



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2024 – 09:55 PM EST

PDB ID : 6NGJ  
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with 6-(3-fluoro-5-(3-(methylamino)prop-1-yn-1-yl)phenethyl)-4-methylpyridin-2-amine  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2018-12-21  
Resolution : 1.76 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

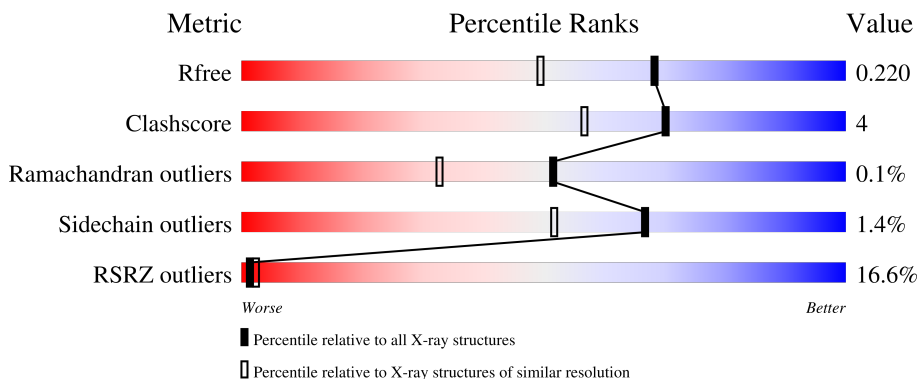
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


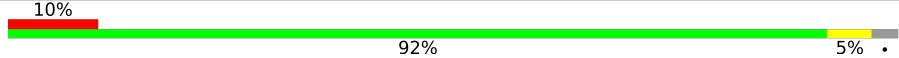
The reported resolution of this entry is 1.76 Å.

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))
$R_{free}$	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	422	
1	B	422	

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7286 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	409	Total 3344	C 2141	N 571	O 610	S 22	0	4	0
1	B	411	Total 3357	C 2148	N 574	O 614	S 21	0	3	0

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



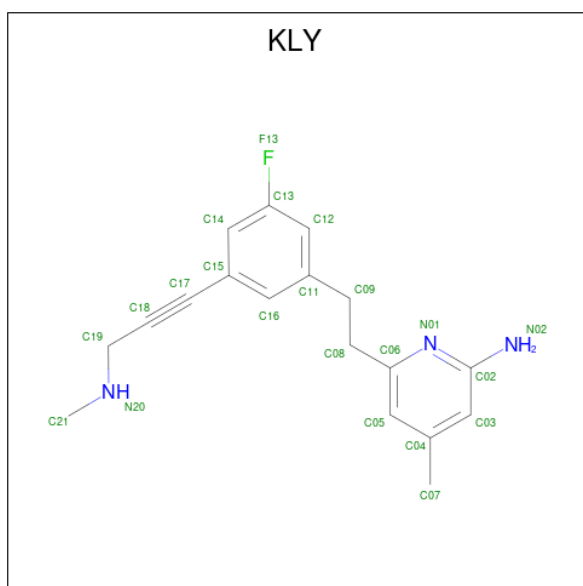
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- 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
			Total	C	N	O		
3	A	1	17	9	5	3	0	0
3	B	1	17	9	5	3	0	0

- Molecule 4 is 6-(2-{3-fluoro-5-[3-(methylamino)prop-1-yn-1-yl]phenyl}ethyl)-4-methylpyridi  
n-2-amine (three-letter code: KLY) (formula:  $C_{18}H_{20}FN_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	F	N		
4	A	1	22	18	1	3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	F	N		
4	B	1	22	18	1	3	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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

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

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

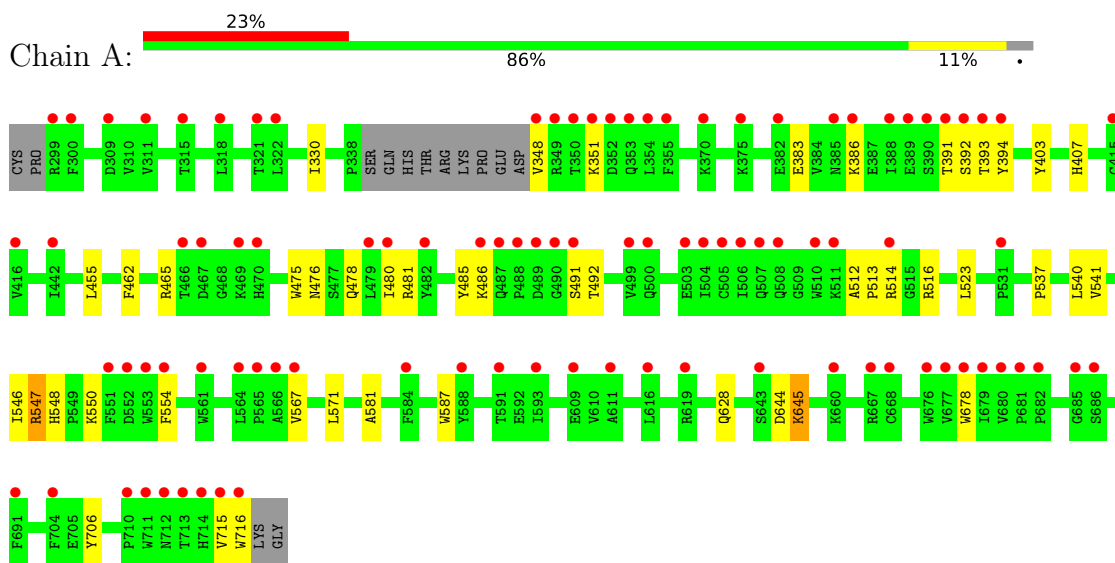
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	166	166	166	0	0
7	B	246	246	246	0	0

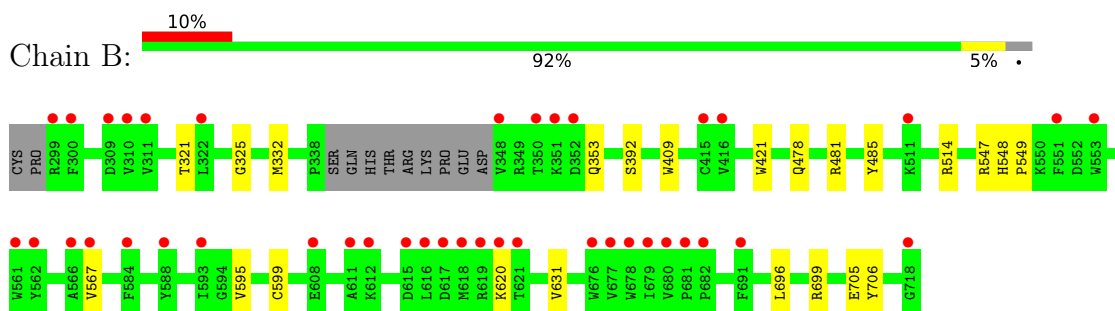
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

- Molecule 1: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.35Å 112.06Å 165.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.32 – 1.76 39.32 – 1.76	Depositor EDS
% Data completeness (in resolution range)	95.7 (39.32-1.76) 96.5 (39.32-1.76)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.54 (at 1.76Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.182 , 0.217 0.186 , 0.220	Depositor DCC
$R_{free}$ test set	4719 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.6	Xtrriage
Anisotropy	0.542	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 58.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7286	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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.

## 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: KLY, HEM, H4B, ZN, ACT

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	0.35	0/3446	0.49	0/4676
1	B	0.38	0/3459	0.50	0/4689
All	All	0.37	0/6905	0.49	0/9365

There are no bond length outliers.

There are no bond angle outliers.

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	3344	0	3261	31	0
1	B	3357	0	3275	12	0
2	A	43	0	30	7	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	22	0	0	3	0
4	B	22	0	0	3	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	166	0	0	5	0
7	B	246	0	0	1	0
All	All	7286	0	6632	49	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 4.

All (49) 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)
2:B:801:HEM:HBD2	4:B:803:KLY:C13	2.16	0.74
1:A:547:ARG:NH2	7:A:902:HOH:O	2.21	0.74
2:A:801:HEM:HBB2	2:A:801:HEM:HHC	1.75	0.69
1:A:480:ILE:HD13	1:A:541:VAL:HG13	1.77	0.67
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.77	0.67
1:B:699:ARG:NH2	1:B:705:GLU:OE1	2.30	0.65
2:A:801:HEM:O1D	7:A:901:HOH:O	2.15	0.63
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.80	0.63
1:A:547:ARG:NH1	1:A:644:ASP:OD1	2.36	0.59
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.87	0.56
2:B:801:HEM:O1D	7:B:901:HOH:O	2.17	0.56
1:A:351:LYS:HE2	1:A:392:SER:HB2	1.88	0.56
1:A:475:TRP:HH2	1:A:716:TRP:HZ3	1.53	0.56
1:B:706:TYR:OH	2:B:801:HEM:O1D	2.21	0.54
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.91	0.53
1:B:567:VAL:HG21	4:B:803:KLY:C13	2.38	0.53
1:A:383:GLU:HA	1:A:386:LYS:HE3	1.92	0.51
1:A:486:LYS:NZ	7:A:908:HOH:O	2.44	0.50
1:B:595:VAL:O	1:B:599:CYS:HB2	2.12	0.49
2:A:801:HEM:HBD1	4:A:803:KLY:C13	2.42	0.49
1:A:706:TYR:OH	2:A:801:HEM:O1D	2.24	0.49
1:B:567:VAL:HG21	4:B:803:KLY:C12	2.43	0.48
1:A:478:GLN:NE2	7:A:907:HOH:O	2.42	0.48
1:A:475:TRP:CH2	1:A:716:TRP:HZ3	2.31	0.48
1:A:628:GLN:HG3	1:B:631:VAL:HG11	1.97	0.47
1:A:645:LYS:HE3	1:A:645:LYS:HB2	1.81	0.47
1:A:486:LYS:HD3	1:A:492:THR:HG23	1.98	0.46
2:A:801:HEM:HBD1	4:A:803:KLY:F13	2.06	0.45
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.99	0.45
1:A:475:TRP:HB2	1:A:523:LEU:HB3	2.00	0.44
1:A:485:TYR:CZ	1:A:514:ARG:HA	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:678:TRP:HZ3	2:A:801:HEM:HBA2	1.82	0.43
1:B:325:GLY:O	1:B:332:MET:HG3	2.19	0.43
1:A:516:ARG:NH2	7:A:911:HOH:O	2.51	0.42
1:A:567:VAL:HG21	4:A:803:KLY:C12	2.50	0.42
1:A:465:ARG:HH12	1:A:571:LEU:HD11	1.85	0.42
1:A:391:THR:O	1:A:392:SER:HB3	2.20	0.42
1:A:548:HIS:CE1	1:A:550:LYS:HB2	2.55	0.42
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.54	0.42
1:A:393:THR:OG1	1:A:394:TYR:N	2.53	0.41
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.08	0.41
1:A:455:LEU:HD12	1:A:587:TRP:HB3	2.01	0.41
1:A:485:TYR:CE1	1:A:514:ARG:HA	2.55	0.41
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.56	0.41
1:A:462:PHE:HB2	1:A:581:ALA:HB3	2.03	0.41
1:A:546:ILE:HG22	1:A:554:PHE:HE2	1.85	0.41
1:A:537:PRO:HB2	1:A:540:LEU:HG	2.03	0.41
1:A:512:ALA:HA	1:A:513:PRO:HD3	1.94	0.41
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.56	0.40

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	408/422 (97%)	395 (97%)	12 (3%)	1 (0%)	47	29
1	B	410/422 (97%)	402 (98%)	8 (2%)	0	100	100
All	All	818/844 (97%)	797 (97%)	20 (2%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	491	SER

### 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	368/377 (98%)	363 (99%)	5 (1%)	67	52
1	B	369/377 (98%)	364 (99%)	5 (1%)	67	52
All	All	737/754 (98%)	727 (99%)	10 (1%)	67	52

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	348	VAL
1	A	476	ASN
1	A	547	ARG
1	A	645	LYS
1	A	715	VAL
1	B	321	THR
1	B	353	GLN
1	B	392	SER
1	B	547	ARG
1	B	620	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

Of 9 ligands modelled in this entry, 1 is 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
3	H4B	B	802	-	16,18,18	0.98	0	11,26,26	2.73	5 (45%)
4	KLY	B	803	-	22,23,23	1.54	1 (4%)	28,30,30	1.76	5 (17%)
3	H4B	A	802	-	16,18,18	0.86	0	11,26,26	2.81	6 (54%)
4	KLY	A	803	-	22,23,23	1.46	1 (4%)	28,30,30	1.32	6 (21%)
5	ACT	B	804	-	3,3,3	0.80	0	3,3,3	0.57	0
5	ACT	A	804	-	3,3,3	0.75	0	3,3,3	0.76	0
2	HEM	B	801	1	41,50,50	1.84	6 (14%)	45,82,82	1.89	10 (22%)
2	HEM	A	801	1	41,50,50	1.94	8 (19%)	45,82,82	1.70	9 (20%)

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	802	-	-	0/8/17/17	0/2/2/2
4	KLY	B	803	-	-	1/8/10/10	0/2/2/2
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2
4	KLY	A	803	-	-	1/8/10/10	0/2/2/2
2	HEM	B	801	1	-	4/12/54/54	-
2	HEM	A	801	1	-	6/12/54/54	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3D-C2D	7.98	1.53	1.36
2	B	801	HEM	C3D-C2D	7.23	1.52	1.36
4	A	803	KLY	C15-C17	-6.26	1.29	1.44
4	B	803	KLY	C15-C17	-6.12	1.29	1.44
2	B	801	HEM	C3C-C2C	-4.09	1.34	1.40
2	A	801	HEM	C3C-C2C	-3.71	1.35	1.40
2	A	801	HEM	C3C-CAC	3.53	1.55	1.47
2	B	801	HEM	C3C-CAC	3.41	1.54	1.47
2	B	801	HEM	CAB-C3B	2.95	1.55	1.47
2	A	801	HEM	CAB-C3B	2.84	1.55	1.47
2	A	801	HEM	CMD-C2D	2.35	1.55	1.50
2	B	801	HEM	C3B-C2B	-2.06	1.33	1.37
2	B	801	HEM	CMD-C2D	2.04	1.55	1.50
2	A	801	HEM	FE-NB	2.04	2.06	1.96
2	A	801	HEM	CMC-C2C	2.02	1.56	1.51
2	A	801	HEM	CMB-C2B	2.02	1.55	1.50

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	CBA-CAA-C2A	-6.15	102.12	112.62
2	A	801	HEM	C4D-ND-C1D	5.27	110.52	105.07
3	A	802	H4B	C8A-C4A-C4	4.96	118.98	114.57
2	B	801	HEM	C4D-ND-C1D	4.95	110.19	105.07
3	B	802	H4B	C8A-C4A-C4	4.85	118.88	114.57
2	A	801	HEM	CBA-CAA-C2A	-4.54	104.88	112.62
4	B	803	KLY	C02-N01-C06	4.35	121.39	118.10
3	A	802	H4B	C4-C4A-N5	4.19	122.63	119.12
2	B	801	HEM	CAD-C3D-C4D	3.93	131.53	124.66
3	B	802	H4B	C2-N3-C4	3.91	122.14	115.93
4	B	803	KLY	C08-C06-N01	3.87	121.71	115.95
4	B	803	KLY	C05-C06-N01	-3.61	119.07	122.90
3	B	802	H4B	N1-C2-N3	-3.60	119.77	125.42
3	A	802	H4B	N1-C2-N3	-3.55	119.85	125.42
4	A	803	KLY	C08-C06-N01	3.38	120.98	115.95
3	A	802	H4B	C2-N3-C4	3.23	121.06	115.93
2	B	801	HEM	CHD-C1D-ND	3.04	127.74	124.43
3	B	802	H4B	C4-C4A-N5	3.02	121.66	119.12
2	A	801	HEM	CHD-C1D-ND	3.01	127.70	124.43
3	A	802	H4B	C2-N1-C8A	3.00	121.25	114.54
2	A	801	HEM	C4B-CHC-C1C	2.99	126.51	122.56
2	B	801	HEM	C4B-CHC-C1C	2.88	126.36	122.56
4	A	803	KLY	C02-N01-C06	2.81	120.23	118.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	802	H4B	C2-N1-C8A	2.67	120.53	114.54
2	B	801	HEM	CAD-C3D-C2D	-2.60	123.04	127.88
2	B	801	HEM	C4C-CHD-C1D	2.53	125.90	122.56
2	B	801	HEM	C3B-C2B-C1B	2.45	108.30	106.49
4	B	803	KLY	C12-C13-C14	-2.38	120.51	123.52
3	A	802	H4B	N2-C2-N3	2.37	120.95	117.25
2	A	801	HEM	CHA-C4D-ND	2.34	127.27	124.38
2	A	801	HEM	CAD-CBD-CGD	-2.29	108.68	113.60
2	A	801	HEM	C4C-CHD-C1D	2.28	125.57	122.56
4	A	803	KLY	C08-C06-C05	-2.22	118.28	121.22
2	B	801	HEM	CMC-C2C-C3C	2.15	128.70	124.68
4	A	803	KLY	C12-C13-C14	-2.14	120.81	123.52
4	B	803	KLY	C09-C11-C12	-2.13	117.05	120.54
2	B	801	HEM	CMA-C3A-C4A	-2.10	125.23	128.46
2	A	801	HEM	CMC-C2C-C3C	2.10	128.60	124.68
4	A	803	KLY	C08-C09-C11	-2.08	105.97	113.28
4	A	803	KLY	C05-C06-N01	-2.07	120.70	122.90
2	A	801	HEM	C3B-C2B-C1B	2.05	108.01	106.49

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	803	KLY	C06-C08-C09-C11
4	B	803	KLY	C06-C08-C09-C11
2	A	801	HEM	C2A-CAA-CBA-CGA
2	B	801	HEM	C4D-C3D-CAD-CBD
2	A	801	HEM	C4D-C3D-CAD-CBD
2	A	801	HEM	C2D-C3D-CAD-CBD
2	B	801	HEM	C2D-C3D-CAD-CBD
2	A	801	HEM	C4B-C3B-CAB-CBB
2	B	801	HEM	C2A-CAA-CBA-CGA
2	A	801	HEM	CAD-CBD-CGD-O1D
2	A	801	HEM	CAD-CBD-CGD-O2D
2	B	801	HEM	C4B-C3B-CAB-CBB

There are no ring outliers.

4 monomers are involved in 14 short contacts:

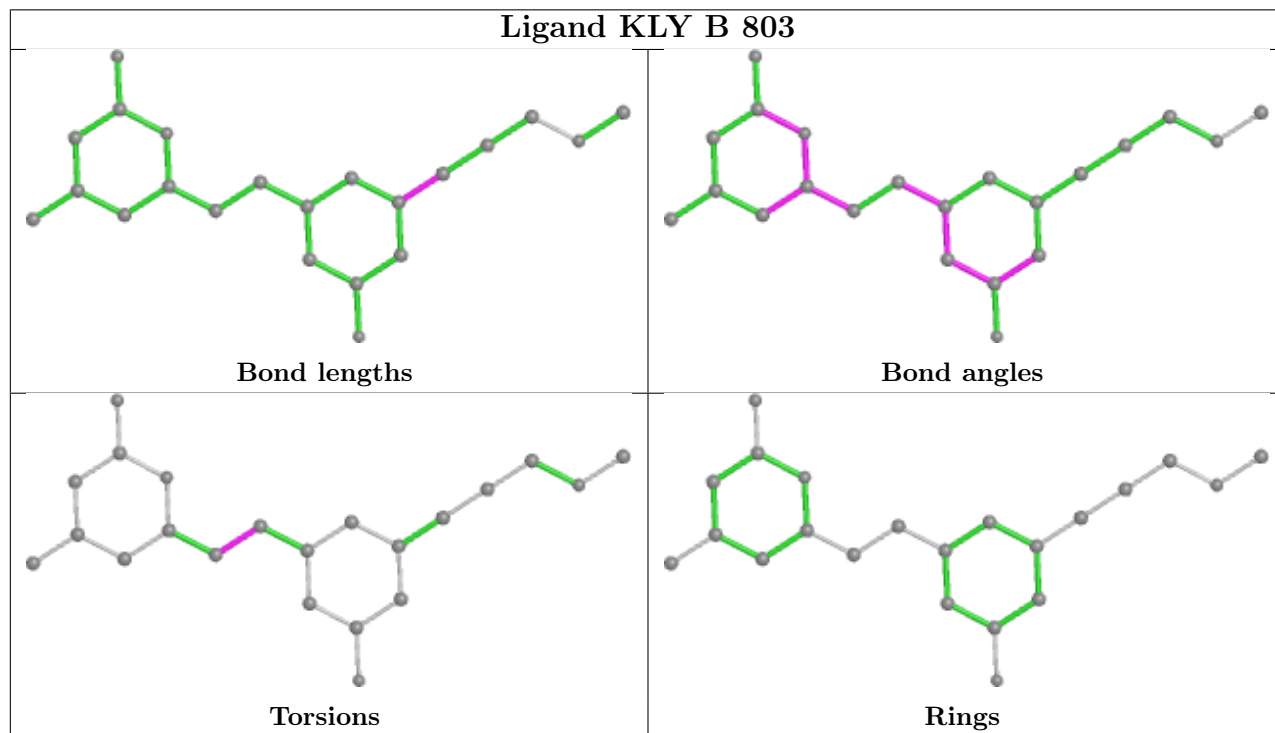
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	803	KLY	3	0

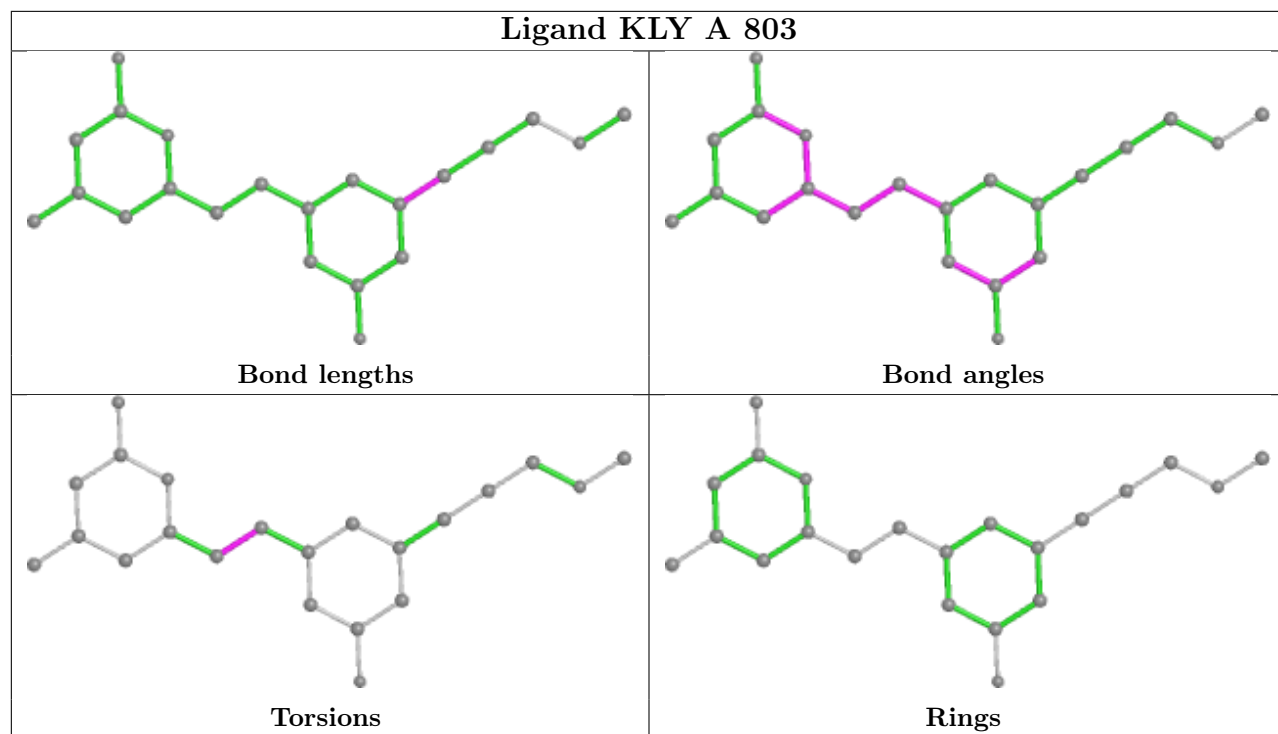
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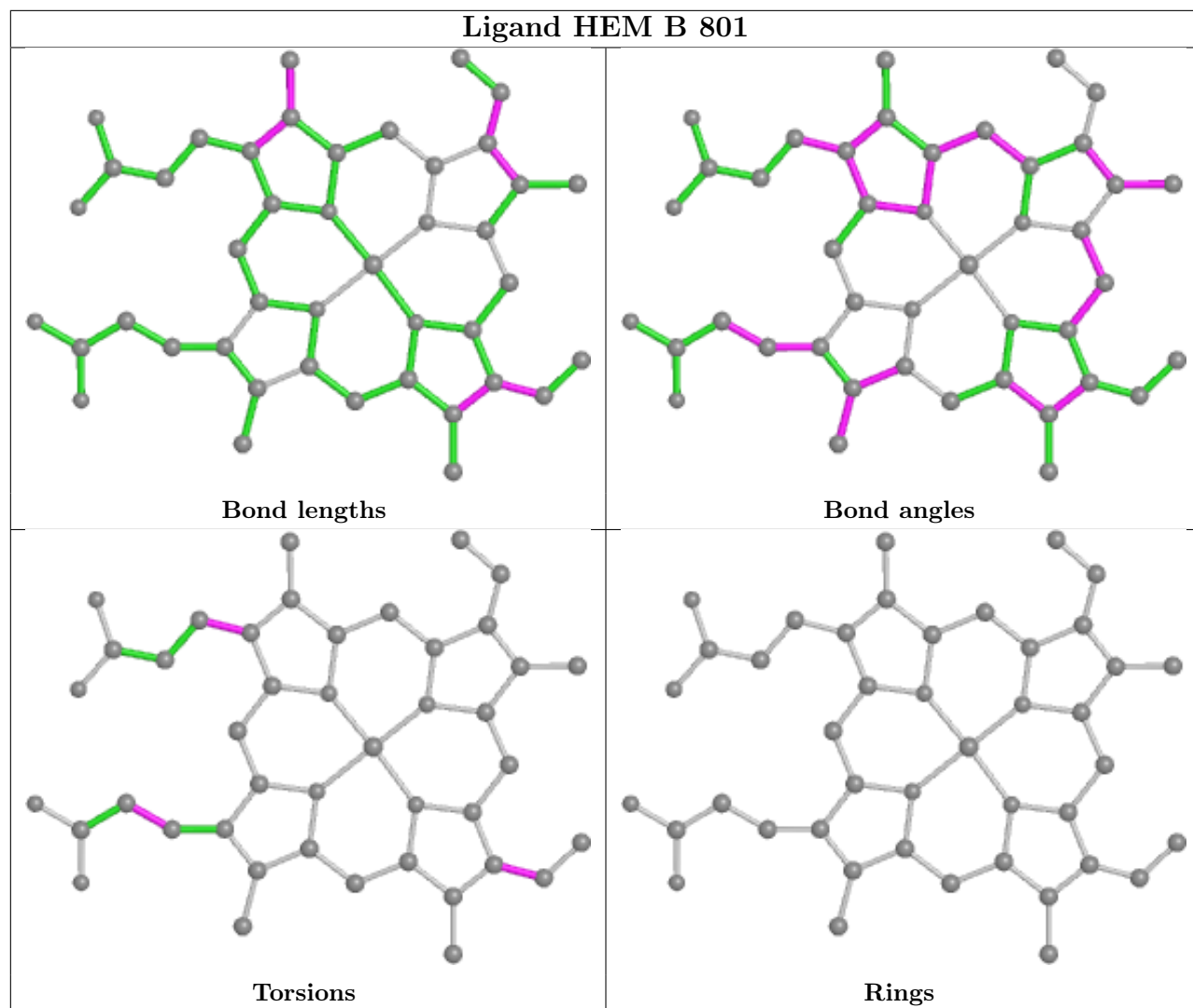
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	803	KLY	3	0
2	B	801	HEM	4	0
2	A	801	HEM	7	0

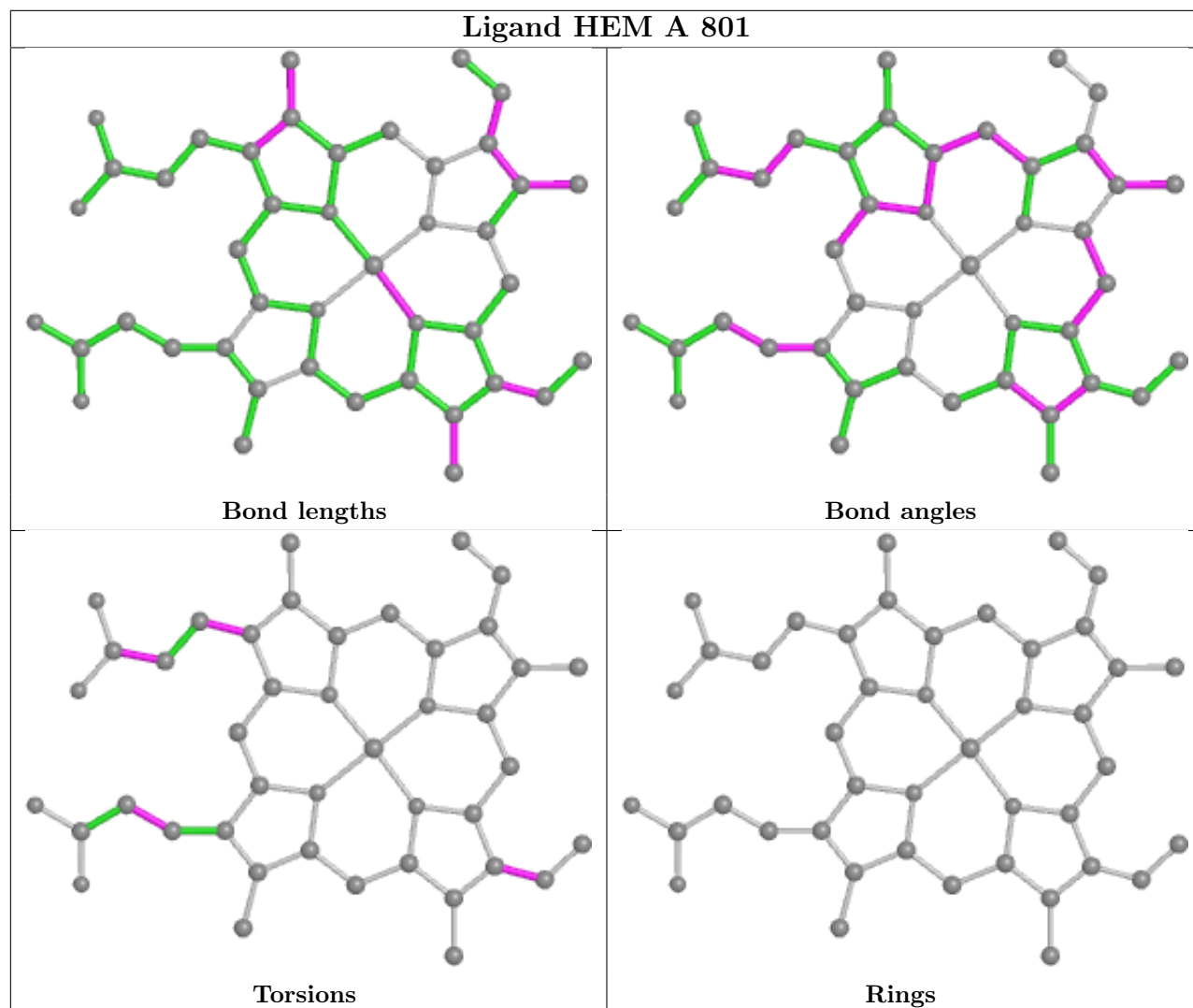
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











## 5.7 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](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	409/422 (96%)	1.26	95 (23%) 0 0	32, 60, 114, 156	0
1	B	411/422 (97%)	0.57	41 (9%) 7 9	28, 47, 84, 113	0
All	All	820/844 (97%)	0.92	136 (16%) 1 2	28, 52, 105, 156	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	715	VAL	9.5
1	B	300	PHE	9.2
1	A	488	PRO	8.9
1	A	348	VAL	8.6
1	A	716	TRP	8.2
1	B	350	THR	7.4
1	A	355	PHE	6.9
1	A	352	ASP	6.7
1	A	322	LEU	6.3
1	A	713	THR	6.1
1	A	551	PHE	6.0
1	A	388	ILE	6.0
1	B	348	VAL	5.8
1	A	349	ARG	5.8
1	A	393	THR	5.7
1	A	350	THR	5.5
1	B	677	VAL	5.4
1	A	679	ILE	5.2
1	A	677	VAL	5.2
1	A	507	GLN	5.1
1	A	489	ASP	5.1
1	A	386	LYS	5.1
1	A	392	SER	5.0
1	A	391	THR	4.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	351	LYS	4.8
1	A	389	GLU	4.7
1	B	718	GLY	4.7
1	A	300	PHE	4.6
1	A	678	TRP	4.5
1	A	469	LYS	4.5
1	A	711	TRP	4.5
1	B	616	LEU	4.5
1	A	506	ILE	4.5
1	A	486	LYS	4.5
1	B	310	VAL	4.4
1	A	619	ARG	4.3
1	A	390	SER	4.3
1	A	385	ASN	4.2
1	B	680	VAL	4.2
1	B	619	ARG	4.1
1	A	466	THR	4.1
1	A	299	ARG	4.1
1	A	712	ASN	4.1
1	A	503	GLU	4.1
1	A	676	TRP	4.0
1	A	480	ILE	4.0
1	A	643	SER	4.0
1	A	714	HIS	3.8
1	A	680	VAL	3.8
1	B	620	LYS	3.8
1	A	353	GLN	3.7
1	A	490	GLY	3.7
1	B	299	ARG	3.7
1	A	470	HIS	3.7
1	A	567	VAL	3.6
1	A	508	GLN	3.6
1	A	553	TRP	3.6
1	A	479	LEU	3.5
1	B	617	ASP	3.5
1	A	561	TRP	3.4
1	B	676	TRP	3.4
1	A	467	ASP	3.4
1	B	611	ALA	3.4
1	A	584	PHE	3.4
1	A	691	PHE	3.4
1	B	678	TRP	3.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	593	ILE	3.3
1	B	309	ASP	3.3
1	B	551	PHE	3.2
1	A	588	TYR	3.2
1	A	710	PRO	3.2
1	B	615	ASP	3.1
1	A	566	ALA	3.1
1	A	415	CYS	3.1
1	B	566	ALA	3.1
1	A	491	SER	3.0
1	A	511	LYS	3.0
1	A	514	ARG	2.9
1	A	321	THR	2.9
1	B	679	ILE	2.9
1	A	487	GLN	2.9
1	B	567	VAL	2.8
1	A	504	ILE	2.8
1	B	691	PHE	2.7
1	A	531	PRO	2.7
1	B	618	MET	2.7
1	A	682	PRO	2.7
1	B	612	LYS	2.7
1	A	681	PRO	2.7
1	A	318	LEU	2.6
1	A	394	TYR	2.6
1	A	500	GLN	2.6
1	B	561	TRP	2.6
1	B	562	TYR	2.6
1	B	322	LEU	2.6
1	A	611	ALA	2.6
1	B	511	LYS	2.5
1	B	621	THR	2.5
1	A	685	GLY	2.5
1	B	352	ASP	2.5
1	A	667	ARG	2.5
1	B	553	TRP	2.5
1	A	499	VAL	2.5
1	A	660	LYS	2.5
1	A	510	TRP	2.5
1	A	416	VAL	2.5
1	A	616	LEU	2.5
1	B	415	CYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	681	PRO	2.4
1	A	375	LYS	2.4
1	B	593	ILE	2.4
1	B	588	TYR	2.4
1	B	351	LYS	2.4
1	A	564	LEU	2.4
1	A	591	THR	2.4
1	B	682	PRO	2.4
1	A	442	ILE	2.3
1	A	311	VAL	2.3
1	A	565	PRO	2.3
1	A	704	PHE	2.3
1	B	608	GLU	2.2
1	A	370	LYS	2.2
1	A	554	PHE	2.2
1	A	668[A]	CYS	2.2
1	A	686	SER	2.2
1	B	416	VAL	2.1
1	A	309	ASP	2.1
1	A	382	GLU	2.1
1	B	311	VAL	2.1
1	A	505	CYS	2.1
1	B	584	PHE	2.1
1	A	552	ASP	2.1
1	A	315	THR	2.0
1	A	482	TYR	2.0
1	A	609	GLU	2.0
1	A	354	LEU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

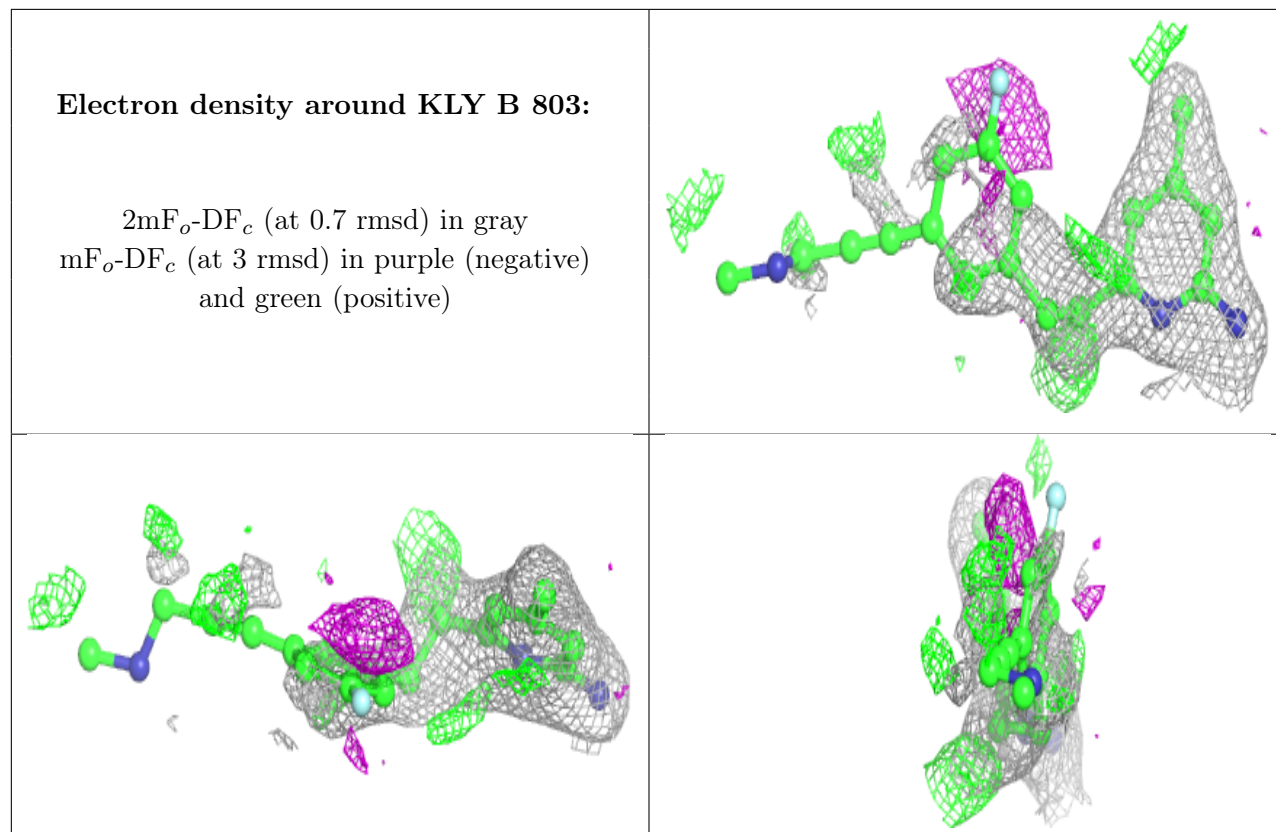
## 6.4 Ligands [i](#)

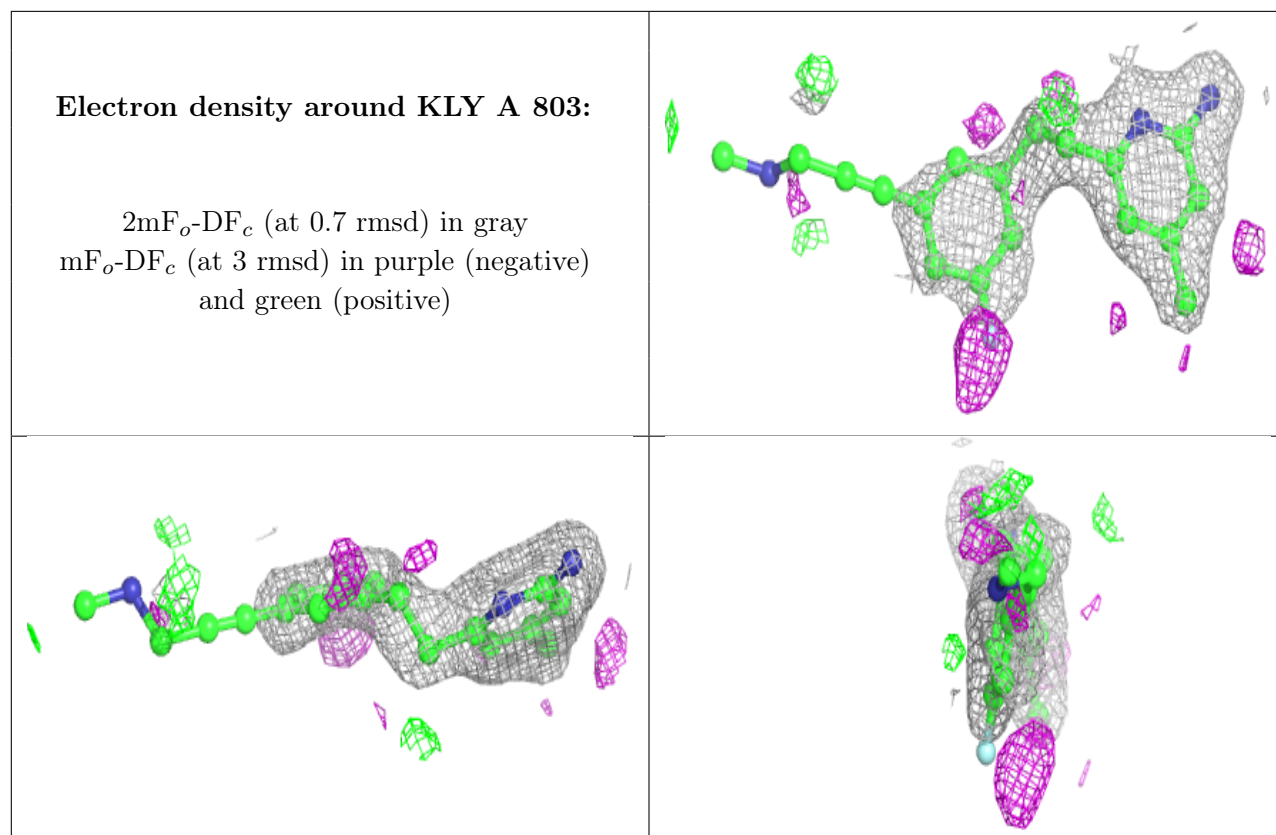
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	KLY	B	803	22/22	0.92	0.27	33,82,112,114	0
5	ACT	B	804	4/4	0.94	0.13	63,68,75,80	0
3	H4B	A	802	17/17	0.95	0.18	33,37,41,41	0
5	ACT	A	804	4/4	0.95	0.19	68,73,75,75	0
4	KLY	A	803	22/22	0.95	0.27	34,71,101,104	0
3	H4B	B	802	17/17	0.96	0.18	31,36,43,44	0
2	HEM	B	801	43/43	0.97	0.17	26,35,56,66	0
2	HEM	A	801	43/43	0.98	0.19	28,39,62,75	0
6	ZN	A	805	1/1	0.99	0.08	38,38,38,38	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

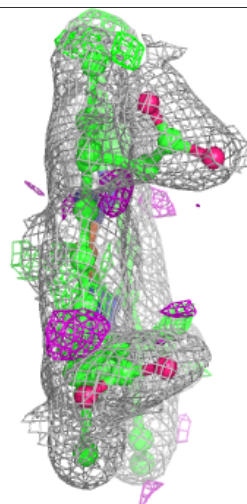
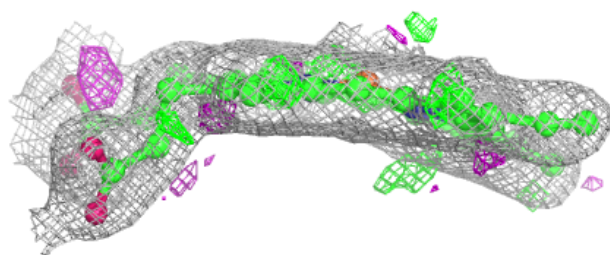
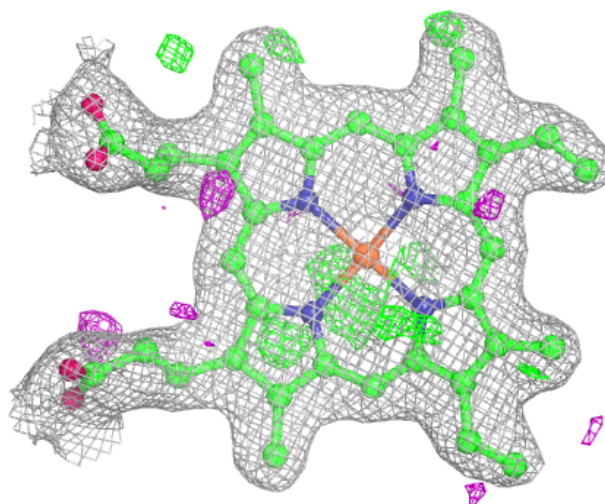


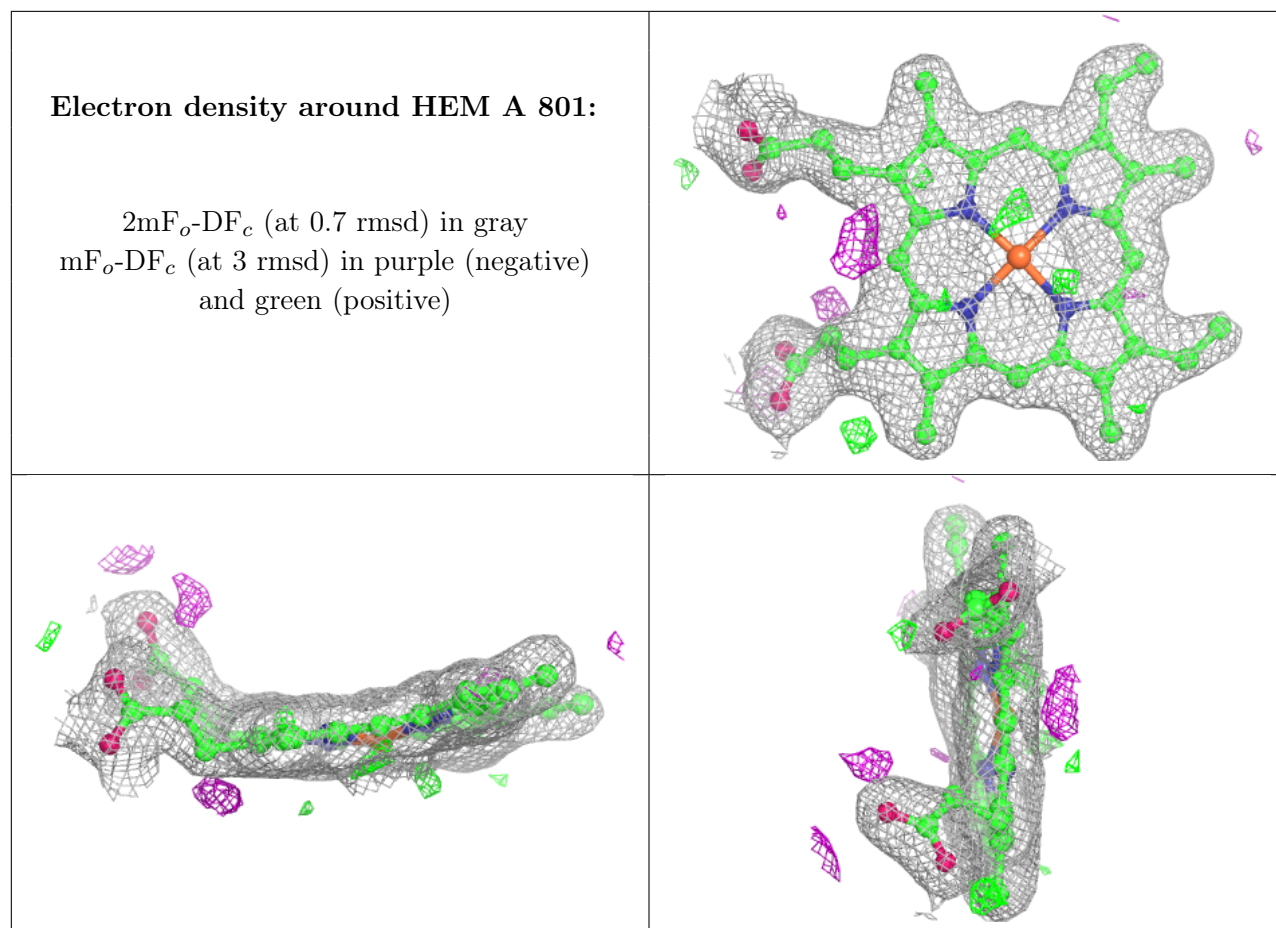




**Electron density around HEM B 801:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.