wwPDB X-ray Structure Validation Summary Report (i)

Aug 26, 2026 – 03:57 am BST

PDB ID	:	2C1U / pdb_00002c1u
Title	:	CRYSTAL STRUCTURE OF THE DI-HAEM CYTOCHROME C PEROXIDASE FROM PARACOCCUS PANTOTROPHUS - OXIDISED FORM
Authors	:	Echalier, A.; Fulop, V.
Deposited on	:	2005-09-21
Resolution	:	1.95 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 (1)) were used in the production of this report:

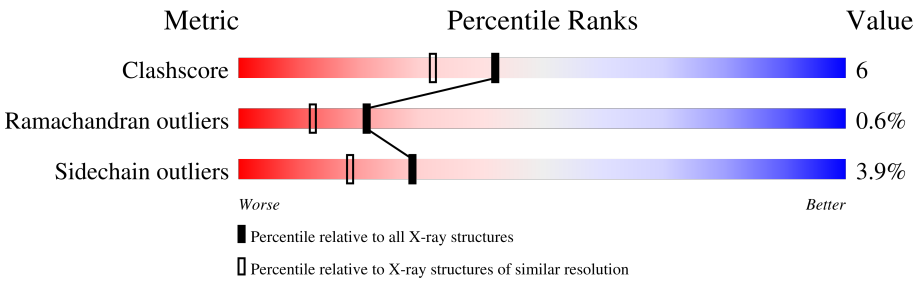
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 1.95 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	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	338	86% 11% •
1	B	338	79% 15% • •
1	C	338	81% 14% •• •
1	D	338	81% 13% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	HEC	A	401	X	-	-	-
2	HEC	A	402	X	-	-	-
2	HEC	B	401	X	-	-	-
2	HEC	B	402	X	-	-	-
2	HEC	C	401	X	-	-	-
2	HEC	C	402	X	-	-	-
2	HEC	D	401	X	-	-	-
2	HEC	D	402	X	-	-	-

2 Entry composition (i)

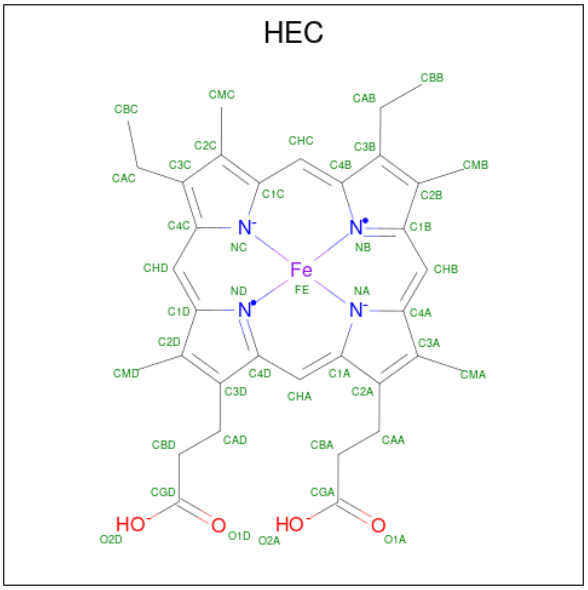
There are 4 unique types of molecules in this entry. The entry contains 11016 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DI-HAEM CYTOCHROME C PEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	329	2479	1566	415	486	12	0	0	0
1	B	324	2446	1545	410	479	12	0	0	0
1	C	329	2479	1567	415	485	12	0	0	0
1	D	322	2431	1537	408	474	12	0	0	0

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



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

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

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	1	1	1	0	0
			Total	Ca		
3	B	1	1	1	0	0
			Total	Ca		
3	C	1	1	1	0	0
			Total	Ca		
3	D	1	1	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	208	208	208	0	0
			Total	O		
4	B	199	199	199	0	0
			Total	O		
4	C	221	221	221	0	0
			Total	O		
4	D	205	205	205	0	0

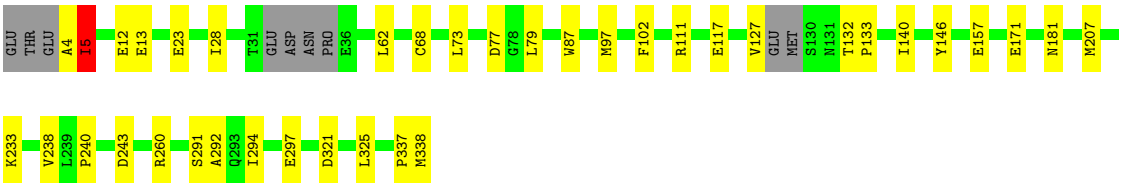
3 Residue-property plots (i)

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. 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.

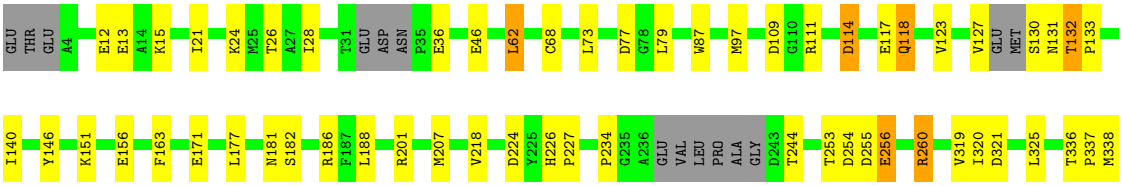
• Molecule 1: DI-HAEM CYTOCHROME C PEROXIDASE

Chain A:



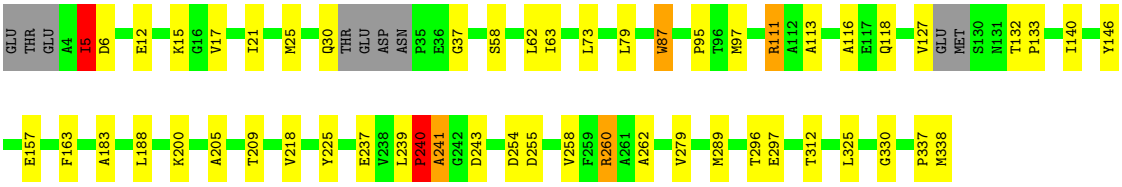
• Molecule 1: DI-HAEM CYTOCHROME C PEROXIDASE

Chain B:



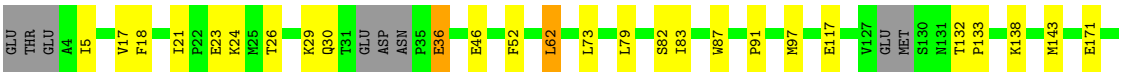
• Molecule 1: DI-HAEM CYTOCHROME C PEROXIDASE

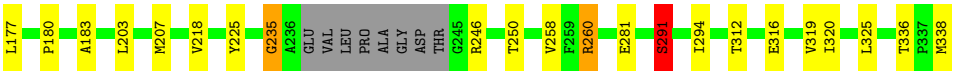
Chain C:



• Molecule 1: DI-HAEM CYTOCHROME C PEROXIDASE

Chain D:




L177
P180
A183
L203
M207
V218
Y225
G235
A236
GLU
VAL
LEU
PRO
ALA
GLY
ASP
THR
G245
R246
T250
V258
F259
R260
E281
S291
I294
T312
E316
V319
I320
L325
T336
P337
M338

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	78.80Å 51.10Å 167.90Å 90.00° 98.20° 90.00°	Depositor
Resolution (Å)	29.88 – 1.95	Depositor
% Data completeness (in resolution range)	88.6 (29.88-1.95)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.9999	Depositor
R, R_{free}	0.169 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11016	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

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: HEC, CA

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	0.92	0/2535	1.04	2/3449 (0.1%)
1	B	0.90	0/2501	1.03	2/3400 (0.1%)
1	C	0.95	2/2536 (0.1%)	1.08	1/3450 (0.0%)
1	D	0.89	1/2486 (0.0%)	1.03	2/3379 (0.1%)
All	All	0.91	3/10058 (0.0%)	1.05	7/13678 (0.1%)

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	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	12	GLU	CD-OE2	6.88	1.38	1.25
1	C	279	VAL	CA-CB	5.40	1.60	1.54
1	D	143	MET	C-O	-5.18	1.20	1.25

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	109	ASP	N-CA-C	6.12	116.51	107.88
1	B	182	SER	N-CA-C	-5.49	103.65	110.41
1	D	235	GLY	N-CA-C	-5.41	102.85	110.75
1	A	102	PHE	N-CA-C	5.37	119.69	113.20
1	D	291	SER	N-CA-C	5.33	117.06	108.32

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	234	PRO	Peptide

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	2479	0	2392	24	0
1	B	2446	0	2358	33	0
1	C	2479	0	2393	42	0
1	D	2431	0	2347	37	0
2	A	86	0	60	2	0
2	B	86	0	60	4	0
2	C	86	0	60	6	0
2	D	86	0	60	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	208	0	0	2	0
4	B	199	0	0	5	0
4	C	221	0	0	3	0
4	D	205	0	0	4	0
All	All	11016	0	9730	126	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 6.

The worst 5 of 126 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:C:296:THR:O	1:C:297:GLU:HG2	1.48	1.12
1:D:83:ILE:CD1	1:D:91:PRO:HA	1.96	0.96
1:D:52:PHE:HE2	1:D:97:MET:HE3	1.40	0.86
1:D:83:ILE:HD13	1:D:91:PRO:HA	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:83:ILE:HD11	1:D:91:PRO:CA	2.13	0.79

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	323/338 (96%)	309 (96%)	12 (4%)	2 (1%)	21	12
1	B	316/338 (94%)	299 (95%)	15 (5%)	2 (1%)	21	12
1	C	323/338 (96%)	312 (97%)	8 (2%)	3 (1%)	14	6
1	D	314/338 (93%)	300 (96%)	13 (4%)	1 (0%)	36	28
All	All	1276/1352 (94%)	1220 (96%)	48 (4%)	8 (1%)	21	12

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	C	5	ILE
1	C	240	PRO
1	C	241	ALA
1	B	244	THR

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	258/267 (97%)	251 (97%)	7 (3%)	39	32
1	B	255/267 (96%)	240 (94%)	15 (6%)	18	7
1	C	258/267 (97%)	249 (96%)	9 (4%)	32	22
1	D	253/267 (95%)	244 (96%)	9 (4%)	31	21
All	All	1024/1068 (96%)	984 (96%)	40 (4%)	28	18

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	237	GLU
1	D	62	LEU
1	C	240	PRO
1	D	26	THR
1	D	260	ARG

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

Mol	Chain	Res	Type
1	B	30	GLN
1	B	106	GLN
1	B	118	GLN
1	C	118	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	HEC	C	401	1	50,50,50	2.01	10 (20%)	68,82,82	1.94	15 (22%)
2	HEC	C	402	1	50,50,50	1.86	7 (14%)	68,82,82	1.45	8 (11%)
2	HEC	B	402	1	50,50,50	1.84	9 (18%)	68,82,82	1.67	14 (20%)
2	HEC	A	401	1	50,50,50	1.77	9 (18%)	68,82,82	1.66	13 (19%)
2	HEC	D	402	1	50,50,50	1.71	7 (14%)	68,82,82	1.37	8 (11%)
2	HEC	A	402	1	50,50,50	1.84	8 (16%)	68,82,82	1.37	6 (8%)
2	HEC	B	401	1	50,50,50	1.73	6 (12%)	68,82,82	1.53	11 (16%)
2	HEC	D	401	1	50,50,50	1.75	8 (16%)	68,82,82	1.70	16 (23%)

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
2	HEC	C	401	1	1/1/3/7	8/14/54/54	-
2	HEC	C	402	1	1/1/3/7	2/14/54/54	-
2	HEC	B	402	1	1/1/3/7	5/14/54/54	-
2	HEC	A	401	1	1/1/3/7	7/14/54/54	-
2	HEC	D	402	1	1/1/3/7	5/14/54/54	-
2	HEC	A	402	1	1/1/3/7	4/14/54/54	-
2	HEC	B	401	1	1/1/3/7	8/14/54/54	-
2	HEC	D	401	1	1/1/3/7	9/14/54/54	-

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	402	HEC	C3D-C2D	8.14	1.54	1.36
2	A	402	HEC	C3D-C2D	7.91	1.53	1.36
2	C	401	HEC	C3D-C2D	7.76	1.53	1.36
2	A	401	HEC	C3D-C2D	7.75	1.53	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	HEC	C3D-C2D	7.53	1.52	1.36

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	HEC	C1D-ND-C4D	6.49	111.78	105.07
2	C	401	HEC	C1D-ND-C4D	6.13	111.40	105.07
2	A	402	HEC	C1D-ND-C4D	5.94	111.21	105.07
2	C	401	HEC	C4A-NA-C1A	5.92	111.15	105.35
2	C	402	HEC	C1D-ND-C4D	5.58	110.83	105.07

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	401	HEC	NA
2	A	402	HEC	NA
2	B	401	HEC	NA
2	B	402	HEC	NA
2	C	401	HEC	NA

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	HEC	C2C-C3C-CAC-CBC
2	B	401	HEC	C2C-C3C-CAC-CBC
2	A	401	HEC	C4C-C3C-CAC-CBC
2	B	401	HEC	C4C-C3C-CAC-CBC
2	D	401	HEC	C2B-C3B-CAB-CBB

There are no ring outliers.

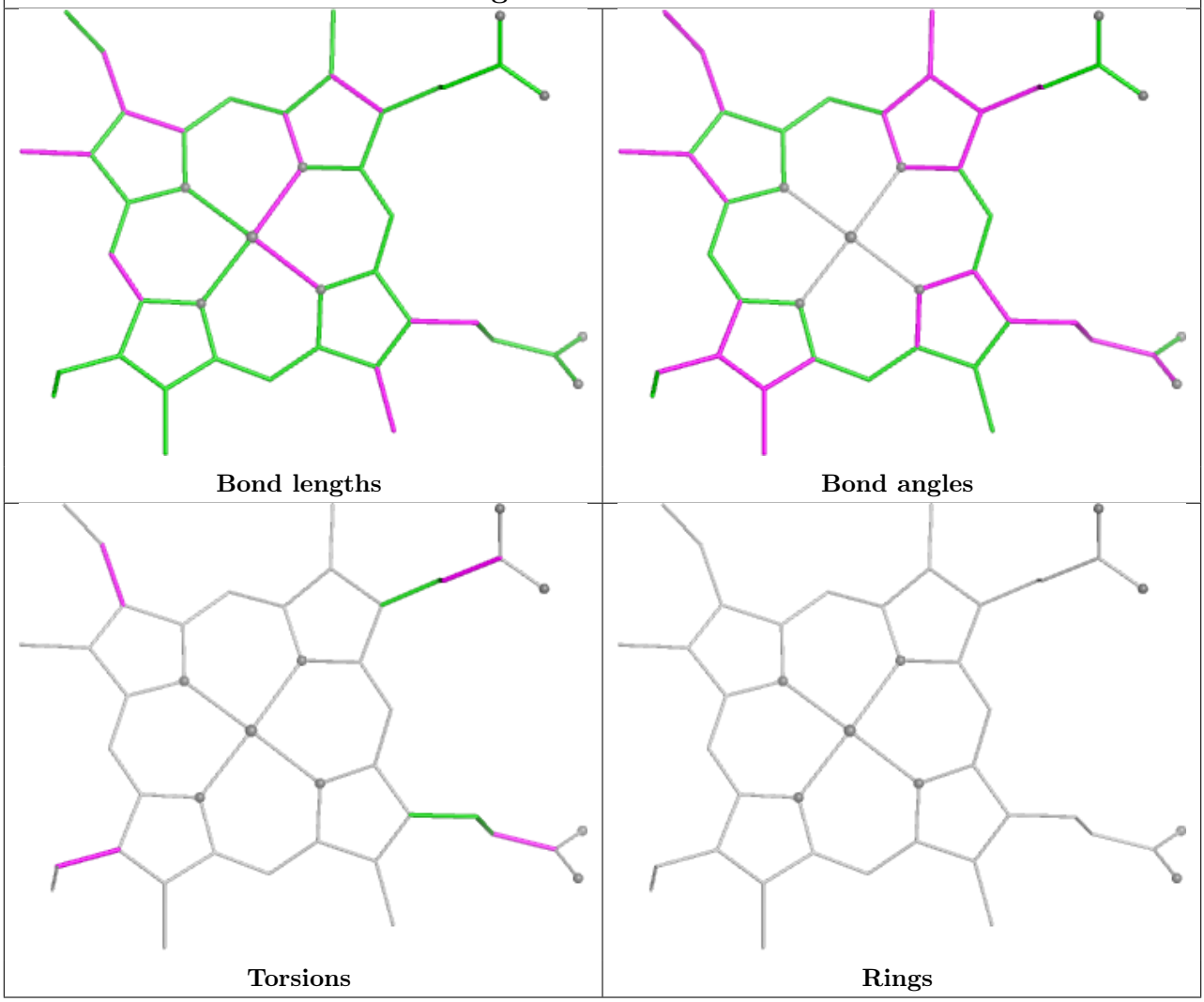
5 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	HEC	3	0
2	C	402	HEC	3	0
2	A	401	HEC	2	0
2	B	401	HEC	4	0
2	D	401	HEC	2	0

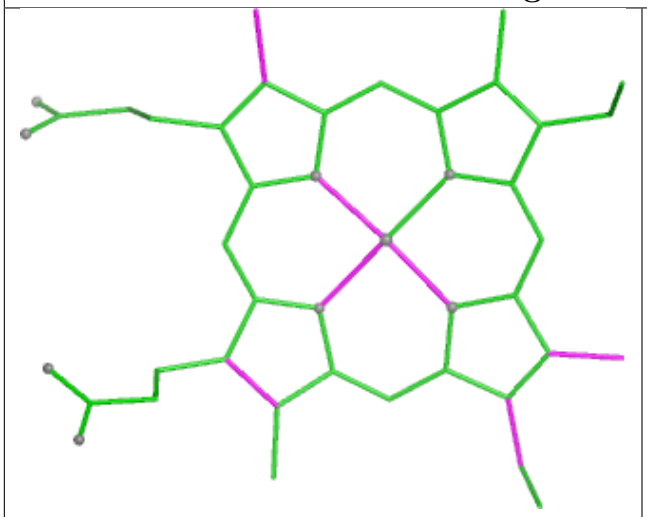
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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.

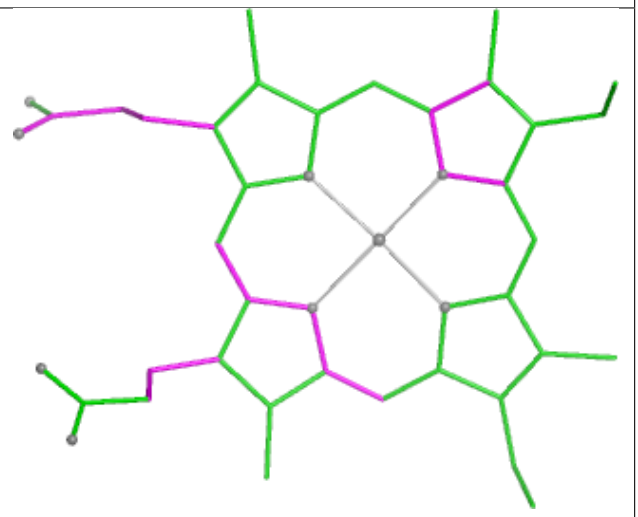
Ligand HEC C 401



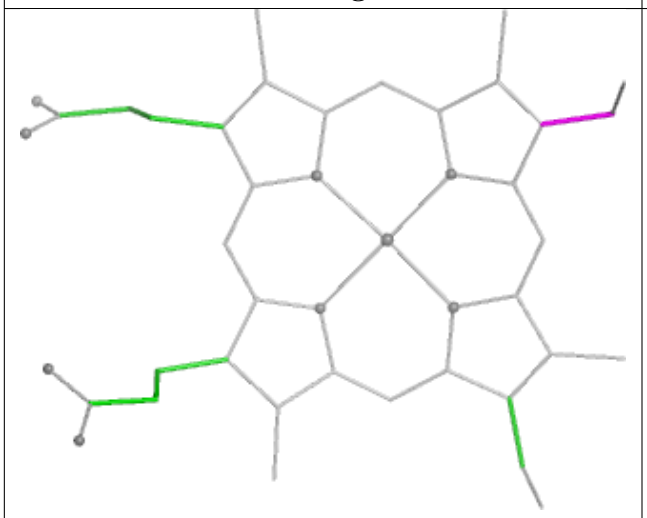
Ligand HEC C 402



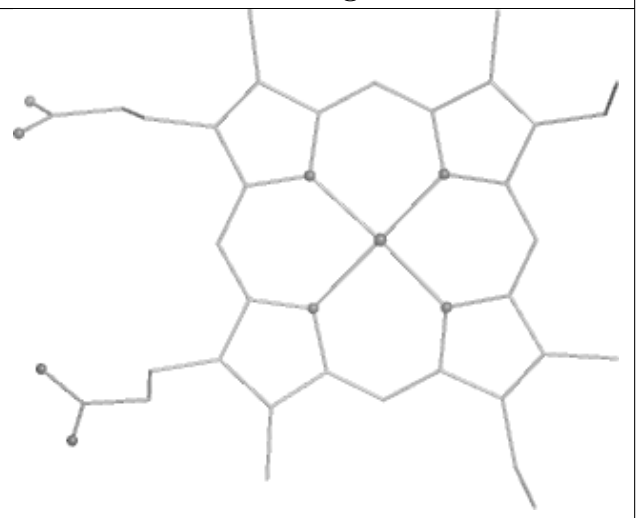
Bond lengths



Bond angles

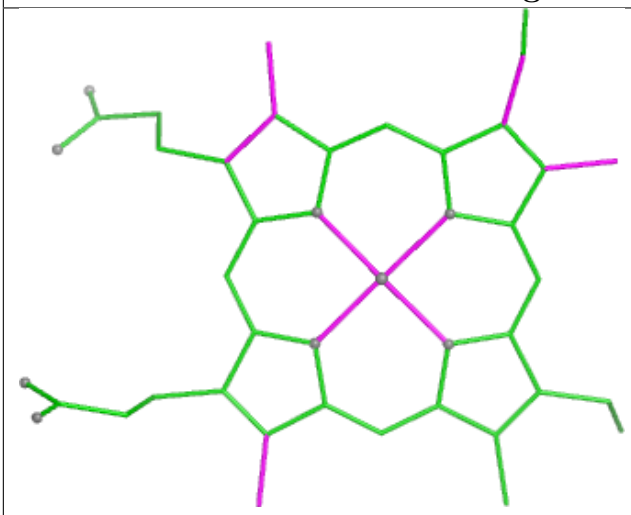


Torsions

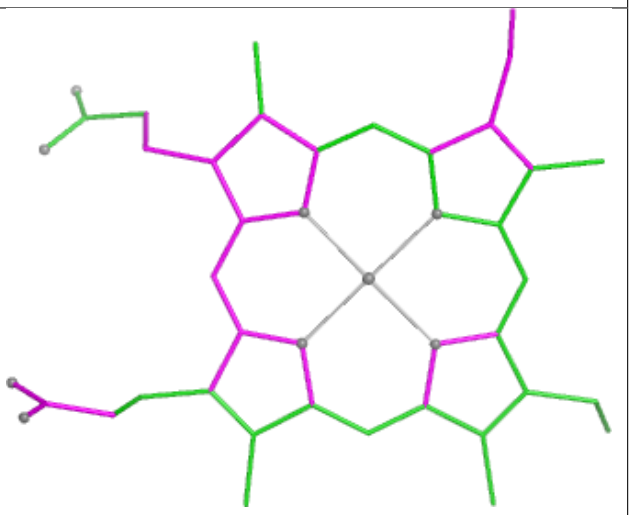


Rings

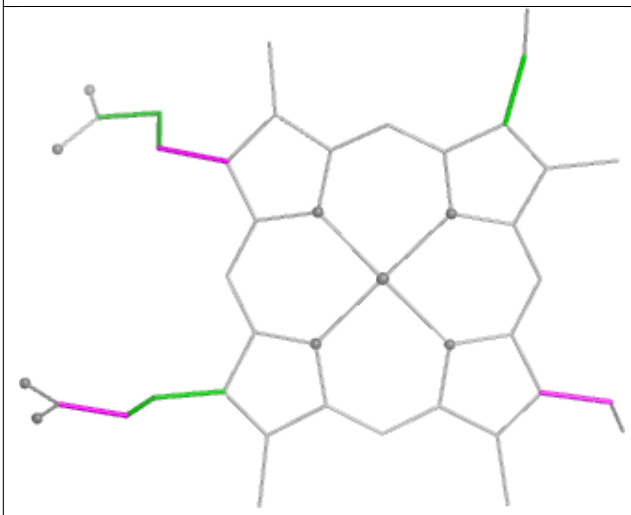
Ligand HEC B 402



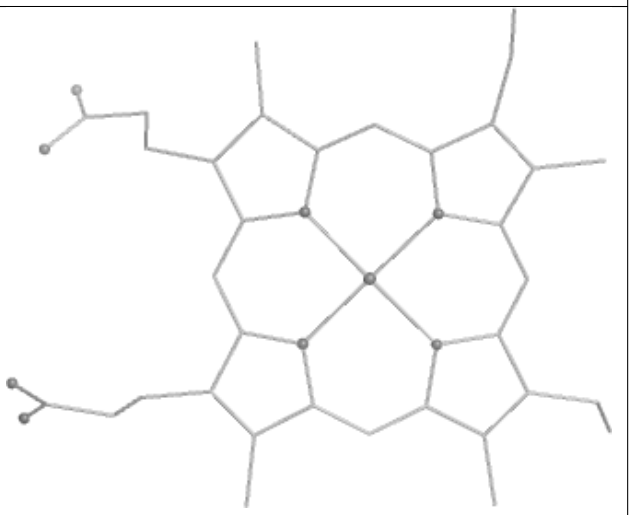
Bond lengths



Bond angles

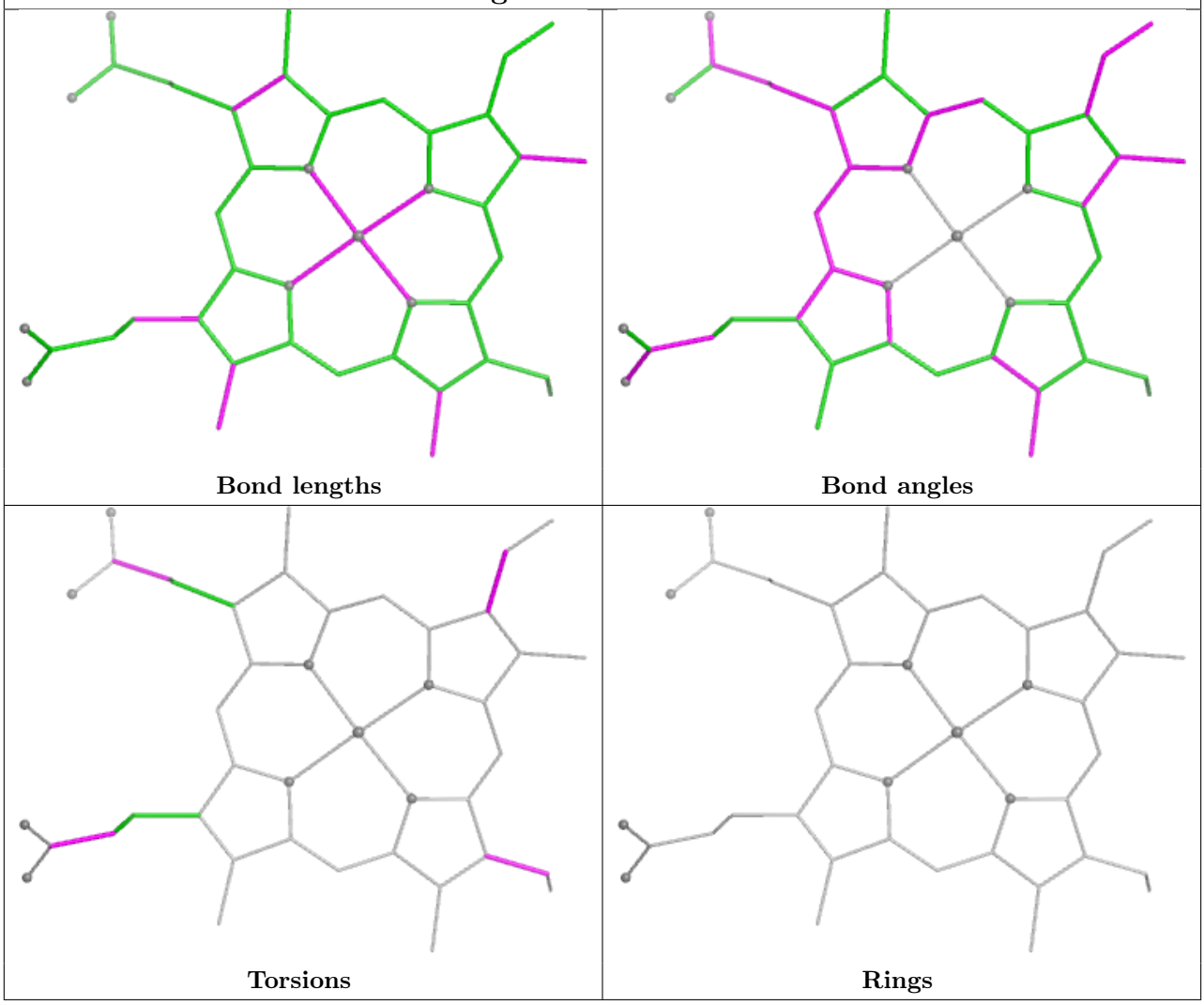


Torsions

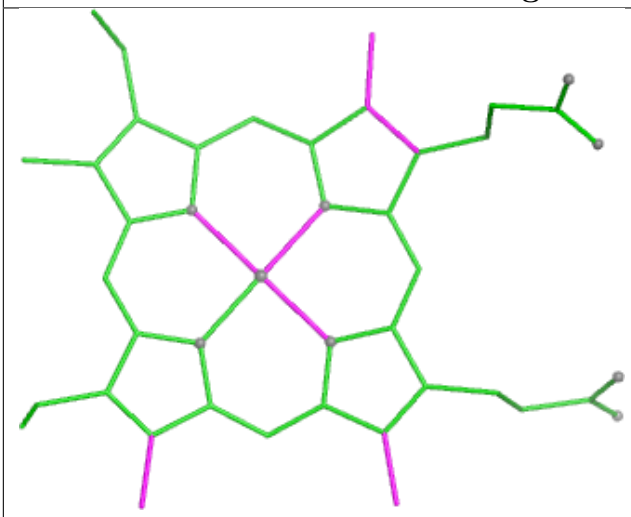


Rings

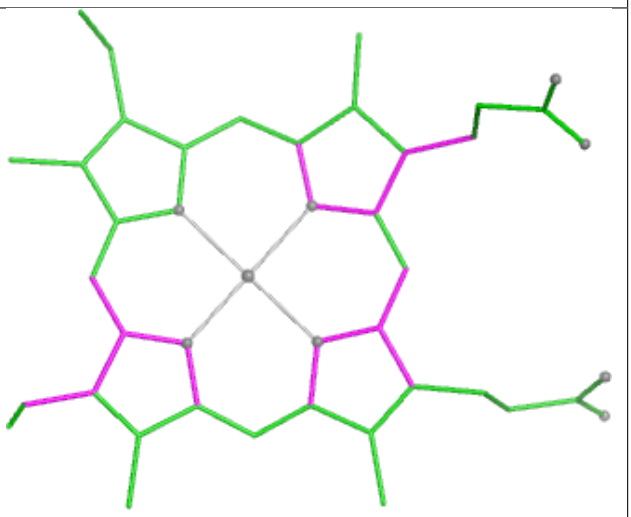
Ligand HEC A 401



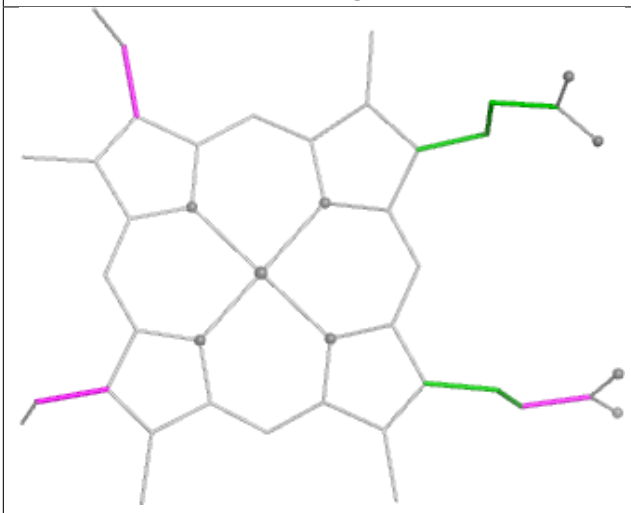
Ligand HEC D 402



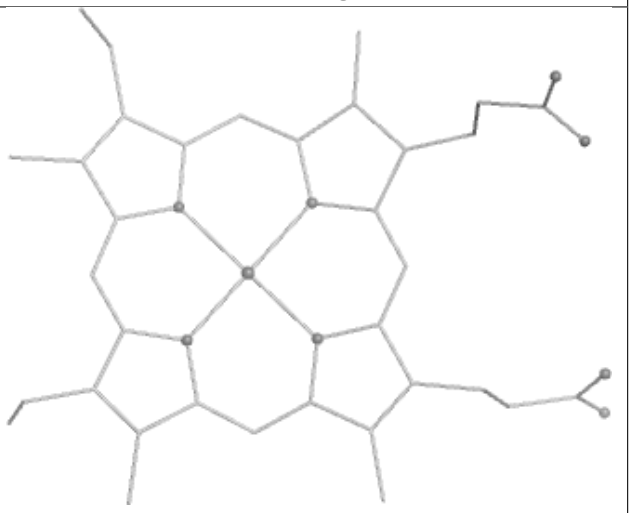
Bond lengths



Bond angles

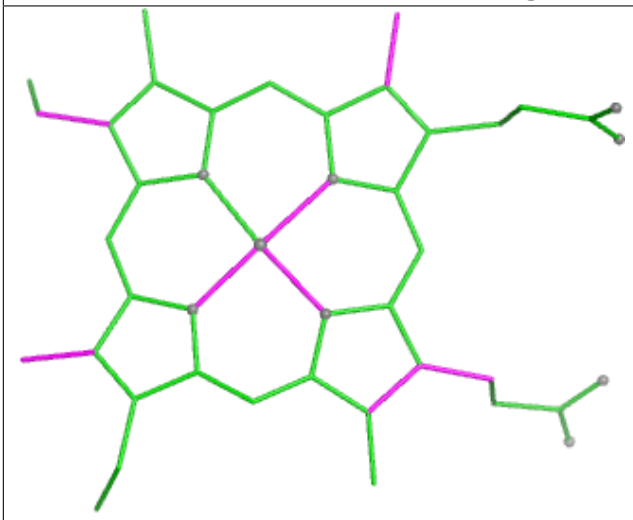


Torsions

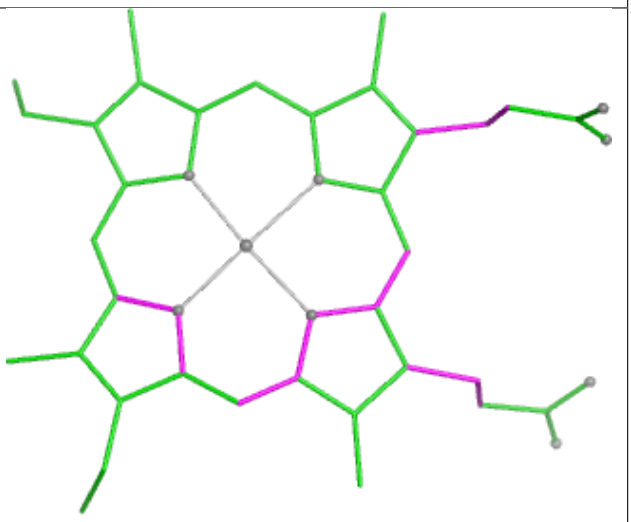


Rings

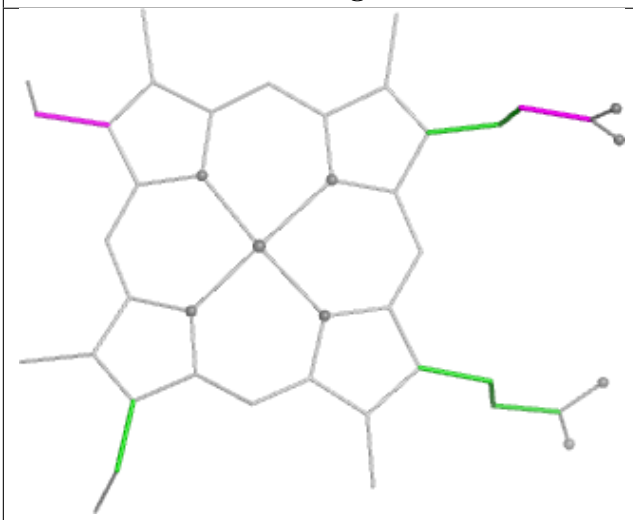
Ligand HEC A 402



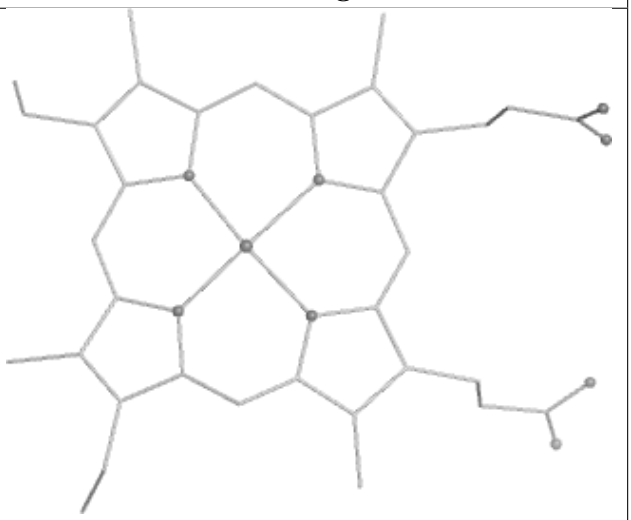
Bond lengths



Bond angles

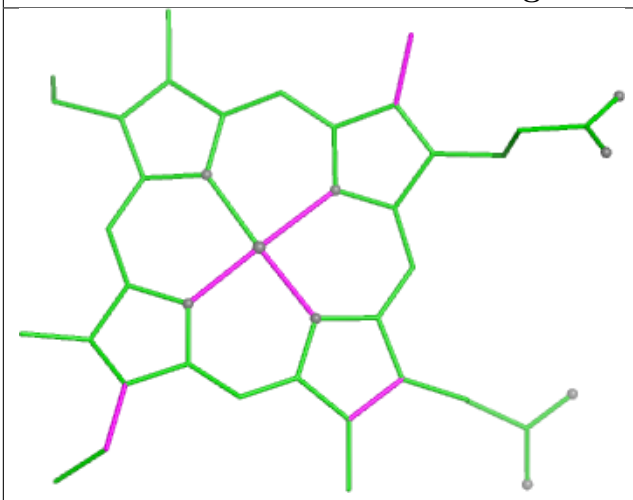


Torsions

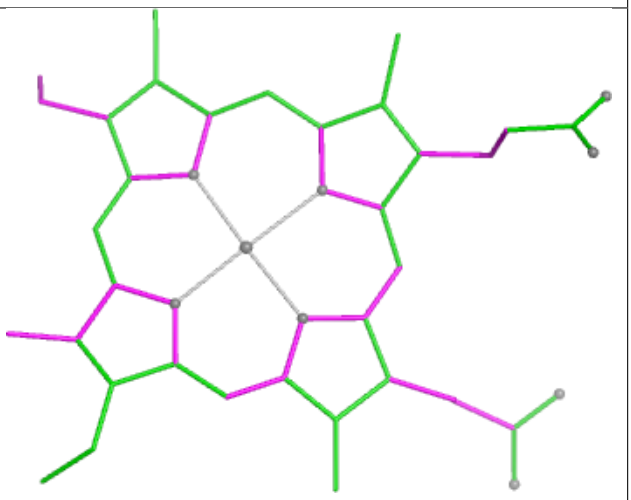


Rings

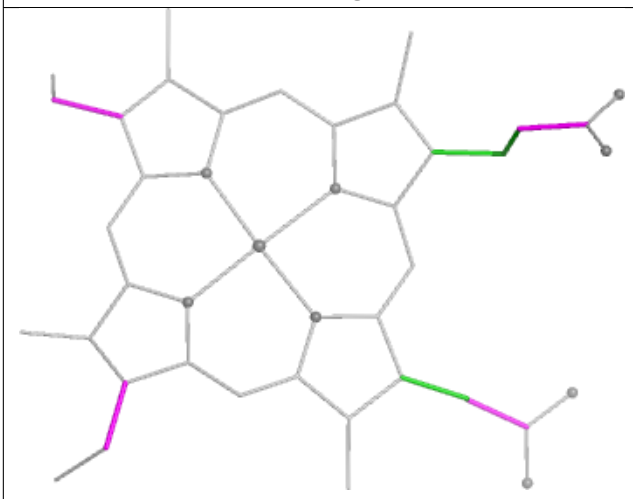
Ligand HEC B 401



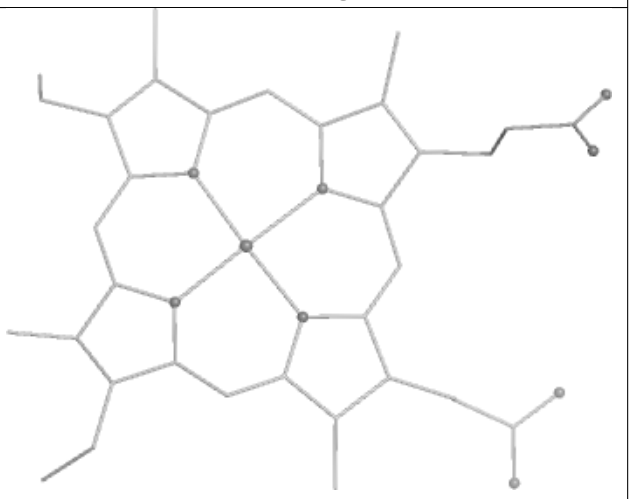
Bond lengths



Bond angles

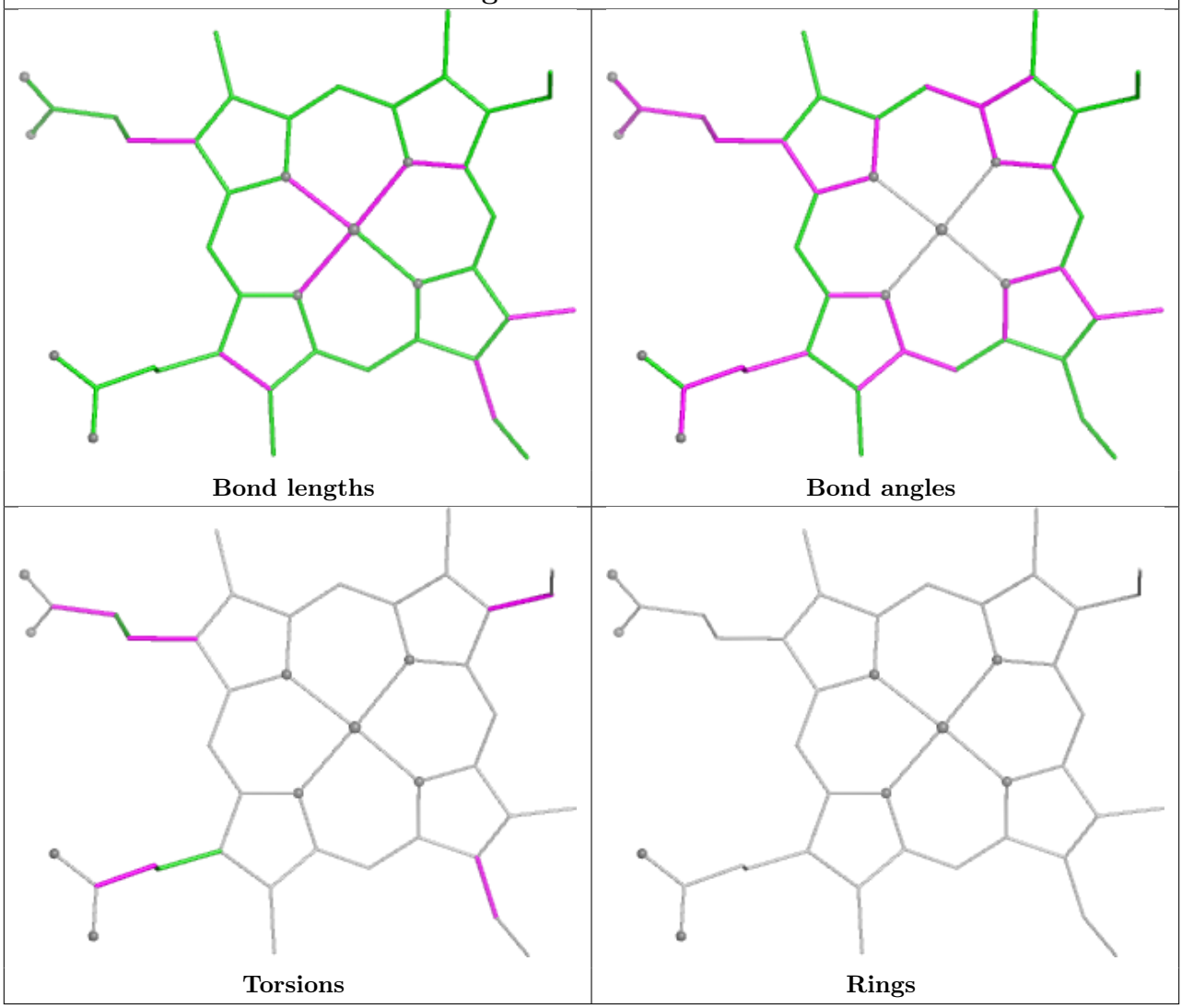


Torsions



Rings

Ligand HEC D 401



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.