



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 29, 2024 – 03:10 PM EDT

PDB ID : 4LM8  
Title : Crystal structure of the outer membrane decaheme cytochrome MtrC  
Authors : Clarke, T.A.; Edwards, M.J.  
Deposited on : 2013-07-10  
Resolution : 1.80 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

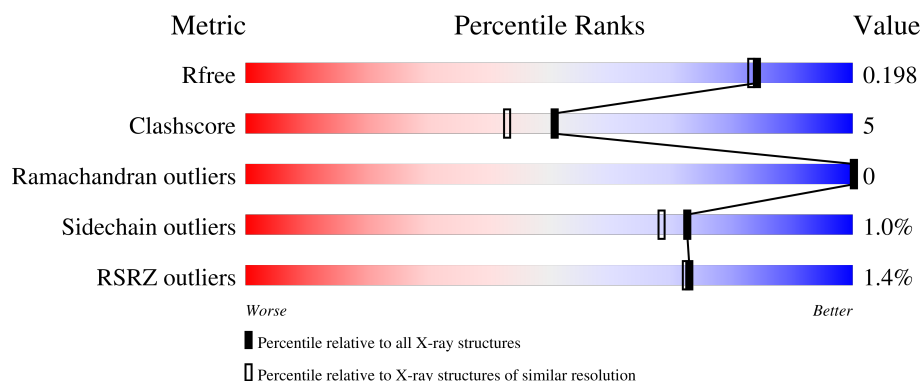
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 1.80 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))
$R_{free}$	164625	7108 (1.80-1.80)
Clashscore	180529	8162 (1.80-1.80)
Ramachandran outliers	177936	8077 (1.80-1.80)
Sidechain outliers	177891	8076 (1.80-1.80)
RSRZ outliers	164620	7108 (1.80-1.80)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	700	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6126 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 Extracellular iron oxide respiratory system surface decaheme cytochrome c component MtrC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	626	Total	C	N	O	S	0	4	0
			4719	2921	813	952	33			

There are 54 discrepancies between the modelled and reference sequences:

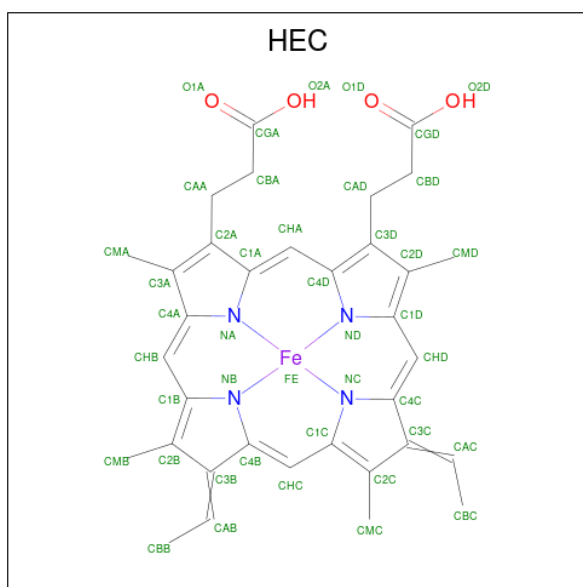
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP Q8EG34
A	3	LYS	-	expression tag	UNP Q8EG34
A	4	PHE	-	expression tag	UNP Q8EG34
A	5	LYS	-	expression tag	UNP Q8EG34
A	6	LEU	-	expression tag	UNP Q8EG34
A	7	ASN	-	expression tag	UNP Q8EG34
A	8	LEU	-	expression tag	UNP Q8EG34
A	9	ILE	-	expression tag	UNP Q8EG34
A	10	THR	-	expression tag	UNP Q8EG34
A	11	LEU	-	expression tag	UNP Q8EG34
A	12	ALA	-	expression tag	UNP Q8EG34
A	13	LEU	-	expression tag	UNP Q8EG34
A	14	LEU	-	expression tag	UNP Q8EG34
A	15	ALA	-	expression tag	UNP Q8EG34
A	16	ASN	-	expression tag	UNP Q8EG34
A	17	THR	-	expression tag	UNP Q8EG34
A	18	GLY	-	expression tag	UNP Q8EG34
A	19	LEU	-	expression tag	UNP Q8EG34
A	20	ALA	-	expression tag	UNP Q8EG34
A	21	VAL	-	expression tag	UNP Q8EG34
A	22	ALA	-	expression tag	UNP Q8EG34
A	23	ALA	-	expression tag	UNP Q8EG34
A	24	ASP	-	expression tag	UNP Q8EG34
A	25	GLY	-	expression tag	UNP Q8EG34
A	672	LYS	-	expression tag	UNP Q8EG34
A	673	GLY	-	expression tag	UNP Q8EG34

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Chain	Residue	Modelled	Actual	Comment	Reference
A	674	GLU	-	expression tag	UNP Q8EG34
A	675	LEU	-	expression tag	UNP Q8EG34
A	676	LYS	-	expression tag	UNP Q8EG34
A	677	LEU	-	expression tag	UNP Q8EG34
A	678	GLU	-	expression tag	UNP Q8EG34
A	679	GLY	-	expression tag	UNP Q8EG34
A	680	LYS	-	expression tag	UNP Q8EG34
A	681	PRO	-	expression tag	UNP Q8EG34
A	682	ILE	-	expression tag	UNP Q8EG34
A	683	PRO	-	expression tag	UNP Q8EG34
A	684	ASN	-	expression tag	UNP Q8EG34
A	685	PRO	-	expression tag	UNP Q8EG34
A	686	LEU	-	expression tag	UNP Q8EG34
A	687	LEU	-	expression tag	UNP Q8EG34
A	688	GLY	-	expression tag	UNP Q8EG34
A	689	LEU	-	expression tag	UNP Q8EG34
A	690	ASP	-	expression tag	UNP Q8EG34
A	691	SER	-	expression tag	UNP Q8EG34
A	692	THR	-	expression tag	UNP Q8EG34
A	693	ARG	-	expression tag	UNP Q8EG34
A	694	THR	-	expression tag	UNP Q8EG34
A	695	GLY	-	expression tag	UNP Q8EG34
A	696	HIS	-	expression tag	UNP Q8EG34
A	697	HIS	-	expression tag	UNP Q8EG34
A	698	HIS	-	expression tag	UNP Q8EG34
A	699	HIS	-	expression tag	UNP Q8EG34
A	700	HIS	-	expression tag	UNP Q8EG34
A	701	HIS	-	expression tag	UNP Q8EG34

- 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 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	Ca	0	0
			5	5		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

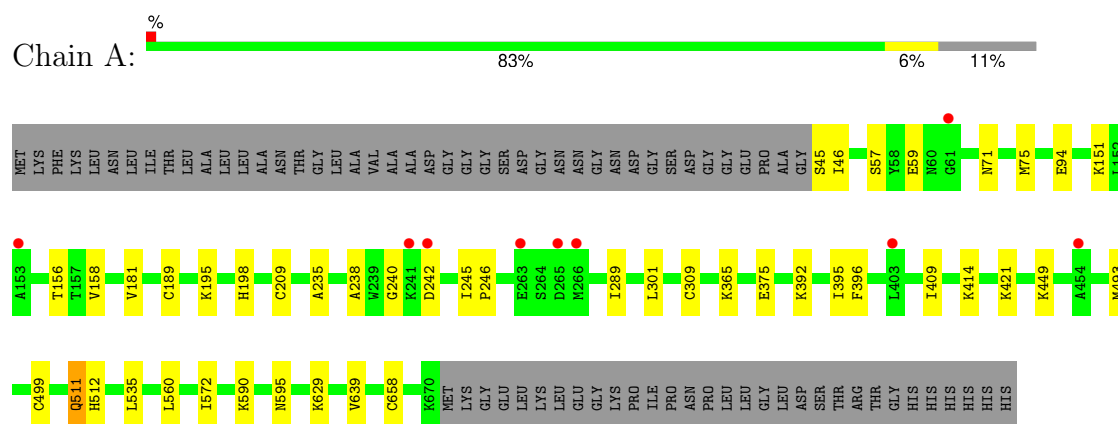
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	936	Total	O	0	0
			936	936		

### 3 Residue-property plots

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: Extracellular iron oxide respiratory system surface decaheme cytochrome c component MtrC





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.12Å 90.44Å 154.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.80 – 1.80 45.80 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.0 (45.80-1.80) 97.0 (45.80-1.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.75 (at 1.80Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.166 , 0.203 0.162 , 0.198	Depositor DCC
$R_{free}$ test set	3427 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.2	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6126	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, EDO, ACT, 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	0.37	0/4808	0.55	0/6530

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	4719	0	4532	40	0
2	A	430	0	303	28	0
3	A	5	0	0	0	0
4	A	32	0	48	0	0
5	A	4	0	3	0	0
6	A	936	0	0	9	0
All	All	6126	0	4886	49	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 5.

The worst 5 of 49 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:209:CYS:SG	2:A:802:HEC:CAC	2.23	1.27
1:A:499:CYS:SG	2:A:806:HEC:CAC	2.23	1.26
1:A:309:CYS:SG	2:A:805:HEC:CAC	2.30	1.20
1:A:209:CYS:SG	2:A:802:HEC:HAC	2.07	0.94
1:A:309:CYS:SG	2:A:805:HEC:HAC	2.07	0.90

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	628/700 (90%)	612 (98%)	16 (2%)	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	517/567 (91%)	512 (99%)	5 (1%)	73	68

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	HIS
1	A	395	ILE

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Mol	Chain	Res	Type
1	A	449	LYS
1	A	511	GLN
1	A	595	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN

### 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 24 ligands modelled in this entry, 5 are monoatomic - leaving 19 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	810	1	32,50,50	2.05	4 (12%)	30,82,82	2.34	8 (26%)
2	HEC	A	807	1	32,50,50	2.03	4 (12%)	30,82,82	2.21	7 (23%)
2	HEC	A	809	1	32,50,50	1.99	5 (15%)	30,82,82	2.38	9 (30%)
2	HEC	A	802	1	32,50,50	1.95	3 (9%)	30,82,82	2.37	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HEC	A	805	1	32,50,50	2.01	3 (9%)	30,82,82	2.28	7 (23%)
4	EDO	A	819	-	3,3,3	0.46	0	2,2,2	0.38	0
2	HEC	A	801	1	32,50,50	2.03	3 (9%)	30,82,82	2.32	9 (30%)
4	EDO	A	823	-	3,3,3	0.41	0	2,2,2	0.40	0
4	EDO	A	822	-	3,3,3	0.45	0	2,2,2	0.38	0
4	EDO	A	817	-	3,3,3	0.39	0	2,2,2	0.62	0
2	HEC	A	808	1	32,50,50	2.04	4 (12%)	30,82,82	2.24	7 (23%)
2	HEC	A	803	1	32,50,50	2.01	4 (12%)	30,82,82	2.08	6 (20%)
2	HEC	A	806	1	32,50,50	2.08	4 (12%)	30,82,82	2.21	8 (26%)
4	EDO	A	818	-	3,3,3	0.50	0	2,2,2	0.35	0
4	EDO	A	816	-	3,3,3	0.43	0	2,2,2	0.46	0
2	HEC	A	804	1	32,50,50	2.01	4 (12%)	30,82,82	2.29	7 (23%)
4	EDO	A	820	-	3,3,3	0.41	0	2,2,2	0.43	0
4	EDO	A	821	-	3,3,3	0.42	0	2,2,2	0.34	0
5	ACT	A	824	-	3,3,3	0.79	0	3,3,3	1.43	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	819	-	-	0/1/1/1	-
2	HEC	A	808	1	-	2/10/54/54	-
4	EDO	A	820	-	-	1/1/1/1	-
2	HEC	A	803	1	-	0/10/54/54	-
2	HEC	A	801	1	-	3/10/54/54	-
2	HEC	A	806	1	-	3/10/54/54	-
4	EDO	A	823	-	-	0/1/1/1	-
4	EDO	A	818	-	-	0/1/1/1	-
2	HEC	A	807	1	-	2/10/54/54	-
2	HEC	A	809	1	-	5/10/54/54	-
4	EDO	A	821	-	-	0/1/1/1	-
4	EDO	A	822	-	-	0/1/1/1	-
4	EDO	A	817	-	-	1/1/1/1	-
2	HEC	A	802	1	-	2/10/54/54	-
4	EDO	A	816	-	-	0/1/1/1	-
2	HEC	A	804	1	-	5/10/54/54	-
2	HEC	A	805	1	-	1/10/54/54	-
2	HEC	A	810	1	-	1/10/54/54	-

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	806	HEC	C2B-C3B	-6.51	1.33	1.40
2	A	807	HEC	C2B-C3B	-5.96	1.34	1.40
2	A	804	HEC	C2B-C3B	-5.58	1.34	1.40
2	A	805	HEC	C2B-C3B	-5.51	1.34	1.40
2	A	810	HEC	C2B-C3B	-5.50	1.34	1.40

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	805	HEC	CBB-CAB-C3B	-7.93	108.93	127.49
2	A	801	HEC	CBB-CAB-C3B	-7.86	109.09	127.49
2	A	809	HEC	CBB-CAB-C3B	-7.06	110.98	127.49
2	A	806	HEC	CBB-CAB-C3B	-7.02	111.06	127.49
2	A	804	HEC	CBB-CAB-C3B	-6.85	111.47	127.49

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	809	HEC	C2A-CAA-CBA-CGA
2	A	801	HEC	C2A-CAA-CBA-CGA
4	A	820	EDO	O1-C1-C2-O2
2	A	804	HEC	C2A-CAA-CBA-CGA
4	A	817	EDO	O1-C1-C2-O2

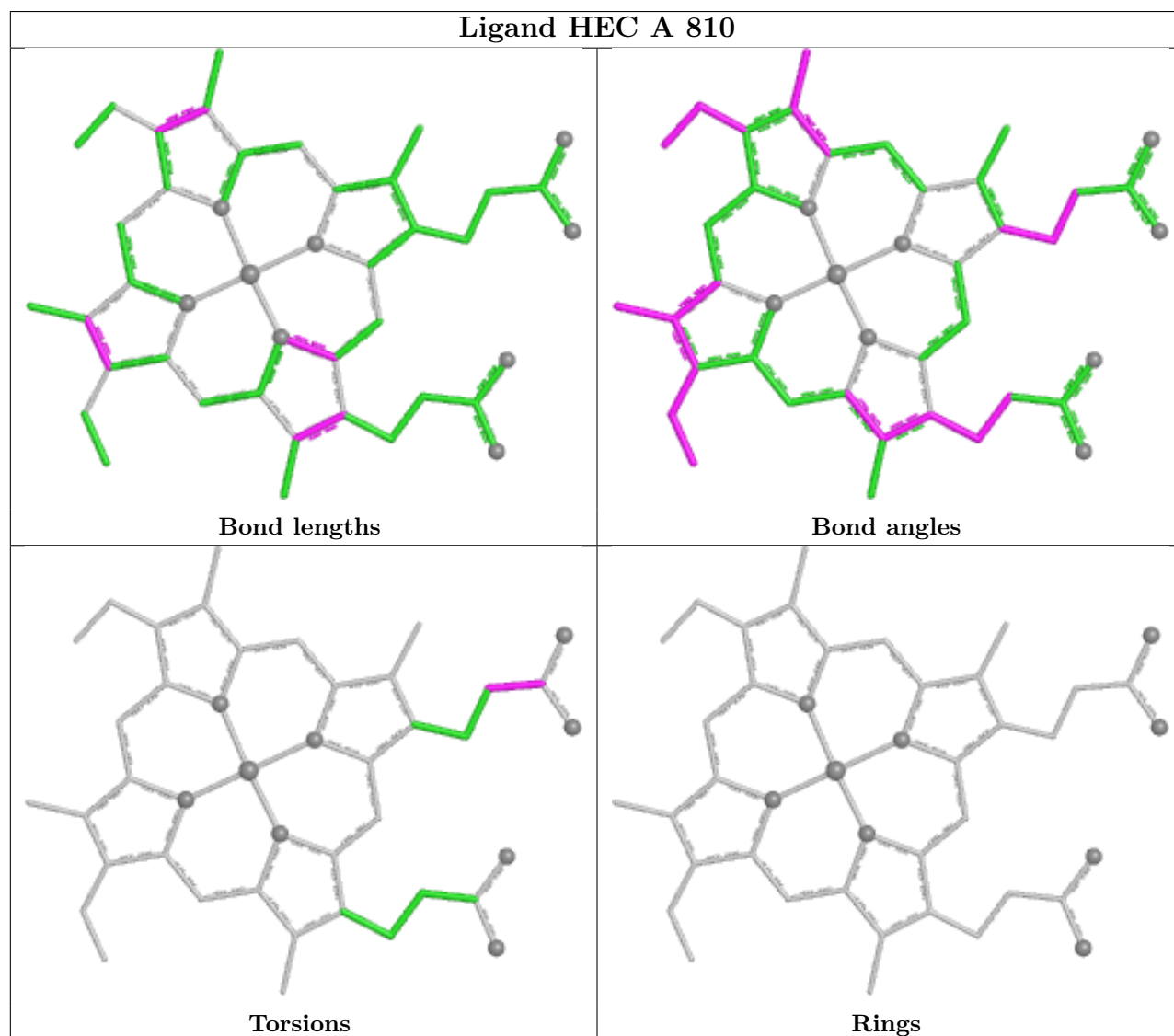
There are no ring outliers.

10 monomers are involved in 28 short contacts:

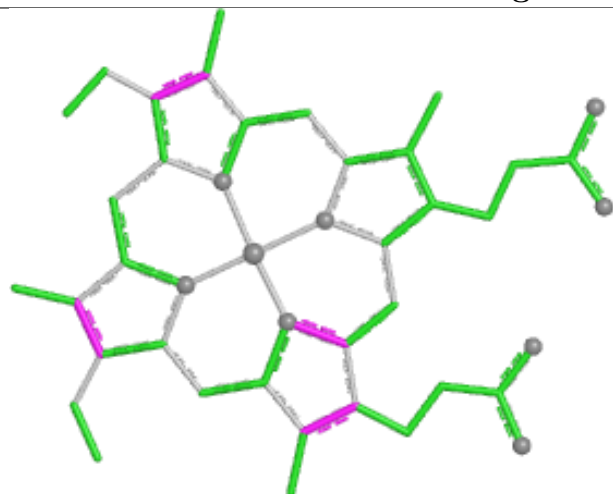
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	810	HEC	3	0
2	A	807	HEC	2	0
2	A	809	HEC	1	0
2	A	802	HEC	5	0
2	A	805	HEC	6	0
2	A	801	HEC	1	0
2	A	808	HEC	1	0
2	A	803	HEC	3	0
2	A	806	HEC	6	0
2	A	804	HEC	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

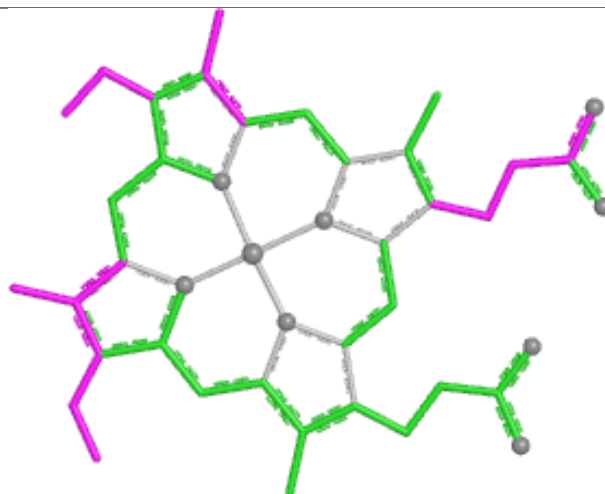
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.



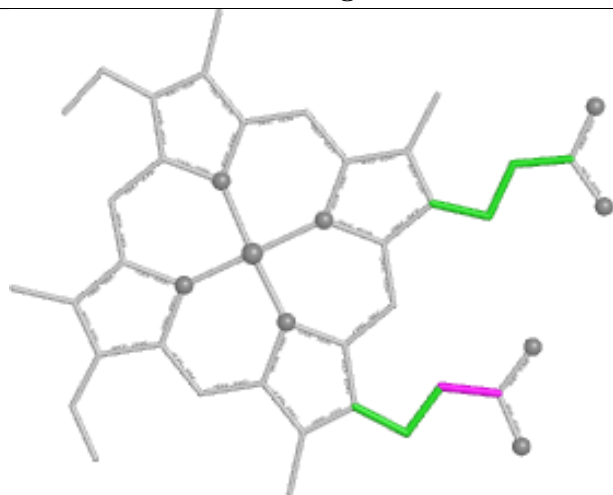
## Ligand HEC A 807



Bond lengths



Bond angles



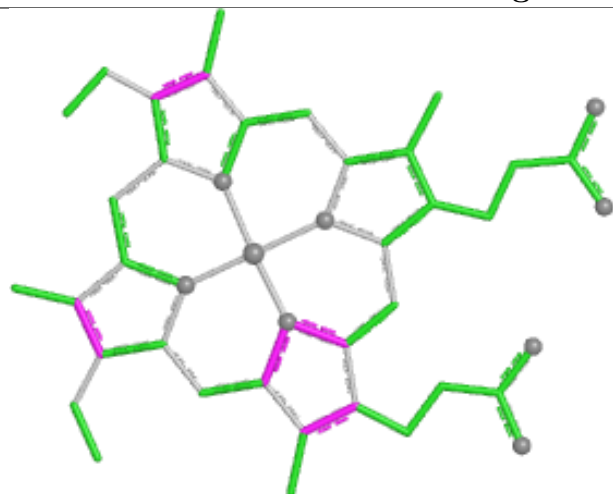
Torsions



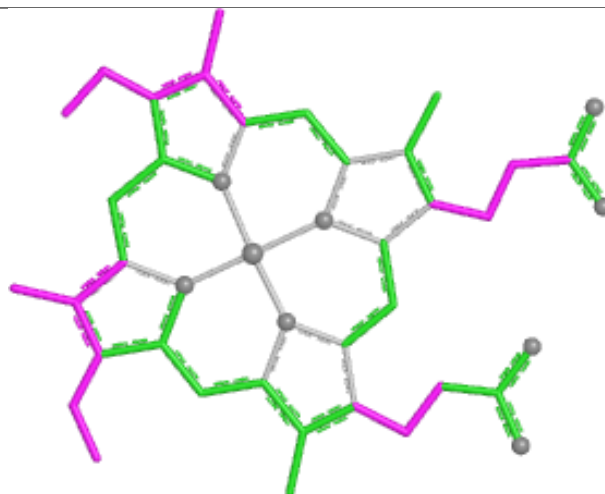
Rings



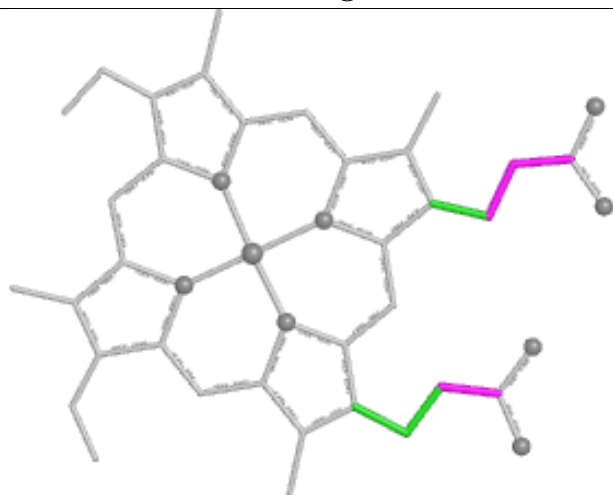
## Ligand HEC A 809



Bond lengths



Bond angles

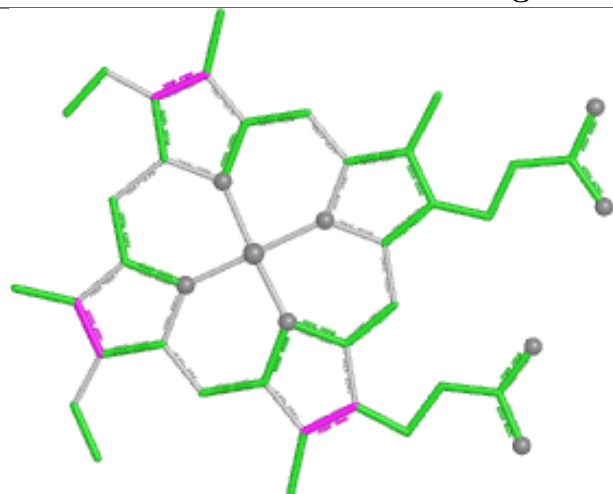


Torsions

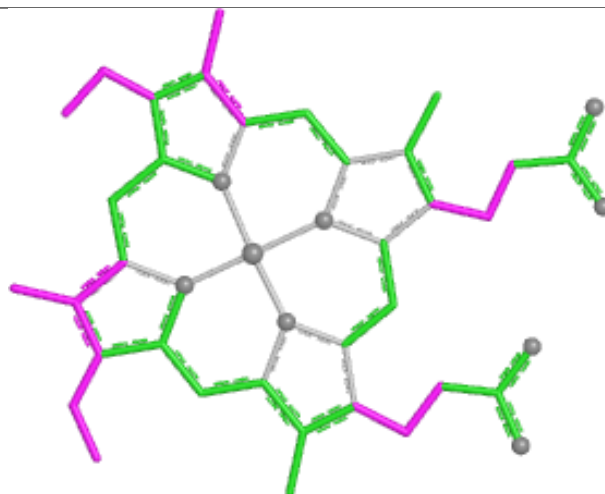


Rings

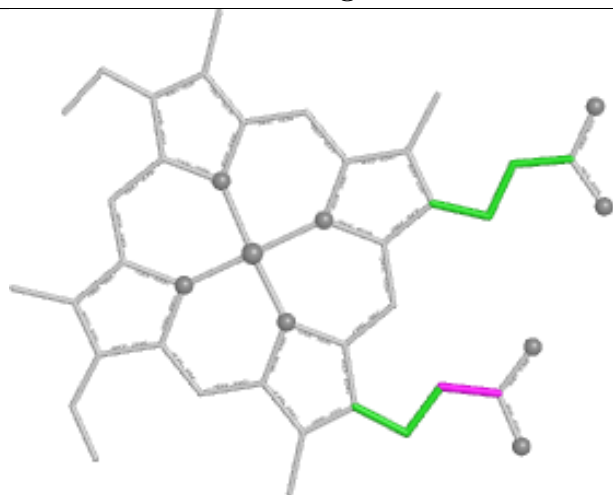
## Ligand HEC A 802



Bond lengths



Bond angles

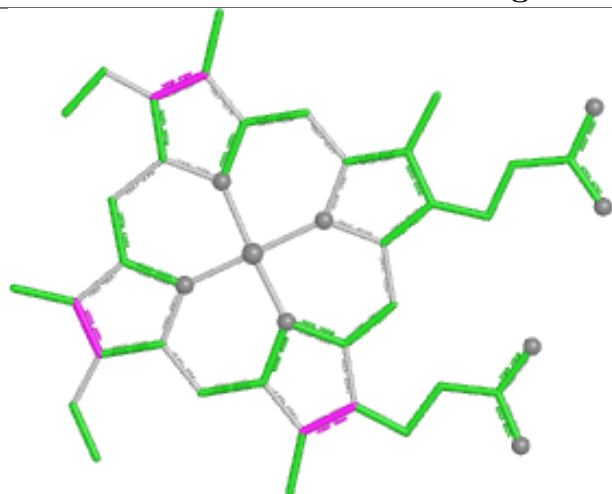


Torsions

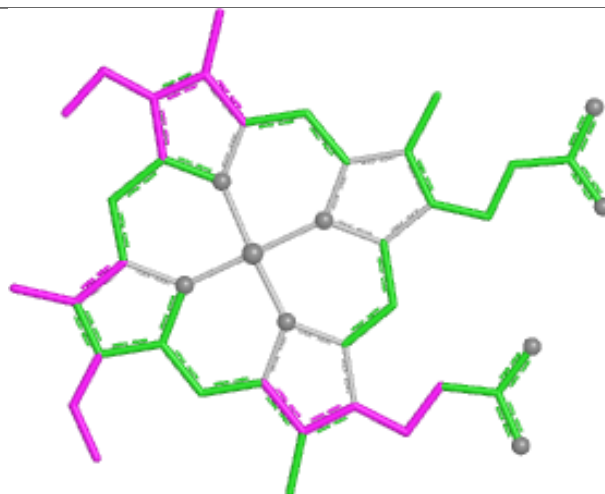


Rings

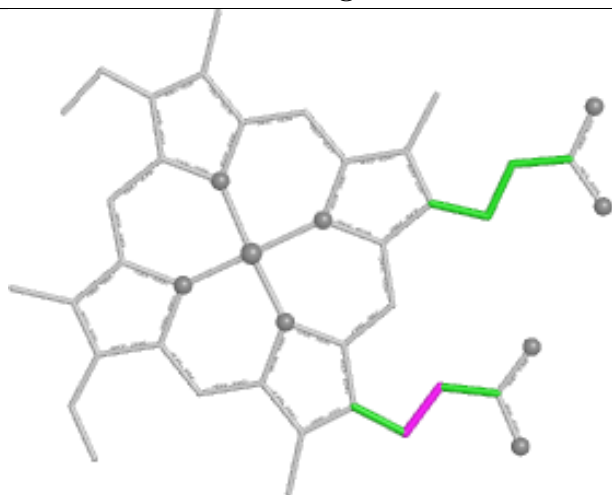
## Ligand HEC A 805



Bond lengths



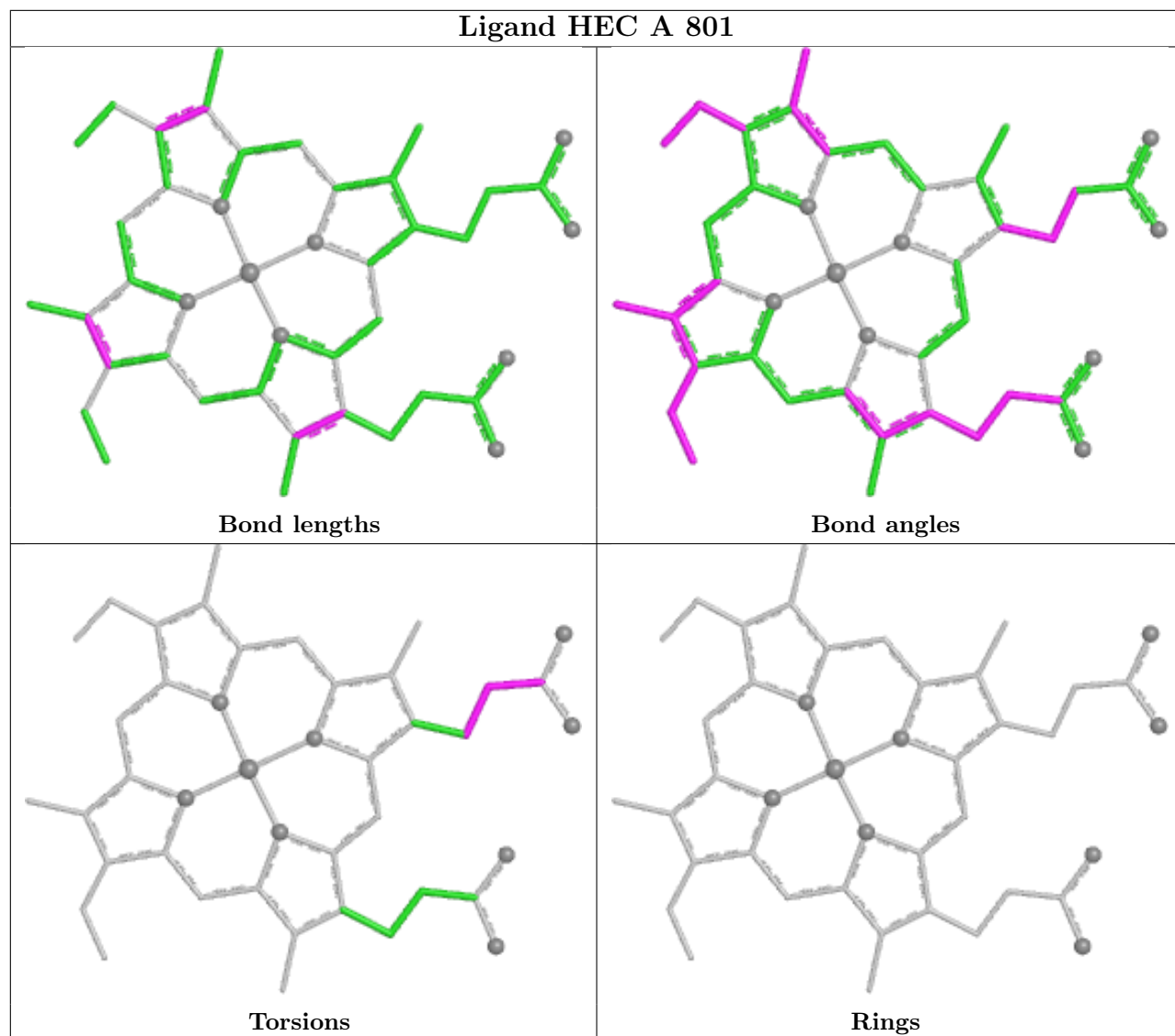
Bond angles



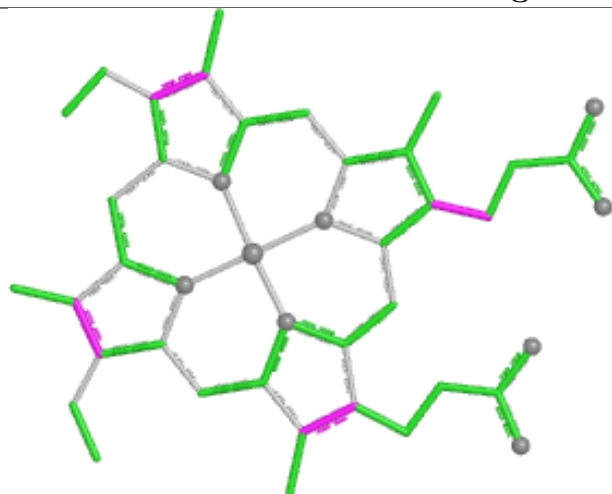
Torsions



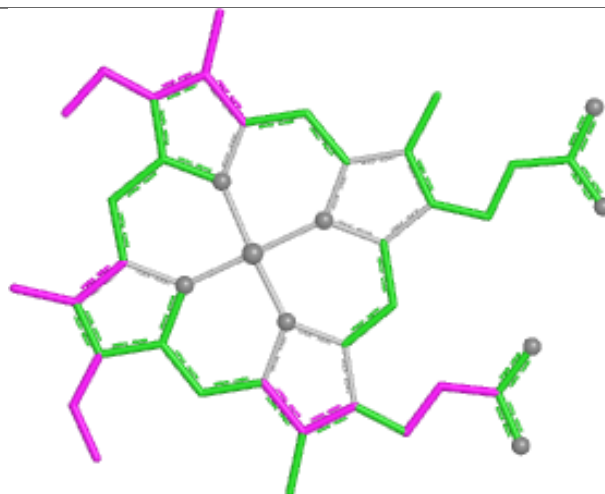
Rings



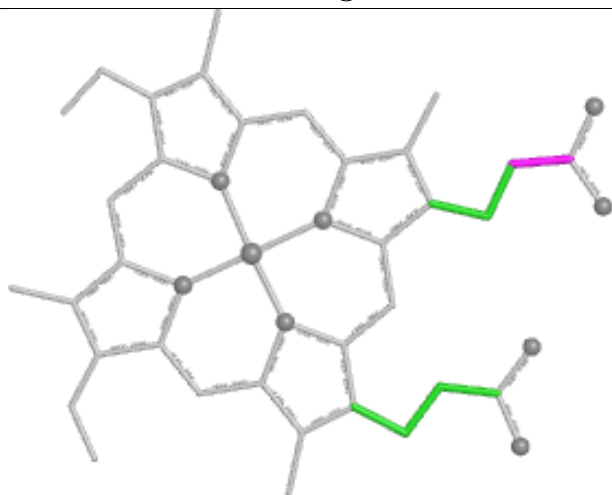
## Ligand HEC A 808



Bond lengths



Bond angles

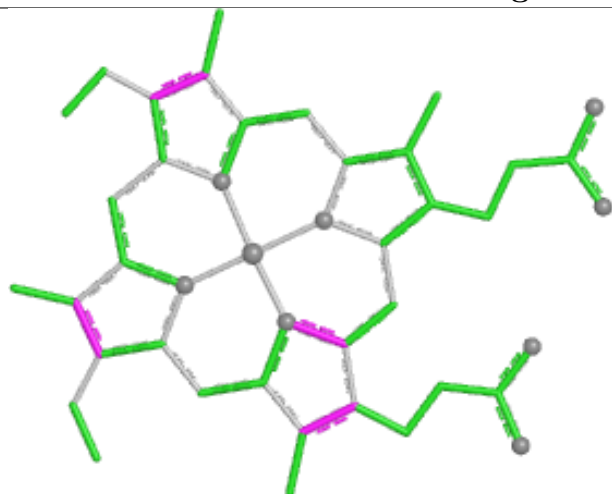


Torsions

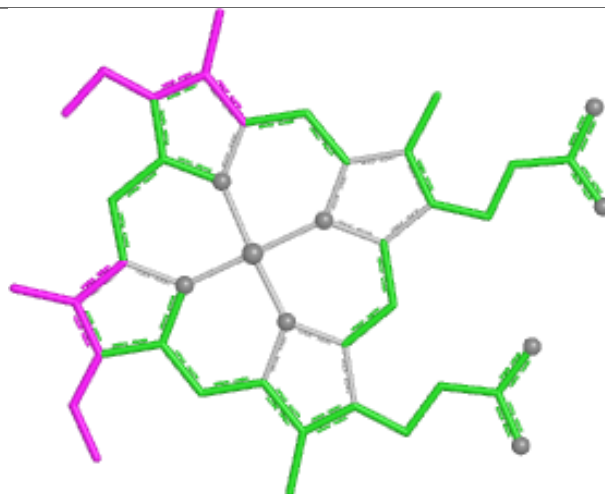


Rings

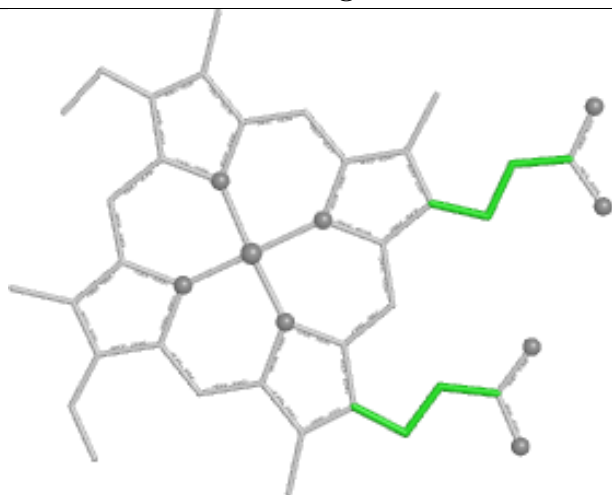
## Ligand HEC A 803



Bond lengths



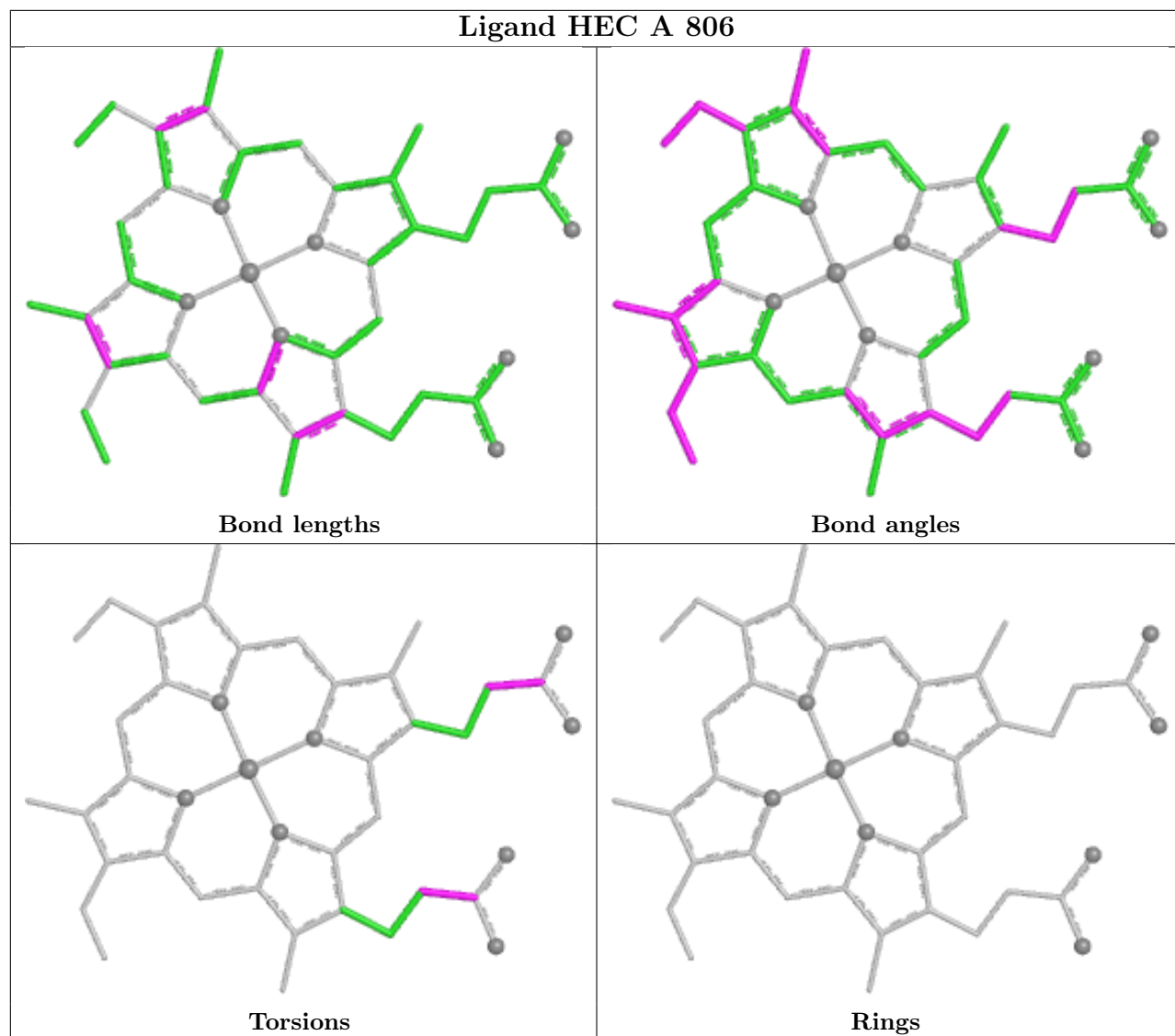
Bond angles

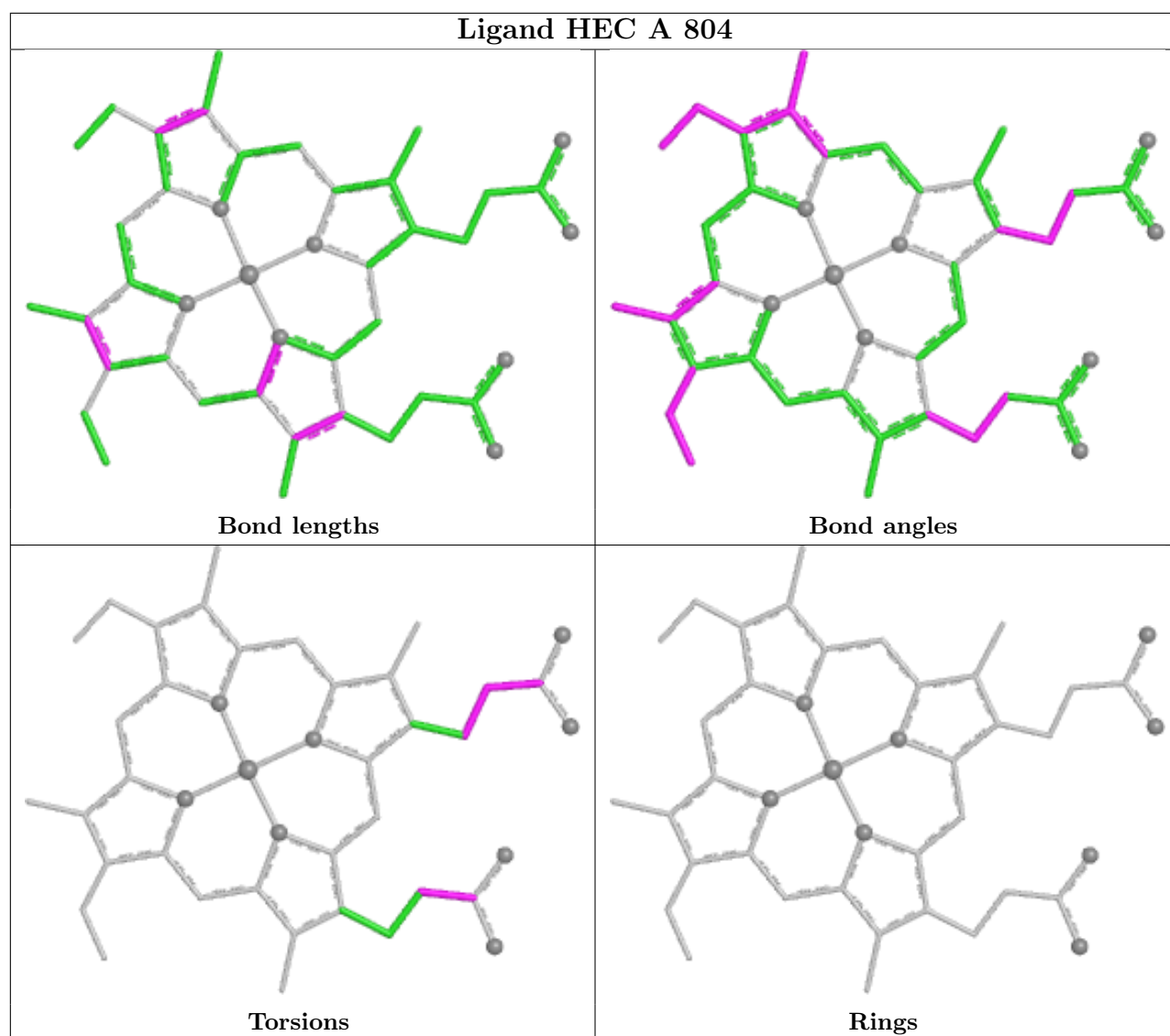


Torsions



Rings





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	626/700 (89%)	-0.38	9 (1%) 73 72	4, 16, 36, 72	4 (0%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	61	GLY	3.2
1	A	241	LYS	2.9
1	A	454	ALA	2.6
1	A	263	GLU	2.6
1	A	265	ASP	2.5

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	ACT	A	824	4/4	0.75	0.25	33,36,38,43	0
4	EDO	A	823	4/4	0.87	0.17	39,39,39,39	0

*Continued on next page...*

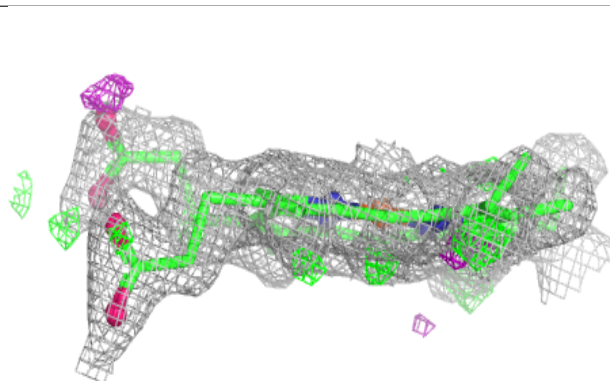
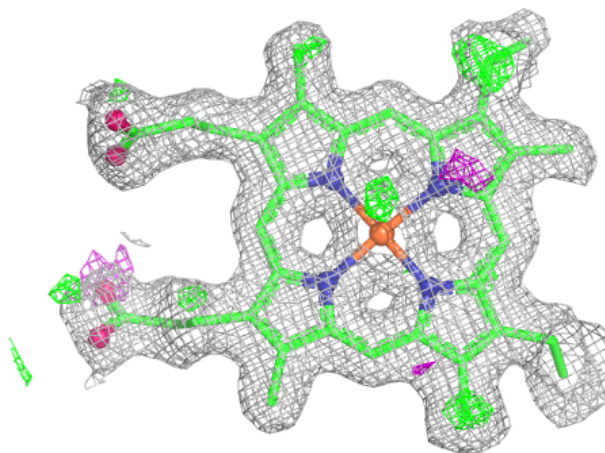
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	817	4/4	0.87	0.12	17,18,23,25	0
4	EDO	A	816	4/4	0.91	0.10	27,29,36,38	0
4	EDO	A	819	4/4	0.92	0.09	30,30,35,35	0
4	EDO	A	820	4/4	0.93	0.09	17,34,35,36	0
4	EDO	A	821	4/4	0.94	0.08	20,21,24,32	0
3	CA	A	814	1/1	0.95	0.07	38,38,38,38	0
4	EDO	A	822	4/4	0.95	0.08	22,22,22,22	0
4	EDO	A	818	4/4	0.96	0.07	15,18,18,23	0
2	HEC	A	805	43/43	0.97	0.08	8,15,34,37	0
2	HEC	A	806	43/43	0.97	0.06	8,10,18,23	0
2	HEC	A	804	43/43	0.98	0.07	5,12,33,49	0
2	HEC	A	801	43/43	0.98	0.06	5,9,21,32	0
2	HEC	A	802	43/43	0.98	0.05	4,8,16,20	0
2	HEC	A	809	43/43	0.98	0.07	6,10,39,47	0
2	HEC	A	810	43/43	0.98	0.06	8,11,23,40	0
3	CA	A	813	1/1	0.99	0.04	15,15,15,15	0
2	HEC	A	808	43/43	0.99	0.04	4,9,11,13	0
3	CA	A	815	1/1	0.99	0.06	14,14,14,14	0
2	HEC	A	803	43/43	0.99	0.04	5,8,10,12	0
2	HEC	A	807	43/43	0.99	0.05	8,12,16,19	0
3	CA	A	812	1/1	0.99	0.15	22,22,22,22	0
3	CA	A	811	1/1	1.00	0.03	8,8,8,8	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.

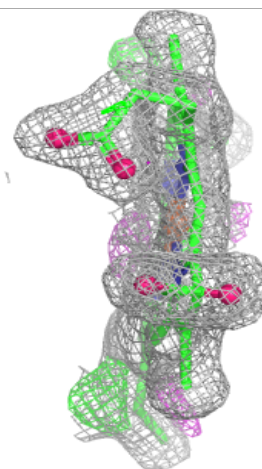
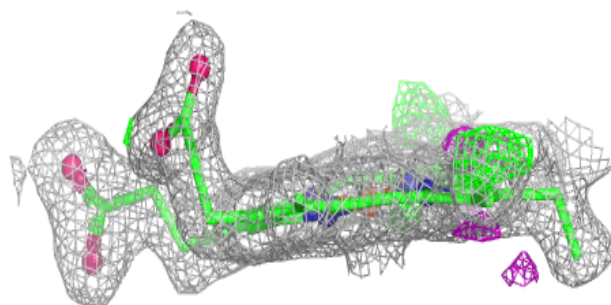
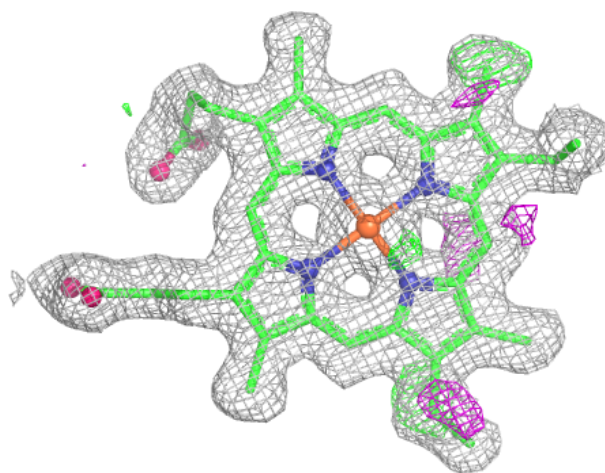
**Electron density around HEC A 805:**

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



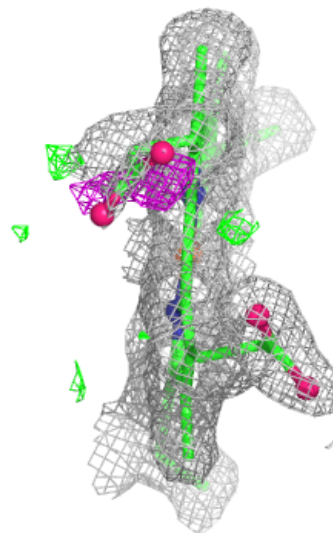
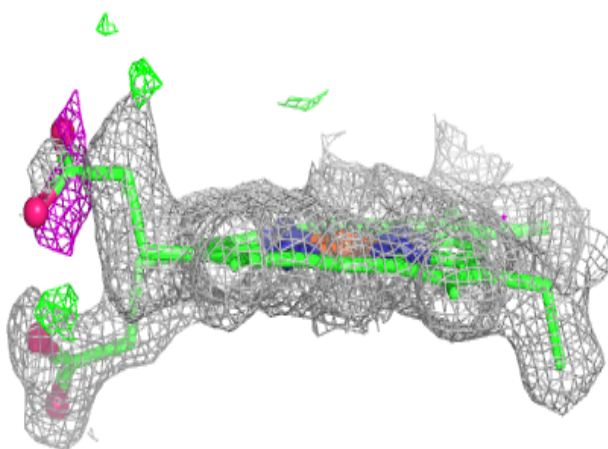
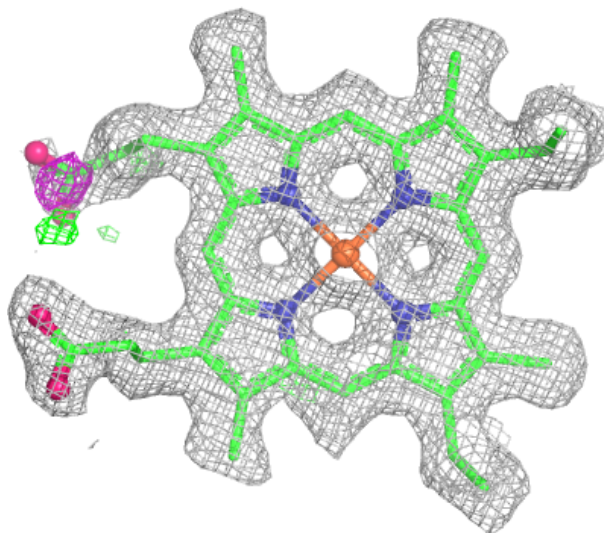
**Electron density around HEC A 806:**

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



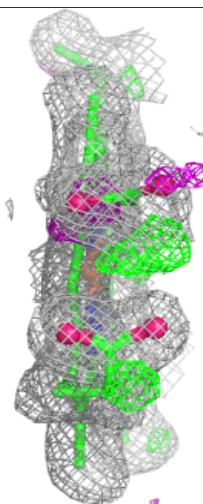
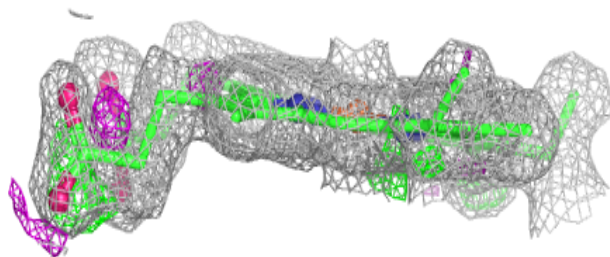
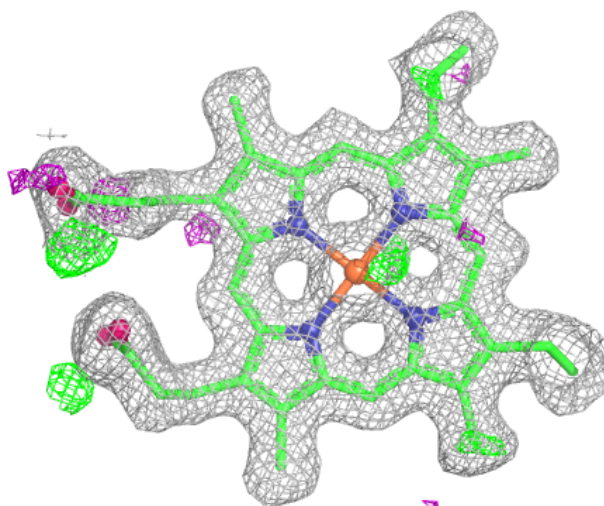
**Electron density around HEC A 804:**

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



**Electron density around HEC A 801:**

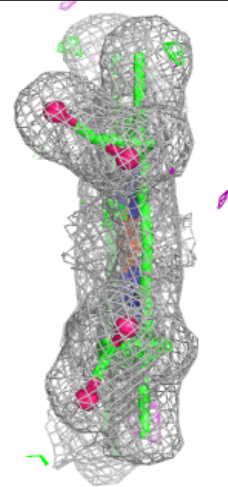
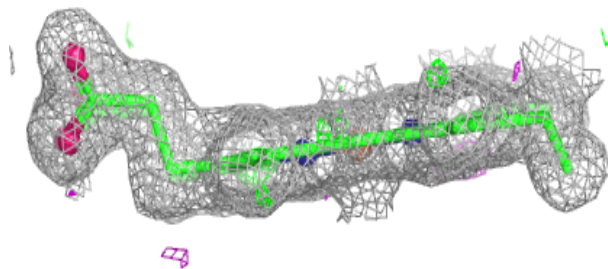
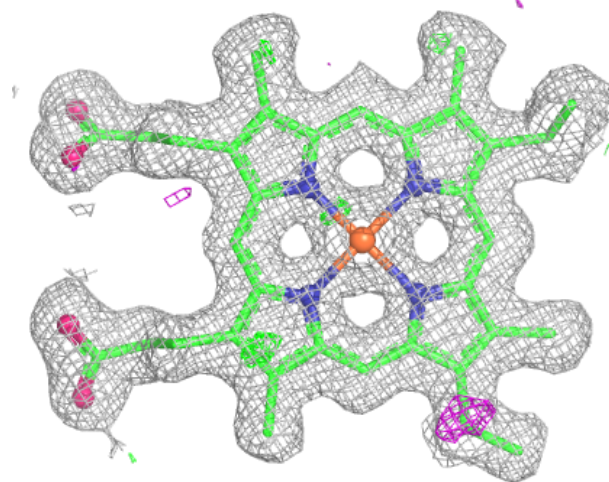
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





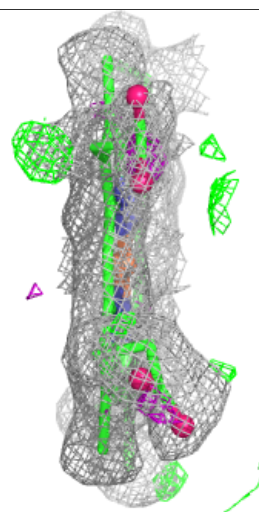
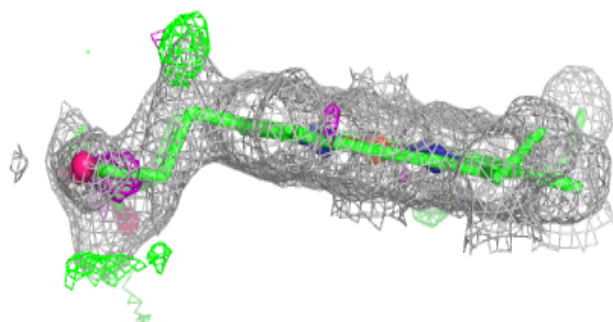
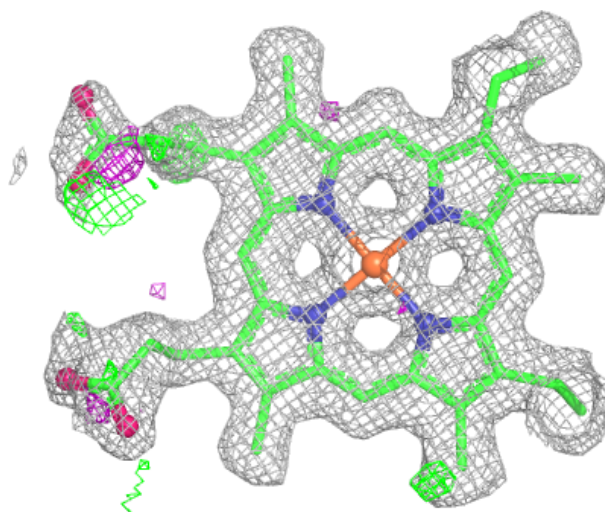
**Electron density around HEC A 802:**

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



**Electron density around HEC A 809:**

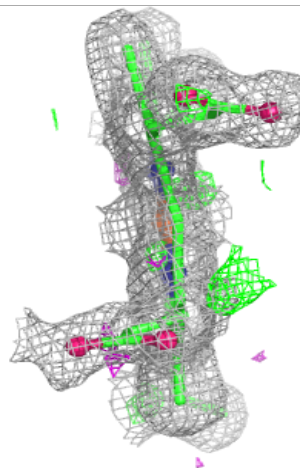
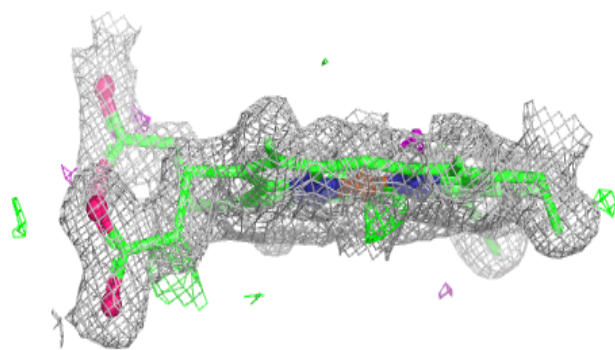
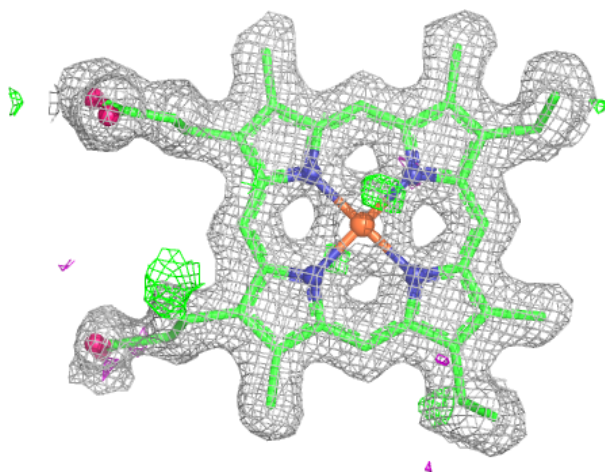
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





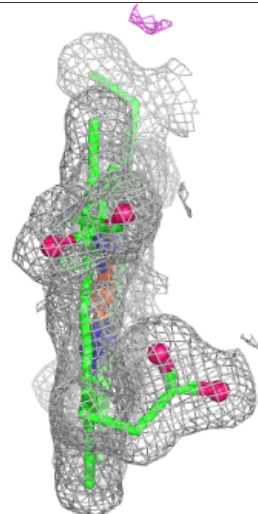
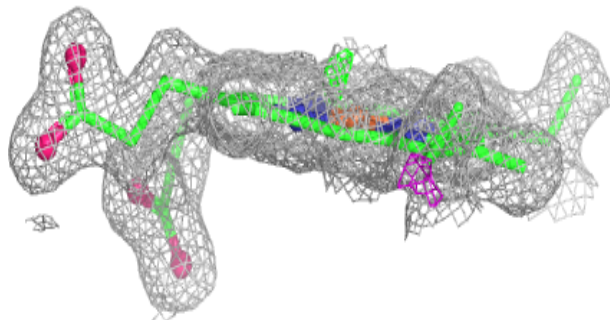
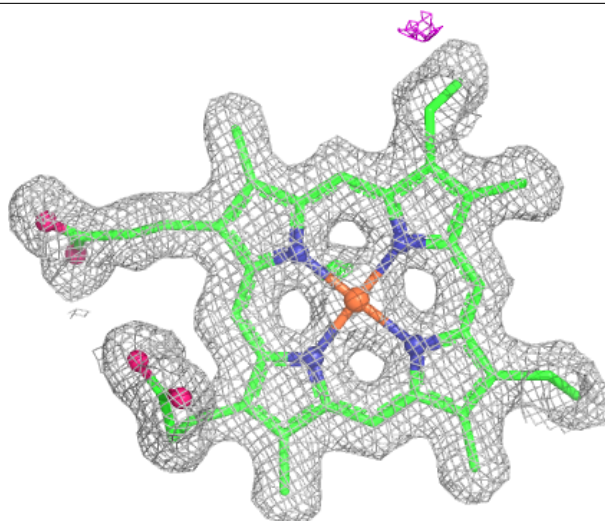
**Electron density around HEC A 810:**

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



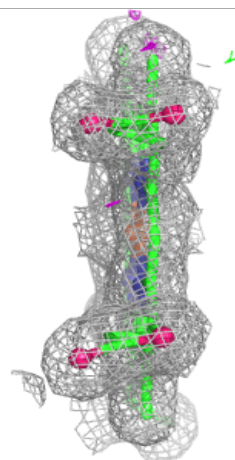
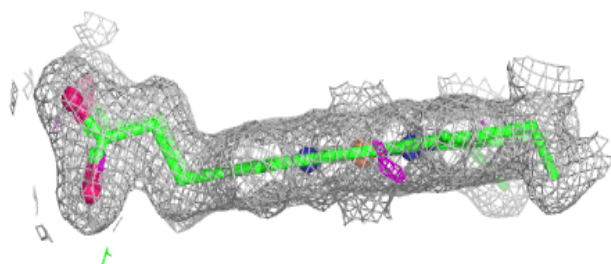
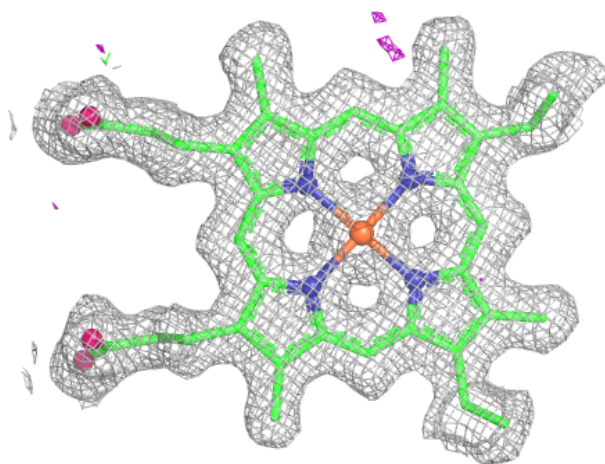
**Electron density around HEC A 808:**

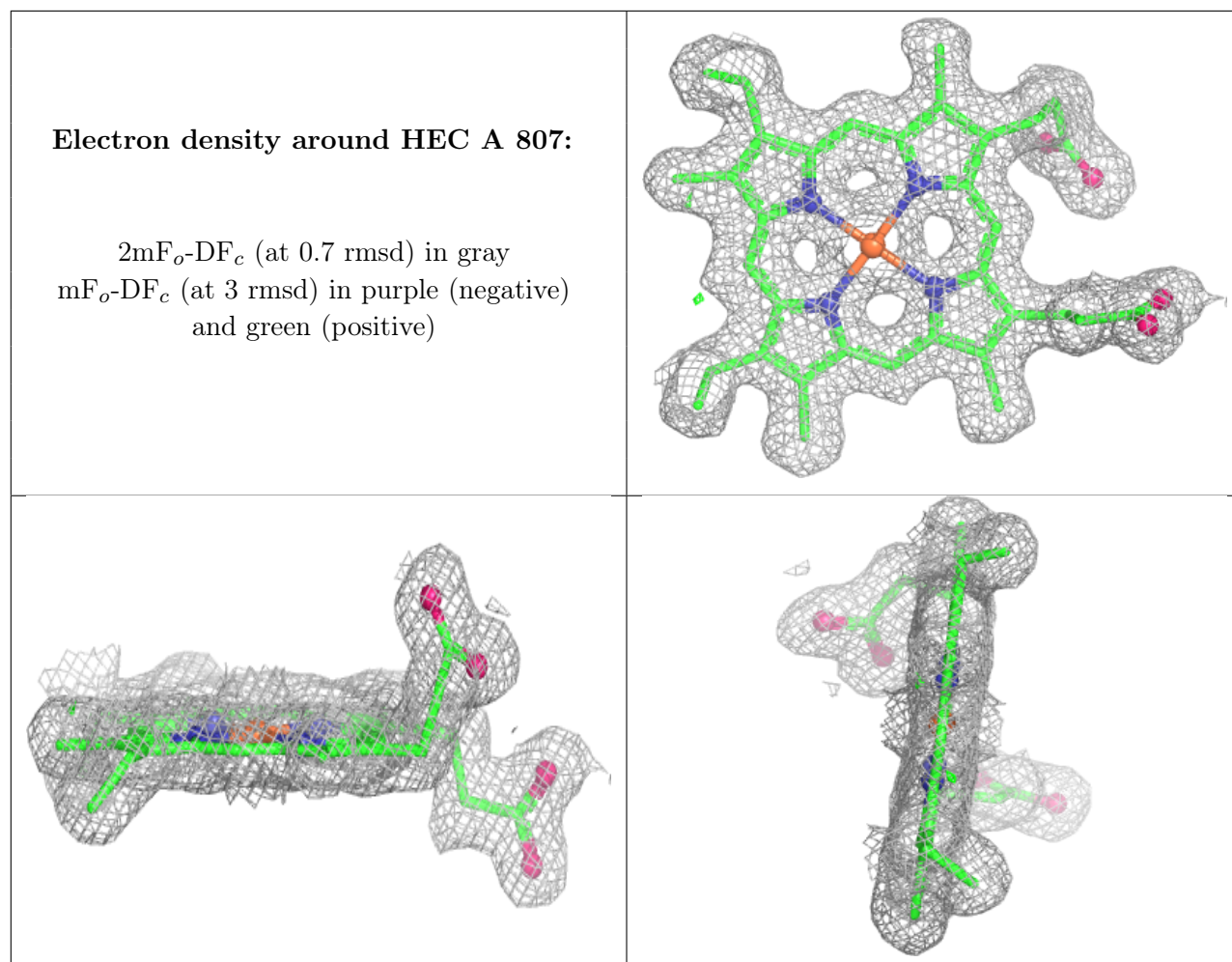
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEC A 803:**

$2mF_o-DF_c$  (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.