



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 01:19 AM UTC

PDB ID : 3SXQ / pdb_00003sxq
Title : Structure of a hexameric multiheme c nitrite reductase from the extremophile bacterium *Thiokalivibrio paradoxus*
Authors : Polyakov, K.M.; Trofimov, A.A.; Tikhonova, T.V.; Tikhonov, A.V.; Boyko, K.M.; Popov, V.O.
Deposited on : 2011-07-15
Resolution : 1.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

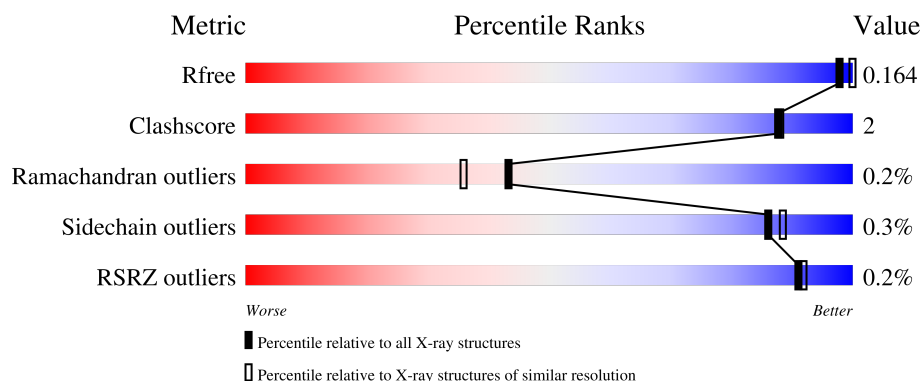
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

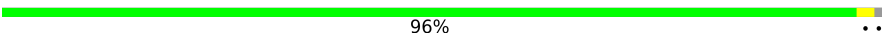
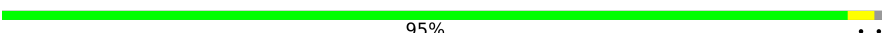
The reported resolution of this entry is 1.90 Å.

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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	525	 96%
1	B	525	 95%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	GOL	A	533	-	-	X	-

2 Entry composition [i](#)

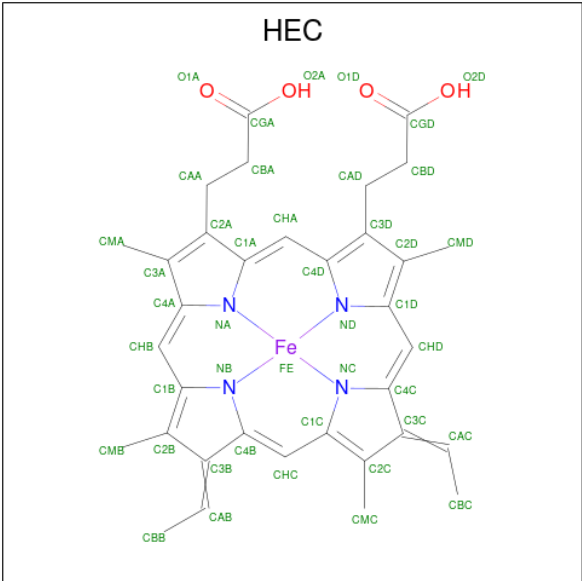
There are 9 unique types of molecules in this entry. The entry contains 10297 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Eight-heme nitrite reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	11	0
			4132	2567	748	783	34			
1	B	518	Total	C	N	O	S	0	12	1
			4115	2558	745	778	34			

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

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

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca		
			1	1	0	0
3	B	1	Total	Ca		
			1	1	0	0

- Molecule 4 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Co		
			2	2	0	0
4	B	2	Total	Co		
			2	2	0	0

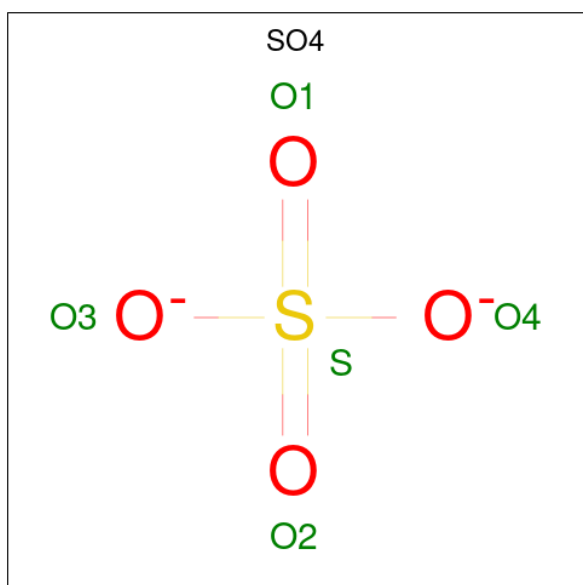
- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		
5	B	1	Total	Na	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

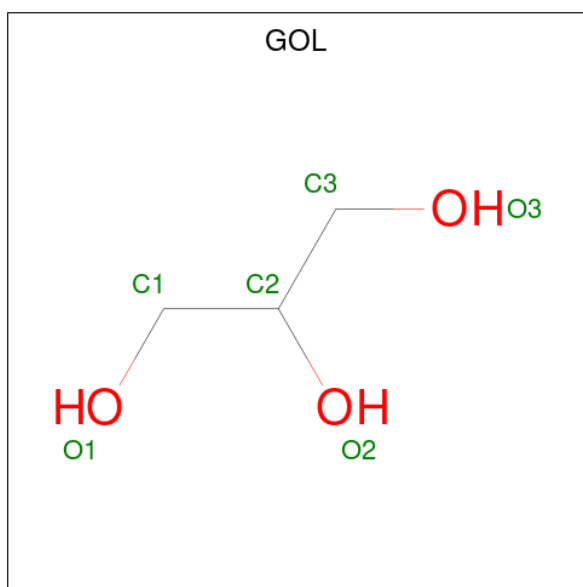
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		
6	B	1	Total	Cl	0	0
			1	1		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

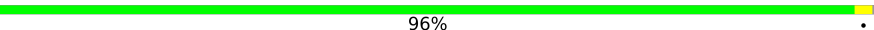
- Molecule 9 is water.

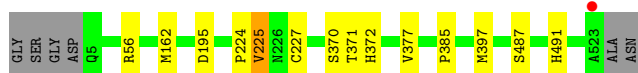
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	649	Total O 649 649	0	0
9	B	635	Total O 635 635	0	0

3 Residue-property plots [i](#)

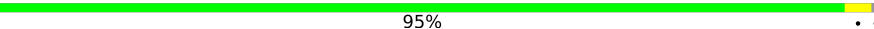
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

- Molecule 1: Eight-heme nitrite reductase

Chain A:  96% ..



- Molecule 1: Eight-heme nitrite reductase

Chain B:  95% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	193.64Å 193.64Å 193.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.90 – 1.90 29.90 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.90-1.90) 98.9 (29.90-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.22 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.138 , 0.162 0.139 , 0.164	Depositor DCC
R_{free} test set	9466 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	14.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.048 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10297	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% 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, GOL, CL, CO, HEC, NA, SO4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.96	0/4305	0.85	0/5850
1	B	0.96	0/4294	0.82	0/5834
All	All	0.96	0/8599	0.84	0/11684

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4132	0	3825	14	0
1	B	4115	0	3805	13	0
2	A	344	0	240	6	0
2	B	344	0	240	6	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	A	10	0	0	0	0
7	B	10	0	0	0	0
8	A	30	0	40	10	0
8	B	18	0	24	1	0
9	A	649	0	0	0	0
9	B	635	0	0	1	0
All	All	10297	0	8174	35	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 2.

All (35) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:PRO:O	1:A:397[B]:MET:HG2	1.78	0.83
1:A:372:HIS:H	8:A:533:GOL:C1	2.01	0.73
1:A:377:VAL:HG22	2:A:1008:HEC:HBC2	1.77	0.67
2:A:1002:HEC:HMC1	2:A:1002:HEC:HBC3	1.78	0.64
1:A:372:HIS:H	8:A:533:GOL:H12	1.64	0.63
1:B:377:VAL:HG22	2:B:1008:HEC:HBC2	1.83	0.60
2:A:1008:HEC:HBC3	2:A:1008:HEC:HMC1	1.86	0.57
2:B:1008:HEC:HBC3	2:B:1008:HEC:HMC1	1.87	0.57
1:B:46:GLU:HG3	9:B:1107:HOH:O	2.08	0.55
8:A:537:GOL:H12	1:B:393:LYS:HA	1.90	0.54
1:A:372:HIS:ND1	8:A:533:GOL:H12	2.25	0.52
8:A:537:GOL:H12	1:B:394:GLU:H	1.74	0.52
1:B:258:PRO:HB2	8:B:533:GOL:H11	1.92	0.51
2:B:1001:HEC:HBC3	2:B:1001:HEC:HMC1	1.92	0.50
2:B:1002:HEC:HMC1	2:B:1002:HEC:HBC3	1.95	0.49
1:B:103:LEU:HD23	1:B:479:TRP:CZ2	2.49	0.48
8:A:537:GOL:C1	1:B:394:GLU:H	2.28	0.47
1:A:372:HIS:H	8:A:533:GOL:H11	1.77	0.47
1:B:103:LEU:HD23	1:B:479:TRP:CE2	2.50	0.46
1:B:399:SER:O	1:B:401[A]:ARG:NH1	2.49	0.45
1:A:227:CYS:HA	2:A:1005:HEC:HHC	1.99	0.45
1:A:487:SER:HB3	1:A:491:HIS:CE1	2.53	0.44
1:A:370:SER:HB2	8:A:533:GOL:H11	2.00	0.43
2:A:1005:HEC:HAA2	2:A:1003:HEC:HBA1	2.01	0.43
2:A:1005:HEC:HAA2	2:A:1003:HEC:CBA	2.50	0.42
2:B:1007:HEC:HMB1	2:B:1007:HEC:HBB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:PRO:HG3	1:B:329:TRP:CD1	2.54	0.41
1:B:227:CYS:HA	2:B:1005:HEC:HHC	2.01	0.41
1:A:56[A]:ARG:NH2	1:A:195:ASP:OD1	2.45	0.41
1:B:430:ILE:HG21	1:B:490:PHE:HA	2.03	0.40
1:A:371:THR:N	8:A:533:GOL:H11	2.35	0.40
1:A:372:HIS:HD1	8:A:533:GOL:H12	1.85	0.40
1:B:487:SER:HB3	1:B:491:HIS:CE1	2.57	0.40
1:A:224:PRO:O	1:A:225:VAL:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	528/525 (101%)	509 (96%)	18 (3%)	1 (0%)	43	36
1	B	528/525 (101%)	508 (96%)	19 (4%)	1 (0%)	43	36
All	All	1056/1050 (101%)	1017 (96%)	37 (4%)	2 (0%)	43	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	VAL
1	B	225	VAL

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	442/440 (100%)	442 (100%)	0	100	100
1	B	439/440 (100%)	435 (99%)	4 (1%)	70	73
All	All	881/880 (100%)	877 (100%)	4 (0%)	86	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	103	LEU
1	B	401[A]	ARG
1	B	401[B]	ARG
1	B	488	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	113	HIS
1	A	138	GLN
1	A	143	GLN
1	B	143	GLN
1	B	223	HIS
1	B	311	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 38 ligands modelled in this entry, 10 are monoatomic - leaving 28 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$
8	GOL	A	535	-	5,5,5	0.35	0	5,5,5	0.17	0
2	HEC	A	1007	1	46,50,50	1.97	9 (19%)	58,82,82	1.82	9 (15%)
8	GOL	A	533	-	5,5,5	0.66	0	5,5,5	1.35	1 (20%)
7	SO4	A	531	-	4,4,4	0.30	0	6,6,6	0.36	0
2	HEC	B	1006	1	46,50,50	1.96	8 (17%)	58,82,82	2.08	8 (13%)
7	SO4	A	532	-	4,4,4	0.43	0	6,6,6	0.63	0
8	GOL	B	533	-	5,5,5	0.39	0	5,5,5	0.44	0
8	GOL	A	537	-	5,5,5	0.56	0	5,5,5	0.69	0
2	HEC	A	1001	1	46,50,50	2.05	7 (15%)	58,82,82	1.98	7 (12%)
2	HEC	A	1005	1	46,50,50	1.92	10 (21%)	58,82,82	1.74	8 (13%)
2	HEC	A	1002	1	46,50,50	1.92	5 (10%)	58,82,82	2.08	6 (10%)
2	HEC	B	1008	1	46,50,50	1.95	6 (13%)	58,82,82	1.92	7 (12%)
2	HEC	B	1002	1	46,50,50	1.93	7 (15%)	58,82,82	1.98	11 (18%)
2	HEC	B	1004	1,9,4	46,50,50	1.93	6 (13%)	58,82,82	1.85	7 (12%)
2	HEC	B	1007	1	46,50,50	1.97	8 (17%)	58,82,82	2.02	10 (17%)
7	SO4	B	531	-	4,4,4	0.29	0	6,6,6	0.45	0
8	GOL	B	535	-	5,5,5	0.61	0	5,5,5	0.70	0
8	GOL	A	534	-	5,5,5	0.41	0	5,5,5	0.35	0
7	SO4	B	532	-	4,4,4	0.32	0	6,6,6	0.22	0
8	GOL	A	536	-	5,5,5	0.42	0	5,5,5	0.86	0
8	GOL	B	534	-	5,5,5	0.45	0	5,5,5	0.29	0
2	HEC	B	1003	1	46,50,50	1.96	9 (19%)	58,82,82	1.84	8 (13%)
2	HEC	A	1008	1	46,50,50	1.97	7 (15%)	58,82,82	2.05	9 (15%)
2	HEC	B	1005	1	46,50,50	1.93	8 (17%)	58,82,82	1.78	10 (17%)
2	HEC	A	1006	1	46,50,50	1.95	7 (15%)	58,82,82	2.05	7 (12%)
2	HEC	A	1003	1	46,50,50	1.95	8 (17%)	58,82,82	1.98	11 (18%)
2	HEC	A	1004	1,9,4	46,50,50	1.98	8 (17%)	58,82,82	1.84	5 (8%)
2	HEC	B	1001	1	46,50,50	2.05	7 (15%)	58,82,82	2.02	9 (15%)

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
8	GOL	A	535	-	-	0/4/4/4	-
2	HEC	A	1007	1	-	4/14/54/54	-
8	GOL	A	533	-	-	1/4/4/4	-
2	HEC	B	1006	1	-	6/14/54/54	-
8	GOL	B	533	-	-	4/4/4/4	-
8	GOL	A	537	-	-	2/4/4/4	-
2	HEC	A	1001	1	-	8/14/54/54	-
2	HEC	A	1005	1	-	6/14/54/54	-
2	HEC	A	1002	1	-	6/14/54/54	-
2	HEC	B	1008	1	-	6/14/54/54	-
2	HEC	B	1002	1	-	6/14/54/54	-
2	HEC	B	1004	1,9,4	-	6/14/54/54	-
2	HEC	B	1007	1	-	6/14/54/54	-
8	GOL	B	535	-	-	0/4/4/4	-
8	GOL	A	534	-	-	0/4/4/4	-
8	GOL	A	536	-	-	1/4/4/4	-
8	GOL	B	534	-	-	0/4/4/4	-
2	HEC	B	1003	1	-	5/14/54/54	-
2	HEC	A	1008	1	-	6/14/54/54	-
2	HEC	B	1005	1	-	6/14/54/54	-
2	HEC	A	1006	1	-	5/14/54/54	-
2	HEC	A	1003	1	-	8/14/54/54	-
2	HEC	A	1004	1,9,4	-	6/14/54/54	-
2	HEC	B	1001	1	-	8/14/54/54	-

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	HEC	CAC-C3C	7.28	1.58	1.35
2	B	1008	HEC	CAC-C3C	7.28	1.58	1.35
2	B	1001	HEC	CAB-C3B	7.23	1.58	1.35
2	A	1001	HEC	CAC-C3C	7.18	1.58	1.35
2	A	1008	HEC	CAC-C3C	7.15	1.58	1.35
2	B	1003	HEC	CAB-C3B	7.10	1.58	1.35
2	A	1004	HEC	CAB-C3B	7.09	1.58	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1003	HEC	CAC-C3C	7.07	1.58	1.35
2	B	1004	HEC	CAB-C3B	7.04	1.57	1.35
2	A	1002	HEC	CAC-C3C	6.93	1.57	1.35
2	A	1001	HEC	CAB-C3B	6.91	1.57	1.35
2	A	1005	HEC	CAC-C3C	6.91	1.57	1.35
2	B	1002	HEC	CAB-C3B	6.90	1.57	1.35
2	B	1007	HEC	CAC-C3C	6.85	1.57	1.35
2	B	1006	HEC	CAC-C3C	6.85	1.57	1.35
2	A	1007	HEC	CAC-C3C	6.84	1.57	1.35
2	B	1005	HEC	CAC-C3C	6.80	1.57	1.35
2	A	1002	HEC	CAB-C3B	6.71	1.56	1.35
2	B	1002	HEC	CAC-C3C	6.69	1.56	1.35
2	A	1006	HEC	CAB-C3B	6.68	1.56	1.35
2	A	1006	HEC	CAC-C3C	6.68	1.56	1.35
2	A	1007	HEC	CAB-C3B	6.64	1.56	1.35
2	B	1003	HEC	CAC-C3C	6.63	1.56	1.35
2	A	1003	HEC	CAB-C3B	6.56	1.56	1.35
2	B	1006	HEC	CAB-C3B	6.52	1.56	1.35
2	A	1004	HEC	CAC-C3C	6.46	1.56	1.35
2	B	1007	HEC	CAB-C3B	6.33	1.55	1.35
2	A	1008	HEC	CAB-C3B	6.33	1.55	1.35
2	A	1005	HEC	CAB-C3B	6.30	1.55	1.35
2	B	1004	HEC	CAC-C3C	6.30	1.55	1.35
2	B	1005	HEC	CAB-C3B	6.25	1.55	1.35
2	B	1008	HEC	CAB-C3B	6.12	1.54	1.35
2	A	1001	HEC	C3D-C2D	5.77	1.53	1.38
2	A	1008	HEC	C3D-C2D	5.23	1.52	1.38
2	B	1006	HEC	C3D-C2D	5.13	1.52	1.38
2	B	1008	HEC	C3D-C2D	5.12	1.52	1.38
2	A	1002	HEC	C3D-C2D	4.97	1.51	1.38
2	B	1001	HEC	C3D-C2D	4.97	1.51	1.38
2	B	1004	HEC	C3D-C2D	4.81	1.51	1.38
2	A	1004	HEC	C3D-C2D	4.74	1.51	1.38
2	B	1002	HEC	C3D-C2D	4.74	1.51	1.38
2	A	1006	HEC	C3D-C2D	4.70	1.51	1.38
2	A	1007	HEC	C3D-C2D	4.59	1.50	1.38
2	B	1005	HEC	C3D-C2D	4.37	1.50	1.38
2	B	1003	HEC	C3D-C2D	4.24	1.50	1.38
2	B	1007	HEC	C3D-C2D	4.19	1.49	1.38
2	A	1005	HEC	C3D-C2D	4.16	1.49	1.38
2	A	1003	HEC	C3D-C2D	3.84	1.48	1.38
2	A	1003	HEC	CMD-C2D	3.49	1.57	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1007	HEC	CMA-C3A	3.29	1.57	1.50
2	B	1005	HEC	CMB-C2B	3.03	1.57	1.50
2	B	1007	HEC	CMC-C2C	3.00	1.56	1.50
2	B	1001	HEC	CMD-C2D	2.94	1.56	1.50
2	A	1004	HEC	CMC-C2C	2.93	1.56	1.50
2	B	1006	HEC	CMB-C2B	2.91	1.56	1.50
2	A	1008	HEC	CMB-C2B	2.86	1.56	1.50
2	A	1001	HEC	CMB-C2B	2.84	1.56	1.50
2	B	1005	HEC	O2D-CGD	-2.84	1.21	1.30
2	A	1006	HEC	CMB-C2B	2.84	1.56	1.50
2	B	1003	HEC	CMB-C2B	2.82	1.56	1.50
2	A	1005	HEC	CMA-C3A	2.77	1.56	1.50
2	A	1007	HEC	CMC-C2C	2.72	1.56	1.50
2	A	1002	HEC	CMD-C2D	2.71	1.56	1.50
2	B	1003	HEC	CMA-C3A	2.71	1.56	1.50
2	B	1004	HEC	CMC-C2C	2.70	1.56	1.50
2	B	1002	HEC	CMB-C2B	2.70	1.56	1.50
2	B	1003	HEC	CMD-C2D	2.67	1.56	1.50
2	B	1001	HEC	CMB-C2B	2.66	1.56	1.50
2	B	1006	HEC	CMA-C3A	2.65	1.56	1.50
2	A	1003	HEC	CMB-C2B	2.62	1.56	1.50
2	B	1008	HEC	CMD-C2D	2.57	1.56	1.50
2	A	1001	HEC	CMD-C2D	2.57	1.56	1.50
2	A	1002	HEC	CMC-C2C	2.55	1.56	1.50
2	A	1006	HEC	CMC-C2C	2.51	1.55	1.50
2	B	1005	HEC	CMD-C2D	2.50	1.55	1.50
2	A	1005	HEC	CMD-C2D	2.49	1.55	1.50
2	A	1005	HEC	O2D-CGD	-2.48	1.22	1.30
2	B	1004	HEC	CMB-C2B	2.47	1.55	1.50
2	A	1008	HEC	CMD-C2D	2.46	1.55	1.50
2	B	1007	HEC	CMB-C2B	2.45	1.55	1.50
2	A	1005	HEC	CMB-C2B	2.42	1.55	1.50
2	A	1007	HEC	CMB-C2B	2.39	1.55	1.50
2	B	1001	HEC	CMC-C2C	2.37	1.55	1.50
2	A	1005	HEC	CBB-CAB	2.36	1.58	1.49
2	A	1003	HEC	CMA-C3A	2.35	1.55	1.50
2	A	1006	HEC	CMA-C3A	2.33	1.55	1.50
2	B	1006	HEC	CMC-C2C	2.32	1.55	1.50
2	B	1002	HEC	CMC-C2C	2.30	1.55	1.50
2	A	1005	HEC	CMC-C2C	2.30	1.55	1.50
2	B	1001	HEC	CMA-C3A	2.29	1.55	1.50
2	A	1007	HEC	CMD-C2D	2.28	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1002	HEC	CMD-C2D	2.27	1.55	1.50
2	B	1005	HEC	CBB-CAB	2.26	1.57	1.49
2	A	1003	HEC	CMC-C2C	2.26	1.55	1.50
2	A	1004	HEC	CMB-C2B	2.24	1.55	1.50
2	A	1004	HEC	CMA-C3A	2.24	1.55	1.50
2	B	1003	HEC	CBB-CAB	2.23	1.57	1.49
2	B	1004	HEC	CMD-C2D	2.23	1.55	1.50
2	B	1007	HEC	C3B-C2B	-2.23	1.33	1.41
2	B	1005	HEC	CMA-C3A	2.22	1.55	1.50
2	A	1004	HEC	CMD-C2D	2.22	1.55	1.50
2	A	1008	HEC	C3B-C2B	-2.20	1.33	1.41
2	B	1002	HEC	CMA-C3A	2.18	1.55	1.50
2	B	1006	HEC	CMD-C2D	2.16	1.55	1.50
2	A	1008	HEC	CMC-C2C	2.15	1.55	1.50
2	B	1007	HEC	CMD-C2D	2.13	1.55	1.50
2	A	1004	HEC	CAA-C2A	2.12	1.56	1.51
2	A	1001	HEC	CMC-C2C	2.12	1.55	1.50
2	A	1007	HEC	CBB-CAB	2.11	1.57	1.49
2	A	1007	HEC	C3B-C2B	-2.09	1.34	1.41
2	B	1008	HEC	CMC-C2C	2.09	1.55	1.50
2	A	1007	HEC	CMA-C3A	2.08	1.55	1.50
2	A	1003	HEC	C3B-C2B	-2.07	1.34	1.41
2	B	1008	HEC	CMB-C2B	2.06	1.55	1.50
2	B	1006	HEC	CBB-CAB	2.05	1.57	1.49
2	A	1006	HEC	CBB-CAB	2.04	1.57	1.49
2	A	1005	HEC	C3B-C2B	-2.03	1.34	1.41
2	A	1001	HEC	CMA-C3A	2.03	1.54	1.50
2	B	1003	HEC	C3B-C2B	-2.01	1.34	1.41
2	B	1003	HEC	O2A-CGA	-2.01	1.24	1.30

All (133) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1008	HEC	CBB-CAB-C3B	-11.82	103.82	127.43
2	B	1008	HEC	CBB-CAB-C3B	-10.71	106.03	127.43
2	A	1006	HEC	CBB-CAB-C3B	-10.44	106.58	127.43
2	B	1007	HEC	CBB-CAB-C3B	-9.95	107.55	127.43
2	B	1006	HEC	CBB-CAB-C3B	-9.93	107.58	127.43
2	A	1002	HEC	CBB-CAB-C3B	-9.68	108.08	127.43
2	A	1003	HEC	CBB-CAB-C3B	-9.66	108.12	127.43
2	A	1001	HEC	CBB-CAB-C3B	-9.66	108.12	127.43
2	A	1007	HEC	CBB-CAB-C3B	-9.45	108.54	127.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1004	HEC	CBB-CAB-C3B	-9.40	108.64	127.43
2	B	1002	HEC	CBB-CAB-C3B	-9.35	108.75	127.43
2	B	1004	HEC	CBB-CAB-C3B	-9.24	108.97	127.43
2	B	1001	HEC	CBB-CAB-C3B	-9.15	109.15	127.43
2	B	1003	HEC	CBB-CAB-C3B	-9.14	109.17	127.43
2	A	1005	HEC	CBB-CAB-C3B	-8.31	110.83	127.43
2	B	1005	HEC	CBB-CAB-C3B	-8.16	111.13	127.43
2	B	1006	HEC	CBC-CAC-C3C	-7.50	112.44	127.43
2	A	1006	HEC	CBC-CAC-C3C	-7.40	112.65	127.43
2	B	1001	HEC	CBC-CAC-C3C	-7.10	113.25	127.43
2	A	1002	HEC	CBC-CAC-C3C	-6.98	113.47	127.43
2	B	1002	HEC	CBC-CAC-C3C	-6.19	115.05	127.43
2	B	1004	HEC	CBC-CAC-C3C	-6.10	115.24	127.43
2	A	1004	HEC	CBC-CAC-C3C	-5.96	115.53	127.43
2	B	1005	HEC	CBC-CAC-C3C	-5.86	115.72	127.43
2	A	1001	HEC	CBC-CAC-C3C	-5.74	115.97	127.43
2	A	1005	HEC	CBC-CAC-C3C	-5.54	116.35	127.43
2	A	1008	HEC	CBC-CAC-C3C	-5.40	116.63	127.43
2	B	1007	HEC	CBC-CAC-C3C	-5.01	117.41	127.43
2	B	1003	HEC	CBC-CAC-C3C	-4.92	117.60	127.43
2	B	1007	HEC	CMB-C2B-C1B	-4.66	118.32	125.42
2	B	1008	HEC	CBC-CAC-C3C	-4.62	118.20	127.43
2	A	1003	HEC	CBC-CAC-C3C	-4.40	118.64	127.43
2	A	1001	HEC	C4D-ND-C1D	4.31	112.85	105.82
2	A	1003	HEC	CAA-CBA-CGA	-4.28	102.32	113.67
2	A	1007	HEC	CBC-CAC-C3C	-3.99	119.47	127.43
2	A	1007	HEC	CMB-C2B-C1B	-3.90	119.47	125.42
2	A	1003	HEC	CBA-CAA-C2A	3.61	122.51	112.53
2	A	1002	HEC	CAA-CBA-CGA	-3.50	104.39	113.67
2	B	1007	HEC	CBD-CAD-C3D	-3.49	102.89	112.53
2	B	1006	HEC	C2A-C1A-NA	-3.34	107.10	110.32
2	B	1002	HEC	C4D-ND-C1D	3.32	111.24	105.82
2	A	1002	HEC	C4D-ND-C1D	3.32	111.23	105.82
2	B	1003	HEC	CMD-C2D-C1D	3.17	130.25	125.42
2	B	1003	HEC	CBD-CAD-C3D	-3.17	103.77	112.53
2	A	1007	HEC	CBD-CAD-C3D	-3.16	103.79	112.53
2	B	1007	HEC	CMD-C2D-C1D	3.14	130.20	125.42
2	A	1003	HEC	CMC-C2C-C1C	-3.11	120.68	125.42
2	B	1001	HEC	CMC-C2C-C1C	-3.08	120.73	125.42
2	A	1001	HEC	CMC-C2C-C1C	-3.06	120.76	125.42
2	A	1002	HEC	CMC-C2C-C1C	-3.04	120.79	125.42
2	B	1007	HEC	CBA-CAA-C2A	-3.04	104.13	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	HEC	CBD-CAD-C3D	-2.89	104.54	112.53
2	A	1003	HEC	CAD-CBD-CGD	-2.88	106.02	113.67
2	B	1003	HEC	CAA-CBA-CGA	-2.88	106.02	113.67
2	B	1008	HEC	CMC-C2C-C1C	-2.88	121.03	125.42
2	B	1001	HEC	CMD-C2D-C1D	2.86	129.77	125.42
2	A	1007	HEC	CBA-CAA-C2A	-2.85	104.64	112.53
2	B	1001	HEC	C4D-ND-C1D	2.85	110.46	105.82
2	B	1003	HEC	CMC-C2C-C1C	-2.76	121.21	125.42
2	B	1001	HEC	CAD-CBD-CGD	-2.76	106.34	113.67
2	A	1005	HEC	C2A-C1A-NA	-2.75	107.67	110.32
2	B	1007	HEC	CMC-C2C-C1C	-2.74	121.25	125.42
2	B	1005	HEC	CMC-C2C-C1C	-2.73	121.26	125.42
2	B	1002	HEC	CAA-CBA-CGA	-2.72	106.46	113.67
2	B	1006	HEC	CMC-C2C-C1C	-2.72	121.28	125.42
2	B	1004	HEC	C4D-ND-C1D	2.70	110.22	105.82
2	A	1007	HEC	CMD-C2D-C1D	2.66	129.47	125.42
2	A	1005	HEC	CBD-CAD-C3D	-2.66	105.19	112.53
2	A	1003	HEC	CBD-CAD-C3D	-2.61	105.31	112.53
2	B	1004	HEC	O2A-CGA-CBA	2.61	122.23	114.00
2	A	1006	HEC	CBD-CAD-C3D	-2.60	105.35	112.53
2	B	1006	HEC	CBD-CAD-C3D	-2.60	105.35	112.53
2	A	1007	HEC	C4D-ND-C1D	2.58	110.03	105.82
2	A	1008	HEC	C4D-ND-C1D	2.58	110.03	105.82
2	B	1004	HEC	CMC-C2C-C1C	-2.58	121.49	125.42
2	B	1005	HEC	O2A-CGA-CBA	2.57	122.13	114.00
2	B	1003	HEC	CMB-C2B-C1B	-2.57	121.51	125.42
2	B	1004	HEC	CMB-C2B-C1B	-2.56	121.53	125.42
2	B	1005	HEC	CBD-CAD-C3D	-2.55	105.47	112.53
2	A	1004	HEC	CMC-C2C-C1C	-2.55	121.53	125.42
2	A	1002	HEC	C2A-C1A-NA	-2.55	107.87	110.32
2	B	1006	HEC	CHB-C4A-NA	2.54	127.22	124.45
2	A	1005	HEC	CMC-C2C-C1C	-2.54	121.56	125.42
2	A	1006	HEC	C2A-C1A-NA	-2.53	107.88	110.32
2	B	1008	HEC	CHC-C4B-NB	2.47	127.14	124.45
2	B	1002	HEC	CHD-C1D-ND	2.47	128.33	123.86
2	B	1008	HEC	C4D-ND-C1D	2.44	109.80	105.82
2	B	1007	HEC	C2B-C1B-NB	-2.43	106.24	110.14
2	A	1004	HEC	CHB-C4A-NA	2.42	127.09	124.45
2	B	1001	HEC	C2A-C1A-NA	-2.41	107.99	110.32
2	A	1007	HEC	CMC-C2C-C1C	-2.41	121.76	125.42
2	B	1006	HEC	C4D-ND-C1D	2.39	109.72	105.82
2	B	1007	HEC	C4D-ND-C1D	2.38	109.71	105.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	HEC	C2A-C1A-NA	-2.37	108.04	110.32
2	B	1005	HEC	CAD-CBD-CGD	-2.37	107.39	113.67
2	A	1008	HEC	O2A-CGA-CBA	2.34	121.39	114.00
2	B	1005	HEC	O1A-CGA-CBA	-2.33	115.70	123.09
2	A	1007	HEC	CAD-C3D-C4D	2.33	129.48	124.94
2	B	1001	HEC	CAA-CBA-CGA	-2.33	107.50	113.67
2	B	1002	HEC	CMC-C2C-C1C	-2.31	121.90	125.42
2	B	1002	HEC	C2A-C1A-NA	-2.31	108.09	110.32
2	A	1003	HEC	CMB-C2B-C1B	-2.29	121.92	125.42
2	B	1002	HEC	CBD-CAD-C3D	-2.28	106.22	112.53
2	A	1003	HEC	O2A-CGA-CBA	2.28	121.19	114.00
2	B	1002	HEC	CAD-C3D-C4D	2.27	129.37	124.94
2	A	1006	HEC	CBA-CAA-C2A	-2.25	106.31	112.53
2	A	1008	HEC	CBA-CAA-C2A	-2.24	106.33	112.53
2	B	1008	HEC	O2A-CGA-CBA	2.21	120.98	114.00
2	B	1001	HEC	CMB-C2B-C1B	-2.21	122.06	125.42
2	A	1001	HEC	C3D-C4D-ND	-2.20	107.71	110.15
2	B	1006	HEC	C4C-NC-C1C	2.19	109.39	105.82
2	B	1008	HEC	CHB-C1B-NB	2.19	127.83	123.86
2	A	1008	HEC	CAD-CBD-CGD	-2.19	107.86	113.67
2	A	1006	HEC	O2D-CGD-CBD	2.18	120.90	114.00
2	A	1008	HEC	CBD-CAD-C3D	-2.18	106.50	112.53
2	A	1005	HEC	CMD-C2D-C1D	2.18	128.73	125.42
2	A	1004	HEC	CMB-C2B-C1B	-2.15	122.15	125.42
2	A	1003	HEC	C1D-C2D-C3D	-2.13	104.38	106.82
8	A	533	GOL	O2-C2-C3	2.12	117.96	109.18
2	A	1005	HEC	O2A-CGA-CBA	2.12	120.69	114.00
2	B	1005	HEC	CHD-C1D-ND	2.12	127.70	123.86
2	A	1008	HEC	CMC-C2C-C1C	-2.10	122.22	125.42
2	B	1004	HEC	C2A-C1A-NA	-2.08	108.32	110.32
2	A	1003	HEC	O1A-CGA-CBA	-2.07	116.52	123.09
2	B	1003	HEC	O2D-CGD-CBD	2.05	120.47	114.00
2	B	1005	HEC	CAD-C3D-C4D	2.05	128.94	124.94
2	A	1006	HEC	CMC-C2C-C1C	-2.04	122.31	125.42
2	B	1007	HEC	O2A-CGA-CBA	2.04	120.45	114.00
2	B	1002	HEC	CMD-C2D-C1D	2.02	128.50	125.42
2	B	1002	HEC	CHA-C1A-NA	2.02	126.65	124.45
2	B	1005	HEC	CHC-C4B-NB	-2.01	122.26	124.45
2	A	1008	HEC	O1A-CGA-CBA	-2.01	116.71	123.09
2	A	1005	HEC	CHB-C4A-NA	2.01	126.64	124.45

There are no chirality outliers.

All (106) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1004	HEC	C2B-C3B-CAB-CBB
2	A	1004	HEC	C4B-C3B-CAB-CBB
2	A	1004	HEC	C2C-C3C-CAC-CBC
2	A	1004	HEC	C4C-C3C-CAC-CBC
2	A	1005	HEC	C2B-C3B-CAB-CBB
2	A	1005	HEC	C4B-C3B-CAB-CBB
2	A	1005	HEC	C2C-C3C-CAC-CBC
2	A	1005	HEC	C4C-C3C-CAC-CBC
2	A	1006	HEC	C2B-C3B-CAB-CBB
2	A	1006	HEC	C4B-C3B-CAB-CBB
2	A	1006	HEC	C2C-C3C-CAC-CBC
2	A	1006	HEC	C4C-C3C-CAC-CBC
2	A	1007	HEC	C2B-C3B-CAB-CBB
2	A	1007	HEC	C4B-C3B-CAB-CBB
2	A	1007	HEC	C2C-C3C-CAC-CBC
2	A	1007	HEC	C4C-C3C-CAC-CBC
2	A	1008	HEC	C2B-C3B-CAB-CBB
2	A	1008	HEC	C2C-C3C-CAC-CBC
2	A	1008	HEC	C4C-C3C-CAC-CBC
2	A	1002	HEC	C2B-C3B-CAB-CBB
2	A	1002	HEC	C4B-C3B-CAB-CBB
2	A	1002	HEC	C2C-C3C-CAC-CBC
2	A	1002	HEC	C4C-C3C-CAC-CBC
2	A	1003	HEC	C2B-C3B-CAB-CBB
2	A	1003	HEC	C4B-C3B-CAB-CBB
2	A	1003	HEC	C2C-C3C-CAC-CBC
2	A	1003	HEC	C4C-C3C-CAC-CBC
2	A	1001	HEC	C2B-C3B-CAB-CBB
2	A	1001	HEC	C4B-C3B-CAB-CBB
2	A	1001	HEC	C2C-C3C-CAC-CBC
2	A	1001	HEC	C4C-C3C-CAC-CBC
2	B	1004	HEC	C2B-C3B-CAB-CBB
2	B	1004	HEC	C4B-C3B-CAB-CBB
2	B	1004	HEC	C2C-C3C-CAC-CBC
2	B	1004	HEC	C4C-C3C-CAC-CBC
2	B	1005	HEC	C2B-C3B-CAB-CBB
2	B	1005	HEC	C4B-C3B-CAB-CBB
2	B	1005	HEC	C2C-C3C-CAC-CBC
2	B	1005	HEC	C4C-C3C-CAC-CBC
2	B	1006	HEC	C2B-C3B-CAB-CBB
2	B	1006	HEC	C4B-C3B-CAB-CBB
2	B	1006	HEC	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
2	B	1006	HEC	C4C-C3C-CAC-CBC
2	B	1007	HEC	C2B-C3B-CAB-CBB
2	B	1007	HEC	C4B-C3B-CAB-CBB
2	B	1007	HEC	C2C-C3C-CAC-CBC
2	B	1007	HEC	C4C-C3C-CAC-CBC
2	B	1008	HEC	C2B-C3B-CAB-CBB
2	B	1008	HEC	C4B-C3B-CAB-CBB
2	B	1008	HEC	C2C-C3C-CAC-CBC
2	B	1008	HEC	C4C-C3C-CAC-CBC
2	B	1002	HEC	C2B-C3B-CAB-CBB
2	B	1002	HEC	C4B-C3B-CAB-CBB
2	B	1002	HEC	C2C-C3C-CAC-CBC
2	B	1002	HEC	C4C-C3C-CAC-CBC
2	B	1003	HEC	C2B-C3B-CAB-CBB
2	B	1003	HEC	C4B-C3B-CAB-CBB
2	B	1003	HEC	C2C-C3C-CAC-CBC
2	B	1003	HEC	C4C-C3C-CAC-CBC
2	B	1001	HEC	C2B-C3B-CAB-CBB
2	B	1001	HEC	C4B-C3B-CAB-CBB
2	B	1001	HEC	C2C-C3C-CAC-CBC
2	B	1001	HEC	C4C-C3C-CAC-CBC
8	A	537	GOL	C1-C2-C3-O3
8	B	533	GOL	O1-C1-C2-C3
8	B	533	GOL	C1-C2-C3-O3
8	A	537	GOL	O2-C2-C3-O3
8	B	533	GOL	O1-C1-C2-O2
8	B	533	GOL	O2-C2-C3-O3
8	A	536	GOL	O1-C1-C2-O2
2	A	1008	HEC	C4B-C3B-CAB-CBB
2	A	1004	HEC	CAA-CBA-CGA-O2A
2	B	1005	HEC	CAA-CBA-CGA-O2A
2	A	1008	HEC	CAD-CBD-CGD-O1D
2	A	1002	HEC	CAA-CBA-CGA-O2A
2	B	1008	HEC	CAD-CBD-CGD-O2D
2	B	1002	HEC	CAA-CBA-CGA-O1A
2	A	1002	HEC	CAA-CBA-CGA-O1A
2	A	1004	HEC	CAA-CBA-CGA-O1A
2	A	1005	HEC	CAA-CBA-CGA-O2A
2	B	1004	HEC	CAA-CBA-CGA-O1A
2	B	1008	HEC	CAD-CBD-CGD-O1D
2	B	1005	HEC	CAA-CBA-CGA-O1A
2	A	1003	HEC	CAA-CBA-CGA-O2A

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Mol	Chain	Res	Type	Atoms
2	A	1003	HEC	CAD-CBD-CGD-O2D
2	B	1004	HEC	CAA-CBA-CGA-O2A
2	A	1005	HEC	CAA-CBA-CGA-O1A
2	A	1003	HEC	CAA-CBA-CGA-O1A
2	A	1008	HEC	CAD-CBD-CGD-O2D
2	B	1001	HEC	CAA-CBA-CGA-O2A
2	B	1001	HEC	CAD-CBD-CGD-O1D
2	B	1002	HEC	CAA-CBA-CGA-O2A
2	B	1001	HEC	CAA-CBA-CGA-O1A
2	B	1001	HEC	CAD-CBD-CGD-O2D
8	A	533	GOL	O2-C2-C3-O3
2	A	1003	HEC	CAD-CBD-CGD-O1D
2	A	1001	HEC	CAD-CBD-CGD-O2D
2	A	1001	HEC	CAD-CBD-CGD-O1D
2	B	1006	HEC	CAA-CBA-CGA-O1A
2	B	1007	HEC	CAA-CBA-CGA-O1A
2	A	1001	HEC	CAA-CBA-CGA-O2A
2	B	1007	HEC	CAA-CBA-CGA-O2A
2	B	1006	HEC	CAA-CBA-CGA-O2A
2	B	1003	HEC	CAA-CBA-CGA-O2A
2	A	1006	HEC	CAA-CBA-CGA-O1A
2	A	1001	HEC	CAA-CBA-CGA-O1A

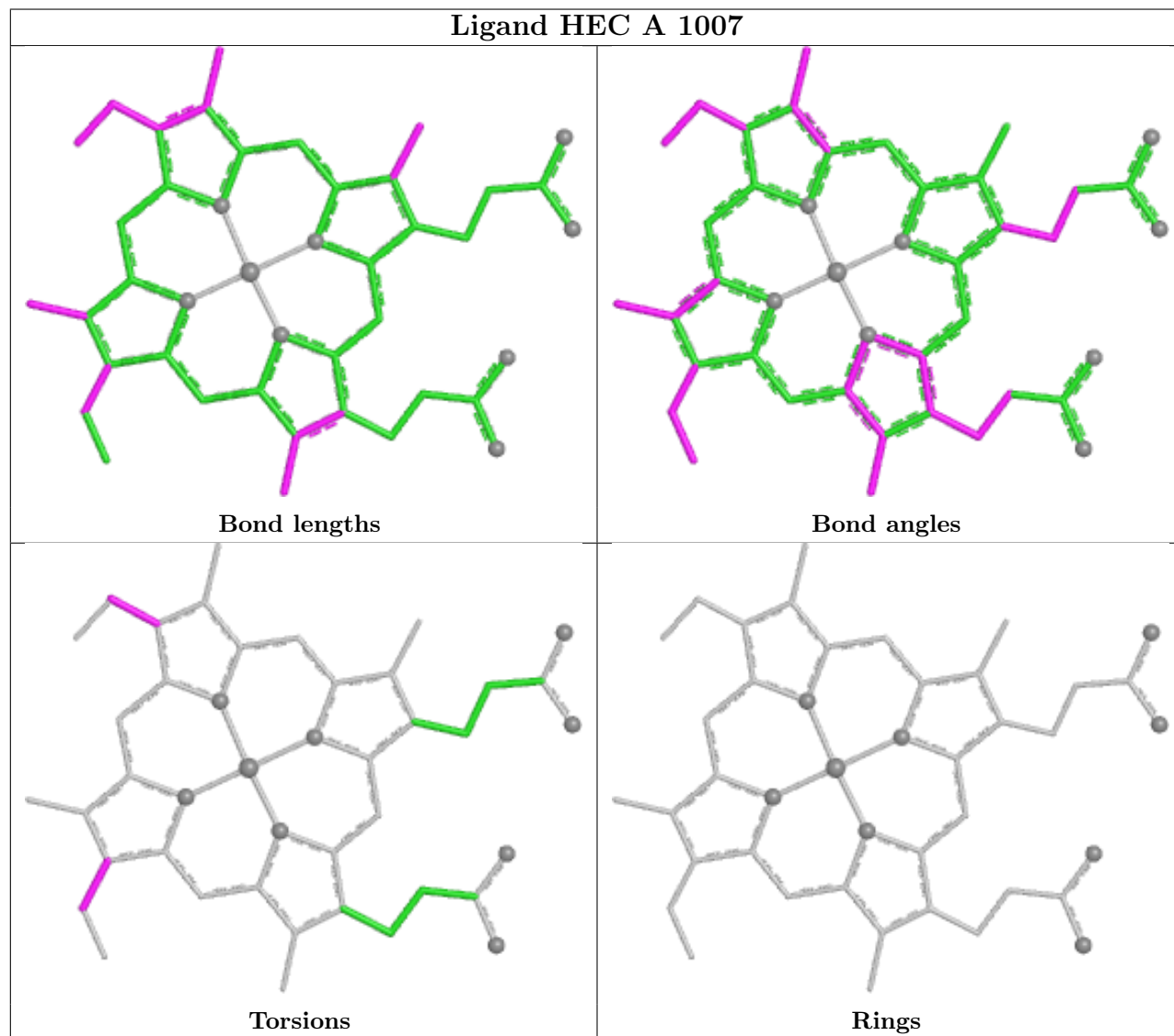
There are no ring outliers.

12 monomers are involved in 23 short contacts:

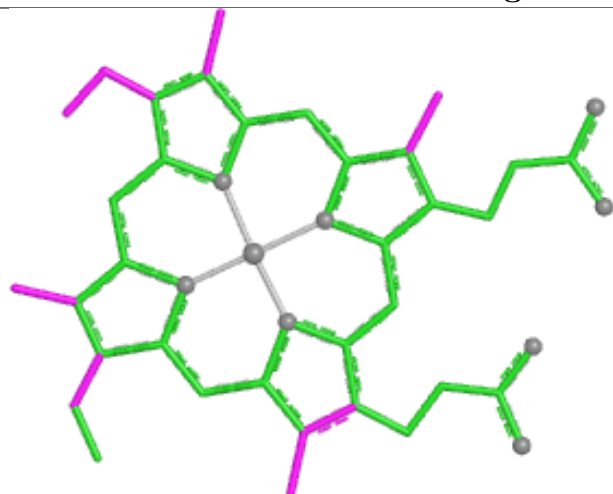
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	533	GOL	7	0
8	B	533	GOL	1	0
8	A	537	GOL	3	0
2	A	1005	HEC	3	0
2	A	1002	HEC	1	0
2	B	1008	HEC	2	0
2	B	1002	HEC	1	0
2	B	1007	HEC	1	0
2	A	1008	HEC	2	0
2	B	1005	HEC	1	0
2	A	1003	HEC	2	0
2	B	1001	HEC	1	0

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

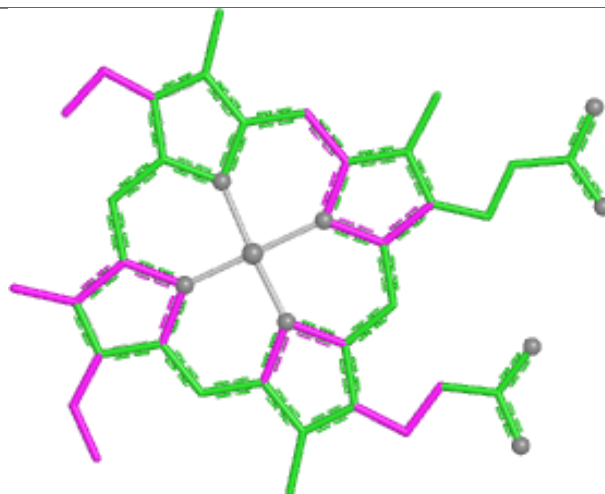
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.



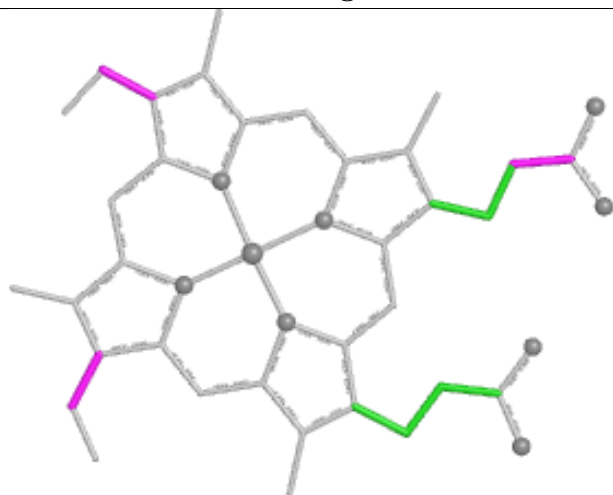
Ligand HEC B 1006



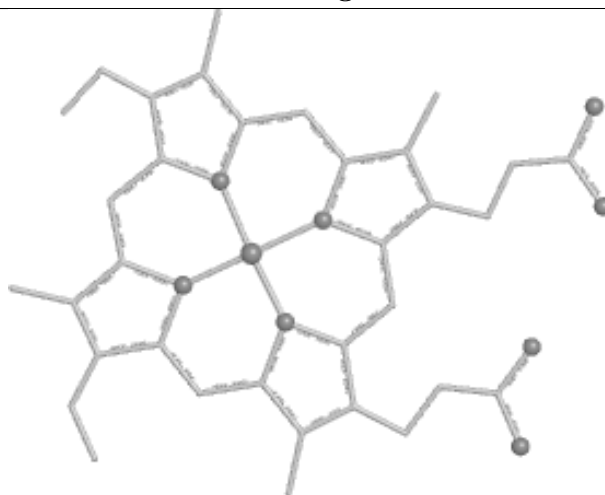
Bond lengths



Bond angles

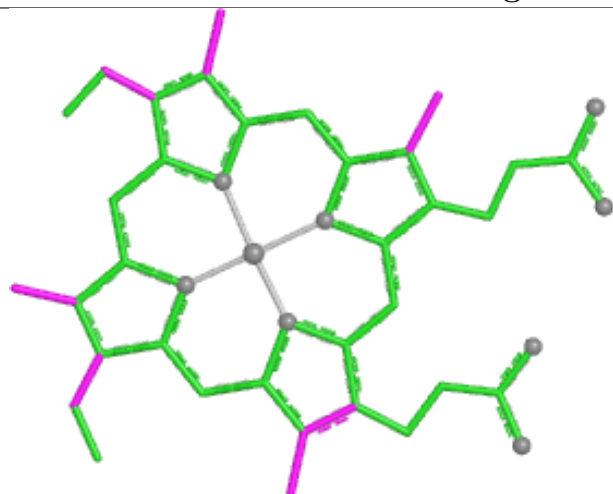


Torsions

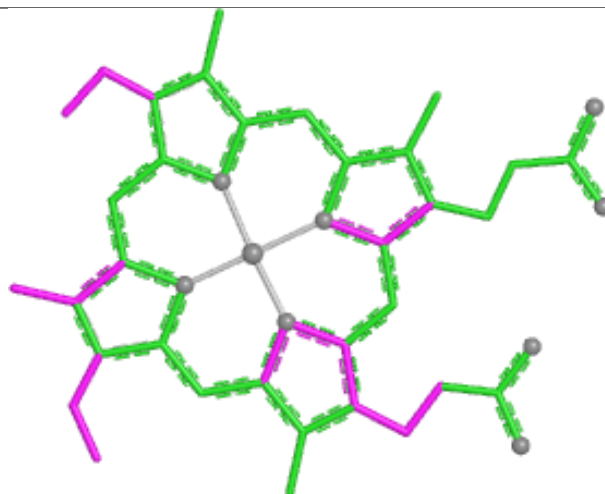


Rings

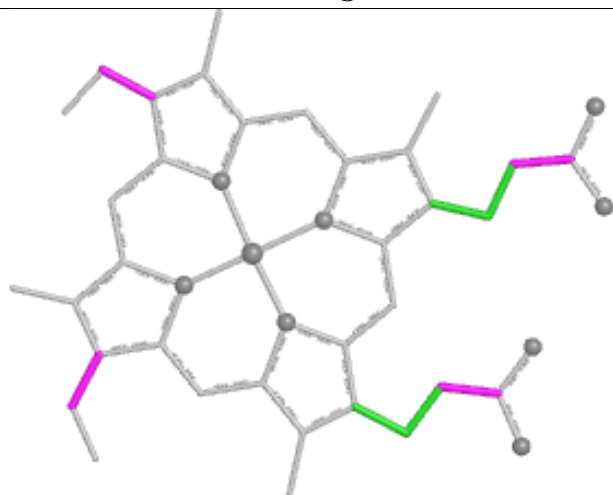
Ligand HEC A 1001



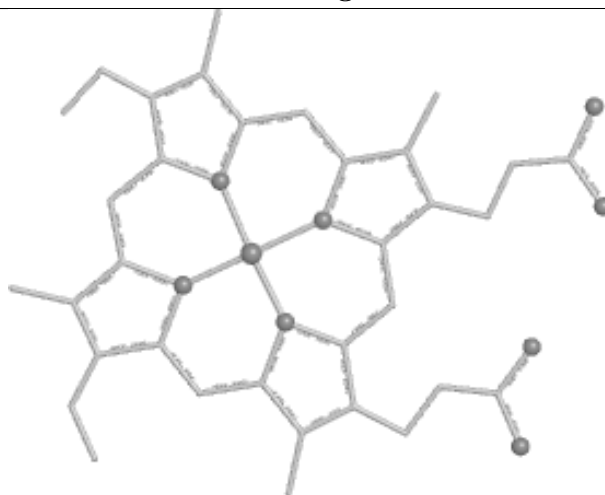
Bond lengths



Bond angles

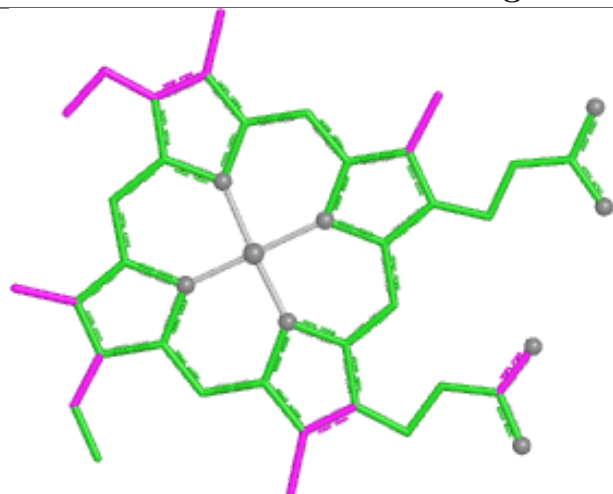


Torsions

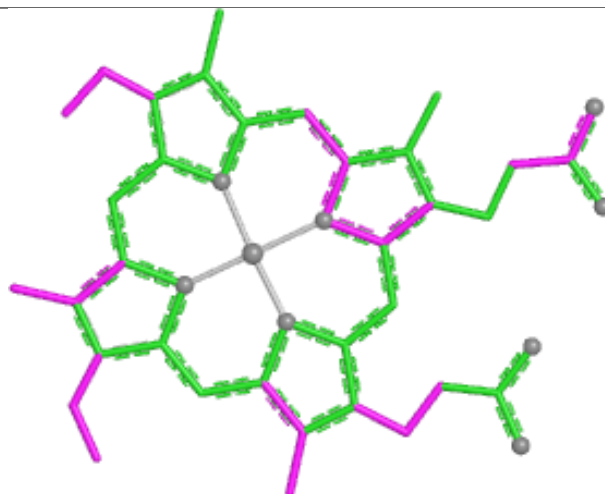


Rings

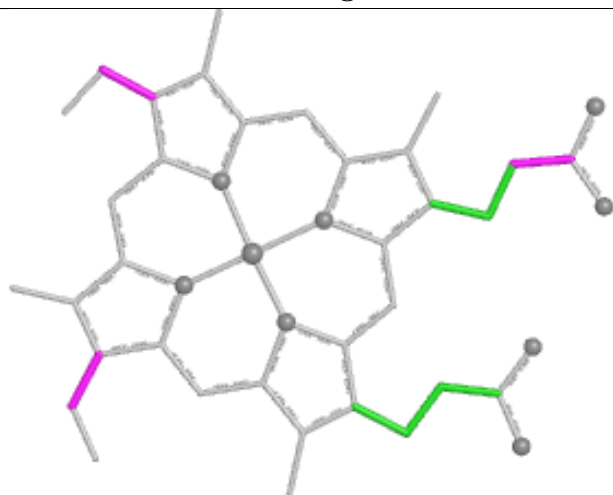
Ligand HEC A 1005



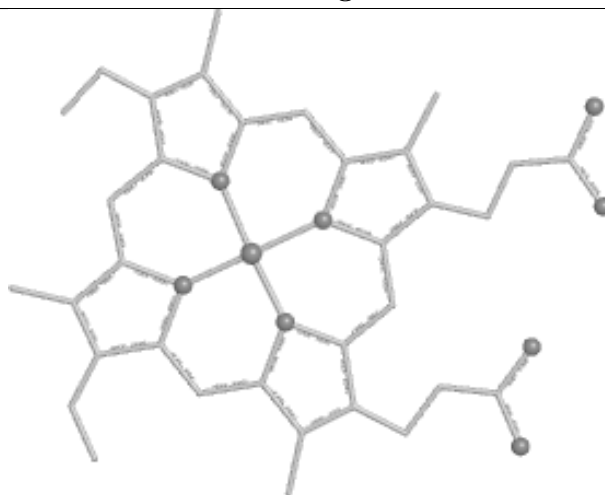
Bond lengths



Bond angles

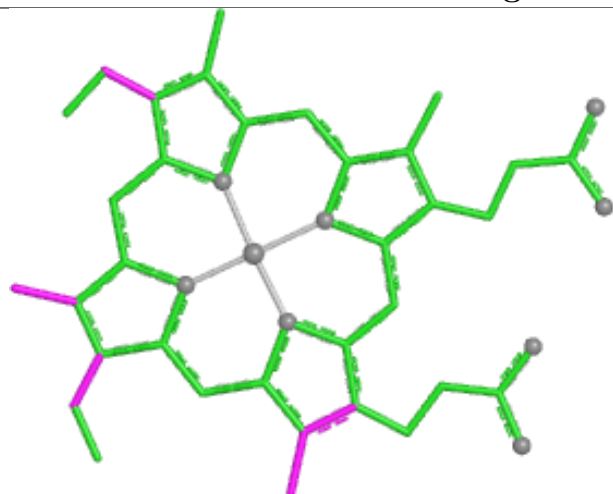


Torsions

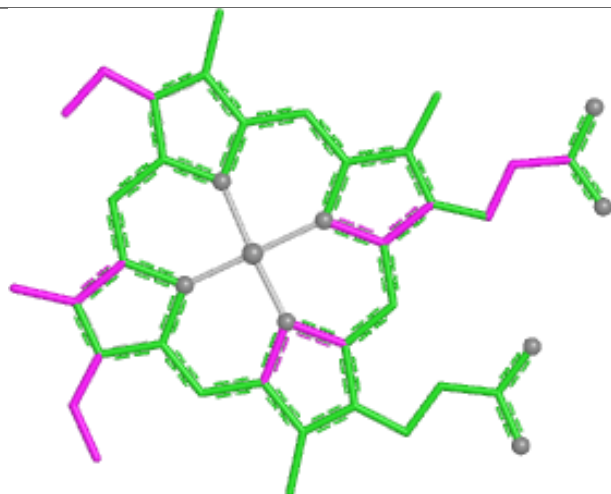


Rings

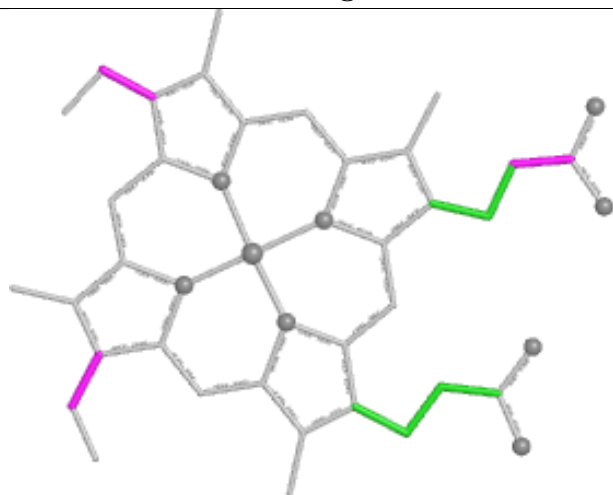
Ligand HEC A 1002



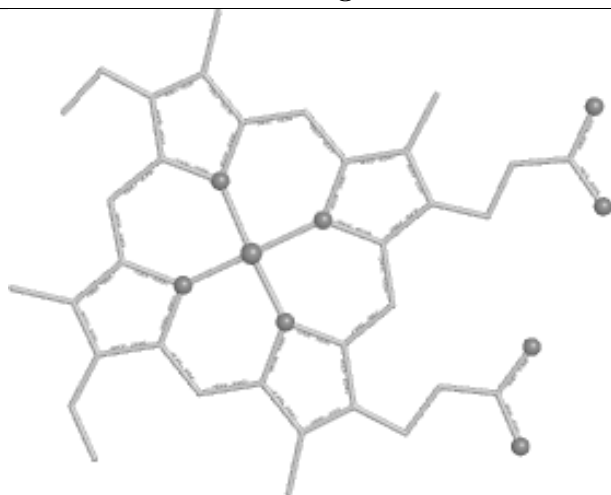
Bond lengths



Bond angles

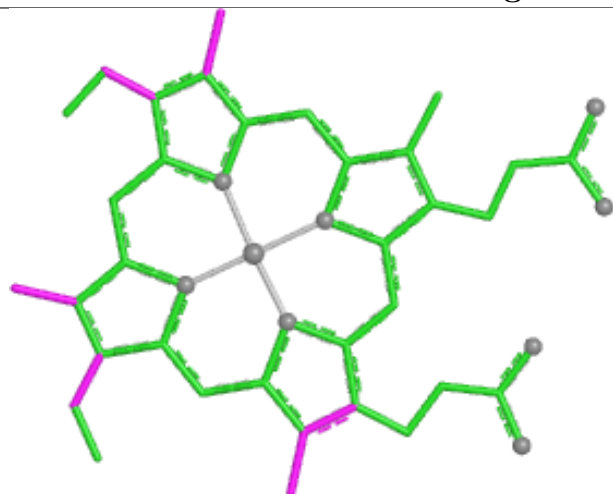


Torsions

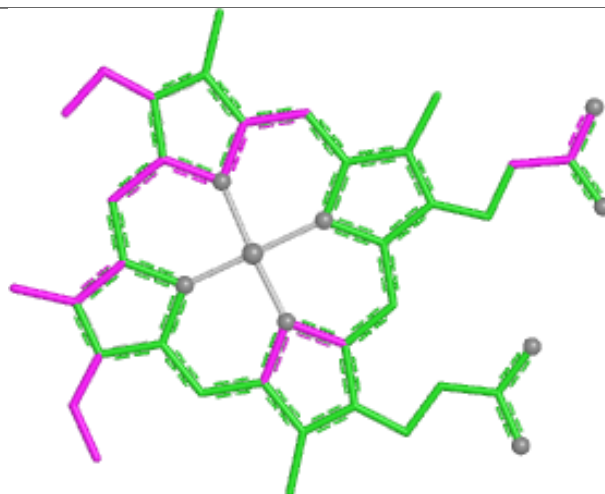


Rings

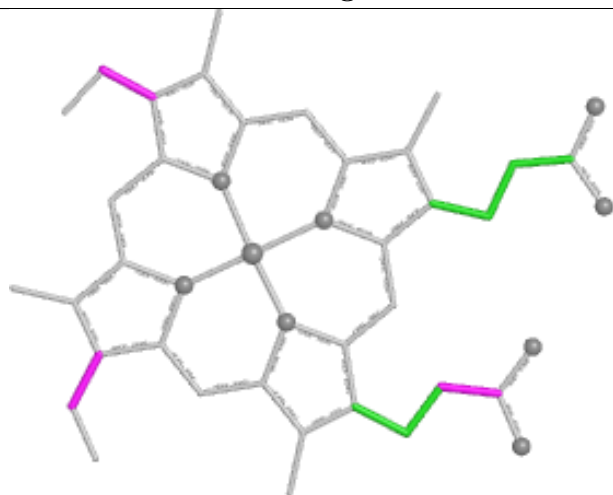
Ligand HEC B 1008



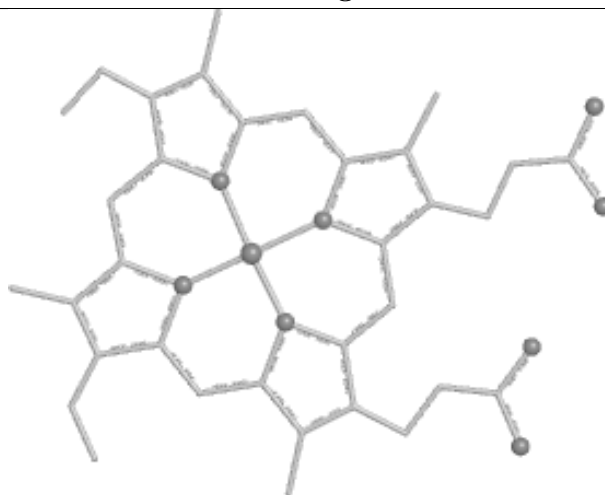
Bond lengths



Bond angles

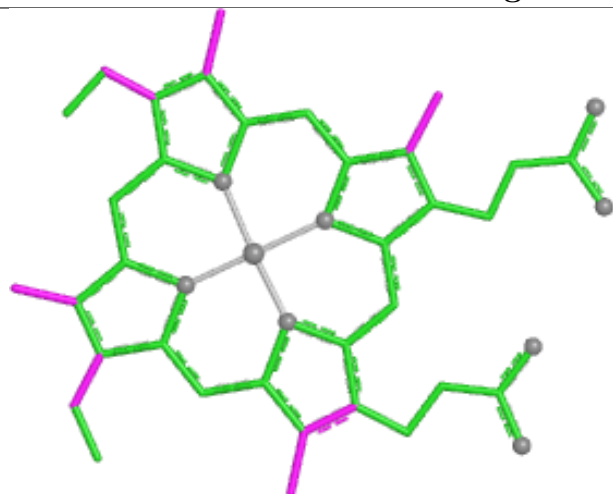


Torsions

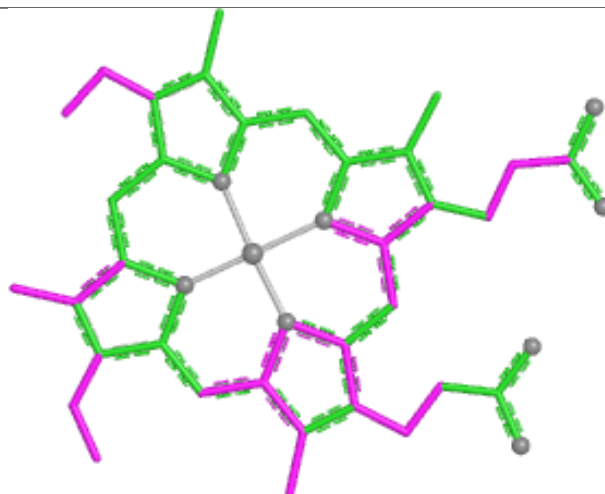


Rings

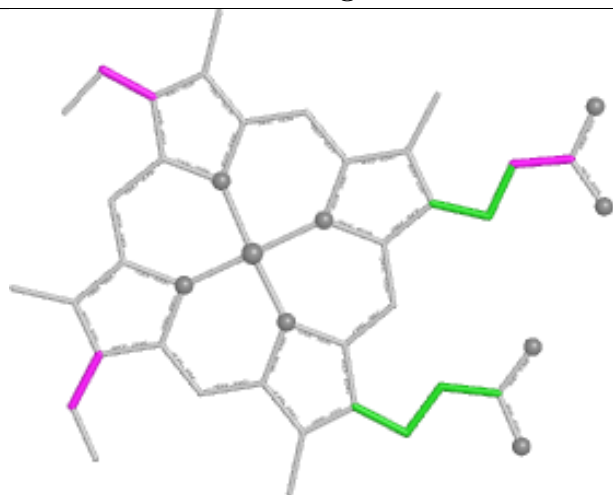
Ligand HEC B 1002



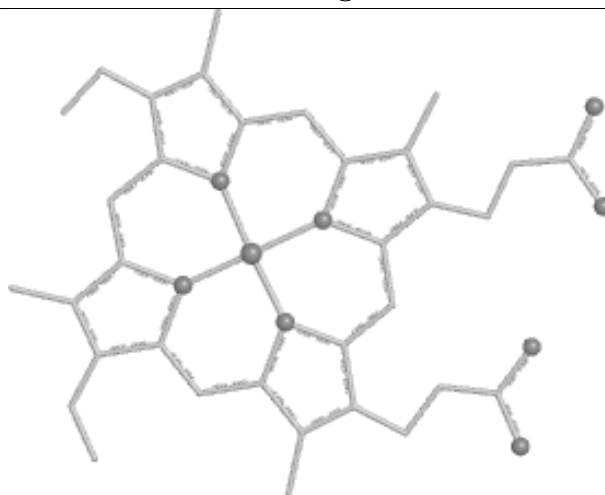
Bond lengths



Bond angles

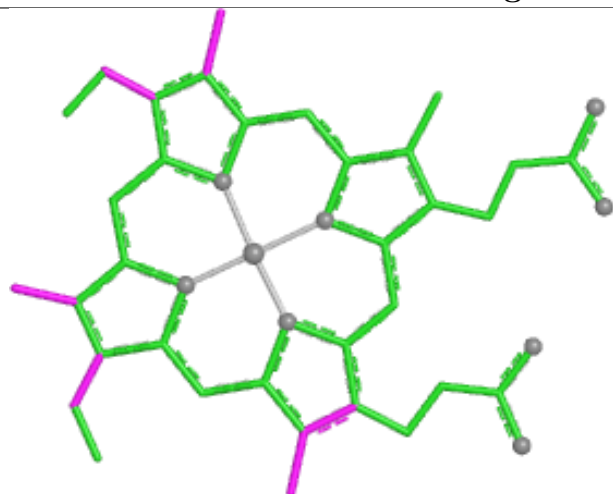


Torsions

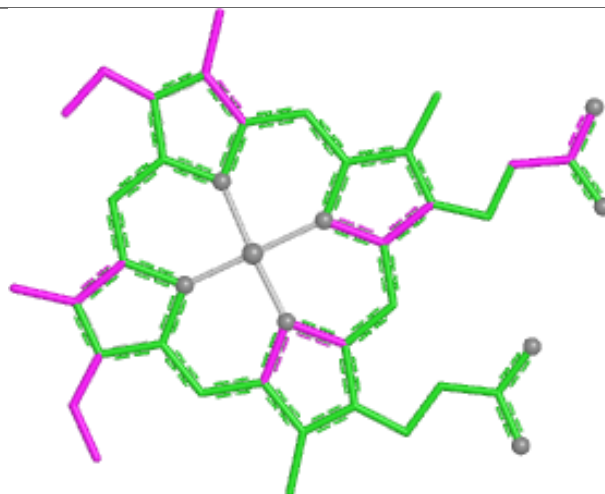


Rings

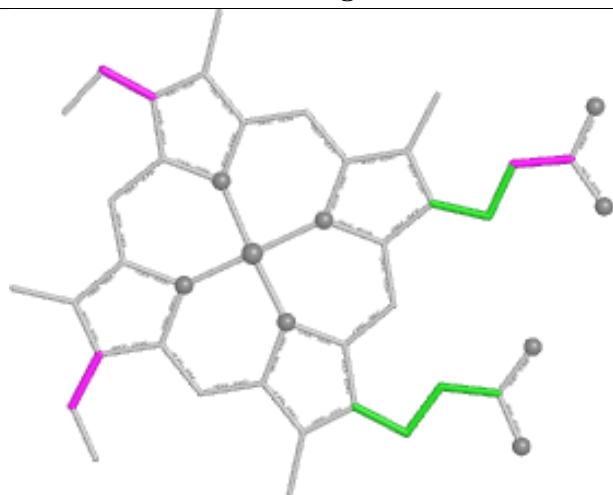
Ligand HEC B 1004



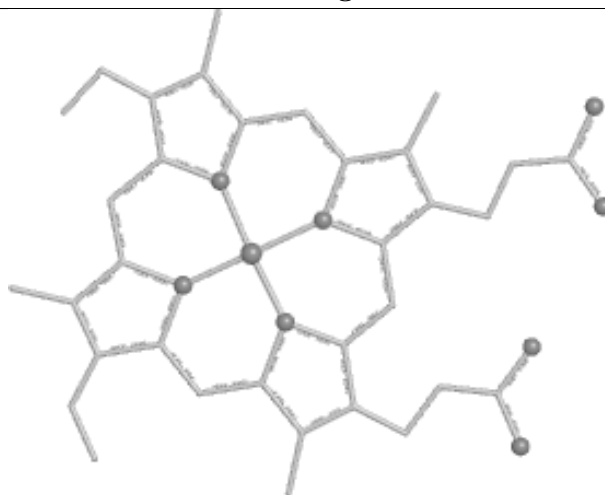
Bond lengths



Bond angles

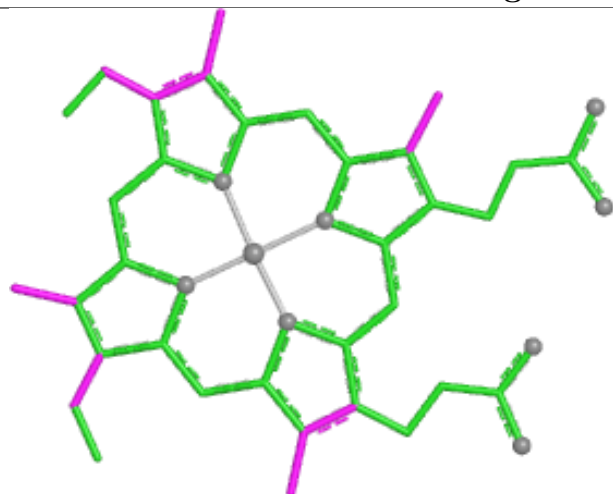


Torsions

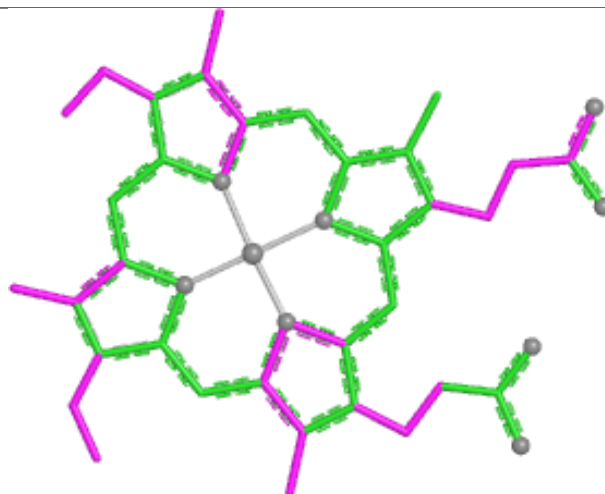


Rings

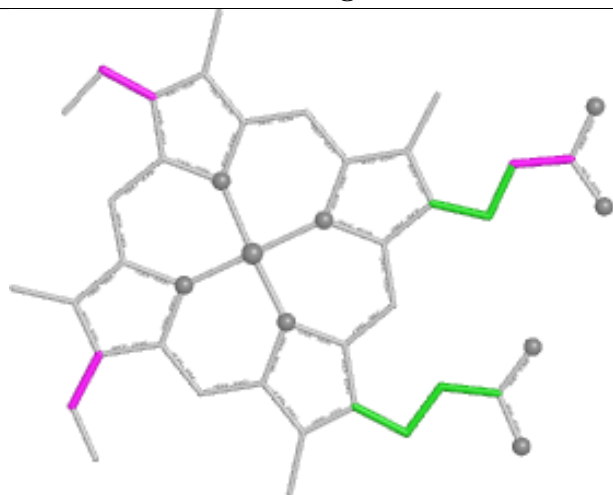
Ligand HEC B 1007



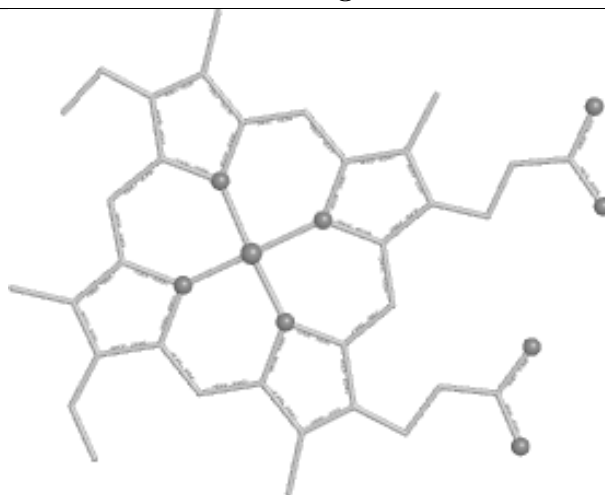
Bond lengths



Bond angles

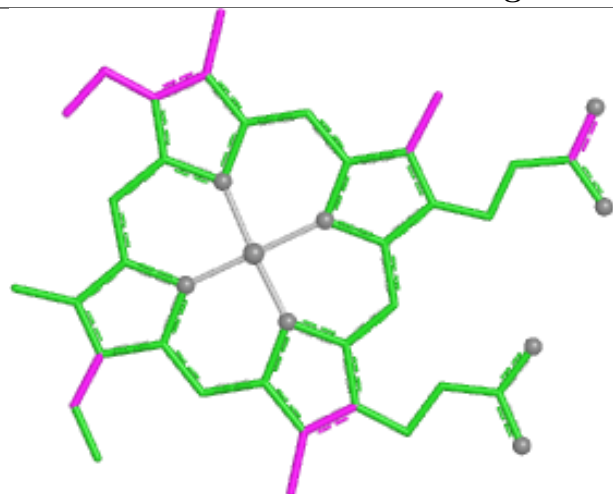


Torsions

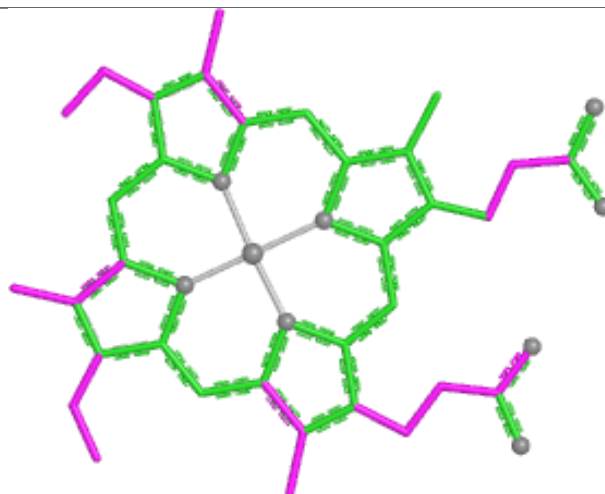


Rings

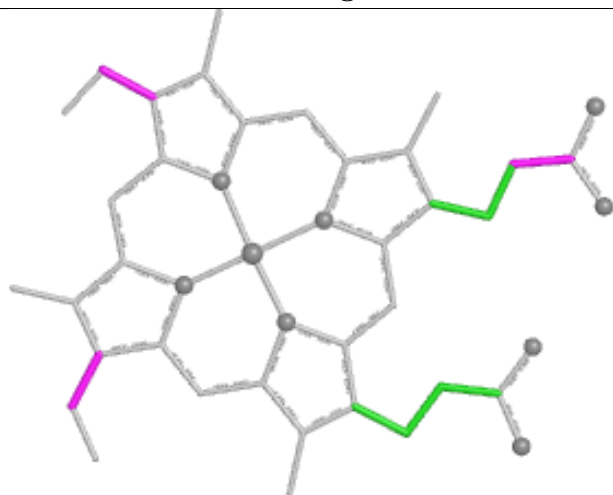
Ligand HEC B 1003



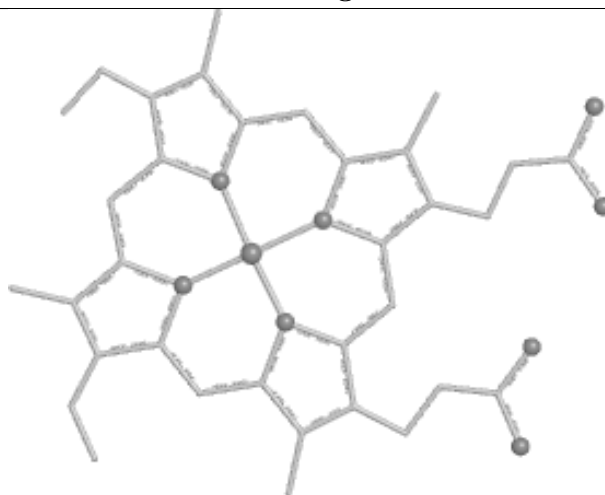
Bond lengths



Bond angles

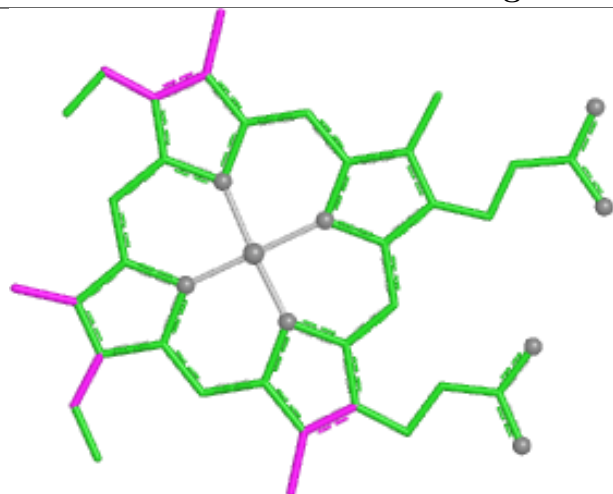


Torsions

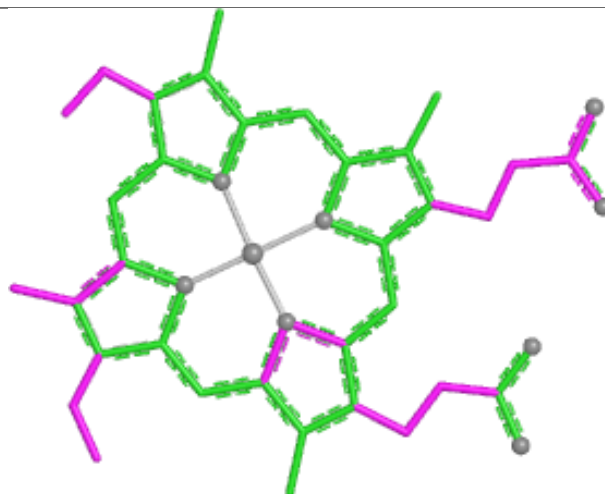


Rings

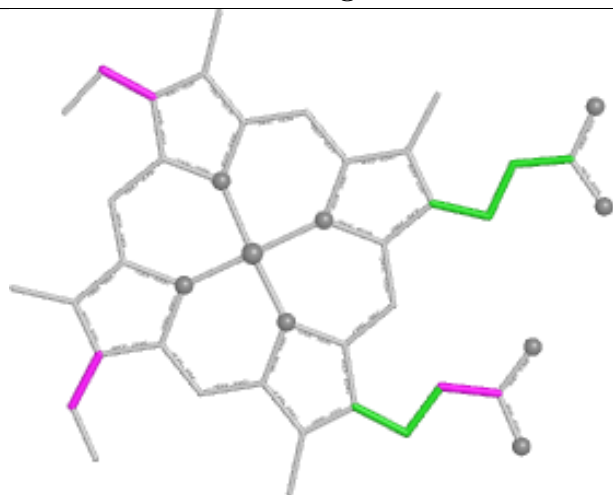
Ligand HEC A 1008



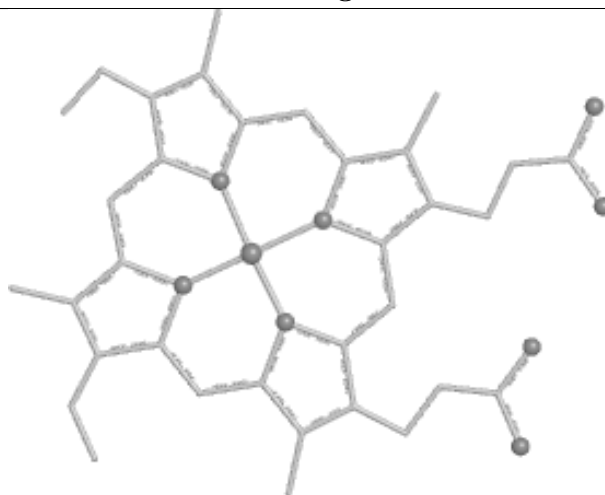
Bond lengths



Bond angles

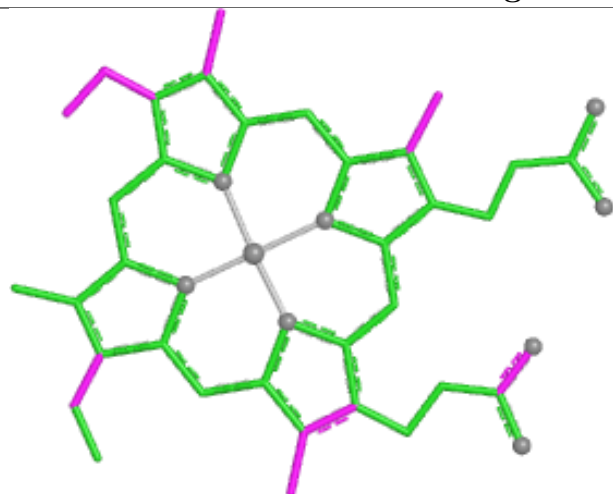


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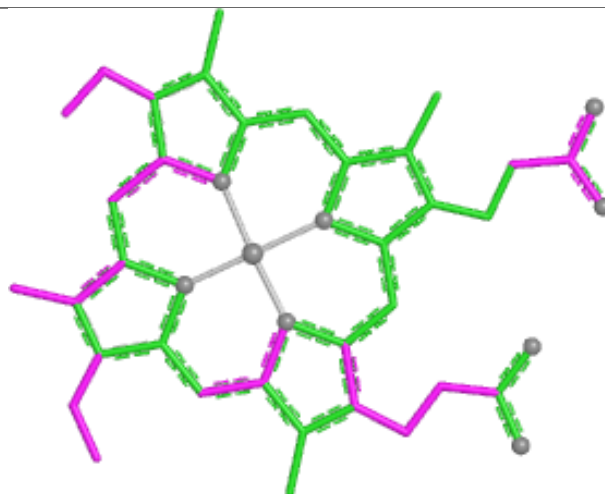


Rings

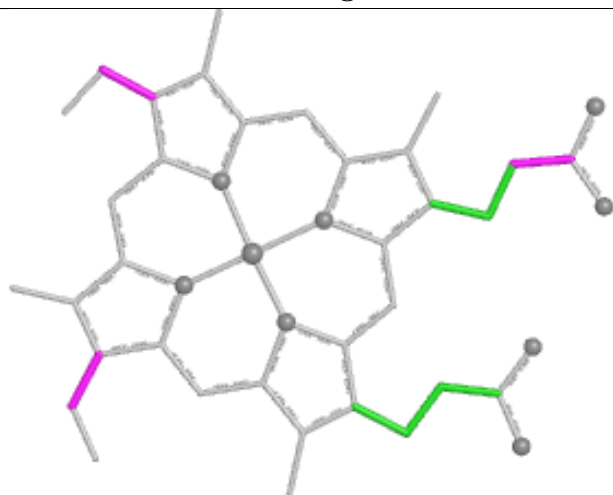
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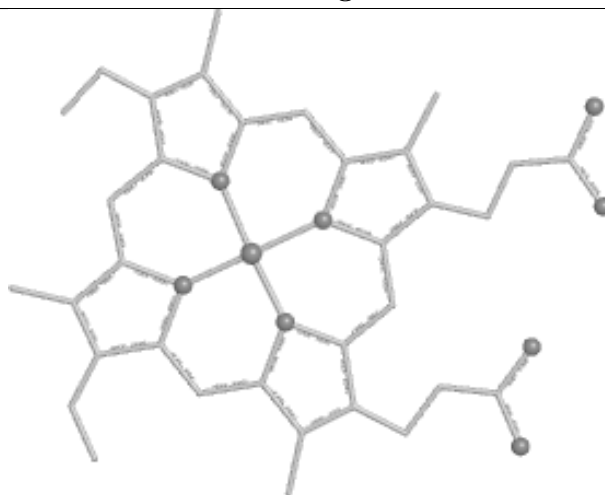
Bond lengths



Bond angles

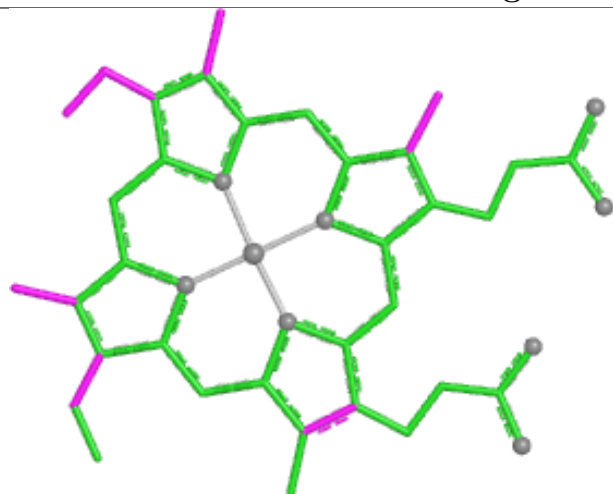


Torsions

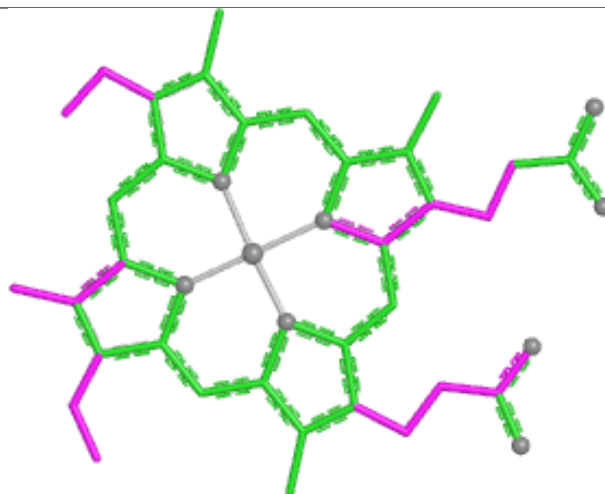


Rings

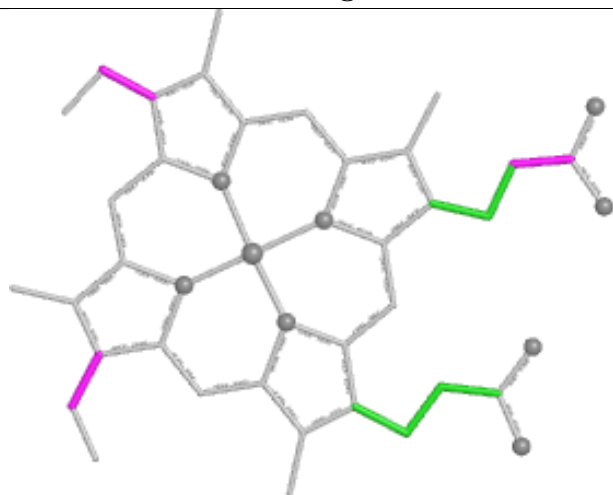
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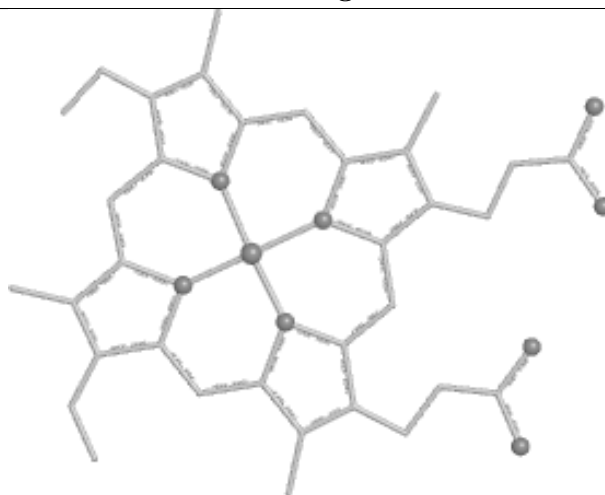
Bond lengths



Bond angles

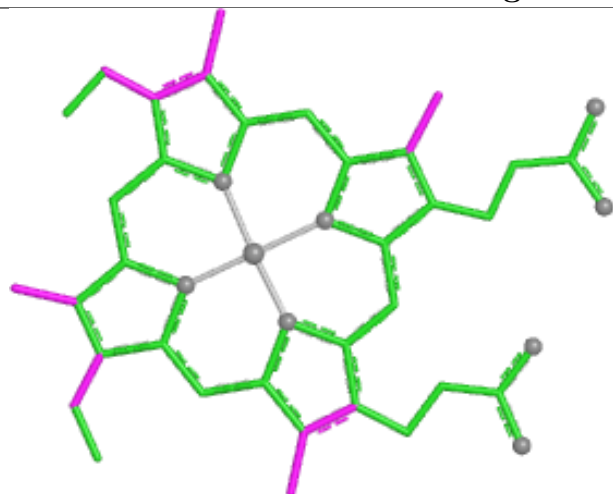


Torsions

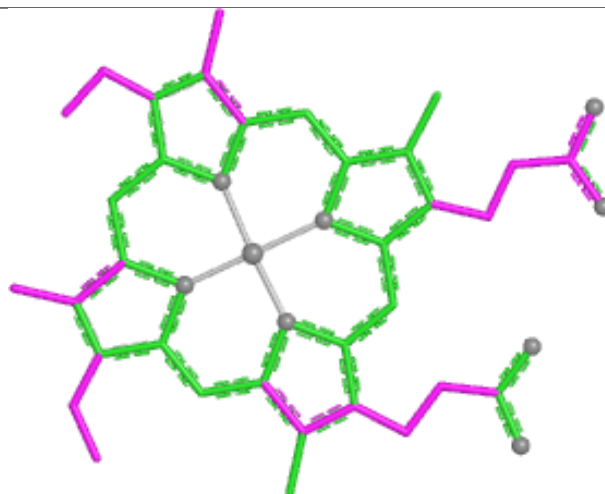


Rings

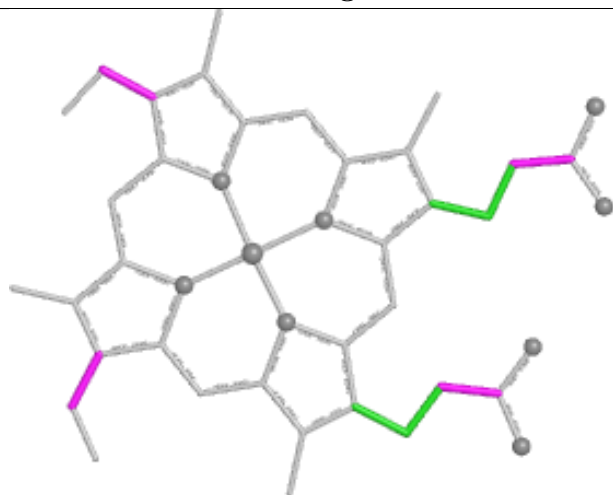
Ligand HEC A 1003



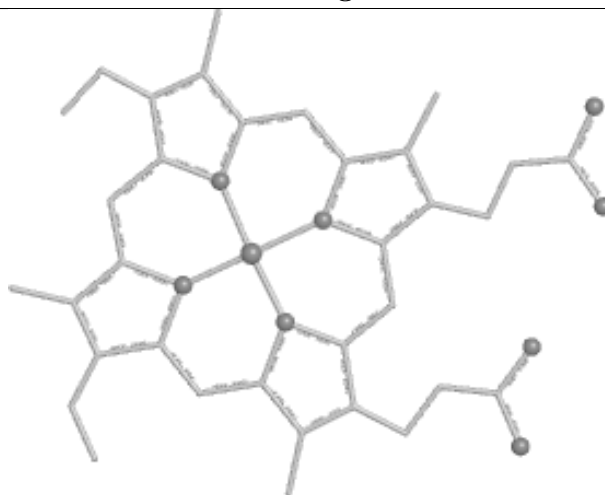
Bond lengths



Bond angles

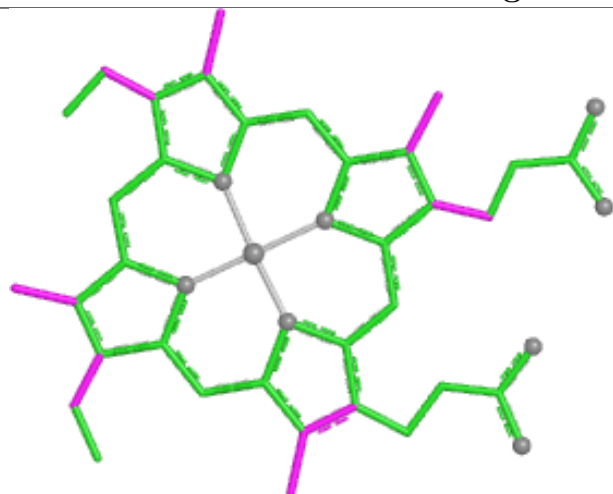


Torsions

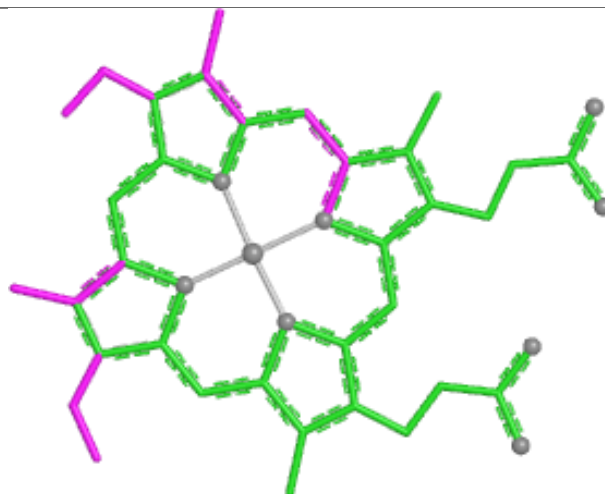


Rings

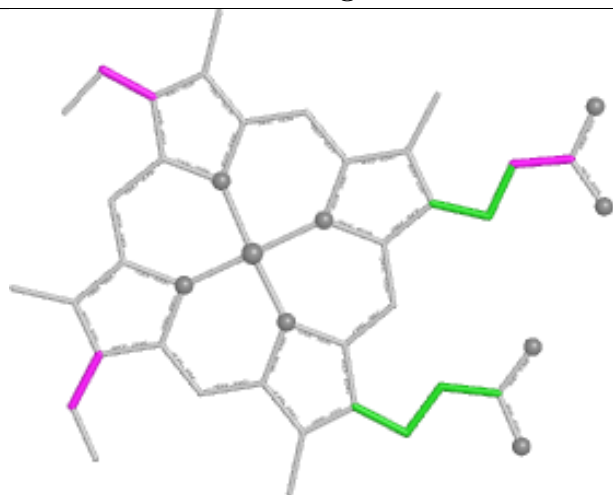
Ligand HEC A 1004



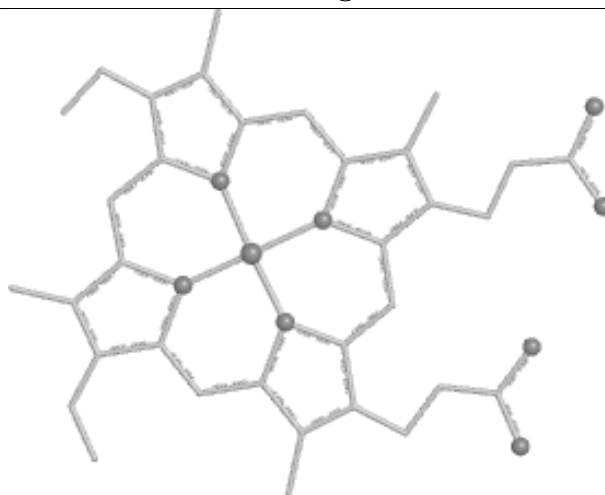
Bond lengths



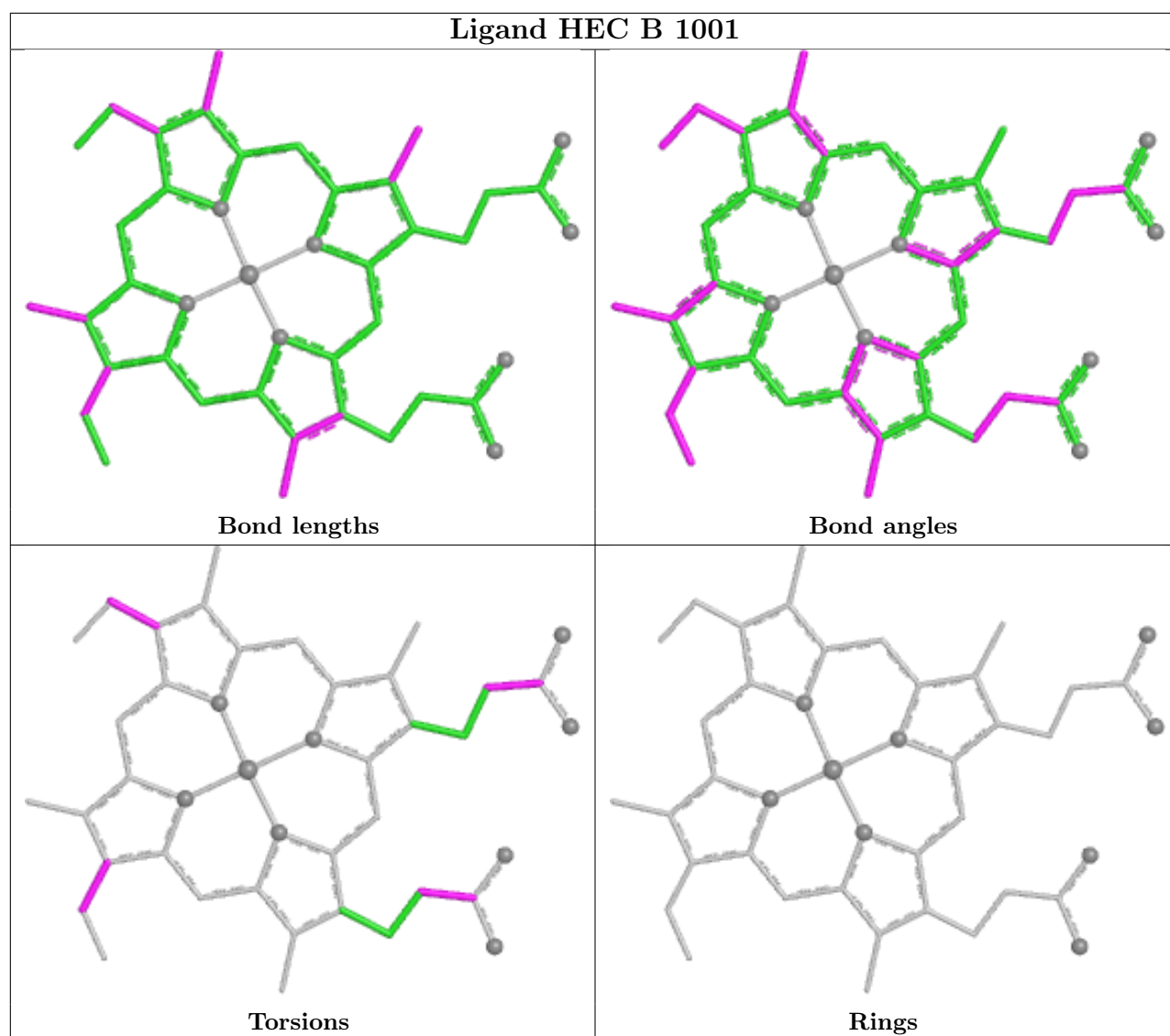
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	519/525 (98%)	-0.84	1 (0%) 91 92	7, 12, 23, 34	12 (2%)
1	B	518/525 (98%)	-0.83	1 (0%) 91 92	8, 13, 24, 39	13 (2%)
All	All	1037/1050 (98%)	-0.84	2 (0%) 91 92	7, 13, 24, 39	25 (2%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	523	ALA	4.1
1	B	522	VAL	2.8

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(Å ²)	Q<0.9
8	GOL	B	535	6/6	0.88	0.15	17,37,46,47	0
8	GOL	A	537	6/6	0.91	0.12	17,27,46,49	0
8	GOL	A	533	6/6	0.92	0.18	17,23,31,37	0

Continued on next page...

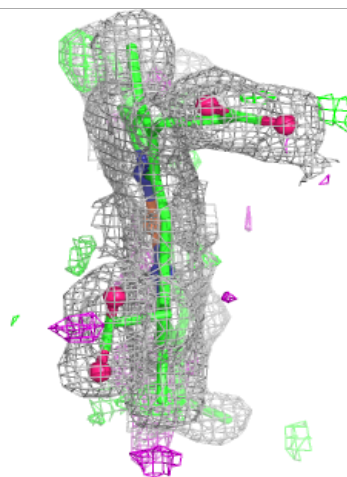
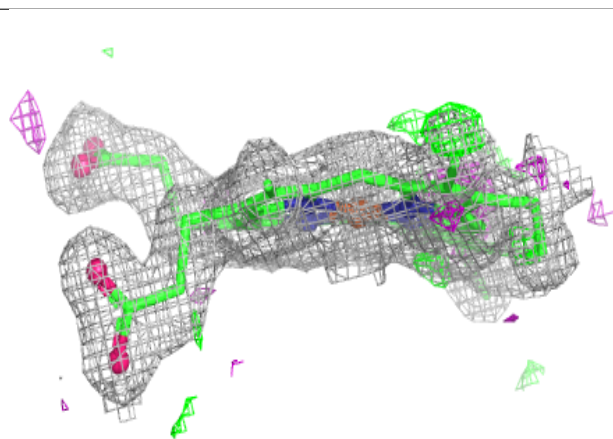
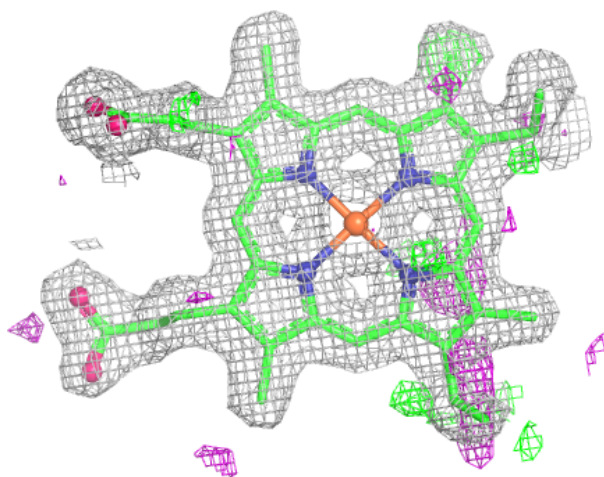
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NA	B	529	1/1	0.93	0.09	27,27,27,27	0
8	GOL	B	533	6/6	0.93	0.12	20,35,49,49	0
8	GOL	B	534	6/6	0.93	0.13	18,26,31,32	0
8	GOL	A	536	6/6	0.93	0.14	27,39,41,49	0
5	NA	A	529	1/1	0.94	0.07	23,23,23,23	0
8	GOL	A	534	6/6	0.96	0.10	18,21,28,36	0
7	SO4	B	532	5/5	0.97	0.07	13,14,17,17	5
8	GOL	A	535	6/6	0.98	0.11	15,30,35,44	0
4	CO	B	527	1/1	0.98	0.15	10,10,10,10	1
2	HEC	B	1008	43/43	0.98	0.07	8,15,28,49	0
2	HEC	B	1002	43/43	0.99	0.04	7,10,14,19	0
2	HEC	B	1003	43/43	0.99	0.06	6,11,37,49	0
2	HEC	B	1001	43/43	0.99	0.05	9,12,19,28	0
4	CO	A	527	1/1	0.99	0.12	9,9,9,9	1
4	CO	A	528	1/1	0.99	0.03	11,11,11,11	1
2	HEC	A	1005	43/43	0.99	0.05	6,9,15,32	0
4	CO	B	528	1/1	0.99	0.04	12,12,12,12	1
2	HEC	A	1006	43/43	0.99	0.04	5,8,11,13	0
2	HEC	A	1007	43/43	0.99	0.05	5,9,16,32	0
6	CL	B	530	1/1	0.99	0.10	23,23,23,23	0
7	SO4	A	531	5/5	0.99	0.05	20,22,23,27	0
7	SO4	A	532	5/5	0.99	0.08	18,19,22,25	0
7	SO4	B	531	5/5	0.99	0.04	17,23,24,29	0
2	HEC	A	1008	43/43	0.99	0.06	8,15,30,49	0
2	HEC	A	1002	43/43	0.99	0.04	8,12,15,24	0
2	HEC	A	1003	43/43	0.99	0.07	7,11,35,49	0
2	HEC	A	1001	43/43	0.99	0.05	9,16,23,33	0
2	HEC	B	1004	43/43	0.99	0.04	6,9,12,13	0
2	HEC	B	1005	43/43	0.99	0.05	5,10,14,41	0
2	HEC	B	1006	43/43	0.99	0.04	6,9,11,12	0
2	HEC	B	1007	43/43	0.99	0.05	6,10,15,29	0
2	HEC	A	1004	43/43	0.99	0.04	5,9,13,14	0
3	CA	B	526	1/1	1.00	0.05	15,15,15,15	0
6	CL	A	530	1/1	1.00	0.10	22,22,22,22	0
3	CA	A	526	1/1	1.00	0.06	14,14,14,14	0

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

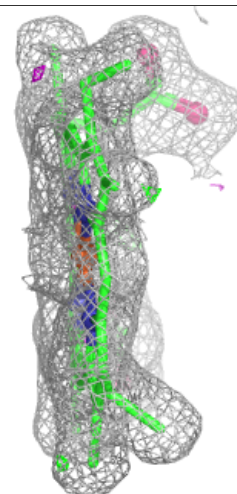
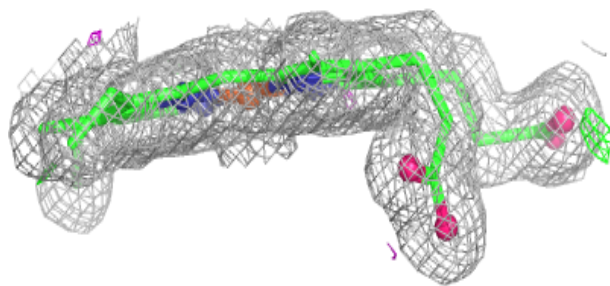
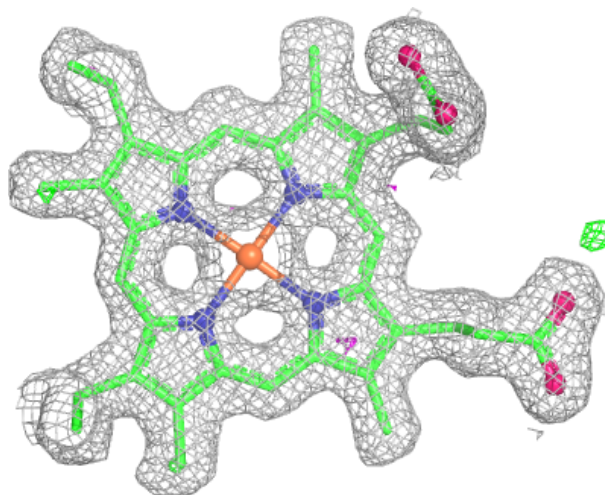
Electron density around HEC B 1008:

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



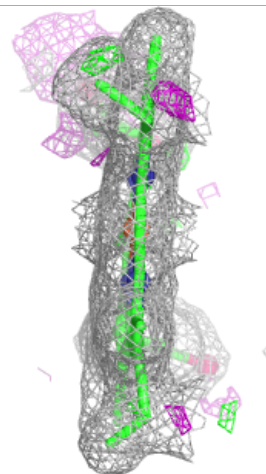
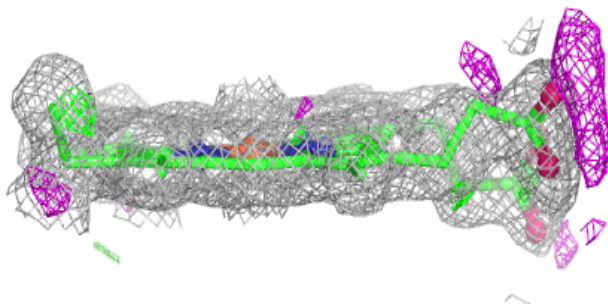
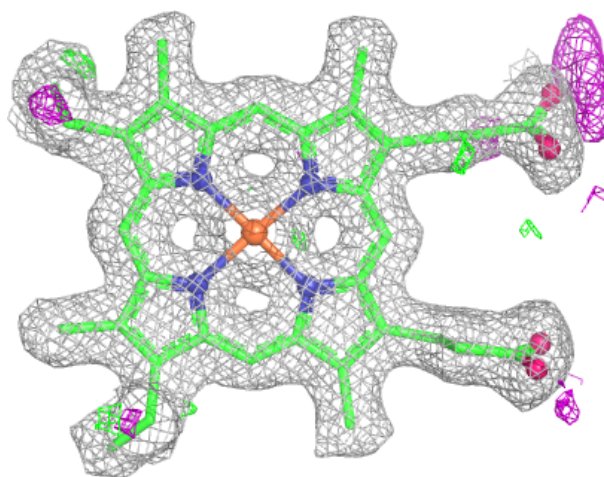
Electron density around HEC B 1002:

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



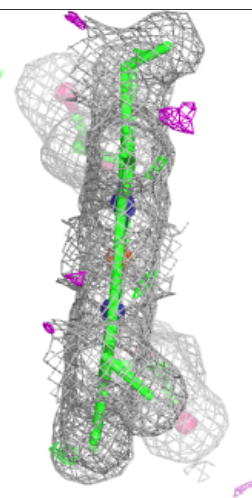
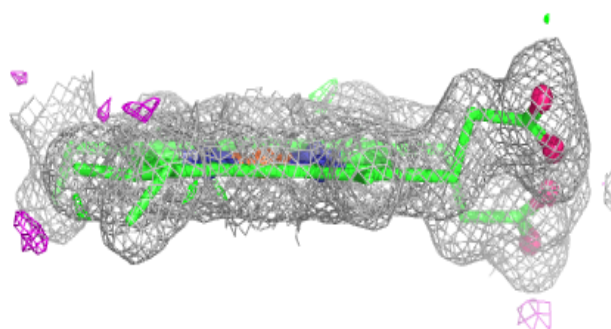
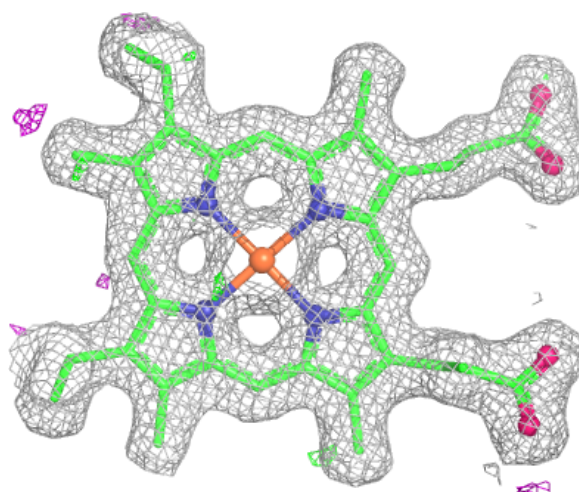
Electron density around HEC B 1003:

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



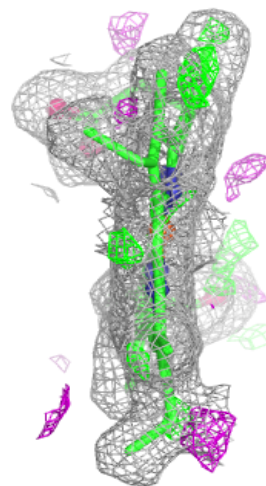
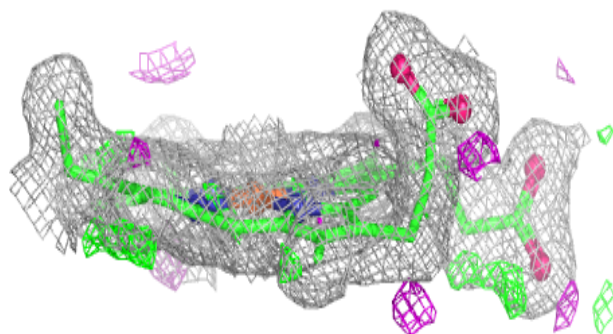
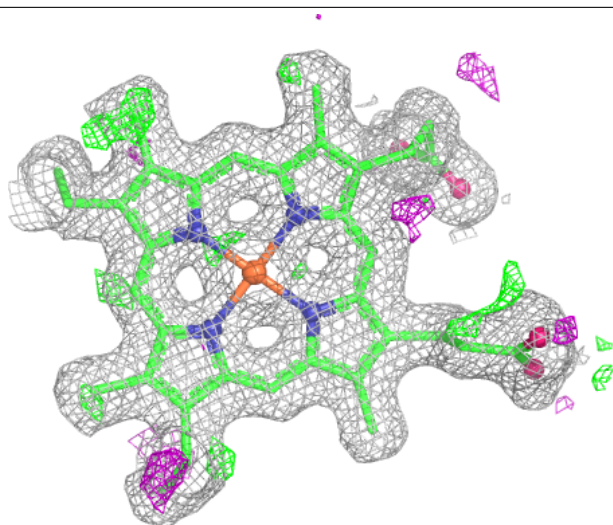
Electron density around HEC B 1001:

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



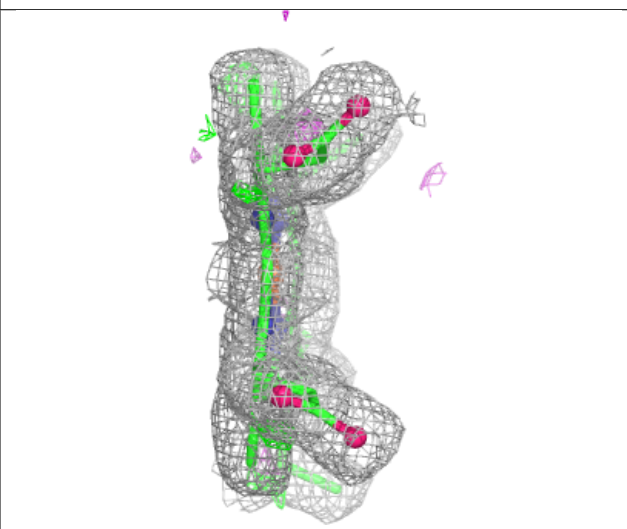
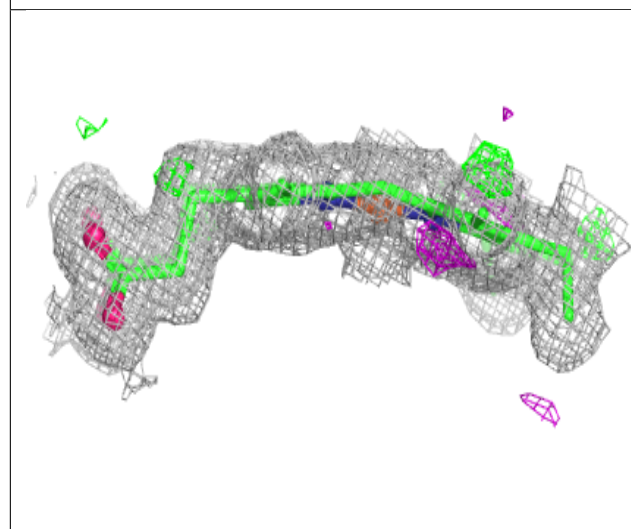
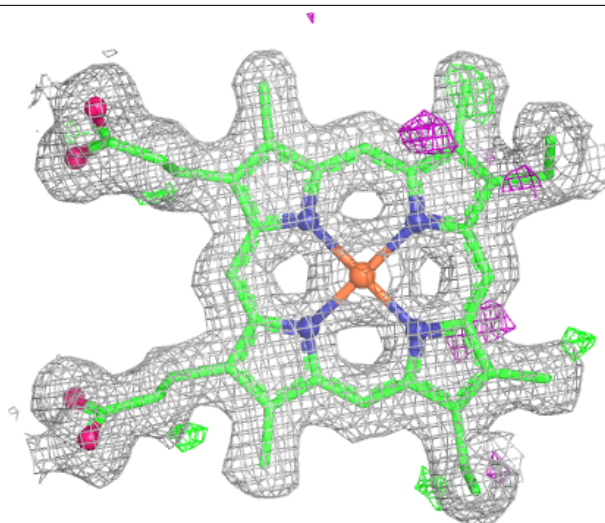
Electron density around HEC A 1005:

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



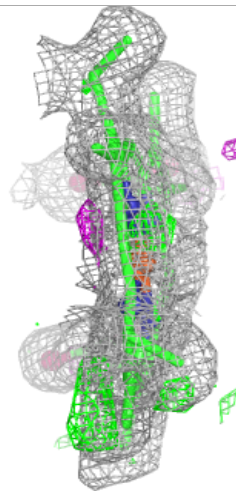
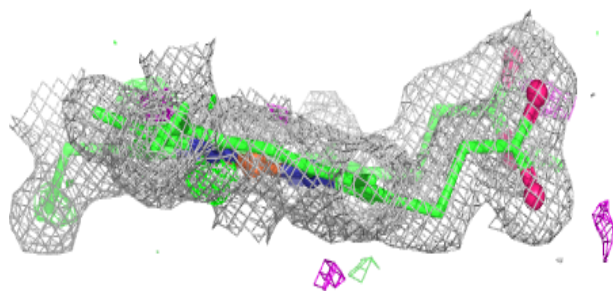
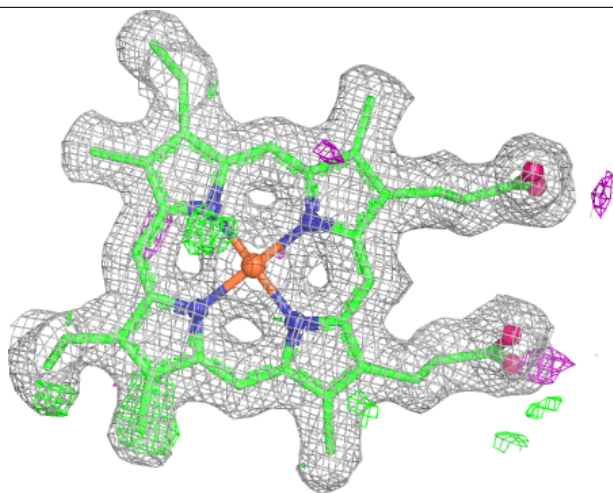
Electron density around HEC A 1006:

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



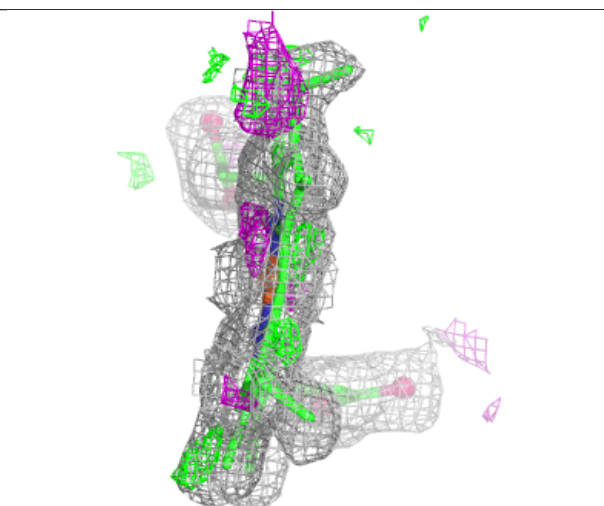
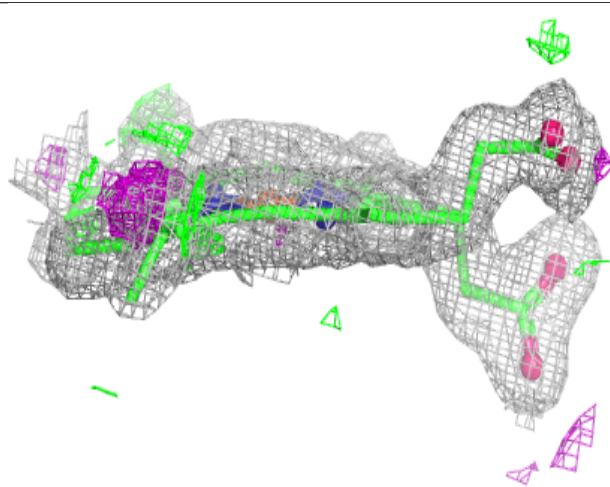
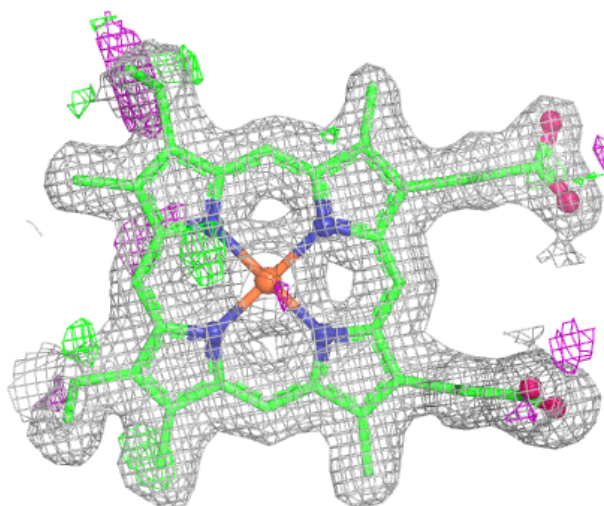
Electron density around HEC A 1007:

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and green (positive)



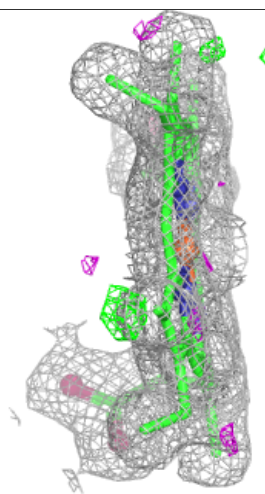
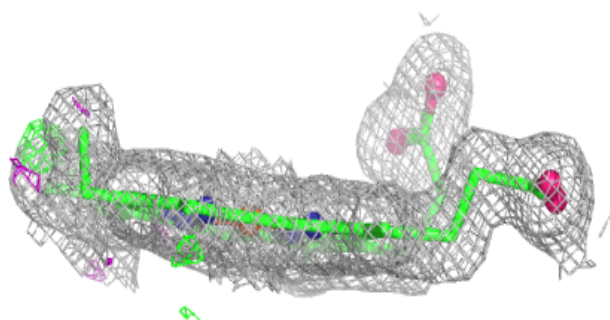
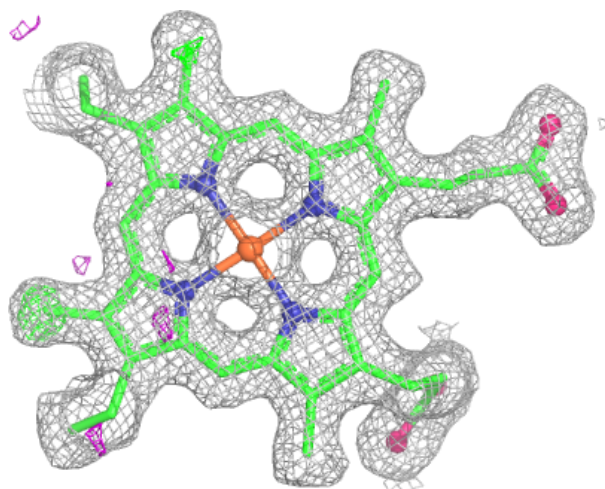
Electron density around HEC A 1008:

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and green (positive)



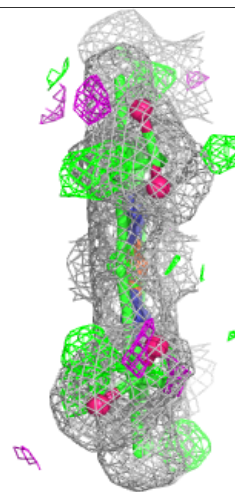
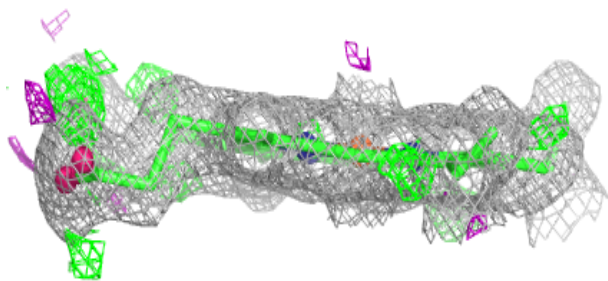
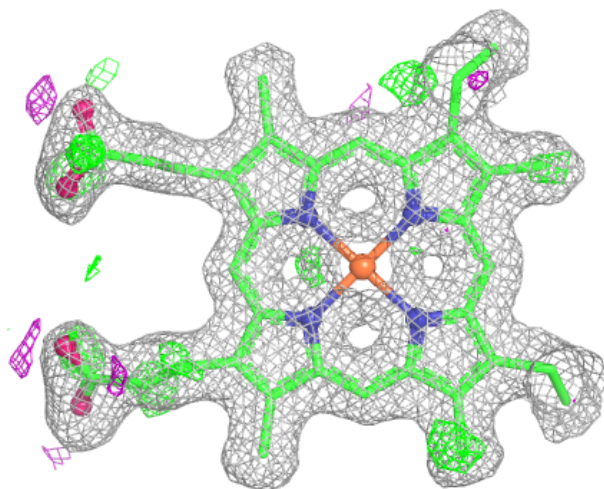
Electron density around HEC A 1002:

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



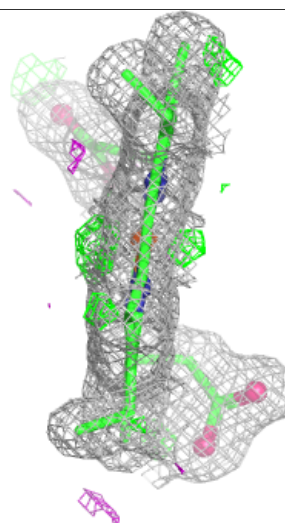
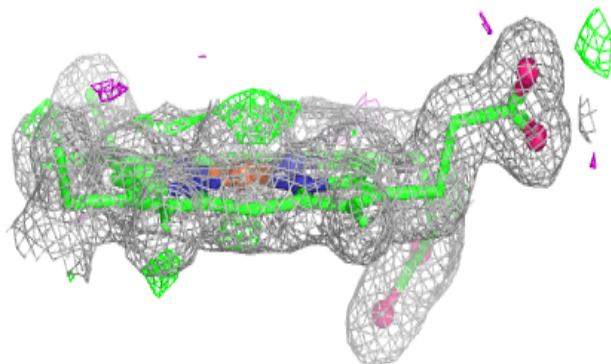
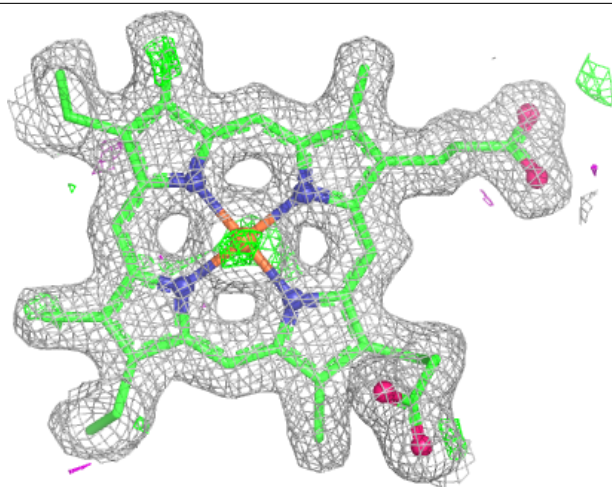
Electron density around HEC A 1003:

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and green (positive)



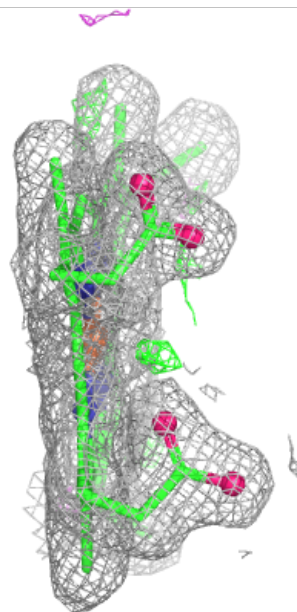
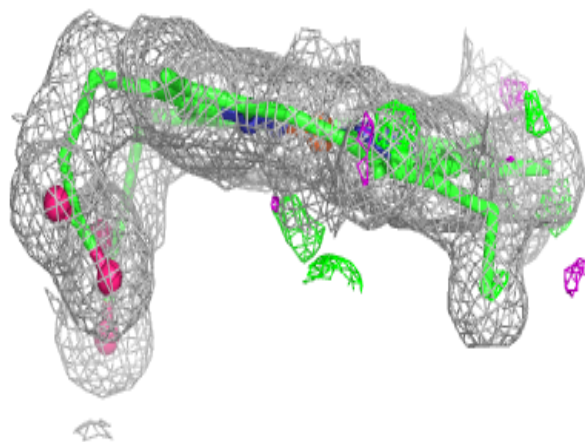
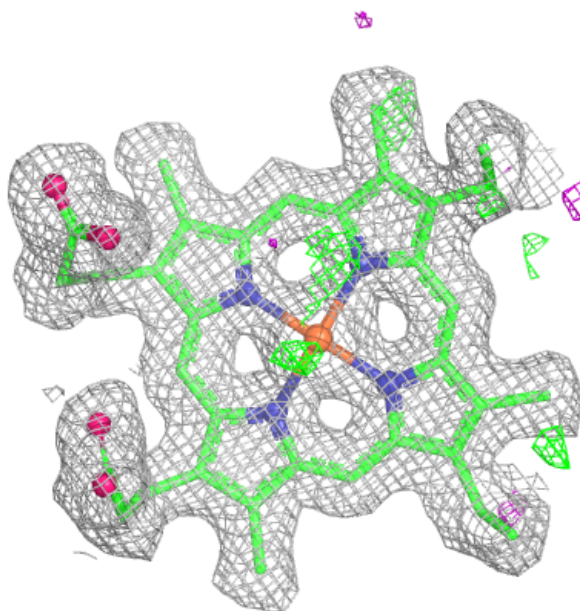
Electron density around HEC A 1001:

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



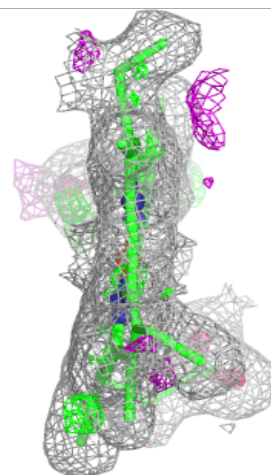
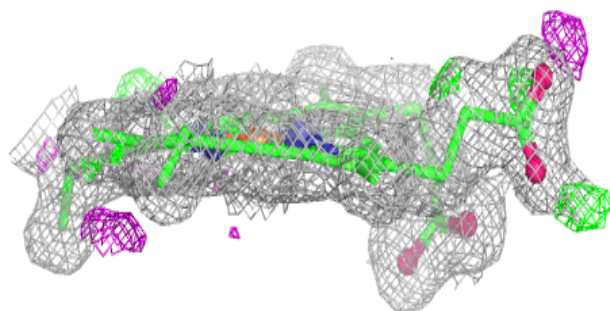
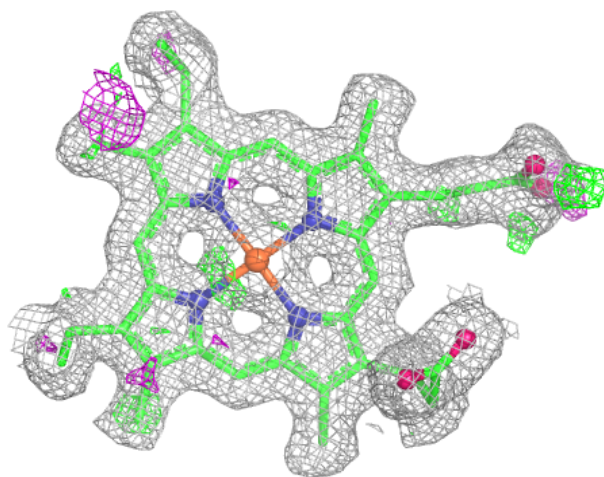
Electron density around HEC B 1004:

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and green (positive)



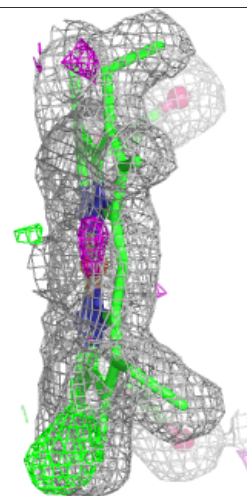
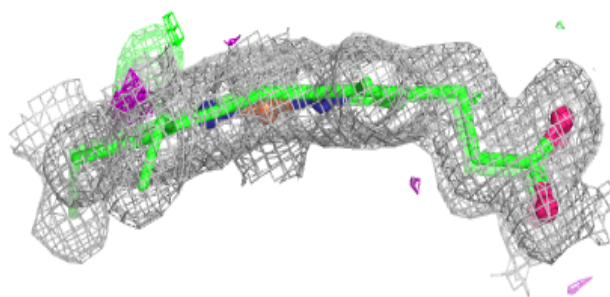
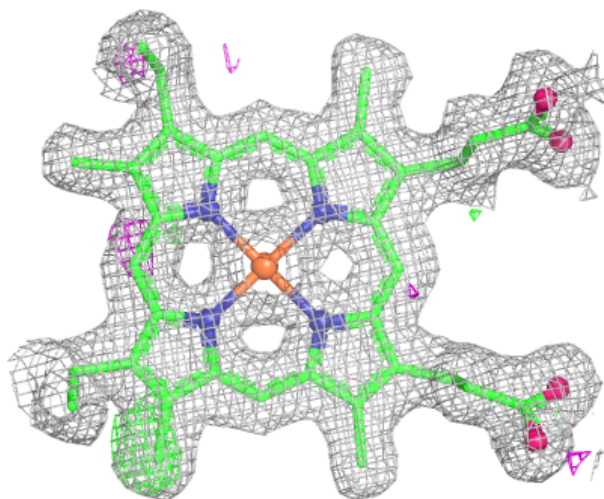
Electron density around HEC B 1005:

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



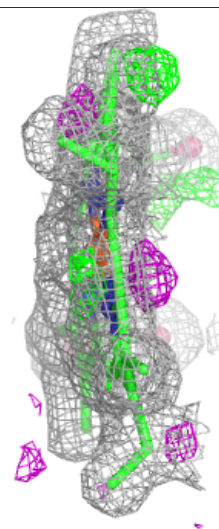
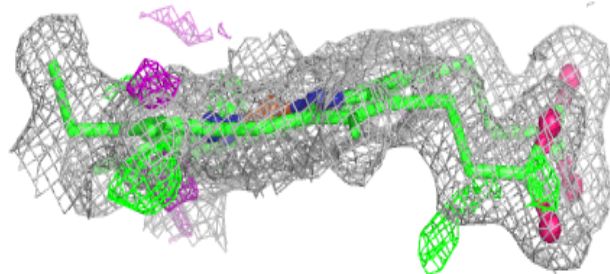
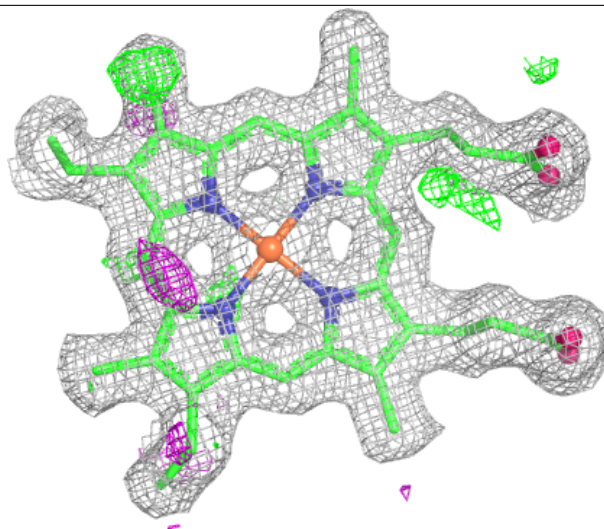
Electron density around HEC B 1006:

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



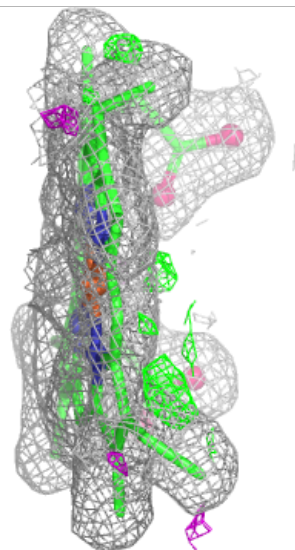
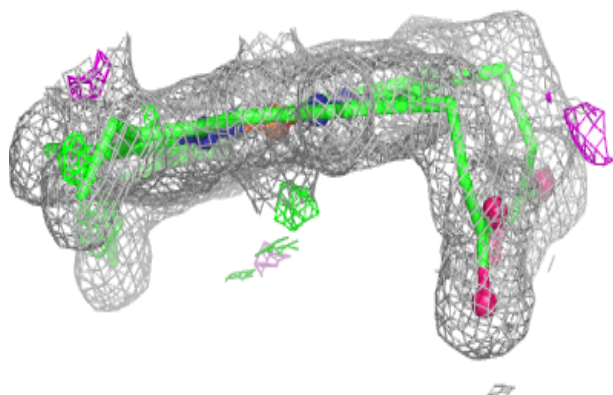
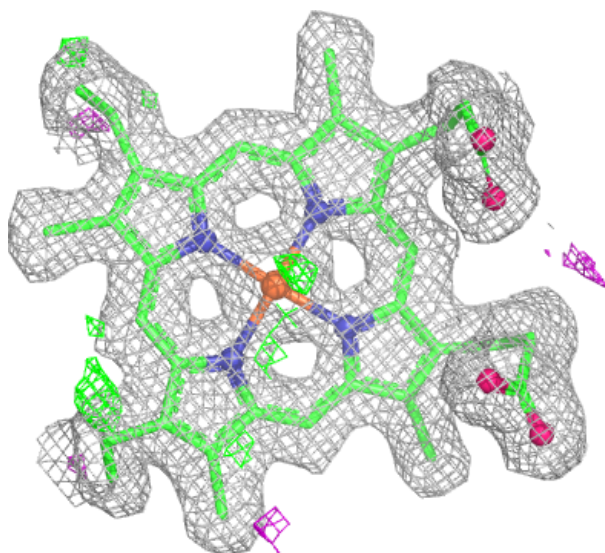
Electron density around HEC B 1007:

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



Electron density around HEC A 1004:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.