



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 6, 2022 – 02:06 PM EDT

PDB ID : 7S40  
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with 7-((3-(((6-aminopyridin-2-yl)methyl)amino)methyl)phenoxy)methyl)quinolin-2-amine  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2021-09-08  
Resolution : 1.80 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)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
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)	:	2.29

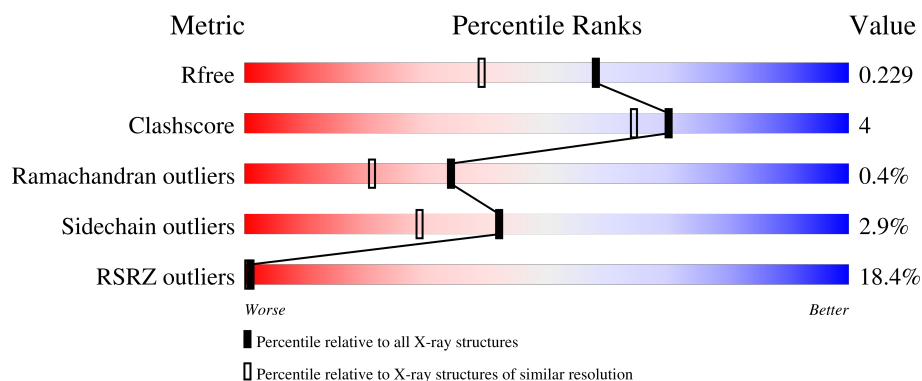
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	<div> <div>26%</div> <div>84%</div> <div>13%</div> <div>.</div> </div>
1	B	422	<div> <div>10%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>

## 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
1	A	411	Total	C	N	O	S	0	2	0
			3348	2141	573	612	22			
1	B	411	Total	C	N	O	S	0	4	0
			3357	2148	574	613	22			

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



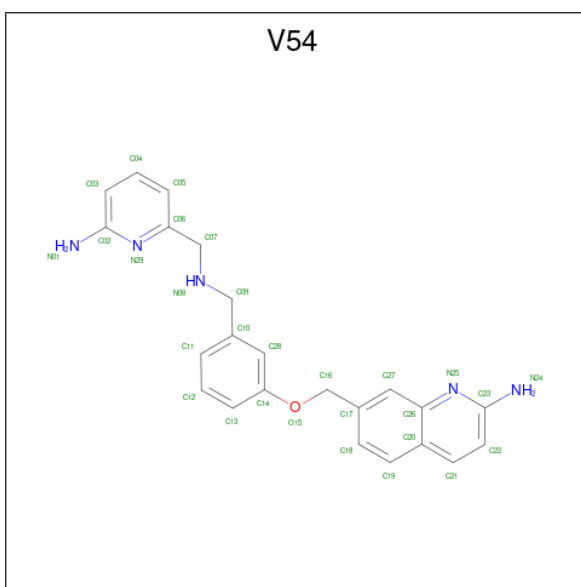
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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 7-{[3-({[(6-aminopyridin-2-yl)methyl]amino}methyl)phenoxy]methyl}quinolin-2-amine (three-letter code: V54) (formula:  $C_{23}H_{23}N_5O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			29	23	5	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			29	23	5	1		

- 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		

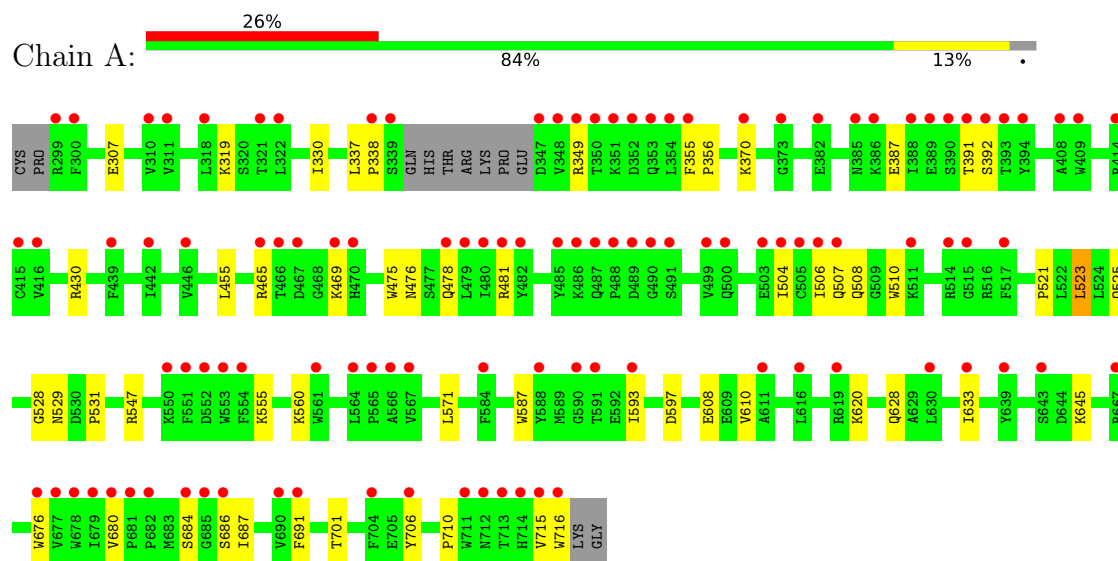
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	157	Total	O	0	0
			157	157		
7	B	237	Total	O	0	0
			237	237		

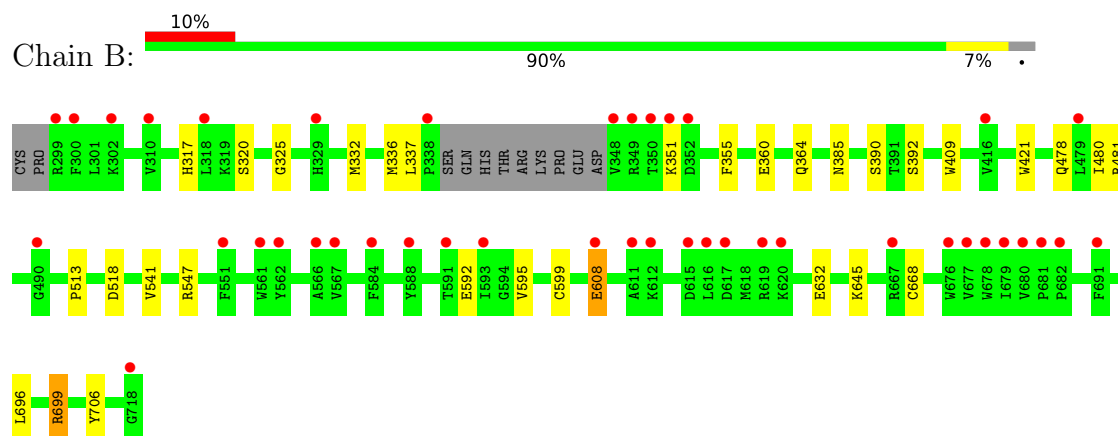
### 3 Residue-property plots [i](#)

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, $\alpha$ , $\beta$ , $\gamma$	52.03Å 111.35Å 164.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.10 – 1.80 39.10 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (39.10-1.80) 99.7 (39.10-1.80)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.11.1-2575_1496	Depositor
R, $R_{free}$	0.192 , 0.229 0.193 , 0.229	Depositor DCC
$R_{free}$ test set	4467 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.8	Xtriage
Anisotropy	0.948	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 57.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7286	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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: ZN, V54, H4B, HEM, 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	0/3444	0.49	0/4672
1	B	0.38	0/3463	0.51	0/4696
All	All	0.36	0/6907	0.50	0/9368

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	3348	0	3257	30	0
1	B	3357	0	3277	16	0
2	A	43	0	30	3	0
2	B	43	0	30	3	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	29	0	0	0	0
4	B	29	0	0	1	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	157	0	0	3	0
7	B	237	0	0	3	0
All	All	7286	0	6630	48	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 (48) 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	1.69	0.75
2:B:801:HEM:HMC2	2:B:801:HEM:HBC2	1.73	0.70
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.75	0.68
1:B:706:TYR:OH	2:B:801:HEM:O2D	2.04	0.67
1:B:668[B]:CYS:SG	7:B:1106:HOH:O	2.52	0.66
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.78	0.66
1:B:364:GLN:OE1	7:B:901:HOH:O	2.13	0.65
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.78	0.65
1:B:592:GLU:OE2	4:B:803:V54:N24	2.33	0.61
2:A:801:HEM:HBB2	2:A:801:HEM:HHC	1.84	0.60
1:A:525:GLN:HE21	1:A:528:GLY:HA2	1.67	0.59
1:A:508:GLN:NE2	1:A:716:TRP:HZ2	2.01	0.59
1:A:706:TYR:OH	2:A:801:HEM:O2D	2.12	0.59
1:A:475:TRP:CH2	1:A:716:TRP:HZ3	2.22	0.57
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.88	0.54
1:B:699:ARG:HH11	1:B:699:ARG:HB3	1.74	0.53
1:A:560:LYS:NZ	7:A:902:HOH:O	2.34	0.53
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.90	0.53
1:A:628:GLN:NE2	1:B:632:GLU:OE2	2.42	0.52
1:A:475:TRP:CE2	1:A:710:PRO:HB2	2.45	0.51
1:A:506:ILE:C	1:A:508:GLN:H	2.15	0.50
1:A:593:ILE:HA	1:A:597:ASP:HB2	1.93	0.50
1:B:595:VAL:O	1:B:599:CYS:HB2	2.12	0.50
1:A:465:ARG:HH12	1:A:571:LEU:HD11	1.78	0.48
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.96	0.48
1:A:686:SER:HA	1:A:691:PHE:CG	2.50	0.46
1:A:510:TRP:CE2	1:A:521:PRO:HD3	2.50	0.46
1:A:307:GLU:HG3	7:B:1038:HOH:O	2.16	0.45
1:B:325:GLY:O	1:B:332:MET:HG3	2.16	0.45
1:A:610:VAL:HG21	1:A:633:ILE:HD11	1.98	0.45
1:A:475:TRP:HH2	1:A:716:TRP:HZ3	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.99	0.44
1:A:684:SER:HB3	1:A:687:ILE:HD11	2.00	0.43
1:B:608:GLU:H	1:B:608:GLU:HG2	1.64	0.43
1:A:387:GLU:O	1:A:391:THR:OG1	2.30	0.43
1:A:525:GLN:HG3	1:A:529:ASN:O	2.19	0.43
1:A:701:THR:HG22	7:A:914:HOH:O	2.18	0.42
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.54	0.42
1:B:480:ILE:HD13	1:B:541:VAL:HG13	2.01	0.42
1:A:370:LYS:HB2	1:A:370:LYS:HE3	1.73	0.42
1:A:676:TRP:CE2	1:A:680:VAL:HG21	2.55	0.41
1:A:504:ILE:O	1:A:508:GLN:HB2	2.20	0.41
1:B:513:PRO:HG2	1:B:518:ASP:CG	2.41	0.41
1:A:355:PHE:N	1:A:356:PRO:HD2	2.36	0.41
1:B:317:HIS:O	1:B:320:SER:HB3	2.21	0.41
1:A:391:THR:O	1:A:392:SER:OG	2.34	0.40
1:A:430:ARG:NH1	7:A:912:HOH:O	2.49	0.40
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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%)	11 (3%)	2 (0%)	29	15
1	B	411/422 (97%)	400 (97%)	10 (2%)	1 (0%)	47	33
All	All	819/844 (97%)	795 (97%)	21 (3%)	3 (0%)	34	21

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	338	PRO

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Mol	Chain	Res	Type
1	B	351	LYS
1	A	507	GLN

### 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	368/377 (98%)	356 (97%)	12 (3%)	38	23
1	B	370/377 (98%)	361 (98%)	9 (2%)	49	36
All	All	738/754 (98%)	717 (97%)	21 (3%)	42	30

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	319	LYS
1	A	337	LEU
1	A	349	ARG
1	A	469	LYS
1	A	476	ASN
1	A	523	LEU
1	A	547	ARG
1	A	555	LYS
1	A	608	GLU
1	A	620	LYS
1	A	645	LYS
1	A	715	VAL
1	B	336	MET
1	B	337	LEU
1	B	360	GLU
1	B	390	SER
1	B	392	SER
1	B	547	ARG
1	B	608	GLU
1	B	645	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 ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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	0.94	0	11,26,26	2.46	5 (45%)
5	ACT	A	804	-	3,3,3	0.75	0	3,3,3	0.78	0
2	HEM	B	801	1	41,50,50	1.59	6 (14%)	45,82,82	1.52	6 (13%)
4	V54	B	803	-	32,32,32	0.88	1 (3%)	42,43,43	1.57	5 (11%)
2	HEM	A	801	1	41,50,50	1.53	6 (14%)	45,82,82	1.52	8 (17%)
5	ACT	B	804	-	3,3,3	0.82	0	3,3,3	0.58	0
3	H4B	A	802	-	16,18,18	0.89	0	11,26,26	2.59	6 (54%)
4	V54	A	803	-	32,32,32	0.83	1 (3%)	42,43,43	1.52	8 (19%)

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
2	HEM	B	801	1	-	1/12/54/54	-
4	V54	B	803	-	-	3/11/11/11	0/4/4/4
2	HEM	A	801	1	-	4/12/54/54	-
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2
4	V54	A	803	-	-	4/11/11/11	0/4/4/4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C3C-C2C	-4.42	1.34	1.40
2	A	801	HEM	C3C-C2C	-3.65	1.35	1.40
2	A	801	HEM	C3C-CAC	3.57	1.55	1.47
2	B	801	HEM	C3C-CAC	3.38	1.54	1.47
2	A	801	HEM	CAB-C3B	2.98	1.55	1.47
2	A	801	HEM	FE-NB	2.81	2.10	1.96
2	B	801	HEM	CAB-C3B	2.73	1.54	1.47
4	A	803	V54	C23-N25	2.59	1.36	1.33
2	B	801	HEM	FE-NB	2.54	2.09	1.96
2	A	801	HEM	CAA-C2A	2.19	1.55	1.52
2	B	801	HEM	CMB-C2B	2.17	1.55	1.50
2	A	801	HEM	CMB-C2B	2.13	1.55	1.50
4	B	803	V54	C27-C26	-2.06	1.38	1.41
2	B	801	HEM	CMD-C2D	2.01	1.55	1.50

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	H4B	C8A-C4A-C4	5.33	119.30	114.57
3	B	802	H4B	C8A-C4A-C4	5.26	119.24	114.57
4	B	803	V54	C06-C07-N08	-4.34	105.19	113.27
4	B	803	V54	C17-C27-C26	-4.10	117.48	121.08
2	B	801	HEM	CBA-CAA-C2A	-3.98	105.82	112.62
4	B	803	V54	C02-N29-C06	3.89	121.05	118.10
4	A	803	V54	C02-N29-C06	3.65	120.86	118.10
2	A	801	HEM	CBA-CAA-C2A	-3.44	106.75	112.62
2	A	801	HEM	C4B-CHC-C1C	3.42	127.08	122.56
2	B	801	HEM	C4B-CHC-C1C	3.30	126.91	122.56
3	A	802	H4B	C2-N3-C4	3.13	120.91	115.93
4	A	803	V54	N24-C23-N25	3.10	120.82	118.26
2	A	801	HEM	CAD-CBD-CGD	-3.07	106.99	113.60
4	A	803	V54	C17-C27-C26	-3.03	118.42	121.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	H4B	N1-C2-N3	-3.02	120.68	125.42
2	A	801	HEM	CMC-C2C-C3C	3.02	130.32	124.68
3	B	802	H4B	C2-N3-C4	2.93	120.59	115.93
3	A	802	H4B	C4-C4A-N5	2.88	121.53	119.12
3	B	802	H4B	N1-C2-N3	-2.87	120.92	125.42
2	B	801	HEM	CHD-C1D-ND	2.79	127.46	124.43
4	A	803	V54	C06-C07-N08	-2.64	108.35	113.27
4	A	803	V54	C16-C17-C18	-2.62	114.50	120.66
2	B	801	HEM	CMC-C2C-C3C	2.50	129.36	124.68
3	A	802	H4B	C2-N1-C8A	2.46	120.05	114.54
4	A	803	V54	C21-C20-C19	-2.41	117.55	123.19
2	A	801	HEM	CHC-C4B-C3B	2.39	128.23	124.57
3	B	802	H4B	C2-N1-C8A	2.39	119.89	114.54
2	A	801	HEM	C3B-C2B-C1B	2.38	108.25	106.49
2	A	801	HEM	CHD-C1D-ND	2.28	126.91	124.43
3	B	802	H4B	C4-C4A-N5	2.27	121.03	119.12
2	B	801	HEM	C4C-CHD-C1D	2.25	125.53	122.56
3	A	802	H4B	N2-C2-N3	2.21	120.69	117.25
4	B	803	V54	C16-O15-C14	-2.19	112.25	117.65
2	A	801	HEM	C4D-ND-C1D	2.18	107.33	105.07
4	A	803	V54	C21-C20-C26	2.18	121.53	118.45
4	B	803	V54	C18-C17-C27	2.08	122.88	118.85
2	B	801	HEM	C4D-ND-C1D	2.02	107.16	105.07
4	A	803	V54	N01-C02-N29	2.00	119.65	116.49

There are no chirality outliers.

All (12) torsion outliers are listed below:

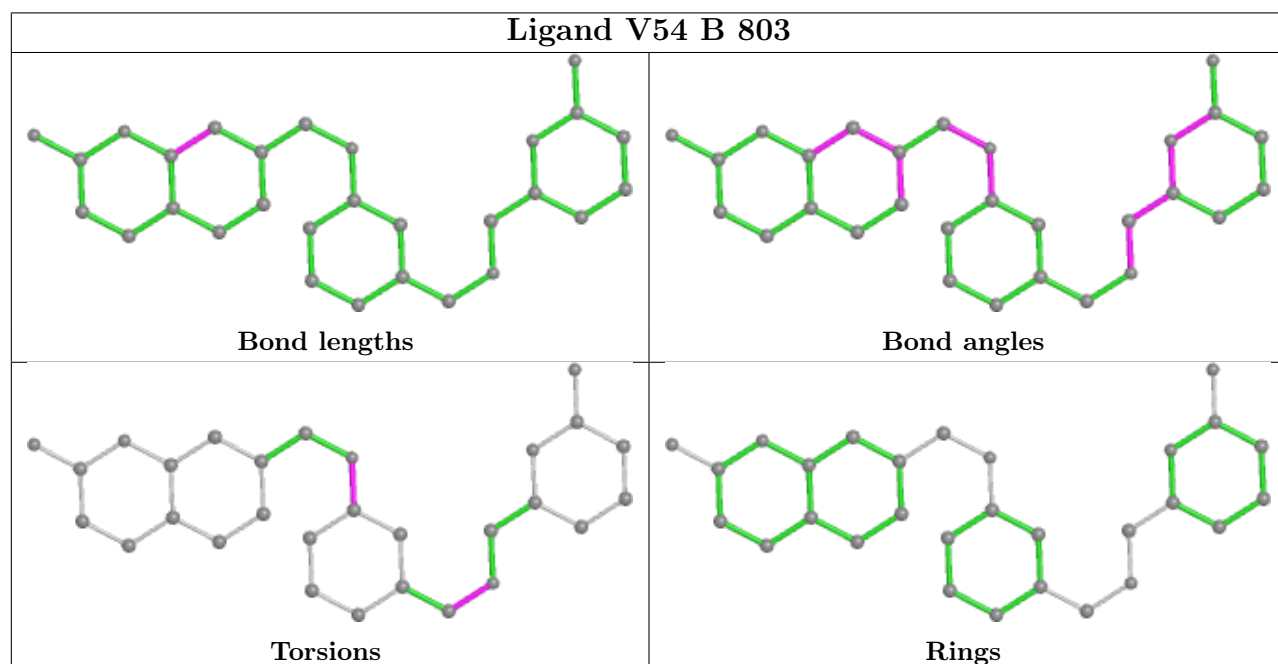
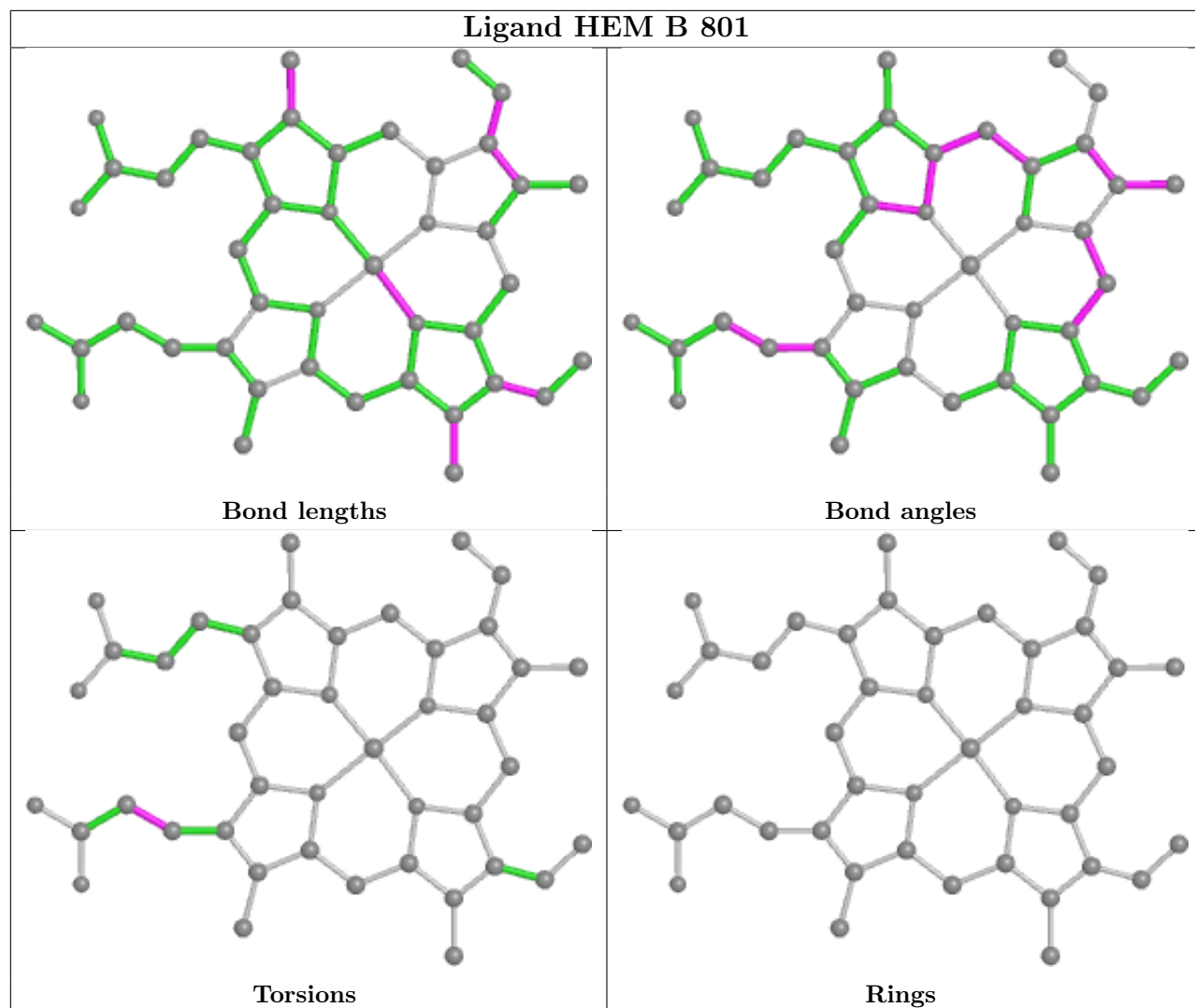
Mol	Chain	Res	Type	Atoms
4	B	803	V54	C28-C14-O15-C16
2	A	801	HEM	C2A-CAA-CBA-CGA
2	B	801	HEM	C2A-CAA-CBA-CGA
4	B	803	V54	C13-C14-O15-C16
4	A	803	V54	C28-C14-O15-C16
4	A	803	V54	C13-C14-O15-C16
4	A	803	V54	C10-C09-N08-C07
4	B	803	V54	C10-C09-N08-C07
2	A	801	HEM	C4B-C3B-CAB-CBB
2	A	801	HEM	CAD-CBD-CGD-O2D
2	A	801	HEM	CAD-CBD-CGD-O1D
4	A	803	V54	C06-C07-N08-C09

There are no ring outliers.

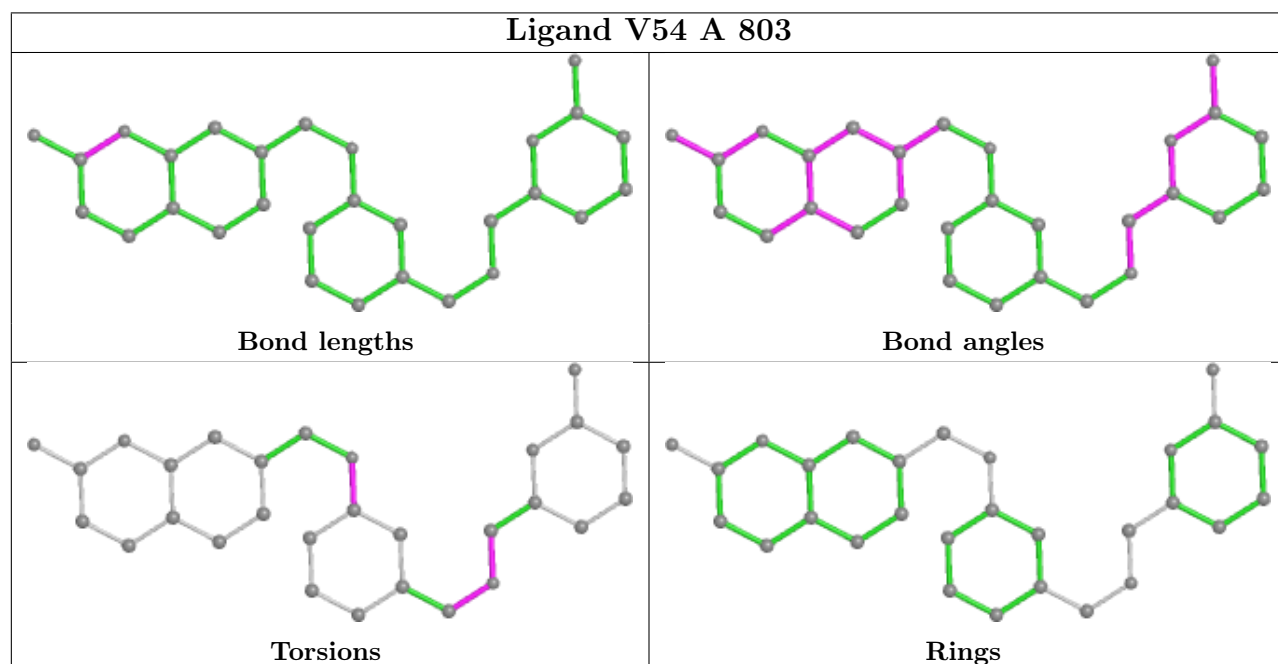
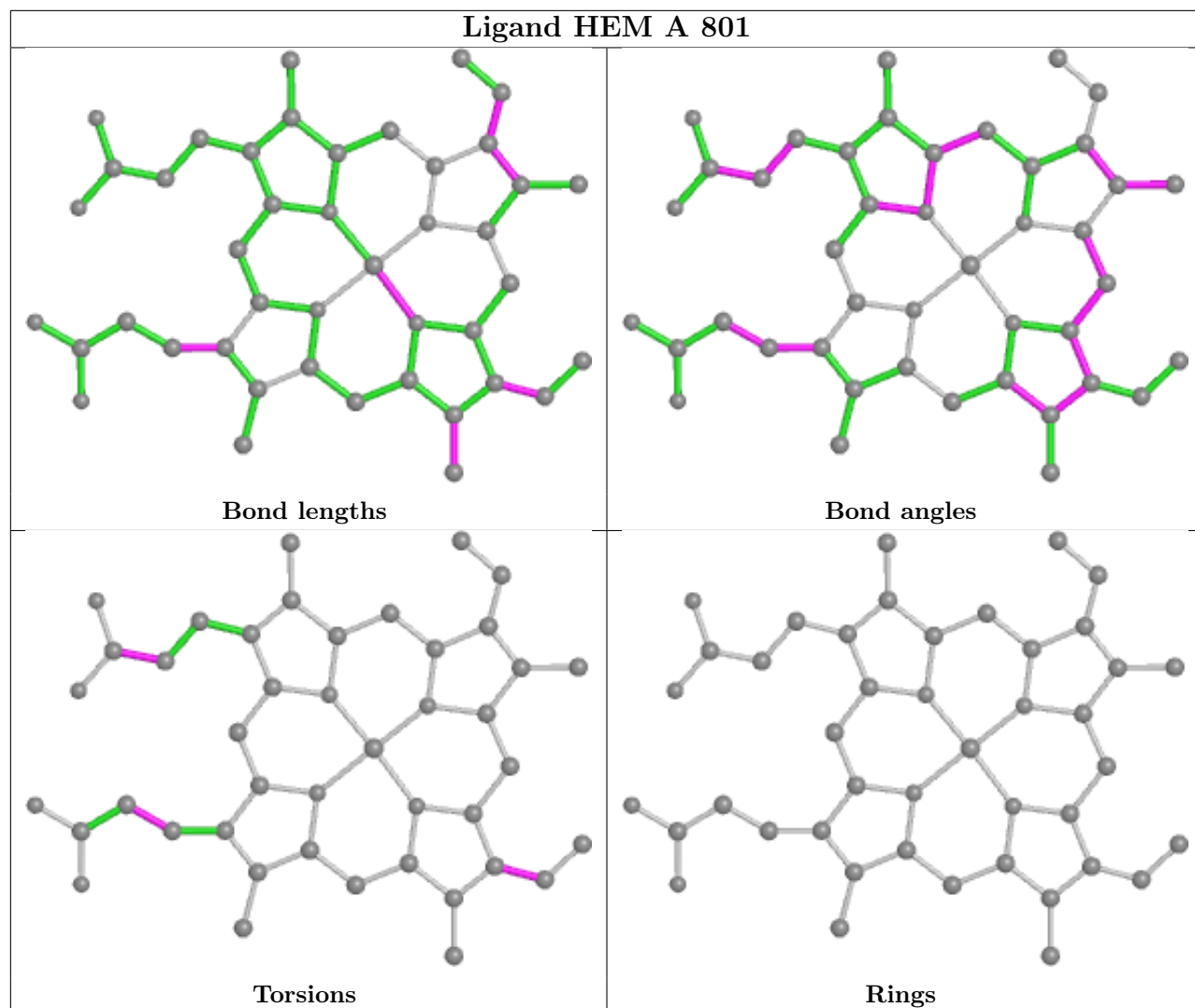
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	HEM	3	0
4	B	803	V54	1	0
2	A	801	HEM	3	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, 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	411/422 (97%)	1.38	109 (26%) <b>0</b> <b>0</b>	37, 63, 114, 147	0
1	B	411/422 (97%)	0.66	42 (10%) <b>6</b> <b>5</b>	35, 53, 90, 113	0
All	All	822/844 (97%)	1.02	151 (18%) <b>1</b> <b>0</b>	35, 57, 106, 147	0

All (151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	348	VAL	14.1
1	B	300	PHE	11.1
1	A	716	TRP	9.3
1	B	348	VAL	9.1
1	A	488	PRO	8.1
1	A	715	VAL	7.3
1	A	347	ASP	7.2
1	A	339	SER	6.5
1	A	355	PHE	6.4
1	A	506	ILE	6.4
1	B	350	THR	6.3
1	A	349	ARG	6.1
1	A	388	ILE	6.0
1	A	490	GLY	5.5
1	A	678	TRP	5.4
1	A	499	VAL	5.4
1	A	350	THR	5.3
1	B	677	VAL	5.2
1	A	507	GLN	5.2
1	A	351	LYS	5.1
1	A	677	VAL	5.1
1	A	352	ASP	5.1
1	A	489	ASP	5.0
1	A	567	VAL	5.0

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Mol	Chain	Res	Type	RSRZ
1	B	680	VAL	5.0
1	A	486	LYS	4.9
1	A	713	THR	4.8
1	A	679	ILE	4.7
1	B	679	ILE	4.6
1	A	584	PHE	4.5
1	B	299	ARG	4.5
1	A	491	SER	4.4
1	A	551	PHE	4.4
1	B	619	ARG	4.4
1	A	479	LEU	4.3
1	B	678	TRP	4.3
1	A	676	TRP	4.3
1	A	566	ALA	4.3
1	A	300	PHE	4.2
1	A	711	TRP	4.1
1	A	469	LYS	4.1
1	A	390	SER	4.0
1	A	389	GLU	4.0
1	A	553	TRP	3.9
1	B	616	LEU	3.8
1	A	480	ILE	3.7
1	A	386	LYS	3.7
1	A	619	ARG	3.7
1	A	391	THR	3.7
1	B	612	LYS	3.6
1	A	393	THR	3.6
1	A	643	SER	3.6
1	B	617	ASP	3.6
1	B	718	GLY	3.6
1	A	385	ASN	3.6
1	A	681	PRO	3.5
1	A	373	GLY	3.5
1	A	487	GLN	3.5
1	B	691	PHE	3.5
1	A	712	ASN	3.5
1	A	392	SER	3.5
1	A	588	TYR	3.4
1	B	567	VAL	3.4
1	A	714	HIS	3.4
1	A	593	ILE	3.4
1	B	676	TRP	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	562	TYR	3.3
1	A	691	PHE	3.3
1	A	322	LEU	3.3
1	B	310	VAL	3.3
1	B	593	ILE	3.2
1	A	466	THR	3.2
1	A	416	VAL	3.2
1	A	680	VAL	3.2
1	A	299	ARG	3.1
1	B	351	LYS	3.1
1	A	353	GLN	3.1
1	A	408	ALA	3.1
1	A	354	LEU	3.1
1	A	503	GLU	3.0
1	B	561	TRP	3.0
1	A	591	THR	3.0
1	A	470	HIS	3.0
1	A	415	CYS	3.0
1	B	615	ASP	3.0
1	A	370	LYS	3.0
1	A	667	ARG	2.9
1	A	311	VAL	2.9
1	B	611	ALA	2.8
1	B	682	PRO	2.8
1	B	588	TYR	2.8
1	B	302	LYS	2.8
1	A	686	SER	2.8
1	A	321	THR	2.8
1	B	591	THR	2.7
1	B	479	LEU	2.7
1	A	706	TYR	2.7
1	B	620	LYS	2.7
1	A	505	CYS	2.7
1	A	564	LEU	2.6
1	B	416	VAL	2.6
1	A	338	PRO	2.6
1	A	446	VAL	2.6
1	B	318	LEU	2.6
1	A	561	TRP	2.6
1	A	511	LYS	2.5
1	B	608	GLU	2.5
1	A	517	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	382	GLU	2.5
1	B	352	ASP	2.5
1	B	584	PHE	2.5
1	A	515	GLY	2.5
1	A	685	GLY	2.5
1	A	682	PRO	2.4
1	A	394	TYR	2.4
1	A	467	ASP	2.4
1	A	630	LEU	2.4
1	A	554	PHE	2.4
1	A	485	TYR	2.4
1	A	611	ALA	2.4
1	A	442	ILE	2.4
1	B	329	HIS	2.4
1	A	565	PRO	2.3
1	A	465	ARG	2.3
1	B	551	PHE	2.3
1	A	639	TYR	2.3
1	A	414	ARG	2.3
1	B	667	ARG	2.3
1	A	504	ILE	2.3
1	B	349	ARG	2.2
1	B	490	GLY	2.2
1	A	318	LEU	2.2
1	B	566	ALA	2.2
1	A	690	VAL	2.2
1	A	500	GLN	2.2
1	B	338	PRO	2.2
1	A	633	ILE	2.2
1	A	550	LYS	2.2
1	A	590	GLY	2.1
1	B	681	PRO	2.1
1	A	409	TRP	2.1
1	A	478	GLN	2.1
1	A	514	ARG	2.1
1	A	684	SER	2.1
1	A	481	ARG	2.1
1	A	482	TYR	2.1
1	A	704	PHE	2.1
1	A	552	ASP	2.1
1	A	616	LEU	2.1
1	A	310	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	439	PHE	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](#)

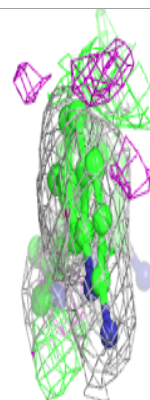
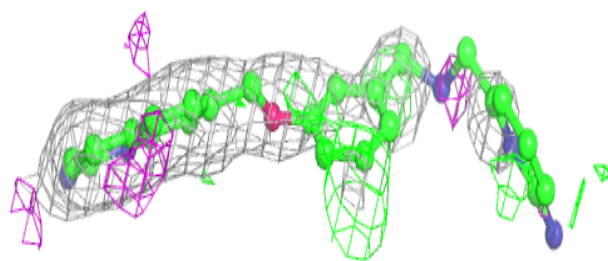
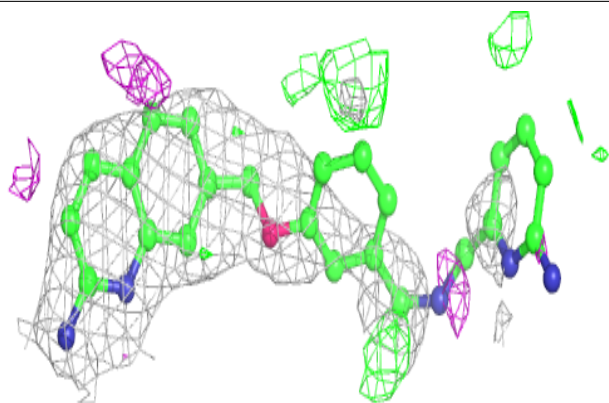
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	V54	A	803	29/29	0.82	0.37	44,105,131,133	0
4	V54	B	803	29/29	0.83	0.36	42,102,129,130	0
5	ACT	A	804	4/4	0.88	0.18	69,75,75,77	0
3	H4B	B	802	17/17	0.93	0.21	47,52,68,79	0
3	H4B	A	802	17/17	0.94	0.17	48,58,71,71	0
5	ACT	B	804	4/4	0.95	0.10	72,74,79,82	0
2	HEM	A	801	43/43	0.97	0.22	35,46,71,74	0
2	HEM	B	801	43/43	0.97	0.19	30,43,65,86	0
6	ZN	A	805	1/1	1.00	0.09	44,44,44,44	0

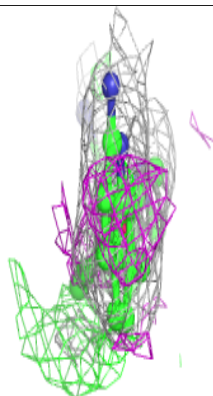
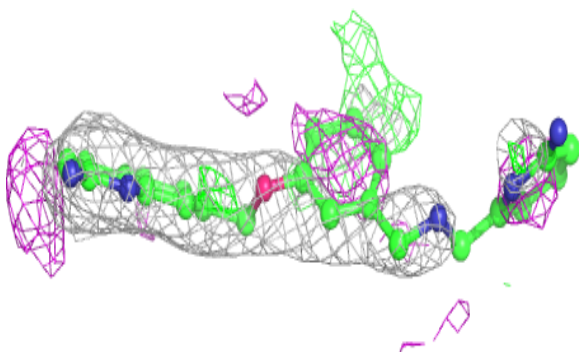
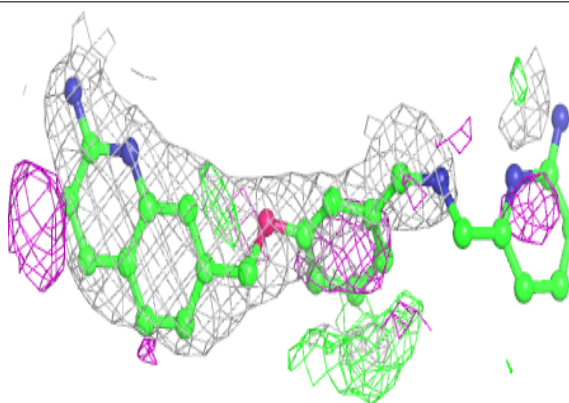
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around V54 A 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 V54 B 803:**

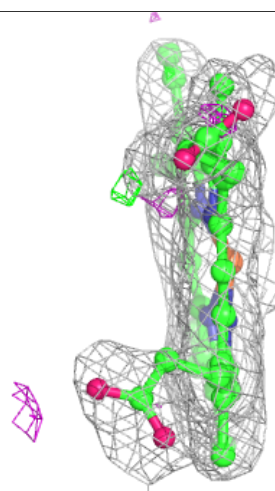
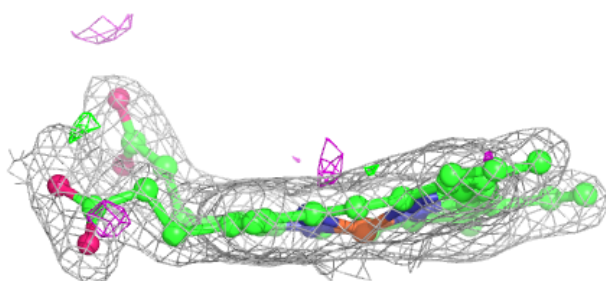
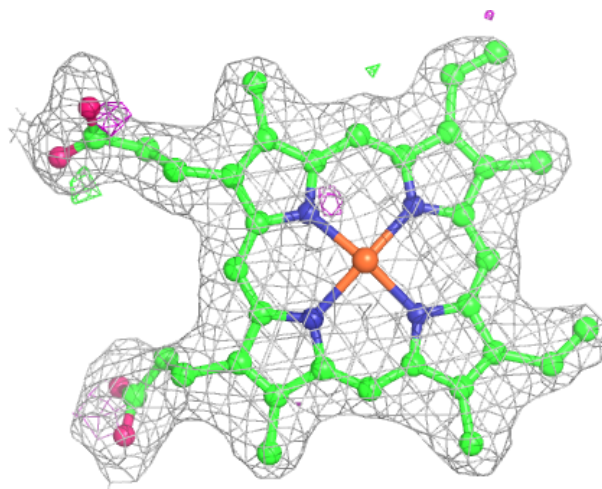
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

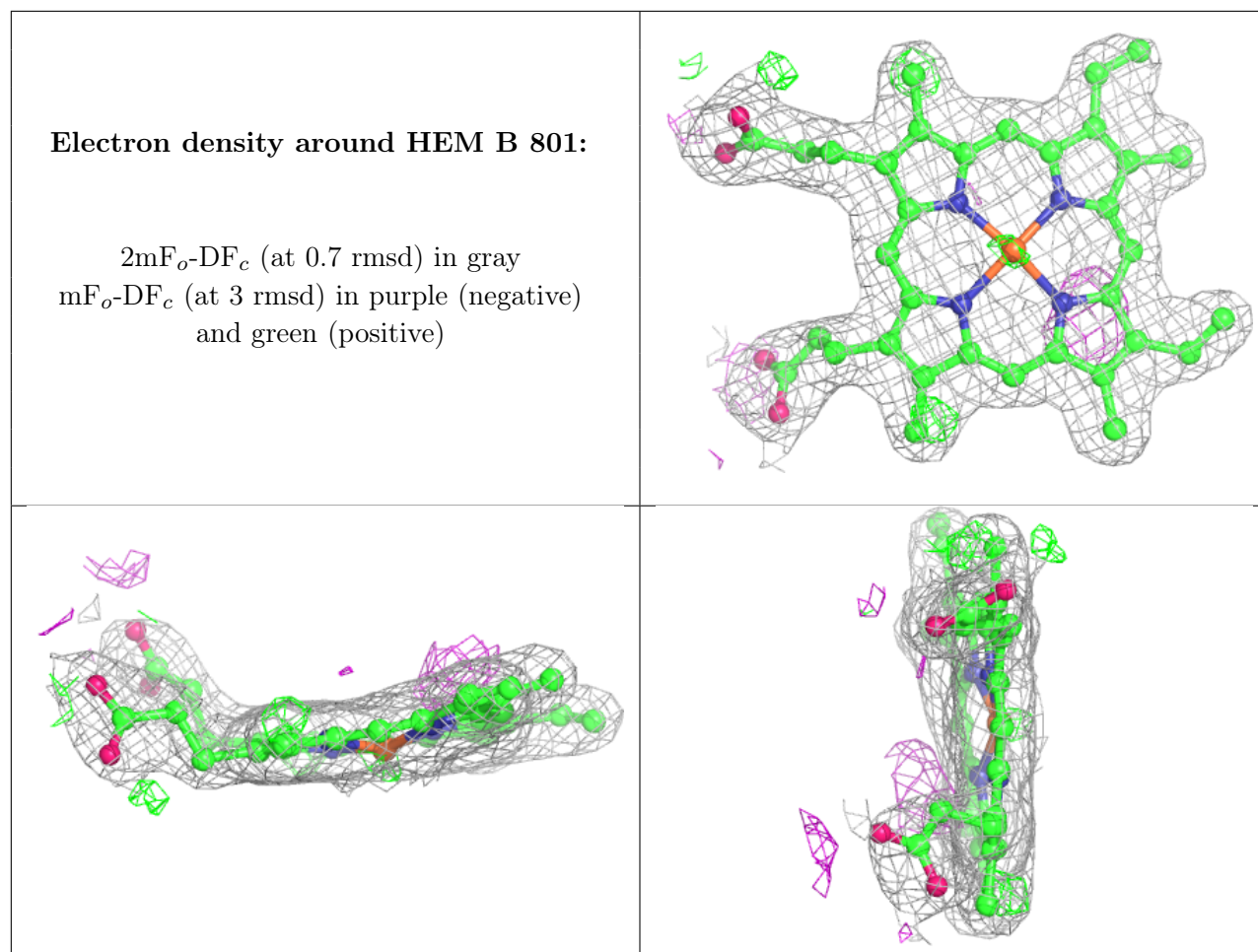




**Electron density around HEM A 801:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.