Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 07:28 pm BST

PDB ID	:	2BQ4
Title	:	Crystal structure of type I cytochrome c3 from Desulfovibrio africanus
Authors	:	Czjzek, M.; Pieulle, L.; Morelli, X.; Guerlesquin, F.; Hatchikian, E.C.
Deposited on	:	2005-04-27
Resolution	:	1.68 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

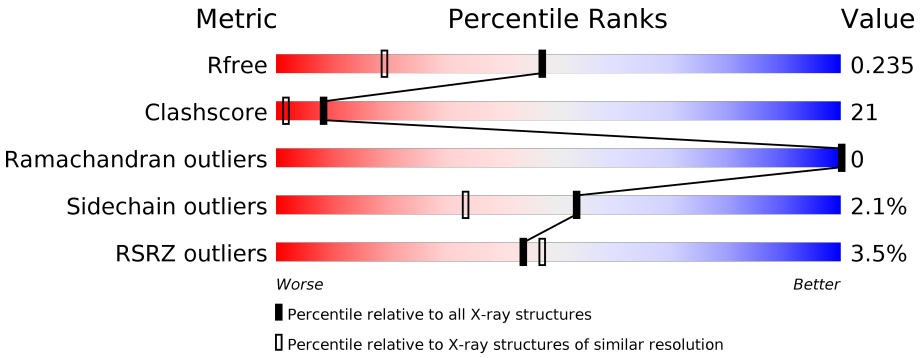
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.68 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	116	3% 86% 11%
1	B	116	3% 84% 15%

2 Entry composition

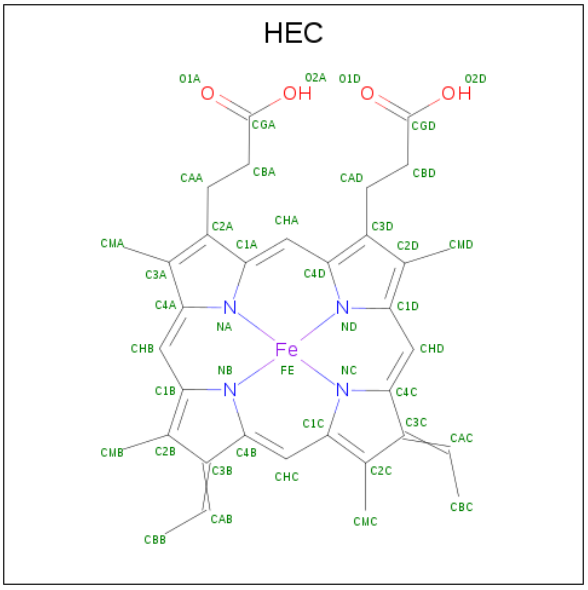
There are 4 unique types of molecules in this entry. The entry contains 2346 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BASIC CYTOCHROME C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	114	Total	C	N	O	S	0	0	0
			854	526	155	162	11			
1	B	115	Total	C	N	O	S	0	0	0
			863	531	157	164	11			

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



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

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

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

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

- Molecule 4 is water.

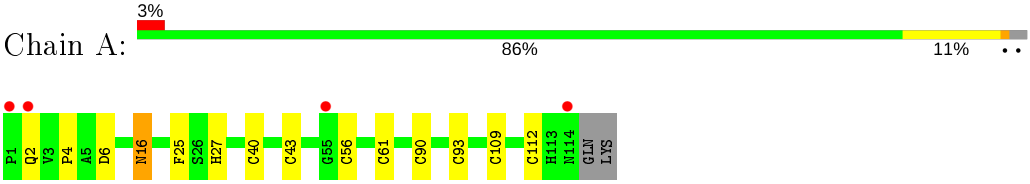
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	134	Total	O	0	0
			134	134		
4	B	149	Total	O	0	0
			149	149		

3 Residue-property plots (i)

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

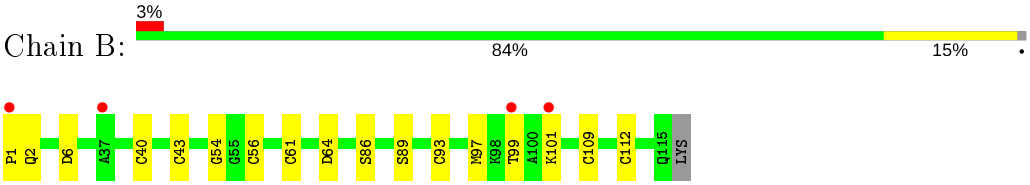
- Molecule 1: BASIC CYTOCHROME C3

Chain A:



- Molecule 1: BASIC CYTOCHROME C3

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	100.90Å 46.30Å 54.82Å 90.00° 118.97° 90.00°	Depositor
Resolution (Å)	48.22 – 1.68 47.96 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.9 (48.22-1.68) 78.9 (47.96-1.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.61 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.200 , 0.240 0.213 , 0.235	Depositor DCC
R_{free} test set	1407 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	2.7	Xtriage
Anisotropy	0.854	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 52.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	2346	wwPDB-VP
Average B, all atoms (Å^2)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 80.78 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.1294e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.36	0/875	0.69	1/1177 (0.1%)
1	B	0.36	0/884	0.72	3/1189 (0.3%)
All	All	0.36	0/1759	0.71	4/2366 (0.2%)

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	B	1	0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1	PRO	N-CA-C	7.45	131.48	112.10
1	A	6	ASP	CB-CG-OD2	5.67	123.40	118.30
1	B	64	ASP	CB-CG-OD2	5.13	122.92	118.30
1	B	6	ASP	CB-CG-OD2	5.03	122.82	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	1	PRO	CA

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	854	0	827	28	0
1	B	863	0	837	28	1
2	A	172	0	124	35	0
2	B	172	0	126	37	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	134	0	0	1	1
4	B	149	0	0	1	2
All	All	2346	0	1914	77	3

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 21.

All (77) 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:B:109:CYS:SG	2:B:1119:HEC:HAB	1.61	1.41
1:B:109:CYS:SG	2:B:1119:HEC:CAB	2.11	1.38
1:A:43:CYS:SG	2:A:1115:HEC:CAC	2.12	1.36
1:A:112:CYS:SG	2:A:1118:HEC:CAC	2.14	1.36
1:B:43:CYS:SG	2:B:1116:HEC:CAC	2.16	1.32
1:A:93:CYS:SG	2:A:1117:HEC:CAC	2.18	1.32
1:B:112:CYS:SG	2:B:1119:HEC:CAC	2.20	1.29
1:B:93:CYS:SG	2:B:1118:HEC:CAC	2.22	1.27
1:A:112:CYS:SG	2:A:1118:HEC:HAC	1.79	1.21
1:A:61:CYS:SG	2:A:1116:HEC:CAC	2.29	1.21
1:B:2:GLN:OE1	4:B:2008:HOH:O	1.58	1.20
1:B:40:CYS:SG	2:B:1116:HEC:HAB	1.79	1.18
1:A:43:CYS:SG	2:A:1115:HEC:HAC	1.81	1.17
1:B:61:CYS:SG	2:B:1117:HEC:CAC	2.39	1.11
1:A:93:CYS:SG	2:A:1117:HEC:HAC	1.92	1.09
1:B:112:CYS:SG	2:B:1119:HEC:HAC	1.89	1.05
1:B:93:CYS:SG	2:B:1118:HEC:HAC	1.92	1.05
1:B:43:CYS:SG	2:B:1116:HEC:HAC	1.92	1.04
1:A:2:GLN:OE1	4:A:2002:HOH:O	1.73	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:CYS:HG	2:B:1119:HEC:CAB	1.62	0.99
1:B:109:CYS:HG	2:B:1119:HEC:HAB	0.74	0.85
1:A:61:CYS:SG	2:A:1116:HEC:HAC	2.18	0.81
2:A:1118:HEC:HBB3	2:A:1118:HEC:HMB1	1.66	0.78
2:B:1118:HEC:HMC1	2:B:1118:HEC:HBC3	1.67	0.77
2:B:1116:HEC:HBC3	2:B:1116:HEC:HMC1	1.67	0.77
2:A:1117:HEC:HBC3	2:A:1117:HEC:HMC1	1.69	0.73
2:A:1118:HEC:HMC1	2:A:1118:HEC:HBC3	1.68	0.73
2:B:1119:HEC:HMC1	2:B:1119:HEC:HBC3	1.72	0.71
1:B:61:CYS:SG	2:B:1117:HEC:HAC	2.29	0.69
2:B:1117:HEC:HMC1	2:B:1117:HEC:HBC3	1.76	0.68
2:A:1115:HEC:HBC3	2:A:1115:HEC:HMC1	1.79	0.65
1:B:40:CYS:SG	2:B:1116:HEC:CBB	2.81	0.65
1:A:40:CYS:SG	2:A:1115:HEC:C3B	2.85	0.64
1:A:93:CYS:SG	2:A:1117:HEC:C3C	2.85	0.64
1:B:56:CYS:SG	2:B:1117:HEC:C3B	2.86	0.63
1:A:112:CYS:SG	2:A:1118:HEC:C3C	2.86	0.63
1:A:61:CYS:SG	2:A:1116:HEC:C3C	2.87	0.63
1:A:109:CYS:SG	2:A:1118:HEC:C3B	2.86	0.63
1:B:93:CYS:SG	2:B:1118:HEC:C3C	2.87	0.62
1:B:112:CYS:SG	2:B:1119:HEC:C3C	2.87	0.62
1:A:56:CYS:SG	2:A:1116:HEC:C3B	2.89	0.61
1:B:43:CYS:SG	2:B:1116:HEC:C3C	2.89	0.61
1:A:56:CYS:SG	2:A:1116:HEC:CBB	2.85	0.60
2:B:1119:HEC:HBB3	2:B:1119:HEC:HMB1	1.82	0.60
1:A:43:CYS:SG	2:A:1115:HEC:C3C	2.90	0.60
2:B:1116:HEC:HBB3	2:B:1116:HEC:HMB1	1.83	0.59
1:B:40:CYS:SG	2:B:1116:HEC:C3B	2.88	0.59
1:B:43:CYS:SG	2:B:1116:HEC:CBC	2.87	0.58
1:A:43:CYS:SG	2:A:1115:HEC:CBC	2.89	0.58
1:A:4:PRO:HD2	1:A:27:HIS:CD2	2.38	0.57
2:A:1118:HEC:HMC1	2:A:1118:HEC:CBC	2.34	0.57
2:B:1117:HEC:HMB1	2:B:1117:HEC:HBB3	1.87	0.57
2:B:1119:HEC:CBC	2:B:1119:HEC:HMC1	2.34	0.57
2:A:1116:HEC:HBB3	2:A:1116:HEC:HMB1	1.88	0.56
2:A:1116:HEC:HMC1	2:A:1116:HEC:HBC3	1.88	0.56
1:A:90:CYS:SG	2:A:1117:HEC:C3B	2.92	0.55
1:A:40:CYS:SG	2:A:1115:HEC:CBB	2.88	0.54
1:B:109:CYS:SG	2:B:1119:HEC:C3B	2.93	0.54
2:B:1118:HEC:HMC1	2:B:1118:HEC:CBC	2.38	0.54
1:B:56:CYS:SG	2:B:1117:HEC:CBB	2.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1117:HEC:HMB1	2:A:1117:HEC:HBB3	1.90	0.53
1:A:90:CYS:SG	2:A:1117:HEC:CBB	2.87	0.52
1:A:61:CYS:SG	2:A:1116:HEC:CBC	2.95	0.52
2:A:1117:HEC:HMC1	2:A:1117:HEC:CBC	2.38	0.52
1:B:61:CYS:SG	2:B:1117:HEC:C3C	2.97	0.51
1:A:109:CYS:SG	2:A:1118:HEC:CBB	2.88	0.50
1:A:93:CYS:SG	2:A:1117:HEC:CBC	2.93	0.48
1:B:61:CYS:SG	2:B:1117:HEC:CBC	2.98	0.48
2:B:1118:HEC:HMB1	2:B:1118:HEC:HBB3	1.95	0.48
2:A:1115:HEC:HMB1	2:A:1115:HEC:HBB3	1.98	0.46
1:A:25:PHE:HE2	1:A:27:HIS:CE1	2.33	0.46
1:A:112:CYS:SG	2:A:1118:HEC:CBC	2.96	0.46
1:A:16:ASN:C	1:A:16:ASN:HD22	2.20	0.45
1:B:54:GLY:HA2	2:B:1116:HEC:HBA2	2.00	0.44
1:B:112:CYS:SG	2:B:1119:HEC:CBC	2.99	0.43
2:A:1118:HEC:HBB3	2:A:1118:HEC:CMB	2.45	0.42
1:B:97:MET:SD	2:B:1118:HEC:HMD3	2.61	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:2070:HOH:O	4:B:2070:HOH:O[2_655]	1.77	0.43
4:B:2043:HOH:O	4:B:2125:HOH:O[4_555]	2.04	0.16
1:B:86:SER:OG	4:A:2002:HOH:O[3_545]	2.13	0.07

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	112/116 (97%)	106 (95%)	6 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	113/116 (97%)	108 (96%)	5 (4%)	0	100	100
All	All	225/232 (97%)	214 (95%)	11 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	93/95 (98%)	92 (99%)	1 (1%)	73	61
1	B	94/95 (99%)	91 (97%)	3 (3%)	39	17
All	All	187/190 (98%)	183 (98%)	4 (2%)	53	33

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

Mol	Chain	Res	Type
1	A	16	ASN
1	B	89	SER
1	B	99	THR
1	B	101	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	114	ASN
1	B	2	GLN
1	B	115	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
2	HEC	A	1117	1	26,50,50	2.49	6 (23%)	18,82,82	1.78	6 (33%)
2	HEC	A	1118	1,3	26,50,50	2.52	7 (26%)	18,82,82	1.54	4 (22%)
2	HEC	B	1118	1	26,50,50	2.50	6 (23%)	18,82,82	1.58	4 (22%)
2	HEC	A	1116	1	26,50,50	2.34	5 (19%)	18,82,82	1.57	3 (16%)
2	HEC	B	1119	1,3	26,50,50	2.55	5 (19%)	18,82,82	1.37	4 (22%)
2	HEC	B	1117	1	26,50,50	2.37	5 (19%)	18,82,82	1.68	5 (27%)
2	HEC	A	1115	1	26,50,50	2.48	6 (23%)	18,82,82	1.95	8 (44%)
2	HEC	B	1116	1	26,50,50	2.47	6 (23%)	18,82,82	1.59	5 (27%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	A	1117	1	-	0/6/54/54	-
2	HEC	A	1118	1,3	-	0/6/54/54	-
2	HEC	B	1118	1	-	0/6/54/54	-
2	HEC	A	1116	1	-	0/6/54/54	-
2	HEC	B	1119	1,3	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	B	1117	1	-	0/6/54/54	-
2	HEC	A	1115	1	-	0/6/54/54	-
2	HEC	B	1116	1	-	0/6/54/54	-

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1119	HEC	C3B-C2B	-6.77	1.33	1.40
2	A	1118	HEC	C3C-C2C	-6.54	1.33	1.40
2	A	1117	HEC	C3B-C2B	-6.51	1.33	1.40
2	B	1119	HEC	C3C-C2C	-6.32	1.34	1.40
2	B	1118	HEC	C3C-C2C	-6.25	1.34	1.40
2	B	1116	HEC	C3C-C2C	-6.19	1.34	1.40
2	B	1117	HEC	C3B-C2B	-6.13	1.34	1.40
2	A	1117	HEC	C3C-C2C	-6.10	1.34	1.40
2	A	1115	HEC	C3C-C2C	-6.10	1.34	1.40
2	A	1118	HEC	C3B-C2B	-5.78	1.34	1.40
2	B	1118	HEC	C3B-C2B	-5.77	1.34	1.40
2	A	1116	HEC	C3B-C2B	-5.76	1.34	1.40
2	A	1115	HEC	C3B-C2B	-5.50	1.35	1.40
2	B	1116	HEC	C3B-C2B	-5.44	1.35	1.40
2	A	1118	HEC	C3D-C2D	5.04	1.52	1.37
2	A	1116	HEC	C3D-C2D	5.02	1.52	1.37
2	A	1115	HEC	C3D-C2D	5.01	1.52	1.37
2	B	1117	HEC	C3C-C2C	-4.97	1.35	1.40
2	B	1116	HEC	C3D-C2D	4.96	1.52	1.37
2	B	1119	HEC	C3D-C2D	4.89	1.52	1.37
2	B	1118	HEC	C3D-C2D	4.89	1.52	1.37
2	B	1117	HEC	C3D-C2D	4.85	1.52	1.37
2	A	1116	HEC	C3C-C2C	-4.62	1.35	1.40
2	A	1117	HEC	C3D-C2D	4.55	1.51	1.37
2	B	1117	HEC	CBC-CAC	-4.08	1.34	1.49
2	A	1115	HEC	CBC-CAC	-3.99	1.34	1.49
2	A	1116	HEC	CBC-CAC	-3.99	1.34	1.49
2	B	1118	HEC	CBC-CAC	-3.91	1.34	1.49
2	A	1115	HEC	CBB-CAB	-3.89	1.34	1.49
2	B	1119	HEC	CBC-CAC	-3.86	1.35	1.49
2	B	1116	HEC	CBB-CAB	-3.86	1.35	1.49
2	A	1116	HEC	CBB-CAB	-3.83	1.35	1.49
2	B	1116	HEC	CBC-CAC	-3.82	1.35	1.49
2	A	1117	HEC	CBB-CAB	-3.80	1.35	1.49
2	A	1118	HEC	CBB-CAB	-3.79	1.35	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1118	HEC	CBB-CAB	-3.76	1.35	1.49
2	B	1119	HEC	CBB-CAB	-3.74	1.35	1.49
2	A	1117	HEC	CBC-CAC	-3.72	1.35	1.49
2	B	1117	HEC	CBB-CAB	-3.67	1.35	1.49
2	A	1118	HEC	CBC-CAC	-3.65	1.35	1.49
2	B	1118	HEC	C1D-ND	2.26	1.40	1.36
2	A	1115	HEC	C1D-ND	2.13	1.40	1.36
2	B	1116	HEC	CAA-C2A	2.09	1.55	1.52
2	A	1117	HEC	C1D-ND	2.08	1.40	1.36
2	A	1118	HEC	CAD-C3D	2.05	1.55	1.52
2	A	1118	HEC	C4D-ND	2.01	1.40	1.36

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1117	HEC	CAA-CBA-CGA	-3.68	106.50	112.67
2	A	1117	HEC	CBA-CAA-C2A	-3.45	106.12	112.48
2	A	1115	HEC	CAD-CBD-CGD	-3.24	107.24	112.67
2	A	1115	HEC	C1D-C2D-C3D	-3.21	104.76	107.00
2	A	1117	HEC	CMC-C2C-C1C	-3.09	123.72	128.46
2	A	1118	HEC	CBA-CAA-C2A	-3.06	106.83	112.48
2	A	1116	HEC	CMC-C2C-C1C	-3.06	123.76	128.46
2	A	1117	HEC	CAD-CBD-CGD	-3.03	107.58	112.67
2	B	1117	HEC	CMC-C2C-C1C	-3.00	123.86	128.46
2	B	1118	HEC	CBA-CAA-C2A	-2.85	107.22	112.48
2	B	1116	HEC	CMB-C2B-C1B	-2.84	124.11	128.46
2	B	1118	HEC	CMB-C2B-C1B	-2.80	124.17	128.46
2	A	1115	HEC	CMB-C2B-C1B	-2.68	124.35	128.46
2	B	1119	HEC	CBA-CAA-C2A	-2.64	107.61	112.48
2	B	1116	HEC	CMC-C2C-C1C	-2.63	124.42	128.46
2	A	1118	HEC	CMC-C2C-C1C	-2.62	124.44	128.46
2	A	1115	HEC	CBA-CAA-C2A	-2.62	107.65	112.48
2	B	1116	HEC	C1D-C2D-C3D	-2.56	105.22	107.00
2	B	1119	HEC	CMC-C2C-C1C	-2.56	124.54	128.46
2	A	1115	HEC	CAA-CBA-CGA	-2.55	108.39	112.67
2	A	1116	HEC	C1D-C2D-C3D	-2.52	105.24	107.00
2	A	1115	HEC	C4C-C3C-C2C	2.47	109.02	106.35
2	A	1118	HEC	CMB-C2B-C1B	-2.39	124.78	128.46
2	B	1117	HEC	CMB-C2B-C1B	-2.39	124.79	128.46
2	B	1118	HEC	CMC-C2C-C1C	-2.37	124.82	128.46
2	A	1117	HEC	C1D-C2D-C3D	-2.29	105.40	107.00
2	A	1118	HEC	C1D-C2D-C3D	-2.29	105.40	107.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1117	HEC	CMC-C2C-C3C	2.29	128.51	125.82
2	A	1115	HEC	CMC-C2C-C1C	-2.28	124.96	128.46
2	B	1119	HEC	CAD-CBD-CGD	-2.27	108.86	112.67
2	B	1117	HEC	C1D-C2D-C3D	-2.26	105.42	107.00
2	B	1118	HEC	CAD-CBD-CGD	-2.25	108.90	112.67
2	A	1116	HEC	CMC-C2C-C3C	2.23	128.45	125.82
2	A	1117	HEC	CMB-C2B-C1B	-2.21	125.07	128.46
2	B	1119	HEC	C1D-C2D-C3D	-2.13	105.52	107.00
2	A	1117	HEC	CBD-CAD-C3D	-2.07	108.67	112.49
2	B	1116	HEC	CAD-CBD-CGD	-2.05	109.24	112.67
2	A	1115	HEC	CMC-C2C-C3C	2.02	128.20	125.82
2	B	1116	HEC	CBD-CAD-C3D	-2.01	108.77	112.49

There are no chirality outliers.

There are no torsion outliers.

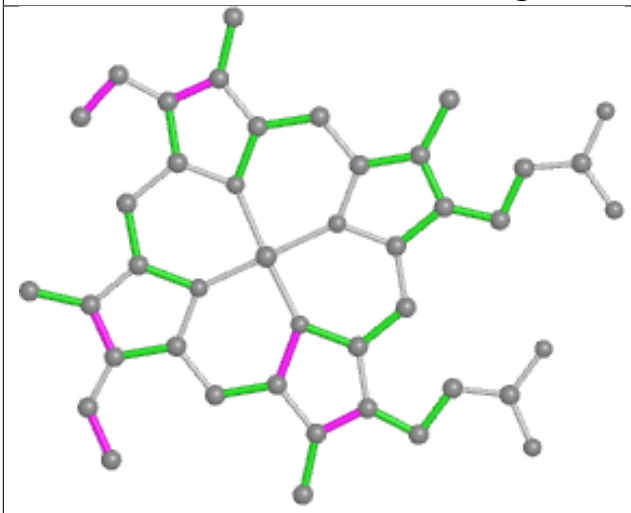
There are no ring outliers.

8 monomers are involved in 72 short contacts:

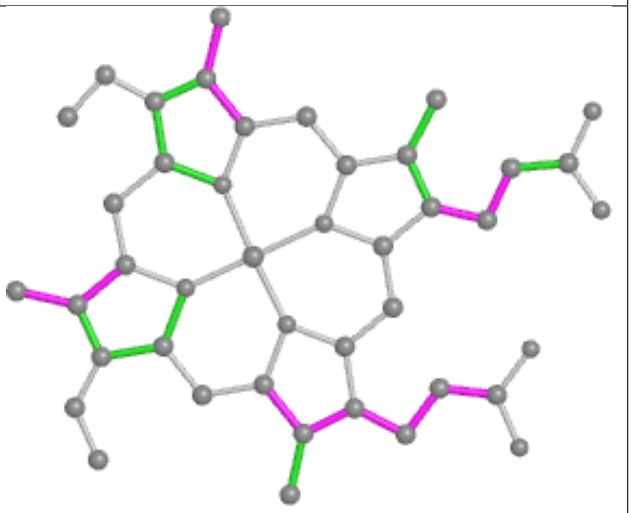
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1117	HEC	9	0
2	A	1118	HEC	10	0
2	B	1118	HEC	7	0
2	A	1116	HEC	8	0
2	B	1119	HEC	12	0
2	B	1117	HEC	8	0
2	A	1115	HEC	8	0
2	B	1116	HEC	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

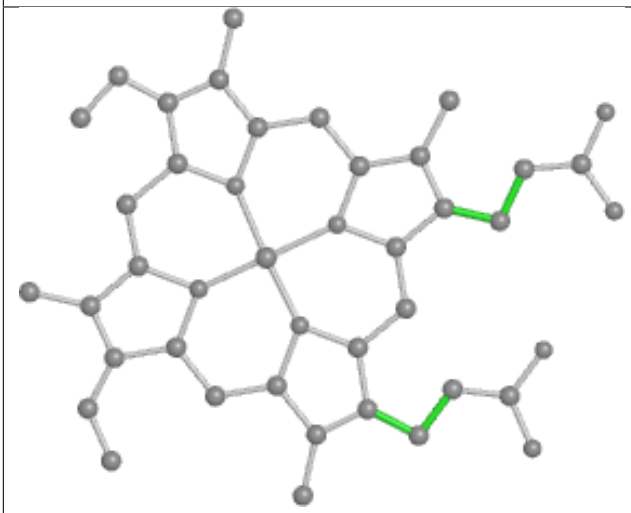
Ligand HEC A 1117



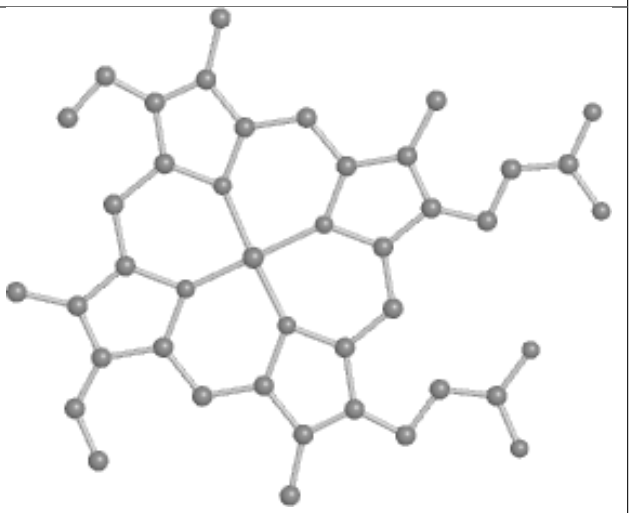
Bond lengths



Bond angles

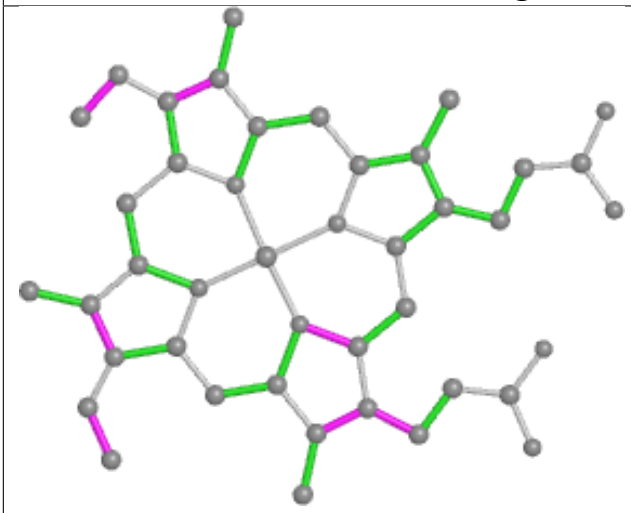


Torsions

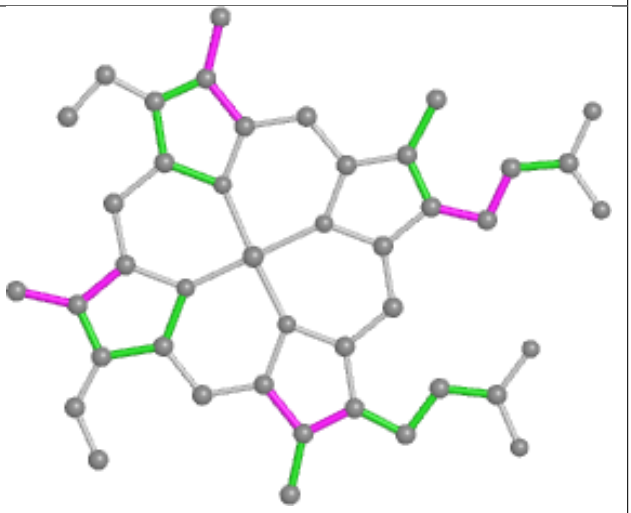


Rings

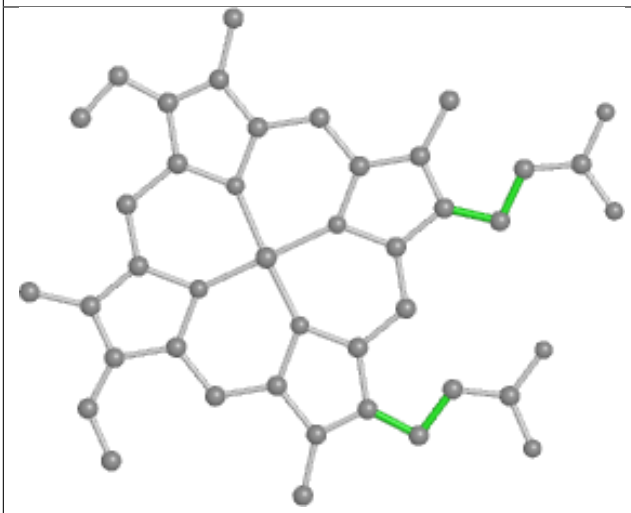
Ligand HEC A 1118



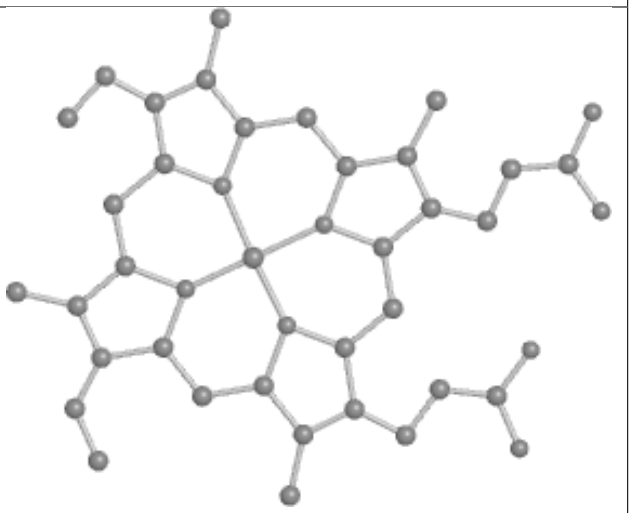
Bond lengths



Bond angles

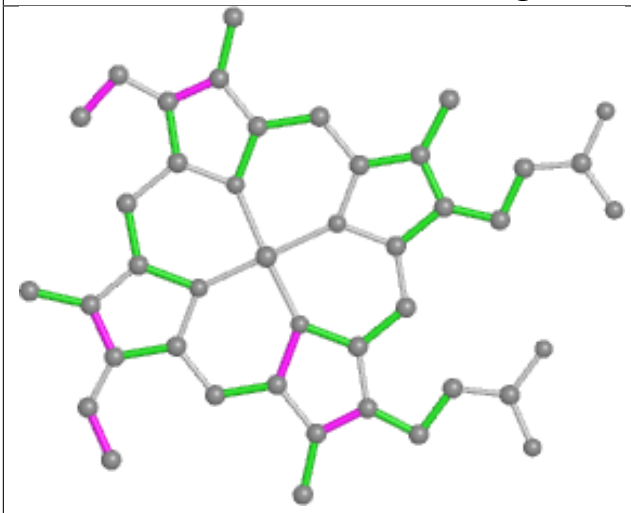


Torsions

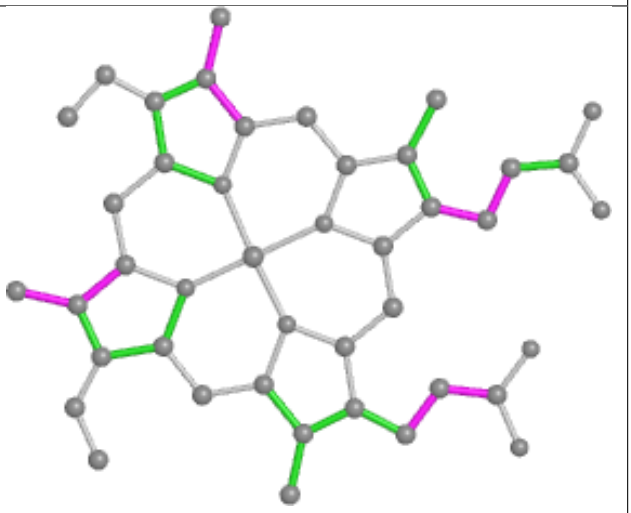


Rings

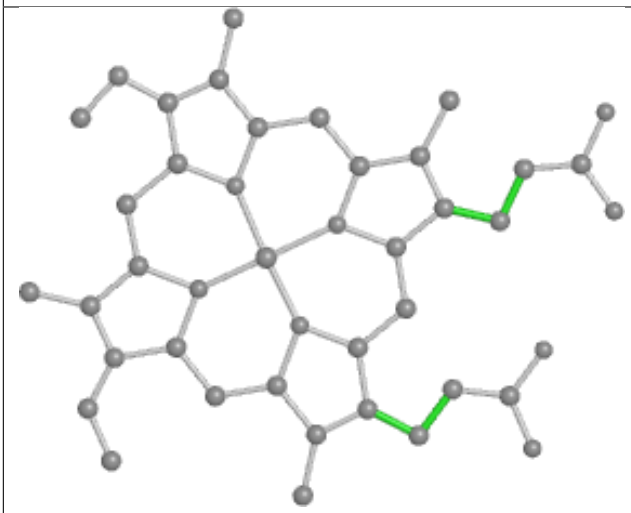
Ligand HEC B 1118



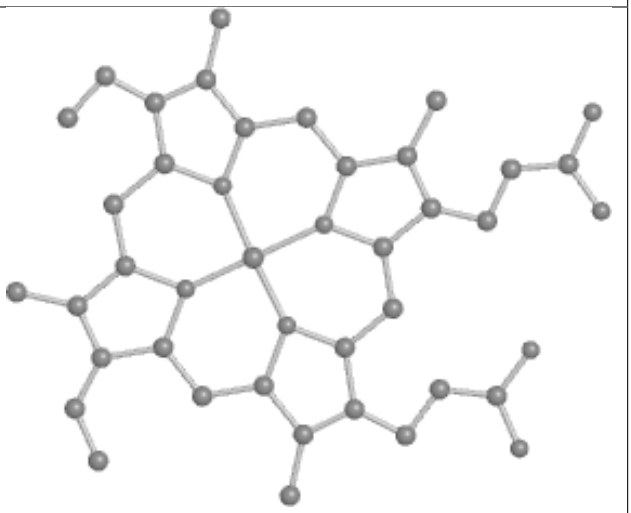
Bond lengths



Bond angles

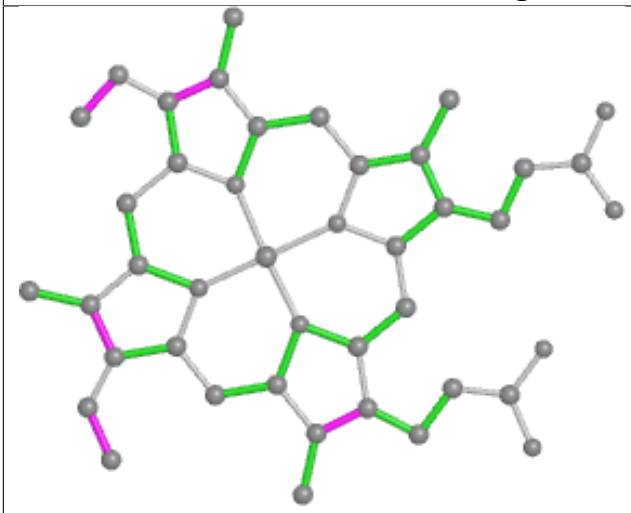


Torsions

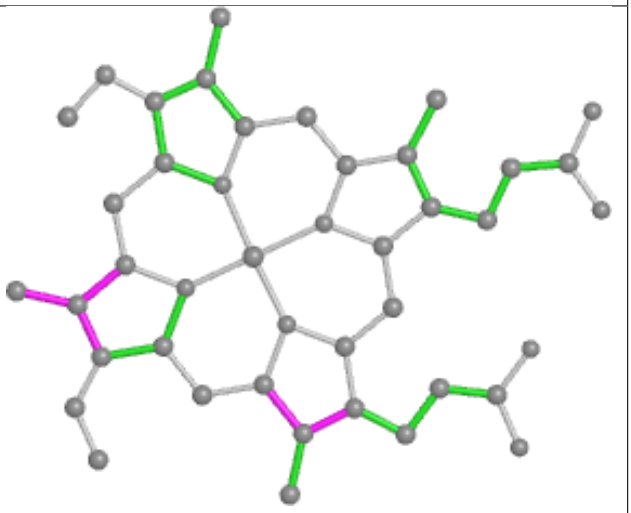


Rings

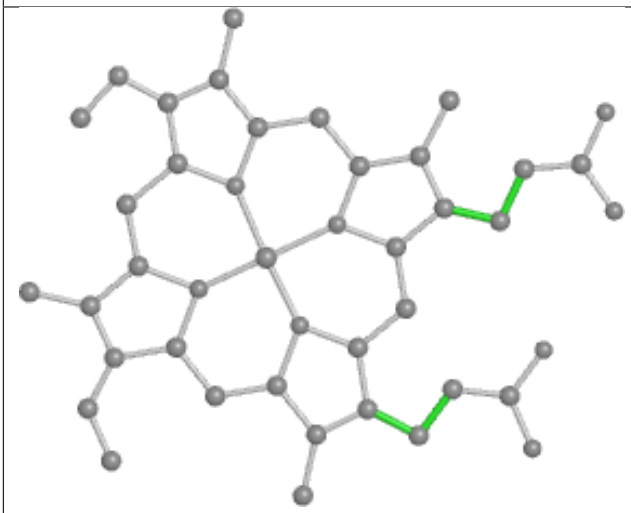
Ligand HEC A 1116



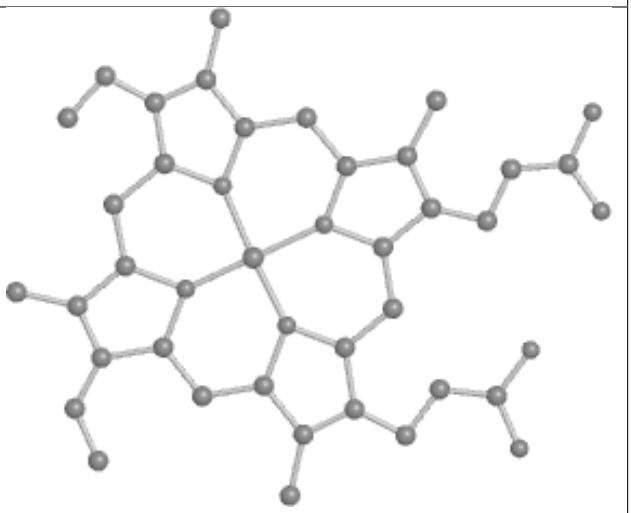
Bond lengths



Bond angles

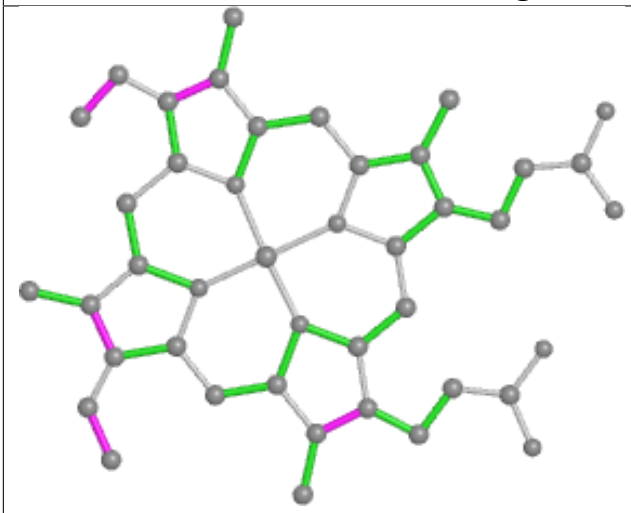


Torsions

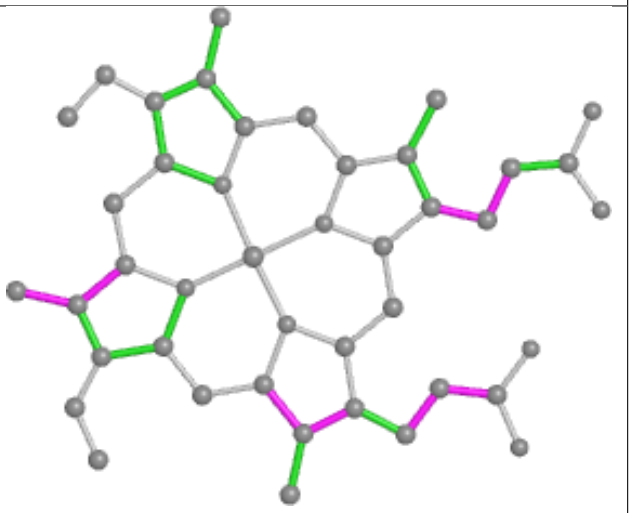


Rings

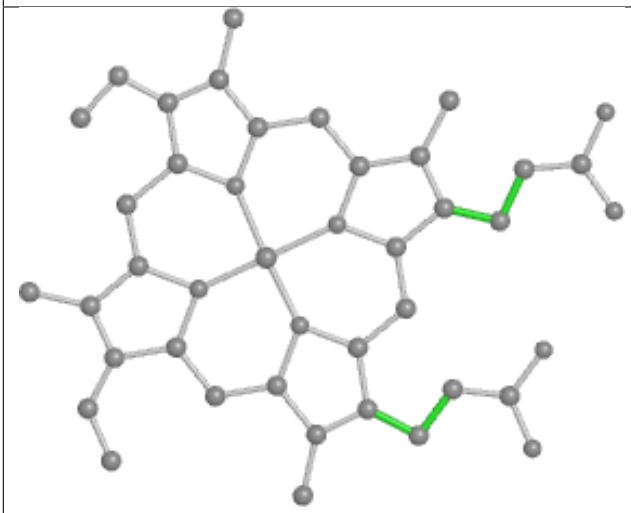
Ligand HEC B 1119



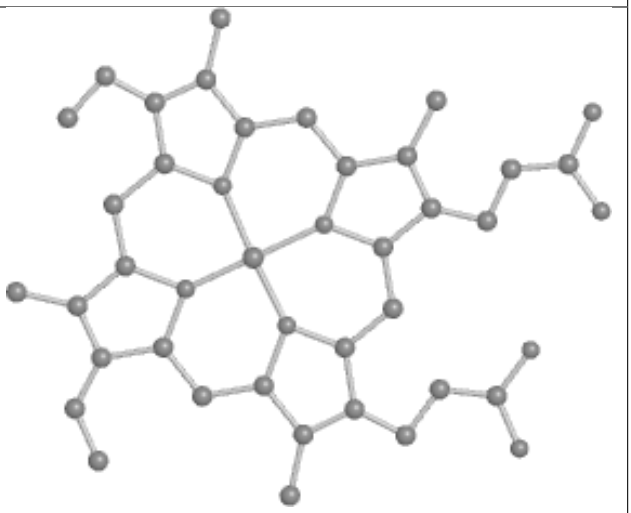
Bond lengths



Bond angles

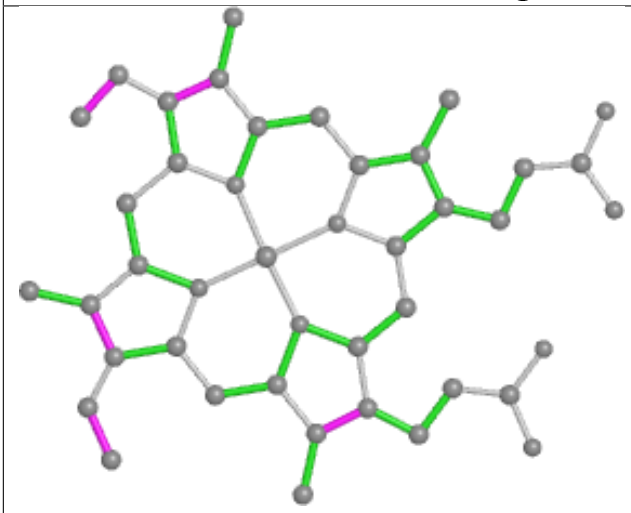


Torsions

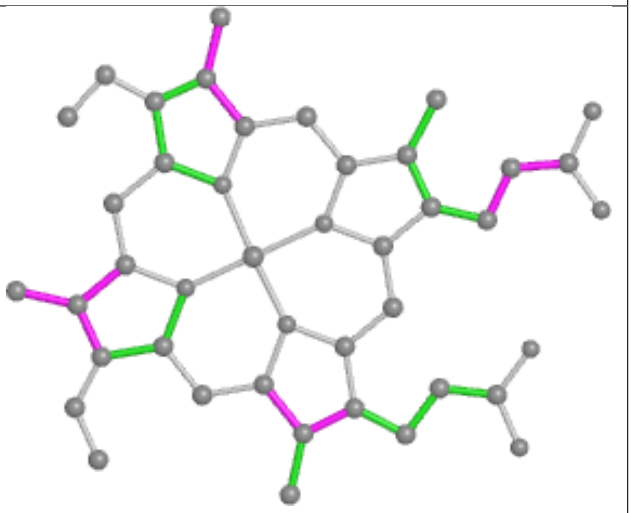


Rings

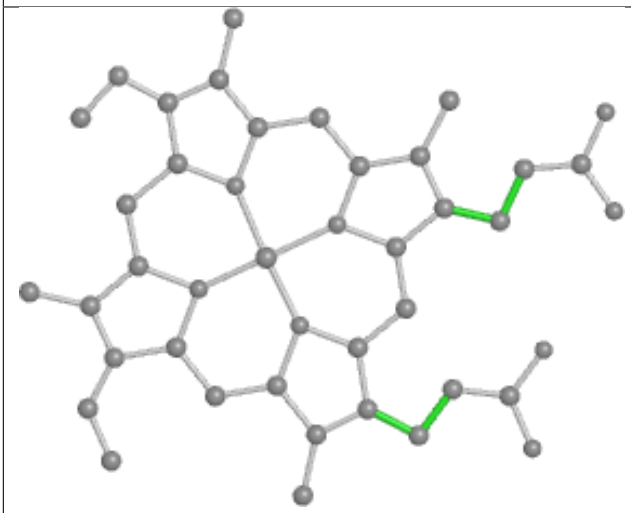
Ligand HEC B 1117



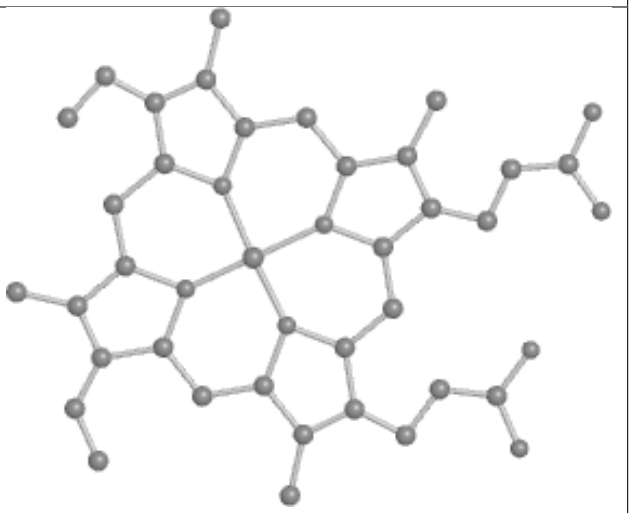
Bond lengths



Bond angles

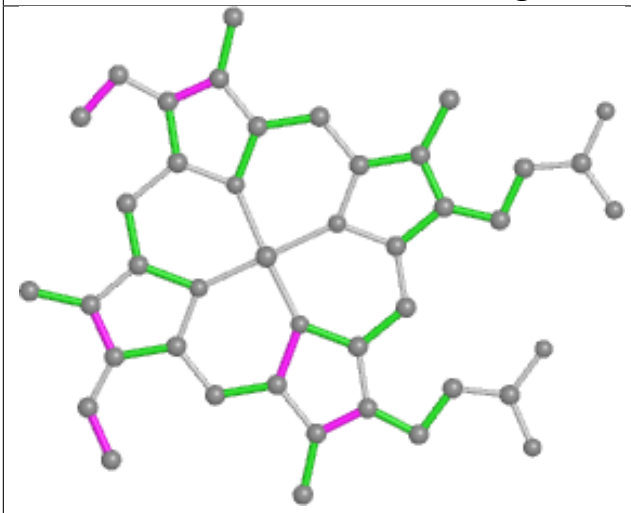


Torsions

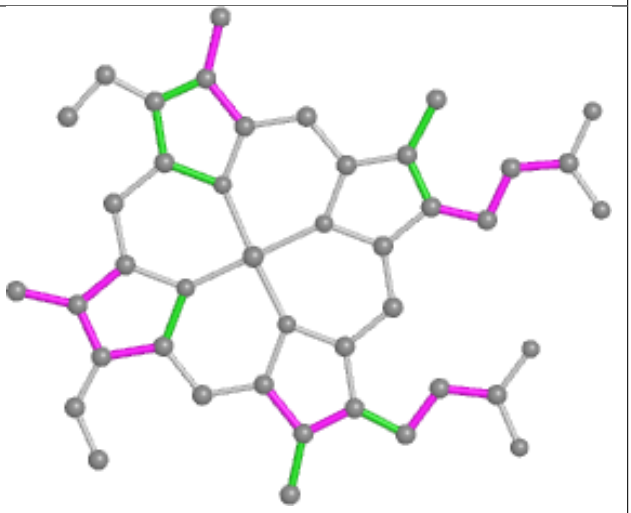


Rings

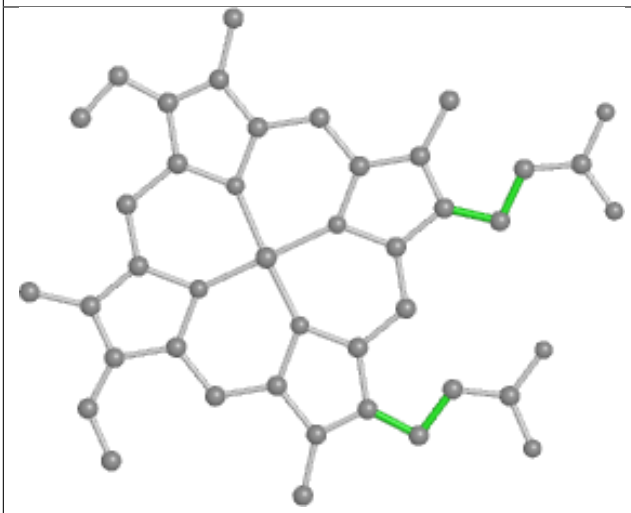
Ligand HEC A 1115



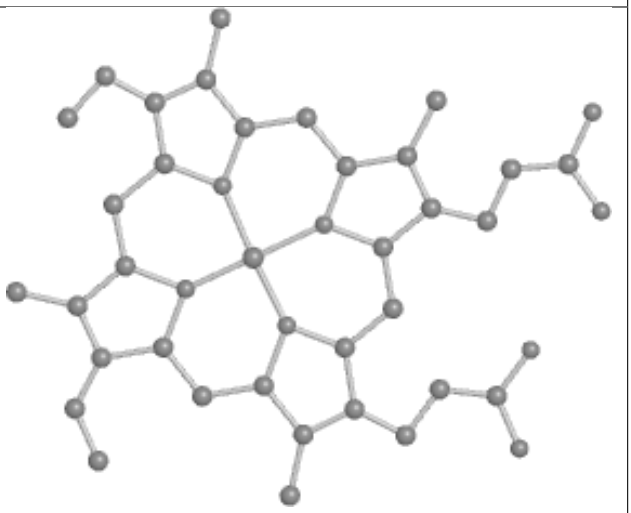
Bond lengths



Bond angles

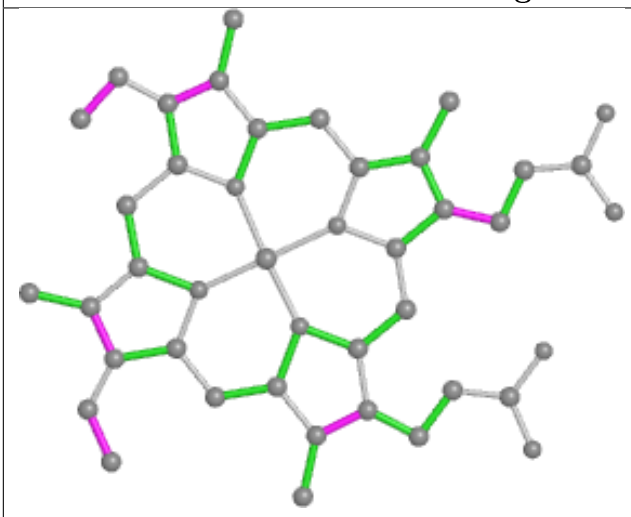


Torsions

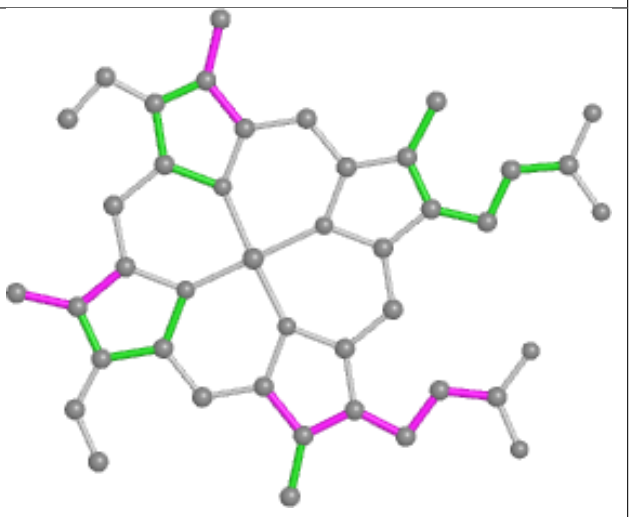


Rings

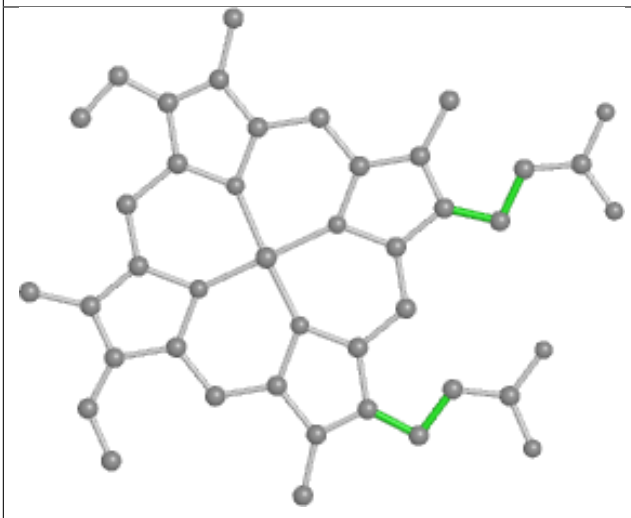
Ligand HEC B 1116



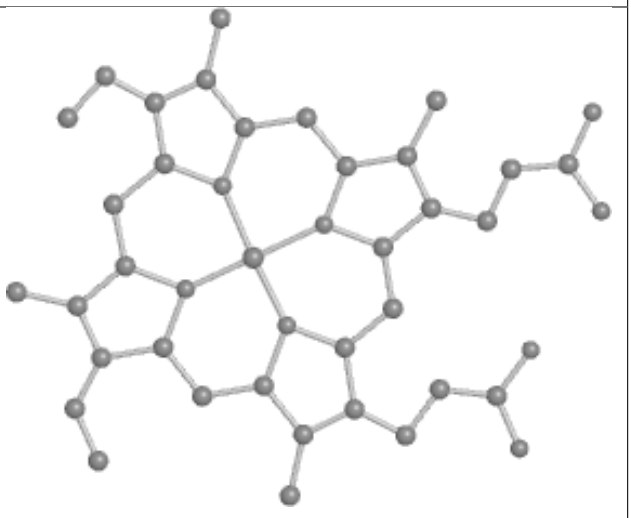
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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, 95^{th} 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	114/116 (98%)	0.39	4 (3%)	44	47	5, 11, 18, 23	0
1	B	115/116 (99%)	0.48	4 (3%)	44	47	2, 9, 19, 31	0
All	All	229/232 (98%)	0.43	8 (3%)	44	47	2, 10, 18, 31	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	PRO	4.1
1	A	114	ASN	3.5
1	B	99	THR	3.4
1	B	1	PRO	3.1
1	A	2	GLN	3.0
1	B	101	LYS	2.3
1	B	37	ALA	2.2
1	A	55	GLY	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

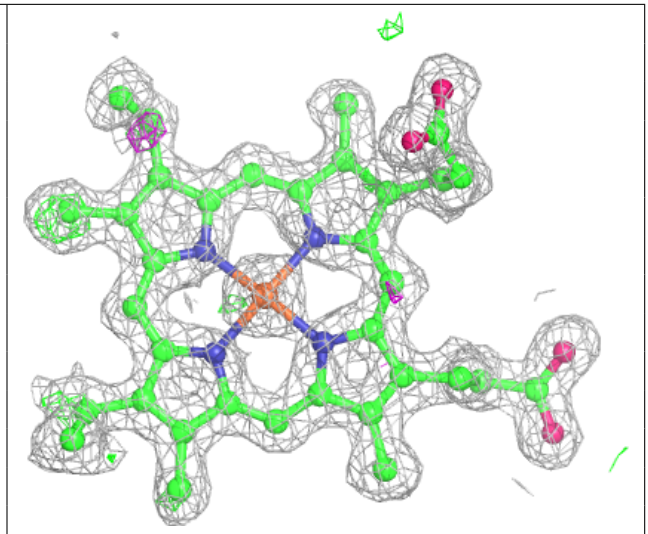
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

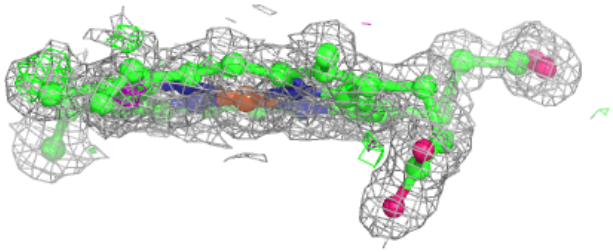
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	HEC	A	1116	43/43	0.96	0.13	6,9,16,20	0
2	HEC	A	1118	43/43	0.97	0.12	7,9,10,11	0
2	HEC	A	1117	43/43	0.97	0.11	4,7,17,20	0
2	HEC	B	1117	43/43	0.97	0.12	3,8,17,21	0
2	HEC	A	1115	43/43	0.97	0.12	5,7,16,23	0
2	HEC	B	1116	43/43	0.97	0.13	2,2,12,17	0
2	HEC	B	1119	43/43	0.98	0.11	6,8,9,11	0
2	HEC	B	1118	43/43	0.98	0.12	2,3,11,15	0
3	CA	B	1120	1/1	0.99	0.08	9,9,9,9	0
3	CA	A	1119	1/1	1.00	0.07	9,9,9,9	0

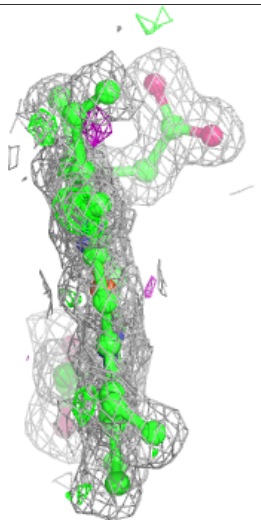
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HEC A 1116:

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

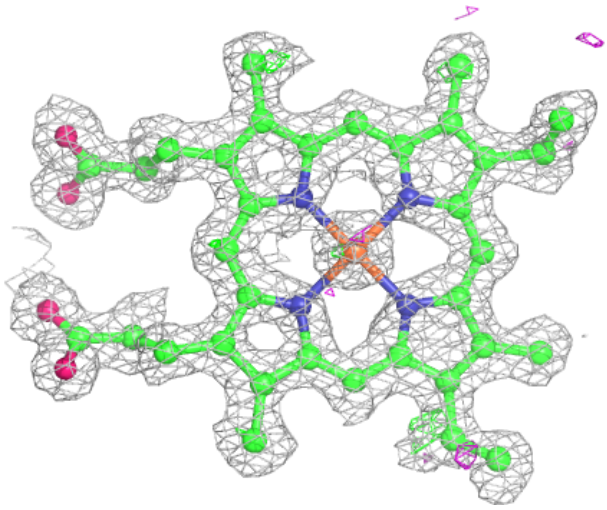


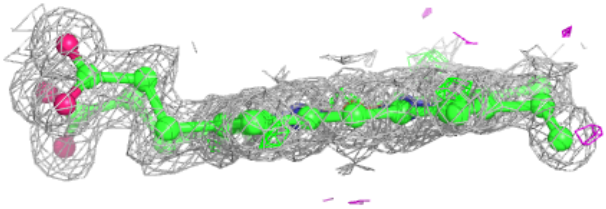




Electron density around HEC A 1118:

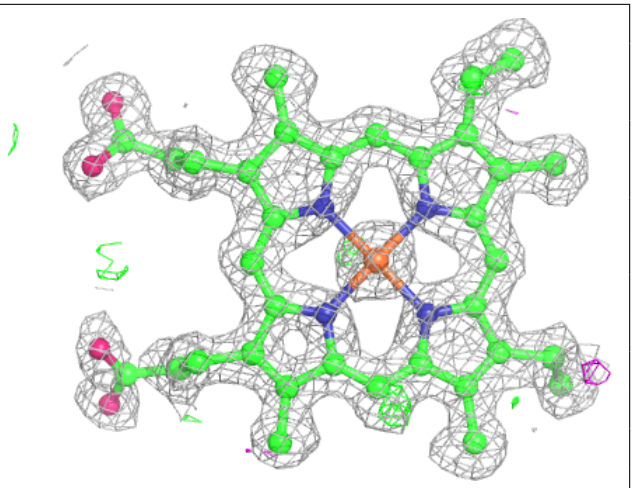
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

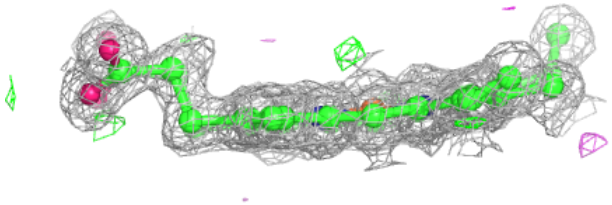


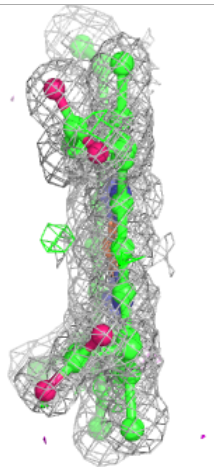


Electron density around HEC A 1117:

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

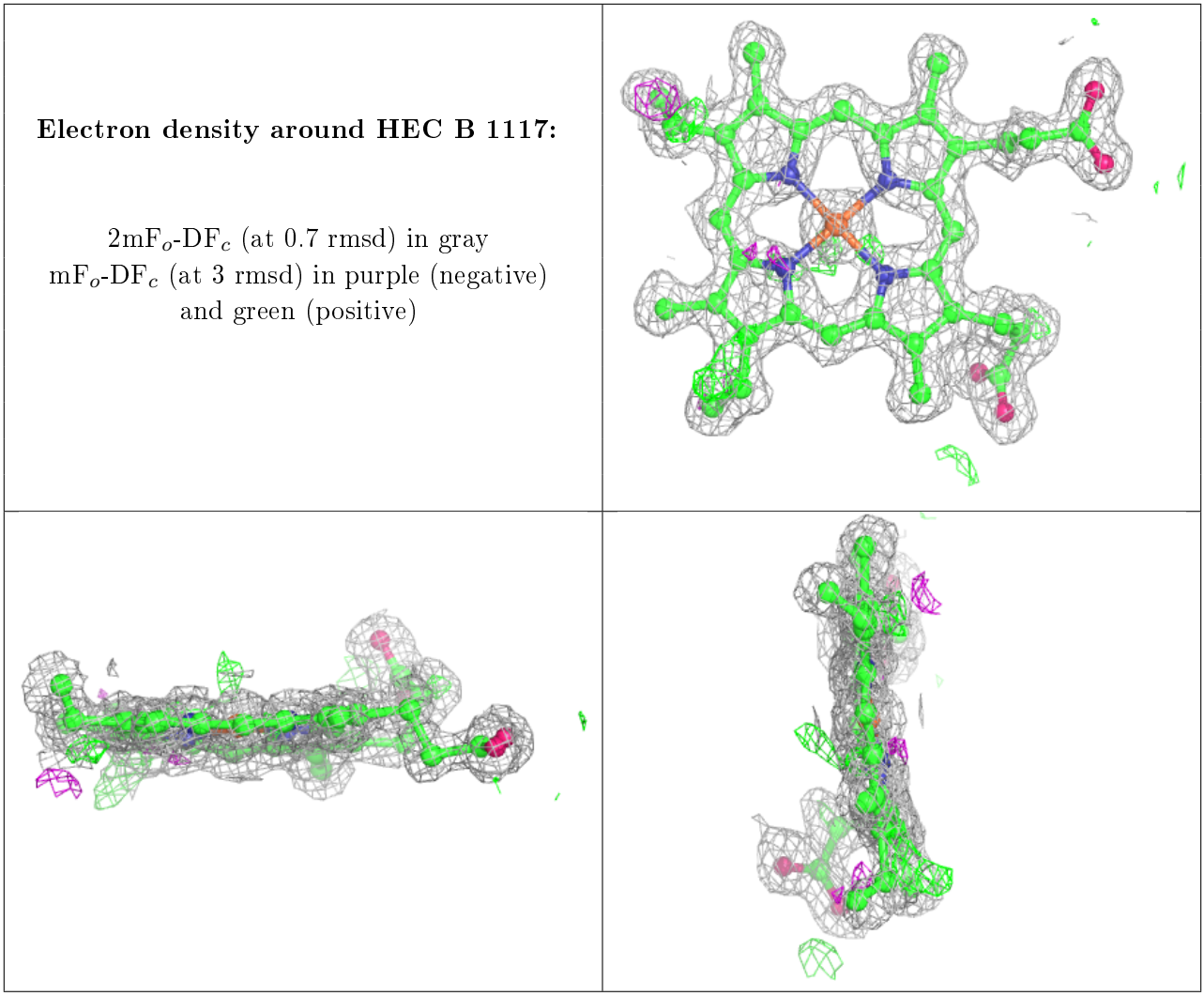






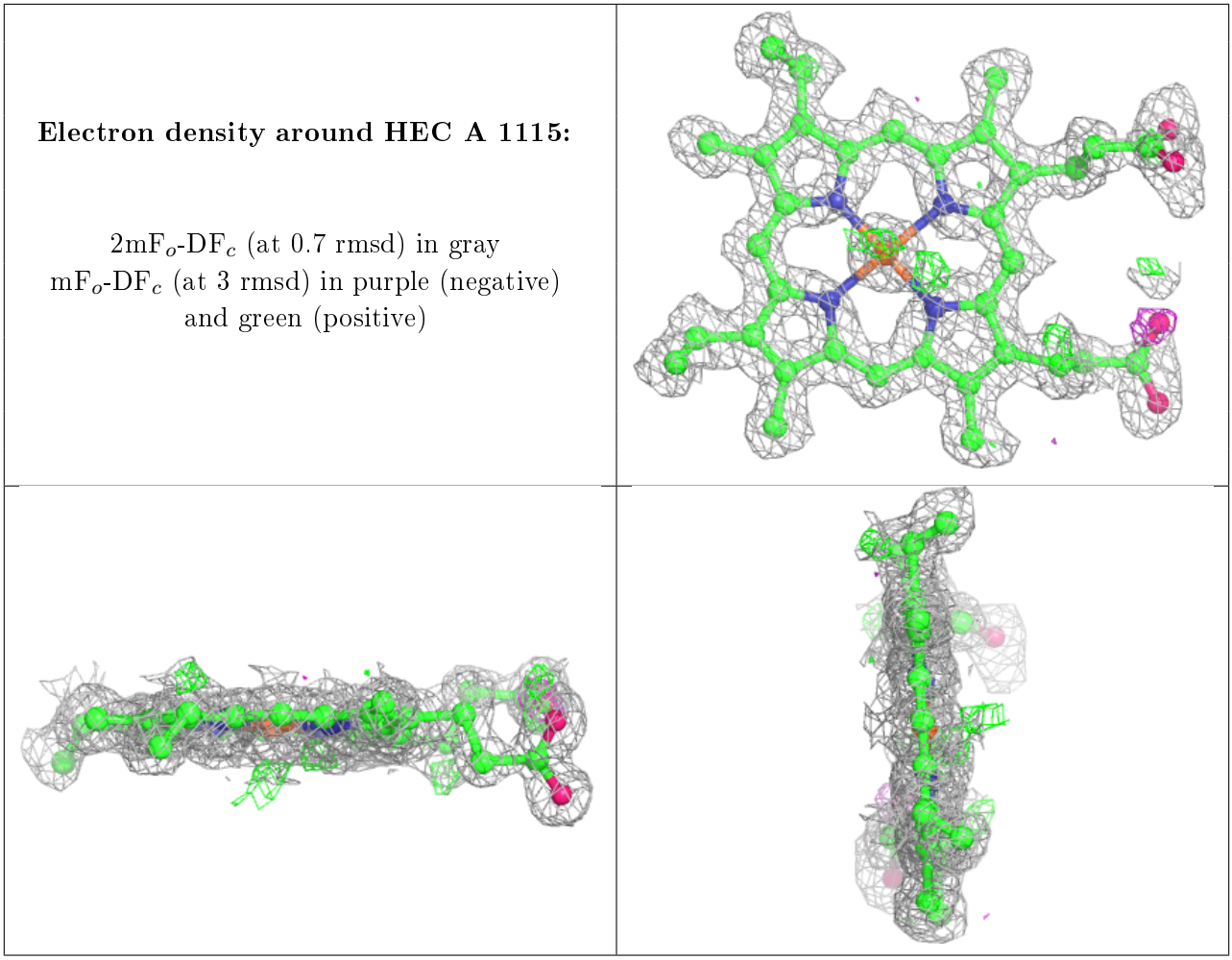
Electron density around HEC B 1117:

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



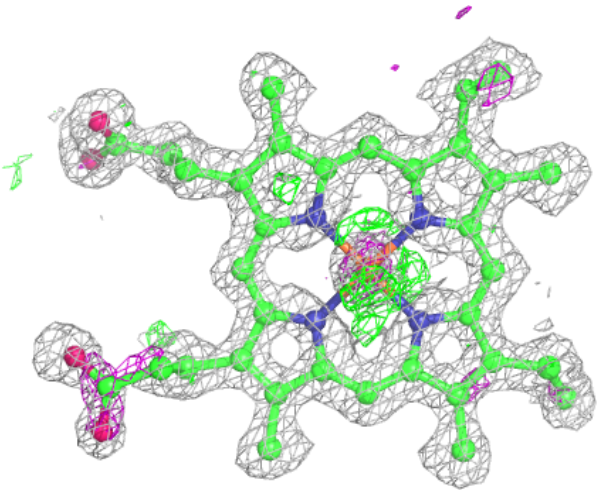
Electron density around HEC A 1115:

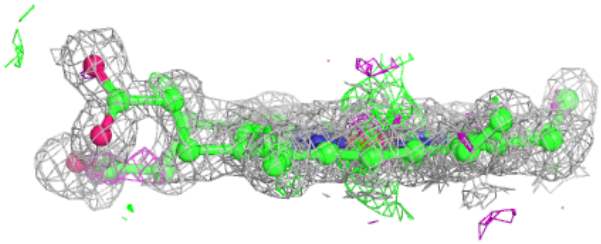
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

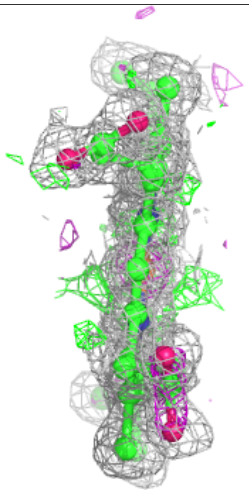


Electron density around HEC B 1116:

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

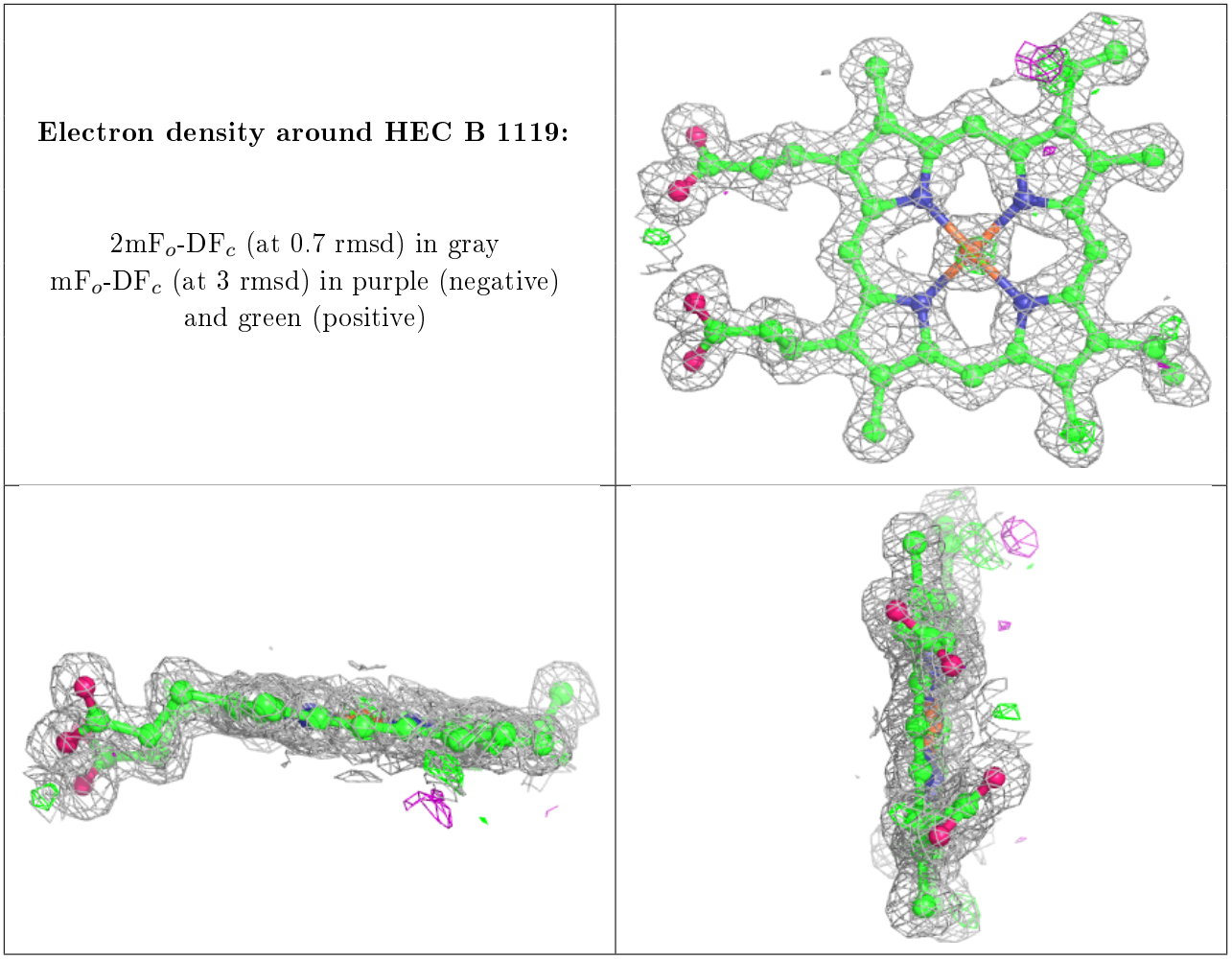






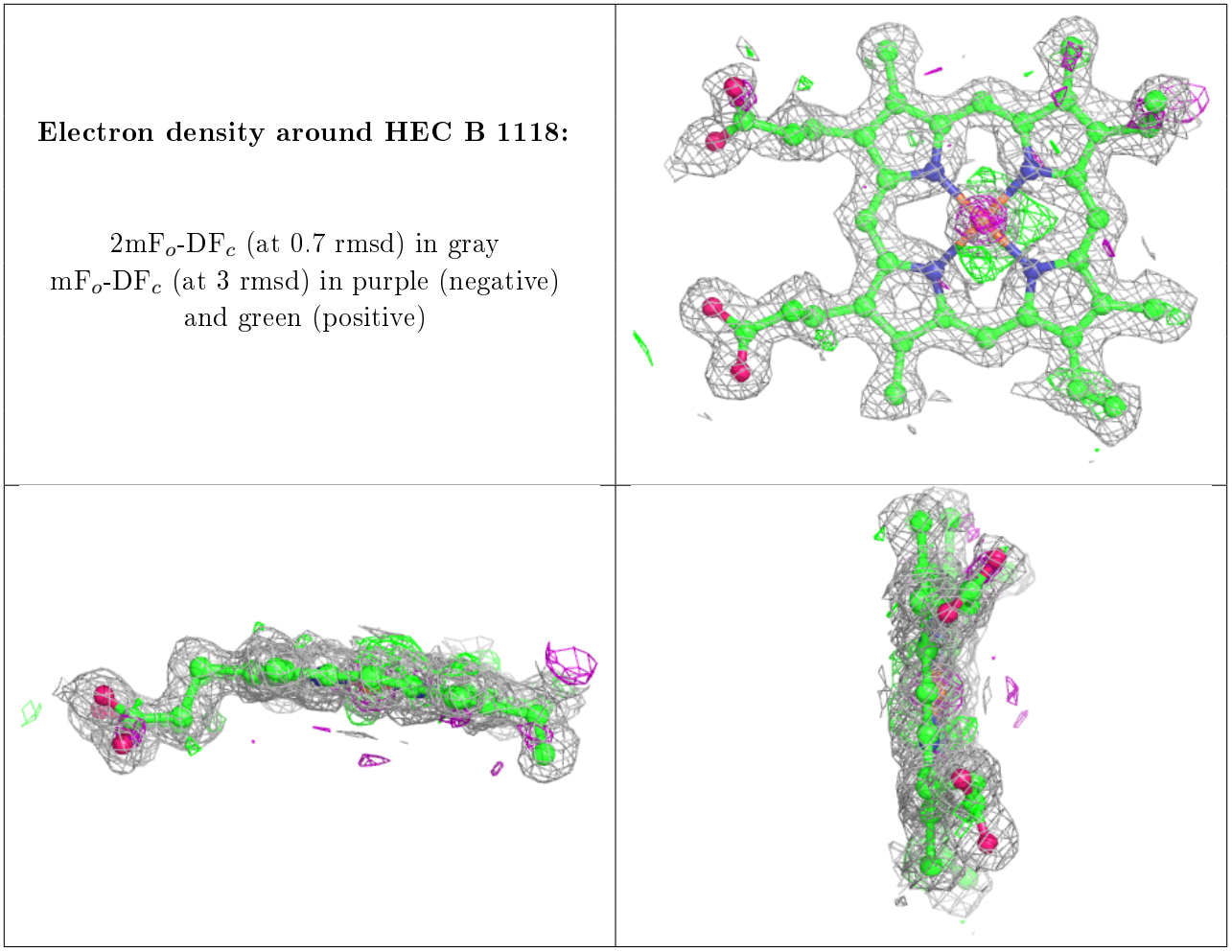
Electron density around HEC B 1119:

$2mF_o$-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 1118:

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



6.5 Other polymers

There are no such residues in this entry.