wwPDB X-ray Structure Validation Summary Report (i)

Sep 19, 2023 – 11:46 PM EDT

PDB ID	:	5IRV
Title	:	Human cytochrome P450 17A1 bound to inhibitor VT-464
Authors	:	Scott, E.E.; Petrunak, E.M.
Deposited on	:	2016-03-14
Resolution	:	3.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

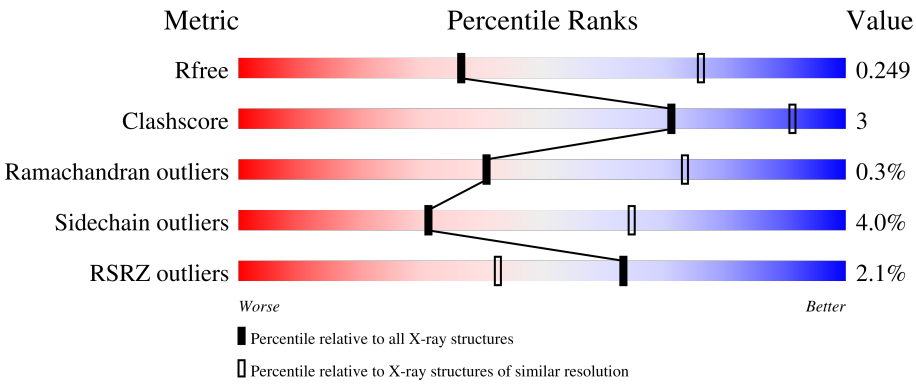
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 <=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	494	.% 87% 8% • 5%
1	B	494	2% 87% 8% 5%
1	C	494	3% 83% 12% • •
1	D	494	2% 85% 9% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 30314 atoms, of which 15005 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 Steroid 17-alpha-hydroxylase/17,20 lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	471	7576	2403	3827	649	682	15	0	0	0
1	B	471	7576	2403	3827	649	682	15	0	0	0
1	C	475	7336	2415	3564	654	688	15	0	0	0
1	D	472	7354	2406	3599	650	684	15	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	MET	-	expression tag	UNP P05093
A	20	ALA	-	expression tag	UNP P05093
A	21	LYS	-	expression tag	UNP P05093
A	22	LYS	-	expression tag	UNP P05093
A	23	THR	-	expression tag	UNP P05093
A	509	HIS	-	expression tag	UNP P05093
A	510	HIS	-	expression tag	UNP P05093
A	511	HIS	-	expression tag	UNP P05093
A	512	HIS	-	expression tag	UNP P05093
B	19	MET	-	expression tag	UNP P05093
B	20	ALA	-	expression tag	UNP P05093
B	21	LYS	-	expression tag	UNP P05093
B	22	LYS	-	expression tag	UNP P05093
B	23	THR	-	expression tag	UNP P05093
B	509	HIS	-	expression tag	UNP P05093
B	510	HIS	-	expression tag	UNP P05093
B	511	HIS	-	expression tag	UNP P05093
B	512	HIS	-	expression tag	UNP P05093
C	19	MET	-	expression tag	UNP P05093
C	20	ALA	-	expression tag	UNP P05093
C	21	LYS	-	expression tag	UNP P05093

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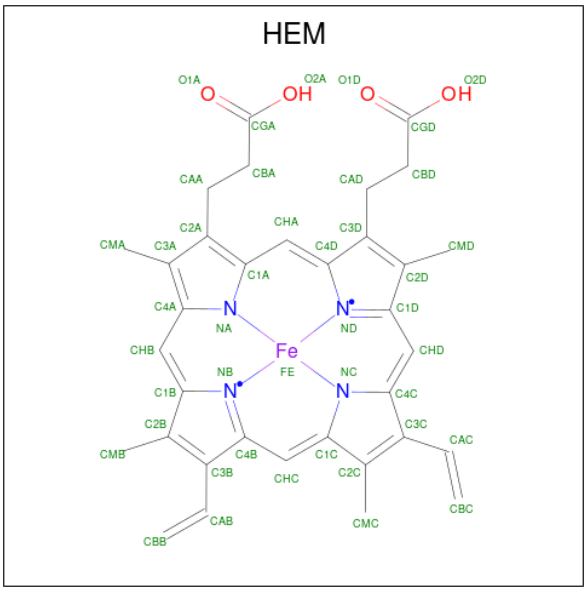
Chain	Residue	Modelled	Actual	Comment	Reference
C	22	LYS	-	expression tag	UNP P05093
C	23	THR	-	expression tag	UNP P05093
C	509	HIS	-	expression tag	UNP P05093
C	510	HIS	-	expression tag	UNP P05093
C	511	HIS	-	expression tag	UNP P05093
C	512	HIS	-	expression tag	UNP P05093
D	19	MET	-	expression tag	UNP P05093
D	20	ALA	-	expression tag	UNP P05093
D	21	LYS	-	expression tag	UNP P05093
D	22	LYS	-	expression tag	UNP P05093
D	23	THR	-	expression tag	UNP P05093
D	509	HIS	-	expression tag	UNP P05093
D	510	HIS	-	expression tag	UNP P05093
D	511	HIS	-	expression tag	UNP P05093
D	512	HIS	-	expression tag	UNP P05093

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Fe	H	N	O		
2	A	1	73	34	1	30	4	4	0	0
			Total	C	Fe	H	N	O		
2	B	1	73	34	1	30	4	4	0	0
			Total	C	Fe	H	N	O		
2	C	1	73	34	1	30	4	4	0	0

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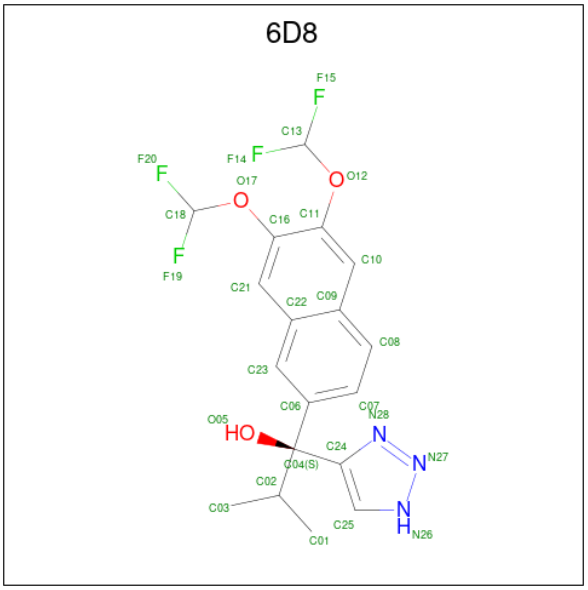
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Fe	H	N	O		
2	D	1	73	34	1	30	4	4	0	0

- Molecule 3 is VT-464 (three-letter code: 6D8) (formula: $C_{18}H_{17}F_4N_3O_3$).



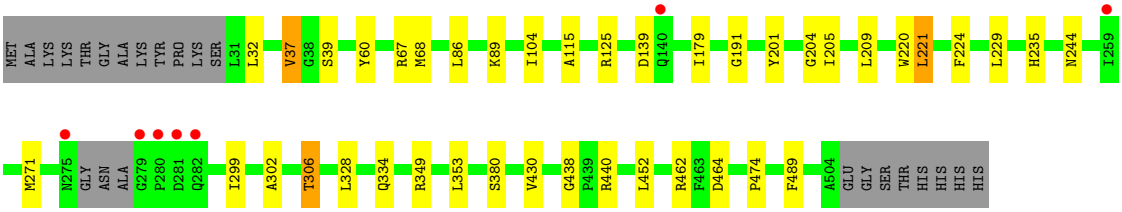
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	F	H	N	O		
3	A	1	45	18	4	17	3	3	0	0
			Total	C	F	H	N	O		
3	B	1	45	18	4	17	3	3	0	0
			Total	C	F	H	N	O		
3	C	1	45	18	4	17	3	3	0	0
			Total	C	F	H	N	O		
3	D	1	45	18	4	17	3	3	0	0

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.

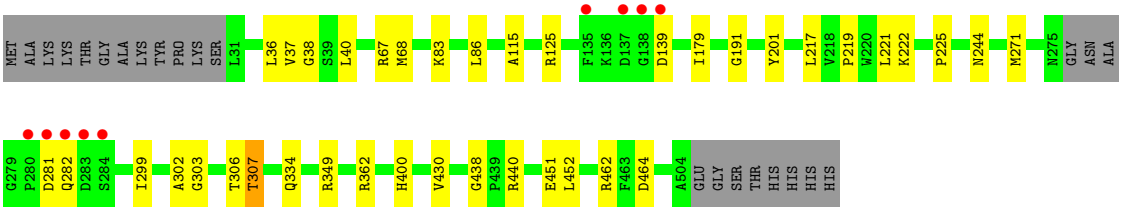
• Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase

Chain A:



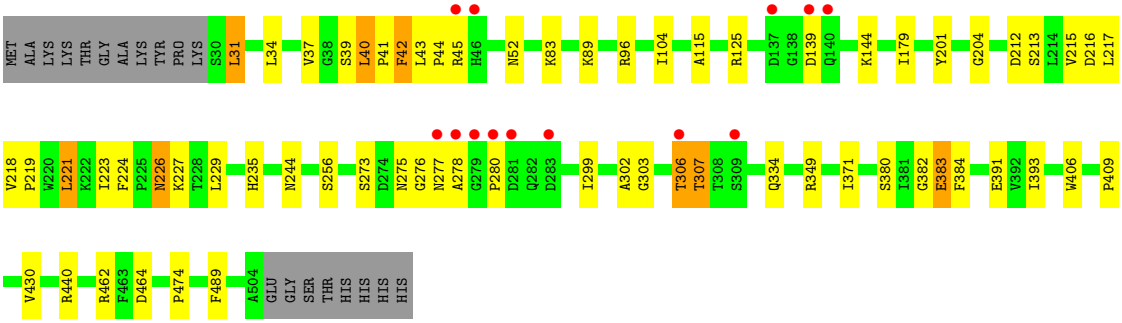
• Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase

Chain B:



• Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase

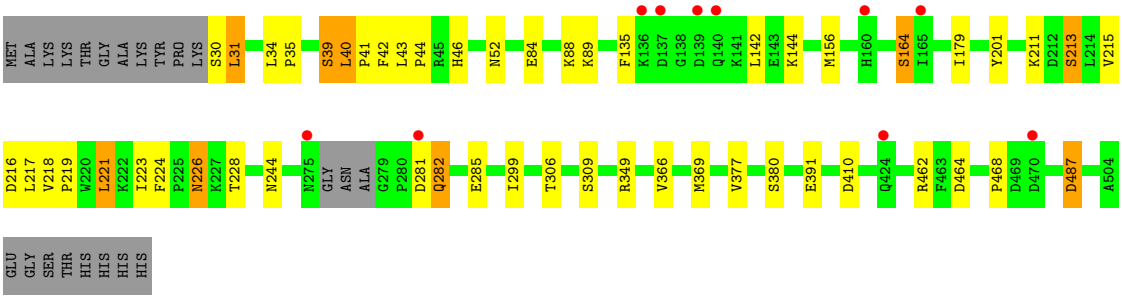
Chain C:



• Molecule 1: Steroid 17-alpha-hydroxylase/17,20 lyase

Chain D:

2%
85%
9%


MET ALA LYS LYS THR GLY ALA LYS TYR PRO LYS S30 L31 L34 P35 S39 L40 P41 F42 L43 P44 R45 H46 N52 E84 K88 K89 F135 K136 D137 G138 D139 Q140 K141 L142 E143 K144 M156 H160 S164 I165 I179 Y201 K211 D212 S213 L214 V215
D216 L217 V218 P219 W220 L221 K222 I223 F224 P225 N226 K227 T228 N244 N275 GLY ASN ALA G279 P280 D281 Q282 E285 I299 T306 S309 R349 V366 M369 V377 S380 E391 D410 Q424 R462 F463 D464 P468 D469 D470 D487 A504
GLU GLY SER THR HIS HIS HIS HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	90.95Å 153.50Å 169.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.44 – 3.10 39.44 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (39.44-3.10) 88.1 (39.44-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 3.12Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.195 , 0.248 0.197 , 0.249	Depositor DCC
R_{free} test set	2163 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	57.7	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 37.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	30314	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 6D8, HEM

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	0.27	0/3830	0.49	1/5186 (0.0%)
1	B	0.27	0/3830	0.49	0/5186
1	C	0.27	0/3854	0.50	0/5220
1	D	0.27	0/3836	0.50	0/5194
All	All	0.27	0/15350	0.50	1/20786 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	221	LEU	CA-CB-CG	5.46	127.85	115.30

There are no chirality outliers.

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	3749	3827	3812	22	0
1	B	3749	3827	3812	24	0
1	C	3772	3564	3832	42	0
1	D	3755	3599	3817	34	0
2	A	43	30	30	4	0
2	B	43	30	30	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	43	30	30	3	0
2	D	43	30	30	1	0
3	A	28	17	0	2	0
3	B	28	17	0	1	0
3	C	28	17	0	0	0
3	D	28	17	0	0	0
All	All	15309	15005	15393	107	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 3.

The worst 5 of 107 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:302:ALA:O	1:A:306:THR:OG1	1.95	0.84
1:B:303:GLY:O	1:B:307:THR:OG1	1.99	0.80
1:C:221:LEU:H	1:C:221:LEU:HD12	1.50	0.75
1:A:37:VAL:O	1:C:41:PRO:HD3	1.90	0.72
1:C:303:GLY:O	1:C:307:THR:OG1	2.08	0.70

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	467/494 (94%)	441 (94%)	25 (5%)	1 (0%)	47 79
1	B	467/494 (94%)	441 (94%)	26 (6%)	0	100 100
1	C	473/494 (96%)	450 (95%)	21 (4%)	2 (0%)	34 69
1	D	468/494 (95%)	443 (95%)	23 (5%)	2 (0%)	34 69
All	All	1875/1976 (95%)	1775 (95%)	95 (5%)	5 (0%)	41 73

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	42	PHE
1	C	383	GLU
1	C	42	PHE
1	D	226	ASN
1	A	32	LEU

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	419/436 (96%)	405 (97%)	14 (3%)	38	69
1	B	419/436 (96%)	407 (97%)	12 (3%)	42	72
1	C	421/436 (97%)	400 (95%)	21 (5%)	24	57
1	D	420/436 (96%)	400 (95%)	20 (5%)	25	58
All	All	1679/1744 (96%)	1612 (96%)	67 (4%)	31	65

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	221	LEU
1	D	281	ASP
1	D	464	ASP
1	B	462	ARG
1	B	349	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	52	ASN
1	D	78	HIS
1	C	46	HIS
1	C	52	ASN
1	C	78	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	6D8	D	601	2	28,30,30	1.68	6 (21%)	36,44,44	1.17	4 (11%)
3	6D8	C	601	2	28,30,30	1.64	6 (21%)	36,44,44	1.09	3 (8%)
2	HEM	D	600	3	41,50,50	1.51	4 (9%)	45,82,82	1.54	12 (26%)
2	HEM	C	600	3	41,50,50	1.49	3 (7%)	45,82,82	1.48	7 (15%)
3	6D8	B	601	2	28,30,30	1.60	5 (17%)	36,44,44	1.11	4 (11%)
3	6D8	A	601	2	28,30,30	1.68	5 (17%)	36,44,44	1.07	2 (5%)
2	HEM	A	600	3	41,50,50	1.54	4 (9%)	45,82,82	1.46	6 (13%)
2	HEM	B	600	3	41,50,50	1.49	4 (9%)	45,82,82	1.42	5 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	6D8	D	601	2	-	1/20/26/26	0/3/3/3
3	6D8	C	601	2	-	3/20/26/26	0/3/3/3
2	HEM	D	600	3	-	1/12/54/54	-
2	HEM	C	600	3	-	2/12/54/54	-
3	6D8	B	601	2	-	4/20/26/26	0/3/3/3
3	6D8	A	601	2	-	3/20/26/26	0/3/3/3
2	HEM	A	600	3	-	2/12/54/54	-
2	HEM	B	600	3	-	2/12/54/54	-

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	HEM	C3C-C2C	-5.49	1.32	1.40
2	D	600	HEM	C3C-C2C	-5.17	1.33	1.40
2	C	600	HEM	C3C-C2C	-4.96	1.33	1.40
2	B	600	HEM	C3C-C2C	-4.82	1.33	1.40
3	D	601	6D8	O12-C11	4.28	1.44	1.37

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	600	HEM	C4B-CHC-C1C	3.53	127.21	122.56
2	D	600	HEM	C4D-ND-C1D	3.45	108.63	105.07
2	A	600	HEM	C4D-ND-C1D	3.33	108.51	105.07
2	C	600	HEM	C4B-CHC-C1C	3.12	126.68	122.56
2	C	600	HEM	C4D-ND-C1D	3.01	108.19	105.07

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	6D8	F20-C18-O17-C16
3	A	601	6D8	F19-C18-O17-C16
3	B	601	6D8	F20-C18-O17-C16
3	C	601	6D8	F14-C13-O12-C11
3	C	601	6D8	F20-C18-O17-C16

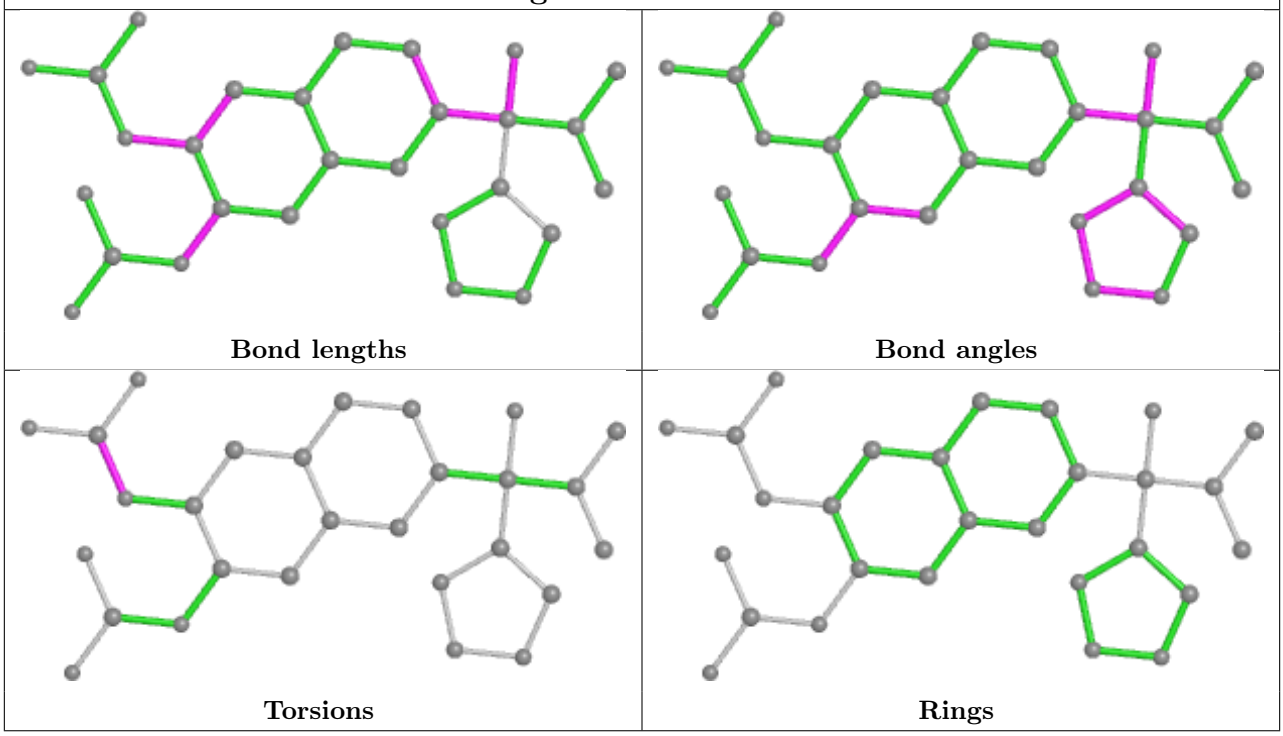
There are no ring outliers.

6 monomers are involved in 15 short contacts:

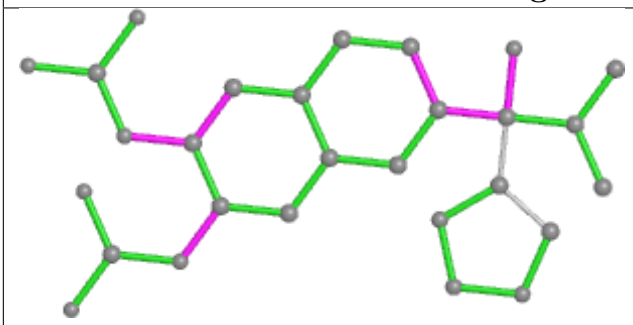
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	600	HEM	1	0
2	C	600	HEM	3	0
3	B	601	6D8	1	0
3	A	601	6D8	2	0
2	A	600	HEM	4	0
2	B	600	HEM	4	0

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.

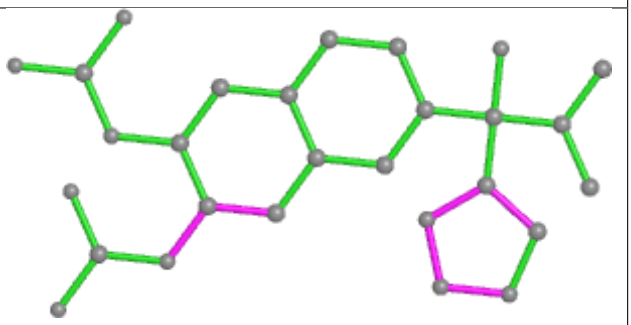
Ligand 6D8 D 601



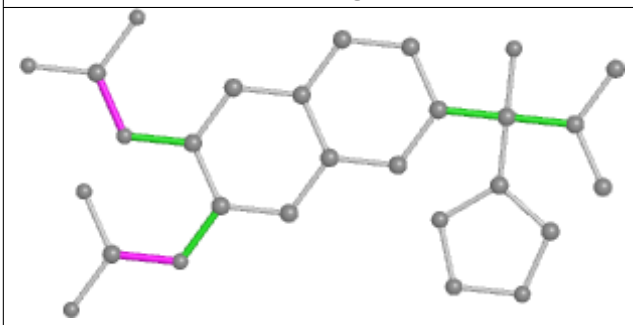
Ligand 6D8 C 601



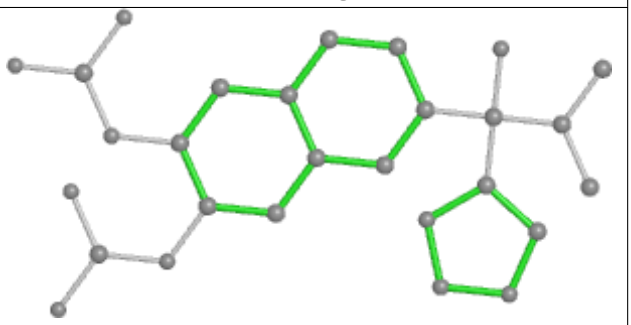
Bond lengths



Bond angles

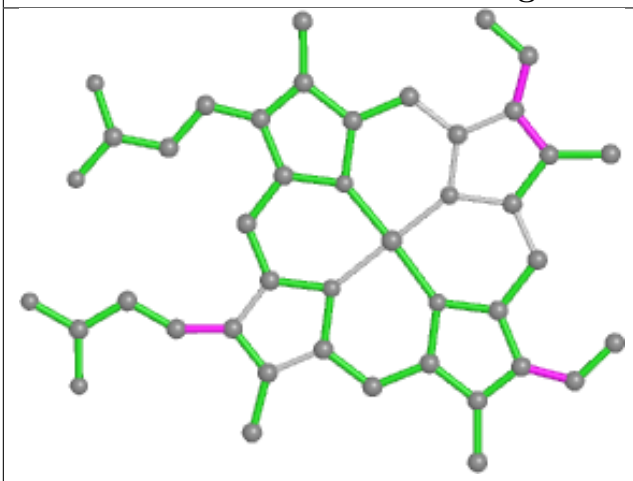


Torsions



Rings

Ligand HEM D 600



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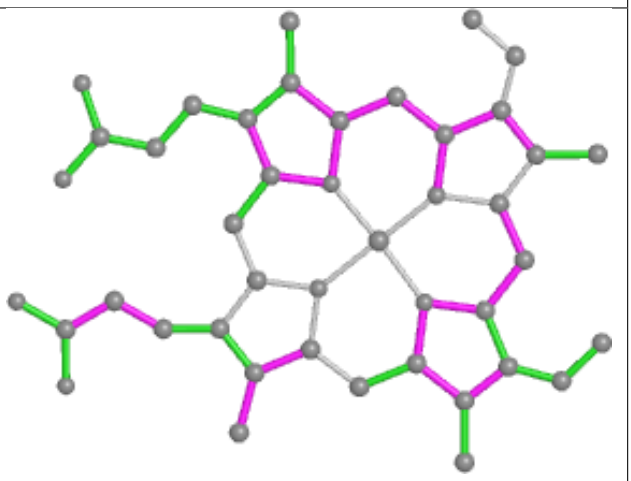

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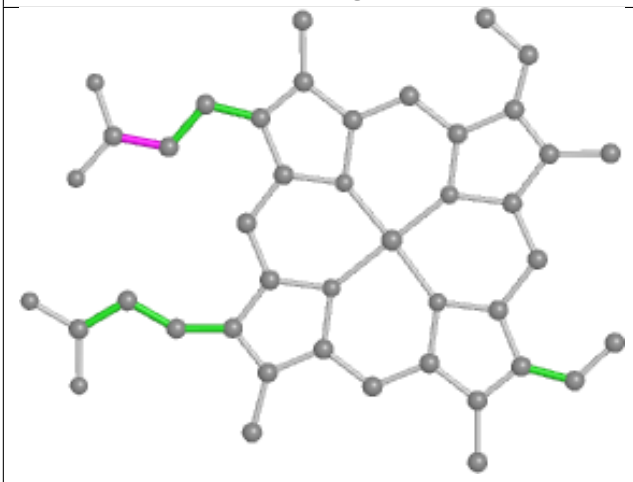

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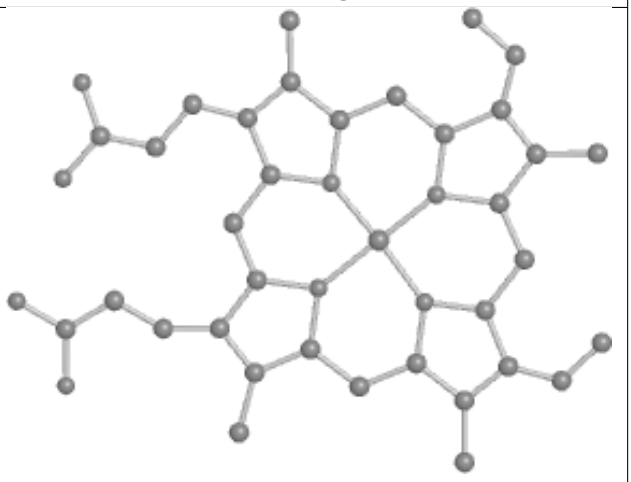
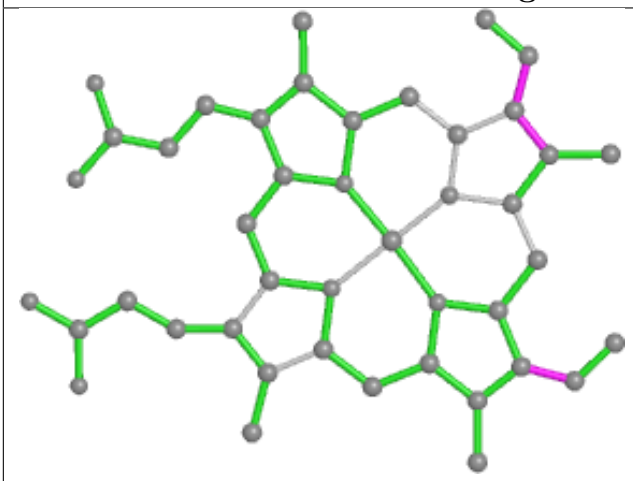
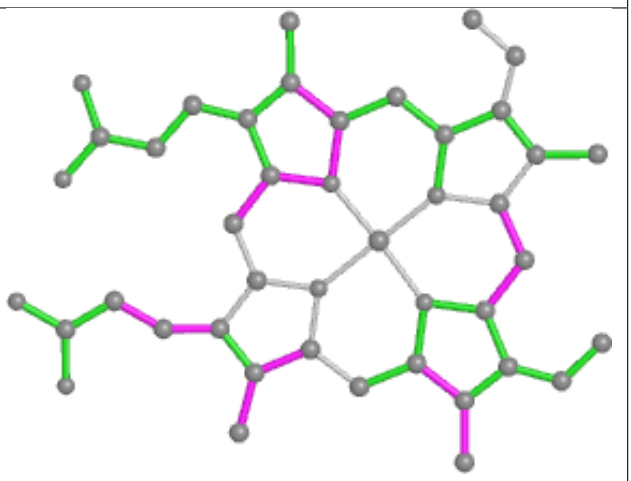


Rings

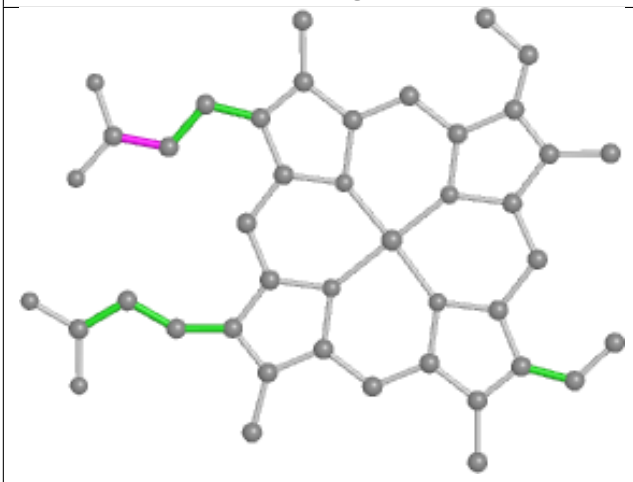
Ligand HEM C 600



Bond lengths



Bond angles



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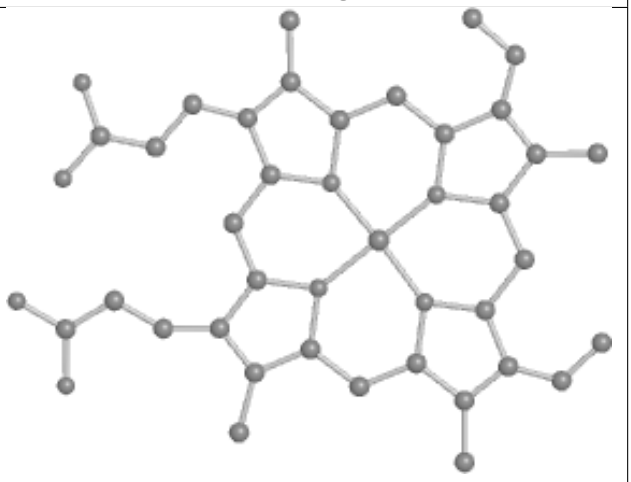
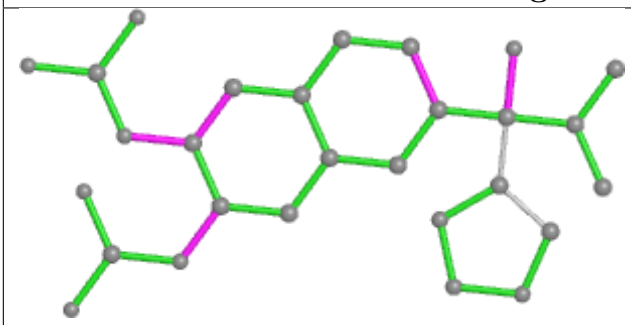
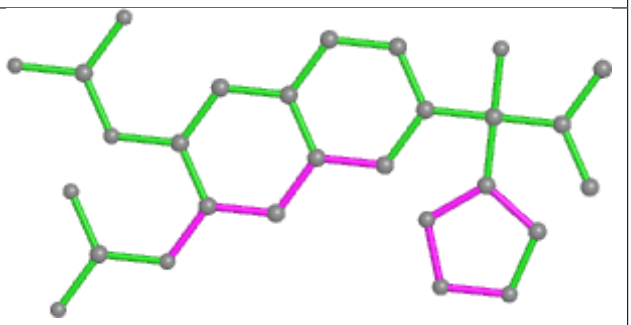


Rings

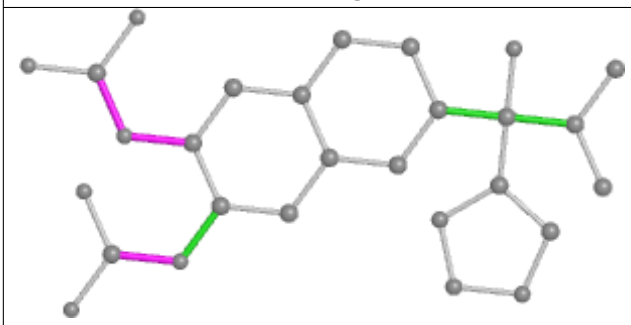
Ligand 6D8 B 601



Bond lengths



Bond angles



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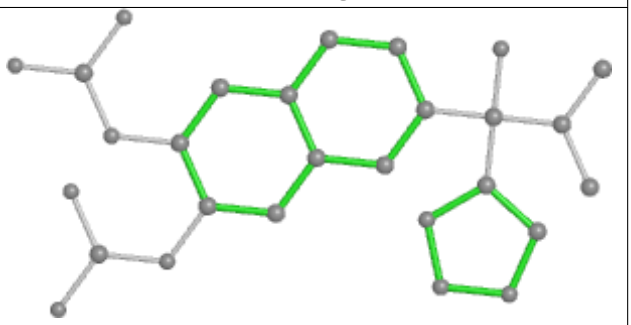
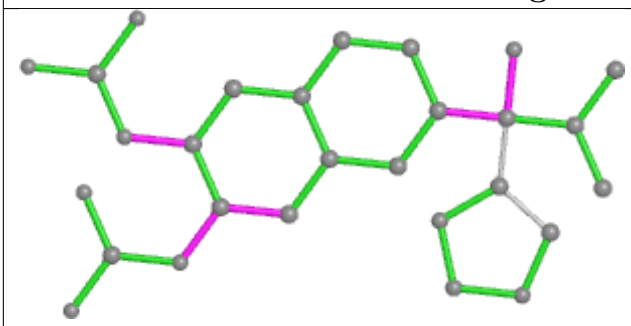


Rings

Ligand 6D8 A 601



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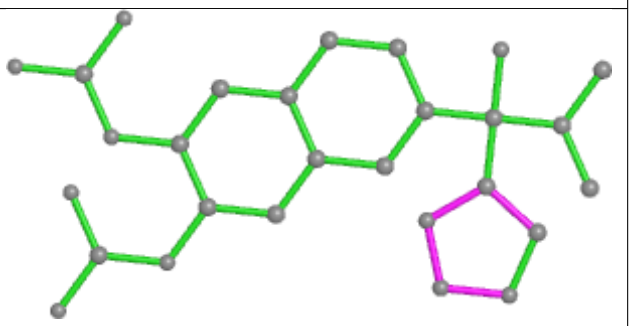
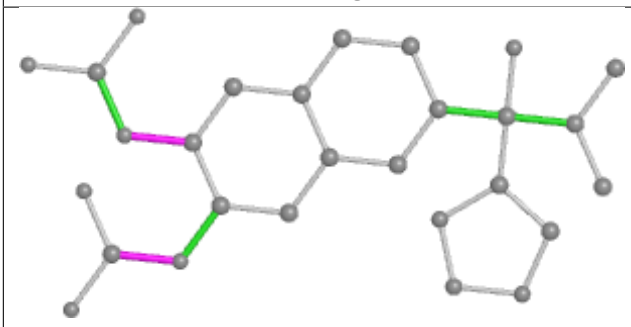


Bond angles



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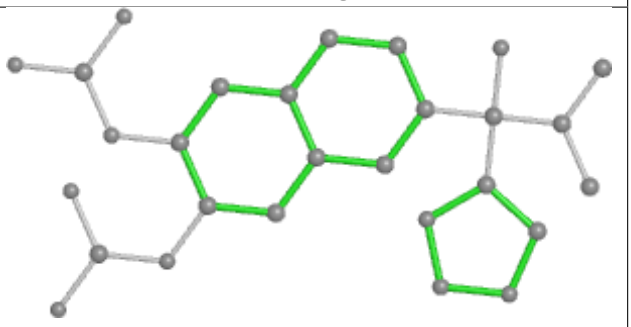
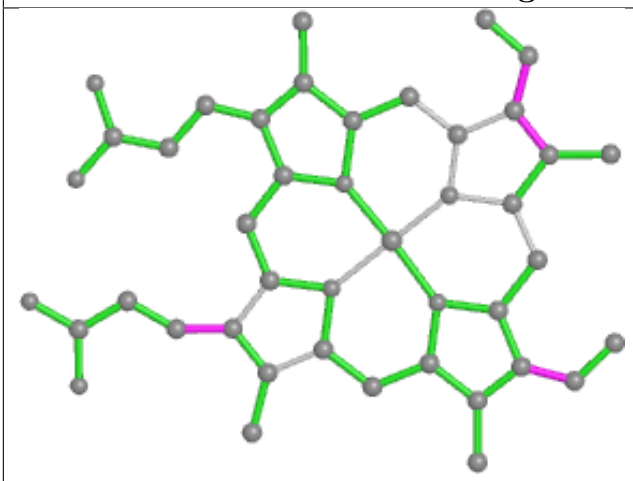


Rings

Ligand HEM A 600



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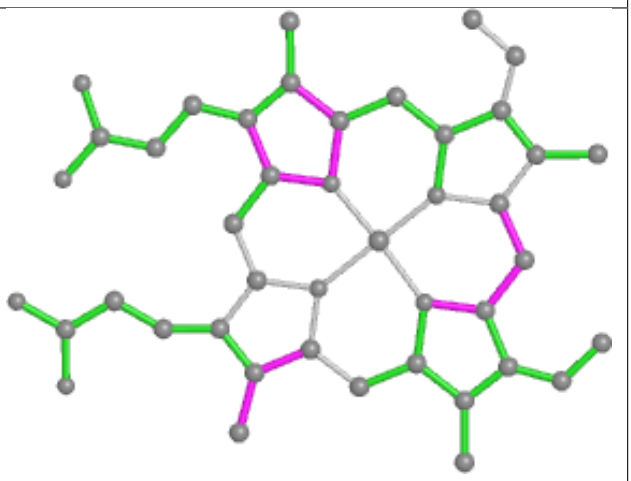
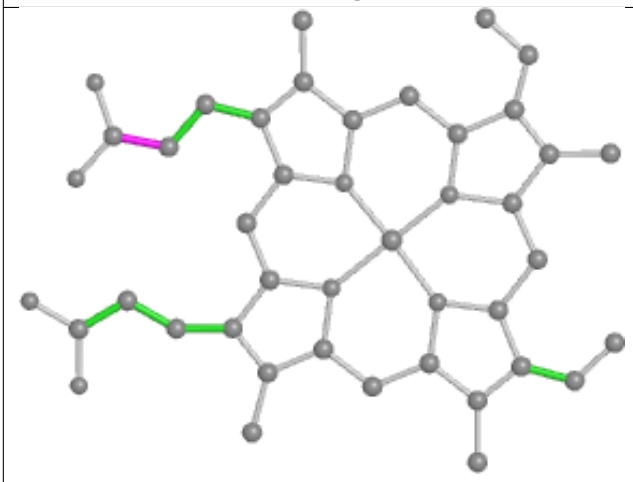


Bond angles



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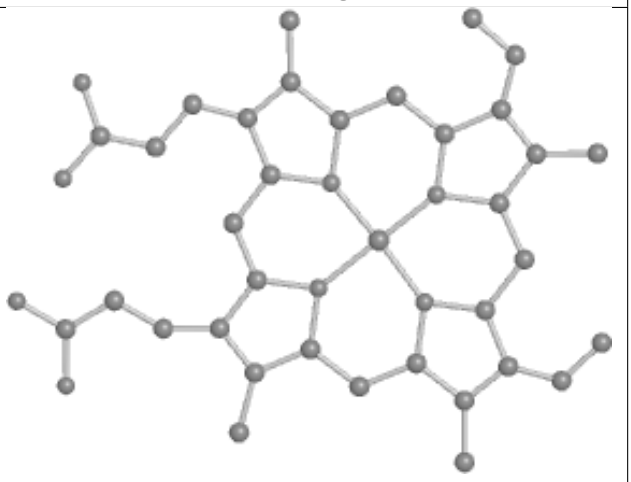
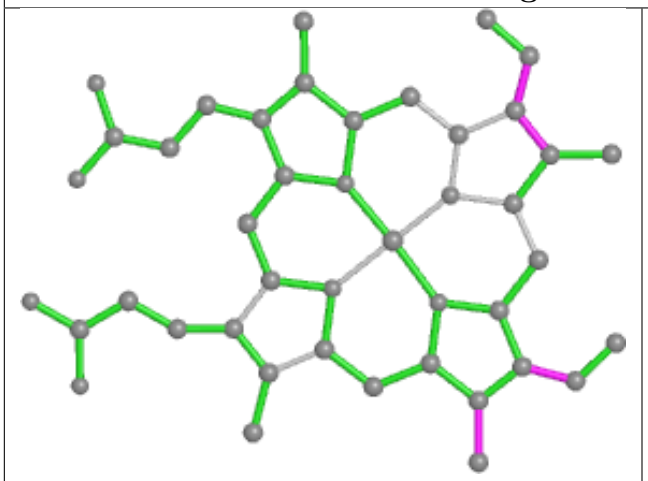


Rings

Ligand HEM B 600



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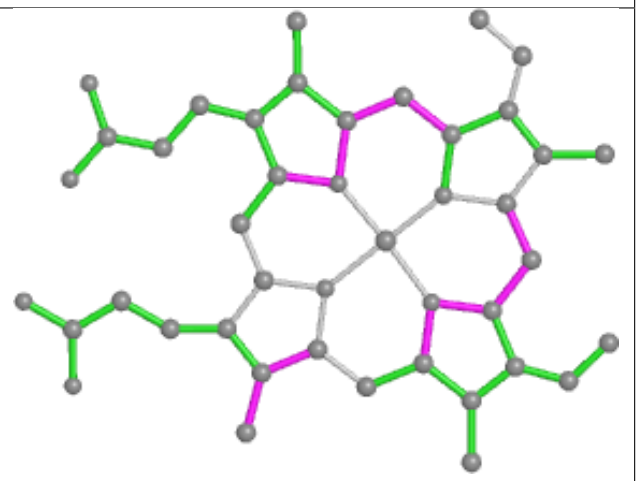
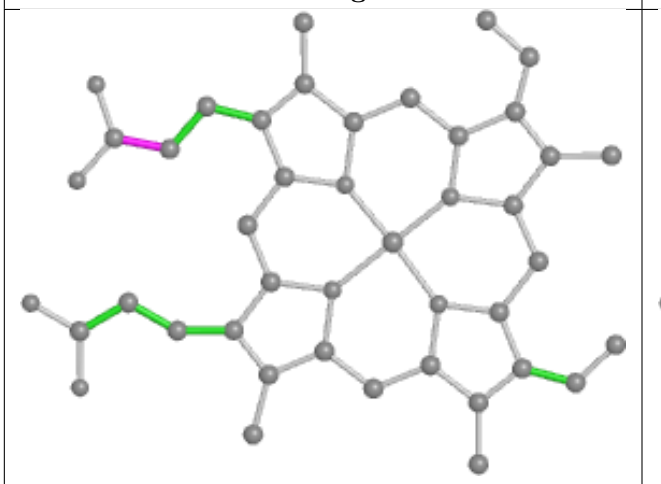
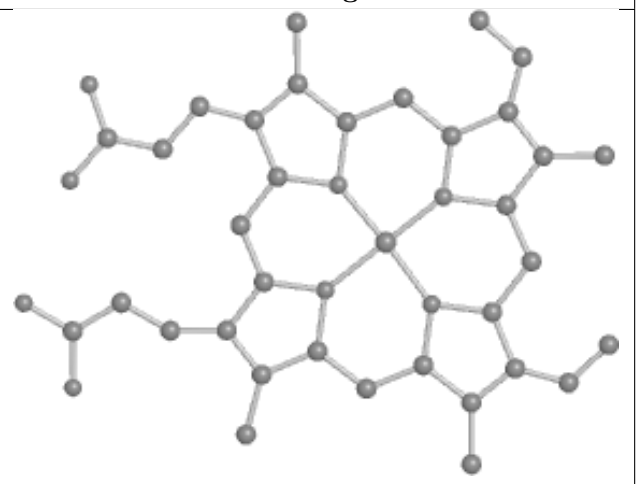


Bond angles



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	471/494 (95%)	-0.02	7 (1%)	73	54	31, 58, 92, 131	0
1	B	471/494 (95%)	0.01	9 (1%)	66	46	31, 60, 93, 129	0
1	C	475/494 (96%)	0.08	13 (2%)	54	31	31, 58, 85, 126	0
1	D	472/494 (95%)	0.06	10 (2%)	63	43	36, 63, 93, 124	0
All	All	1889/1976 (95%)	0.03	39 (2%)	63	43	31, 59, 91, 131	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	139	ASP	5.4
1	C	277	ASN	5.0
1	B	139	ASP	4.5
1	A	279	GLY	4.3
1	B	280	PRO	4.1

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)

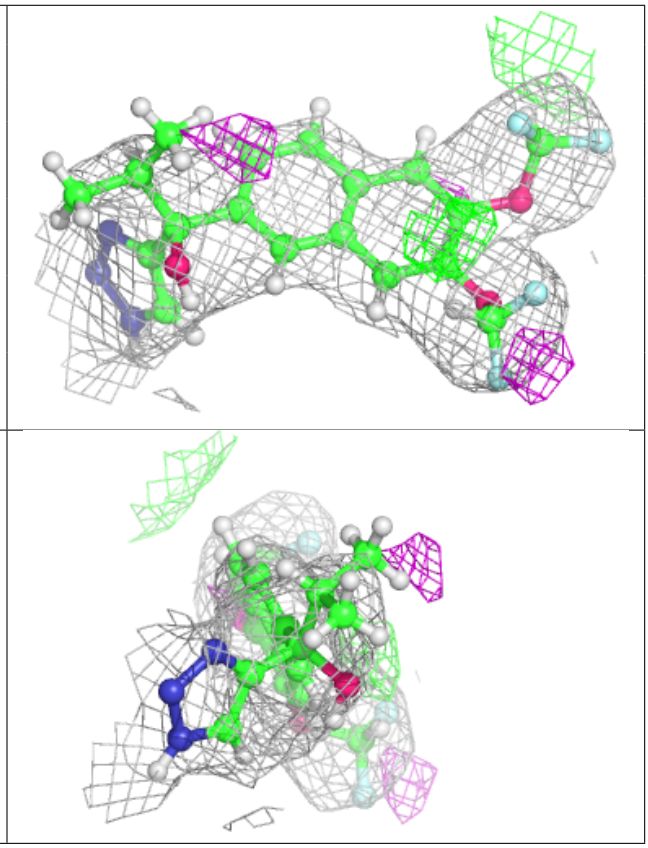
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	6D8	B	601	28/28	0.92	0.30	32,50,59,67	0
3	6D8	D	601	28/28	0.92	0.29	33,44,58,69	0
3	6D8	C	601	28/28	0.93	0.30	28,40,58,61	0
3	6D8	A	601	28/28	0.95	0.28	34,45,57,60	0
2	HEM	C	600	43/43	0.96	0.33	28,53,68,80	0
2	HEM	D	600	43/43	0.96	0.34	40,58,73,76	0
2	HEM	A	600	43/43	0.97	0.30	35,49,67,72	0
2	HEM	B	600	43/43	0.97	0.33	33,51,65,68	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.

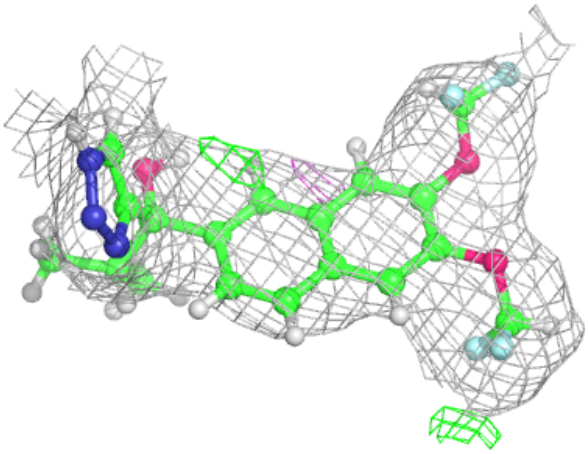
Electron density around 6D8 B 601:

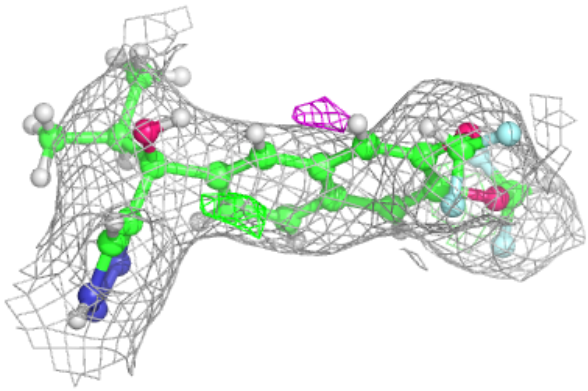
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

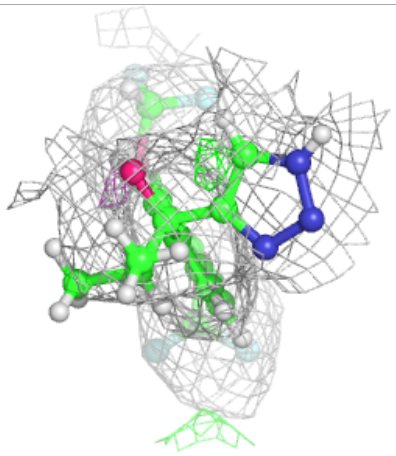


Electron density around 6D8 D 601:

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

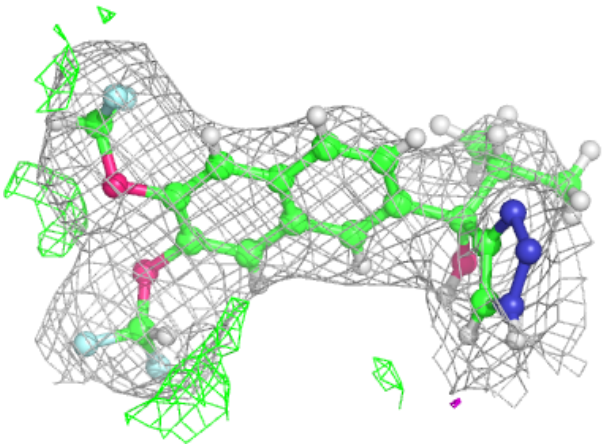


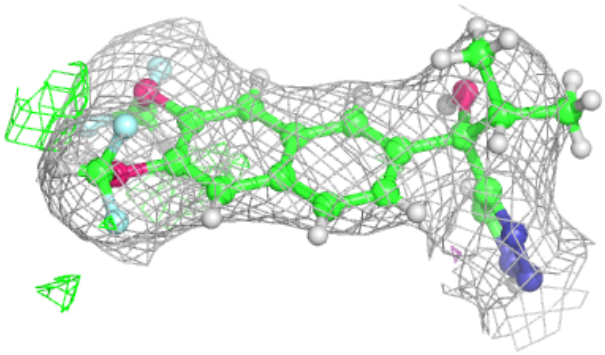


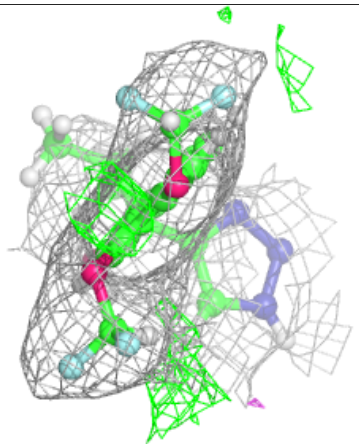


Electron density around 6D8 C 601:

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

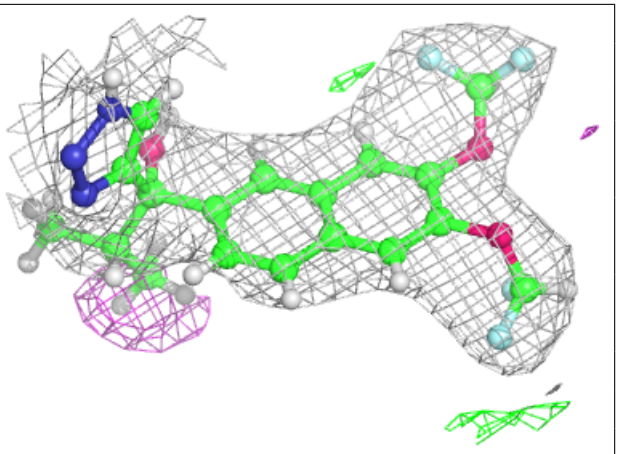


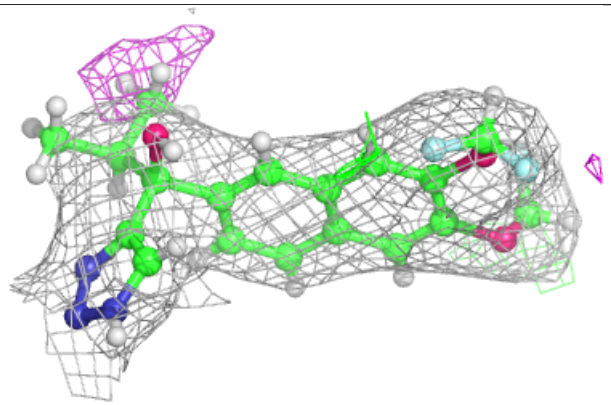


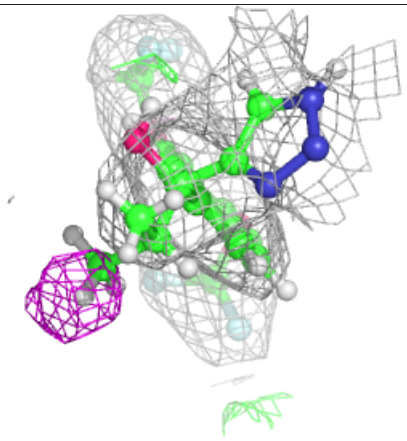


Electron density around 6D8 A 601:

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

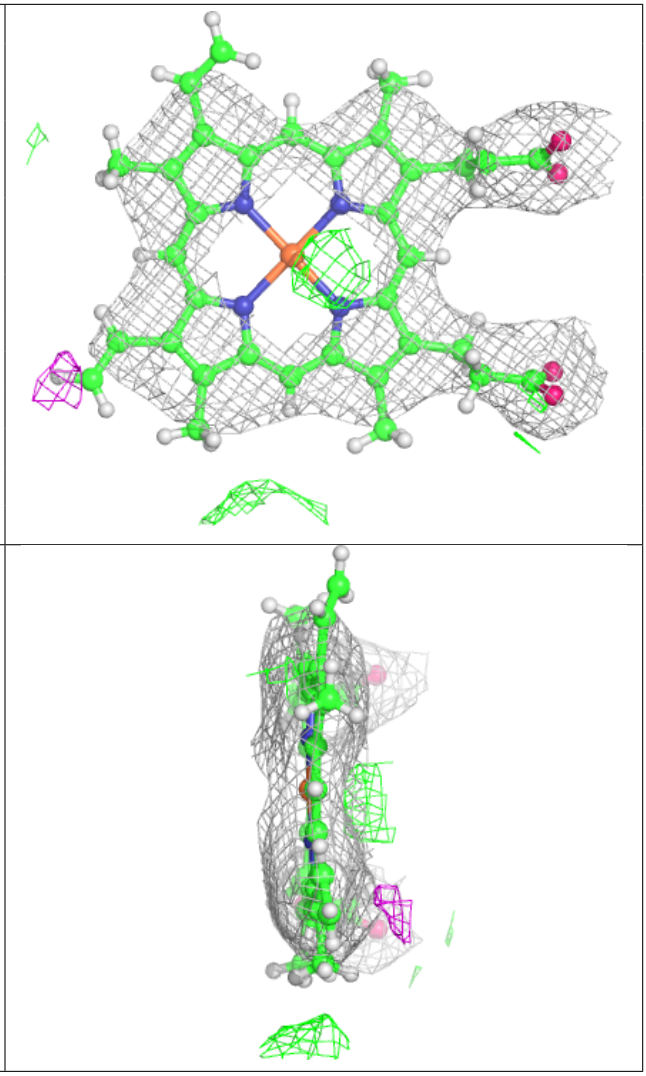






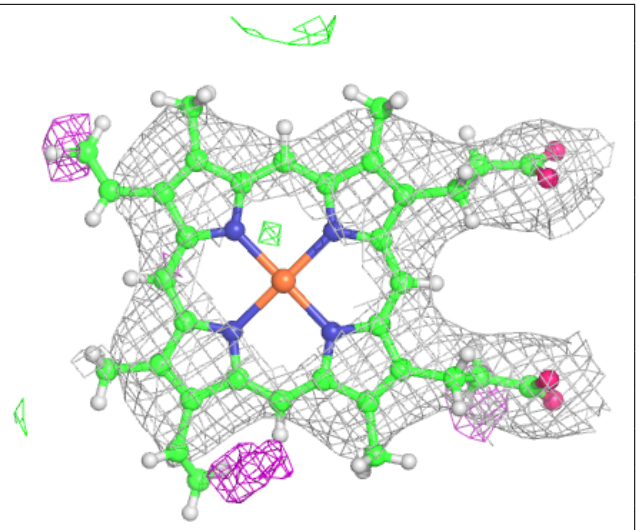
Electron density around HEM C 600:

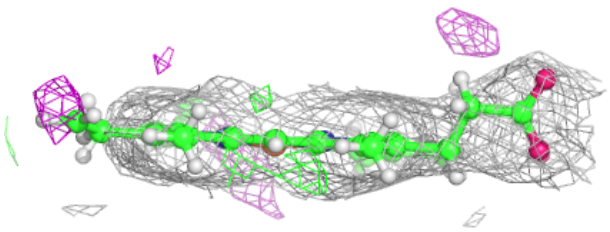
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

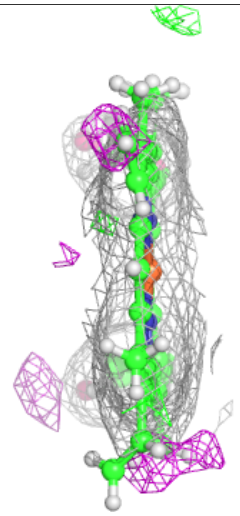


Electron density around HEM D 600:

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

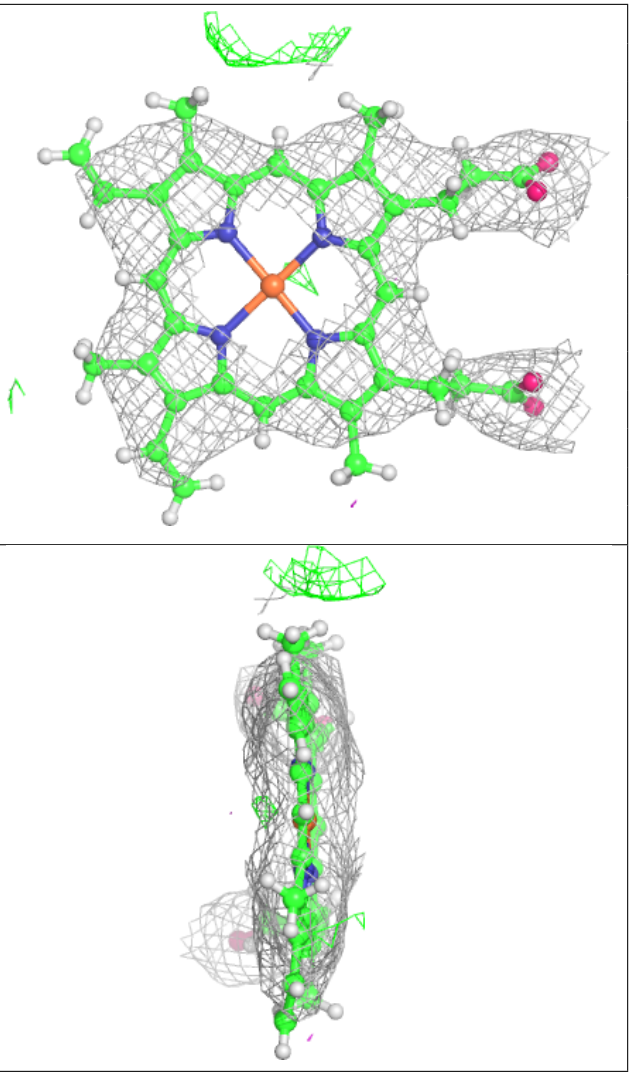


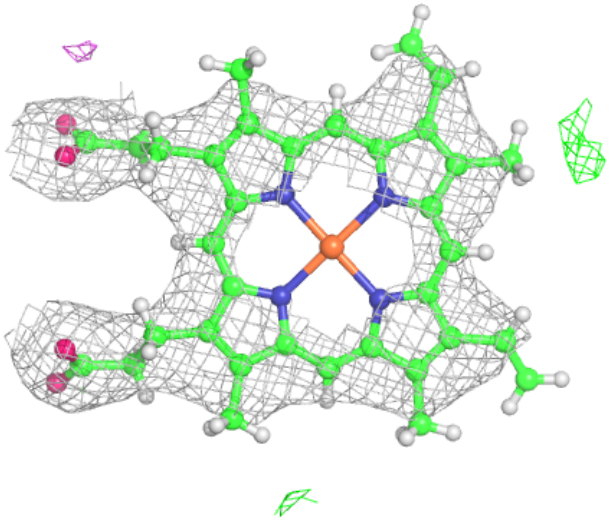
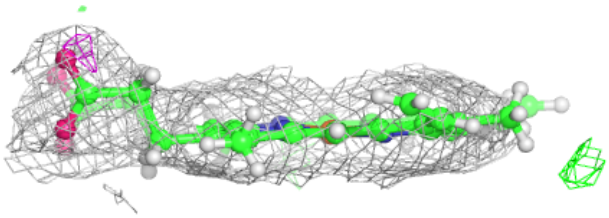
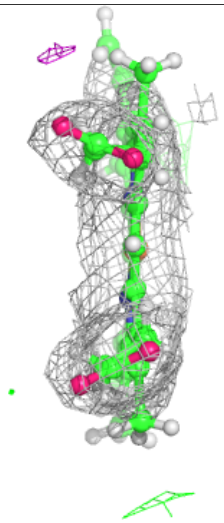




Electron density around HEM A 600:

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



Electron density around HEM B 600: 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.