wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 05:16 AM EDT

PDB ID	:	6NLM
Title	:	1.90 A resolution structure of WT BfrB from Pseudomonas aeruginosa in complex with a protein-protein interaction inhibitor (analog 15)
Authors	:	Lovell, S.; Punchi-Hewage, A.; Battaile, K.P.; Yao, H.; Nammalwar, B.; Gnanasekaran, K.K.; Bunce, R.A.; Reitz, A.B.; Rivera, M.
Deposited on	:	2019-01-08
Resolution	:	1.90 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:

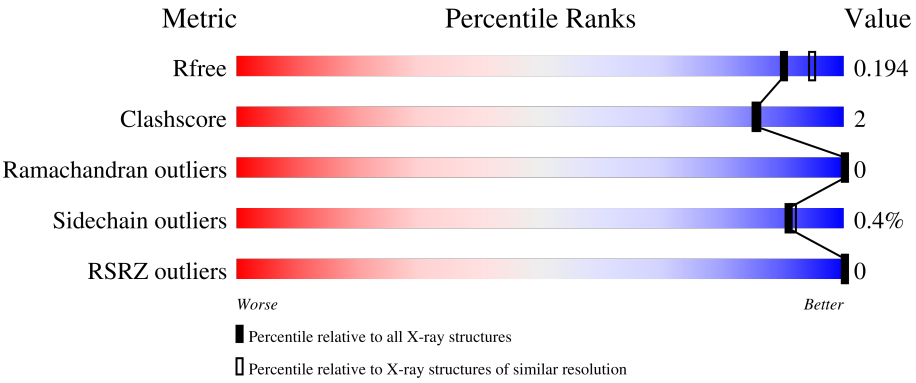
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	158	95%
1	B	158	95%
1	C	158	95%
1	D	158	96%

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Mol	Chain	Length	Quality of chain
1	E	158	97%
1	F	158	94%
1	G	158	97%
1	H	158	96%
1	I	158	94%
1	J	158	92% 6%
1	K	158	92% 6%
1	L	158	96%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 17216 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 Ferroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	1	0
			1263	803	213	240	7			
1	B	155	Total	C	N	O	S	0	1	0
			1261	800	216	238	7			
1	C	155	Total	C	N	O	S	0	1	0
			1260	800	213	240	7			
1	D	155	Total	C	N	O	S	0	1	0
			1269	804	218	240	7			
1	E	156	Total	C	N	O	S	0	2	0
			1271	807	214	243	7			
1	F	155	Total	C	N	O	S	0	1	0
			1258	798	215	238	7			
1	G	155	Total	C	N	O	S	0	1	0
			1255	797	212	239	7			
1	H	155	Total	C	N	O	S	0	1	0
			1256	797	215	237	7			
1	I	155	Total	C	N	O	S	0	1	0
			1257	798	212	240	7			
1	J	155	Total	C	N	O	S	0	1	0
			1259	797	215	240	7			
1	K	155	Total	C	N	O	S	0	1	0
			1256	798	212	239	7			
1	L	156	Total	C	N	O	S	0	1	0
			1265	802	216	240	7			

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		

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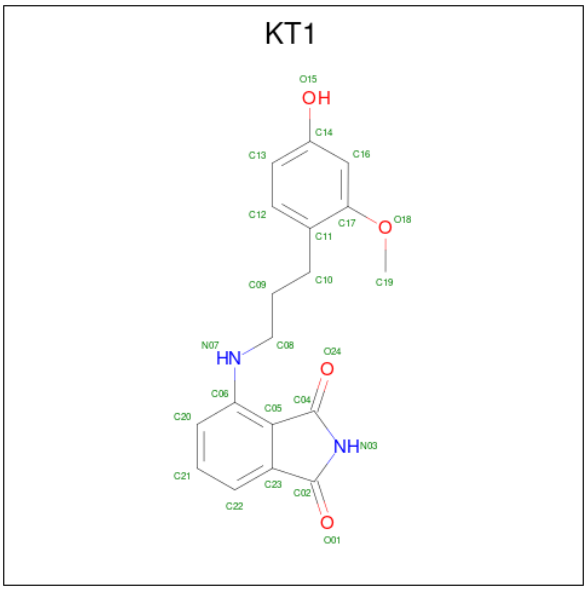
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Fe 1 1	0	0

- Molecule 3 is 4-{[3-(4-hydroxy-2-methoxyphenyl)propyl]amino}-1H-isoindole-1,3(2H)-dione (three-letter code: KT1) (formula: $C_{18}H_{18}N_2O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 24 18 2 4	0	0
3	B	1	Total C N O 24 18 2 4	0	0
3	C	1	Total C N O 24 18 2 4	0	0
3	D	1	Total C N O 24 18 2 4	0	0
3	E	1	Total C N O 24 18 2 4	0	0
3	F	1	Total C N O 24 18 2 4	0	0
3	G	1	Total C N O 24 18 2 4	0	0
3	H	1	Total C N O 24 18 2 4	0	0
3	I	1	Total C N O 24 18 2 4	0	0
3	J	1	Total C N O 24 18 2 4	0	0

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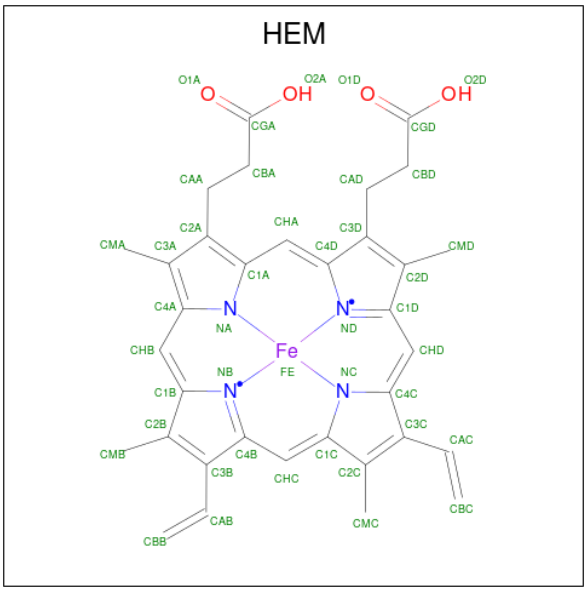
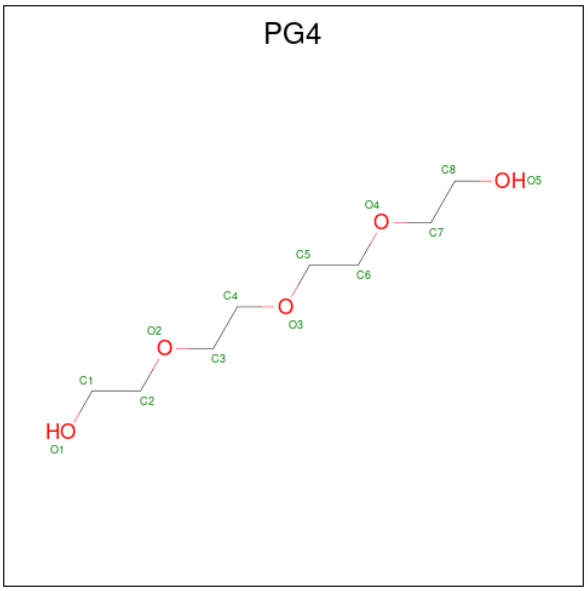
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	K	1	Total	C	N	O	0	0
			24	18	2	4		
3	L	1	Total	C	N	O	0	0
			24	18	2	4		

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	H	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	L	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 10 6 4	0	0
5	B	1	Total C O 8 5 3	0	0
5	B	1	Total C O 6 4 2	0	0
5	B	1	Total C O 9 6 3	0	0
5	C	1	Total C O 11 7 4	0	0
5	D	1	Total C O 10 6 4	0	0
5	D	1	Total C O 8 5 3	0	0
5	E	1	Total C O 10 6 4	0	0
5	E	1	Total C O 8 5 3	0	0
5	F	1	Total C O 10 6 4	0	0
5	G	1	Total C O 10 6 4	0	0
5	H	1	Total C O 8 5 3	0	0
5	H	1	Total C O 9 6 3	0	0
5	I	1	Total C O 8 5 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	J	1	Total C O 13 8 5	0	0
5	J	1	Total C O 13 8 5	0	0
5	K	1	Total C O 11 7 4	0	0

- Molecule 6 is water.

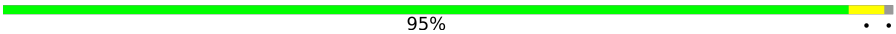
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	112	Total O 112 112	0	0
6	B	117	Total O 117 117	0	0
6	C	100	Total O 100 100	0	0
6	D	108	Total O 108 108	0	0
6	E	114	Total O 114 114	0	0
6	F	104	Total O 104 104	0	0
6	G	113	Total O 113 113	0	0
6	H	121	Total O 121 121	0	0
6	I	104	Total O 104 104	0	0
6	J	122	Total O 122 122	0	0
6	K	111	Total O 111 111	0	0
6	L	106	Total O 106 106	0	0

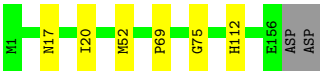
3 Residue-property plots (i)

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: Ferroxidase

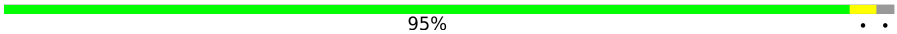
Chain A:

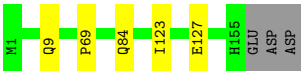




- Molecule 1: Ferroxidase

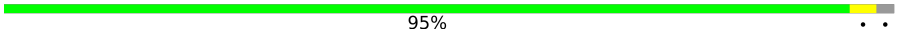
Chain B:





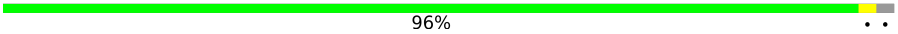
- Molecule 1: Ferroxidase

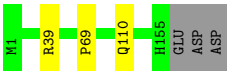
Chain C:



- Molecule 1: Ferroxidase

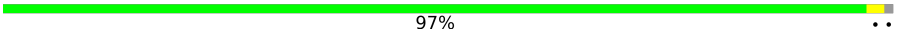
Chain D:





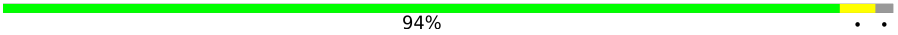
- Molecule 1: Ferroxidase

Chain E:



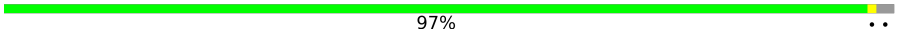
- Molecule 1: Ferroxidase

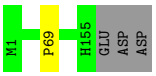
Chain F:



• Molecule 1: Ferroxidase

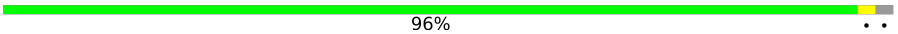
Chain G:

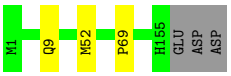




• Molecule 1: Ferroxidase

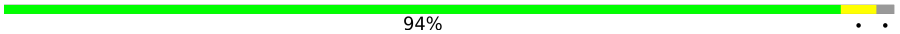
Chain H:

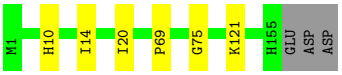




• Molecule 1: Ferroxidase

Chain I:



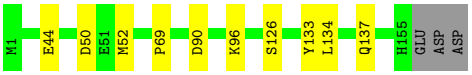


• Molecule 1: Ferroxidase

Chain J:

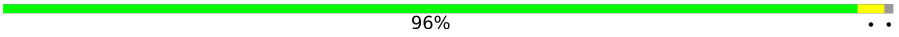
• Molecule 1: Ferroxidase

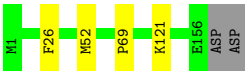
Chain K:



• Molecule 1: Ferroxidase

Chain L:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	130.25Å 194.97Å 203.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.93 – 1.90 48.74 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.93-1.90) 100.0 (48.74-1.90)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.12 (at 1.90Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.152 , 0.184 0.165 , 0.194	Depositor DCC
R_{free} test set	10145 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	18.4	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 54.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	17216	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KT1, FE2, PG4, 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	0.45	0/1286	0.55	0/1732
1	B	0.45	0/1285	0.55	0/1732
1	C	0.47	0/1284	0.56	0/1731
1	D	0.45	0/1293	0.55	0/1741
1	E	0.50	0/1298	0.55	0/1750
1	F	0.46	0/1282	0.55	0/1729
1	G	0.47	0/1279	0.55	0/1725
1	H	0.46	0/1280	0.55	0/1726
1	I	0.45	0/1281	0.54	0/1728
1	J	0.45	0/1283	0.53	0/1731
1	K	0.44	0/1280	0.54	0/1726
1	L	0.46	0/1289	0.53	0/1738
All	All	0.46	0/15420	0.55	0/20789

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	1263	0	1242	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1261	0	1236	4	0
1	C	1260	0	1231	3	0
1	D	1269	0	1254	3	0
1	E	1271	0	1239	3	0
1	F	1258	0	1227	4	0
1	G	1255	0	1223	1	0
1	H	1256	0	1228	3	0
1	I	1257	0	1222	3	0
1	J	1259	0	1225	5	0
1	K	1256	0	1225	8	0
1	L	1265	0	1234	4	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	D	1	0	0	0	0
3	A	24	0	0	1	0
3	B	24	0	0	1	0
3	C	24	0	0	1	0
3	D	24	0	0	1	0
3	E	24	0	0	1	0
3	F	24	0	0	1	0
3	G	24	0	0	1	0
3	H	24	0	0	1	0
3	I	24	0	0	1	0
3	J	24	0	0	1	0
3	K	24	0	0	1	0
3	L	24	0	0	1	0
4	A	43	0	30	3	0
4	B	43	0	30	4	0
4	C	43	0	30	3	0
4	D	43	0	30	3	0
4	F	43	0	30	6	0
4	H	43	0	30	3	0
4	L	43	0	30	6	0
5	A	10	0	13	0	0
5	B	23	0	21	2	0
5	C	11	0	13	1	0
5	D	18	0	21	0	0
5	E	18	0	22	0	0
5	F	10	0	13	0	0
5	G	10	0	13	0	0
5	H	17	0	19	1	0
5	I	8	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	J	26	0	36	1	0
5	K	11	0	13	0	0
6	A	112	0	0	2	1
6	B	117	0	0	2	1
6	C	100	0	0	0	0
6	D	108	0	0	2	0
6	E	114	0	0	1	0
6	F	104	0	0	0	0
6	G	113	0	0	1	1
6	H	121	0	0	0	0
6	I	104	0	0	0	0
6	J	122	0	0	0	0
6	K	111	0	0	4	0
6	L	106	0	0	1	1
All	All	17216	0	15189	68	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 68 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)
4:F:202:HEM:HMC2	4:F:202:HEM:HBC2	1.63	0.79
4:H:202:HEM:HMC1	4:H:202:HEM:HBC2	1.68	0.75
4:D:203:HEM:HMC1	4:D:203:HEM:HBC2	1.69	0.73
4:C:202:HEM:HMC2	4:C:202:HEM:HBC2	1.70	0.73
4:L:202:HEM:O1D	6:L:301:HOH:O	2.08	0.71

All (2) 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)
6:B:362:HOH:O	6:L:391:HOH:O[3_554]	2.01	0.19
6:A:391:HOH:O	6:G:395:HOH:O[3_554]	2.16	0.04

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	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
1	B	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
1	C	154/158 (98%)	154 (100%)	0	0	100	100
1	D	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
1	E	156/158 (99%)	156 (100%)	0	0	100	100
1	F	154/158 (98%)	154 (100%)	0	0	100	100
1	G	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
1	H	154/158 (98%)	154 (100%)	0	0	100	100
1	I	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
1	J	154/158 (98%)	154 (100%)	0	0	100	100
1	K	154/158 (98%)	152 (99%)	2 (1%)	0	100	100
1	L	155/158 (98%)	155 (100%)	0	0	100	100
All	All	1852/1896 (98%)	1845 (100%)	7 (0%)	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	135/144 (94%)	135 (100%)	0	100	100
1	B	135/144 (94%)	135 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	135/144 (94%)	134 (99%)	1 (1%)	84 84
1	D	138/144 (96%)	138 (100%)	0	100 100
1	E	136/144 (94%)	136 (100%)	0	100 100
1	F	134/144 (93%)	133 (99%)	1 (1%)	84 84
1	G	134/144 (93%)	134 (100%)	0	100 100
1	H	134/144 (93%)	134 (100%)	0	100 100
1	I	134/144 (93%)	133 (99%)	1 (1%)	84 84
1	J	135/144 (94%)	133 (98%)	2 (2%)	65 62
1	K	134/144 (93%)	134 (100%)	0	100 100
1	L	135/144 (94%)	134 (99%)	1 (1%)	84 84
All	All	1619/1728 (94%)	1613 (100%)	6 (0%)	91 91

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	84	GLN
1	J	121	LYS
1	L	121	LYS
1	F	121	LYS
1	C	121	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 39 ligands modelled in this entry, 3 are monoatomic - leaving 36 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	KT1	B	202	-	26,26,26	1.85	6 (23%)	36,36,36	1.50	4 (11%)
4	HEM	A	203	1	41,50,50	1.49	7 (17%)	45,82,82	1.65	13 (28%)
5	PG4	B	205	-	5,5,12	0.61	0	4,4,11	0.32	0
5	PG4	G	202	-	9,9,12	0.60	0	8,8,11	0.37	0
5	PG4	C	203	-	10,10,12	0.48	0	9,9,11	0.29	0
3	KT1	I	201	-	26,26,26	1.78	5 (19%)	36,36,36	1.77	6 (16%)
4	HEM	C	202	1	41,50,50	1.46	5 (12%)	45,82,82	1.57	10 (22%)
4	HEM	D	203	1	41,50,50	1.46	4 (9%)	45,82,82	1.50	7 (15%)
5	PG4	J	202	-	12,12,12	0.42	0	11,11,11	0.38	0
5	PG4	K	202	-	10,10,12	0.56	0	9,9,11	0.29	0
3	KT1	J	201	-	26,26,26	1.84	6 (23%)	36,36,36	1.63	6 (16%)
5	PG4	H	204	-	8,8,12	0.52	0	7,7,11	0.36	0
5	PG4	E	202	-	9,9,12	0.52	0	8,8,11	0.23	0
5	PG4	F	203	-	9,9,12	0.55	0	8,8,11	0.23	0
5	PG4	D	204	-	9,9,12	0.49	0	8,8,11	0.28	0
5	PG4	A	204	-	9,9,12	0.52	0	8,8,11	0.20	0
5	PG4	E	203	-	7,7,12	0.50	0	6,6,11	0.25	0
5	PG4	I	202	-	7,7,12	0.55	0	6,6,11	0.21	0
4	HEM	F	202	1	41,50,50	1.44	4 (9%)	45,82,82	1.60	9 (20%)
3	KT1	L	201	-	26,26,26	1.75	5 (19%)	36,36,36	1.27	5 (13%)
5	PG4	B	204	-	7,7,12	0.53	0	6,6,11	0.21	0
5	PG4	B	206	-	8,8,12	0.49	0	7,7,11	0.45	0
3	KT1	K	201	-	26,26,26	1.77	6 (23%)	36,36,36	1.36	2 (5%)
5	PG4	H	203	-	7,7,12	0.49	0	6,6,11	0.31	0
4	HEM	H	202	1	41,50,50	1.52	5 (12%)	45,82,82	1.72	12 (26%)
3	KT1	C	201	-	26,26,26	1.73	6 (23%)	36,36,36	1.40	4 (11%)
3	KT1	D	202	-	26,26,26	1.74	6 (23%)	36,36,36	1.35	4 (11%)
3	KT1	A	202	-	26,26,26	1.85	6 (23%)	36,36,36	1.59	5 (13%)
4	HEM	B	203	1	41,50,50	1.41	4 (9%)	45,82,82	1.59	12 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	KT1	G	201	-	26,26,26	1.84	6 (23%)	36,36,36	1.31	4 (11%)
3	KT1	F	201	-	26,26,26	1.90	6 (23%)	36,36,36	1.41	4 (11%)
3	KT1	E	201	-	26,26,26	1.81	5 (19%)	36,36,36	1.32	3 (8%)
5	PG4	D	205	-	7,7,12	0.41	0	6,6,11	0.39	0
5	PG4	J	203	-	12,12,12	0.43	0	11,11,11	0.57	0
4	HEM	L	202	1	41,50,50	1.48	5 (12%)	45,82,82	1.49	7 (15%)
3	KT1	H	201	-	26,26,26	1.83	6 (23%)	36,36,36	1.47	5 (13%)

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	KT1	B	202	-	-	3/9/21/21	0/3/3/3
4	HEM	A	203	1	-	4/12/54/54	-
5	PG4	B	205	-	-	2/3/3/10	-
5	PG4	G	202	-	-	0/7/7/10	-
5	PG4	C	203	-	-	1/8/8/10	-
3	KT1	I	201	-	-	4/9/21/21	0/3/3/3
4	HEM	C	202	1	-	4/12/54/54	-
4	HEM	D	203	1	-	6/12/54/54	-
5	PG4	J	202	-	-	1/10/10/10	-
5	PG4	K	202	-	-	1/8/8/10	-
3	KT1	J	201	-	-	2/9/21/21	0/3/3/3
5	PG4	H	204	-	-	0/6/6/10	-
5	PG4	E	202	-	-	0/7/7/10	-
5	PG4	F	203	-	-	0/7/7/10	-
5	PG4	D	204	-	-	0/7/7/10	-
5	PG4	A	204	-	-	1/7/7/10	-
5	PG4	E	203	-	-	1/5/5/10	-
5	PG4	I	202	-	-	0/5/5/10	-
4	HEM	F	202	1	-	4/12/54/54	-
3	KT1	L	201	-	-	0/9/21/21	0/3/3/3
5	PG4	B	204	-	-	0/5/5/10	-
5	PG4	B	206	-	-	2/6/6/10	-
3	KT1	K	201	-	-	2/9/21/21	0/3/3/3
5	PG4	H	203	-	-	0/5/5/10	-
4	HEM	H	202	1	-	4/12/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	KT1	C	201	-	-	0/9/21/21	0/3/3/3
3	KT1	D	202	-	-	1/9/21/21	0/3/3/3
3	KT1	A	202	-	-	3/9/21/21	0/3/3/3
4	HEM	B	203	1	-	4/12/54/54	-
3	KT1	G	201	-	-	0/9/21/21	0/3/3/3
3	KT1	F	201	-	-	0/9/21/21	0/3/3/3
3	KT1	E	201	-	-	1/9/21/21	0/3/3/3
5	PG4	D	205	-	-	1/5/5/10	-
5	PG4	J	203	-	-	5/10/10/10	-
4	HEM	L	202	1	-	4/12/54/54	-
3	KT1	H	201	-	-	3/9/21/21	0/3/3/3

The worst 5 of 103 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	202	HEM	C3C-C2C	-4.83	1.33	1.40
3	F	201	KT1	C04-N03	4.75	1.45	1.38
3	A	202	KT1	C04-N03	4.67	1.45	1.38
3	C	201	KT1	C23-C02	4.60	1.55	1.48
3	H	201	KT1	C02-N03	4.55	1.45	1.38

The worst 5 of 122 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	202	KT1	C04-N03-C02	-6.02	107.39	112.52
3	J	201	KT1	C05-C06-N07	-5.07	115.31	121.32
3	I	201	KT1	C23-C05-C06	-5.00	118.47	121.91
3	K	201	KT1	C05-C06-N07	-4.72	115.73	121.32
3	B	202	KT1	C05-C06-N07	-4.71	115.74	121.32

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	201	KT1	C20-C06-N07-C08
3	I	201	KT1	C05-C06-N07-C08
3	J	201	KT1	C11-C17-O18-C19
5	J	203	PG4	O3-C5-C6-O4
3	A	202	KT1	N07-C08-C09-C10

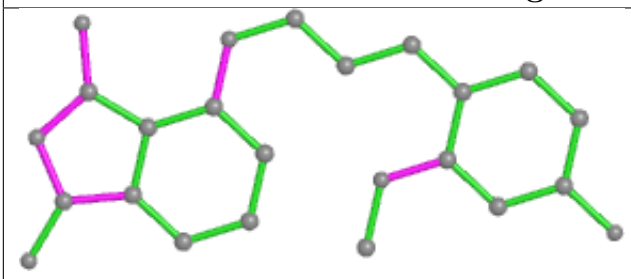
There are no ring outliers.

24 monomers are involved in 45 short contacts:

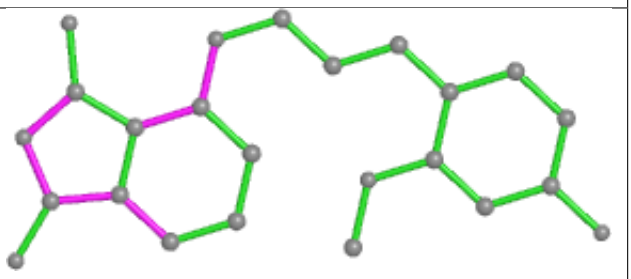
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	202	KT1	1	0
4	A	203	HEM	3	0
5	C	203	PG4	1	0
3	I	201	KT1	1	0
4	C	202	HEM	3	0
4	D	203	HEM	3	0
3	J	201	KT1	1	0
5	H	204	PG4	1	0
4	F	202	HEM	6	0
3	L	201	KT1	1	0
5	B	204	PG4	1	0
5	B	206	PG4	1	0
3	K	201	KT1	1	0
4	H	202	HEM	3	0
3	C	201	KT1	1	0
3	D	202	KT1	1	0
3	A	202	KT1	1	0
4	B	203	HEM	4	0
3	G	201	KT1	1	0
3	F	201	KT1	1	0
3	E	201	KT1	1	0
5	J	203	PG4	1	0
4	L	202	HEM	6	0
3	H	201	KT1	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 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.

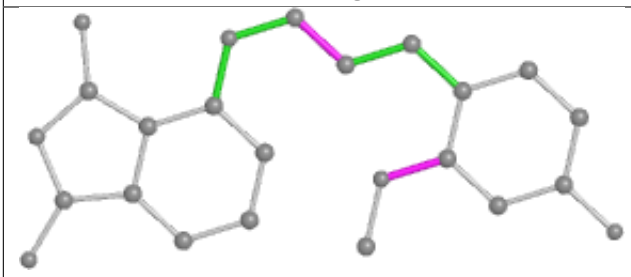
Ligand KT1 B 202



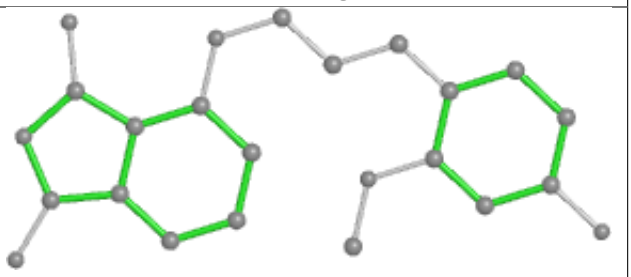
Bond lengths



Bond angles

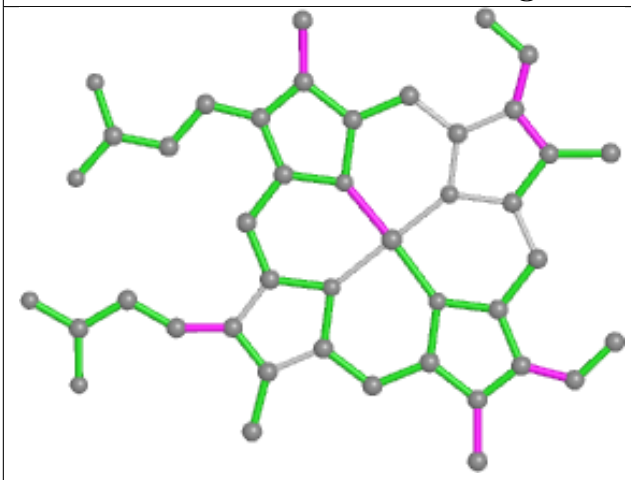


Torsions



Rings

Ligand HEM A 203



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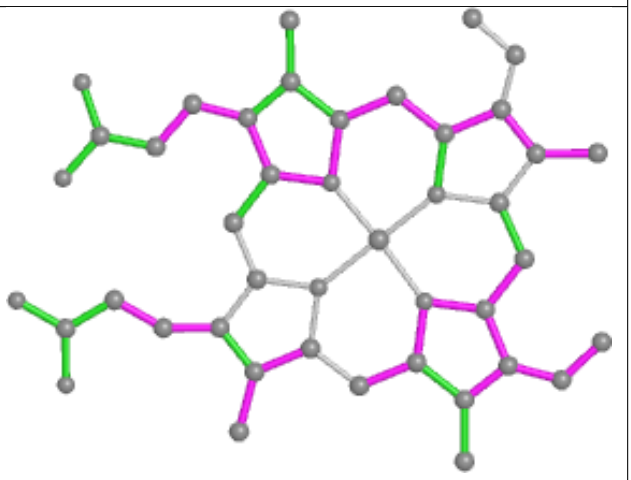
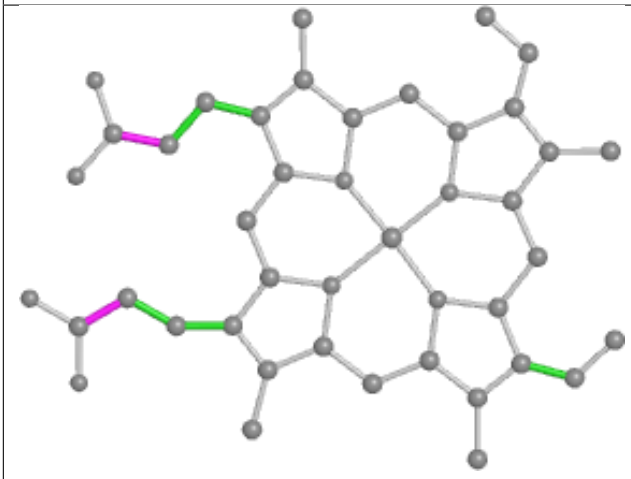


Bond angles



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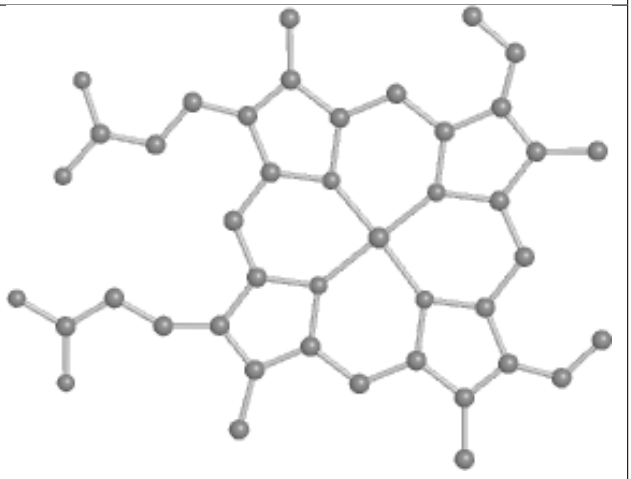
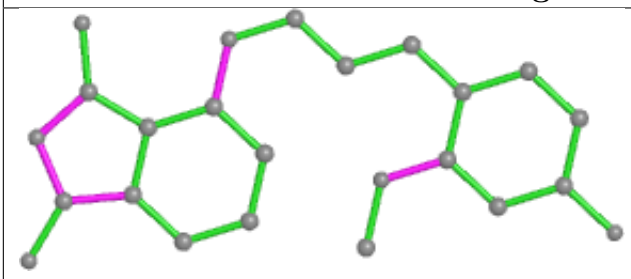


Rings

Ligand KT1 I 201



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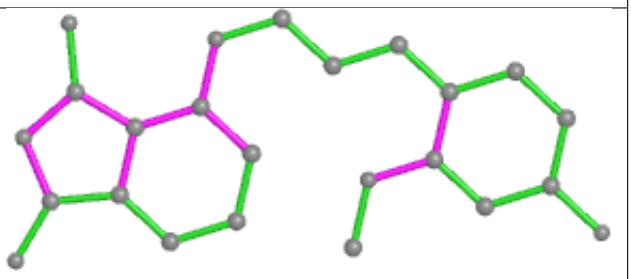
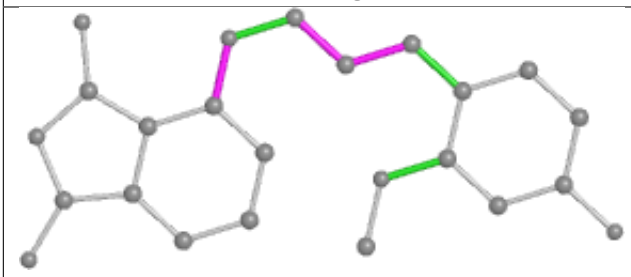
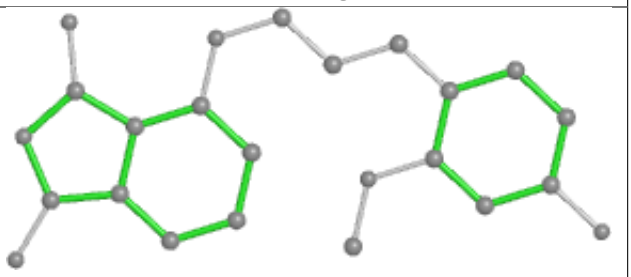


Bond angles

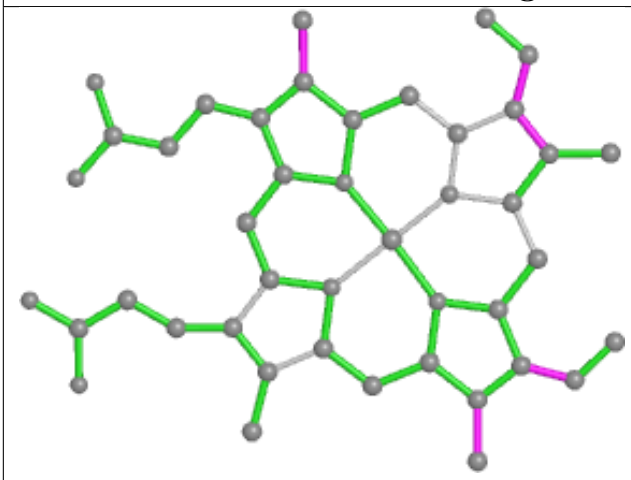


Torsions

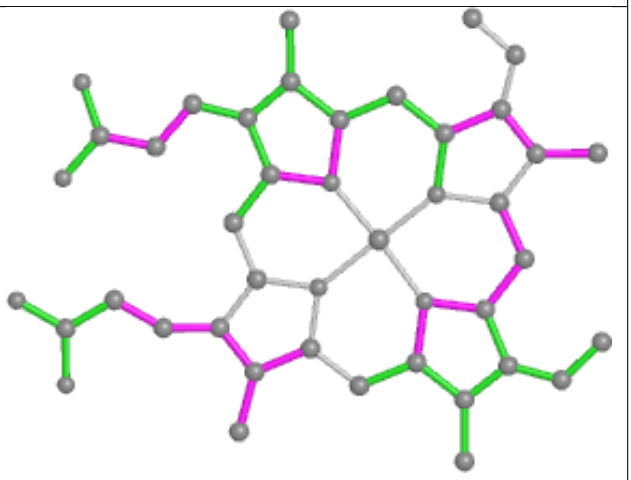


Rings

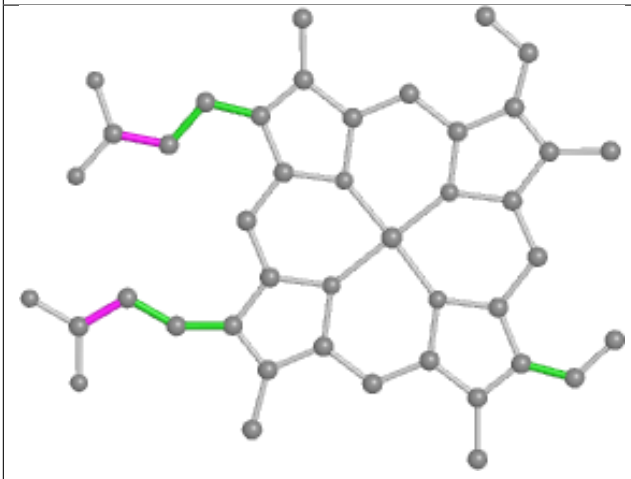
Ligand HEM C 202



Bond lengths



Bond angles



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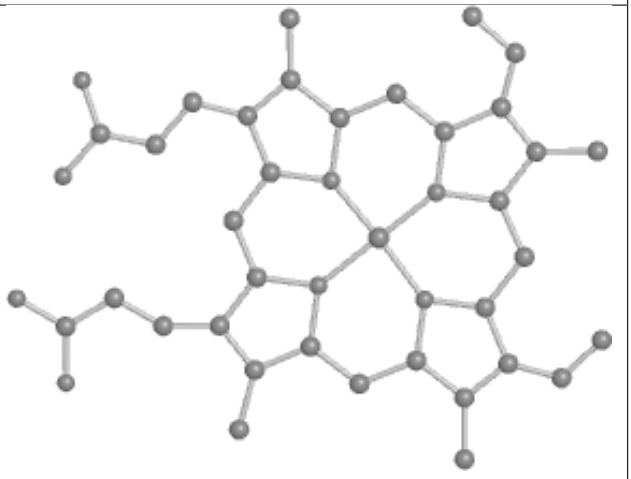
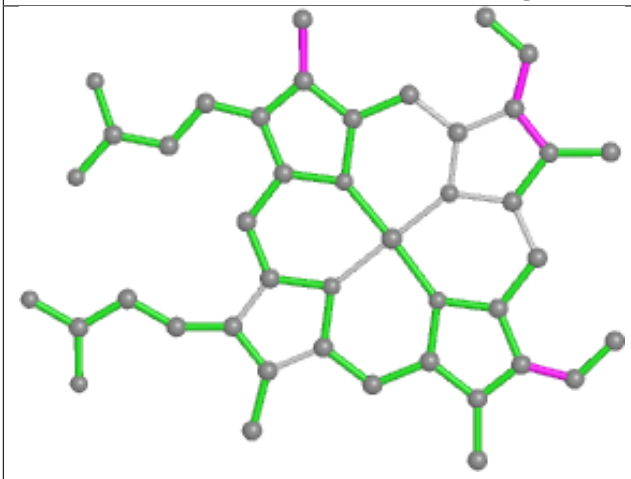
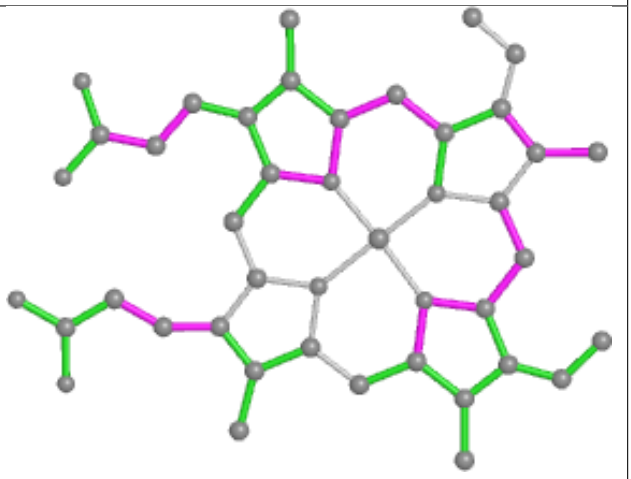


Rings

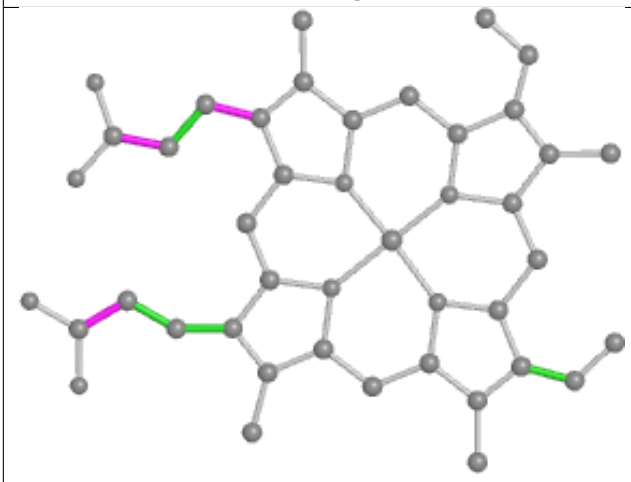
Ligand HEM D 203



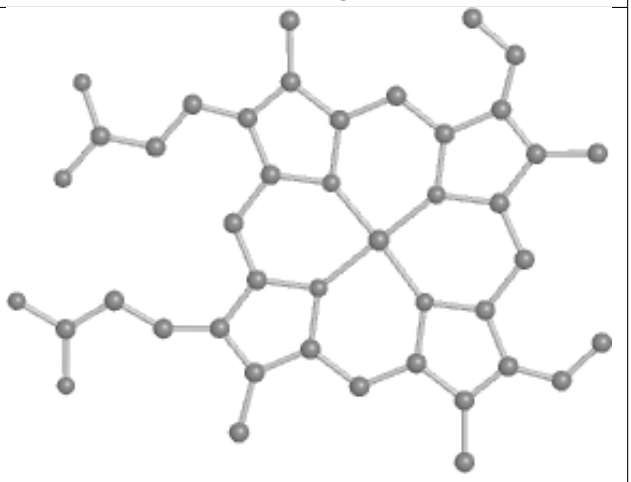
Bond lengths



Bond angles

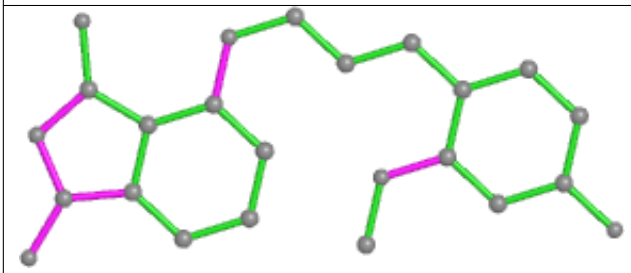


Torsions



Rings

Ligand KT1 J 201



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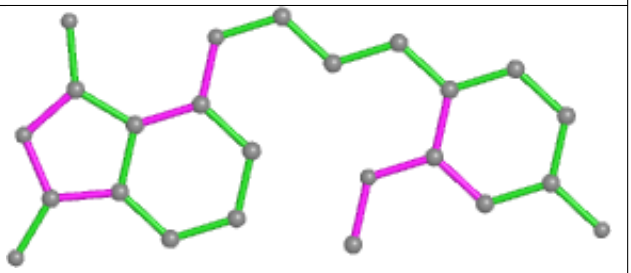

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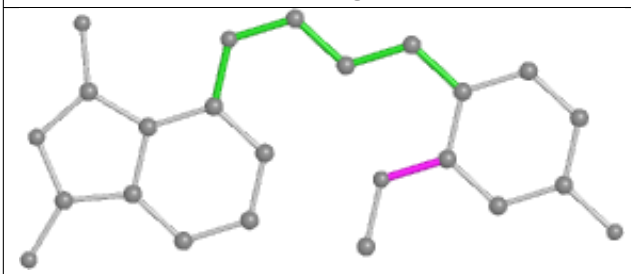

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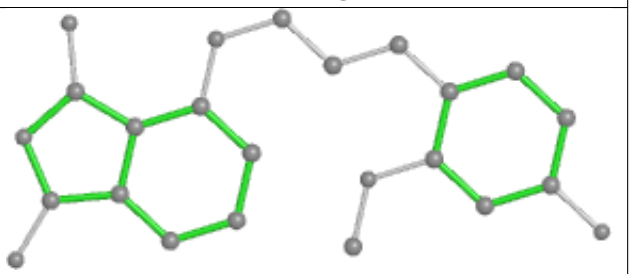
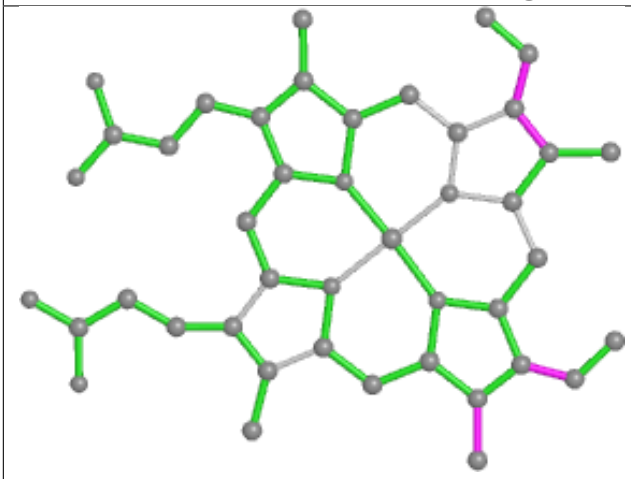


Rings

Ligand HEM F 202



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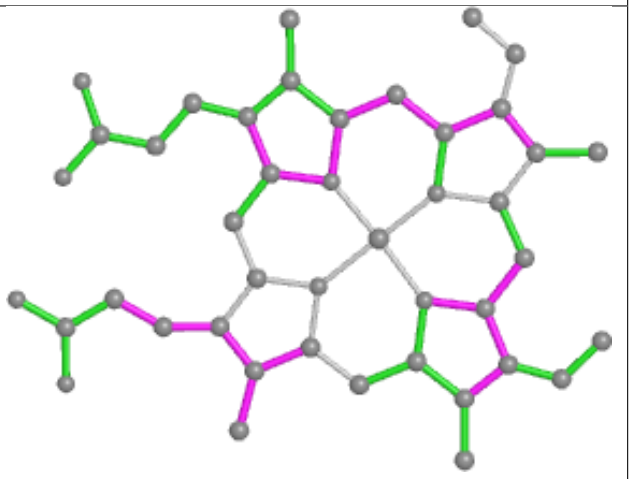

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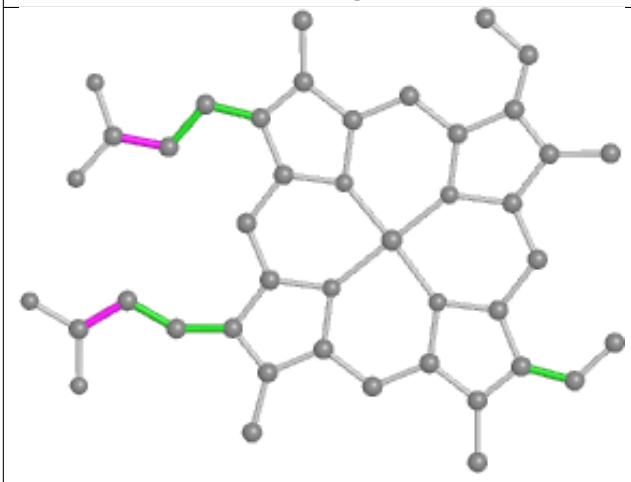

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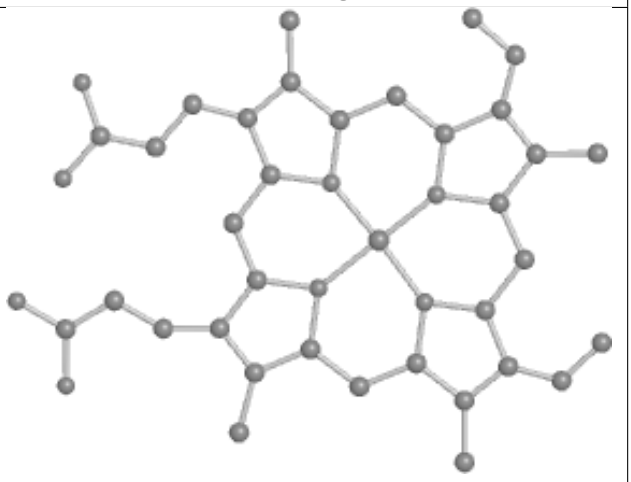
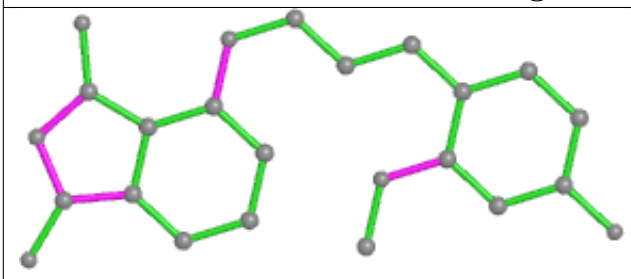


Rings

Ligand KT1 L 201



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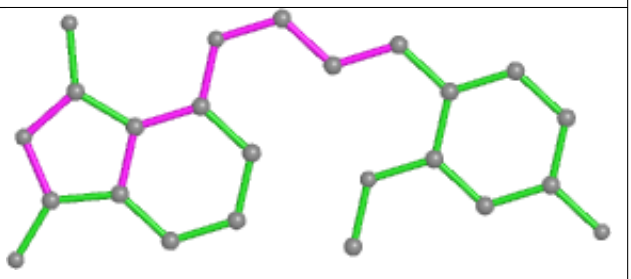

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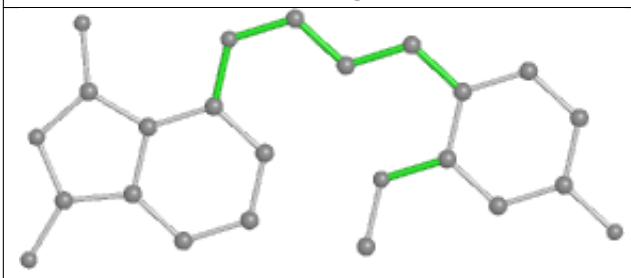

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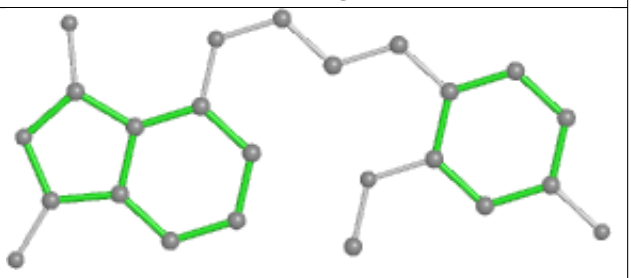
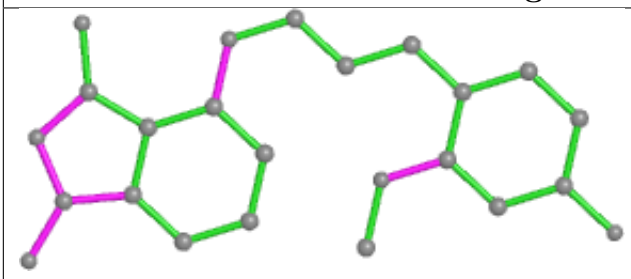


Rings

Ligand KT1 K 201



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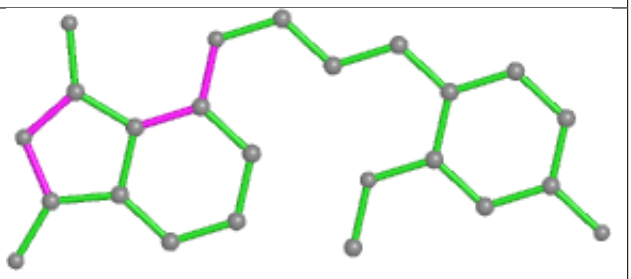
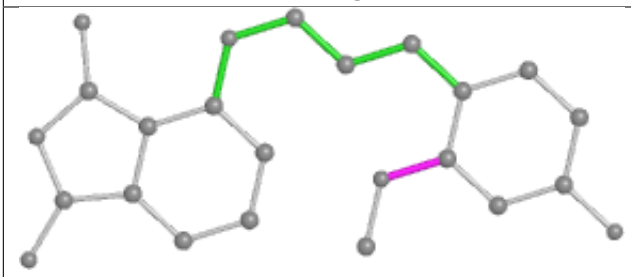


Bond angles



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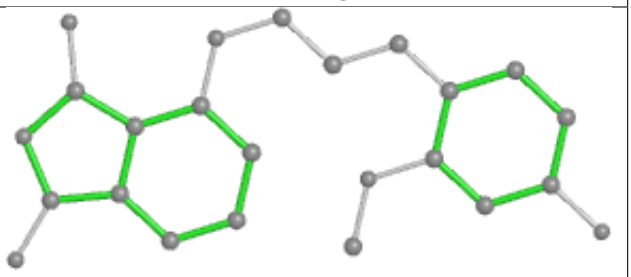
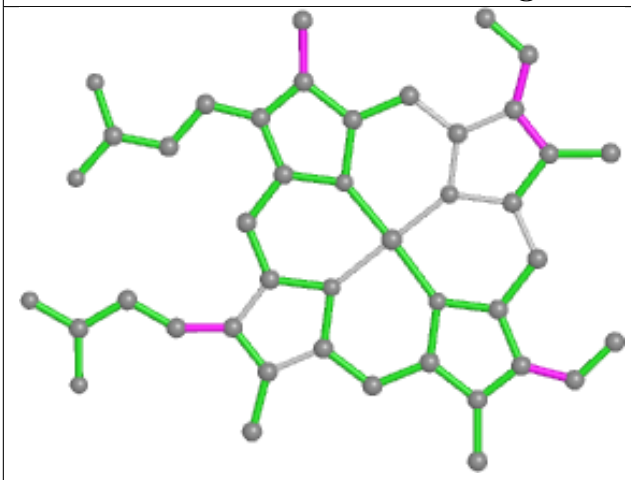


Rings

Ligand HEM H 202



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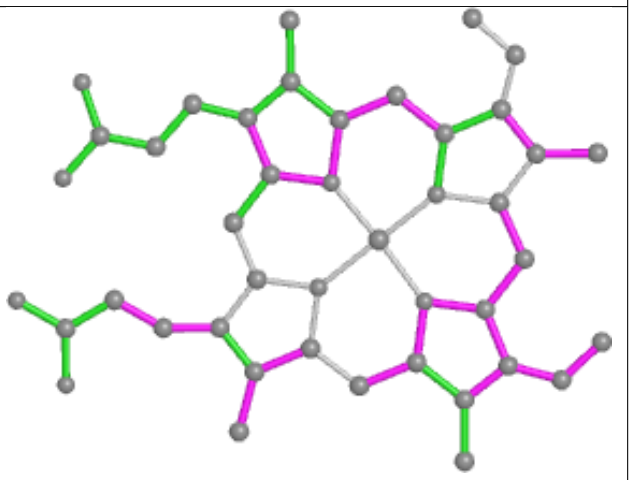

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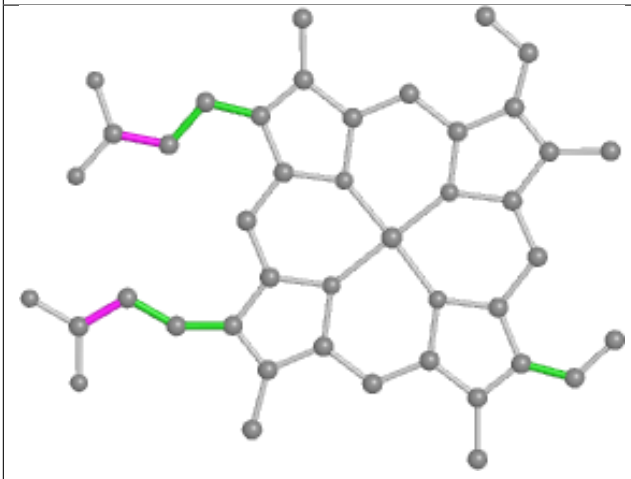

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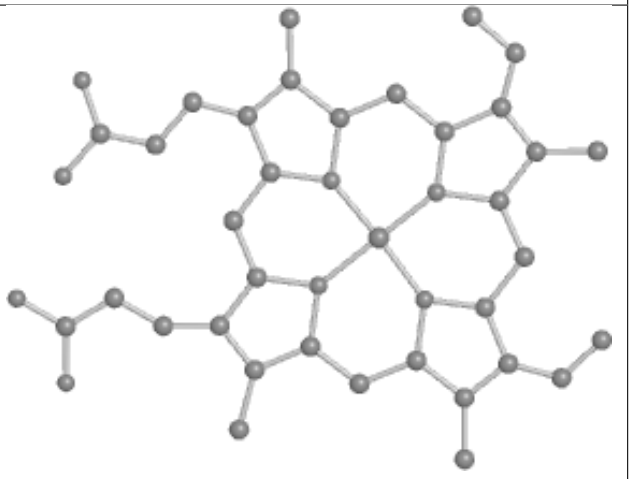
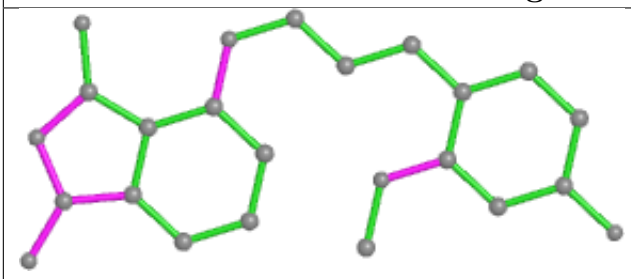


Rings

Ligand KT1 C 201



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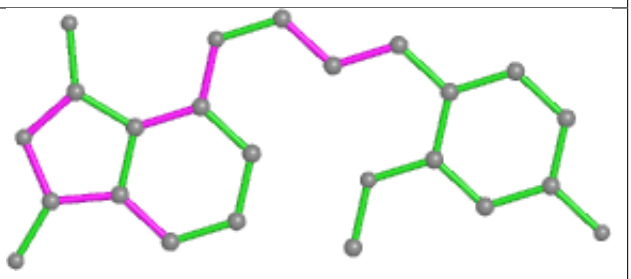
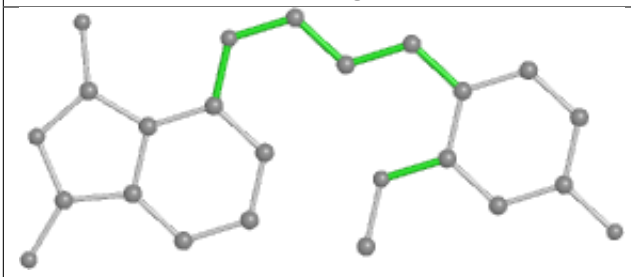


Bond angles



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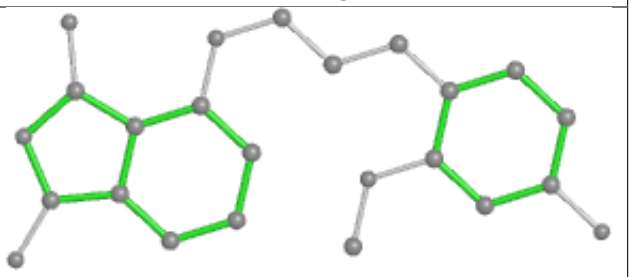
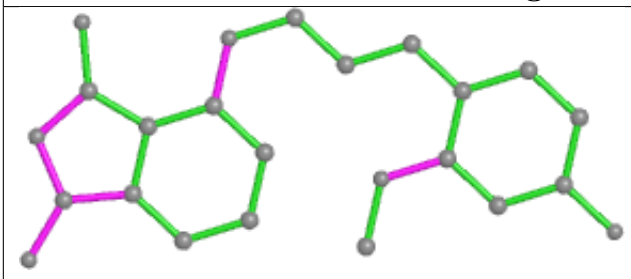


Rings

Ligand KT1 D 202



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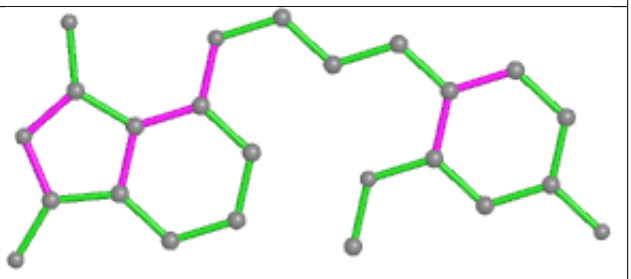
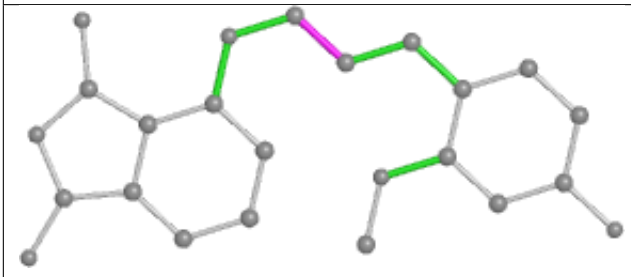


Bond angles



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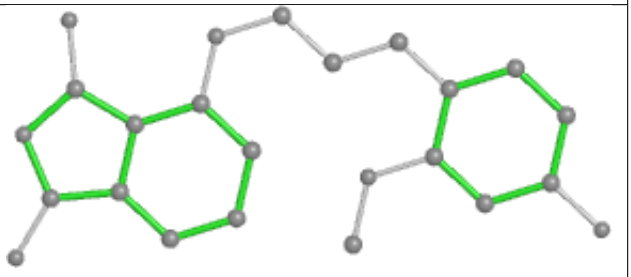
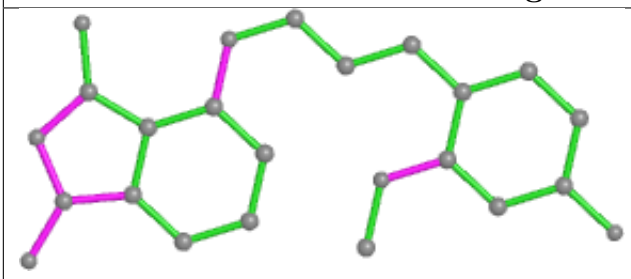


Rings

Ligand KT1 A 202



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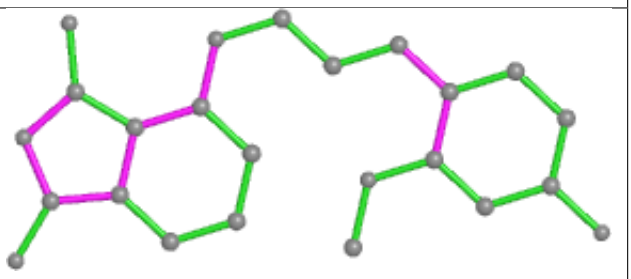
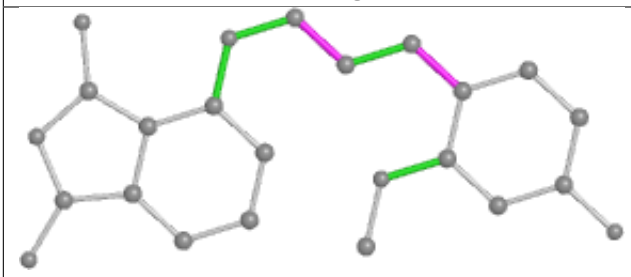
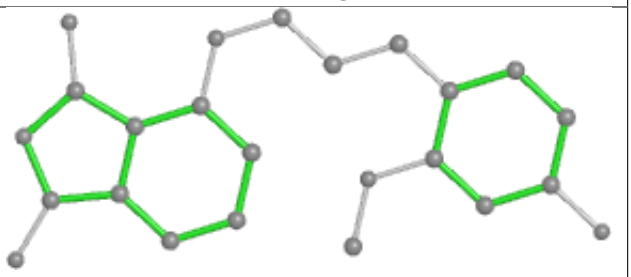


Bond angles

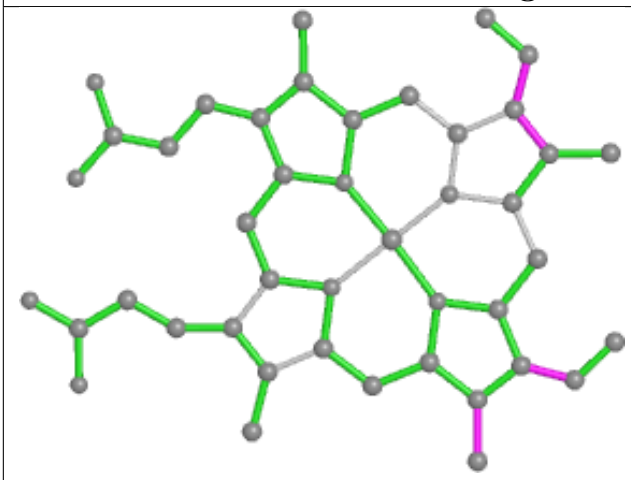


Torsions

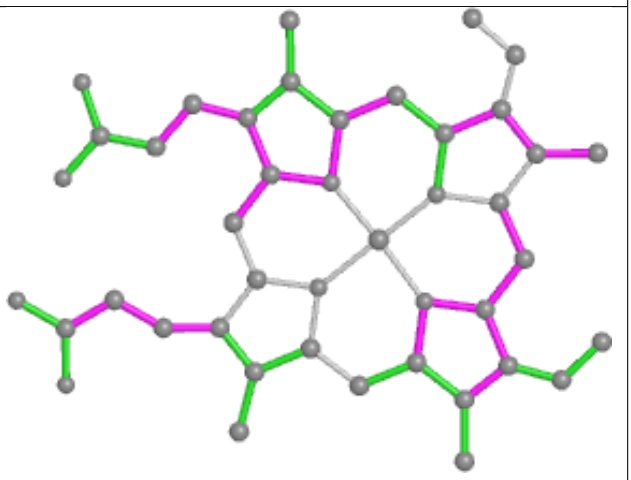


Rings

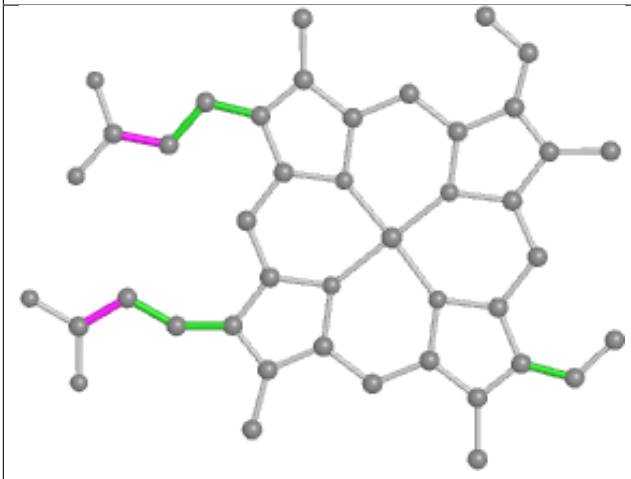
Ligand HEM B 203



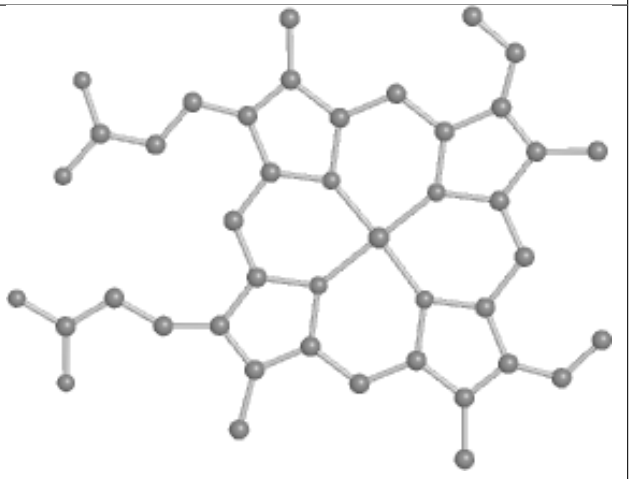
Bond lengths



Bond angles

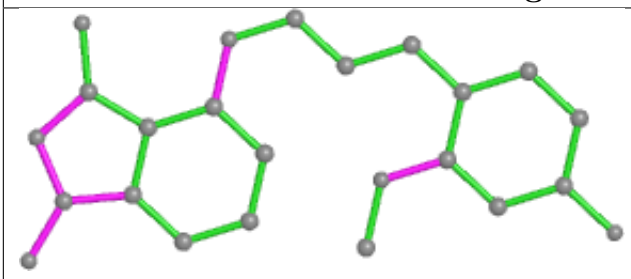


Torsions



Rings

Ligand KT1 G 201



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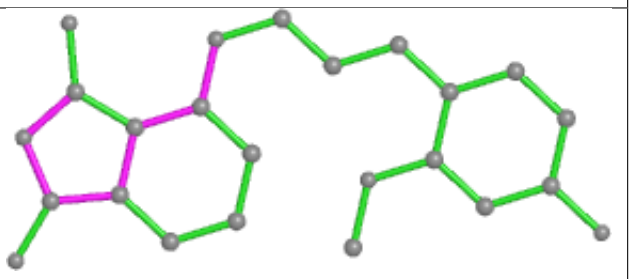
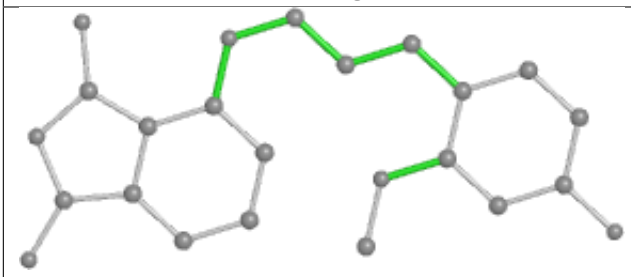


Bond angles



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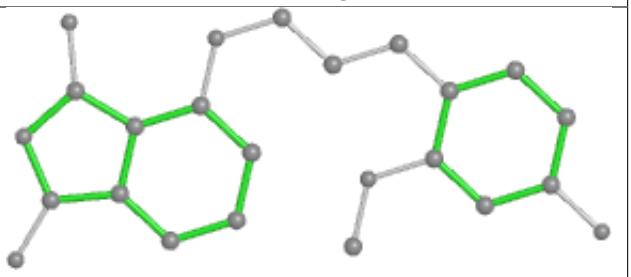
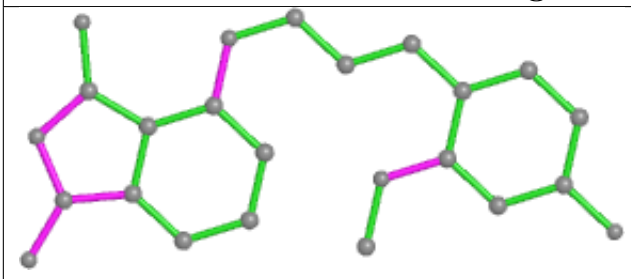
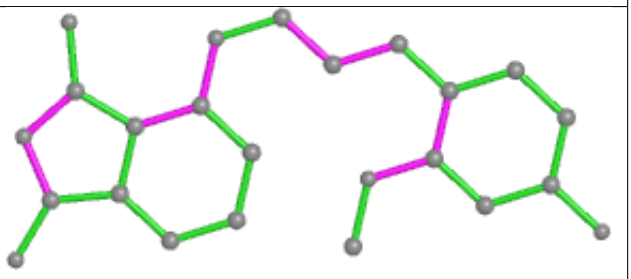


Rings

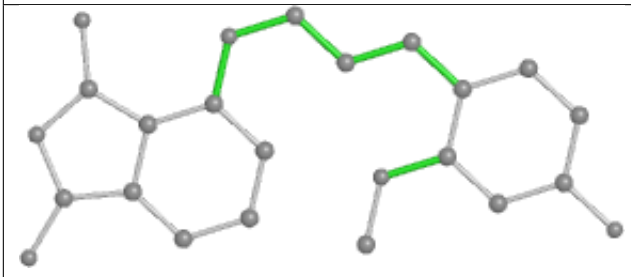
Ligand KT1 F 201



Bond lengths



Bond angles



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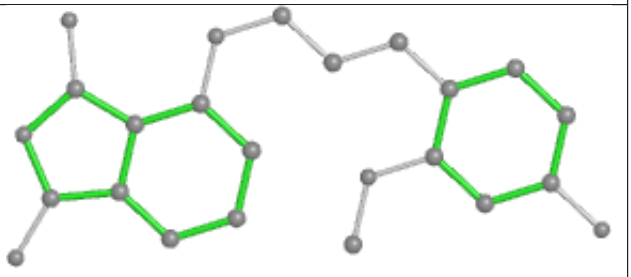
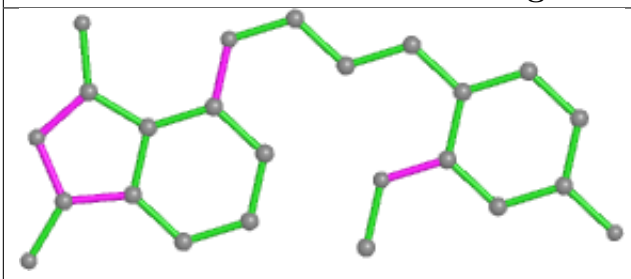


Rings

Ligand KT1 E 201



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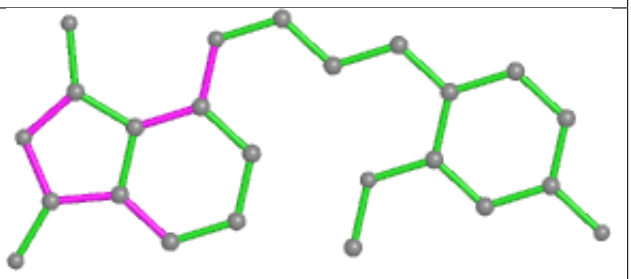
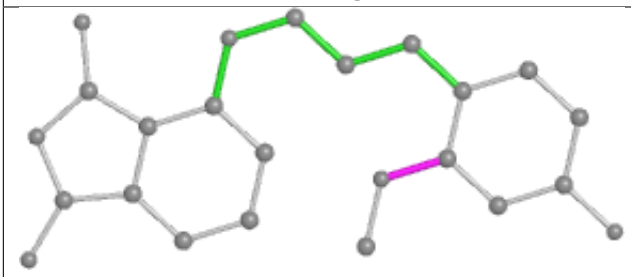
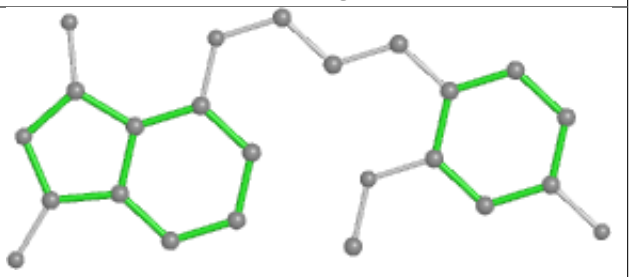


Bond angles

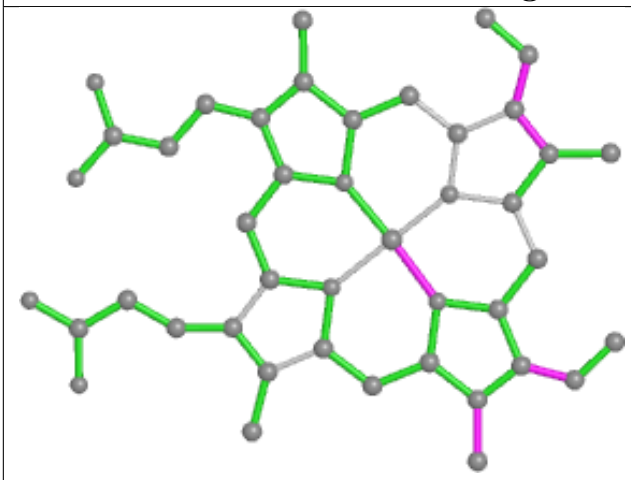


Torsions



Rings

Ligand HEM L 202



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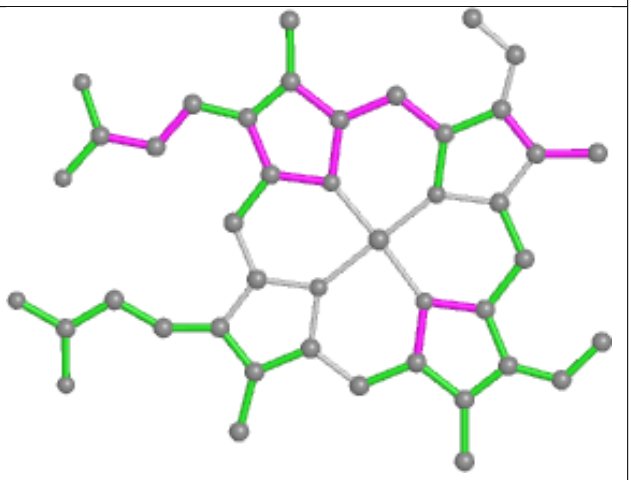
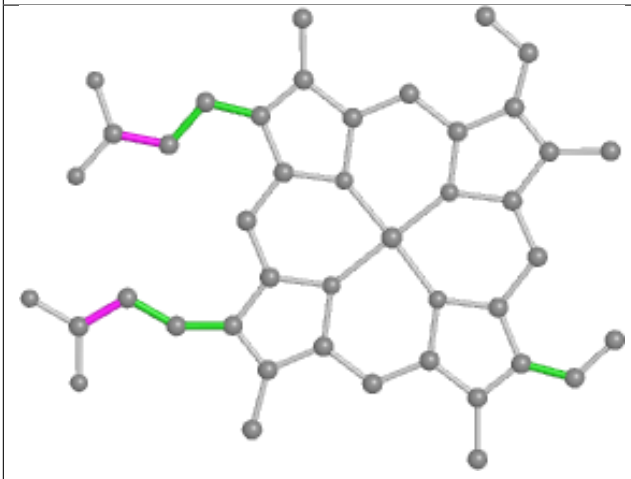
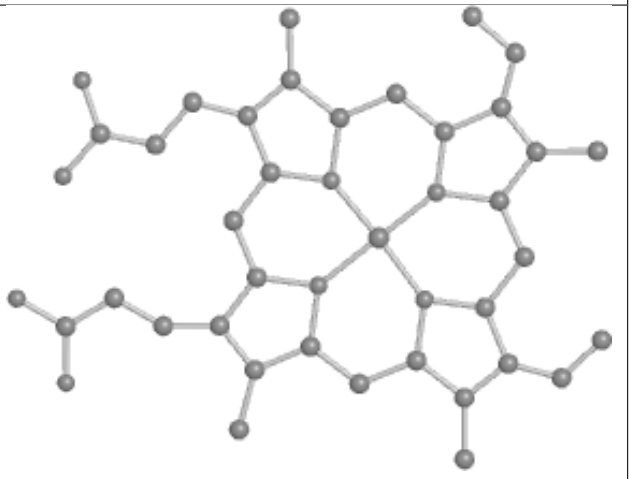


Bond angles

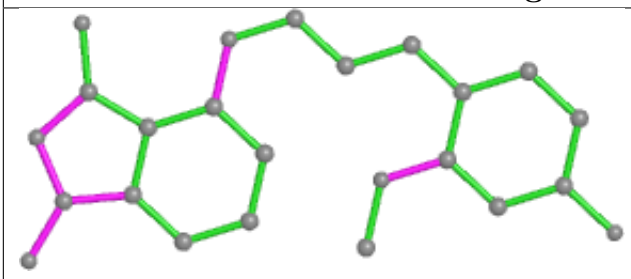


Torsions

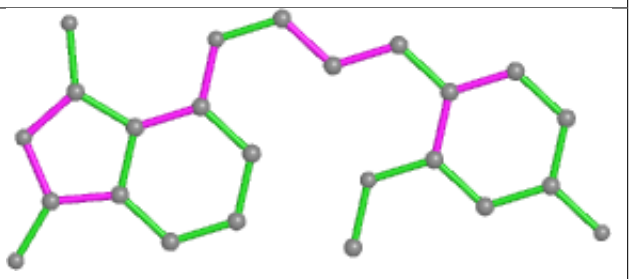


Rings

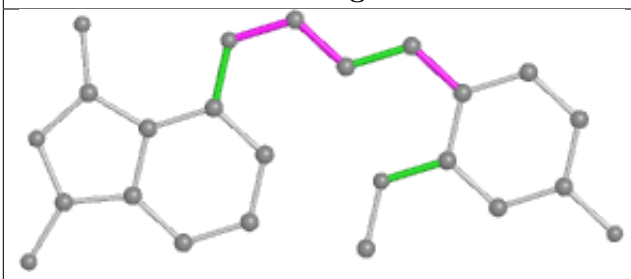
Ligand KT1 H 201



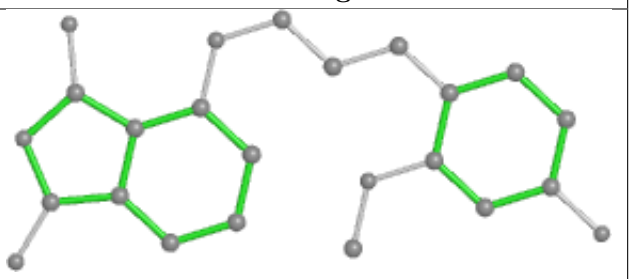
Bond lengths



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

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	156/158 (98%)	-0.49	0	100	100	13, 17, 26, 48	0
1	B	155/158 (98%)	-0.50	0	100	100	13, 17, 28, 44	0
1	C	155/158 (98%)	-0.46	0	100	100	12, 17, 27, 42	0
1	D	155/158 (98%)	-0.53	0	100	100	13, 17, 27, 42	0
1	E	156/158 (98%)	-0.47	0	100	100	12, 16, 25, 47	0
1	F	155/158 (98%)	-0.49	0	100	100	13, 18, 28, 43	0
1	G	155/158 (98%)	-0.54	0	100	100	12, 17, 25, 44	0
1	H	155/158 (98%)	-0.48	0	100	100	13, 17, 26, 44	0
1	I	155/158 (98%)	-0.51	0	100	100	13, 18, 27, 42	0
1	J	155/158 (98%)	-0.48	0	100	100	12, 16, 26, 42	0
1	K	155/158 (98%)	-0.49	0	100	100	13, 17, 28, 43	0
1	L	156/158 (98%)	-0.49	0	100	100	12, 17, 28, 49	0
All	All	1863/1896 (98%)	-0.49	0	100	100	12, 17, 27, 49	0

There are no RSRZ outliers to report.

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 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^{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
5	PG4	D	205	8/13	0.77	0.20	37,42,51,56	0
5	PG4	B	206	9/13	0.83	0.22	30,39,52,54	0
5	PG4	H	204	9/13	0.83	0.19	29,36,44,49	0
5	PG4	G	202	10/13	0.84	0.17	24,27,41,46	0
3	KT1	F	201	24/24	0.86	0.19	22,34,52,53	0
3	KT1	H	201	24/24	0.86	0.23	19,32,47,53	0
5	PG4	E	202	10/13	0.86	0.15	26,33,40,42	0
3	KT1	I	201	24/24	0.86	0.20	21,34,50,55	0
5	PG4	B	204	8/13	0.86	0.17	29,33,35,40	0
5	PG4	I	202	8/13	0.86	0.14	28,31,37,48	0
5	PG4	B	205	6/13	0.87	0.14	37,40,43,47	0
5	PG4	D	204	10/13	0.88	0.16	30,33,41,45	0
5	PG4	H	203	8/13	0.88	0.14	25,31,33,40	0
3	KT1	C	201	24/24	0.88	0.21	21,34,52,60	0
3	KT1	E	201	24/24	0.88	0.22	19,34,47,53	0
3	KT1	B	202	24/24	0.89	0.18	17,33,51,56	0
5	PG4	E	203	8/13	0.89	0.19	33,39,52,53	0
3	KT1	K	201	24/24	0.90	0.19	21,31,51,54	0
3	KT1	G	201	24/24	0.90	0.14	20,32,41,44	0
3	KT1	J	201	24/24	0.90	0.15	20,30,46,48	0
5	PG4	J	203	13/13	0.90	0.14	26,34,45,51	0
5	PG4	F	203	10/13	0.91	0.15	24,30,37,37	0
3	KT1	L	201	24/24	0.91	0.15	18,33,43,50	0
5	PG4	A	204	10/13	0.92	0.16	28,35,48,51	0
5	PG4	C	203	11/13	0.92	0.11	23,32,41,49	0
5	PG4	K	202	11/13	0.92	0.15	25,34,40,43	0
3	KT1	A	202	24/24	0.93	0.14	14,26,37,41	0
3	KT1	D	202	24/24	0.94	0.14	19,27,38,40	0
5	PG4	J	202	13/13	0.94	0.11	23,30,39,46	0
4	HEM	B	203	43/43	0.95	0.12	13,16,34,37	0
4	HEM	F	202	43/43	0.96	0.10	12,18,36,42	0
4	HEM	H	202	43/43	0.96	0.12	12,18,34,38	0
4	HEM	L	202	43/43	0.96	0.12	12,17,24,30	43
4	HEM	C	202	43/43	0.96	0.12	14,19,35,45	0
4	HEM	A	203	43/43	0.97	0.10	11,17,34,39	0
4	HEM	D	203	43/43	0.97	0.10	11,16,23,26	43
2	FE2	A	201	1/1	1.00	0.06	13,13,13,13	0

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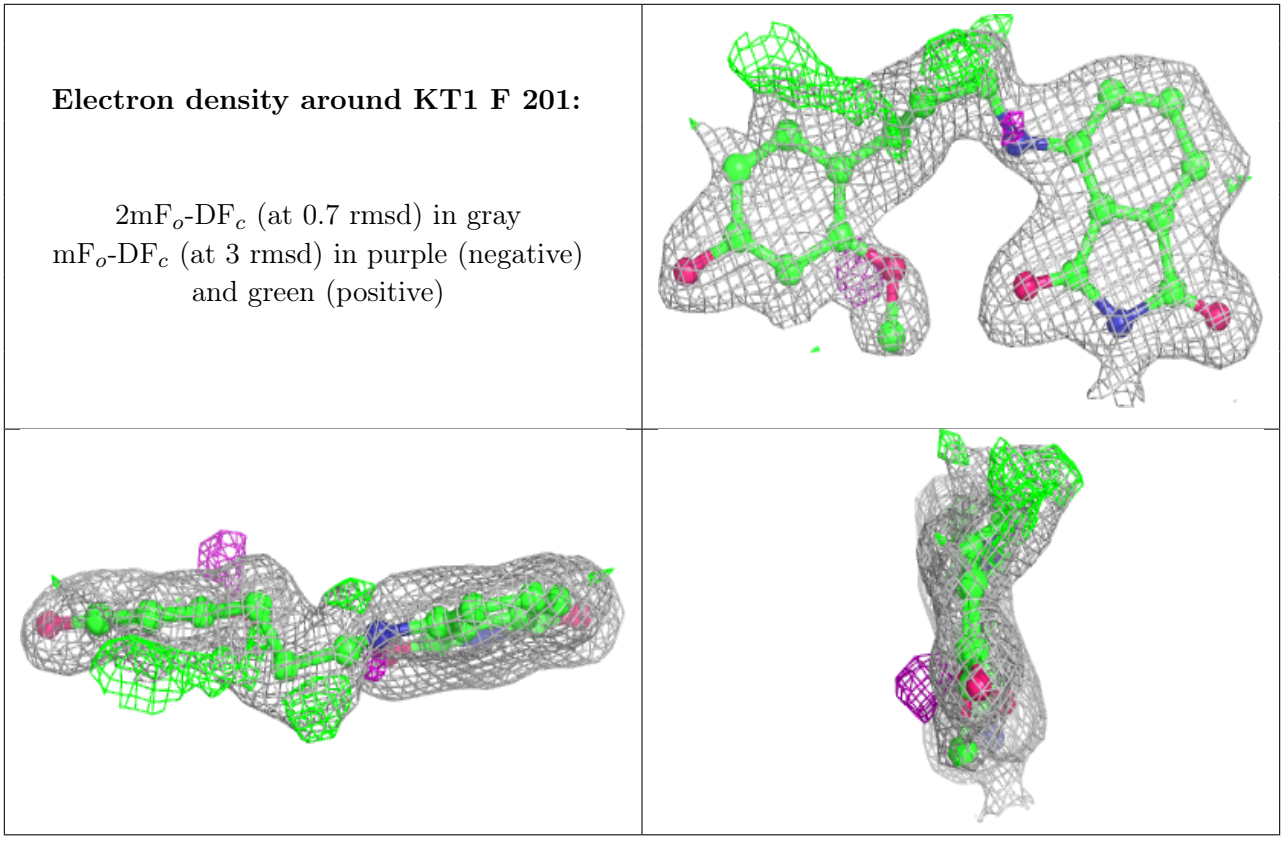
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	FE2	B	201	1/1	1.00	0.07	13,13,13,13	0
2	FE2	D	201	1/1	1.00	0.07	14,14,14,14	0

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

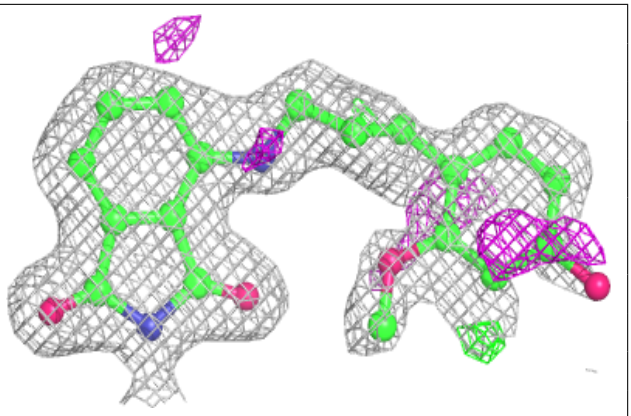
Electron density around KT1 F 201:

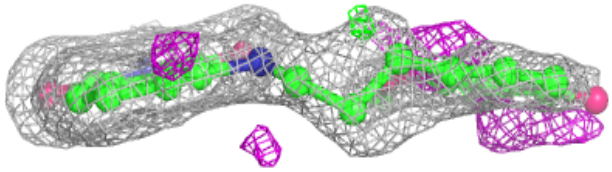
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

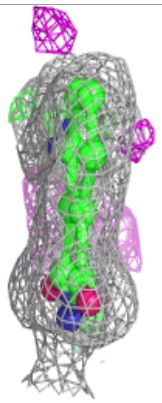


Electron density around KT1 H 201:

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

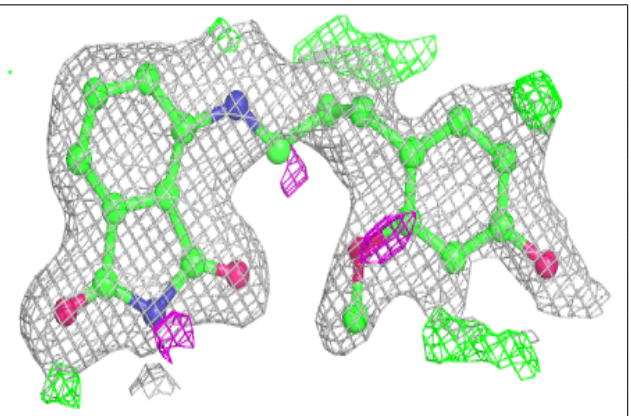


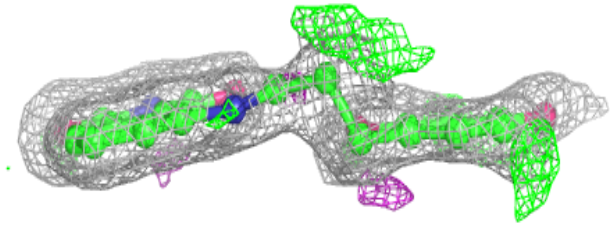


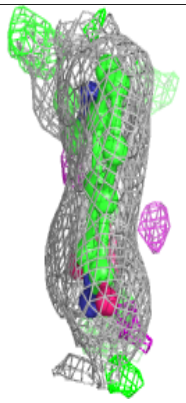


Electron density around KT1 I 201:

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

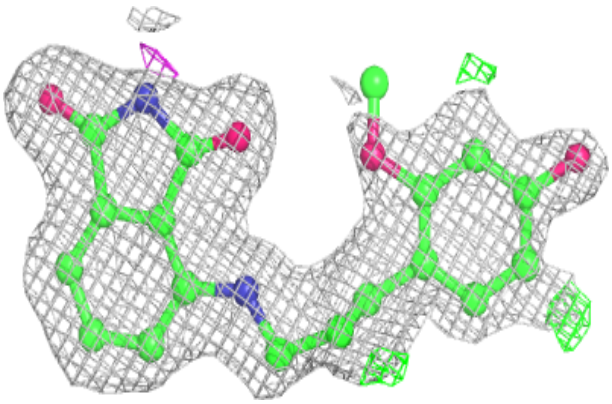


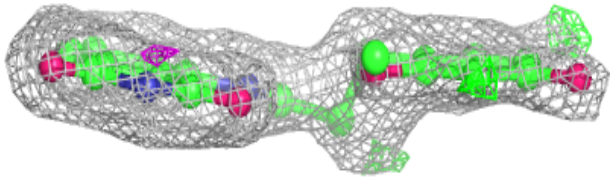


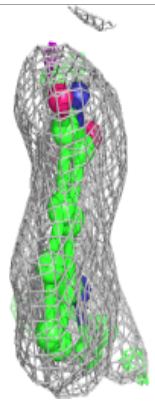


Electron density around KT1 C 201:

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

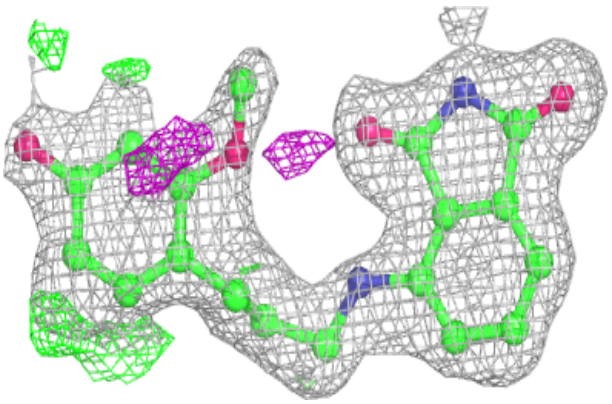


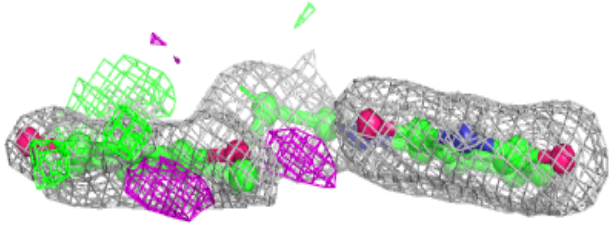


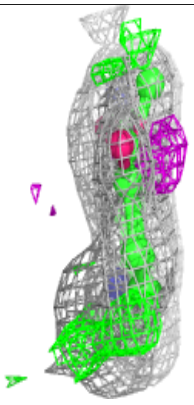


Electron density around KT1 E 201:

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

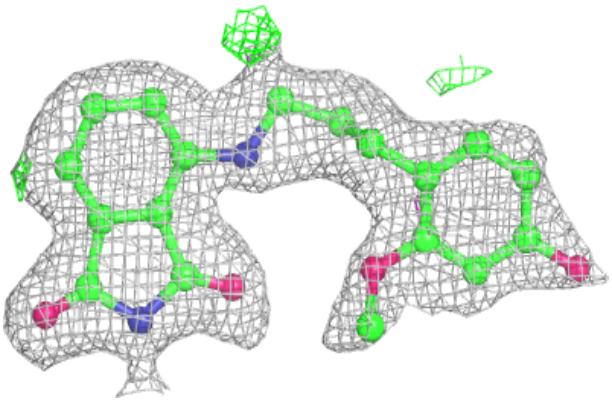


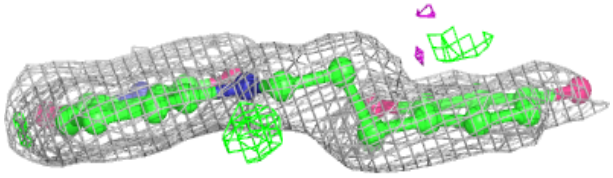


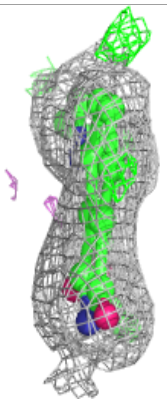


Electron density around KT1 B 202:

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

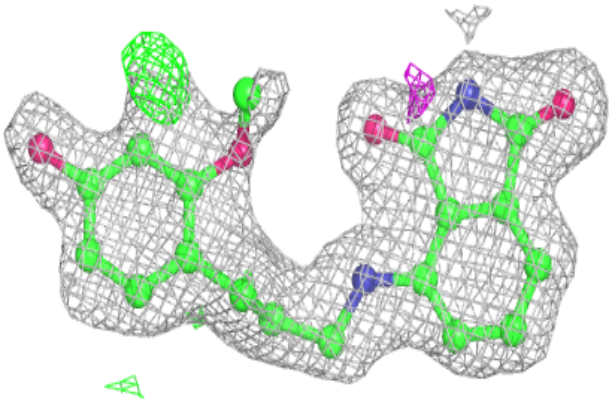


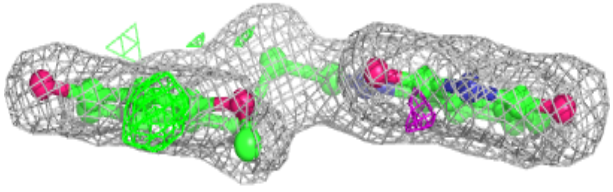


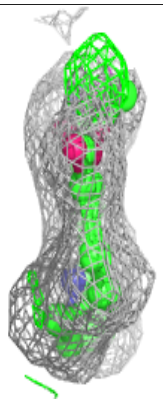


Electron density around KT1 K 201:

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

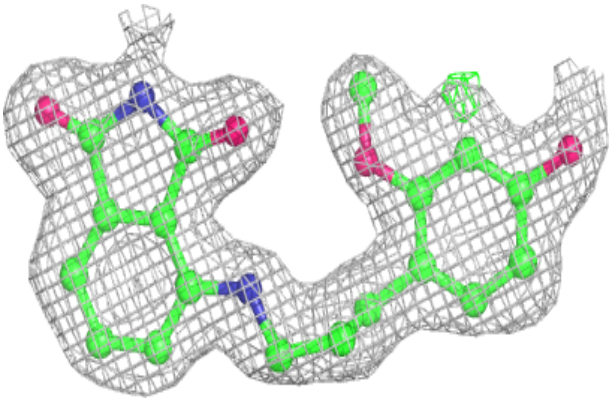


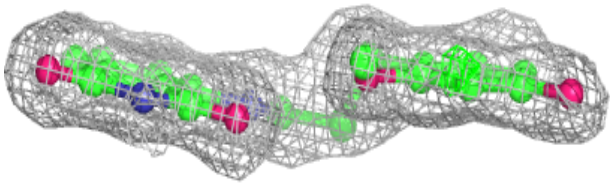


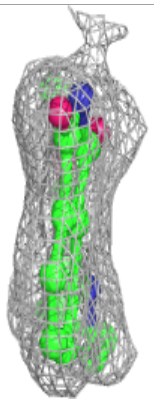


Electron density around KT1 G 201:

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

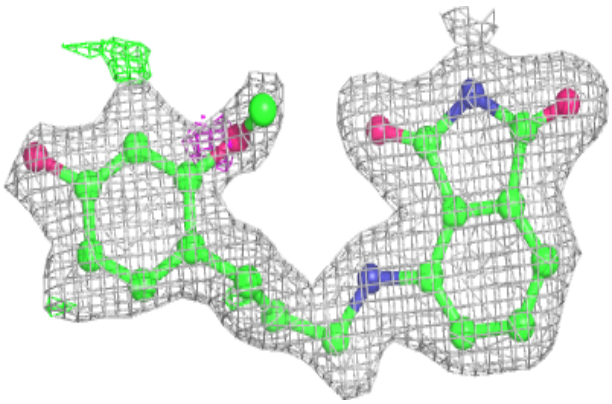


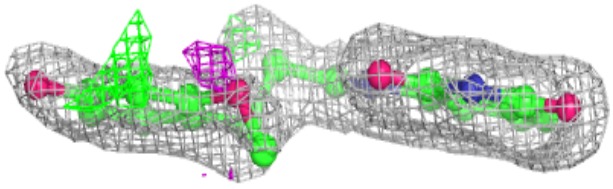


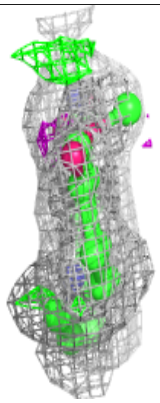


Electron density around KT1 J 201:

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

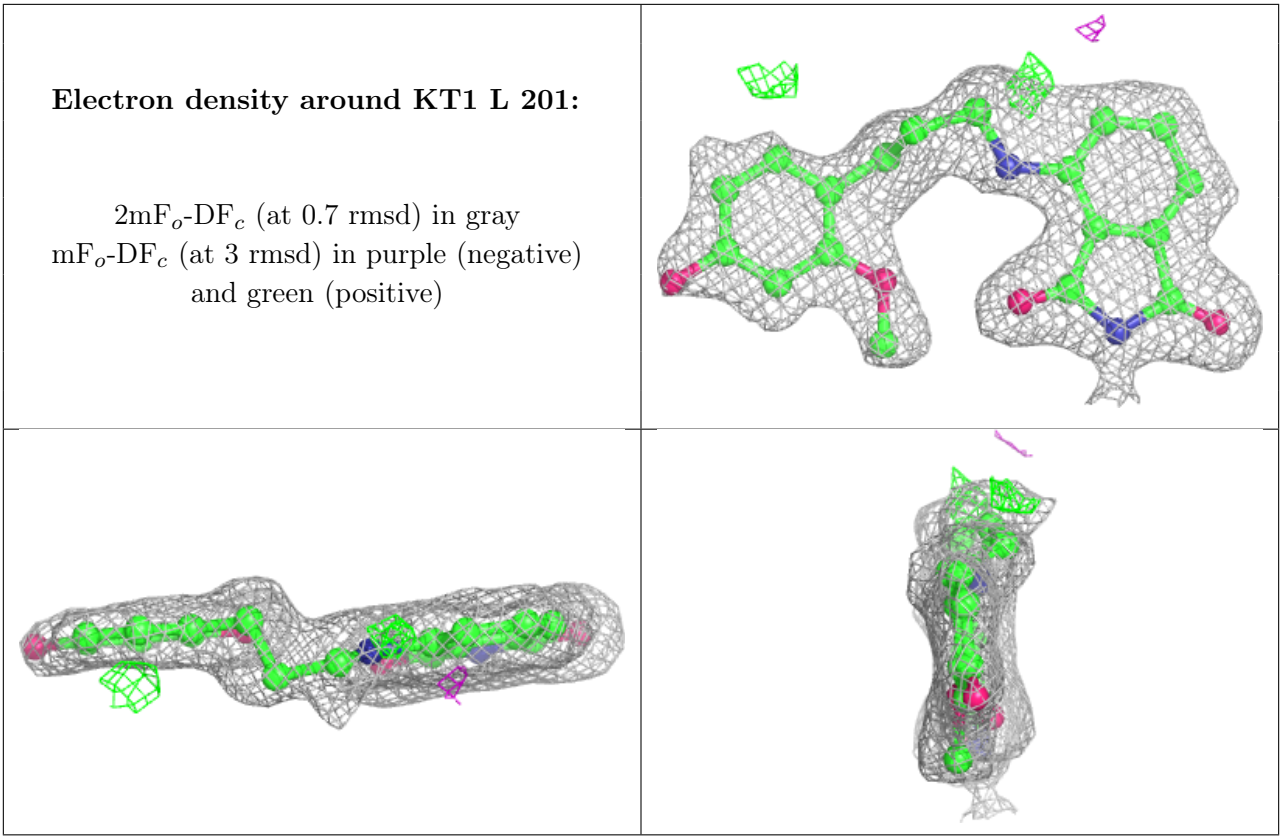






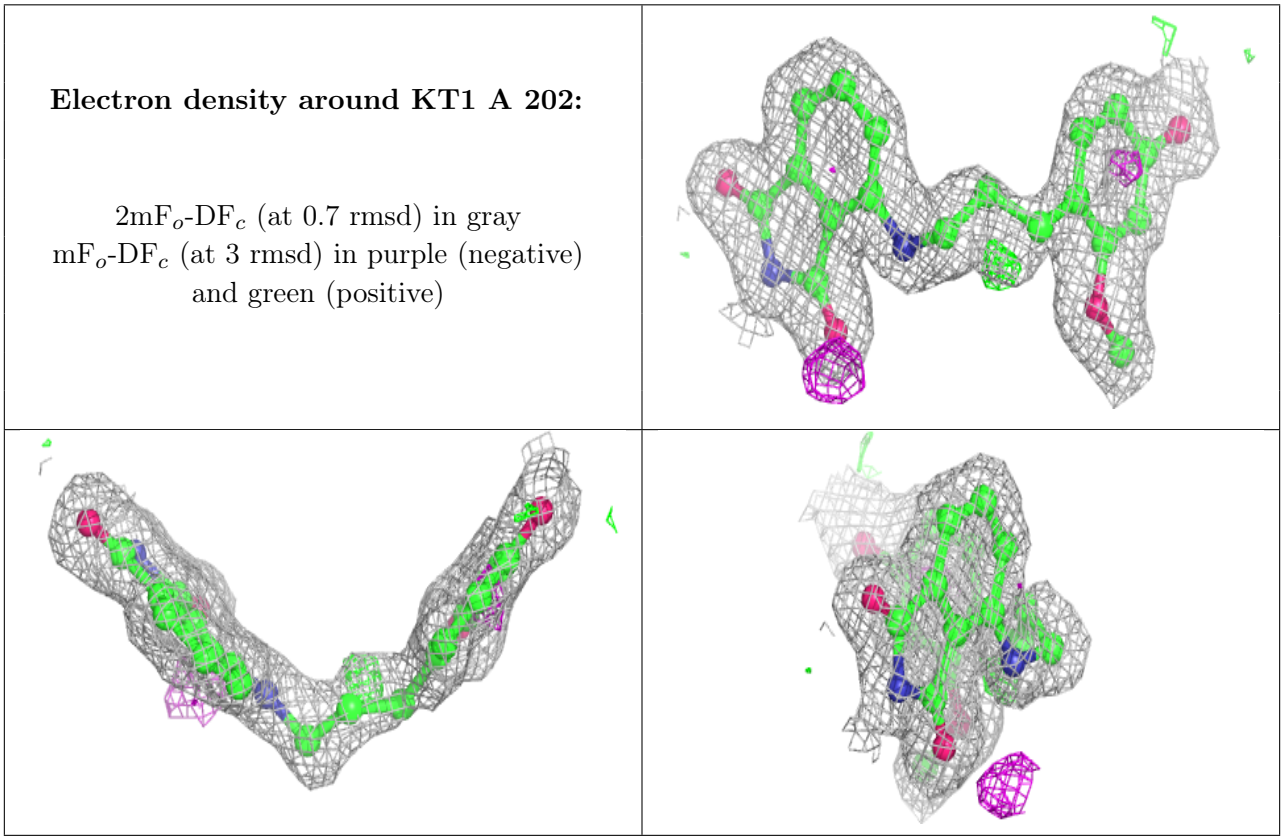
Electron density around KT1 L 201:

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



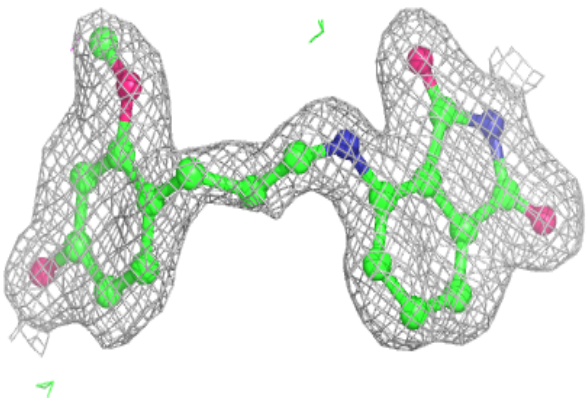
Electron density around KT1 A 202:

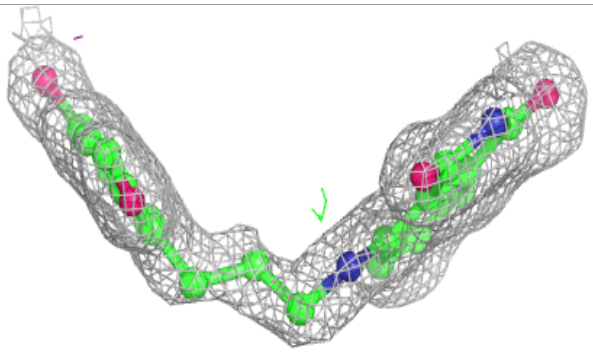
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

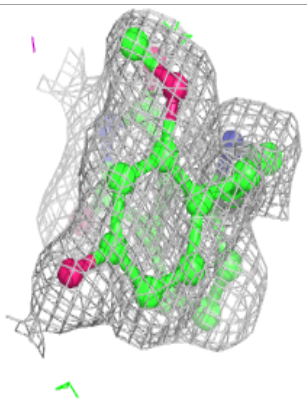


Electron density around KT1 D 202:

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

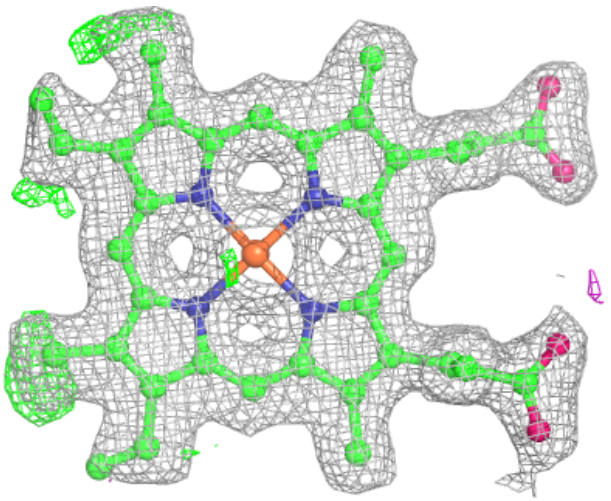


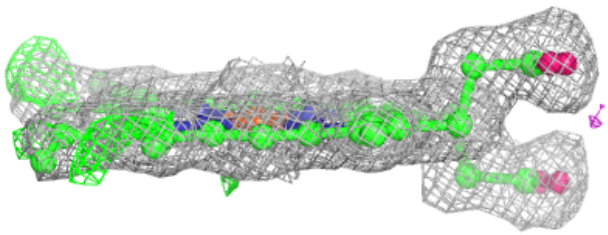


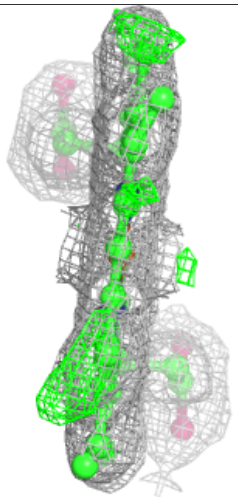


Electron density around HEM B 203:

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

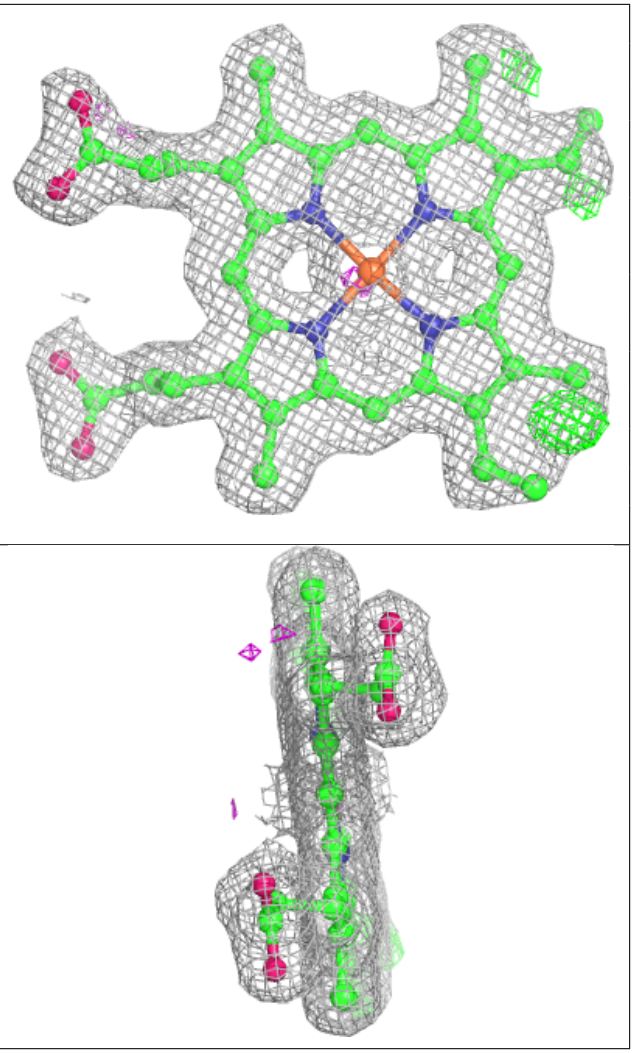






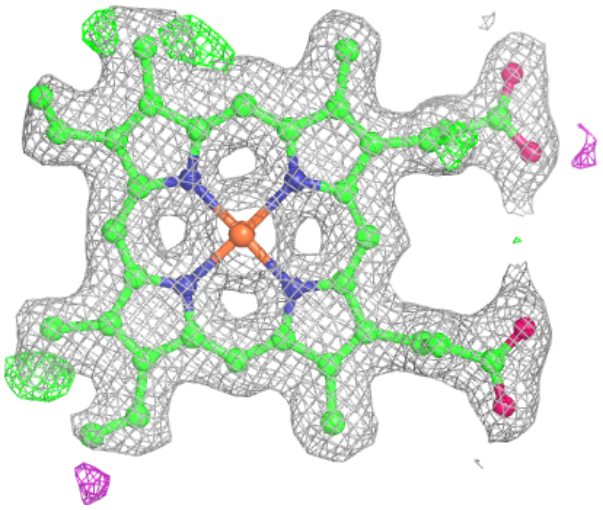
Electron density around HEM F 202:

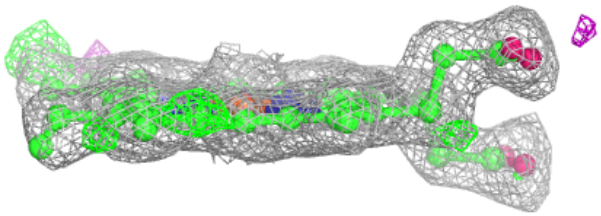
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

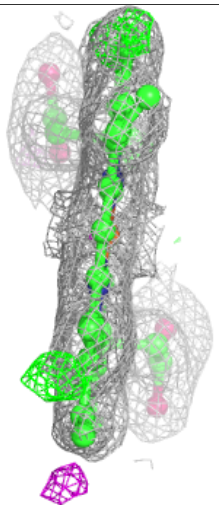


Electron density around HEM H 202:

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

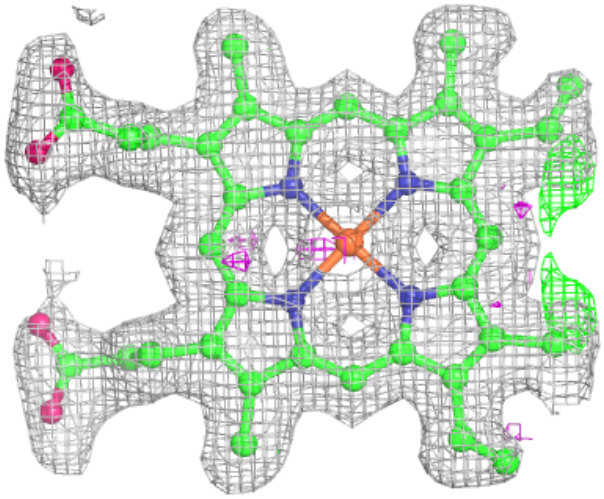


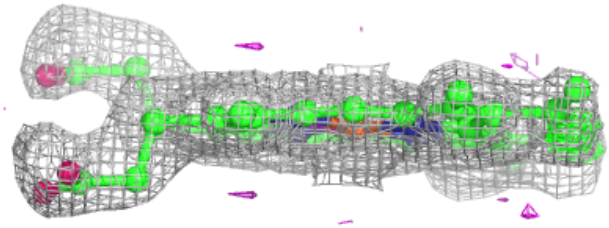


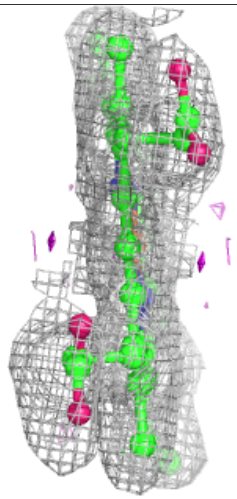


Electron density around HEM L 202:

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

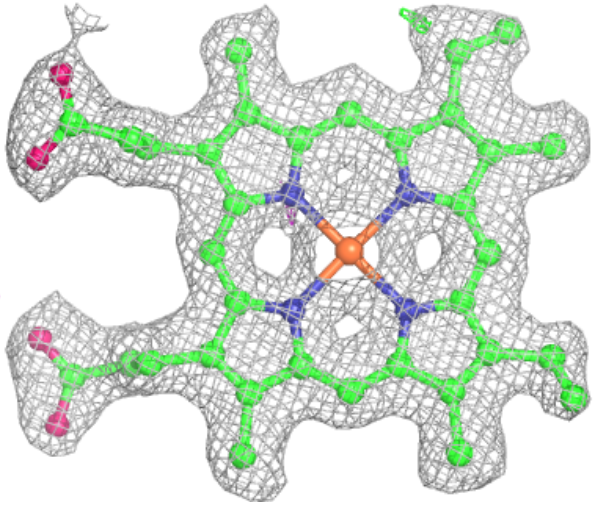


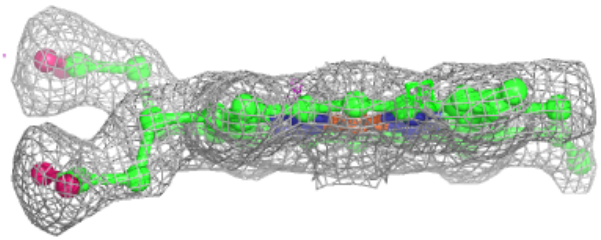


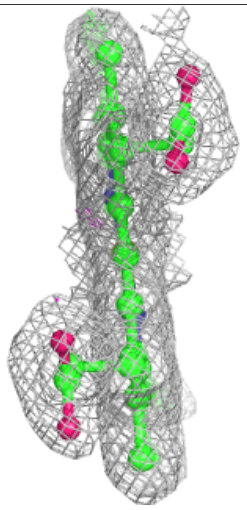


Electron density around HEM C 202:

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

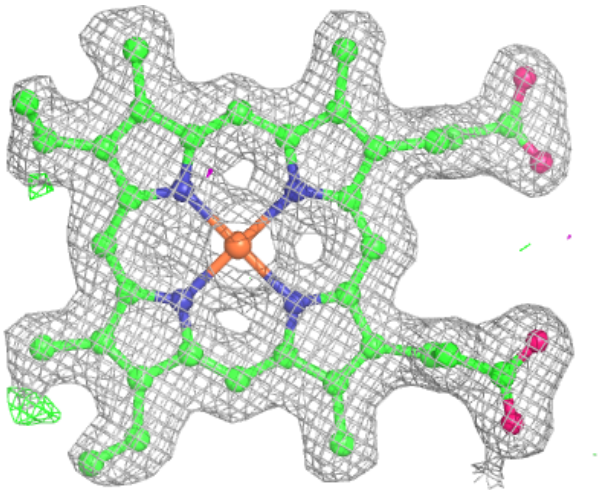


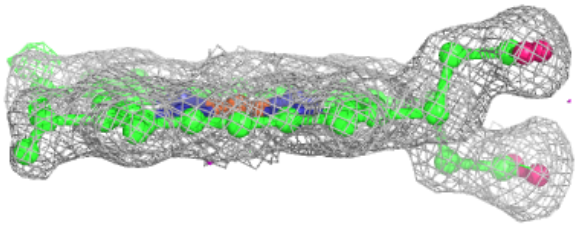


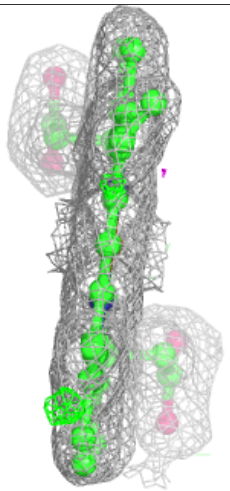


Electron density around HEM A 203:

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

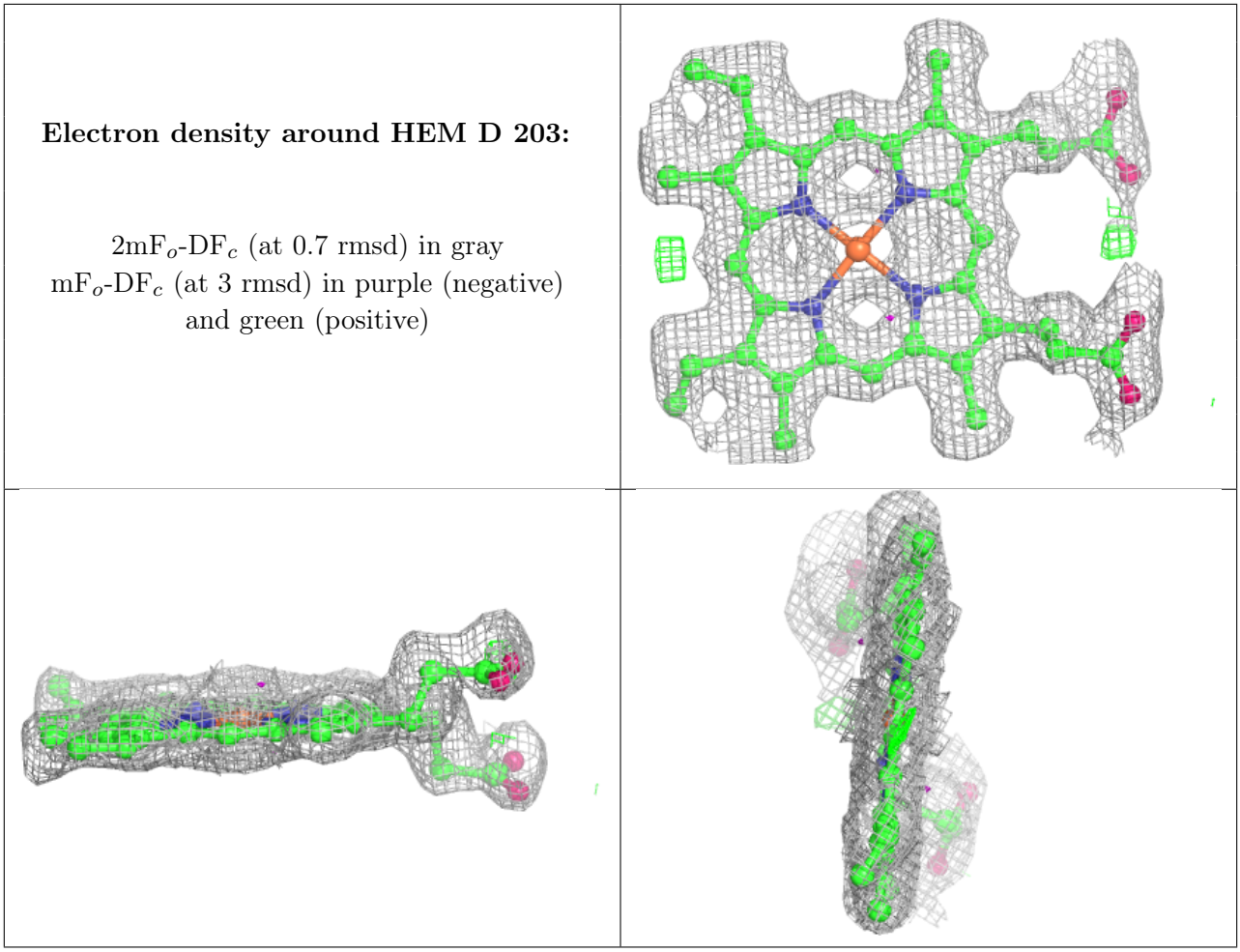






Electron density around HEM D 203:

$2mF_o$-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.