



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 08:21 am BST

PDB ID : 2RDZ  
Title : High Resolution Crystal Structure of the Escherichia coli Cytochrome c Nitrite Reductase.  
Authors : Clarke, T.A.; Hemmings, A.M.; Richardson, D.J.  
Deposited on : 2007-09-25  
Resolution : 1.74 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](mailto: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.

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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

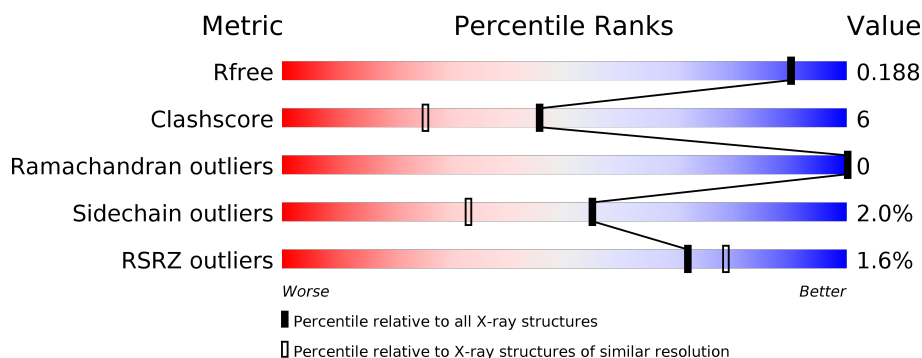
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.74 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	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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  $\geq 3$ , 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	452	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div>..</div> </div> </div>
1	B	452	<div> <div>87%</div> <div>10%</div> <div>..</div> </div>
1	C	452	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>9%</div> <div>..</div> </div> </div>
1	D	452	<div> <div>87%</div> <div>10%</div> <div>..</div> </div>

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
5	EDO	C	21	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17176 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

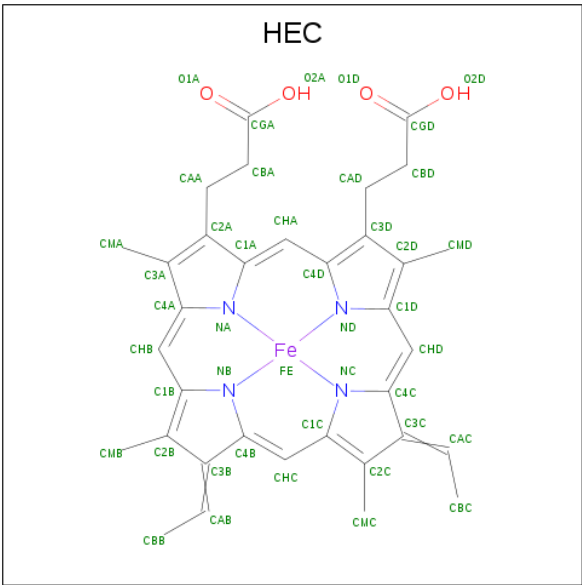
- Molecule 1 is a protein called Cytochrome c-552.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	2	0
			3487	2187	619	659	22			
1	B	441	Total	C	N	O	S	0	8	0
			3520	2209	622	667	22			
1	C	441	Total	C	N	O	S	0	5	0
			3502	2197	620	662	23			
1	D	441	Total	C	N	O	S	0	7	0
			3514	2203	623	666	22			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 3 is HEME C (three-letter code: HEC) (formula: C<sub>34</sub>H<sub>34</sub>FeN<sub>4</sub>O<sub>4</sub>).



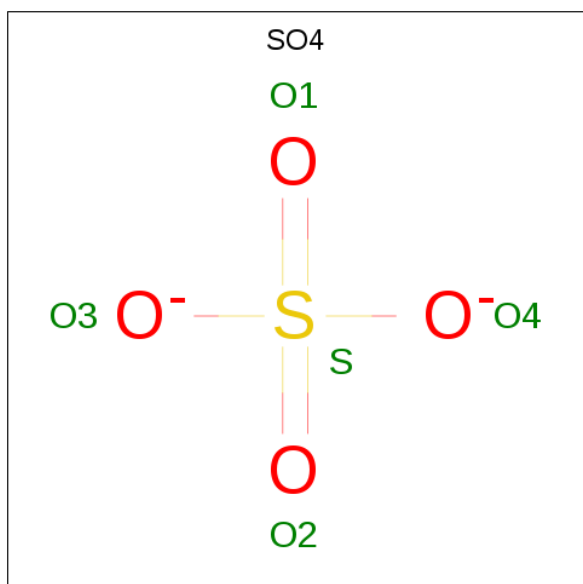
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0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

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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O S	0	0
			5 4 1			
4	B	1	Total	O S	0	0
			5 4 1			
4	C	1	Total	O S	0	0
			5 4 1			
4	D	1	Total	O S	0	0
			5 4 1			

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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

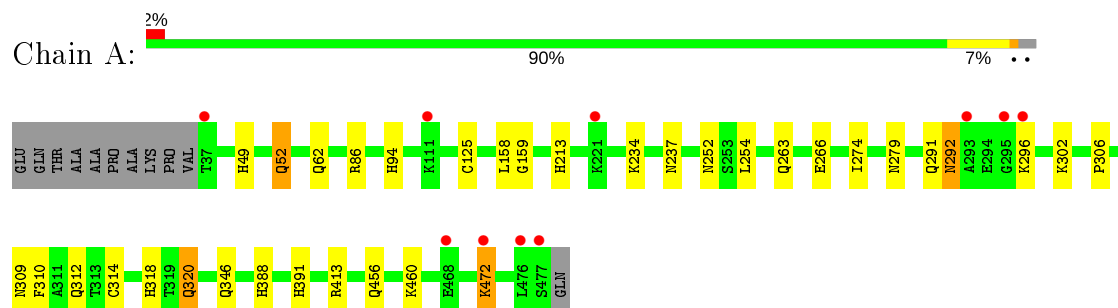
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	547	Total O 548 548	0	1
6	B	553	Total O 554 554	0	1
6	C	490	Total O 491 491	0	1
6	D	559	Total O 560 560	0	1

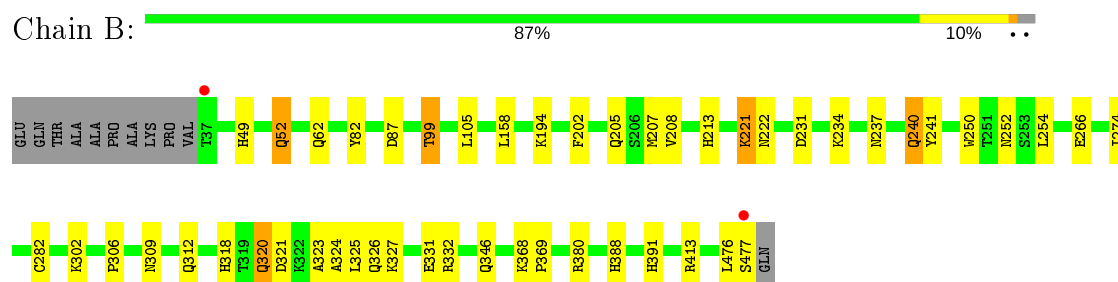
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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.

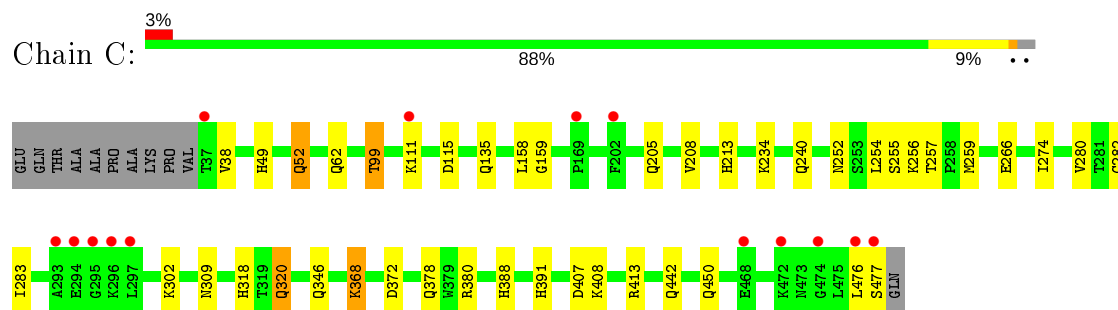
#### • Molecule 1: Cytochrome c-552



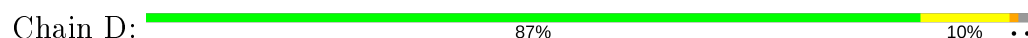
#### • Molecule 1: Cytochrome c-552

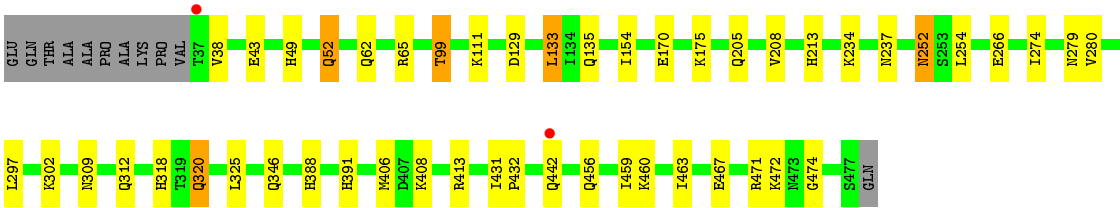


#### • Molecule 1: Cytochrome c-552



#### • Molecule 1: Cytochrome c-552





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.46 Å 79.30 Å 137.58 Å 90.00° 101.57° 90.00°	Depositor
Resolution (Å)	39.65 – 1.74 39.65 – 1.74	Depositor EDS
% Data completeness (in resolution range)	99.1 (39.65-1.74) 99.1 (39.65-1.74)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.73 (at 1.74 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.154 , 0.189 0.154 , 0.188	Depositor DCC
$R_{free}$ test set	9756 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.3	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 64.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17176	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, HEC, EDO, SO4

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	0.58	0/3577	0.60	0/4839
1	B	0.60	0/3628	0.62	0/4906
1	C	0.56	0/3601	0.59	0/4870
1	D	0.62	0/3619	0.62	0/4895
All	All	0.59	0/14425	0.61	0/19510

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

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	3487	0	3382	31	0
1	B	3520	0	3422	41	0
1	C	3502	0	3400	42	0
1	D	3514	0	3411	45	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	215	0	151	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	215	0	150	12	0
3	C	215	0	150	13	0
3	D	215	0	150	11	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
5	A	32	0	48	4	0
5	B	24	0	36	0	0
5	C	24	0	36	4	0
5	D	32	0	48	2	0
6	A	548	0	0	5	0
6	B	554	0	0	10	0
6	C	491	0	0	10	0
6	D	560	0	0	13	0
All	All	17176	0	14384	188	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 6.

The worst 5 of 188 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:125:CYS:SG	3:A:1:HEC:CAC	2.28	1.20
1:C:476:LEU:HB3	1:C:477:SER:HA	1.20	1.12
5:A:11:EDO:H22	1:B:332:ARG:HH12	1.27	0.99
1:C:476:LEU:HB3	1:C:477:SER:CA	2.00	0.92
1:B:99:THR:HG21	6:B:882:HOH:O	1.70	0.90

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	441/452 (98%)	432 (98%)	9 (2%)	0	100	100
1	B	447/452 (99%)	437 (98%)	10 (2%)	0	100	100
1	C	444/452 (98%)	432 (97%)	12 (3%)	0	100	100
1	D	446/452 (99%)	436 (98%)	10 (2%)	0	100	100
All	All	1778/1808 (98%)	1737 (98%)	41 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	364/370 (98%)	357 (98%)	7 (2%)	57	36
1	B	370/370 (100%)	363 (98%)	7 (2%)	57	36
1	C	367/370 (99%)	361 (98%)	6 (2%)	62	44
1	D	369/370 (100%)	359 (97%)	10 (3%)	44	21
All	All	1470/1480 (99%)	1440 (98%)	30 (2%)	55	33

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	325	LEU
1	C	234	LYS
1	D	325	LEU
1	C	99	THR
1	C	309	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	326	GLN
1	B	469	GLN
1	D	371	GLN

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Mol	Chain	Res	Type
1	B	371	GLN
1	C	52	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 60 ligands modelled in this entry, 8 are monoatomic - leaving 52 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	HEC	D	2	1	26,50,50	2.09	4 (15%)	18,82,82	1.84	7 (38%)
5	EDO	B	17	-	3,3,3	0.44	0	2,2,2	0.42	0
5	EDO	D	481	-	3,3,3	0.33	0	2,2,2	0.36	0
5	EDO	B	16	-	3,3,3	0.52	0	2,2,2	0.29	0
3	HEC	A	5	1	26,50,50	2.19	4 (15%)	18,82,82	2.10	7 (38%)
3	HEC	D	1	1,6	26,50,50	2.27	5 (19%)	18,82,82	1.75	5 (27%)
3	HEC	A	2	1	26,50,50	2.04	3 (11%)	18,82,82	1.74	4 (22%)
5	EDO	A	13	-	3,3,3	0.39	0	2,2,2	0.64	0
5	EDO	B	20	-	3,3,3	0.44	0	2,2,2	0.53	0
5	EDO	D	24	-	3,3,3	0.47	0	2,2,2	0.37	0
4	SO4	D	2001	-	4,4,4	0.07	0	6,6,6	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	EDO	B	19	-	3,3,3	0.48	0	2,2,2	0.16	0
5	EDO	C	481	-	3,3,3	0.51	0	2,2,2	0.25	0
3	HEC	D	3	1,2	26,50,50	2.08	4 (15%)	18,82,82	1.96	7 (38%)
5	EDO	A	15	-	3,3,3	0.40	0	2,2,2	0.36	0
3	HEC	A	4	1,2	26,50,50	2.30	4 (15%)	18,82,82	2.01	6 (33%)
3	HEC	C	4	1,2	26,50,50	2.18	3 (11%)	18,82,82	1.66	5 (27%)
5	EDO	C	12	-	3,3,3	0.42	0	2,2,2	0.73	0
5	EDO	A	21	-	3,3,3	0.42	0	2,2,2	0.43	0
5	EDO	D	482	-	3,3,3	0.50	0	2,2,2	0.21	0
5	EDO	D	22	-	3,3,3	0.44	0	2,2,2	0.69	0
3	HEC	B	4	1,2	26,50,50	2.23	5 (19%)	18,82,82	1.96	4 (22%)
3	HEC	B	3	1,2	26,50,50	2.23	4 (15%)	18,82,82	1.70	4 (22%)
5	EDO	D	6	-	3,3,3	0.56	0	2,2,2	0.18	0
4	SO4	B	2001	-	4,4,4	0.26	0	6,6,6	0.29	0
5	EDO	B	481	-	3,3,3	0.57	0	2,2,2	0.27	0
5	EDO	A	22	-	3,3,3	0.44	0	2,2,2	0.39	0
3	HEC	C	3	1,2	26,50,50	2.14	3 (11%)	18,82,82	1.95	7 (38%)
3	HEC	D	5	1	26,50,50	2.39	5 (19%)	18,82,82	2.05	7 (38%)
3	HEC	C	1	1,6	26,50,50	2.21	4 (15%)	18,82,82	1.74	5 (27%)
3	HEC	B	1	1,6	26,50,50	2.03	3 (11%)	18,82,82	1.62	5 (27%)
3	HEC	B	5	1	26,50,50	2.30	5 (19%)	18,82,82	2.01	7 (38%)
3	HEC	C	2	1	26,50,50	2.14	4 (15%)	18,82,82	1.84	5 (27%)
5	EDO	A	481	-	3,3,3	0.40	0	2,2,2	0.26	0
5	EDO	C	25	-	3,3,3	0.39	0	2,2,2	0.50	0
5	EDO	D	25	-	3,3,3	0.51	0	2,2,2	0.11	0
5	EDO	C	21	-	3,3,3	0.36	0	2,2,2	0.61	0
5	EDO	A	11	-	3,3,3	0.38	0	2,2,2	0.74	0
5	EDO	A	14	-	3,3,3	0.39	0	2,2,2	0.37	0
5	EDO	A	20	-	3,3,3	0.50	0	2,2,2	0.10	0
4	SO4	C	2001	-	4,4,4	0.17	0	6,6,6	0.40	0
5	EDO	B	18	-	3,3,3	0.43	0	2,2,2	0.34	0
5	EDO	D	23	-	3,3,3	0.47	0	2,2,2	0.41	0
3	HEC	C	5	1	26,50,50	2.12	4 (15%)	18,82,82	1.67	4 (22%)
5	EDO	C	23	-	3,3,3	0.43	0	2,2,2	0.41	0
3	HEC	B	2	1	26,50,50	3.68	6 (23%)	18,82,82	3.67	7 (38%)
5	EDO	C	22	-	3,3,3	0.46	0	2,2,2	0.22	0
5	EDO	D	21	-	3,3,3	0.49	0	2,2,2	0.46	0
3	HEC	A	1	1,6	26,50,50	2.09	5 (19%)	18,82,82	1.69	5 (27%)
3	HEC	A	3	1,2	26,50,50	2.28	5 (19%)	18,82,82	1.75	4 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	HEC	D	4	1	26,50,50	2.15	4 (15%)	18,82,82	1.84	7 (38%)
4	SO4	A	2001	-	4,4,4	0.08	0	6,6,6	0.34	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	D	2	1	-	0/6/54/54	-
5	EDO	B	17	-	-	0/1/1/1	-
5	EDO	D	481	-	-	0/1/1/1	-
5	EDO	B	16	-	-	0/1/1/1	-
3	HEC	A	5	1	-	0/6/54/54	-
3	HEC	D	1	1,6	-	0/6/54/54	-
3	HEC	A	2	1	-	0/6/54/54	-
5	EDO	A	13	-	-	0/1/1/1	-
5	EDO	B	20	-	-	0/1/1/1	-
5	EDO	D	24	-	-	1/1/1/1	-
5	EDO	B	19	-	-	0/1/1/1	-
5	EDO	C	481	-	-	0/1/1/1	-
3	HEC	D	3	1,2	-	0/6/54/54	-
5	EDO	A	15	-	-	1/1/1/1	-
3	HEC	A	4	1,2	-	0/6/54/54	-
3	HEC	C	4	1,2	-	0/6/54/54	-
5	EDO	C	12	-	-	0/1/1/1	-
5	EDO	A	21	-	-	1/1/1/1	-
5	EDO	D	482	-	-	0/1/1/1	-
3	HEC	B	4	1,2	-	0/6/54/54	-
3	HEC	B	3	1,2	-	0/6/54/54	-
5	EDO	D	6	-	-	0/1/1/1	-
5	EDO	B	481	-	-	0/1/1/1	-
5	EDO	A	22	-	-	1/1/1/1	-
3	HEC	C	3	1,2	-	0/6/54/54	-
3	HEC	D	5	1	-	0/6/54/54	-
3	HEC	C	1	1,6	-	0/6/54/54	-
3	HEC	B	1	1,6	-	0/6/54/54	-
3	HEC	B	5	1	-	0/6/54/54	-
3	HEC	C	2	1	-	0/6/54/54	-
5	EDO	A	481	-	-	0/1/1/1	-
5	EDO	C	25	-	-	0/1/1/1	-
5	EDO	D	25	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	C	21	-	-	1/1/1/1	-
5	EDO	A	11	-	-	0/1/1/1	-
5	EDO	A	14	-	-	0/1/1/1	-
5	EDO	A	20	-	-	1/1/1/1	-
5	EDO	B	18	-	-	0/1/1/1	-
5	EDO	D	23	-	-	1/1/1/1	-
3	HEC	C	5	1	-	0/6/54/54	-
5	EDO	C	23	-	-	1/1/1/1	-
3	HEC	B	2	1	-	0/6/54/54	-
5	EDO	C	22	-	-	0/1/1/1	-
5	EDO	D	21	-	-	1/1/1/1	-
3	HEC	A	1	1,6	-	0/6/54/54	-
3	HEC	A	3	1,2	-	0/6/54/54	-
3	HEC	D	4	1	-	1/6/54/54	-
5	EDO	D	22	-	-	1/1/1/1	-

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2	HEC	C1D-ND	14.10	1.65	1.36
3	B	3	HEC	C3B-C2B	-6.43	1.34	1.40
3	B	5	HEC	C3B-C2B	-6.38	1.34	1.40
3	B	4	HEC	C3B-C2B	-6.27	1.34	1.40
3	D	5	HEC	C3C-C2C	-6.22	1.34	1.40

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2	HEC	C1D-C2D-C3D	12.00	115.35	107.00
3	B	2	HEC	CMD-C2D-C1D	-6.88	117.89	128.46
3	B	4	HEC	CMC-C2C-C1C	-4.51	121.53	128.46
3	B	5	HEC	CMC-C2C-C1C	-4.05	122.23	128.46
3	A	5	HEC	CMC-C2C-C1C	-3.91	122.45	128.46

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	4	HEC	C2A-CAA-CBA-CGA
5	C	21	EDO	O1-C1-C2-O2
5	A	22	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
5	D	25	EDO	O1-C1-C2-O2
5	A	21	EDO	O1-C1-C2-O2

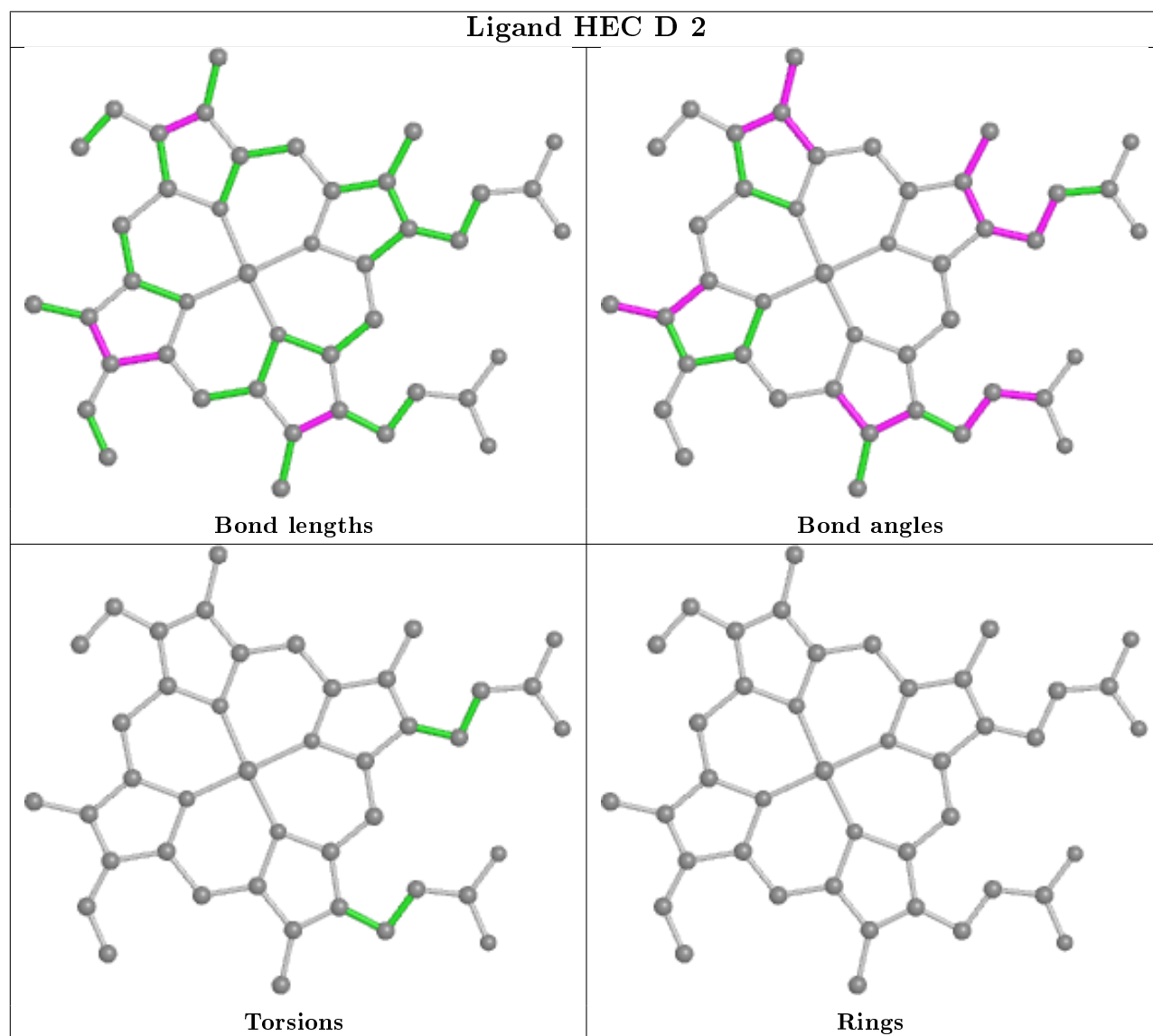
There are no ring outliers.

24 monomers are involved in 65 short contacts:

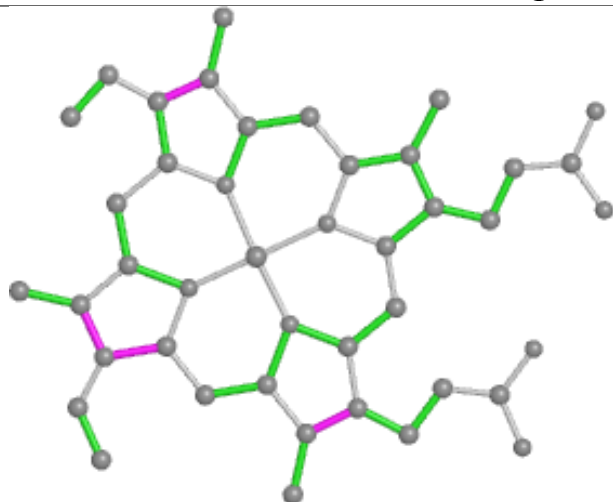
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	HEC	2	0
5	D	481	EDO	1	0
3	A	5	HEC	3	0
3	D	1	HEC	1	0
3	A	2	HEC	4	0
3	A	4	HEC	4	0
3	C	4	HEC	4	0
5	A	21	EDO	1	0
3	B	4	HEC	4	0
3	B	3	HEC	2	0
3	C	3	HEC	2	0
3	D	5	HEC	5	0
3	C	1	HEC	1	0
3	B	1	HEC	1	0
3	B	5	HEC	2	0
3	C	2	HEC	2	0
5	D	25	EDO	1	0
5	C	21	EDO	4	0
5	A	11	EDO	3	0
3	C	5	HEC	4	0
3	B	2	HEC	3	0
3	A	1	HEC	6	0
3	A	3	HEC	2	0
3	D	4	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.

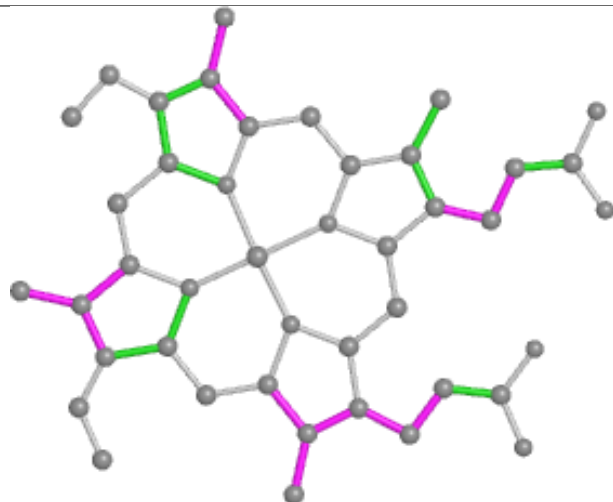
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



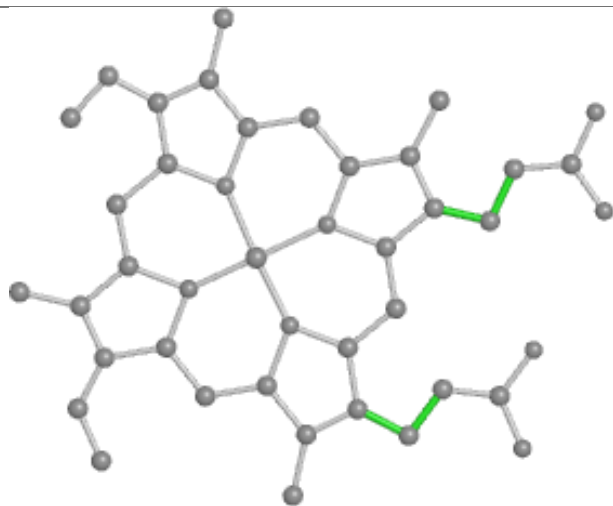
## Ligand HEC A 5



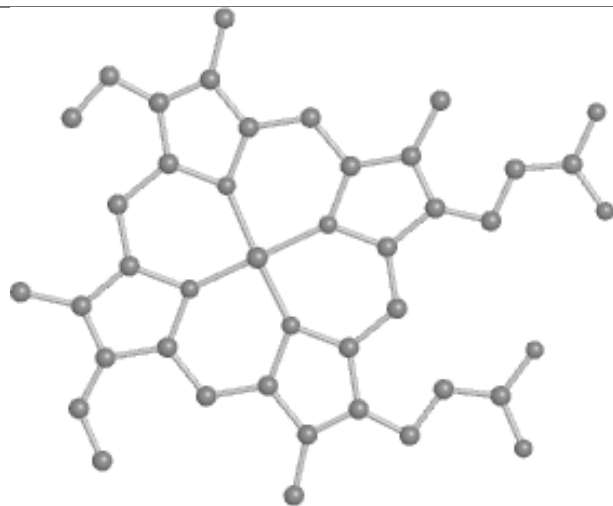
Bond lengths



Bond angles

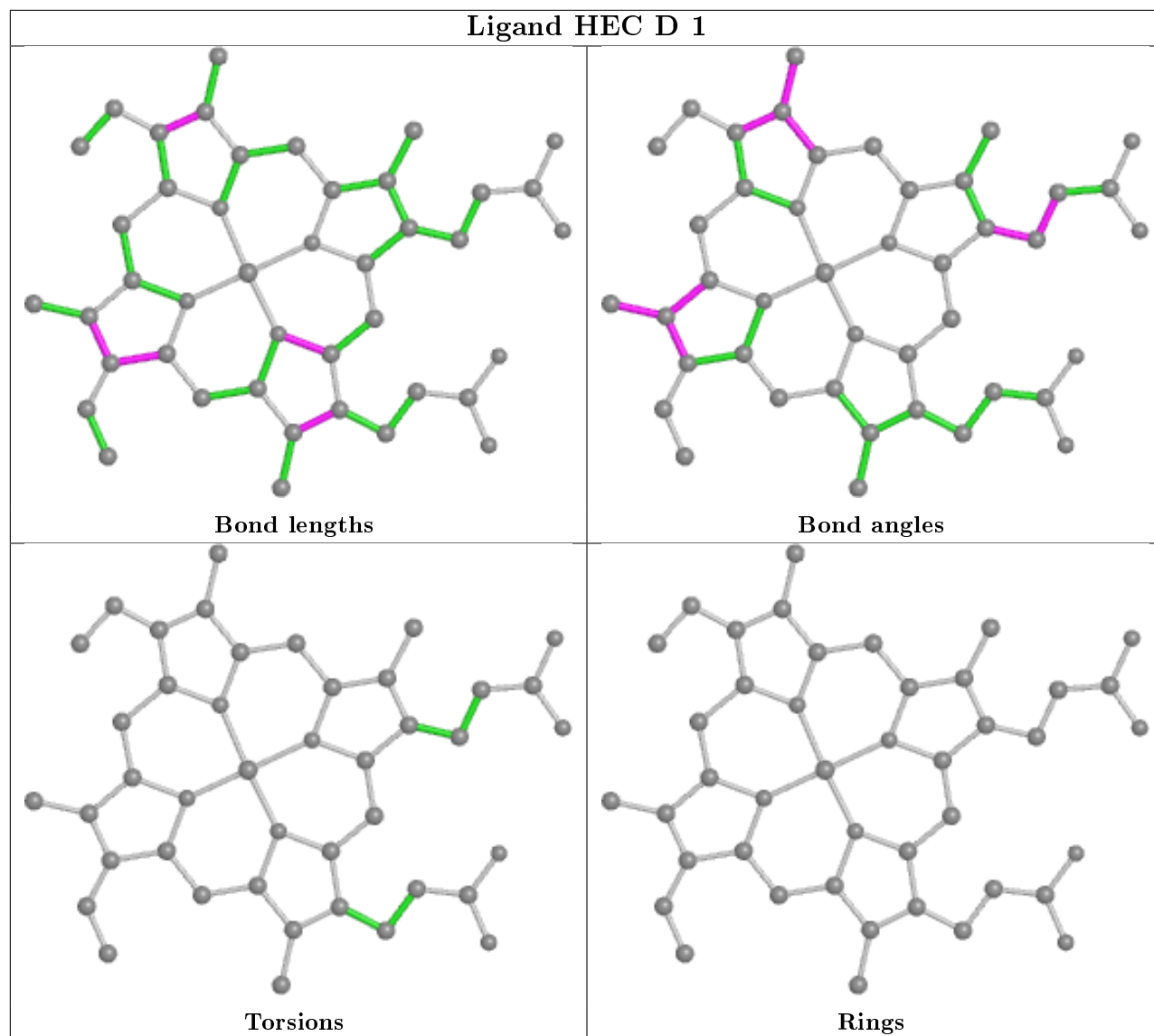


Torsions

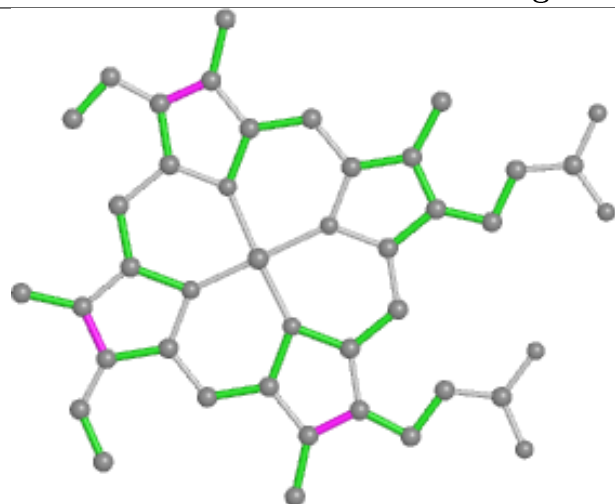


Rings

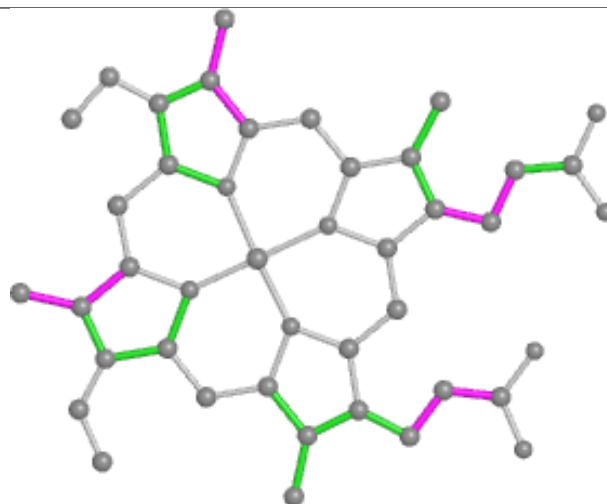
## Ligand HEC D 1



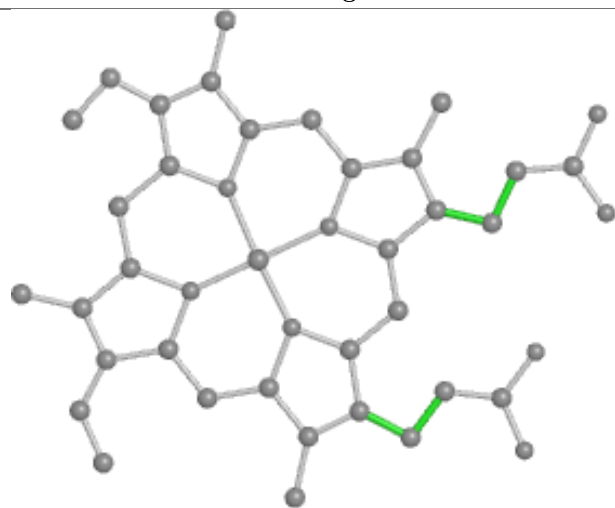
## Ligand HEC A 2



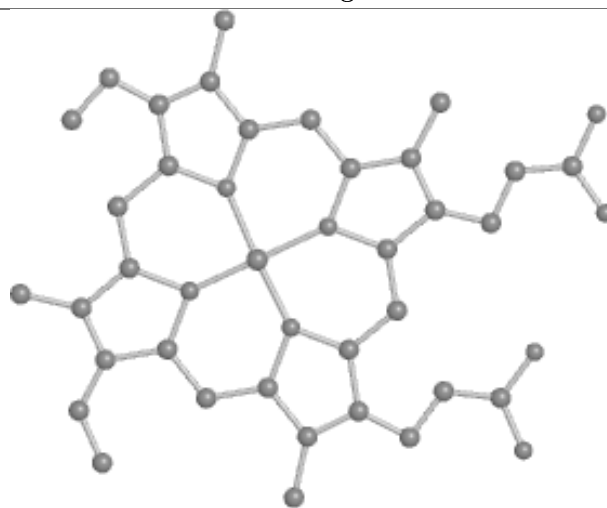
Bond lengths



Bond angles

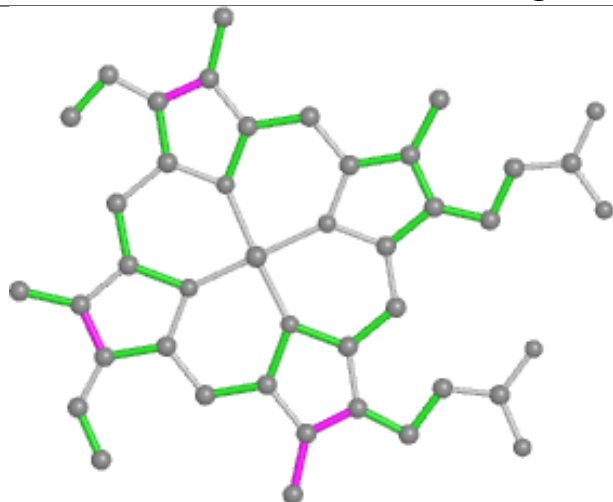


Torsions

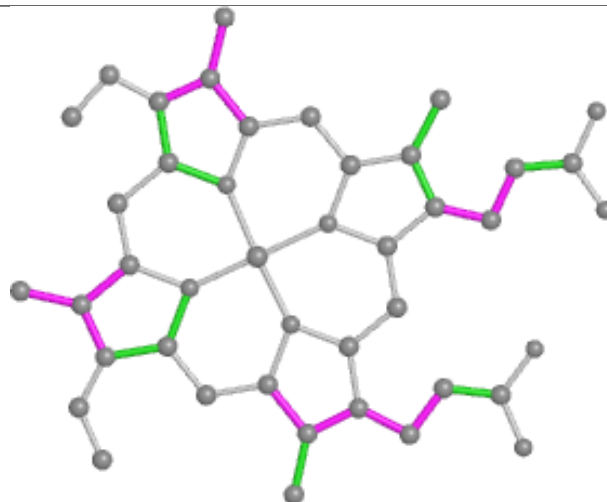


Rings

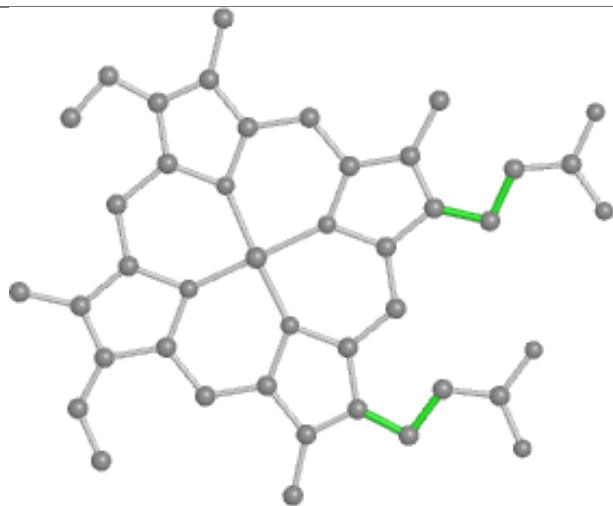
## Ligand HEC D 3



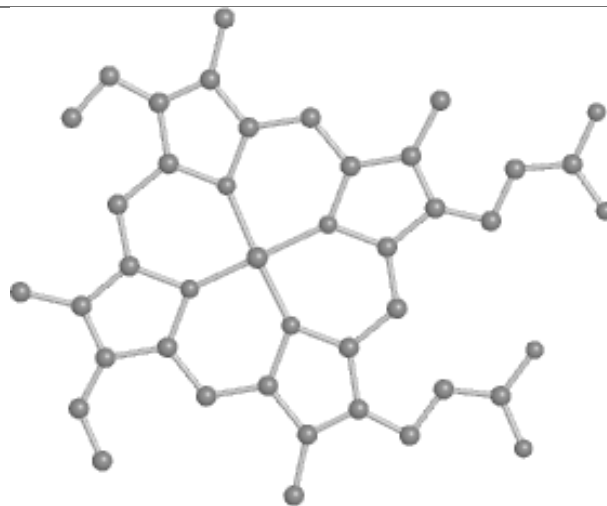
Bond lengths



Bond angles

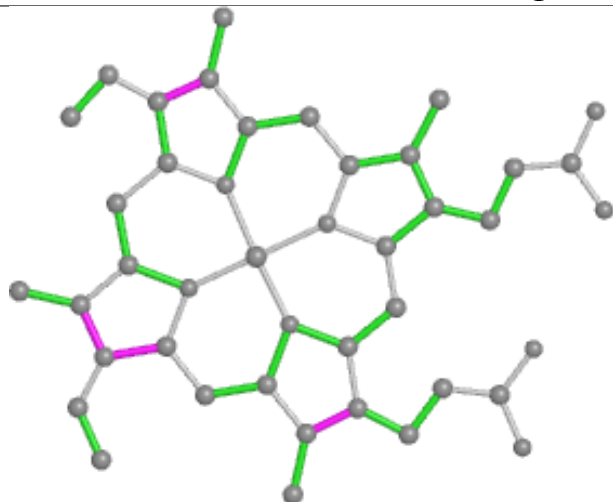


Torsions

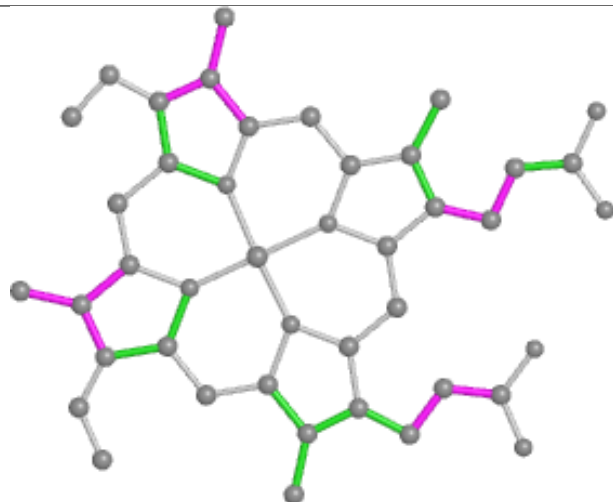


Rings

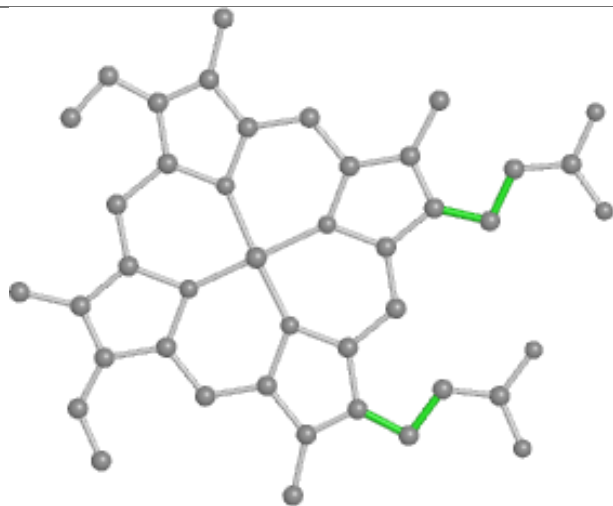
## Ligand HEC A 4



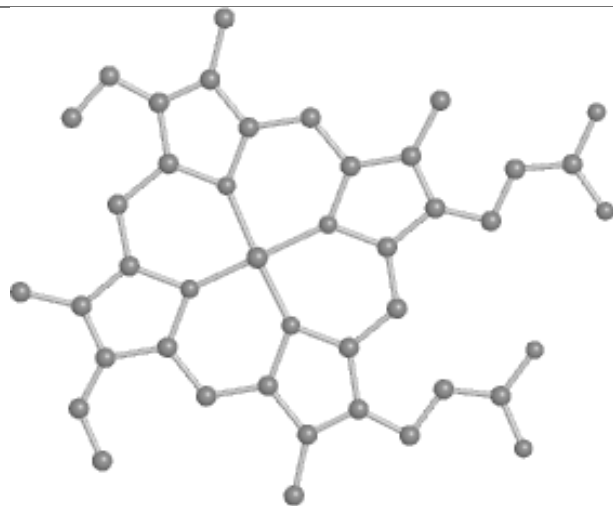
Bond lengths



Bond angles

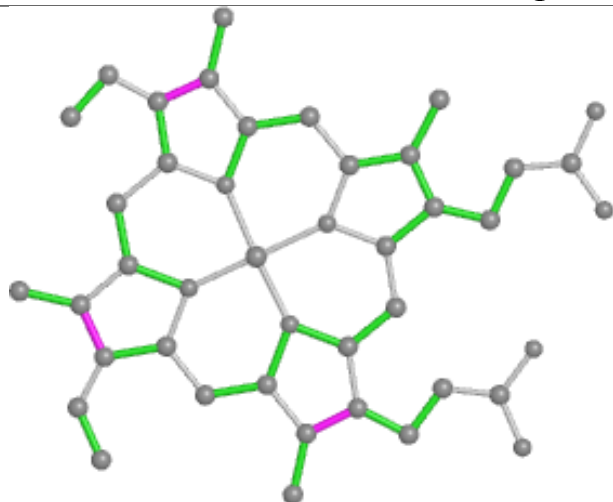


Torsions

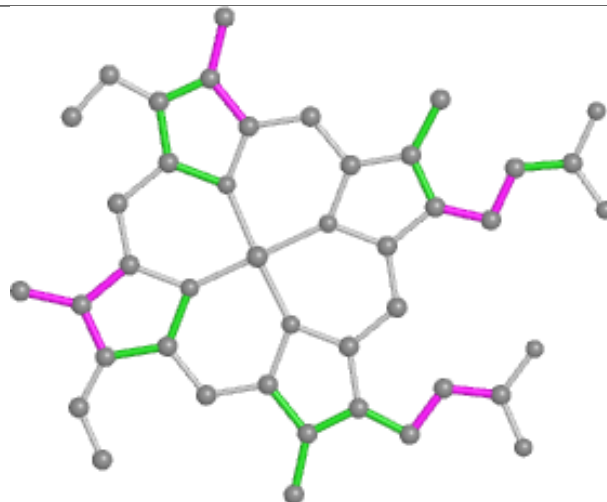


Rings

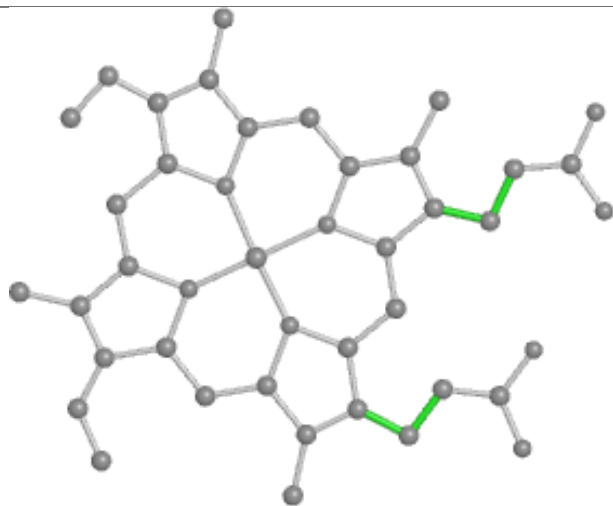
## Ligand HEC C 4



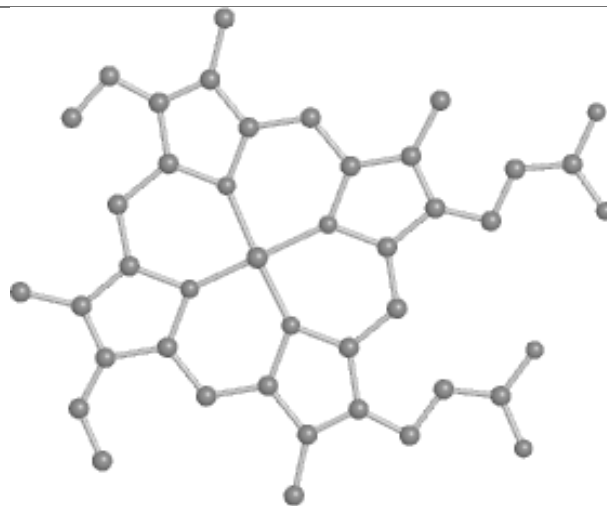
Bond lengths



Bond angles

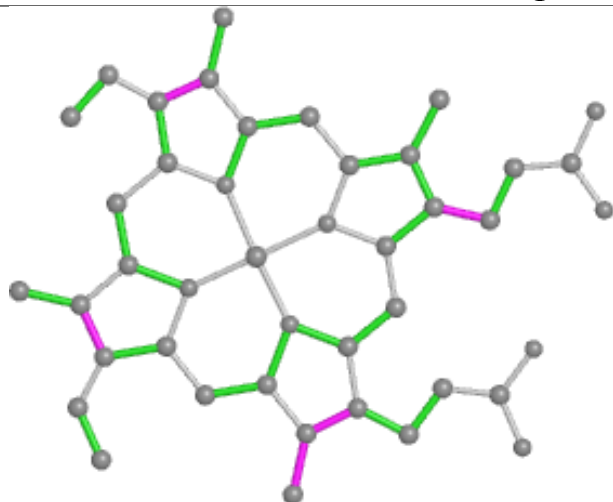


Torsions

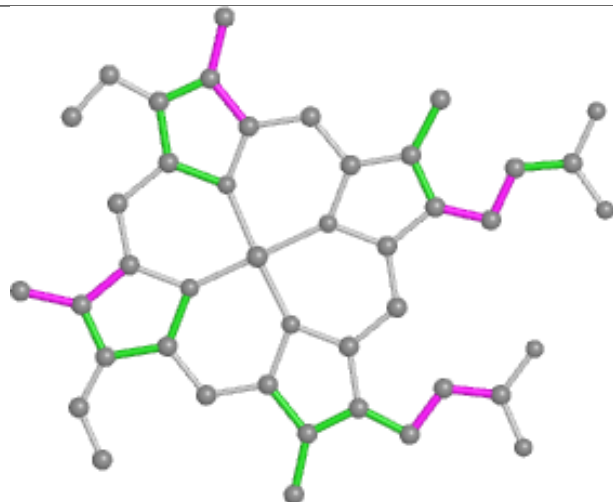


Rings

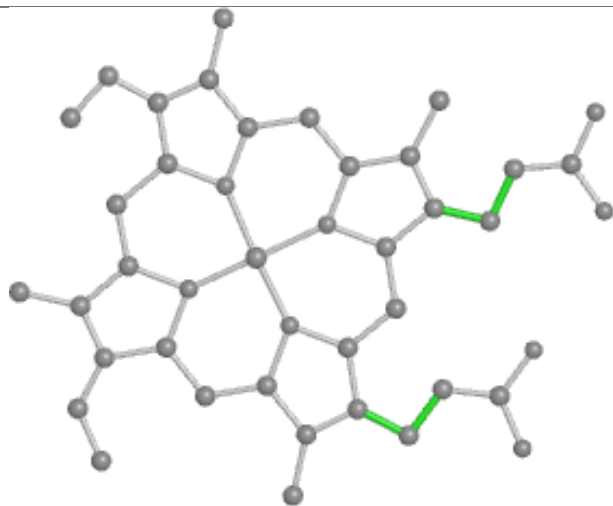
## Ligand HEC B 4



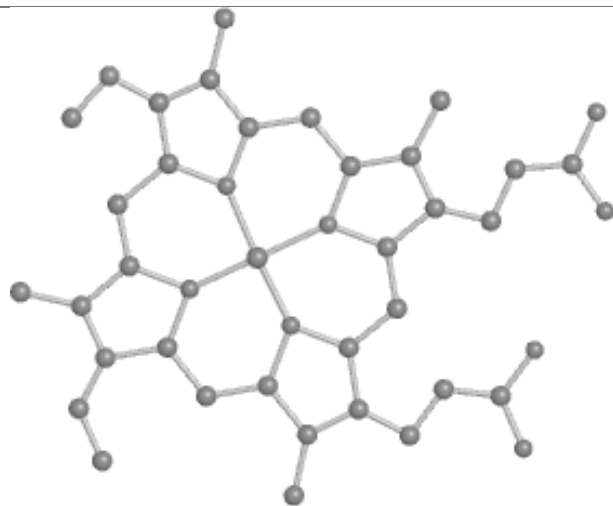
Bond lengths



Bond angles

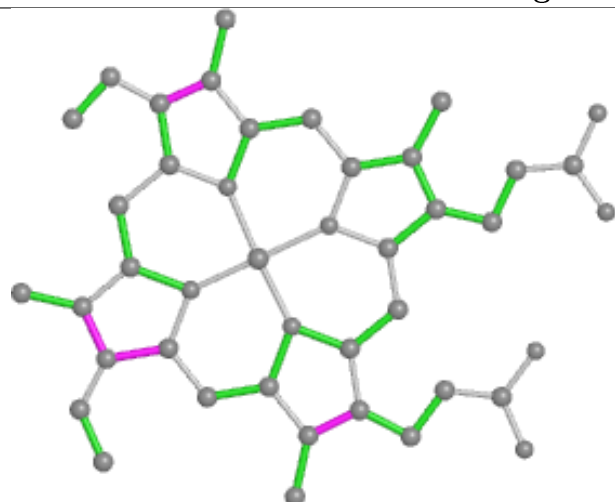


Torsions

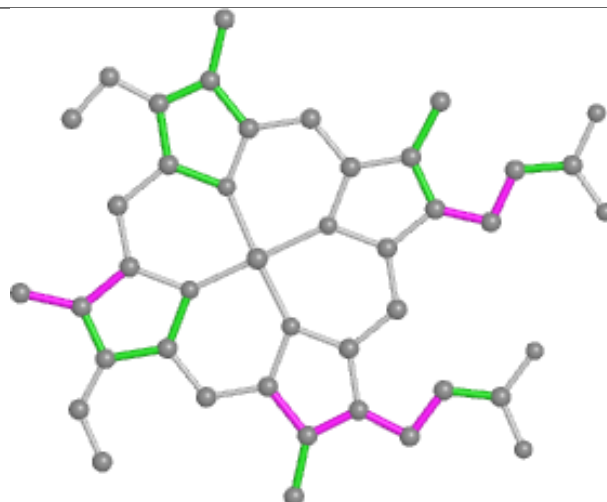


Rings

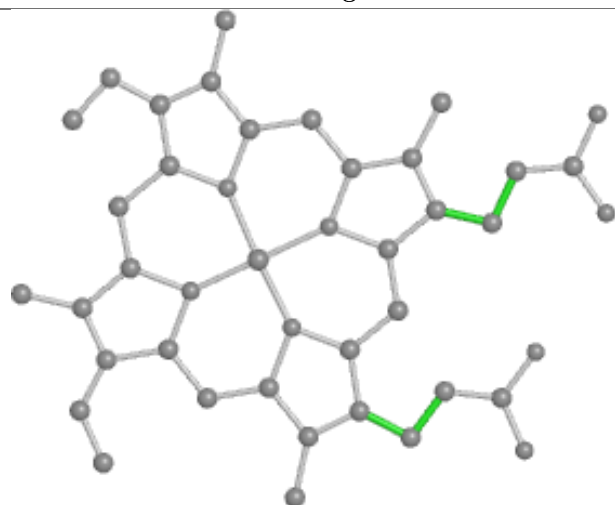
## Ligand HEC B 3



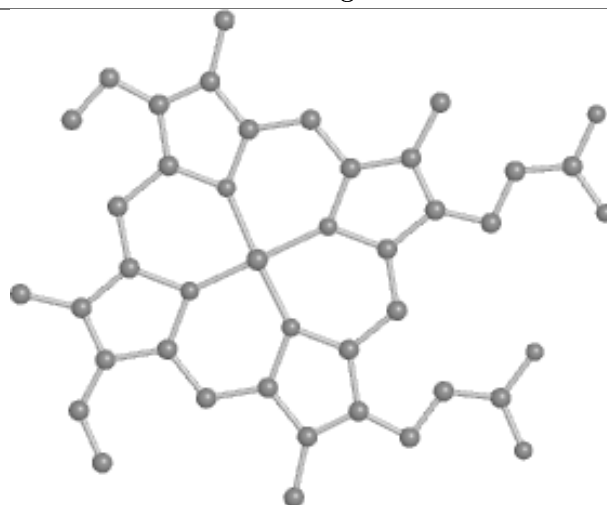
Bond lengths



Bond angles

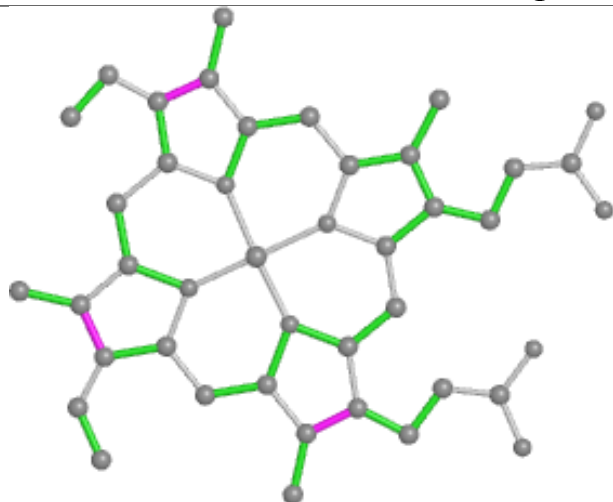


Torsions

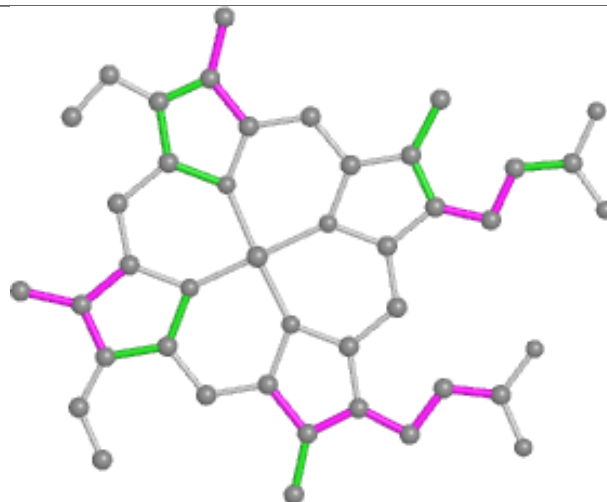


Rings

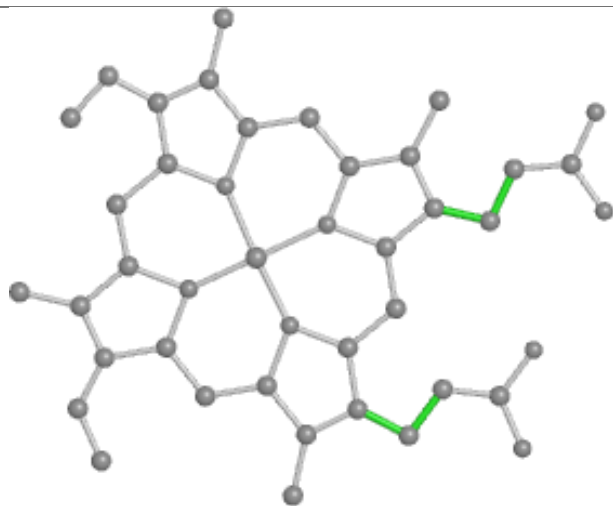
## Ligand HEC C 3



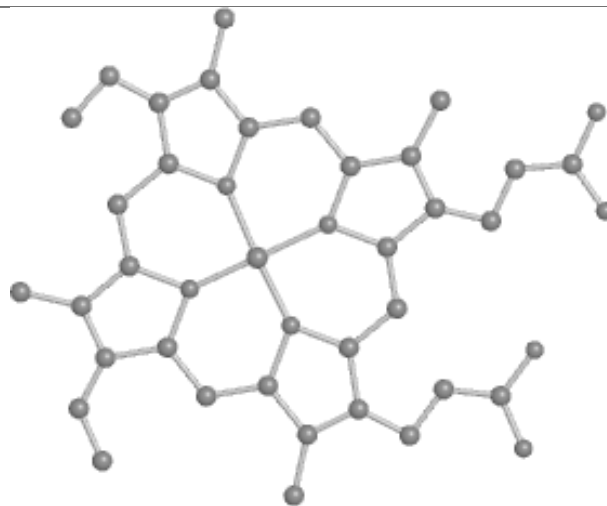
Bond lengths



Bond angles

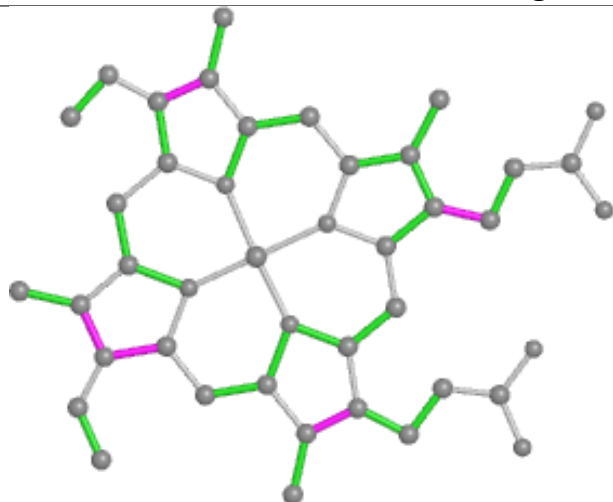


Torsions

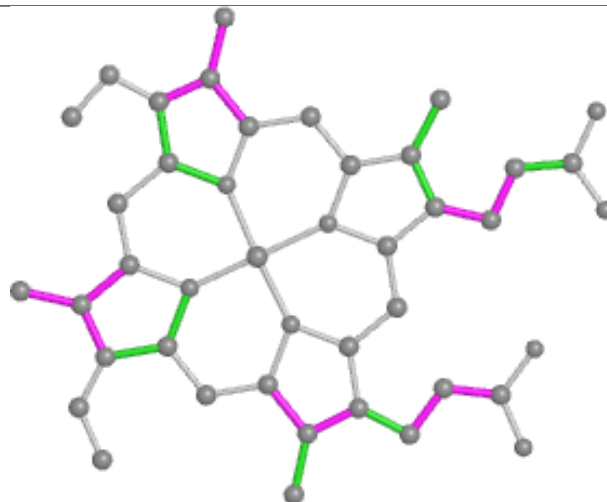


Rings

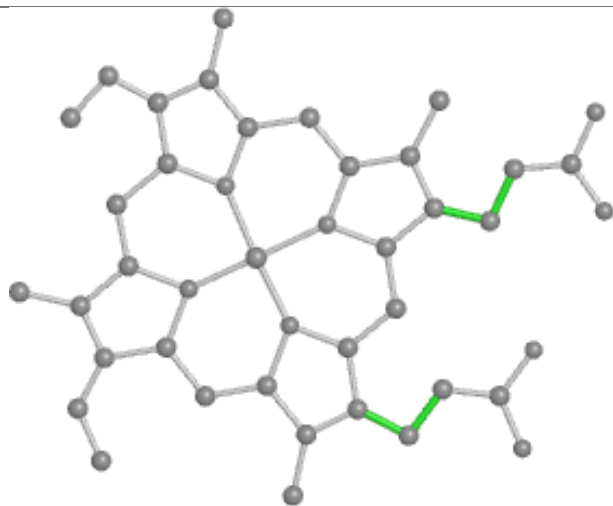
## Ligand HEC D 5



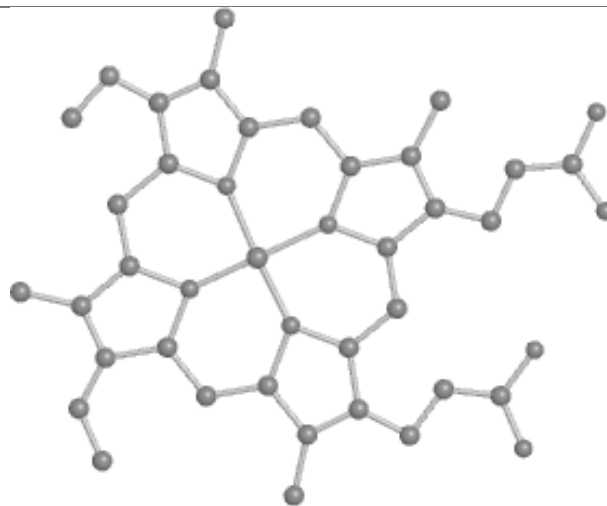
Bond lengths



Bond angles

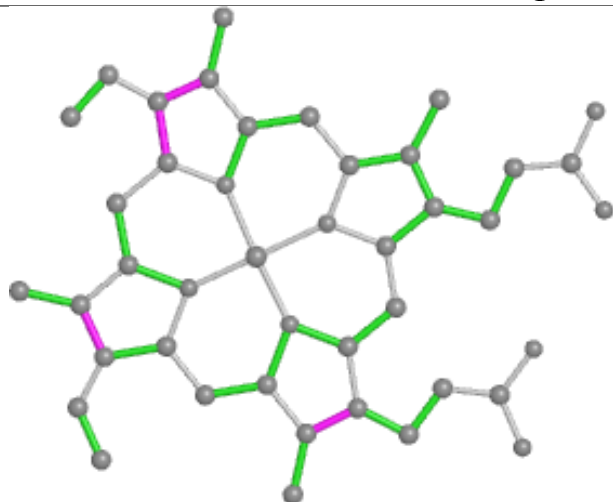


Torsions

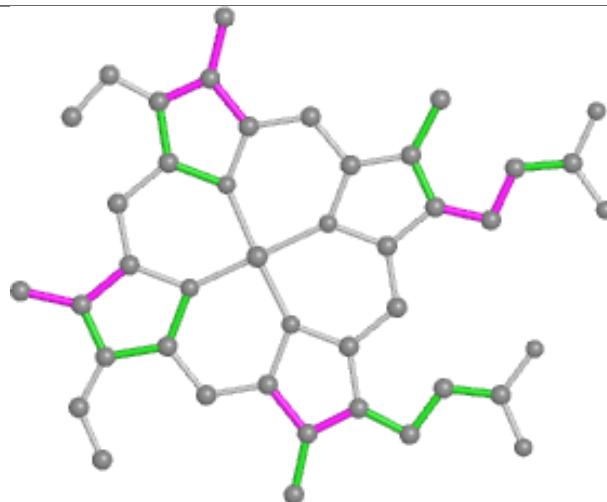


Rings

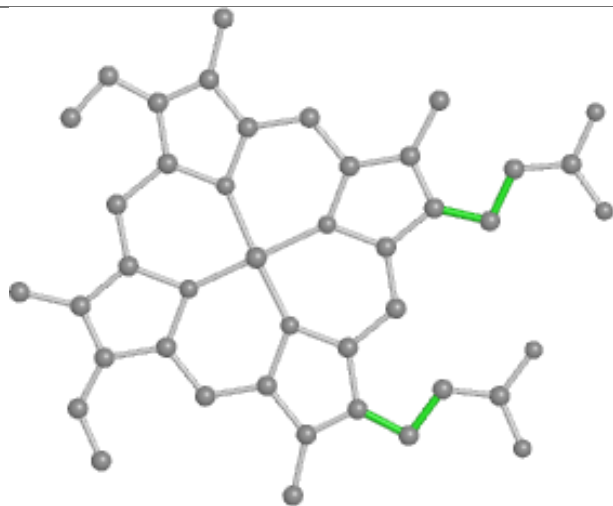
## Ligand HEC C 1



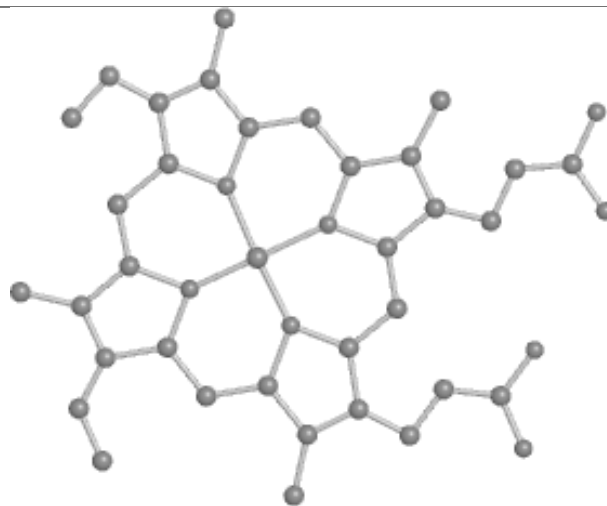
Bond lengths



Bond angles

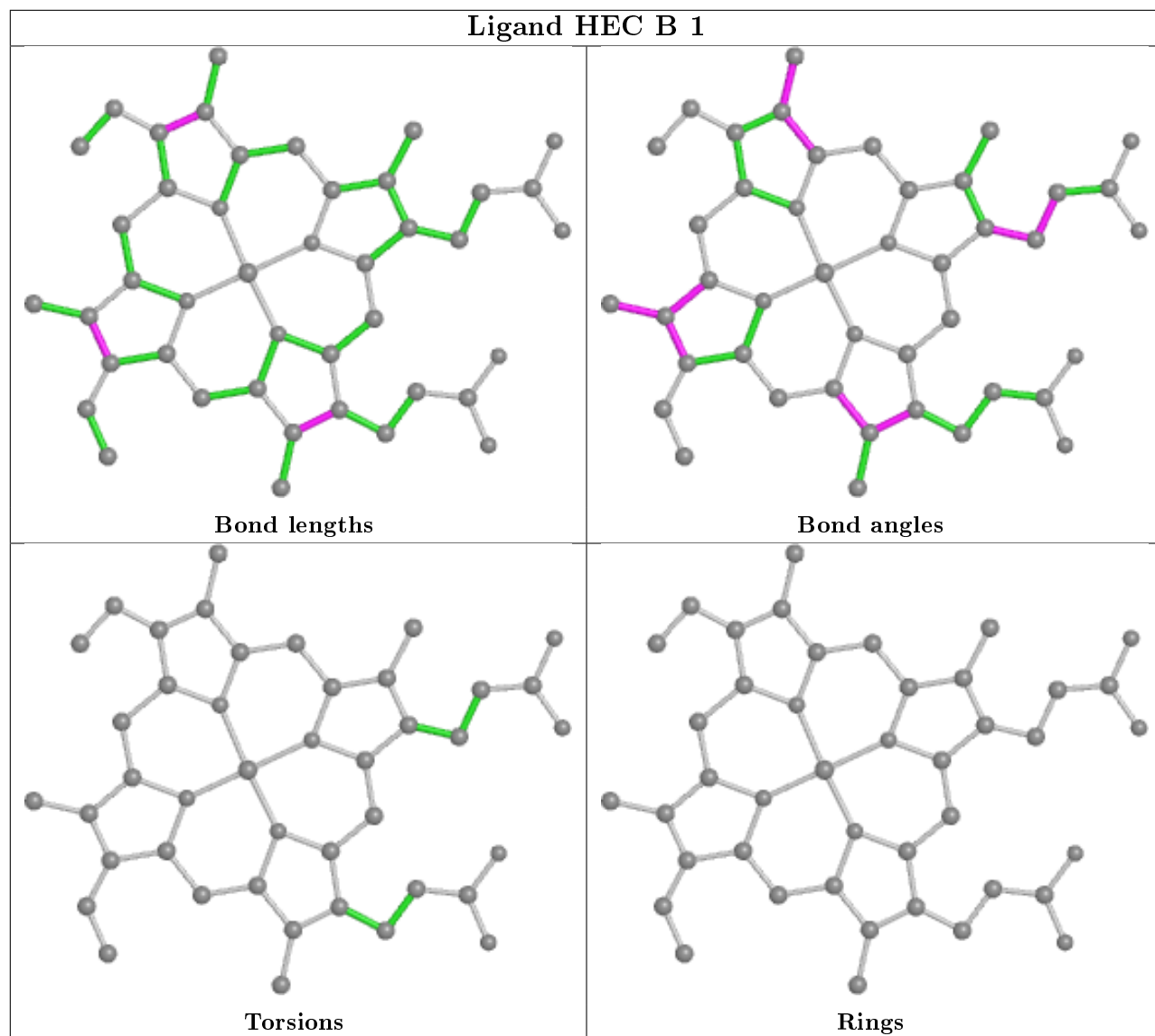


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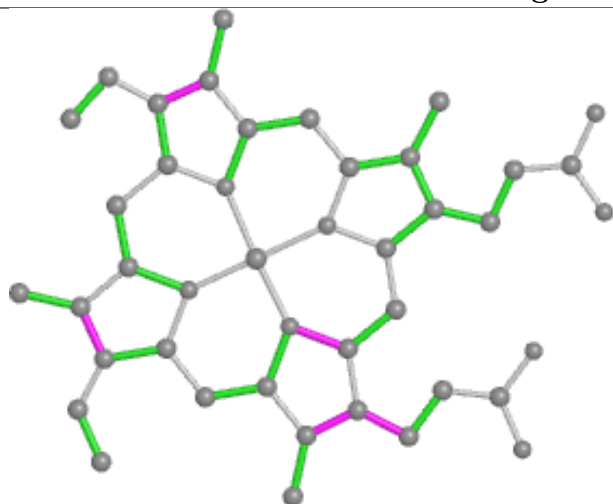


Rings

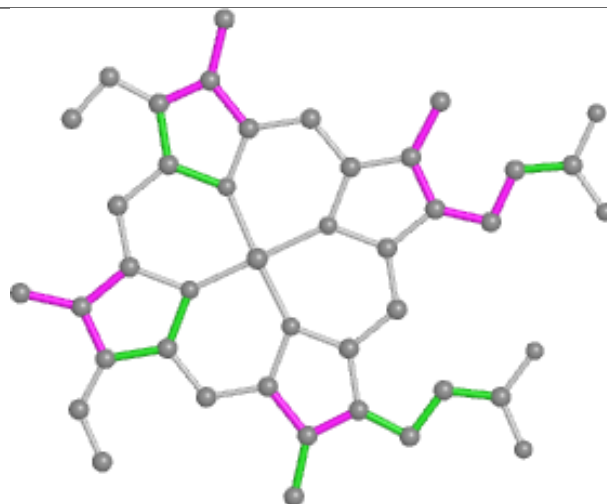
## Ligand HEC B 1



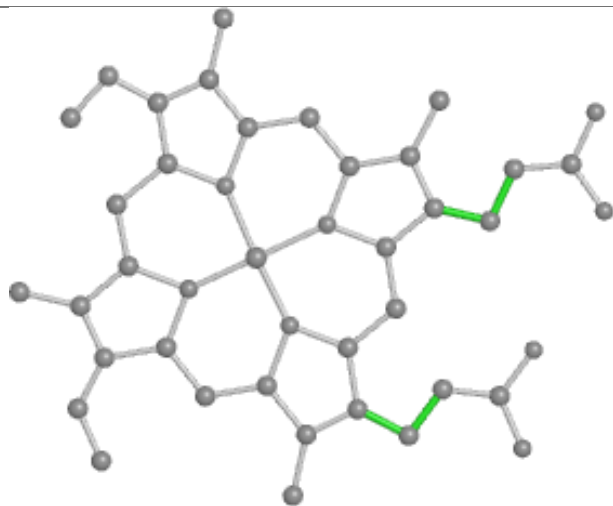
## Ligand HEC B 5



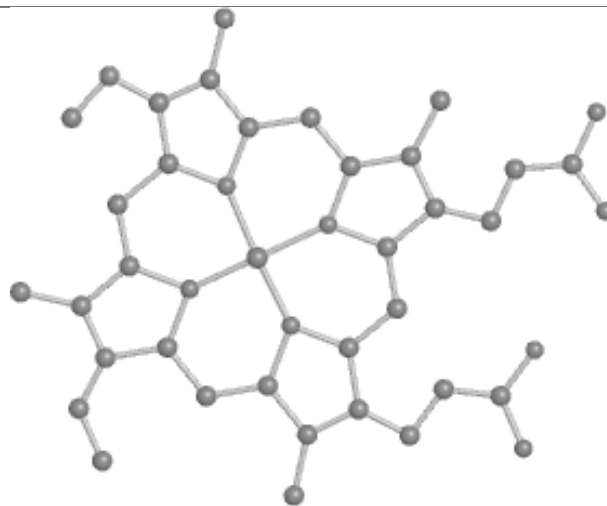
Bond lengths



Bond angles

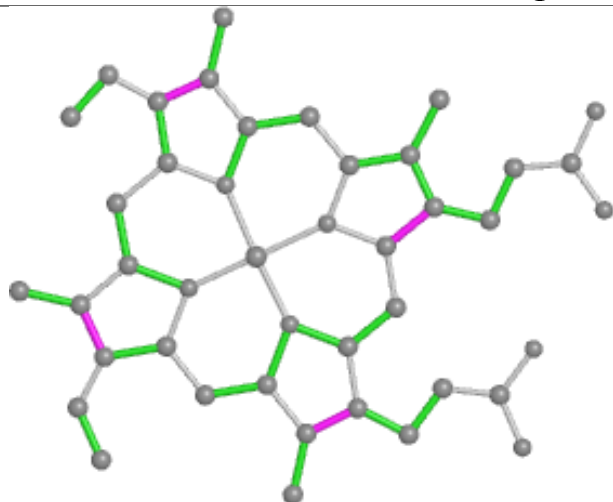


Torsions

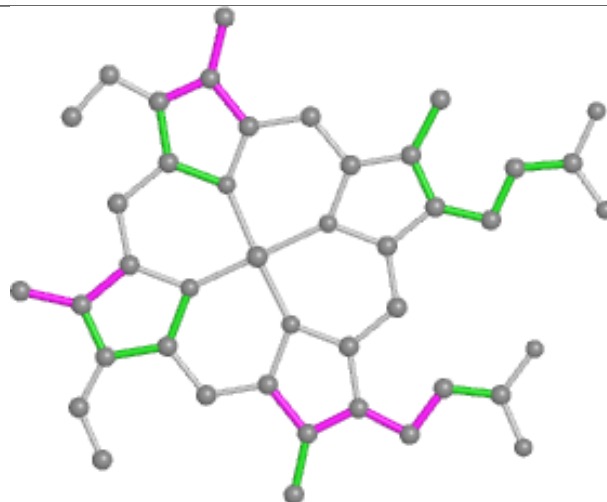


Rings

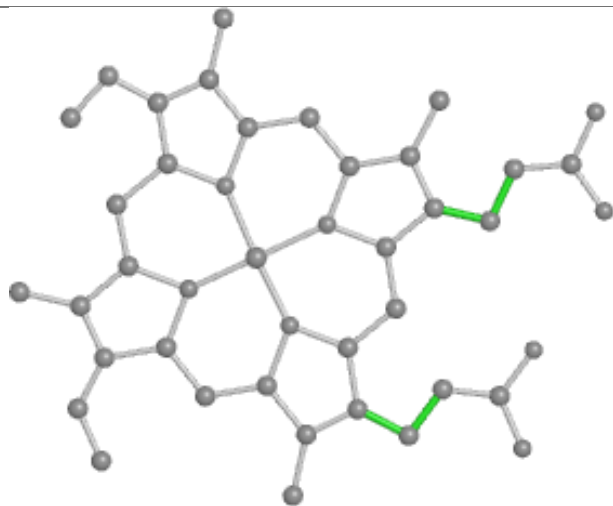
## Ligand HEC C 2



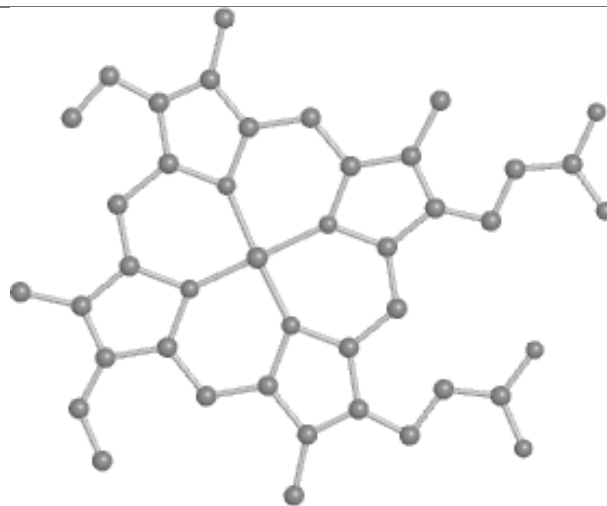
Bond lengths



Bond angles

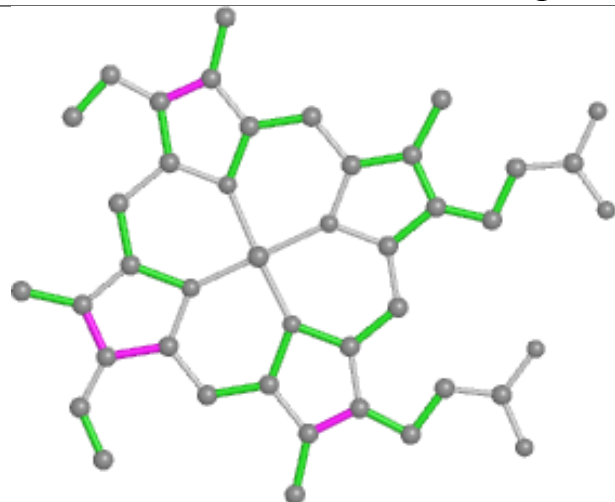


Torsions

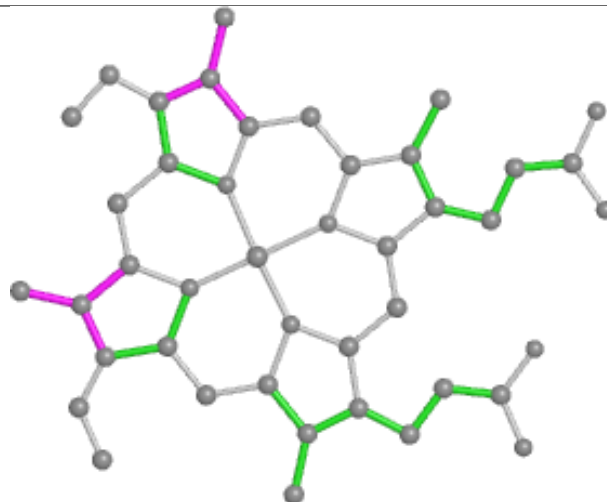


Rings

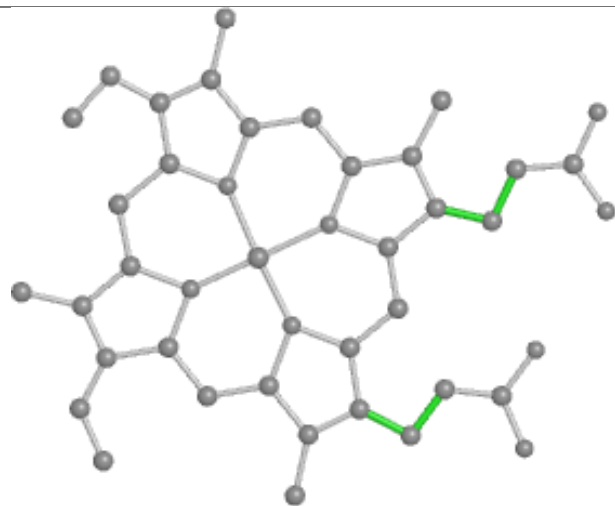
## Ligand HEC C 5



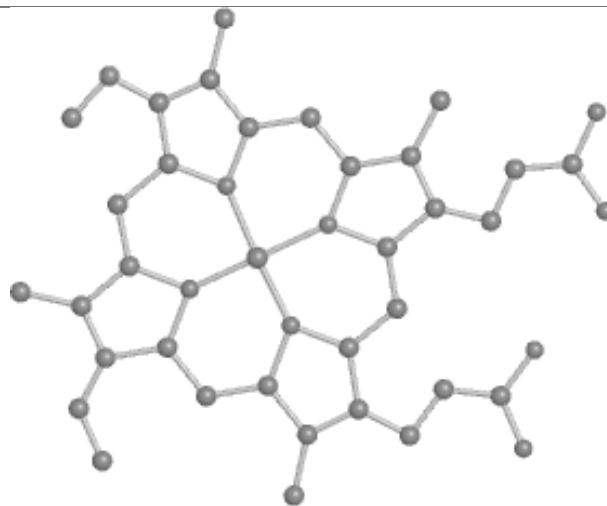
Bond lengths



Bond angles

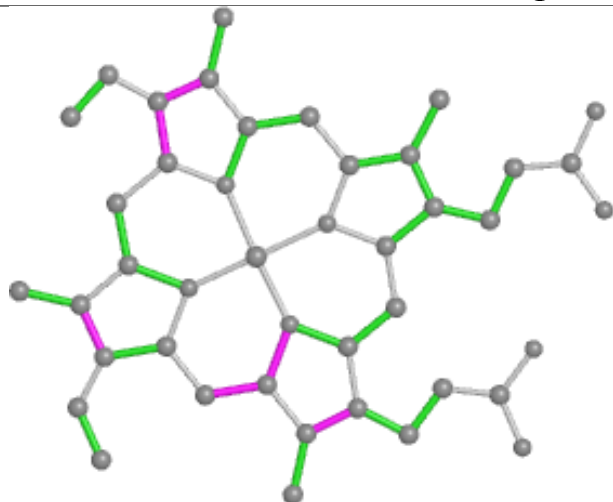


Torsions

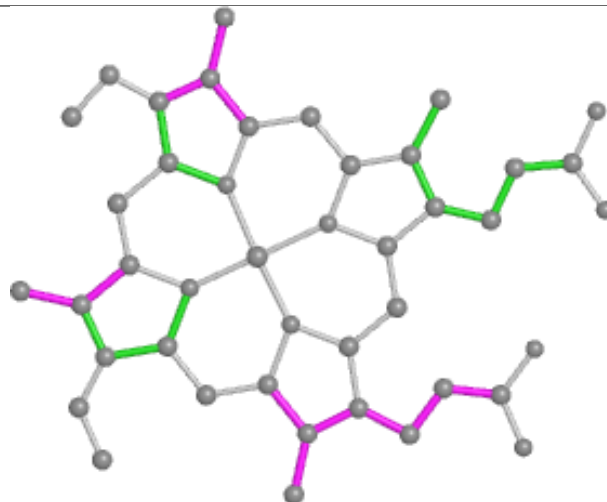


Rings

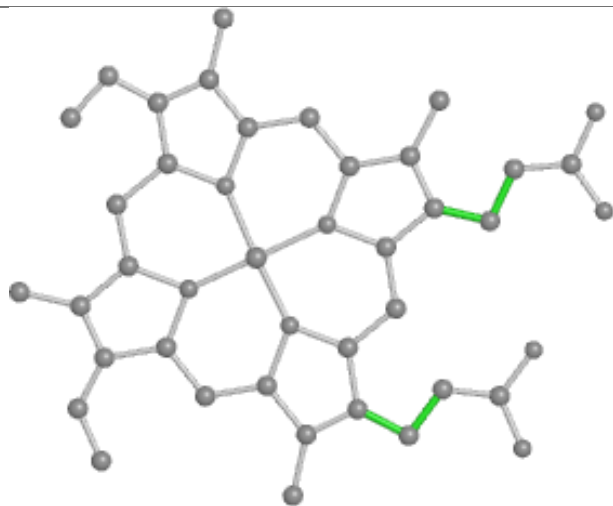
## Ligand HEC B 2



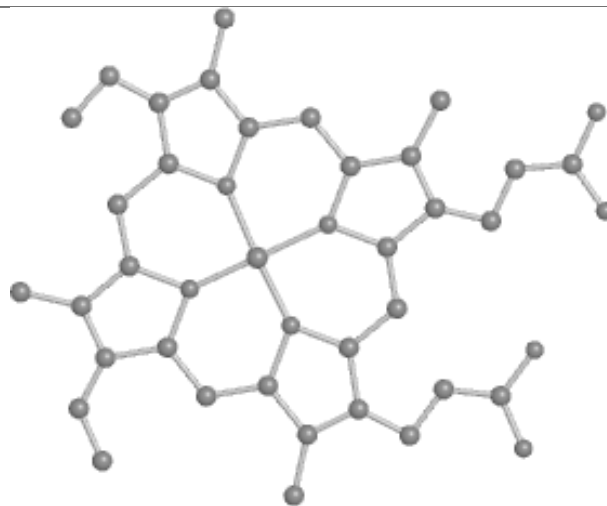
Bond lengths



Bond angles

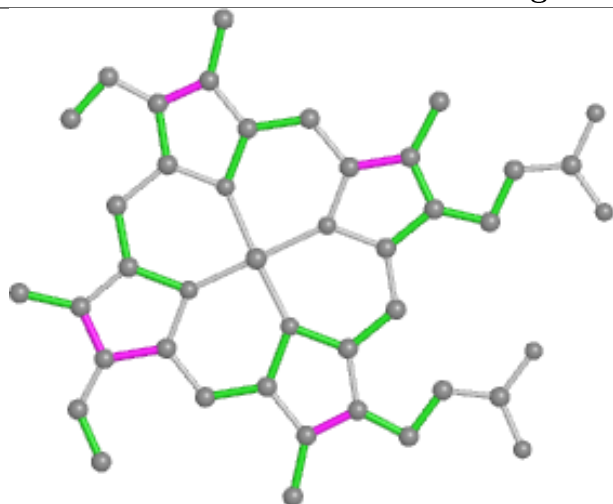


Torsions

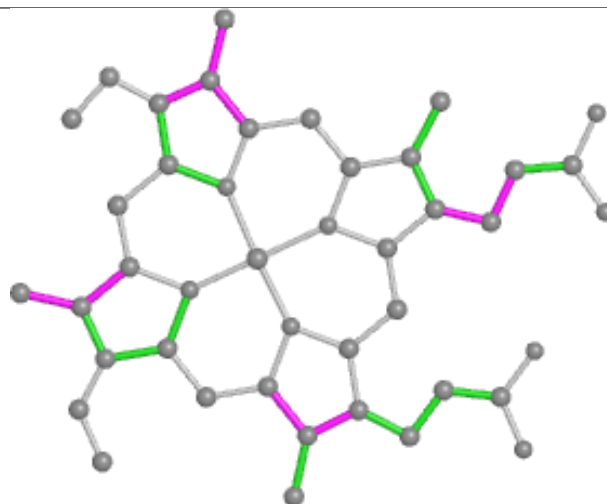


Rings

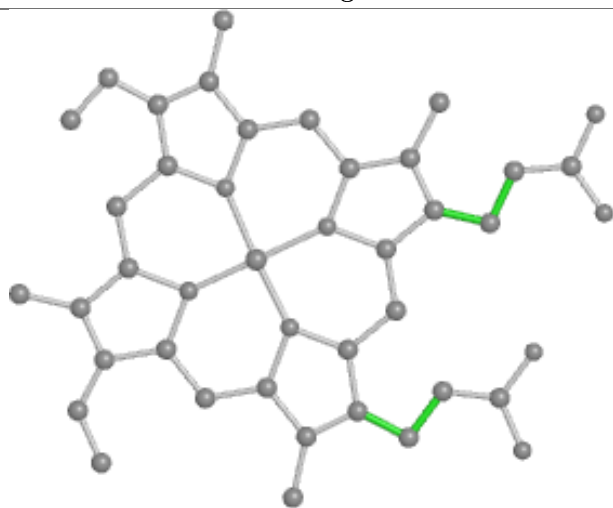
## Ligand HEC A 1



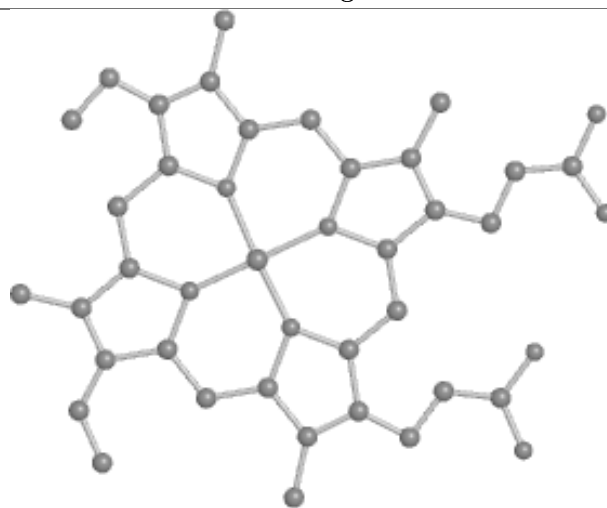
Bond lengths



Bond angles

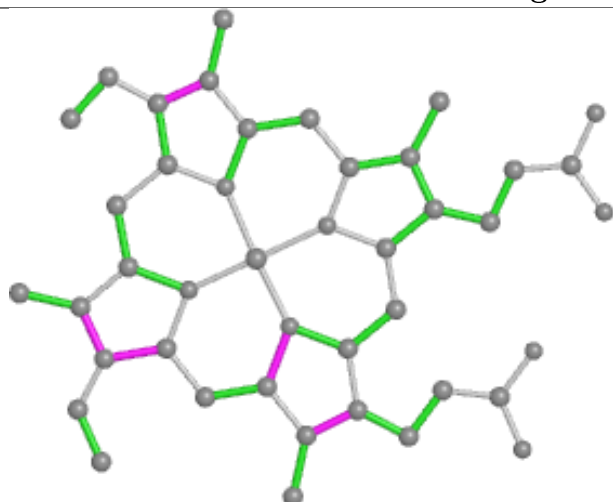


Torsions

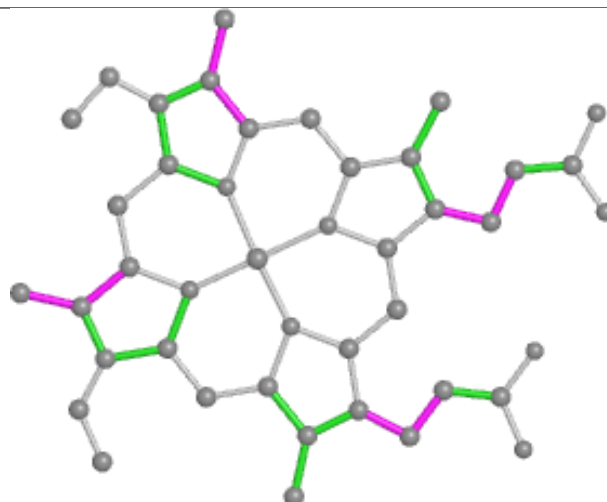


Rings

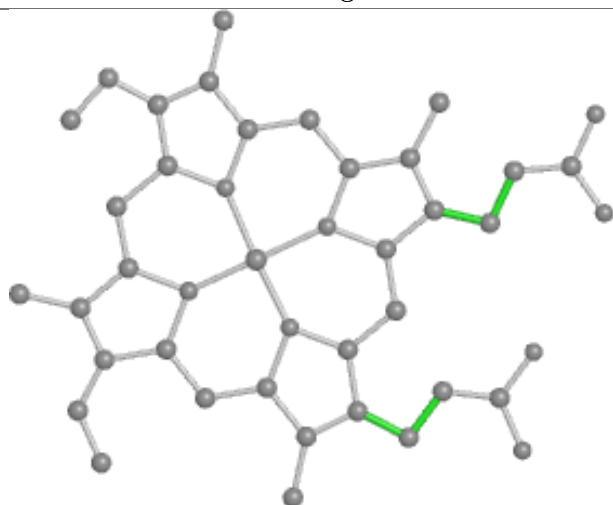
## Ligand HEC A 3



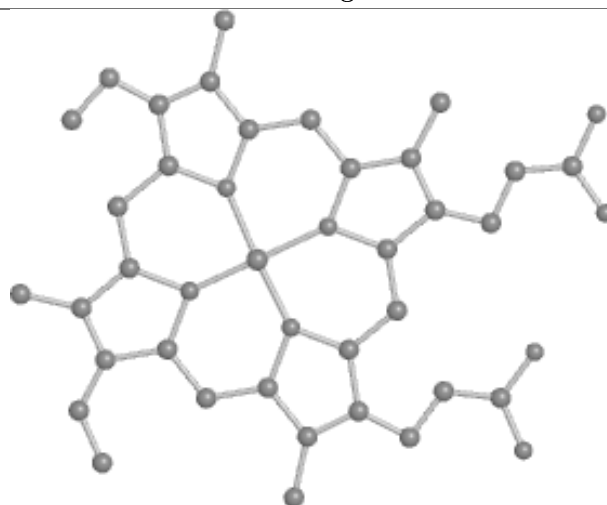
Bond lengths



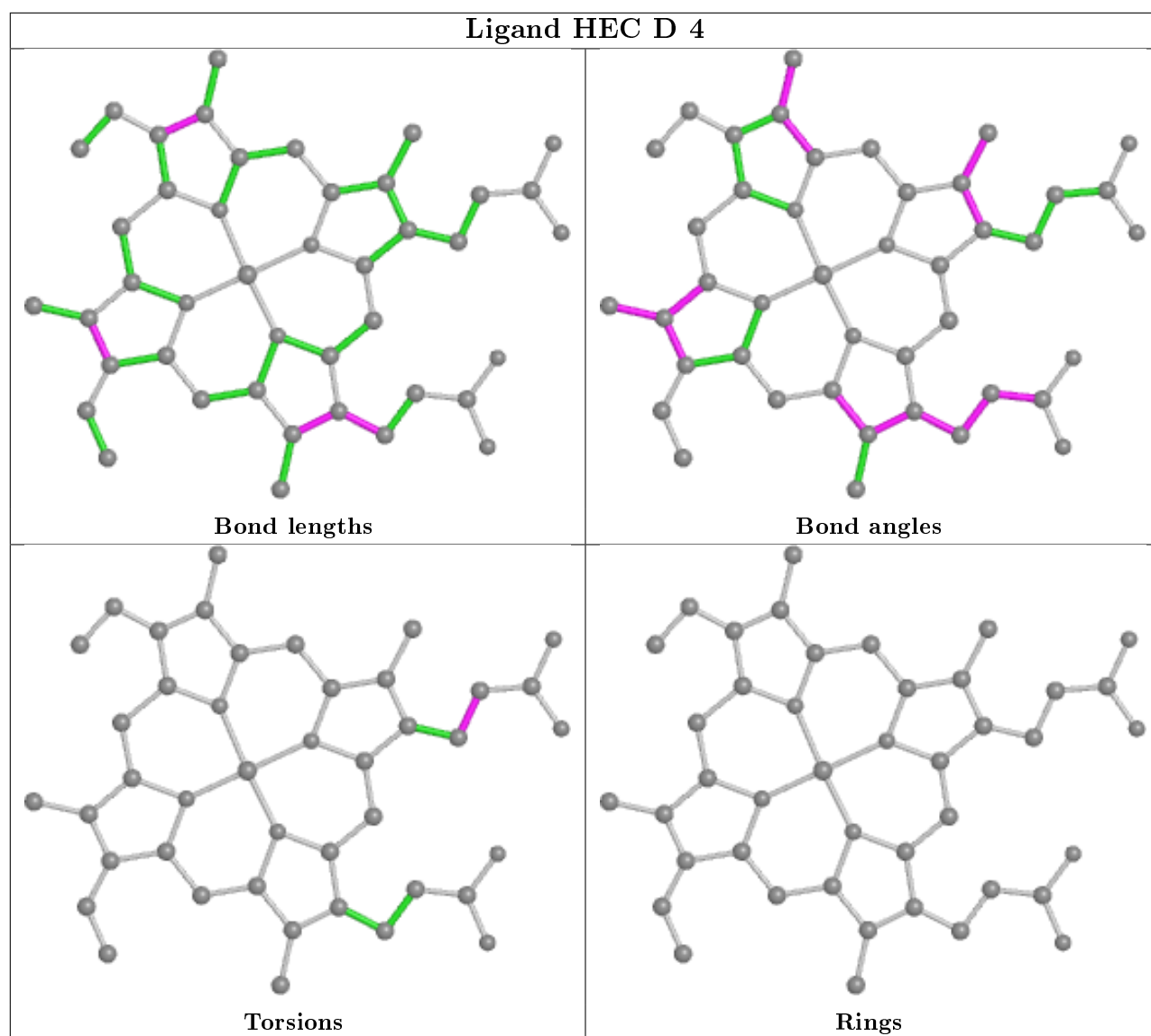
Bond angles



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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	441/452 (97%)	-0.19	10 (2%) 60 66	7, 13, 25, 34	8 (1%)
1	B	441/452 (97%)	-0.34	2 (0%) 91 93	6, 13, 22, 28	9 (2%)
1	C	441/452 (97%)	-0.08	14 (3%) 47 53	8, 16, 28, 38	9 (2%)
1	D	441/452 (97%)	-0.32	2 (0%) 91 93	6, 12, 21, 27	8 (1%)
All	All	1764/1808 (97%)	-0.23	28 (1%) 72 78	6, 14, 24, 38	34 (1%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	477	SER	5.0
1	A	476	LEU	4.0
1	C	476	LEU	3.9
1	C	293	ALA	3.8
1	A	111	LYS	3.7

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
5	EDO	D	22	4/4	0.82	0.17	33,33,33,35	0
5	EDO	A	11	4/4	0.82	0.17	26,26,29,30	0
5	EDO	D	25	4/4	0.83	0.17	27,27,30,30	0
5	EDO	C	12	4/4	0.84	0.14	28,29,30,32	0
5	EDO	B	20	4/4	0.87	0.17	23,28,30,35	0
5	EDO	C	21	4/4	0.88	0.17	34,35,35,36	0
5	EDO	D	23	4/4	0.90	0.12	24,28,30,34	0
5	EDO	D	21	4/4	0.90	0.14	23,29,32,35	0
5	EDO	A	21	4/4	0.91	0.12	32,32,32,34	0
5	EDO	D	481	4/4	0.92	0.16	34,34,35,35	0
5	EDO	B	18	4/4	0.92	0.12	27,28,28,28	0
2	CA	D	1502	1/1	0.93	0.11	16,16,16,16	1
5	EDO	C	25	4/4	0.93	0.12	23,23,26,28	0
5	EDO	A	22	4/4	0.94	0.12	20,25,28,31	0
2	CA	A	1502	1/1	0.95	0.07	28,28,28,28	0
5	EDO	A	14	4/4	0.95	0.11	30,31,31,33	0
4	SO4	C	2001	5/5	0.95	0.11	36,36,38,39	0
5	EDO	B	19	4/4	0.95	0.12	20,25,25,25	0
2	CA	C	1502	1/1	0.95	0.07	31,31,31,31	0
5	EDO	C	23	4/4	0.95	0.17	35,35,35,36	0
5	EDO	B	17	4/4	0.95	0.08	28,29,30,31	0
4	SO4	D	2001	5/5	0.96	0.13	33,33,34,37	0
5	EDO	A	13	4/4	0.96	0.09	22,23,25,28	0
5	EDO	C	481	4/4	0.96	0.09	13,16,18,19	0
5	EDO	D	24	4/4	0.96	0.12	20,21,22,22	0
5	EDO	A	15	4/4	0.96	0.09	27,27,27,27	0
2	CA	B	1502	1/1	0.96	0.06	25,25,25,25	0
4	SO4	A	2001	5/5	0.96	0.10	23,25,27,31	0
5	EDO	A	481	4/4	0.97	0.09	11,12,14,17	0
3	HEC	A	2	43/43	0.97	0.10	10,12,15,16	0
3	HEC	C	4	43/43	0.97	0.10	9,12,20,28	0
3	HEC	C	5	43/43	0.97	0.09	11,14,22,30	0
4	SO4	B	2001	5/5	0.97	0.08	21,21,25,27	0
5	EDO	B	481	4/4	0.97	0.10	12,14,16,18	0
5	EDO	B	16	4/4	0.97	0.08	16,17,17,19	0
3	HEC	C	2	43/43	0.97	0.11	12,16,17,19	0
3	HEC	B	4	43/43	0.98	0.10	6,8,17,25	0
5	EDO	D	6	4/4	0.98	0.07	12,13,15,18	0
3	HEC	A	4	43/43	0.98	0.10	5,9,18,26	0
3	HEC	A	5	43/43	0.98	0.08	8,10,19,24	0
3	HEC	D	1	43/43	0.98	0.08	5,7,9,10	0
5	EDO	A	20	4/4	0.98	0.07	18,19,19,20	0
3	HEC	C	3	43/43	0.98	0.08	9,11,14,15	0

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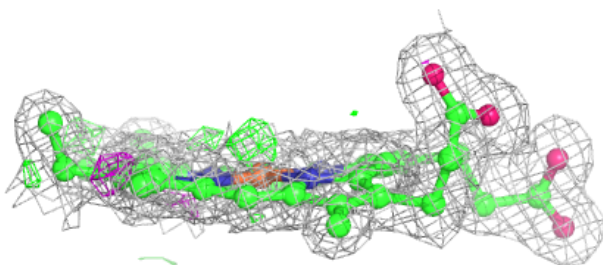
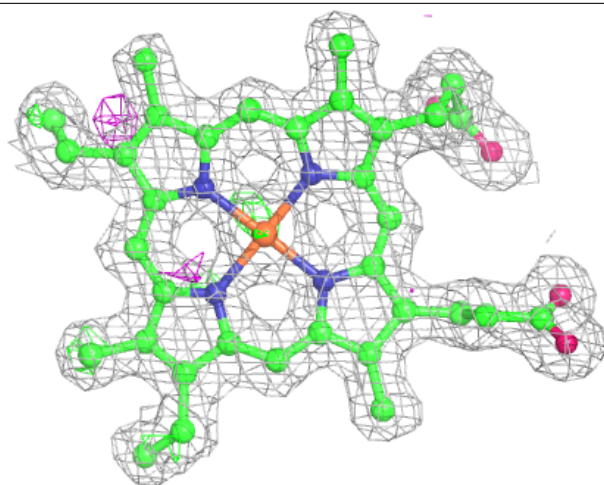
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	HEC	D	5	43/43	0.98	0.09	7,11,22,24	0
3	HEC	C	1	43/43	0.98	0.10	9,12,13,13	0
3	HEC	B	1	43/43	0.98	0.09	6,8,10,11	0
3	HEC	B	5	43/43	0.98	0.09	7,10,19,23	0
3	HEC	B	2	43/43	0.98	0.08	7,9,12,12	0
3	HEC	D	4	43/43	0.98	0.08	5,8,16,26	0
3	HEC	D	3	43/43	0.98	0.08	4,7,9,12	0
3	HEC	A	1	43/43	0.98	0.10	7,9,10,11	0
3	HEC	A	3	43/43	0.98	0.08	7,9,11,13	0
5	EDO	D	482	4/4	0.98	0.06	17,18,18,19	0
3	HEC	D	2	43/43	0.98	0.08	7,10,12,14	0
5	EDO	C	22	4/4	0.99	0.06	18,18,20,21	0
3	HEC	B	3	43/43	0.99	0.08	5,7,10,11	0
2	CA	A	1501	1/1	1.00	0.08	10,10,10,10	0
2	CA	B	1501	1/1	1.00	0.06	10,10,10,10	0
2	CA	D	1501	1/1	1.00	0.08	8,8,8,8	0
2	CA	C	1501	1/1	1.00	0.09	11,11,11,11	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.

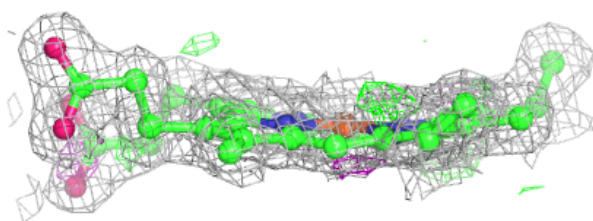
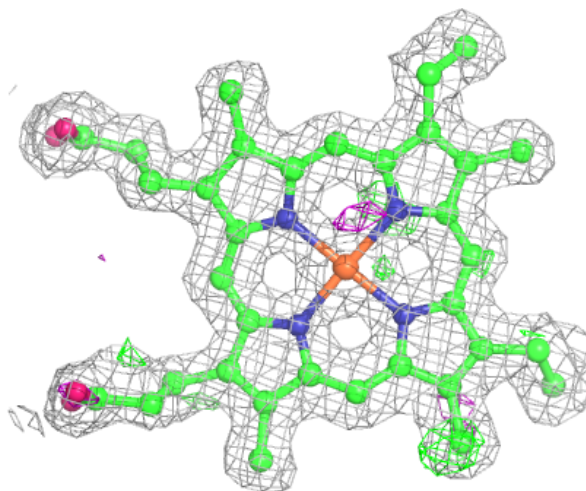
**Electron density around HEC A 2:**

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



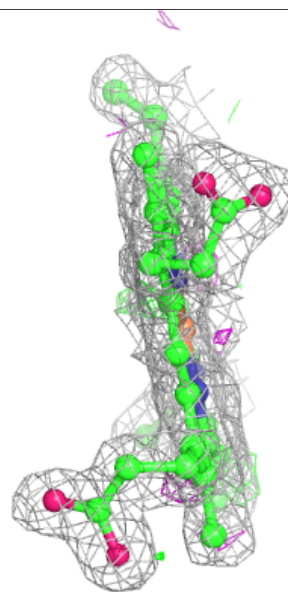
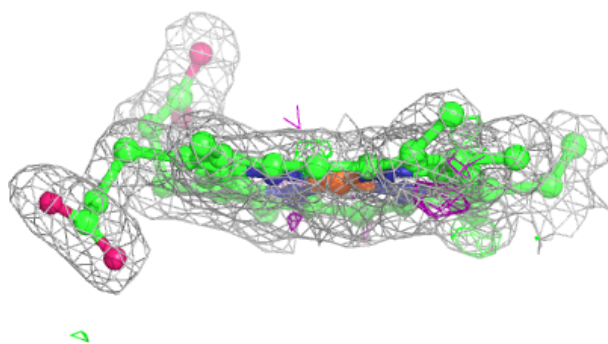
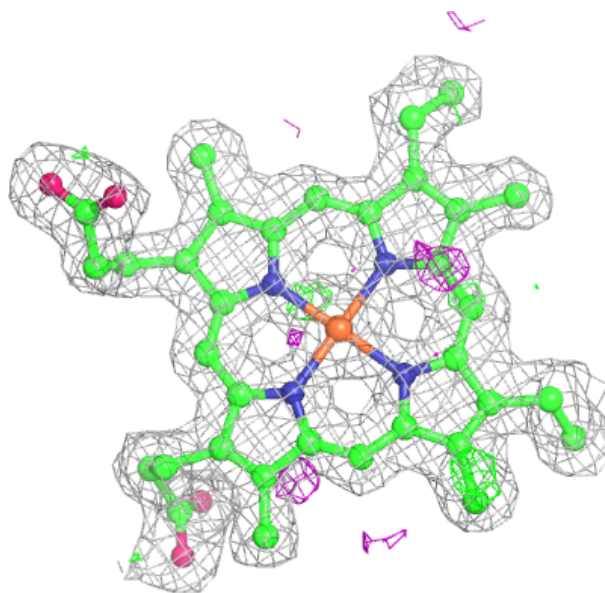
**Electron density around HEC C 4:**

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and green (positive)



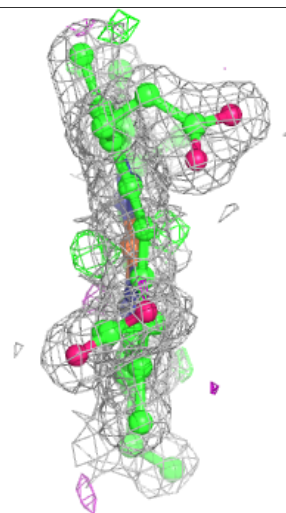
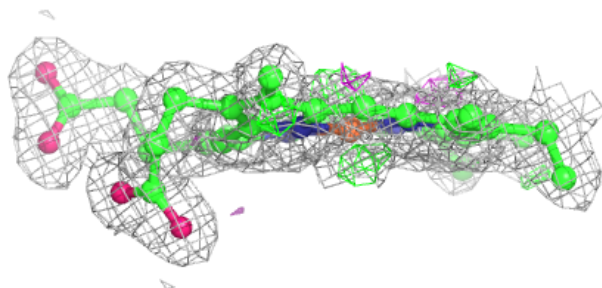
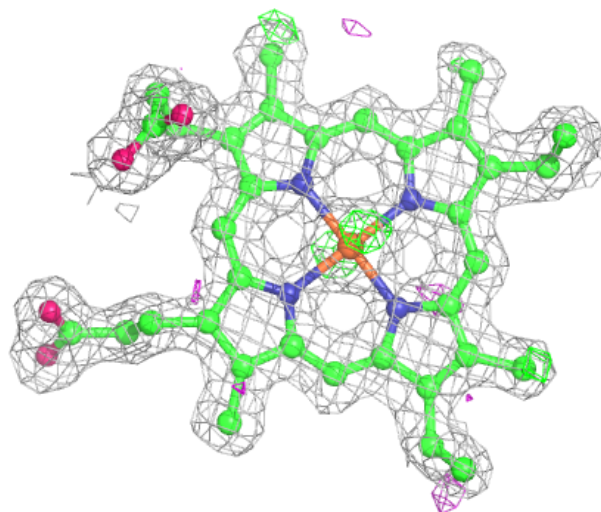
**Electron density around HEC C 5:**

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



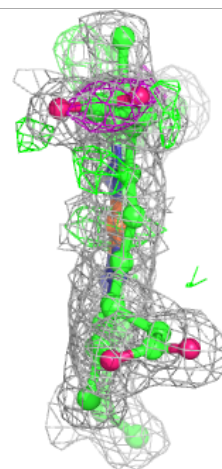
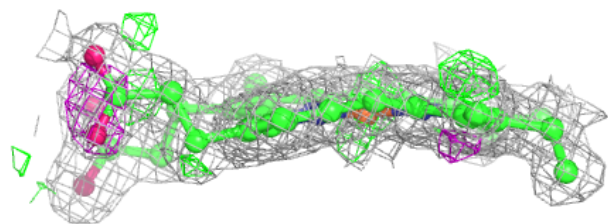
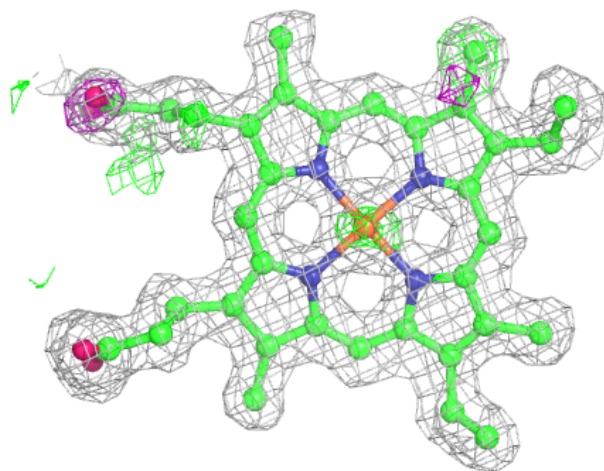
**Electron density around HEC C 2:**

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



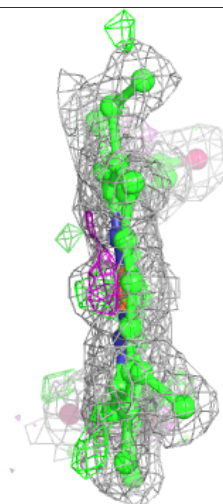
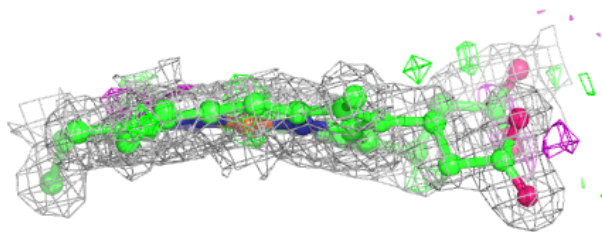
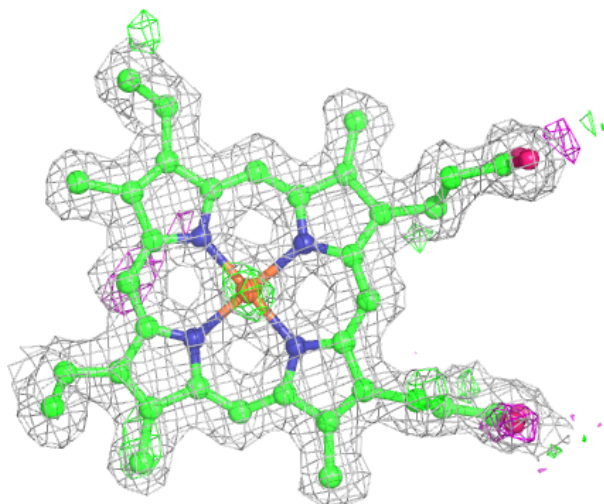
**Electron density around HEC B 4:**

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



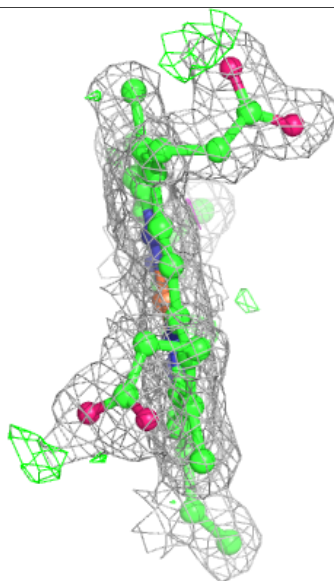
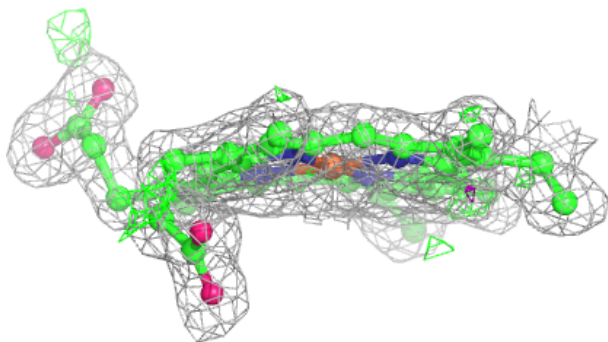
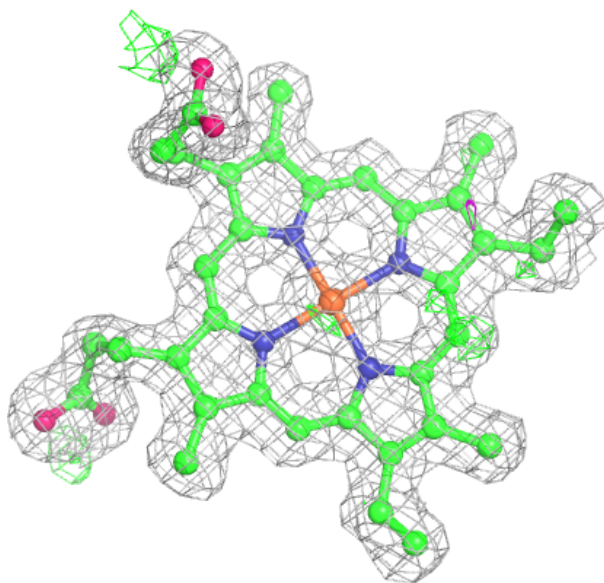
**Electron density around HEC A 4:**

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



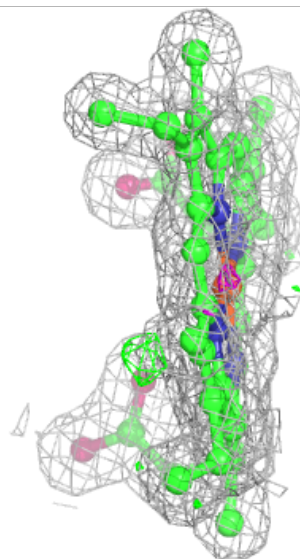
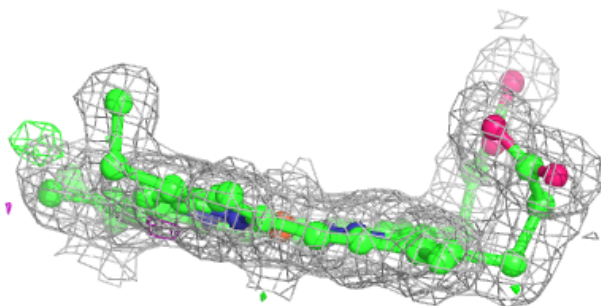
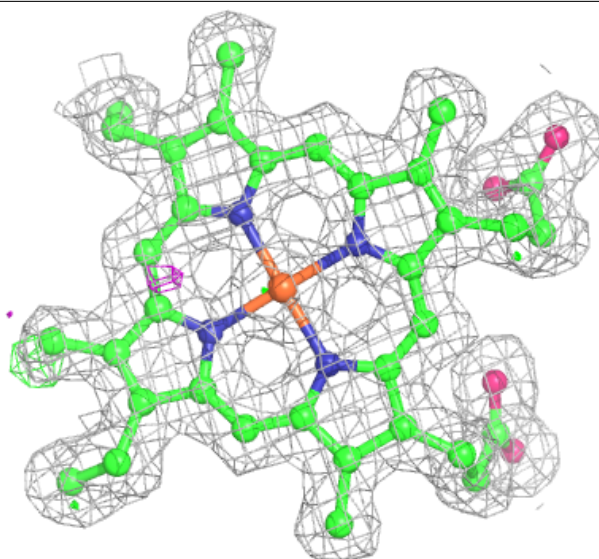
**Electron density around HEC A 5:**

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



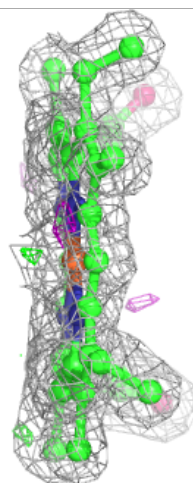
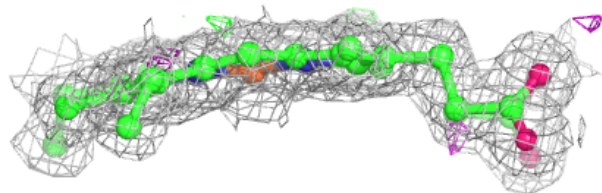
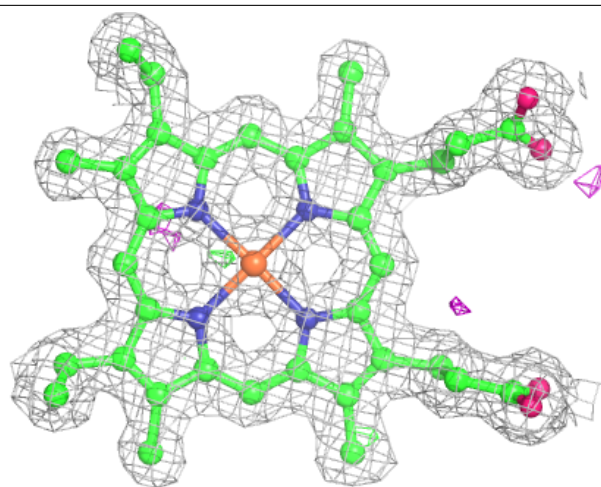
**Electron density around HEC D 1:**

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



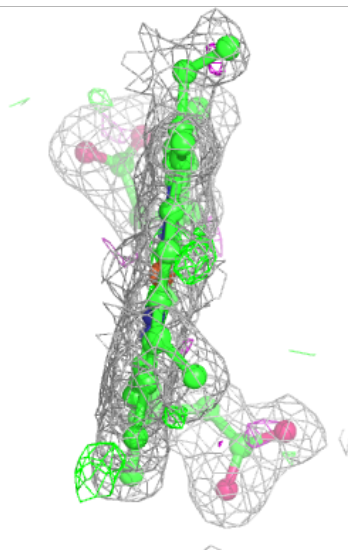
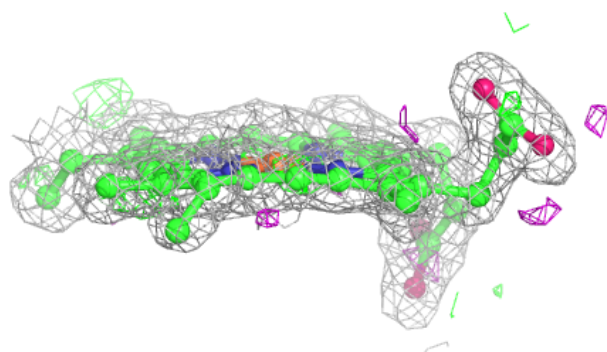
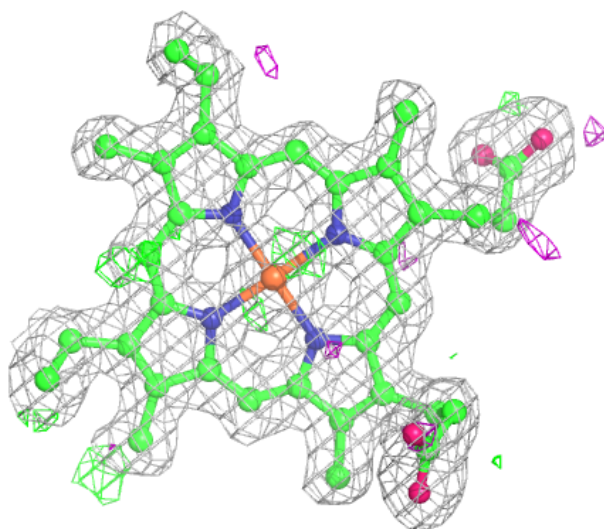
**Electron density around HEC C 3:**

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



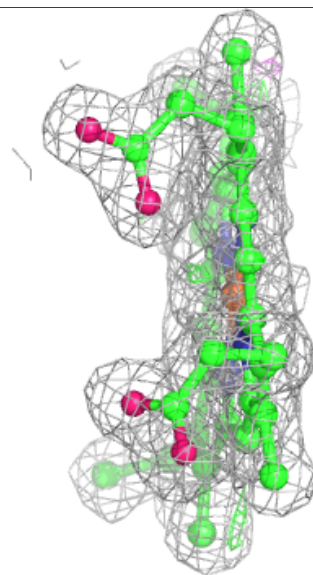
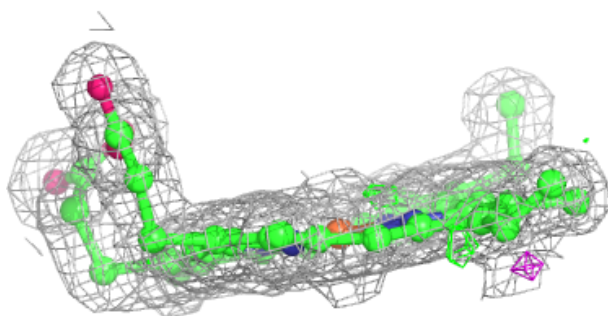
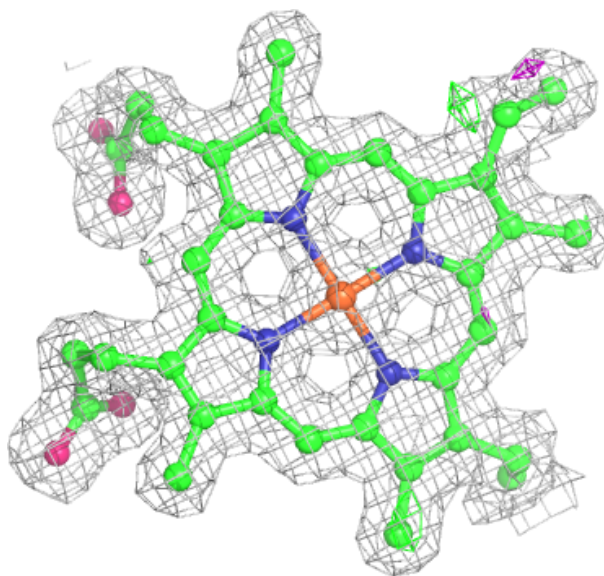
**Electron density around HEC D 5:**

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



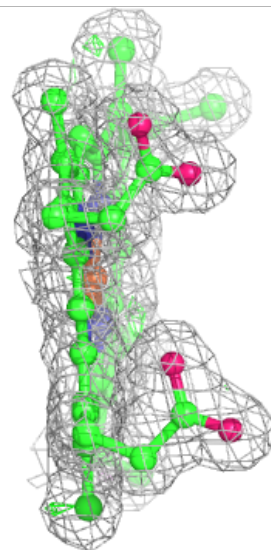
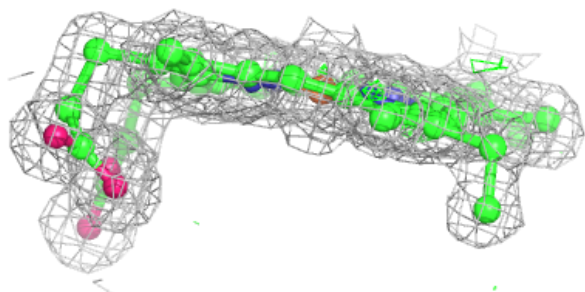
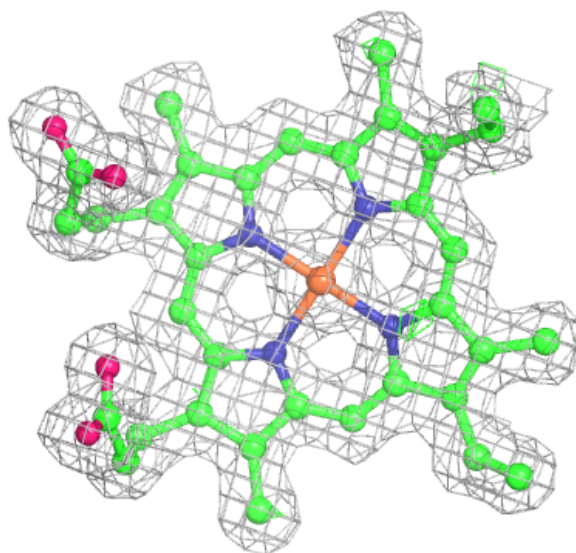
**Electron density around HEC C 1:**

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and green (positive)



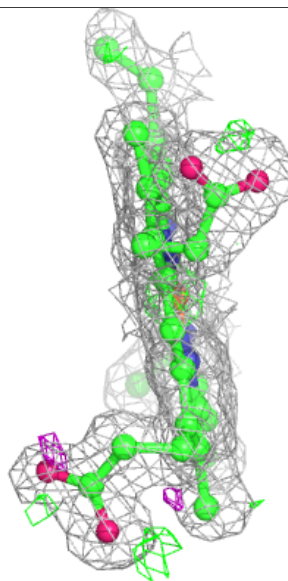
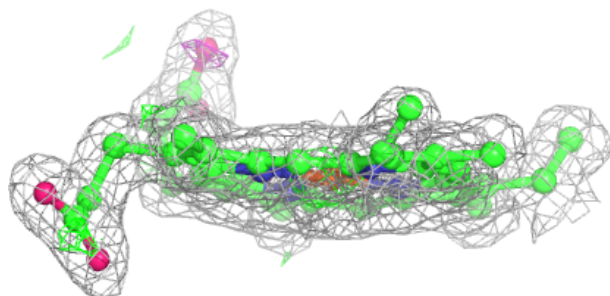
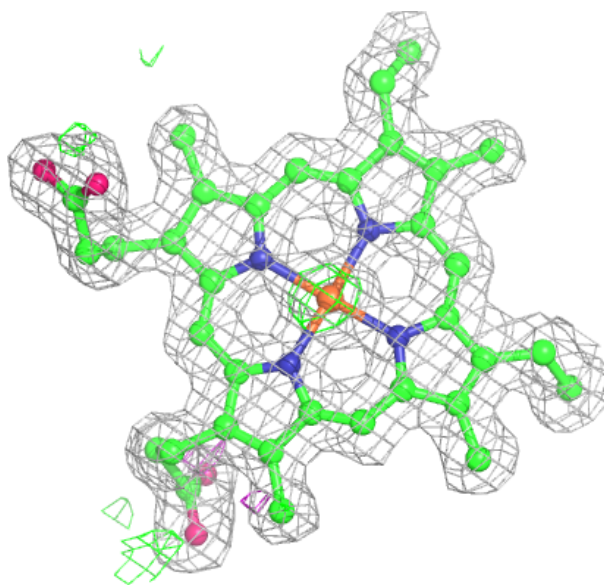
**Electron density around HEC B 1:**

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



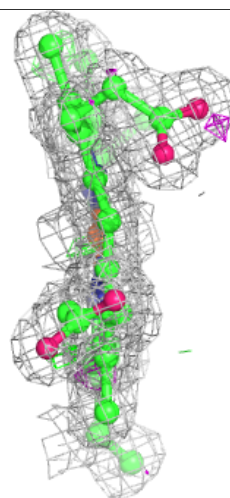
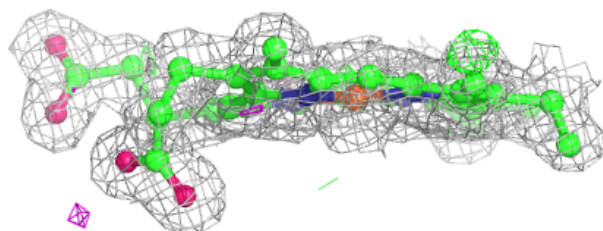
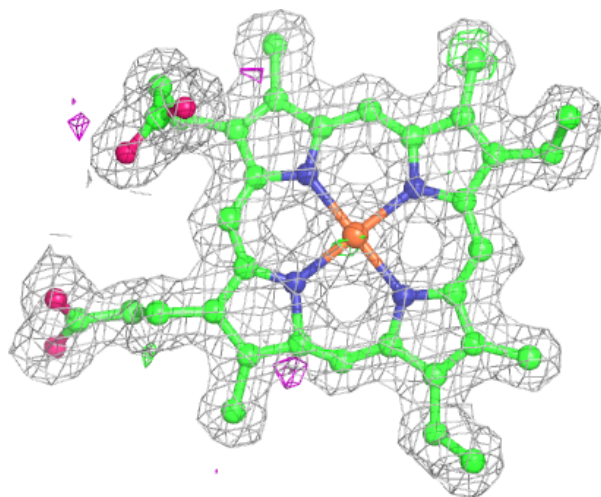
**Electron density around HEC B 5:**

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



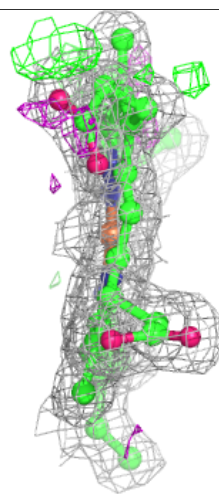
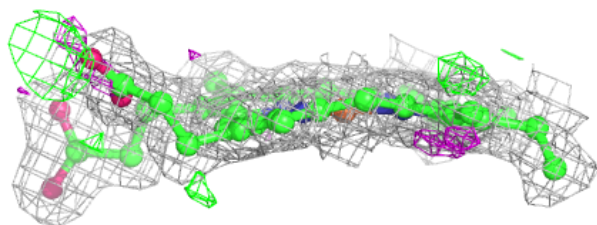
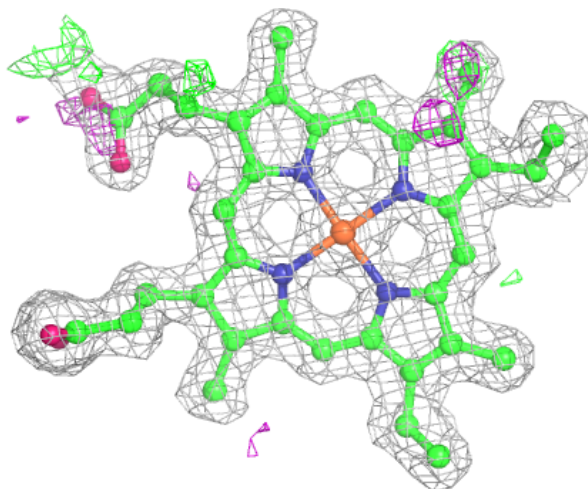
**Electron density around HEC B 2:**

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



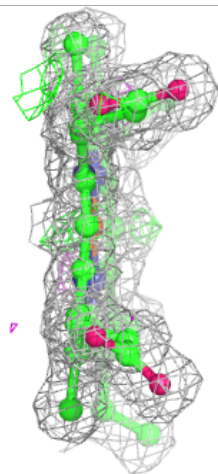
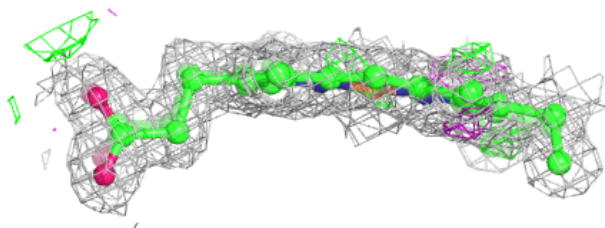
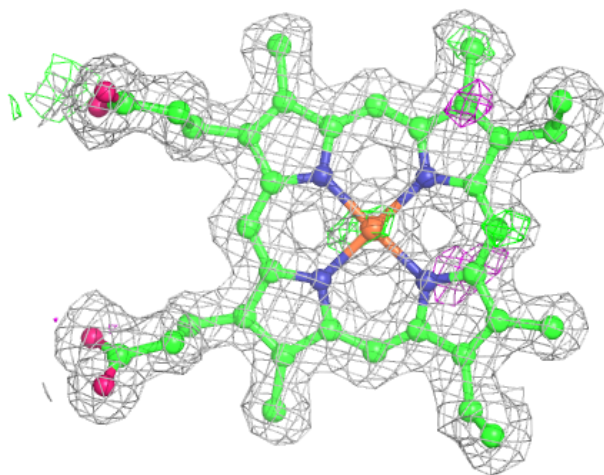
**Electron density around HEC D 4:**

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



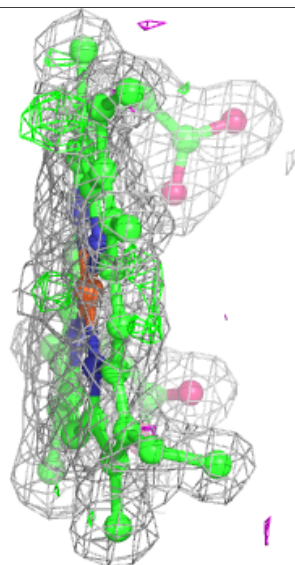
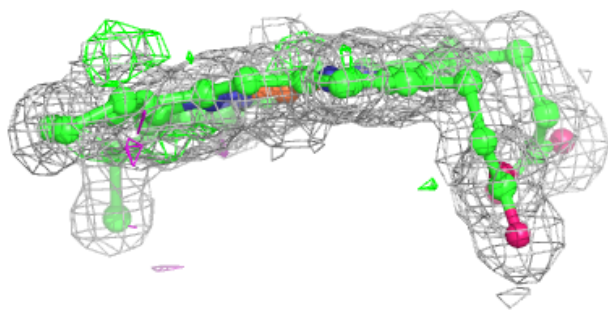
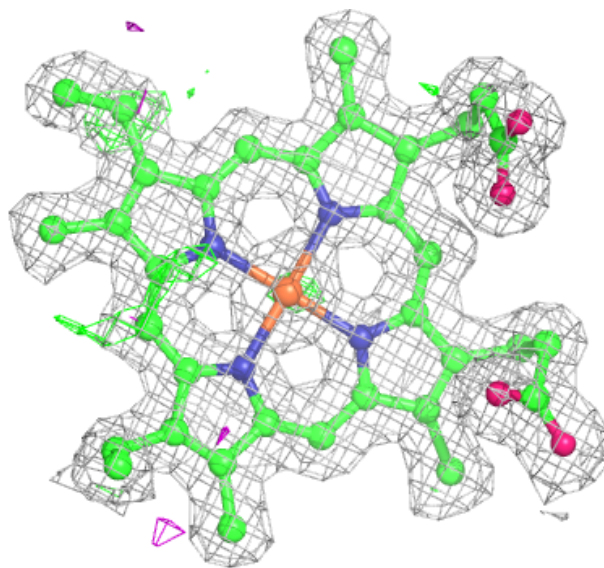
**Electron density around HEC D 3:**

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



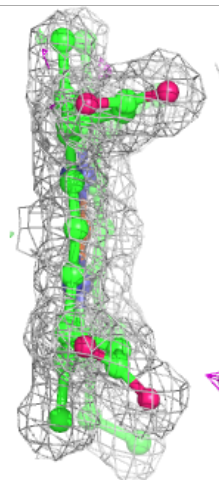
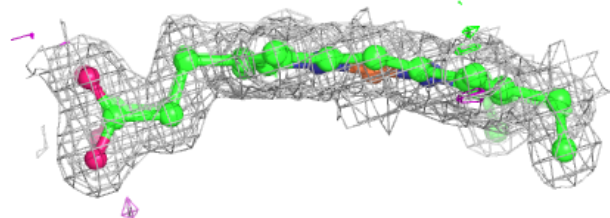
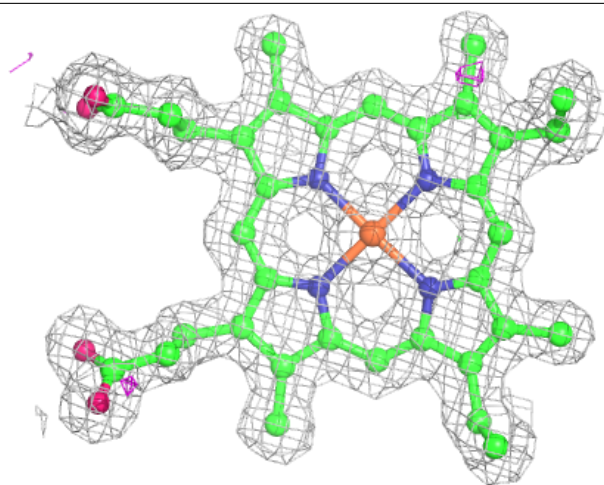
**Electron density around HEC A 1:**

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



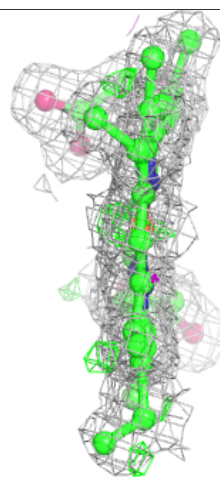
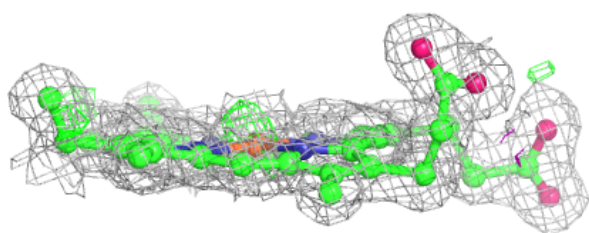
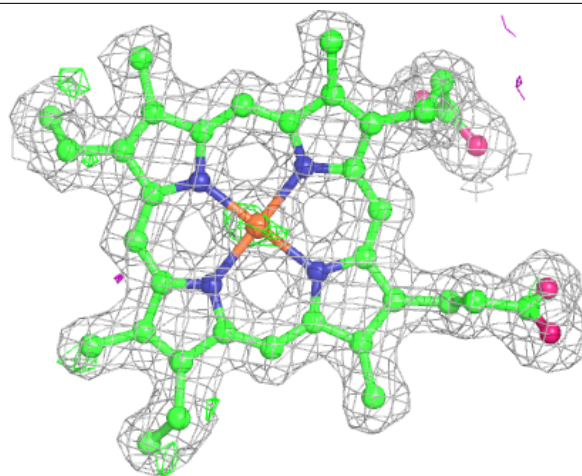
**Electron density around HEC A 3:**

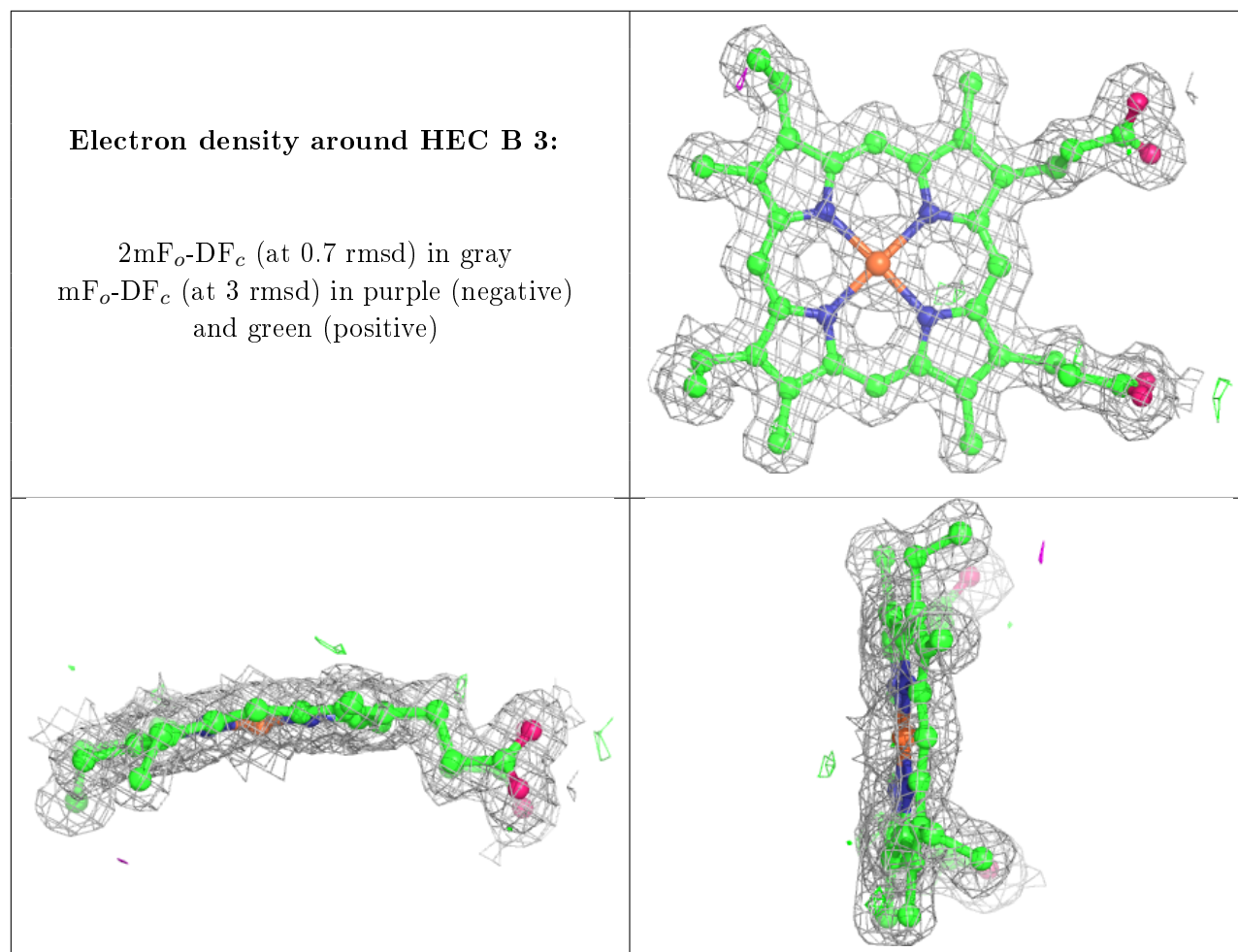
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEC D 2:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.