



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2026 – 06:36 am BST

PDB ID : 1H29 / pdb_00001h29
Title : Sulfate respiration in *Desulfovibrio vulgaris* Hildenborough: Structure of the 16-heme Cytochrome c HmcA at 2.5 Å resolution and a view of its role in transmembrane electron transfer
Authors : Matias, P.M.; Coelho, A.V.; Valente, F.M.A.; Placido, D.; Legall, J.; Xavier, A.V.; Pereira, I.A.C.; Carrondo, M.A.
Deposited on : 2002-08-01
Resolution : 2.51 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

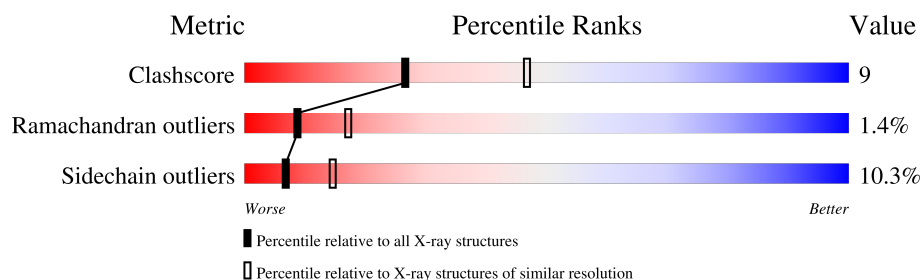
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	514	
1	B	514	
1	C	514	
1	D	514	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	HEC	A	1102	X	-	-	-
2	HEC	A	1103	X	-	-	-
2	HEC	A	1104	X	-	-	-
2	HEC	A	1105	X	-	-	-
2	HEC	A	1106	X	-	-	-
2	HEC	A	1107	X	-	-	-
2	HEC	A	1108	X	-	-	-
2	HEC	A	1109	X	-	-	-
2	HEC	A	1110	X	-	-	-
2	HEC	A	1111	X	-	-	-
2	HEC	A	1113	X	-	-	-
2	HEC	A	1114	X	-	-	-
2	HEC	A	1115	X	-	-	-
2	HEC	A	1116	X	-	-	-
2	HEC	B	1102	X	-	-	-
2	HEC	B	1103	X	-	-	-
2	HEC	B	1104	X	-	-	-
2	HEC	B	1105	X	-	-	-
2	HEC	B	1106	X	-	-	-
2	HEC	B	1107	X	-	-	-
2	HEC	B	1108	X	-	-	-
2	HEC	B	1109	X	-	-	-
2	HEC	B	1110	X	-	-	-
2	HEC	B	1111	X	-	-	-
2	HEC	B	1113	X	-	-	-
2	HEC	B	1114	X	-	-	-
2	HEC	B	1115	X	-	-	-
2	HEC	B	1116	X	-	-	-
2	HEC	C	1101	X	-	-	-
2	HEC	C	1102	X	-	-	-
2	HEC	C	1103	X	-	-	-
2	HEC	C	1104	X	-	-	-
2	HEC	C	1105	X	-	-	-
2	HEC	C	1106	X	-	-	-
2	HEC	C	1107	X	-	-	-
2	HEC	C	1108	X	-	-	-
2	HEC	C	1109	X	-	-	-
2	HEC	C	1110	X	-	-	-
2	HEC	C	1111	X	-	-	-
2	HEC	C	1112	X	-	-	-
2	HEC	C	1113	X	-	-	-
2	HEC	C	1114	X	-	-	-
2	HEC	C	1115	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	HEC	C	1116	X	-	-	-
2	HEC	D	1101	X	-	-	-
2	HEC	D	1102	X	-	-	-
2	HEC	D	1103	X	-	-	-
2	HEC	D	1105	X	-	-	-
2	HEC	D	1106	X	-	-	-
2	HEC	D	1107	X	-	-	-
2	HEC	D	1108	X	-	-	-
2	HEC	D	1109	X	-	-	-
2	HEC	D	1110	X	-	-	-
2	HEC	D	1111	X	-	-	-
2	HEC	D	1113	X	-	-	-
2	HEC	D	1114	X	-	-	-
2	HEC	D	1115	X	-	-	-
2	HEC	D	1116	X	-	-	-

2 Entry composition [i](#)

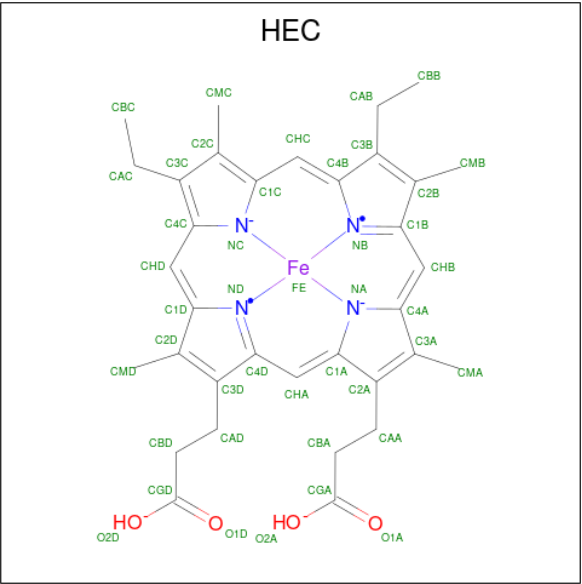
There are 3 unique types of molecules in this entry. The entry contains 18287 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HIGH-MOLECULAR-WEIGHT CYTOCHROME C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	38	0	0
			3783	2323	717	699	44			
1	B	499	Total	C	N	O	S	75	0	0
			3763	2312	712	695	44			
1	C	501	Total	C	N	O	S	90	0	0
			3777	2320	714	699	44			
1	D	492	Total	C	N	O	S	70	0	0
			3715	2284	699	688	44			

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



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

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

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

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

- Molecule 3 is water.

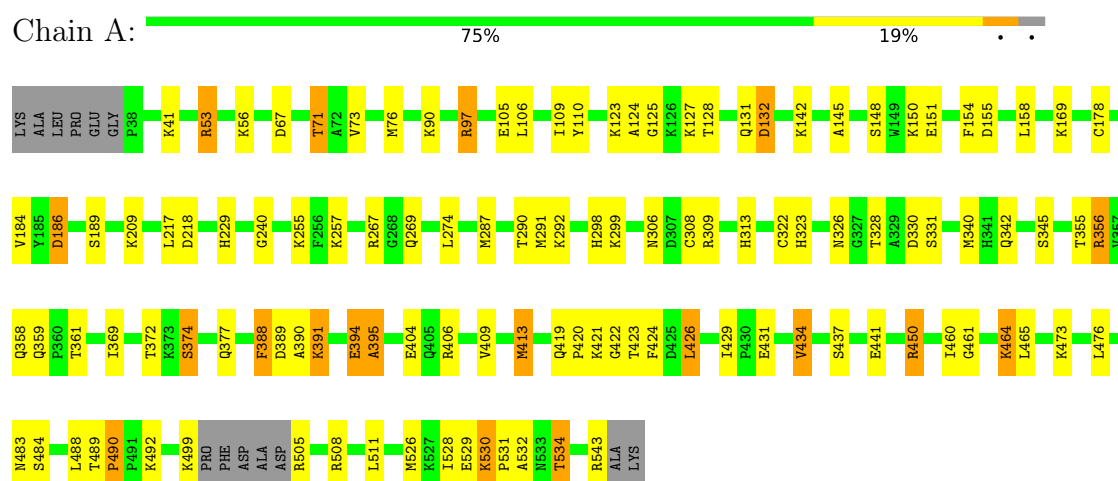
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	123	Total 123	O 123	0	0
3	B	126	Total 126	O 126	0	0
3	C	136	Total 136	O 136	0	0
3	D	112	Total 112	O 112	0	0

3 Residue-property plots

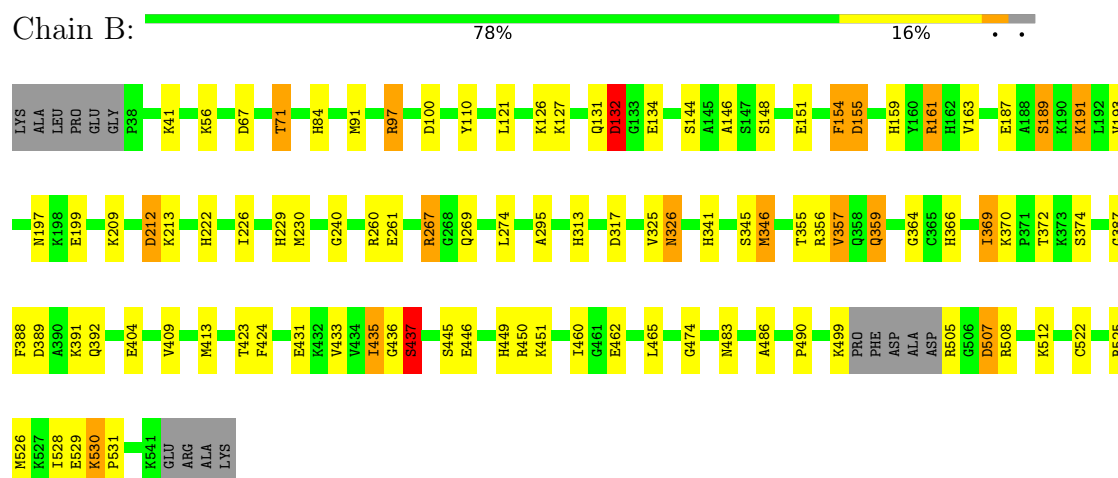
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

• Molecule 1: HIGH-MOLECULAR-WEIGHT CYTOCHROME C

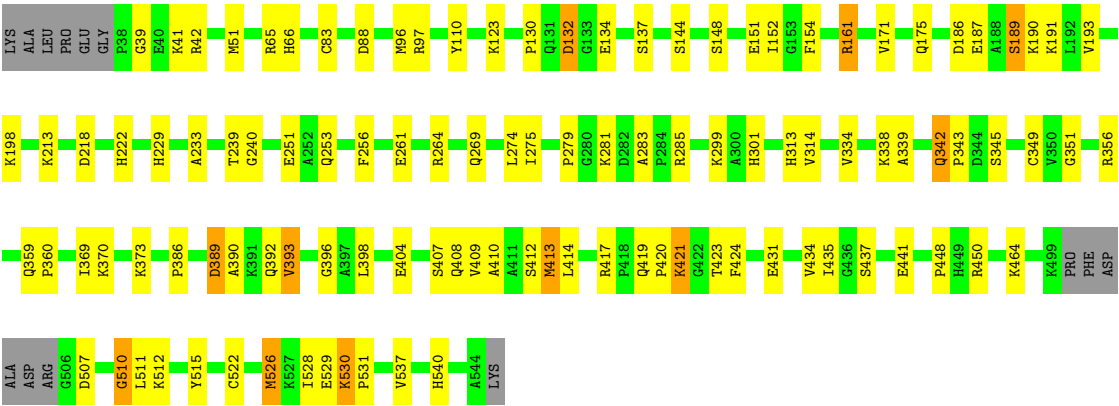


• Molecule 1: HIGH-MOLECULAR-WEIGHT CYTOCHROME C

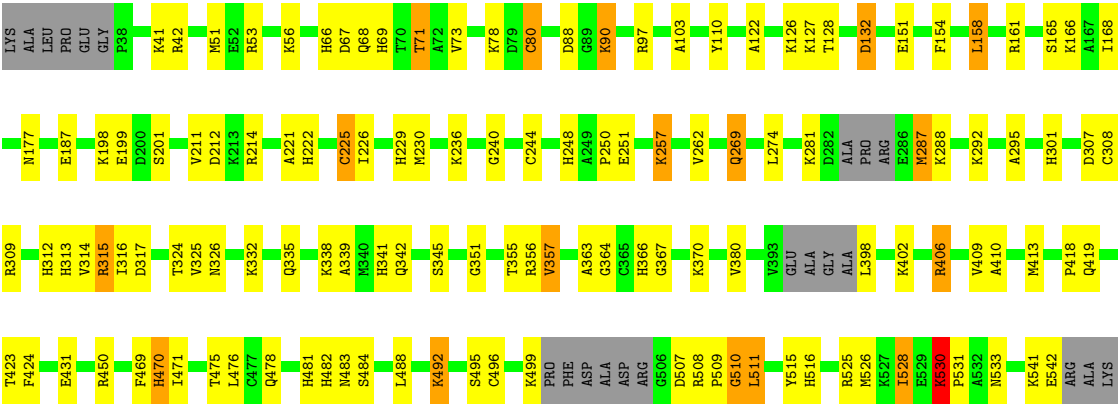


• Molecule 1: HIGH-MOLECULAR-WEIGHT CYTOCHROME C





● Molecule 1: HIGH-MOLECULAR-WEIGHT CYTOCHROME C



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α , β , γ	220.39Å 220.39Å 102.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.51	Depositor
% Data completeness (in resolution range)	92.1 (30.00-2.51)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.192 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	18287	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

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: HEC

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	0.76	4/3864 (0.1%)	1.01	4/5201 (0.1%)
1	B	0.74	4/3844 (0.1%)	1.00	0/5175
1	C	0.73	2/3858 (0.1%)	1.04	7/5194 (0.1%)
1	D	0.68	0/3793	1.01	3/5103 (0.1%)
All	All	0.73	10/15359 (0.1%)	1.02	14/20673 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	D	0	1
All	All	0	5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	413	MET	SD-CE	-6.73	1.62	1.79
1	A	125	GLY	CA-C	6.51	1.58	1.51
1	C	526	MET	SD-CE	-6.28	1.63	1.79
1	B	346	MET	SD-CE	-6.27	1.63	1.79
1	B	189	SER	C-O	6.18	1.32	1.24

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	396	GLY	N-CA-C	12.20	126.63	113.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	421	LYS	N-CA-C	-8.04	97.50	110.20
1	D	510	GLY	N-CA-C	-6.41	103.67	112.25
1	A	389	ASP	N-CA-C	6.24	118.57	108.34
1	C	96	MET	N-CA-C	6.06	119.78	111.54

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	GLN	Peptide
1	A	217	LEU	Peptide
1	B	131	GLN	Peptide
1	B	154	PHE	Peptide
1	D	470	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3783	0	3716	63	0
1	B	3763	0	3697	68	0
1	C	3777	0	3708	75	0
1	D	3715	0	3644	82	0
2	A	688	0	480	18	0
2	B	688	0	480	23	0
2	C	688	0	480	24	0
2	D	688	0	480	34	0
3	A	123	0	0	1	0
3	B	126	0	0	2	0
3	C	136	0	0	2	0
3	D	112	0	0	1	0
All	All	18287	0	16685	313	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 9.

The worst 5 of 313 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:C:522:CYS:SG	1:C:526:MET:HE2	1.67	1.35
1:C:409:VAL:HG12	1:C:413:MET:HE2	1.21	1.10
1:D:530:LYS:HB3	1:D:531:PRO:CD	1.85	1.07
1:B:530:LYS:HB2	1:B:531:PRO:HD3	1.34	1.06
1:D:530:LYS:HB3	1:D:531:PRO:HD3	1.29	1.06

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	497/514 (97%)	463 (93%)	25 (5%)	9 (2%)	6	12
1	B	495/514 (96%)	460 (93%)	28 (6%)	7 (1%)	9	17
1	C	497/514 (97%)	468 (94%)	24 (5%)	5 (1%)	12	24
1	D	484/514 (94%)	451 (93%)	26 (5%)	7 (1%)	9	17
All	All	1973/2056 (96%)	1842 (93%)	103 (5%)	28 (1%)	9	17

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	ASP
1	A	218	ASP
1	A	390	ALA
1	A	395	ALA
1	B	132	ASP

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	405/414 (98%)	358 (88%)	47 (12%)	5	11
1	B	403/414 (97%)	362 (90%)	41 (10%)	7	15
1	C	404/414 (98%)	371 (92%)	33 (8%)	10	23
1	D	400/414 (97%)	355 (89%)	45 (11%)	5	12
All	All	1612/1656 (97%)	1446 (90%)	166 (10%)	7	14

5 of 166 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	435	ILE
1	D	288	LYS
1	C	512	LYS
1	D	132	ASP
1	D	355	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	483	ASN
1	D	483	ASN
1	C	377	GLN
1	D	377	GLN
1	C	358	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

64 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	A	1111	1	50,50,50	2.00	9 (18%)	68,82,82	1.27	8 (11%)
2	HEC	B	1108	1	50,50,50	1.85	9 (18%)	68,82,82	1.45	6 (8%)
2	HEC	B	1107	1	50,50,50	1.73	7 (14%)	68,82,82	1.35	8 (11%)
2	HEC	C	1116	1	50,50,50	1.91	7 (14%)	68,82,82	1.30	7 (10%)
2	HEC	A	1104	1	50,50,50	1.83	6 (12%)	68,82,82	1.34	8 (11%)
2	HEC	A	1112	1	50,50,50	1.93	11 (22%)	68,82,82	1.28	5 (7%)
2	HEC	A	1116	1	50,50,50	1.81	8 (16%)	68,82,82	1.33	9 (13%)
2	HEC	A	1107	1	50,50,50	1.78	8 (16%)	68,82,82	1.63	14 (20%)
2	HEC	C	1102	1	50,50,50	1.84	7 (14%)	68,82,82	1.29	5 (7%)
2	HEC	C	1110	1	50,50,50	1.88	8 (16%)	68,82,82	1.55	11 (16%)
2	HEC	D	1102	1	50,50,50	1.86	9 (18%)	68,82,82	1.29	7 (10%)
2	HEC	C	1104	1	50,50,50	1.81	7 (14%)	68,82,82	1.43	9 (13%)
2	HEC	C	1108	1	50,50,50	1.77	8 (16%)	68,82,82	1.32	4 (5%)
2	HEC	C	1115	1	50,50,50	2.14	10 (20%)	68,82,82	1.73	14 (20%)
2	HEC	D	1108	1	50,50,50	1.93	8 (16%)	68,82,82	1.76	15 (22%)
2	HEC	C	1106	1	50,50,50	1.84	10 (20%)	68,82,82	1.38	10 (14%)
2	HEC	D	1109	1	50,50,50	1.90	9 (18%)	68,82,82	1.18	6 (8%)
2	HEC	A	1101	1	50,50,50	1.97	10 (20%)	68,82,82	1.35	6 (8%)
2	HEC	B	1110	1	50,50,50	1.82	10 (20%)	68,82,82	1.51	11 (16%)
2	HEC	B	1101	1	50,50,50	2.00	9 (18%)	68,82,82	1.62	9 (13%)
2	HEC	C	1103	1	50,50,50	1.77	9 (18%)	68,82,82	1.49	8 (11%)
2	HEC	A	1109	1	50,50,50	2.09	7 (14%)	68,82,82	1.24	5 (7%)
2	HEC	B	1103	1	50,50,50	1.91	10 (20%)	68,82,82	1.26	5 (7%)
2	HEC	B	1114	1	50,50,50	1.96	10 (20%)	68,82,82	1.31	6 (8%)
2	HEC	A	1102	1	50,50,50	1.93	8 (16%)	68,82,82	1.43	4 (5%)
2	HEC	B	1116	1	50,50,50	1.88	8 (16%)	68,82,82	1.30	8 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	B	1111	1	50,50,50	1.93	9 (18%)	68,82,82	1.38	8 (11%)
2	HEC	C	1113	1	50,50,50	1.98	9 (18%)	68,82,82	1.48	10 (14%)
2	HEC	D	1105	1	50,50,50	2.02	9 (18%)	68,82,82	1.50	8 (11%)
2	HEC	B	1112	1	50,50,50	1.86	8 (16%)	68,82,82	1.23	7 (10%)
2	HEC	C	1105	1	50,50,50	1.86	6 (12%)	68,82,82	1.39	8 (11%)
2	HEC	B	1102	1	50,50,50	1.85	6 (12%)	68,82,82	1.26	5 (7%)
2	HEC	A	1115	1	50,50,50	1.91	8 (16%)	68,82,82	1.49	9 (13%)
2	HEC	B	1104	1	50,50,50	1.84	9 (18%)	68,82,82	1.58	10 (14%)
2	HEC	B	1115	1	50,50,50	2.00	10 (20%)	68,82,82	1.45	12 (17%)
2	HEC	D	1107	1	50,50,50	1.87	8 (16%)	68,82,82	1.42	8 (11%)
2	HEC	C	1112	1	50,50,50	1.76	9 (18%)	68,82,82	1.17	5 (7%)
2	HEC	D	1110	1	50,50,50	2.02	13 (26%)	68,82,82	1.38	9 (13%)
2	HEC	D	1101	1	50,50,50	1.98	9 (18%)	68,82,82	1.48	7 (10%)
2	HEC	D	1112	1	50,50,50	1.94	9 (18%)	68,82,82	1.24	3 (4%)
2	HEC	B	1109	1	50,50,50	1.92	10 (20%)	68,82,82	1.18	3 (4%)
2	HEC	C	1107	1	50,50,50	1.79	6 (12%)	68,82,82	1.48	8 (11%)
2	HEC	A	1113	1	50,50,50	1.81	7 (14%)	68,82,82	1.31	6 (8%)
2	HEC	A	1108	1	50,50,50	1.92	9 (18%)	68,82,82	1.45	10 (14%)
2	HEC	C	1101	1	50,50,50	1.79	7 (14%)	68,82,82	1.24	6 (8%)
2	HEC	B	1113	1	50,50,50	1.87	7 (14%)	68,82,82	1.51	11 (16%)
2	HEC	D	1113	1	50,50,50	1.89	8 (16%)	68,82,82	1.36	5 (7%)
2	HEC	A	1106	1	50,50,50	1.88	10 (20%)	68,82,82	1.30	6 (8%)
2	HEC	A	1110	1	50,50,50	1.87	8 (16%)	68,82,82	1.31	4 (5%)
2	HEC	D	1106	1	50,50,50	1.83	7 (14%)	68,82,82	1.41	6 (8%)
2	HEC	B	1106	1	50,50,50	1.77	8 (16%)	68,82,82	1.51	9 (13%)
2	HEC	C	1114	1	50,50,50	1.96	10 (20%)	68,82,82	1.28	5 (7%)
2	HEC	D	1114	1	50,50,50	1.93	10 (20%)	68,82,82	1.37	7 (10%)
2	HEC	A	1105	1	50,50,50	1.80	8 (16%)	68,82,82	1.32	5 (7%)
2	HEC	D	1103	1	50,50,50	1.89	8 (16%)	68,82,82	1.43	8 (11%)
2	HEC	A	1114	1	50,50,50	2.01	8 (16%)	68,82,82	1.62	11 (16%)
2	HEC	C	1109	1	50,50,50	1.86	8 (16%)	68,82,82	1.16	4 (5%)
2	HEC	D	1116	1	50,50,50	1.81	8 (16%)	68,82,82	1.20	7 (10%)
2	HEC	D	1111	1	50,50,50	1.98	10 (20%)	68,82,82	1.43	9 (13%)
2	HEC	D	1115	1	50,50,50	2.03	11 (22%)	68,82,82	1.40	8 (11%)
2	HEC	B	1105	1	50,50,50	1.91	10 (20%)	68,82,82	1.42	8 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	D	1104	1	50,50,50	1.87	8 (16%)	68,82,82	1.44	8 (11%)
2	HEC	A	1103	1	50,50,50	1.78	11 (22%)	68,82,82	1.49	11 (16%)
2	HEC	C	1111	1	50,50,50	1.87	8 (16%)	68,82,82	1.16	5 (7%)

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
2	HEC	A	1111	1	1/1/3/7	5/14/54/54	-
2	HEC	B	1108	1	1/1/3/7	4/14/54/54	-
2	HEC	B	1107	1	1/1/3/7	6/14/54/54	-
2	HEC	C	1116	1	1/1/3/7	4/14/54/54	-
2	HEC	A	1104	1	1/1/3/7	5/14/54/54	-
2	HEC	A	1112	1	-	6/14/54/54	-
2	HEC	A	1116	1	1/1/3/7	4/14/54/54	-
2	HEC	A	1107	1	1/1/3/7	8/14/54/54	-
2	HEC	C	1102	1	1/1/3/7	6/14/54/54	-
2	HEC	C	1110	1	1/1/3/7	7/14/54/54	-
2	HEC	D	1102	1	1/1/3/7	4/14/54/54	-
2	HEC	C	1104	1	1/1/3/7	5/14/54/54	-
2	HEC	C	1108	1	1/1/3/7	4/14/54/54	-
2	HEC	C	1115	1	1/1/3/7	8/14/54/54	-
2	HEC	D	1108	1	1/1/3/7	5/14/54/54	-
2	HEC	C	1106	1	1/1/3/7	6/14/54/54	-
2	HEC	D	1109	1	1/1/3/7	9/14/54/54	-
2	HEC	B	1110	1	1/1/3/7	8/14/54/54	-
2	HEC	A	1101	1	-	5/14/54/54	-
2	HEC	B	1101	1	-	4/14/54/54	-
2	HEC	C	1103	1	1/1/3/7	6/14/54/54	-
2	HEC	A	1109	1	1/1/3/7	9/14/54/54	-
2	HEC	B	1103	1	1/1/3/7	4/14/54/54	-
2	HEC	B	1114	1	1/1/3/7	1/14/54/54	-
2	HEC	A	1102	1	1/1/3/7	6/14/54/54	-
2	HEC	B	1116	1	1/1/3/7	5/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	B	1111	1	1/1/3/7	7/14/54/54	-
2	HEC	C	1113	1	1/1/3/7	4/14/54/54	-
2	HEC	D	1105	1	1/1/3/7	10/14/54/54	-
2	HEC	B	1112	1	-	6/14/54/54	-
2	HEC	C	1105	1	1/1/3/7	9/14/54/54	-
2	HEC	B	1102	1	1/1/3/7	6/14/54/54	-
2	HEC	A	1115	1	1/1/3/7	8/14/54/54	-
2	HEC	B	1104	1	1/1/3/7	7/14/54/54	-
2	HEC	B	1115	1	1/1/3/7	6/14/54/54	-
2	HEC	D	1107	1	1/1/3/7	4/14/54/54	-
2	HEC	C	1112	1	1/1/3/7	6/14/54/54	-
2	HEC	D	1110	1	1/1/3/7	10/14/54/54	-
2	HEC	D	1101	1	1/1/3/7	5/14/54/54	-
2	HEC	D	1112	1	-	8/14/54/54	-
2	HEC	B	1109	1	1/1/3/7	4/14/54/54	-
2	HEC	C	1107	1	1/1/3/7	5/14/54/54	-
2	HEC	A	1113	1	1/1/3/7	5/14/54/54	-
2	HEC	A	1108	1	1/1/3/7	7/14/54/54	-
2	HEC	C	1101	1	1/1/3/7	7/14/54/54	-
2	HEC	B	1113	1	1/1/3/7	4/14/54/54	-
2	HEC	D	1113	1	1/1/3/7	4/14/54/54	-
2	HEC	A	1106	1	1/1/3/7	6/14/54/54	-
2	HEC	A	1110	1	1/1/3/7	6/14/54/54	-
2	HEC	D	1106	1	1/1/3/7	6/14/54/54	-
2	HEC	B	1106	1	1/1/3/7	6/14/54/54	-
2	HEC	C	1114	1	1/1/3/7	1/14/54/54	-
2	HEC	D	1114	1	1/1/3/7	2/14/54/54	-
2	HEC	A	1105	1	1/1/3/7	6/14/54/54	-
2	HEC	D	1103	1	1/1/3/7	6/14/54/54	-
2	HEC	A	1114	1	1/1/3/7	4/14/54/54	-
2	HEC	C	1109	1	1/1/3/7	9/14/54/54	-
2	HEC	D	1116	1	1/1/3/7	4/14/54/54	-
2	HEC	D	1111	1	1/1/3/7	7/14/54/54	-
2	HEC	D	1115	1	1/1/3/7	6/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	B	1105	1	1/1/3/7	8/14/54/54	-
2	HEC	D	1104	1	-	5/14/54/54	-
2	HEC	A	1103	1	1/1/3/7	6/14/54/54	-
2	HEC	C	1111	1	1/1/3/7	10/14/54/54	-

The worst 5 of 549 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1110	HEC	C3D-C2D	8.72	1.55	1.36
2	A	1108	HEC	C3D-C2D	8.63	1.55	1.36
2	B	1114	HEC	C3D-C2D	8.50	1.54	1.36
2	D	1105	HEC	C3D-C2D	8.50	1.54	1.36
2	D	1114	HEC	C3D-C2D	8.36	1.54	1.36

The worst 5 of 487 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1101	HEC	C1D-ND-C4D	7.19	112.50	105.07
2	A	1114	HEC	C1D-ND-C4D	6.89	112.19	105.07
2	D	1108	HEC	C1D-ND-C4D	6.84	112.14	105.07
2	A	1102	HEC	C1D-ND-C4D	6.74	112.03	105.07
2	D	1114	HEC	C1D-ND-C4D	6.51	111.80	105.07

5 of 58 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1102	HEC	NA
2	A	1103	HEC	NA
2	A	1104	HEC	NA
2	A	1105	HEC	NA
2	A	1106	HEC	NA

5 of 374 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1105	HEC	C1A-C2A-CAA-CBA
2	A	1105	HEC	C3A-C2A-CAA-CBA
2	A	1107	HEC	C1A-C2A-CAA-CBA
2	A	1109	HEC	C1A-C2A-CAA-CBA
2	A	1109	HEC	C3A-C2A-CAA-CBA

There are no ring outliers.

48 monomers are involved in 99 short contacts:

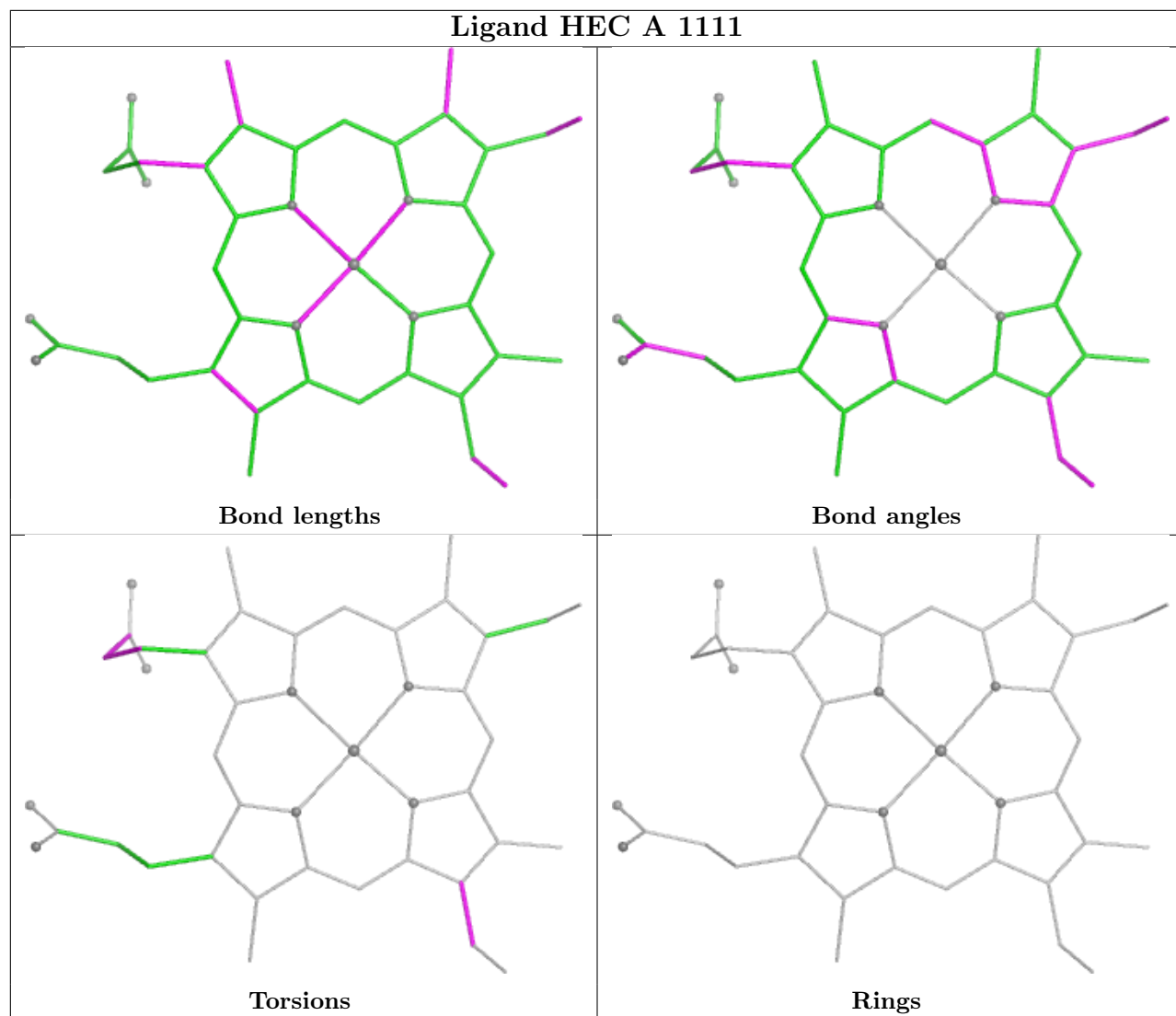
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1111	HEC	1	0
2	B	1107	HEC	3	0
2	A	1104	HEC	3	0
2	A	1112	HEC	2	0
2	C	1102	HEC	1	0
2	C	1110	HEC	3	0
2	D	1102	HEC	3	0
2	C	1104	HEC	1	0
2	C	1108	HEC	1	0
2	C	1115	HEC	5	0
2	D	1108	HEC	3	0
2	C	1106	HEC	1	0
2	D	1109	HEC	4	0
2	B	1110	HEC	1	0
2	C	1103	HEC	1	0
2	A	1109	HEC	2	0
2	B	1114	HEC	1	0
2	A	1102	HEC	2	0
2	B	1116	HEC	1	0
2	B	1111	HEC	2	0
2	B	1112	HEC	1	0
2	B	1102	HEC	2	0
2	A	1115	HEC	1	0
2	B	1104	HEC	1	0
2	B	1115	HEC	7	0
2	D	1107	HEC	2	0
2	D	1110	HEC	4	0
2	D	1101	HEC	3	0
2	D	1112	HEC	2	0
2	B	1109	HEC	1	0
2	C	1107	HEC	2	0
2	A	1113	HEC	2	0
2	A	1108	HEC	2	0
2	C	1101	HEC	2	0
2	B	1113	HEC	1	0
2	D	1113	HEC	1	0
2	A	1110	HEC	2	0
2	D	1106	HEC	4	0
2	B	1106	HEC	2	0
2	C	1114	HEC	2	0

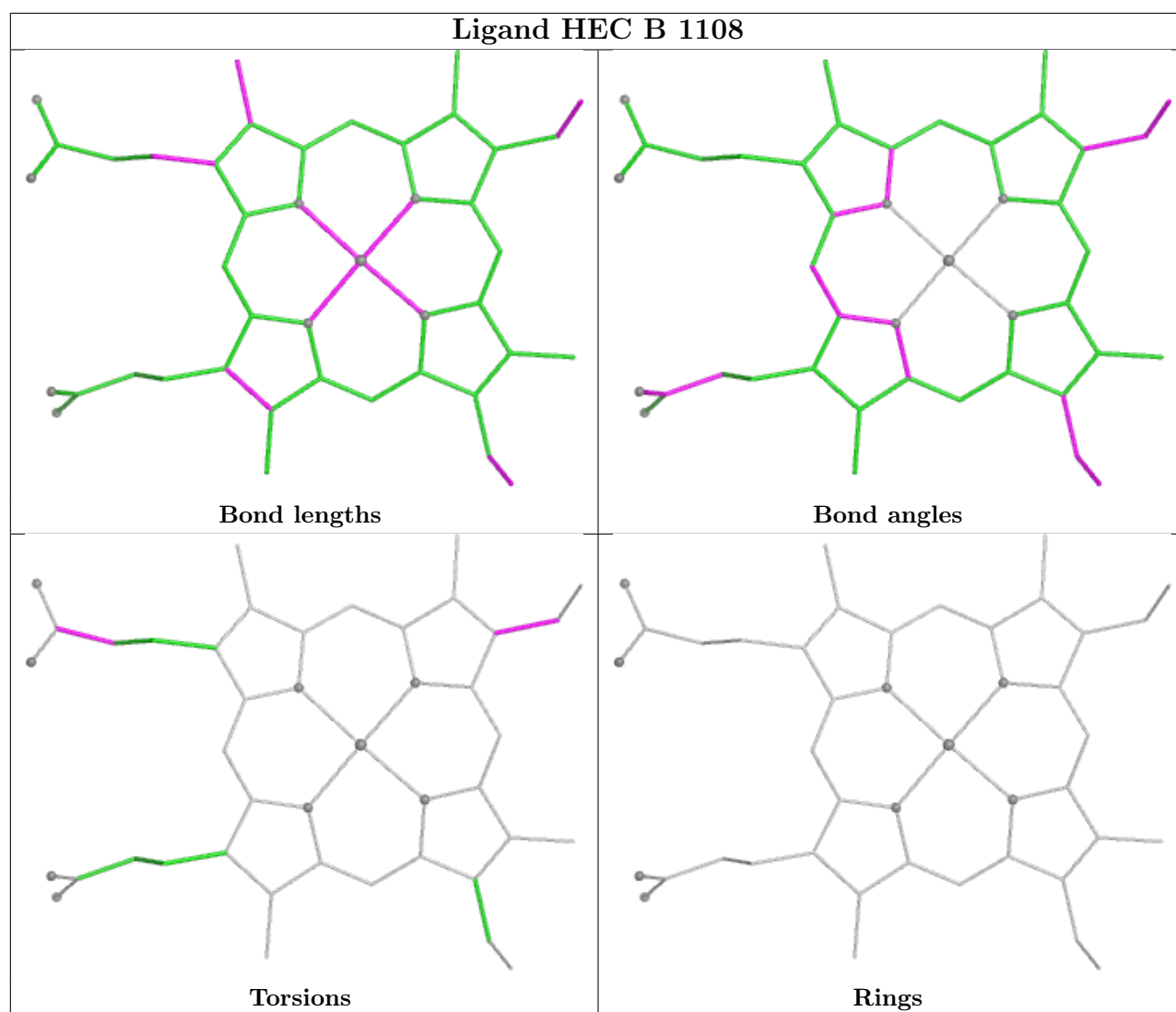
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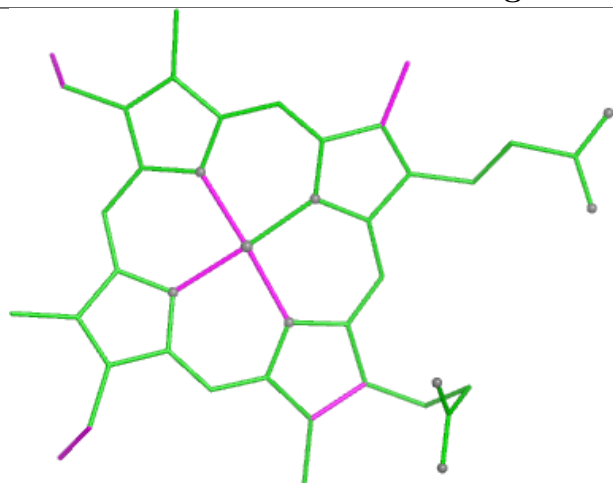
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1114	HEC	2	0
2	D	1103	HEC	2	0
2	A	1114	HEC	1	0
2	C	1109	HEC	5	0
2	D	1111	HEC	1	0
2	D	1115	HEC	1	0
2	D	1104	HEC	7	0
2	C	1111	HEC	1	0

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

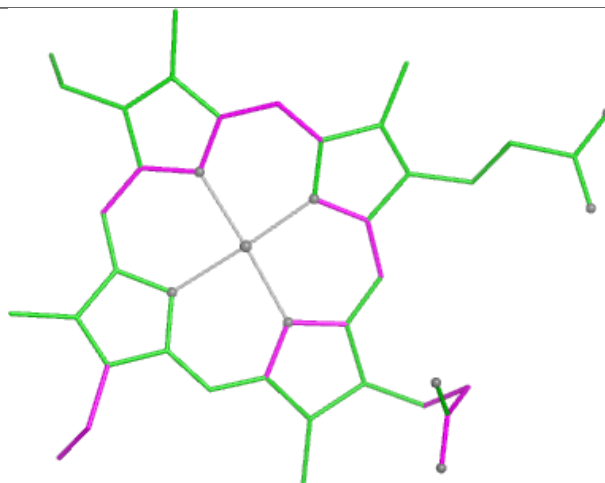




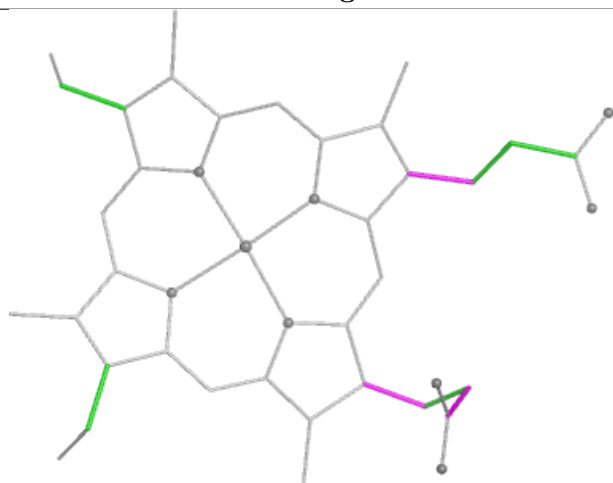
Ligand HEC B 1107



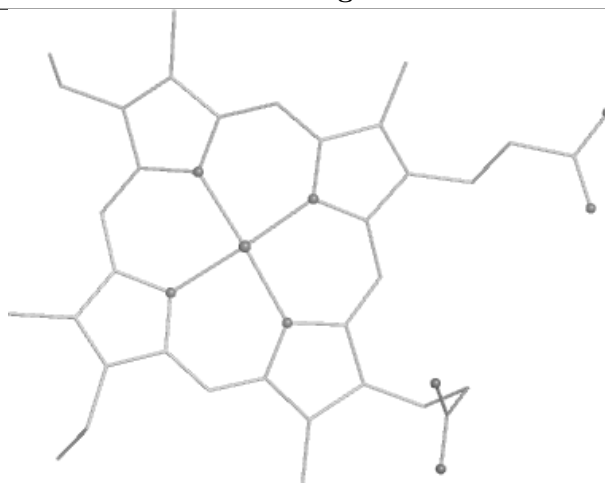
Bond lengths



Bond angles

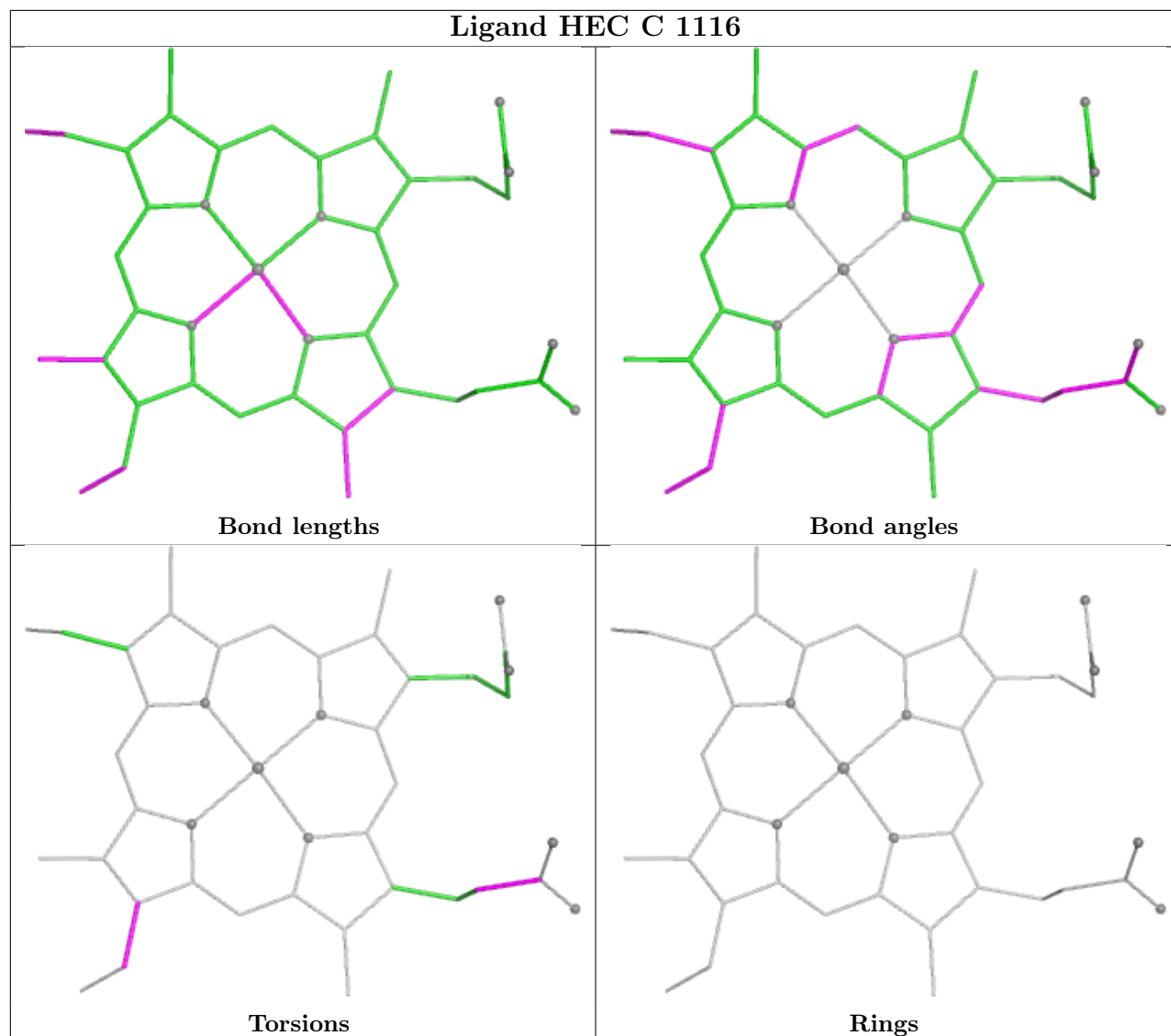


Torsions

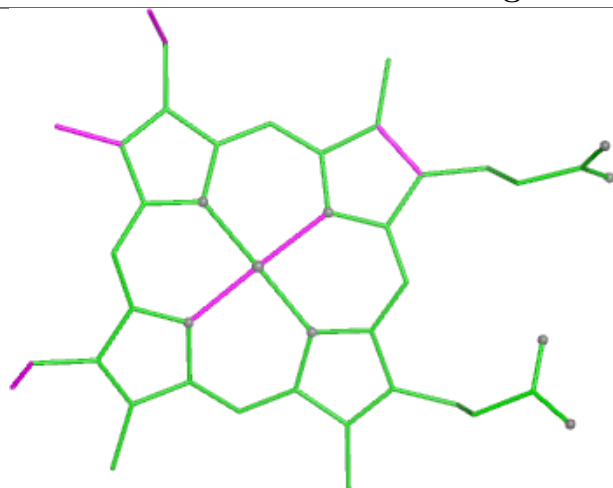


Rings

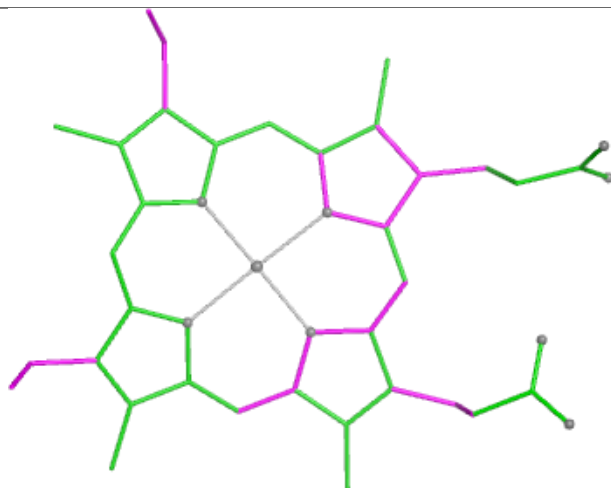
Ligand HEC C 1116



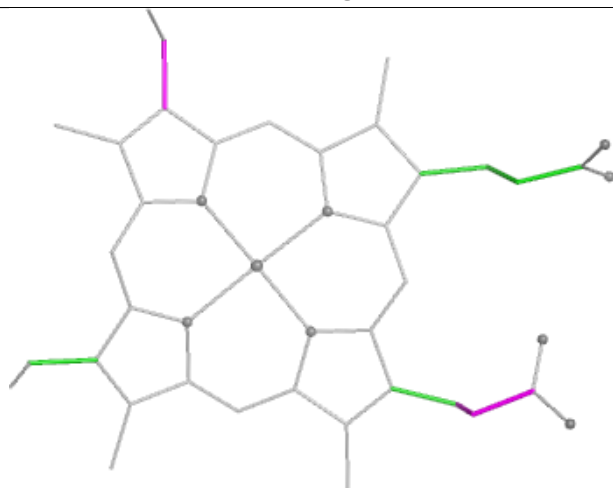
Ligand HEC A 1104



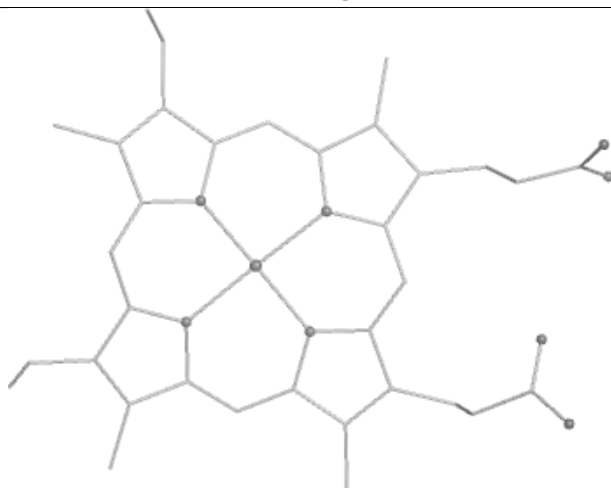
Bond lengths



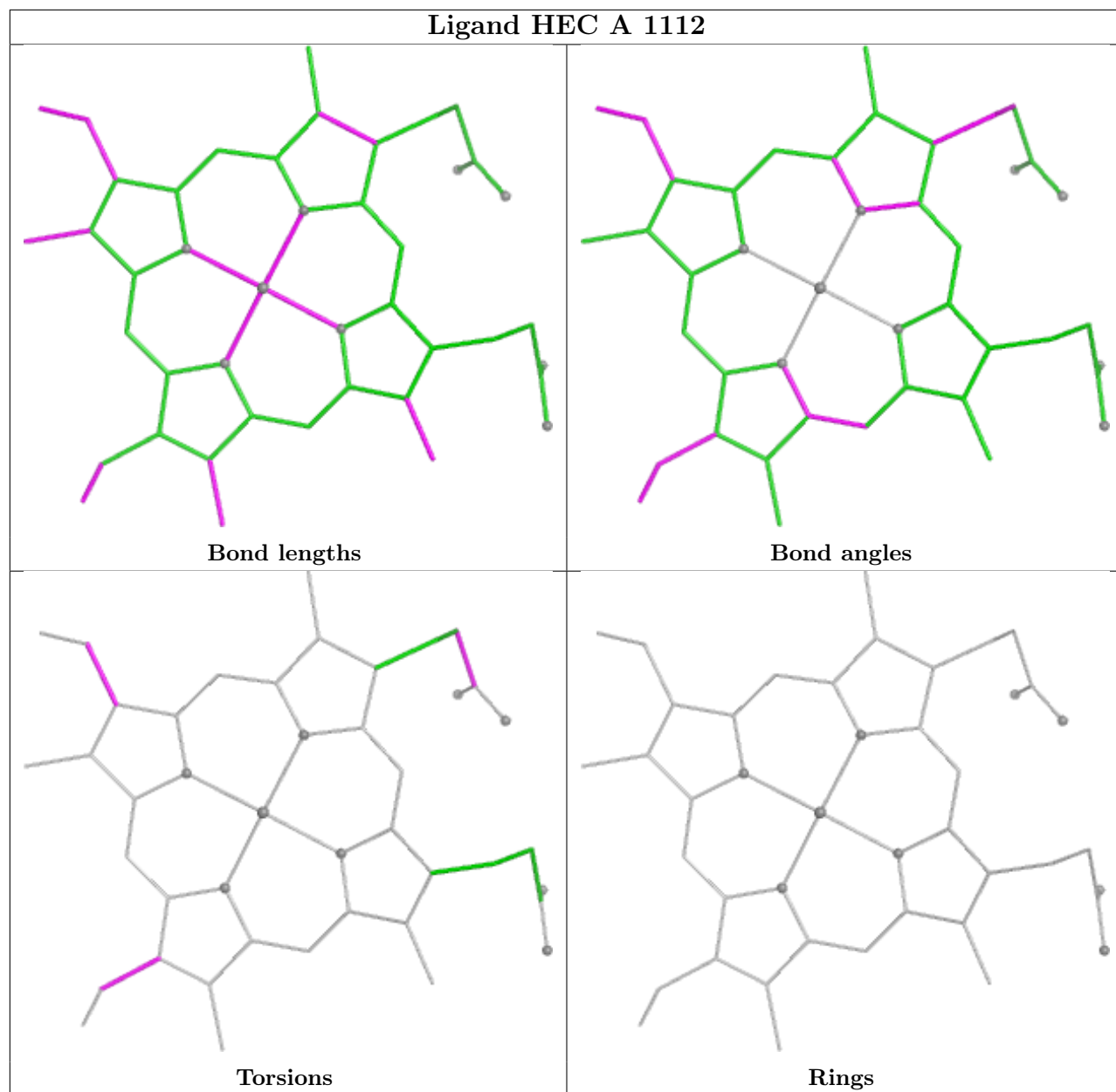
Bond angles

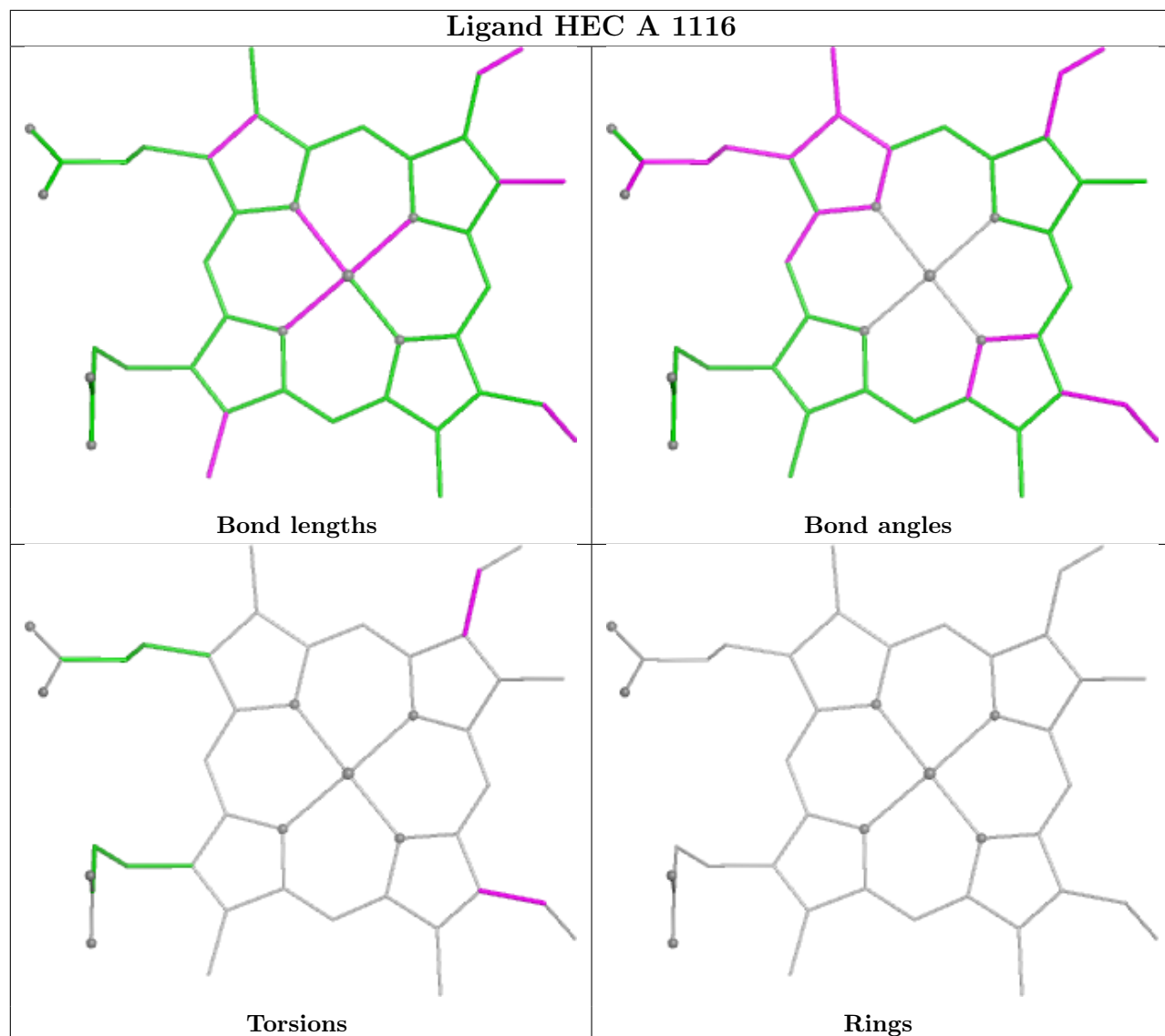


Torsions

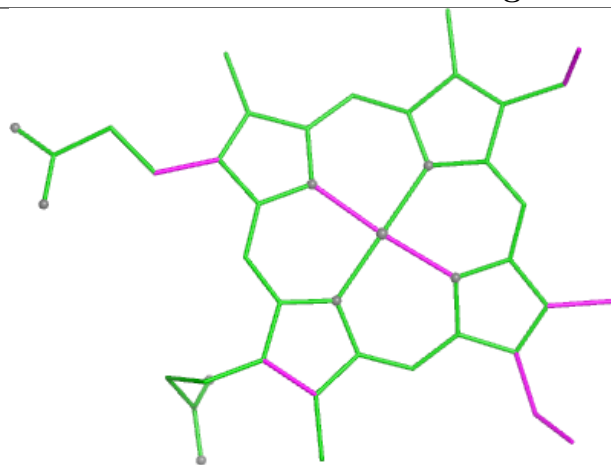


Rings

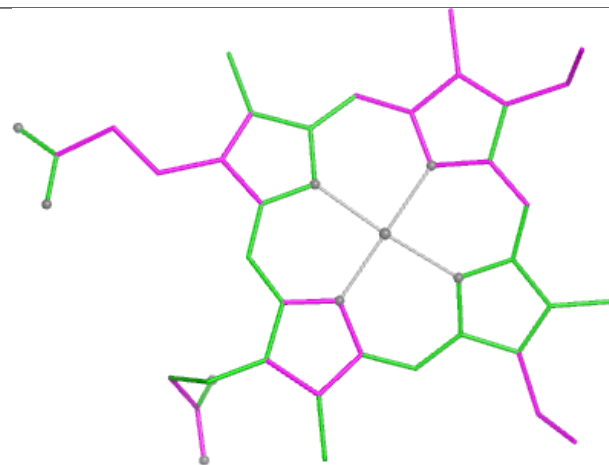




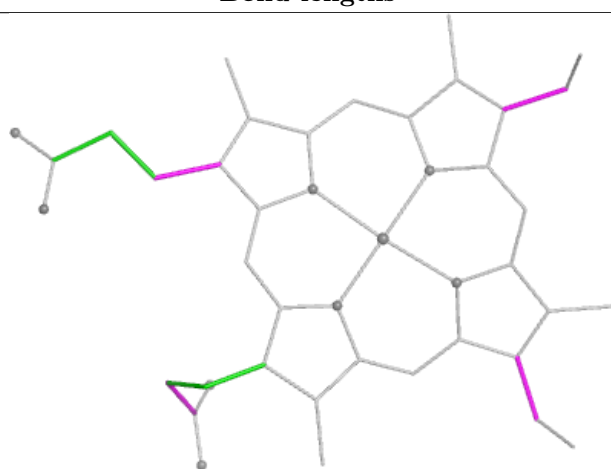
Ligand HEC A 1107



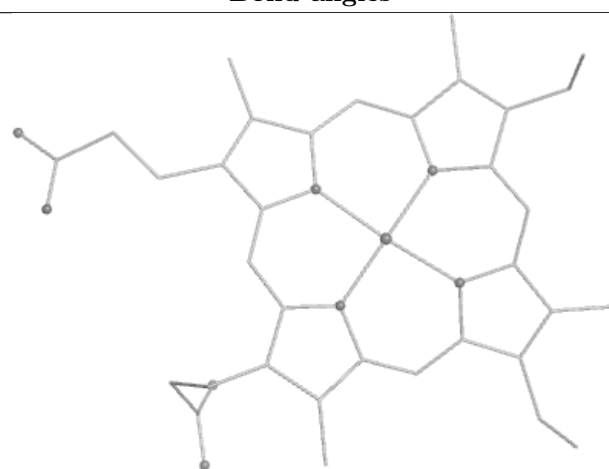
Bond lengths



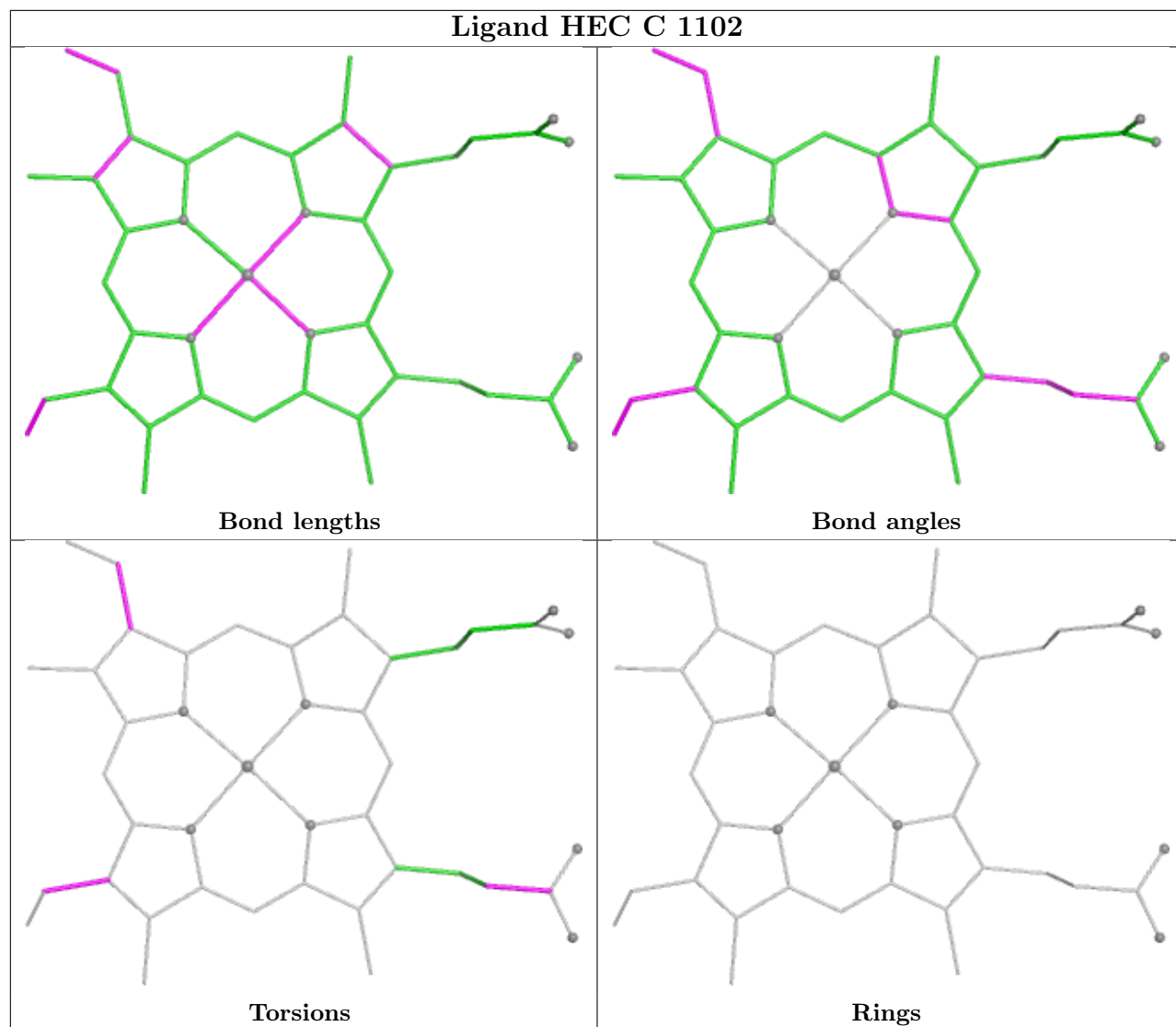
Bond angles



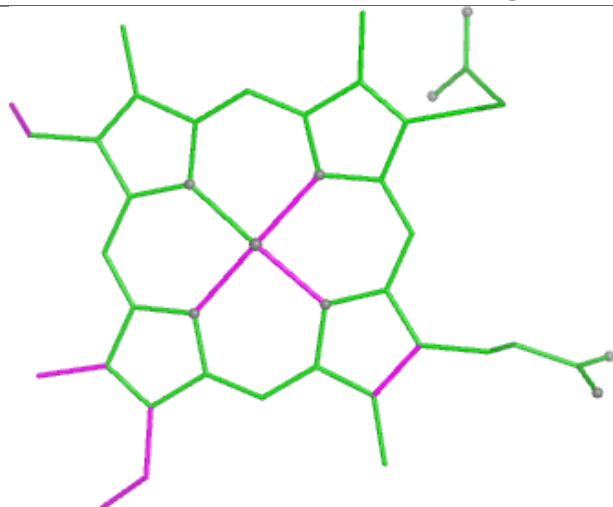
Torsions



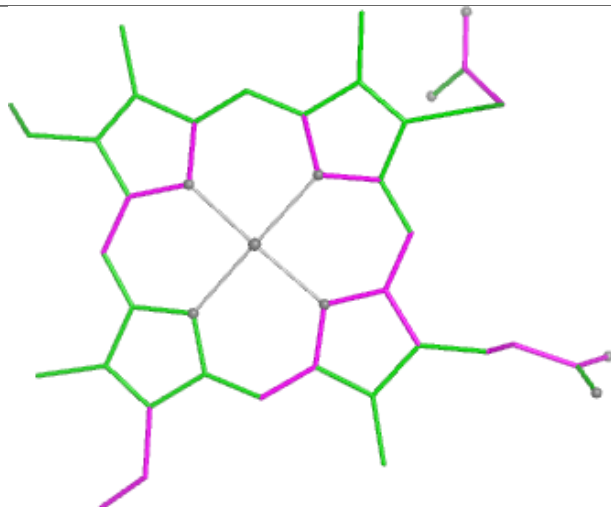
Rings



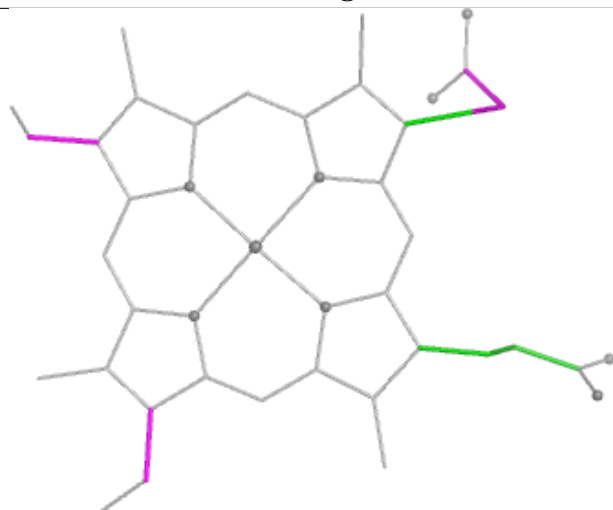
Ligand HEC C 1110



Bond lengths



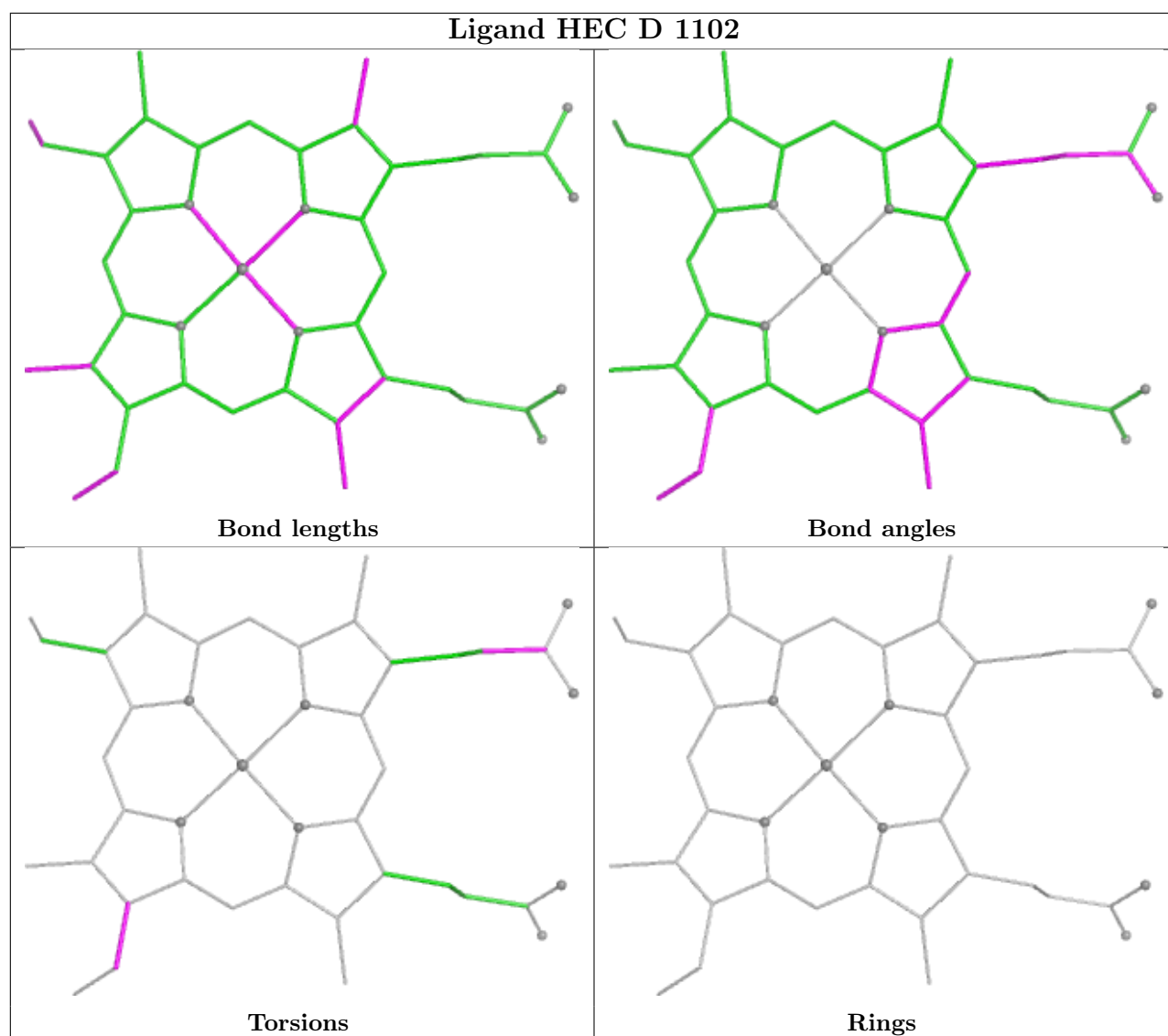
Bond angles



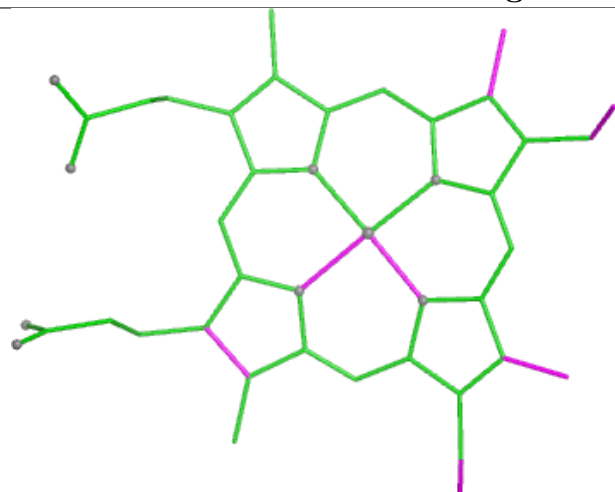
Torsions



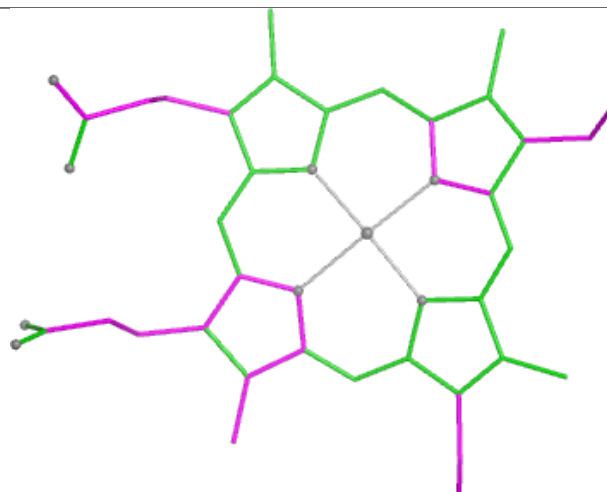
Rings



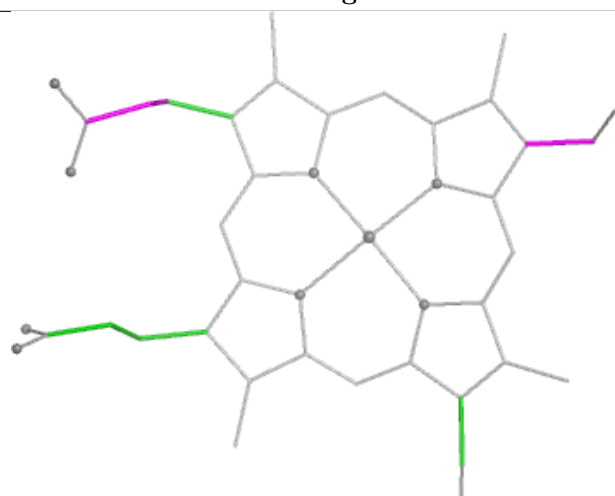
Ligand HEC C 1104



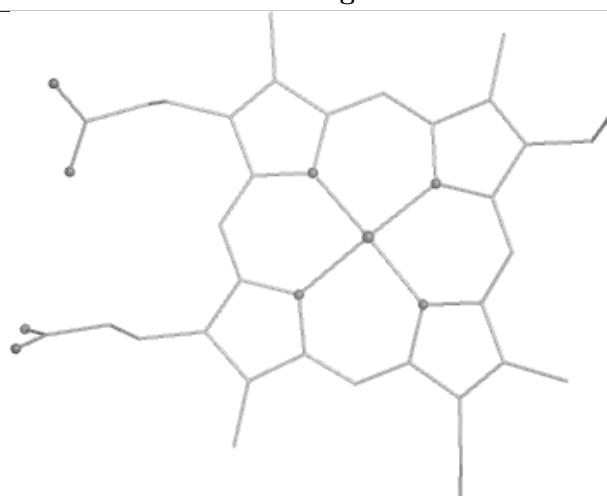
Bond lengths



Bond angles

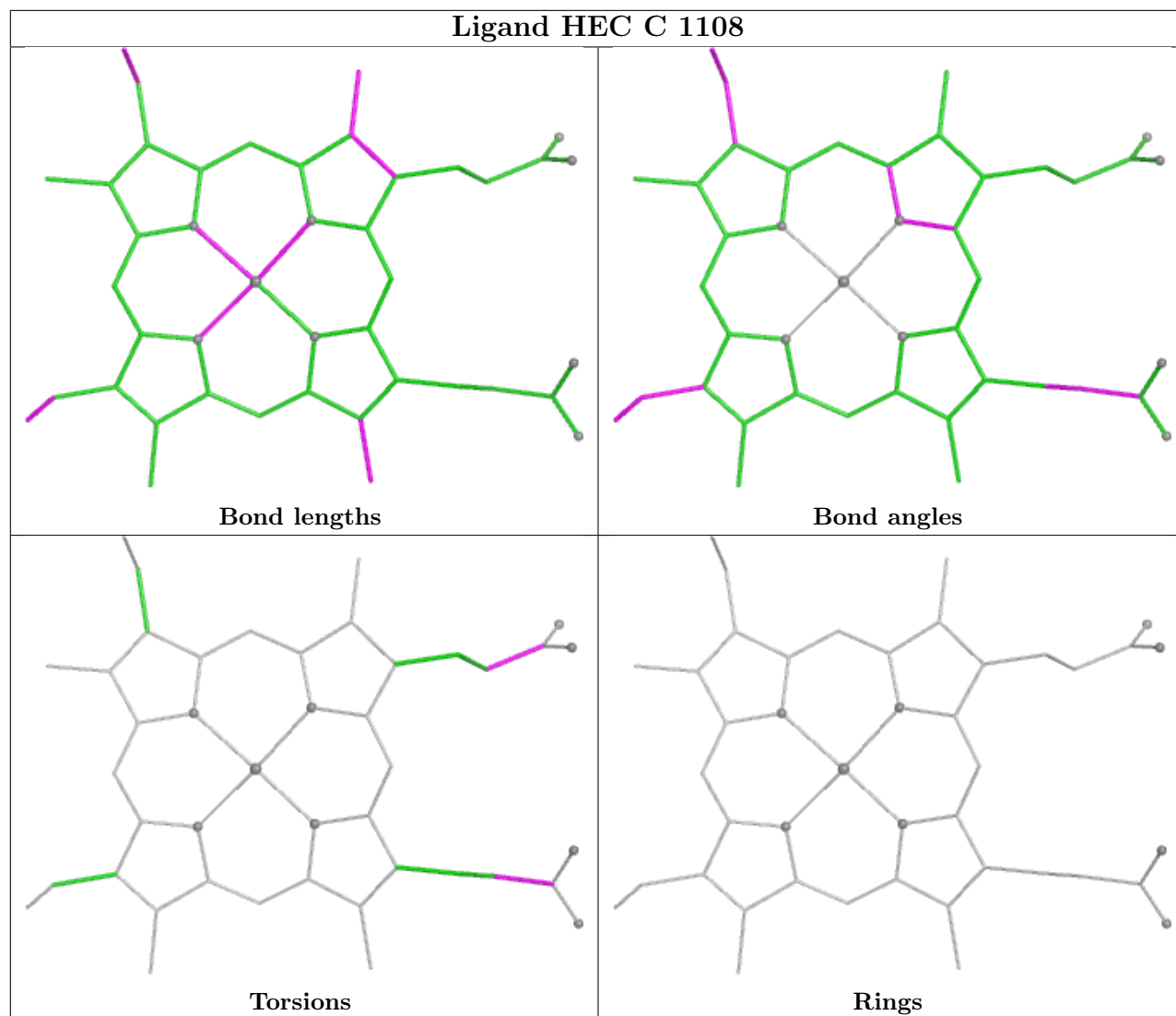


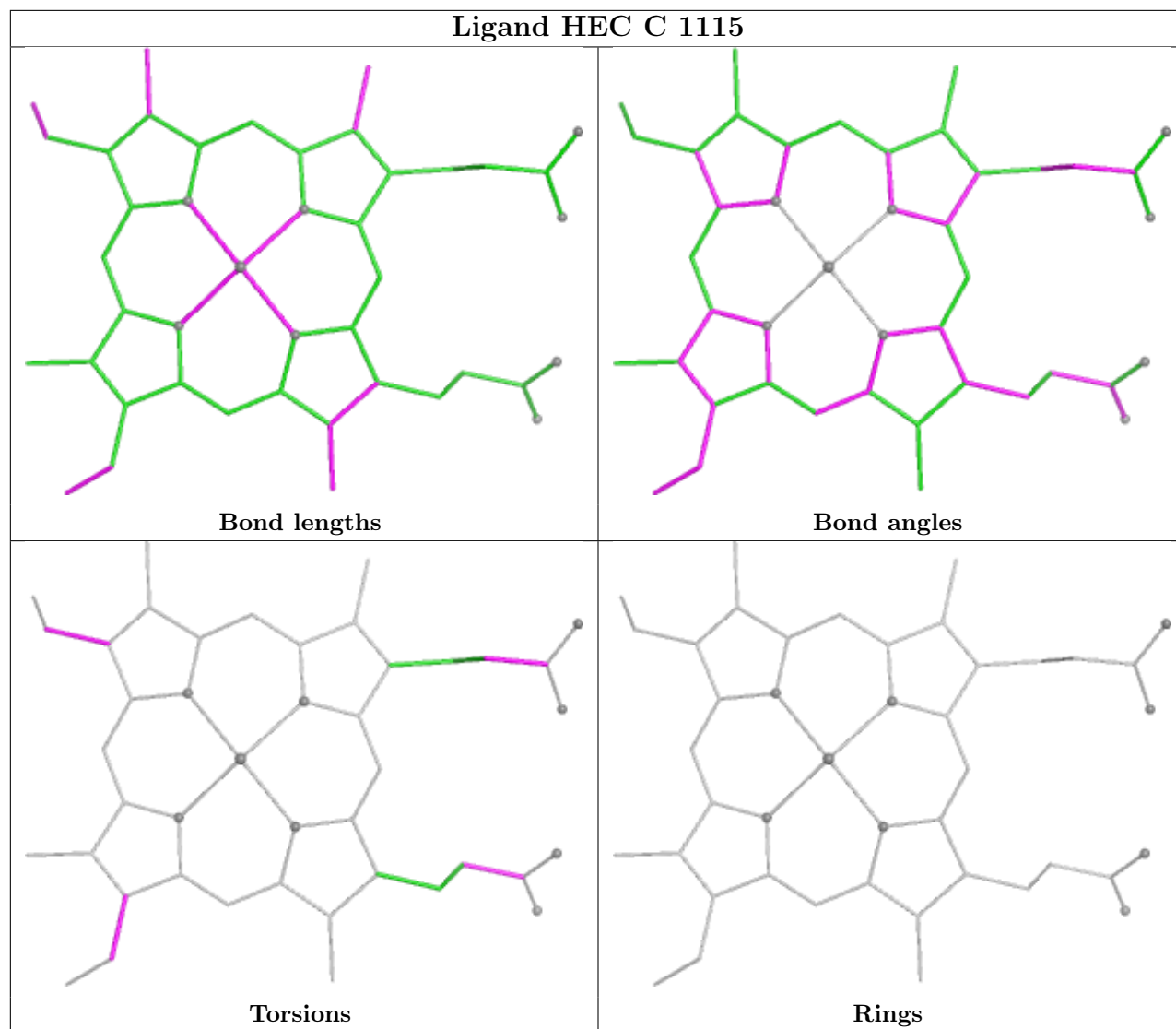
Torsions



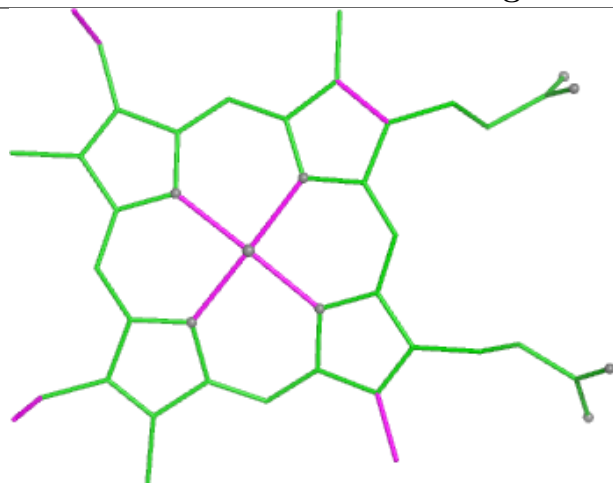
Rings

Ligand HEC C 1108

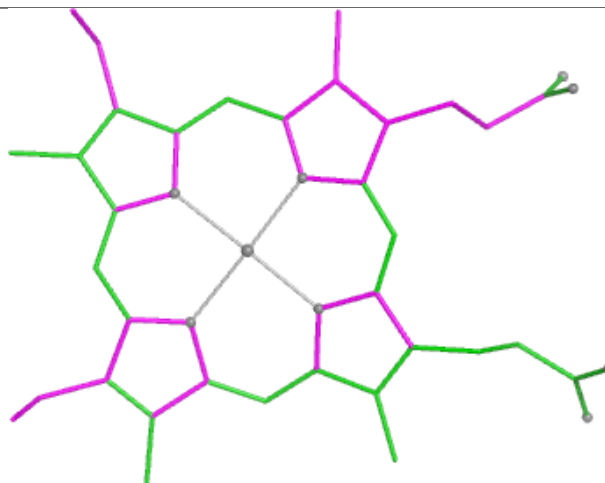




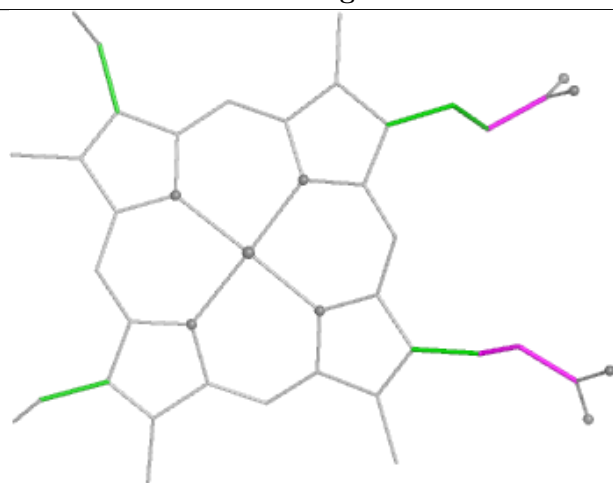
Ligand HEC D 1108



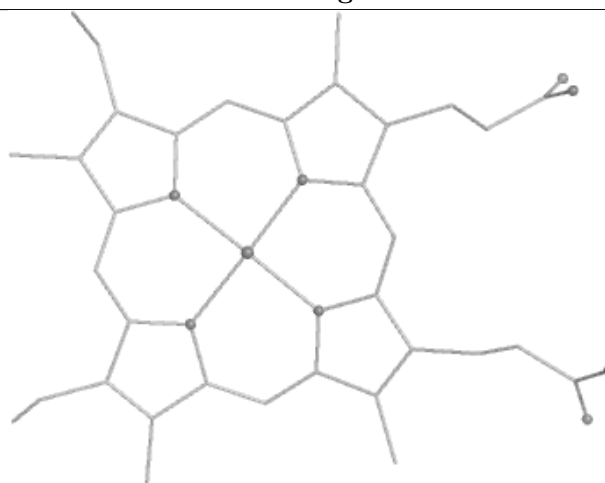
Bond lengths



Bond angles

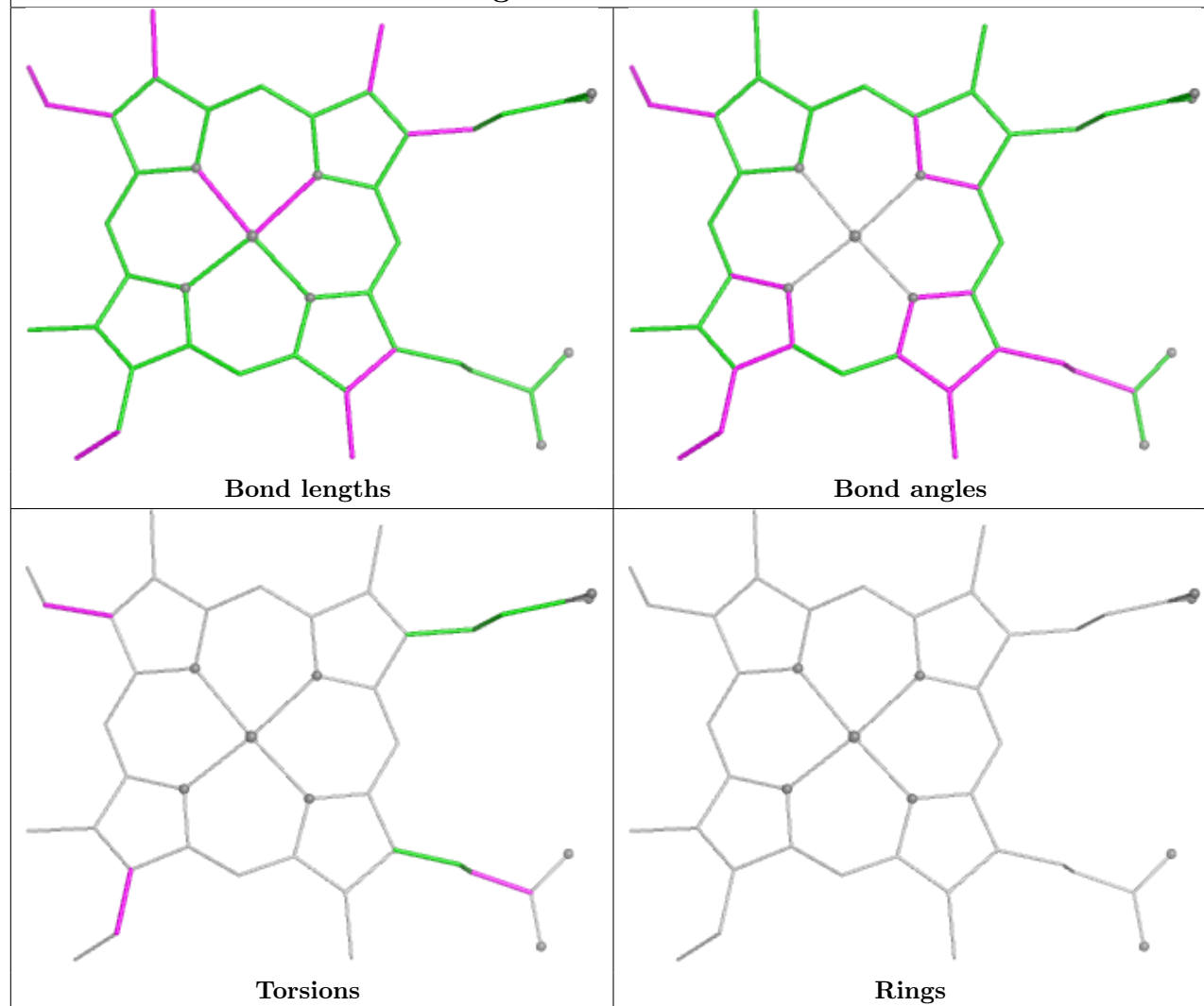


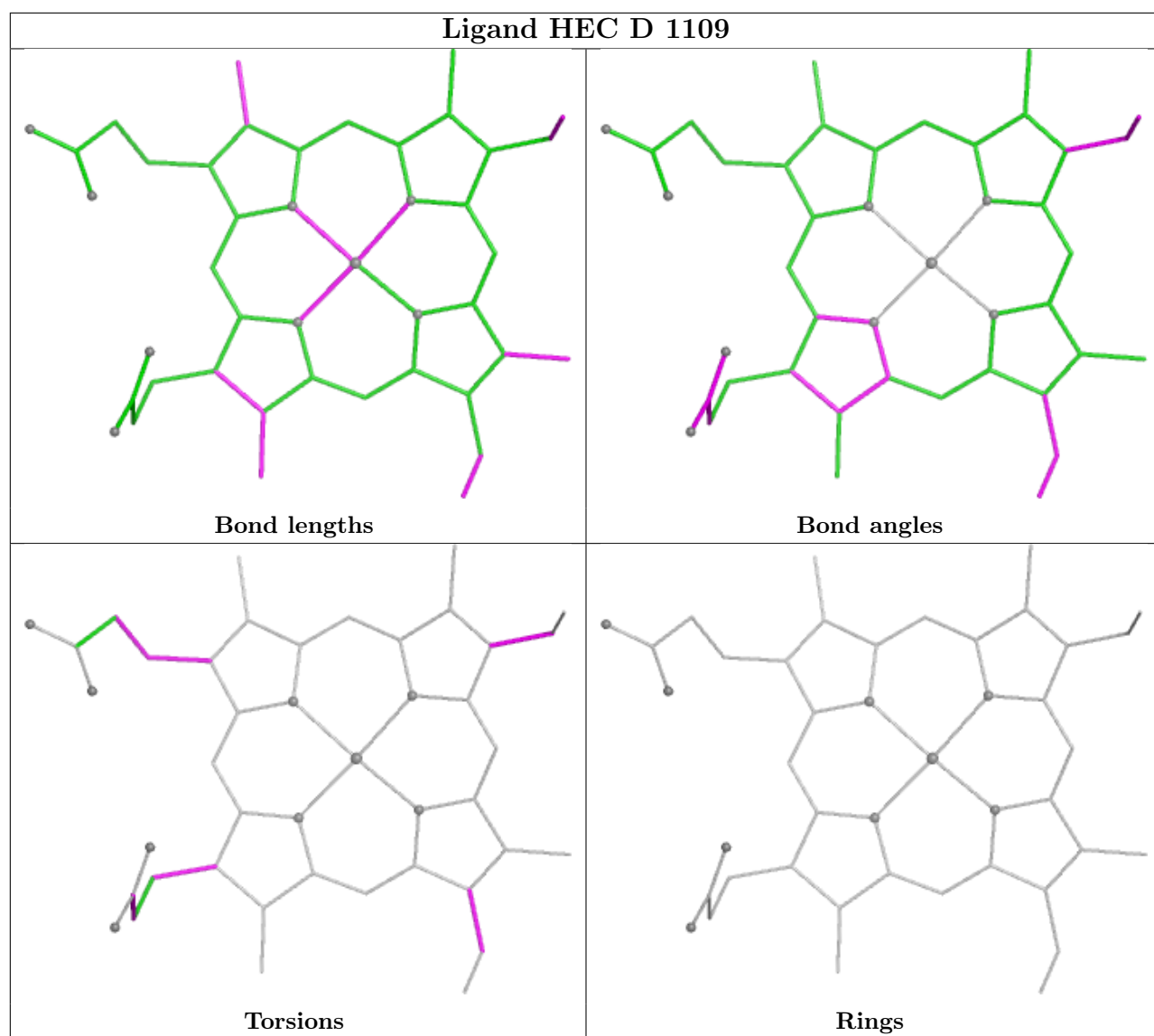
Torsions



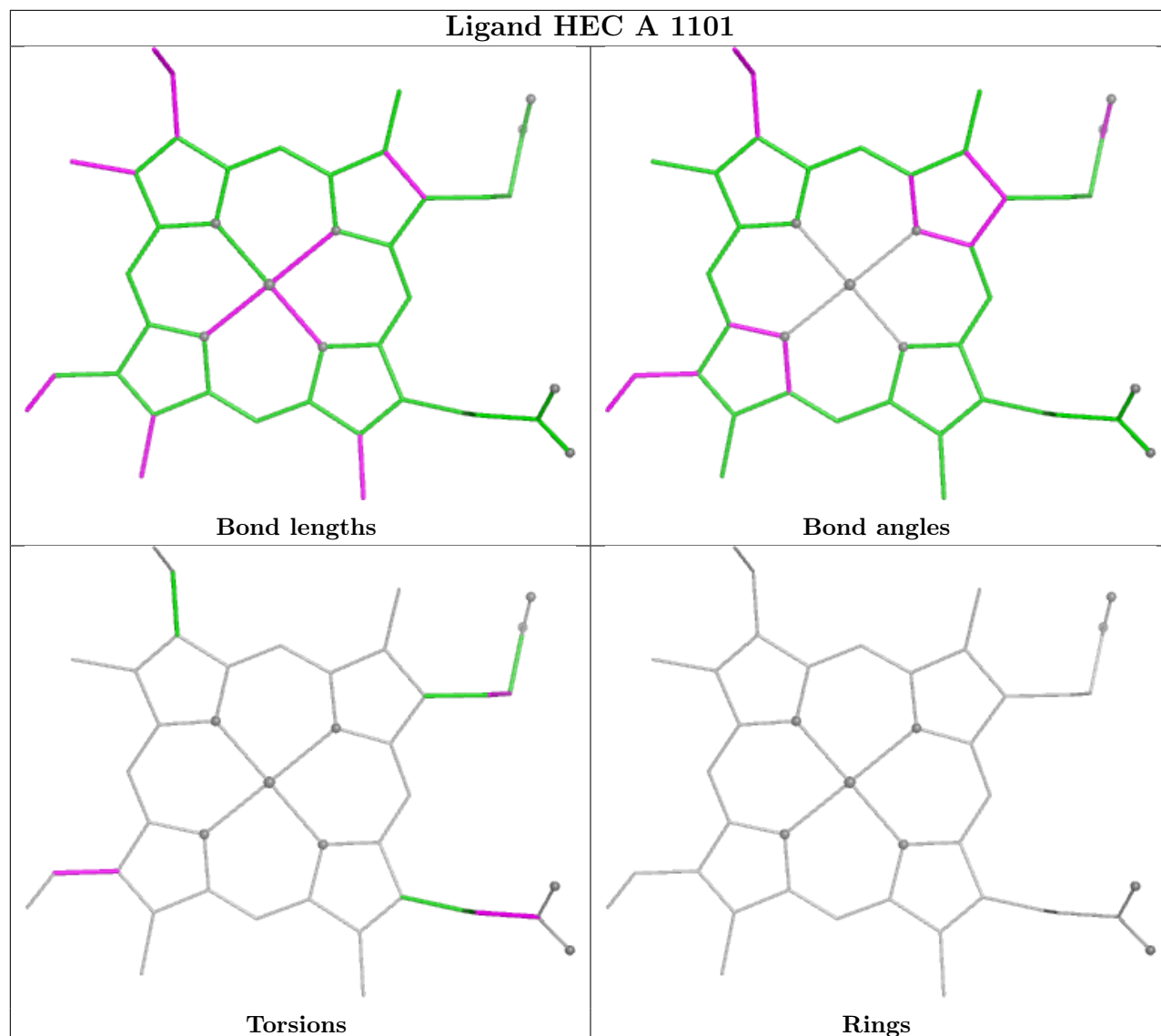
Rings

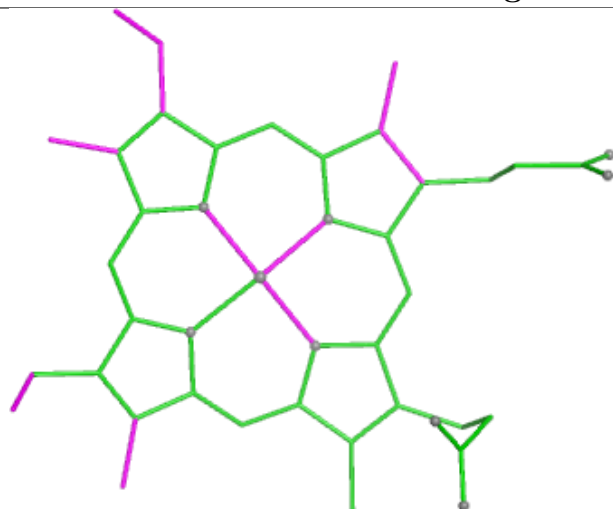
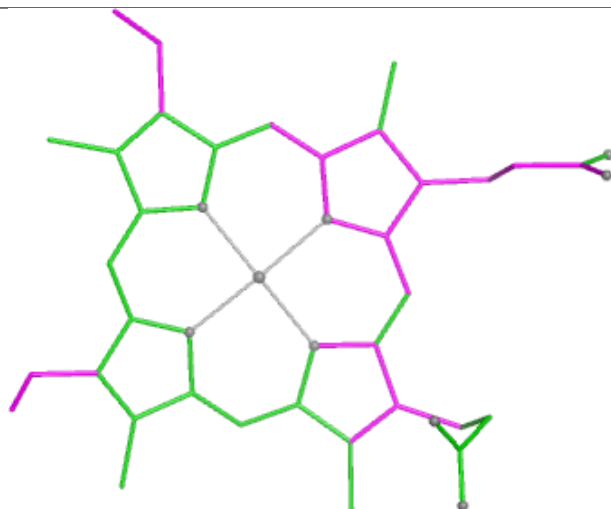
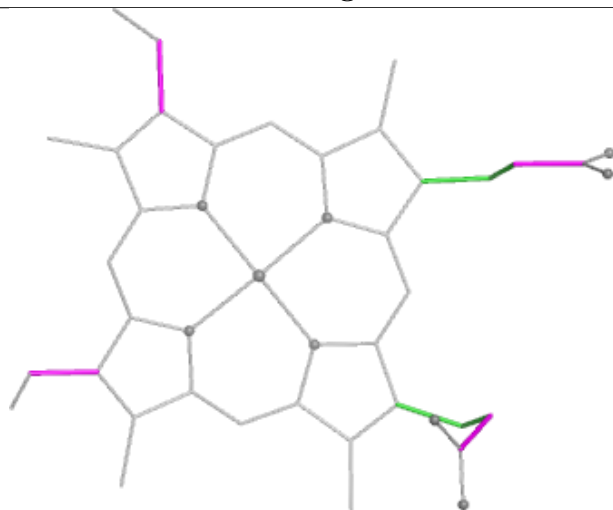
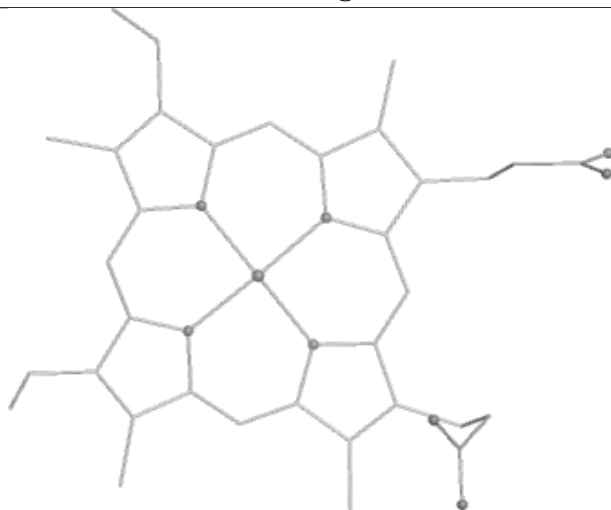
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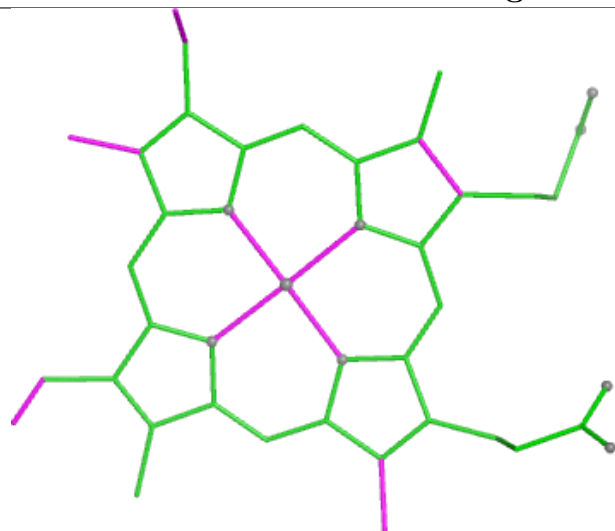
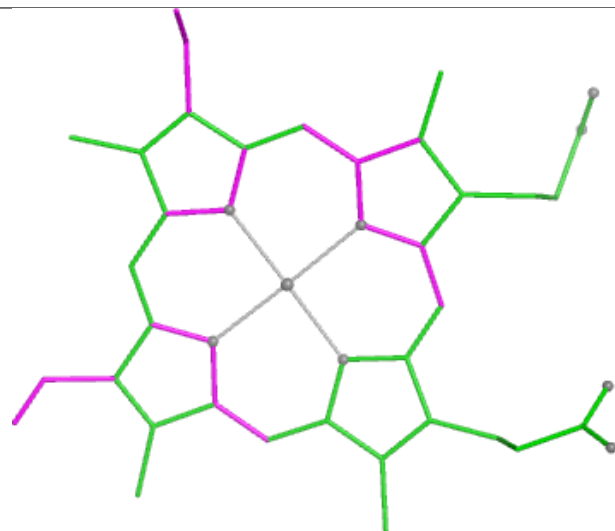
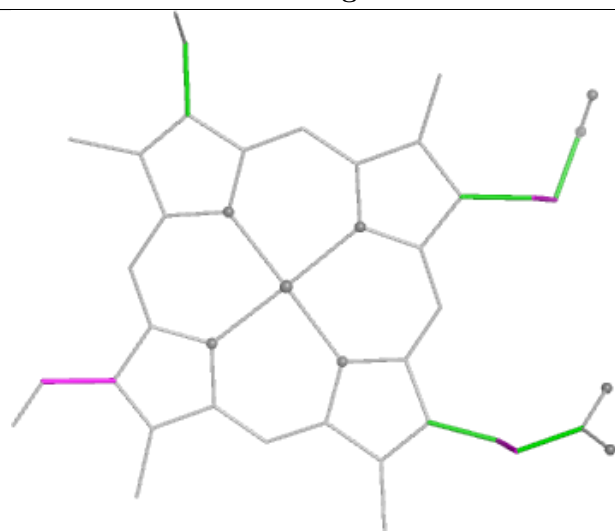
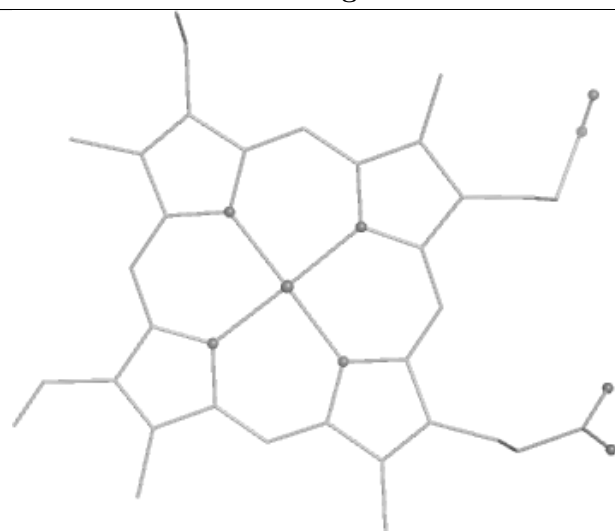




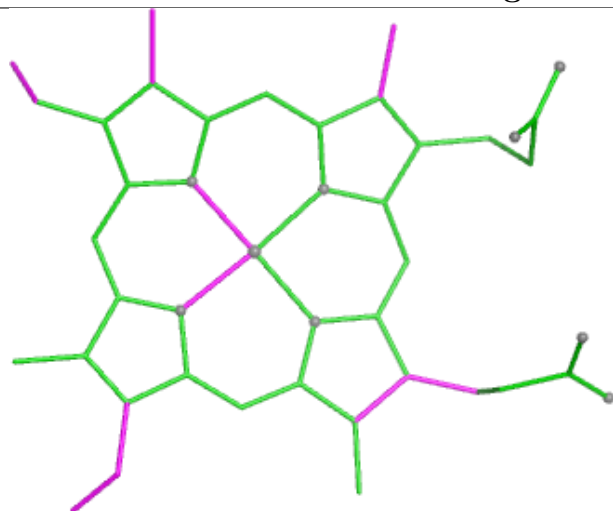
Ligand HEC A 1101



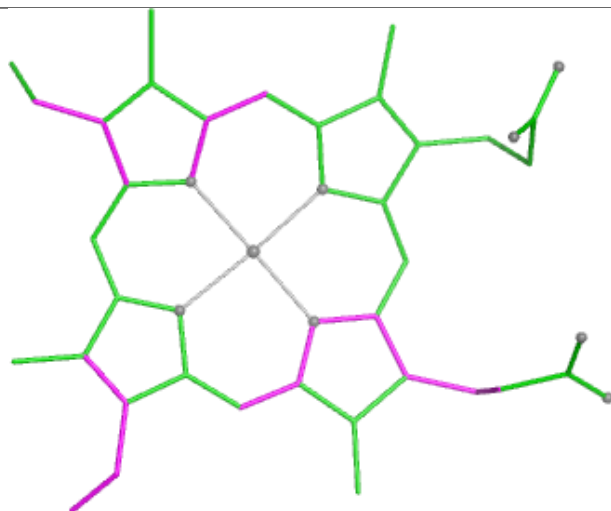
Ligand HEC B 1110**Bond lengths****Bond angles****Torsions****Rings**

Ligand HEC B 1101**Bond lengths****Bond angles****Torsions****Rings**

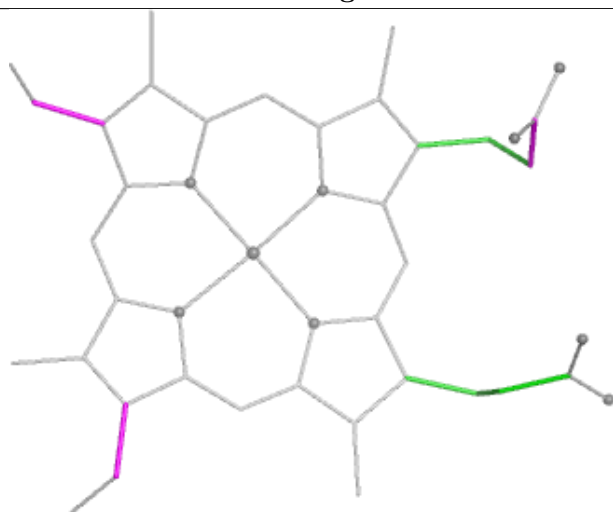
Ligand HEC C 1103



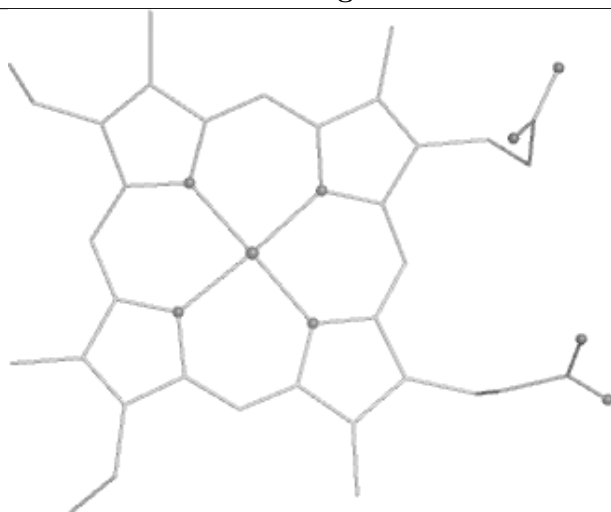
Bond lengths



Bond angles

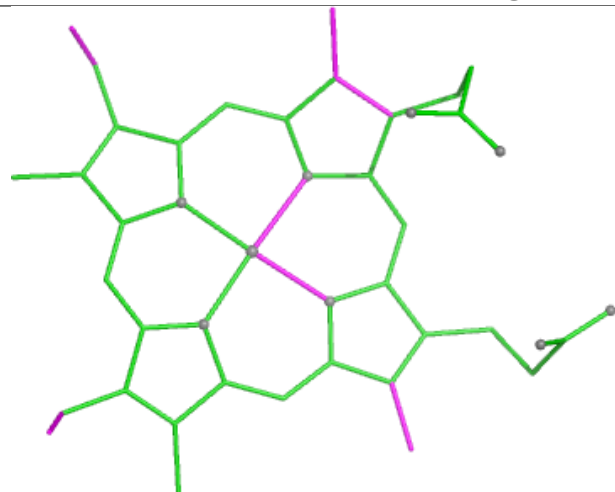


Torsions

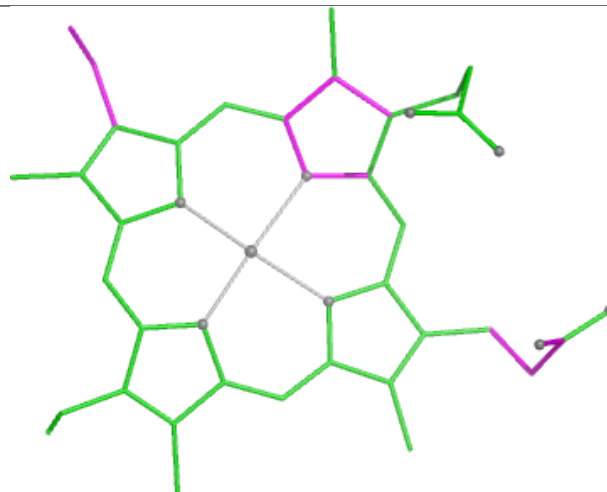


Rings

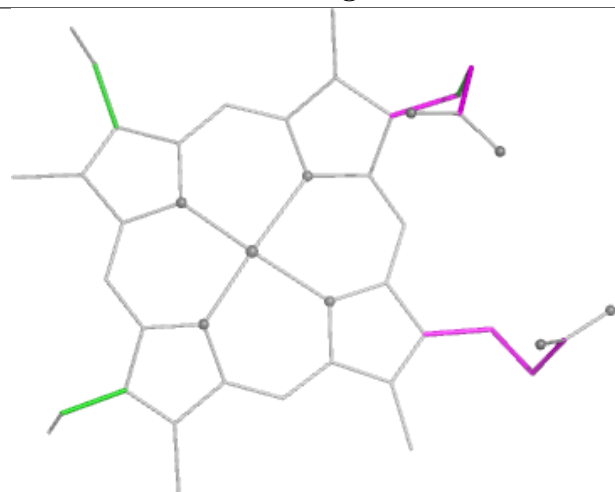
Ligand HEC A 1109



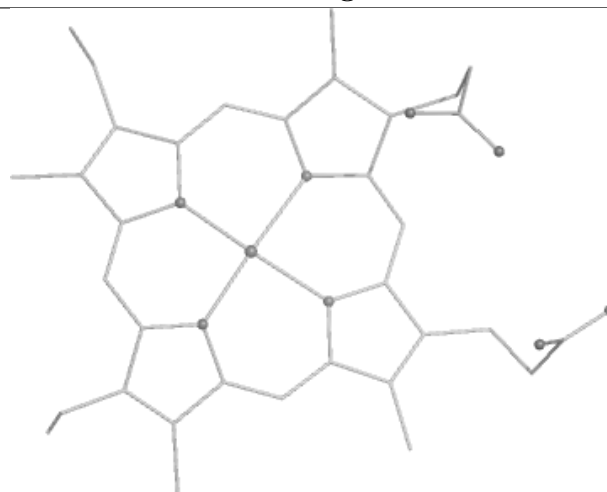
Bond lengths



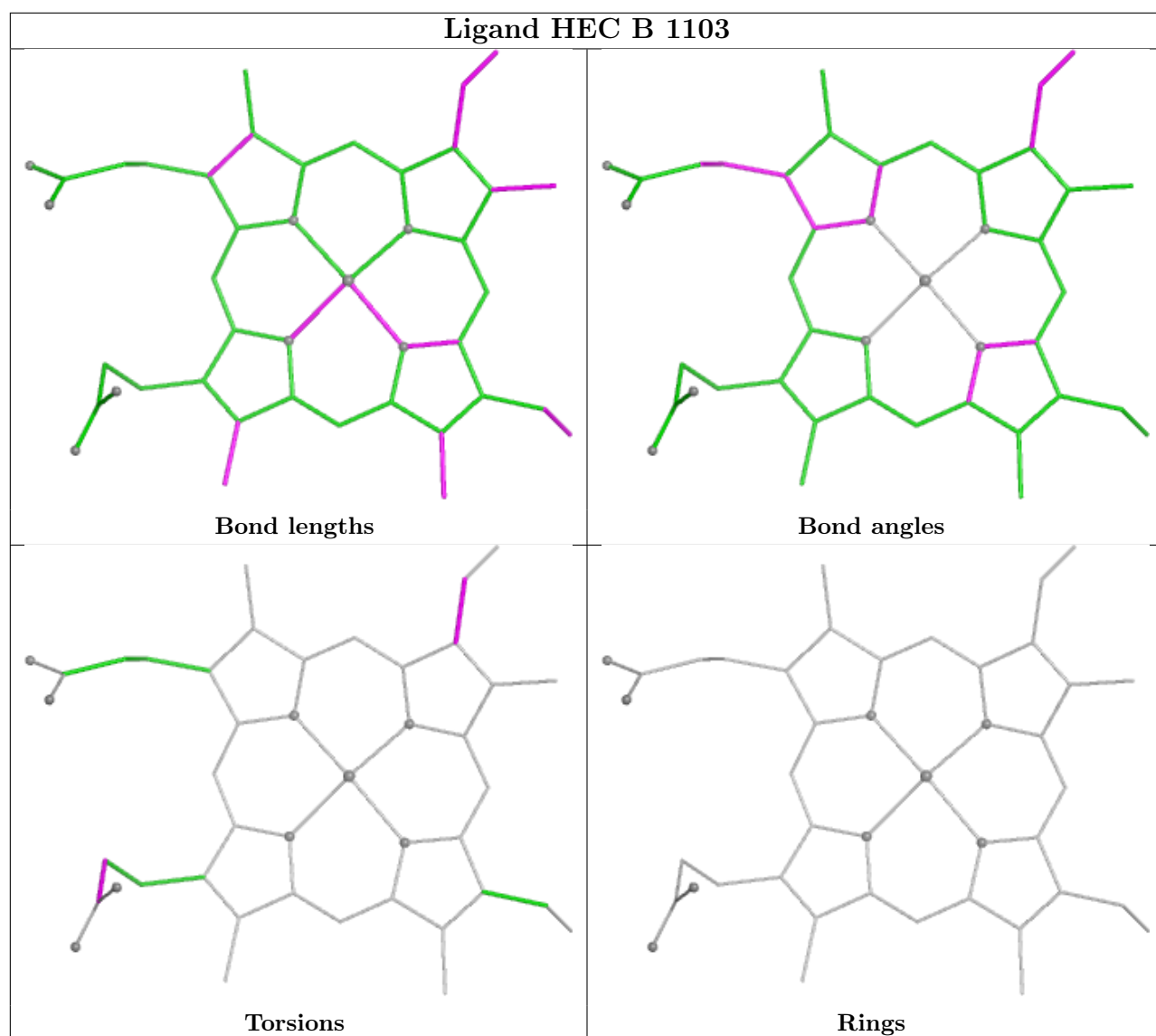
Bond angles

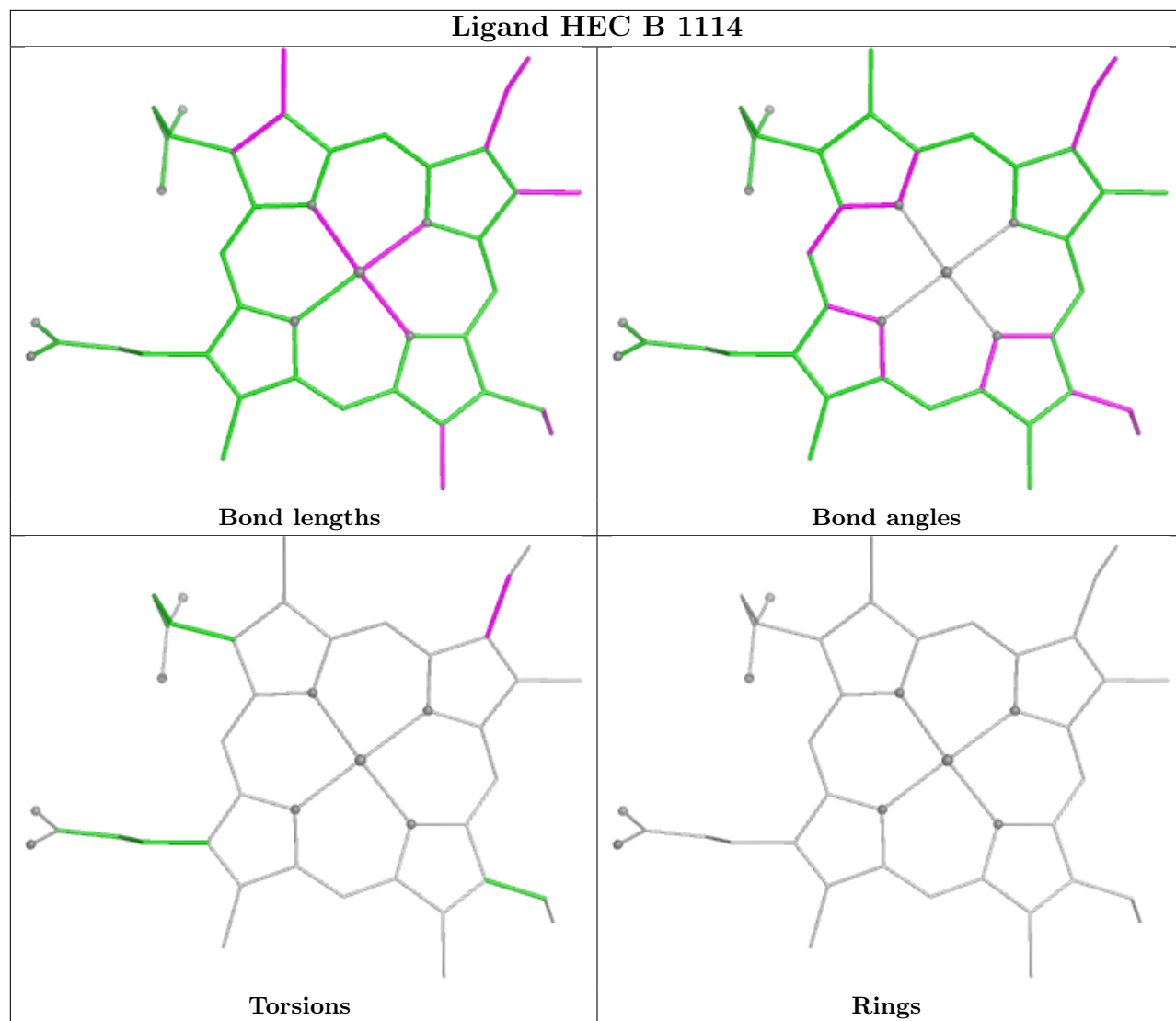


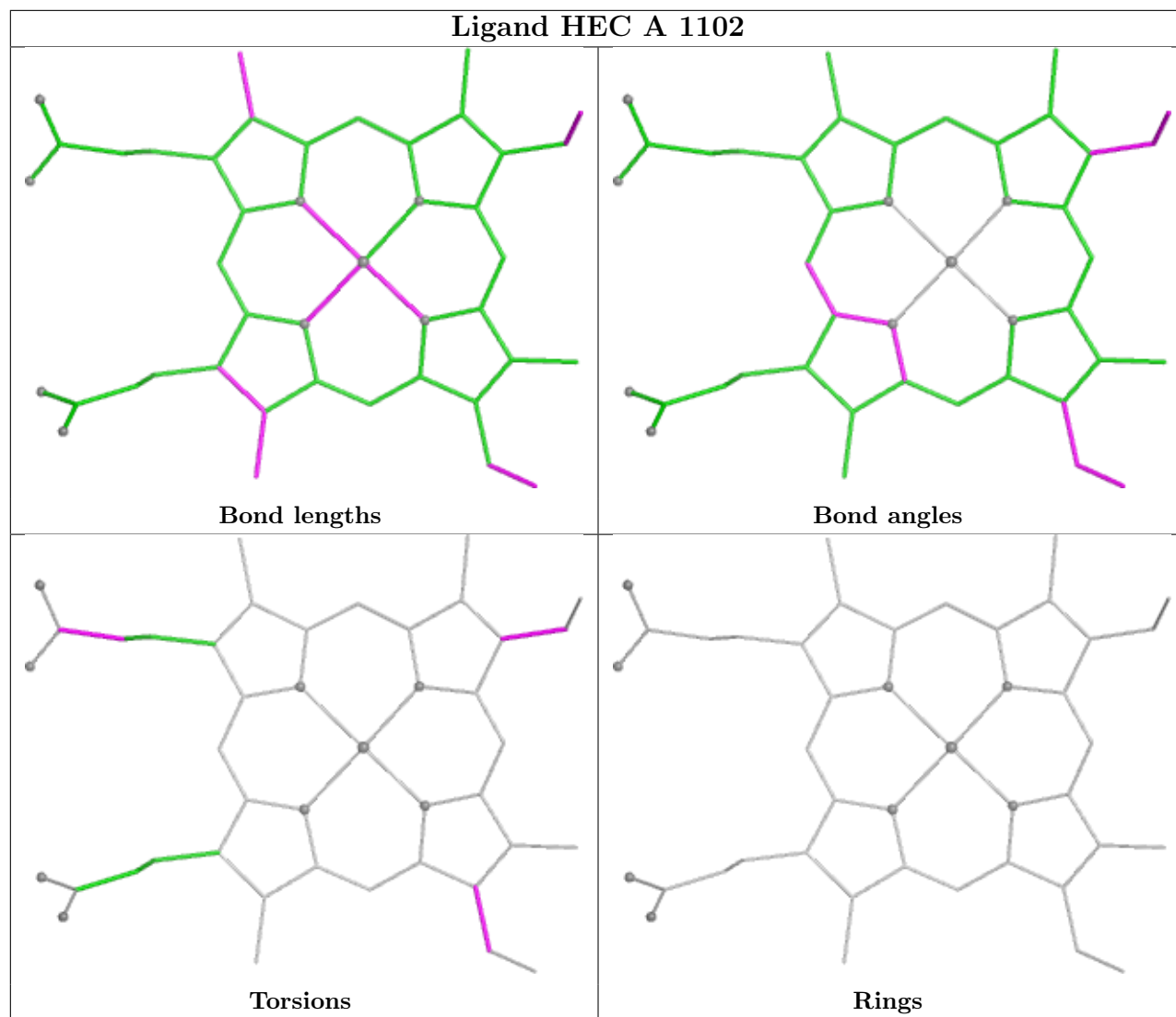
Torsions

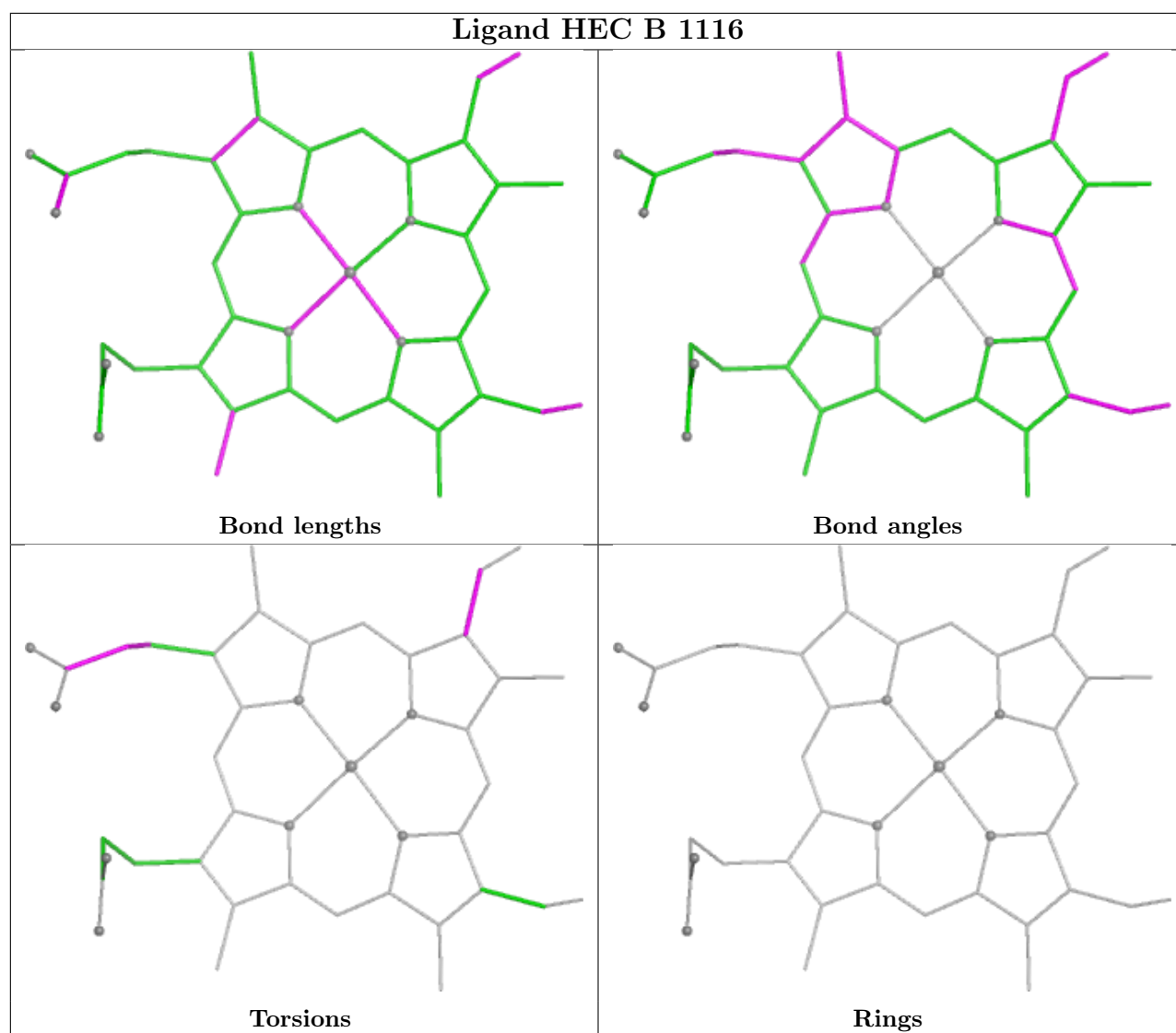


Rings

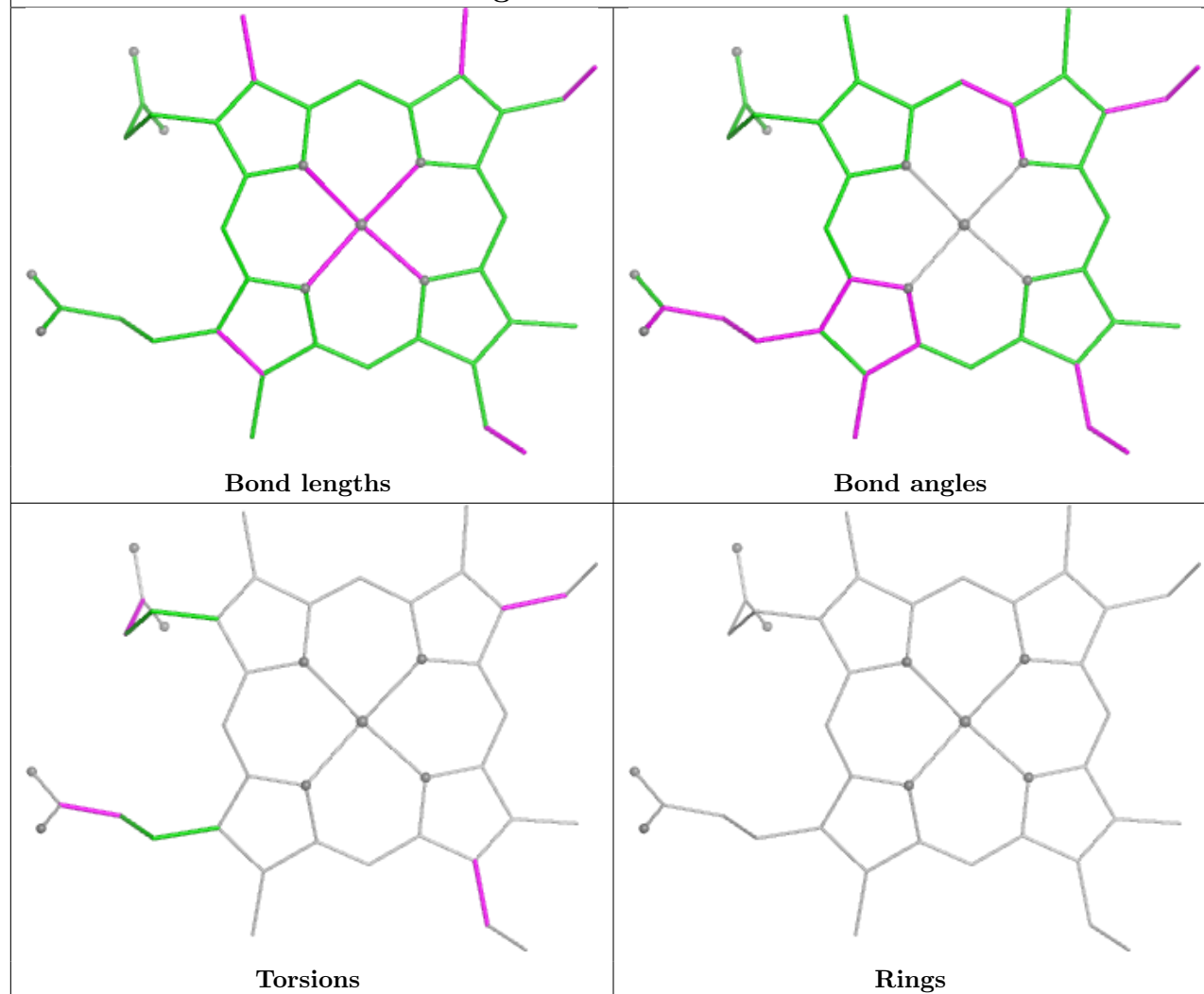


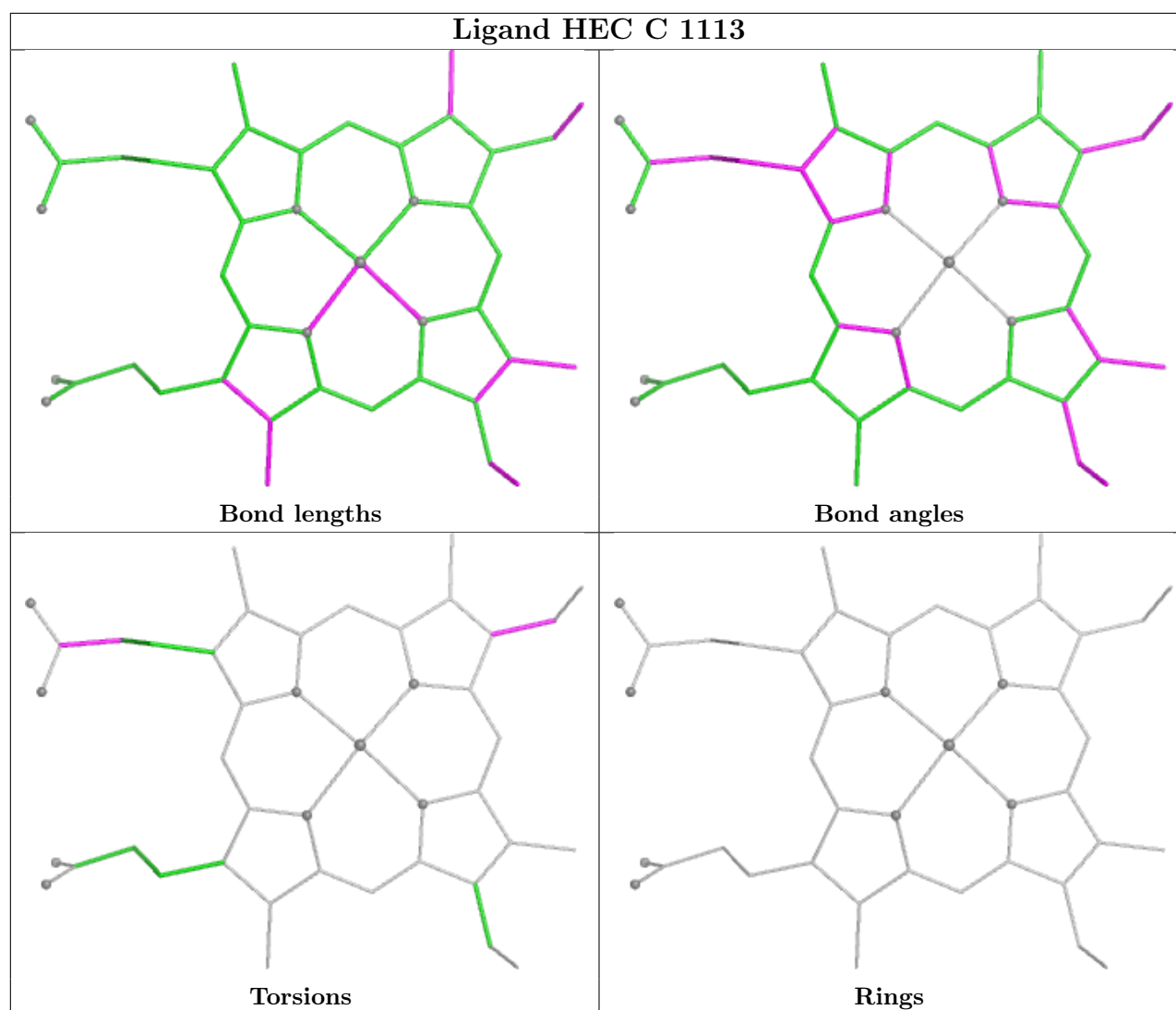




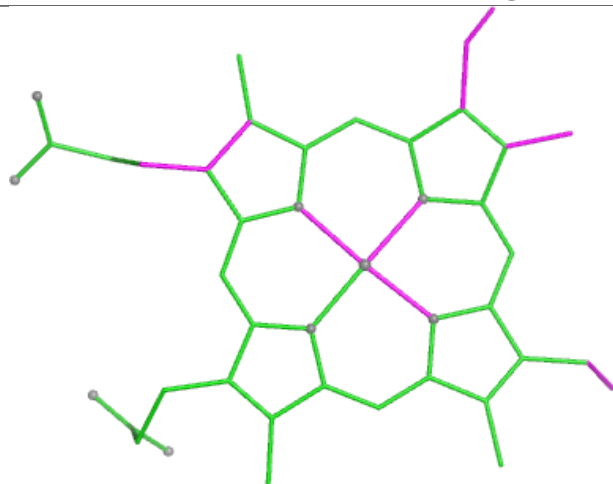


Ligand HEC B 1111

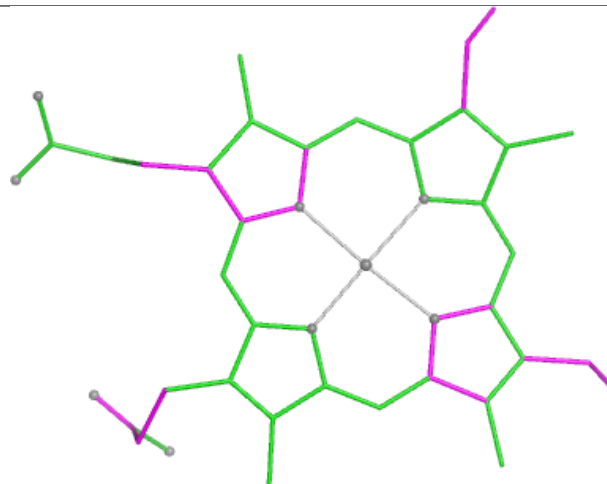




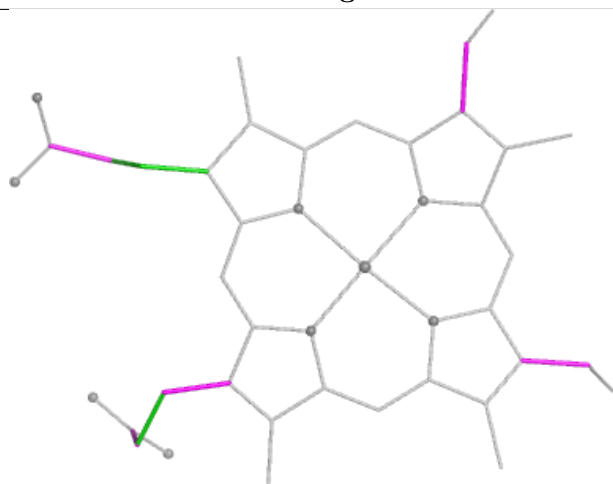
Ligand HEC D 1105



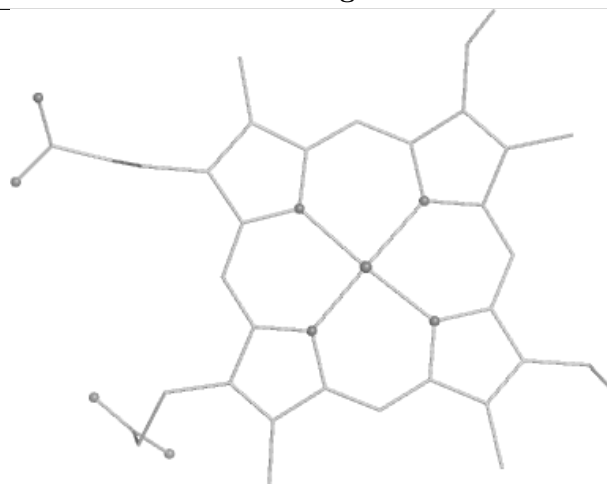
Bond lengths



Bond angles

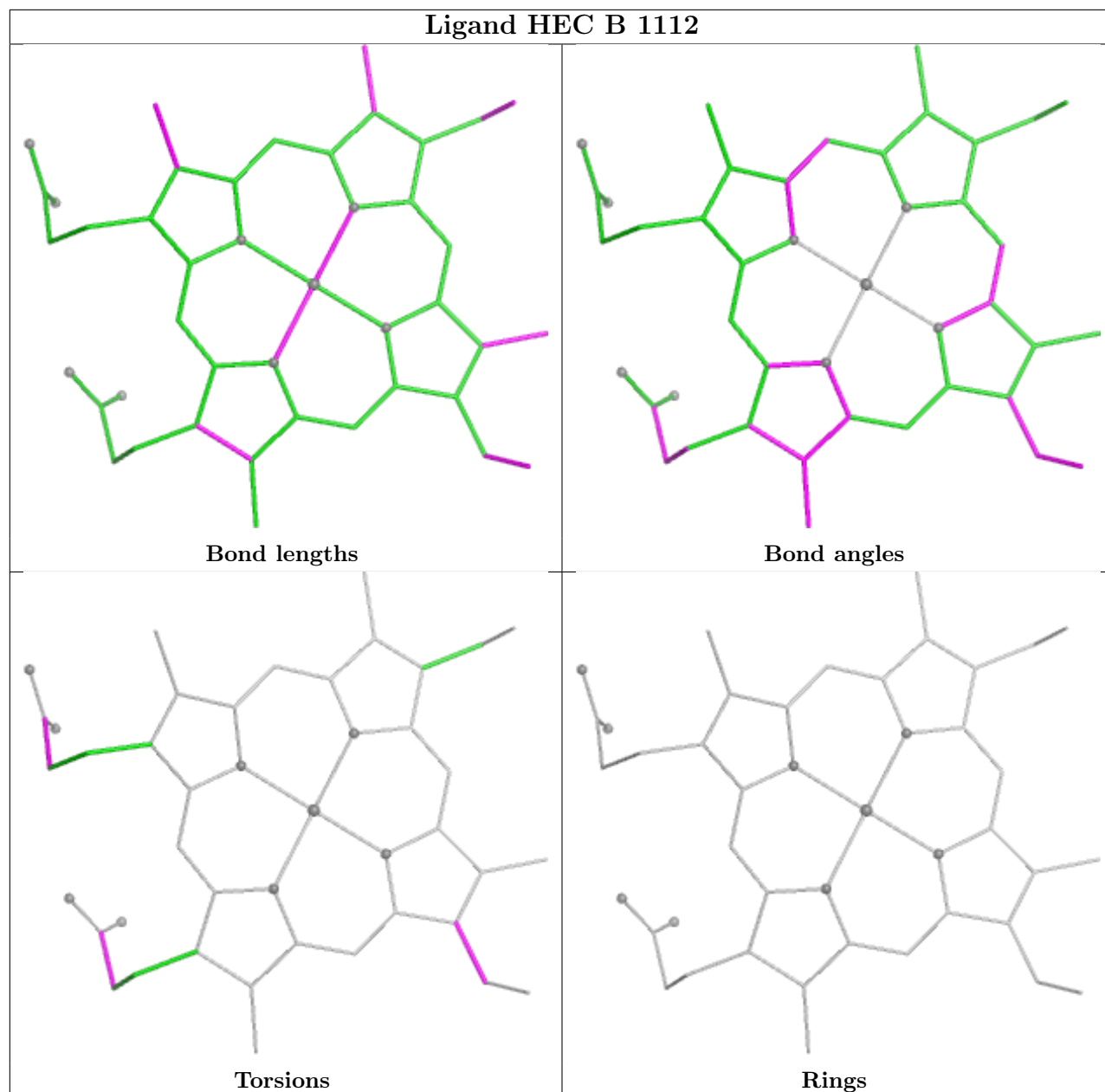


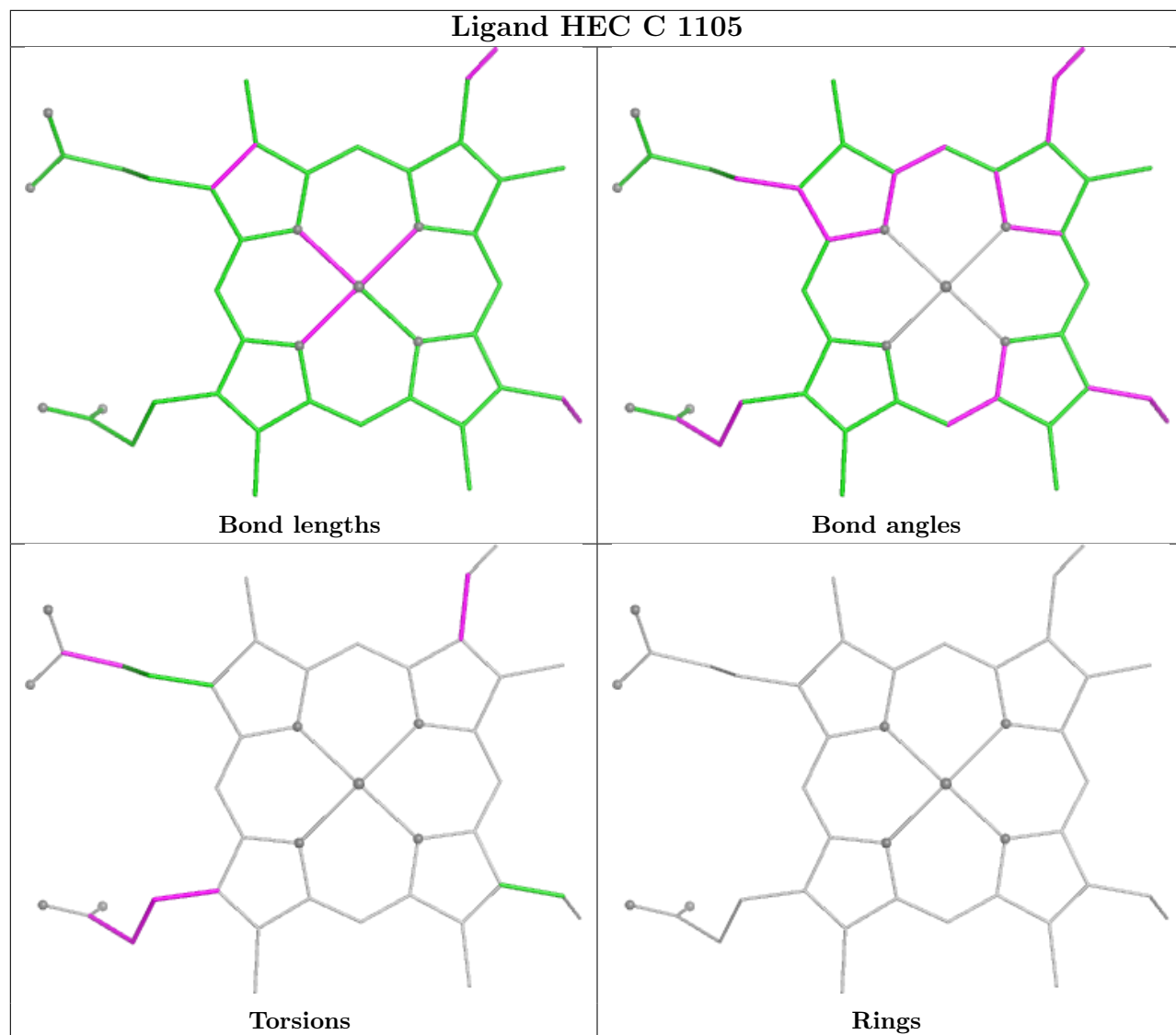
Torsions

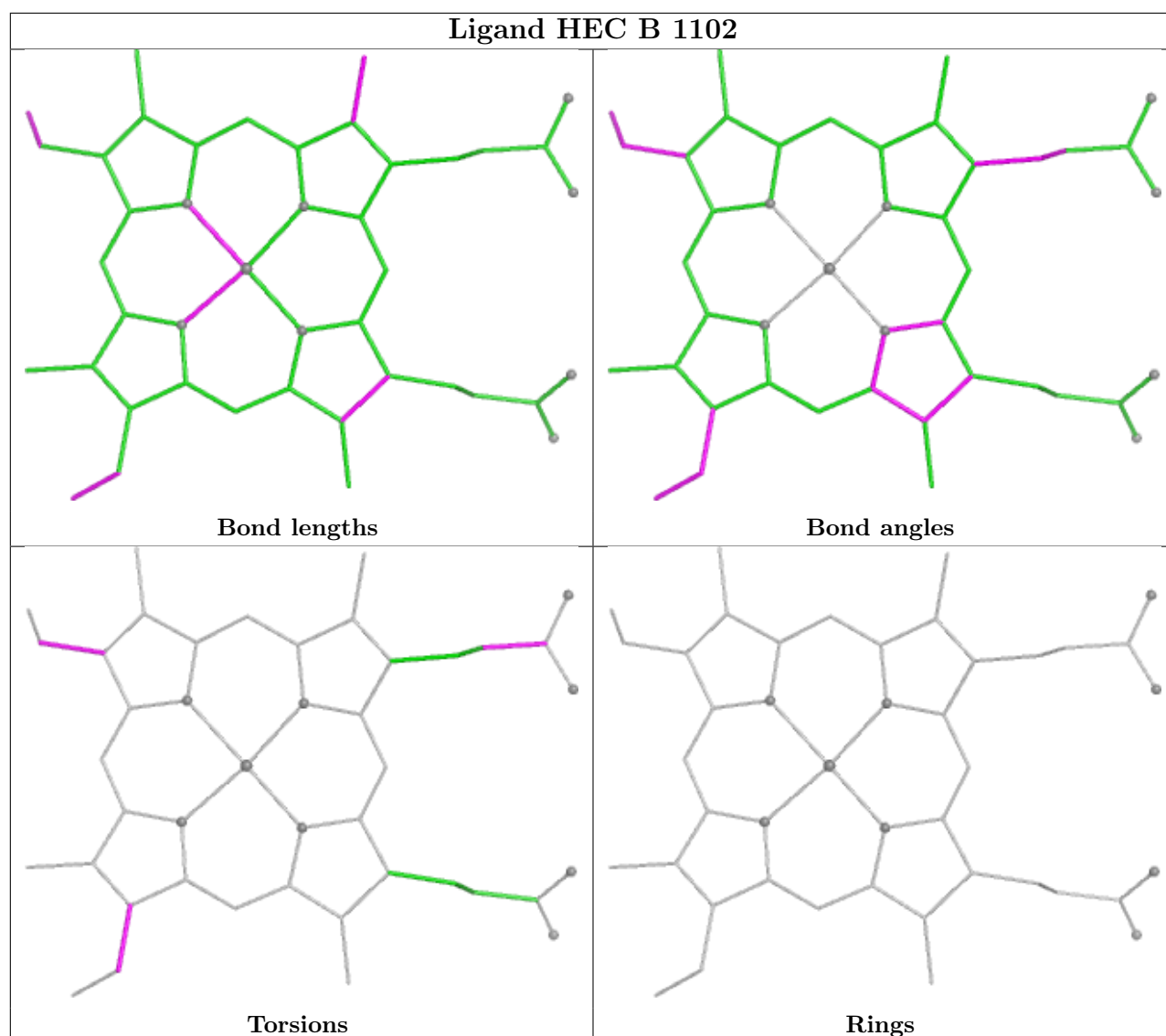


Rings

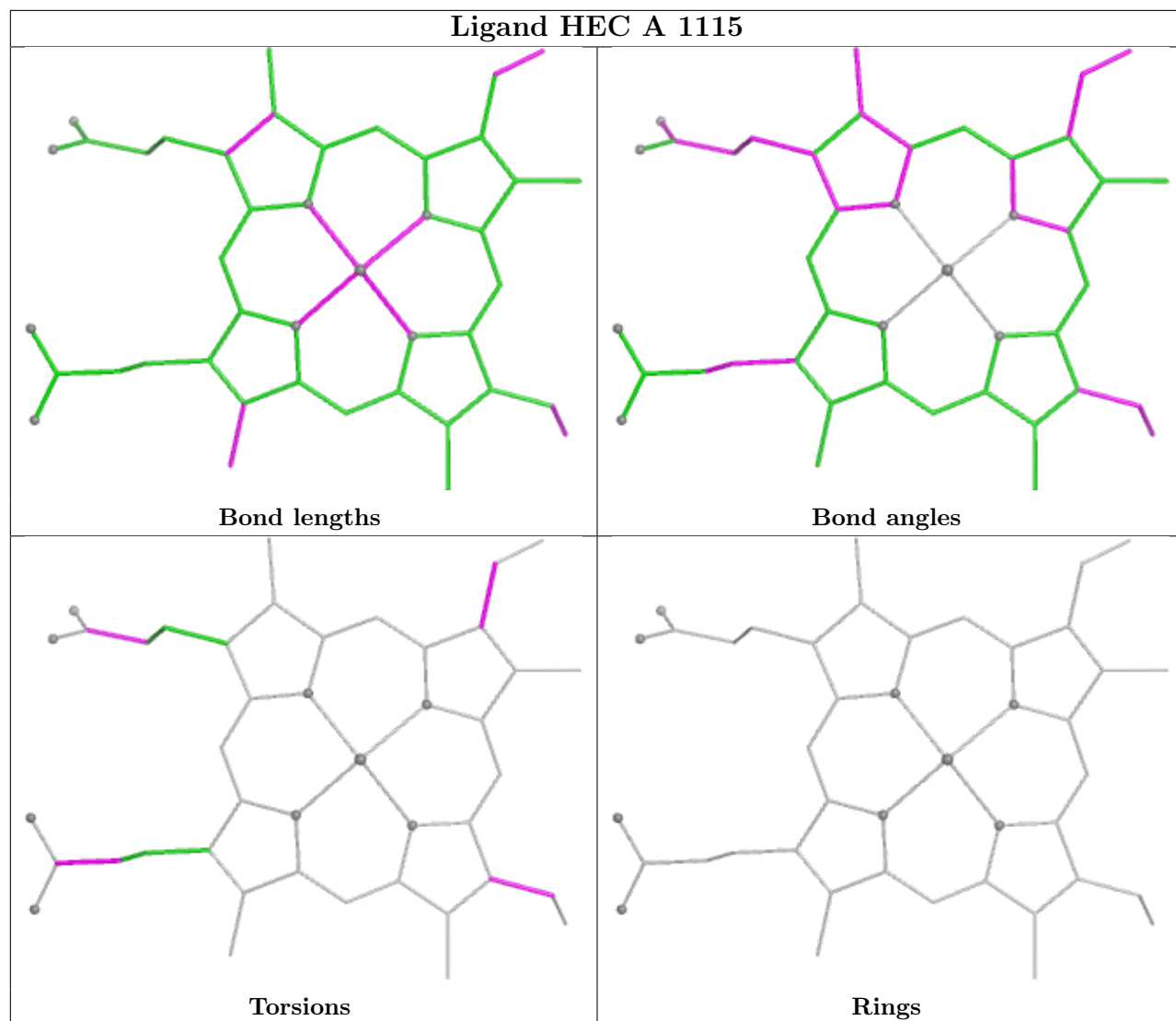
Ligand HEC B 1112

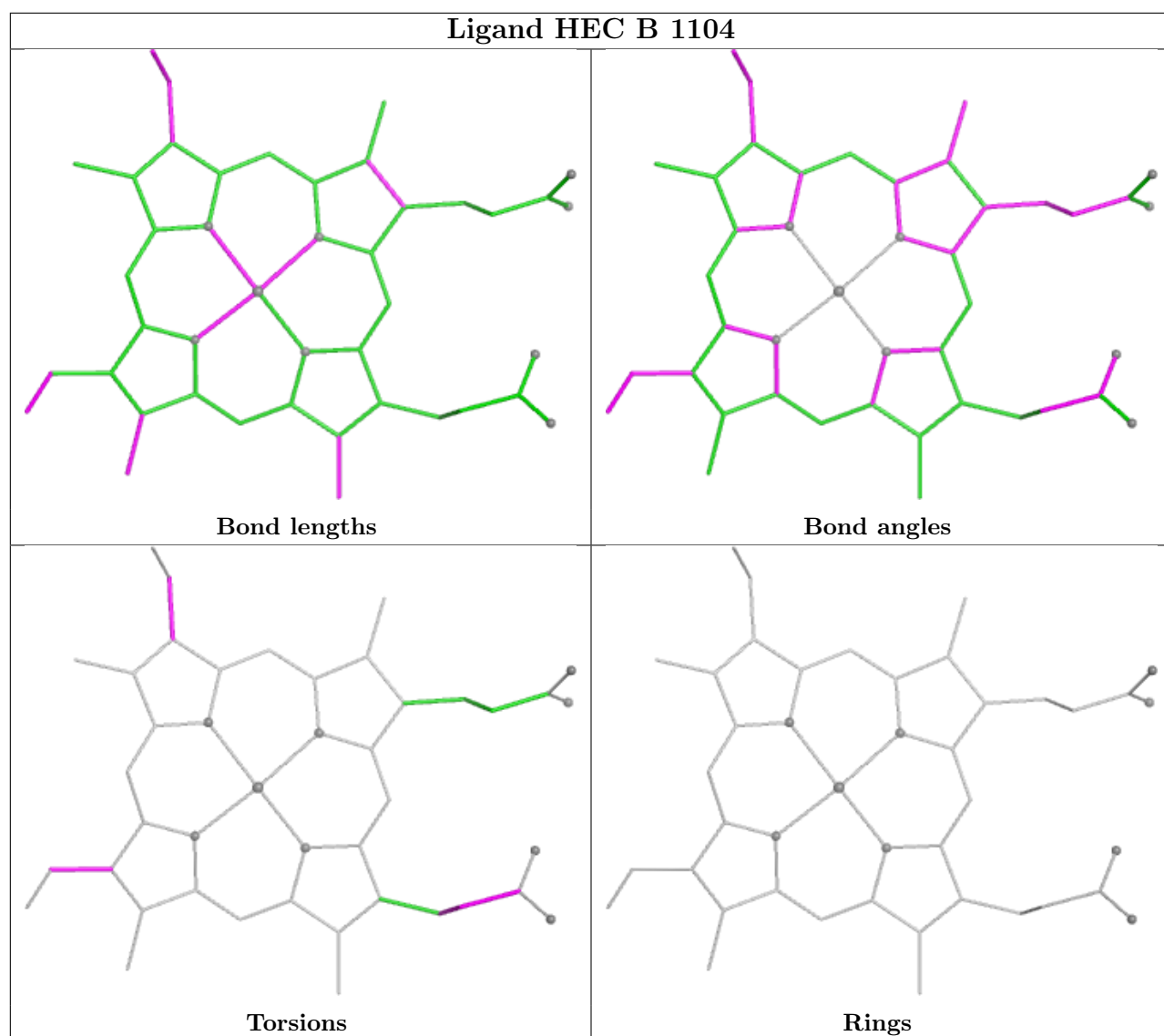




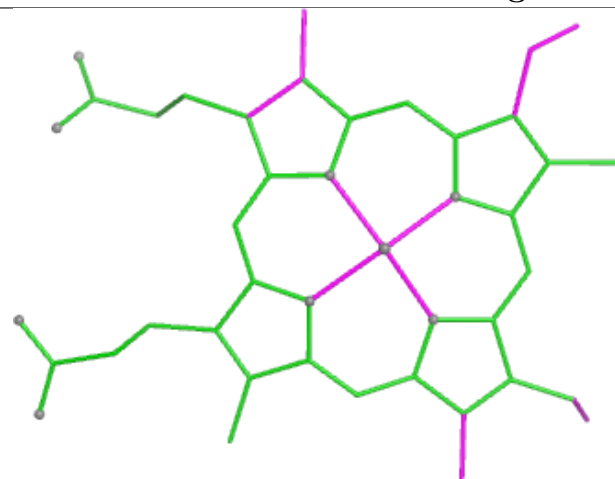


Ligand HEC A 1115

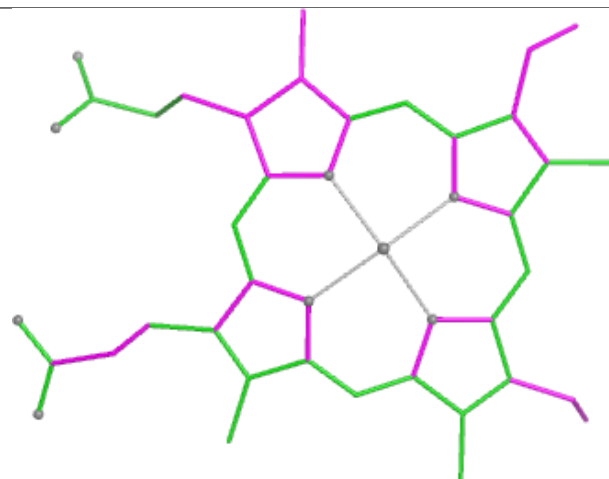




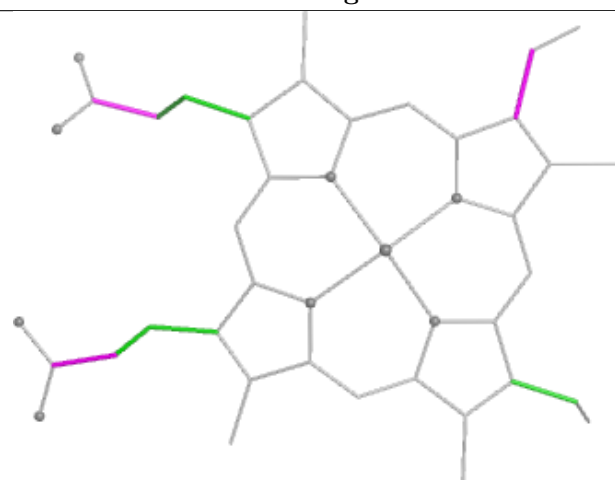
Ligand HEC B 1115



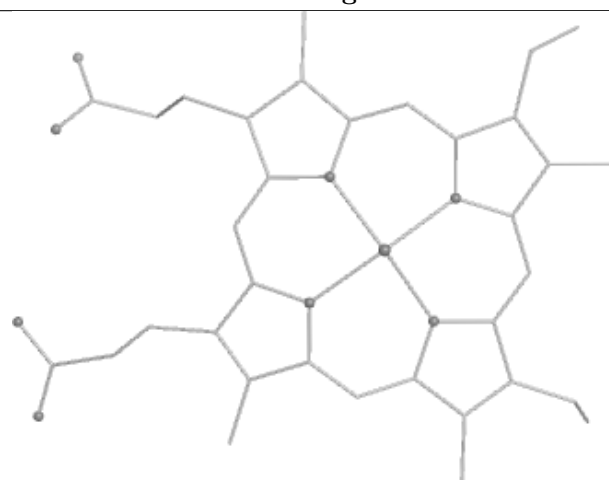
Bond lengths



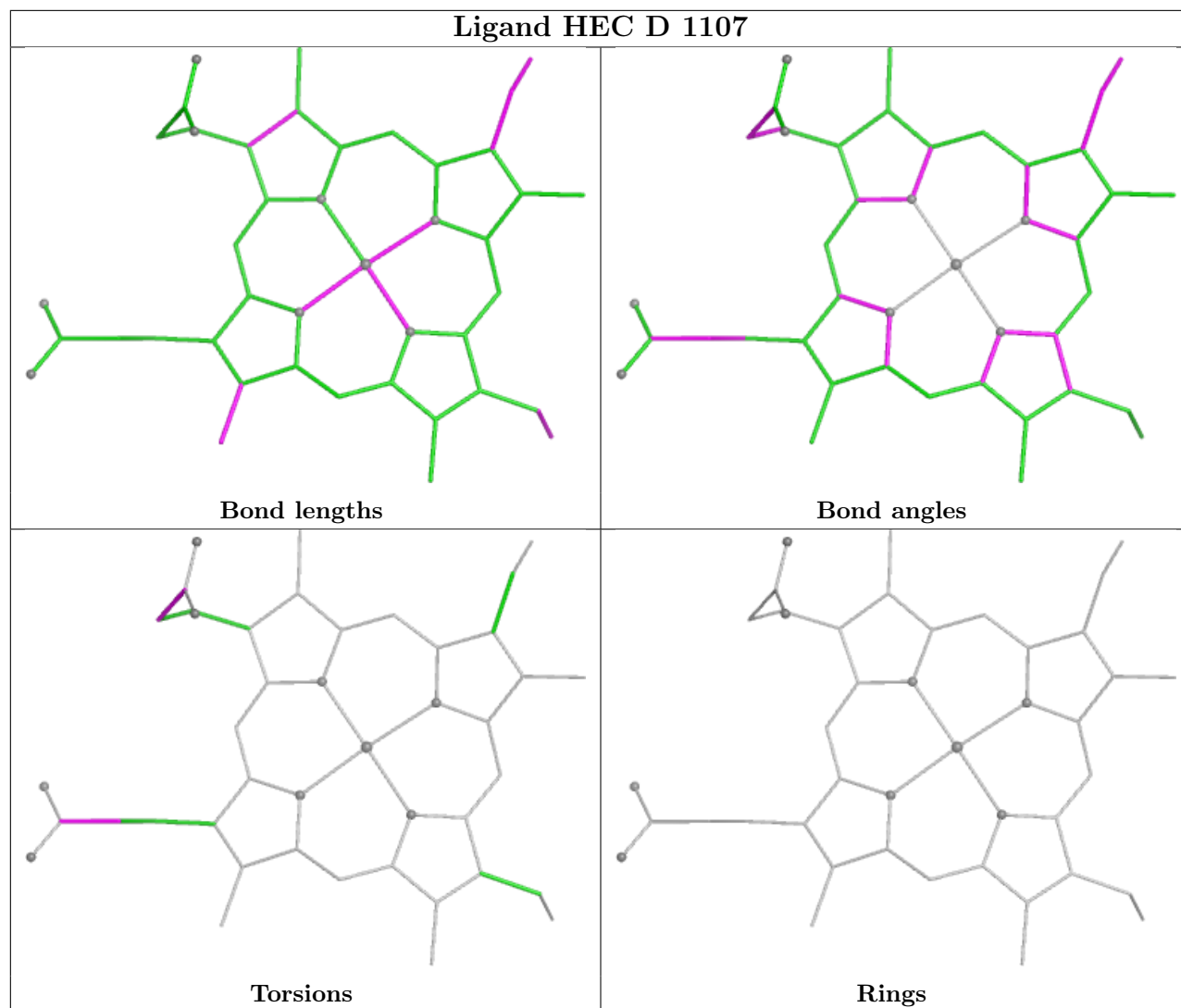
Bond angles



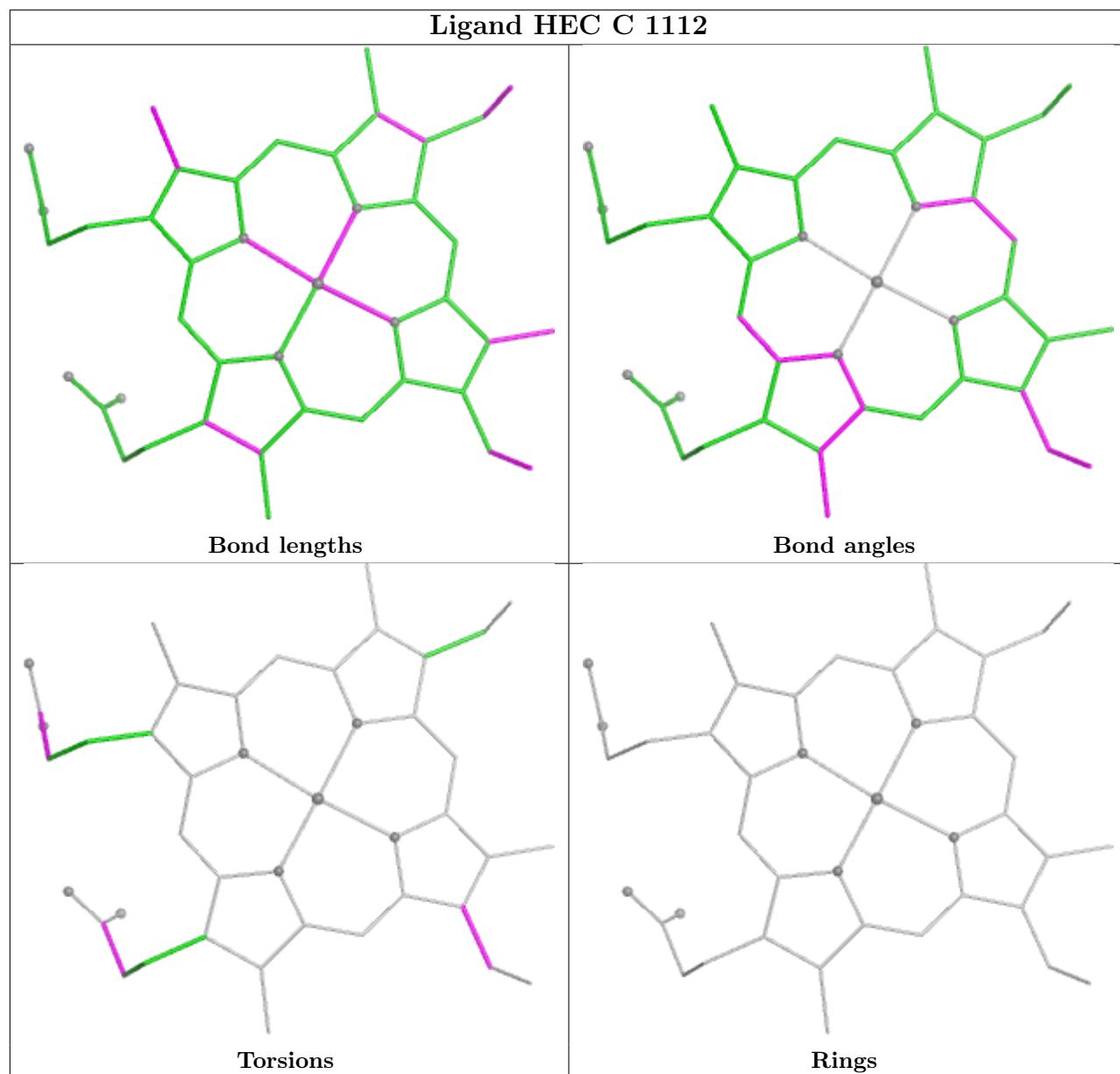
Torsions

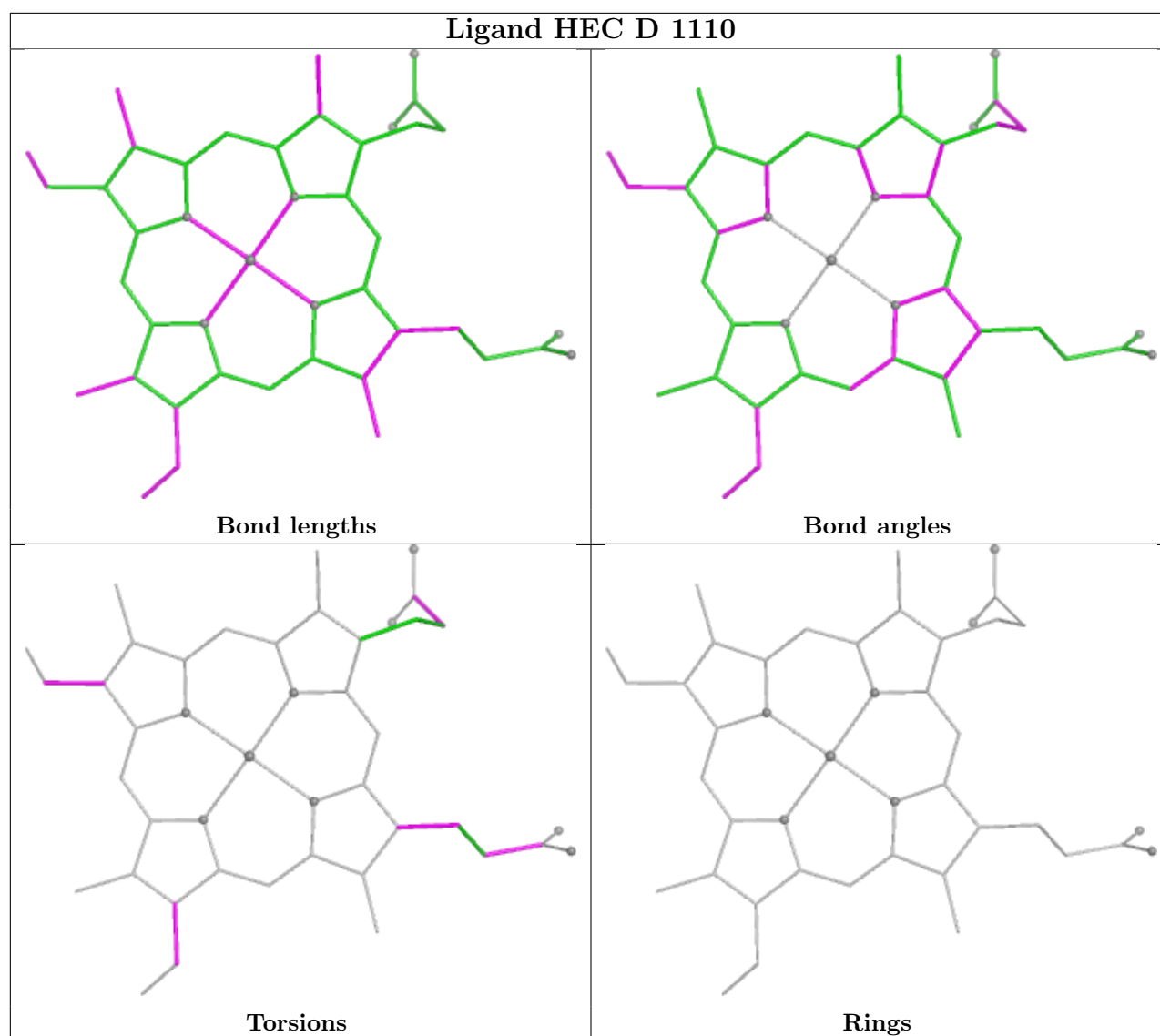


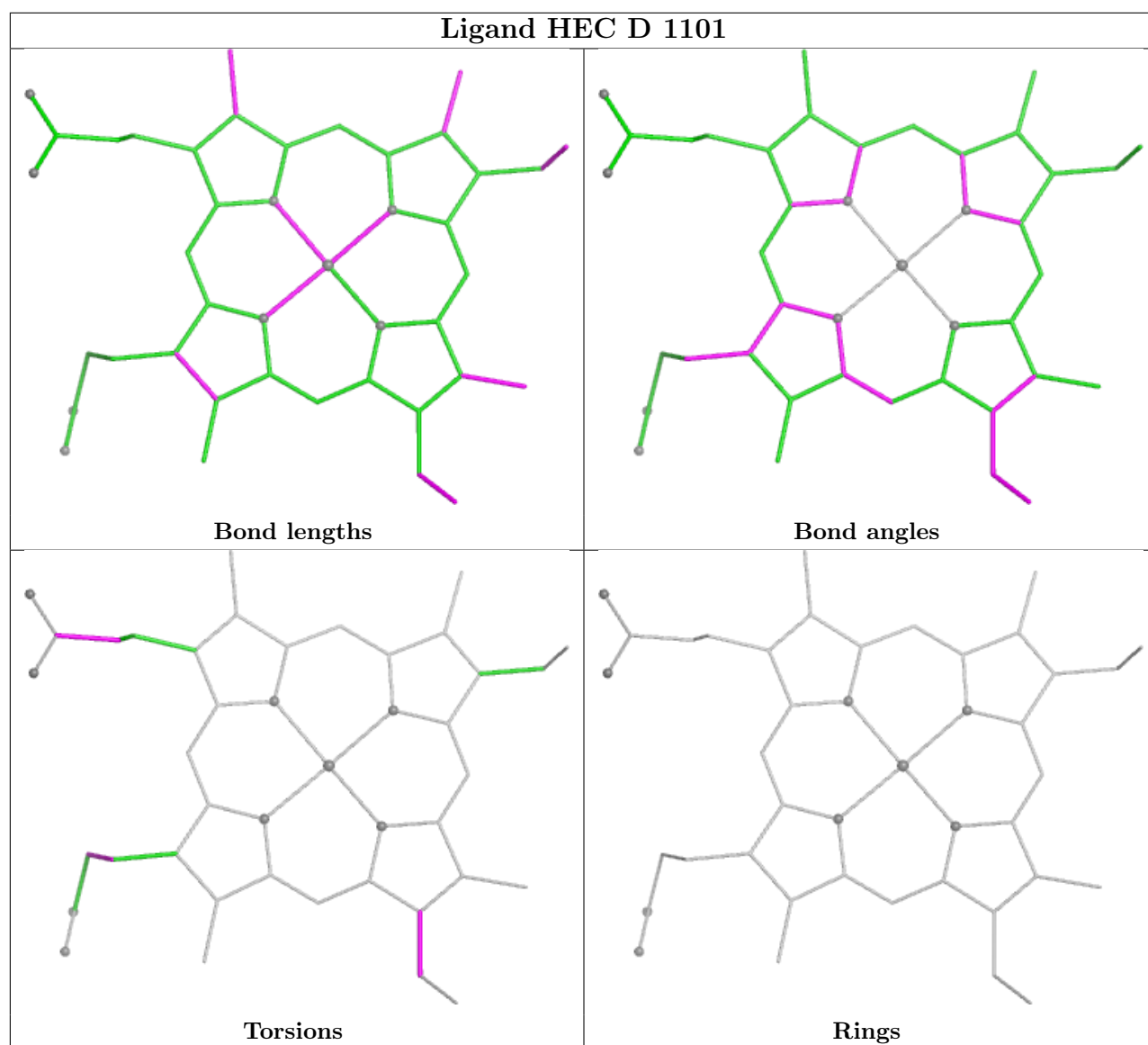
Rings



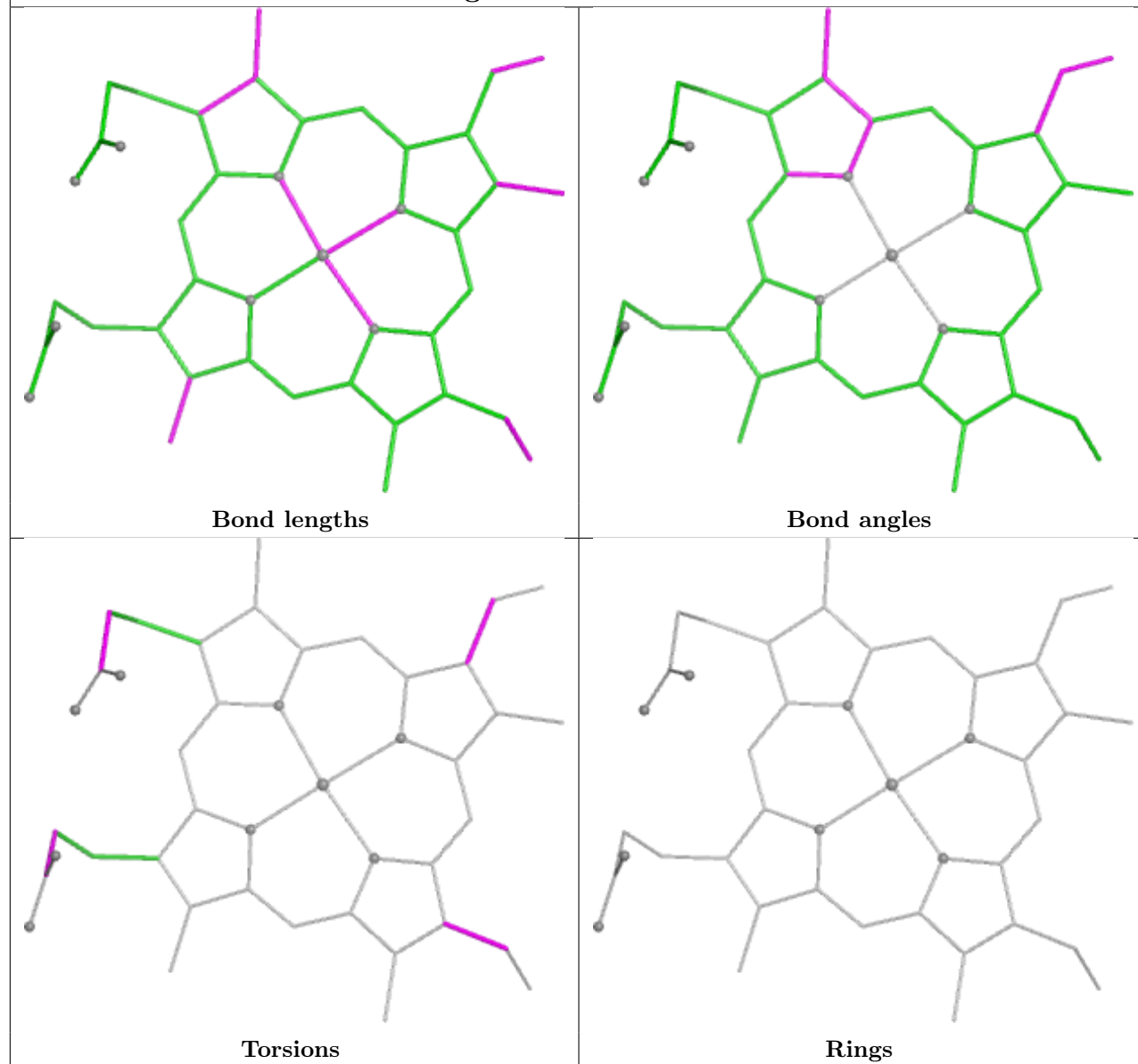
Ligand HEC C 1112



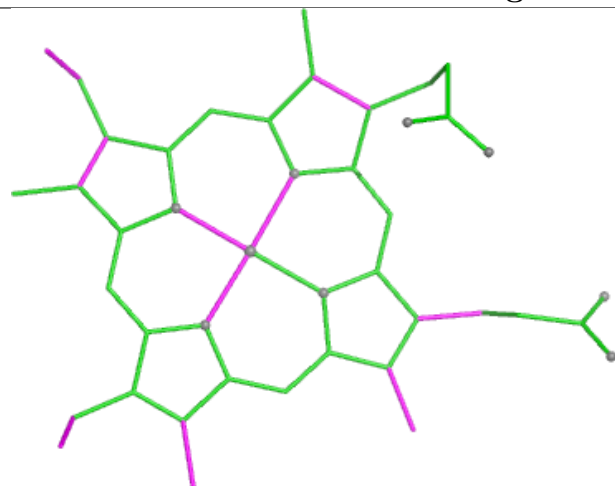




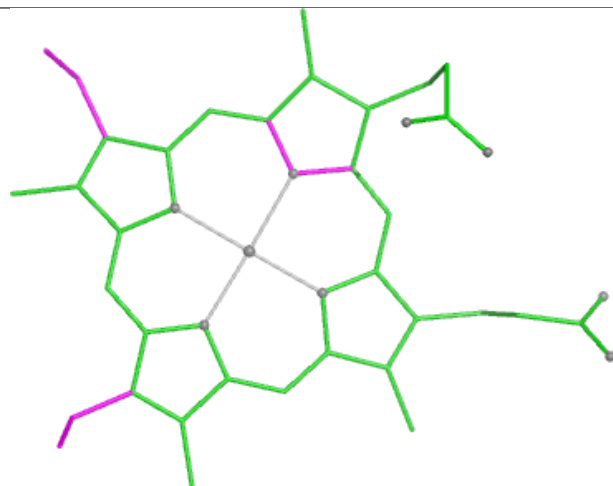
Ligand HEC D 1112



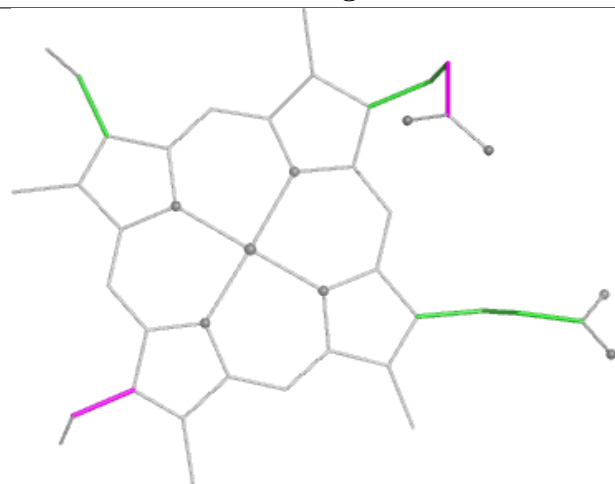
Ligand HEC B 1109



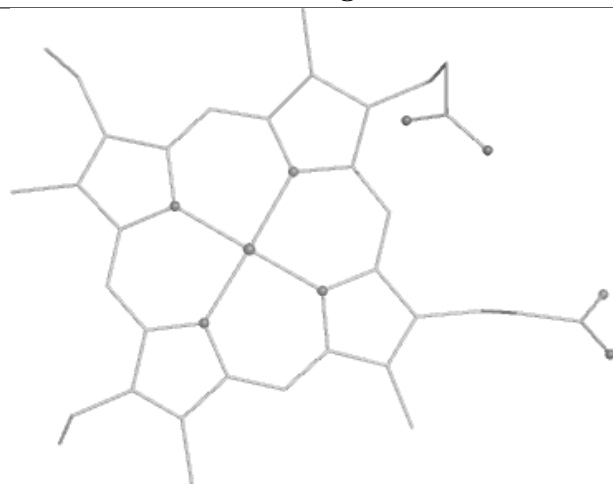
Bond lengths



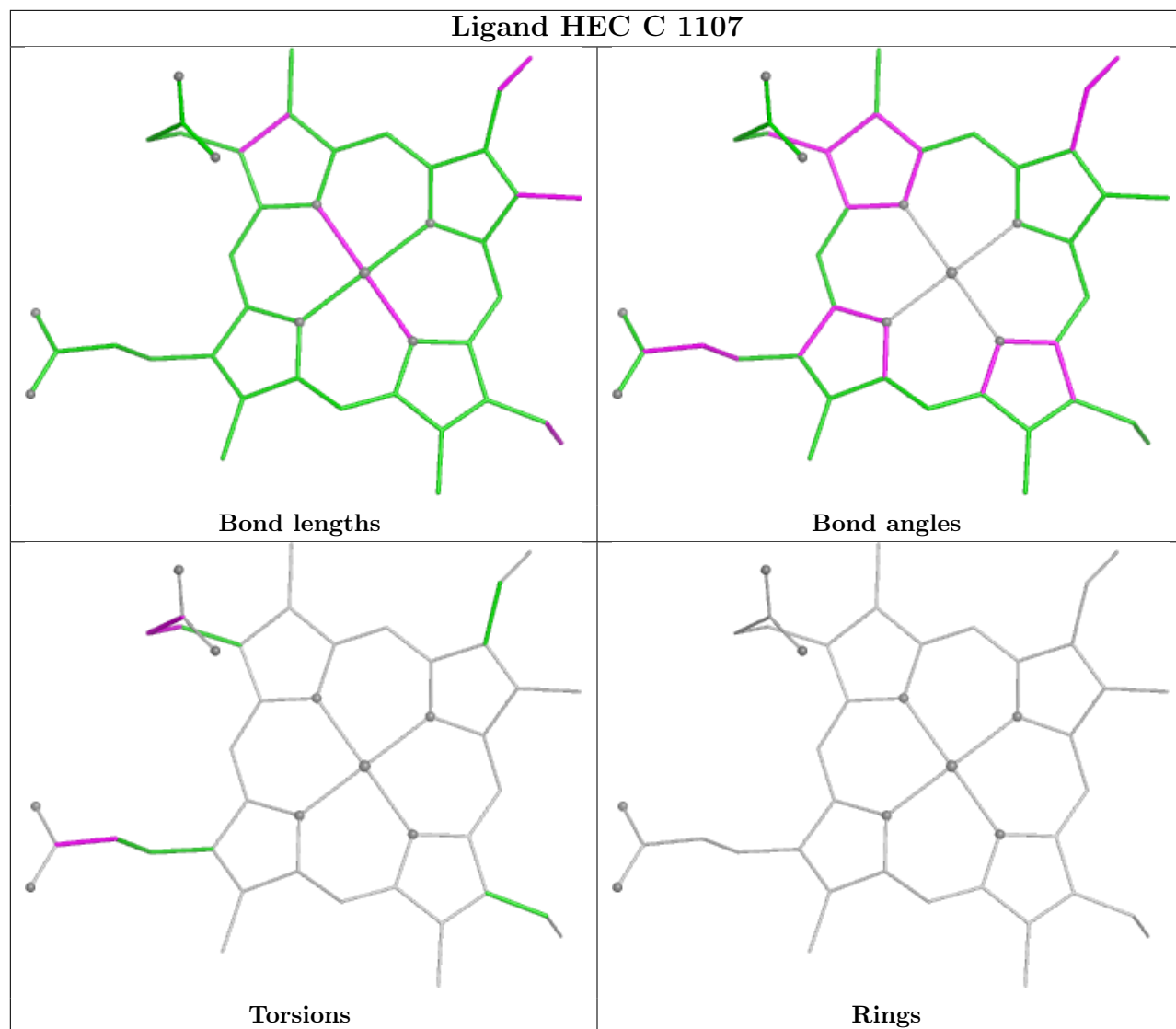
Bond angles



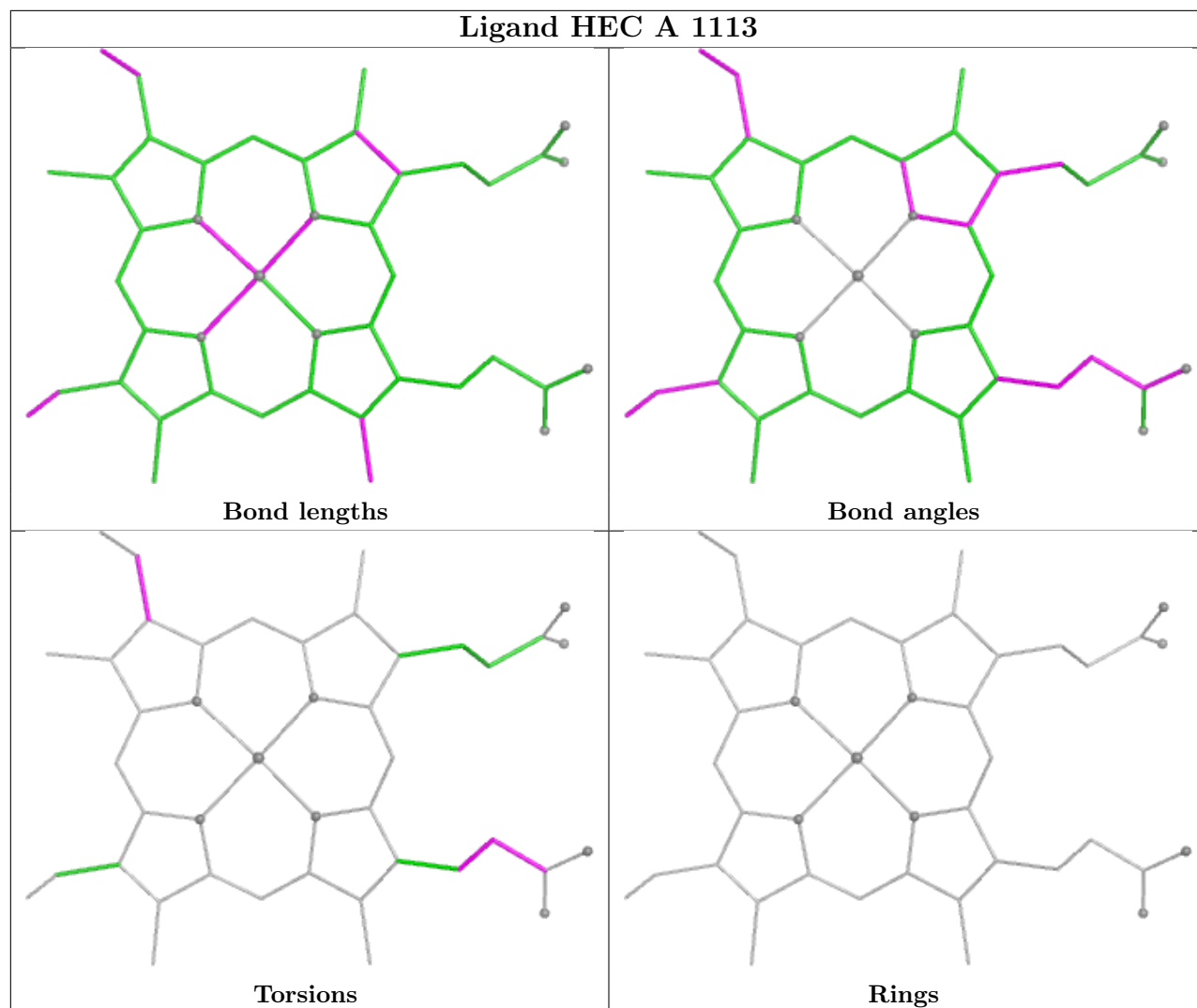
Torsions

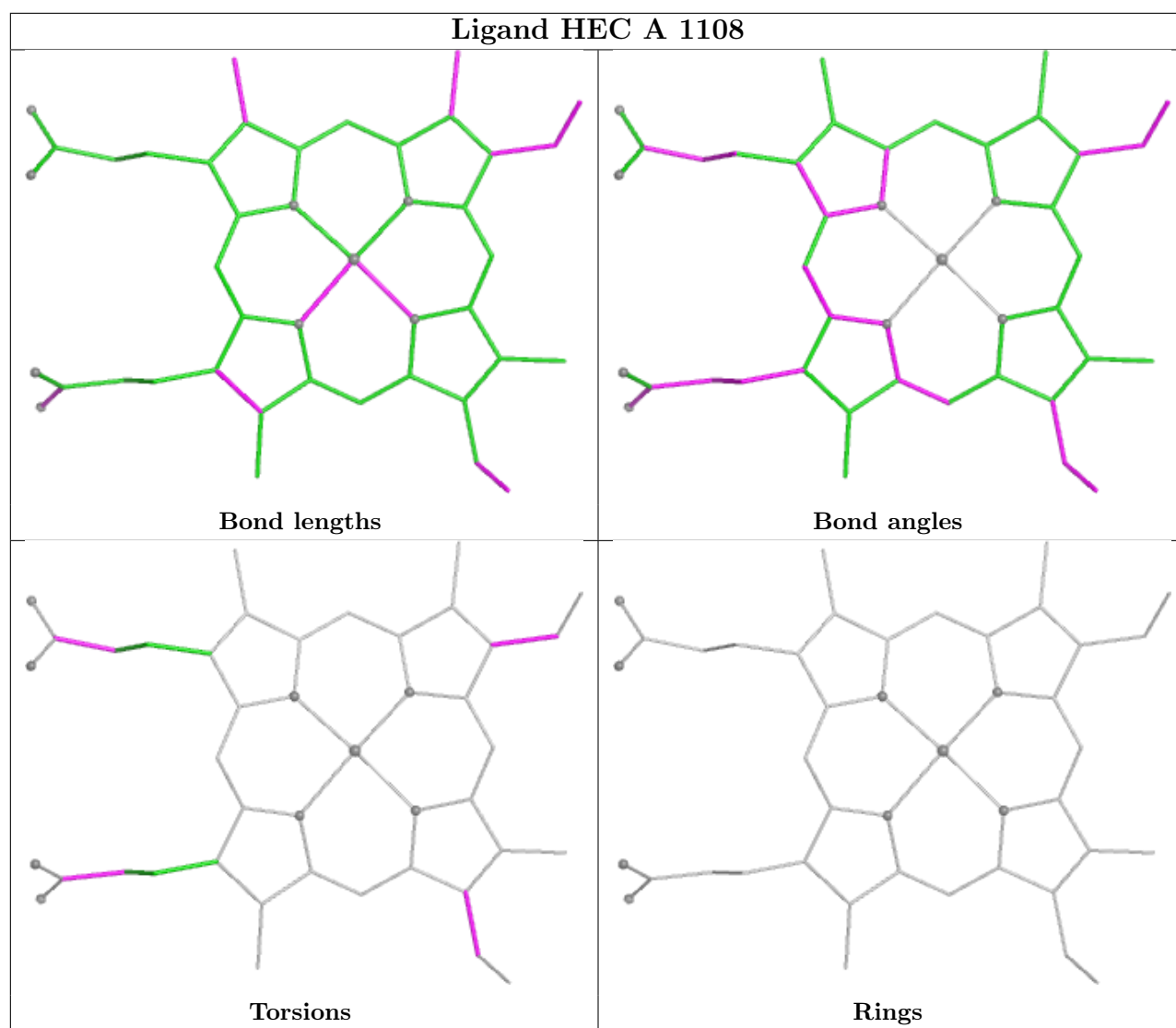


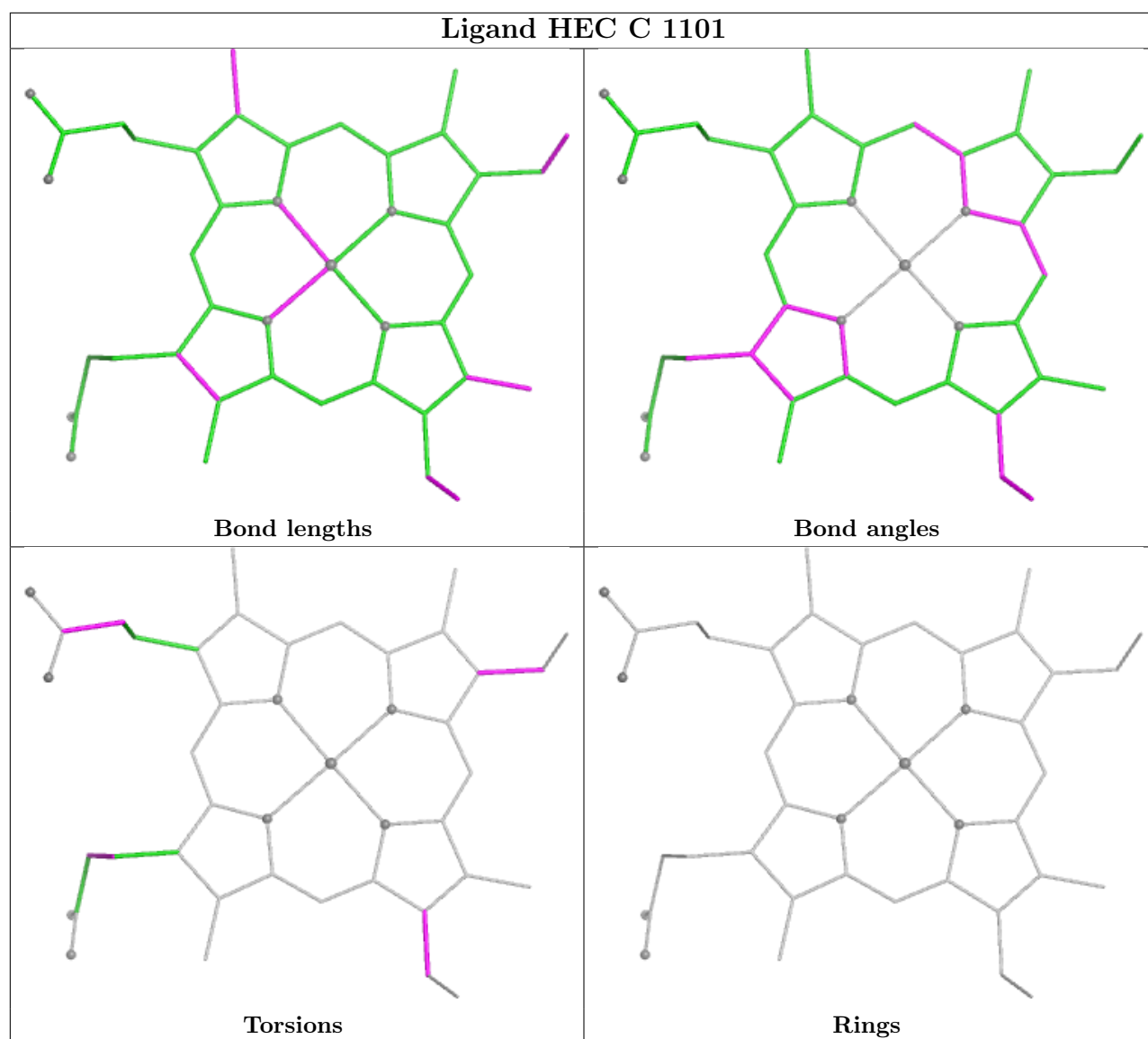
Rings

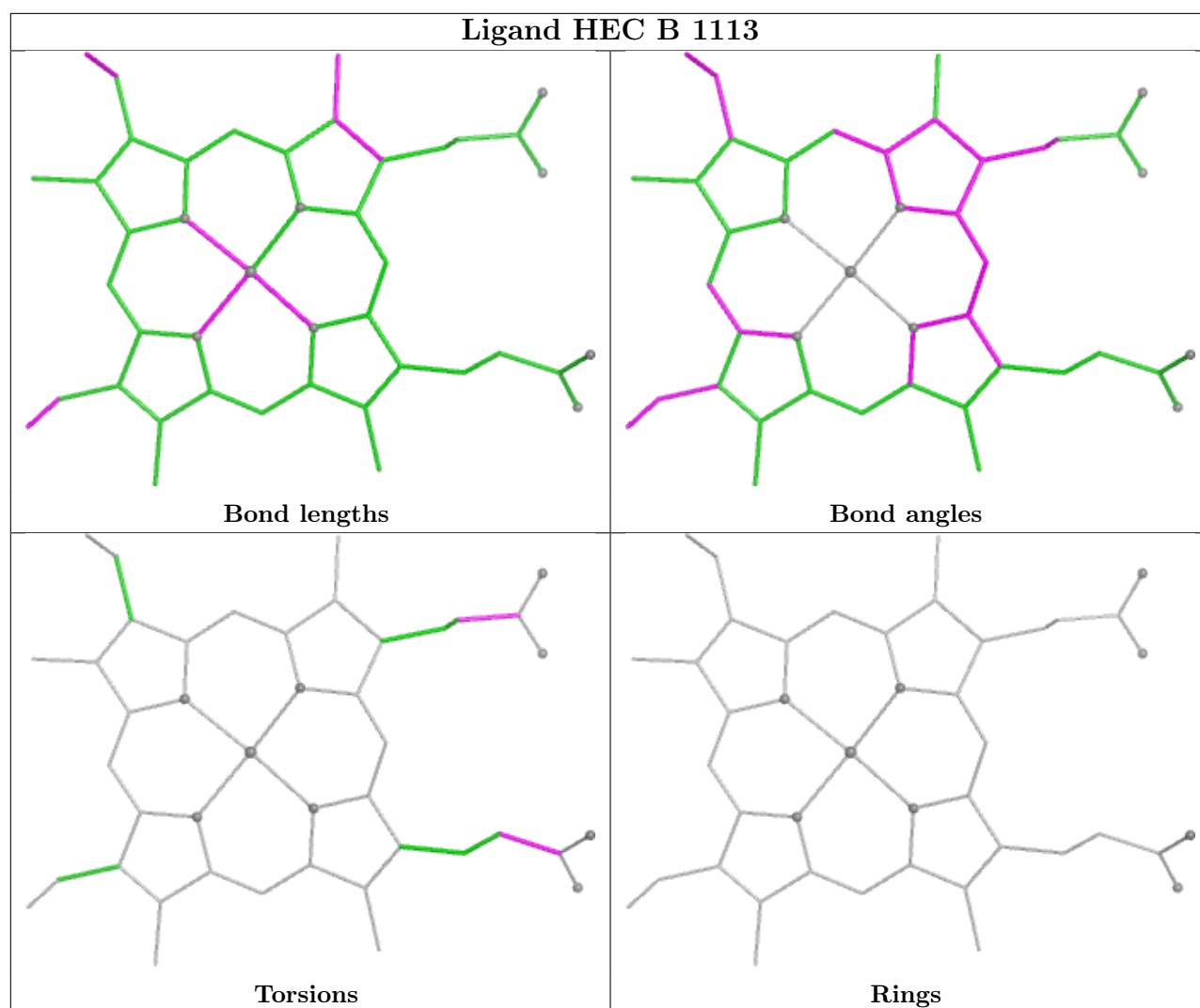


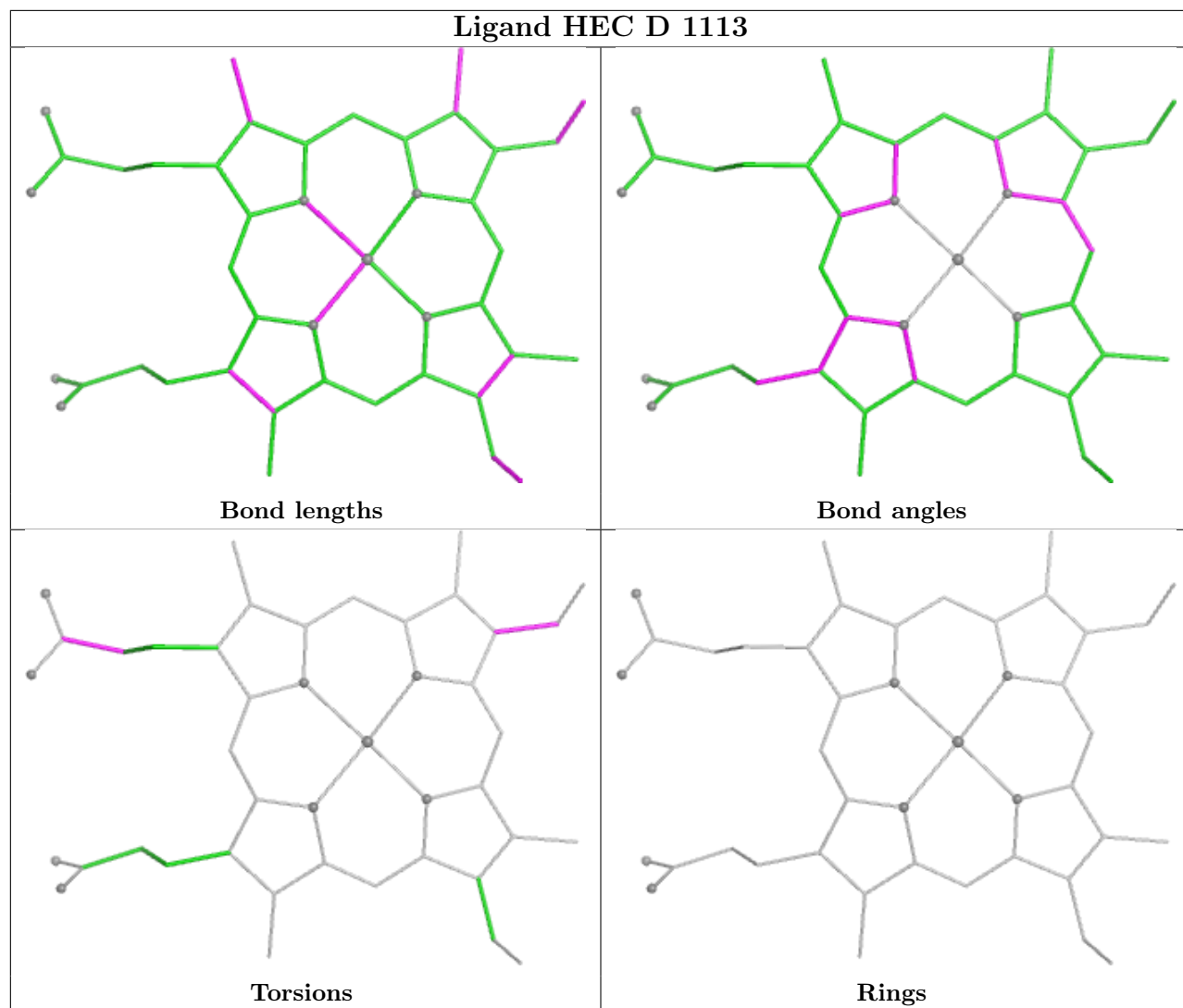
Ligand HEC A 1113



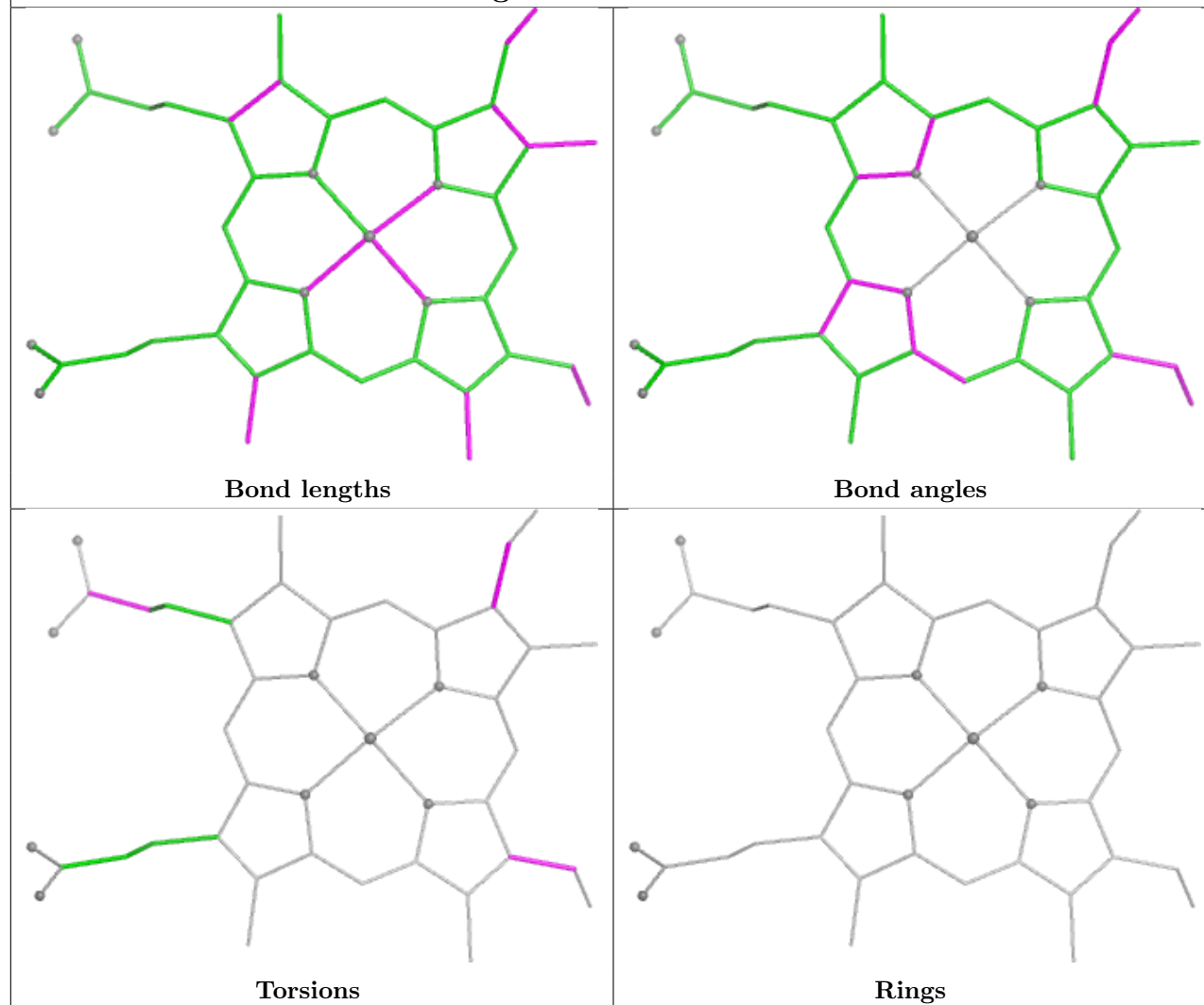




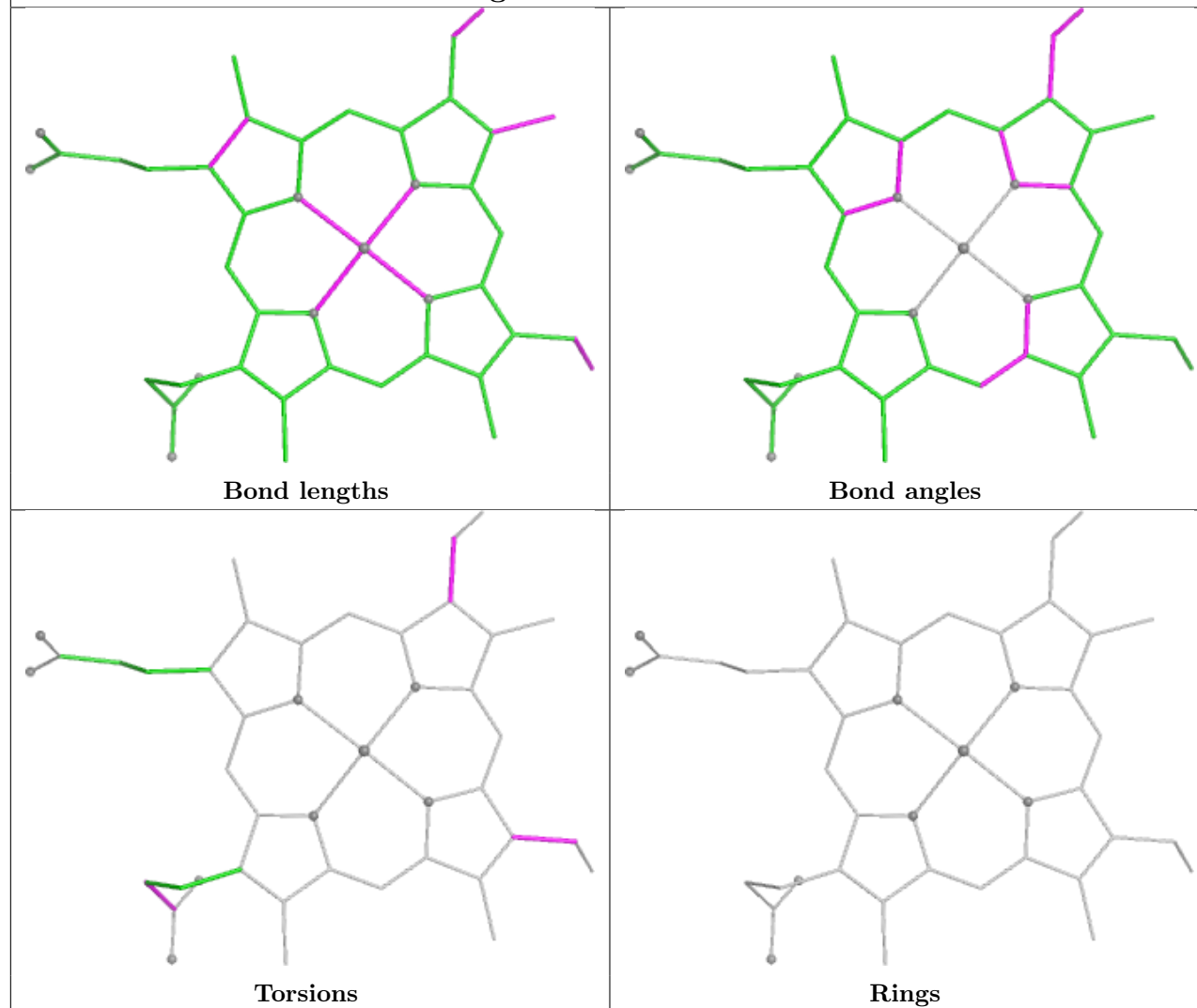


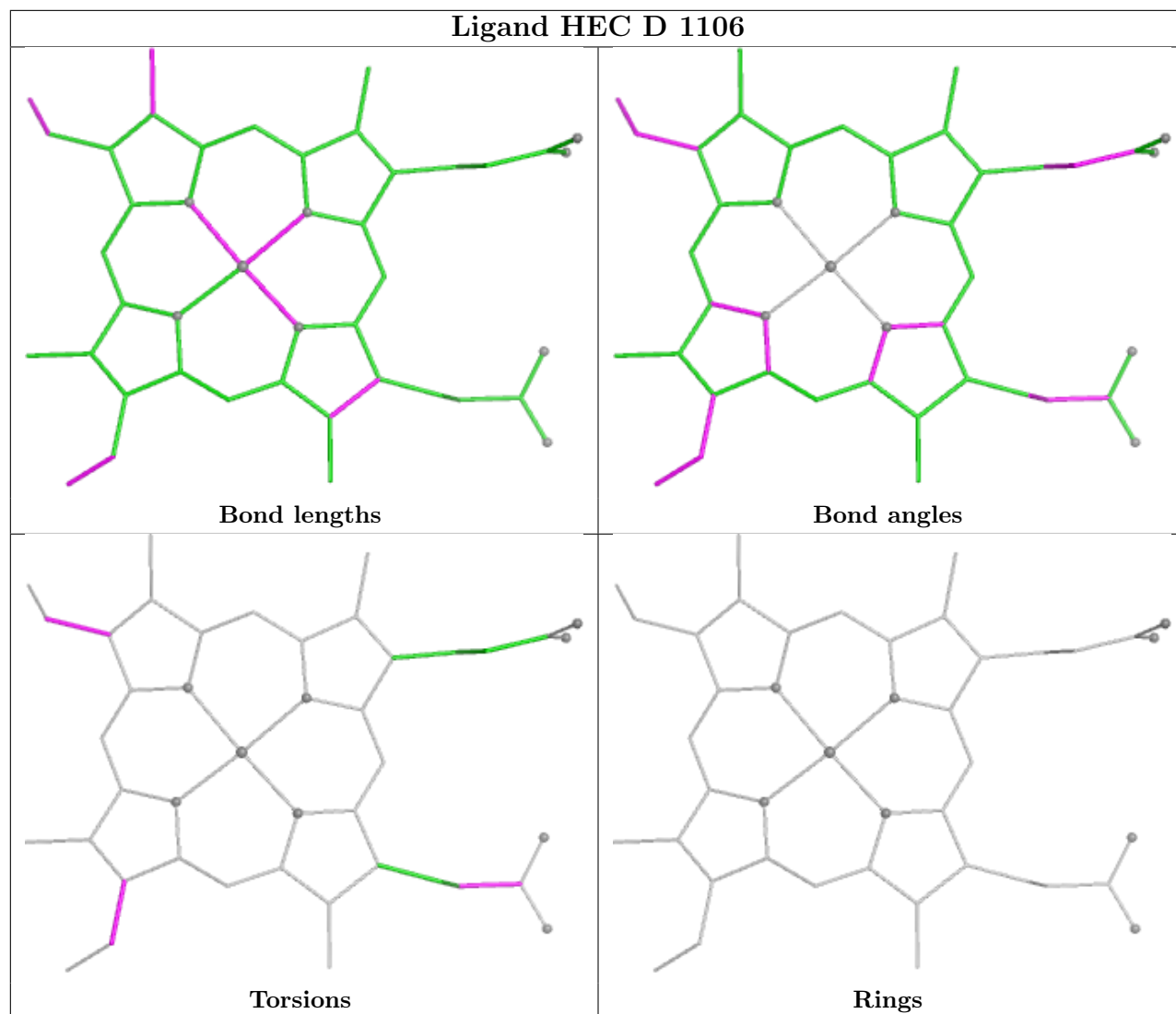


Ligand HEC A 1106

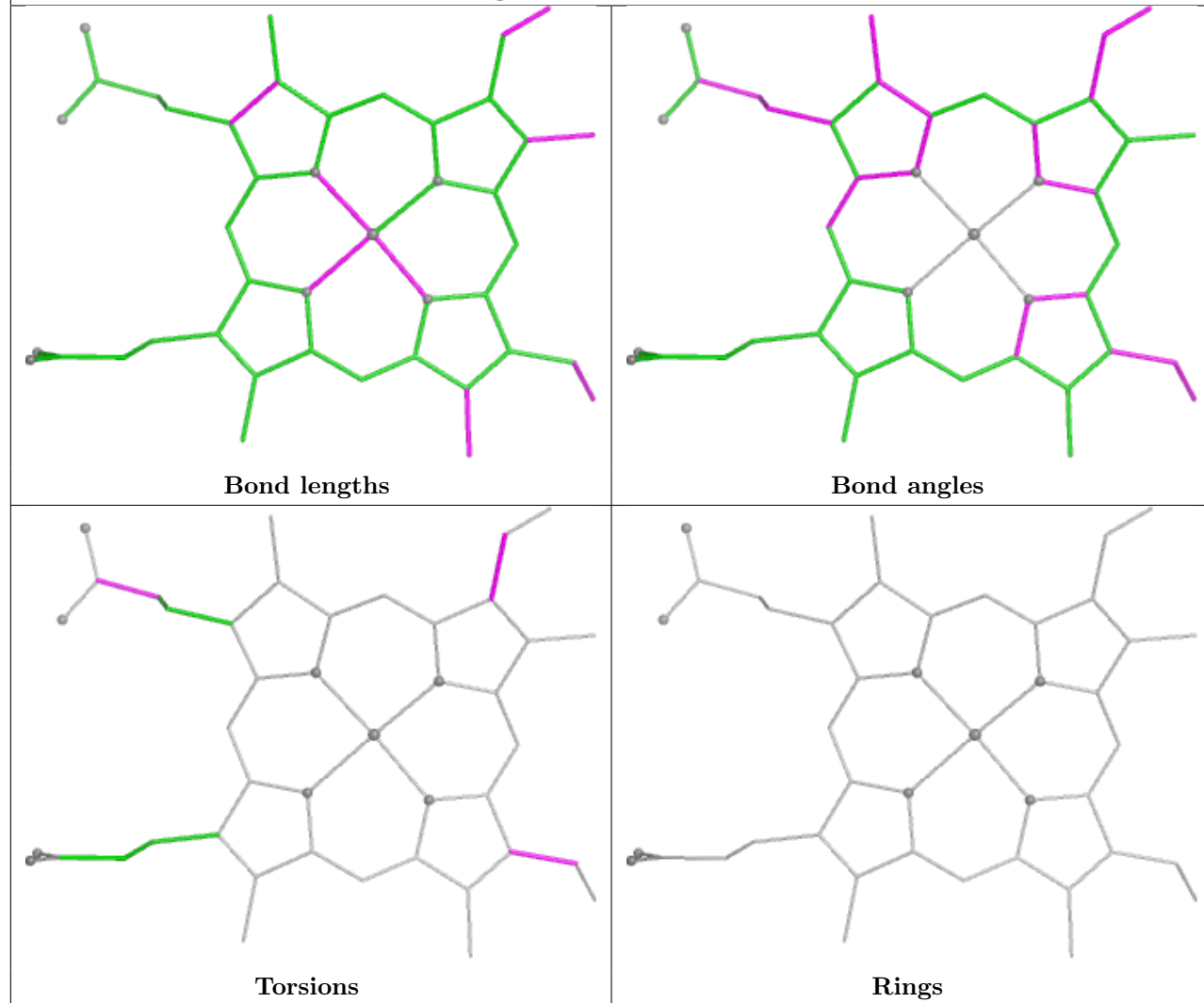


Ligand HEC A 1110

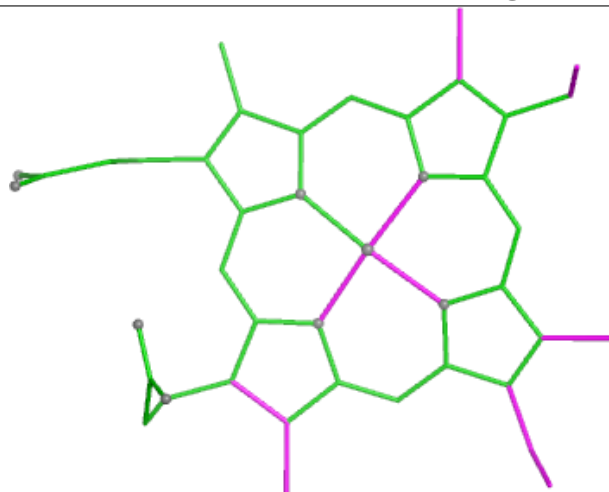




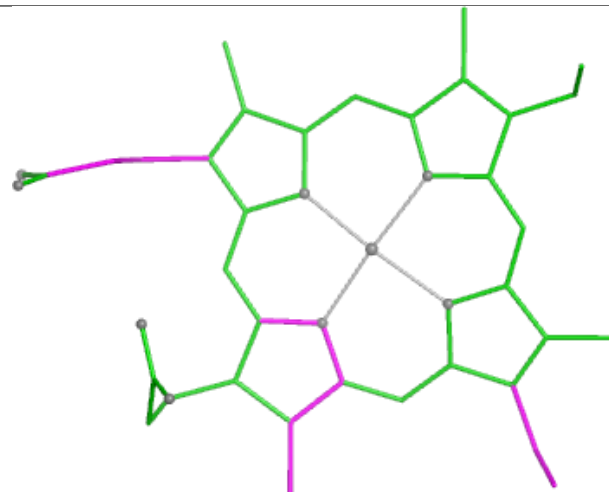
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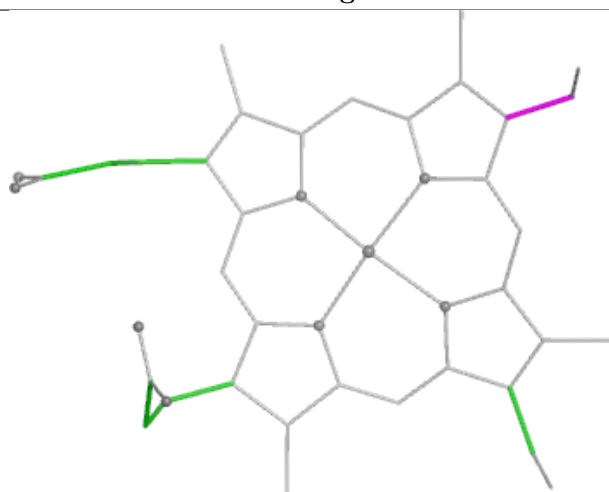
Ligand HEC C 1114



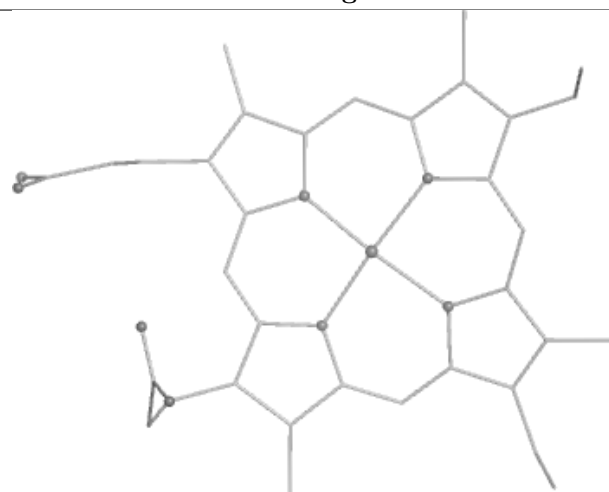
Bond lengths



Bond angles

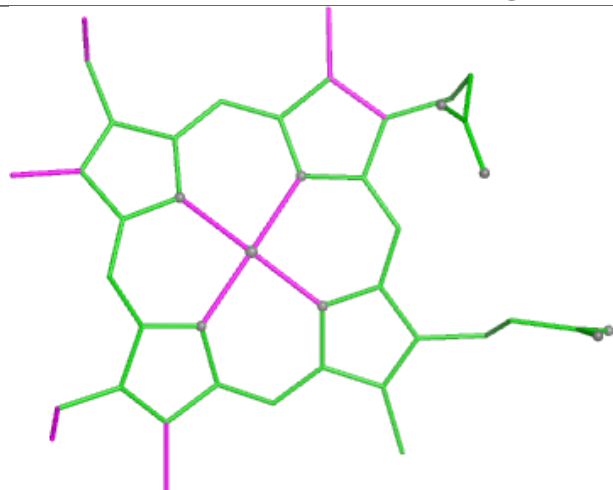


Torsions

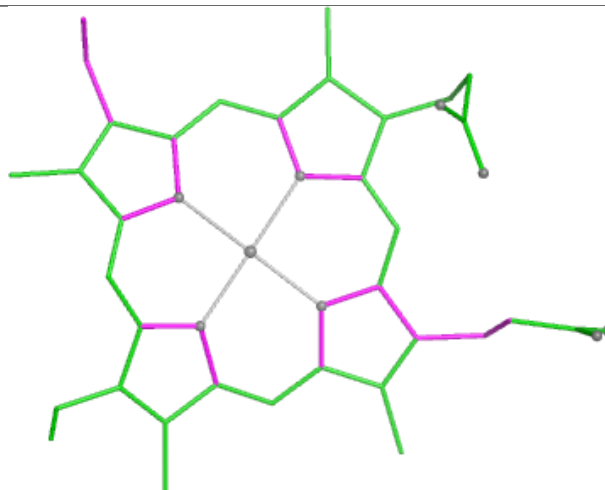


Rings

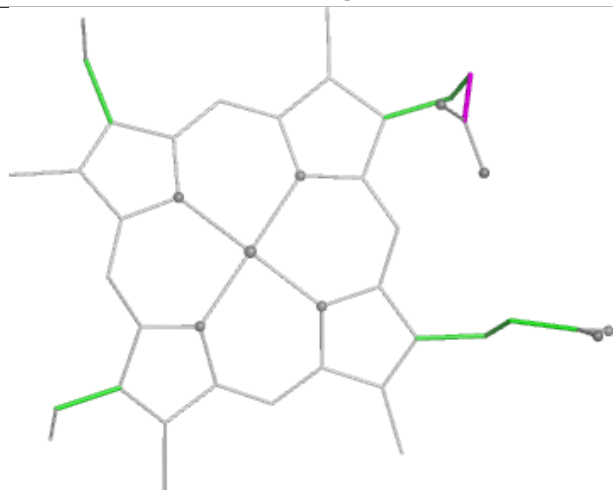
Ligand HEC D 1114



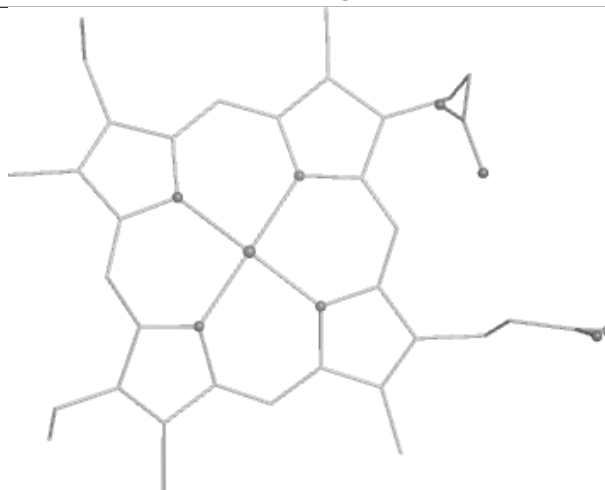
Bond lengths



Bond angles

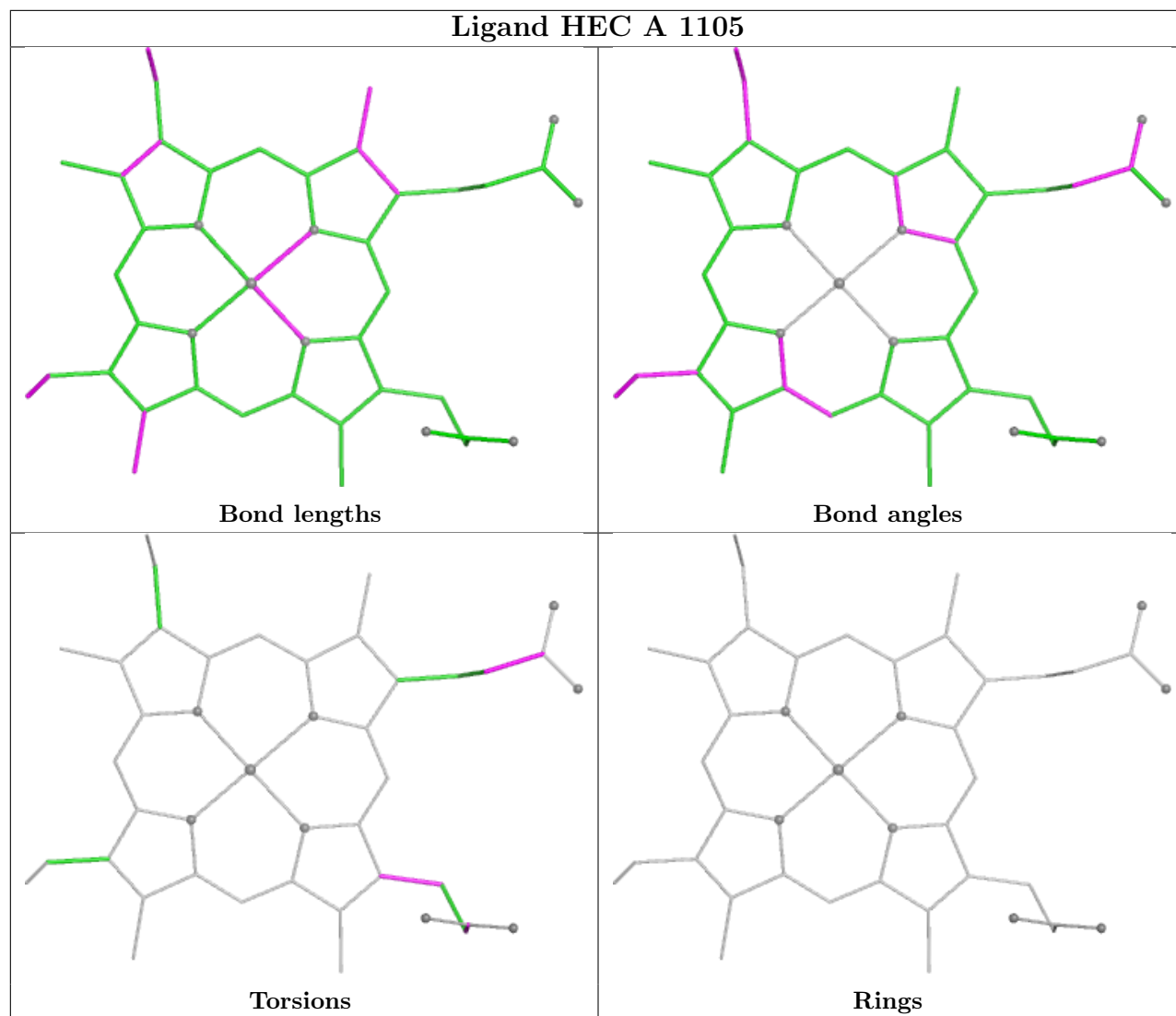


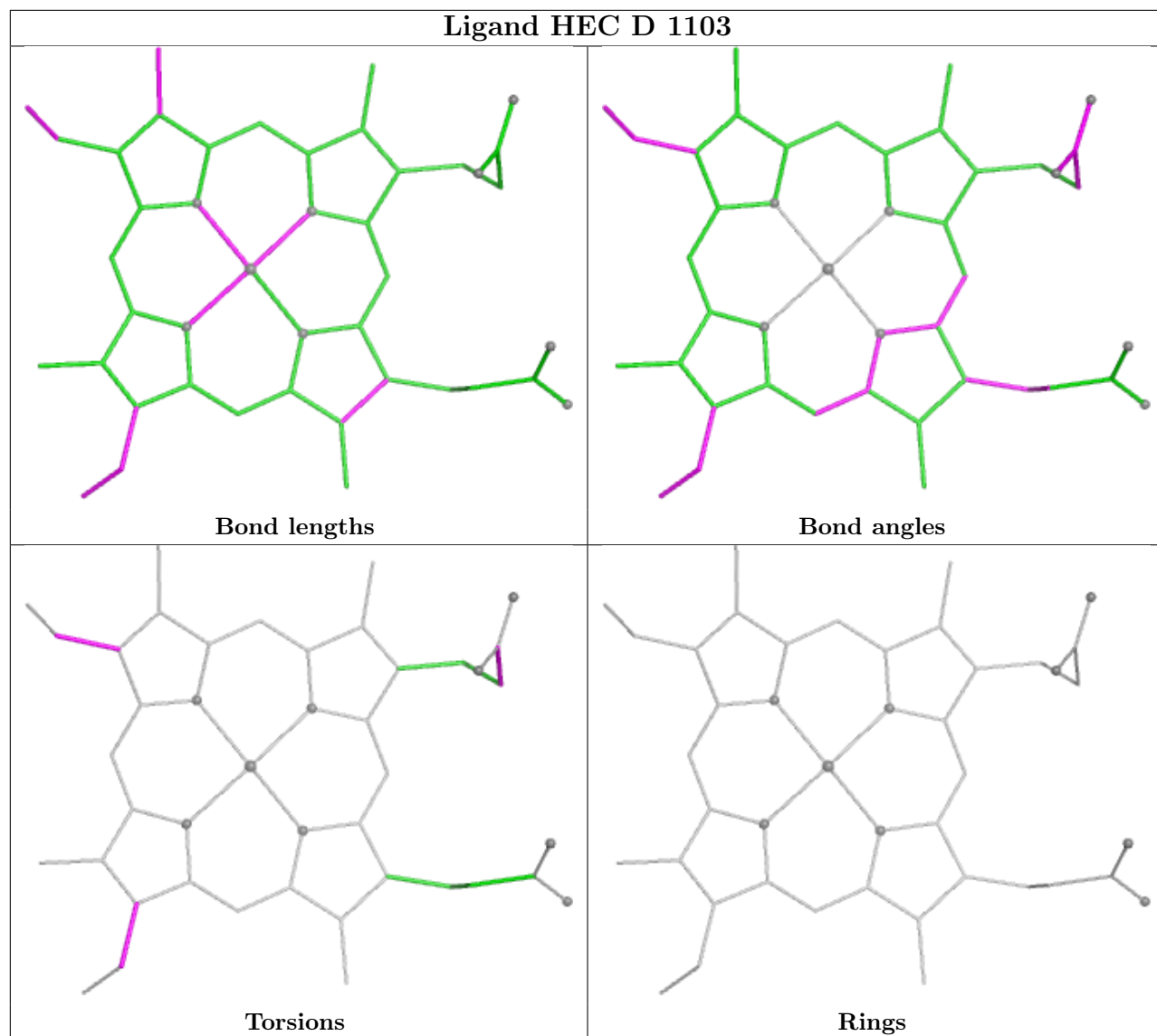
Torsions



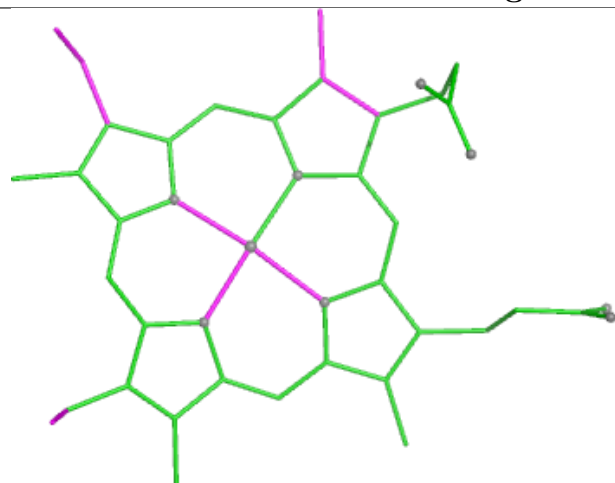
Rings

Ligand HEC A 1105

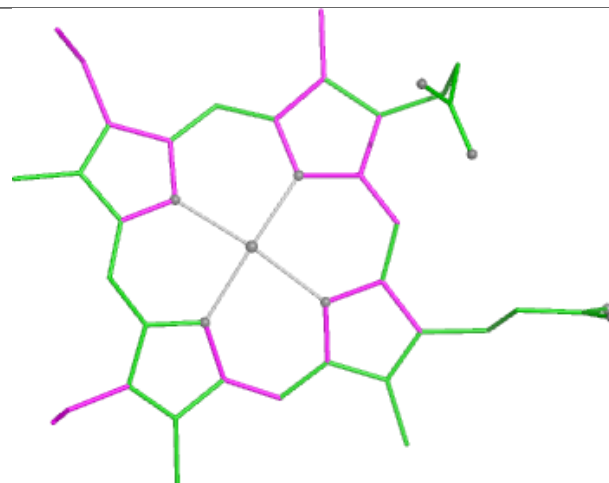




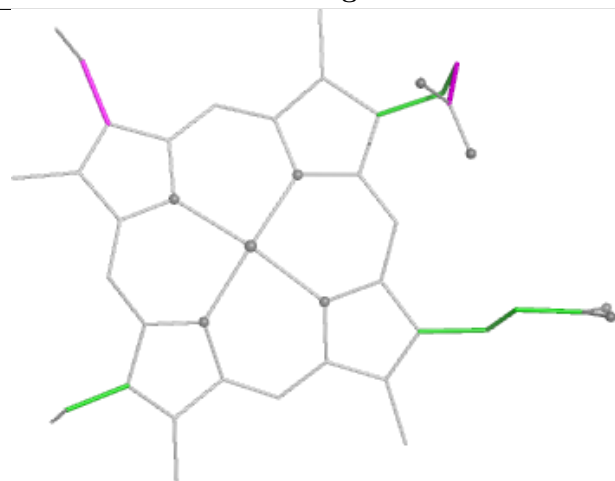
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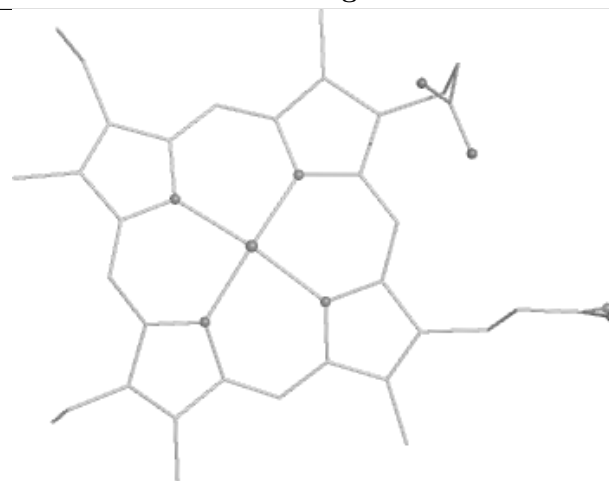
Bond lengths



Bond angles

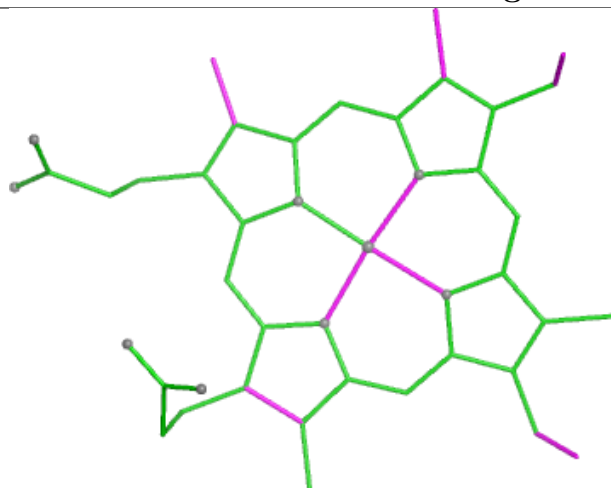


Torsions

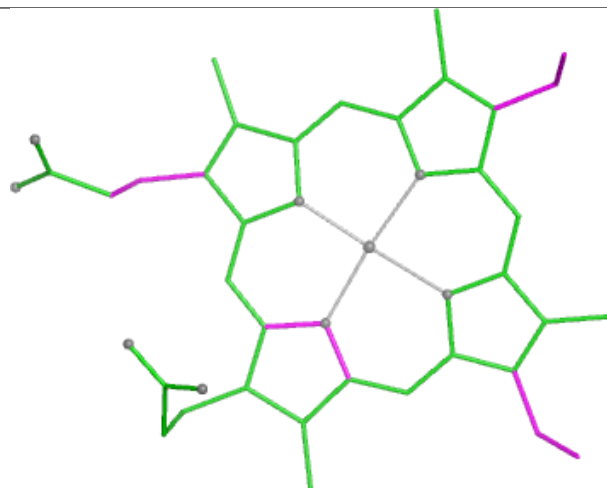


Rings

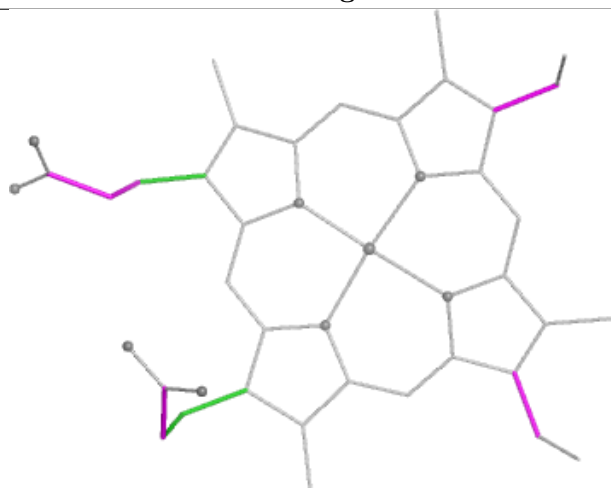
Ligand HEC C 1109



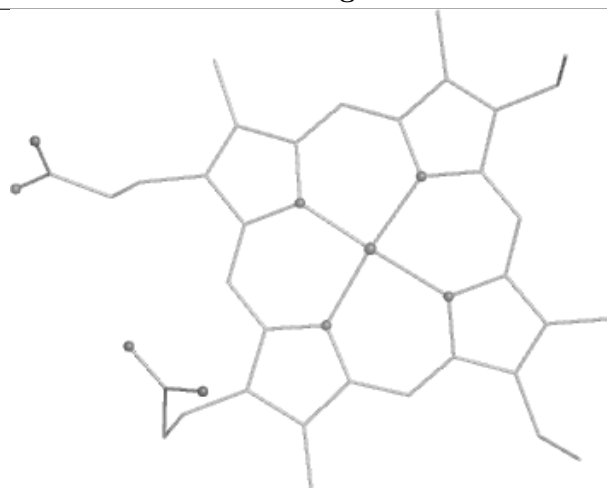
Bond lengths



Bond angles

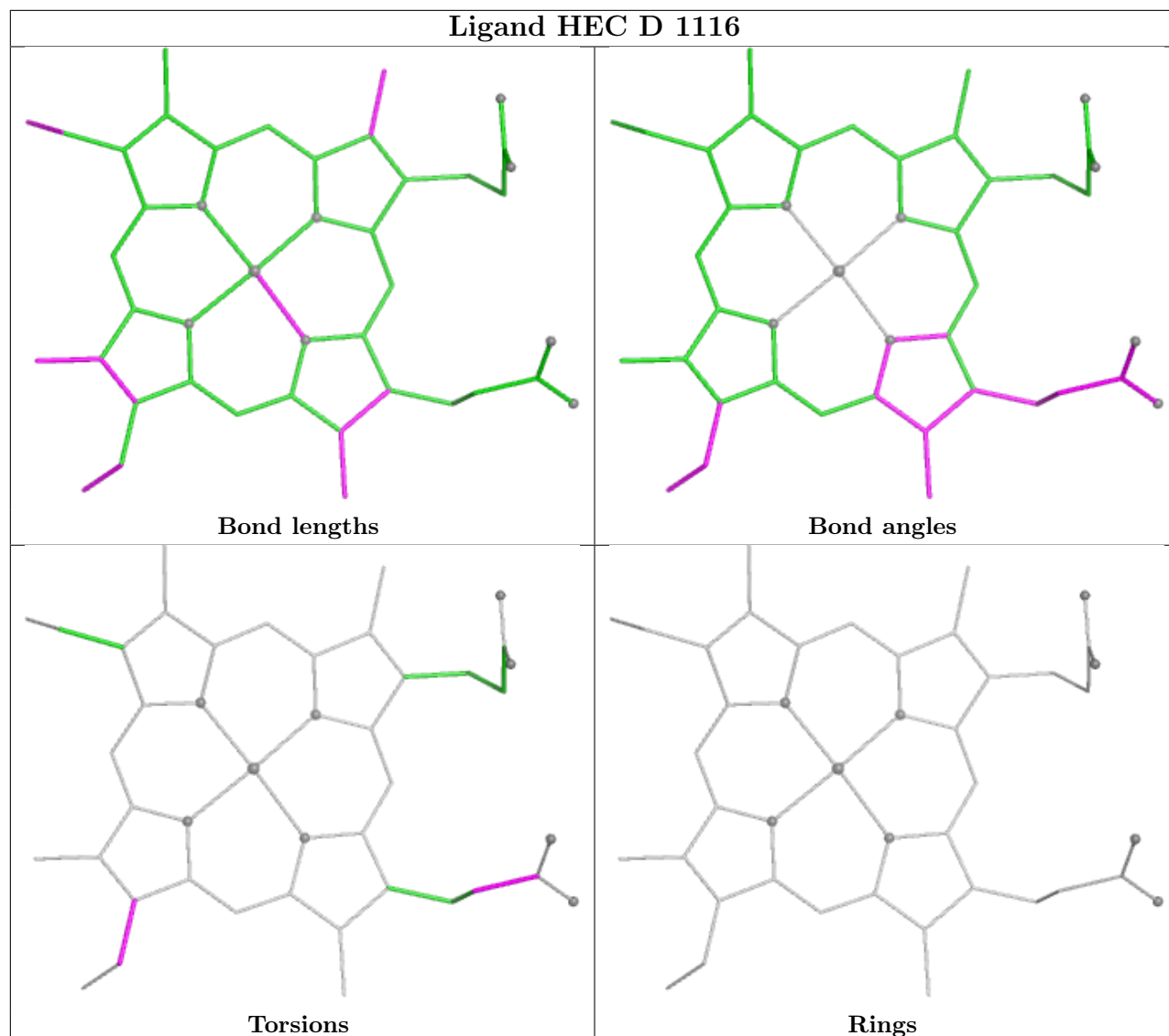


Torsions

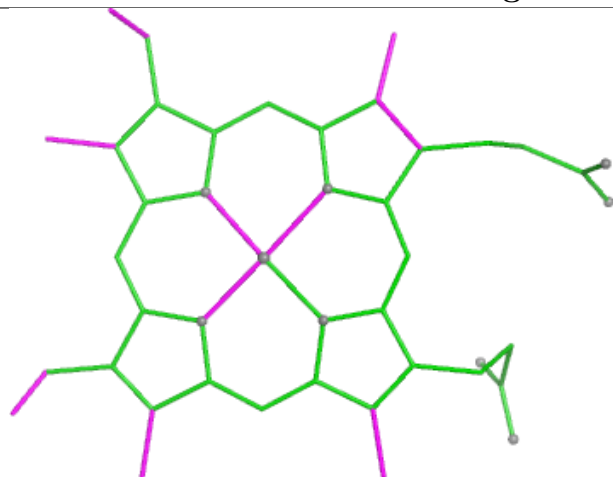


Rings

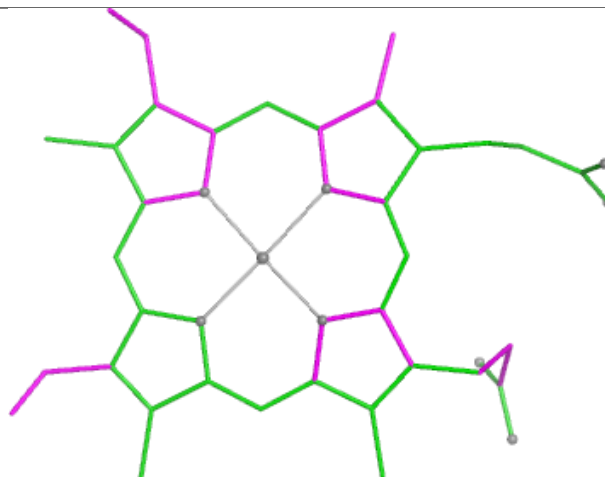
Ligand HEC D 1116



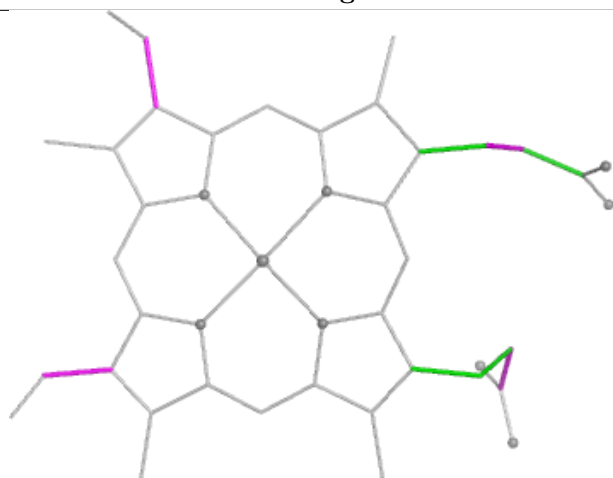
Ligand HEC D 1111



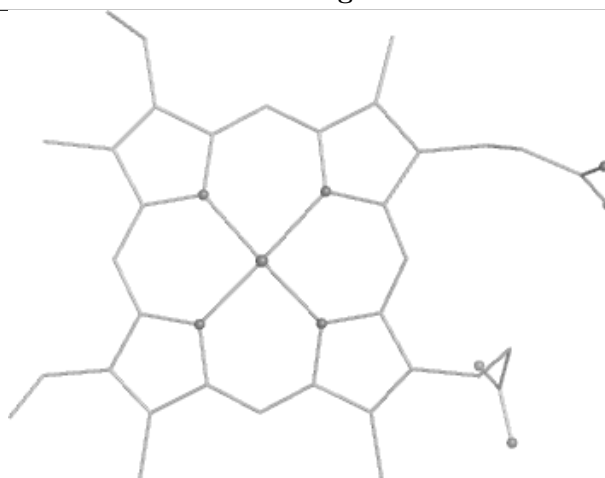
Bond lengths



Bond angles

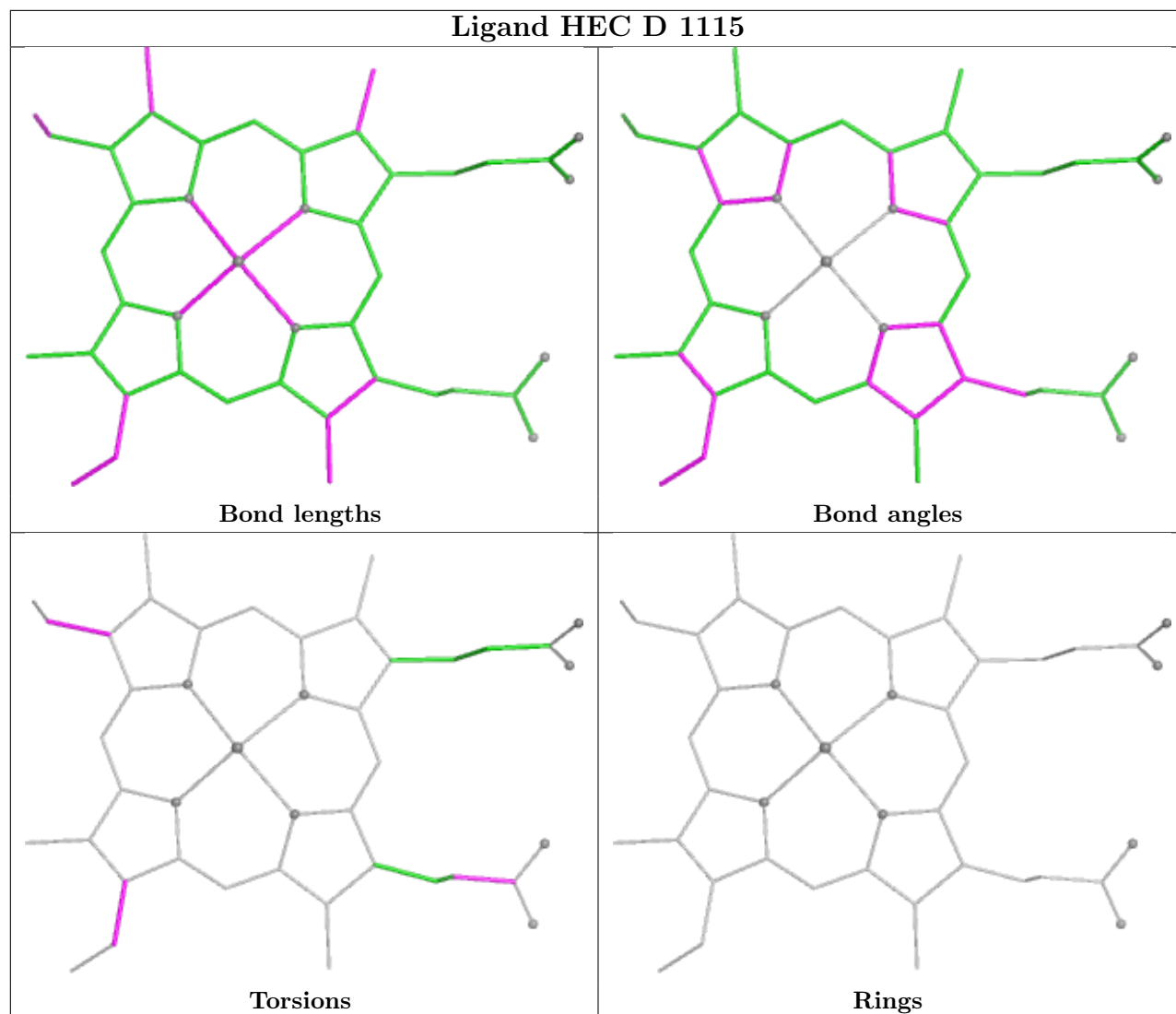


Torsions

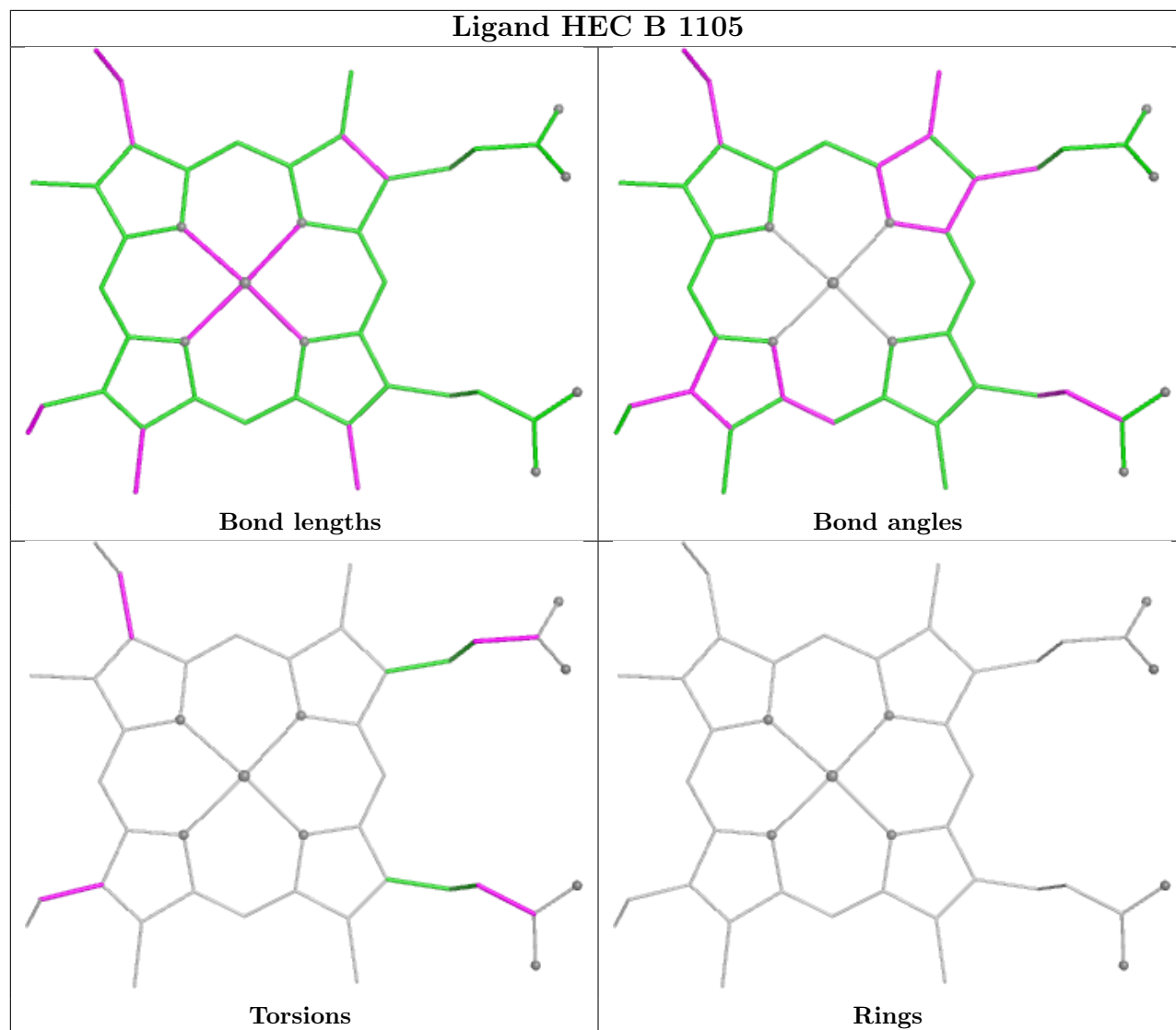


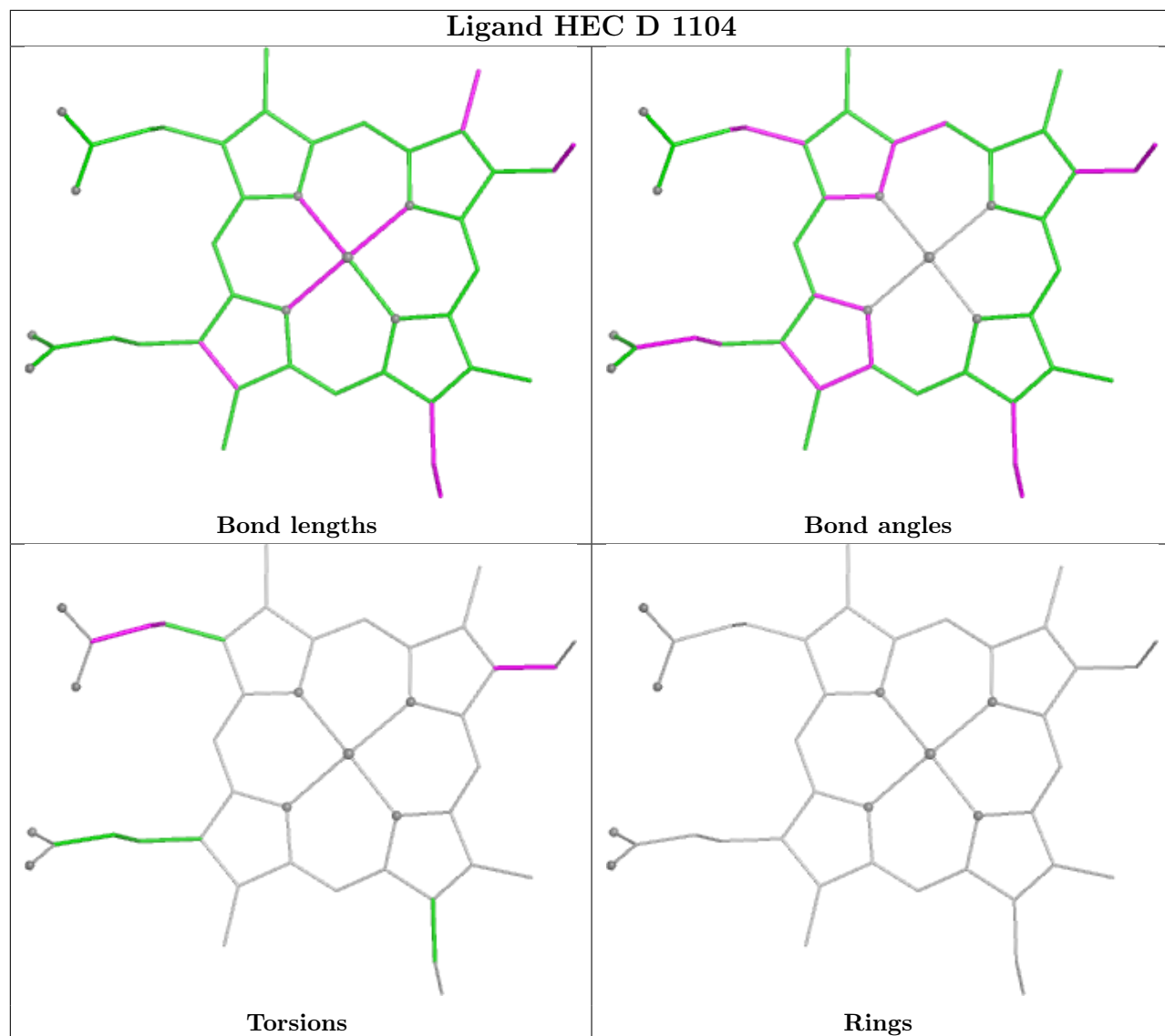
Rings

Ligand HEC D 1115

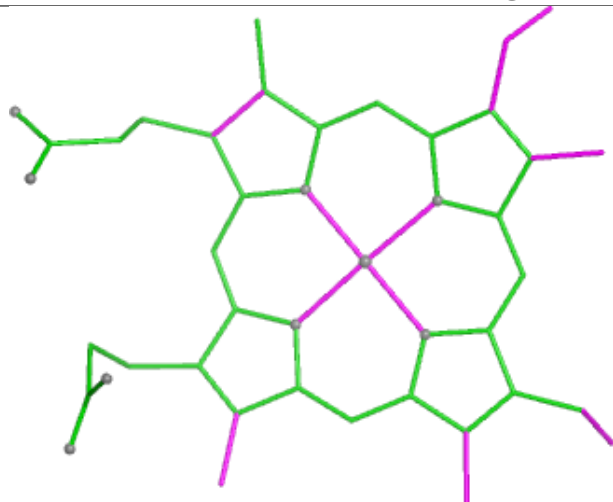


Ligand HEC B 1105

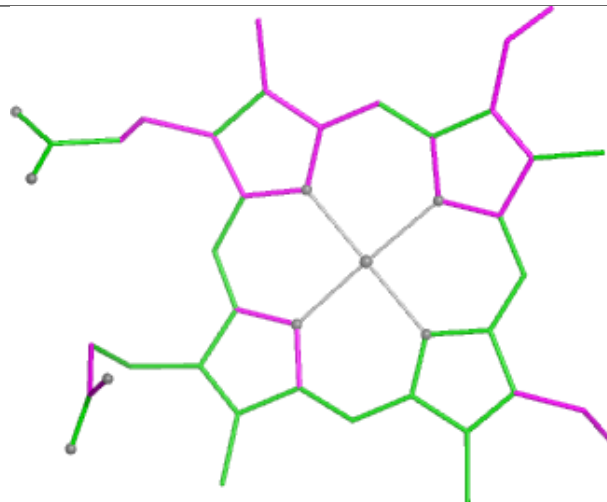




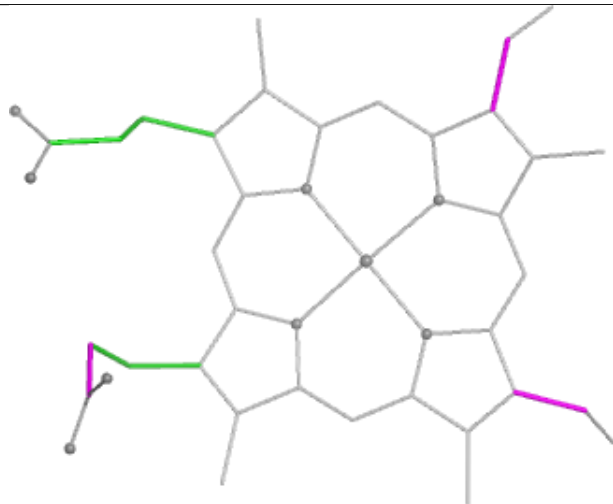
Ligand HEC A 1103



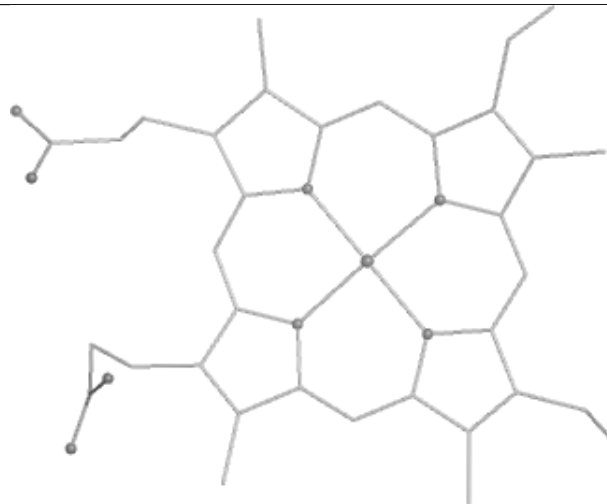
Bond lengths



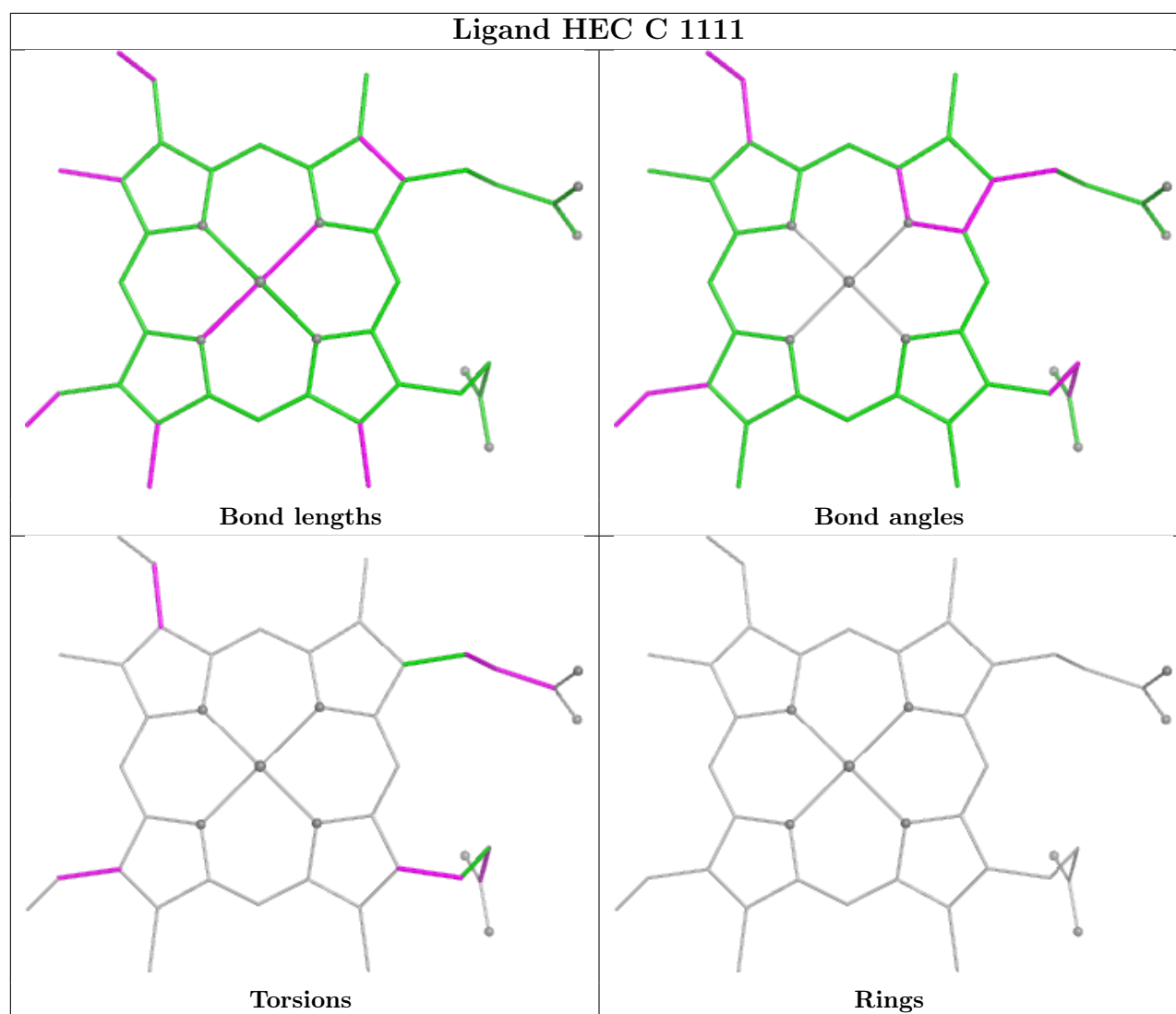
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.