wwPDB X-ray Structure Validation Summary Report (i)

May 25, 2020 – 01:02 pm BST

PDB ID	:	1QO8
Title	:	The structure of the open conformation of a flavocytochrome c3 fumarate reductase
Authors	:	Bamford, V.; Dobbin, P.S.; Richardson, D.J.; Hemmings, A.M.
Deposited on	:	1999-11-04
Resolution	:	2.15 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 following versions of software and data (see references (1)) were used in the production of this report:

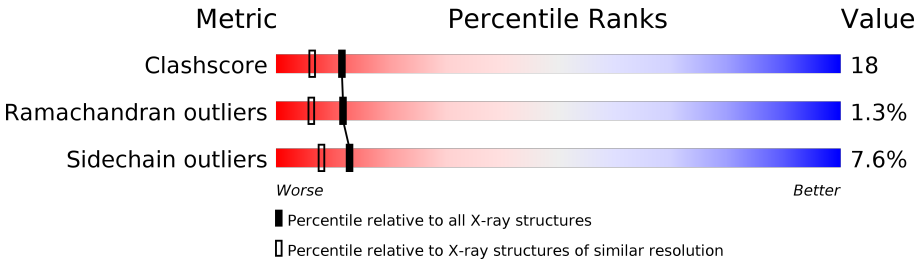
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.15 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))
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	566	68% 23% 6%
1	D	566	63% 30% 6%

2 Entry composition

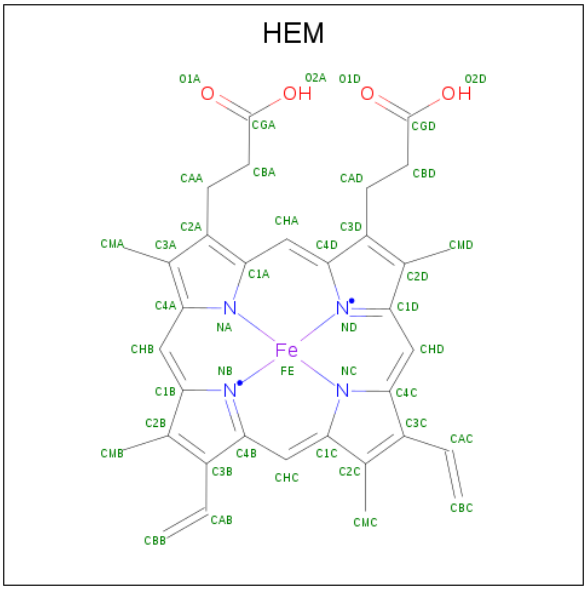
There are 4 unique types of molecules in this entry. The entry contains 9425 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FLAVOCYTOCHROME C3 FUMARATE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	564	Total	C	N	O	S	0	0	0
			4234	2627	753	826	28			
1	D	564	Total	C	N	O	S	0	0	0
			4234	2627	753	826	28			

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

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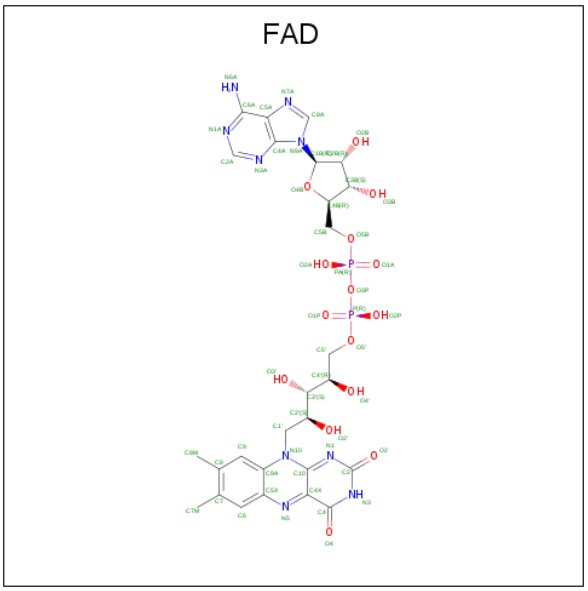
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	358	Total	O	0	0
			358	358		
4	D	149	Total	O	0	0
			149	149		

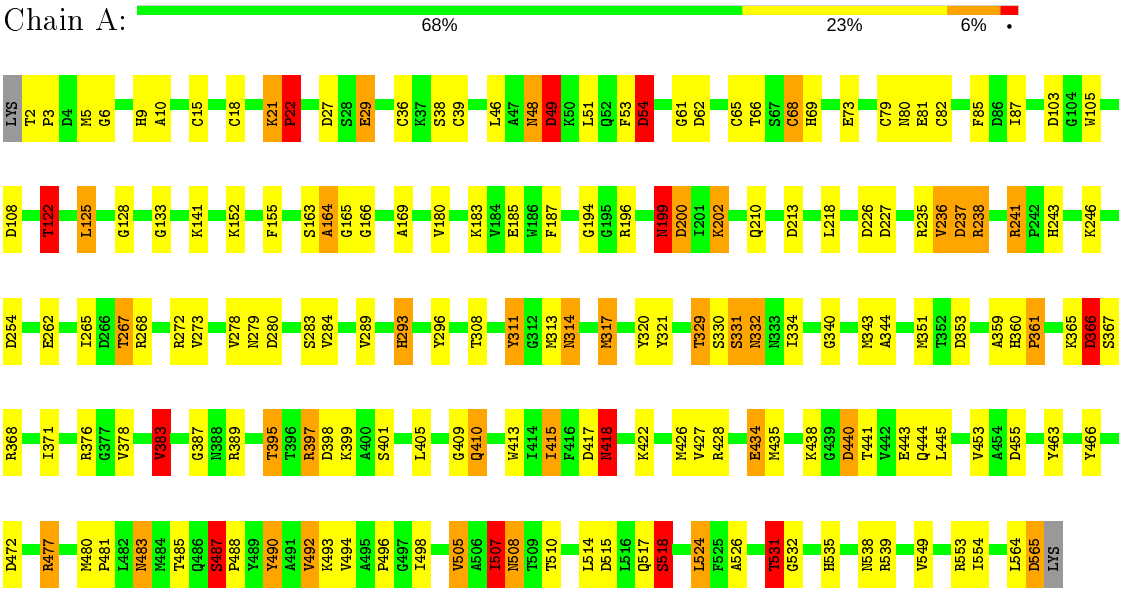
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

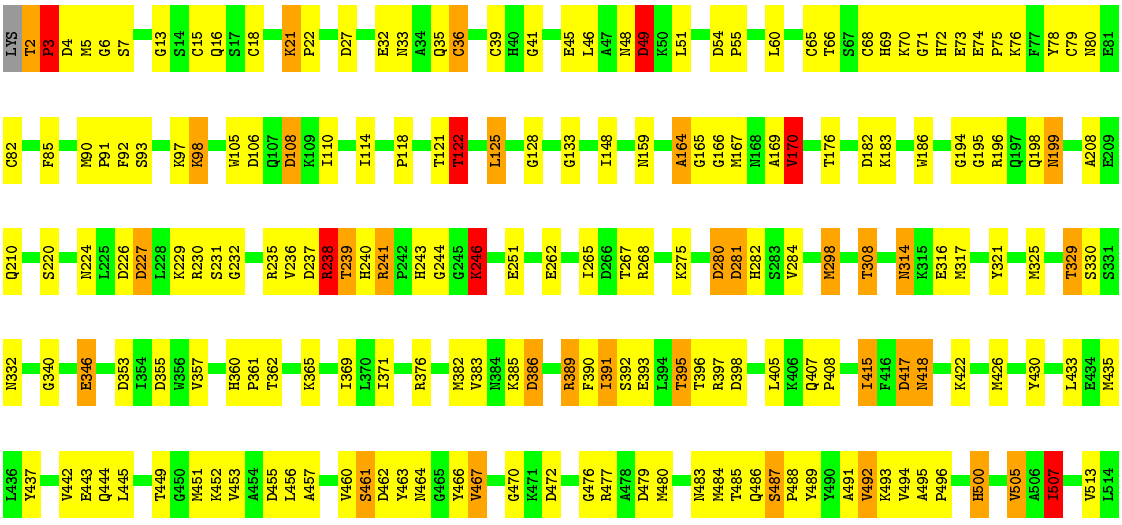
- Molecule 1: FLAVOCYTOCHROME C3 FUMARATE REDUCTASE

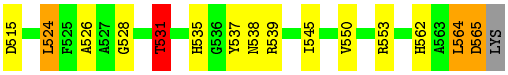
Chain A:



- Molecule 1: FLAVOCYTOCHROME C3 FUMARATE REDUCTASE

Chain D:




D515
L524
F525
A526
A527
G528
T531
H535
G536
Y537
N538
R539
I545
V550
R553
H562
A563
L564
D565
LYS

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.77Å 109.69Å 227.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.15	Depositor
% Data completeness (in resolution range)	93.4 (20.00-2.15)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.225 , 0.281	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9425	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.94	4/4312 (0.1%)	1.94	119/5820 (2.0%)
1	D	0.61	0/4312	1.47	49/5820 (0.8%)
All	All	0.79	4/8624 (0.0%)	1.72	168/11640 (1.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	10
1	D	0	2
All	All	0	12

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	164	ALA	CA-CB	6.30	1.65	1.52
1	A	330	SER	CB-OG	5.81	1.49	1.42
1	A	61	GLY	CA-C	5.12	1.60	1.51
1	A	330	SER	CA-CB	5.09	1.60	1.52

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	376	ARG	NE-CZ-NH2	23.64	132.12	120.30
1	A	428	ARG	NE-CZ-NH1	18.82	129.71	120.30
1	D	196	ARG	NE-CZ-NH2	-16.45	112.08	120.30
1	A	368	ARG	NE-CZ-NH1	16.34	128.47	120.30
1	A	241	ARG	NE-CZ-NH1	16.24	128.42	120.30

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	21	LYS	Peptide
1	A	246	LYS	Peptide
1	A	311	TYR	Mainchain
1	A	5	MET	Mainchain
1	A	68	CYS	Mainchain

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	4234	0	4153	138	0
1	D	4234	0	4154	157	0
2	A	172	0	120	42	0
2	D	172	0	120	33	0
3	A	53	0	30	1	0
3	D	53	0	31	0	0
4	A	358	0	0	17	1
4	D	149	0	0	11	1
All	All	9425	0	8608	307	1

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 18.

The worst 5 of 307 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:CYS:SG	2:A:602:HEM:CAB	2.34	1.15
1:A:36:CYS:SG	2:A:603:HEM:CAB	2.35	1.13
1:A:82:CYS:SG	2:A:601:HEM:CAC	2.39	1.11
1:A:79:CYS:SG	2:A:601:HEM:CAB	2.39	1.10
1:A:68:CYS:SG	2:A:602:HEM:CAC	2.41	1.07

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2135:HOH:O	4:D:2105:HOH:O[3_655]	2.19	0.01

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	562/566 (99%)	523 (93%)	33 (6%)	6 (1%)	14 8
1	D	562/566 (99%)	511 (91%)	42 (8%)	9 (2%)	9 4
All	All	1124/1132 (99%)	1034 (92%)	75 (7%)	15 (1%)	12 6

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	22	PRO
1	D	3	PRO
1	D	391	ILE
1	D	487	SER
1	A	49	ASP

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	446/448 (100%)	420 (94%)	26 (6%)	20 15
1	D	446/448 (100%)	404 (91%)	42 (9%)	8 4
All	All	892/896 (100%)	824 (92%)	68 (8%)	13 8

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	98	LYS
1	D	199	ASN
1	D	467	VAL
1	D	105	TRP
1	D	122	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	508	ASN
1	D	197	GLN
1	D	360	HIS
1	A	483	ASN
1	D	388	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

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	FAD	A	605	-	51,58,58	2.19	18 (35%)	60,89,89	1.92	19 (31%)
2	HEM	A	602	1	27,50,50	2.49	11 (40%)	17,82,82	2.60	8 (47%)
2	HEM	D	603	1	27,50,50	1.96	5 (18%)	17,82,82	2.84	7 (41%)
2	HEM	A	601	1	27,50,50	2.44	6 (22%)	17,82,82	2.40	7 (41%)
2	HEM	A	604	1	27,50,50	2.29	8 (29%)	17,82,82	3.58	10 (58%)
2	HEM	D	604	1	27,50,50	2.00	5 (18%)	17,82,82	7.55	10 (58%)
2	HEM	A	603	1	27,50,50	2.27	10 (37%)	17,82,82	2.36	8 (47%)
2	HEM	D	601	1	27,50,50	2.15	7 (25%)	17,82,82	1.97	7 (41%)
3	FAD	D	605	-	51,58,58	1.98	15 (29%)	60,89,89	2.18	19 (31%)
2	HEM	D	602	1	27,50,50	1.97	6 (22%)	17,82,82	2.84	7 (41%)

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	FAD	A	605	-	-	3/30/50/50	0/6/6/6
2	HEM	A	602	1	-	0/6/54/54	-
2	HEM	D	603	1	-	2/6/54/54	-
2	HEM	A	601	1	-	0/6/54/54	-
2	HEM	A	604	1	-	0/6/54/54	-
2	HEM	D	604	1	-	2/6/54/54	-
2	HEM	A	603	1	-	0/6/54/54	-
2	HEM	D	601	1	-	0/6/54/54	-
3	FAD	D	605	-	-	4/30/50/50	0/6/6/6
2	HEM	D	602	1	-	1/6/54/54	-

The worst 5 of 91 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	605	FAD	C4X-C10	7.51	1.46	1.38
2	A	604	HEM	C3C-C2C	-7.05	1.30	1.40
2	A	602	HEM	C3B-C2B	-6.16	1.31	1.40
2	D	601	HEM	C3C-C2C	-6.07	1.31	1.40
2	A	603	HEM	C3B-C2B	-5.83	1.32	1.40

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	604	HEM	CAD-CBD-CGD	24.25	153.35	112.67
2	D	604	HEM	CBD-CAD-C3D	-13.66	87.30	112.48
2	D	604	HEM	CBA-CAA-C2A	10.63	132.10	112.49
2	D	603	HEM	CBD-CAD-C3D	-9.41	95.14	112.48
2	A	604	HEM	CAA-CBA-CGA	7.74	125.66	112.67

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	604	HEM	C1A-C2A-CAA-CBA
2	D	604	HEM	C3A-C2A-CAA-CBA
3	D	605	FAD	N10-C1'-C2'-C3'
2	D	602	HEM	C2A-CAA-CBA-CGA
3	A	605	FAD	O2'-C2'-C3'-C4'

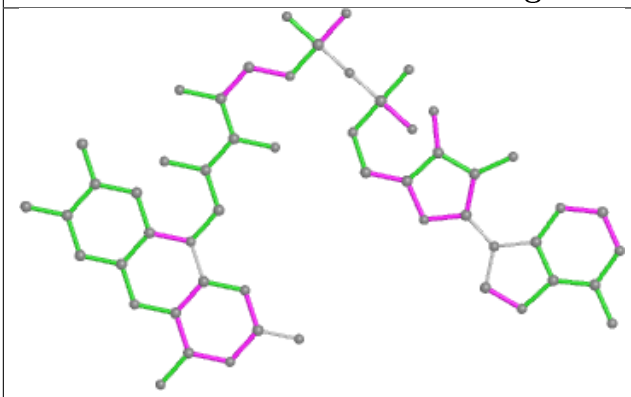
There are no ring outliers.

9 monomers are involved in 76 short contacts:

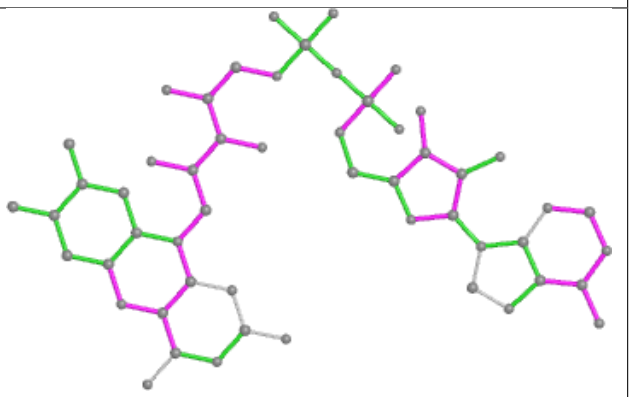
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	605	FAD	1	0
2	A	602	HEM	13	0
2	D	603	HEM	6	0
2	A	601	HEM	11	0
2	A	604	HEM	12	0
2	D	604	HEM	9	0
2	A	603	HEM	8	0
2	D	601	HEM	10	0
2	D	602	HEM	12	0

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.

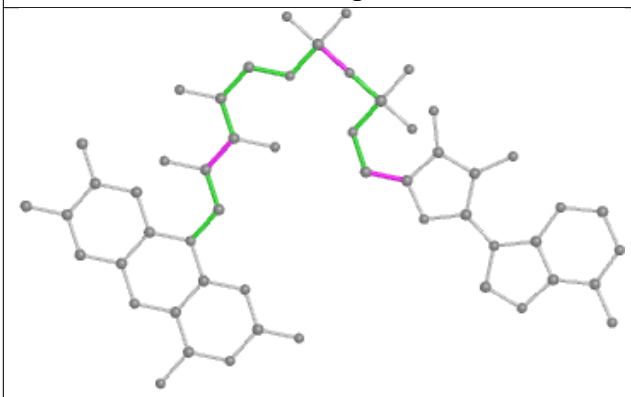
Ligand FAD A 605



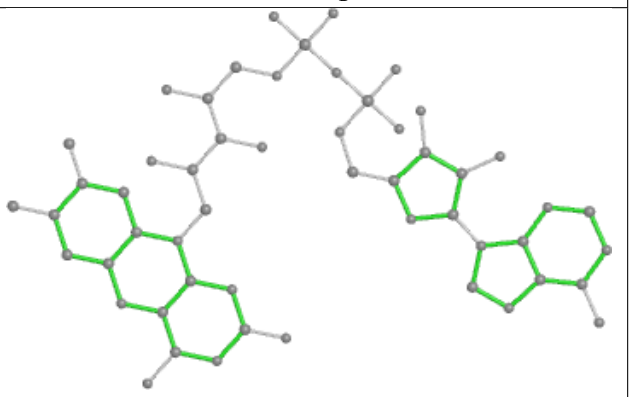
Bond lengths



Bond angles

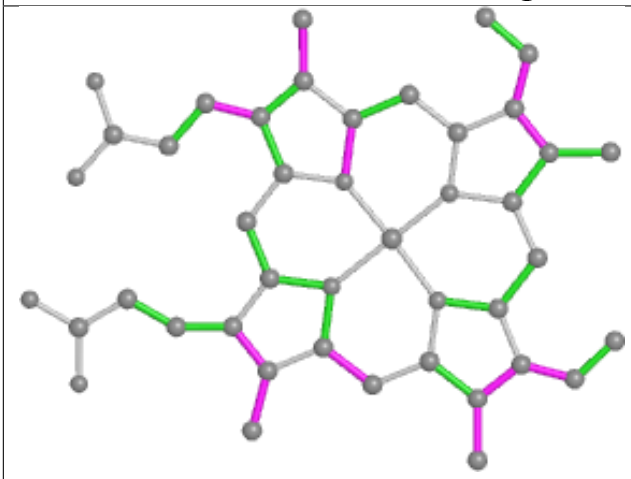


Torsions

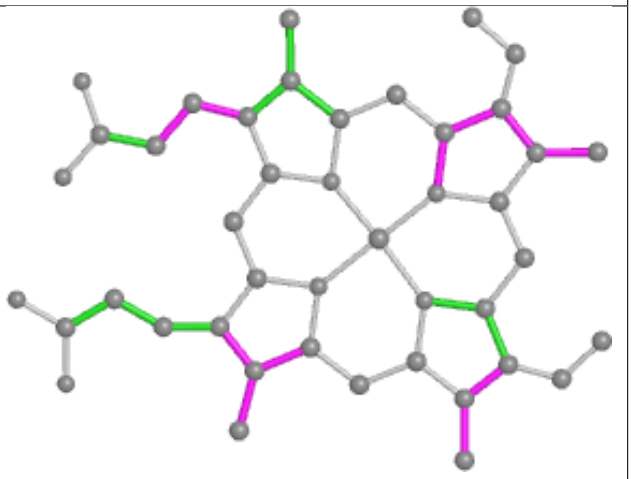


Rings

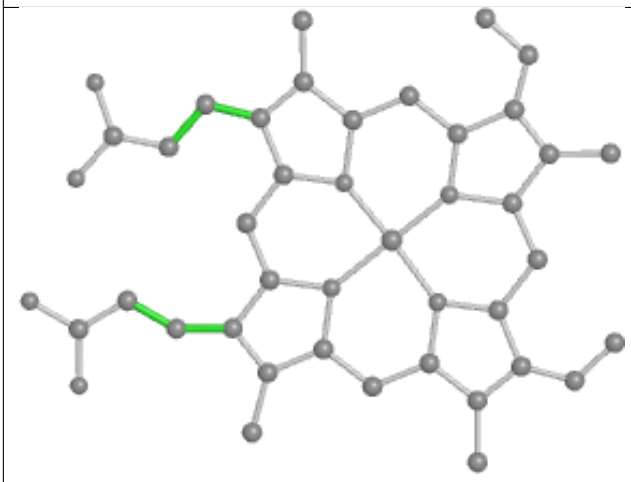
Ligand HEM A 602



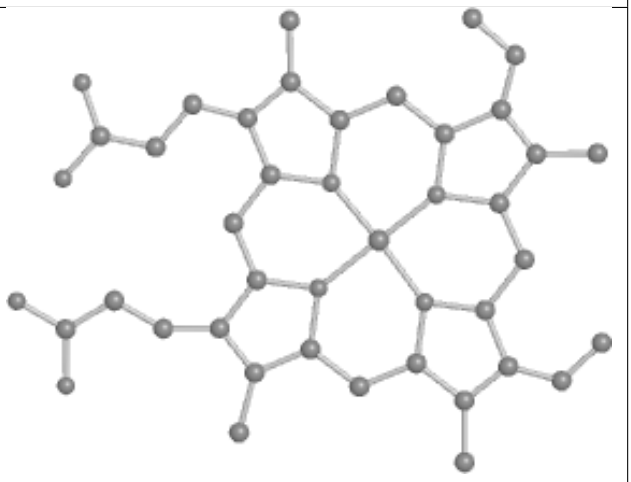
Bond lengths



Bond angles

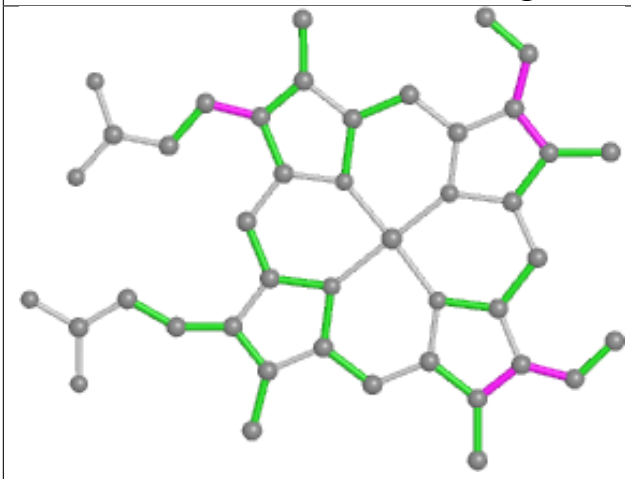


Torsions

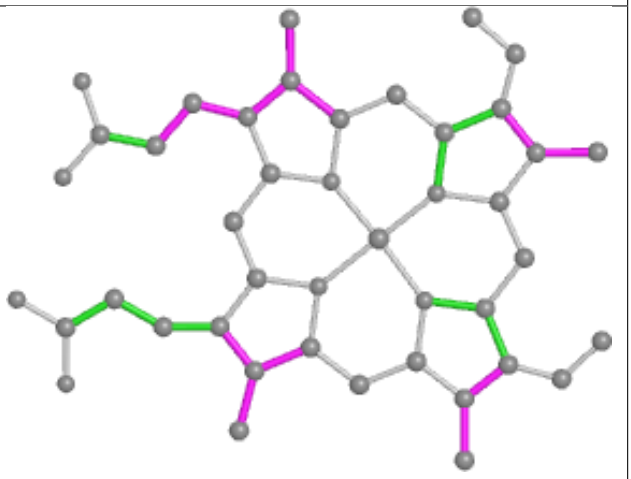


Rings

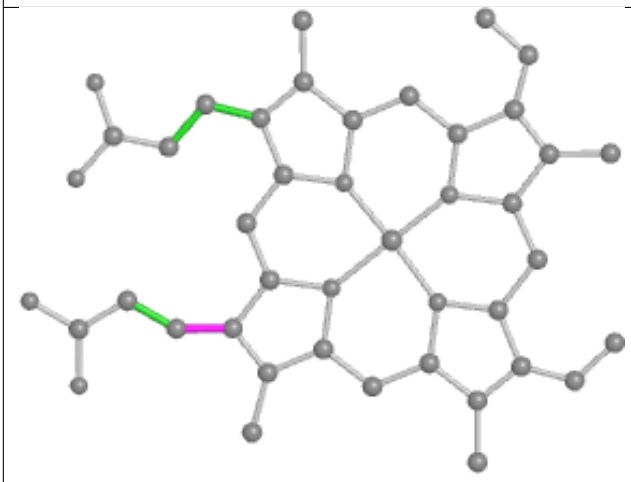
Ligand HEM D 603



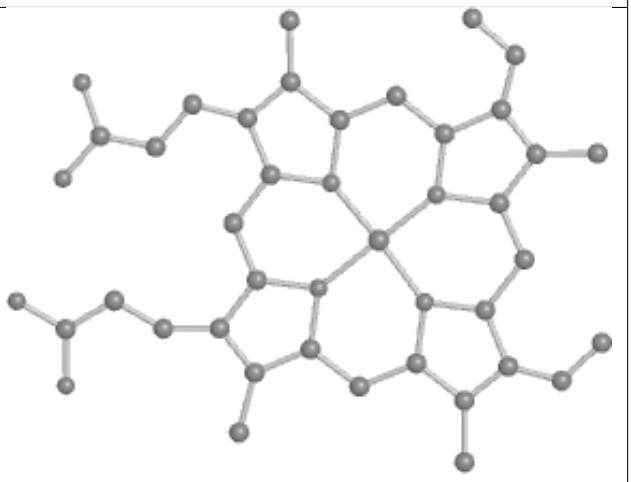
Bond lengths



Bond angles

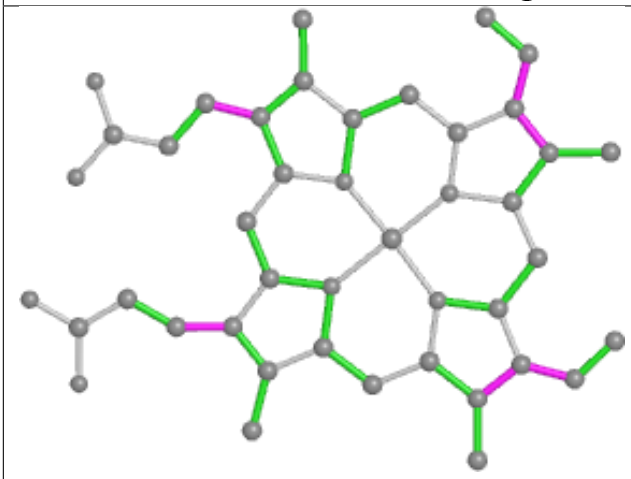


Torsions

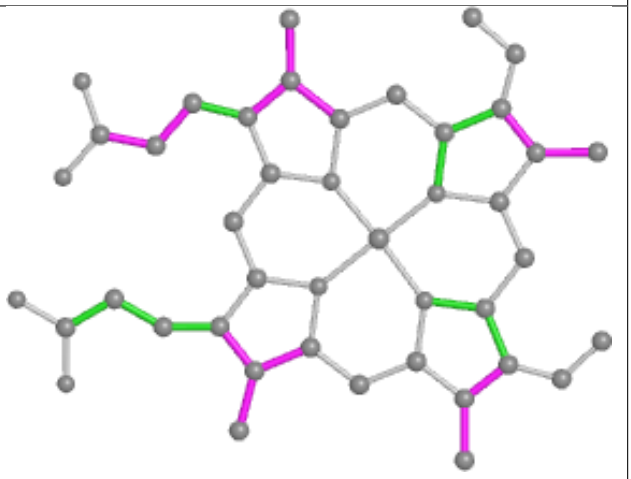


Rings

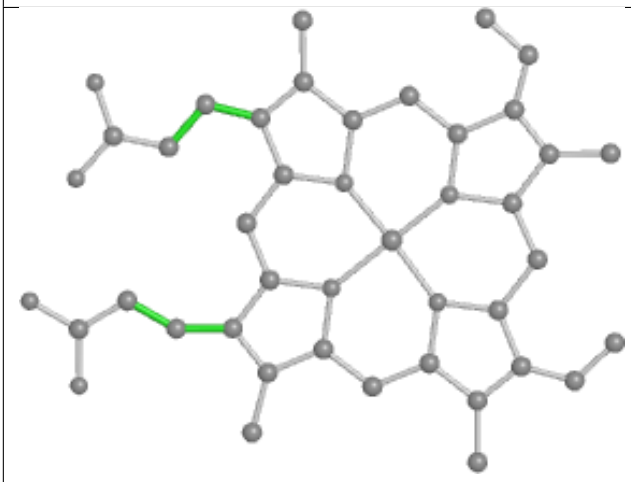
Ligand HEM A 601



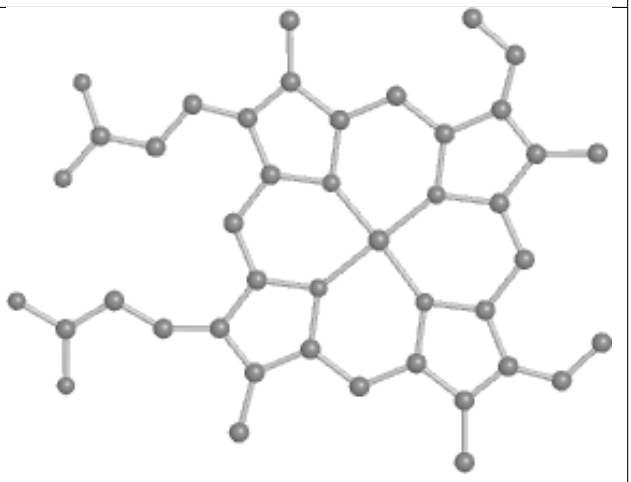
Bond lengths



Bond angles

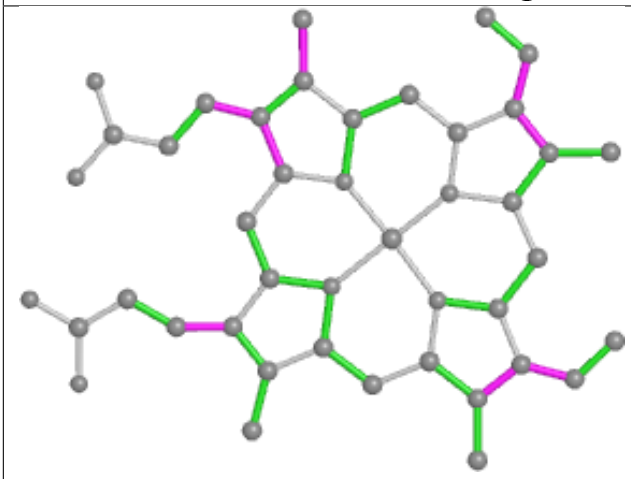


Torsions

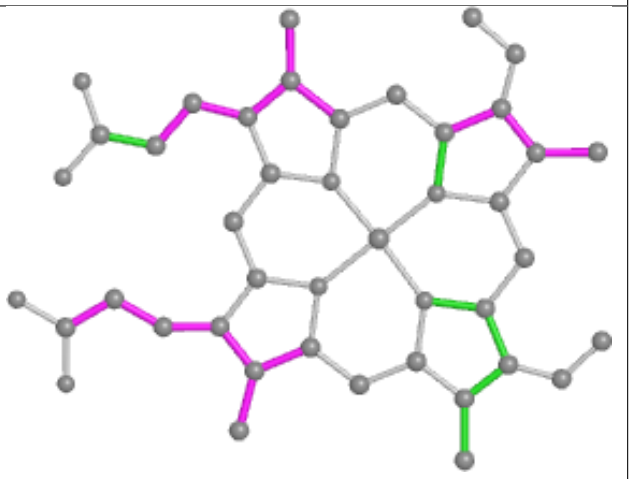


Rings

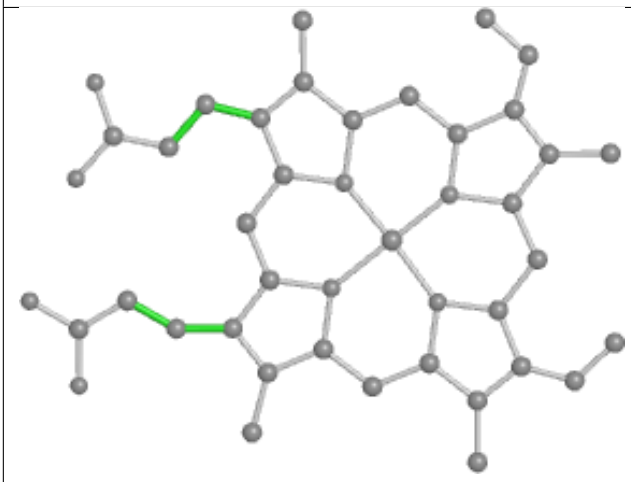
Ligand HEM A 604



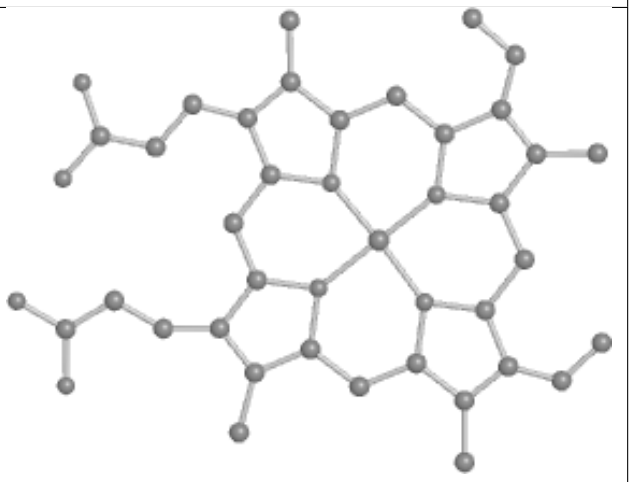
Bond lengths



Bond angles

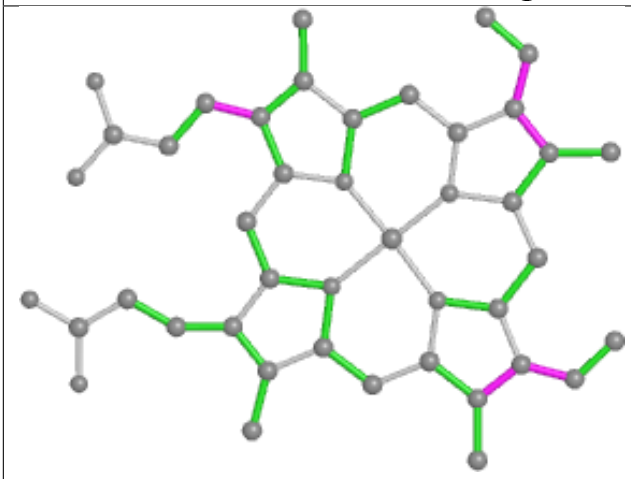


Torsions

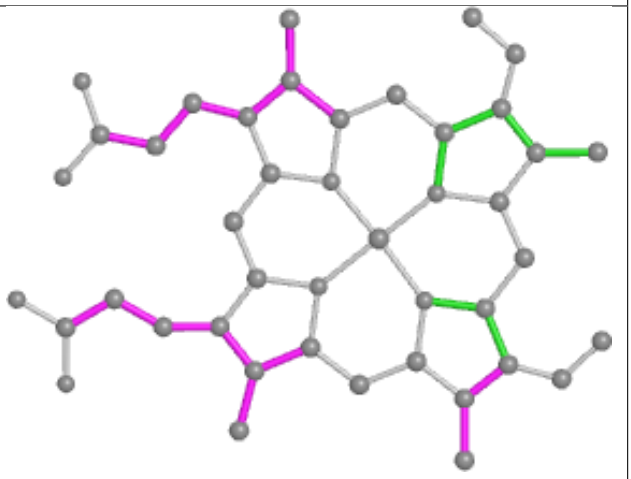


Rings

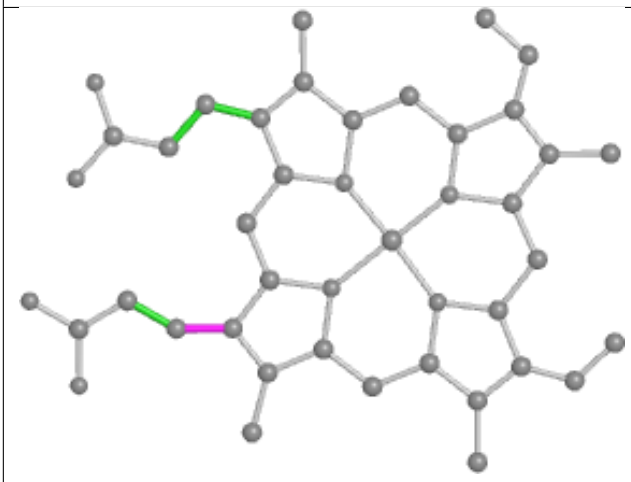
Ligand HEM D 604



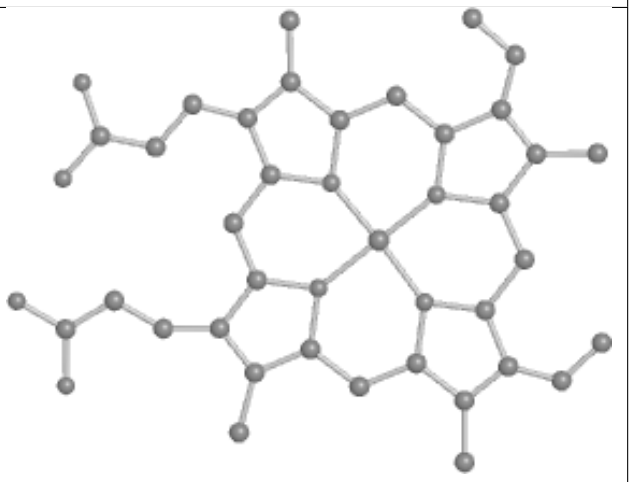
Bond lengths



Bond angles

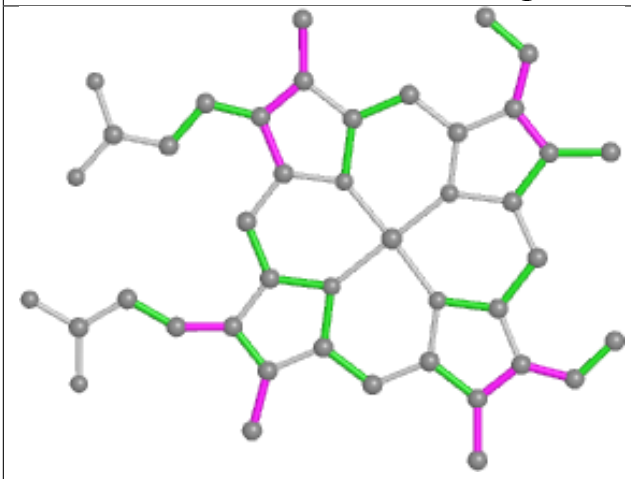


Torsions

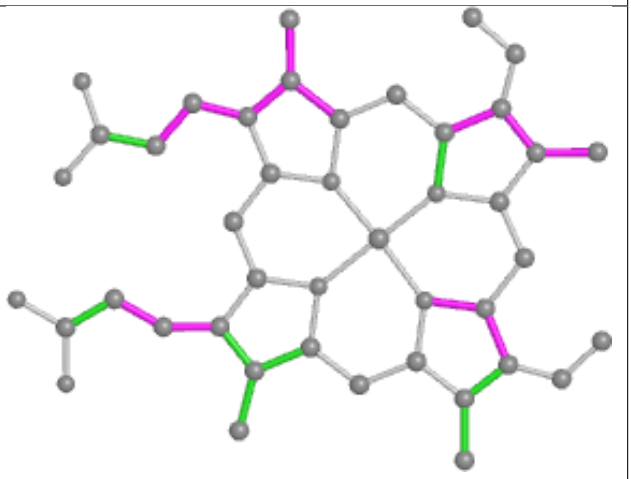


Rings

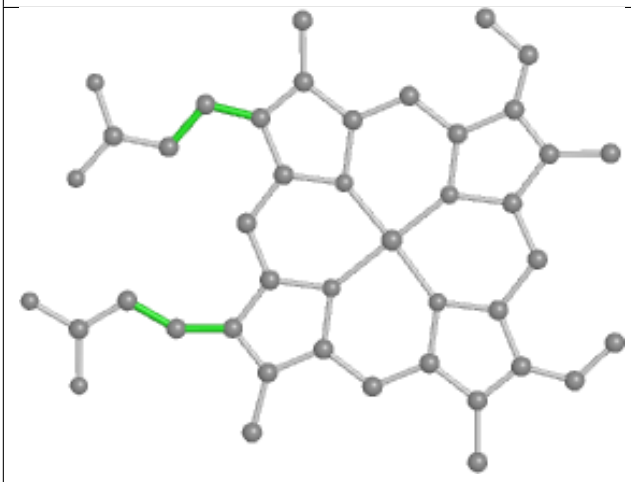
Ligand HEM A 603



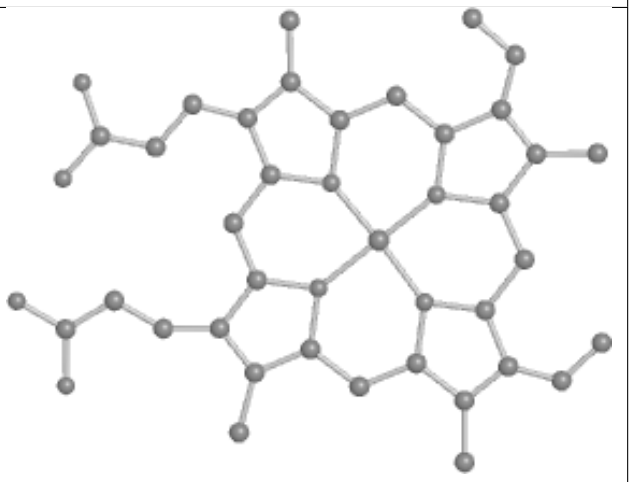
Bond lengths



Bond angles

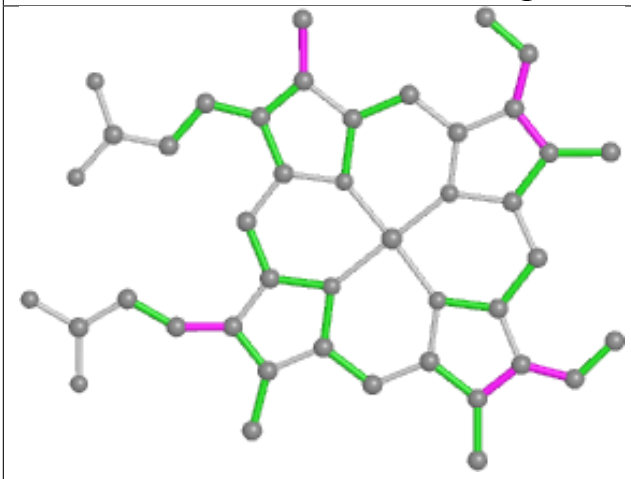


Torsions

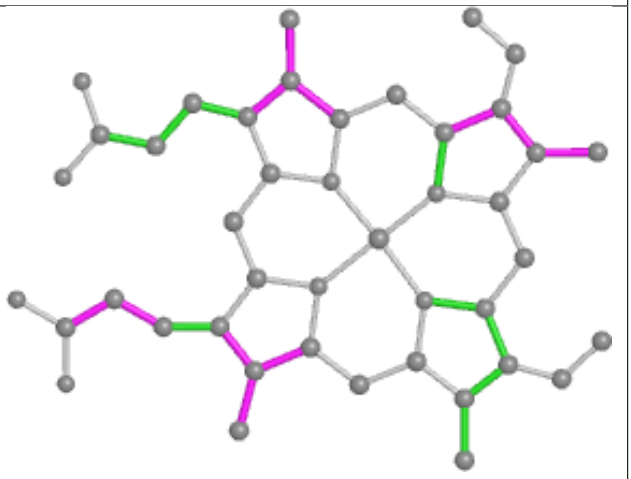


Rings

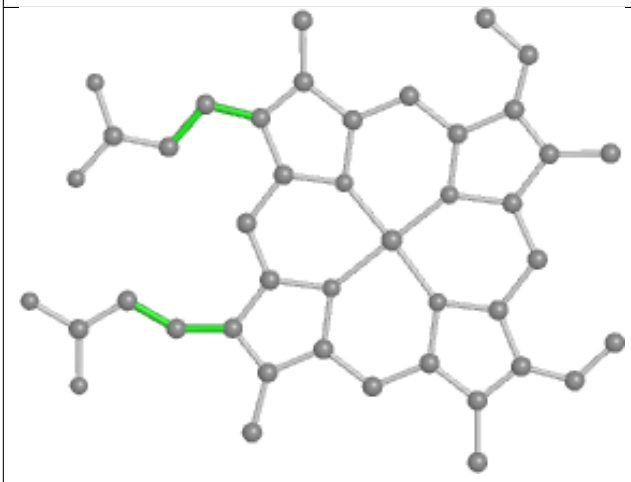
Ligand HEM D 601



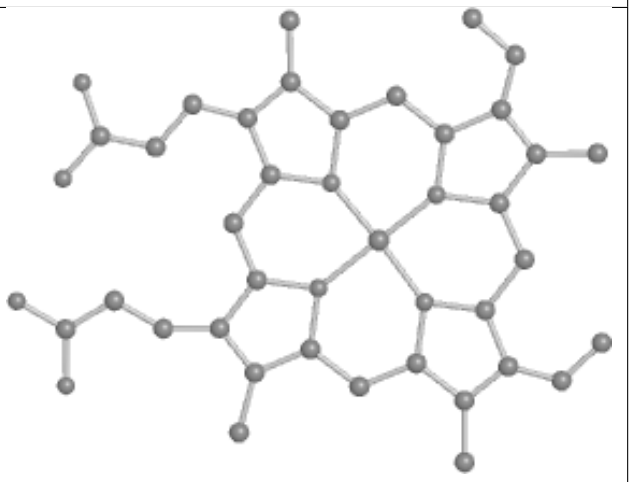
Bond lengths



Bond angles

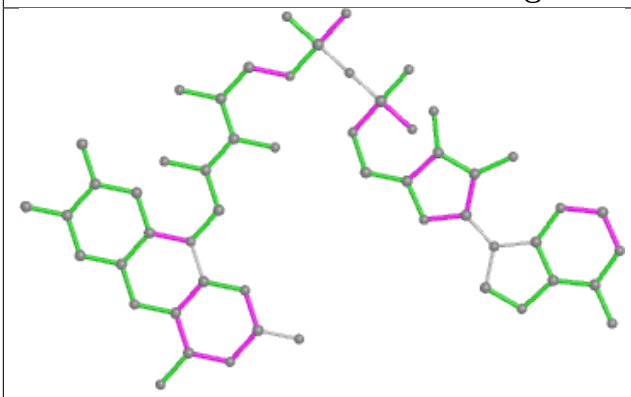


Torsions

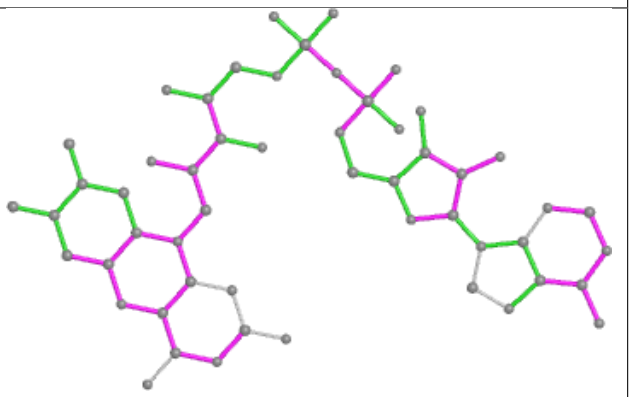


Rings

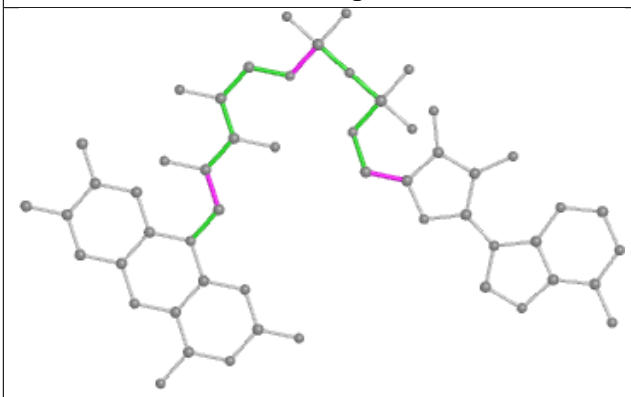
Ligand FAD D 605



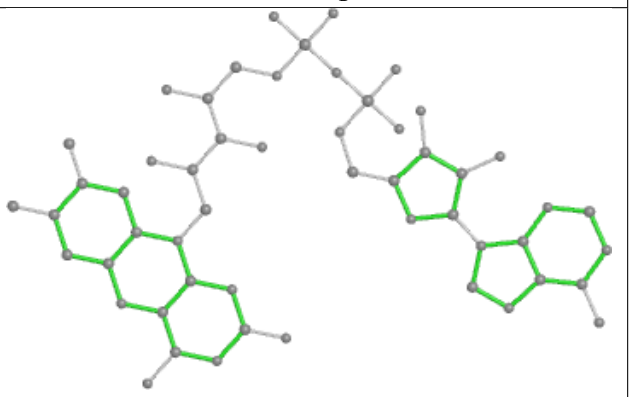
Bond lengths



Bond angles

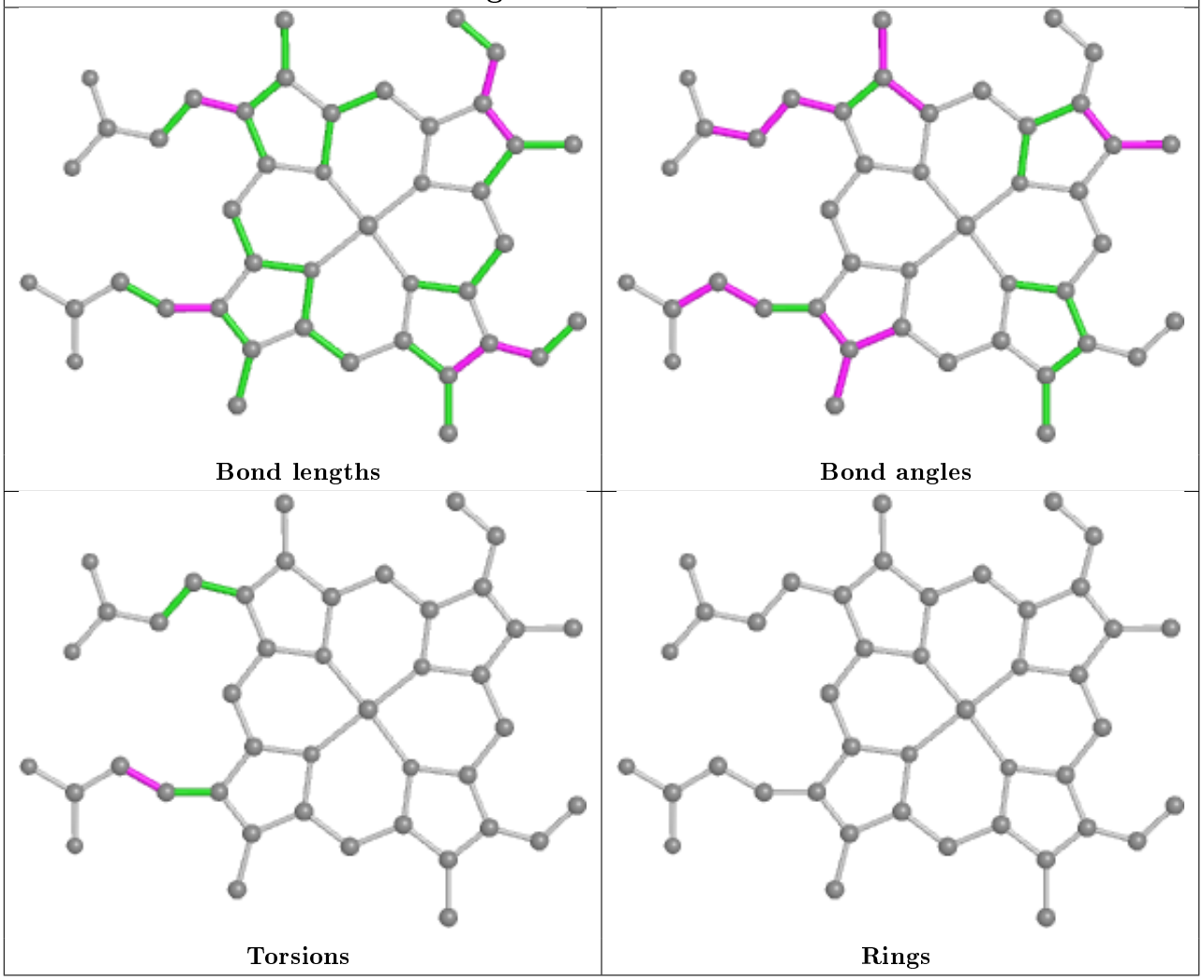


Torsions



Rings

Ligand HEM D 602



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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.