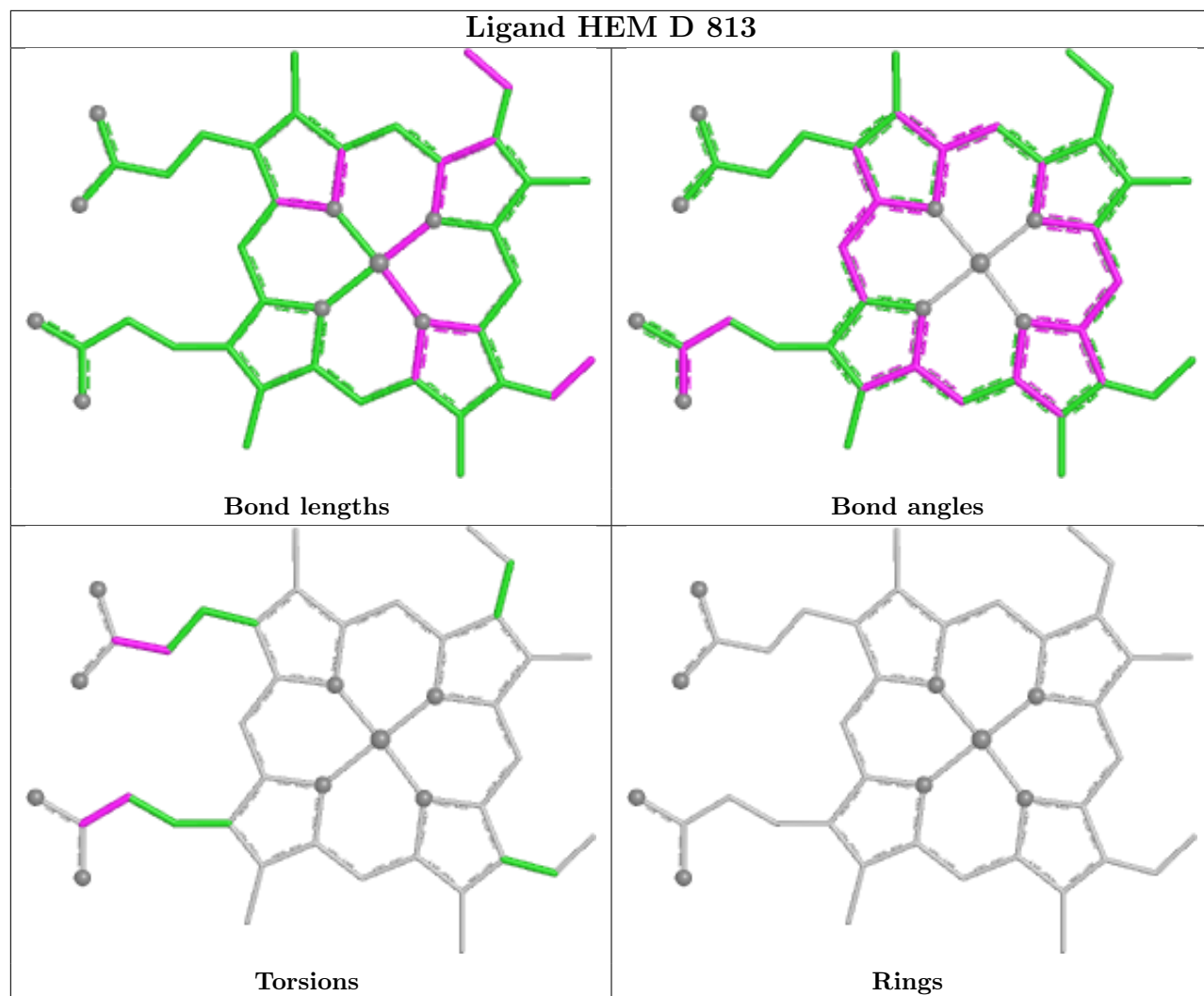


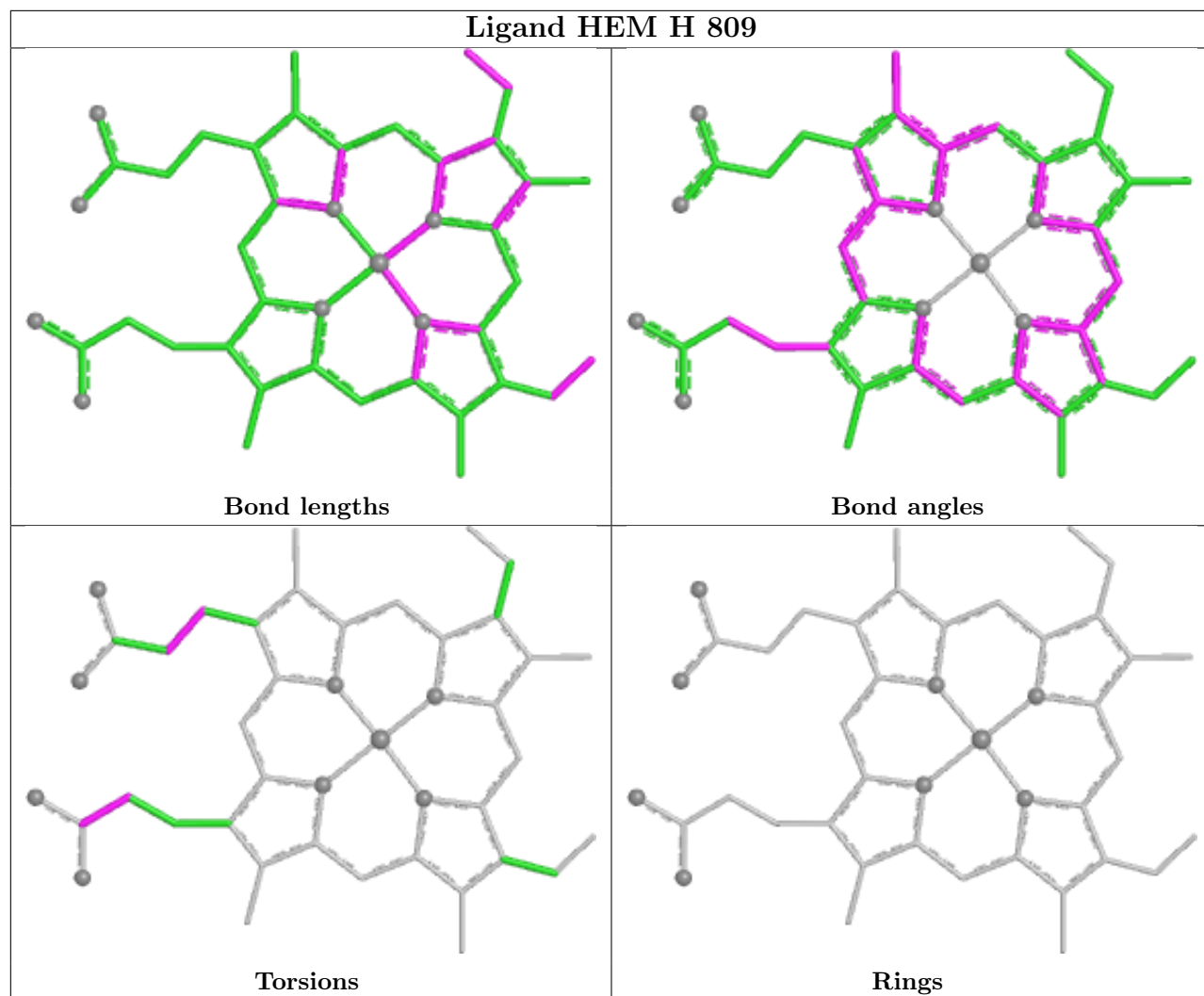
Rings

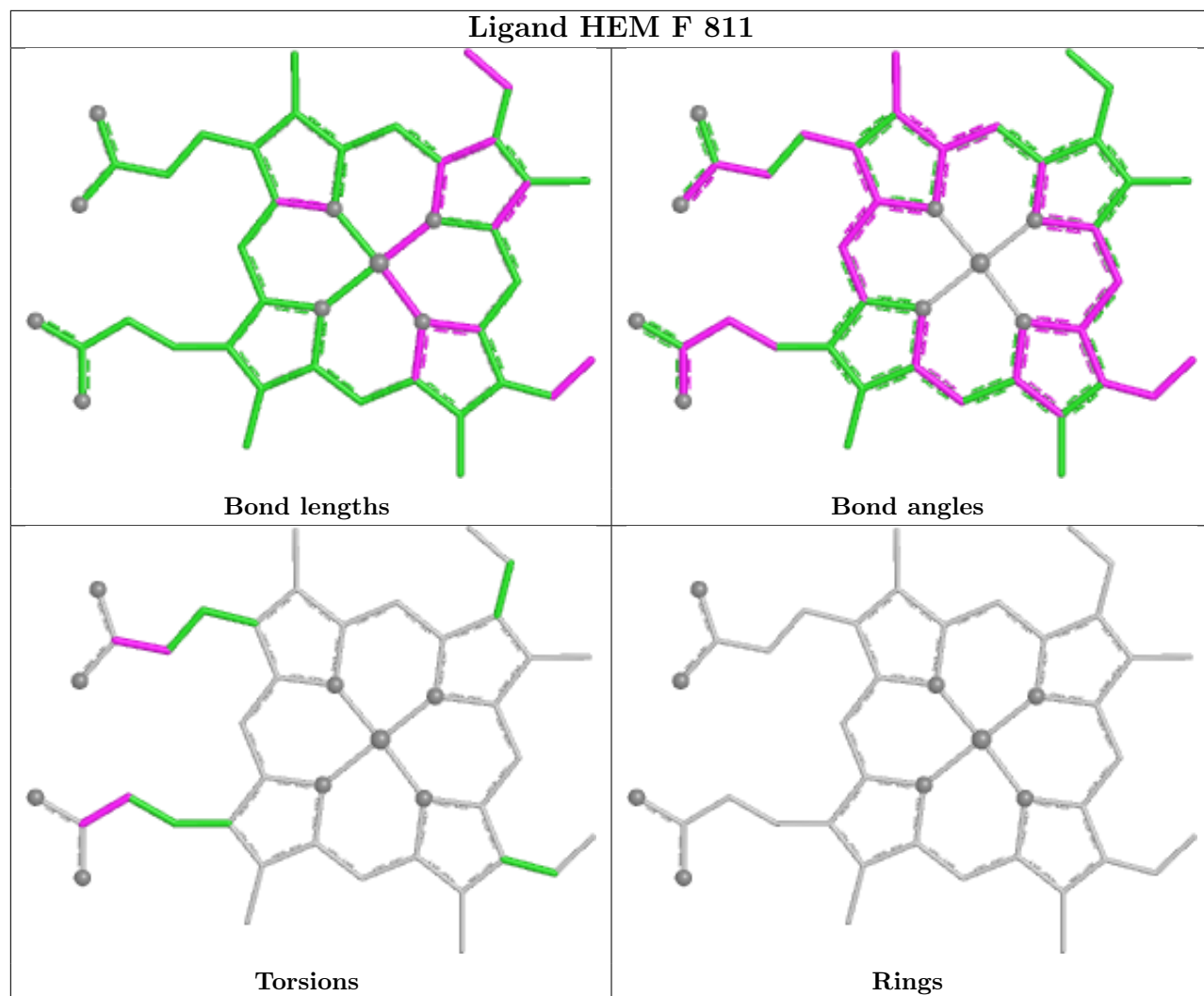


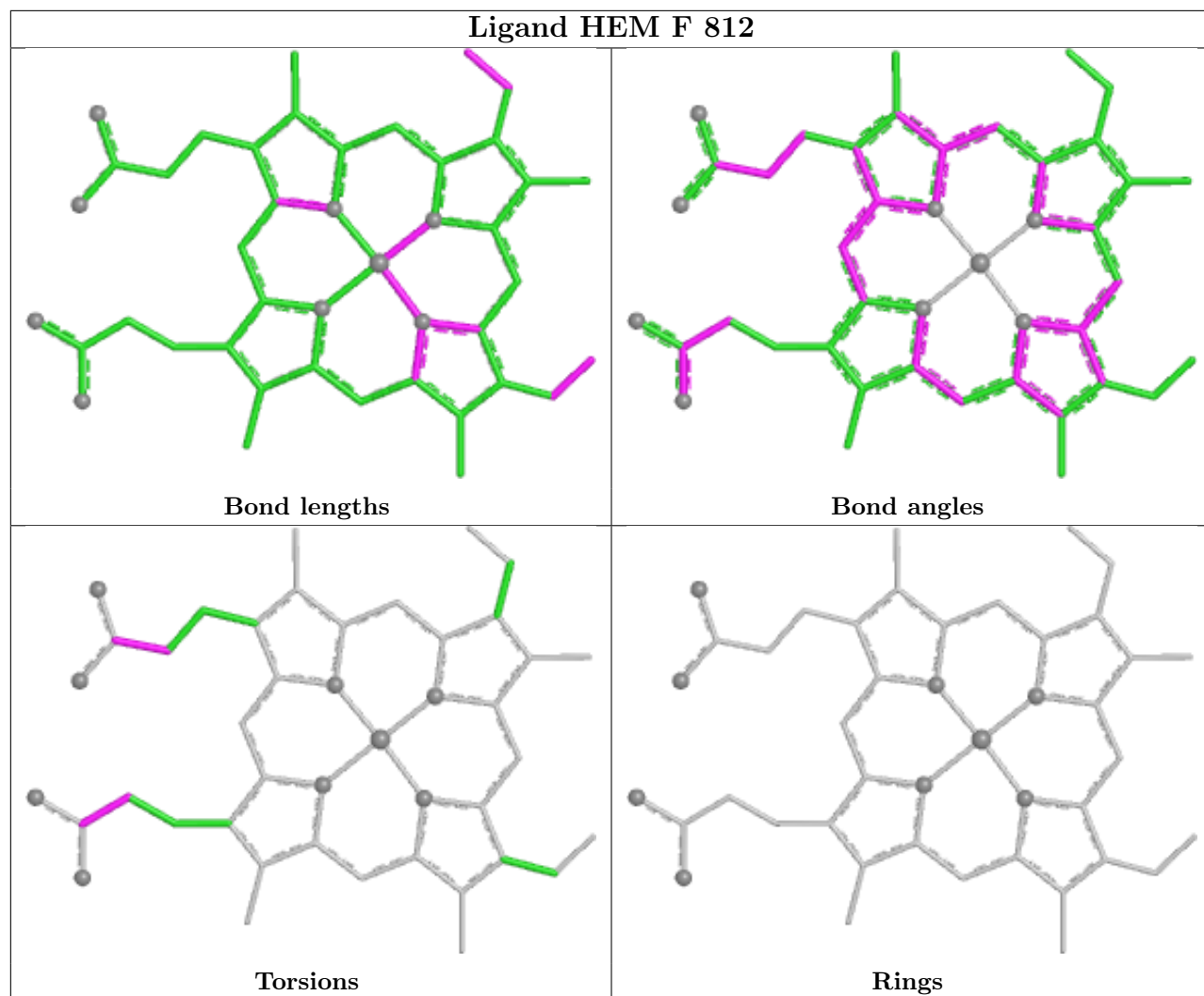


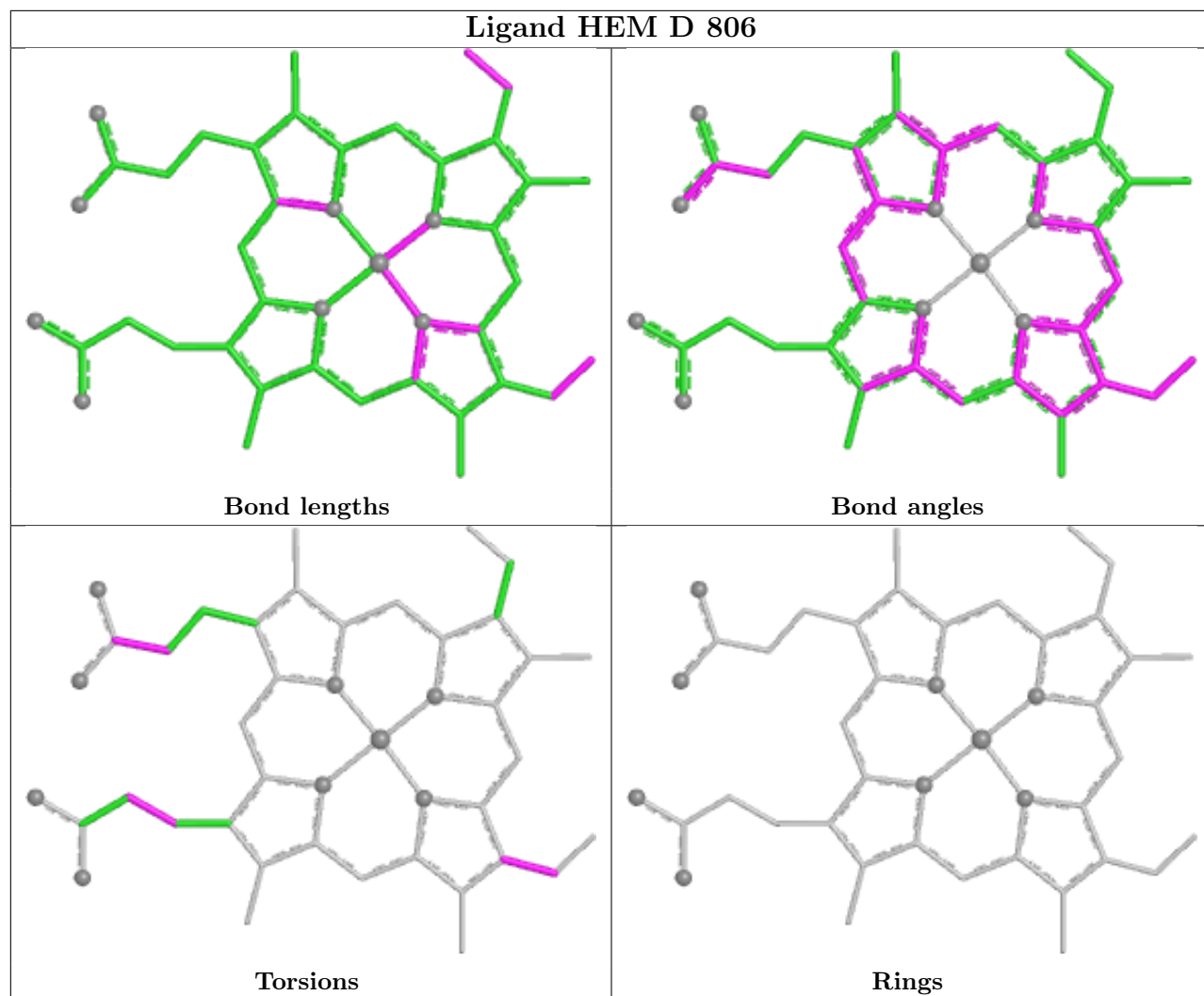


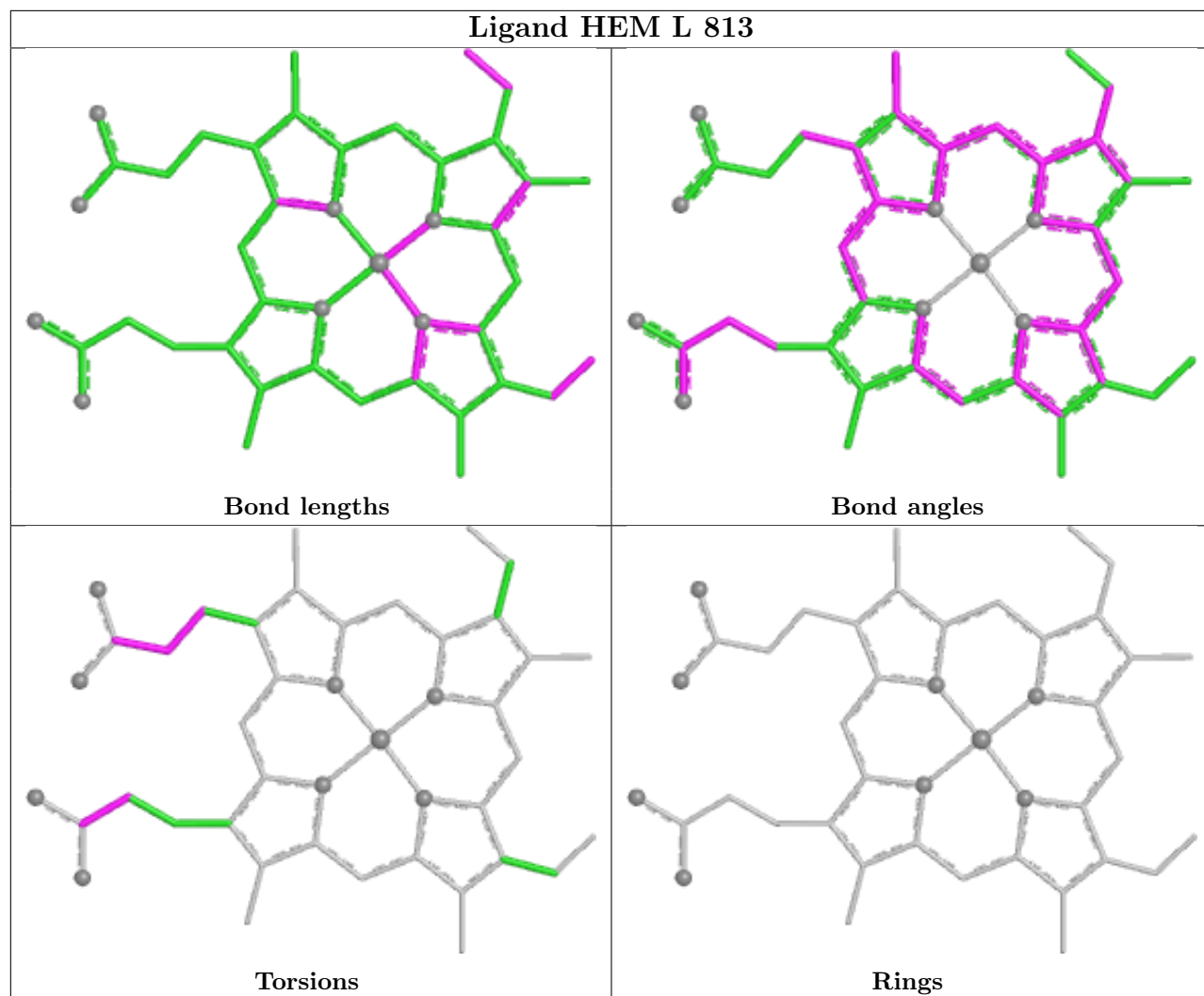


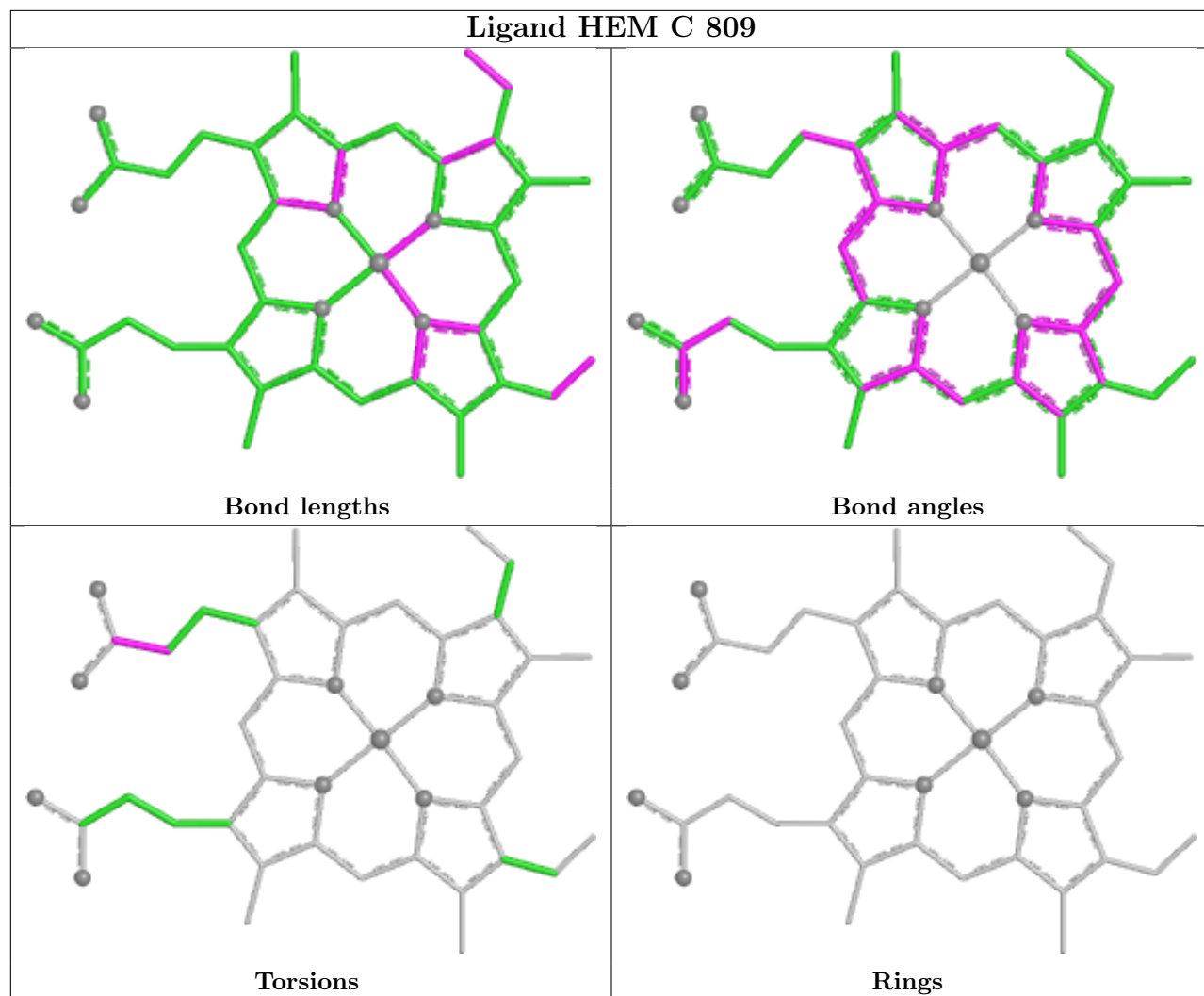


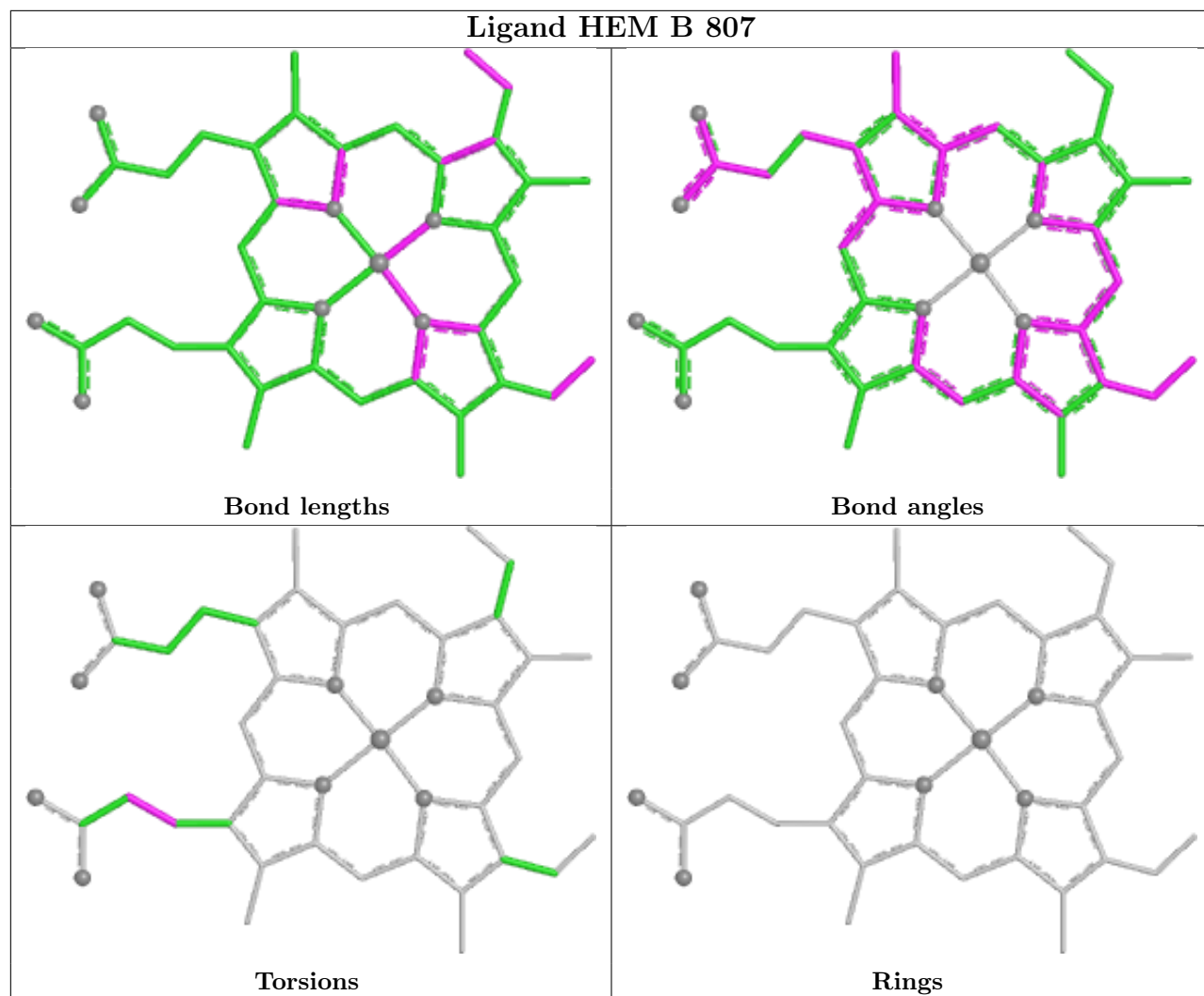


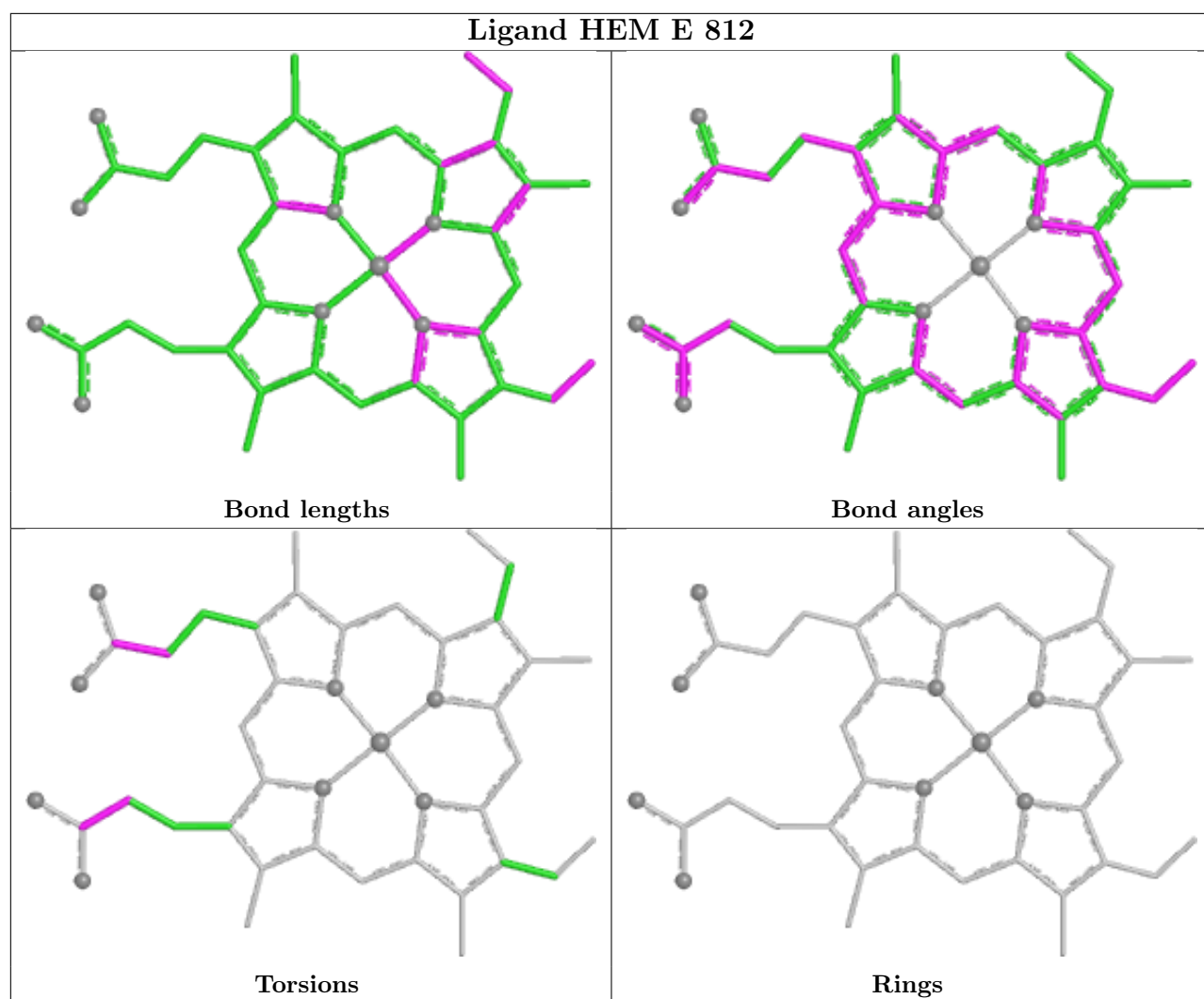


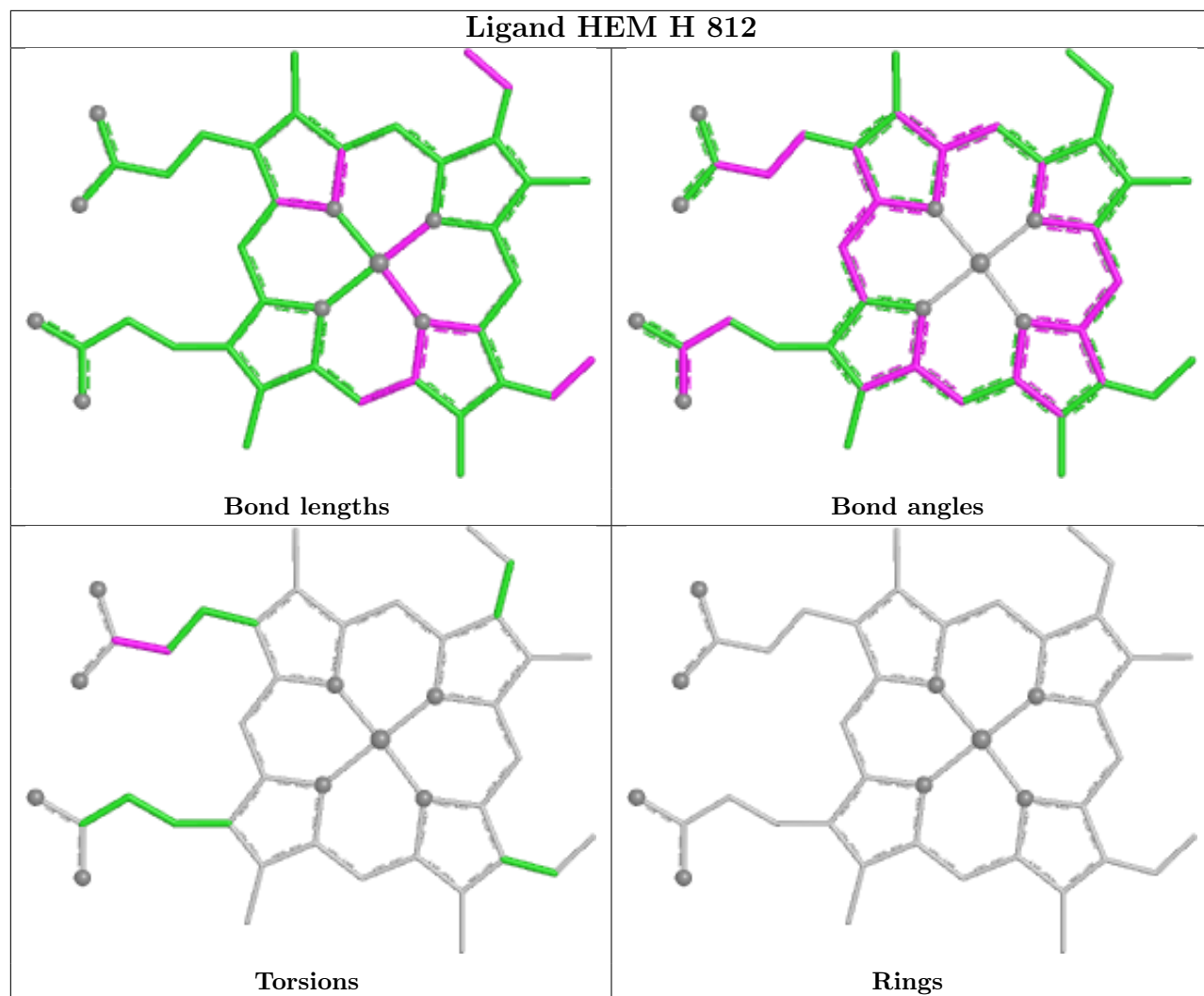


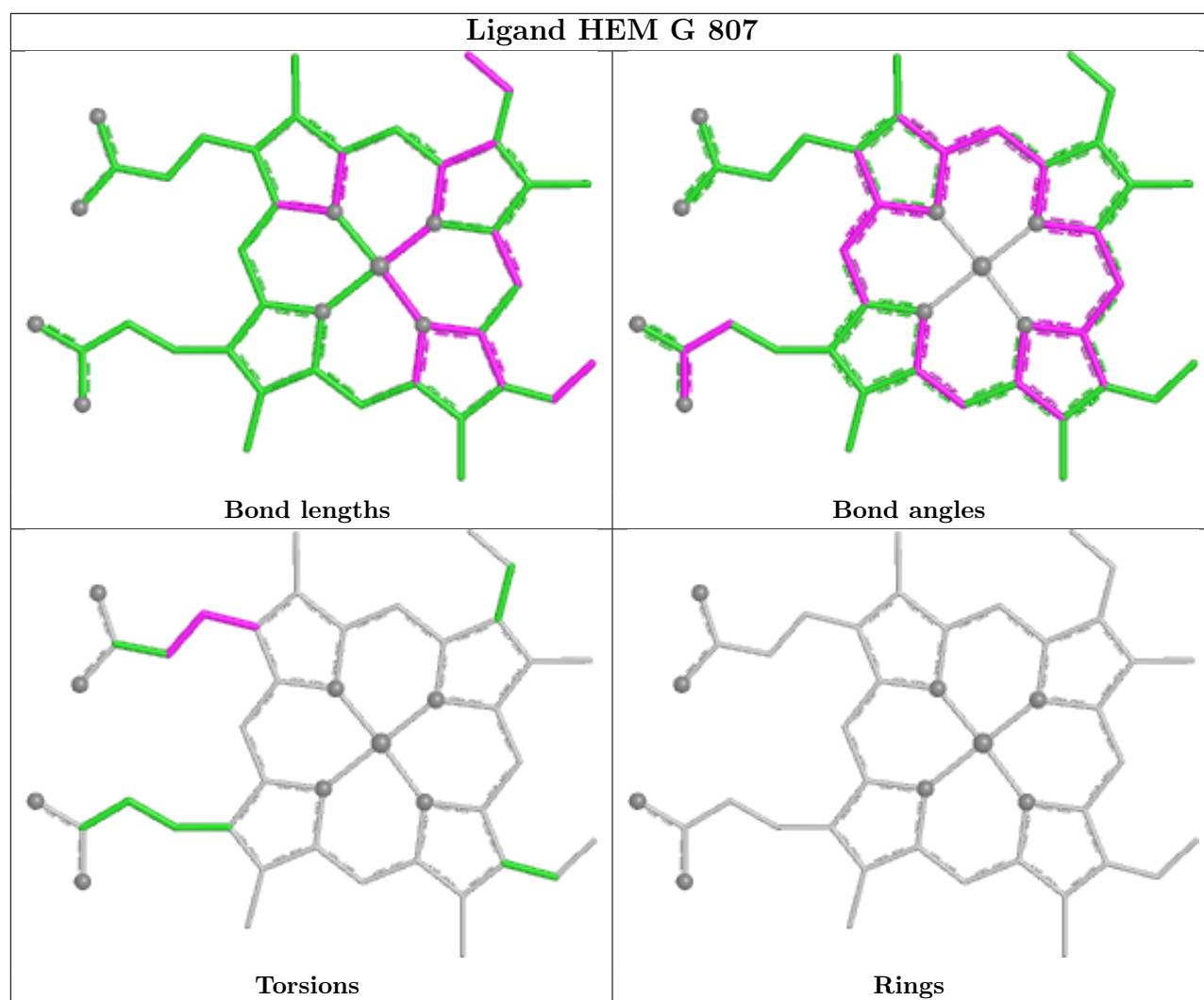


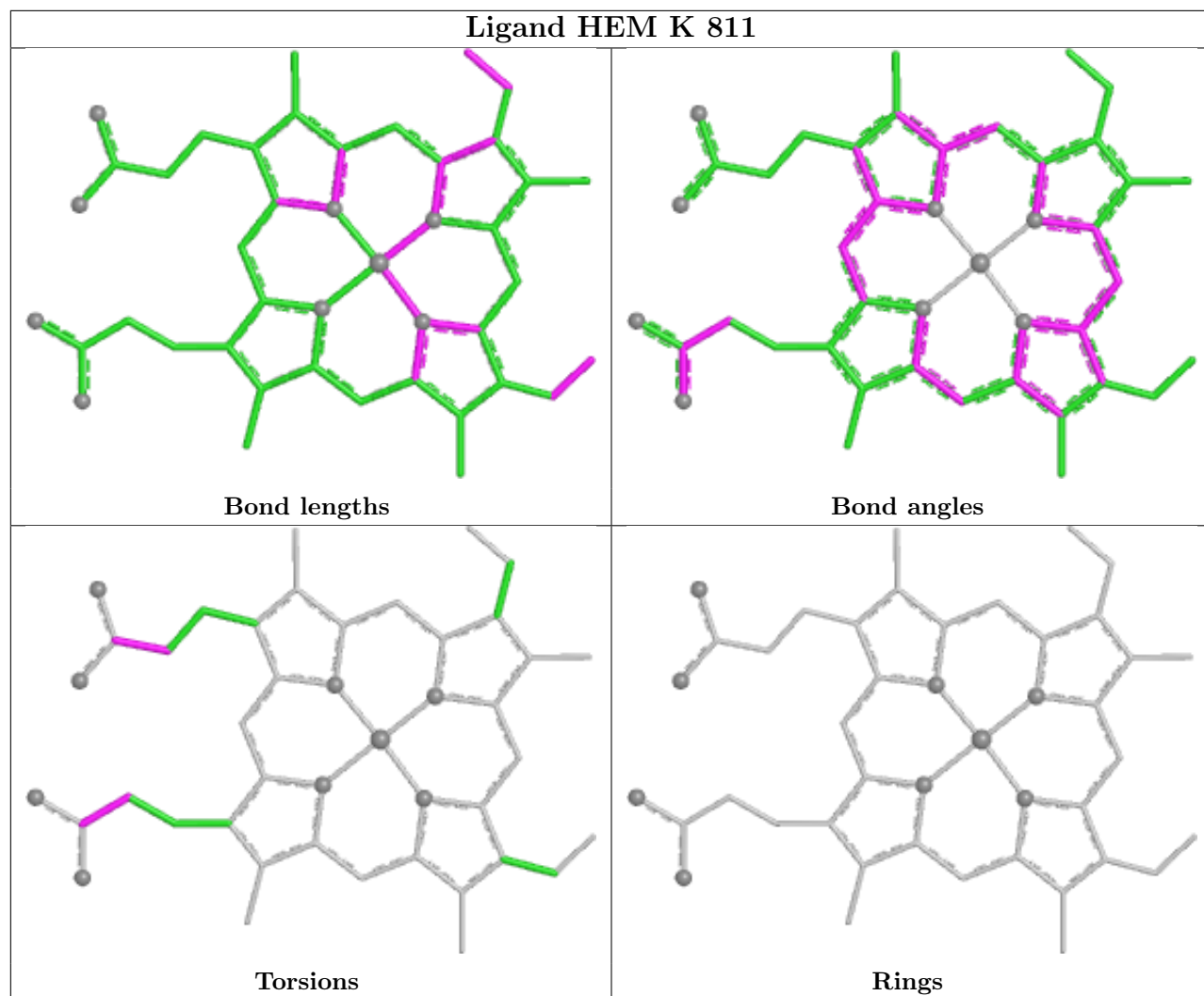


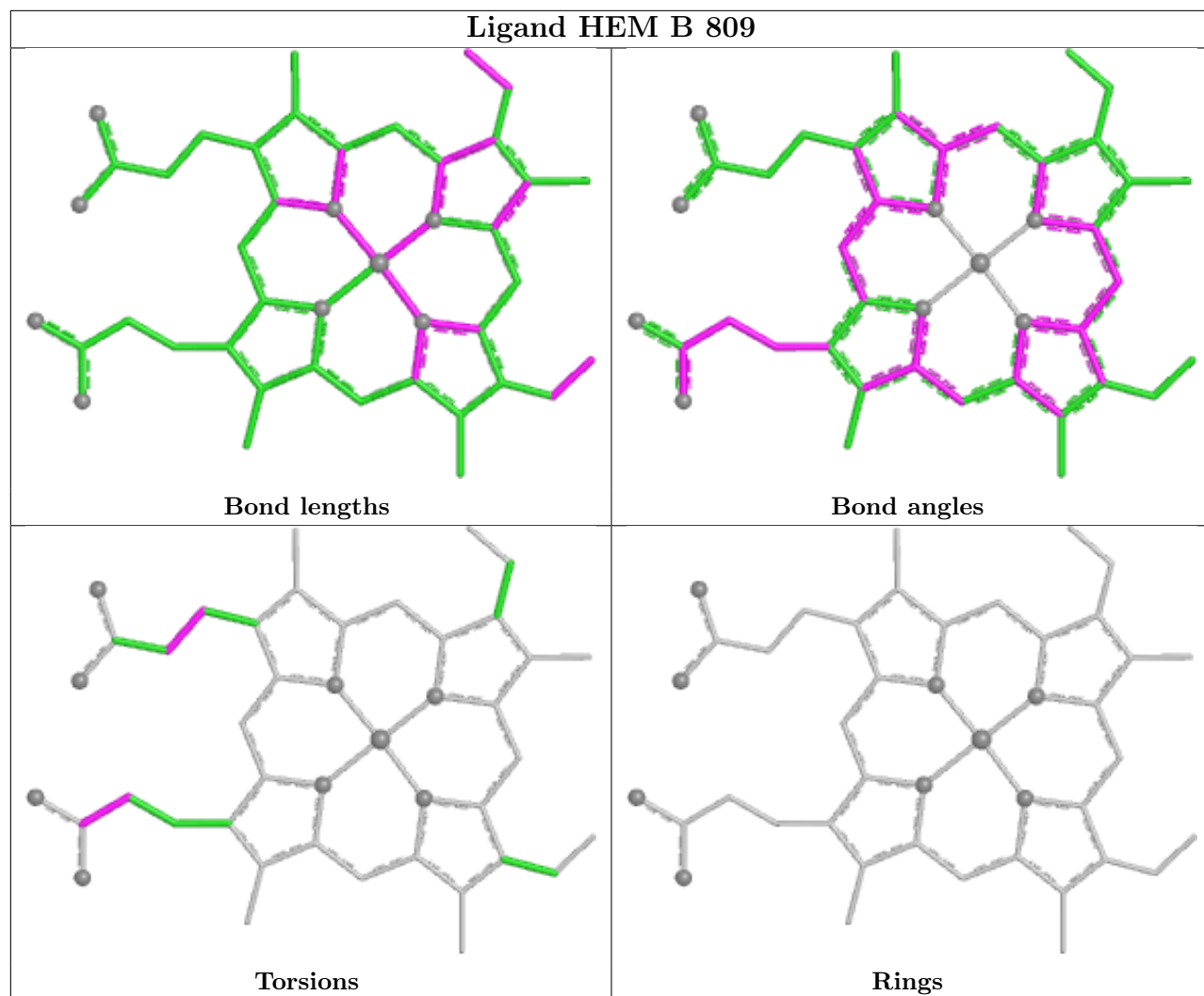


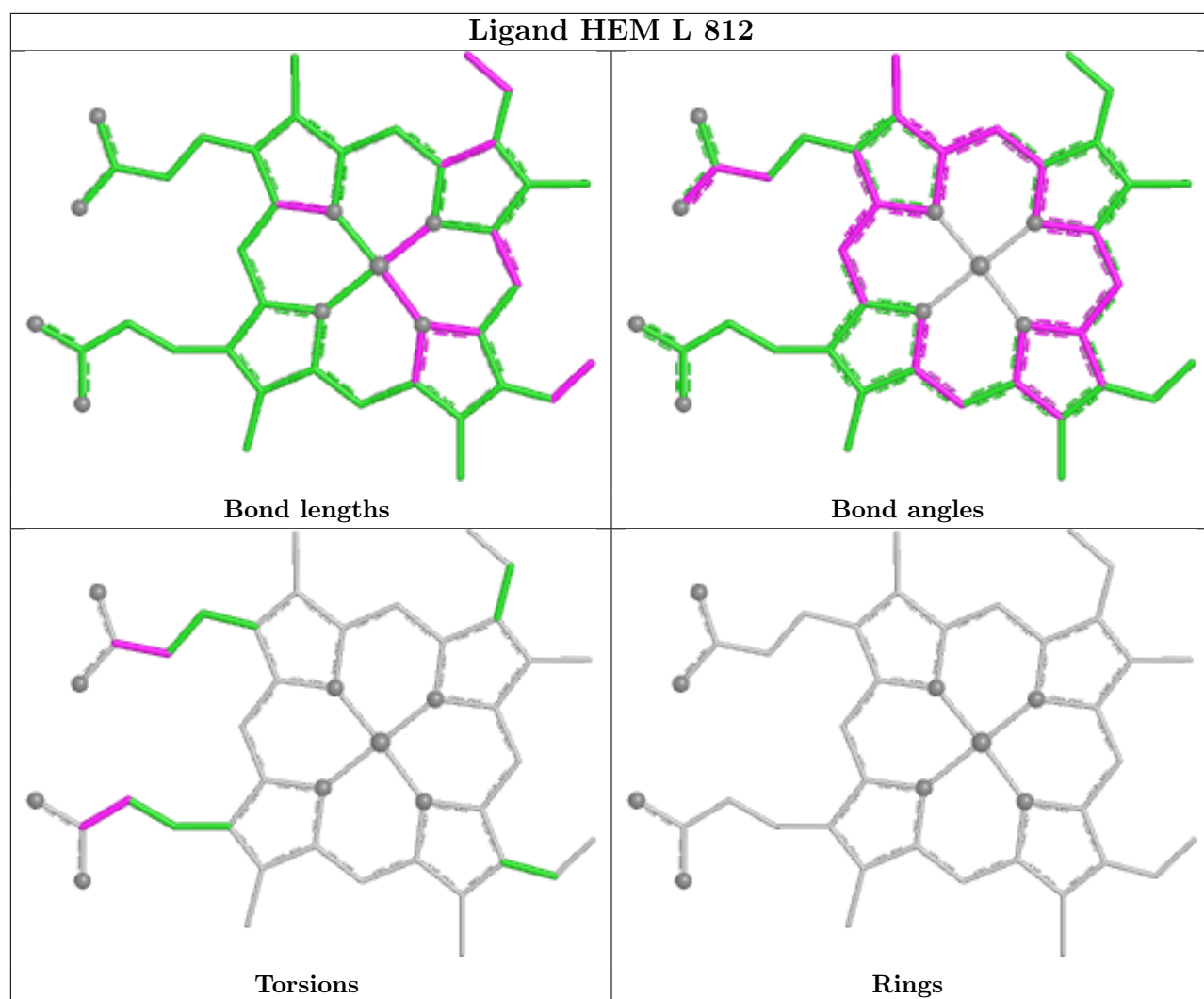


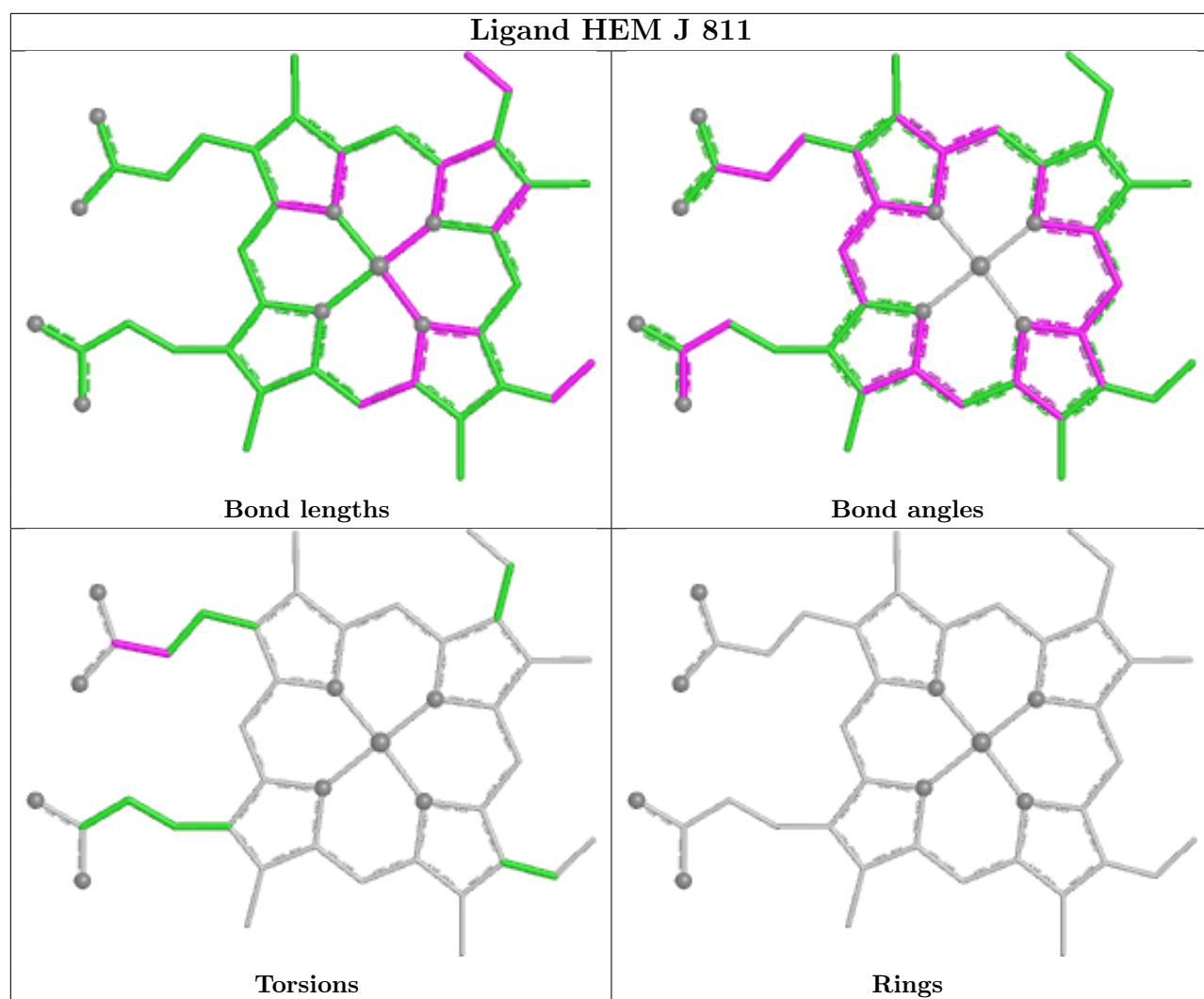


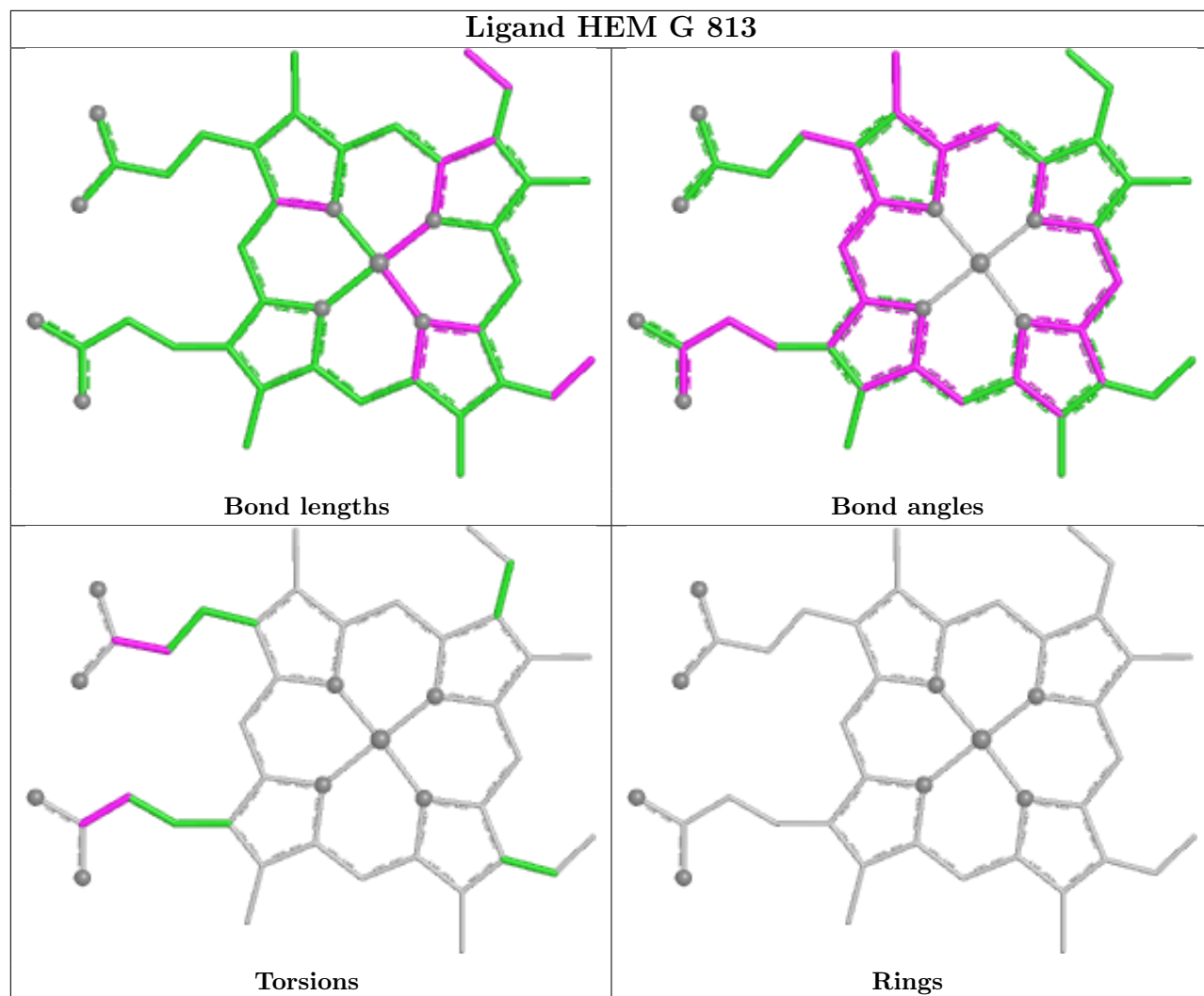


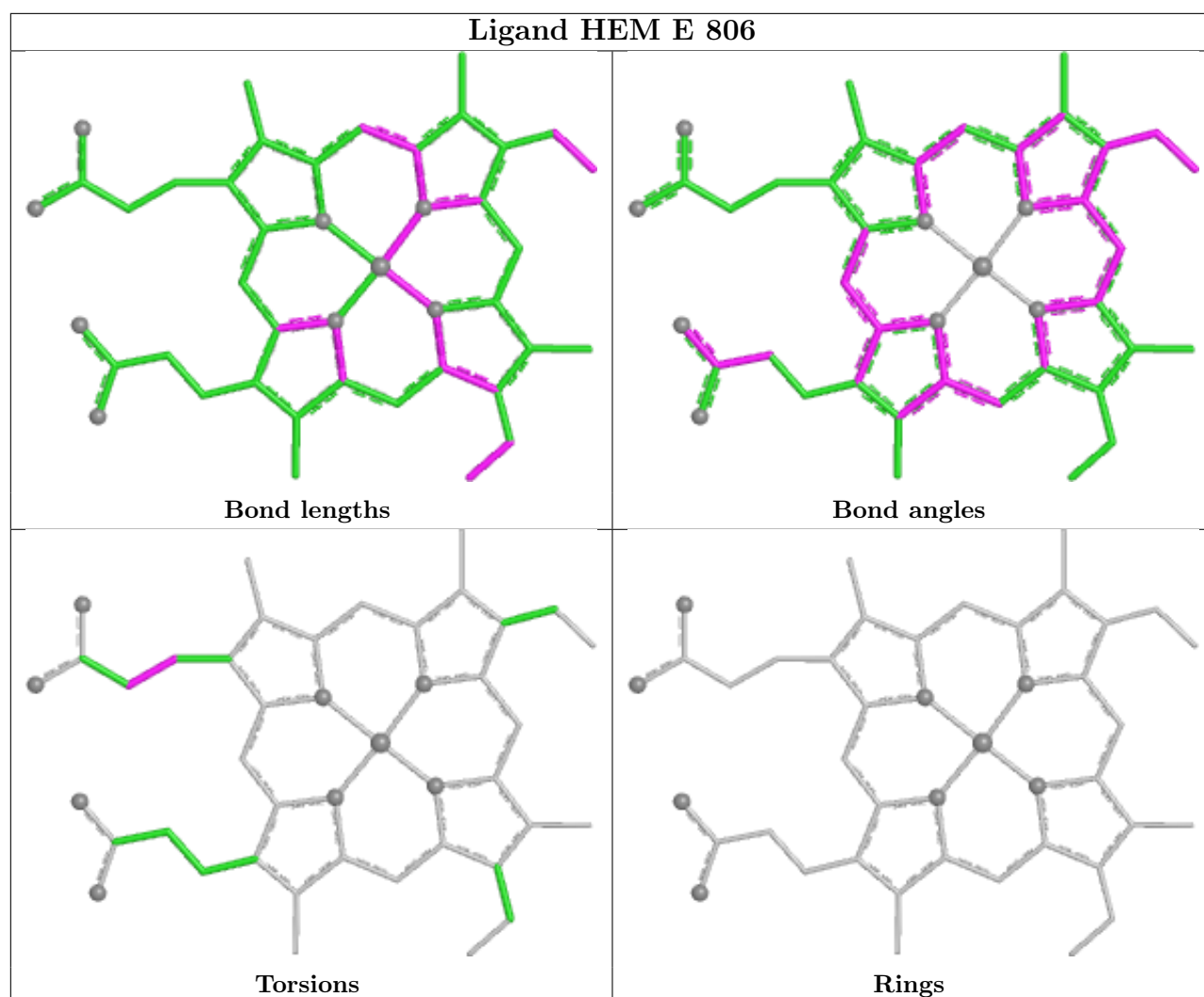


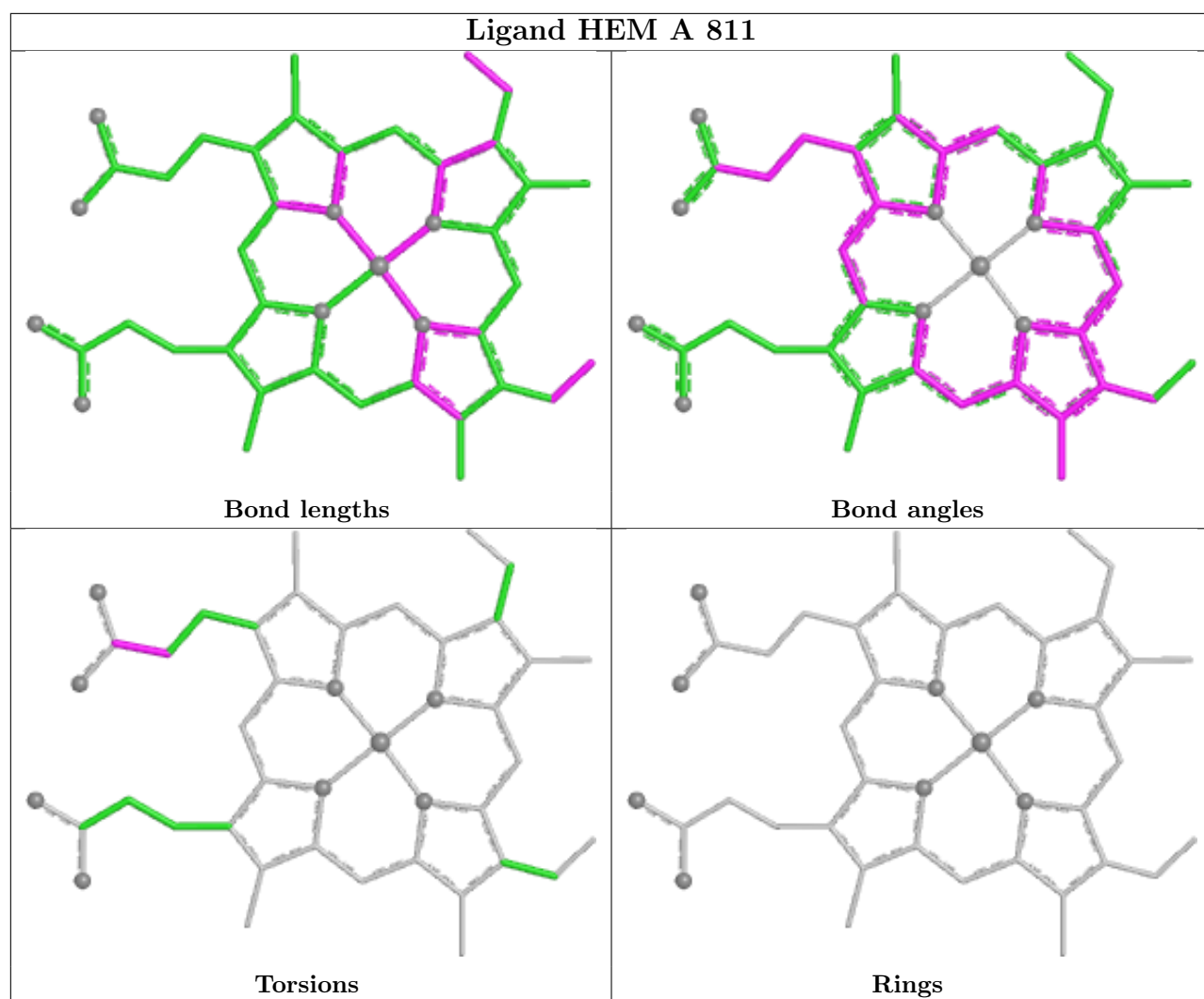


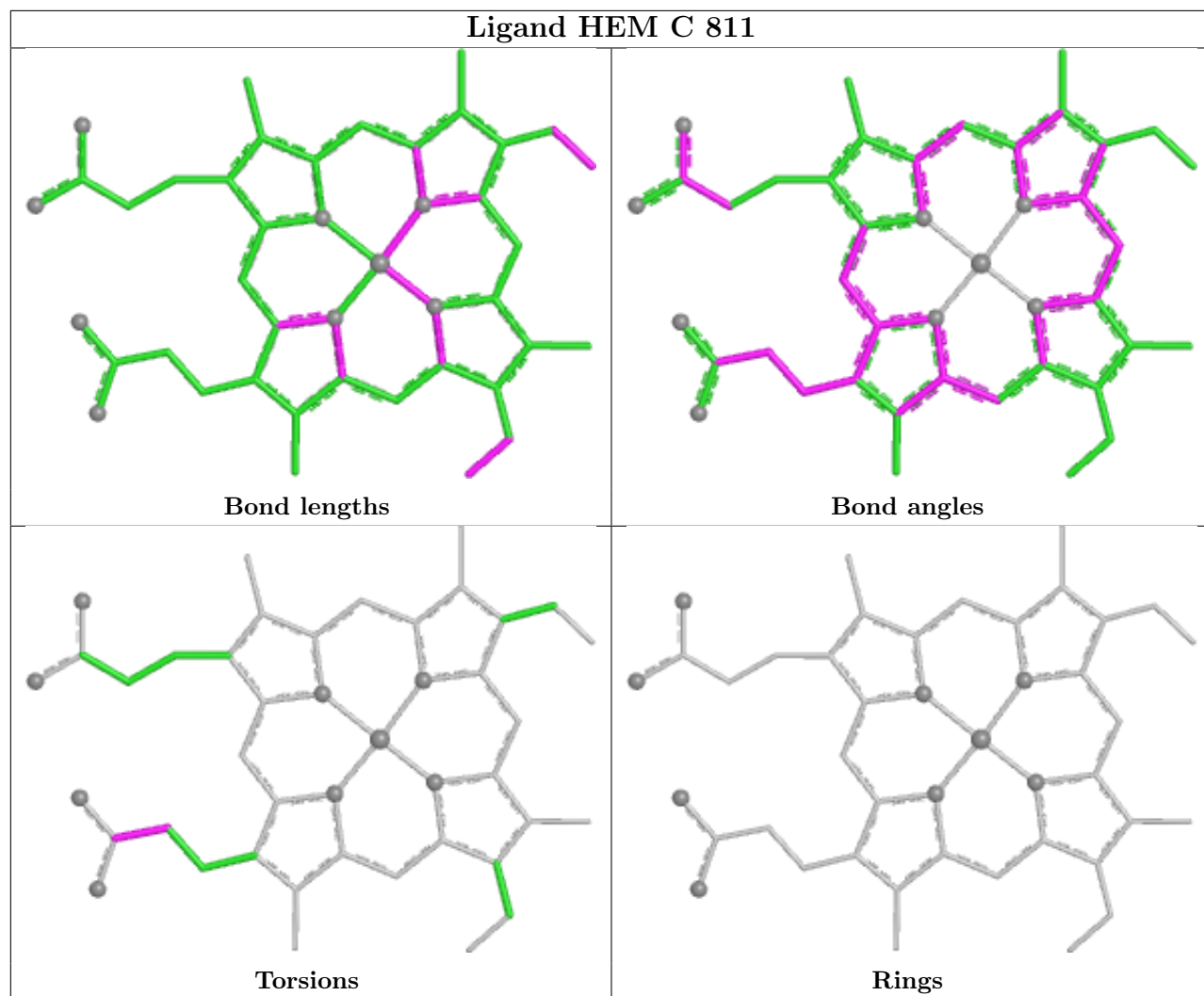




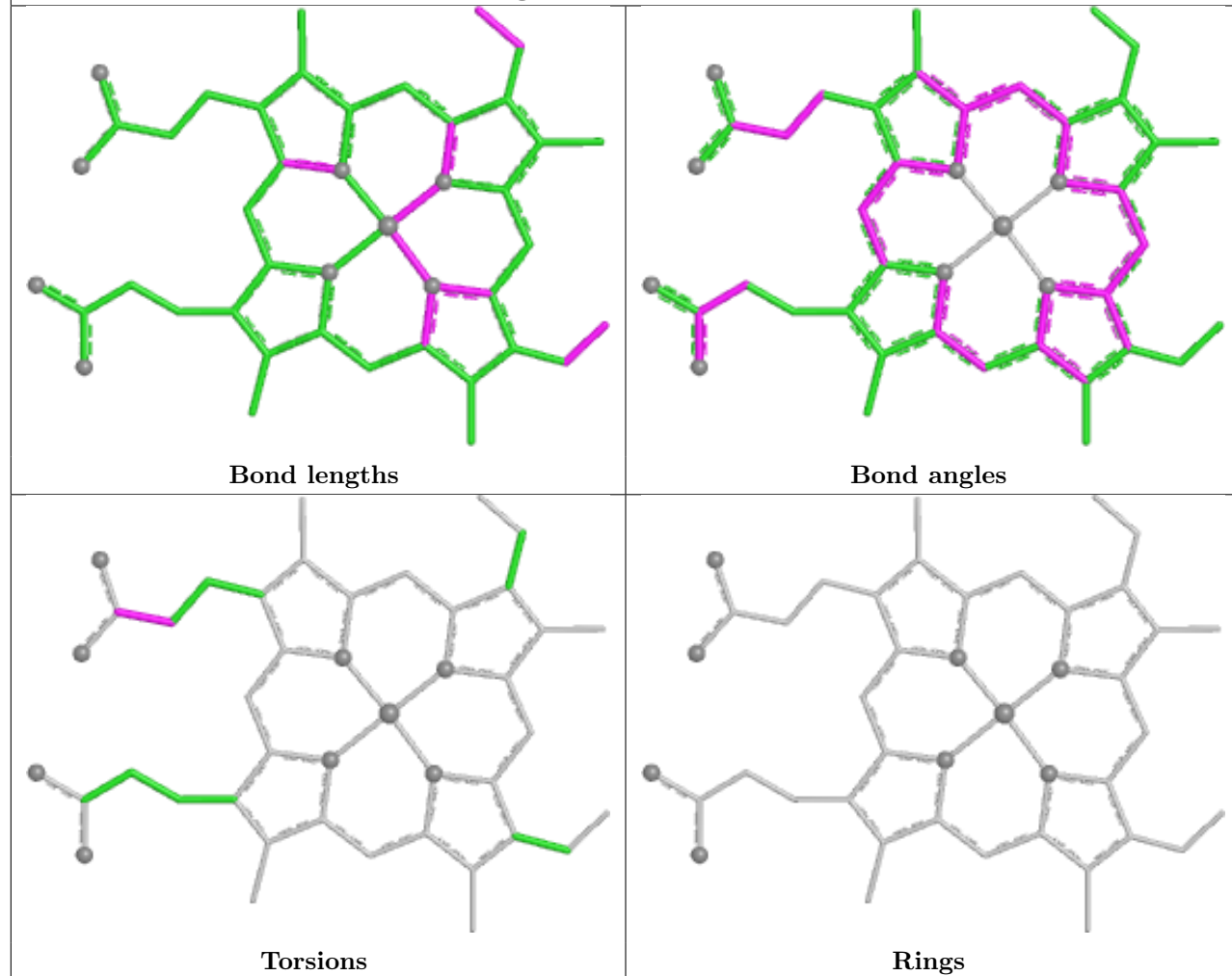


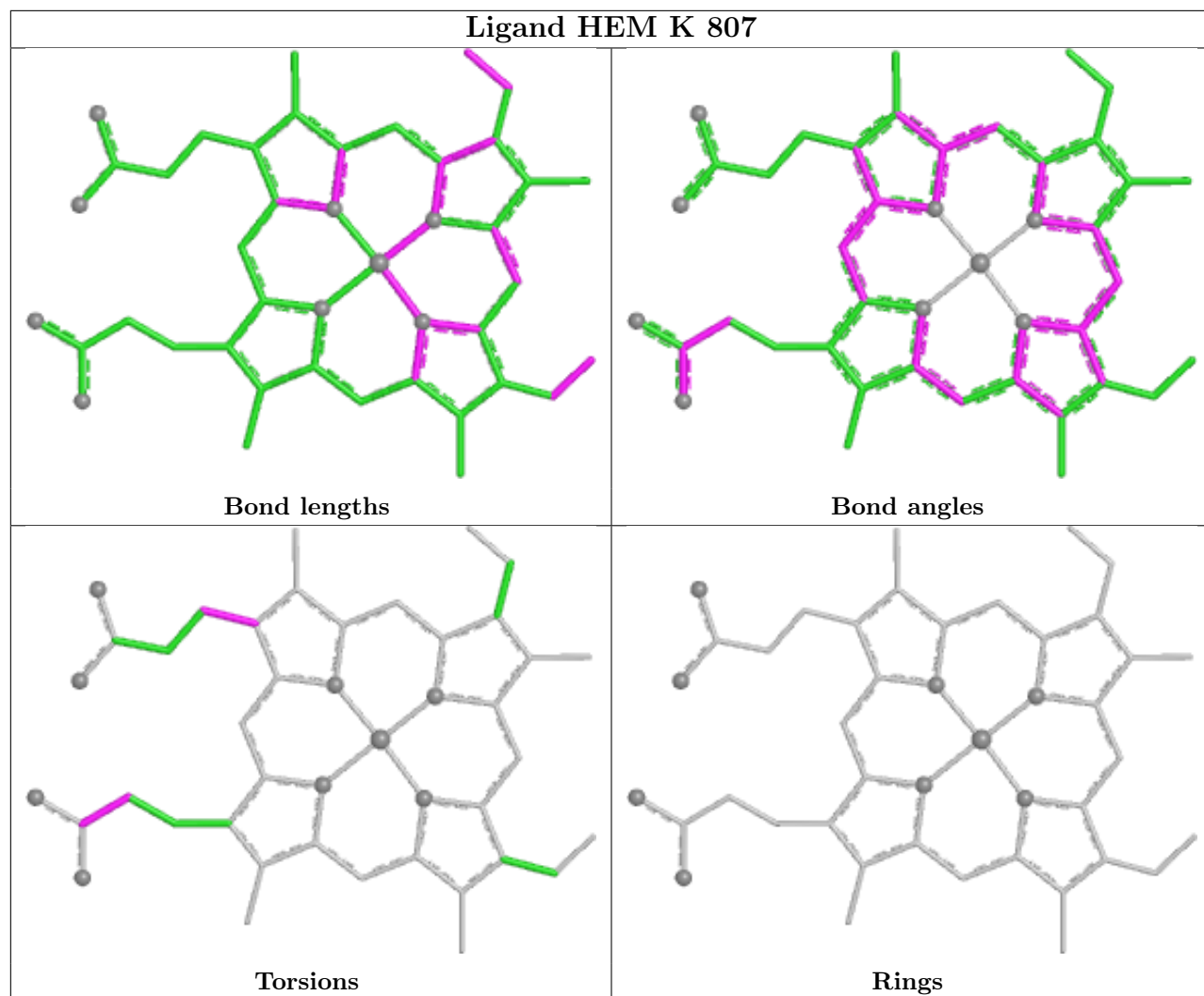


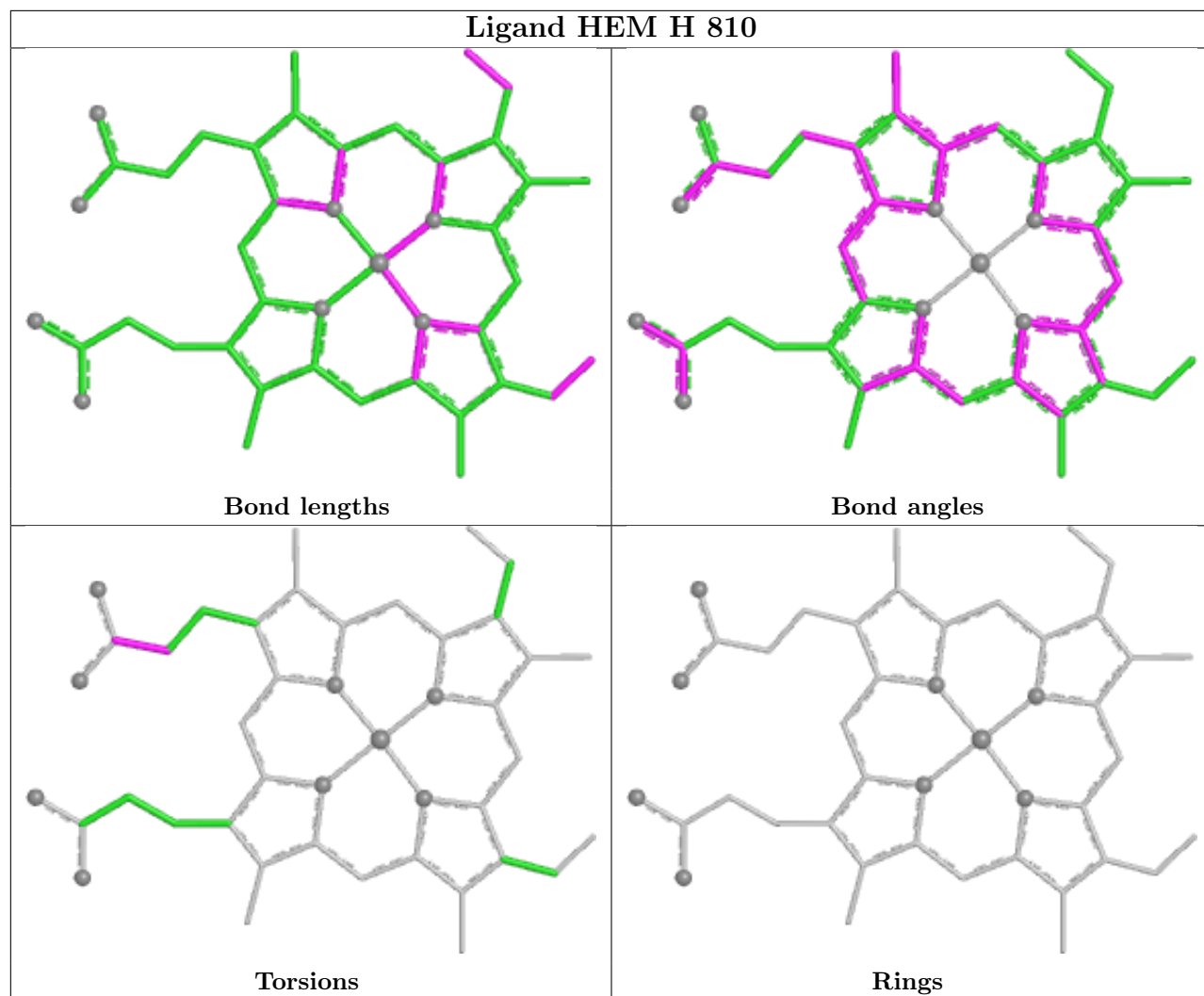


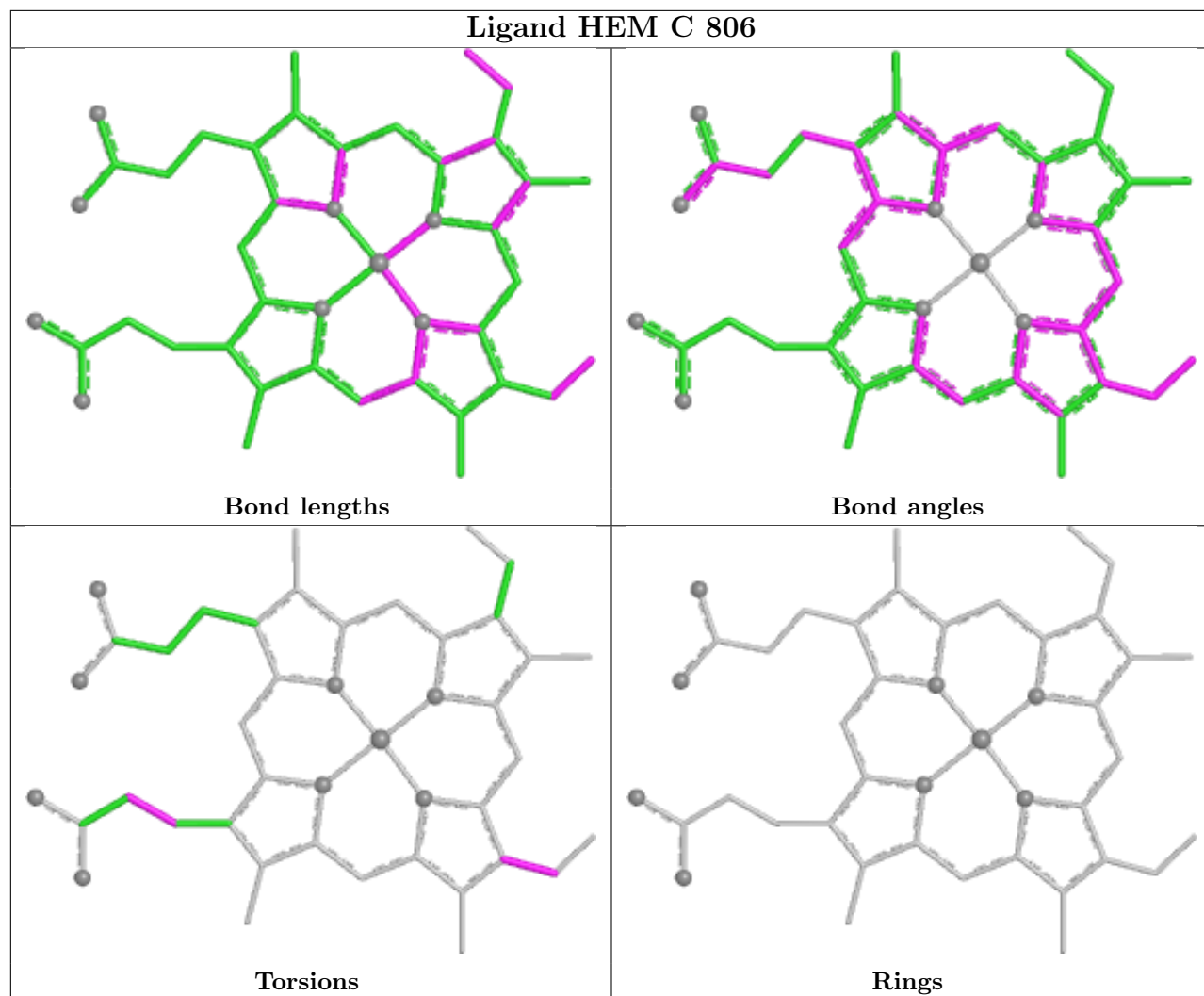


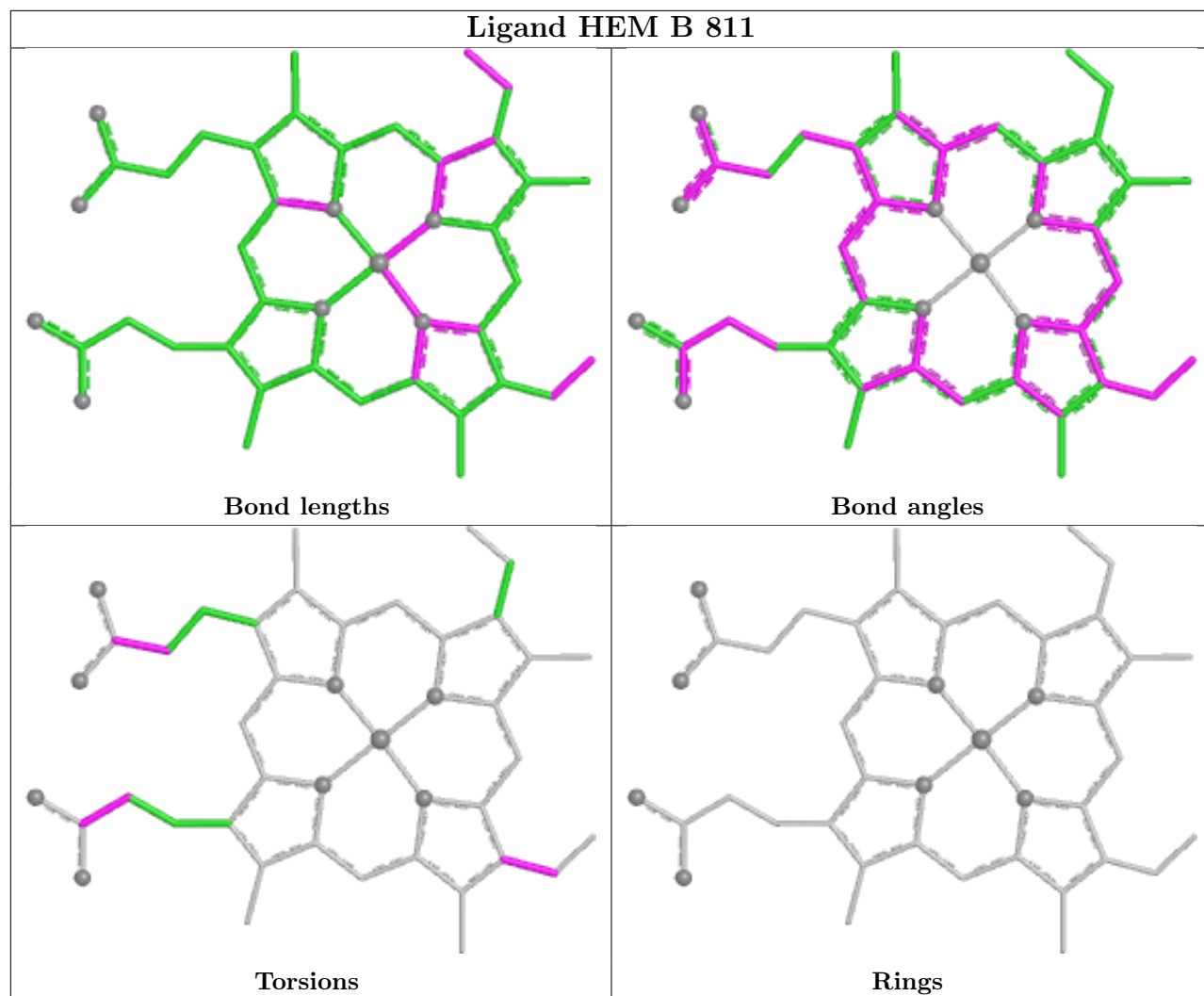
Ligand HEM I 811

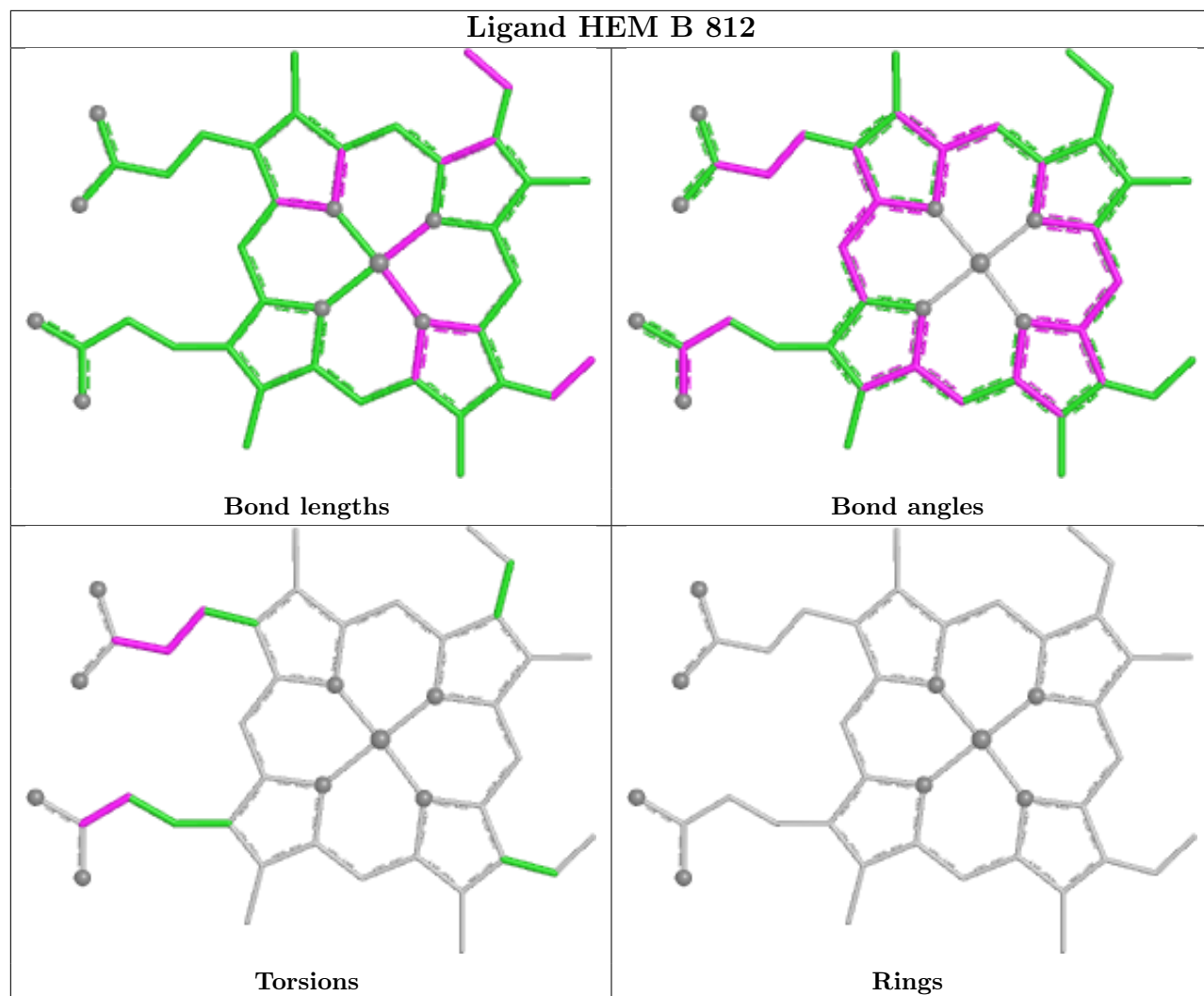


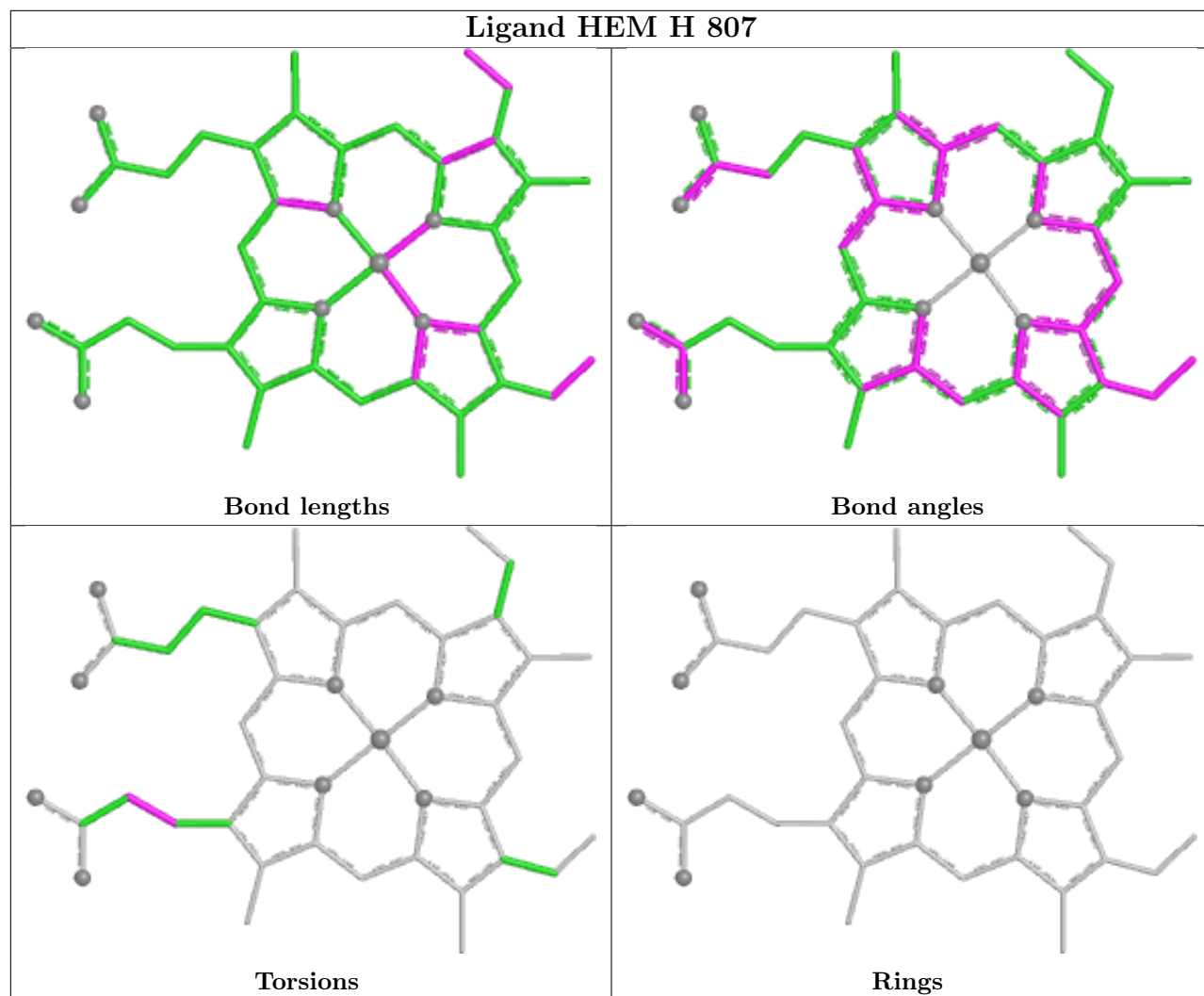


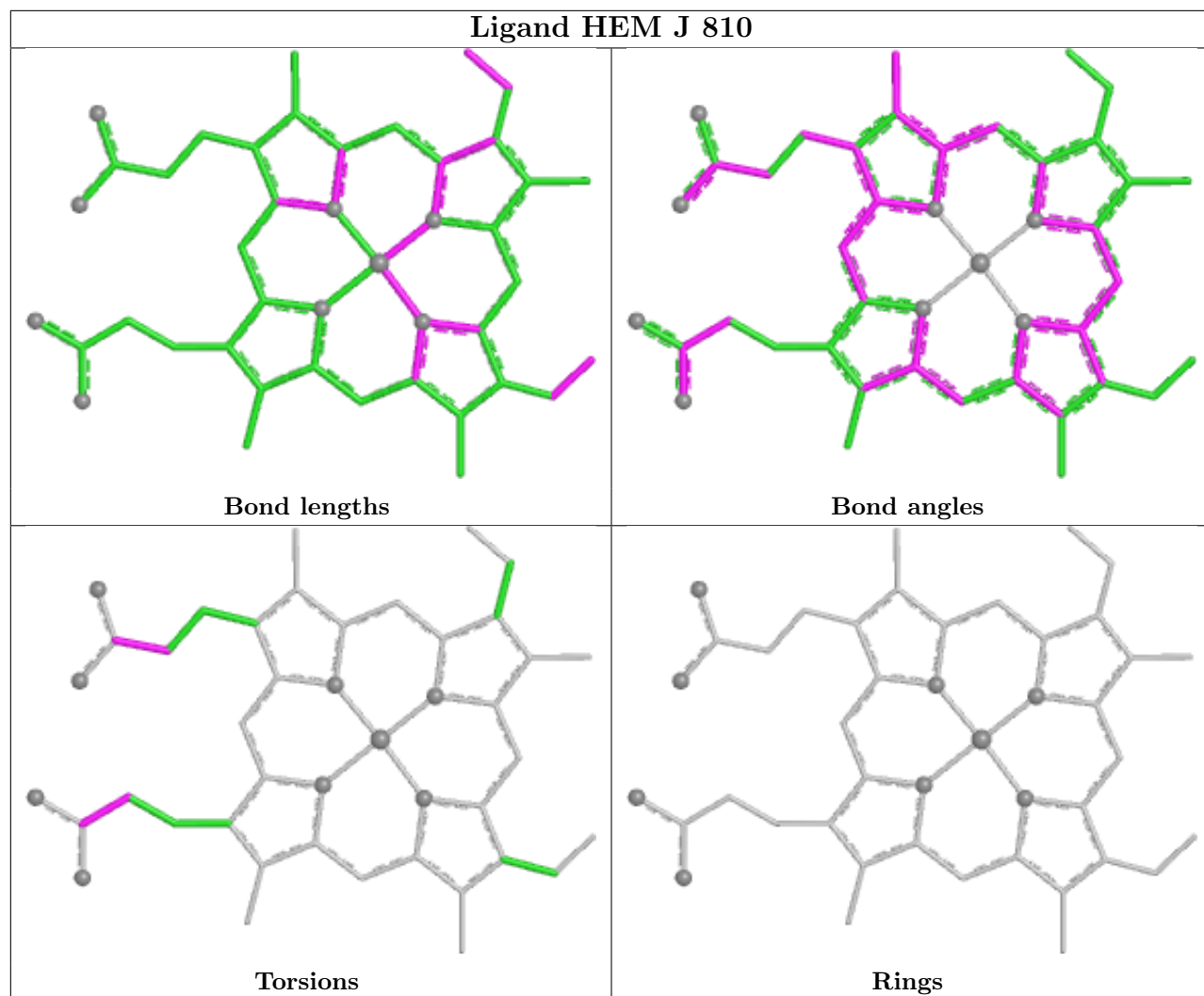


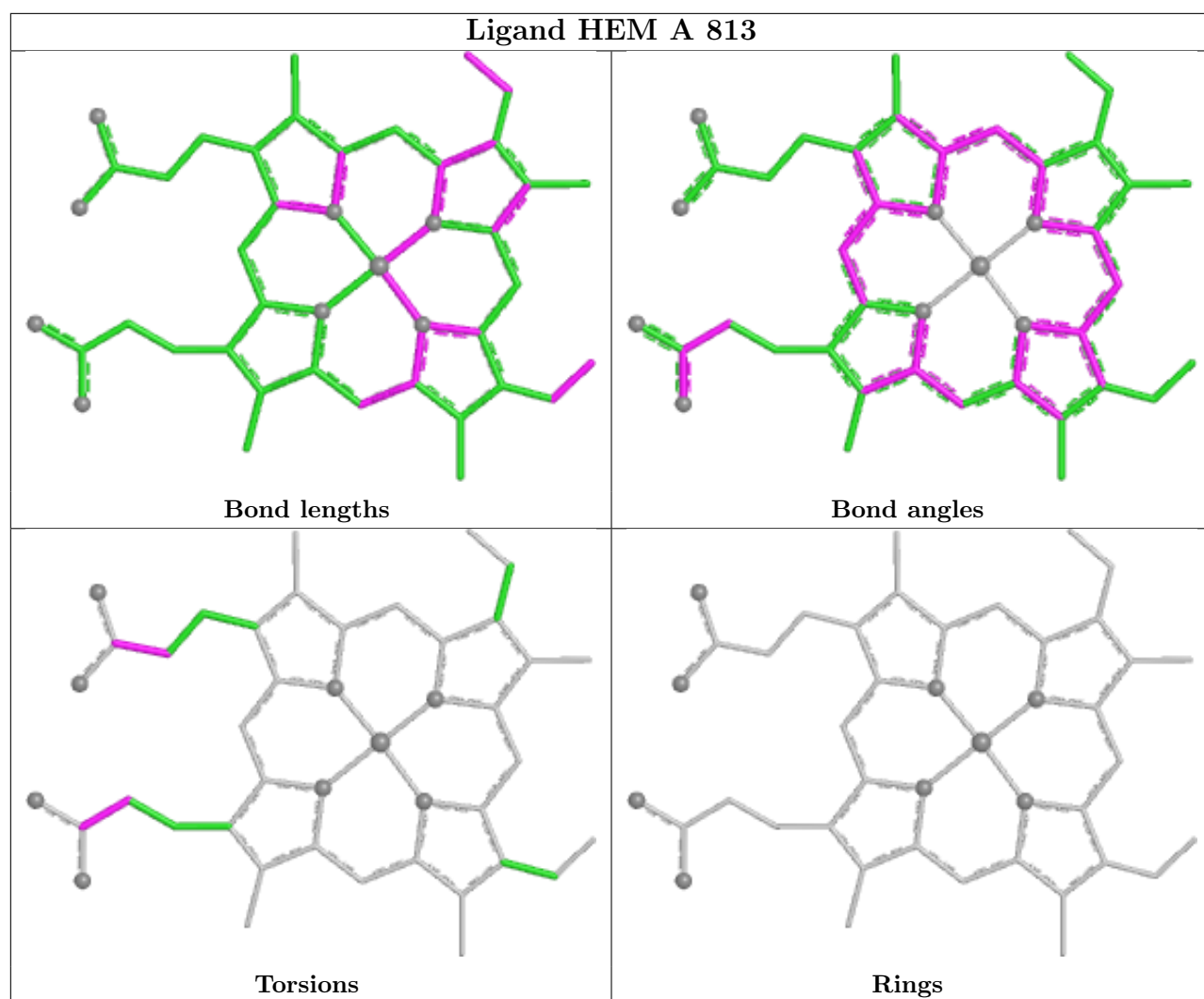


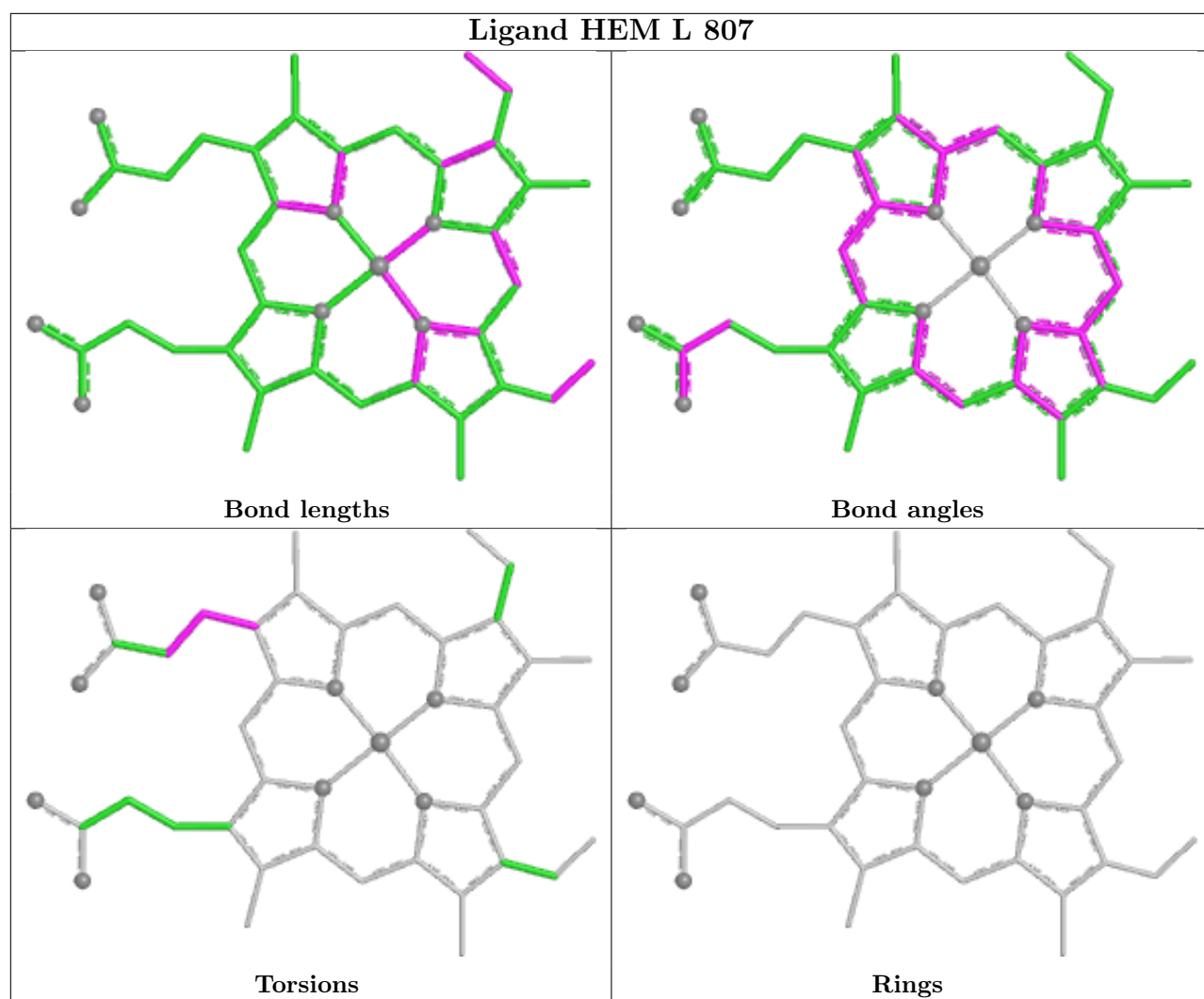


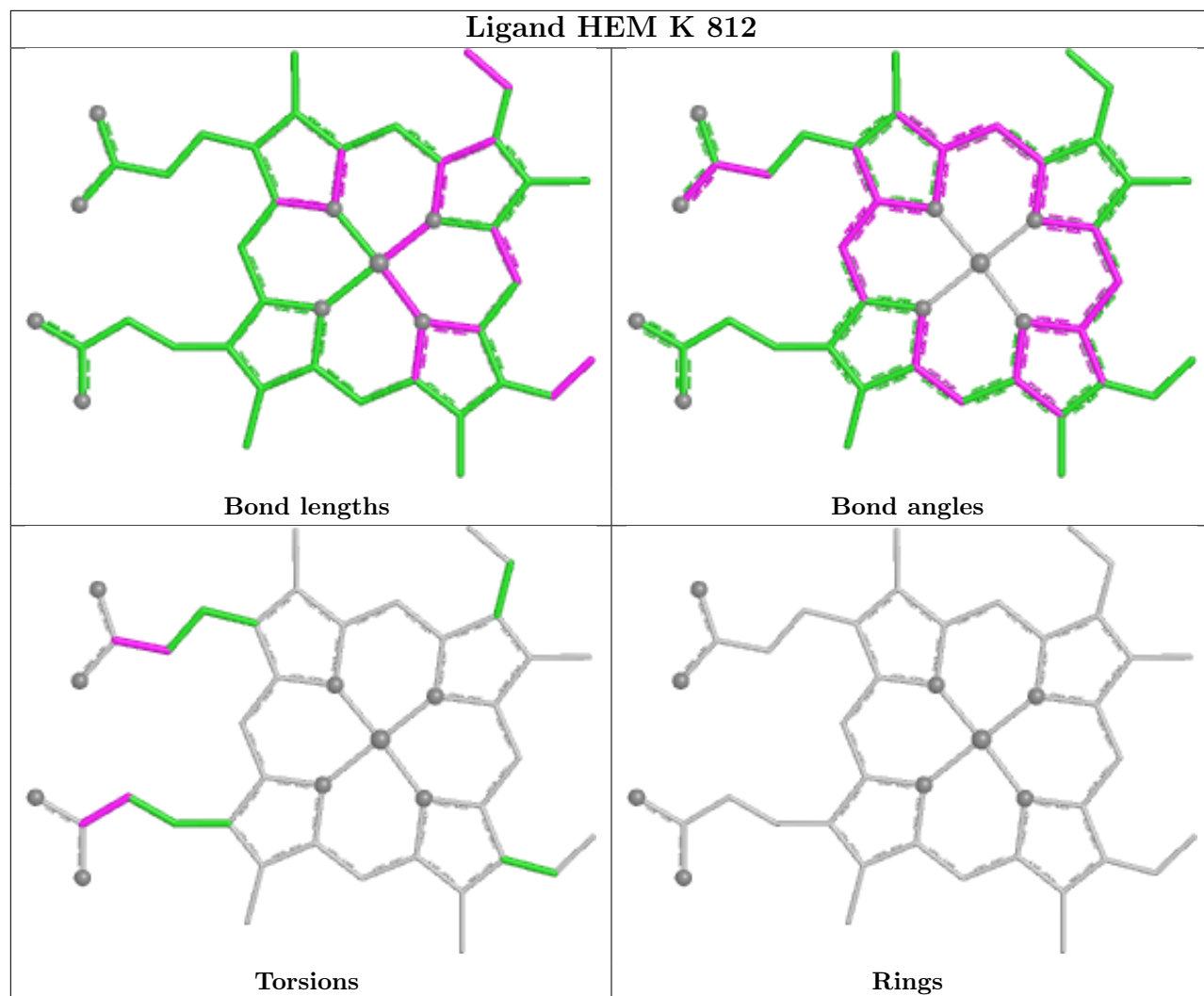


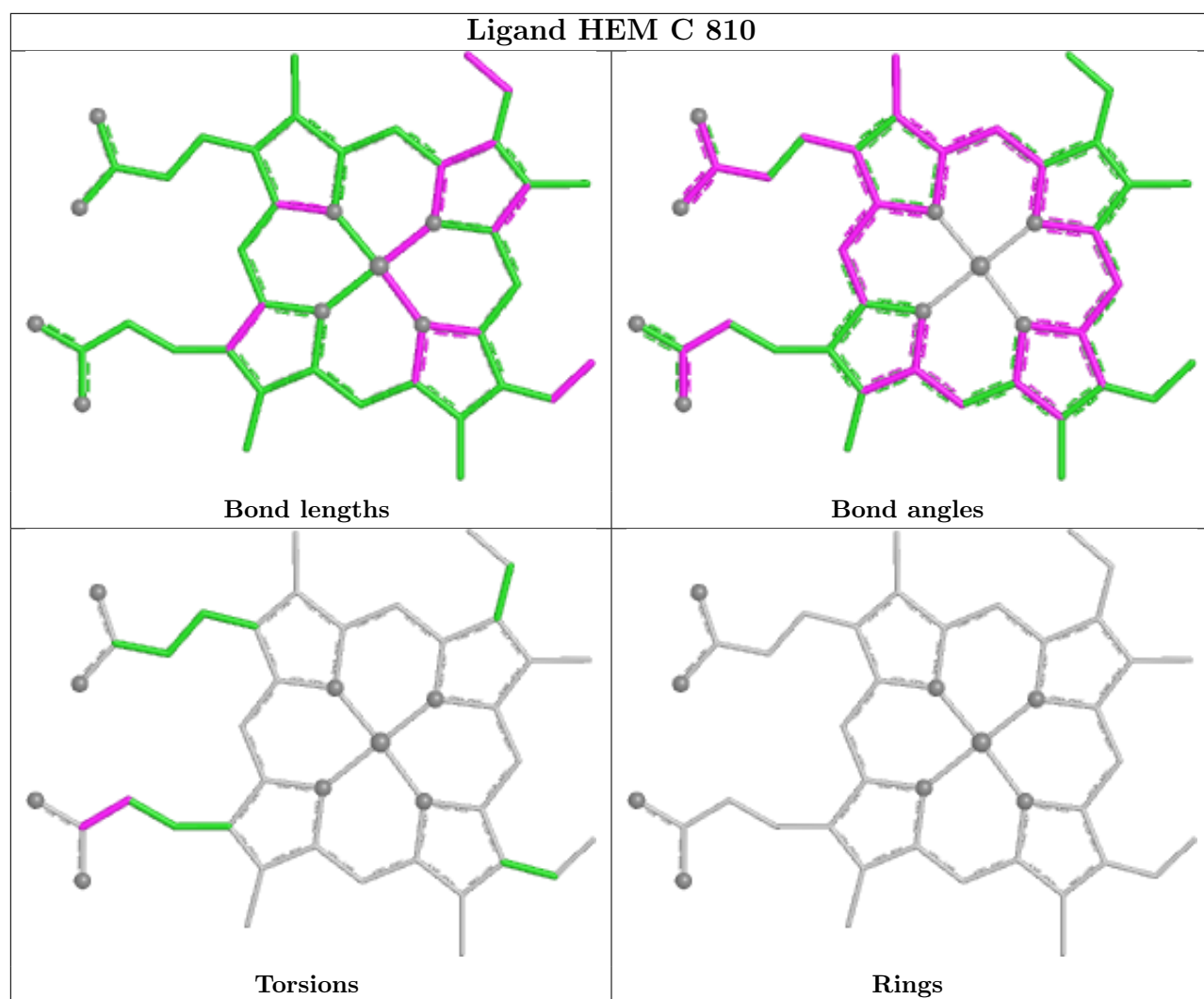




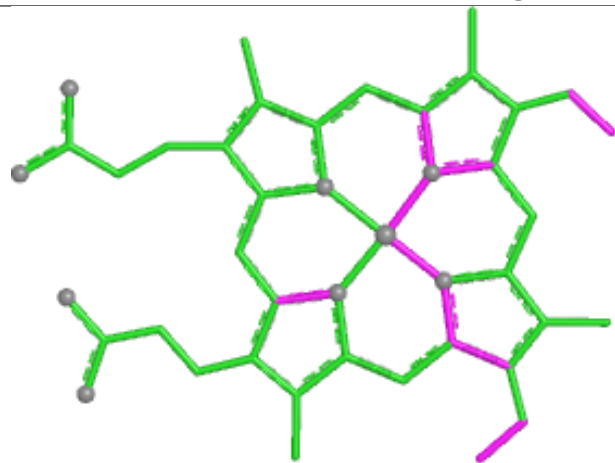




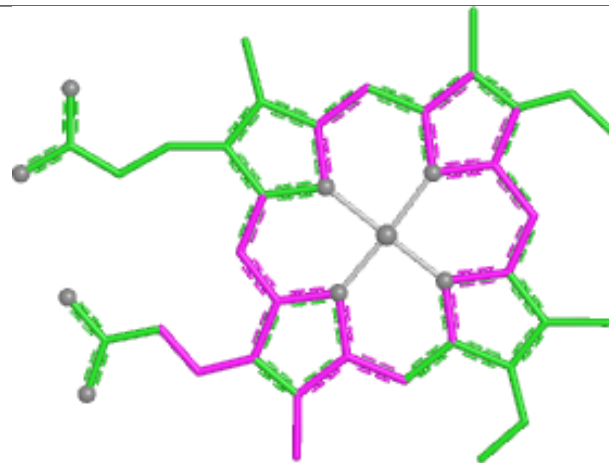




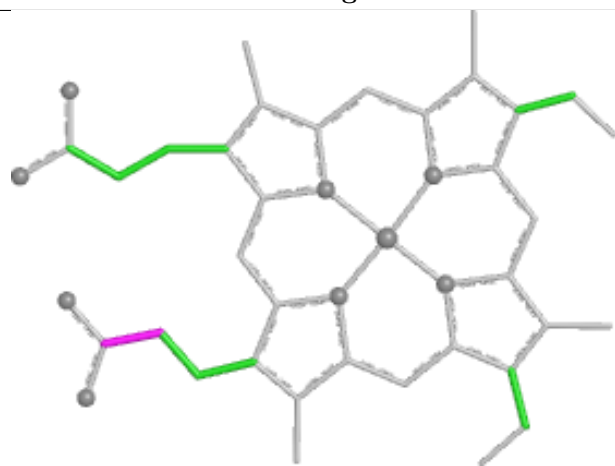
Ligand HEM K 809



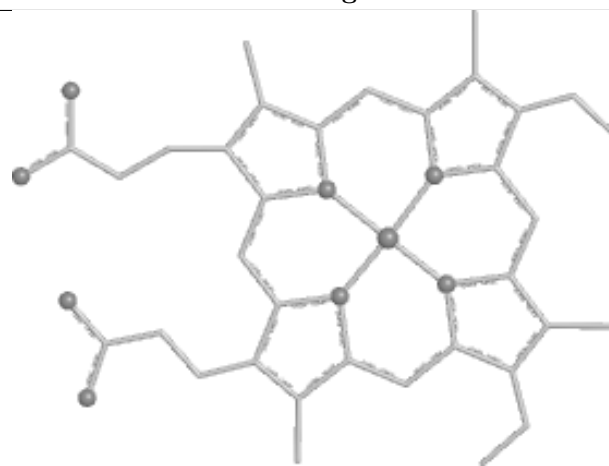
Bond lengths



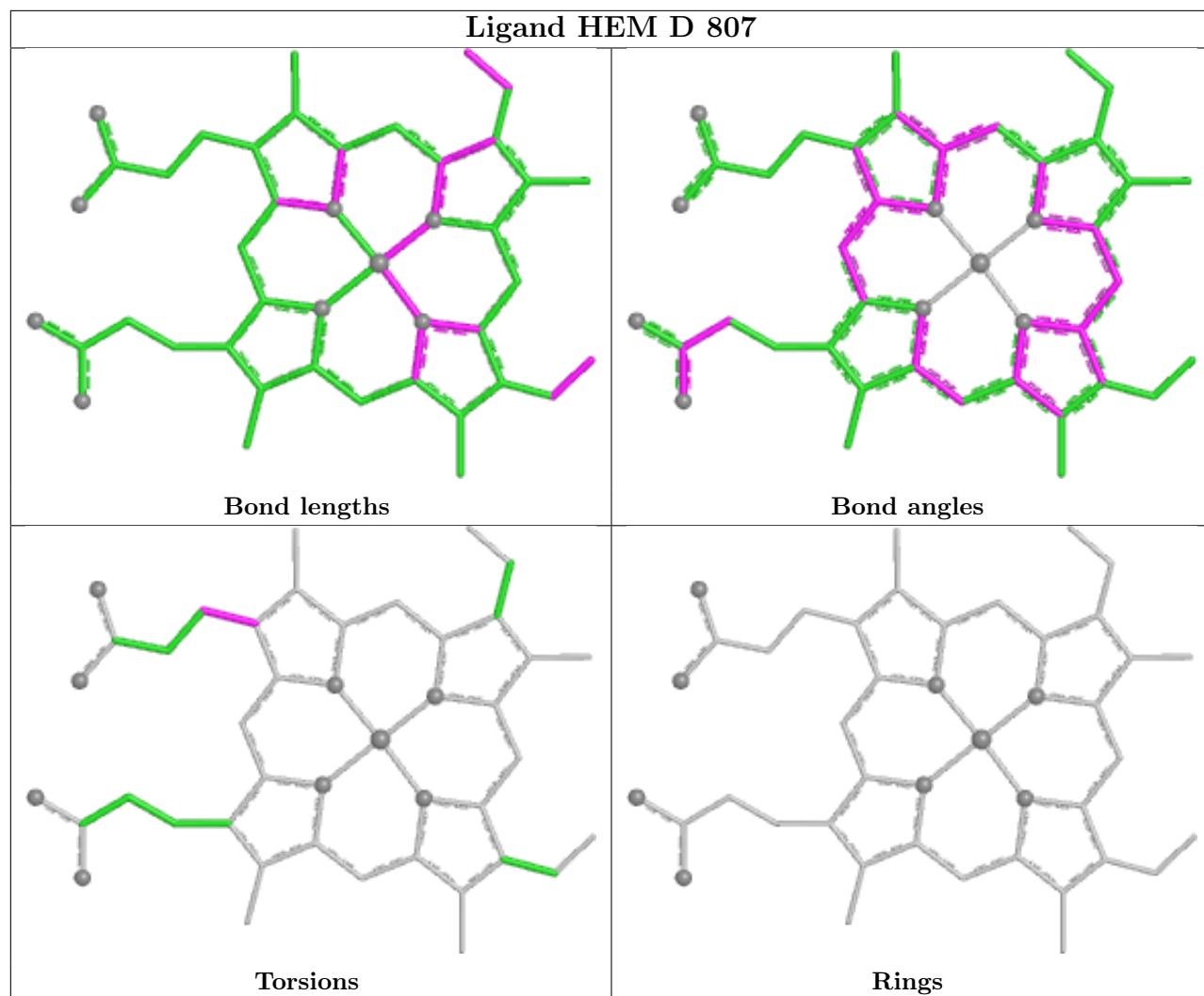
Bond angles

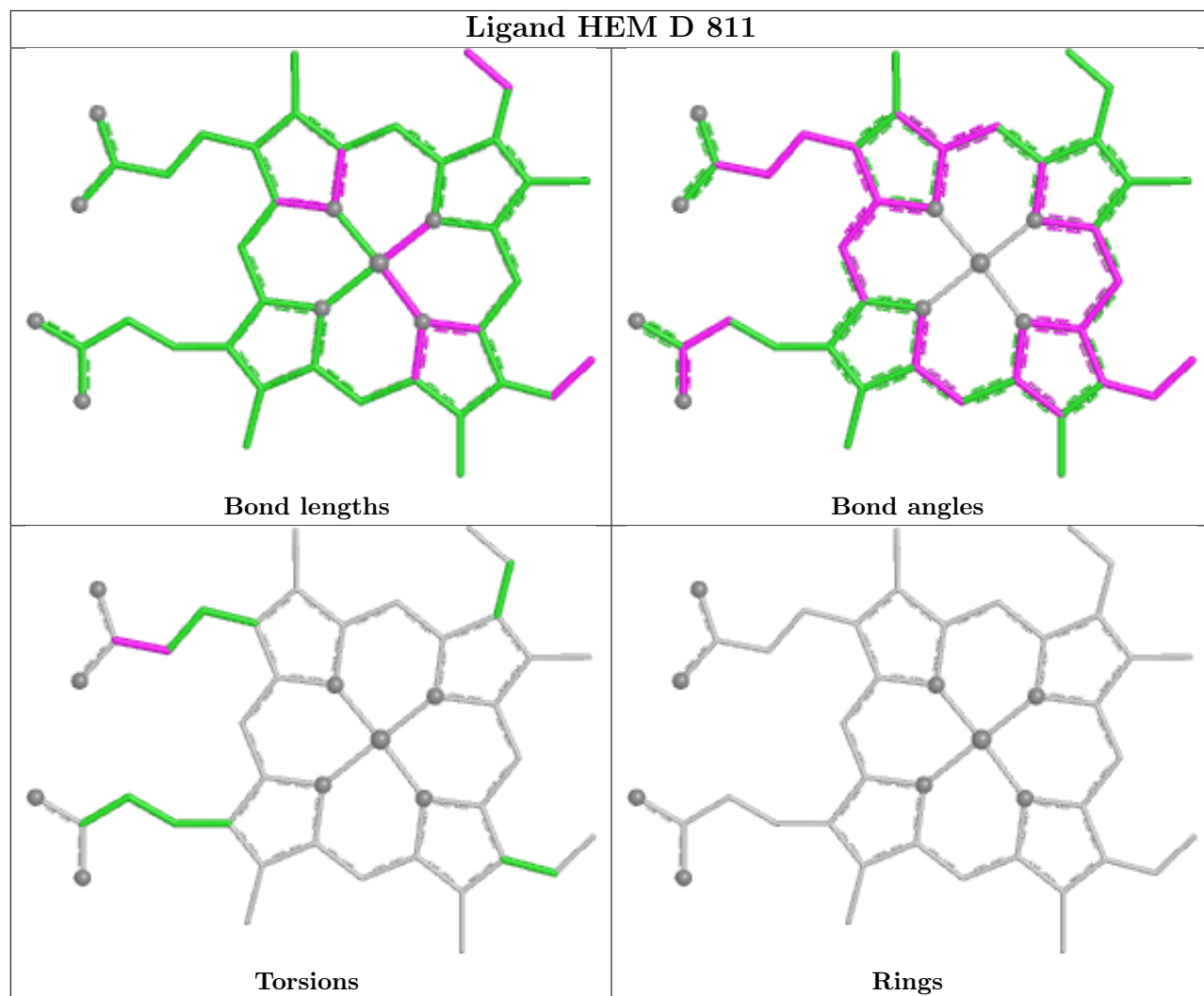


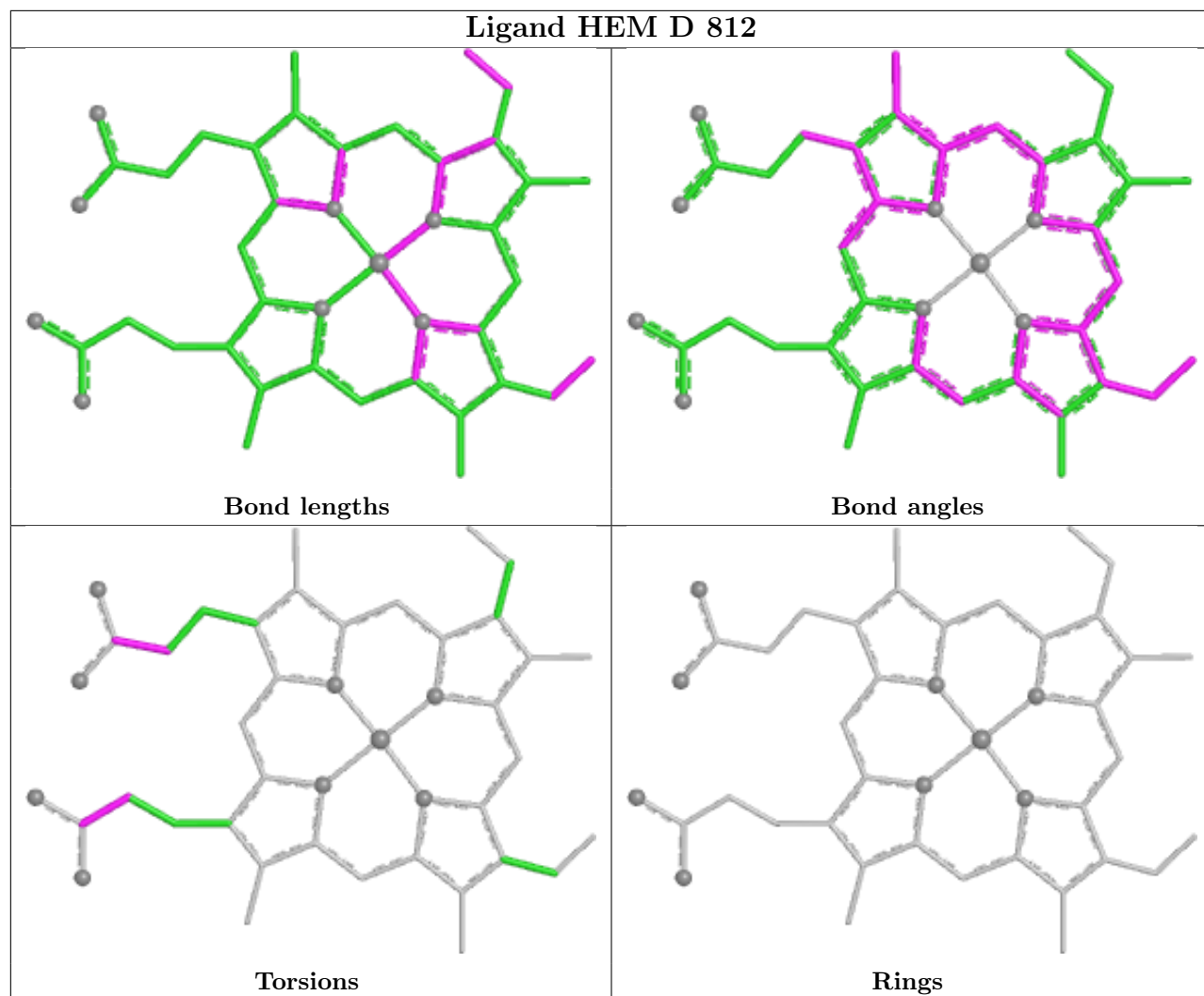
Torsions

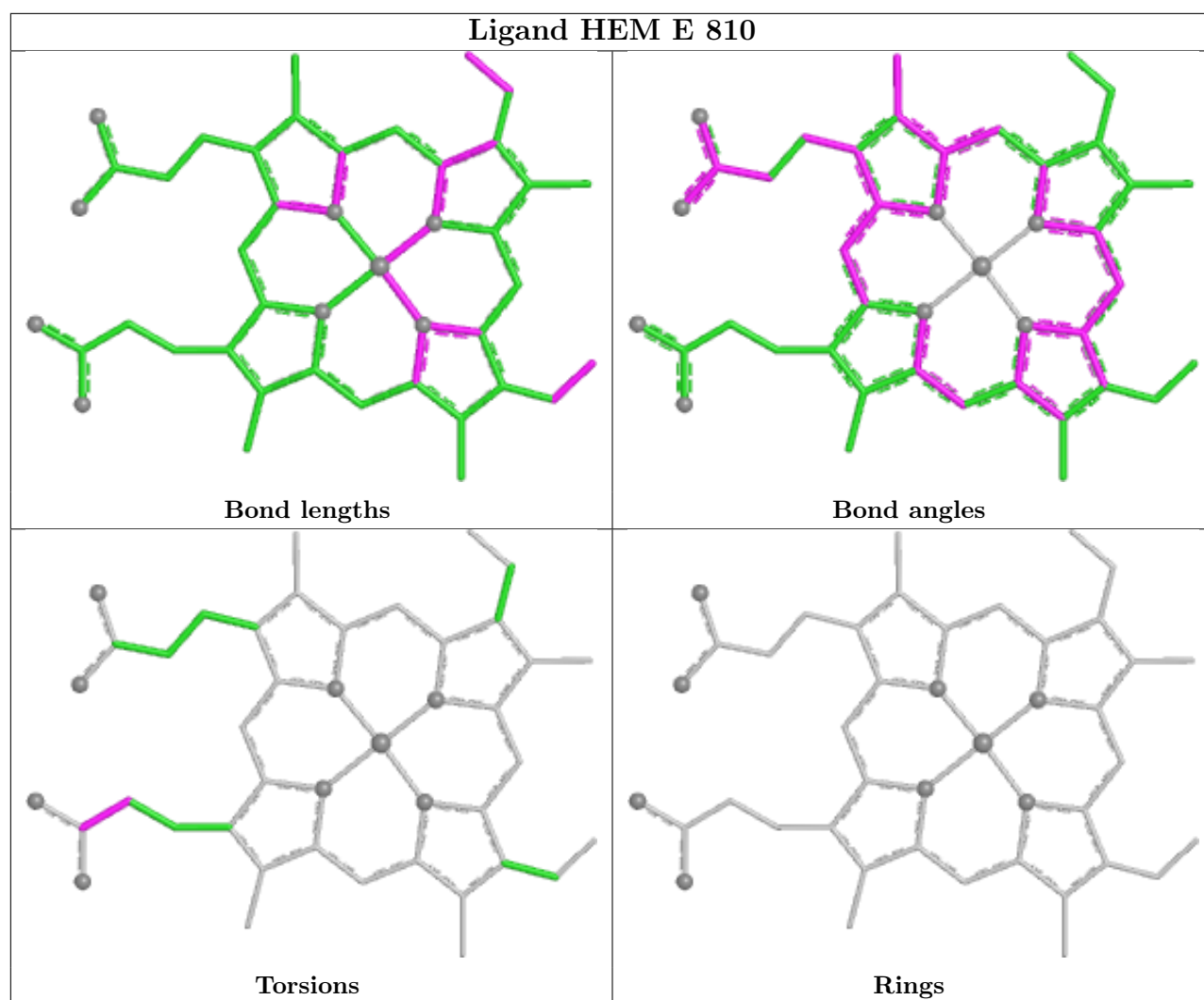


Rings

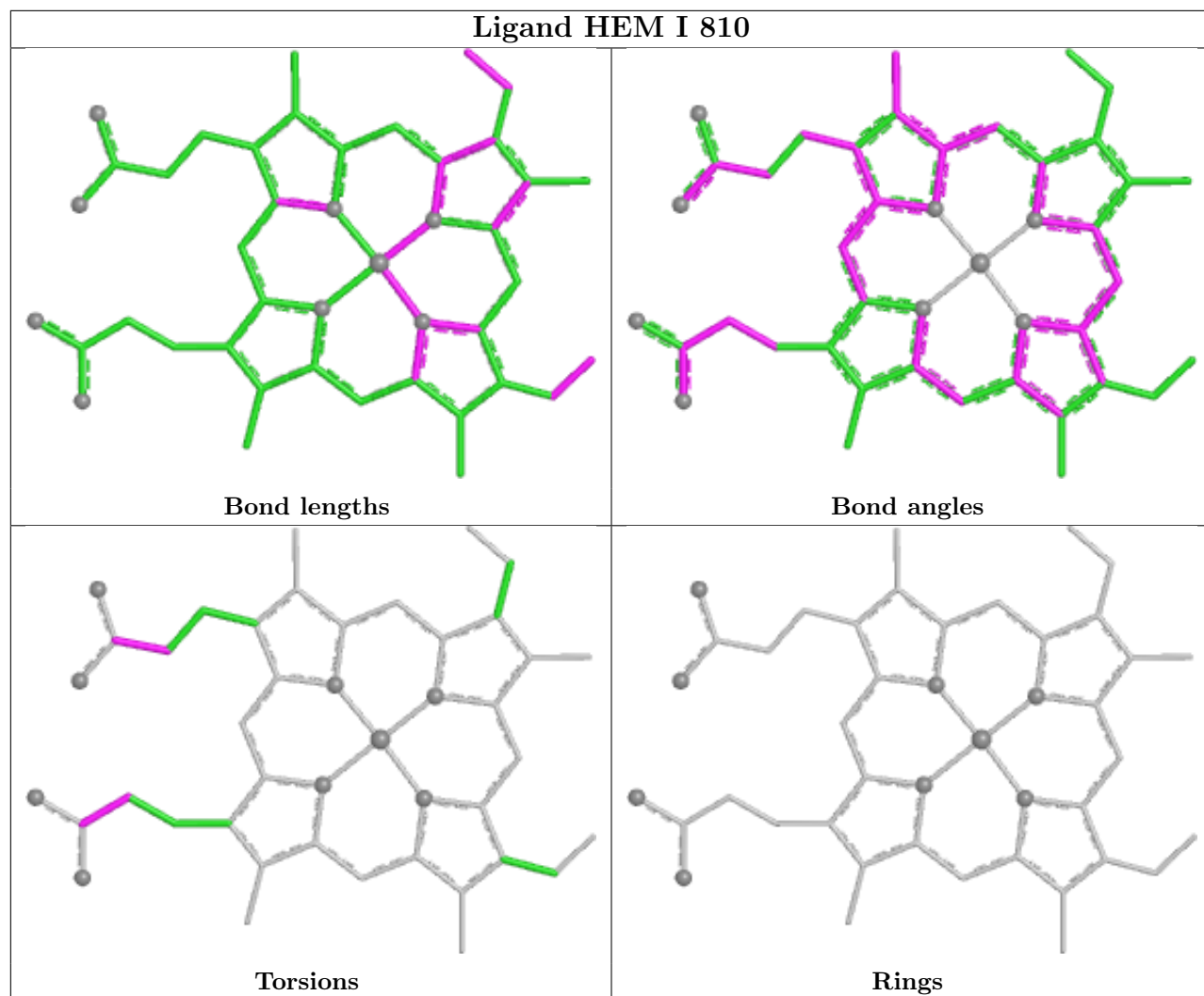


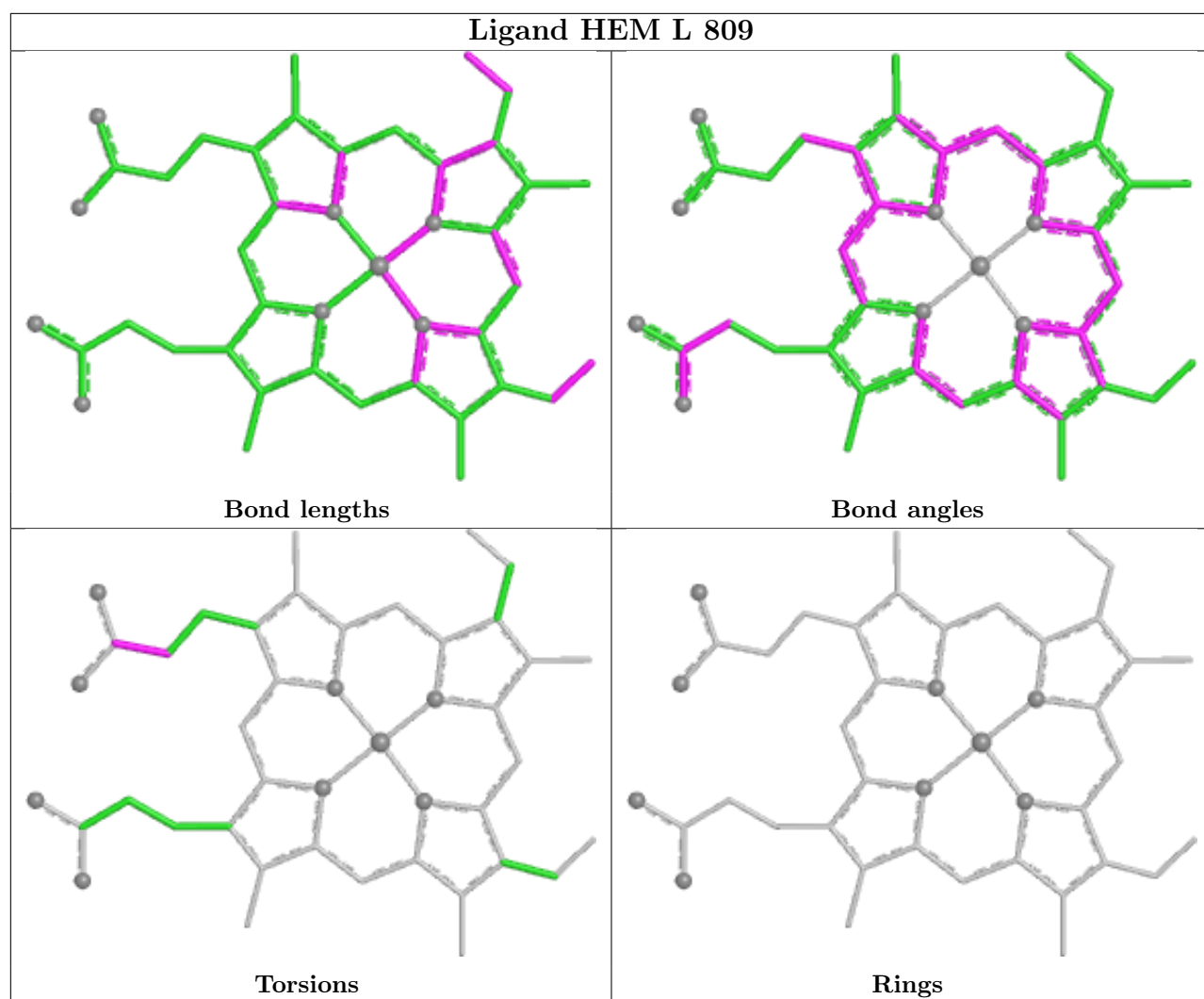




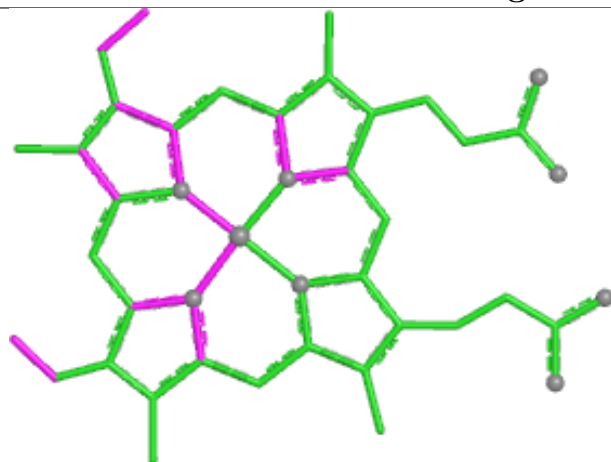


Ligand HEM I 810

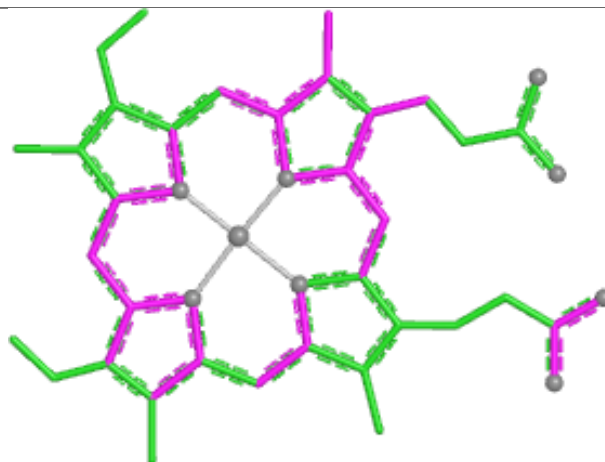




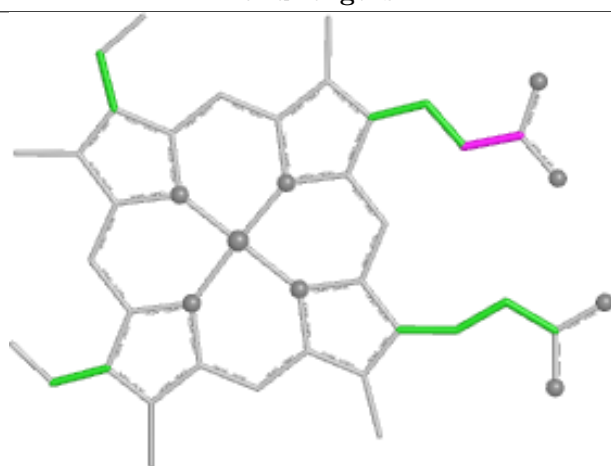
Ligand HEM D 809



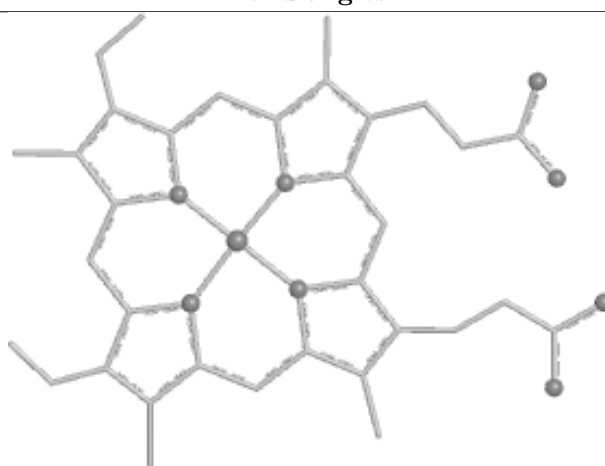
Bond lengths



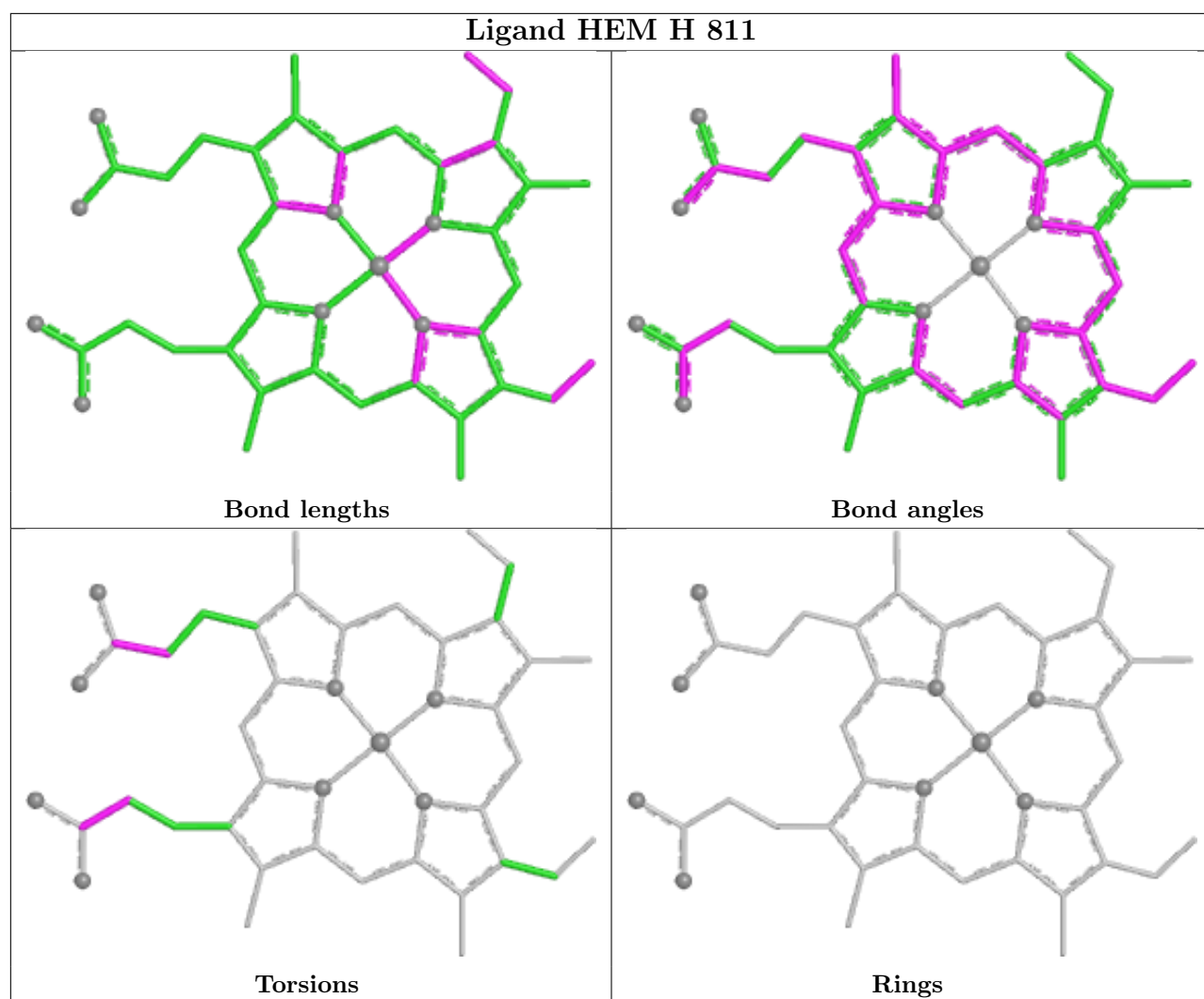
Bond angles

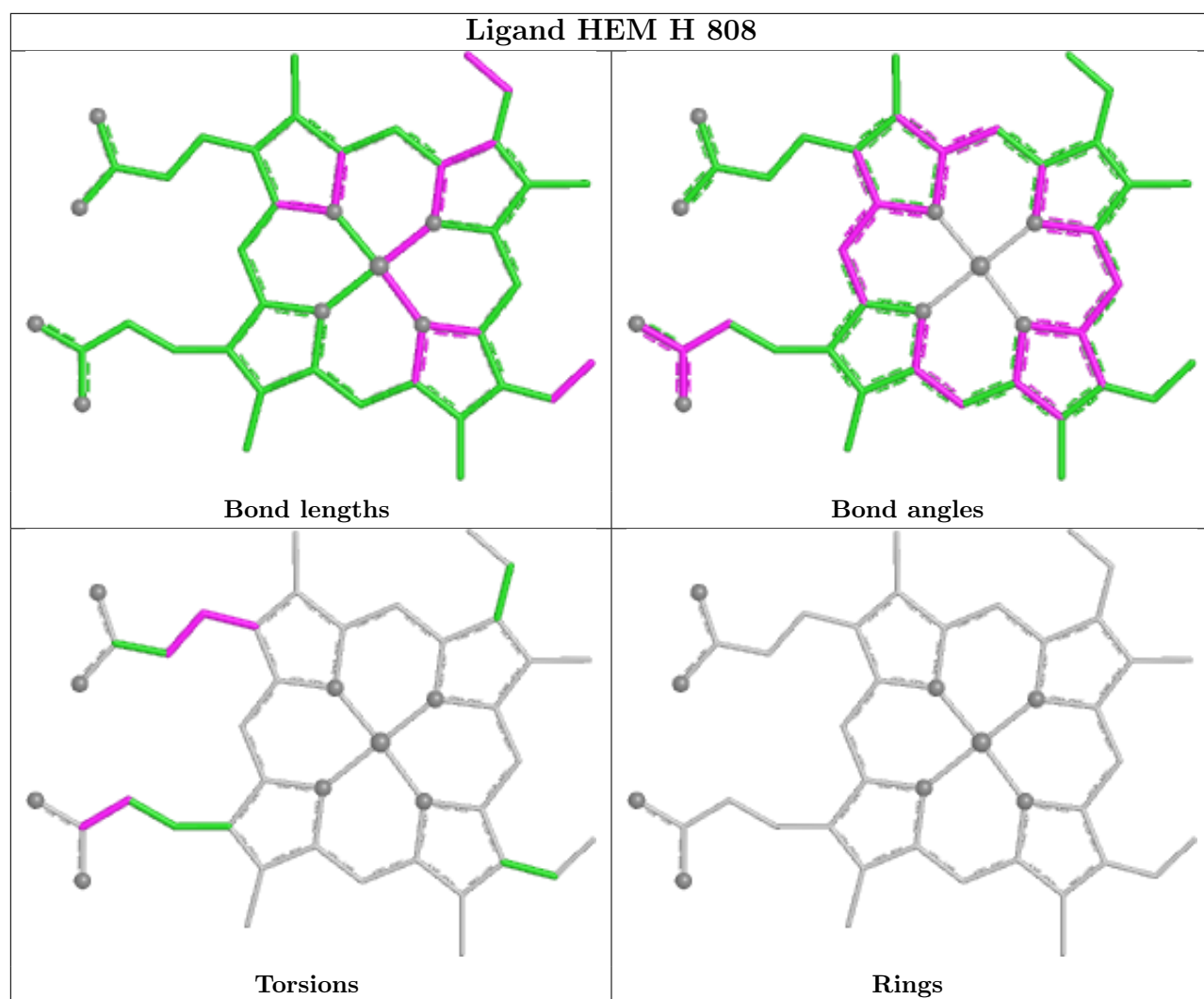


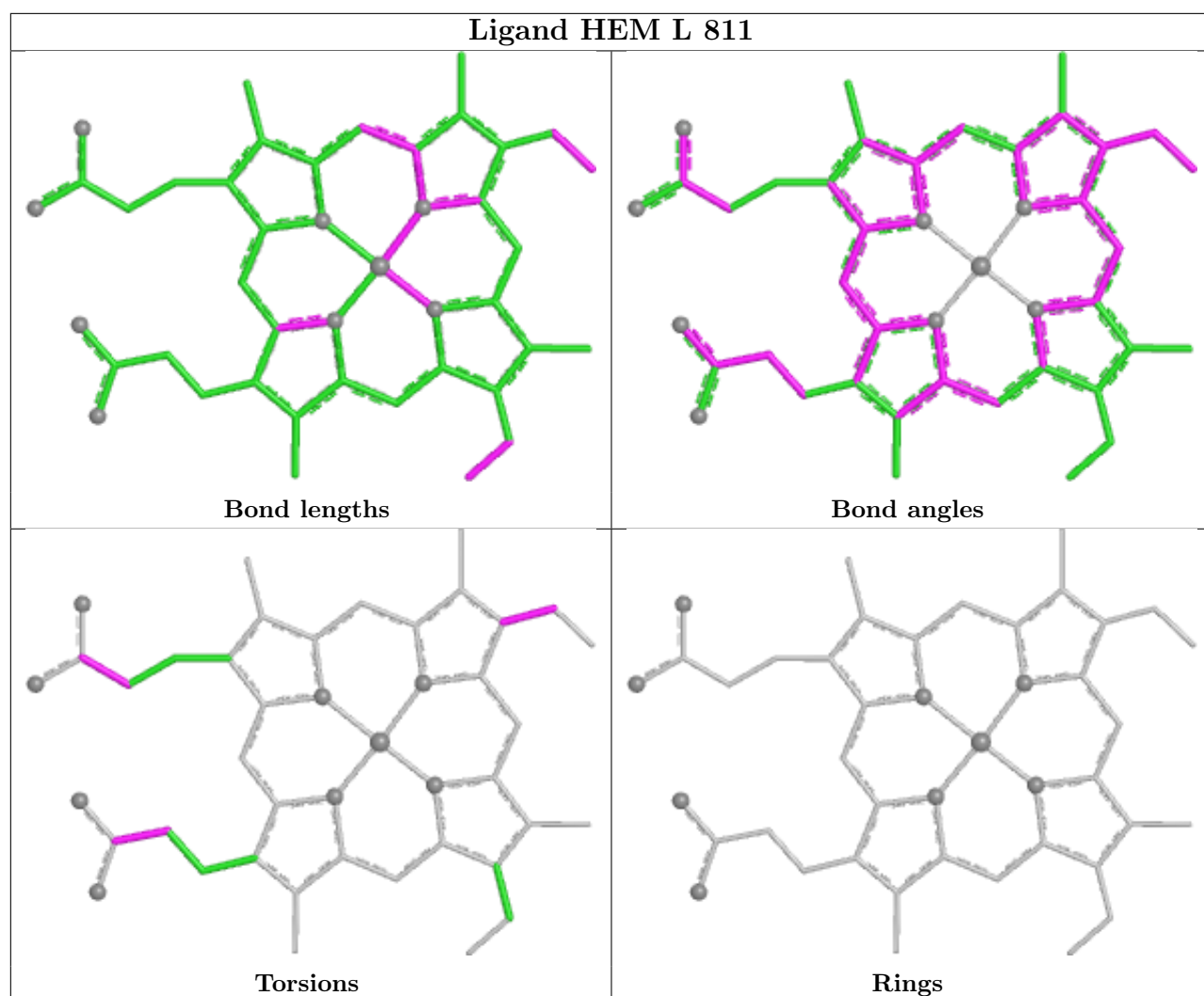
Torsions

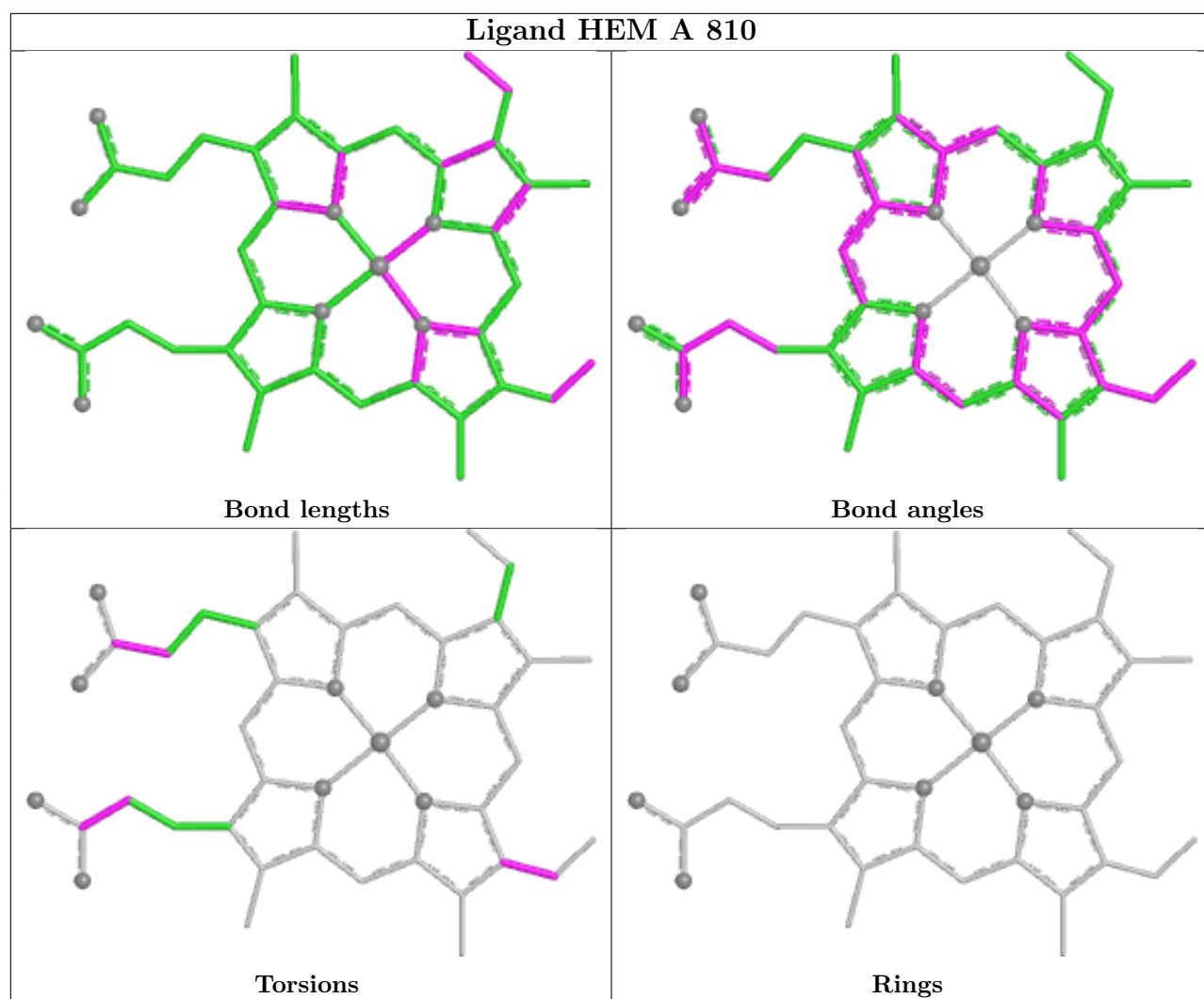


Rings

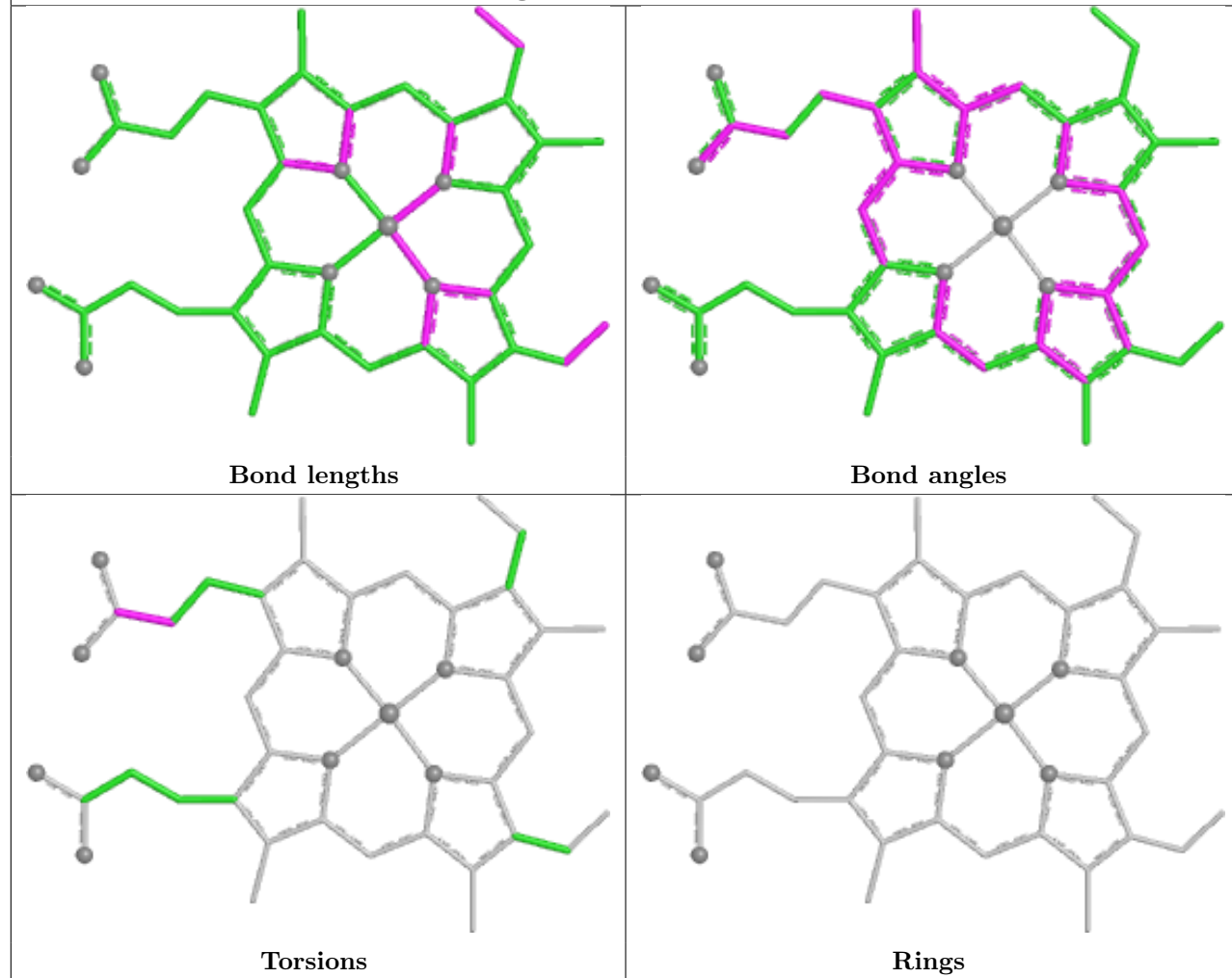




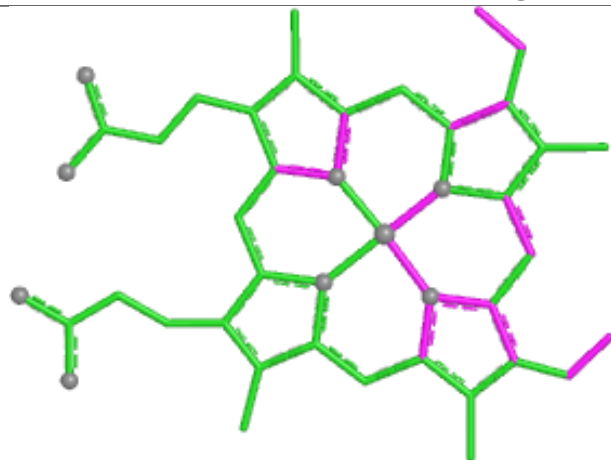




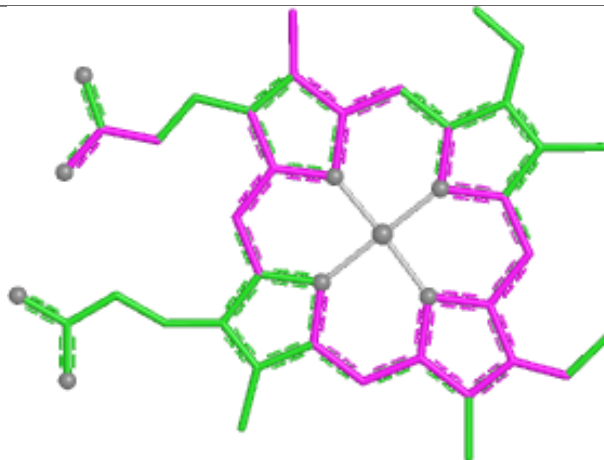
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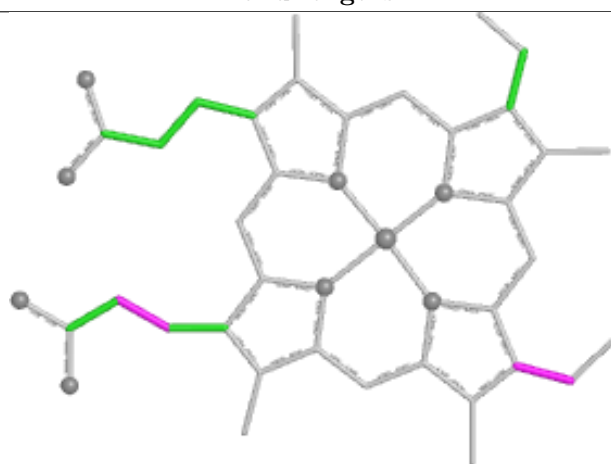
Ligand HEM J 806



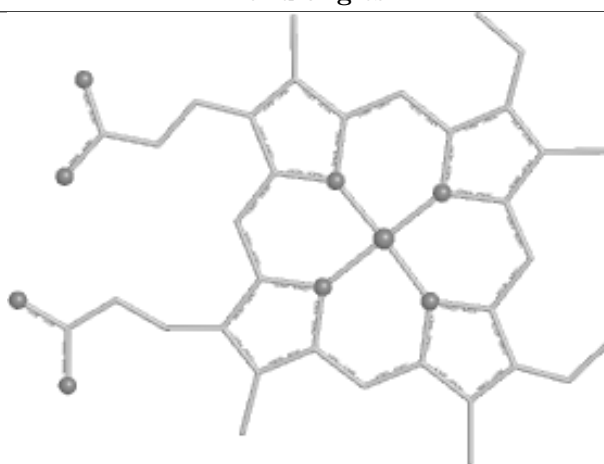
Bond lengths



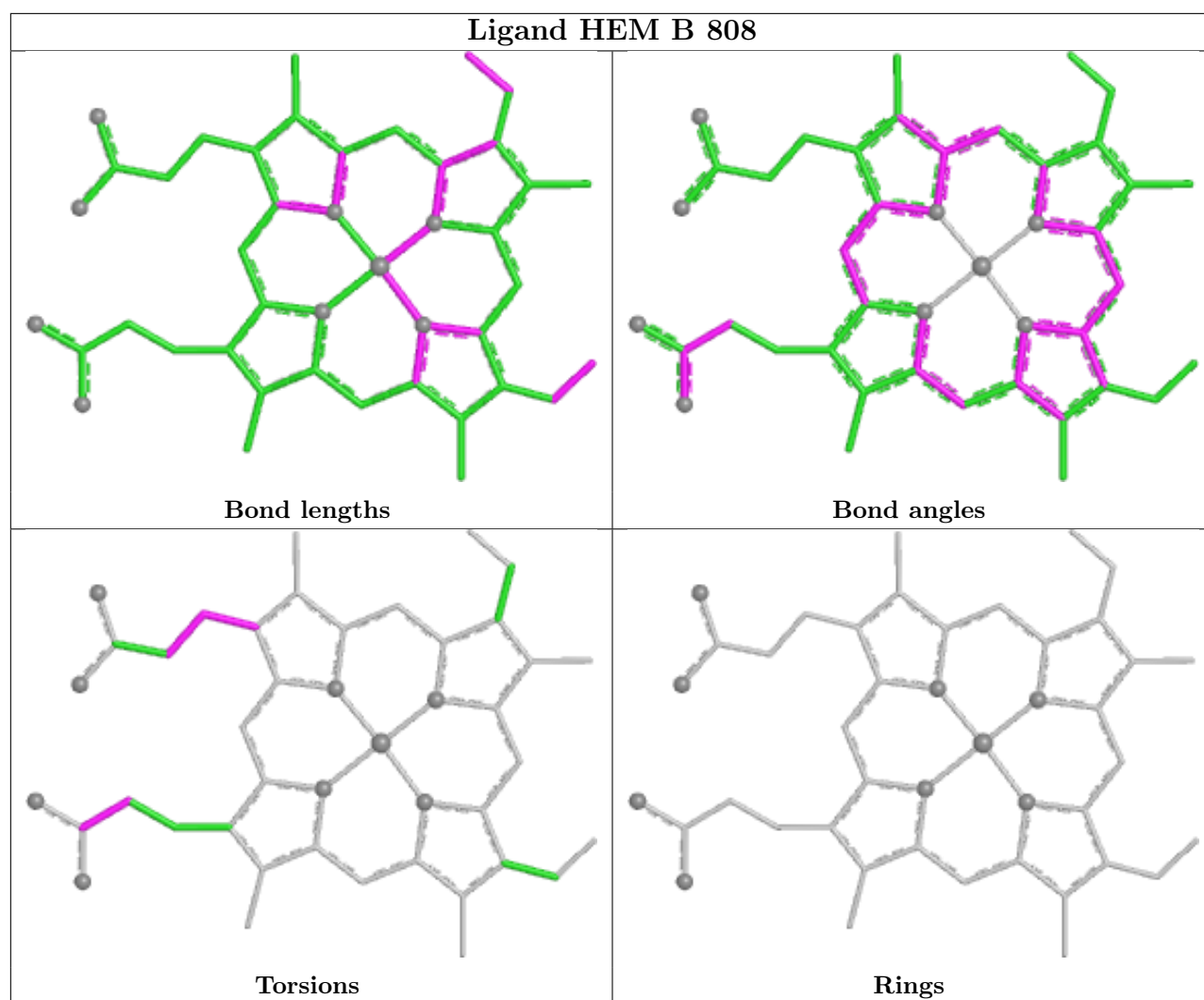
Bond angles

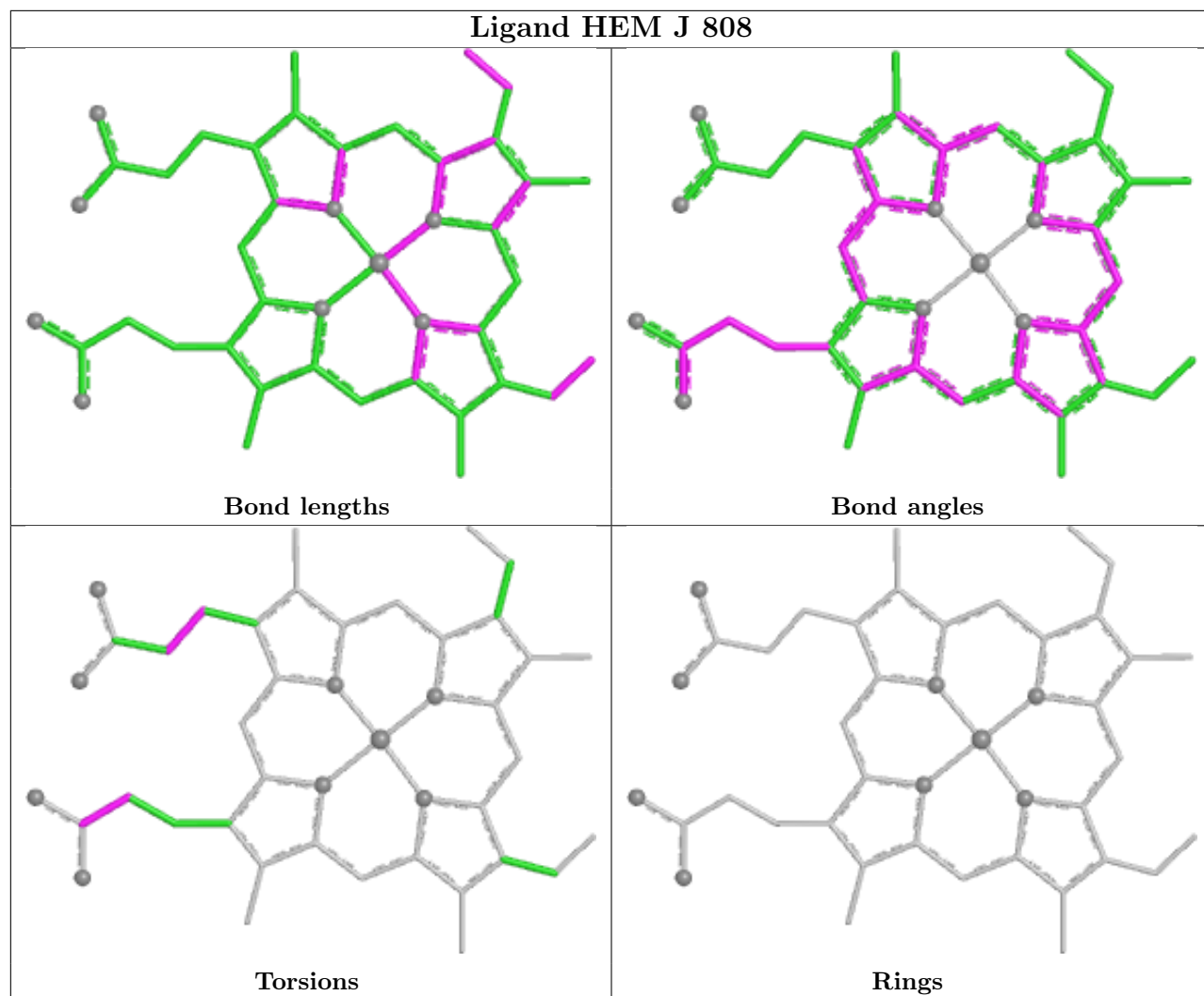


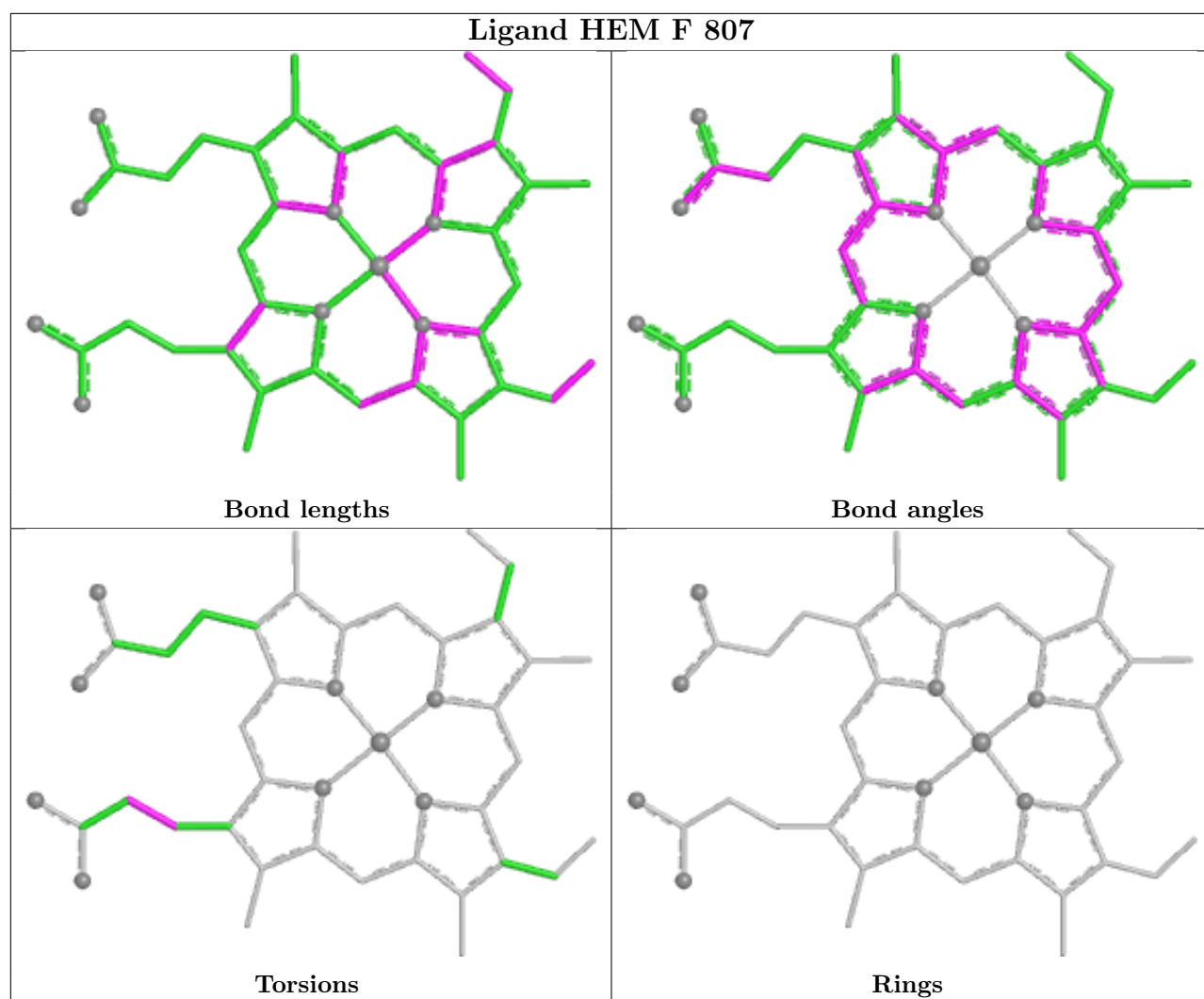
Torsions

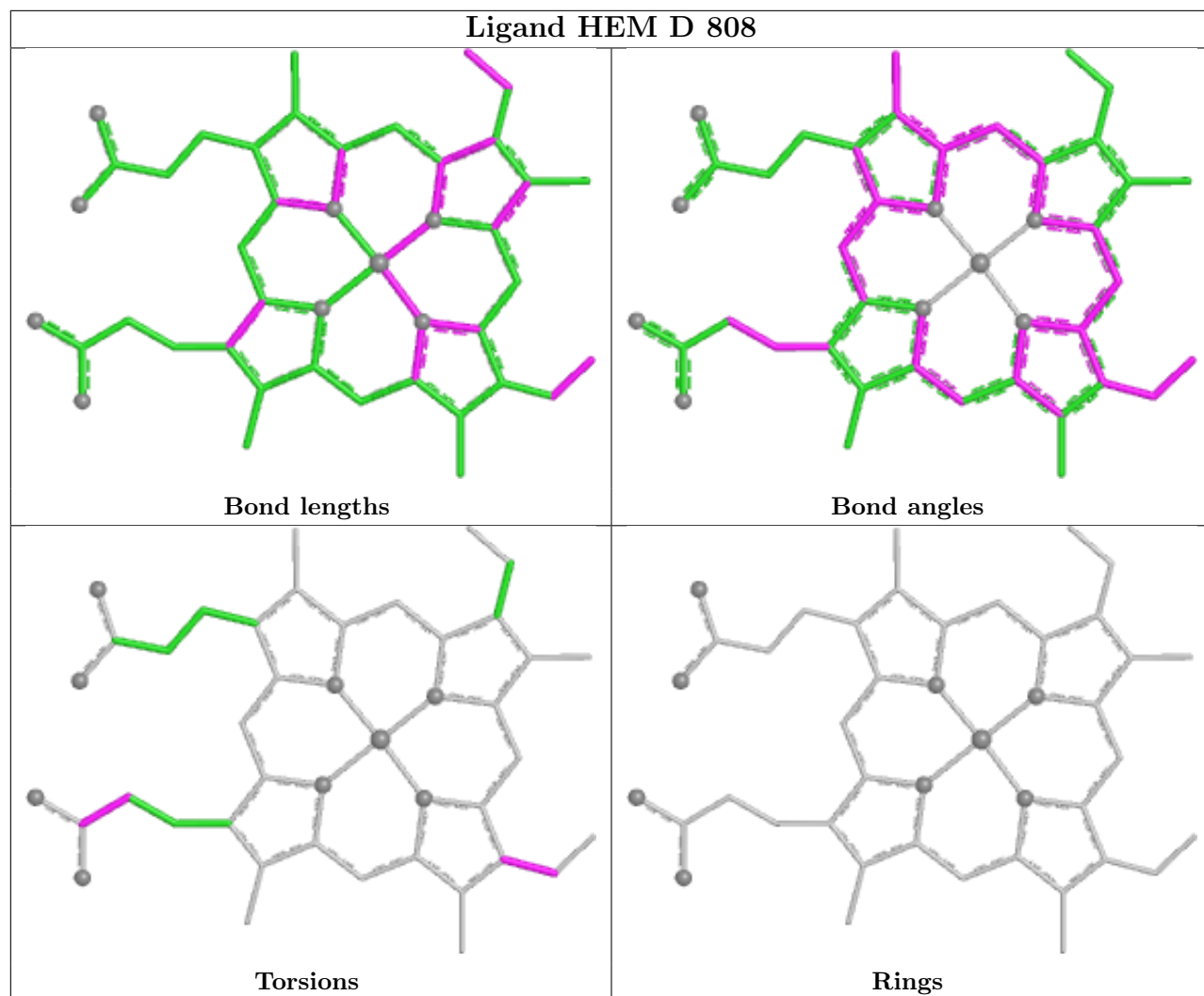


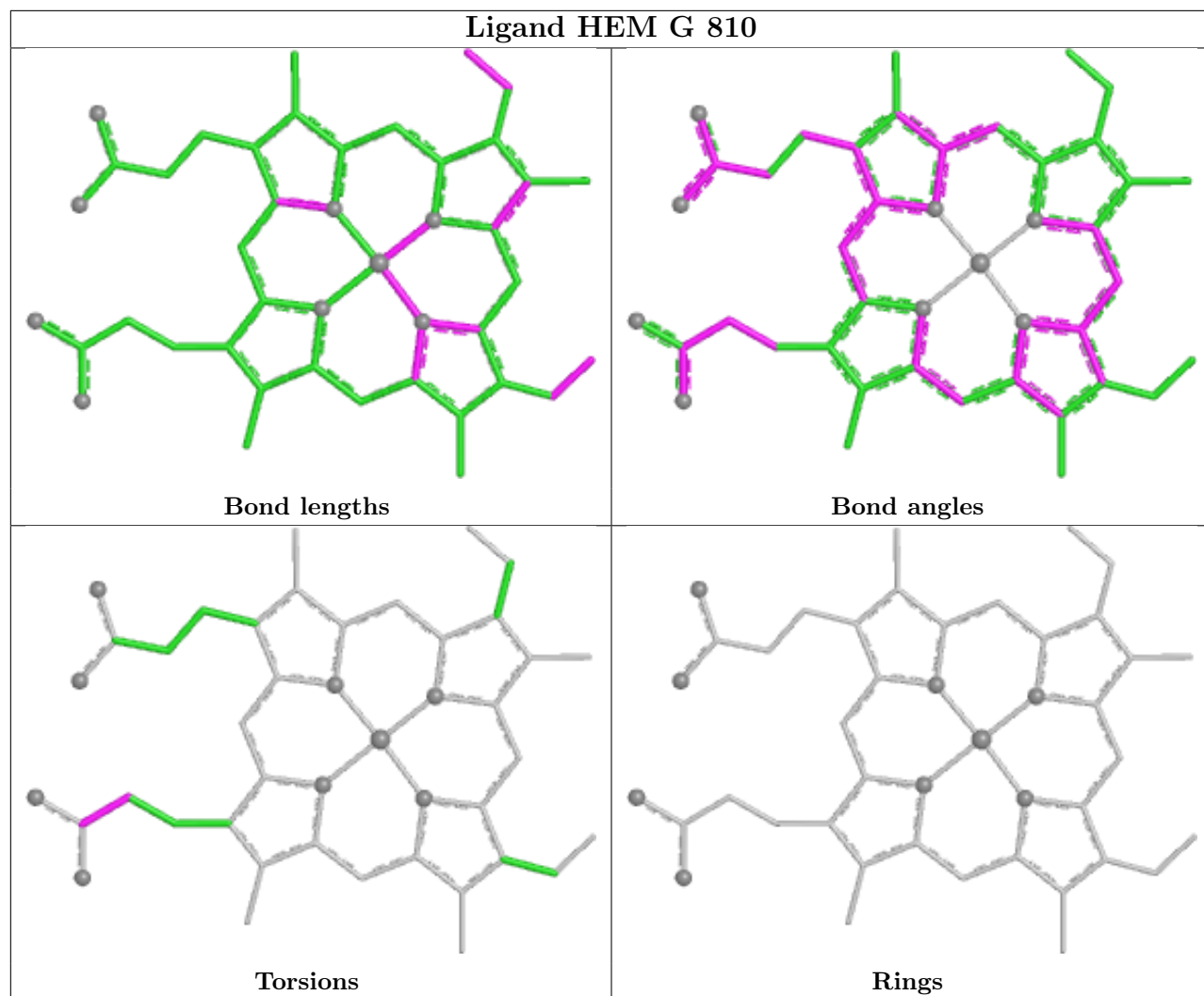
Rings

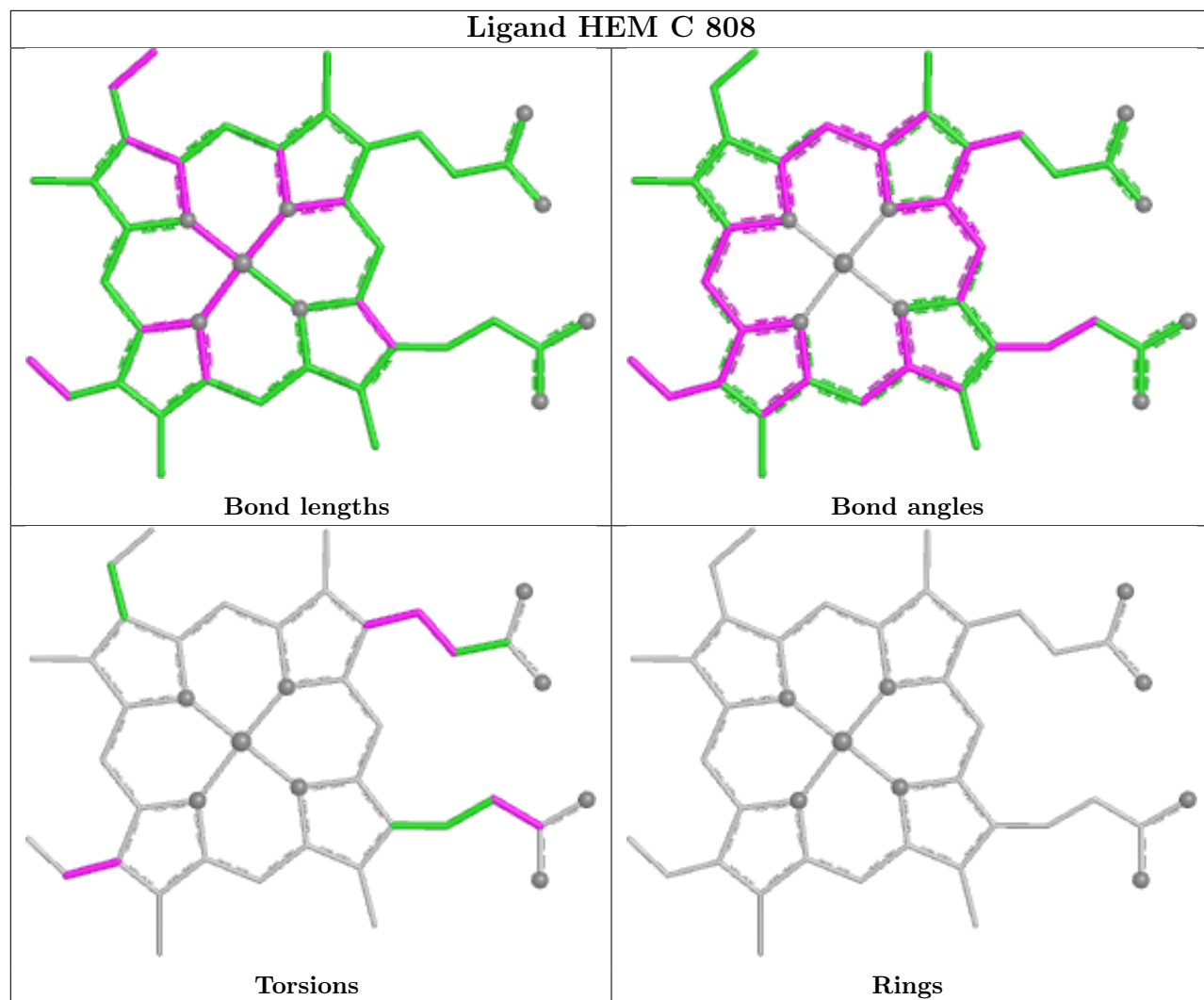


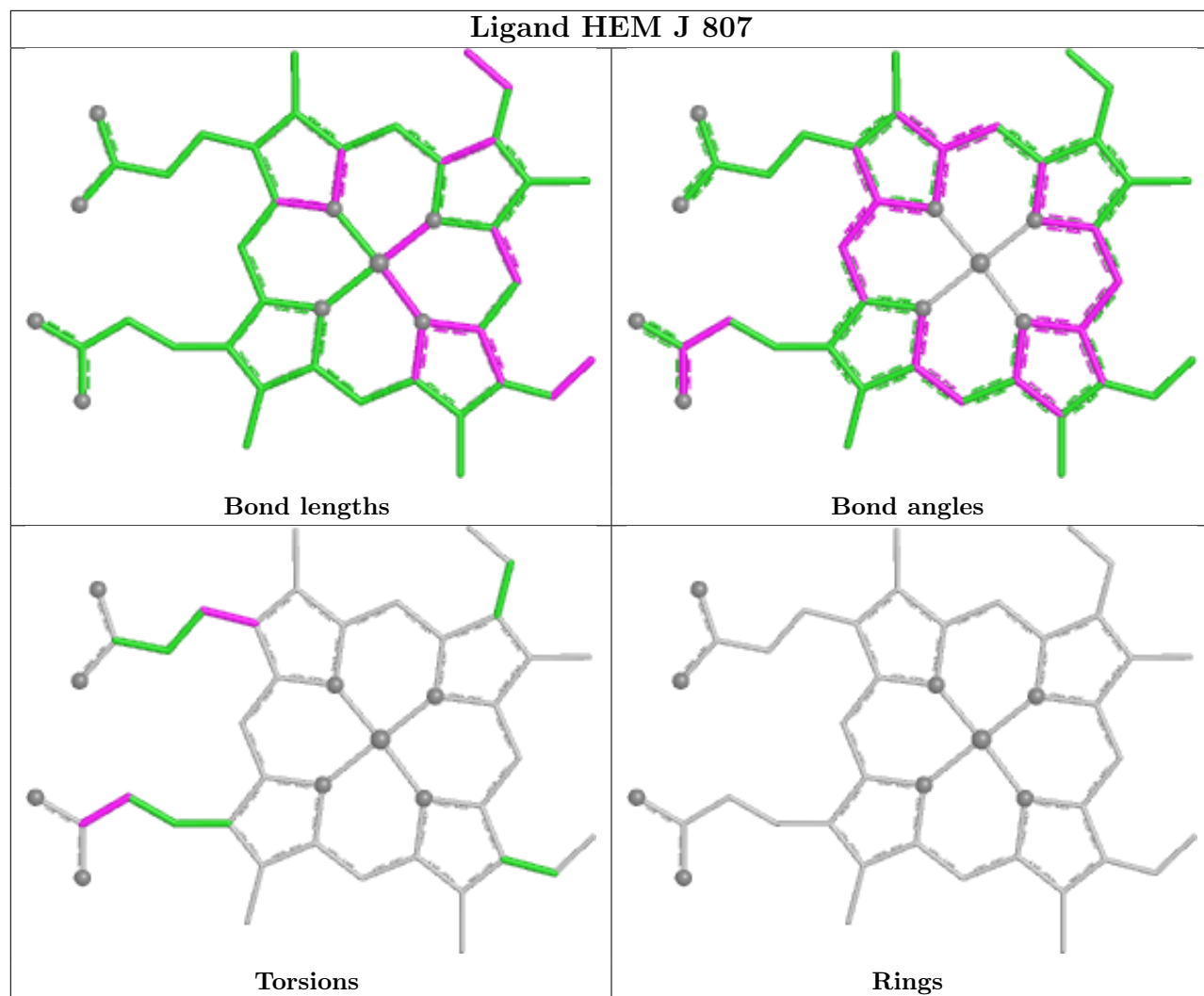


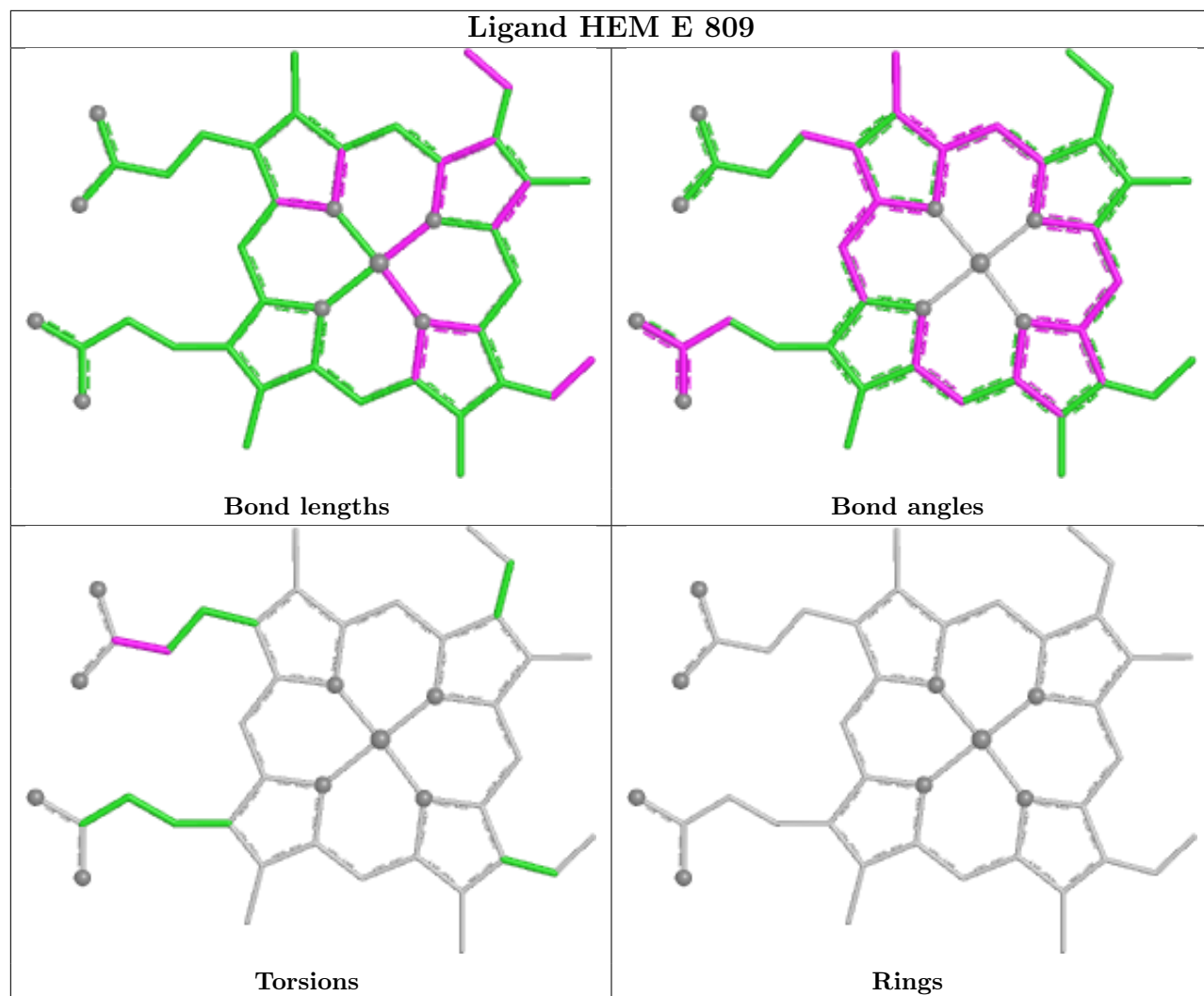




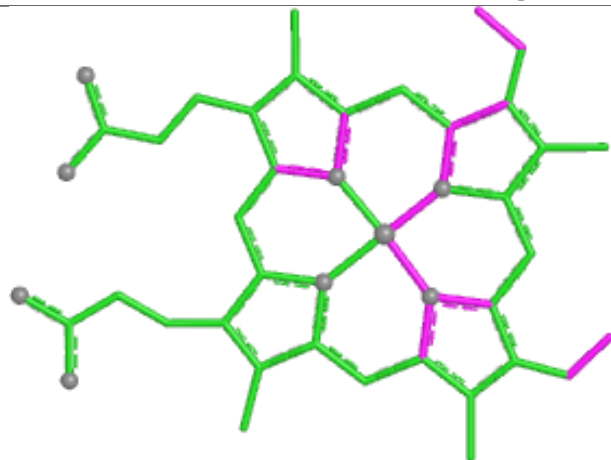




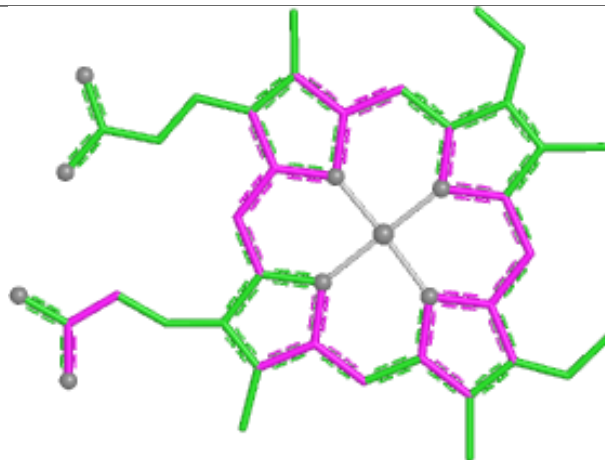




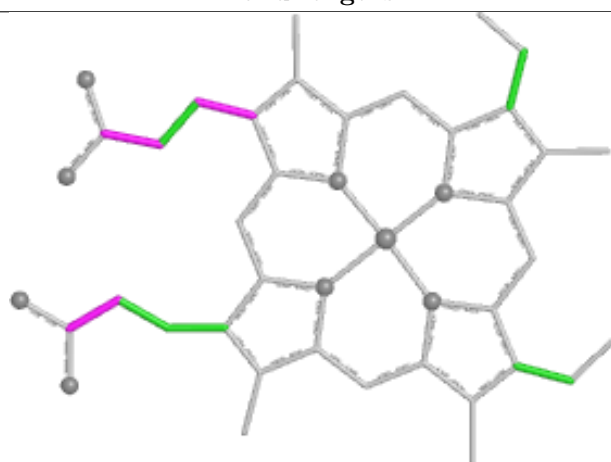
Ligand HEM J 813



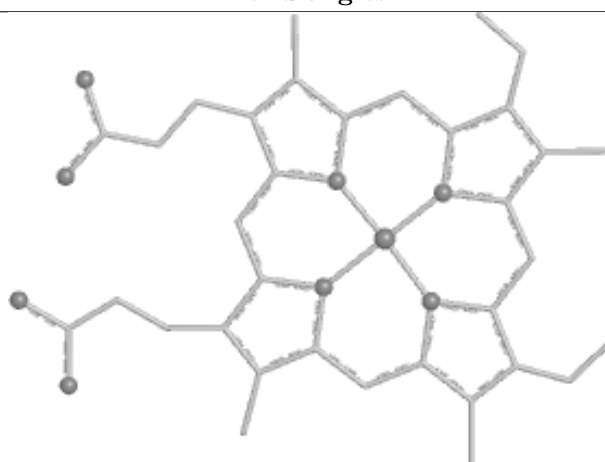
Bond lengths



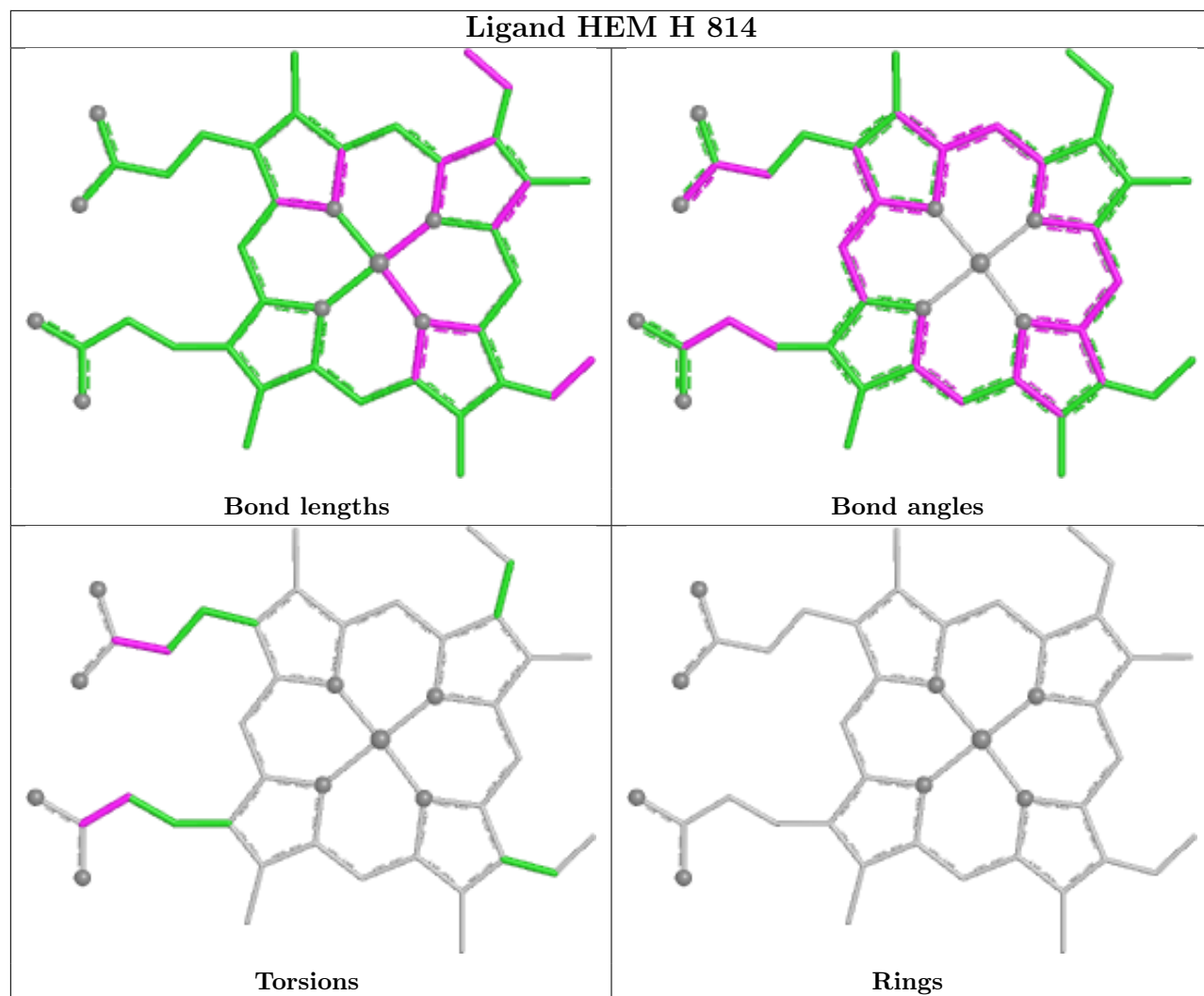
Bond angles

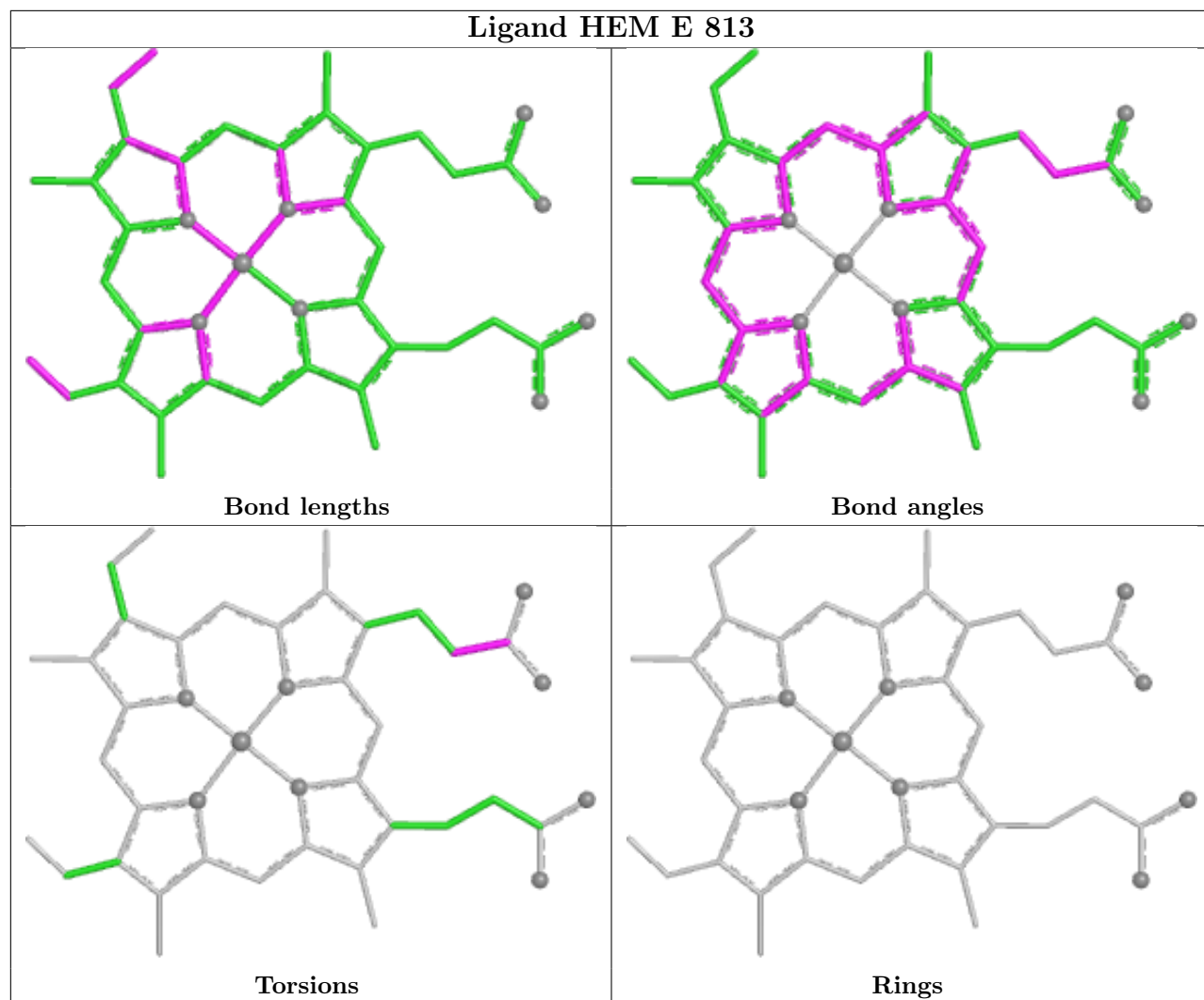


Torsions

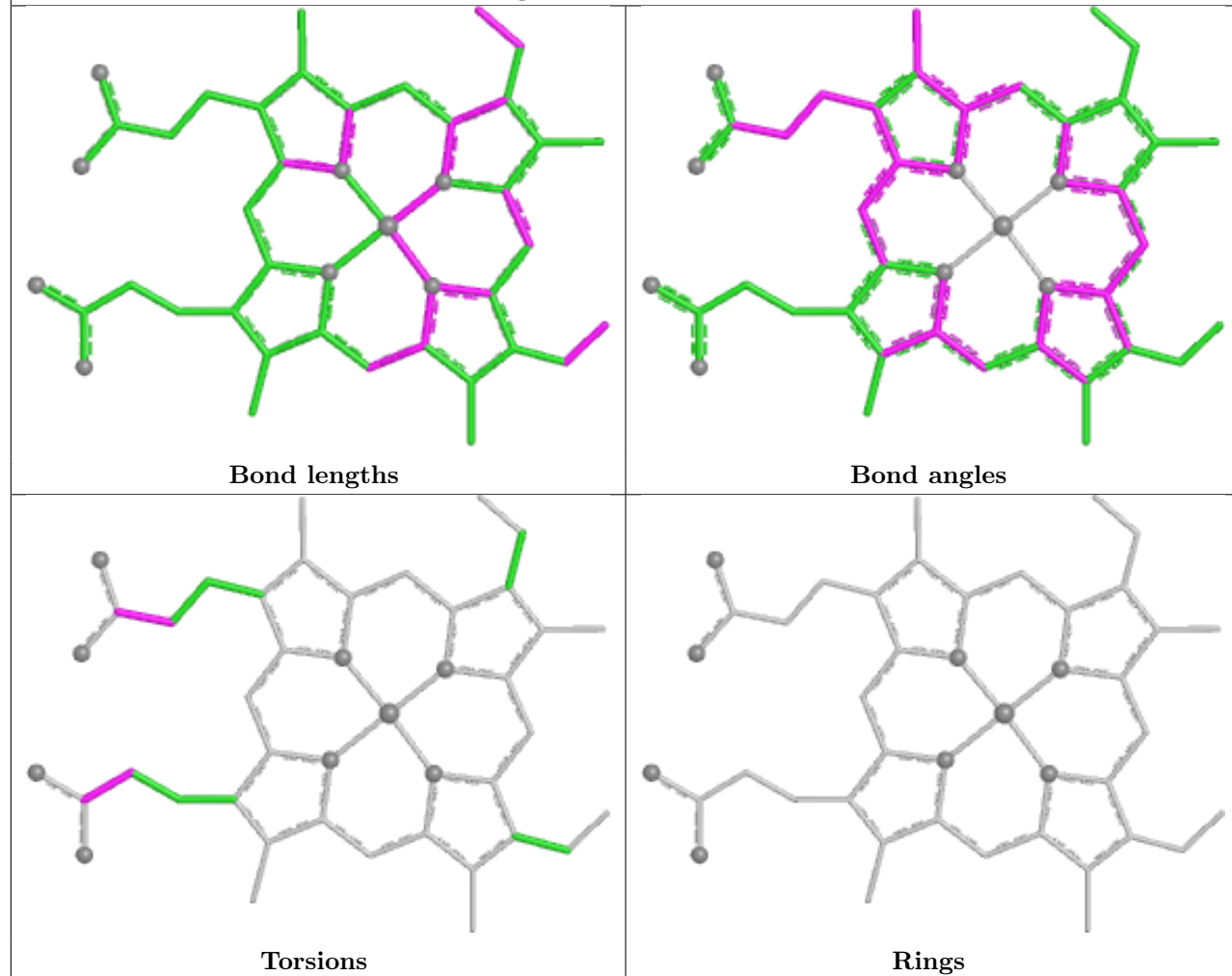


Rings

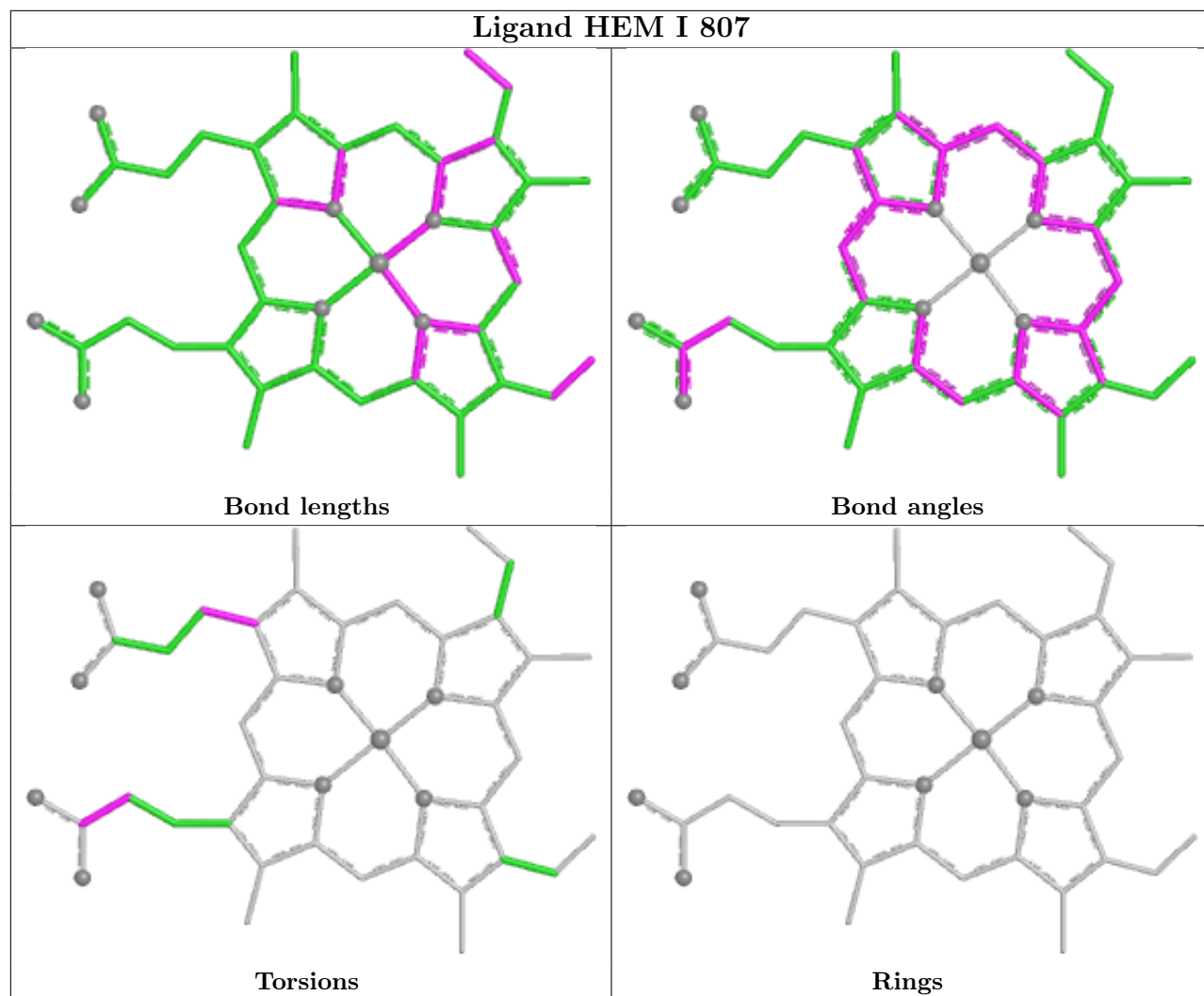


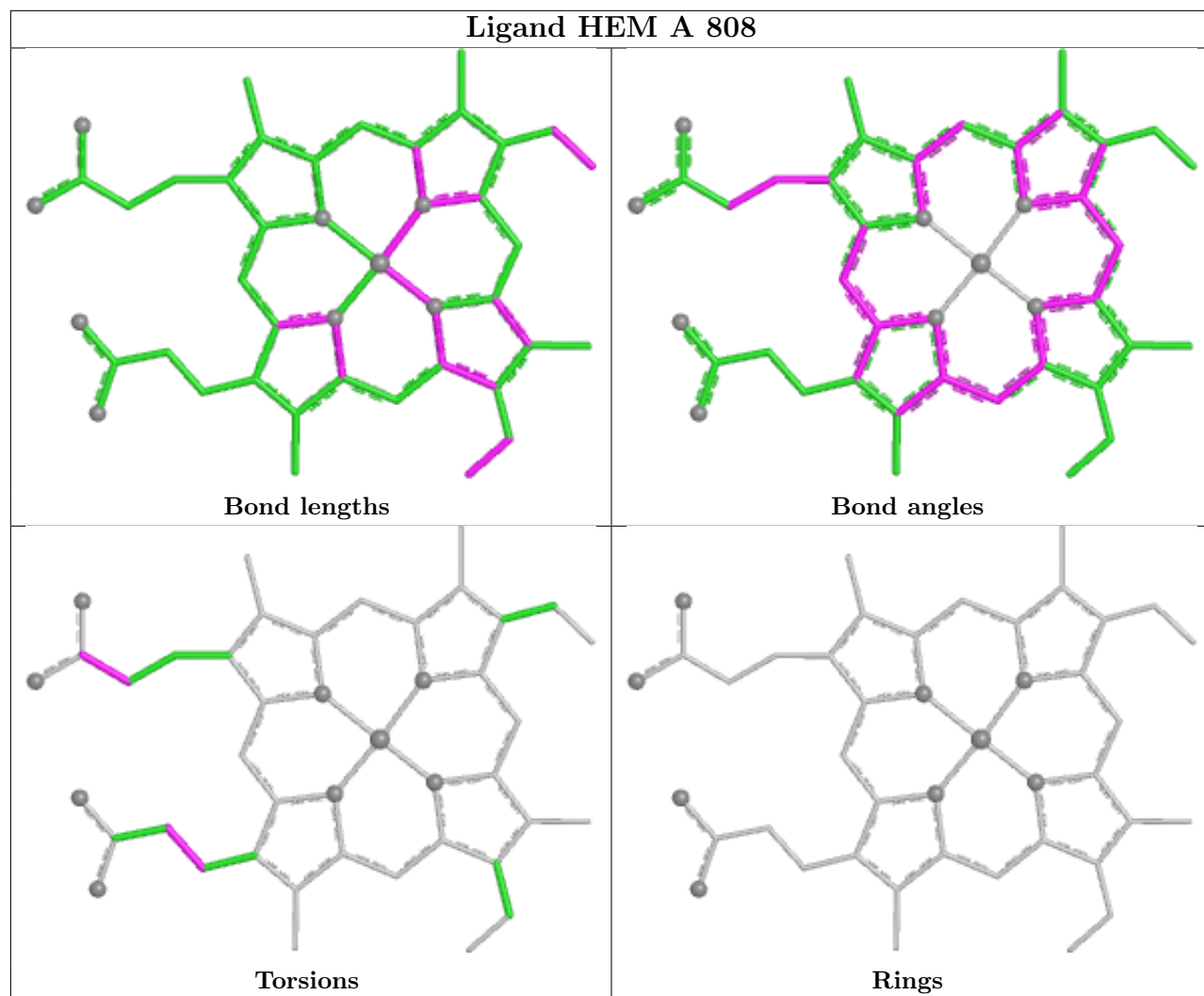


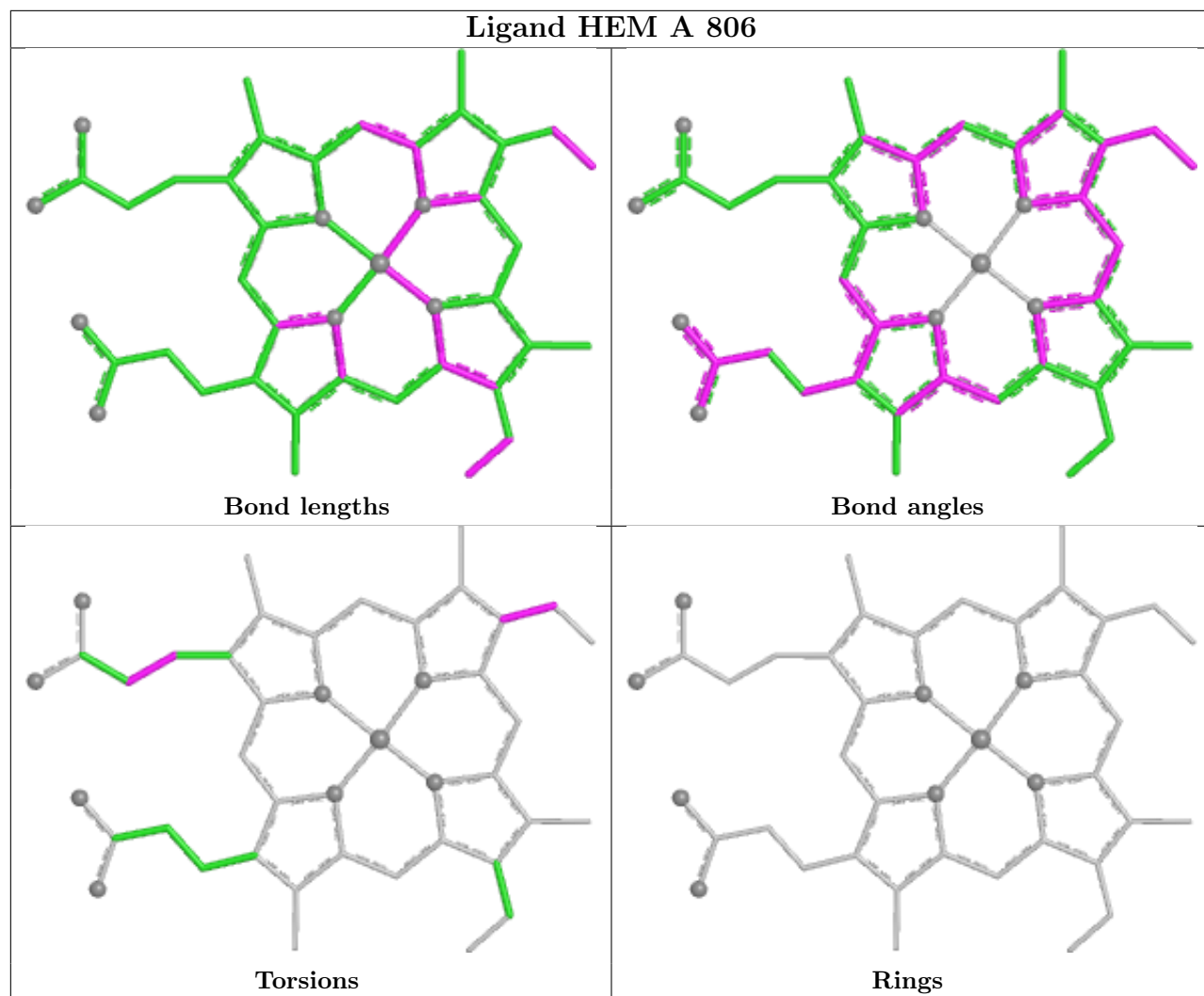
Ligand HEM I 813

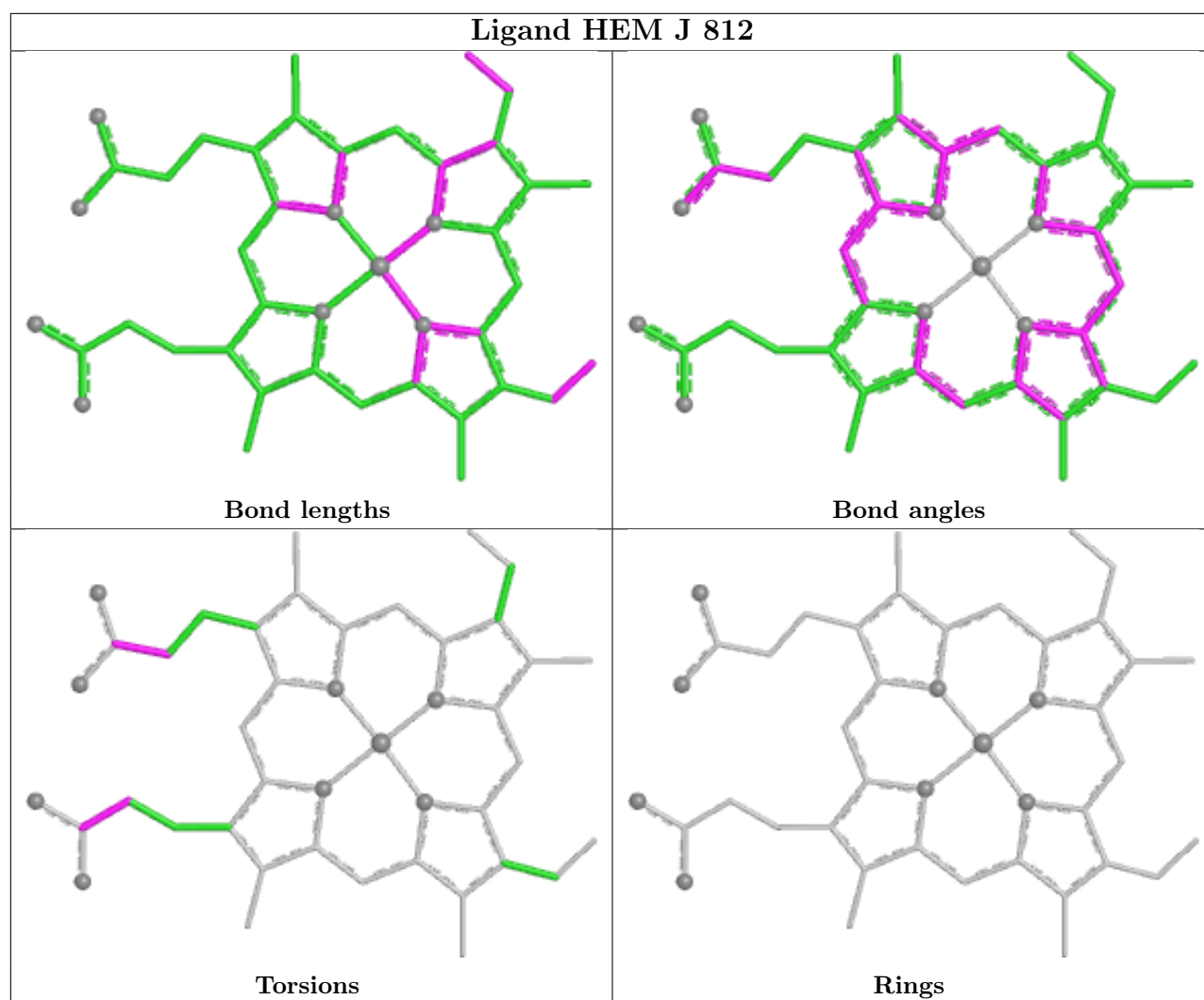


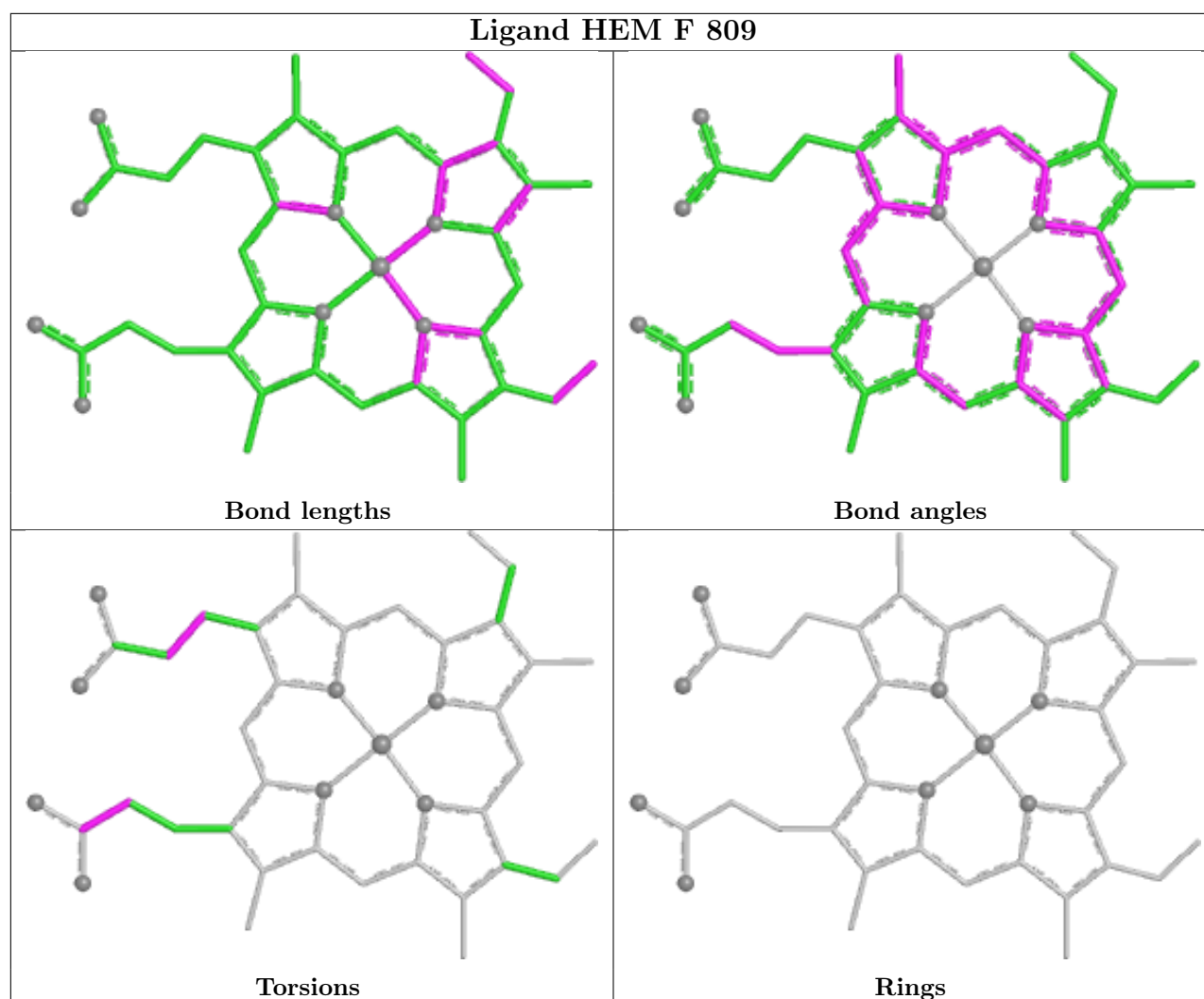
Ligand HEM I 807

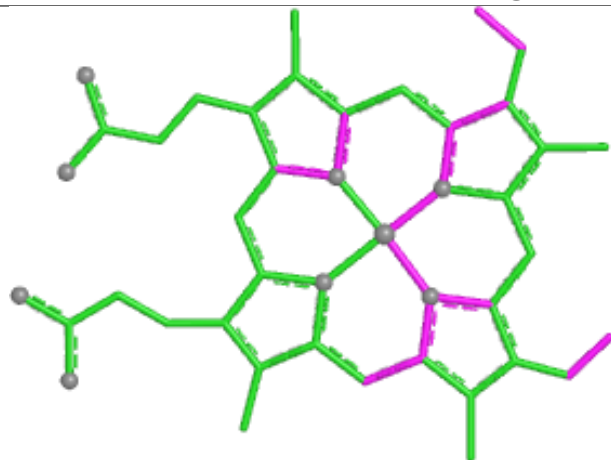




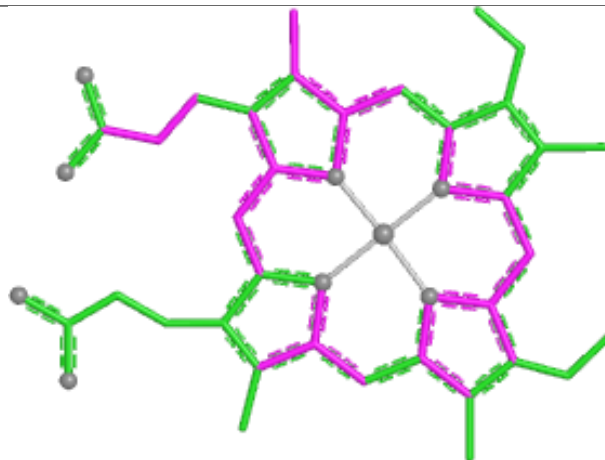




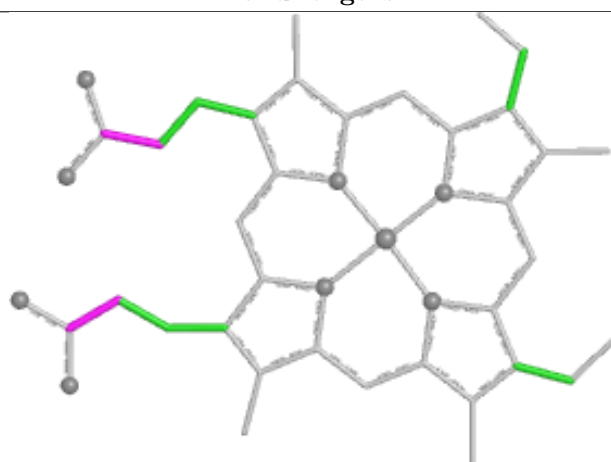


Ligand HEM K 813

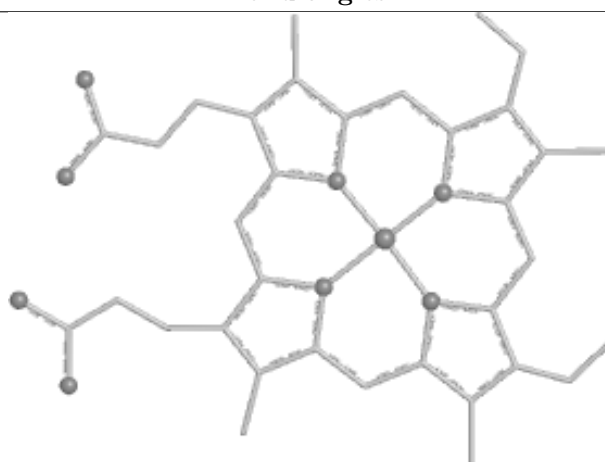
Bond lengths



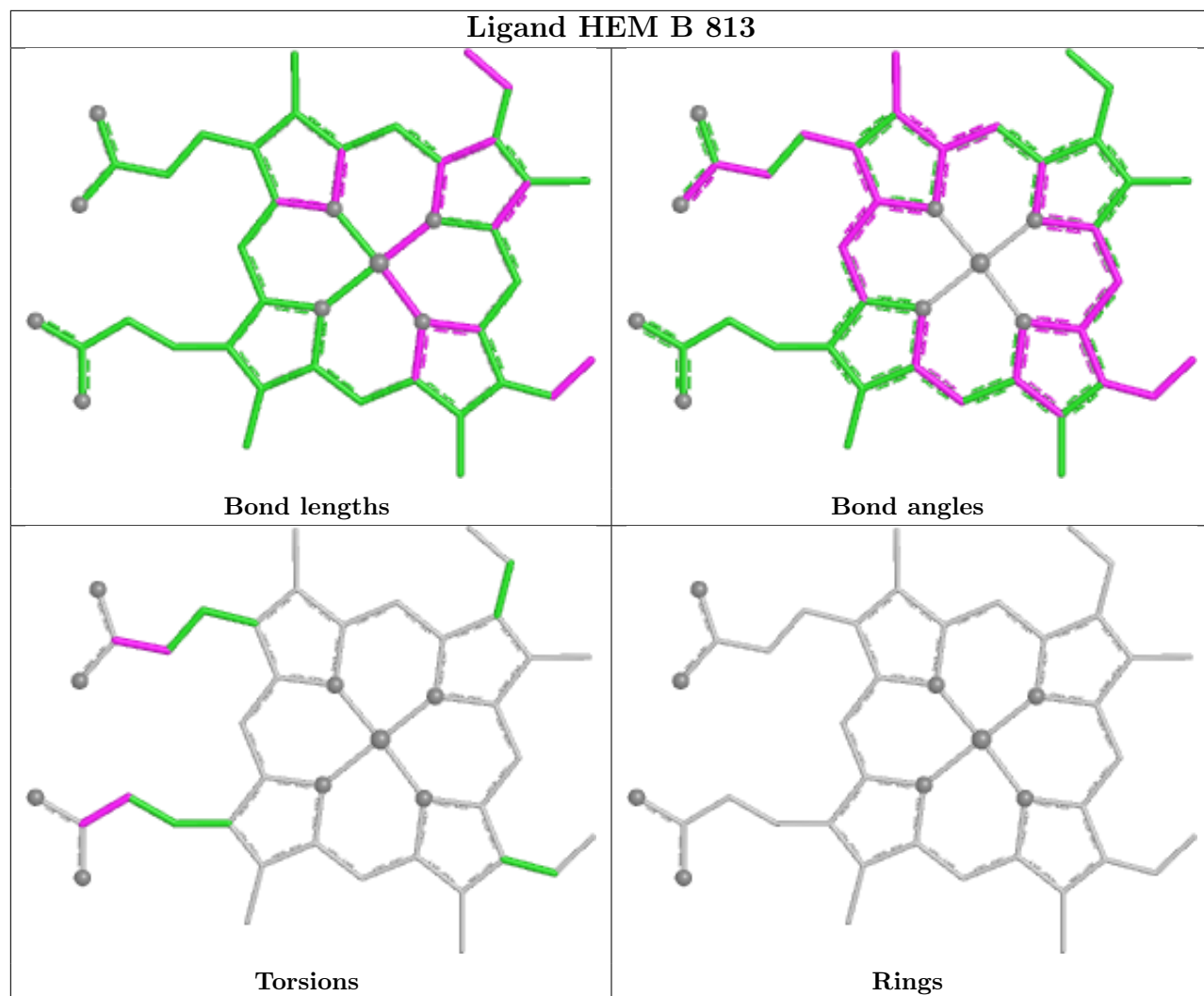
Bond angles

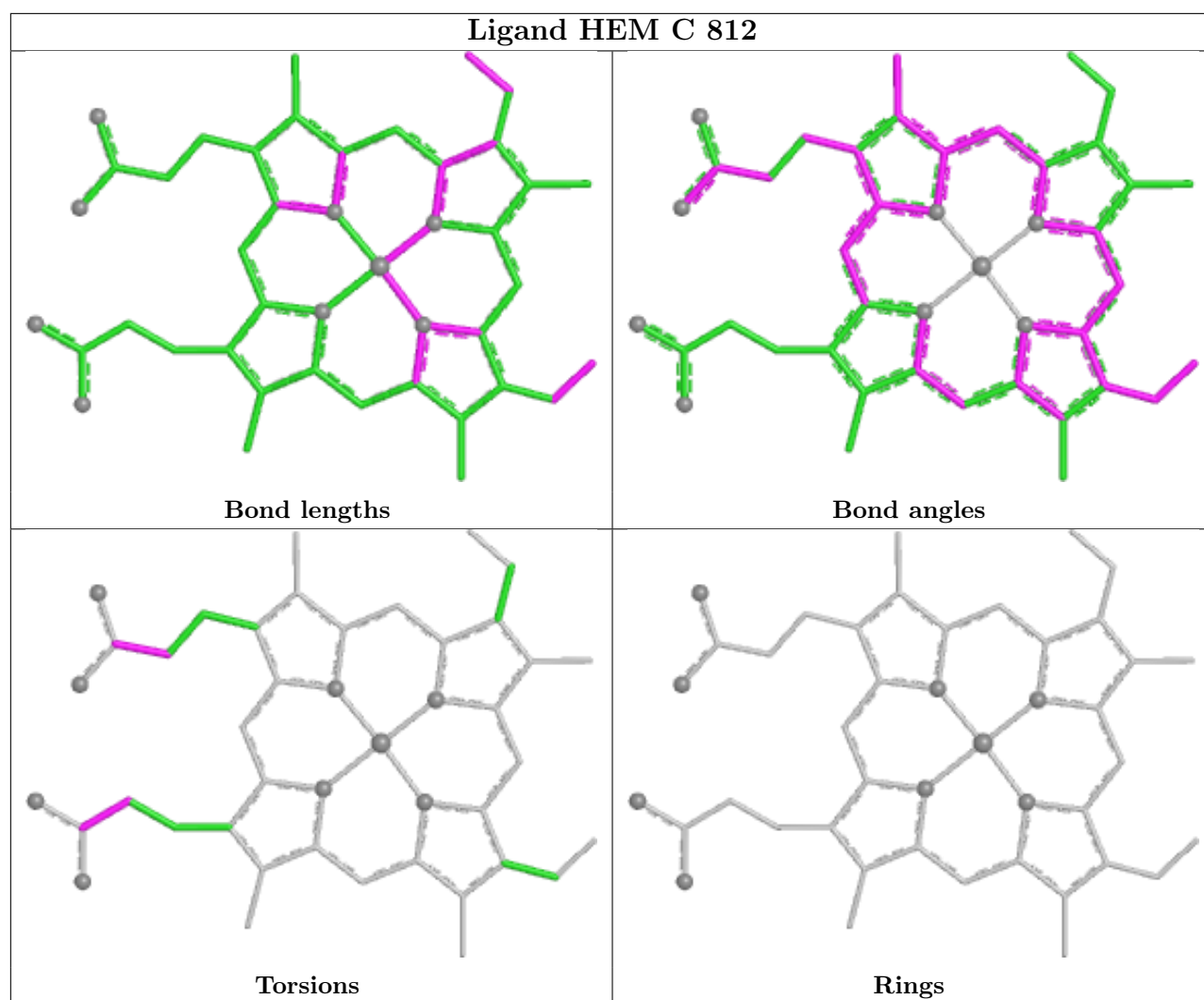


Torsions

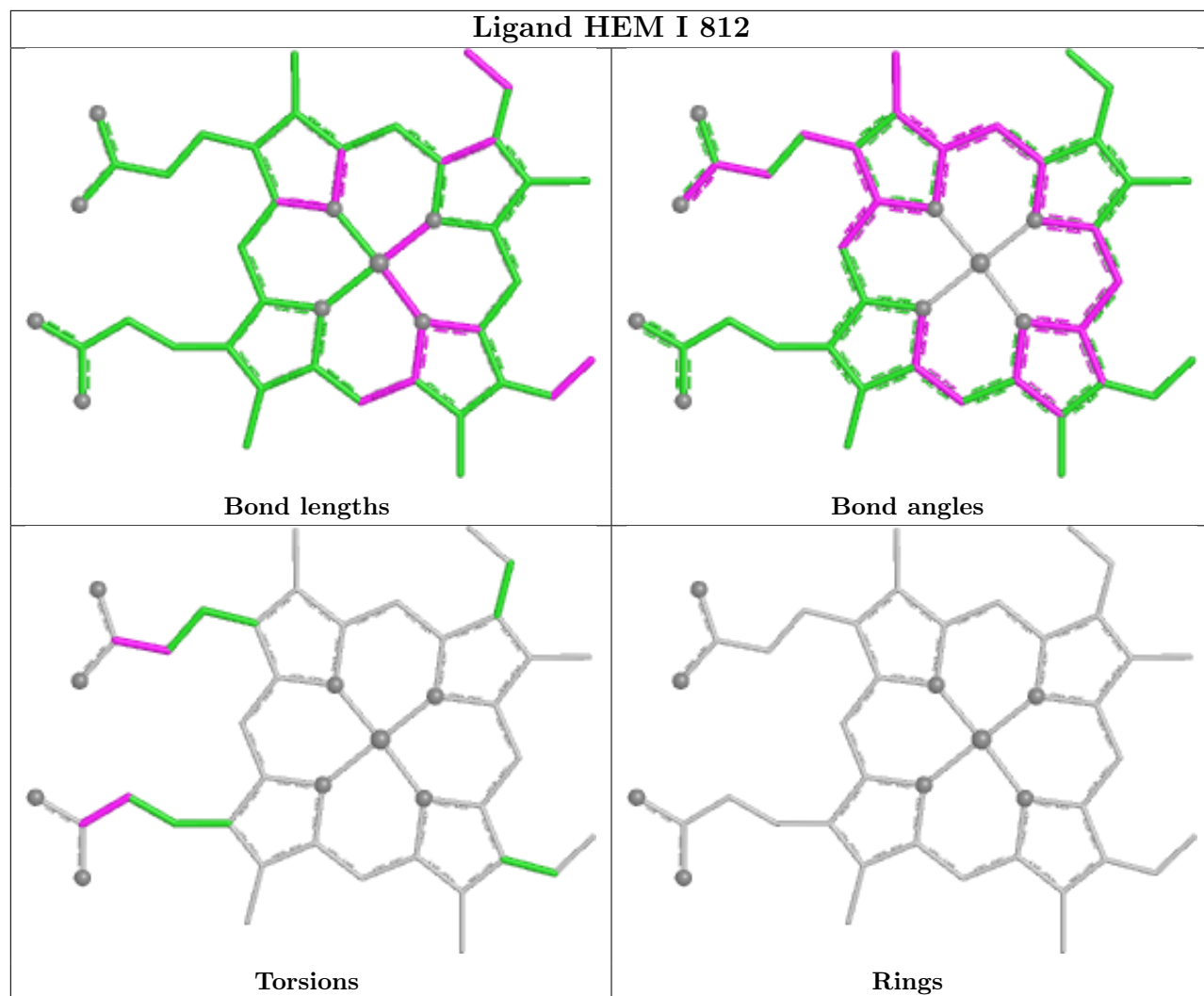


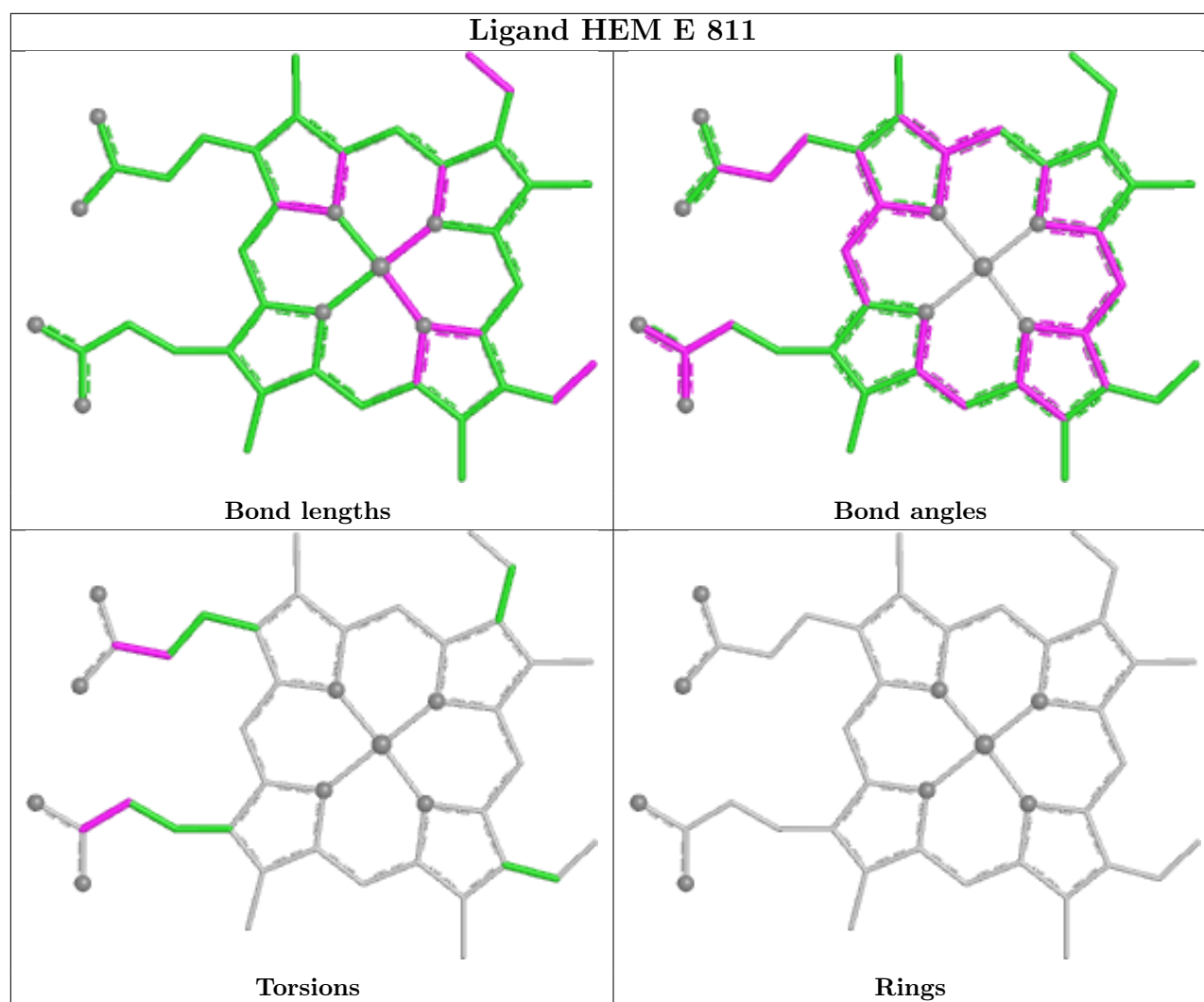
Rings

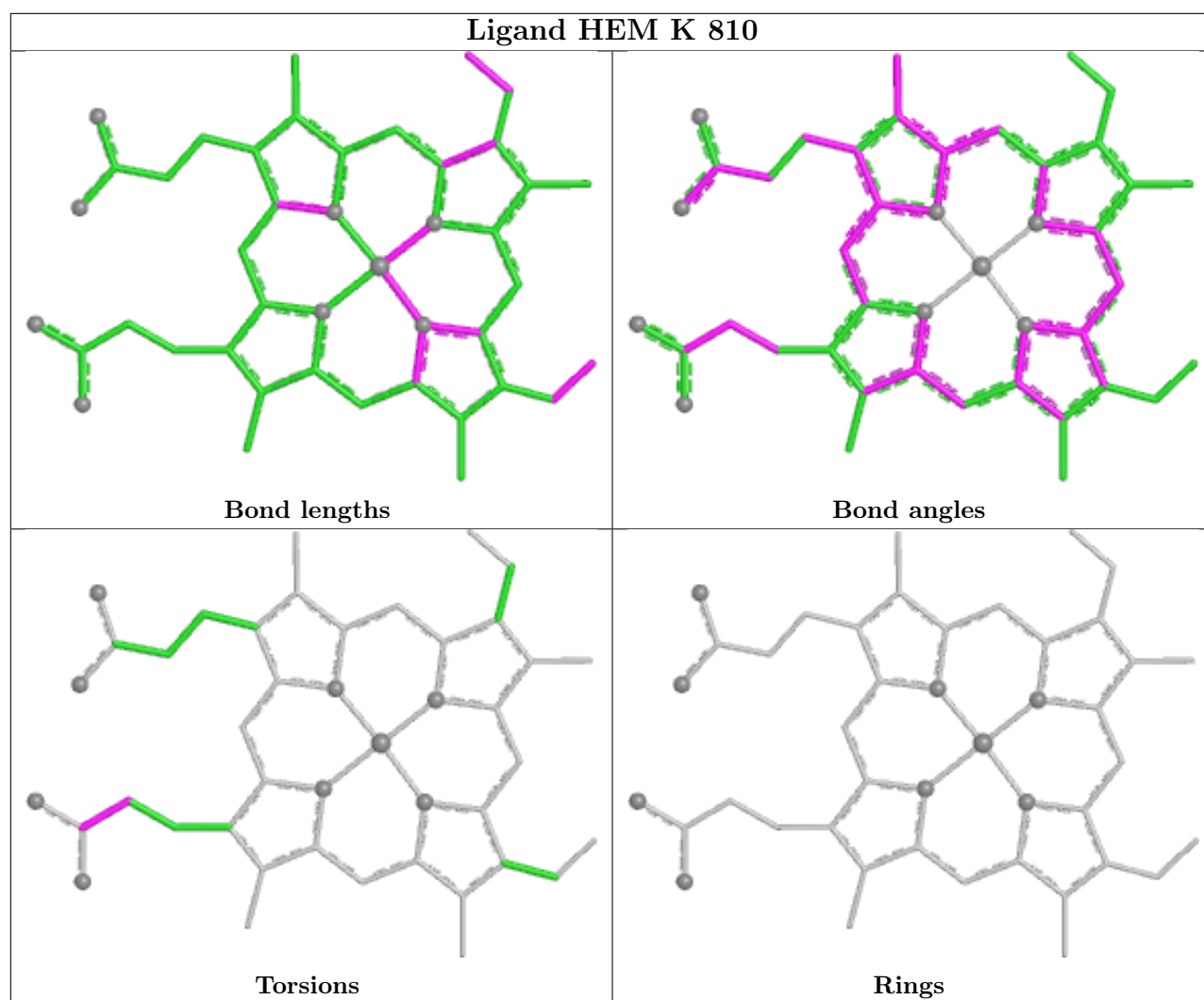


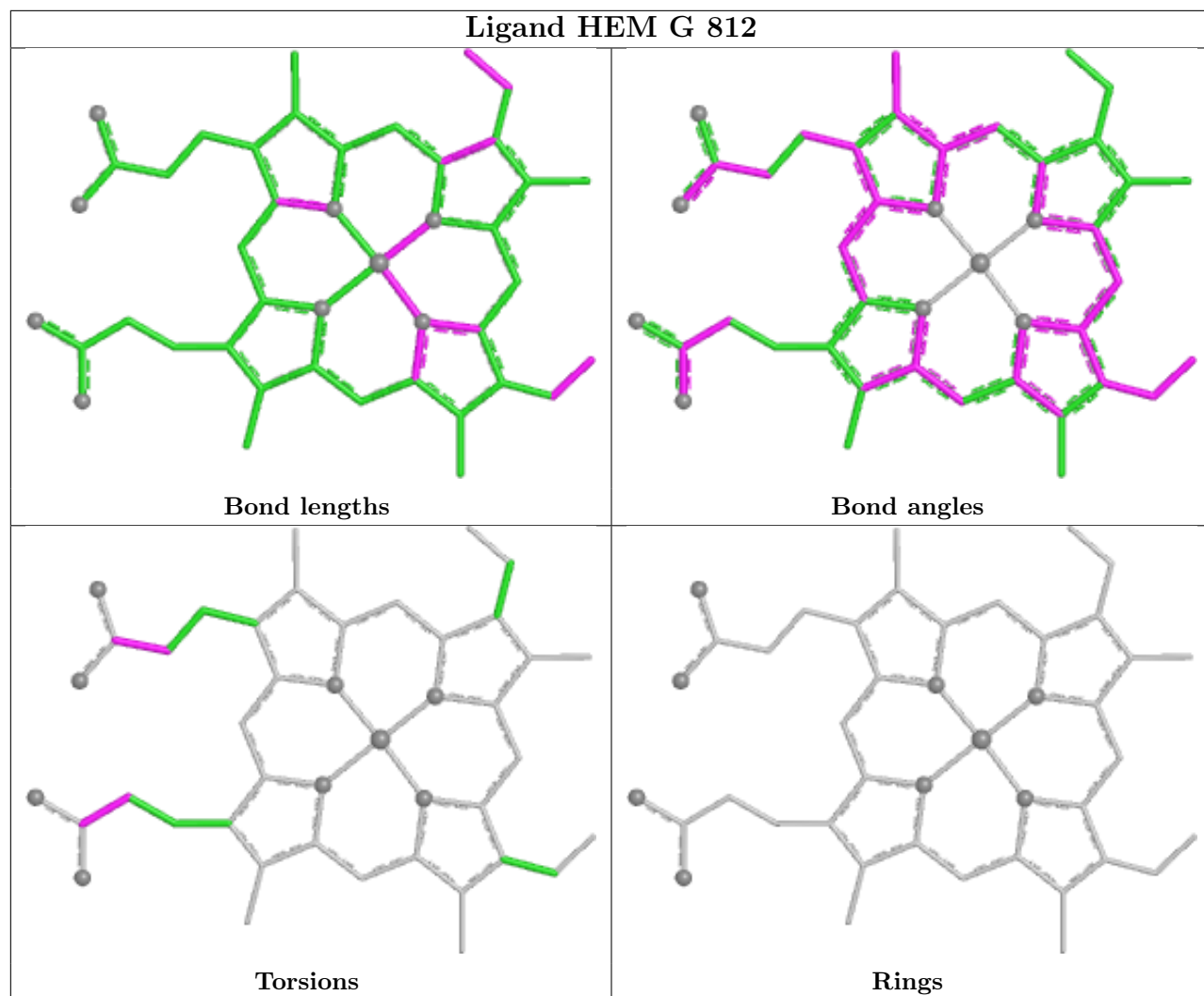


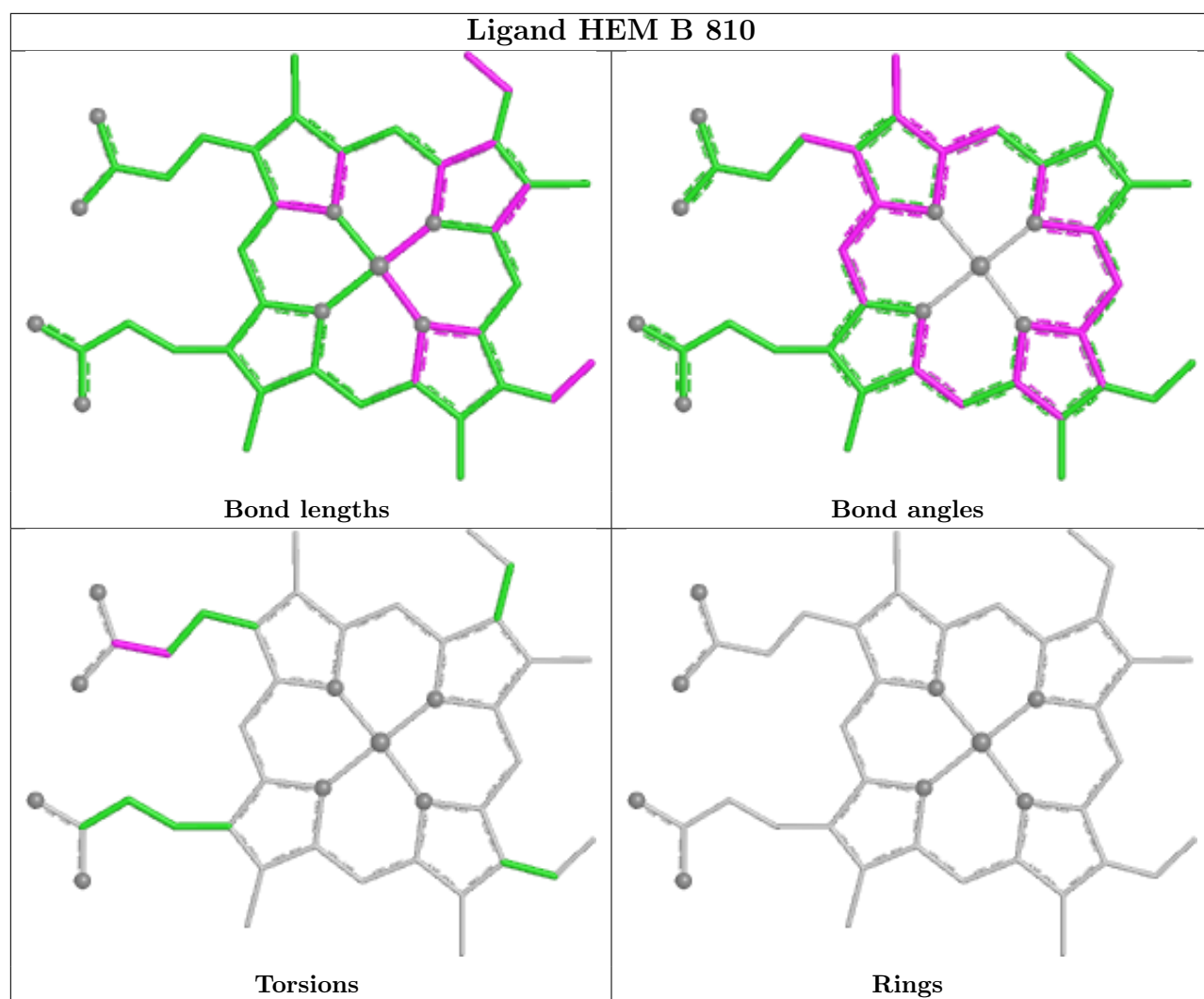
Ligand HEM I 812

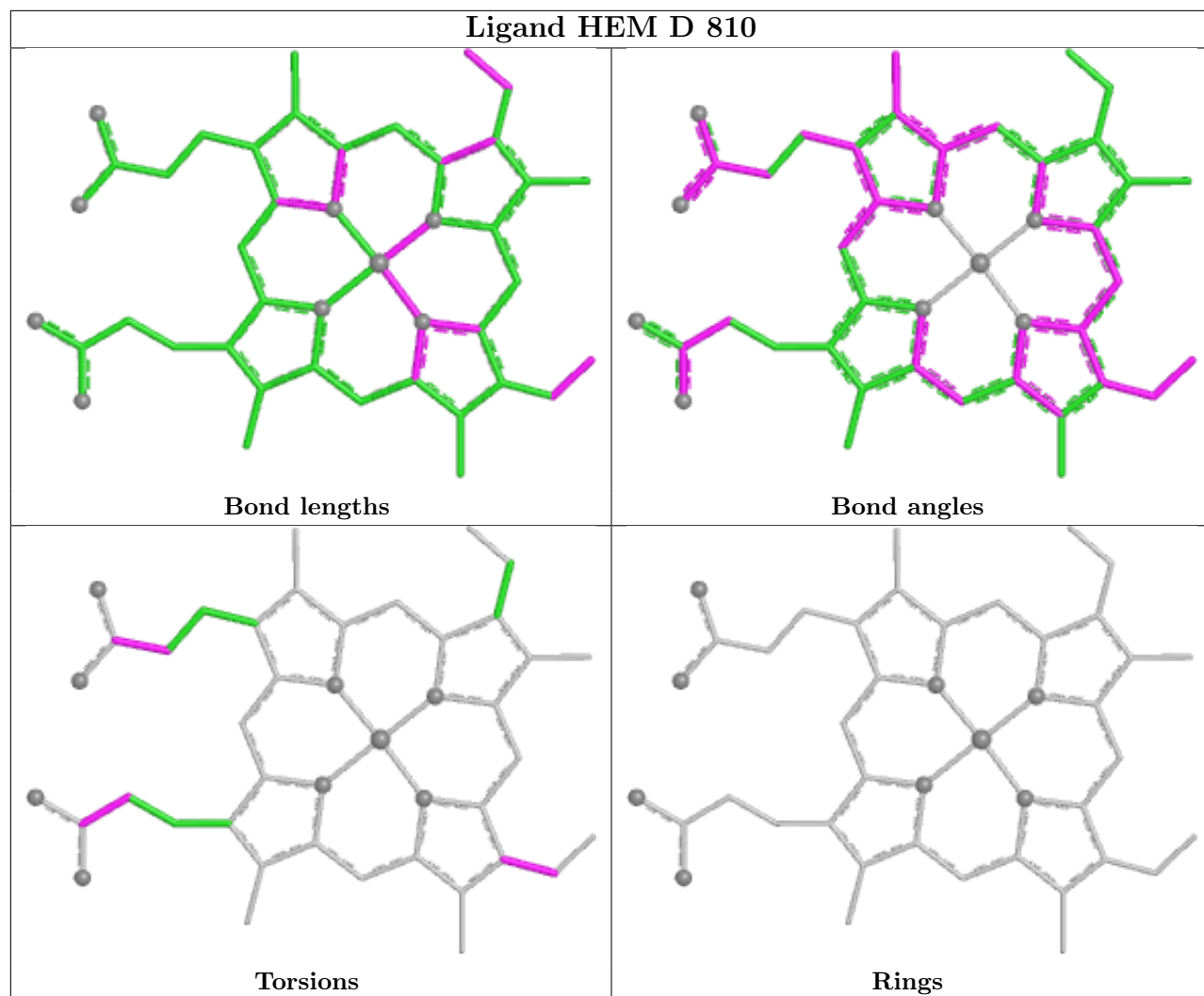


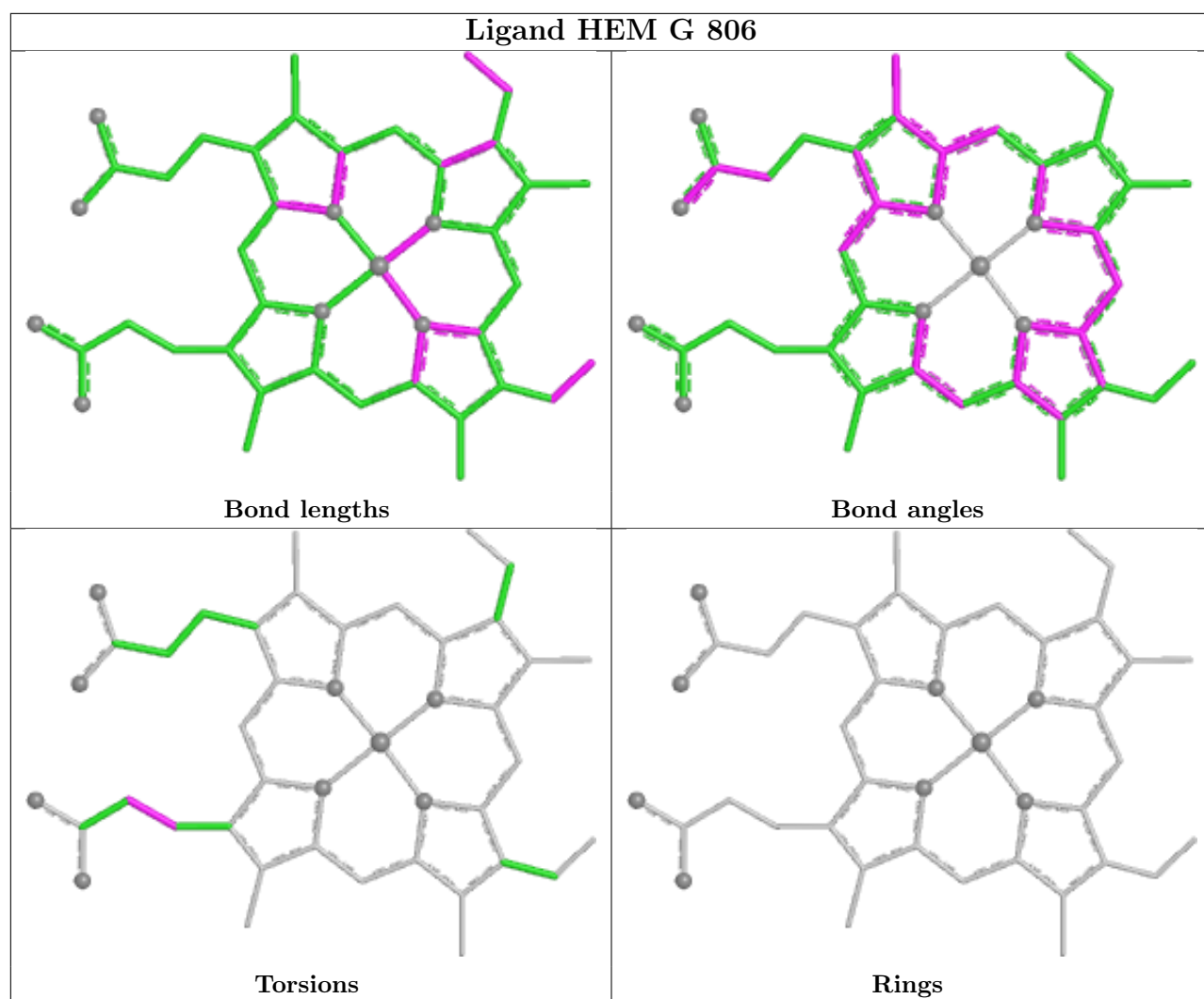


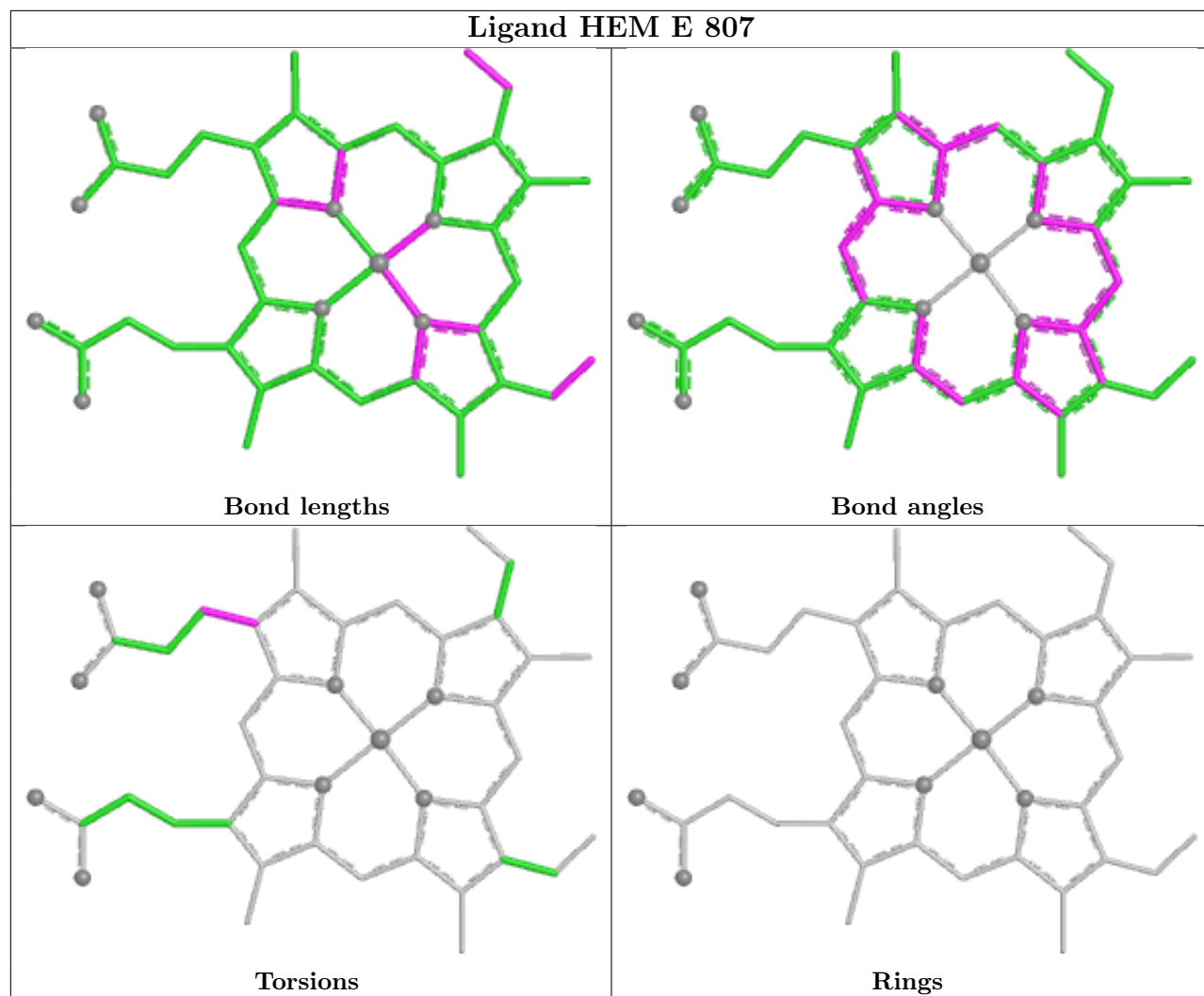


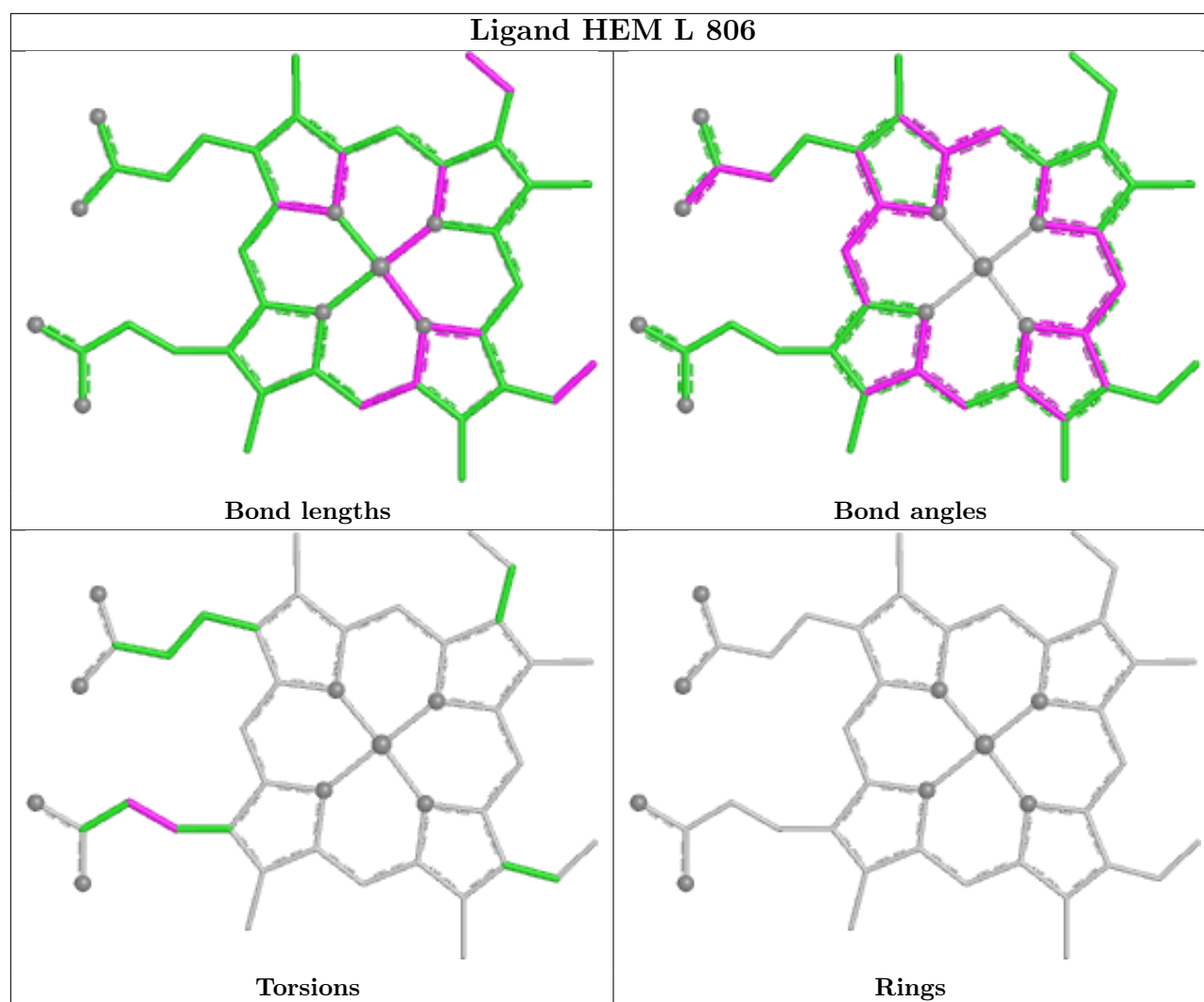


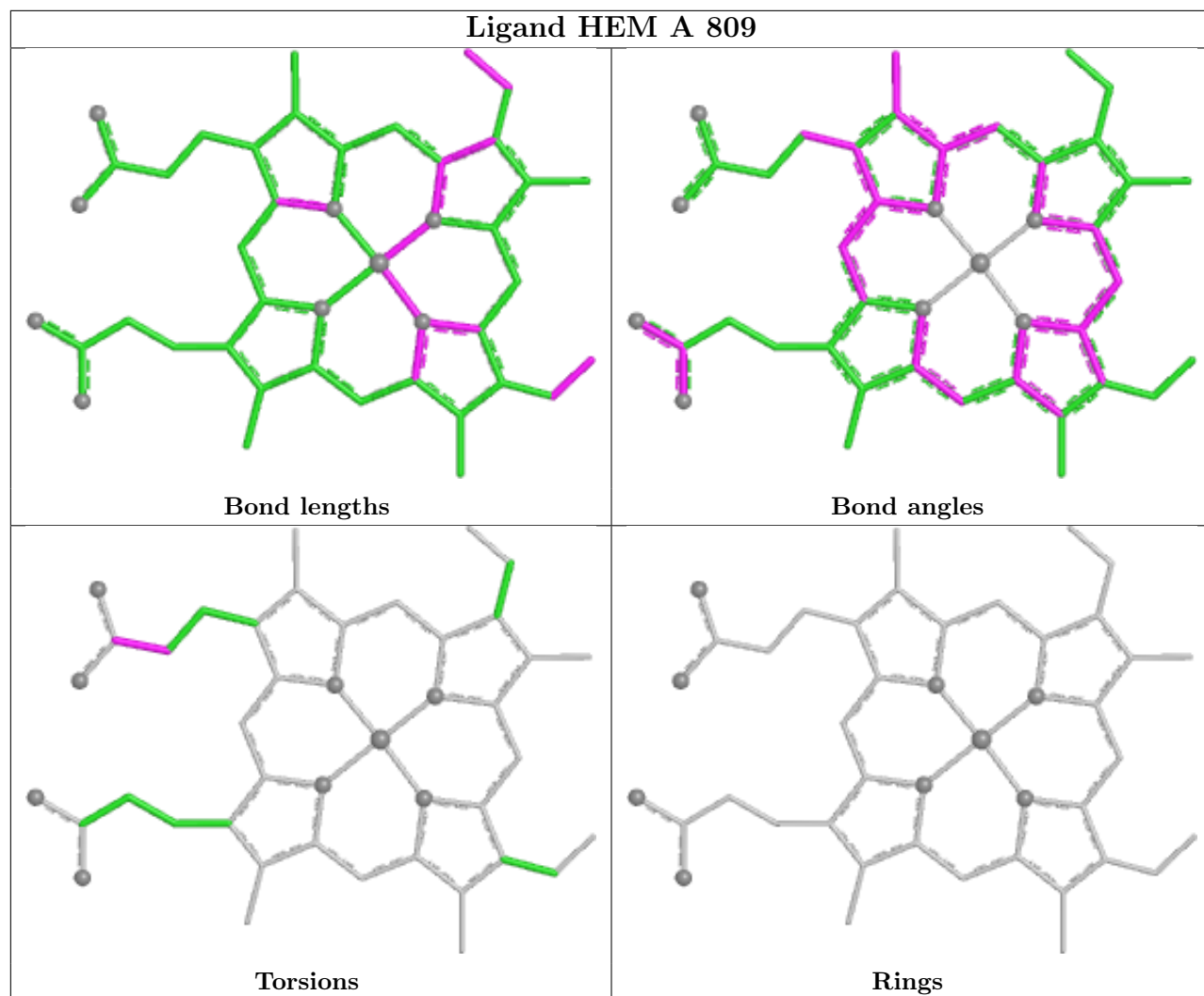


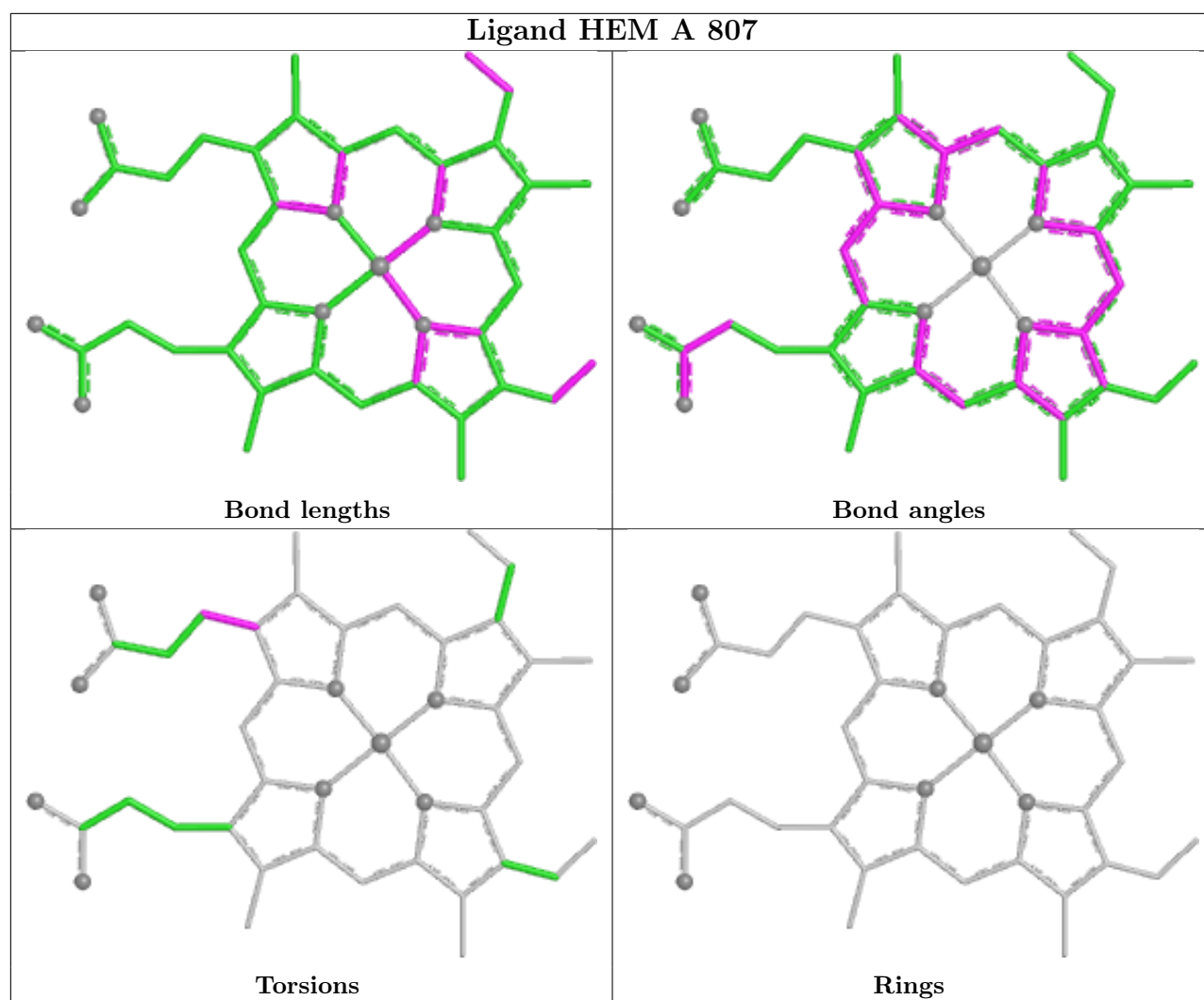


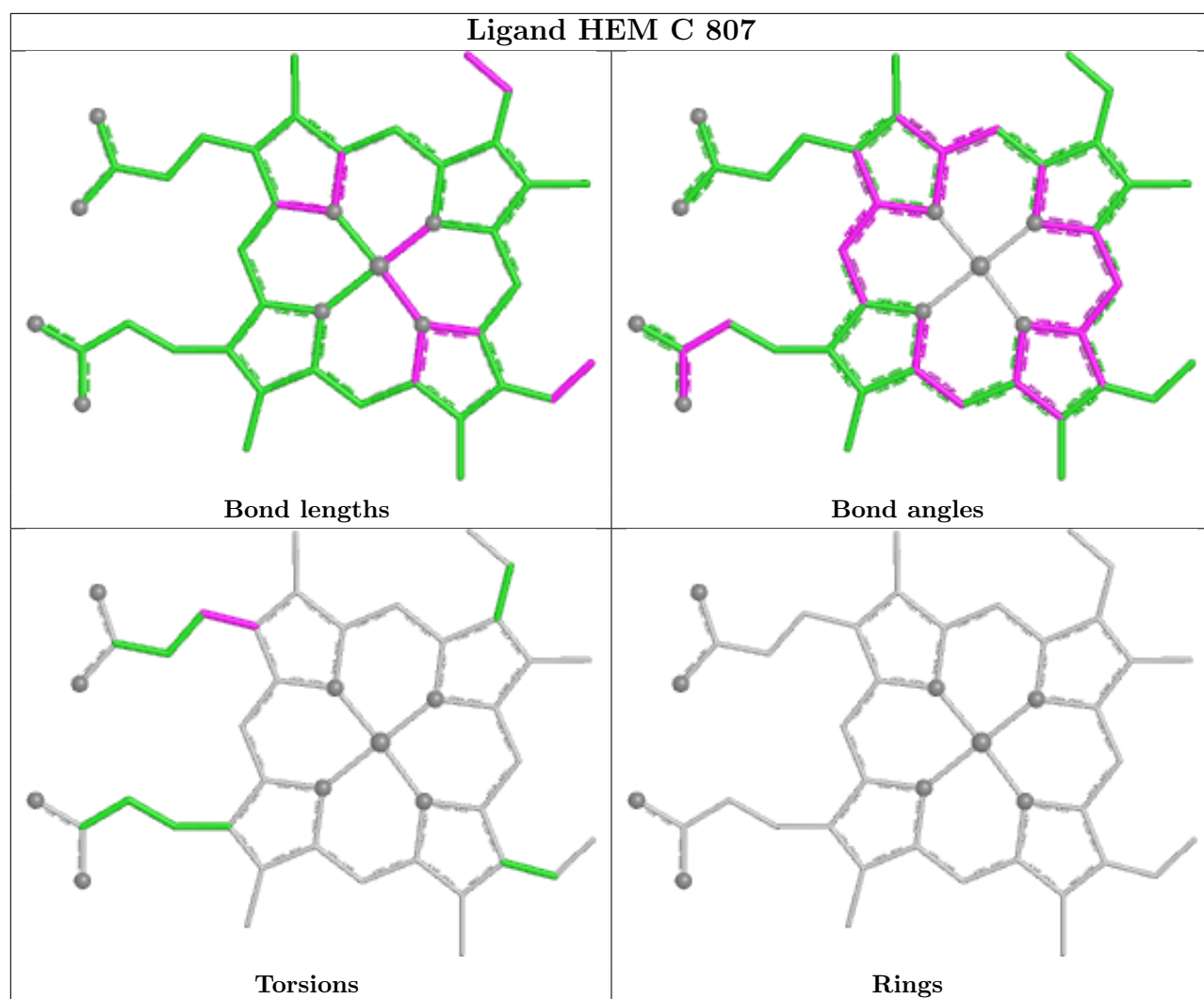


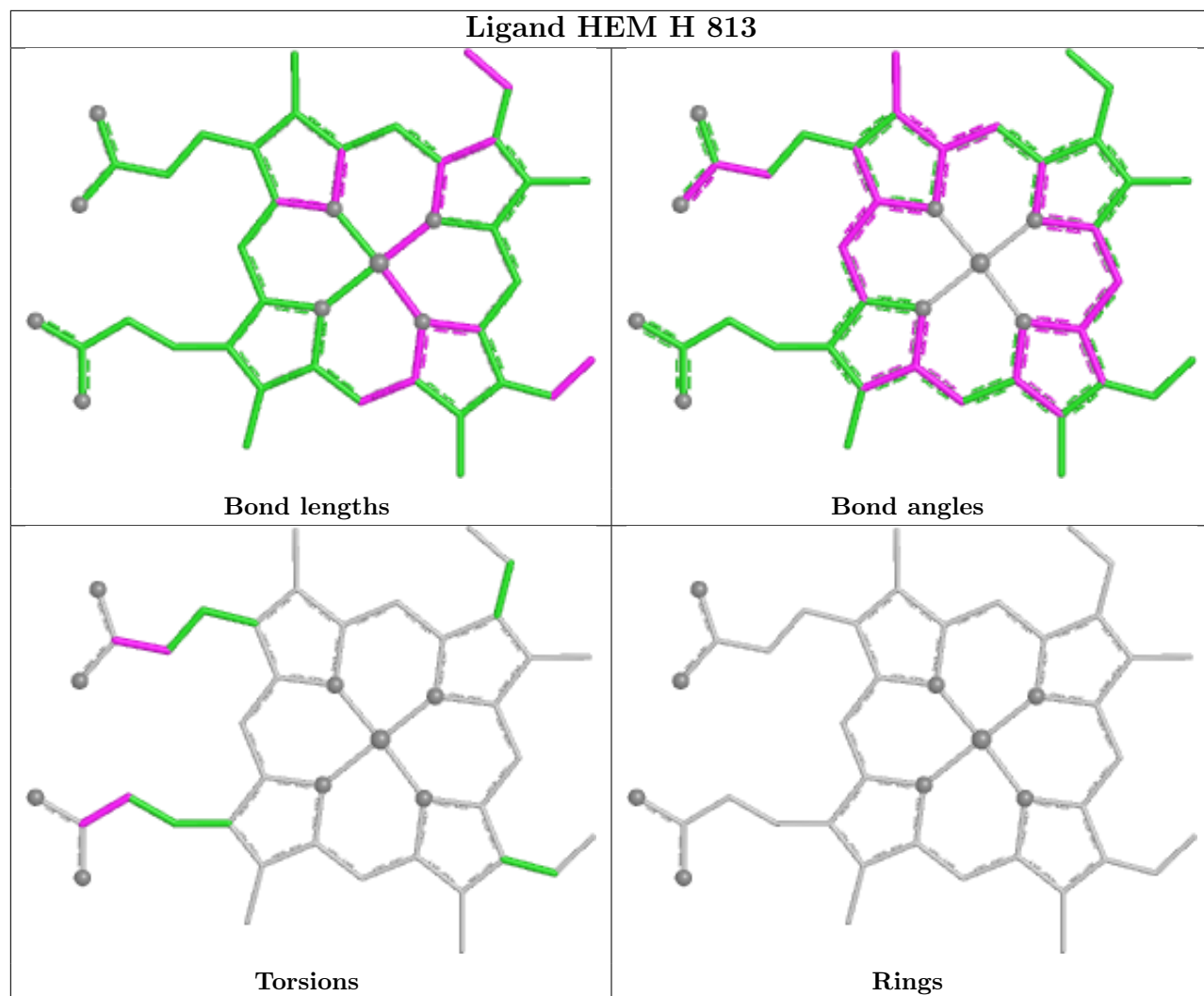


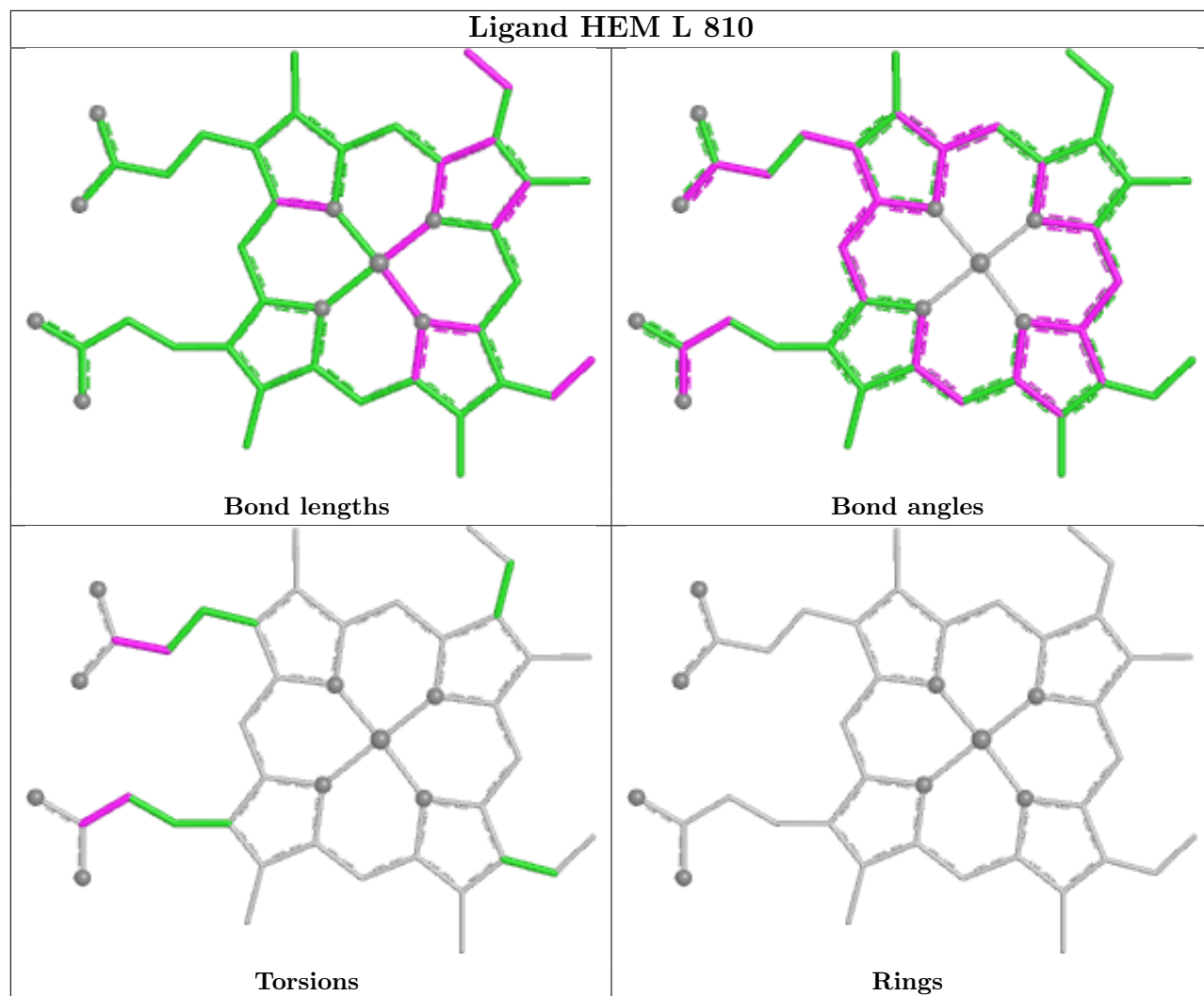


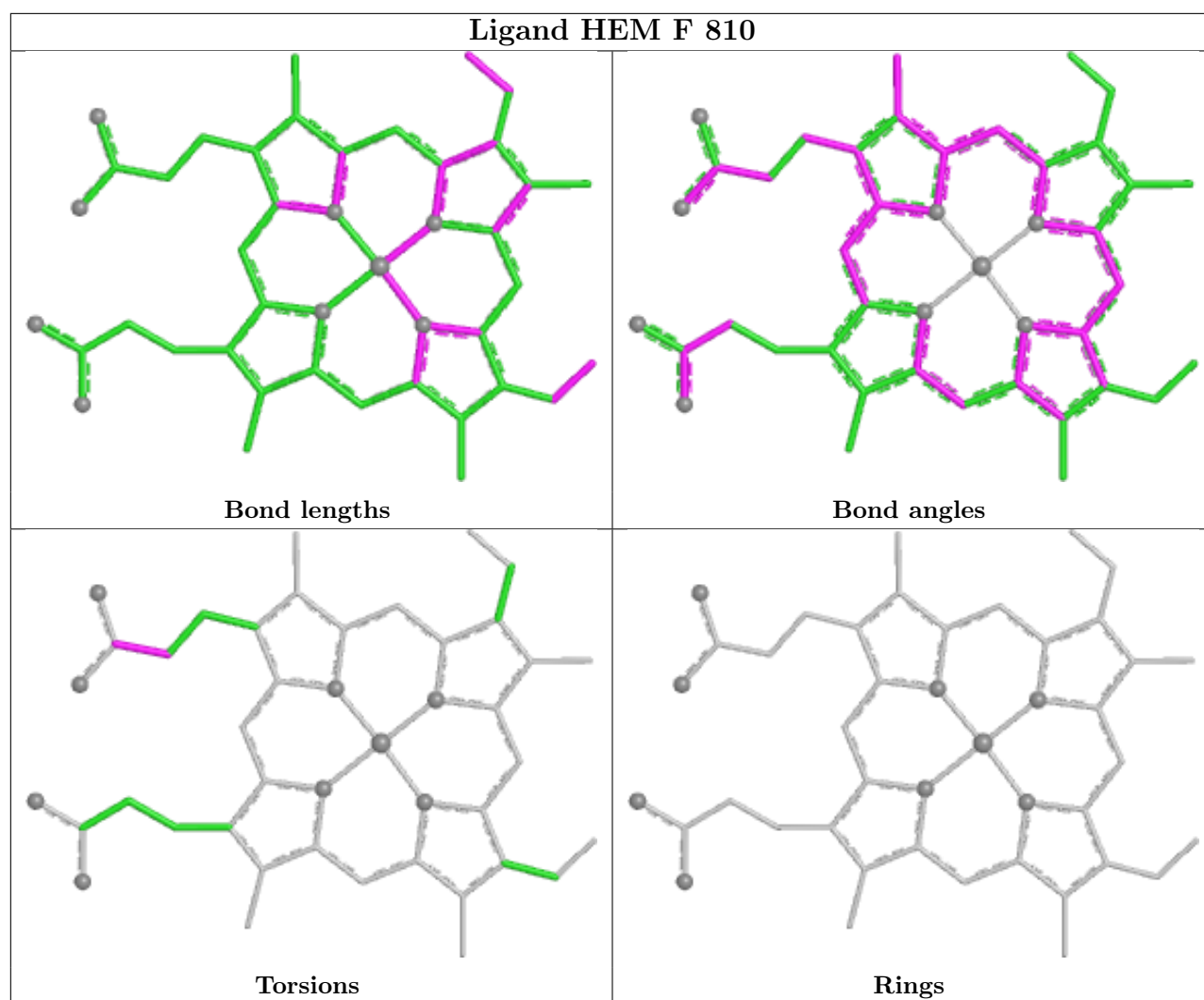












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	659/732 (90%)	-0.42	7 (1%) 78 76	16, 24, 45, 95	0
1	B	660/732 (90%)	-0.23	2 (0%) 90 88	20, 33, 49, 82	0
1	C	659/732 (90%)	-0.18	8 (1%) 76 74	18, 32, 54, 86	0
1	D	659/732 (90%)	-0.21	14 (2%) 63 60	21, 32, 56, 102	0
1	E	659/732 (90%)	0.02	11 (1%) 69 66	23, 38, 59, 104	0
1	F	659/732 (90%)	0.12	7 (1%) 78 76	21, 38, 63, 107	0
1	G	658/732 (89%)	-0.02	10 (1%) 72 69	25, 37, 57, 93	0
1	H	660/732 (90%)	0.01	5 (0%) 82 80	25, 37, 61, 95	0
1	I	659/732 (90%)	0.04	3 (0%) 87 85	26, 39, 58, 76	0
1	J	659/732 (90%)	0.34	13 (1%) 65 62	27, 46, 69, 96	0
1	K	659/732 (90%)	0.35	6 (0%) 81 79	25, 46, 68, 85	0
1	L	659/732 (90%)	0.49	18 (2%) 56 53	30, 51, 76, 89	0
All	All	7909/8784 (90%)	0.03	104 (1%) 75 73	16, 37, 65, 107	0

The worst 5 of 104 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	690	LEU	5.9
1	F	629	VAL	4.9
1	H	690	LEU	4.5
1	J	629	VAL	4.4
1	E	629	VAL	4.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BU3	K	804	6/6	0.77	0.22	74,77,78,79	0
5	ACT	H	806	4/4	0.79	0.27	59,63,64,64	0
4	BU3	E	804	6/6	0.80	0.25	77,79,79,79	0
4	BU3	L	804	6/6	0.80	0.19	69,70,70,72	0
4	BU3	H	805	6/6	0.80	0.20	49,50,51,53	0
5	ACT	K	805	4/4	0.80	0.22	58,58,58,59	0
5	ACT	A	805	4/4	0.81	0.21	47,50,50,51	0
5	ACT	B	806	4/4	0.81	0.20	46,47,48,49	0
5	ACT	D	805	4/4	0.83	0.25	59,62,62,63	0
4	BU3	I	804	6/6	0.83	0.20	60,61,62,62	0
4	BU3	J	804	6/6	0.83	0.20	64,65,66,66	0
4	BU3	K	803	6/6	0.84	0.23	56,58,59,60	0
4	BU3	L	803	6/6	0.84	0.20	57,58,58,60	0
4	BU3	C	804	6/6	0.85	0.16	48,49,49,50	0
4	BU3	A	803	6/6	0.85	0.19	47,47,48,48	0
4	BU3	F	805	6/6	0.85	0.21	58,60,61,62	0
4	BU3	A	804	6/6	0.85	0.17	40,41,42,43	0
4	BU3	C	803	6/6	0.85	0.20	52,53,54,55	0
5	ACT	C	805	4/4	0.86	0.23	58,59,61,61	0
5	ACT	F	806	4/4	0.86	0.18	54,56,56,56	0
5	ACT	G	805	4/4	0.86	0.20	51,51,52,52	0
7	SO2	I	802	3/3	0.86	0.16	63,63,64,71	0
4	BU3	F	804	6/6	0.87	0.16	62,63,64,65	0
4	BU3	D	804	6/6	0.87	0.14	45,46,47,47	0
4	BU3	B	803	6/6	0.87	0.19	50,51,52,52	0
4	BU3	D	803	6/6	0.88	0.18	50,54,54,55	0
5	ACT	L	805	4/4	0.88	0.22	61,63,63,64	0
4	BU3	H	803	6/6	0.88	0.21	62,63,64,65	0
3	SX	B	802	2/2	0.88	0.17	51,51,51,52	0
4	BU3	F	803	6/6	0.89	0.16	49,50,50,50	0
5	ACT	J	805	4/4	0.89	0.23	62,62,62,63	0
4	BU3	I	803	6/6	0.89	0.16	48,50,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BU3	E	803	6/6	0.89	0.18	50,51,54,55	0
4	BU3	H	804	6/6	0.89	0.16	61,62,62,64	0
4	BU3	G	803	6/6	0.89	0.14	49,50,51,52	0
4	BU3	B	804	6/6	0.90	0.14	50,52,53,53	0
4	BU3	G	804	6/6	0.90	0.16	58,59,61,61	0
5	ACT	E	805	4/4	0.90	0.19	58,60,61,61	0
4	BU3	B	805	6/6	0.90	0.16	55,59,59,60	0
3	SX	A	802	2/2	0.90	0.17	45,45,45,50	2
4	BU3	J	803	6/6	0.91	0.18	55,57,58,58	0
3	SX	F	802	2/2	0.91	0.21	69,69,69,73	0
3	SX	K	802	2/2	0.92	0.12	67,67,67,71	0
3	SX	E	802	2/2	0.92	0.16	66,66,66,68	0
5	ACT	I	805	4/4	0.92	0.16	50,50,52,52	0
3	SX	H	802	2/2	0.92	0.13	58,58,58,61	0
3	SX	C	802	2/2	0.93	0.19	55,55,55,56	0
3	SX	G	802	2/2	0.94	0.16	31,31,31,32	2
7	SO2	G	814	3/3	0.94	0.21	74,74,74,76	3
3	SX	J	802	2/2	0.95	0.09	57,57,57,62	0
6	HEM	L	813	43/43	0.95	0.10	46,48,58,65	0
7	SO2	A	814	3/3	0.95	0.12	16,16,16,16	3
2	CU1	H	801	1/1	0.95	0.07	45,45,45,45	0
3	SX	L	802	2/2	0.95	0.10	65,65,65,68	0
6	HEM	J	807	43/43	0.96	0.08	34,36,38,39	0
6	HEM	J	811	43/43	0.96	0.09	29,31,41,51	0
6	HEM	K	813	43/43	0.96	0.09	39,41,52,55	0
6	HEM	L	807	43/43	0.96	0.09	37,39,42,44	0
6	HEM	L	810	43/43	0.96	0.09	31,32,39,43	0
6	HEM	L	811	43/43	0.96	0.09	34,37,45,49	0
6	HEM	L	812	43/43	0.96	0.09	37,39,41,42	0
6	HEM	C	813	43/43	0.96	0.08	30,32,45,50	0
6	HEM	H	807	43/43	0.96	0.08	32,33,35,36	0
7	SO2	D	802	3/3	0.96	0.13	51,51,53,54	0
6	HEM	I	809	43/43	0.96	0.09	26,27,30,32	0
6	HEM	I	813	43/43	0.96	0.09	33,35,46,49	0
6	HEM	D	810	43/43	0.97	0.07	21,22,25,28	0
6	HEM	E	807	43/43	0.97	0.07	28,29,31,33	0
6	HEM	E	808	43/43	0.97	0.07	23,24,25,27	0
6	HEM	E	809	43/43	0.97	0.07	24,25,26,26	0
6	HEM	E	810	43/43	0.97	0.07	24,25,29,34	0
6	HEM	E	811	43/43	0.97	0.08	27,29,36,43	0
6	HEM	E	812	43/43	0.97	0.07	26,28,31,32	0
6	HEM	E	813	43/43	0.97	0.08	30,32,44,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	HEM	F	807	43/43	0.97	0.07	25,29,32,33	0
6	HEM	F	808	43/43	0.97	0.08	25,28,32,35	0
6	HEM	F	809	43/43	0.97	0.08	28,29,30,31	0
6	HEM	F	811	43/43	0.97	0.07	21,22,26,31	0
6	HEM	F	812	43/43	0.97	0.08	21,23,32,42	0
6	HEM	F	813	43/43	0.97	0.07	21,23,24,26	0
6	HEM	F	814	43/43	0.97	0.08	24,26,34,39	0
2	CU1	L	801	1/1	0.97	0.05	55,55,55,55	0
6	HEM	H	808	43/43	0.97	0.07	24,29,31,33	0
6	HEM	H	809	43/43	0.97	0.08	29,31,34,39	0
6	HEM	H	810	43/43	0.97	0.07	28,30,31,32	0
6	HEM	H	811	43/43	0.97	0.08	25,27,30,33	0
6	HEM	H	812	43/43	0.97	0.08	23,26,35,43	0
6	HEM	H	813	43/43	0.97	0.07	26,27,28,29	0
6	HEM	H	814	43/43	0.97	0.08	25,26,36,40	0
6	HEM	I	806	43/43	0.97	0.07	27,30,32,32	0
6	HEM	I	807	43/43	0.97	0.07	29,32,33,34	0
6	HEM	I	808	43/43	0.97	0.09	27,28,30,30	0
2	CU1	J	801	1/1	0.97	0.05	51,51,51,51	0
6	HEM	I	810	43/43	0.97	0.07	24,26,30,35	0
6	HEM	I	811	43/43	0.97	0.08	25,26,35,43	0
6	HEM	I	812	43/43	0.97	0.08	27,28,31,33	0
6	HEM	A	811	43/43	0.97	0.07	19,20,28,33	0
6	HEM	J	806	43/43	0.97	0.07	28,30,32,34	0
6	HEM	A	812	43/43	0.97	0.07	18,19,22,25	0
6	HEM	J	808	43/43	0.97	0.07	27,28,29,30	0
6	HEM	J	809	43/43	0.97	0.07	29,31,33,35	0
6	HEM	A	813	43/43	0.97	0.07	21,23,31,34	0
6	HEM	J	812	43/43	0.97	0.08	34,36,37,39	0
6	HEM	J	813	43/43	0.97	0.09	37,40,53,62	0
6	HEM	K	806	43/43	0.97	0.08	26,28,31,32	0
6	HEM	K	807	43/43	0.97	0.09	38,41,45,49	0
6	HEM	K	808	43/43	0.97	0.07	27,27,29,31	0
6	HEM	K	809	43/43	0.97	0.08	28,31,34,35	0
6	HEM	K	810	43/43	0.97	0.08	27,29,33,37	0
6	HEM	K	811	43/43	0.97	0.08	27,30,39,47	0
6	HEM	K	812	43/43	0.97	0.08	31,34,36,37	0
6	HEM	B	807	43/43	0.97	0.07	21,22,23,24	0
6	HEM	L	806	43/43	0.97	0.07	24,30,33,34	0
6	HEM	B	811	43/43	0.97	0.07	21,22,28,34	0
6	HEM	L	808	43/43	0.97	0.08	31,33,35,38	0
6	HEM	L	809	43/43	0.97	0.09	32,34,38,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	HEM	B	812	43/43	0.97	0.07	23,24,33,43	0
6	HEM	B	813	43/43	0.97	0.08	24,26,29,30	0
6	HEM	B	814	43/43	0.97	0.08	29,31,43,46	0
6	HEM	C	811	43/43	0.97	0.07	24,26,36,46	0
6	HEM	G	806	43/43	0.97	0.07	27,28,29,29	0
6	HEM	G	808	43/43	0.97	0.07	25,26,28,30	0
6	HEM	G	809	43/43	0.97	0.07	24,27,28,28	0
6	HEM	G	810	43/43	0.97	0.07	24,24,29,31	0
6	HEM	G	811	43/43	0.97	0.09	28,31,43,49	0
6	HEM	G	812	43/43	0.97	0.07	26,28,32,33	0
6	HEM	G	813	43/43	0.97	0.08	28,31,38,45	0
2	CU1	K	801	1/1	0.97	0.07	53,53,53,53	0
6	HEM	D	806	43/43	0.97	0.08	28,30,32,33	0
6	HEM	D	807	43/43	0.97	0.07	21,22,24,25	0
6	HEM	D	808	43/43	0.97	0.07	25,27,31,35	0
6	HEM	C	808	43/43	0.98	0.07	18,19,21,23	0
6	HEM	C	809	43/43	0.98	0.07	18,20,21,21	0
6	HEM	C	810	43/43	0.98	0.06	20,21,24,28	0
6	HEM	A	809	43/43	0.98	0.06	14,15,17,19	0
6	HEM	C	812	43/43	0.98	0.06	23,25,28,31	0
6	HEM	B	808	43/43	0.98	0.06	24,25,26,28	0
6	HEM	F	810	43/43	0.98	0.07	25,27,27,27	0
6	HEM	B	809	43/43	0.98	0.07	20,22,23,27	0
6	HEM	B	810	43/43	0.98	0.06	20,23,25,27	0
6	HEM	A	810	43/43	0.98	0.07	16,17,21,24	0
6	HEM	D	809	43/43	0.98	0.06	21,22,23,25	0
6	HEM	G	807	43/43	0.98	0.06	25,26,28,29	0
6	HEM	J	810	43/43	0.98	0.07	26,28,33,37	0
6	HEM	A	806	43/43	0.98	0.07	19,20,21,21	0
6	HEM	D	811	43/43	0.98	0.07	21,23,33,42	0
6	HEM	D	812	43/43	0.98	0.07	20,22,24,27	0
6	HEM	D	813	43/43	0.98	0.07	25,26,34,36	0
6	HEM	E	806	43/43	0.98	0.07	23,24,26,26	0
6	HEM	A	807	43/43	0.98	0.07	16,16,17,17	0
6	HEM	A	808	43/43	0.98	0.06	17,18,20,23	0
6	HEM	C	806	43/43	0.98	0.05	16,17,18,19	0
6	HEM	C	807	43/43	0.98	0.07	21,23,23,24	0
2	CU1	C	801	1/1	0.99	0.02	31,31,31,31	0
2	CU1	D	801	1/1	0.99	0.03	33,33,33,33	0
2	CU1	G	801	1/1	0.99	0.03	34,34,34,34	0
2	CU1	E	801	1/1	0.99	0.03	37,37,37,37	0
2	CU1	F	801	1/1	0.99	0.03	38,38,38,38	0

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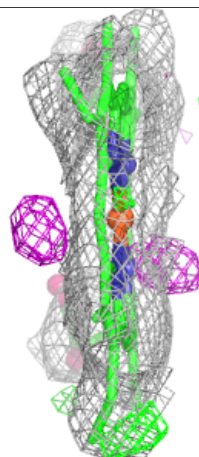
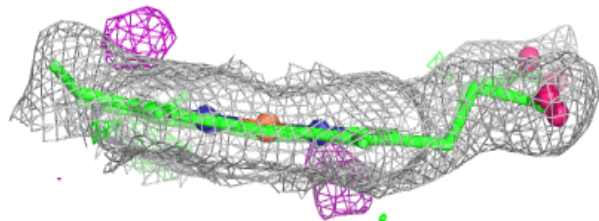
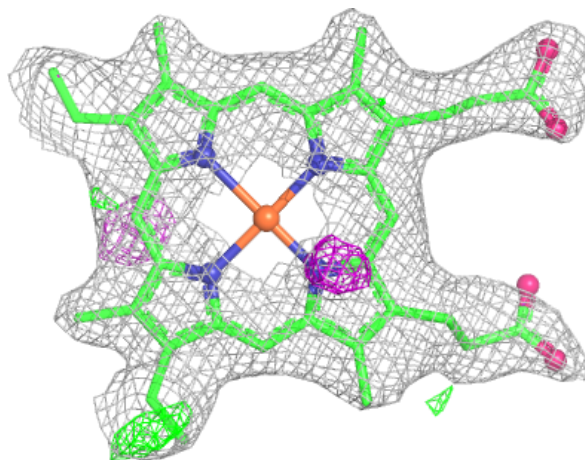
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CU1	A	801	1/1	0.99	0.03	26,26,26,26	0
2	CU1	I	801	1/1	0.99	0.03	39,39,39,39	0
2	CU1	B	801	1/1	0.99	0.02	35,35,35,35	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

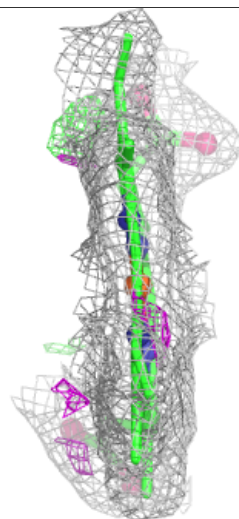
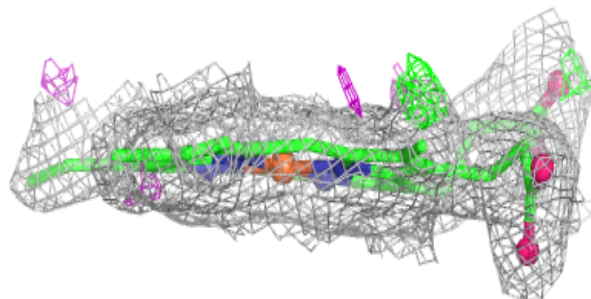
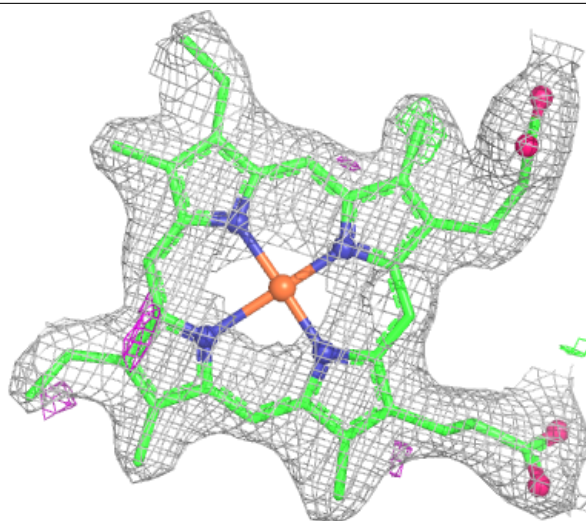
Electron density around HEM L 813:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



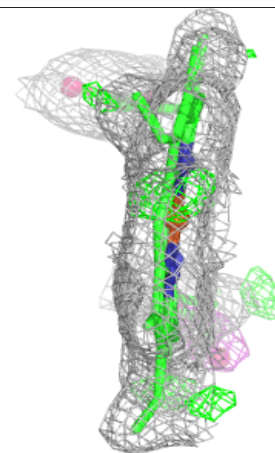
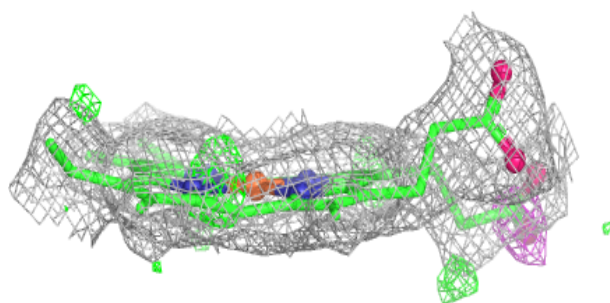
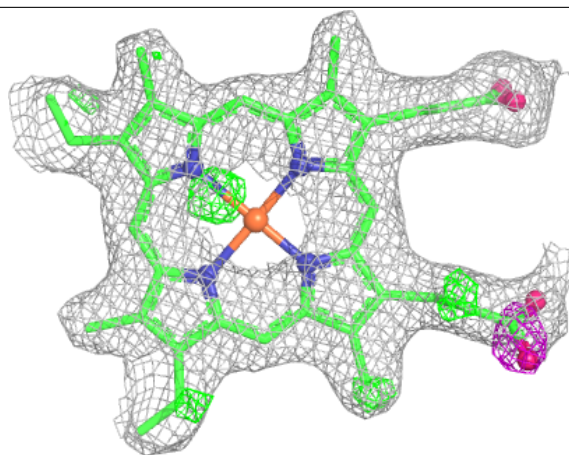
Electron density around HEM J 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



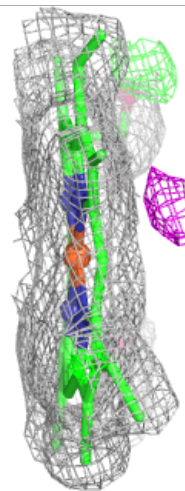
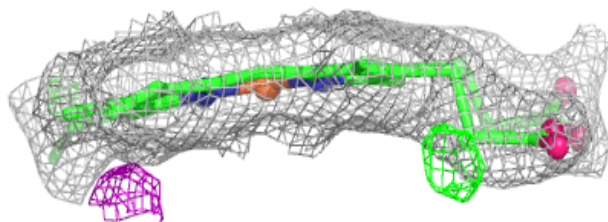
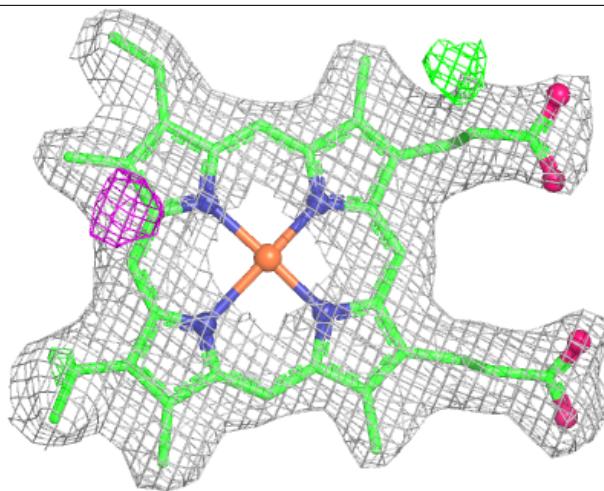
Electron density around HEM J 811:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



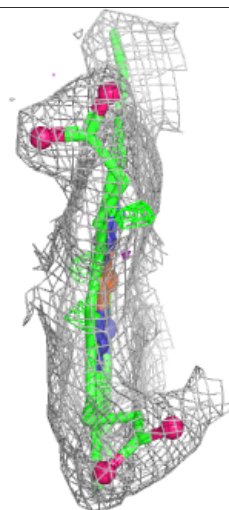
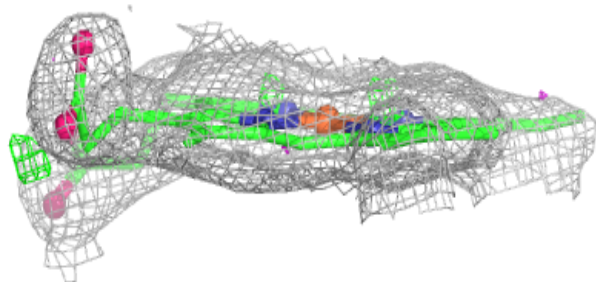
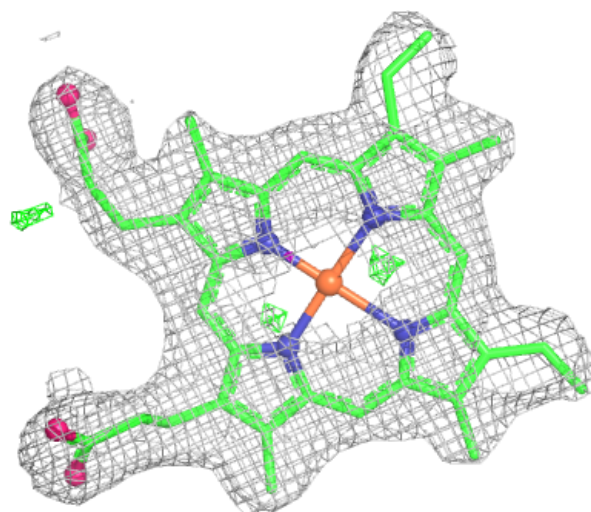
Electron density around HEM K 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



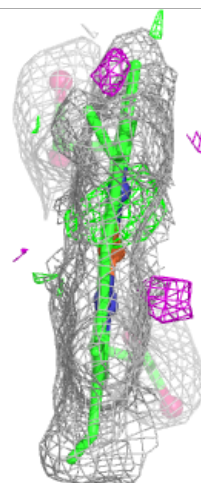
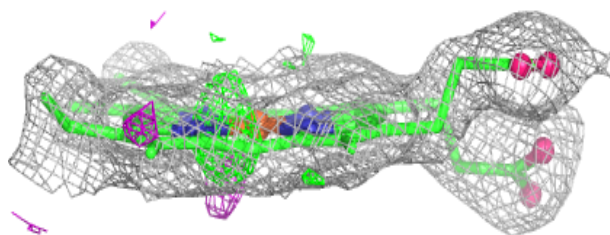
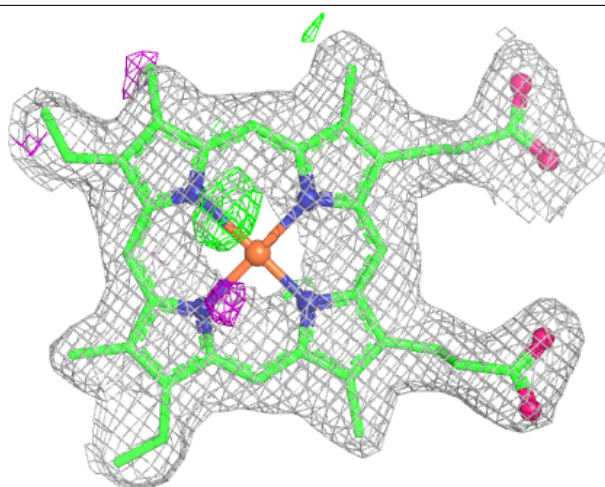
Electron density around HEM L 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



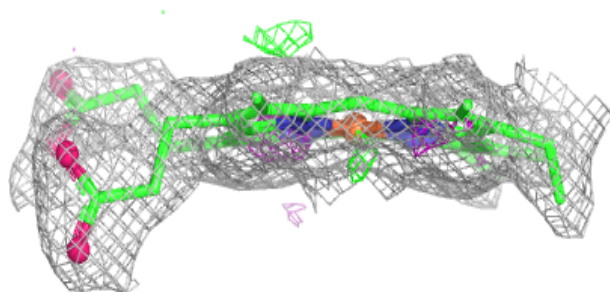
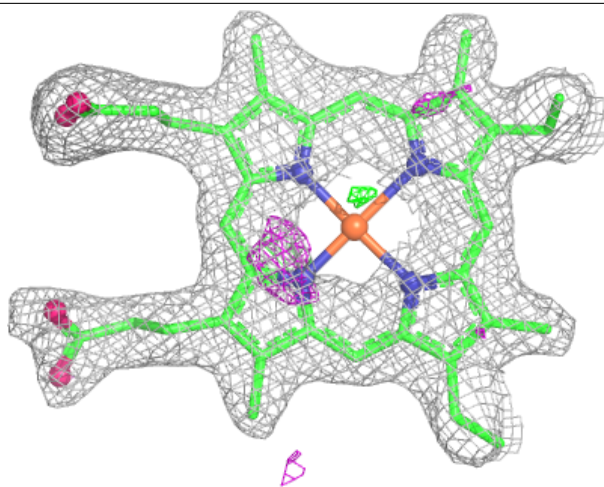
Electron density around HEM L 810:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



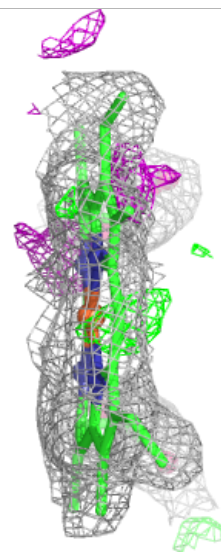
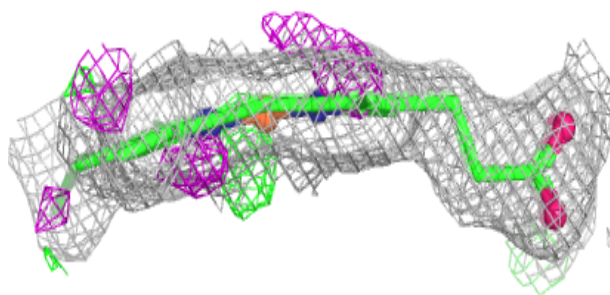
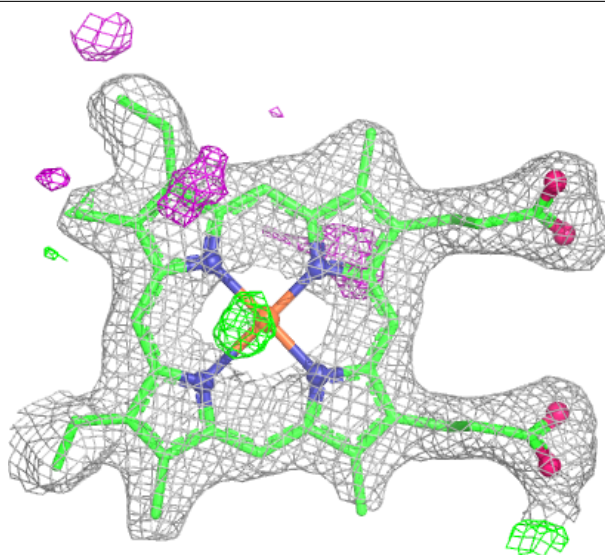
Electron density around HEM L 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



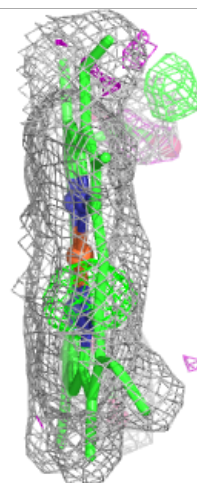
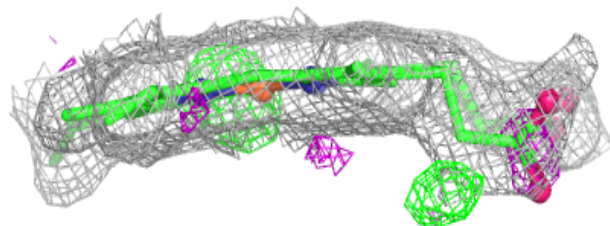
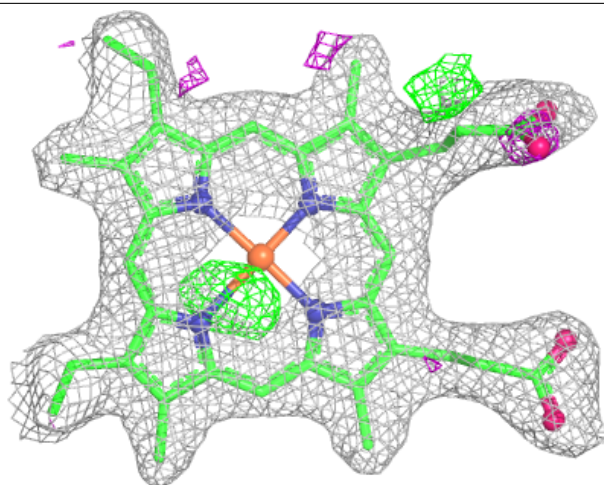
Electron density around HEM L 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



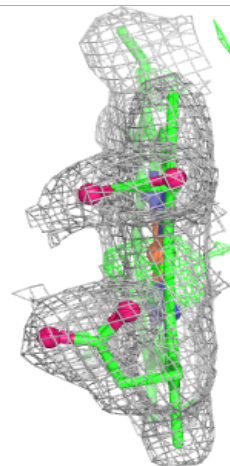
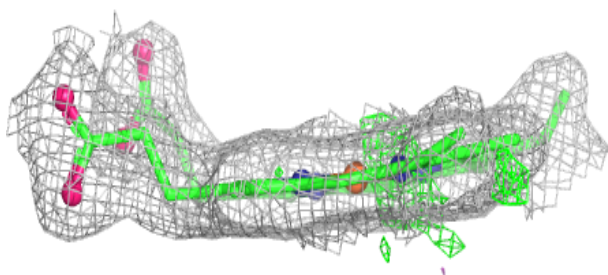
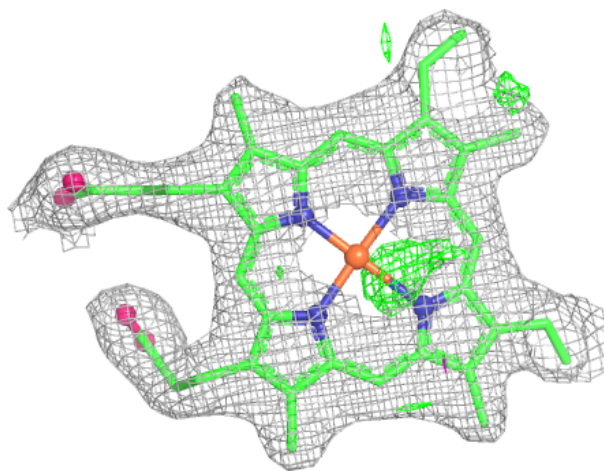
Electron density around HEM C 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



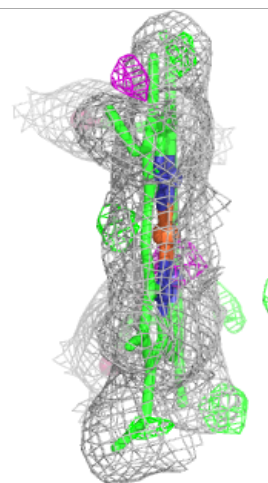
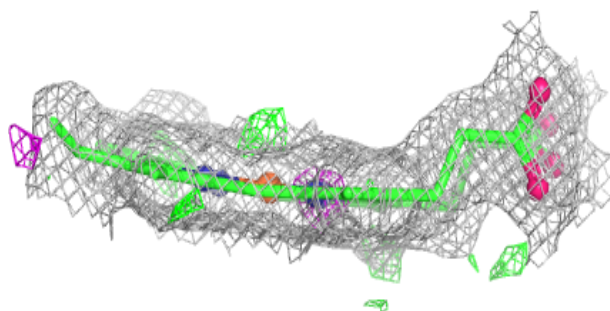
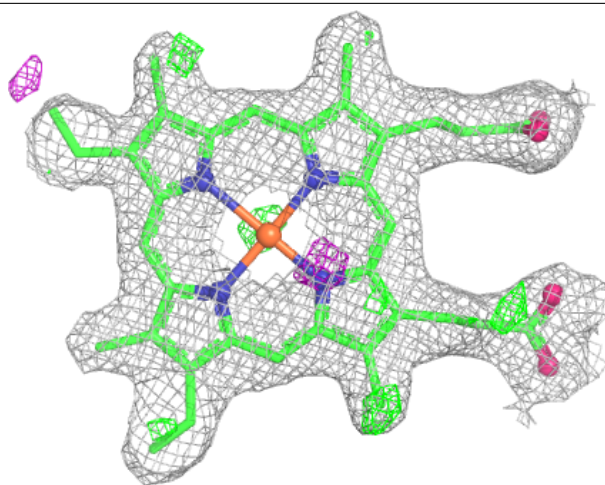
Electron density around HEM H 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



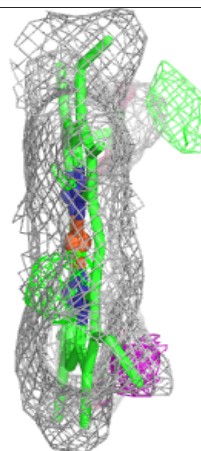
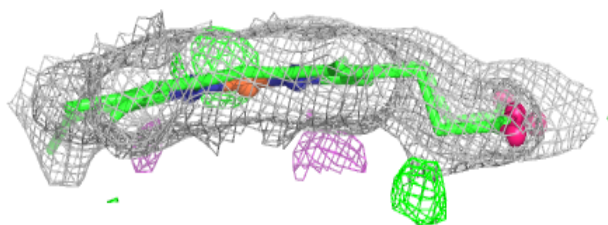
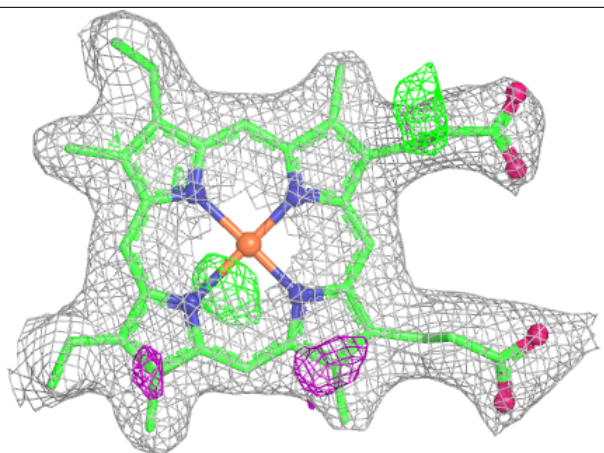
Electron density around HEM I 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



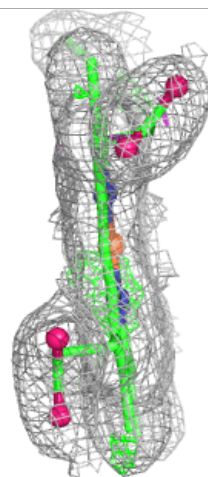
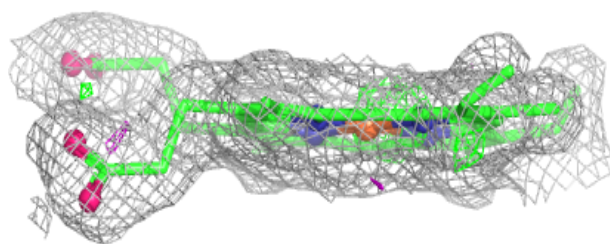
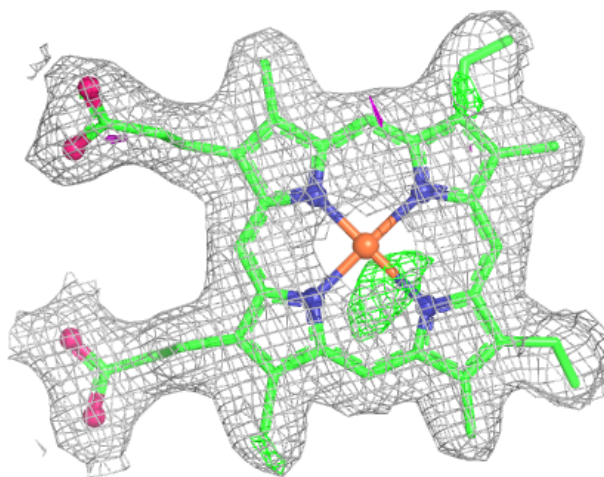
Electron density around HEM I 813:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



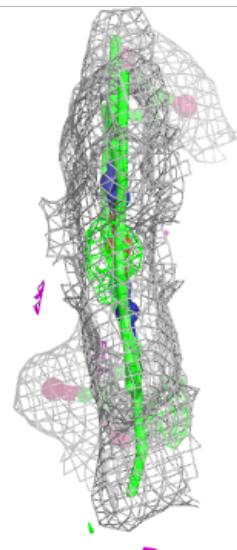
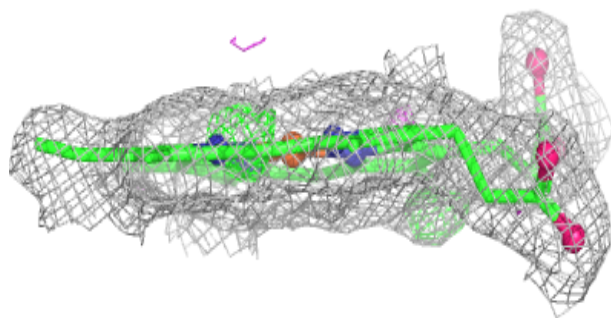
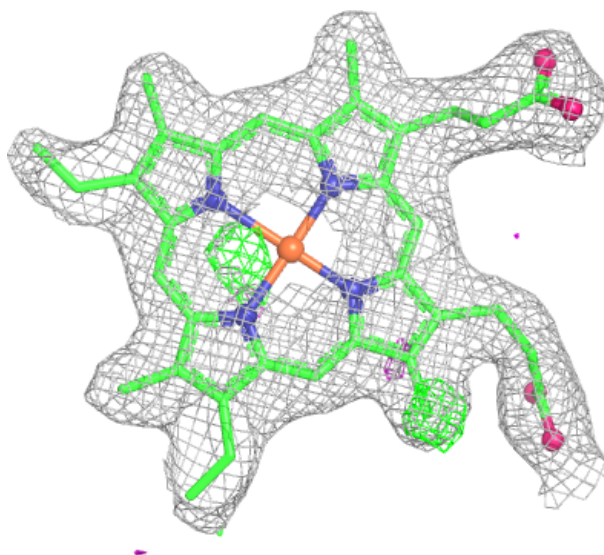
Electron density around HEM D 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



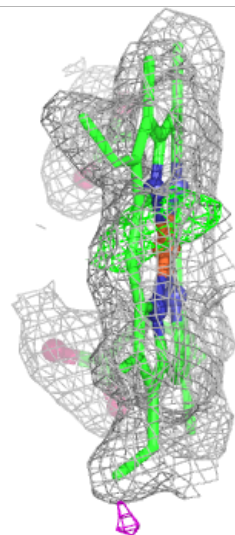
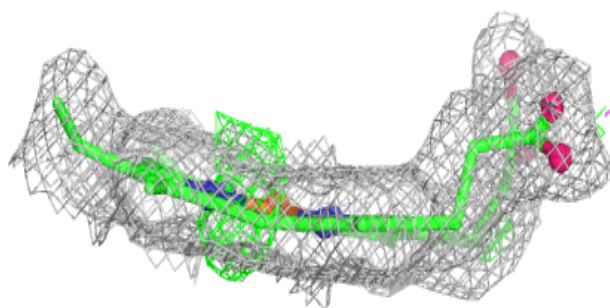
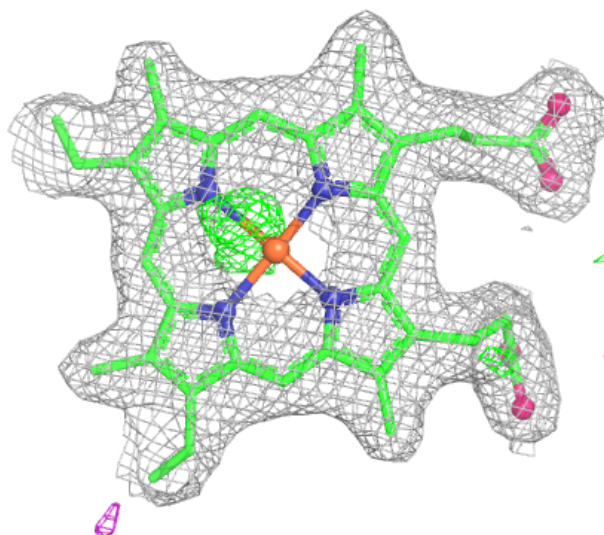
Electron density around HEM E 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



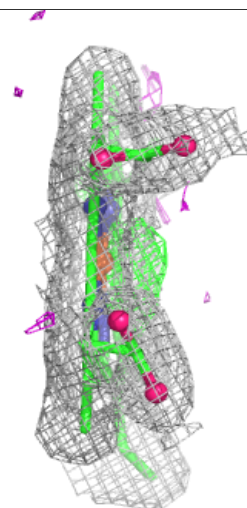
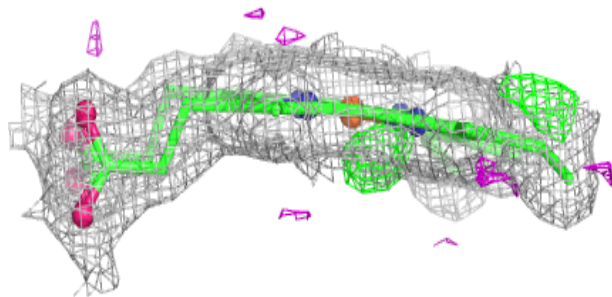
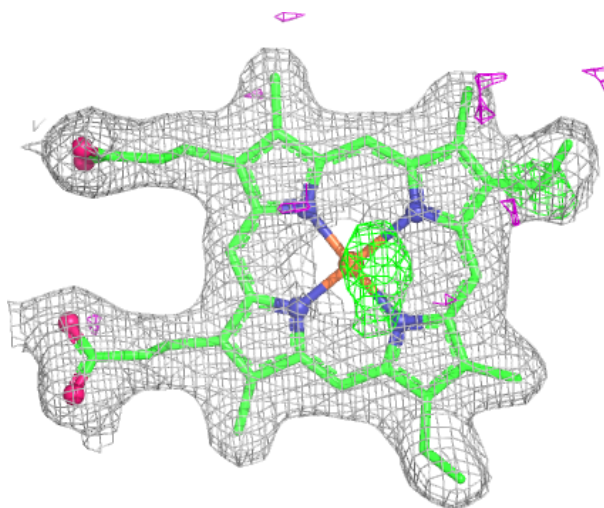
Electron density around HEM E 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



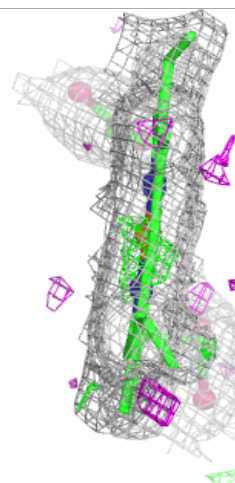
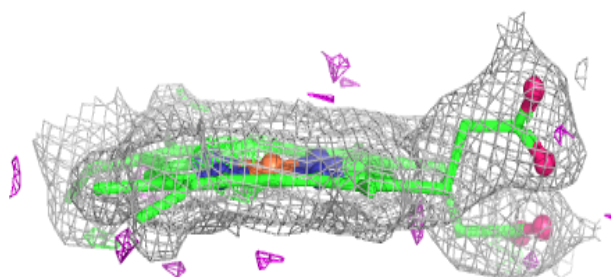
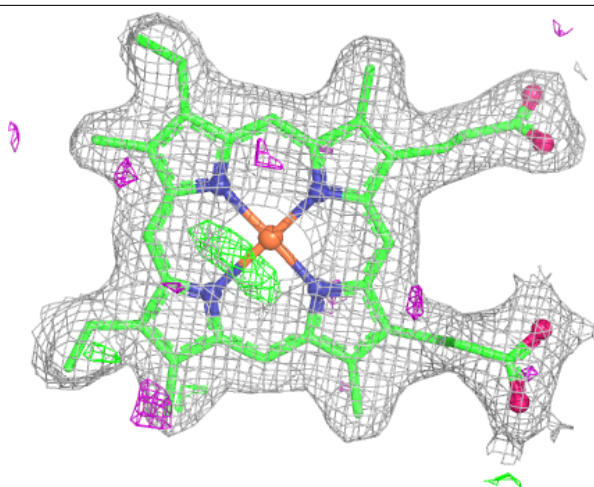
Electron density around HEM E 809:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



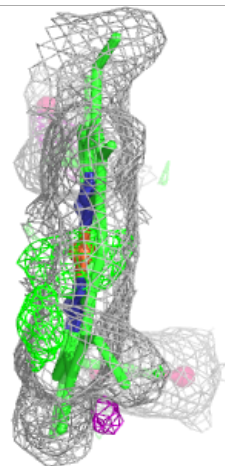
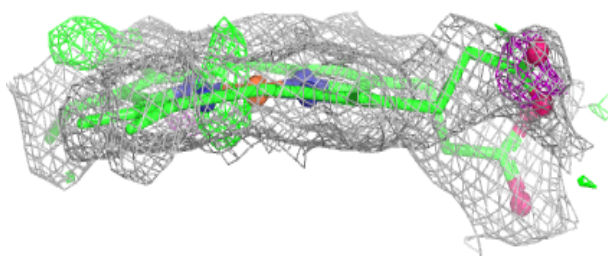
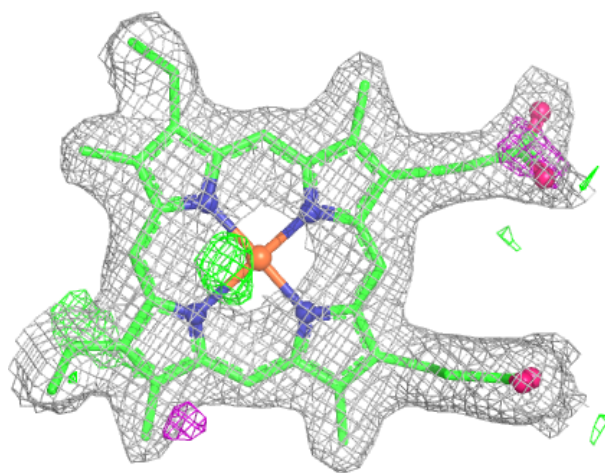
Electron density around HEM E 810:

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and green (positive)



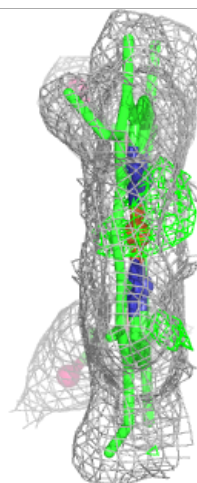
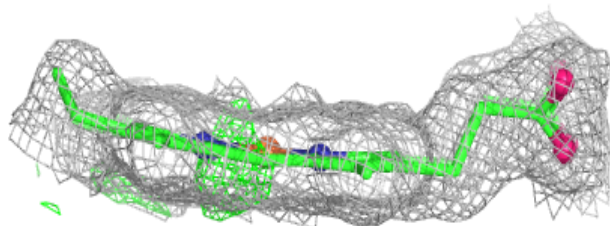
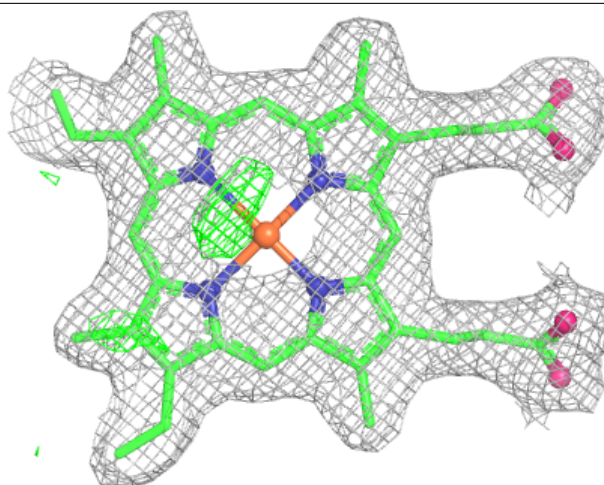
Electron density around HEM E 811:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



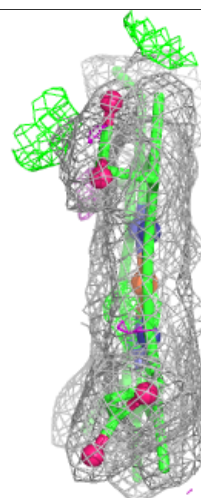
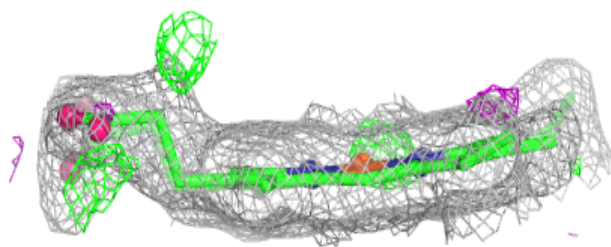
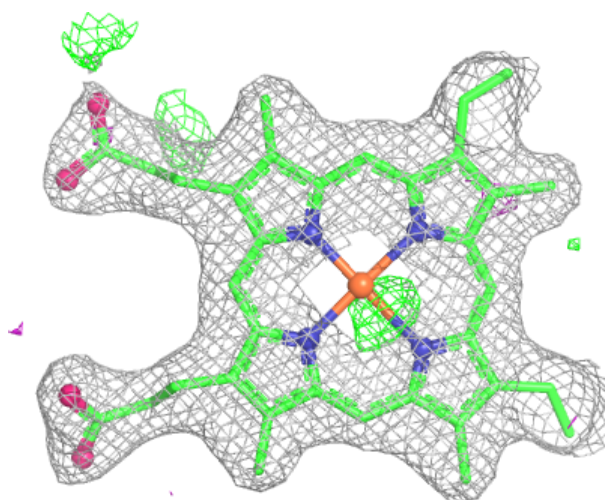
Electron density around HEM E 812:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



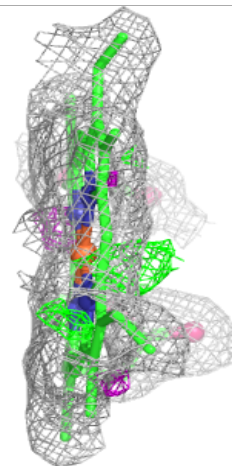
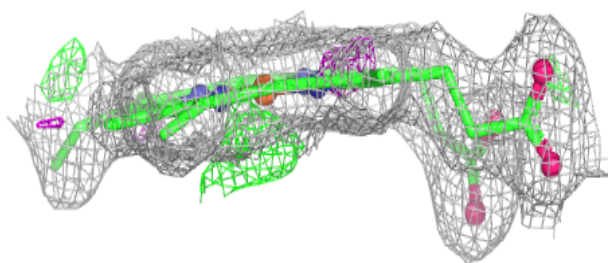
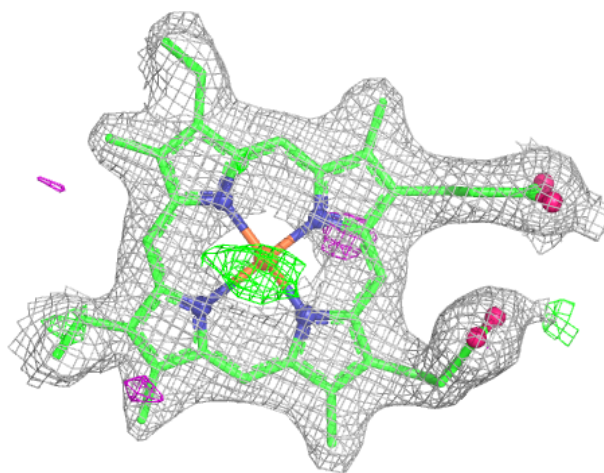
Electron density around HEM E 813:

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and green (positive)



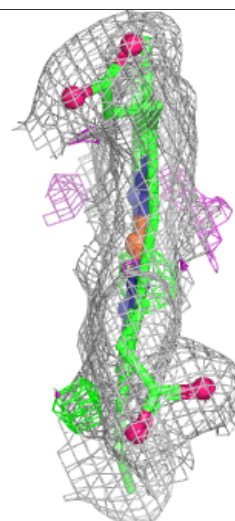
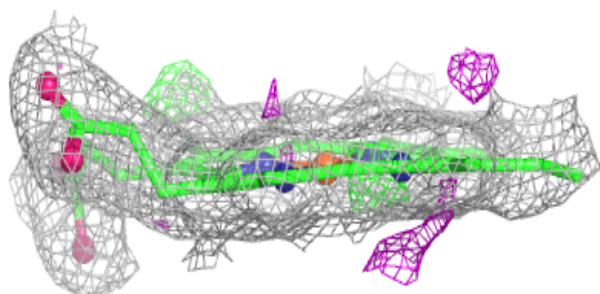
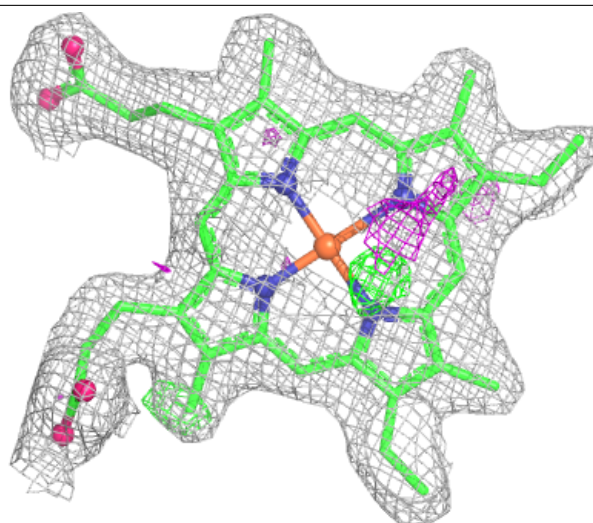
Electron density around HEM F 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



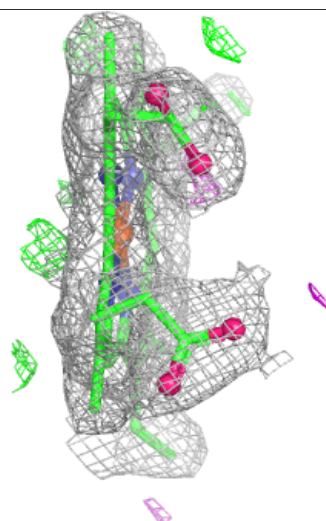
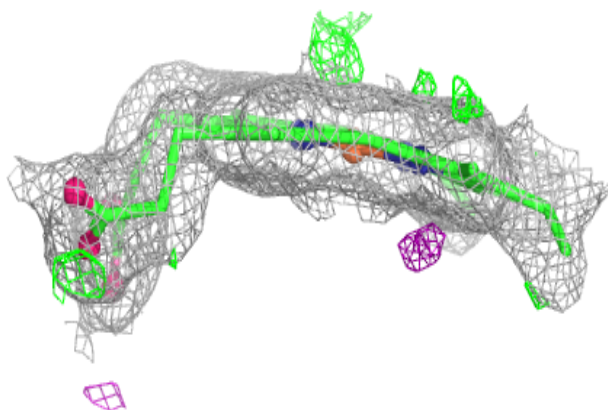
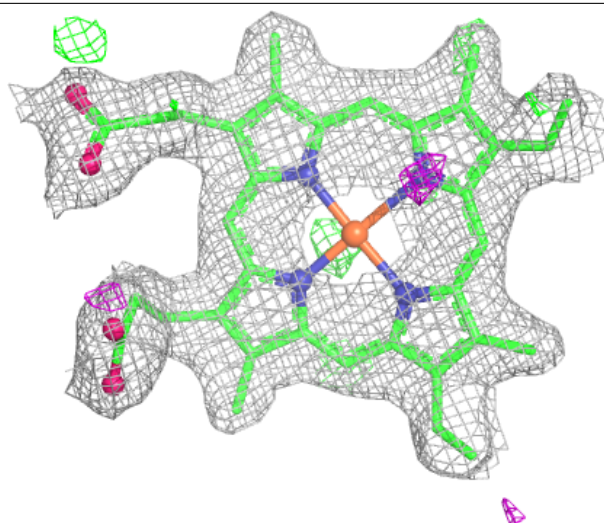
Electron density around HEM F 808:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



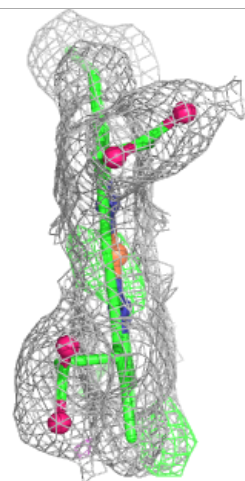
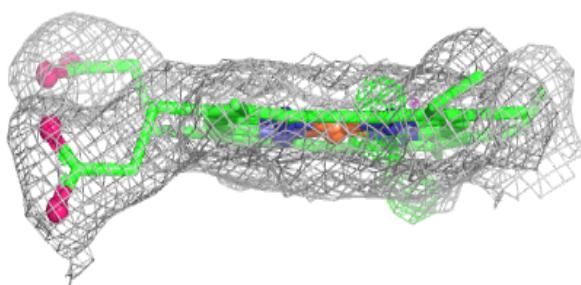
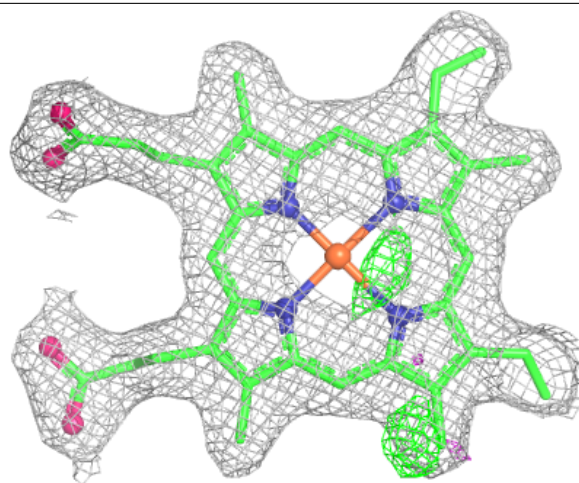
Electron density around HEM F 809:

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and green (positive)



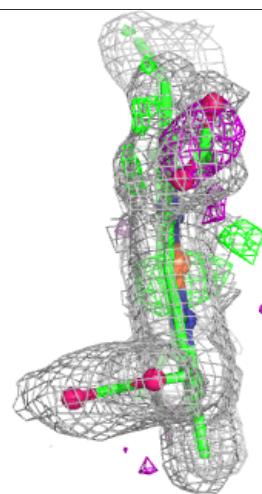
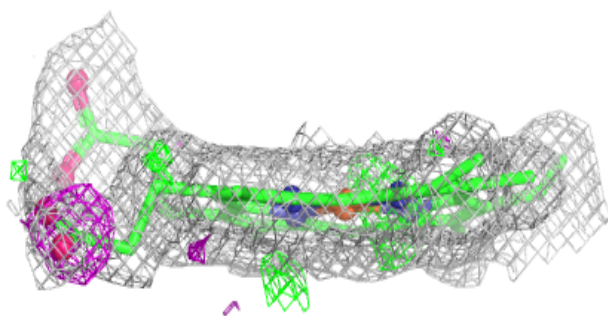
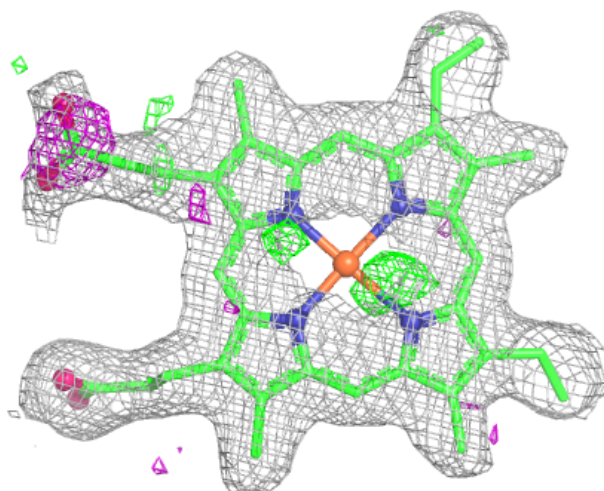
Electron density around HEM F 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



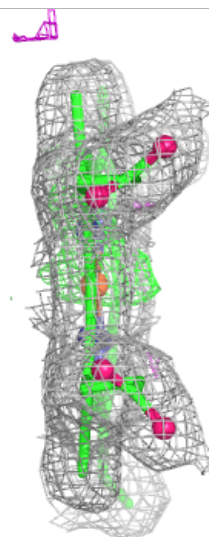
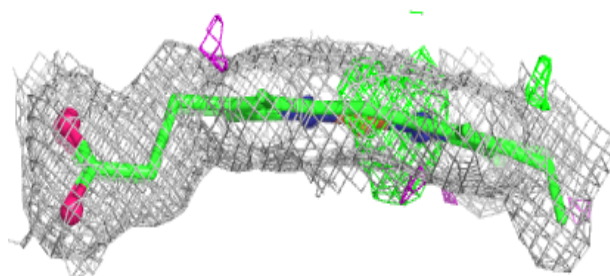
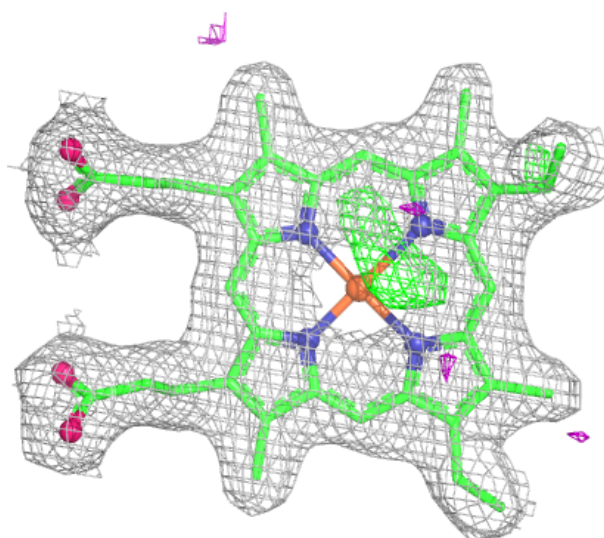
Electron density around HEM F 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



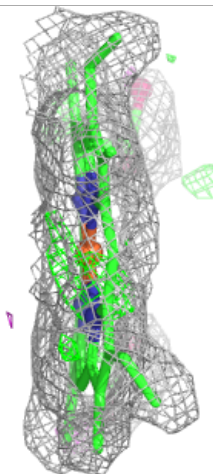
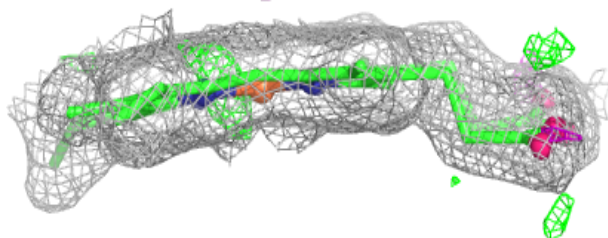
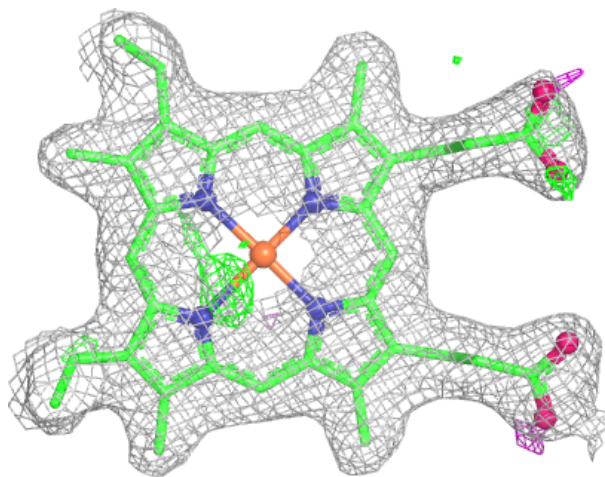
Electron density around HEM F 813:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



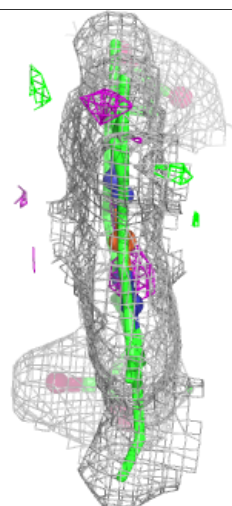
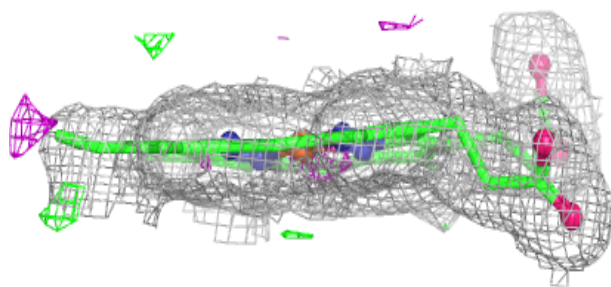
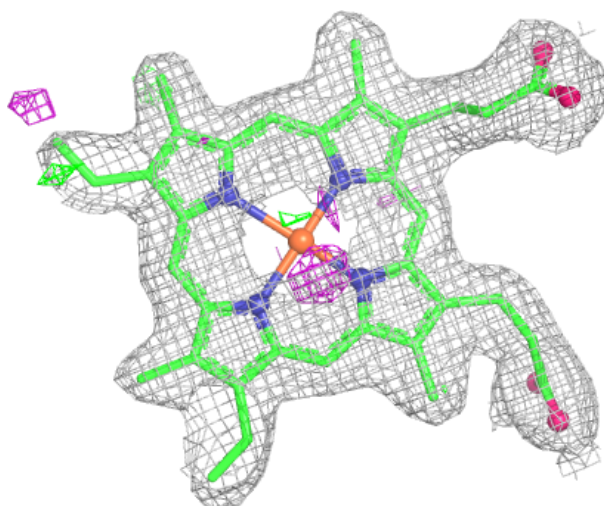
Electron density around HEM F 814:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



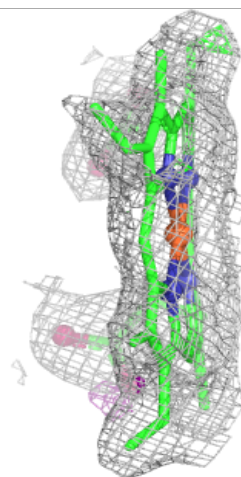
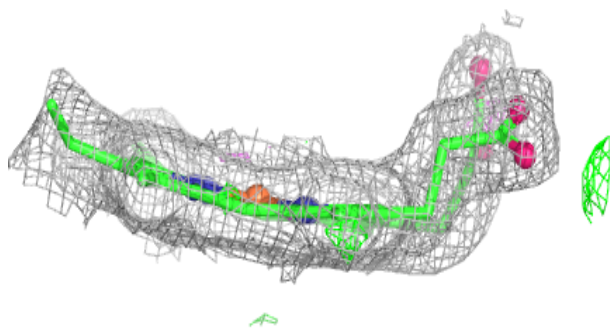
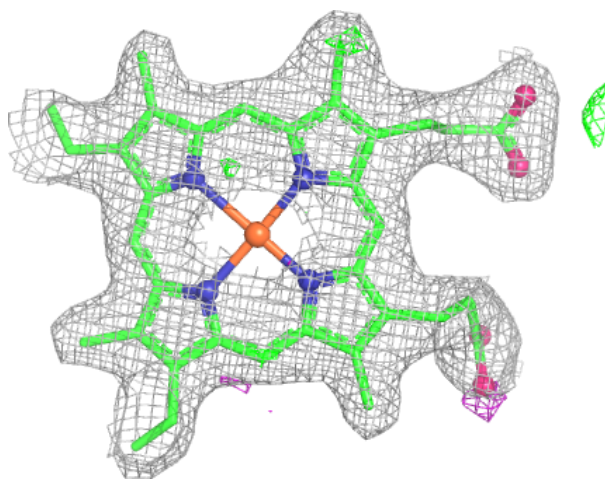
Electron density around HEM H 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



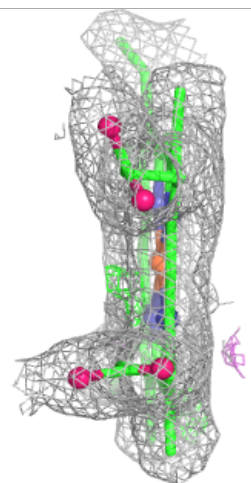
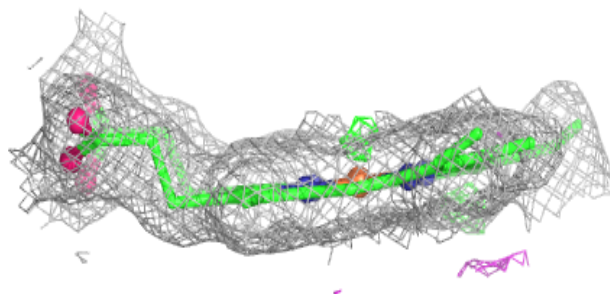
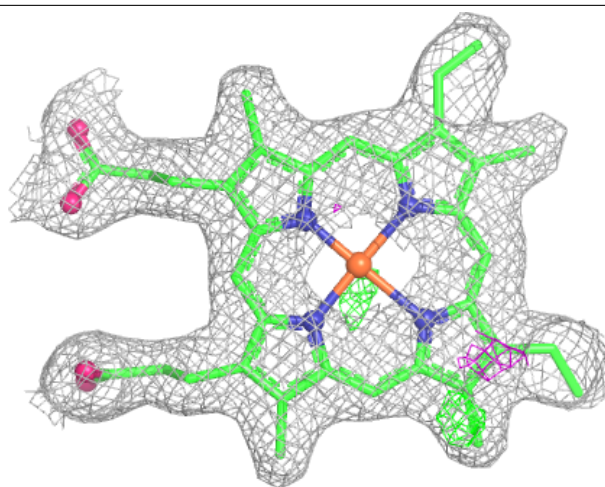
Electron density around HEM H 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



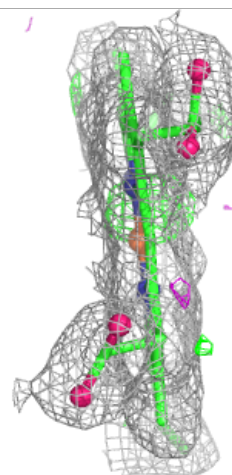
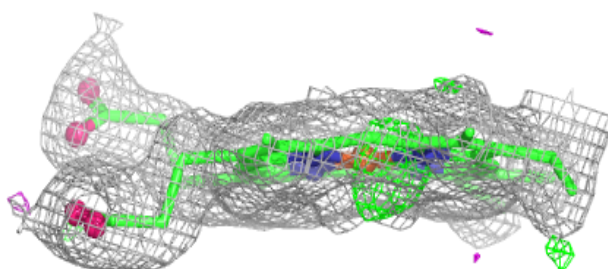
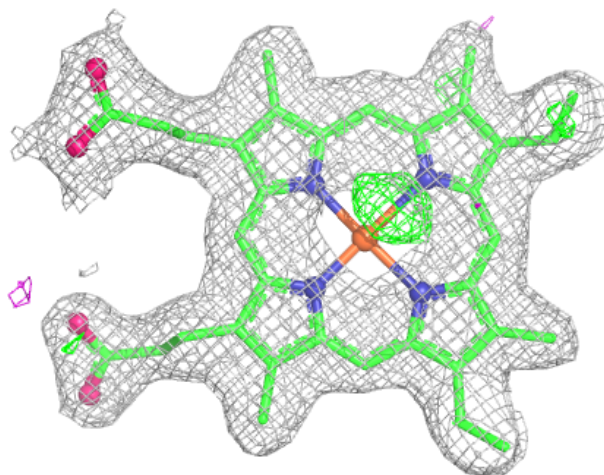
Electron density around HEM H 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



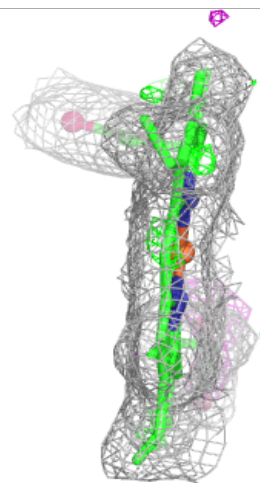
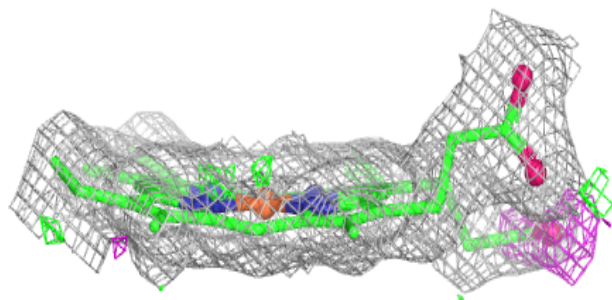
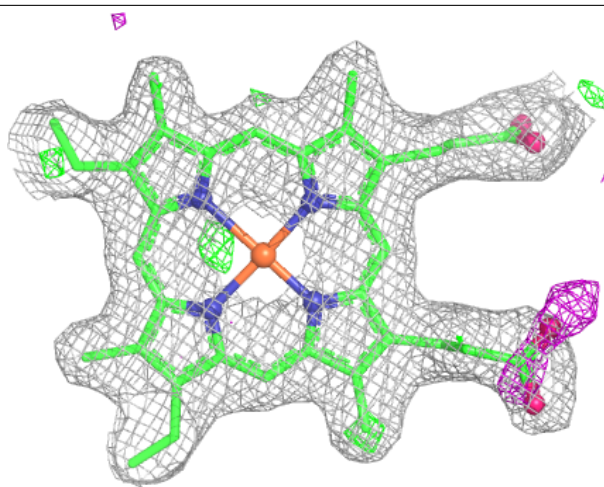
Electron density around HEM H 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



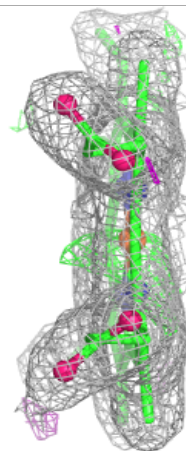
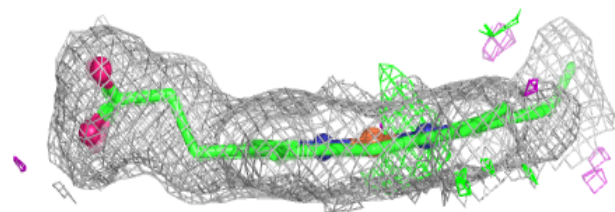
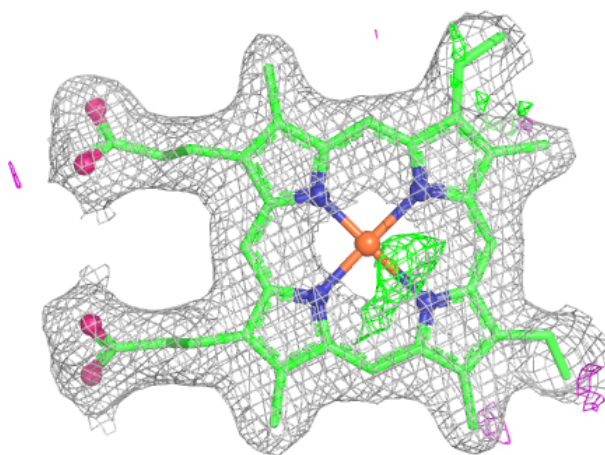
Electron density around HEM H 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



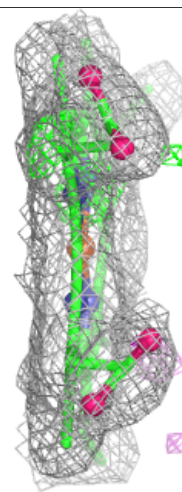
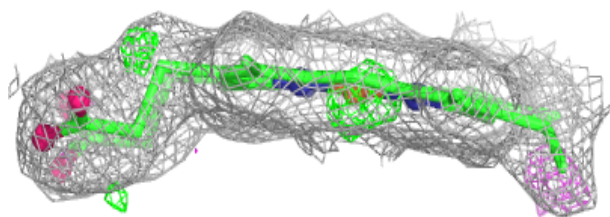
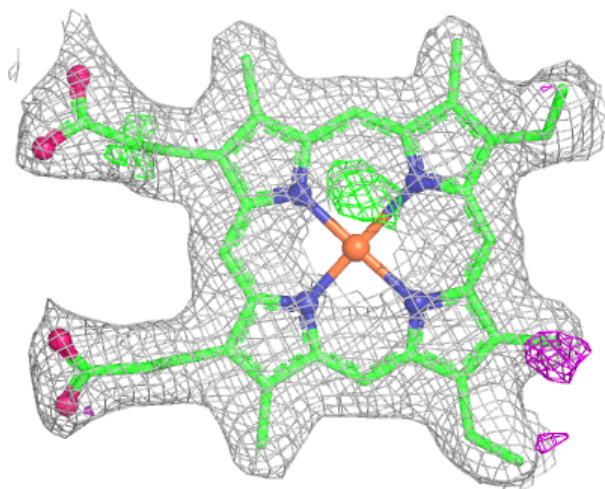
Electron density around HEM H 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



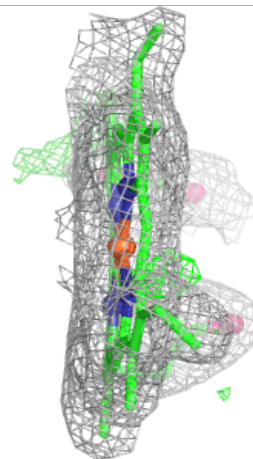
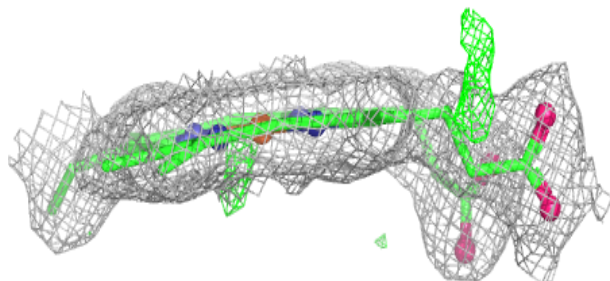
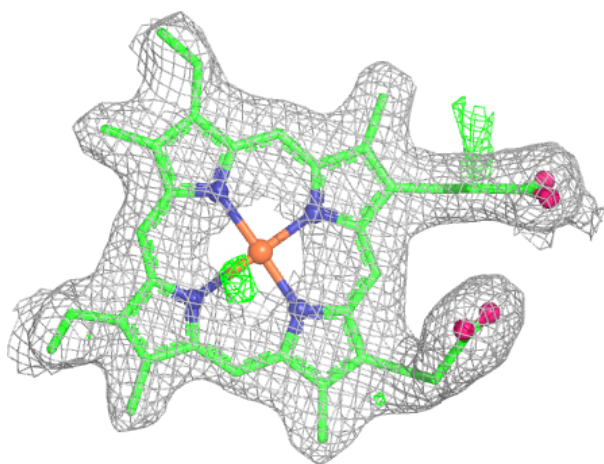
Electron density around HEM H 814:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



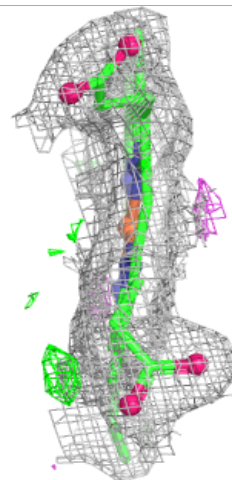
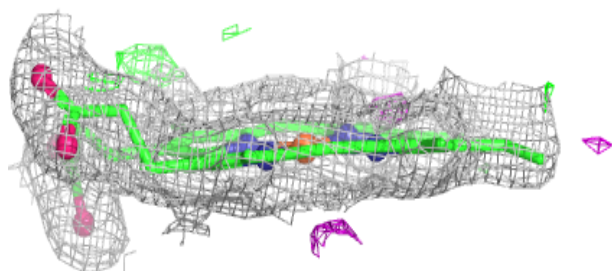
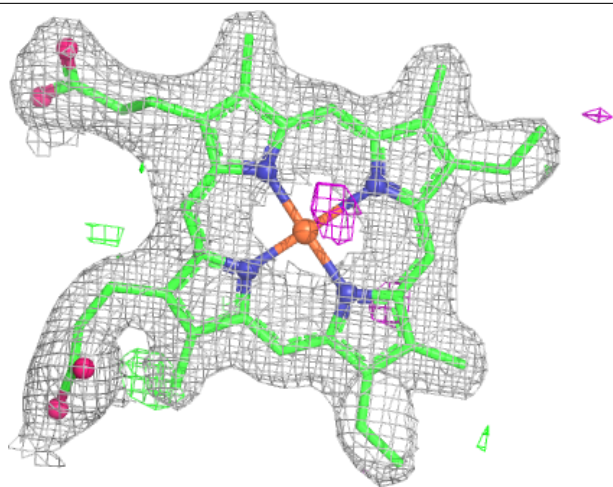
Electron density around HEM I 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



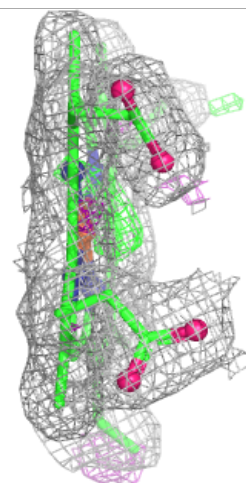
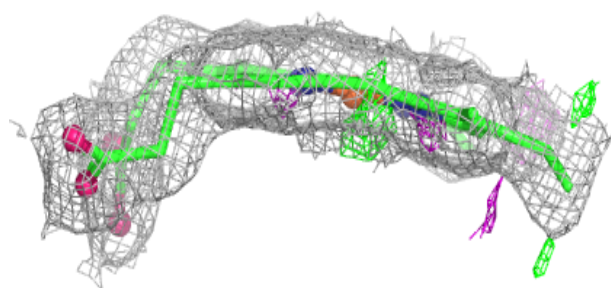
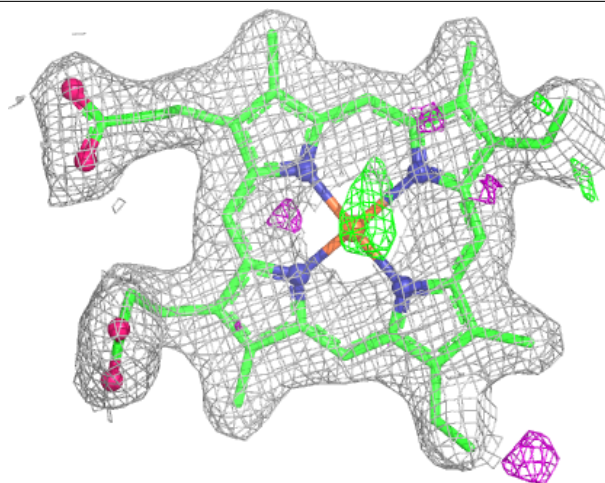
Electron density around HEM I 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



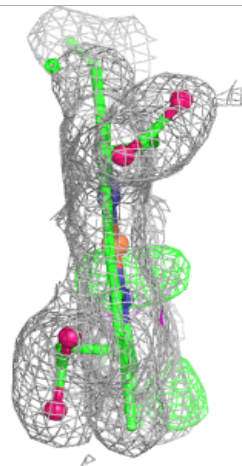
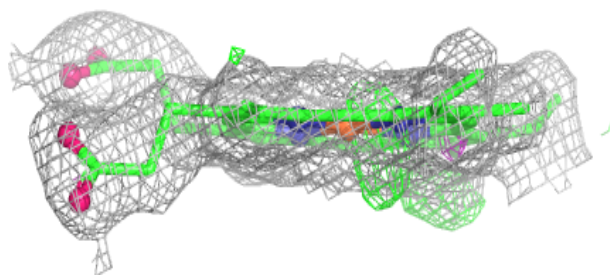
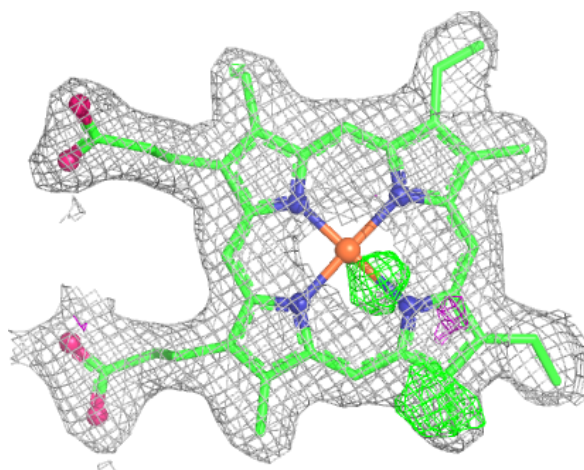
Electron density around HEM I 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



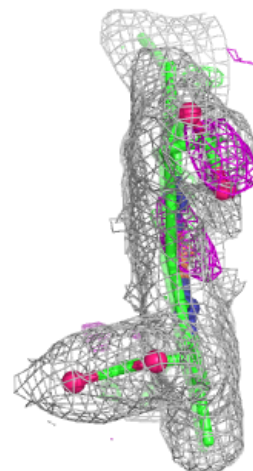
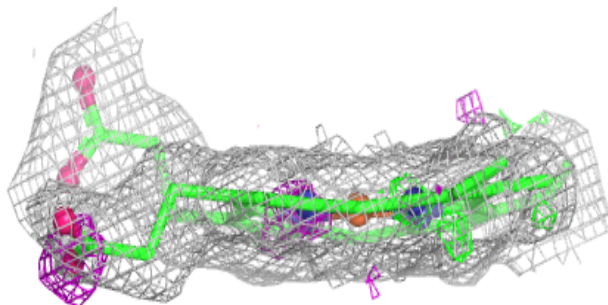
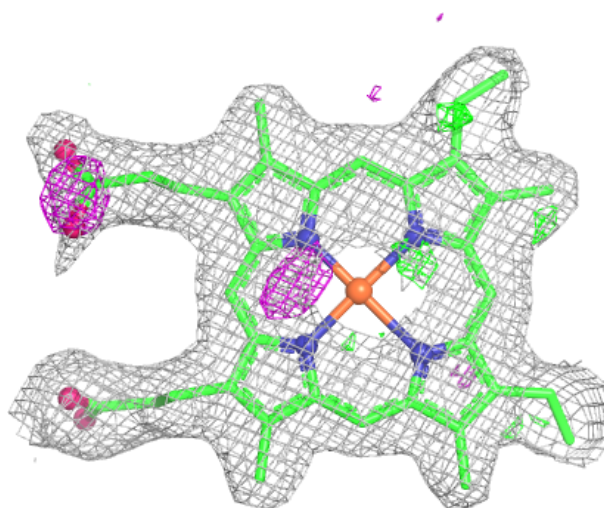
Electron density around HEM I 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



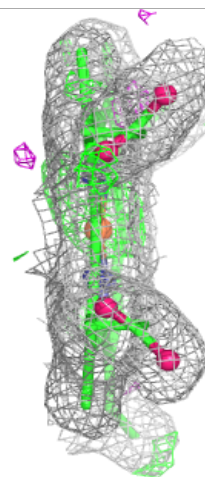
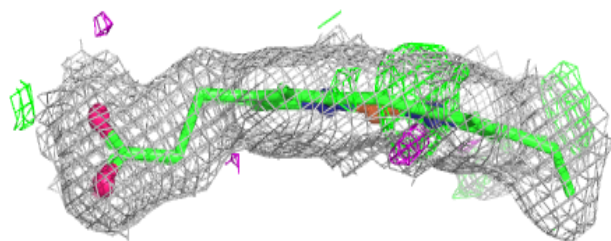
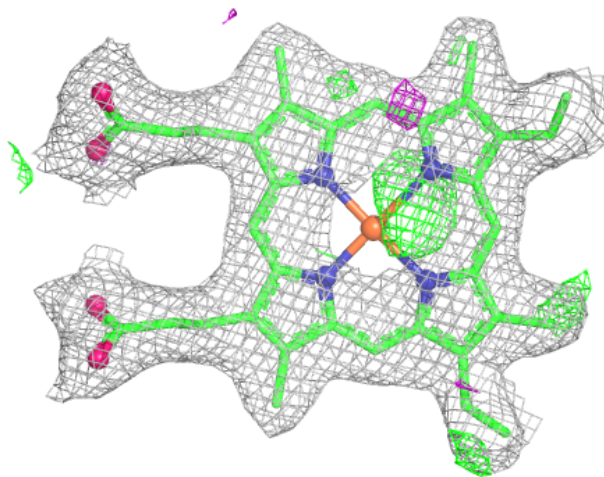
Electron density around HEM I 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



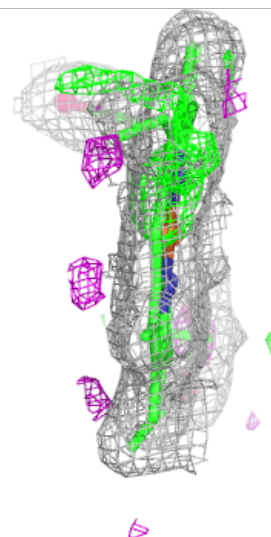
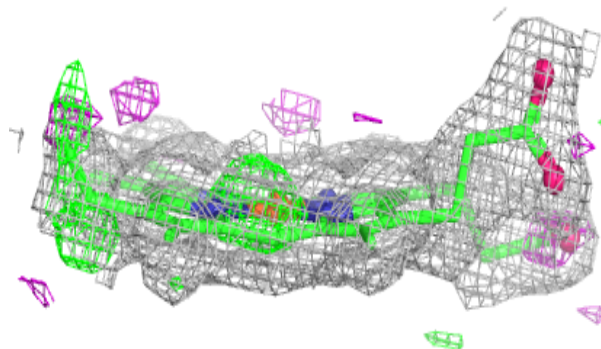
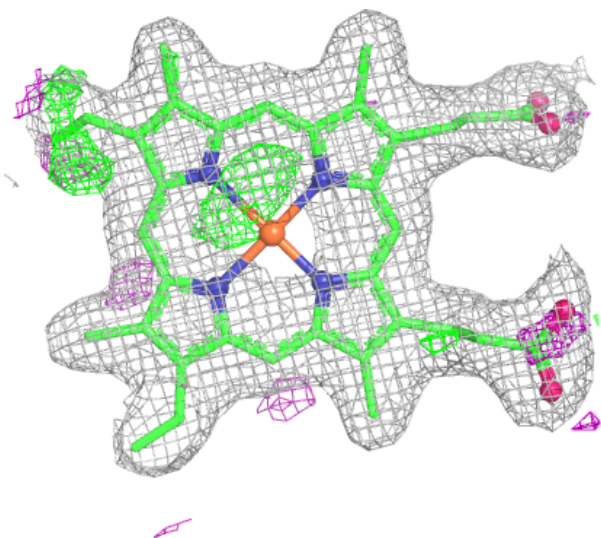
Electron density around HEM I 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



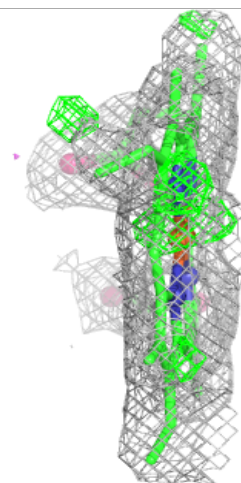
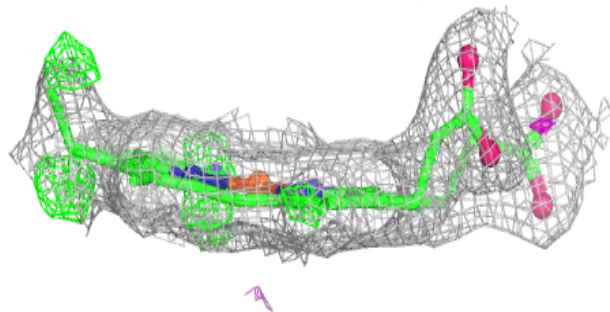
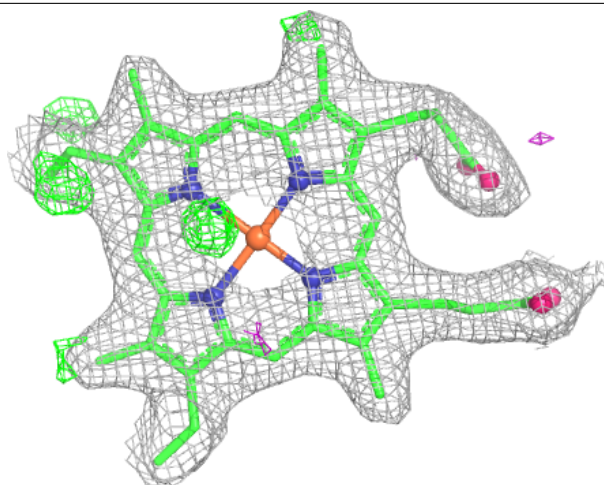
Electron density around HEM A 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



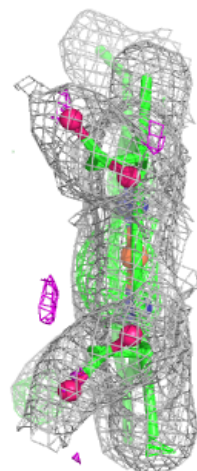
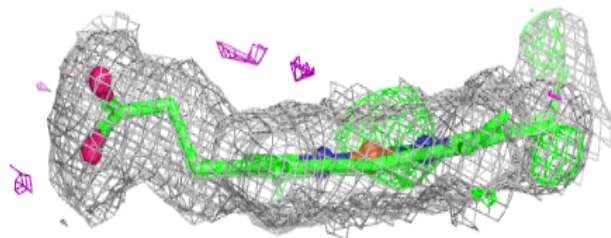
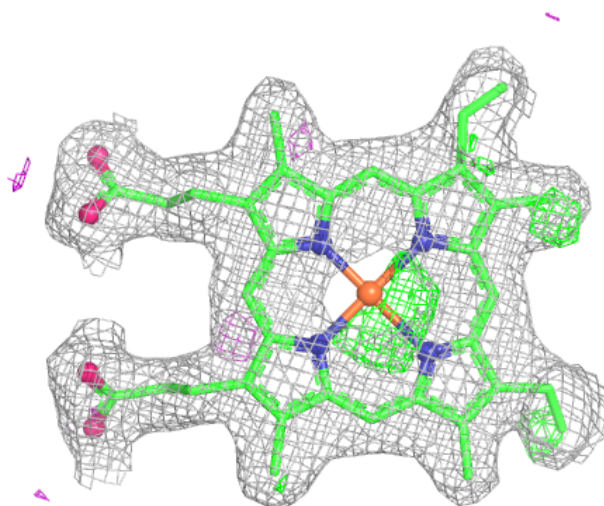
Electron density around HEM J 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



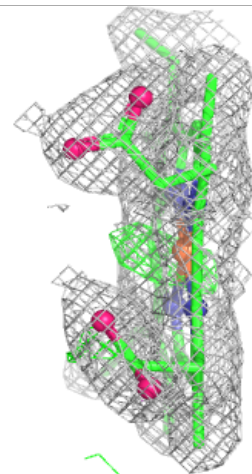
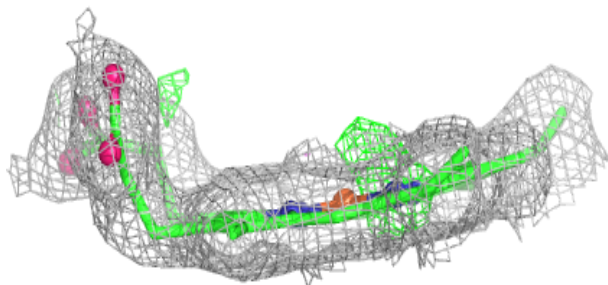
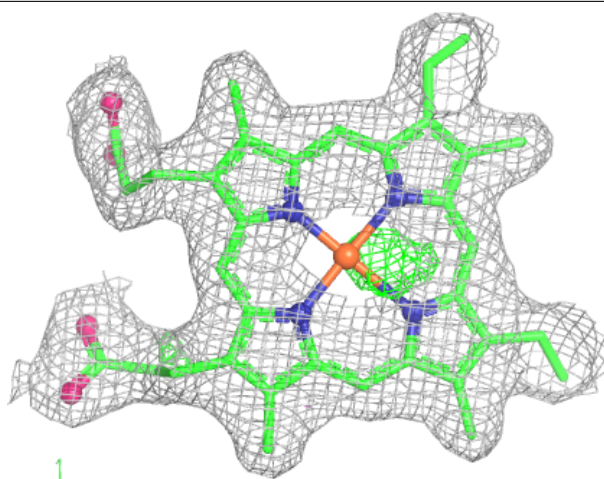
Electron density around HEM A 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



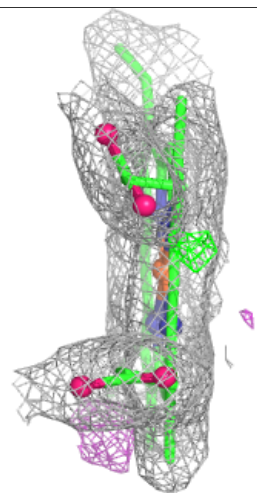
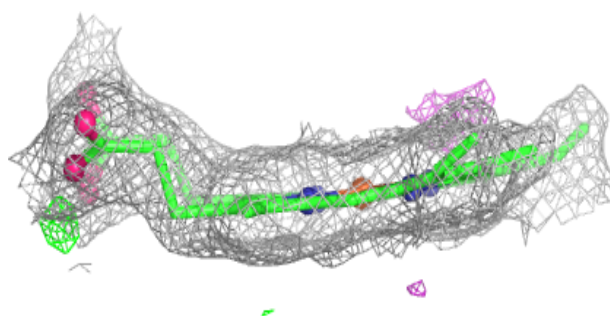
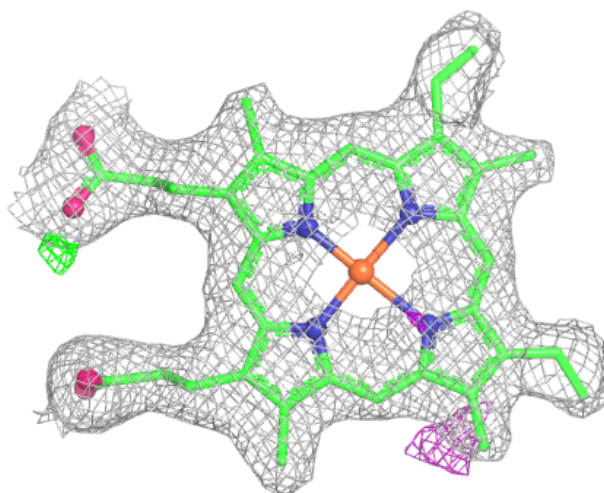
Electron density around HEM J 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



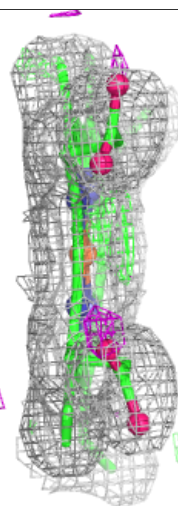
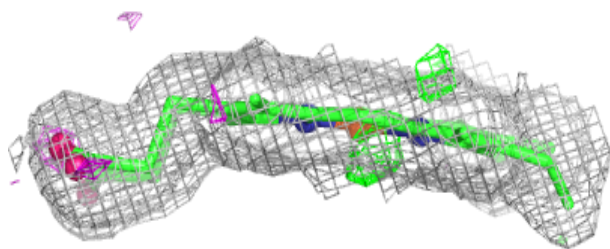
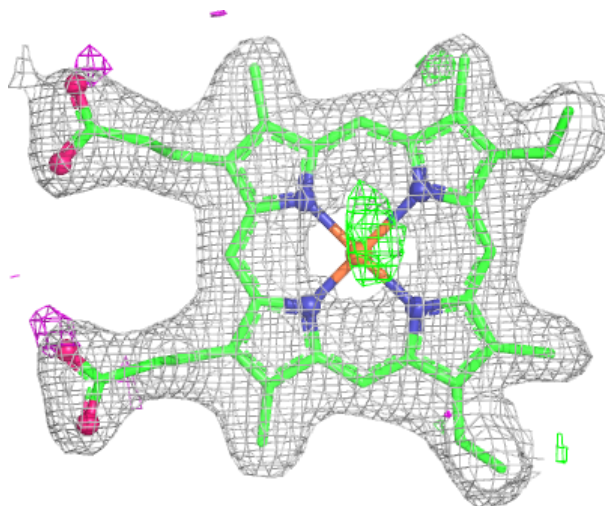
Electron density around HEM J 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



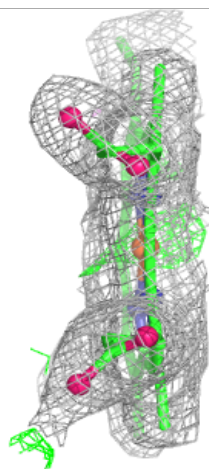
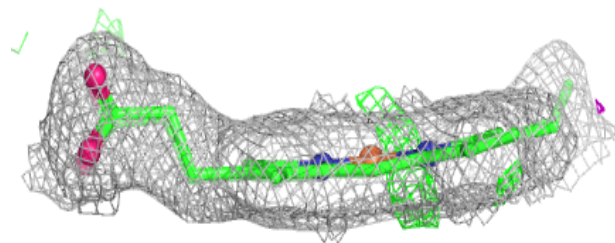
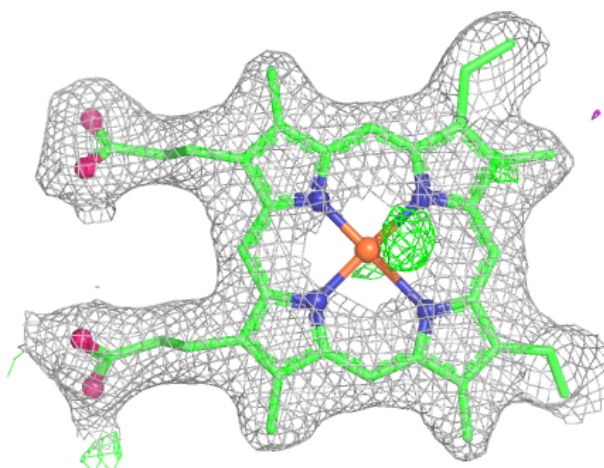
Electron density around HEM A 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



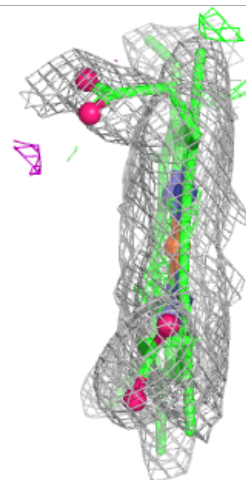
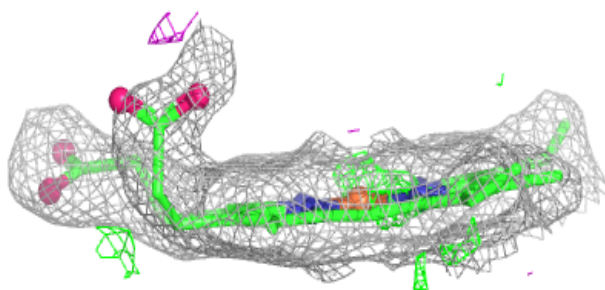
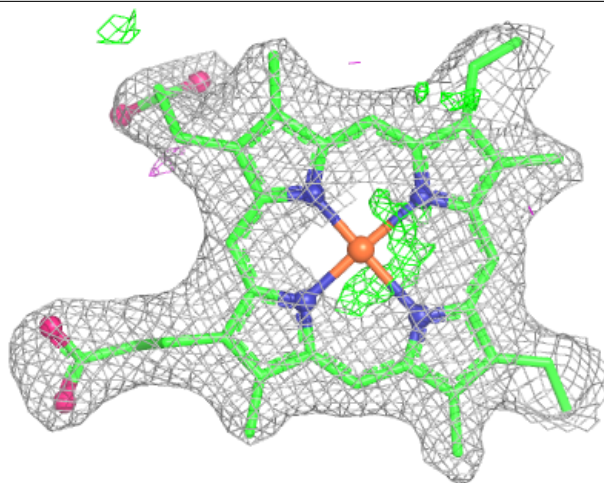
Electron density around HEM J 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



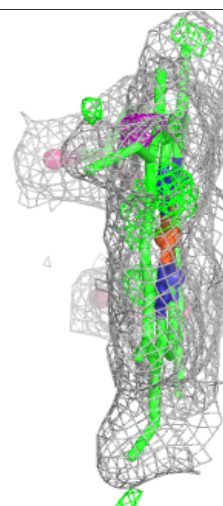
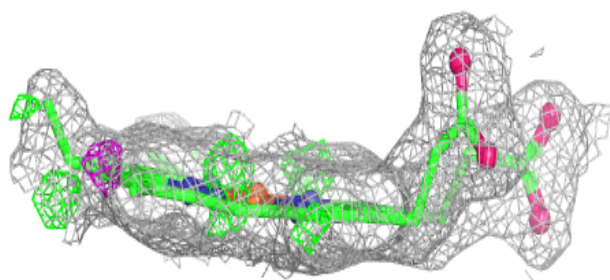
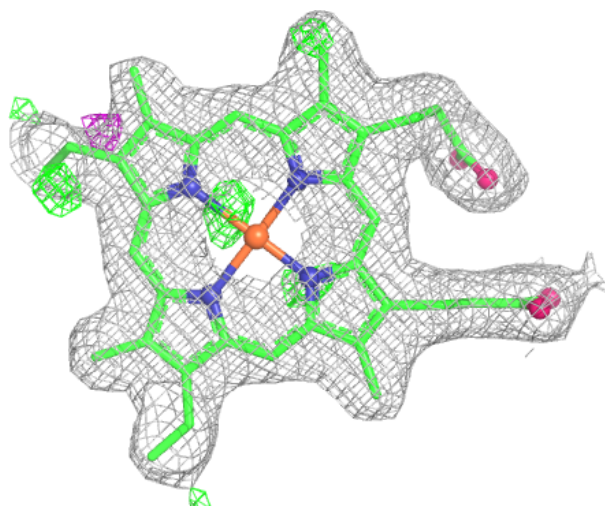
Electron density around HEM J 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



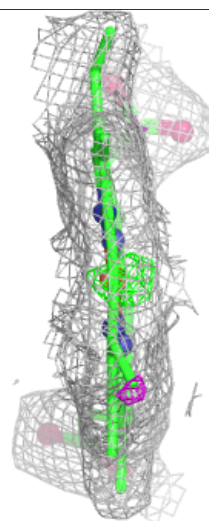
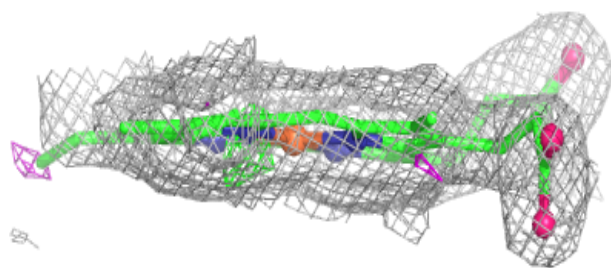
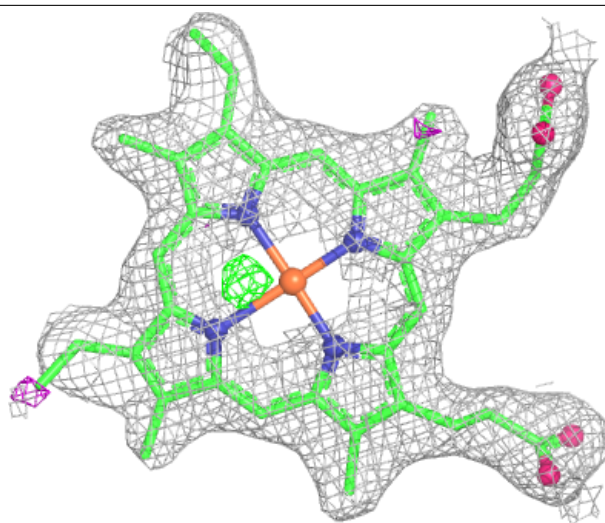
Electron density around HEM K 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



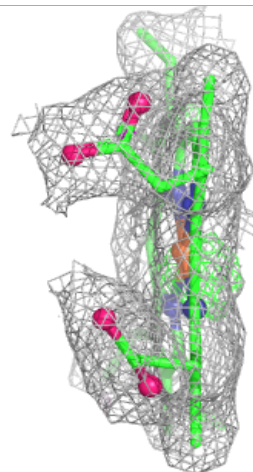
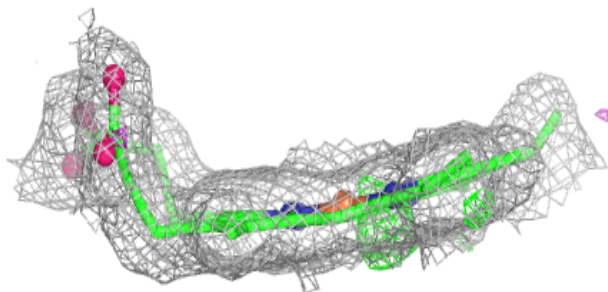
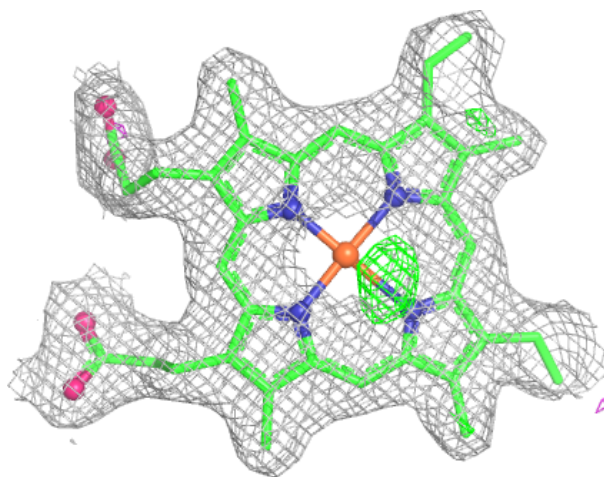
Electron density around HEM K 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



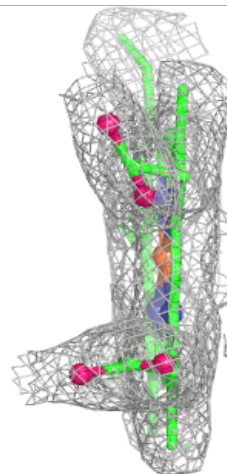
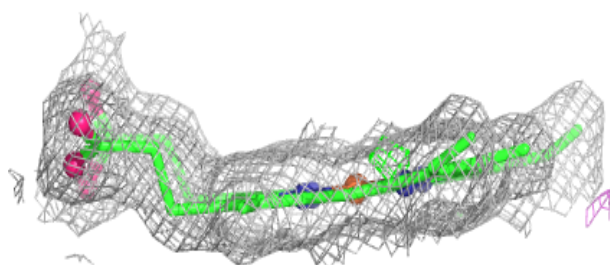
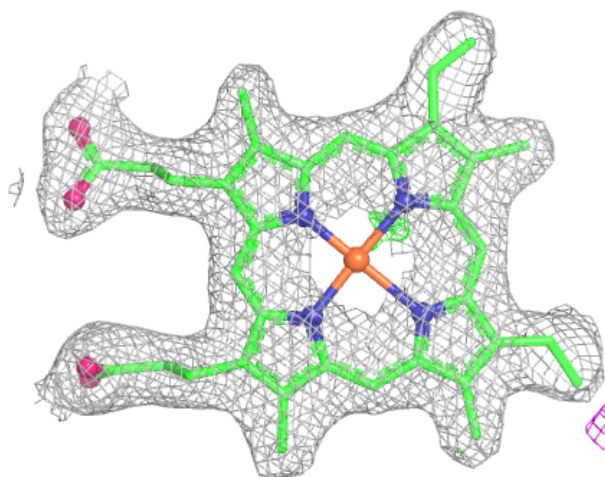
Electron density around HEM K 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



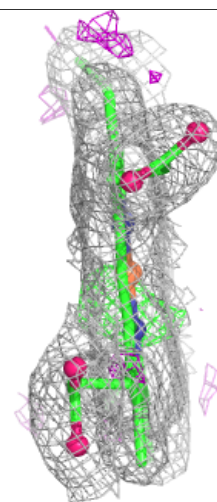
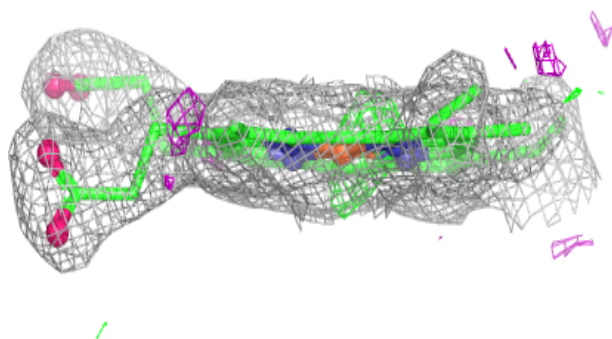
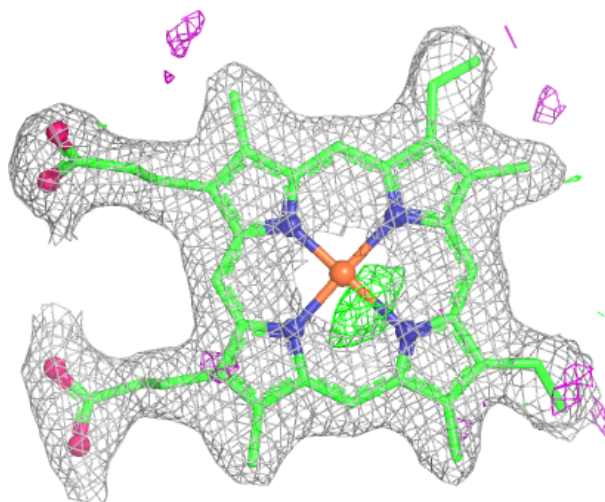
Electron density around HEM K 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



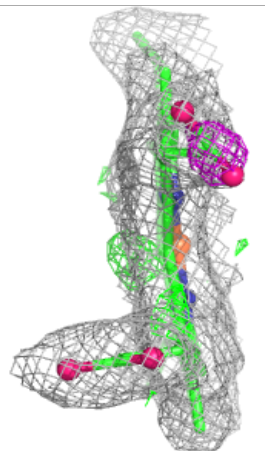
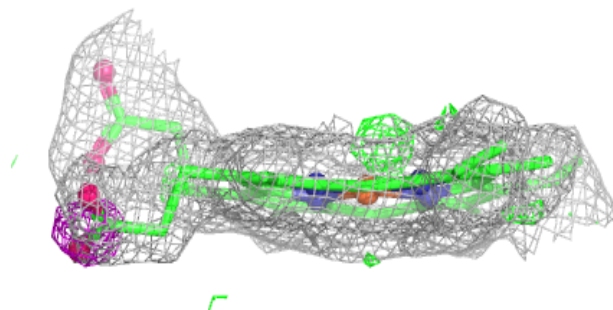
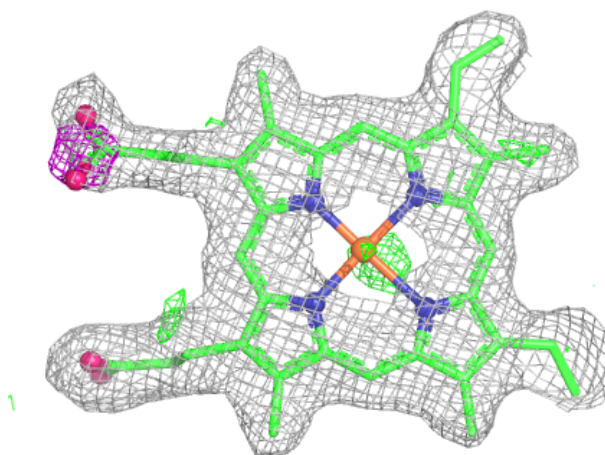
Electron density around HEM K 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



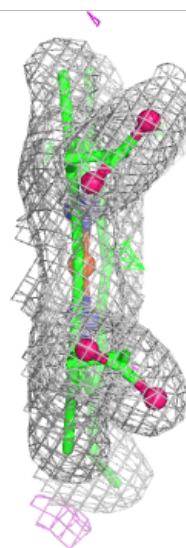
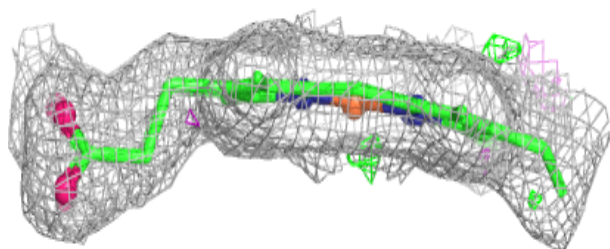
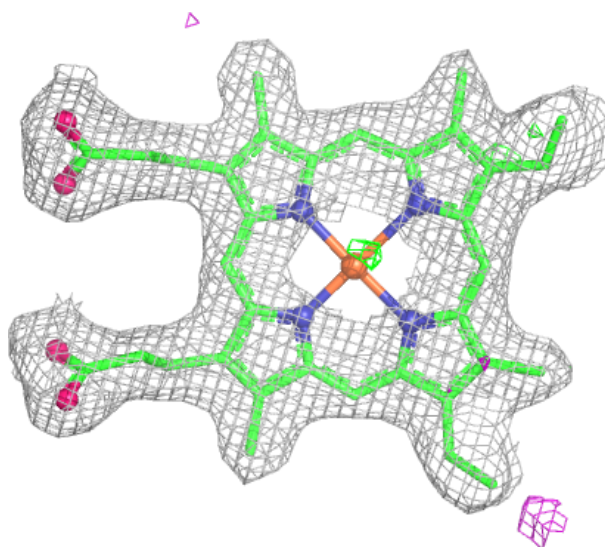
Electron density around HEM K 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



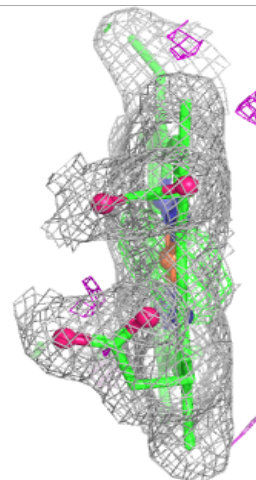
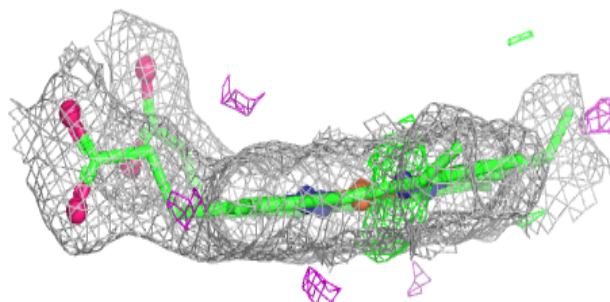
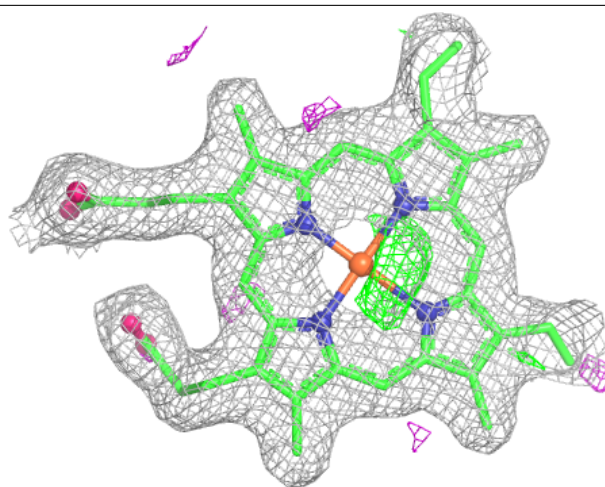
Electron density around HEM K 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



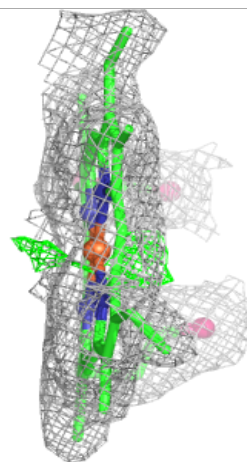
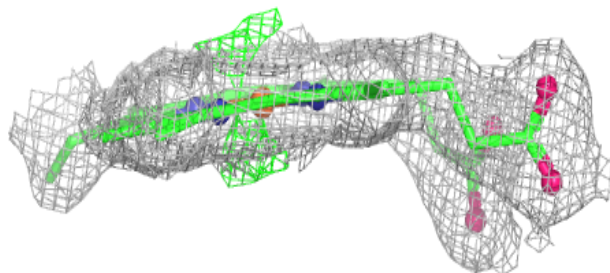
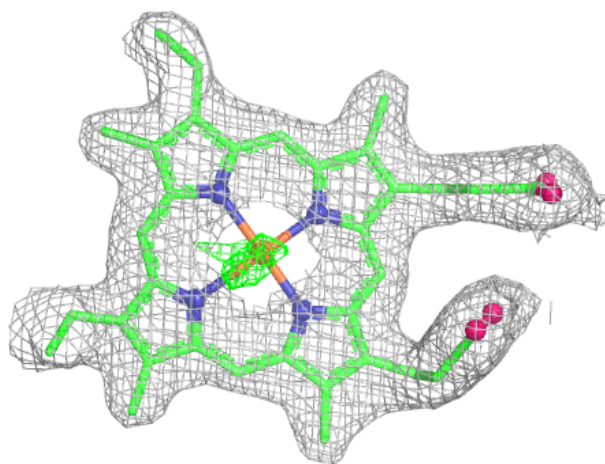
Electron density around HEM B 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



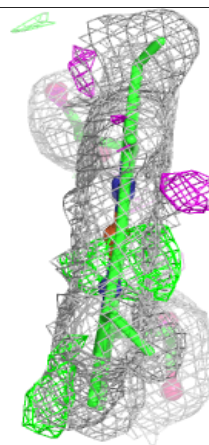
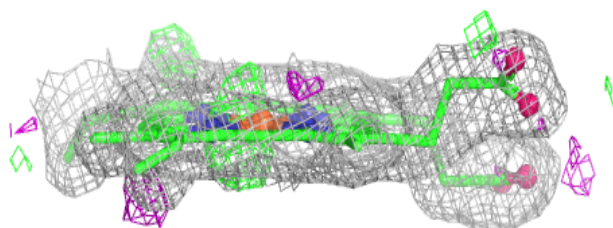
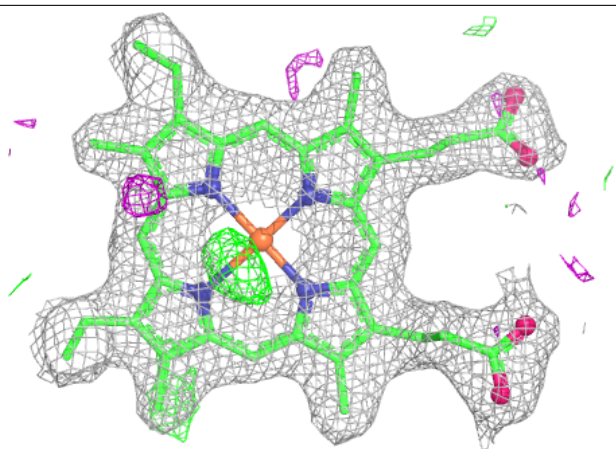
Electron density around HEM L 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



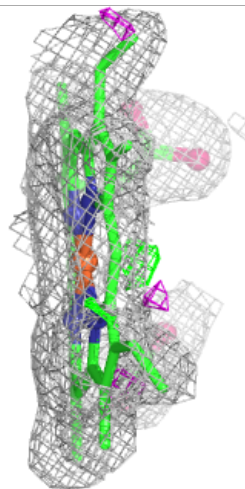
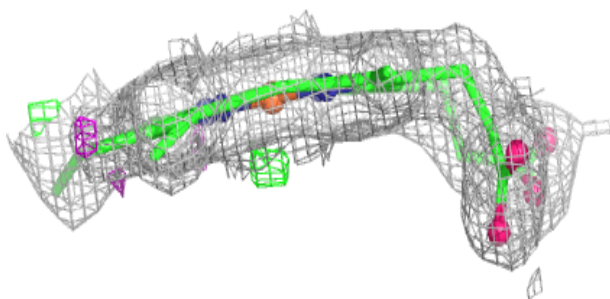
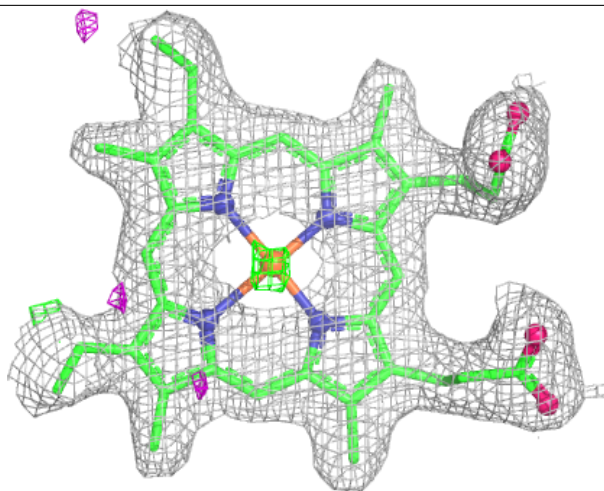
Electron density around HEM B 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



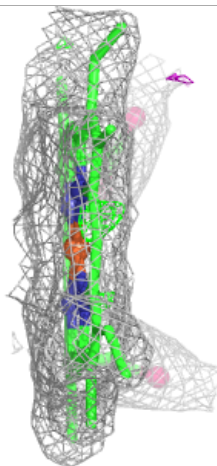
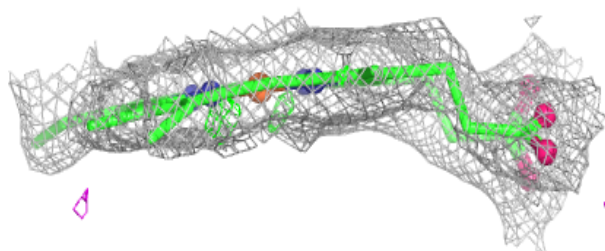
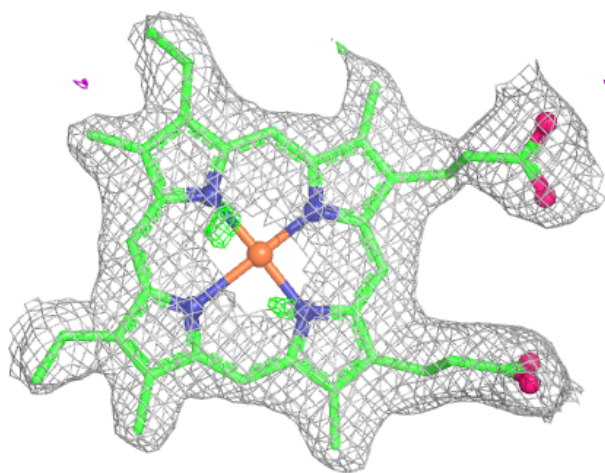
Electron density around HEM L 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



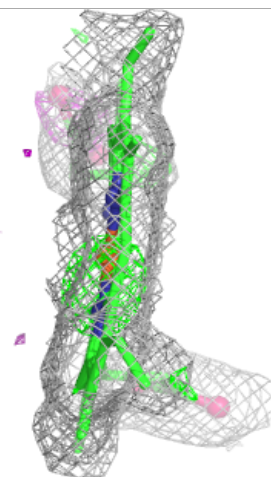
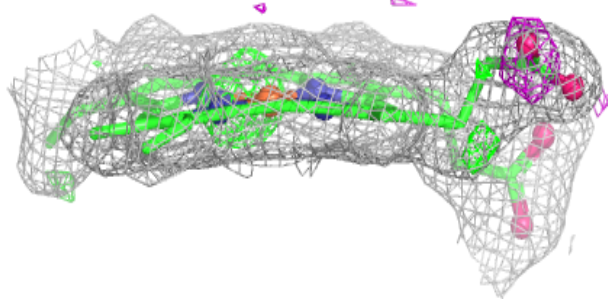
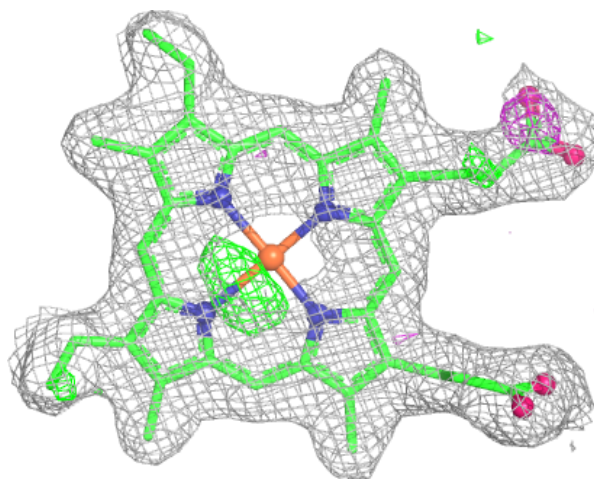
Electron density around HEM L 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



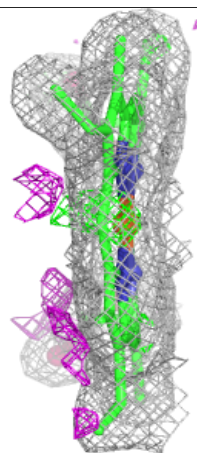
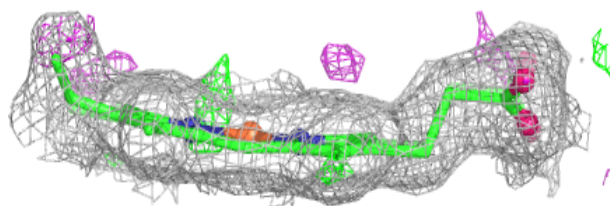
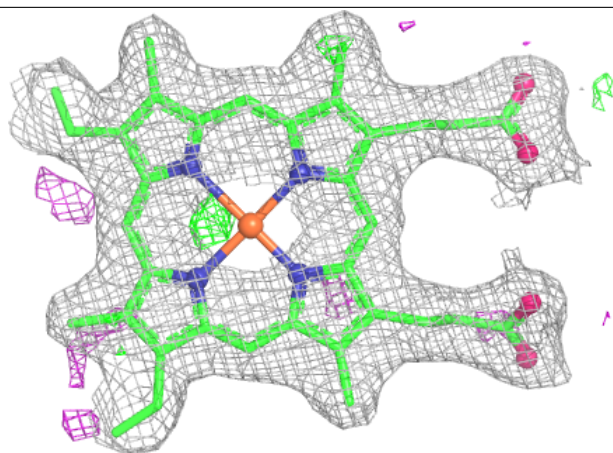
Electron density around HEM B 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



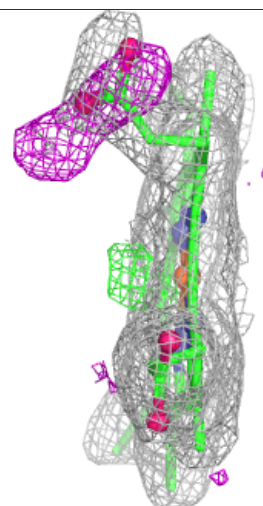
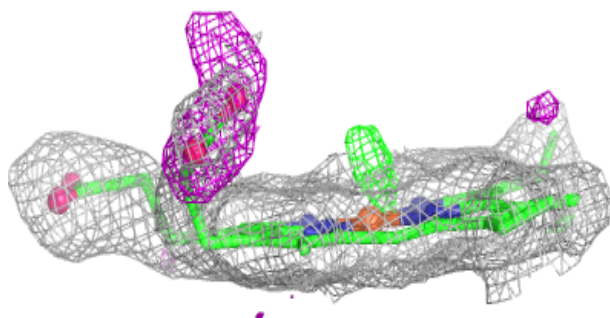
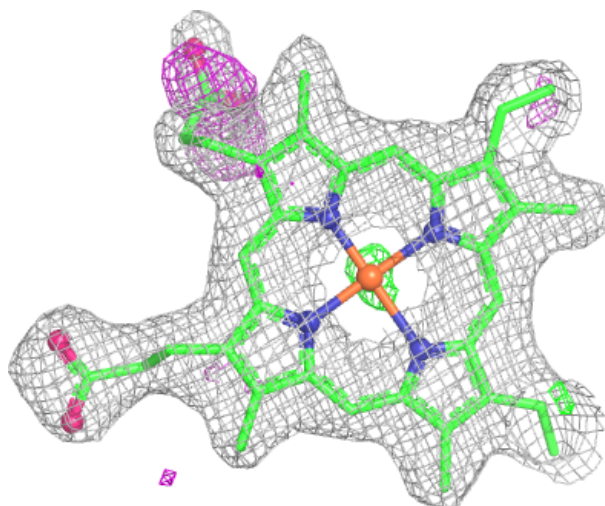
Electron density around HEM B 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



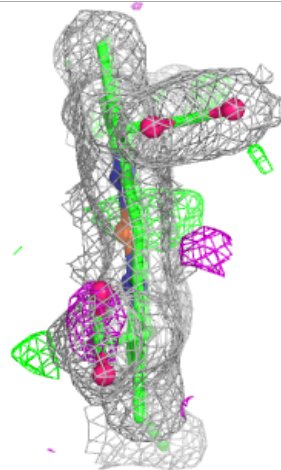
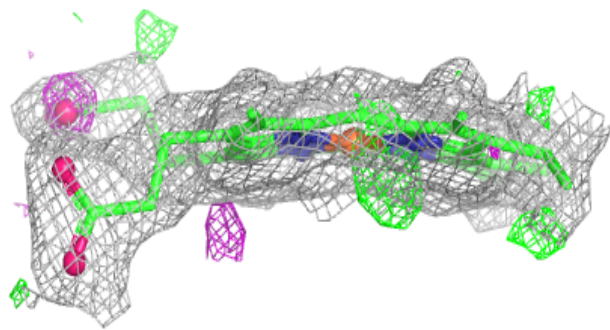
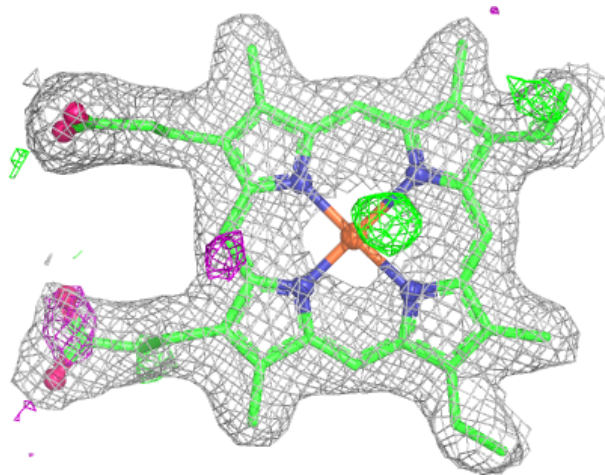
Electron density around HEM B 814:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



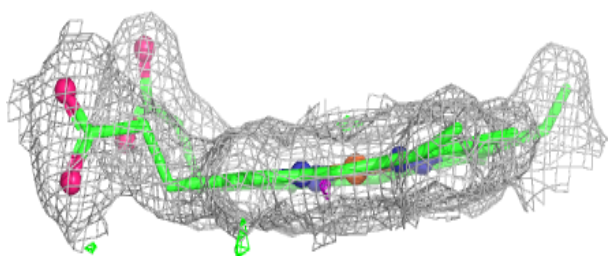
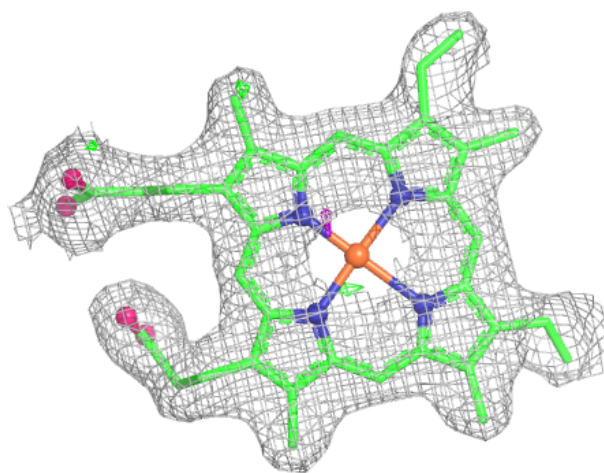
Electron density around HEM C 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



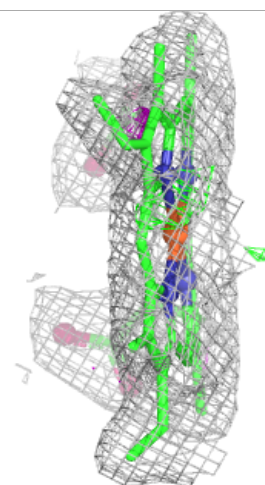
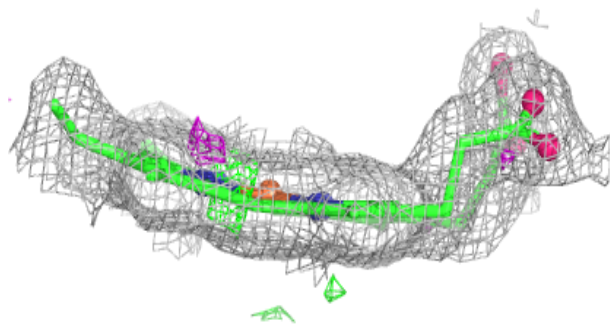
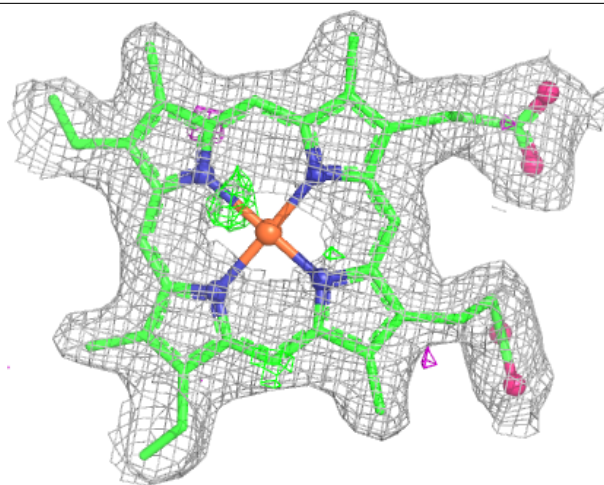
Electron density around HEM G 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



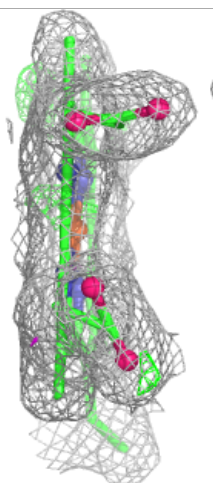
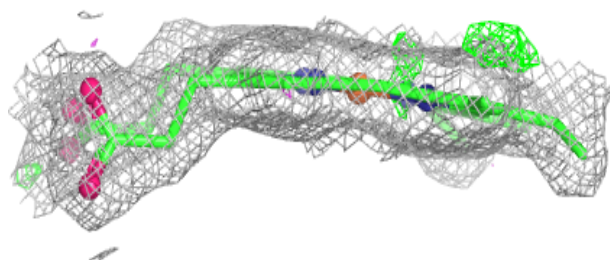
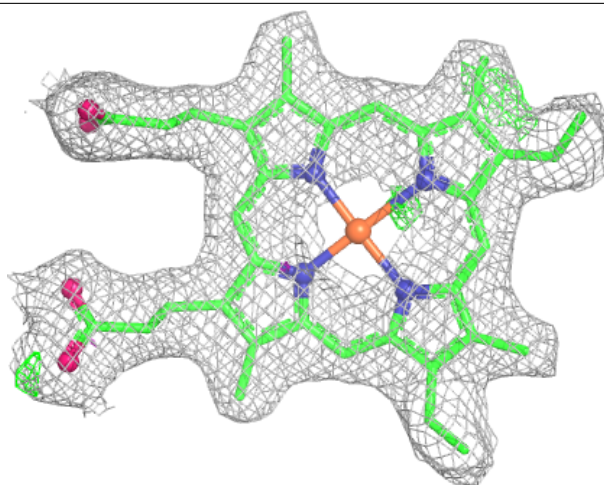
Electron density around HEM G 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



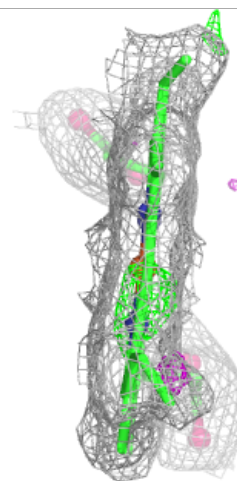
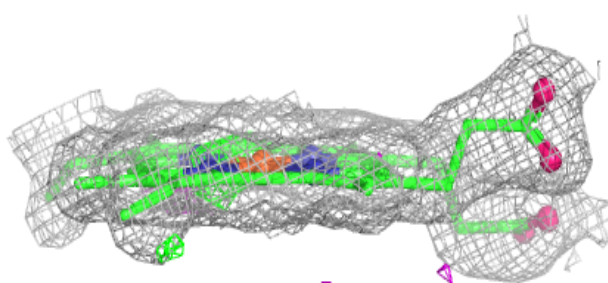
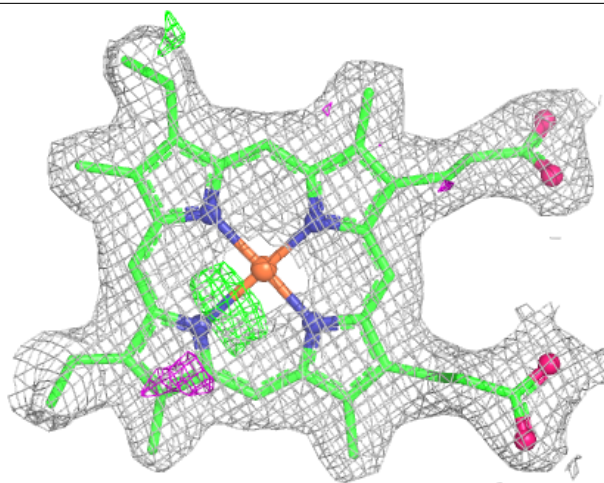
Electron density around HEM G 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



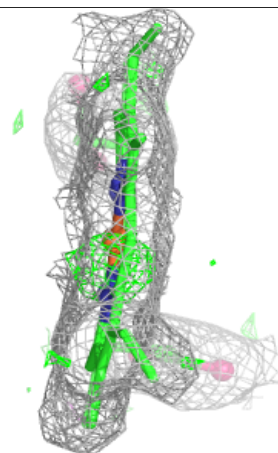
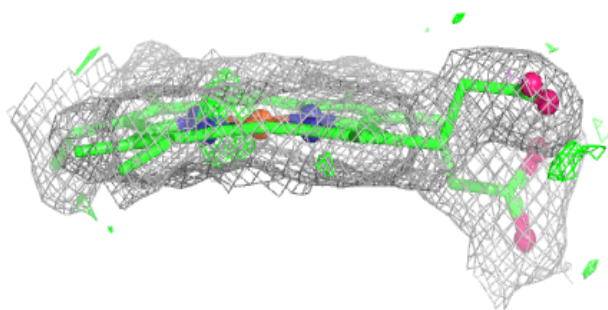
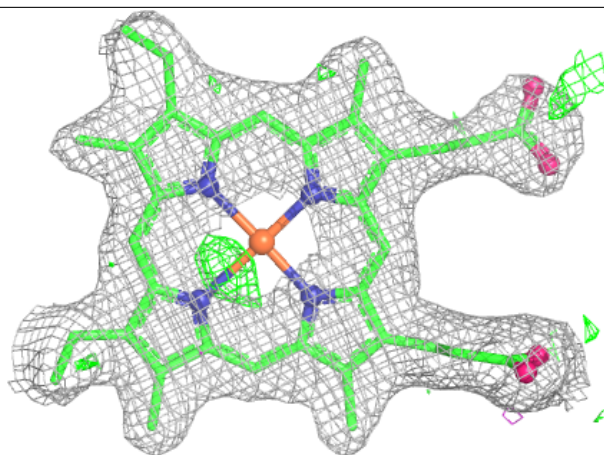
Electron density around HEM G 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



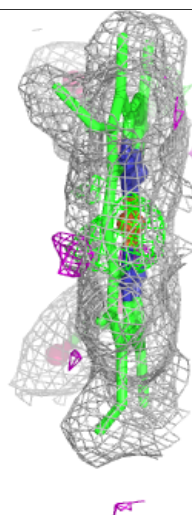
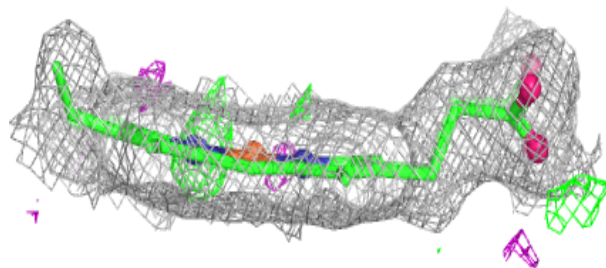
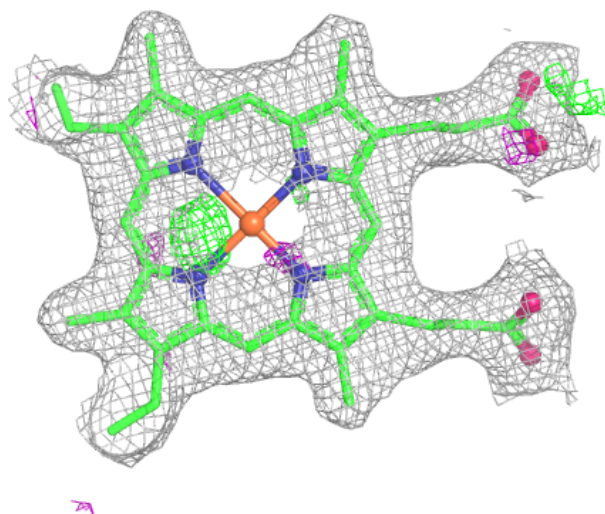
Electron density around HEM G 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



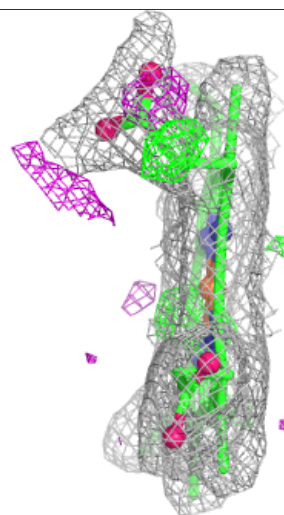
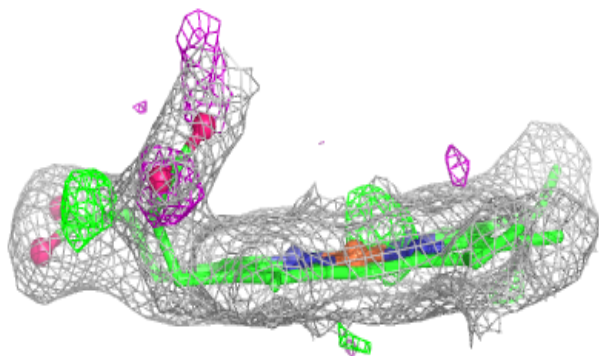
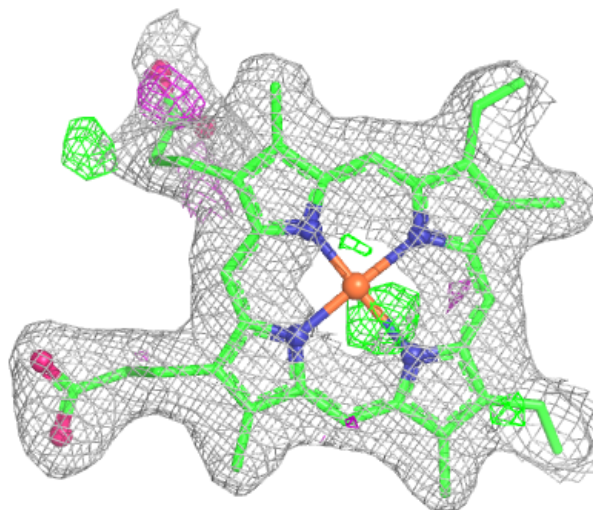
Electron density around HEM G 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



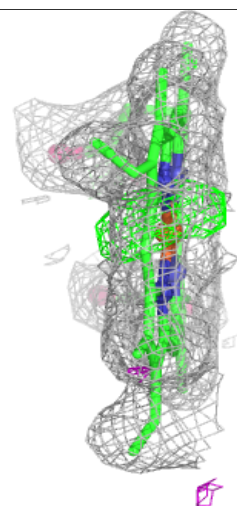
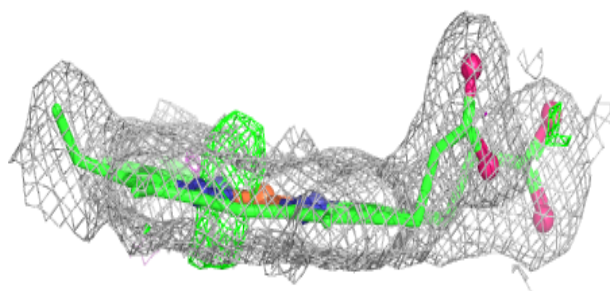
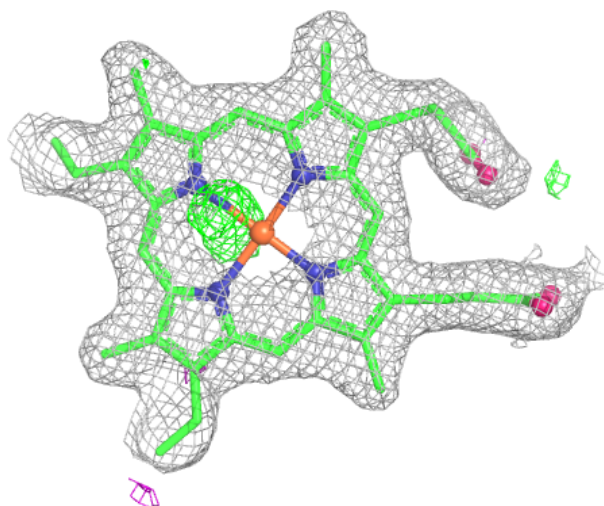
Electron density around HEM G 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



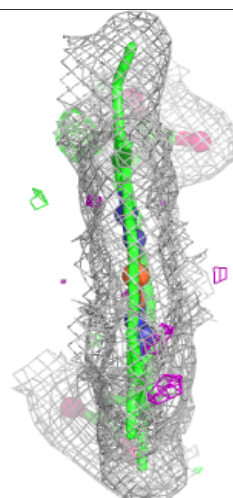
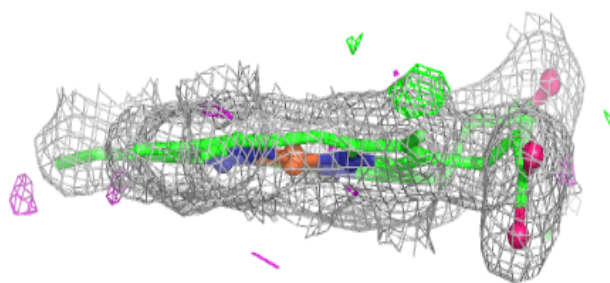
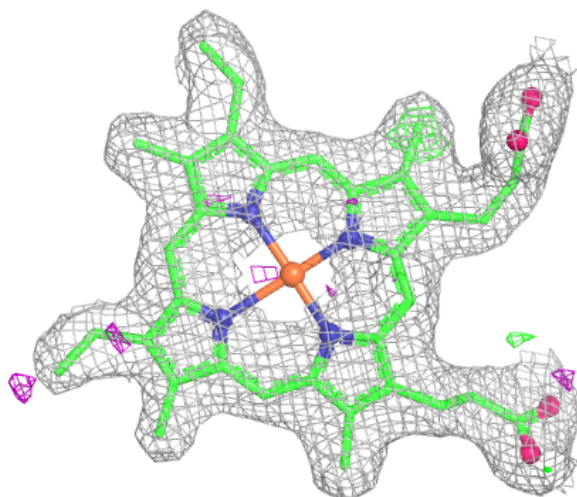
Electron density around HEM D 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



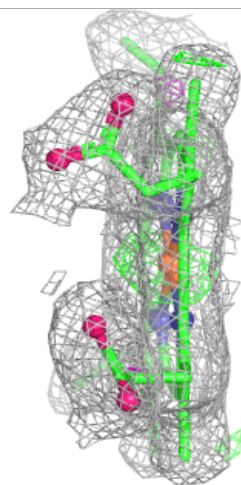
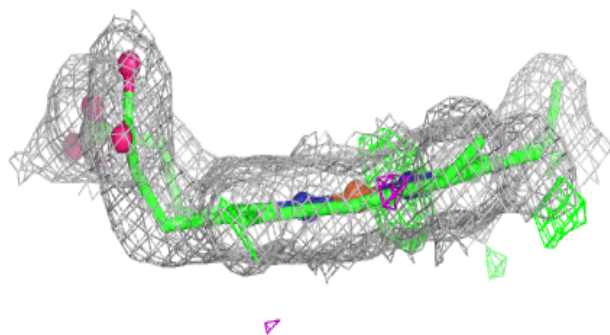
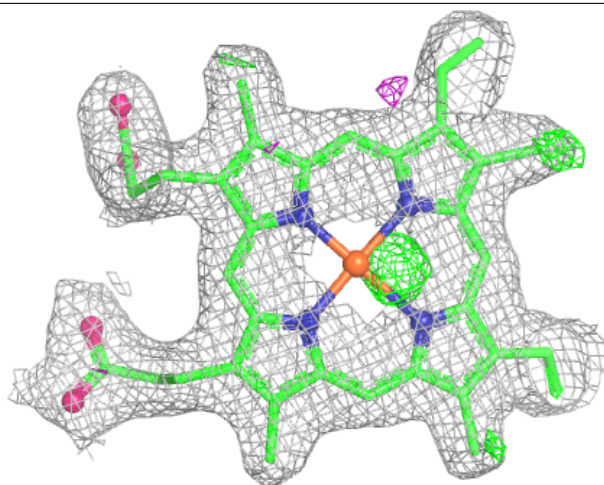
Electron density around HEM D 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



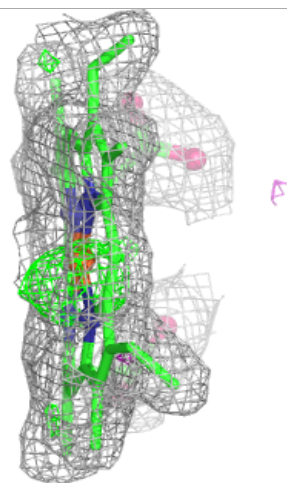
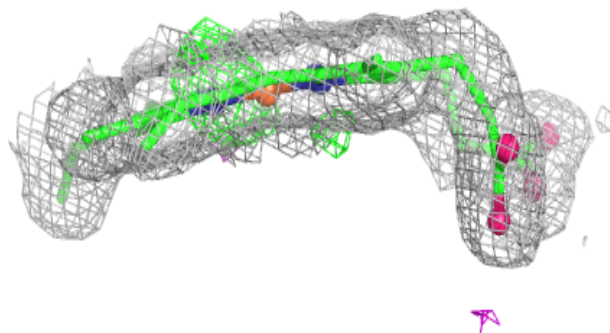
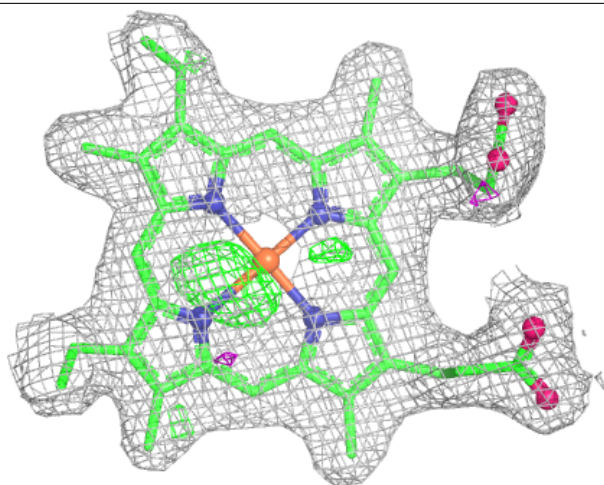
Electron density around HEM D 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



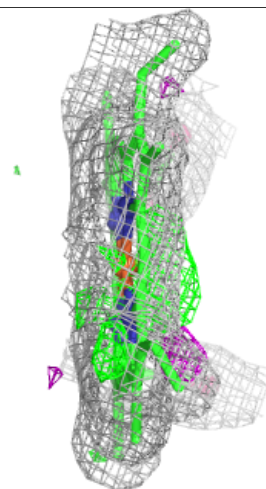
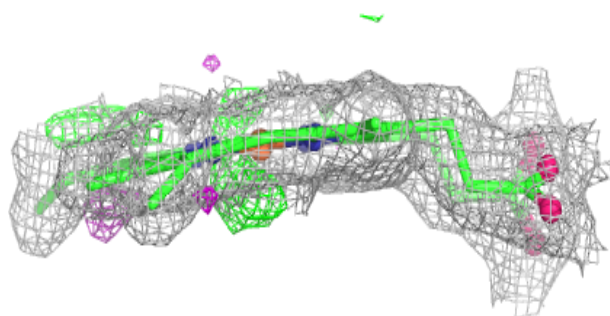
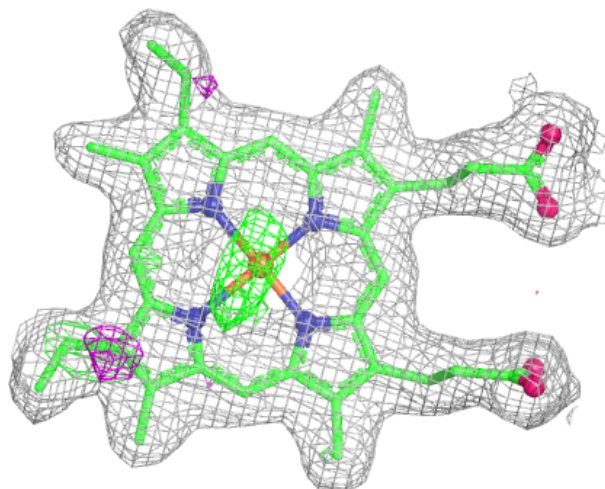
Electron density around HEM C 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



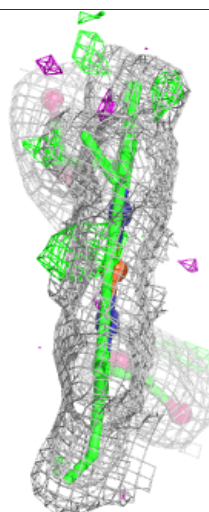
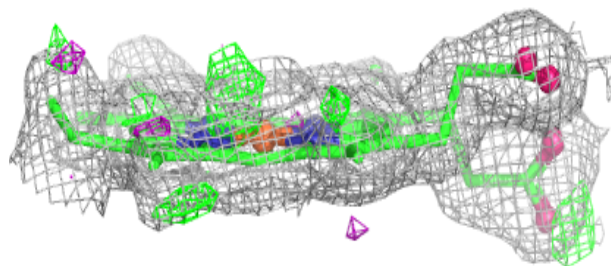
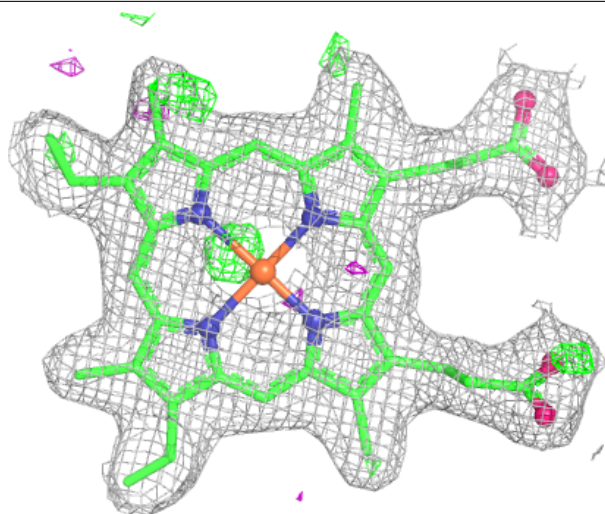
Electron density around HEM C 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



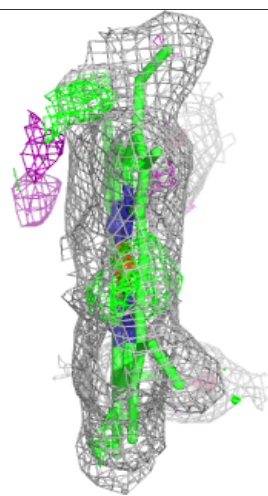
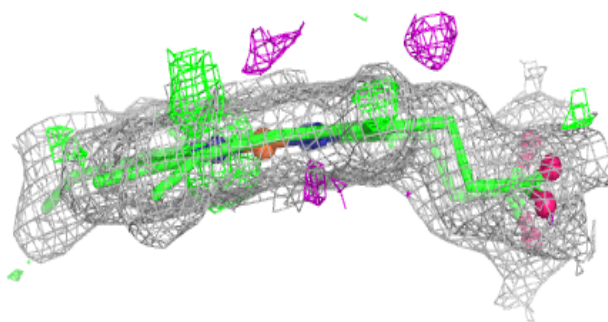
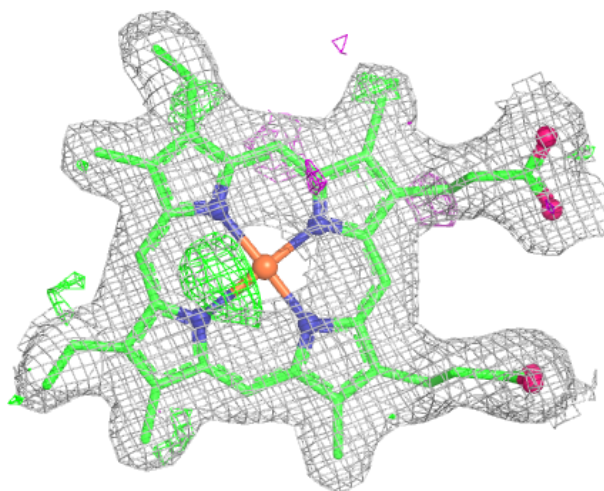
Electron density around HEM C 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



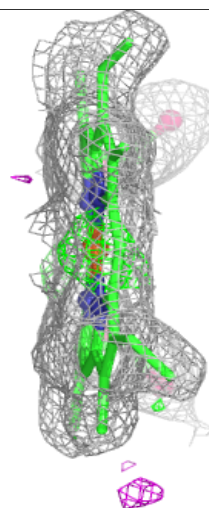
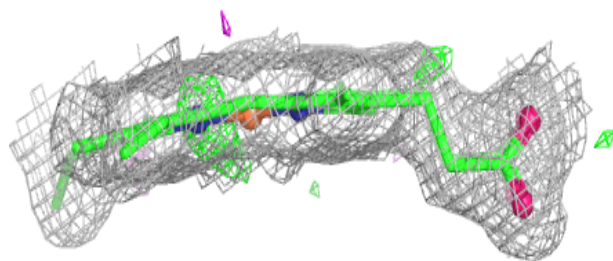
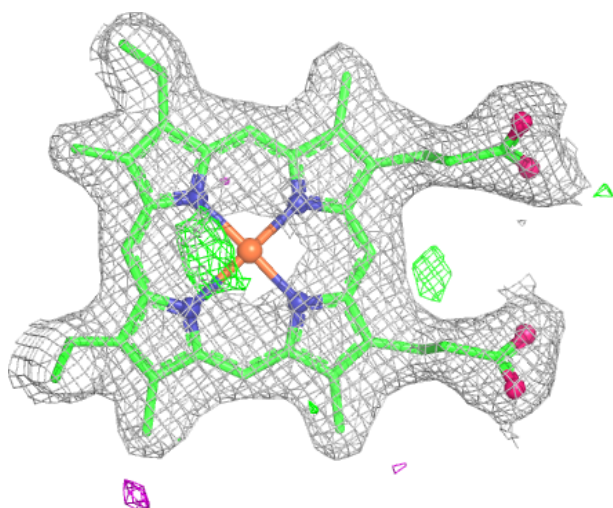
Electron density around HEM A 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



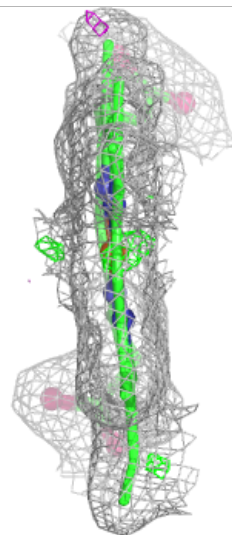
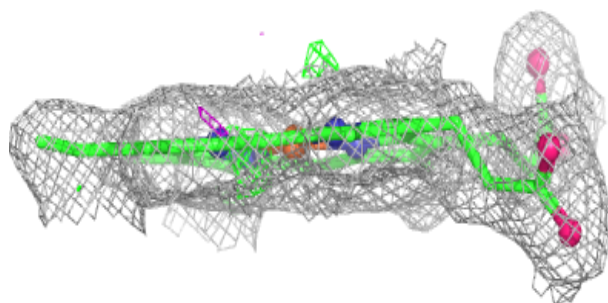
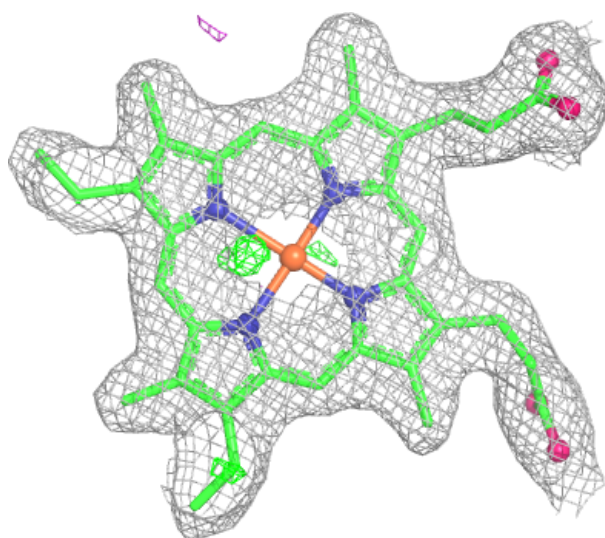
Electron density around HEM C 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



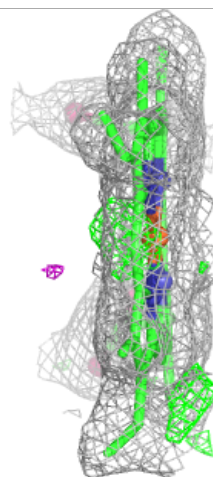
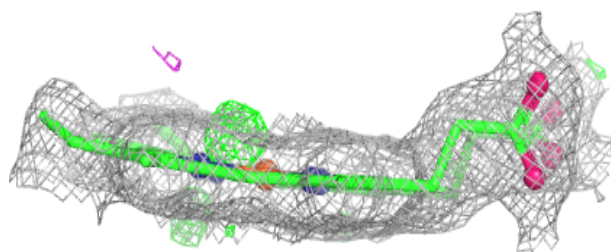
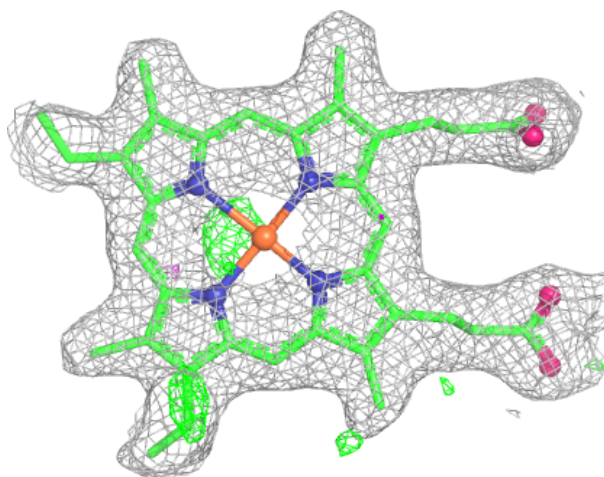
Electron density around HEM B 808:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



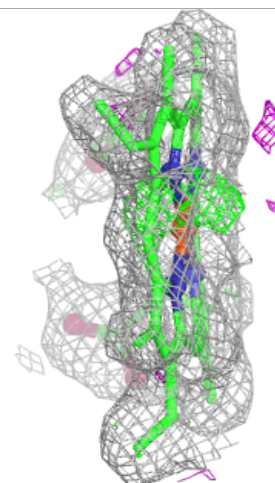
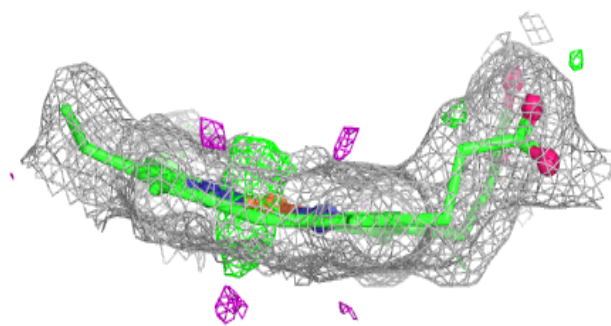
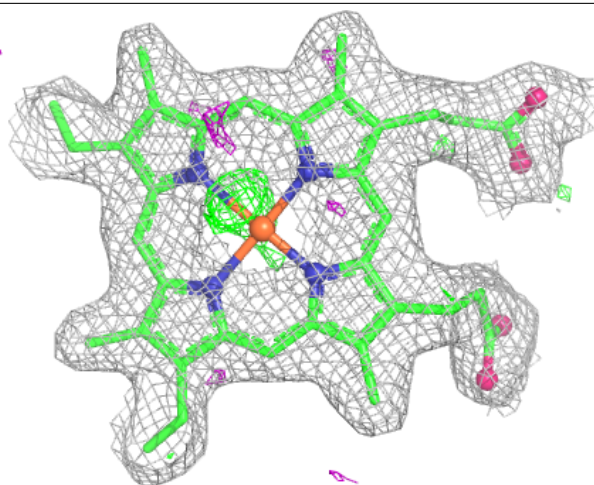
Electron density around HEM F 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



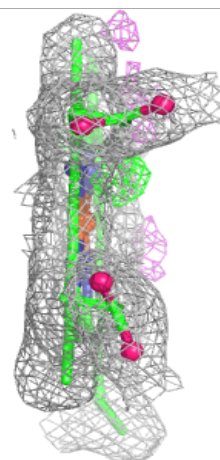
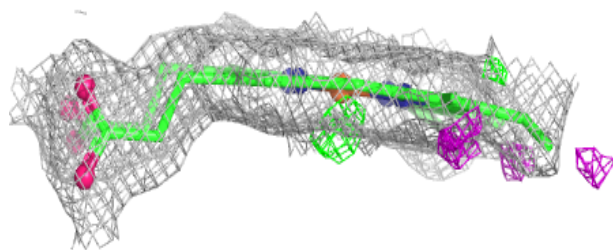
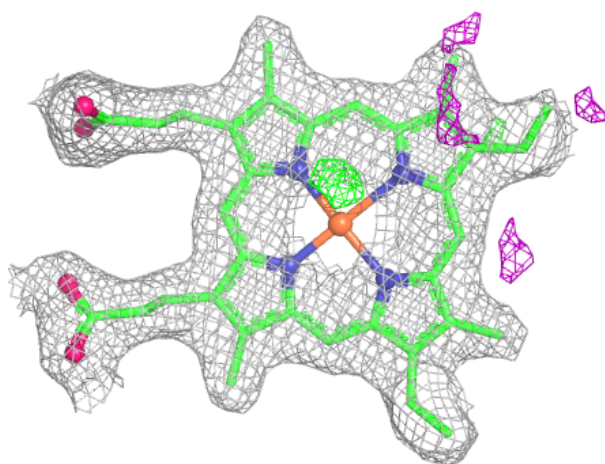
Electron density around HEM B 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



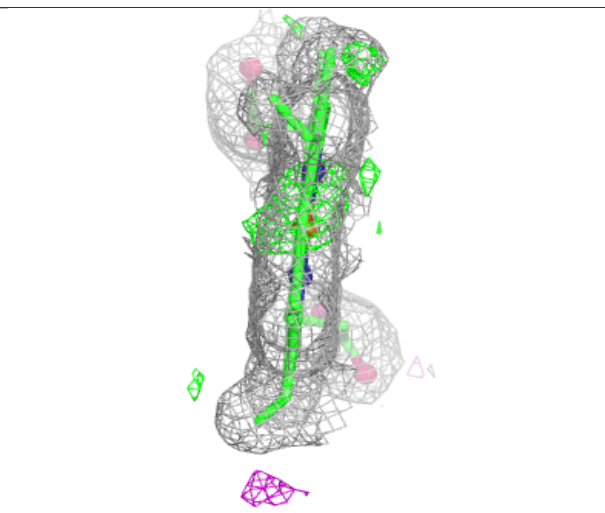
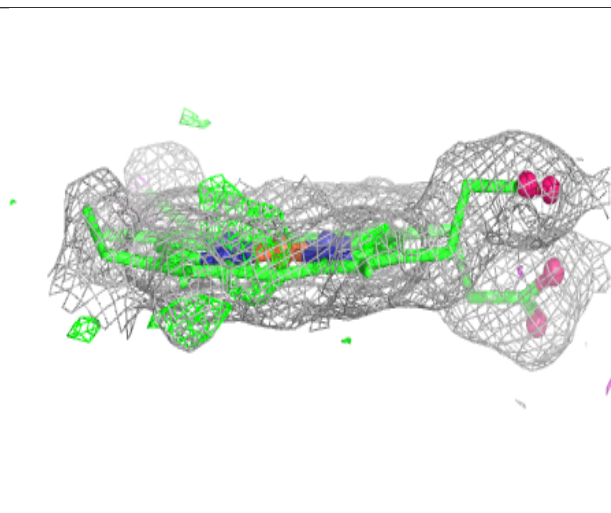
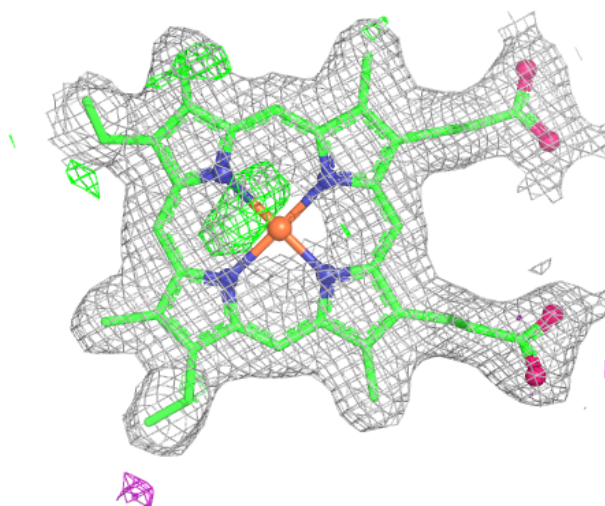
Electron density around HEM B 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



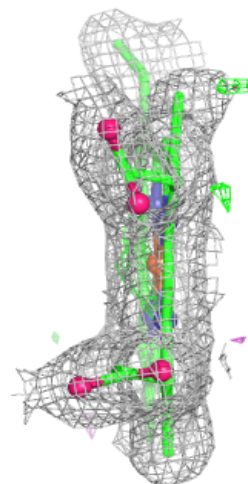
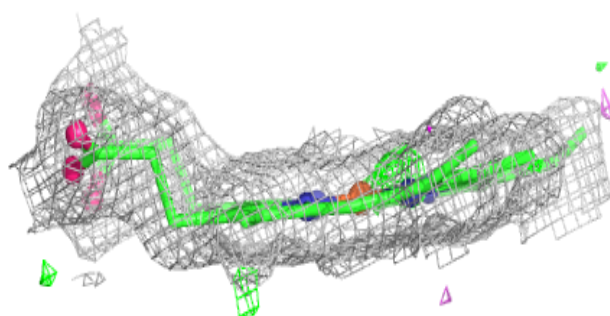
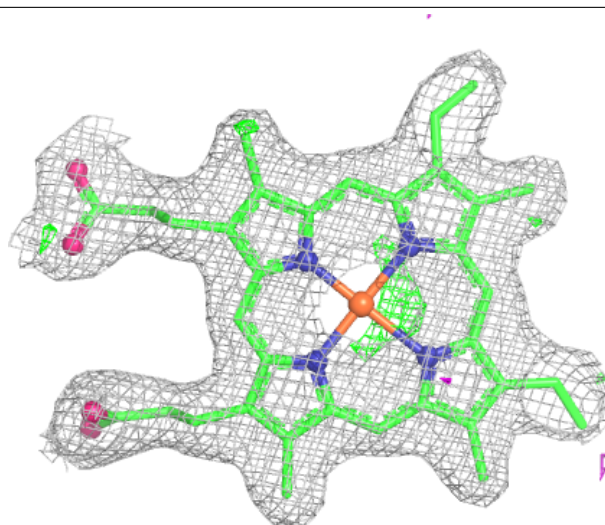
Electron density around HEM A 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



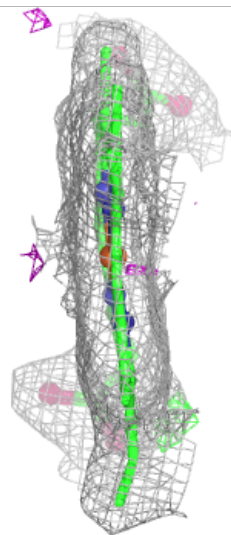
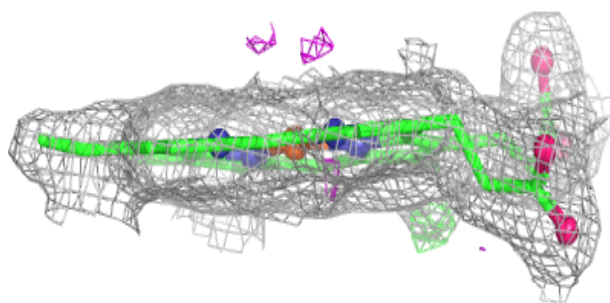
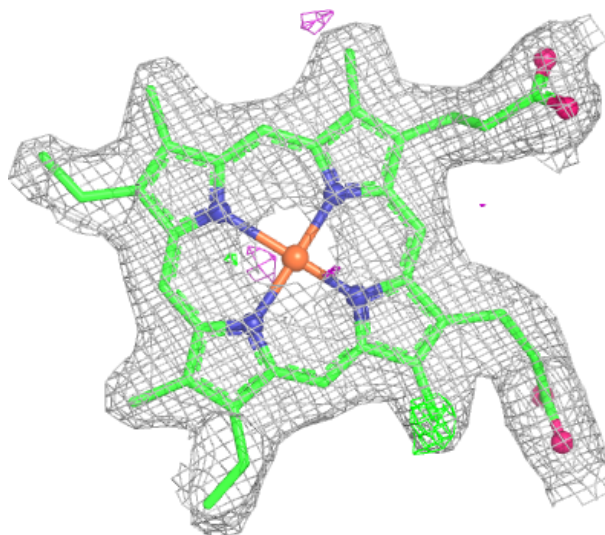
Electron density around HEM D 809:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



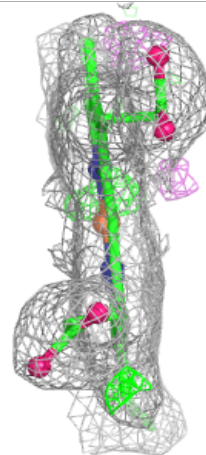
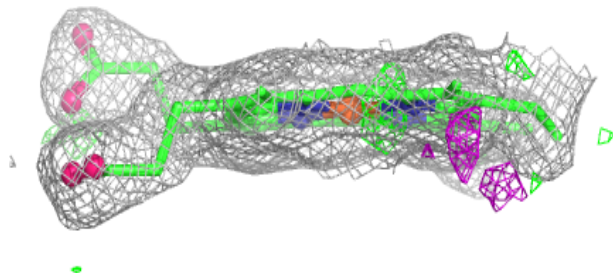
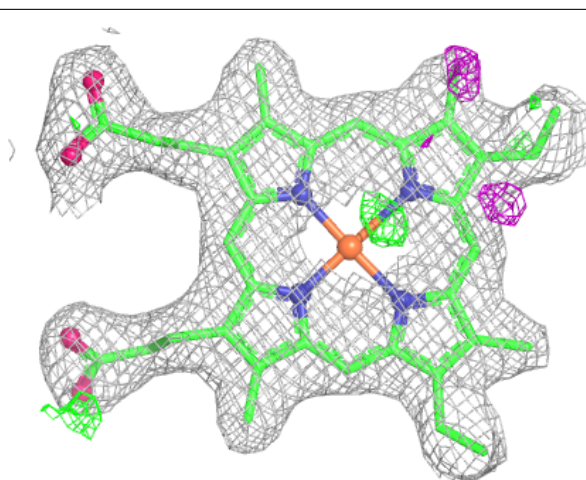
Electron density around HEM G 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



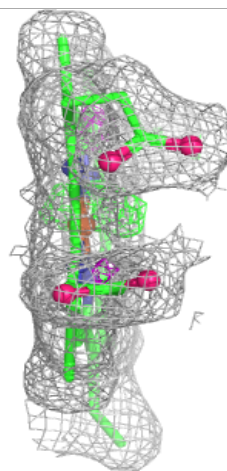
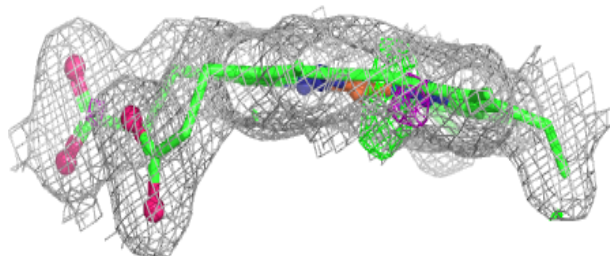
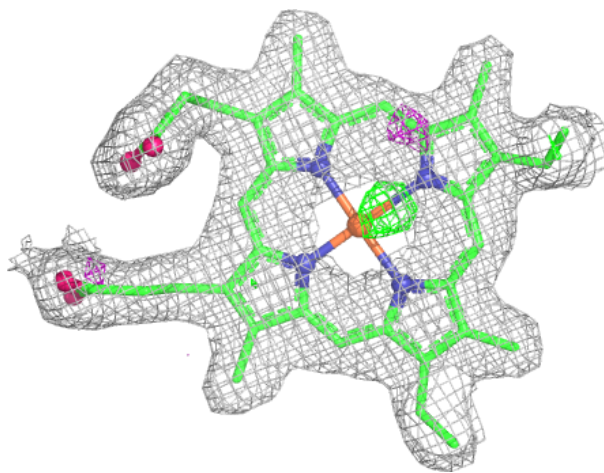
Electron density around HEM J 810:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



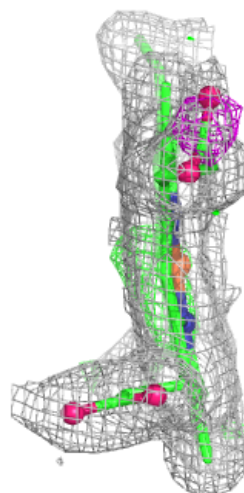
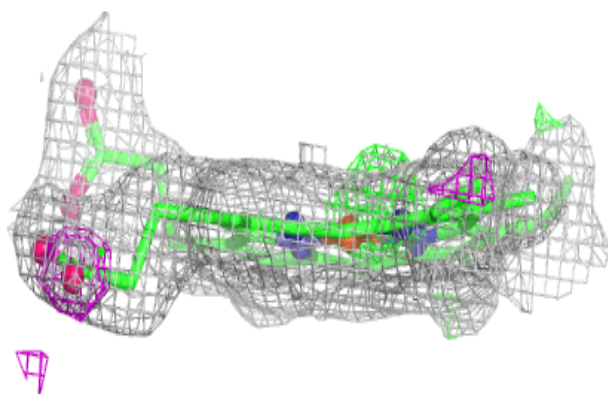
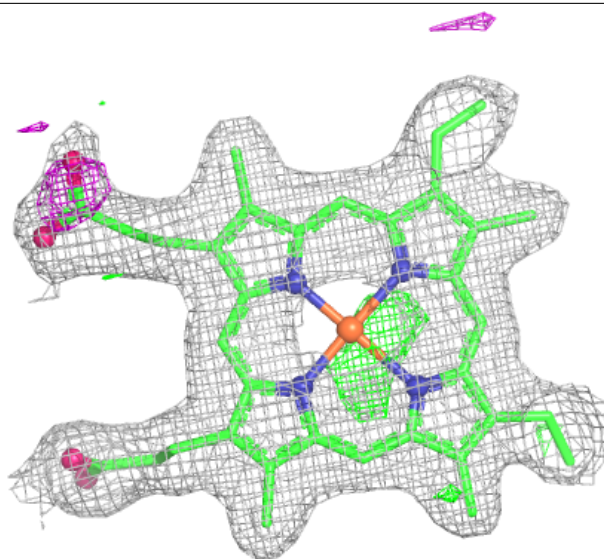
Electron density around HEM A 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



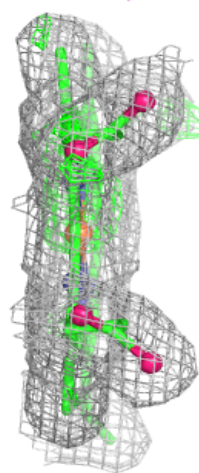
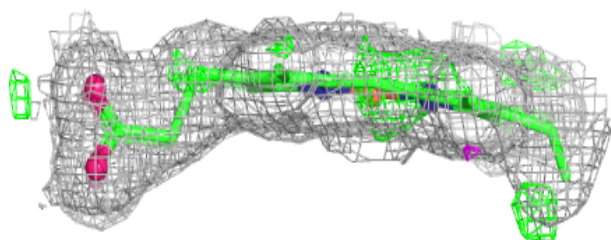
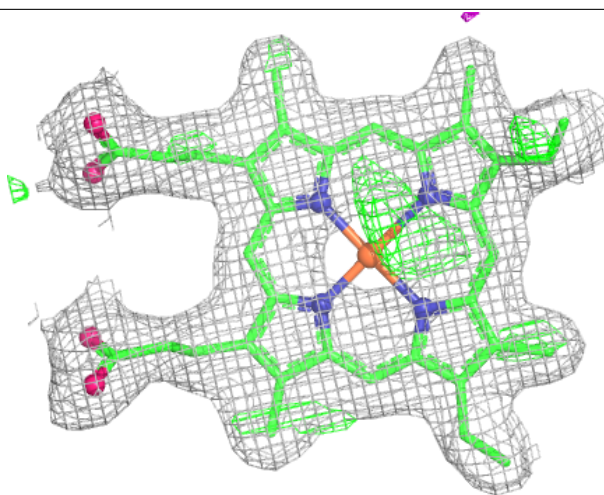
Electron density around HEM D 811:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



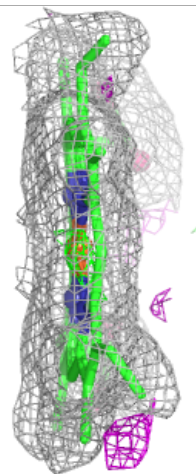
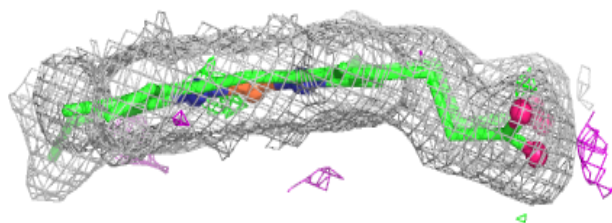
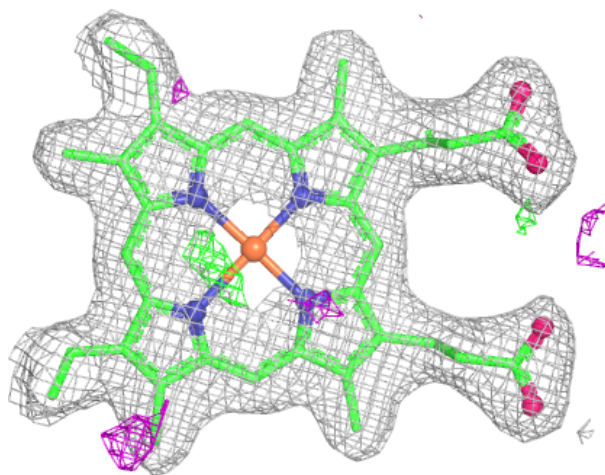
Electron density around HEM D 812:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



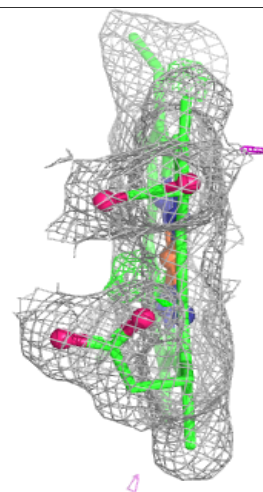
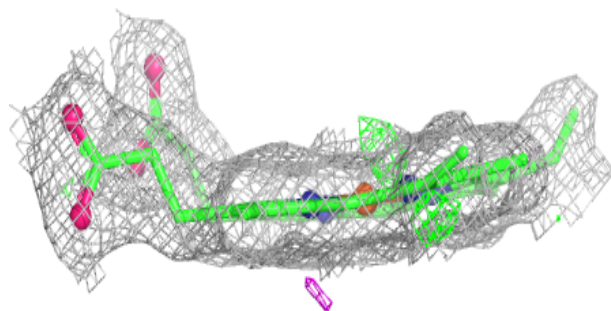
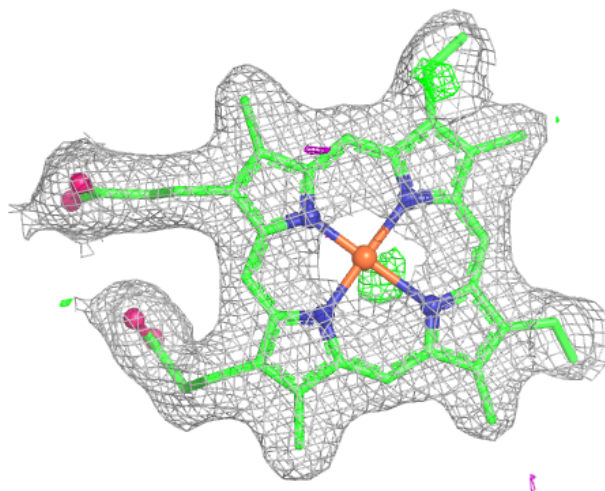
Electron density around HEM D 813:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



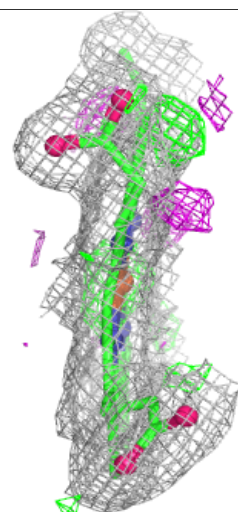
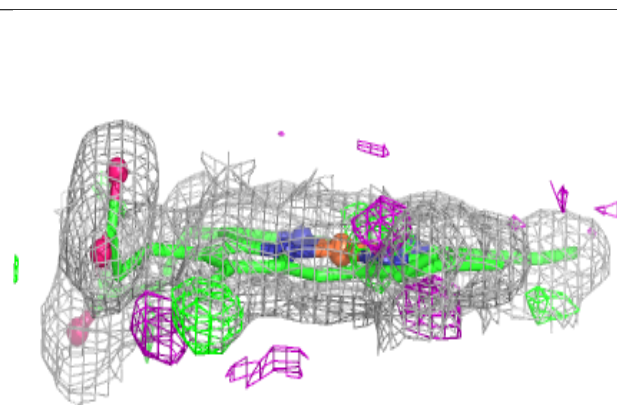
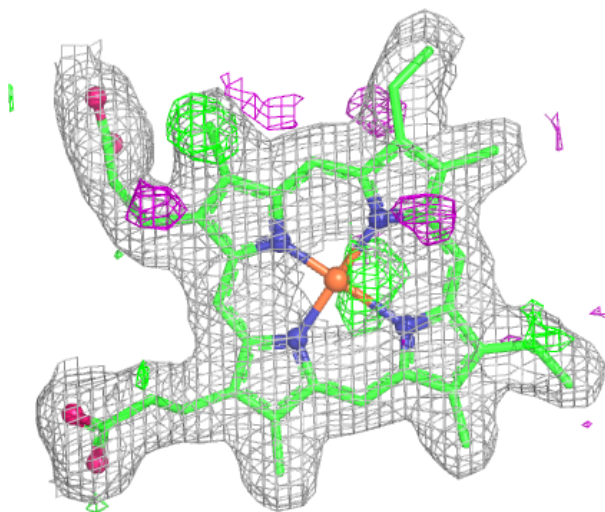
Electron density around HEM E 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



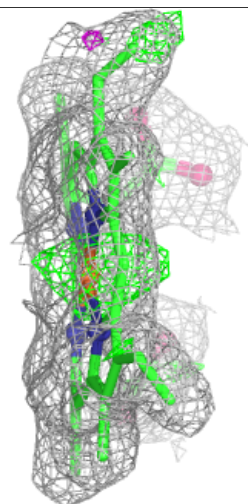
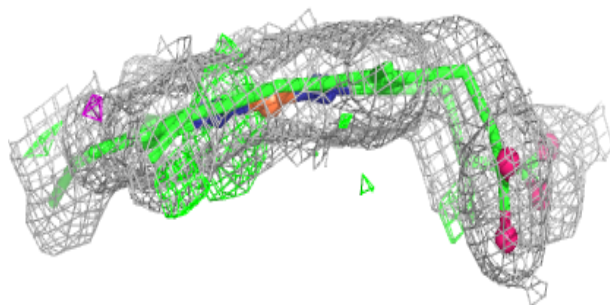
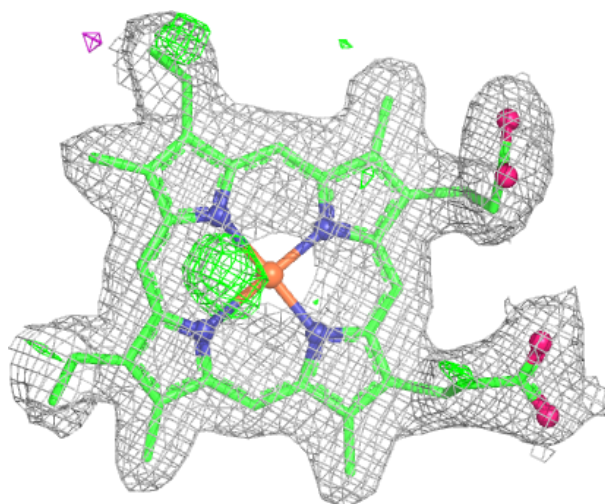
Electron density around HEM A 807:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



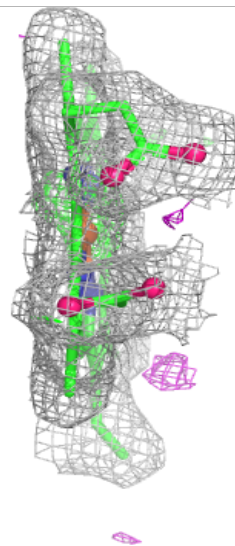
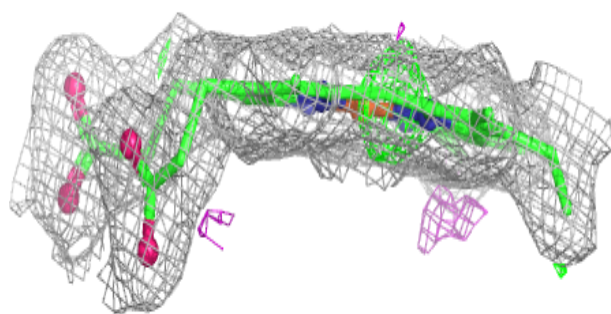
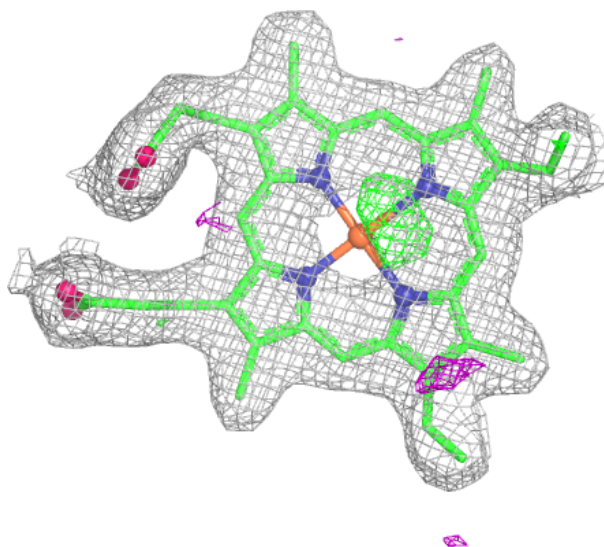
Electron density around HEM A 808:

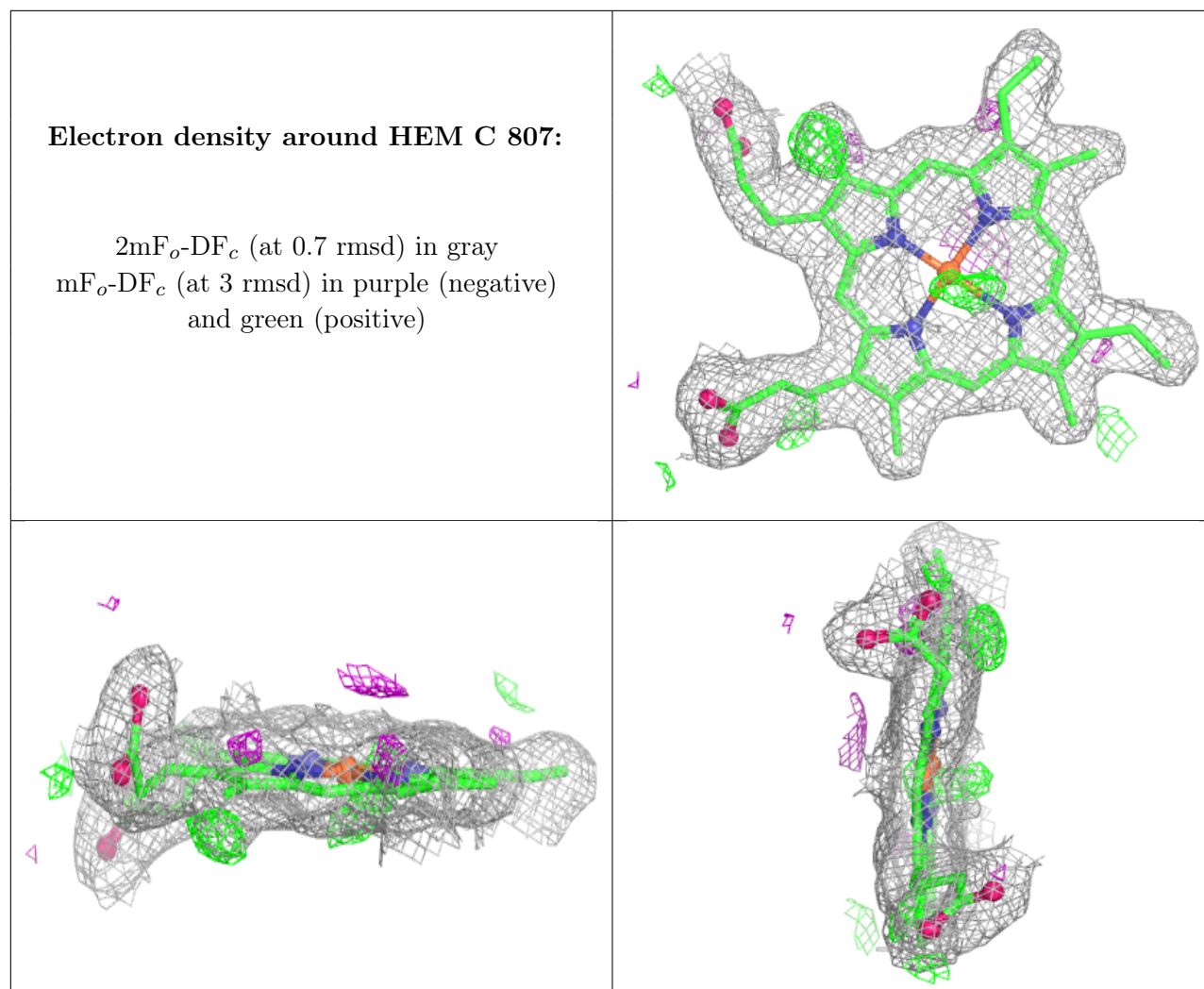
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM C 806:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers ⓘ

There are no such residues in this entry.