Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 09:39 pm BST

PDB ID	:	5FVP
Title	:	Structure of rat neuronal nitric oxide synthase heme domain in complex with 4-methyl-6-[2-(5-morpholin-4-ylpyridin-3-yl)ethyl]pyridin-2-amine
Authors	:	Li, H.; Poulos, T.L.
Deposited on	:	2016-02-10
Resolution	:	2.10 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 following versions of software and data (see references ⓘ) were used in the production of this report:

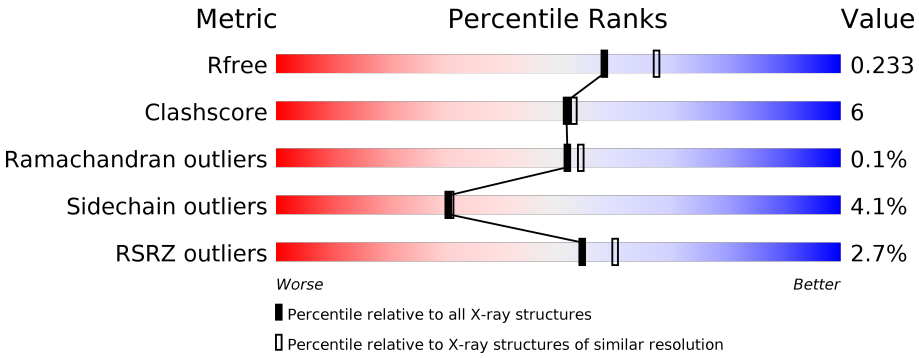
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	4% 79% 17%
1	B	422	2% 82% 15%

2 Entry composition

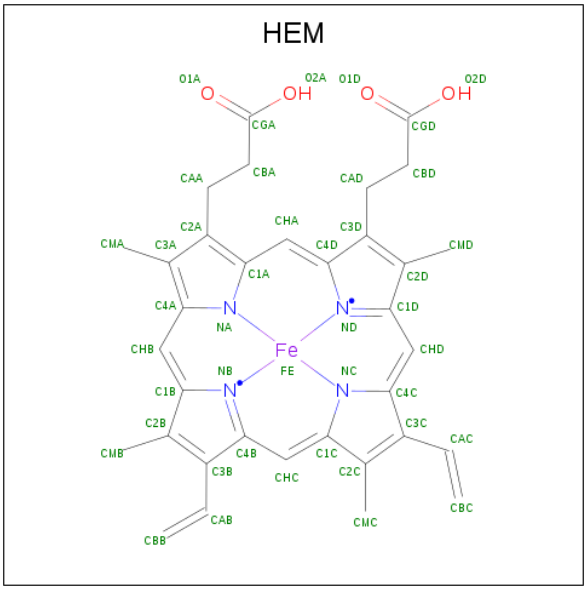
There are 7 unique types of molecules in this entry. The entry contains 7052 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

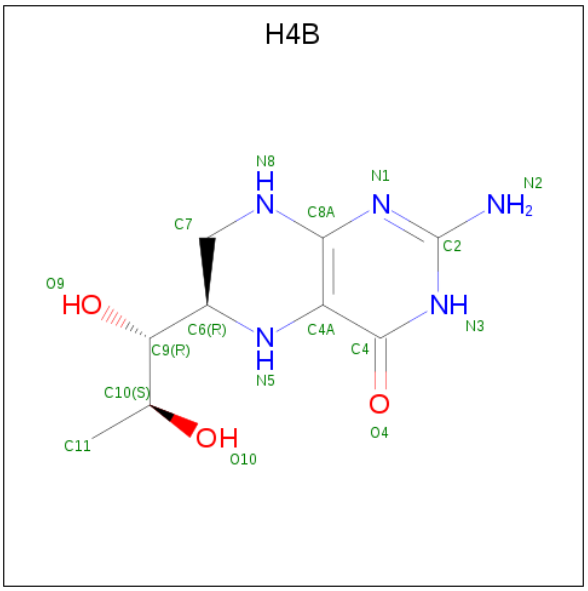
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	3	1
			3323	2127	567	607	22			
1	B	411	Total	C	N	O	S	0	3	0
			3357	2148	574	614	21			

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



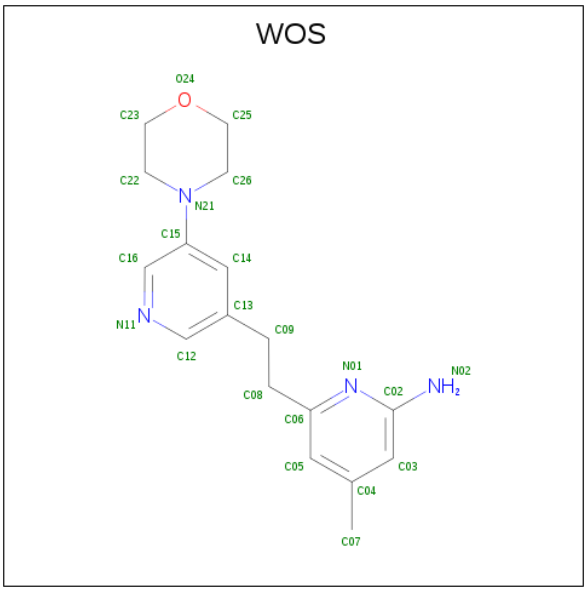
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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 4-methyl-6-[2-(5-morpholin-4-ylpyridin-3-yl)ethyl]pyridin-2-amine (three-letter code: WOS) (formula: $C_{17}H_{22}N_4O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			22	17	4	1		

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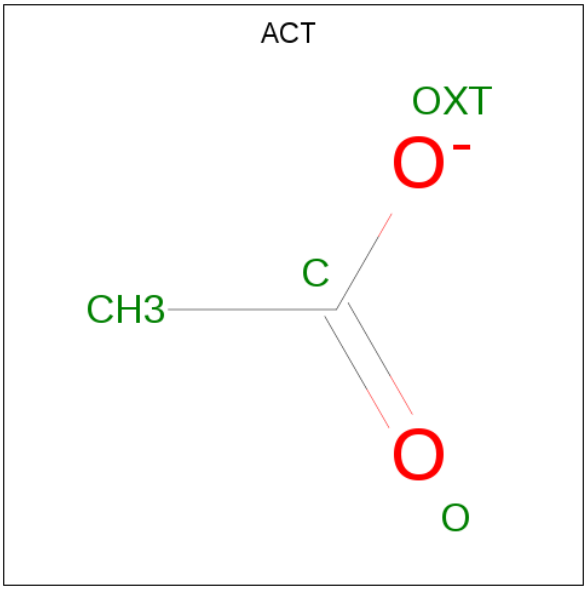
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N O 22 17 4 1	0	0

- 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 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

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

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

- Molecule 7 is water.

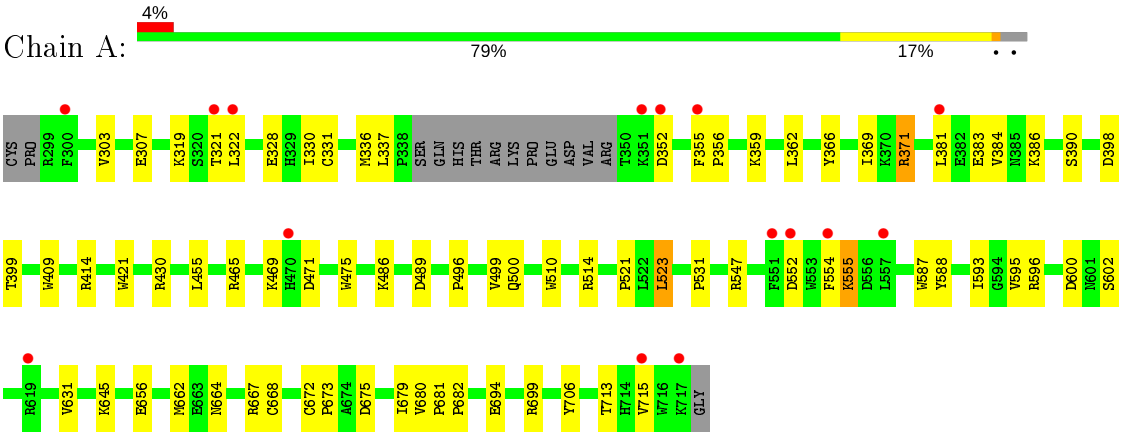
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	91	Total O 91 91	0	0
7	B	108	Total O 108 108	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

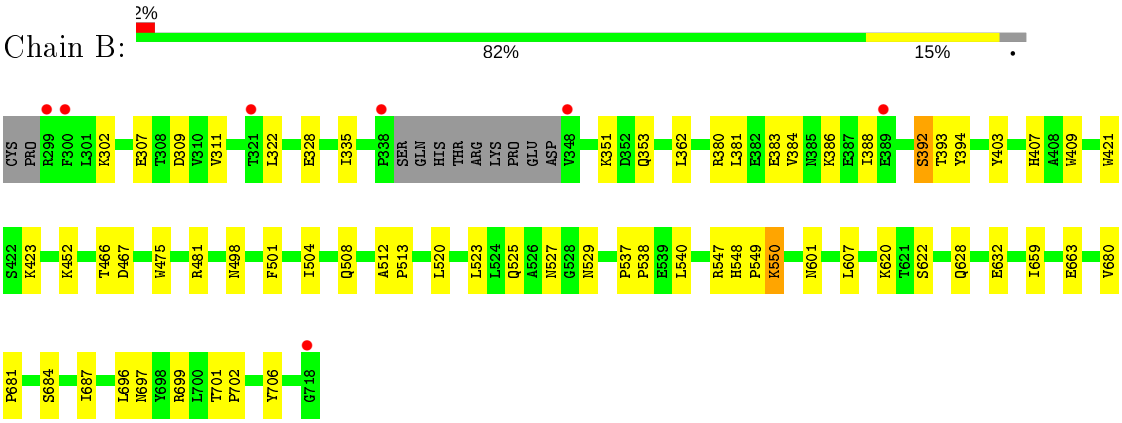
- Molecule 1: NITRIC OXIDE SYNTHASE, BRAIN

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	51.54Å 111.36Å 163.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.99 – 2.10 49.06 – 2.10	Depositor EDS
% Data completeness (in resolution range)	71.3 (40.99-2.10) 71.3 (49.06-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.58 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.173 , 0.232 0.173 , 0.233	Depositor DCC
R_{free} test set	1980 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	29.0	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 57.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7052	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% 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: HEM, ZN, H4B, WOS, 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	0.40	0/3422	0.55	0/4643
1	B	0.41	0/3459	0.56	0/4689
All	All	0.41	0/6881	0.55	0/9332

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

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	3323	0	3232	38	0
1	B	3357	0	3275	39	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	22	0	0	0	0
4	B	22	0	0	0	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	91	0	0	5	0
7	B	108	0	0	2	0
All	All	7052	0	6603	75	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 6.

All (75) 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	1.64	0.80
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.62	0.78
1:B:706:TYR:OH	2:B:750:HEM:O2D	2.00	0.78
2:B:750:HEM:HBC2	2:B:750:HEM:HMC2	1.67	0.76
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.69	0.74
1:B:322:LEU:HD13	1:B:699:ARG:HH21	1.62	0.64
1:A:667:ARG:NH1	1:A:668[A]:CYS:SG	2.71	0.62
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.82	0.60
1:B:393:THR:OG1	1:B:394:TYR:N	2.36	0.58
1:B:380:ARG:NH1	1:B:383:GLU:OE1	2.34	0.57
1:B:362:LEU:HD12	1:B:381:LEU:HD23	1.87	0.57
1:A:369:ILE:HG13	1:A:371:ARG:HB2	1.89	0.55
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.88	0.55
1:A:675:ASP:O	1:A:679:ILE:HG12	2.08	0.54
1:A:706:TYR:OH	2:A:750:HEM:O2D	2.09	0.54
1:A:602:SER:OG	1:B:307[B]:GLU:OE1	2.20	0.53
1:B:501:PHE:HD2	1:B:520:LEU:HD13	1.73	0.53
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.45	0.51
1:B:481:ARG:NH1	1:B:498:ASN:OD1	2.44	0.51
1:A:321:THR:HG23	1:A:322:LEU:HG	1.93	0.50
1:B:362:LEU:HD11	1:B:384:VAL:HG21	1.92	0.50
1:A:694:GLU:HB3	1:B:335:ILE:HD13	1.94	0.49
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.95	0.49
1:A:486:LYS:HE2	1:A:499:VAL:HG11	1.93	0.49
1:A:554:PHE:HB3	7:A:2058:HOH:O	2.11	0.49
1:A:596:ARG:NH2	1:A:600:ASP:OD2	2.45	0.48
1:A:664:ASN:OD1	1:A:667:ARG:NH2	2.40	0.48
1:A:631:VAL:HG11	1:B:628:GLN:HG3	1.95	0.48
1:B:388:ILE:O	1:B:392:SER:N	2.38	0.48
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.43	0.48
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307[A]:GLU:OE2	1:B:601:ASN:ND2	2.47	0.47
1:B:328:GLU:OE1	1:B:328:GLU:N	2.47	0.47
1:B:550:LYS:HB3	1:B:550:LYS:HE2	1.77	0.47
1:B:322:LEU:HD13	1:B:699:ARG:NH2	2.28	0.47
1:B:659:ILE:O	1:B:663:GLU:HG3	2.15	0.47
1:B:680:VAL:HA	1:B:681:PRO:HD3	1.81	0.46
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.97	0.46
1:A:359:LYS:HG3	1:A:381:LEU:HD11	1.97	0.45
1:A:496:PRO:HA	1:A:499:VAL:HG23	1.99	0.45
1:B:475:TRP:HB2	1:B:523:LEU:HB3	1.97	0.45
1:A:430:ARG:NH1	7:A:2013:HOH:O	2.43	0.45
1:B:409:TRP:CZ3	1:B:421:TRP:HA	2.52	0.45
1:B:501:PHE:CD2	1:B:520:LEU:HD13	2.52	0.45
1:A:362:LEU:HD11	1:A:384:VAL:HG21	1.99	0.44
1:B:620:LYS:HD2	1:B:622:SER:OG	2.16	0.44
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.52	0.44
1:A:331:CYS:HB3	1:B:697:ASN:HB3	1.99	0.44
1:B:504:ILE:O	1:B:508:GLN:HG2	2.18	0.44
1:B:452:LYS:HB2	7:B:2037:HOH:O	2.18	0.43
1:B:699:ARG:HA	7:B:2020:HOH:O	2.18	0.43
1:B:302:LYS:HE3	1:B:311:VAL:HG11	1.98	0.43
1:A:588:TYR:CD2	1:A:593:ILE:HD11	2.55	0.42
1:A:595:VAL:HG11	1:A:682:PRO:HB2	2.02	0.42
1:B:537:PRO:HA	1:B:538:PRO:HD3	1.89	0.42
1:A:366:TYR:HA	1:A:369:ILE:HG12	2.02	0.42
1:A:383:GLU:HA	1:A:386:LYS:HD2	2.01	0.42
1:A:414:ARG:NH1	1:A:706:TYR:OH	2.50	0.42
1:B:512:ALA:HA	1:B:513:PRO:HD3	1.93	0.42
1:B:607:LEU:HA	1:B:607:LEU:HD23	1.87	0.41
1:A:455:LEU:HD12	1:A:587:TRP:CB	2.50	0.41
1:A:672:CYS:HA	1:A:673:PRO:HD2	1.93	0.41
1:A:322:LEU:HB2	1:A:699:ARG:HB2	2.02	0.41
1:A:399:THR:HG23	7:A:2015:HOH:O	2.20	0.41
1:A:680:VAL:HA	1:A:681:PRO:HD3	1.92	0.41
1:B:525:GLN:HG3	1:B:529:ASN:O	2.21	0.41
1:A:500:GLN:HG3	7:A:2054:HOH:O	2.21	0.41
1:A:555:LYS:N	7:A:2058:HOH:O	2.45	0.41
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.08	0.41
1:A:355:PHE:N	1:A:356:PRO:HD2	2.36	0.41
1:A:510:TRP:CE2	1:A:521:PRO:HD3	2.56	0.41
1:A:465:ARG:HG3	1:A:471:ASP:OD1	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:THR:OG1	1:B:467:ASP:N	2.51	0.40
1:B:701:THR:HA	1:B:702:PRO:C	2.41	0.40
1:B:684:SER:HB3	1:B:687:ILE:HD11	2.03	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	406/422 (96%)	392 (97%)	13 (3%)	1 (0%)	47 49
1	B	410/422 (97%)	400 (98%)	10 (2%)	0	100 100
All	All	816/844 (97%)	792 (97%)	23 (3%)	1 (0%)	51 54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	514	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%)	345 (94%)	20 (6%)	21 19
1	B	369/377 (98%)	359 (97%)	10 (3%)	44 48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	734/754 (97%)	704 (96%)	30 (4%)	30 31

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	VAL
1	A	319	LYS
1	A	328	GLU
1	A	336	MET
1	A	337	LEU
1	A	352	ASP
1	A	371	ARG
1	A	390	SER
1	A	398	ASP
1	A	469	LYS
1	A	489	ASP
1	A	523	LEU
1	A	547	ARG
1	A	552	ASP
1	A	555	LYS
1	A	645	LYS
1	A	656	GLU
1	A	662	MET
1	A	713	THR
1	A	715	VAL
1	B	309	ASP
1	B	351	LYS
1	B	353	GLN
1	B	386	LYS
1	B	392	SER
1	B	423	LYS
1	B	527	ASN
1	B	540	LEU
1	B	547	ARG
1	B	550	LYS

Some 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 (i)

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

5.5 Carbohydrates (i)

There are no carbohydrates 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	$\#\|Z\| > 2$
5	ACT	A	860	-	1,3,3	1.65	0	0,3,3	0.00	-
4	WOS	A	800	-	24,24,24	0.48	0	31,32,32	2.31	10 (32%)
4	WOS	B	800	-	24,24,24	0.50	0	31,32,32	2.06	9 (29%)
5	ACT	B	860	-	1,3,3	1.94	0	0,3,3	0.00	-
3	H4B	B	760	-	16,18,18	0.85	0	11,26,26	2.60	5 (45%)
2	HEM	B	750	1	27,50,50	2.16	5 (18%)	17,82,82	2.38	3 (17%)
2	HEM	A	750	1	27,50,50	2.12	6 (22%)	17,82,82	1.84	5 (29%)
3	H4B	A	760	-	16,18,18	0.75	0	11,26,26	2.54	5 (45%)

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
4	WOS	A	800	-	-	1/9/17/17	0/3/3/3
4	WOS	B	800	-	-	3/9/17/17	0/3/3/3
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
2	HEM	B	750	1	-	0/6/54/54	-
2	HEM	A	750	1	-	3/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3B-C2B	-5.40	1.32	1.40
2	B	750	HEM	C3D-C2D	5.08	1.52	1.37
2	A	750	HEM	C3D-C2D	4.81	1.51	1.37
2	B	750	HEM	C3B-C2B	-4.45	1.34	1.40
2	B	750	HEM	C3C-C2C	-4.17	1.34	1.40
2	B	750	HEM	C3C-CAC	3.83	1.55	1.47
2	A	750	HEM	C3C-C2C	-3.77	1.35	1.40
2	A	750	HEM	C3B-CAB	3.47	1.55	1.47
2	B	750	HEM	C3B-CAB	3.27	1.54	1.47
2	A	750	HEM	C3C-CAC	3.17	1.54	1.47
2	A	750	HEM	CMC-C2C	2.04	1.56	1.51

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	750	HEM	CBA-CAA-C2A	-6.77	99.99	112.49
4	A	800	WOS	C25-C26-N21	-6.77	97.53	110.02
4	B	800	WOS	C02-N01-C06	5.73	122.44	118.10
2	B	750	HEM	CBD-CAD-C3D	-5.16	102.96	112.48
3	B	760	H4B	C4-C4A-C8A	4.84	118.87	114.57
4	A	800	WOS	C23-C22-N21	-4.77	101.23	110.02
3	A	760	H4B	C4-C4A-C8A	4.67	118.72	114.57
4	A	800	WOS	C02-N01-C06	4.54	121.54	118.10
2	A	750	HEM	CBD-CAD-C3D	-4.45	104.28	112.48
4	B	800	WOS	C25-C26-N21	-4.16	102.34	110.02
4	B	800	WOS	C23-C22-N21	-3.89	102.84	110.02
3	B	760	H4B	C4-N3-C2	3.70	121.81	115.93
4	B	800	WOS	C05-C06-N01	-3.57	119.11	122.90
3	A	760	H4B	C4-C4A-N5	3.47	122.03	119.12
2	B	750	HEM	C1D-C2D-C3D	-3.43	104.61	107.00
4	B	800	WOS	C26-N21-C22	3.32	118.85	111.52
3	B	760	H4B	N3-C2-N1	-3.30	120.24	125.42
3	A	760	H4B	C4-N3-C2	3.29	121.16	115.93
3	A	760	H4B	N3-C2-N1	-3.16	120.46	125.42
3	B	760	H4B	C4-C4A-N5	3.16	121.78	119.12
4	A	800	WOS	C26-N21-C22	2.99	118.12	111.52
4	A	800	WOS	C09-C13-C12	-2.84	117.26	121.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	750	HEM	C4C-C3C-C2C	2.79	108.85	106.90
4	B	800	WOS	C14-C15-N21	-2.77	118.35	121.33
4	A	800	WOS	C05-C06-N01	-2.70	120.04	122.90
2	A	750	HEM	CAD-CBD-CGD	-2.69	108.17	112.67
4	B	800	WOS	C15-C16-N11	-2.68	119.95	122.92
3	A	760	H4B	C2-N1-C8A	2.68	120.54	114.54
4	A	800	WOS	C08-C09-C13	-2.55	104.32	113.28
2	A	750	HEM	C1D-C2D-C3D	-2.42	105.31	107.00
4	A	800	WOS	C15-C14-C13	-2.42	117.49	120.43
4	A	800	WOS	C14-C13-C12	2.32	118.95	116.71
4	B	800	WOS	C12-N11-C16	2.31	120.63	117.48
2	A	750	HEM	CMC-C2C-C3C	2.27	128.93	124.68
3	B	760	H4B	C2-N1-C8A	2.27	119.62	114.54
4	B	800	WOS	N02-C02-N01	2.25	120.05	116.49
4	A	800	WOS	C15-C16-N11	-2.24	120.44	122.92

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	750	HEM	C2A-CAA-CBA-CGA
4	B	800	WOS	N01-C06-C08-C09
4	B	800	WOS	C05-C06-C08-C09
2	A	750	HEM	C1A-C2A-CAA-CBA
2	A	750	HEM	C3A-C2A-CAA-CBA
4	A	800	WOS	C08-C09-C13-C14
4	B	800	WOS	C08-C09-C13-C14

There are no ring outliers.

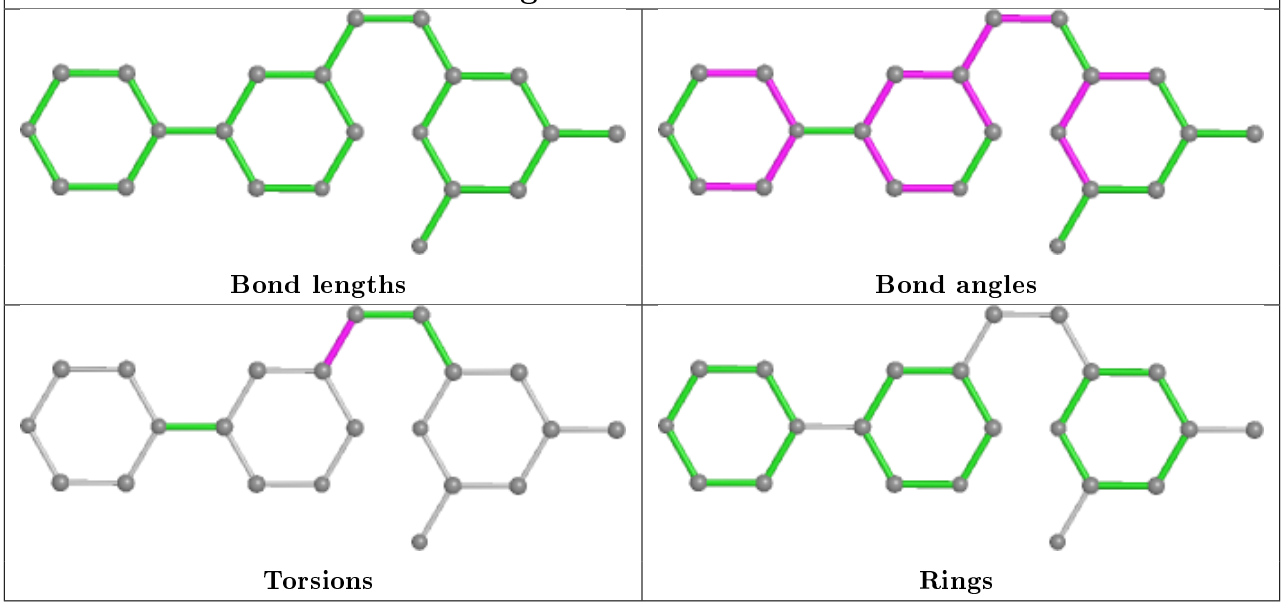
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	750	HEM	3	0
2	A	750	HEM	3	0

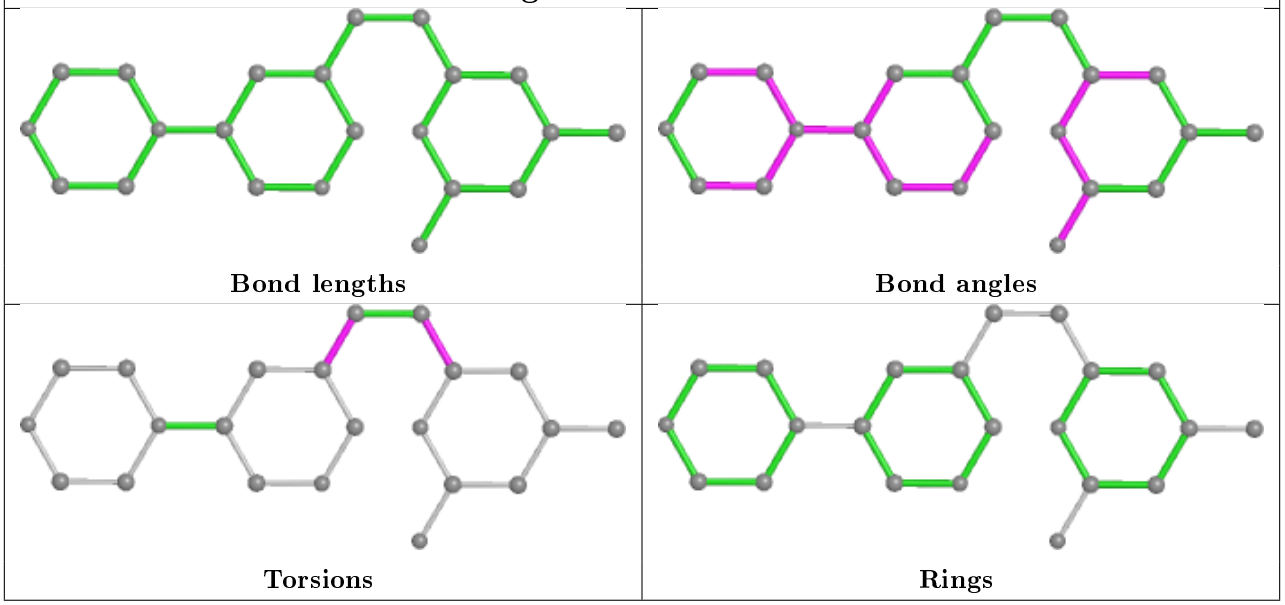
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

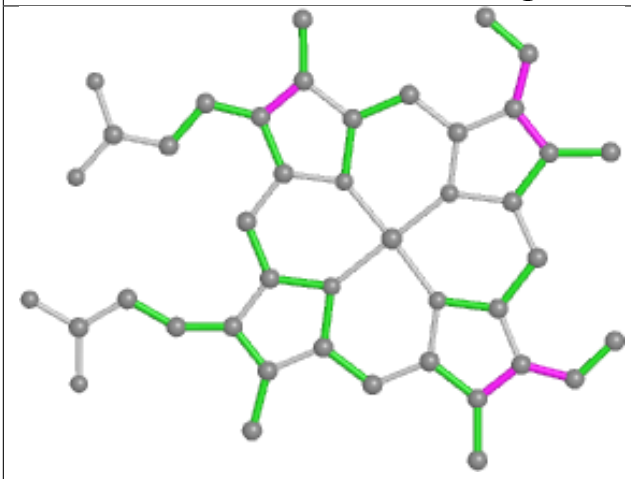
Ligand WOS A 800



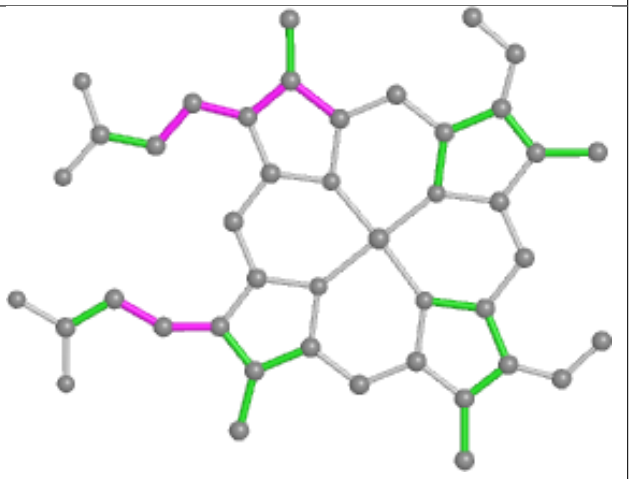
Ligand WOS B 800



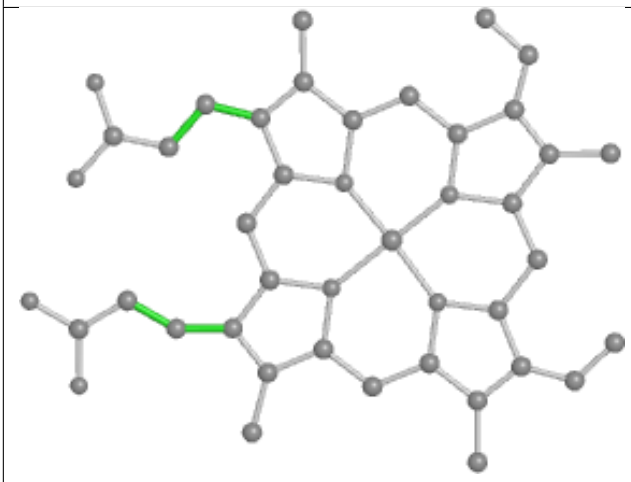
Ligand HEM B 750



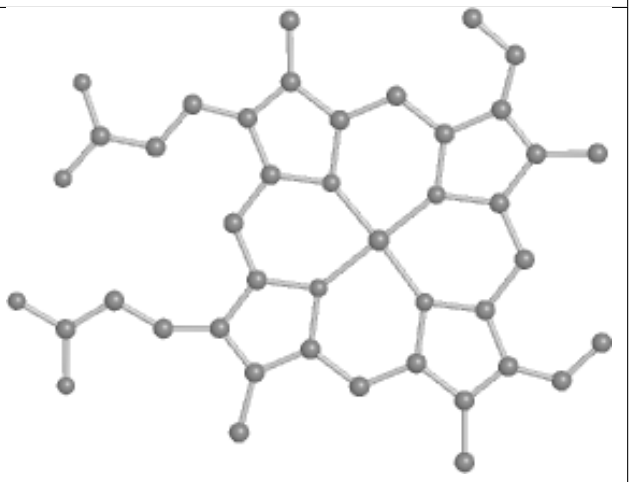
Bond lengths



Bond angles

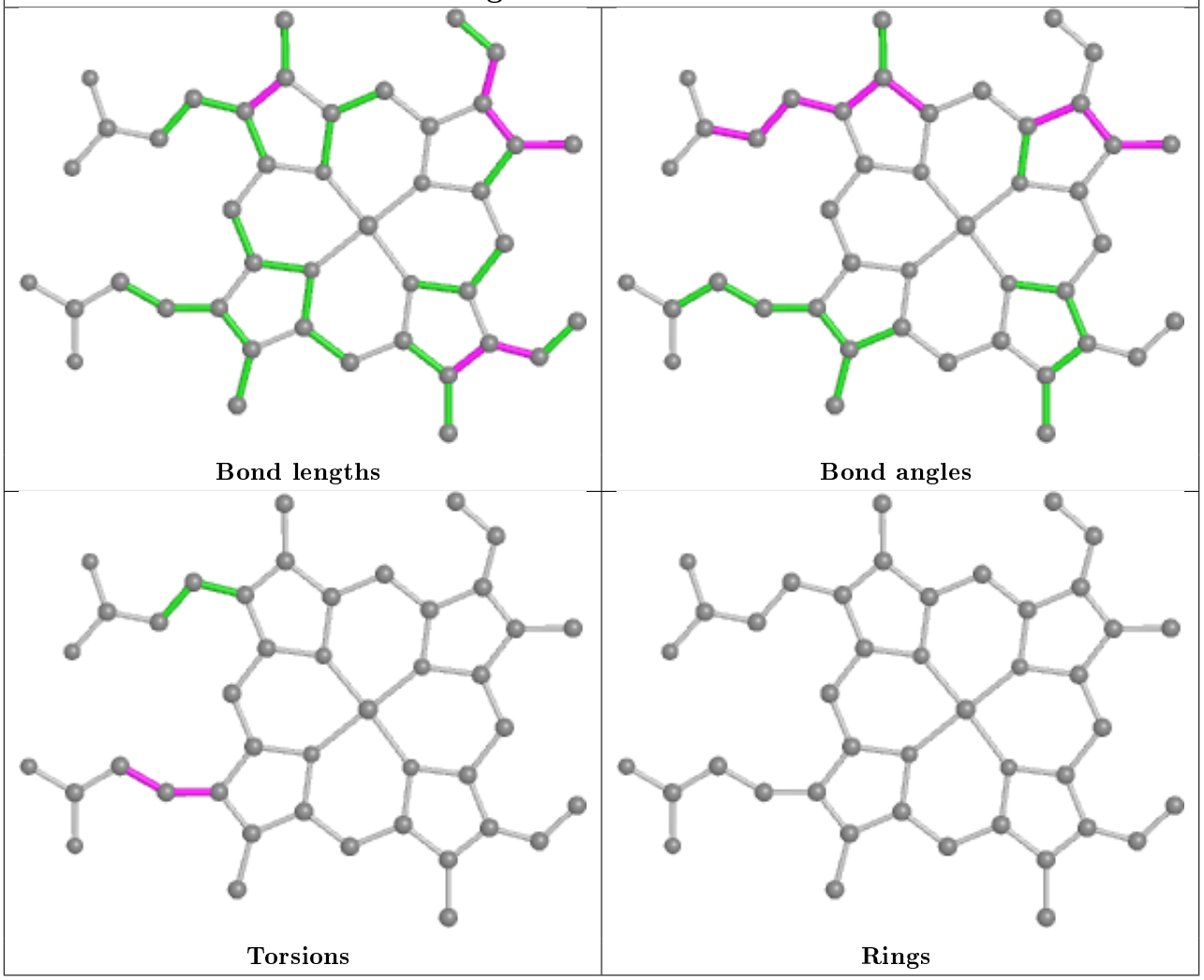


Torsions



Rings

Ligand HEM A 750



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^{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	408/422 (96%)	0.04	15 (3%) 41 48	20, 54, 98, 130	0
1	B	411/422 (97%)	-0.22	7 (1%) 70 74	21, 43, 79, 104	0
All	All	819/844 (97%)	-0.09	22 (2%) 54 60	20, 47, 93, 130	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	717	LYS	7.7
1	A	321	THR	3.5
1	B	300	PHE	3.4
1	A	355	PHE	3.4
1	A	322	LEU	3.1
1	B	338	PRO	3.1
1	A	554	PHE	2.9
1	A	552	ASP	2.8
1	A	715	VAL	2.8
1	A	300	PHE	2.6
1	A	551	PHE	2.5
1	B	718	GLY	2.5
1	A	557	LEU	2.4
1	B	389	GLU	2.4
1	A	381	LEU	2.4
1	B	321	THR	2.3
1	A	352	ASP	2.3
1	B	348	VAL	2.3
1	A	351	LYS	2.2
1	B	299	ARG	2.2
1	A	470	HIS	2.1
1	A	619	ARG	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 carbohydrates in this entry.

6.4 Ligands (i)

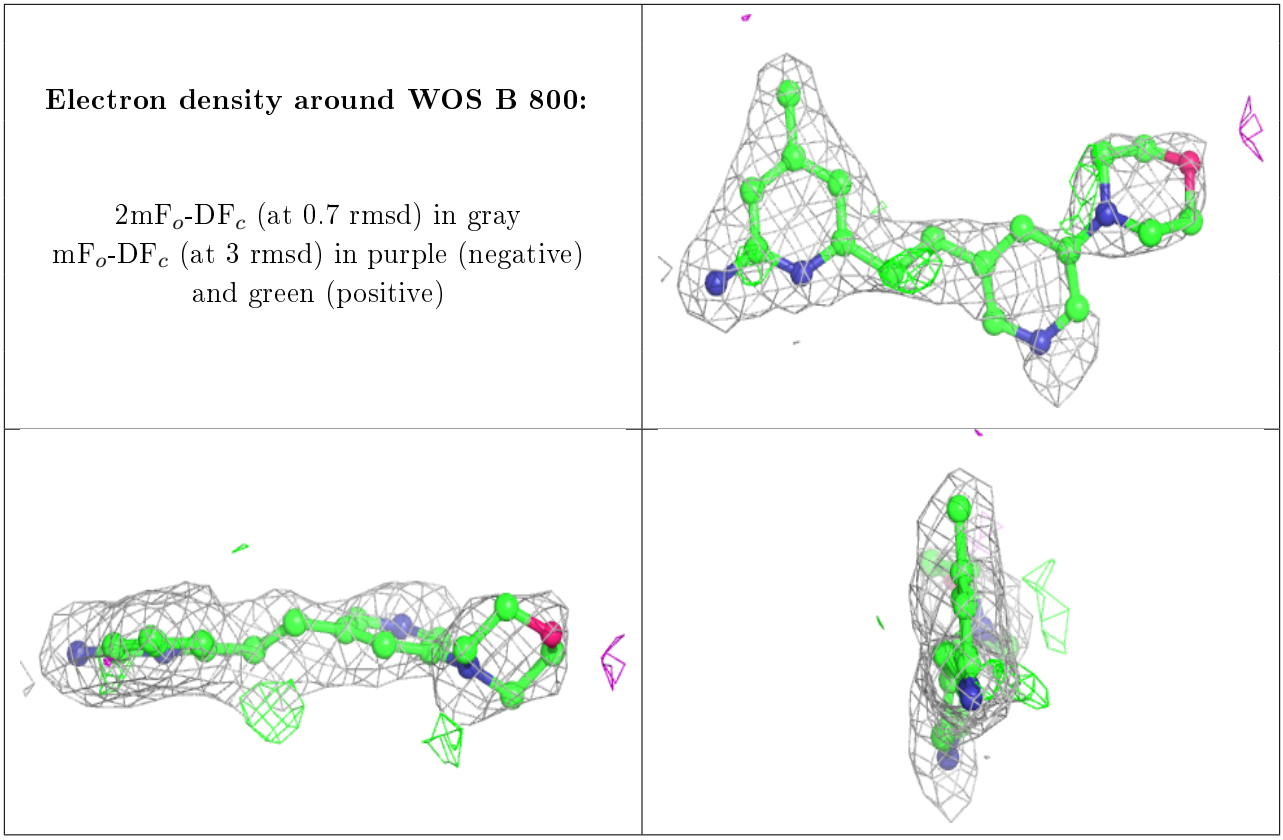
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	H4B	B	760	17/17	0.90	0.12	38,49,57,62	0
3	H4B	A	760	17/17	0.91	0.11	35,50,56,58	0
5	ACT	B	860	4/4	0.94	0.11	55,60,62,62	0
4	WOS	B	800	22/22	0.95	0.17	22,77,90,93	0
5	ACT	A	860	4/4	0.96	0.22	59,61,62,65	0
4	WOS	A	800	22/22	0.96	0.19	23,84,105,106	0
2	HEM	A	750	43/43	0.99	0.12	17,30,63,72	0
2	HEM	B	750	43/43	0.99	0.12	16,30,61,78	0
6	ZN	B	900	1/1	1.00	0.10	42,42,42,42	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.

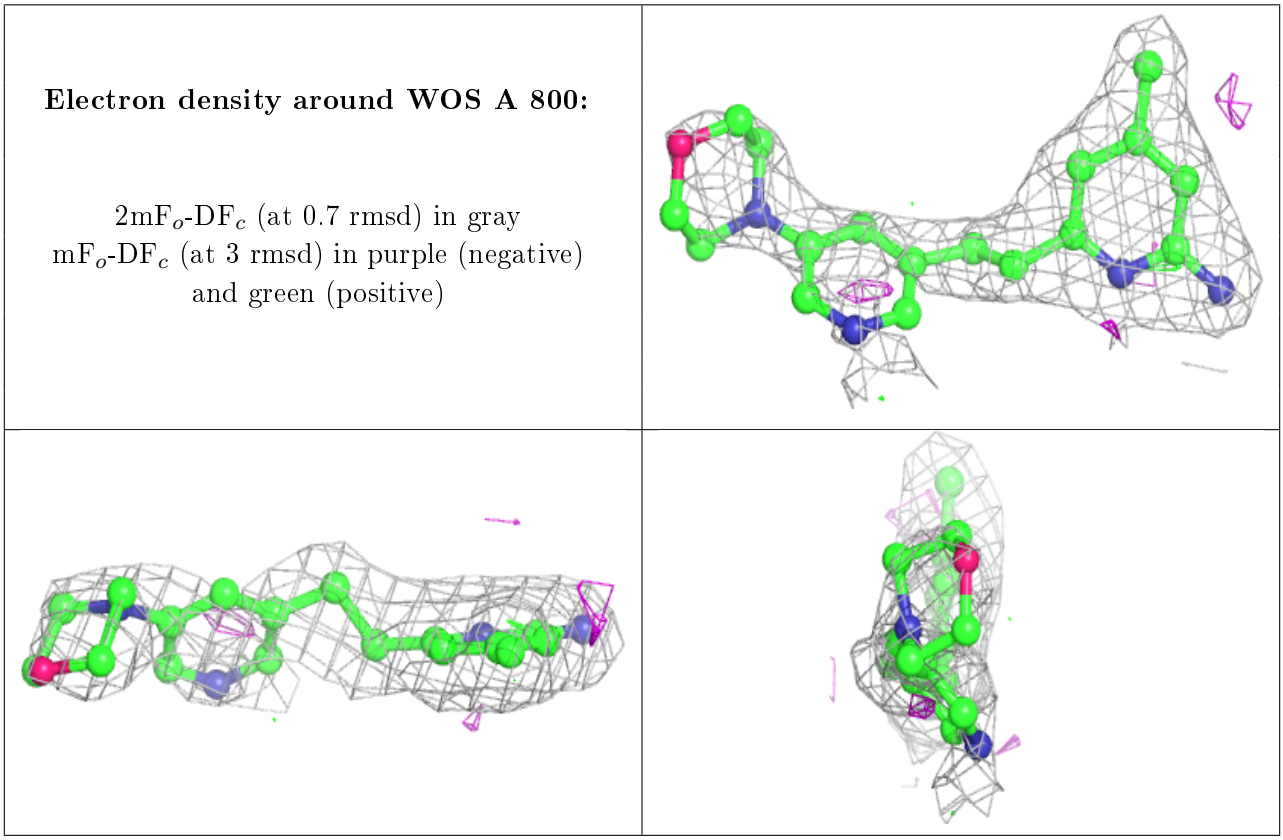
Electron density around WOS B 800:

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



Electron density around WOS A 800:

$2mF_o$-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 750:

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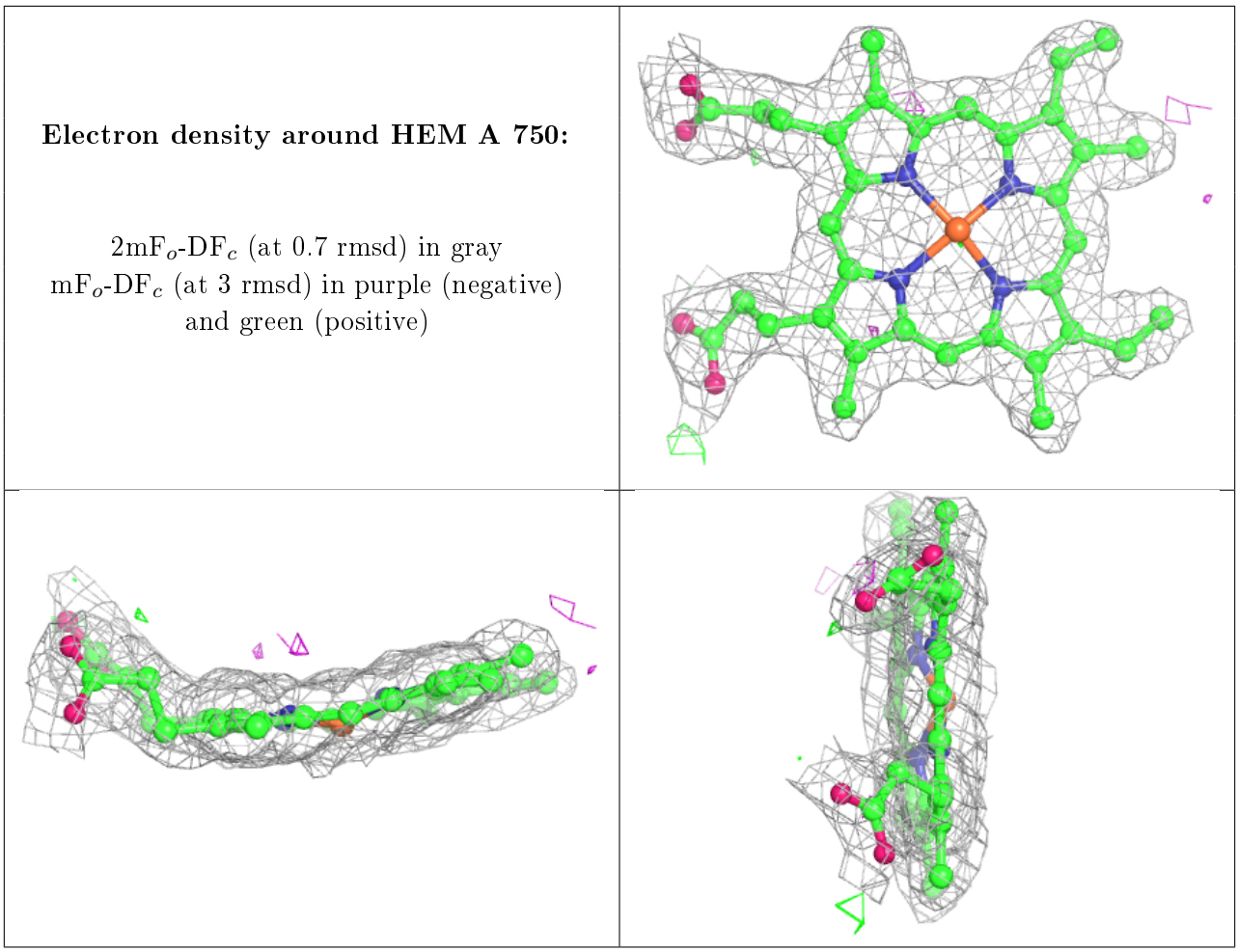
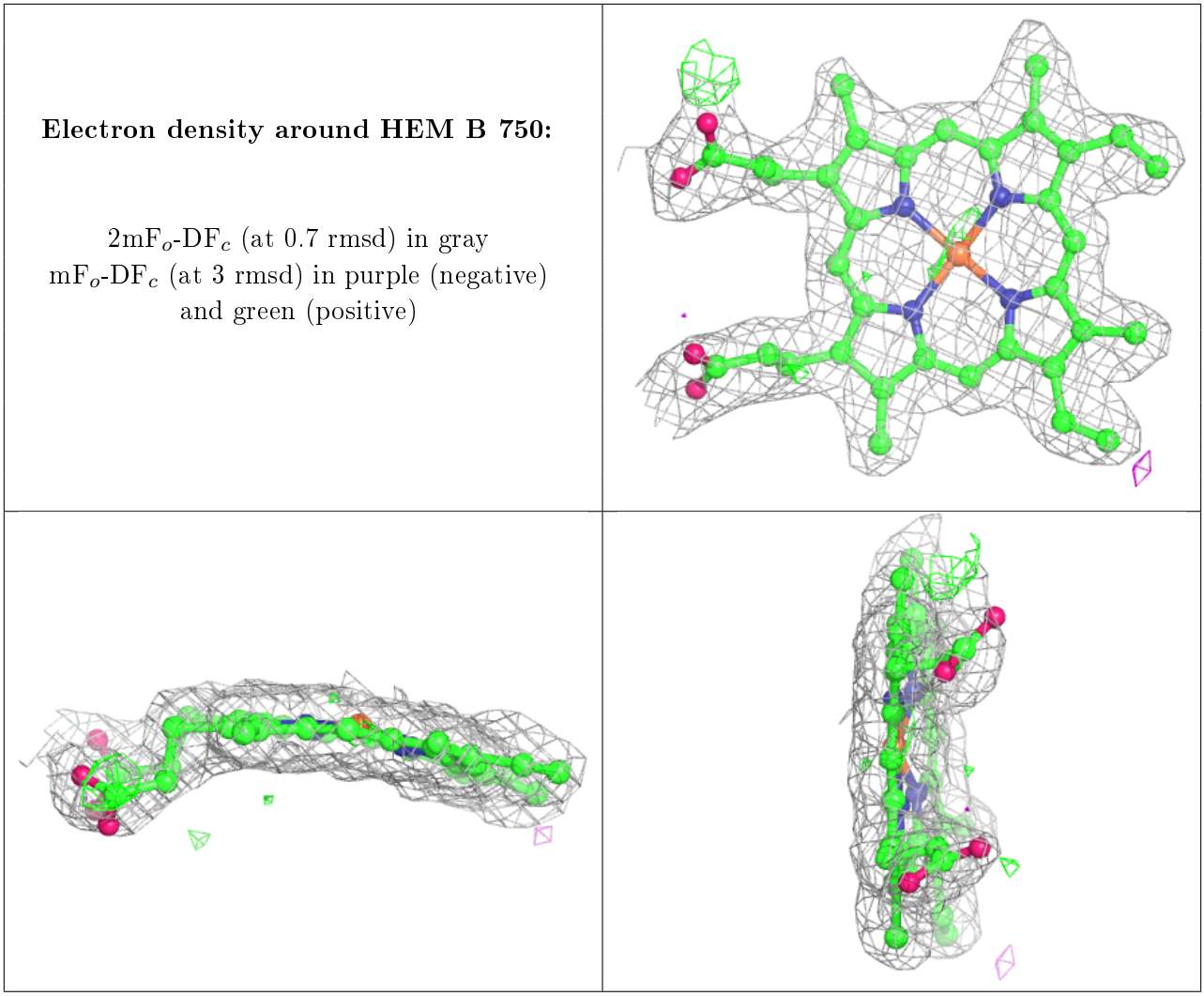
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around HEM B 750:

$2mF_o$-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.