

# Full wwPDB X-ray Structure Validation Report (i)

### Mar 4, 2024 - 01:48 PM EST

PDB ID : 1JFC

Title: X-ray structure of nitric oxide reductase (cytochrome P450nor) in the ferrous

CO state at atomic resolution

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nomics/Proteomics Initiative (RSGI)

Deposited on : 2001-06-20

Resolution : 1.05 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
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: 4.02b-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)

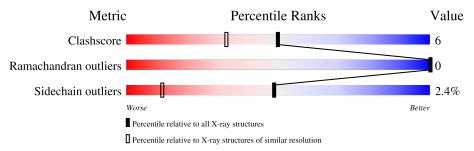
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.05 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
Clashscore	141614	1252 (1.10-1.02)
Ramachandran outliers	138981	1204 (1.10-1.02)
Sidechain outliers	138945	1202 (1.10-1.02)

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	٨	40.4						
1	A	404	84%	13%	• •			



## 2 Entry composition (i)

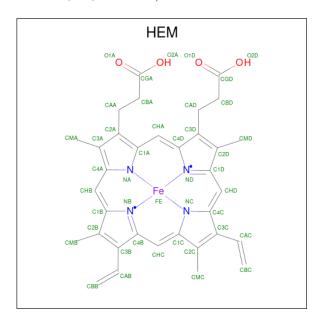
There are 5 unique types of molecules in this entry. The entry contains 7743 atoms, of which 3447 are hydrogens and 0 are deuteriums.

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 nitric-oxide reductase Cytochrome P450 55A1.

Mo	l Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total 6697	C 2113	H 3387	N 560	O 621	S 16	0	43	0

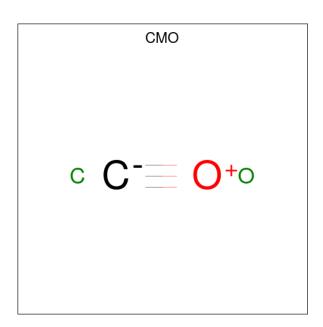
• Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
2	A	1	Total 146	C 68	Fe 2	H 60	N 8	O 8	0	1

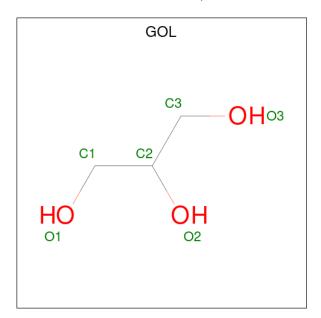
• Molecule 3 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).





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

 $\bullet$  Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $\mathrm{C_3H_8O_3}).$ 



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

• Molecule 5 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	892	Total O 892 892	0	152

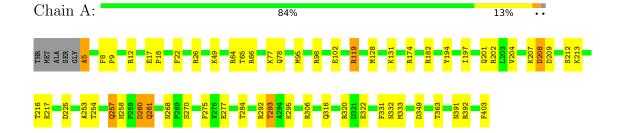


## 3 Residue-property plots (i)

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: nitric-oxide reductase Cytochrome P450 55A1





# 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	54.87Å 82.25Å 85.80Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	10.00 - 1.05	Depositor	
% Data completeness	96.9 (10.00-1.05)	Depositor	
(in resolution range)	30.3 (10.00 1.09)		
$R_{merge}$	0.07	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	SHELXL-97	Depositor	
$R, R_{free}$	0.117 , $0.152$	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	7743	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	16.0	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: CMO, HEM, GOL

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	Boı	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.82	$2/3528 \ (0.1\%)$	1.23	38/4785 (0.8%)	

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$Ideal(\AA)$
1	A	5	ALA	N-CA	19.79	1.85	1.46
1	A	26	ARG	CZ-NH1	-5.96	1.25	1.33

### All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	26	ARG	NE-CZ-NH2	12.76	126.68	120.30
1	A	306	ARG	NE-CZ-NH2	-11.47	114.57	120.30
1	A	5	ALA	N-CA-CB	9.27	123.07	110.10
1	A	174	ARG	NE-CZ-NH2	-9.18	115.71	120.30
1	A	261[A]	GLN	CA-CB-CG	8.71	132.56	113.40
1	A	261[B]	GLN	CA-CB-CG	8.71	132.56	113.40
1	A	174	ARG	NE-CZ-NH1	8.42	124.51	120.30
1	A	349	ASP	CB-CG-OD1	7.51	125.06	118.30
1	A	320	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	A	119[A]	ARG	NE-CZ-NH2	6.89	123.75	120.30
1	A	119[B]	ARG	NE-CZ-NH2	6.89	123.75	120.30
1	A	194	TYR	CG-CD2-CE2	6.88	126.80	121.30
1	A	66	ARG	NE-CZ-NH1	-6.66	116.97	120.30
1	A	208[A]	ASP	CB-CA-C	6.57	123.54	110.40
1	A	208[B]	ASP	CB-CA-C	6.57	123.54	110.40
1	A	292	ARG	NE-CZ-NH2	-6.50	117.05	120.30
1	A	293[A]	THR	CA-CB-CG2	-6.46	103.35	112.40
1	A	293[B]	THR	CA-CB-CG2	-6.46	103.35	112.40
1	A	194	TYR	CB-CG-CD2	6.33	124.80	121.00

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Mol	Chain	Res	Type	Atoms	${f Z}$	$Observed(^o)$	$Ideal(^{o})$
1	A	260	ASP	CB-CG-OD1	-6.33	112.61	118.30
1	A	306	ARG	NE-CZ-NH1	6.30	123.45	120.30
1	A	320	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	A	225	ASP	CB-CG-OD1	-6.13	112.78	118.30
1	A	119[A]	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	A	119[B]	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	A	22	PHE	CD1-CE1-CZ	6.00	127.30	120.10
1	A	182	ARG	NE-CZ-NH1	-5.92	117.34	120.30
1	A	119[A]	ARG	NH1-CZ-NH2	-5.90	112.91	119.40
1	A	119[B]	ARG	NH1-CZ-NH2	-5.90	112.91	119.40
1	A	403	PHE	CB-CG-CD2	-5.83	116.72	120.80
1	A	64	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	A	98	ARG	NE-CZ-NH1	5.61	123.10	120.30
1	A	403	PHE	CB-CG-CD1	5.52	124.67	120.80
1	A	26	ARG	NH1-CZ-NH2	-5.45	113.41	119.40
1	A	349	ASP	OD1-CG-OD2	-5.44	112.96	123.30
1	A	392[A]	ARG	CD-NE-CZ	5.37	131.12	123.60
1	A	392[B]	ARG	CD-NE-CZ	5.37	131.12	123.60
1	A	322	GLU	CB-CG-CD	5.01	127.72	114.20

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	3310	3387	3376	38	0
2	A	86	60	60	1	0
3	A	2	0	0	0	0
4	A	6	0	8	0	0
5	A	892	0	0	22	0
All	All	4296	3447	3444	40	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.

All (40) close contacts within the same asymmetric unit are listed below, sorted by their clash



## magnitude.

Atom-1	Atom-2	Interatomic	Clash
		${\rm distance}  (\mathring{\rm A})$	$-$ overlap $(\mathring{A})$
1:A:5:ALA:N	1:A:5:ALA:CA	1.85	1.39
1:A:260:ASP:HB2	5:A:1455[B]:HOH:O	1.85	0.77
1:A:213[B]:LYS:HG2	1:A:217[B]:GLU:OE2	1.87	0.73
1:A:95[A]:MET:HE2	5:A:1299:HOH:O	1.87	0.73
1:A:277[A]:GLU:HG2	5:A:935:HOH:O	1.94	0.67
1:A:49[A]:LYS:HG2	5:A:1228:HOH:O	1.97	0.63
1:A:216[B]:THR:HG22	5:A:796:HOH:O	1.98	0.62
1:A:363[B]:THR:HG21	5:A:953:HOH:O	2.00	0.61
1:A:254:THR:O	1:A:258[B]:HIS:HD2	1.85	0.59
1:A:268:ASN:OD1	1:A:270[A]:SER:HB2	2.03	0.58
1:A:131[B]:LYS:HB3	5:A:1269:HOH:O	2.05	0.57
1:A:65:THR:HG23	5:A:980:HOH:O	2.04	0.55
1:A:201[B]:GLN:HG2	5:A:1008:HOH:O	2.05	0.55
1:A:102[B]:GLU:HG2	5:A:993:HOH:O	2.06	0.54
1:A:213[B]:LYS:HE2	5:A:1335:HOH:O	2.07	0.53
1:A:5:ALA:N	1:A:5:ALA:C	2.61	0.51
1:A:293[B]:THR:HG22	5:A:626:HOH:O	2.10	0.50
1:A:212:SER:O	1:A:216[B]:THR:HG23	2.11	0.50
1:A:18:PRO:HB3	1:A:316[A]:GLN:CD	2.34	0.48
1:A:275:PHE:HB2	1:A:333:MET:HE3	1.93	0.48
1:A:363[A]:THR:HG22	5:A:1230:HOH:O	2.13	0.48
1:A:202:ARG:CZ	1:A:207:LYS:HD2	2.44	0.47
1:A:8:PHE:CG	1:A:9:PRO:HA	2.51	0.46
1:A:207:LYS:HE3	5:A:793:HOH:O	2.15	0.45
1:A:18:PRO:HB3	1:A:316[A]:GLN:OE1	2.17	0.44
1:A:208[B]:ASP:O	1:A:209:ASP:HB3	2.17	0.44
2:A:501[B]:HEM:HBC1	5:A:605:HOH:O	2.17	0.44
1:A:131[A]:LYS:HB3	5:A:1269:HOH:O	2.17	0.44
1:A:119[B]:ARG:NH1	5:A:1199:HOH:O	2.50	0.43
1:A:204[B]:VAL:HG23	5:A:1008:HOH:O	2.18	0.42
1:A:253:ALA:O	1:A:257[A]:GLN:HG2	2.19	0.42
1:A:213[B]:LYS:HD2	5:A:1156:HOH:O	2.19	0.42
1:A:295[A]:LYS:NZ	5:A:1422[A]:HOH:O	2.47	0.42
1:A:258[B]:HIS:CE1	1:A:331:PHE:HB3	2.54	0.42
1:A:257[B]:GLN:NE2	5:A:742:HOH:O	2.46	0.42
1:A:18:PRO:HB3	1:A:316[A]:GLN:NE2	2.34	0.42
1:A:12:ARG:HB3	1:A:17:GLU:O	2.20	0.41
1:A:284:THR:HB	1:A:316[A]:GLN:HG2	2.02	0.41

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	441/404 (109%)	429 (97%)	12 (3%)	0	100 100

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	384/343 (112%)	372 (97%)	12 (3%)	40 7	

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	LYS
1	A	78	GLN
1	A	128[A]	MET
1	A	128[B]	MET
1	A	197[A]	ILE
1	A	197[B]	ILE
1	A	257[A]	GLN
1	A	257[B]	GLN
1	A	261[A]	GLN
1	A	261[B]	GLN
1	A	332	ASN
1	A	391	ASN



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	176	ASN
1	A	223	ASN
1	A	332	ASN
1	A	340	GLN
1	A	391	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 monosaccharides in this entry.

## 5.6 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	Во	ond leng	${ m ths}$	В	ond ang	cles
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	CMO	A	502	2	0,1,1	-	-	-		
2	HEM	A	501[A]	3,1	41,50,50	1.55	8 (19%)	45,82,82	1.25	4 (8%)
4	GOL	A	503	-	5,5,5	1.71	2 (40%)	5,5,5	0.65	0
2	HEM	A	501[B]	3,1	41,50,50	1.36	4 (9%)	45,82,82	1.42	6 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral



centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

$\mathbf{Mol}$	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	501[A]	3,1	-	4/12/54/54	-
4	GOL	A	503	-	-	0/4/4/4	-
2	HEM	A	501[B]	3,1	-	4/12/54/54	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(Å)	$\operatorname{Ideal}(\text{\AA})$
2	A	501[A]	HEM	C3C-C2C	-4.38	1.34	1.40
2	A	501[A]	HEM	CAA-C2A	-4.20	1.45	1.52
2	A	501[B]	HEM	C3C-C2C	-3.46	1.35	1.40
4	A	503	GOL	O3-C3	3.02	1.55	1.42
2	A	501[B]	HEM	CHA-C4D	2.69	1.41	1.35
2	A	501[B]	HEM	O2D-CGD	-2.66	1.21	1.30
2	A	501[A]	HEM	C1A-NA	2.48	1.41	1.36
2	A	501[A]	HEM	C4A-NA	2.46	1.41	1.36
2	A	501[A]	HEM	C2C-C1C	2.38	1.48	1.42
4	A	503	GOL	C1-C2	2.24	1.60	1.51
2	A	501[B]	HEM	CAA-C2A	-2.23	1.48	1.52
2	A	501[A]	HEM	C3B-C2B	-2.18	1.32	1.37
2	A	501[A]	HEM	CHB-C1B	2.15	1.40	1.35
2	A	501[A]	HEM	CBB-CAB	2.02	1.40	1.30

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
2	A	501[B]	HEM	C4C-CHD-C1D	4.69	128.75	122.56
2	A	501[B]	HEM	C4B-CHC-C1C	4.45	128.44	122.56
2	A	501[A]	HEM	C4C-CHD-C1D	4.37	128.33	122.56
2	A	501[A]	HEM	C4B-CHC-C1C	3.53	127.22	122.56
2	A	501[B]	HEM	CMC-C2C-C3C	2.89	130.08	124.68
2	A	501[A]	HEM	CMC-C2C-C3C	2.57	129.49	124.68
2	A	501[B]	HEM	O1D-CGD-CBD	-2.40	115.37	123.08
2	A	501[B]	HEM	CHD-C1D-ND	-2.28	121.96	124.43
2	A	501[A]	HEM	CMB-C2B-C1B	-2.16	121.75	125.04
2	A	501[B]	HEM	C2D-C1D-ND	2.06	112.35	109.88

There are no chirality outliers.

All (8) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	A	501[B]	HEM	C2B-C3B-CAB-CBB
2	A	501[B]	HEM	C4B-C3B-CAB-CBB
2	A	501[A]	HEM	CAA-CBA-CGA-O1A
2	A	501[A]	HEM	CAA-CBA-CGA-O2A
2	A	501[B]	HEM	CAD-CBD-CGD-O2D
2	A	501[A]	HEM	CAD-CBD-CGD-O2D
2	A	501[A]	HEM	CAD-CBD-CGD-O1D
2	A	501[B]	HEM	CAD-CBD-CGD-O1D

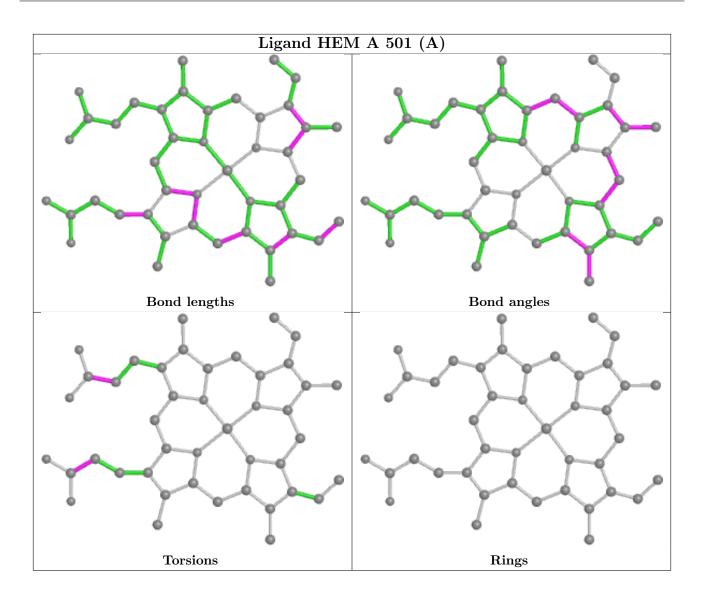
There are no ring outliers.

1 monomer is involved in 1 short contact:

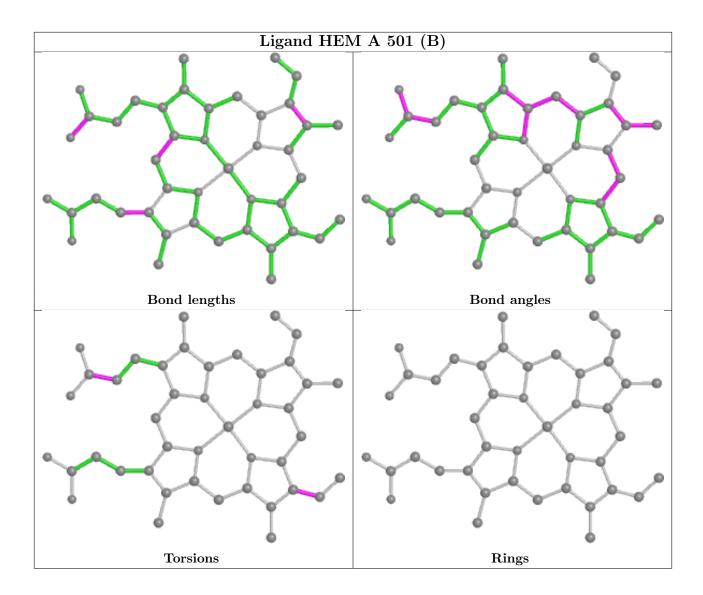
Mol					Symm-Clashes
2	A	501[B]	HEM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 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.

