wwPDB X-ray Structure Validation Summary Report (i)

Oct 7, 2023 – 10:53 PM EDT

PDB ID	:	6DWN
Title	:	Structure of Human Cytochrome P450 1A1 with Erlotinib
Authors	:	Bart, A.G.; Scott, E.E.
Deposited on	:	2018-06-26
Resolution	:	3.00 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:

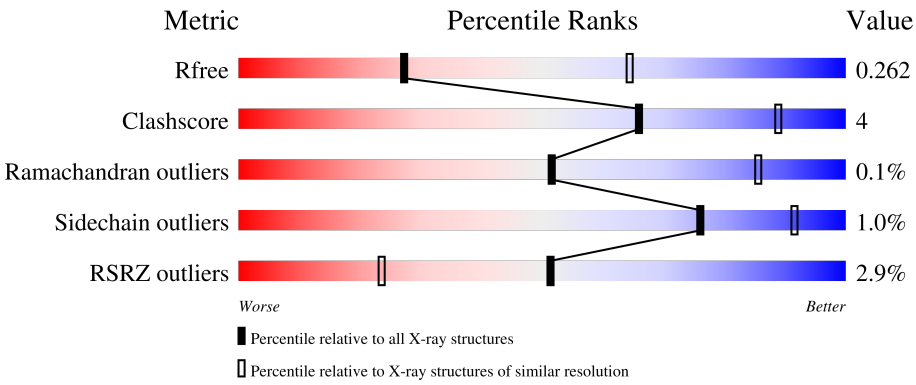
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	491	2%, 88%, 9%, •
1	B	491	85%, 9%, 5%
1	C	491	5%, 85%, 9%, 6%
1	D	491	3%, 84%, 8%, 8%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 30308 atoms, of which 15121 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 Cytochrome P450 1A1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	476	7619	2440	3807	663	688	21	0	0	0
1	B	465	7437	2384	3718	647	667	21	0	0	0
1	C	462	7395	2371	3697	643	663	21	0	0	0
1	D	453	7251	2325	3628	629	648	21	0	0	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MET	-	expression tag	UNP P04798
A	29	ALA	-	expression tag	UNP P04798
A	30	LYS	-	expression tag	UNP P04798
A	31	LYS	-	expression tag	UNP P04798
A	32	THR	-	expression tag	UNP P04798
A	33	SER	-	expression tag	UNP P04798
A	34	SER	-	expression tag	UNP P04798
A	513	HIS	-	expression tag	UNP P04798
A	514	HIS	-	expression tag	UNP P04798
A	515	HIS	-	expression tag	UNP P04798
A	516	HIS	-	expression tag	UNP P04798
A	517	HIS	-	expression tag	UNP P04798
A	518	HIS	-	expression tag	UNP P04798
B	28	MET	-	expression tag	UNP P04798
B	29	ALA	-	expression tag	UNP P04798
B	30	LYS	-	expression tag	UNP P04798
B	31	LYS	-	expression tag	UNP P04798
B	32	THR	-	expression tag	UNP P04798
B	33	SER	-	expression tag	UNP P04798
B	34	SER	-	expression tag	UNP P04798
B	513	HIS	-	expression tag	UNP P04798

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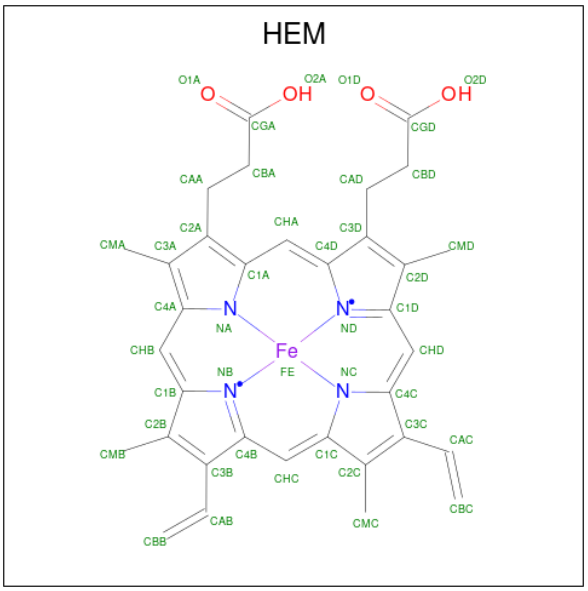
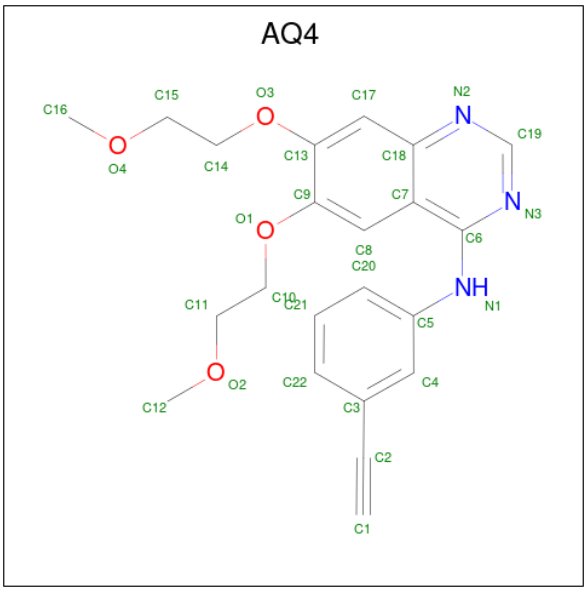
Chain	Residue	Modelled	Actual	Comment	Reference
B	514	HIS	-	expression tag	UNP P04798
B	515	HIS	-	expression tag	UNP P04798
B	516	HIS	-	expression tag	UNP P04798
B	517	HIS	-	expression tag	UNP P04798
B	518	HIS	-	expression tag	UNP P04798
C	28	MET	-	expression tag	UNP P04798
C	29	ALA	-	expression tag	UNP P04798
C	30	LYS	-	expression tag	UNP P04798
C	31	LYS	-	expression tag	UNP P04798
C	32	THR	-	expression tag	UNP P04798
C	33	SER	-	expression tag	UNP P04798
C	34	SER	-	expression tag	UNP P04798
C	513	HIS	-	expression tag	UNP P04798
C	514	HIS	-	expression tag	UNP P04798
C	515	HIS	-	expression tag	UNP P04798
C	516	HIS	-	expression tag	UNP P04798
C	517	HIS	-	expression tag	UNP P04798
C	518	HIS	-	expression tag	UNP P04798
D	28	MET	-	expression tag	UNP P04798
D	29	ALA	-	expression tag	UNP P04798
D	30	LYS	-	expression tag	UNP P04798
D	31	LYS	-	expression tag	UNP P04798
D	32	THR	-	expression tag	UNP P04798
D	33	SER	-	expression tag	UNP P04798
D	34	SER	-	expression tag	UNP P04798
D	513	HIS	-	expression tag	UNP P04798
D	514	HIS	-	expression tag	UNP P04798
D	515	HIS	-	expression tag	UNP P04798
D	516	HIS	-	expression tag	UNP P04798
D	517	HIS	-	expression tag	UNP P04798
D	518	HIS	-	expression tag	UNP P04798

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



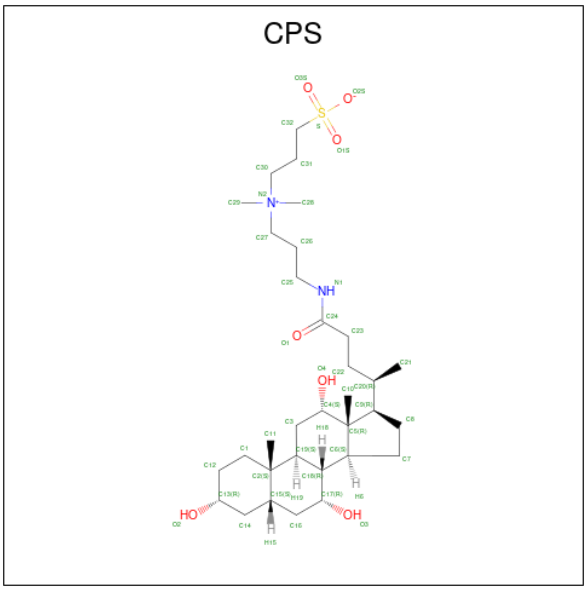
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Fe	H	N	O		
2	A	1	73	34	1	30	4	4	0	0
			Total	C	Fe	H	N	O		
2	B	1	73	34	1	30	4	4	0	0
			Total	C	Fe	H	N	O		
2	C	1	73	34	1	30	4	4	0	0
			Total	C	Fe	H	N	O		
2	D	1	73	34	1	30	4	4	0	0

- Molecule 3 is [6,7-BIS(2-METHOXY-ETHOXY)QUINAZOLINE-4-YL]-(3-ETHYNYLPHENYL)AMINE (three-letter code: AQ4) (formula: $C_{22}H_{23}N_3O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
3	A	1	52	22	23	3	4	0	0
			Total	C	H	N	O		
3	B	1	52	22	23	3	4	0	0
			Total	C	H	N	O		
3	C	1	36	18	13	3	2	0	0
			Total	C	H	N	O		
3	D	1	33	17	11	3	2	0	0

- Molecule 4 is 3-[(3-CHOLAMIDOPROPYL)DIMETHYLAMMONIO]-1-PROPANESULFONATE (three-letter code: CPS) (formula: $C_{32}H_{58}N_2O_7S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	65	23	39		3	0	0
			Total	C	H	N	O		
4	B	1	72	25	42	1	4	0	0

- Molecule 5 is water.

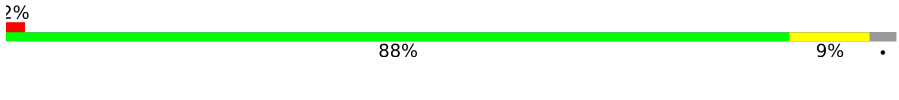
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	3	3	3	0	0
			Total	O		
5	B	1	1	1	0	0

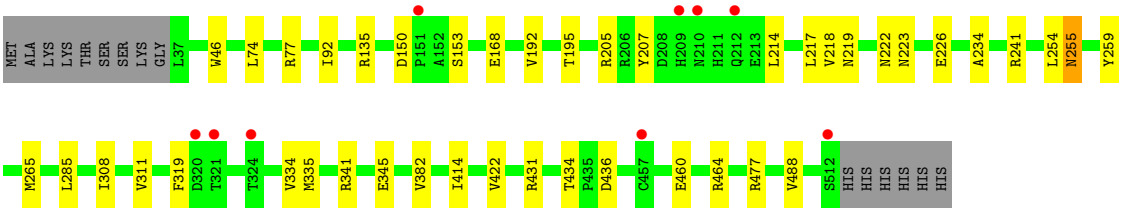
3 Residue-property plots (i)

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: Cytochrome P450 1A1

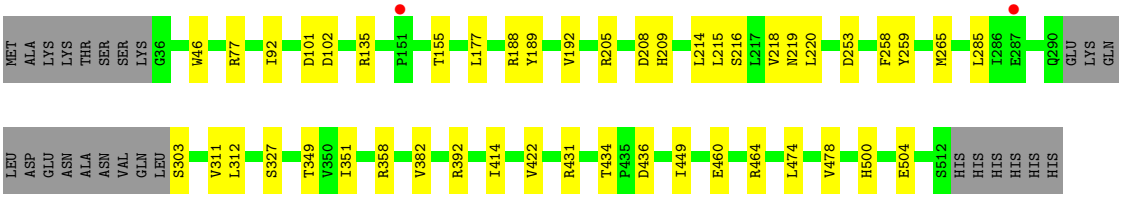
Chain A:





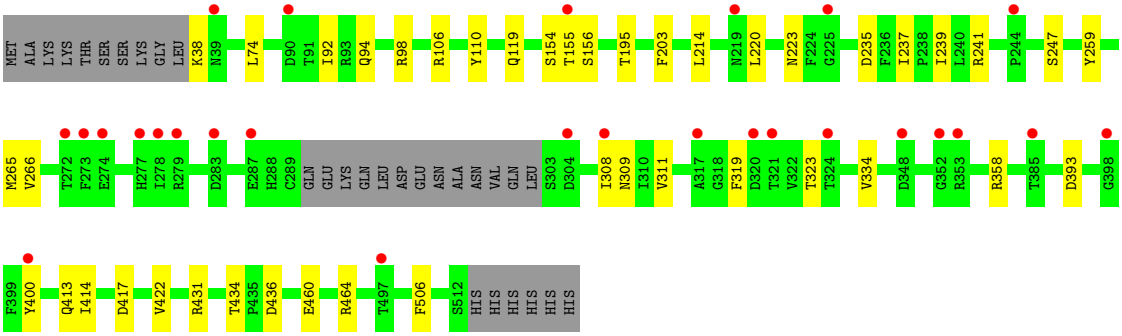
• Molecule 1: Cytochrome P450 1A1

Chain B:



• Molecule 1: Cytochrome P450 1A1

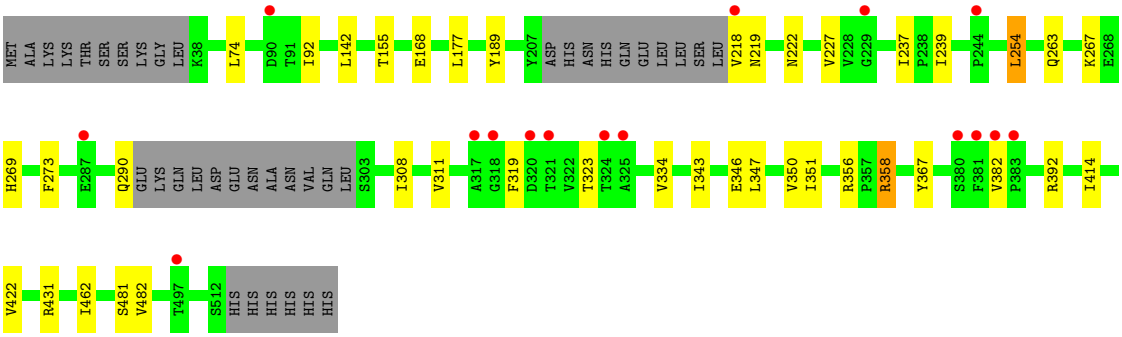
Chain C:



• Molecule 1: Cytochrome P450 1A1

Chain D:

3%
84%
8%
8%


MET ALA LYS LYS THR SER SER LYS GLY LEU K38 L74 D90 T91 I92 L142 T155 E168 L177 Y189 Y207 ASP HIS ASN HIS GLN GLU LEU LEU SER LEU V218 N219 N222 V227 V228 G229 I237 P238 I239 P244 L254 Q263 K267 E268
H269 F273 E287 Q290 GLU LYS GLN LEU ASP GLU ASN ALA ASN VAL GLN LEU S303 I308 V311 A317 G318 F319 D320 T321 V322 T323 T324 A325 V334 I343 E346 L347 V350 I351 R356 P357 R358 Y367 S380 F381 V382 P383 R392 I414
V422 R431 I462 S481 V482 T497 S512 HIS HIS 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	64.86Å 195.08Å 238.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.98 – 3.00 38.98 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (38.98-3.00) 93.0 (38.98-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.14 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.241 , 0.261 0.241 , 0.262	Depositor DCC
R_{free} test set	1997 reflections (3.26%)	wwPDB-VP
Wilson B-factor (Å^2)	73.9	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 39.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	30308	wwPDB-VP
Average B, all atoms (Å^2)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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: HEM, AQ4, CPS

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	0/3907	0.44	0/5295
1	B	0.26	0/3813	0.43	0/5166
1	C	0.25	0/3792	0.41	0/5138
1	D	0.26	0/3714	0.42	0/5030
All	All	0.26	0/15226	0.43	0/20629

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 (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	3812	3807	3806	28	0
1	B	3719	3718	3716	27	0
1	C	3698	3697	3694	22	0
1	D	3623	3628	3625	22	0
2	A	43	30	30	5	0
2	B	43	30	30	5	0
2	C	43	30	30	5	0
2	D	43	30	30	4	0
3	A	29	23	23	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	29	23	23	2	0
3	C	23	13	11	2	0
3	D	22	11	9	2	0
4	A	26	39	37	1	0
4	B	30	42	40	0	0
5	A	3	0	0	0	0
5	B	1	0	0	0	0
All	All	15187	15121	15104	120	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 4.

The worst 5 of 120 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:ARG:NH2	1:B:504:GLU:OE2	2.08	0.85
1:A:255:ASN:ND2	3:A:602:AQ4:O4	2.16	0.78
1:C:434:THR:OG1	1:C:436:ASP:OD1	2.04	0.76
1:D:155:THR:OG1	1:D:358:ARG:NH2	2.20	0.74
1:D:92:ILE:HD12	1:D:414:ILE:HD11	1.71	0.72

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	474/491 (96%)	463 (98%)	11 (2%)	0	100 100
1	B	461/491 (94%)	449 (97%)	11 (2%)	1 (0%)	47 82
1	C	458/491 (93%)	447 (98%)	11 (2%)	0	100 100
1	D	447/491 (91%)	437 (98%)	10 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1840/1964 (94%)	1796 (98%)	43 (2%)	1 (0%)	51 85

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	449	ILE

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	426/439 (97%)	422 (99%)	4 (1%)	78 92
1	B	415/439 (94%)	411 (99%)	4 (1%)	76 91
1	C	413/439 (94%)	410 (99%)	3 (1%)	84 94
1	D	404/439 (92%)	399 (99%)	5 (1%)	71 90
All	All	1658/1756 (94%)	1642 (99%)	16 (1%)	76 91

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	358	ARG
1	D	290	GLN
1	C	38	LYS
1	D	254	LEU
1	B	303	SER

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

Mol	Chain	Res	Type
1	A	222	ASN
1	A	255	ASN
1	B	344	GLN
1	C	416	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)

10 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	AQ4	A	602	-	31,31,31	1.25	3 (9%)	40,40,40	1.16	5 (12%)
3	AQ4	D	602	-	24,24,31	1.26	2 (8%)	33,33,40	1.33	4 (12%)
2	HEM	A	601	1	41,50,50	1.46	4 (9%)	45,82,82	1.45	6 (13%)
4	CPS	B	603	-	33,33,45	0.66	0	52,52,70	1.91	17 (32%)
2	HEM	D	601	-	41,50,50	1.46	4 (9%)	45,82,82	1.19	4 (8%)
3	AQ4	C	602	-	25,25,31	1.17	2 (8%)	34,34,40	1.37	6 (17%)
3	AQ4	B	602	-	31,31,31	1.19	2 (6%)	40,40,40	1.09	4 (10%)
4	CPS	A	603	-	29,29,45	1.01	1 (3%)	47,47,70	2.02	15 (31%)
2	HEM	B	601	-	41,50,50	1.47	4 (9%)	45,82,82	1.03	2 (4%)
2	HEM	C	601	-	41,50,50	1.46	4 (9%)	45,82,82	1.31	4 (8%)

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	AQ4	A	602	-	-	7/16/16/16	0/3/3/3
3	AQ4	D	602	-	-	3/8/8/16	0/3/3/3
2	HEM	A	601	1	-	2/12/54/54	-
4	CPS	B	603	-	-	3/11/76/90	0/4/4/4
2	HEM	D	601	-	-	2/12/54/54	-
3	AQ4	C	602	-	-	4/9/9/16	0/3/3/3
3	AQ4	B	602	-	-	5/16/16/16	0/3/3/3
4	CPS	A	603	-	-	0/6/71/90	0/4/4/4
2	HEM	B	601	-	-	4/12/54/54	-
2	HEM	C	601	-	-	2/12/54/54	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	HEM	C3C-C2C	-4.17	1.34	1.40
2	C	601	HEM	C3C-C2C	-4.03	1.34	1.40
2	D	601	HEM	C3C-C2C	-4.02	1.34	1.40
3	D	602	AQ4	C6-N1	3.83	1.42	1.36
3	A	602	AQ4	C6-N1	3.79	1.42	1.36

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	603	CPS	C5-C9-C20	-6.14	112.16	119.50
4	B	603	CPS	C5-C9-C20	-5.88	112.47	119.50
4	A	603	CPS	C19-C18-C6	-4.70	103.26	109.71
4	A	603	CPS	C5-C6-C18	-4.00	109.63	114.74
4	B	603	CPS	C22-C23-C24	-3.88	104.38	113.04

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	AQ4	C1-C2-C3-C4
3	A	602	AQ4	C1-C2-C3-C22
3	A	602	AQ4	O1-C10-C11-O2
3	A	602	AQ4	O3-C14-C15-O4
3	D	602	AQ4	C13-C9-O1-C10

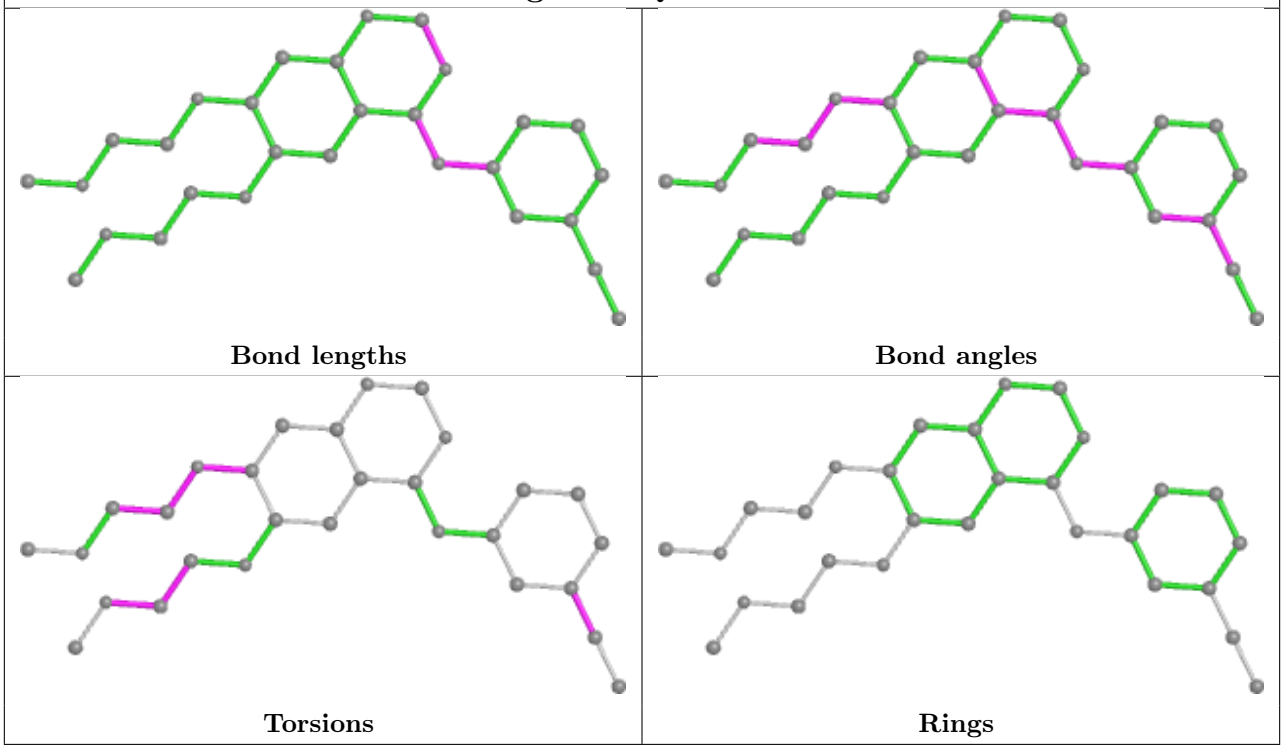
There are no ring outliers.

9 monomers are involved in 33 short contacts:

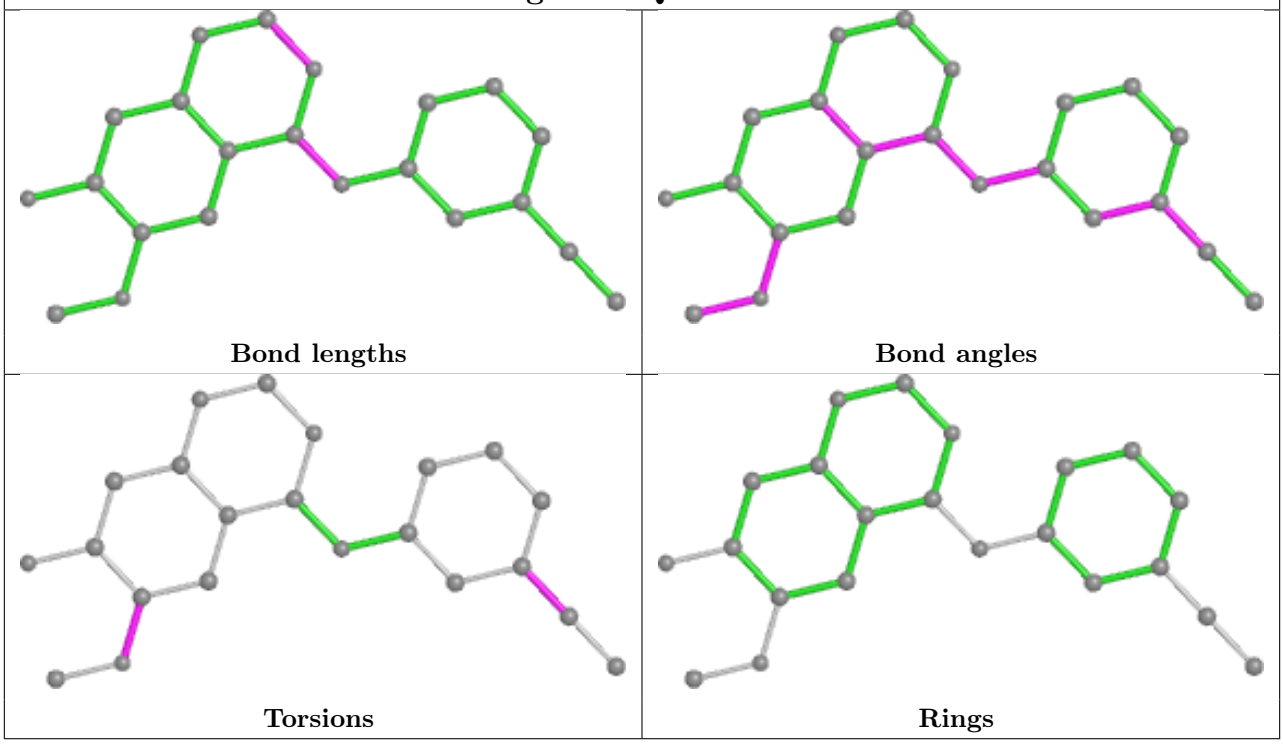
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	AQ4	7	0
3	D	602	AQ4	2	0
2	A	601	HEM	5	0
2	D	601	HEM	4	0
3	C	602	AQ4	2	0
3	B	602	AQ4	2	0
4	A	603	CPS	1	0
2	B	601	HEM	5	0
2	C	601	HEM	5	0

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.

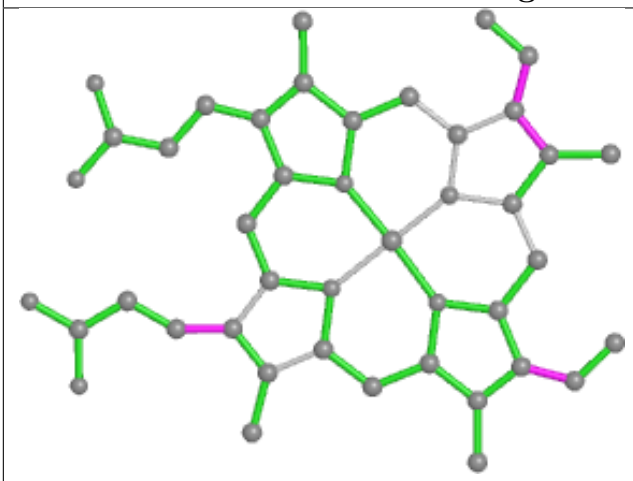
Ligand AQ4 A 602



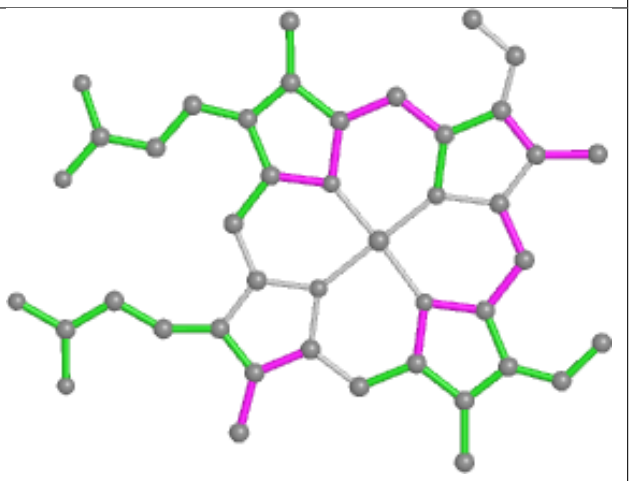
Ligand AQ4 D 602



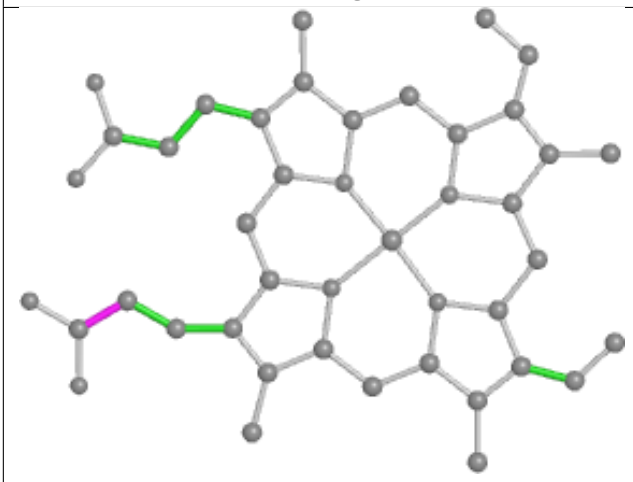
Ligand HEM A 601



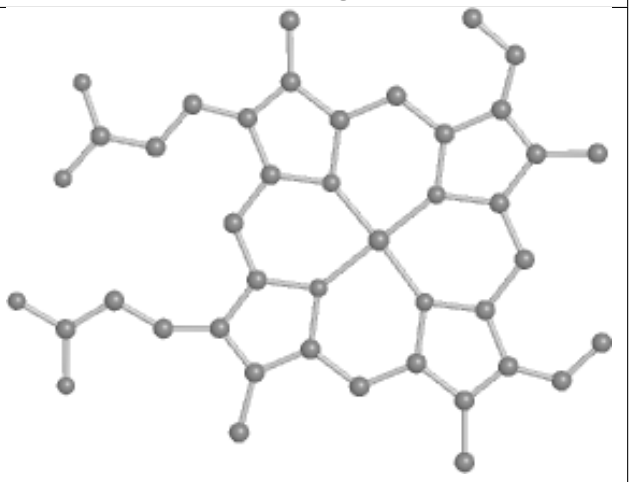
Bond lengths



Bond angles

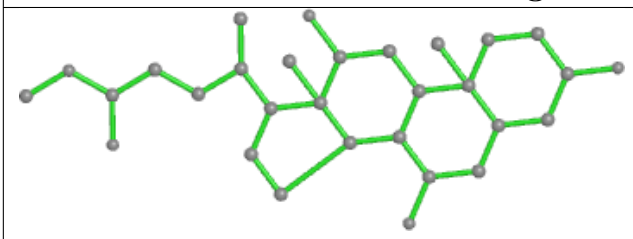


Torsions

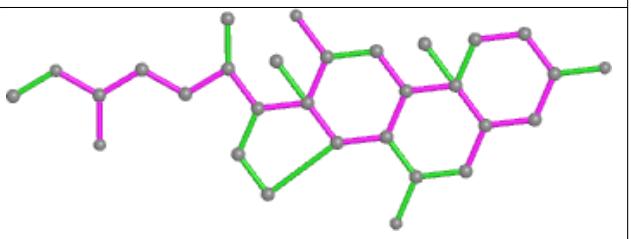


Rings

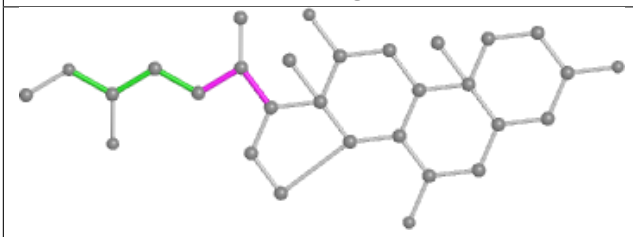
Ligand CPS B 603



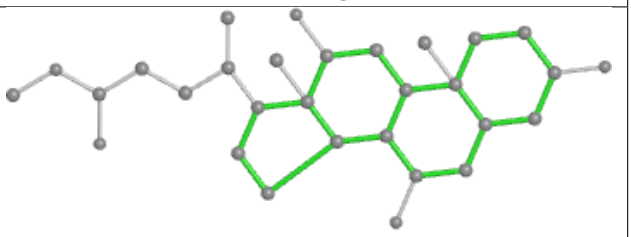
Bond lengths



Bond angles

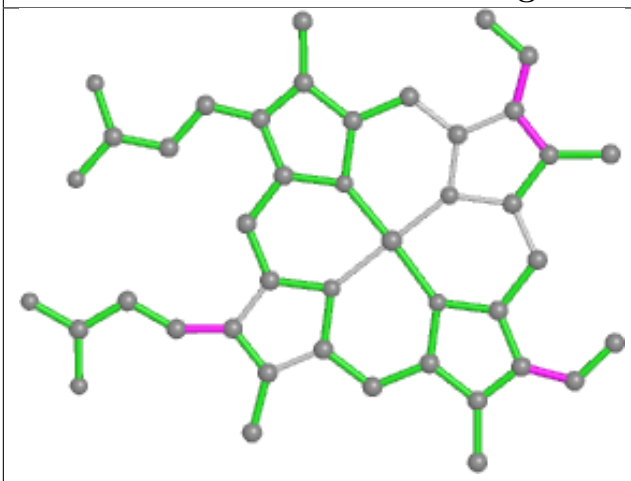


Torsions

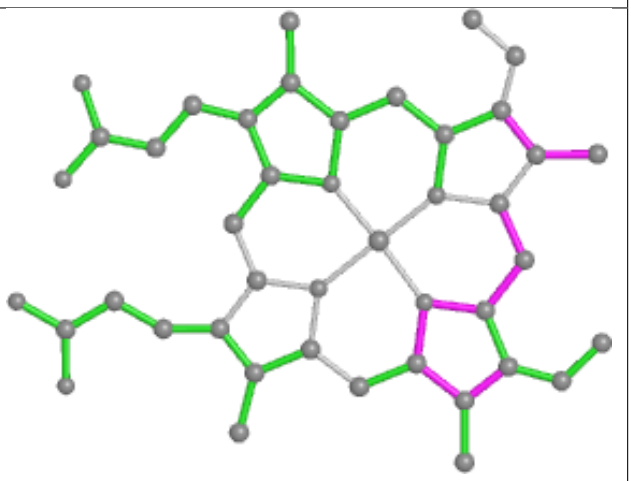


Rings

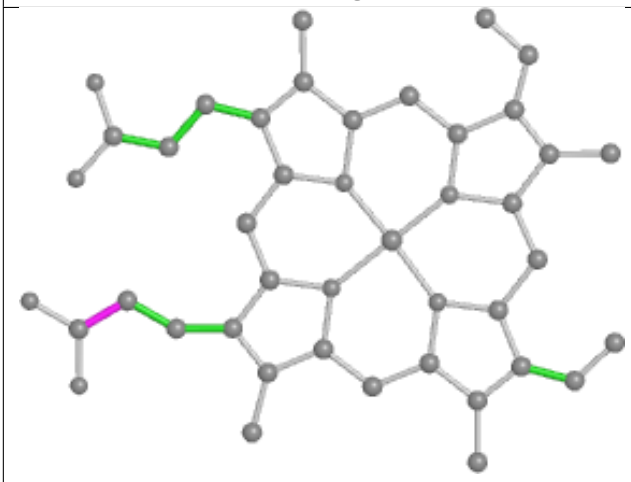
Ligand HEM D 601



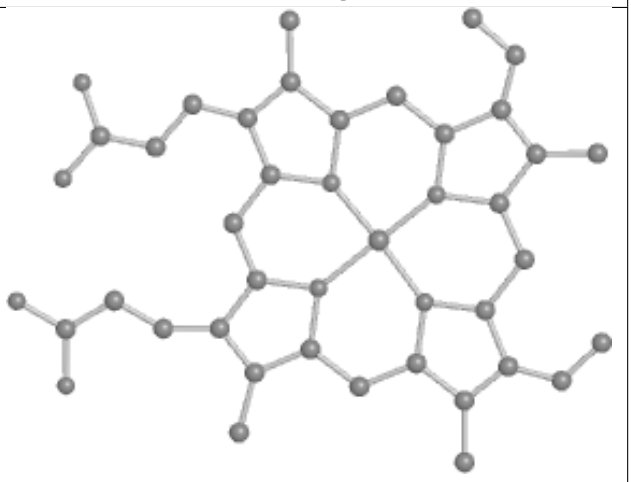
Bond lengths



Bond angles

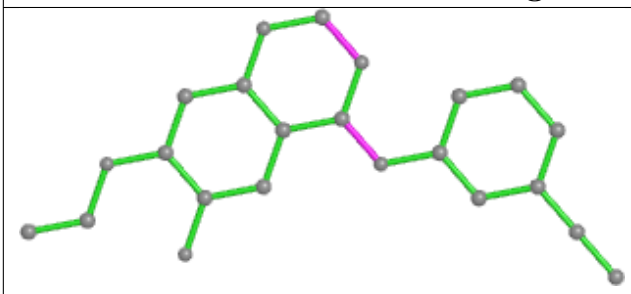


Torsions

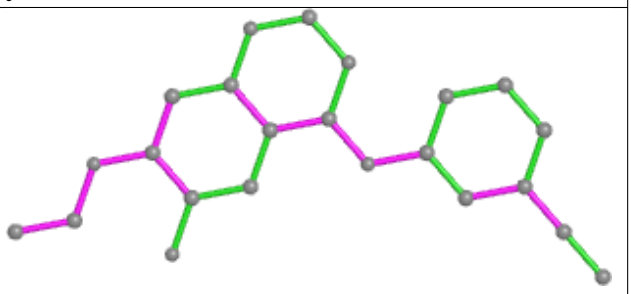


Rings

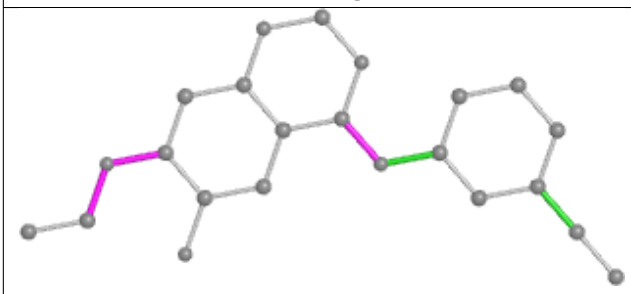
Ligand AQ4 C 602



Bond lengths



Bond angles



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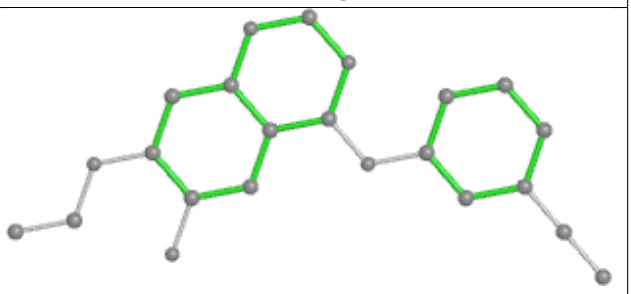
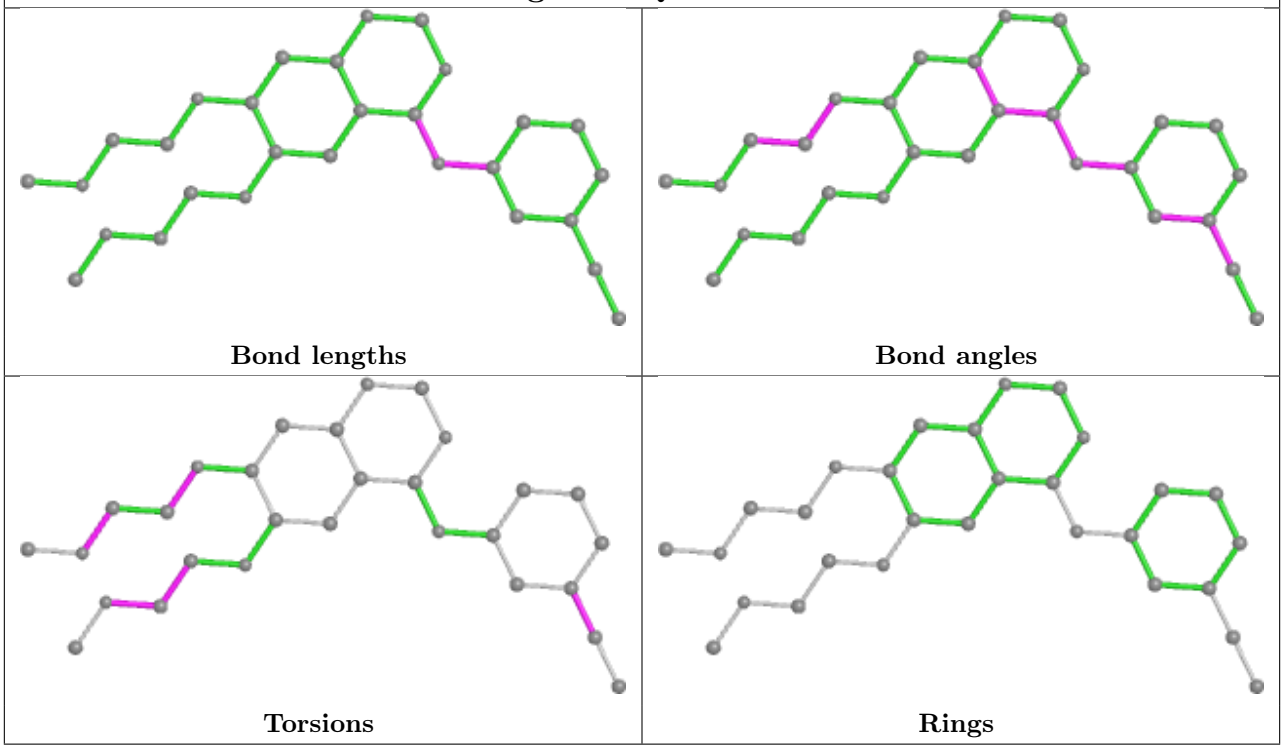
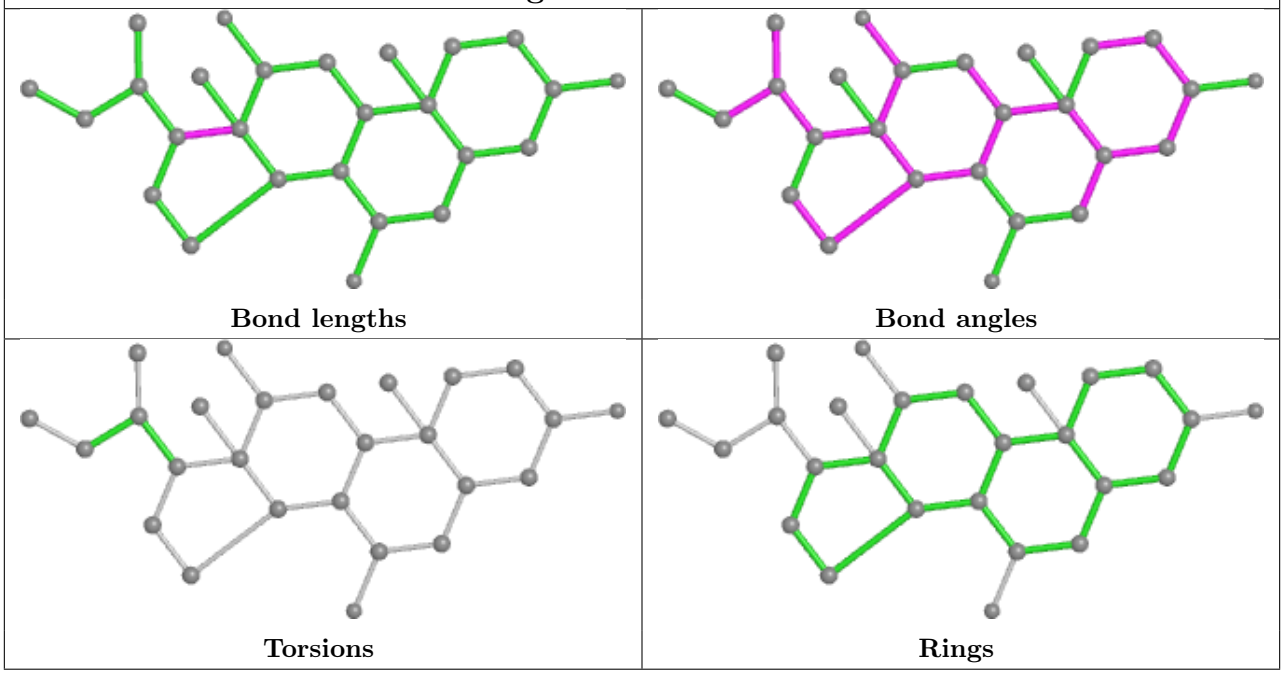


Rings

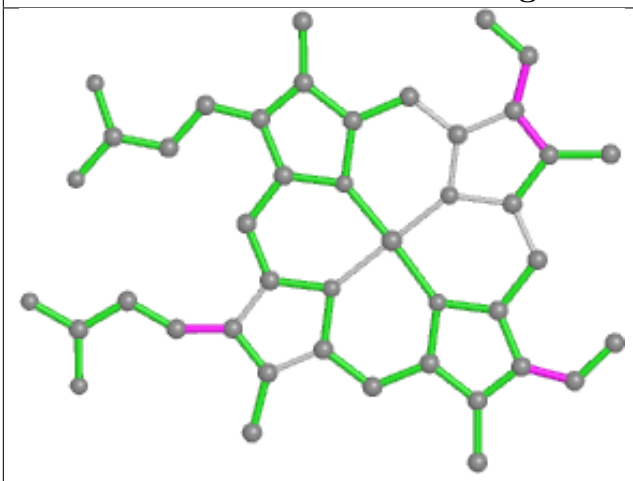
Ligand AQ4 B 602



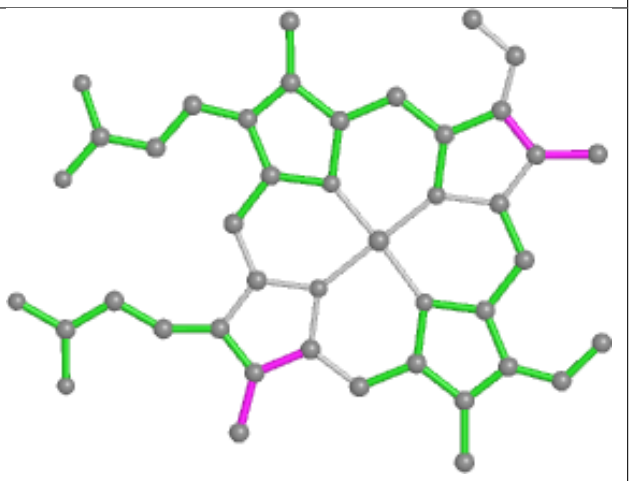
Ligand CPS A 603



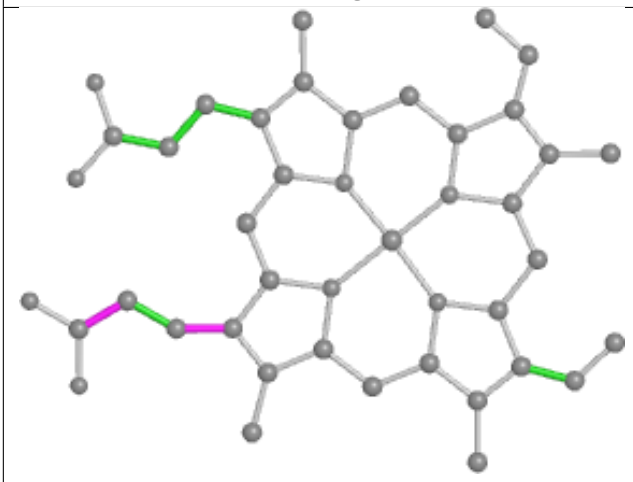
Ligand HEM B 601



Bond lengths



Bond angles



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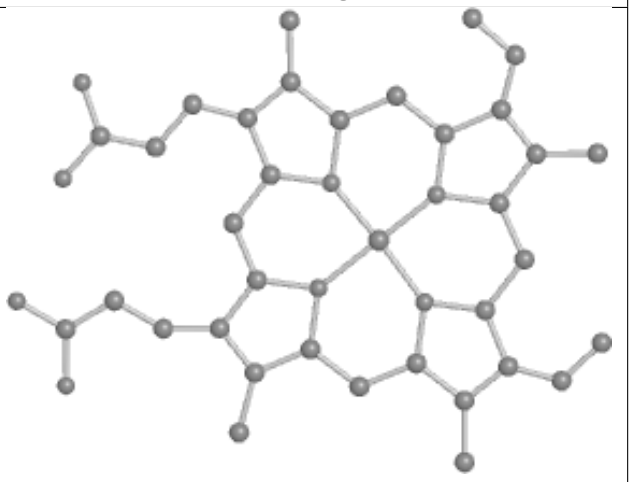
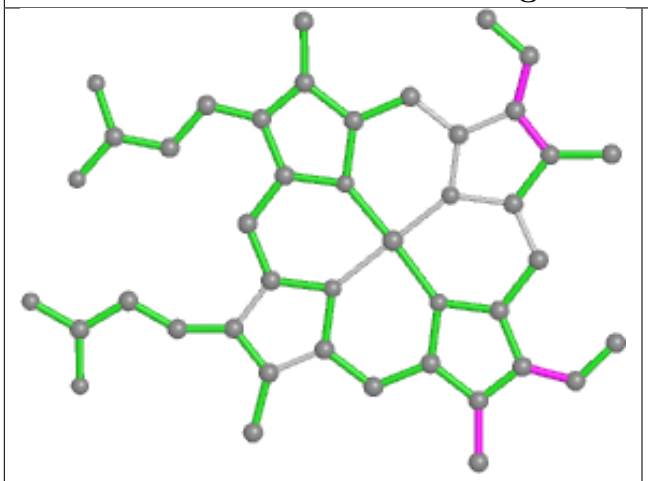


Rings

Ligand HEM C 601



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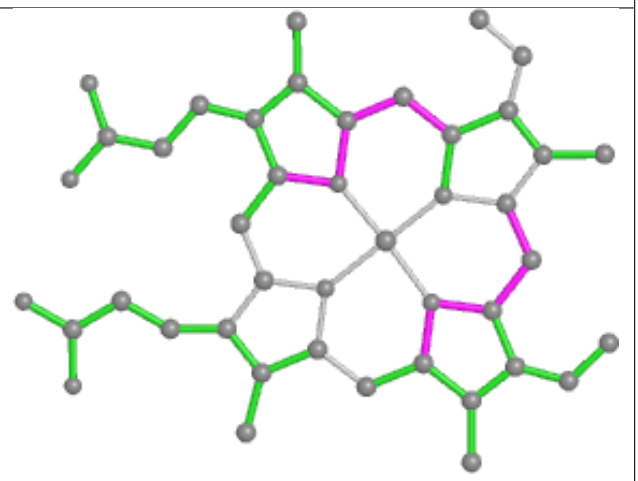
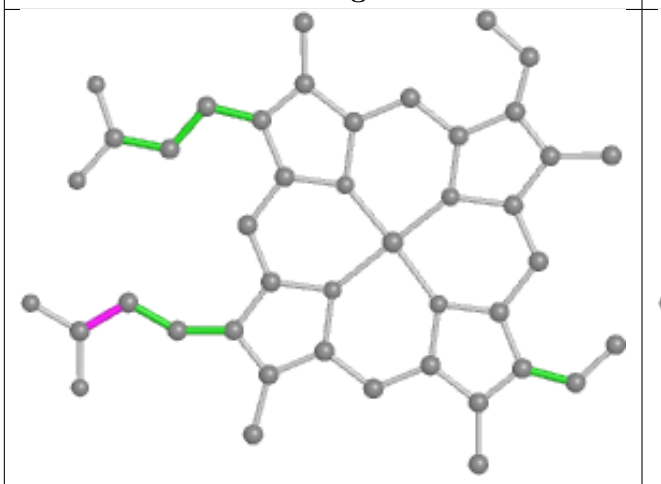


Bond angles



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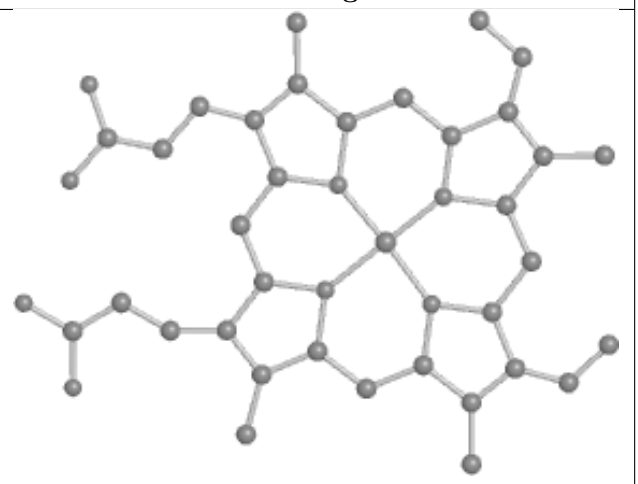


Rings

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	476/491 (96%)	0.19	9 (1%)	66	37	47, 70, 107, 137	0
1	B	465/491 (94%)	0.17	2 (0%)	92	79	47, 75, 116, 143	0
1	C	462/491 (94%)	0.44	27 (5%)	23	7	82, 109, 129, 150	0
1	D	453/491 (92%)	0.41	16 (3%)	44	18	69, 98, 124, 141	0
All	All	1856/1964 (94%)	0.30	54 (2%)	51	23	47, 90, 124, 150	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	398	GLY	4.5
1	C	273	PHE	3.4
1	C	320	ASP	3.2
1	C	308	ILE	3.2
1	D	317	ALA	3.2

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)

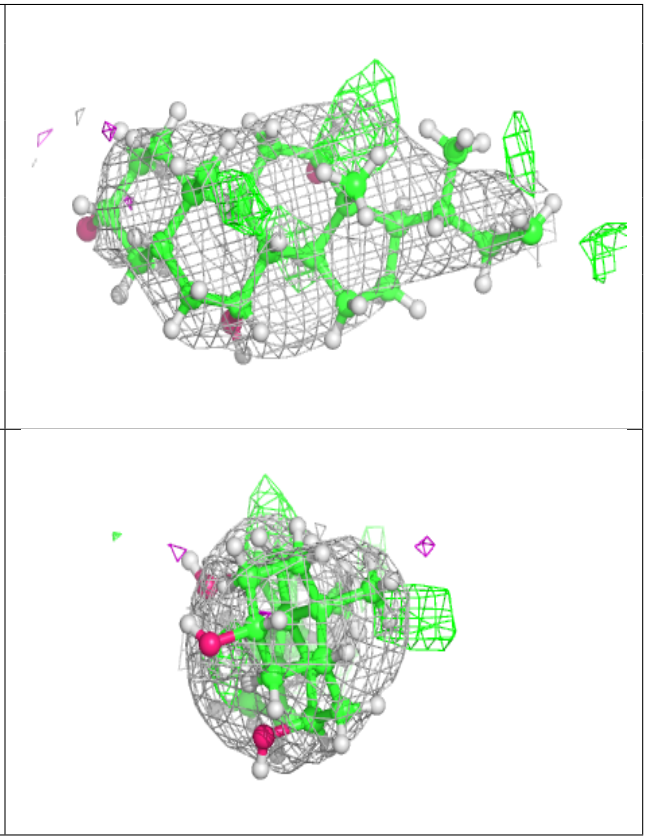
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	CPS	A	603	26/42	0.82	0.36	72,93,110,115	0
4	CPS	B	603	30/42	0.83	0.46	92,119,131,148	0
3	AQ4	B	602	29/29	0.85	0.33	66,81,101,103	0
2	HEM	A	601	43/43	0.85	0.39	43,52,67,162	0
2	HEM	B	601	43/43	0.85	0.43	54,77,90,240	0
3	AQ4	A	602	29/29	0.88	0.35	47,66,92,102	0
3	AQ4	D	602	22/29	0.89	0.35	79,96,116,117	0
2	HEM	D	601	43/43	0.90	0.45	75,87,105,116	0
3	AQ4	C	602	23/29	0.92	0.37	89,105,127,132	0
2	HEM	C	601	43/43	0.94	0.45	84,100,121,125	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.

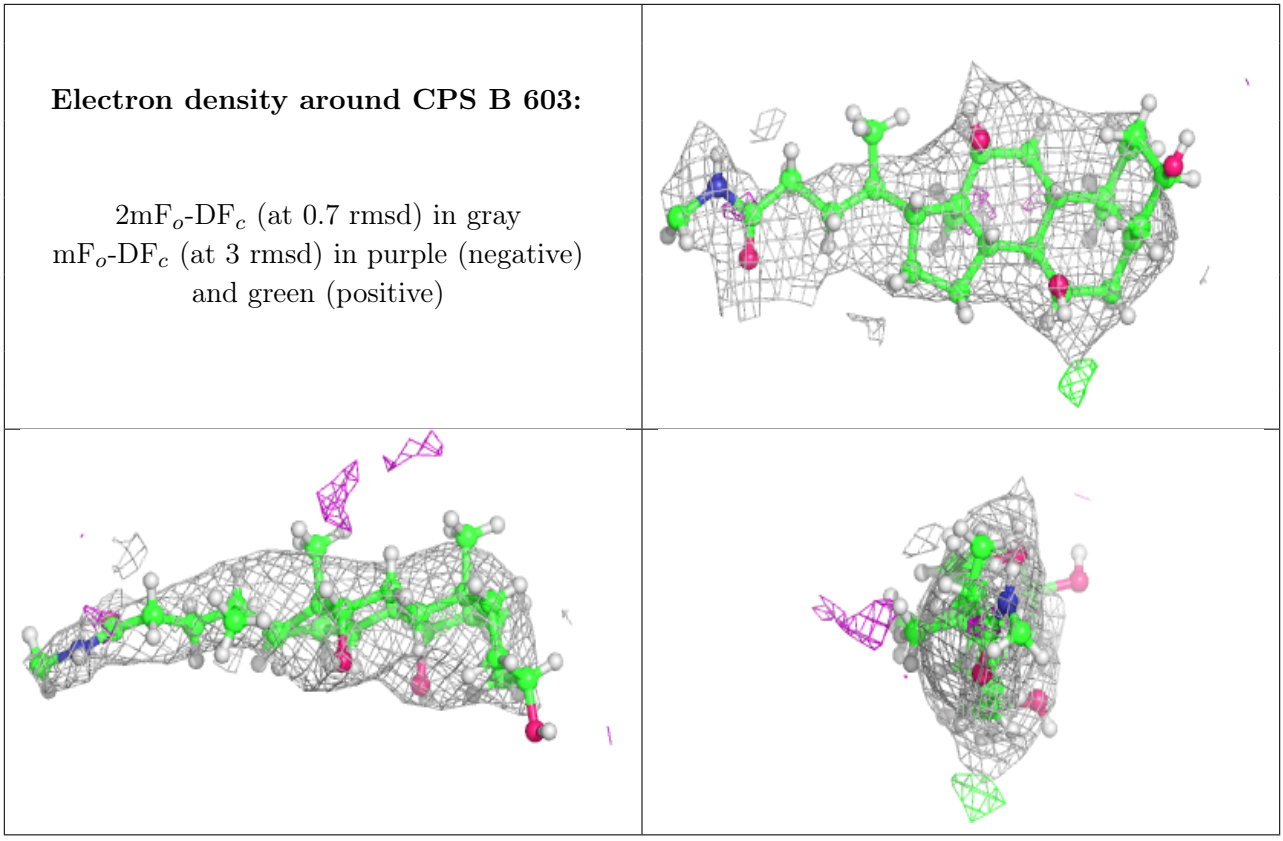
Electron density around CPS A 603:

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 CPS B 603:

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



Electron density around AQ4 B 602:

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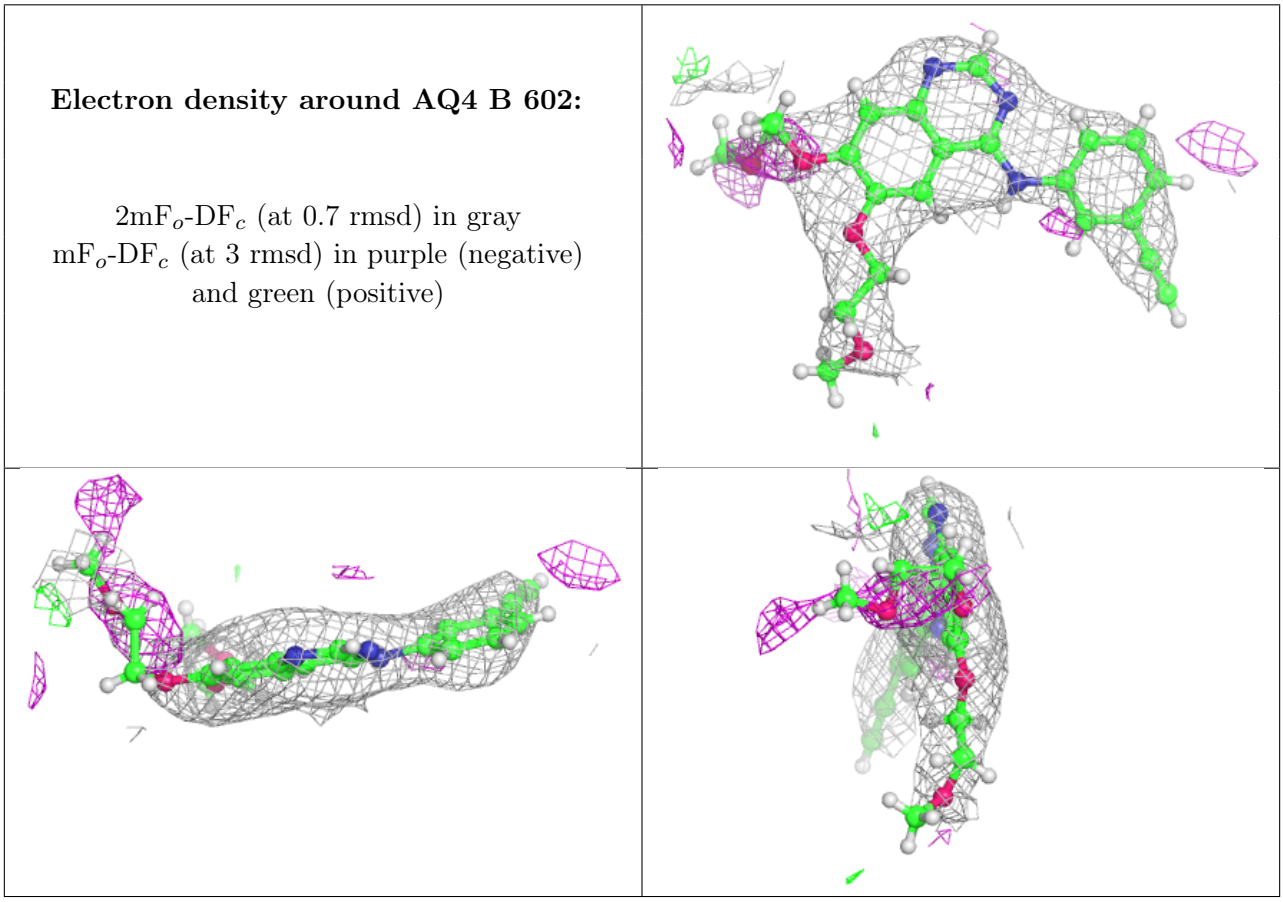
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 601:

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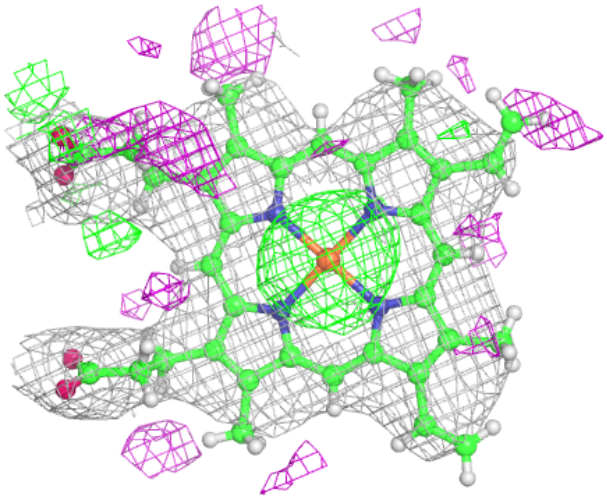
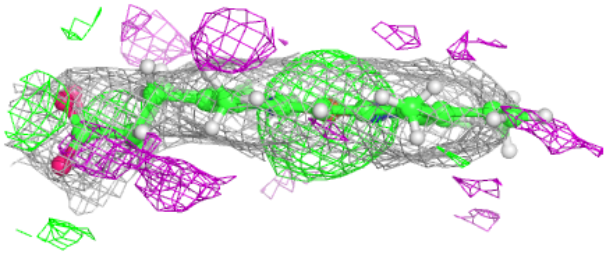
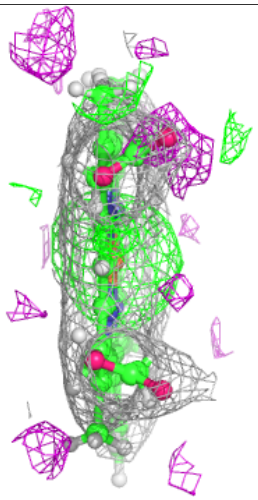
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around HEM B 601:

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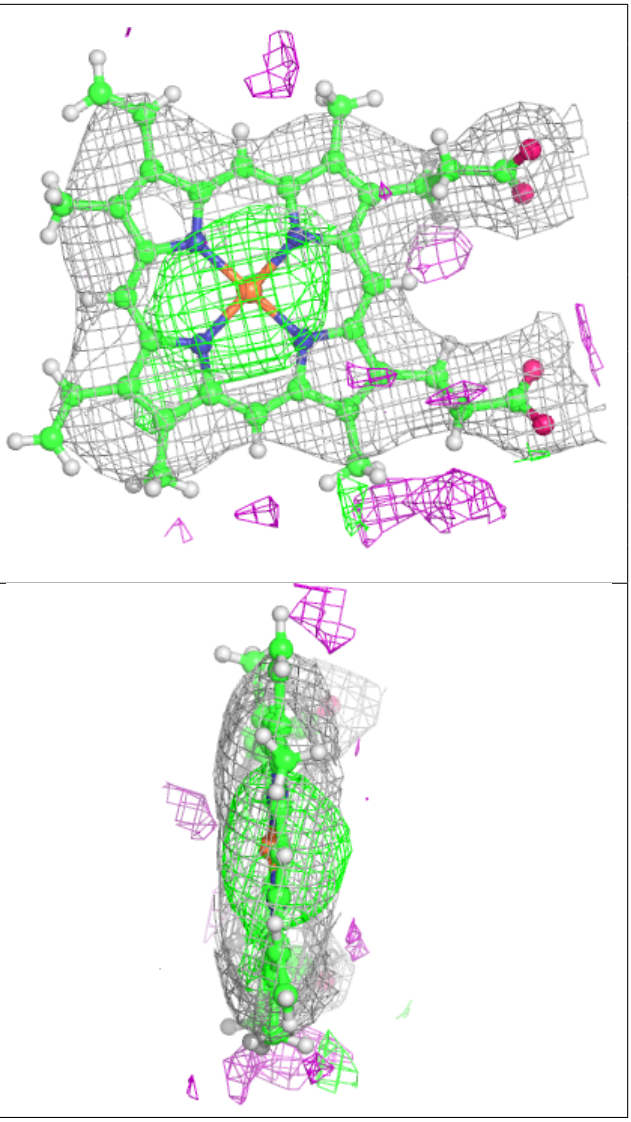
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around AQ4 A 602:

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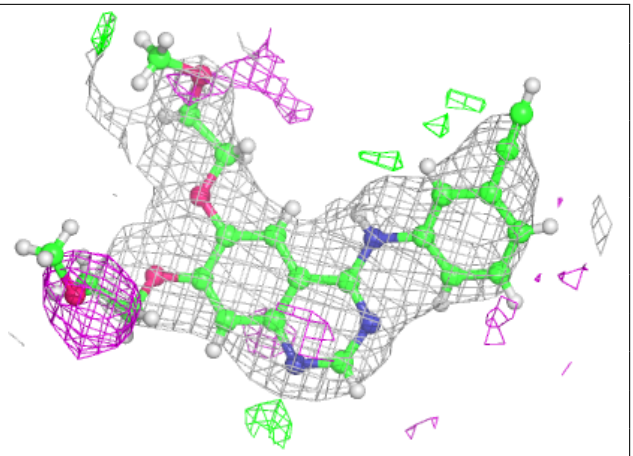
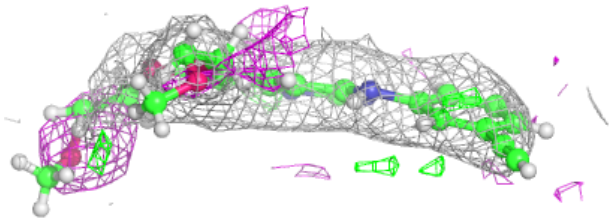
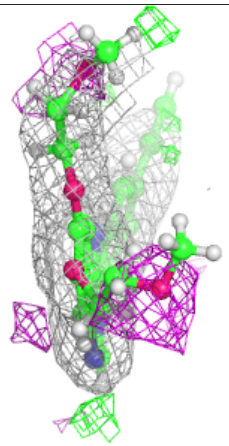
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around AQ4 D 602:

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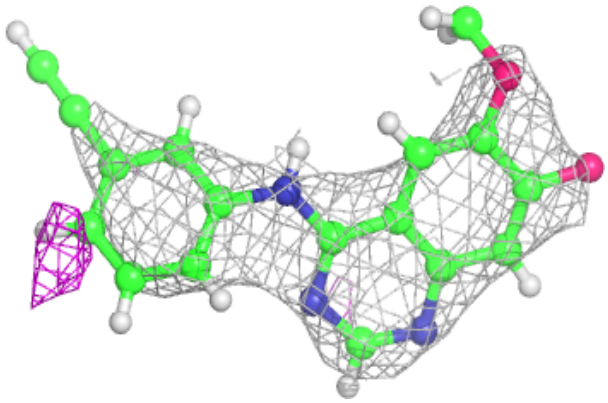
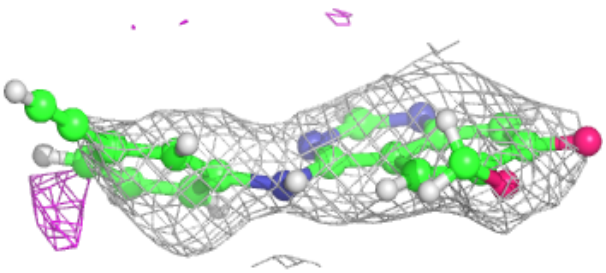
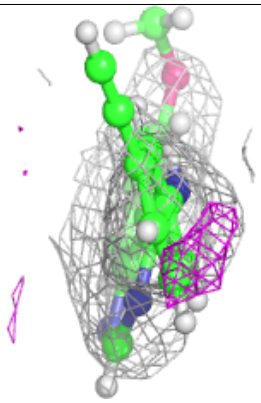
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

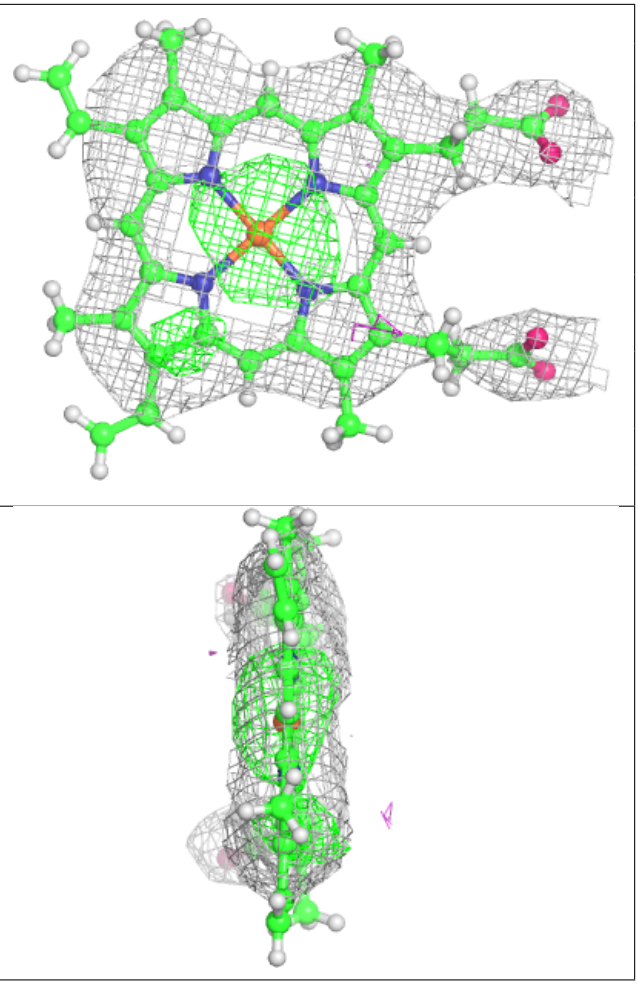






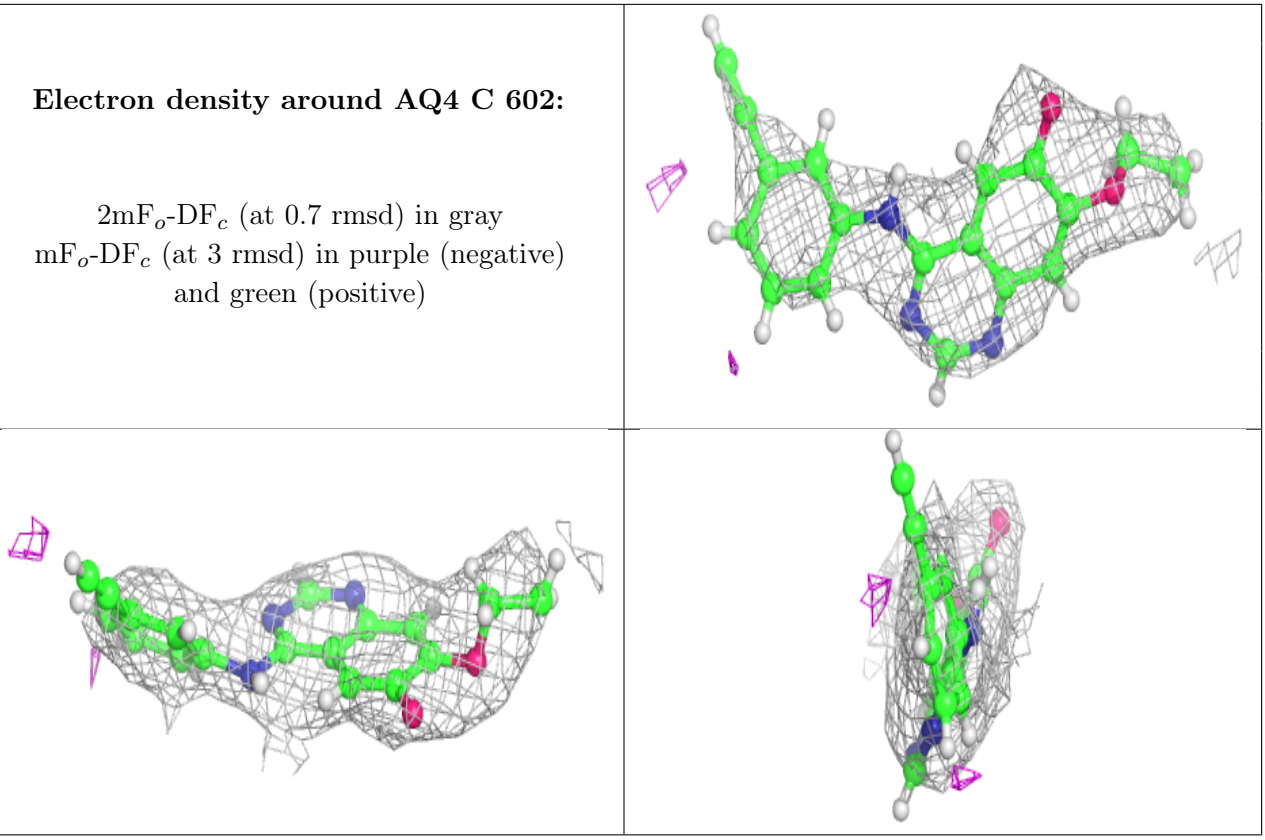
Electron density around HEM D 601:

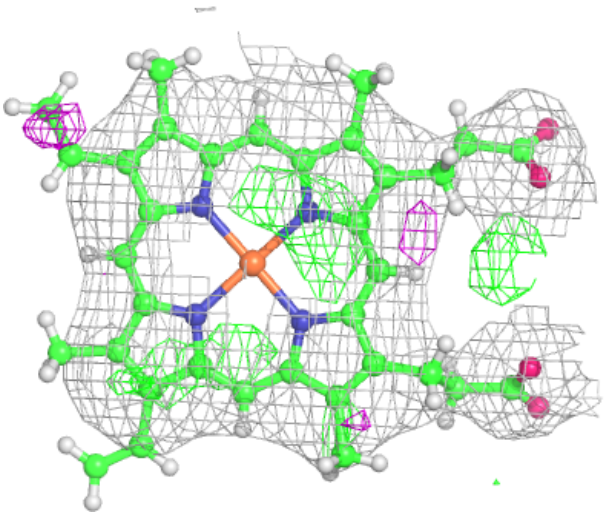
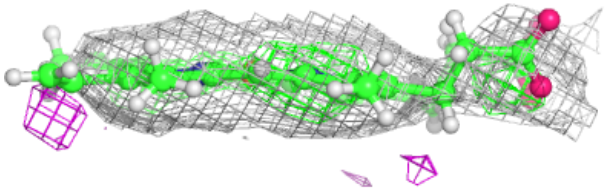
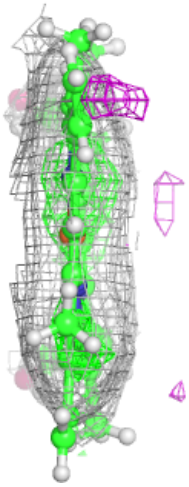
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around AQ4 C 602:

$2mF_o$-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 601: 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.