



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 05:03 pm BST

PDB ID : 2J7A
Title : Crystal structure of cytochrome c nitrite reductase NrfHA complex from *Desulfovibrio vulgaris*
Authors : Rodrigues, M.L.; Oliveira, T.F.; Pereira, I.A.C.; Archer, M.
Deposited on : 2006-10-06
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

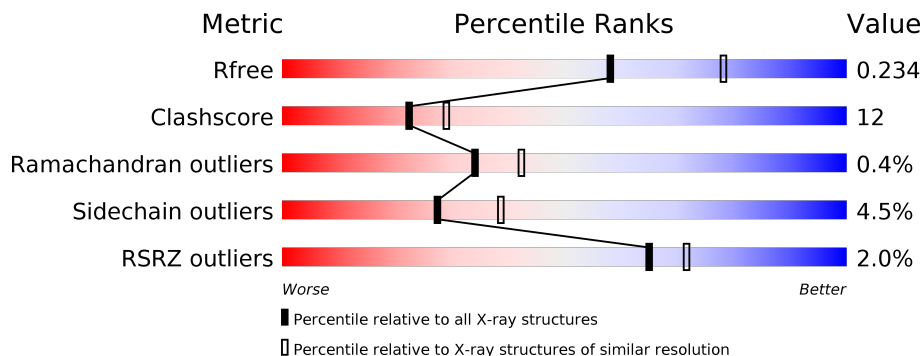
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 on 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	500	 84% 14% ..
1	B	500	 82% 16% .
1	D	500	 84% 14% ..
1	E	500	 81% 15% ..
1	G	500	 84% 13% ..
1	H	500	 83% 15% ..

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Mol	Chain	Length	Quality of chain
1	J	500	<p>82% 16% ..</p>
1	K	500	<p>81% 17% ..</p>
1	M	500	<p>79% 18% ..</p>
1	N	500	<p>83% 15% .</p>
1	P	500	<p>81% 16% ..</p>
1	Q	500	<p>78% 19% ..</p>
2	C	159	<p>72% 18% . 9%</p>
2	F	159	<p>70% 18% . 9%</p>
2	I	159	<p>69% 21% . 9%</p>
2	L	159	<p>69% 21% . 9%</p>
2	O	159	<p>69% 19% . 9%</p>
2	R	159	<p>65% 24% . 9%</p>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 60930 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 CYTOCHROME C NITRITE REDUCTASE NRFA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	495	Total 4022	C 2556	N 695	O 742	S 29	0	2	0
1	B	498	Total 4032	C 2560	N 697	O 746	S 29	0	1	0
1	D	494	Total 4009	C 2546	N 693	O 741	S 29	0	1	0
1	E	494	Total 4009	C 2546	N 693	O 741	S 29	0	1	0
1	G	494	Total 4008	C 2545	N 691	O 743	S 29	0	1	0
1	H	497	Total 4037	C 2563	N 694	O 751	S 29	0	3	0
1	J	494	Total 4021	C 2554	N 693	O 745	S 29	0	3	0
1	K	496	Total 4014	C 2549	N 693	O 743	S 29	0	0	0
1	M	494	Total 4014	C 2549	N 693	O 743	S 29	0	2	0
1	N	498	Total 4032	C 2560	N 697	O 746	S 29	0	1	0
1	P	494	Total 4007	C 2544	N 691	O 743	S 29	0	1	0
1	Q	495	Total 4016	C 2551	N 694	O 742	S 29	0	1	0

- Molecule 2 is a protein called CYTOCHROME C QUINOL DEHYDROGENASE NRFH.

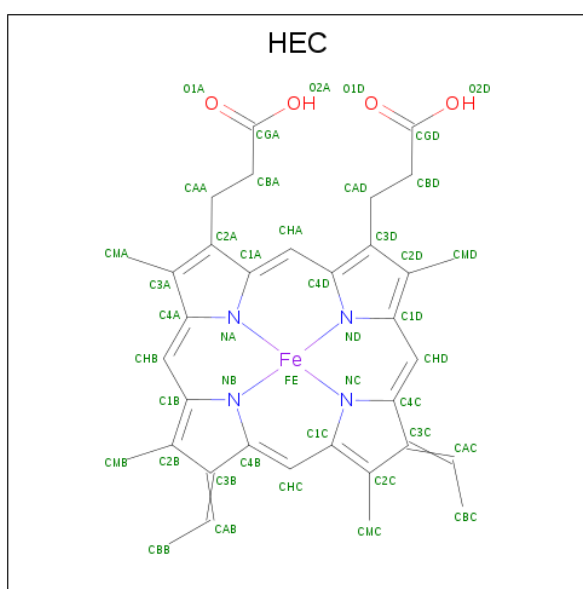
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	145	Total 1094	C 680	N 201	O 197	S 16	0	1	0
2	F	145	Total 1093	C 679	N 199	O 199	S 16	0	1	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	145	Total	C	N	O	S	0	0	0
			1087	675	199	197	16			
2	L	145	Total	C	N	O	S	0	0	0
			1087	675	199	197	16			
2	O	144	Total	C	N	O	S	0	0	0
			1078	669	197	196	16			
2	R	145	Total	C	N	O	S	0	0	0
			1087	675	199	197	16			

- Molecule 3 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

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

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

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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	R	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	R	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	R	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	R	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

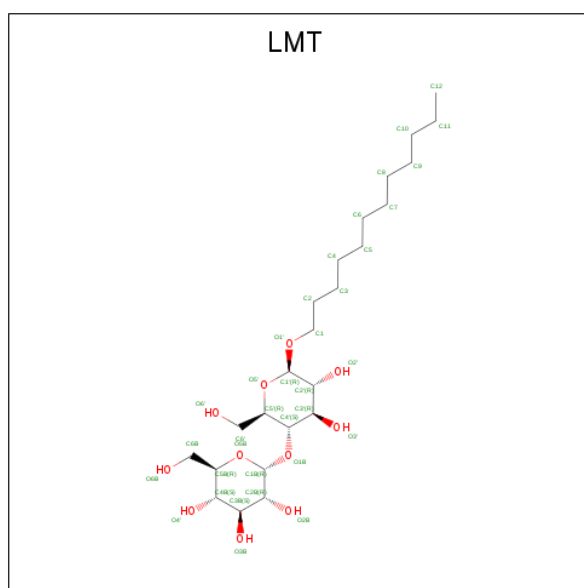
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	2	Total 2	Ca 2	0	0
4	G	2	Total 2	Ca 2	0	0
4	J	2	Total 2	Ca 2	0	0
4	Q	2	Total 2	Ca 2	0	0
4	D	2	Total 2	Ca 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	K	2	Total Ca 2 2	0	0
4	E	2	Total Ca 2 2	0	0
4	H	2	Total Ca 2 2	0	0
4	B	2	Total Ca 2 2	0	0
4	A	2	Total Ca 2 2	0	0
4	N	2	Total Ca 2 2	0	0
4	M	2	Total Ca 2 2	0	0

- Molecule 5 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



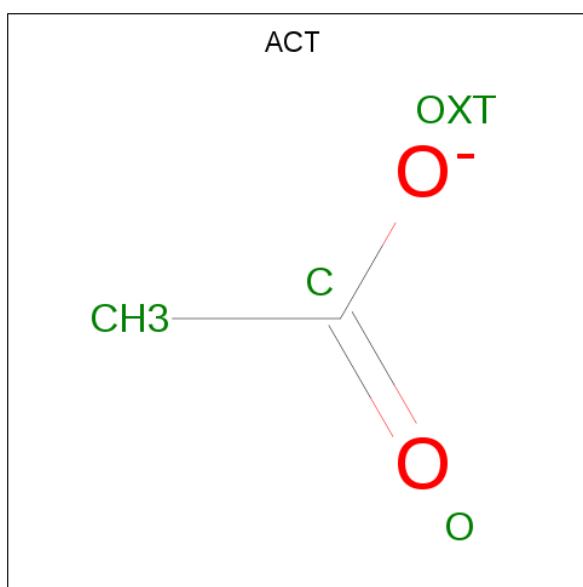
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 35 24 11	0	0
5	F	1	Total C O 35 24 11	0	0
5	I	1	Total C O 35 24 11	0	0
5	L	1	Total C O 35 24 11	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	O	1	Total	C	O	0	0
			35	24	11		
5	R	1	Total	C	O	0	0
			35	24	11		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			4	2	2		
6	I	1	Total	C	O	0	0
			4	2	2		
6	O	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	201	Total	O	0	0
			201	201		
7	B	188	Total	O	0	0
			188	188		
7	C	50	Total	O	0	0
			50	50		
7	D	170	Total	O	0	0
			170	170		

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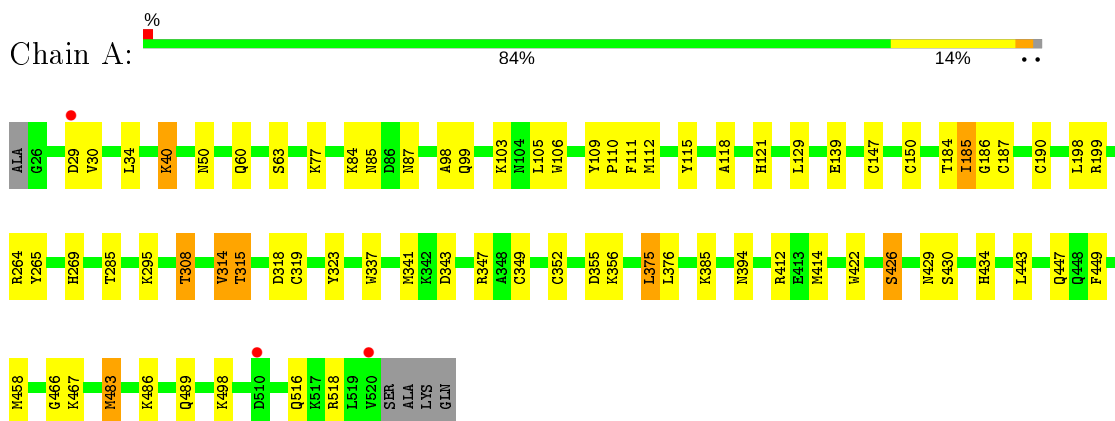
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	E	155	Total 155	O 155	0	0
7	F	42	Total 42	O 42	0	0
7	G	160	Total 160	O 160	0	0
7	H	194	Total 194	O 194	0	0
7	I	40	Total 40	O 40	0	0
7	J	168	Total 168	O 168	0	0
7	K	106	Total 106	O 106	0	0
7	L	43	Total 43	O 43	0	0
7	M	203	Total 203	O 203	0	0
7	N	206	Total 206	O 206	0	0
7	O	50	Total 50	O 50	0	0
7	P	173	Total 173	O 173	0	0
7	Q	132	Total 132	O 132	0	0
7	R	44	Total 44	O 44	0	0

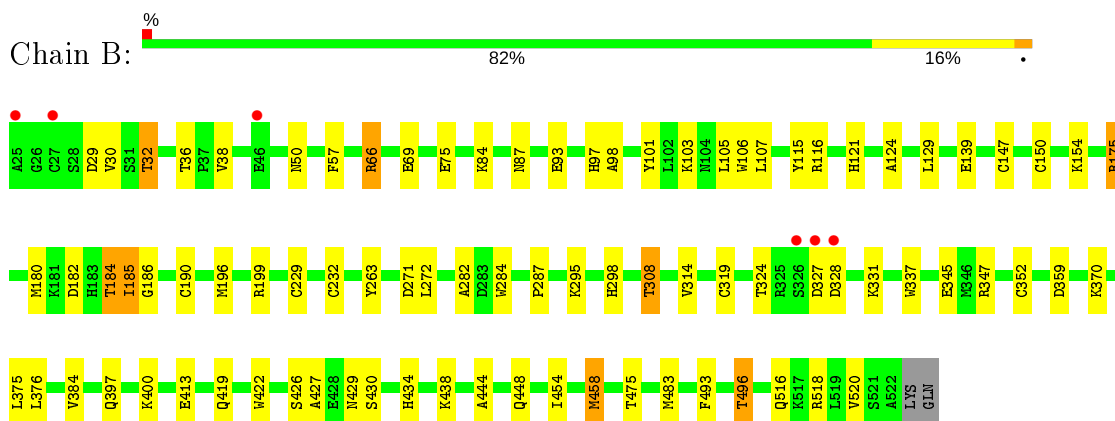
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

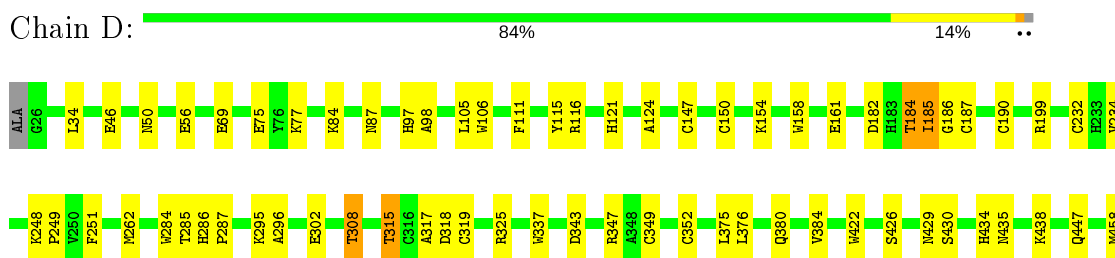
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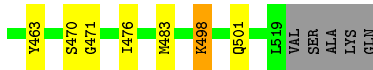


- Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

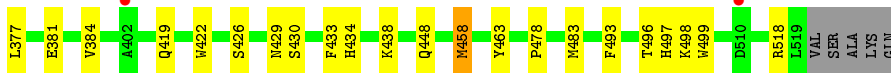
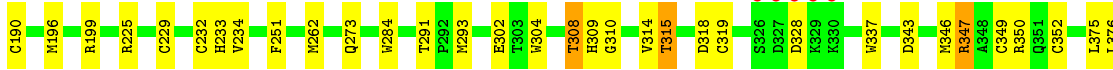
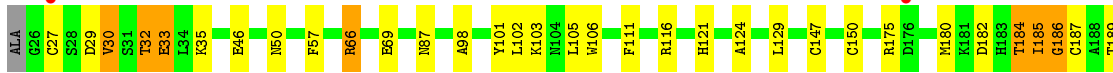
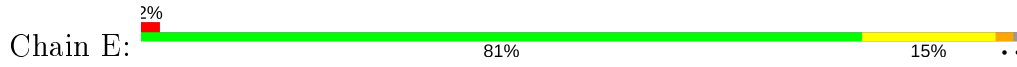


- Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

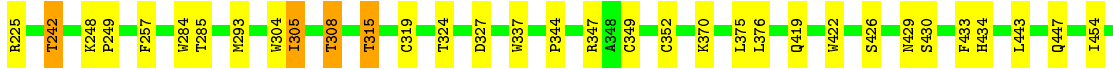
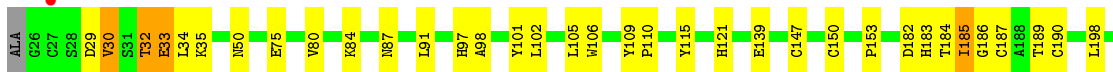
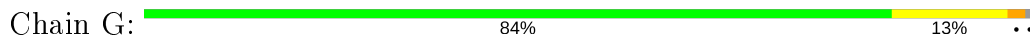




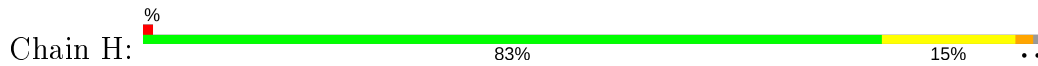
- Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



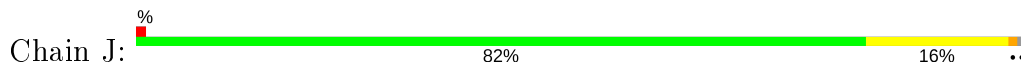
- Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

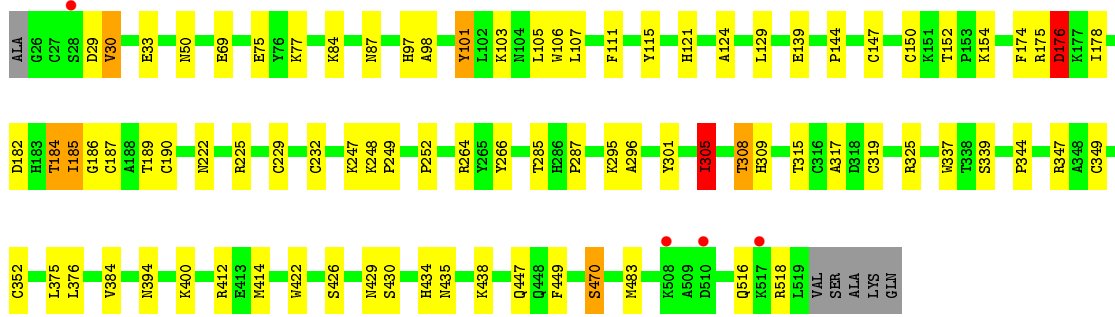


- Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

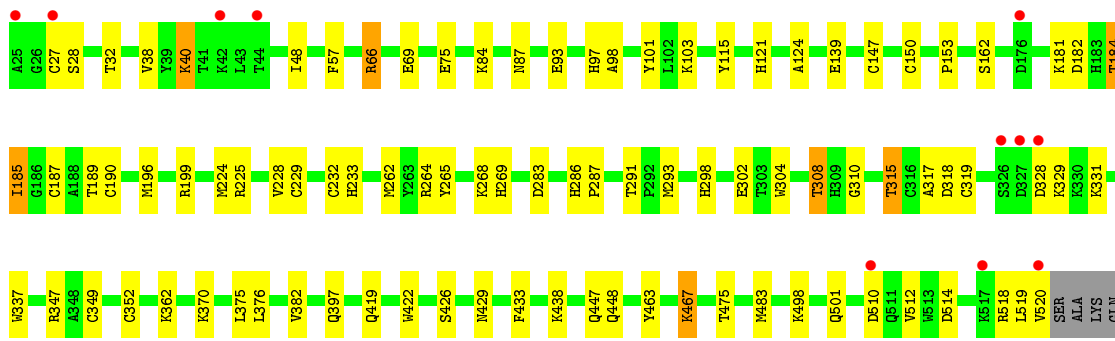
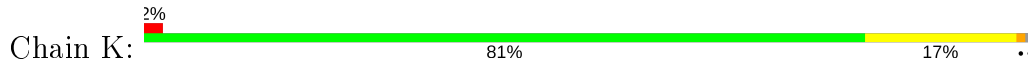


- Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

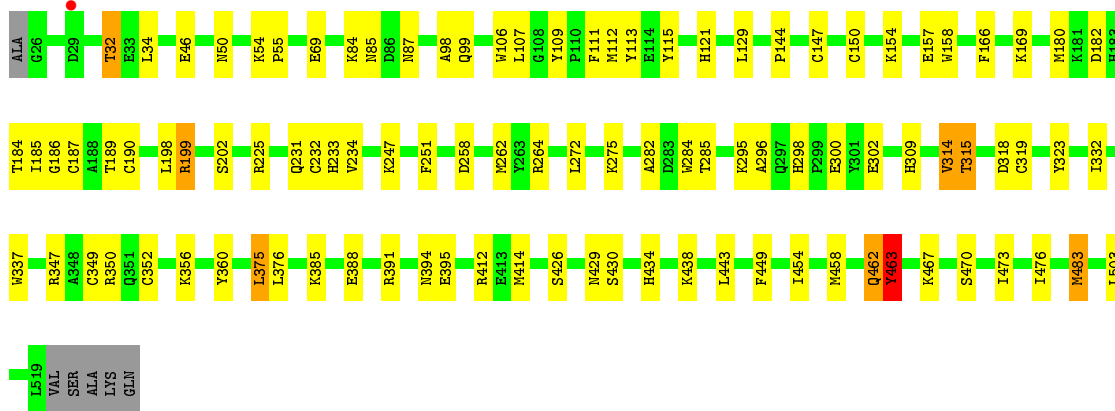
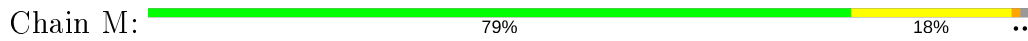




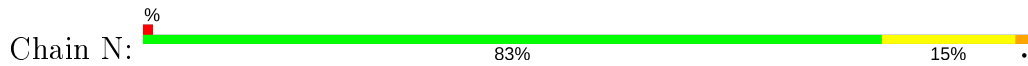
● Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

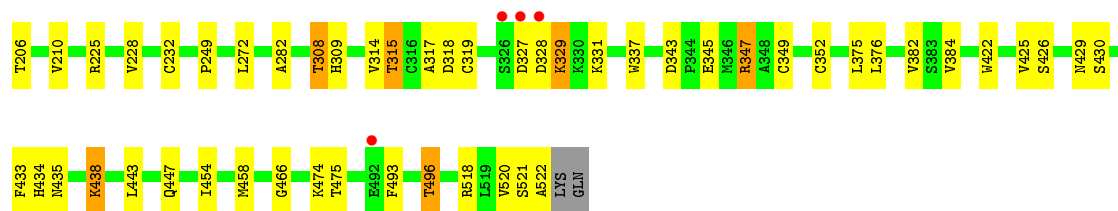


● Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

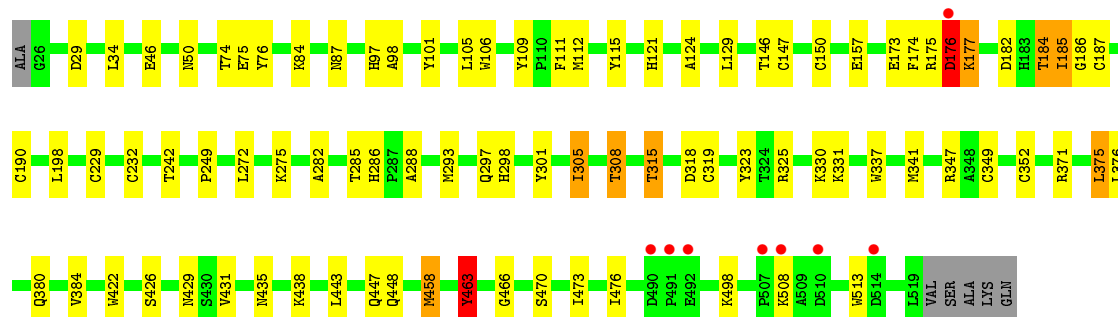
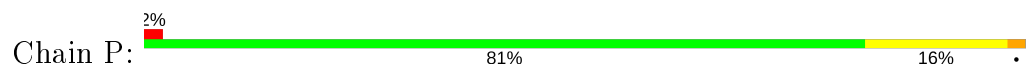


● Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

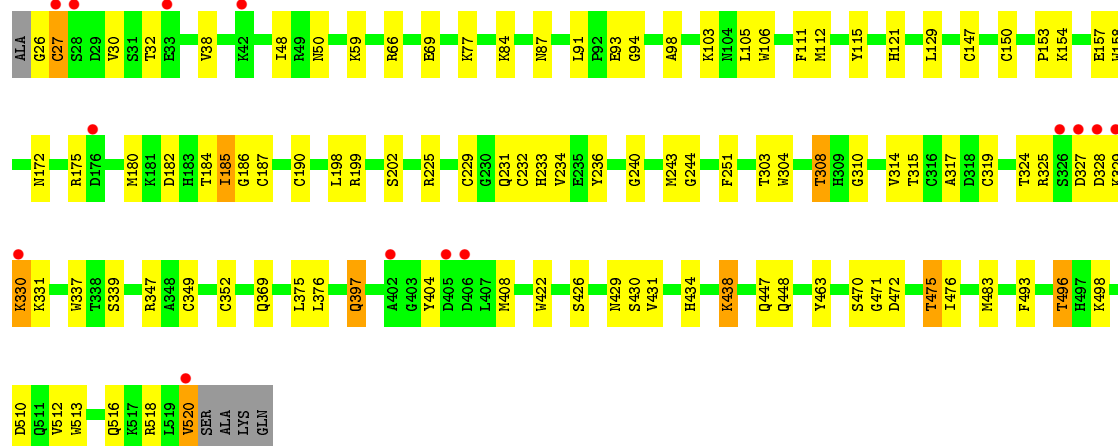
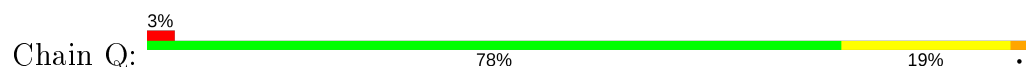




● Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



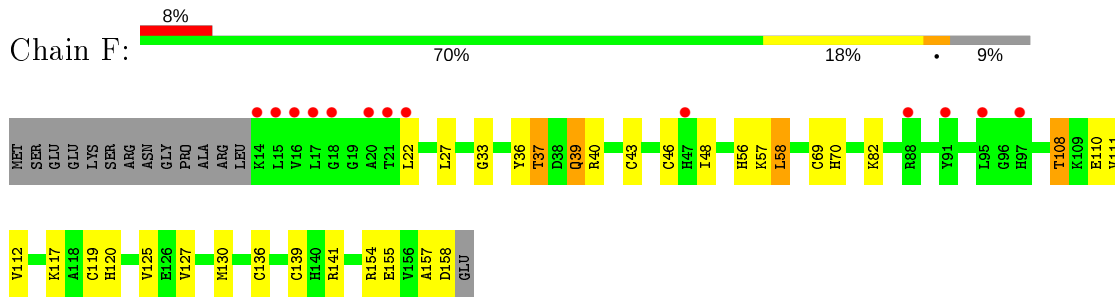
● Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



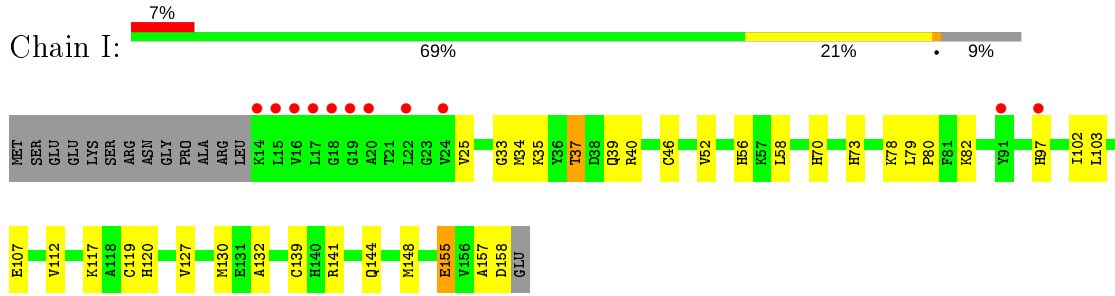
● Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH



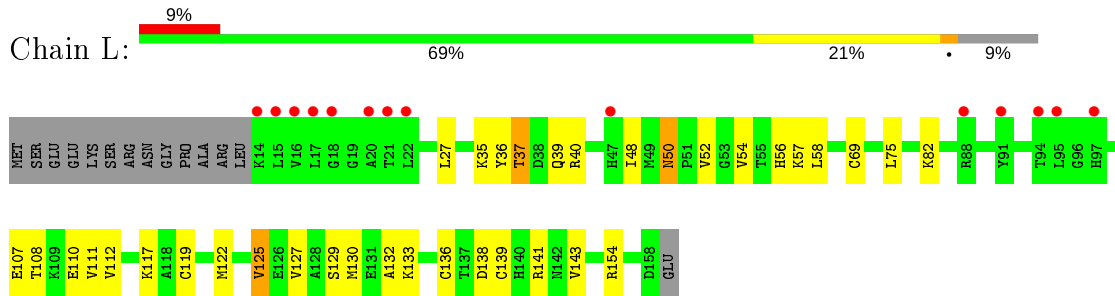
● Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH



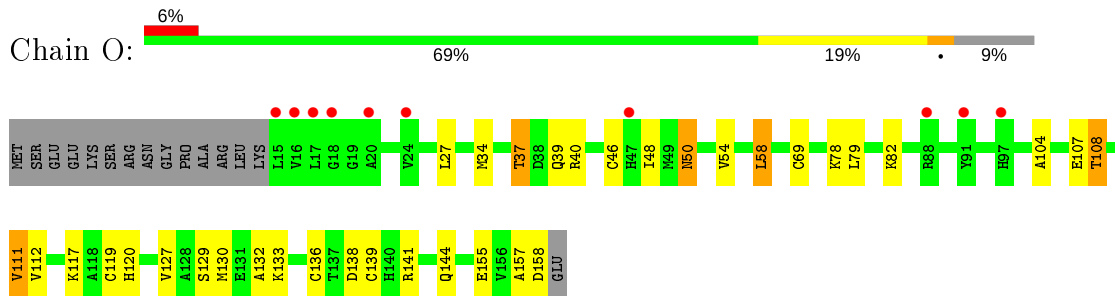
● Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH



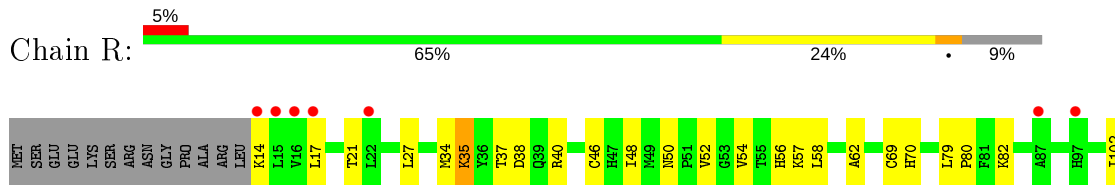
● Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH



● Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH



● Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.66Å 258.12Å 580.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	288.67 – 2.30 53.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	83.7 (288.67-2.30) 83.7 (53.69-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.201 , 0.240 0.197 , 0.234	Depositor DCC
R_{free} test set	22270 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtrriage
Anisotropy	0.524	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	60930	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.81% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, HEC, LMT, ACT

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	0.56	0/4143	0.65	0/5605
1	B	0.56	0/4150	0.67	1/5616 (0.0%)
1	D	0.55	0/4127	0.65	0/5584
1	E	0.55	0/4127	0.65	0/5584
1	G	0.57	0/4125	0.68	0/5581
1	H	0.55	0/4160	0.66	1/5629 (0.0%)
1	J	0.58	0/4145	0.66	1/5608 (0.0%)
1	K	0.56	0/4128	0.65	0/5586
1	M	0.62	2/4135 (0.0%)	0.68	1/5595 (0.0%)
1	N	0.57	0/4150	0.66	1/5616 (0.0%)
1	P	0.58	0/4124	0.68	2/5580 (0.0%)
1	Q	0.55	0/4134	0.67	1/5594 (0.0%)
2	C	0.51	0/1118	0.73	1/1513 (0.1%)
2	F	0.52	0/1116	0.72	0/1509
2	I	0.50	0/1107	0.68	0/1497
2	L	0.51	0/1107	0.77	0/1497
2	O	0.53	0/1098	0.74	0/1486
2	R	0.47	0/1107	0.69	0/1497
All	All	0.56	2/56301 (0.0%)	0.67	9/76177 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	G	0	1
1	M	0	3
1	Q	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	462	GLN	C-N	-12.07	1.06	1.34
1	M	463	TYR	C-N	-10.40	1.14	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	463	TYR	O-C-N	5.94	133.30	123.20
1	Q	27	CYS	N-CA-C	5.67	126.31	111.00
1	M	463	TYR	CA-C-N	-5.66	104.89	116.20
1	J	305	ILE	CB-CA-C	-5.65	100.30	111.60
1	B	175	ARG	NE-CZ-NH2	-5.49	117.56	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	314	VAL	Peptide
1	G	327	ASP	Peptide
1	M	314	VAL	Peptide
1	M	462	GLN	Mainchain
1	M	463	TYR	Mainchain

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	4022	0	3896	77	0
1	B	4032	0	3896	69	0
1	D	4009	0	3874	64	0
1	E	4009	0	3875	86	0
1	G	4008	0	3874	80	0
1	H	4037	0	3903	90	0
1	J	4021	0	3886	76	0
1	K	4014	0	3882	83	0
1	M	4014	0	3877	78	0
1	N	4032	0	3899	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	4007	0	3870	85	0
1	Q	4016	0	3884	121	0
2	C	1094	0	1095	32	0
2	F	1093	0	1096	47	0
2	I	1087	0	1089	39	0
2	L	1087	0	1090	46	0
2	O	1078	0	1077	45	0
2	R	1087	0	1090	53	0
3	A	215	0	156	36	0
3	B	215	0	154	28	0
3	C	172	0	122	21	0
3	D	215	0	156	38	0
3	E	215	0	157	38	0
3	F	172	0	124	29	0
3	G	215	0	157	44	0
3	H	215	0	157	39	0
3	I	172	0	123	18	0
3	J	215	0	156	38	0
3	K	215	0	157	40	0
3	L	172	0	124	26	0
3	M	215	0	157	41	0
3	N	215	0	157	37	0
3	O	172	0	124	23	0
3	P	215	0	156	40	0
3	Q	215	0	157	50	0
3	R	172	0	124	25	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
4	J	2	0	0	0	0
4	K	2	0	0	0	0
4	M	2	0	0	0	0
4	N	2	0	0	0	0
4	P	2	0	0	0	0
4	Q	2	0	0	0	0
5	C	35	0	46	2	0
5	F	35	0	46	0	0
5	I	35	0	46	3	0
5	L	35	0	46	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	O	35	0	46	0	0
5	R	35	0	46	0	0
6	C	4	0	3	0	0
6	I	4	0	3	0	0
6	O	4	0	3	0	0
7	A	201	0	0	7	0
7	B	188	0	0	6	0
7	C	50	0	0	0	0
7	D	170	0	0	3	0
7	E	155	0	0	2	0
7	F	42	0	0	1	0
7	G	160	0	0	7	0
7	H	194	0	0	4	0
7	I	40	0	0	1	0
7	J	168	0	0	2	0
7	K	106	0	0	5	0
7	L	43	0	0	5	0
7	M	203	0	0	6	0
7	N	206	0	0	5	0
7	O	50	0	0	3	0
7	P	173	0	0	7	0
7	Q	132	0	0	3	0
7	R	44	0	0	4	0
All	All	60930	0	56056	1278	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 12.

The worst 5 of 1278 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:K:319:CYS:SG	3:K:1004:HEC:HAC	1.30	1.72
1:N:187:CYS:SG	3:N:1002:HEC:HAB	1.21	1.71
2:L:69:CYS:SG	3:L:1002:HEC:HAC	1.32	1.70
1:K:150:CYS:SG	3:K:1001:HEC:HAC	1.32	1.68
1:J:147:CYS:SG	3:J:1001:HEC:HAB	1.26	1.67

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	495/500 (99%)	481 (97%)	13 (3%)	1 (0%)	47	58
1	B	497/500 (99%)	482 (97%)	14 (3%)	1 (0%)	47	58
1	D	493/500 (99%)	478 (97%)	13 (3%)	2 (0%)	34	42
1	E	493/500 (99%)	474 (96%)	17 (3%)	2 (0%)	34	42
1	G	493/500 (99%)	479 (97%)	12 (2%)	2 (0%)	34	42
1	H	498/500 (100%)	483 (97%)	13 (3%)	2 (0%)	34	42
1	J	495/500 (99%)	477 (96%)	16 (3%)	2 (0%)	34	42
1	K	494/500 (99%)	473 (96%)	19 (4%)	2 (0%)	34	42
1	M	494/500 (99%)	477 (97%)	15 (3%)	2 (0%)	34	42
1	N	497/500 (99%)	476 (96%)	19 (4%)	2 (0%)	34	42
1	P	493/500 (99%)	474 (96%)	15 (3%)	4 (1%)	19	23
1	Q	494/500 (99%)	473 (96%)	19 (4%)	2 (0%)	34	42
2	C	144/159 (91%)	139 (96%)	5 (4%)	0	100	100
2	F	144/159 (91%)	138 (96%)	5 (4%)	1 (1%)	22	26
2	I	143/159 (90%)	142 (99%)	1 (1%)	0	100	100
2	L	143/159 (90%)	136 (95%)	7 (5%)	0	100	100
2	O	142/159 (89%)	139 (98%)	3 (2%)	0	100	100
2	R	143/159 (90%)	139 (97%)	4 (3%)	0	100	100
All	All	6795/6954 (98%)	6560 (96%)	210 (3%)	25 (0%)	34	42

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	185	ILE
1	E	186	GLY
1	N	329	LYS
1	J	176	ASP

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Mol	Chain	Res	Type
1	M	463	TYR

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	431/432 (100%)	417 (97%)	14 (3%)	39	54
1	B	431/432 (100%)	408 (95%)	23 (5%)	22	31
1	D	429/432 (99%)	413 (96%)	16 (4%)	34	48
1	E	429/432 (99%)	409 (95%)	20 (5%)	26	37
1	G	429/432 (99%)	413 (96%)	16 (4%)	34	48
1	H	433/432 (100%)	419 (97%)	14 (3%)	39	54
1	J	431/432 (100%)	418 (97%)	13 (3%)	41	57
1	K	429/432 (99%)	408 (95%)	21 (5%)	25	35
1	M	430/432 (100%)	412 (96%)	18 (4%)	30	42
1	N	431/432 (100%)	415 (96%)	16 (4%)	34	48
1	P	429/432 (99%)	413 (96%)	16 (4%)	34	48
1	Q	430/432 (100%)	408 (95%)	22 (5%)	24	33
2	C	120/131 (92%)	113 (94%)	7 (6%)	20	27
2	F	120/131 (92%)	109 (91%)	11 (9%)	9	11
2	I	119/131 (91%)	112 (94%)	7 (6%)	19	27
2	L	119/131 (91%)	108 (91%)	11 (9%)	9	11
2	O	118/131 (90%)	111 (94%)	7 (6%)	19	27
2	R	119/131 (91%)	107 (90%)	12 (10%)	7	9
All	All	5877/5970 (98%)	5613 (96%)	264 (4%)	27	39

5 of 264 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	470	SER

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Mol	Chain	Res	Type
1	K	101	TYR
1	Q	375	LEU
2	I	35	LYS
1	J	184	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	447	GLN
1	J	394	ASN
1	Q	397	GLN
1	H	298	HIS
2	I	73	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 117 ligands modelled in this entry, 24 are monoatomic - leaving 93 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
3	HEC	K	1004	1,4	26,50,50	2.45	6 (23%)	18,82,82	2.17	8 (44%)
3	HEC	M	1004	1,4	26,50,50	2.35	5 (19%)	18,82,82	2.22	9 (50%)
3	HEC	O	1003	2	26,50,50	2.36	7 (26%)	18,82,82	1.78	6 (33%)
3	HEC	L	1003	2	26,50,50	2.40	7 (26%)	18,82,82	2.04	8 (44%)
3	HEC	R	1002	2	26,50,50	2.53	8 (30%)	18,82,82	1.97	5 (27%)
3	HEC	J	1003	1,4	26,50,50	2.63	7 (26%)	18,82,82	1.47	3 (16%)
3	HEC	H	1004	1,4	26,50,50	2.46	5 (19%)	18,82,82	2.02	8 (44%)
3	HEC	C	1001	2	26,50,50	2.54	5 (19%)	18,82,82	1.66	4 (22%)
3	HEC	D	1002	1	26,50,50	2.35	6 (23%)	18,82,82	1.92	5 (27%)
3	HEC	J	1001	1,7	26,50,50	2.47	7 (26%)	18,82,82	1.58	4 (22%)
3	HEC	R	1003	2	26,50,50	2.37	8 (30%)	18,82,82	1.71	5 (27%)
3	HEC	D	1003	1,4	26,50,50	2.62	9 (34%)	18,82,82	1.45	3 (16%)
3	HEC	G	1002	1	26,50,50	2.52	6 (23%)	18,82,82	1.74	3 (16%)
3	HEC	F	1002	2	26,50,50	2.57	6 (23%)	18,82,82	1.91	8 (44%)
3	HEC	G	1004	1,4	26,50,50	2.42	6 (23%)	18,82,82	2.17	8 (44%)
3	HEC	B	1003	1,4	26,50,50	2.44	7 (26%)	18,82,82	1.65	5 (27%)
3	HEC	J	1005	1	26,50,50	2.60	6 (23%)	18,82,82	1.45	3 (16%)
3	HEC	H	1001	1,7	26,50,50	2.46	6 (23%)	18,82,82	1.58	2 (11%)
3	HEC	L	1004	1,2	26,50,50	2.46	9 (34%)	18,82,82	2.37	5 (27%)
3	HEC	K	1005	1	26,50,50	2.38	5 (19%)	18,82,82	1.53	5 (27%)
3	HEC	M	1005	1	26,50,50	2.55	9 (34%)	18,82,82	1.56	3 (16%)
3	HEC	F	1004	1,2	26,50,50	2.41	9 (34%)	18,82,82	2.24	7 (38%)
3	HEC	H	1003	1,4	26,50,50	2.51	7 (26%)	18,82,82	1.76	5 (27%)
3	HEC	J	1002	1	26,50,50	2.36	9 (34%)	18,82,82	1.86	7 (38%)
3	HEC	N	1001	1,7	26,50,50	2.56	6 (23%)	18,82,82	1.63	4 (22%)
3	HEC	K	1003	1,4	26,50,50	2.52	7 (26%)	18,82,82	1.63	3 (16%)
3	HEC	C	1003	2	26,50,50	2.36	7 (26%)	18,82,82	2.03	7 (38%)
3	HEC	C	1002	2	26,50,50	2.49	6 (23%)	18,82,82	2.19	9 (50%)
3	HEC	N	1004	1,4	26,50,50	2.42	6 (23%)	18,82,82	1.94	5 (27%)
3	HEC	A	1004	1,4	26,50,50	2.56	6 (23%)	18,82,82	1.78	5 (27%)
3	HEC	B	1004	1,4	26,50,50	2.41	5 (19%)	18,82,82	2.22	8 (44%)
3	HEC	L	1002	2	26,50,50	2.55	6 (23%)	18,82,82	1.67	6 (33%)
3	HEC	G	1005	1	26,50,50	2.32	7 (26%)	18,82,82	2.01	6 (33%)
3	HEC	Q	1004	1,4	26,50,50	2.39	6 (23%)	18,82,82	1.71	7 (38%)
3	HEC	B	1002	1	26,50,50	2.49	6 (23%)	18,82,82	1.62	4 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	I	1004	1,2	26,50,50	2.30	5 (19%)	18,82,82	1.94	6 (33%)
5	LMT	R	1005	-	36,36,36	0.57	0	47,47,47	1.03	2 (4%)
5	LMT	C	1005	-	36,36,36	0.56	0	47,47,47	0.83	1 (2%)
3	HEC	P	1004	1,4	26,50,50	2.34	5 (19%)	18,82,82	1.75	6 (33%)
3	HEC	Q	1002	1	26,50,50	2.56	7 (26%)	18,82,82	1.69	4 (22%)
3	HEC	A	1001	1,7	26,50,50	2.39	6 (23%)	18,82,82	1.78	4 (22%)
3	HEC	M	1001	1	26,50,50	2.43	5 (19%)	18,82,82	1.58	3 (16%)
6	ACT	C	1006	-	1,3,3	0.47	0	0,3,3	0.00	-
5	LMT	L	1005	-	36,36,36	0.58	0	47,47,47	0.68	1 (2%)
3	HEC	P	1002	1	26,50,50	2.52	6 (23%)	18,82,82	1.74	5 (27%)
3	HEC	G	1003	1,4	26,50,50	2.50	8 (30%)	18,82,82	1.41	2 (11%)
3	HEC	G	1001	1,7	26,50,50	2.51	7 (26%)	18,82,82	1.48	4 (22%)
3	HEC	M	1002	1	26,50,50	2.48	6 (23%)	18,82,82	1.76	4 (22%)
6	ACT	O	1006	-	1,3,3	1.31	0	0,3,3	0.00	-
3	HEC	E	1003	1,4	26,50,50	2.41	7 (26%)	18,82,82	1.81	7 (38%)
3	HEC	B	1001	1,7	26,50,50	2.50	8 (30%)	18,82,82	1.45	5 (27%)
3	HEC	L	1101	2	26,50,50	2.65	6 (23%)	18,82,82	1.77	6 (33%)
3	HEC	O	1001	2	26,50,50	2.60	5 (19%)	18,82,82	1.61	3 (16%)
3	HEC	E	1004	1,4	26,50,50	2.43	7 (26%)	18,82,82	1.92	7 (38%)
3	HEC	K	1001	1	26,50,50	2.52	7 (26%)	18,82,82	1.42	3 (16%)
3	HEC	O	1002	2	26,50,50	2.48	6 (23%)	18,82,82	2.17	7 (38%)
6	ACT	I	1006	-	1,3,3	1.30	0	0,3,3	0.00	-
3	HEC	K	1002	1	26,50,50	2.52	6 (23%)	18,82,82	1.43	3 (16%)
3	HEC	D	1001	1	26,50,50	2.54	8 (30%)	18,82,82	1.63	5 (27%)
3	HEC	Q	1001	1,7	26,50,50	2.58	8 (30%)	18,82,82	1.28	1 (5%)
3	HEC	P	1003	1,4	26,50,50	2.40	6 (23%)	18,82,82	1.72	6 (33%)
3	HEC	Q	1003	1,4	26,50,50	2.48	5 (19%)	18,82,82	1.83	5 (27%)
3	HEC	B	1005	1	26,50,50	2.32	5 (19%)	18,82,82	1.47	3 (16%)
3	HEC	D	1005	1	26,50,50	2.51	7 (26%)	18,82,82	1.66	5 (27%)
3	HEC	I	1001	2	26,50,50	2.49	6 (23%)	18,82,82	1.82	5 (27%)
5	LMT	O	1005	-	36,36,36	0.65	1 (2%)	47,47,47	0.79	1 (2%)
3	HEC	F	1003	2	26,50,50	2.48	8 (30%)	18,82,82	1.67	7 (38%)
3	HEC	H	1005	1	26,50,50	2.46	9 (34%)	18,82,82	1.68	4 (22%)
3	HEC	E	1002	1	26,50,50	2.40	7 (26%)	18,82,82	1.65	5 (27%)
3	HEC	I	1003	2	26,50,50	2.30	8 (30%)	18,82,82	2.06	8 (44%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	F	1001	2	26,50,50	2.53	5 (19%)	18,82,82	1.48	2 (11%)
3	HEC	O	1004	1,2	26,50,50	2.56	9 (34%)	18,82,82	2.13	5 (27%)
3	HEC	N	1003	1,4	26,50,50	2.53	6 (23%)	18,82,82	1.66	5 (27%)
3	HEC	Q	1005	1	26,50,50	2.40	5 (19%)	18,82,82	2.04	6 (33%)
3	HEC	E	1005	1	26,50,50	2.53	7 (26%)	18,82,82	1.84	3 (16%)
3	HEC	E	1001	1,7	26,50,50	2.58	7 (26%)	18,82,82	1.40	2 (11%)
5	LMT	I	1005	-	36,36,36	0.58	0	47,47,47	0.90	2 (4%)
3	HEC	R	1001	2	26,50,50	2.58	6 (23%)	18,82,82	2.19	6 (33%)
3	HEC	N	1002	1	26,50,50	2.45	7 (26%)	18,82,82	1.66	5 (27%)
3	HEC	C	1004	1,2	26,50,50	2.41	5 (19%)	18,82,82	1.95	6 (33%)
3	HEC	D	1004	1,4	26,50,50	2.34	7 (26%)	18,82,82	2.12	7 (38%)
3	HEC	N	1005	1	26,50,50	2.43	5 (19%)	18,82,82	1.96	5 (27%)
3	HEC	P	1005	1	26,50,50	2.57	8 (30%)	18,82,82	1.68	4 (22%)
3	HEC	H	1002	1	26,50,50	2.45	6 (23%)	18,82,82	1.71	4 (22%)
3	HEC	I	1002	2	26,50,50	2.60	7 (26%)	18,82,82	1.79	5 (27%)
3	HEC	M	1003	1,4	26,50,50	2.46	7 (26%)	18,82,82	2.23	8 (44%)
3	HEC	A	1005	1	26,50,50	2.48	7 (26%)	18,82,82	2.40	8 (44%)
3	HEC	A	1003	1,4	26,50,50	2.56	7 (26%)	18,82,82	1.87	8 (44%)
3	HEC	P	1001	1,7	26,50,50	2.46	8 (30%)	18,82,82	1.23	1 (5%)
5	LMT	F	1005	-	36,36,36	0.63	0	47,47,47	0.90	2 (4%)
3	HEC	R	1004	1,2	26,50,50	2.49	6 (23%)	18,82,82	2.23	6 (33%)
3	HEC	A	1002	1	26,50,50	2.40	6 (23%)	18,82,82	2.18	6 (33%)
3	HEC	J	1004	1,4	26,50,50	2.36	7 (26%)	18,82,82	1.90	6 (33%)

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
3	HEC	K	1004	1,4	-	0/6/54/54	-
3	HEC	M	1004	1,4	-	0/6/54/54	-
3	HEC	O	1003	2	-	0/6/54/54	-
3	HEC	L	1003	2	-	0/6/54/54	-
3	HEC	R	1002	2	-	2/6/54/54	-
3	HEC	J	1003	1,4	-	0/6/54/54	-
3	HEC	H	1004	1,4	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	C	1001	2	-	0/6/54/54	-
3	HEC	D	1002	1	-	0/6/54/54	-
3	HEC	J	1001	1,7	-	0/6/54/54	-
3	HEC	R	1003	2	-	0/6/54/54	-
3	HEC	D	1003	1,4	-	0/6/54/54	-
3	HEC	G	1002	1	-	1/6/54/54	-
3	HEC	F	1002	2	-	2/6/54/54	-
3	HEC	G	1004	1,4	-	0/6/54/54	-
3	HEC	B	1003	1,4	-	0/6/54/54	-
3	HEC	J	1005	1	-	0/6/54/54	-
3	HEC	H	1001	1,7	-	0/6/54/54	-
3	HEC	L	1004	1,2	-	0/6/54/54	-
3	HEC	K	1005	1	-	0/6/54/54	-
3	HEC	M	1005	1	-	0/6/54/54	-
3	HEC	F	1004	1,2	-	0/6/54/54	-
3	HEC	H	1003	1,4	-	0/6/54/54	-
3	HEC	J	1002	1	-	0/6/54/54	-
3	HEC	N	1001	1,7	-	0/6/54/54	-
3	HEC	K	1003	1,4	-	0/6/54/54	-
3	HEC	C	1003	2	-	0/6/54/54	-
3	HEC	C	1002	2	-	2/6/54/54	-
3	HEC	N	1004	1,4	-	0/6/54/54	-
3	HEC	A	1004	1,4	-	0/6/54/54	-
3	HEC	B	1004	1,4	-	0/6/54/54	-
3	HEC	L	1002	2	-	2/6/54/54	-
3	HEC	G	1005	1	-	0/6/54/54	-
3	HEC	Q	1004	1,4	-	3/6/54/54	-
3	HEC	B	1002	1	-	0/6/54/54	-
3	HEC	I	1004	1,2	-	0/6/54/54	-
5	LMT	R	1005	-	-	8/21/61/61	0/2/2/2
5	LMT	C	1005	-	-	7/21/61/61	0/2/2/2
3	HEC	P	1004	1,4	-	0/6/54/54	-
3	HEC	Q	1002	1	-	0/6/54/54	-
3	HEC	A	1001	1,7	-	0/6/54/54	-
3	HEC	M	1001	1	-	0/6/54/54	-
5	LMT	L	1005	-	-	9/21/61/61	0/2/2/2
3	HEC	P	1002	1	-	0/6/54/54	-
3	HEC	G	1003	1,4	-	0/6/54/54	-
3	HEC	G	1001	1,7	-	0/6/54/54	-
3	HEC	M	1002	1	-	0/6/54/54	-
3	HEC	E	1003	1,4	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	B	1001	1,7	-	0/6/54/54	-
3	HEC	L	1101	2	-	0/6/54/54	-
3	HEC	O	1001	2	-	0/6/54/54	-
3	HEC	E	1004	1,4	-	0/6/54/54	-
3	HEC	K	1001	1	-	0/6/54/54	-
3	HEC	O	1002	2	-	2/6/54/54	-
3	HEC	K	1002	1	-	0/6/54/54	-
3	HEC	D	1001	1	-	0/6/54/54	-
3	HEC	Q	1001	1,7	-	0/6/54/54	-
3	HEC	P	1003	1,4	-	0/6/54/54	-
3	HEC	Q	1003	1,4	-	0/6/54/54	-
3	HEC	B	1005	1	-	0/6/54/54	-
3	HEC	D	1005	1	-	1/6/54/54	-
3	HEC	I	1001	2	-	0/6/54/54	-
5	LMT	O	1005	-	-	8/21/61/61	0/2/2/2
3	HEC	F	1003	2	-	0/6/54/54	-
3	HEC	H	1005	1	-	0/6/54/54	-
3	HEC	E	1002	1	-	0/6/54/54	-
3	HEC	I	1003	2	-	0/6/54/54	-
3	HEC	F	1001	2	-	0/6/54/54	-
3	HEC	O	1004	1,2	-	0/6/54/54	-
3	HEC	N	1003	1,4	-	0/6/54/54	-
3	HEC	Q	1005	1	-	1/6/54/54	-
3	HEC	E	1005	1	-	1/6/54/54	-
3	HEC	E	1001	1,7	-	0/6/54/54	-
5	LMT	I	1005	-	-	8/21/61/61	0/2/2/2
3	HEC	R	1001	2	-	1/6/54/54	-
3	HEC	N	1002	1	-	0/6/54/54	-
3	HEC	C	1004	1,2	-	0/6/54/54	-
3	HEC	D	1004	1,4	-	0/6/54/54	-
3	HEC	N	1005	1	-	1/6/54/54	-
3	HEC	P	1005	1	-	0/6/54/54	-
3	HEC	H	1002	1	-	0/6/54/54	-
3	HEC	I	1002	2	-	2/6/54/54	-
3	HEC	M	1003	1,4	-	0/6/54/54	-
3	HEC	A	1005	1	-	0/6/54/54	-
3	HEC	A	1003	1,4	-	2/6/54/54	-
3	HEC	P	1001	1,7	-	0/6/54/54	-
5	LMT	F	1005	-	-	7/21/61/61	0/2/2/2
3	HEC	R	1004	1,2	-	0/6/54/54	-
3	HEC	A	1002	1	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	J	1004	1,4	-	0/6/54/54	-

The worst 5 of 556 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	O	1004	HEC	C3B-C2B	-7.14	1.33	1.40
3	D	1003	HEC	C3B-C2B	-6.96	1.33	1.40
3	L	1101	HEC	C3B-C2B	-6.95	1.33	1.40
3	L	1002	HEC	C3B-C2B	-6.94	1.33	1.40
3	N	1001	HEC	C3B-C2B	-6.90	1.33	1.40

The worst 5 of 443 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	R	1004	HEC	CBA-CAA-C2A	-6.66	100.20	112.48
3	O	1004	HEC	CBA-CAA-C2A	-6.59	100.33	112.48
3	L	1004	HEC	CBA-CAA-C2A	-6.50	100.50	112.48
3	F	1004	HEC	CBA-CAA-C2A	-5.96	101.50	112.48
3	K	1004	HEC	CBA-CAA-C2A	-5.51	102.33	112.48

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	R	1002	HEC	C1A-C2A-CAA-CBA
3	R	1002	HEC	C3A-C2A-CAA-CBA
3	F	1002	HEC	C1A-C2A-CAA-CBA
3	F	1002	HEC	C3A-C2A-CAA-CBA
3	C	1002	HEC	C1A-C2A-CAA-CBA

There are no ring outliers.

87 monomers are involved in 617 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	1004	HEC	9	0
3	M	1004	HEC	9	0
3	O	1003	HEC	5	0
3	L	1003	HEC	9	0
3	R	1002	HEC	11	0
3	J	1003	HEC	8	0
3	H	1004	HEC	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1001	HEC	3	0
3	D	1002	HEC	11	0
3	J	1001	HEC	5	0
3	R	1003	HEC	6	0
3	D	1003	HEC	5	0
3	G	1002	HEC	9	0
3	F	1002	HEC	12	0
3	G	1004	HEC	11	0
3	B	1003	HEC	8	0
3	J	1005	HEC	10	0
3	H	1001	HEC	10	0
3	L	1004	HEC	8	0
3	K	1005	HEC	4	0
3	M	1005	HEC	12	0
3	F	1004	HEC	8	0
3	H	1003	HEC	5	0
3	J	1002	HEC	6	0
3	N	1001	HEC	8	0
3	K	1003	HEC	10	0
3	C	1003	HEC	4	0
3	C	1002	HEC	5	0
3	N	1004	HEC	9	0
3	A	1004	HEC	7	0
3	B	1004	HEC	7	0
3	L	1002	HEC	8	0
3	G	1005	HEC	11	0
3	Q	1004	HEC	8	0
3	B	1002	HEC	6	0
3	I	1004	HEC	8	0
5	C	1005	LMT	2	0
3	P	1004	HEC	8	0
3	Q	1002	HEC	12	0
3	A	1001	HEC	5	0
3	M	1001	HEC	4	0
5	L	1005	LMT	3	0
3	P	1002	HEC	12	0
3	G	1003	HEC	2	0
3	G	1001	HEC	11	0
3	M	1002	HEC	11	0
3	E	1003	HEC	7	0
3	B	1001	HEC	5	0
3	L	1101	HEC	1	0

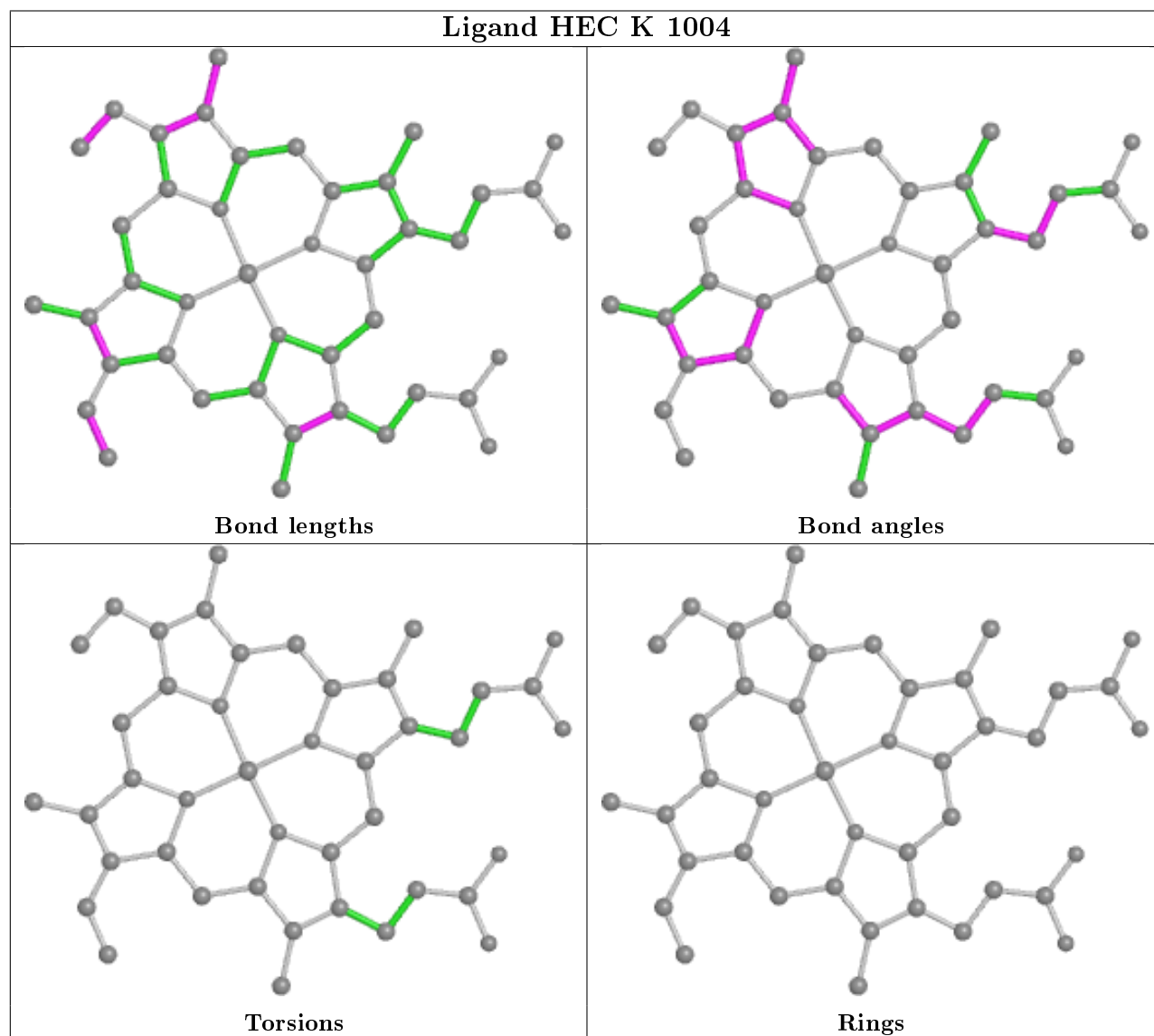
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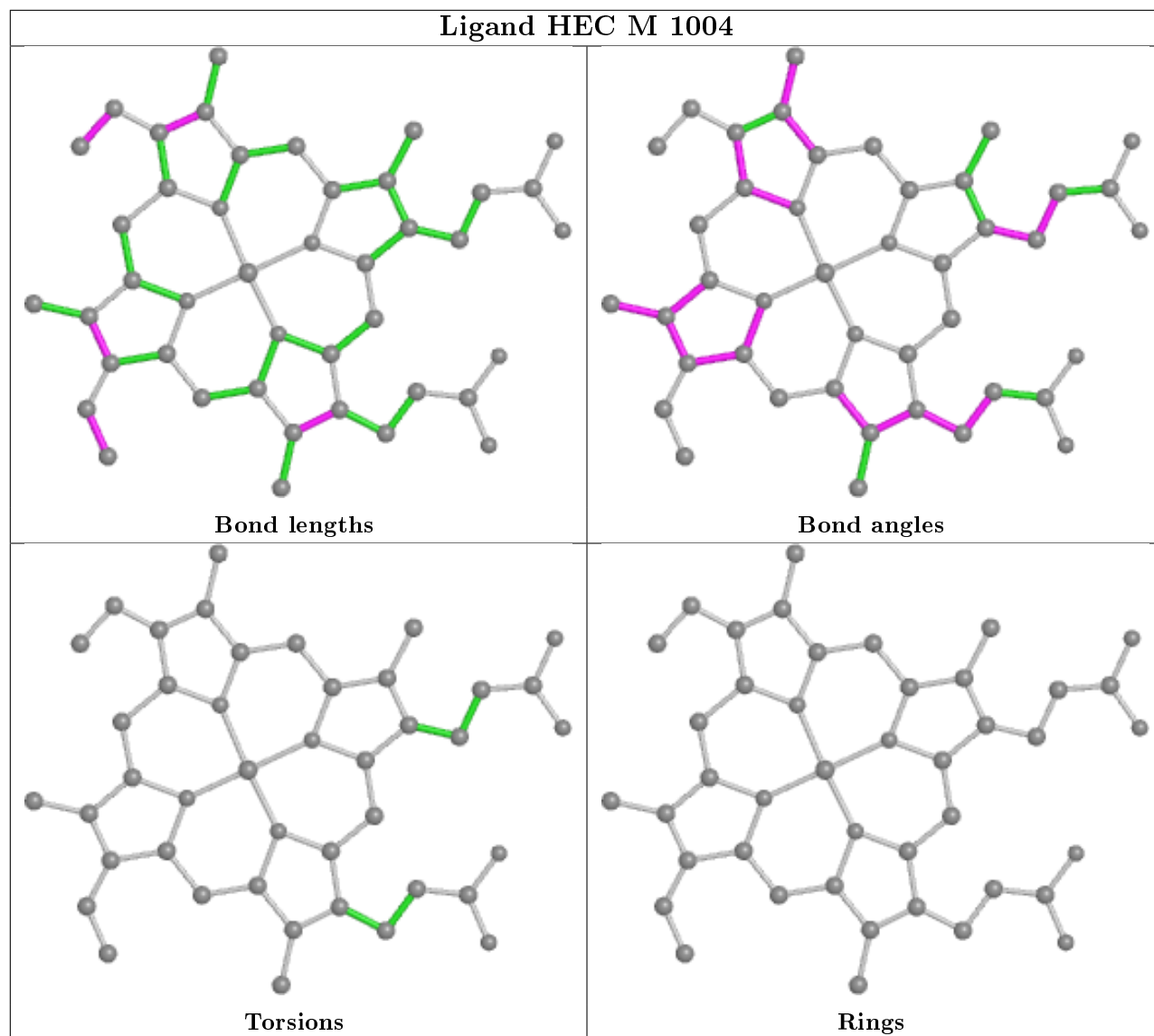
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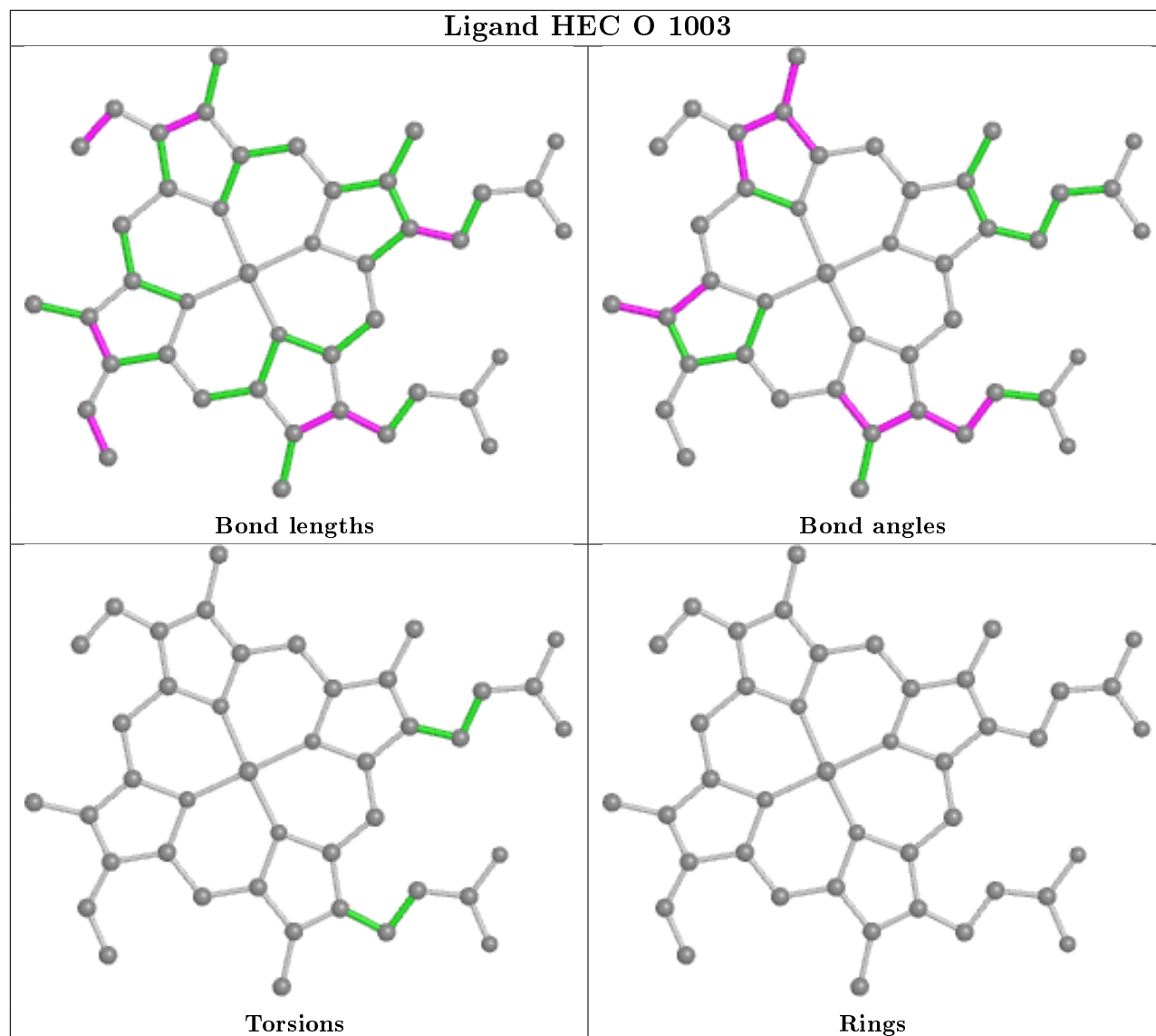
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	O	1001	HEC	2	0
3	E	1004	HEC	5	0
3	K	1001	HEC	9	0
3	O	1002	HEC	7	0
3	K	1002	HEC	11	0
3	D	1001	HEC	5	0
3	Q	1001	HEC	10	0
3	P	1003	HEC	6	0
3	Q	1003	HEC	9	0
3	B	1005	HEC	4	0
3	D	1005	HEC	9	0
3	I	1001	HEC	2	0
3	F	1003	HEC	4	0
3	H	1005	HEC	9	0
3	E	1002	HEC	12	0
3	I	1003	HEC	4	0
3	F	1001	HEC	5	0
3	O	1004	HEC	9	0
3	N	1003	HEC	6	0
3	Q	1005	HEC	13	0
3	E	1005	HEC	8	0
3	E	1001	HEC	8	0
5	I	1005	LMT	3	0
3	R	1001	HEC	4	0
3	N	1002	HEC	8	0
3	C	1004	HEC	9	0
3	D	1004	HEC	10	0
3	N	1005	HEC	9	0
3	P	1005	HEC	7	0
3	H	1002	HEC	8	0
3	I	1002	HEC	5	0
3	M	1003	HEC	8	0
3	A	1005	HEC	10	0
3	A	1003	HEC	4	0
3	P	1001	HEC	8	0
3	R	1004	HEC	5	0
3	A	1002	HEC	12	0
3	J	1004	HEC	10	0

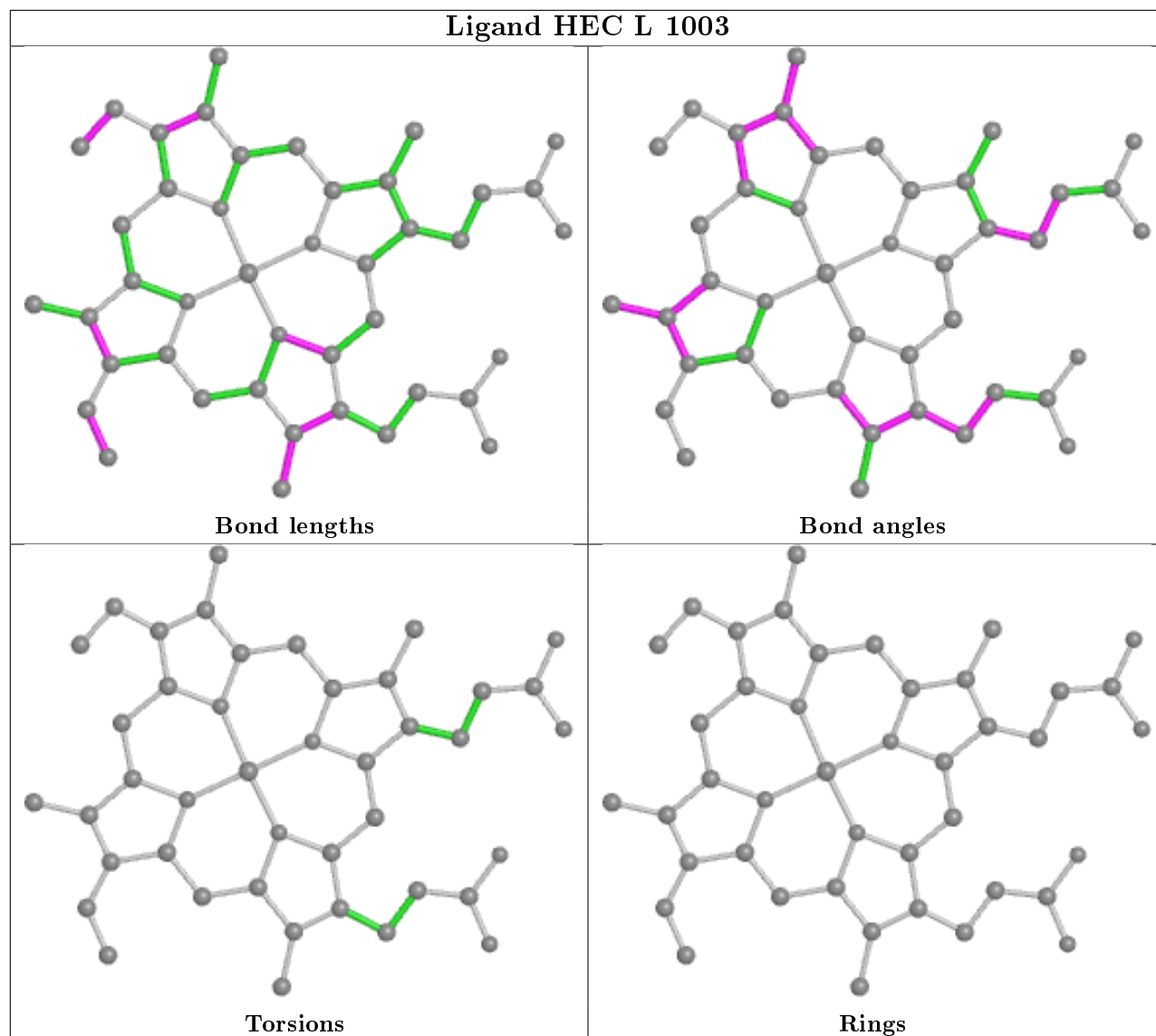
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

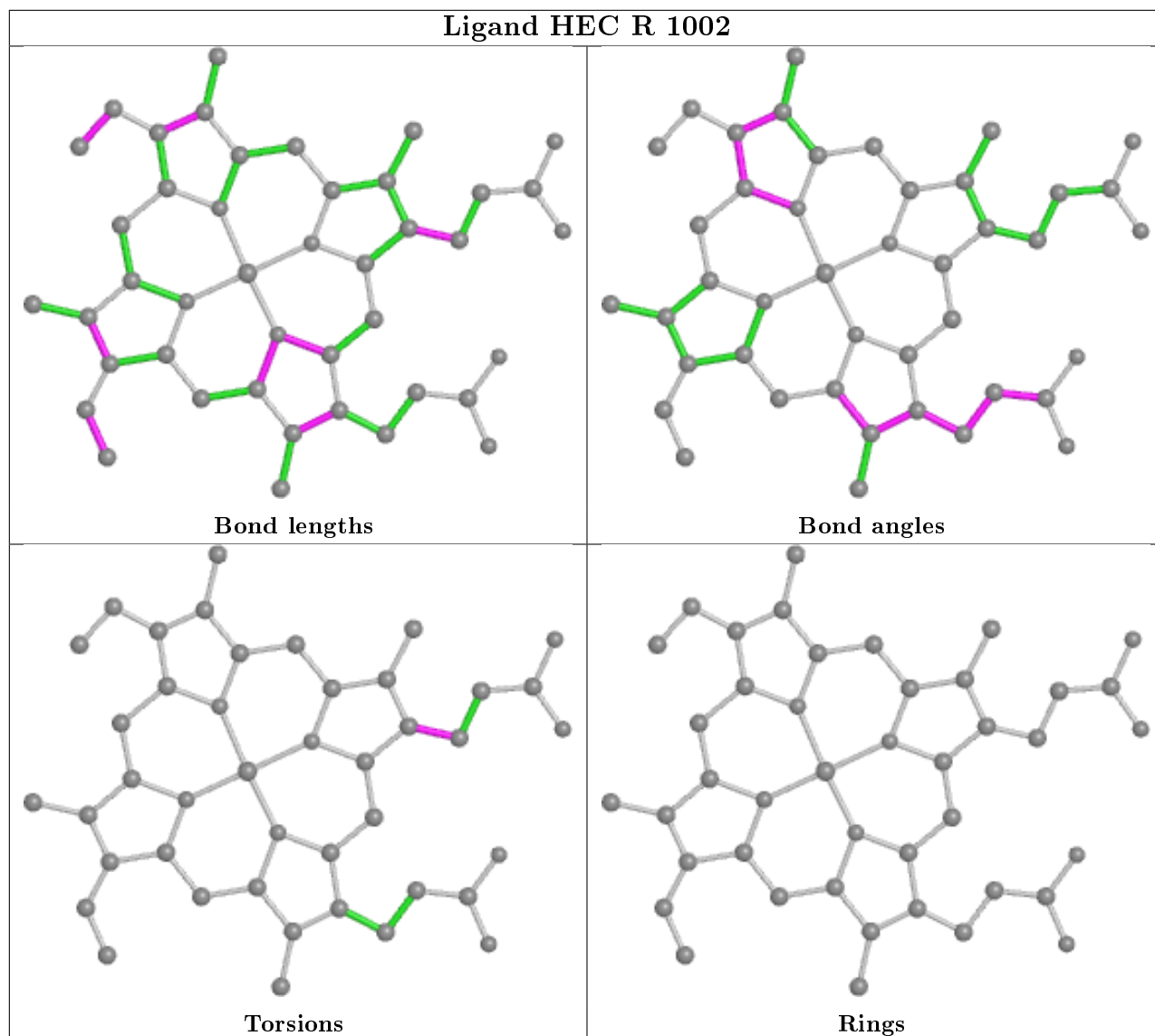
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

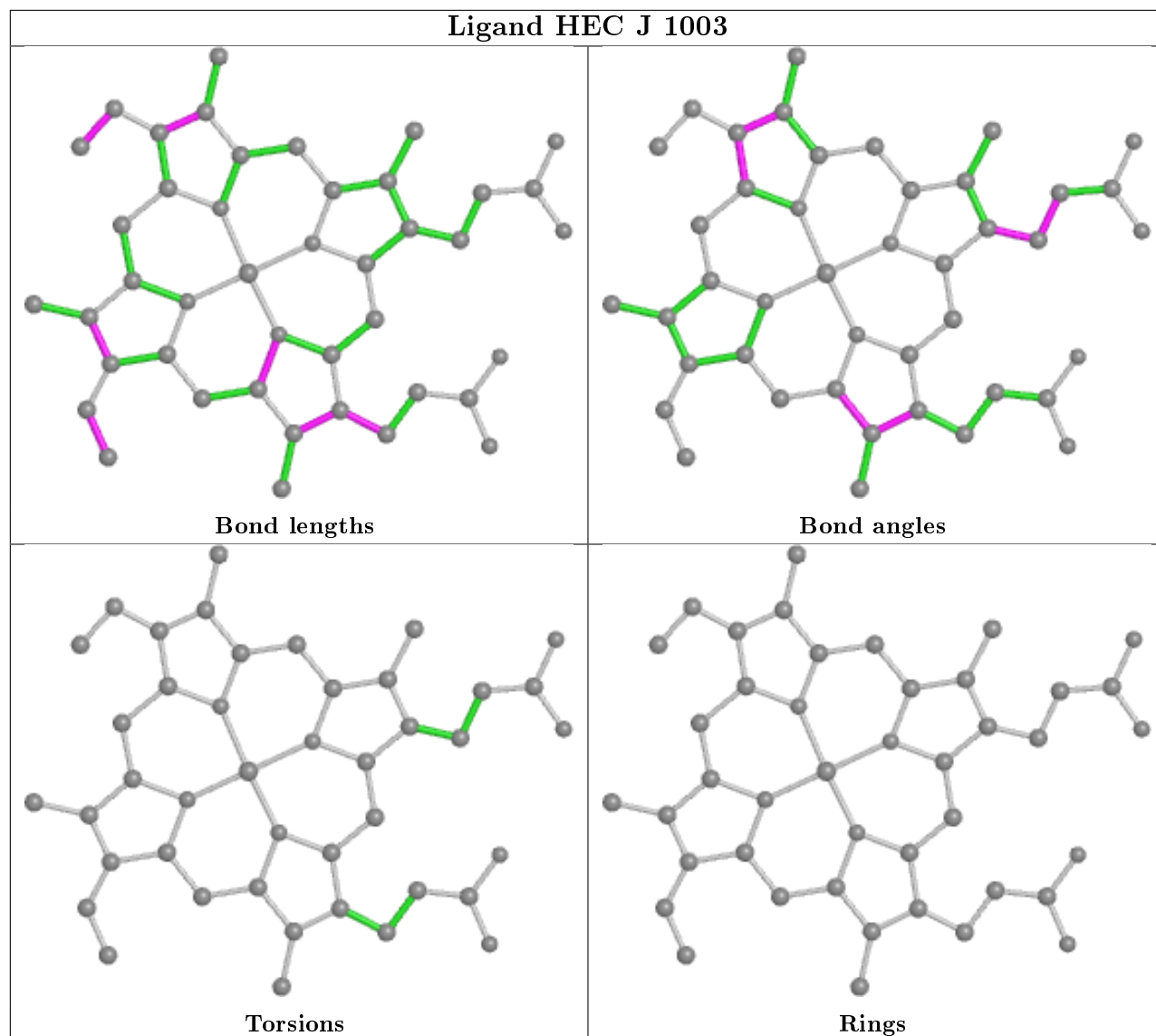


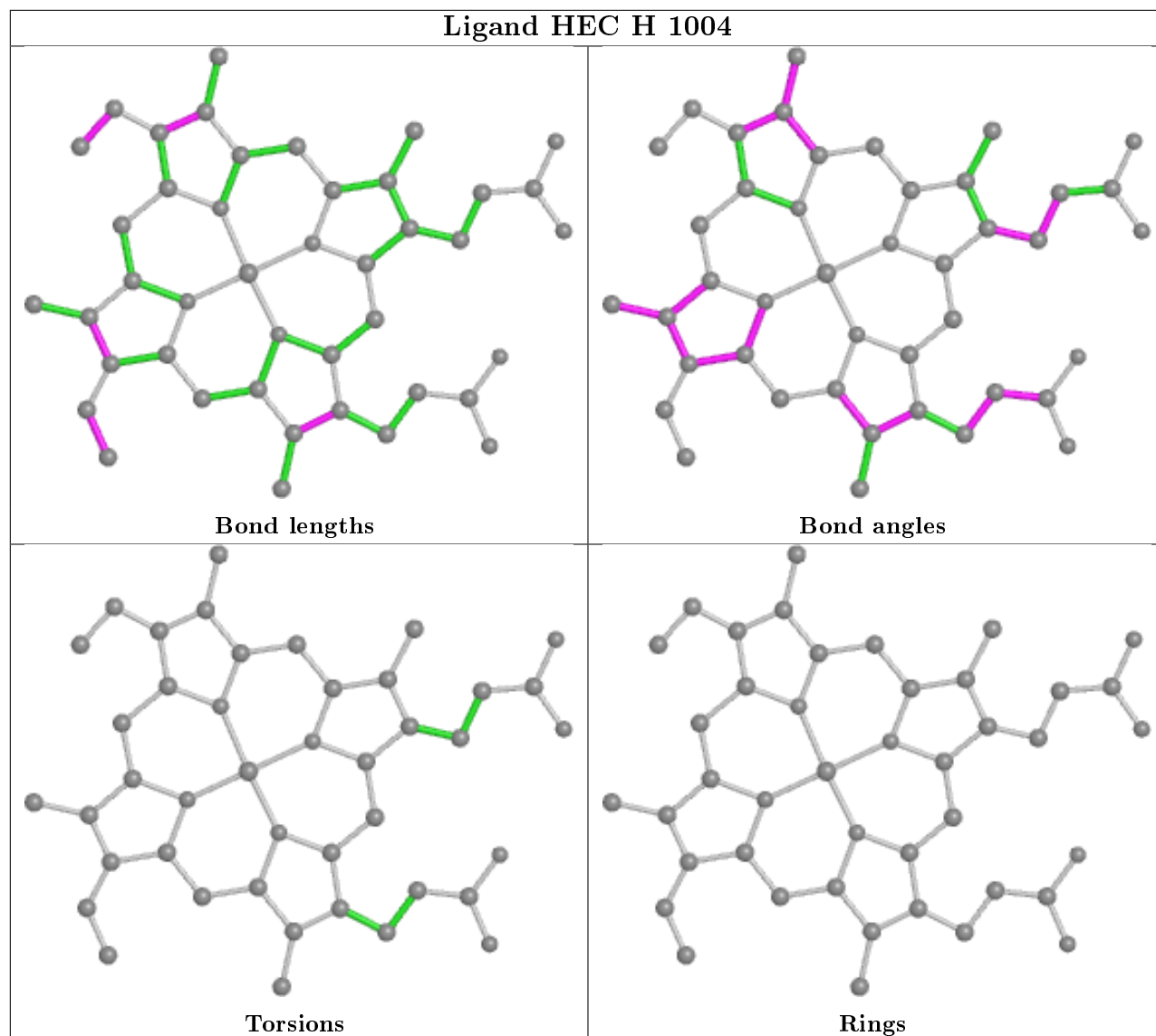


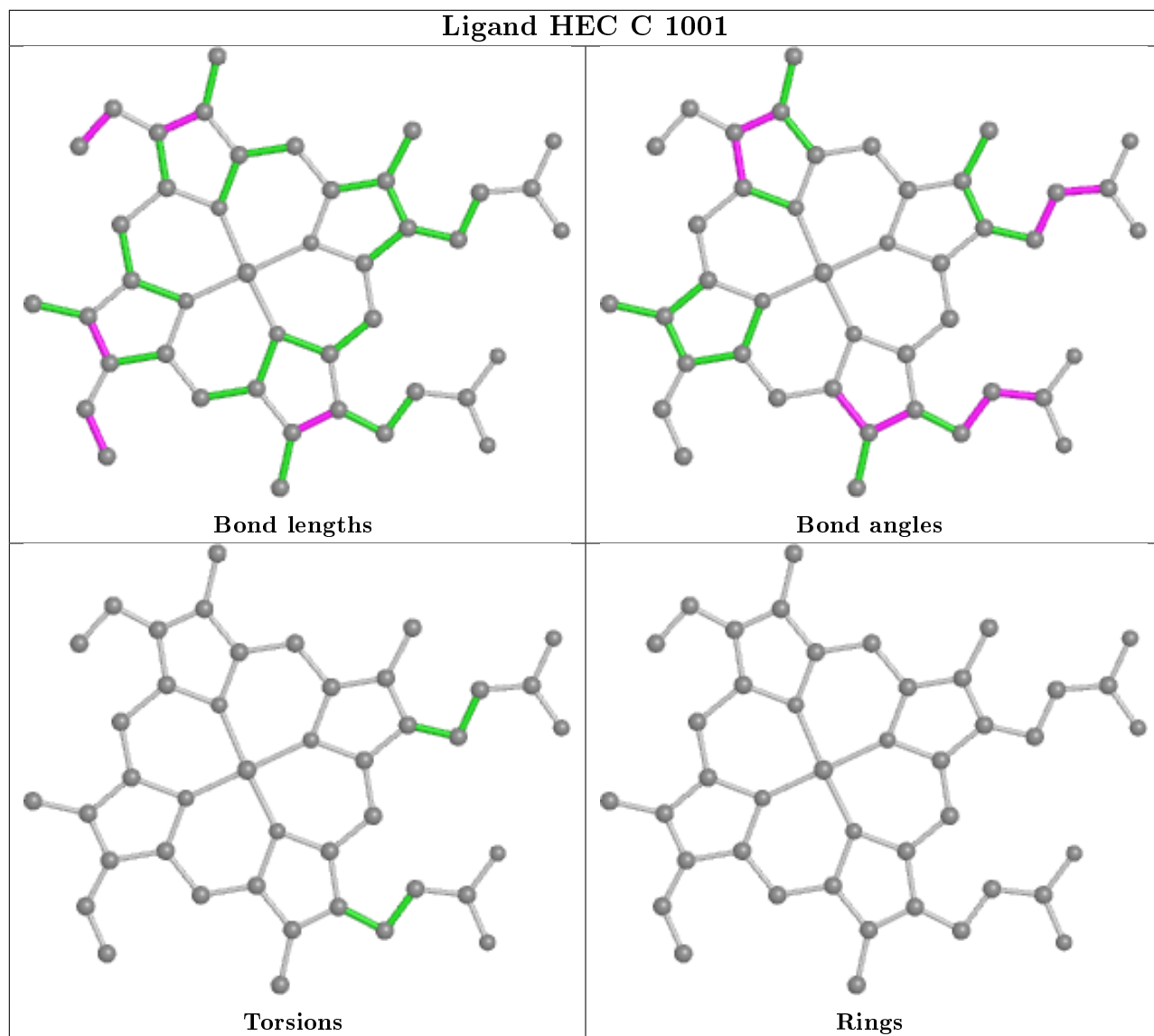


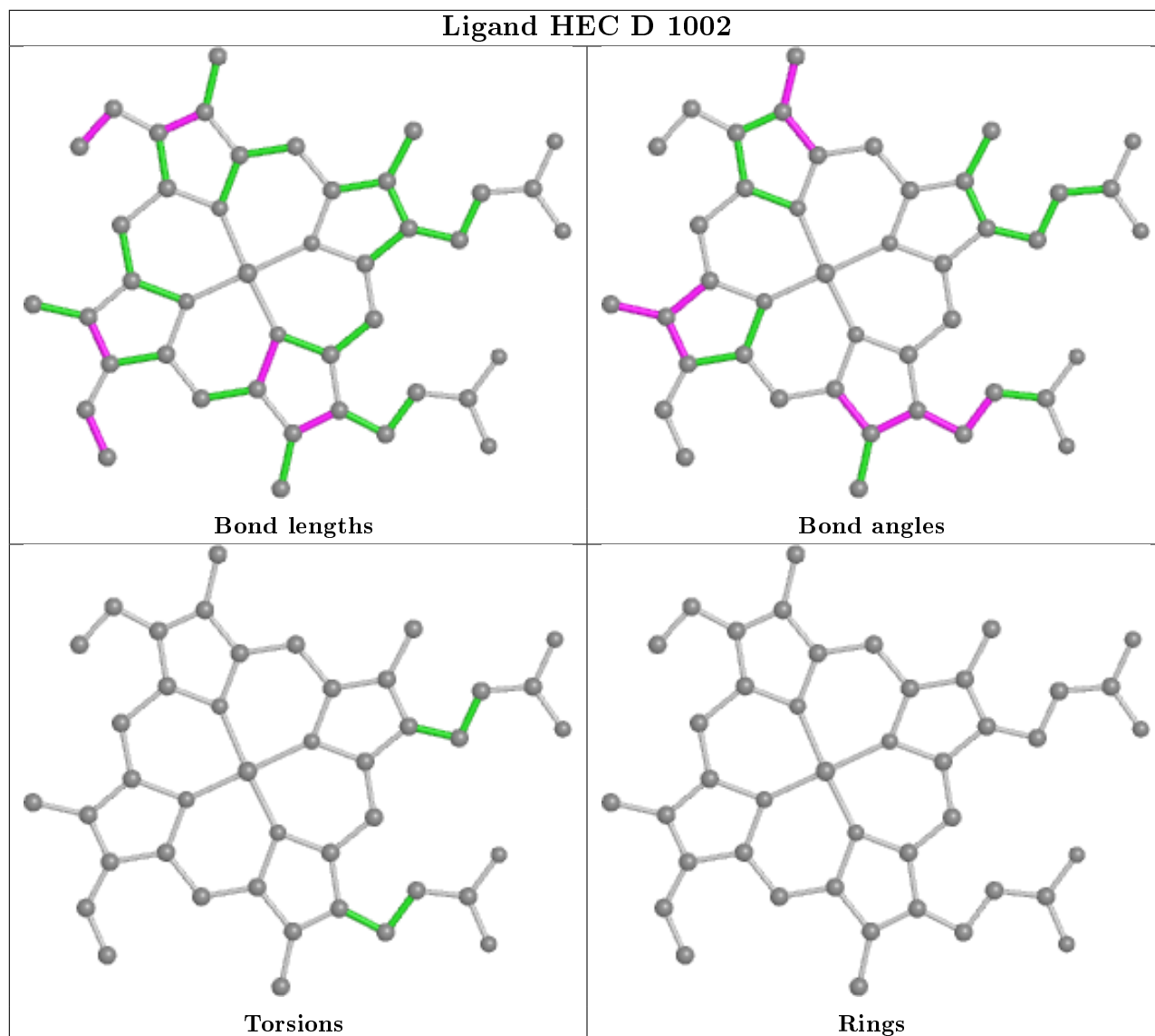


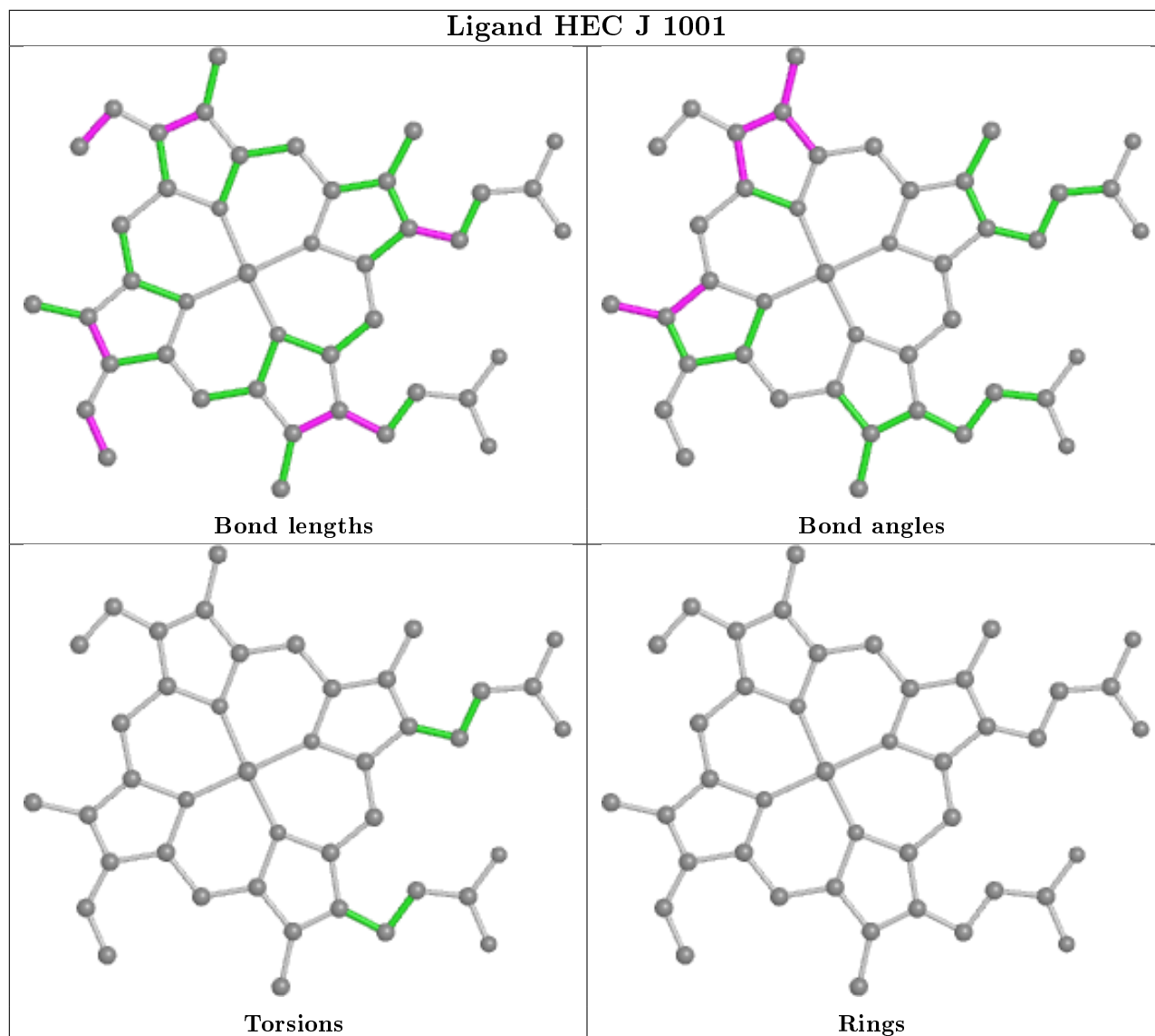


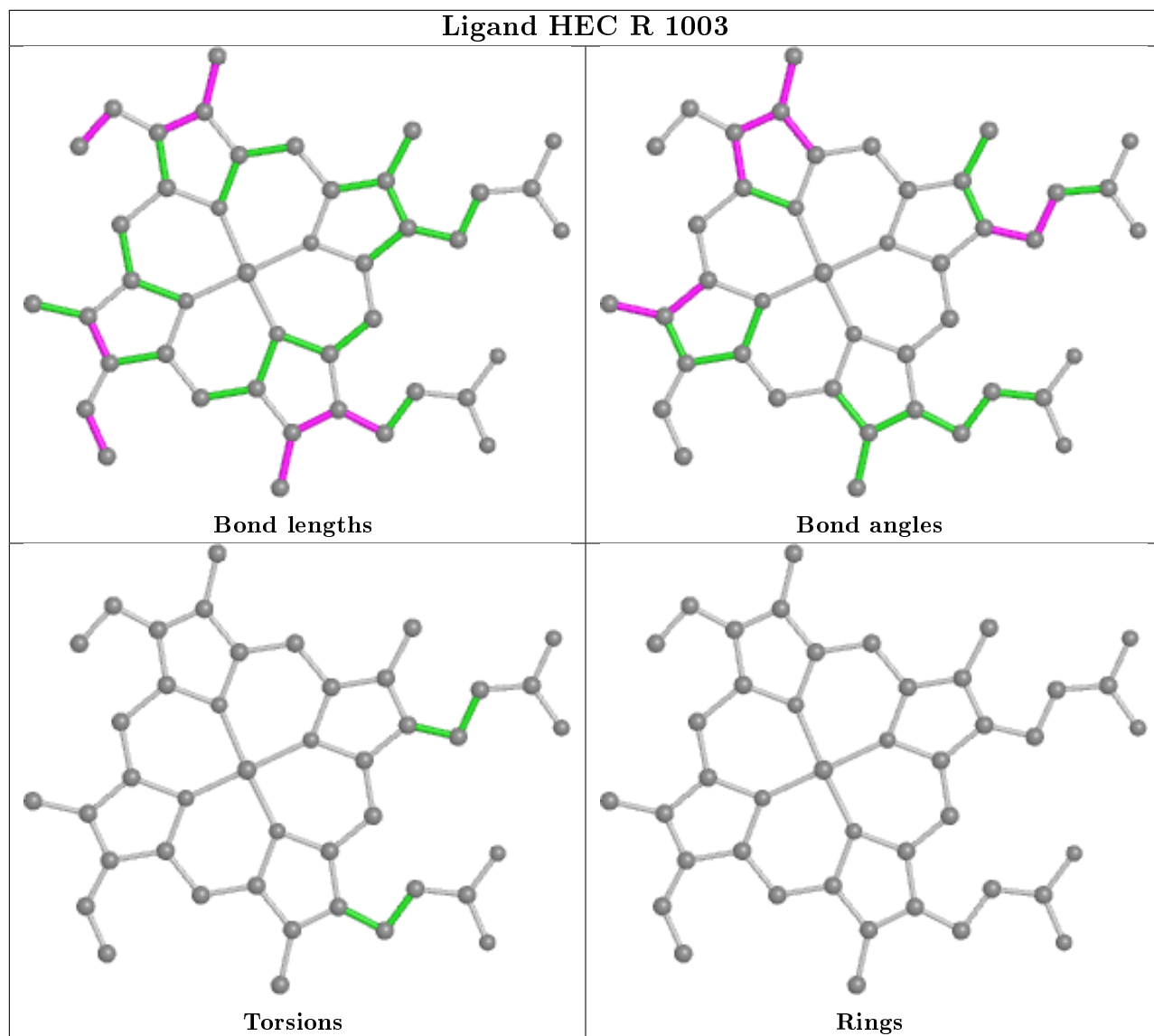


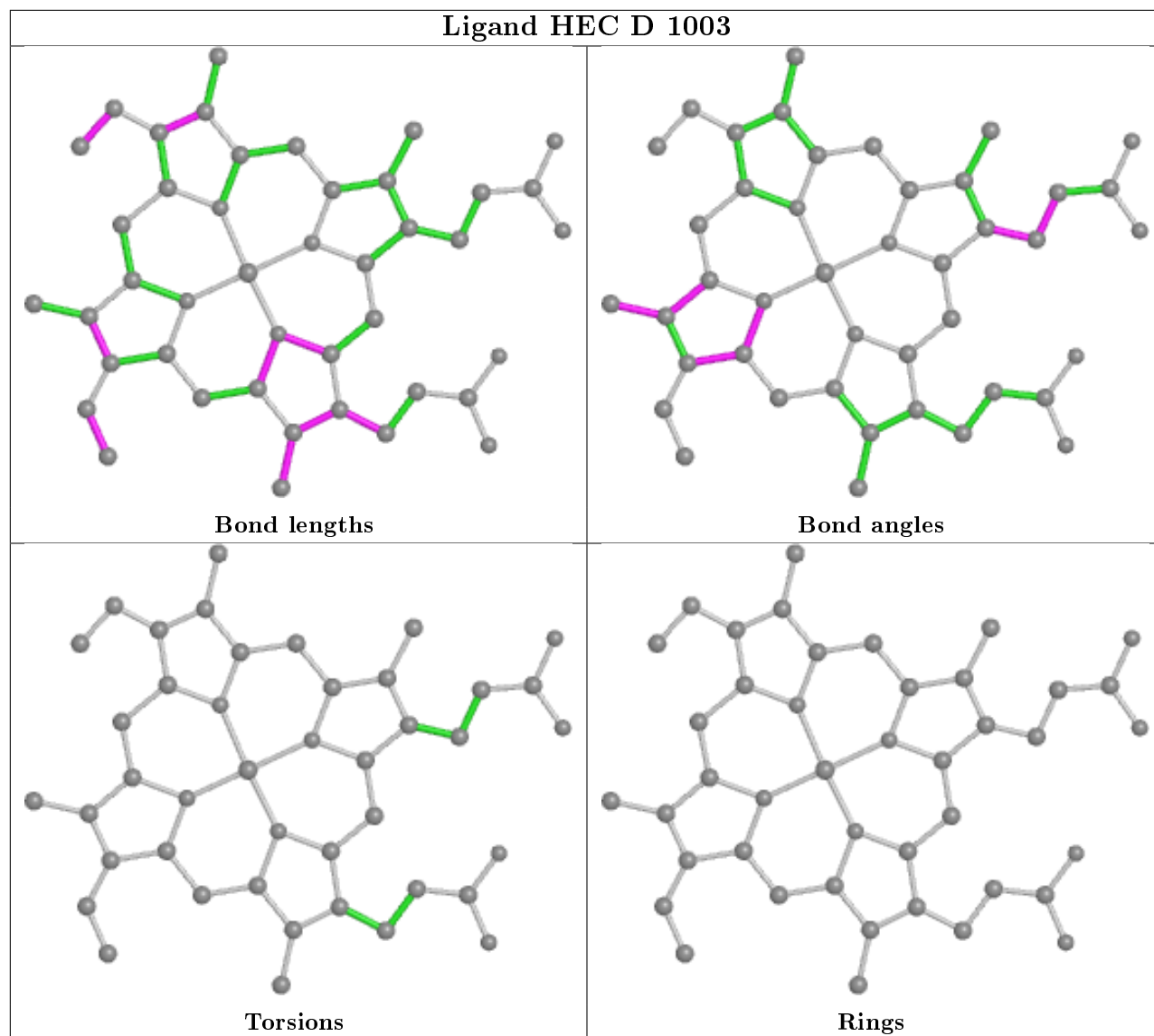


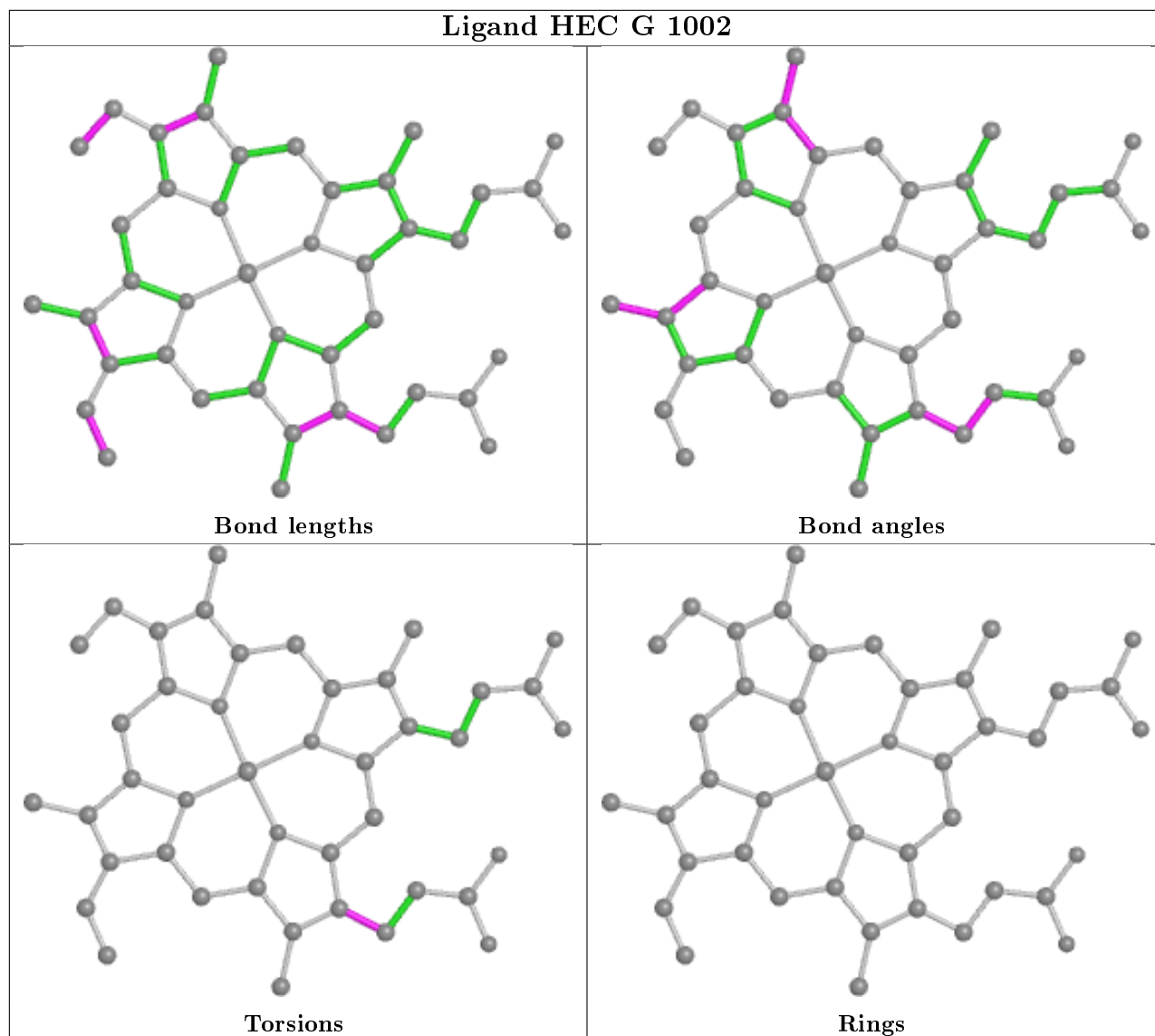


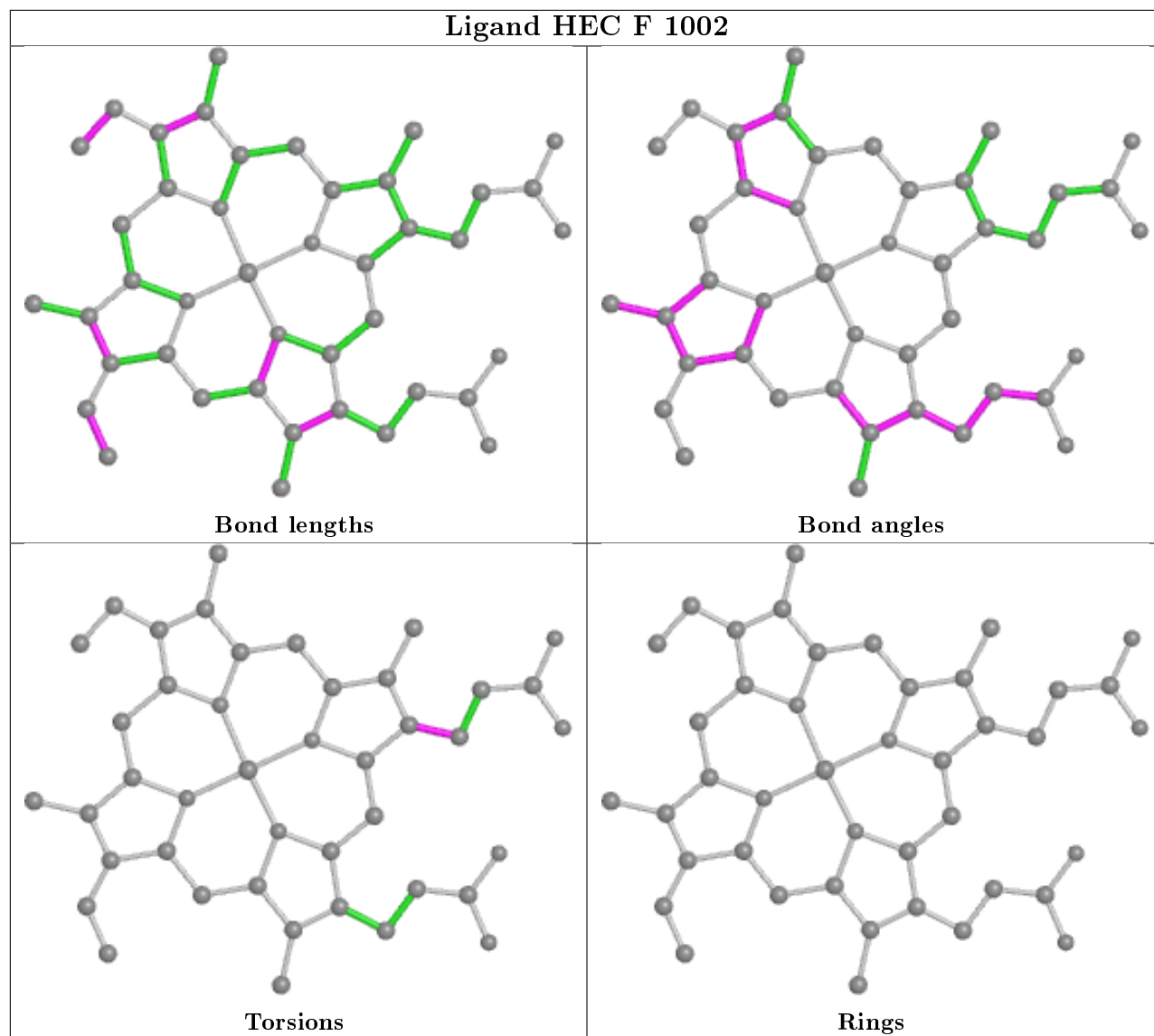


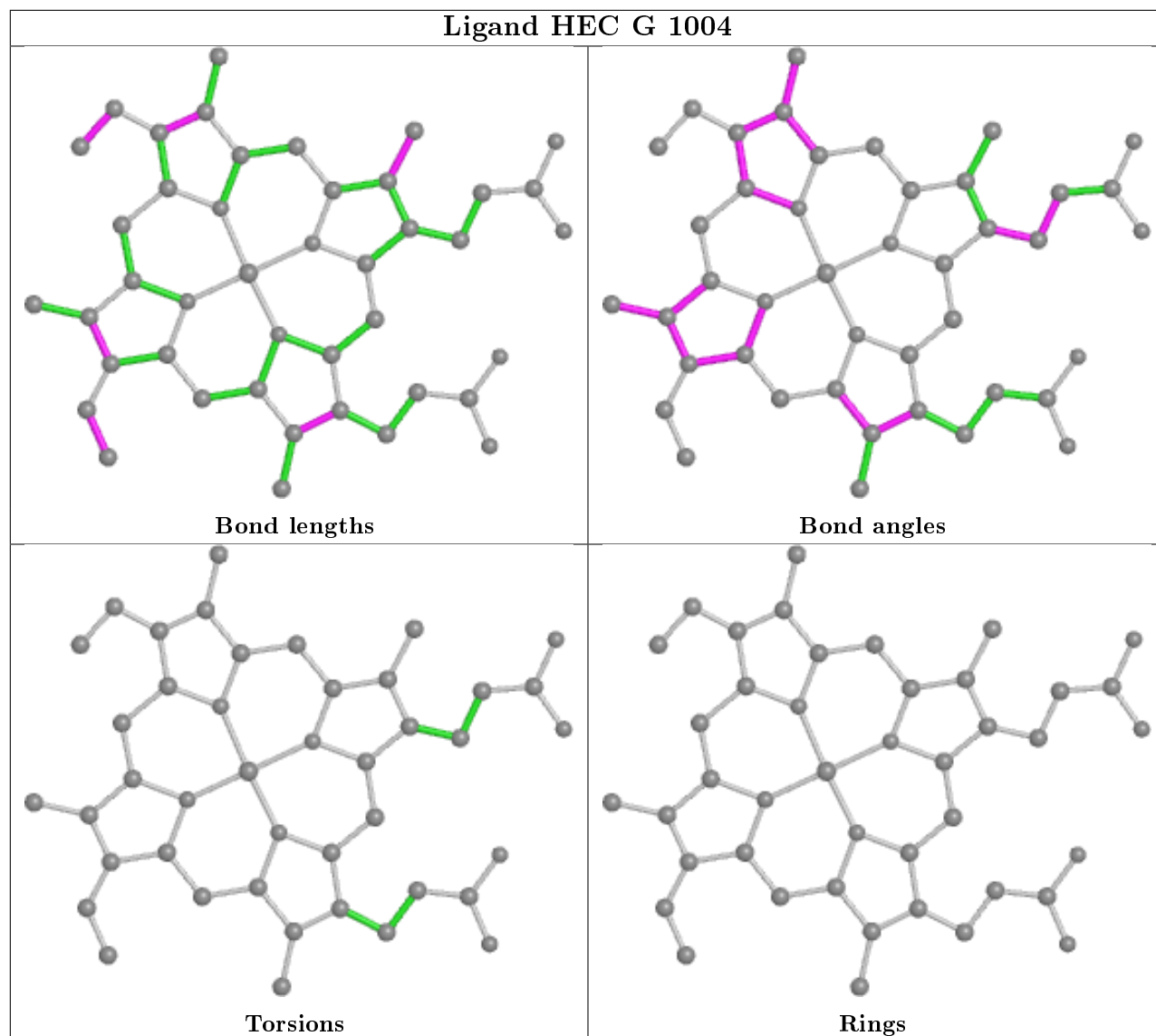


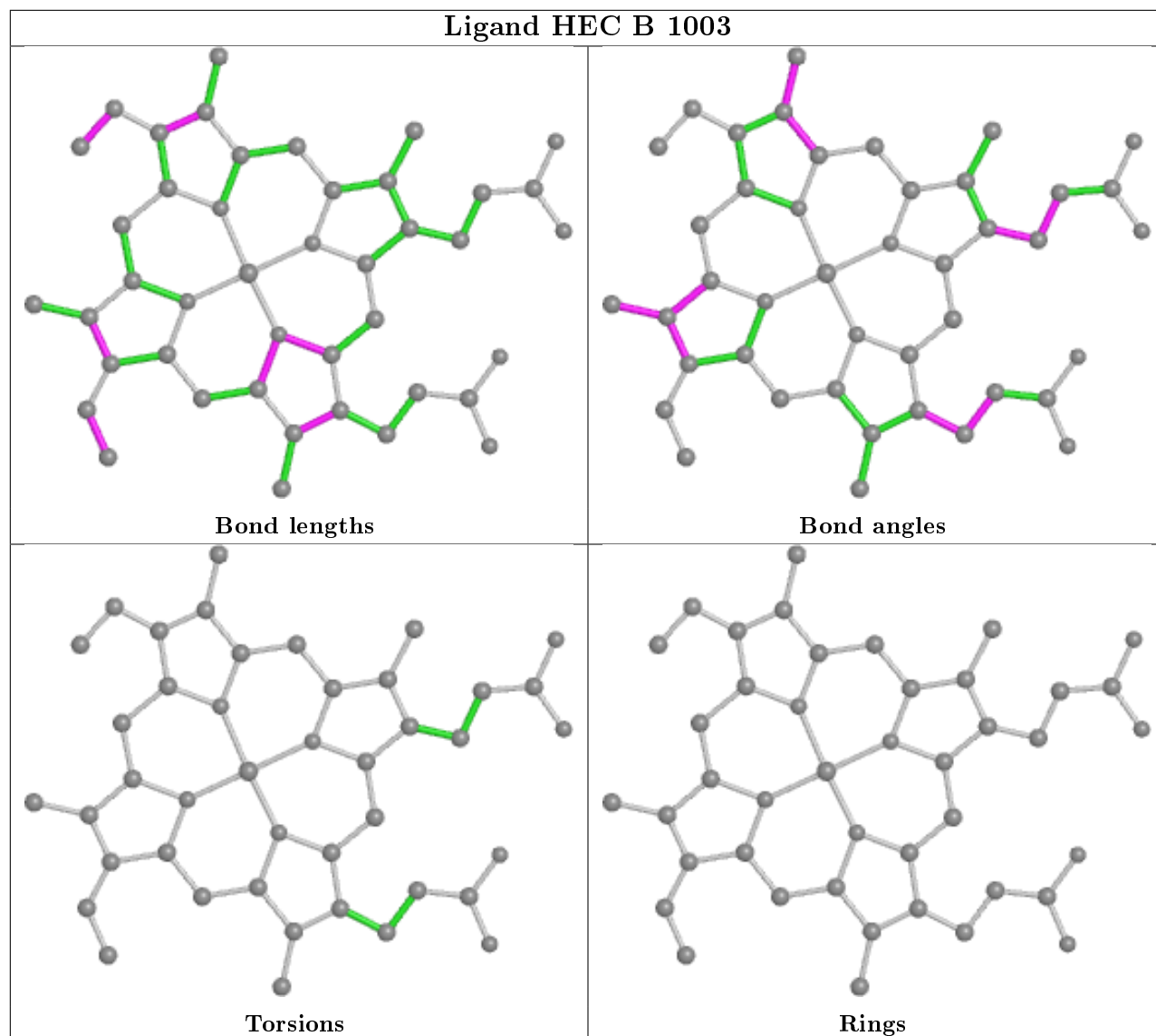


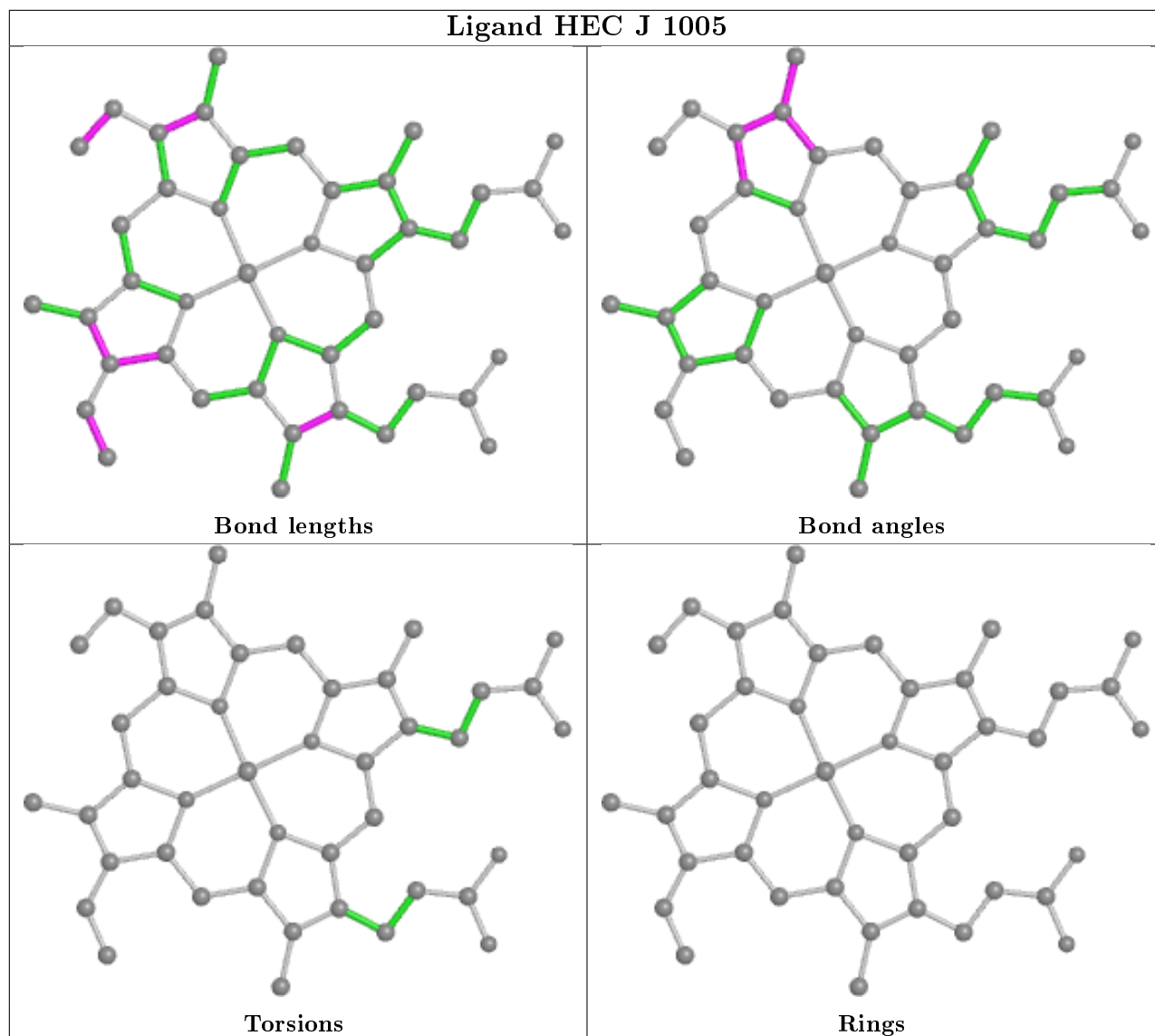


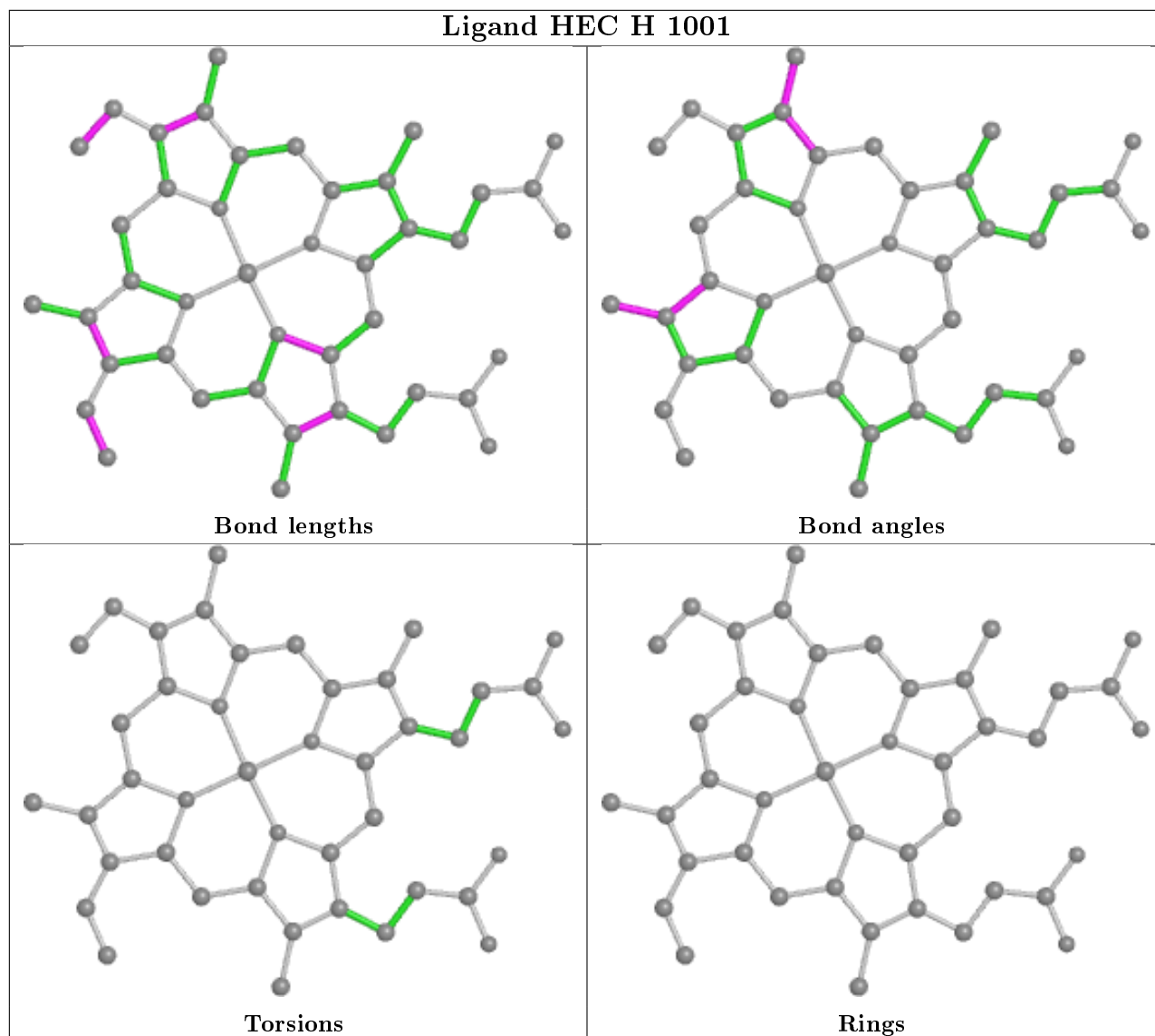


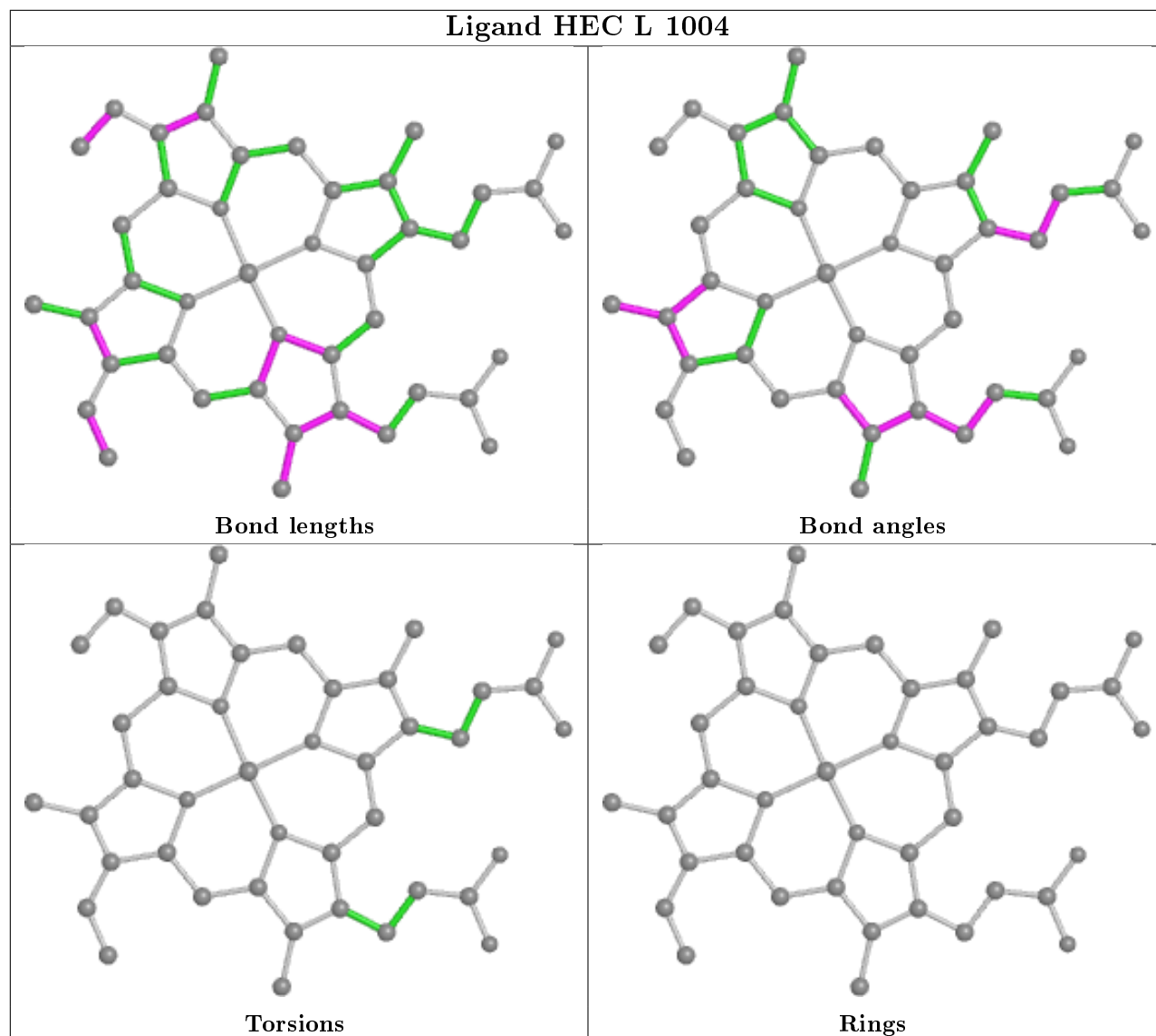


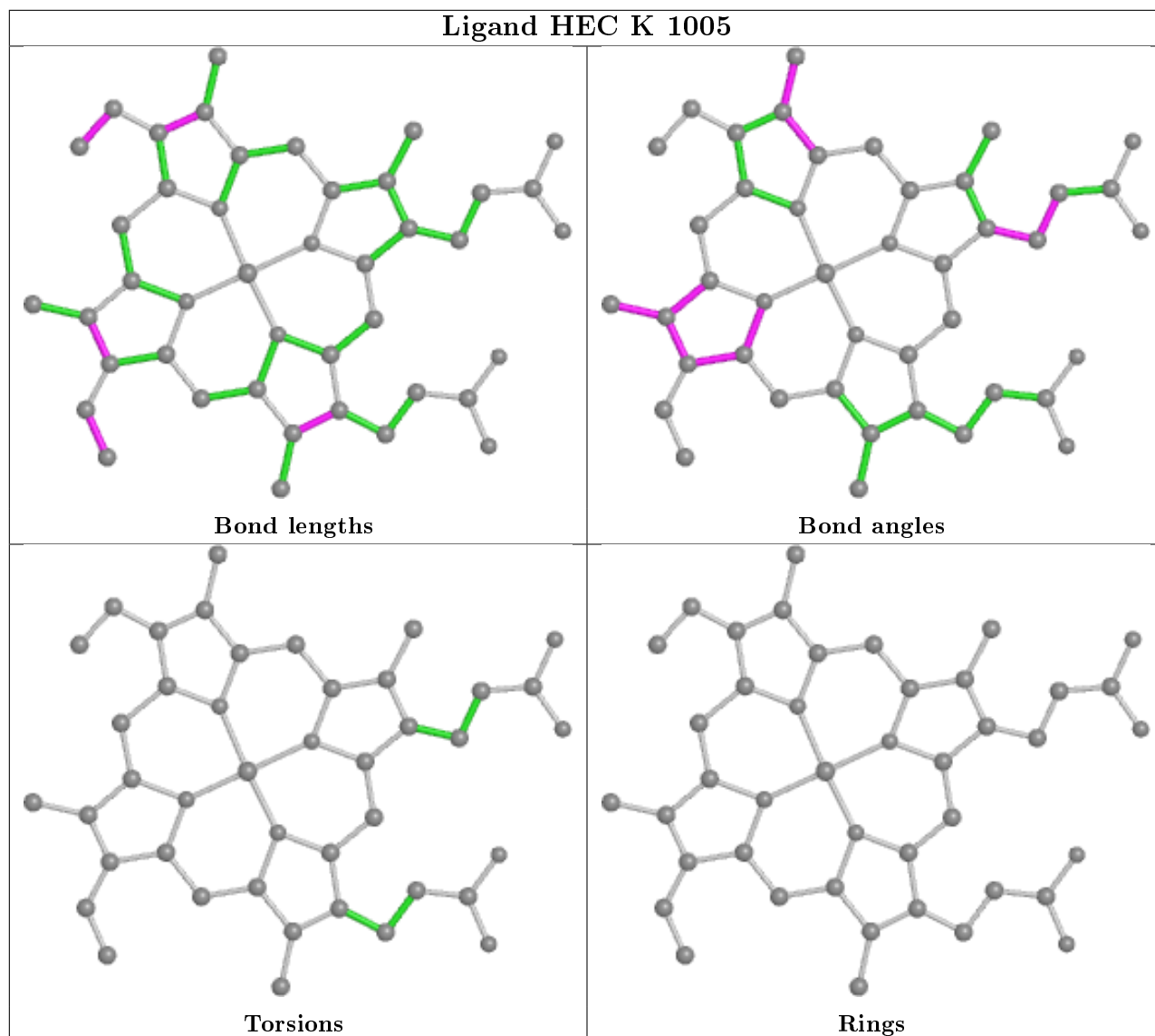


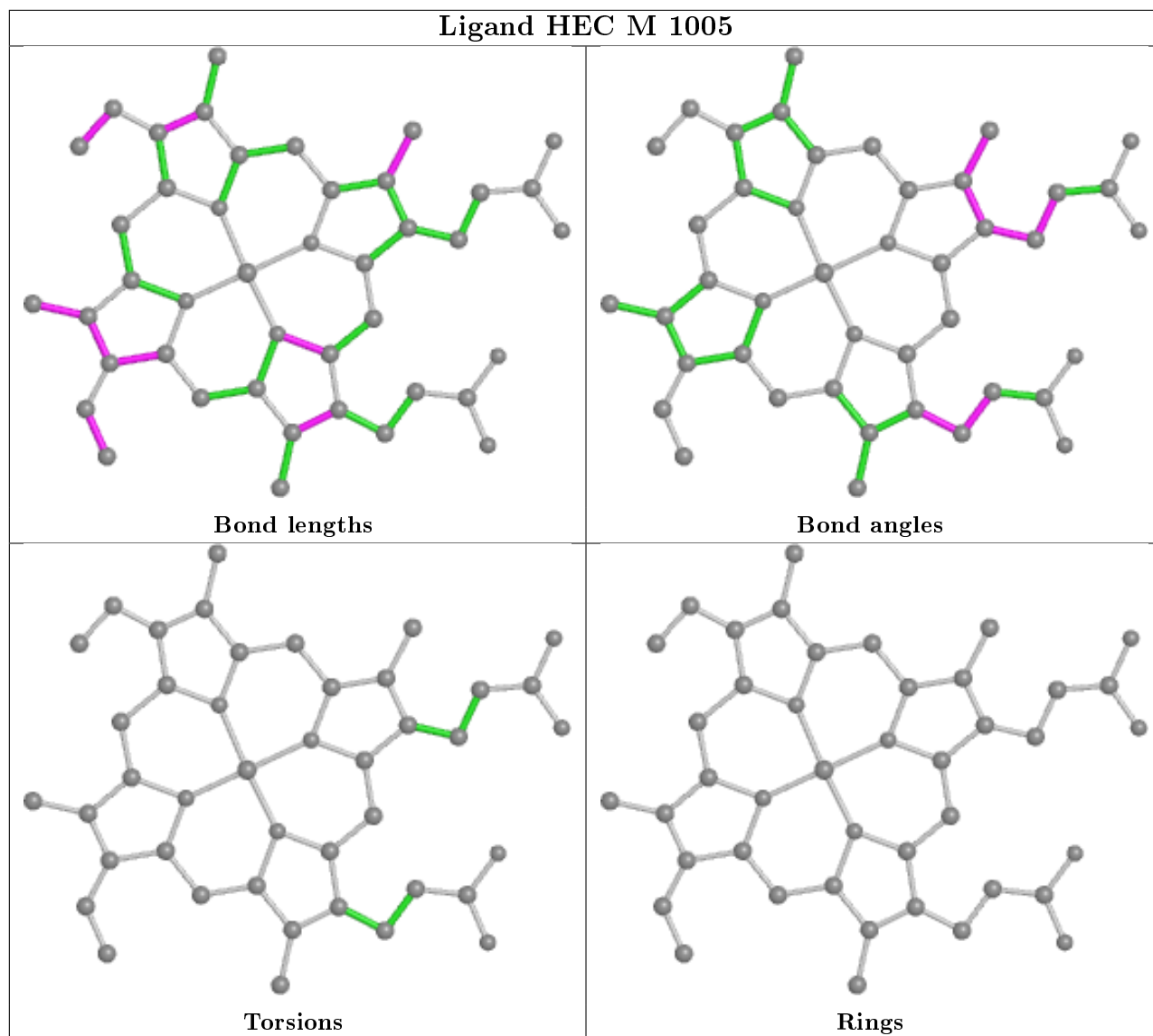


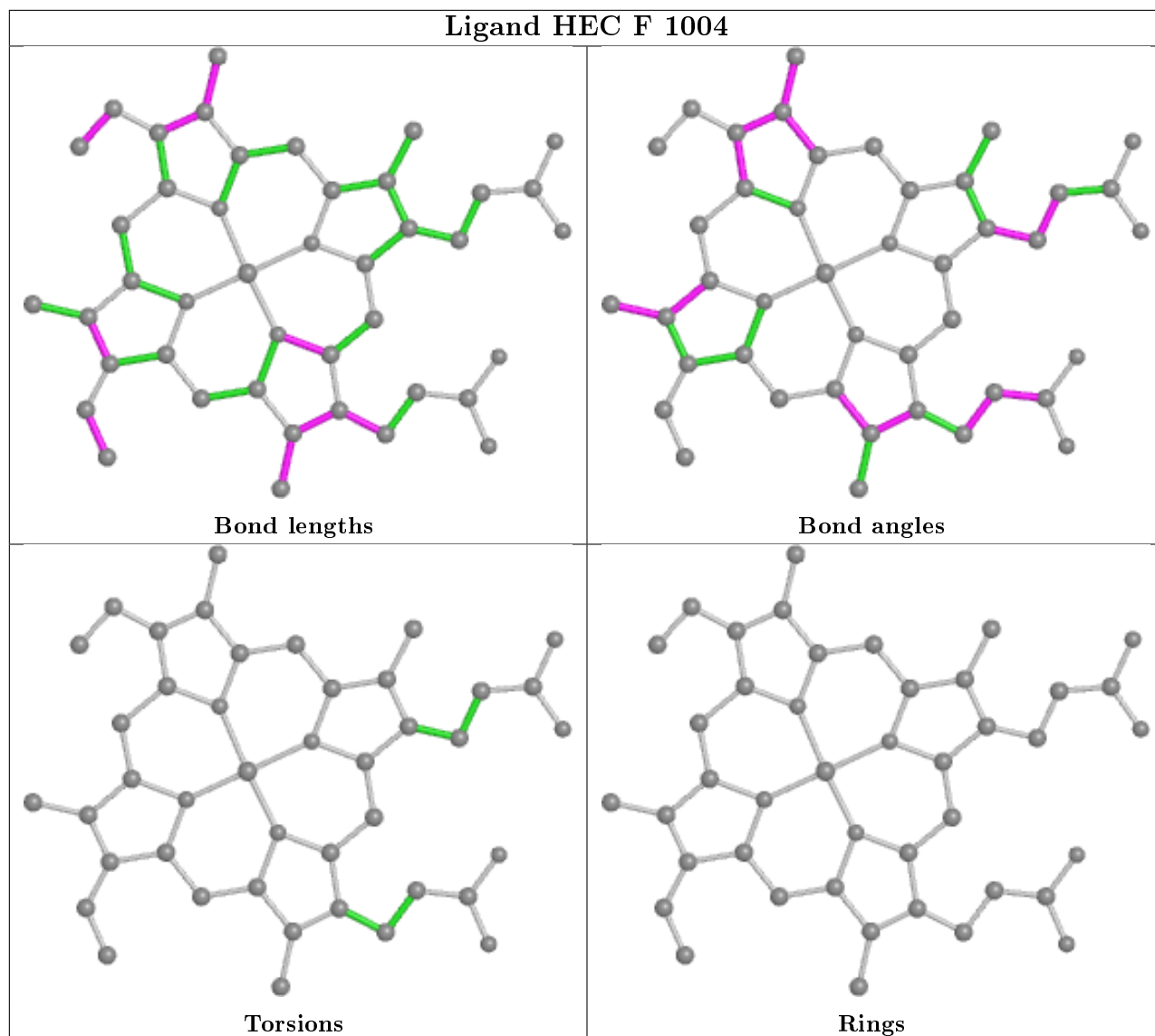


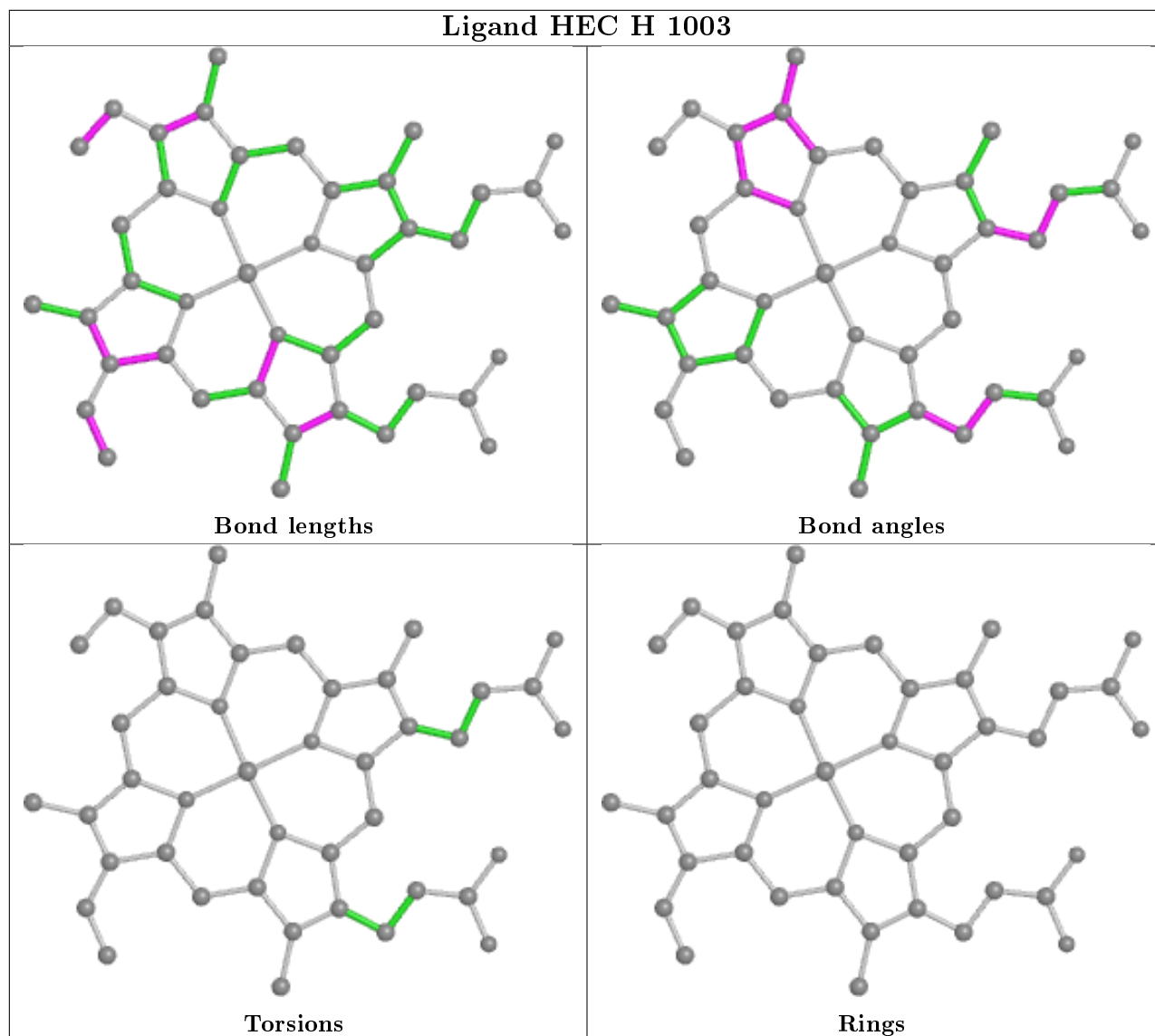


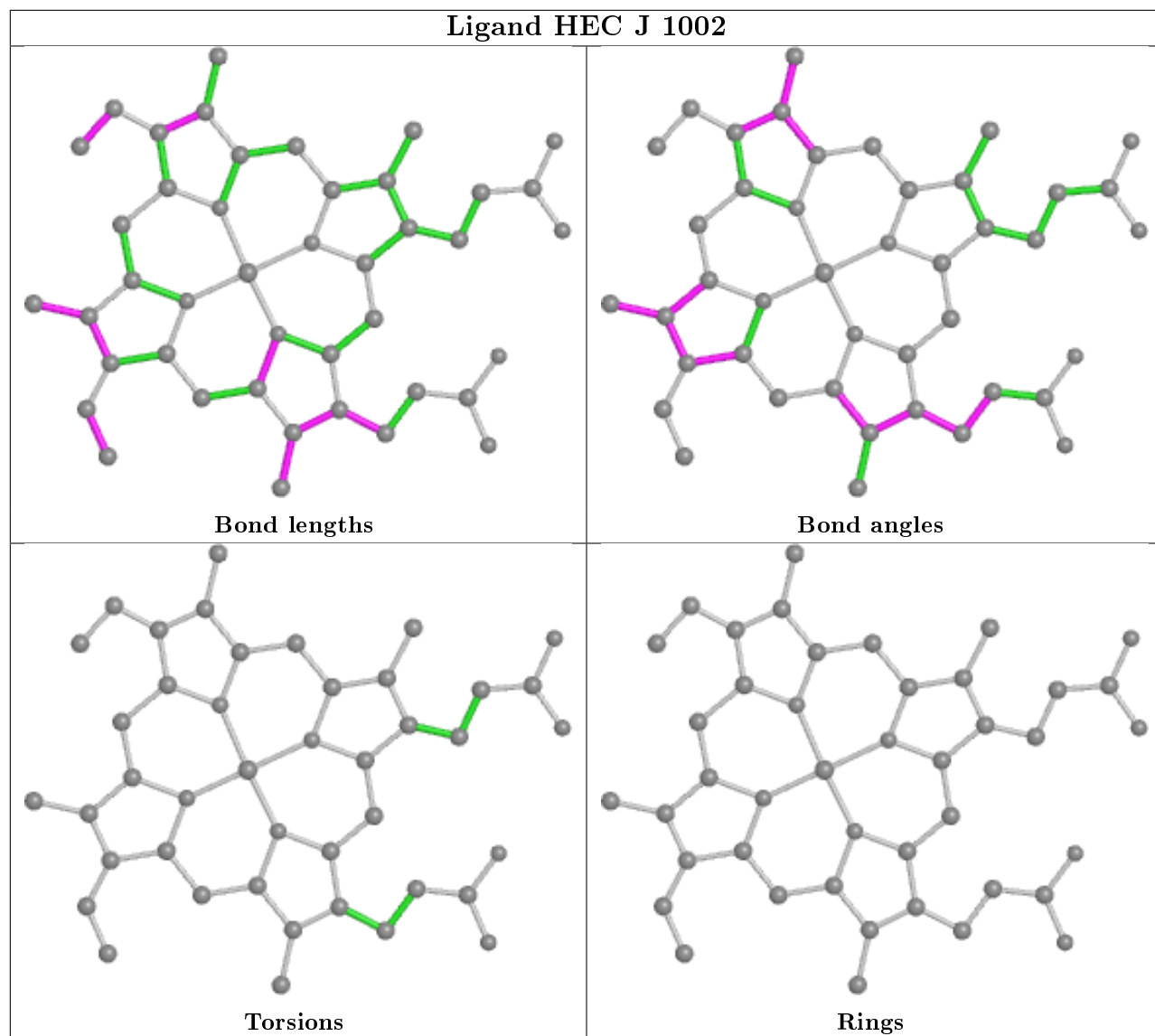


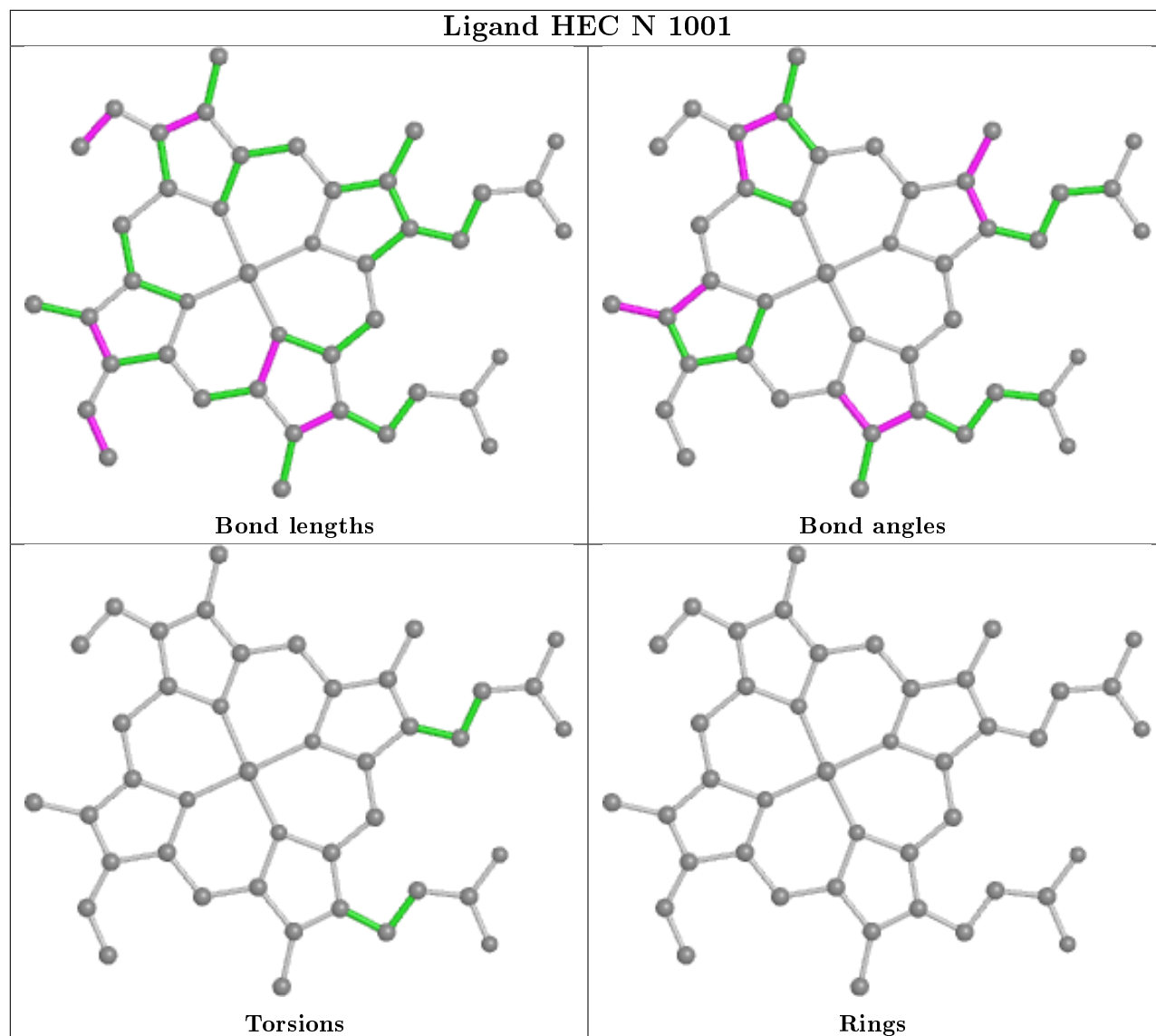


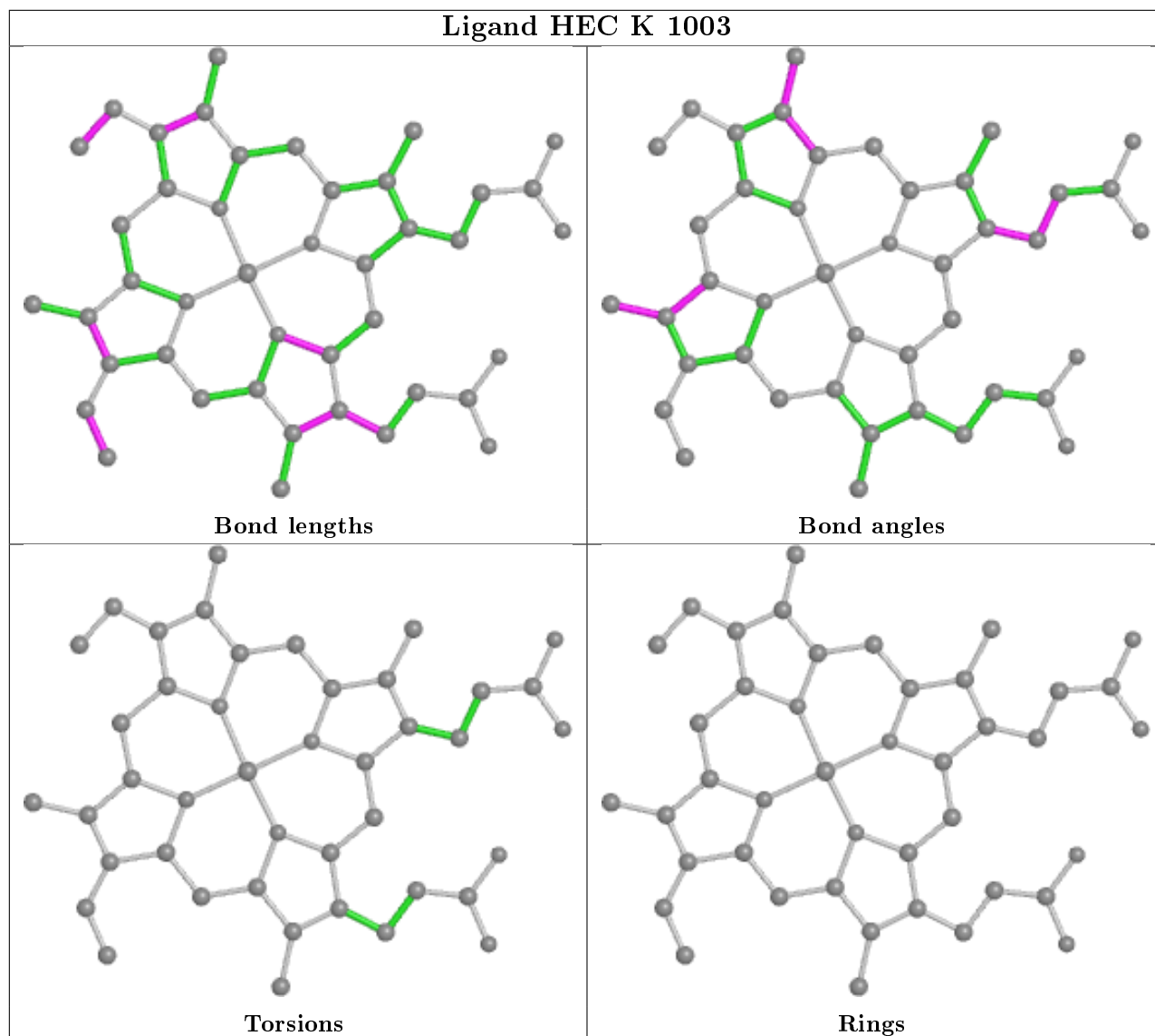


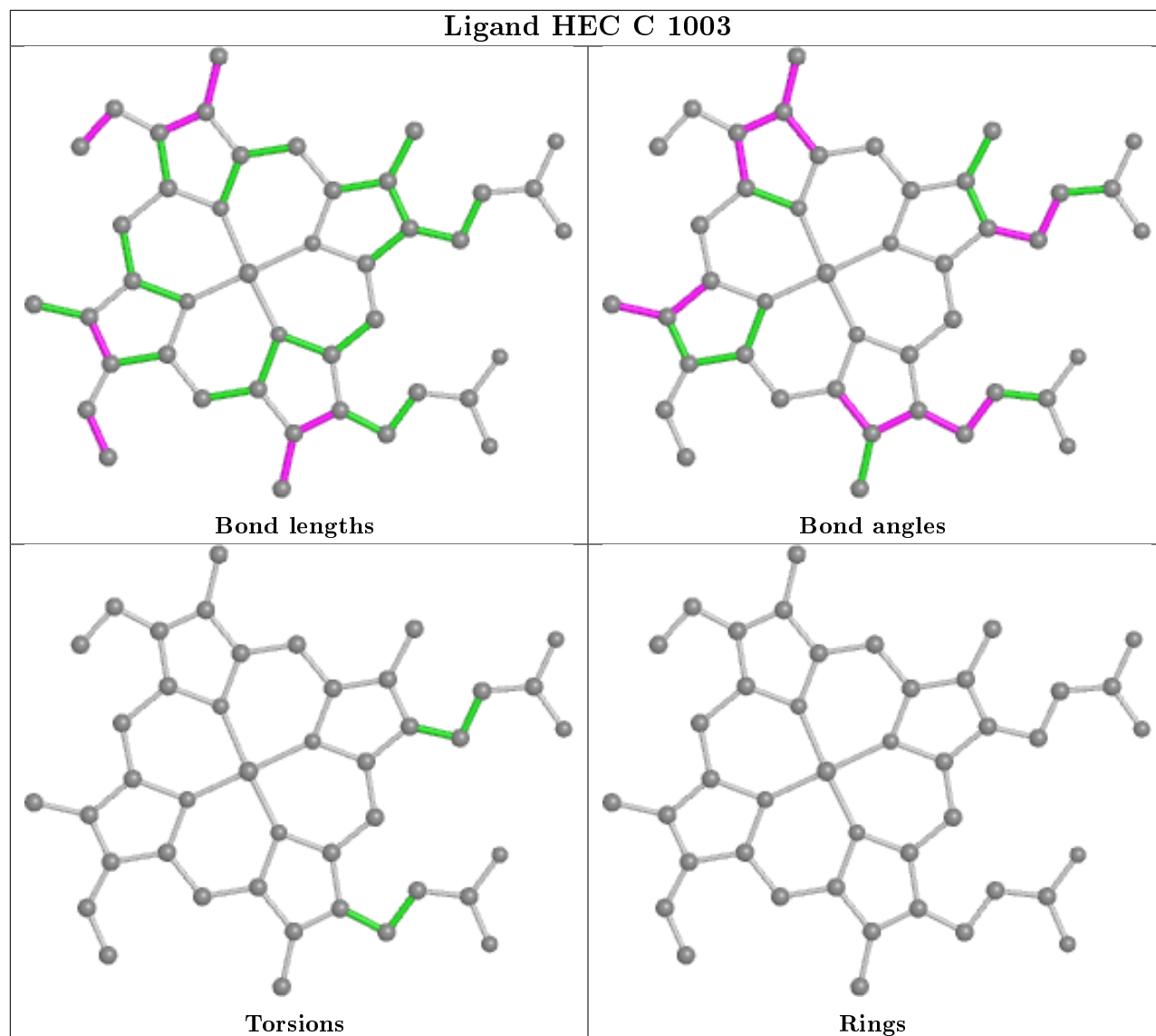


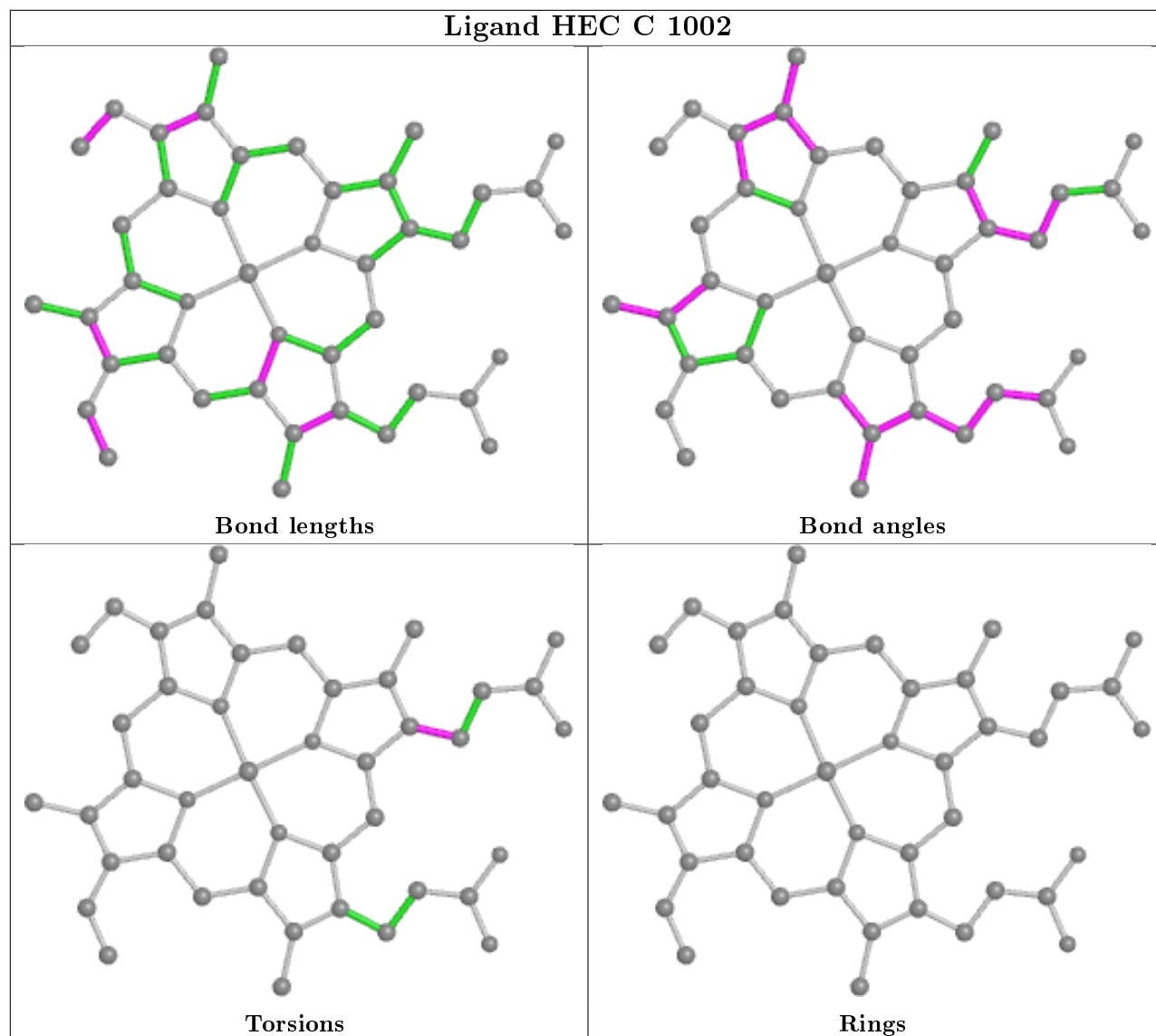


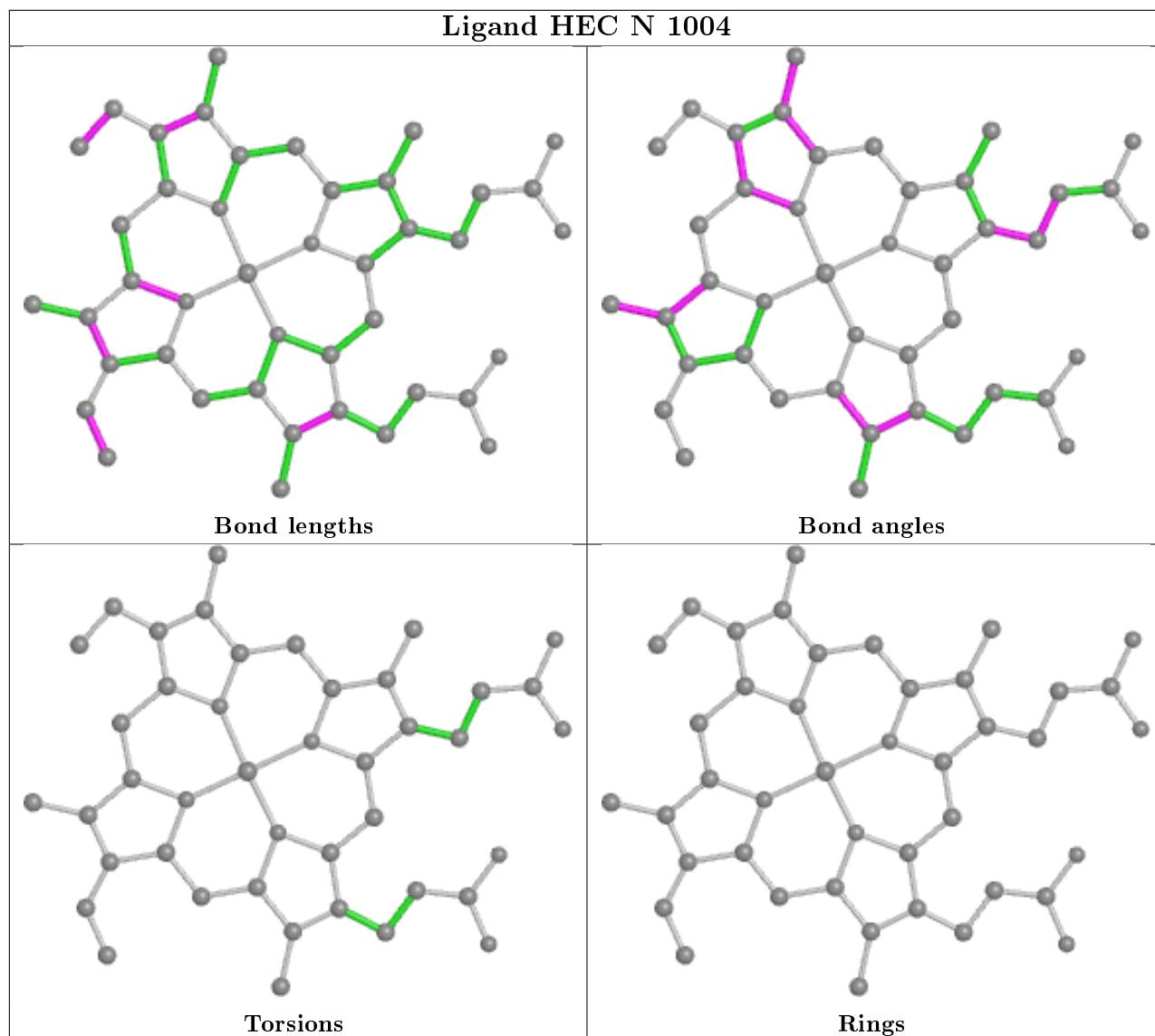


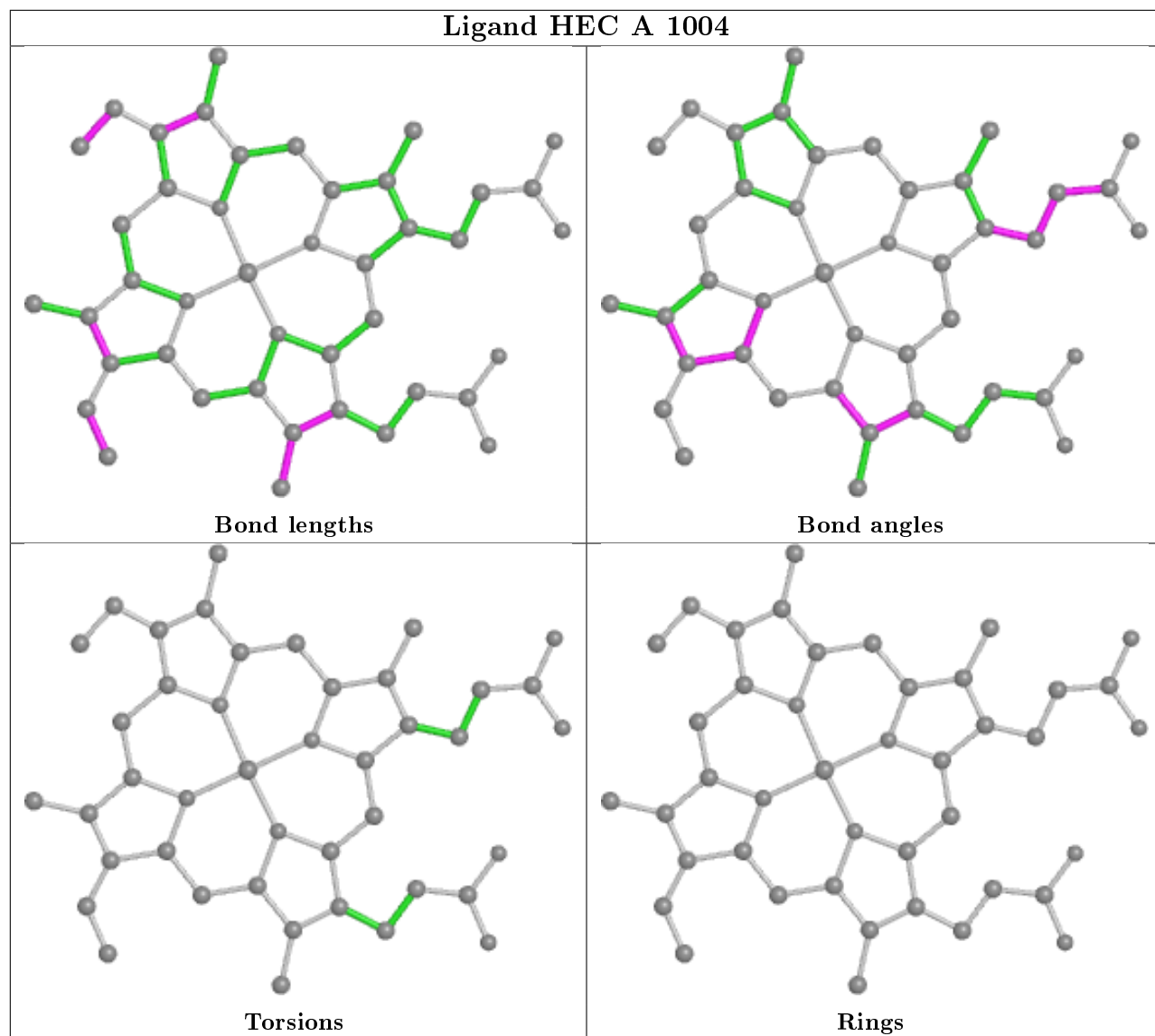


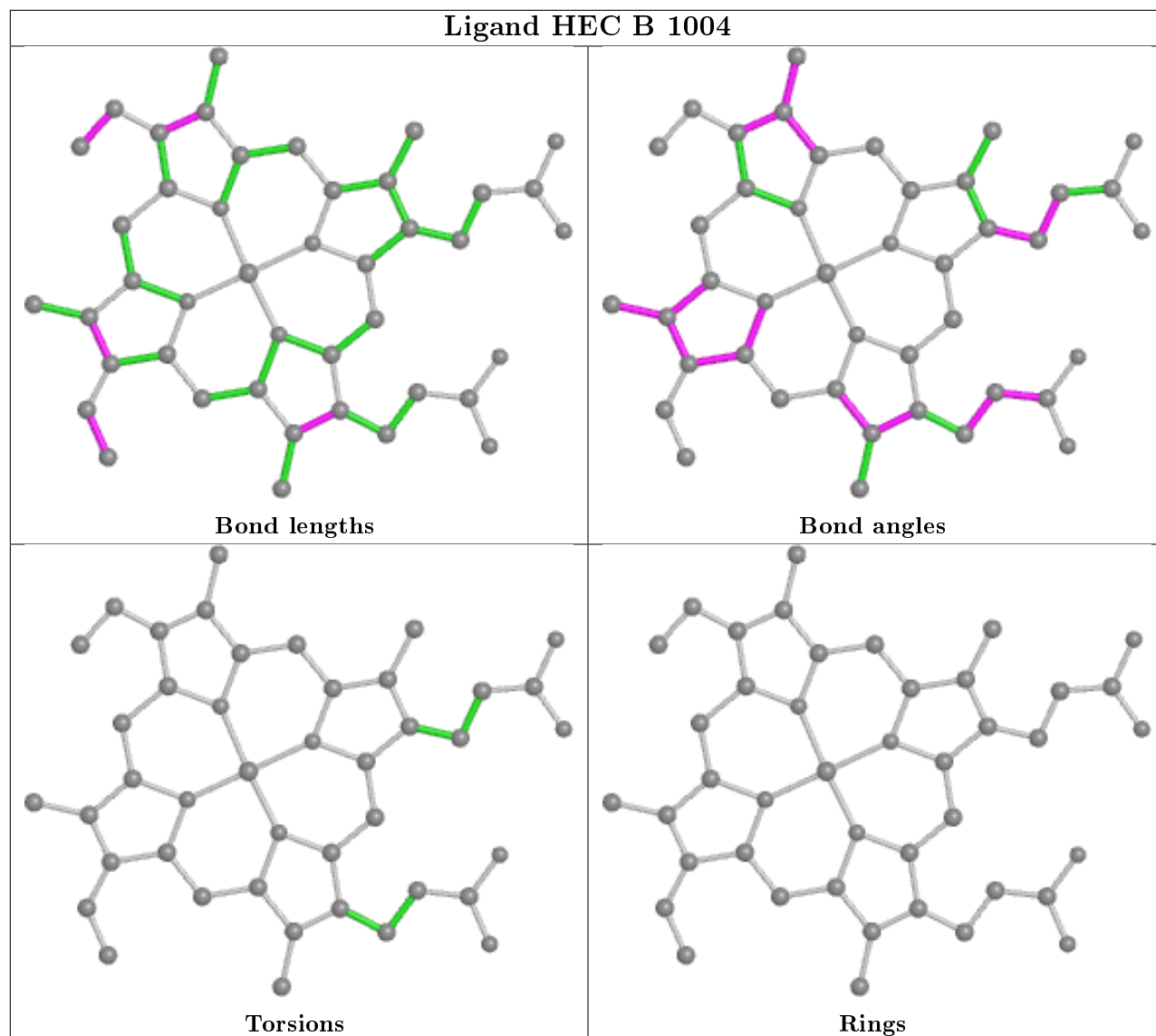


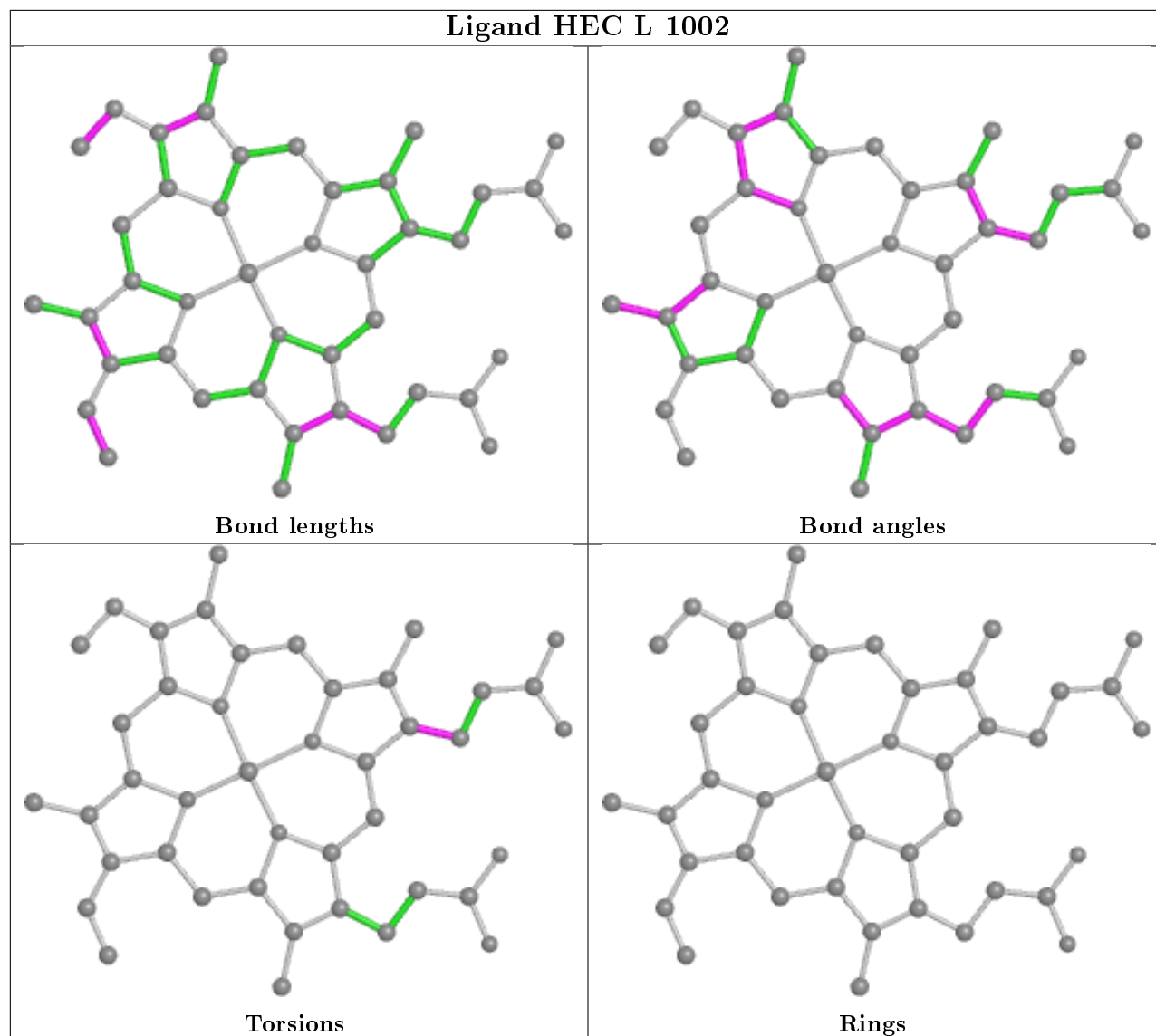


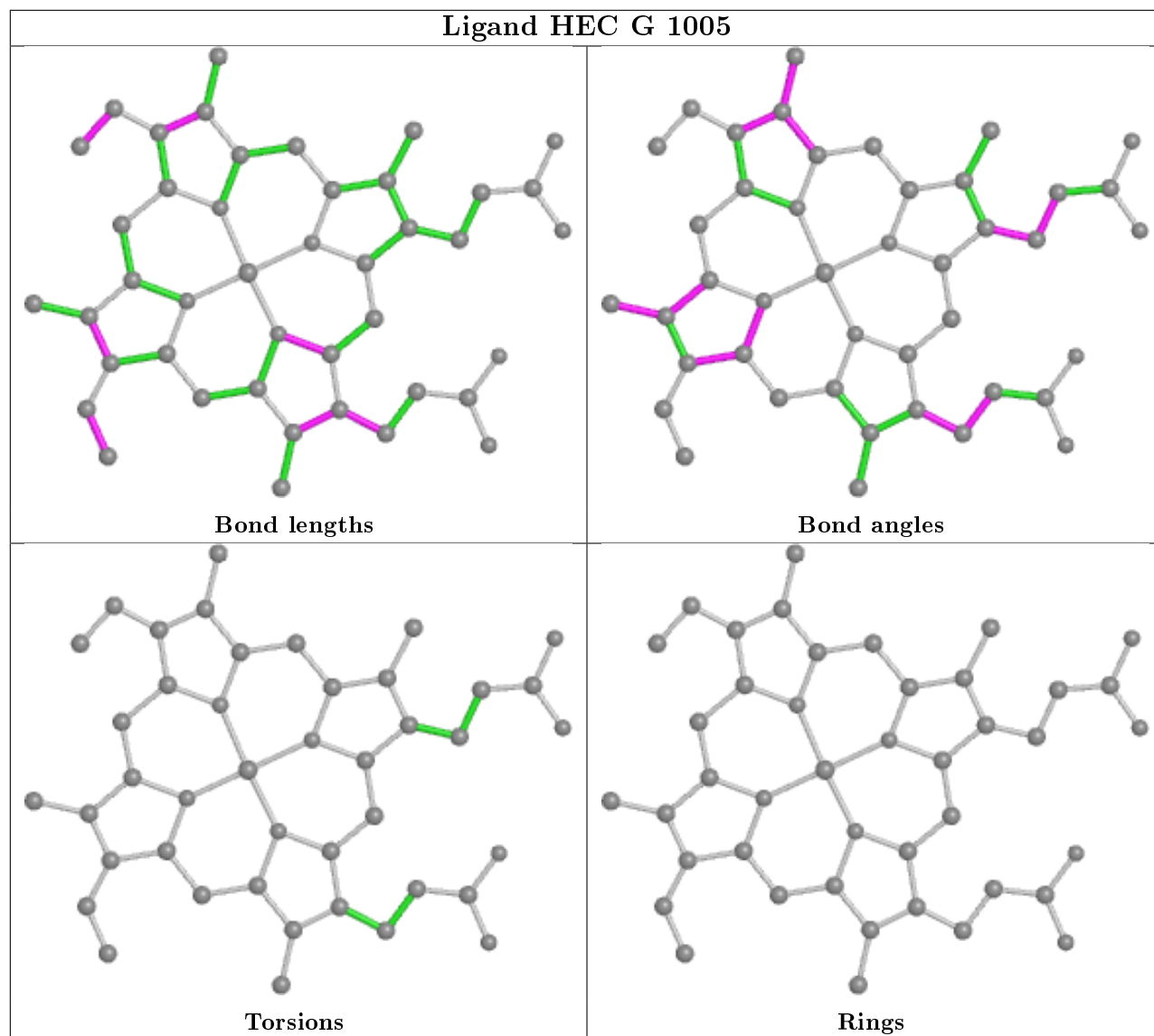


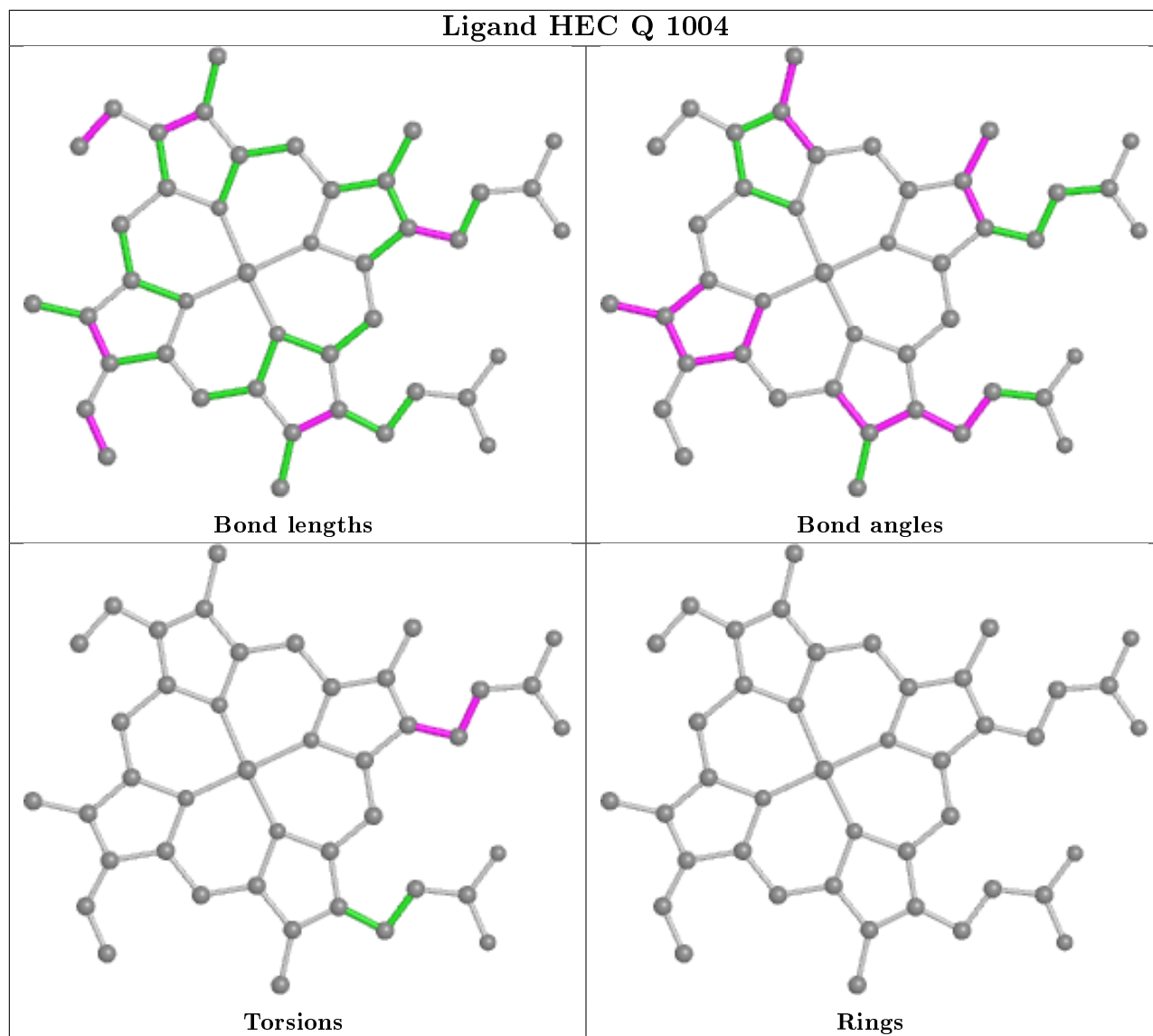


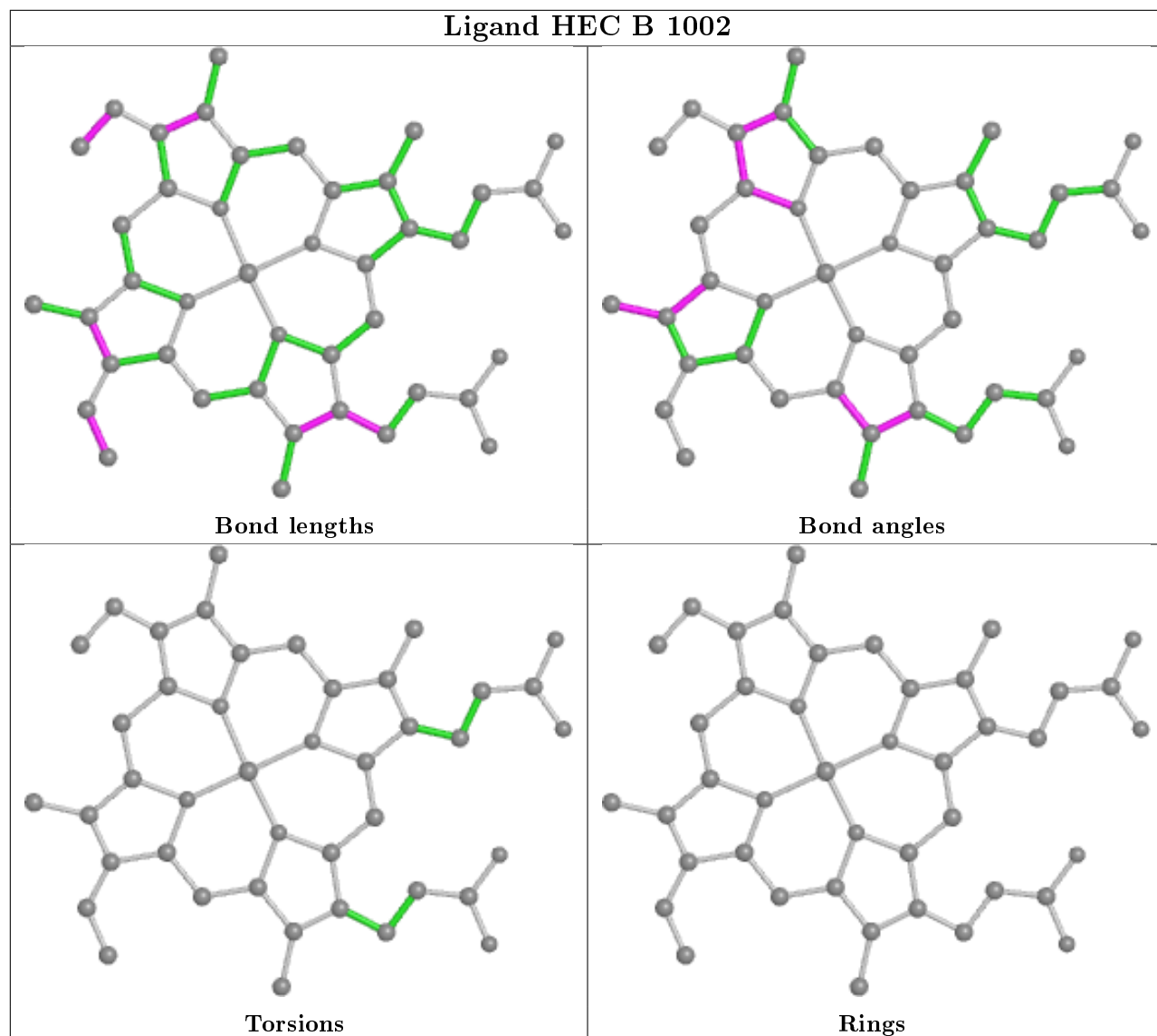


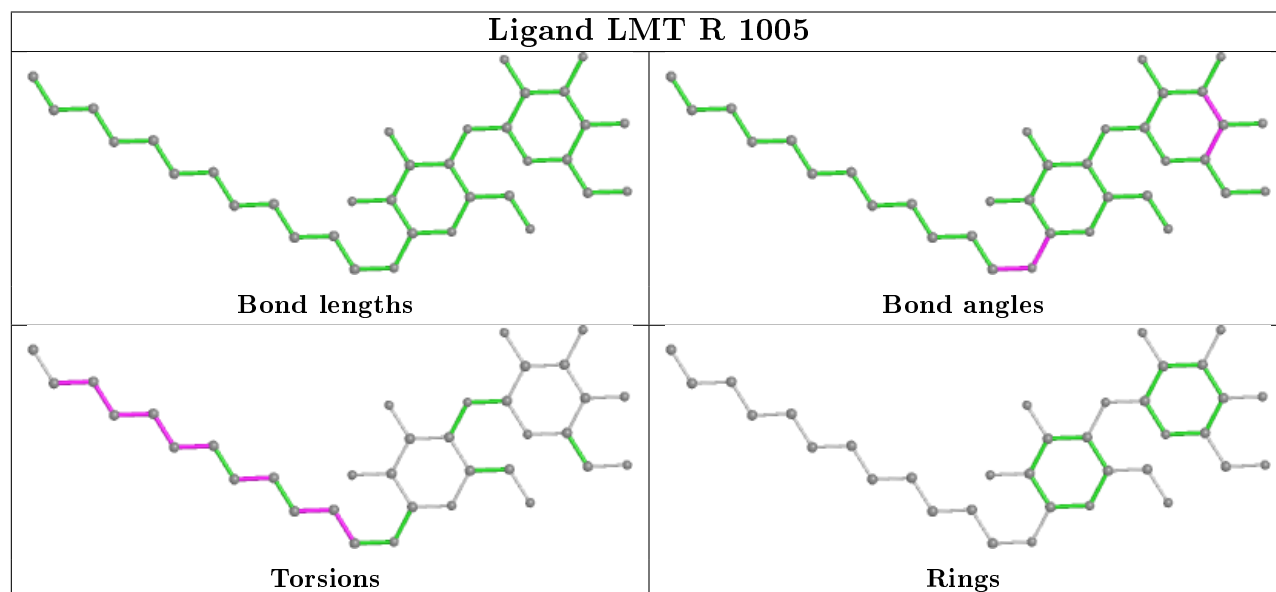
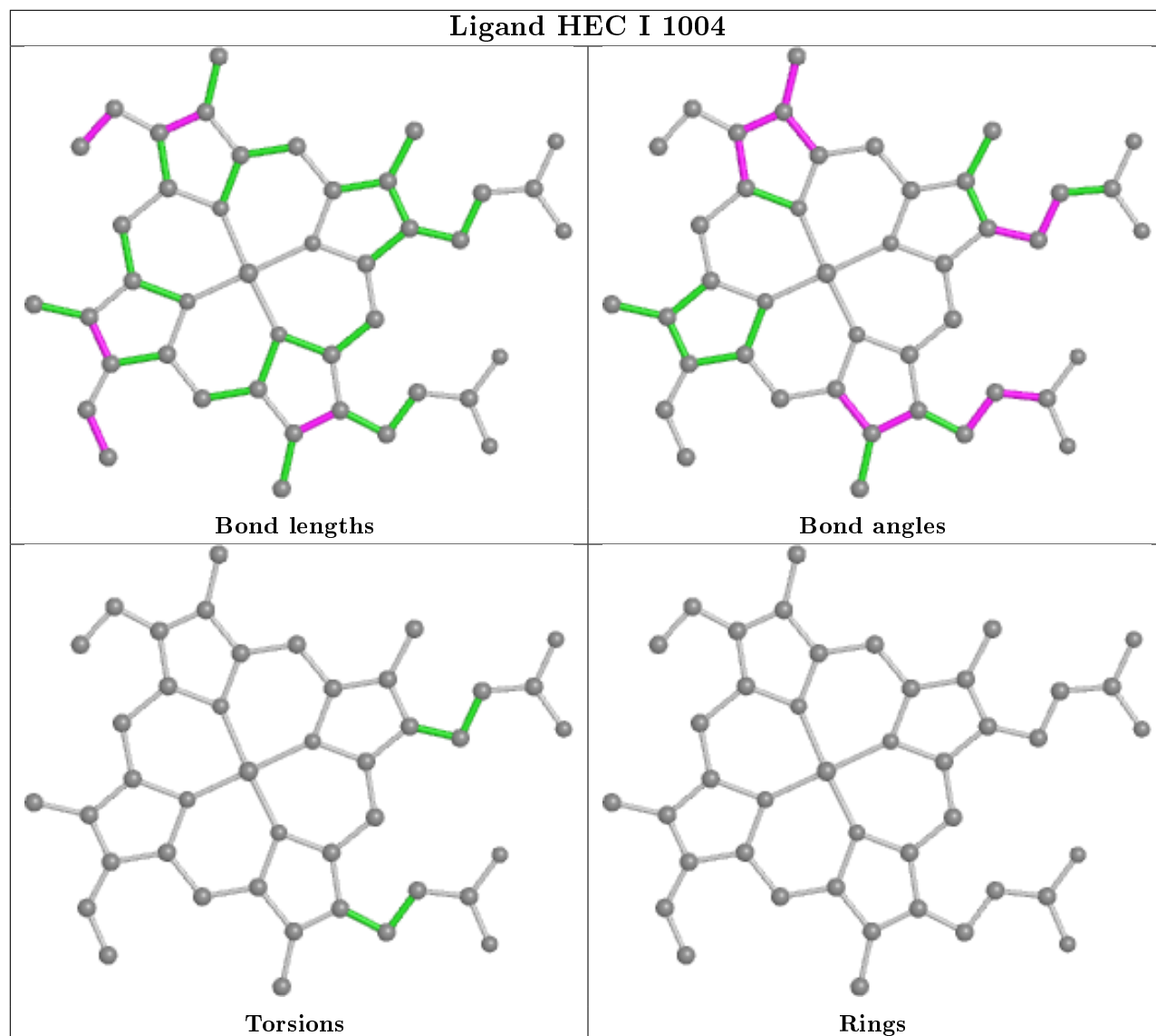


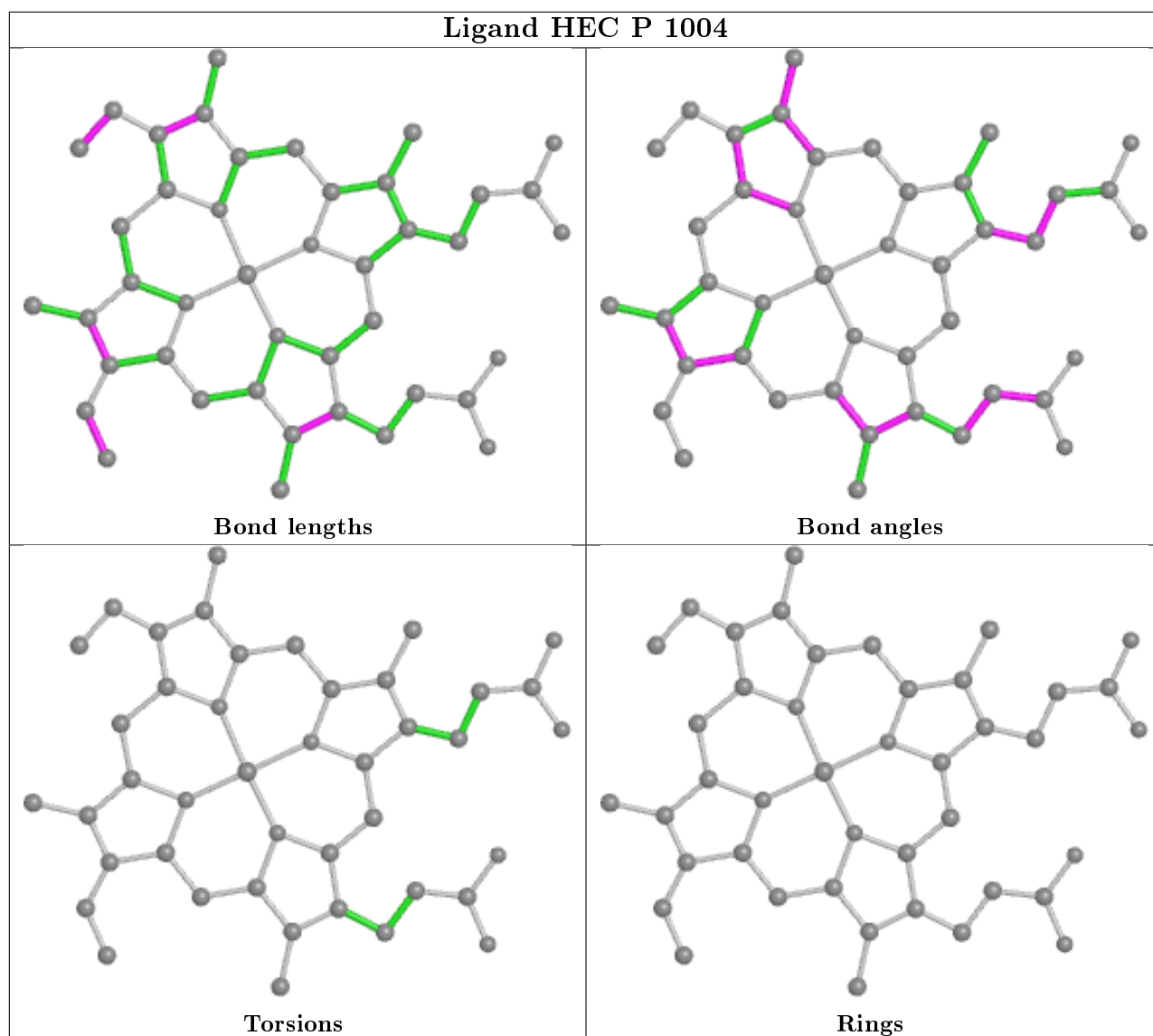
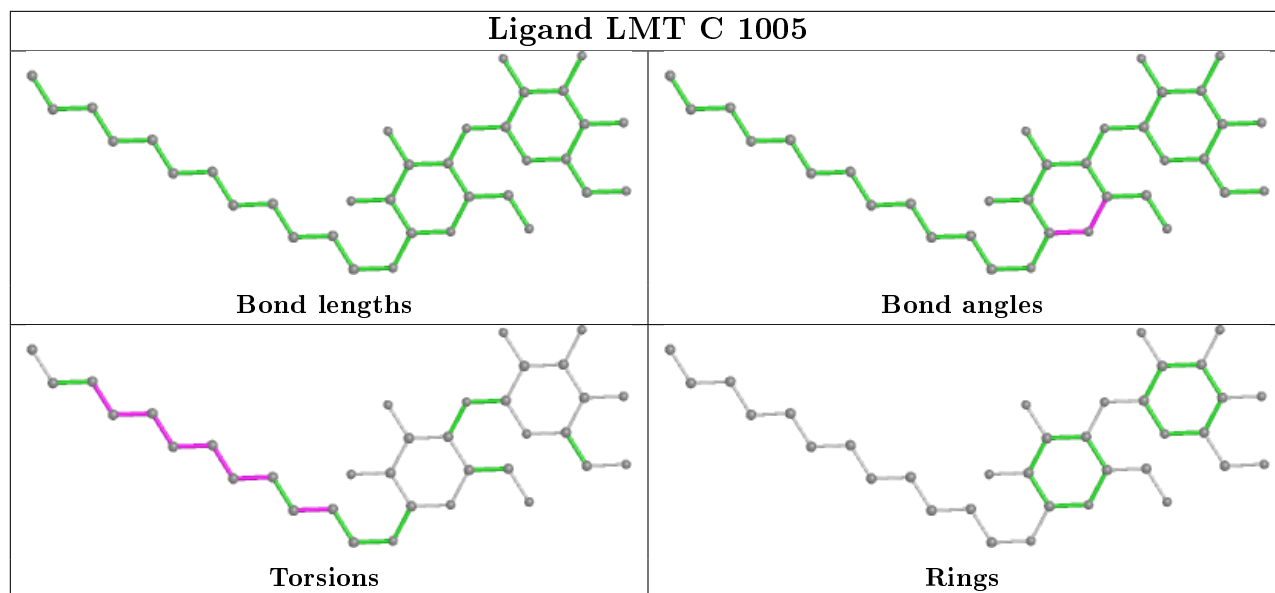


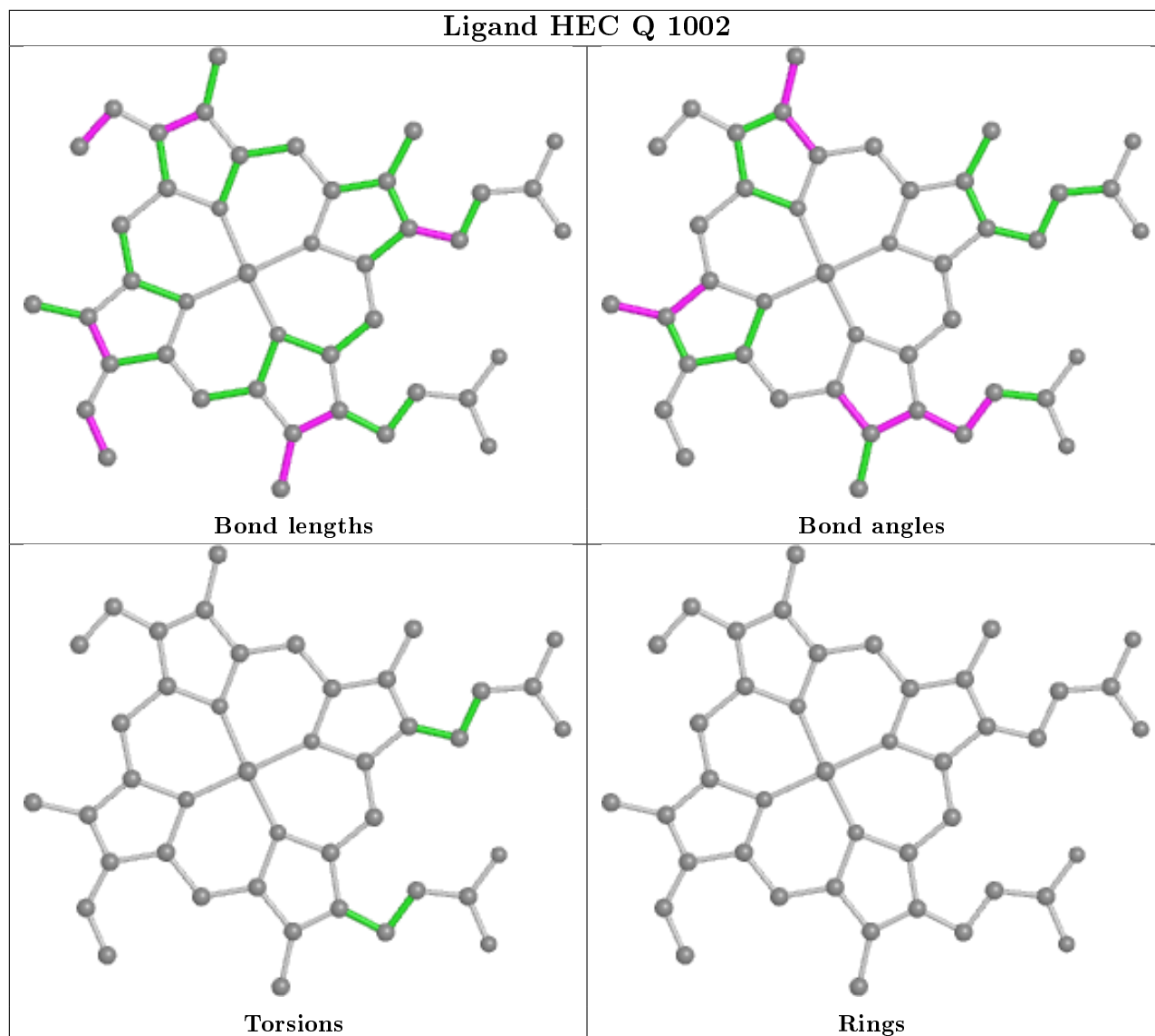


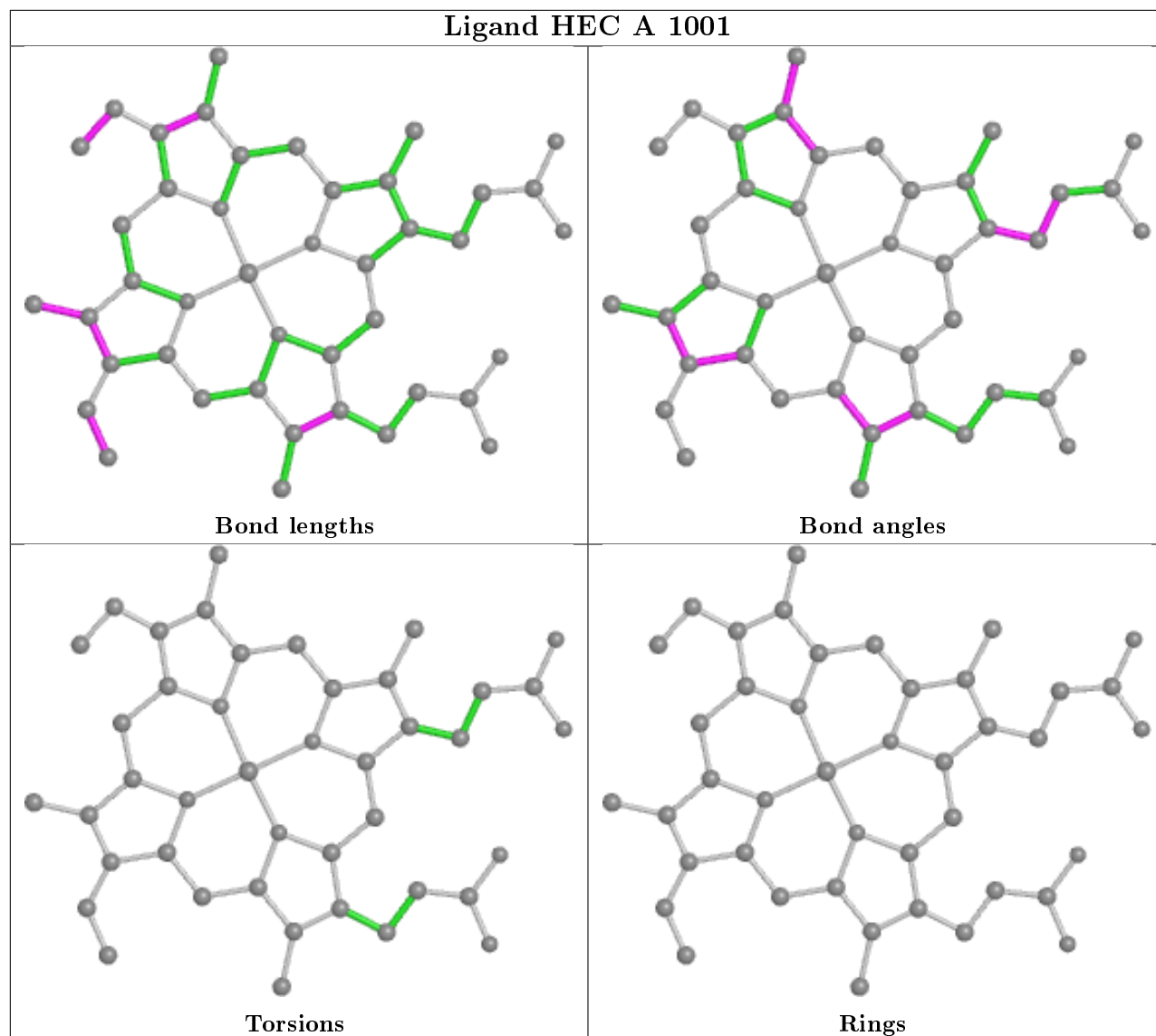


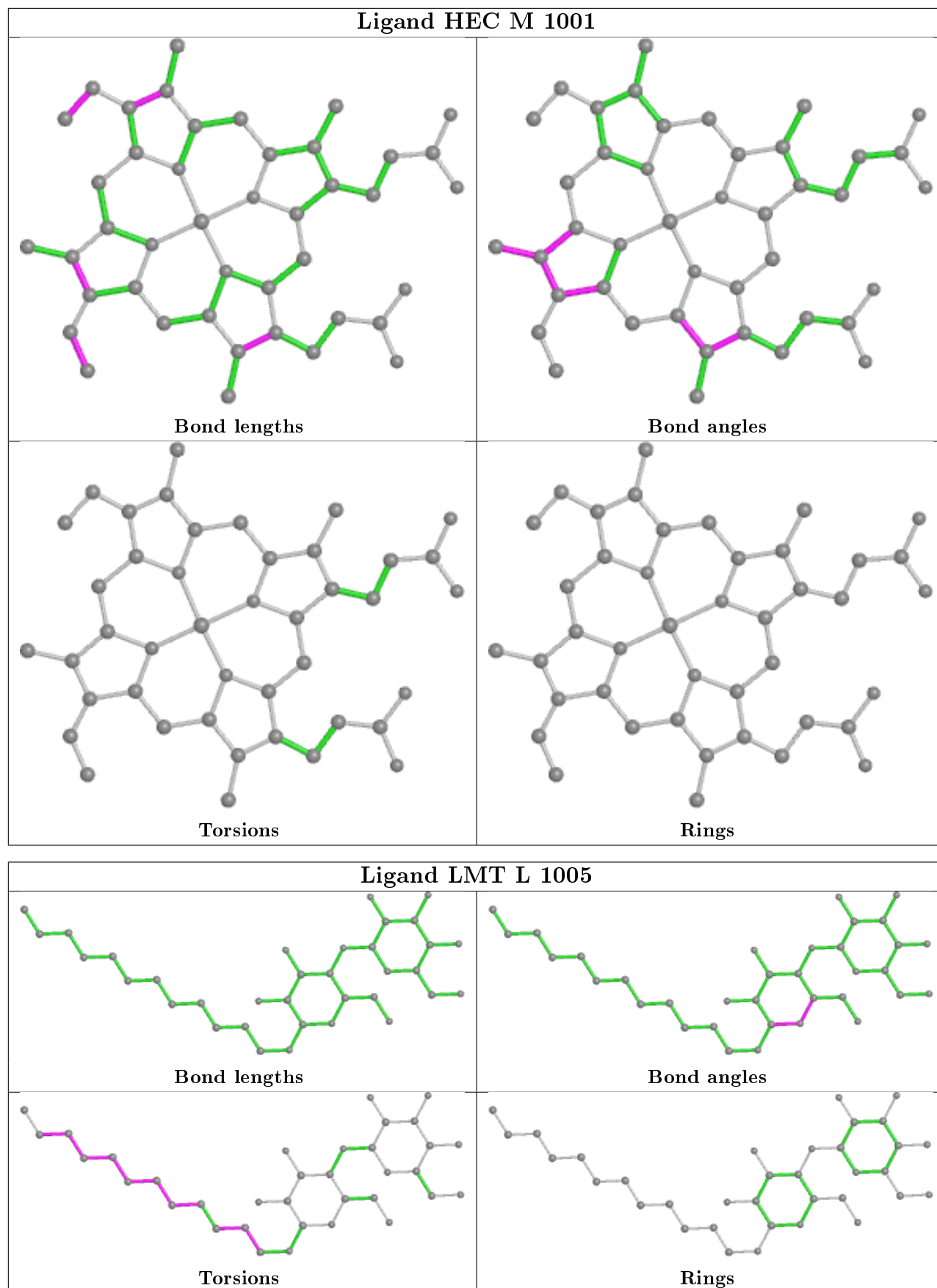


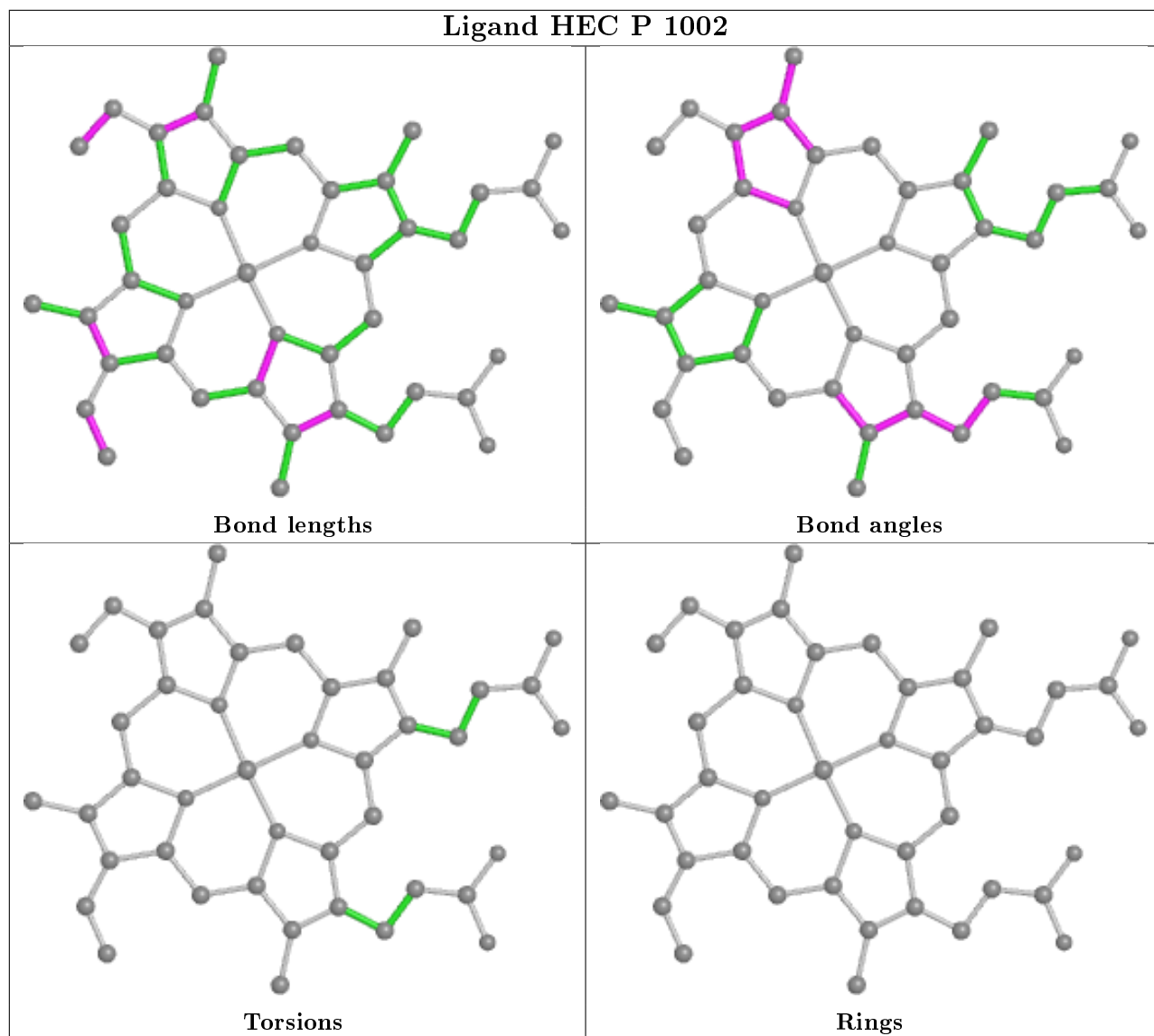


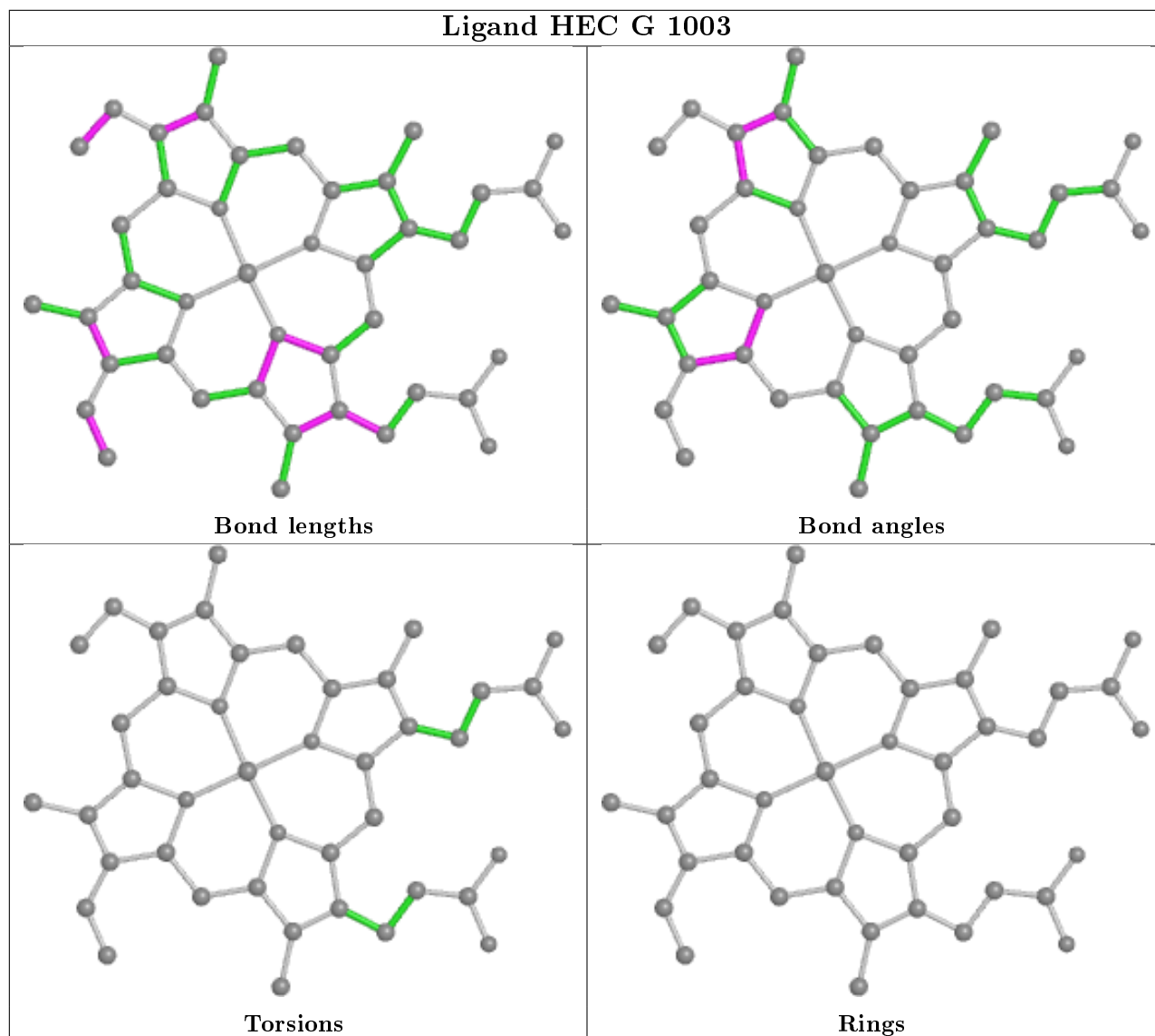


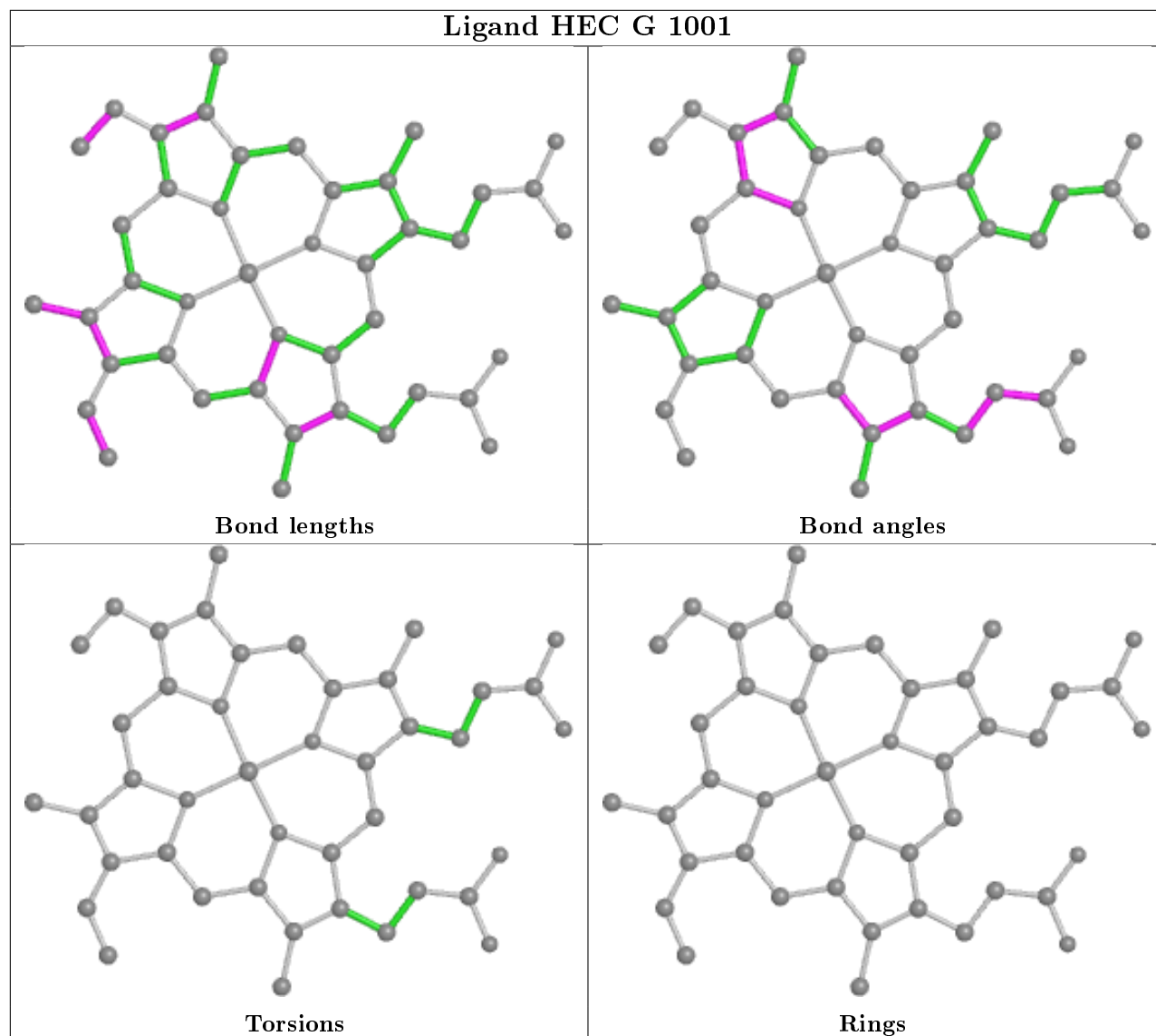


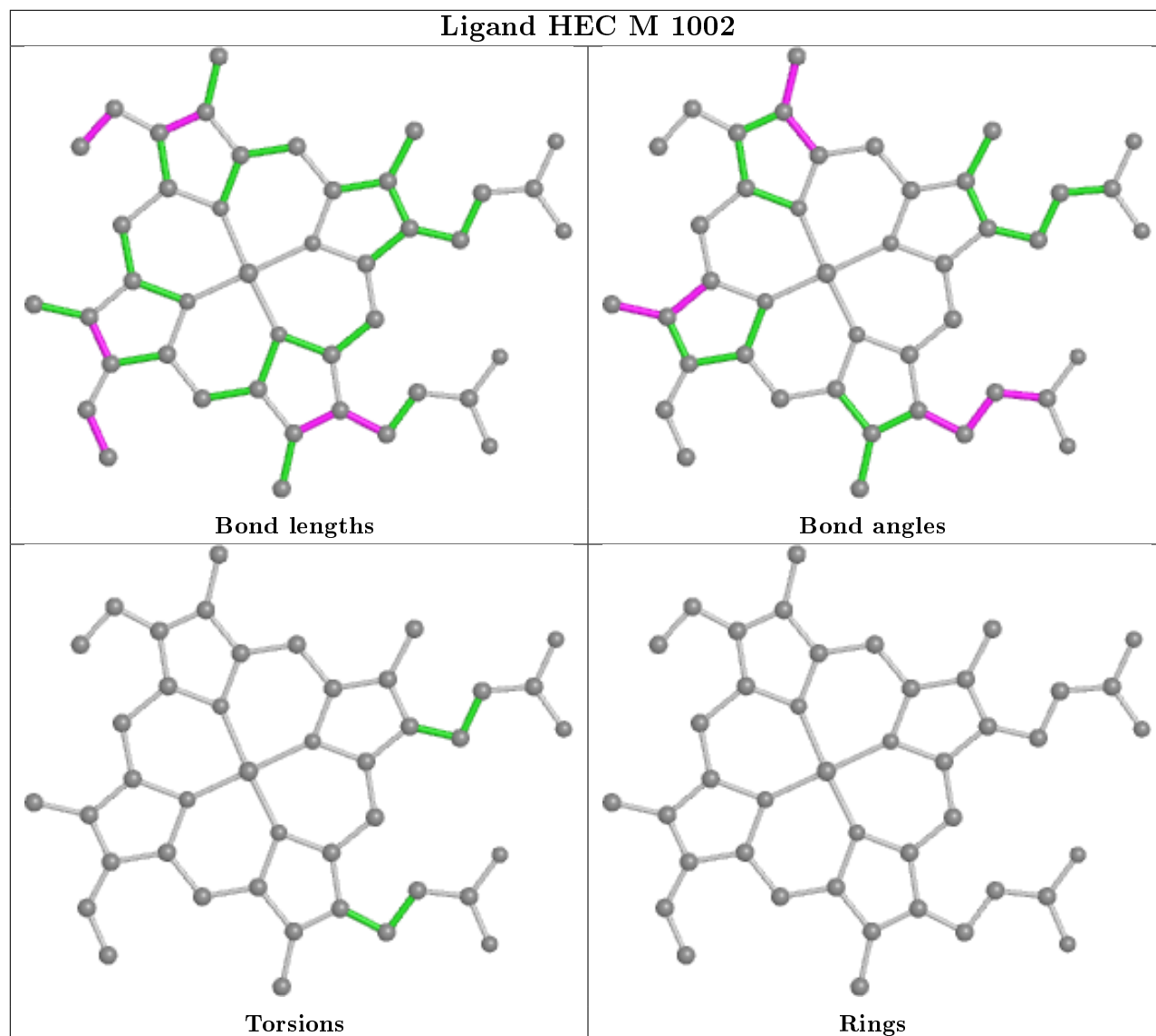


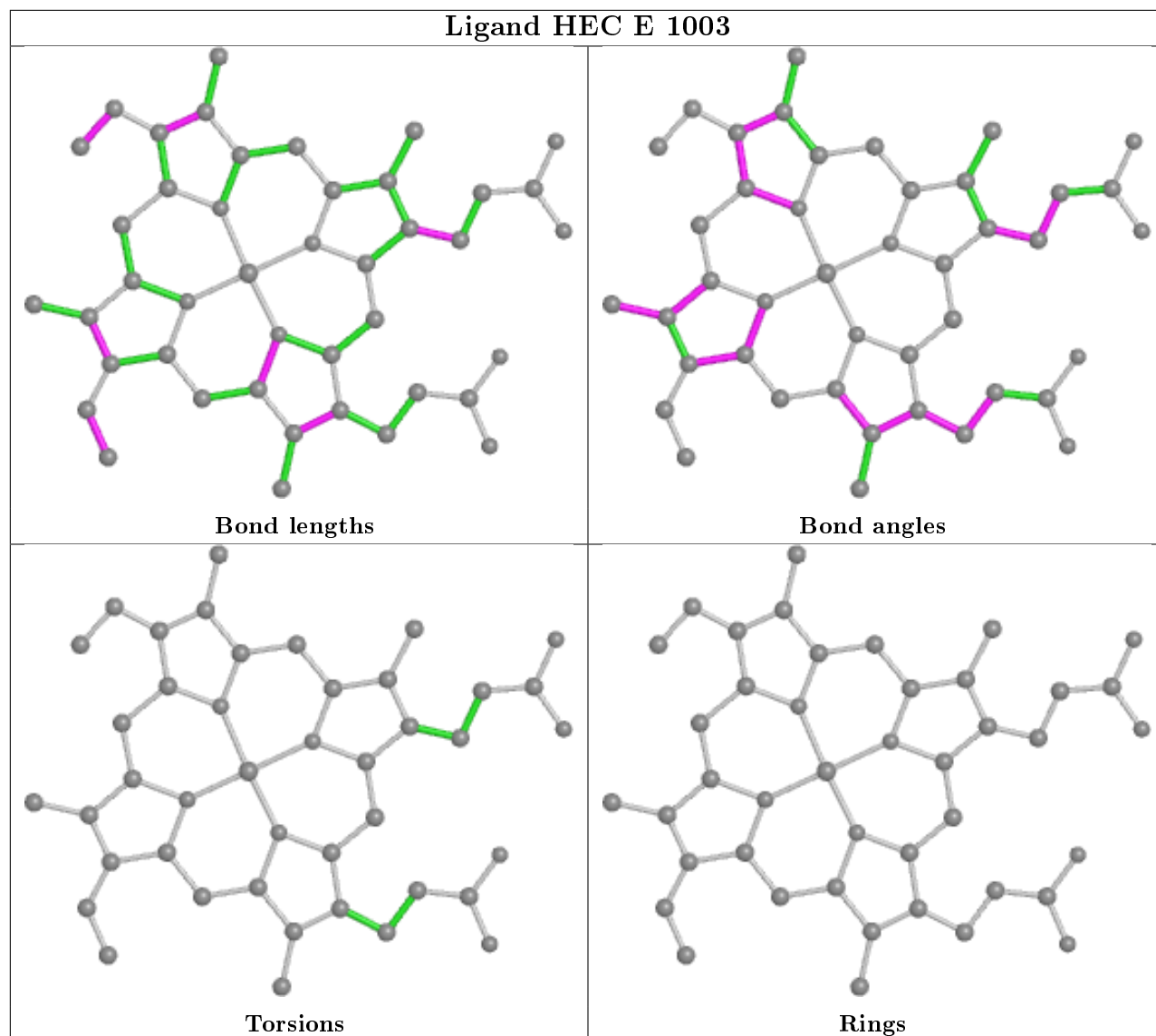


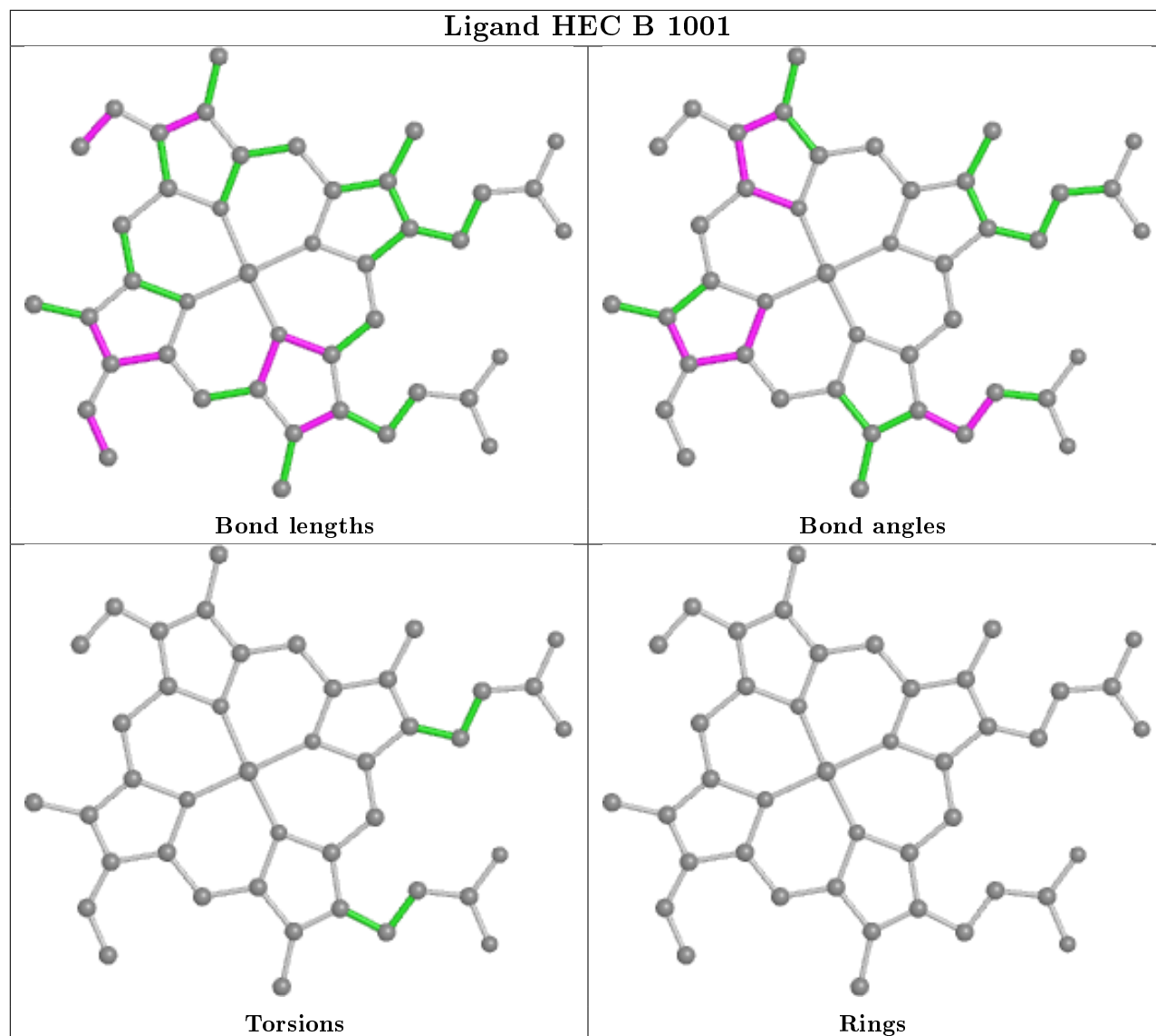


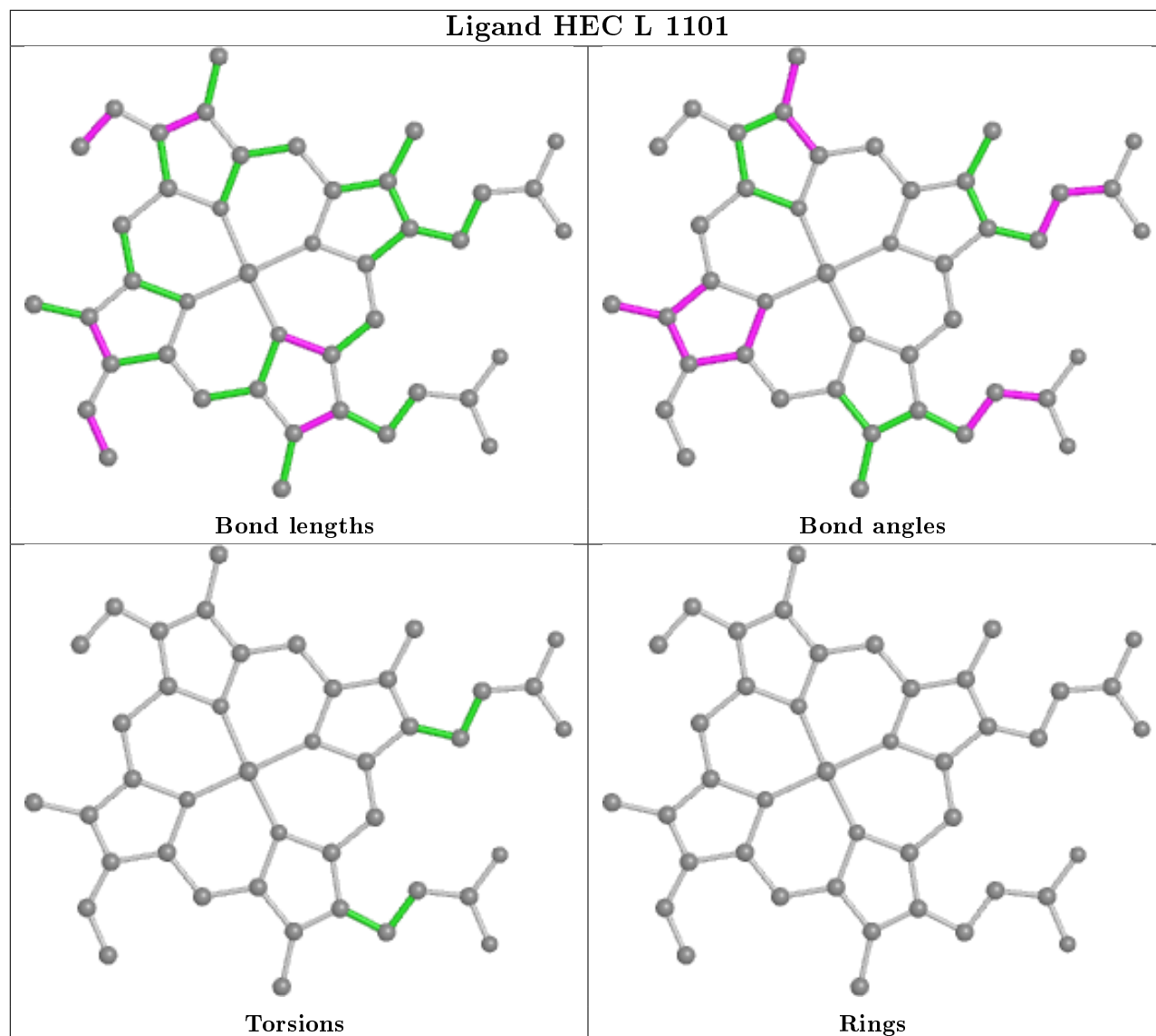


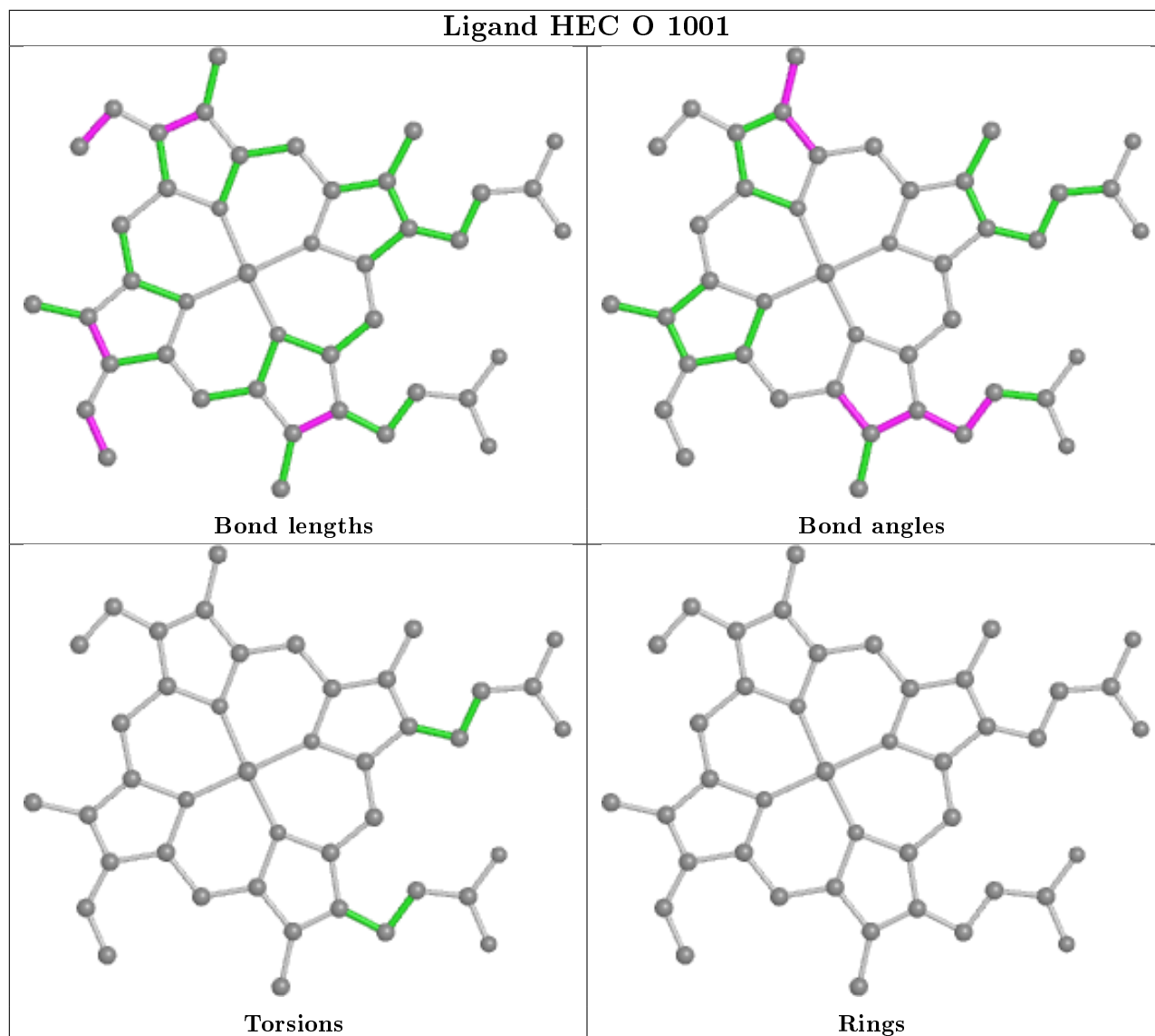


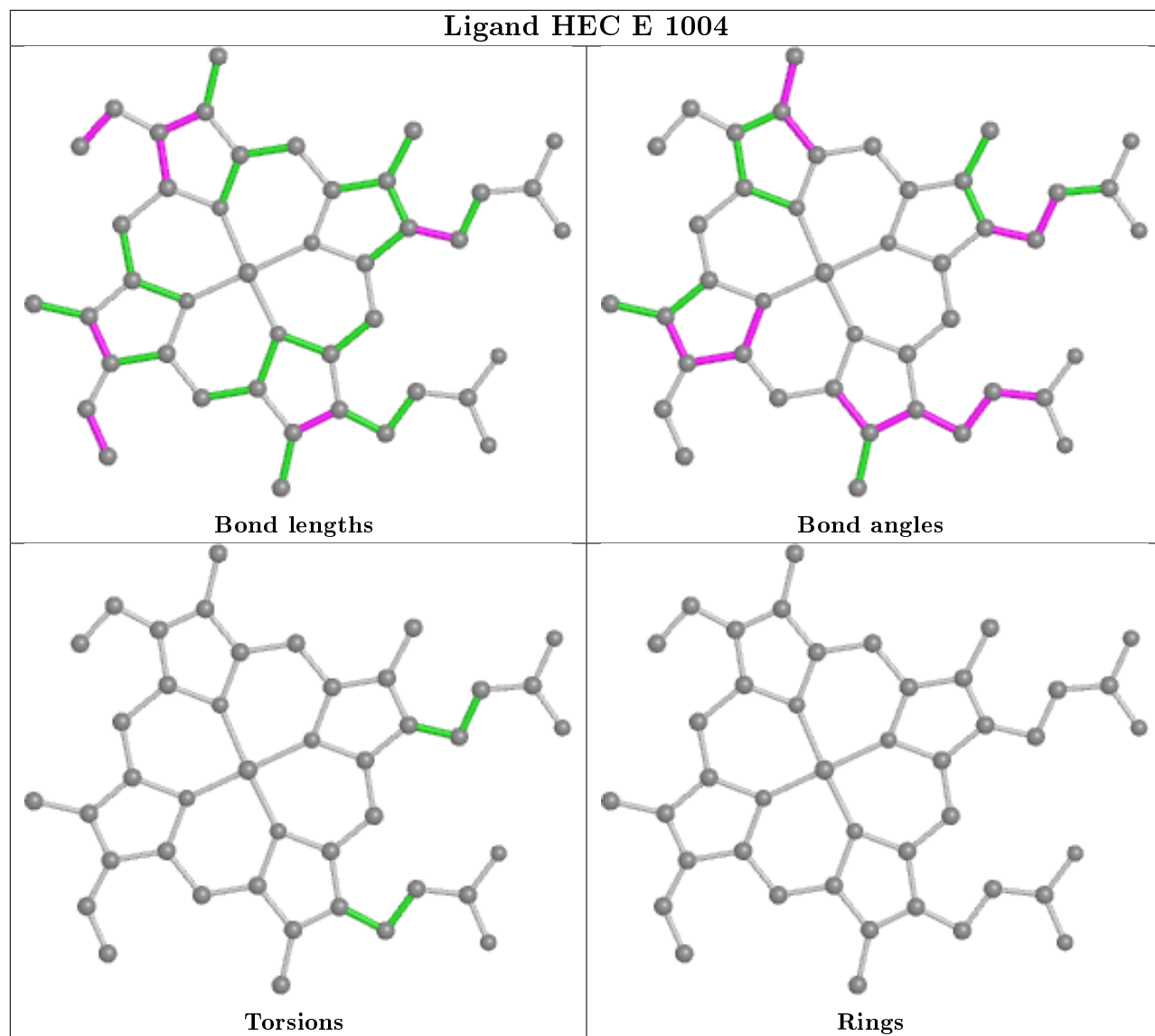


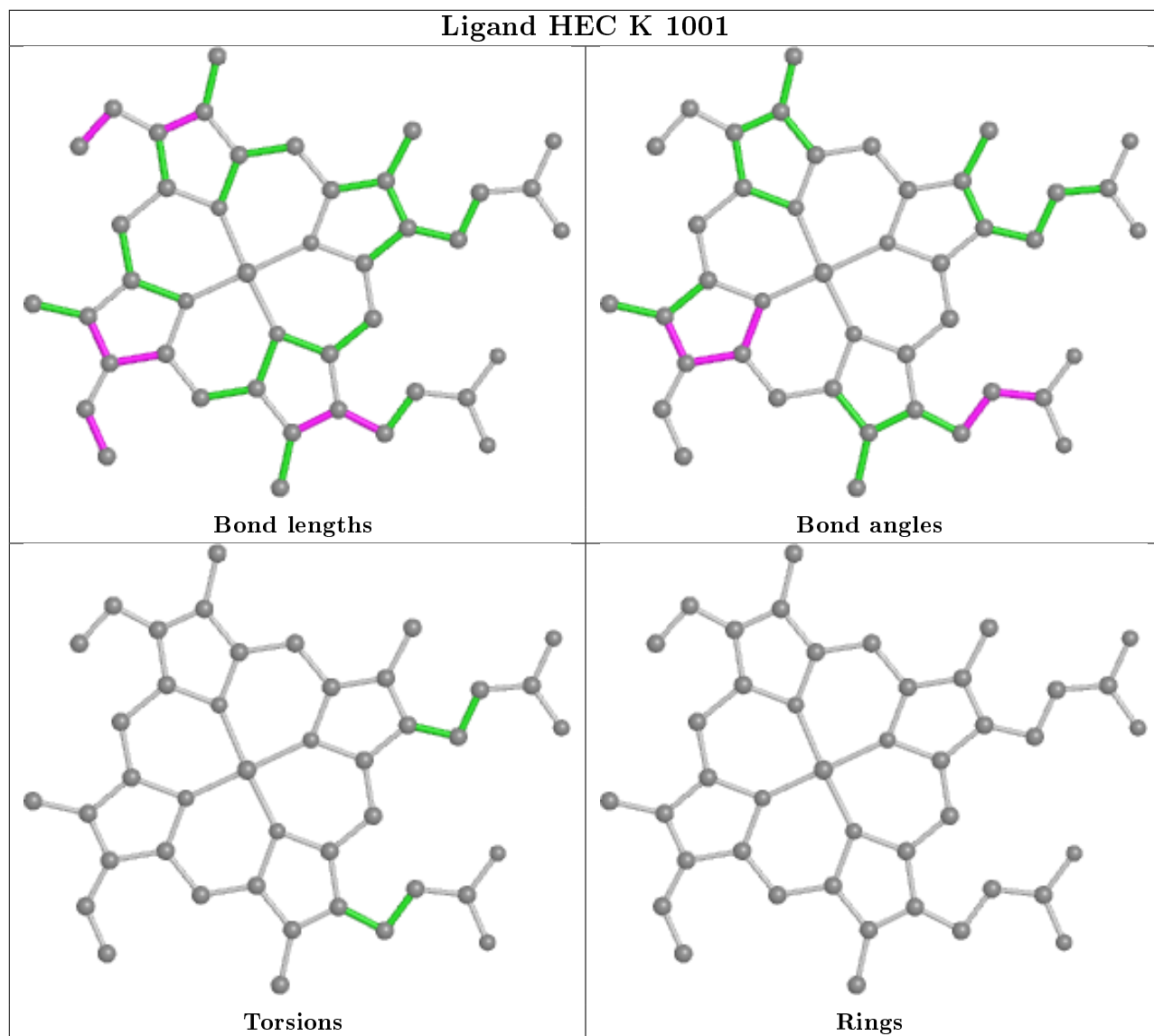


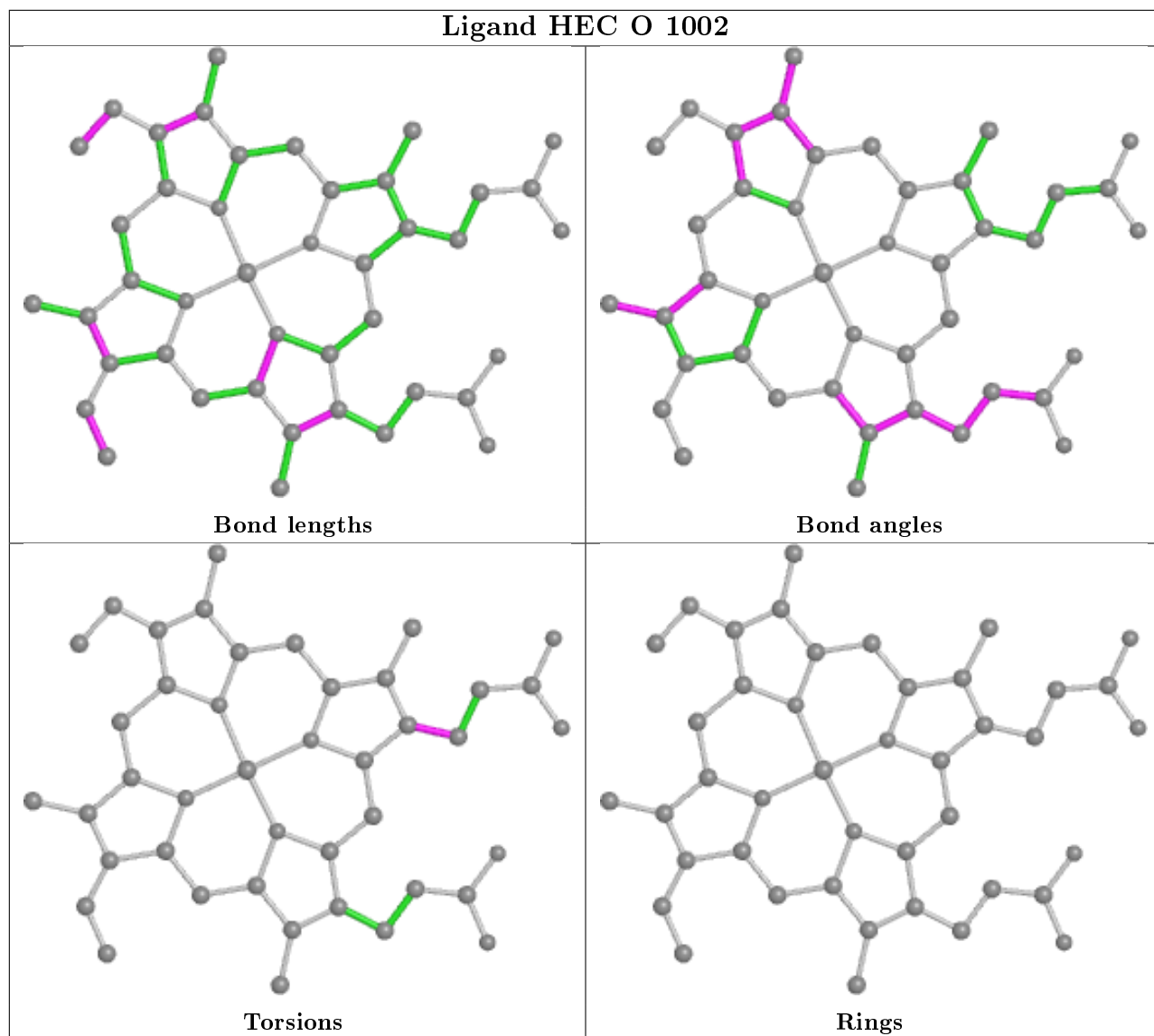


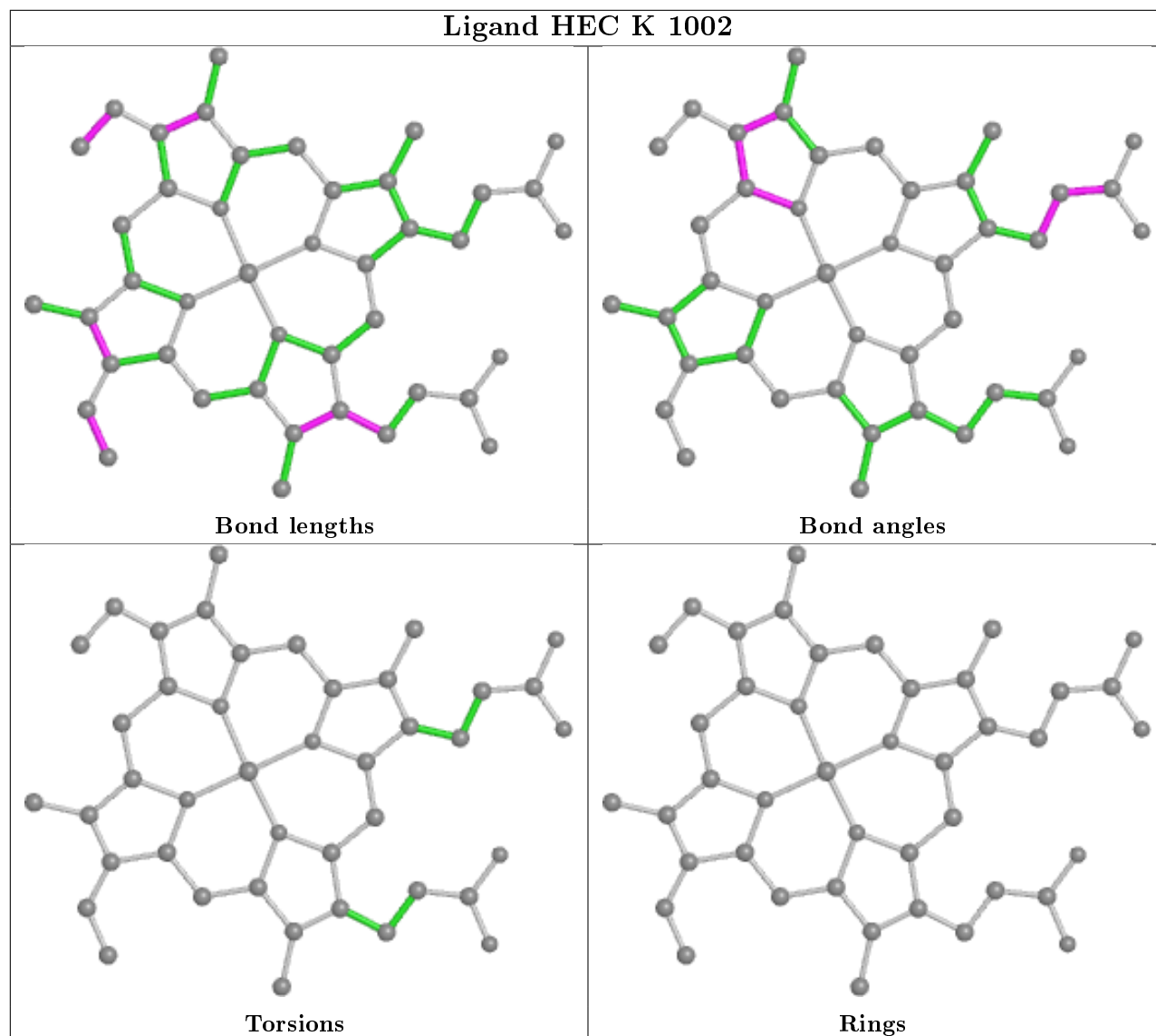


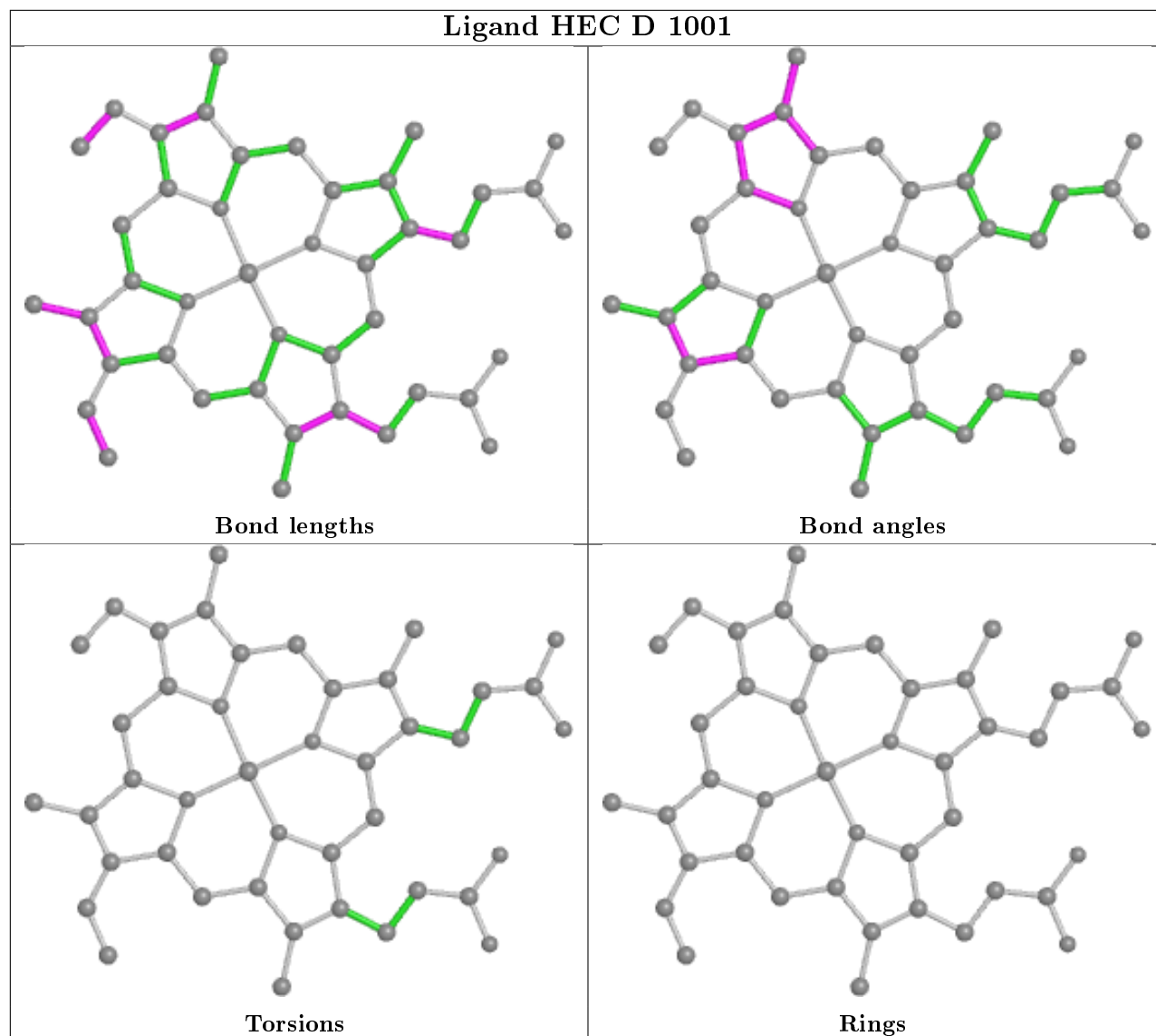


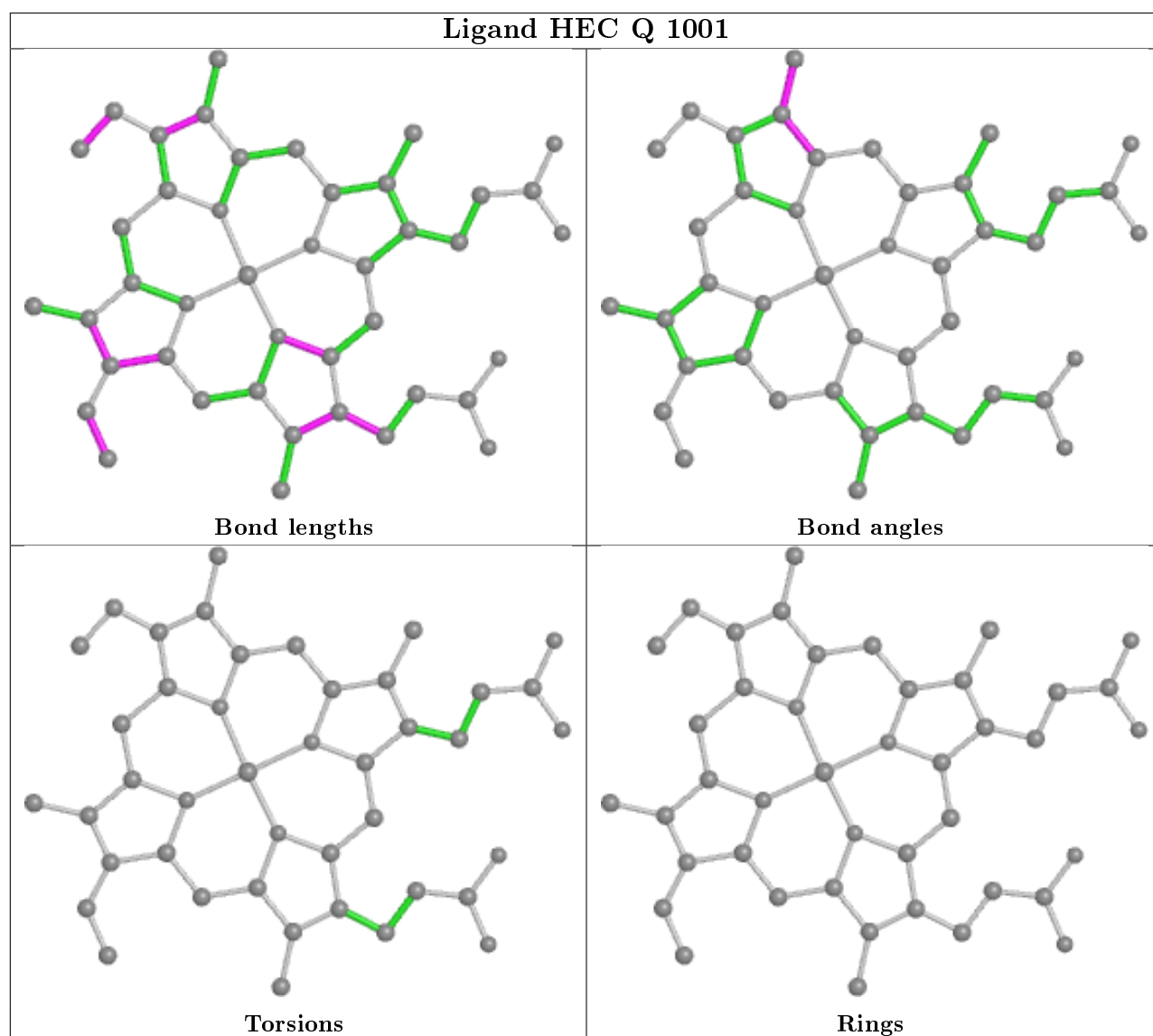


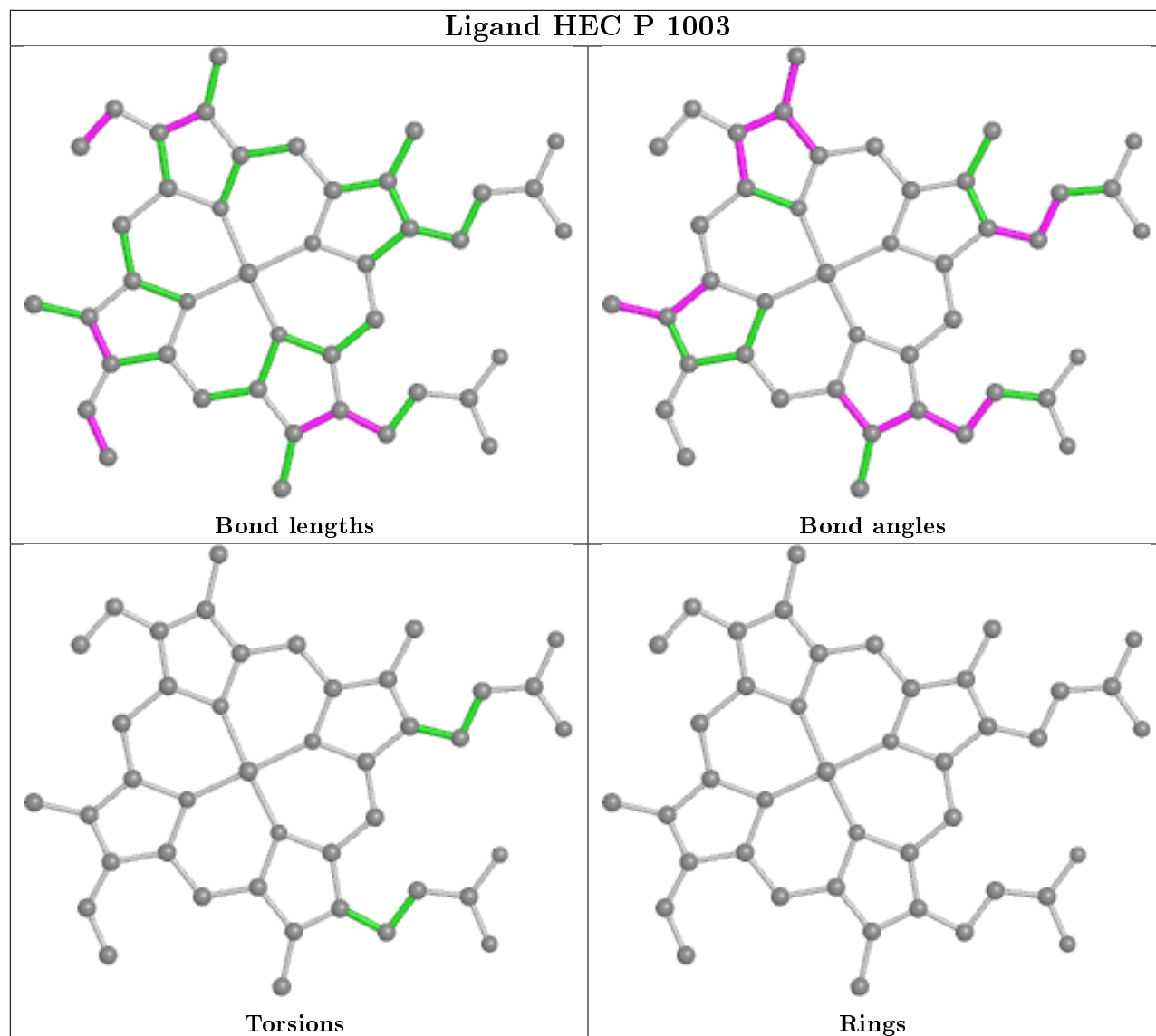


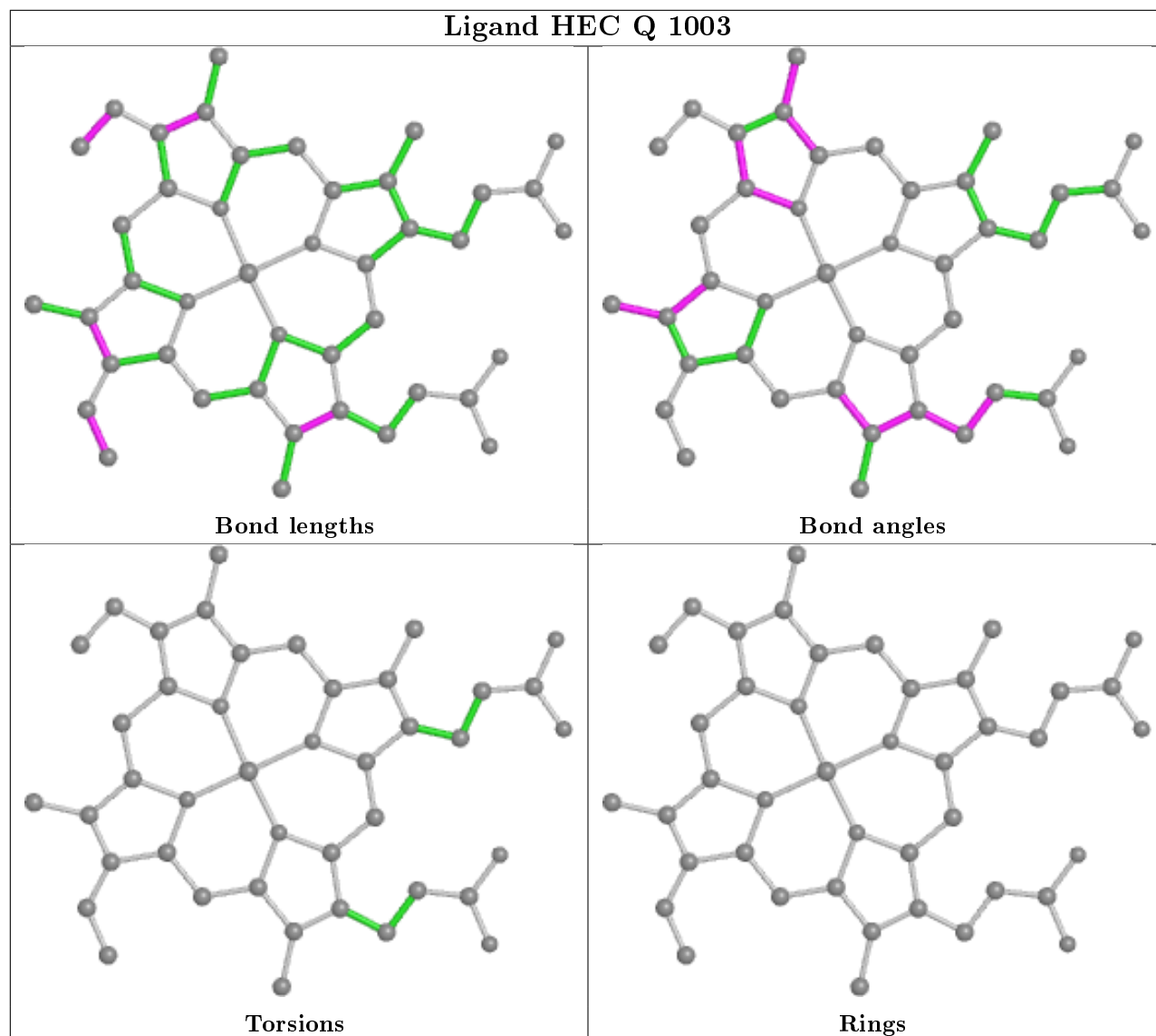


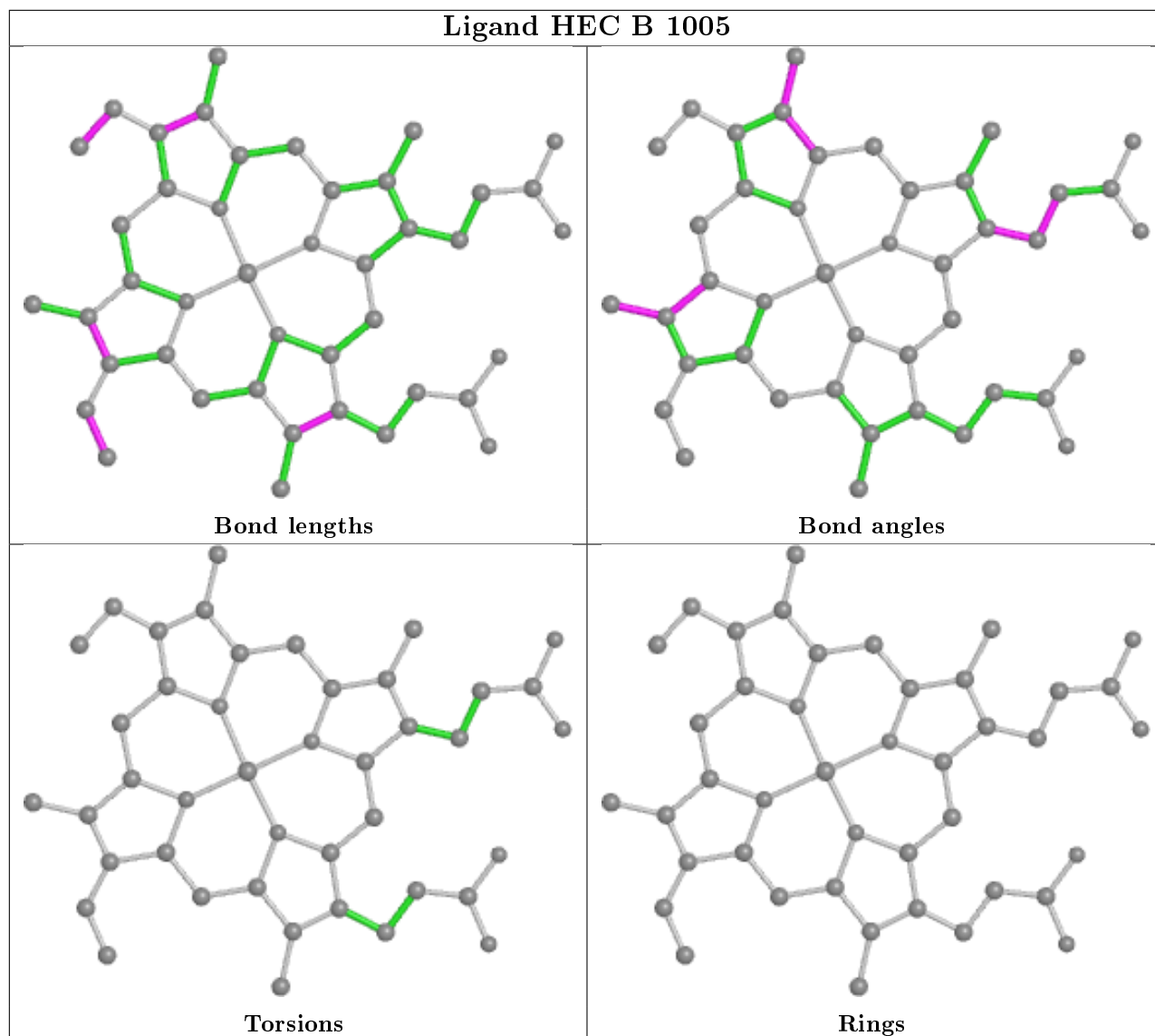


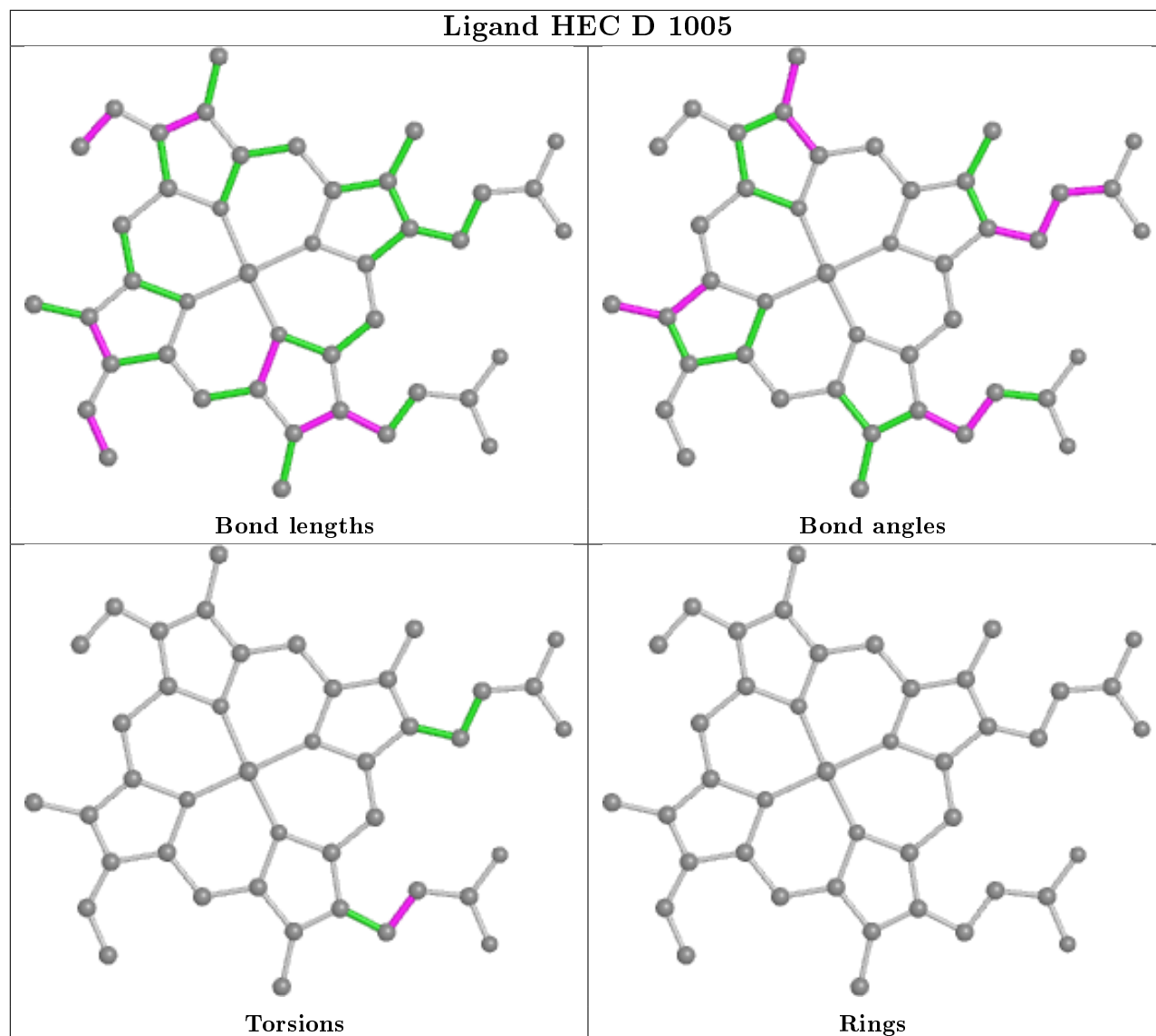


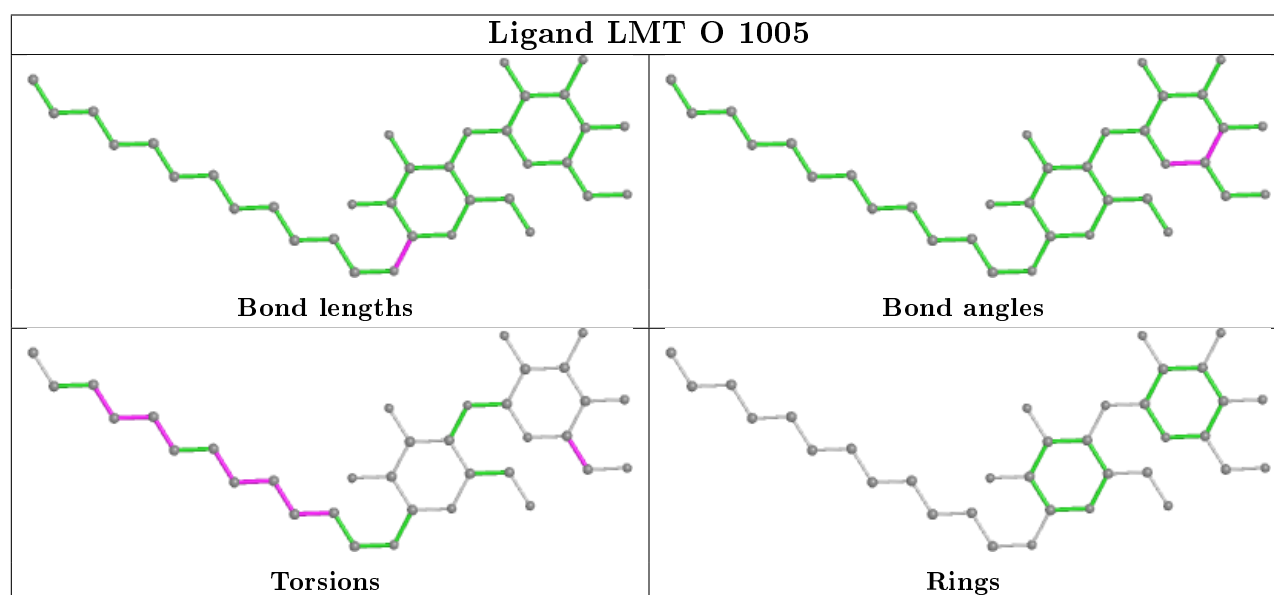
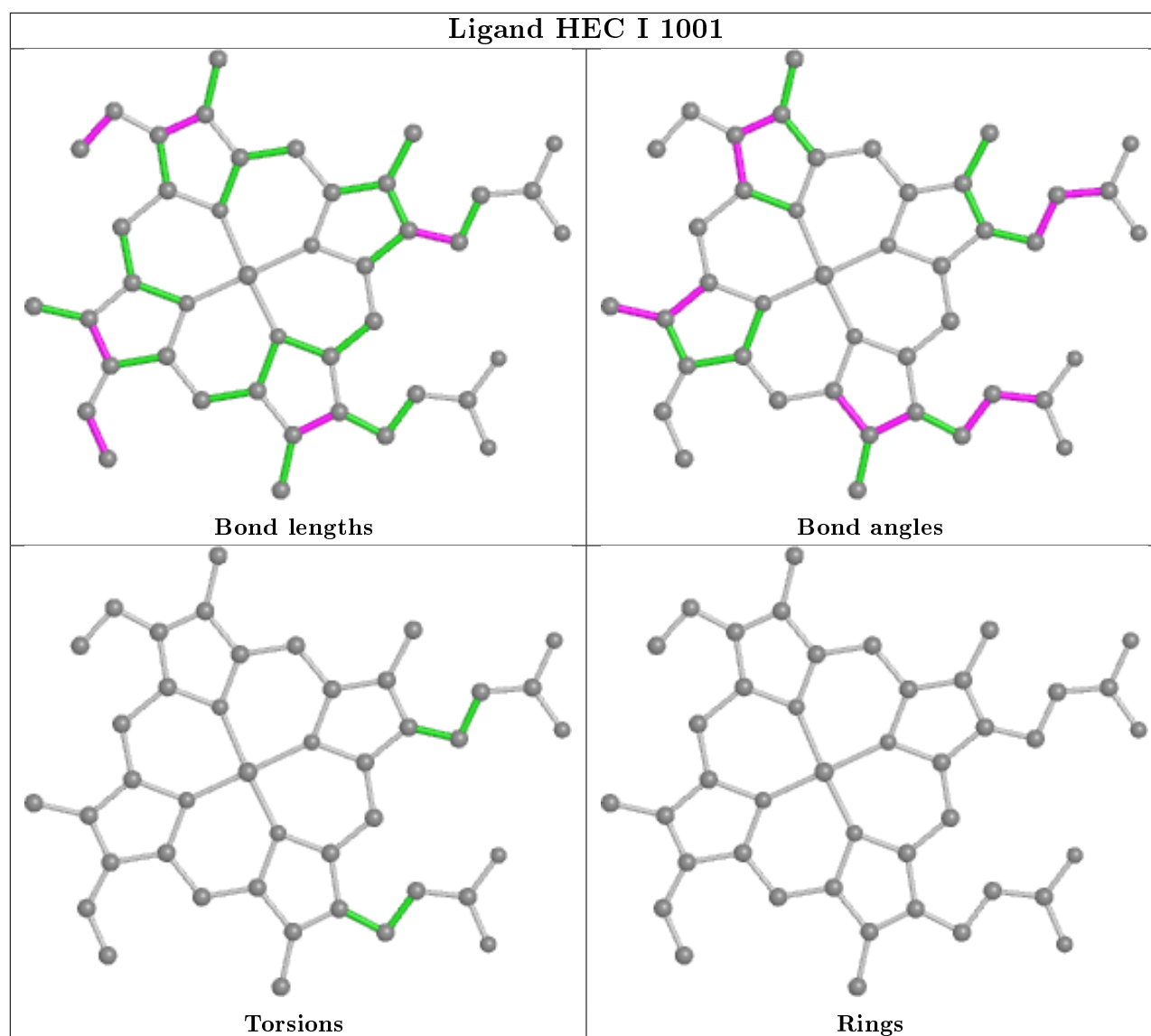


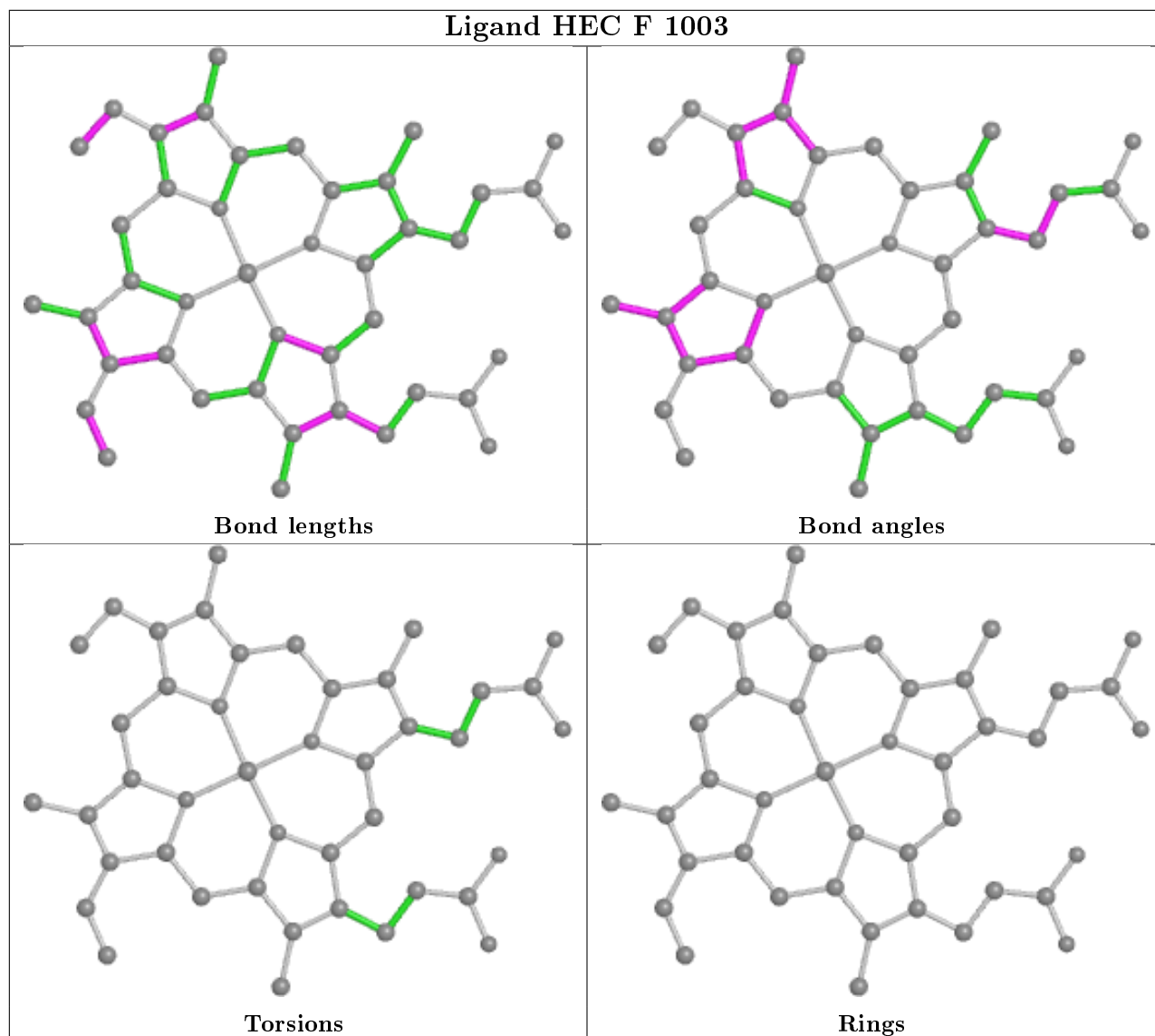


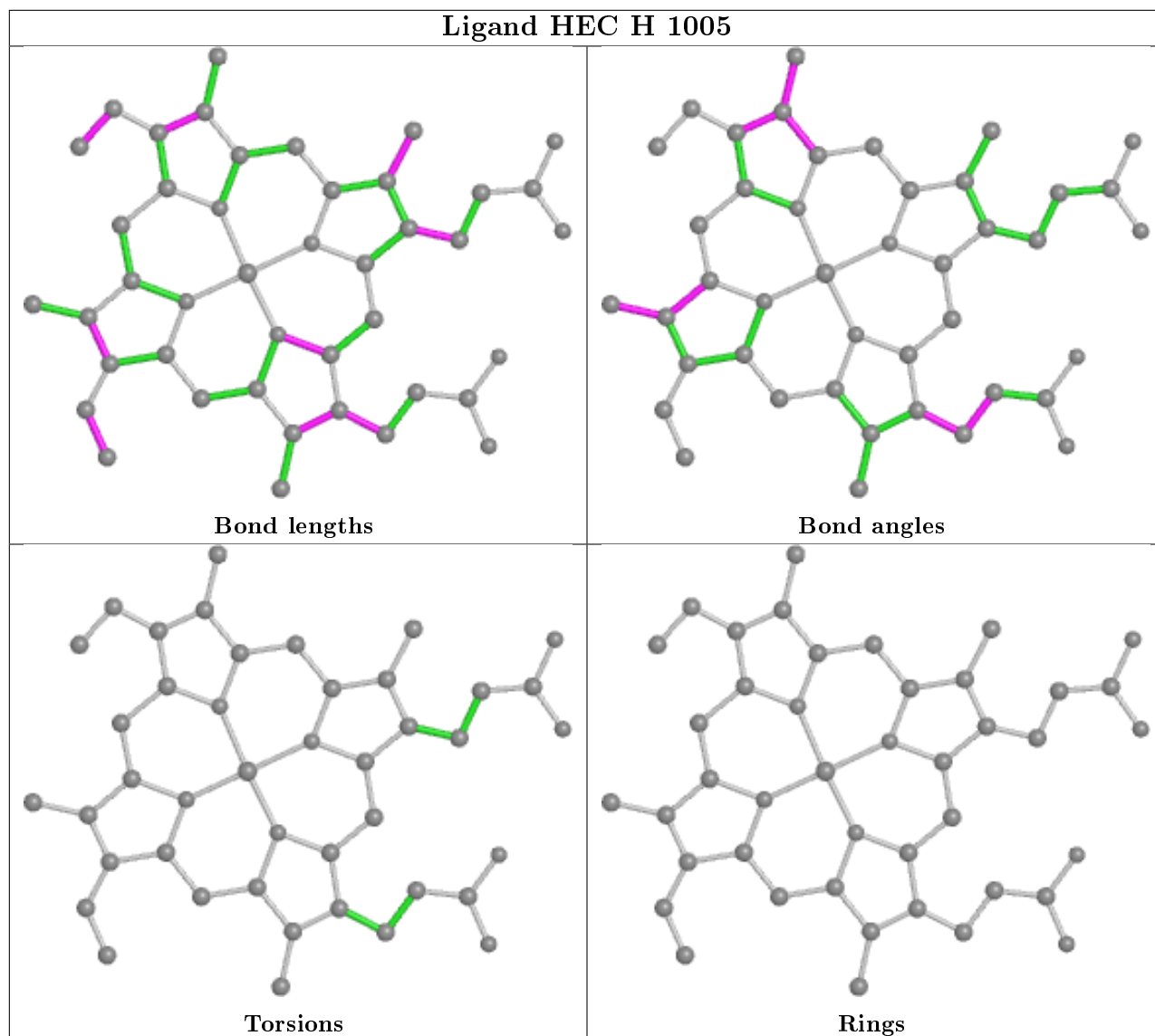


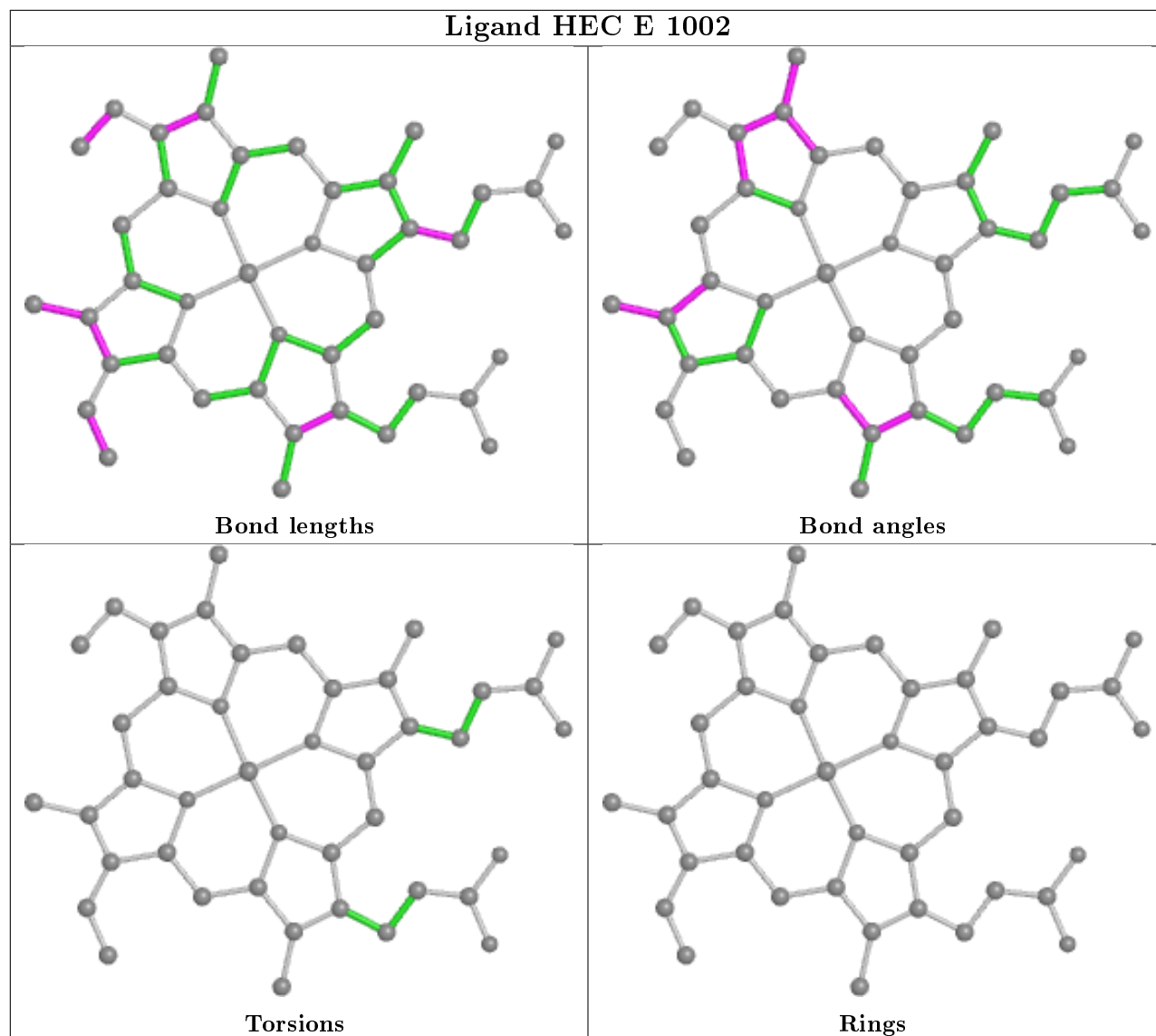


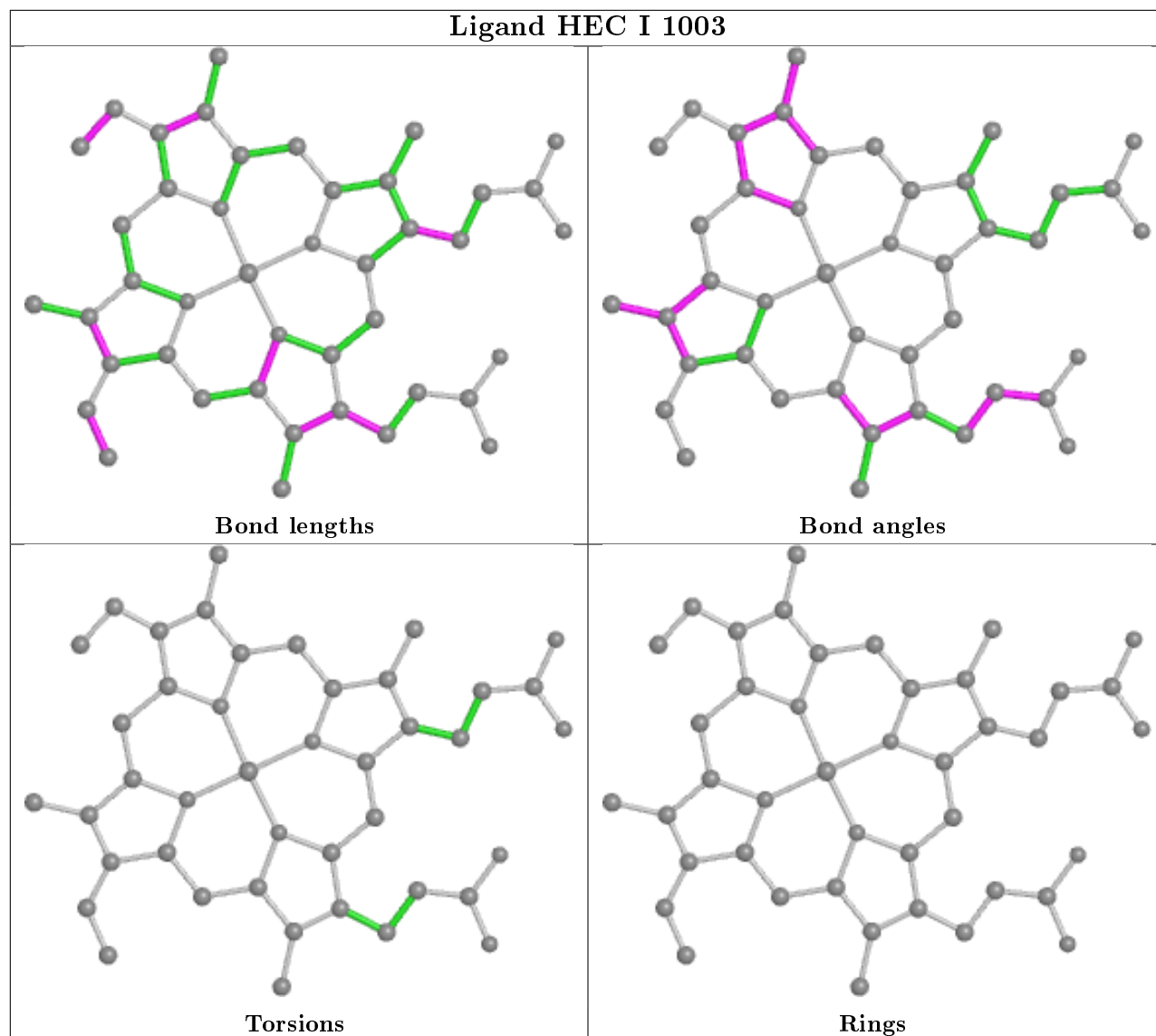


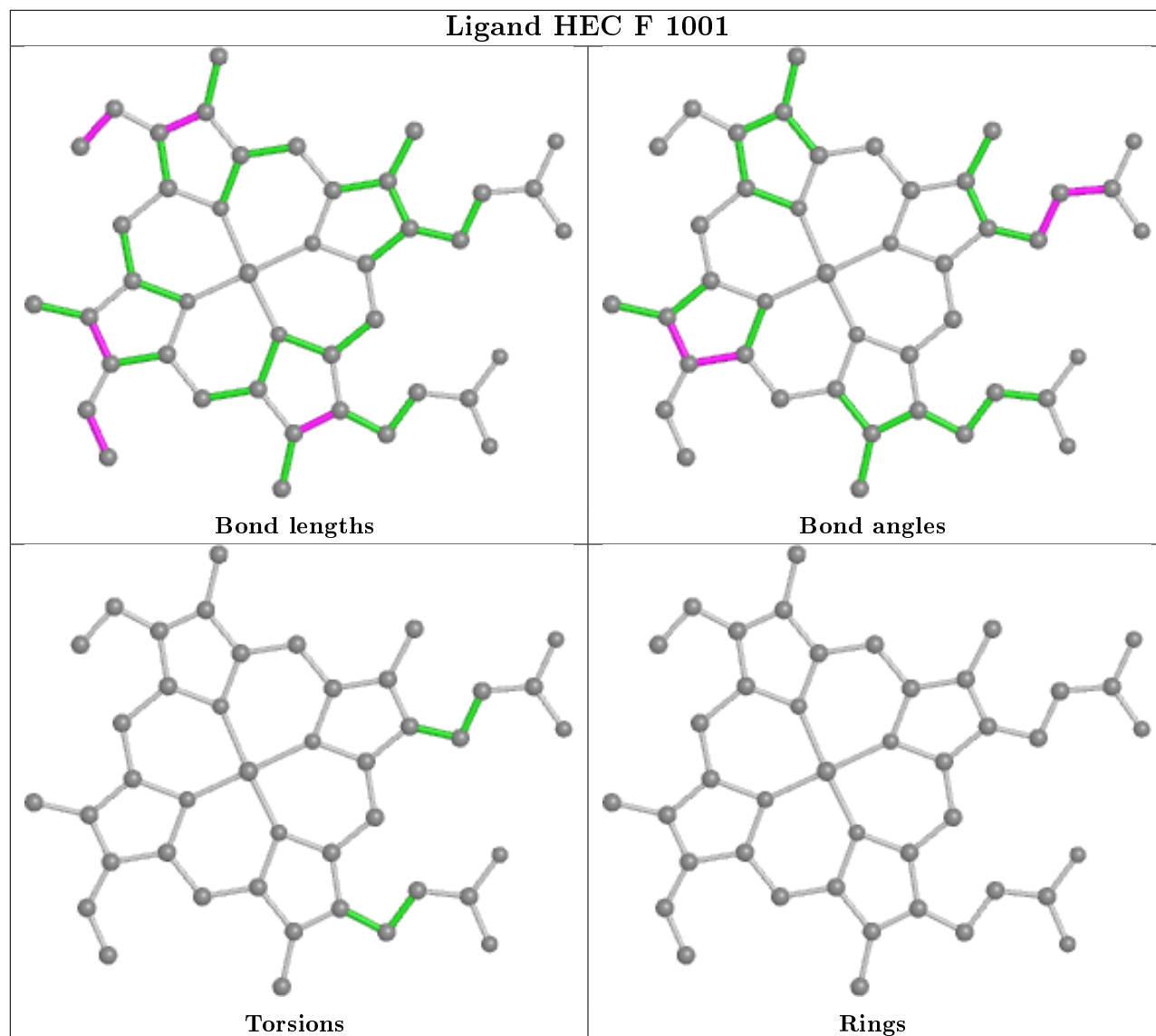


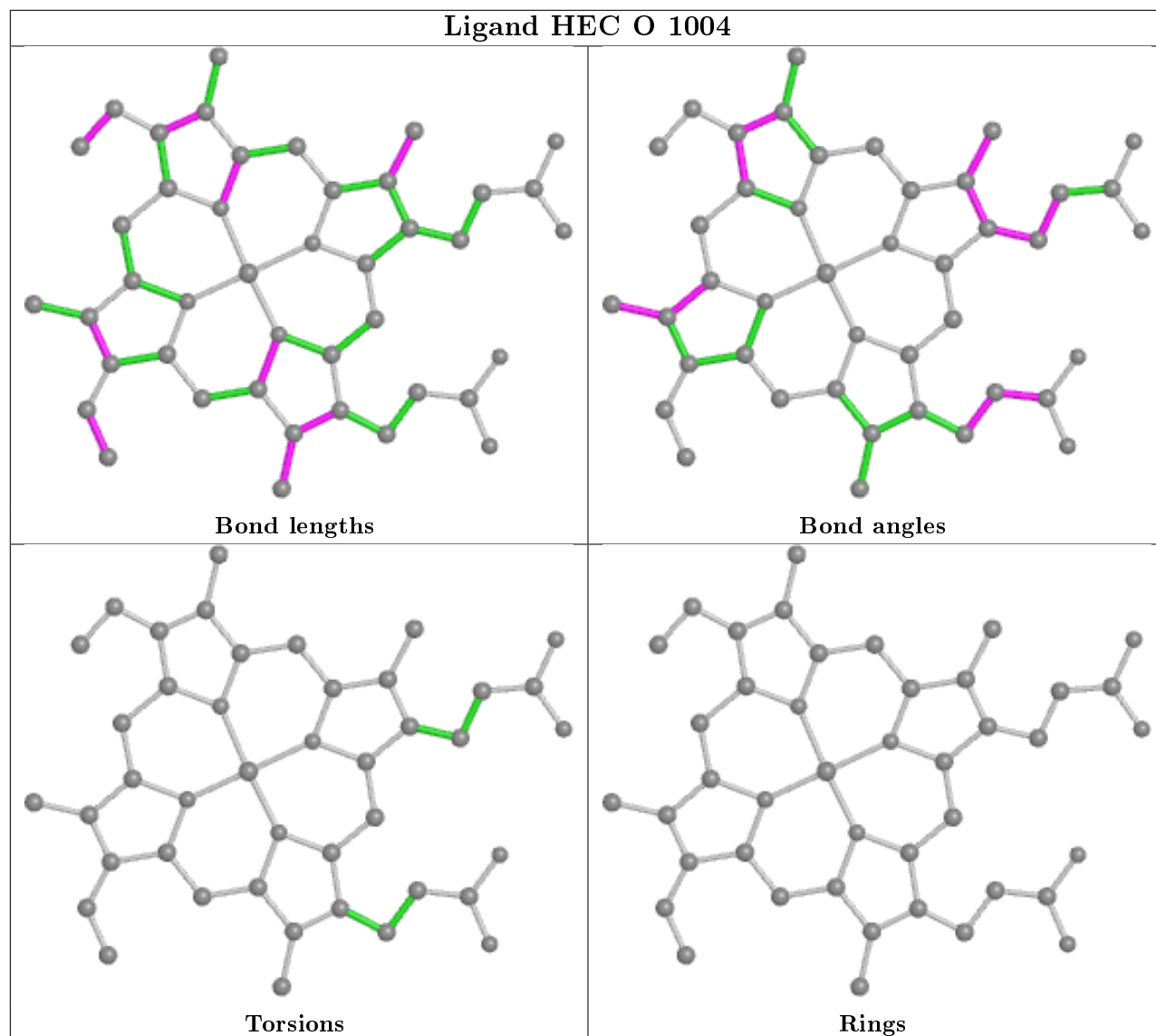


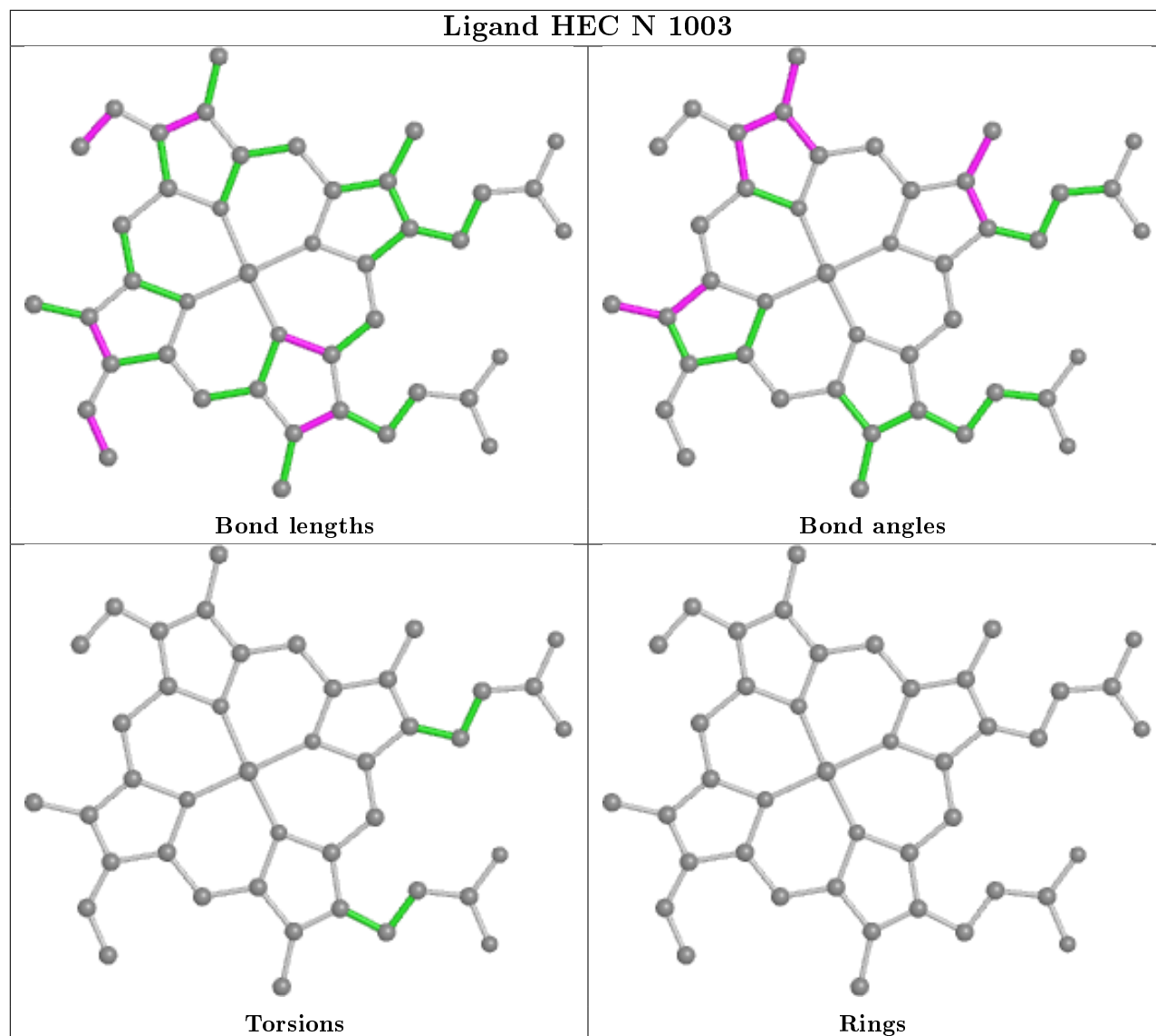


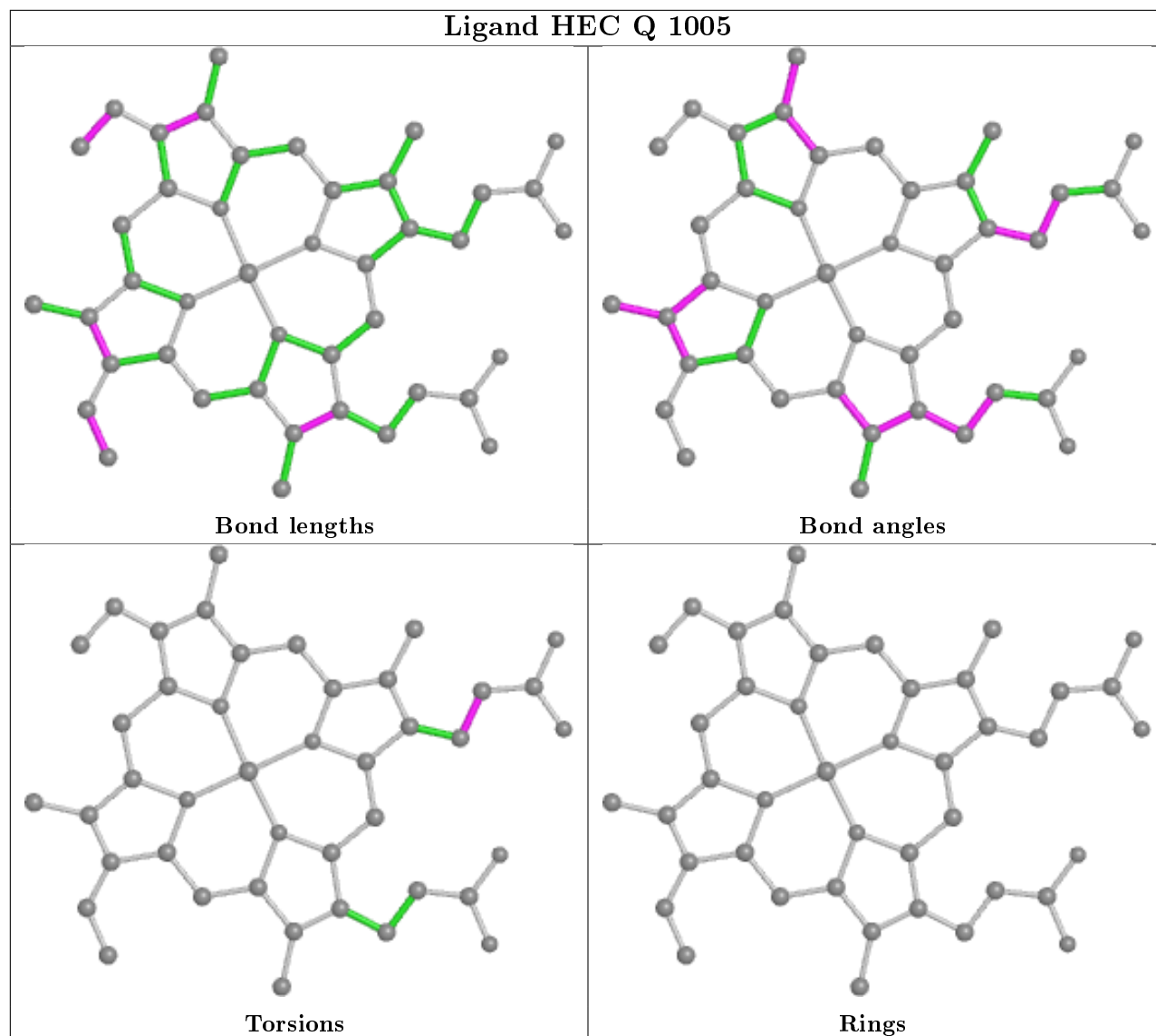


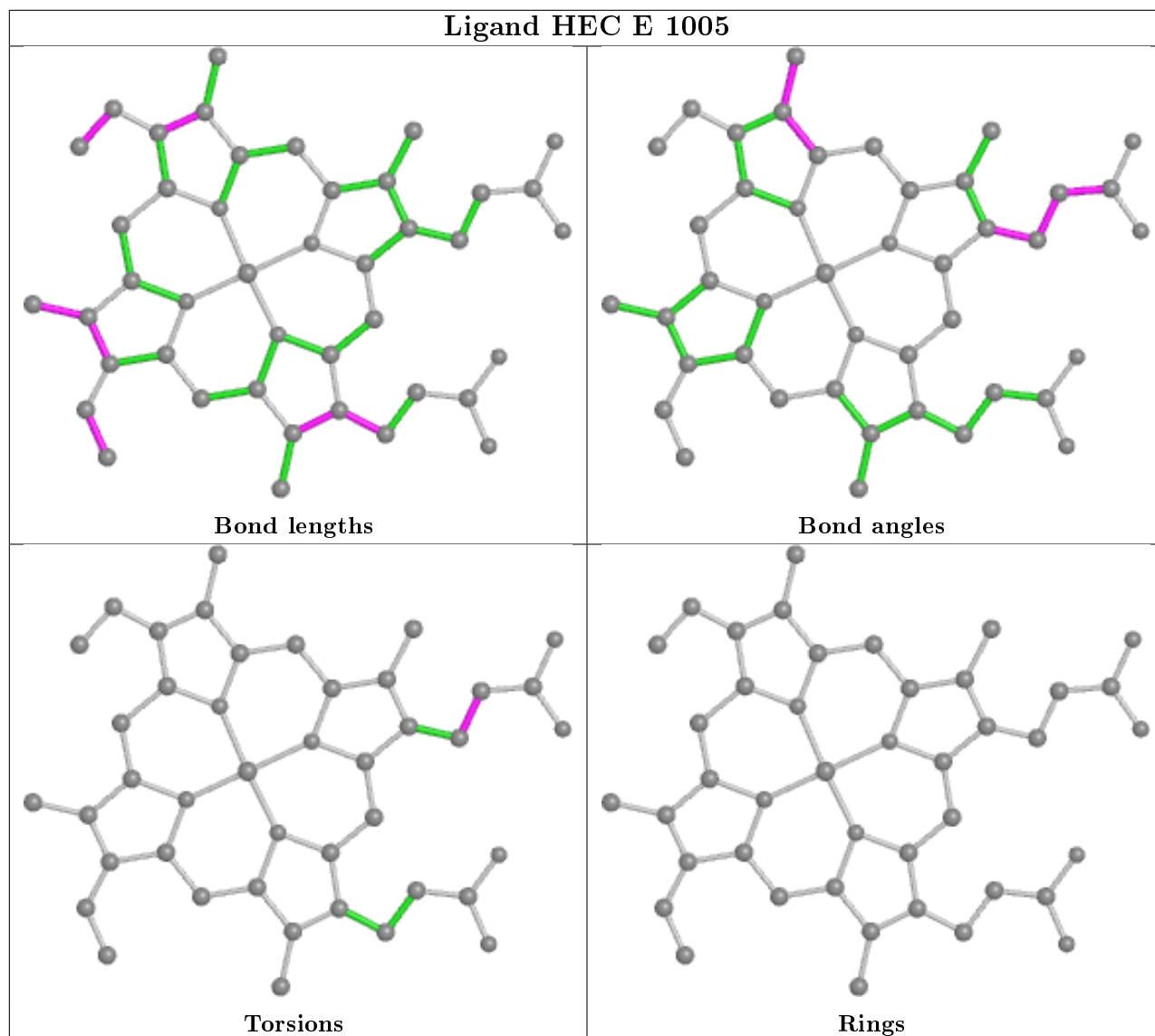


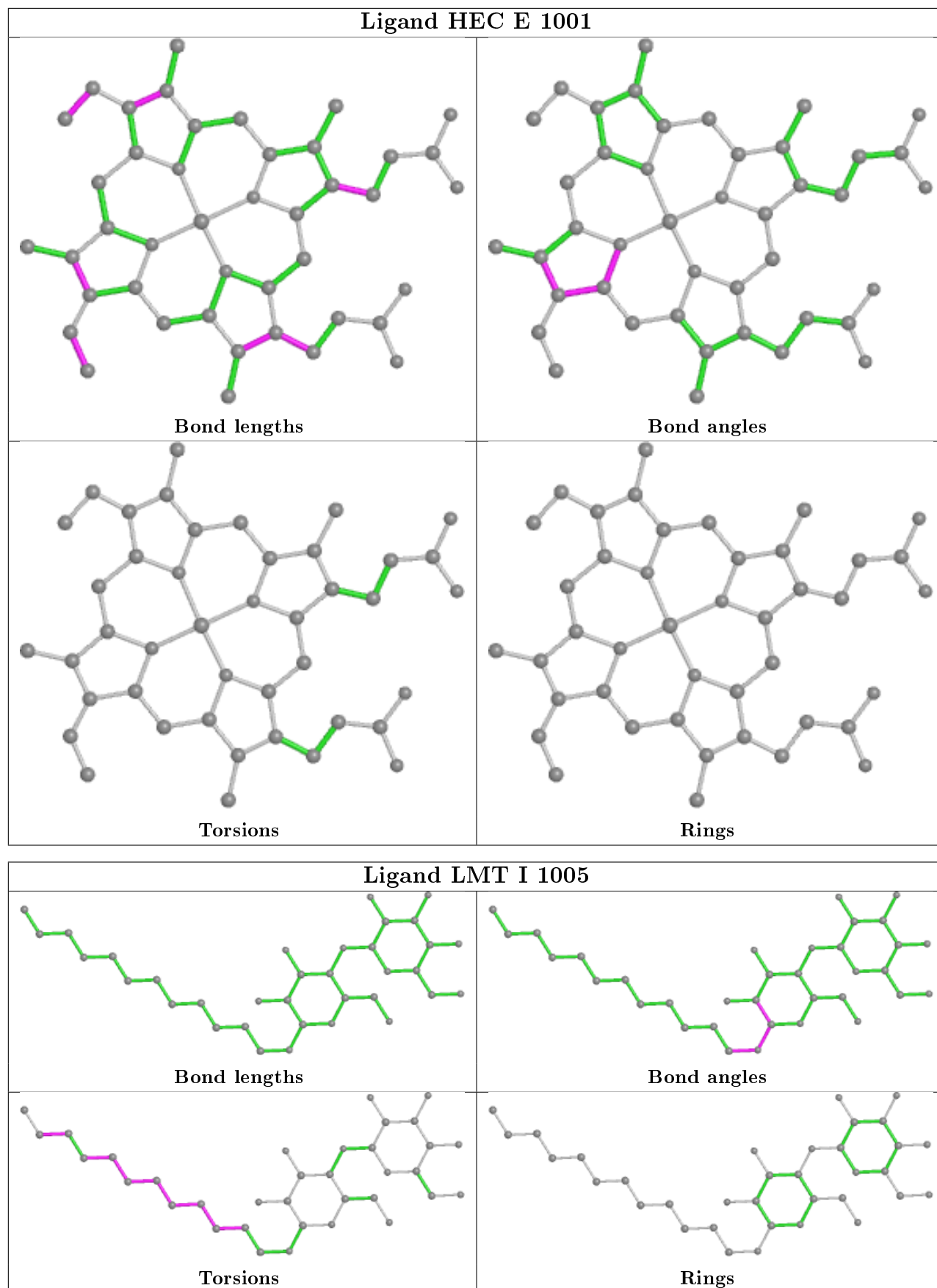


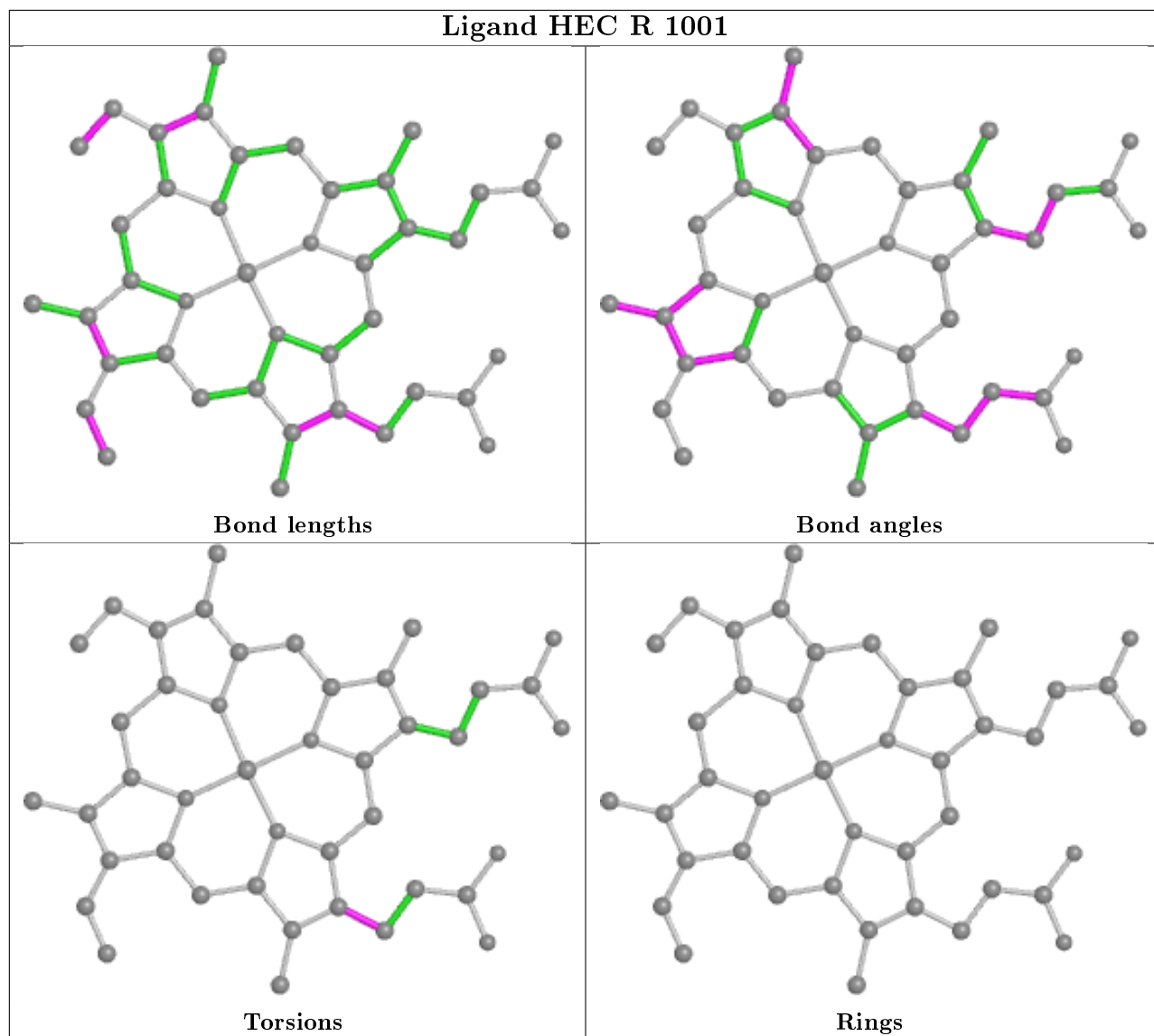


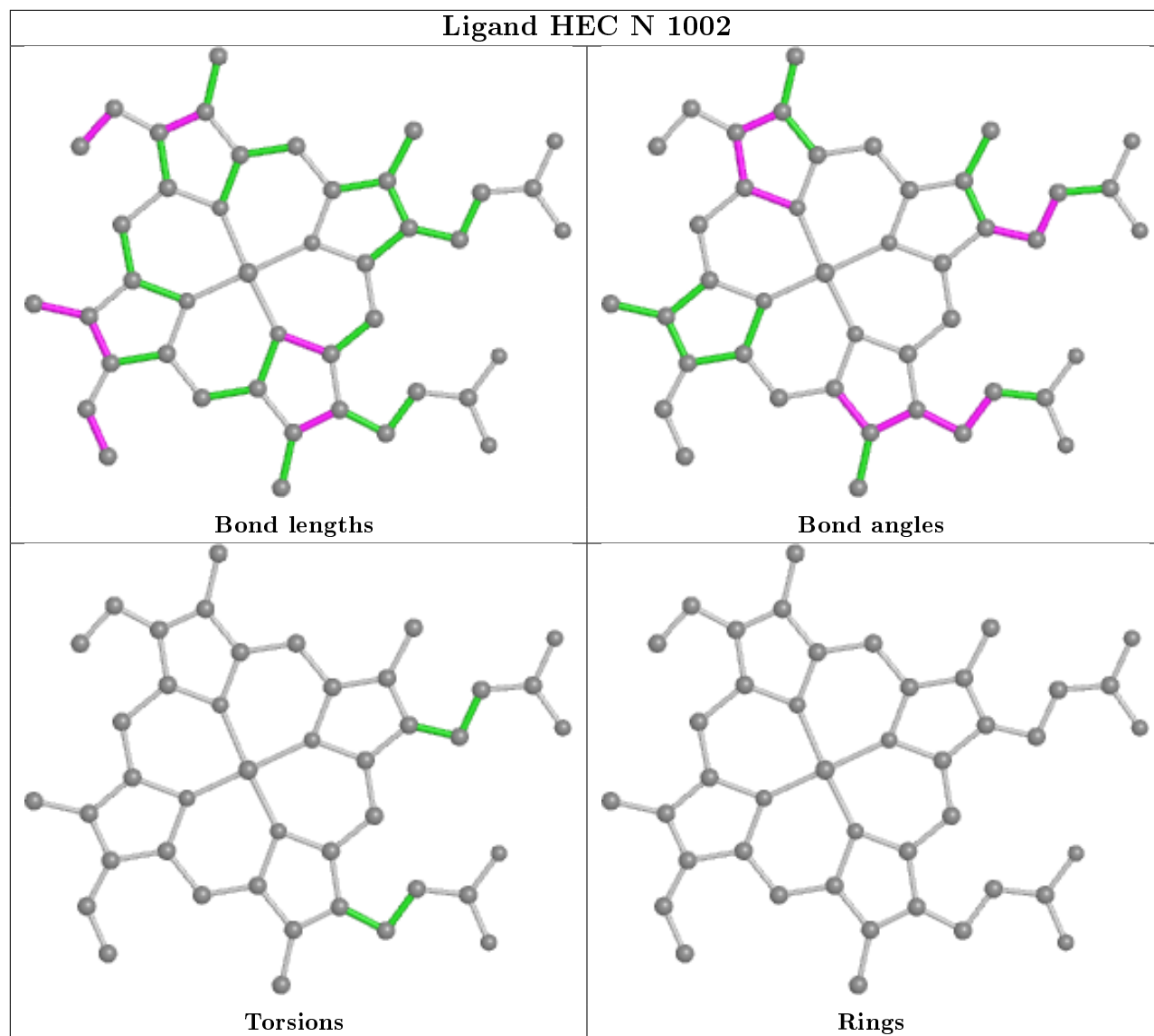


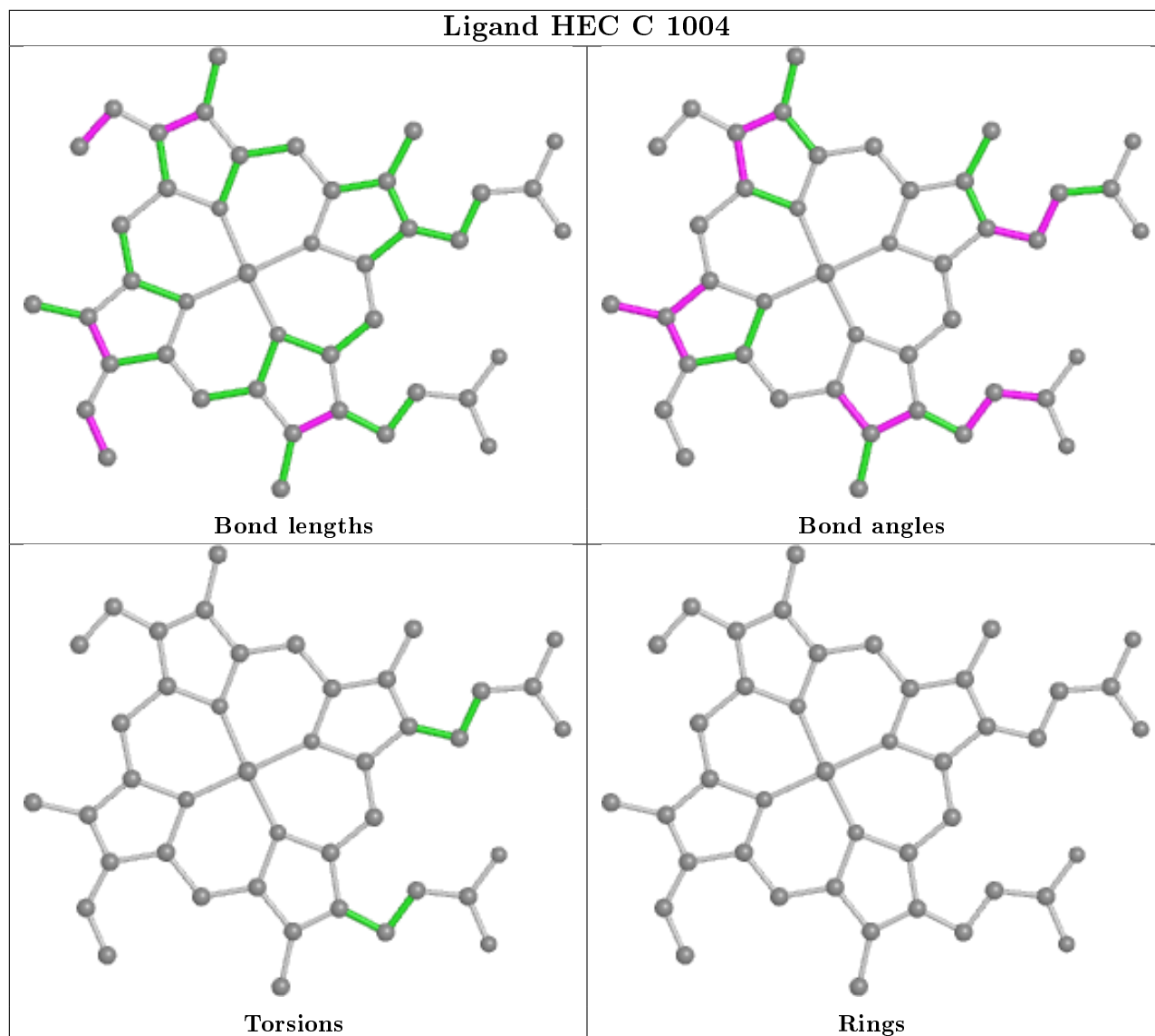


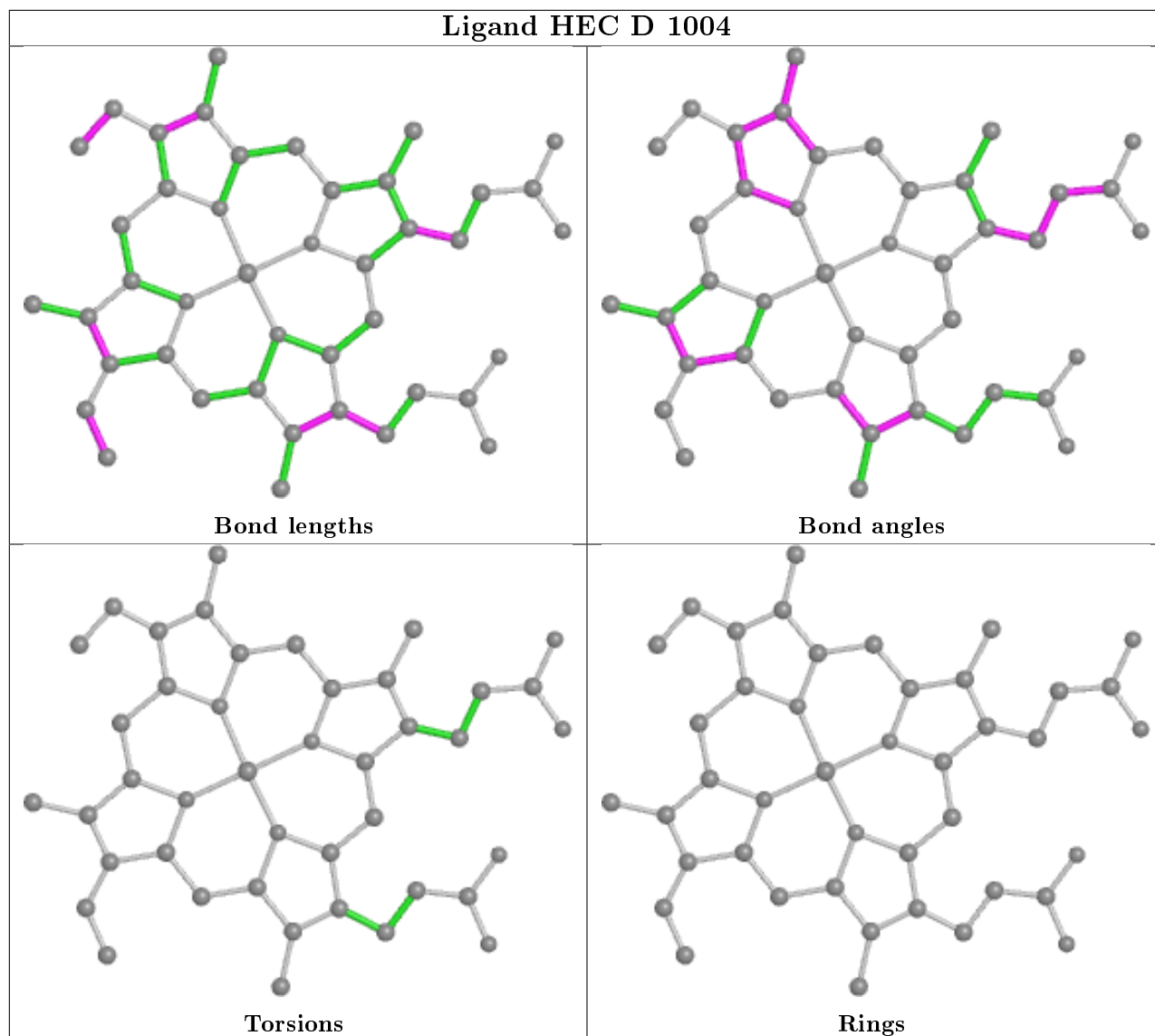


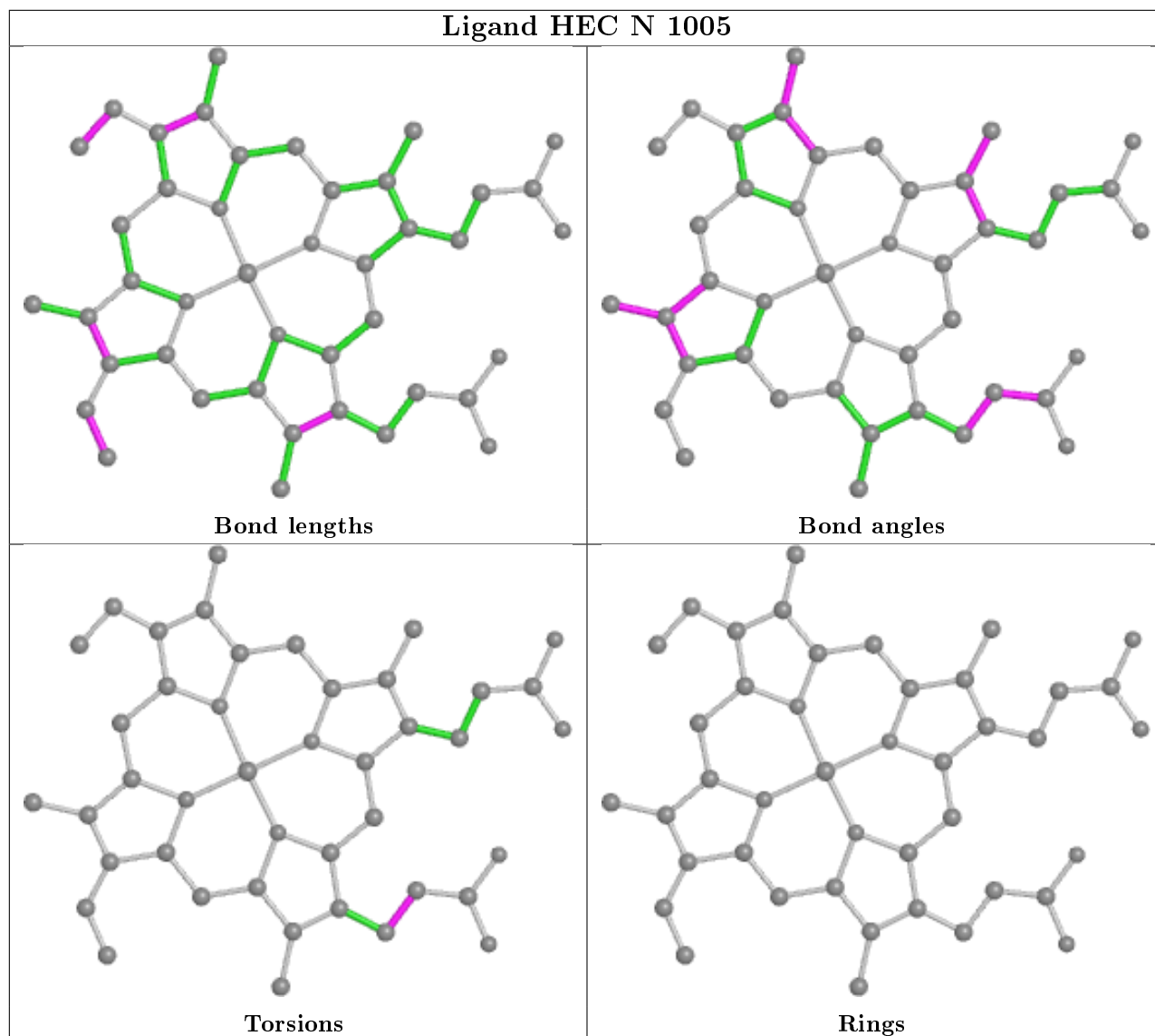


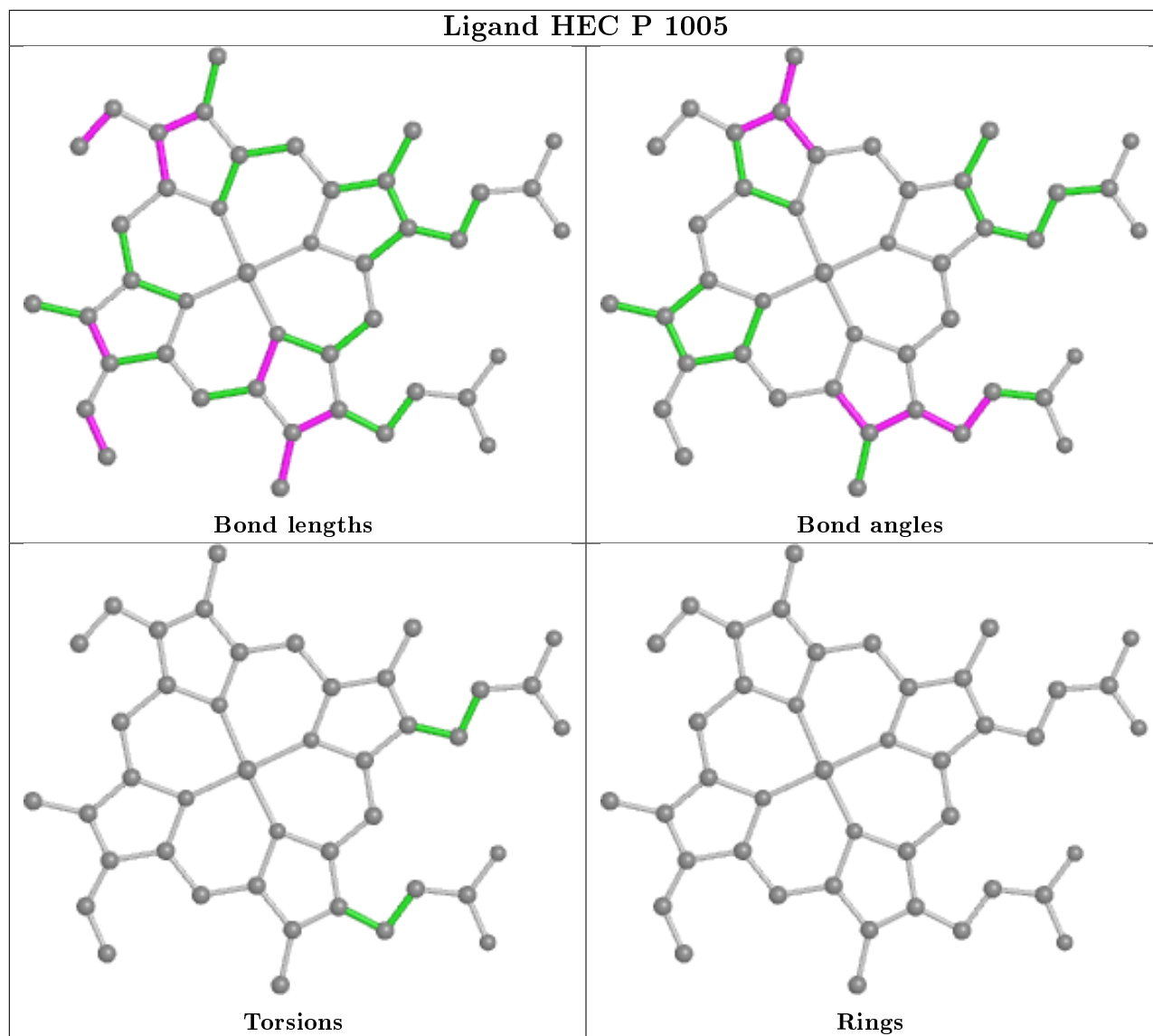


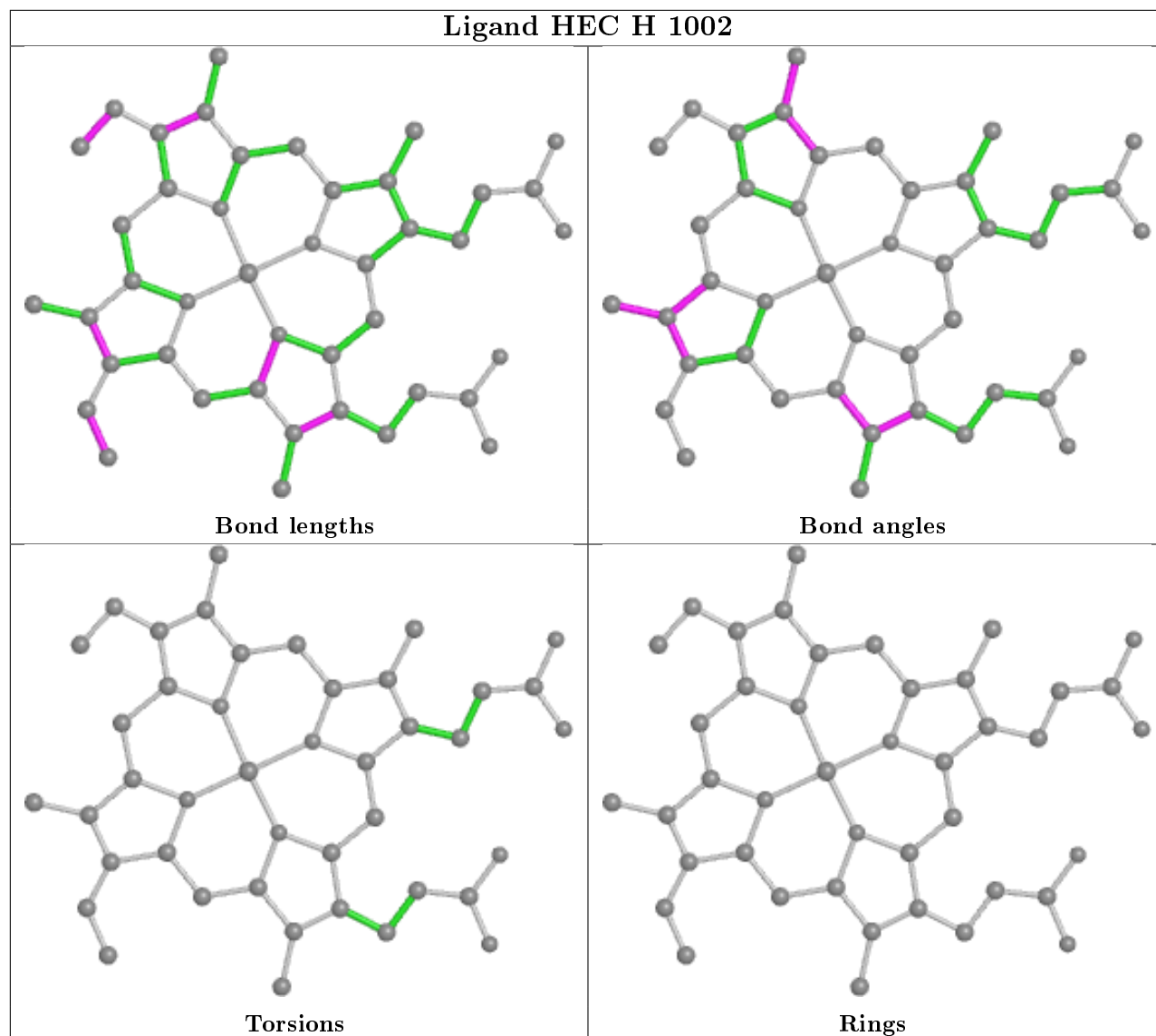


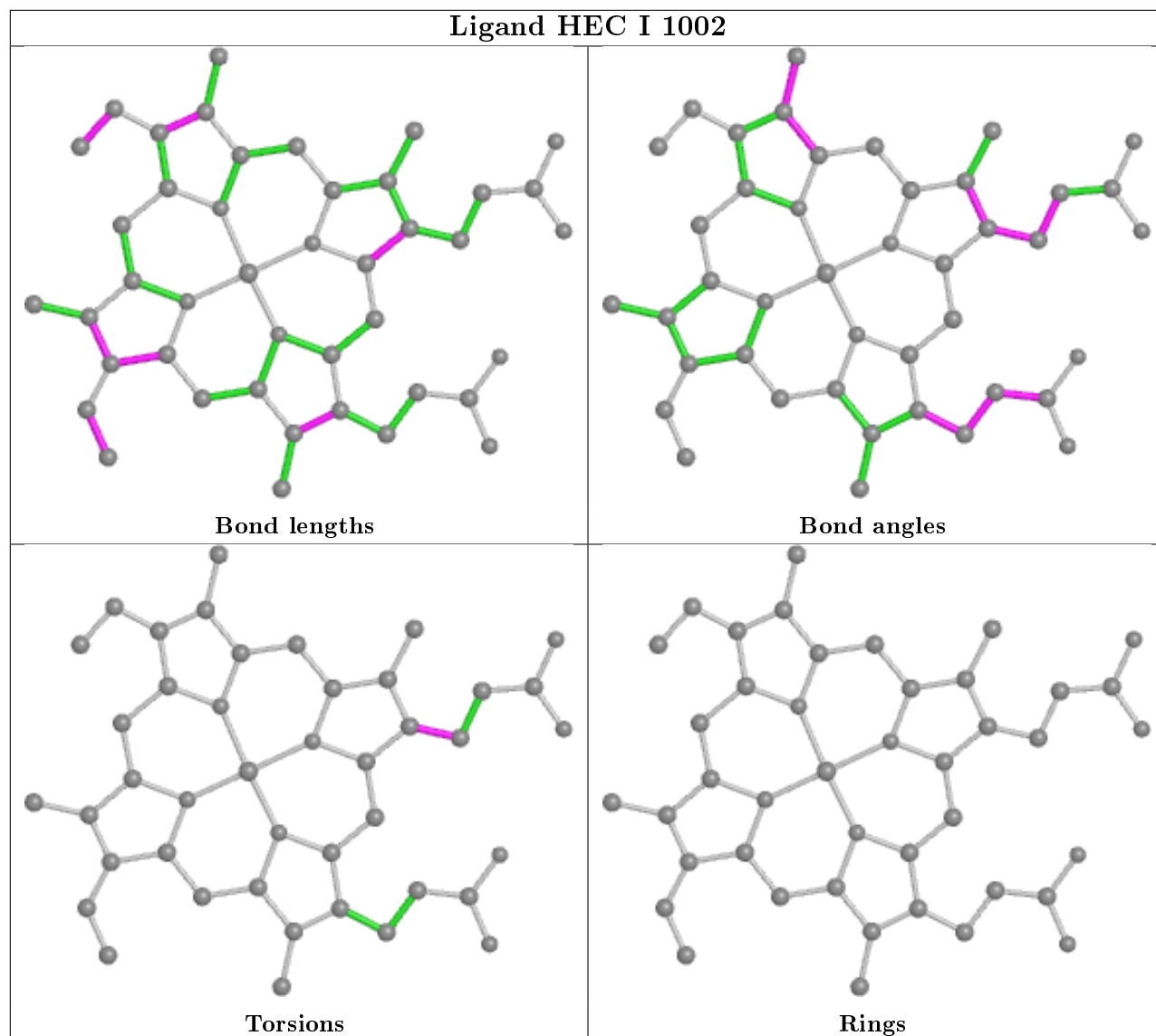


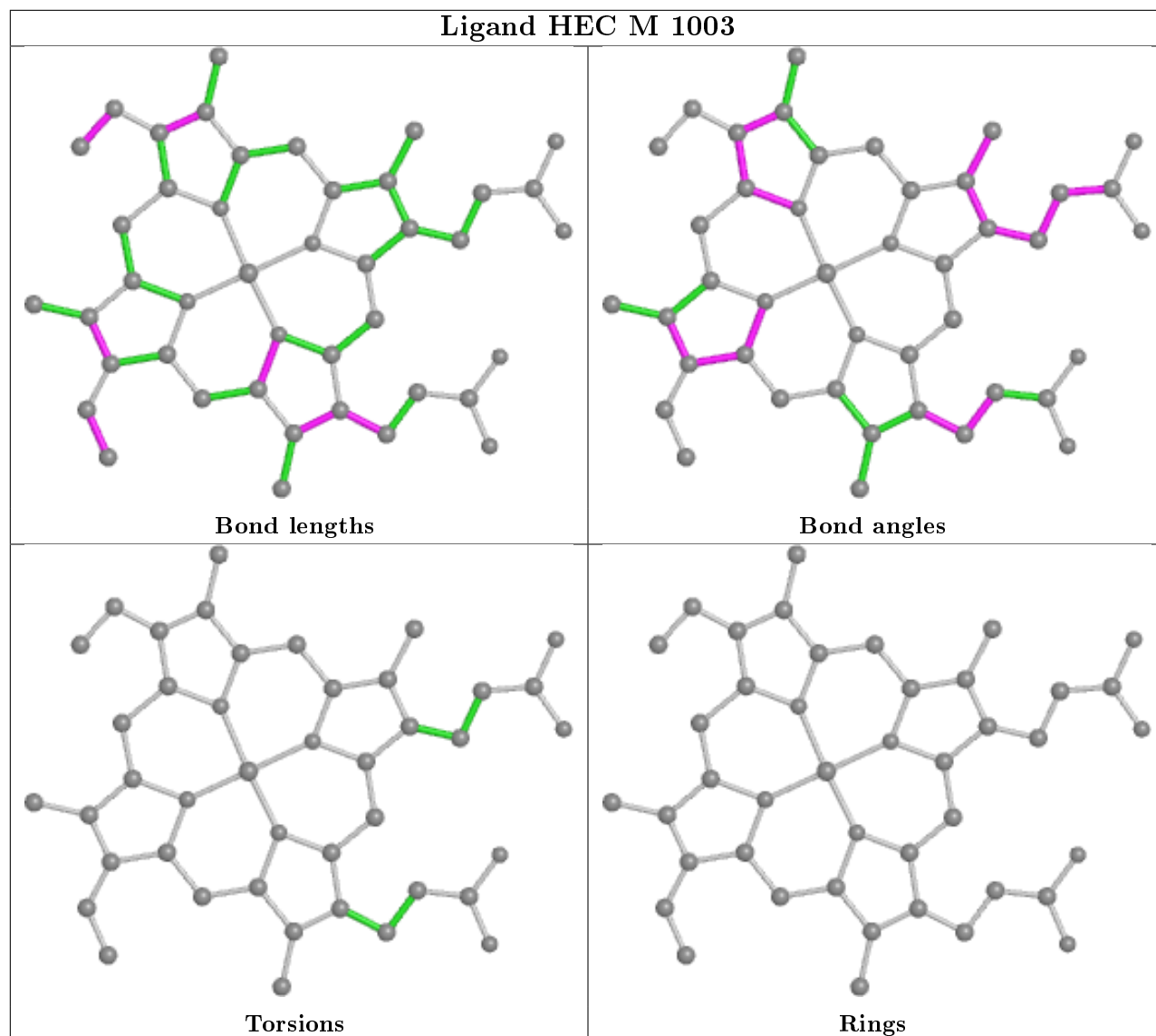


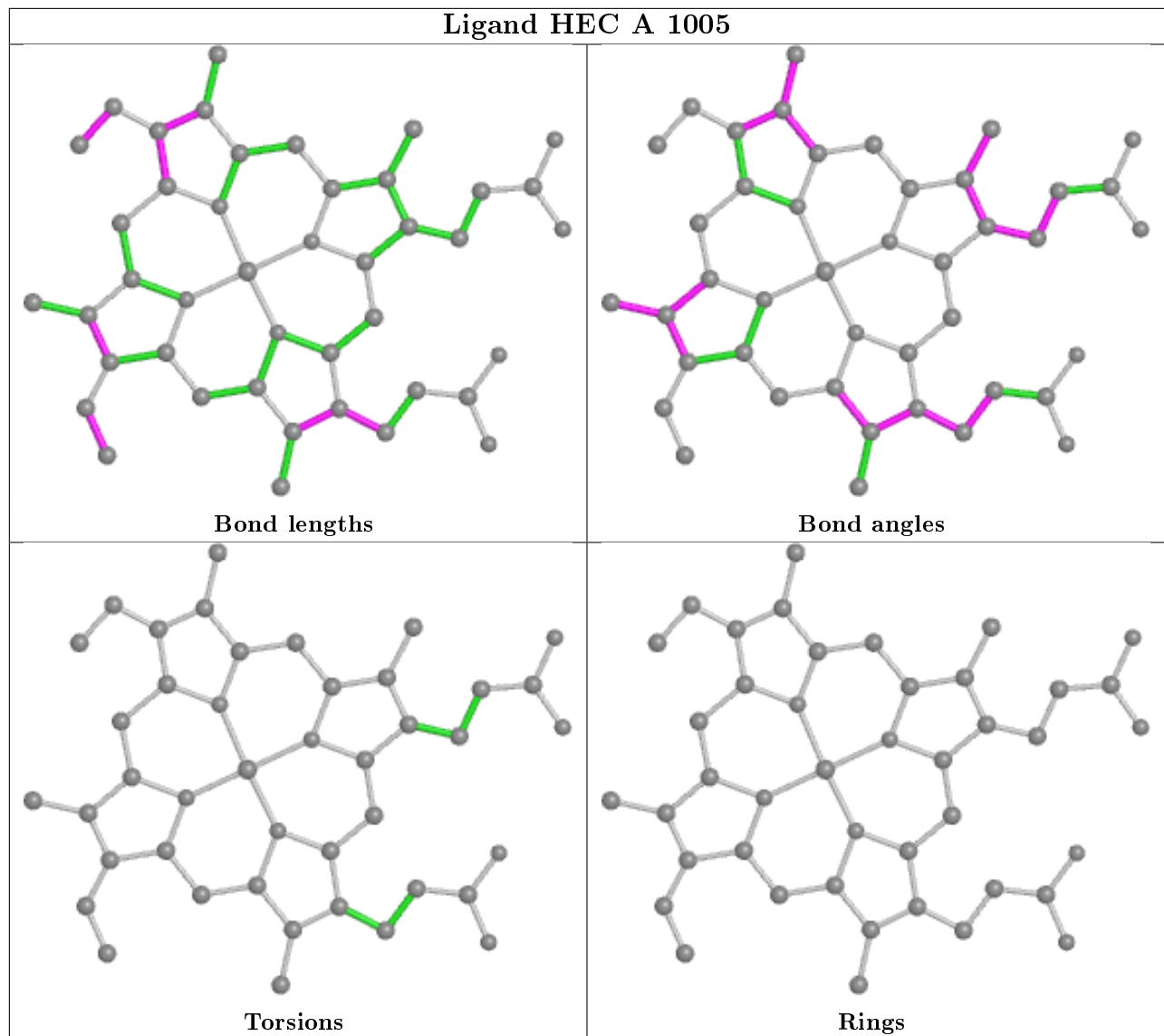


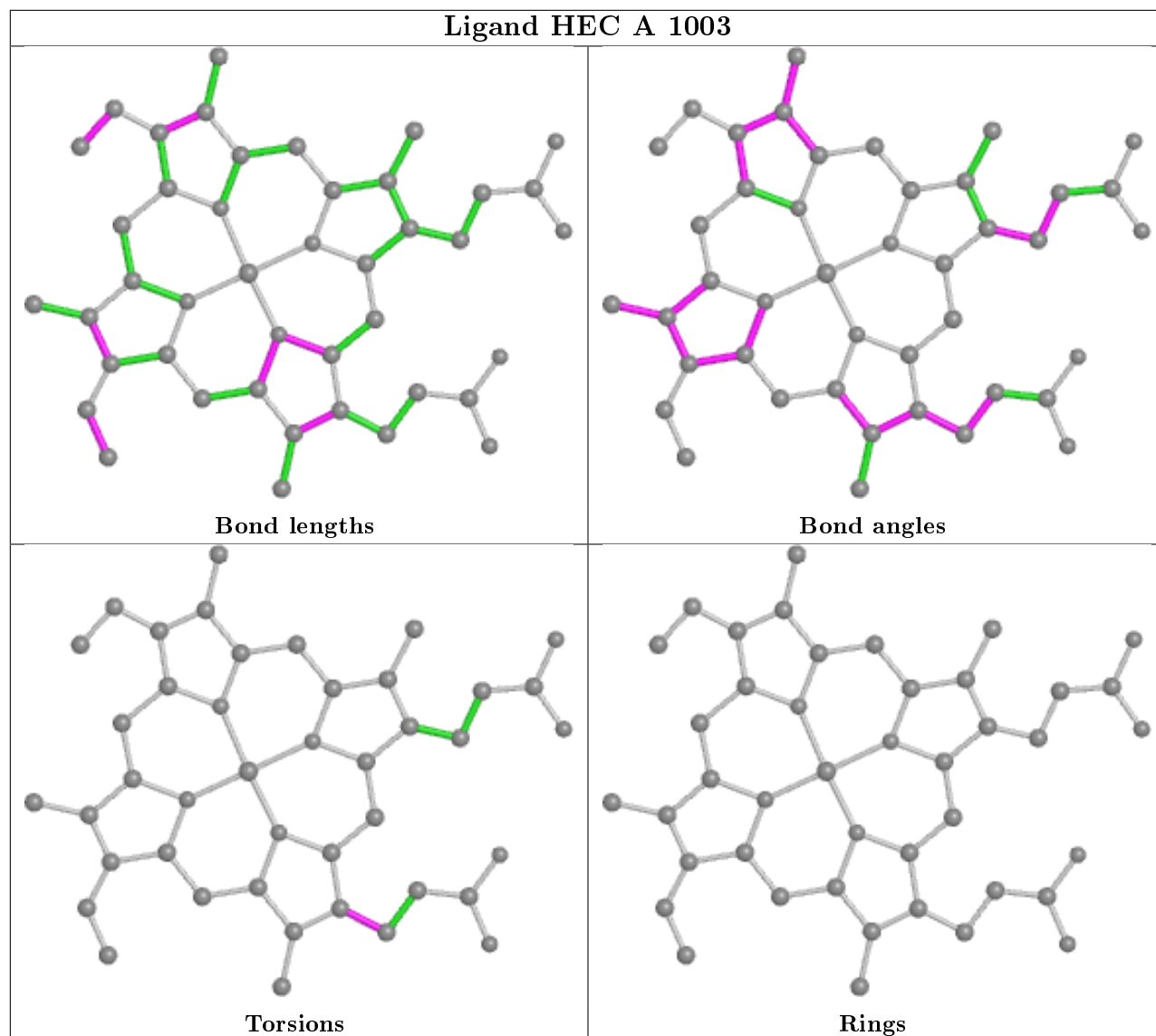


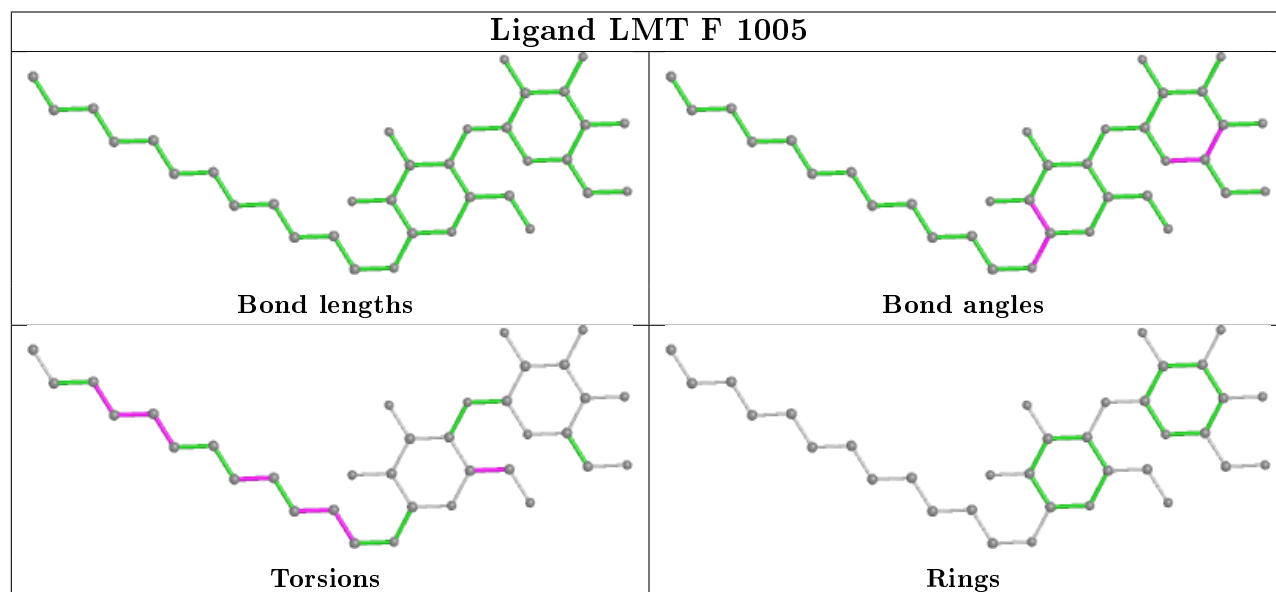
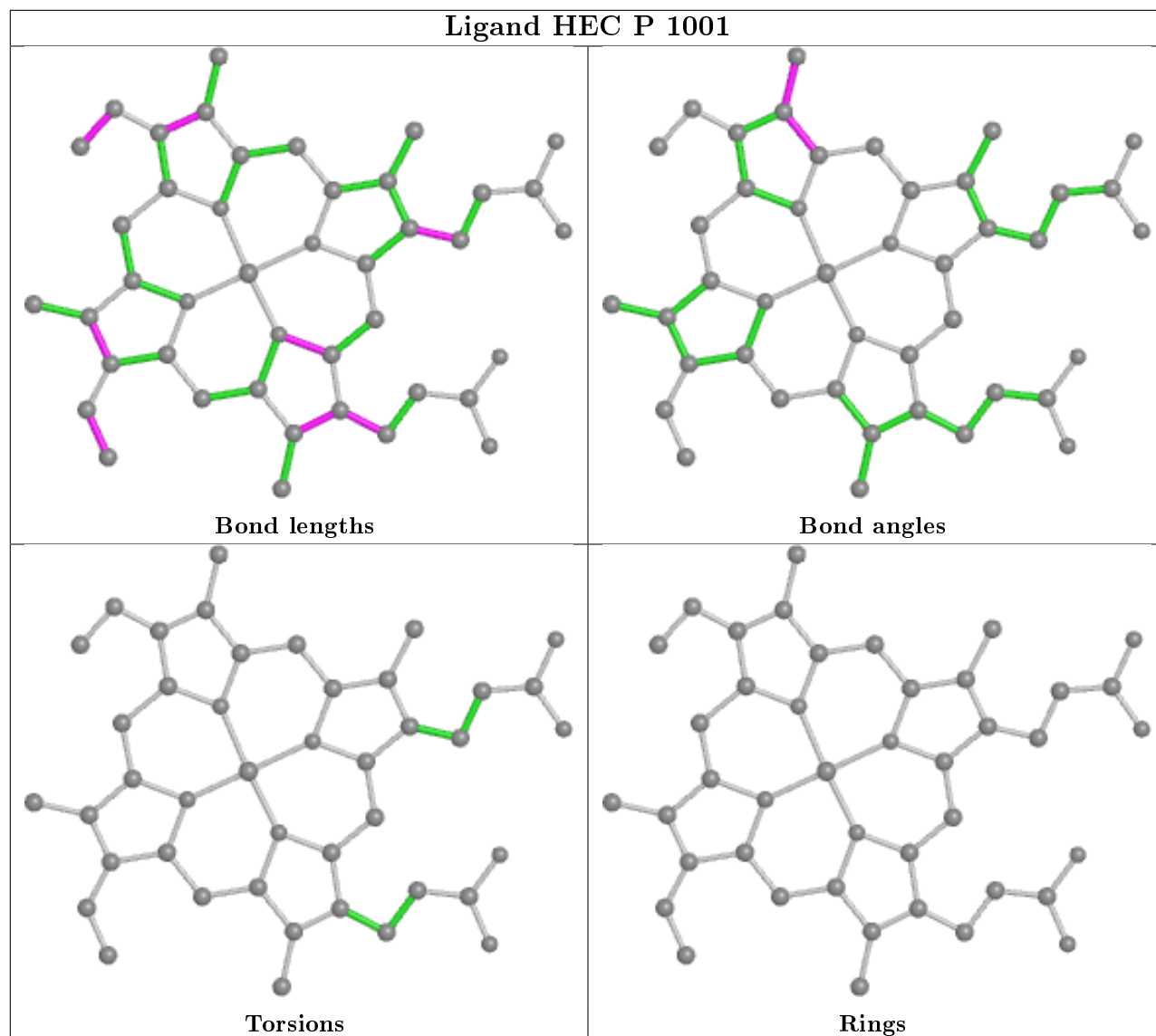


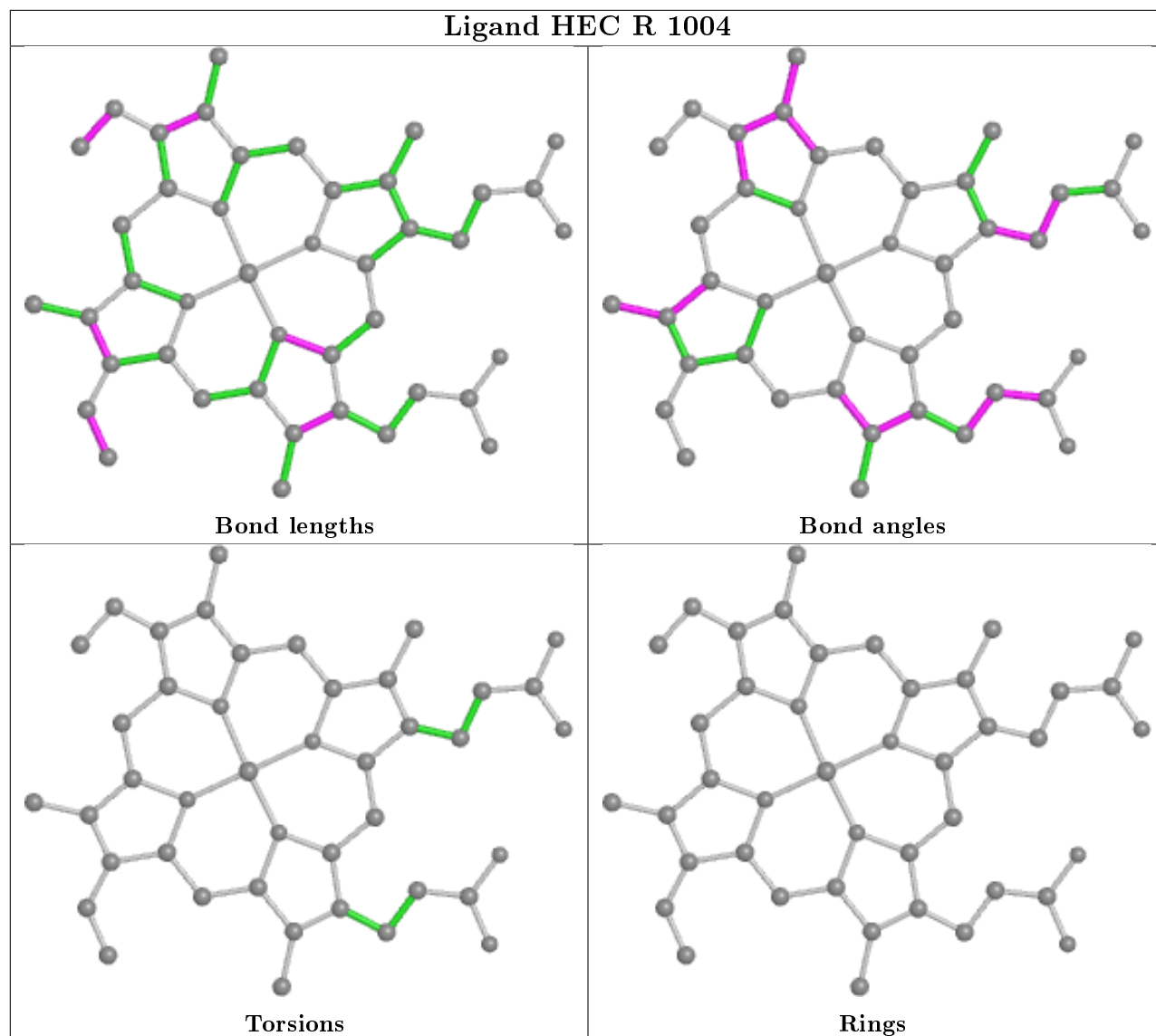


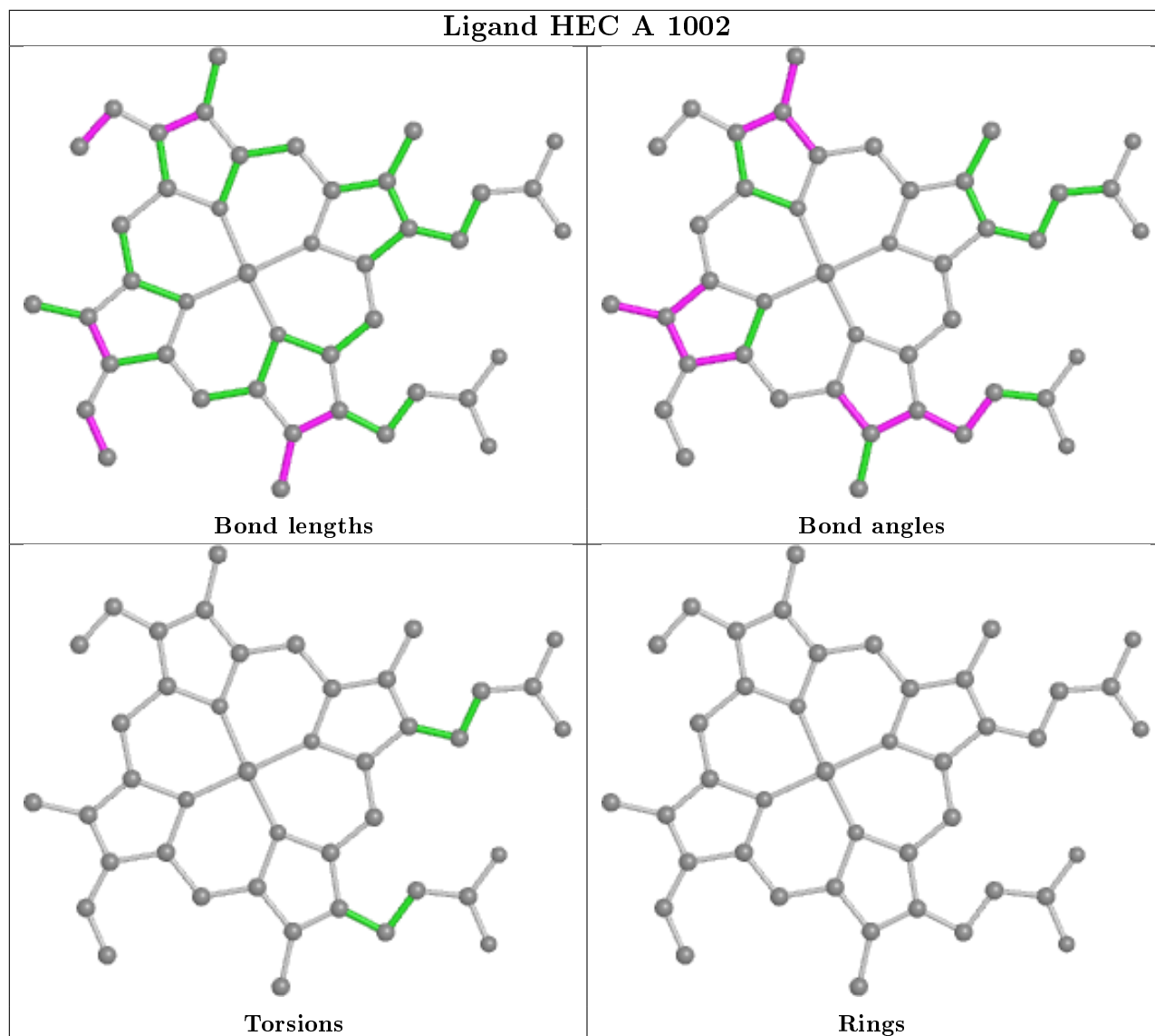


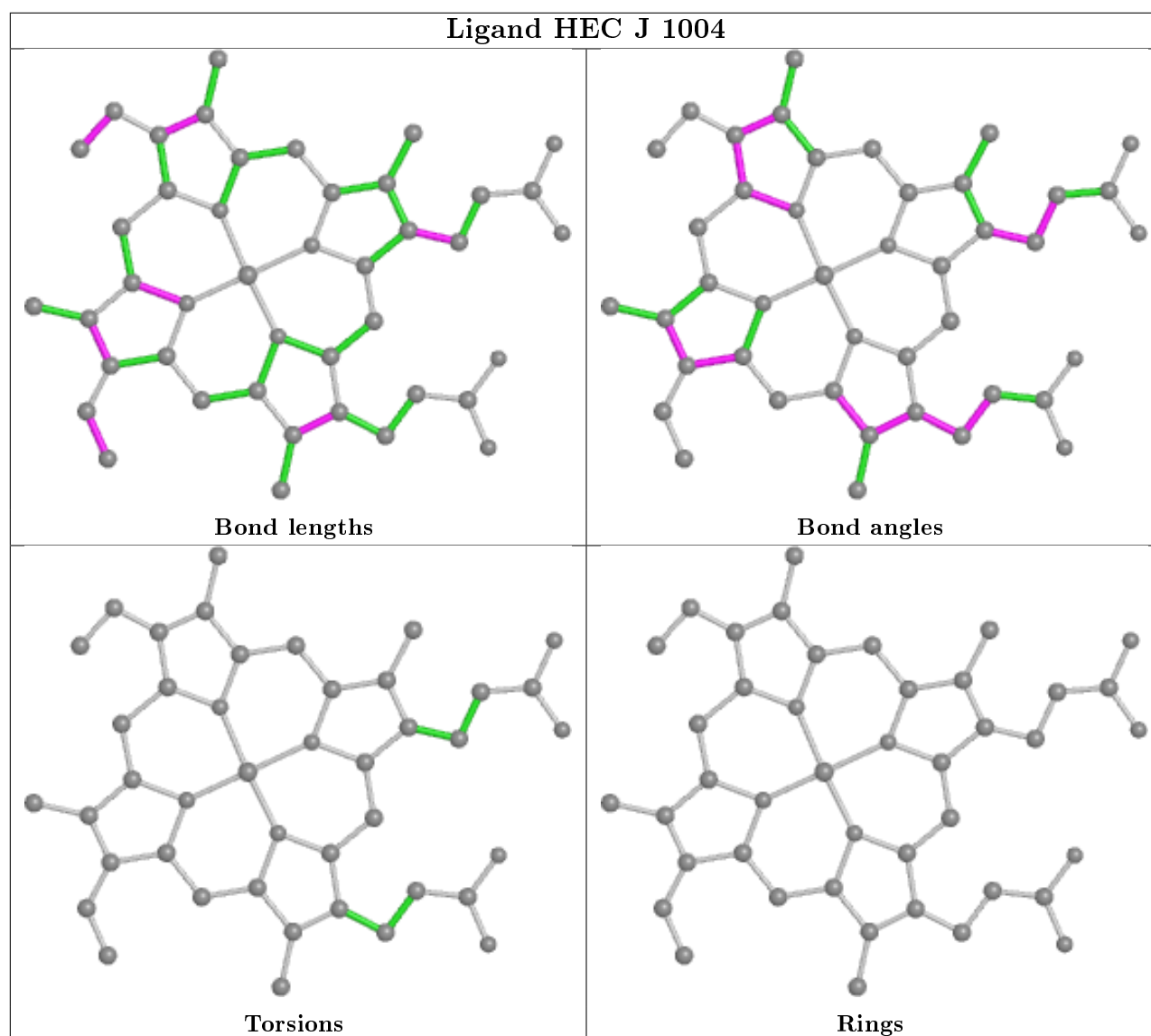












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	M	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	463:TYR	C	464:GLY	N	1.14
1	M	462:GLN	C	463:TYR	N	1.06

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	495/500 (99%)	-0.36	3 (0%) 89 92	5, 17, 32, 50	0
1	B	498/500 (99%)	-0.33	6 (1%) 79 83	5, 16, 33, 52	0
1	D	494/500 (98%)	-0.40	0 100 100	6, 18, 34, 50	0
1	E	494/500 (98%)	-0.23	9 (1%) 68 74	8, 21, 37, 53	0
1	G	494/500 (98%)	-0.36	1 (0%) 95 96	6, 17, 32, 50	0
1	H	497/500 (99%)	-0.36	4 (0%) 86 89	5, 17, 33, 51	0
1	J	494/500 (98%)	-0.36	4 (0%) 86 89	7, 18, 34, 50	0
1	K	496/500 (99%)	-0.18	11 (2%) 62 69	9, 21, 38, 53	0
1	M	494/500 (98%)	-0.37	1 (0%) 95 96	5, 17, 32, 50	0
1	N	498/500 (99%)	-0.35	6 (1%) 79 83	6, 16, 33, 51	0
1	P	494/500 (98%)	-0.31	8 (1%) 72 77	8, 19, 34, 49	0
1	Q	495/500 (99%)	-0.18	14 (2%) 53 60	9, 21, 37, 53	0
2	C	145/159 (91%)	0.12	11 (7%) 13 18	8, 21, 80, 97	0
2	F	145/159 (91%)	0.30	13 (8%) 9 12	8, 26, 80, 96	0
2	I	145/159 (91%)	0.10	11 (7%) 13 18	8, 22, 80, 96	0
2	L	145/159 (91%)	0.21	14 (9%) 7 10	11, 27, 81, 96	0
2	O	144/159 (90%)	0.07	10 (6%) 16 22	9, 21, 76, 96	0
2	R	145/159 (91%)	0.13	8 (5%) 25 31	10, 27, 80, 96	0
All	All	6812/6954 (97%)	-0.26	134 (1%) 65 71	5, 19, 38, 97	0

The worst 5 of 134 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	15	LEU	9.2
2	C	16	VAL	7.7
2	R	15	LEU	6.9

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Mol	Chain	Res	Type	RSRZ
2	L	16	VAL	6.6
2	F	17	LEU	6.6

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 carbohydrates 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(\AA^2)	Q<0.9
5	LMT	R	1005	35/35	0.84	0.28	41,49,75,75	0
5	LMT	O	1005	35/35	0.85	0.28	38,45,74,75	0
5	LMT	L	1005	35/35	0.88	0.24	40,46,66,67	0
5	LMT	F	1005	35/35	0.89	0.21	37,44,70,71	0
5	LMT	I	1005	35/35	0.90	0.29	36,41,72,73	0
5	LMT	C	1005	35/35	0.91	0.25	36,41,72,73	0
6	ACT	O	1006	4/4	0.93	0.20	32,32,33,33	0
6	ACT	C	1006	4/4	0.94	0.22	34,34,34,34	0
6	ACT	I	1006	4/4	0.95	0.25	38,39,39,39	0
3	HEC	R	1001	43/43	0.95	0.15	22,26,37,42	0
3	HEC	L	1101	43/43	0.95	0.14	23,27,33,36	0
3	HEC	C	1001	43/43	0.96	0.13	17,20,29,34	0
3	HEC	K	1002	43/43	0.97	0.11	18,21,23,24	0
3	HEC	Q	1001	43/43	0.97	0.11	13,18,20,22	0
3	HEC	Q	1003	43/43	0.97	0.11	14,17,20,23	0
3	HEC	I	1001	43/43	0.97	0.12	18,21,29,32	0
3	HEC	K	1005	43/43	0.97	0.14	9,15,23,26	0
3	HEC	F	1001	43/43	0.97	0.13	20,24,27,31	0
3	HEC	E	1001	43/43	0.97	0.11	14,16,18,20	0
3	HEC	L	1002	43/43	0.97	0.12	16,18,26,29	0
3	HEC	K	1001	43/43	0.97	0.12	15,19,23,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HEC	I	1002	43/43	0.97	0.13	11,15,26,29	0
3	HEC	R	1002	43/43	0.97	0.12	17,20,28,32	0
3	HEC	B	1002	43/43	0.98	0.10	6,10,15,17	0
3	HEC	I	1004	43/43	0.98	0.12	3,6,16,20	0
3	HEC	J	1003	43/43	0.98	0.11	5,8,12,16	0
3	HEC	O	1003	43/43	0.98	0.12	8,12,17,20	0
3	HEC	P	1004	43/43	0.98	0.13	5,8,13,18	0
3	HEC	Q	1002	43/43	0.98	0.11	19,21,22,23	0
4	CA	Q	1007	1/1	0.98	0.06	20,20,20,20	0
3	HEC	M	1001	43/43	0.98	0.10	3,9,11,12	0
3	HEC	J	1001	43/43	0.98	0.11	8,12,16,16	0
4	CA	H	1007	1/1	0.98	0.09	16,16,16,16	0
3	HEC	P	1002	43/43	0.98	0.11	6,9,17,24	0
3	HEC	G	1003	43/43	0.98	0.12	4,7,11,13	0
3	HEC	G	1001	43/43	0.98	0.10	3,8,11,13	0
3	HEC	M	1002	43/43	0.98	0.10	6,11,13,17	0
4	CA	M	1006	1/1	0.98	0.08	12,12,12,12	0
3	HEC	R	1003	43/43	0.98	0.13	7,11,17,21	0
4	CA	K	1006	1/1	0.98	0.10	16,16,16,16	0
3	HEC	E	1003	43/43	0.98	0.12	12,14,16,18	0
3	HEC	B	1001	43/43	0.98	0.11	5,10,13,16	0
3	HEC	G	1002	43/43	0.98	0.11	7,9,14,19	0
3	HEC	O	1001	43/43	0.98	0.10	17,20,28,34	0
3	HEC	E	1004	43/43	0.98	0.12	7,11,14,21	0
3	HEC	F	1002	43/43	0.98	0.12	14,17,27,30	0
3	HEC	O	1002	43/43	0.98	0.12	12,14,23,29	0
3	HEC	H	1001	43/43	0.98	0.11	5,11,13,14	0
3	HEC	L	1004	43/43	0.98	0.12	7,10,19,21	0
3	HEC	D	1001	43/43	0.98	0.11	6,12,16,19	0
3	HEC	L	1003	43/43	0.98	0.12	8,11,16,21	0
3	HEC	P	1003	43/43	0.98	0.10	6,9,12,14	0
3	HEC	F	1004	43/43	0.98	0.12	3,6,16,24	0
3	HEC	B	1005	43/43	0.98	0.14	4,8,18,21	0
3	HEC	D	1005	43/43	0.98	0.15	6,12,18,19	0
3	HEC	J	1002	43/43	0.98	0.11	9,11,16,21	0
3	HEC	N	1001	43/43	0.98	0.11	6,9,12,13	0
3	HEC	F	1003	43/43	0.98	0.13	7,10,18,24	0
3	HEC	H	1005	43/43	0.98	0.15	5,8,18,22	0
3	HEC	E	1002	43/43	0.98	0.11	13,16,19,21	0
3	HEC	I	1003	43/43	0.98	0.12	7,12,19,24	0
3	HEC	K	1003	43/43	0.98	0.12	9,15,17,18	0
3	HEC	O	1004	43/43	0.98	0.13	5,8,20,23	0

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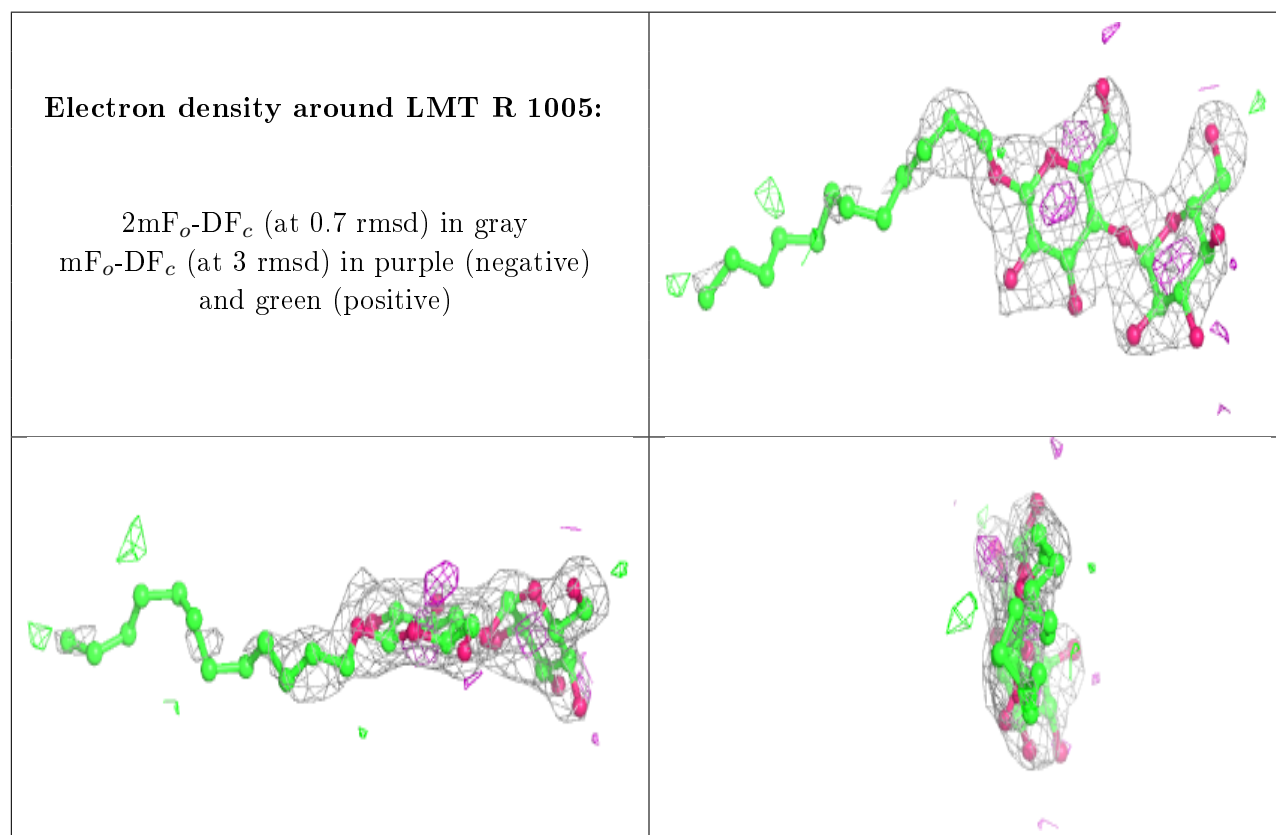
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HEC	Q	1005	43/43	0.98	0.14	12,15,20,29	0
3	HEC	E	1005	43/43	0.98	0.14	11,14,20,24	0
3	HEC	C	1003	43/43	0.98	0.12	8,11,15,23	0
3	HEC	C	1002	43/43	0.98	0.12	8,13,27,29	0
3	HEC	K	1004	43/43	0.98	0.12	7,13,21,25	0
3	HEC	N	1002	43/43	0.98	0.10	6,10,12,14	0
3	HEC	C	1004	43/43	0.98	0.14	3,8,17,22	0
3	HEC	D	1004	43/43	0.98	0.13	2,5,10,16	0
3	HEC	N	1005	43/43	0.98	0.14	3,8,21,24	0
3	HEC	P	1005	43/43	0.98	0.14	8,13,18,22	0
3	HEC	H	1002	43/43	0.98	0.10	6,9,14,21	0
3	HEC	G	1005	43/43	0.98	0.15	5,8,12,16	0
3	HEC	M	1003	43/43	0.98	0.10	3,7,12,14	0
3	HEC	P	1001	43/43	0.98	0.12	12,16,21,24	0
3	HEC	Q	1004	43/43	0.98	0.12	7,11,18,19	0
3	HEC	A	1002	43/43	0.98	0.10	5,9,14,18	0
3	HEC	J	1004	43/43	0.98	0.13	3,6,13,21	0
4	CA	J	1007	1/1	0.99	0.09	11,11,11,11	0
4	CA	E	1007	1/1	0.99	0.10	18,18,18,18	0
3	HEC	M	1004	43/43	0.99	0.12	2,5,14,16	0
3	HEC	D	1003	43/43	0.99	0.10	2,5,8,11	0
3	HEC	N	1003	43/43	0.99	0.11	3,7,8,11	0
4	CA	E	1006	1/1	0.99	0.09	17,17,17,17	0
3	HEC	M	1005	43/43	0.99	0.14	4,7,16,21	0
4	CA	D	1007	1/1	0.99	0.09	11,11,11,11	0
3	HEC	H	1003	43/43	0.99	0.11	3,8,10,13	0
4	CA	D	1006	1/1	0.99	0.09	16,16,16,16	0
3	HEC	A	1001	43/43	0.99	0.10	2,7,12,15	0
3	HEC	D	1002	43/43	0.99	0.10	4,7,13,19	0
4	CA	K	1007	1/1	0.99	0.11	17,17,17,17	0
4	CA	P	1006	1/1	0.99	0.07	16,16,16,16	0
4	CA	G	1007	1/1	0.99	0.11	16,16,16,16	0
4	CA	J	1006	1/1	0.99	0.11	13,13,13,13	0
4	CA	N	1007	1/1	0.99	0.09	11,11,11,11	0
3	HEC	G	1004	43/43	0.99	0.13	2,5,12,14	0
3	HEC	N	1004	43/43	0.99	0.12	2,5,8,13	0
3	HEC	A	1004	43/43	0.99	0.13	2,5,11,14	0
3	HEC	B	1004	43/43	0.99	0.13	2,5,7,12	0
3	HEC	A	1005	43/43	0.99	0.16	2,7,16,22	0
3	HEC	A	1003	43/43	0.99	0.11	2,6,9,12	0
4	CA	P	1007	1/1	0.99	0.09	15,15,15,15	0
3	HEC	B	1003	43/43	0.99	0.11	5,7,9,13	0

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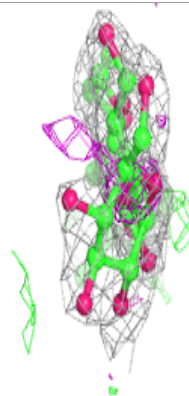
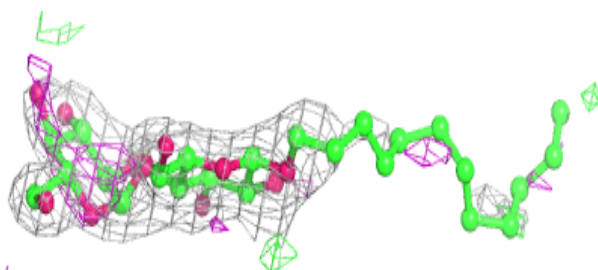
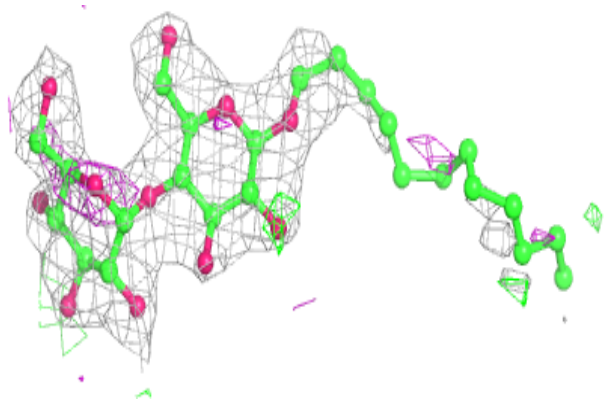
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HEC	J	1005	43/43	0.99	0.13	10,13,19,22	0
3	HEC	R	1004	43/43	0.99	0.11	3,8,16,21	0
3	HEC	H	1004	43/43	0.99	0.13	3,6,8,12	0
4	CA	Q	1006	1/1	0.99	0.10	17,17,17,17	0
4	CA	B	1007	1/1	0.99	0.09	13,13,13,13	0
4	CA	A	1006	1/1	1.00	0.09	13,13,13,13	0
4	CA	A	1007	1/1	1.00	0.09	11,11,11,11	0
4	CA	N	1006	1/1	1.00	0.10	10,10,10,10	0
4	CA	B	1006	1/1	1.00	0.08	11,11,11,11	0
4	CA	H	1006	1/1	1.00	0.10	11,11,11,11	0
4	CA	G	1006	1/1	1.00	0.08	13,13,13,13	0
4	CA	M	1007	1/1	1.00	0.08	14,14,14,14	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.

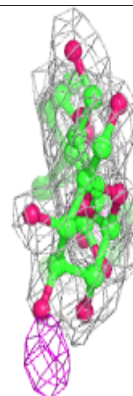
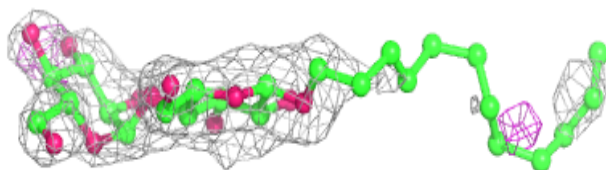
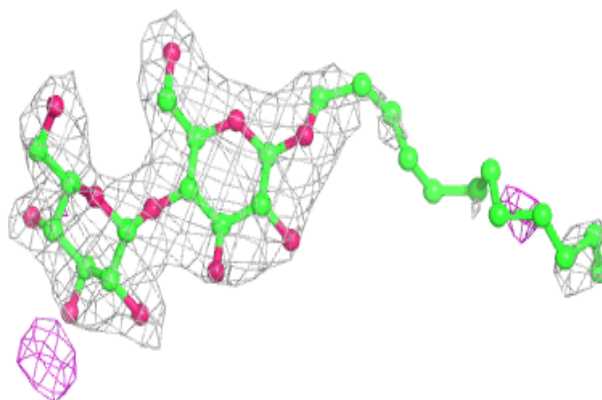


Electron density around LMT O 1005:

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

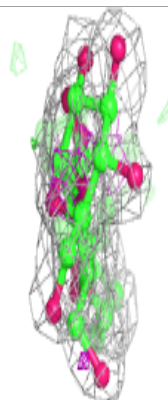
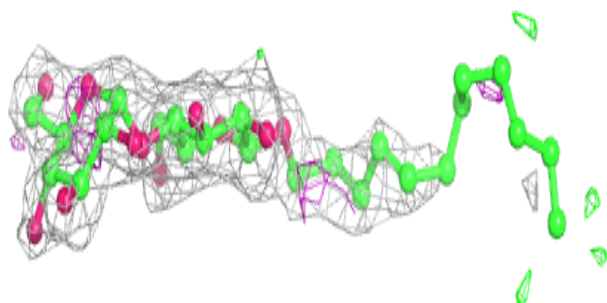
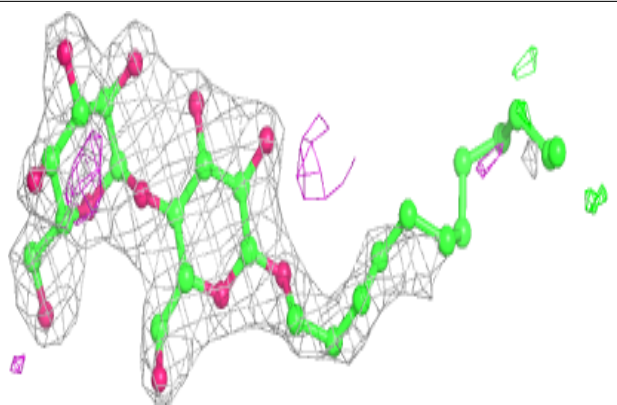
**Electron density around LMT L 1005:**

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

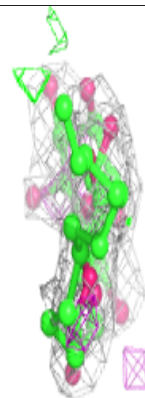
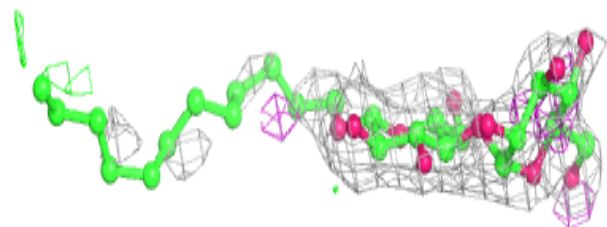
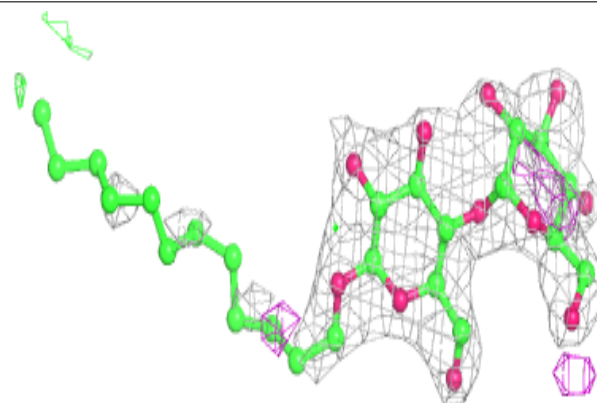


Electron density around LMT F 1005:

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

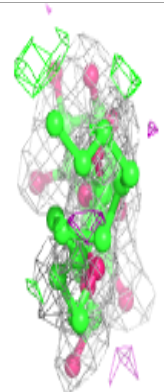
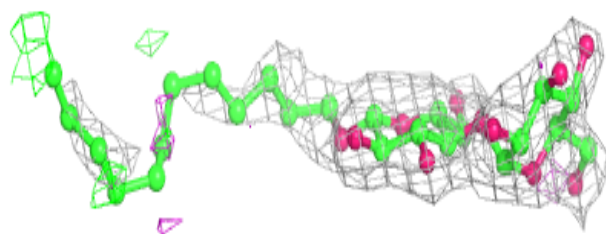
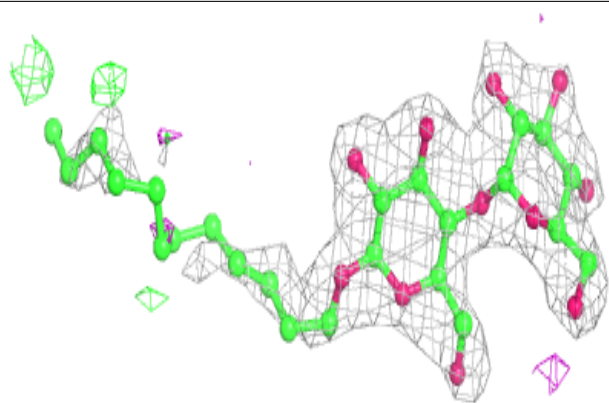
**Electron density around LMT I 1005:**

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



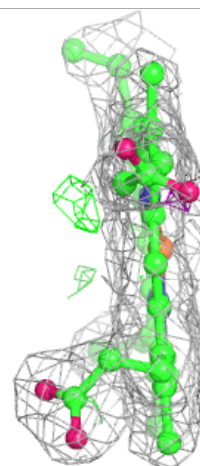
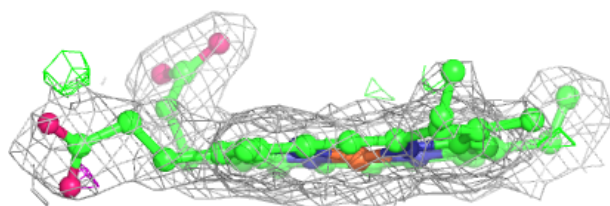
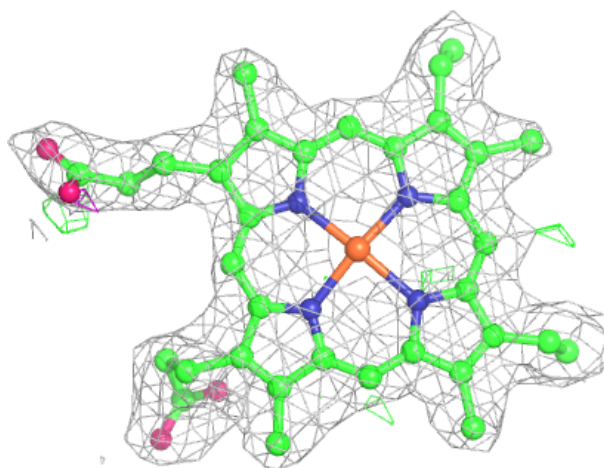
Electron density around LMT C 1005:

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



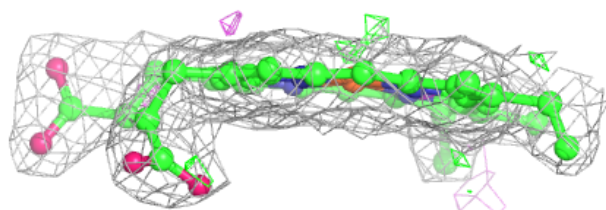
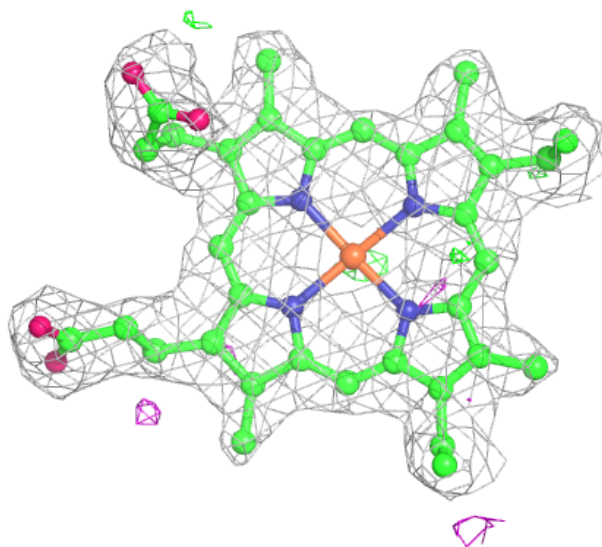
Electron density around HEC R 1001:

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



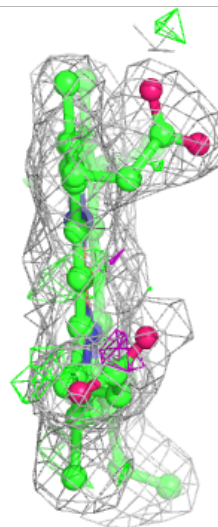
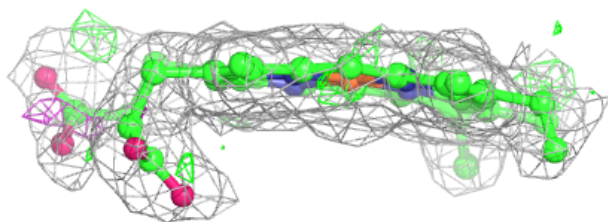
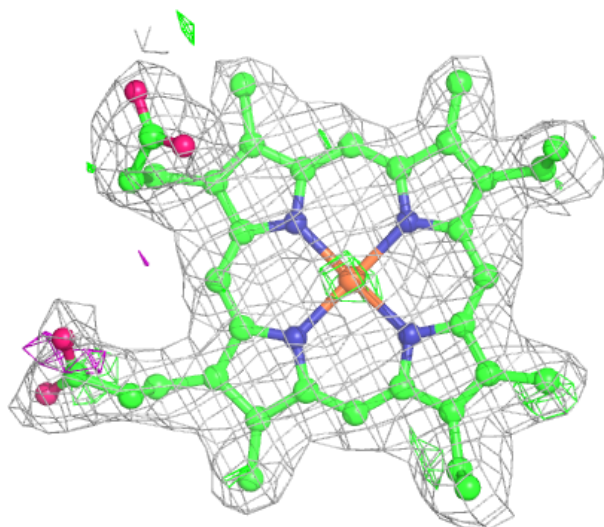
Electron density around HEC L 1101:

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



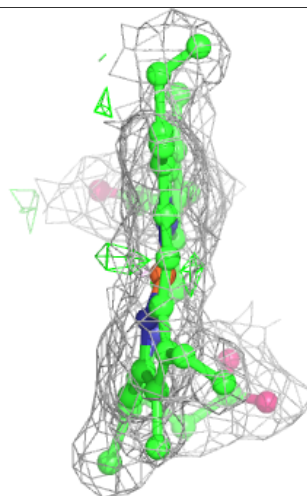
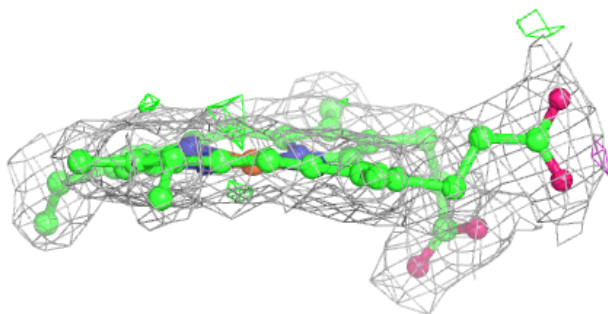
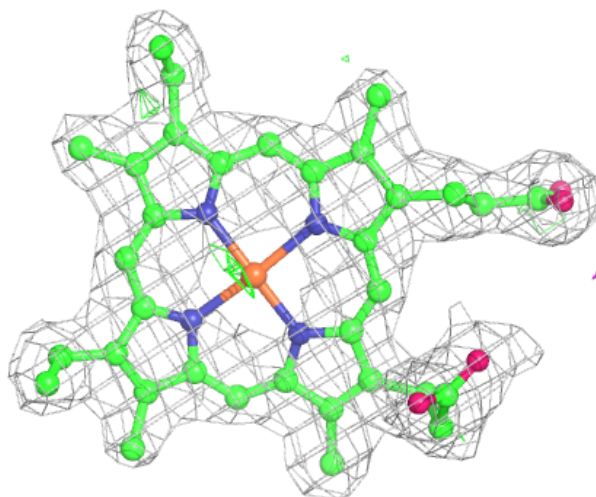
Electron density around HEC C 1001:

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



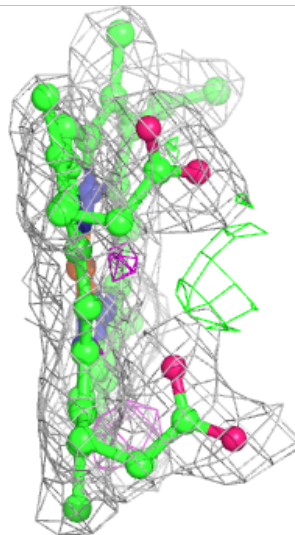
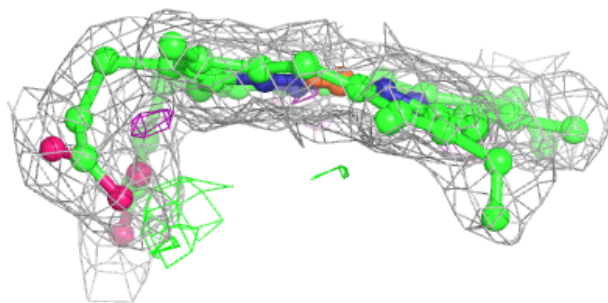
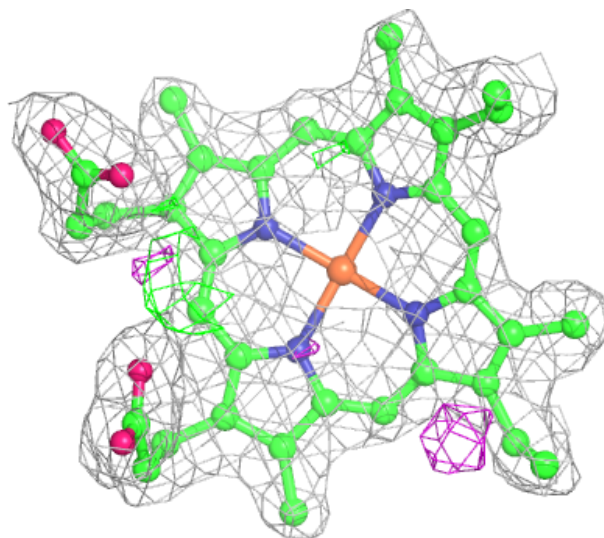
Electron density around HEC K 1002:

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



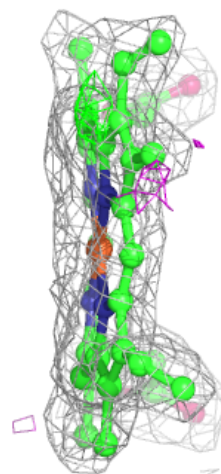
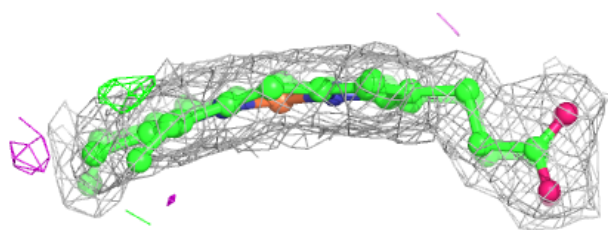
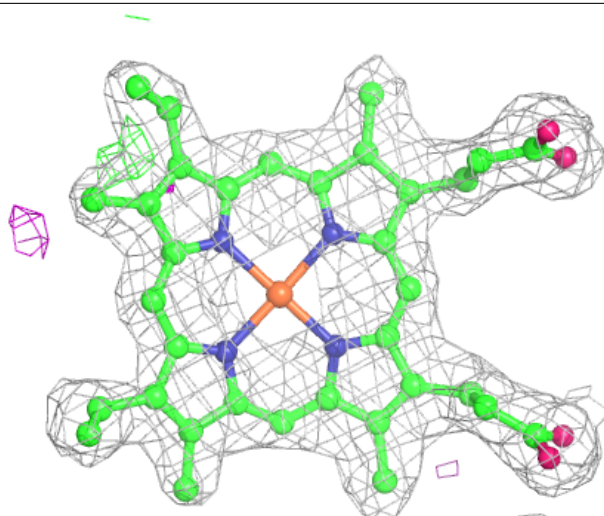
Electron density around HEC Q 1001:

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



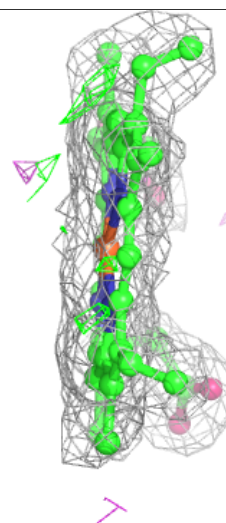
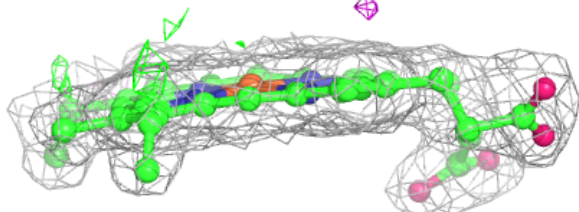
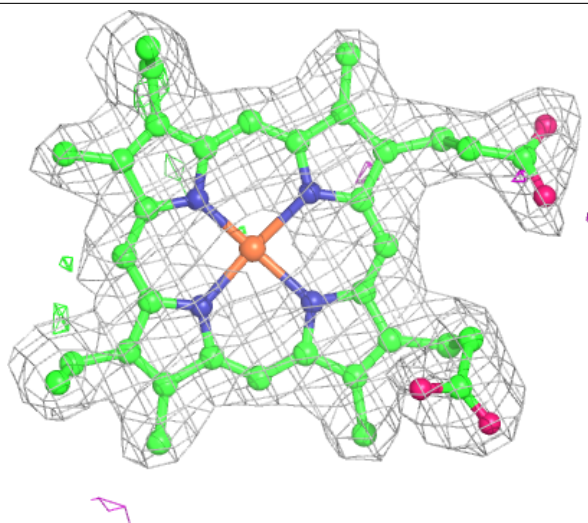
Electron density around HEC Q 1003:

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



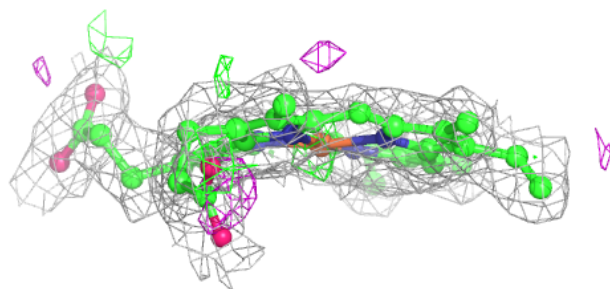
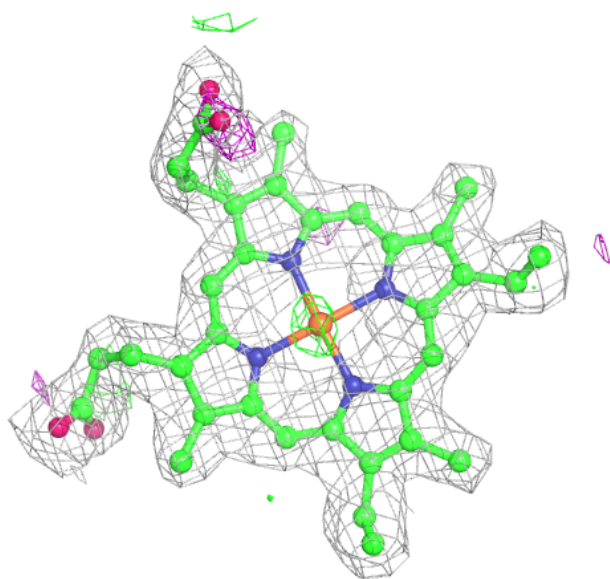
Electron density around HEC I 1001:

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



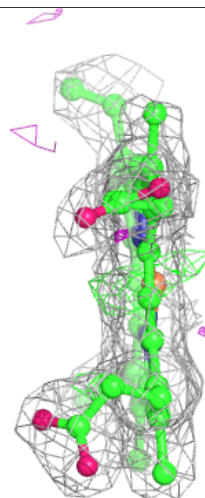
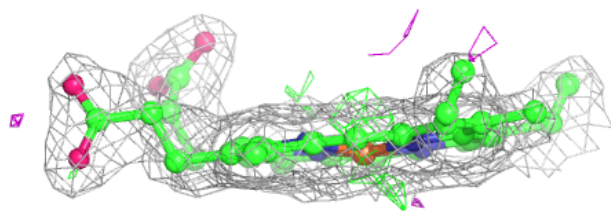
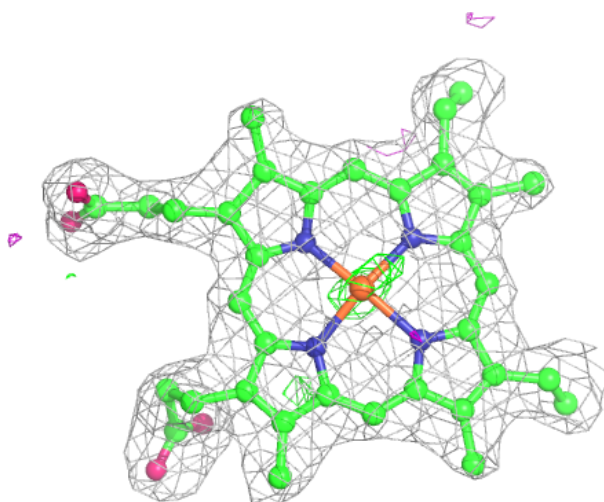
Electron density around HEC K 1005:

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



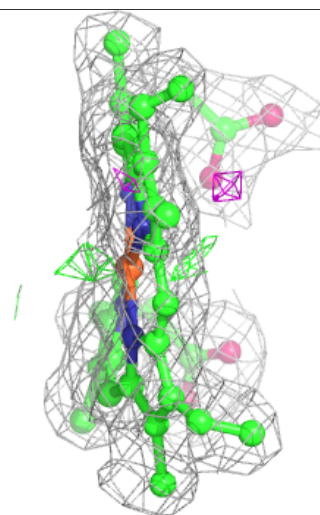
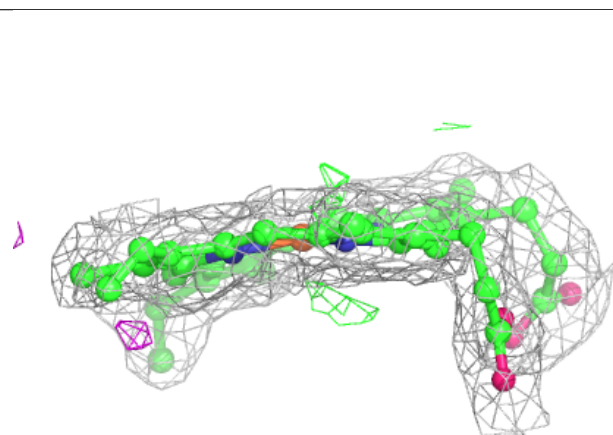
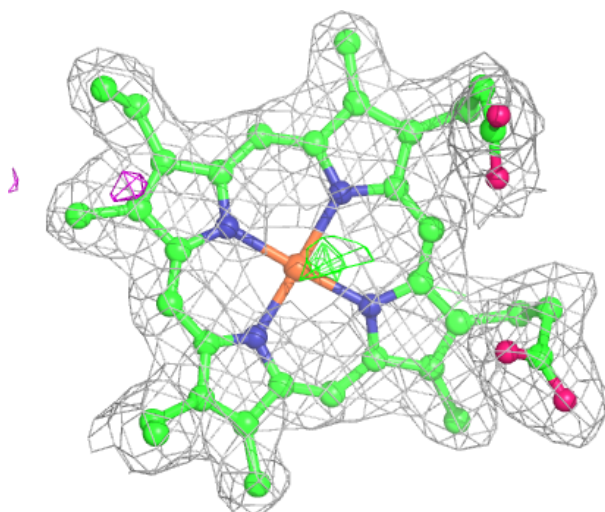
Electron density around HEC F 1001:

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



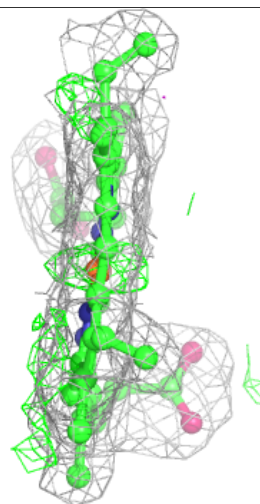
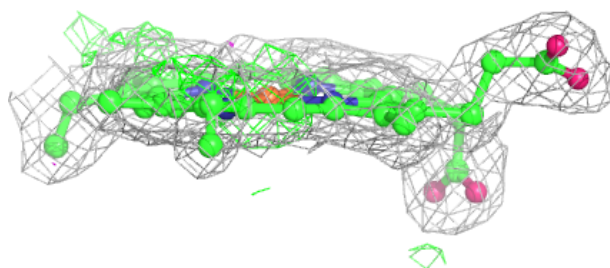
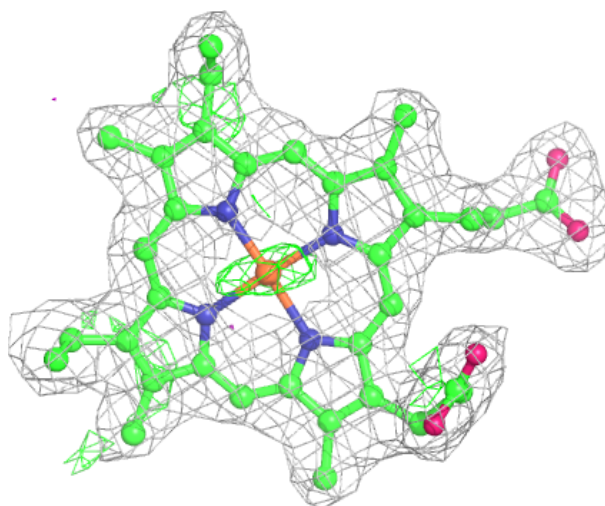
Electron density around HEC E 1001:

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



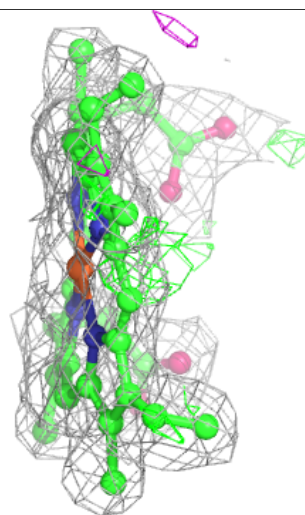
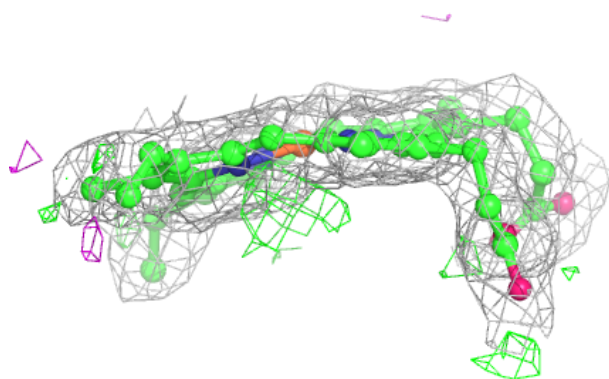
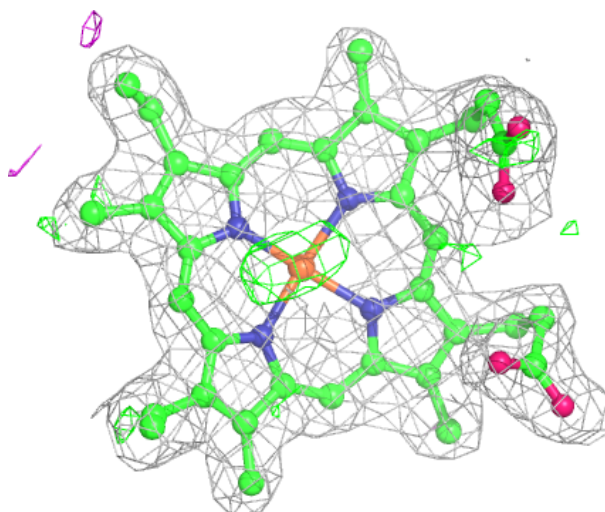
Electron density around HEC L 1002:

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



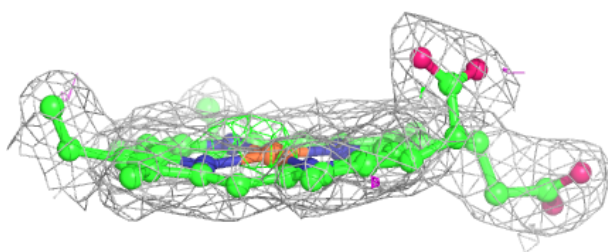
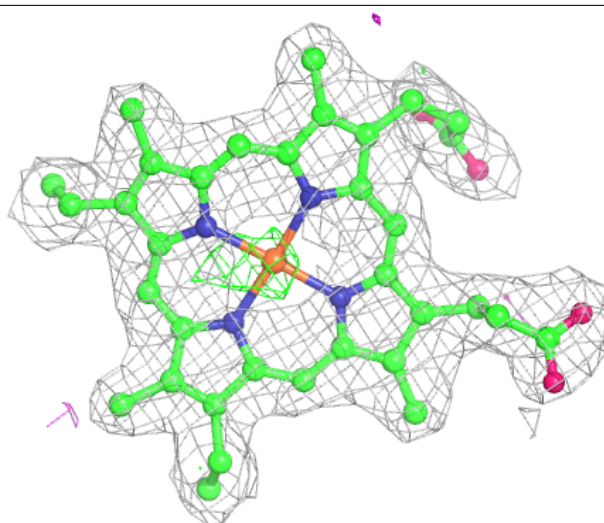
Electron density around HEC K 1001:

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



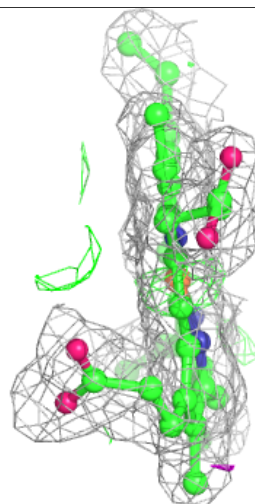
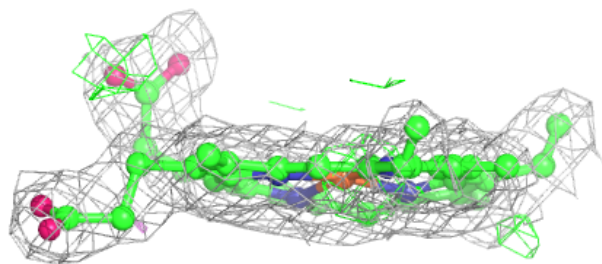
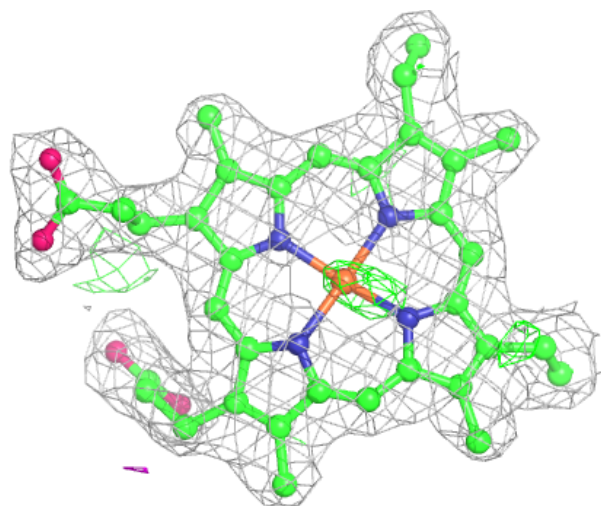
Electron density around HEC I 1002:

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



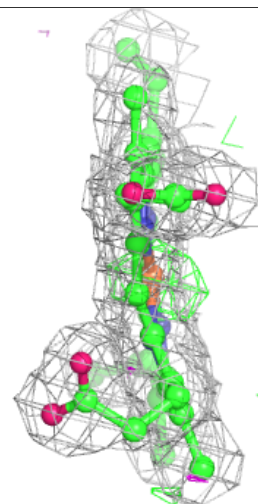
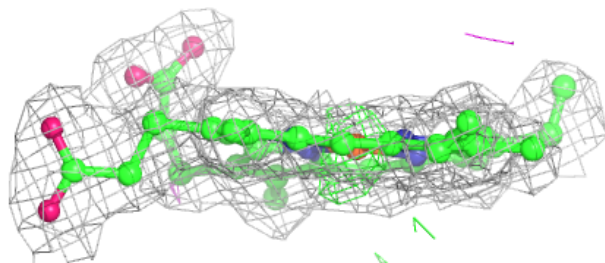
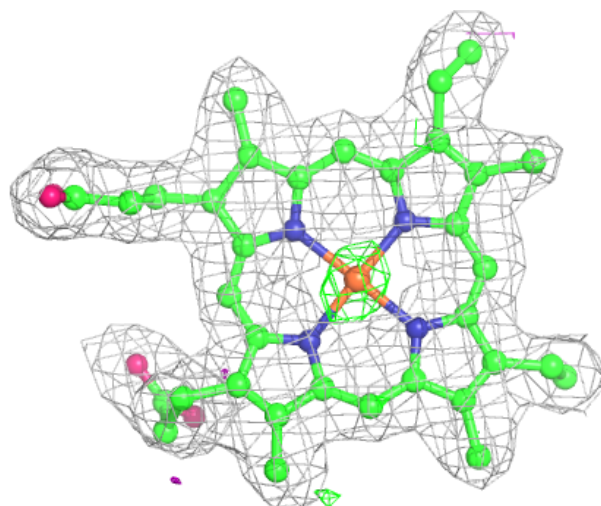
Electron density around HEC R 1002:

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



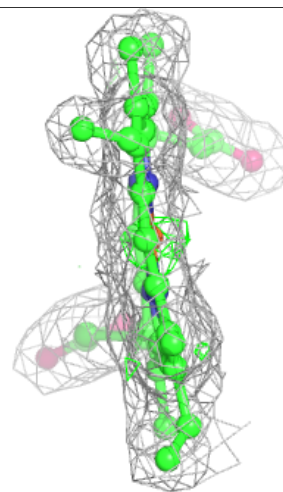
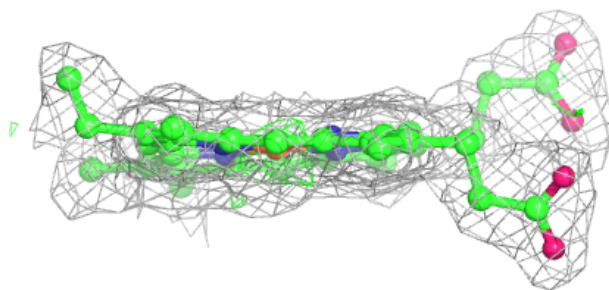
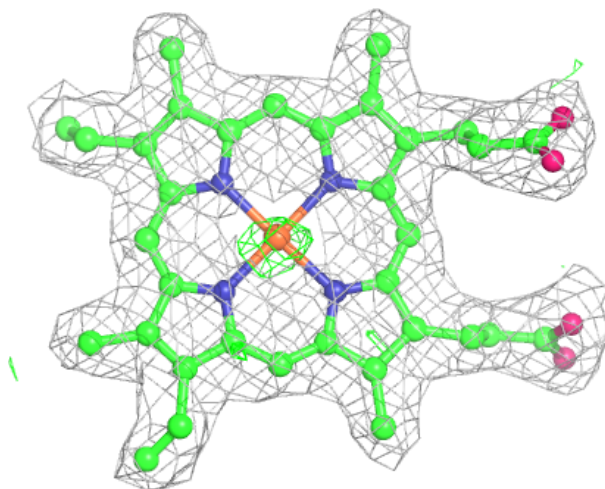
Electron density around HEC B 1002:

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



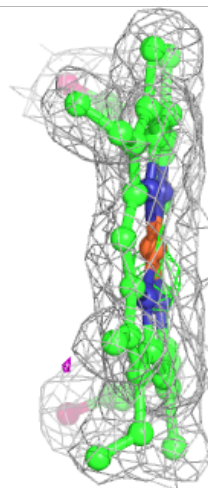
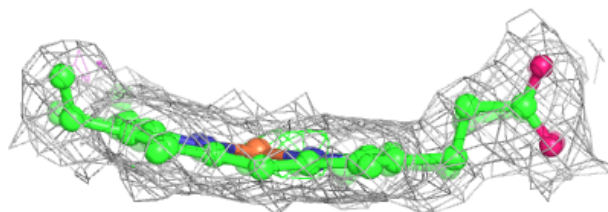
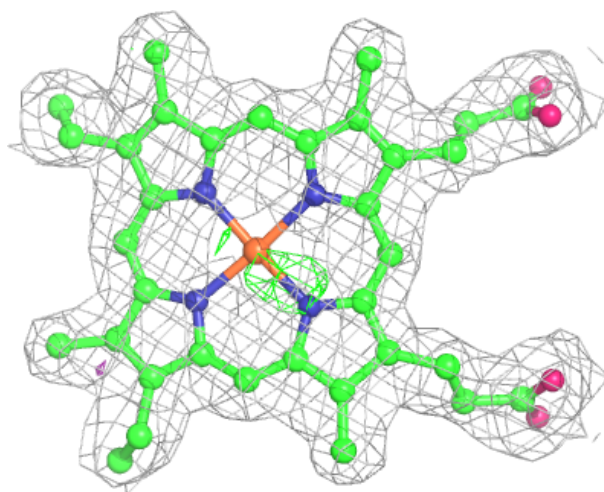
Electron density around HEC I 1004:

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



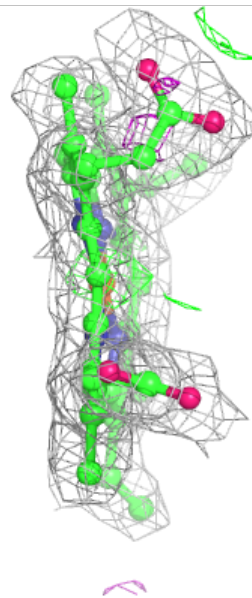
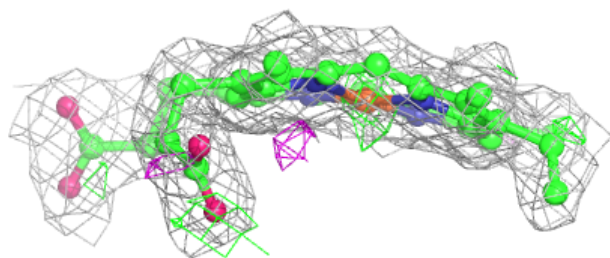
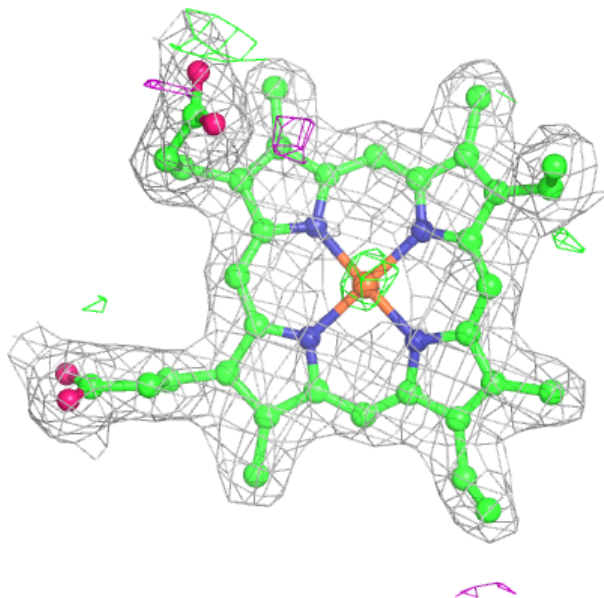
Electron density around HEC J 1003:

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



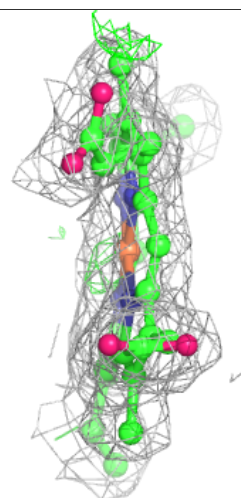
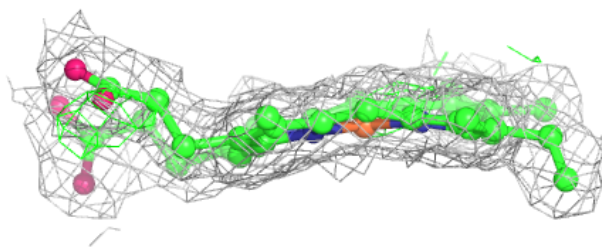
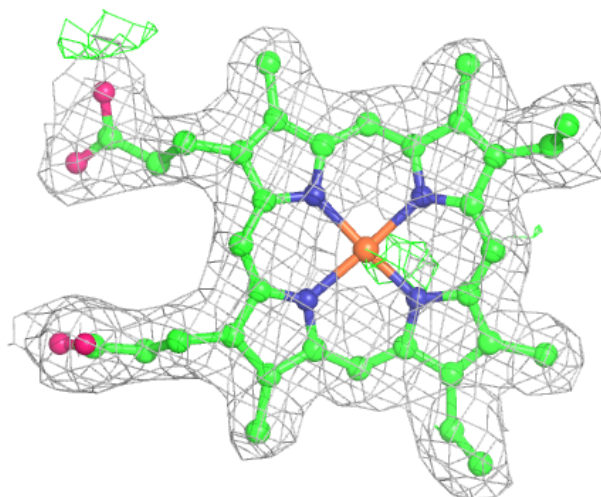
Electron density around HEC O 1003:

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



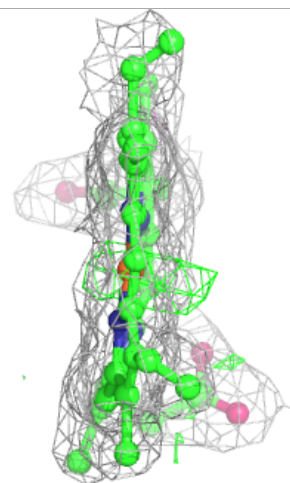
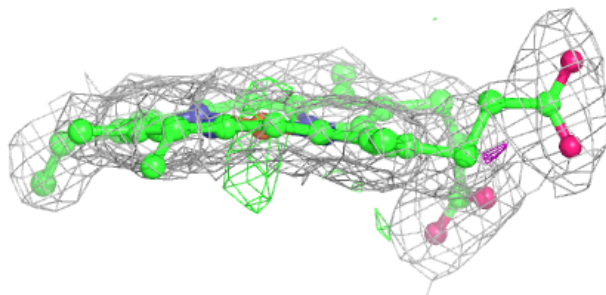
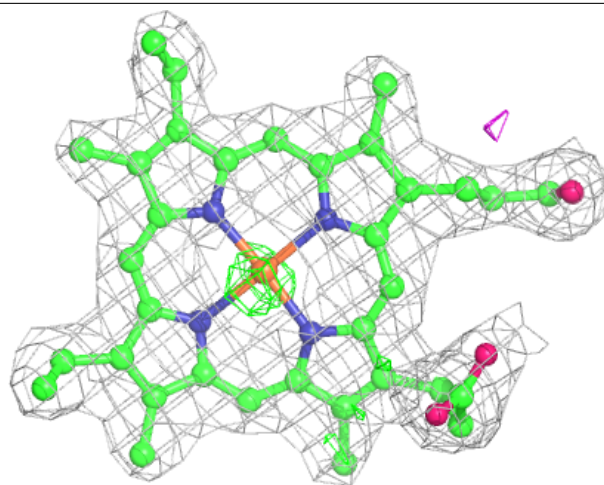
Electron density around HEC P 1004:

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



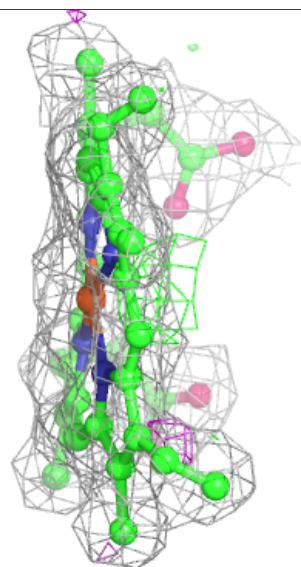
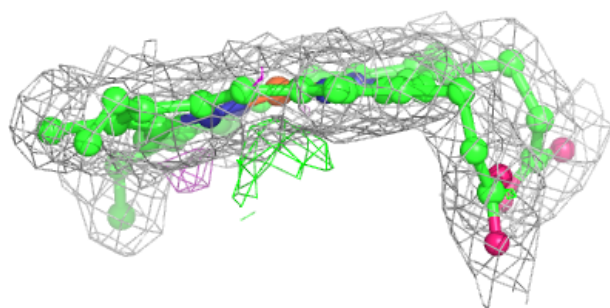
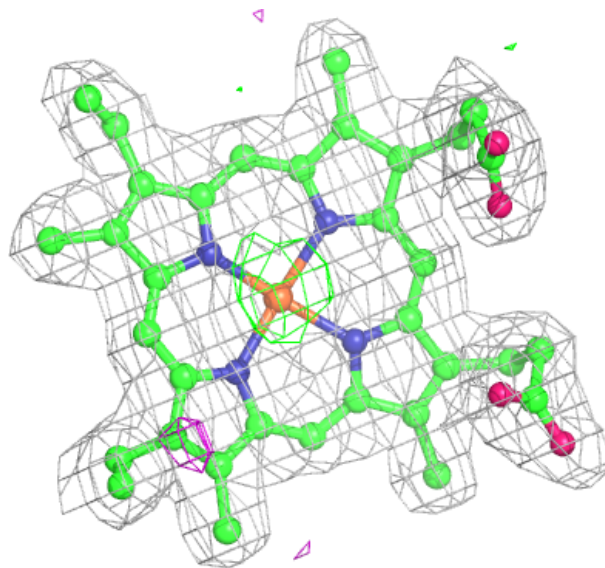
Electron density around HEC Q 1002:

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



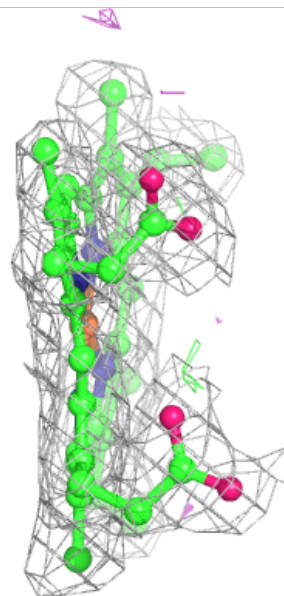
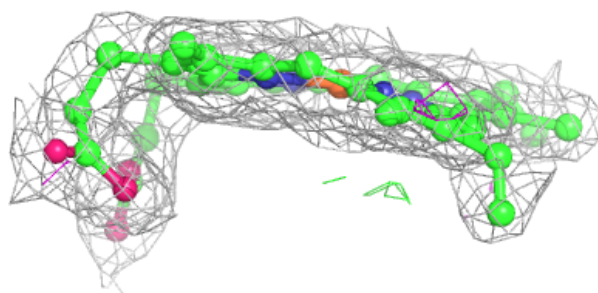
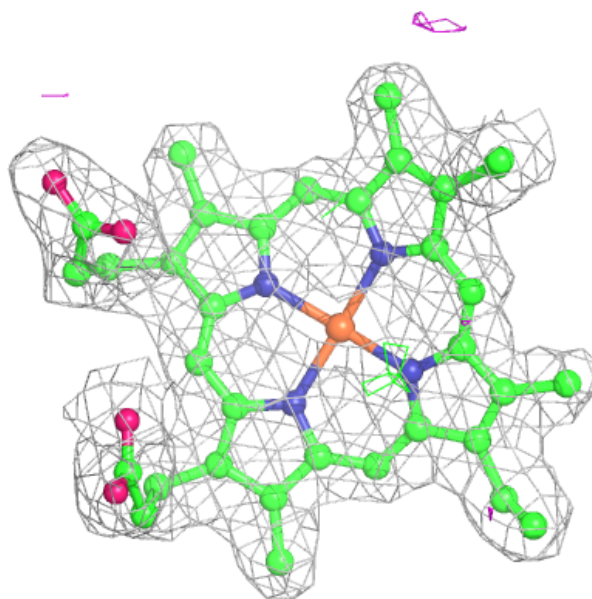
Electron density around HEC M 1001:

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



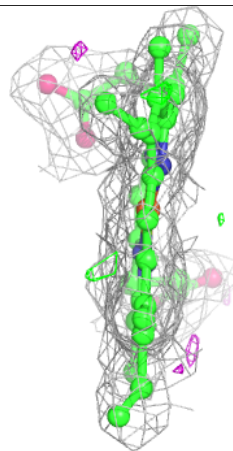
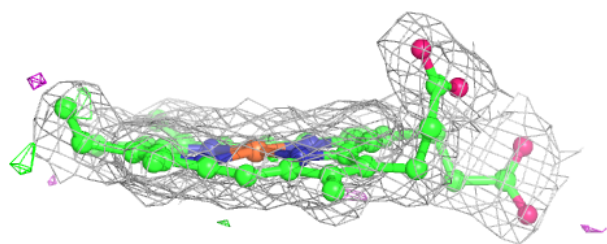
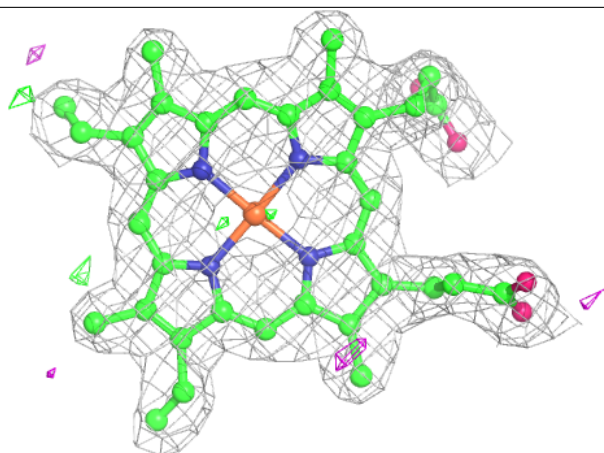
Electron density around HEC J 1001:

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



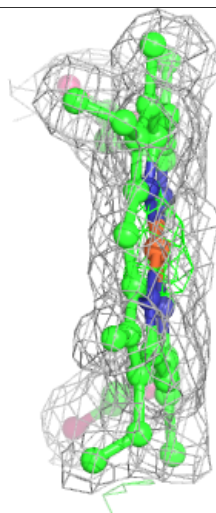
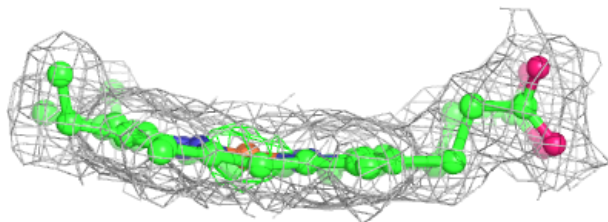
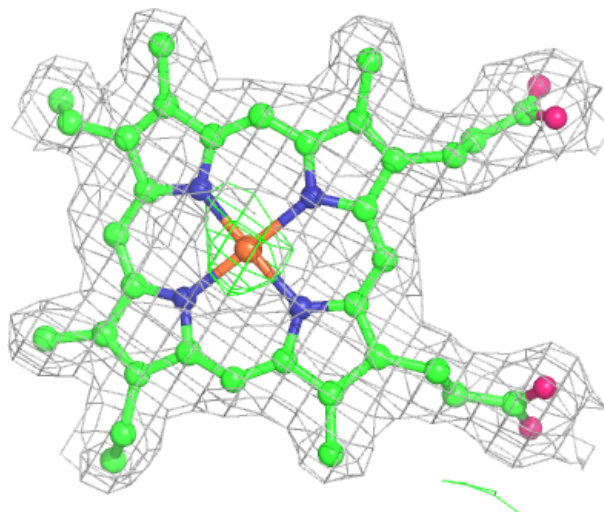
Electron density around HEC P 1002:

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



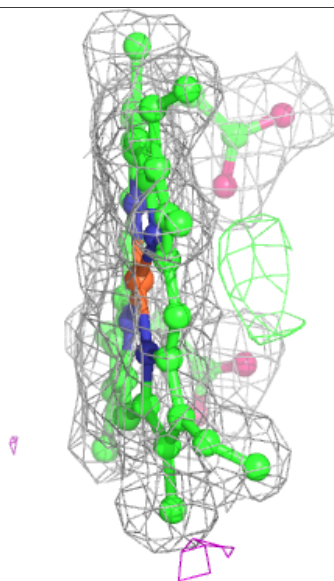
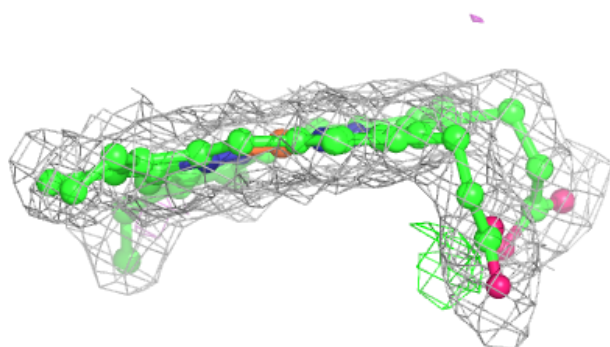
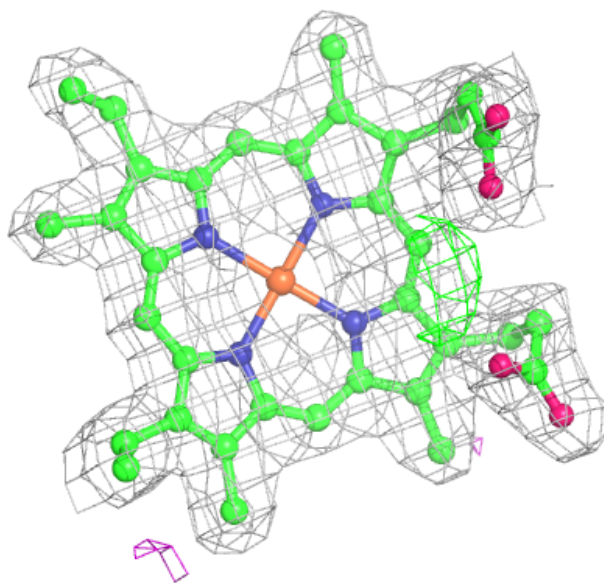
Electron density around HEC G 1003:

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



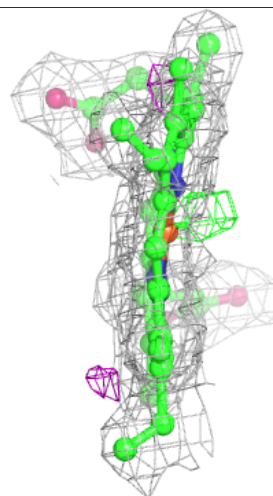
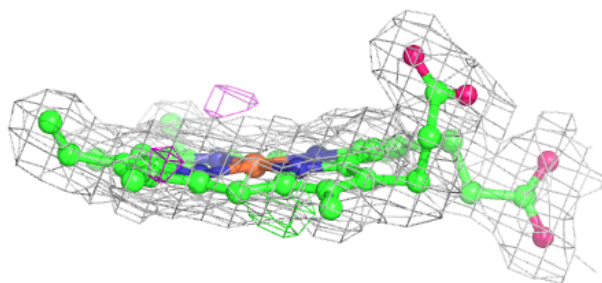
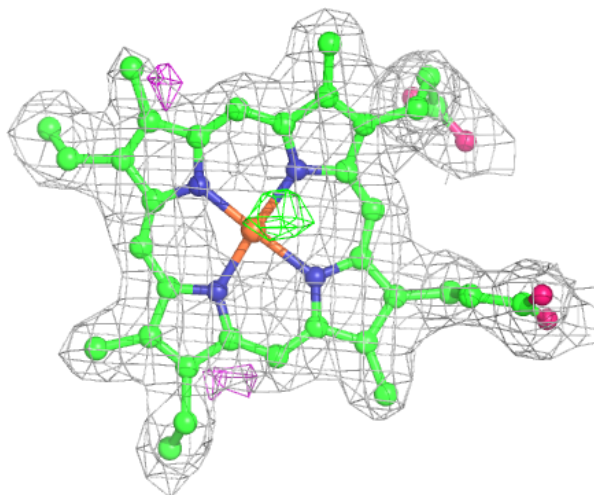
Electron density around HEC G 1001:

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



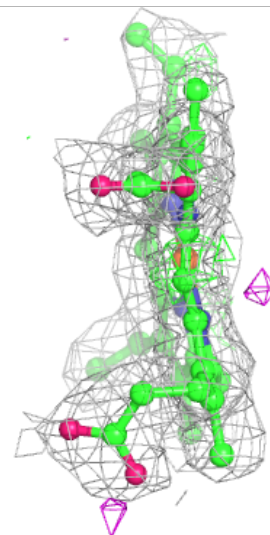
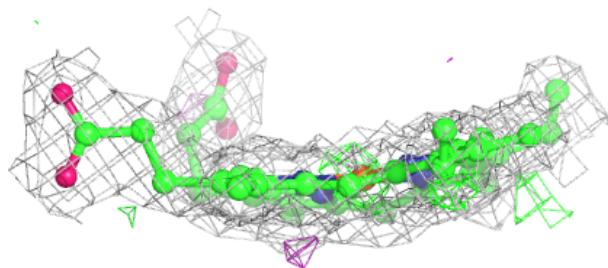
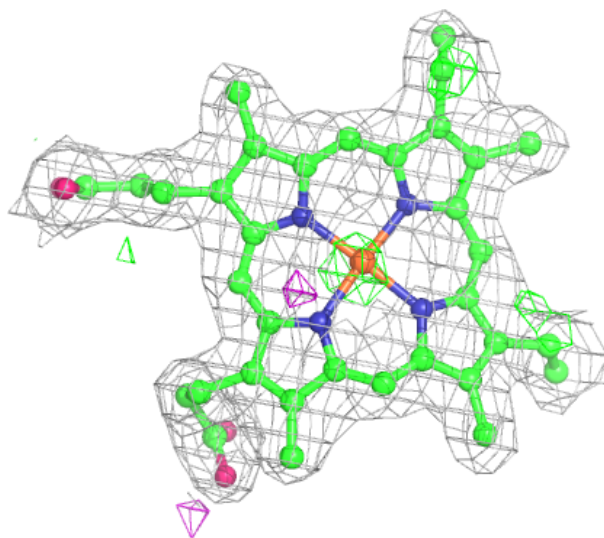
Electron density around HEC M 1002:

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



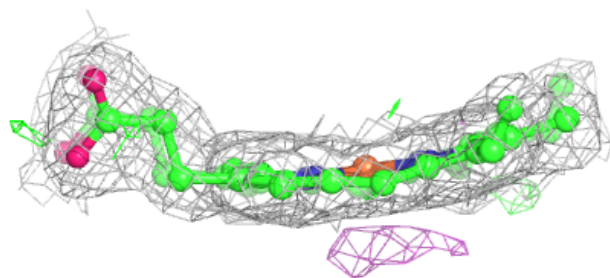
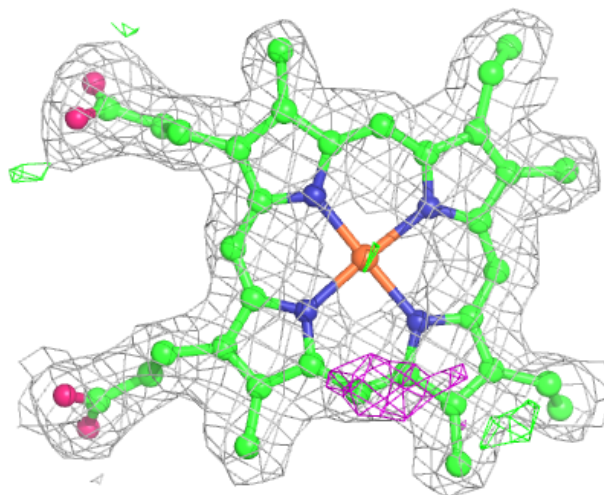
Electron density around HEC R 1003:

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



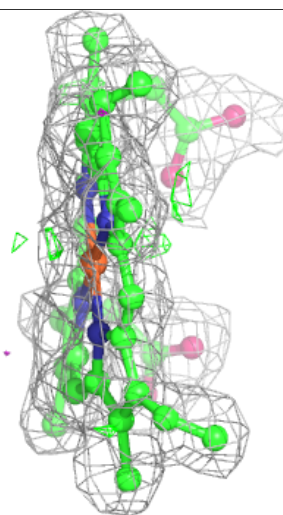
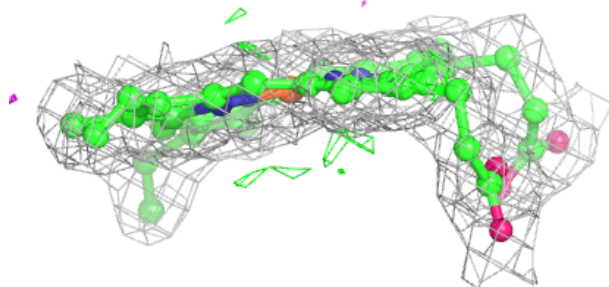
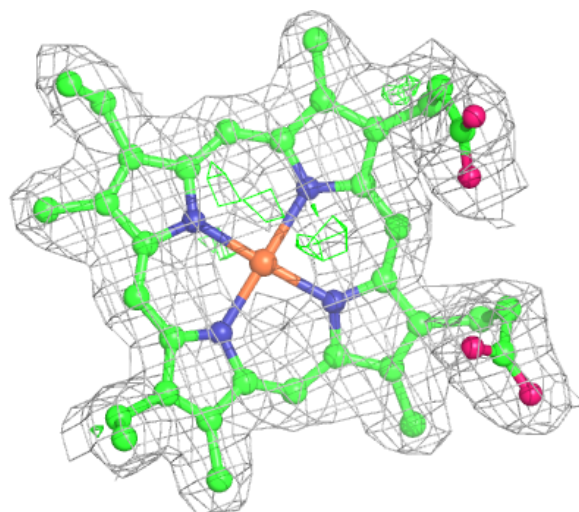
Electron density around HEC E 1003:

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



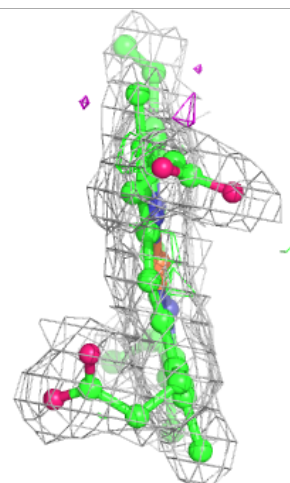
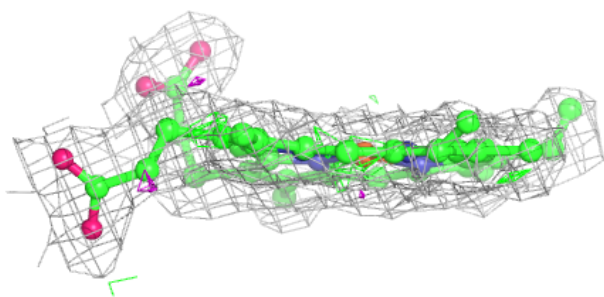
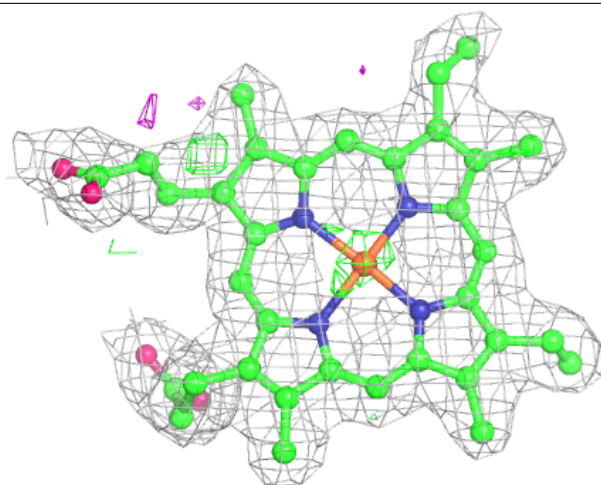
Electron density around HEC B 1001:

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



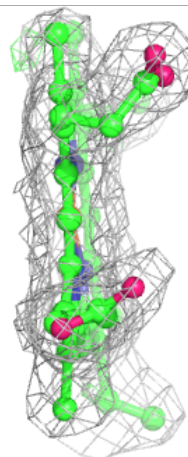
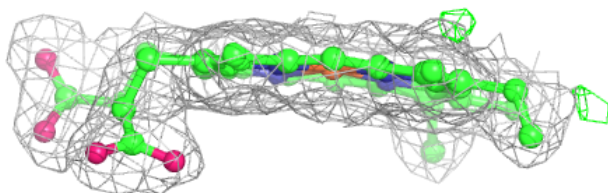
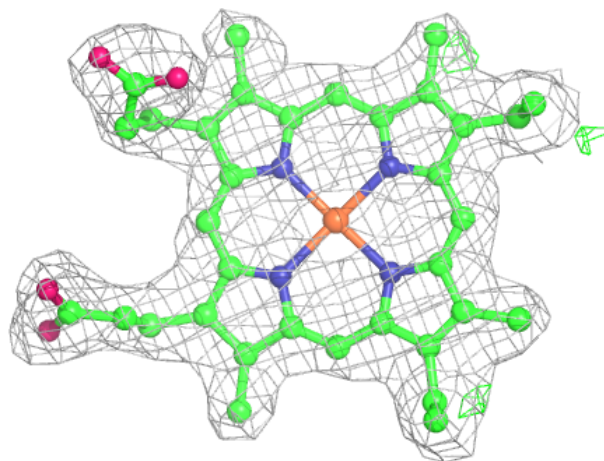
Electron density around HEC G 1002:

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



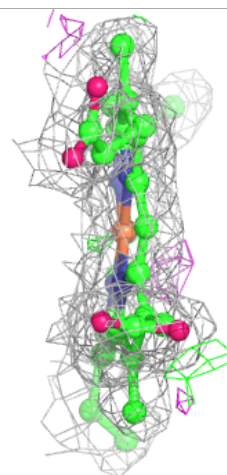
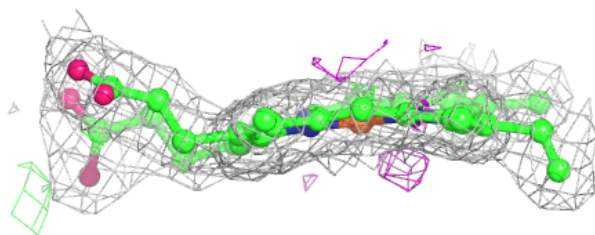
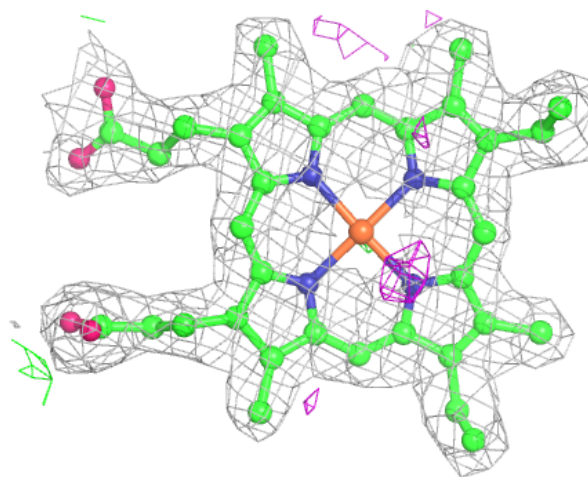
Electron density around HEC O 1001:

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



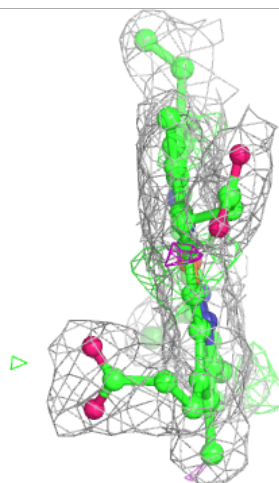
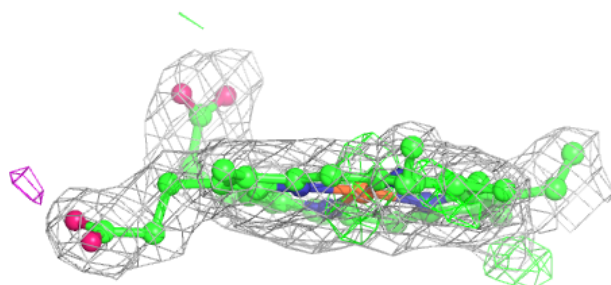
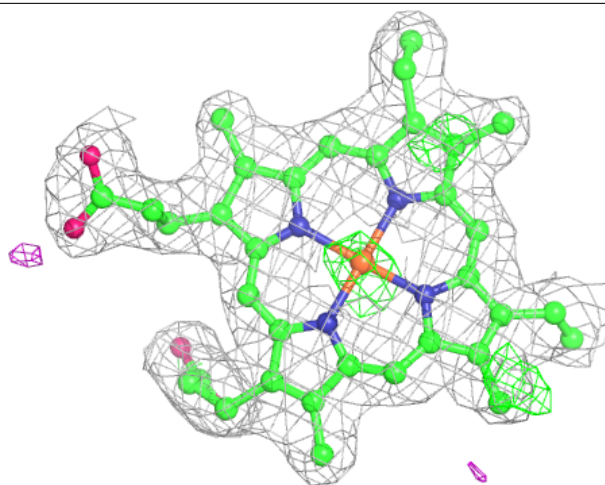
Electron density around HEC E 1004:

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



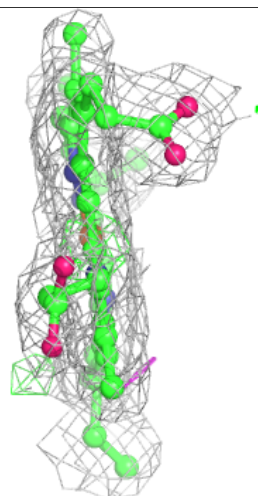
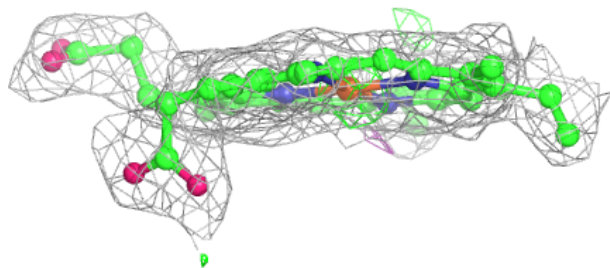
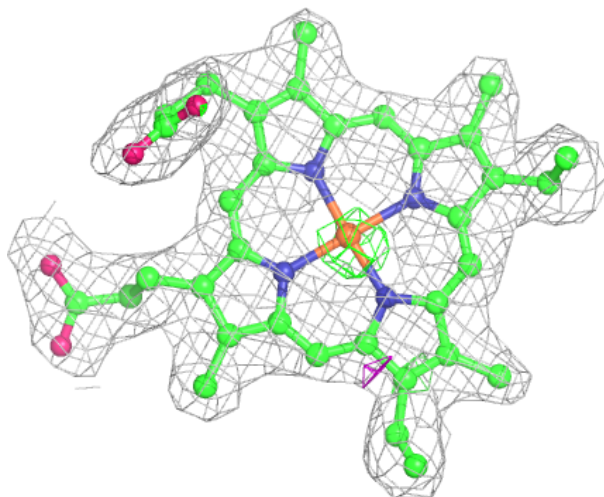
Electron density around HEC F 1002:

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



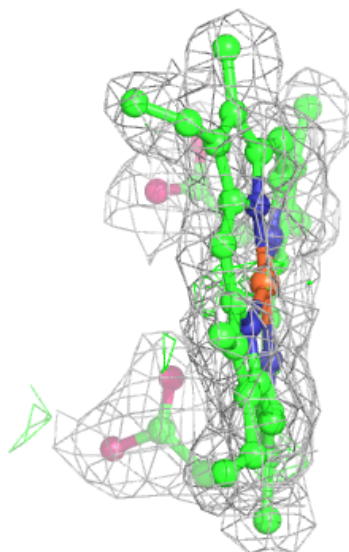
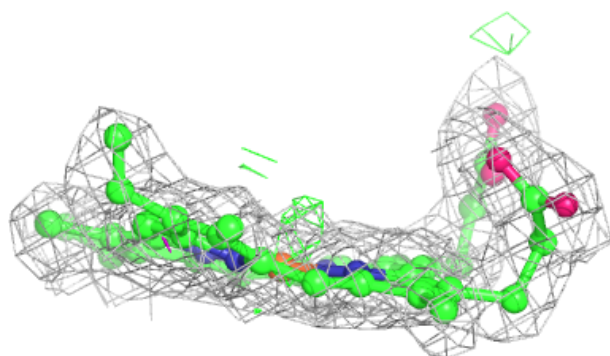
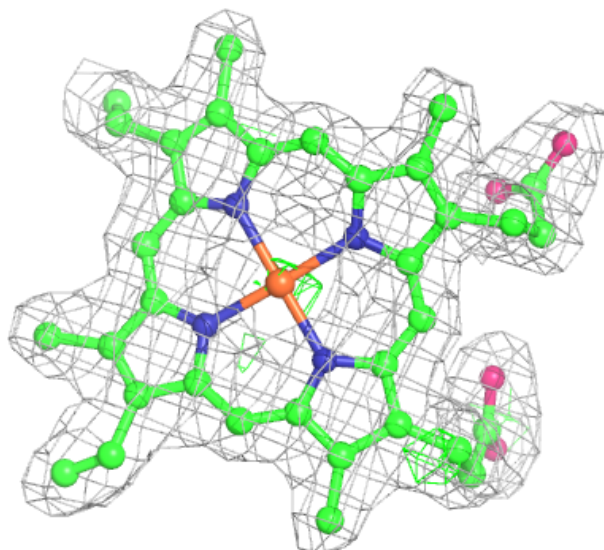
Electron density around HEC O 1002:

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



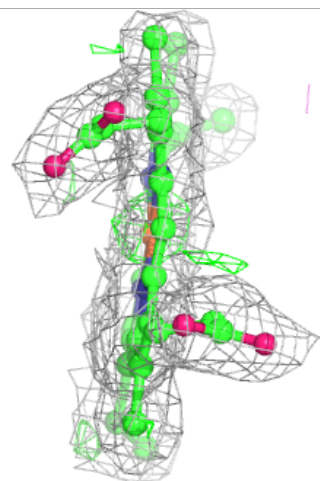
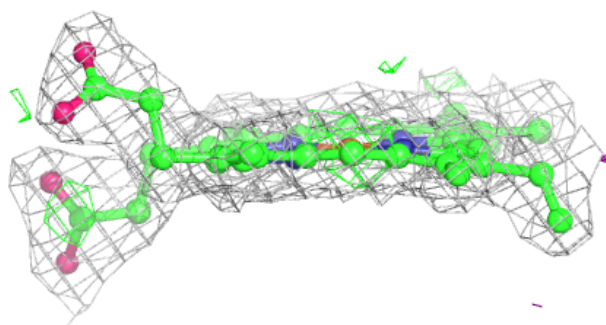
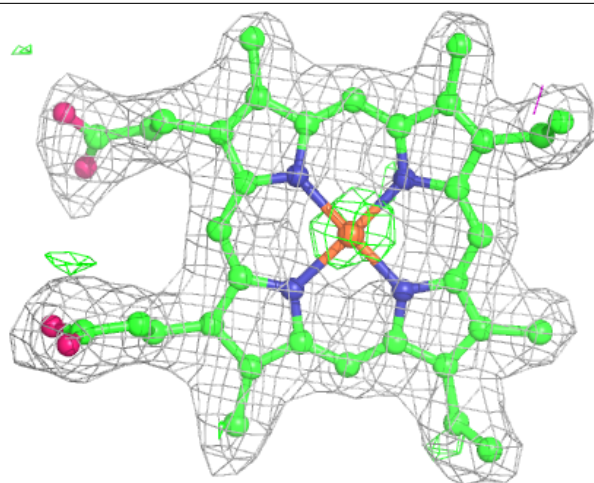
Electron density around HEC H 1001:

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



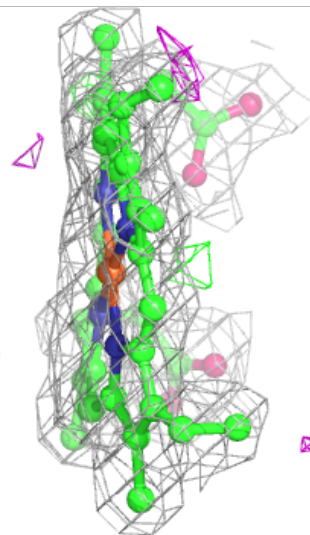
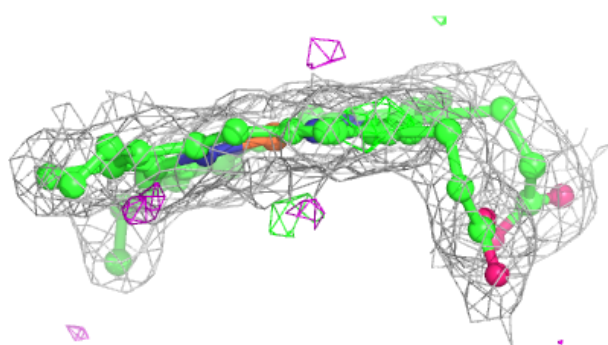
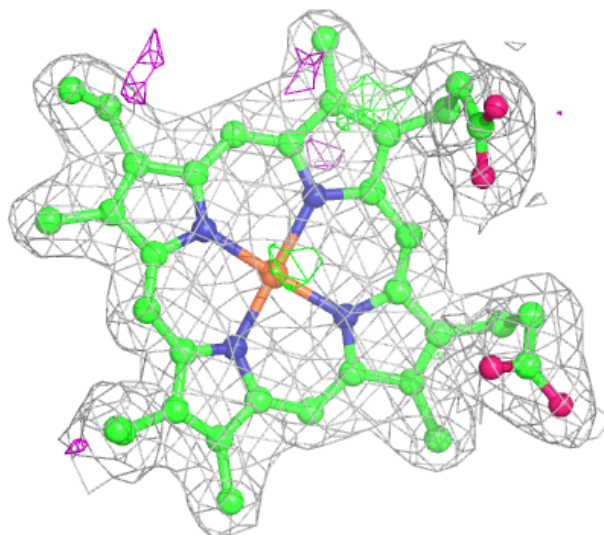
Electron density around HEC L 1004:

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



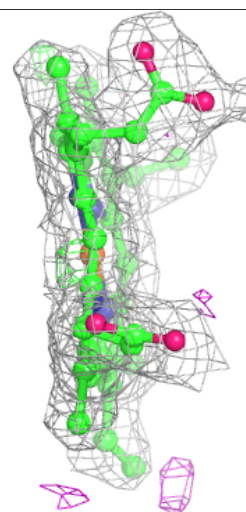
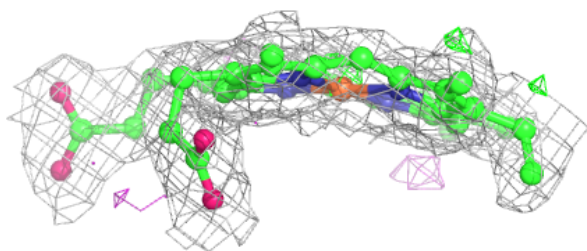
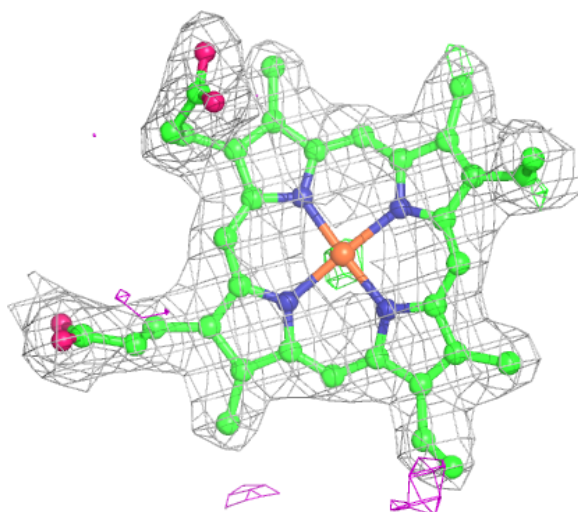
Electron density around HEC D 1001:

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



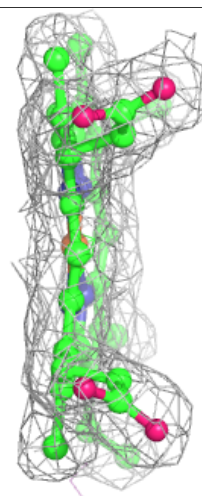
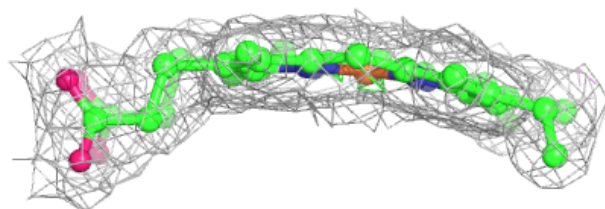
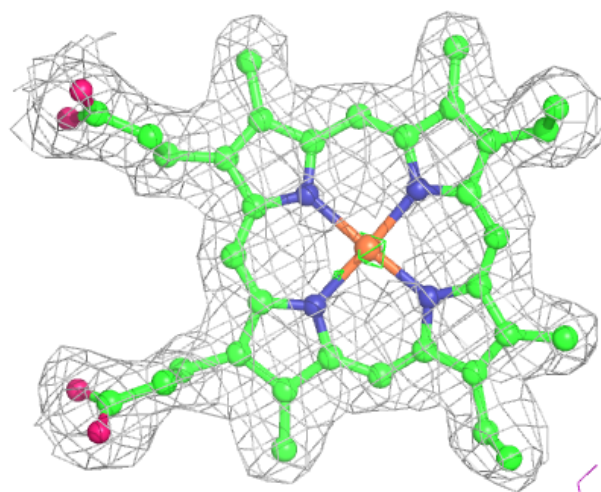
Electron density around HEC L 1003:

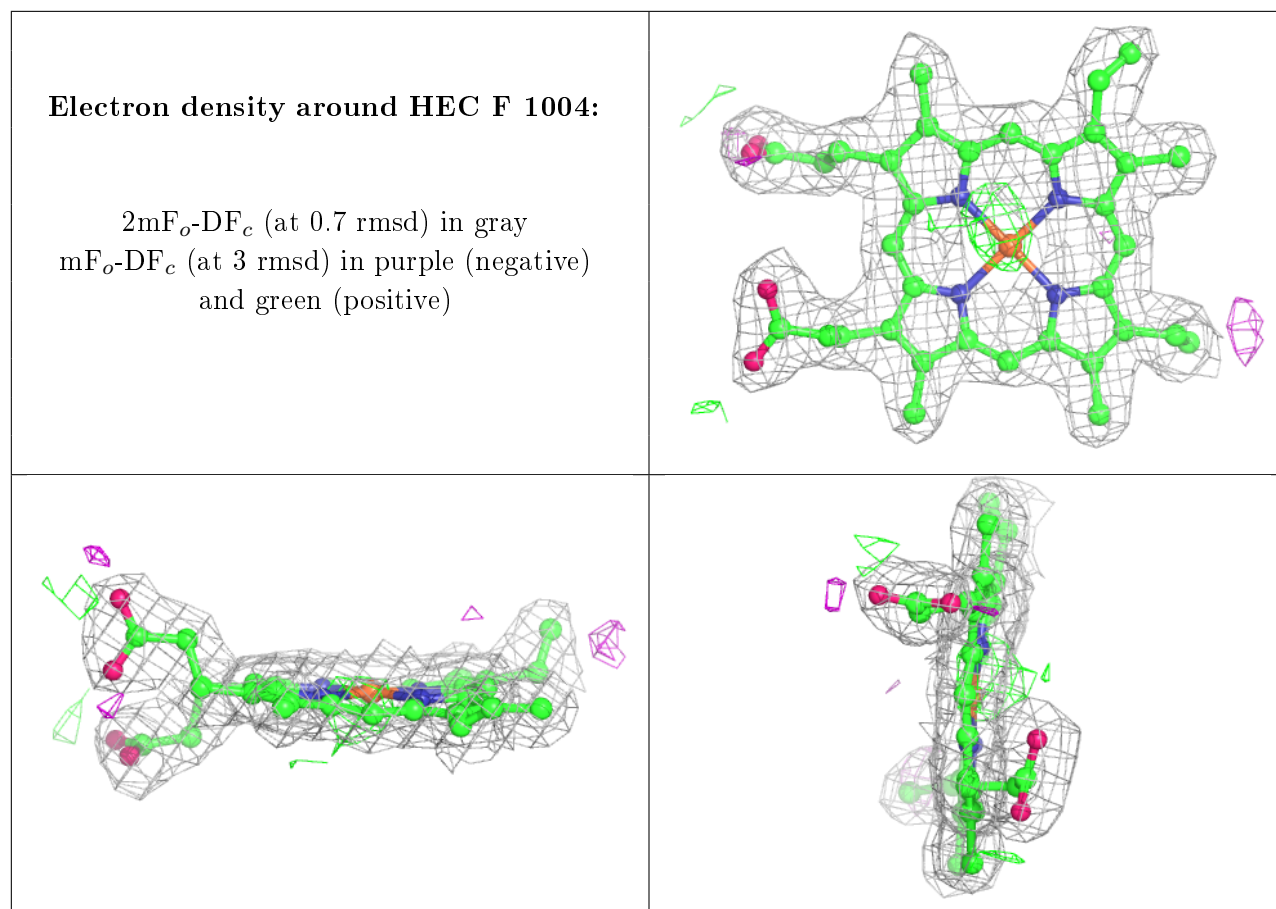
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC P 1003:

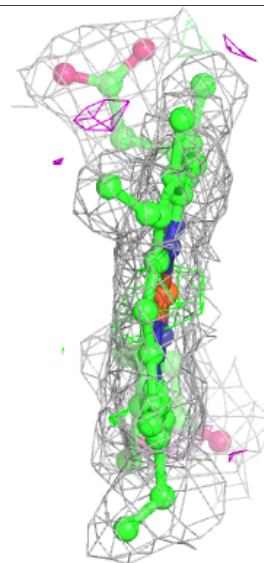
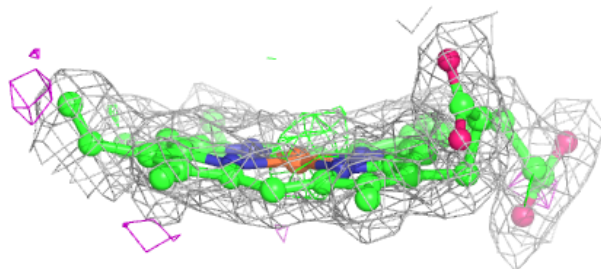
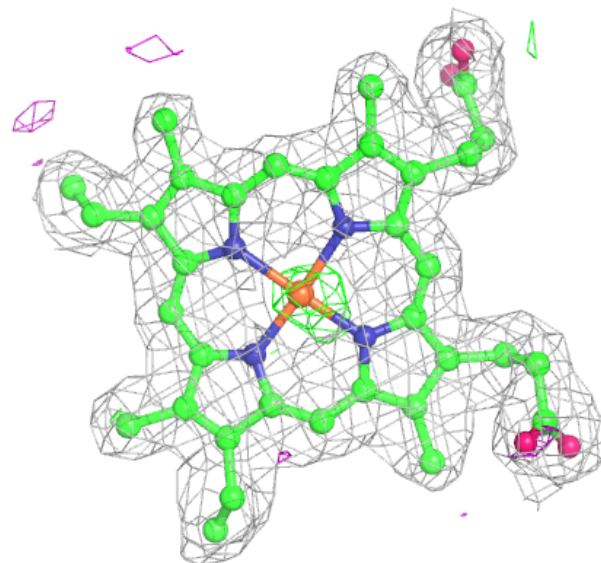
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





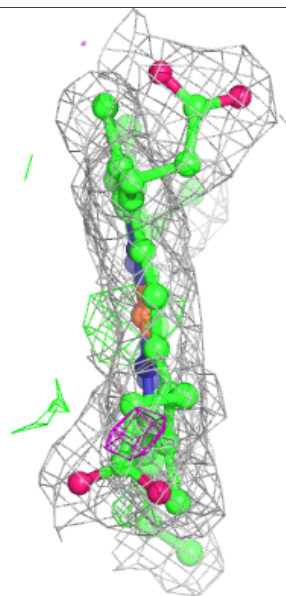
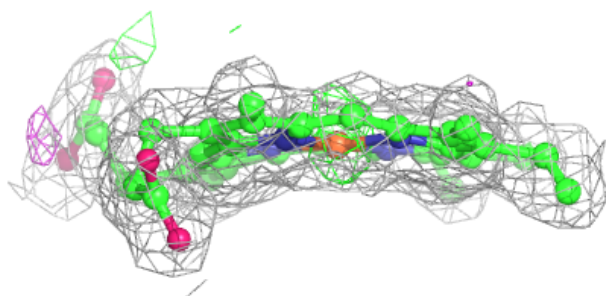
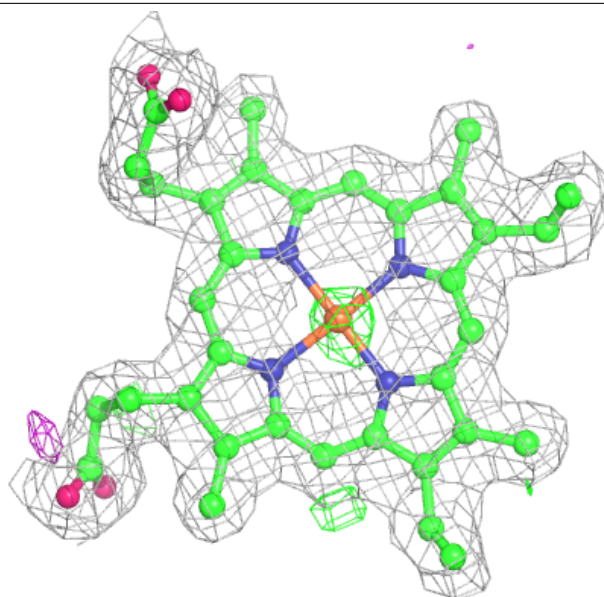
Electron density around HEC B 1005:

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



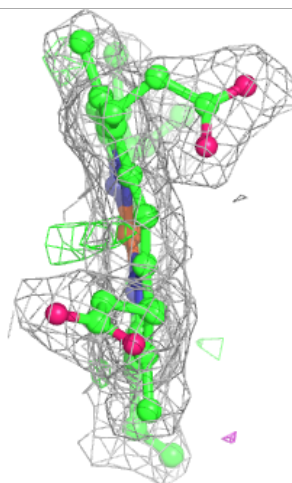
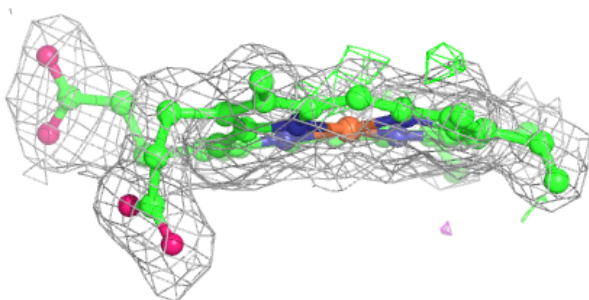
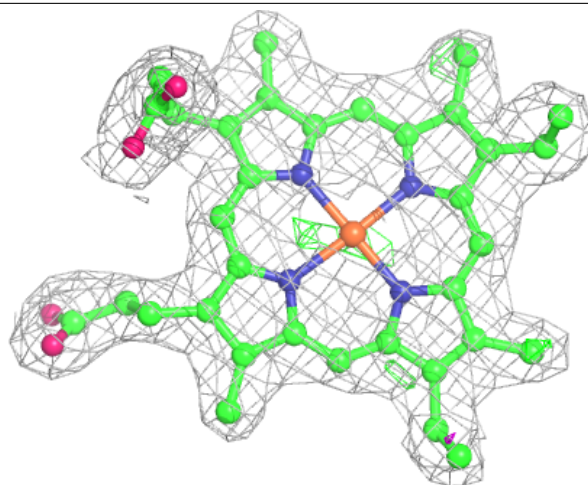
Electron density around HEC D 1005:

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



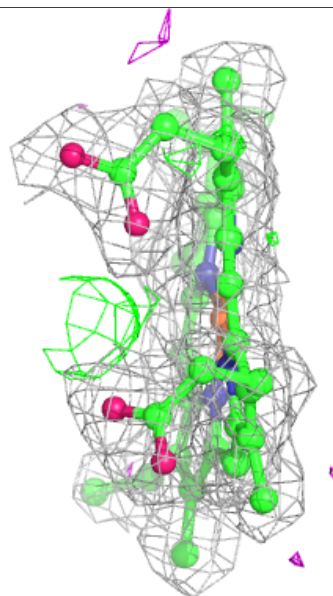
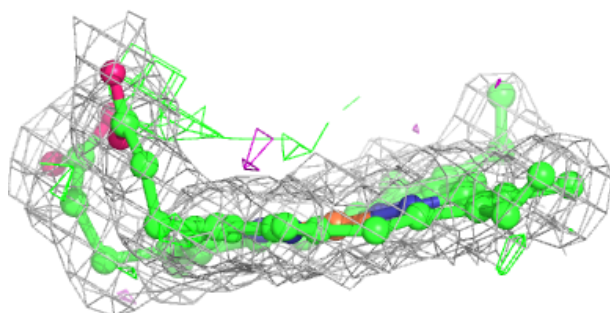
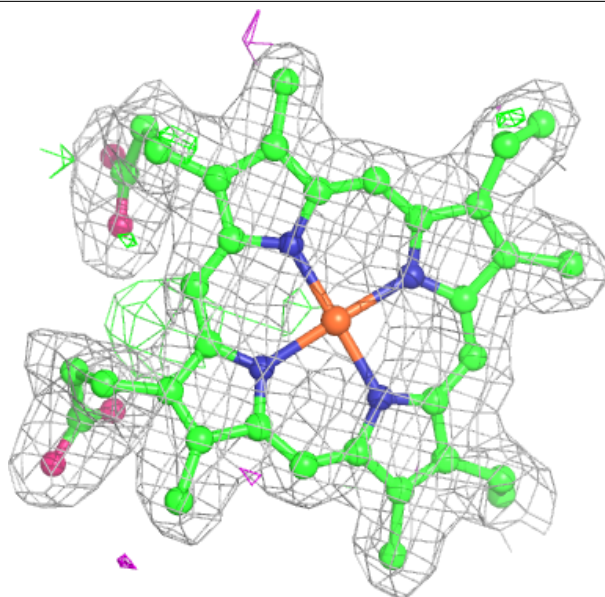
Electron density around HEC J 1002:

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



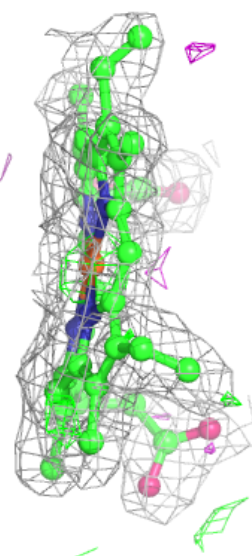
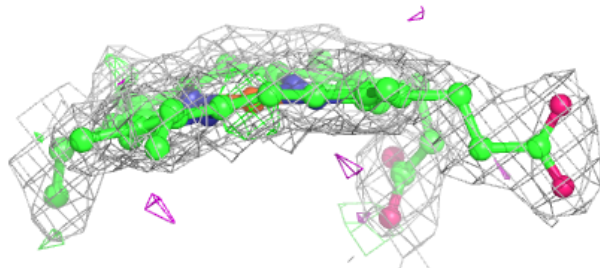
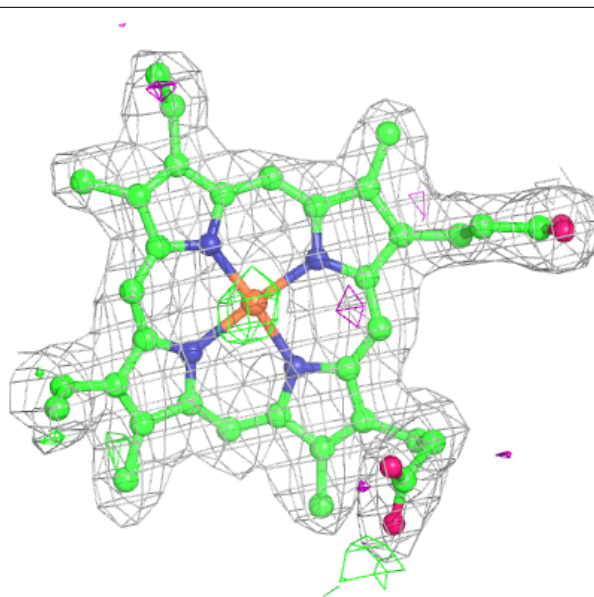
Electron density around HEC N 1001:

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



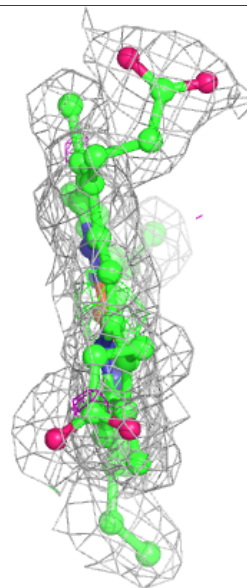
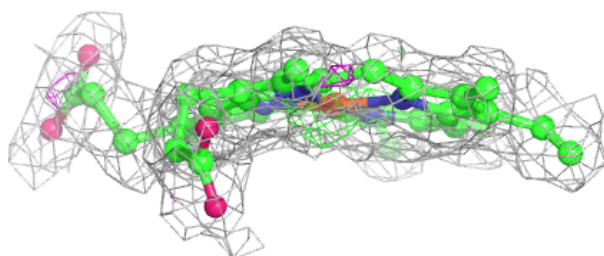
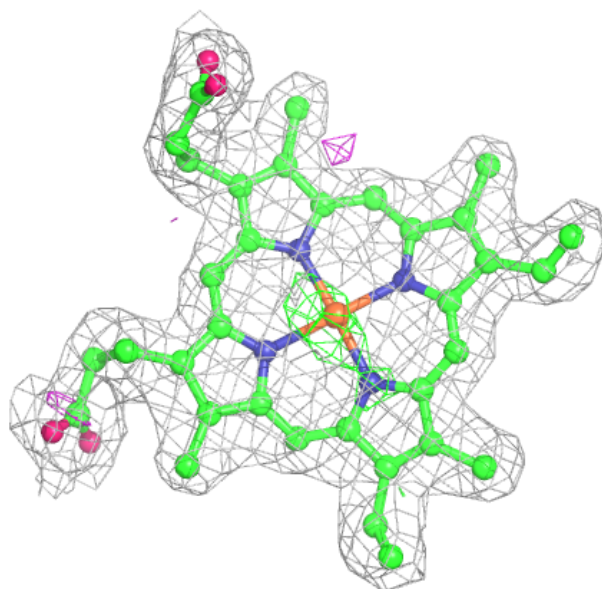
Electron density around HEC F 1003:

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



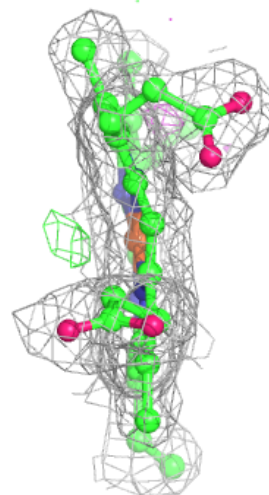
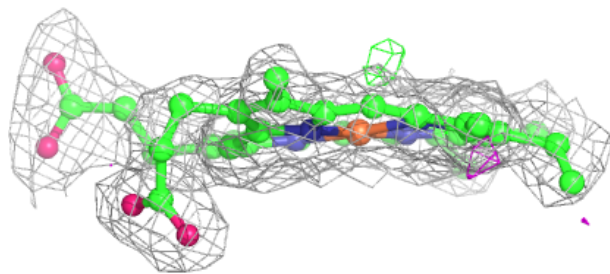
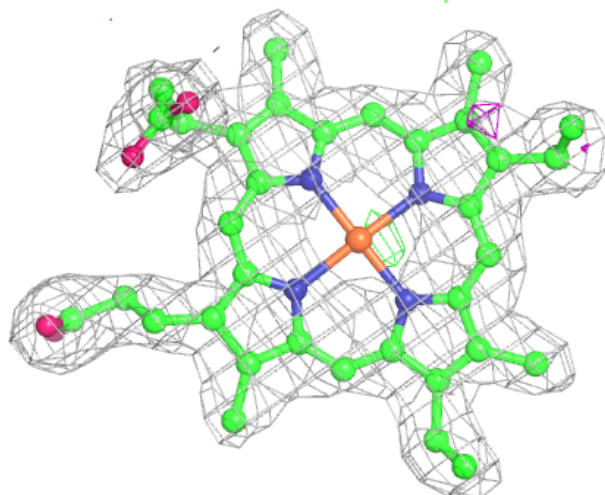
Electron density around HEC H 1005:

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



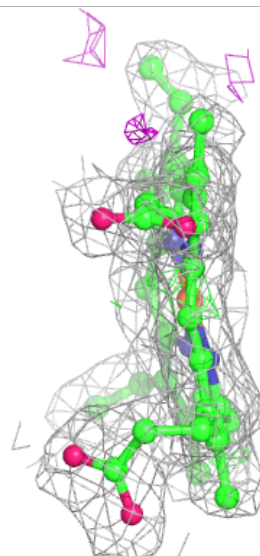
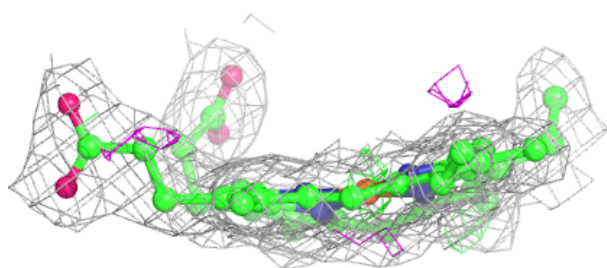
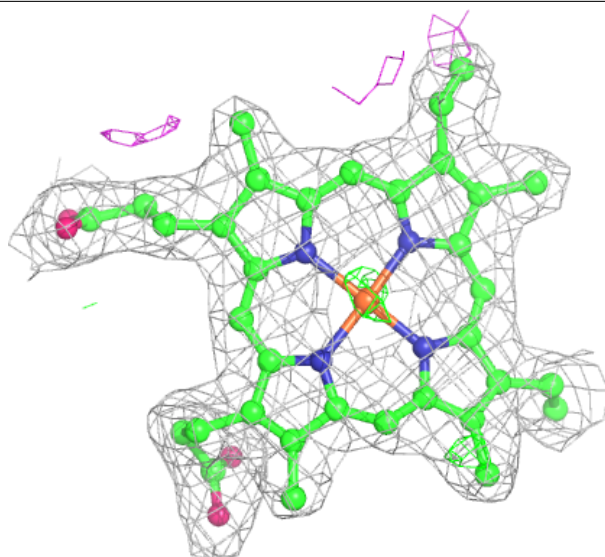
Electron density around HEC E 1002:

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



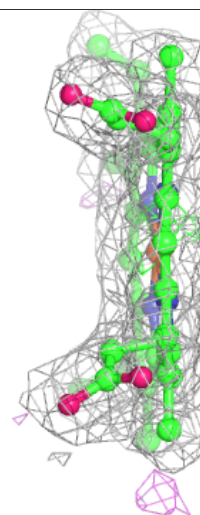
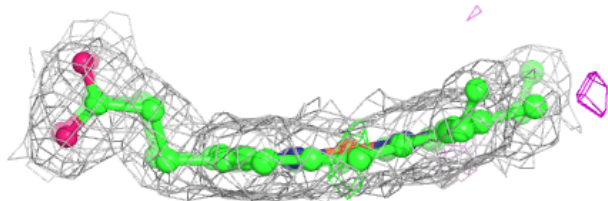
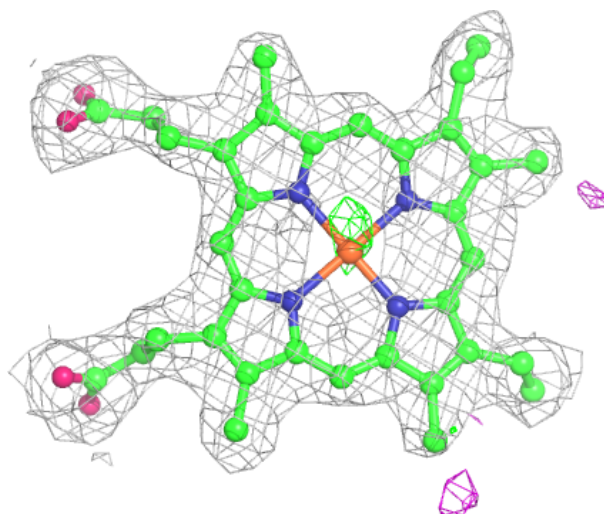
Electron density around HEC I 1003:

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



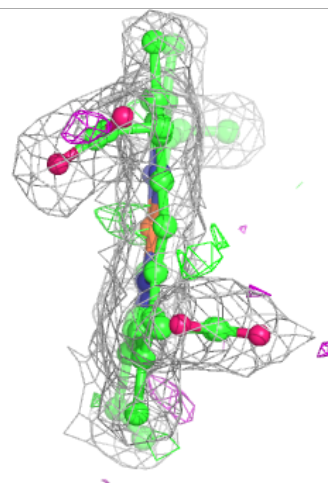
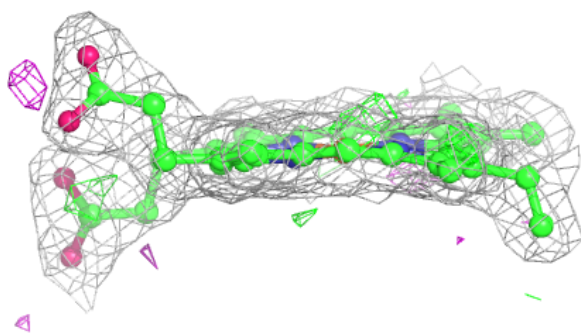
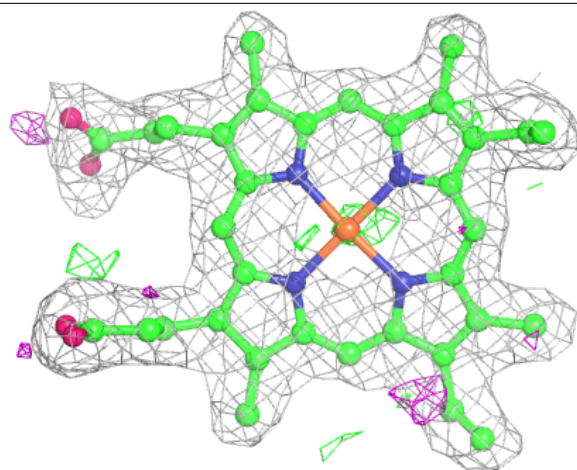
Electron density around HEC K 1003:

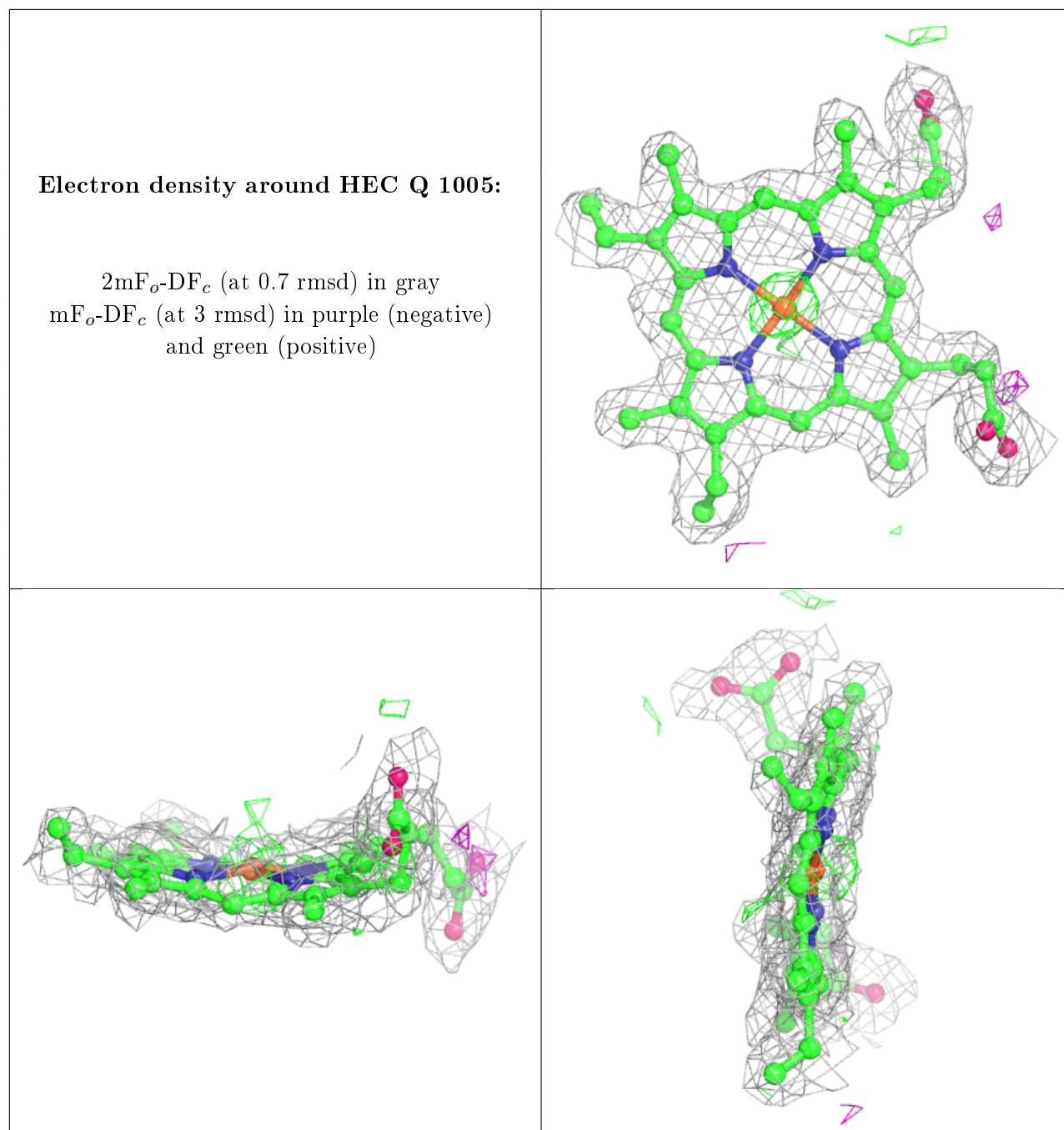
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC O 1004:

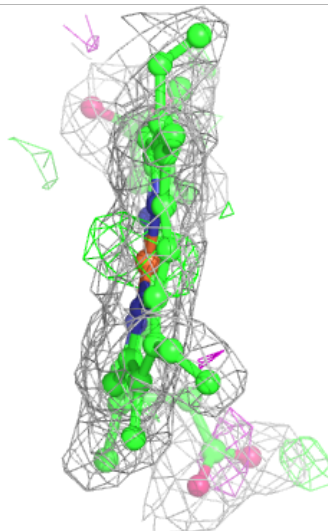
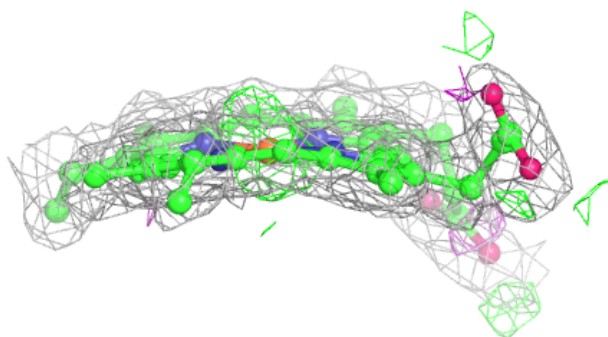
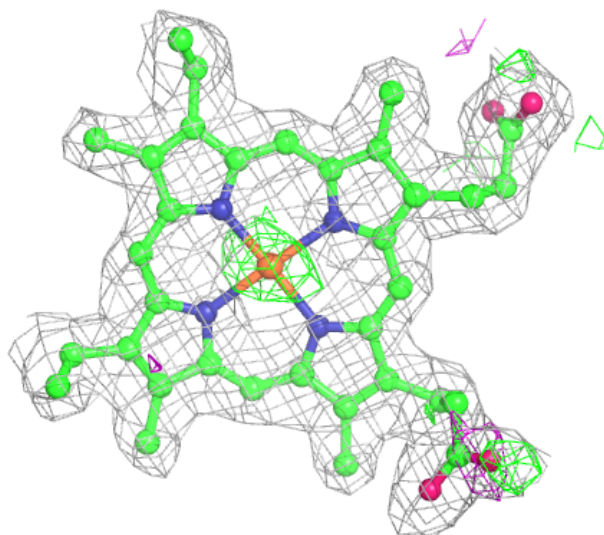
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





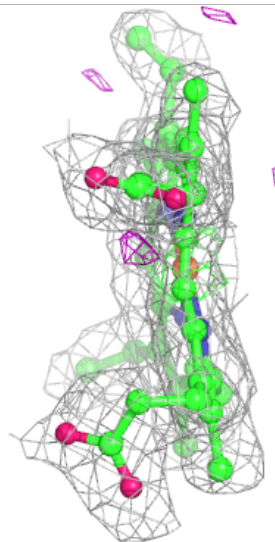
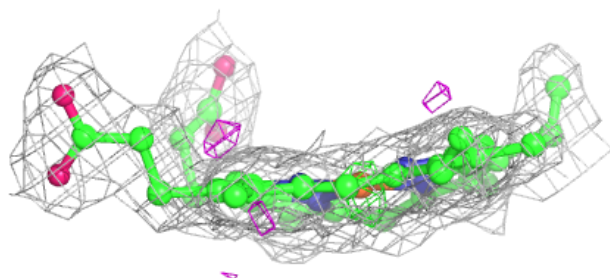
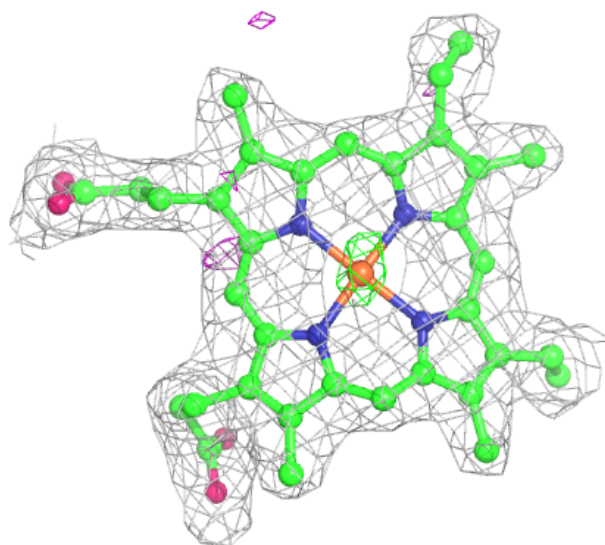
Electron density around HEC E 1005:

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



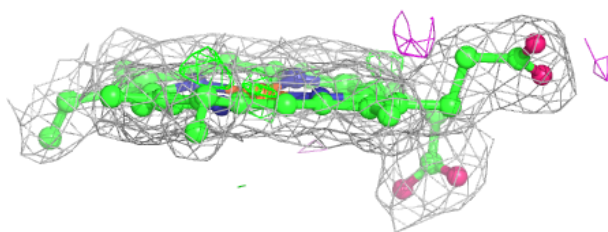
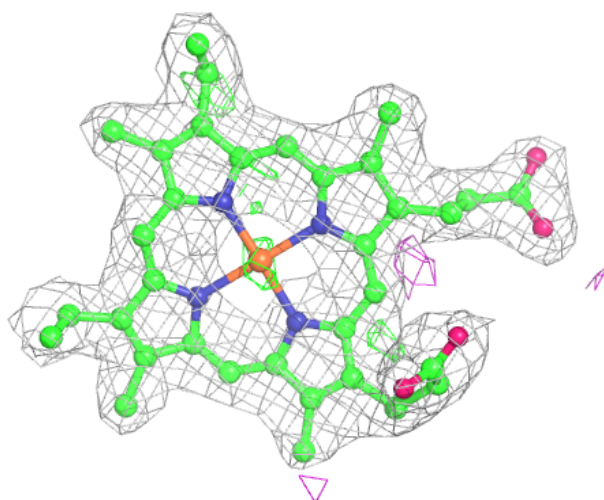
Electron density around HEC C 1003:

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



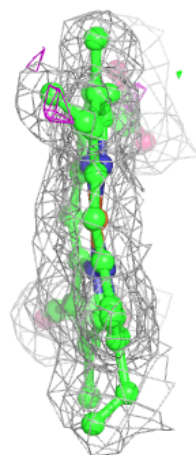
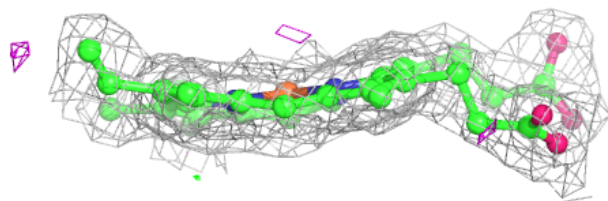
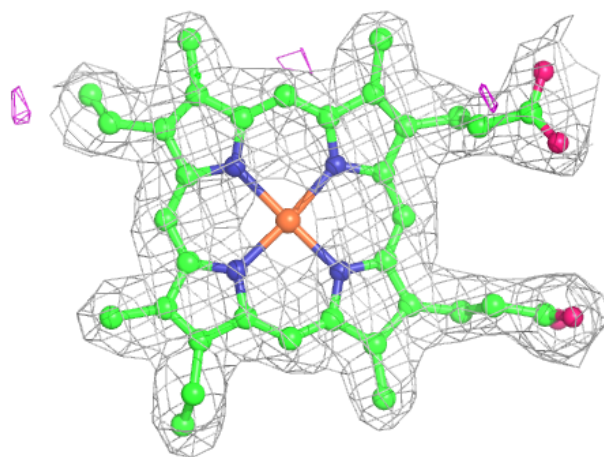
Electron density around HEC C 1002:

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



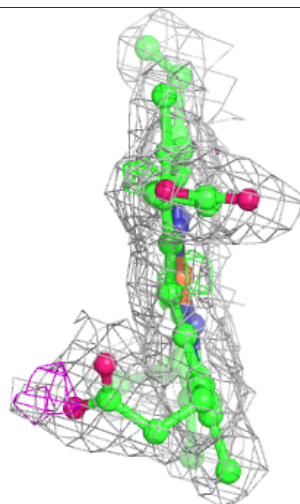
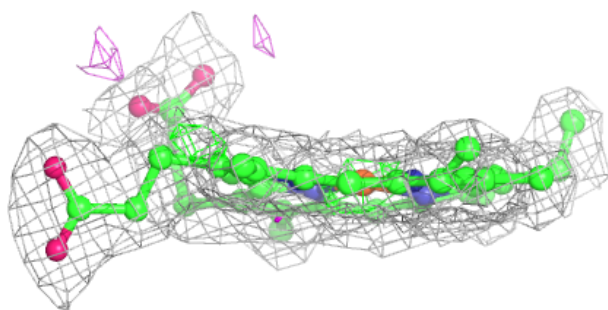
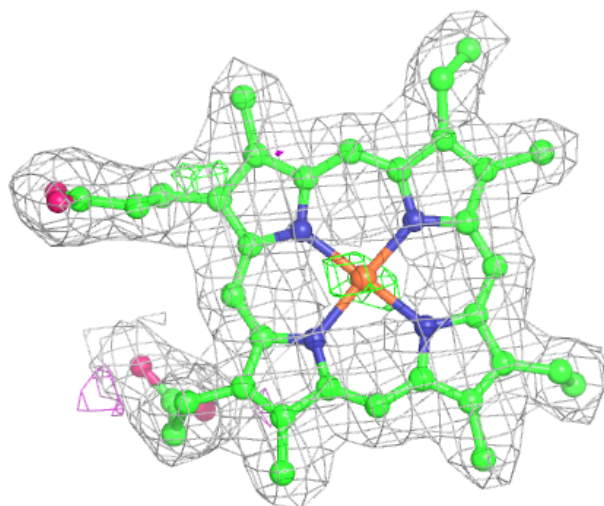
Electron density around HEC K 1004:

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



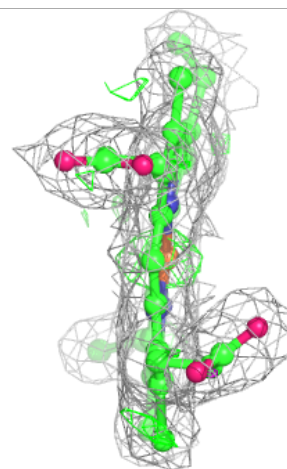
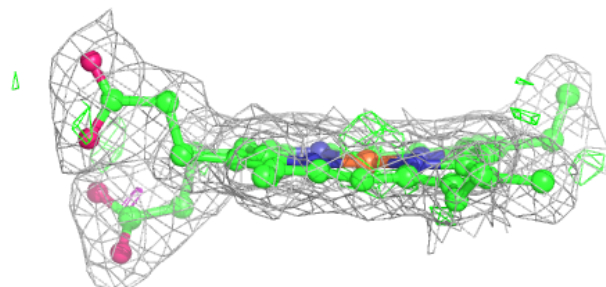
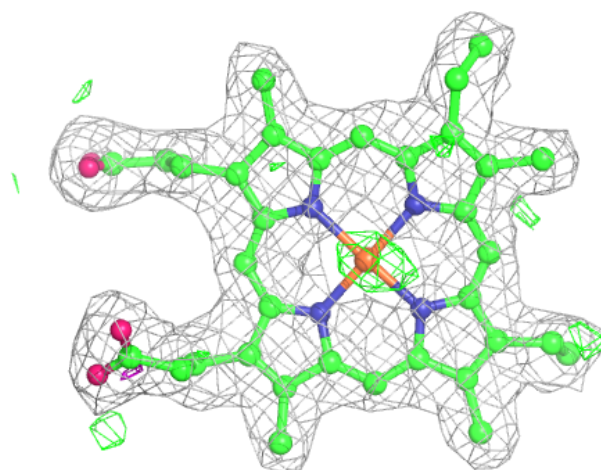
Electron density around HEC N 1002:

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



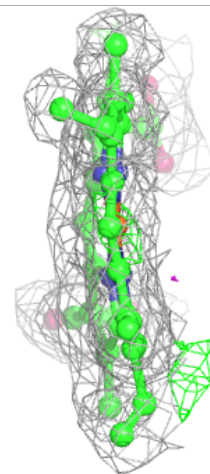
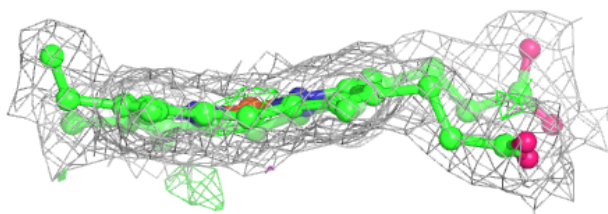
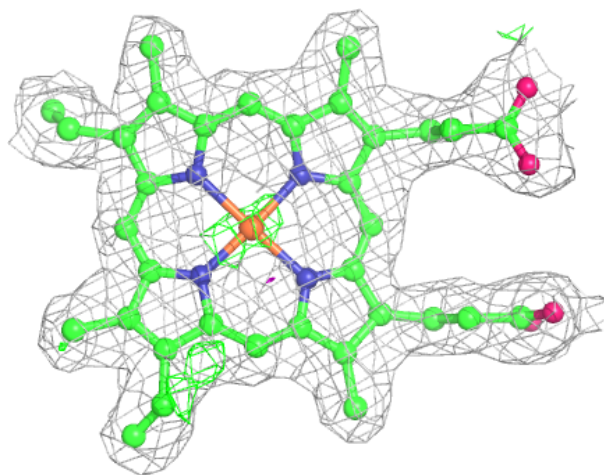
Electron density around HEC C 1004:

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



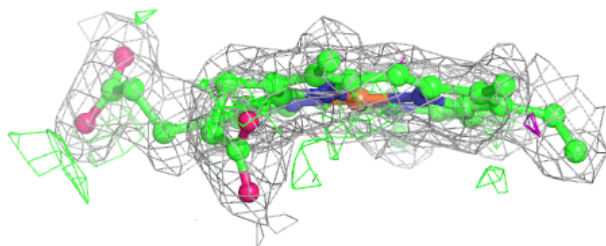
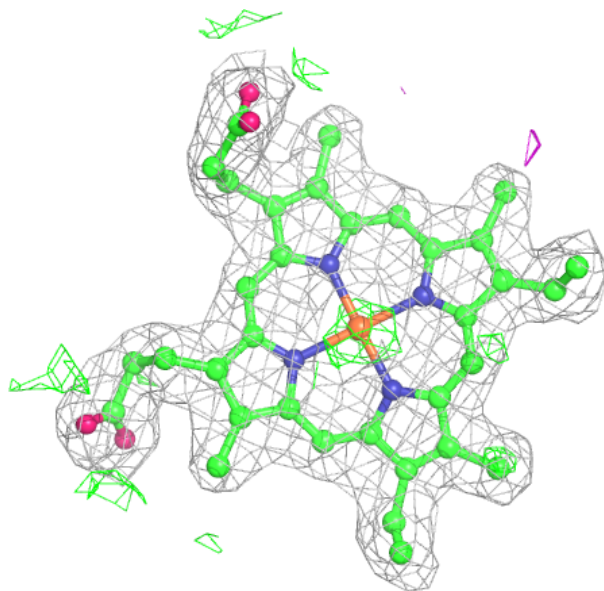
Electron density around HEC D 1004:

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



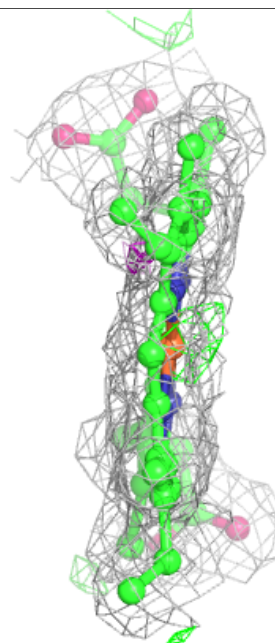
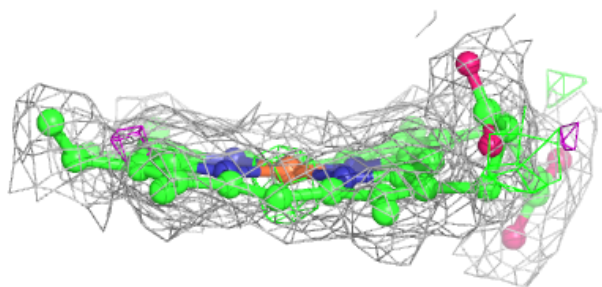
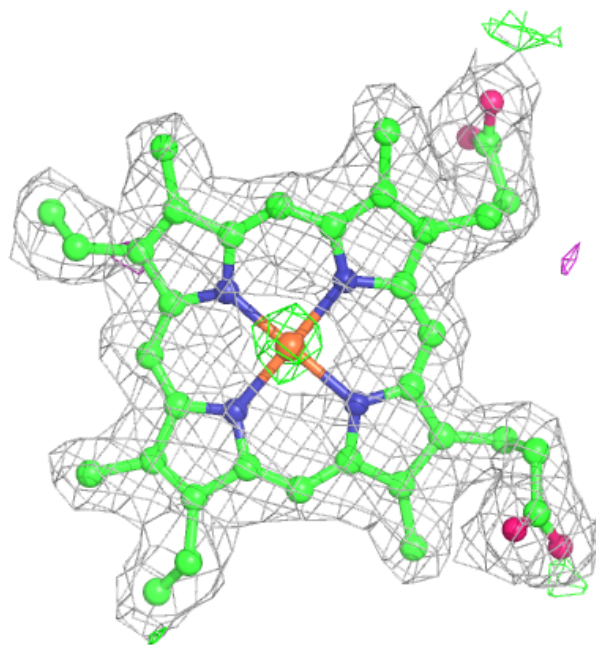
Electron density around HEC N 1005:

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



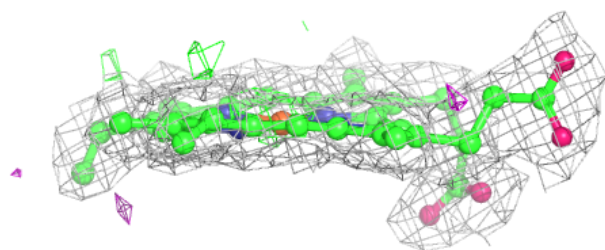
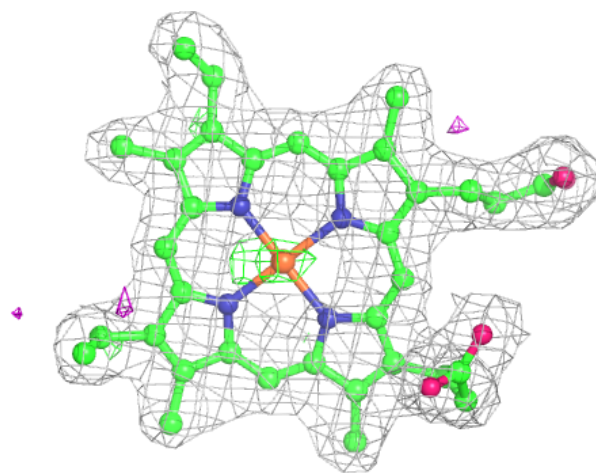
Electron density around HEC P 1005:

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



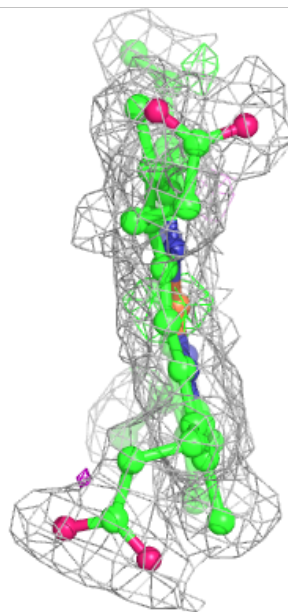
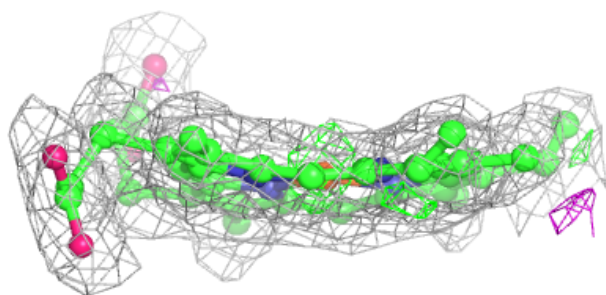
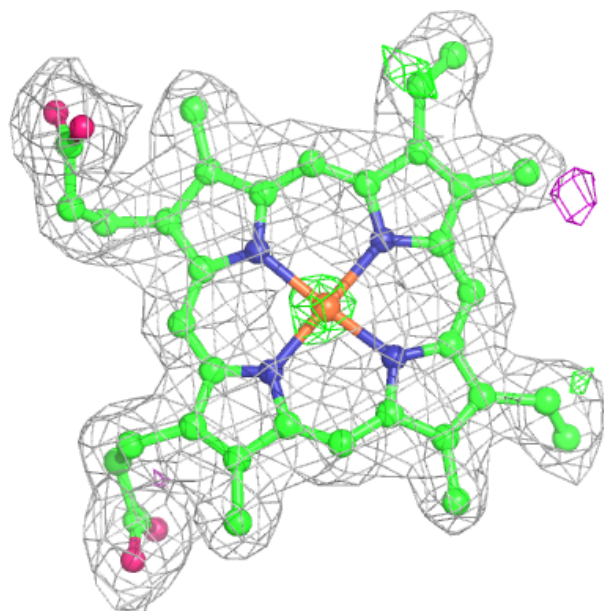
Electron density around HEC H 1002:

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



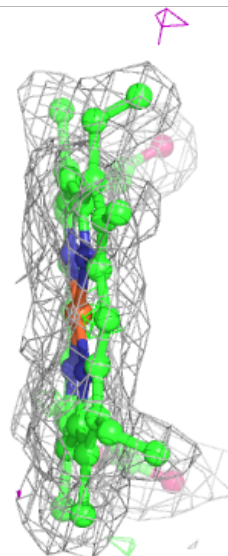
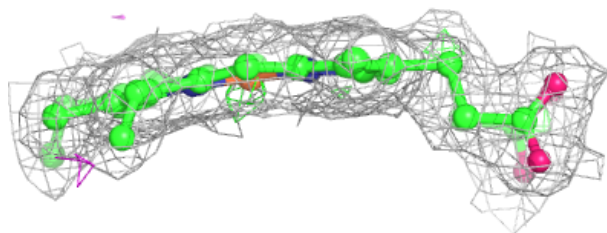
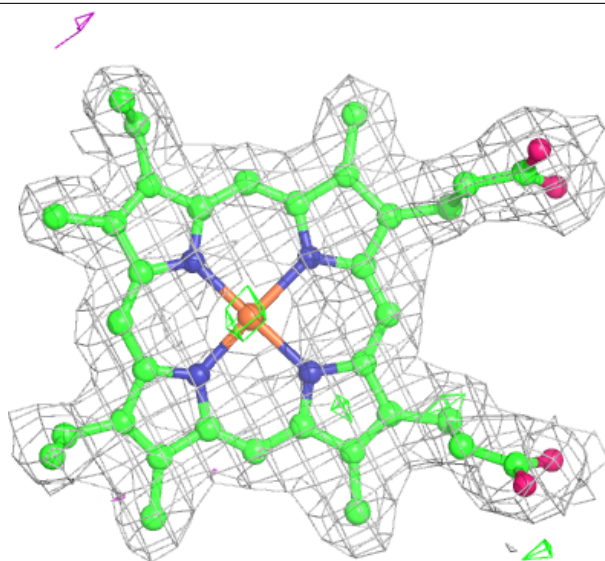
Electron density around HEC G 1005:

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



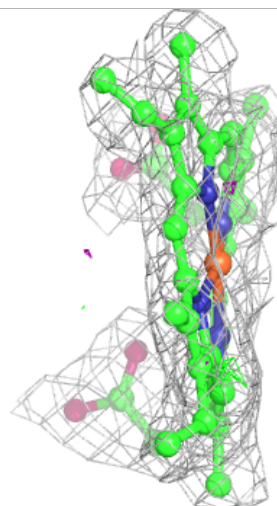
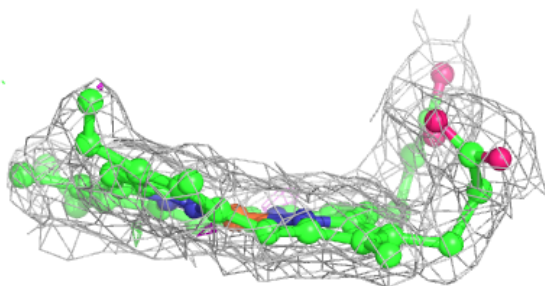
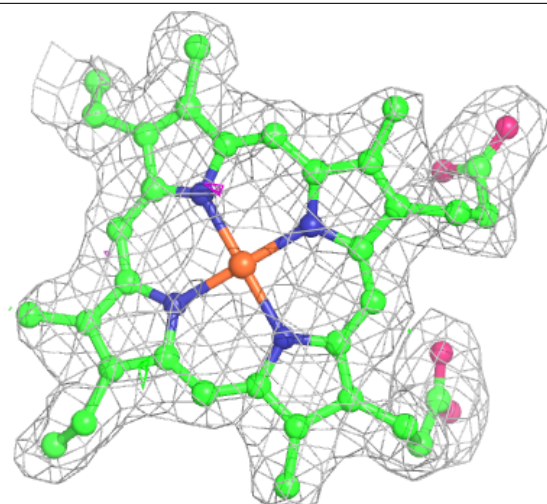
Electron density around HEC M 1003:

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



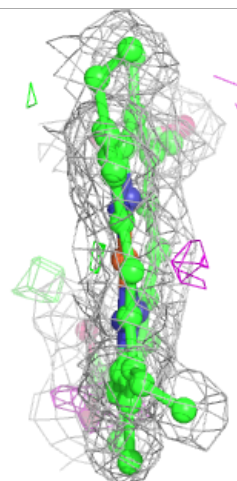
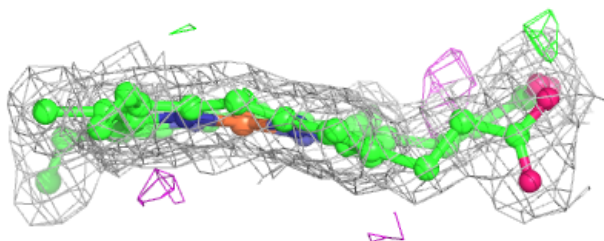
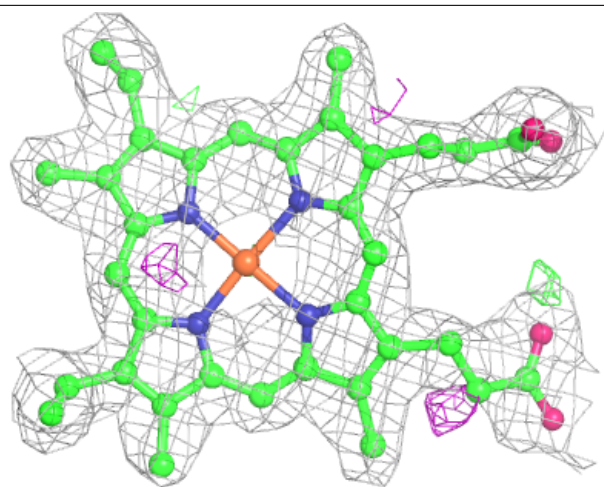
Electron density around HEC P 1001:

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



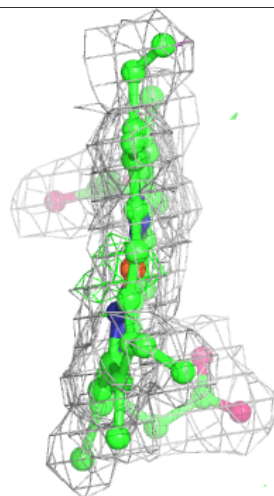
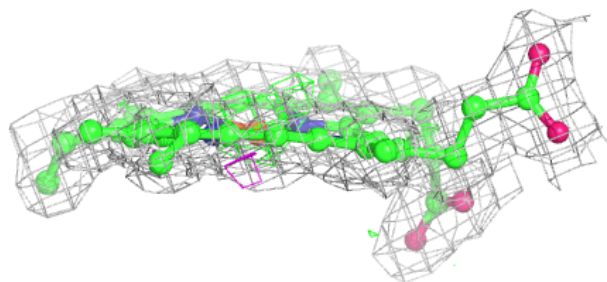
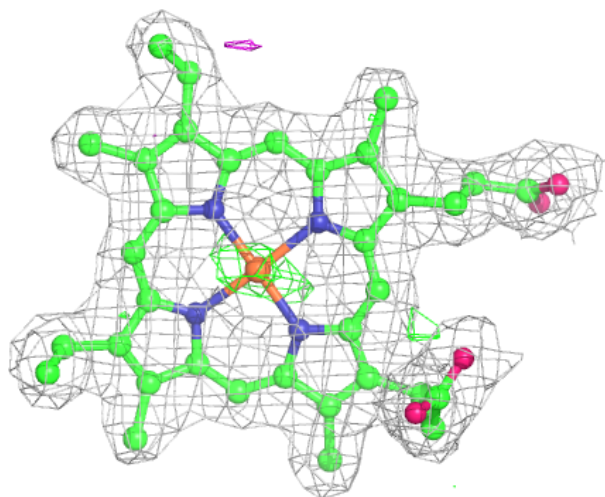
Electron density around HEC Q 1004:

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



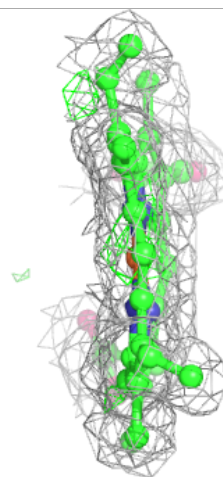
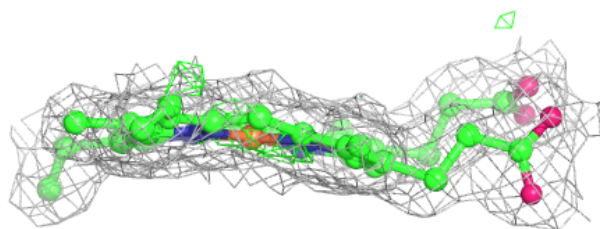
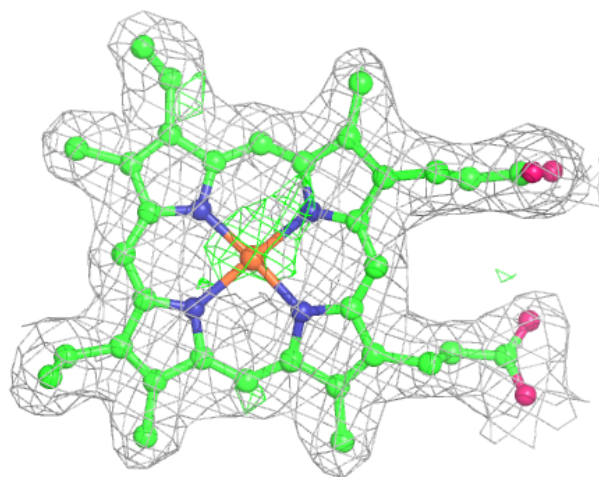
Electron density around HEC A 1002:

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



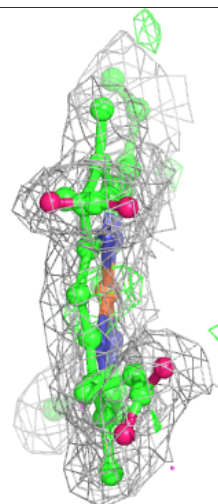
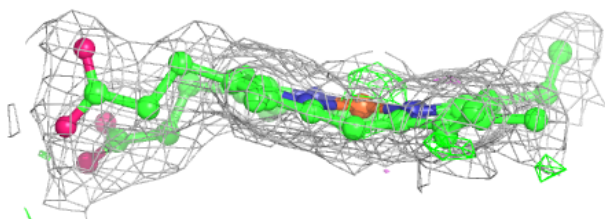
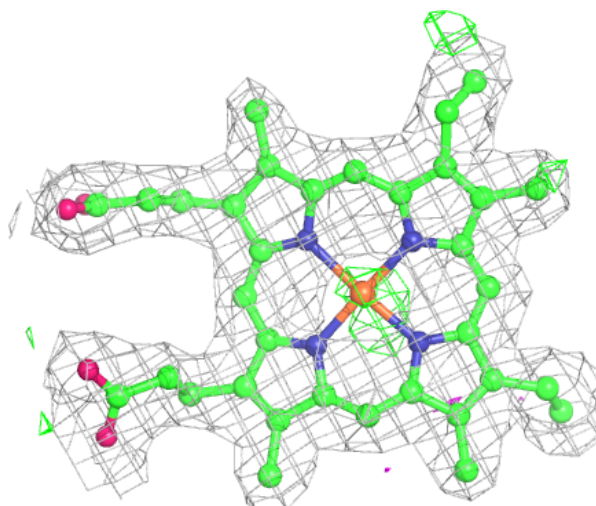
Electron density around HEC J 1004:

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



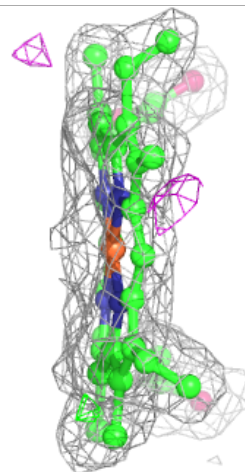
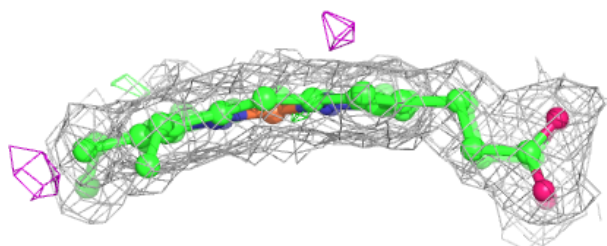
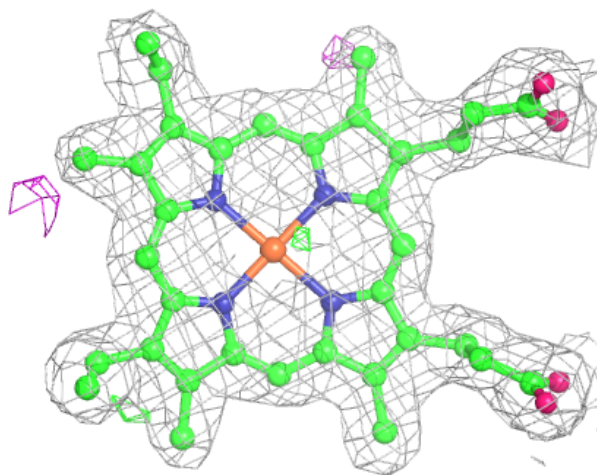
Electron density around HEC M 1004:

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



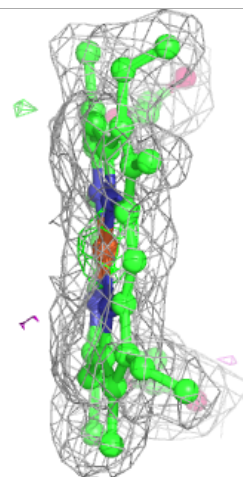
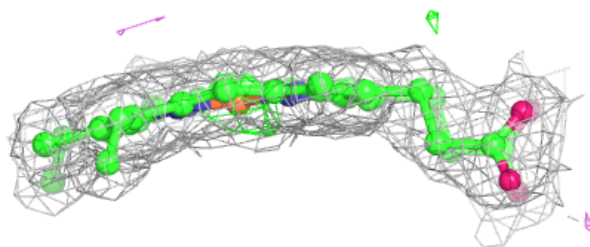
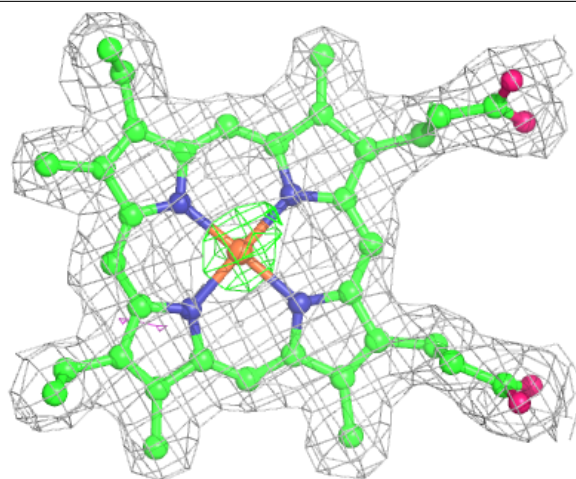
Electron density around HEC D 1003:

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



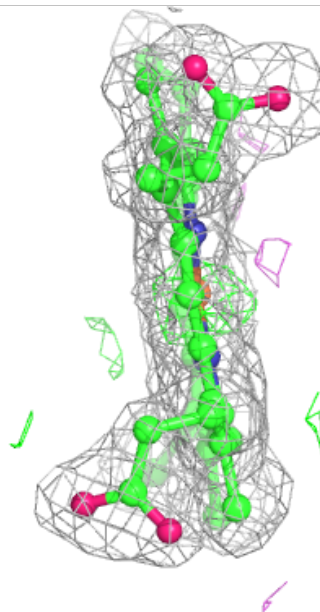
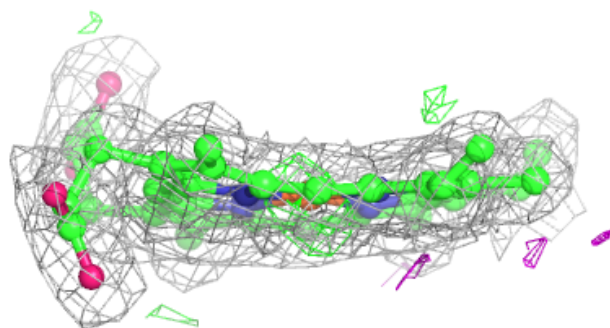
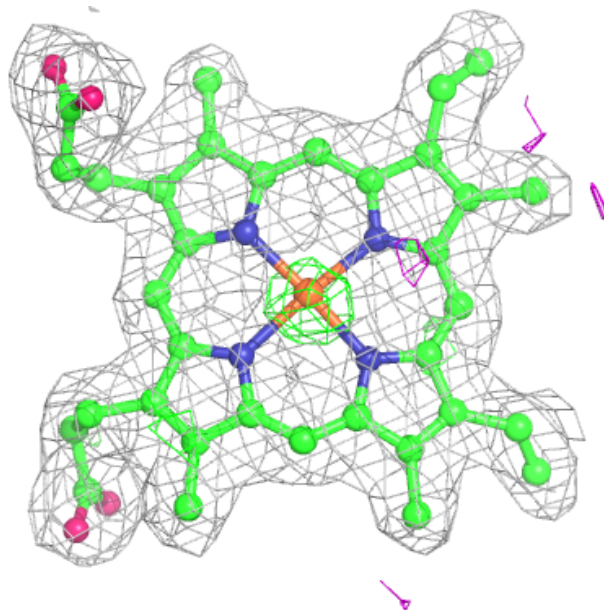
Electron density around HEC N 1003:

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



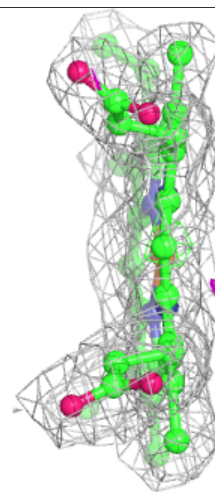
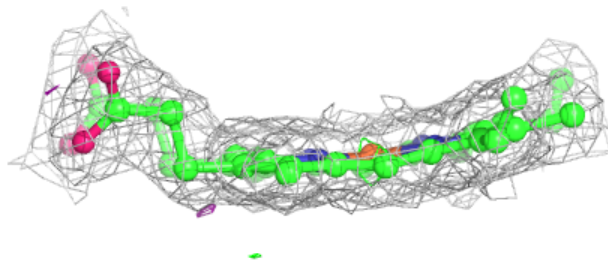
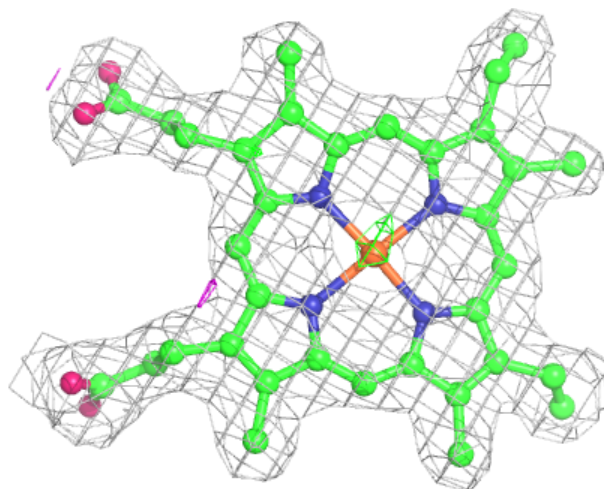
Electron density around HEC M 1005:

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



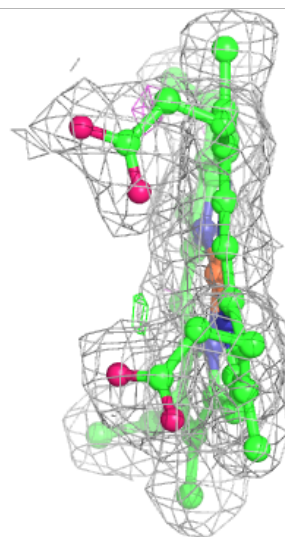
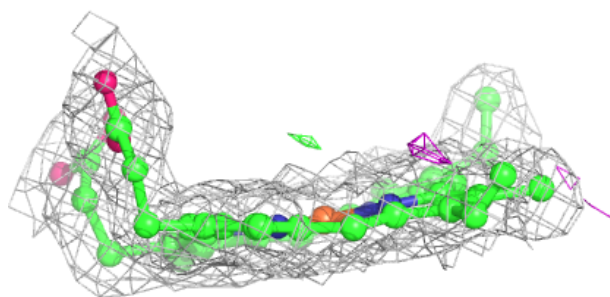
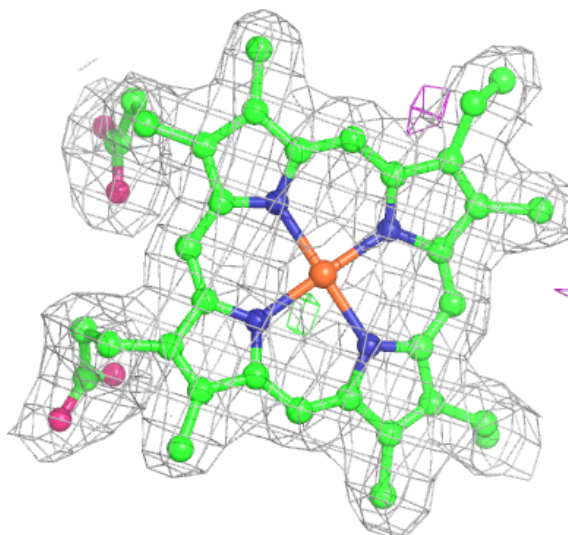
Electron density around HEC H 1003:

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



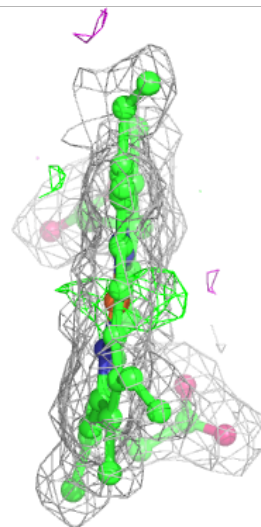
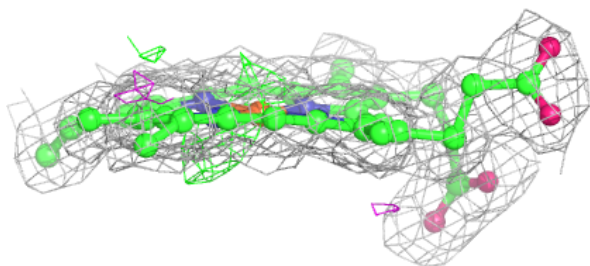
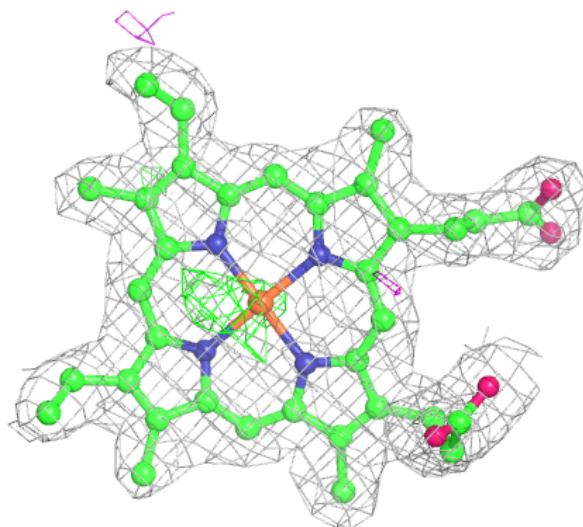
Electron density around HEC A 1001:

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



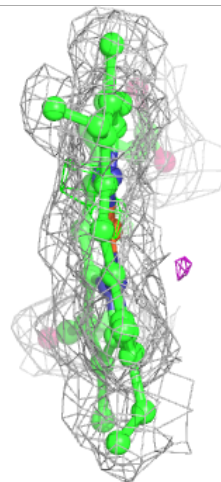
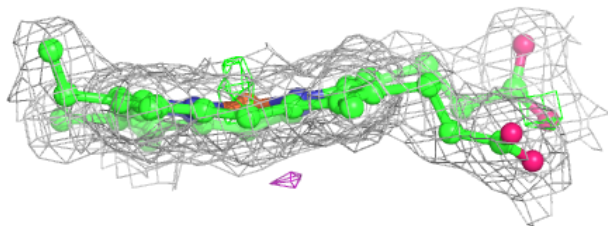
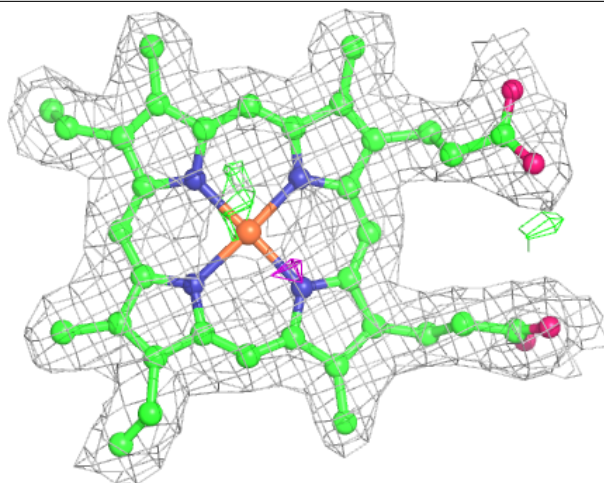
Electron density around HEC D 1002:

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



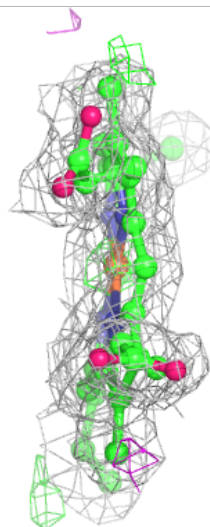
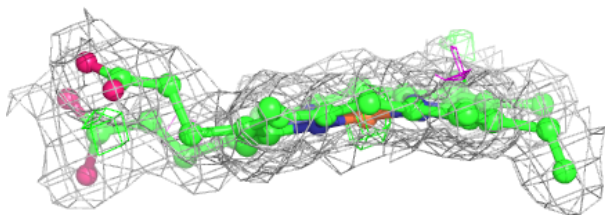
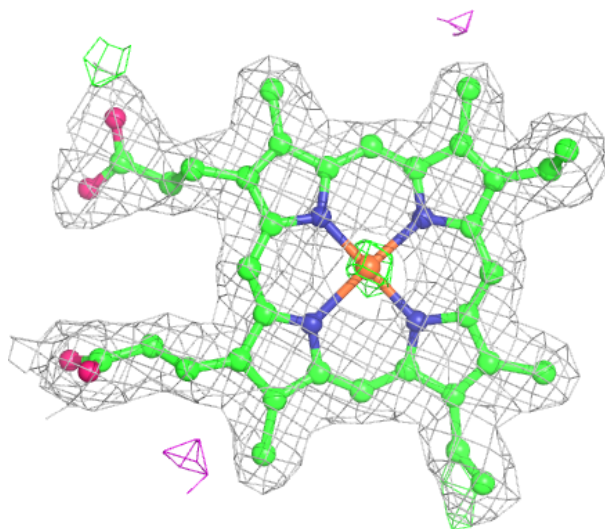
Electron density around HEC G 1004:

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



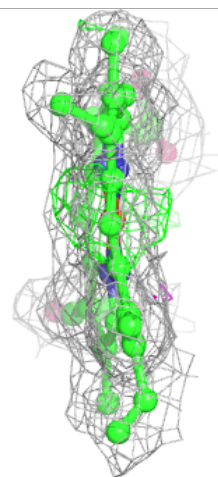
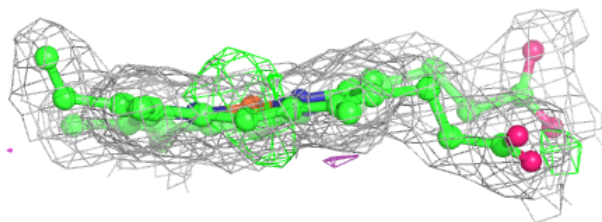
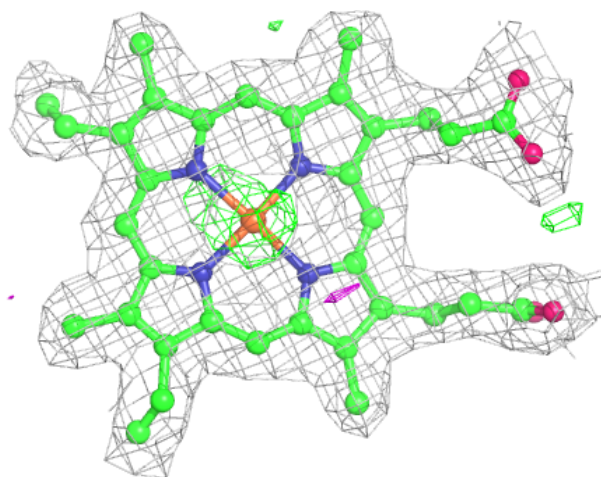
Electron density around HEC N 1004:

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



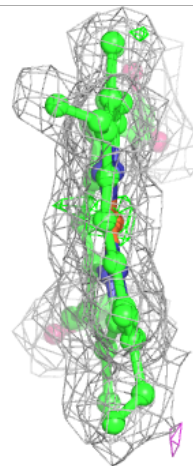
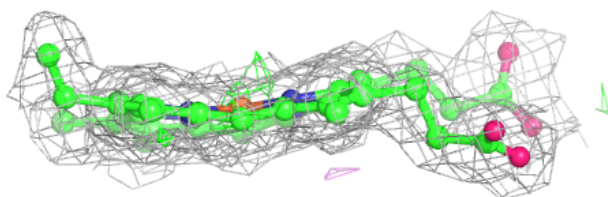
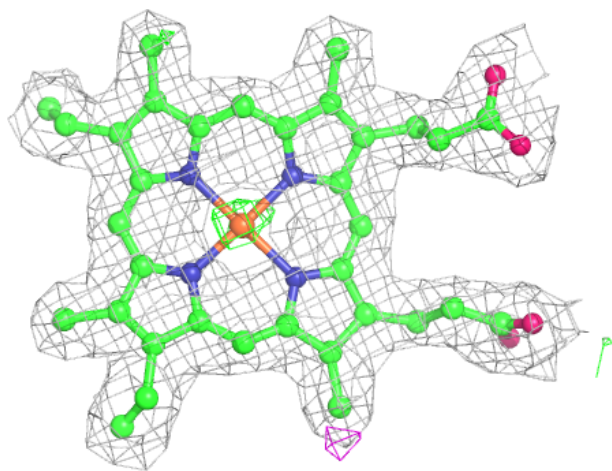
Electron density around HEC A 1004:

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



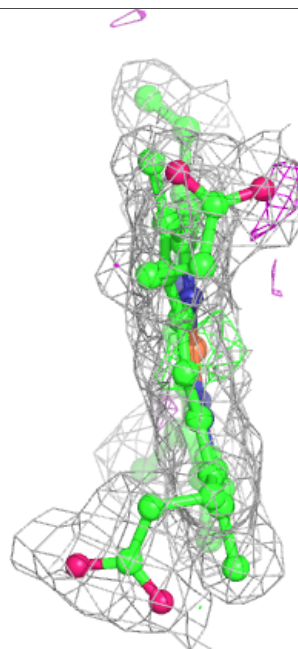
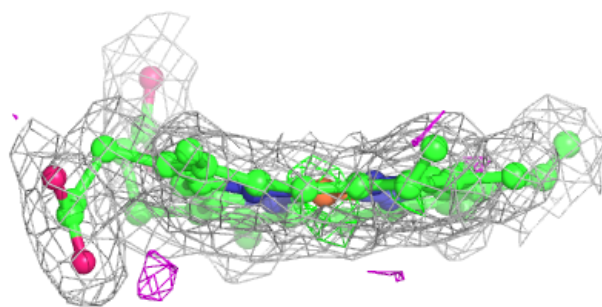
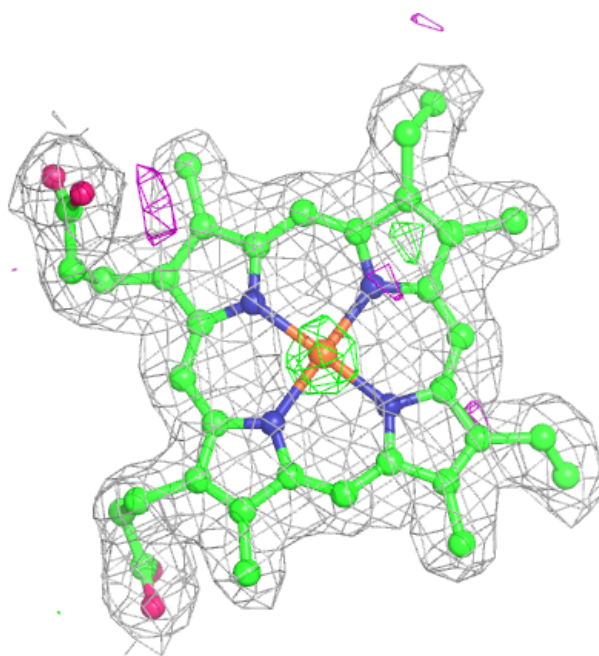
Electron density around HEC B 1004:

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



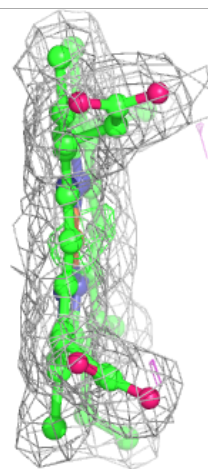
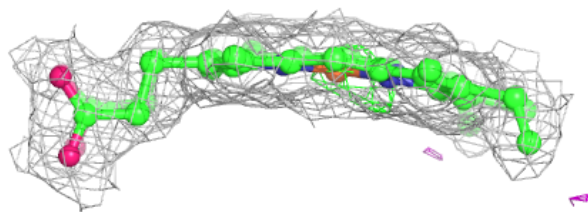
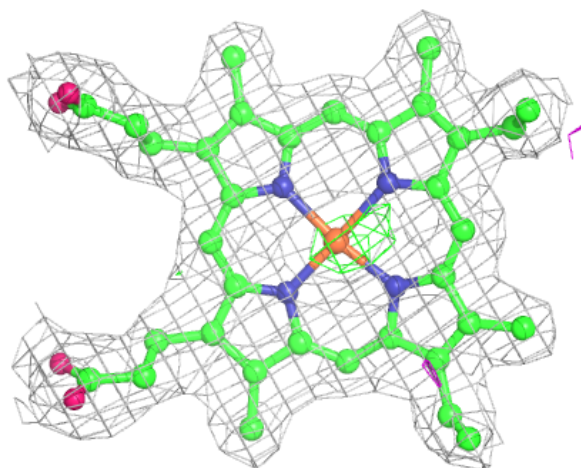
Electron density around HEC A 1005:

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



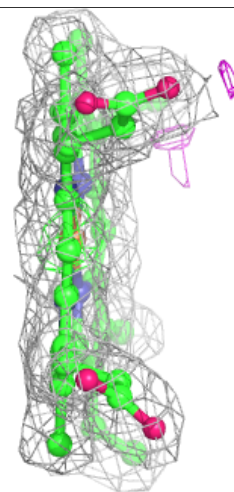
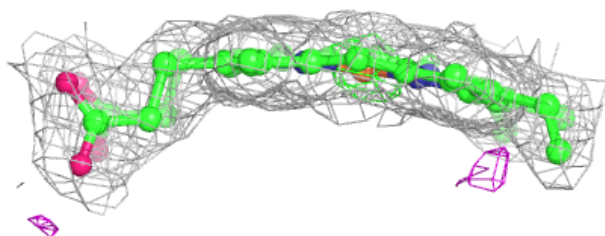
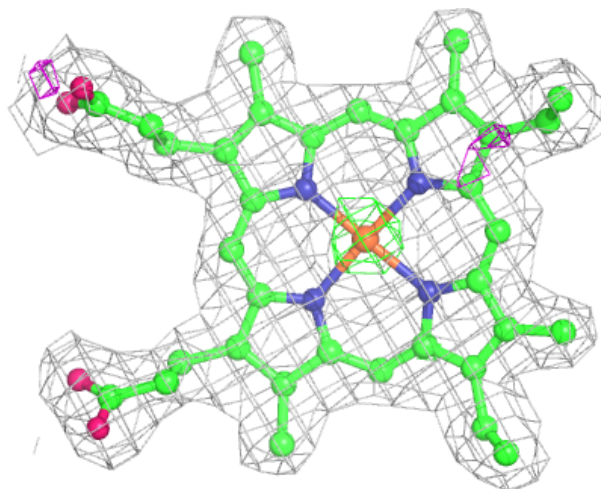
Electron density around HEC A 1003:

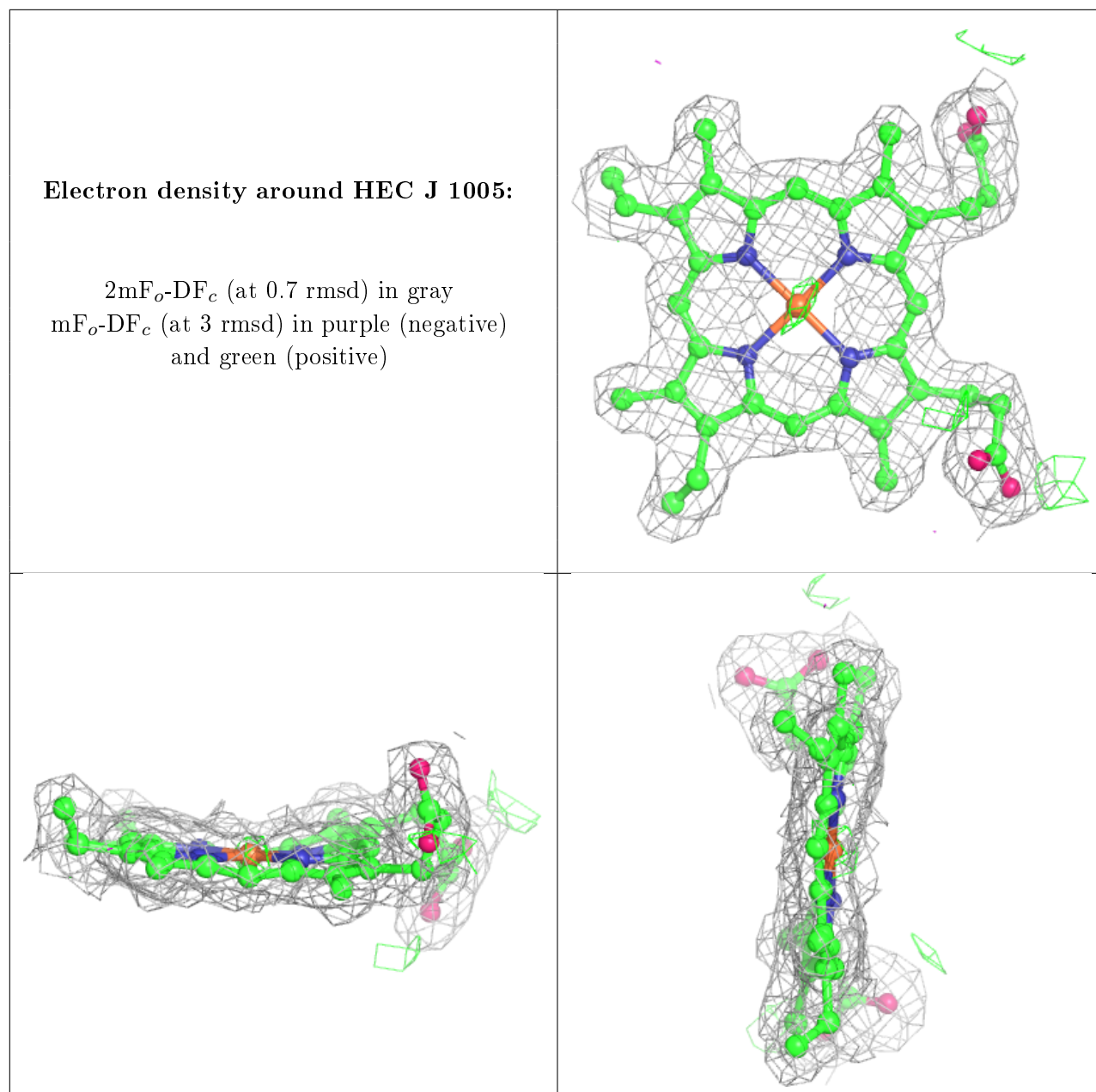
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC B 1003:

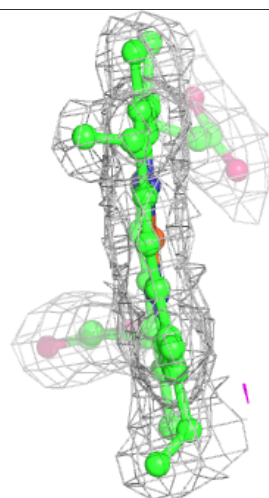
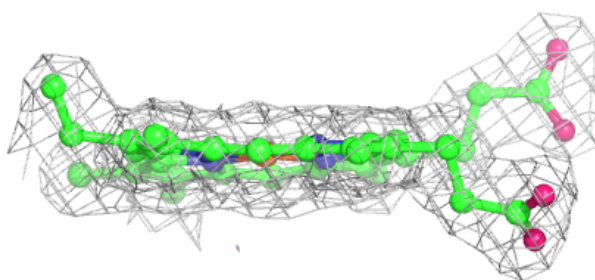
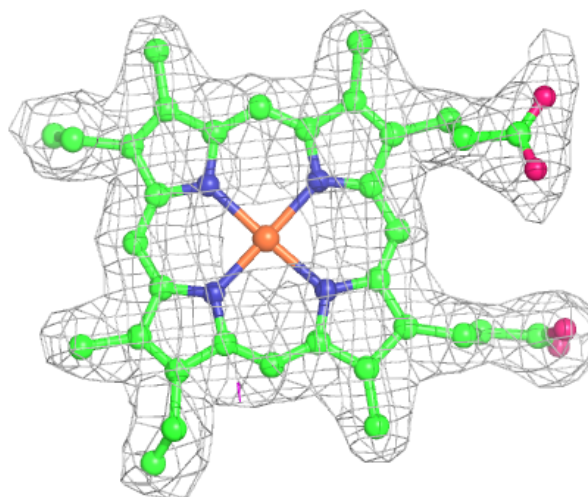
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

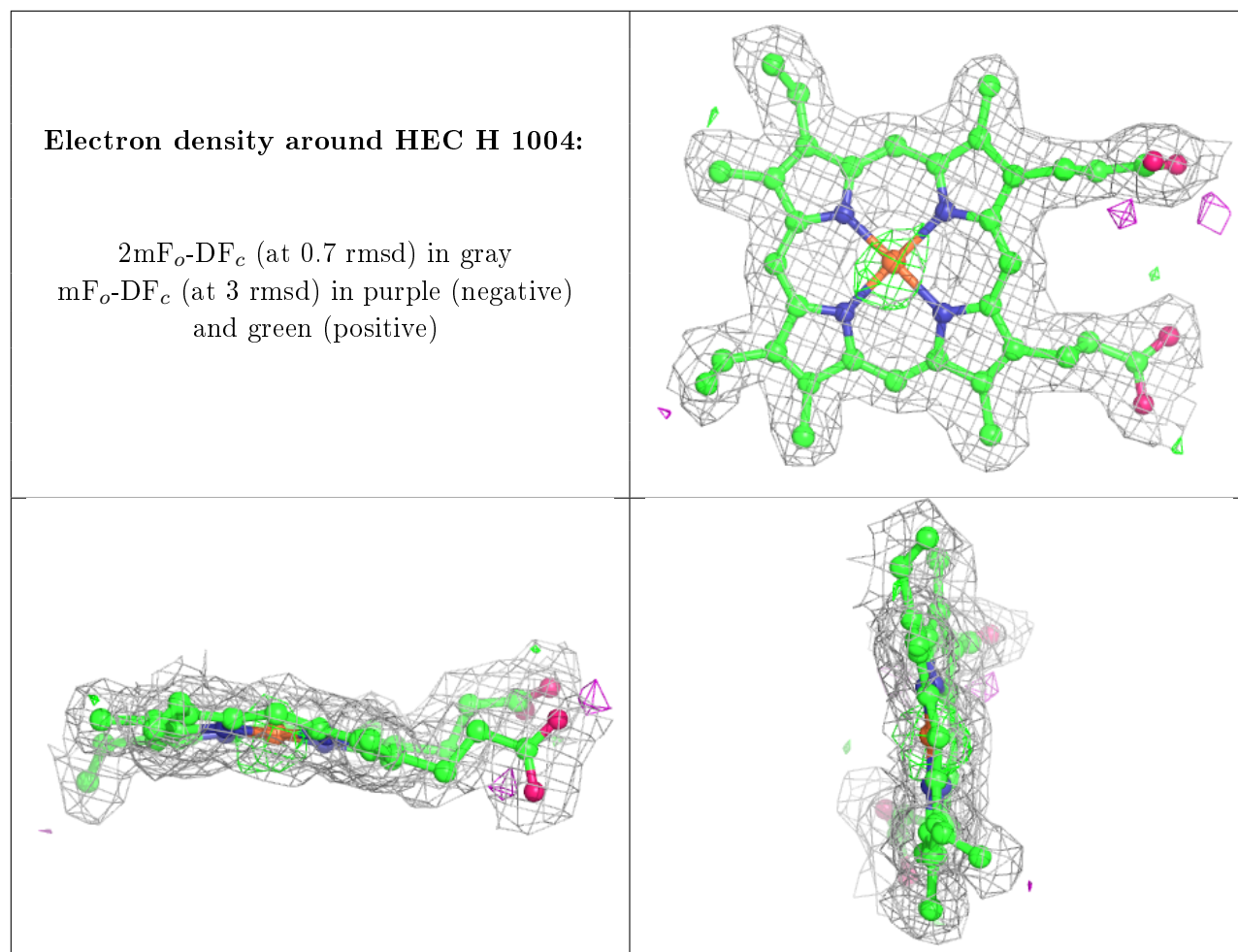




Electron density around HEC R 1004:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.