Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:20 AM UTC

PDB ID	:	6AUW / pdb_00006auw
Title	:	Structure of rat neuronal nitric oxide synthase heme domain in complex with 4-Methyl-6-(2-(5-(4-((methylamino)methyl)phenyl)pyridin-3-yl)ethyl)pyridin-2-amine
Authors	:	Li, H.; Poulos, T.L.
Deposited on	:	2017-09-01
Resolution	:	1.70 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:

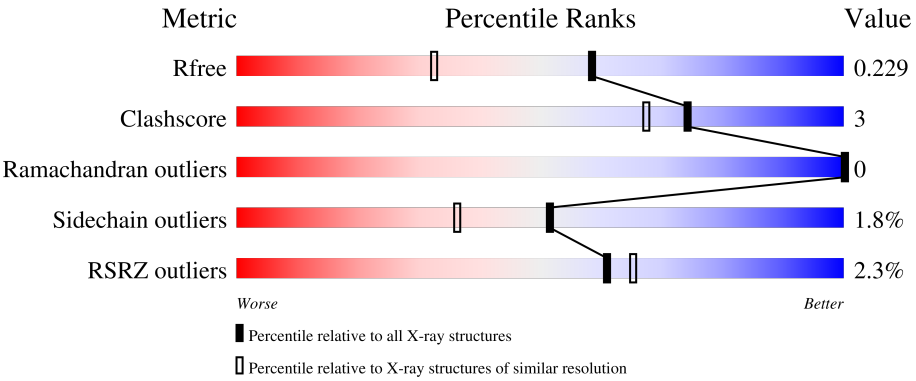
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 <=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	3% 86% 9% .
1	B	422	2% 89% 8% .

2 Entry composition

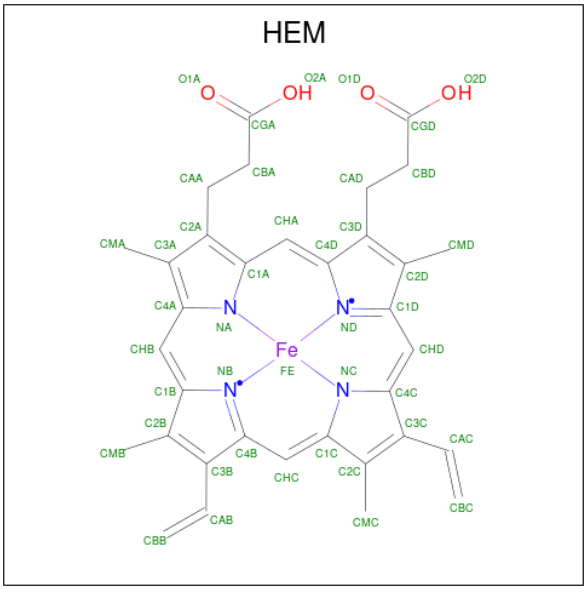
There are 7 unique types of molecules in this entry. The entry contains 7265 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

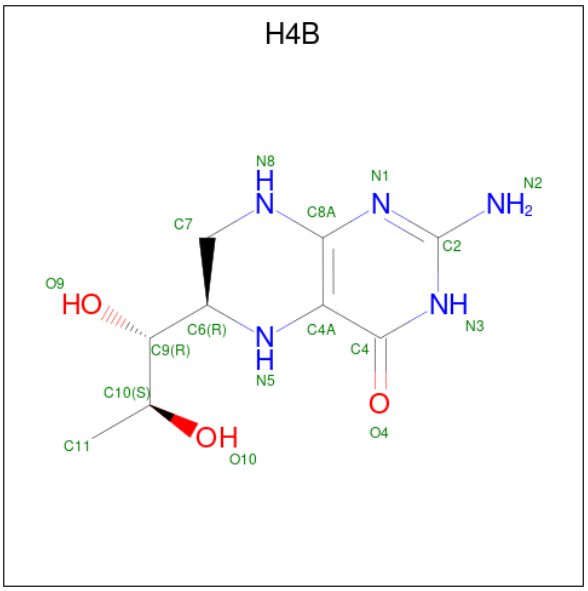
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	4	0
			3326	2130	566	608	22			
1	B	411	Total	C	N	O	S	0	4	0
			3365	2156	574	614	21			

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



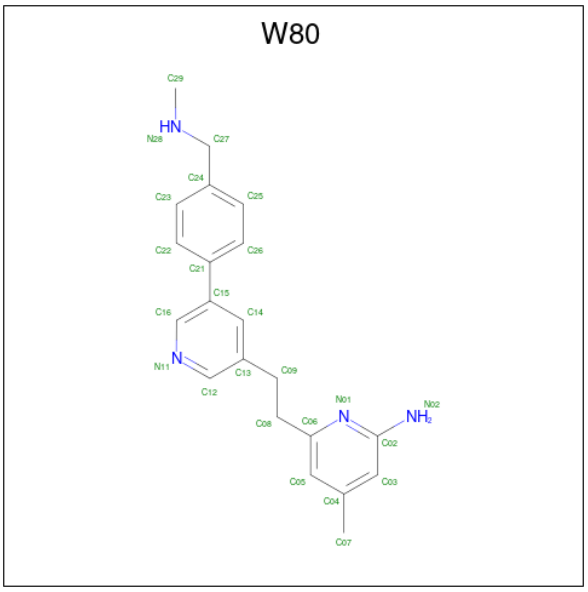
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



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

- Molecule 4 is 4-methyl-6-[2-(5-{4-[(methylamino)methyl]phenyl}pyridin-3-yl)ethyl]pyridin-2-amine (CCD ID: W80) (formula: $C_{21}H_{24}N_4$).



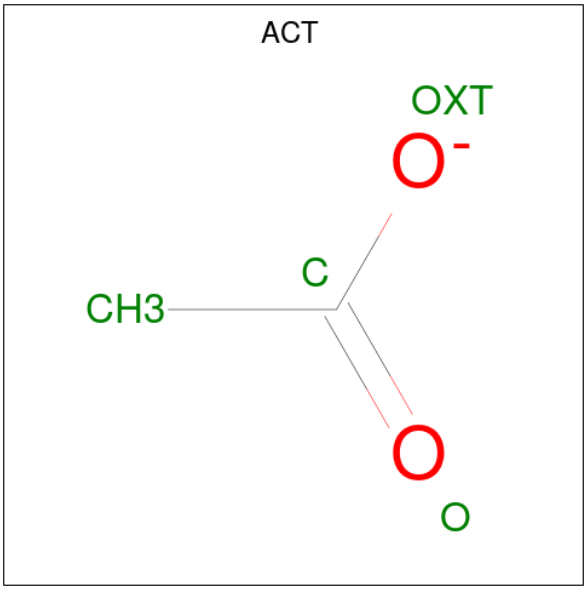
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N 25 21 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N 25 21 4	0	0

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 7 is water.

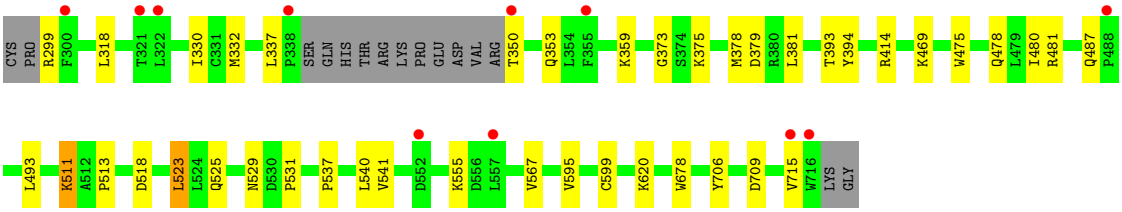
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	163	Total O 163 163	0	0
7	B	232	Total O 232 232	0	0

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.

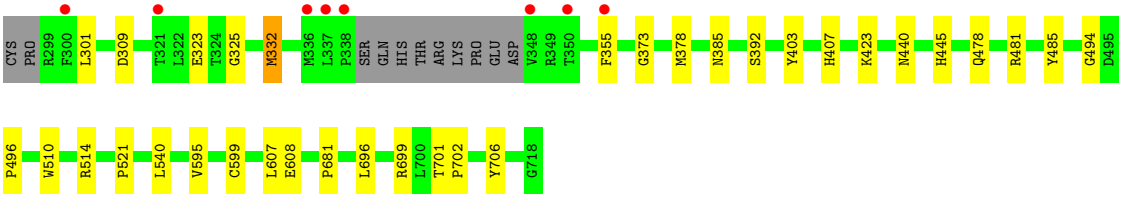
• Molecule 1: Nitric oxide synthase, brain

Chain A:



• Molecule 1: Nitric oxide synthase, brain

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	51.91Å 111.07Å 164.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.96 – 1.70 38.96 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.0 (38.96-1.70) 96.8 (38.96-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.25 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.194 , 0.229 0.194 , 0.229	Depositor DCC
R_{free} test set	5065 reflections (4.01%)	wwPDB-VP
Wilson B-factor (Å^2)	30.5	Xtriage
Anisotropy	0.599	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 47.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7265	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: W80, H4B, ZN, ACT, HEM

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	0.41	0/3428	0.75	2/4652 (0.0%)
1	B	0.45	0/3471	0.76	2/4706 (0.0%)
All	All	0.43	0/6899	0.75	4/9358 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	709	ASP	CA-C-N	5.38	125.46	119.32
1	A	709	ASP	C-N-CA	5.38	125.46	119.32
1	B	681	PRO	CA-C-N	5.11	125.79	120.12
1	B	681	PRO	C-N-CA	5.11	125.79	120.12

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3326	0	3239	22	0
1	B	3365	0	3284	19	0
2	A	43	0	30	3	0
2	B	43	0	30	3	0
3	A	17	0	15	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	15	0	0
4	A	25	0	0	1	0
4	B	25	0	0	0	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0
7	A	163	0	0	0	0
7	B	232	0	0	1	0
All	All	7265	0	6619	42	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 3.

All (42) 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	1.65	0.77
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.69	0.73
2:A:801:HEM:HBB2	2:A:801:HEM:HHC	1.76	0.68
2:B:801:HEM:HMC2	2:B:801:HEM:HBC2	1.76	0.68
1:A:487:GLN:HE21	1:A:493:LEU:HB2	1.59	0.66
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.80	0.63
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.79	0.62
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.82	0.60
1:B:706:TYR:OH	2:B:801:HEM:O1D	2.17	0.55
1:A:330:ILE:HD11	1:B:696:LEU:HB3	1.91	0.53
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.90	0.53
1:B:595:VAL:O	1:B:599:CYS:HB2	2.11	0.51
1:A:706:TYR:OH	2:A:801:HEM:O1D	2.19	0.50
1:A:299:ARG:HG3	1:A:318:LEU:HD21	1.94	0.49
1:A:567:VAL:HG22	4:A:803:W80:C12	2.42	0.49
1:B:494:GLY:O	1:B:496:PRO:HD3	2.14	0.47
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.02	0.47
1:A:511:LYS:HE2	1:A:511:LYS:C	2.40	0.46
1:A:393:THR:OG1	1:A:394:TYR:N	2.46	0.45
1:A:525:GLN:HG3	1:A:529:ASN:O	2.16	0.45
1:B:373:GLY:HA2	1:B:378:MET:HE3	1.99	0.44
1:A:375:LYS:NZ	1:A:379:ASP:OD1	2.51	0.44
1:A:513:PRO:HG2	1:A:518:ASP:CG	2.43	0.43
1:B:325:GLY:O	1:B:332:MET:HG3	2.19	0.43
1:A:373:GLY:HA2	1:A:378:MET:HE3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.54	0.42
1:A:537:PRO:HB2	1:A:540:LEU:HG	2.01	0.42
1:A:330:ILE:HD11	1:B:696:LEU:HD22	2.01	0.42
1:B:355[A]:PHE:CE1	1:B:385:ASN:HB2	2.55	0.42
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.54	0.42
1:A:414:ARG:HD3	1:A:678:TRP:CD2	2.55	0.42
1:B:301:LEU:HD23	1:B:301:LEU:HA	1.91	0.42
1:A:359:LYS:HE2	1:A:381:LEU:HD21	2.00	0.42
1:A:350:THR:N	1:A:353:GLN:OE1	2.53	0.41
1:B:445:HIS:CD2	1:B:445:HIS:C	2.98	0.41
1:B:440:ASN:ND2	7:B:919:HOH:O	2.53	0.41
1:B:701:THR:HA	1:B:702:PRO:C	2.45	0.41
1:A:595:VAL:O	1:A:599:CYS:HB2	2.21	0.41
1:B:323:GLU:O	1:B:699:ARG:HD3	2.21	0.41
1:A:480:ILE:HD13	1:A:541:VAL:HG13	2.03	0.41
1:A:332:MET:HE1	1:B:301:LEU:HD22	2.02	0.40
1:B:607:LEU:HD23	1:B:607:LEU:HA	1.96	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	406/422 (96%)	395 (97%)	11 (3%)	0	100	100
1	B	411/422 (97%)	406 (99%)	5 (1%)	0	100	100
All	All	817/844 (97%)	801 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	366/377 (97%)	359 (98%)	7 (2%)	50 34
1	B	370/377 (98%)	364 (98%)	6 (2%)	55 41
All	All	736/754 (98%)	723 (98%)	13 (2%)	51 36

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	337	LEU
1	A	469	LYS
1	A	511	LYS
1	A	523	LEU
1	A	555	LYS
1	A	620	LYS
1	A	715	VAL
1	B	309	ASP
1	B	332	MET
1	B	392	SER
1	B	423	LYS
1	B	540	LEU
1	B	608	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	487	GLN
1	B	407	HIS
1	B	425	GLN

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 oligosaccharides 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	$\#\|Z\| > 2$
2	HEM	A	801	1	50,50,50	2.08	11 (22%)	67,82,82	1.40	7 (10%)
2	HEM	B	801	1	50,50,50	1.97	11 (22%)	67,82,82	1.36	7 (10%)
5	ACT	A	804	-	3,3,3	0.81	0	3,3,3	0.74	0
4	W80	B	803	-	27,27,27	0.45	0	34,36,36	1.94	10 (29%)
4	W80	A	803	-	27,27,27	0.53	0	34,36,36	2.29	11 (32%)
5	ACT	B	804	-	3,3,3	0.83	0	3,3,3	0.65	0
3	H4B	B	802	-	17,18,18	0.83	0	14,26,26	1.82	4 (28%)
3	H4B	A	802	-	17,18,18	0.73	0	14,26,26	1.95	5 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	801	1	-	3/14/54/54	-
2	HEM	B	801	1	-	3/14/54/54	-
4	W80	B	803	-	-	5/12/12/12	0/3/3/3
4	W80	A	803	-	-	6/12/12/12	0/3/3/3
3	H4B	B	802	-	-	0/8/17/17	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3D-C2D	7.30	1.52	1.36
2	B	801	HEM	C3D-C2D	7.17	1.52	1.36
2	A	801	HEM	FE-NA	5.95	2.14	1.95
2	B	801	HEM	FE-NA	5.42	2.13	1.95
2	A	801	HEM	FE-NB	5.01	2.10	1.94
2	A	801	HEM	FE-NC	4.59	2.10	1.95
2	B	801	HEM	FE-NC	4.16	2.08	1.95
2	B	801	HEM	FE-NB	3.64	2.06	1.94
2	A	801	HEM	FE-ND	3.30	2.05	1.94
2	B	801	HEM	FE-ND	3.26	2.04	1.94
2	B	801	HEM	CAC-C3C	3.07	1.55	1.47
2	A	801	HEM	CAC-C3C	3.05	1.55	1.47
2	B	801	HEM	CAB-C3B	2.99	1.55	1.47
2	A	801	HEM	CAB-C3B	2.98	1.55	1.47
2	B	801	HEM	CMC-C2C	2.43	1.55	1.50
2	A	801	HEM	CMD-C2D	2.30	1.55	1.50
2	A	801	HEM	CMC-C2C	2.28	1.55	1.50
2	A	801	HEM	CMA-C3A	2.27	1.55	1.50
2	B	801	HEM	CMB-C2B	2.20	1.55	1.50
2	B	801	HEM	CMD-C2D	2.20	1.55	1.50
2	B	801	HEM	CMA-C3A	2.17	1.55	1.50
2	A	801	HEM	CMB-C2B	2.12	1.55	1.50

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	803	W80	C02-N01-C06	8.14	124.16	118.07
4	B	803	W80	C02-N01-C06	5.83	122.43	118.07
4	A	803	W80	C05-C06-N01	-4.80	117.26	122.73
2	B	801	HEM	C4D-ND-C1D	4.44	110.46	105.21
2	A	801	HEM	CBD-CAD-C3D	-4.41	100.33	112.53
2	A	801	HEM	C4D-ND-C1D	4.40	110.41	105.21
3	A	802	H4B	C2-N1-C8A	4.34	121.01	113.36
3	B	802	H4B	C2-N1-C8A	4.09	120.57	113.36
4	A	803	W80	C16-C15-C21	-4.08	114.73	121.62
2	B	801	HEM	CBA-CAA-C2A	-3.54	102.76	112.53
4	B	803	W80	C05-C06-N01	-3.50	118.74	122.73

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	803	W80	C16-C15-C21	-3.38	115.91	121.62
2	A	801	HEM	CMD-C2D-C1D	3.25	130.11	125.03
2	B	801	HEM	C2A-C1A-NA	-3.06	106.76	110.15
3	B	802	H4B	O4-C4-C4A	-3.01	120.00	127.26
4	A	803	W80	C09-C13-C14	2.98	125.55	120.54
4	A	803	W80	C14-C15-C16	2.92	120.23	117.10
4	B	803	W80	C09-C13-C12	-2.88	116.61	121.73
2	B	801	HEM	CHD-C1D-ND	2.87	127.51	124.42
3	A	802	H4B	O4-C4-C4A	-2.77	120.57	127.26
2	B	801	HEM	CAD-C3D-C4D	2.77	129.52	124.70
3	B	802	H4B	C4A-C4-N3	2.72	119.59	112.13
4	B	803	W80	C14-C15-C16	2.68	119.97	117.10
3	A	802	H4B	C2-N3-C4	-2.63	120.33	125.11
3	A	802	H4B	C4A-C4-N3	2.63	119.35	112.13
4	B	803	W80	C08-C06-N01	2.62	120.03	116.06
2	A	801	HEM	C4C-NC-C1C	2.58	110.02	105.82
4	B	803	W80	C09-C13-C14	2.54	124.82	120.54
4	A	803	W80	C09-C13-C12	-2.54	117.22	121.73
4	B	803	W80	C15-C14-C13	-2.52	117.85	121.20
4	A	803	W80	C14-C15-C21	2.49	125.02	120.84
4	B	803	W80	C22-C21-C15	-2.40	117.12	121.25
3	B	802	H4B	C2-N3-C4	-2.33	120.88	125.11
4	B	803	W80	N02-C02-N01	2.25	120.21	116.59
4	A	803	W80	C15-C14-C13	-2.25	118.20	121.20
2	B	801	HEM	CMD-C2D-C1D	2.15	128.40	125.03
2	B	801	HEM	CBD-CAD-C3D	-2.14	106.62	112.53
4	A	803	W80	C08-C06-C05	2.13	124.73	121.65
2	A	801	HEM	CBA-CAA-C2A	-2.11	106.69	112.53
4	A	803	W80	C22-C21-C15	-2.09	117.64	121.25
2	A	801	HEM	C1D-C2D-C3D	-2.07	104.80	106.98
2	A	801	HEM	C3B-C2B-C1B	2.07	107.96	106.41
3	A	802	H4B	C11-C10-C9	-2.02	109.64	112.11
4	A	803	W80	C09-C08-C06	2.02	117.50	113.01

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	803	W80	C24-C27-N28-C29
4	A	803	W80	C16-C15-C21-C26
4	A	803	W80	C16-C15-C21-C22
4	A	803	W80	C14-C15-C21-C22

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	803	W80	C14-C15-C21-C26
2	A	801	HEM	C2A-CAA-CBA-CGA
2	A	801	HEM	C4B-C3B-CAB-CBB
2	A	801	HEM	C1A-C2A-CAA-CBA
2	B	801	HEM	C4B-C3B-CAB-CBB
4	B	803	W80	C05-C06-C08-C09
4	A	803	W80	C05-C06-C08-C09
4	A	803	W80	N01-C06-C08-C09
4	B	803	W80	N01-C06-C08-C09
4	B	803	W80	C08-C09-C13-C14
4	B	803	W80	C08-C09-C13-C12
2	B	801	HEM	CAA-CBA-CGA-O2A
2	B	801	HEM	CAA-CBA-CGA-O1A

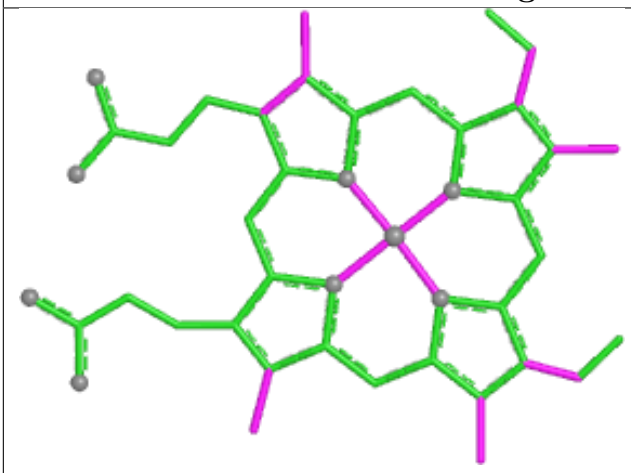
There are no ring outliers.

3 monomers are involved in 7 short contacts:

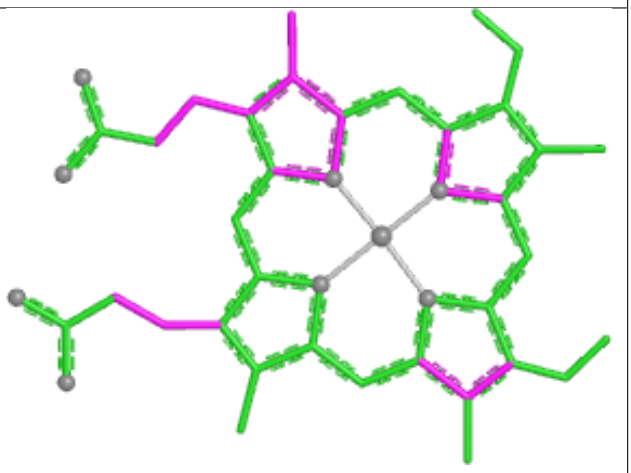
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	3	0
2	B	801	HEM	3	0
4	A	803	W80	1	0

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 then 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.

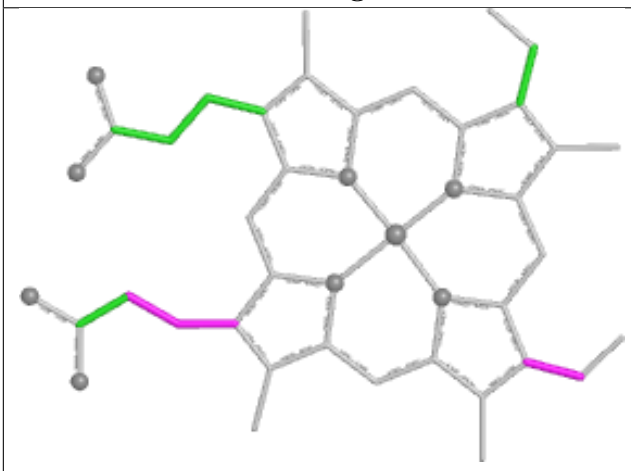
Ligand HEM A 801



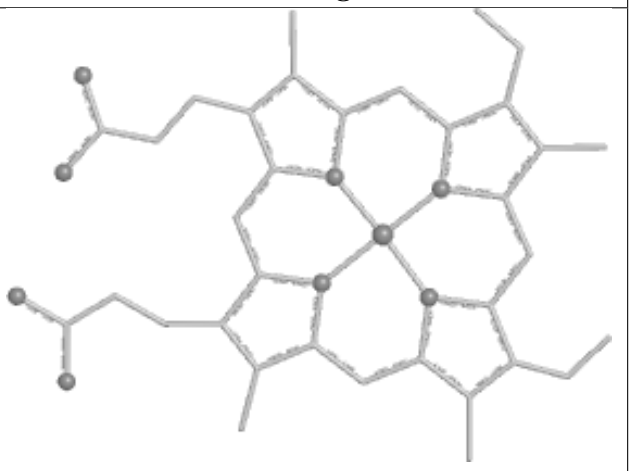
Bond lengths



Bond angles

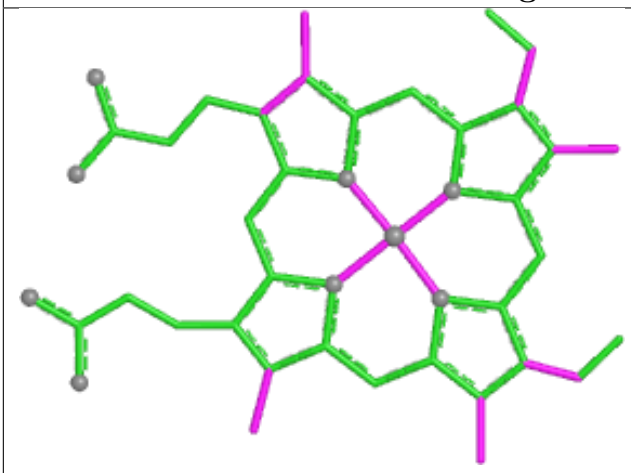


Torsions

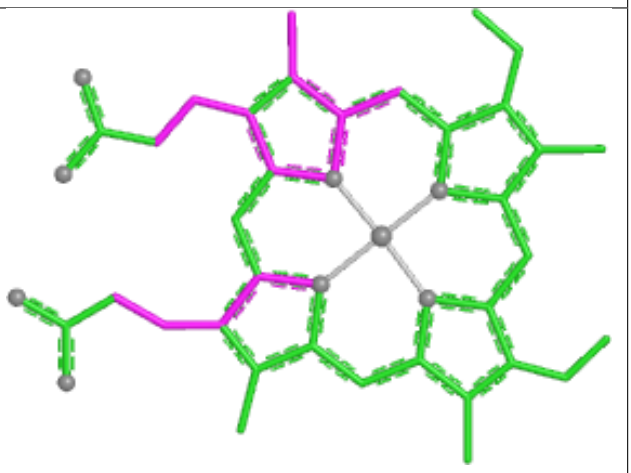


Rings

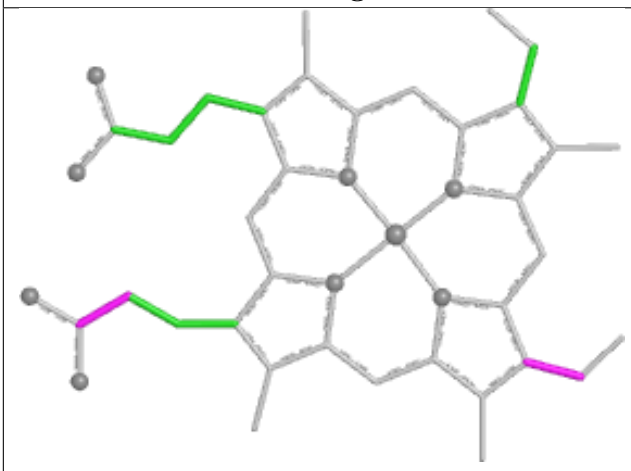
Ligand HEM B 801



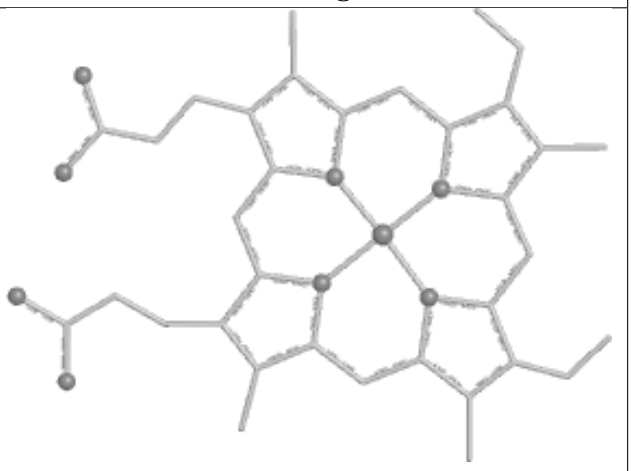
Bond lengths



Bond angles

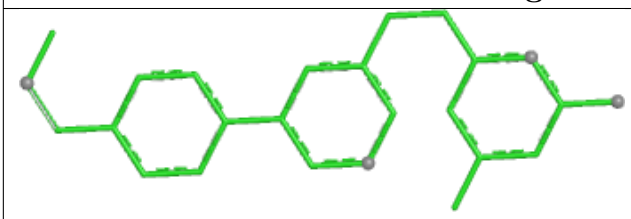


Torsions

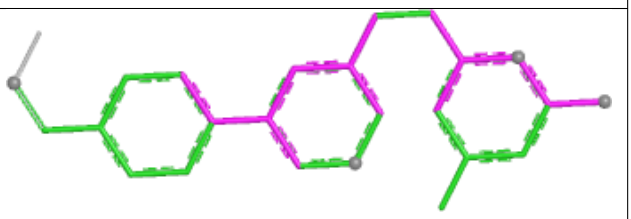


Rings

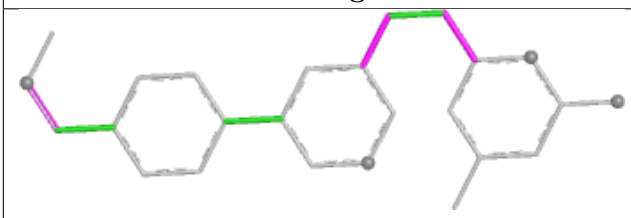
Ligand W80 B 803



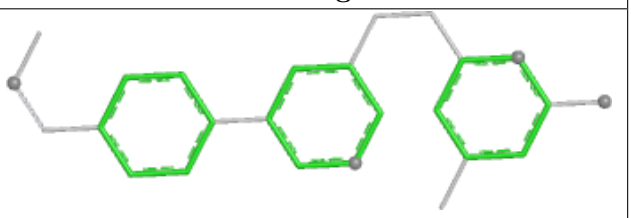
Bond lengths



Bond angles

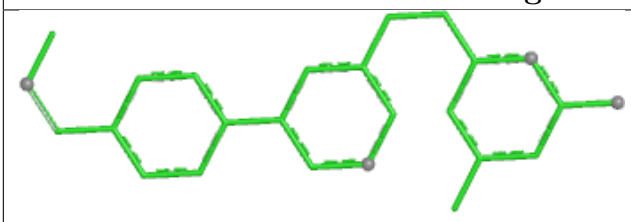


Torsions

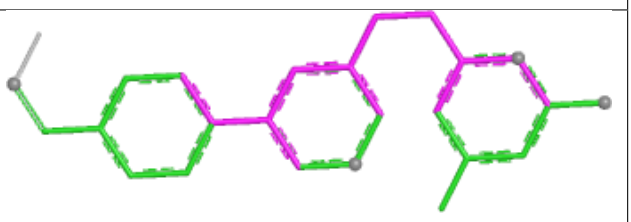


Rings

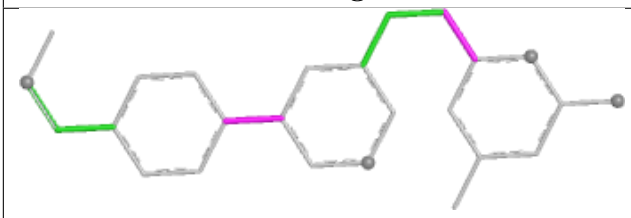
Ligand W80 A 803



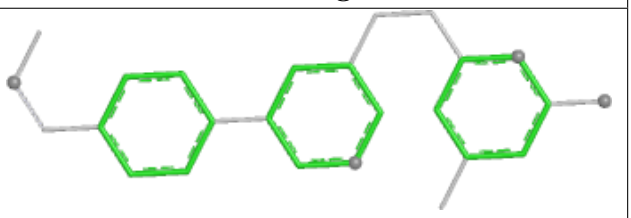
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	407/422 (96%)	0.43	11 (2%)	56	60	28, 59, 104, 149	3 (0%)
1	B	411/422 (97%)	0.10	8 (1%)	66	71	27, 46, 76, 103	4 (0%)
All	All	818/844 (96%)	0.26	19 (2%)	61	65	27, 50, 97, 149	7 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	338	PRO	5.1
1	B	348	VAL	4.4
1	A	338	PRO	4.0
1	B	355[A]	PHE	4.0
1	A	355	PHE	3.9
1	A	300	PHE	3.4
1	A	716	TRP	3.0
1	A	321	THR	3.0
1	A	715	VAL	2.5
1	A	557	LEU	2.4
1	B	300	PHE	2.4
1	B	337	LEU	2.4
1	A	322	LEU	2.4
1	A	488	PRO	2.4
1	B	350	THR	2.4
1	B	336	MET	2.3
1	A	350	THR	2.2
1	B	321	THR	2.1
1	A	552	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

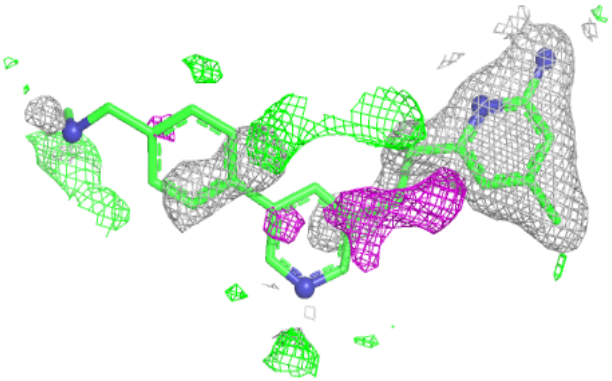
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

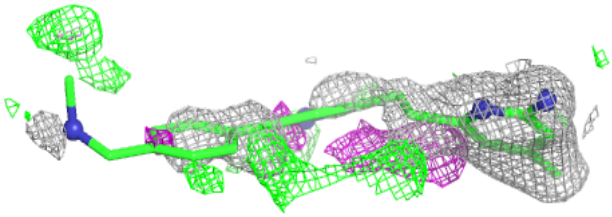
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	W80	B	803	25/25	0.83	0.22	35,117,127,129	0
4	W80	A	803	25/25	0.85	0.20	31,114,130,134	0
5	ACT	A	804	4/4	0.88	0.15	73,75,78,80	0
3	H4B	B	802	17/17	0.95	0.08	34,43,48,50	0
3	H4B	A	802	17/17	0.95	0.08	37,48,53,53	0
5	ACT	B	804	4/4	0.96	0.09	57,71,72,75	0
2	HEM	A	801	43/43	0.98	0.07	29,38,65,74	0
2	HEM	B	801	43/43	0.98	0.07	27,37,64,69	0
6	ZN	A	805	1/1	0.99	0.04	37,37,37,37	0

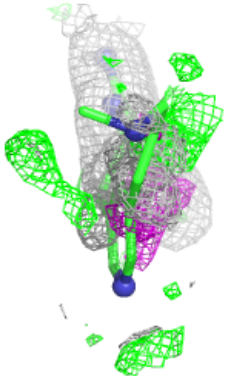
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around W80 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)

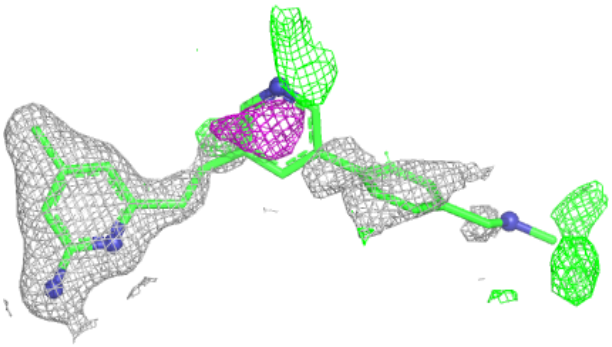


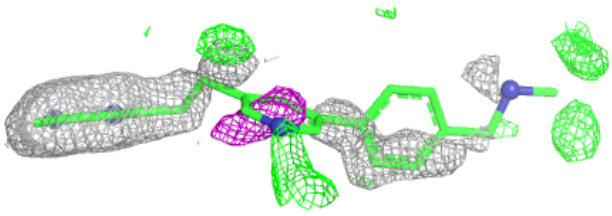


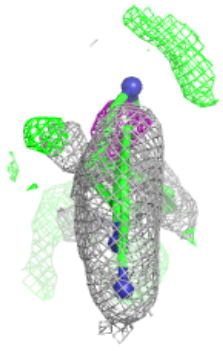


Electron density around W80 A 803:

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

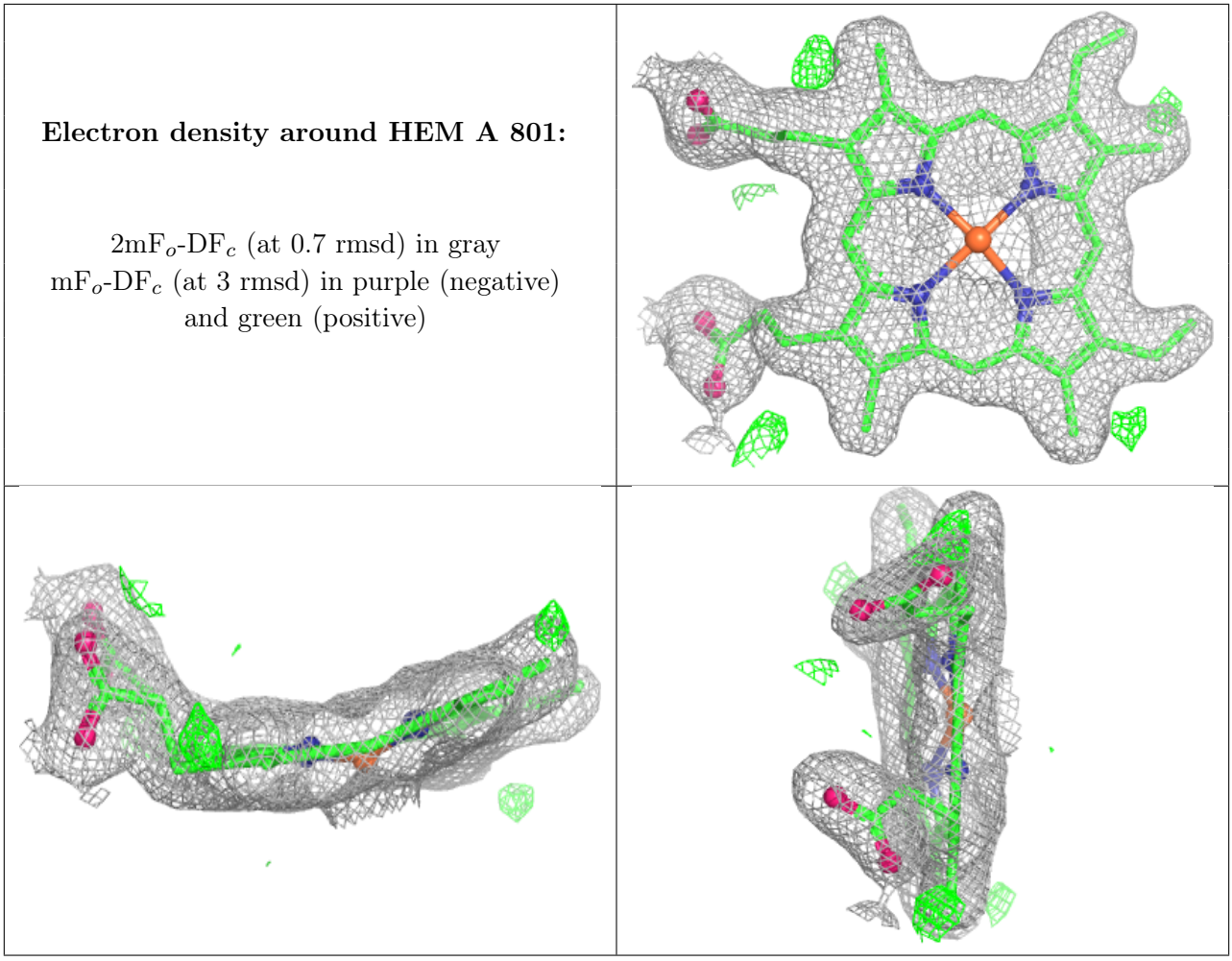






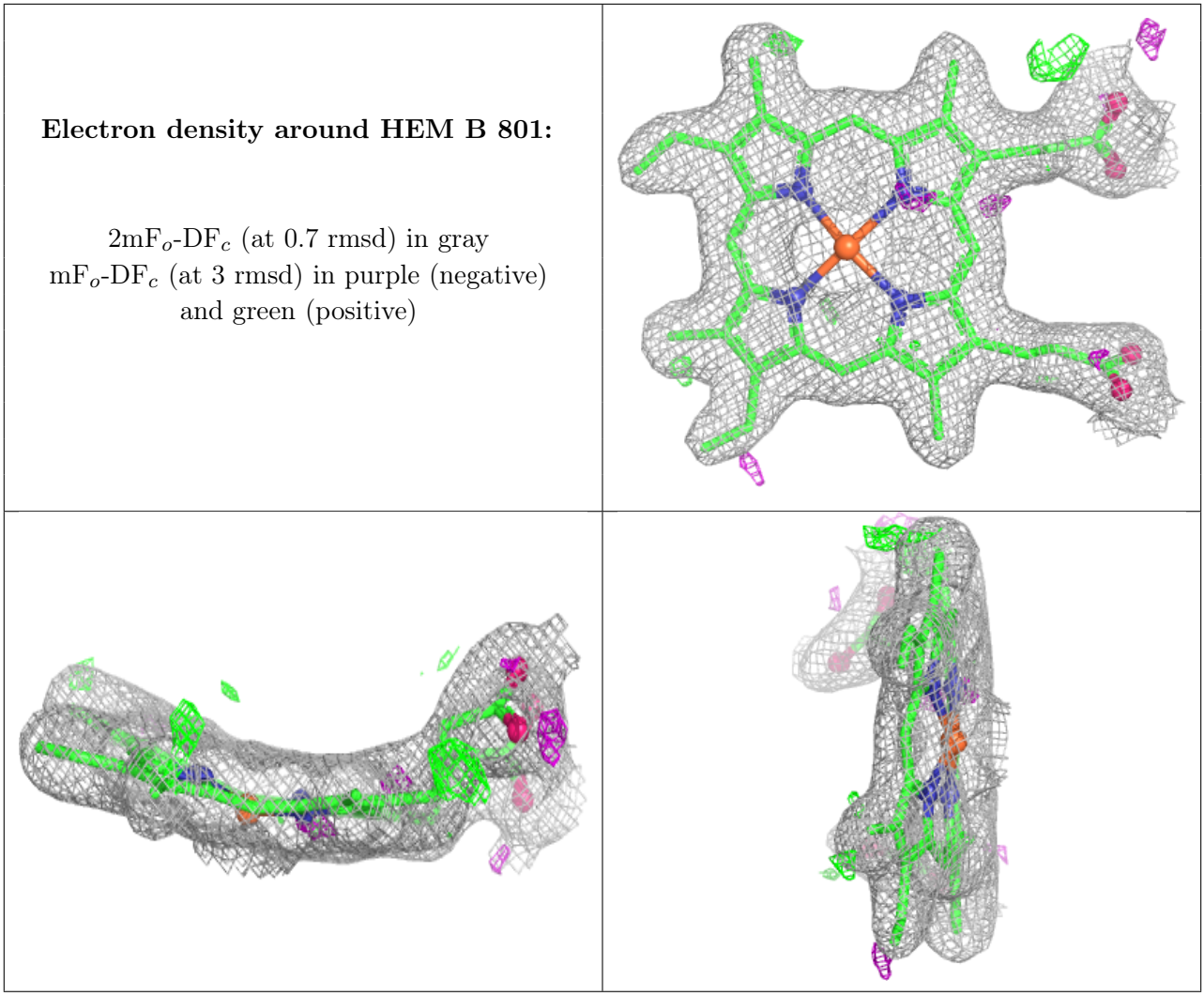
Electron density around HEM A 801:

$2mF_o$-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

There are no such residues in this entry.