



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 3, 2024 – 03:33 PM EST

PDB ID : 1MBC  
Title : X-RAY STRUCTURE AND REFINEMENT OF CARBON-MONOXY (FE II)-MYOGLOBIN AT 1.5 ANGSTROMS RESOLUTION  
Authors : Kuriyan, J.; Petsko, G.A.  
Deposited on : 1988-09-15  
Resolution : 1.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (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) : 2.36

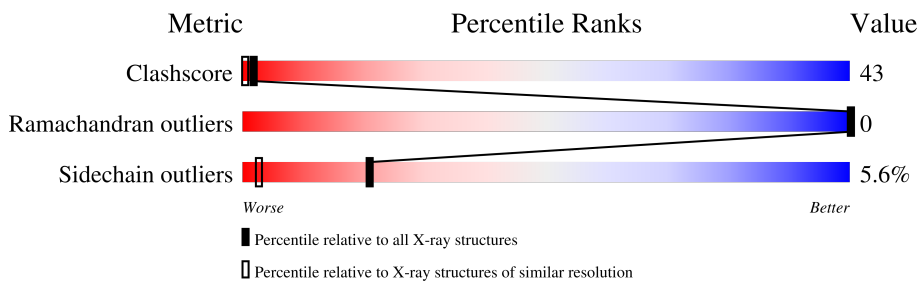
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	153	 44% 37% 16% .

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 1432 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 MYOGLOBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	153	1244	802	222	217	3	0	7	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



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

- Molecule 4 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
			Total	C			O
4	A	1	3	1	2	0	1

- Molecule 5 is water.

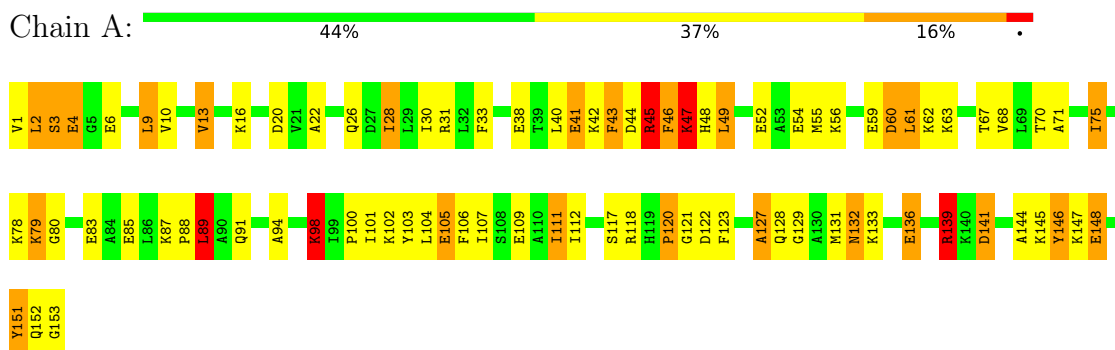
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	137	Total 137	O 137	0	0

### 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: MYOGLOBIN



## 4 Data and refinement statistics

Xtrriage (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, $\alpha$ , $\beta$ , $\gamma$	64.18Å 30.84Å 34.69Å 90.00° 105.84° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.50)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.171 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1432	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	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: HEM, CMO, SO4

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	1.84	23/1307 (1.8%)	2.26	50/1751 (2.9%)

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	3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	109	GLU	CD-OE2	15.08	1.42	1.25
1	A	80	GLY	N-CA	8.87	1.59	1.46
1	A	59	GLU	CD-OE2	8.07	1.34	1.25
1	A	41	GLU	CD-OE2	7.95	1.34	1.25
1	A	4	GLU	CD-OE2	7.08	1.33	1.25
1	A	3	SER	CB-OG	6.78	1.51	1.42
1	A	129	GLY	N-CA	6.62	1.55	1.46
1	A	136	GLU	CD-OE2	6.06	1.32	1.25
1	A	28	ILE	N-CA	6.03	1.58	1.46
1	A	85	GLU	CD-OE2	5.99	1.32	1.25
1	A	118	ARG	C-O	5.76	1.34	1.23
1	A	105	GLU	CD-OE1	-5.70	1.19	1.25
1	A	83	GLU	CD-OE2	5.64	1.31	1.25
1	A	70	THR	CB-OG1	-5.54	1.32	1.43
1	A	107	ILE	N-CA	5.52	1.57	1.46
1	A	148	GLU	CD-OE1	-5.32	1.19	1.25
1	A	13	VAL	C-O	5.21	1.33	1.23
1	A	111	ILE	C-O	5.20	1.33	1.23

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	120	PRO	N-CD	5.18	1.55	1.47
1	A	31	ARG	NE-CZ	5.10	1.39	1.33
1	A	38	GLU	CG-CD	-5.04	1.44	1.51
1	A	136	GLU	C-O	5.04	1.32	1.23
1	A	132	ASN	CG-OD1	5.03	1.35	1.24

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	141	ASP	CB-CG-OD1	19.51	135.86	118.30
1	A	139	ARG	NE-CZ-NH2	14.81	127.70	120.30
1	A	109	GLU	OE1-CD-OE2	-12.36	108.47	123.30
1	A	60	ASP	CB-CG-OD1	-10.76	108.62	118.30
1	A	31	ARG	CD-NE-CZ	-10.37	109.08	123.60
1	A	141	ASP	OD1-CG-OD2	-8.71	106.74	123.30
1	A	38	GLU	OE1-CD-OE2	-8.60	112.98	123.30
1	A	43	PHE	CB-CG-CD1	-8.54	114.82	120.80
1	A	41	GLU	OE1-CD-OE2	-8.26	113.39	123.30
1	A	31	ARG	NE-CZ-NH2	-8.23	116.19	120.30
1	A	109	GLU	CG-CD-OE1	8.21	134.71	118.30
1	A	151	TYR	CB-CG-CD1	8.14	125.89	121.00
1	A	98	LYS	CA-CB-CG	8.03	131.06	113.40
1	A	41	GLU	CG-CD-OE1	7.93	134.17	118.30
1	A	141	ASP	CA-CB-CG	-7.54	96.82	113.40
1	A	127	ALA	N-CA-CB	-7.44	99.68	110.10
1	A	103	TYR	CB-CG-CD1	7.29	125.38	121.00
1	A	89	LEU	CB-CA-C	7.28	124.02	110.20
1	A	106	PHE	CB-CG-CD1	-7.10	115.83	120.80
1	A	144	ALA	CB-CA-C	6.97	120.55	110.10
1	A	118	ARG	NE-CZ-NH1	-6.96	116.82	120.30
1	A	55	MET	CA-CB-CG	-6.75	101.83	113.30
1	A	33	PHE	CB-CG-CD1	-6.69	116.12	120.80
1	A	43	PHE	CB-CG-CD2	6.55	125.38	120.80
1	A	46	PHE	CB-CG-CD2	6.55	125.38	120.80
1	A	103	TYR	CB-CG-CD2	-6.35	117.19	121.00
1	A	2	LEU	O-C-N	6.17	132.57	122.70
1	A	146	TYR	CA-CB-CG	6.14	125.06	113.40
1	A	118	ARG	NE-CZ-NH2	6.05	123.33	120.30
1	A	61[A]	LEU	O-C-N	-5.88	113.30	122.70
1	A	61[B]	LEU	O-C-N	-5.88	113.30	122.70
1	A	70	THR	CA-CB-CG2	-5.83	104.23	112.40
1	A	98	LYS	CB-CG-CD	5.70	126.42	111.60

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	46	PHE	CB-CG-CD1	-5.69	116.82	120.80
1	A	63	LYS	CA-CB-CG	5.67	125.88	113.40
1	A	132	ASN	CB-CG-OD1	-5.66	110.28	121.60
1	A	20	ASP	O-C-N	5.61	131.67	122.70
1	A	31	ARG	NH1-CZ-NH2	5.60	125.56	119.40
1	A	103	TYR	O-C-N	-5.53	113.85	122.70
1	A	112	ILE	O-C-N	-5.50	113.89	122.70
1	A	45[A]	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	A	45[B]	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	A	146	TYR	CG-CD1-CE1	5.43	125.64	121.30
1	A	67	THR	N-CA-CB	5.43	120.61	110.30
1	A	117	SER	N-CA-CB	5.37	118.56	110.50
1	A	54	GLU	OE1-CD-OE2	-5.29	116.96	123.30
1	A	47	LYS	CB-CA-C	-5.27	99.87	110.40
1	A	79	LYS	C-N-CA	-5.25	111.28	122.30
1	A	41	GLU	CB-CG-CD	5.19	128.22	114.20
1	A	4	GLU	CG-CD-OE2	-5.03	108.24	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	139	ARG	Sidechain
1	A	45[A]	ARG	Sidechain
1	A	45[B]	ARG	Sidechain

CLOSE-CONTACTS INFOmissingINFO

## 5.2 Torsion angles [i](#)

### 5.2.1 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	158/153 (103%)	152 (96%)	6 (4%)	0	<b>100</b> <b>100</b>

There are no Ramachandran outliers to report.

### 5.2.2 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	132/125 (106%)	124 (94%)	8 (6%)	18 2

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	VAL
1	A	9	LEU
1	A	47	LYS
1	A	49	LEU
1	A	75[A]	ILE
1	A	75[B]	ILE
1	A	89	LEU
1	A	98	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	36	HIS
1	A	81	HIS
1	A	128	GLN
1	A	152	GLN

### 5.2.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.3 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.4 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.5 Ligand geometry [i](#)

4 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
4	CMO	A	201[B]	3	0,1,1	-	-	-		
3	HEM	A	155	1,4	41,50,50	2.02	13 (31%)	45,82,82	2.71	24 (53%)
4	CMO	A	201[A]	3	0,1,1	-	-	-		
2	SO4	A	154	-	4,4,4	1.02	0	6,6,6	1.38	1 (16%)

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	HEM	A	155	1,4	-	4/12/54/54	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	155	HEM	C3C-CAC	5.71	1.59	1.47
3	A	155	HEM	C1D-C2D	4.12	1.52	1.44
3	A	155	HEM	C3C-C2C	-3.42	1.35	1.40
3	A	155	HEM	CMB-C2B	3.04	1.57	1.50
3	A	155	HEM	CBD-CGD	-2.93	1.43	1.50
3	A	155	HEM	C4A-NA	2.82	1.42	1.36
3	A	155	HEM	C3B-C2B	-2.71	1.31	1.37
3	A	155	HEM	O2D-CGD	-2.64	1.21	1.30
3	A	155	HEM	CHA-C4D	2.64	1.41	1.35
3	A	155	HEM	CMD-C2D	2.48	1.56	1.50

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	155	HEM	O1D-CGD	2.41	1.30	1.22
3	A	155	HEM	CHB-C1B	2.15	1.40	1.35
3	A	155	HEM	C1A-CHA	-2.12	1.35	1.41

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	155	HEM	C4B-CHC-C1C	7.99	133.10	122.56
3	A	155	HEM	C4C-CHD-C1D	-6.24	114.32	122.56
3	A	155	HEM	CHD-C1D-ND	5.80	130.73	124.43
3	A	155	HEM	CMA-C3A-C4A	-4.63	121.34	128.46
3	A	155	HEM	CAD-CBD-CGD	4.63	123.56	113.60
3	A	155	HEM	CHD-C1D-C2D	-3.81	119.03	124.98
3	A	155	HEM	C1D-C2D-C3D	-3.59	103.18	106.96
3	A	155	HEM	O1D-CGD-CBD	-3.38	112.22	123.08
3	A	155	HEM	C3B-C2B-C1B	2.96	108.68	106.49
2	A	154	SO4	O3-S-O2	2.93	124.60	109.31
3	A	155	HEM	CBB-CAB-C3B	-2.81	113.65	127.62
3	A	155	HEM	CHA-C4D-ND	2.79	127.83	124.38
3	A	155	HEM	CAD-C3D-C2D	-2.71	122.83	127.88
3	A	155	HEM	O1A-CGA-CBA	-2.68	114.47	123.08
3	A	155	HEM	C4D-C3D-C2D	2.62	110.72	106.90
3	A	155	HEM	O2A-CGA-CBA	2.60	122.37	114.03
3	A	155	HEM	CMA-C3A-C2A	2.58	129.81	124.94
3	A	155	HEM	O2D-CGD-O1D	2.51	129.55	123.30
3	A	155	HEM	C4A-C3A-C2A	2.25	108.56	107.00
3	A	155	HEM	CHC-C4B-NB	-2.24	122.00	124.43
3	A	155	HEM	CMD-C2D-C3D	2.23	132.18	126.12
3	A	155	HEM	CHB-C1B-NB	-2.20	121.66	124.38
3	A	155	HEM	CHC-C4B-C3B	2.18	127.90	124.57
3	A	155	HEM	CHA-C4D-C3D	-2.17	121.25	125.33
3	A	155	HEM	CMB-C2B-C1B	-2.03	121.95	125.04

There are no chirality outliers.

All (4) torsion outliers are listed below:

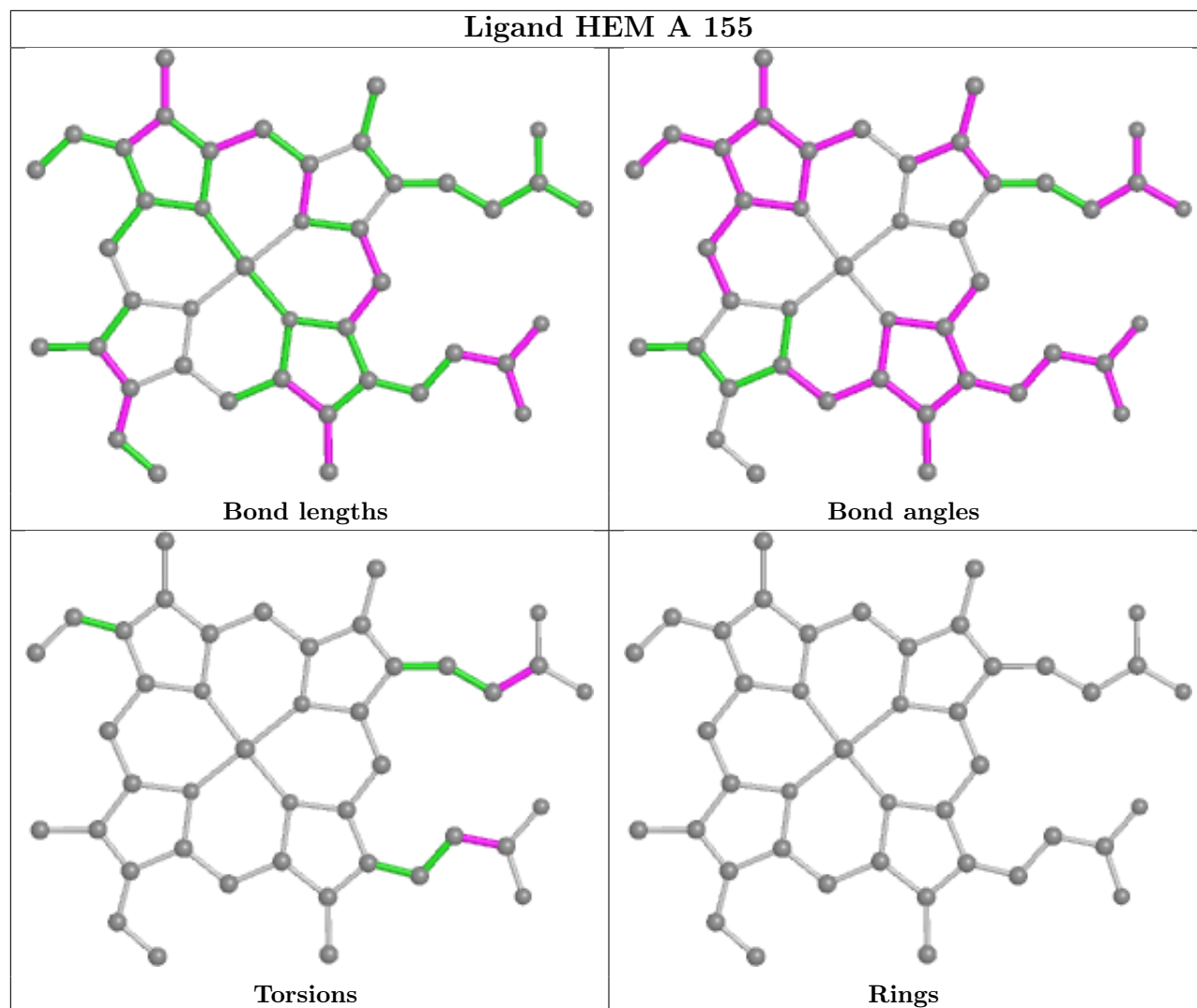
Mol	Chain	Res	Type	Atoms
3	A	155	HEM	CAA-CBA-CGA-O2A
3	A	155	HEM	CAA-CBA-CGA-O1A
3	A	155	HEM	CAD-CBD-CGD-O2D
3	A	155	HEM	CAD-CBD-CGD-O1D

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	201[B]	CMO	1	0
3	A	155	HEM	10	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 than 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.



## 5.6 Other polymers [i](#)

There are no such residues in this entry.

## 5.7 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.