



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 07:52 am BST

PDB ID : 4LMH
Title : Crystal structure of the outer membrane decaheme cytochrome OmcA
Authors : Edwards, M.J.; Baiden, N.; Clarke, T.A.
Deposited on : 2013-07-10
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

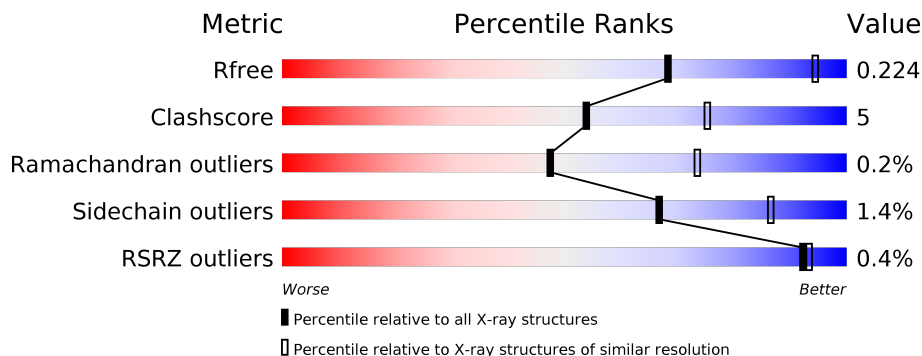
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	760	 82% 9% 9%
1	B	760	 81% 10% 9%
1	C	760	 83% 8% 9%
1	D	760	 83% 8% 9%

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

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	DMS	D	815	-	-	-	X

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 24443 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 Extracellular iron oxide respiratory system surface decaheme cytochrome c component OmcA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	693	5222	3229	916	1047	30	0	0	0
1	B	694	5231	3235	918	1048	30	0	0	0
1	C	692	5215	3224	915	1046	30	0	0	0
1	D	695	5235	3237	919	1049	30	0	0	0

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	MET	-	INITIATING METHIONINE	UNP Q8EG33
A	7	LYS	-	EXPRESSION TAG	UNP Q8EG33
A	8	PHE	-	EXPRESSION TAG	UNP Q8EG33
A	9	LYS	-	EXPRESSION TAG	UNP Q8EG33
A	10	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	11	ASN	-	EXPRESSION TAG	UNP Q8EG33
A	12	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	13	ILE	-	EXPRESSION TAG	UNP Q8EG33
A	14	THR	-	EXPRESSION TAG	UNP Q8EG33
A	15	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	16	ALA	-	EXPRESSION TAG	UNP Q8EG33
A	17	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	18	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	19	ALA	-	EXPRESSION TAG	UNP Q8EG33
A	20	ASN	-	EXPRESSION TAG	UNP Q8EG33
A	21	THR	-	EXPRESSION TAG	UNP Q8EG33
A	22	GLY	-	EXPRESSION TAG	UNP Q8EG33
A	23	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	24	ALA	-	EXPRESSION TAG	UNP Q8EG33
A	25	VAL	-	EXPRESSION TAG	UNP Q8EG33

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Chain	Residue	Modelled	Actual	Comment	Reference
A	26	ALA	-	EXPRESSION TAG	UNP Q8EG33
A	27	ALA	-	EXPRESSION TAG	UNP Q8EG33
A	736	LYS	-	EXPRESSION TAG	UNP Q8EG33
A	737	GLY	-	EXPRESSION TAG	UNP Q8EG33
A	738	GLU	-	EXPRESSION TAG	UNP Q8EG33
A	739	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	740	LYS	-	EXPRESSION TAG	UNP Q8EG33
A	741	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	742	GLU	-	EXPRESSION TAG	UNP Q8EG33
A	743	GLY	-	EXPRESSION TAG	UNP Q8EG33
A	744	LYS	-	EXPRESSION TAG	UNP Q8EG33
A	745	PRO	-	EXPRESSION TAG	UNP Q8EG33
A	746	ILE	-	EXPRESSION TAG	UNP Q8EG33
A	747	PRO	-	EXPRESSION TAG	UNP Q8EG33
A	748	ASN	-	EXPRESSION TAG	UNP Q8EG33
A	749	PRO	-	EXPRESSION TAG	UNP Q8EG33
A	750	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	751	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	752	GLY	-	EXPRESSION TAG	UNP Q8EG33
A	753	LEU	-	EXPRESSION TAG	UNP Q8EG33
A	754	ASP	-	EXPRESSION TAG	UNP Q8EG33
A	755	SER	-	EXPRESSION TAG	UNP Q8EG33
A	756	THR	-	EXPRESSION TAG	UNP Q8EG33
A	757	ARG	-	EXPRESSION TAG	UNP Q8EG33
A	758	THR	-	EXPRESSION TAG	UNP Q8EG33
A	759	GLY	-	EXPRESSION TAG	UNP Q8EG33
A	760	HIS	-	EXPRESSION TAG	UNP Q8EG33
A	761	HIS	-	EXPRESSION TAG	UNP Q8EG33
A	762	HIS	-	EXPRESSION TAG	UNP Q8EG33
A	763	HIS	-	EXPRESSION TAG	UNP Q8EG33
A	764	HIS	-	EXPRESSION TAG	UNP Q8EG33
A	765	HIS	-	EXPRESSION TAG	UNP Q8EG33
B	6	MET	-	INITIATING METHIONINE	UNP Q8EG33
B	7	LYS	-	EXPRESSION TAG	UNP Q8EG33
B	8	PHE	-	EXPRESSION TAG	UNP Q8EG33
B	9	LYS	-	EXPRESSION TAG	UNP Q8EG33
B	10	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	11	ASN	-	EXPRESSION TAG	UNP Q8EG33
B	12	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	13	ILE	-	EXPRESSION TAG	UNP Q8EG33
B	14	THR	-	EXPRESSION TAG	UNP Q8EG33
B	15	LEU	-	EXPRESSION TAG	UNP Q8EG33

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Chain	Residue	Modelled	Actual	Comment	Reference
B	16	ALA	-	EXPRESSION TAG	UNP Q8EG33
B	17	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	18	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	19	ALA	-	EXPRESSION TAG	UNP Q8EG33
B	20	ASN	-	EXPRESSION TAG	UNP Q8EG33
B	21	THR	-	EXPRESSION TAG	UNP Q8EG33
B	22	GLY	-	EXPRESSION TAG	UNP Q8EG33
B	23	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	24	ALA	-	EXPRESSION TAG	UNP Q8EG33
B	25	VAL	-	EXPRESSION TAG	UNP Q8EG33
B	26	ALA	-	EXPRESSION TAG	UNP Q8EG33
B	27	ALA	-	EXPRESSION TAG	UNP Q8EG33
B	736	LYS	-	EXPRESSION TAG	UNP Q8EG33
B	737	GLY	-	EXPRESSION TAG	UNP Q8EG33
B	738	GLU	-	EXPRESSION TAG	UNP Q8EG33
B	739	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	740	LYS	-	EXPRESSION TAG	UNP Q8EG33
B	741	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	742	GLU	-	EXPRESSION TAG	UNP Q8EG33
B	743	GLY	-	EXPRESSION TAG	UNP Q8EG33
B	744	LYS	-	EXPRESSION TAG	UNP Q8EG33
B	745	PRO	-	EXPRESSION TAG	UNP Q8EG33
B	746	ILE	-	EXPRESSION TAG	UNP Q8EG33
B	747	PRO	-	EXPRESSION TAG	UNP Q8EG33
B	748	ASN	-	EXPRESSION TAG	UNP Q8EG33
B	749	PRO	-	EXPRESSION TAG	UNP Q8EG33
B	750	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	751	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	752	GLY	-	EXPRESSION TAG	UNP Q8EG33
B	753	LEU	-	EXPRESSION TAG	UNP Q8EG33
B	754	ASP	-	EXPRESSION TAG	UNP Q8EG33
B	755	SER	-	EXPRESSION TAG	UNP Q8EG33
B	756	THR	-	EXPRESSION TAG	UNP Q8EG33
B	757	ARG	-	EXPRESSION TAG	UNP Q8EG33
B	758	THR	-	EXPRESSION TAG	UNP Q8EG33
B	759	GLY	-	EXPRESSION TAG	UNP Q8EG33
B	760	HIS	-	EXPRESSION TAG	UNP Q8EG33
B	761	HIS	-	EXPRESSION TAG	UNP Q8EG33
B	762	HIS	-	EXPRESSION TAG	UNP Q8EG33
B	763	HIS	-	EXPRESSION TAG	UNP Q8EG33
B	764	HIS	-	EXPRESSION TAG	UNP Q8EG33
B	765	HIS	-	EXPRESSION TAG	UNP Q8EG33

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Chain	Residue	Modelled	Actual	Comment	Reference
C	6	MET	-	INITIATING METHIONINE	UNP Q8EG33
C	7	LYS	-	EXPRESSION TAG	UNP Q8EG33
C	8	PHE	-	EXPRESSION TAG	UNP Q8EG33
C	9	LYS	-	EXPRESSION TAG	UNP Q8EG33
C	10	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	11	ASN	-	EXPRESSION TAG	UNP Q8EG33
C	12	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	13	ILE	-	EXPRESSION TAG	UNP Q8EG33
C	14	THR	-	EXPRESSION TAG	UNP Q8EG33
C	15	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	16	ALA	-	EXPRESSION TAG	UNP Q8EG33
C	17	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	18	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	19	ALA	-	EXPRESSION TAG	UNP Q8EG33
C	20	ASN	-	EXPRESSION TAG	UNP Q8EG33
C	21	THR	-	EXPRESSION TAG	UNP Q8EG33
C	22	GLY	-	EXPRESSION TAG	UNP Q8EG33
C	23	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	24	ALA	-	EXPRESSION TAG	UNP Q8EG33
C	25	VAL	-	EXPRESSION TAG	UNP Q8EG33
C	26	ALA	-	EXPRESSION TAG	UNP Q8EG33
C	27	ALA	-	EXPRESSION TAG	UNP Q8EG33
C	736	LYS	-	EXPRESSION TAG	UNP Q8EG33
C	737	GLY	-	EXPRESSION TAG	UNP Q8EG33
C	738	GLU	-	EXPRESSION TAG	UNP Q8EG33
C	739	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	740	LYS	-	EXPRESSION TAG	UNP Q8EG33
C	741	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	742	GLU	-	EXPRESSION TAG	UNP Q8EG33
C	743	GLY	-	EXPRESSION TAG	UNP Q8EG33
C	744	LYS	-	EXPRESSION TAG	UNP Q8EG33
C	745	PRO	-	EXPRESSION TAG	UNP Q8EG33
C	746	ILE	-	EXPRESSION TAG	UNP Q8EG33
C	747	PRO	-	EXPRESSION TAG	UNP Q8EG33
C	748	ASN	-	EXPRESSION TAG	UNP Q8EG33
C	749	PRO	-	EXPRESSION TAG	UNP Q8EG33
C	750	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	751	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	752	GLY	-	EXPRESSION TAG	UNP Q8EG33
C	753	LEU	-	EXPRESSION TAG	UNP Q8EG33
C	754	ASP	-	EXPRESSION TAG	UNP Q8EG33
C	755	SER	-	EXPRESSION TAG	UNP Q8EG33

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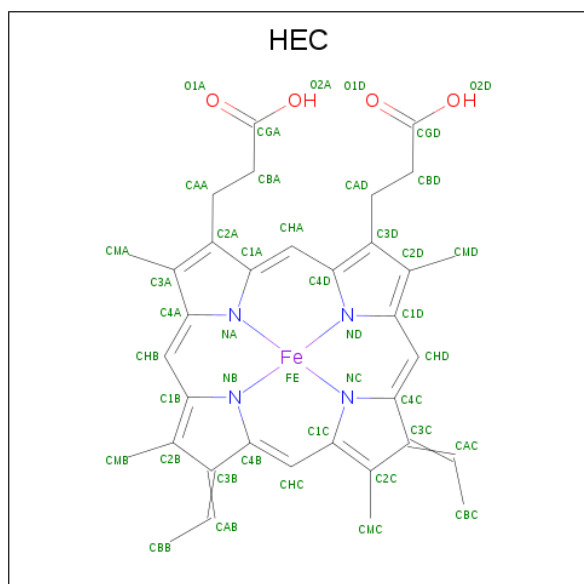
Chain	Residue	Modelled	Actual	Comment	Reference
C	756	THR	-	EXPRESSION TAG	UNP Q8EG33
C	757	ARG	-	EXPRESSION TAG	UNP Q8EG33
C	758	THR	-	EXPRESSION TAG	UNP Q8EG33
C	759	GLY	-	EXPRESSION TAG	UNP Q8EG33
C	760	HIS	-	EXPRESSION TAG	UNP Q8EG33
C	761	HIS	-	EXPRESSION TAG	UNP Q8EG33
C	762	HIS	-	EXPRESSION TAG	UNP Q8EG33
C	763	HIS	-	EXPRESSION TAG	UNP Q8EG33
C	764	HIS	-	EXPRESSION TAG	UNP Q8EG33
C	765	HIS	-	EXPRESSION TAG	UNP Q8EG33
D	6	MET	-	INITIATING METHIONINE	UNP Q8EG33
D	7	LYS	-	EXPRESSION TAG	UNP Q8EG33
D	8	PHE	-	EXPRESSION TAG	UNP Q8EG33
D	9	LYS	-	EXPRESSION TAG	UNP Q8EG33
D	10	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	11	ASN	-	EXPRESSION TAG	UNP Q8EG33
D	12	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	13	ILE	-	EXPRESSION TAG	UNP Q8EG33
D	14	THR	-	EXPRESSION TAG	UNP Q8EG33
D	15	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	16	ALA	-	EXPRESSION TAG	UNP Q8EG33
D	17	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	18	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	19	ALA	-	EXPRESSION TAG	UNP Q8EG33
D	20	ASN	-	EXPRESSION TAG	UNP Q8EG33
D	21	THR	-	EXPRESSION TAG	UNP Q8EG33
D	22	GLY	-	EXPRESSION TAG	UNP Q8EG33
D	23	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	24	ALA	-	EXPRESSION TAG	UNP Q8EG33
D	25	VAL	-	EXPRESSION TAG	UNP Q8EG33
D	26	ALA	-	EXPRESSION TAG	UNP Q8EG33
D	27	ALA	-	EXPRESSION TAG	UNP Q8EG33
D	736	LYS	-	EXPRESSION TAG	UNP Q8EG33
D	737	GLY	-	EXPRESSION TAG	UNP Q8EG33
D	738	GLU	-	EXPRESSION TAG	UNP Q8EG33
D	739	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	740	LYS	-	EXPRESSION TAG	UNP Q8EG33
D	741	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	742	GLU	-	EXPRESSION TAG	UNP Q8EG33
D	743	GLY	-	EXPRESSION TAG	UNP Q8EG33
D	744	LYS	-	EXPRESSION TAG	UNP Q8EG33
D	745	PRO	-	EXPRESSION TAG	UNP Q8EG33

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Chain	Residue	Modelled	Actual	Comment	Reference
D	746	ILE	-	EXPRESSION TAG	UNP Q8EG33
D	747	PRO	-	EXPRESSION TAG	UNP Q8EG33
D	748	ASN	-	EXPRESSION TAG	UNP Q8EG33
D	749	PRO	-	EXPRESSION TAG	UNP Q8EG33
D	750	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	751	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	752	GLY	-	EXPRESSION TAG	UNP Q8EG33
D	753	LEU	-	EXPRESSION TAG	UNP Q8EG33
D	754	ASP	-	EXPRESSION TAG	UNP Q8EG33
D	755	SER	-	EXPRESSION TAG	UNP Q8EG33
D	756	THR	-	EXPRESSION TAG	UNP Q8EG33
D	757	ARG	-	EXPRESSION TAG	UNP Q8EG33
D	758	THR	-	EXPRESSION TAG	UNP Q8EG33
D	759	GLY	-	EXPRESSION TAG	UNP Q8EG33
D	760	HIS	-	EXPRESSION TAG	UNP Q8EG33
D	761	HIS	-	EXPRESSION TAG	UNP Q8EG33
D	762	HIS	-	EXPRESSION TAG	UNP Q8EG33
D	763	HIS	-	EXPRESSION TAG	UNP Q8EG33
D	764	HIS	-	EXPRESSION TAG	UNP Q8EG33
D	765	HIS	-	EXPRESSION TAG	UNP Q8EG33

- Molecule 2 is HEME C (three-letter code: HEC) (formula: C₃₄H₃₄FeN₄O₄).



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

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

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

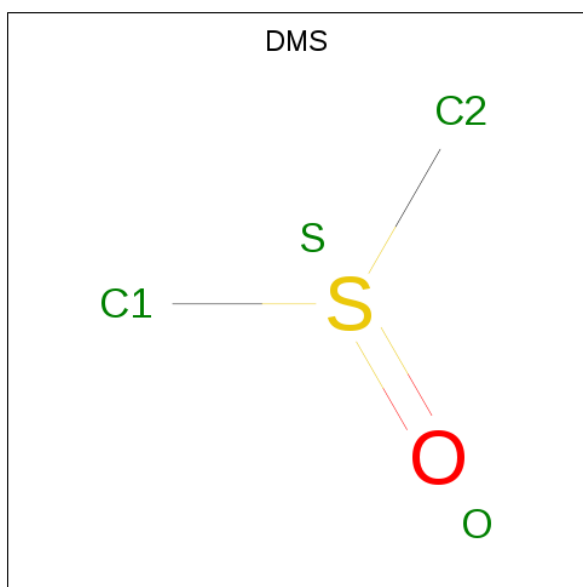
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Ca 2 2	0	0
3	D	2	Total Ca 2 2	0	0
3	C	2	Total Ca 2 2	0	0

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O S 4 2 1 1	0	0
4	A	1	Total C O S 4 2 1 1	0	0
4	A	1	Total C O S 4 2 1 1	0	0
4	A	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total 4	C 2	O 1	S 1	0	0
4	C	1	Total 4	C 2	O 1	S 1	0	0
4	C	1	Total 4	C 2	O 1	S 1	0	0
4	C	1	Total 4	C 2	O 1	S 1	0	0
4	D	1	Total 4	C 2	O 1	S 1	0	0
4	D	1	Total 4	C 2	O 1	S 1	0	0
4	D	1	Total 4	C 2	O 1	S 1	0	0
4	D	1	Total 4	C 2	O 1	S 1	0	0

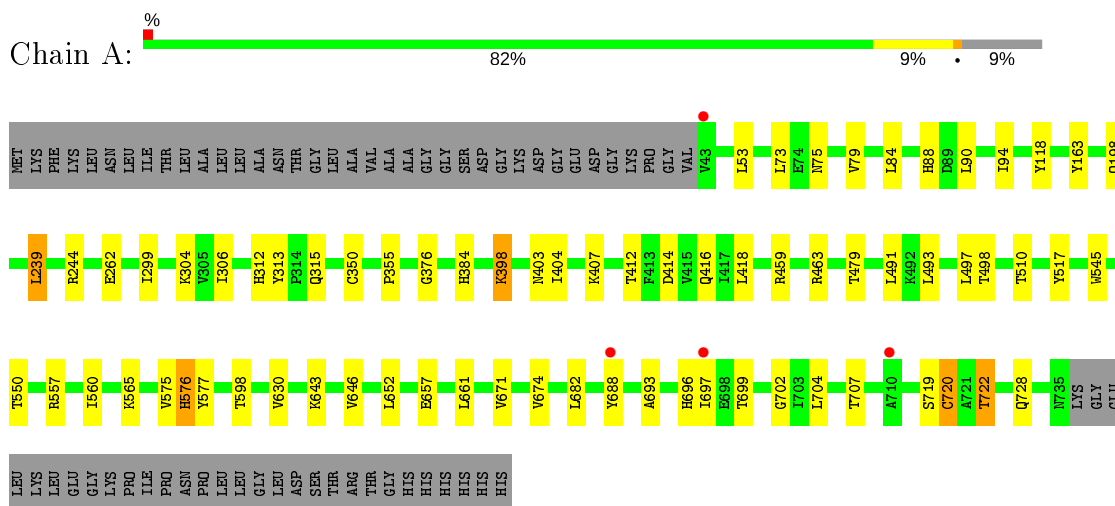
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	397	Total 397	O 397	0	0
5	B	420	Total 420	O 420	0	0
5	C	380	Total 380	O 380	0	0
5	D	551	Total 551	O 551	0	0

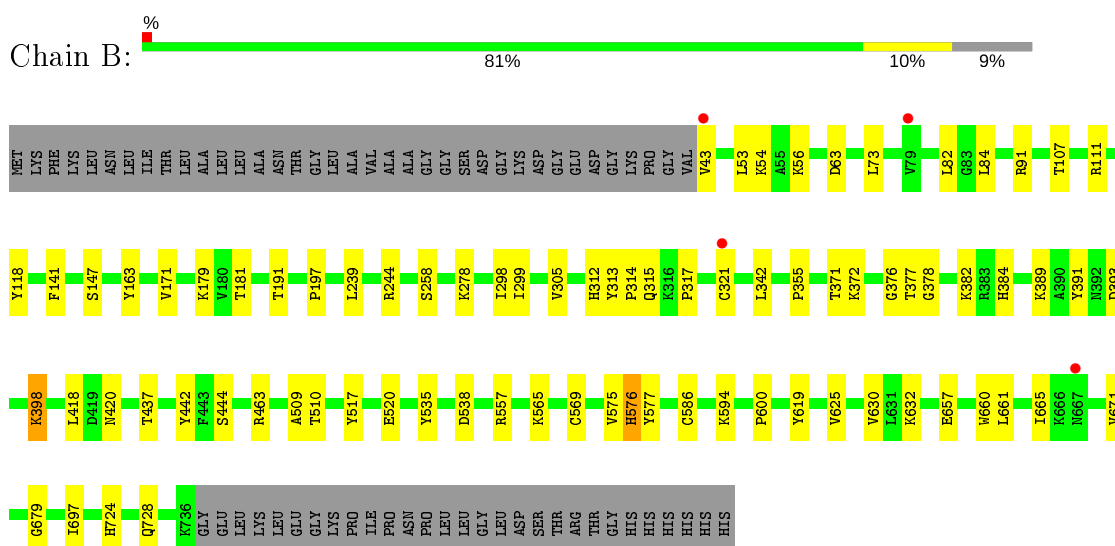
3 Residue-property plots

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.


- Molecule 1: Extracellular iron oxide respiratory system surface decaheme cytochrome c component OmcA

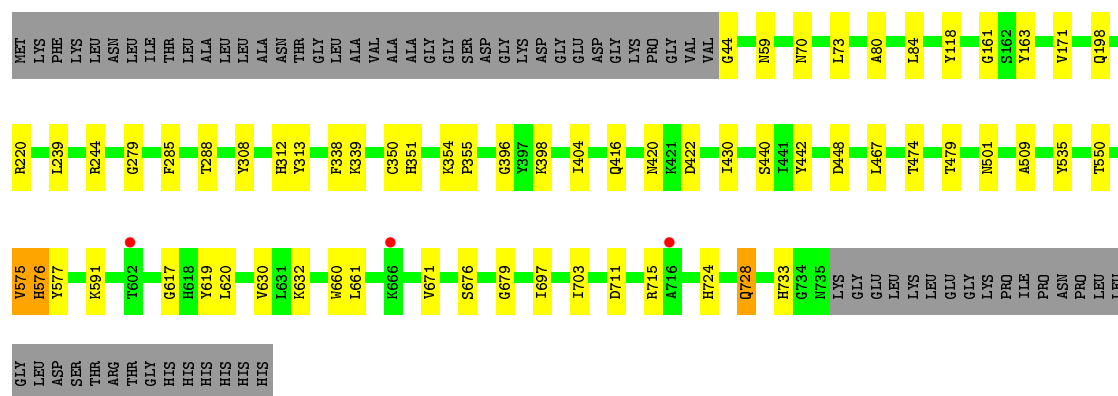


- Molecule 1: Extracellular iron oxide respiratory system surface decaheme cytochrome c component OmcA




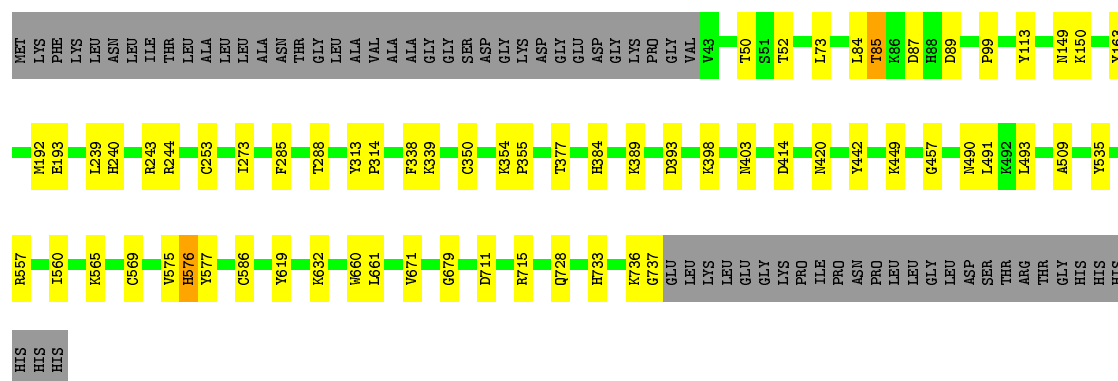
- Molecule 1: Extracellular iron oxide respiratory system surface decaheme cytochrome c component OmcA

Chain C:  83% 8% 9%



- Molecule 1: Extracellular iron oxide respiratory system surface decaheme cytochrome c component OmcA

Chain D:  83% 8% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.64Å 245.38Å 135.63Å 90.00° 97.89° 90.00°	Depositor
Resolution (Å)	50.97 – 2.70 52.54 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.4 (50.97-2.70) 98.4 (52.54-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.69Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.193 , 0.230 0.186 , 0.224	Depositor DCC
R_{free} test set	8083 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtrriage
Anisotropy	0.039	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	24443	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.27	0/5337	0.44	0/7254
1	B	0.27	0/5346	0.44	0/7265
1	C	0.27	0/5330	0.43	0/7244
1	D	0.28	0/5350	0.44	0/7270
All	All	0.27	0/21363	0.44	0/29033

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5222	0	4957	50	0
1	B	5231	0	4971	59	0
1	C	5215	0	4948	48	0
1	D	5235	0	4974	47	0
2	A	430	0	301	24	0
2	B	430	0	302	35	0
2	C	430	0	301	17	0
2	D	430	0	302	28	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	16	0	24	3	0
4	B	16	0	24	1	0
4	C	16	0	24	2	0
4	D	16	0	24	1	0
5	A	397	0	0	5	0
5	B	420	0	0	2	0
5	C	380	0	0	2	0
5	D	551	0	0	0	0
All	All	24443	0	21152	222	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 5.

All (222) 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:D:253:CYS:SG	2:D:802:HEC:HAC	1.35	1.63
1:D:350:CYS:SG	2:D:804:HEC:HAC	1.53	1.47
1:C:350:CYS:SG	2:C:804:HEC:HAC	1.56	1.44
1:A:350:CYS:SG	2:A:804:HEC:HAC	1.64	1.34
1:B:586:CYS:SG	2:B:908:HEC:HAC	1.70	1.25
1:A:350:CYS:HG	2:A:804:HEC:HAC	0.95	1.02
1:D:569:CYS:SG	2:D:806:HEC:C3C	2.69	0.80
1:C:350:CYS:SG	2:C:804:HEC:C3C	2.70	0.80
1:D:350:CYS:SG	2:D:804:HEC:C3C	2.69	0.79
1:B:569:CYS:SG	2:B:907:HEC:C3C	2.72	0.77
1:D:239:LEU:HD13	2:D:802:HEC:HMB2	1.65	0.77
1:D:586:CYS:SG	2:D:807:HEC:C3C	2.73	0.76
1:A:350:CYS:SG	2:A:804:HEC:C3C	2.73	0.75
1:A:576:HIS:HE1	2:A:807:HEC:ND	1.83	0.75
1:C:239:LEU:HD13	2:C:802:HEC:HMB2	1.69	0.74
1:B:586:CYS:SG	2:B:908:HEC:C3C	2.76	0.73
1:D:85:THR:HG23	1:D:87:ASP:H	1.53	0.72
1:A:407:LYS:HD3	1:A:412:THR:HG21	1.73	0.71
1:B:239:LEU:HD13	2:B:903:HEC:HMB2	1.71	0.71
1:B:576:HIS:HE1	2:B:908:HEC:ND	1.88	0.71
1:D:253:CYS:SG	2:D:802:HEC:C3C	2.81	0.69
1:B:724:HIS:HA	1:B:728:GLN:HG2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:557:ARG:NH2	2:A:808:HEC:O1D	2.28	0.67
1:A:239:LEU:HD13	2:A:802:HEC:HMB2	1.76	0.67
1:B:557:ARG:NH2	2:B:909:HEC:O1D	2.29	0.65
2:D:810:HEC:HBD2	2:D:810:HEC:HHA	1.78	0.65
1:A:661:LEU:HD11	1:A:671:VAL:HG13	1.80	0.64
1:B:43:VAL:N	5:B:1357:HOH:O	2.31	0.64
1:A:697:ILE:HG22	1:A:702:GLY:HA3	1.79	0.64
1:B:73:LEU:HD11	1:B:84:LEU:HD22	1.84	0.60
2:B:904:HEC:HBB2	2:B:905:HEC:C4C	2.32	0.60
1:A:719:SER:O	1:A:722:THR:OG1	2.21	0.59
1:C:44:GLY:N	5:C:1113:HOH:O	2.34	0.59
1:A:652:LEU:HD23	1:A:720:CYS:HB2	1.84	0.58
1:B:377:THR:OG1	1:B:378:GLY:N	2.36	0.58
1:D:149:ASN:OD1	1:D:150:LYS:NZ	2.36	0.58
1:B:600:PRO:HB2	1:B:665:ILE:HB	1.86	0.57
1:A:491:LEU:HD21	1:A:493:LEU:HD13	1.87	0.57
1:A:244:ARG:NH2	2:A:802:HEC:HBC2	2.20	0.57
1:C:73:LEU:HD11	1:C:84:LEU:HD22	1.85	0.56
1:B:382:LYS:NZ	1:B:520:GLU:O	2.39	0.56
1:C:404:ILE:HD12	1:C:550:THR:HG21	1.87	0.56
1:D:557:ARG:NH2	2:D:808:HEC:O1D	2.39	0.55
1:D:660:TRP:CD1	1:D:679:GLY:HA3	2.41	0.55
1:D:89:ASP:OD2	1:D:243:ARG:NH1	2.40	0.55
1:D:244:ARG:NH2	2:D:802:HEC:HBC2	2.21	0.55
1:C:351:HIS:HB3	1:C:355:PRO:HB3	1.89	0.55
1:C:312:HIS:N	5:C:973:HOH:O	2.30	0.54
1:B:371:THR:OG1	1:B:372:LYS:N	2.41	0.53
1:B:384:HIS:CE1	2:B:904:HEC:HBB3	2.43	0.53
1:B:312:HIS:HB2	4:B:915:DMS:H22	1.91	0.53
1:C:59:ASN:OD1	1:C:70:ASN:ND2	2.42	0.53
1:B:313:TYR:CE1	2:B:902:HEC:HBC2	2.43	0.53
1:C:711:ASP:OD1	1:C:715:ARG:NH1	2.40	0.52
1:D:403:ASN:ND2	1:D:414:ASP:OD2	2.35	0.52
2:C:806:HEC:HMA2	2:C:807:HEC:HMA1	1.92	0.52
1:C:733:HIS:CD2	2:C:809:HEC:ND	2.77	0.52
1:D:576:HIS:HE1	2:D:807:HEC:ND	2.05	0.51
1:A:198:GLN:OE1	1:A:198:GLN:N	2.44	0.51
1:A:244:ARG:CZ	2:A:802:HEC:HBC2	2.40	0.51
1:B:661:LEU:HD11	1:B:671:VAL:HG13	1.91	0.51
2:A:802:HEC:HBC3	2:A:802:HEC:HMC1	1.92	0.51
1:C:244:ARG:NH2	2:C:802:HEC:HBC2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:CYS:CB	2:D:802:HEC:CAC	2.89	0.51
1:B:278:LYS:HE2	2:B:905:HEC:HMD3	1.92	0.50
1:A:577:TYR:CE2	2:A:807:HEC:HBC2	2.47	0.50
1:D:491:LEU:HD21	1:D:493:LEU:HD13	1.93	0.50
1:B:444:SER:OG	1:B:463:ARG:NH2	2.44	0.50
1:B:244:ARG:NH2	2:B:903:HEC:HBC2	2.27	0.50
1:C:244:ARG:CZ	2:C:802:HEC:HBC2	2.42	0.50
1:B:437:THR:HG23	1:B:577:TYR:CZ	2.47	0.50
1:B:557:ARG:HH22	2:B:909:HEC:CGD	2.25	0.50
1:D:449:LYS:O	1:D:557:ARG:HD2	2.12	0.49
1:D:736:LYS:HG2	1:D:737:GLY:H	1.77	0.49
2:B:911:HEC:HHA	2:B:911:HEC:HBD2	1.93	0.49
1:C:509:ALA:HA	1:C:535:TYR:HA	1.92	0.49
1:C:724:HIS:HA	1:C:728:GLN:HG2	1.93	0.49
1:C:285:PHE:O	1:C:354:LYS:HD3	2.12	0.49
1:C:661:LEU:HD11	1:C:671:VAL:HG13	1.94	0.49
1:A:262:GLU:HB2	1:A:299:ILE:HB	1.94	0.49
2:D:802:HEC:HMC1	2:D:802:HEC:HBC3	1.93	0.49
1:B:660:TRP:CD1	1:B:679:GLY:HA3	2.48	0.49
1:C:239:LEU:HD22	2:C:802:HEC:CHB	2.43	0.49
1:B:317:PRO:HG3	1:B:391:TYR:CE2	2.48	0.49
1:D:565:LYS:O	2:D:806:HEC:HMC3	2.14	0.48
1:C:198:GLN:OE1	1:C:198:GLN:N	2.42	0.48
1:A:304:LYS:NZ	1:A:306:ILE:HD11	2.28	0.48
1:B:442:TYR:CZ	2:B:908:HEC:HBC1	2.49	0.48
2:B:909:HEC:HBB2	2:B:910:HEC:HBC2	1.95	0.48
1:D:73:LEU:HD11	1:D:84:LEU:HD22	1.95	0.48
1:B:577:TYR:CE2	2:B:908:HEC:HBC2	2.49	0.48
1:D:355:PRO:HG3	2:D:805:HEC:C1B	2.44	0.48
1:D:384:HIS:CE1	2:D:803:HEC:HBB3	2.48	0.48
1:D:661:LEU:HD11	1:D:671:VAL:HG13	1.95	0.48
1:A:53:LEU:HD21	1:A:73:LEU:HD22	1.96	0.48
1:B:510:THR:HB	5:B:1143:HOH:O	2.14	0.48
1:D:244:ARG:CZ	2:D:802:HEC:HBC2	2.44	0.48
1:B:577:TYR:CZ	2:B:908:HEC:HBC2	2.49	0.47
1:A:510:THR:HB	5:A:904:HOH:O	2.13	0.47
2:A:807:HEC:HHA	2:A:807:HEC:HBA1	1.97	0.47
1:C:620:LEU:HD13	2:C:801:HEC:HBD1	1.95	0.47
1:A:630:VAL:HG13	2:A:806:HEC:HBC2	1.97	0.47
1:A:557:ARG:HH22	2:A:808:HEC:CGD	2.28	0.47
1:D:442:TYR:CZ	2:D:807:HEC:HBC1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:696:HIS:HD2	2:A:810:HEC:NA	2.09	0.47
1:C:630:VAL:HG13	2:C:806:HEC:HBC2	1.97	0.47
1:B:625:VAL:HG22	2:B:902:HEC:CGD	2.45	0.47
1:B:576:HIS:HE1	2:B:908:HEC:C4D	2.27	0.47
1:A:313:TYR:CE1	2:A:801:HEC:HBC2	2.50	0.46
2:A:804:HEC:O1D	5:A:1270:HOH:O	2.21	0.46
2:C:802:HEC:HBC3	2:C:802:HEC:HMC1	1.97	0.46
1:A:313:TYR:CE2	1:A:315:GLN:HB2	2.51	0.46
1:A:498:THR:OG1	5:A:1266:HOH:O	2.21	0.46
1:A:384:HIS:CE1	2:A:803:HEC:HBB3	2.51	0.46
1:B:630:VAL:HG13	2:B:907:HEC:HBC2	1.96	0.46
1:A:693:ALA:O	1:A:697:ILE:HG12	2.16	0.46
1:B:565:LYS:O	2:B:907:HEC:HMC3	2.15	0.46
1:C:80:ALA:HB1	1:C:161:GLY:HA3	1.98	0.46
1:A:404:ILE:HD12	1:A:550:THR:HG21	1.99	0.45
1:A:376:GLY:HA3	1:A:517:TYR:CE2	2.52	0.45
1:B:657:GLU:H	1:B:657:GLU:CD	2.20	0.45
1:C:577:TYR:CE2	2:C:807:HEC:HBC2	2.51	0.45
1:D:240:HIS:O	1:D:243:ARG:HG2	2.17	0.45
1:B:244:ARG:CZ	2:B:903:HEC:HBC2	2.47	0.45
1:D:84:LEU:HB3	1:D:163:TYR:CE2	2.51	0.45
1:B:244:ARG:HG2	2:B:903:HEC:HMC2	1.98	0.45
1:C:118:TYR:CE1	1:C:171:VAL:HG13	2.51	0.45
1:D:711:ASP:OD2	1:D:715:ARG:NH1	2.50	0.45
1:D:733:HIS:CD2	2:D:809:HEC:ND	2.84	0.45
1:A:646:VAL:HG22	5:A:1267:HOH:O	2.17	0.45
1:C:313:TYR:CE1	2:C:801:HEC:HBC2	2.52	0.45
1:D:193:GLU:OE1	1:D:243:ARG:NH2	2.49	0.45
1:A:497:LEU:O	1:A:545:TRP:HB3	2.17	0.44
1:A:576:HIS:HE1	2:A:807:HEC:C4D	2.30	0.44
2:B:904:HEC:HBB3	2:B:904:HEC:HMB1	1.98	0.44
1:A:355:PRO:HG3	2:A:805:HEC:C1B	2.47	0.44
1:B:298:ILE:HG21	2:B:903:HEC:HAA1	1.99	0.44
1:C:396:GLY:HA3	1:C:420:ASN:HB3	1.99	0.44
1:B:179:LYS:NZ	1:B:181:THR:OG1	2.49	0.44
1:B:314:PRO:HB3	2:B:907:HEC:C2D	2.47	0.44
1:C:430:ILE:HG21	1:C:467:LEU:HD12	1.99	0.44
1:B:315:GLN:HG2	1:B:569:CYS:O	2.17	0.44
2:D:810:HEC:CHA	2:D:810:HEC:HBD2	2.47	0.44
1:A:398:LYS:HD2	1:A:418:LEU:HB2	1.99	0.44
1:A:565:LYS:O	2:A:806:HEC:HMC3	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:LEU:HD11	1:B:73:LEU:HB3	2.00	0.44
1:C:338:PHE:CZ	1:C:339:LYS:HE3	2.53	0.44
1:A:674:VAL:HG13	1:A:704:LEU:HD23	2.00	0.44
1:C:279:GLY:HA2	1:C:308:TYR:O	2.18	0.43
1:A:416:GLN:NE2	1:A:479:THR:O	2.51	0.43
1:D:420:ASN:OD1	1:D:420:ASN:N	2.51	0.43
1:D:99:PRO:HG3	1:D:113:TYR:CE1	2.53	0.43
1:A:463:ARG:NH1	5:A:1213:HOH:O	2.50	0.43
1:D:560:ILE:HG21	2:D:808:HEC:HBD2	1.99	0.43
1:B:389:LYS:HE2	1:B:393:ASP:OD2	2.19	0.43
1:D:619:TYR:CD1	1:D:632:LYS:HG2	2.54	0.43
1:A:84:LEU:HB3	1:A:163:TYR:CE2	2.52	0.43
1:A:403:ASN:ND2	1:A:414:ASP:OD2	2.42	0.43
1:C:728:GLN:HB2	1:C:728:GLN:HE21	1.66	0.43
1:B:141:PHE:O	1:B:258:SER:HA	2.18	0.43
1:A:312:HIS:HB2	4:A:814:DMS:H22	2.00	0.43
1:C:442:TYR:CZ	2:C:807:HEC:HBC1	2.54	0.43
1:B:118:TYR:CE1	1:B:171:VAL:HG13	2.54	0.42
1:B:244:ARG:HD3	2:B:903:HEC:C2C	2.48	0.42
1:D:577:TYR:CZ	2:D:807:HEC:HBC2	2.54	0.42
1:A:75:ASN:OD1	1:A:79:VAL:N	2.52	0.42
1:C:535:TYR:CE2	1:C:577:TYR:HA	2.54	0.42
1:C:591:LYS:NZ	2:C:807:HEC:O2D	2.44	0.42
1:D:314:PRO:HB3	2:D:806:HEC:C2D	2.49	0.42
2:A:803:HEC:HBB2	2:A:804:HEC:C3C	2.49	0.42
1:A:88:HIS:O	1:A:90:LEU:N	2.52	0.42
1:C:440:SER:HB2	1:C:442:TYR:CE1	2.53	0.42
1:D:576:HIS:HE1	2:D:807:HEC:C4D	2.33	0.42
1:B:355:PRO:HG3	2:B:906:HEC:C1B	2.49	0.42
1:C:420:ASN:OD1	1:C:420:ASN:N	2.47	0.42
1:C:575:VAL:HG13	1:C:576:HIS:HD2	1.84	0.42
2:B:903:HEC:HBC3	2:B:903:HEC:HMC1	2.01	0.42
1:C:220:ARG:HH22	2:C:803:HEC:CGA	2.33	0.42
1:C:660:TRP:CD1	1:C:679:GLY:HA3	2.55	0.42
1:B:84:LEU:HB3	1:B:163:TYR:CE2	2.53	0.42
1:B:398:LYS:HB3	1:B:538:ASP:HB3	2.02	0.42
1:D:273:ILE:HG13	2:D:803:HEC:HMD2	2.02	0.42
1:D:509:ALA:HA	1:D:535:TYR:HA	2.01	0.42
1:A:94:ILE:HG23	1:A:118:TYR:HB2	2.01	0.42
1:B:314:PRO:HD3	2:B:902:HEC:HMD2	2.02	0.42
2:B:905:HEC:HMA3	2:B:906:HEC:C2A	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:448:ASP:OD1	1:C:501:ASN:ND2	2.51	0.42
1:A:560:ILE:HG21	2:A:808:HEC:HBD2	2.00	0.42
1:D:389:LYS:NZ	1:D:393:ASP:OD2	2.49	0.42
1:B:197:PRO:HB2	1:C:422:ASP:O	2.20	0.42
1:B:697:ILE:HG12	2:B:911:HEC:HMB2	2.02	0.42
1:C:619:TYR:CD1	1:C:632:LYS:HG2	2.55	0.42
1:C:617:GLY:HA2	4:C:815:DMS:H11	2.01	0.41
1:D:50:THR:OG1	1:D:52:THR:O	2.31	0.41
1:D:313:TYR:CE1	2:D:801:HEC:HBC2	2.54	0.41
1:B:111:ARG:HD3	1:B:342:LEU:O	2.20	0.41
1:C:84:LEU:HB3	1:C:163:TYR:CE2	2.55	0.41
1:C:416:GLN:NE2	1:C:479:THR:O	2.50	0.41
1:C:697:ILE:HG12	2:C:810:HEC:HMB2	2.03	0.41
1:B:509:ALA:HA	1:B:535:TYR:HA	2.02	0.41
2:B:904:HEC:HBB2	2:B:905:HEC:C3C	2.50	0.41
1:A:459:ARG:O	1:A:463:ARG:HG3	2.21	0.41
1:B:377:THR:HB	2:B:906:HEC:HBD2	2.02	0.41
1:D:457:GLY:HA2	1:D:490:ASN:O	2.20	0.41
1:B:398:LYS:HD2	1:B:418:LEU:HB2	2.02	0.41
1:D:338:PHE:CZ	1:D:339:LYS:HE3	2.56	0.41
1:C:118:TYR:CZ	1:C:171:VAL:HG13	2.55	0.41
1:C:703:ILE:HD11	1:C:715:ARG:O	2.21	0.41
1:B:619:TYR:CD1	1:B:632:LYS:HG2	2.56	0.41
1:B:54:LYS:HE3	1:B:56:LYS:HG2	2.03	0.41
1:B:91:ARG:HG2	1:B:147:SER:HA	2.01	0.41
1:A:239:LEU:HD22	2:A:802:HEC:CHB	2.51	0.40
2:D:805:HEC:CHD	4:D:813:DMS:H22	2.51	0.40
1:C:312:HIS:HB2	4:C:815:DMS:H12	2.03	0.40
1:A:657:GLU:OE1	1:A:657:GLU:N	2.41	0.40
1:A:682:LEU:HD11	1:A:704:LEU:HD22	2.04	0.40
2:A:806:HEC:HAD2	4:A:814:DMS:H22	2.04	0.40
4:A:816:DMS:O	2:B:906:HEC:HBC2	2.20	0.40
1:D:285:PHE:O	1:D:354:LYS:HD3	2.21	0.40
1:B:299:ILE:HD12	1:B:305:VAL:HG22	2.03	0.40
1:B:376:GLY:HA3	1:B:517:TYR:CE2	2.56	0.40
1:D:377:THR:HB	2:D:805:HEC:HBD2	2.03	0.40

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	691/760 (91%)	656 (95%)	34 (5%)	1 (0%)	51	78
1	B	692/760 (91%)	669 (97%)	22 (3%)	1 (0%)	51	78
1	C	690/760 (91%)	664 (96%)	24 (4%)	2 (0%)	41	66
1	D	693/760 (91%)	670 (97%)	22 (3%)	1 (0%)	51	78
All	All	2766/3040 (91%)	2659 (96%)	102 (4%)	5 (0%)	47	73

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	575	VAL
1	A	575	VAL
1	C	676	SER
1	D	575	VAL
1	C	575	VAL

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	558/609 (92%)	547 (98%)	11 (2%)	55	81
1	B	559/609 (92%)	550 (98%)	9 (2%)	62	85
1	C	557/609 (92%)	552 (99%)	5 (1%)	78	92
1	D	559/609 (92%)	553 (99%)	6 (1%)	73	90
All	All	2233/2436 (92%)	2202 (99%)	31 (1%)	67	86

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	239	LEU
1	A	398	LYS
1	A	576	HIS
1	A	598	THR
1	A	643	LYS
1	A	688	TYR
1	A	699	THR
1	A	707	THR
1	A	720	CYS
1	A	722	THR
1	A	728	GLN
1	B	63	ASP
1	B	82	LEU
1	B	107	THR
1	B	191	THR
1	B	321	CYS
1	B	398	LYS
1	B	420	ASN
1	B	576	HIS
1	B	594	LYS
1	C	288	THR
1	C	398	LYS
1	C	474	THR
1	C	576	HIS
1	C	728	GLN
1	D	85	THR
1	D	192	MET
1	D	288	THR
1	D	398	LYS
1	D	576	HIS
1	D	728	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	ASN
1	A	713	GLN
1	C	59	ASN
1	C	70	ASN
1	C	735	ASN
1	D	735	ASN

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 64 ligands modelled in this entry, 8 are monoatomic - leaving 56 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
4	DMS	B	914	-	3,3,3	2.66	1 (33%)	3,3,3	0.40	0
4	DMS	A	815	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
2	HEC	C	801	1	26,50,50	2.36	3 (11%)	18,82,82	1.49	2 (11%)
2	HEC	A	808	1	26,50,50	2.35	3 (11%)	18,82,82	1.52	4 (22%)
2	HEC	A	801	1	26,50,50	2.35	3 (11%)	18,82,82	1.57	5 (27%)
2	HEC	D	803	1	26,50,50	2.32	3 (11%)	18,82,82	1.45	3 (16%)
4	DMS	B	901	-	3,3,3	2.65	1 (33%)	3,3,3	0.38	0
2	HEC	B	911	1	26,50,50	2.30	4 (15%)	18,82,82	1.36	2 (11%)
2	HEC	A	805	1	26,50,50	2.30	3 (11%)	18,82,82	1.71	4 (22%)
4	DMS	D	813	-	3,3,3	2.65	1 (33%)	3,3,3	0.41	0
2	HEC	C	803	1	26,50,50	2.32	3 (11%)	18,82,82	1.54	3 (16%)
2	HEC	C	806	1	26,50,50	2.29	3 (11%)	18,82,82	1.75	5 (27%)
2	HEC	B	903	1,3	26,50,50	2.28	3 (11%)	18,82,82	1.49	4 (22%)
2	HEC	D	801	1	26,50,50	2.33	3 (11%)	18,82,82	1.39	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	C	802	1,3	26,50,50	2.25	4 (15%)	18,82,82	1.40	2 (11%)
2	HEC	A	809	1	26,50,50	2.33	3 (11%)	18,82,82	1.62	4 (22%)
2	HEC	D	802	1,3	26,50,50	2.33	4 (15%)	18,82,82	1.36	3 (16%)
4	DMS	D	816	-	3,3,3	2.68	1 (33%)	3,3,3	0.60	0
4	DMS	C	816	-	3,3,3	2.69	1 (33%)	3,3,3	0.53	0
2	HEC	C	804	1	26,50,50	2.29	4 (15%)	18,82,82	1.41	3 (16%)
2	HEC	C	807	1	26,50,50	2.26	3 (11%)	18,82,82	1.56	3 (16%)
2	HEC	A	802	1,3	26,50,50	2.28	4 (15%)	18,82,82	1.42	2 (11%)
2	HEC	B	904	1	26,50,50	2.14	5 (19%)	18,82,82	1.65	2 (11%)
4	DMS	A	813	-	3,3,3	2.63	1 (33%)	3,3,3	0.46	0
2	HEC	C	809	1	26,50,50	2.31	3 (11%)	18,82,82	1.50	3 (16%)
2	HEC	A	810	1	26,50,50	2.34	4 (15%)	18,82,82	1.36	2 (11%)
4	DMS	C	813	-	3,3,3	2.64	1 (33%)	3,3,3	0.45	0
2	HEC	C	805	1	26,50,50	2.28	4 (15%)	18,82,82	1.47	3 (16%)
2	HEC	B	902	1	26,50,50	2.32	3 (11%)	18,82,82	1.33	2 (11%)
2	HEC	B	906	1	26,50,50	2.30	4 (15%)	18,82,82	1.46	2 (11%)
2	HEC	B	910	1	26,50,50	2.32	3 (11%)	18,82,82	1.54	4 (22%)
4	DMS	A	814	-	3,3,3	2.65	1 (33%)	3,3,3	0.51	0
2	HEC	D	810	1	26,50,50	2.38	4 (15%)	18,82,82	1.39	1 (5%)
2	HEC	B	905	1	26,50,50	2.27	4 (15%)	18,82,82	1.57	3 (16%)
4	DMS	B	915	-	3,3,3	2.68	1 (33%)	3,3,3	0.55	0
4	DMS	D	815	-	3,3,3	2.69	1 (33%)	3,3,3	0.56	0
4	DMS	D	814	-	3,3,3	2.60	1 (33%)	3,3,3	0.41	0
4	DMS	B	916	-	3,3,3	2.67	1 (33%)	3,3,3	0.57	0
2	HEC	B	908	1	26,50,50	2.21	3 (11%)	18,82,82	1.56	4 (22%)
2	HEC	C	810	1	26,50,50	2.34	4 (15%)	18,82,82	1.41	2 (11%)
2	HEC	B	907	1	26,50,50	2.37	3 (11%)	18,82,82	1.70	4 (22%)
2	HEC	B	909	1	26,50,50	2.31	3 (11%)	18,82,82	1.47	2 (11%)
2	HEC	A	806	1	26,50,50	2.33	3 (11%)	18,82,82	1.75	5 (27%)
4	DMS	A	816	-	3,3,3	2.66	1 (33%)	3,3,3	0.36	0
2	HEC	D	809	1	26,50,50	2.32	3 (11%)	18,82,82	1.54	4 (22%)
4	DMS	C	814	-	3,3,3	2.61	1 (33%)	3,3,3	0.46	0
2	HEC	D	804	1	26,50,50	2.35	4 (15%)	18,82,82	1.38	3 (16%)
2	HEC	A	804	1	26,50,50	2.30	3 (11%)	18,82,82	1.64	6 (33%)
2	HEC	D	807	1	26,50,50	2.19	3 (11%)	18,82,82	1.50	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	A	803	1	26,50,50	2.30	3 (11%)	18,82,82	1.60	4 (22%)
2	HEC	D	805	1	26,50,50	2.31	4 (15%)	18,82,82	1.47	3 (16%)
2	HEC	A	807	1	26,50,50	2.28	4 (15%)	18,82,82	1.27	1 (5%)
4	DMS	C	815	-	3,3,3	2.67	1 (33%)	3,3,3	0.56	0
2	HEC	D	808	1	26,50,50	2.26	4 (15%)	18,82,82	1.67	5 (27%)
2	HEC	D	806	1	26,50,50	2.31	3 (11%)	18,82,82	1.84	5 (27%)
2	HEC	C	808	1	26,50,50	2.30	4 (15%)	18,82,82	1.53	3 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	C	801	1	-	0/6/54/54	-
2	HEC	A	808	1	-	0/6/54/54	-
2	HEC	A	801	1	-	0/6/54/54	-
2	HEC	D	803	1	-	0/6/54/54	-
2	HEC	B	911	1	-	3/6/54/54	-
2	HEC	A	805	1	-	0/6/54/54	-
2	HEC	D	804	1	-	1/6/54/54	-
2	HEC	C	803	1	-	0/6/54/54	-
2	HEC	C	806	1	-	0/6/54/54	-
2	HEC	B	903	1,3	-	0/6/54/54	-
2	HEC	D	801	1	-	0/6/54/54	-
2	HEC	A	809	1	-	0/6/54/54	-
2	HEC	D	802	1,3	-	0/6/54/54	-
2	HEC	B	904	1	-	0/6/54/54	-
2	HEC	C	807	1	-	1/6/54/54	-
2	HEC	A	802	1,3	-	0/6/54/54	-
2	HEC	C	804	1	-	1/6/54/54	-
2	HEC	C	809	1	-	0/6/54/54	-
2	HEC	A	810	1	-	0/6/54/54	-
2	HEC	C	805	1	-	0/6/54/54	-
2	HEC	C	802	1,3	-	0/6/54/54	-
2	HEC	B	906	1	-	0/6/54/54	-
2	HEC	B	910	1	-	0/6/54/54	-
2	HEC	D	810	1	-	3/6/54/54	-
2	HEC	B	905	1	-	1/6/54/54	-
2	HEC	B	908	1	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	C	810	1	-	3/6/54/54	-
2	HEC	B	907	1	-	0/6/54/54	-
2	HEC	B	909	1	-	0/6/54/54	-
2	HEC	A	806	1	-	0/6/54/54	-
2	HEC	D	809	1	-	0/6/54/54	-
2	HEC	A	804	1	-	0/6/54/54	-
2	HEC	D	807	1	-	1/6/54/54	-
2	HEC	A	803	1	-	0/6/54/54	-
2	HEC	D	805	1	-	0/6/54/54	-
2	HEC	A	807	1	-	2/6/54/54	-
2	HEC	B	902	1	-	0/6/54/54	-
2	HEC	D	808	1	-	0/6/54/54	-
2	HEC	D	806	1	-	0/6/54/54	-
2	HEC	C	808	1	-	0/6/54/54	-

All (154) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	907	HEC	C3B-C2B	-6.41	1.34	1.40
2	A	805	HEC	C3B-C2B	-6.22	1.34	1.40
2	D	810	HEC	C3B-C2B	-6.21	1.34	1.40
2	B	902	HEC	C3C-C2C	-6.18	1.34	1.40
2	D	802	HEC	C3B-C2B	-6.16	1.34	1.40
2	C	806	HEC	C3B-C2B	-6.16	1.34	1.40
2	A	806	HEC	C3B-C2B	-6.14	1.34	1.40
2	B	904	HEC	C3C-C2C	-6.14	1.34	1.40
2	A	803	HEC	C3B-C2B	-6.11	1.34	1.40
2	B	903	HEC	C3B-C2B	-6.11	1.34	1.40
2	C	801	HEC	C3B-C2B	-6.10	1.34	1.40
2	A	809	HEC	C3B-C2B	-6.10	1.34	1.40
2	A	804	HEC	C3B-C2B	-6.09	1.34	1.40
2	A	801	HEC	C3C-C2C	-6.06	1.34	1.40
2	B	909	HEC	C3B-C2B	-6.05	1.34	1.40
2	A	810	HEC	C3C-C2C	-6.05	1.34	1.40
2	A	801	HEC	C3B-C2B	-6.03	1.34	1.40
2	A	809	HEC	C3C-C2C	-6.02	1.34	1.40
2	B	908	HEC	C3B-C2B	-6.02	1.34	1.40
2	D	804	HEC	C3C-C2C	-5.99	1.34	1.40
2	A	808	HEC	C3B-C2B	-5.98	1.34	1.40
2	D	803	HEC	C3C-C2C	-5.98	1.34	1.40
2	C	809	HEC	C3C-C2C	-5.98	1.34	1.40
2	C	801	HEC	C3C-C2C	-5.97	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	910	HEC	C3B-C2B	-5.97	1.34	1.40
2	A	808	HEC	C3C-C2C	-5.97	1.34	1.40
2	C	810	HEC	C3C-C2C	-5.95	1.34	1.40
2	D	804	HEC	C3B-C2B	-5.95	1.34	1.40
2	A	807	HEC	C3B-C2B	-5.94	1.34	1.40
2	D	809	HEC	C3B-C2B	-5.92	1.34	1.40
2	A	802	HEC	C3B-C2B	-5.91	1.34	1.40
2	D	809	HEC	C3C-C2C	-5.91	1.34	1.40
2	C	802	HEC	C3B-C2B	-5.91	1.34	1.40
2	D	801	HEC	C3C-C2C	-5.91	1.34	1.40
2	D	801	HEC	C3B-C2B	-5.90	1.34	1.40
2	D	808	HEC	C3B-C2B	-5.89	1.34	1.40
2	C	809	HEC	C3B-C2B	-5.88	1.34	1.40
2	C	810	HEC	C3B-C2B	-5.88	1.34	1.40
2	B	907	HEC	C3C-C2C	-5.88	1.34	1.40
2	D	805	HEC	C3B-C2B	-5.88	1.34	1.40
2	D	806	HEC	C3C-C2C	-5.88	1.34	1.40
2	C	805	HEC	C3B-C2B	-5.87	1.34	1.40
2	B	910	HEC	C3C-C2C	-5.87	1.34	1.40
2	D	806	HEC	C3B-C2B	-5.86	1.34	1.40
2	C	804	HEC	C3B-C2B	-5.84	1.34	1.40
2	B	911	HEC	C3C-C2C	-5.82	1.34	1.40
2	B	905	HEC	C3B-C2B	-5.82	1.34	1.40
2	D	810	HEC	C3C-C2C	-5.81	1.34	1.40
2	D	803	HEC	C3B-C2B	-5.79	1.34	1.40
2	B	911	HEC	C3B-C2B	-5.78	1.34	1.40
2	C	804	HEC	C3C-C2C	-5.77	1.34	1.40
2	C	803	HEC	C3B-C2B	-5.77	1.34	1.40
2	C	803	HEC	C3C-C2C	-5.77	1.34	1.40
2	B	909	HEC	C3C-C2C	-5.76	1.34	1.40
2	C	808	HEC	C3B-C2B	-5.76	1.34	1.40
2	C	807	HEC	C3B-C2B	-5.76	1.34	1.40
2	B	906	HEC	C3C-C2C	-5.72	1.34	1.40
2	A	804	HEC	C3C-C2C	-5.71	1.34	1.40
2	B	902	HEC	C3B-C2B	-5.71	1.34	1.40
2	D	805	HEC	C3D-C2D	5.69	1.54	1.37
2	A	803	HEC	C3C-C2C	-5.68	1.34	1.40
2	A	810	HEC	C3B-C2B	-5.68	1.34	1.40
2	C	808	HEC	C3C-C2C	-5.68	1.34	1.40
2	B	906	HEC	C3B-C2B	-5.68	1.34	1.40
2	A	806	HEC	C3C-C2C	-5.66	1.34	1.40
2	C	807	HEC	C3C-C2C	-5.66	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	906	HEC	C3D-C2D	5.65	1.54	1.37
2	C	805	HEC	C3D-C2D	5.65	1.54	1.37
2	D	808	HEC	C3C-C2C	-5.64	1.34	1.40
2	D	804	HEC	C3D-C2D	5.60	1.54	1.37
2	D	807	HEC	C3B-C2B	-5.60	1.34	1.40
2	A	810	HEC	C3D-C2D	5.59	1.54	1.37
2	D	810	HEC	C3D-C2D	5.57	1.54	1.37
2	C	806	HEC	C3C-C2C	-5.57	1.34	1.40
2	C	810	HEC	C3D-C2D	5.55	1.54	1.37
2	B	905	HEC	C3D-C2D	5.54	1.54	1.37
2	B	904	HEC	C3D-C2D	5.54	1.54	1.37
2	D	802	HEC	C3C-C2C	-5.53	1.35	1.40
2	D	806	HEC	C3D-C2D	5.53	1.54	1.37
2	C	808	HEC	C3D-C2D	5.53	1.54	1.37
2	A	805	HEC	C3D-C2D	5.52	1.54	1.37
2	C	804	HEC	C3D-C2D	5.51	1.54	1.37
2	A	802	HEC	C3D-C2D	5.51	1.54	1.37
2	C	803	HEC	C3D-C2D	5.49	1.53	1.37
2	C	801	HEC	C3D-C2D	5.49	1.53	1.37
2	B	911	HEC	C3D-C2D	5.46	1.53	1.37
2	B	907	HEC	C3D-C2D	5.46	1.53	1.37
2	A	805	HEC	C3C-C2C	-5.46	1.35	1.40
2	A	806	HEC	C3D-C2D	5.45	1.53	1.37
2	A	801	HEC	C3D-C2D	5.45	1.53	1.37
2	D	801	HEC	C3D-C2D	5.45	1.53	1.37
2	A	804	HEC	C3D-C2D	5.44	1.53	1.37
2	A	808	HEC	C3D-C2D	5.43	1.53	1.37
2	C	809	HEC	C3D-C2D	5.42	1.53	1.37
2	D	803	HEC	C3D-C2D	5.41	1.53	1.37
2	C	806	HEC	C3D-C2D	5.41	1.53	1.37
2	B	903	HEC	C3C-C2C	-5.41	1.35	1.40
2	D	809	HEC	C3D-C2D	5.40	1.53	1.37
2	C	802	HEC	C3D-C2D	5.40	1.53	1.37
2	A	807	HEC	C3D-C2D	5.40	1.53	1.37
2	D	802	HEC	C3D-C2D	5.40	1.53	1.37
2	B	910	HEC	C3D-C2D	5.39	1.53	1.37
2	A	809	HEC	C3D-C2D	5.38	1.53	1.37
2	A	807	HEC	C3C-C2C	-5.38	1.35	1.40
2	D	805	HEC	C3C-C2C	-5.38	1.35	1.40
2	A	803	HEC	C3D-C2D	5.37	1.53	1.37
2	B	909	HEC	C3D-C2D	5.36	1.53	1.37
2	B	903	HEC	C3D-C2D	5.36	1.53	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	905	HEC	C3C-C2C	-5.36	1.35	1.40
2	B	902	HEC	C3D-C2D	5.35	1.53	1.37
2	C	805	HEC	C3C-C2C	-5.34	1.35	1.40
2	D	807	HEC	C3C-C2C	-5.32	1.35	1.40
2	C	807	HEC	C3D-C2D	5.31	1.53	1.37
2	D	808	HEC	C3D-C2D	5.26	1.53	1.37
2	D	807	HEC	C3D-C2D	5.22	1.53	1.37
2	B	908	HEC	C3C-C2C	-5.21	1.35	1.40
2	A	802	HEC	C3C-C2C	-5.21	1.35	1.40
2	C	802	HEC	C3C-C2C	-5.20	1.35	1.40
2	B	908	HEC	C3D-C2D	5.18	1.53	1.37
4	D	815	DMS	O-S	4.52	1.80	1.50
4	C	816	DMS	O-S	4.50	1.80	1.50
4	B	915	DMS	O-S	4.49	1.80	1.50
4	B	914	DMS	O-S	4.48	1.80	1.50
4	C	815	DMS	O-S	4.48	1.80	1.50
4	B	916	DMS	O-S	4.48	1.80	1.50
4	D	816	DMS	O-S	4.48	1.80	1.50
4	D	813	DMS	O-S	4.48	1.80	1.50
4	A	815	DMS	O-S	4.47	1.80	1.50
4	A	816	DMS	O-S	4.47	1.80	1.50
4	A	814	DMS	O-S	4.45	1.80	1.50
4	B	901	DMS	O-S	4.45	1.80	1.50
4	C	813	DMS	O-S	4.44	1.80	1.50
4	A	813	DMS	O-S	4.41	1.80	1.50
4	C	814	DMS	O-S	4.39	1.79	1.50
4	D	814	DMS	O-S	4.36	1.79	1.50
2	D	810	HEC	CAD-C3D	2.62	1.55	1.52
2	D	804	HEC	CAD-C3D	2.35	1.55	1.52
2	A	802	HEC	CAD-C3D	2.30	1.55	1.52
2	B	904	HEC	C3B-C4B	2.28	1.47	1.43
2	B	911	HEC	CAD-C3D	2.27	1.55	1.52
2	C	810	HEC	CAD-C3D	2.22	1.55	1.52
2	C	805	HEC	CAD-C3D	2.19	1.55	1.52
2	B	905	HEC	CAD-C3D	2.18	1.55	1.52
2	D	805	HEC	CAD-C3D	2.17	1.55	1.52
2	B	906	HEC	CAD-C3D	2.12	1.55	1.52
2	D	802	HEC	CAD-C3D	2.12	1.55	1.52
2	A	810	HEC	CAD-C3D	2.10	1.55	1.52
2	C	808	HEC	CAD-C3D	2.09	1.55	1.52
2	B	904	HEC	C1D-ND	2.09	1.40	1.36
2	A	807	HEC	CAD-C3D	2.08	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	904	HEC	C3B-C2B	-2.06	1.38	1.40
2	C	802	HEC	CAD-C3D	2.04	1.55	1.52
2	D	808	HEC	CAA-C2A	2.03	1.55	1.52
2	C	804	HEC	CAD-C3D	2.01	1.55	1.52

All (127) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	905	HEC	CMC-C2C-C1C	-4.42	121.67	128.46
2	B	904	HEC	CMC-C2C-C1C	-4.42	121.68	128.46
2	D	806	HEC	CBA-CAA-C2A	-4.14	104.86	112.48
2	B	907	HEC	CBA-CAA-C2A	-3.85	105.39	112.48
2	A	806	HEC	CBA-CAA-C2A	-3.78	105.51	112.48
2	D	804	HEC	CMC-C2C-C1C	-3.52	123.06	128.46
2	C	804	HEC	CMC-C2C-C1C	-3.40	123.25	128.46
2	A	804	HEC	CMC-C2C-C1C	-3.37	123.28	128.46
2	A	806	HEC	CBD-CAD-C3D	-3.36	106.28	112.49
2	A	805	HEC	CMC-C2C-C1C	-3.34	123.33	128.46
2	B	908	HEC	CMC-C2C-C1C	-3.33	123.34	128.46
2	A	803	HEC	CMC-C2C-C1C	-3.31	123.38	128.46
2	D	805	HEC	CMC-C2C-C1C	-3.25	123.46	128.46
2	D	807	HEC	CMC-C2C-C1C	-3.24	123.49	128.46
2	C	803	HEC	CMC-C2C-C1C	-3.23	123.50	128.46
2	D	806	HEC	CBD-CAD-C3D	-3.19	106.60	112.49
2	A	802	HEC	CMC-C2C-C1C	-3.18	123.57	128.46
2	A	801	HEC	CBD-CAD-C3D	-3.15	106.68	112.49
2	C	806	HEC	CBA-CAA-C2A	-3.11	106.74	112.48
2	A	809	HEC	CBD-CAD-C3D	-3.07	106.81	112.49
2	B	903	HEC	CMC-C2C-C1C	-3.07	123.74	128.46
2	A	807	HEC	CMC-C2C-C1C	-3.07	123.74	128.46
2	C	807	HEC	CMC-C2C-C1C	-3.06	123.76	128.46
2	C	802	HEC	CMC-C2C-C1C	-3.03	123.81	128.46
2	D	809	HEC	CMC-C2C-C1C	-3.03	123.81	128.46
2	C	801	HEC	CMC-C2C-C1C	-3.02	123.83	128.46
2	B	906	HEC	CMC-C2C-C1C	-2.93	123.95	128.46
2	A	805	HEC	CAA-CBA-CGA	-2.92	107.78	112.67
2	C	806	HEC	CMC-C2C-C1C	-2.90	124.01	128.46
2	D	808	HEC	CMC-C2C-C1C	-2.89	124.02	128.46
2	C	805	HEC	CMC-C2C-C1C	-2.86	124.07	128.46
2	A	801	HEC	CMC-C2C-C1C	-2.85	124.08	128.46
2	B	910	HEC	CBD-CAD-C3D	-2.85	107.23	112.49
2	D	801	HEC	CMC-C2C-C1C	-2.85	124.08	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	802	HEC	CMC-C2C-C1C	-2.84	124.09	128.46
2	B	909	HEC	CMC-C2C-C1C	-2.82	124.14	128.46
2	D	806	HEC	CMC-C2C-C1C	-2.80	124.16	128.46
2	D	808	HEC	CMB-C2B-C1B	-2.75	124.23	128.46
2	C	803	HEC	CAD-CBD-CGD	-2.73	108.09	112.67
2	B	907	HEC	CMC-C2C-C1C	-2.72	124.28	128.46
2	D	808	HEC	C1D-C2D-C3D	-2.71	105.11	107.00
2	B	904	HEC	C1D-C2D-C3D	-2.71	105.11	107.00
2	D	808	HEC	CBD-CAD-C3D	-2.71	107.49	112.49
2	C	808	HEC	CMC-C2C-C1C	-2.66	124.37	128.46
2	C	809	HEC	CMC-C2C-C1C	-2.64	124.41	128.46
2	A	804	HEC	CBD-CAD-C3D	-2.63	107.64	112.49
2	C	806	HEC	CBD-CAD-C3D	-2.62	107.65	112.49
2	A	809	HEC	CMC-C2C-C1C	-2.62	124.44	128.46
2	A	810	HEC	CMC-C2C-C1C	-2.61	124.45	128.46
2	D	809	HEC	CMB-C2B-C1B	-2.60	124.47	128.46
2	D	806	HEC	CMB-C2B-C1B	-2.59	124.48	128.46
2	C	808	HEC	CMB-C2B-C1B	-2.58	124.50	128.46
2	C	806	HEC	C1D-C2D-C3D	-2.55	105.22	107.00
2	B	907	HEC	CBD-CAD-C3D	-2.54	107.80	112.49
2	C	807	HEC	CAA-CBA-CGA	-2.51	108.45	112.67
2	B	903	HEC	CBD-CAD-C3D	-2.50	107.88	112.49
2	C	810	HEC	CMC-C2C-C1C	-2.49	124.63	128.46
2	C	801	HEC	CMB-C2B-C1B	-2.49	124.63	128.46
2	A	806	HEC	CMC-C2C-C1C	-2.48	124.66	128.46
2	B	910	HEC	CMC-C2C-C1C	-2.47	124.66	128.46
2	A	801	HEC	C1D-C2D-C3D	-2.45	105.29	107.00
2	D	809	HEC	CBD-CAD-C3D	-2.44	107.98	112.49
2	A	804	HEC	C1D-C2D-C3D	-2.43	105.30	107.00
2	A	804	HEC	CAD-CBD-CGD	-2.43	108.59	112.67
2	D	809	HEC	C1D-C2D-C3D	-2.42	105.31	107.00
2	A	808	HEC	CMB-C2B-C1B	-2.42	124.75	128.46
2	C	806	HEC	CMB-C2B-C1B	-2.40	124.78	128.46
2	D	803	HEC	CMC-C2C-C1C	-2.40	124.78	128.46
2	A	808	HEC	CMC-C2C-C1C	-2.40	124.78	128.46
2	A	805	HEC	C1D-C2D-C3D	-2.39	105.33	107.00
2	C	808	HEC	CBA-CAA-C2A	-2.39	108.07	112.48
2	A	809	HEC	C1D-C2D-C3D	-2.37	105.35	107.00
2	A	806	HEC	C4B-C3B-C2B	2.37	108.91	106.35
2	A	803	HEC	CMB-C2B-C1B	-2.36	124.83	128.46
2	B	909	HEC	CMB-C2B-C1B	-2.35	124.85	128.46
2	C	804	HEC	C1D-C2D-C3D	-2.35	105.36	107.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	HEC	CMB-C2B-C1B	-2.35	124.86	128.46
2	D	808	HEC	CAD-CBD-CGD	-2.34	108.74	112.67
2	B	911	HEC	CMC-C2C-C1C	-2.34	124.87	128.46
2	A	803	HEC	C1D-C2D-C3D	-2.33	105.37	107.00
2	B	903	HEC	C1D-C2D-C3D	-2.33	105.38	107.00
2	B	905	HEC	CMB-C2B-C1B	-2.32	124.89	128.46
2	A	806	HEC	C1D-C2D-C3D	-2.32	105.38	107.00
2	B	910	HEC	CMB-C2B-C1B	-2.32	124.90	128.46
2	A	809	HEC	CMB-C2B-C1B	-2.31	124.92	128.46
2	D	806	HEC	C1D-C2D-C3D	-2.30	105.39	107.00
2	B	910	HEC	C1D-C2D-C3D	-2.29	105.40	107.00
2	D	807	HEC	CMC-C2C-C3C	2.29	128.51	125.82
2	C	807	HEC	CMB-C2B-C1B	-2.27	124.97	128.46
2	D	802	HEC	CBD-CAD-C3D	-2.27	108.30	112.49
2	A	808	HEC	C1D-C2D-C3D	-2.27	105.42	107.00
2	B	907	HEC	C1D-C2D-C3D	-2.27	105.42	107.00
2	B	908	HEC	CAA-CBA-CGA	-2.27	108.87	112.67
2	A	810	HEC	CMB-C2B-C1B	-2.24	125.02	128.46
2	B	903	HEC	CMB-C2B-C1B	-2.24	125.03	128.46
2	C	810	HEC	CMB-C2B-C1B	-2.22	125.06	128.46
2	B	908	HEC	CMB-C2B-C1B	-2.20	125.08	128.46
2	B	902	HEC	CMB-C2B-C1B	-2.19	125.10	128.46
2	A	805	HEC	CMB-C2B-C1B	-2.17	125.12	128.46
2	B	905	HEC	C1D-C2D-C3D	-2.17	105.49	107.00
2	D	807	HEC	CAA-CBA-CGA	-2.17	109.03	112.67
2	D	802	HEC	CMB-C2B-C1B	-2.15	125.16	128.46
2	B	902	HEC	CMC-C2C-C1C	-2.15	125.16	128.46
2	C	802	HEC	CMB-C2B-C1B	-2.15	125.16	128.46
2	A	803	HEC	CAD-CBD-CGD	-2.14	109.09	112.67
2	A	801	HEC	CBA-CAA-C2A	-2.13	108.55	112.48
2	D	804	HEC	C1D-C2D-C3D	-2.12	105.52	107.00
2	C	805	HEC	C1D-C2D-C3D	-2.12	105.52	107.00
2	C	805	HEC	CBA-CAA-C2A	-2.11	108.59	112.48
2	C	804	HEC	CMB-C2B-C1B	-2.10	125.23	128.46
2	D	803	HEC	CBD-CAD-C3D	-2.08	108.65	112.49
2	D	805	HEC	C1D-C2D-C3D	-2.08	105.55	107.00
2	B	906	HEC	CMB-C2B-C1B	-2.07	125.28	128.46
2	A	802	HEC	CMB-C2B-C1B	-2.06	125.29	128.46
2	C	809	HEC	C1D-C2D-C3D	-2.06	105.56	107.00
2	D	803	HEC	CMB-C2B-C1B	-2.06	125.30	128.46
2	D	805	HEC	CBA-CAA-C2A	-2.05	108.70	112.48
2	A	808	HEC	CAD-CBD-CGD	-2.04	109.24	112.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	911	HEC	CMB-C2B-C1B	-2.04	125.33	128.46
2	C	803	HEC	CMB-C2B-C1B	-2.04	125.33	128.46
2	C	809	HEC	CMB-C2B-C1B	-2.03	125.34	128.46
2	A	804	HEC	CBA-CAA-C2A	-2.02	108.75	112.48
2	A	801	HEC	CMB-C2B-C1B	-2.02	125.36	128.46
2	D	804	HEC	CMB-C2B-C1B	-2.01	125.37	128.46
2	D	810	HEC	CMB-C2B-C1B	-2.01	125.37	128.46
2	B	908	HEC	CAD-CBD-CGD	-2.01	109.31	112.67
2	A	804	HEC	CMB-C2B-C1B	-2.01	125.38	128.46

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	911	HEC	C2D-C3D-CAD-CBD
2	B	911	HEC	C4D-C3D-CAD-CBD
2	B	911	HEC	C3D-CAD-CBD-CGD
2	C	807	HEC	C2A-CAA-CBA-CGA
2	D	810	HEC	C2D-C3D-CAD-CBD
2	D	810	HEC	C4D-C3D-CAD-CBD
2	D	810	HEC	C3D-CAD-CBD-CGD
2	C	810	HEC	C2D-C3D-CAD-CBD
2	C	810	HEC	C4D-C3D-CAD-CBD
2	D	807	HEC	C2A-CAA-CBA-CGA
2	A	807	HEC	C1A-C2A-CAA-CBA
2	A	807	HEC	C3A-C2A-CAA-CBA
2	C	804	HEC	C3D-CAD-CBD-CGD
2	C	810	HEC	C3D-CAD-CBD-CGD
2	D	804	HEC	C3D-CAD-CBD-CGD
2	B	905	HEC	C3D-CAD-CBD-CGD

There are no ring outliers.

42 monomers are involved in 108 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	HEC	2	0
2	A	808	HEC	3	0
2	A	801	HEC	1	0
2	D	803	HEC	2	0
2	B	911	HEC	2	0
2	A	805	HEC	1	0

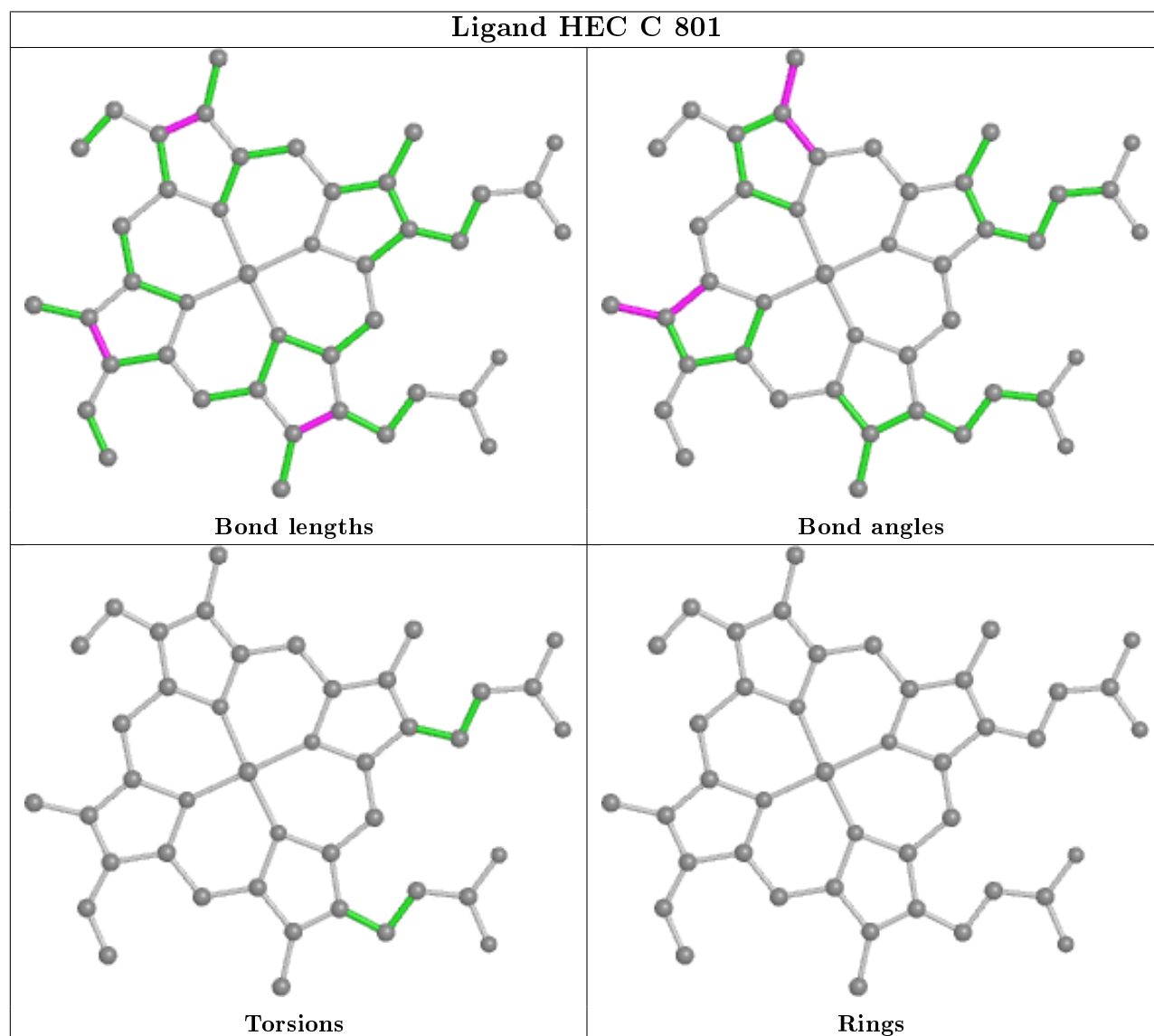
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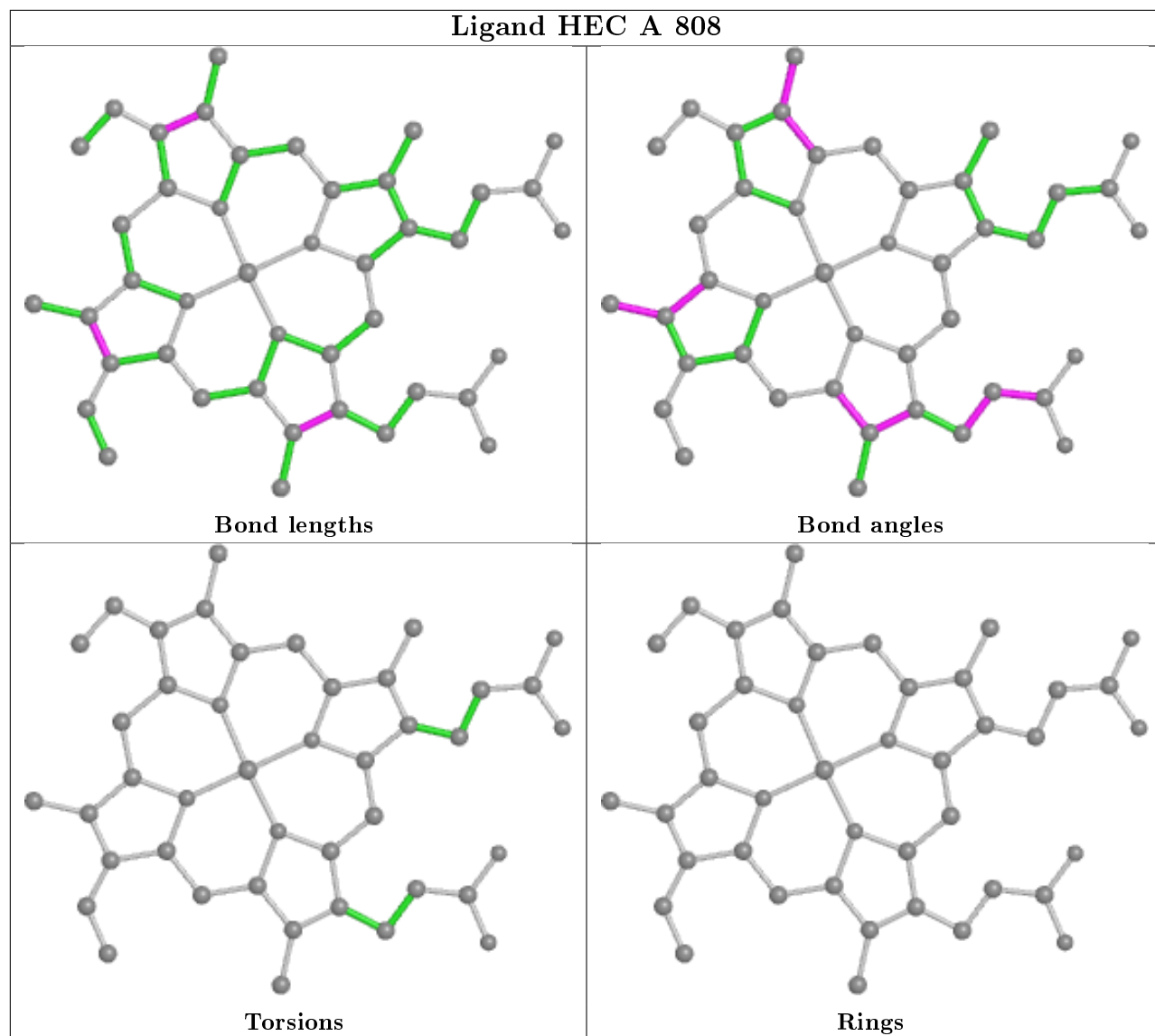
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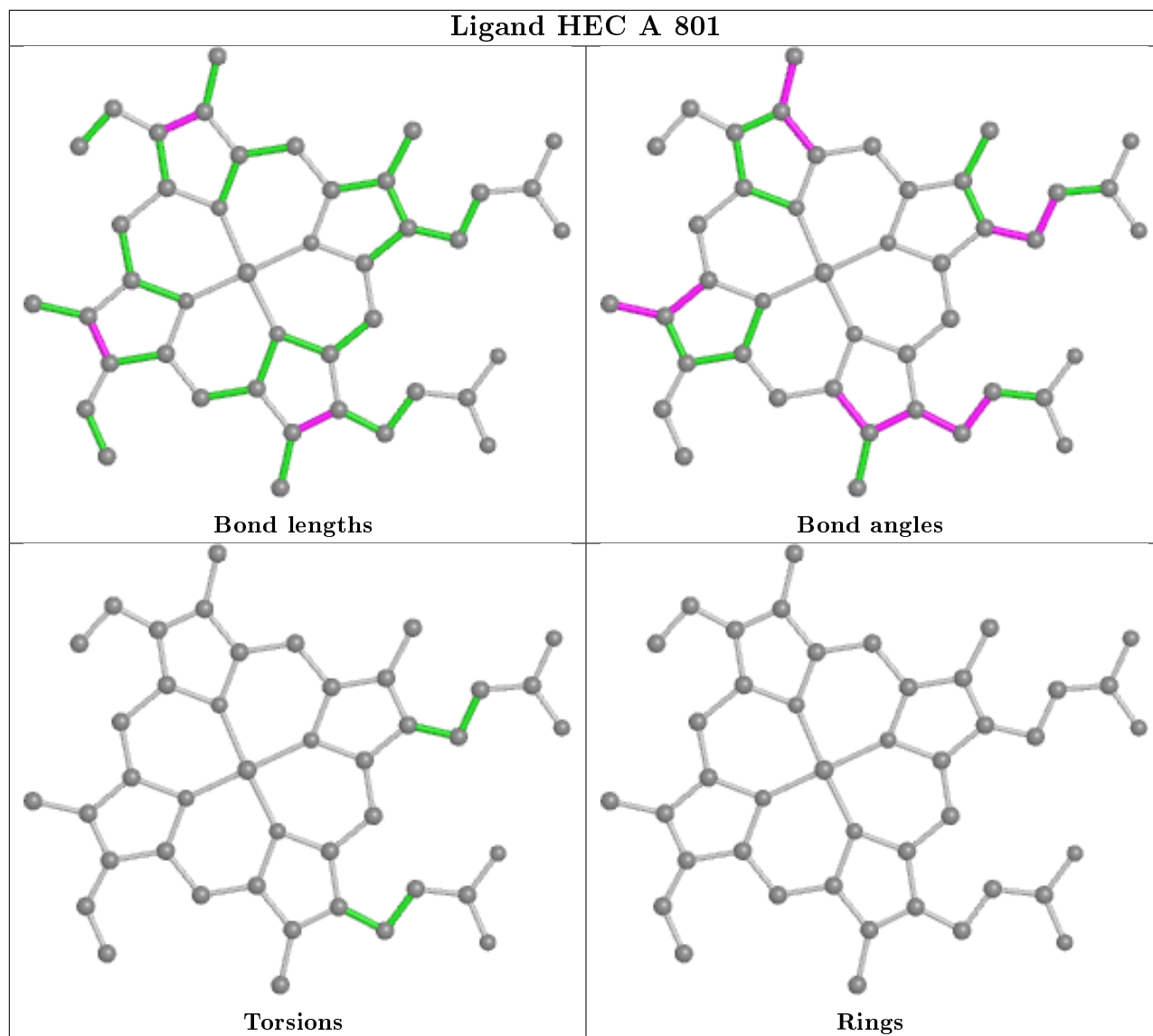
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	813	DMS	1	0
2	C	803	HEC	1	0
2	C	806	HEC	2	0
2	B	903	HEC	7	0
2	D	801	HEC	1	0
2	C	802	HEC	5	0
2	D	802	HEC	7	0
2	C	804	HEC	2	0
2	C	807	HEC	4	0
2	A	802	HEC	5	0
2	B	904	HEC	4	0
2	C	809	HEC	1	0
2	A	810	HEC	1	0
2	B	902	HEC	3	0
2	B	906	HEC	4	0
2	B	910	HEC	1	0
4	A	814	DMS	2	0
2	D	810	HEC	2	0
2	B	905	HEC	4	0
4	B	915	DMS	1	0
2	B	908	HEC	7	0
2	C	810	HEC	1	0
2	B	907	HEC	4	0
2	B	909	HEC	3	0
2	A	806	HEC	3	0
4	A	816	DMS	1	0
2	D	809	HEC	1	0
2	D	804	HEC	2	0
2	A	804	HEC	5	0
2	D	807	HEC	5	0
2	A	803	HEC	2	0
2	D	805	HEC	3	0
2	A	807	HEC	4	0
4	C	815	DMS	2	0
2	D	808	HEC	2	0
2	D	806	HEC	3	0

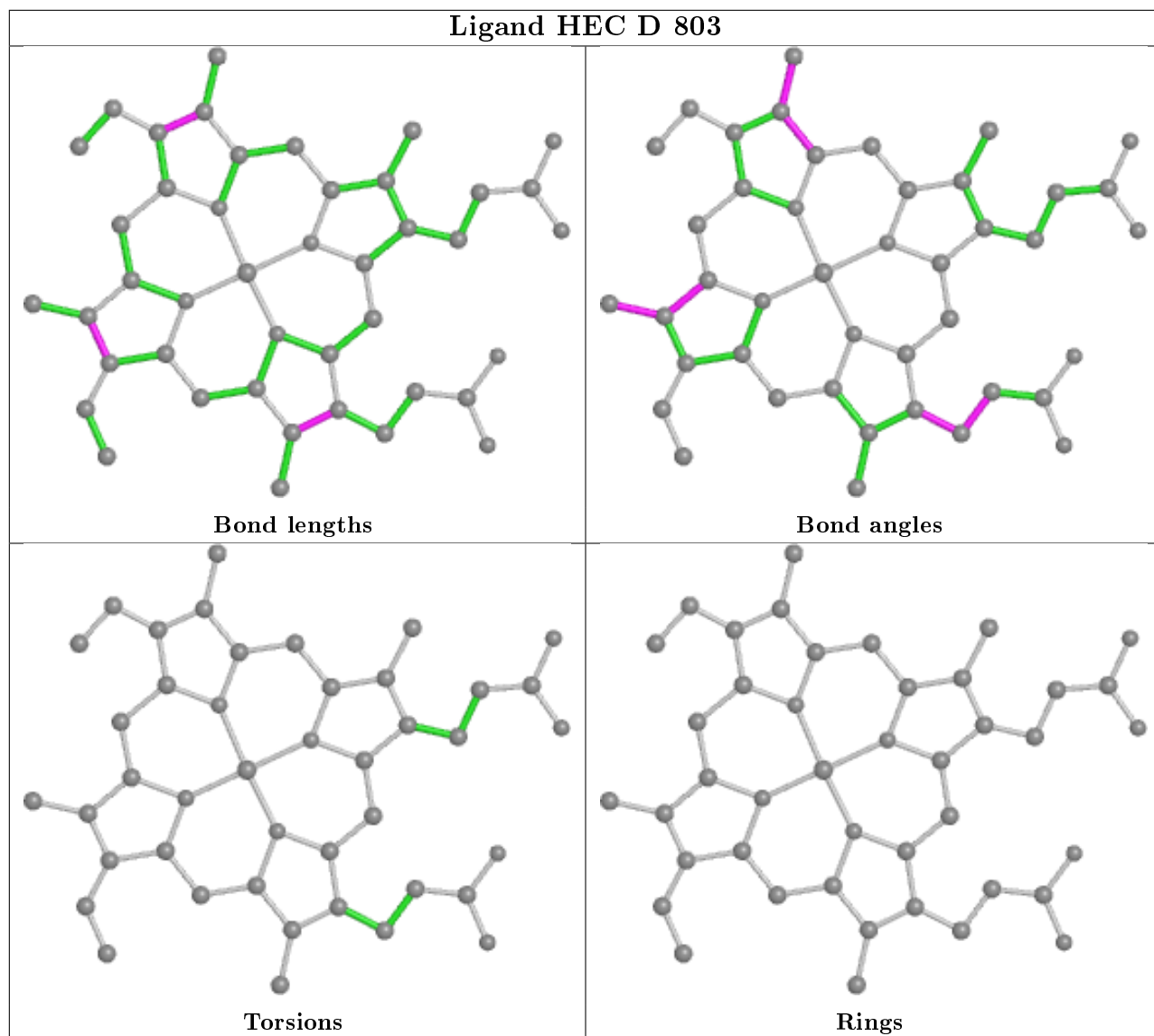
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

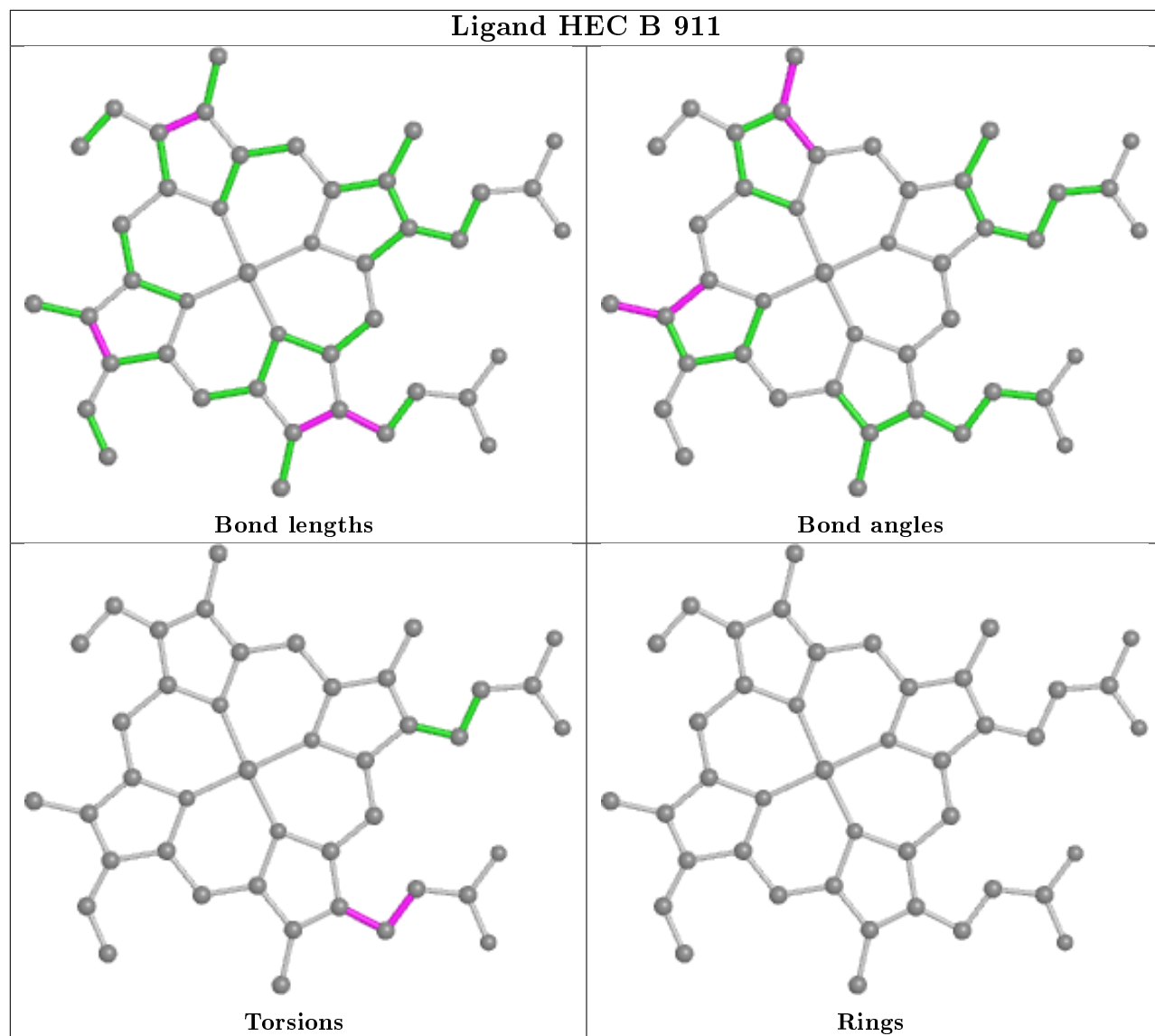
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

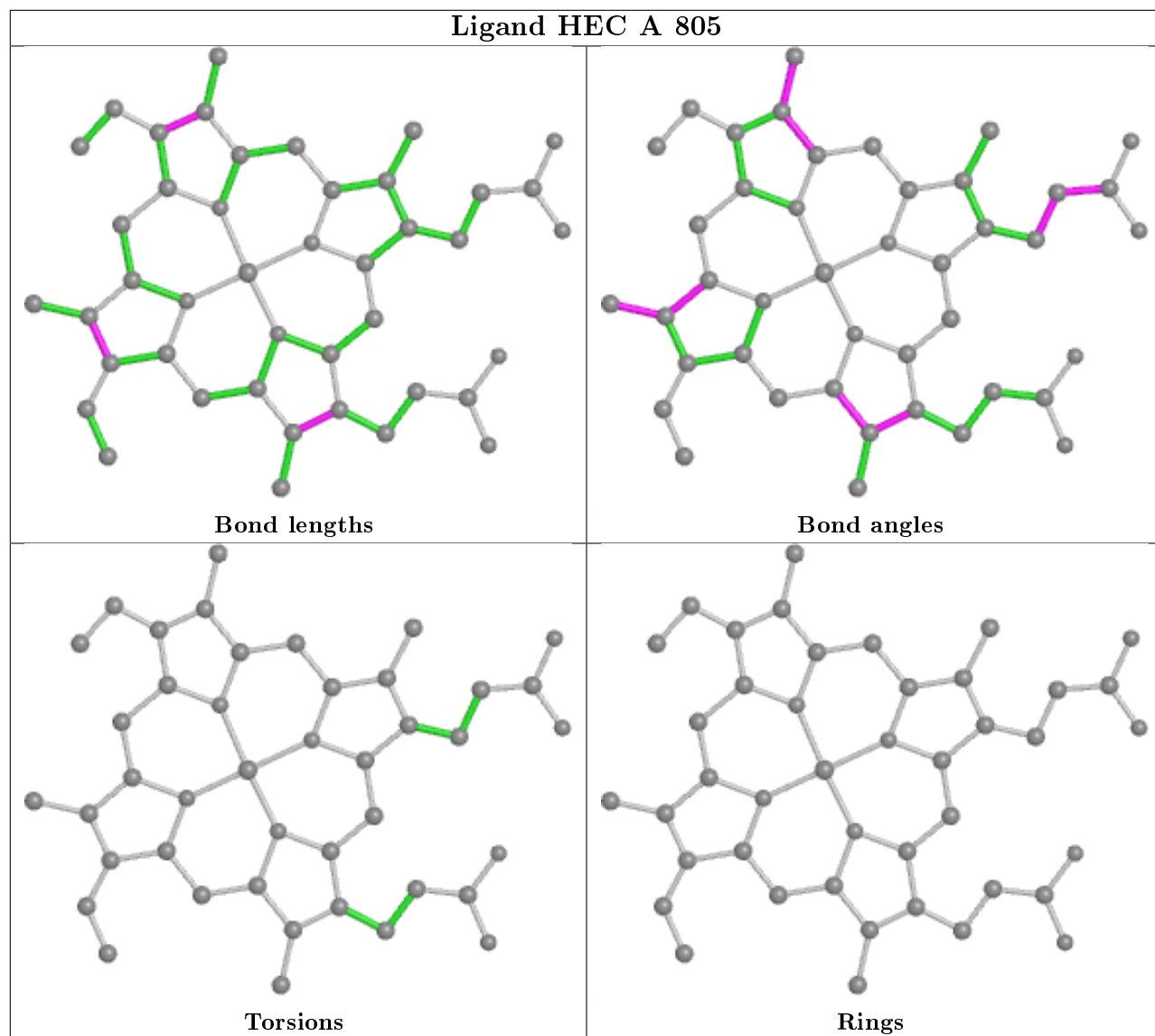


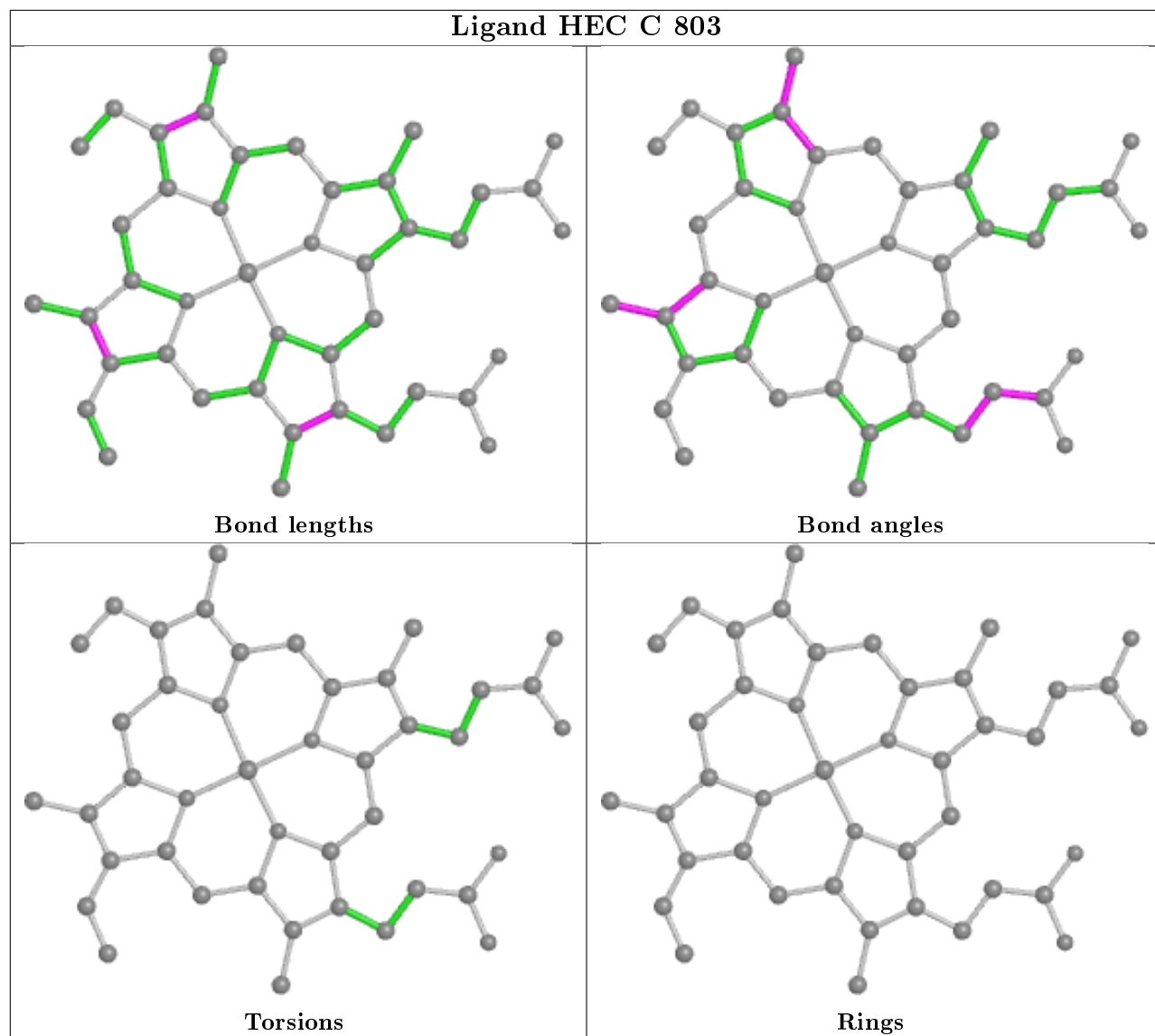


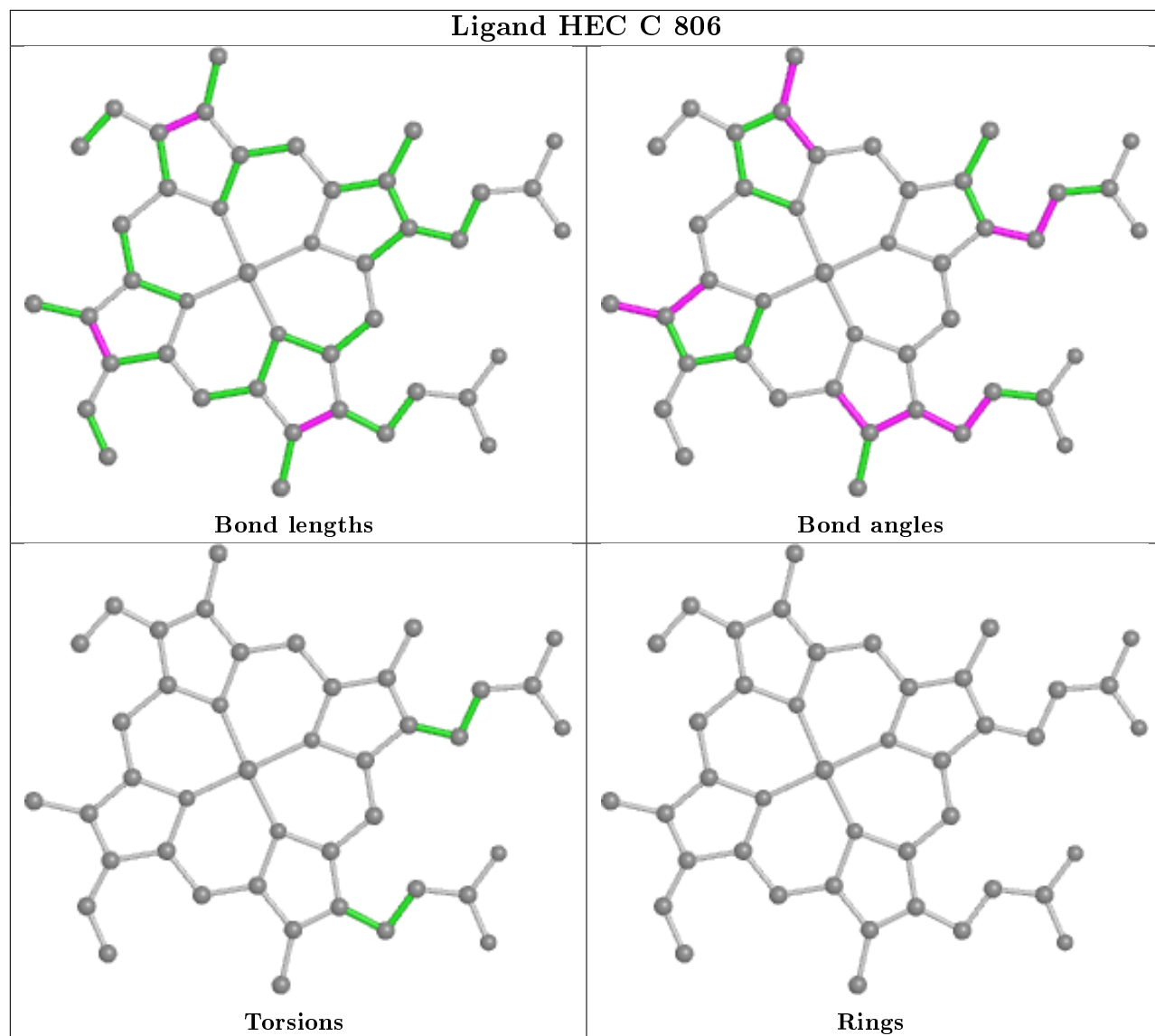


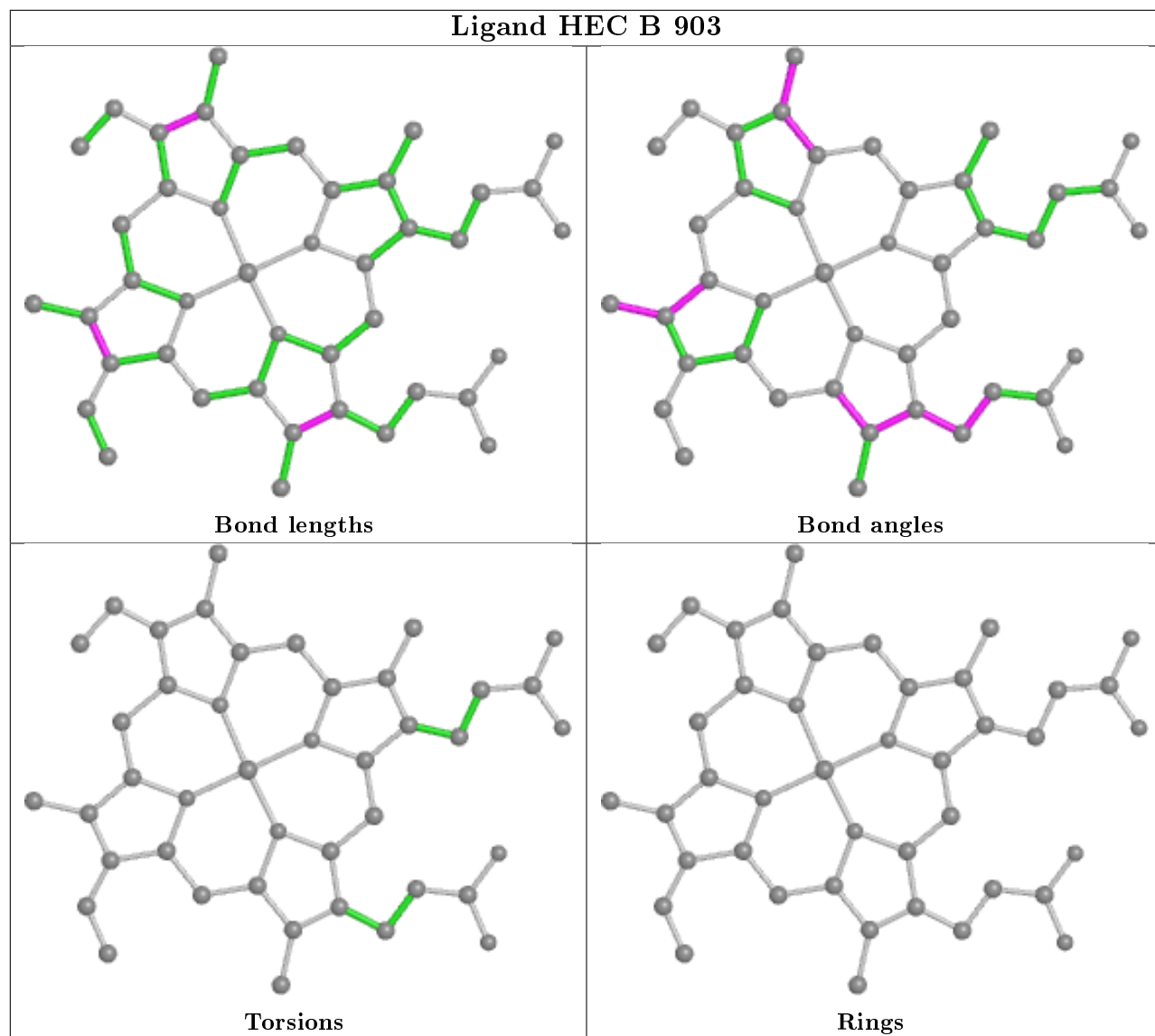


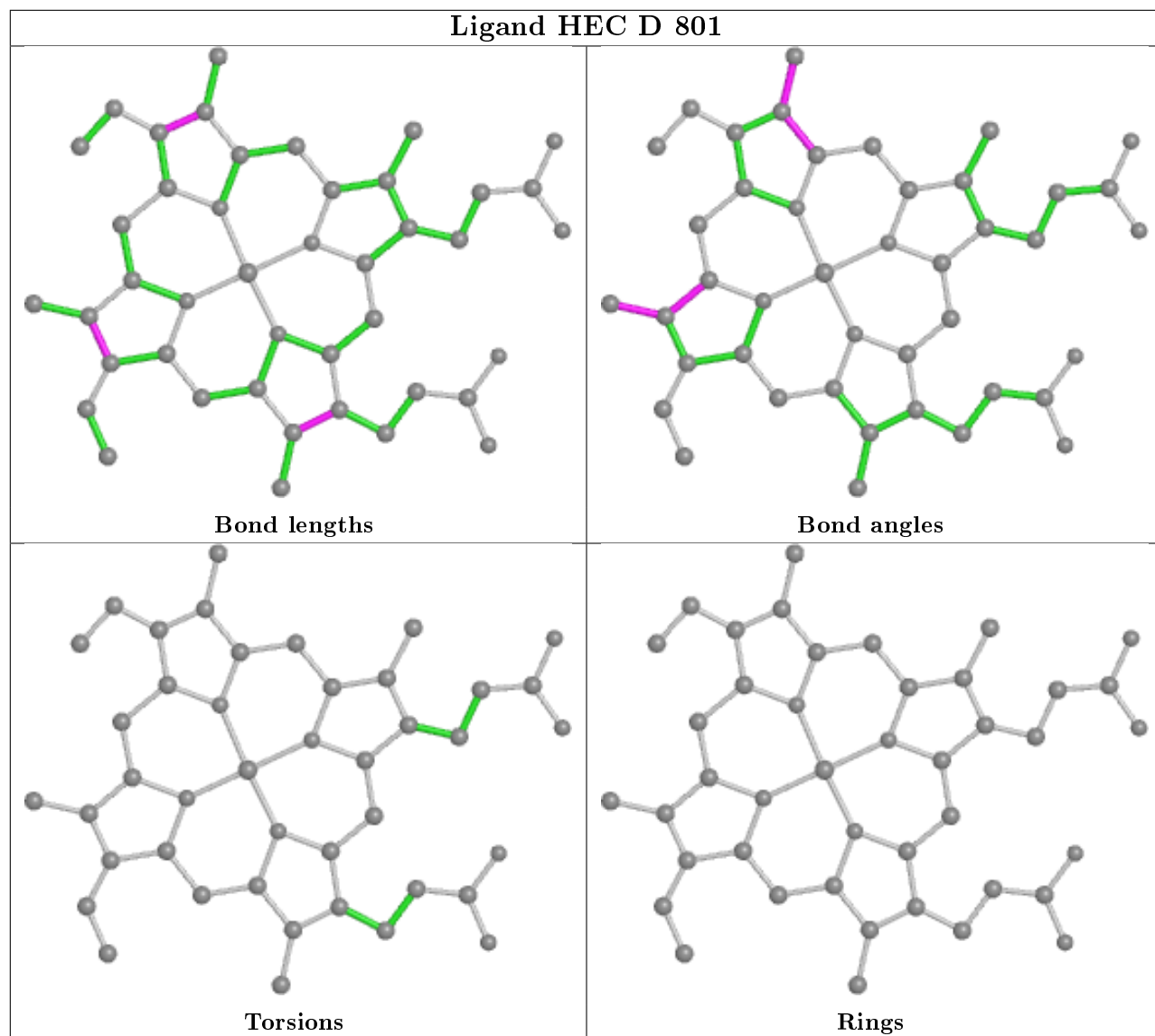


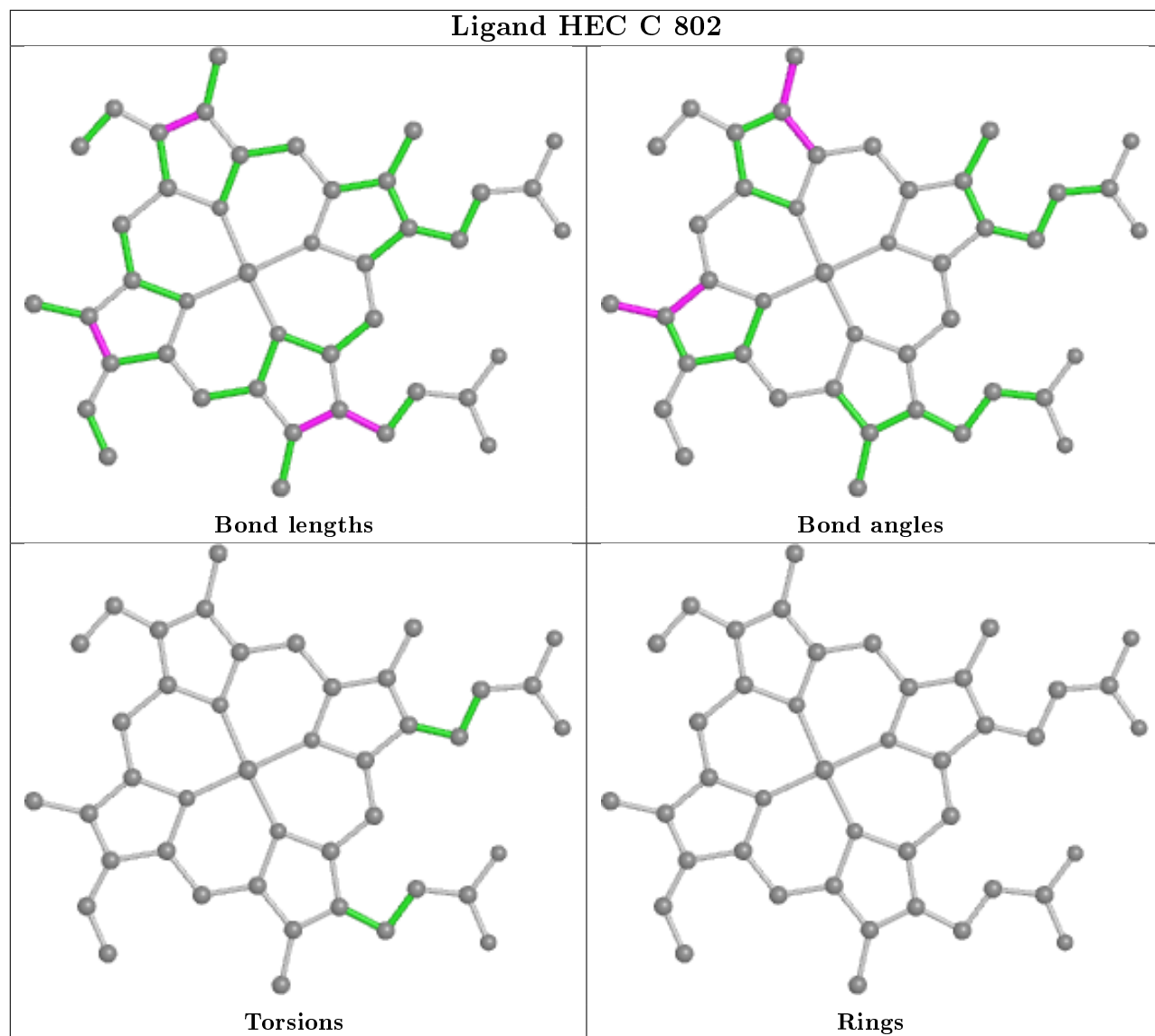


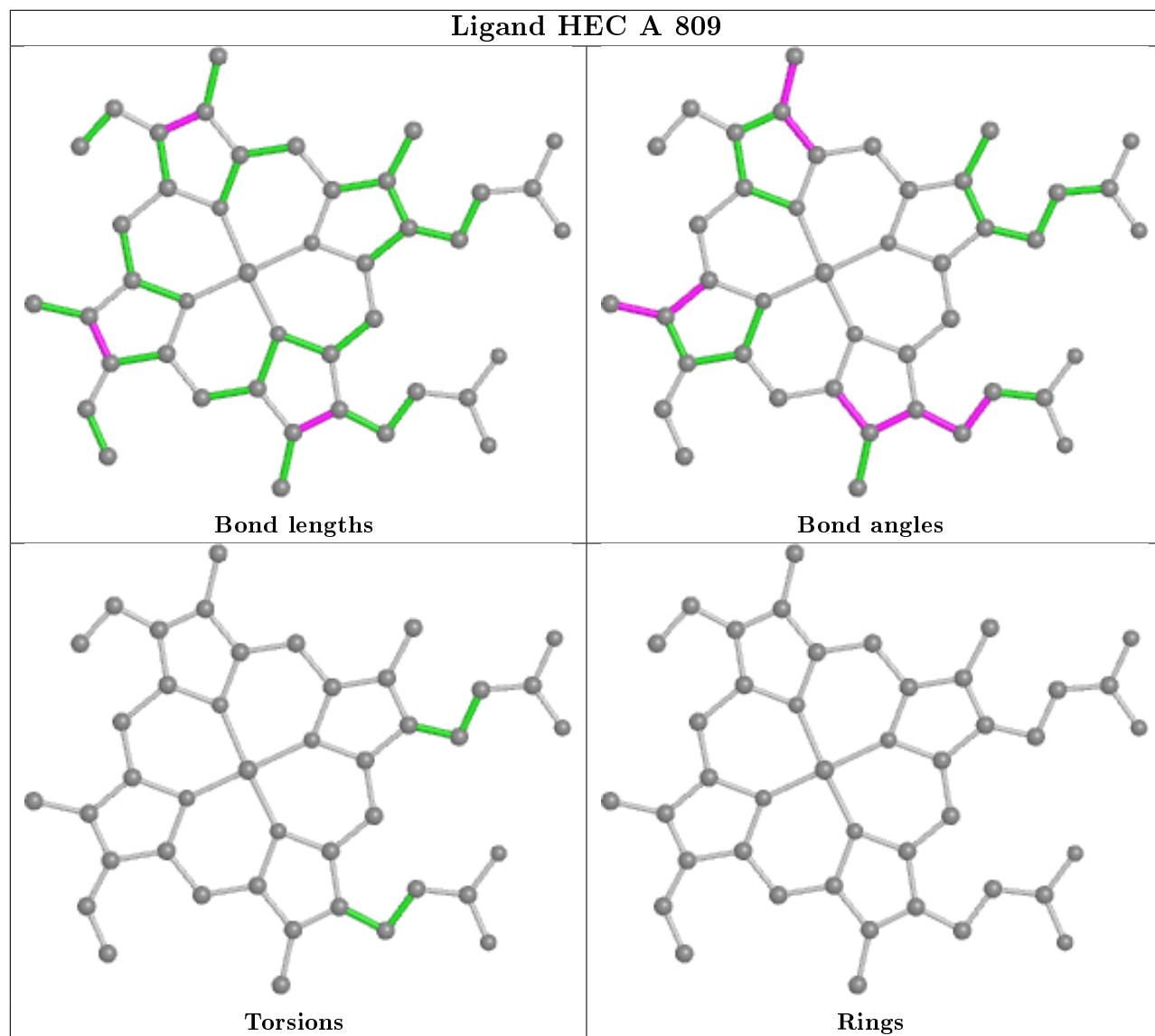


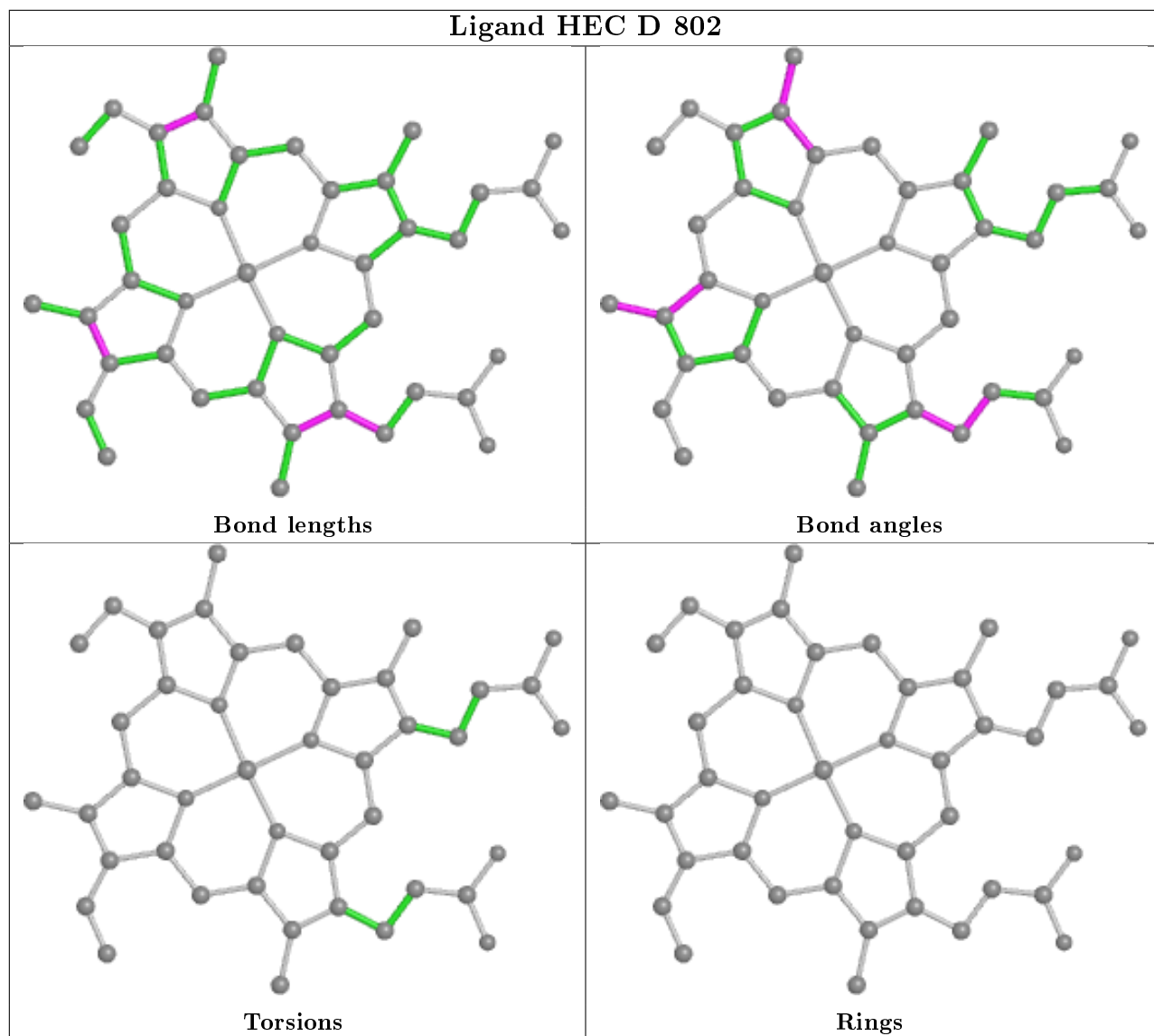


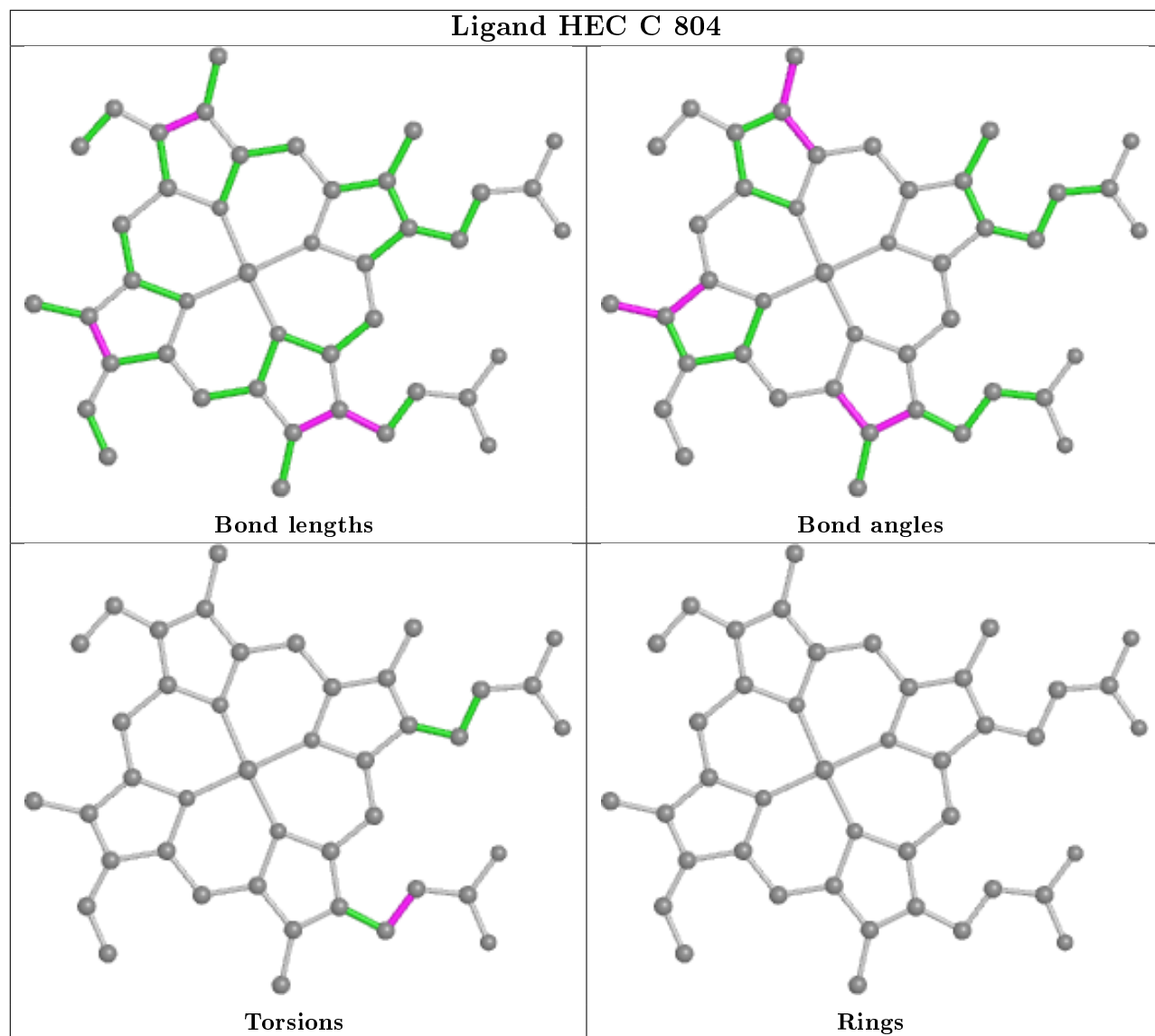


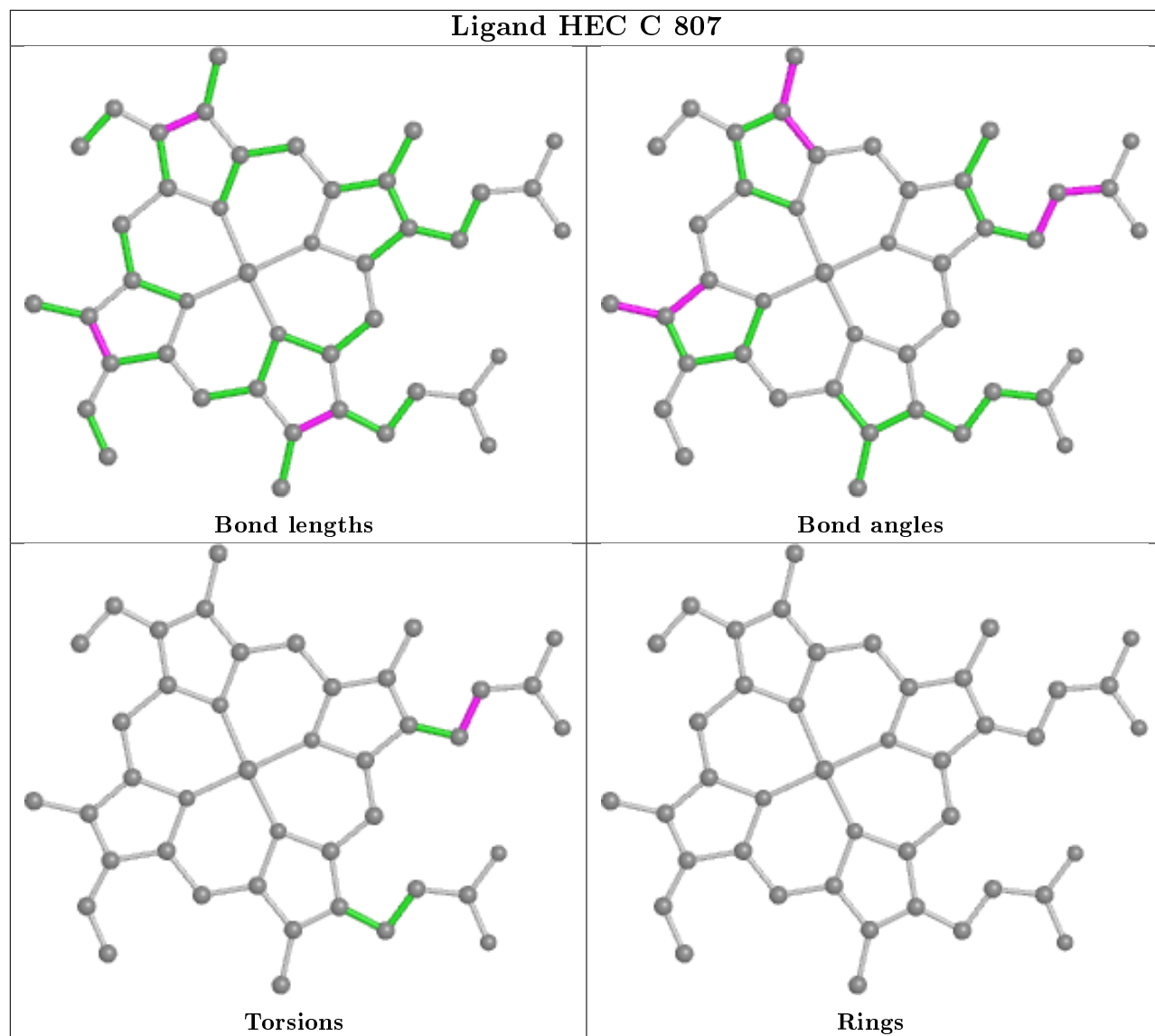


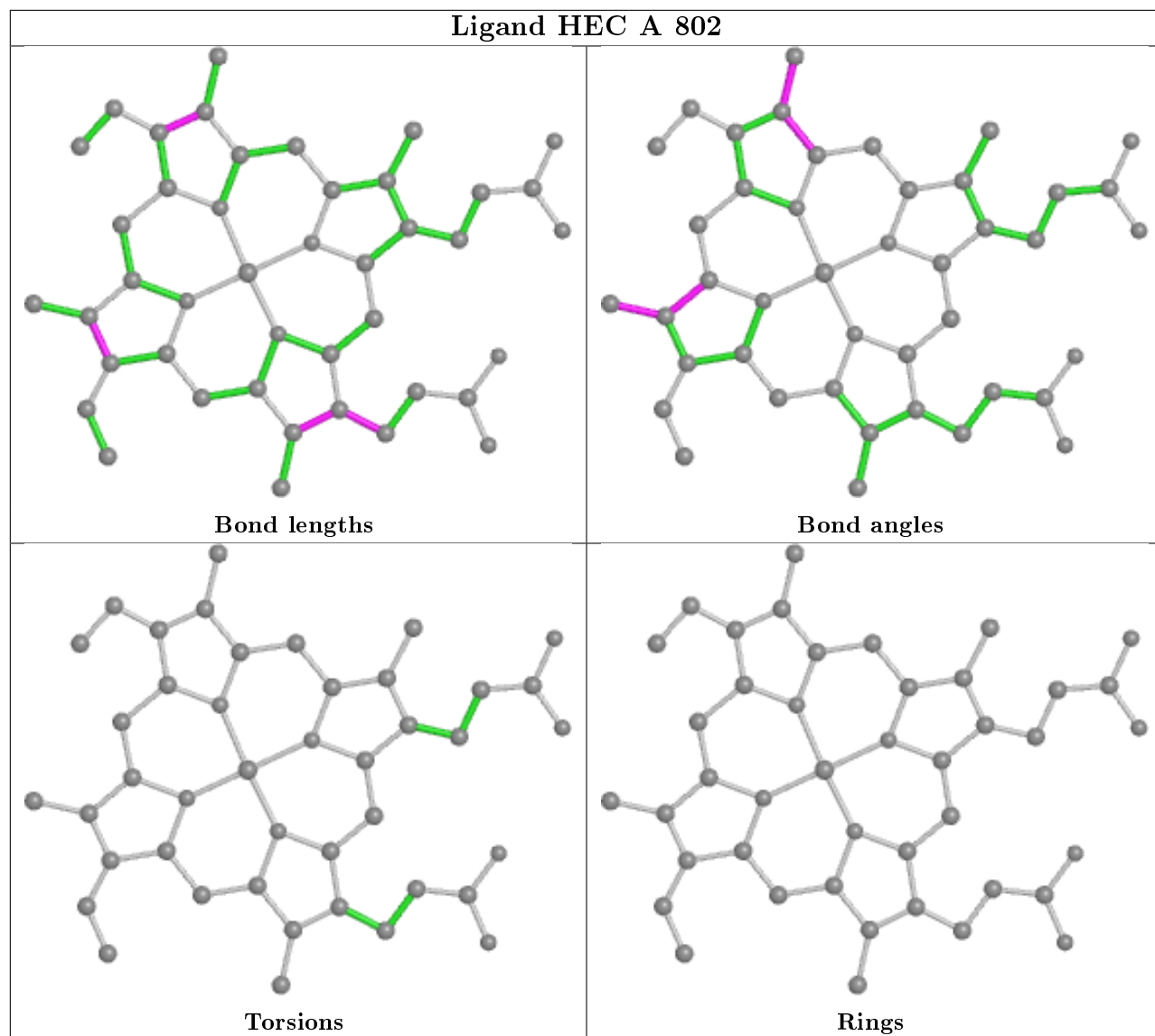


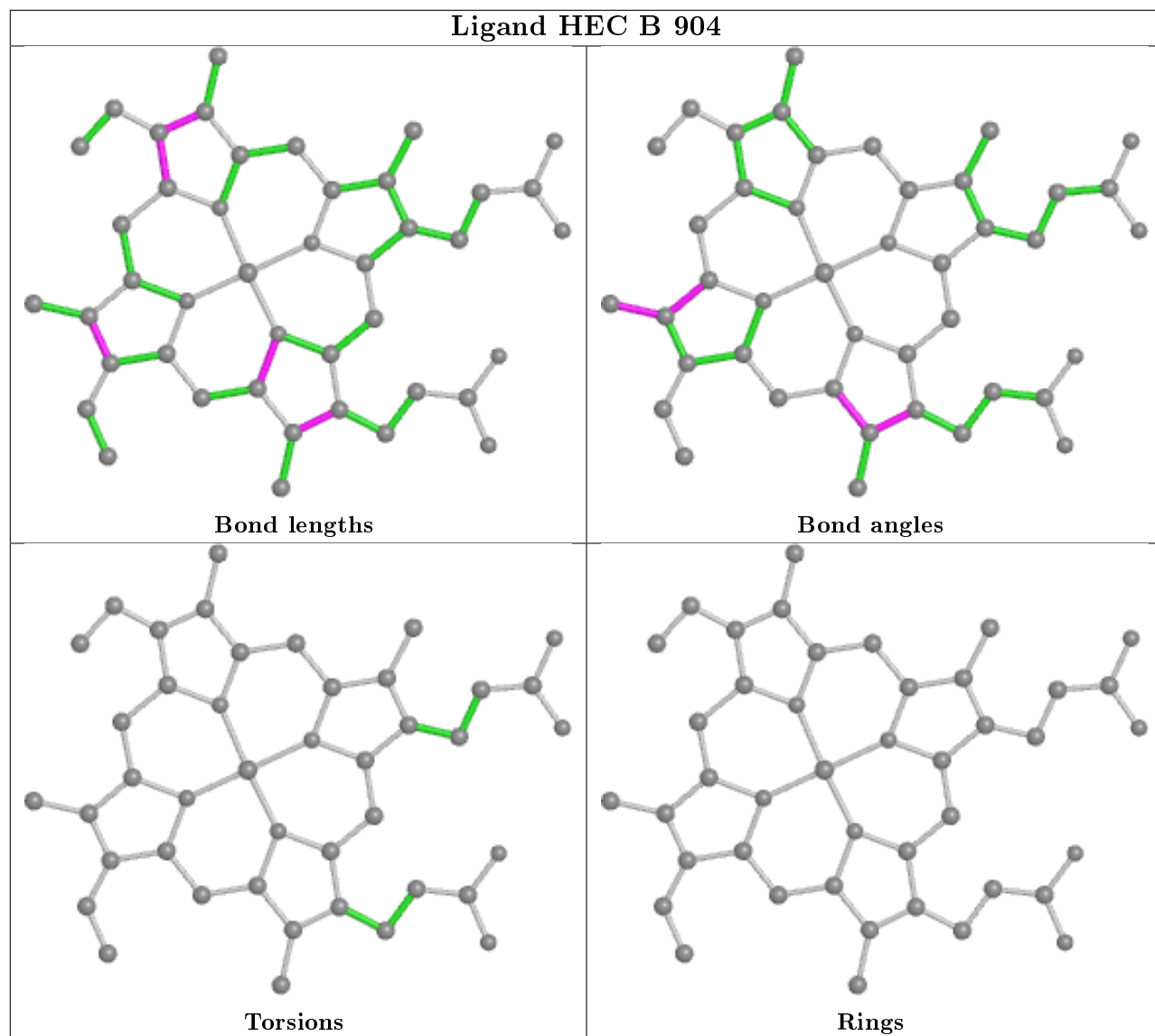


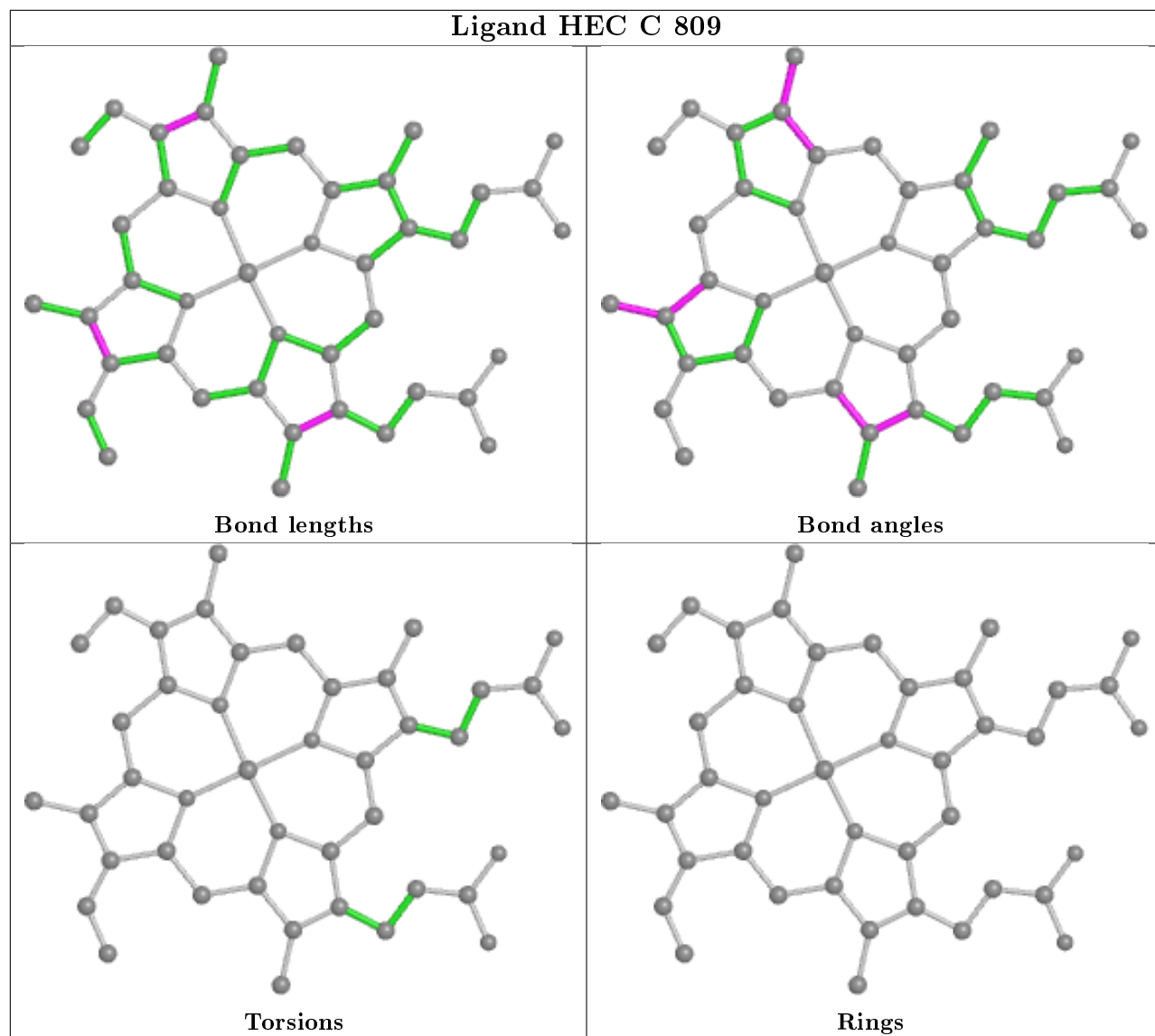


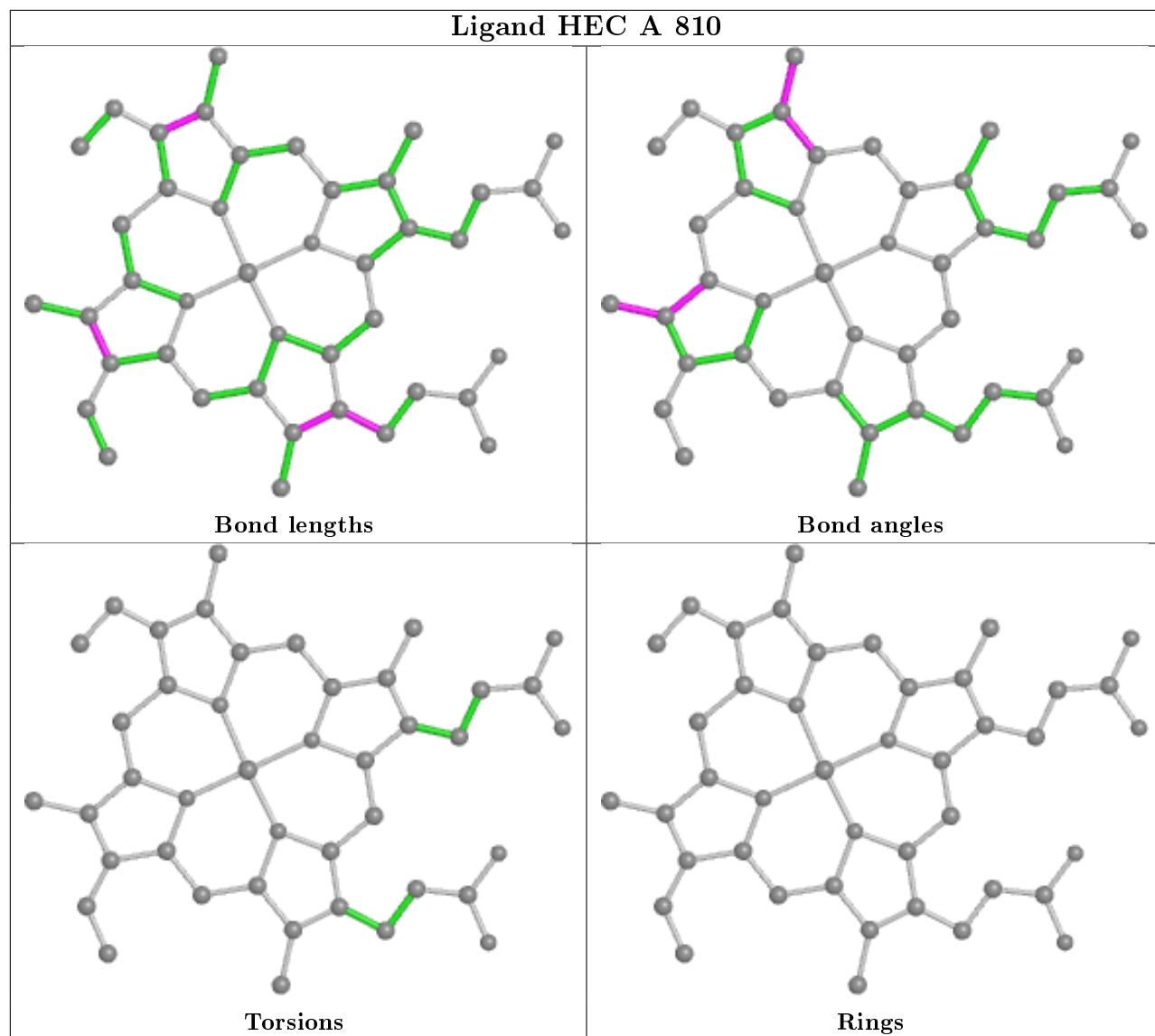


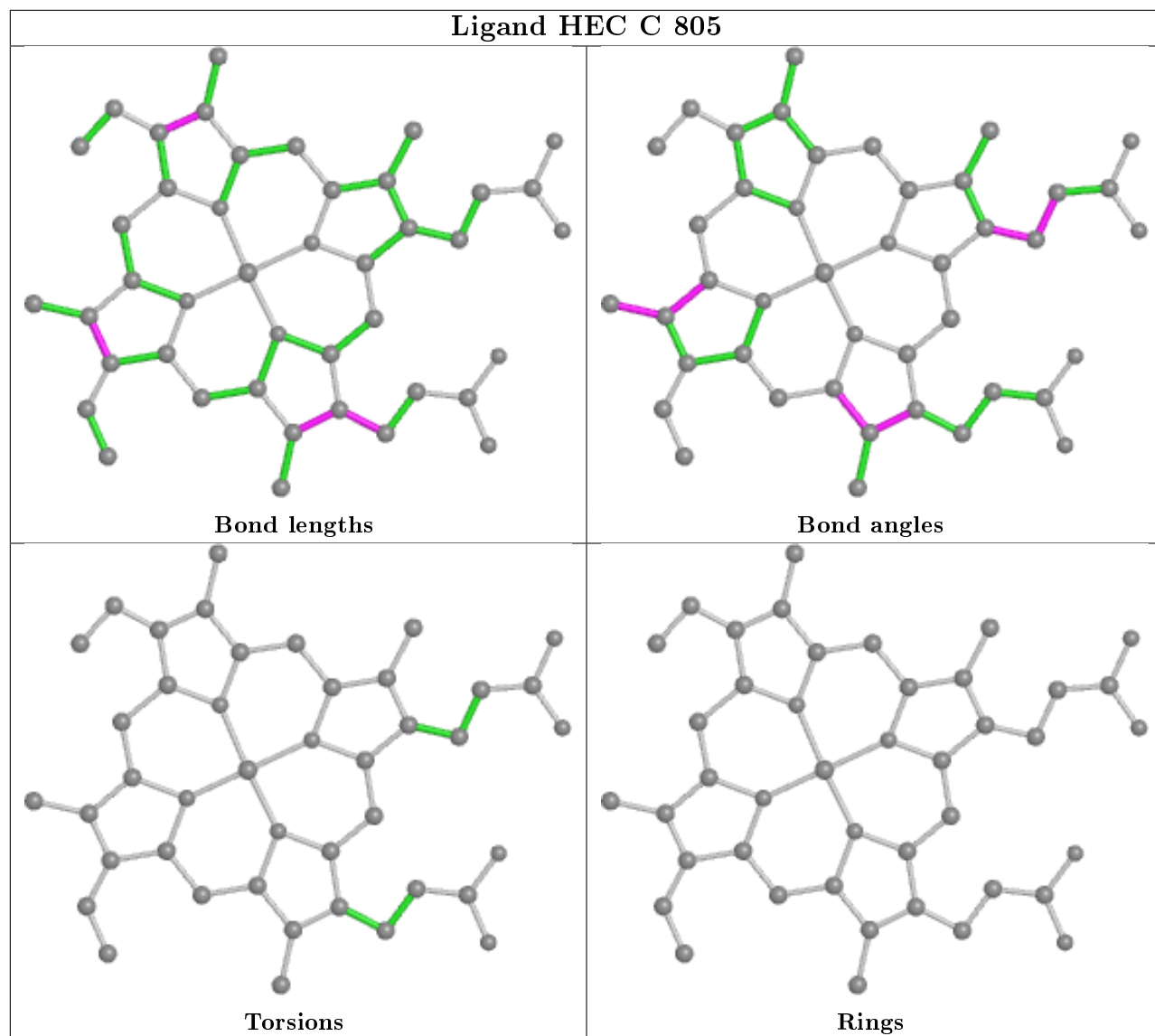


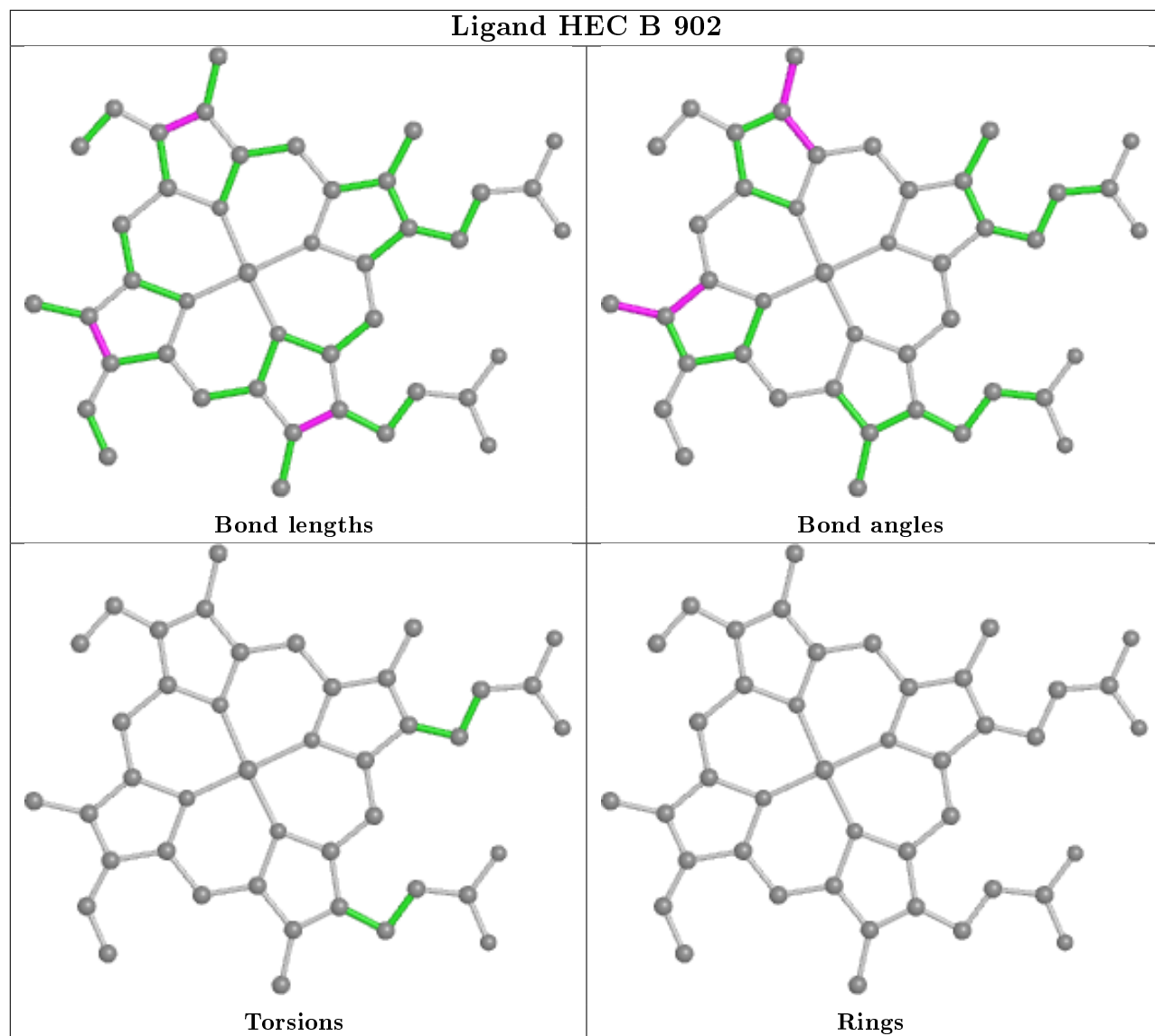


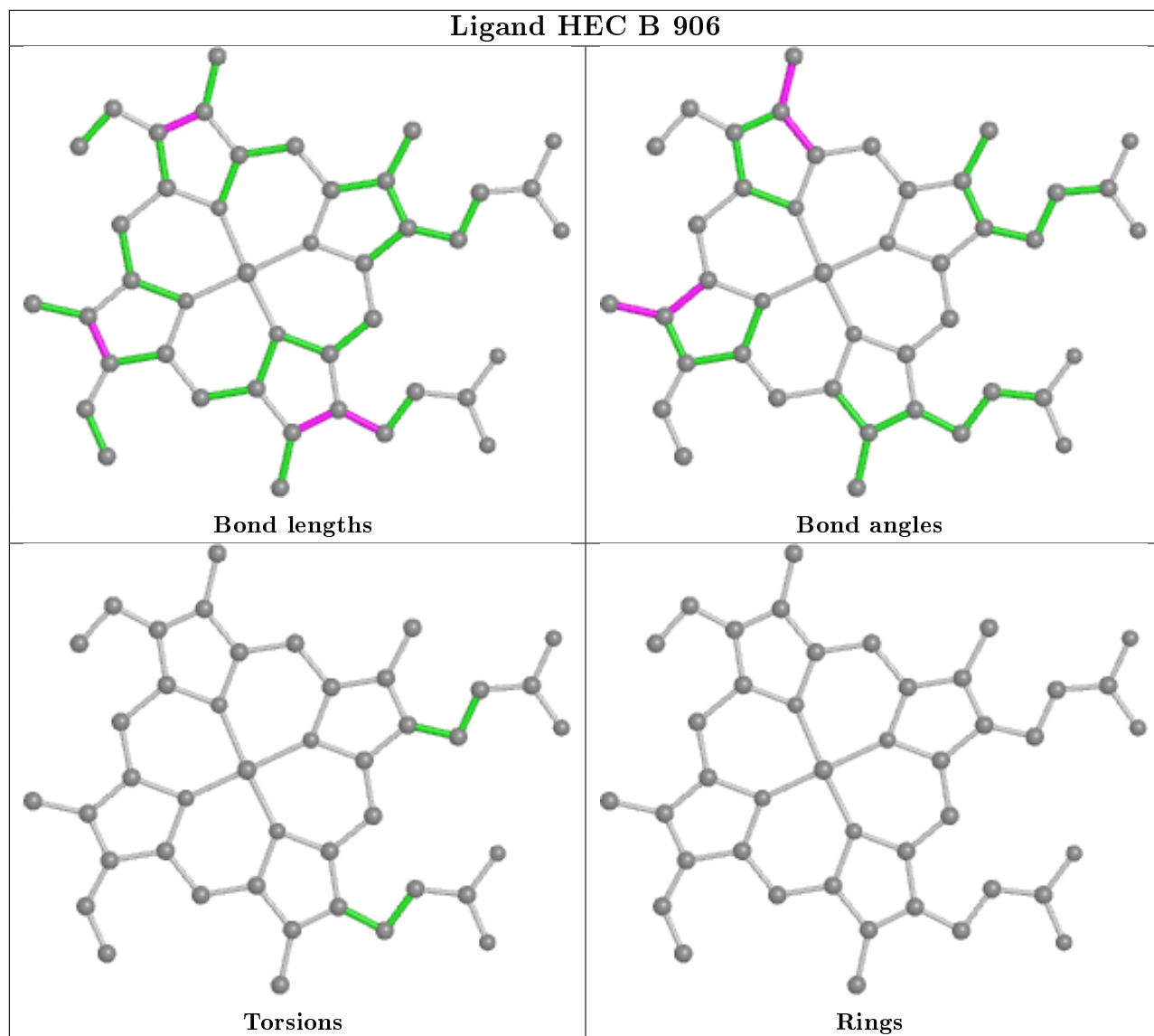


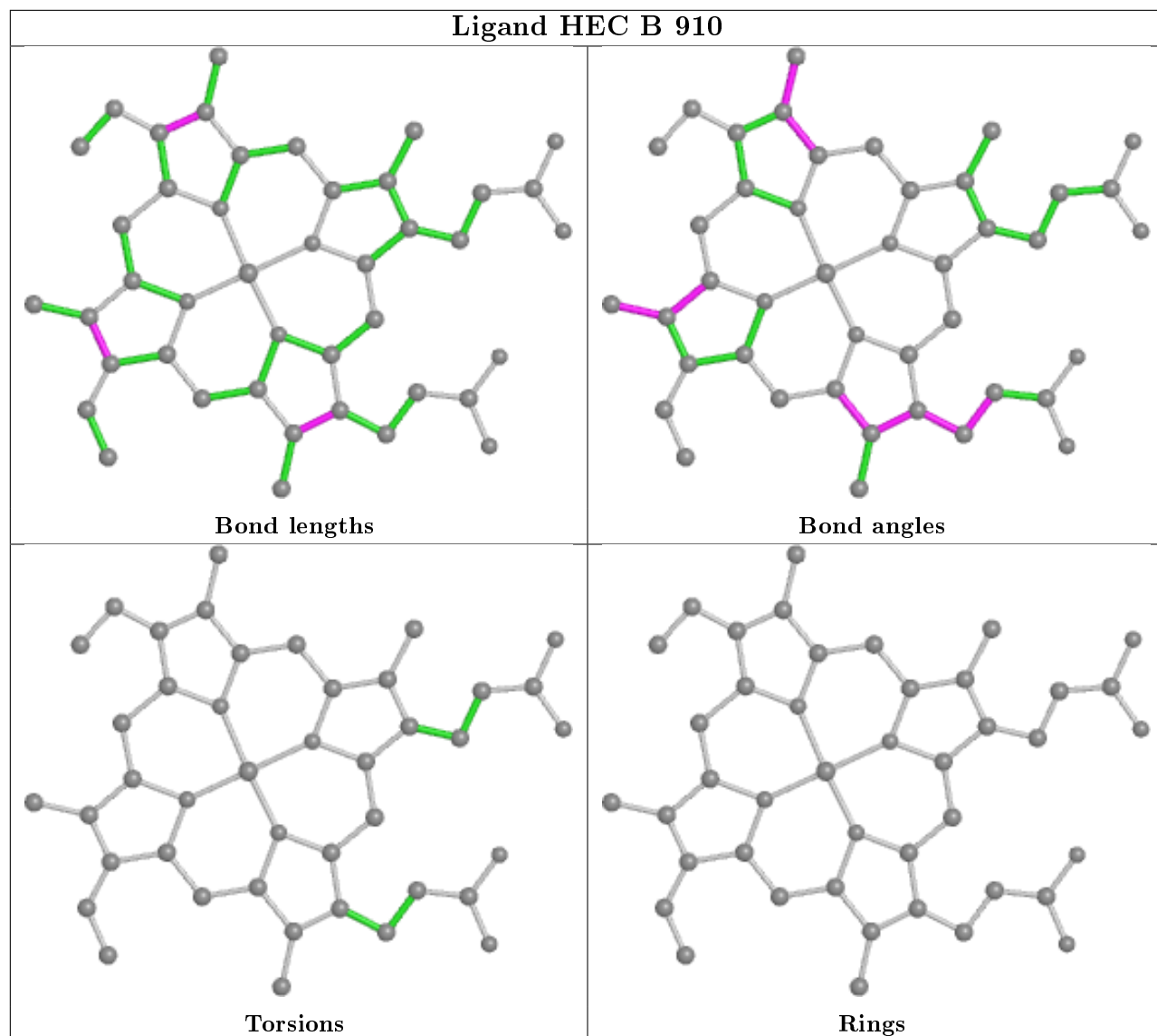


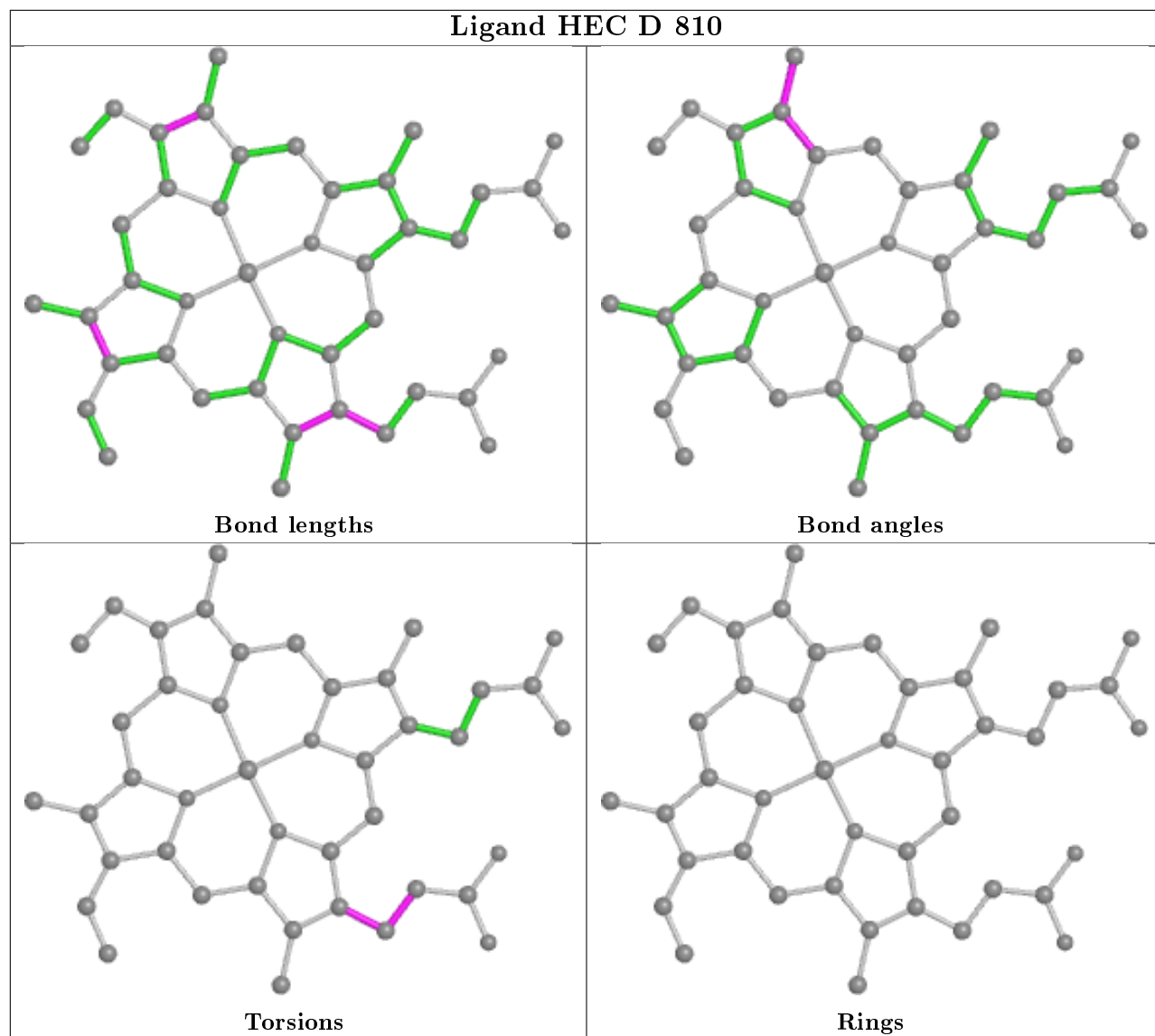


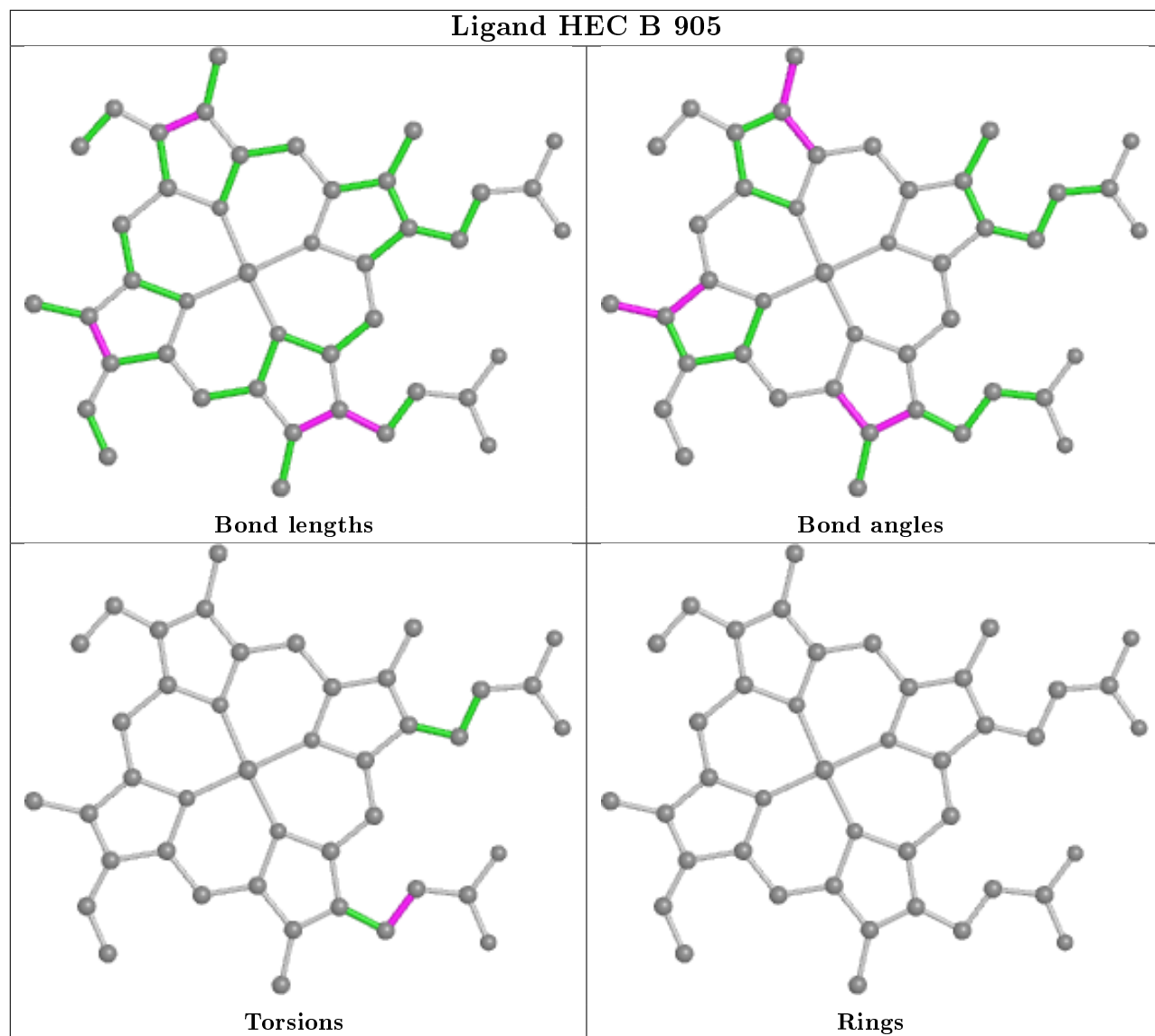


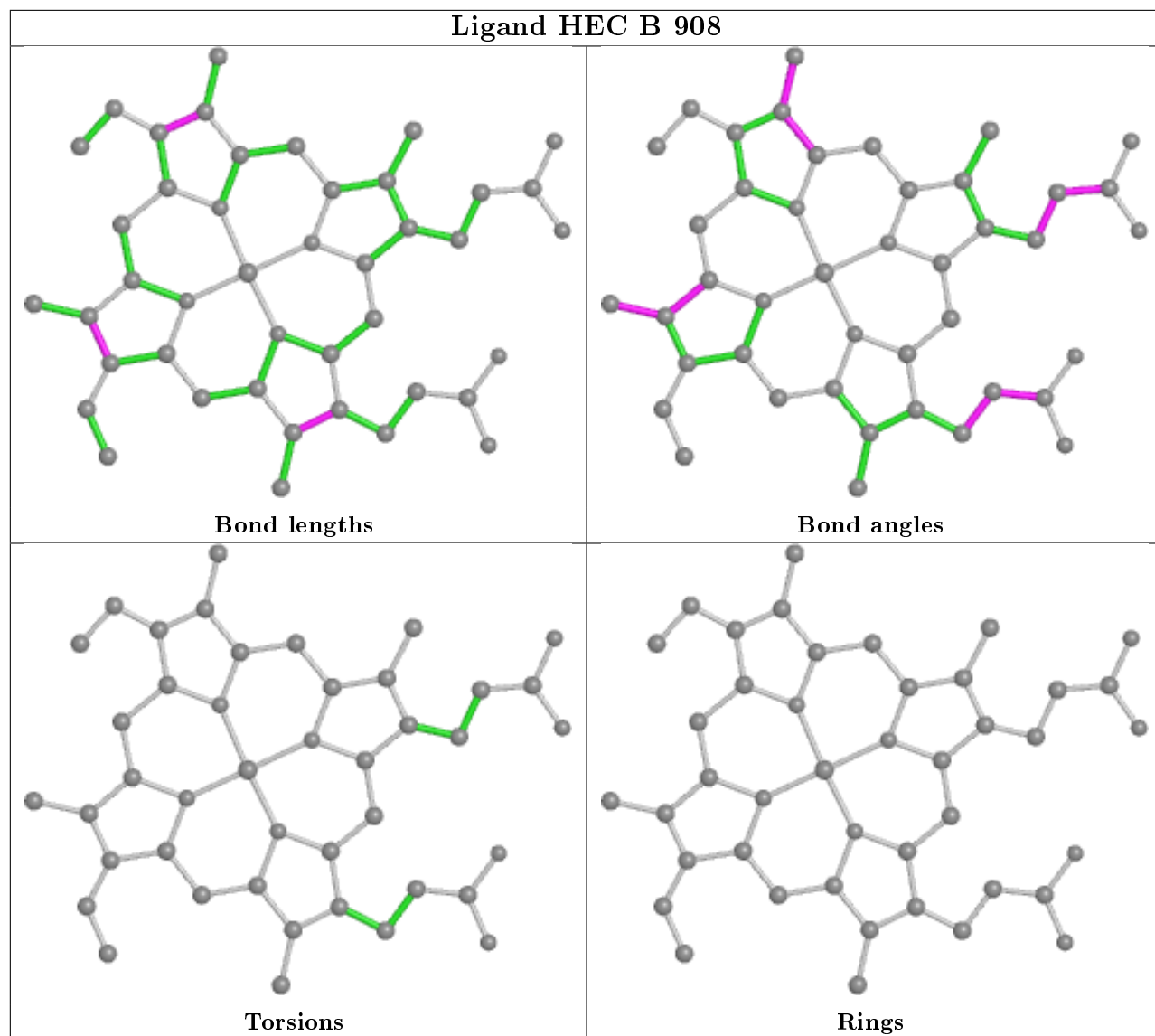


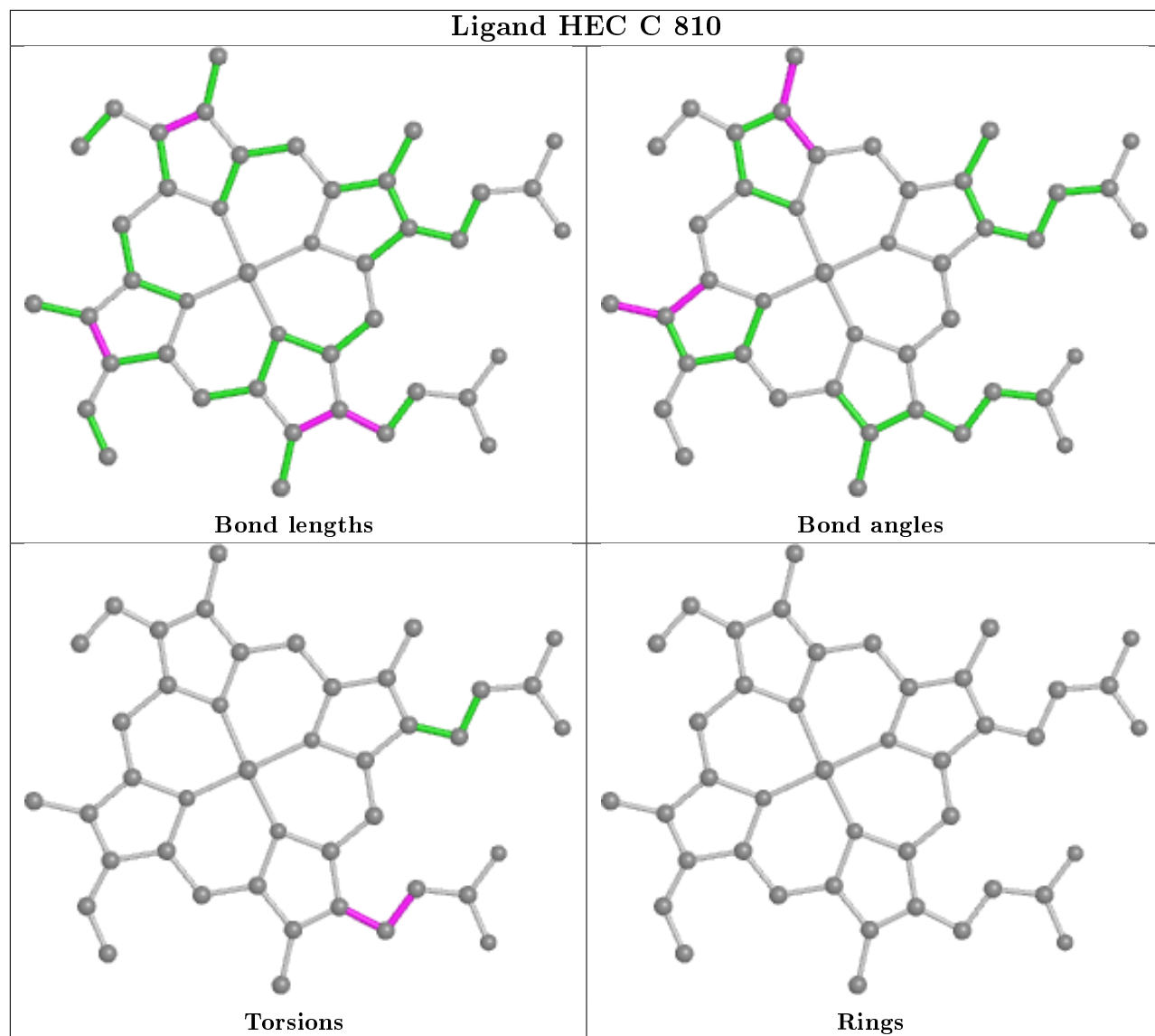


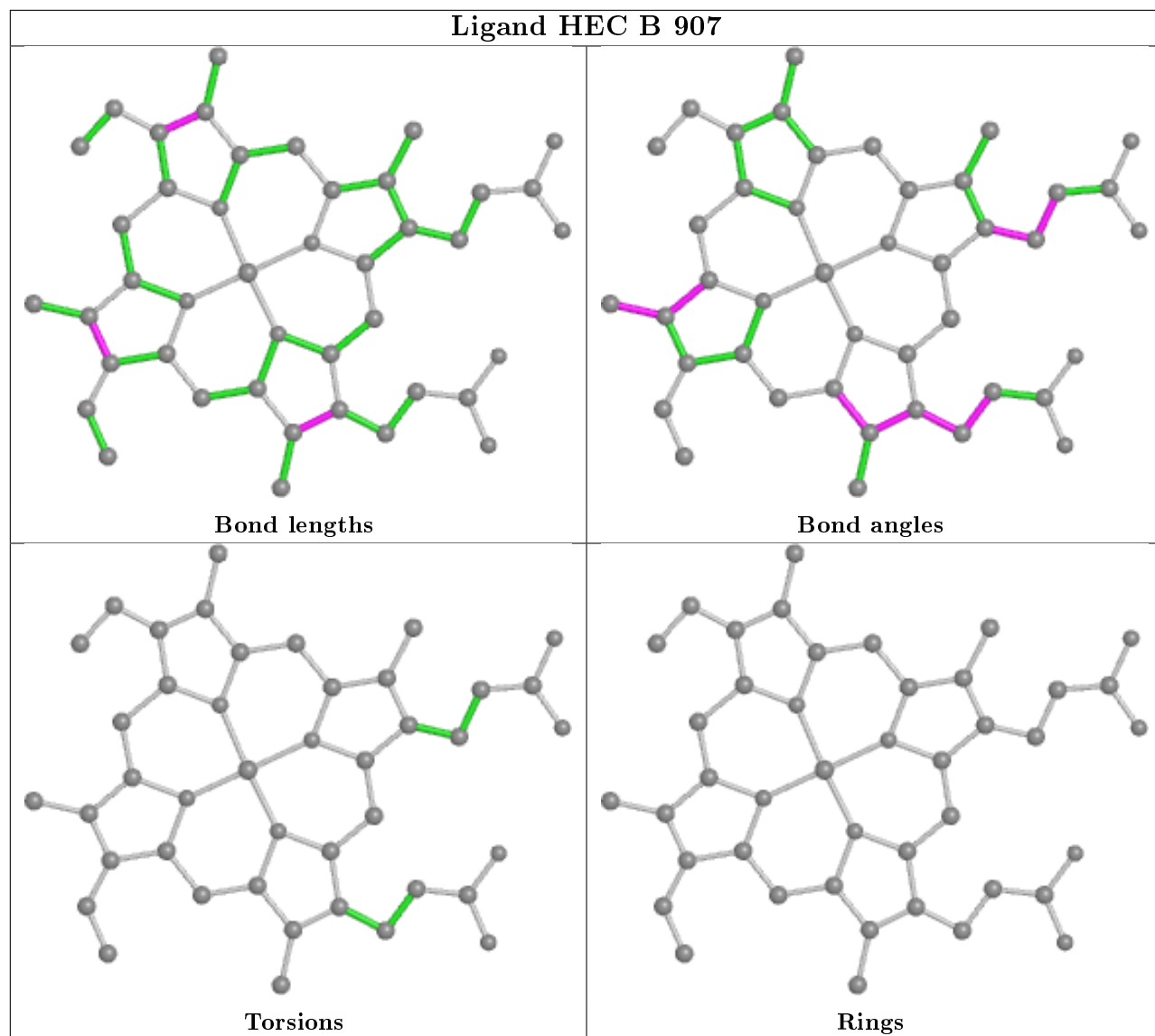


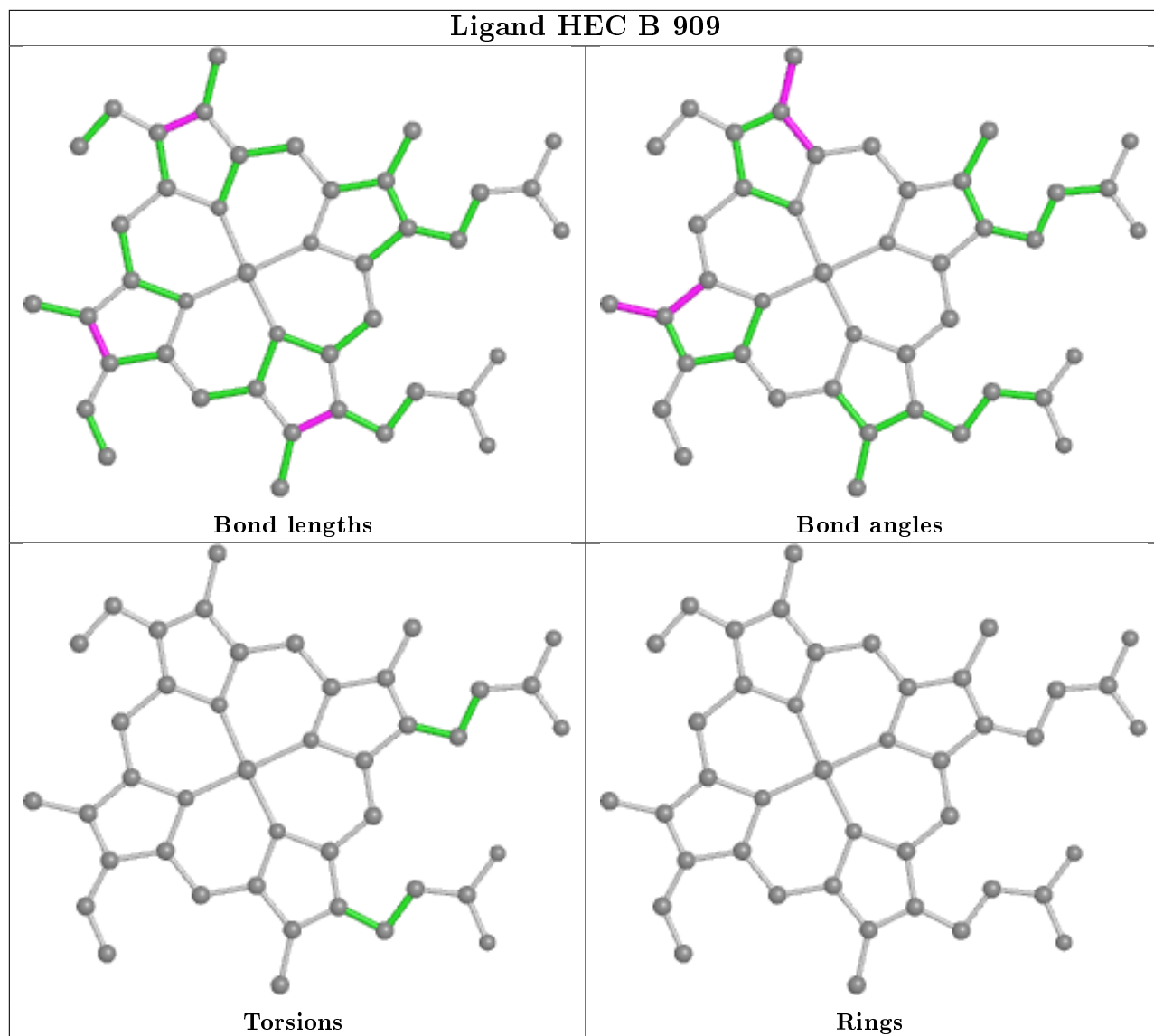


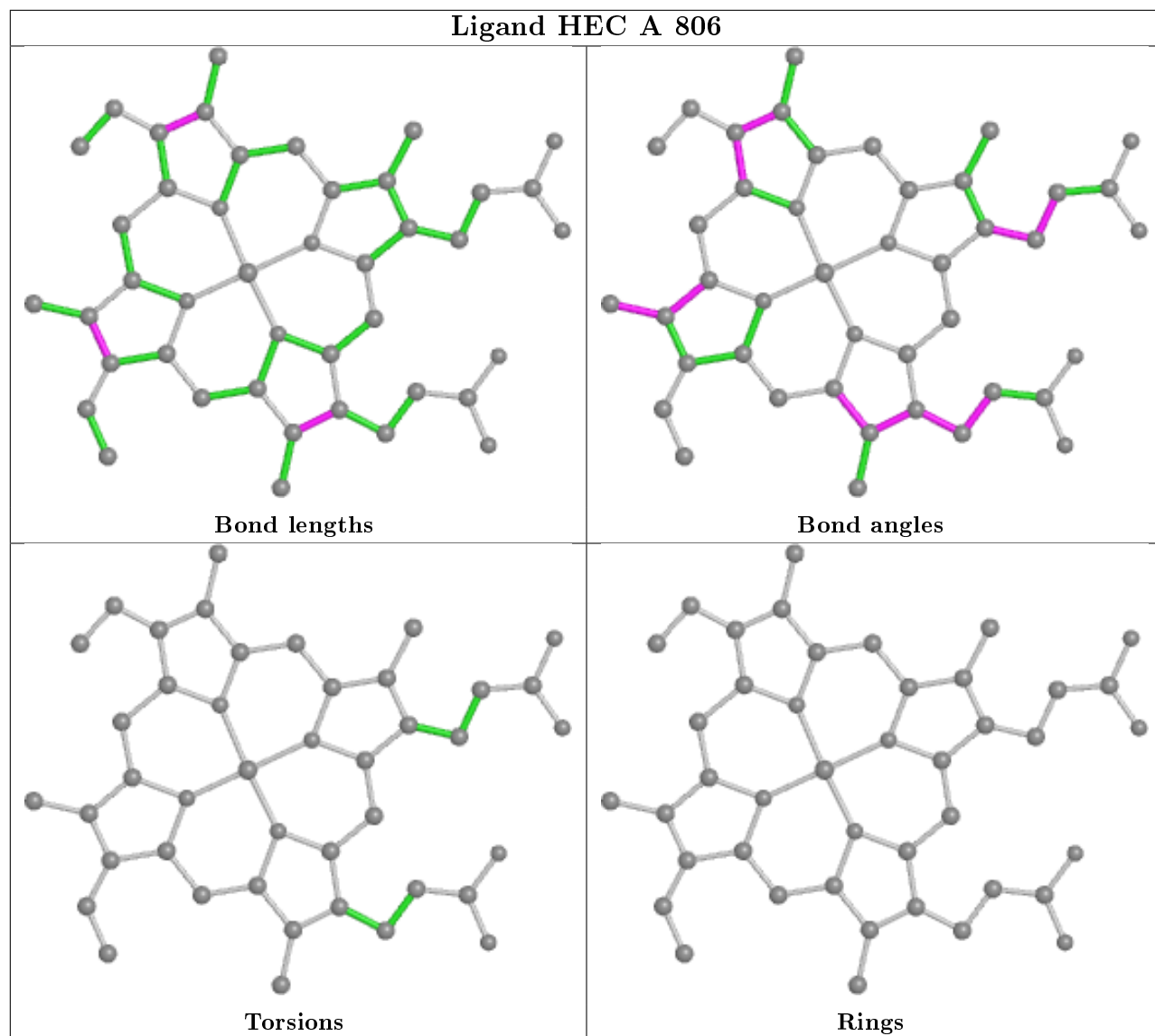


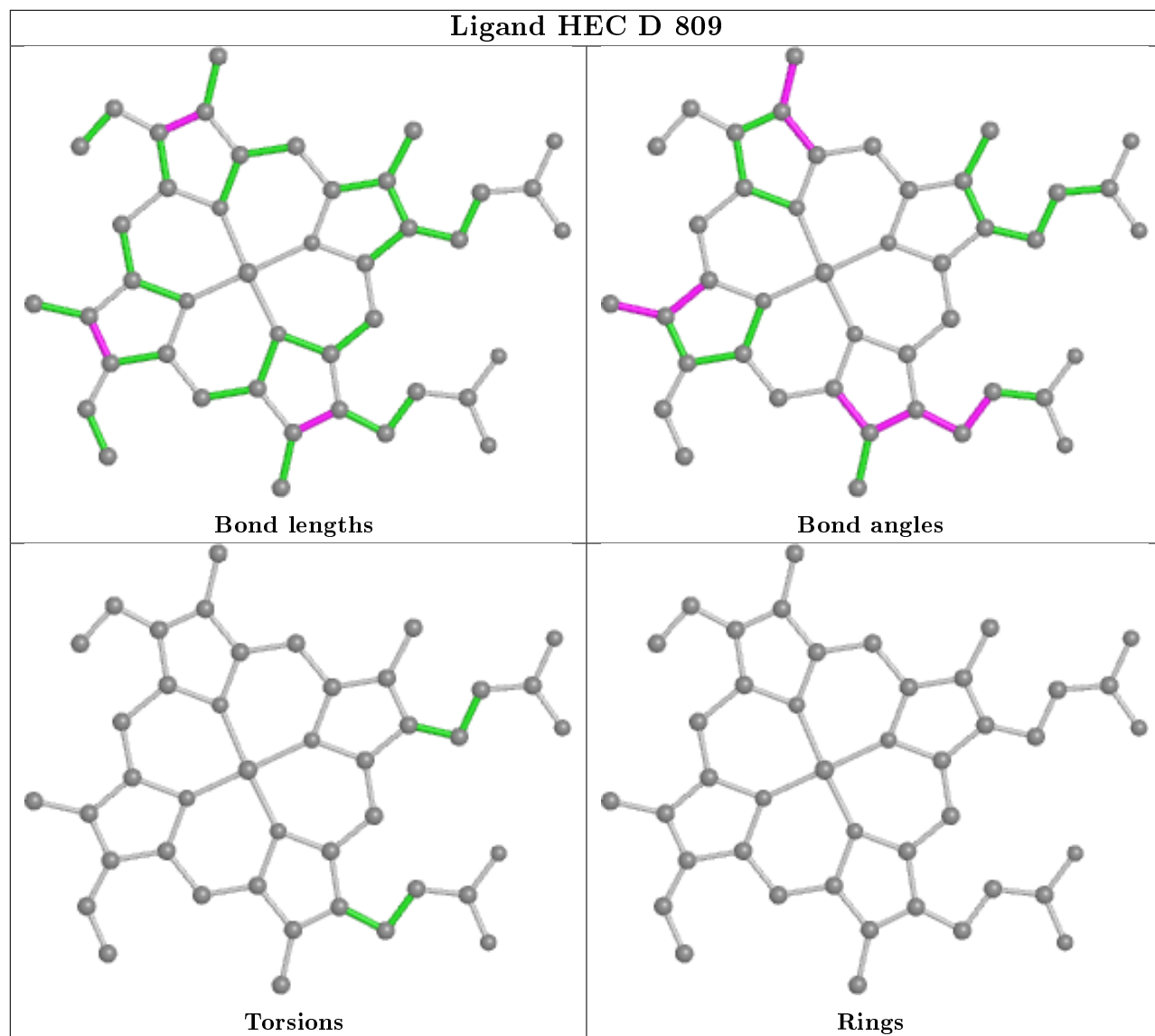


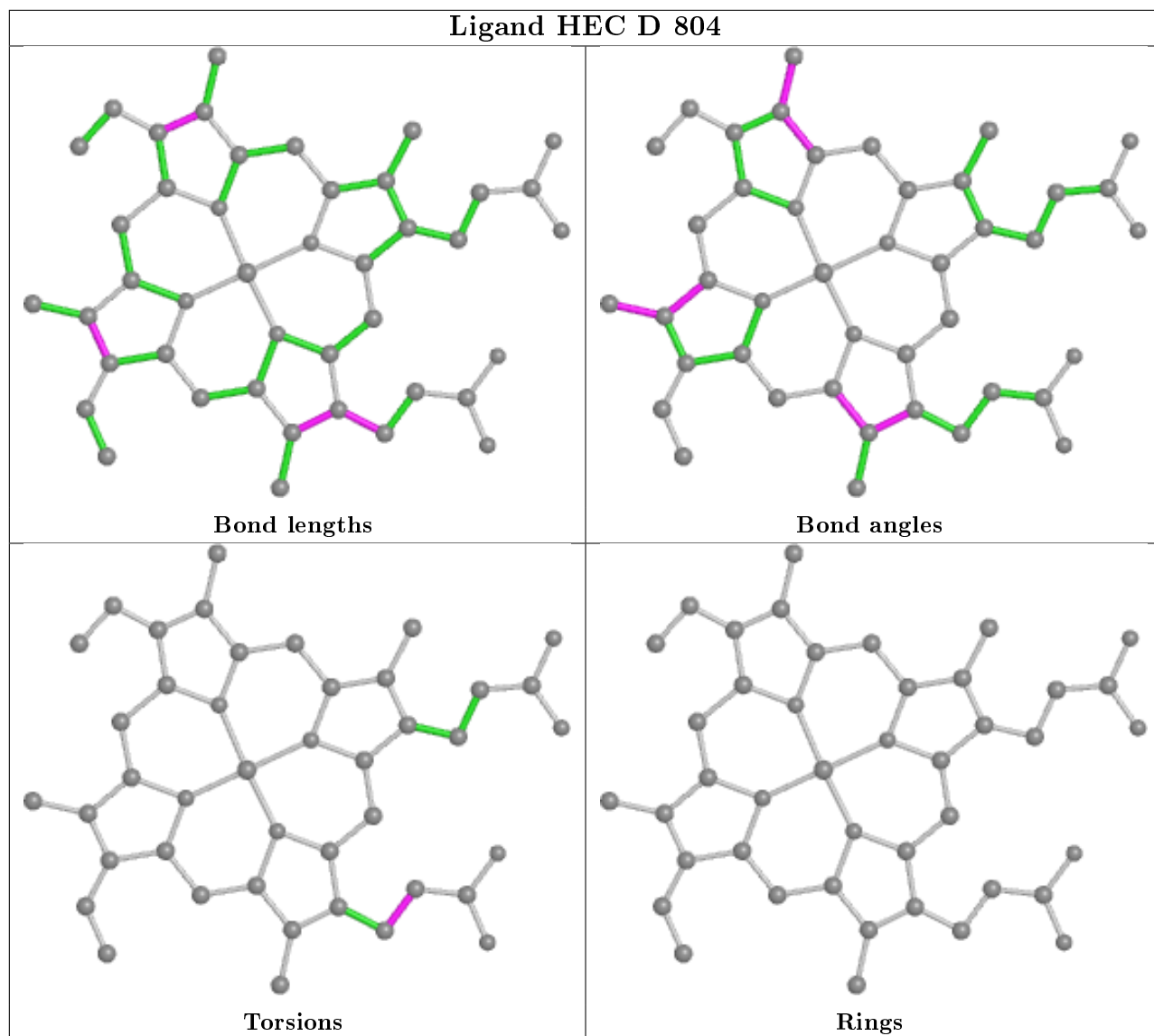


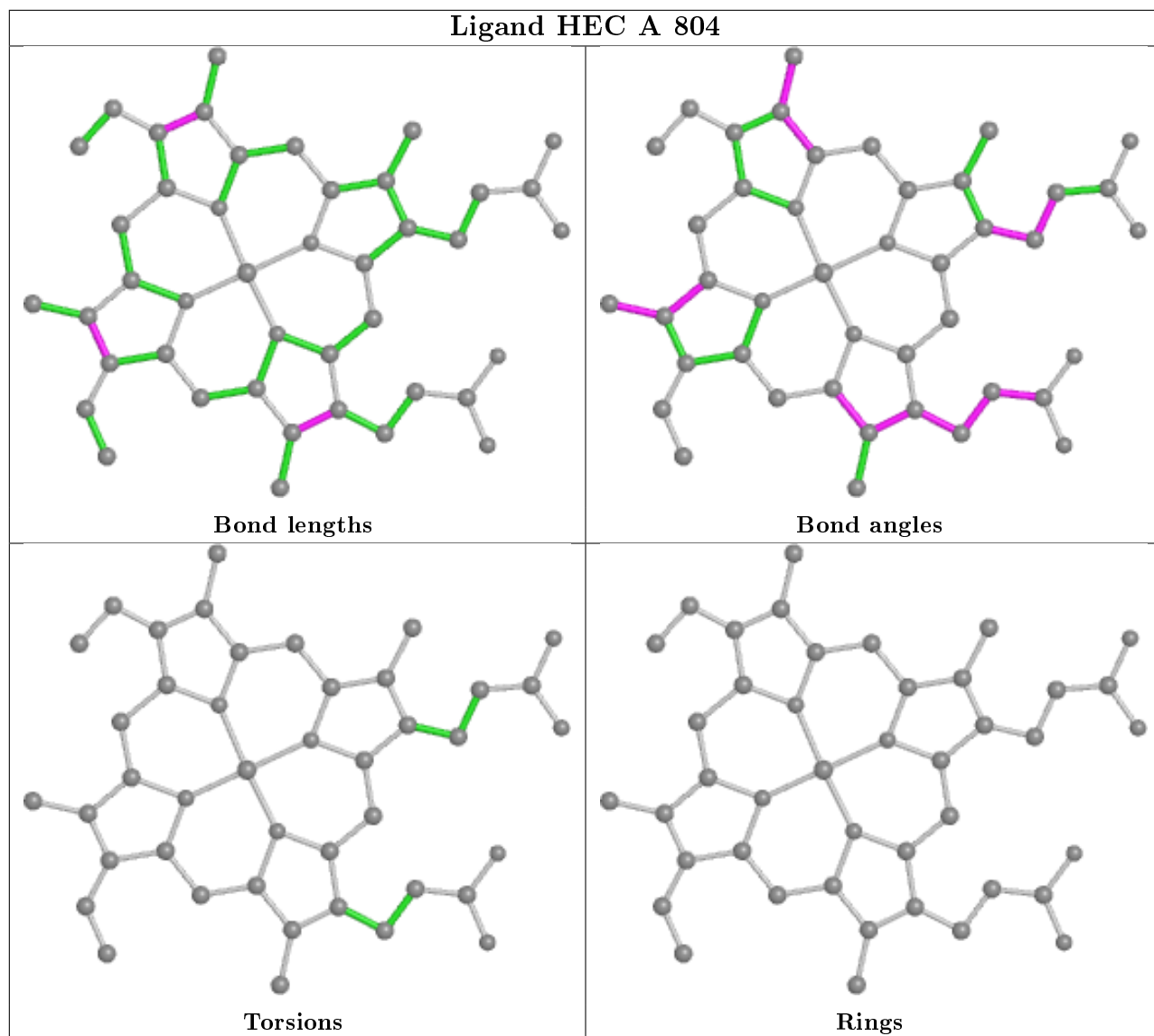


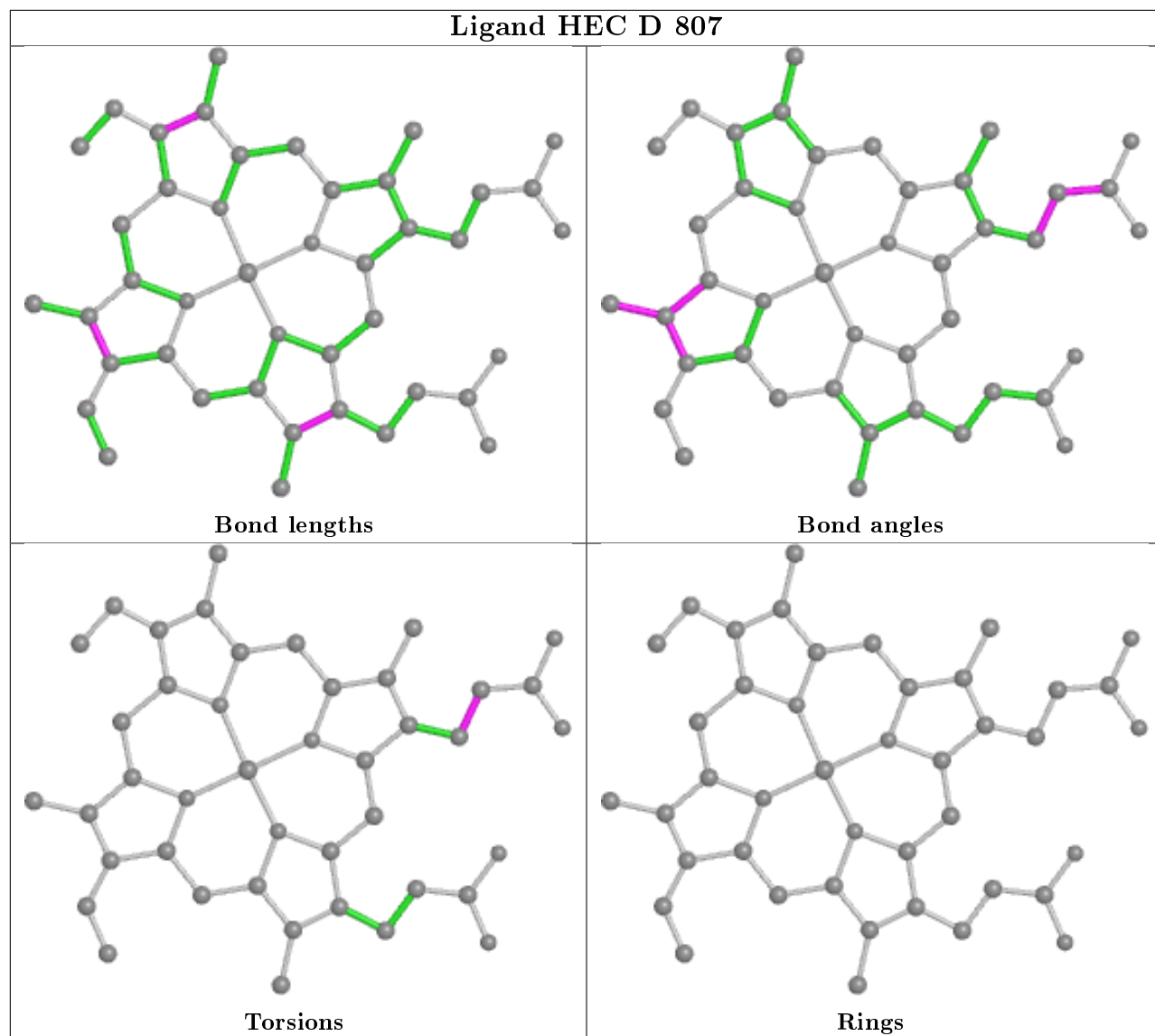


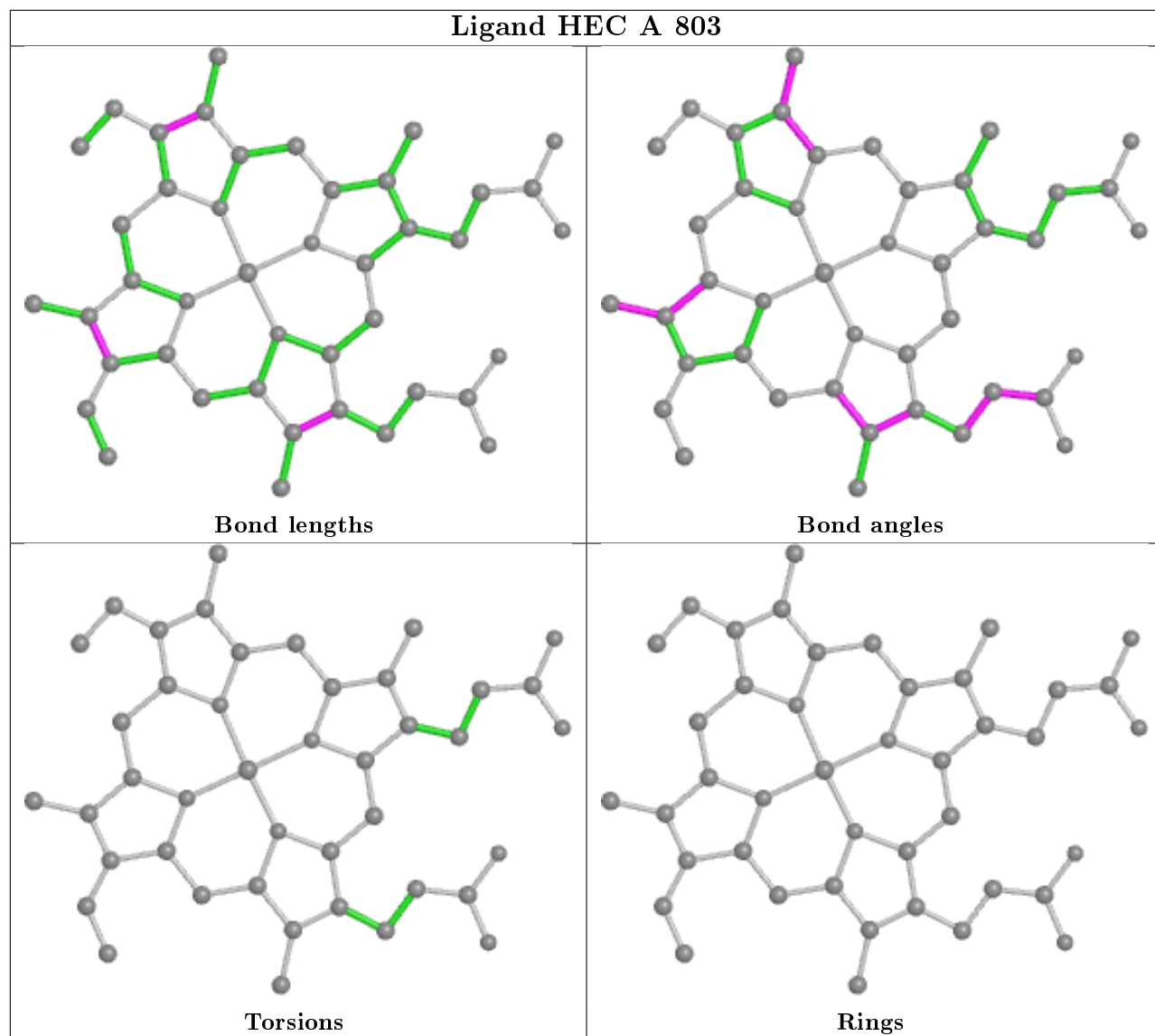


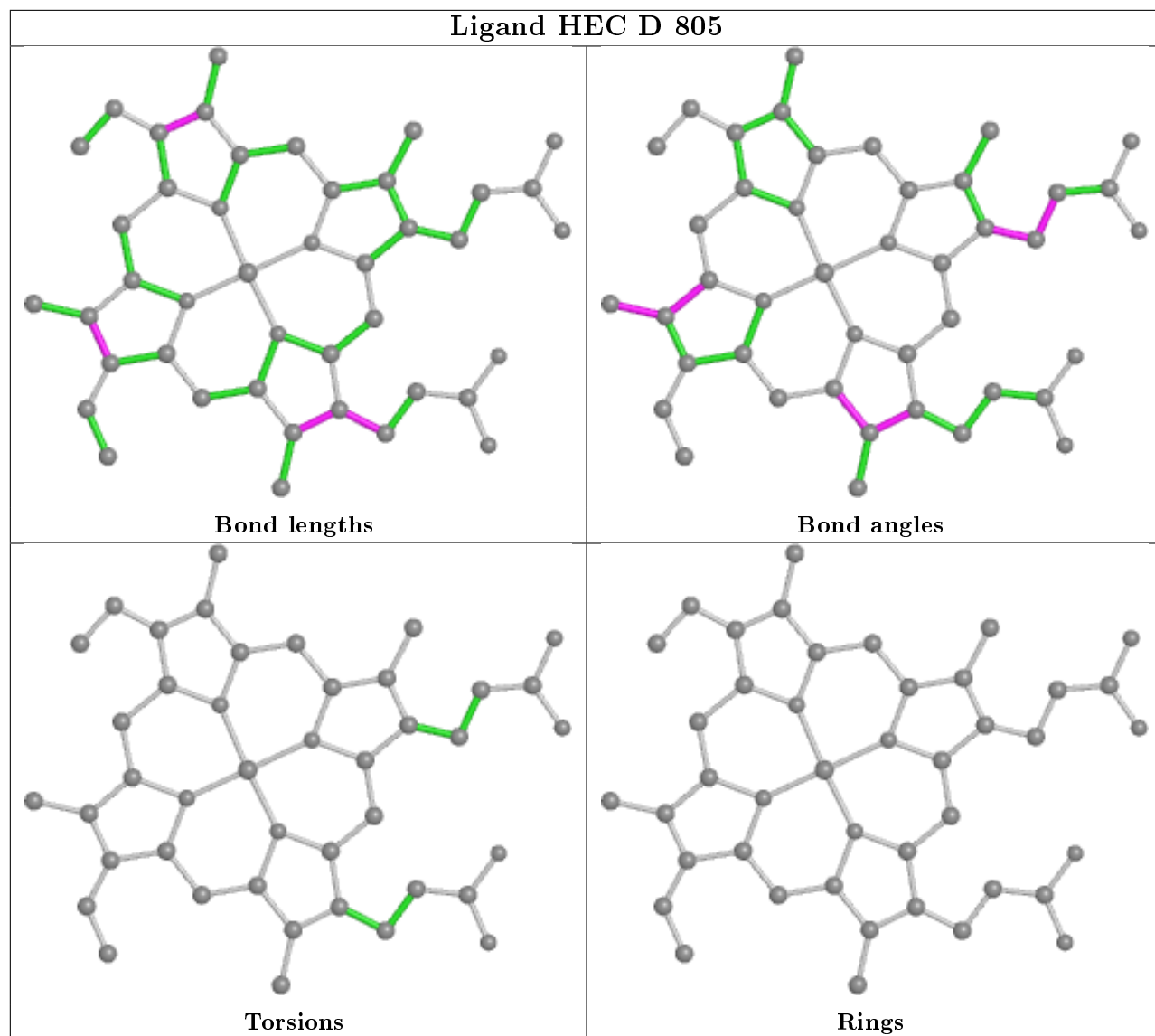


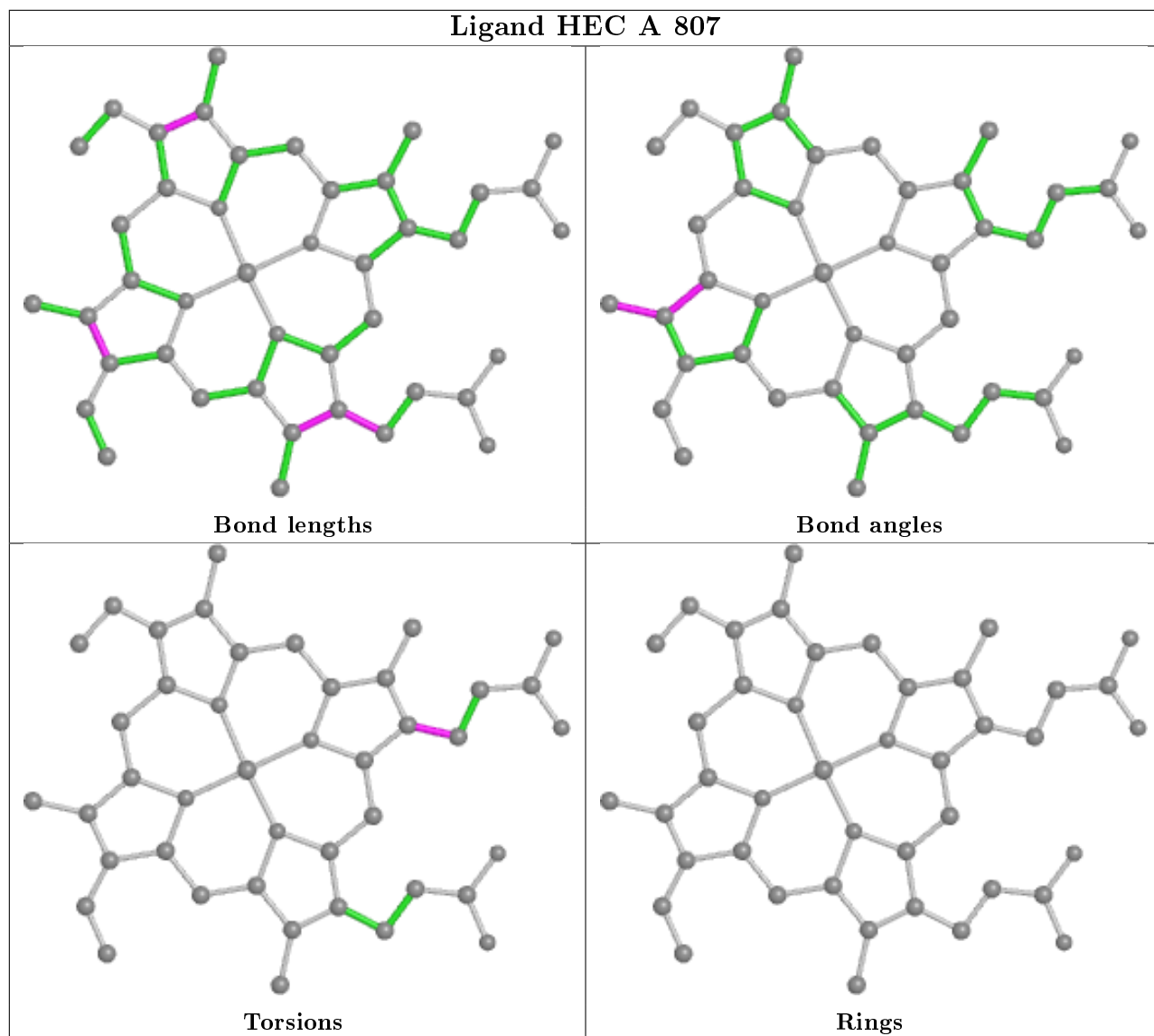


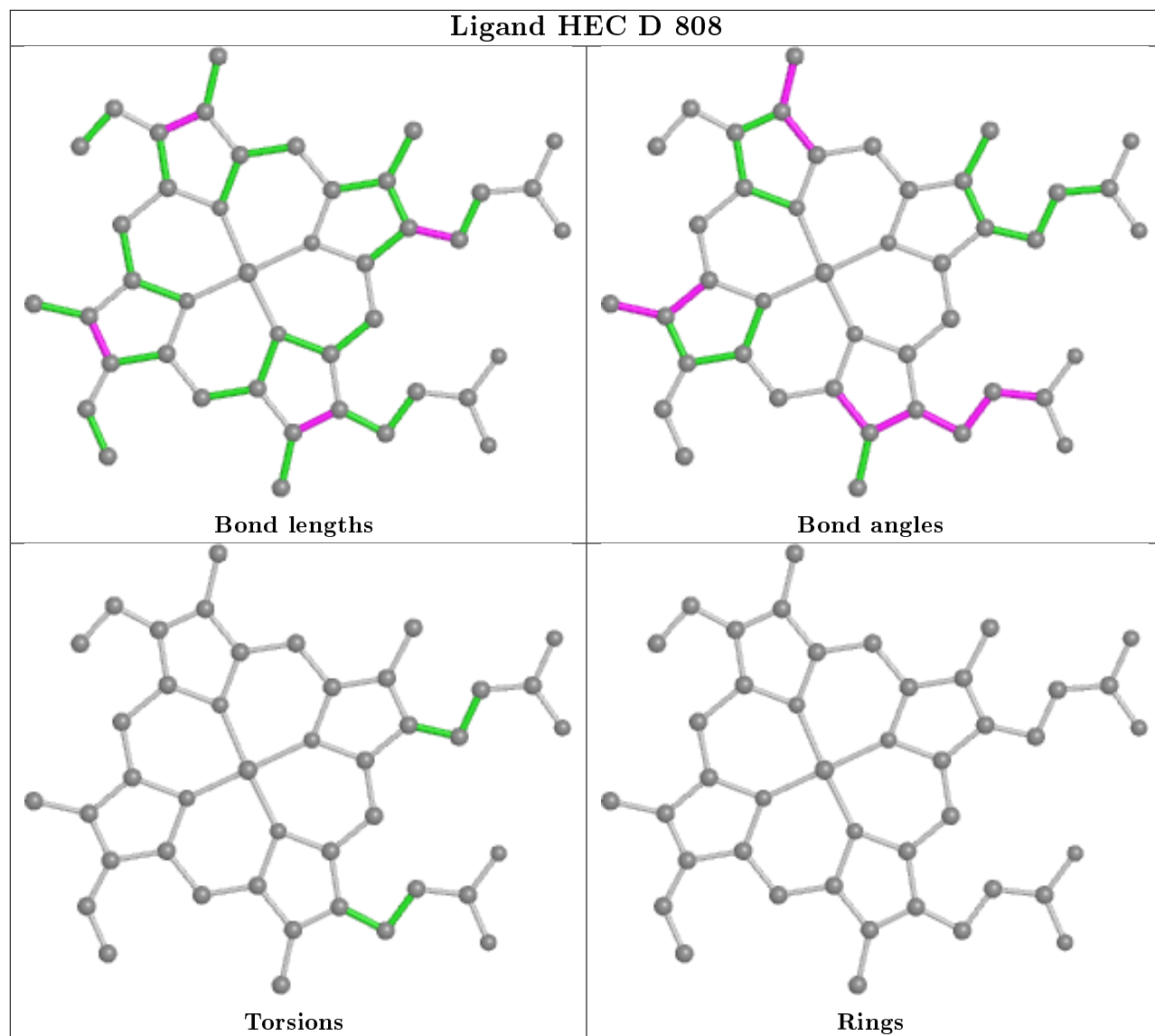


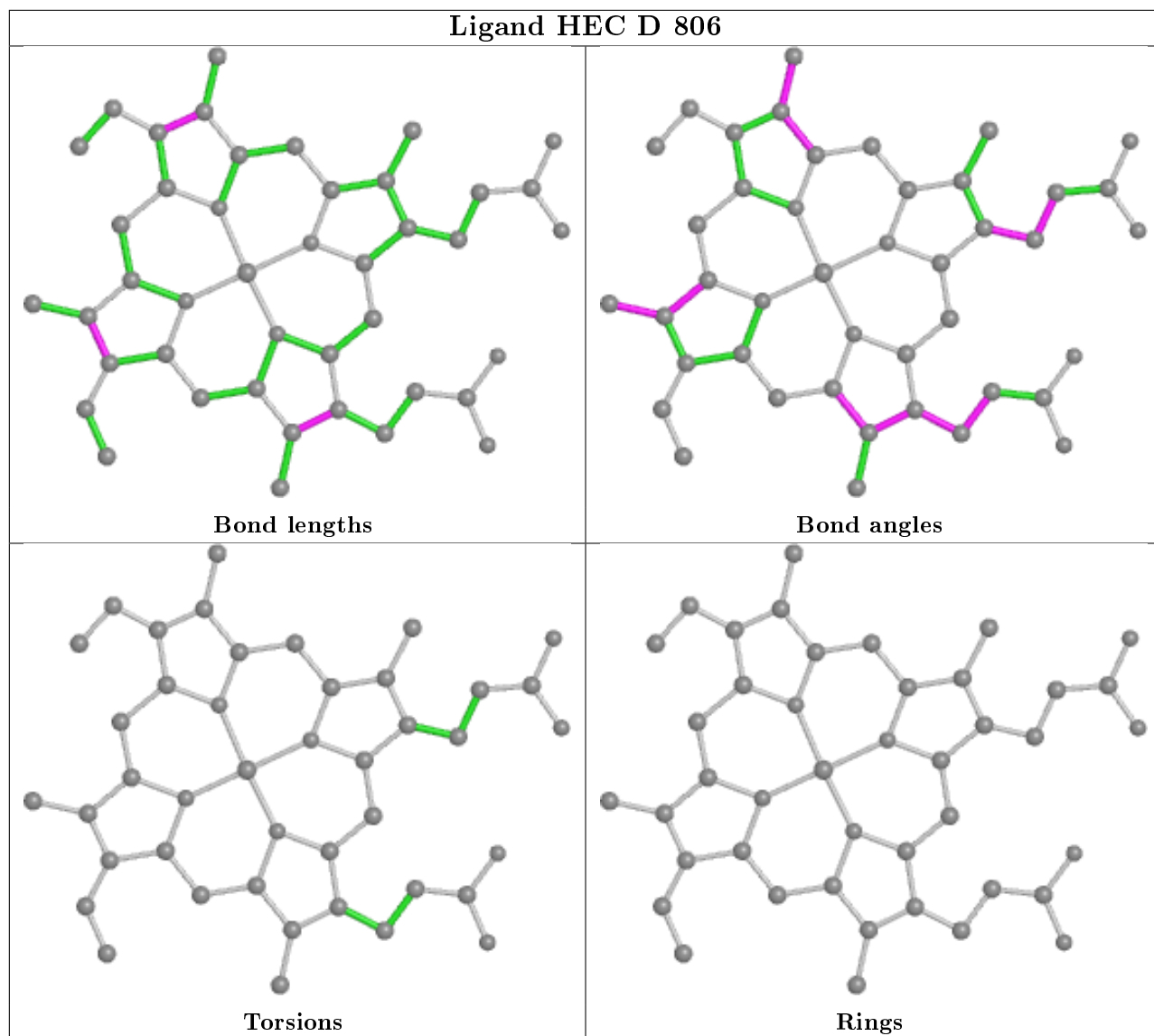


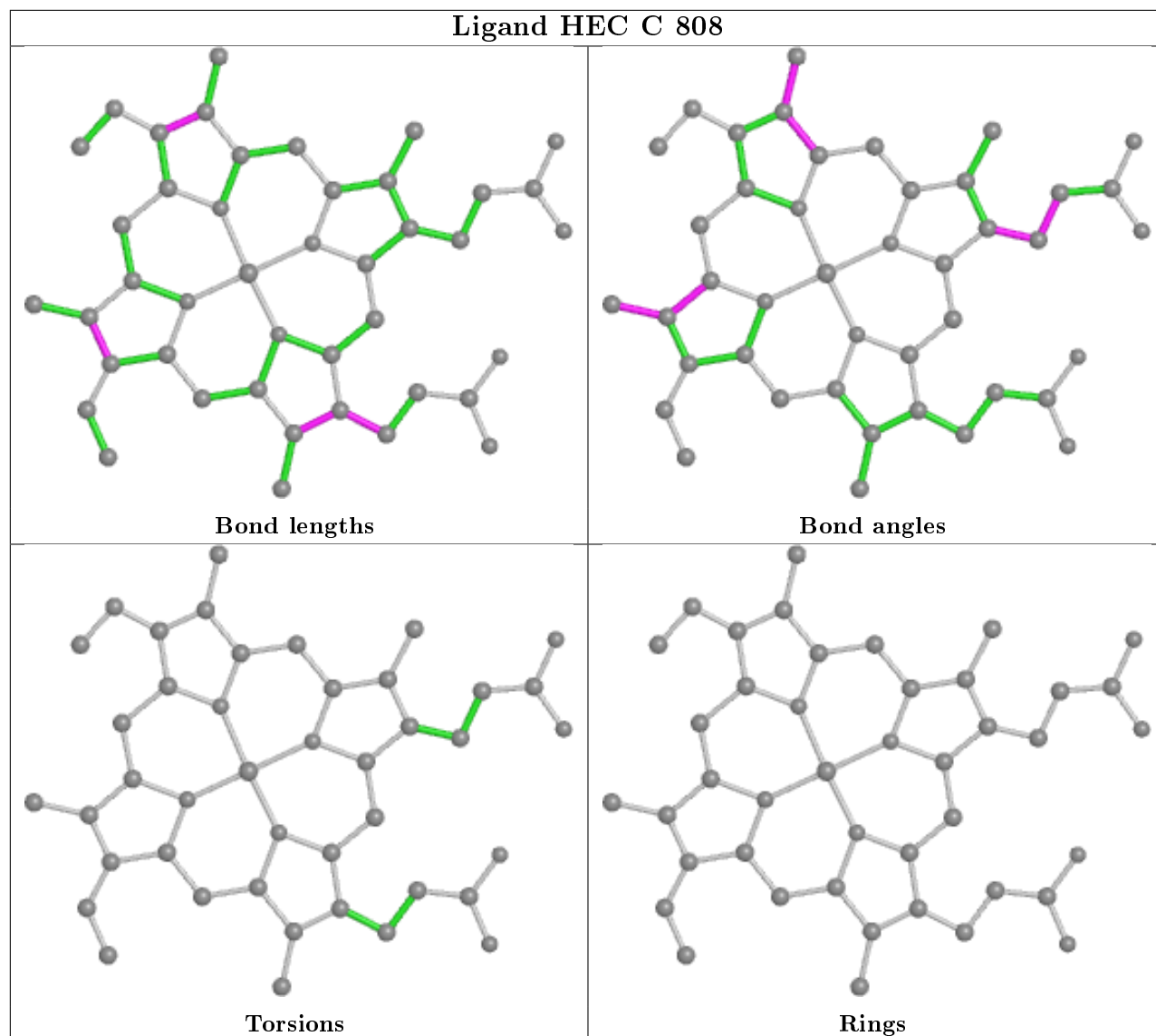












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	693/760 (91%)	-0.28	4 (0%) 89 91	18, 36, 70, 148	0
1	B	694/760 (91%)	-0.25	4 (0%) 89 91	18, 35, 63, 113	0
1	C	692/760 (91%)	-0.23	3 (0%) 92 93	17, 37, 74, 110	0
1	D	695/760 (91%)	-0.40	0 100 100	15, 31, 55, 111	0
All	All	2774/3040 (91%)	-0.29	11 (0%) 92 93	15, 34, 67, 148	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	688	TYR	3.2
1	A	43	VAL	2.7
1	B	321	CYS	2.7
1	A	710	ALA	2.3
1	C	716	ALA	2.3
1	A	697	ILE	2.3
1	C	666	LYS	2.3
1	B	43	VAL	2.2
1	C	602	THR	2.2
1	B	667	ASN	2.1
1	B	79	VAL	2.1

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(Å ²)	Q<0.9
4	DMS	D	815	4/4	0.52	0.56	115,115,115,115	0
3	CA	A	812	1/1	0.69	0.23	69,69,69,69	0
4	DMS	B	915	4/4	0.78	0.34	92,92,92,92	0
4	DMS	C	815	4/4	0.86	0.28	84,84,84,84	0
4	DMS	C	816	4/4	0.88	0.22	56,67,67,88	0
3	CA	D	812	1/1	0.88	0.14	60,60,60,60	0
4	DMS	A	814	4/4	0.89	0.28	61,67,77,91	0
3	CA	C	812	1/1	0.91	0.13	57,57,57,57	0
4	DMS	D	816	4/4	0.92	0.19	66,66,66,66	0
4	DMS	A	815	4/4	0.93	0.18	57,58,61,80	0
4	DMS	C	814	4/4	0.94	0.23	59,59,59,59	0
3	CA	C	811	1/1	0.94	0.13	39,39,39,39	0
4	DMS	B	914	4/4	0.95	0.29	46,49,57,59	0
4	DMS	B	916	4/4	0.95	0.17	46,48,50,71	0
2	HEC	C	810	43/43	0.95	0.21	62,71,76,83	0
2	HEC	A	809	43/43	0.96	0.15	40,53,71,81	0
2	HEC	C	809	43/43	0.96	0.18	46,60,71,75	0
2	HEC	A	810	43/43	0.96	0.18	58,67,75,80	0
3	CA	A	811	1/1	0.97	0.14	30,30,30,30	0
2	HEC	B	903	43/43	0.97	0.15	24,31,43,46	0
2	HEC	B	905	43/43	0.97	0.15	26,33,42,50	0
2	HEC	B	911	43/43	0.97	0.16	26,32,52,58	0
3	CA	B	913	1/1	0.97	0.16	58,58,58,58	0
2	HEC	C	807	43/43	0.97	0.15	28,34,46,63	0
2	HEC	B	904	43/43	0.97	0.16	25,32,37,40	0
2	HEC	D	802	43/43	0.97	0.16	21,27,36,44	0
4	DMS	D	813	4/4	0.97	0.21	36,43,45,52	0
4	DMS	C	813	4/4	0.97	0.21	41,42,46,47	0
3	CA	D	811	1/1	0.97	0.07	38,38,38,38	0
2	HEC	C	804	43/43	0.98	0.15	20,27,37,43	0
2	HEC	B	906	43/43	0.98	0.15	27,34,37,39	0
2	HEC	B	910	43/43	0.98	0.15	24,31,67,73	0
2	HEC	A	805	43/43	0.98	0.15	25,30,35,37	0
2	HEC	D	810	43/43	0.98	0.14	22,27,44,48	0
2	HEC	A	802	43/43	0.98	0.15	15,22,29,35	0
3	CA	B	912	1/1	0.98	0.08	51,51,51,51	0
2	HEC	D	804	43/43	0.98	0.15	24,31,36,51	0

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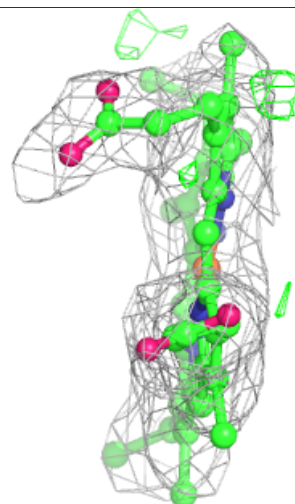
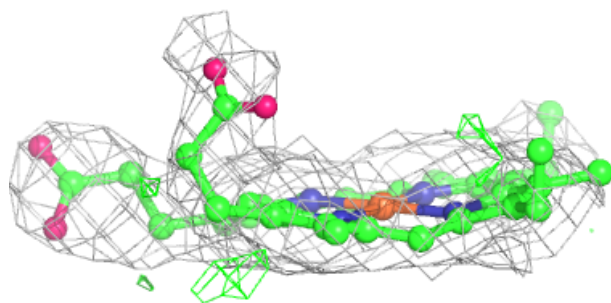
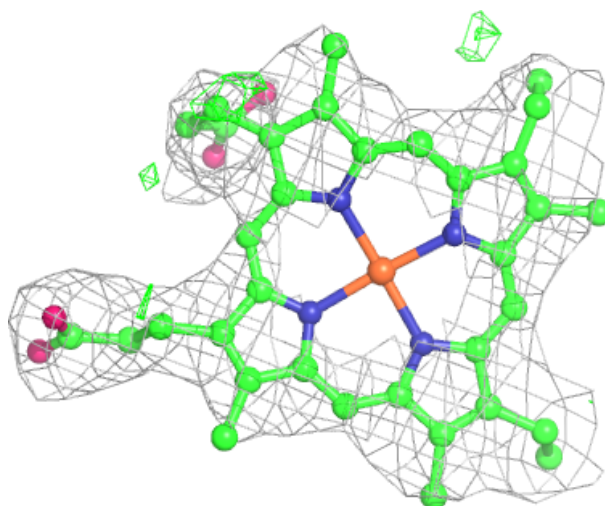
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	HEC	C	803	43/43	0.98	0.14	18,23,27,32	0
4	DMS	D	814	4/4	0.98	0.19	23,35,38,42	0
2	HEC	C	806	43/43	0.98	0.14	27,31,43,52	0
2	HEC	B	908	43/43	0.98	0.16	19,26,35,54	0
2	HEC	A	808	43/43	0.98	0.13	28,38,43,44	0
2	HEC	B	907	43/43	0.98	0.16	18,24,35,42	0
2	HEC	B	909	43/43	0.98	0.13	17,24,28,32	0
2	HEC	C	801	43/43	0.98	0.14	20,23,28,30	0
2	HEC	A	806	43/43	0.98	0.14	23,29,41,45	0
2	HEC	D	809	43/43	0.98	0.14	21,29,59,69	0
2	HEC	C	805	43/43	0.98	0.14	23,28,34,46	0
2	HEC	A	804	43/43	0.98	0.14	20,27,33,51	0
2	HEC	D	807	43/43	0.98	0.16	18,25,36,62	0
2	HEC	D	805	43/43	0.98	0.13	23,32,39,46	0
2	HEC	A	807	43/43	0.98	0.14	27,33,41,49	0
2	HEC	C	802	43/43	0.98	0.17	16,23,30,36	0
2	HEC	D	806	43/43	0.98	0.15	17,22,36,43	0
2	HEC	C	808	43/43	0.98	0.16	29,37,43,48	0
2	HEC	D	803	43/43	0.99	0.13	19,26,30,33	0
2	HEC	A	803	43/43	0.99	0.14	16,20,24,32	0
4	DMS	B	901	4/4	0.99	0.21	31,36,37,45	0
4	DMS	A	816	4/4	0.99	0.16	28,31,36,41	0
2	HEC	B	902	43/43	0.99	0.15	19,24,27,30	0
2	HEC	D	808	43/43	0.99	0.13	16,23,27,30	0
2	HEC	A	801	43/43	0.99	0.13	18,22,29,34	0
4	DMS	A	813	4/4	0.99	0.22	46,50,53,58	0
2	HEC	D	801	43/43	0.99	0.14	16,20,26,28	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.

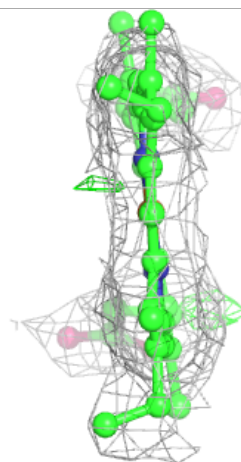
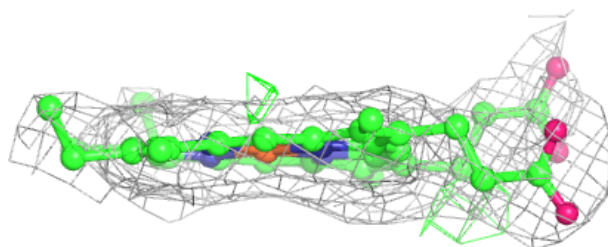
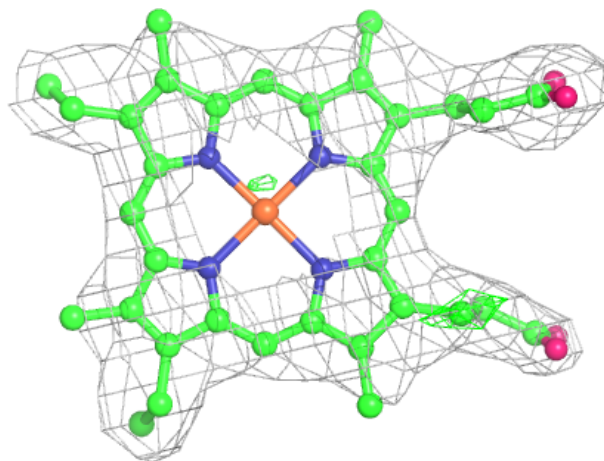
Electron density around HEC C 810:

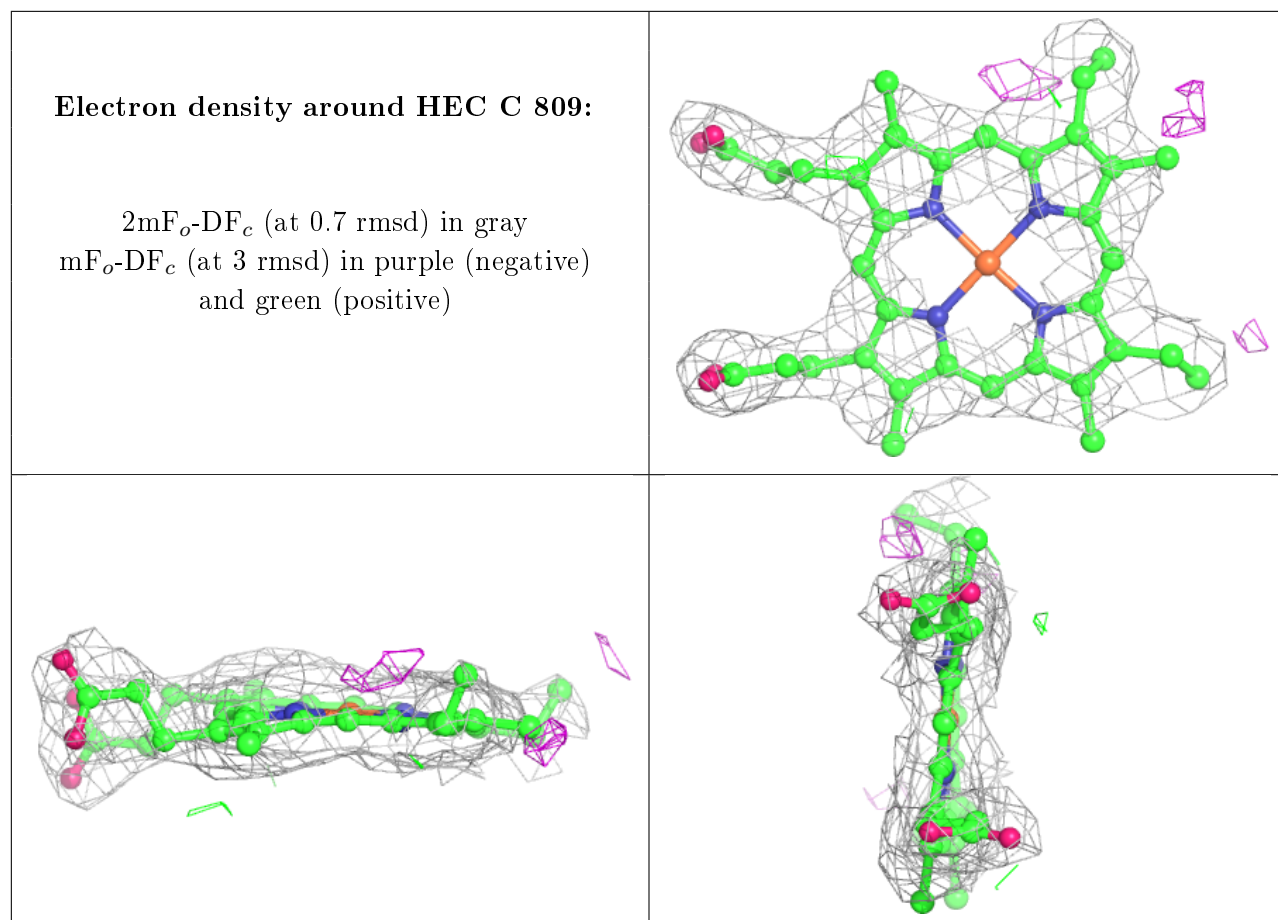
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 809:

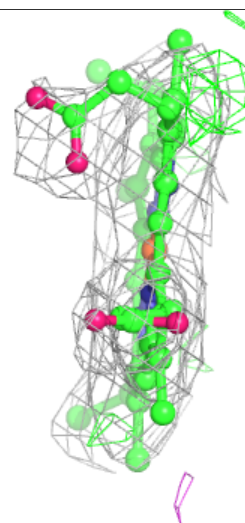
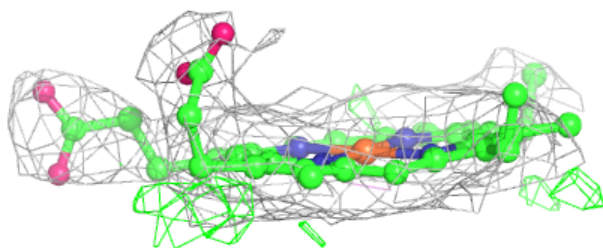
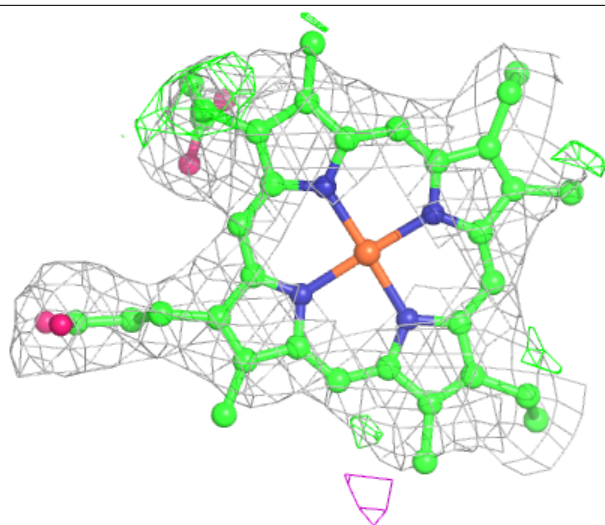
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

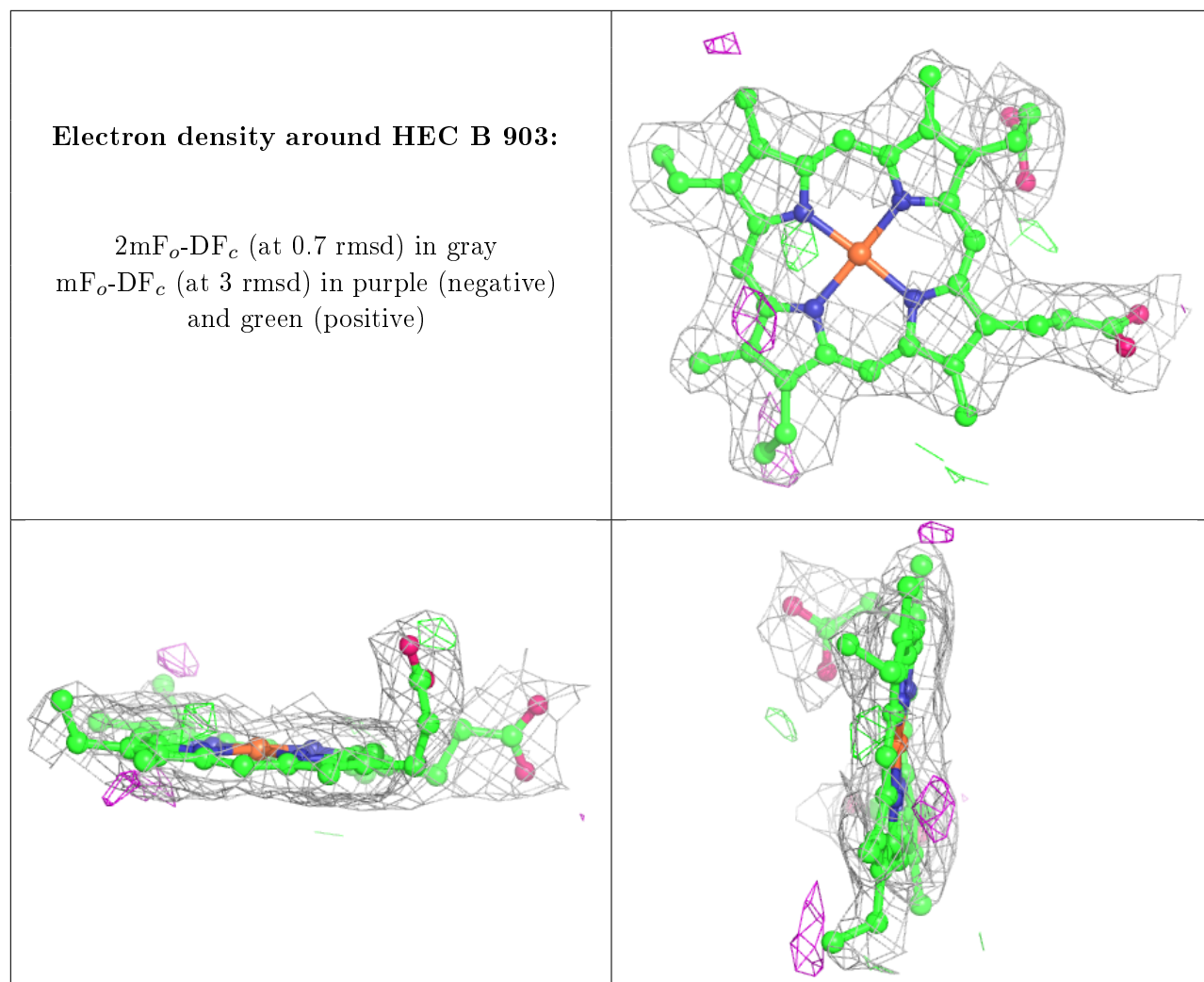


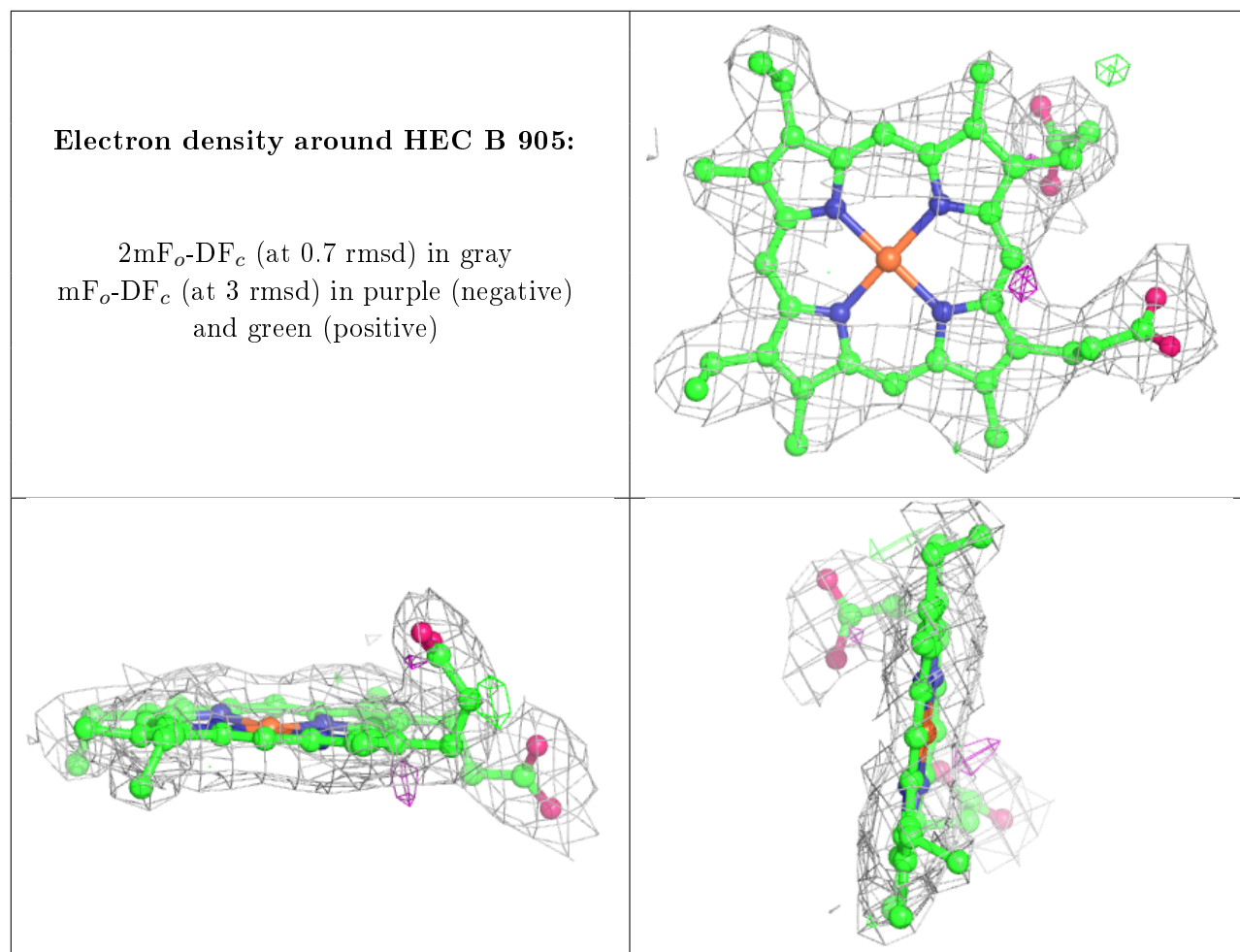


Electron density around HEC A 810:

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

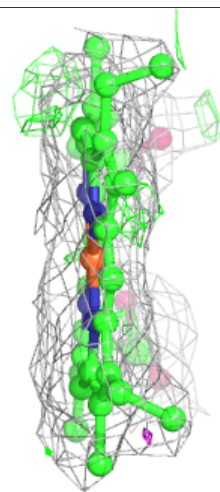
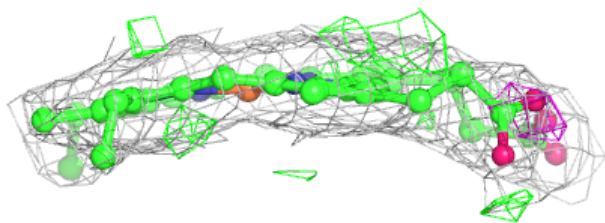
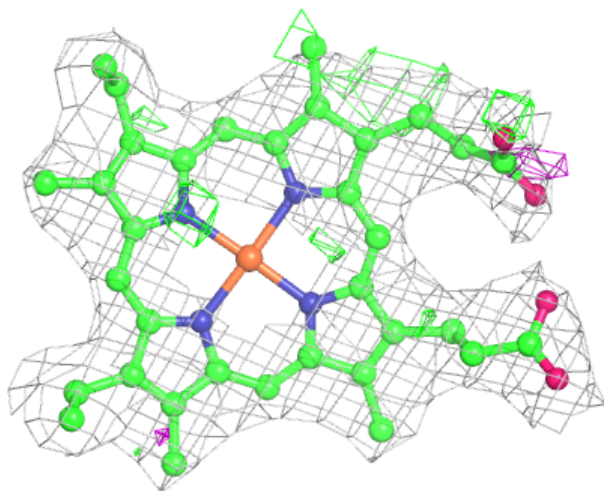






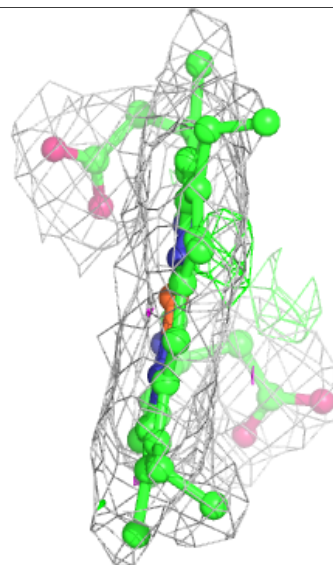
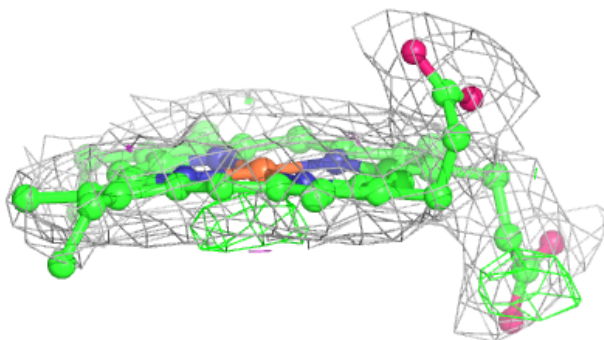
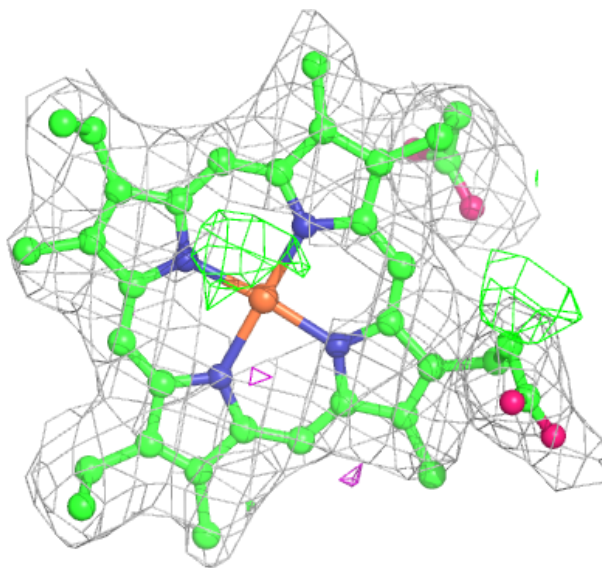
Electron density around HEC B 911:

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



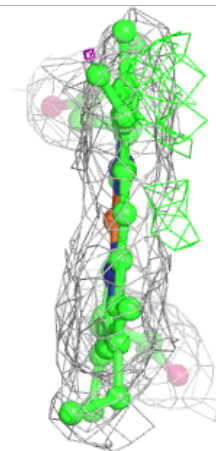
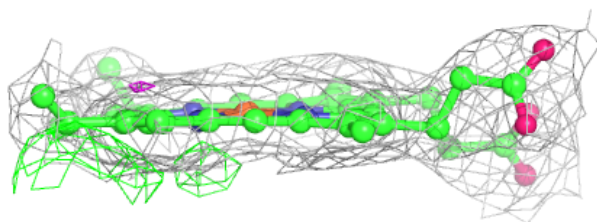
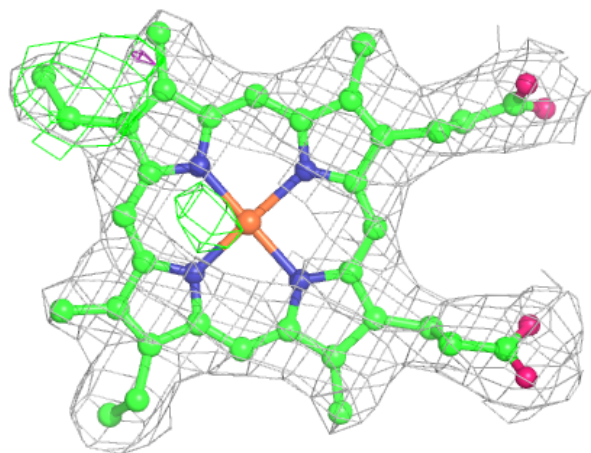
Electron density around HEC C 807:

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



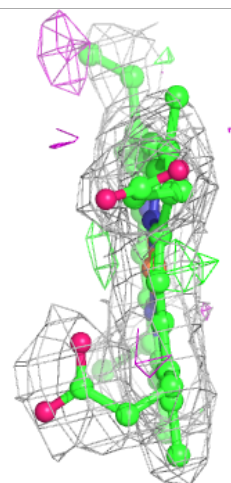
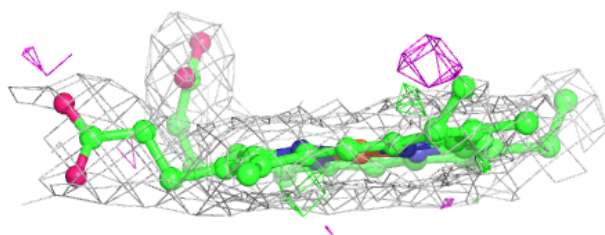
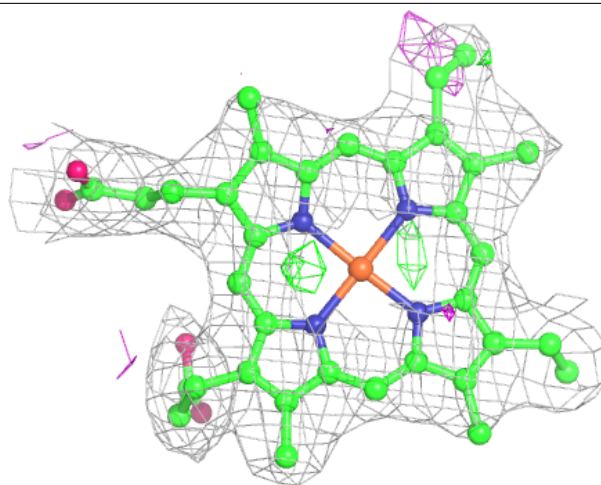
Electron density around HEC B 904:

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



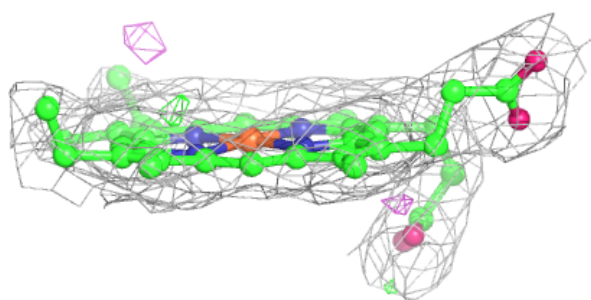
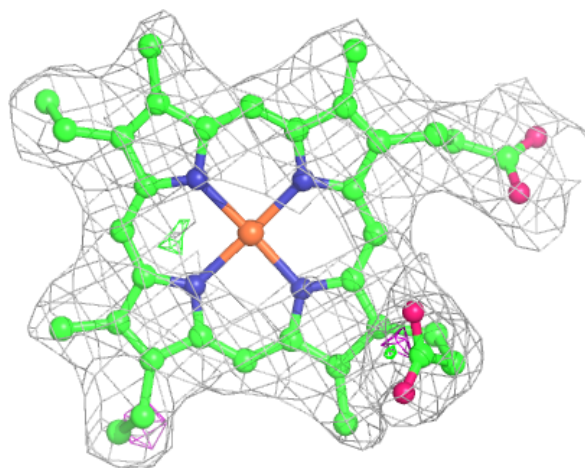
Electron density around HEC D 802:

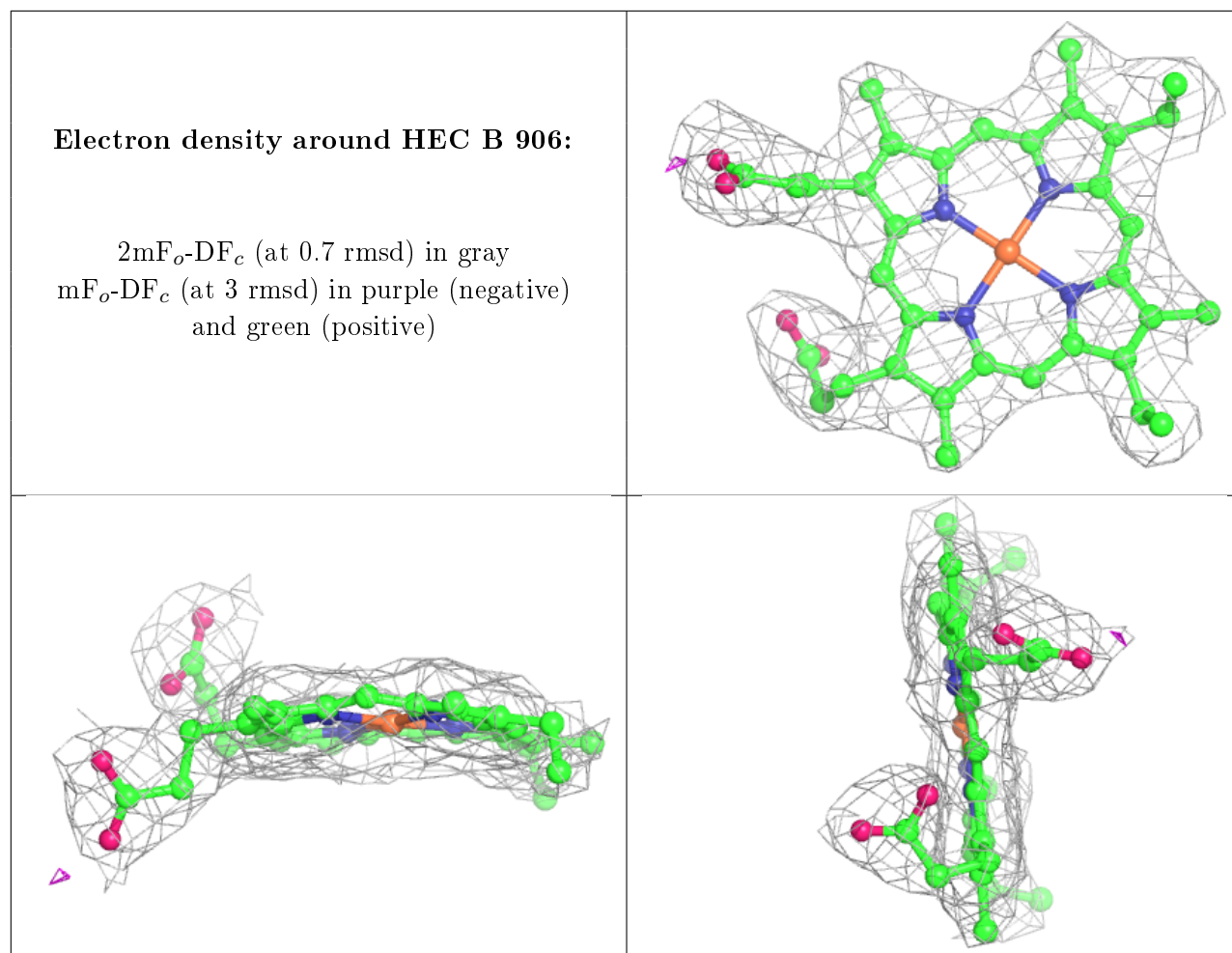
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC C 804:

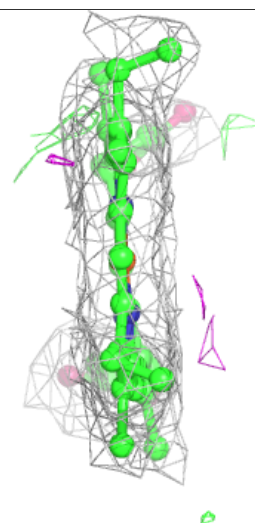
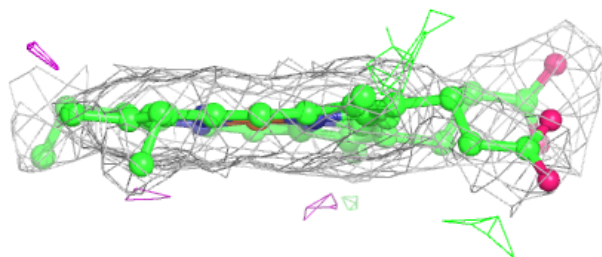
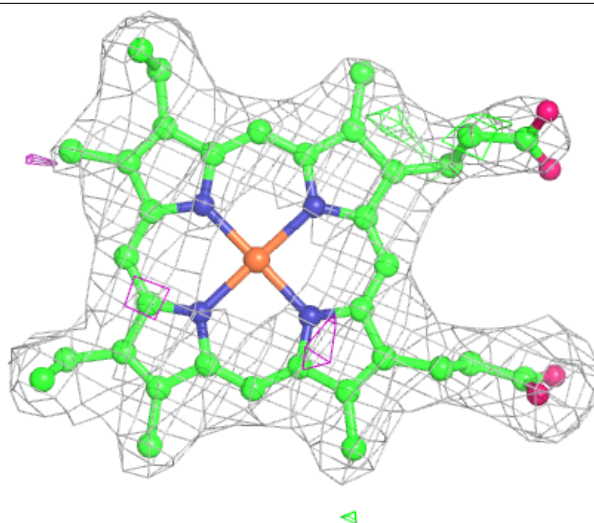
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





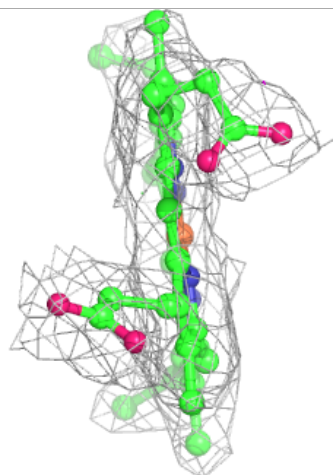
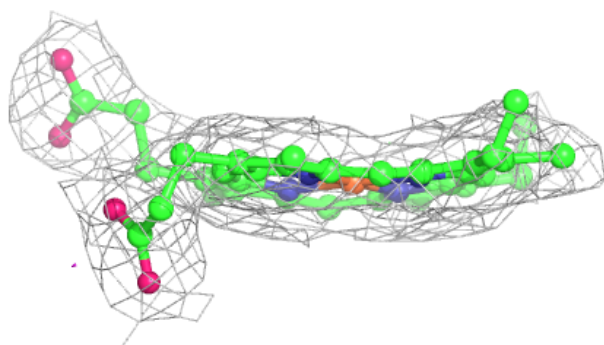
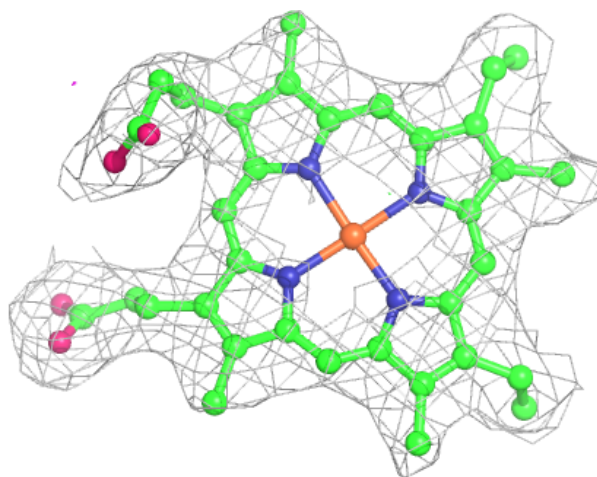
Electron density around HEC B 910:

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



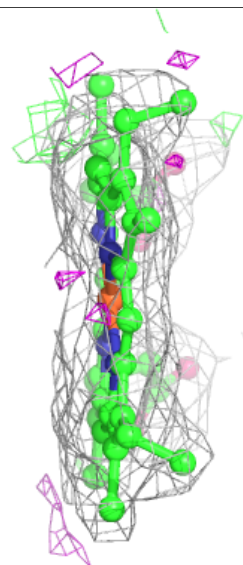
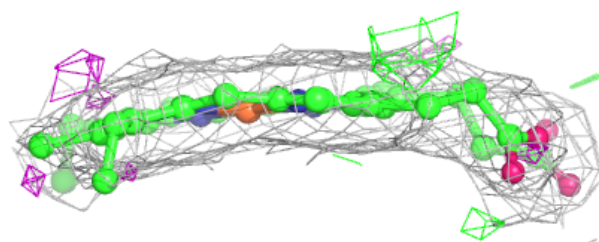
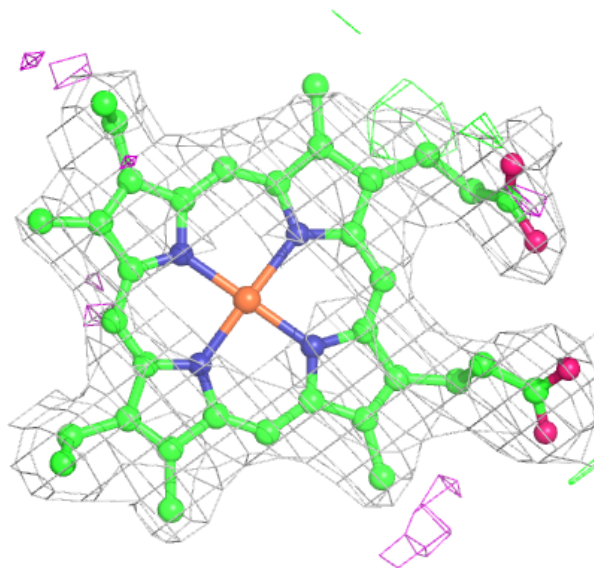
Electron density around HEC A 805:

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



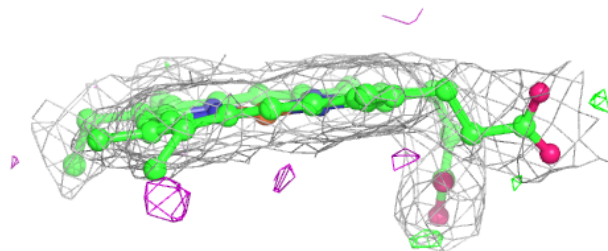
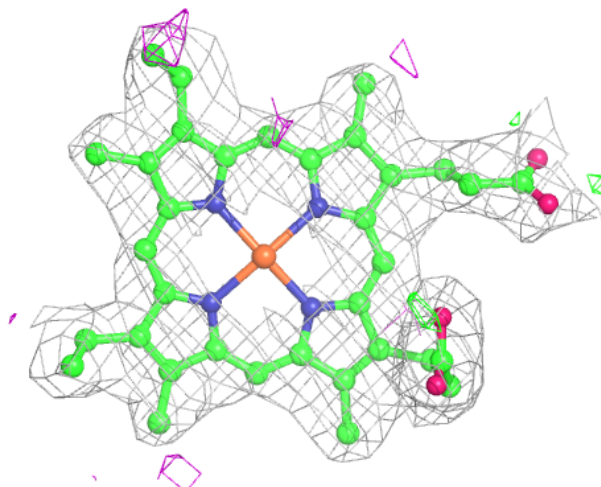
Electron density around HEC D 810:

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



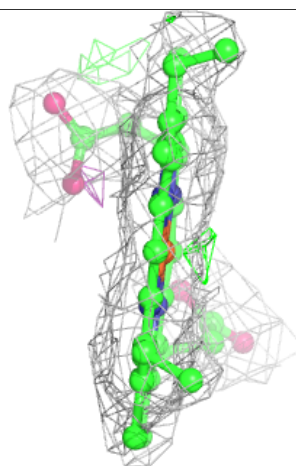
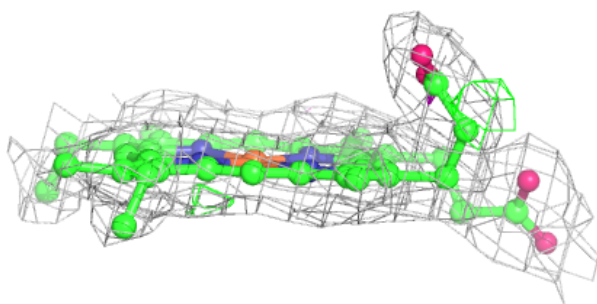
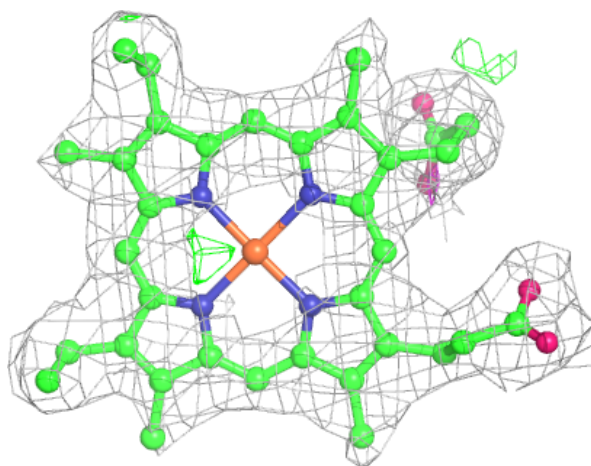
Electron density around HEC A 802:

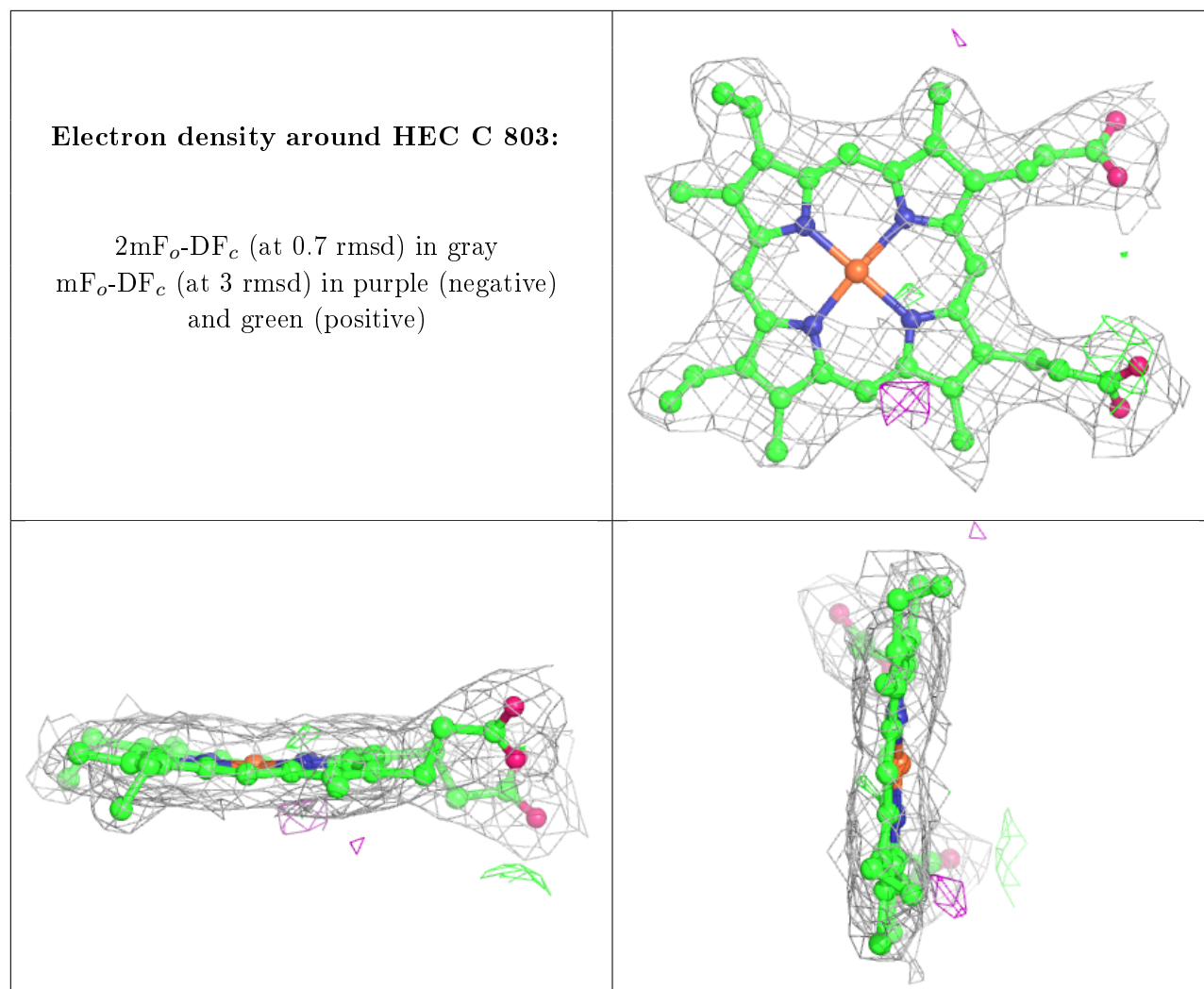
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

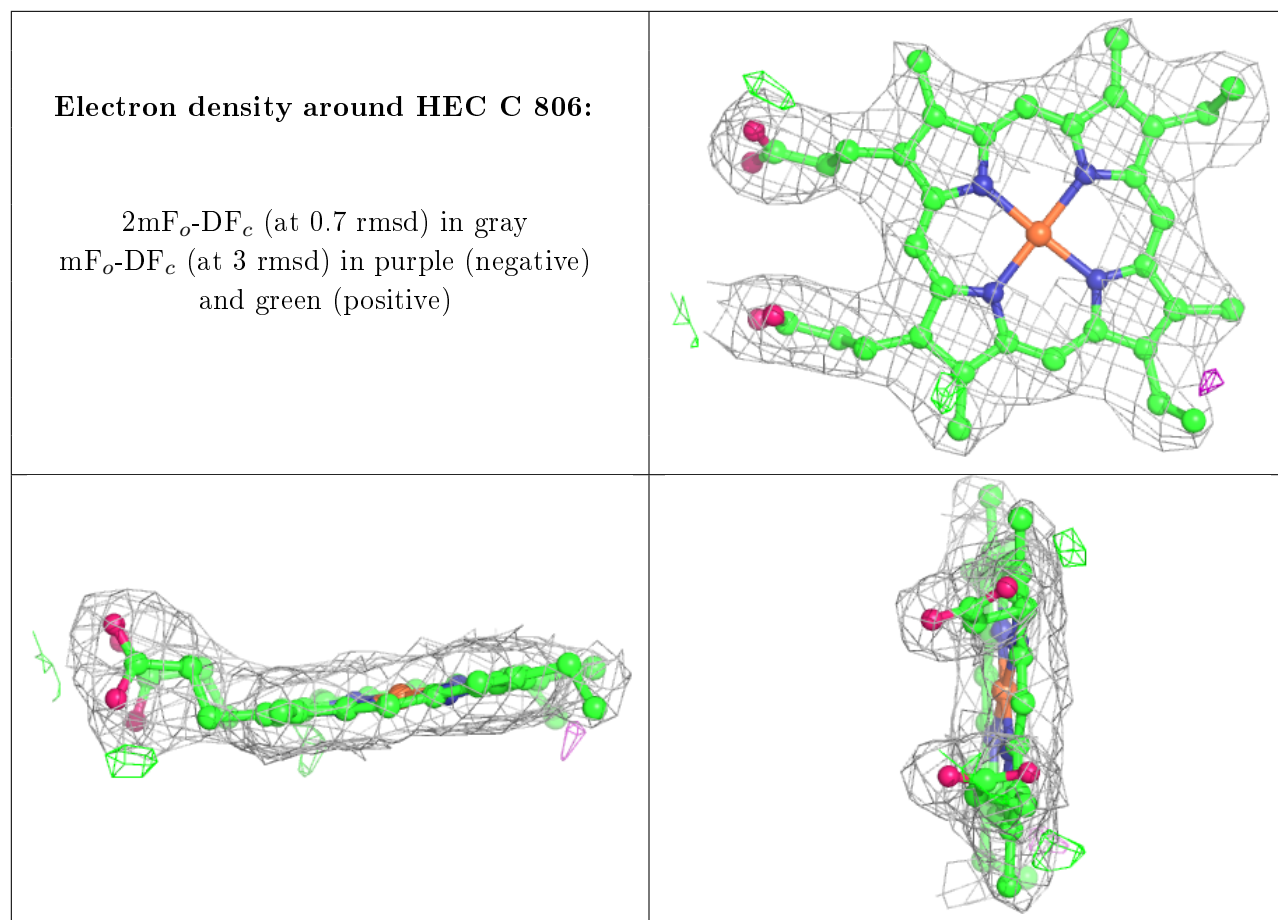


Electron density around HEC D 804:

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

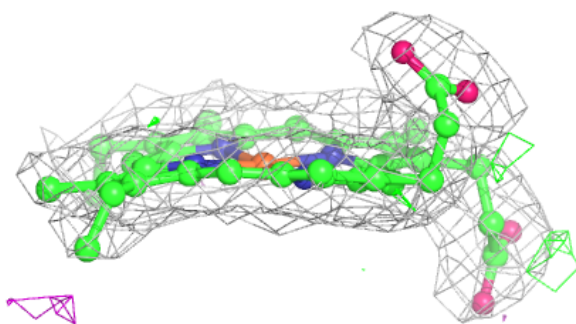
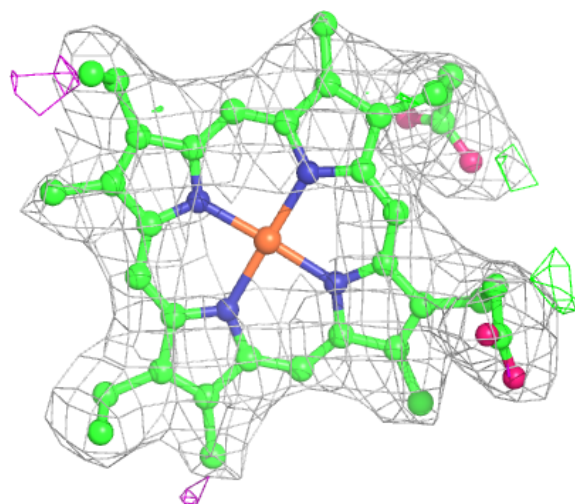


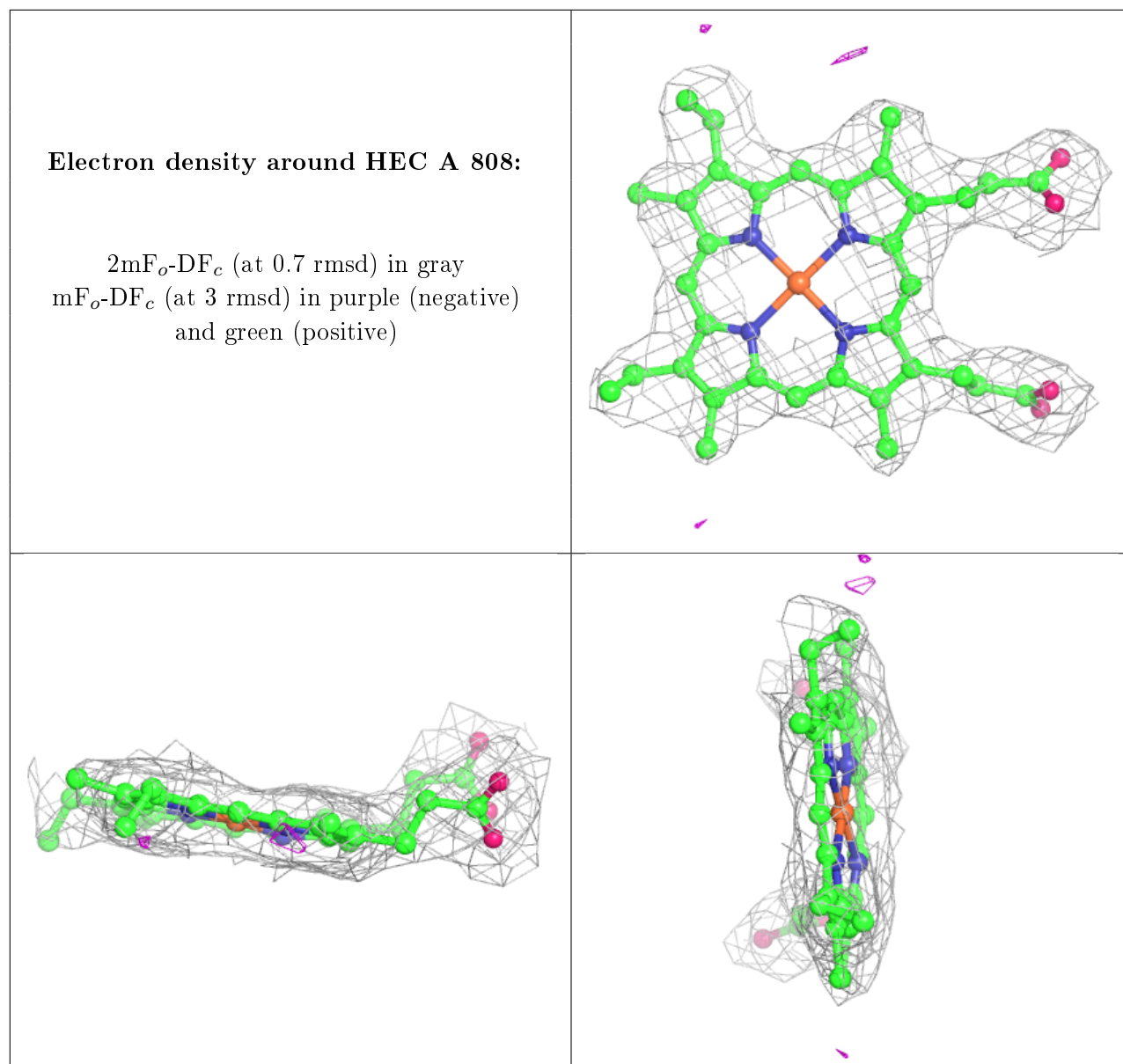


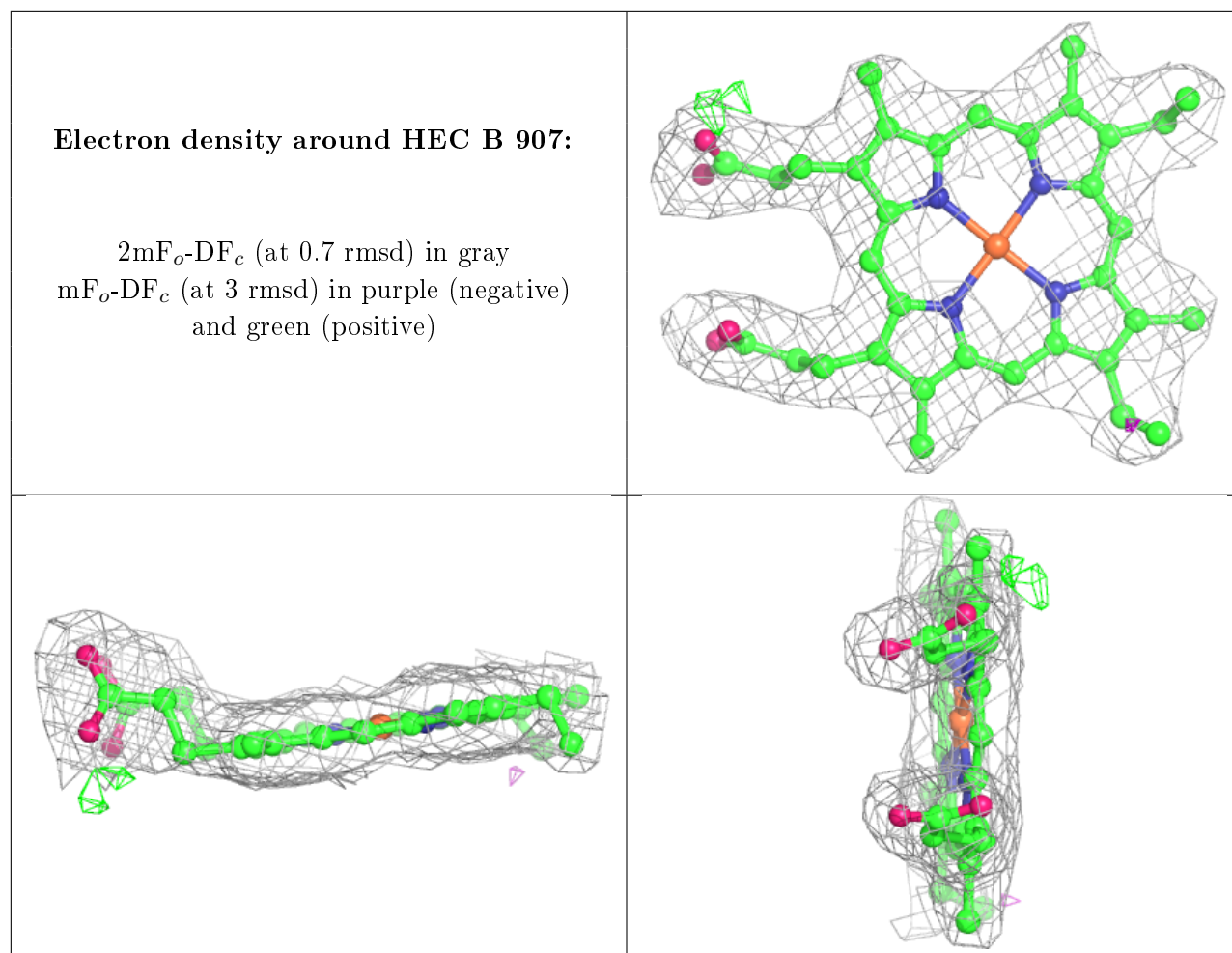


Electron density around HEC B 908:

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

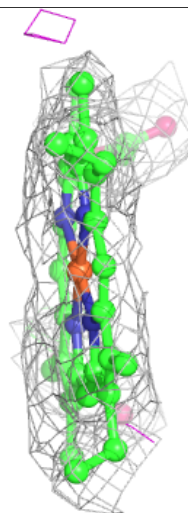
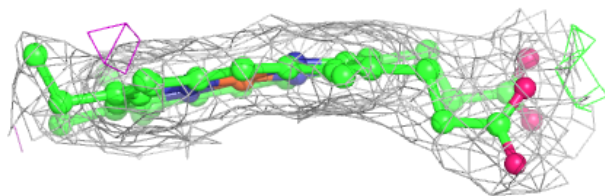
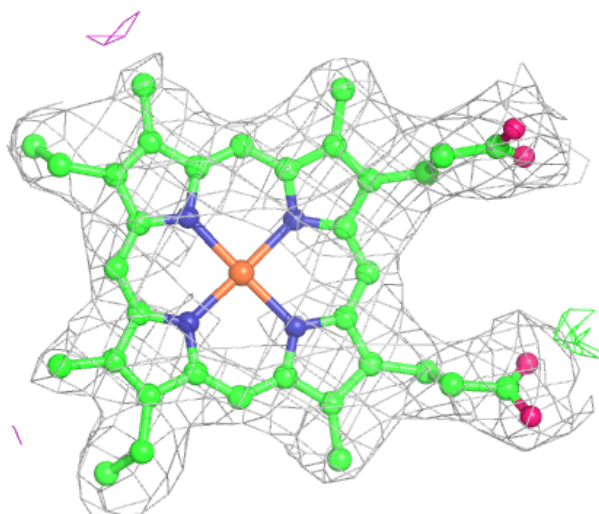


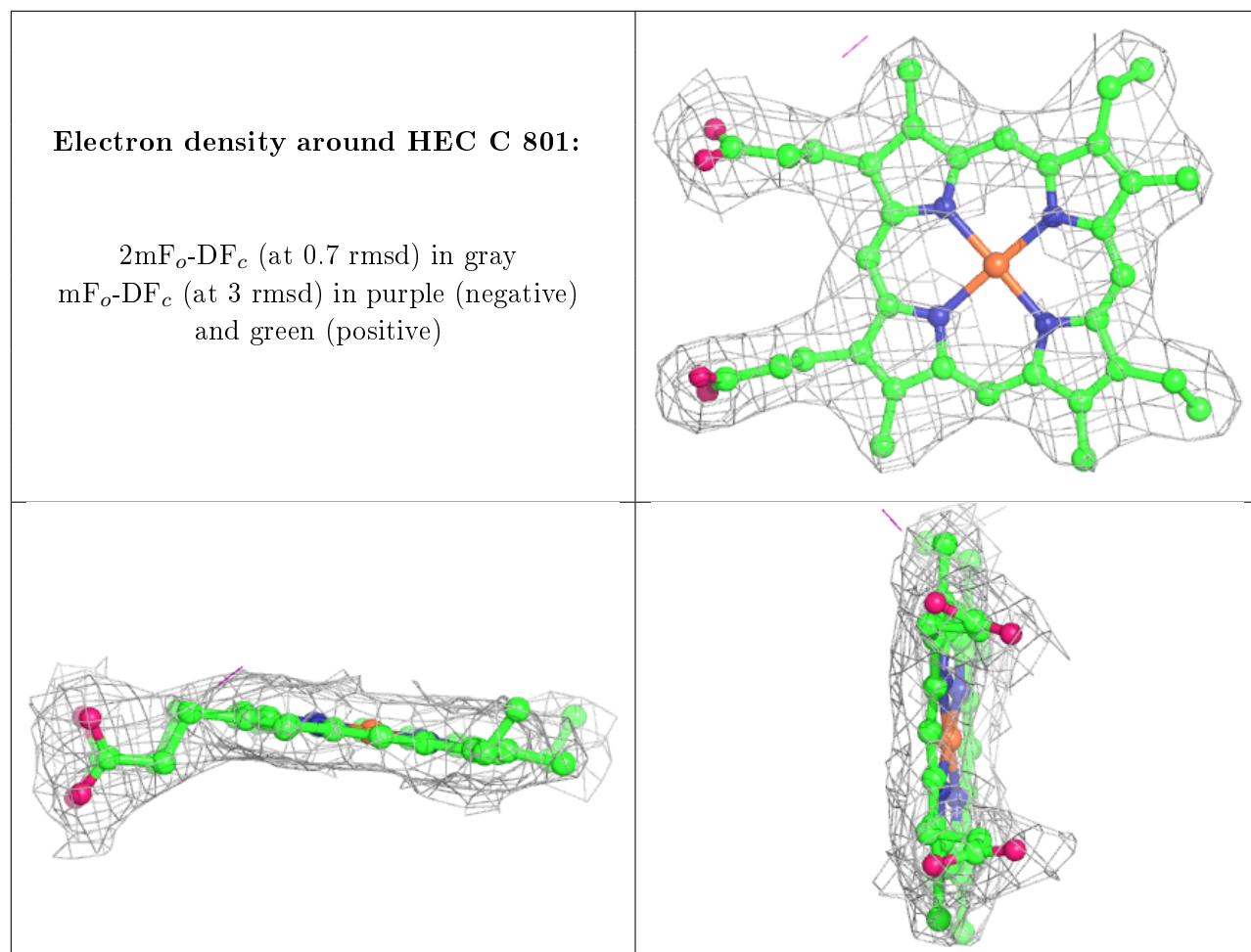




Electron density around HEC B 909:

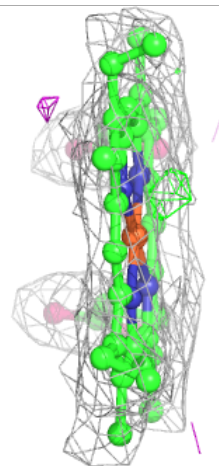
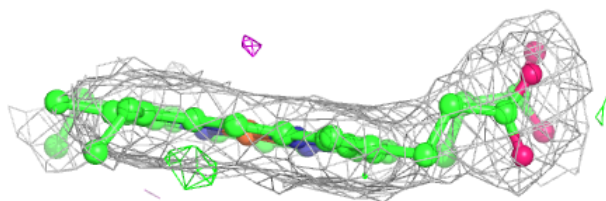
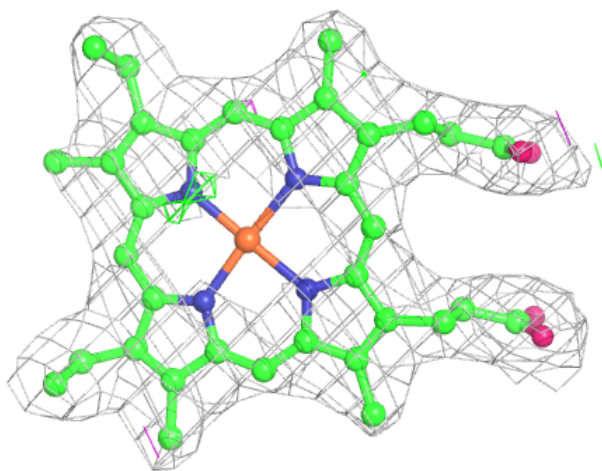
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





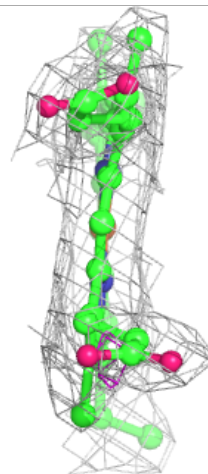
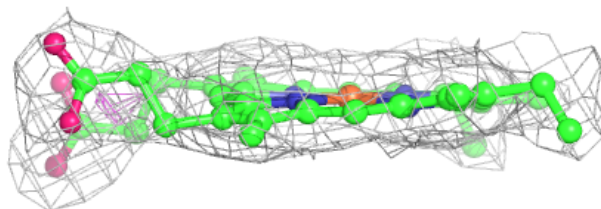
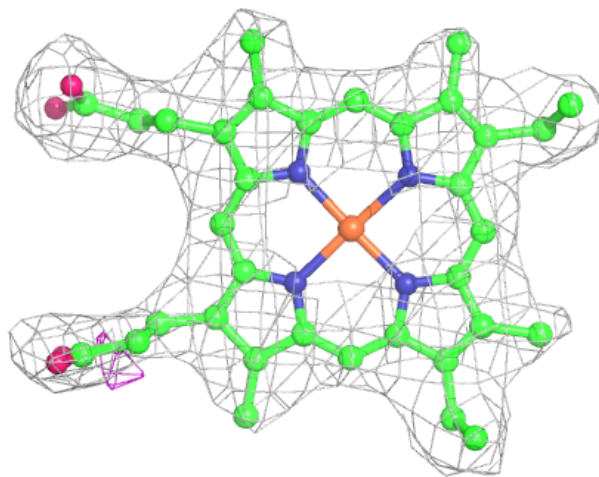
Electron density around HEC A 806:

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



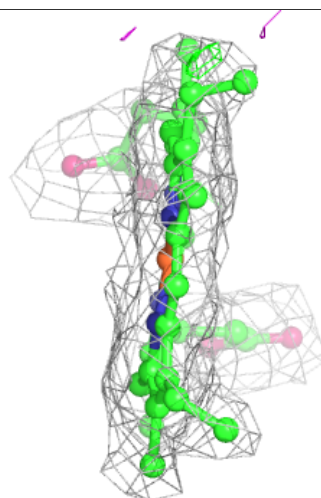
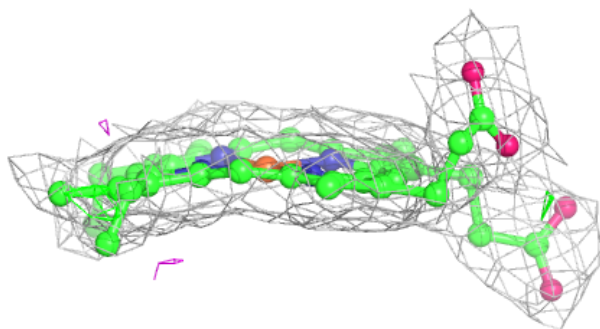
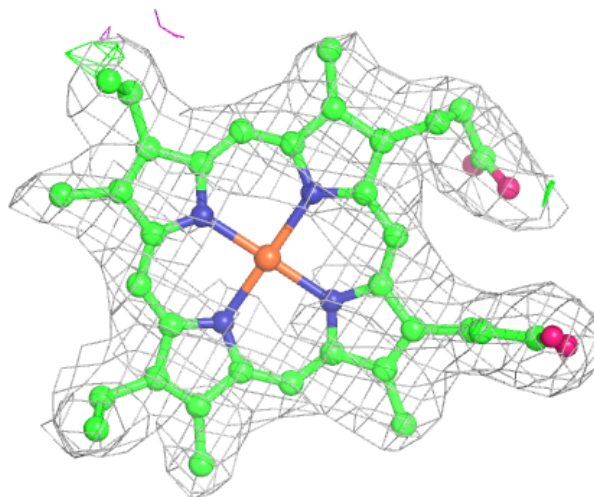
Electron density around HEC D 809:

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



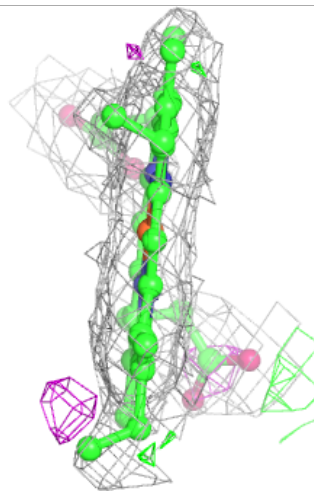
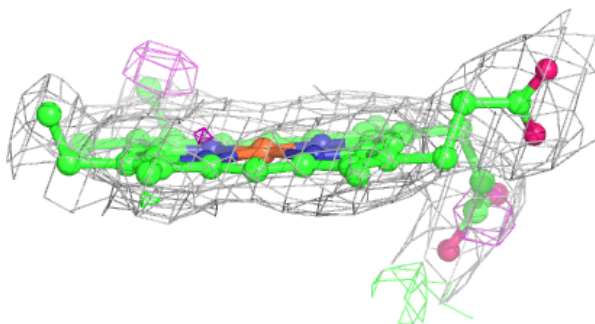
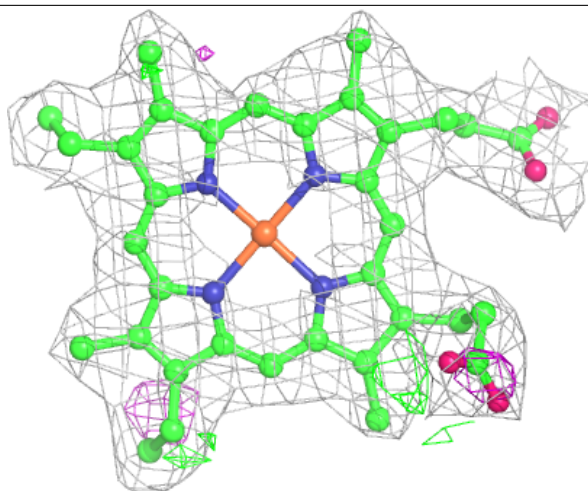
Electron density around HEC C 805:

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



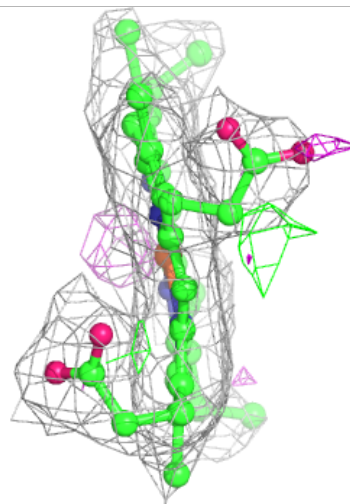
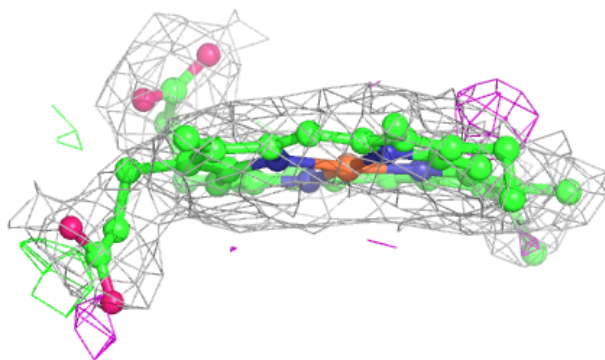
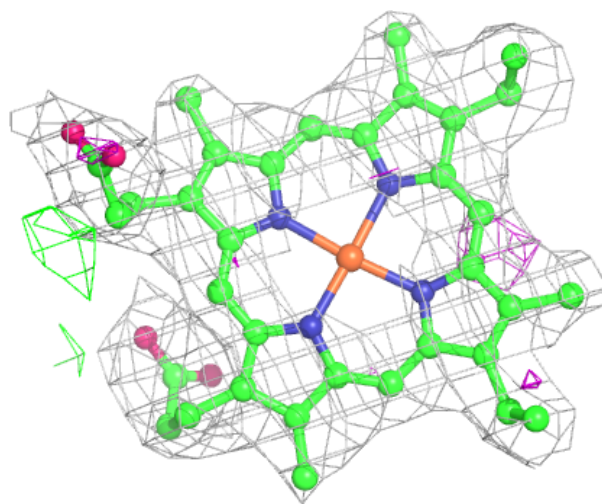
Electron density around HEC A 804:

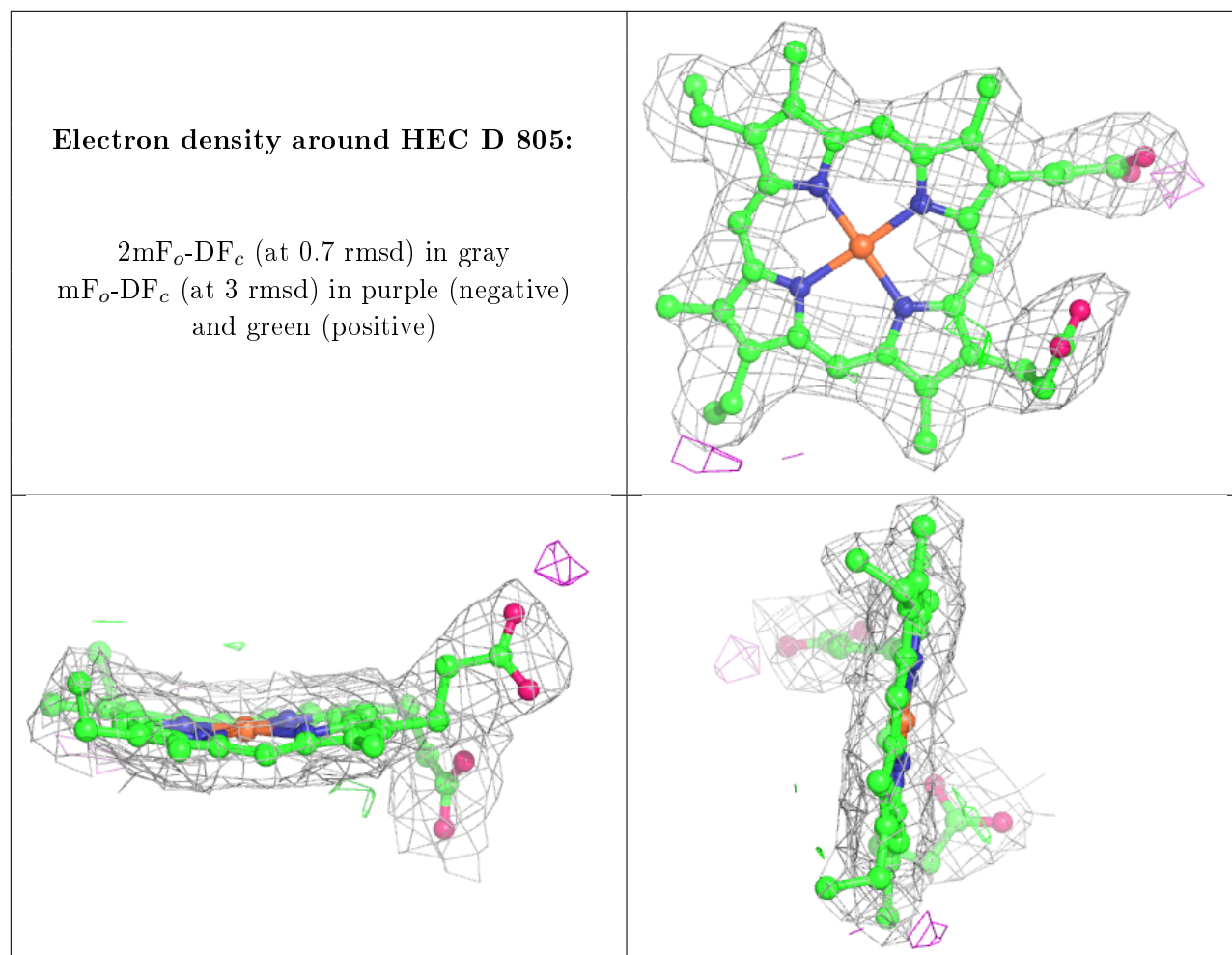
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC D 807:

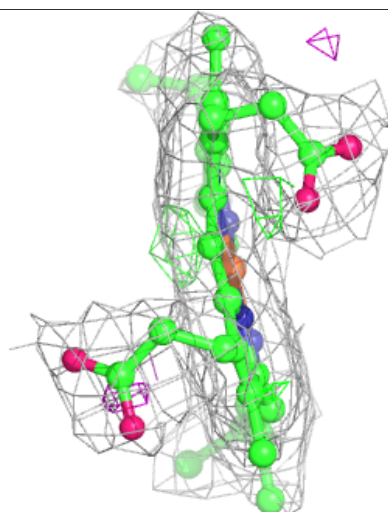
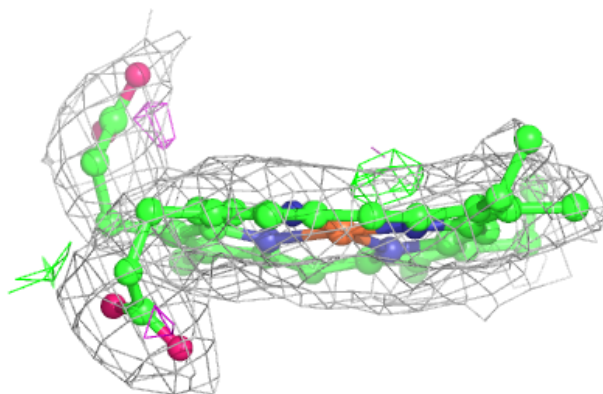
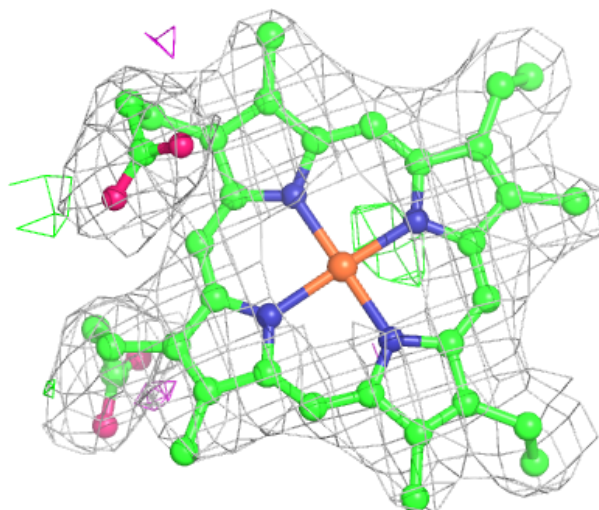
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





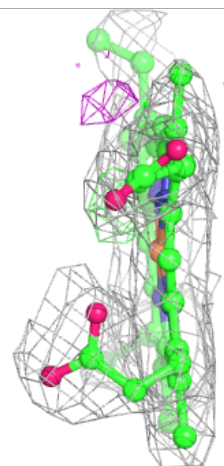
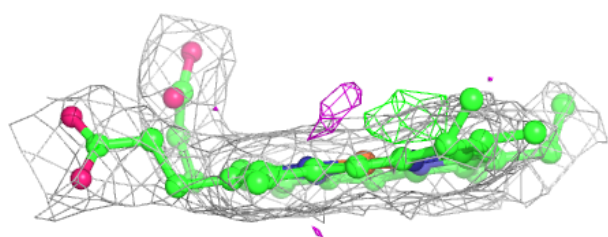
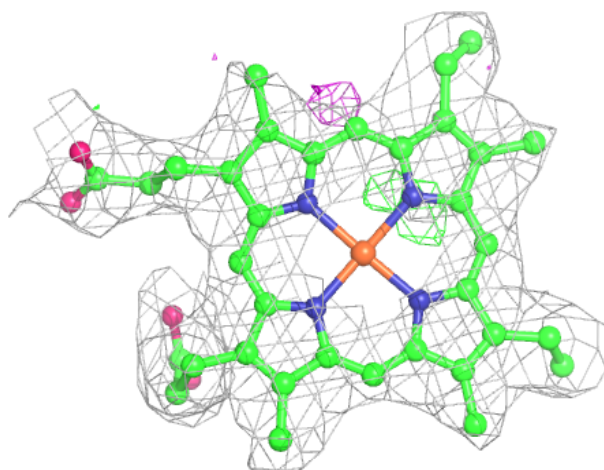
Electron density around HEC A 807:

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



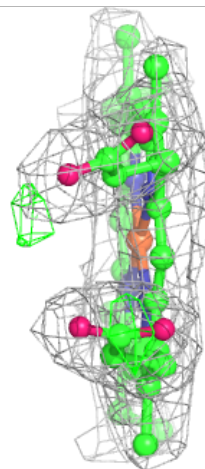
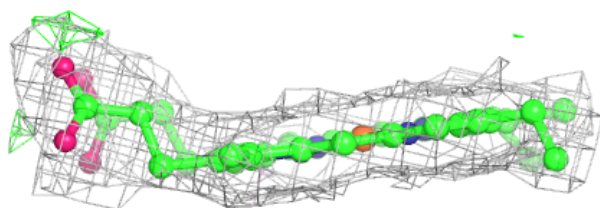
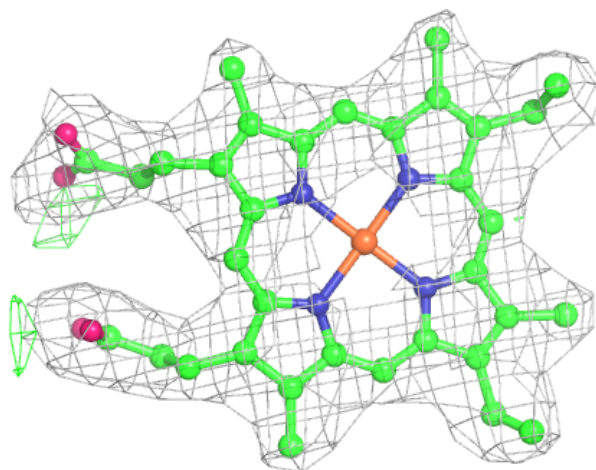
Electron density around HEC C 802:

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



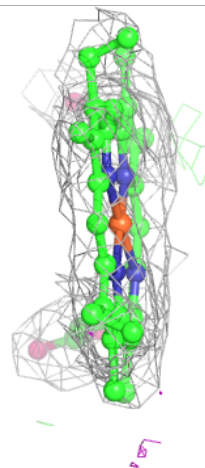
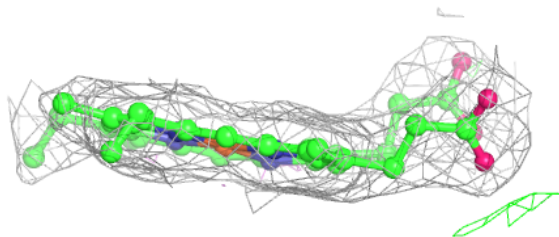
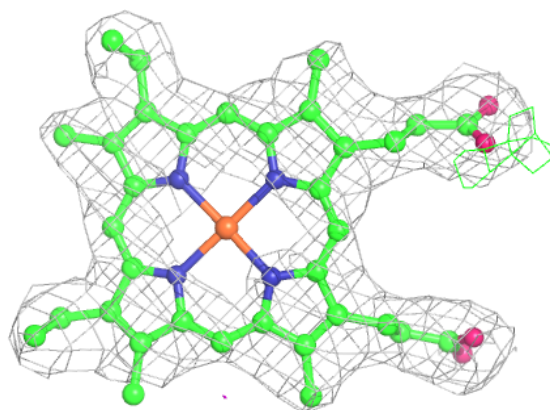
Electron density around HEC D 806:

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



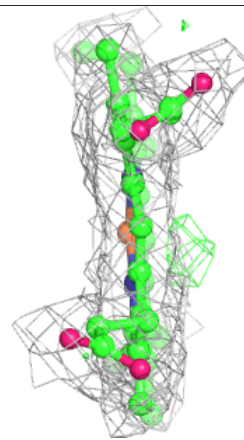
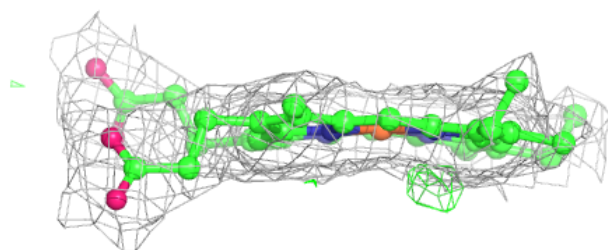
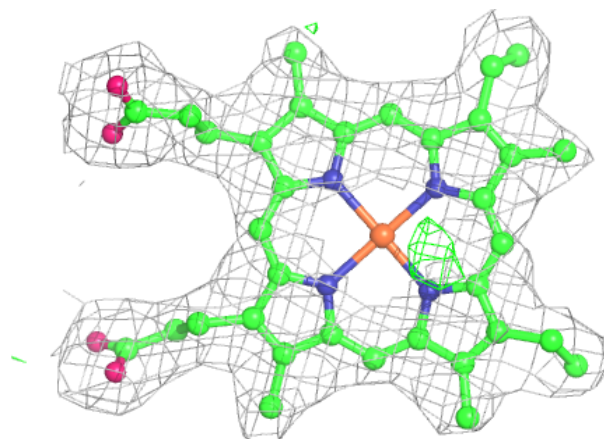
Electron density around HEC C 808:

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



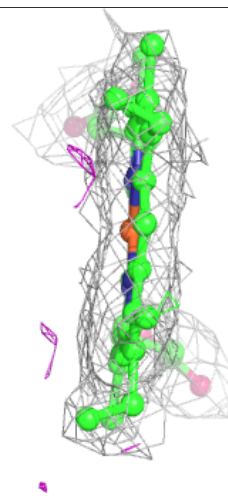
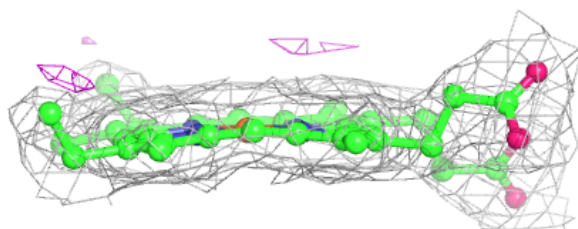
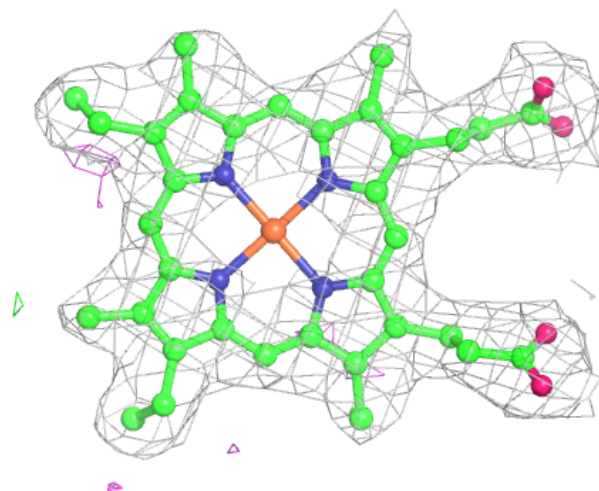
Electron density around HEC D 803:

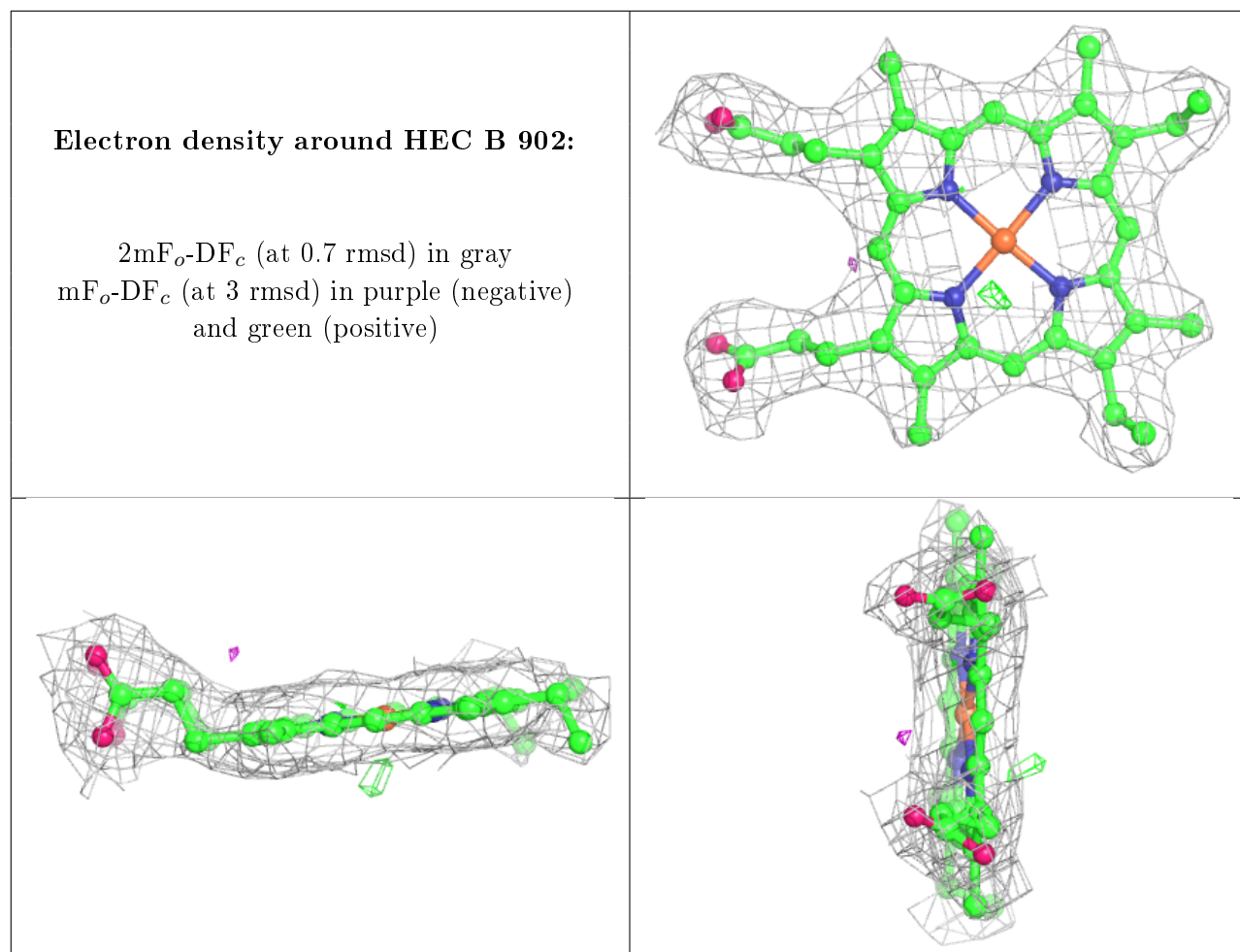
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 803:

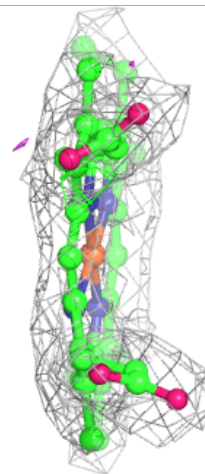
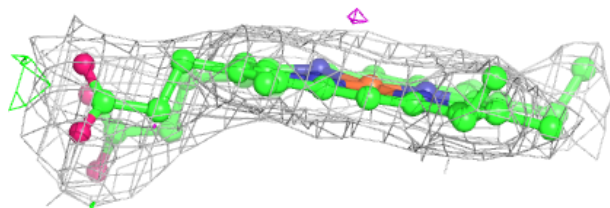
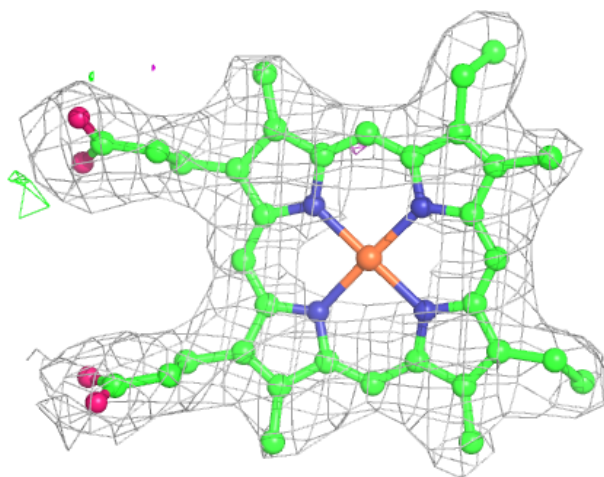
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

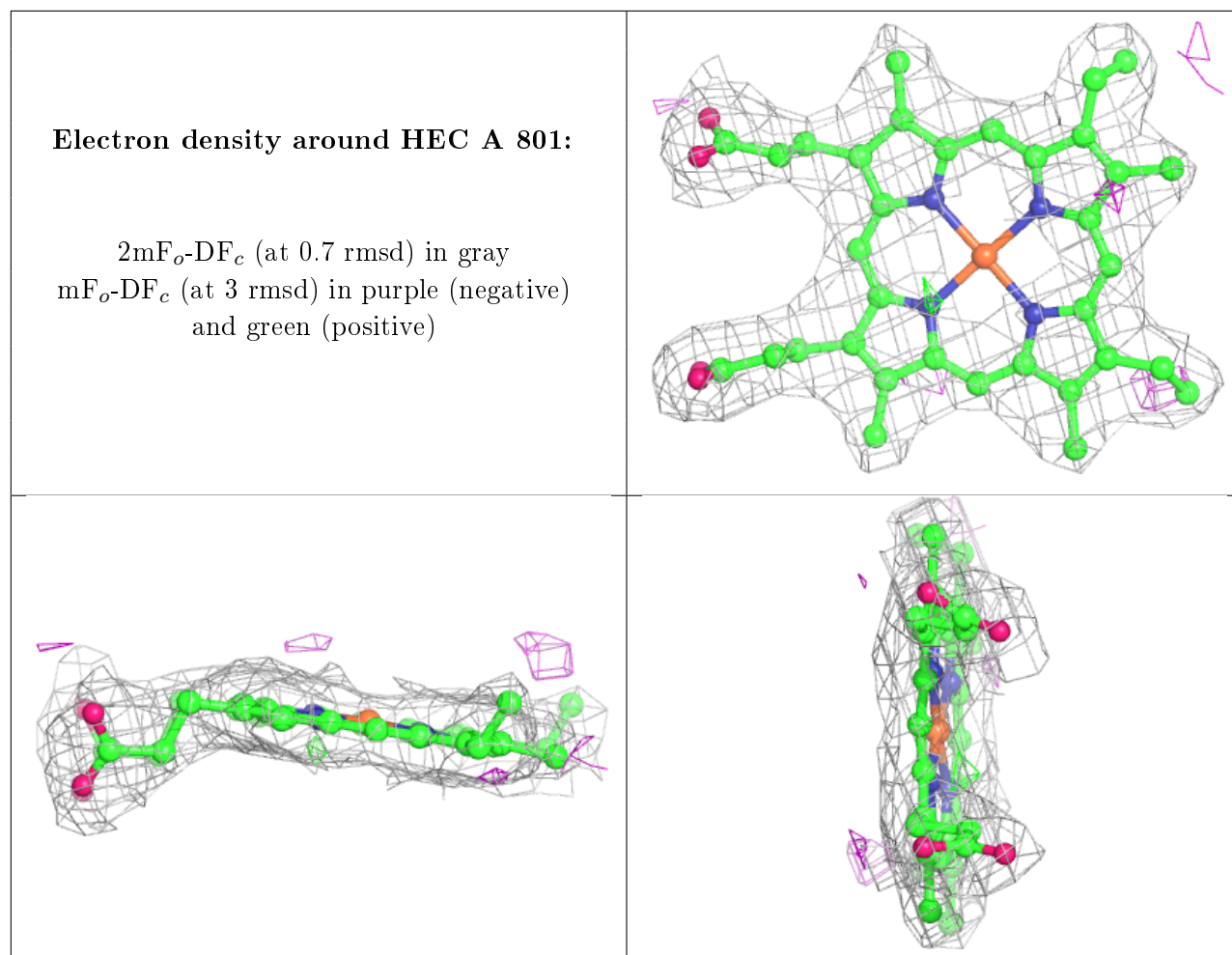


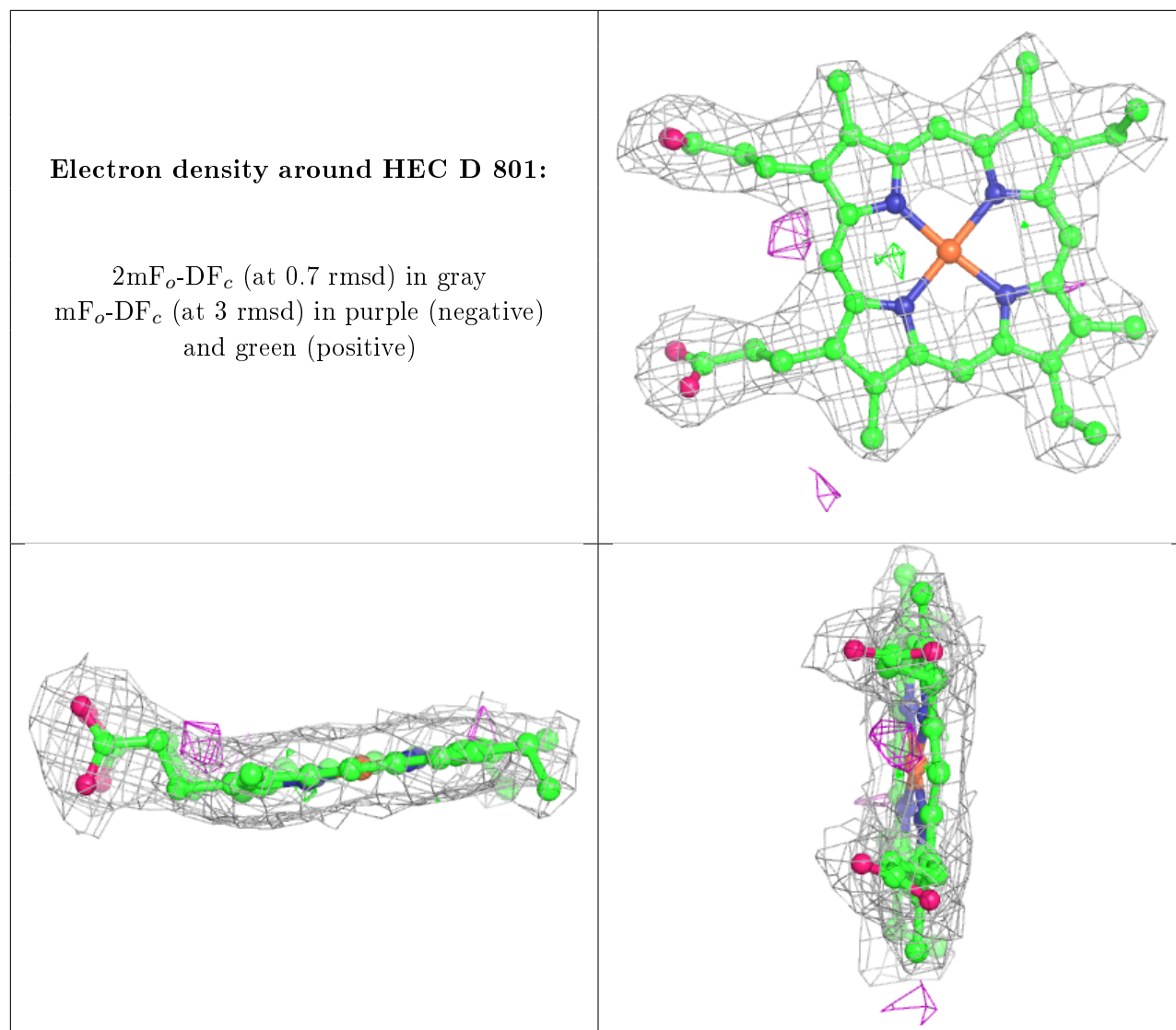


Electron density around HEC D 808:

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







6.5 Other polymers ⓘ

There are no such residues in this entry.