wwPDB X-ray Structure Validation Summary Report (i)

Dec 9, 2023 – 09:26 am GMT

PDB ID	:	1OFY
Title	:	three dimensional structure of the reduced form of nine-heme cytochrome c at ph 7.5
Authors	:	Bento, I.; Teixeira, V.H.; Baptista, A.M.; Soares, C.M.; Matias, P.M.; Carrondo, M.A.
Deposited on	:	2003-04-22
Resolution	:	2.00 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

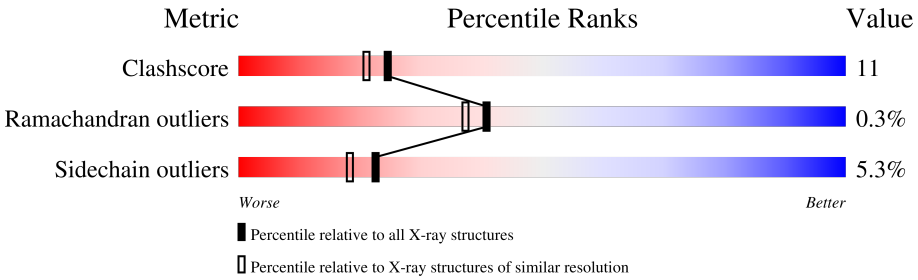
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	296	82% 15%
1	B	296	76% 21%

2 Entry composition (i)

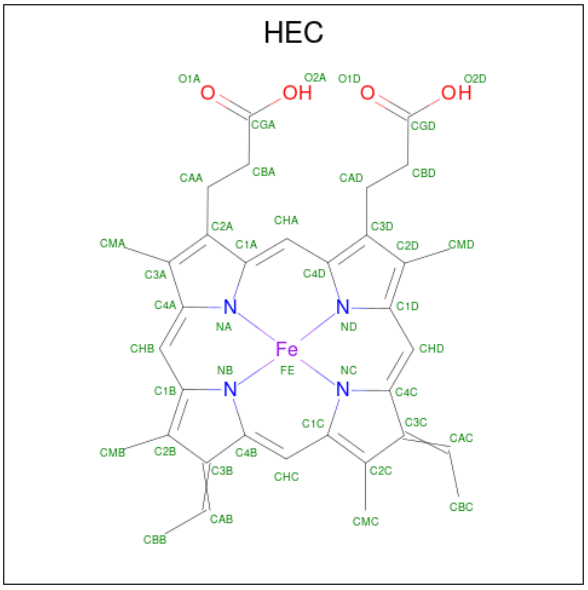
There are 5 unique types of molecules in this entry. The entry contains 5755 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NINE HEME CYTOCHROME C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	22	4	1
			2223	1363	412	420	28			
1	B	293	Total	C	N	O	S	21	5	1
			2237	1371	413	425	28			

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

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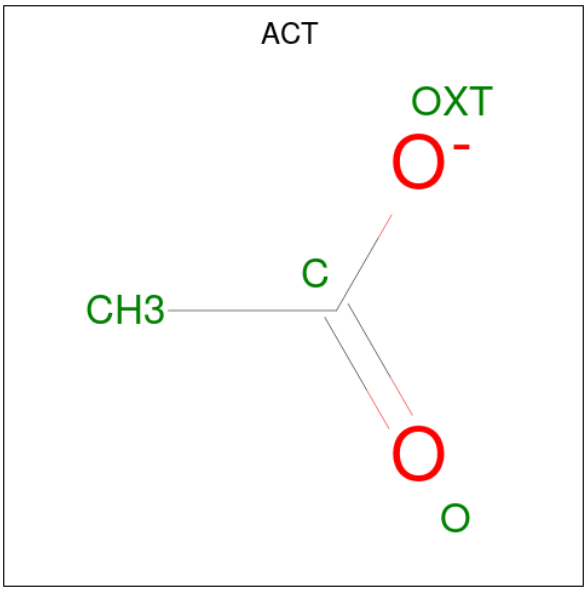
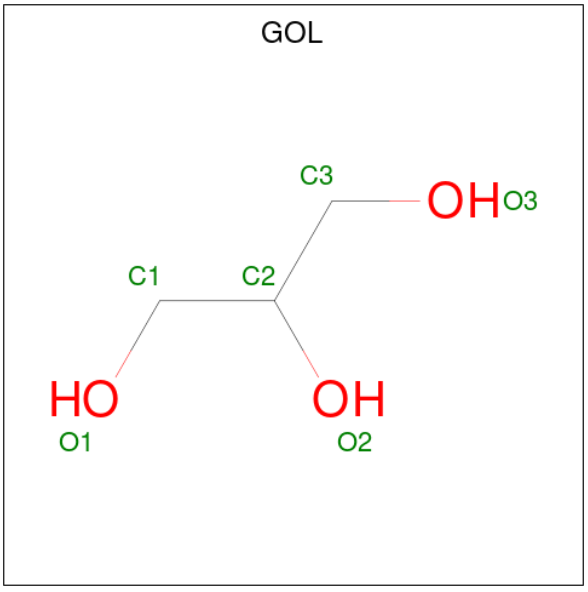
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0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

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	263	Total O 263 263	0	0
5	B	242	Total O 242 242	0	0

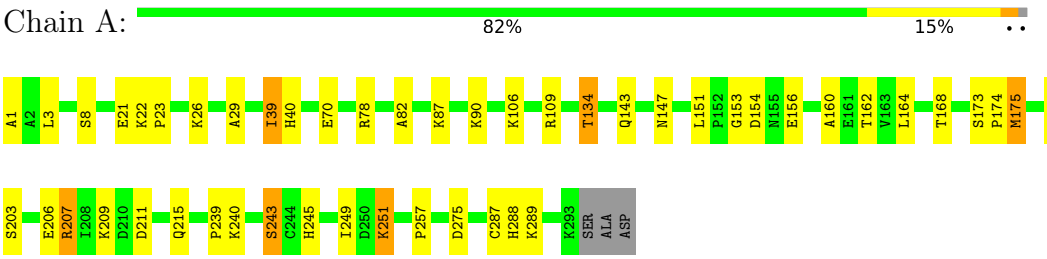
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

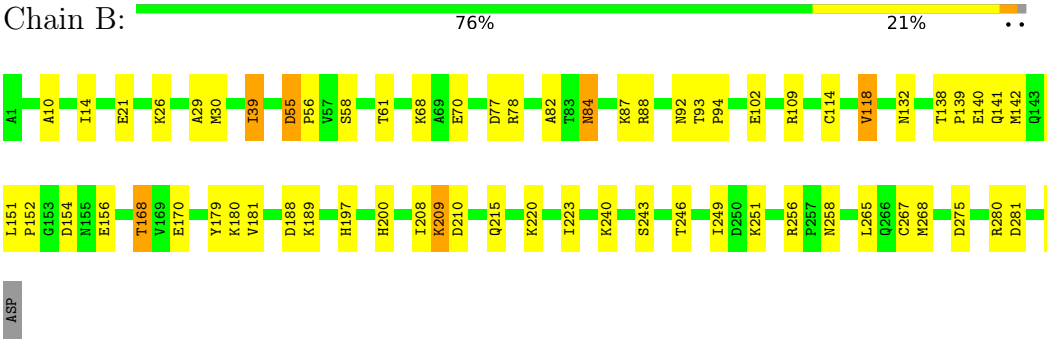
• Molecule 1: NINE HEME CYTOCHROME C

Chain A:



• Molecule 1: NINE HEME CYTOCHROME C

Chain B:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	60.40Å 105.66Å 80.94Å 90.00° 103.35° 90.00°	Depositor
Resolution (Å)	25.00 – 2.00	Depositor
% Data completeness (in resolution range)	92.7 (25.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.242 , 0.275	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5755	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, GOL, 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	0.36	0/2297	0.91	2/3117 (0.1%)
1	B	0.31	0/2304	0.86	0/3127
All	All	0.34	0/4601	0.89	2/6244 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	207	ARG	NE-CZ-NH1	7.85	124.22	120.30
1	A	1	ALA	O-C-N	5.72	131.85	122.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2223	0	2163	33	0
1	B	2237	0	2170	46	0
2	A	387	0	270	23	0
2	B	387	0	270	27	0
3	A	4	0	3	1	0
4	A	6	0	8	0	0
4	B	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	263	0	0	8	0
5	B	242	0	0	8	0
All	All	5755	0	4892	110	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 11.

The worst 5 of 110 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ARG:HH21	1:A:275:ASP:HB2	1.45	0.80
1:B:138:THR:OG1	1:B:141:GLN:HG3	1.84	0.78
1:B:68:LYS:HG3	1:B:70:GLU:OE1	1.85	0.76
1:A:39:ILE:HD12	2:A:1295:HEC:HBD1	1.70	0.74
1:B:152:PRO:O	1:B:156:GLU:HG3	1.90	0.71

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	295/296 (100%)	288 (98%)	7 (2%)	0	100	100
1	B	296/296 (100%)	281 (95%)	13 (4%)	2 (1%)	22	16
All	All	591/592 (100%)	569 (96%)	20 (3%)	2 (0%)	41	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	188	ASP
1	B	292	PRO

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	250/249 (100%)	239 (96%)	11 (4%)	28 25
1	B	251/249 (101%)	235 (94%)	16 (6%)	17 13
All	All	501/498 (101%)	474 (95%)	27 (5%)	22 18

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	84	ASN
1	B	168	THR
1	B	256	ARG
1	B	118	VAL
1	B	170	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	B	72	ASN
1	B	194	ASN
1	B	215	GLN
1	B	266	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

21 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	HEC	A	1301	1	32,50,50	1.78	2 (6%)	24,82,82	2.13	9 (37%)
4	GOL	B	1302	-	5,5,5	0.21	0	5,5,5	0.50	0
2	HEC	B	1298	1	32,50,50	1.71	2 (6%)	24,82,82	1.64	6 (25%)
2	HEC	A	1295	1	32,50,50	1.76	2 (6%)	24,82,82	2.00	6 (25%)
2	HEC	B	1299	1	32,50,50	1.69	2 (6%)	24,82,82	1.83	7 (29%)
2	HEC	B	1294	1	32,50,50	1.67	2 (6%)	24,82,82	1.41	5 (20%)
2	HEC	A	1297	1	32,50,50	1.65	2 (6%)	24,82,82	1.43	6 (25%)
2	HEC	A	1294	1	32,50,50	1.71	2 (6%)	24,82,82	1.60	3 (12%)
2	HEC	A	1293	1	32,50,50	1.75	2 (6%)	24,82,82	1.36	5 (20%)
2	HEC	B	1300	1	32,50,50	1.80	2 (6%)	24,82,82	1.67	5 (20%)
2	HEC	B	1295	1	32,50,50	1.81	2 (6%)	24,82,82	1.93	6 (25%)
2	HEC	A	1300	1	32,50,50	1.82	2 (6%)	24,82,82	1.92	6 (25%)
4	GOL	A	1303	-	5,5,5	0.15	0	5,5,5	0.35	0
2	HEC	A	1298	1	32,50,50	1.79	2 (6%)	24,82,82	1.45	4 (16%)
2	HEC	A	1299	1	32,50,50	1.75	2 (6%)	24,82,82	1.73	7 (29%)
2	HEC	B	1296	1	32,50,50	1.68	2 (6%)	24,82,82	1.43	4 (16%)
2	HEC	B	1297	1	32,50,50	1.77	2 (6%)	24,82,82	1.37	5 (20%)
3	ACT	A	1302	-	3,3,3	1.18	0	3,3,3	0.72	0
2	HEC	A	1296	1	32,50,50	1.75	2 (6%)	24,82,82	1.59	9 (37%)
2	HEC	B	1293	1	32,50,50	1.69	2 (6%)	24,82,82	2.05	6 (25%)
2	HEC	B	1301	1	32,50,50	1.74	2 (6%)	24,82,82	1.78	5 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	A	1301	1	-	1/10/54/54	-
2	HEC	A	1296	1	-	4/10/54/54	-
4	GOL	B	1302	-	-	2/4/4/4	-
2	HEC	B	1298	1	-	1/10/54/54	-
2	HEC	A	1295	1	-	4/10/54/54	-
2	HEC	B	1299	1	-	3/10/54/54	-
2	HEC	B	1294	1	-	3/10/54/54	-
2	HEC	A	1297	1	-	4/10/54/54	-
2	HEC	A	1294	1	-	0/10/54/54	-
2	HEC	A	1293	1	-	3/10/54/54	-
2	HEC	B	1300	1	-	5/10/54/54	-
2	HEC	B	1295	1	-	4/10/54/54	-
2	HEC	A	1300	1	-	4/10/54/54	-
2	HEC	A	1298	1	-	0/10/54/54	-
2	HEC	A	1299	1	-	4/10/54/54	-
2	HEC	B	1296	1	-	4/10/54/54	-
2	HEC	B	1297	1	-	4/10/54/54	-
4	GOL	A	1303	-	-	2/4/4/4	-
2	HEC	B	1293	1	-	3/10/54/54	-
2	HEC	B	1301	1	-	1/10/54/54	-

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1300	HEC	C3C-C2C	-6.26	1.34	1.40
2	B	1295	HEC	C3C-C2C	-6.23	1.34	1.40
2	B	1297	HEC	C2B-C3B	-6.19	1.34	1.40
2	A	1298	HEC	C3C-C2C	-6.04	1.34	1.40
2	A	1301	HEC	C2B-C3B	-6.01	1.34	1.40

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1293	HEC	CMB-C2B-C3B	5.22	131.95	125.82
2	A	1300	HEC	CMC-C2C-C3C	5.11	131.83	125.82
2	B	1293	HEC	CMB-C2B-C1B	-4.80	121.09	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1301	HEC	CMC-C2C-C3C	4.73	131.38	125.82
2	A	1301	HEC	CMD-C2D-C1D	-4.57	121.45	128.46

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1294	HEC	C3D-CAD-CBD-CGD
4	A	1303	GOL	O1-C1-C2-C3
2	B	1300	HEC	C2A-CAA-CBA-CGA
4	B	1302	GOL	O1-C1-C2-C3
4	A	1303	GOL	O1-C1-C2-O2

There are no ring outliers.

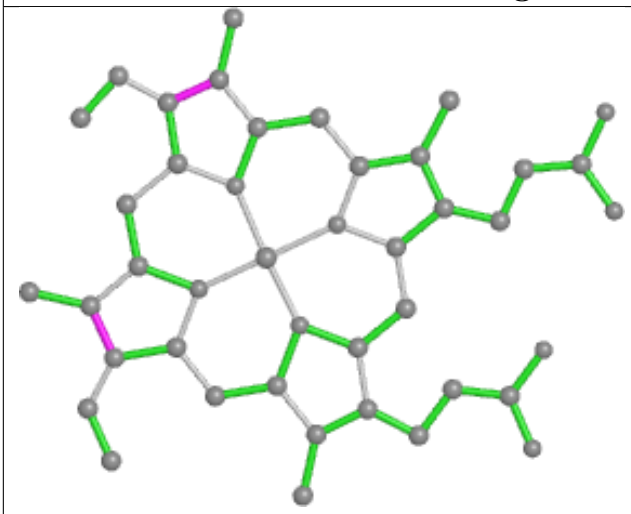
20 monomers are involved in 52 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301	HEC	2	0
4	B	1302	GOL	1	0
2	B	1298	HEC	5	0
2	A	1295	HEC	4	0
2	B	1299	HEC	2	0
2	B	1294	HEC	2	0
2	A	1297	HEC	3	0
2	A	1294	HEC	2	0
2	A	1293	HEC	3	0
2	B	1300	HEC	4	0
2	B	1295	HEC	3	0
2	A	1300	HEC	3	0
2	A	1298	HEC	2	0
2	A	1299	HEC	2	0
2	B	1296	HEC	4	0
2	B	1297	HEC	3	0
3	A	1302	ACT	1	0
2	A	1296	HEC	2	0
2	B	1293	HEC	2	0
2	B	1301	HEC	2	0

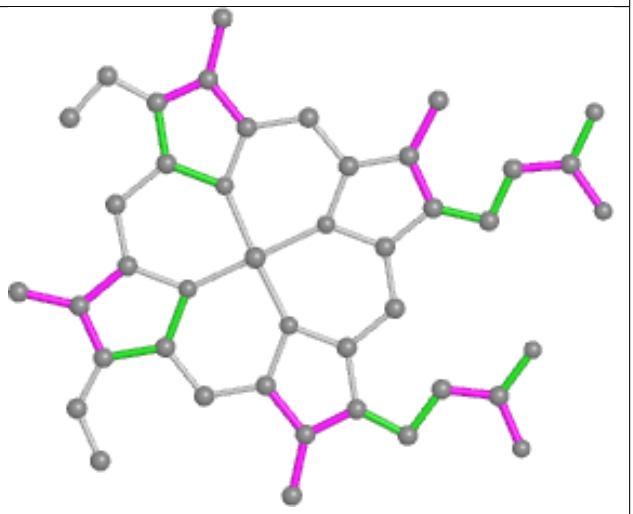
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

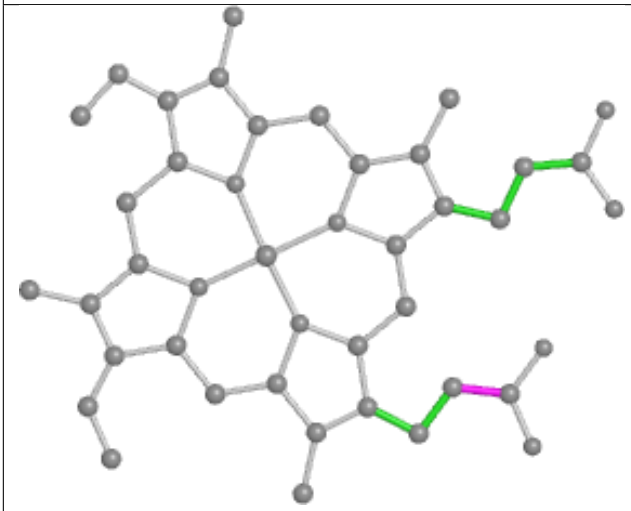
Ligand HEC A 1301



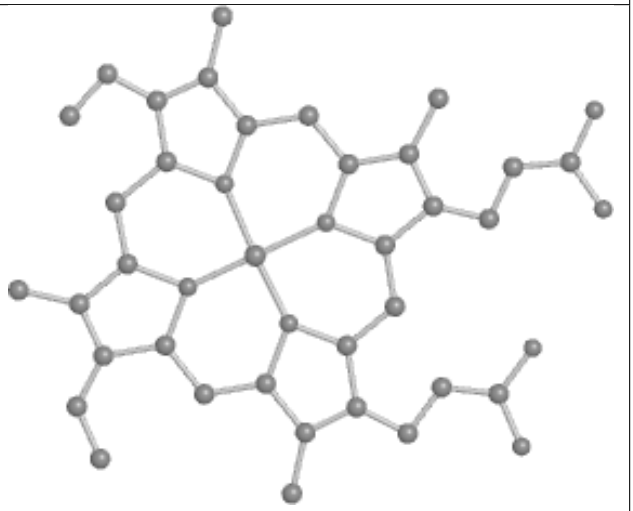
Bond lengths



Bond angles

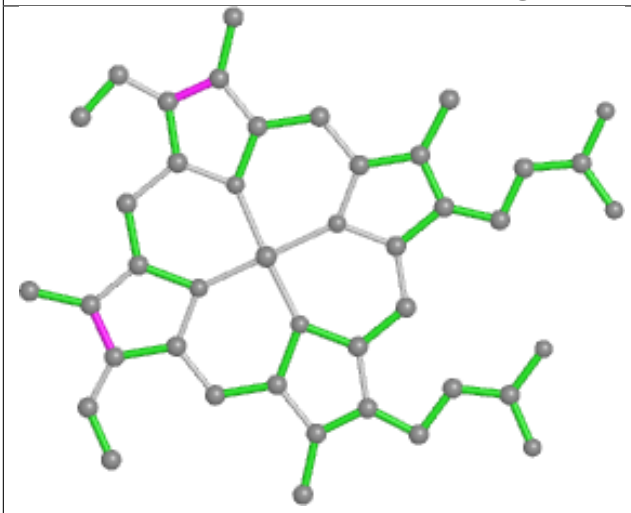


Torsions

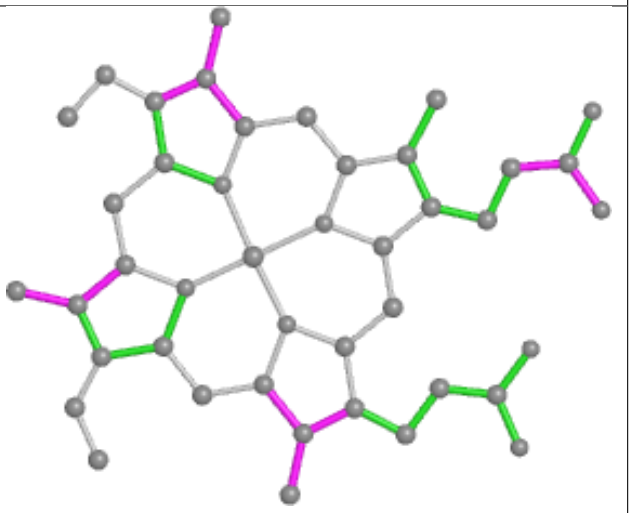


Rings

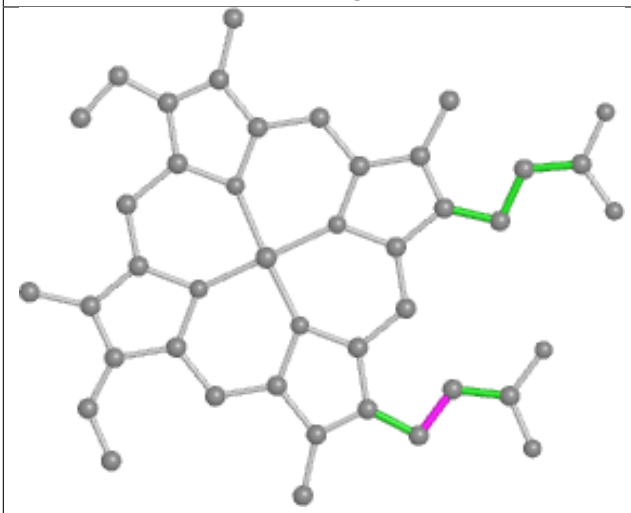
Ligand HEC B 1298



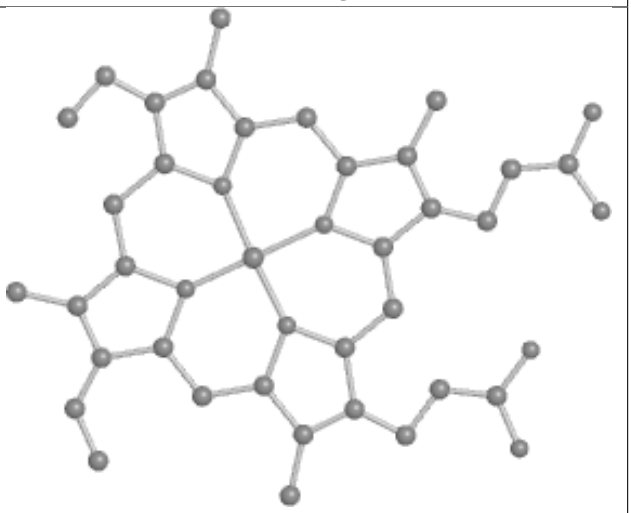
Bond lengths



Bond angles

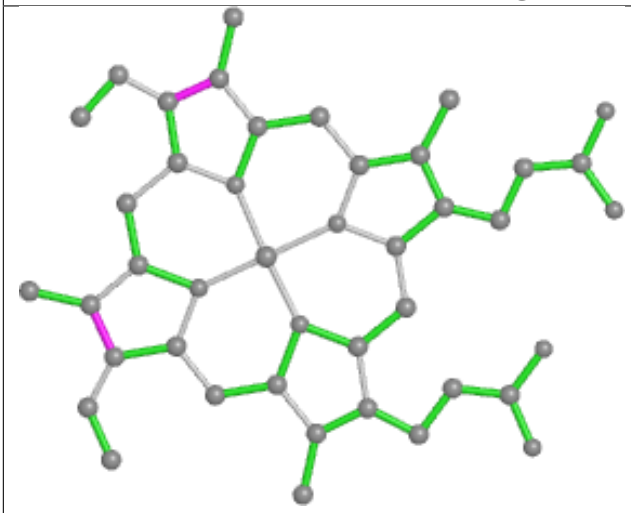


Torsions



Rings

Ligand HEC A 1295



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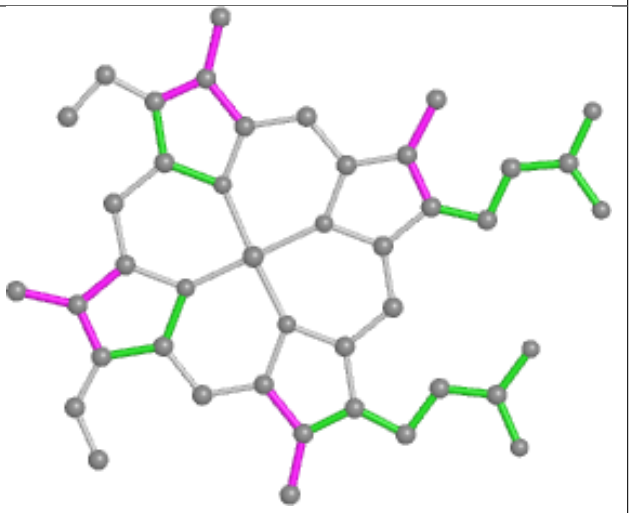
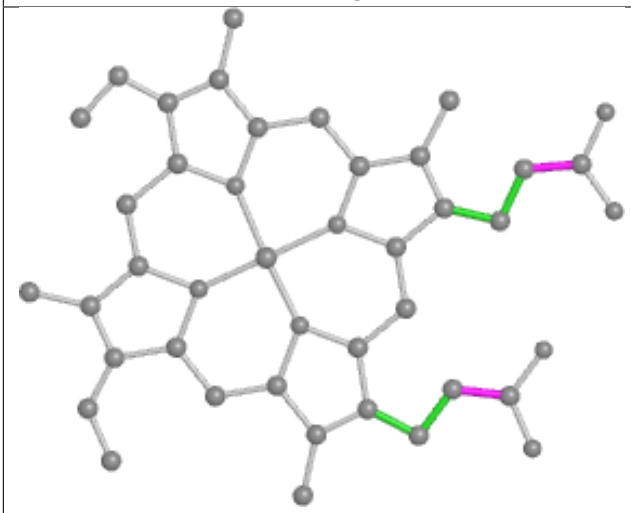


Bond angles



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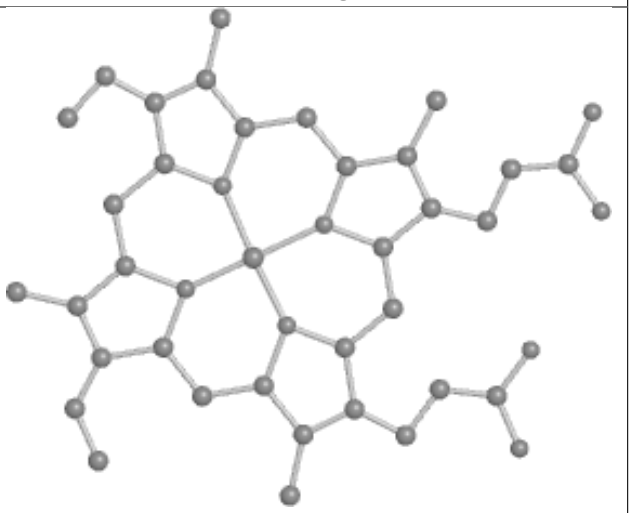
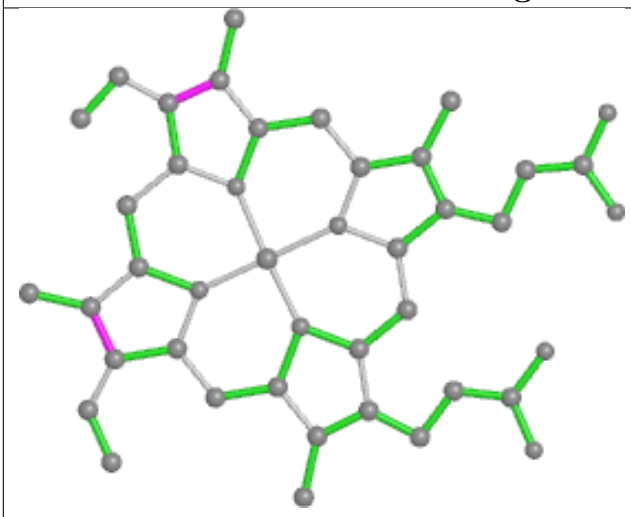


Rings

Ligand HEC B 1299



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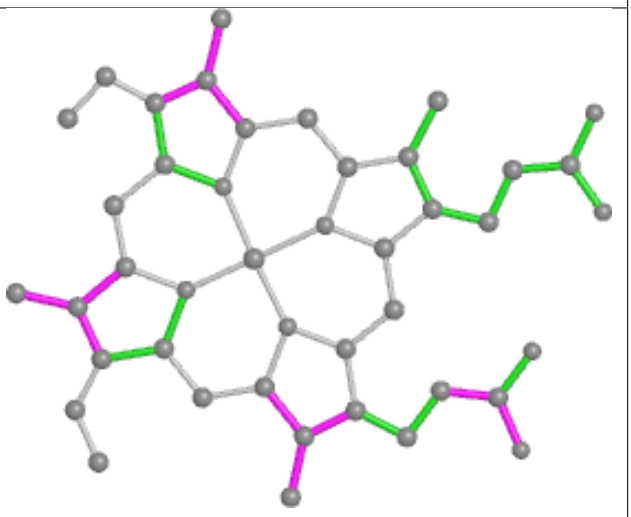
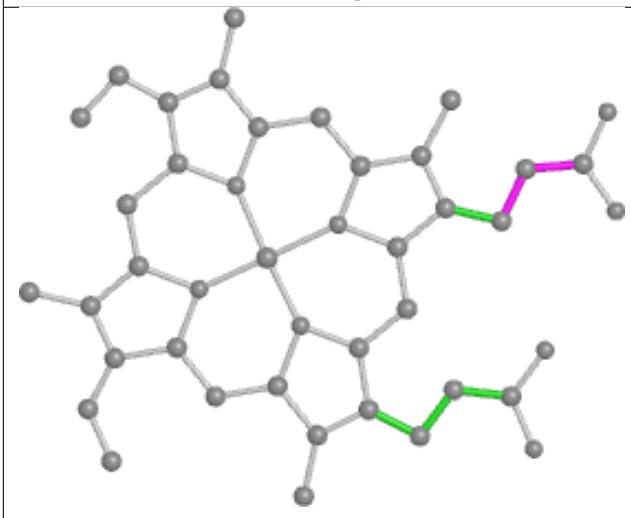


Bond angles



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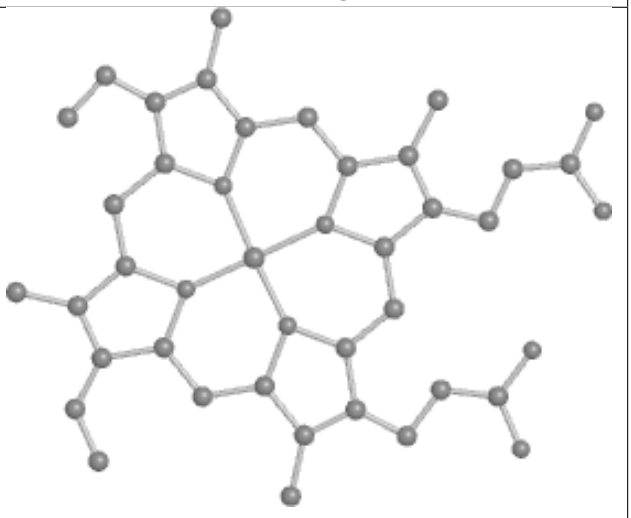
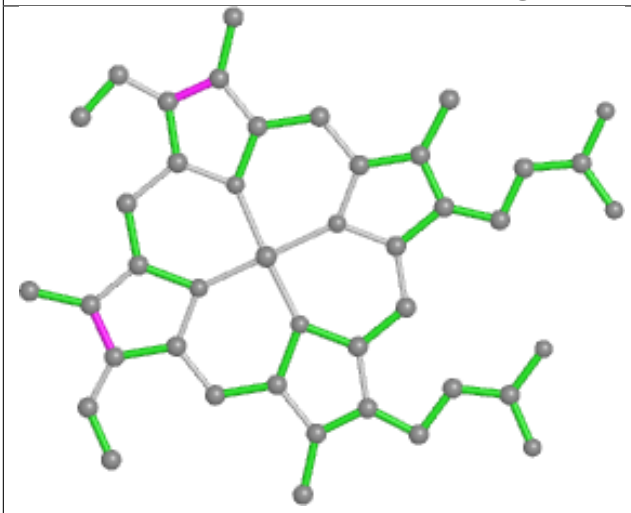
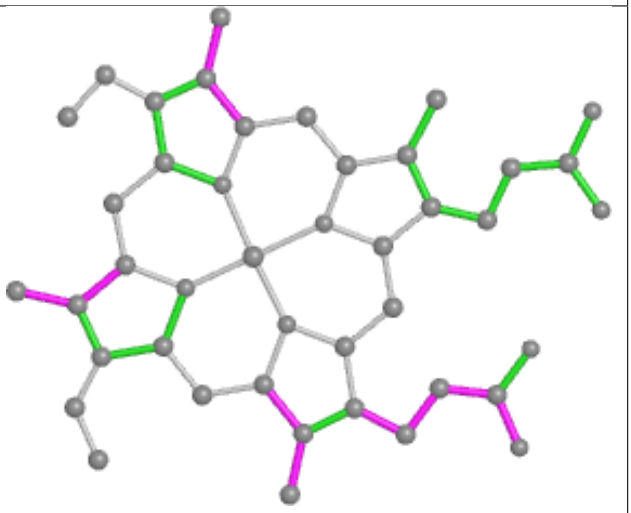


Rings

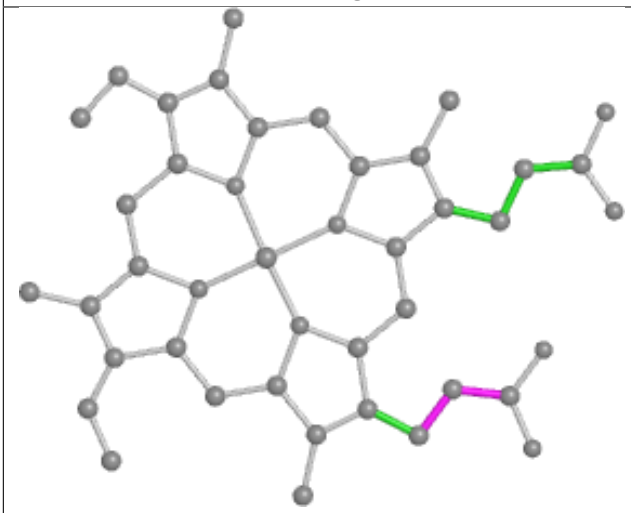
Ligand HEC B 1294



Bond lengths



Bond angles



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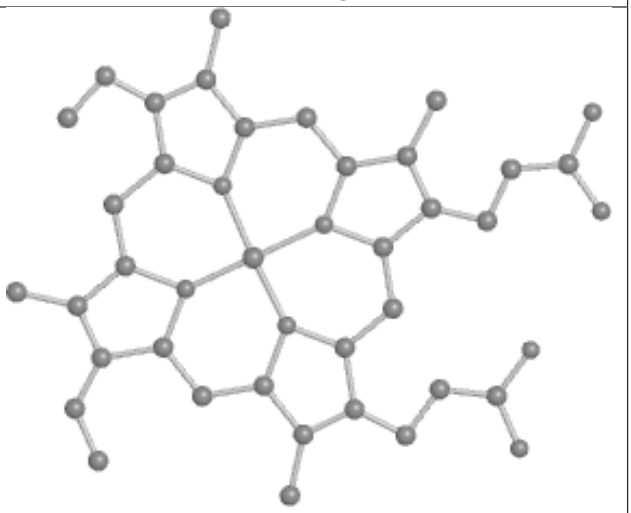
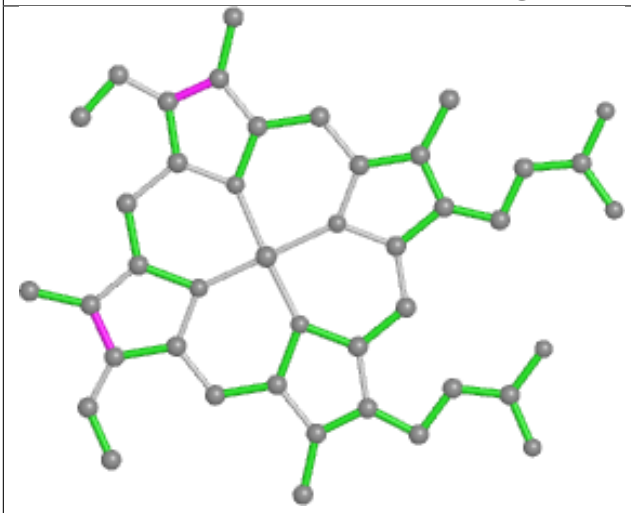


Rings

Ligand HEC A 1297



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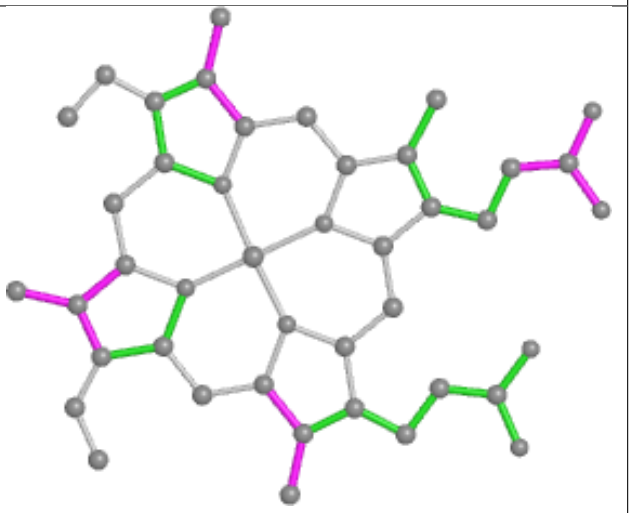
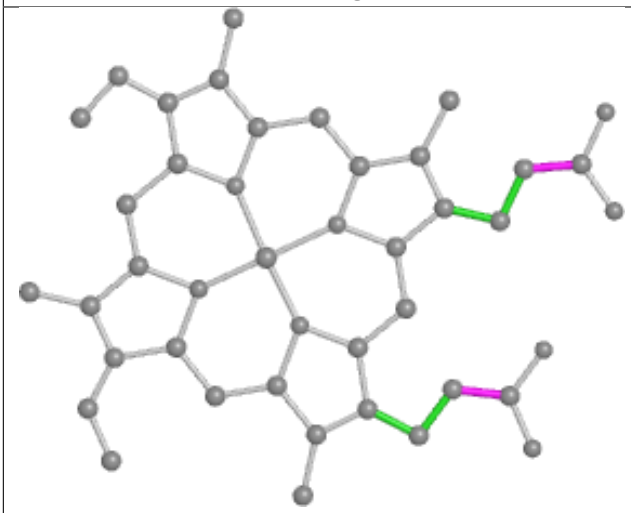


Bond angles



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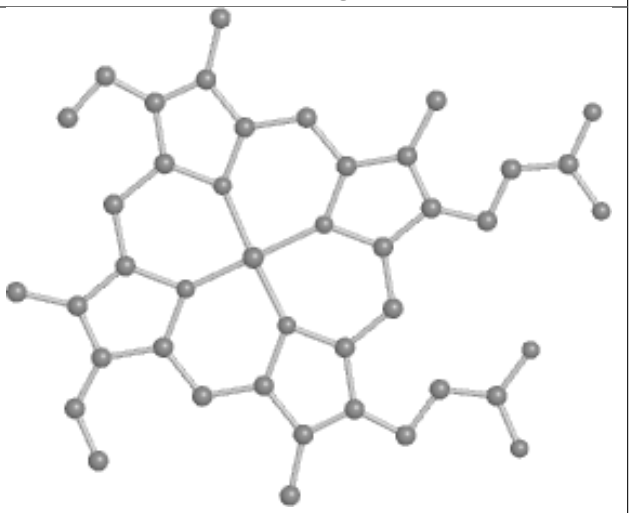
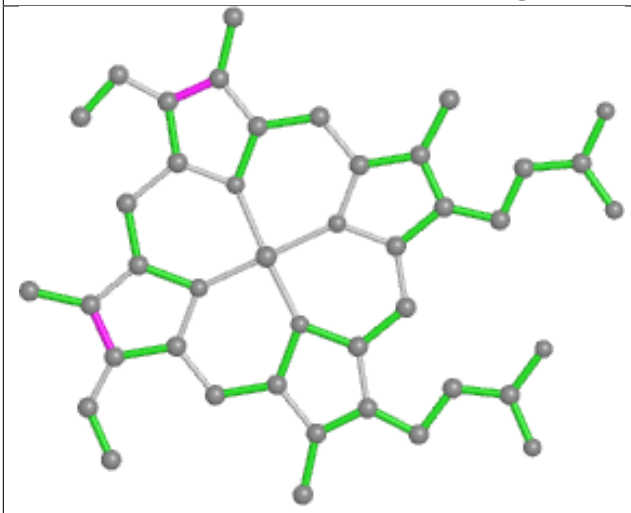


Rings

Ligand HEC A 1294



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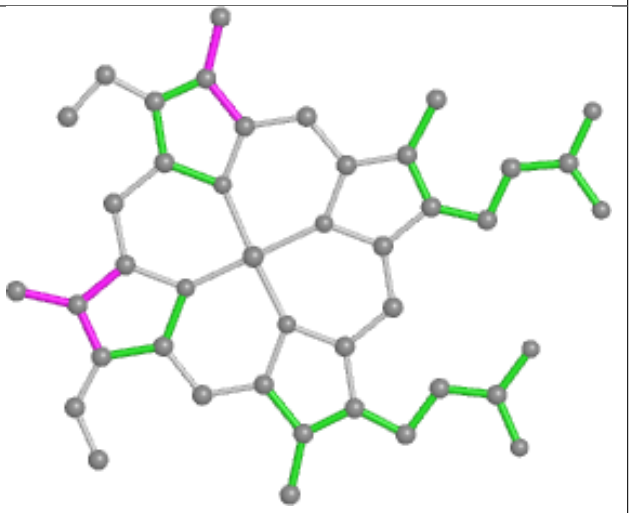

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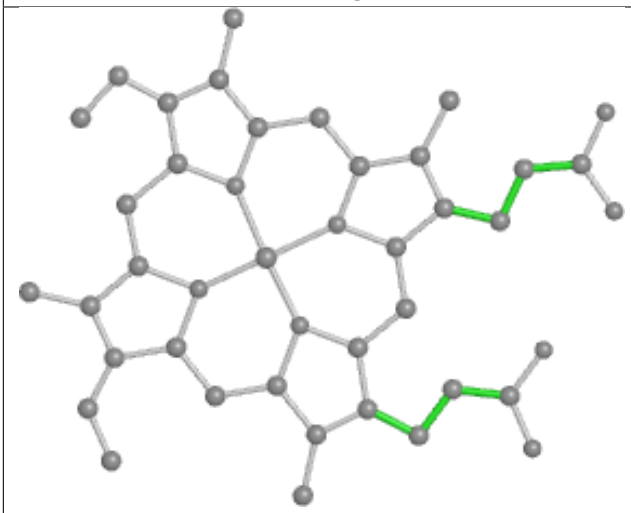
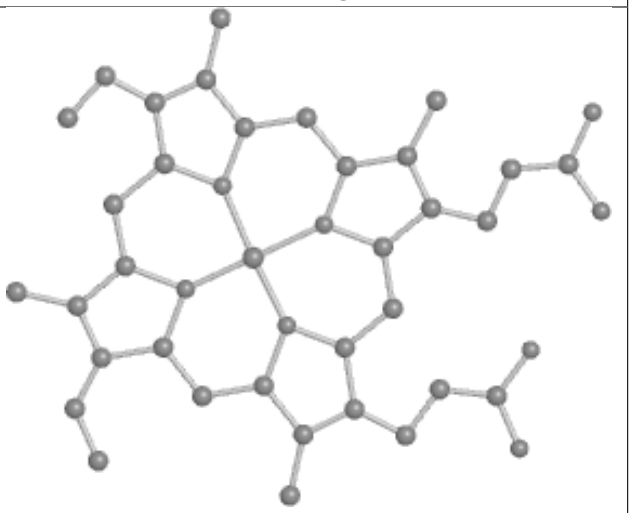
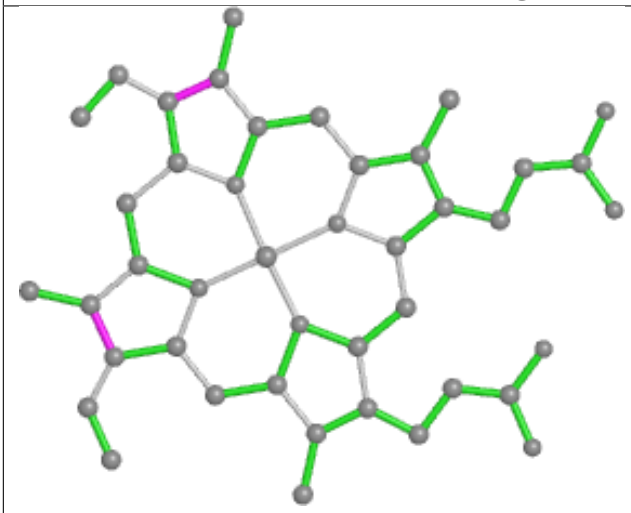


Torsions



Rings

Ligand HEC A 1293



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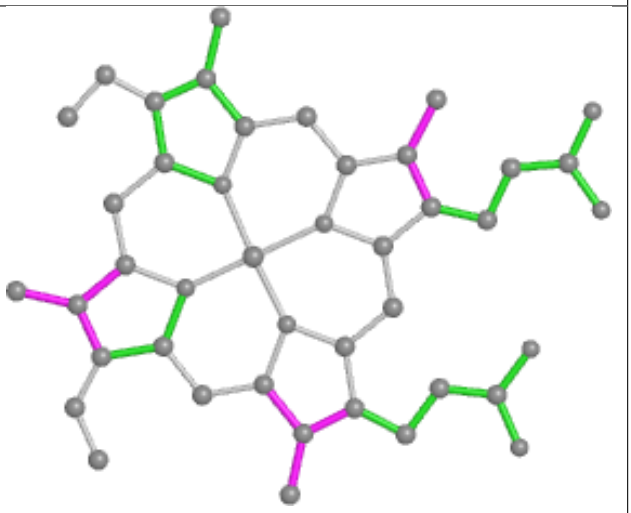
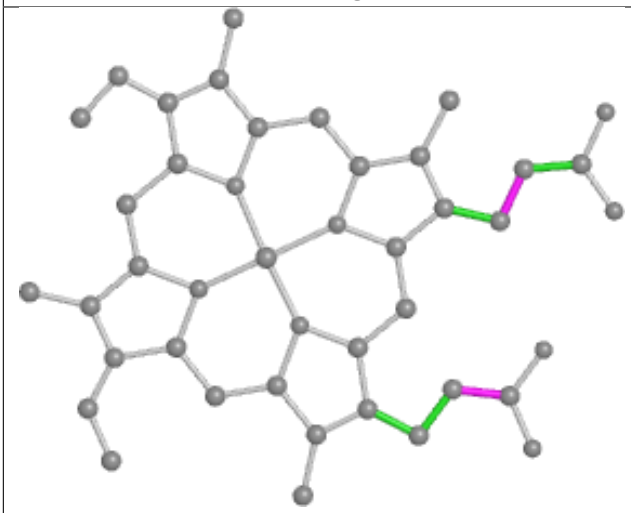


Bond angles



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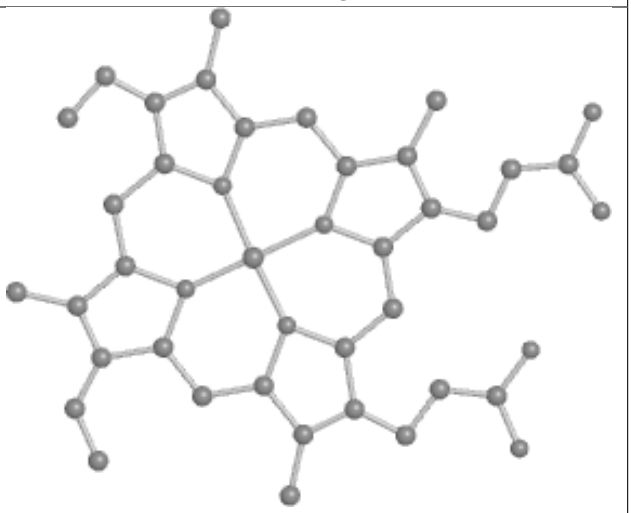
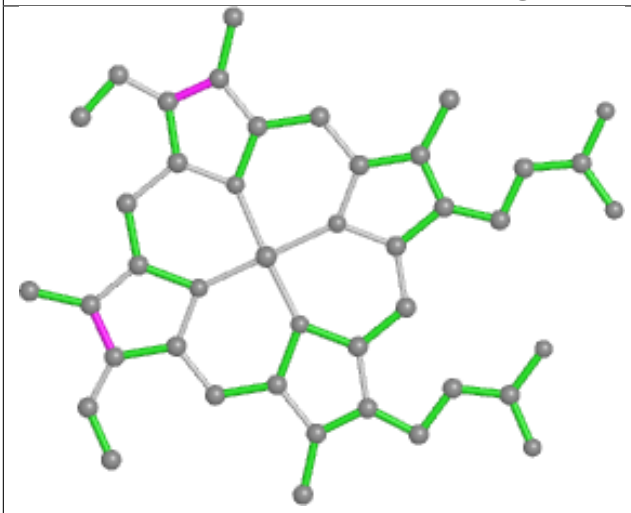


Rings

Ligand HEC B 1300



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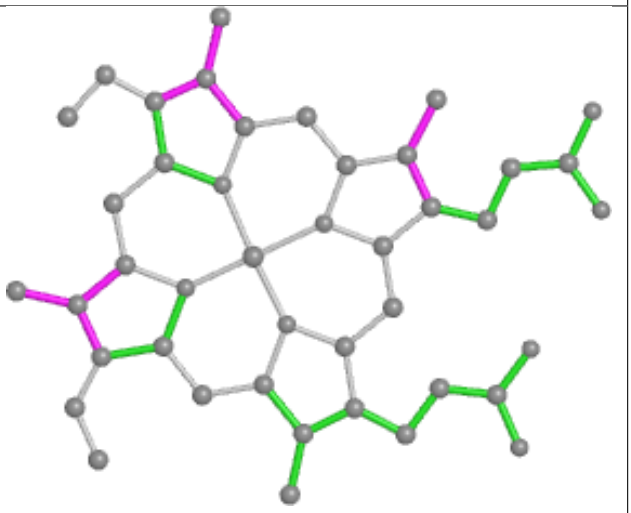
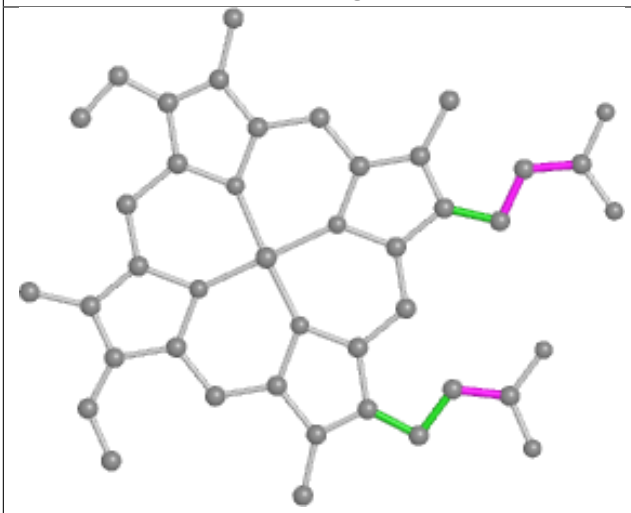


Bond angles



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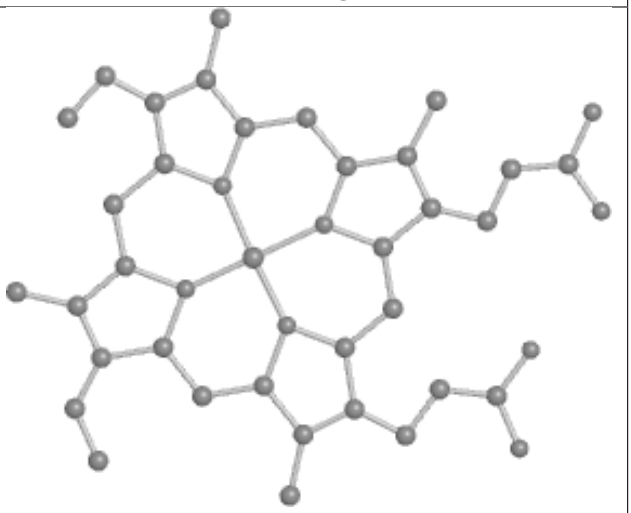
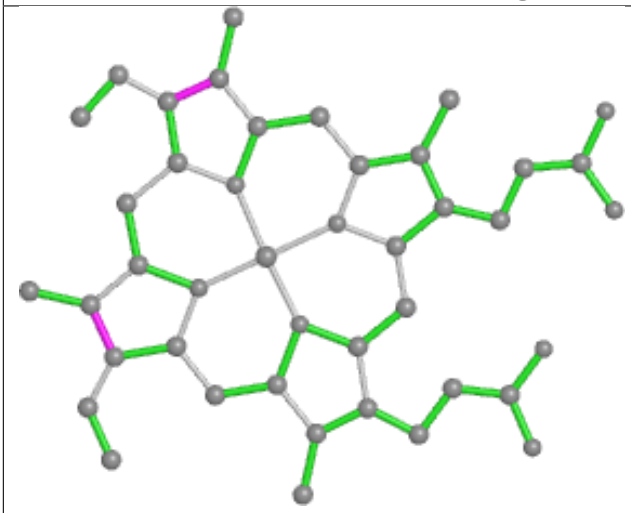
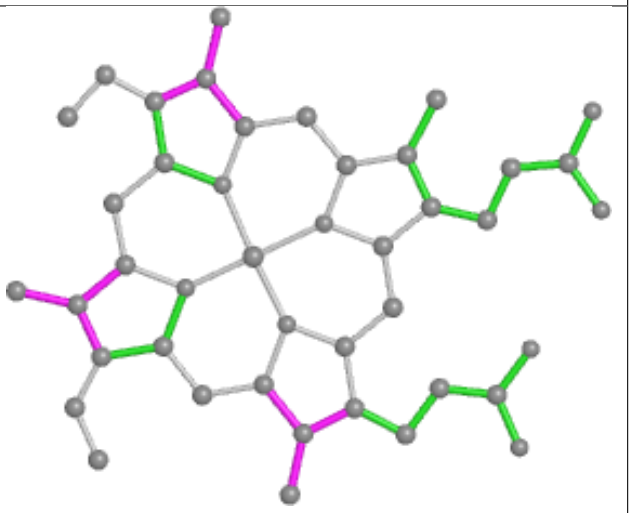


Rings

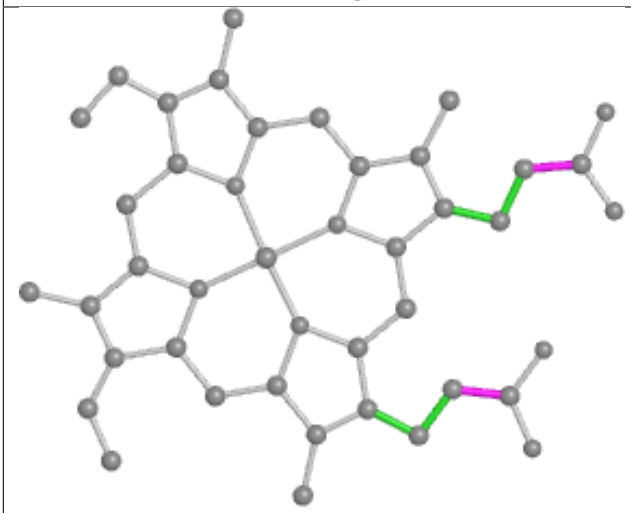
Ligand HEC B 1295



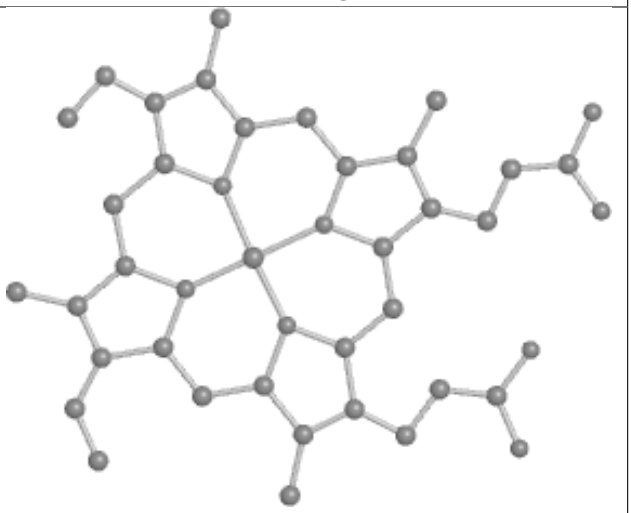
Bond lengths



Bond angles

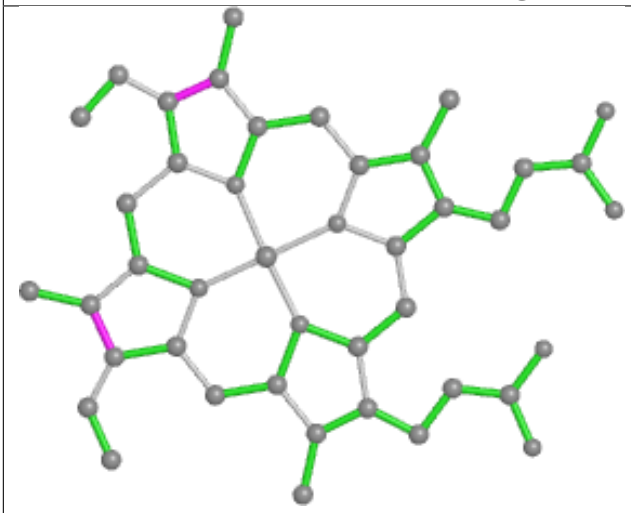


Torsions



Rings

Ligand HEC A 1300



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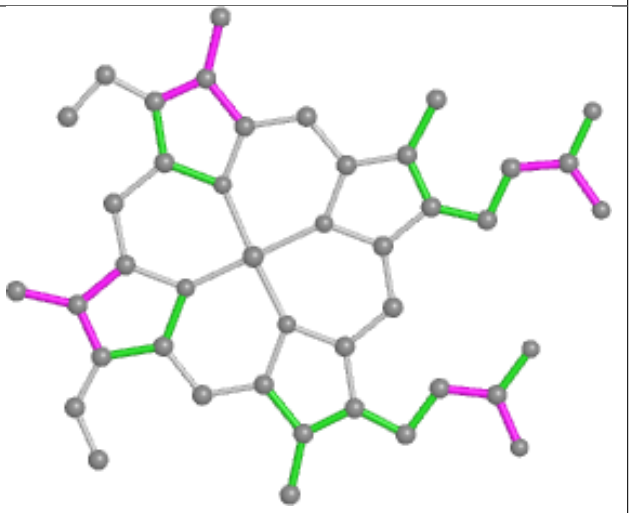
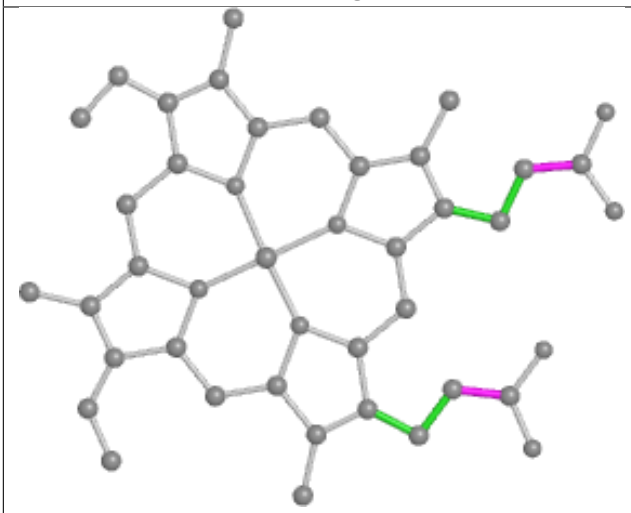
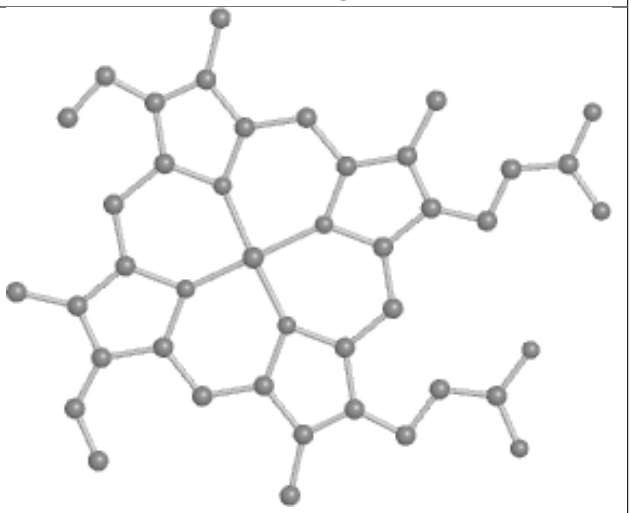


Bond angles

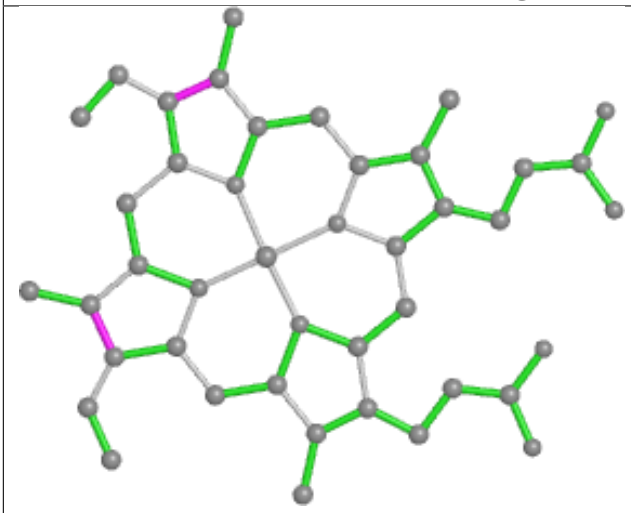


Torsions



Rings

Ligand HEC A 1298



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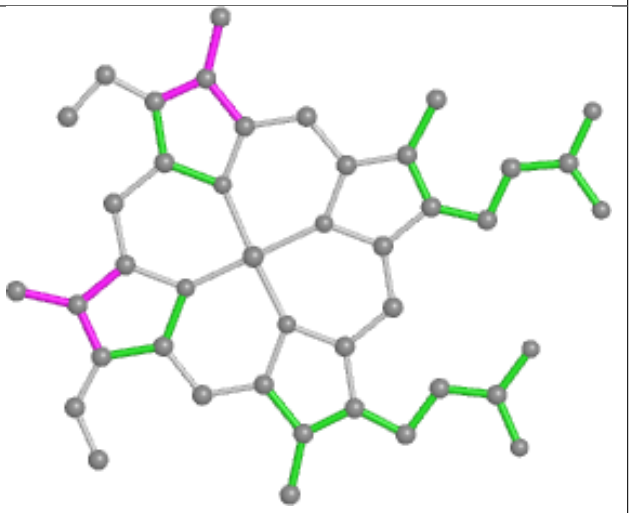
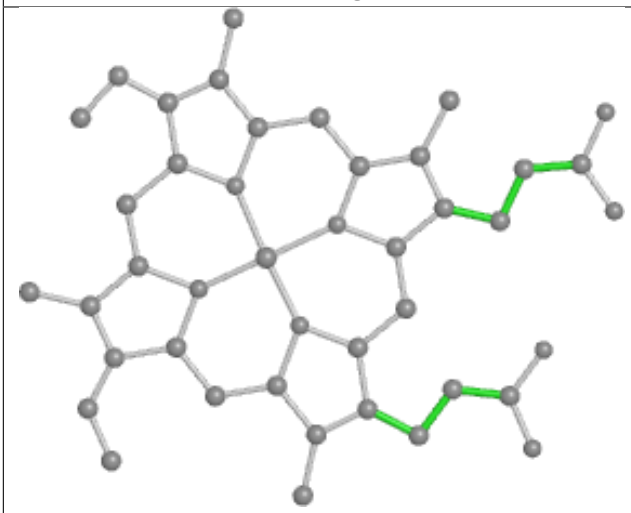


Bond angles



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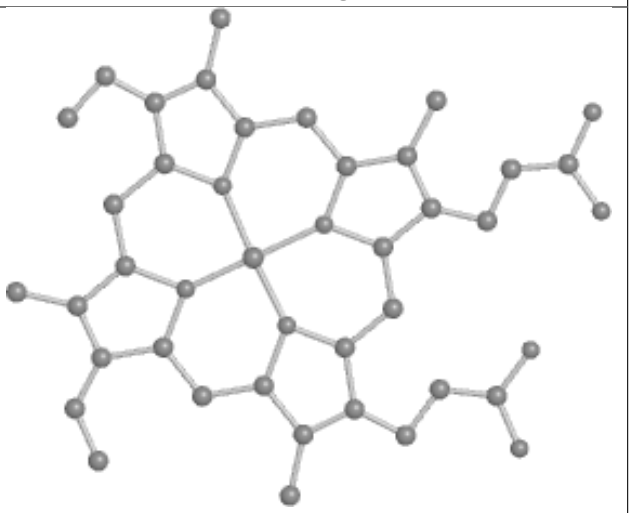
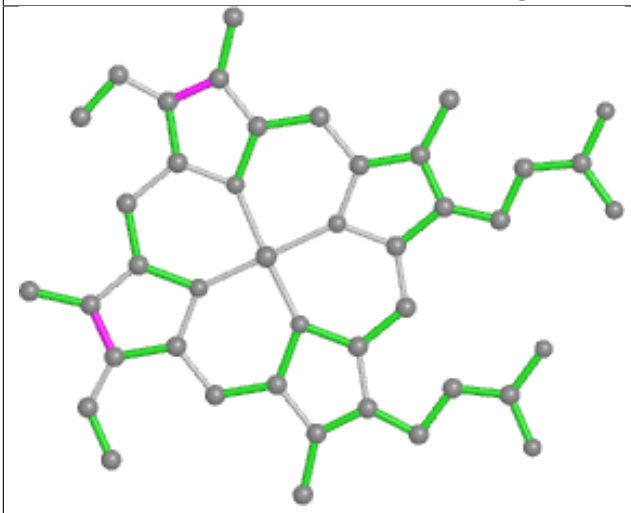


Rings

Ligand HEC A 1299



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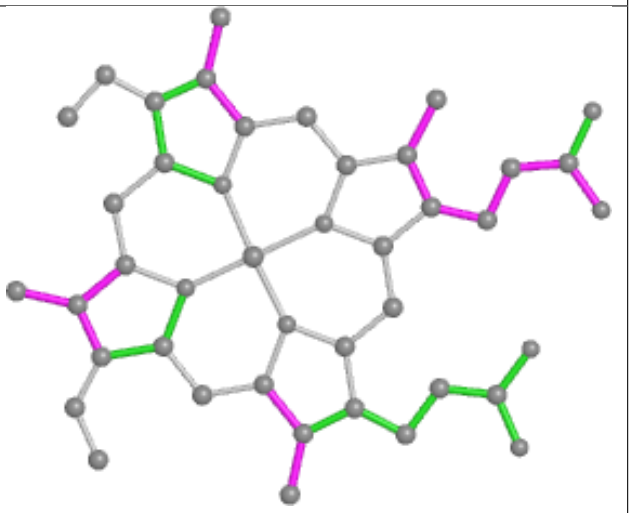
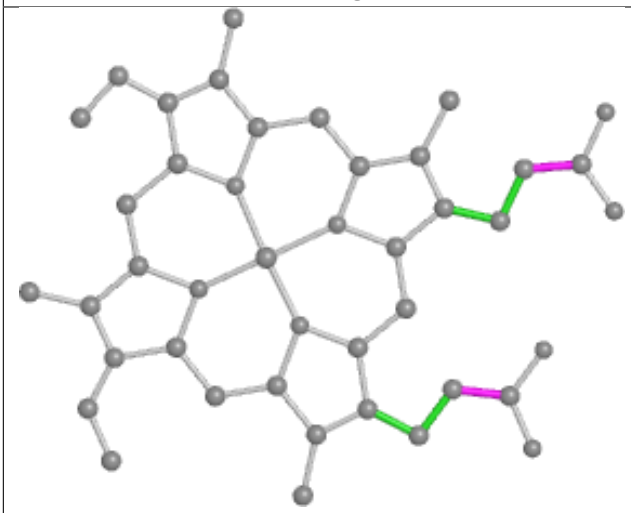
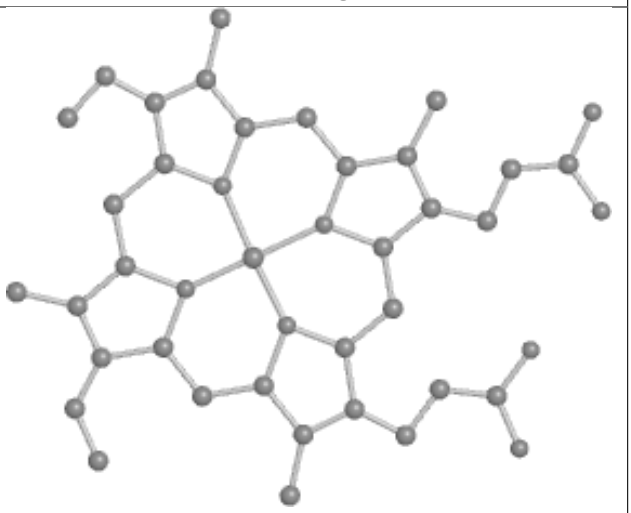


Bond angles

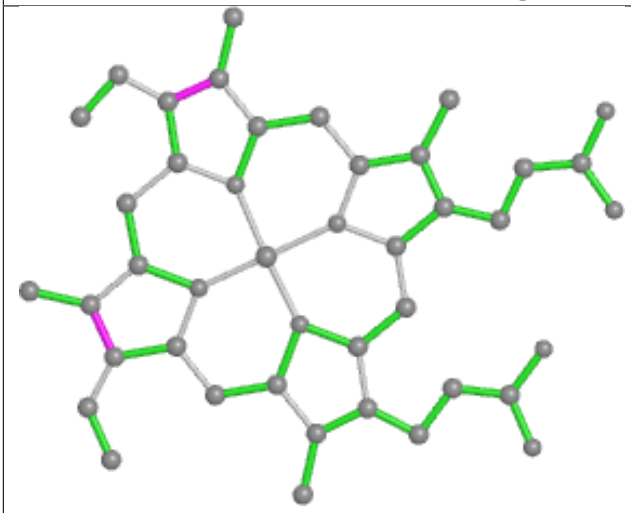


Torsions

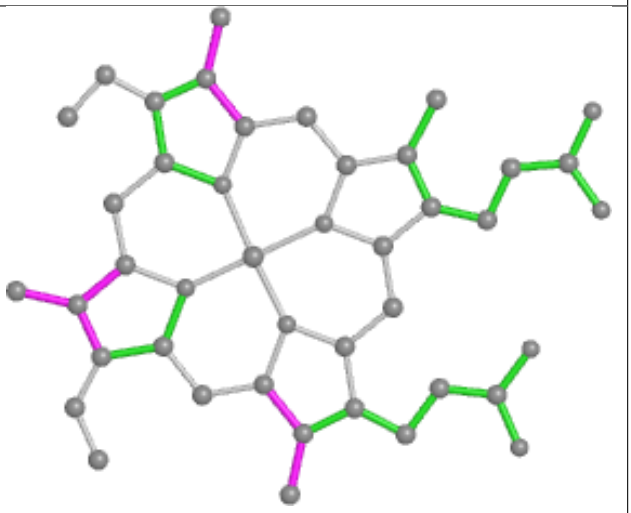


Rings

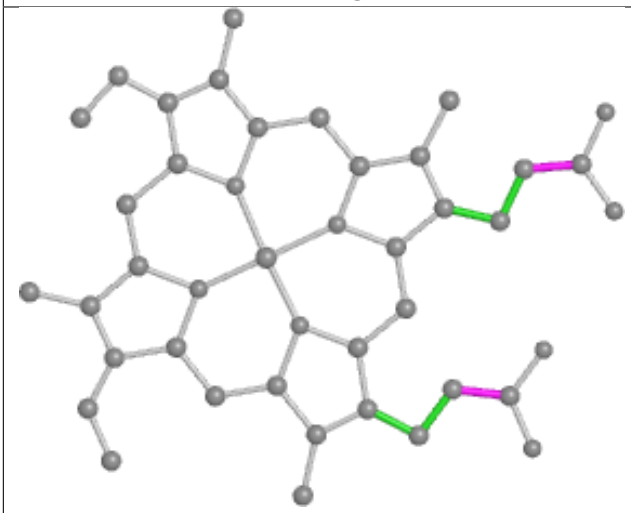
Ligand HEC B 1296



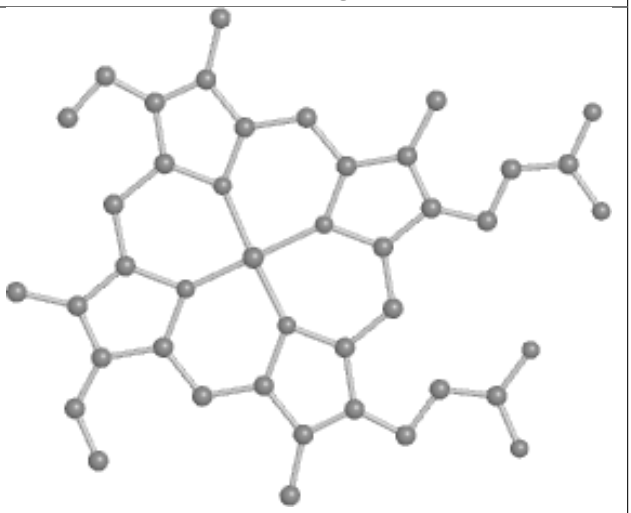
Bond lengths



Bond angles

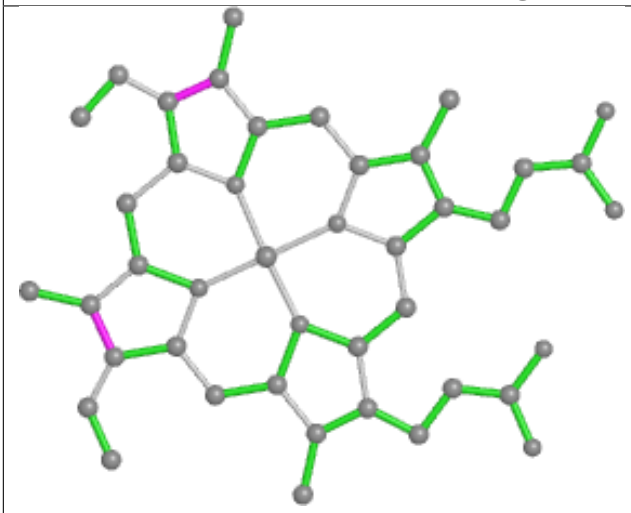


Torsions

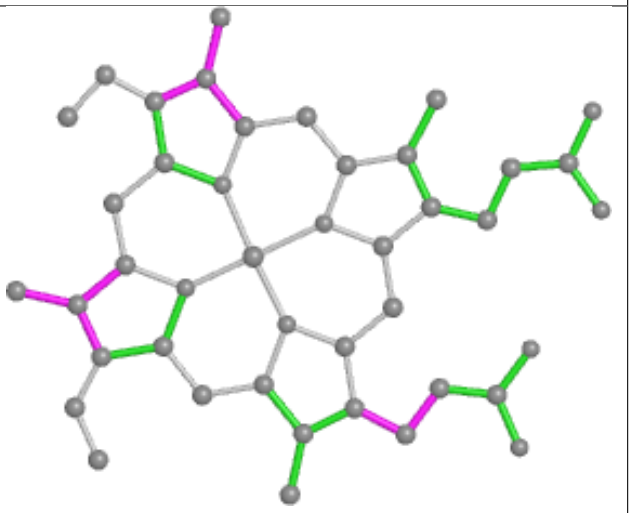


Rings

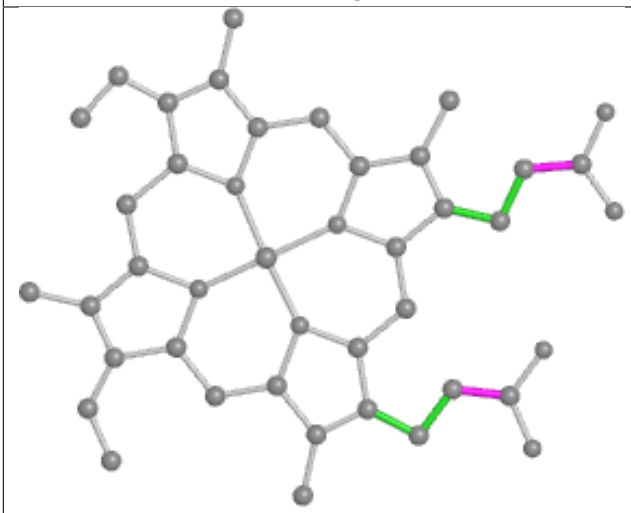
Ligand HEC B 1297



Bond lengths



Bond angles



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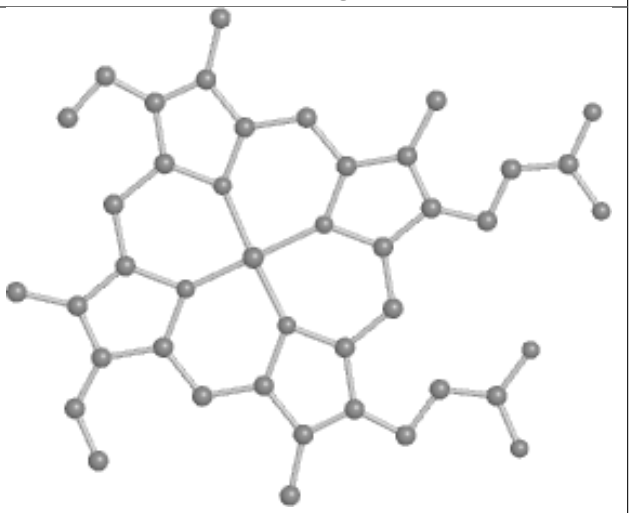
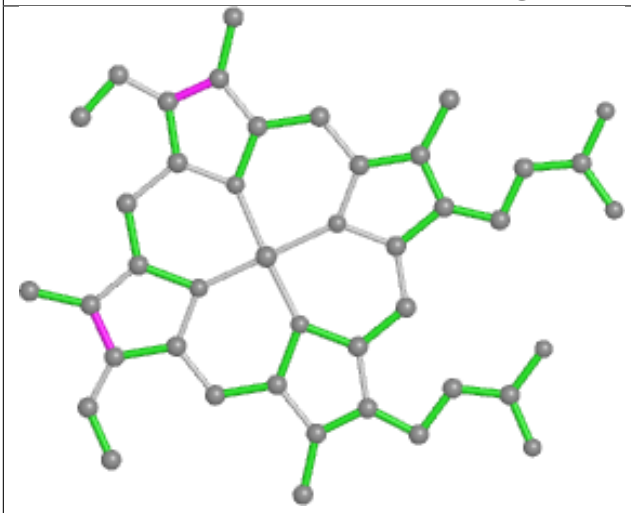
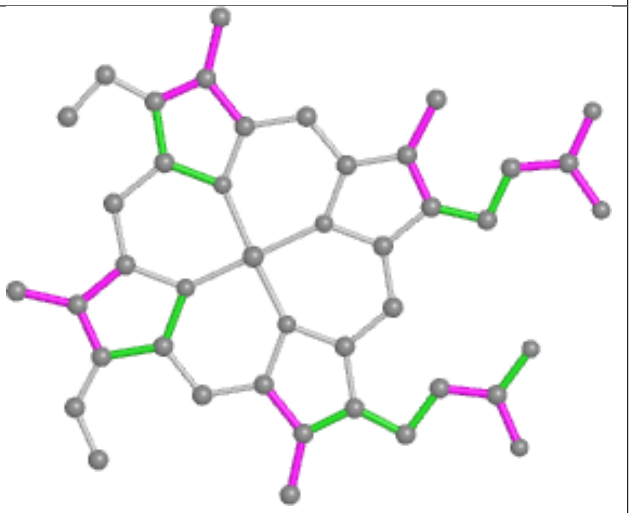


Rings

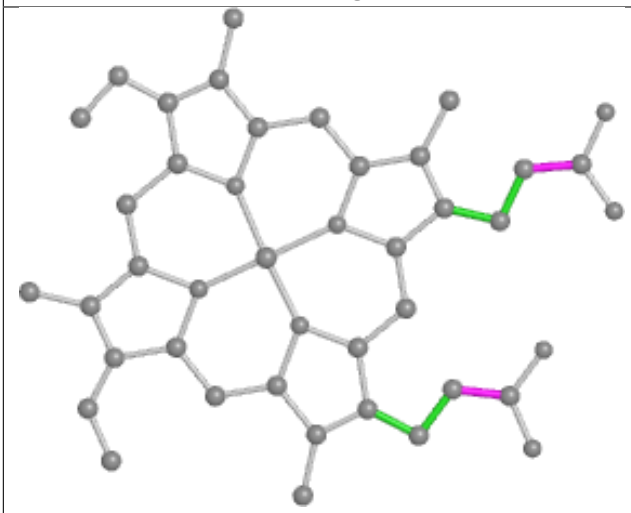
Ligand HEC A 1296



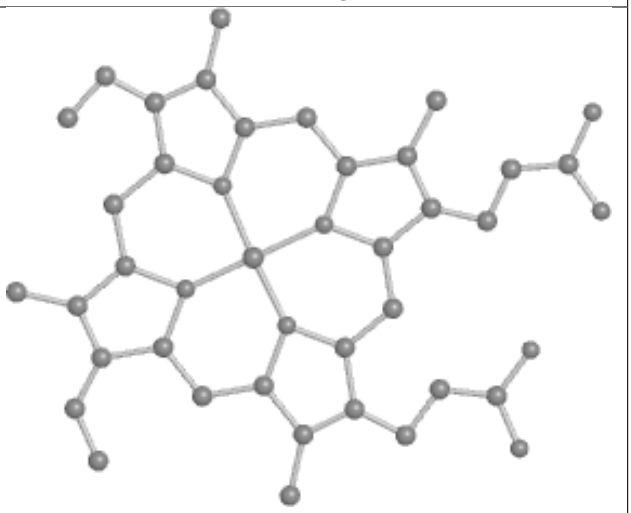
Bond lengths



Bond angles

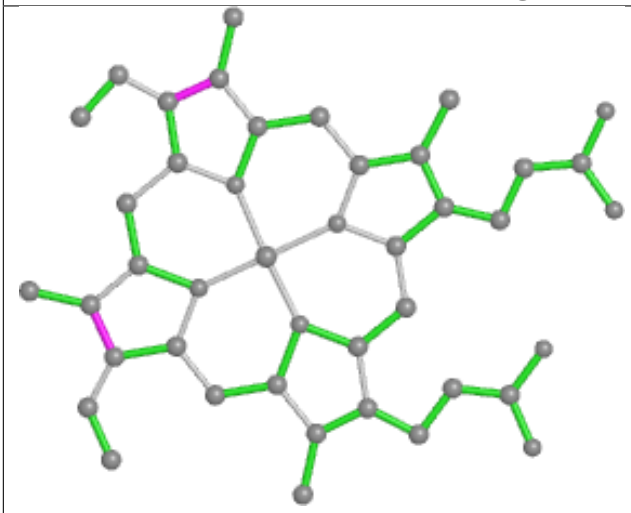


Torsions

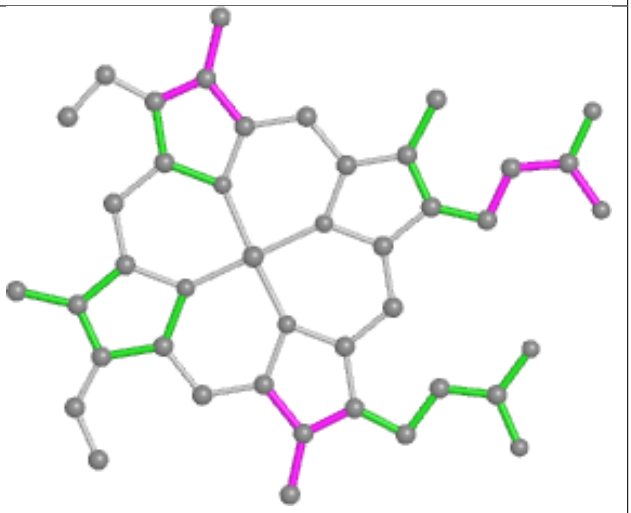


Rings

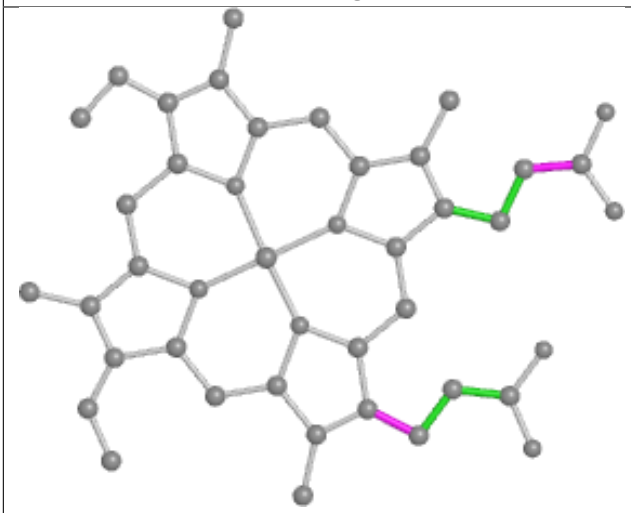
Ligand HEC B 1293



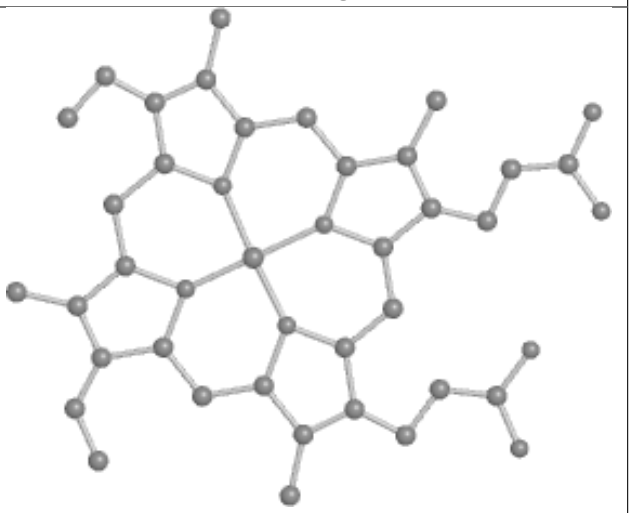
Bond lengths



Bond angles

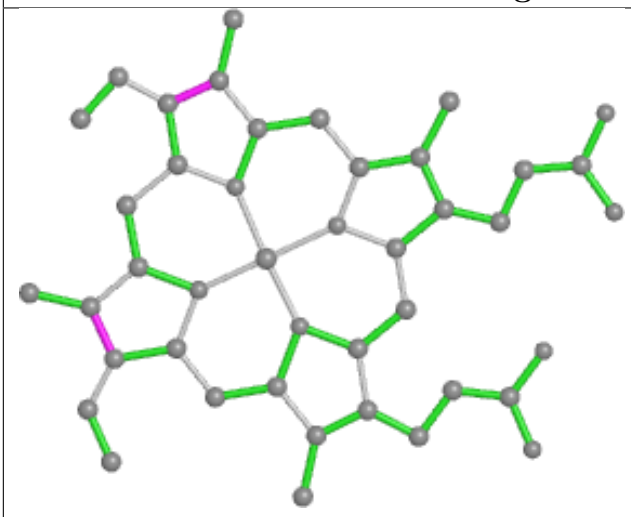


Torsions

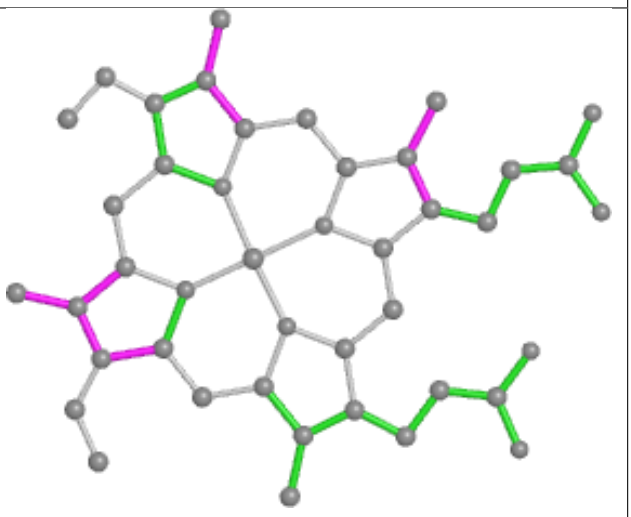


Rings

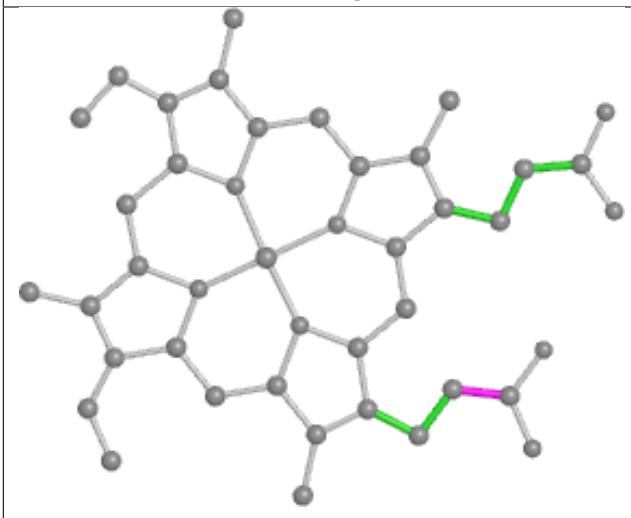
Ligand HEC B 1301



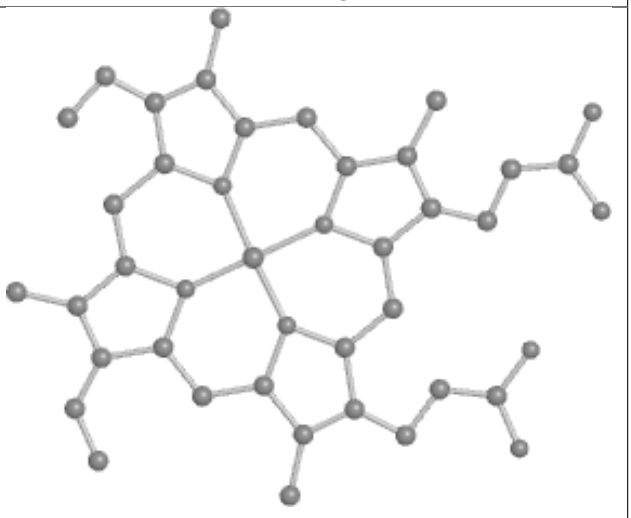
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.