



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 24, 2026 – 11:54 PM UTC

PDB ID : 2J7A / pdb_00002j7a
Title : Crystal structure of cytochrome c nitrite reductase NrfHA complex from *Desulfovibrio vulgaris*
Authors : Rodrigues, M.L.; Oliveira, T.F.; Pereira, I.A.C.; Archer, M.
Deposited on : 2006-10-06
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

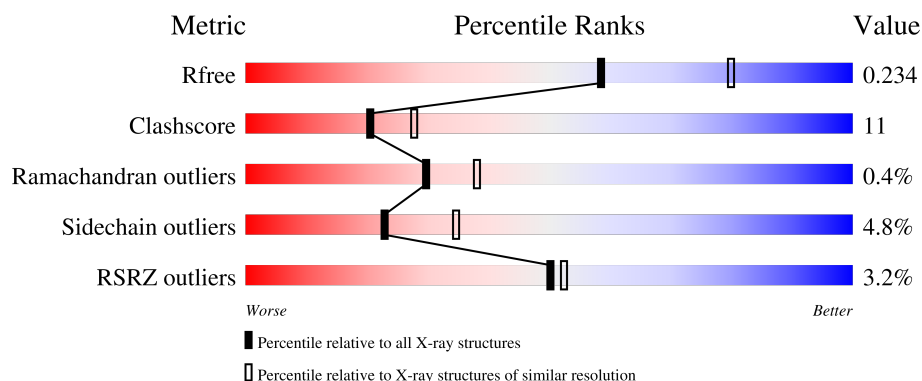
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	500	% 83% 14% ..
1	B	500	2% 81% 17% .
1	D	500	83% 15% ..
1	E	500	3% 80% 17% ...
1	G	500	% 83% 14% ..

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Mol	Chain	Length	Quality of chain
1	H	500	
1	J	500	
1	K	500	
1	M	500	
1	N	500	
1	P	500	
1	Q	500	
2	C	159	
2	F	159	
2	I	159	
2	L	159	
2	O	159	
2	R	159	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 60930 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called CYTOCHROME C NITRITE REDUCTASE NRFA.

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

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

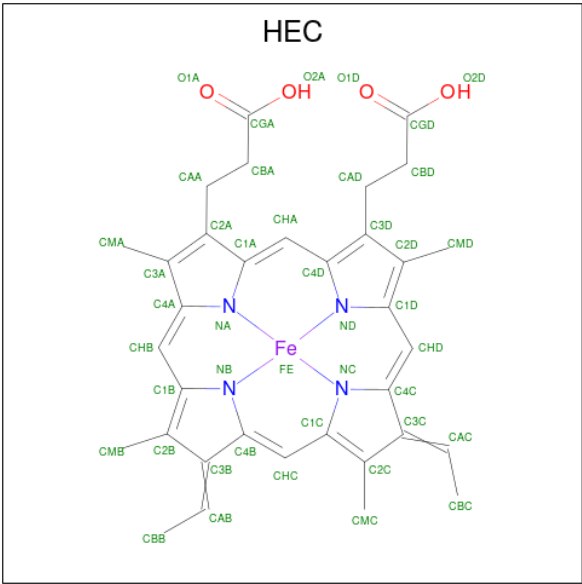
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	145	Total	C	N	O	S	0	1	0
			1094	680	201	197	16			
2	F	145	Total	C	N	O	S	0	1	0
			1093	679	199	199	16			

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

- Molecule 3 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₄FeN₄O₄).



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

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

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

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

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

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

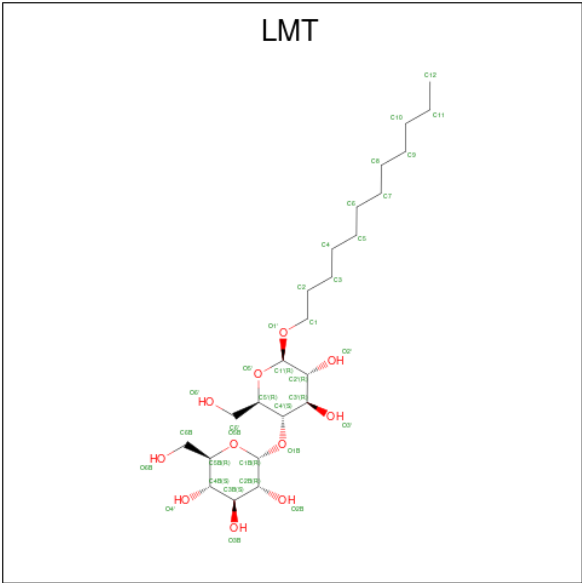
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Ca 2	0	0
4	B	2	Total 2	Ca 2	0	0
4	D	2	Total 2	Ca 2	0	0
4	E	2	Total 2	Ca 2	0	0
4	G	2	Total 2	Ca 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	2	Total	Ca	0	0
			2	2		
4	J	2	Total	Ca	0	0
			2	2		
4	K	2	Total	Ca	0	0
			2	2		
4	M	2	Total	Ca	0	0
			2	2		
4	N	2	Total	Ca	0	0
			2	2		
4	P	2	Total	Ca	0	0
			2	2		
4	Q	2	Total	Ca	0	0
			2	2		

- Molecule 5 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



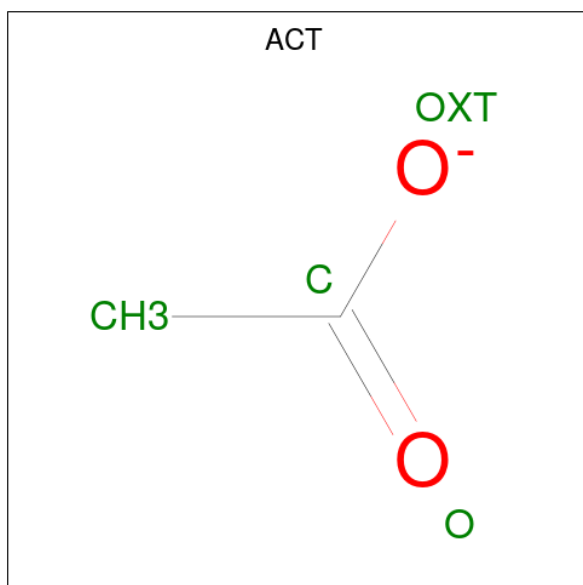
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			35	24	11		
5	F	1	Total	C	O	0	0
			35	24	11		
5	I	1	Total	C	O	0	0
			35	24	11		
5	L	1	Total	C	O	0	0
			35	24	11		

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

- Molecule 6 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 7 is water.

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

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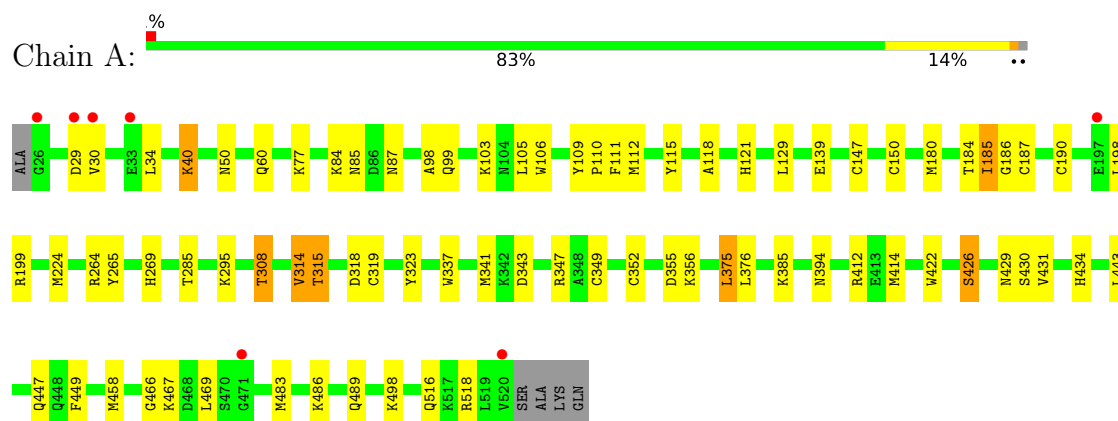
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	E	155	Total 155	O 155	0	0
7	F	42	Total 42	O 42	0	0
7	G	160	Total 160	O 160	0	0
7	H	194	Total 194	O 194	0	0
7	I	40	Total 40	O 40	0	0
7	J	168	Total 168	O 168	0	0
7	K	106	Total 106	O 106	0	0
7	L	43	Total 43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

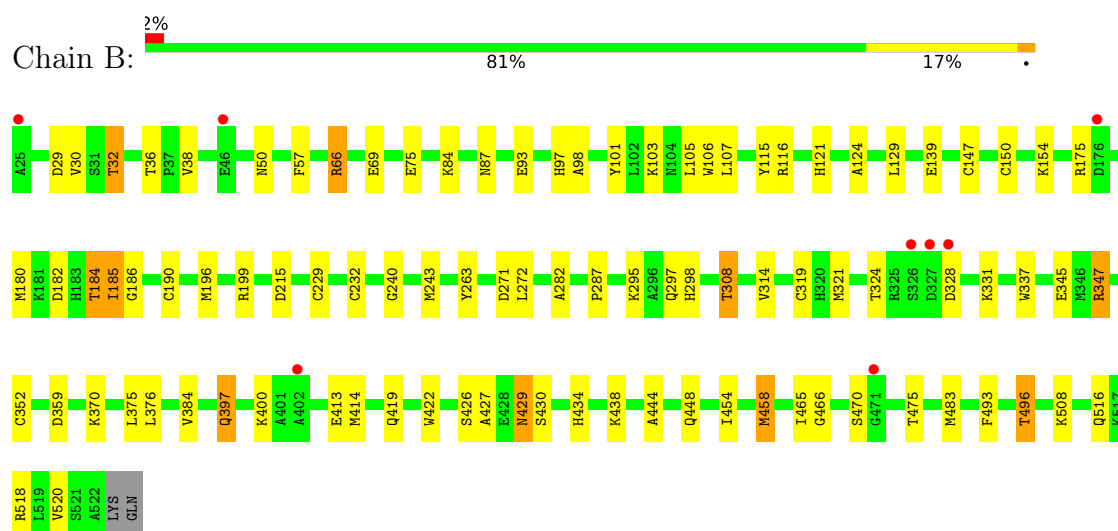
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, 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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

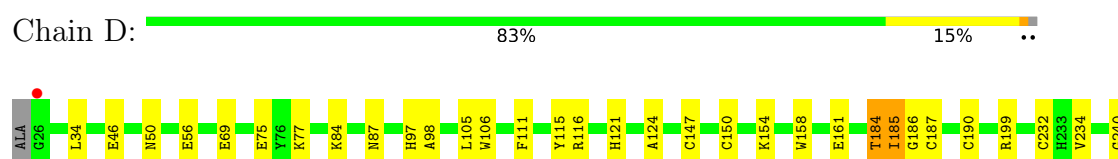
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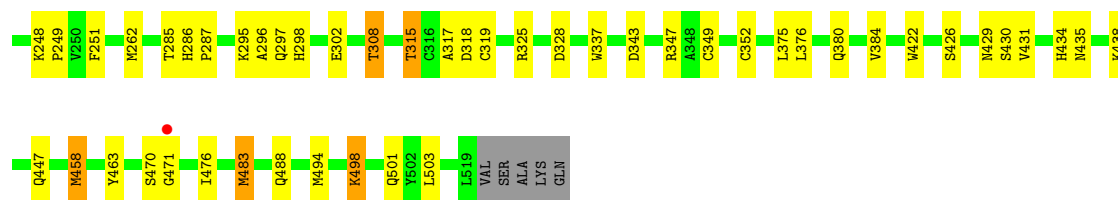


• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

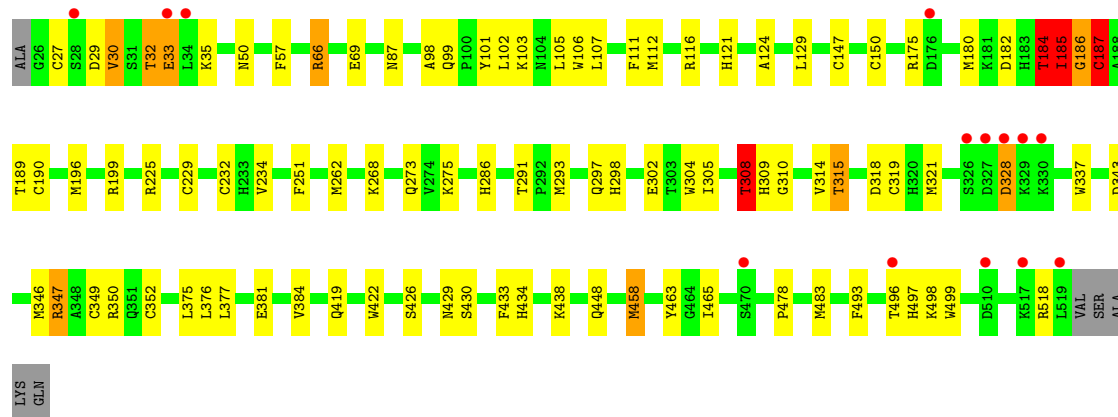
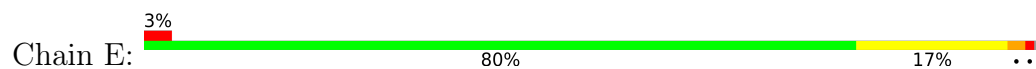


• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

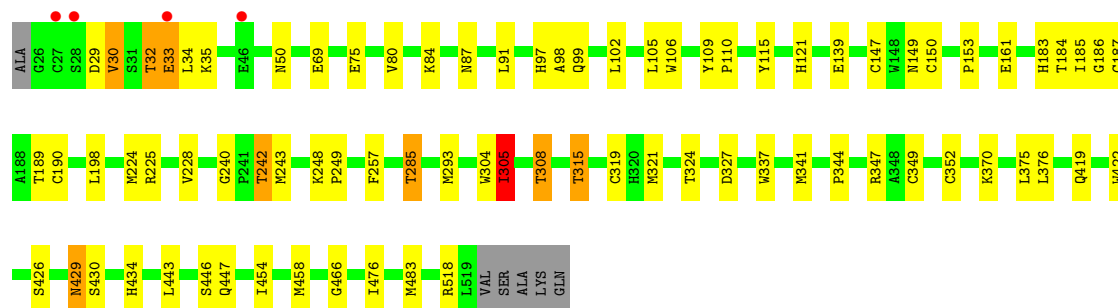
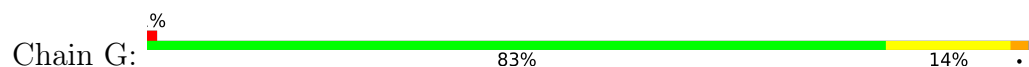




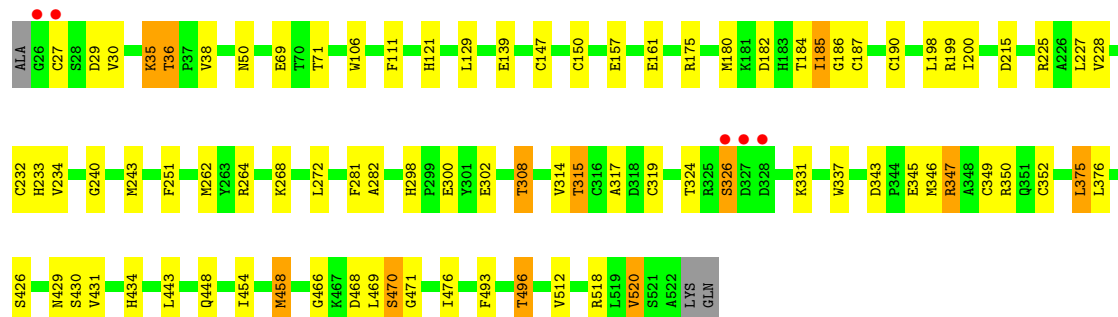
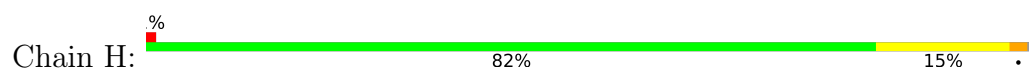
• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



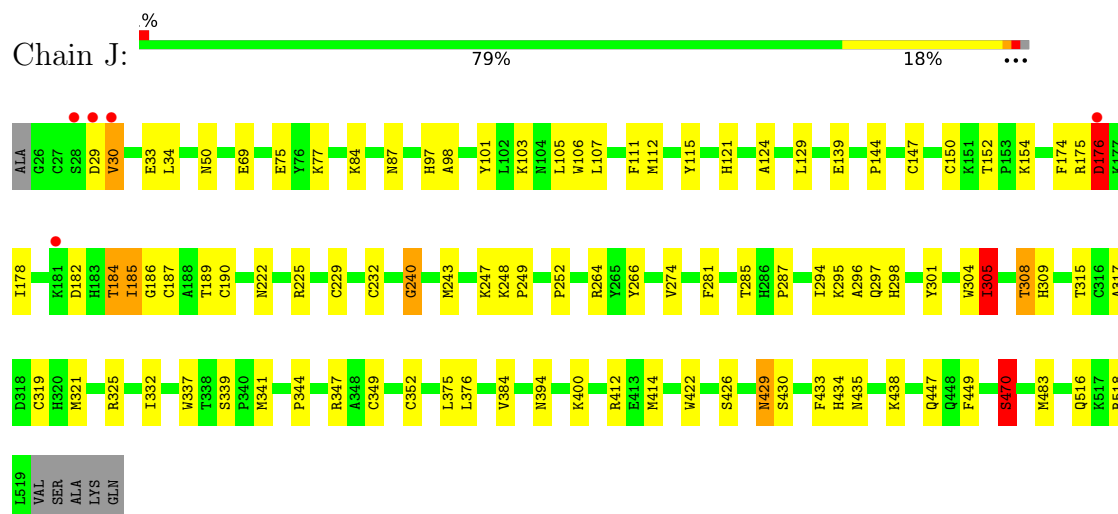
• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



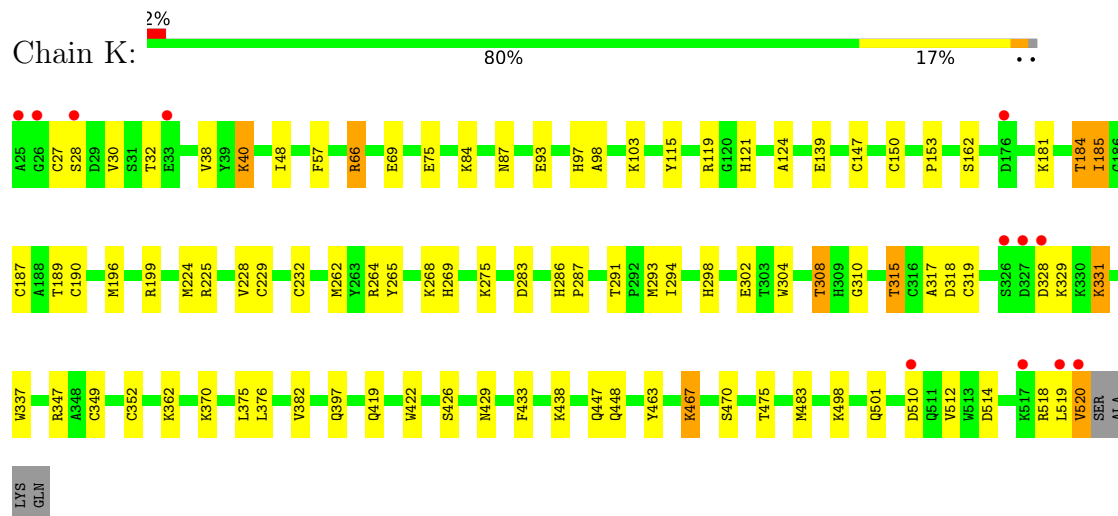
• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



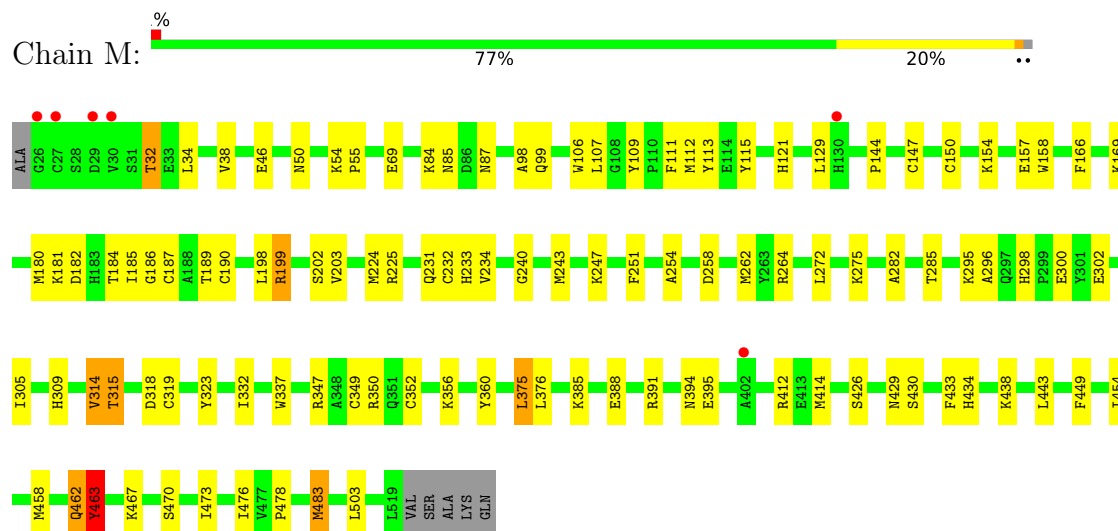
• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



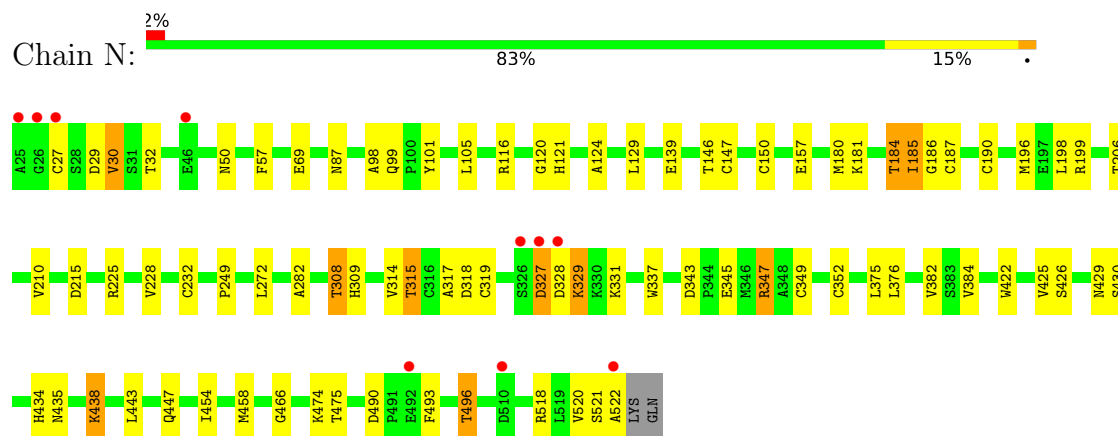
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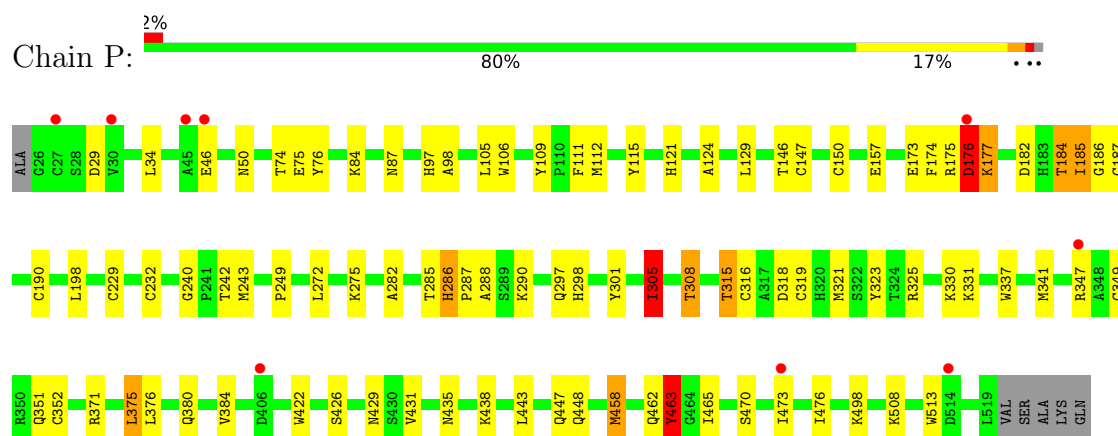
• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



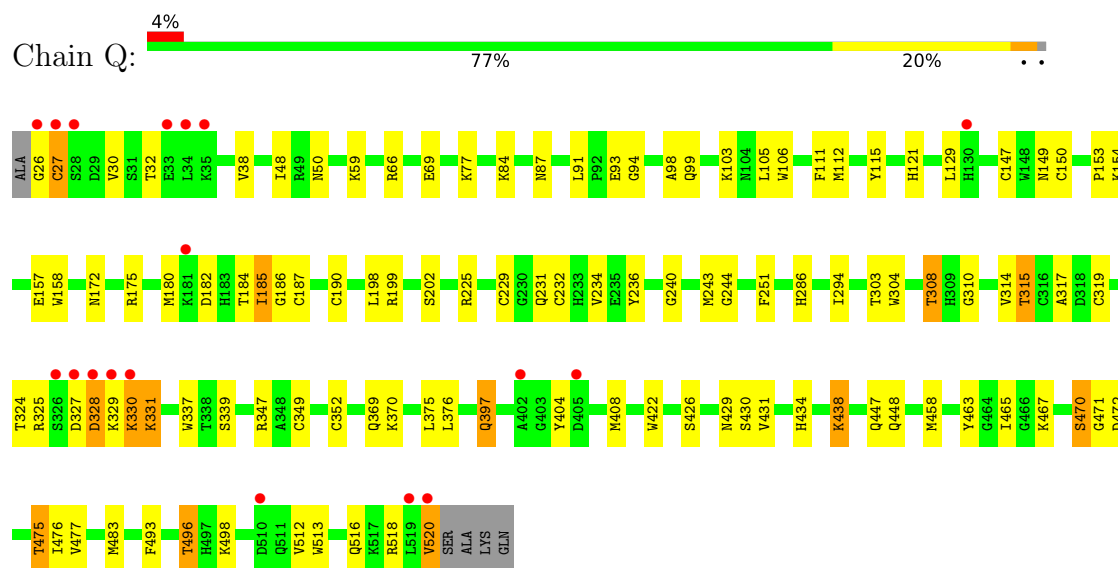
• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA



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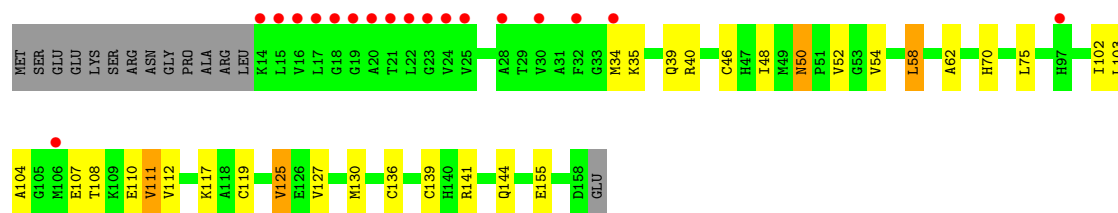


• Molecule 1: CYTOCHROME C NITRITE REDUCTASE NRFA

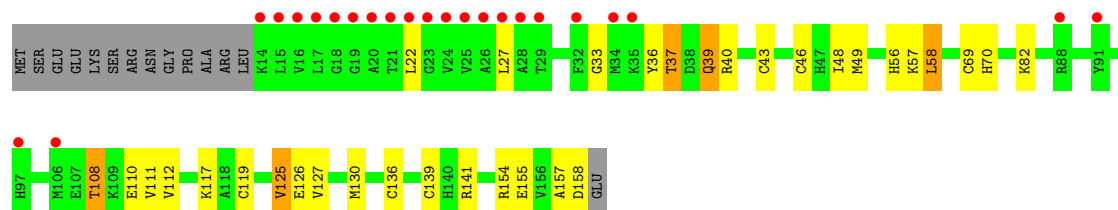


• Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH

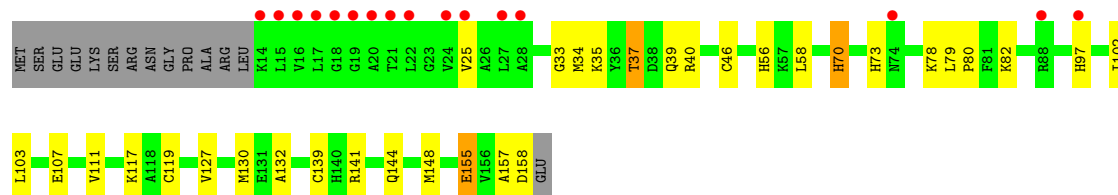




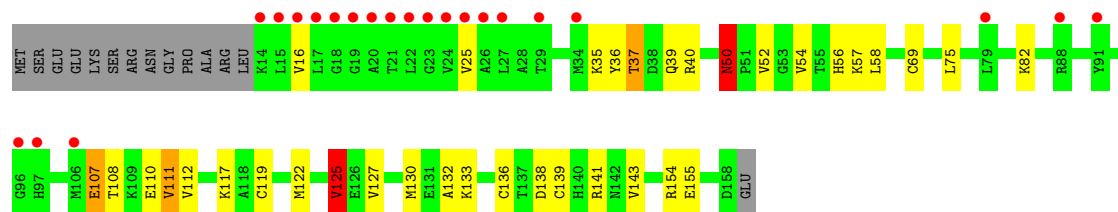
• Molecule 2: CYTOCHROME C QUINOL DEHYDROGENASE NRFH



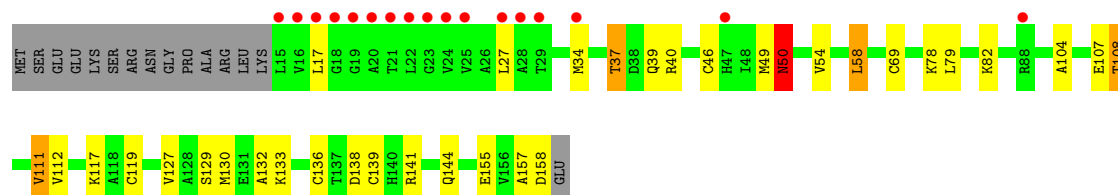
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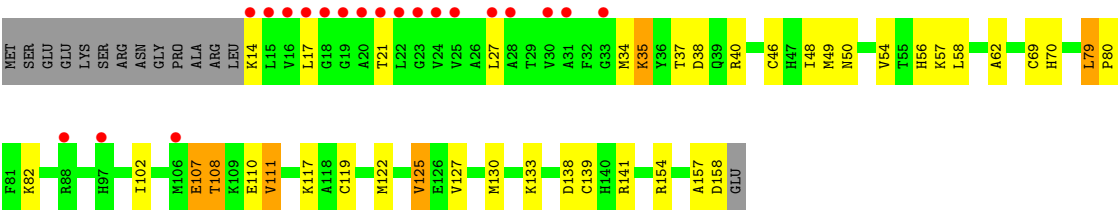
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.66Å 258.12Å 580.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	288.67 – 2.30 288.67 – 2.30	Depositor EDS
% Data completeness (in resolution range)	83.7 (288.67-2.30) 83.7 (288.67-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.201 , 0.240 0.197 , 0.234	Depositor DCC
R_{free} test set	22270 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.524	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	60930	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.70	0/4143	0.94	0/5605
1	B	0.71	0/4150	0.96	4/5616 (0.1%)
1	D	0.68	0/4127	0.95	3/5584 (0.1%)
1	E	0.68	0/4127	0.93	10/5584 (0.2%)
1	G	0.70	1/4125 (0.0%)	0.98	8/5581 (0.1%)
1	H	0.69	0/4160	0.94	5/5629 (0.1%)
1	J	0.71	0/4145	0.95	7/5608 (0.1%)
1	K	0.69	0/4128	0.94	1/5586 (0.0%)
1	M	0.82	3/4135 (0.1%)	0.96	9/5595 (0.2%)
1	N	0.71	0/4150	0.94	6/5616 (0.1%)
1	P	0.71	3/4124 (0.1%)	0.99	6/5580 (0.1%)
1	Q	0.69	0/4134	0.98	10/5594 (0.2%)
2	C	0.71	0/1118	1.02	3/1513 (0.2%)
2	F	0.69	0/1116	1.05	1/1509 (0.1%)
2	I	0.69	0/1107	0.99	1/1497 (0.1%)
2	L	0.68	0/1107	1.09	3/1497 (0.2%)
2	O	0.72	0/1098	1.06	1/1486 (0.1%)
2	R	0.65	0/1107	1.02	0/1497
All	All	0.71	7/56301 (0.0%)	0.97	78/76177 (0.1%)

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

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

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	462	GLN	C-N	-19.57	1.06	1.33
1	M	463	TYR	C-N	-14.93	1.14	1.34
1	P	462	GLN	C-N	-7.60	1.23	1.33
1	P	305	ILE	CA-CB	6.80	1.62	1.54
1	P	463	TYR	C-N	-6.77	1.25	1.33

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	27	CYS	N-CA-C	10.59	126.31	112.12
1	Q	470	SER	N-CA-C	8.42	120.53	111.36
1	M	305	ILE	N-CA-C	8.10	118.88	110.62
1	P	463	TYR	O-C-N	8.05	133.30	122.59
1	J	305	ILE	CB-CA-C	-7.65	100.30	112.16

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

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

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4022	0	3896	76	0
1	B	4032	0	3896	80	0
1	D	4009	0	3874	67	0
1	E	4009	0	3875	87	0
1	G	4008	0	3874	82	0
1	H	4037	0	3903	86	0
1	J	4021	0	3886	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	4014	0	3882	80	0
1	M	4014	0	3878	82	0
1	N	4032	0	3899	76	0
1	P	4007	0	3871	89	0
1	Q	4016	0	3884	116	0
2	C	1094	0	1095	32	0
2	F	1093	0	1096	48	0
2	I	1087	0	1089	35	0
2	L	1087	0	1090	45	0
2	O	1078	0	1077	46	0
2	R	1087	0	1090	51	0
3	A	215	0	156	28	0
3	B	215	0	154	25	0
3	C	172	0	122	20	0
3	D	215	0	156	31	0
3	E	215	0	157	32	0
3	F	172	0	124	26	0
3	G	215	0	157	36	0
3	H	215	0	157	32	0
3	I	172	0	123	12	0
3	J	215	0	156	33	0
3	K	215	0	157	35	0
3	L	172	0	124	21	0
3	M	215	0	157	36	0
3	N	215	0	157	31	0
3	O	172	0	124	18	0
3	P	215	0	156	37	0
3	Q	215	0	157	42	0
3	R	172	0	124	21	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
4	J	2	0	0	0	0
4	K	2	0	0	0	0
4	M	2	0	0	0	0
4	N	2	0	0	0	0
4	P	2	0	0	0	0
4	Q	2	0	0	0	0
5	C	35	0	46	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	35	0	46	0	0
5	I	35	0	46	3	0
5	L	35	0	46	3	0
5	O	35	0	46	0	0
5	R	35	0	46	0	0
6	C	4	0	3	0	0
6	I	4	0	3	0	0
6	O	4	0	3	0	0
7	A	201	0	0	8	0
7	B	188	0	0	6	0
7	C	50	0	0	0	0
7	D	170	0	0	3	0
7	E	155	0	0	2	0
7	F	42	0	0	1	0
7	G	160	0	0	8	0
7	H	194	0	0	4	0
7	I	40	0	0	1	0
7	J	168	0	0	3	0
7	K	106	0	0	5	0
7	L	43	0	0	4	0
7	M	203	0	0	6	0
7	N	206	0	0	4	0
7	O	50	0	0	3	0
7	P	173	0	0	7	0
7	Q	132	0	0	3	0
7	R	44	0	0	4	0
All	All	60930	0	56058	1232	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 1232 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:319:CYS:SG	3:K:1004:HEC:HAC	1.30	1.72
1:N:187:CYS:SG	3:N:1002:HEC:HAB	1.21	1.71
2:L:69:CYS:SG	3:L:1002:HEC:HAC	1.32	1.70
1:K:150:CYS:SG	3:K:1001:HEC:HAC	1.32	1.68
1:J:147:CYS:SG	3:J:1001:HEC:HAB	1.26	1.67

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	495/500 (99%)	481 (97%)	13 (3%)	1 (0%)	43	55
1	B	497/500 (99%)	482 (97%)	14 (3%)	1 (0%)	43	55
1	D	493/500 (99%)	478 (97%)	13 (3%)	2 (0%)	30	38
1	E	493/500 (99%)	474 (96%)	17 (3%)	2 (0%)	30	38
1	G	493/500 (99%)	479 (97%)	12 (2%)	2 (0%)	30	38
1	H	498/500 (100%)	483 (97%)	13 (3%)	2 (0%)	30	38
1	J	495/500 (99%)	477 (96%)	16 (3%)	2 (0%)	30	38
1	K	494/500 (99%)	473 (96%)	19 (4%)	2 (0%)	30	38
1	M	494/500 (99%)	477 (97%)	15 (3%)	2 (0%)	30	38
1	N	497/500 (99%)	476 (96%)	19 (4%)	2 (0%)	30	38
1	P	493/500 (99%)	474 (96%)	15 (3%)	4 (1%)	16	20
1	Q	494/500 (99%)	473 (96%)	19 (4%)	2 (0%)	30	38
2	C	144/159 (91%)	139 (96%)	5 (4%)	0	100	100
2	F	144/159 (91%)	138 (96%)	5 (4%)	1 (1%)	18	23
2	I	143/159 (90%)	142 (99%)	1 (1%)	0	100	100
2	L	143/159 (90%)	136 (95%)	7 (5%)	0	100	100
2	O	142/159 (89%)	139 (98%)	3 (2%)	0	100	100
2	R	143/159 (90%)	139 (97%)	4 (3%)	0	100	100
All	All	6795/6954 (98%)	6560 (96%)	210 (3%)	25 (0%)	30	38

5 of 25 Ramachandran outliers are listed below:

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

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Mol	Chain	Res	Type
1	M	463	TYR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	431/432 (100%)	418 (97%)	13 (3%)	36	53
1	B	431/432 (100%)	407 (94%)	24 (6%)	19	28
1	D	429/432 (99%)	413 (96%)	16 (4%)	30	45
1	E	429/432 (99%)	408 (95%)	21 (5%)	22	34
1	G	429/432 (99%)	414 (96%)	15 (4%)	32	48
1	H	433/432 (100%)	414 (96%)	19 (4%)	25	38
1	J	431/432 (100%)	416 (96%)	15 (4%)	32	48
1	K	429/432 (99%)	405 (94%)	24 (6%)	19	28
1	M	430/432 (100%)	412 (96%)	18 (4%)	26	40
1	N	431/432 (100%)	416 (96%)	15 (4%)	32	48
1	P	429/432 (99%)	413 (96%)	16 (4%)	30	45
1	Q	430/432 (100%)	405 (94%)	25 (6%)	18	26
2	C	120/131 (92%)	113 (94%)	7 (6%)	18	26
2	F	120/131 (92%)	107 (89%)	13 (11%)	6	7
2	I	119/131 (91%)	111 (93%)	8 (7%)	15	21
2	L	119/131 (91%)	106 (89%)	13 (11%)	6	7
2	O	118/131 (90%)	110 (93%)	8 (7%)	14	20
2	R	119/131 (91%)	105 (88%)	14 (12%)	5	6
All	All	5877/5970 (98%)	5593 (95%)	284 (5%)	23	35

5 of 284 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	182	ASP

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Mol	Chain	Res	Type
1	P	315	THR
1	Q	370	LYS
1	G	69	GLU
1	G	32	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
2	O	50	ASN
1	P	97	HIS
1	P	451	GLN
2	F	74	ASN
2	F	56	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 117 ligands modelled in this entry, 24 are monoatomic - leaving 93 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	N	1005	1	46,50,50	2.06	8 (17%)	58,82,82	1.27	7 (12%)
3	HEC	A	1003	1,4	46,50,50	2.07	7 (15%)	58,82,82	1.26	5 (8%)
5	LMT	F	1005	-	36,36,36	0.64	0	47,47,47	0.90	2 (4%)
5	LMT	I	1005	-	36,36,36	0.59	0	47,47,47	0.90	2 (4%)
3	HEC	Q	1003	1,4	46,50,50	2.04	6 (13%)	58,82,82	1.38	6 (10%)
6	ACT	O	1006	-	3,3,3	0.76	0	3,3,3	1.29	0
3	HEC	P	1004	1,4	46,50,50	2.01	7 (15%)	58,82,82	1.36	8 (13%)
3	HEC	Q	1004	1,4	46,50,50	2.04	7 (15%)	58,82,82	1.32	9 (15%)
3	HEC	H	1003	1,4	46,50,50	2.04	10 (21%)	58,82,82	1.41	8 (13%)
3	HEC	E	1001	1,7	46,50,50	2.07	8 (17%)	58,82,82	1.35	6 (10%)
3	HEC	R	1003	2	46,50,50	2.05	8 (17%)	58,82,82	1.34	6 (10%)
3	HEC	F	1002	2	46,50,50	1.97	9 (19%)	58,82,82	1.56	14 (24%)
3	HEC	D	1001	1	46,50,50	2.02	8 (17%)	58,82,82	1.30	7 (12%)
3	HEC	B	1005	1	46,50,50	2.03	8 (17%)	58,82,82	1.19	4 (6%)
6	ACT	I	1006	-	3,3,3	0.76	0	3,3,3	1.12	0
3	HEC	D	1003	1,4	46,50,50	2.03	8 (17%)	58,82,82	1.21	4 (6%)
3	HEC	J	1001	1,7	46,50,50	2.04	7 (15%)	58,82,82	1.14	3 (5%)
3	HEC	C	1001	2	46,50,50	2.03	10 (21%)	58,82,82	1.44	6 (10%)
3	HEC	H	1005	1	46,50,50	2.11	8 (17%)	58,82,82	1.17	3 (5%)
3	HEC	K	1002	1	46,50,50	2.09	9 (19%)	58,82,82	1.35	6 (10%)
3	HEC	M	1002	1	46,50,50	2.06	10 (21%)	58,82,82	1.31	5 (8%)
3	HEC	F	1001	2	46,50,50	2.01	8 (17%)	58,82,82	1.32	8 (13%)
3	HEC	M	1003	1,4	46,50,50	2.02	9 (19%)	58,82,82	1.46	8 (13%)
3	HEC	P	1002	1	46,50,50	2.05	8 (17%)	58,82,82	1.19	5 (8%)
5	LMT	O	1005	-	36,36,36	0.66	1 (2%)	47,47,47	0.79	1 (2%)
3	HEC	A	1001	1,7	46,50,50	2.01	7 (15%)	58,82,82	1.41	6 (10%)
3	HEC	D	1005	1	46,50,50	2.05	9 (19%)	58,82,82	1.35	4 (6%)
3	HEC	G	1002	1	46,50,50	2.04	8 (17%)	58,82,82	1.19	4 (6%)
3	HEC	O	1001	2	46,50,50	2.03	10 (21%)	58,82,82	1.51	9 (15%)
3	HEC	G	1003	1,4	46,50,50	1.99	8 (17%)	58,82,82	1.32	5 (8%)
3	HEC	A	1004	1,4	46,50,50	2.08	9 (19%)	58,82,82	1.46	7 (12%)
3	HEC	H	1004	1,4	46,50,50	2.07	10 (21%)	58,82,82	1.35	8 (13%)
3	HEC	Q	1005	1	46,50,50	2.05	9 (19%)	58,82,82	1.37	10 (17%)
3	HEC	J	1005	1	46,50,50	2.06	9 (19%)	58,82,82	1.17	3 (5%)
3	HEC	R	1001	2	46,50,50	2.01	9 (19%)	58,82,82	1.66	12 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	B	1004	1,4	46,50,50	2.05	8 (17%)	58,82,82	1.41	7 (12%)
3	HEC	H	1002	1	46,50,50	2.04	8 (17%)	58,82,82	1.20	5 (8%)
3	HEC	O	1002	2	46,50,50	2.05	9 (19%)	58,82,82	1.54	12 (20%)
3	HEC	C	1002	2	46,50,50	2.02	9 (19%)	58,82,82	1.82	15 (25%)
6	ACT	C	1006	-	3,3,3	0.83	0	3,3,3	0.89	0
3	HEC	L	1003	2	46,50,50	2.05	8 (17%)	58,82,82	1.38	6 (10%)
3	HEC	R	1002	2	46,50,50	2.02	8 (17%)	58,82,82	1.56	12 (20%)
3	HEC	O	1004	1,2	46,50,50	2.01	10 (21%)	58,82,82	1.58	9 (15%)
3	HEC	M	1005	1	46,50,50	2.12	9 (19%)	58,82,82	1.41	8 (13%)
3	HEC	K	1003	1,4	46,50,50	2.04	7 (15%)	58,82,82	1.19	3 (5%)
3	HEC	I	1001	2	46,50,50	1.98	9 (19%)	58,82,82	1.42	7 (12%)
3	HEC	E	1002	1	46,50,50	2.12	9 (19%)	58,82,82	1.35	6 (10%)
3	HEC	P	1005	1	46,50,50	2.08	10 (21%)	58,82,82	1.32	5 (8%)
3	HEC	D	1004	1,4	46,50,50	2.07	10 (21%)	58,82,82	1.37	8 (13%)
3	HEC	G	1005	1	46,50,50	2.07	8 (17%)	58,82,82	1.42	6 (10%)
3	HEC	C	1003	2	46,50,50	2.07	8 (17%)	58,82,82	1.43	9 (15%)
3	HEC	D	1002	1	46,50,50	2.04	7 (15%)	58,82,82	1.15	5 (8%)
3	HEC	L	1002	2	46,50,50	1.97	9 (19%)	58,82,82	1.67	8 (13%)
3	HEC	E	1004	1,4	46,50,50	2.02	8 (17%)	58,82,82	1.50	10 (17%)
3	HEC	F	1003	2	46,50,50	2.04	9 (19%)	58,82,82	1.43	8 (13%)
5	LMT	C	1005	-	36,36,36	0.58	0	47,47,47	0.83	1 (2%)
3	HEC	I	1002	2	46,50,50	2.02	9 (19%)	58,82,82	1.77	10 (17%)
3	HEC	Q	1001	1,7	46,50,50	2.05	8 (17%)	58,82,82	1.40	8 (13%)
3	HEC	A	1005	1	46,50,50	2.12	9 (19%)	58,82,82	1.60	12 (20%)
3	HEC	B	1003	1,4	46,50,50	2.10	9 (19%)	58,82,82	1.28	5 (8%)
3	HEC	H	1001	1,7	46,50,50	2.13	9 (19%)	58,82,82	1.44	7 (12%)
3	HEC	M	1004	1,4	46,50,50	2.00	6 (13%)	58,82,82	1.55	8 (13%)
3	HEC	F	1004	1,2	46,50,50	2.09	9 (19%)	58,82,82	1.42	6 (10%)
3	HEC	G	1004	1,4	46,50,50	2.04	9 (19%)	58,82,82	1.56	10 (17%)
3	HEC	A	1002	1	46,50,50	2.09	9 (19%)	58,82,82	1.47	7 (12%)
3	HEC	J	1004	1,4	46,50,50	2.00	7 (15%)	58,82,82	1.39	9 (15%)
3	HEC	K	1005	1	46,50,50	2.08	8 (17%)	58,82,82	1.25	6 (10%)
3	HEC	L	1101	2	46,50,50	2.03	9 (19%)	58,82,82	1.50	8 (13%)
3	HEC	Q	1002	1	46,50,50	2.13	8 (17%)	58,82,82	1.34	6 (10%)
3	HEC	N	1004	1,4	46,50,50	2.07	7 (15%)	58,82,82	1.46	9 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	O	1003	2	46,50,50	2.05	9 (19%)	58,82,82	1.30	6 (10%)
3	HEC	J	1002	1	46,50,50	2.03	9 (19%)	58,82,82	1.25	5 (8%)
3	HEC	G	1001	1,7	46,50,50	2.08	7 (15%)	58,82,82	1.20	5 (8%)
3	HEC	J	1003	1,4	46,50,50	2.04	10 (21%)	58,82,82	1.36	6 (10%)
3	HEC	M	1001	1	46,50,50	2.00	7 (15%)	58,82,82	1.32	4 (6%)
3	HEC	N	1002	1	46,50,50	2.09	10 (21%)	58,82,82	1.39	6 (10%)
3	HEC	L	1004	1,2	46,50,50	2.03	8 (17%)	58,82,82	1.57	9 (15%)
3	HEC	C	1004	1,2	46,50,50	2.02	9 (19%)	58,82,82	1.47	8 (13%)
3	HEC	K	1004	1,4	46,50,50	2.07	8 (17%)	58,82,82	1.55	8 (13%)
3	HEC	R	1004	1,2	46,50,50	2.07	9 (19%)	58,82,82	1.58	10 (17%)
3	HEC	E	1003	1,4	46,50,50	2.03	9 (19%)	58,82,82	1.44	6 (10%)
3	HEC	B	1001	1,7	46,50,50	2.06	8 (17%)	58,82,82	1.57	10 (17%)
3	HEC	N	1001	1,7	46,50,50	2.10	10 (21%)	58,82,82	1.55	8 (13%)
5	LMT	R	1005	-	36,36,36	0.57	0	47,47,47	1.03	2 (4%)
3	HEC	I	1004	1,2	46,50,50	1.98	8 (17%)	58,82,82	1.31	6 (10%)
3	HEC	B	1002	1	46,50,50	2.06	9 (19%)	58,82,82	1.46	4 (6%)
3	HEC	N	1003	1,4	46,50,50	2.07	10 (21%)	58,82,82	1.22	4 (6%)
3	HEC	P	1001	1,7	46,50,50	2.05	6 (13%)	58,82,82	1.33	8 (13%)
3	HEC	E	1005	1	46,50,50	2.14	9 (19%)	58,82,82	1.29	6 (10%)
3	HEC	I	1003	2	46,50,50	2.03	6 (13%)	58,82,82	1.37	5 (8%)
5	LMT	L	1005	-	36,36,36	0.59	0	47,47,47	0.68	1 (2%)
3	HEC	P	1003	1,4	46,50,50	2.04	7 (15%)	58,82,82	1.32	5 (8%)
3	HEC	K	1001	1	46,50,50	2.08	8 (17%)	58,82,82	1.26	5 (8%)

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	N	1005	1	-	7/14/54/54	-
3	HEC	A	1003	1,4	-	5/14/54/54	-
5	LMT	F	1005	-	-	7/21/61/61	0/2/2/2
5	LMT	I	1005	-	-	8/21/61/61	0/2/2/2
3	HEC	Q	1003	1,4	-	4/14/54/54	-
3	HEC	P	1004	1,4	-	4/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	Q	1004	1,4	-	7/14/54/54	-
3	HEC	H	1003	1,4	-	4/14/54/54	-
3	HEC	E	1001	1,7	-	6/14/54/54	-
3	HEC	R	1003	2	-	4/14/54/54	-
3	HEC	F	1002	2	-	10/14/54/54	-
3	HEC	D	1001	1	-	6/14/54/54	-
3	HEC	B	1005	1	-	6/14/54/54	-
3	HEC	D	1003	1,4	-	4/14/54/54	-
3	HEC	J	1001	1,7	-	5/14/54/54	-
3	HEC	C	1001	2	-	9/14/54/54	-
3	HEC	H	1005	1	-	7/14/54/54	-
3	HEC	K	1002	1	-	6/14/54/54	-
3	HEC	M	1002	1	-	6/14/54/54	-
3	HEC	F	1001	2	-	7/14/54/54	-
3	HEC	M	1003	1,4	-	4/14/54/54	-
3	HEC	P	1002	1	-	6/14/54/54	-
5	LMT	O	1005	-	-	8/21/61/61	0/2/2/2
3	HEC	A	1001	1,7	-	6/14/54/54	-
3	HEC	D	1005	1	-	9/14/54/54	-
3	HEC	G	1002	1	-	10/14/54/54	-
3	HEC	O	1001	2	-	8/14/54/54	-
3	HEC	G	1003	1,4	-	4/14/54/54	-
3	HEC	A	1004	1,4	-	6/14/54/54	-
3	HEC	H	1004	1,4	-	6/14/54/54	-
3	HEC	Q	1005	1	-	7/14/54/54	-
3	HEC	J	1005	1	-	6/14/54/54	-
3	HEC	R	1001	2	-	9/14/54/54	-
3	HEC	B	1004	1,4	-	6/14/54/54	-
3	HEC	H	1002	1	-	6/14/54/54	-
3	HEC	O	1002	2	-	10/14/54/54	-
3	HEC	C	1002	2	-	10/14/54/54	-
3	HEC	L	1003	2	-	6/14/54/54	-
3	HEC	R	1002	2	-	10/14/54/54	-
3	HEC	O	1004	1,2	-	4/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	M	1005	1	-	8/14/54/54	-
3	HEC	K	1003	1,4	-	4/14/54/54	-
3	HEC	I	1001	2	-	8/14/54/54	-
3	HEC	E	1002	1	-	6/14/54/54	-
3	HEC	P	1005	1	-	8/14/54/54	-
3	HEC	D	1004	1,4	-	6/14/54/54	-
3	HEC	G	1005	1	-	8/14/54/54	-
3	HEC	C	1003	2	-	8/14/54/54	-
3	HEC	D	1002	1	-	6/14/54/54	-
3	HEC	L	1002	2	-	9/14/54/54	-
3	HEC	E	1004	1,4	-	4/14/54/54	-
3	HEC	F	1003	2	-	6/14/54/54	-
5	LMT	C	1005	-	-	7/21/61/61	0/2/2/2
3	HEC	I	1002	2	-	9/14/54/54	-
3	HEC	Q	1001	1,7	-	6/14/54/54	-
3	HEC	A	1005	1	-	8/14/54/54	-
3	HEC	B	1003	1,4	-	4/14/54/54	-
3	HEC	H	1001	1,7	-	6/14/54/54	-
3	HEC	M	1004	1,4	-	4/14/54/54	-
3	HEC	F	1004	1,2	-	7/14/54/54	-
3	HEC	G	1004	1,4	-	6/14/54/54	-
3	HEC	A	1002	1	-	6/14/54/54	-
3	HEC	J	1004	1,4	-	6/14/54/54	-
3	HEC	K	1005	1	-	9/14/54/54	-
3	HEC	L	1101	2	-	7/14/54/54	-
3	HEC	Q	1002	1	-	6/14/54/54	-
3	HEC	N	1004	1,4	-	6/14/54/54	-
3	HEC	O	1003	2	-	6/14/54/54	-
3	HEC	J	1002	1	-	6/14/54/54	-
3	HEC	G	1001	1,7	-	6/14/54/54	-
3	HEC	J	1003	1,4	-	4/14/54/54	-
3	HEC	M	1001	1	-	6/14/54/54	-
3	HEC	N	1002	1	-	6/14/54/54	-
3	HEC	L	1004	1,2	-	5/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	C	1004	1,2	-	7/14/54/54	-
3	HEC	K	1004	1,4	-	6/14/54/54	-
3	HEC	R	1004	1,2	-	6/14/54/54	-
3	HEC	E	1003	1,4	-	4/14/54/54	-
3	HEC	B	1001	1,7	-	6/14/54/54	-
3	HEC	N	1001	1,7	-	6/14/54/54	-
5	LMT	R	1005	-	-	8/21/61/61	0/2/2/2
3	HEC	I	1004	1,2	-	4/14/54/54	-
3	HEC	B	1002	1	-	6/14/54/54	-
3	HEC	N	1003	1,4	-	4/14/54/54	-
3	HEC	P	1001	1,7	-	6/14/54/54	-
3	HEC	E	1005	1	-	7/14/54/54	-
3	HEC	I	1003	2	-	6/14/54/54	-
5	LMT	L	1005	-	-	9/21/61/61	0/2/2/2
3	HEC	P	1003	1,4	-	4/14/54/54	-
3	HEC	K	1001	1	-	6/14/54/54	-

The worst 5 of 707 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1002	HEC	CAC-C3C	7.06	1.57	1.35
3	I	1004	HEC	CAC-C3C	7.00	1.57	1.35
3	F	1004	HEC	CAC-C3C	6.93	1.57	1.35
3	B	1003	HEC	CAC-C3C	6.92	1.57	1.35
3	C	1003	HEC	CAC-C3C	6.89	1.57	1.35

The worst 5 of 599 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	1002	HEC	CBB-CAB-C3B	-5.95	115.54	127.43
3	C	1004	HEC	CBB-CAB-C3B	-5.30	116.84	127.43
3	F	1004	HEC	CBB-CAB-C3B	-5.22	117.00	127.43
3	B	1001	HEC	C4D-ND-C1D	5.18	114.27	105.82
3	O	1002	HEC	CBB-CAB-C3B	-5.16	117.12	127.43

There are no chirality outliers.

5 of 575 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	HEC	C2C-C3C-CAC-CBC
3	A	1001	HEC	C4C-C3C-CAC-CBC
3	A	1002	HEC	C2B-C3B-CAB-CBB
3	A	1002	HEC	C4B-C3B-CAB-CBB
3	A	1002	HEC	C2C-C3C-CAC-CBC

There are no ring outliers.

86 monomers are involved in 523 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	N	1005	HEC	9	0
3	A	1003	HEC	2	0
5	I	1005	LMT	3	0
3	Q	1003	HEC	8	0
3	P	1004	HEC	7	0
3	Q	1004	HEC	7	0
3	H	1003	HEC	4	0
3	E	1001	HEC	6	0
3	R	1003	HEC	4	0
3	F	1002	HEC	10	0
3	D	1001	HEC	4	0
3	B	1005	HEC	4	0
3	D	1003	HEC	4	0
3	J	1001	HEC	4	0
3	C	1001	HEC	4	0
3	H	1005	HEC	8	0
3	K	1002	HEC	10	0
3	M	1002	HEC	10	0
3	F	1001	HEC	5	0
3	M	1003	HEC	8	0
3	P	1002	HEC	13	0
3	A	1001	HEC	3	0
3	D	1005	HEC	8	0
3	G	1002	HEC	9	0
3	O	1001	HEC	1	0
3	G	1003	HEC	1	0
3	A	1004	HEC	6	0
3	H	1004	HEC	6	0
3	Q	1005	HEC	12	0
3	J	1005	HEC	8	0
3	R	1001	HEC	4	0
3	B	1004	HEC	6	0
3	H	1002	HEC	7	0

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

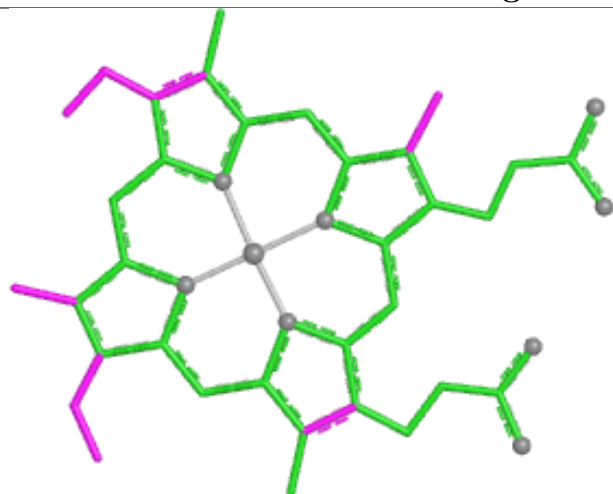
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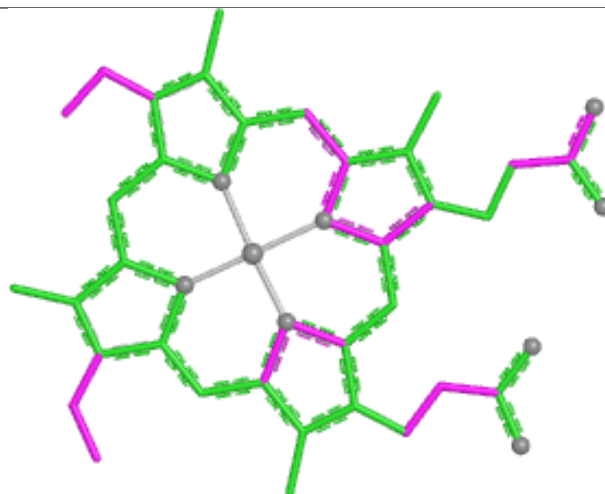
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1001	HEC	3	0
3	N	1001	HEC	6	0
3	I	1004	HEC	6	0
3	B	1002	HEC	6	0
3	N	1003	HEC	5	0
3	P	1001	HEC	6	0
3	E	1005	HEC	8	0
3	I	1003	HEC	3	0
5	L	1005	LMT	3	0
3	P	1003	HEC	6	0
3	K	1001	HEC	7	0

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.

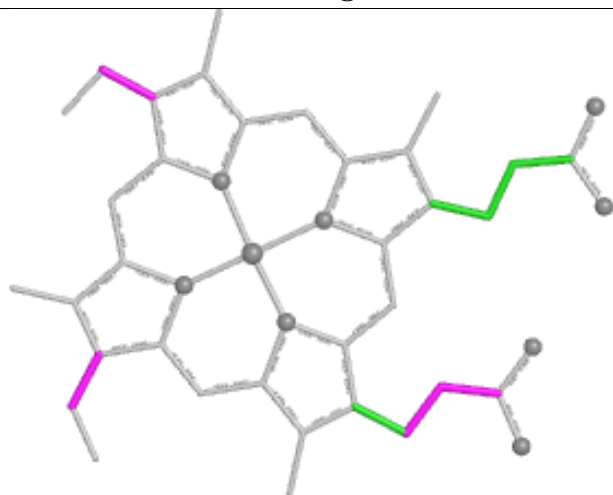
Ligand HEC N 1005



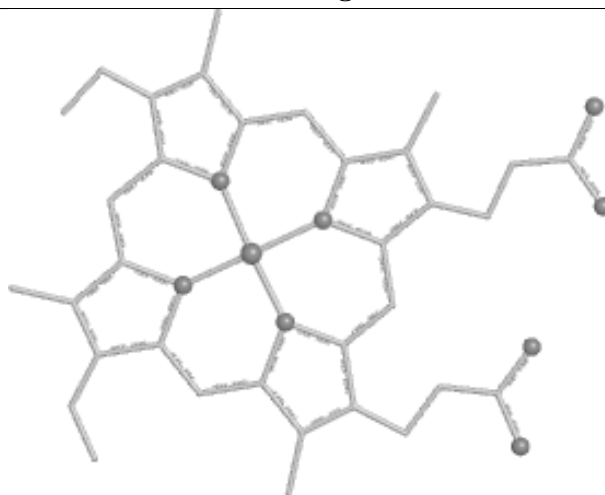
Bond lengths



Bond angles

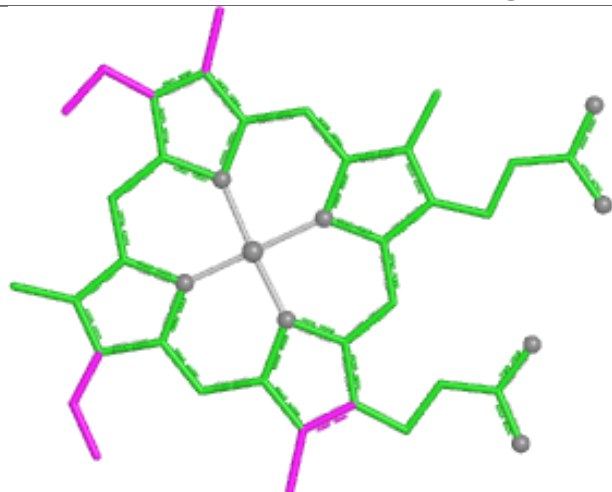


Torsions

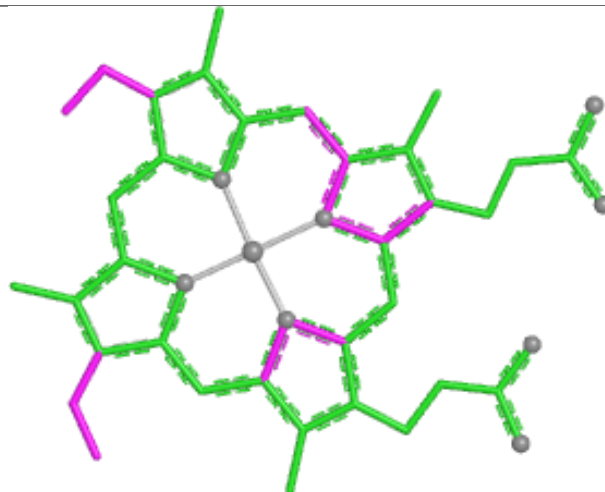


Rings

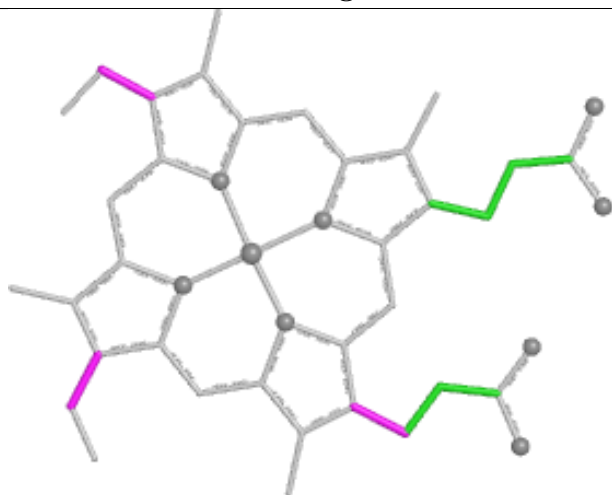
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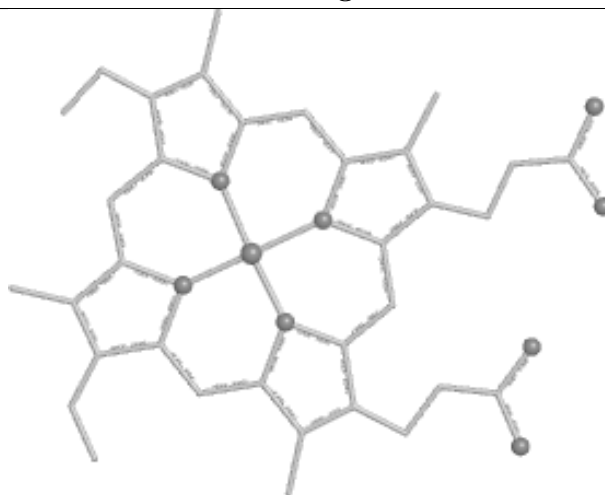
Bond lengths



Bond angles

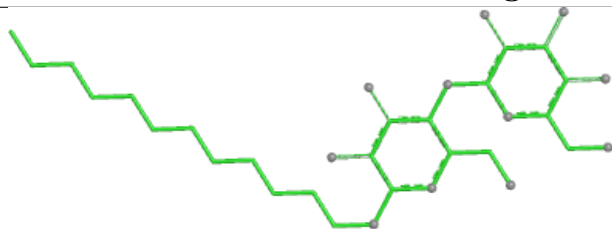


Torsions

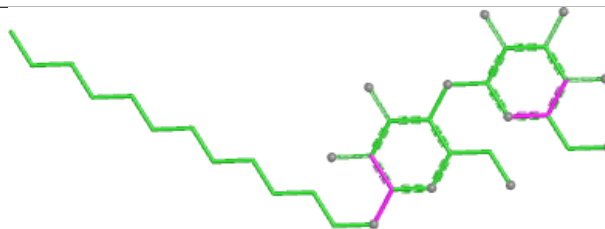


Rings

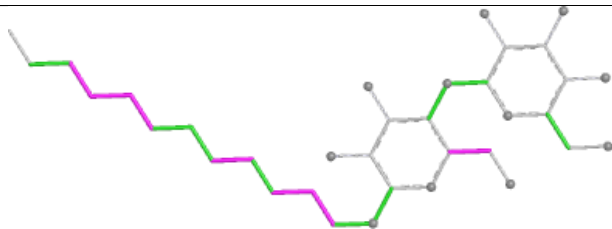
Ligand LMT F 1005



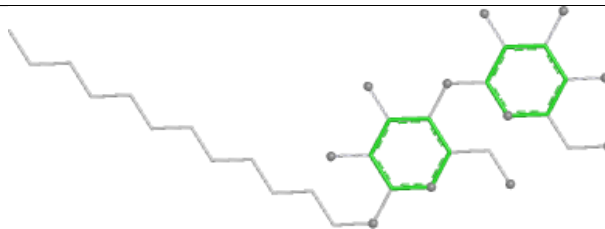
Bond lengths



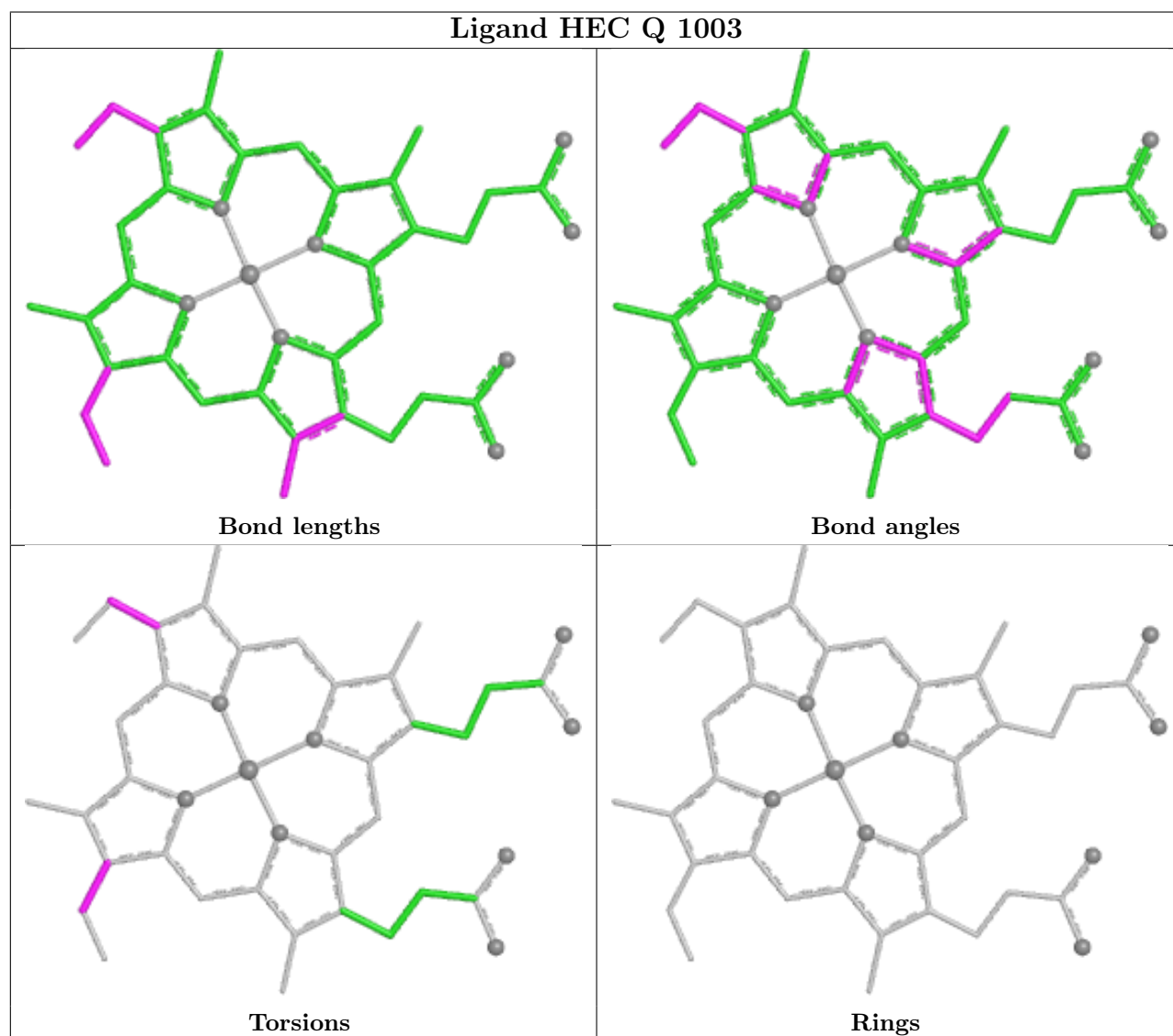
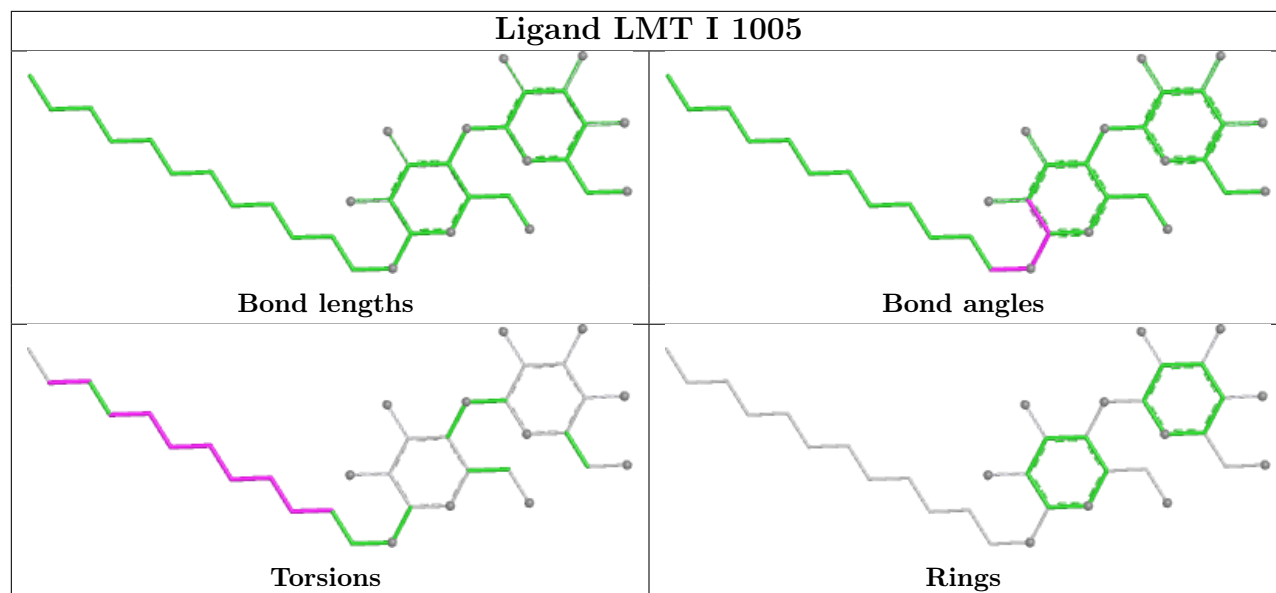
Bond angles



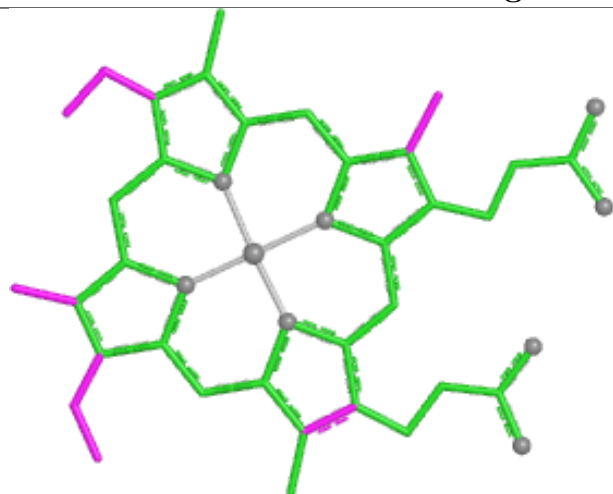
Torsions



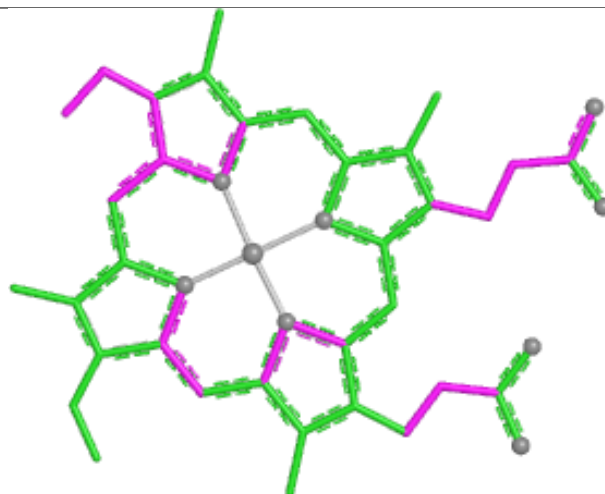
Rings



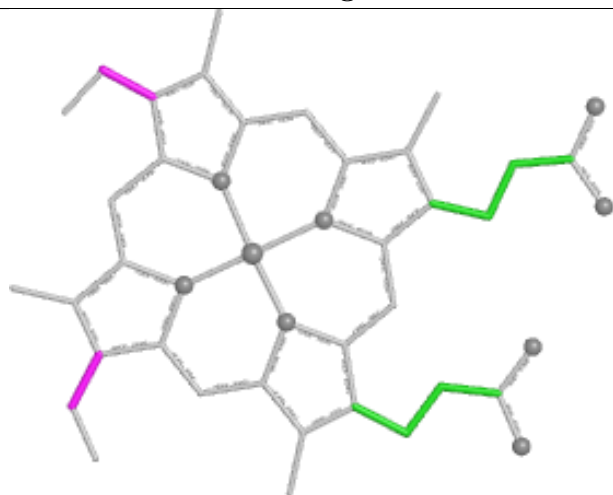
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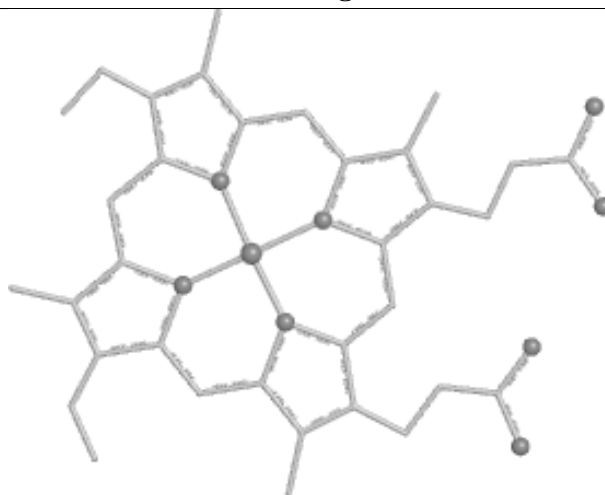
Bond lengths



Bond angles

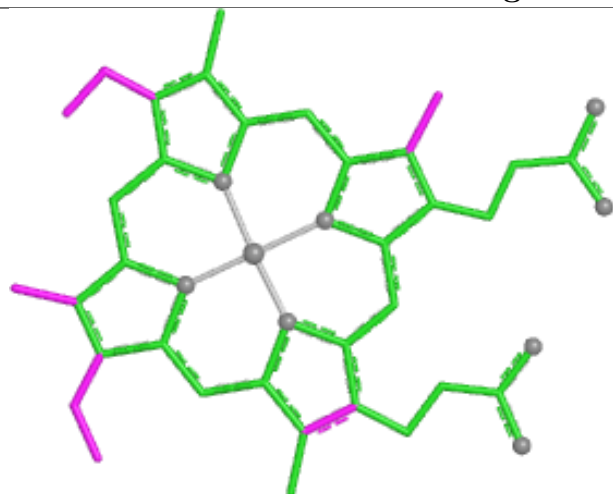


Torsions

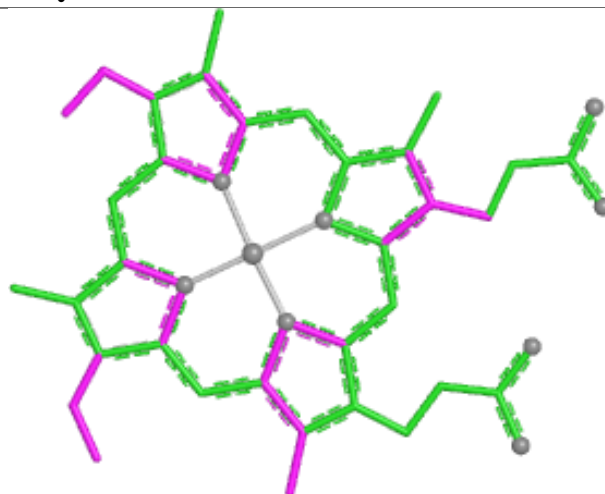


Rings

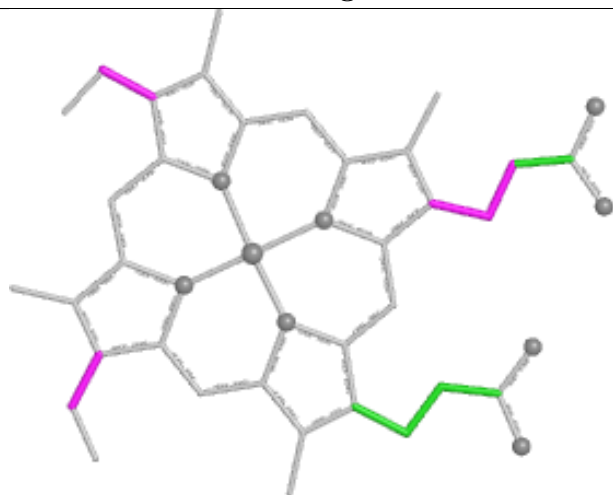
Ligand HEC Q 1004



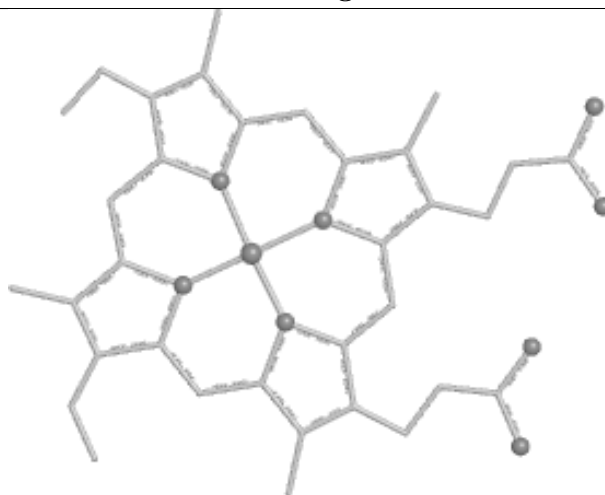
Bond lengths



Bond angles

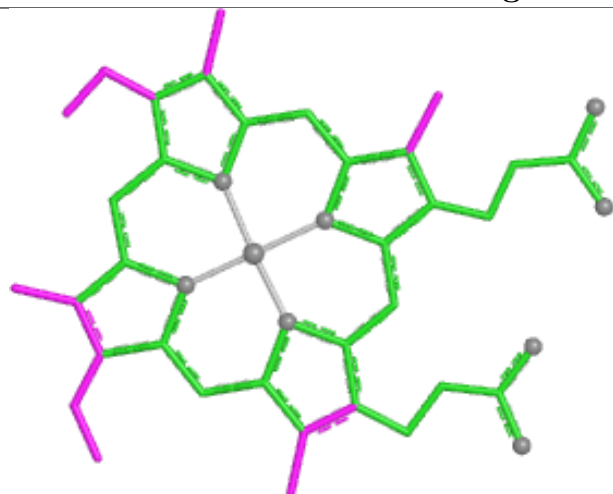


Torsions

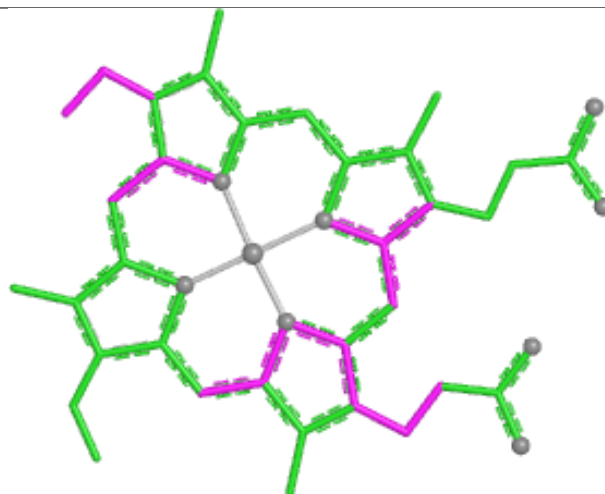


Rings

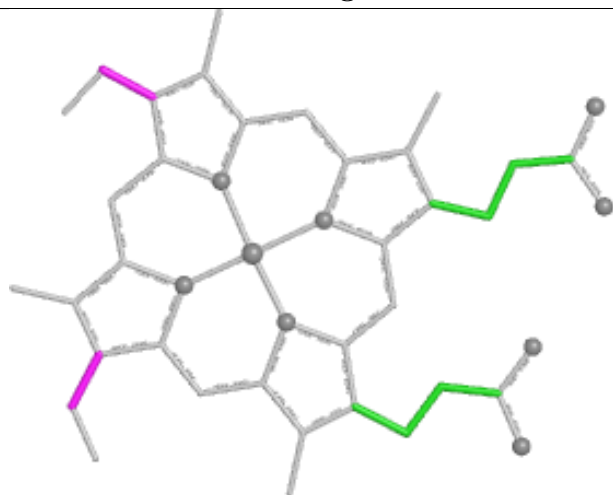
Ligand HEC H 1003



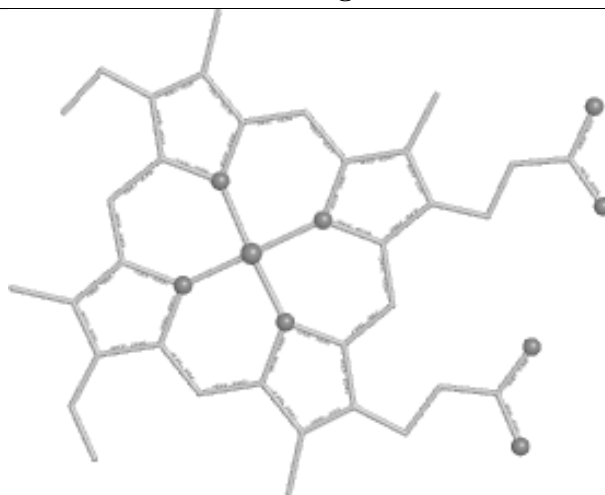
Bond lengths



Bond angles

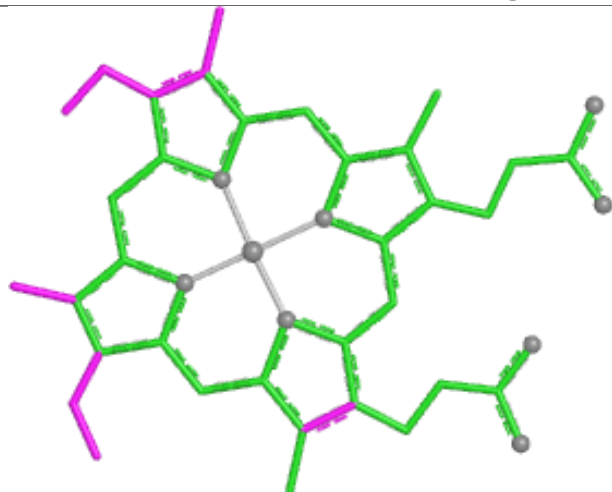


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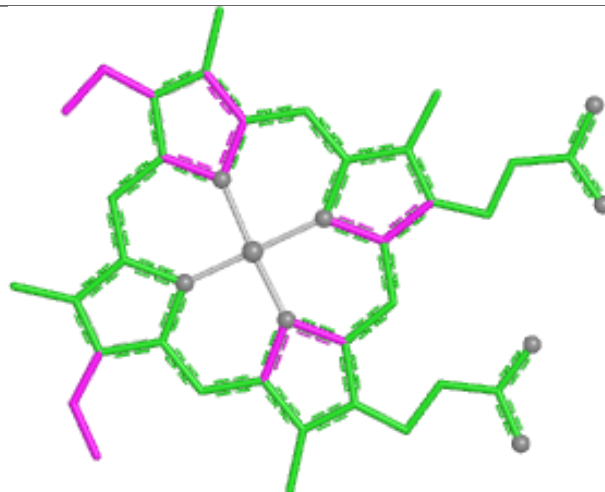


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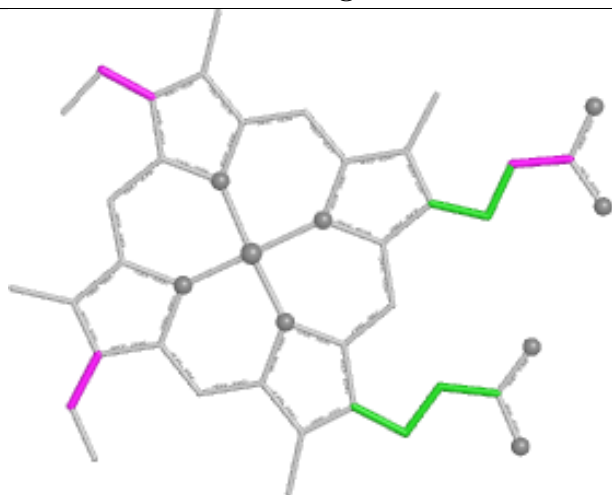
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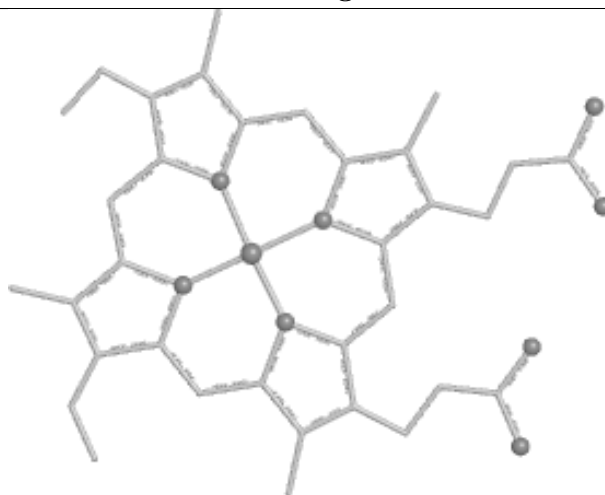
Bond lengths



Bond angles

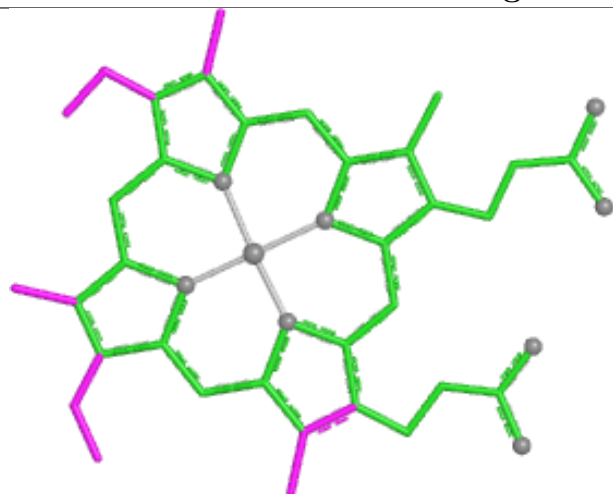


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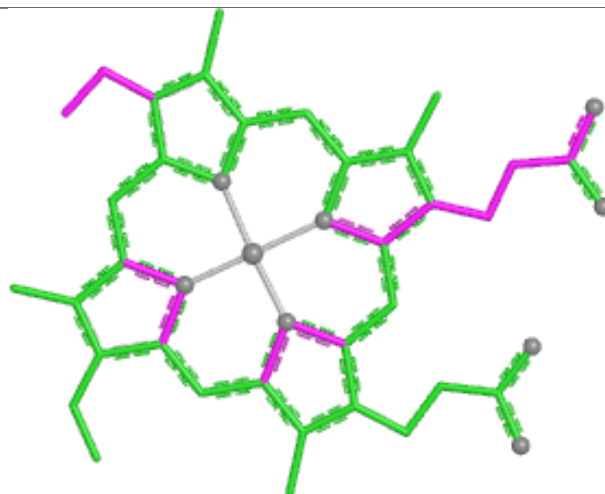


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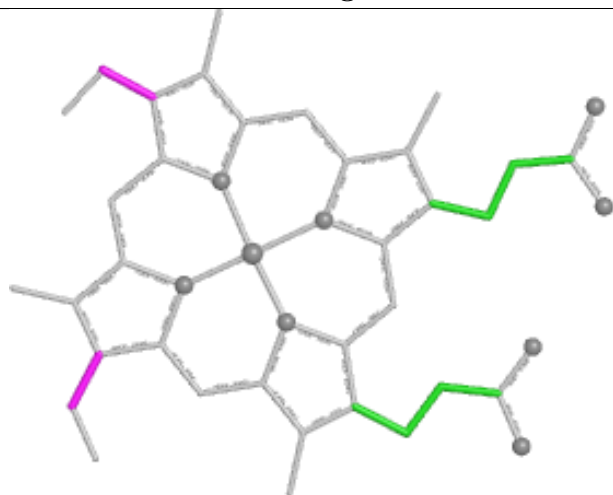
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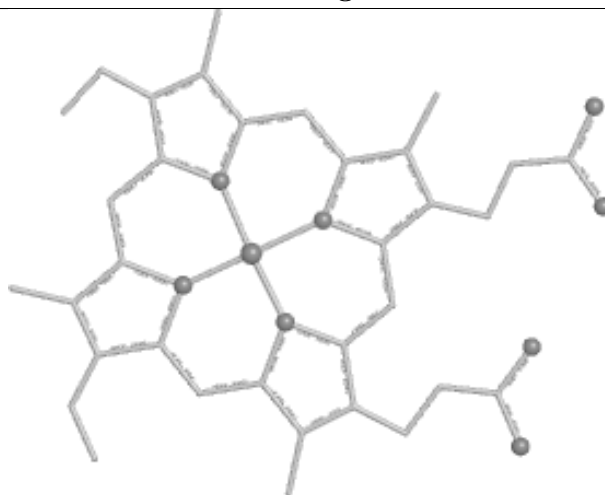
Bond lengths



Bond angles

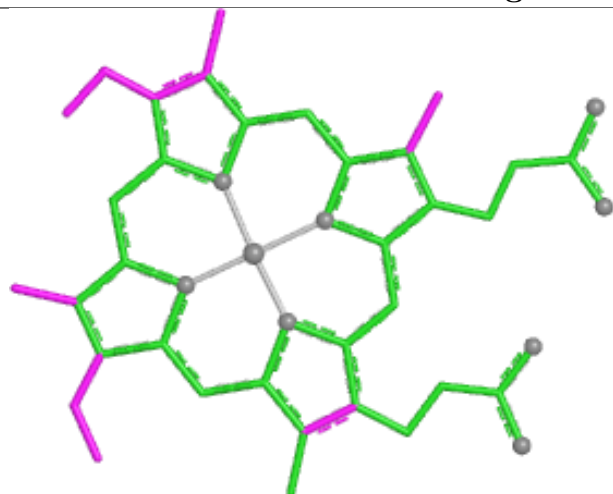


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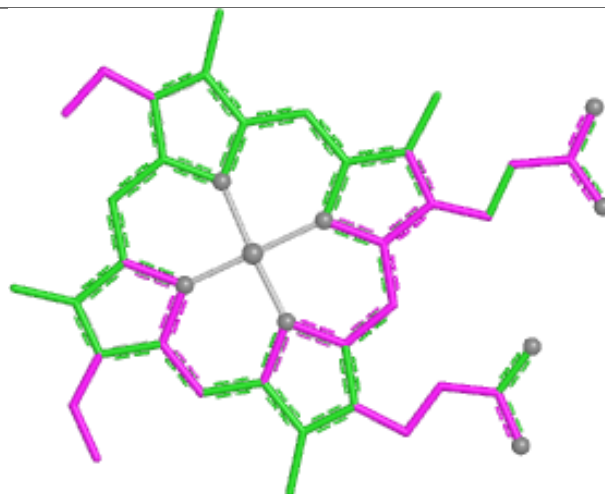


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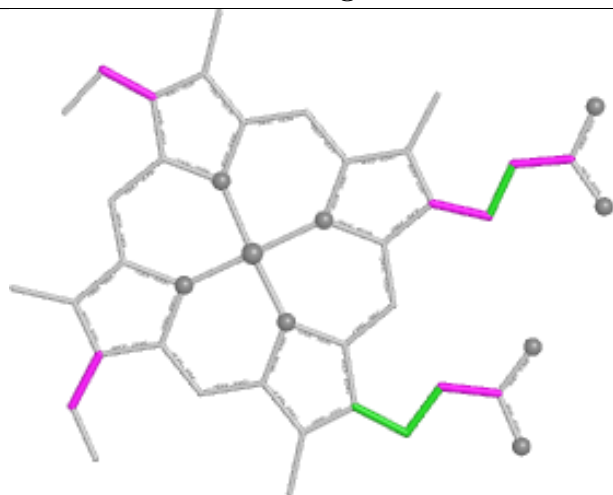
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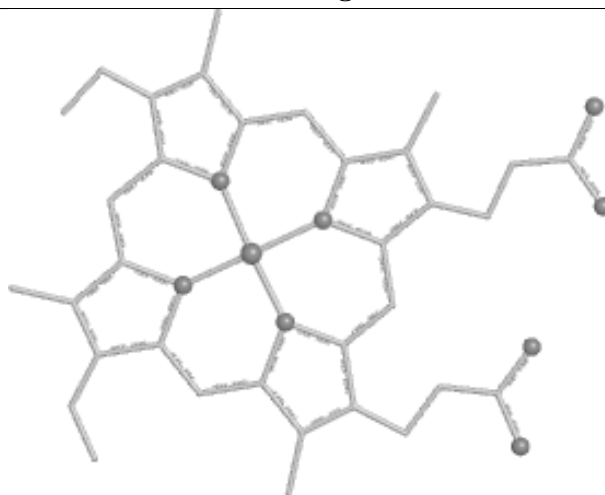
Bond lengths



Bond angles

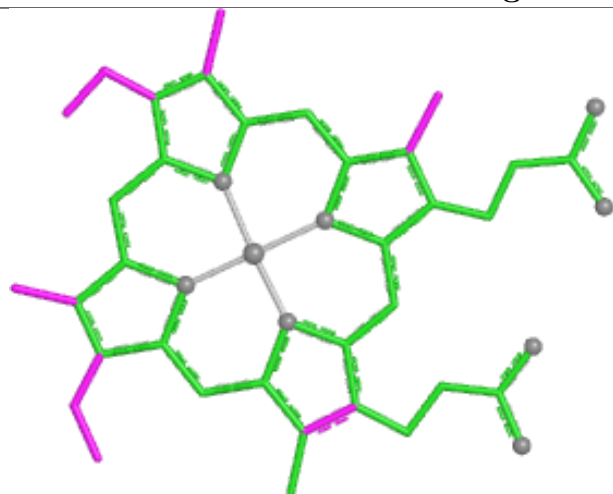


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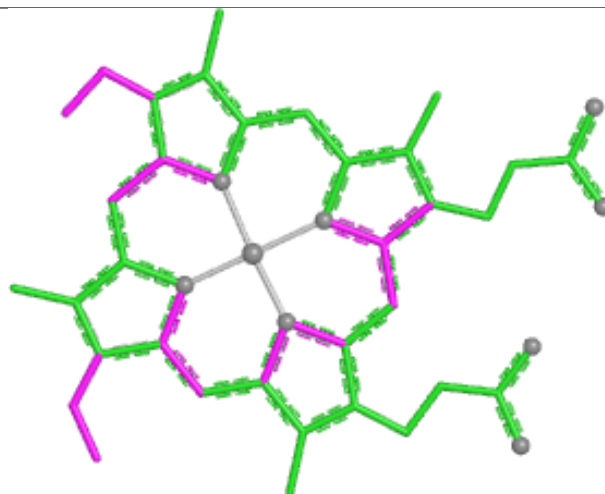


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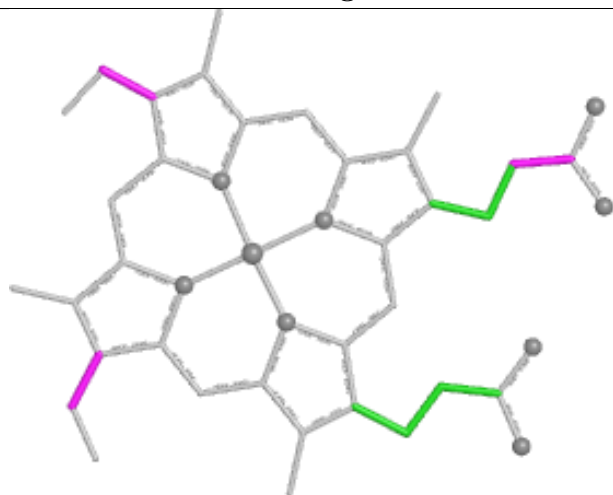
Ligand HEC D 1001



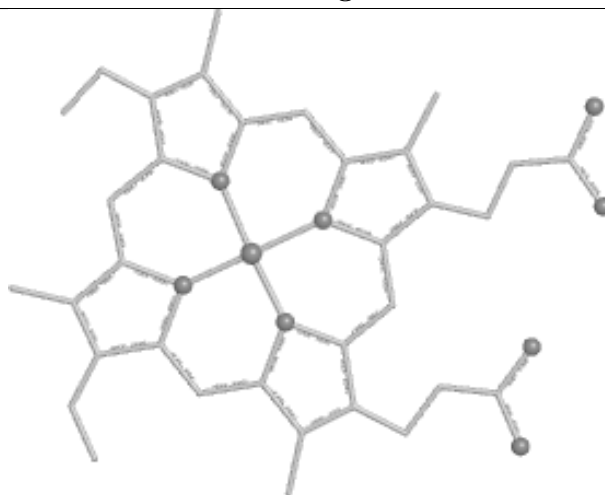
Bond lengths



Bond angles

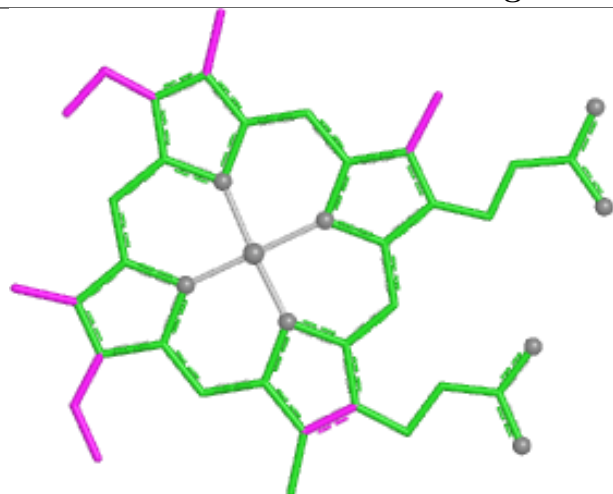


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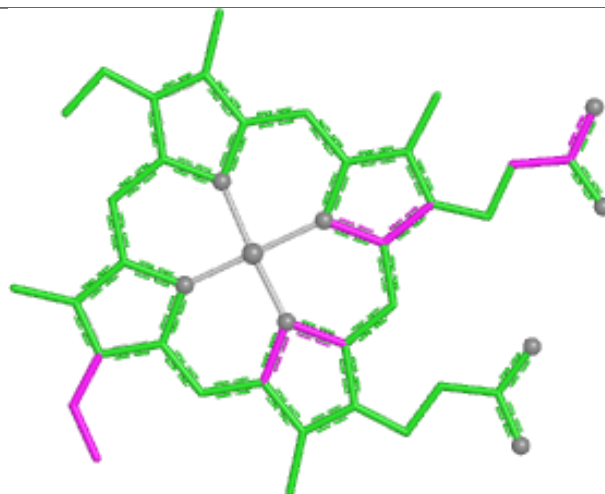


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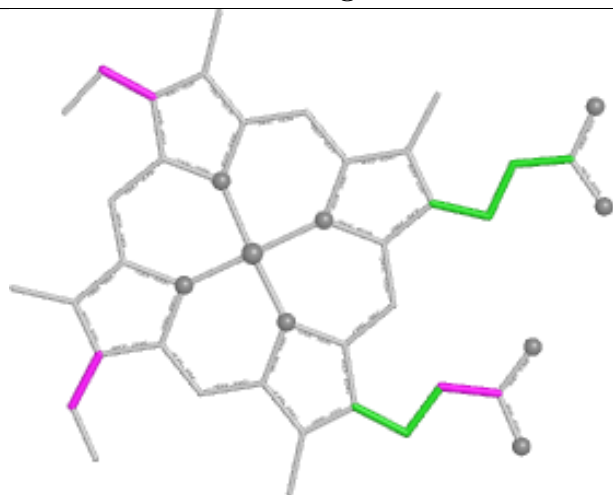
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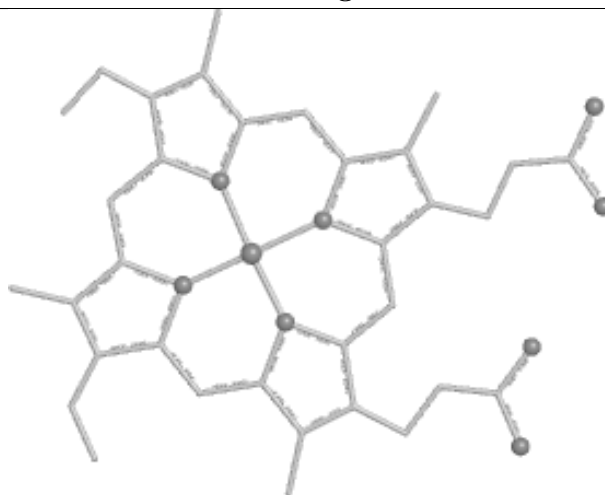
Bond lengths



Bond angles

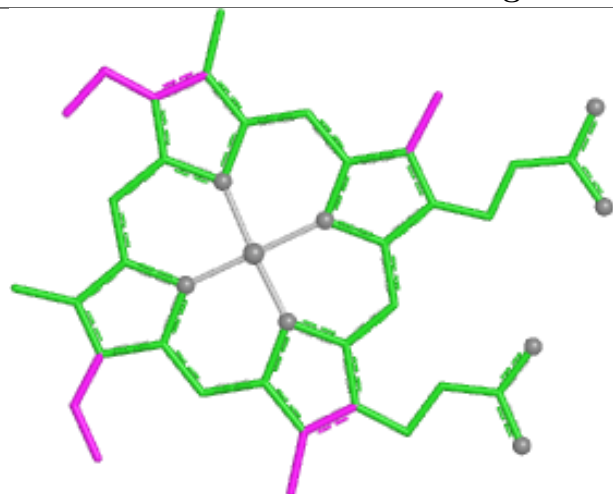


Torsions

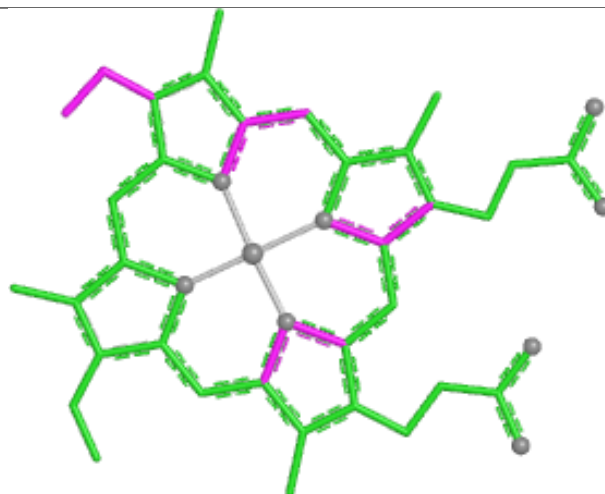


Rings

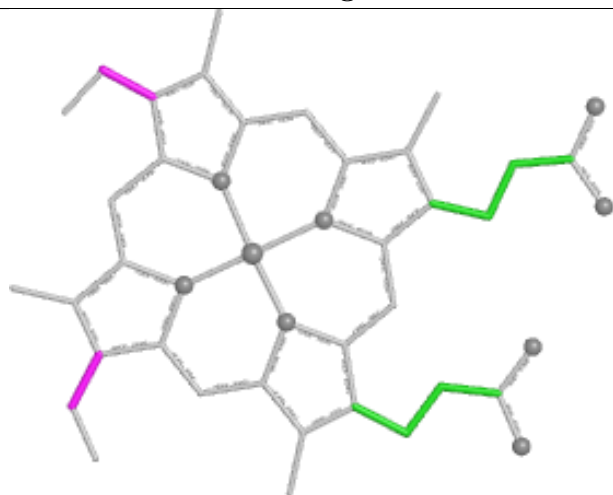
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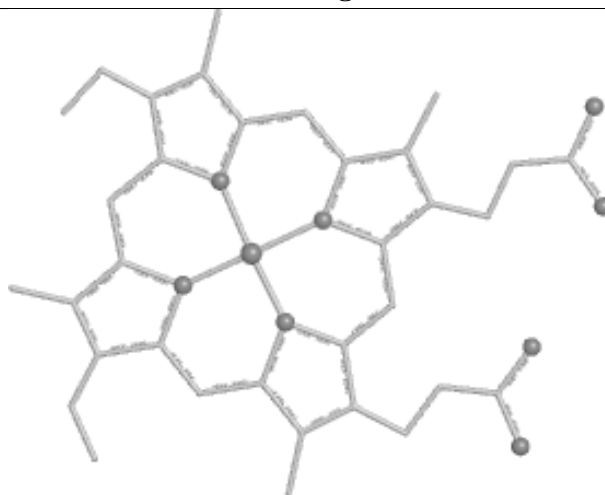
Bond lengths



Bond angles

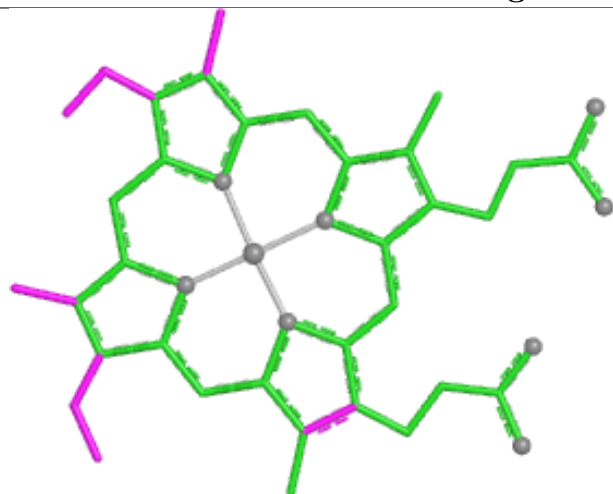


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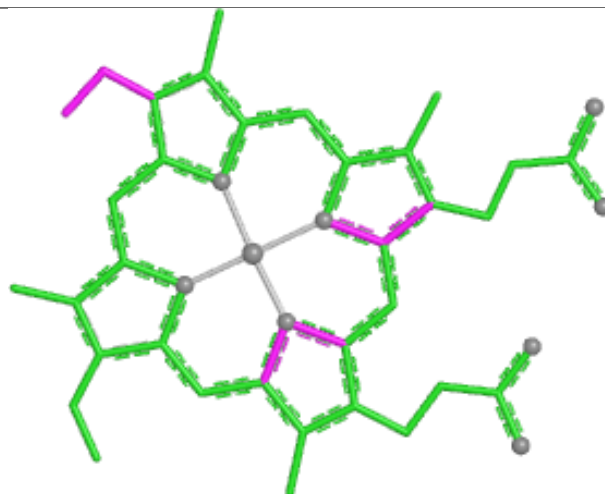


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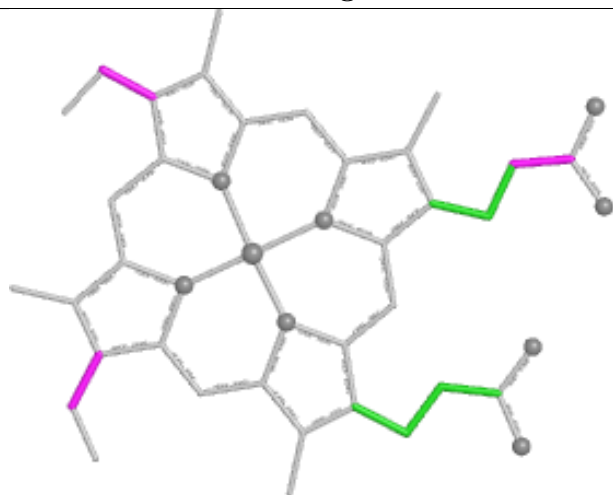
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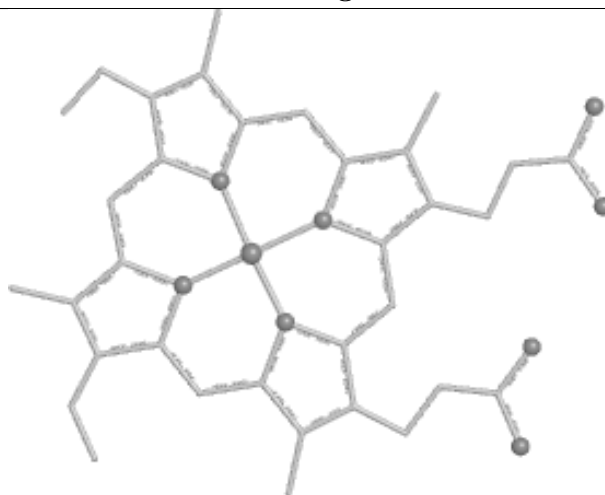
Bond lengths



Bond angles

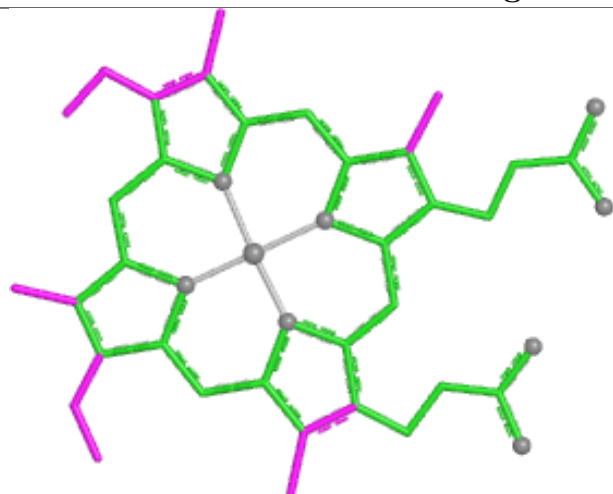


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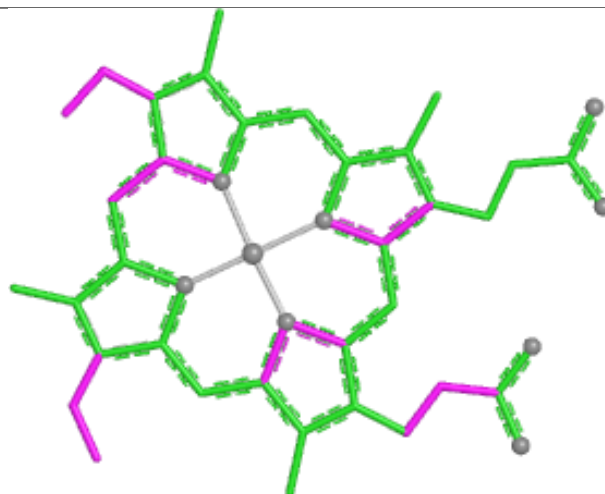


Rings

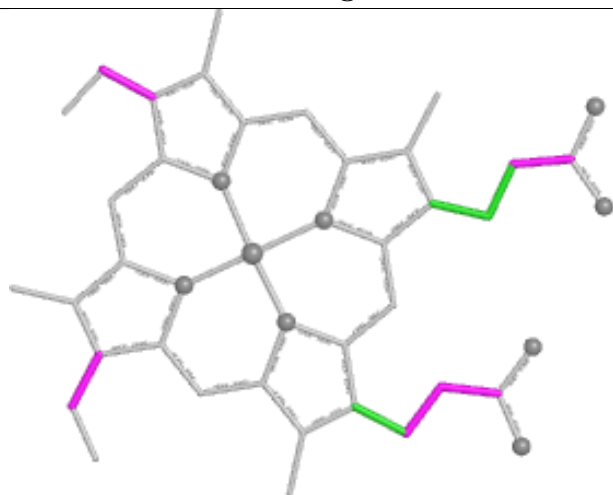
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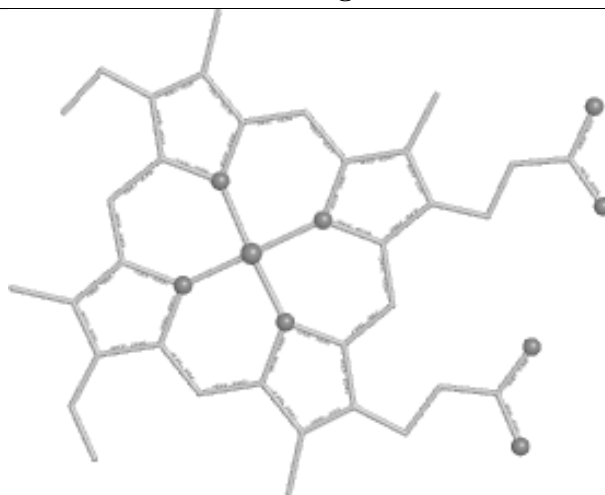
Bond lengths



Bond angles

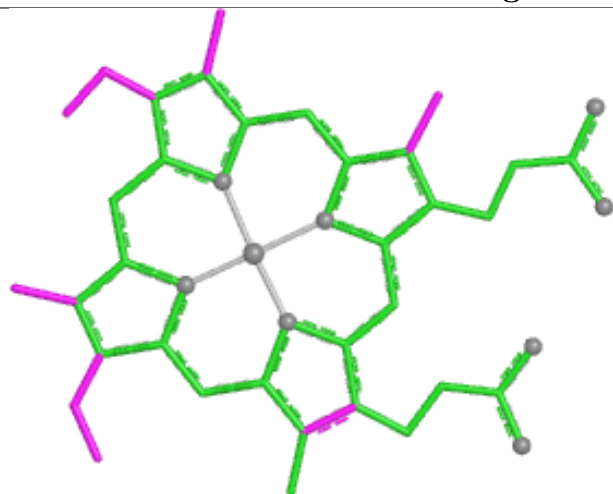


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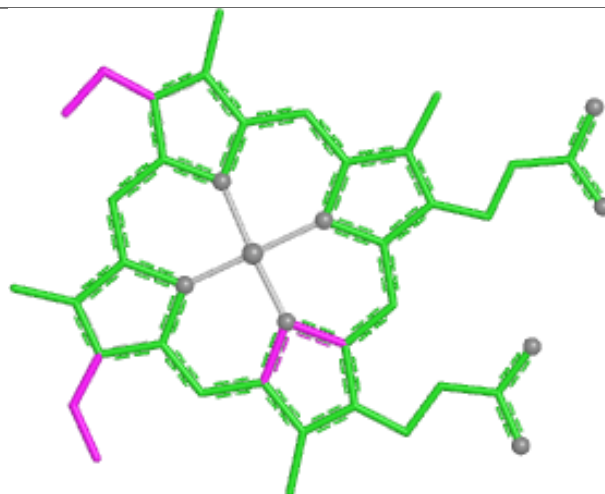


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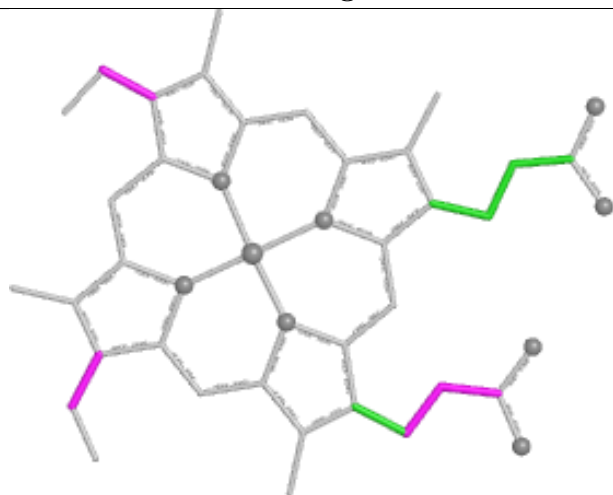
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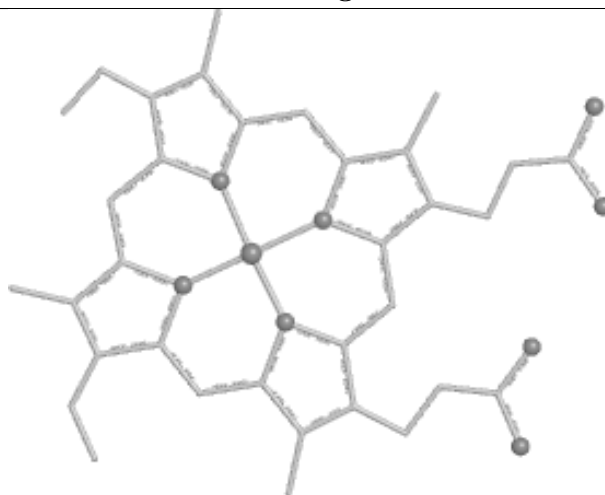
Bond lengths



Bond angles

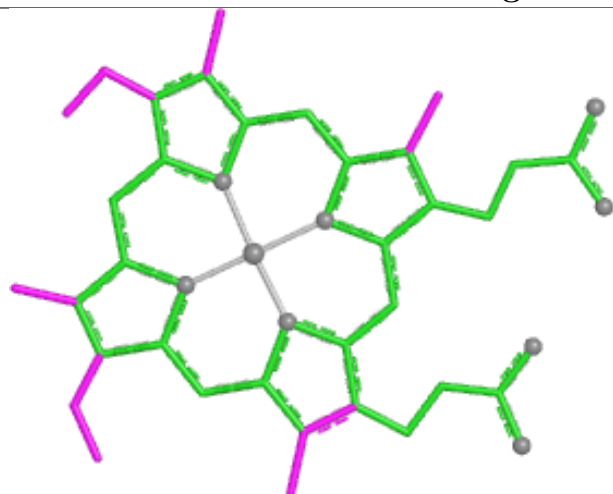


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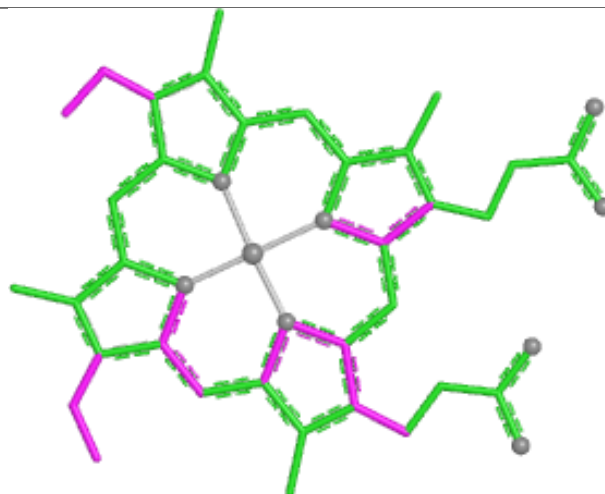


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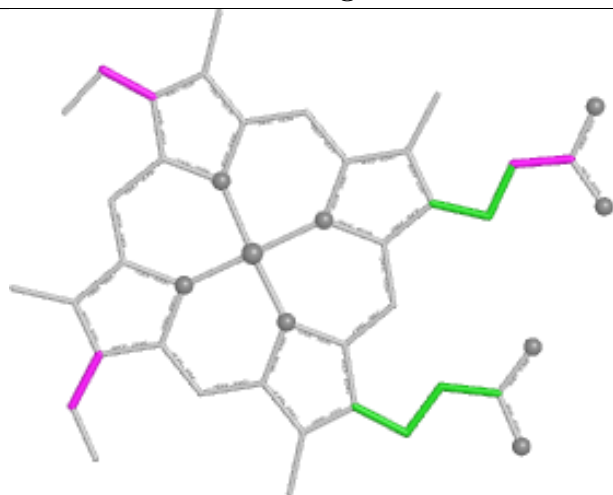
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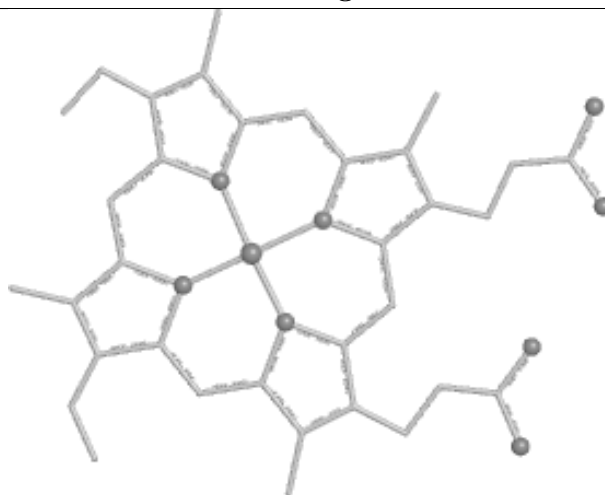
Bond lengths



Bond angles

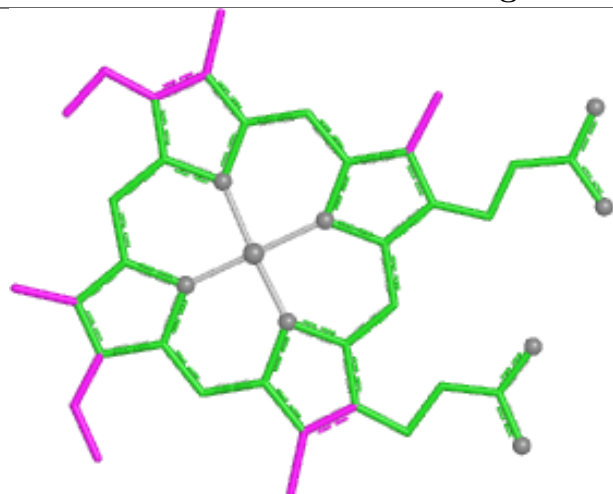


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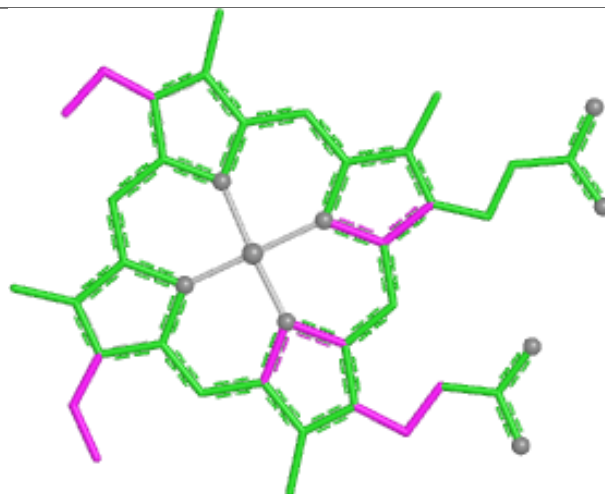


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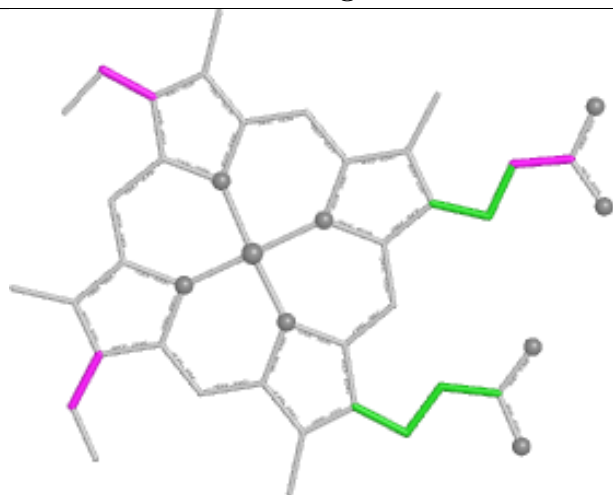
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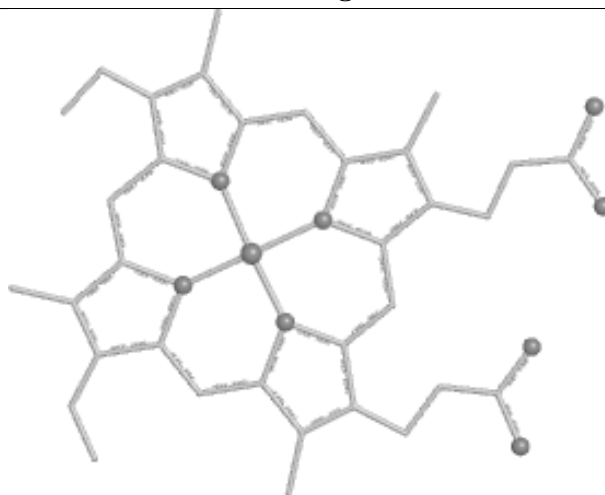
Bond lengths



Bond angles

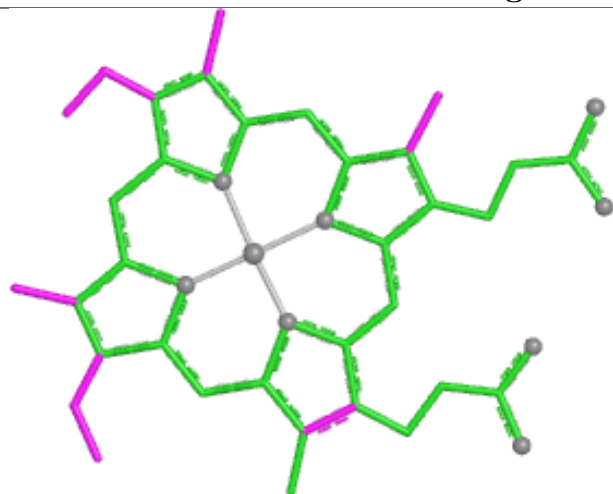


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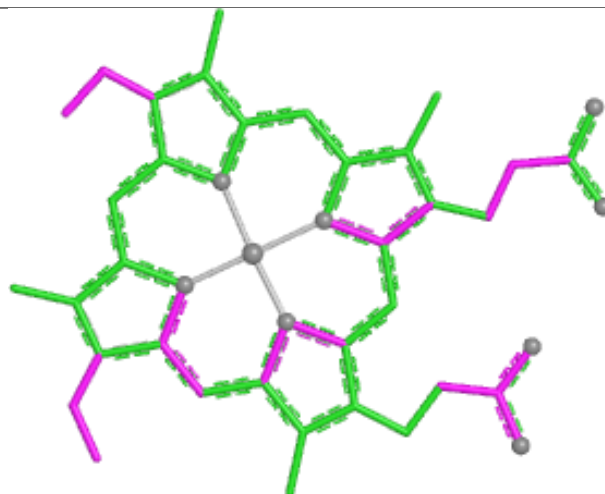


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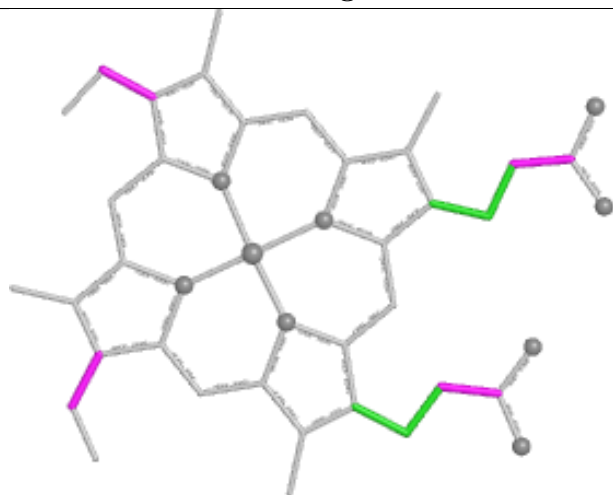
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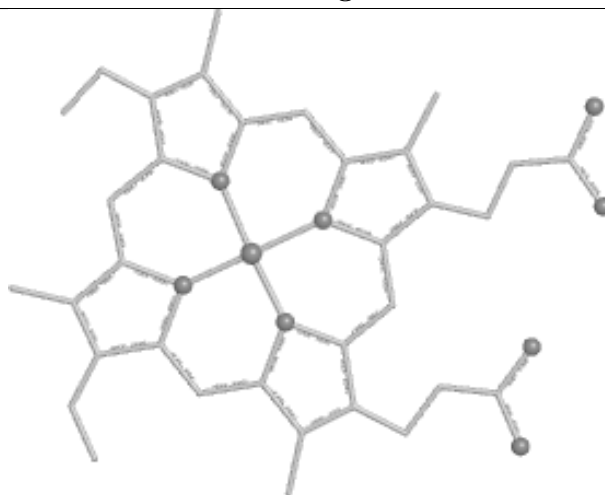
Bond lengths



Bond angles

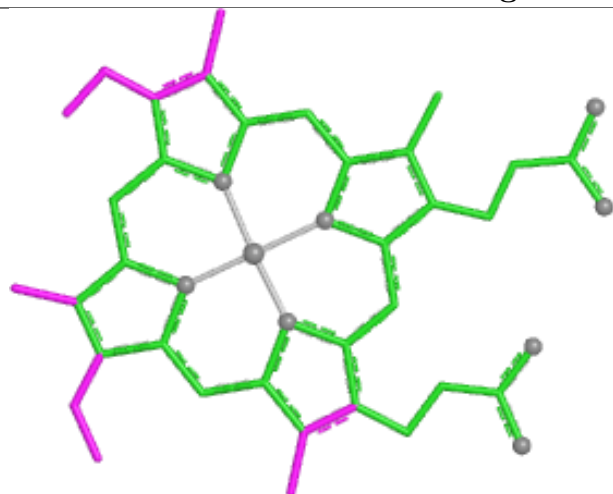


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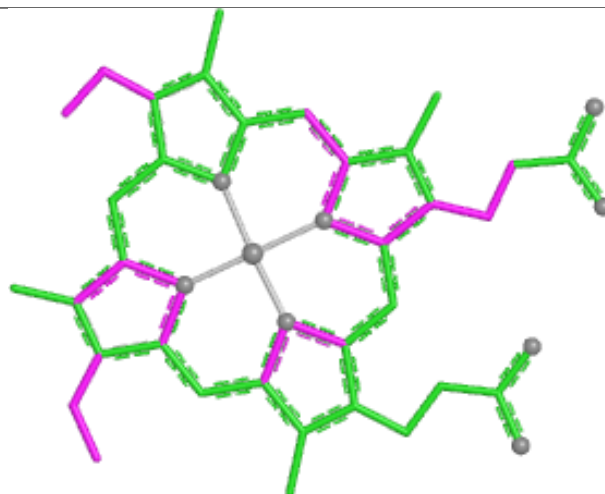


Rings

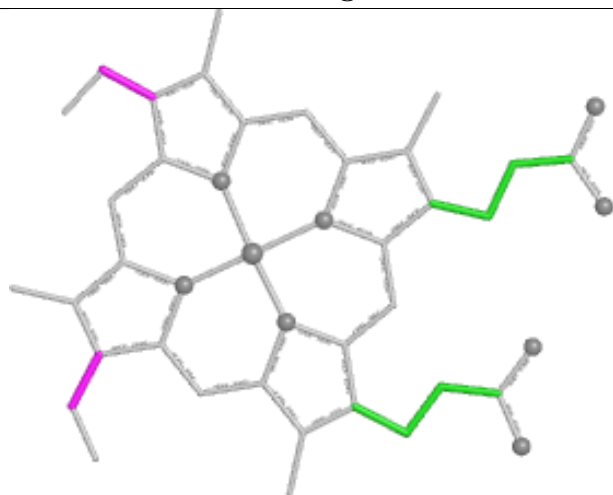
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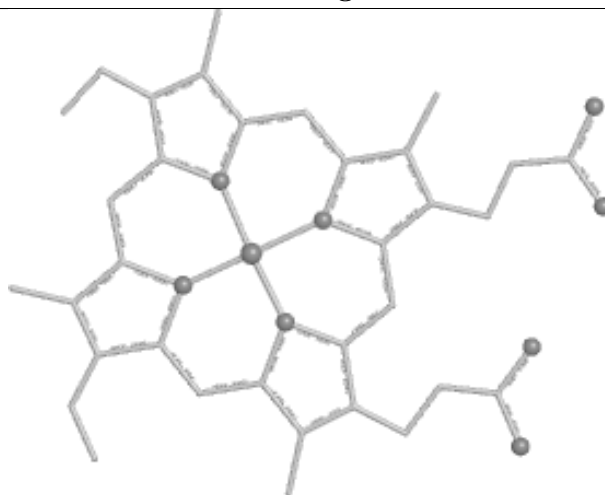
Bond lengths



Bond angles

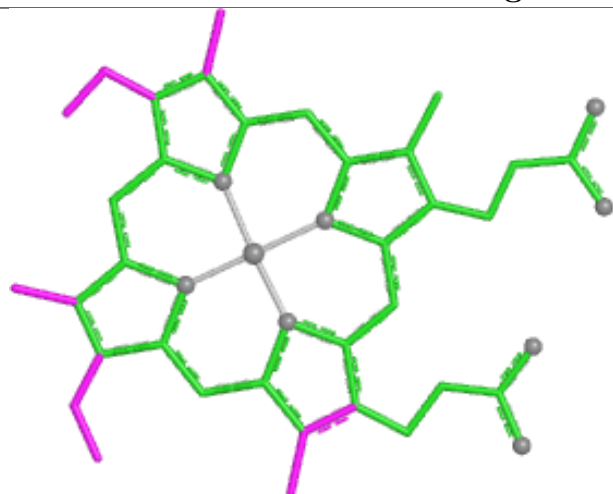


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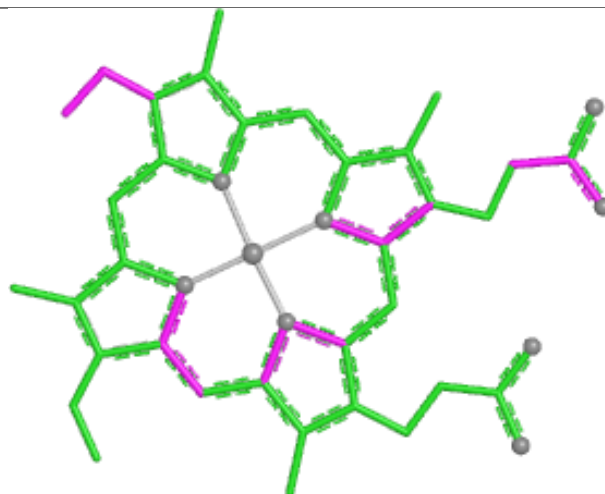


Rings

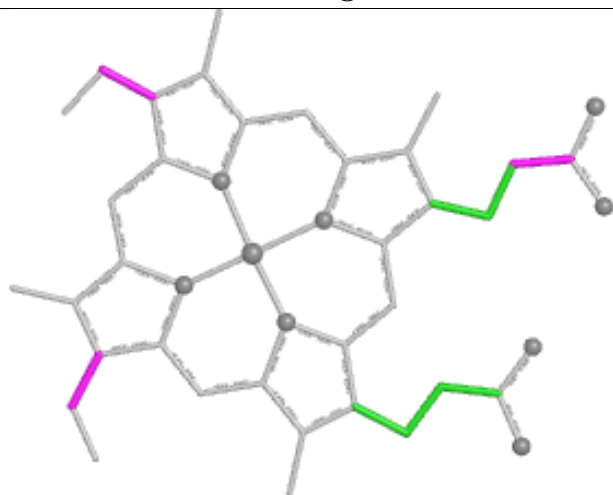
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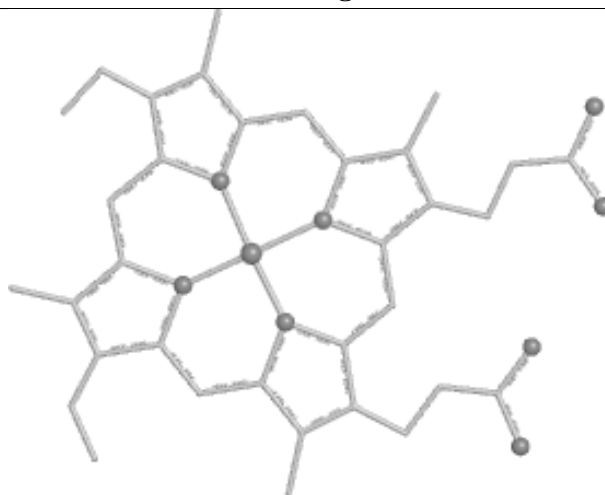
Bond lengths



Bond angles

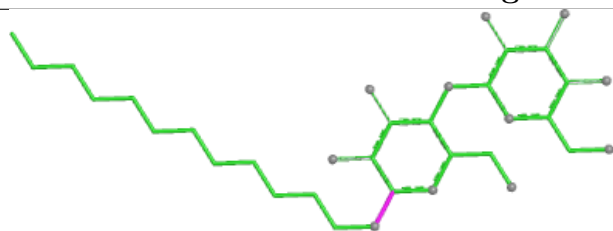


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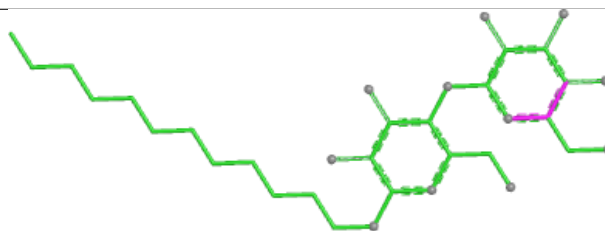


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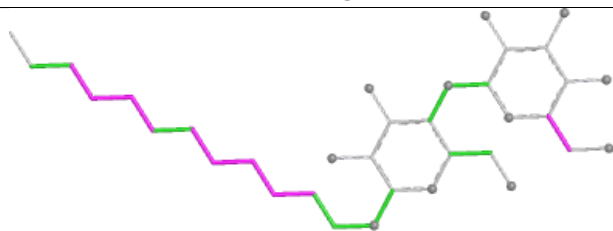
Ligand LMT O 1005



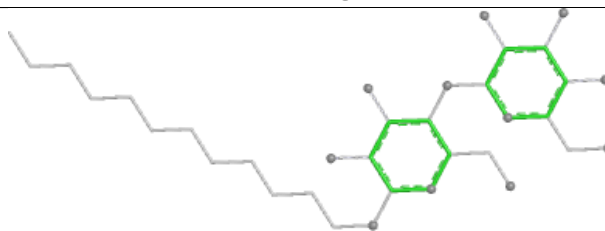
Bond lengths



Bond angles

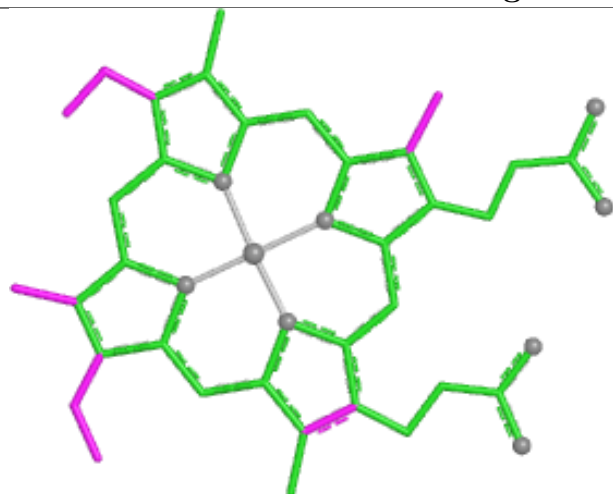


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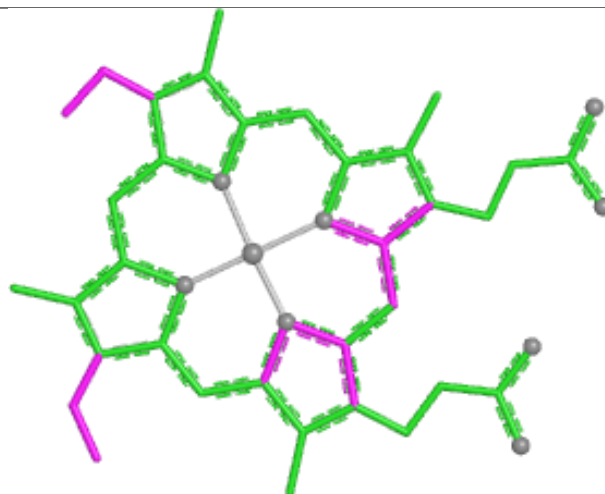


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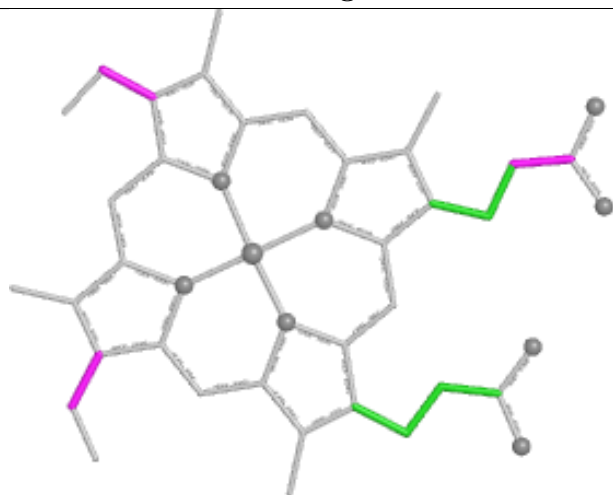
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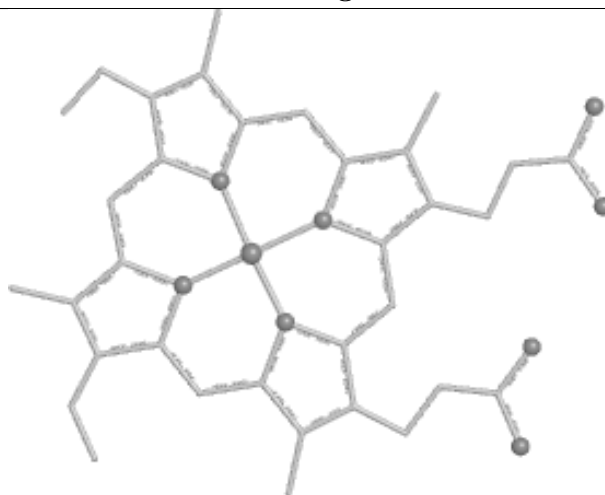
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Bond angles

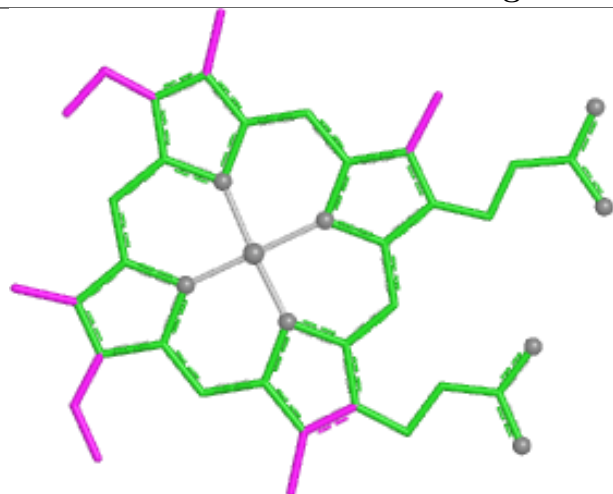


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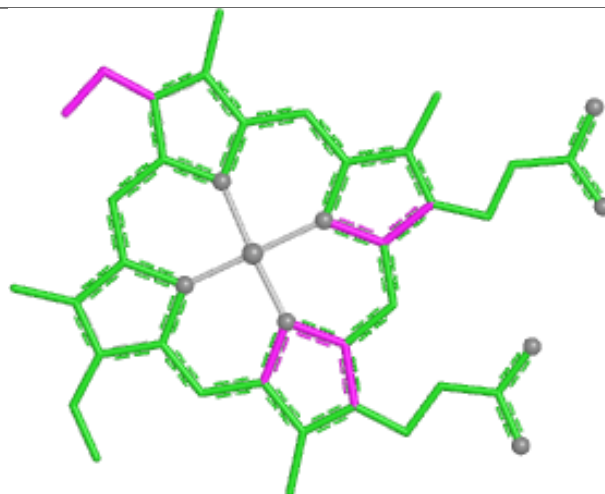


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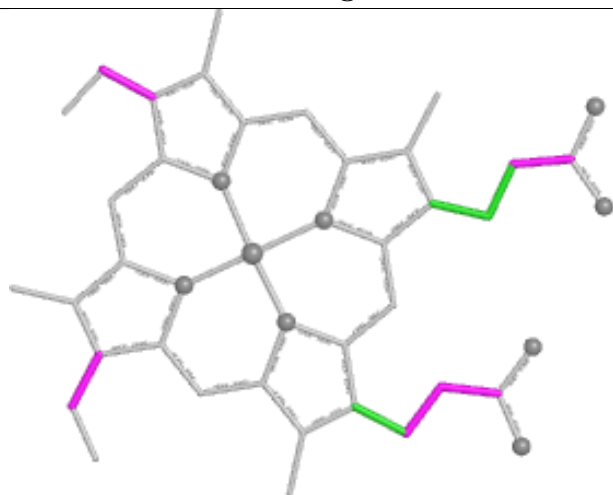
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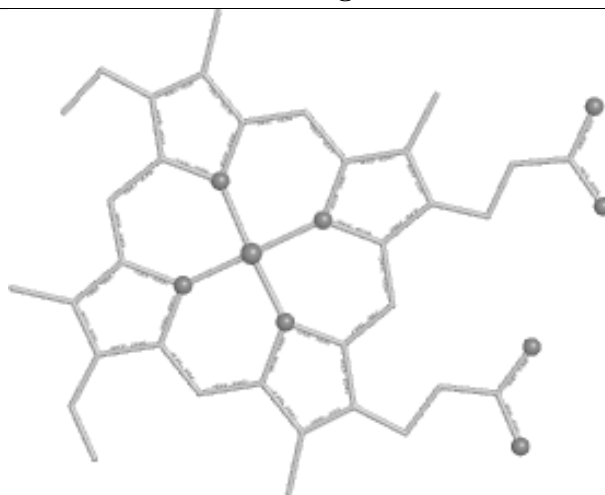
Bond lengths



Bond angles

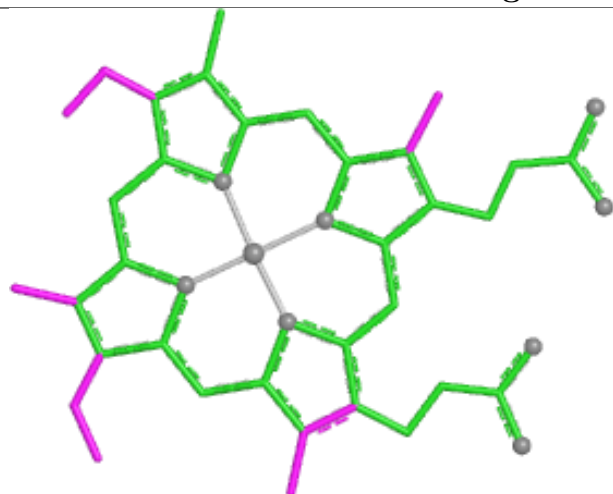


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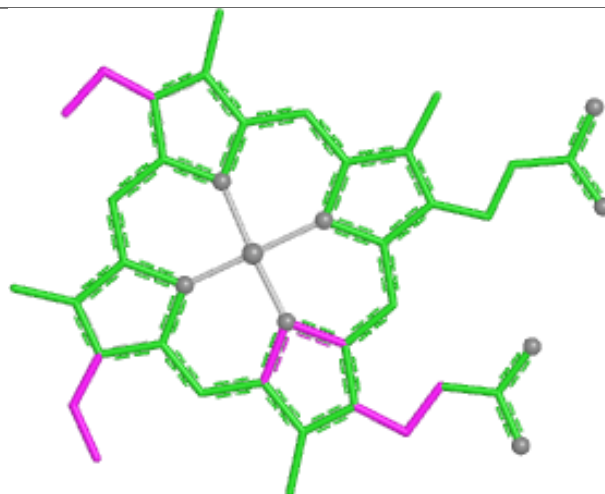


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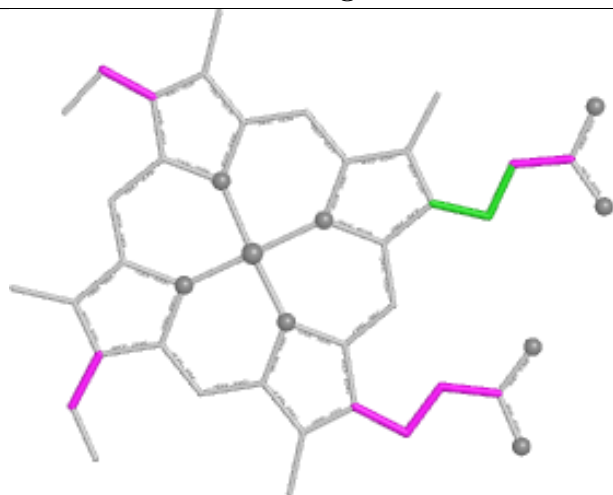
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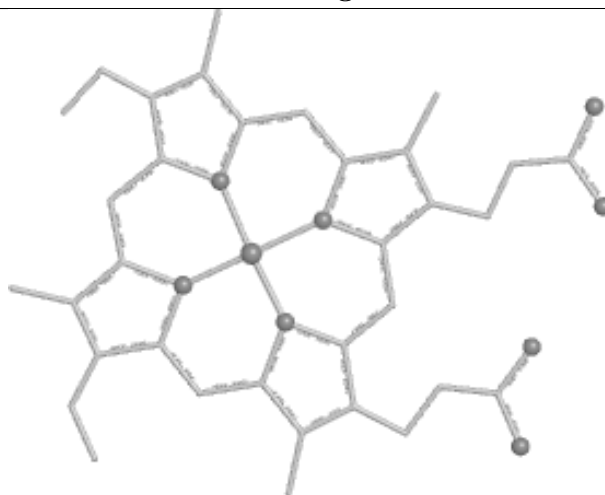
Bond lengths



Bond angles

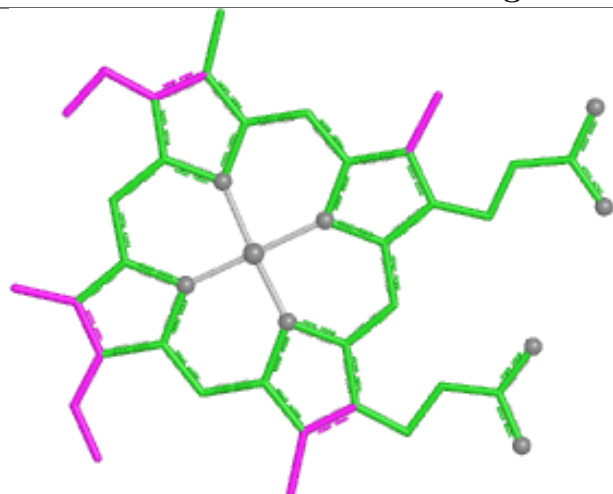


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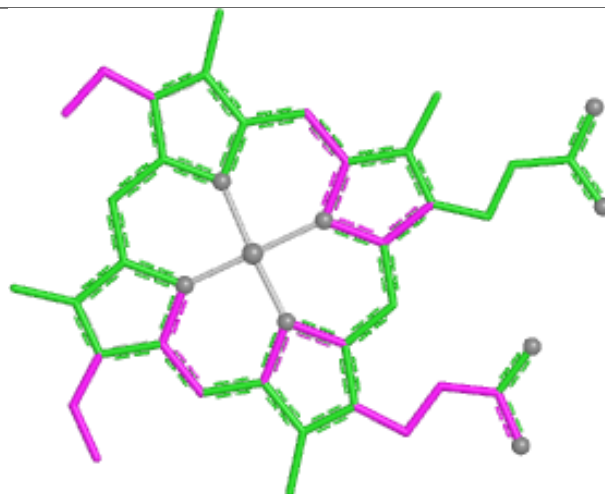


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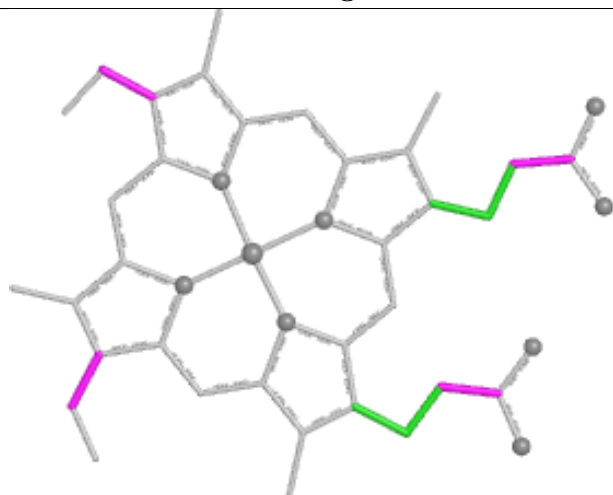
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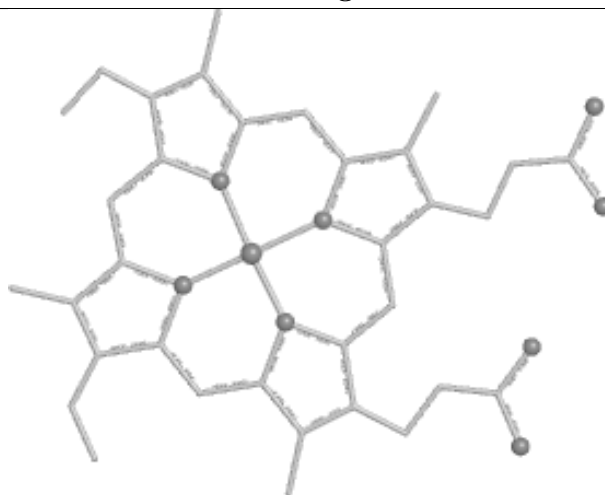
Bond lengths



Bond angles

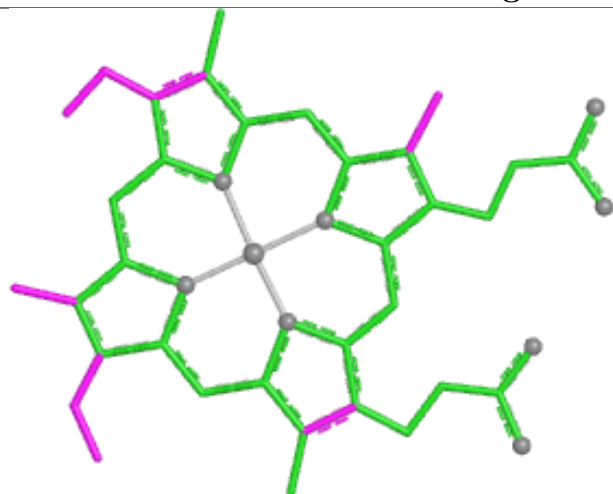


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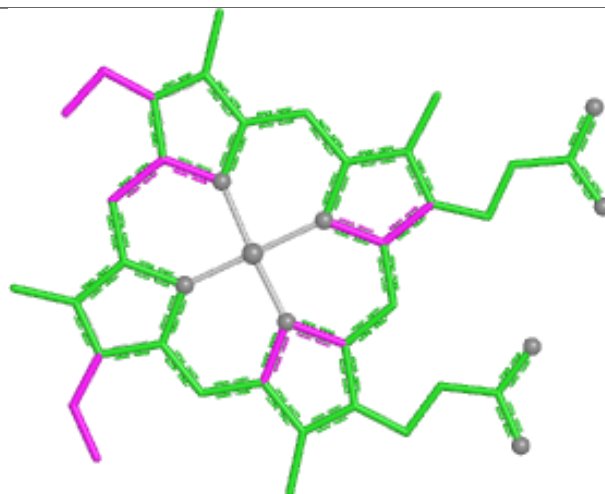


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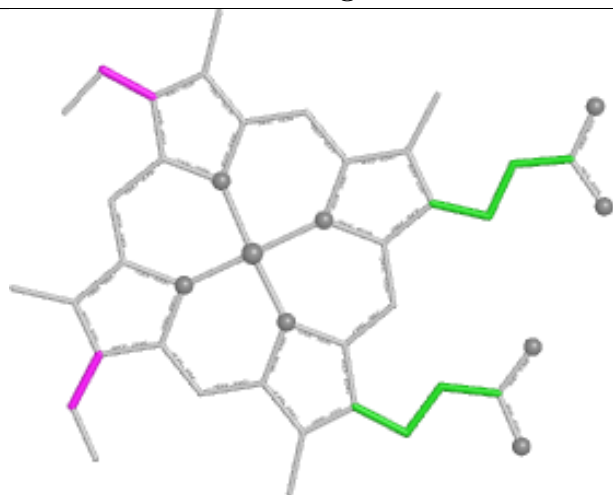
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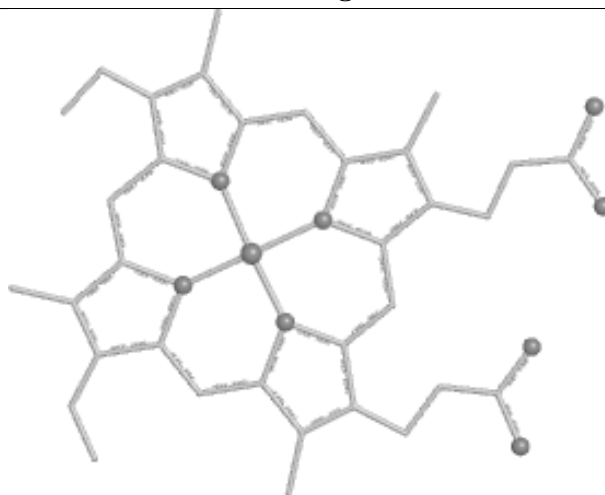
Bond lengths



Bond angles

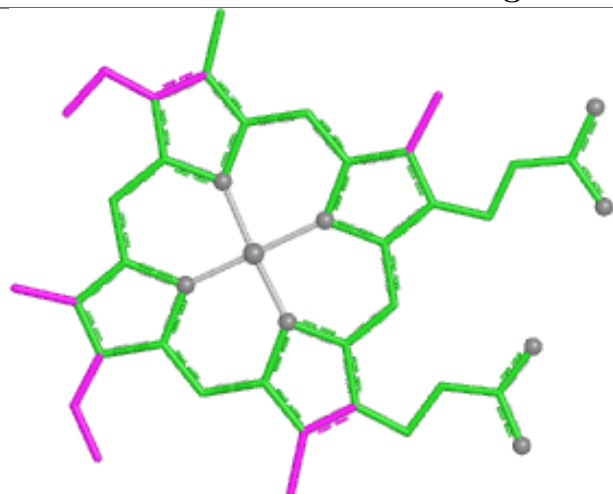


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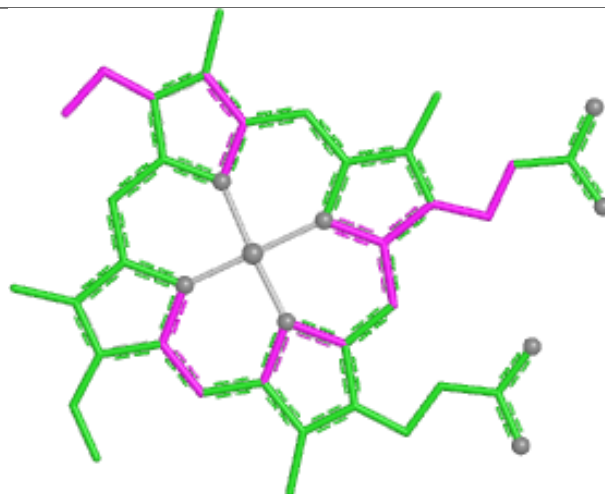


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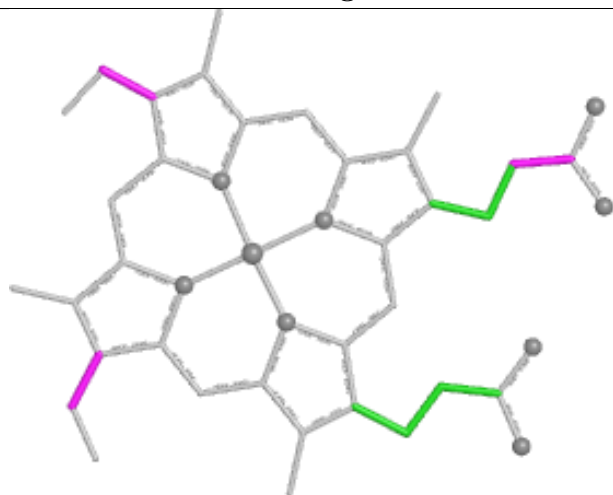
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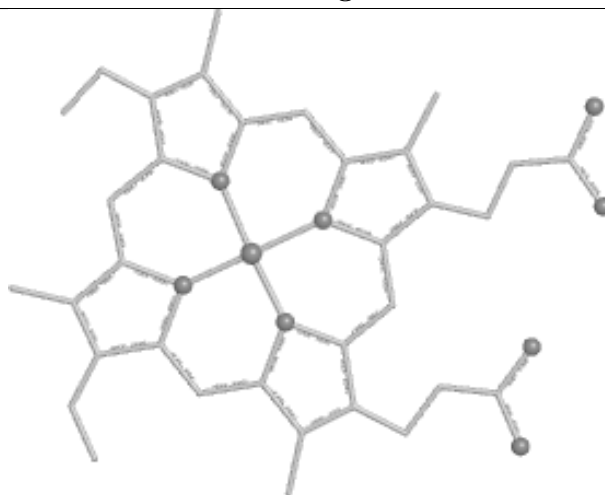
Bond lengths



Bond angles

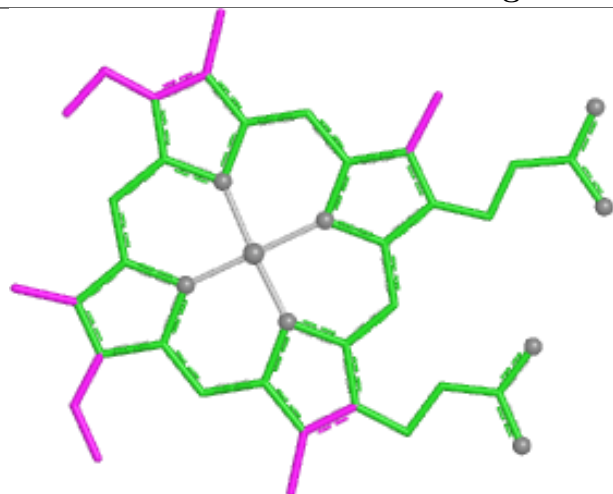


Torsions

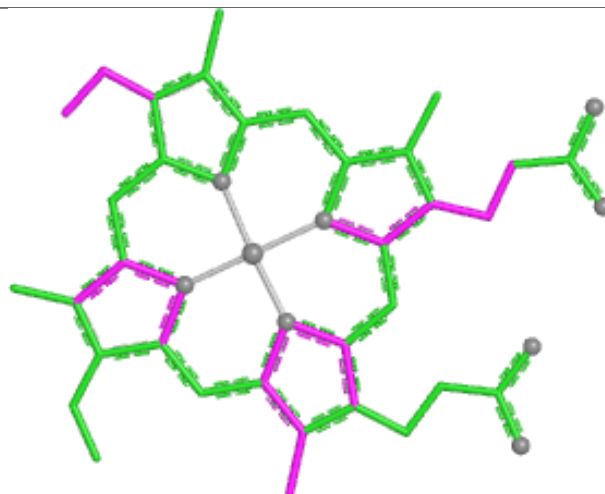


Rings

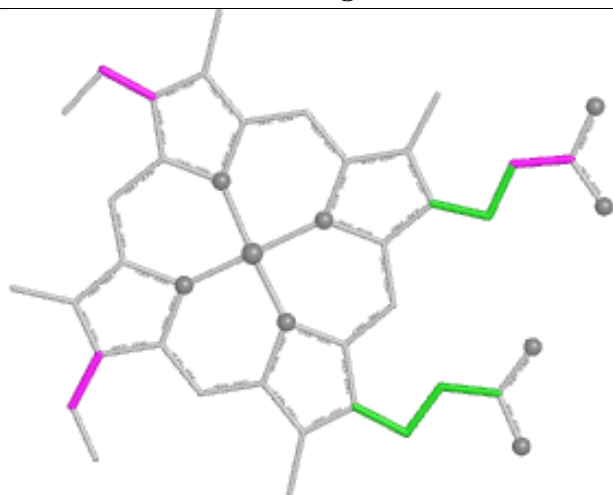
Ligand HEC H 1004



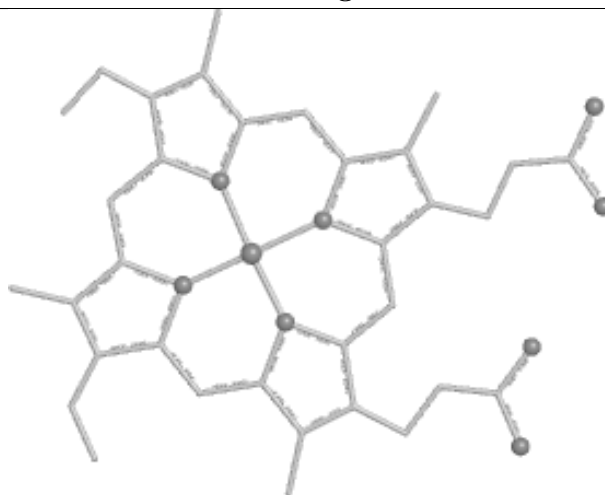
Bond lengths



Bond angles

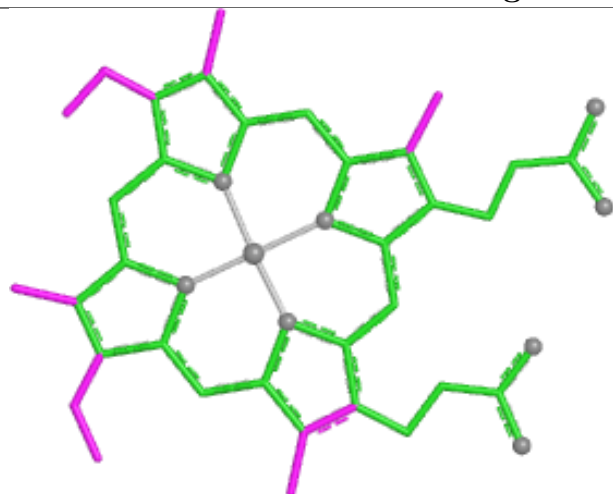


Torsions

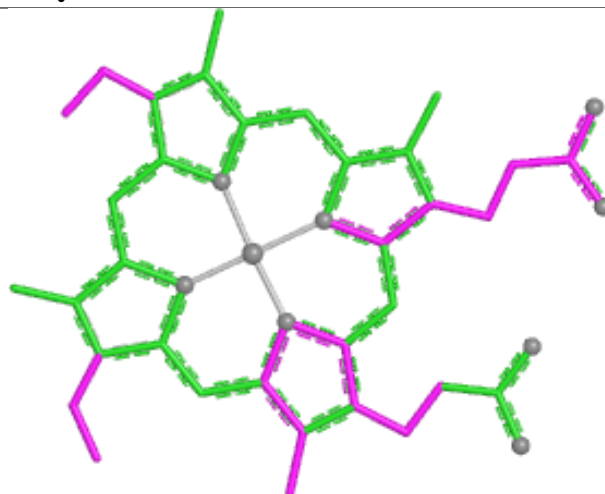


Rings

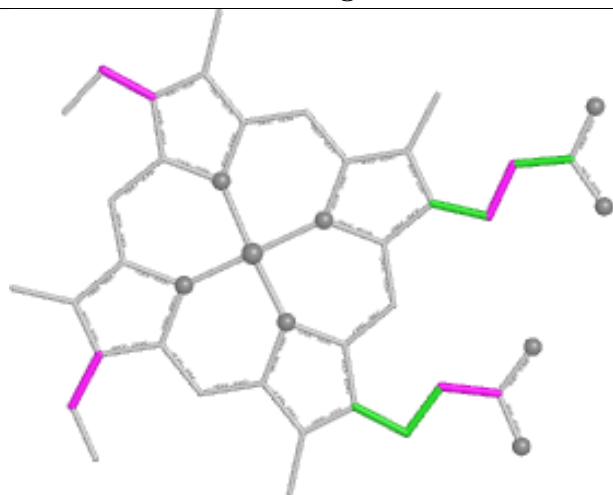
Ligand HEC Q 1005



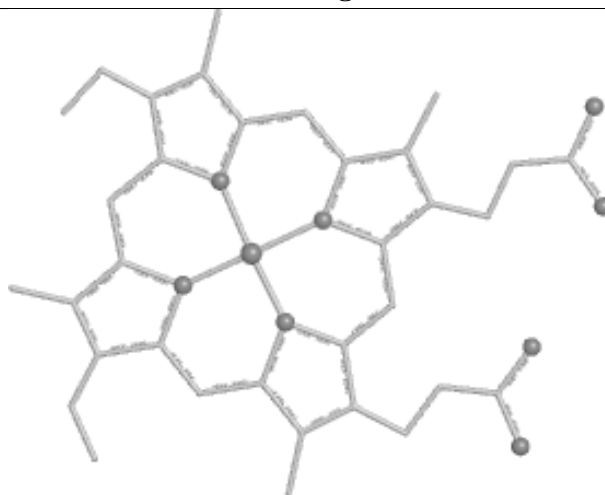
Bond lengths



Bond angles

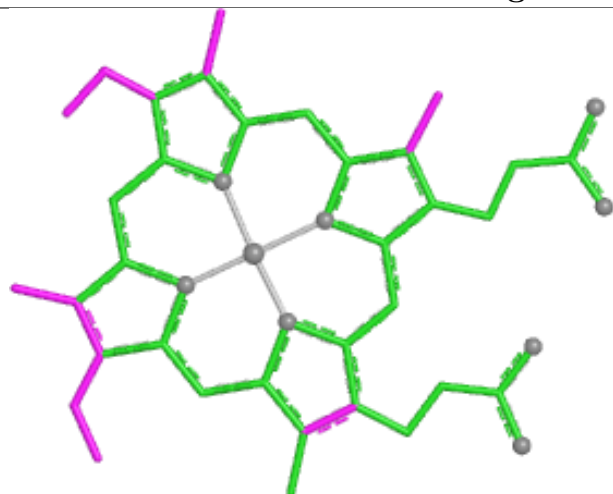


Torsions

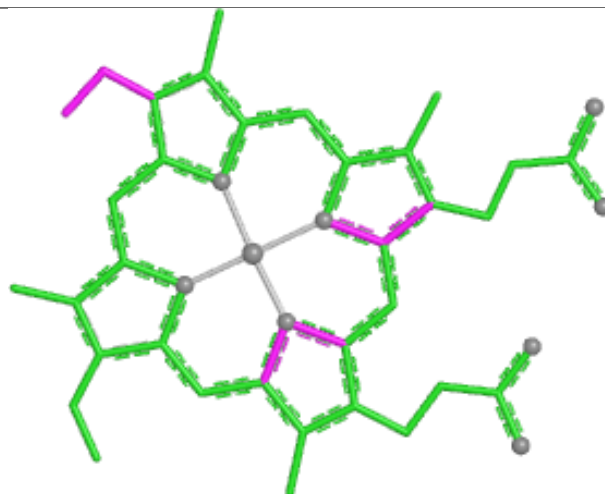


Rings

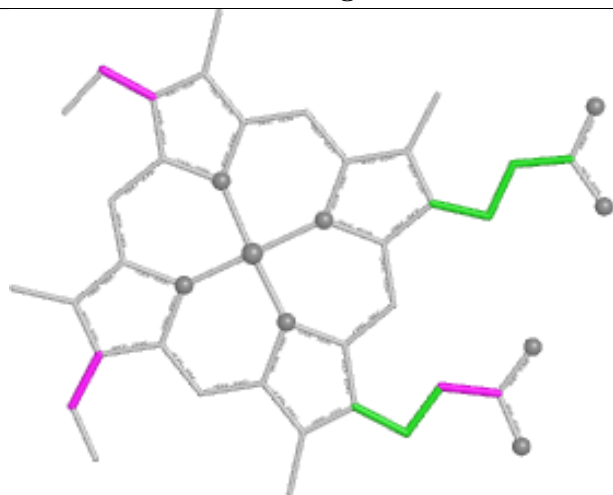
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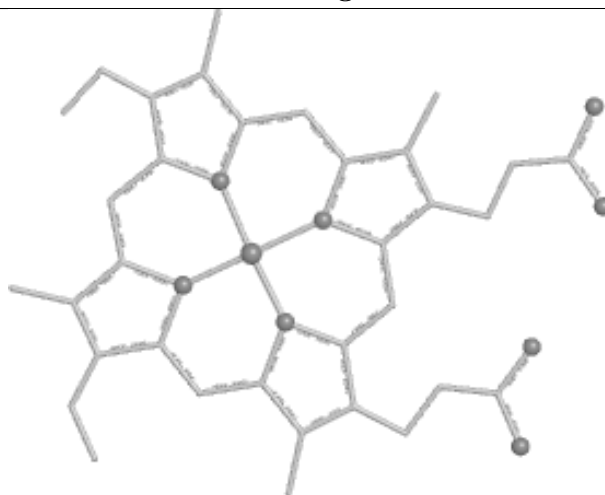
Bond lengths



Bond angles

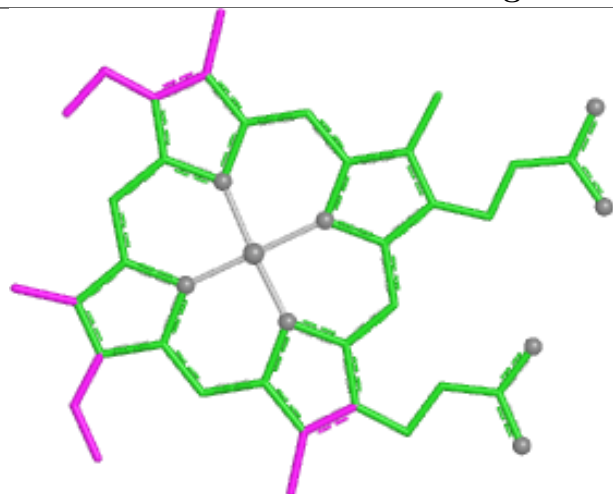


Torsions

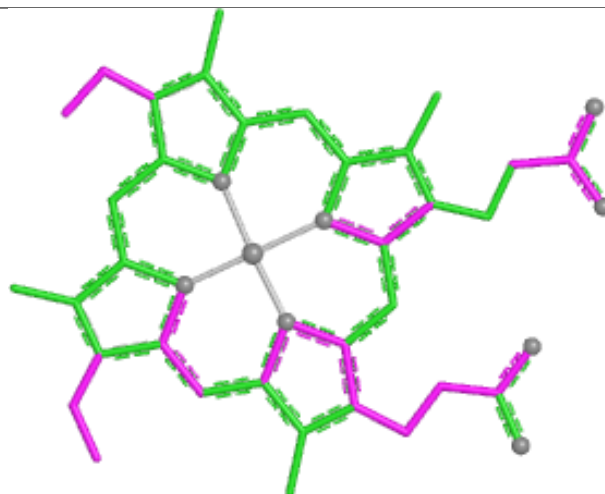


Rings

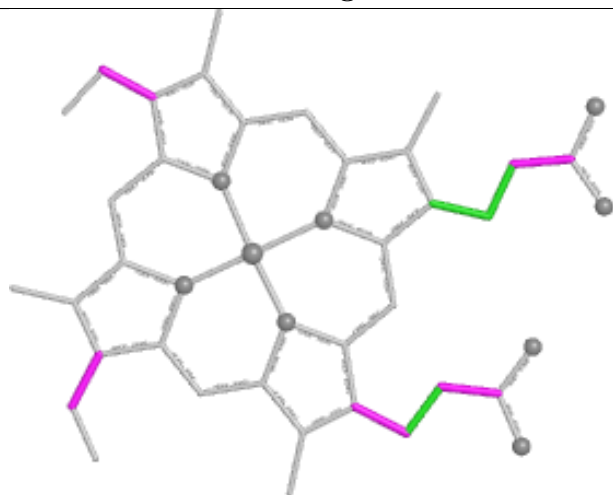
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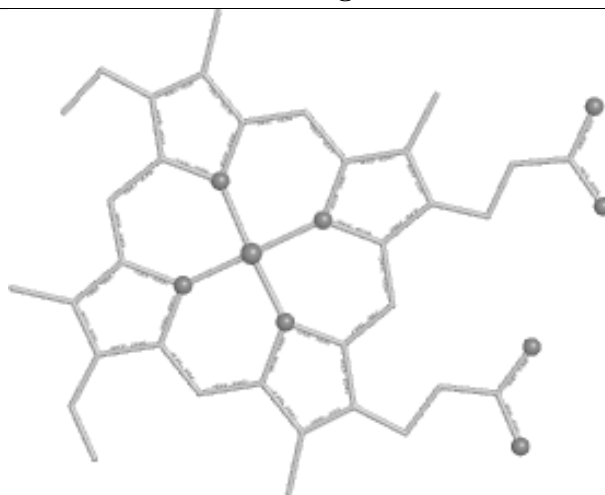
Bond lengths



Bond angles

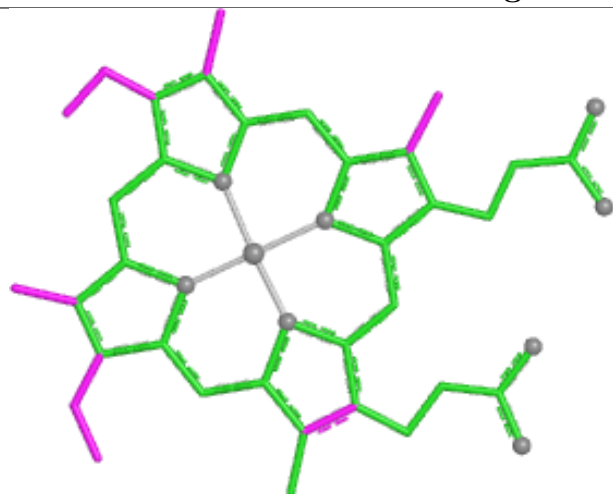


Torsions

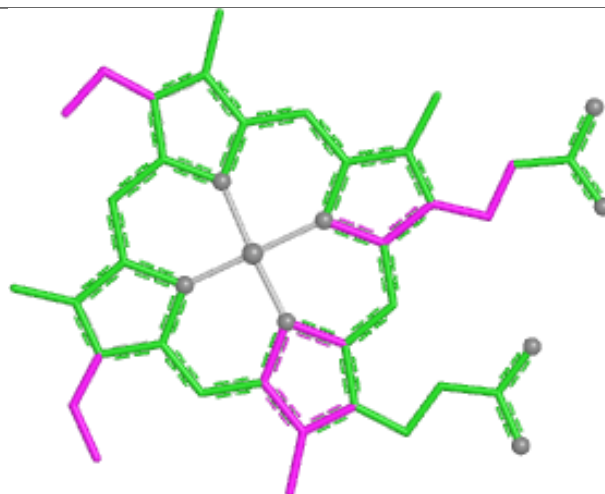


Rings

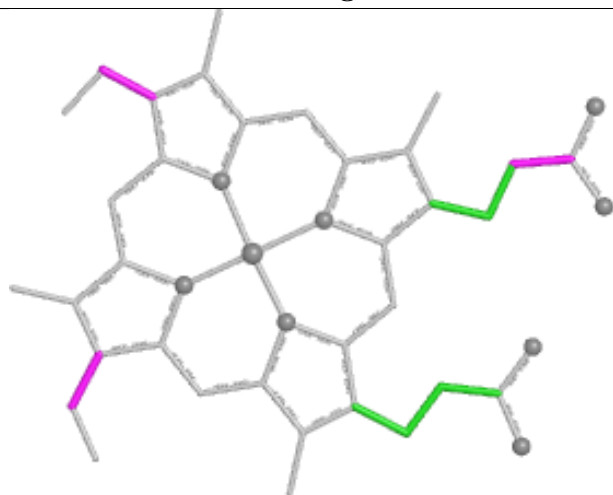
Ligand HEC B 1004



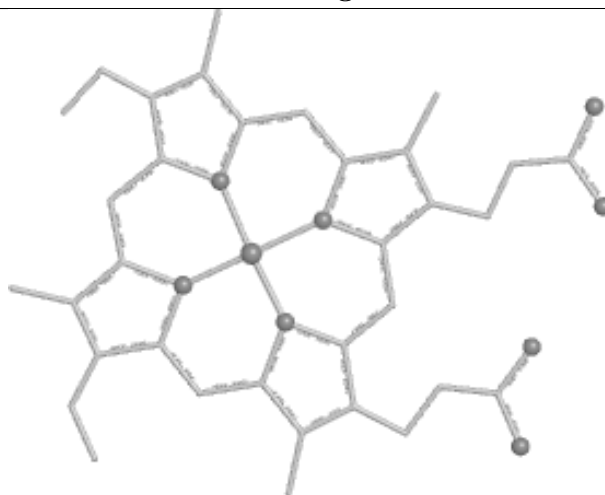
Bond lengths



Bond angles

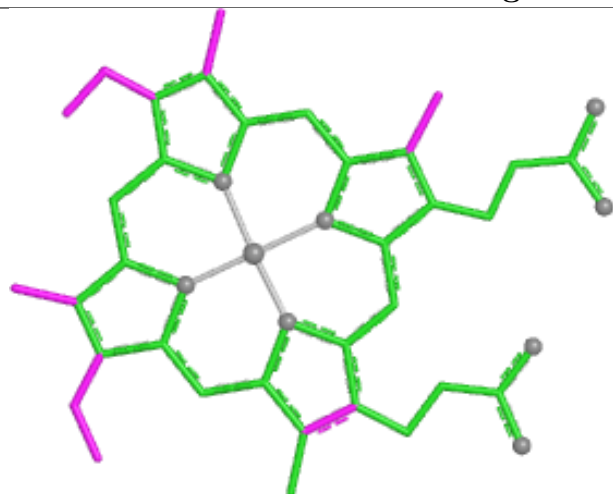


Torsions

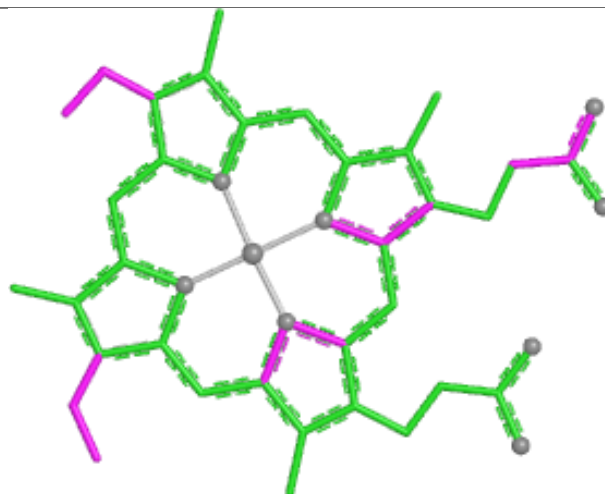


Rings

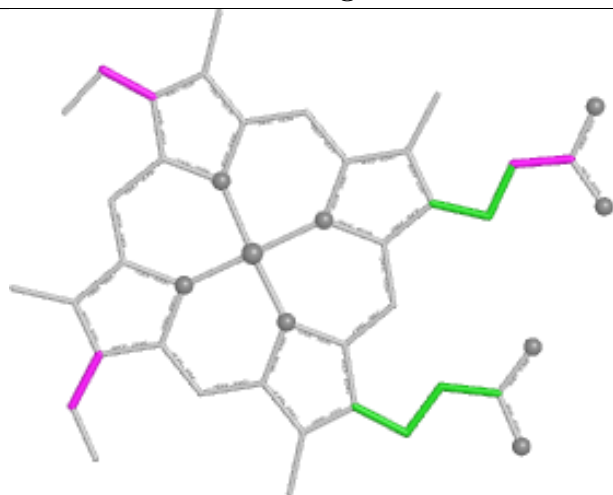
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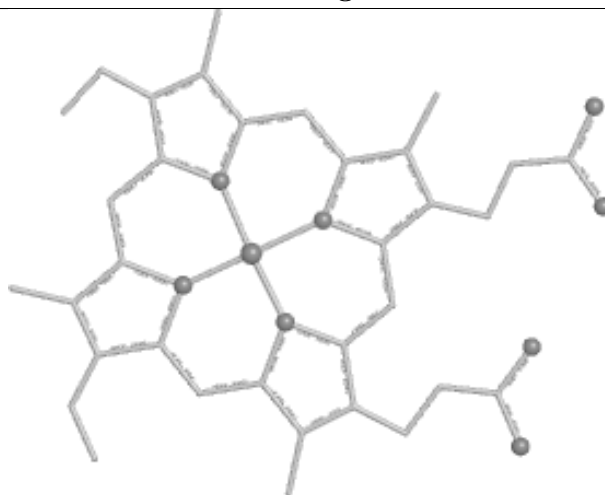
Bond lengths



Bond angles

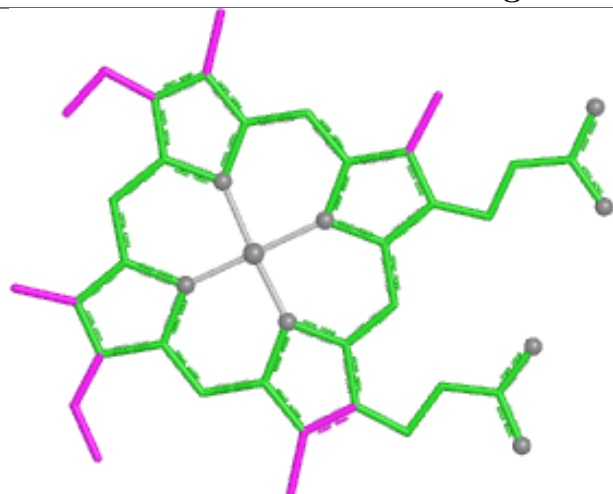


Torsions

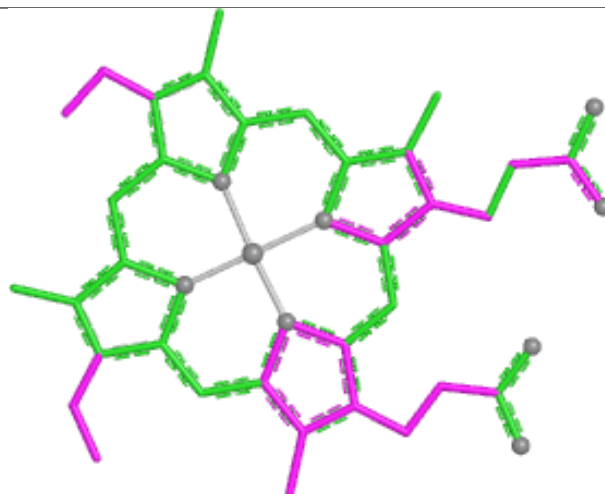


Rings

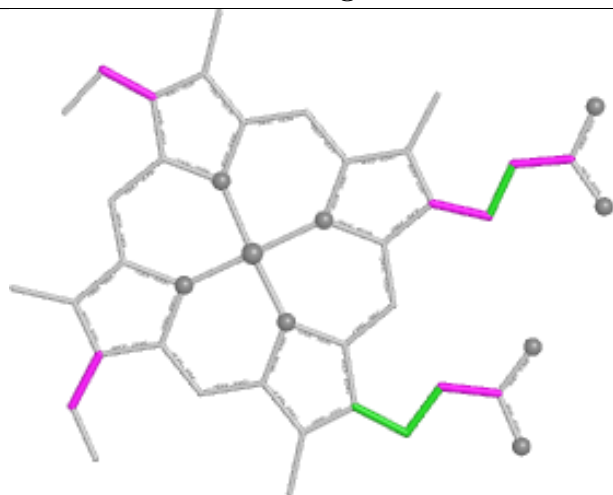
Ligand HEC O 1002



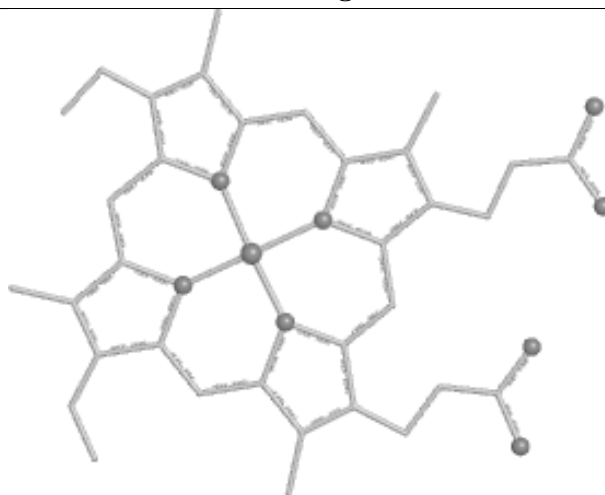
Bond lengths



Bond angles

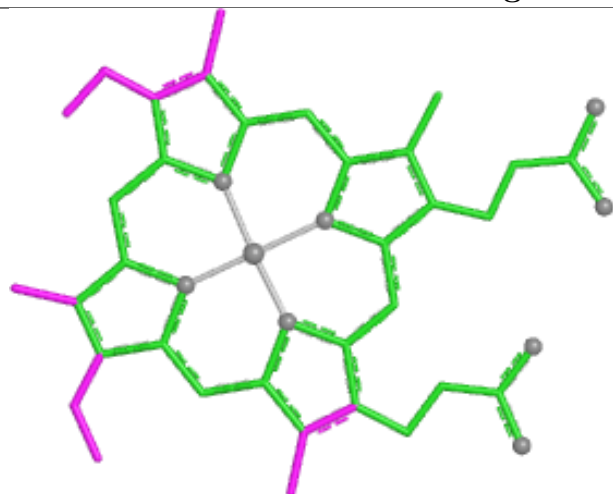


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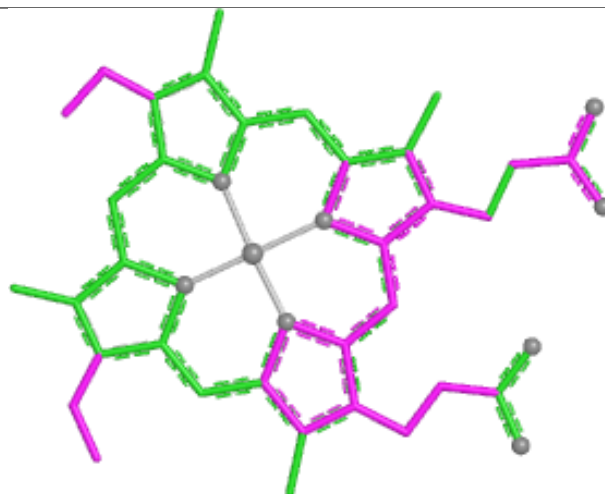


Rings

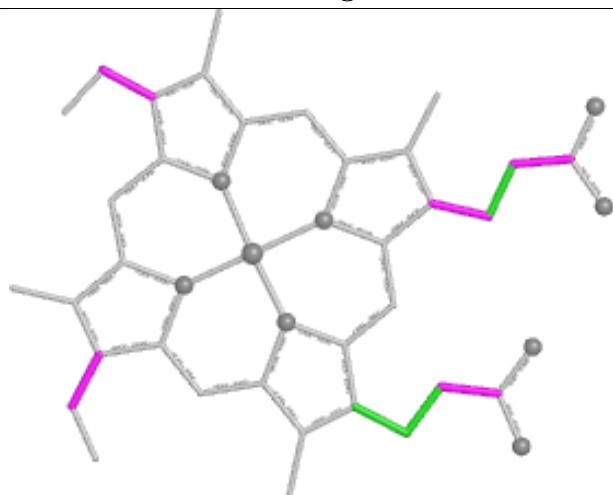
Ligand HEC C 1002



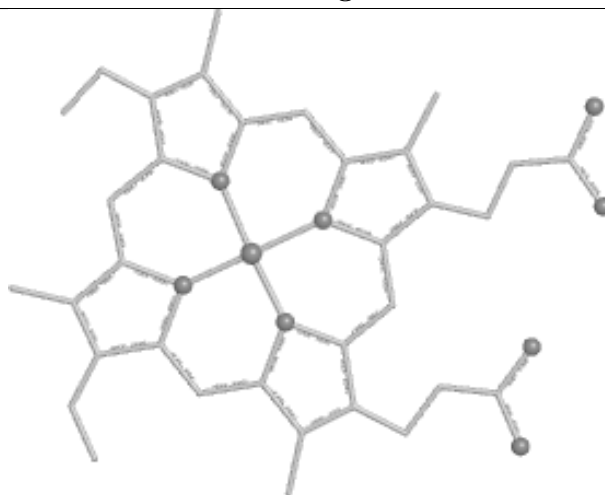
Bond lengths



Bond angles

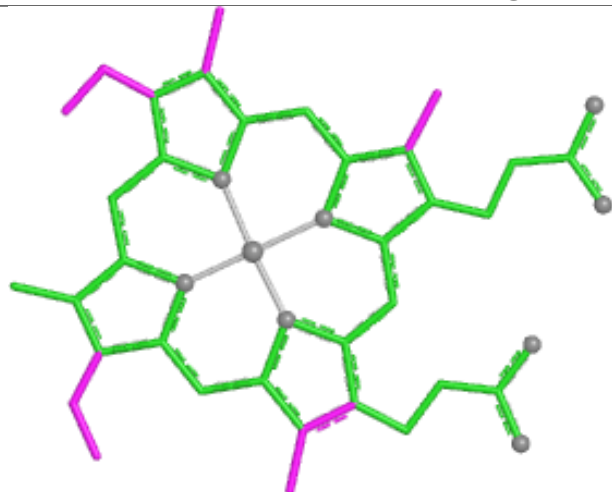


Torsions

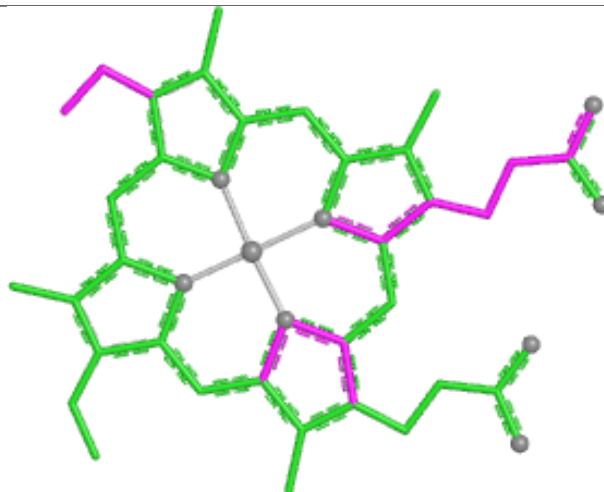


Rings

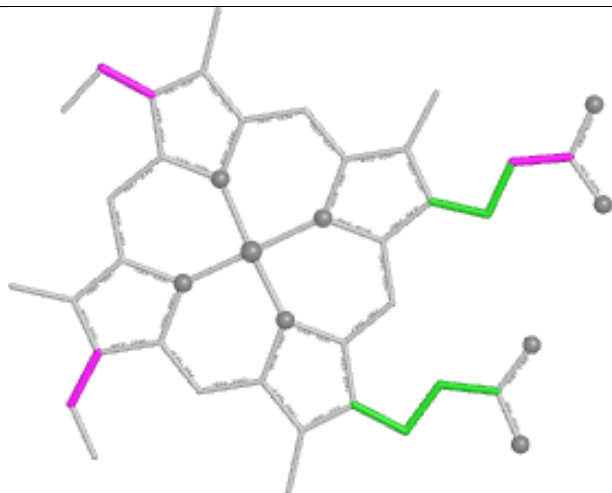
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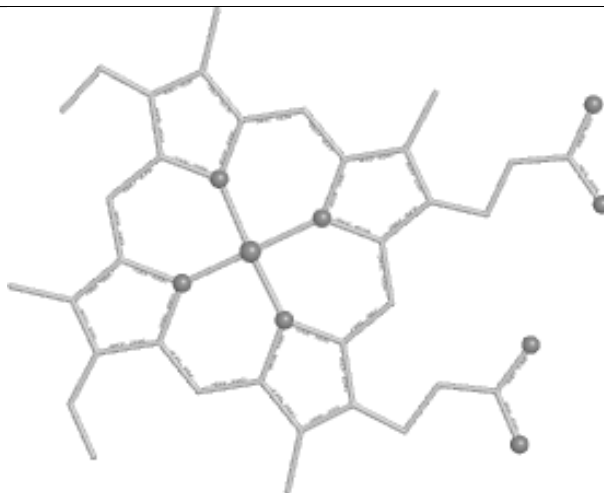
Bond lengths



Bond angles

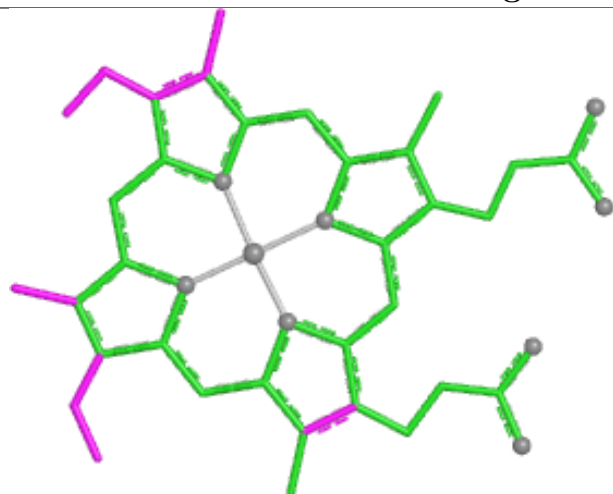


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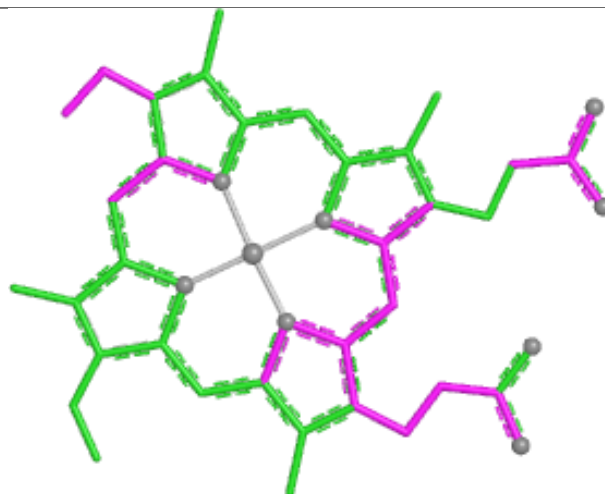


Rings

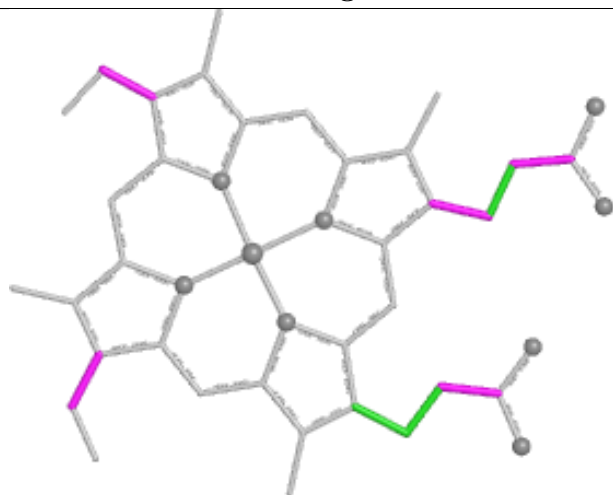
Ligand HEC R 1002



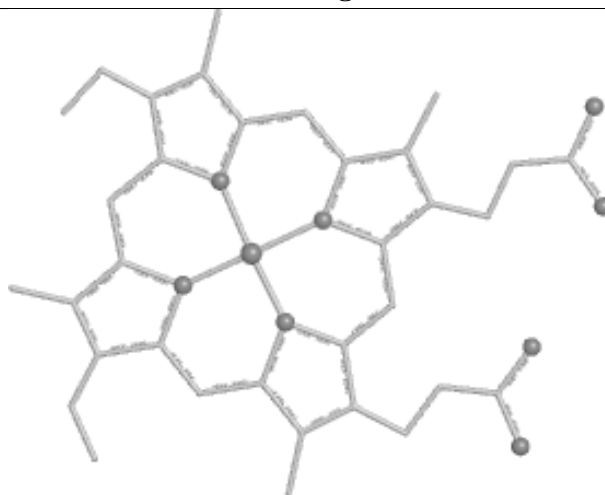
Bond lengths



Bond angles

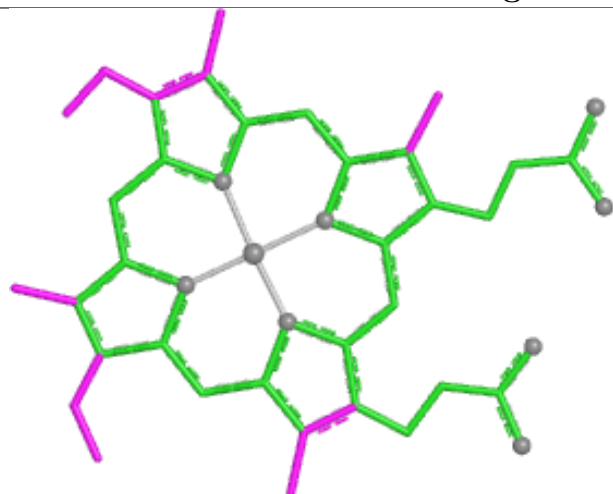


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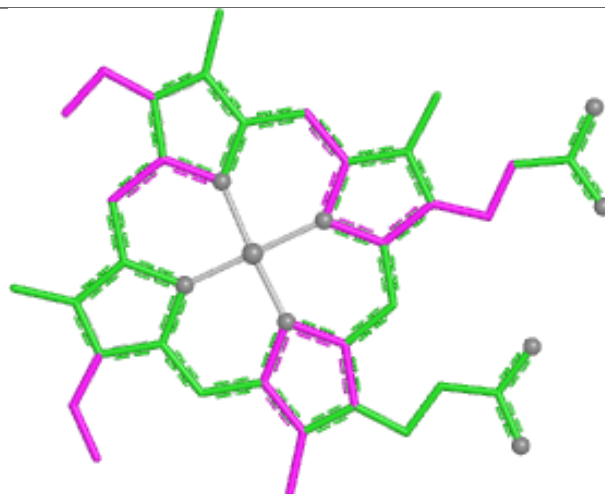


Rings

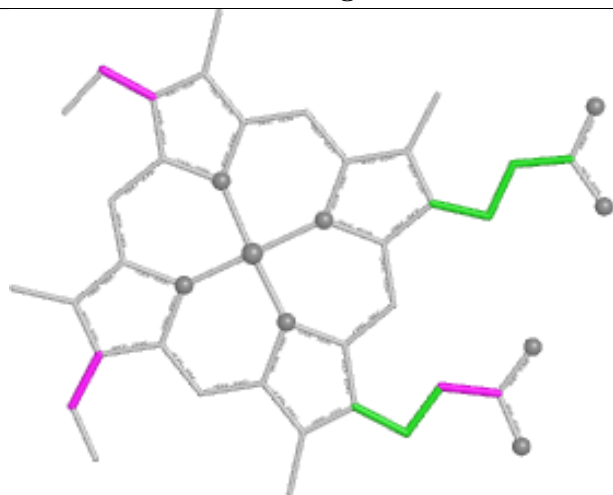
Ligand HEC O 1004



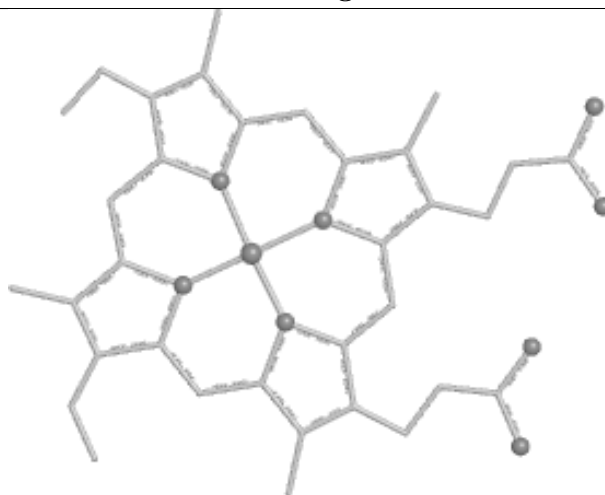
Bond lengths



Bond angles

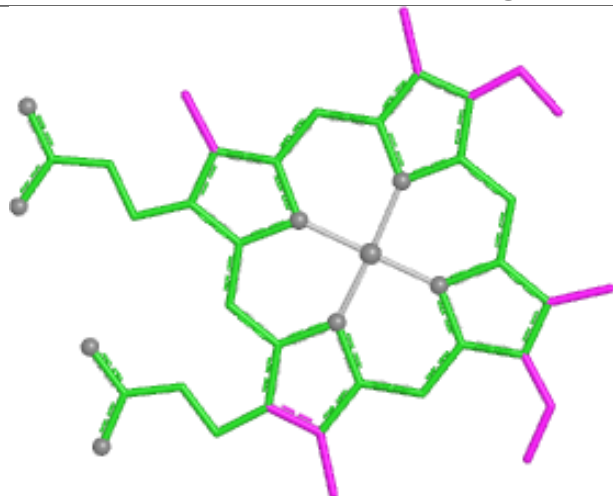


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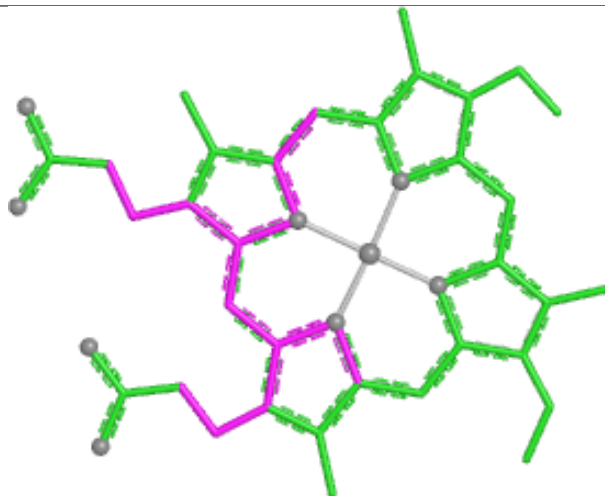


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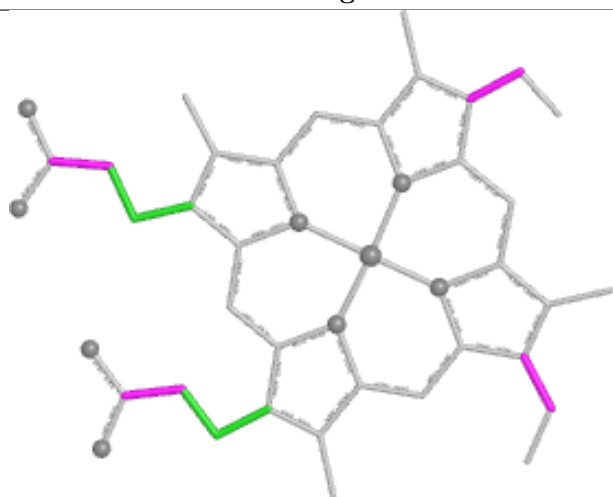
Ligand HEC M 1005



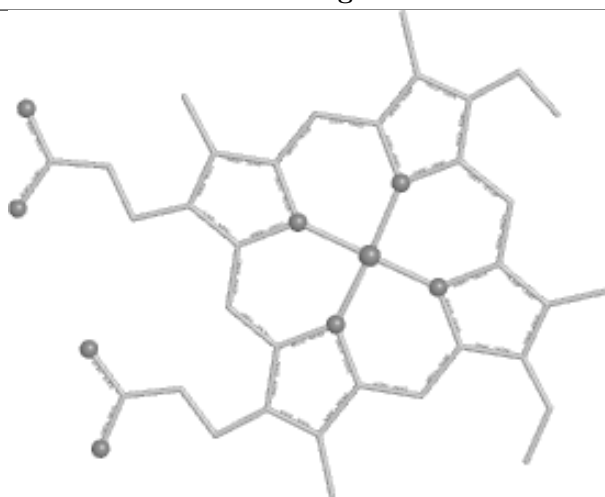
Bond lengths



Bond angles

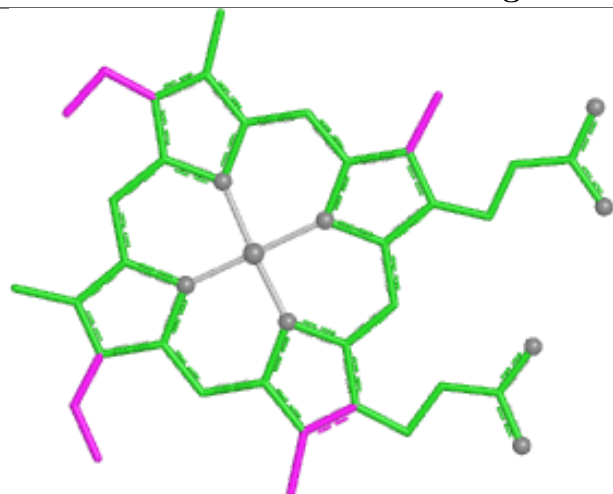


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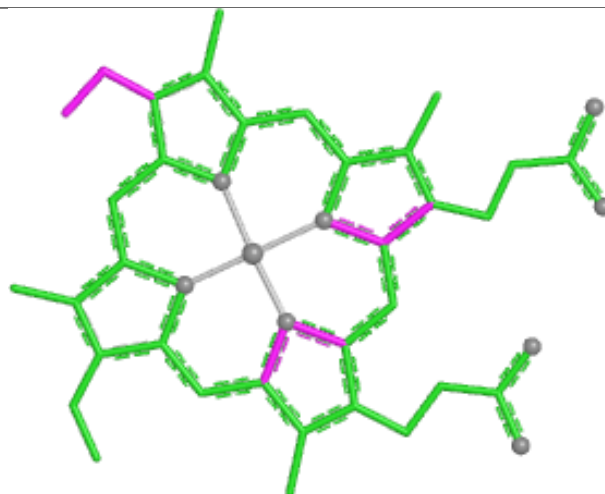


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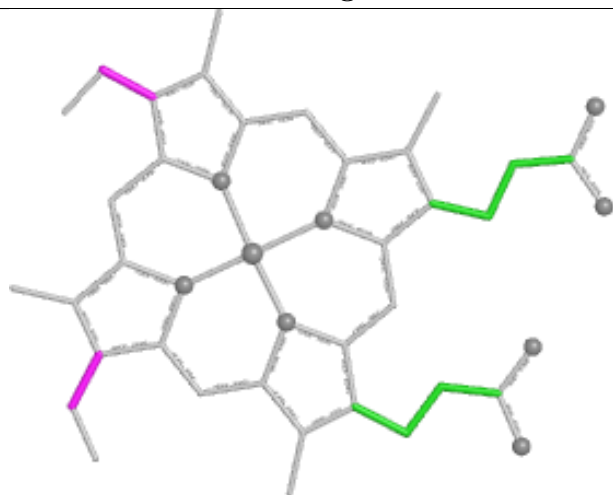
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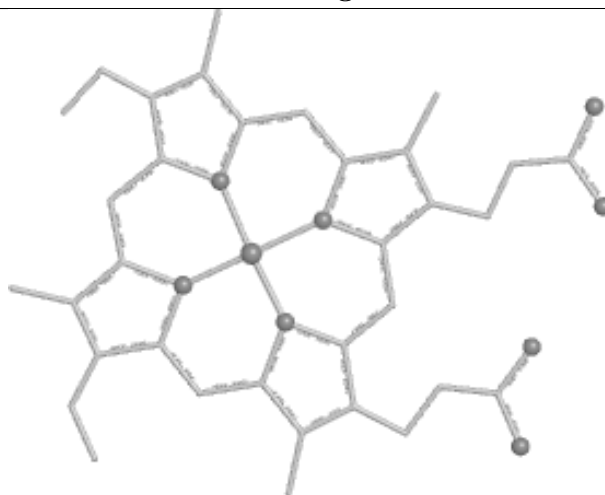
Bond lengths



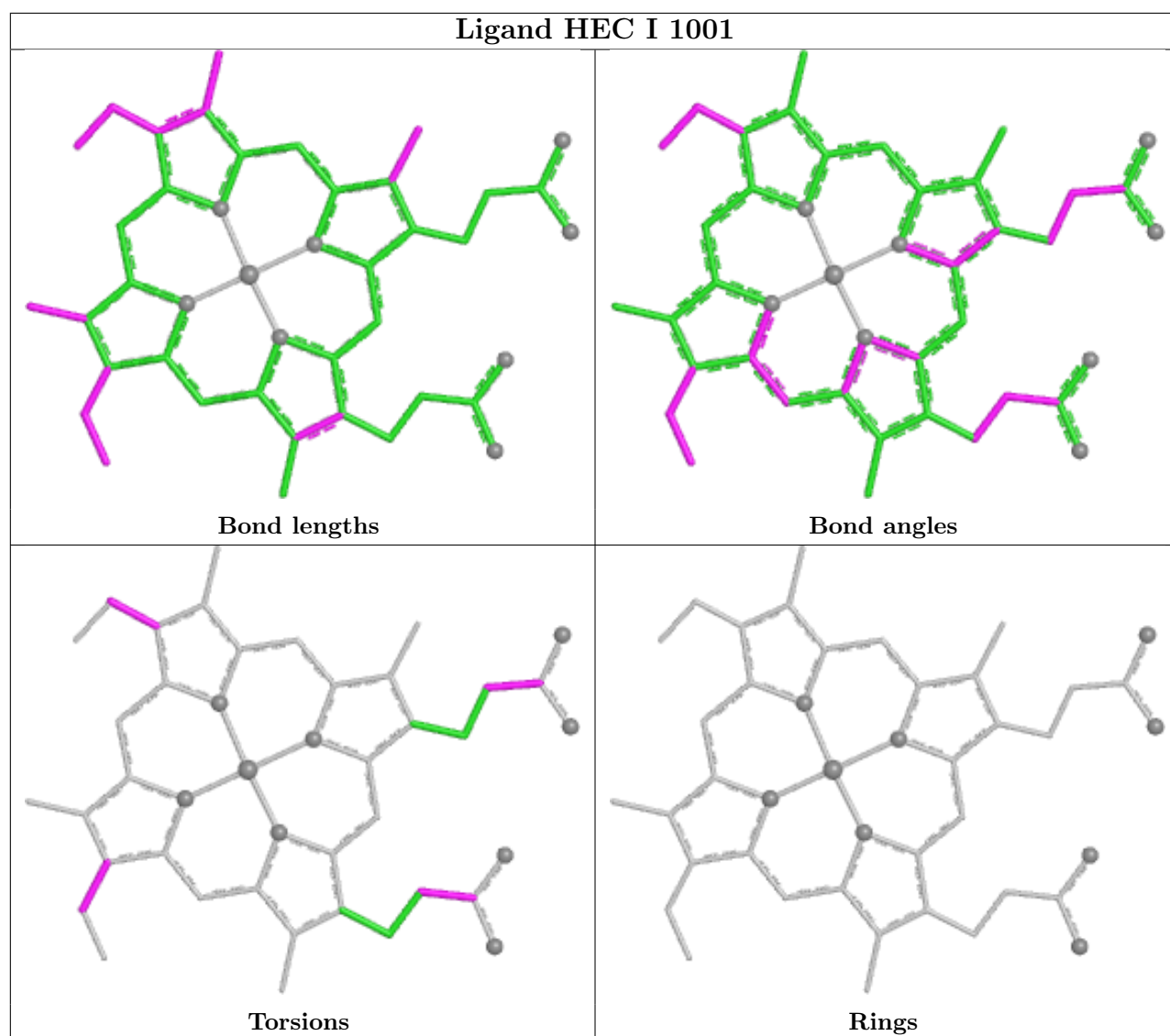
Bond angles



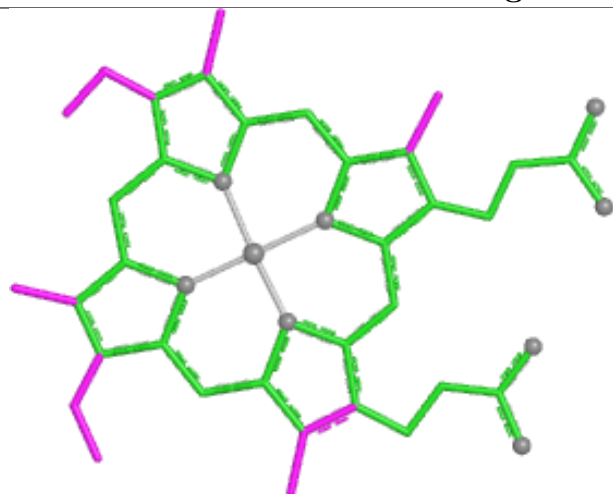
Torsions



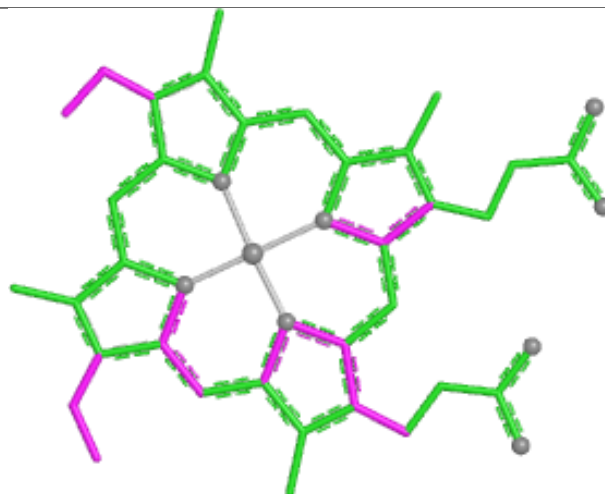
Rings



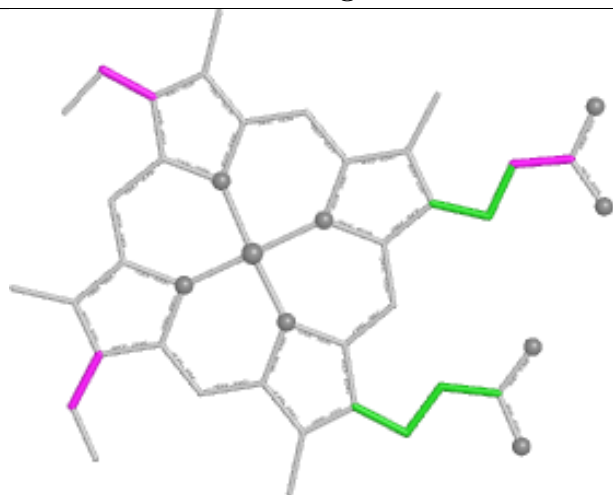
Ligand HEC E 1002



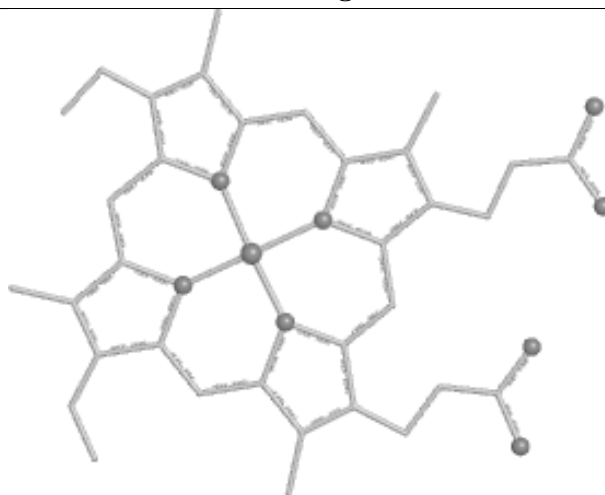
Bond lengths



Bond angles

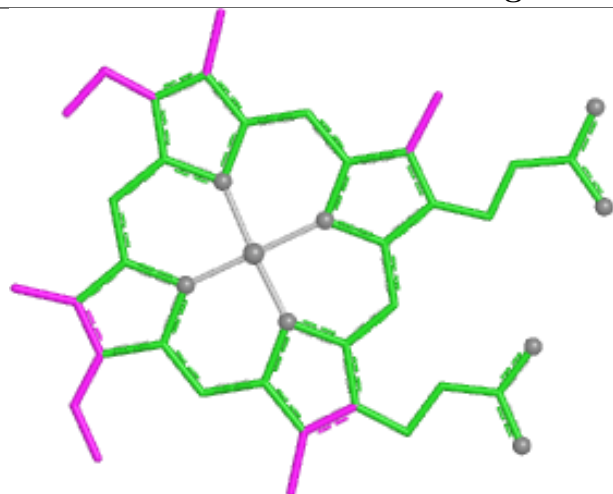


Torsions

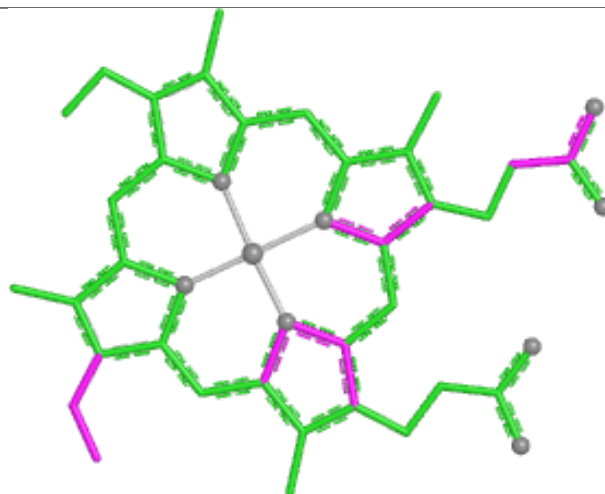


Rings

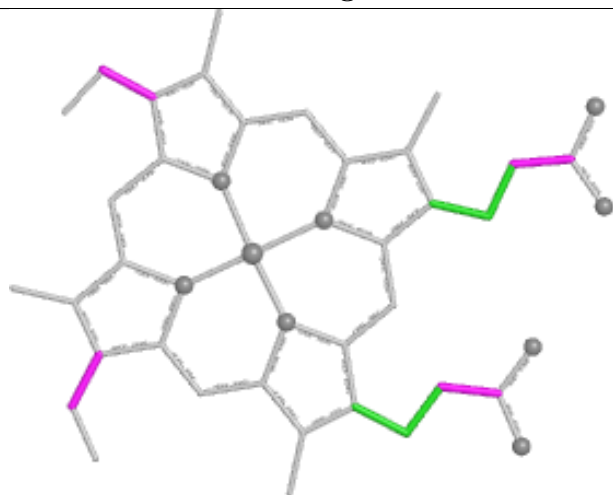
Ligand HEC P 1005



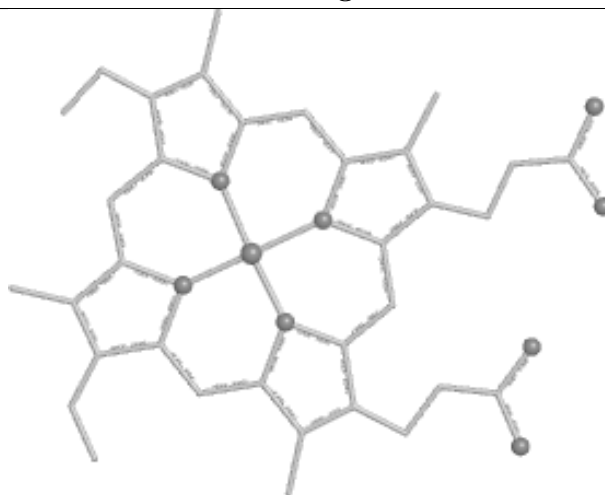
Bond lengths



Bond angles

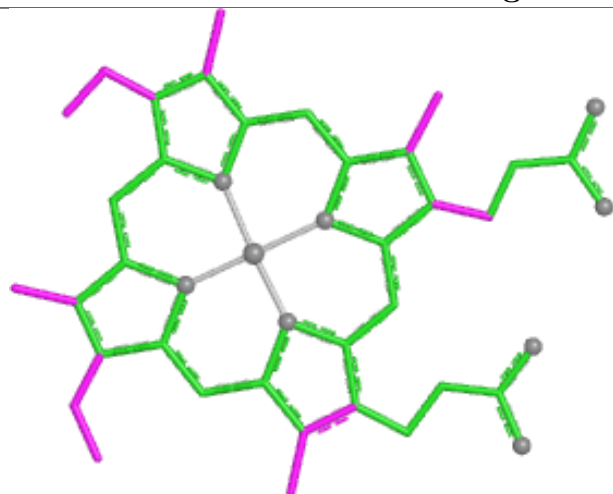


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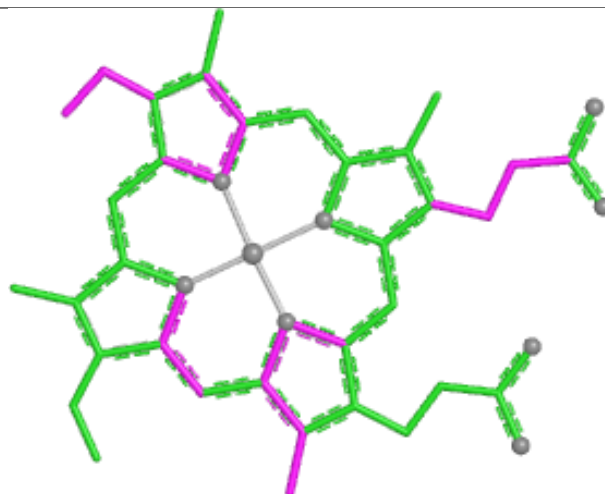


Rings

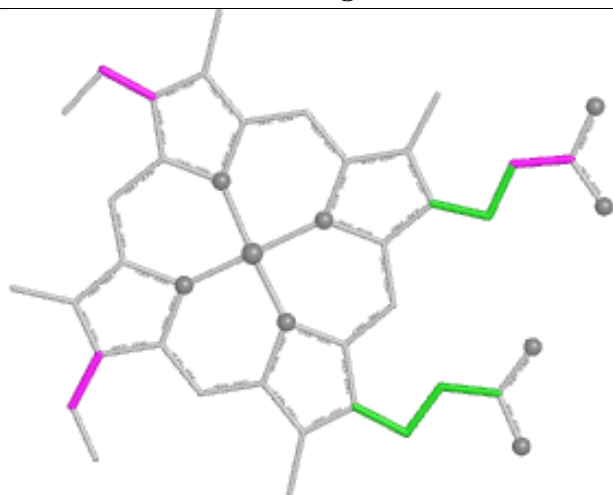
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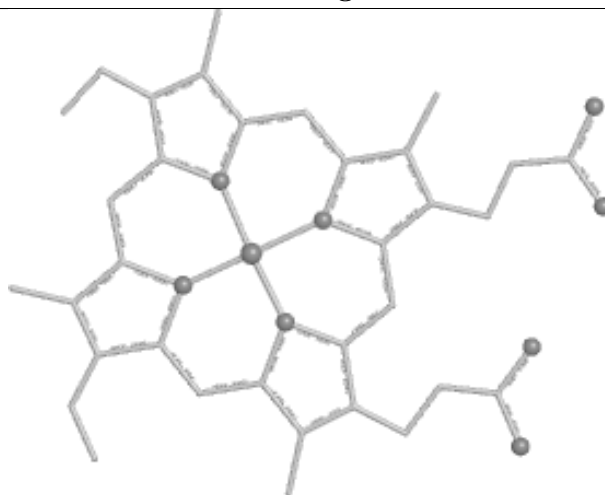
Bond lengths



Bond angles

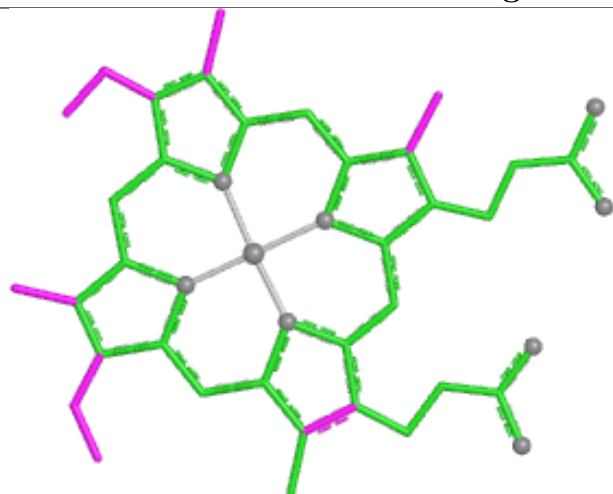


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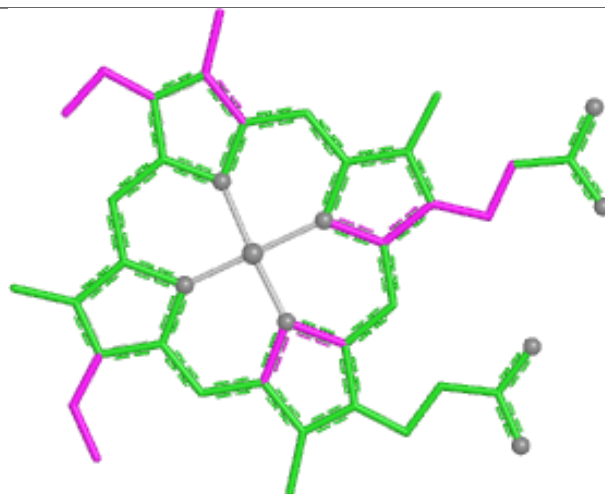


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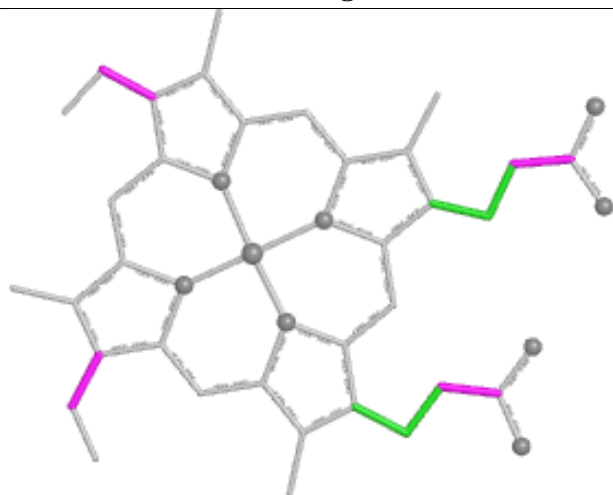
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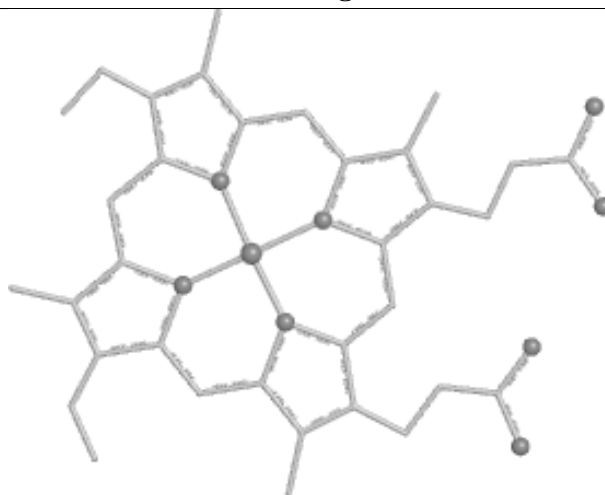
Bond lengths



Bond angles

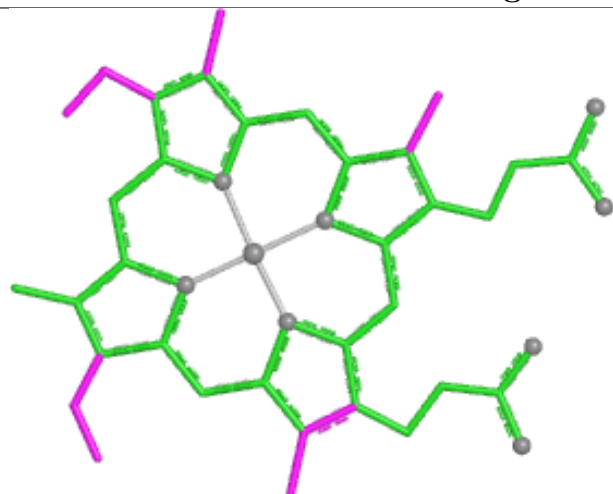


Torsions

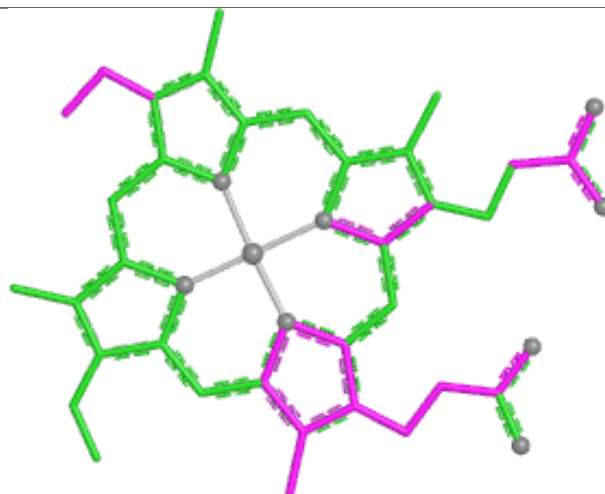


Rings

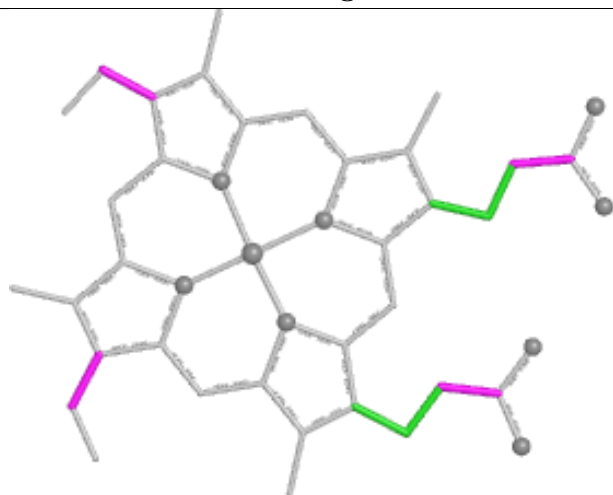
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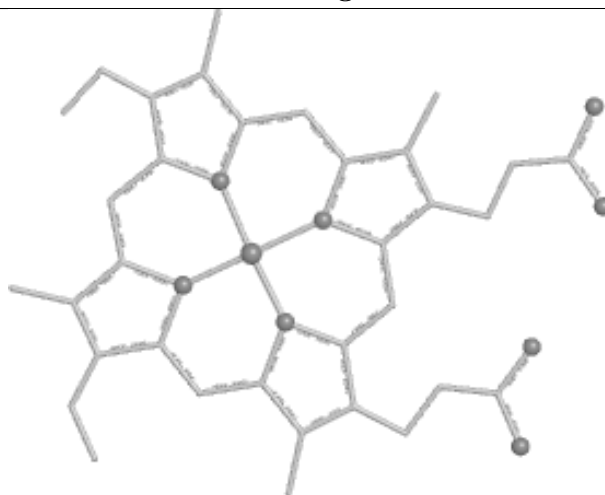
Bond lengths



Bond angles

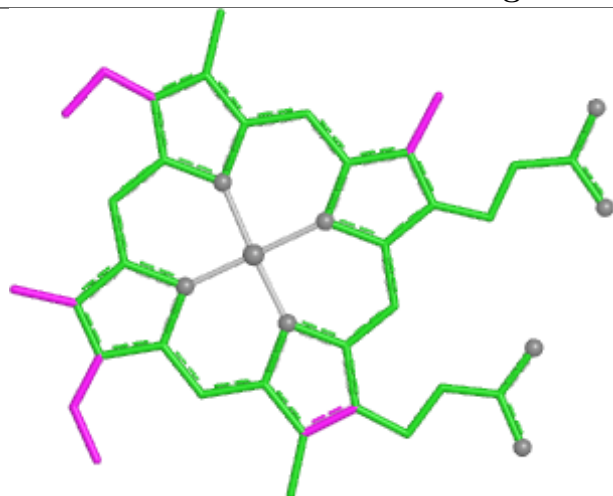


Torsions

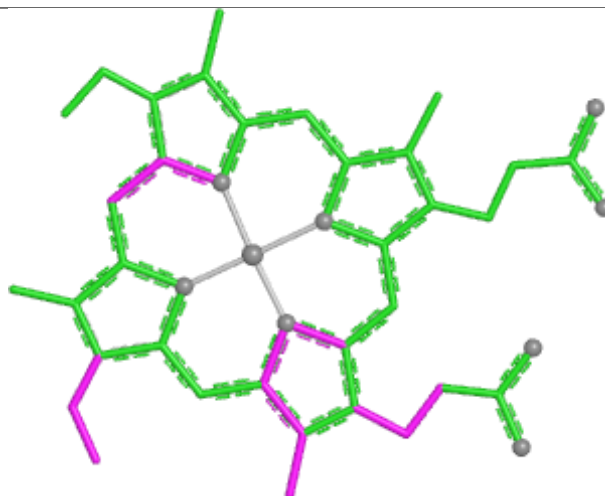


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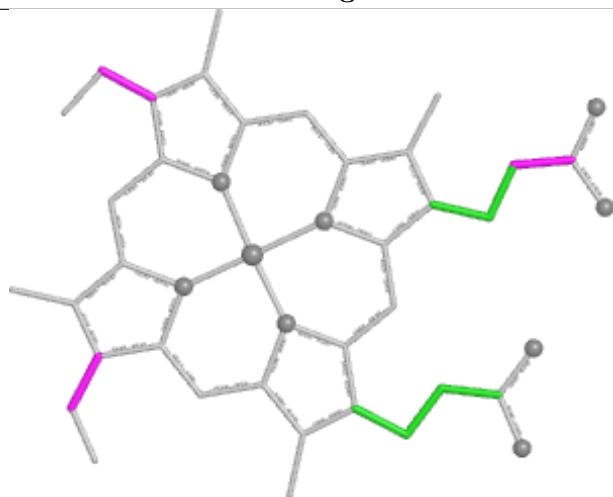
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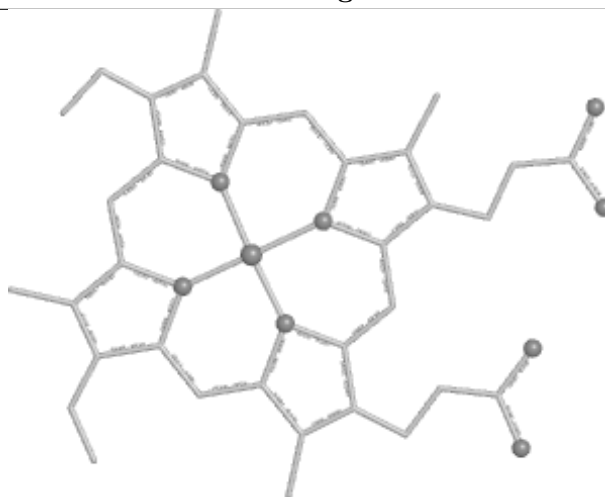
Bond lengths



Bond angles

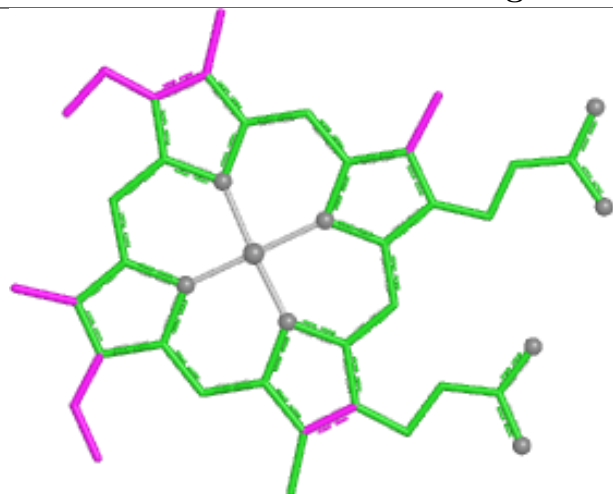


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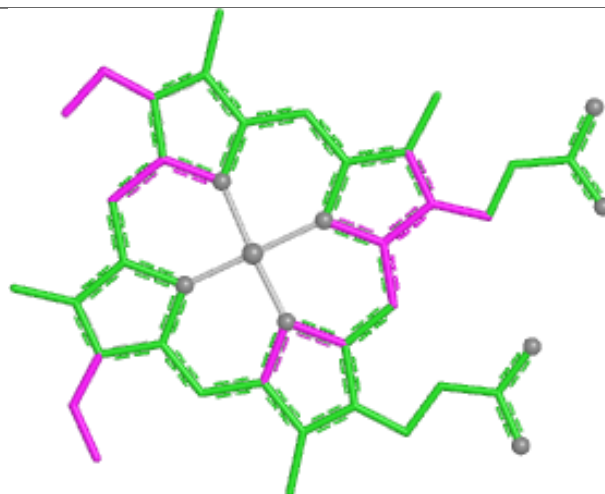


Rings

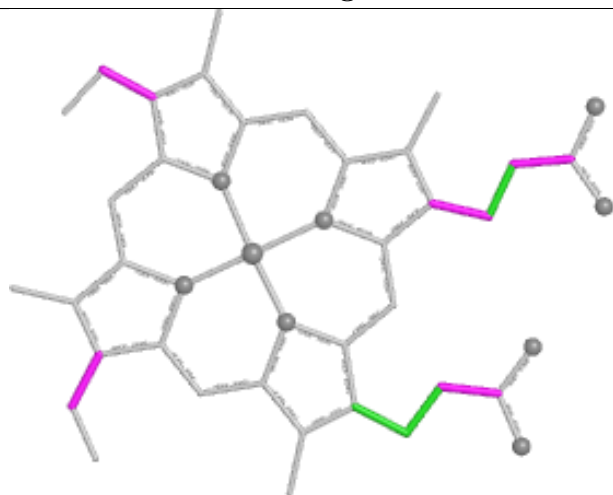
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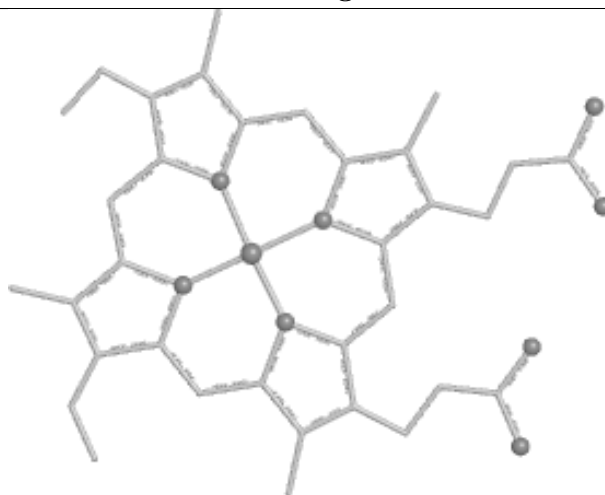
Bond lengths



Bond angles

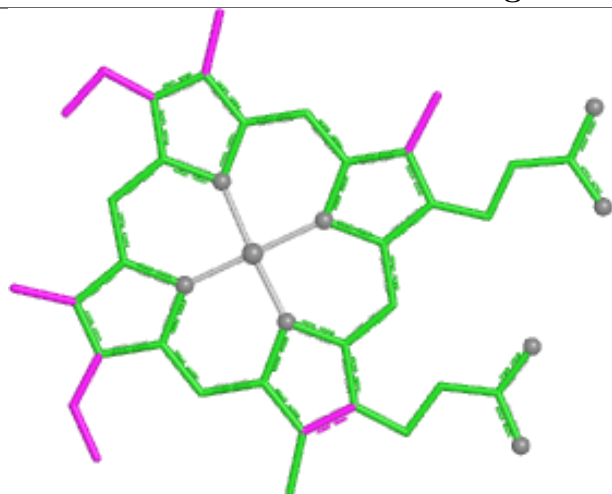


Torsions

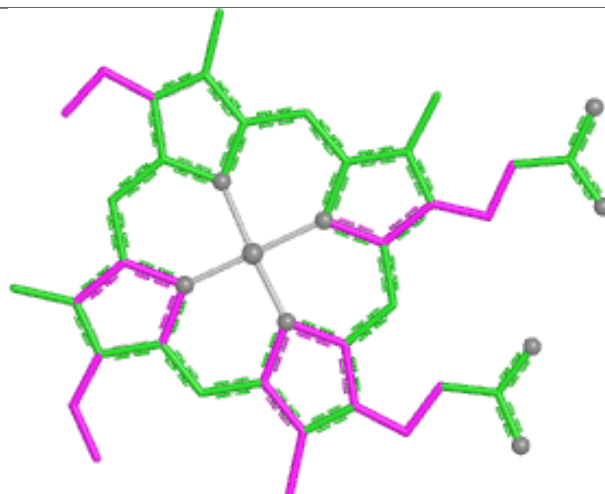


Rings

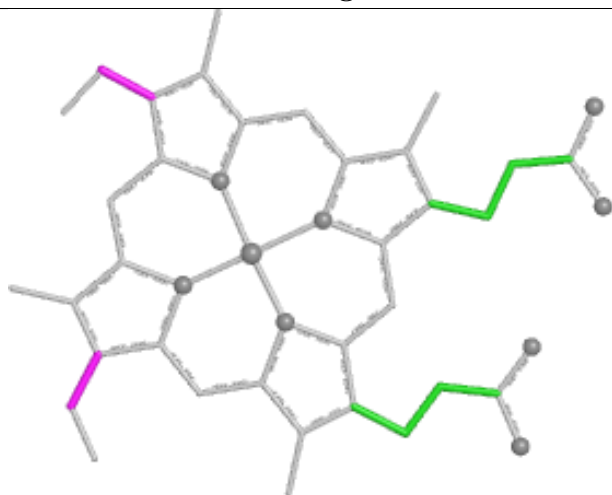
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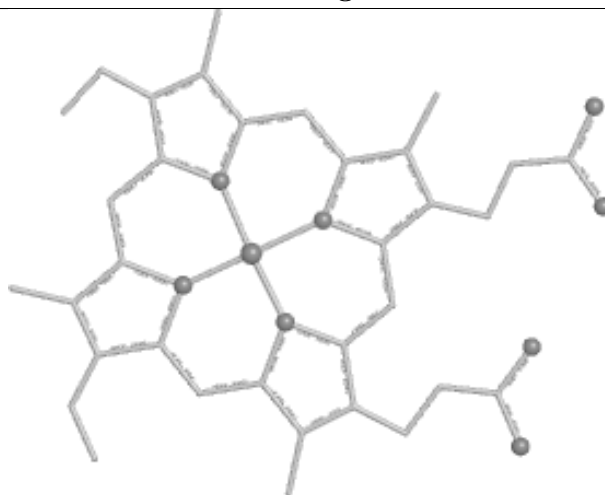
Bond lengths



Bond angles

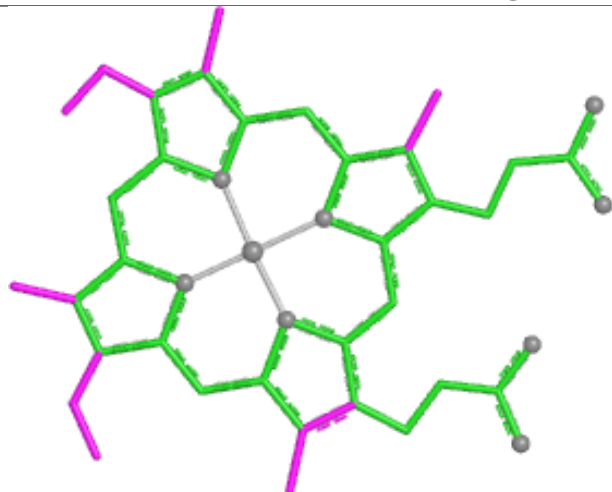


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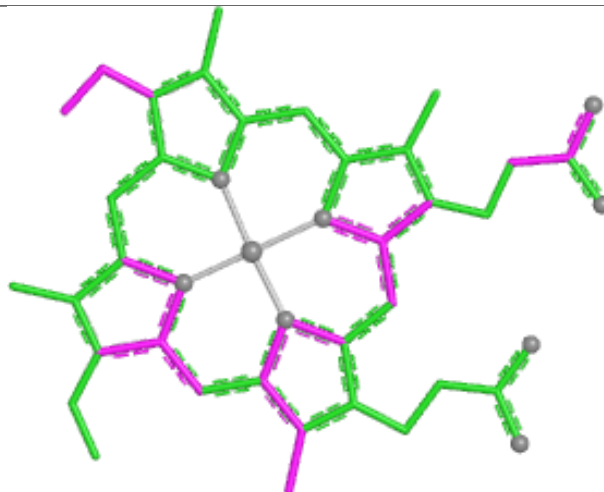


Rings

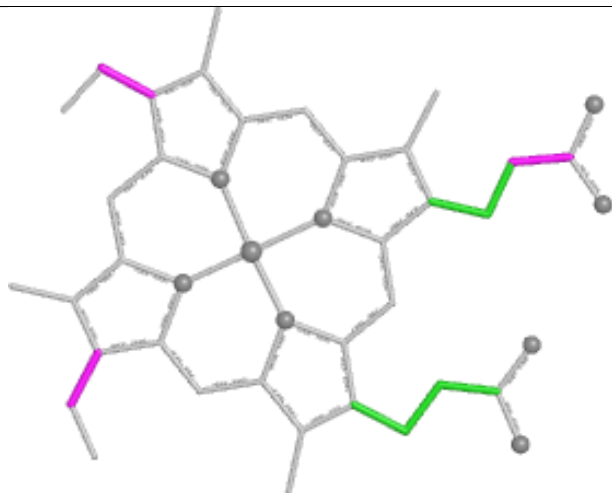
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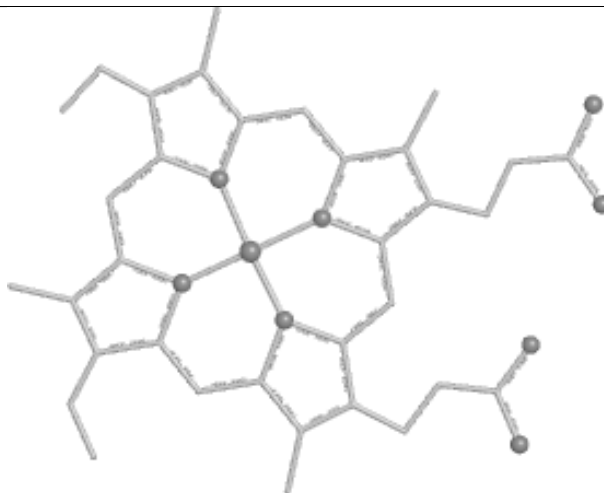
Bond lengths



Bond angles

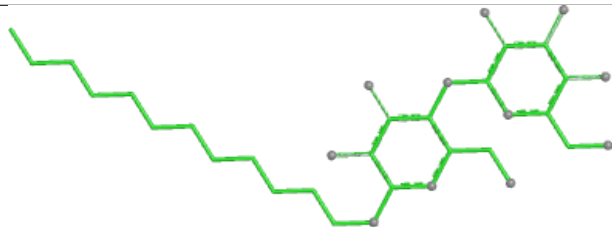


Torsions

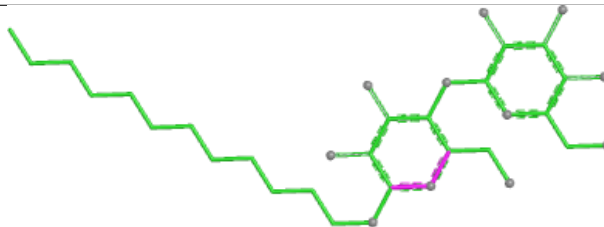


Rings

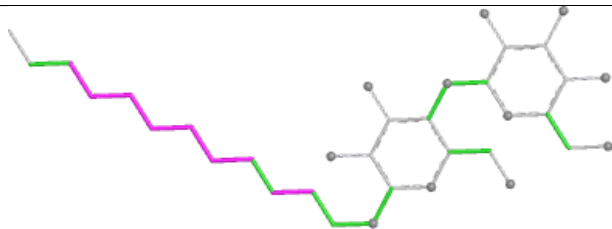
Ligand LMT C 1005



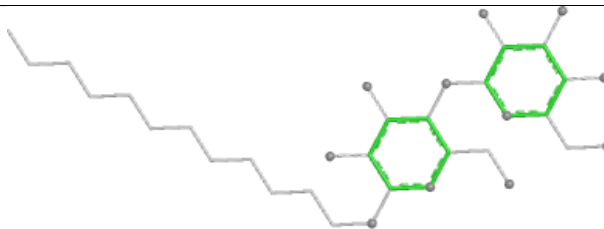
Bond lengths



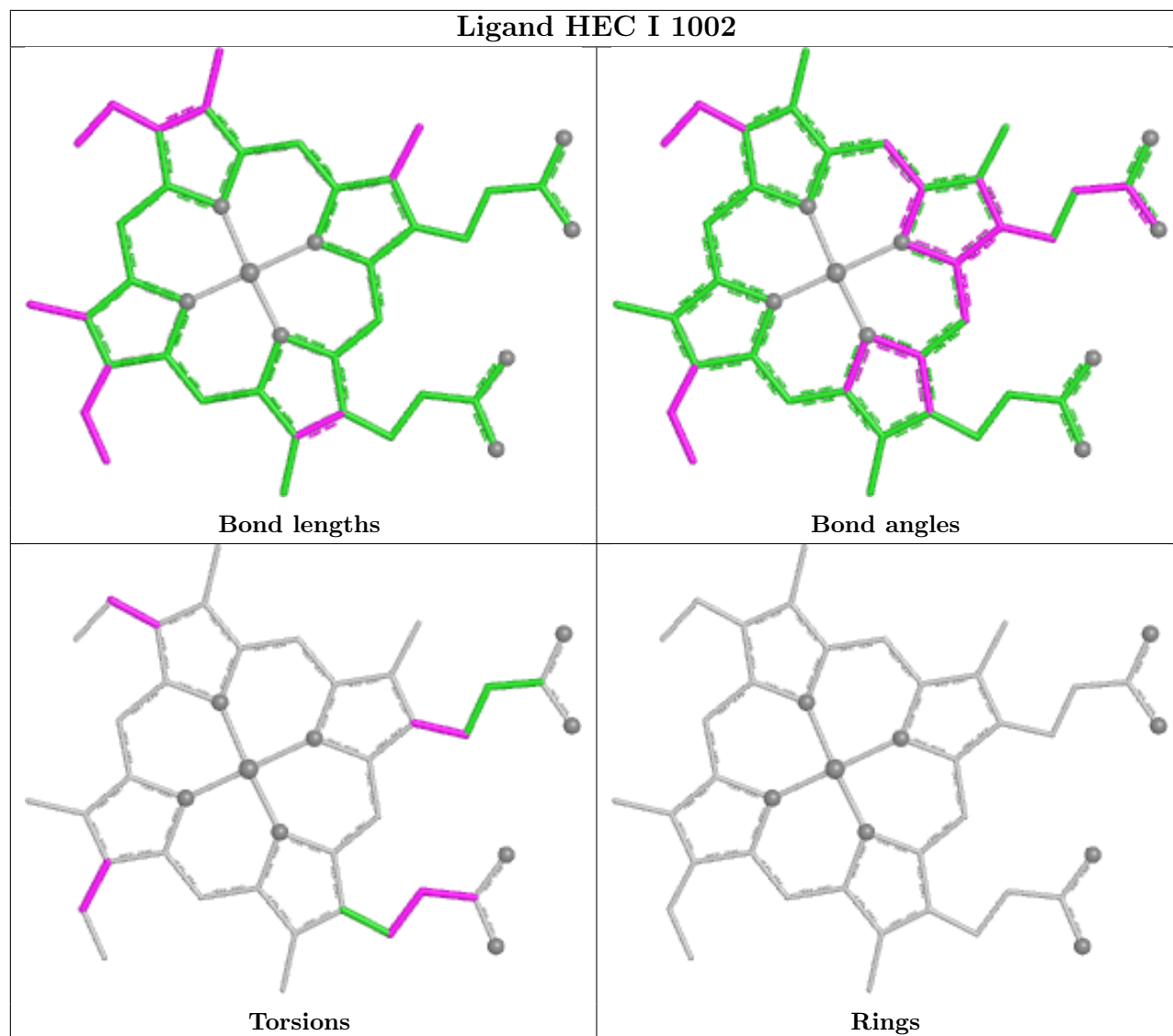
Bond angles



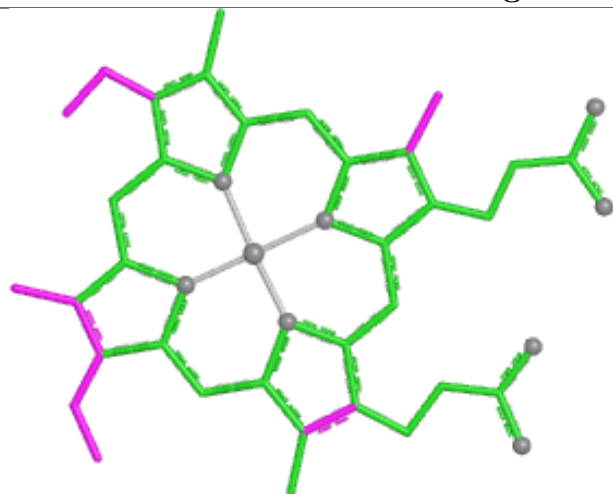
Torsions



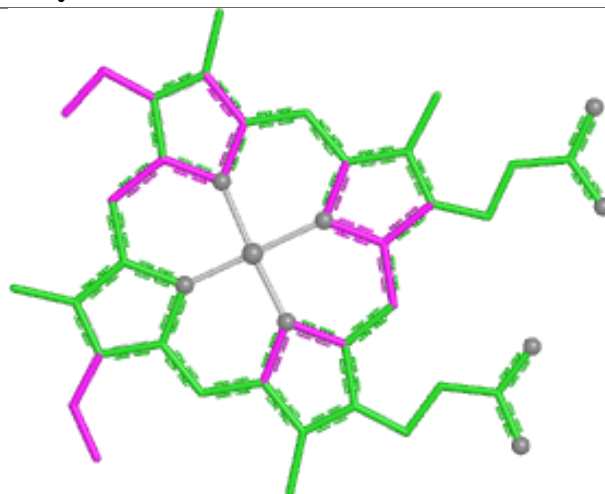
Rings



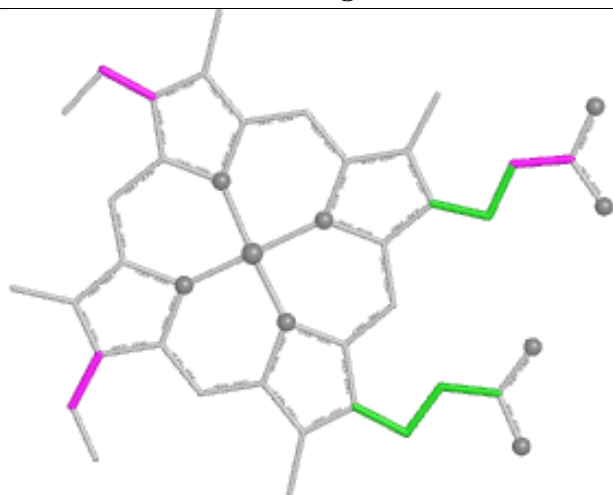
Ligand HEC Q 1001



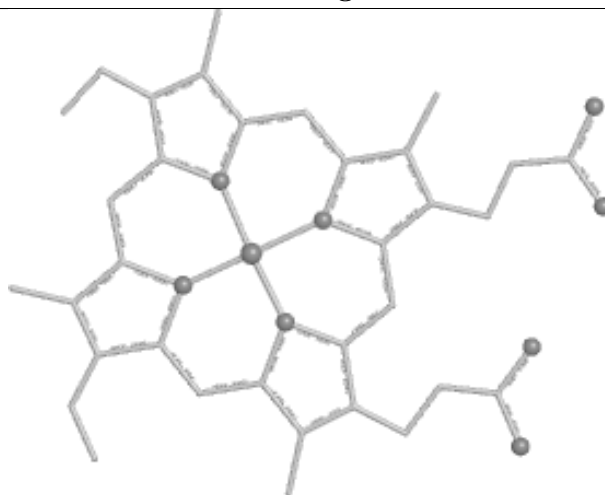
Bond lengths



Bond angles

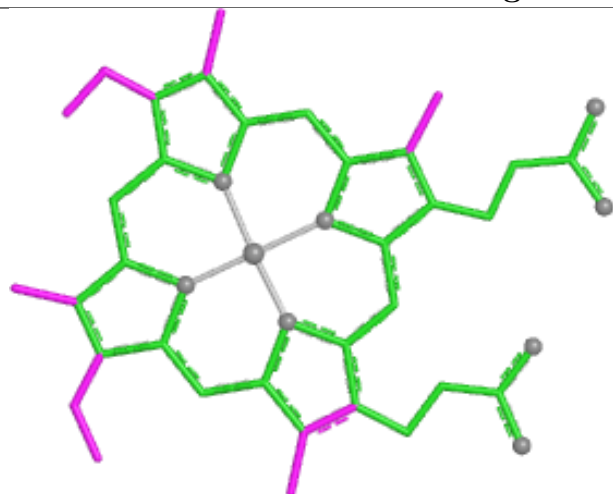


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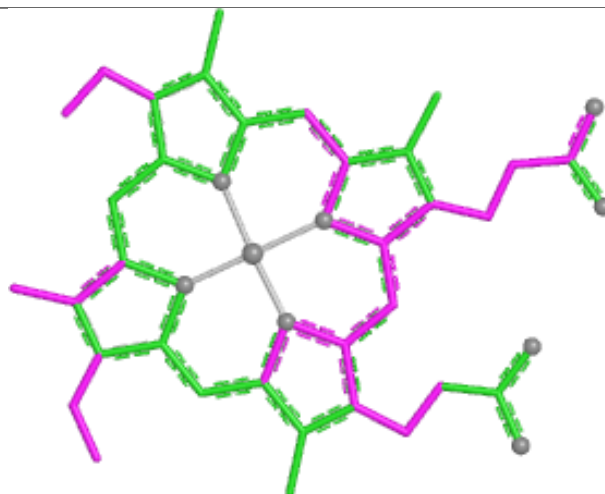


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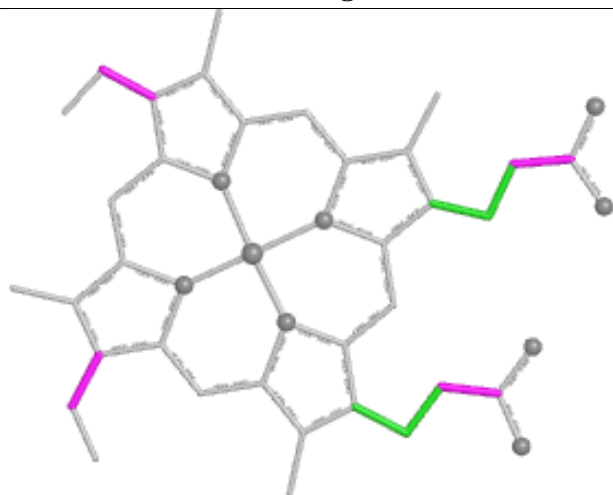
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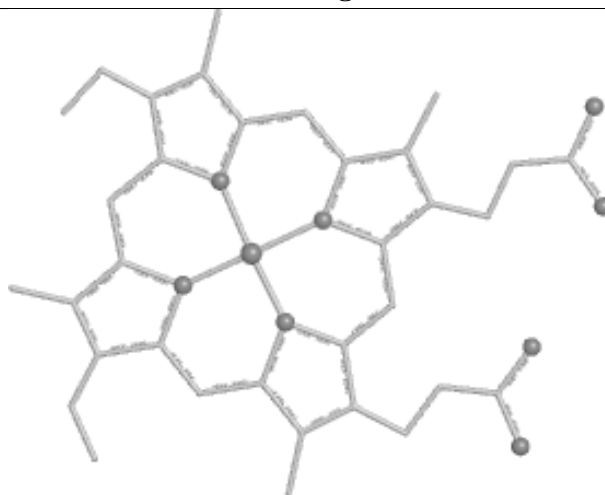
Bond lengths



Bond angles

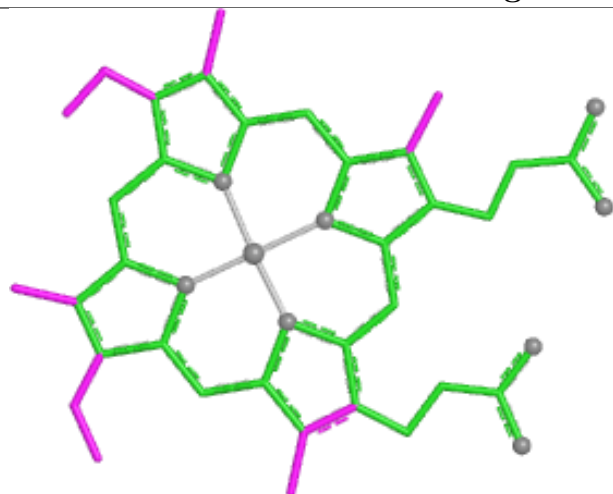


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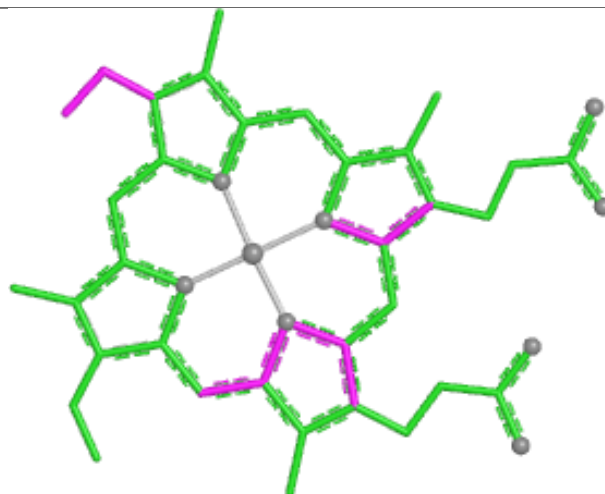


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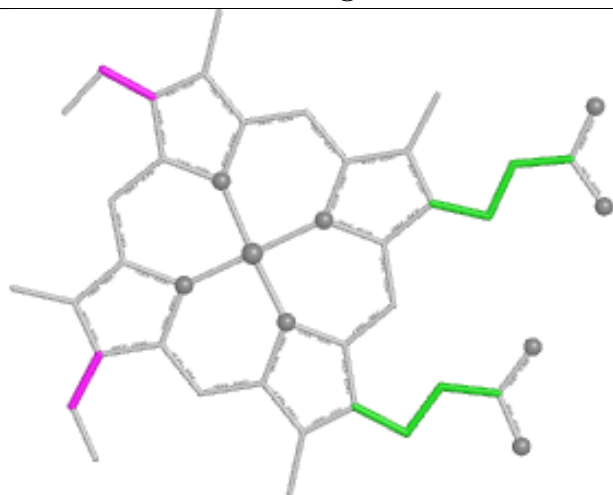
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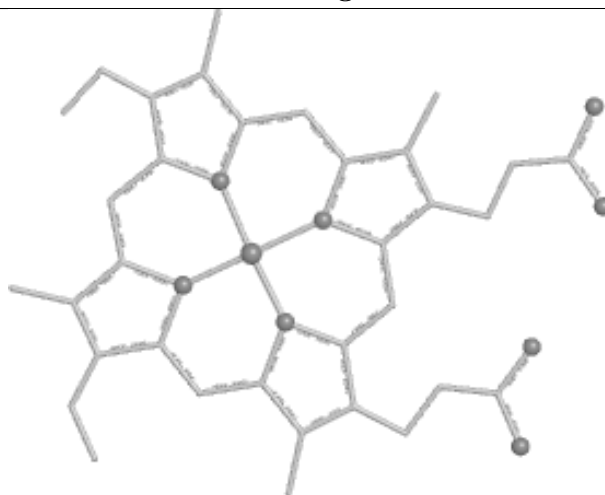
Bond lengths



Bond angles

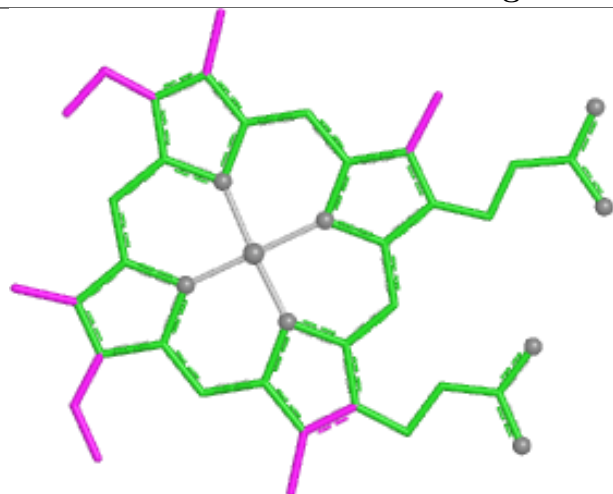


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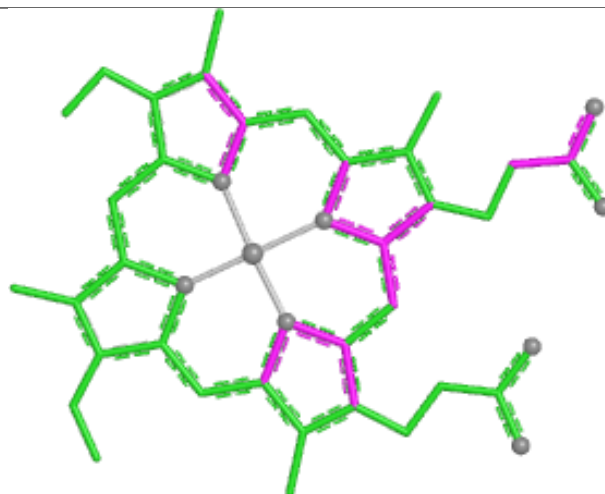


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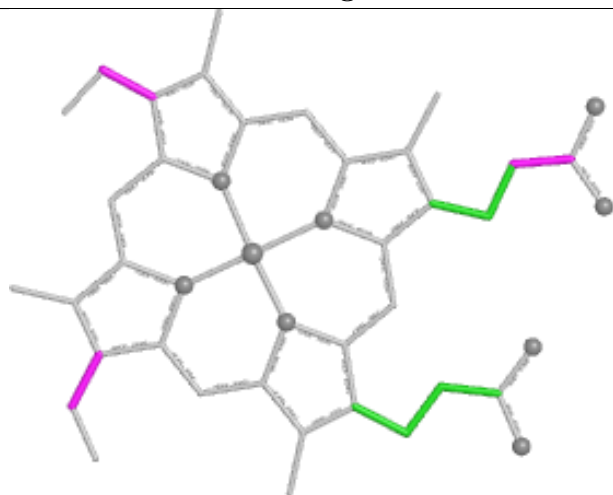
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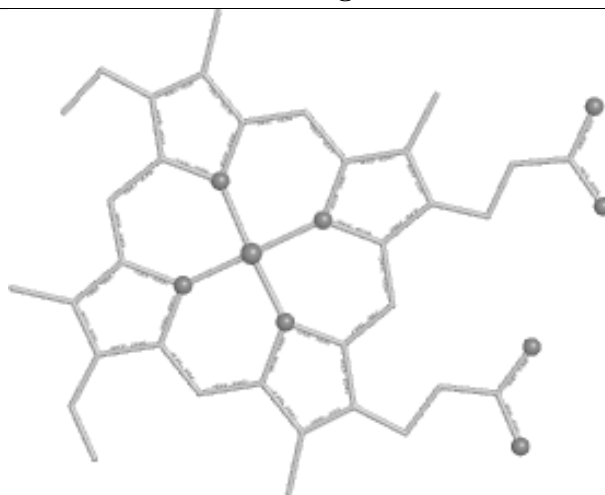
Bond lengths



Bond angles

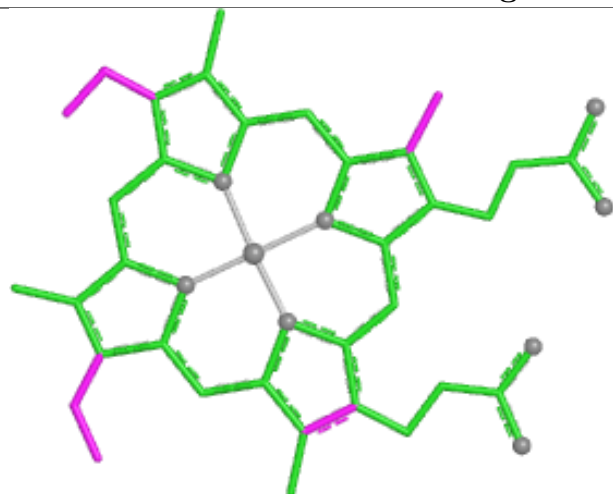


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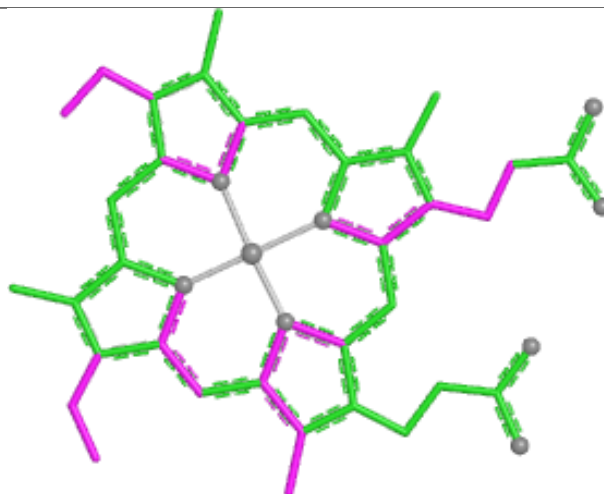


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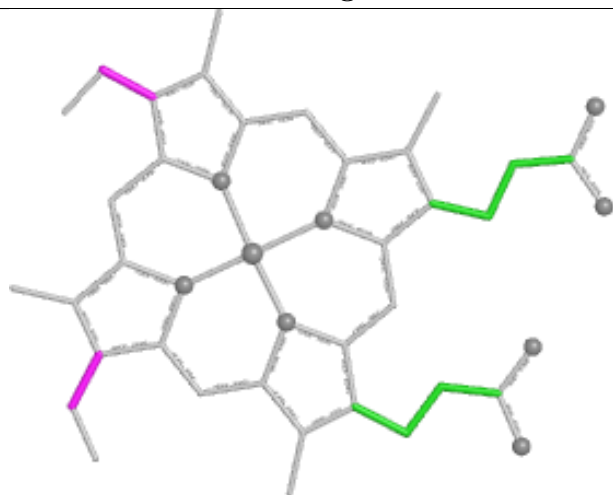
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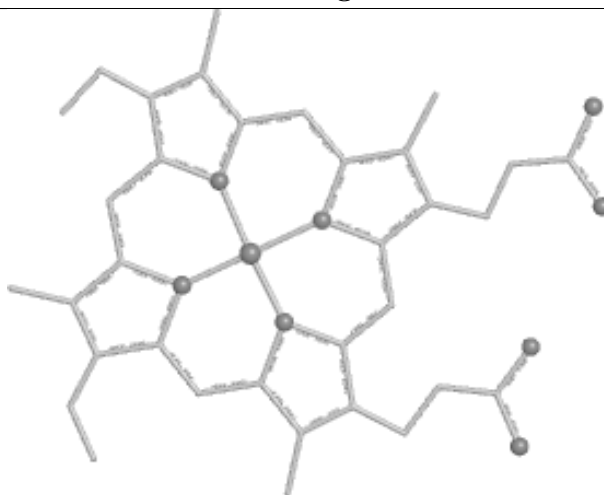
Bond lengths



Bond angles

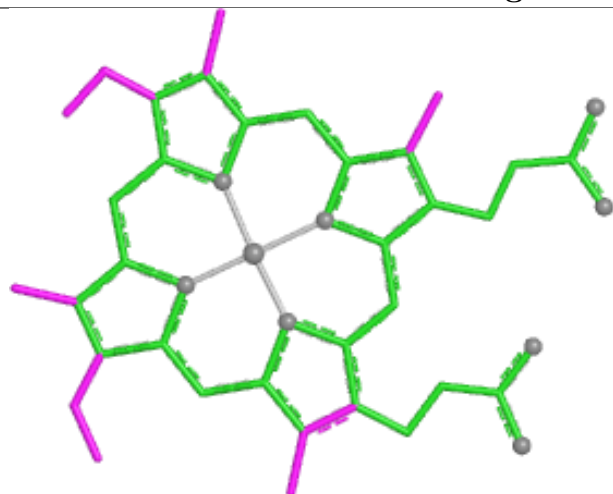


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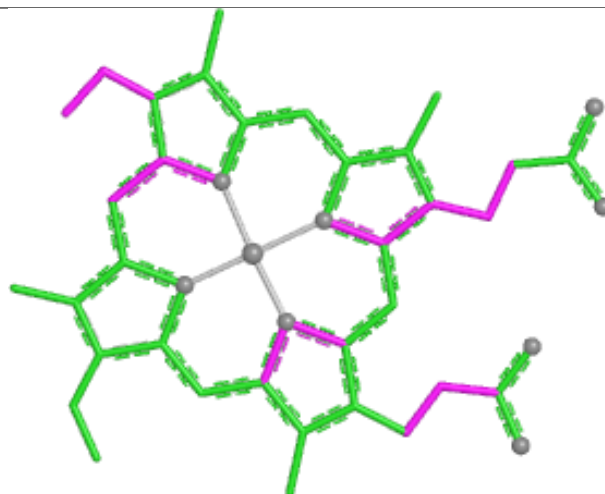


Rings

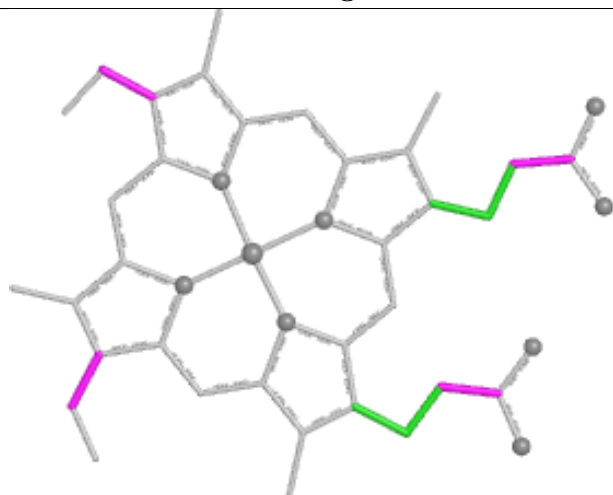
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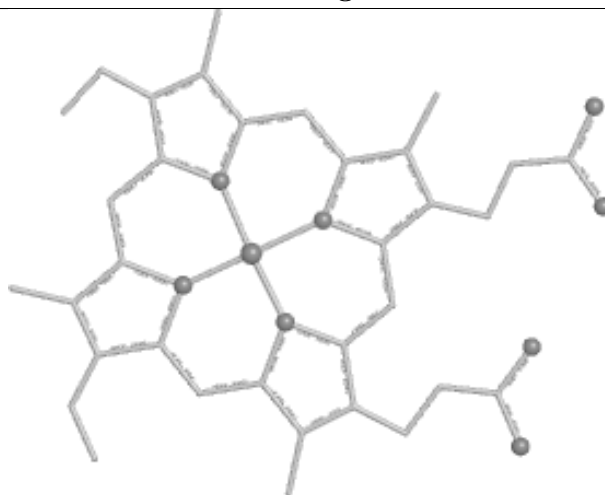
Bond lengths



Bond angles

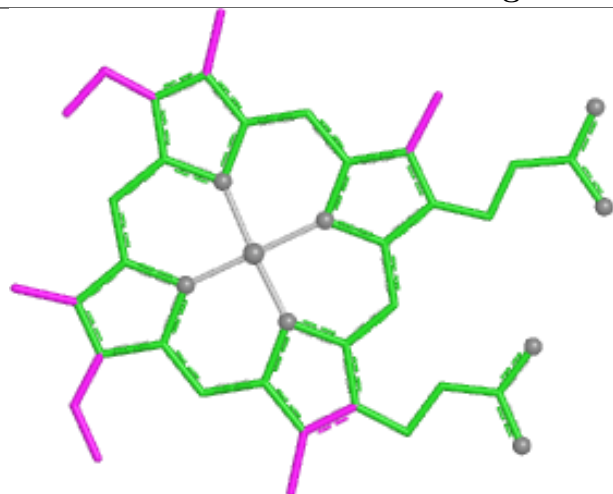


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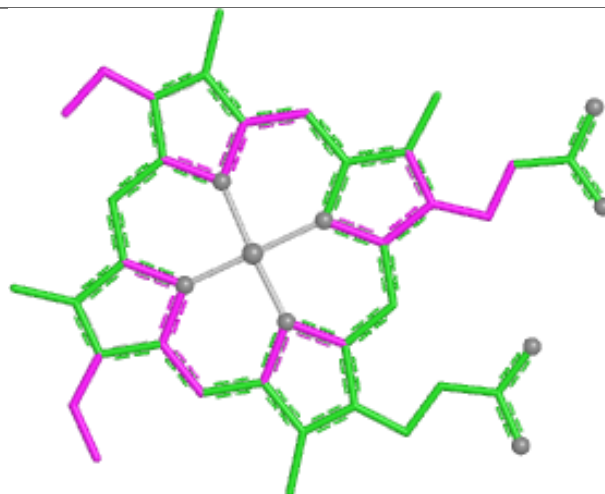


Rings

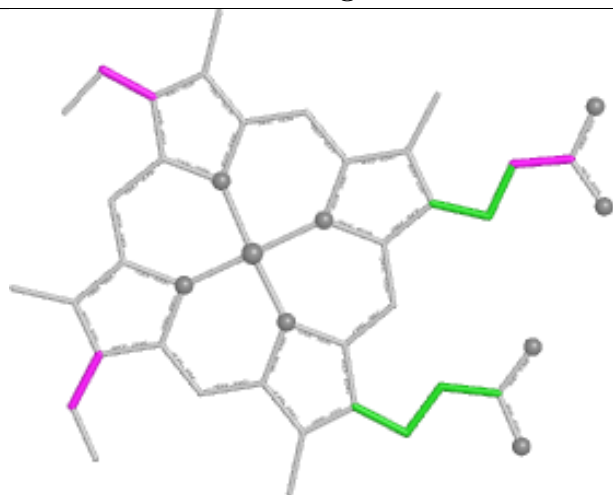
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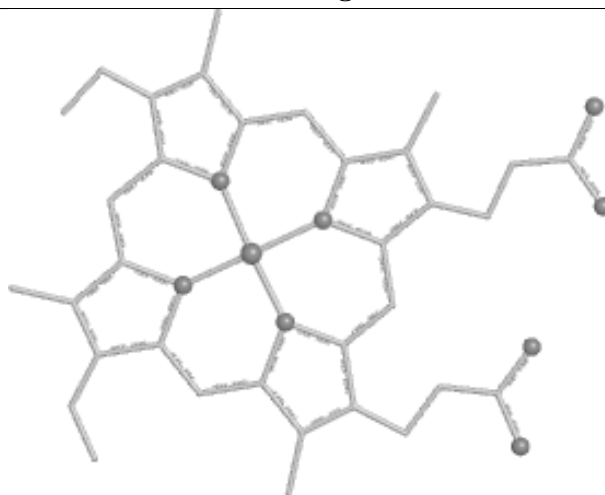
Bond lengths



Bond angles

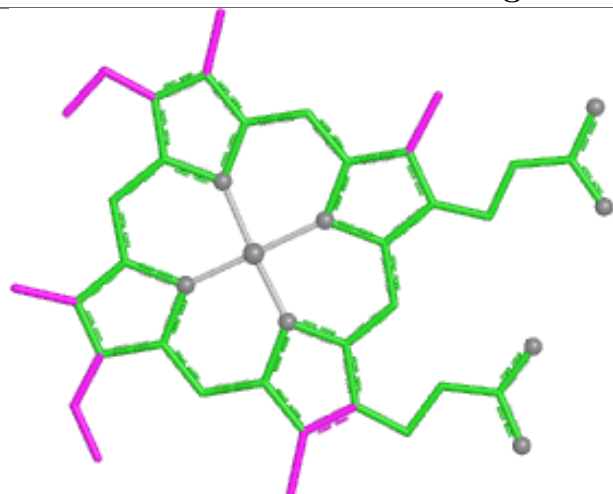


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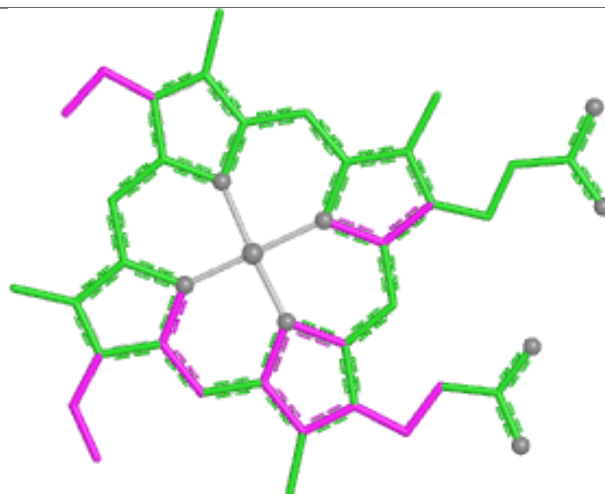


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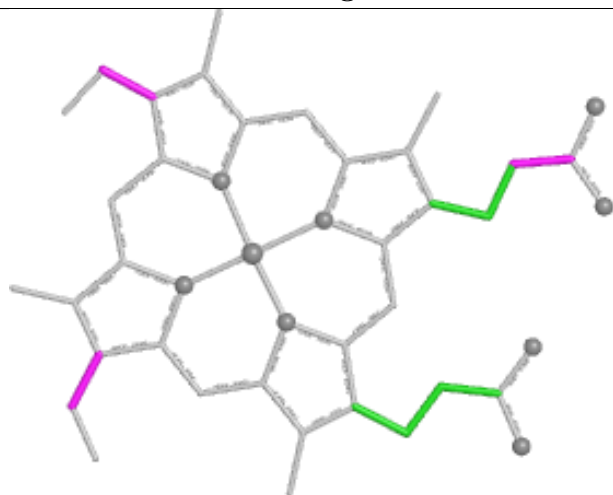
Ligand HEC A 1002



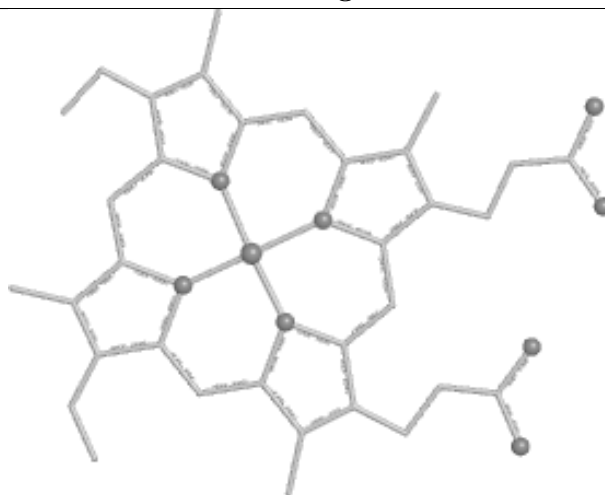
Bond lengths



Bond angles

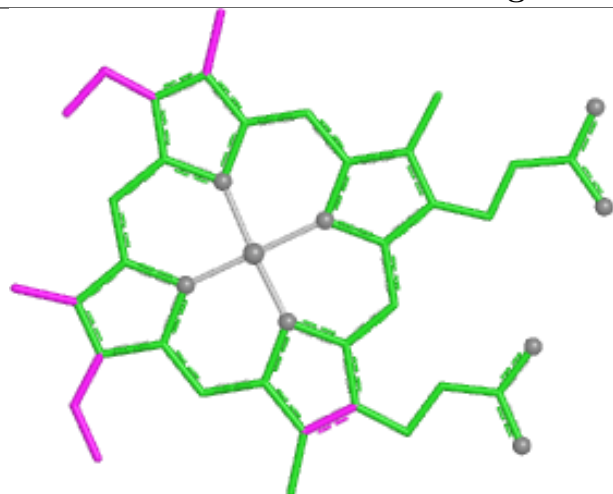


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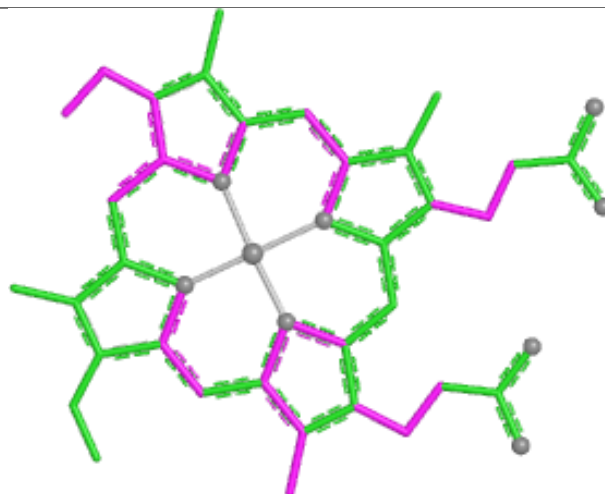


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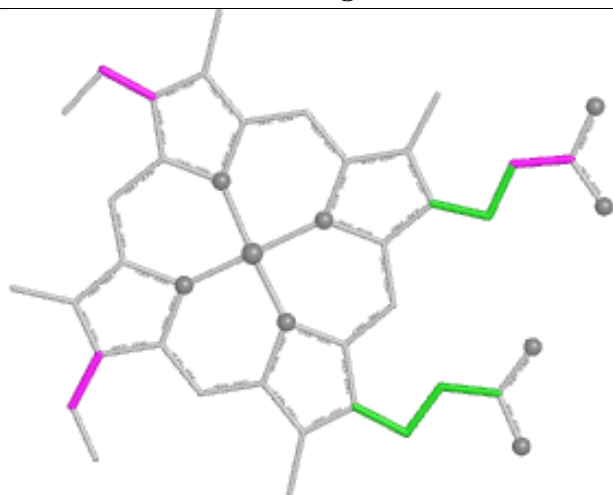
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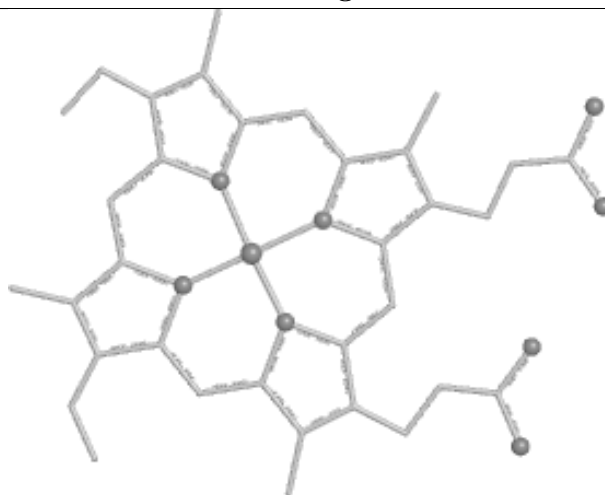
Bond lengths



Bond angles

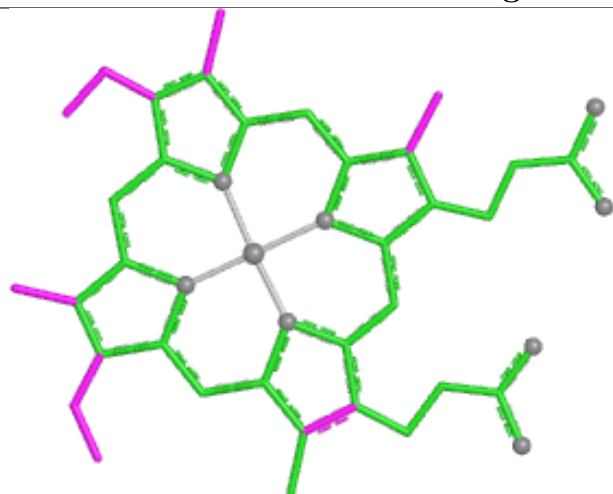


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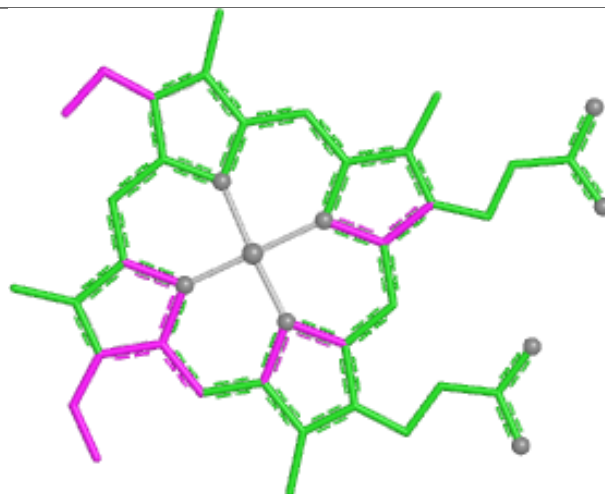


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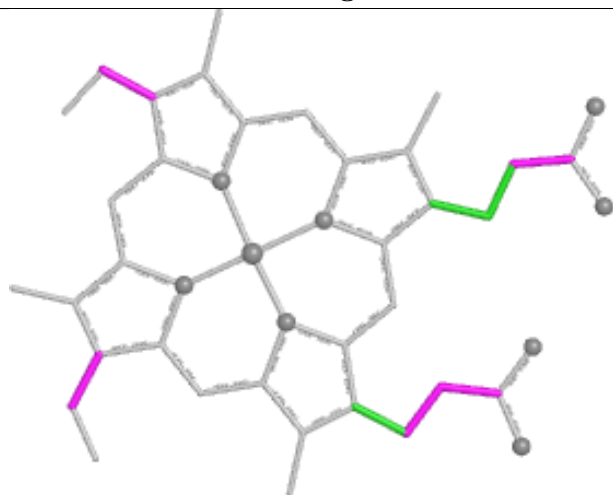
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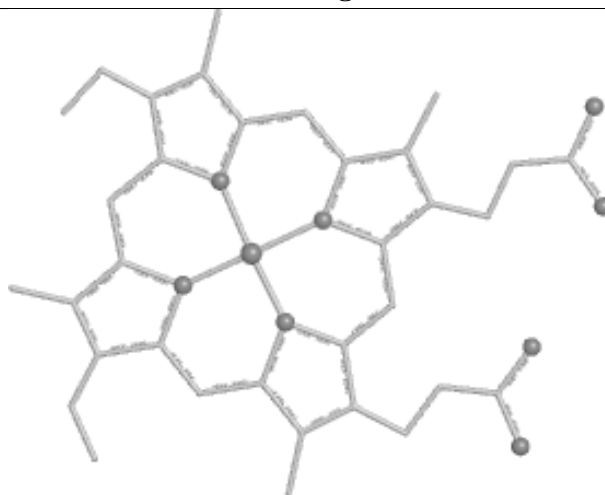
Bond lengths



Bond angles

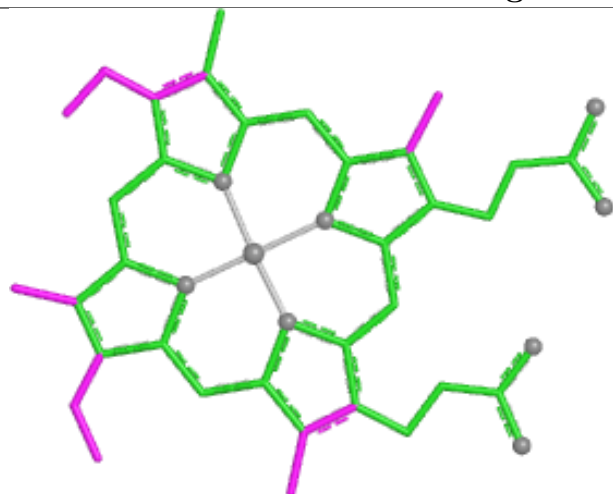


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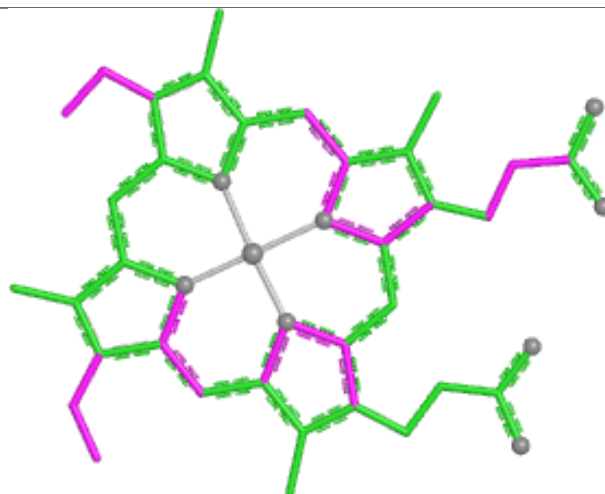


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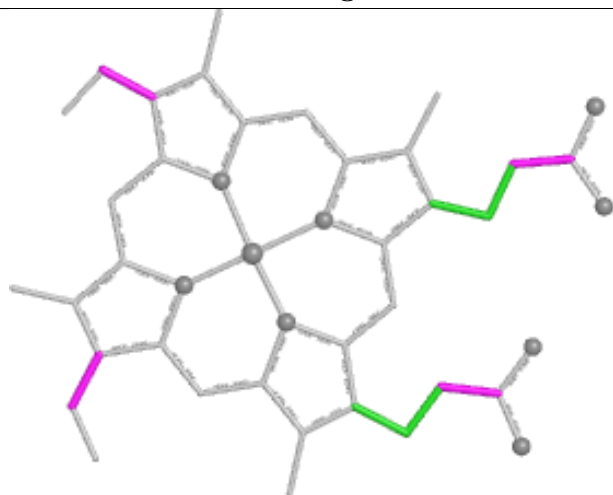
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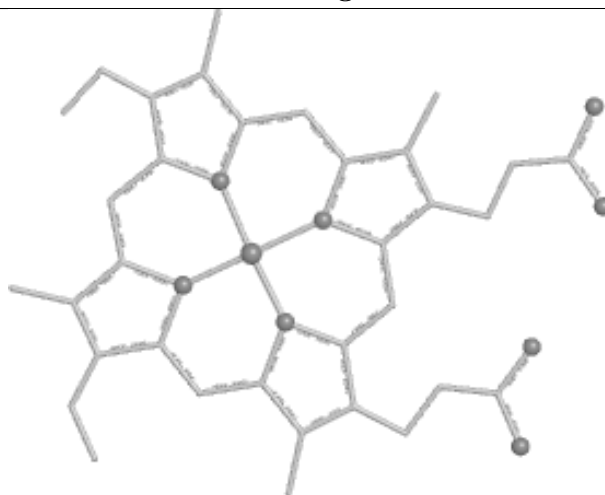
Bond lengths



Bond angles

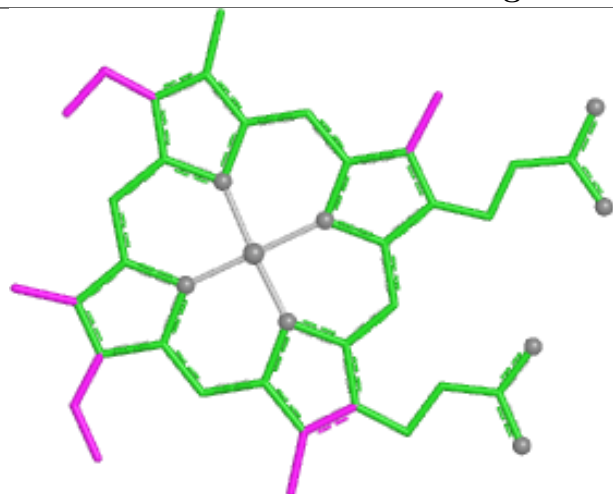


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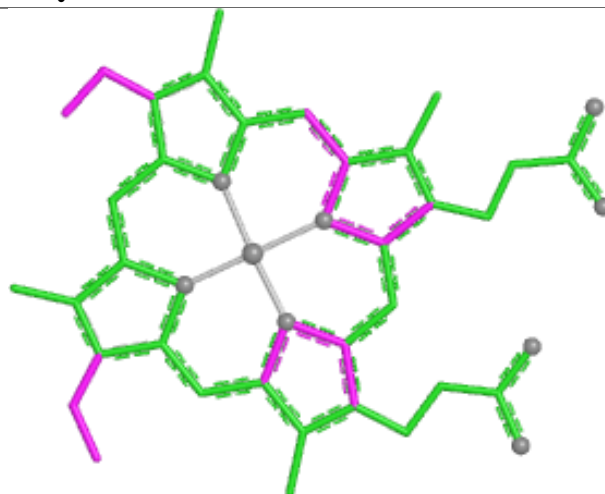


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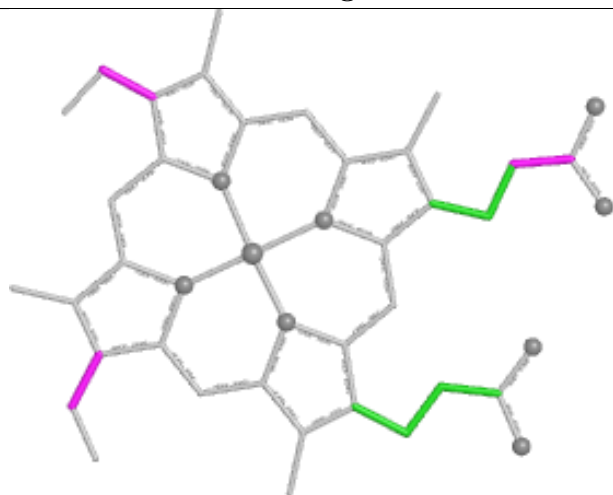
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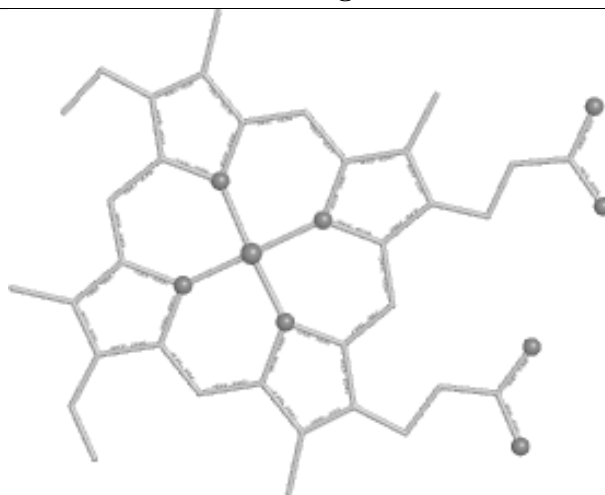
Bond lengths



Bond angles

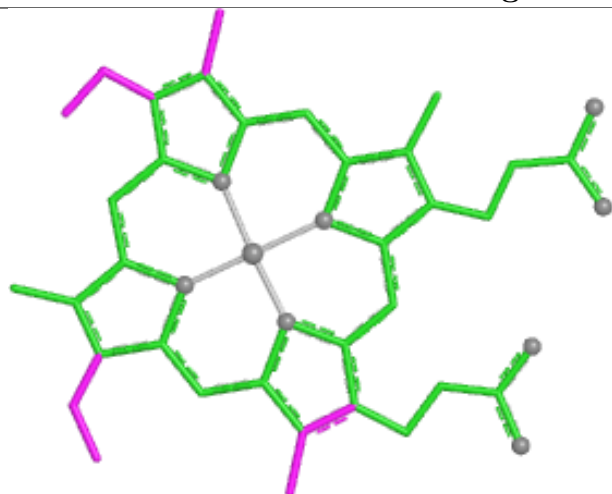


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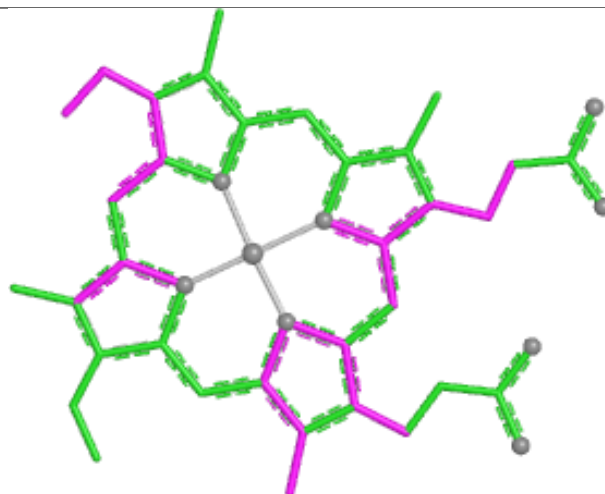


Rings

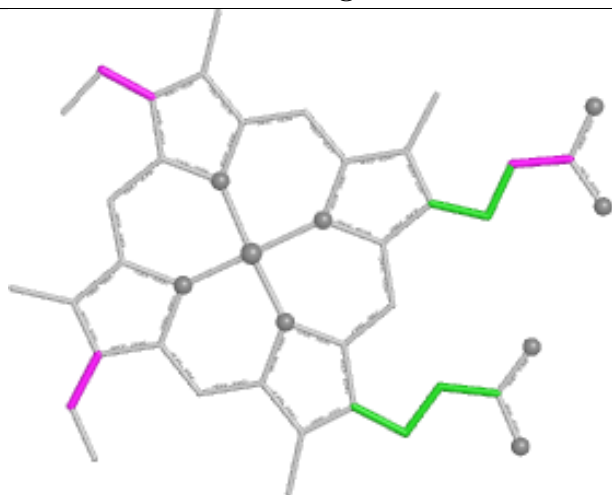
Ligand HEC N 1004



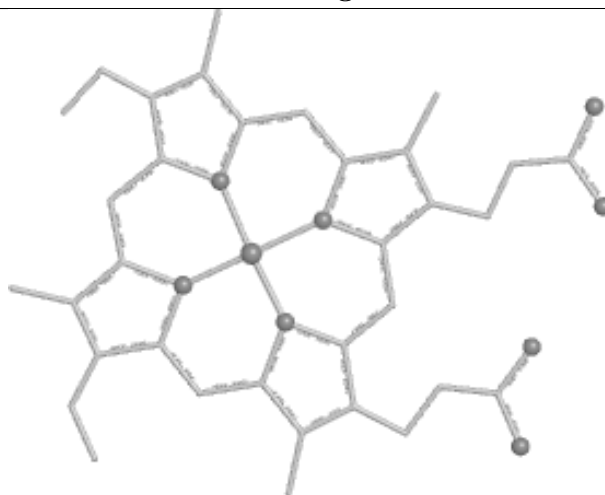
Bond lengths



Bond angles

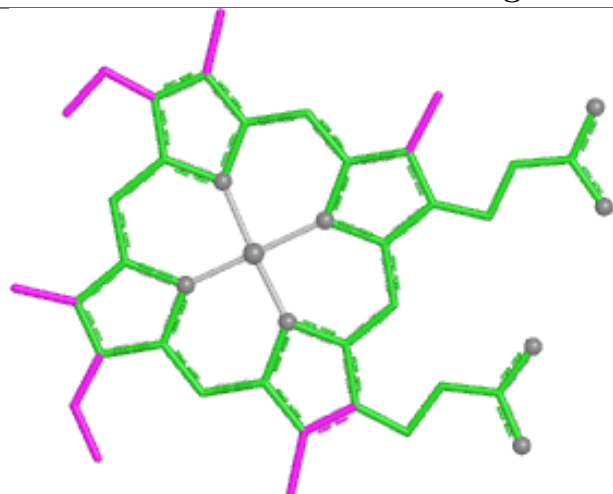


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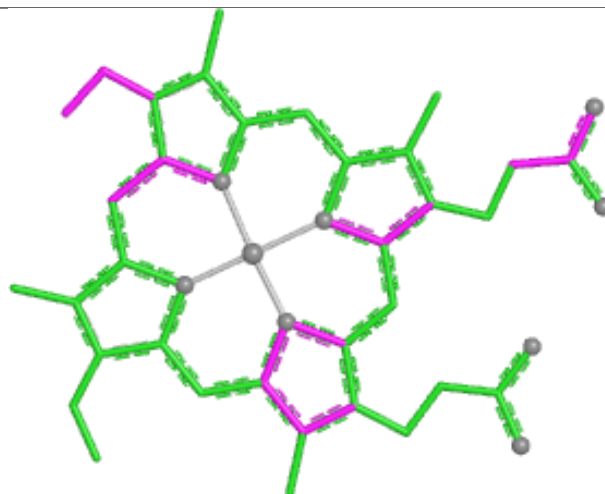


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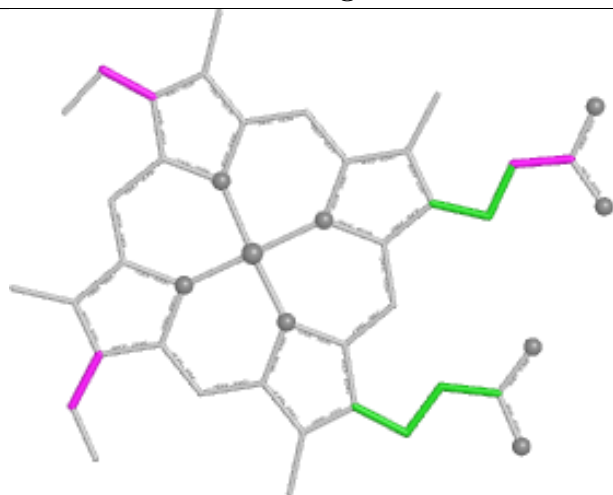
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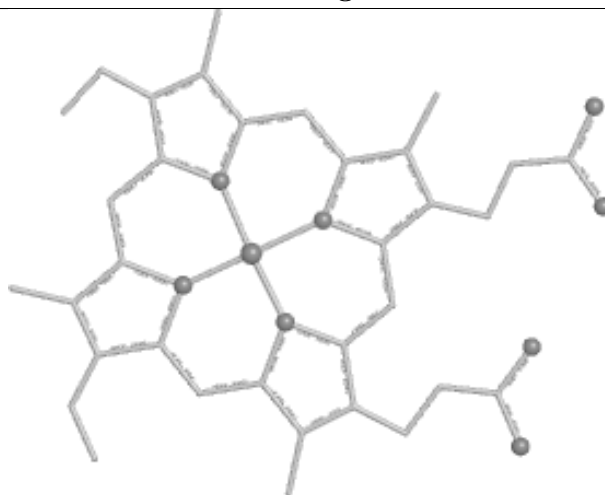
Bond lengths



Bond angles

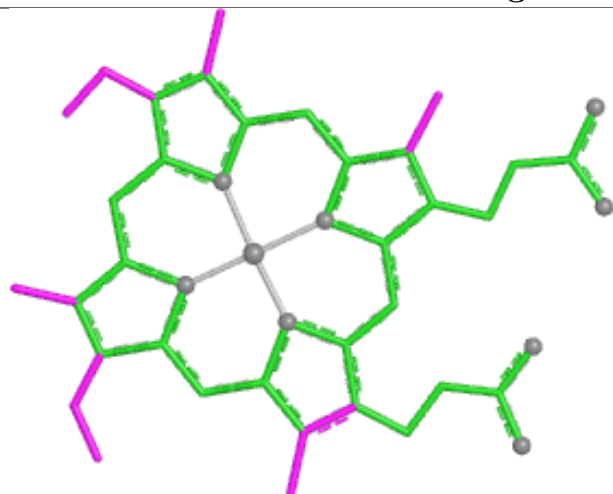


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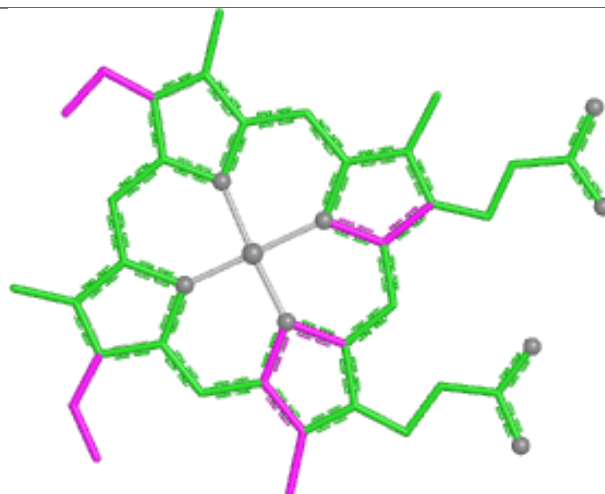


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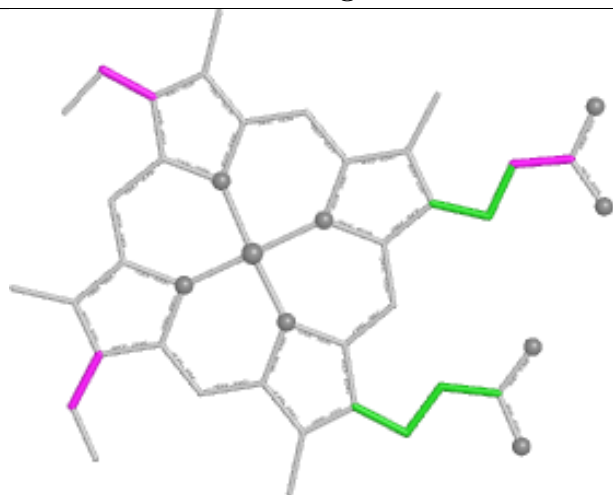
Ligand HEC J 1002



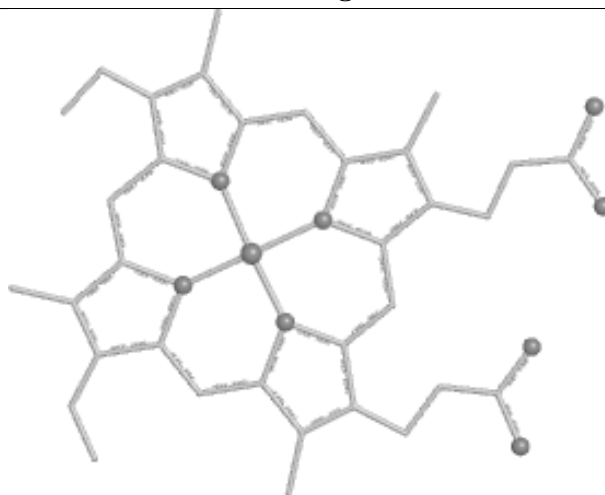
Bond lengths



Bond angles

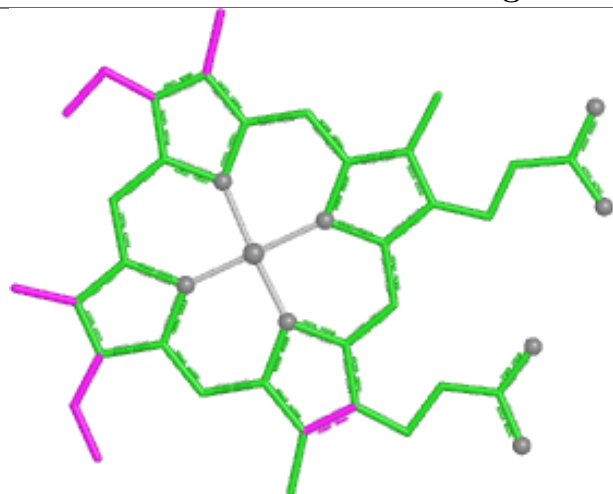


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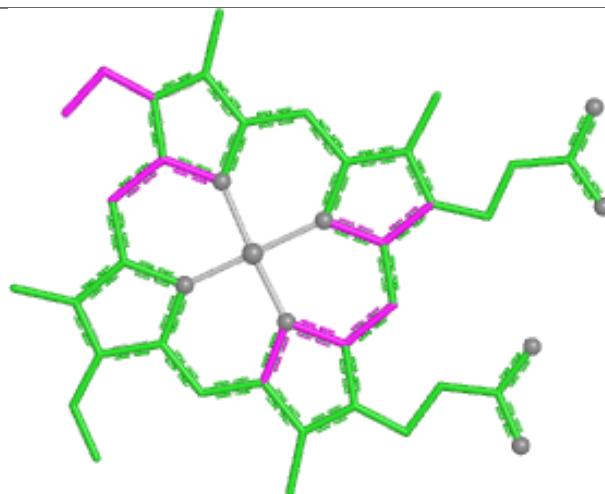


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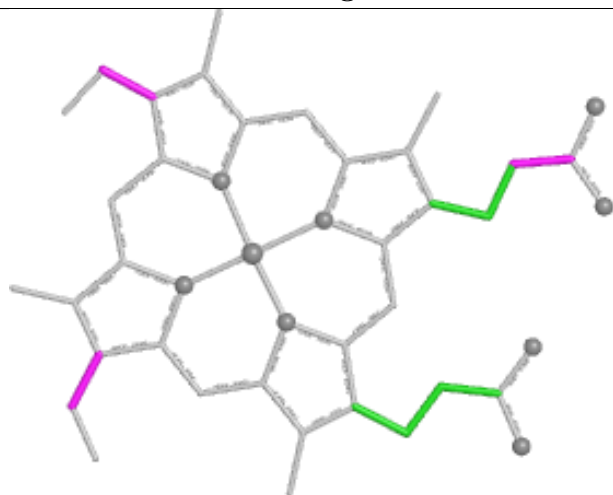
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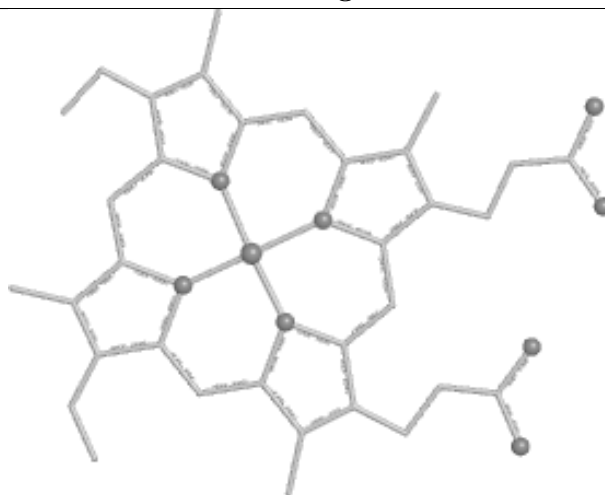
Bond lengths



Bond angles

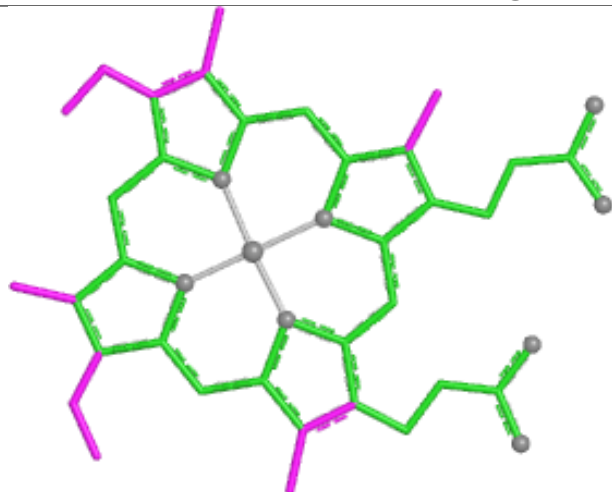


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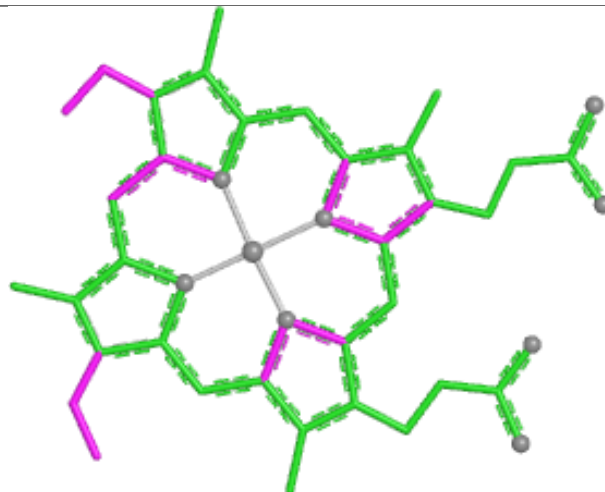


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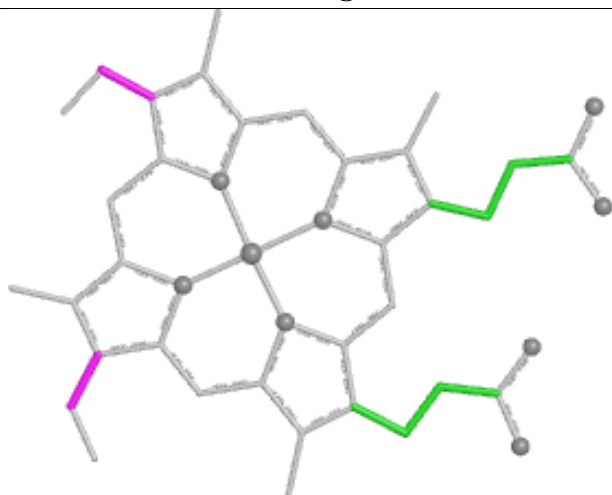
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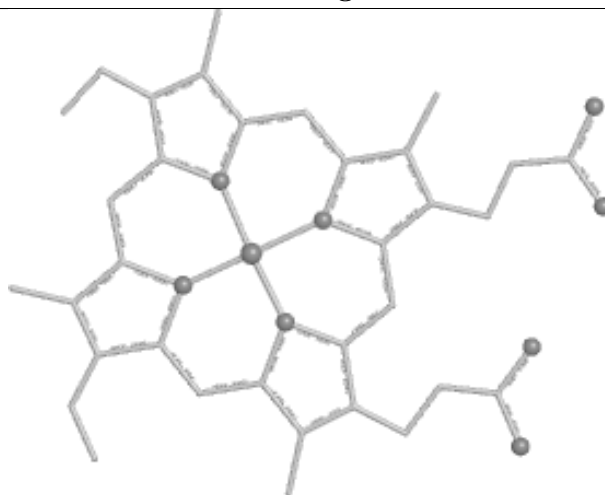
Bond lengths



Bond angles

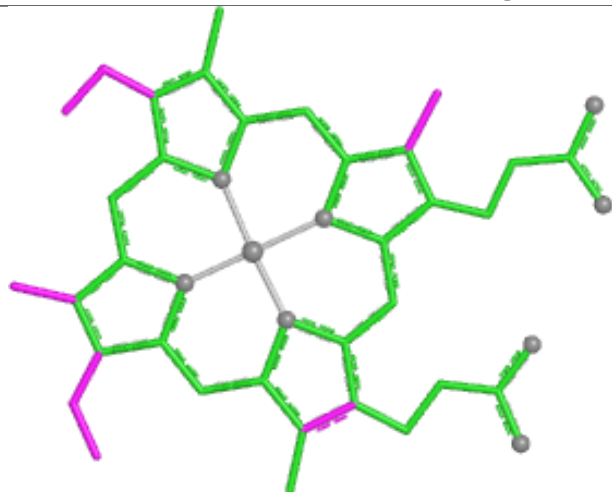


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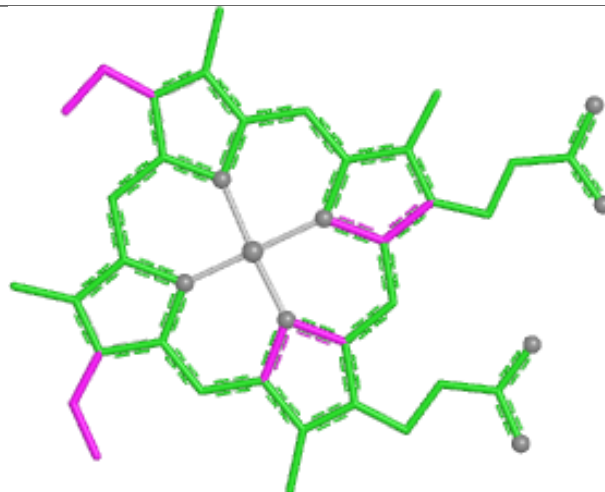


Rings

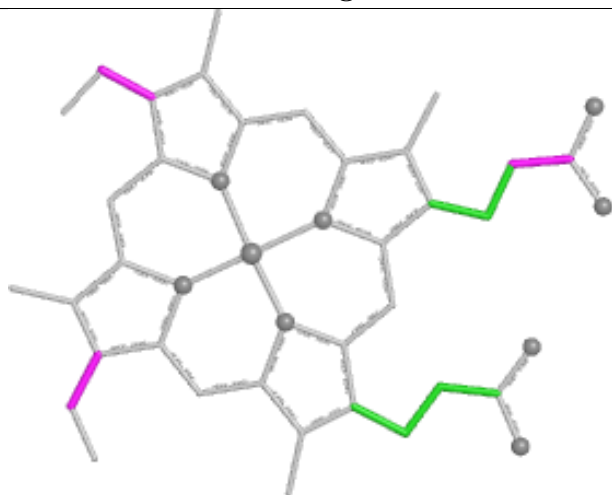
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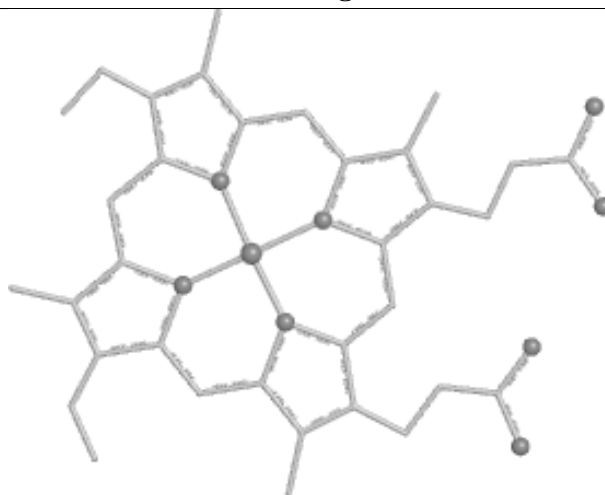
Bond lengths



Bond angles

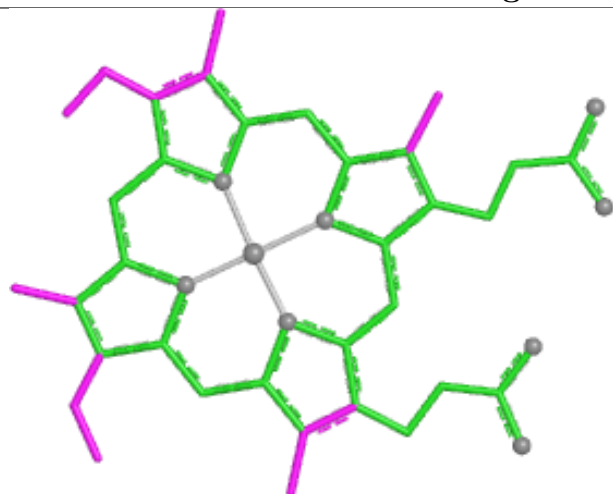


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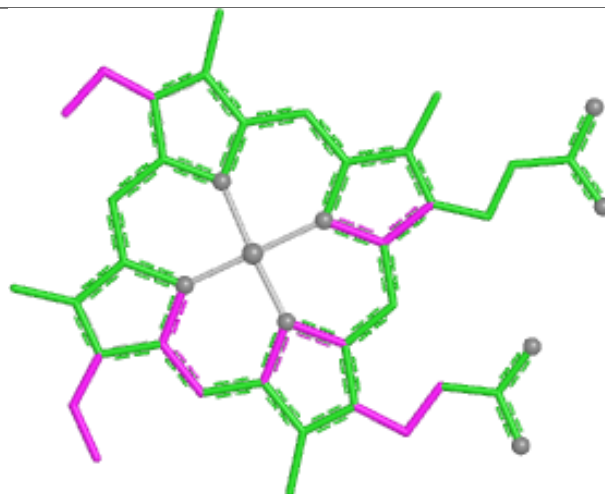


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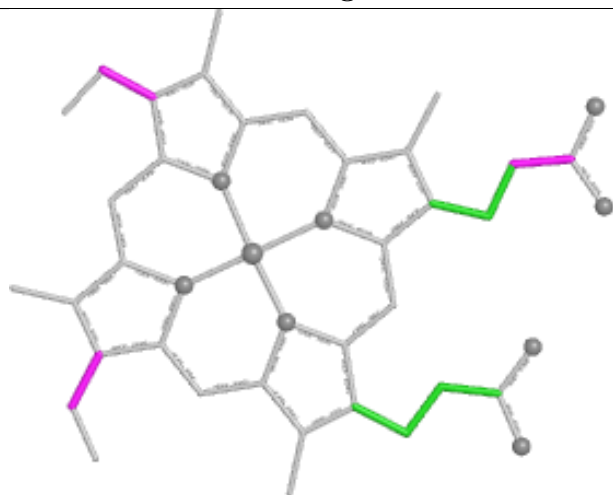
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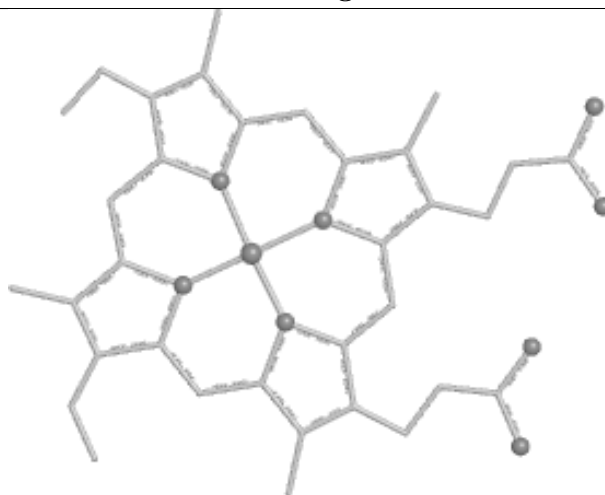
Bond lengths



Bond angles

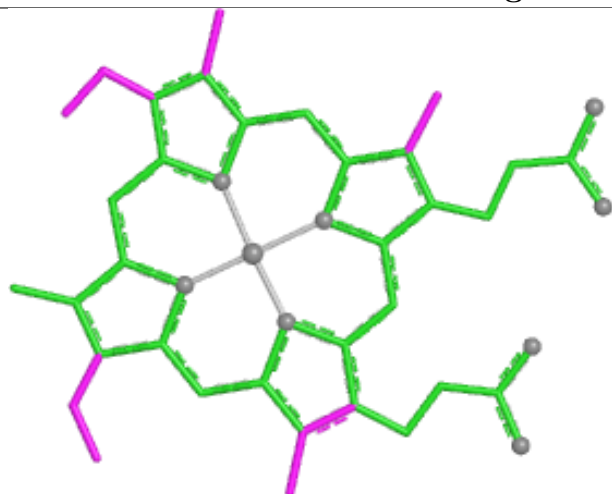


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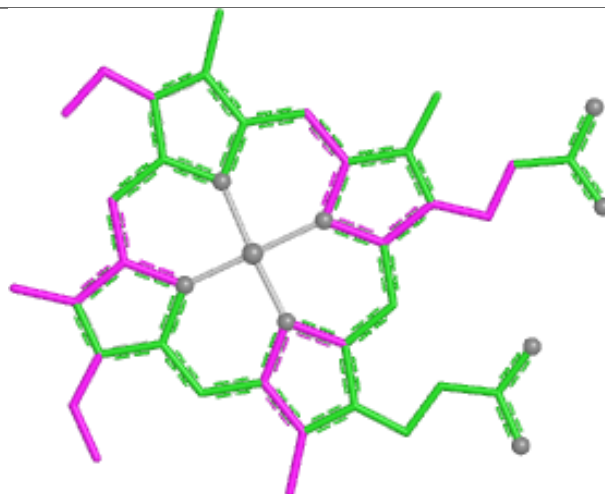


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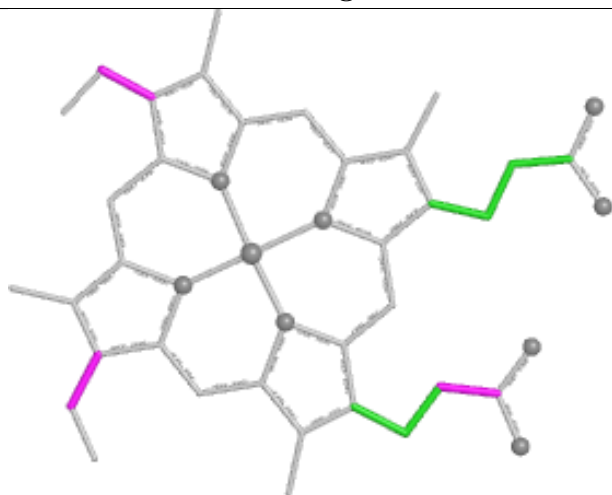
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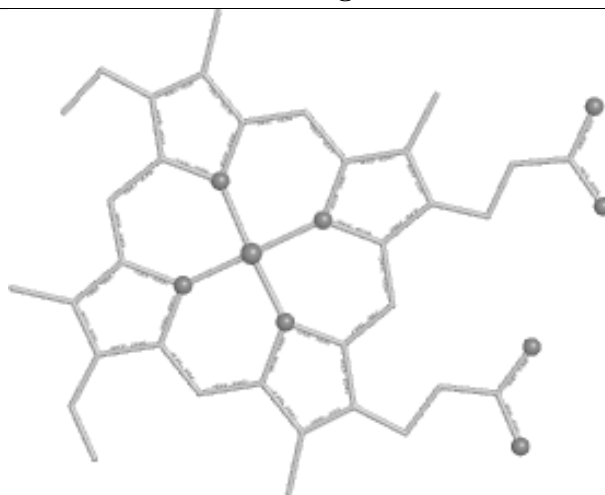
Bond lengths



Bond angles

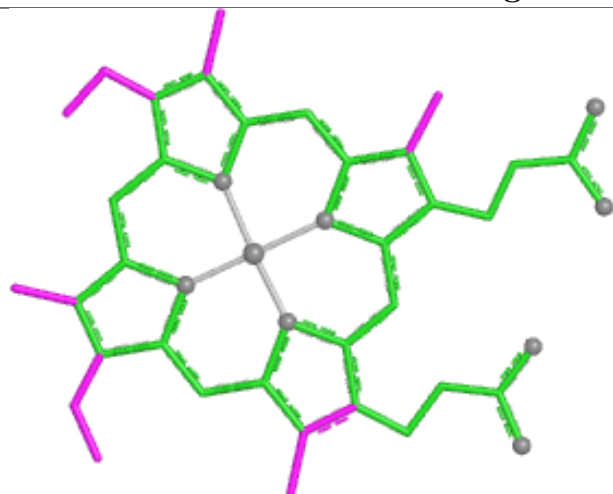


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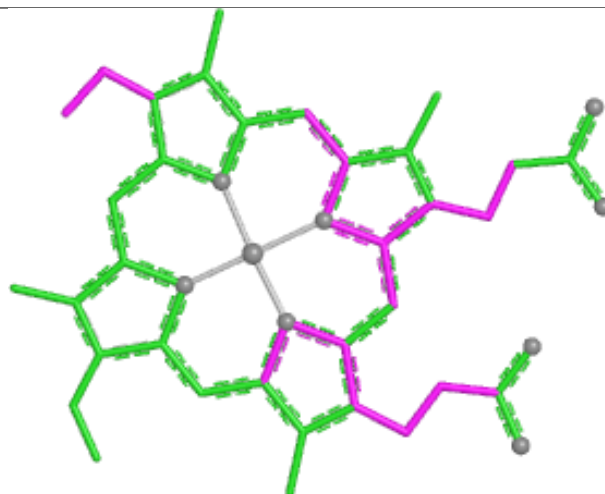


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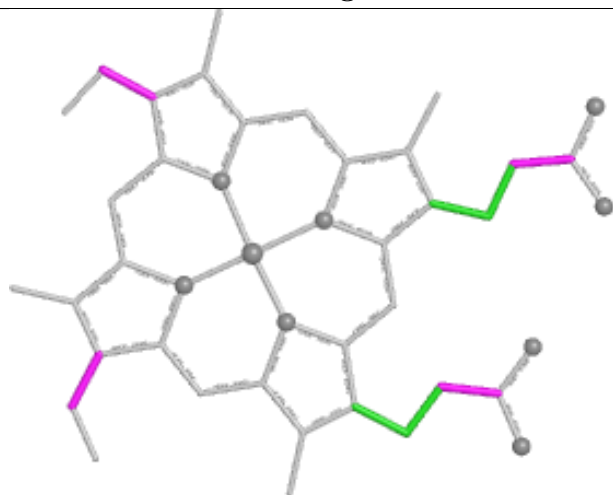
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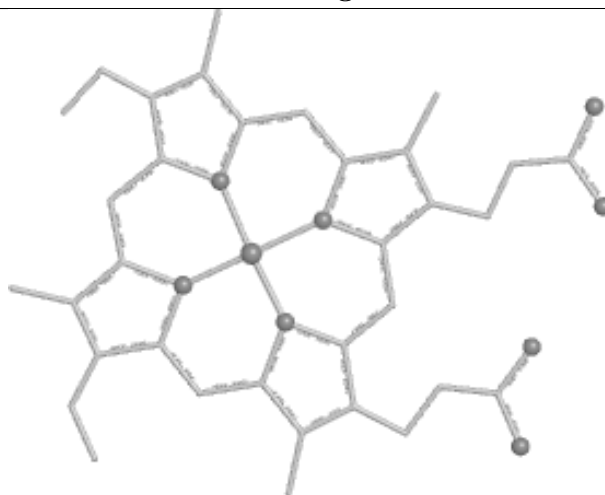
Bond lengths



Bond angles

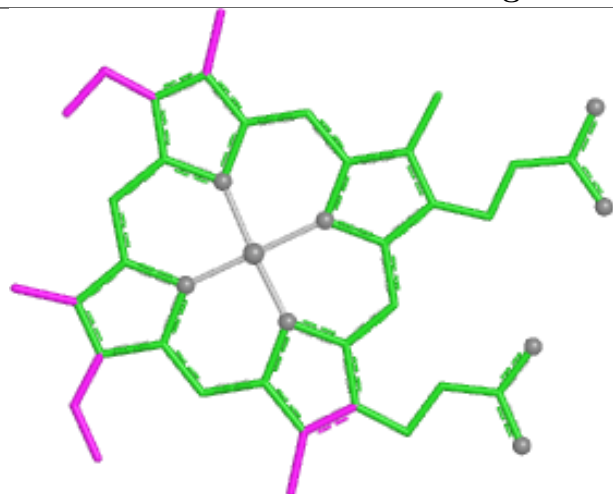


Torsions

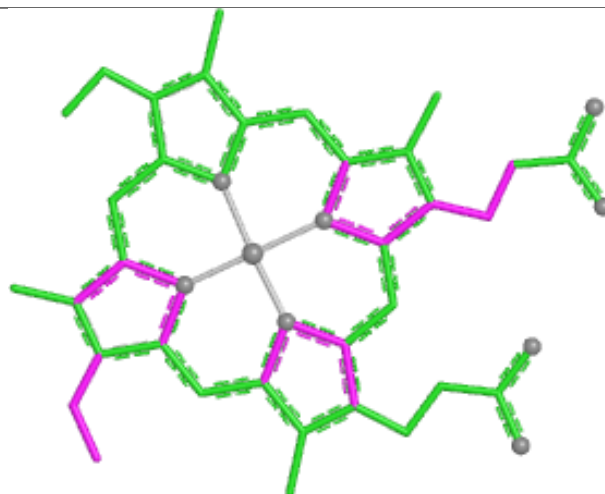


Rings

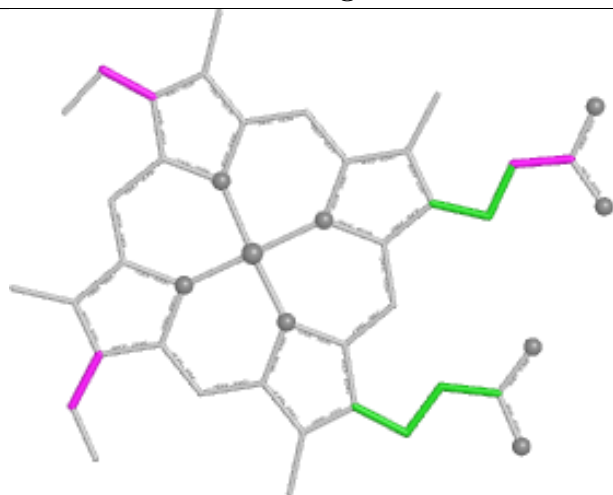
Ligand HEC K 1004



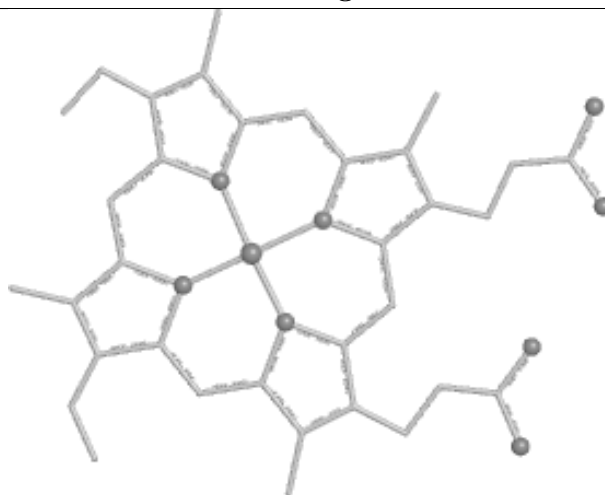
Bond lengths



Bond angles

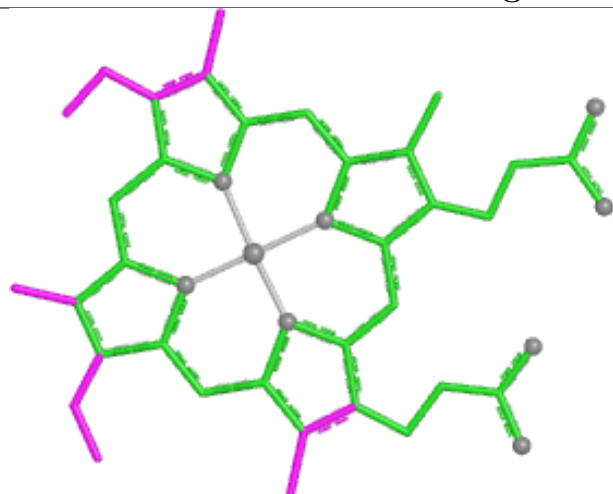


Torsions

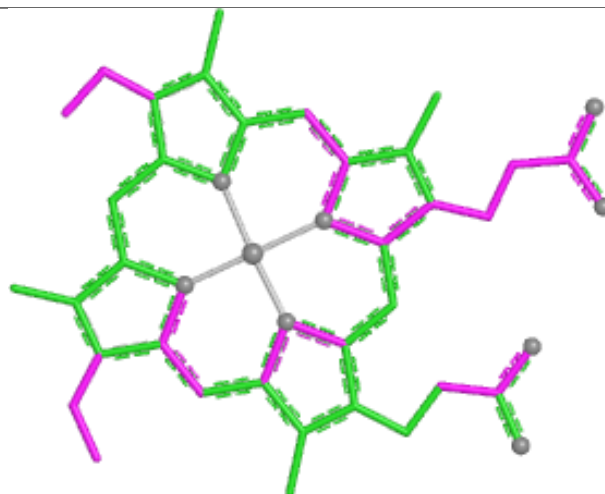


Rings

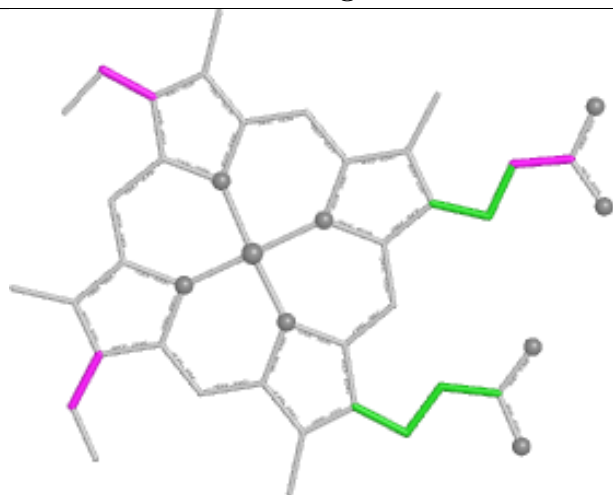
Ligand HEC R 1004



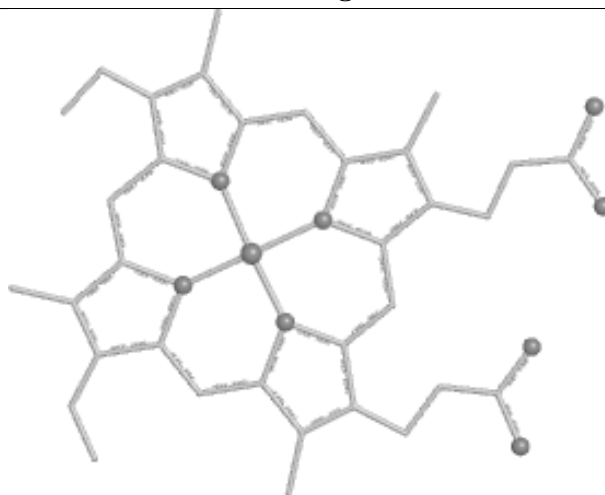
Bond lengths



Bond angles

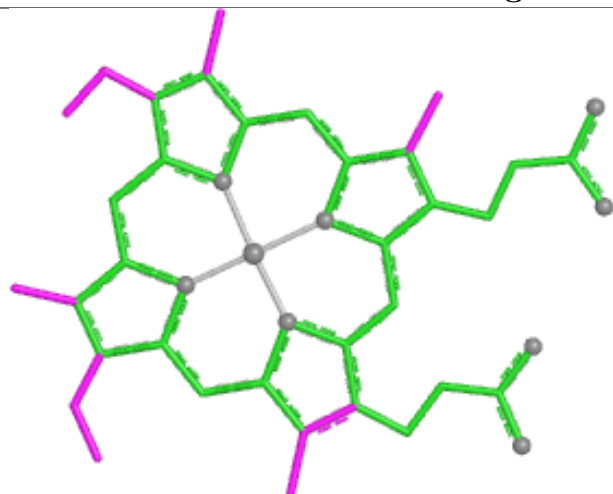


Torsions

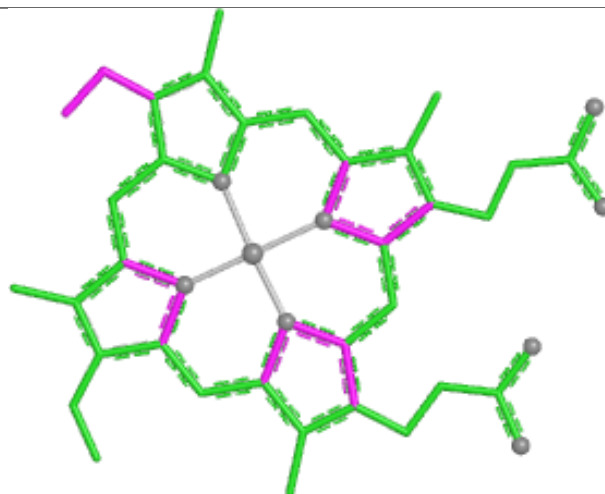


Rings

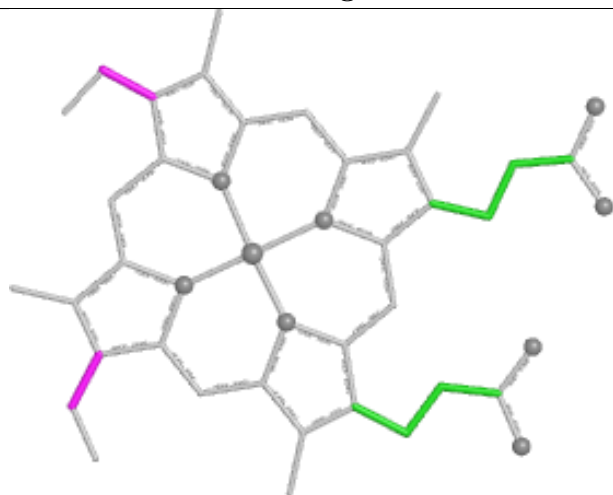
Ligand HEC E 1003



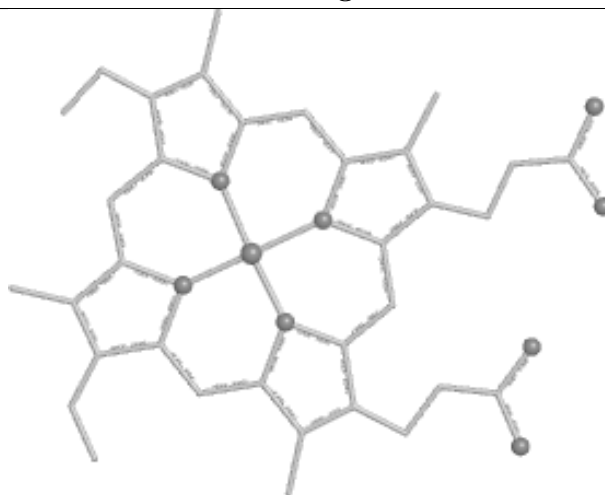
Bond lengths



Bond angles

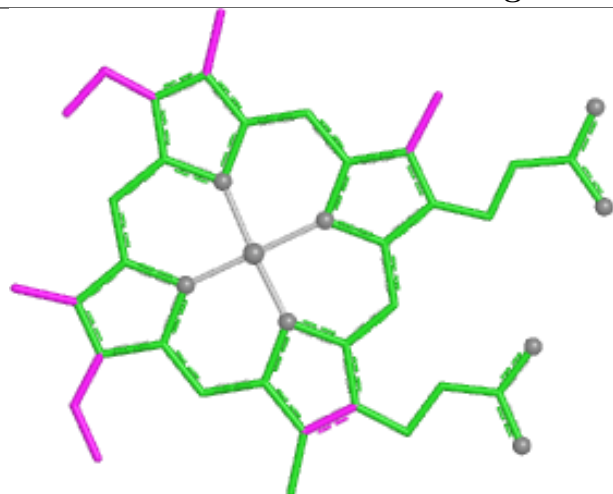


Torsions

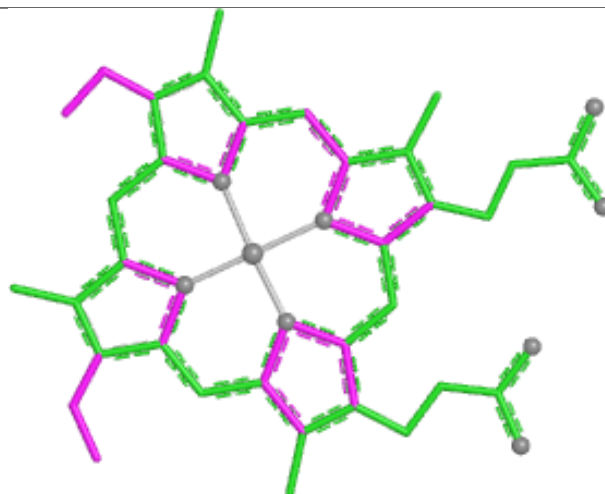


Rings

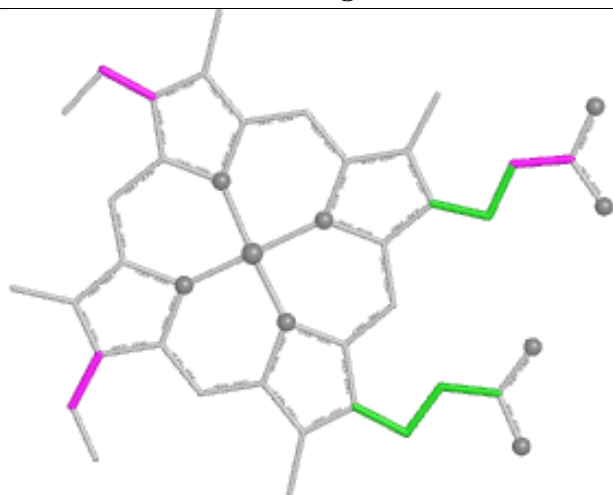
Ligand HEC B 1001



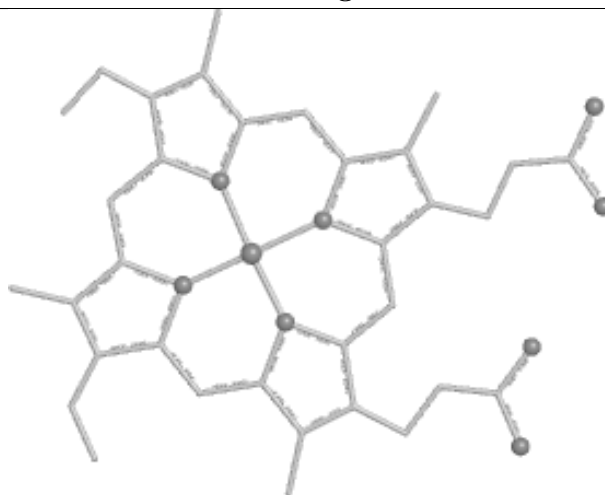
Bond lengths



Bond angles

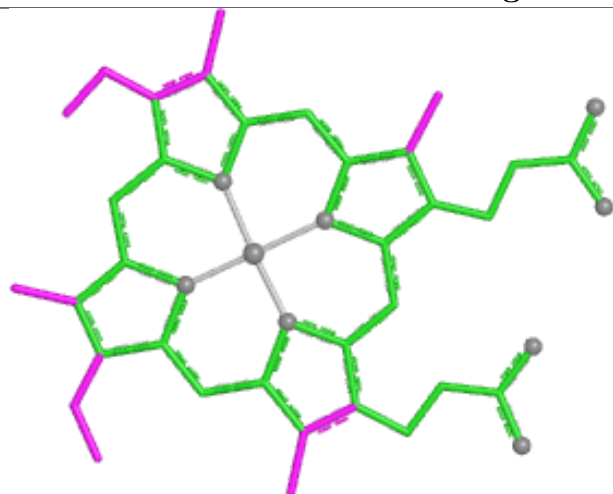


Torsions

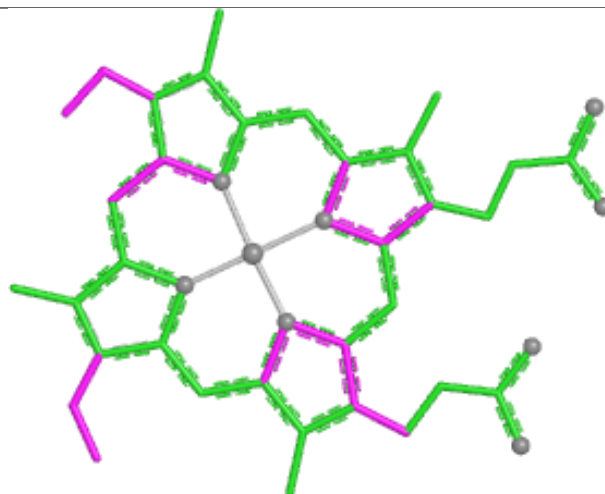


Rings

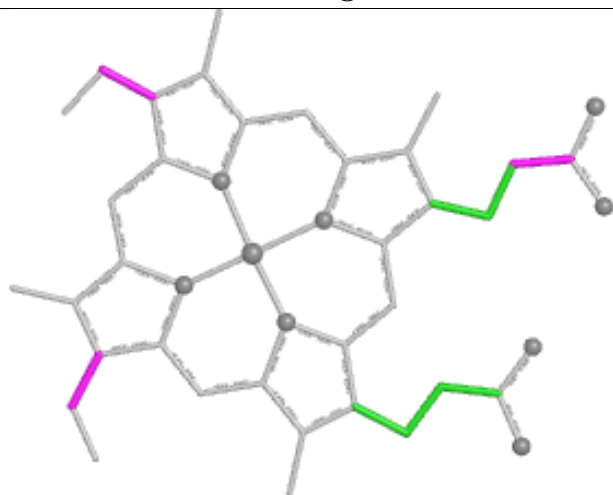
Ligand HEC N 1001



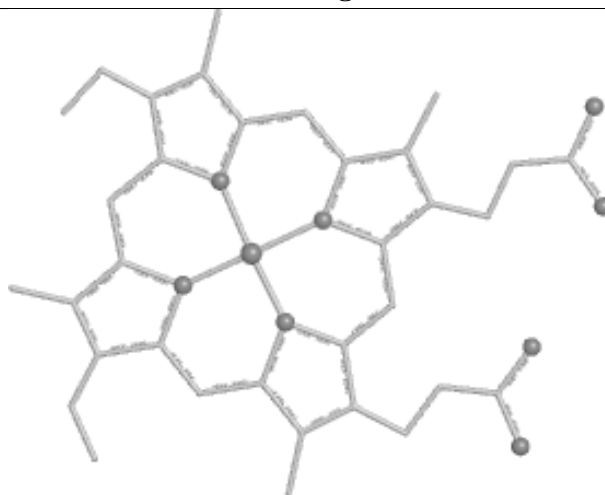
Bond lengths



Bond angles

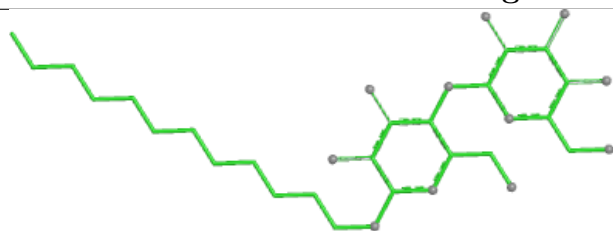


Torsions

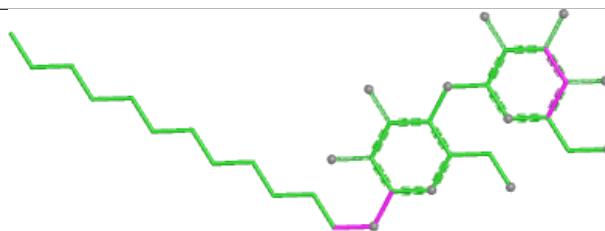


Rings

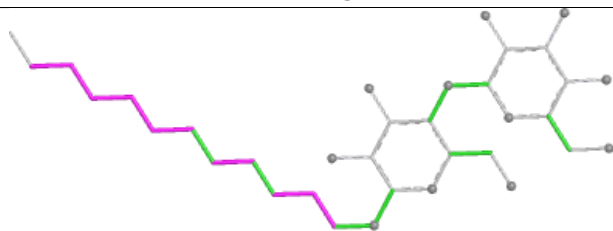
Ligand LMT R 1005



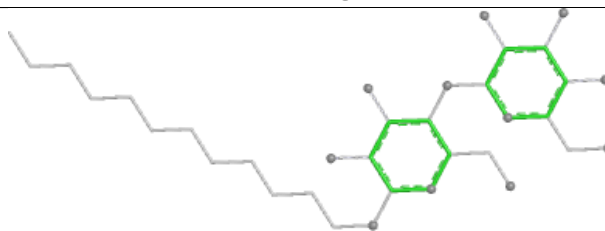
Bond lengths



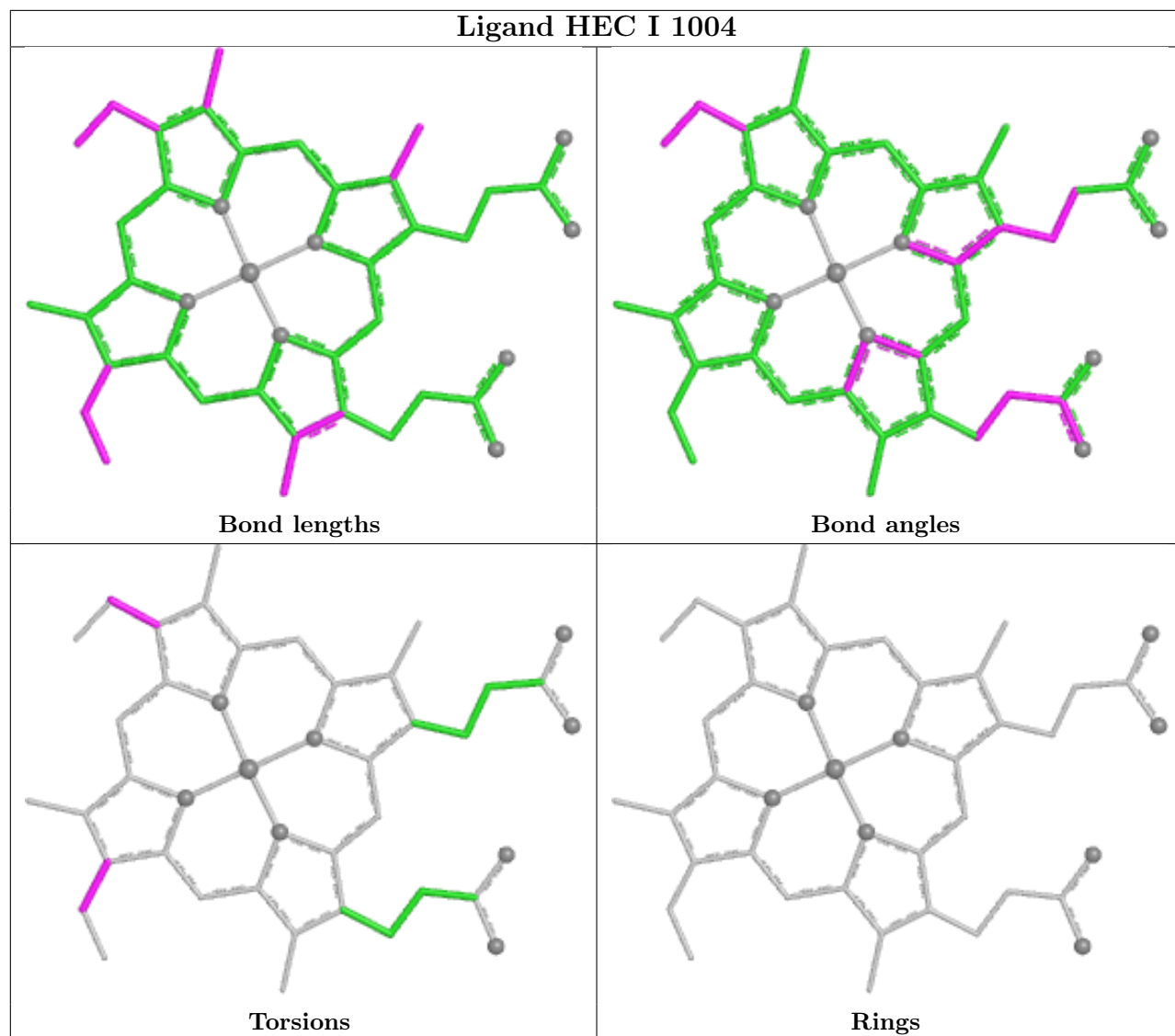
Bond angles



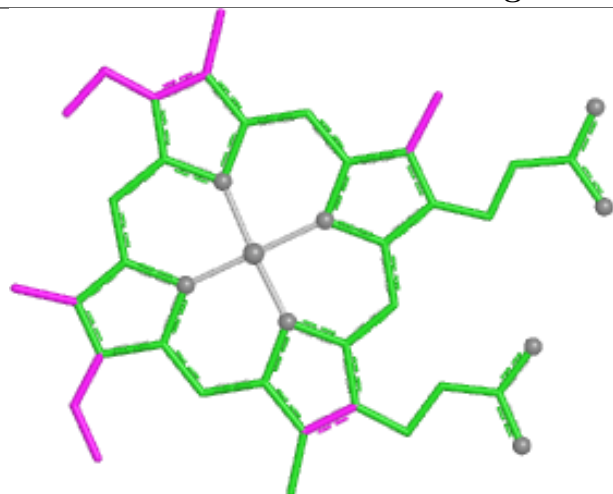
Torsions



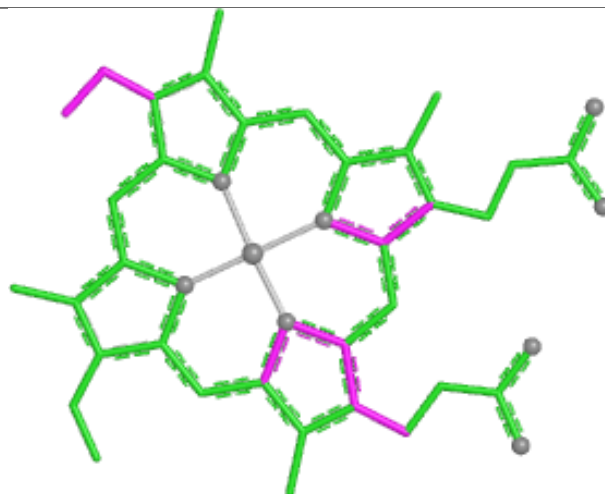
Rings



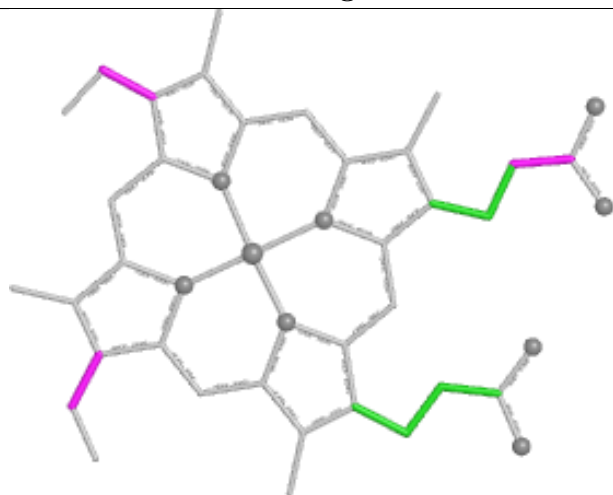
Ligand HEC B 1002



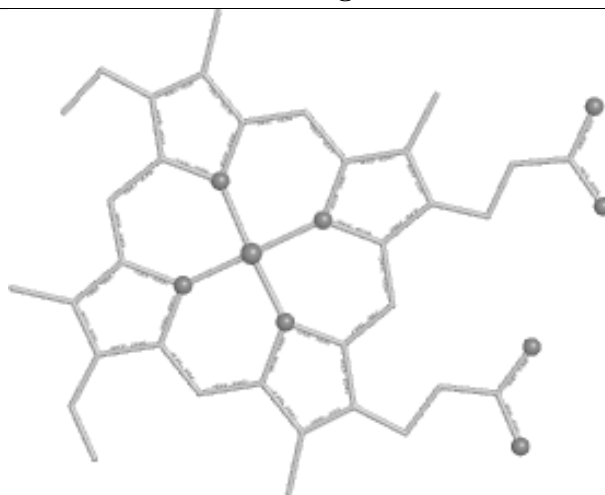
Bond lengths



Bond angles

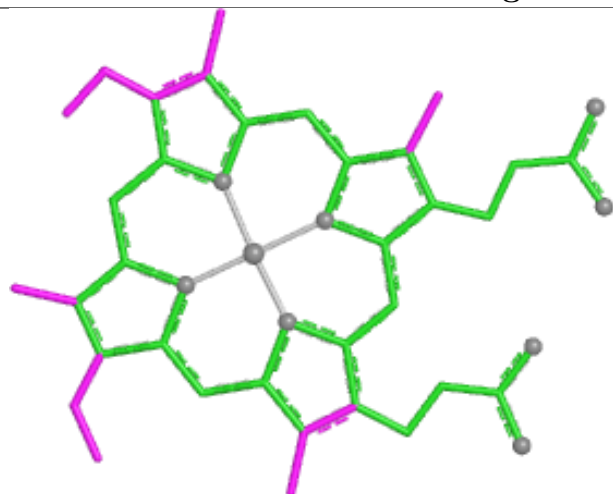


Torsions

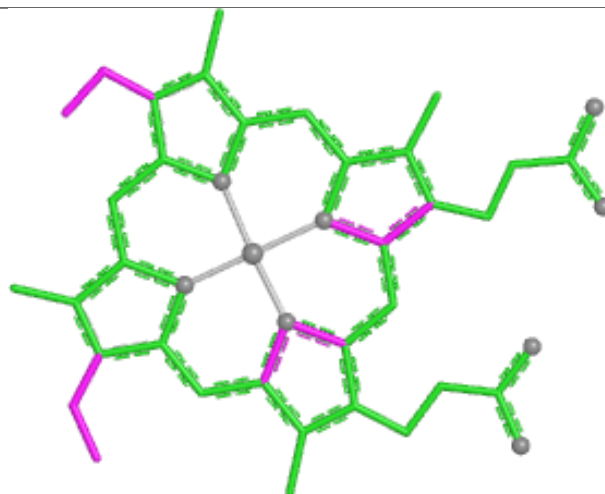


Rings

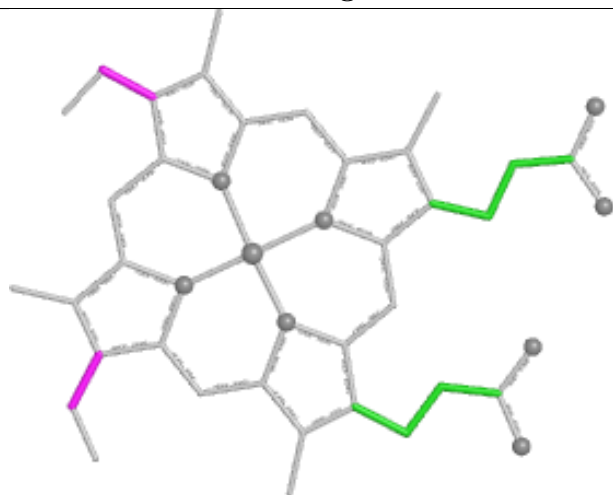
Ligand HEC N 1003



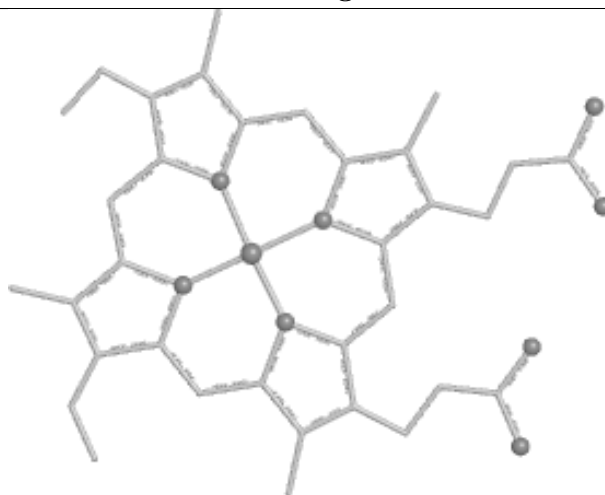
Bond lengths



Bond angles

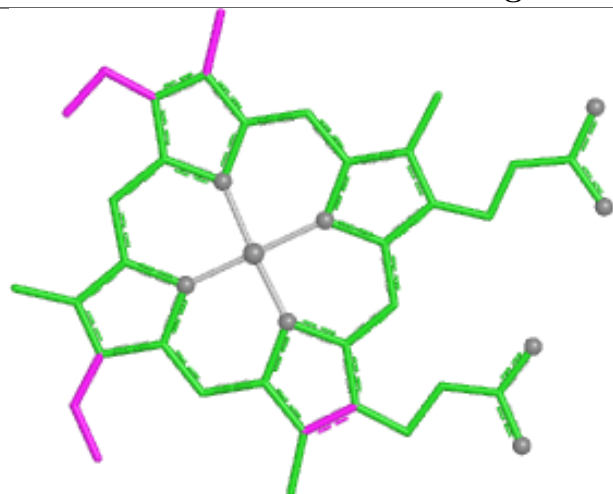


Torsions

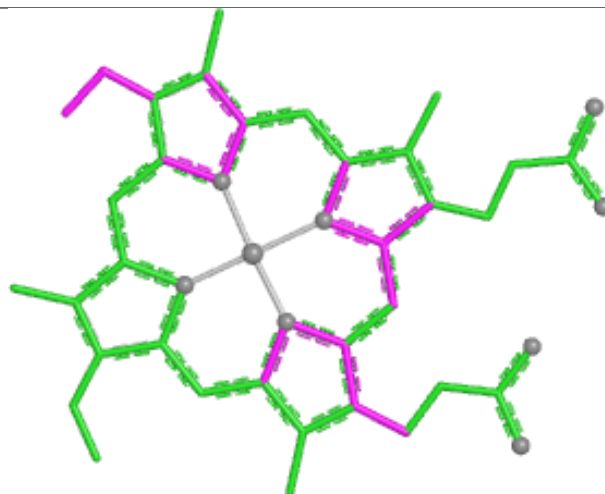


Rings

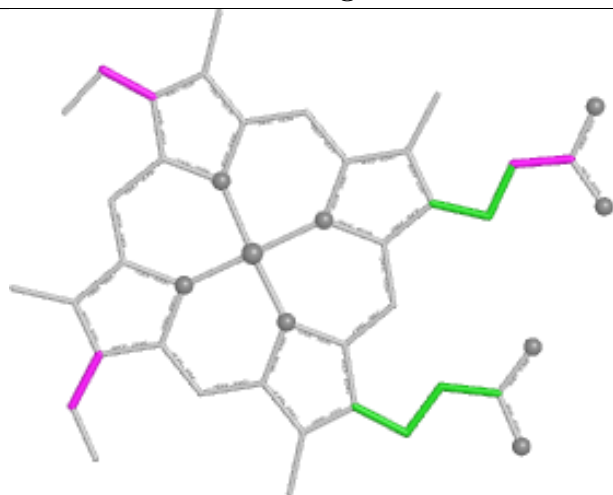
Ligand HEC P 1001



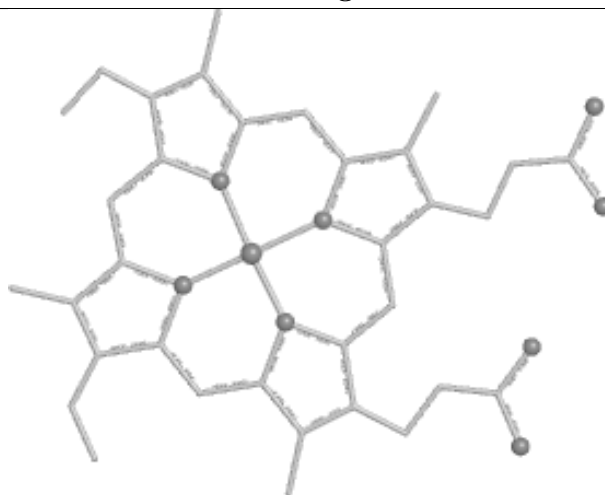
Bond lengths



Bond angles

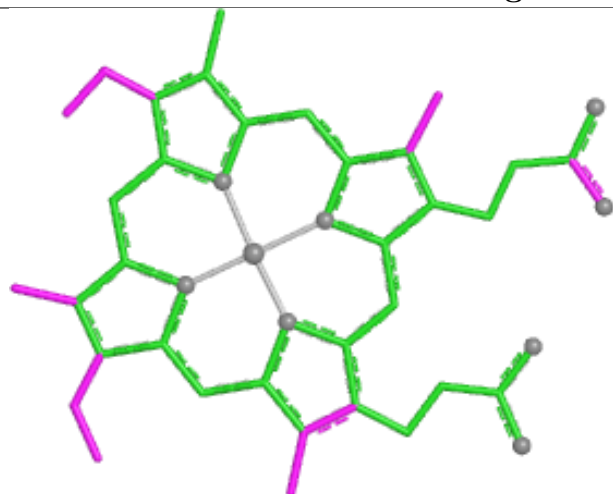


Torsions

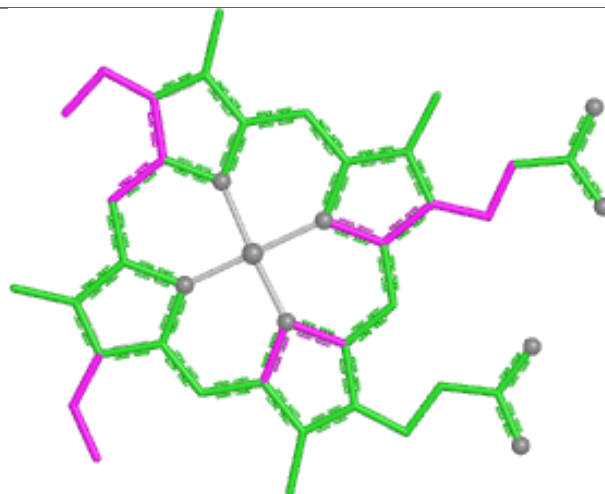


Rings

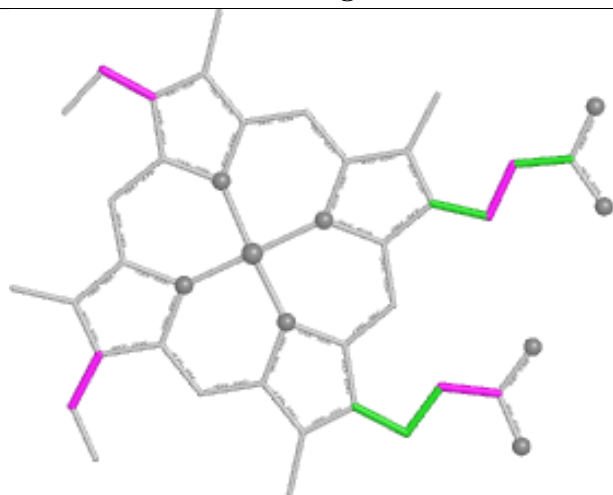
Ligand HEC E 1005



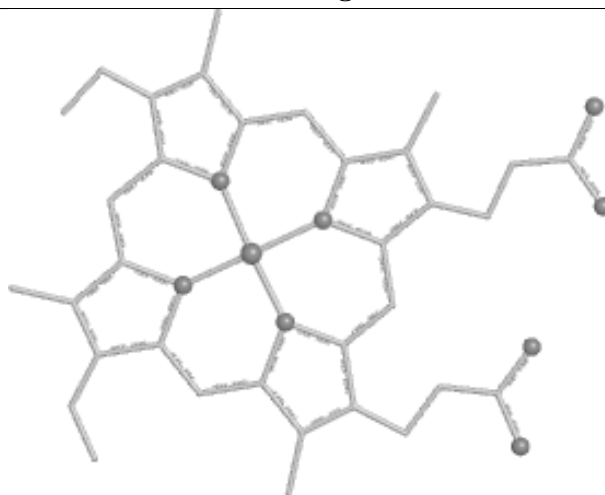
Bond lengths



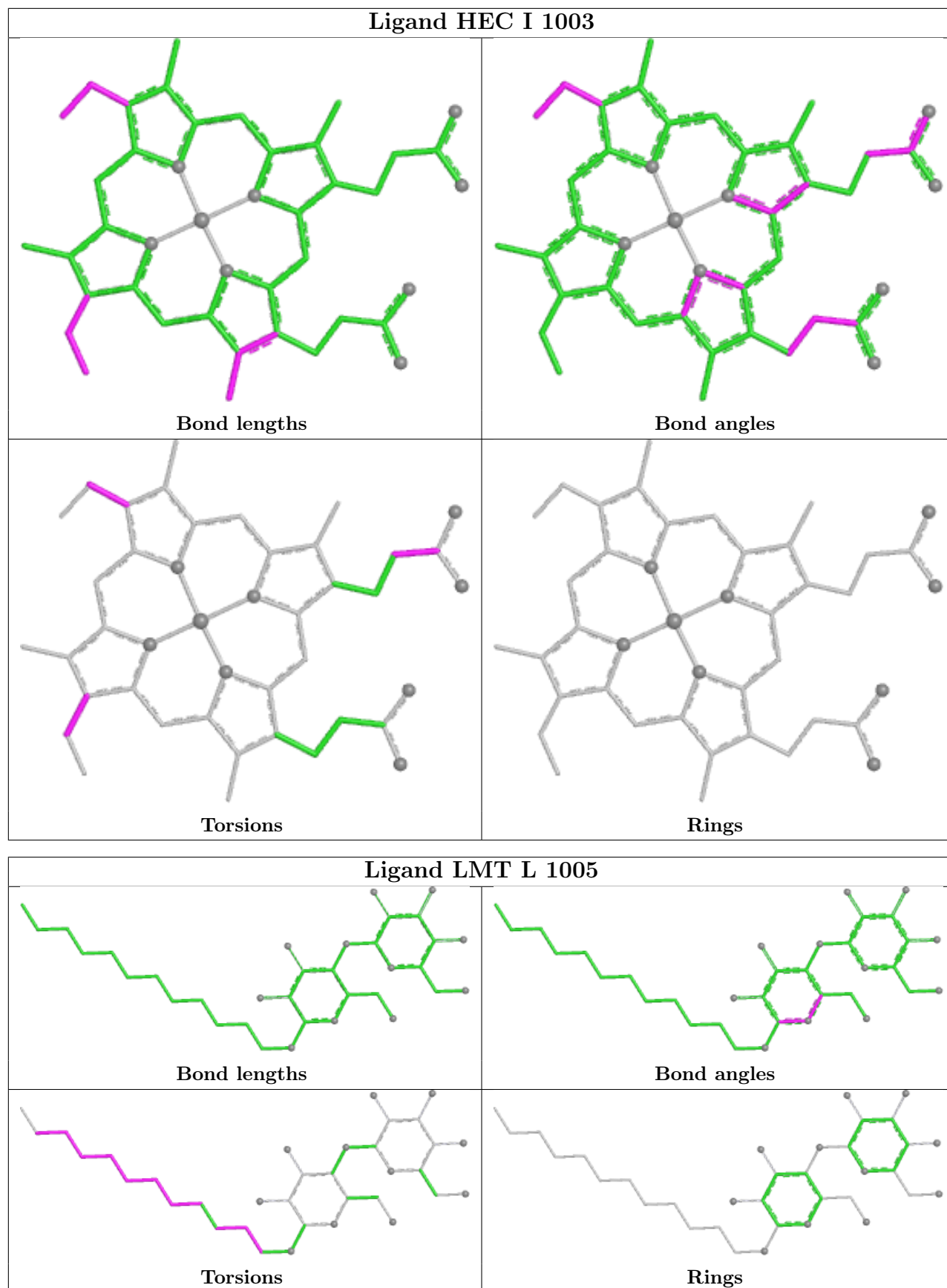
Bond angles



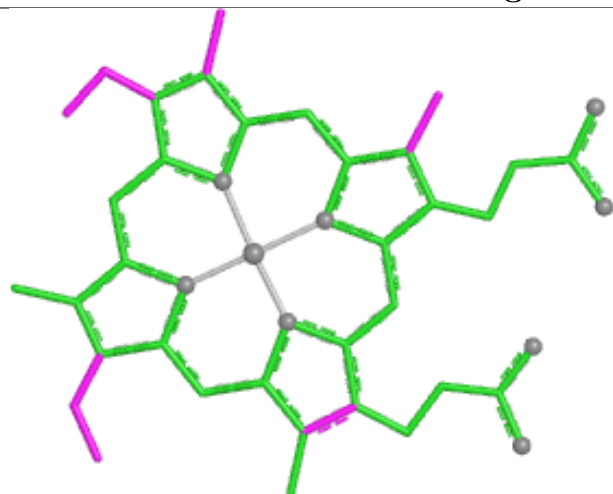
Torsions



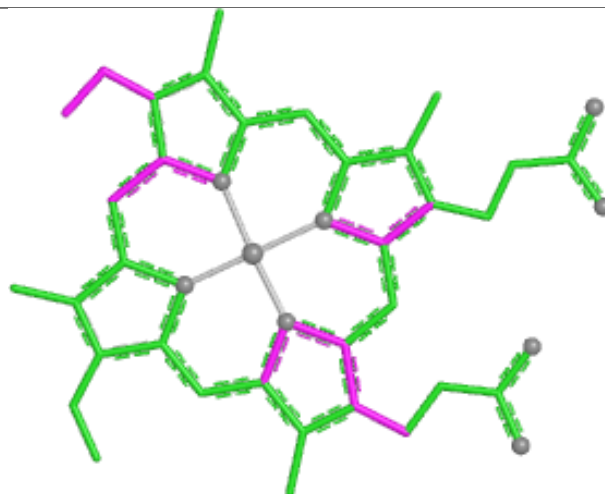
Rings



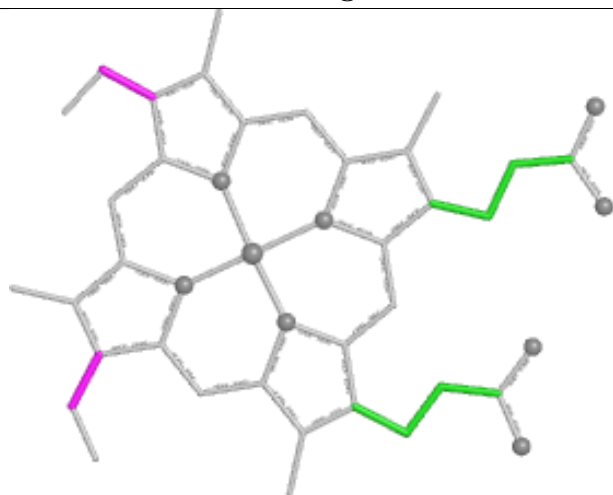
Ligand HEC P 1003



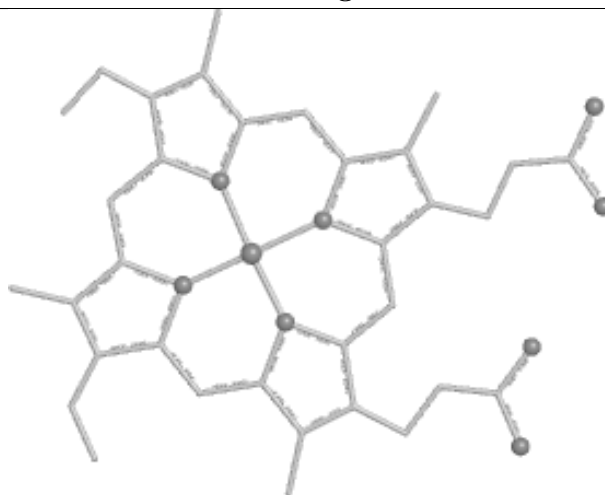
Bond lengths



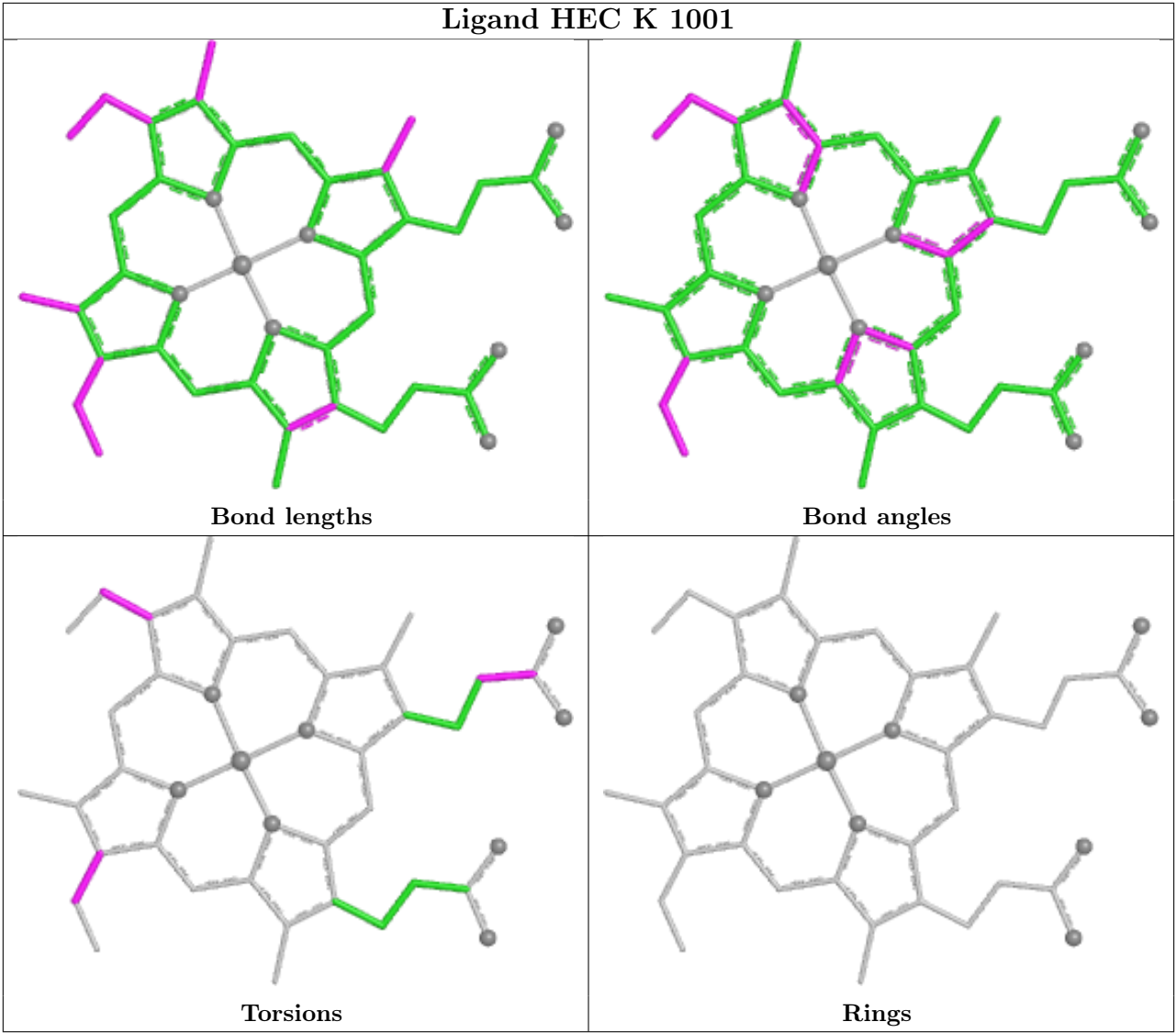
Bond angles



Torsions



Rings



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	M	2

All chain breaks are listed below:

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

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	495/500 (99%)	-0.19	7 (1%) 73 75	5, 17, 32, 50	2 (0%)
1	B	498/500 (99%)	-0.25	8 (1%) 70 72	5, 16, 33, 52	1 (0%)
1	D	494/500 (98%)	-0.20	2 (0%) 88 89	6, 18, 34, 50	1 (0%)
1	E	494/500 (98%)	-0.00	14 (2%) 55 57	8, 21, 37, 53	1 (0%)
1	G	494/500 (98%)	-0.21	4 (0%) 82 83	6, 17, 32, 50	1 (0%)
1	H	497/500 (99%)	-0.23	5 (1%) 79 80	5, 16, 33, 51	3 (0%)
1	J	494/500 (98%)	-0.12	5 (1%) 79 80	7, 18, 34, 50	3 (0%)
1	K	496/500 (99%)	0.08	12 (2%) 59 62	9, 21, 38, 53	0
1	M	494/500 (98%)	-0.19	6 (1%) 76 77	5, 17, 32, 50	2 (0%)
1	N	498/500 (99%)	-0.21	10 (2%) 65 66	6, 16, 33, 51	1 (0%)
1	P	494/500 (98%)	-0.09	9 (1%) 67 69	8, 19, 34, 49	1 (0%)
1	Q	495/500 (99%)	0.06	18 (3%) 46 48	9, 21, 37, 53	1 (0%)
2	C	145/159 (91%)	0.48	18 (12%) 8 9	8, 21, 80, 97	1 (0%)
2	F	145/159 (91%)	0.70	23 (15%) 5 5	8, 26, 80, 96	1 (0%)
2	I	145/159 (91%)	0.49	16 (11%) 10 11	8, 22, 80, 96	0
2	L	145/159 (91%)	0.72	22 (15%) 5 6	11, 27, 81, 96	0
2	O	144/159 (90%)	0.55	17 (11%) 9 10	9, 21, 76, 96	0
2	R	145/159 (91%)	0.71	20 (13%) 6 7	10, 27, 80, 96	0
All	All	6812/6954 (97%)	-0.04	216 (3%) 50 52	5, 19, 38, 97	19 (0%)

The worst 5 of 216 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	15	LEU	8.2
2	O	15	LEU	7.7
2	F	15	LEU	7.6

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Mol	Chain	Res	Type	RSRZ
2	I	15	LEU	7.2
2	R	15	LEU	7.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	LMT	R	1005	35/35	0.78	0.22	41,49,75,75	0
5	LMT	O	1005	35/35	0.81	0.20	38,45,74,75	0
5	LMT	I	1005	35/35	0.82	0.19	36,41,72,73	0
5	LMT	L	1005	35/35	0.82	0.20	40,46,66,67	0
5	LMT	C	1005	35/35	0.83	0.19	36,41,72,73	0
5	LMT	F	1005	35/35	0.83	0.19	37,44,70,71	0
6	ACT	C	1006	4/4	0.86	0.14	34,34,34,34	0
6	ACT	I	1006	4/4	0.86	0.14	38,39,39,39	0
6	ACT	O	1006	4/4	0.89	0.15	32,32,33,33	0
3	HEC	E	1005	43/43	0.94	0.10	11,14,20,24	0
3	HEC	L	1101	43/43	0.94	0.11	23,27,33,36	0
3	HEC	R	1001	43/43	0.94	0.11	22,26,37,42	0
3	HEC	C	1001	43/43	0.94	0.11	17,20,29,34	0
3	HEC	K	1002	43/43	0.95	0.10	18,21,23,24	0
3	HEC	K	1005	43/43	0.95	0.09	9,15,23,26	0
3	HEC	L	1002	43/43	0.95	0.10	16,18,26,29	0
3	HEC	A	1003	43/43	0.95	0.07	2,6,9,12	0
3	HEC	M	1001	43/43	0.95	0.07	3,9,11,12	0
3	HEC	N	1004	43/43	0.95	0.08	2,5,8,13	0
3	HEC	O	1001	43/43	0.95	0.10	17,20,28,34	0
3	HEC	O	1003	43/43	0.95	0.09	8,12,17,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HEC	Q	1005	43/43	0.95	0.09	12,15,20,29	0
3	HEC	A	1004	43/43	0.95	0.08	2,5,11,14	0
3	HEC	R	1002	43/43	0.95	0.10	17,20,28,32	0
3	HEC	F	1001	43/43	0.95	0.10	20,24,27,31	0
3	HEC	F	1003	43/43	0.95	0.09	7,10,18,24	0
3	HEC	G	1003	43/43	0.95	0.08	4,7,11,13	0
3	HEC	H	1004	43/43	0.95	0.08	3,6,8,12	0
3	HEC	H	1005	43/43	0.95	0.09	5,8,18,22	0
3	HEC	I	1001	43/43	0.95	0.10	18,21,29,32	0
3	HEC	I	1002	43/43	0.95	0.10	11,15,26,29	0
3	HEC	I	1003	43/43	0.95	0.08	7,12,19,24	0
3	HEC	K	1001	43/43	0.95	0.09	15,19,23,25	0
3	HEC	B	1005	43/43	0.96	0.09	4,8,18,21	0
3	HEC	A	1002	43/43	0.96	0.08	5,9,14,18	0
3	HEC	C	1002	43/43	0.96	0.09	8,13,27,29	0
3	HEC	C	1003	43/43	0.96	0.08	8,11,15,23	0
3	HEC	I	1004	43/43	0.96	0.08	3,6,16,20	0
3	HEC	J	1001	43/43	0.96	0.07	8,12,16,16	0
3	HEC	J	1002	43/43	0.96	0.08	9,11,16,21	0
3	HEC	J	1003	43/43	0.96	0.07	5,8,12,16	0
3	HEC	J	1004	43/43	0.96	0.08	3,6,13,21	0
3	HEC	J	1005	43/43	0.96	0.08	10,13,19,22	0
3	HEC	C	1004	43/43	0.96	0.08	3,8,17,22	0
3	HEC	D	1002	43/43	0.96	0.07	4,7,13,19	0
3	HEC	K	1003	43/43	0.96	0.08	9,15,17,18	0
3	HEC	K	1004	43/43	0.96	0.08	7,13,21,25	0
3	HEC	D	1005	43/43	0.96	0.08	6,12,18,19	0
3	HEC	E	1001	43/43	0.96	0.08	14,16,18,20	0
3	HEC	L	1003	43/43	0.96	0.08	8,11,16,21	0
3	HEC	L	1004	43/43	0.96	0.08	7,10,19,21	0
3	HEC	E	1002	43/43	0.96	0.08	13,16,19,21	0
3	HEC	E	1003	43/43	0.96	0.08	12,14,16,18	0
3	HEC	M	1002	43/43	0.96	0.08	6,11,13,17	0
3	HEC	M	1003	43/43	0.96	0.07	3,7,12,14	0
3	HEC	M	1004	43/43	0.96	0.07	2,5,14,16	0
3	HEC	M	1005	43/43	0.96	0.07	4,7,16,21	0
3	HEC	N	1001	43/43	0.96	0.08	6,9,12,13	0
3	HEC	N	1002	43/43	0.96	0.08	6,10,12,14	0
3	HEC	N	1003	43/43	0.96	0.08	3,7,8,11	0
3	HEC	E	1004	43/43	0.96	0.08	7,11,14,21	0
3	HEC	N	1005	43/43	0.96	0.09	3,8,21,24	0
3	HEC	A	1005	43/43	0.96	0.07	2,7,16,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HEC	O	1002	43/43	0.96	0.09	12,14,23,29	0
3	HEC	B	1001	43/43	0.96	0.08	5,10,13,16	0
3	HEC	O	1004	43/43	0.96	0.08	5,8,20,23	0
3	HEC	P	1001	43/43	0.96	0.09	12,16,21,24	0
3	HEC	P	1002	43/43	0.96	0.08	6,9,17,24	0
3	HEC	P	1003	43/43	0.96	0.07	6,9,12,14	0
3	HEC	P	1005	43/43	0.96	0.08	8,13,18,22	0
3	HEC	Q	1001	43/43	0.96	0.09	13,18,20,22	0
3	HEC	Q	1002	43/43	0.96	0.09	19,21,22,23	0
3	HEC	Q	1003	43/43	0.96	0.09	14,17,20,23	0
3	HEC	F	1002	43/43	0.96	0.10	14,17,27,30	0
3	HEC	B	1002	43/43	0.96	0.08	6,10,15,17	0
3	HEC	F	1004	43/43	0.96	0.08	3,6,16,24	0
3	HEC	R	1003	43/43	0.96	0.08	7,11,17,21	0
3	HEC	R	1004	43/43	0.96	0.07	3,8,16,21	0
3	HEC	G	1001	43/43	0.96	0.07	3,8,11,13	0
3	HEC	G	1002	43/43	0.96	0.09	7,9,14,19	0
3	HEC	B	1003	43/43	0.96	0.08	5,7,9,13	0
3	HEC	G	1004	43/43	0.96	0.07	2,5,12,14	0
3	HEC	G	1005	43/43	0.96	0.07	5,8,12,16	0
3	HEC	H	1001	43/43	0.96	0.08	5,11,13,14	0
3	HEC	H	1002	43/43	0.96	0.08	6,9,14,21	0
3	HEC	H	1003	43/43	0.96	0.08	3,8,10,13	0
3	HEC	B	1004	43/43	0.96	0.07	2,5,7,12	0
3	HEC	D	1001	43/43	0.97	0.08	6,12,16,19	0
3	HEC	A	1001	43/43	0.97	0.07	2,7,12,15	0
3	HEC	D	1003	43/43	0.97	0.07	2,5,8,11	0
3	HEC	Q	1004	43/43	0.97	0.08	7,11,18,19	0
3	HEC	P	1004	43/43	0.97	0.07	5,8,13,18	0
3	HEC	D	1004	43/43	0.97	0.07	2,5,10,16	0
4	CA	Q	1007	1/1	0.98	0.02	20,20,20,20	0
4	CA	J	1006	1/1	0.98	0.02	13,13,13,13	0
4	CA	J	1007	1/1	0.99	0.02	11,11,11,11	0
4	CA	K	1006	1/1	0.99	0.02	16,16,16,16	0
4	CA	K	1007	1/1	0.99	0.02	17,17,17,17	0
4	CA	M	1006	1/1	0.99	0.02	12,12,12,12	0
4	CA	M	1007	1/1	0.99	0.02	14,14,14,14	0
4	CA	N	1007	1/1	0.99	0.02	11,11,11,11	0
4	CA	P	1007	1/1	0.99	0.02	15,15,15,15	0
4	CA	Q	1006	1/1	0.99	0.02	17,17,17,17	0
4	CA	B	1006	1/1	0.99	0.01	11,11,11,11	0
4	CA	B	1007	1/1	0.99	0.02	13,13,13,13	0

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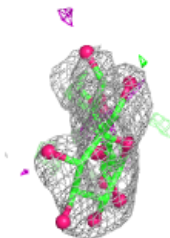
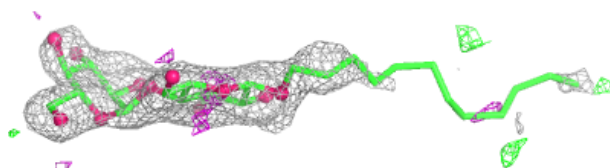
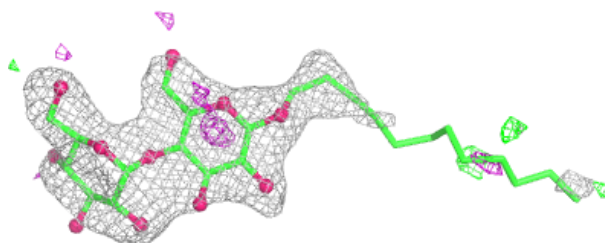
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	D	1006	1/1	0.99	0.02	16,16,16,16	0
4	CA	D	1007	1/1	0.99	0.01	11,11,11,11	0
4	CA	E	1006	1/1	0.99	0.02	17,17,17,17	0
4	CA	E	1007	1/1	0.99	0.02	18,18,18,18	0
4	CA	G	1006	1/1	0.99	0.01	13,13,13,13	0
4	CA	G	1007	1/1	0.99	0.03	16,16,16,16	0
4	CA	H	1007	1/1	0.99	0.02	16,16,16,16	0
4	CA	A	1006	1/1	0.99	0.01	13,13,13,13	0
4	CA	A	1007	1/1	1.00	0.01	11,11,11,11	0
4	CA	N	1006	1/1	1.00	0.01	10,10,10,10	0
4	CA	H	1006	1/1	1.00	0.02	11,11,11,11	0
4	CA	P	1006	1/1	1.00	0.01	16,16,16,16	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

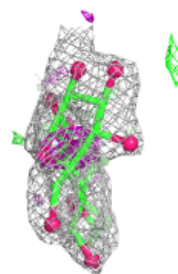
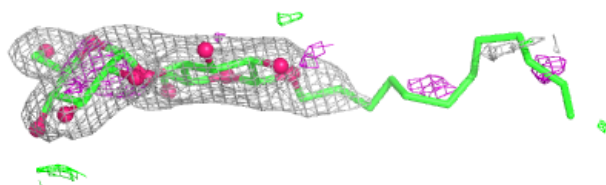
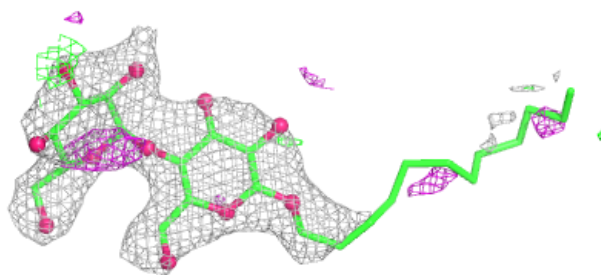
Electron density around LMT R 1005:

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

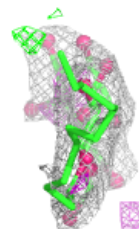
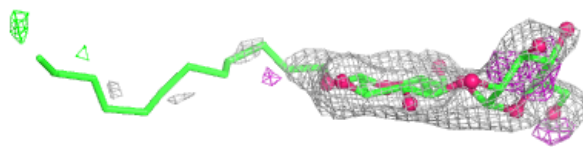
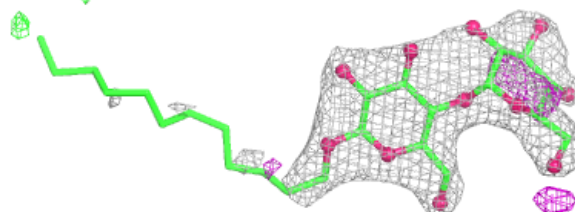


Electron density around LMT O 1005:

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

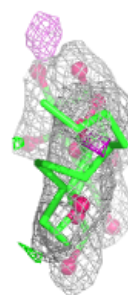
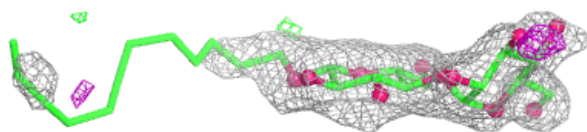
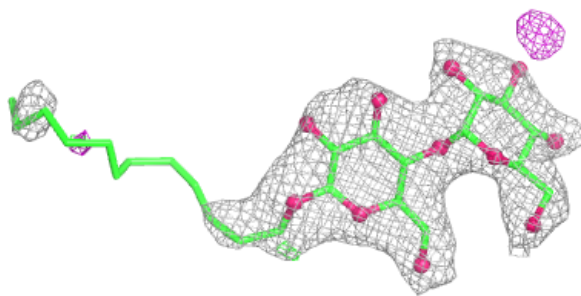
**Electron density around LMT I 1005:**

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

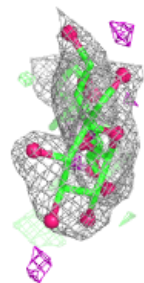
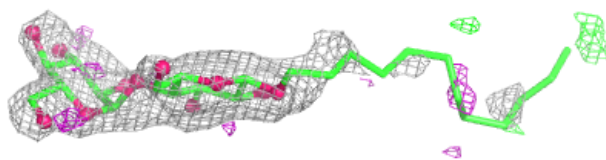
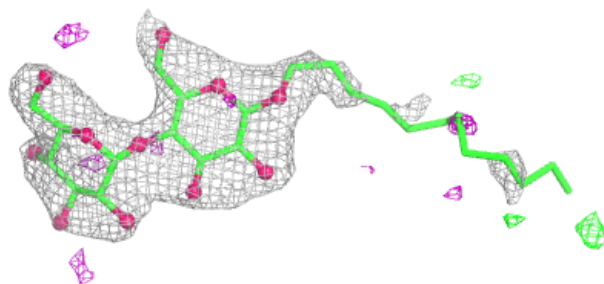


Electron density around LMT L 1005:

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and green (positive)

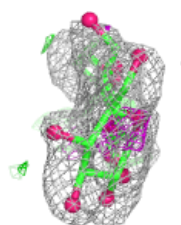
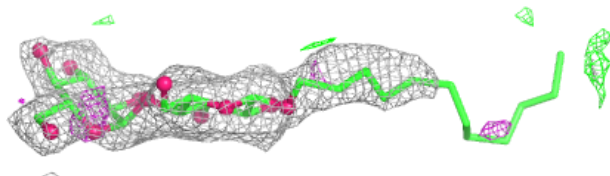
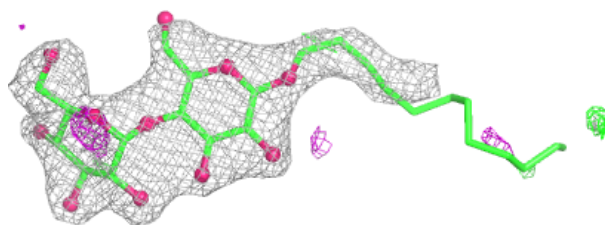
**Electron density around LMT C 1005:**

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



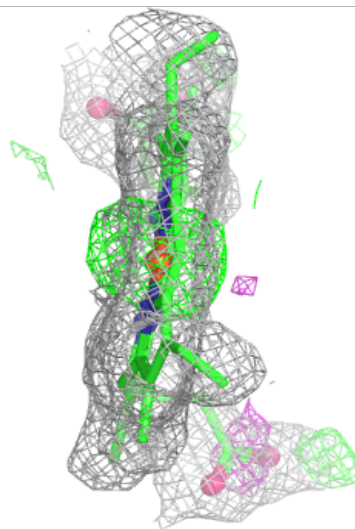
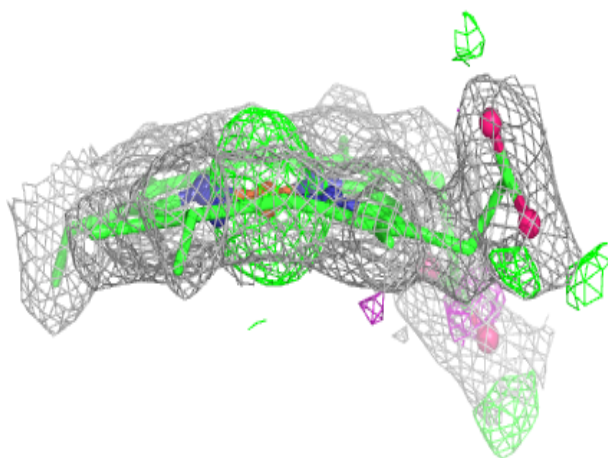
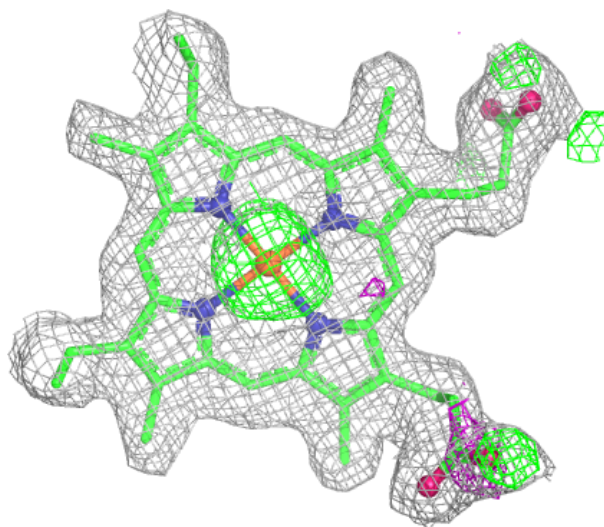
Electron density around LMT F 1005:

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



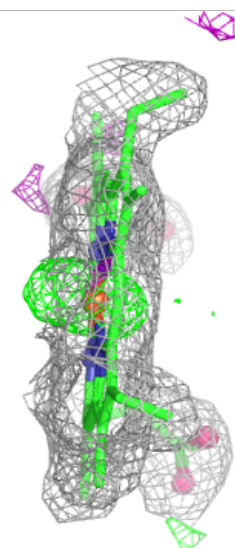
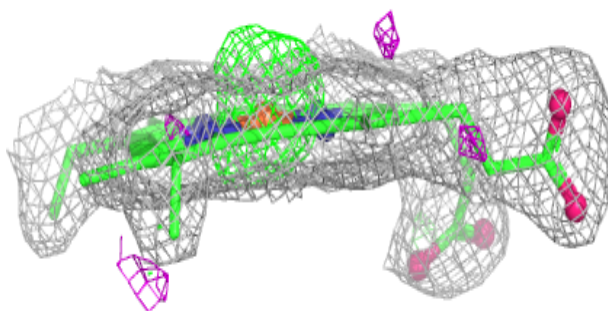
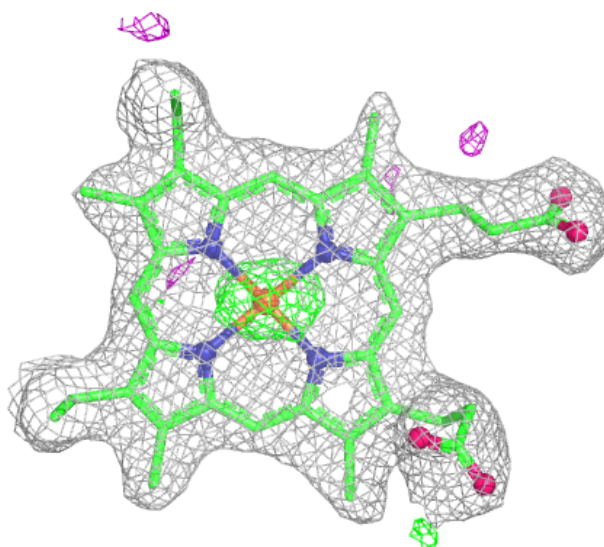
Electron density around HEC E 1005:

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



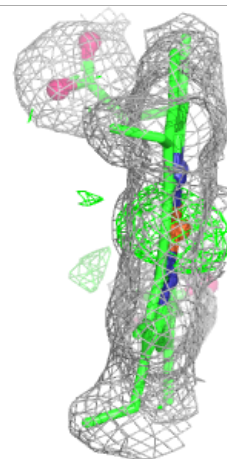
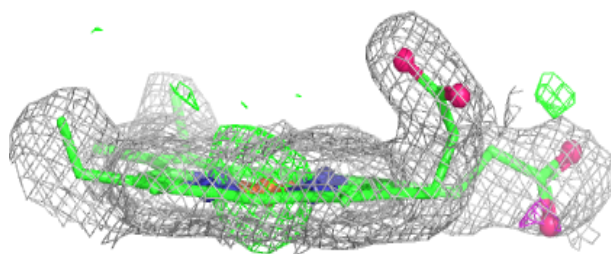
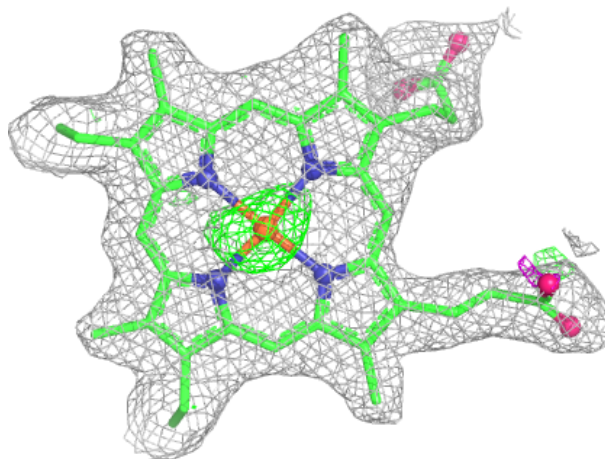
Electron density around HEC L 1101:

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and green (positive)



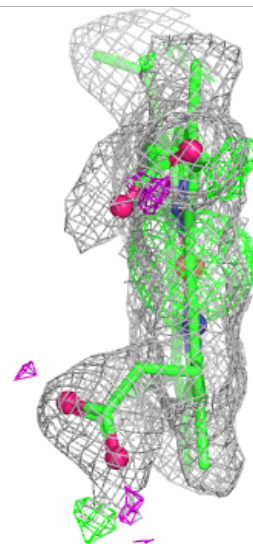
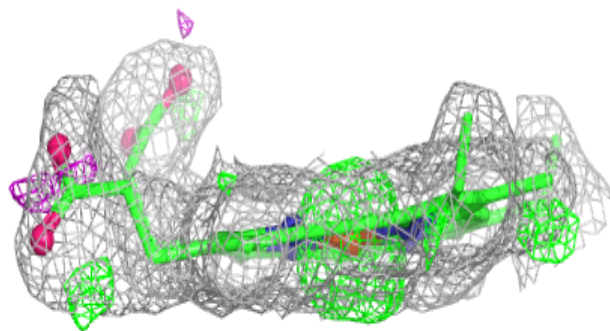
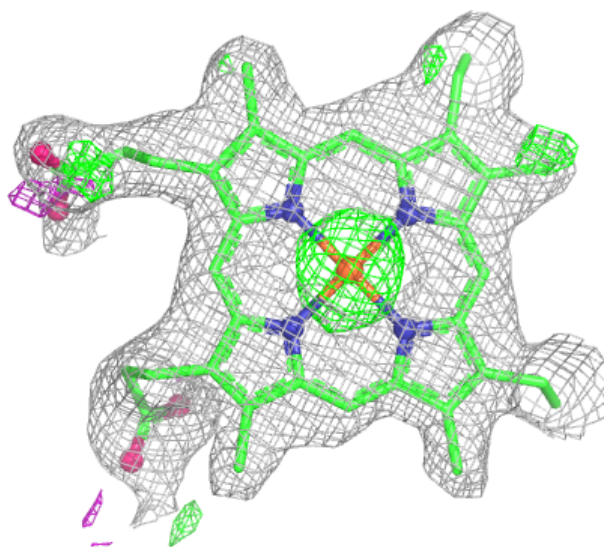
Electron density around HEC R 1001:

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and green (positive)



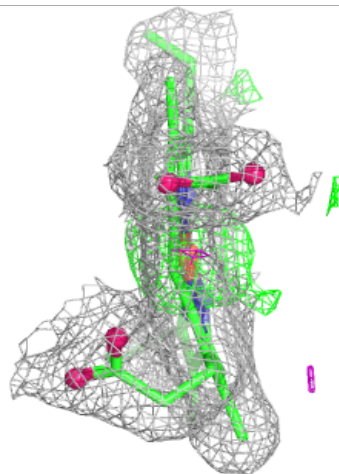
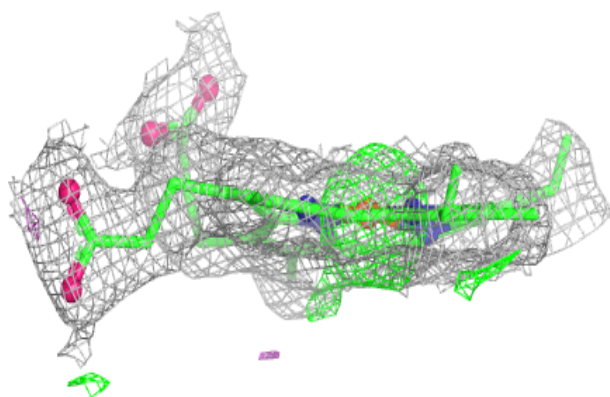
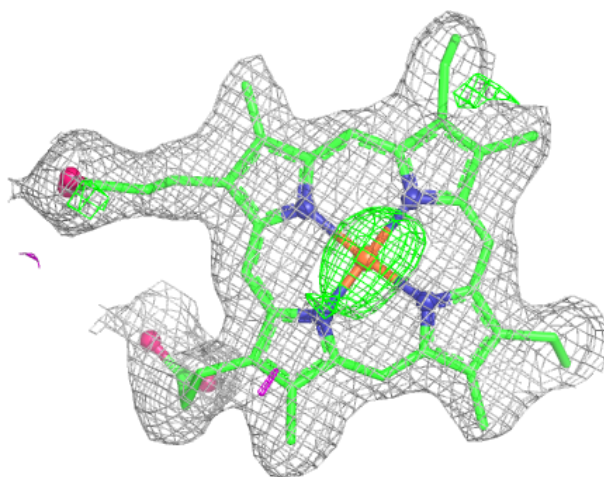
Electron density around HEC C 1001:

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and green (positive)



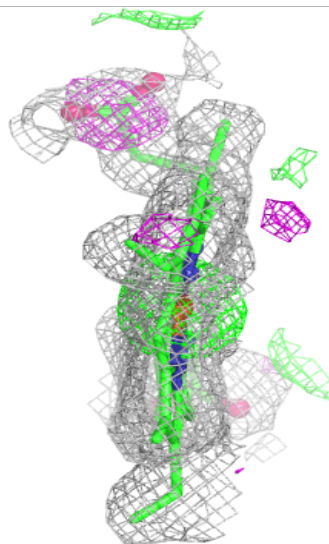
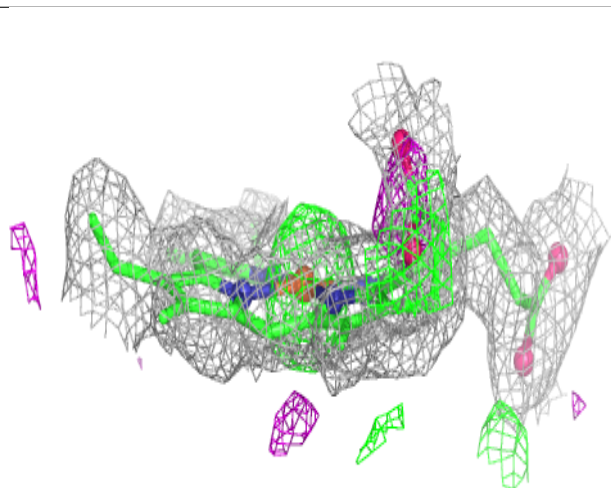
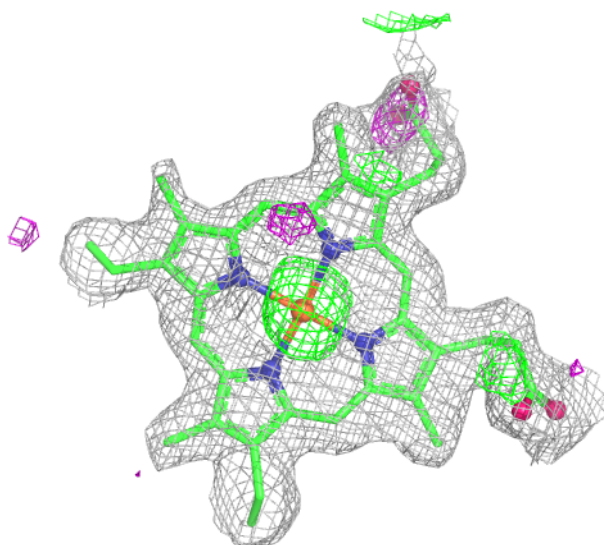
Electron density around HEC K 1002:

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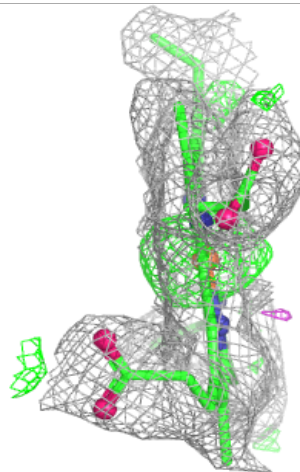
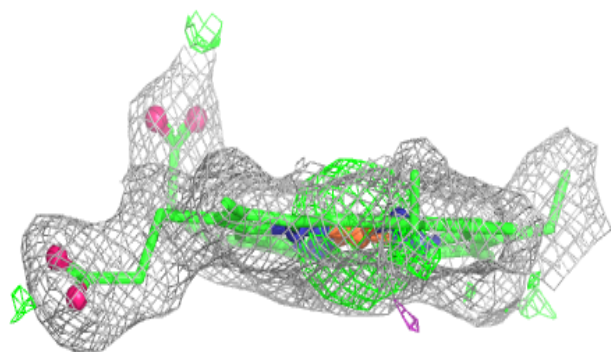
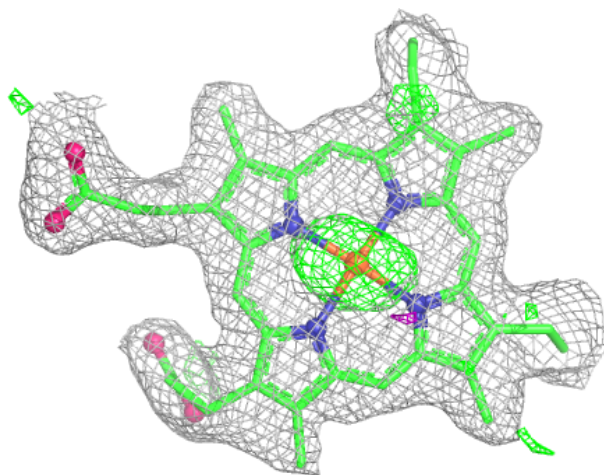
Electron density around HEC K 1005:

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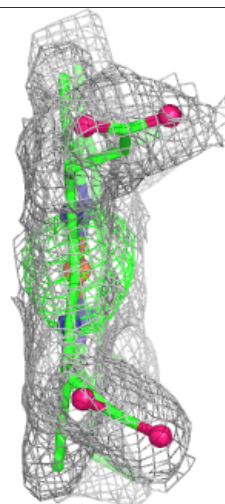
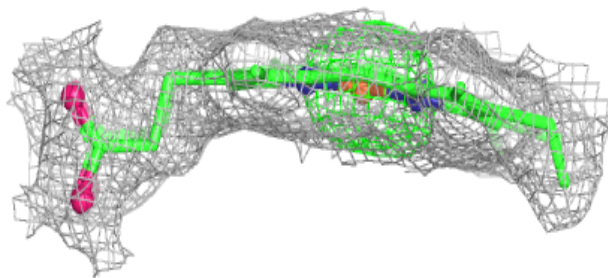
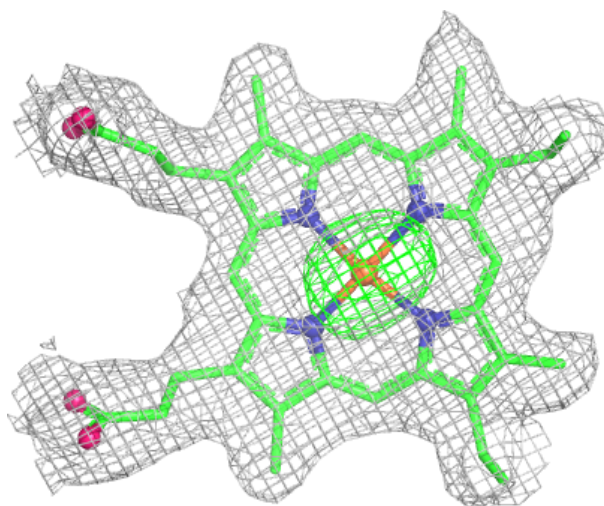
Electron density around HEC L 1002:

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and green (positive)



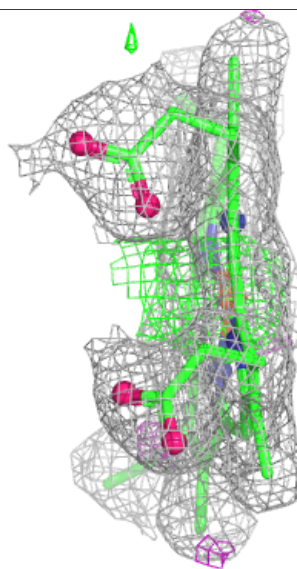
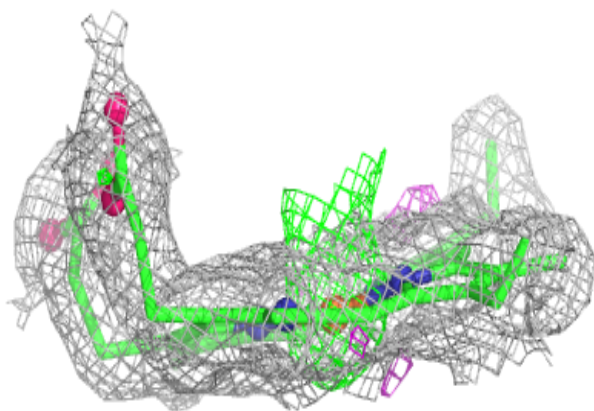
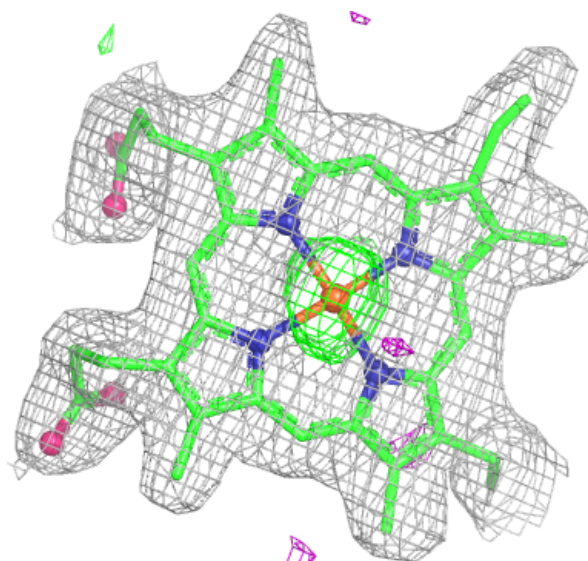
Electron density around HEC A 1003:

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



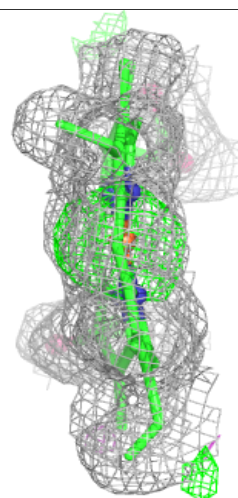
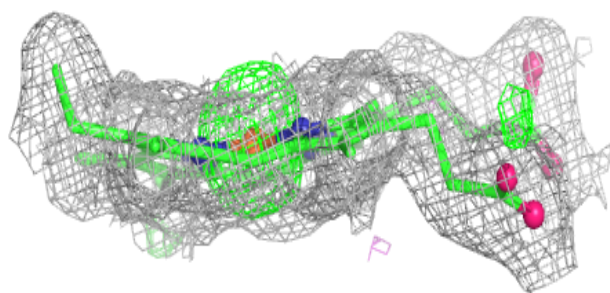
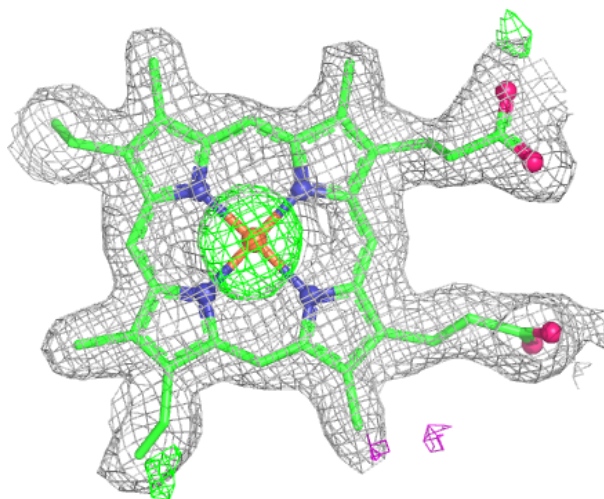
Electron density around HEC M 1001:

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and green (positive)



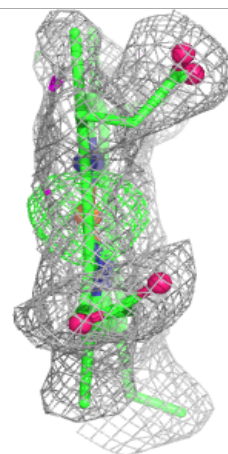
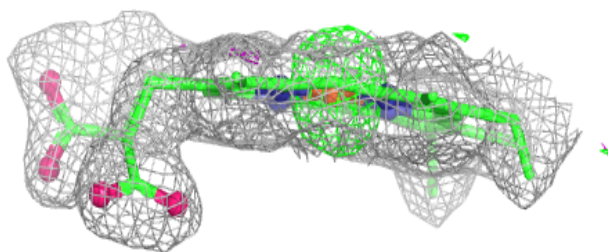
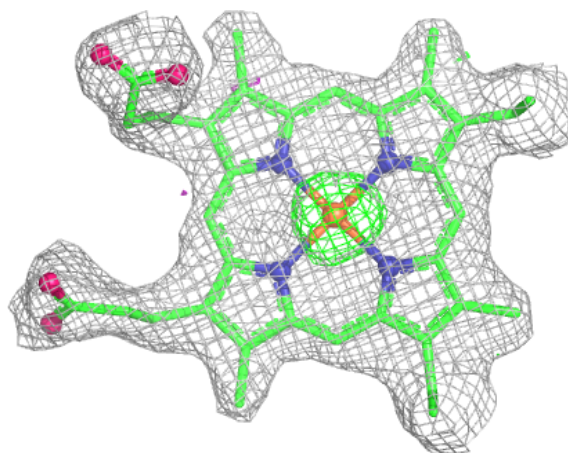
Electron density around HEC N 1004:

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and green (positive)



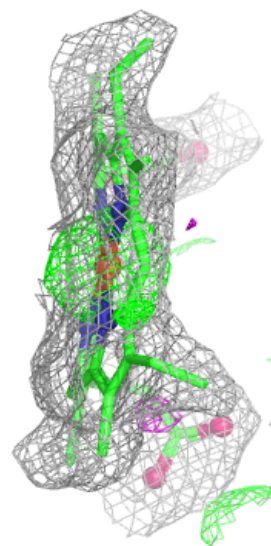
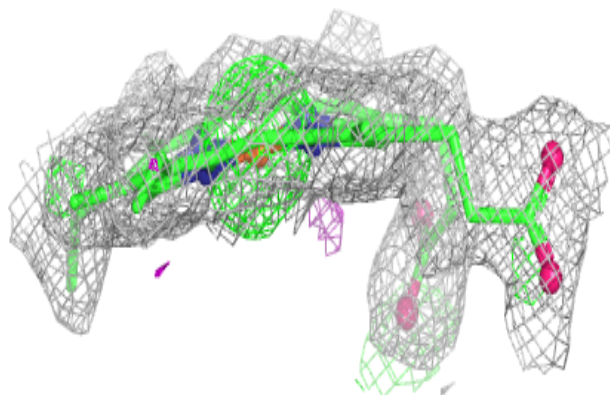
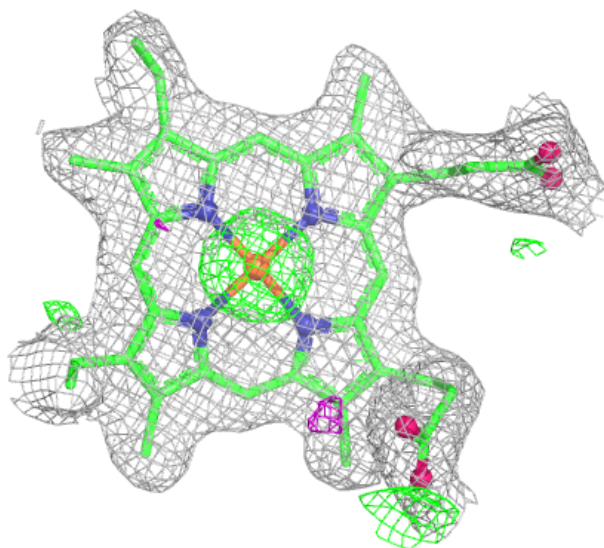
Electron density around HEC O 1001:

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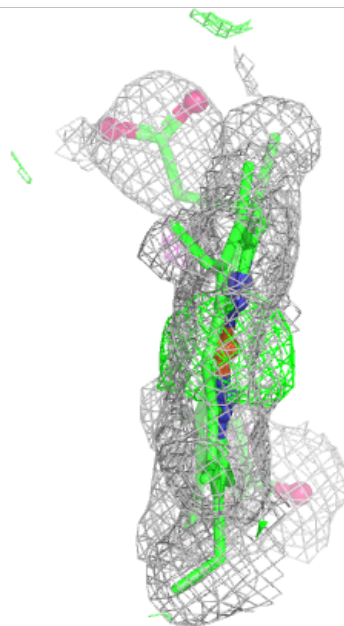
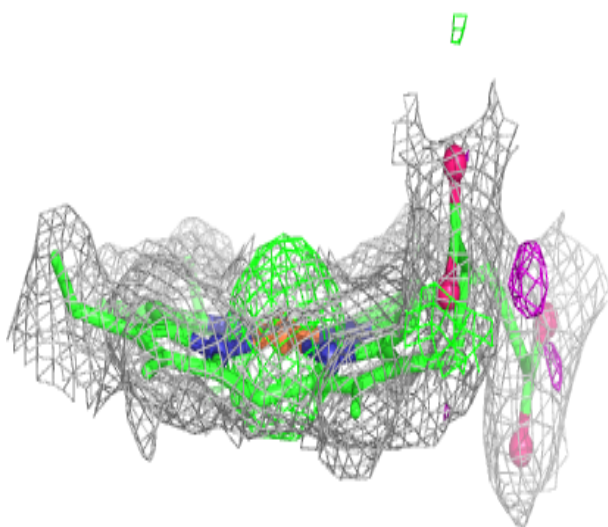
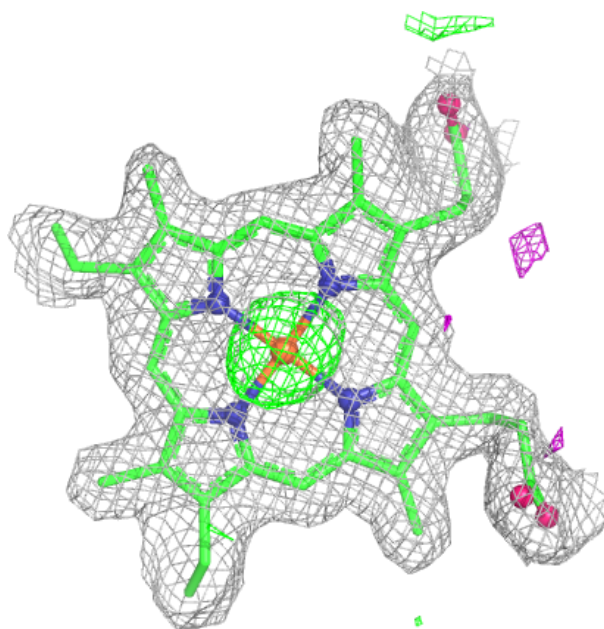
Electron density around HEC O 1003:

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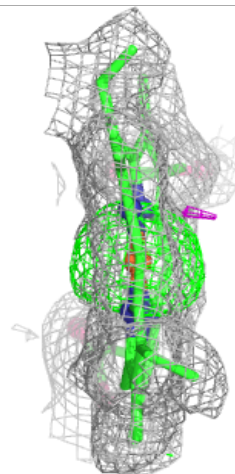
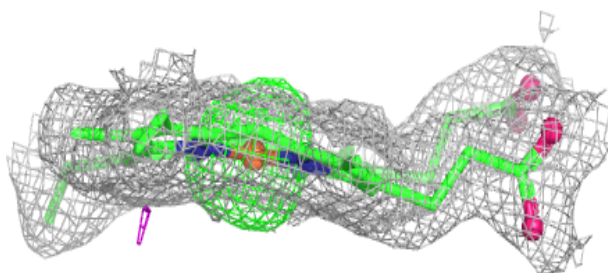
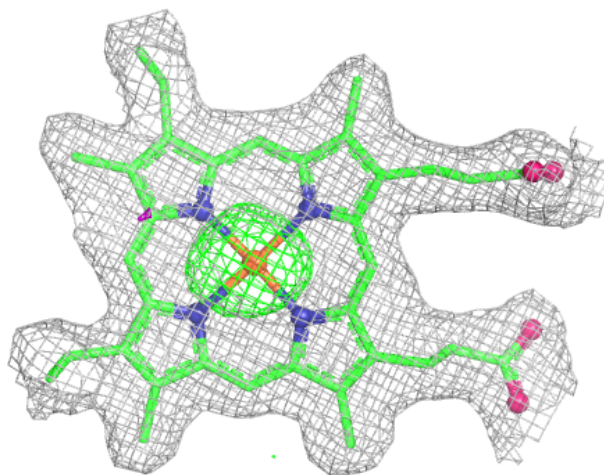
Electron density around HEC Q 1005:

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and green (positive)



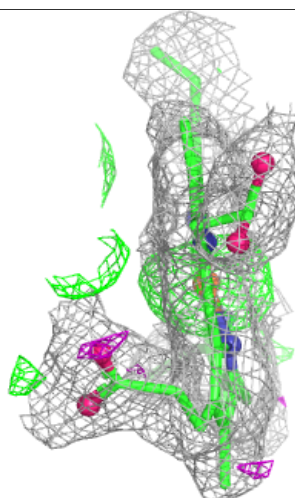
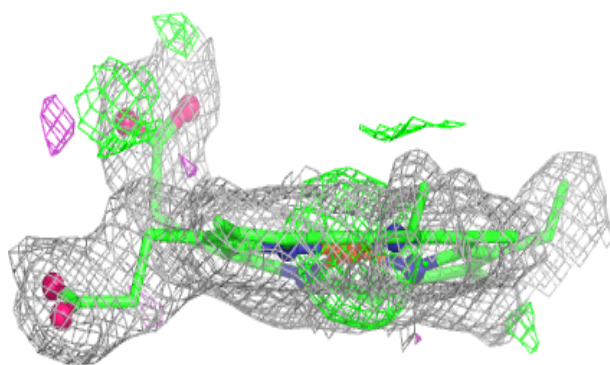
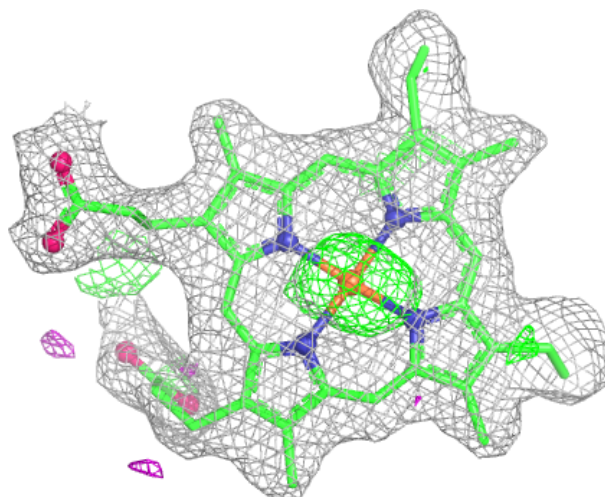
Electron density around HEC A 1004:

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and green (positive)



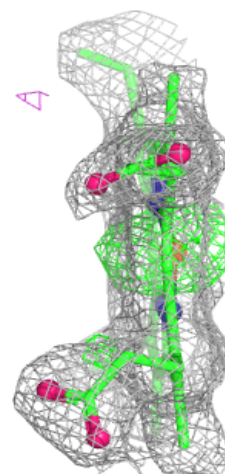
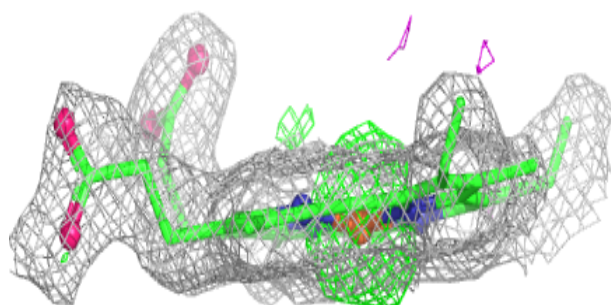
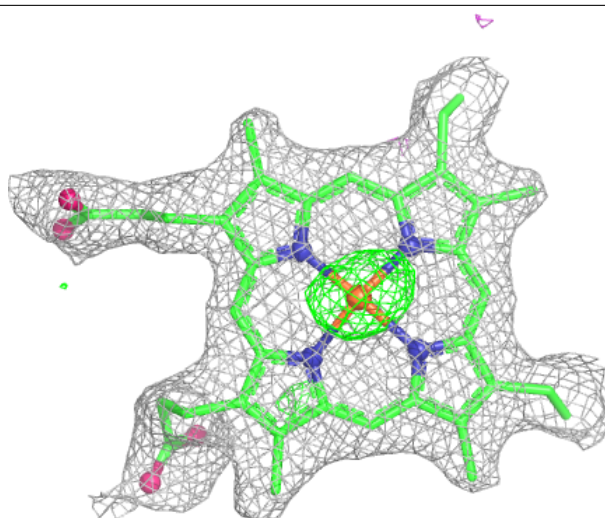
Electron density around HEC R 1002:

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



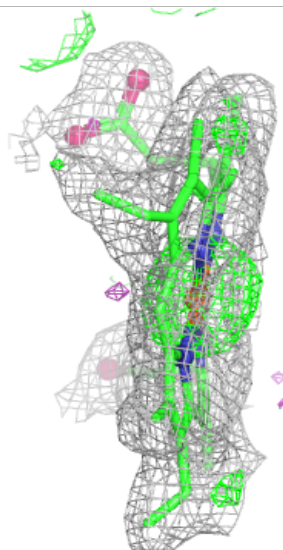
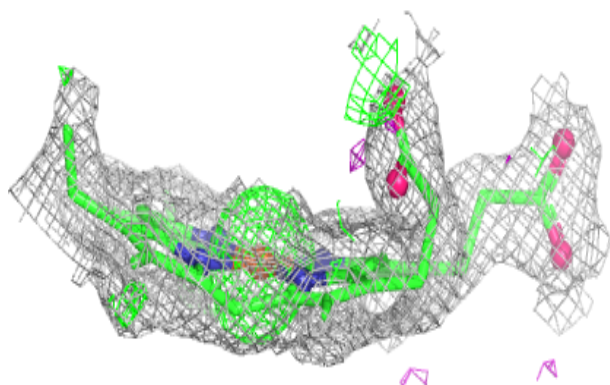
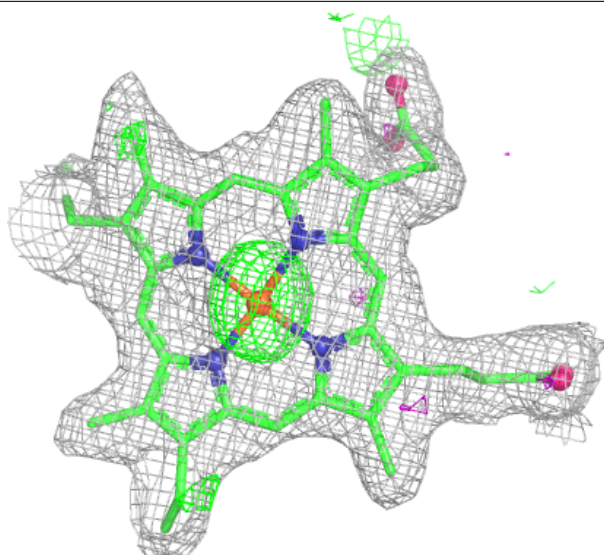
Electron density around HEC F 1001:

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



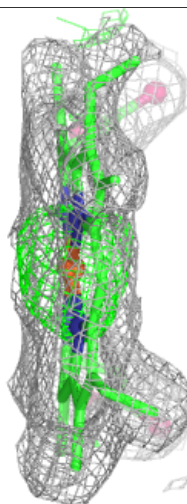
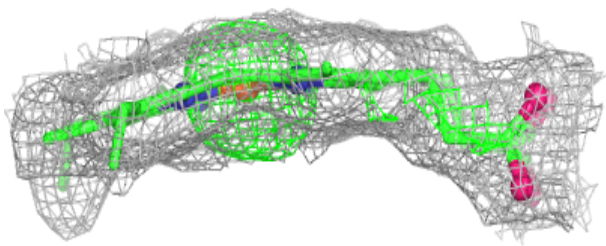
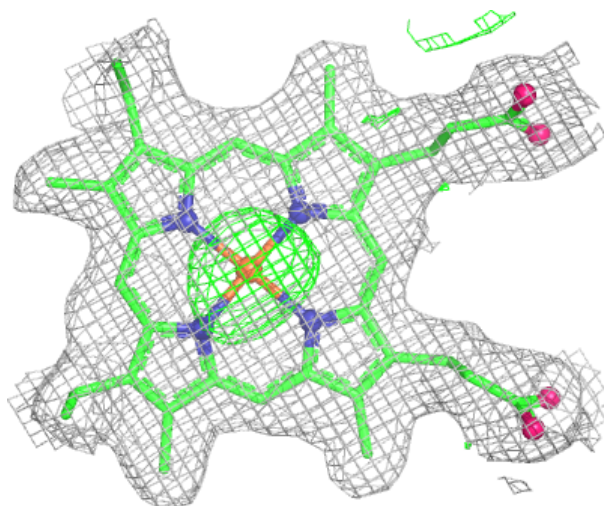
Electron density around HEC F 1003:

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



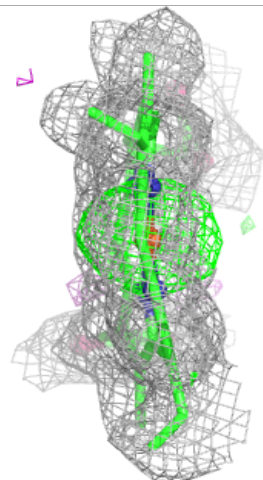
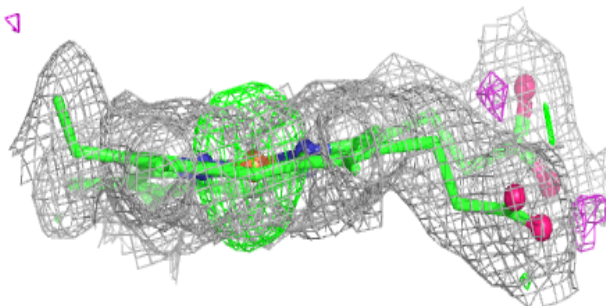
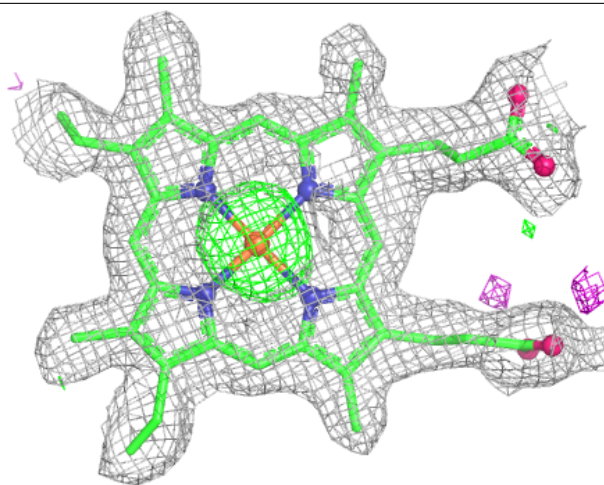
Electron density around HEC G 1003:

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



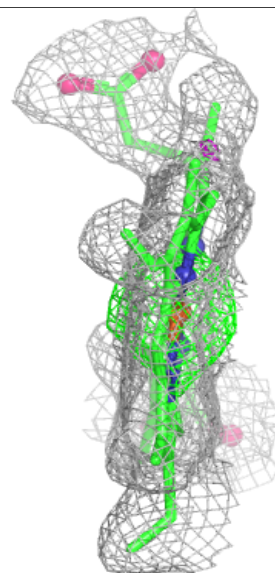
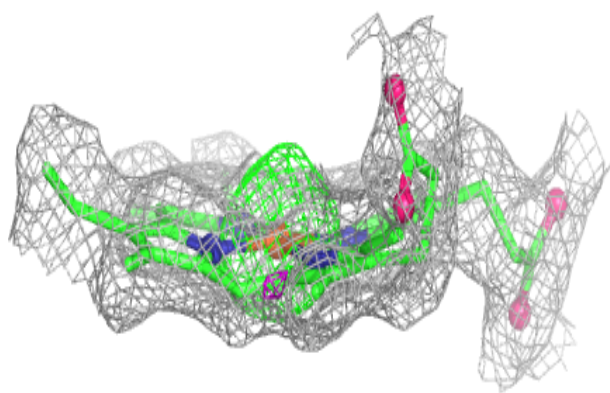
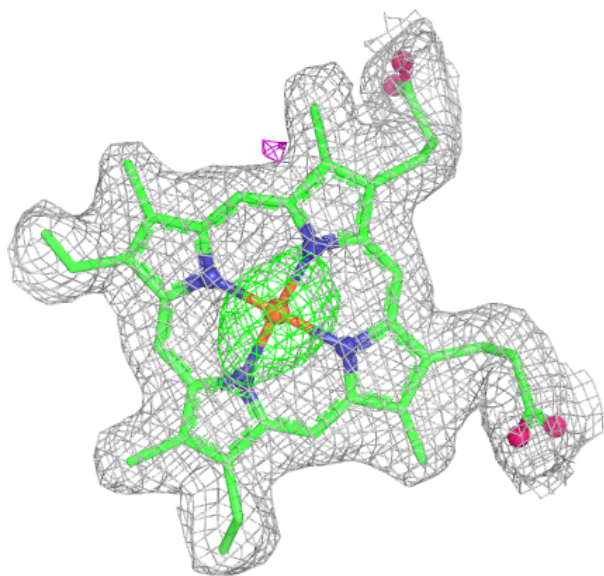
Electron density around HEC H 1004:

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



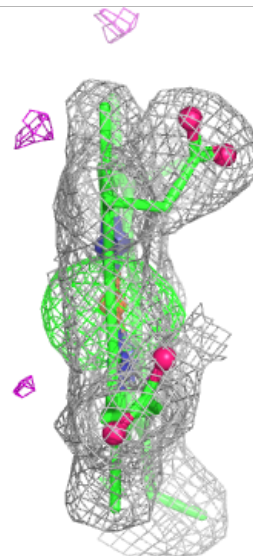
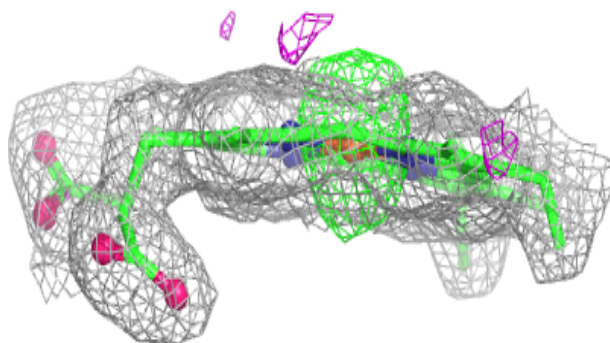
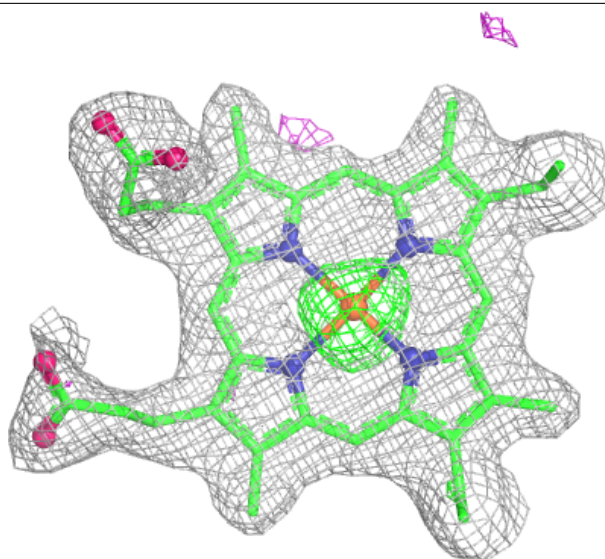
Electron density around HEC H 1005:

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



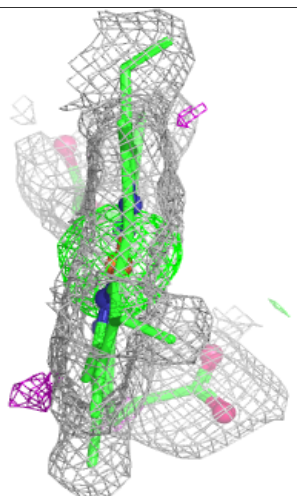
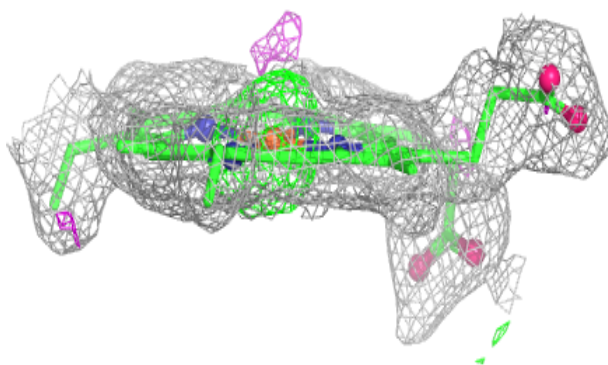
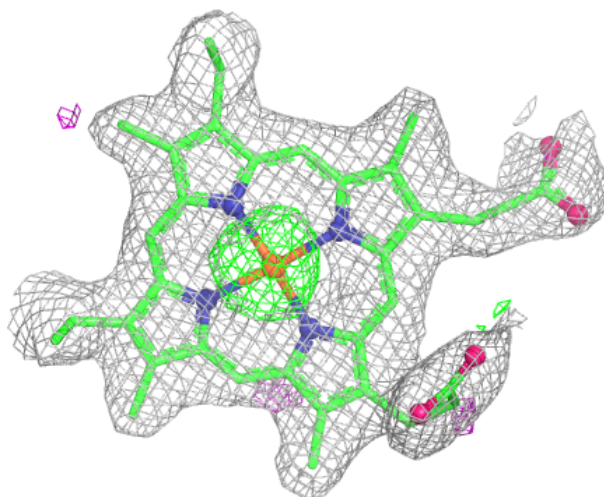
Electron density around HEC I 1001:

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



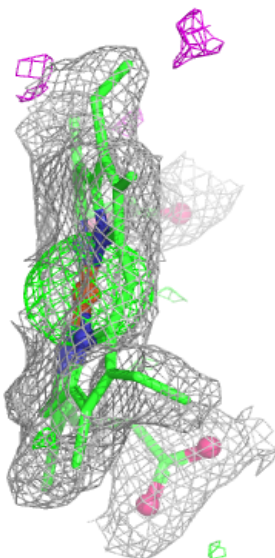
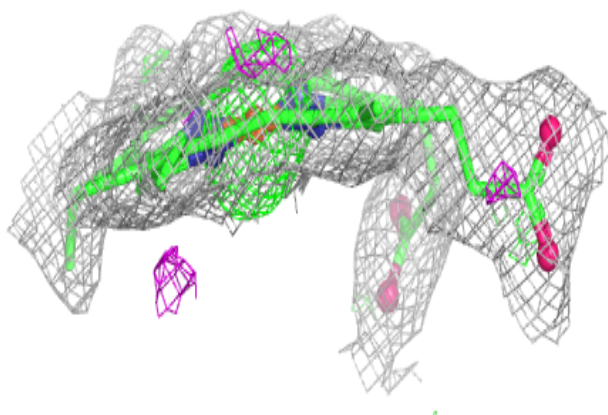
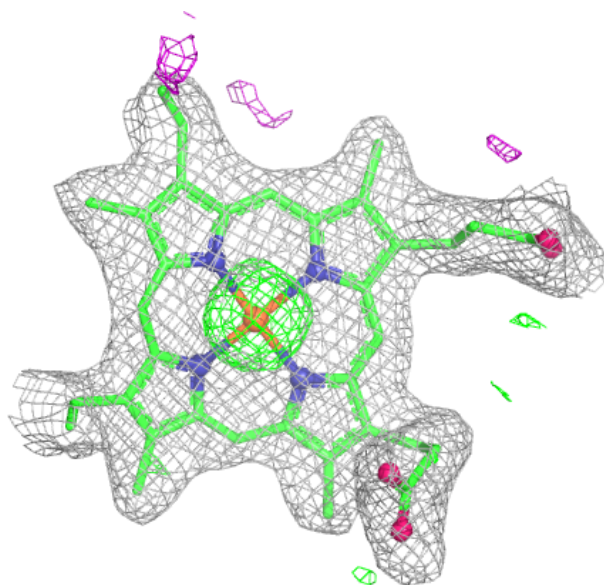
Electron density around HEC I 1002:

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



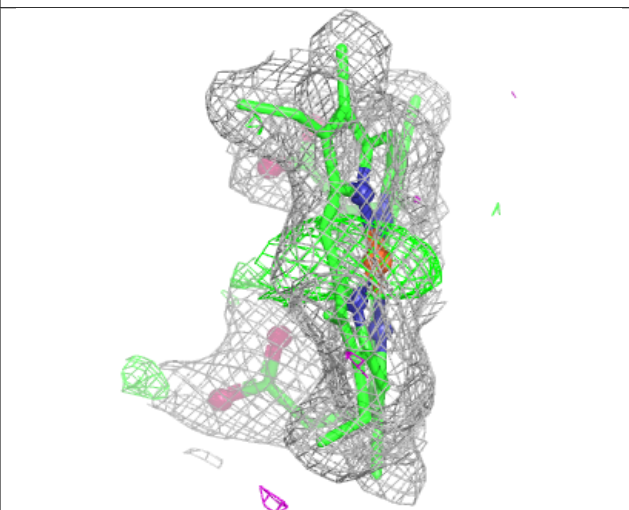
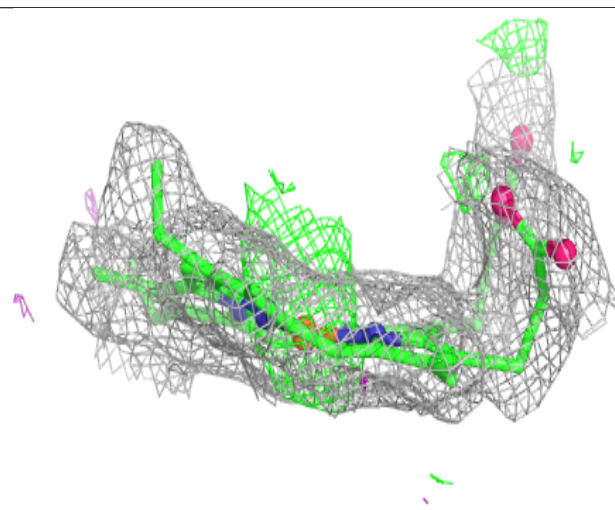
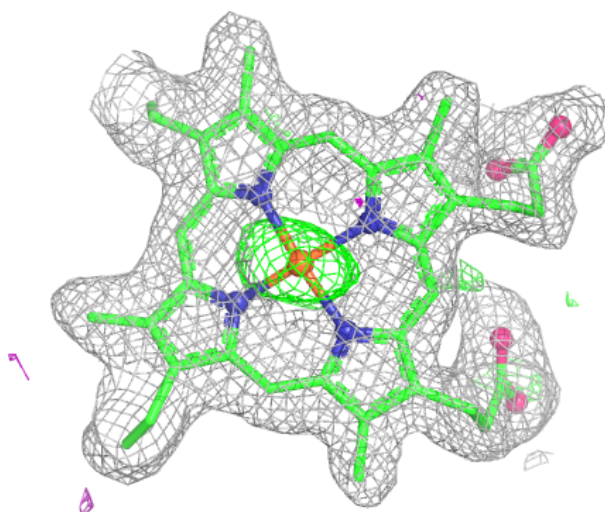
Electron density around HEC I 1003:

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



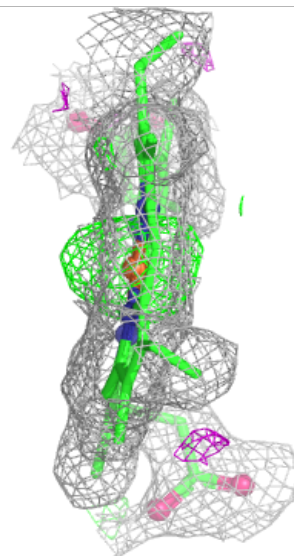
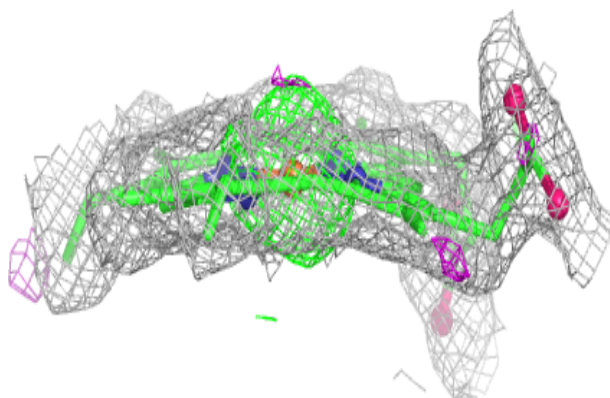
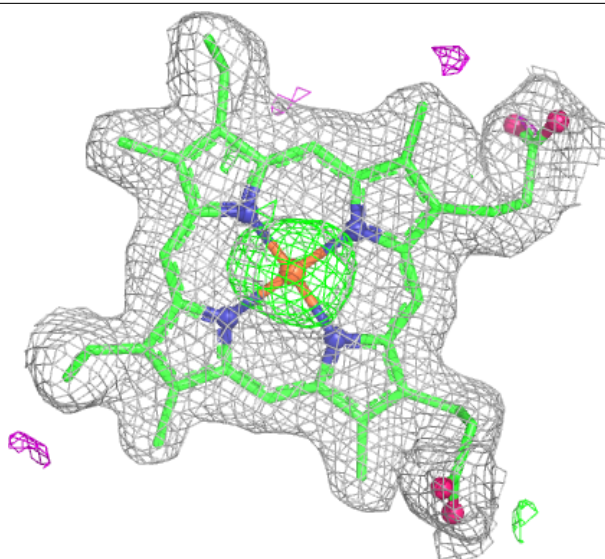
Electron density around HEC K 1001:

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



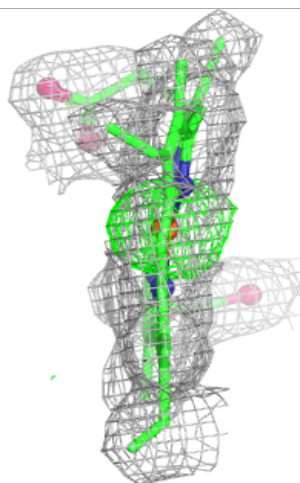
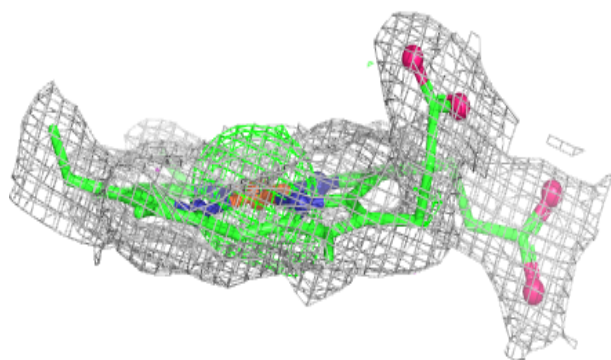
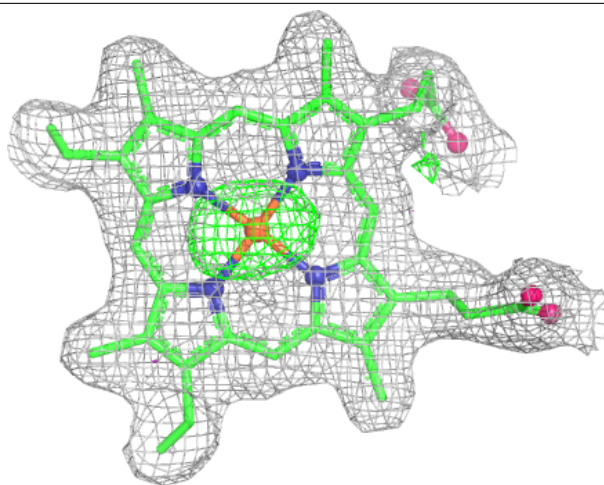
Electron density around HEC B 1005:

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



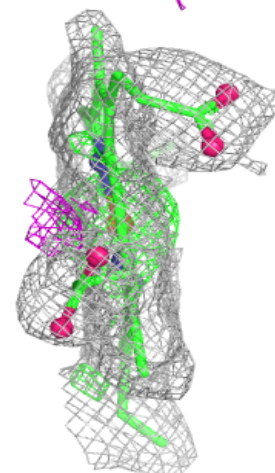
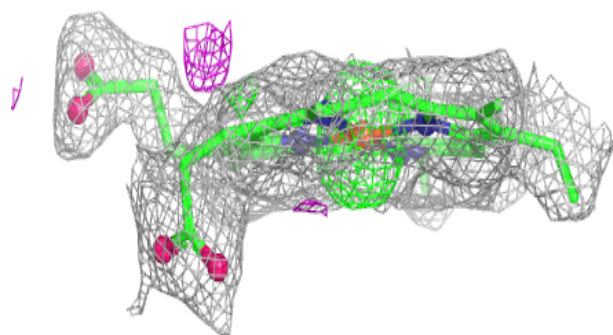
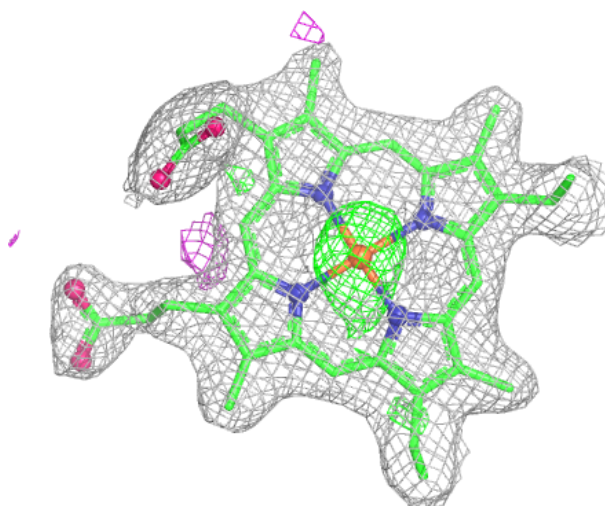
Electron density around HEC A 1002:

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



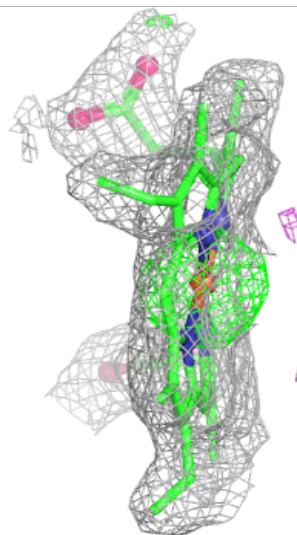
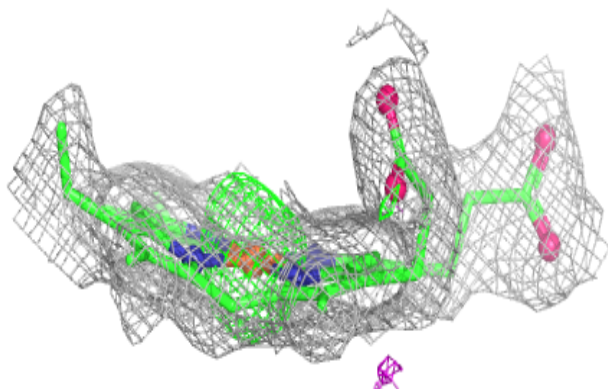
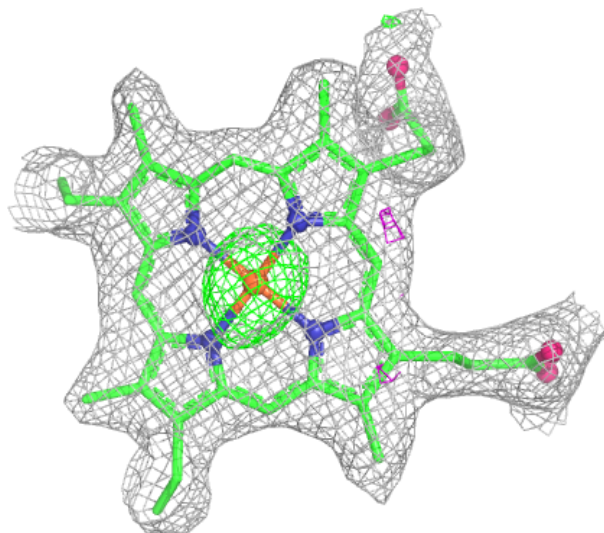
Electron density around HEC C 1002:

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



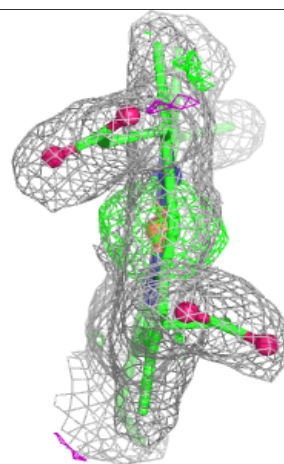
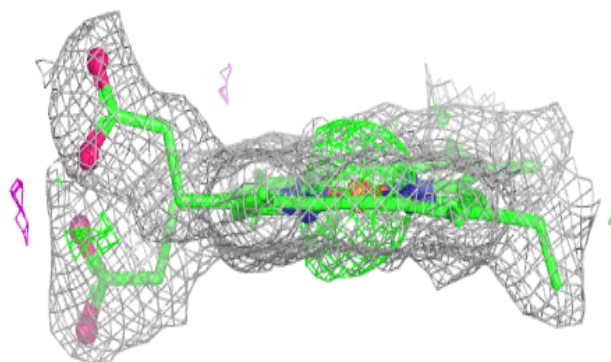
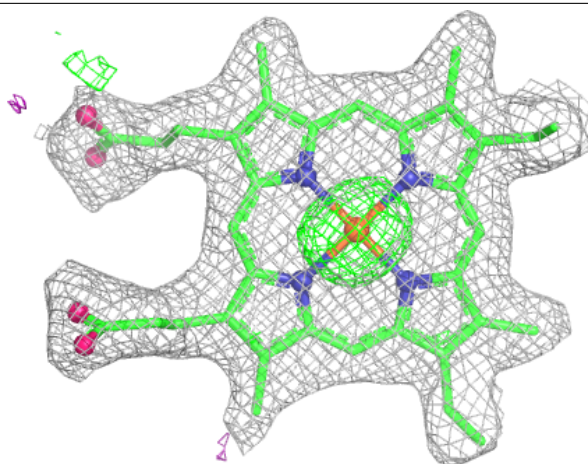
Electron density around HEC C 1003:

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



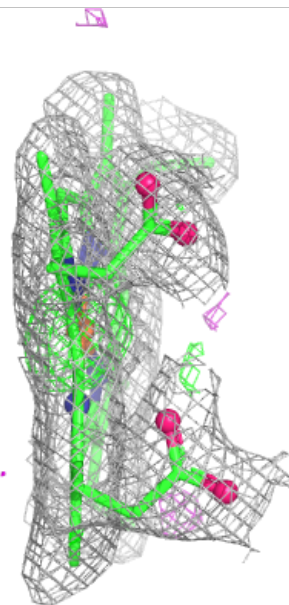
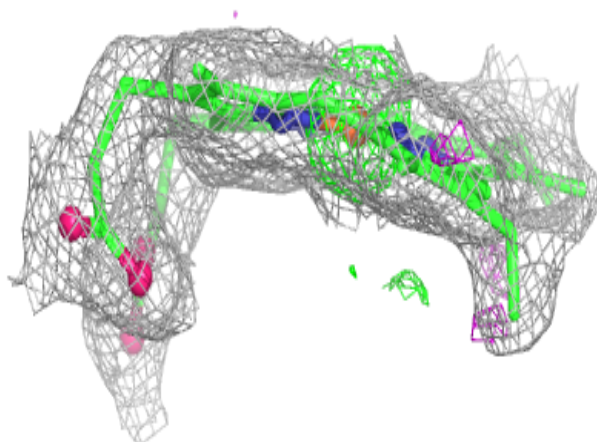
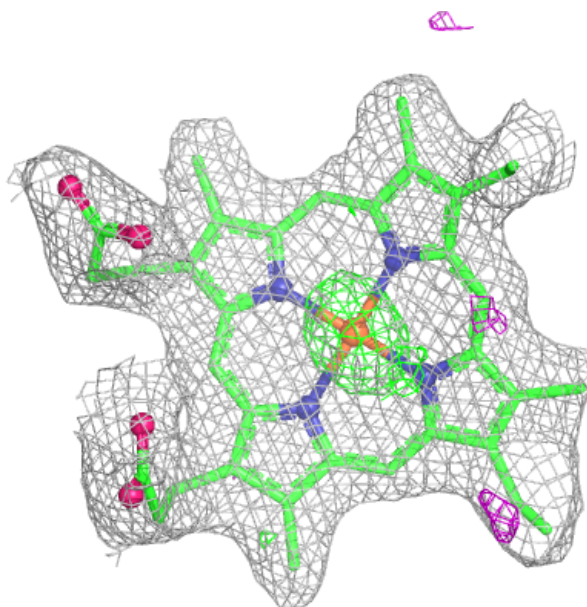
Electron density around HEC I 1004:

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



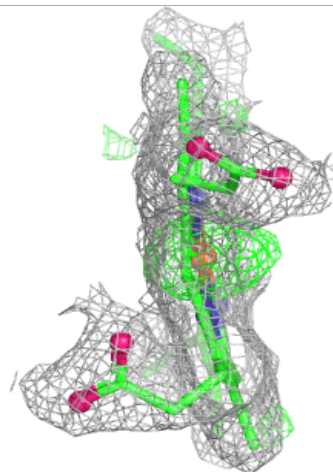
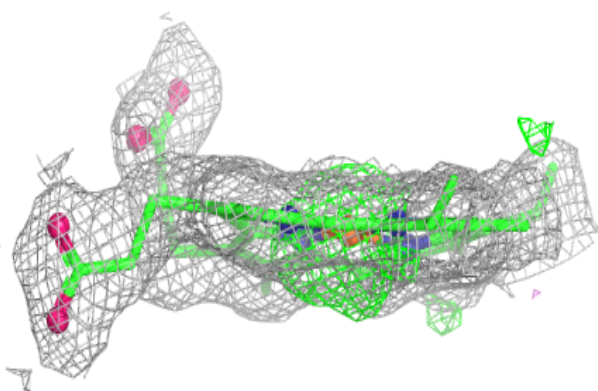
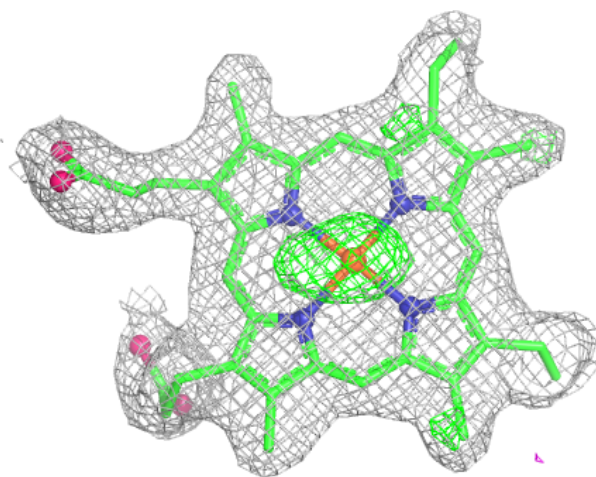
Electron density around HEC J 1001:

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



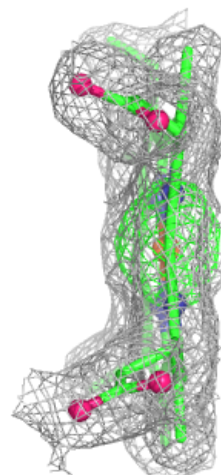
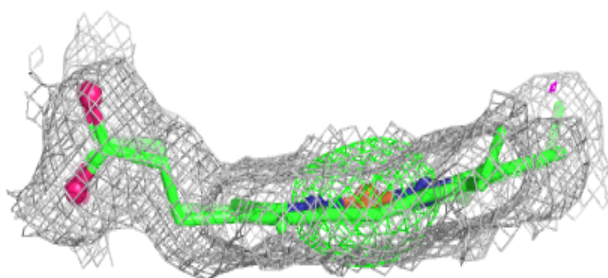
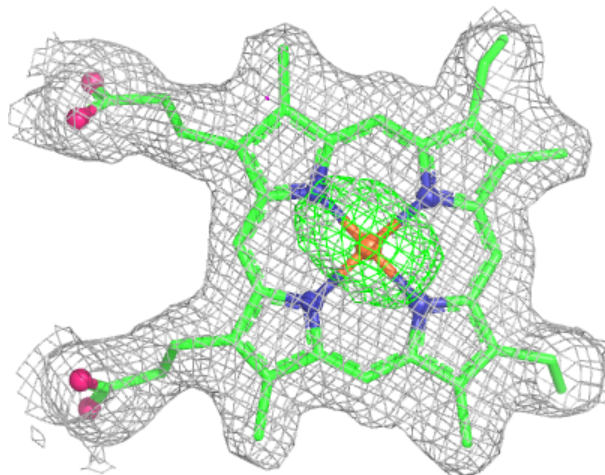
Electron density around HEC J 1002:

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



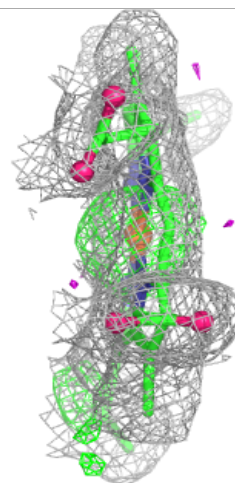
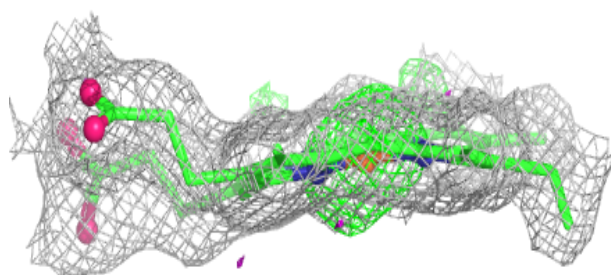
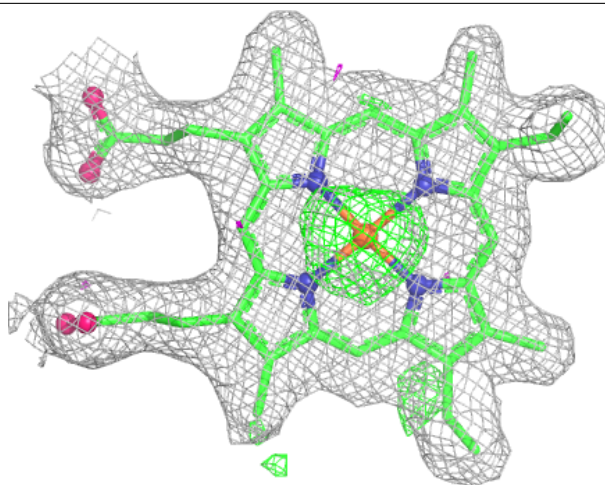
Electron density around HEC J 1003:

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



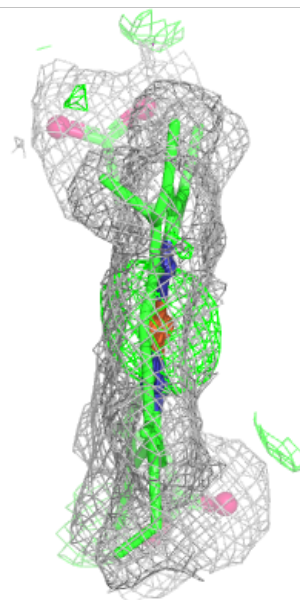
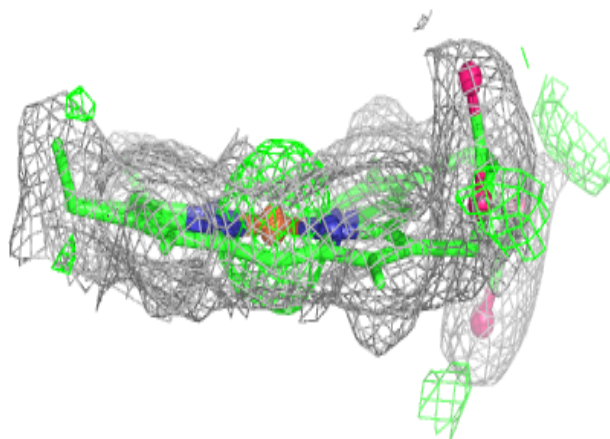
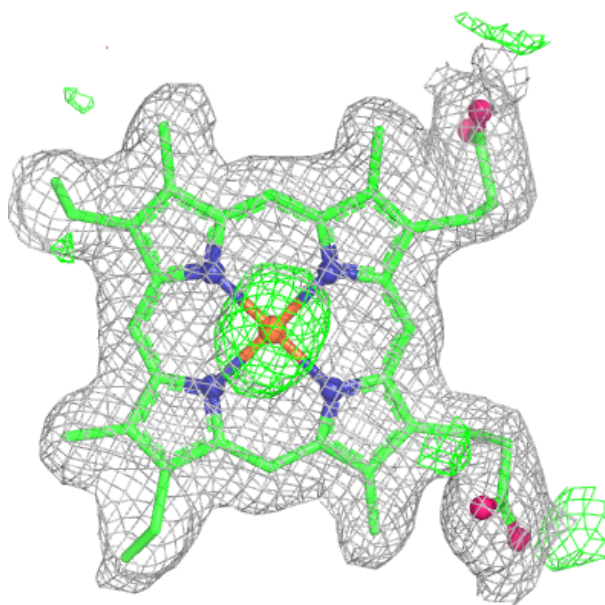
Electron density around HEC J 1004:

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



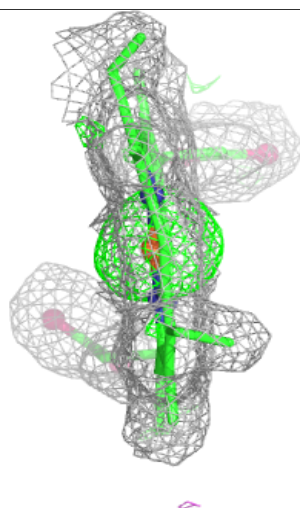
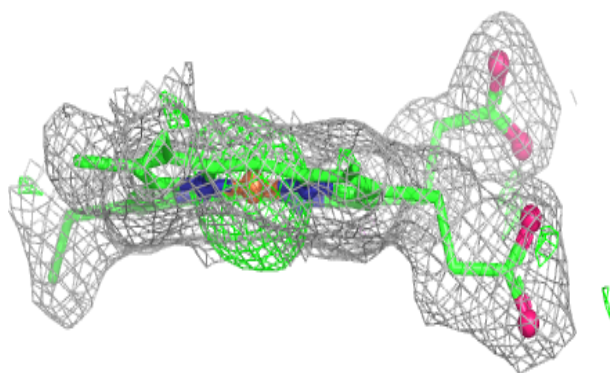
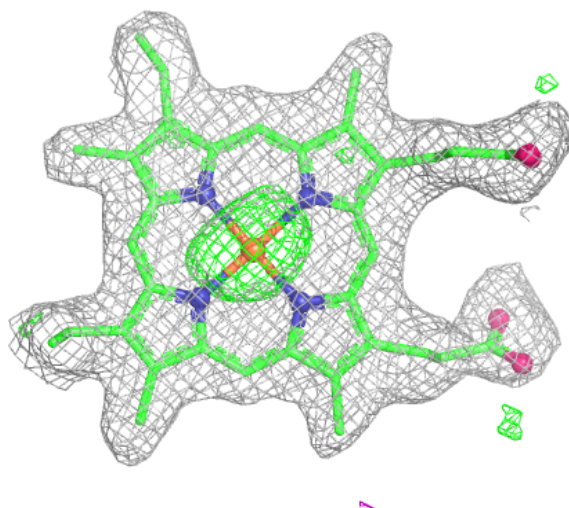
Electron density around HEC J 1005:

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



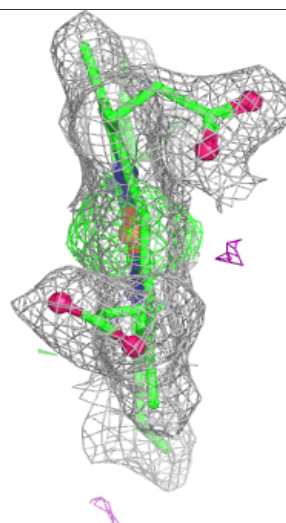
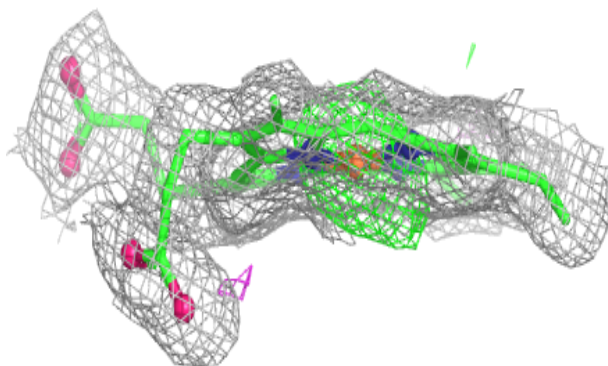
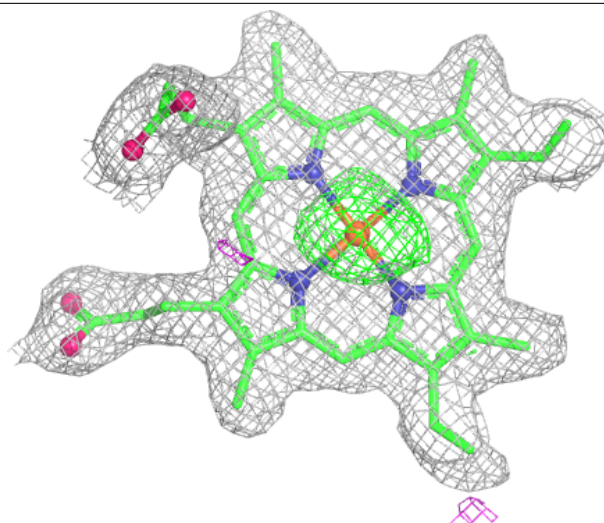
Electron density around HEC C 1004:

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



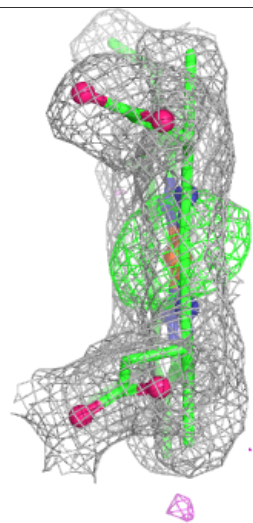
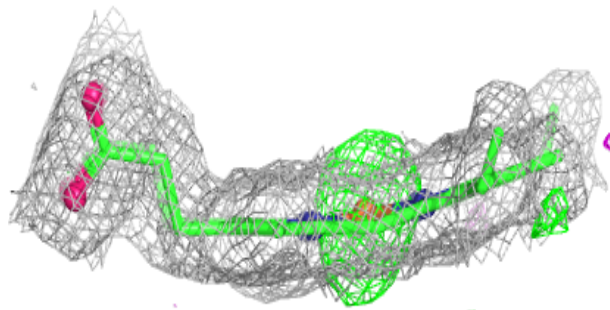
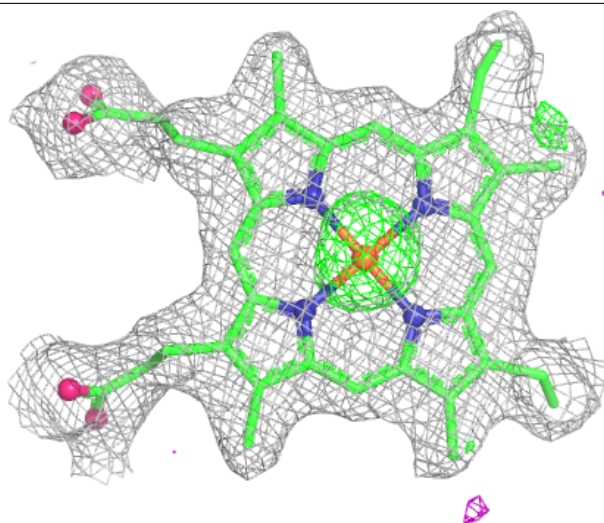
Electron density around HEC D 1002:

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



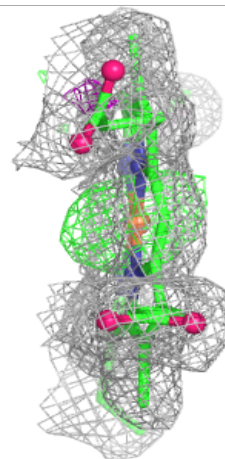
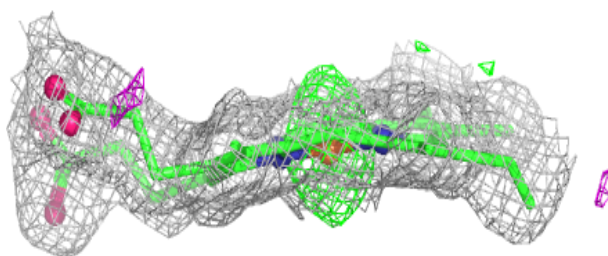
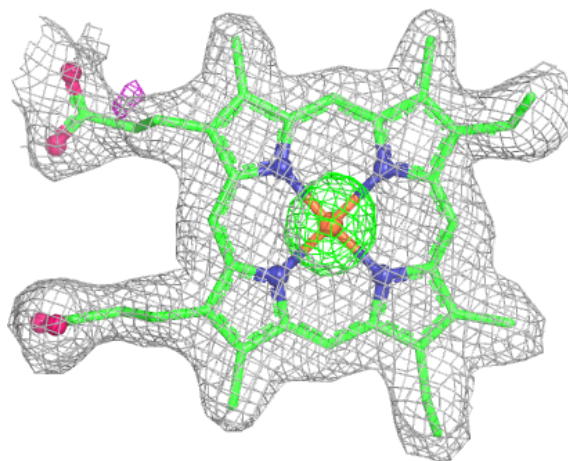
Electron density around HEC K 1003:

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



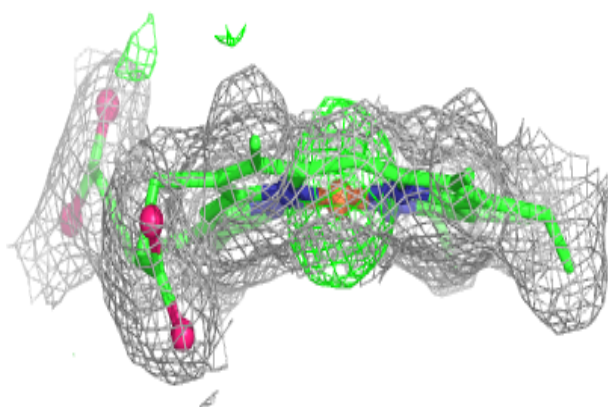
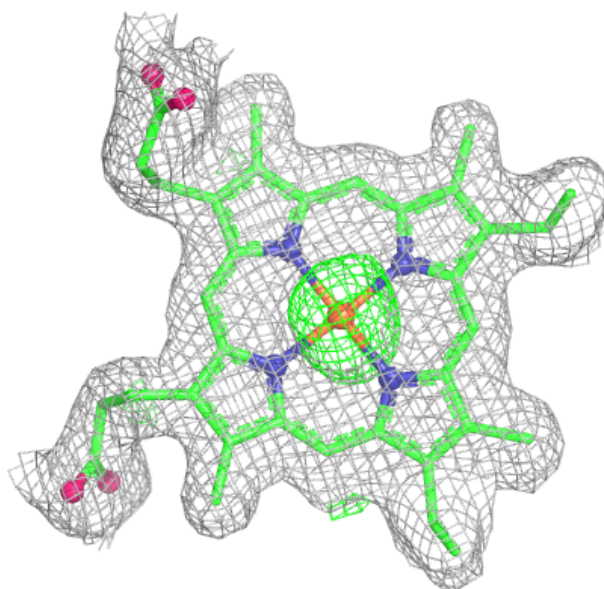
Electron density around HEC K 1004:

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



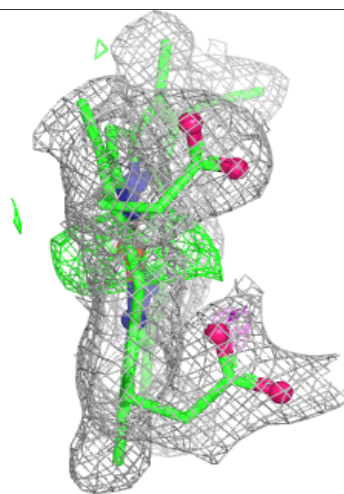
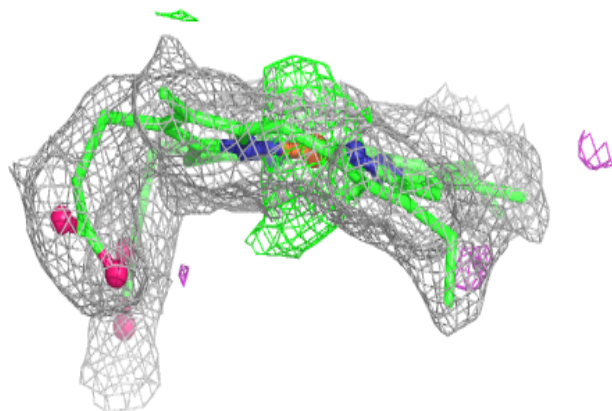
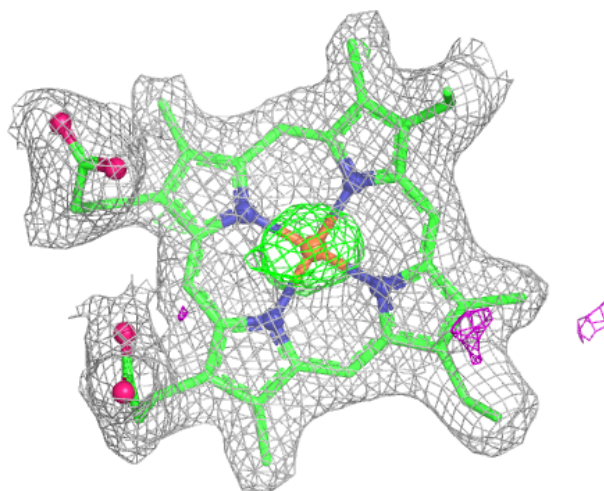
Electron density around HEC D 1005:

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



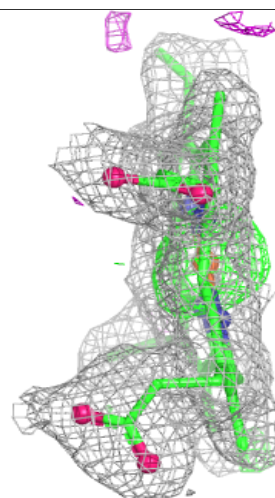
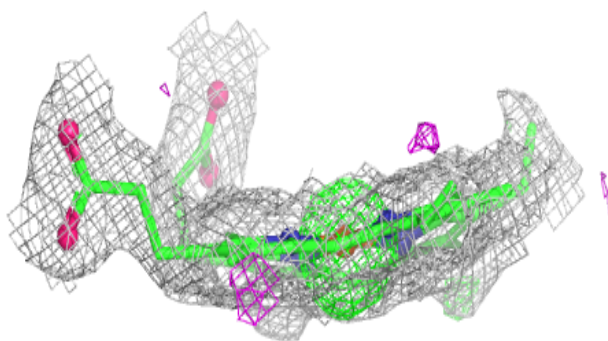
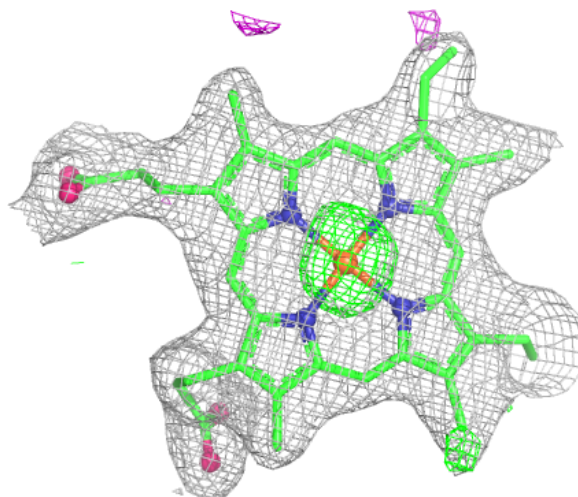
Electron density around HEC E 1001:

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



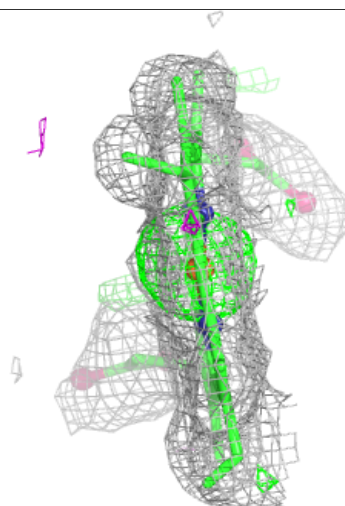
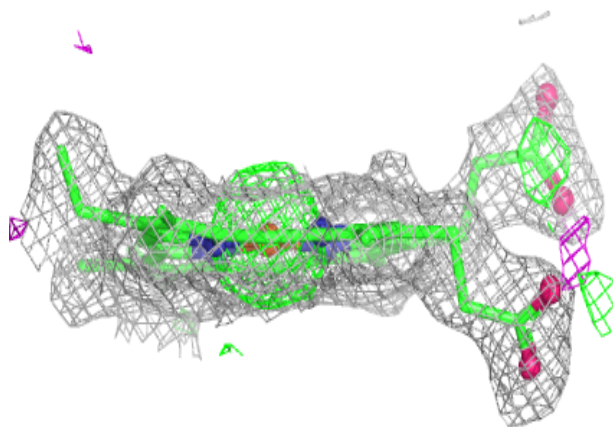
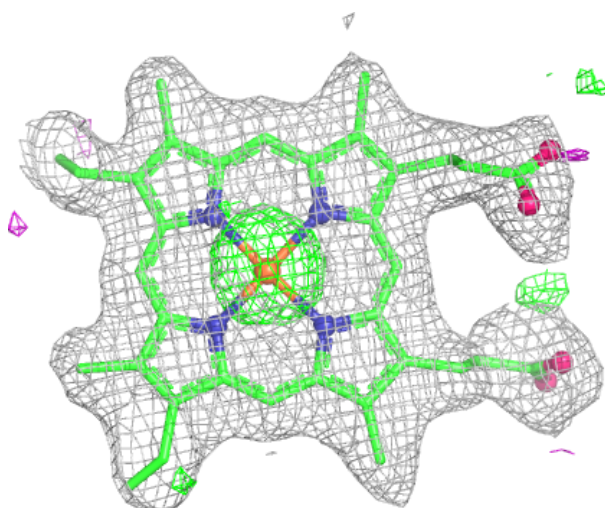
Electron density around HEC L 1003:

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



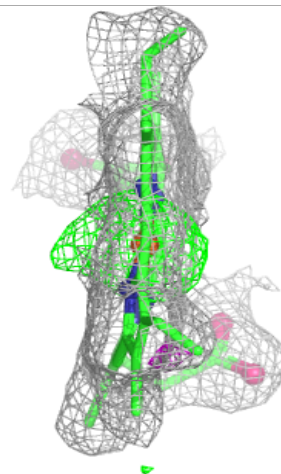
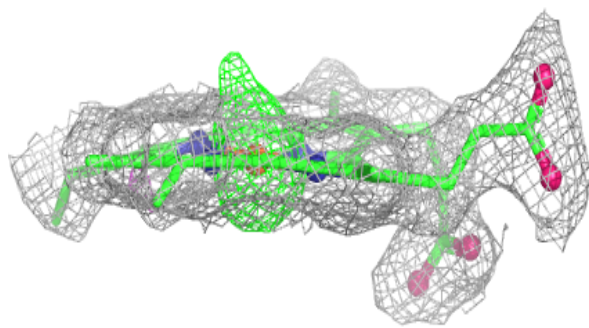
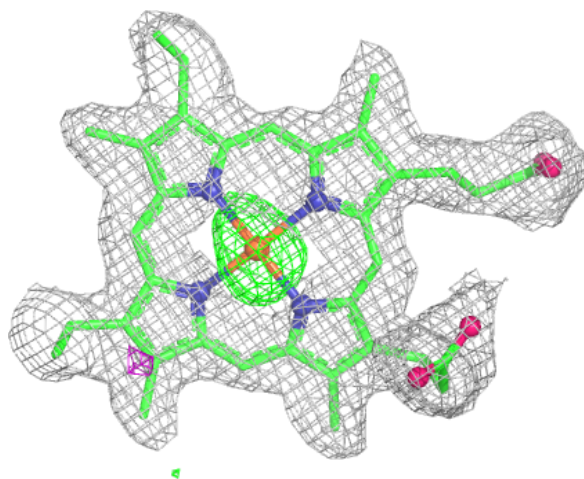
Electron density around HEC L 1004:

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



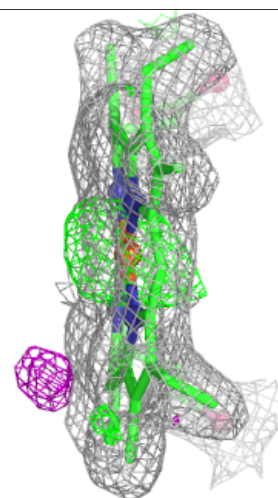
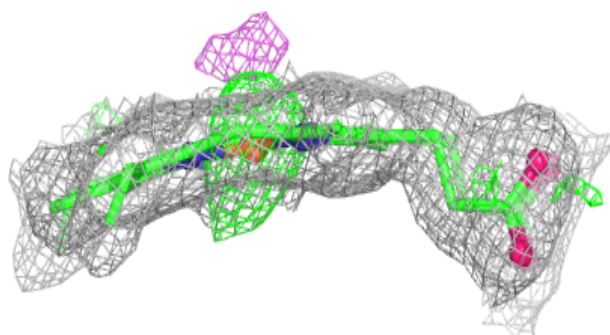
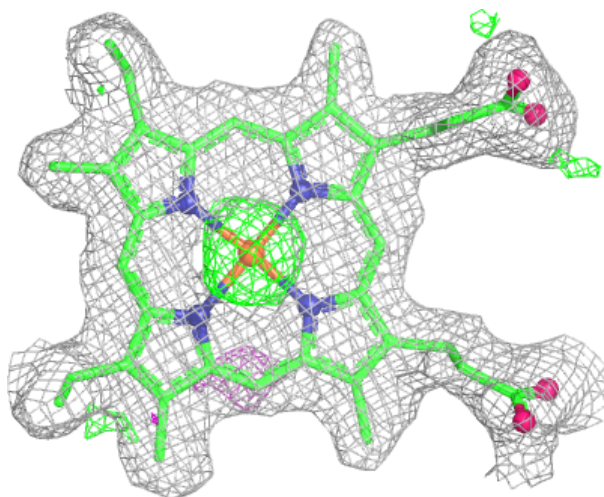
Electron density around HEC E 1002:

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



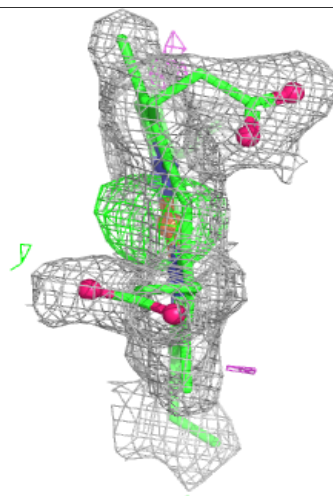
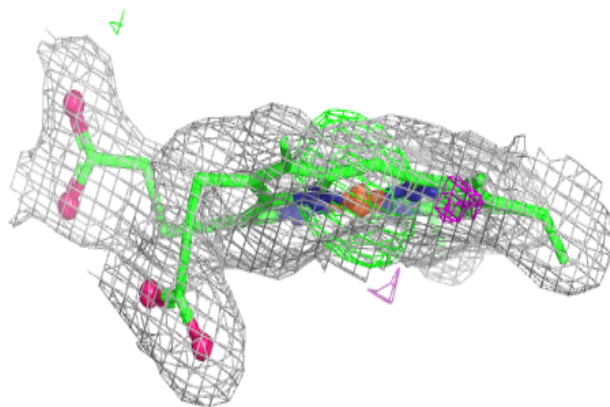
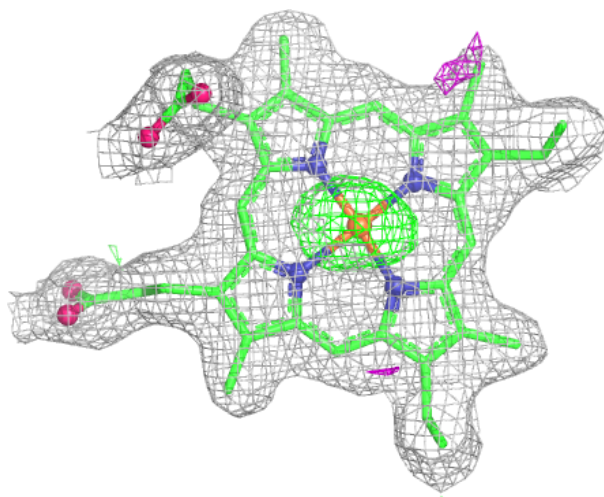
Electron density around HEC E 1003:

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



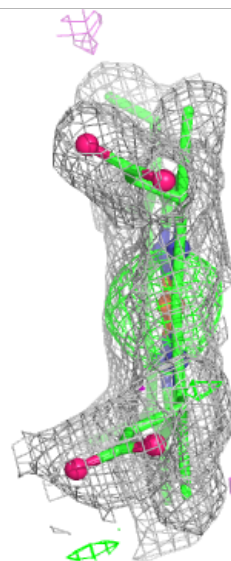
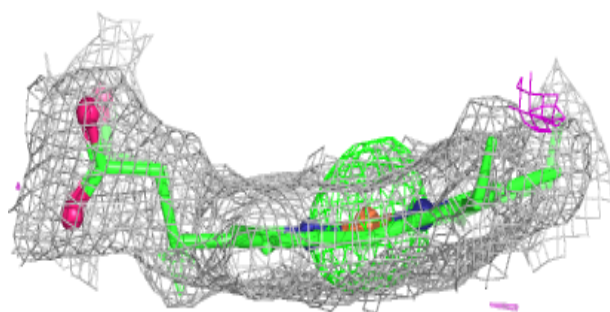
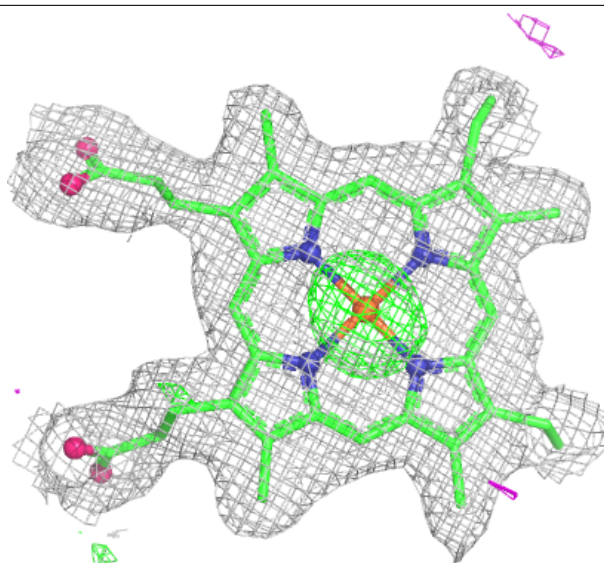
Electron density around HEC M 1002:

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



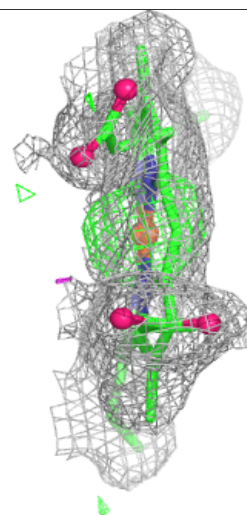
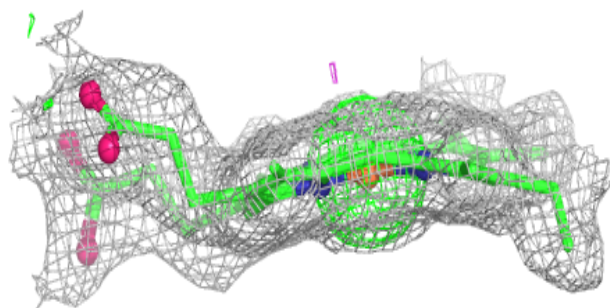
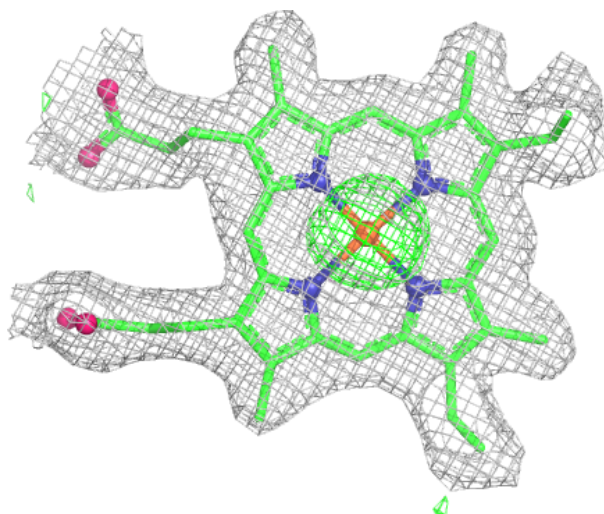
Electron density around HEC M 1003:

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



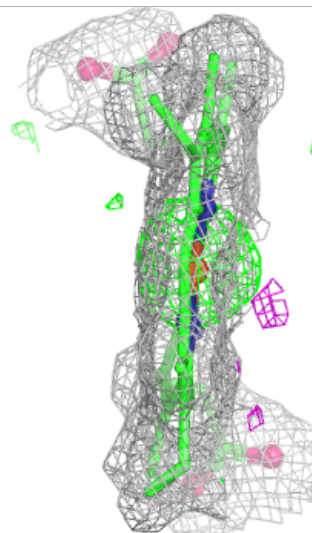
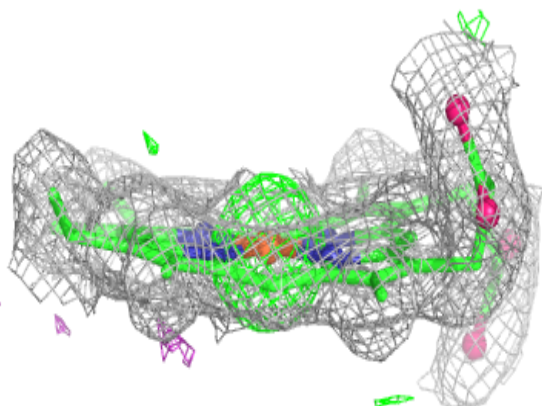
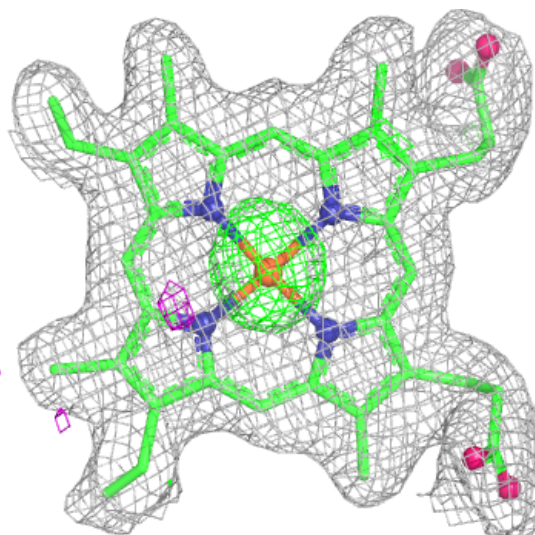
Electron density around HEC M 1004:

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



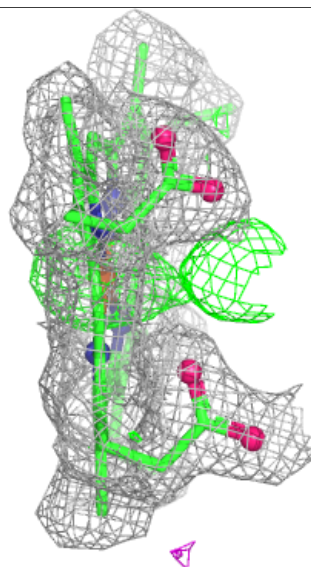
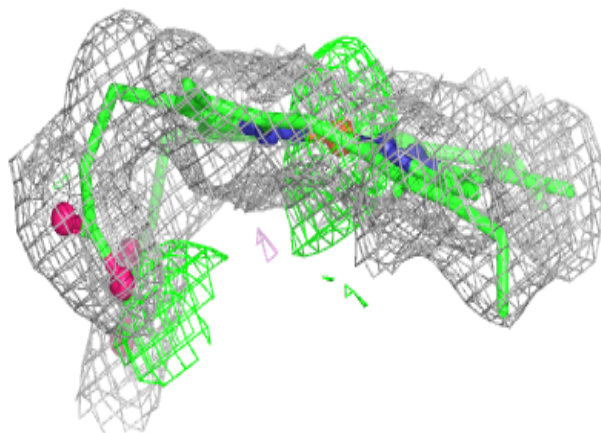
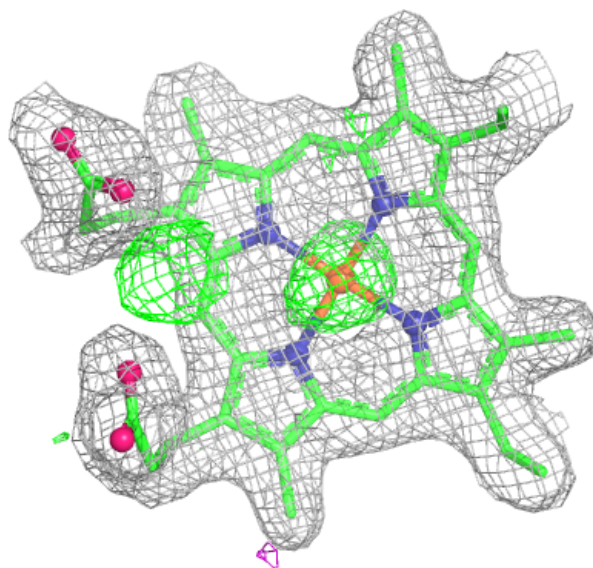
Electron density around HEC M 1005:

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



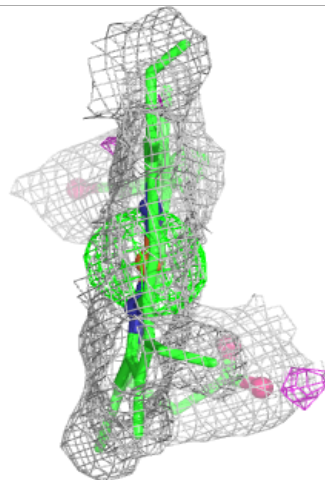
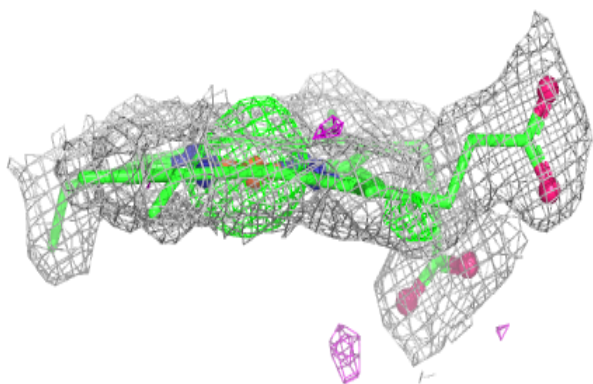
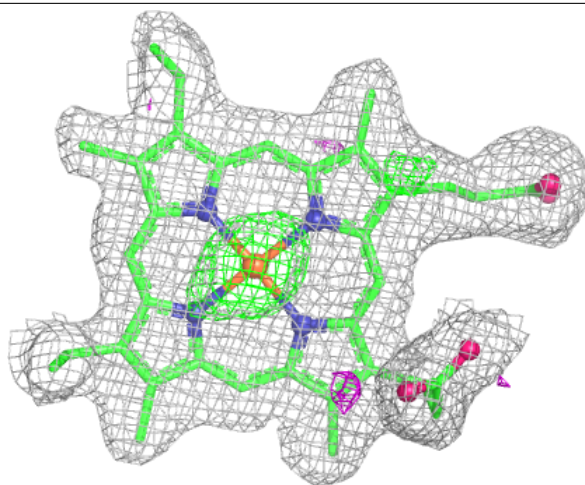
Electron density around HEC N 1001:

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



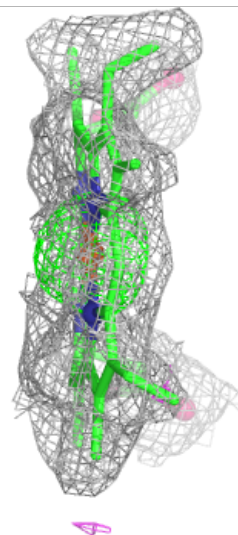
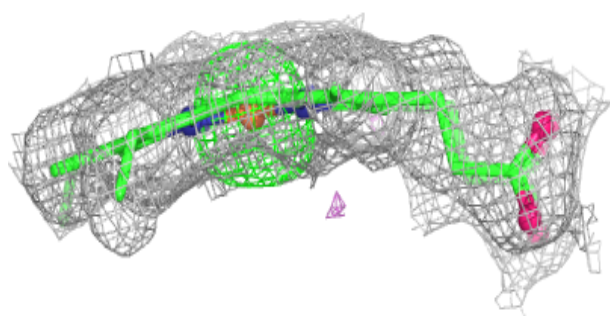
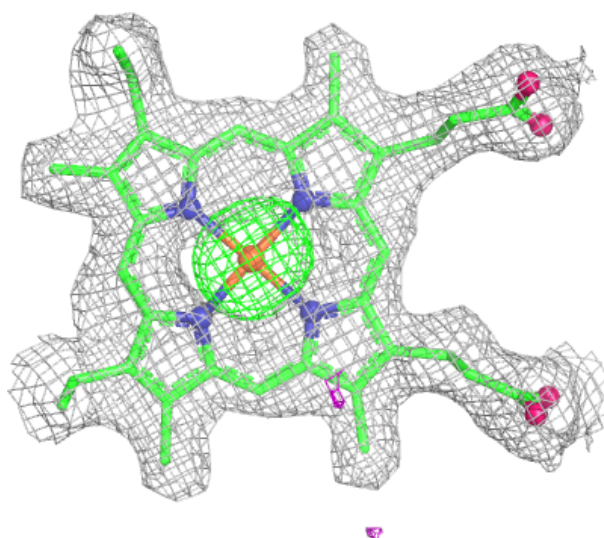
Electron density around HEC N 1002:

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



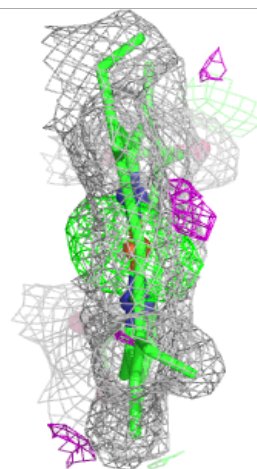
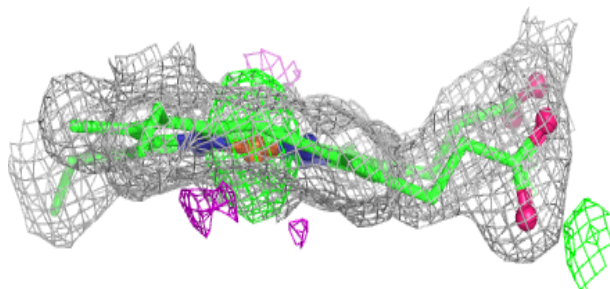
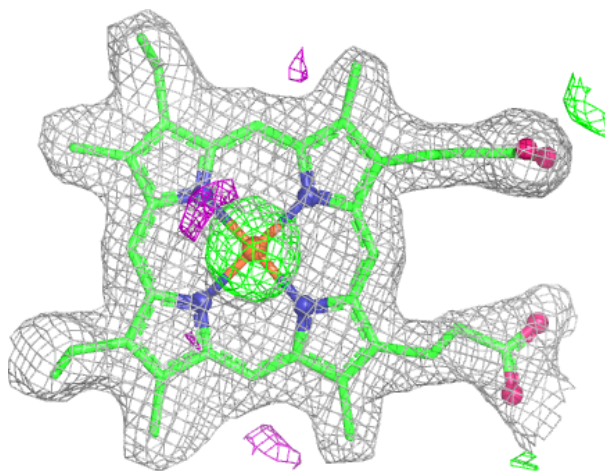
Electron density around HEC N 1003:

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



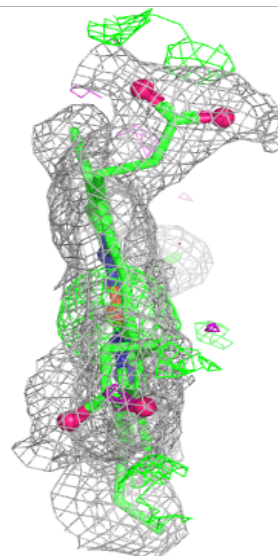
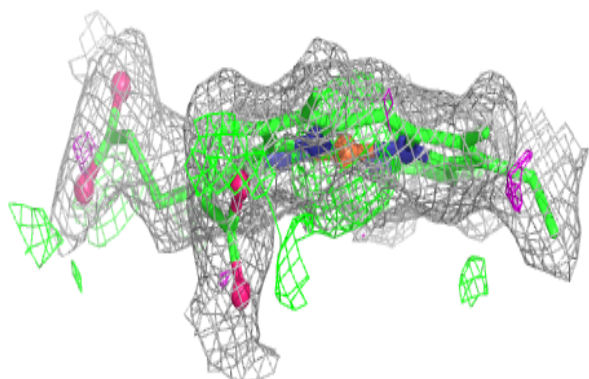
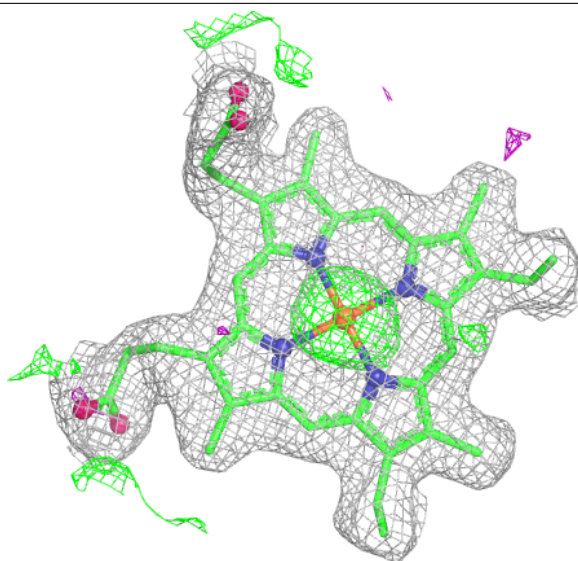
Electron density around HEC E 1004:

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



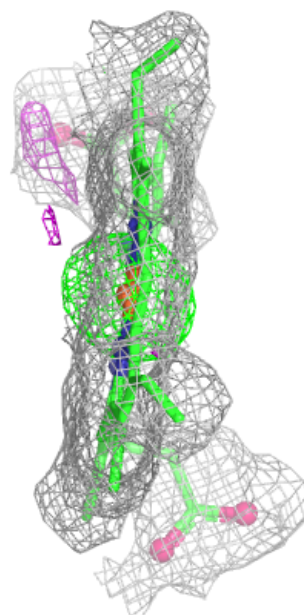
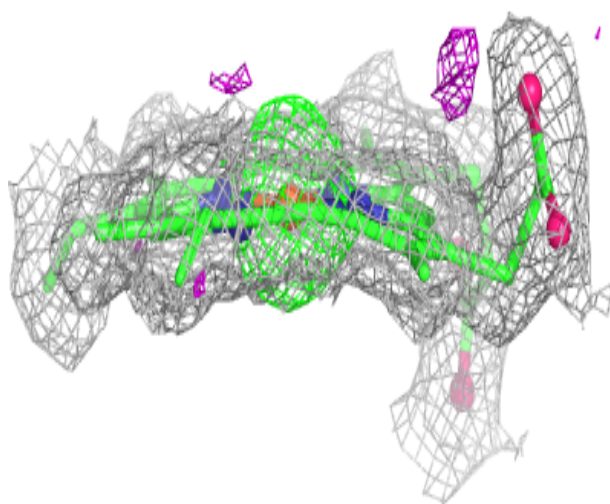
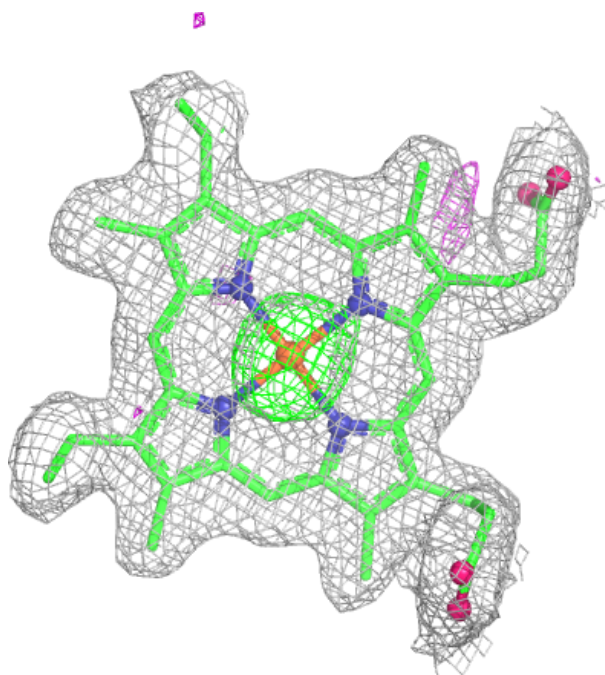
Electron density around HEC N 1005:

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



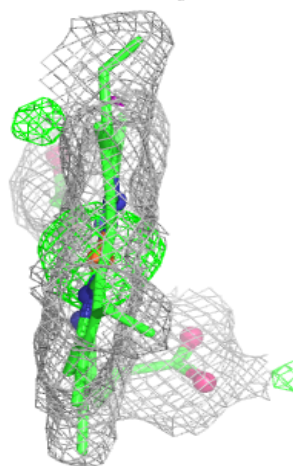
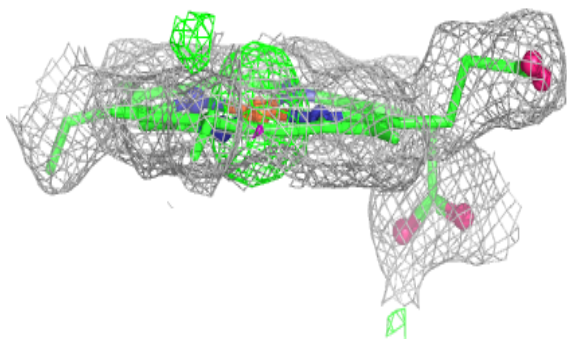
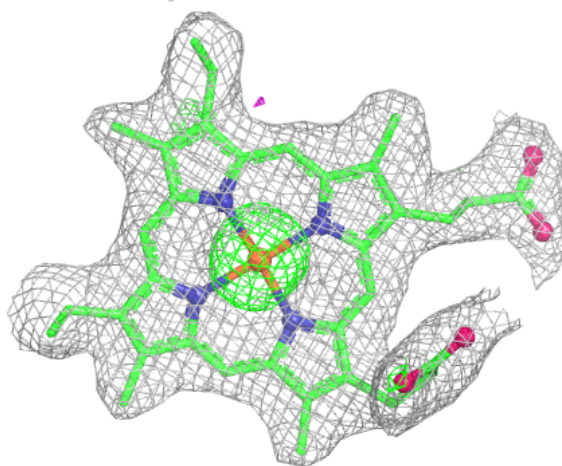
Electron density around HEC A 1005:

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



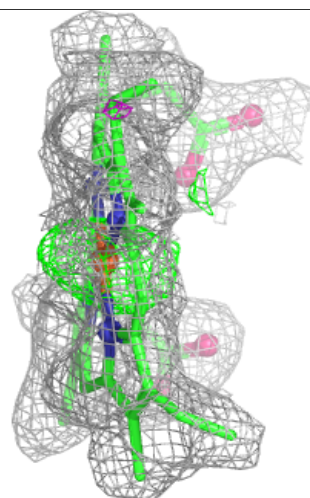
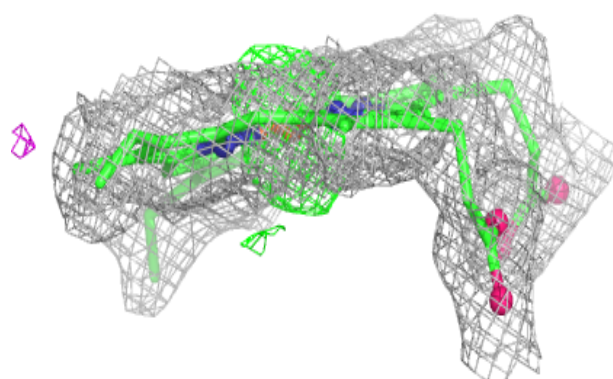
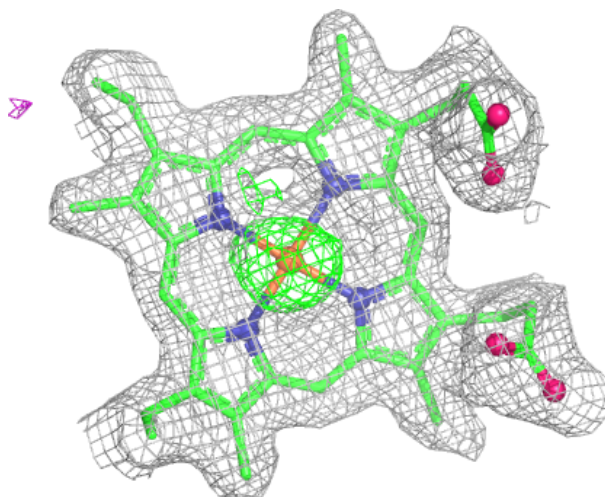
Electron density around HEC O 1002:

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



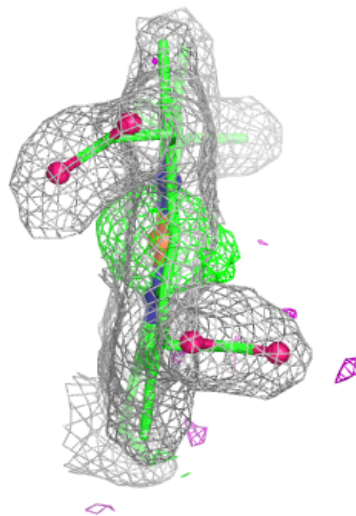
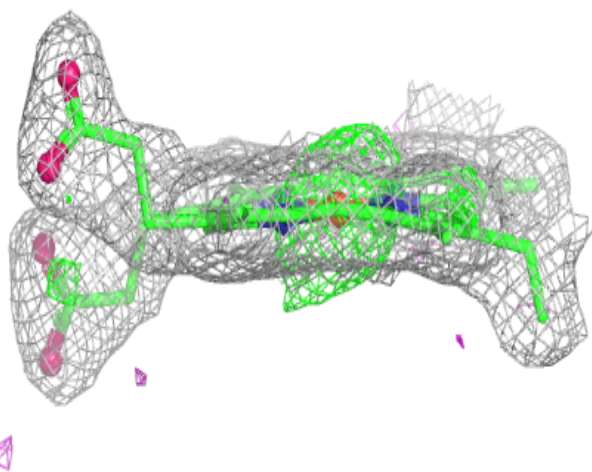
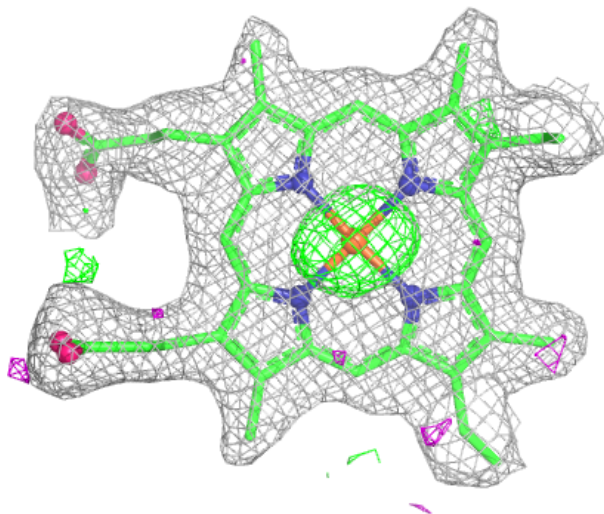
Electron density around HEC B 1001:

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



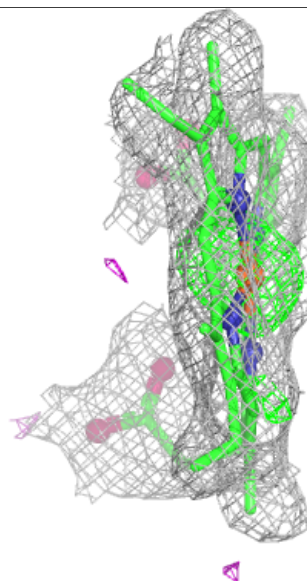
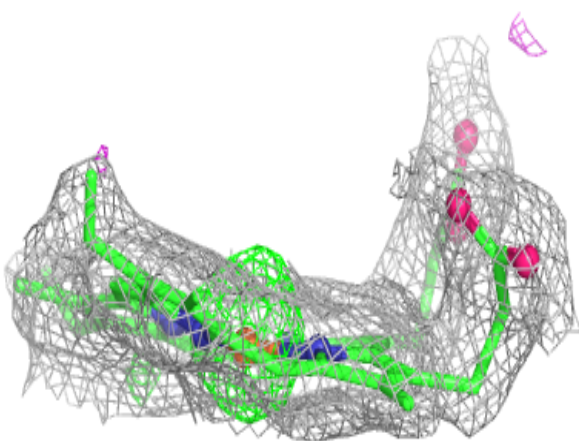
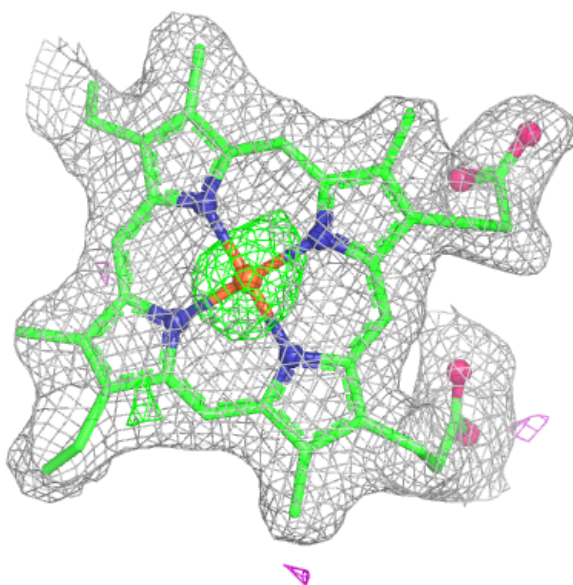
Electron density around HEC O 1004:

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



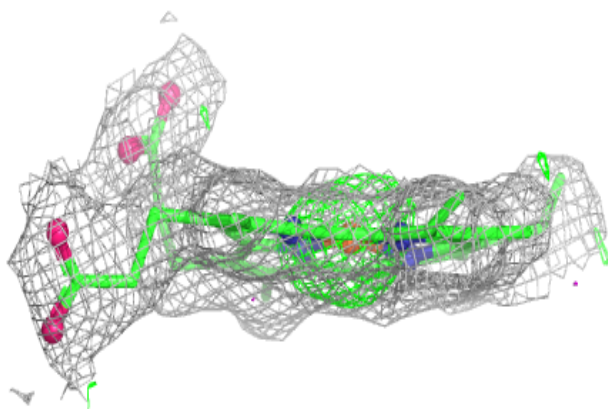
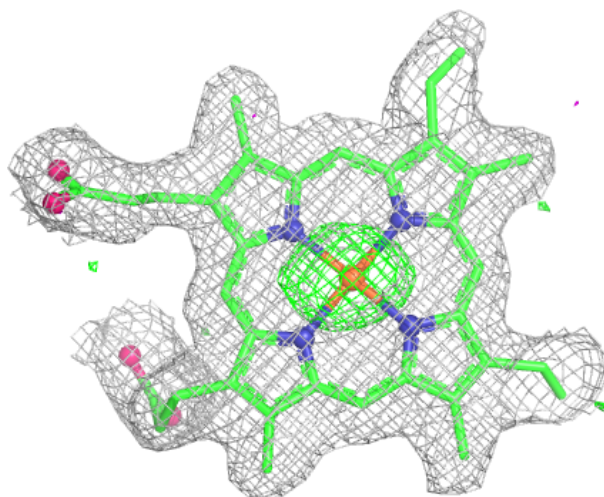
Electron density around HEC P 1001:

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



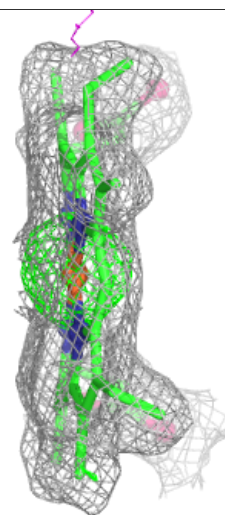
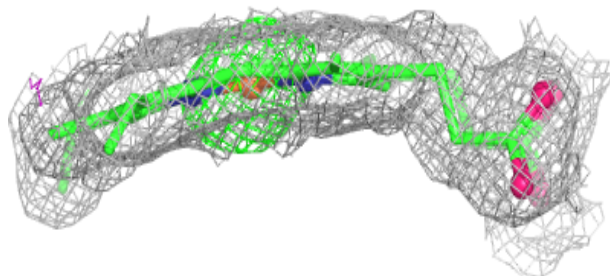
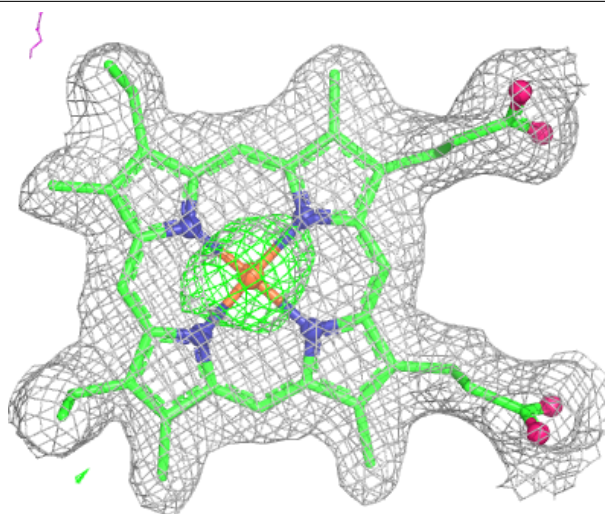
Electron density around HEC P 1002:

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



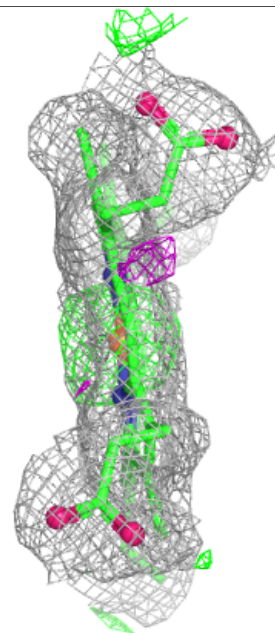
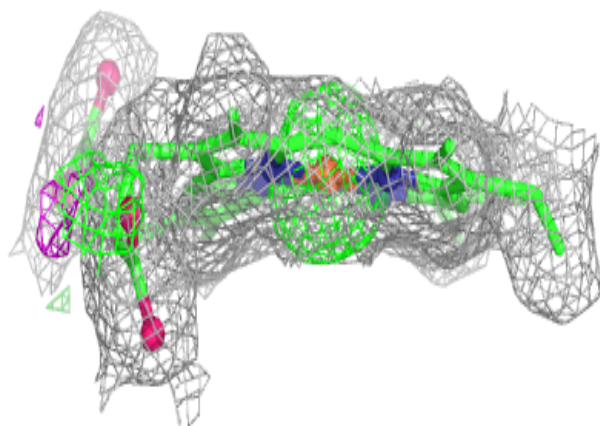
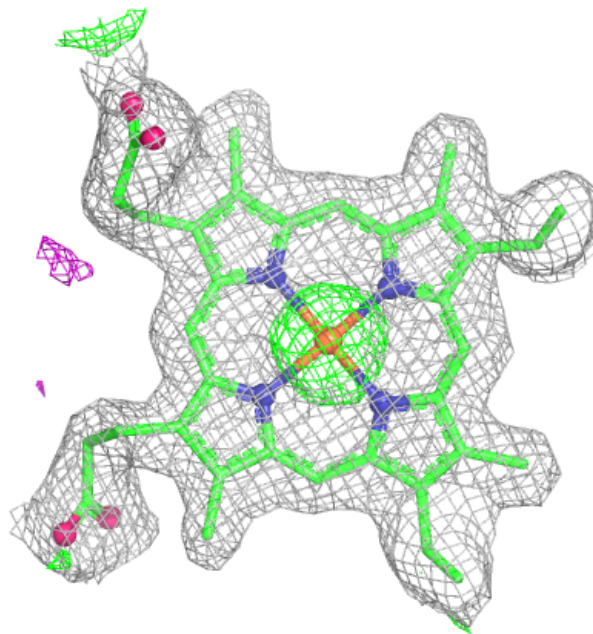
Electron density around HEC P 1003:

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



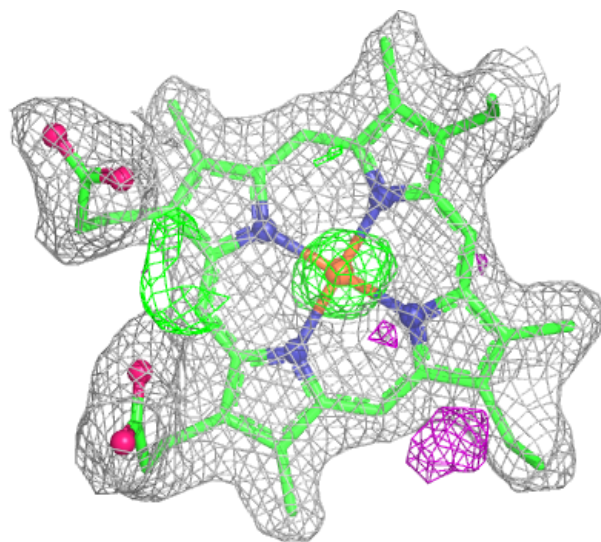
Electron density around HEC P 1005:

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

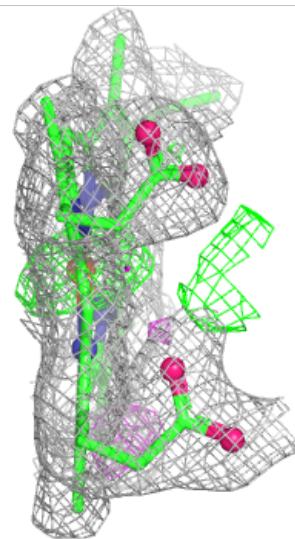
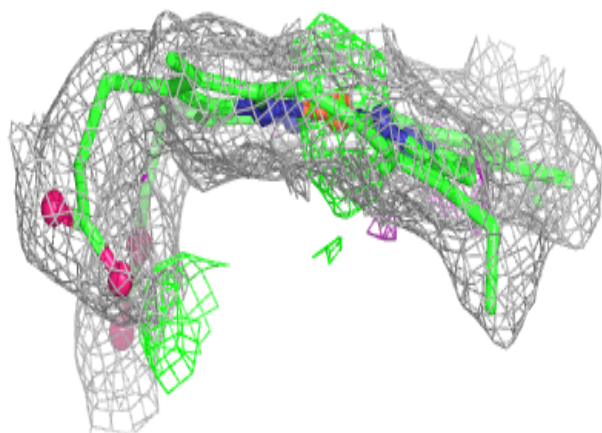


Electron density around HEC Q 1001:

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



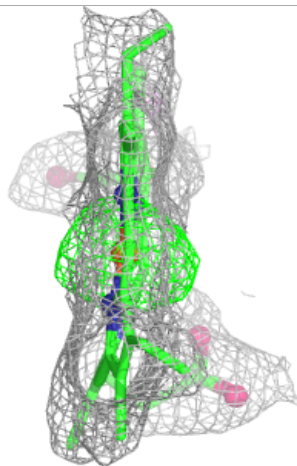
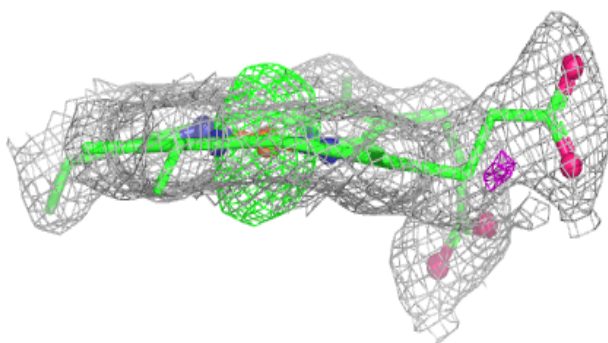
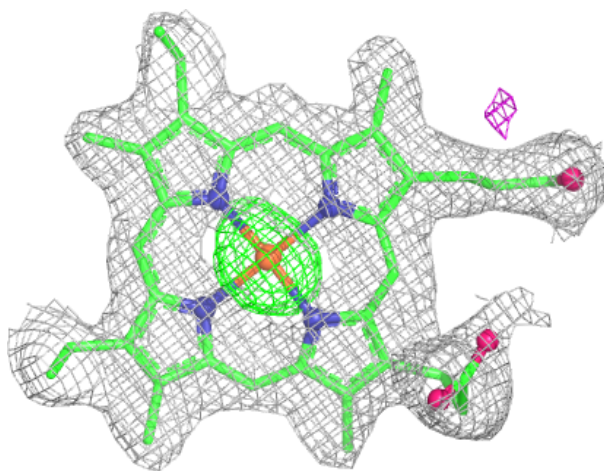
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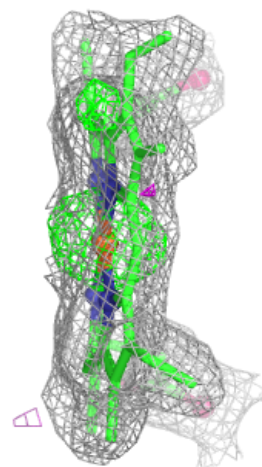
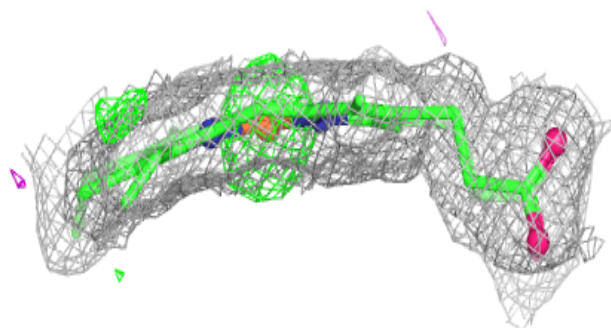
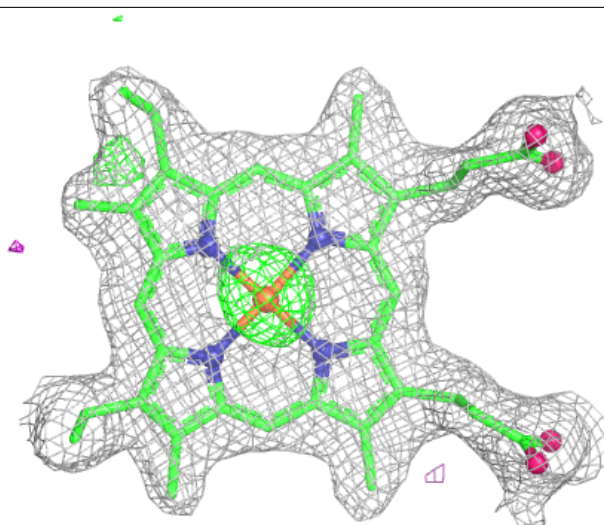
Electron density around HEC Q 1002:

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



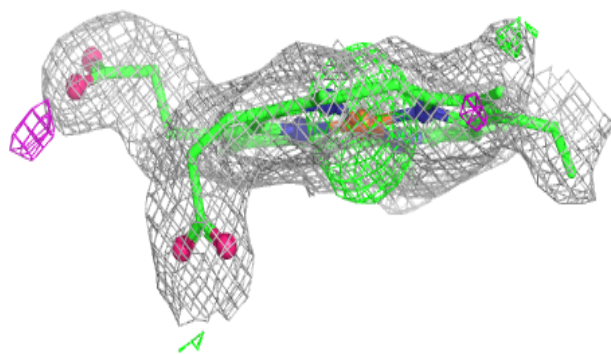
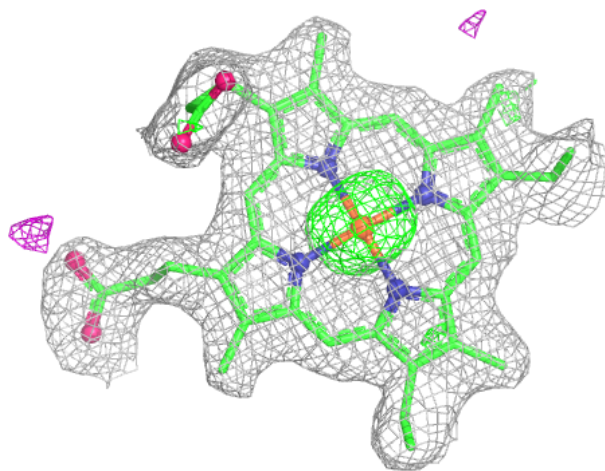
Electron density around HEC Q 1003:

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



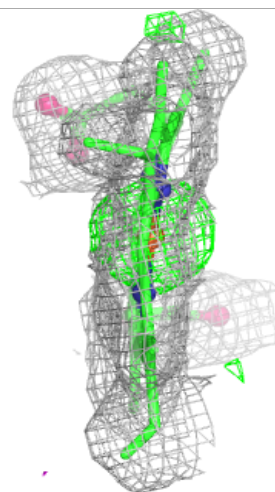
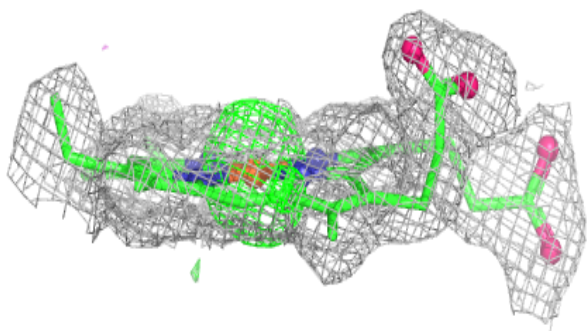
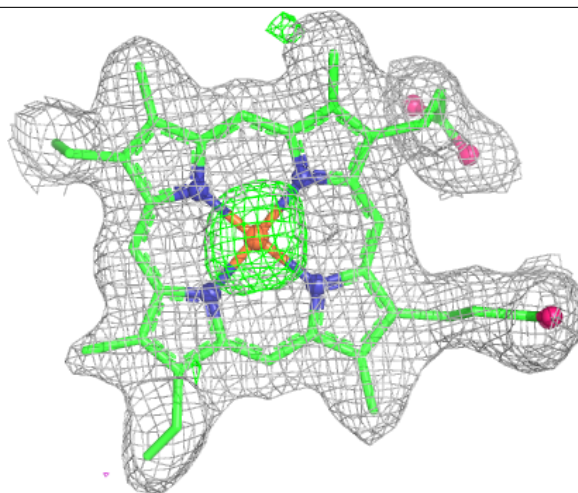
Electron density around HEC F 1002:

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



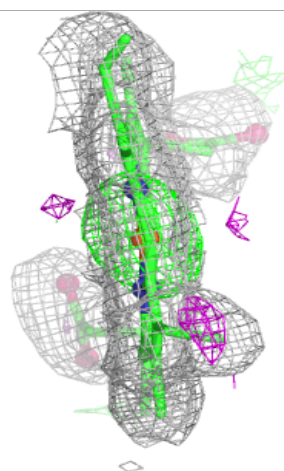
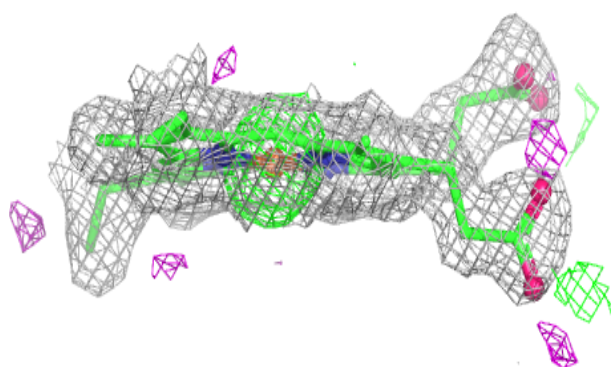
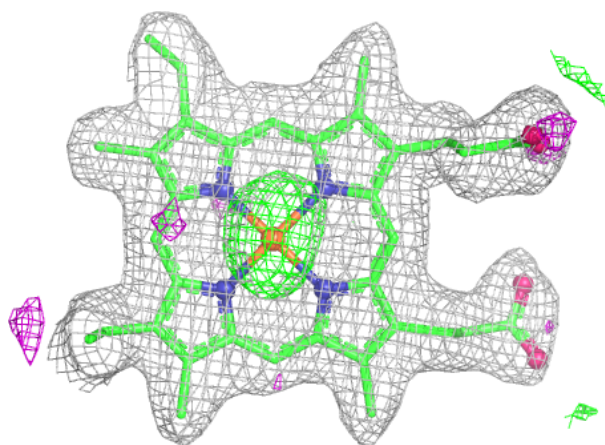
Electron density around HEC B 1002:

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



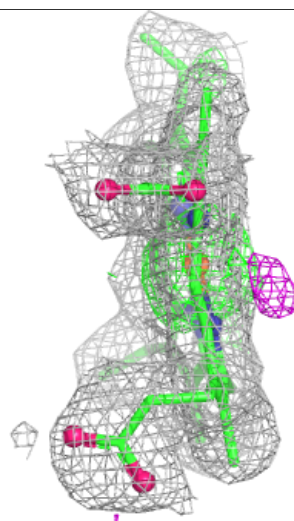
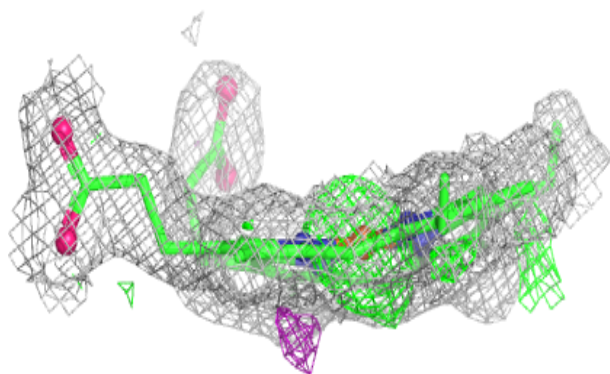
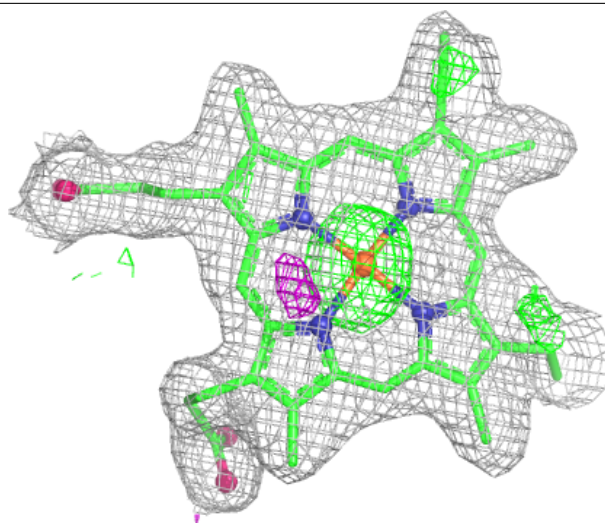
Electron density around HEC F 1004:

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



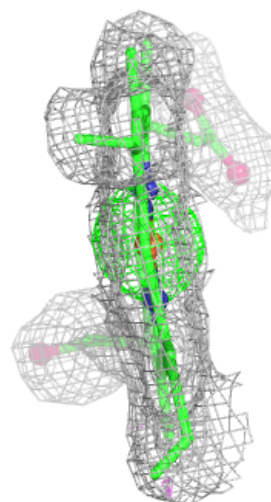
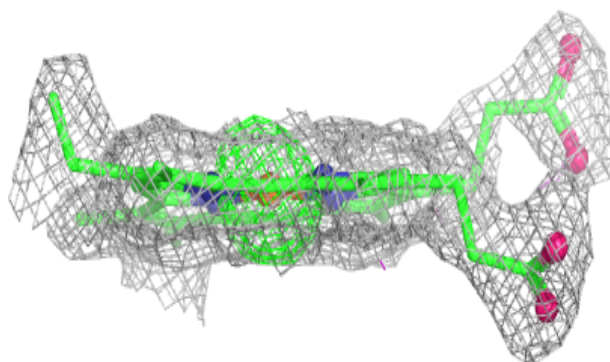
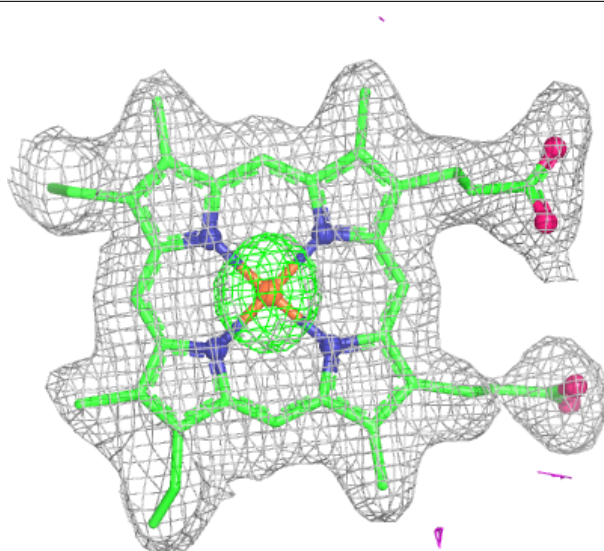
Electron density around HEC R 1003:

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



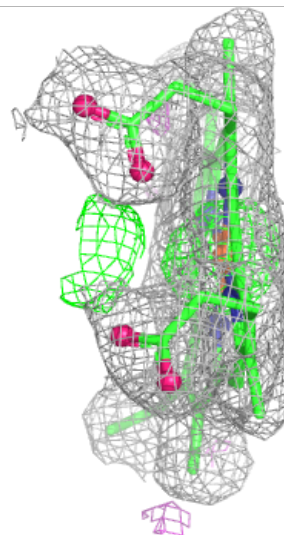
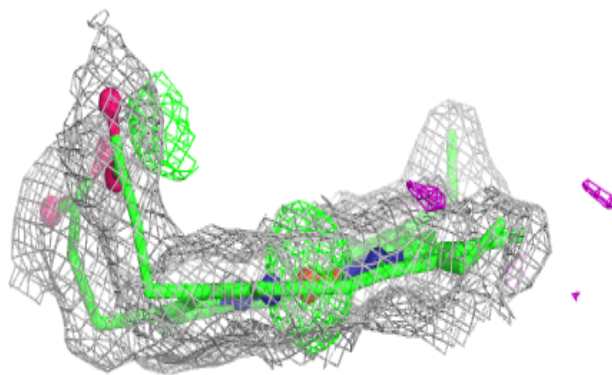
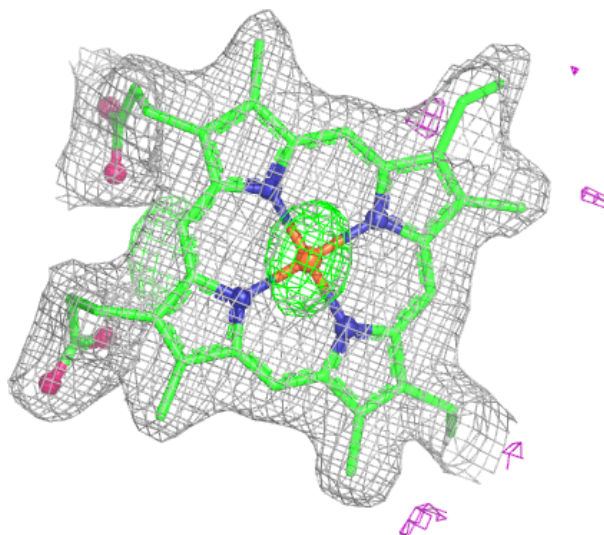
Electron density around HEC R 1004:

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



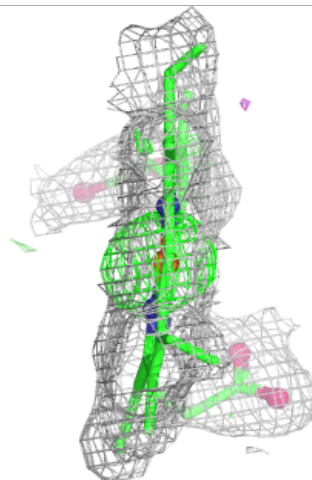
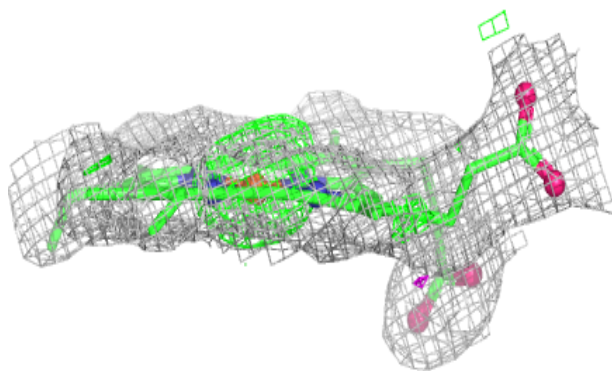
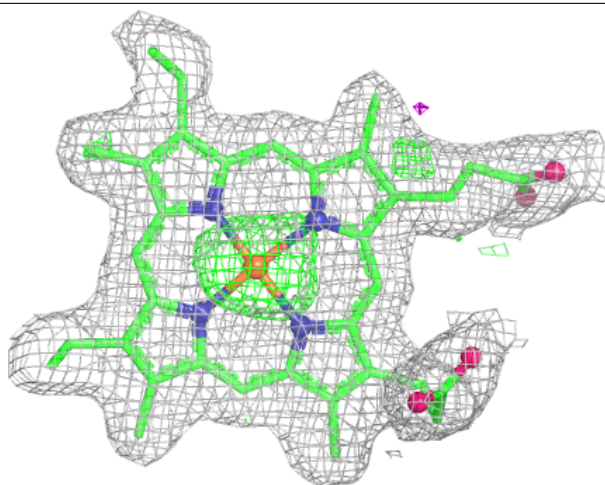
Electron density around HEC G 1001:

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



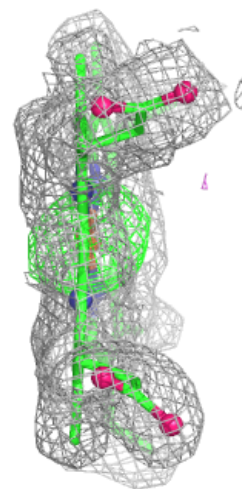
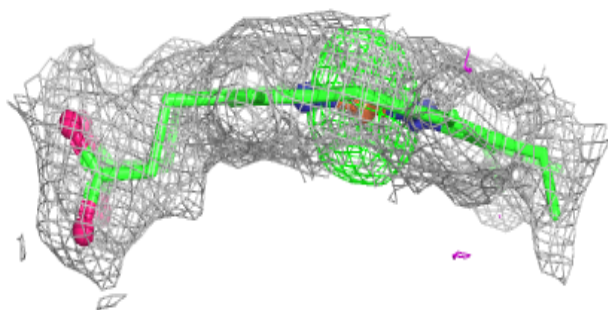
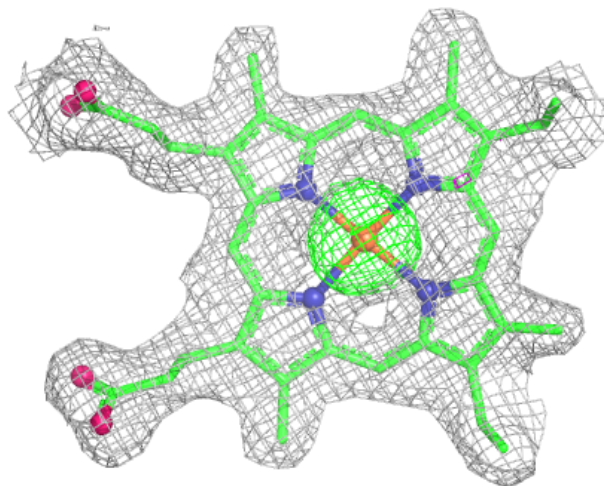
Electron density around HEC G 1002:

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



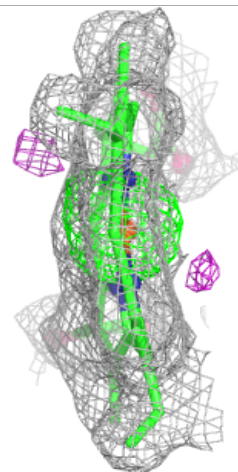
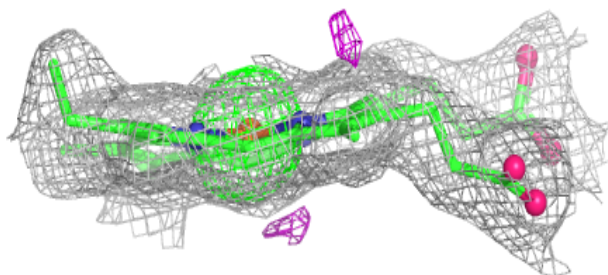
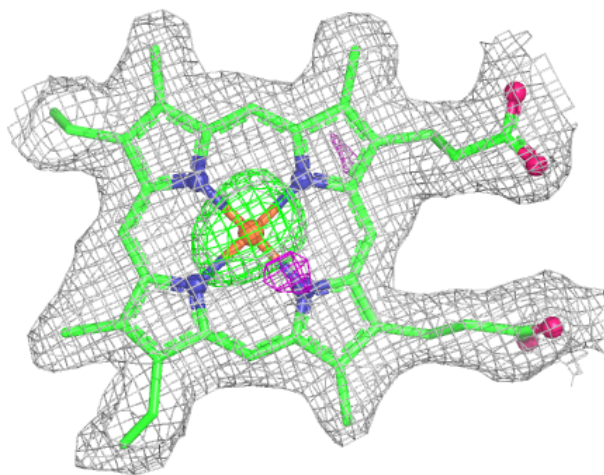
Electron density around HEC B 1003:

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



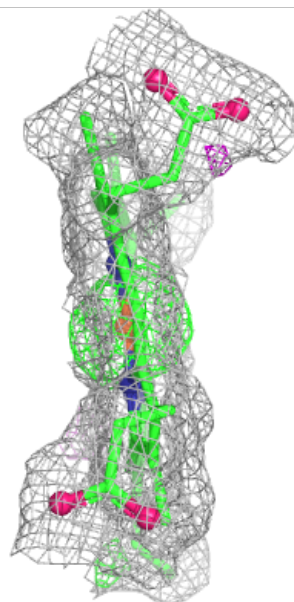
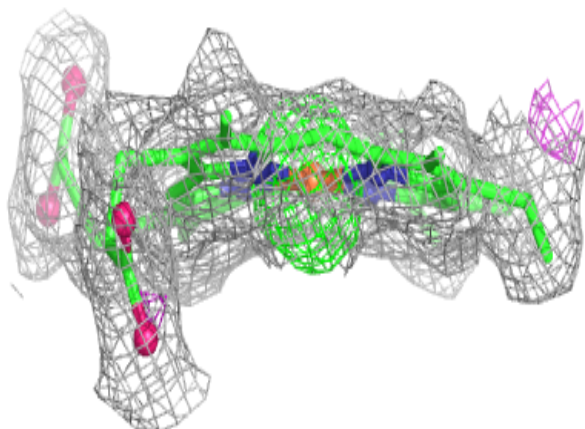
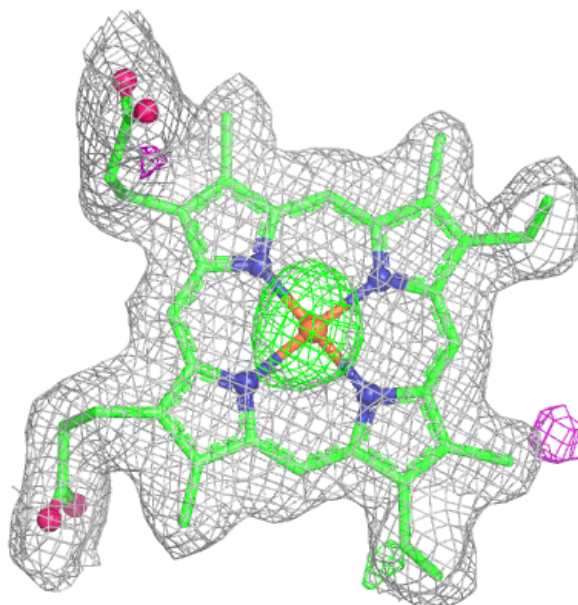
Electron density around HEC G 1004:

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



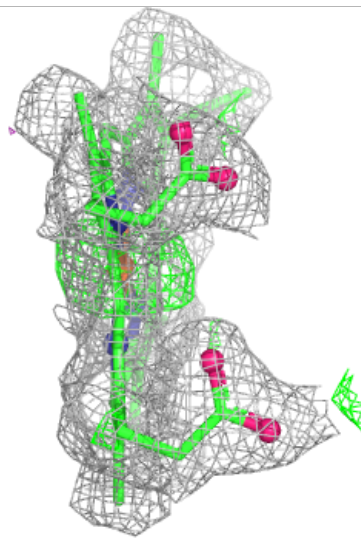
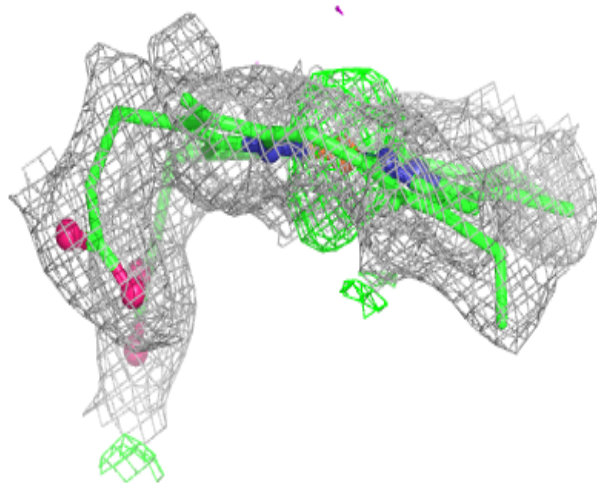
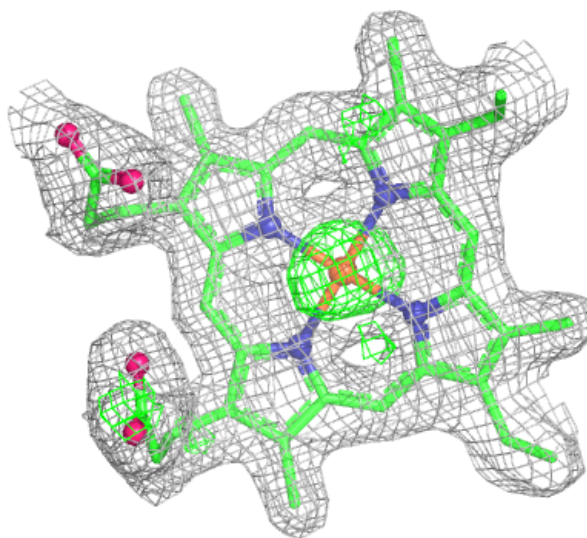
Electron density around HEC G 1005:

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



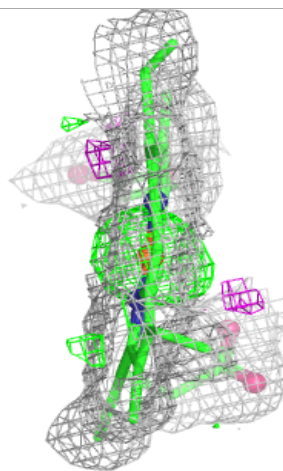
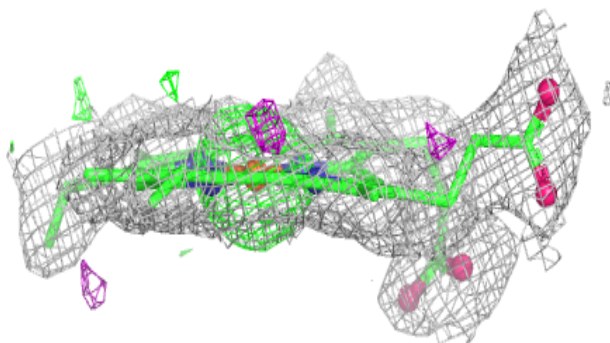
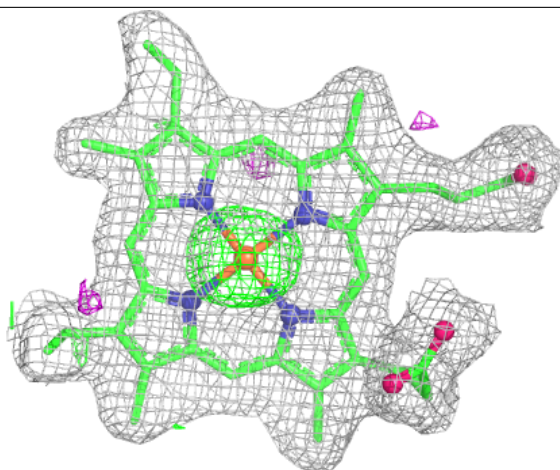
Electron density around HEC H 1001:

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



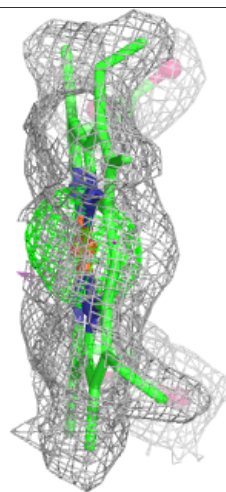
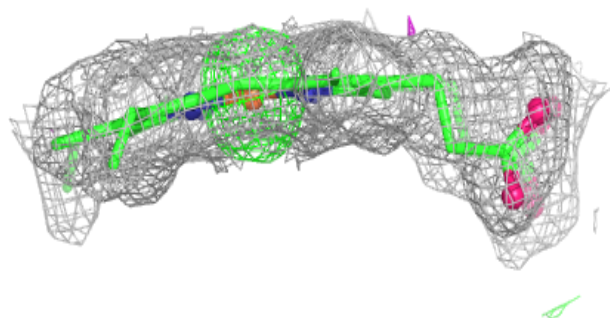
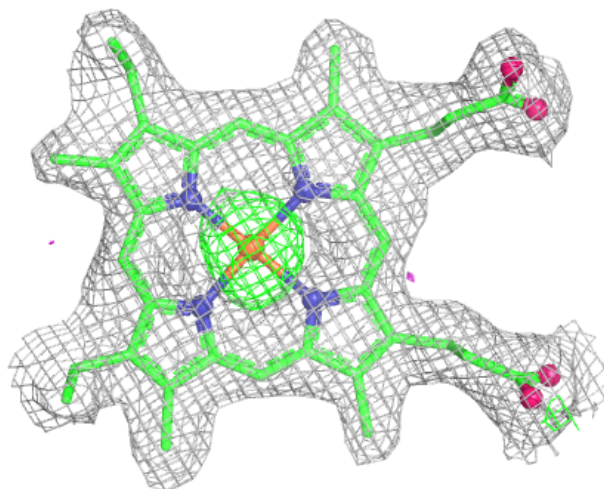
Electron density around HEC H 1002:

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



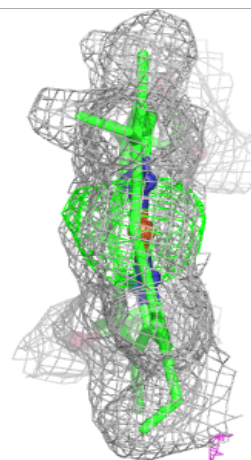
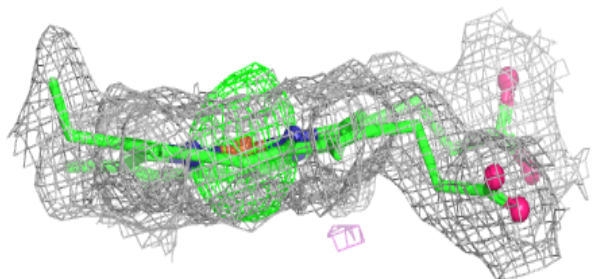
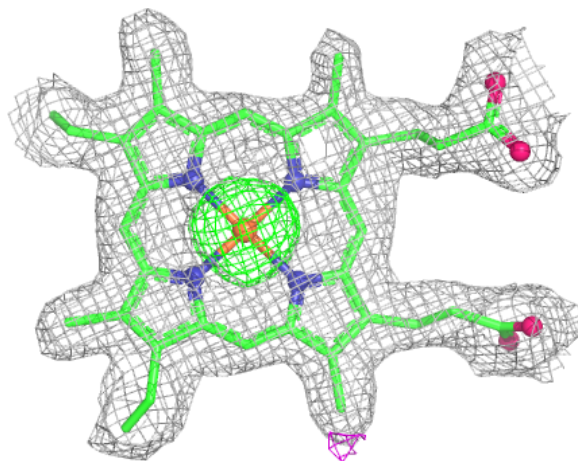
Electron density around HEC H 1003:

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



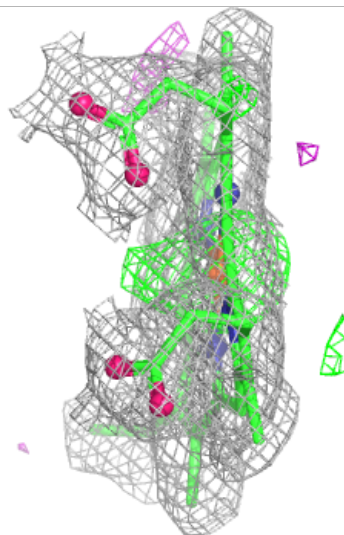
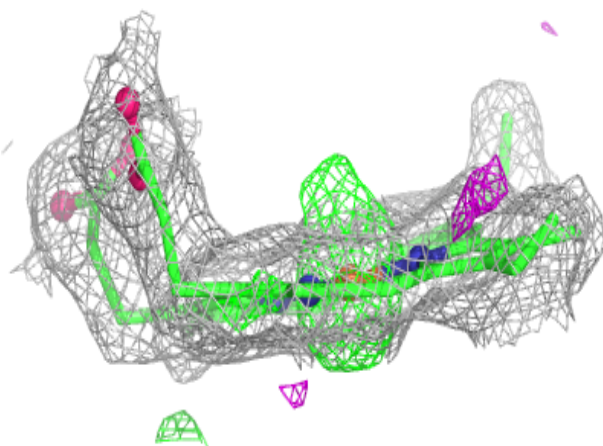
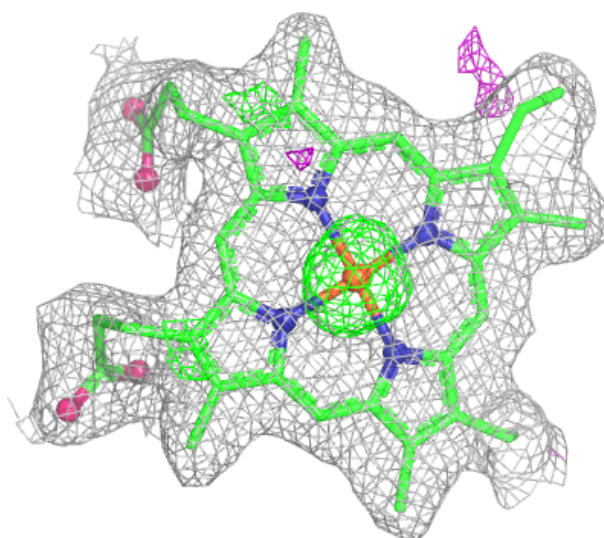
Electron density around HEC B 1004:

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



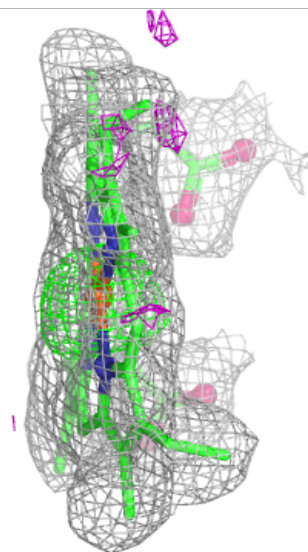
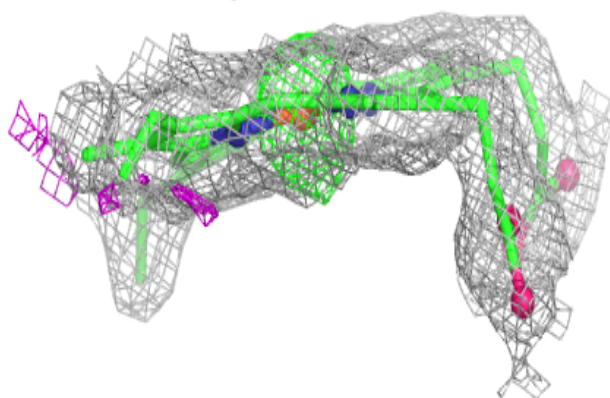
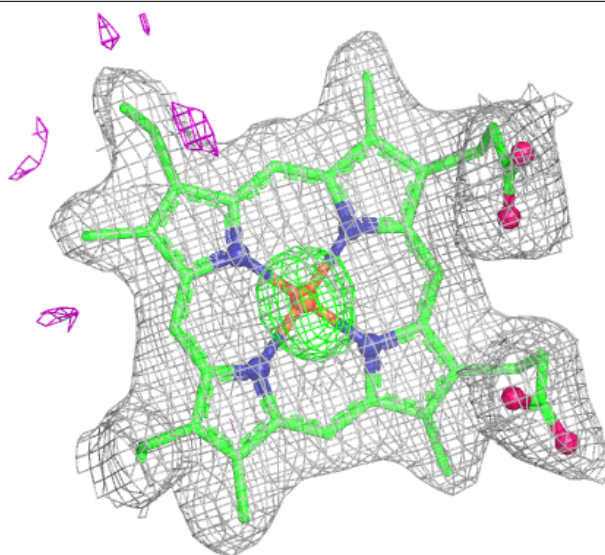
Electron density around HEC D 1001:

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



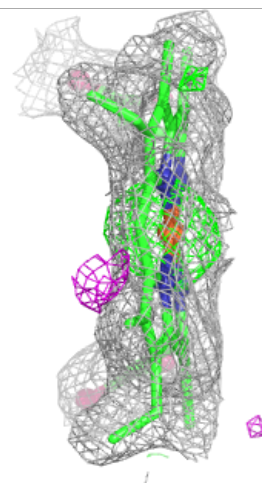
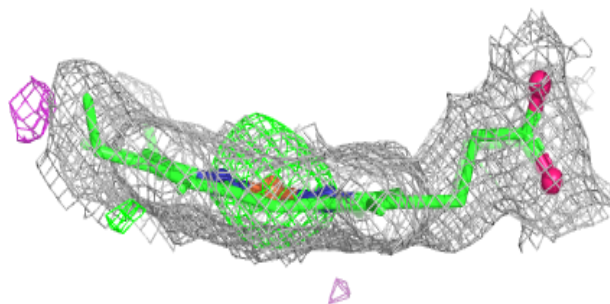
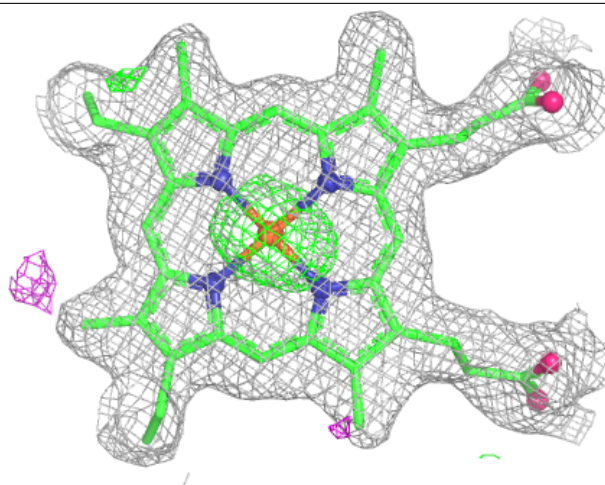
Electron density around HEC A 1001:

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



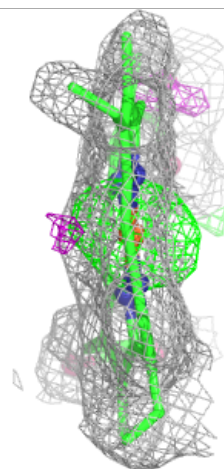
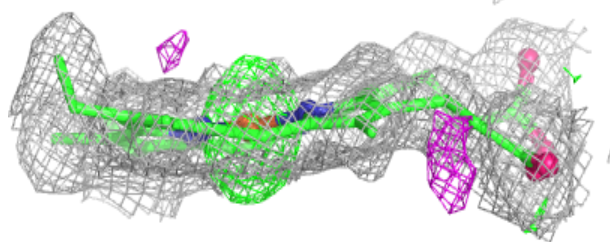
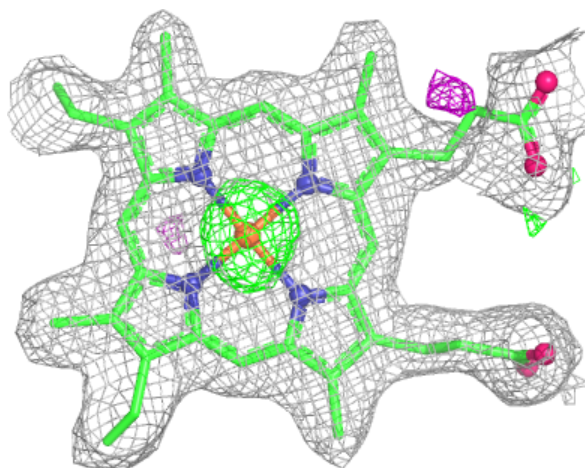
Electron density around HEC D 1003:

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



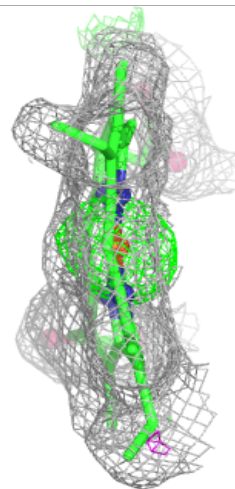
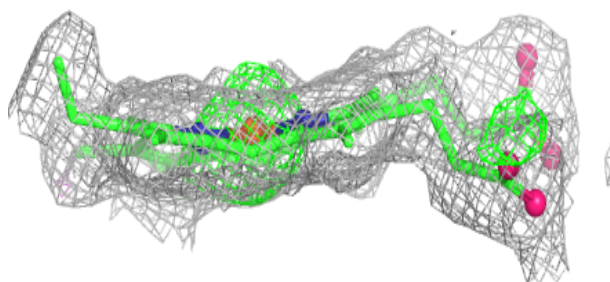
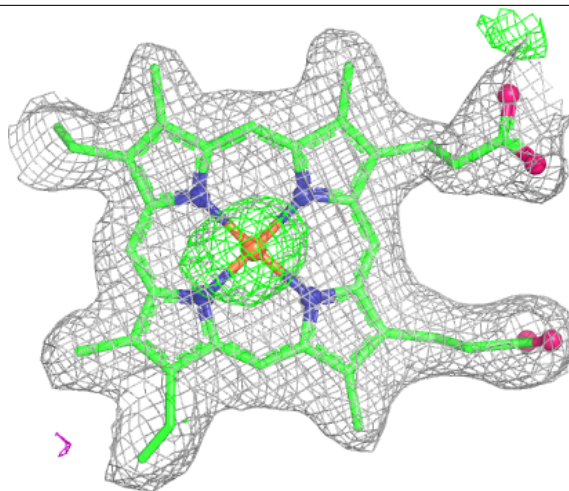
Electron density around HEC Q 1004:

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



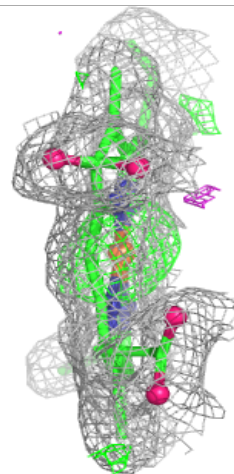
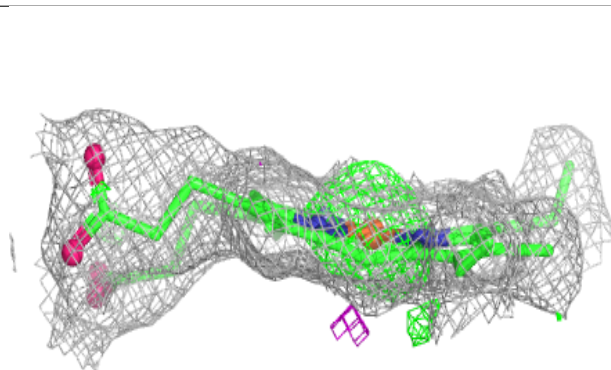
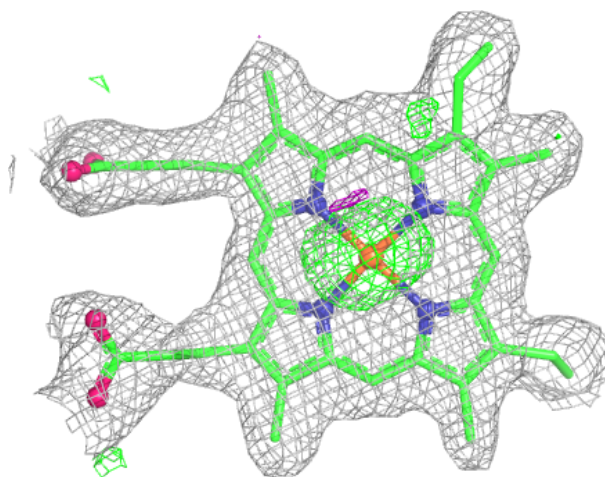
Electron density around HEC P 1004:

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



Electron density around HEC D 1004:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.