



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2023 – 04:41 AM EDT

PDB ID : 6V59  
Title : Crystal structure of the diheme peroxidase BthA Y463M variant from Burkholderia thailandensis E264  
Authors : Cohen, S.E.; Drennan, C.L.  
Deposited on : 2019-12-03  
Resolution : 1.59 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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : **FAILED**  
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) : 2.35.1

## 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 1.59 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13840 atoms, of which 6362 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.

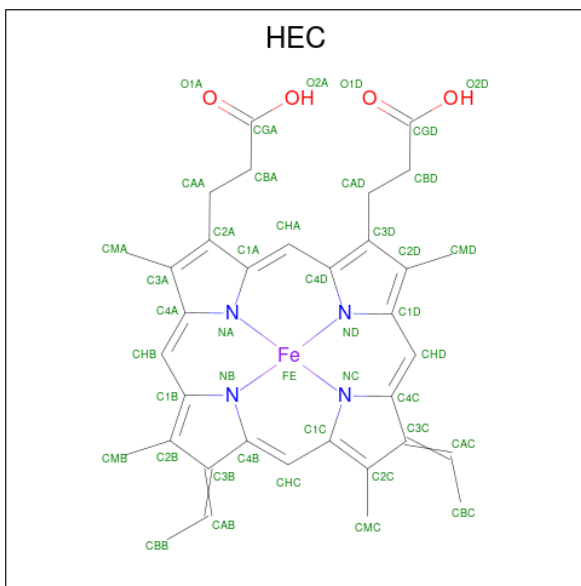
- Molecule 1 is a protein called Di-haem cytochrome c peroxidase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	419	6242	1987	3071	585	580	19	0	0	0
1	B	419	6265	1998	3076	580	591	20	0	3	0

There are 4 discrepancies between the modelled and reference sequences:

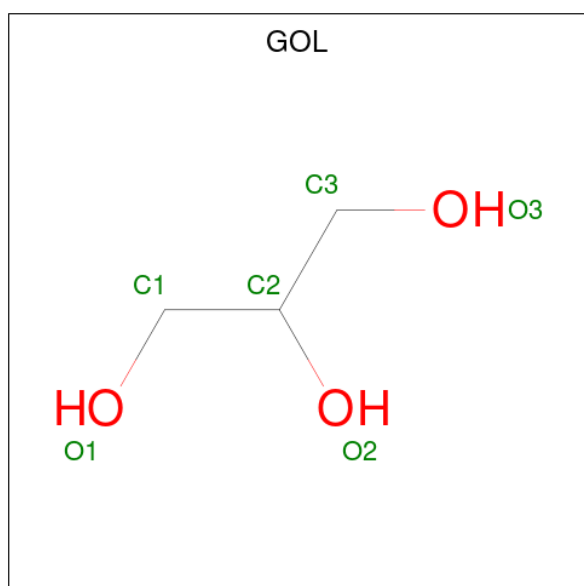
Chain	Residue	Modelled	Actual	Comment	Reference
A	68	SER	-	insertion	UNP Q2T6B0
A	463	MET	TYR	engineered mutation	UNP Q2T6B0
B	68	SER	-	insertion	UNP Q2T6B0
B	463	MET	TYR	engineered mutation	UNP Q2T6B0

- Molecule 2 is HEME C (three-letter code: HEC) (formula:  $C_{34}H_{34}FeN_4O_4$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Fe	H	N			O
2	A	1	Total 75	C 34	Fe 1	H 32	N 4	O 4	0	0
2	A	1	Total 75	C 34	Fe 1	H 32	N 4	O 4	0	0
2	B	1	Total 75	C 34	Fe 1	H 32	N 4	O 4	0	0
2	B	1	Total 75	C 34	Fe 1	H 32	N 4	O 4	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	Total 14	C 3	H 8	O 3	0	0
3	A	1	Total 14	C 3	H 8	O 3	0	0
3	A	1	Total 14	C 3	H 8	O 3	0	0
3	A	1	Total 14	C 3	H 8	O 3	0	0
3	B	1	Total 14	C 3	H 8	O 3	0	0
3	B	1	Total 14	C 3	H 8	O 3	0	0
3	B	1	Total 13	C 3	H 7	O 3	0	0
3	B	1	Total 14	C 3	H 8	O 3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		
4	B	2	Total	Cl	0	0
			2	2		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	458	Total	O	0	0
			458	458		
6	B	417	Total	O	0	0
			417	417		

MolProbity and EDS failed to run properly - this section is therefore empty.

### 3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.97Å 87.61Å 184.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.23 – 1.59	Depositor
% Data completeness (in resolution range)	98.5 (48.23-1.59)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 1.59Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.151 , 0.177	Depositor
Wilson B-factor (Å <sup>2</sup> )	17.8	Xtrriage
Anisotropy	0.663	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	13840	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

### 4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 5 are monoatomic - leaving 15 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	B	601	1	32,50,50	2.11	5 (15%)	24,82,82	1.44	4 (16%)
3	GOL	A	605	-	5,5,5	0.66	0	5,5,5	0.97	0
3	GOL	B	604	-	5,5,5	0.78	0	5,5,5	0.95	0
3	GOL	A	604	-	5,5,5	0.82	0	5,5,5	1.06	0
3	GOL	A	606	-	5,5,5	0.81	0	5,5,5	1.03	0
3	GOL	B	603	-	5,5,5	0.91	0	5,5,5	0.83	0
2	HEC	A	601	1,6	32,50,50	2.08	3 (9%)	24,82,82	1.73	6 (25%)
3	GOL	B	606	-	5,5,5	0.74	0	5,5,5	0.90	0
2	HEC	A	602	1	32,50,50	2.18	3 (9%)	24,82,82	1.52	4 (16%)
3	GOL	B	609	-	5,5,5	0.84	0	5,5,5	0.96	0
3	GOL	A	603	-	5,5,5	0.83	0	5,5,5	0.91	0
3	GOL	B	605	-	5,5,5	0.71	0	5,5,5	1.04	0
2	HEC	B	602	1	32,50,50	2.19	3 (9%)	24,82,82	1.38	4 (16%)
3	GOL	B	608	-	5,5,5	0.80	0	5,5,5	0.94	0
3	GOL	B	607	-	5,5,5	0.90	0	5,5,5	0.97	0

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	B	601	1	-	1/10/54/54	-
3	GOL	A	605	-	-	3/4/4/4	-
3	GOL	B	604	-	-	0/4/4/4	-
3	GOL	A	604	-	-	2/4/4/4	-
3	GOL	A	606	-	-	0/4/4/4	-
3	GOL	B	603	-	-	4/4/4/4	-
2	HEC	A	601	1,6	-	1/10/54/54	-
3	GOL	B	606	-	-	0/4/4/4	-
2	HEC	A	602	1	-	1/10/54/54	-
3	GOL	B	609	-	-	0/4/4/4	-
3	GOL	A	603	-	-	0/4/4/4	-
3	GOL	B	605	-	-	0/4/4/4	-
2	HEC	B	602	1	-	1/10/54/54	-
3	GOL	B	608	-	-	2/4/4/4	-
3	GOL	B	607	-	-	0/4/4/4	-



All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	602	HEC	C2B-C3B	-7.22	1.33	1.40
2	A	602	HEC	C3C-C2C	-6.56	1.33	1.40
2	A	602	HEC	C2B-C3B	-6.44	1.34	1.40
2	B	601	HEC	C2B-C3B	-6.08	1.34	1.40
2	B	601	HEC	C3C-C2C	-6.07	1.34	1.40
2	A	601	HEC	C3C-C2C	-5.98	1.34	1.40
2	A	601	HEC	C2B-C3B	-5.96	1.34	1.40
2	B	602	HEC	C3C-C2C	-5.77	1.34	1.40
2	A	601	HEC	C3D-C2D	4.97	1.52	1.37
2	A	602	HEC	C3D-C2D	4.94	1.52	1.37
2	B	601	HEC	C3D-C2D	4.90	1.52	1.37
2	B	602	HEC	C3D-C2D	4.70	1.51	1.37
2	B	601	HEC	CAA-C2A	2.11	1.55	1.52
2	B	601	HEC	C4D-ND	2.05	1.40	1.36

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	HEC	CMB-C2B-C1B	-3.70	122.77	128.46
2	A	601	HEC	CMC-C2C-C1C	-3.36	123.29	128.46
2	A	601	HEC	CBD-CAD-C3D	-3.23	107.11	112.62
2	A	602	HEC	CMC-C2C-C1C	-3.02	123.82	128.46
2	B	601	HEC	CMB-C2B-C1B	-2.97	123.89	128.46
2	A	602	HEC	C1D-C2D-C3D	-2.92	104.96	107.00
2	B	601	HEC	CBD-CAD-C3D	-2.75	107.93	112.62
2	B	602	HEC	CMC-C2C-C1C	-2.74	124.25	128.46
2	A	602	HEC	CMB-C2B-C1B	-2.69	124.33	128.46
2	B	602	HEC	CMB-C2B-C1B	-2.63	124.42	128.46
2	B	601	HEC	CMC-C2C-C1C	-2.56	124.52	128.46
2	A	602	HEC	CBD-CAD-C3D	-2.34	108.62	112.62
2	A	601	HEC	CBA-CAA-C2A	-2.25	108.82	112.60
2	B	601	HEC	O1A-CGA-CBA	-2.23	115.92	123.08
2	B	602	HEC	CBD-CAD-C3D	-2.12	109.00	112.62
2	A	601	HEC	O2A-CGA-CBA	2.11	120.81	114.03
2	A	601	HEC	O1A-CGA-CBA	-2.04	116.53	123.08
2	B	602	HEC	C1D-C2D-C3D	-2.02	105.59	107.00

There are no chirality outliers.

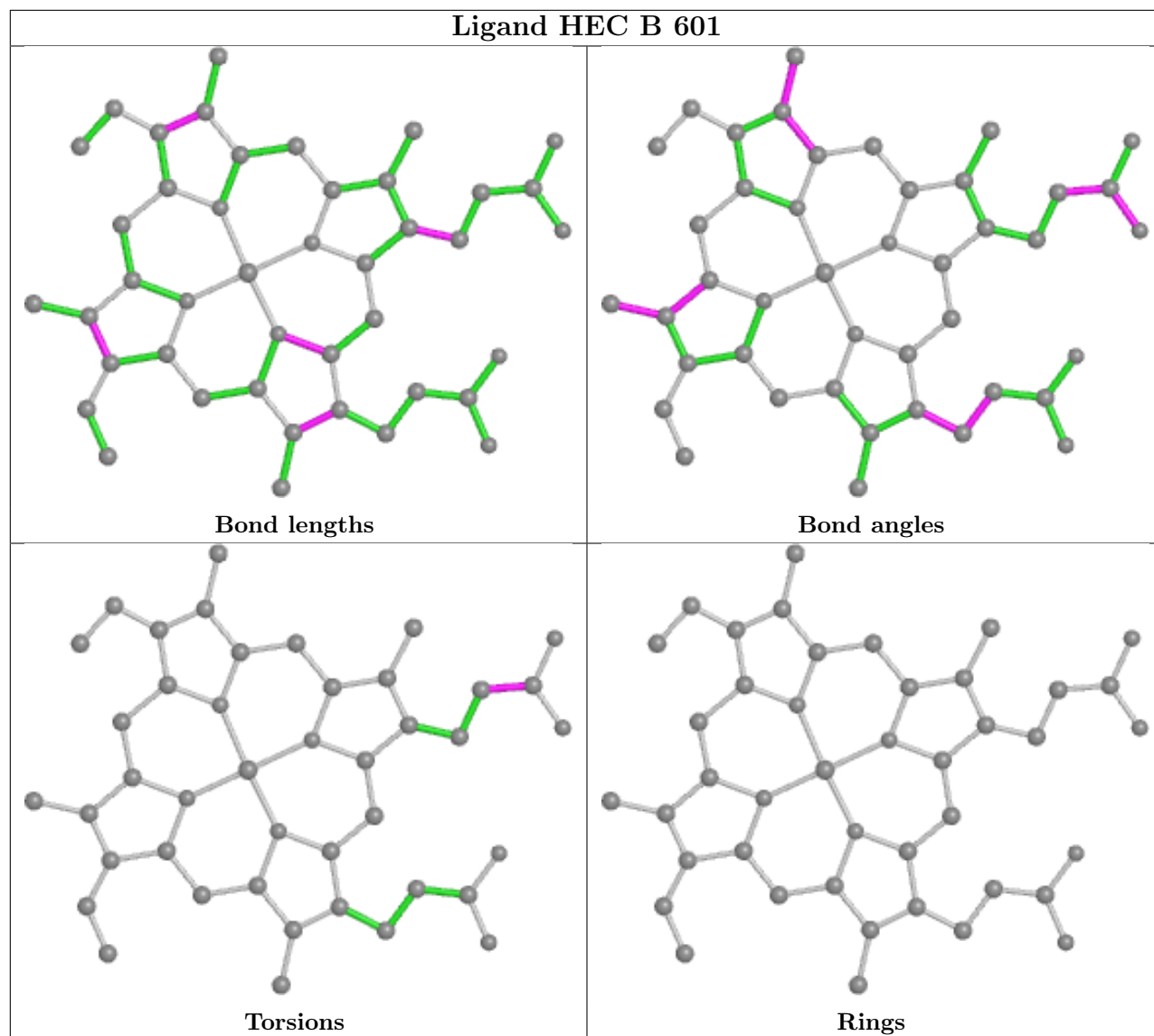
All (15) torsion outliers are listed below:

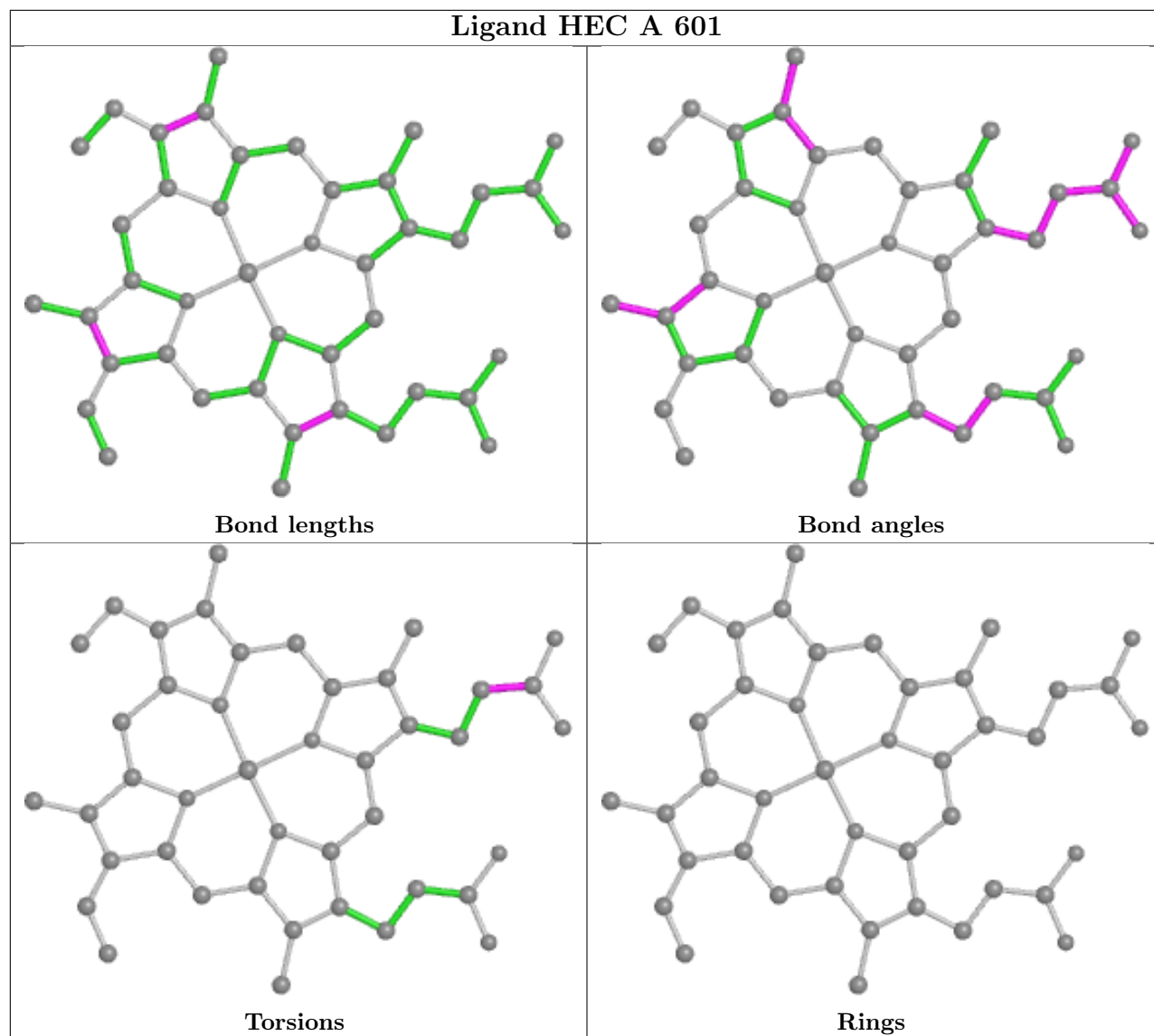
Mol	Chain	Res	Type	Atoms
3	A	605	GOL	C1-C2-C3-O3
3	A	605	GOL	O2-C2-C3-O3
3	B	603	GOL	C1-C2-C3-O3
3	B	603	GOL	O2-C2-C3-O3
3	B	608	GOL	O1-C1-C2-C3
3	A	604	GOL	O1-C1-C2-C3
3	B	603	GOL	O1-C1-C2-C3
3	B	608	GOL	O1-C1-C2-O2
3	B	603	GOL	O1-C1-C2-O2
2	A	602	HEC	CAA-CBA-CGA-O2A
3	A	605	GOL	O1-C1-C2-C3
2	B	602	HEC	CAD-CBD-CGD-O1D
3	A	604	GOL	O1-C1-C2-O2
2	A	601	HEC	CAA-CBA-CGA-O1A
2	B	601	HEC	CAA-CBA-CGA-O2A

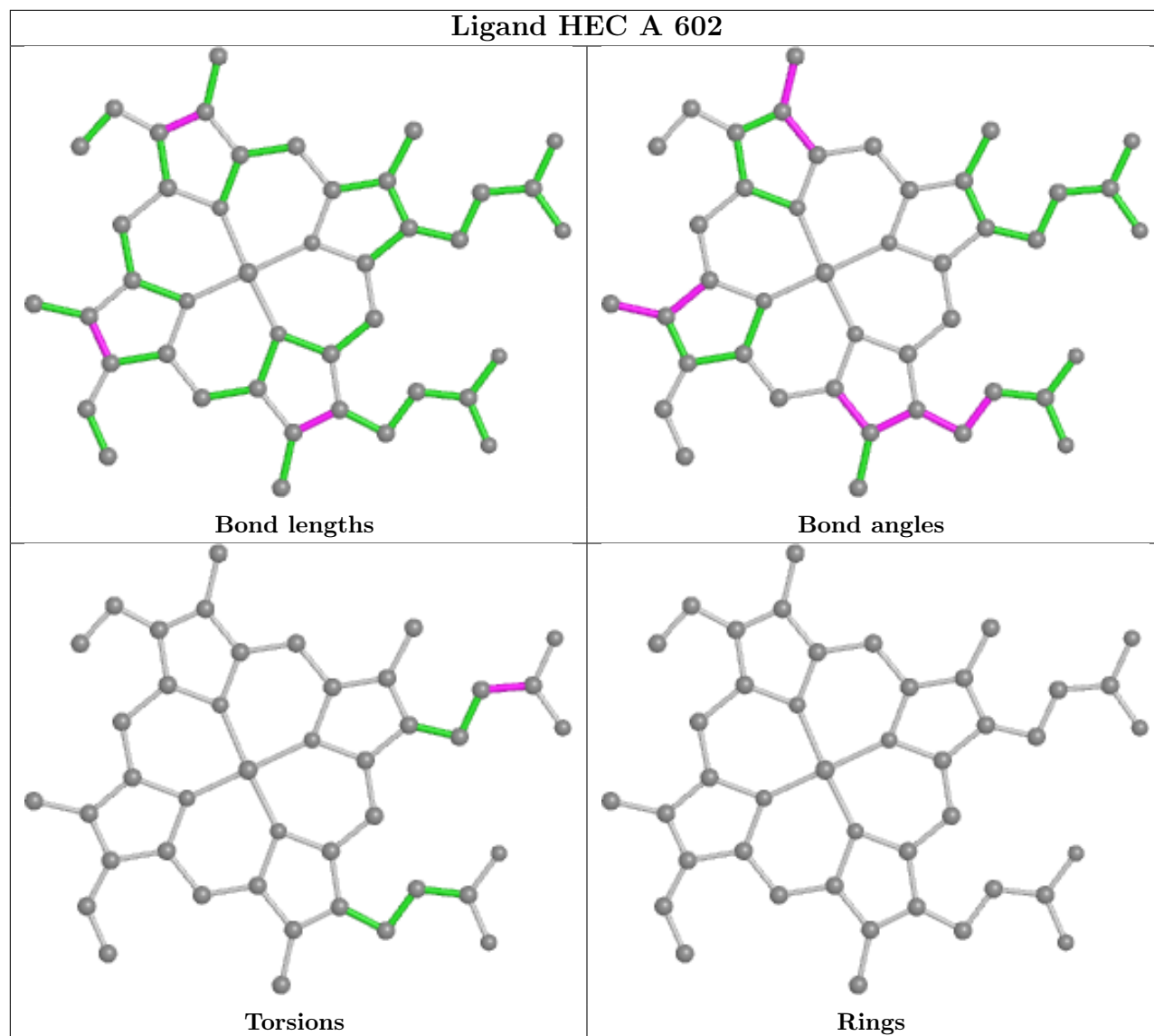
There are no ring outliers.

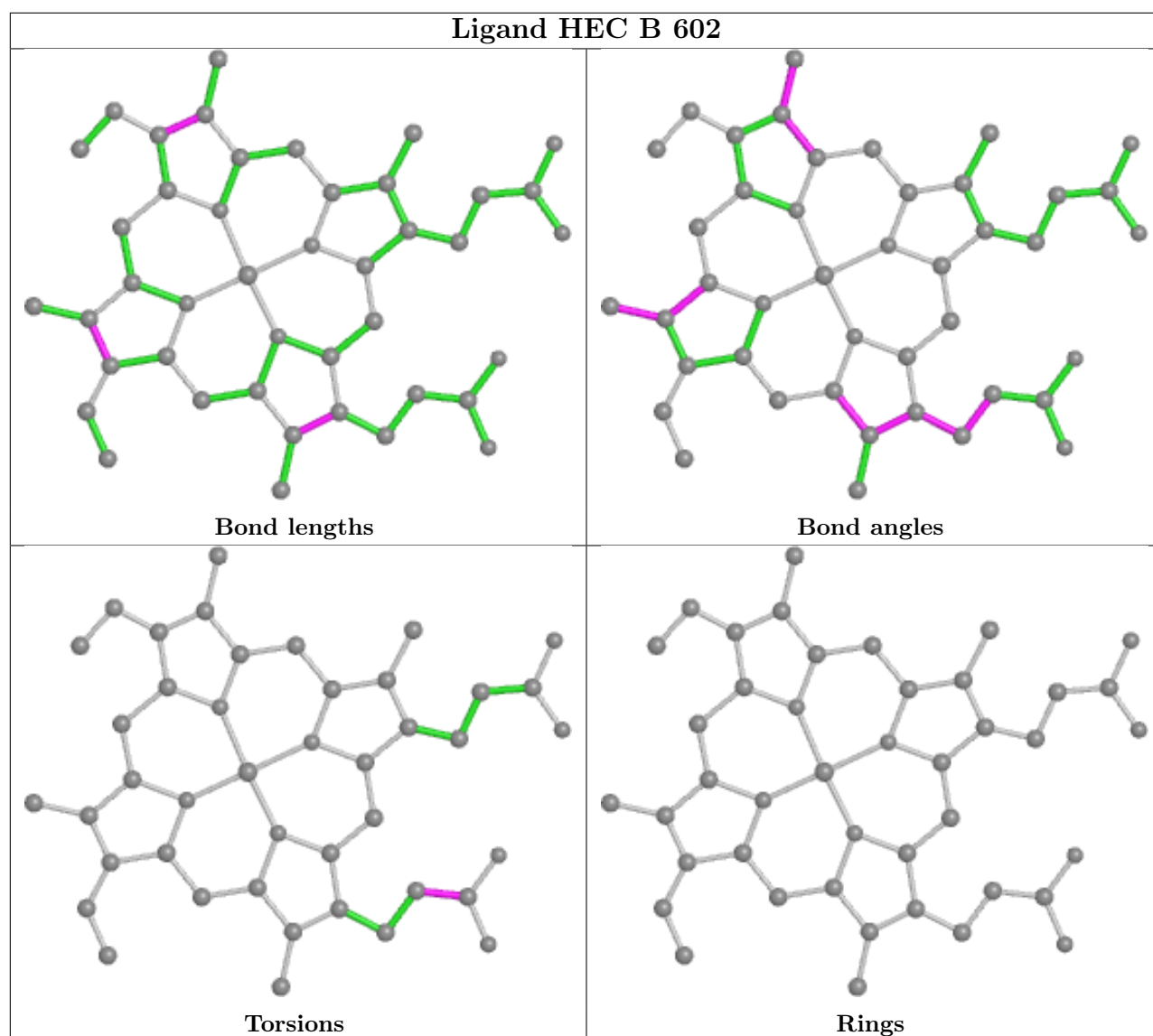
No monomer is involved in short contacts.

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.









#### 4.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

#### 4.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

## 5 Fit of model and data

### 5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 5.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 5.5 Other polymers

EDS failed to run properly - this section is therefore empty.