



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 03:41 AM EDT

PDB ID : 6NGY
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with (R)-6-(2,3-difluoro-5-(2-(1-methylpyrrolidin-2-yl)ethyl)phenethyl)-4-methylpyridin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2018-12-21
Resolution : 1.93 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
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)	:	2.36.2

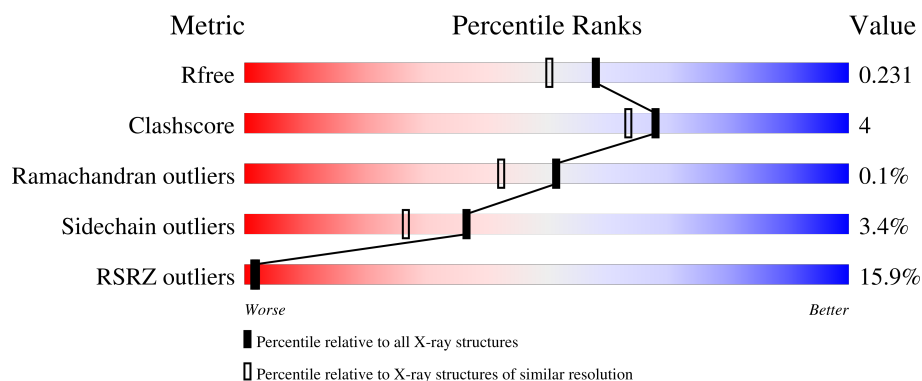
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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 $\leq 5\%$. 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	<div> <div>20%</div> <div>86%</div> <div>10%</div> <div>.</div> </div>
1	B	422	<div> <div>11%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7220 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
1	A	408	Total	C	N	O	S	0	2	0
			3322	2126	567	607	22			
1	B	416	Total	C	N	O	S	0	3	0
			3397	2170	585	620	22			

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



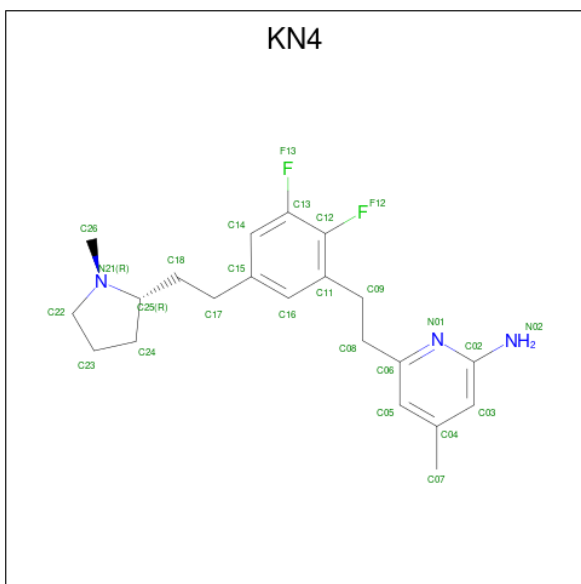
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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 6-[2-(2,3-difluoro-5-{2-[(2R)-1-methylpyrrolidin-2-yl]ethyl}phenyl)ethyl]-4-methylpyridin-2-amine (three-letter code: KN4) (formula: C₂₁H₂₇F₂N₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	N	0	0
			26	21	2	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	F	N	0	0
			26	21	2	3		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

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

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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

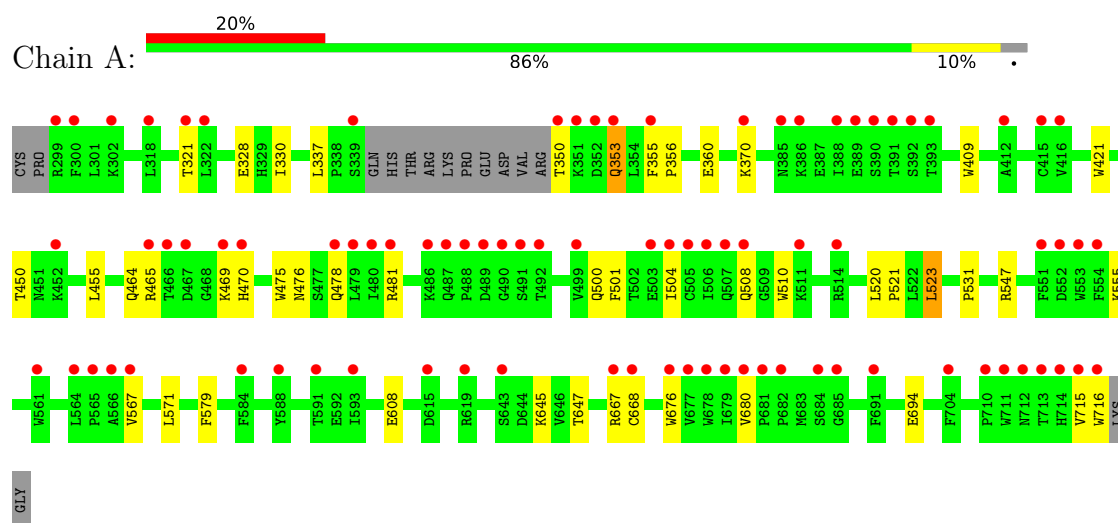
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	121	Total	O	0	0
			121	121		
8	B	187	Total	O	0	0
			187	187		

3 Residue-property plots

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.84Å 111.11Å 164.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.00 – 1.93 39.00 – 1.93	Depositor EDS
% Data completeness (in resolution range)	98.6 (39.00-1.93) 99.1 (39.00-1.93)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 1.92Å)	Xtriage
Refinement program	PHENIX (1.11.1-2575_1496: ???)	Depositor
R, R_{free}	0.187 , 0.230 0.187 , 0.231	Depositor DCC
R_{free} test set	3556 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.998	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 59.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7220	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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.

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: KN4, ZN, HEM, H4B, GOL, 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	0/3418	0.50	0/4637
1	B	0.39	0/3500	0.52	0/4744
All	All	0.37	0/6918	0.51	0/9381

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	3322	0	3231	20	0
1	B	3397	0	3314	27	0
2	A	43	0	30	2	0
2	B	43	0	30	5	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	26	0	0	1	0
4	B	26	0	0	4	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	B	12	0	16	2	0
8	A	121	0	0	1	0
8	B	187	0	0	1	0
All	All	7220	0	6657	51	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 (51) 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)
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.70	0.73
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.70	0.71
1:B:706:TYR:OH	2:B:801:HEM:O2D	2.08	0.69
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.74	0.68
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.75	0.67
1:B:364:GLN:NE2	8:B:901:HOH:O	2.13	0.65
2:B:801:HEM:HMC2	2:B:801:HEM:HBC2	1.78	0.64
2:A:801:HEM:HBB2	2:A:801:HEM:HHC	1.79	0.64
1:B:663:GLU:HB3	1:B:667:ARG:HH12	1.63	0.62
1:A:350:THR:N	1:A:353:GLN:OE1	2.33	0.61
1:B:663:GLU:HB3	1:B:667:ARG:NH1	2.15	0.61
1:A:667:ARG:NH1	1:A:668[A]:CYS:SG	2.75	0.60
1:B:525:GLN:HE21	1:B:528:GLY:HA2	1.67	0.59
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.85	0.59
1:B:494:GLY:O	7:B:805:GOL:H12	2.06	0.56
1:A:455:LEU:HD12	1:A:647:THR:HB	1.88	0.54
1:B:567:VAL:HG21	4:B:803:KN4:C12	2.36	0.54
1:A:510:TRP:CE2	1:A:521:PRO:HD3	2.43	0.54
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.90	0.53
1:B:340:GLN:O	1:B:699:ARG:NH2	2.41	0.53
1:B:570:MET:SD	4:B:803:KN4:F13	2.57	0.52
1:B:607:LEU:HD13	1:B:626:LYS:HG2	1.91	0.52
1:A:567:VAL:HG21	4:A:803:KN4:C12	2.43	0.49
1:B:362:LEU:HD11	1:B:384:VAL:HG21	1.94	0.48
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.51	0.45
1:A:370:LYS:HB2	1:A:370:LYS:HE3	1.79	0.45
8:A:979:HOH:O	1:B:307:GLU:HG3	2.16	0.45
2:B:801:HEM:HBD2	4:B:803:KN4:C13	2.47	0.45
1:B:516:ARG:HD2	7:B:805:GOL:O1	2.18	0.44
1:A:355:PHE:N	1:A:356:PRO:HD2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:TRP:CZ2	1:A:680:VAL:HG21	2.53	0.44
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.53	0.43
1:B:620:LYS:H	1:B:620:LYS:HD3	1.83	0.43
1:A:465:ARG:HH12	1:A:571:LEU:HD11	1.83	0.43
1:B:595:VAL:O	1:B:599:CYS:HB2	2.18	0.43
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.50	0.42
2:B:801:HEM:HBA1	4:B:803:KN4:C09	2.49	0.42
1:A:464:GLN:HB3	1:A:579:PHE:CE2	2.55	0.42
1:A:500:GLN:O	1:A:504:ILE:HG13	2.19	0.41
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.56	0.41
1:B:511:LYS:HA	1:B:511:LYS:HD3	1.80	0.41
1:B:322:LEU:HD12	1:B:699:ARG:HG2	2.02	0.41
1:A:501:PHE:HD2	1:A:520:LEU:HD13	1.85	0.41
1:A:450:THR:HA	1:A:455:LEU:HD23	2.02	0.41
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.56	0.41
1:B:323:GLU:O	1:B:699:ARG:NH1	2.45	0.41
1:A:330:ILE:HD11	1:B:696:LEU:HB3	2.02	0.41
1:B:504:ILE:O	1:B:508:GLN:HG2	2.21	0.40
1:A:510:TRP:CD1	1:A:521:PRO:HG3	2.56	0.40
1:A:694:GLU:HB3	1:B:335:ILE:HD13	2.04	0.40
1:B:478:GLN:HB2	1:B:481:ARG:CG	2.47	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	405/422 (96%)	392 (97%)	13 (3%)	0	100	100
1	B	415/422 (98%)	405 (98%)	9 (2%)	1 (0%)	47	38
All	All	820/844 (97%)	797 (97%)	22 (3%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	349	ARG

5.3.2 Protein sidechains ⓘ

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	365/377 (97%)	349 (96%)	16 (4%)	28	18
1	B	374/377 (99%)	365 (98%)	9 (2%)	49	41
All	All	739/754 (98%)	714 (97%)	25 (3%)	37	27

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	321	THR
1	A	328	GLU
1	A	337	LEU
1	A	353	GLN
1	A	360	GLU
1	A	469	LYS
1	A	470	HIS
1	A	476	ASN
1	A	508	GLN
1	A	523	LEU
1	A	547	ARG
1	A	555	LYS
1	A	608	GLU
1	A	645	LYS
1	A	715	VAL
1	A	716	TRP
1	B	332	MET
1	B	341	HIS
1	B	351	LYS
1	B	392	SER
1	B	547	ARG
1	B	609	GLU

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Mol	Chain	Res	Type
1	B	612	LYS
1	B	620	LYS
1	B	699	ARG

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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	0.99	0	11,26,26	2.47	5 (45%)
7	GOL	B	805	-	5,5,5	0.36	0	5,5,5	0.44	0
2	HEM	B	801	1	41,50,50	1.55	8 (19%)	45,82,82	1.63	11 (24%)
2	HEM	A	801	1	41,50,50	1.50	8 (19%)	45,82,82	1.60	9 (20%)
7	GOL	B	806	-	5,5,5	0.37	0	5,5,5	0.22	0
5	ACT	B	804	-	3,3,3	0.78	0	3,3,3	0.64	0
5	ACT	A	804	-	3,3,3	0.76	0	3,3,3	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	KN4	B	803	-	28,28,28	0.37	0	33,39,39	1.81	8 (24%)
4	KN4	A	803	-	28,28,28	0.32	0	33,39,39	1.71	6 (18%)
3	H4B	A	802	-	16,18,18	0.79	0	11,26,26	2.58	6 (54%)

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
7	GOL	B	805	-	-	2/4/4/4	-
2	HEM	B	801	1	-	2/12/54/54	-
2	HEM	A	801	1	-	8/12/54/54	-
7	GOL	B	806	-	-	1/4/4/4	-
4	KN4	B	803	-	-	3/10/20/20	0/3/3/3
4	KN4	A	803	-	-	3/10/20/20	0/3/3/3
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C3C-C2C	-4.18	1.34	1.40
2	A	801	HEM	C3C-C2C	-3.53	1.35	1.40
2	A	801	HEM	C3C-CAC	3.45	1.54	1.47
2	B	801	HEM	C3C-CAC	3.33	1.54	1.47
2	A	801	HEM	CAB-C3B	3.08	1.55	1.47
2	B	801	HEM	CAB-C3B	2.98	1.55	1.47
2	B	801	HEM	FE-NB	2.77	2.10	1.96
2	B	801	HEM	CMB-C2B	2.47	1.56	1.50
2	A	801	HEM	C3B-C2B	-2.43	1.32	1.37
2	A	801	HEM	FE-NB	2.34	2.08	1.96
2	A	801	HEM	CAA-C2A	2.30	1.55	1.52
2	A	801	HEM	CMB-C2B	2.20	1.55	1.50
2	A	801	HEM	CMD-C2D	2.14	1.55	1.50
2	B	801	HEM	C3B-C2B	-2.09	1.33	1.37
2	B	801	HEM	CMC-C2C	2.08	1.56	1.51
2	B	801	HEM	CAA-C2A	2.03	1.55	1.52

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	802	H4B	C8A-C4A-C4	4.92	118.94	114.57
3	A	802	H4B	C8A-C4A-C4	4.35	118.44	114.57
4	B	803	KN4	C09-C08-C06	-4.18	103.63	112.99
4	B	803	KN4	C02-N01-C06	4.13	121.23	118.10
4	A	803	KN4	C02-N01-C06	3.82	120.99	118.10
4	B	803	KN4	C16-C11-C12	3.67	120.12	116.76
3	A	802	H4B	C4-C4A-N5	3.67	122.20	119.12
4	A	803	KN4	C08-C06-N01	3.64	121.37	115.95
4	A	803	KN4	C09-C11-C12	-3.61	117.83	120.73
2	B	801	HEM	C4B-CHC-C1C	3.59	127.30	122.56
3	A	802	H4B	C2-N3-C4	3.54	121.55	115.93
2	A	801	HEM	C4B-CHC-C1C	3.33	126.95	122.56
3	B	802	H4B	C2-N3-C4	3.33	121.22	115.93
4	A	803	KN4	C05-C06-N01	-3.29	119.42	122.90
3	A	802	H4B	N1-C2-N3	-3.24	120.33	125.42
3	B	802	H4B	N1-C2-N3	-3.22	120.37	125.42
4	B	803	KN4	F12-C12-C11	3.21	121.24	117.85
2	B	801	HEM	CAD-C3D-C4D	3.11	130.10	124.66
2	B	801	HEM	CAD-C3D-C2D	-3.07	122.16	127.88
4	A	803	KN4	C16-C11-C12	2.96	119.47	116.76
2	B	801	HEM	CAD-CBD-CGD	-2.92	107.33	113.60
2	A	801	HEM	C1B-NB-C4B	2.83	108.00	105.07
4	B	803	KN4	C08-C06-N01	2.82	120.14	115.95
2	B	801	HEM	CHD-C1D-ND	2.81	127.49	124.43
2	A	801	HEM	CMC-C2C-C3C	2.78	129.88	124.68
2	A	801	HEM	CAD-CBD-CGD	-2.69	107.81	113.60
2	A	801	HEM	C3B-C2B-C1B	2.67	108.47	106.49
4	B	803	KN4	C17-C15-C14	-2.66	116.18	120.54
2	A	801	HEM	C4C-CHD-C1D	2.63	126.03	122.56
3	B	802	H4B	C2-N1-C8A	2.61	120.39	114.54
3	A	802	H4B	C2-N1-C8A	2.52	120.18	114.54
4	B	803	KN4	C09-C11-C12	-2.48	118.73	120.73
4	A	803	KN4	F12-C12-C11	2.48	120.47	117.85
4	B	803	KN4	C05-C06-N01	-2.47	120.28	122.90
2	A	801	HEM	CBD-CAD-C3D	2.32	119.08	112.63
3	B	802	H4B	C4-C4A-N5	2.30	121.05	119.12
2	B	801	HEM	CBA-CAA-C2A	-2.25	108.78	112.62
2	A	801	HEM	C2B-C1B-NB	-2.18	107.25	109.84
2	B	801	HEM	C4C-CHD-C1D	2.18	125.44	122.56
2	B	801	HEM	C4D-ND-C1D	2.18	107.32	105.07
2	B	801	HEM	C3D-C4D-ND	-2.16	107.76	110.17
2	A	801	HEM	CAB-C3B-C2B	-2.10	121.69	128.60
3	A	802	H4B	N2-C2-N3	2.08	120.48	117.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	C4A-C3A-C2A	2.04	108.41	107.00
2	B	801	HEM	CMC-C2C-C3C	2.03	128.48	124.68

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	HEM	C1A-C2A-CAA-CBA
2	A	801	HEM	C3A-C2A-CAA-CBA
2	B	801	HEM	C2A-CAA-CBA-CGA
4	A	803	KN4	C06-C08-C09-C11
4	B	803	KN4	C06-C08-C09-C11
2	A	801	HEM	C2A-CAA-CBA-CGA
7	B	805	GOL	O1-C1-C2-C3
2	A	801	HEM	C4D-C3D-CAD-CBD
7	B	805	GOL	O1-C1-C2-O2
2	A	801	HEM	C2D-C3D-CAD-CBD
2	A	801	HEM	C4B-C3B-CAB-CBB
2	B	801	HEM	C4B-C3B-CAB-CBB
4	B	803	KN4	C16-C15-C17-C18
4	A	803	KN4	C16-C15-C17-C18
4	A	803	KN4	C14-C15-C17-C18
4	B	803	KN4	C14-C15-C17-C18
2	A	801	HEM	CAD-CBD-CGD-O1D
2	A	801	HEM	CAD-CBD-CGD-O2D
7	B	806	GOL	O1-C1-C2-O2

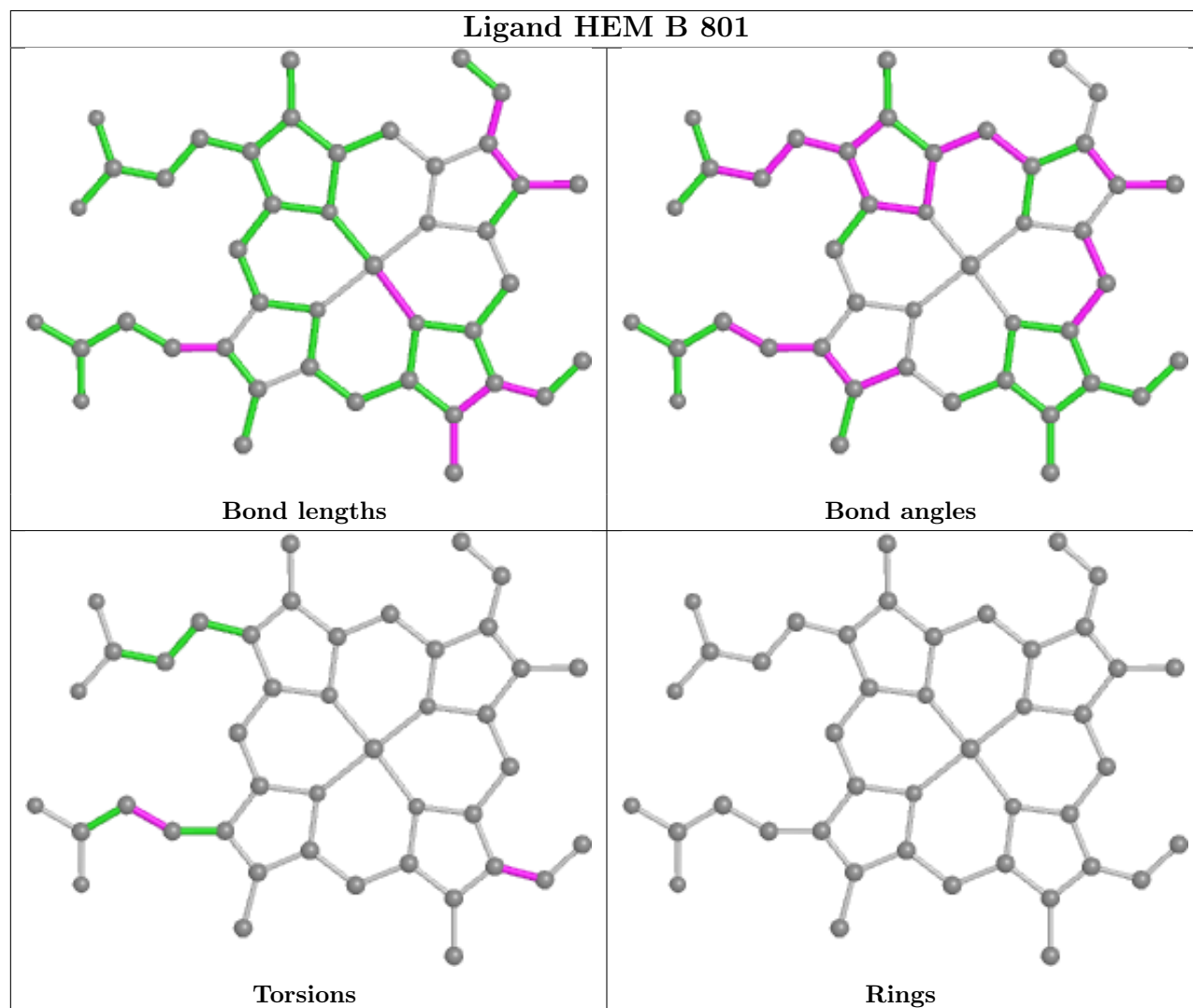
There are no ring outliers.

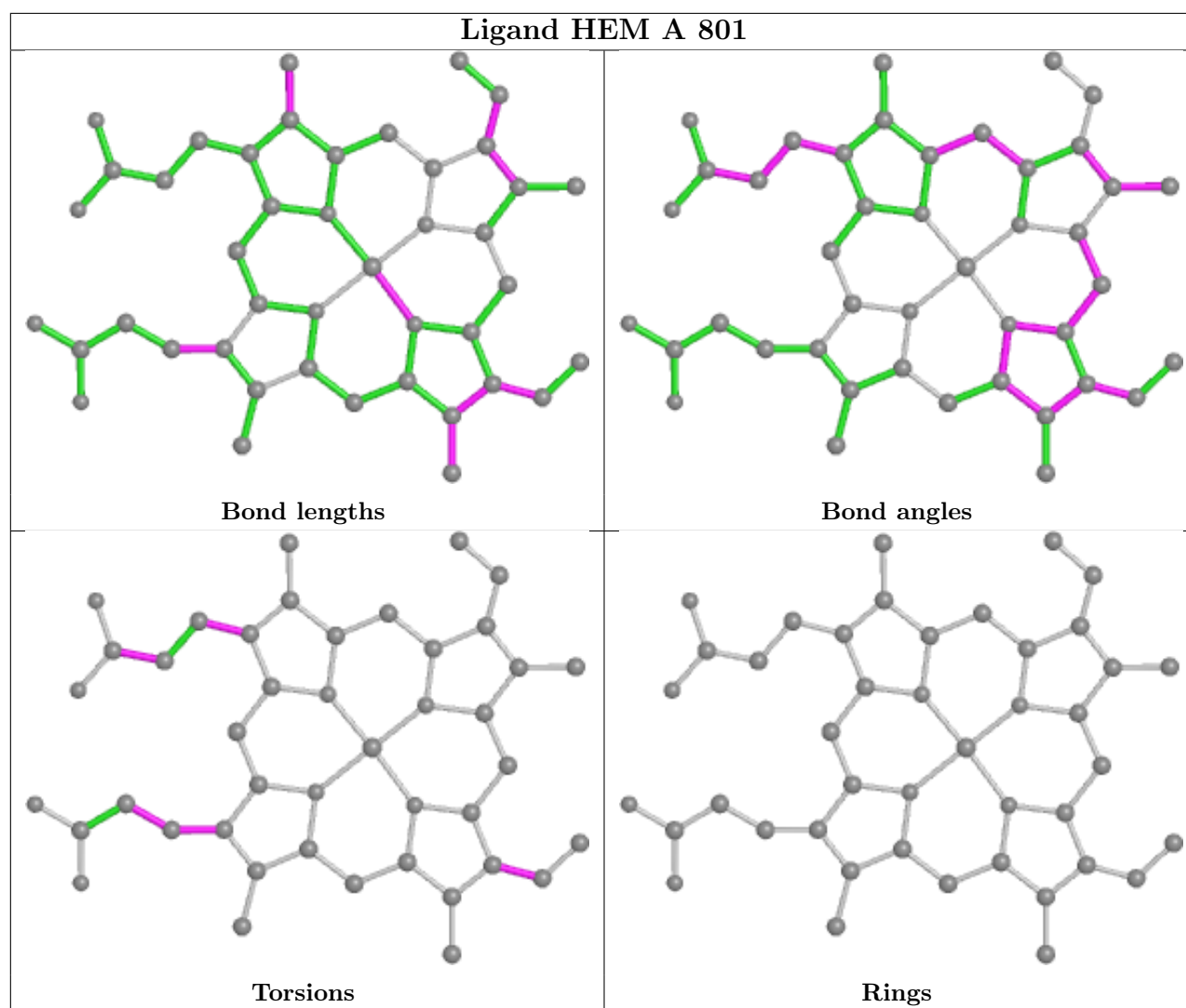
5 monomers are involved in 12 short contacts:

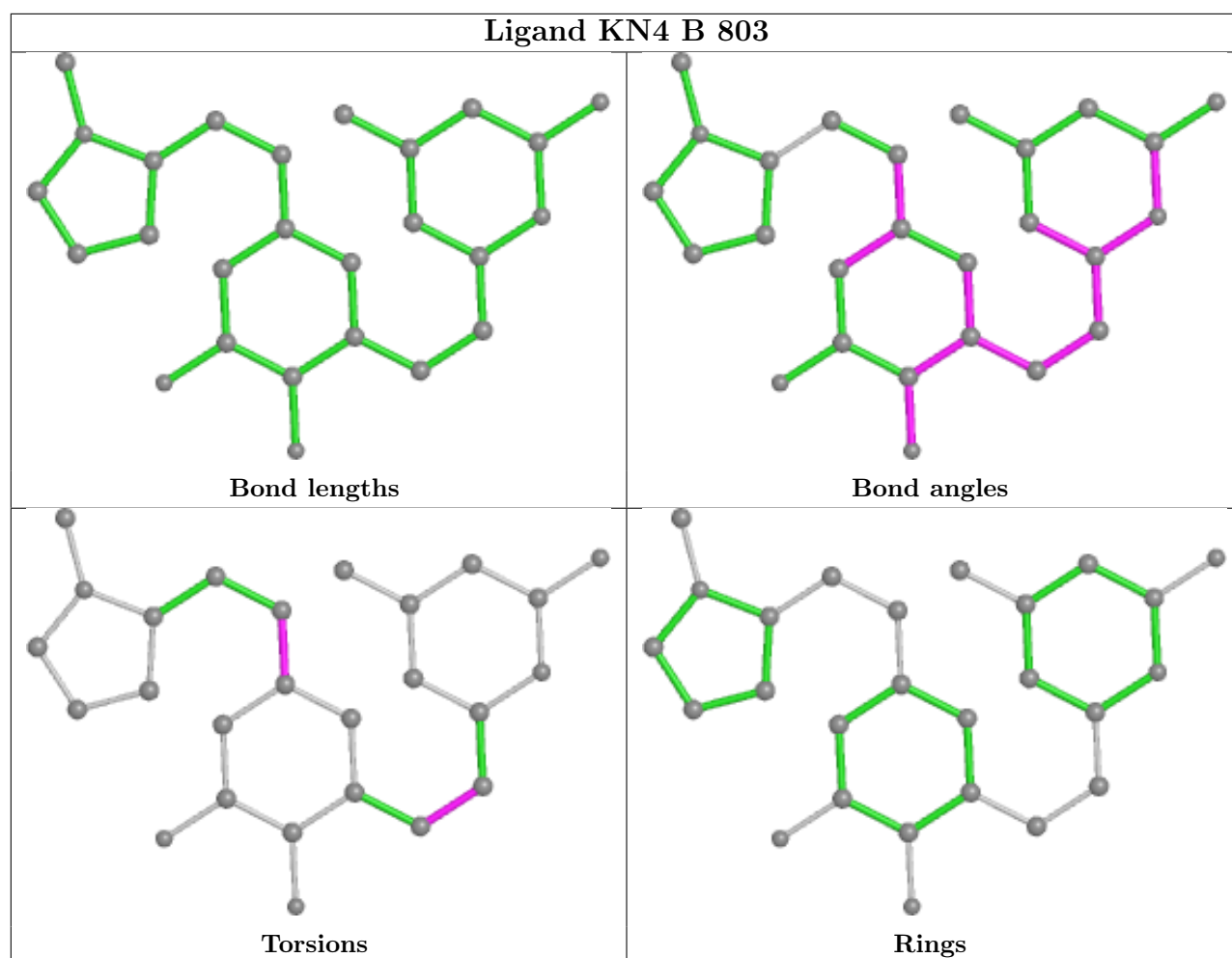
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	805	GOL	2	0
2	B	801	HEM	5	0
2	A	801	HEM	2	0
4	B	803	KN4	4	0
4	A	803	KN4	1	0

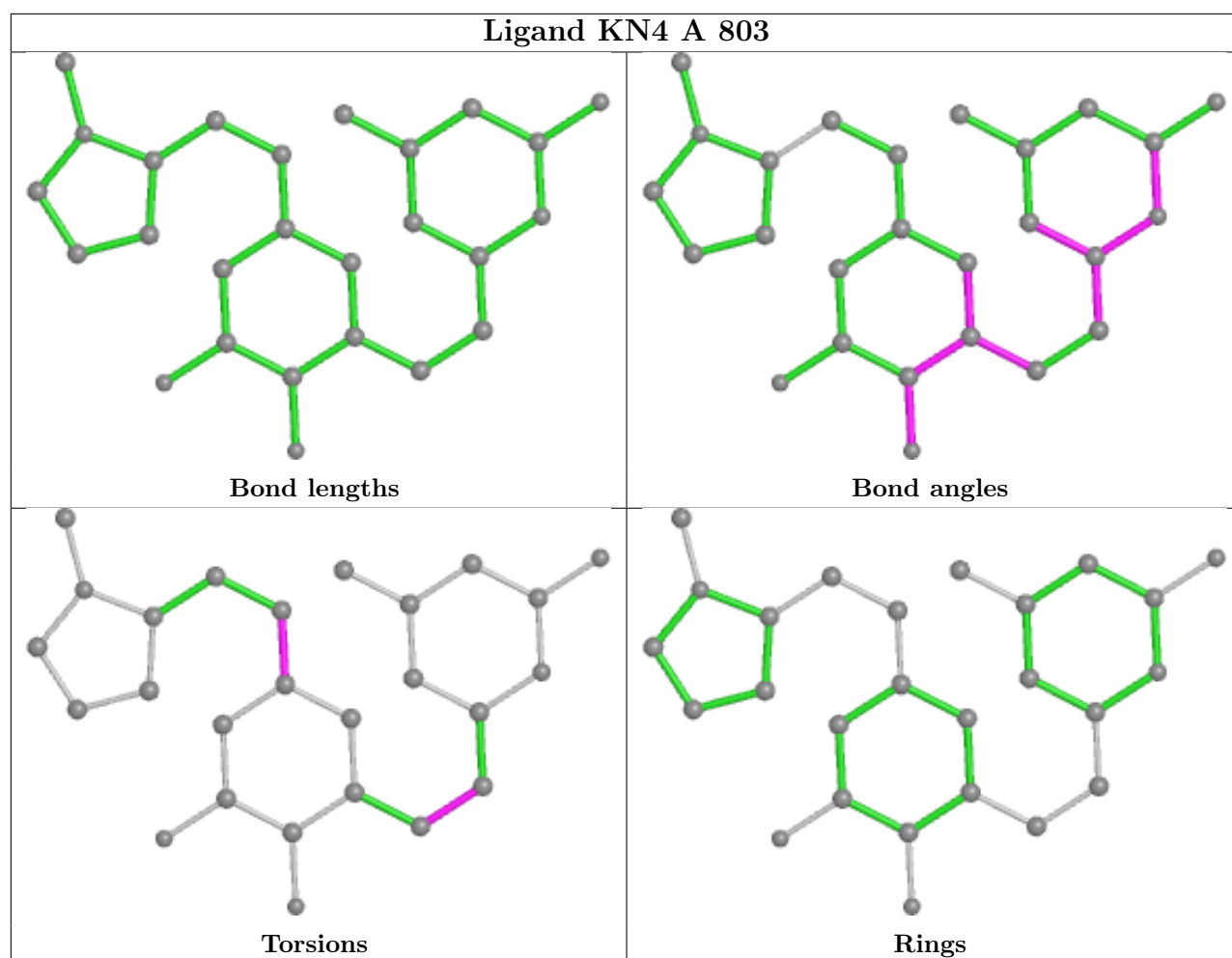
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

6.1 Protein, DNA and RNA chains

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, 95th 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 ²)	Q<0.9
1	A	408/422 (96%)	1.13	86 (21%) 1 0	36, 67, 112, 151	0
1	B	416/422 (98%)	0.61	45 (10%) 5 7	33, 55, 97, 120	0
All	All	824/844 (97%)	0.87	131 (15%) 1 2	33, 60, 107, 151	0

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	715	VAL	12.5
1	A	716	TRP	7.7
1	B	300	PHE	7.5
1	B	348	VAL	6.9
1	A	488	PRO	6.7
1	A	388	ILE	5.9
1	B	342	THR	5.8
1	A	506	ILE	5.8
1	B	350	THR	5.6
1	B	677	VAL	5.4
1	A	352	ASP	5.2
1	A	489	ASP	5.2
1	A	713	THR	5.1
1	A	507	GLN	5.0
1	A	355	PHE	5.0
1	A	677	VAL	4.8
1	A	351	LYS	4.6
1	A	480	ILE	4.5
1	A	322	LEU	4.4
1	A	678	TRP	4.4
1	A	390	SER	4.4
1	B	616	LEU	4.4
1	A	350	THR	4.3
1	A	679	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	340	GLN	4.3
1	A	389	GLU	4.3
1	A	711	TRP	4.3
1	B	718	GLY	4.3
1	B	680	VAL	4.2
1	A	551	PHE	4.2
1	A	714	HIS	4.2
1	A	712	ASN	4.1
1	A	386	LYS	3.9
1	A	393	THR	3.9
1	A	508	GLN	3.9
1	A	681	PRO	3.9
1	A	499	VAL	3.8
1	A	339	SER	3.8
1	B	678	TRP	3.8
1	A	566	ALA	3.8
1	A	643	SER	3.8
1	A	553	TRP	3.8
1	A	676	TRP	3.8
1	A	503	GLU	3.8
1	A	391	THR	3.7
1	B	341	HIS	3.7
1	A	567	VAL	3.7
1	B	619	ARG	3.7
1	B	617	ASP	3.6
1	B	299	ARG	3.6
1	B	302	LYS	3.6
1	A	470	HIS	3.5
1	A	385	ASN	3.5
1	A	392	SER	3.5
1	A	479	LEU	3.5
1	A	486	LYS	3.5
1	A	593	ILE	3.5
1	A	680	VAL	3.5
1	A	685	GLY	3.5
1	A	487	GLN	3.5
1	A	619	ARG	3.4
1	B	310	VAL	3.4
1	A	584	PHE	3.4
1	B	676	TRP	3.4
1	B	343	ARG	3.3
1	B	566	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	620	LYS	3.2
1	A	299	ARG	3.2
1	B	679	ILE	3.2
1	A	353	GLN	3.1
1	B	352	ASP	3.1
1	A	466	THR	3.1
1	A	514	ARG	3.1
1	A	490	GLY	3.1
1	B	301	LEU	3.0
1	A	300	PHE	3.0
1	A	691	PHE	3.0
1	A	467	ASP	3.0
1	A	504	ILE	2.9
1	A	416	VAL	2.9
1	B	337	LEU	2.9
1	A	667	ARG	2.9
1	B	615	ASP	2.8
1	B	611	ALA	2.8
1	B	561	TRP	2.8
1	A	302	LYS	2.7
1	B	309	ASP	2.7
1	A	505	CYS	2.7
1	B	562	TYR	2.7
1	A	554	PHE	2.7
1	A	588	TYR	2.7
1	B	567	VAL	2.7
1	B	667	ARG	2.7
1	A	511	LYS	2.6
1	A	564	LEU	2.6
1	A	469	LYS	2.6
1	A	710	PRO	2.6
1	A	668[A]	CYS	2.6
1	B	691	PHE	2.5
1	A	415	CYS	2.5
1	B	608	GLU	2.5
1	B	681	PRO	2.5
1	B	717	LYS	2.5
1	A	492	THR	2.5
1	A	491	SER	2.5
1	A	412	ALA	2.4
1	B	612	LYS	2.4
1	B	339	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	615	ASP	2.4
1	B	591	THR	2.4
1	B	609	GLU	2.4
1	B	479	LEU	2.4
1	A	565	PRO	2.4
1	B	550	LYS	2.4
1	A	552	ASP	2.3
1	A	481	ARG	2.3
1	A	370	LYS	2.3
1	A	478	GLN	2.2
1	B	329	HIS	2.2
1	B	682	PRO	2.2
1	B	351	LYS	2.2
1	A	561	TRP	2.2
1	A	465	ARG	2.2
1	A	704	PHE	2.2
1	A	452	LYS	2.2
1	A	682	PRO	2.1
1	A	318	LEU	2.1
1	A	321	THR	2.1
1	A	684	SER	2.1
1	B	311	VAL	2.0
1	A	591	THR	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](#)

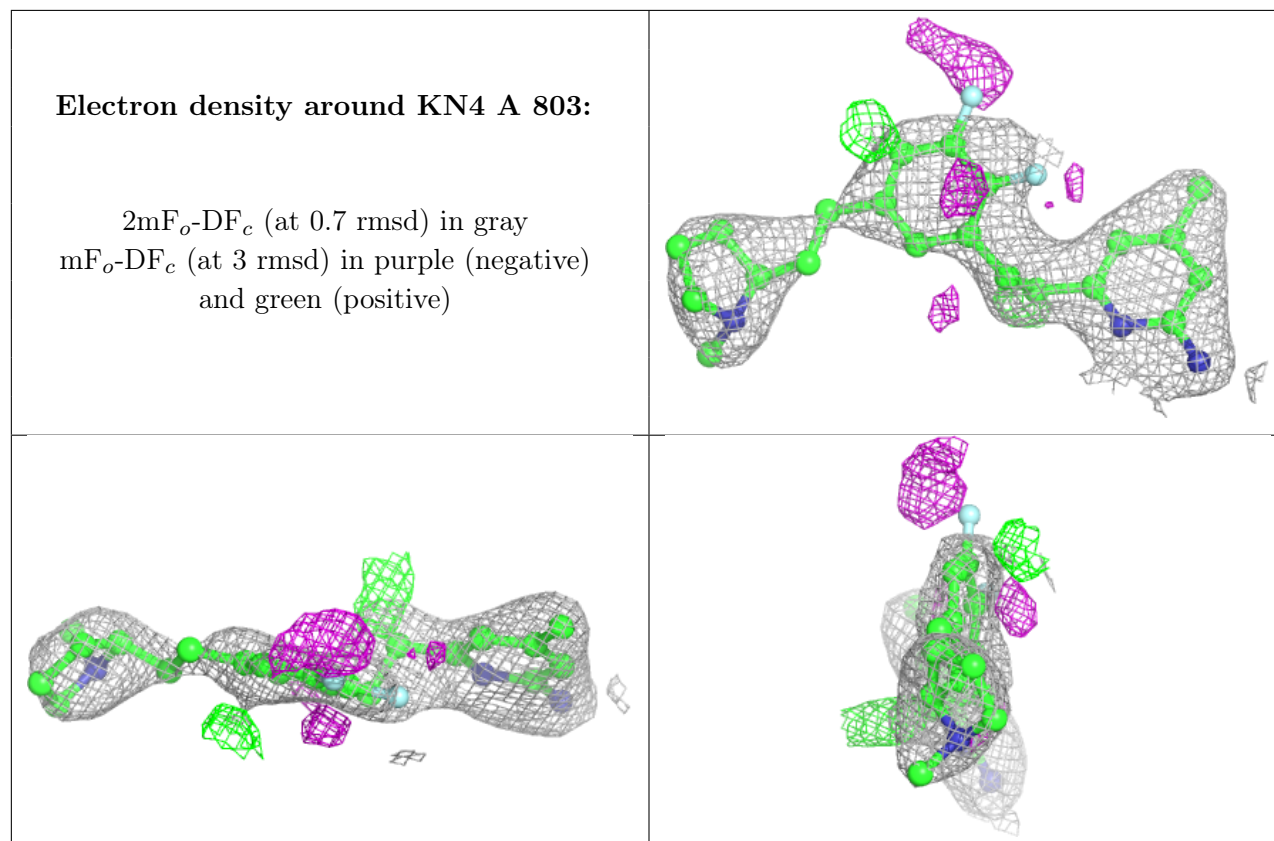
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

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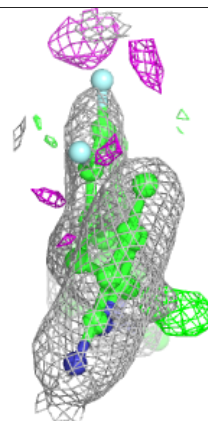
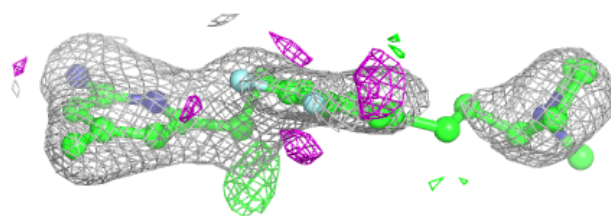
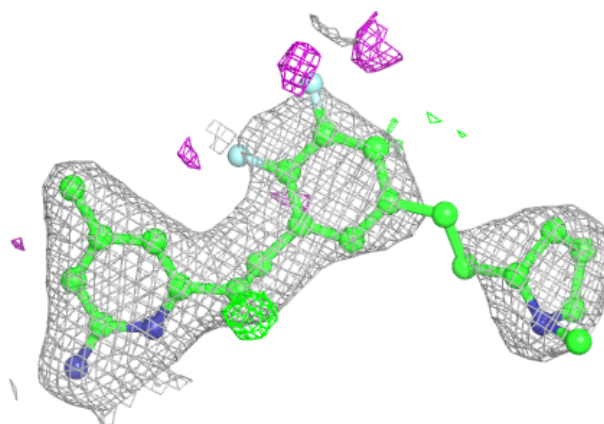
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	GOL	B	805	6/6	0.66	0.24	81,82,87,87	0
7	GOL	B	806	6/6	0.73	0.33	83,88,94,103	0
4	KN4	A	803	26/26	0.90	0.34	40,89,108,115	0
4	KN4	B	803	26/26	0.91	0.32	37,95,104,107	0
3	H4B	A	802	17/17	0.93	0.22	39,50,60,60	0
3	H4B	B	802	17/17	0.94	0.23	43,48,53,55	0
5	ACT	B	804	4/4	0.95	0.16	73,76,78,81	0
5	ACT	A	804	4/4	0.97	0.10	73,74,76,78	0
2	HEM	A	801	43/43	0.98	0.23	29,44,63,73	0
2	HEM	B	801	43/43	0.98	0.22	30,43,71,74	0
6	ZN	A	805	1/1	0.99	0.08	46,46,46,46	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.



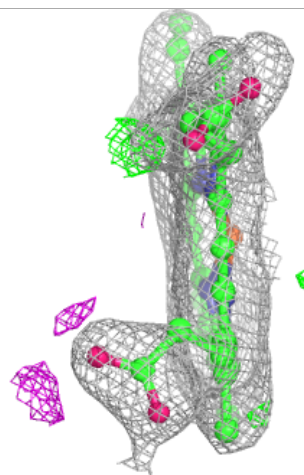
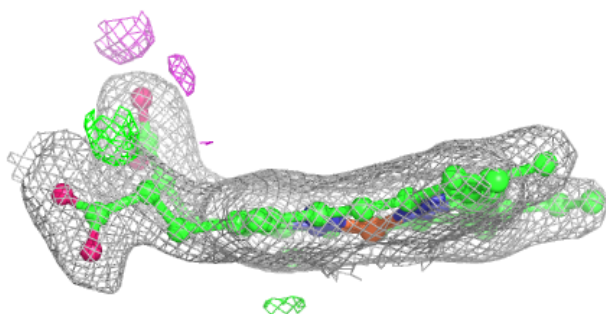
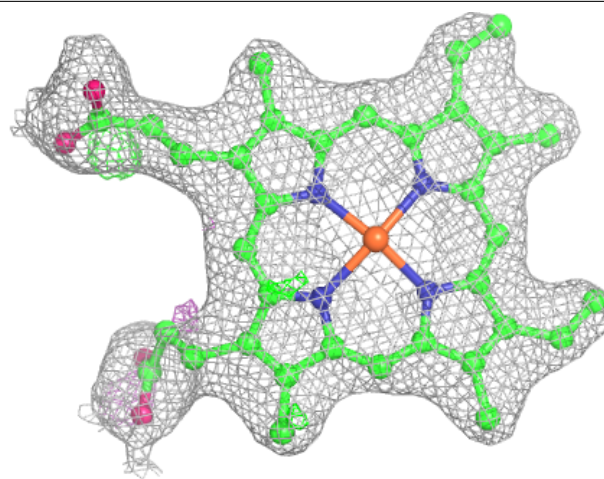
Electron density around KN4 B 803:

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



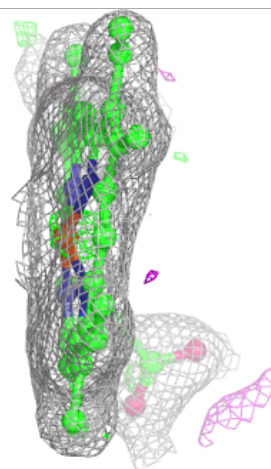
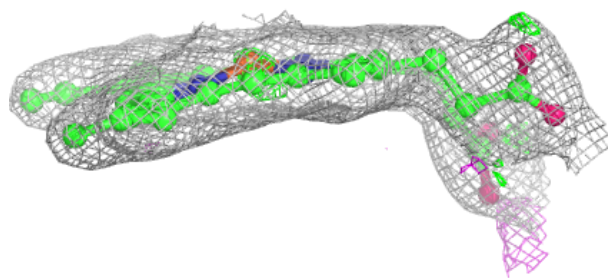
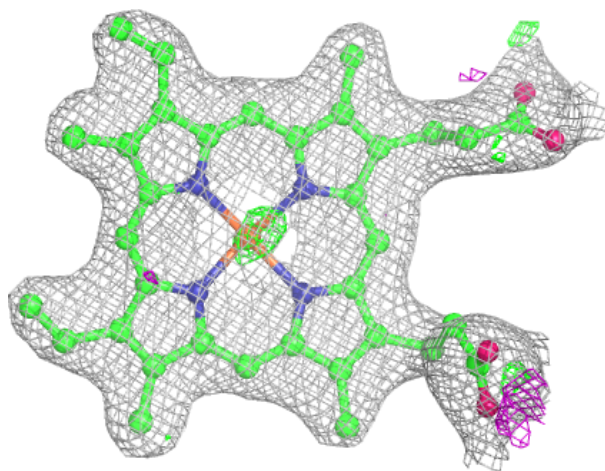
Electron density around HEM A 801:

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



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.