



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2023 – 05:21 AM EDT

PDB ID : 6PO5
Title : Structure of human neuronal nitric oxide synthase R354A/G357D mutant heme domain in complex with 7-(3-(Aminomethyl)-4-(cyclobutylmethoxy)phenyl)-4-methylquinolin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2019-07-03
Resolution : 1.82 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 ⓘ 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 : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (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 1.82 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 7 unique types of molecules in this entry. The entry contains 7701 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.

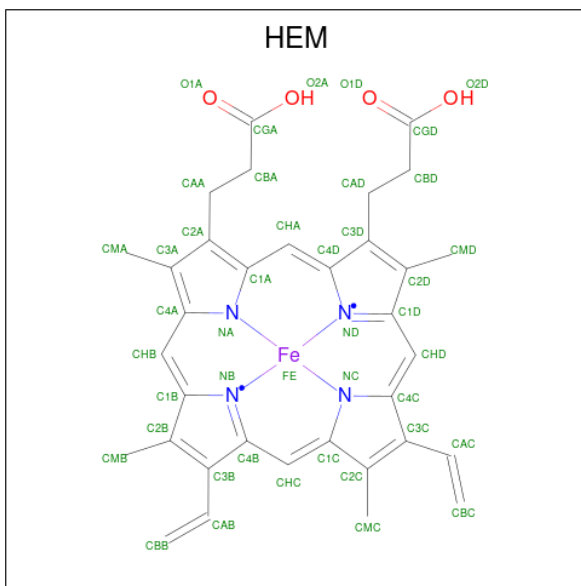
- Molecule 1 is a protein called Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	417	Total 3416	C 2186	N 582	O 625	S 23	0	5	0
1	B	411	Total 3362	C 2154	N 572	O 615	S 21	0	3	0

There are 4 discrepancies between the modelled and reference sequences:

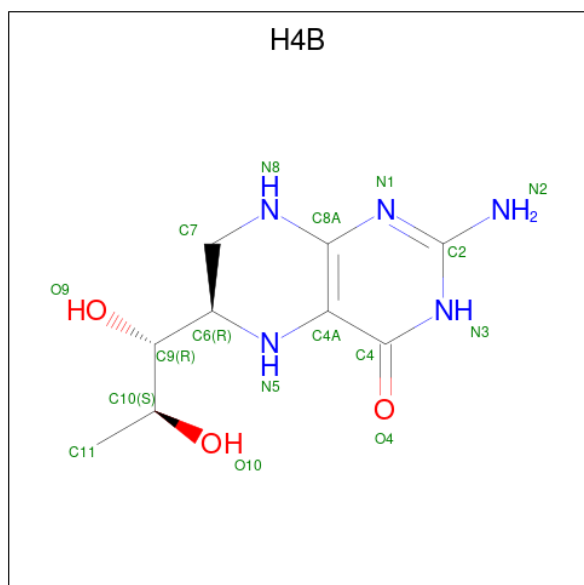
Chain	Residue	Modelled	Actual	Comment	Reference
A	354	ALA	ARG	engineered mutation	UNP P29475
A	357	ASP	GLY	engineered mutation	UNP P29475
B	354	ALA	ARG	engineered mutation	UNP P29475
B	357	ASP	GLY	engineered mutation	UNP P29475

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



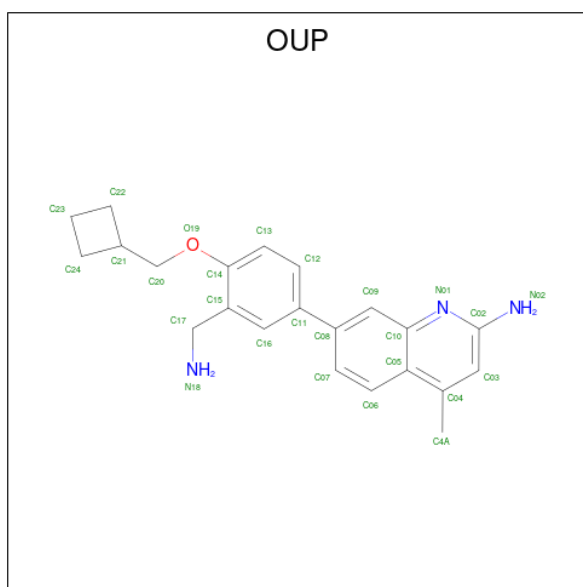
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is 7-[3-(aminomethyl)-4-(cyclobutylmethoxy)phenyl]-4-methylquinolin-2-amine (three-letter code: OUP) (formula: $C_{22}H_{25}N_3O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	26	22	3	1	0	0
4	B	1	26	22	3	1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Zn	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	407	Total	O	0	0
			407	407		
7	B	325	Total	O	0	0
			325	325		

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, α , β , γ	52.24Å 123.73Å 165.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.58 – 1.82	Depositor
% Data completeness (in resolution range)	98.8 (41.58-1.82)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 1.82Å)	Xtrriage
Refinement program	PHENIX (1.11.1-2575_1496: ???)	Depositor
R, R_{free}	0.189 , 0.228	Depositor
Wilson B-factor (Å ²)	31.9	Xtrriage
Anisotropy	0.589	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	7701	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

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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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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
3	H4B	B	803	-	16,18,18	0.97	0	11,26,26	2.78	6 (54%)
4	OUP	A	803	-	29,29,29	0.94	1 (3%)	40,41,41	1.50	4 (10%)
4	OUP	B	804	-	29,29,29	0.97	2 (6%)	40,41,41	1.53	6 (15%)
5	GOL	B	805	-	5,5,5	0.36	0	5,5,5	0.22	0
2	HEM	B	802	1	41,50,50	1.49	6 (14%)	45,82,82	1.92	8 (17%)
5	GOL	A	804	-	5,5,5	0.37	0	5,5,5	0.27	0
3	H4B	A	802	-	16,18,18	0.71	0	11,26,26	2.79	7 (63%)
2	HEM	A	801	1	41,50,50	1.41	5 (12%)	45,82,82	1.84	12 (26%)
5	GOL	A	805	-	5,5,5	0.43	0	5,5,5	0.55	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
3	H4B	B	803	-	-	3/8/17/17	0/2/2/2
4	OUP	A	803	-	-	3/11/17/17	0/4/4/4
4	OUP	B	804	-	-	6/11/17/17	0/4/4/4
5	GOL	B	805	-	-	2/4/4/4	-
2	HEM	B	802	1	-	5/12/54/54	-
5	GOL	A	804	-	-	2/4/4/4	-
3	H4B	A	802	-	-	3/8/17/17	0/2/2/2
2	HEM	A	801	1	-	5/12/54/54	-
5	GOL	A	805	-	-	4/4/4/4	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	802	HEM	C3C-C2C	-3.98	1.34	1.40
2	B	802	HEM	C3C-CAC	3.82	1.55	1.47
2	A	801	HEM	C3C-C2C	-3.79	1.35	1.40
2	A	801	HEM	C3C-CAC	3.41	1.54	1.47
2	B	802	HEM	CAB-C3B	2.96	1.55	1.47
2	A	801	HEM	CAB-C3B	2.96	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	802	HEM	CMD-C2D	2.36	1.55	1.50
4	B	804	OUP	C05-C10	-2.30	1.38	1.42
2	A	801	HEM	C3B-C2B	-2.26	1.32	1.37
2	B	802	HEM	C3B-C2B	-2.12	1.33	1.37
2	B	802	HEM	CMB-C2B	2.11	1.55	1.50
2	A	801	HEM	CMB-C2B	2.02	1.55	1.50
4	A	803	OUP	C05-C10	-2.02	1.39	1.42
4	B	804	OUP	C02-N01	2.01	1.36	1.33

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	802	HEM	CBA-CAA-C2A	-7.63	99.59	112.62
2	A	801	HEM	CBA-CAA-C2A	-5.94	102.47	112.62
3	B	803	H4B	C8A-C4A-C4	5.51	119.46	114.57
3	A	802	H4B	C8A-C4A-C4	4.49	118.56	114.57
4	B	804	OUP	C04-C05-C10	4.45	120.42	118.01
3	A	802	H4B	C4-C4A-N5	4.44	122.85	119.12
4	A	803	OUP	C04-C05-C10	4.17	120.27	118.01
4	A	803	OUP	O19-C14-C15	4.10	121.14	115.78
2	A	801	HEM	CMA-C3A-C4A	-3.91	122.45	128.46
3	A	802	H4B	C2-N3-C4	3.83	122.02	115.93
3	B	803	H4B	C2-N3-C4	3.74	121.88	115.93
3	B	803	H4B	N1-C2-N3	-3.72	119.59	125.42
4	B	804	OUP	C05-C10-N01	-3.68	118.91	122.81
2	B	802	HEM	C4B-CHC-C1C	3.65	127.38	122.56
4	A	803	OUP	C05-C10-N01	-3.45	119.15	122.81
2	A	801	HEM	C4B-CHC-C1C	3.32	126.94	122.56
3	A	802	H4B	N1-C2-N3	-3.29	120.26	125.42
2	B	802	HEM	C3B-C2B-C1B	3.05	108.75	106.49
4	B	804	OUP	O19-C14-C15	3.03	119.74	115.78
2	A	801	HEM	CAD-C3D-C4D	-2.88	119.62	124.66
2	A	801	HEM	CAD-C3D-C2D	2.81	133.12	127.88
3	B	803	H4B	N2-C2-N3	2.74	121.51	117.25
2	B	802	HEM	C4D-ND-C1D	2.69	107.86	105.07
3	B	803	H4B	C2-N1-C8A	2.68	120.54	114.54
2	B	802	HEM	CMA-C3A-C4A	-2.64	124.41	128.46
2	A	801	HEM	CHA-C4D-ND	2.63	127.63	124.38
2	A	801	HEM	CMA-C3A-C2A	2.59	129.82	124.94
2	A	801	HEM	CBD-CAD-C3D	2.49	119.53	112.63
2	B	802	HEM	CMC-C2C-C3C	2.35	129.08	124.68
3	A	802	H4B	C2-N1-C8A	2.34	119.77	114.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	802	HEM	CHA-C4D-ND	2.33	127.26	124.38
4	B	804	OUP	C07-C08-C11	-2.26	117.44	121.36
2	A	801	HEM	CMC-C2C-C3C	2.23	128.86	124.68
2	A	801	HEM	CAD-CBD-CGD	-2.20	108.88	113.60
3	B	803	H4B	C4-C4A-N5	2.18	120.95	119.12
4	A	803	OUP	O19-C14-C13	-2.16	119.30	123.97
2	B	802	HEM	O1D-CGD-CBD	-2.15	116.16	123.08
3	A	802	H4B	C4A-N5-C6	-2.15	115.30	121.16
2	A	801	HEM	C3B-C2B-C1B	2.12	108.06	106.49
4	B	804	OUP	C03-C04-C05	2.09	119.84	117.78
2	A	801	HEM	CAB-C3B-C2B	-2.07	121.78	128.60
4	B	804	OUP	C06-C05-C04	-2.06	119.72	123.66
3	A	802	H4B	N2-C2-N3	2.04	120.42	117.25

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	HEM	C2D-C3D-CAD-CBD
2	B	802	HEM	C2D-C3D-CAD-CBD
2	B	802	HEM	C4D-C3D-CAD-CBD
4	A	803	OUP	O19-C20-C21-C22
4	B	804	OUP	O19-C20-C21-C22
4	B	804	OUP	O19-C20-C21-C24
5	A	804	GOL	O1-C1-C2-C3
5	A	805	GOL	O1-C1-C2-C3
5	B	805	GOL	O1-C1-C2-C3
2	A	801	HEM	C4D-C3D-CAD-CBD
5	A	805	GOL	C1-C2-C3-O3
5	A	805	GOL	O1-C1-C2-O2
5	A	805	GOL	O2-C2-C3-O3
5	B	805	GOL	O1-C1-C2-O2
3	B	803	H4B	C7-C6-C9-O9
4	B	804	OUP	C13-C14-O19-C20
4	B	804	OUP	C21-C20-O19-C14
5	A	804	GOL	O1-C1-C2-O2
4	B	804	OUP	C15-C14-O19-C20
3	A	802	H4B	C7-C6-C9-C10
3	B	803	H4B	C7-C6-C9-C10
3	A	802	H4B	C7-C6-C9-O9
2	B	802	HEM	C4B-C3B-CAB-CBB
4	A	803	OUP	C13-C14-O19-C20

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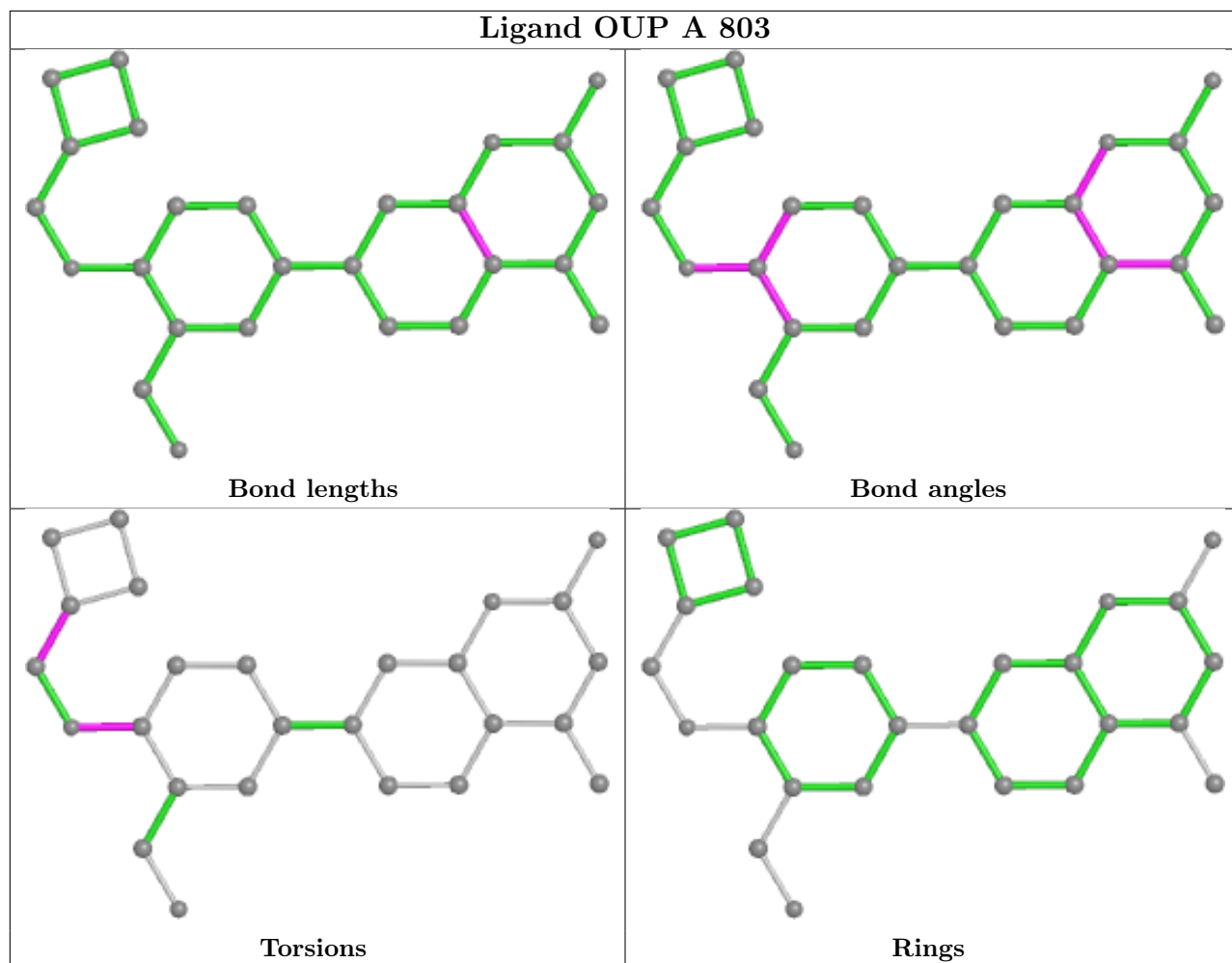
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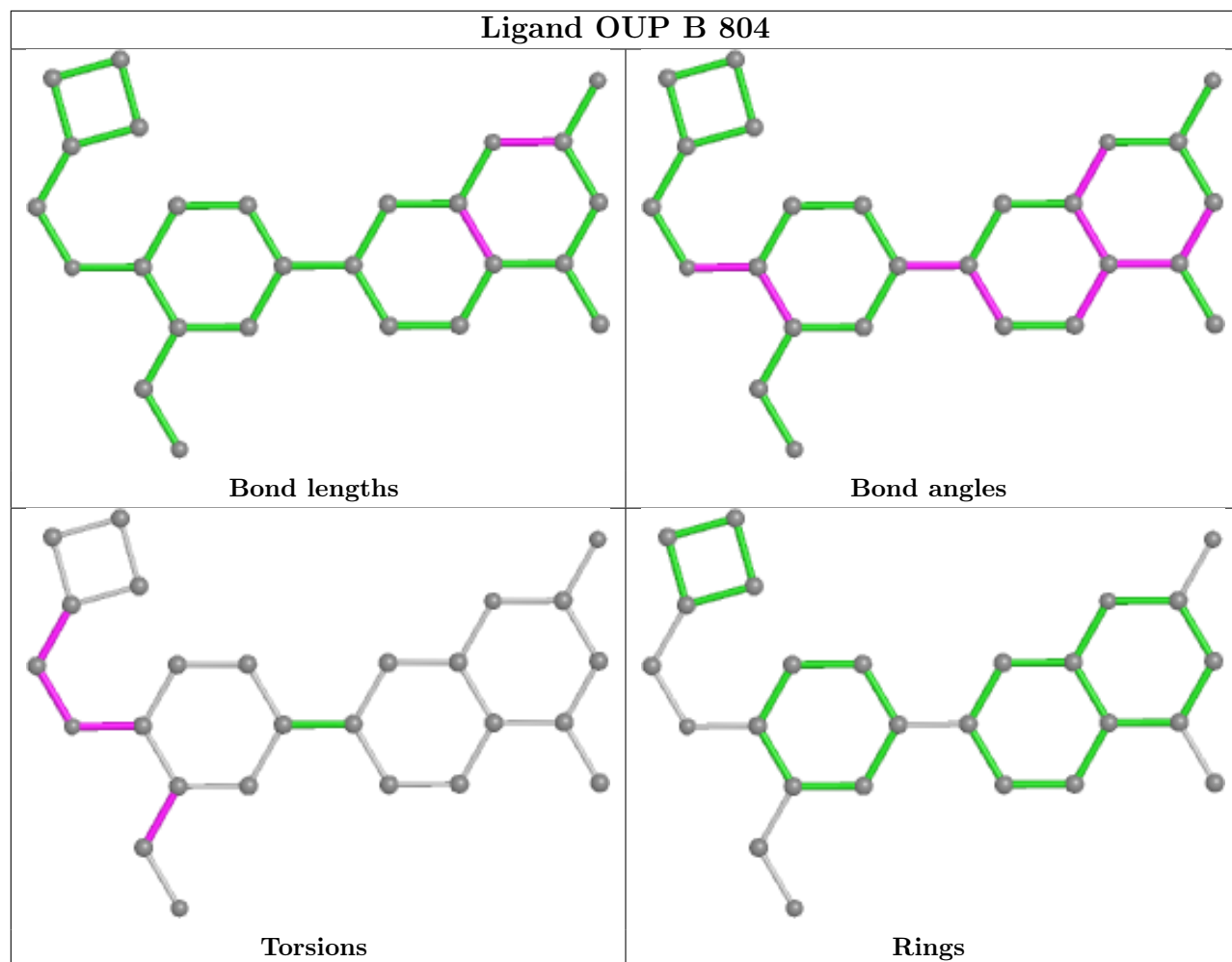
Mol	Chain	Res	Type	Atoms
4	A	803	OUP	C15-C14-O19-C20
2	A	801	HEM	C3D-CAD-CBD-CGD
3	A	802	H4B	N5-C6-C9-O9
3	B	803	H4B	N5-C6-C9-O9
2	B	802	HEM	CAD-CBD-CGD-O2D
4	B	804	OUP	C14-C15-C17-N18
2	B	802	HEM	CAD-CBD-CGD-O1D
2	A	801	HEM	CAD-CBD-CGD-O2D
2	A	801	HEM	CAD-CBD-CGD-O1D

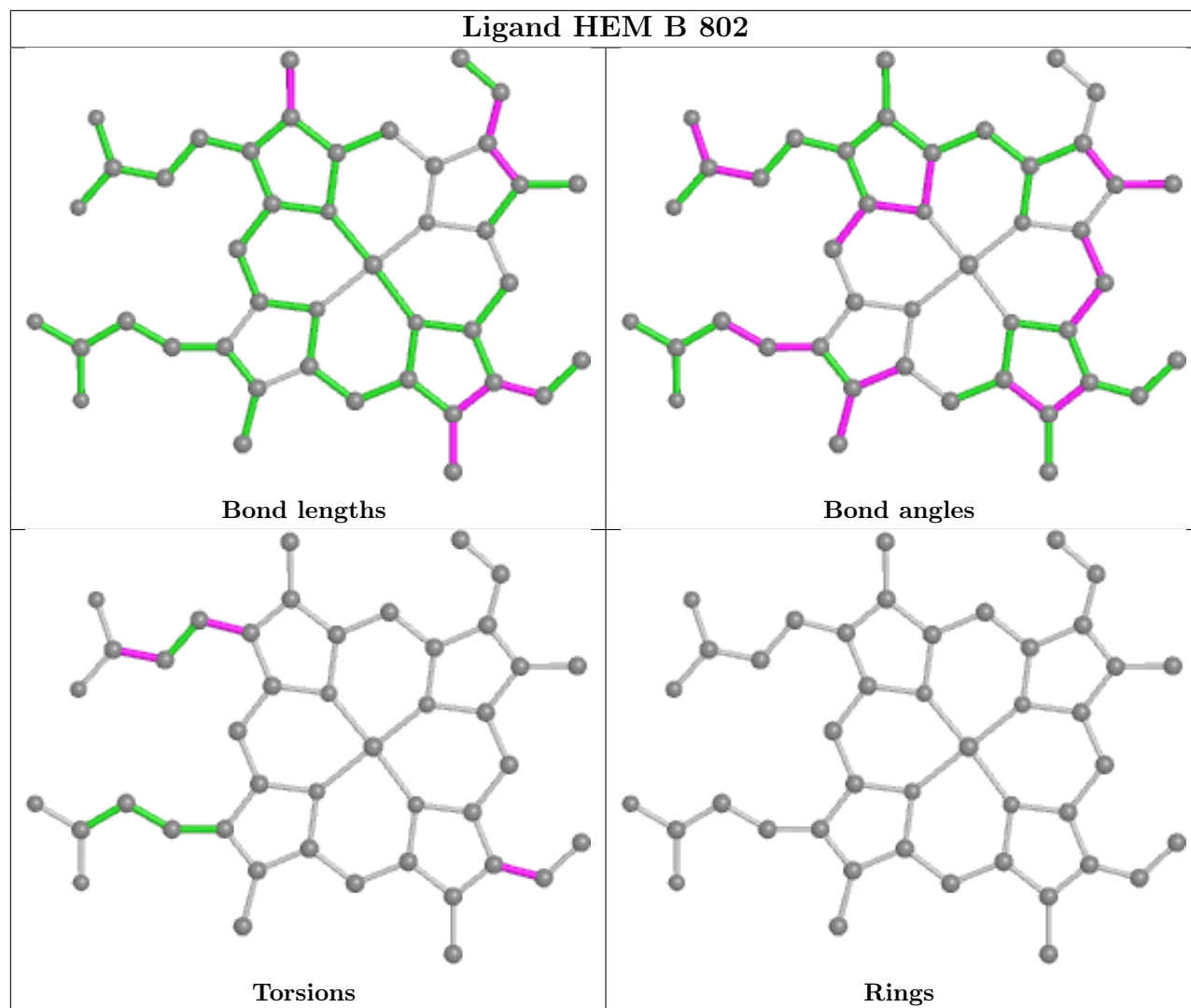
There are no ring outliers.

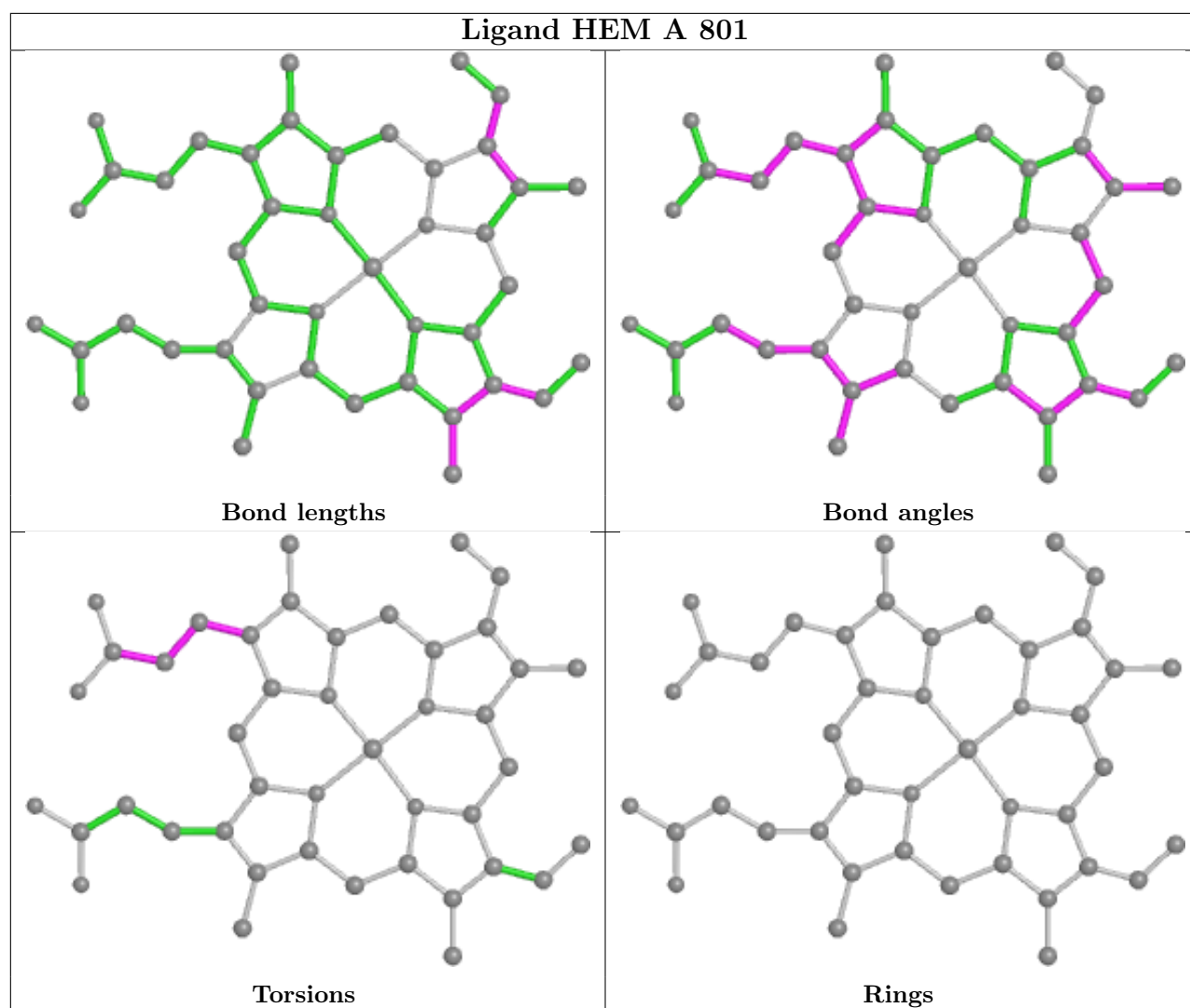
No monomer is involved in short contacts.

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 [i](#)

5.1 Protein, DNA and RNA chains [i](#)

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

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

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

5.3 Carbohydrates [i](#)

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

5.4 Ligands [i](#)

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

5.5 Other polymers [i](#)

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