Full wwPDB X-ray Structure Validation Report (i)

Aug 28, 2023 – 02:02 AM EDT

PDB ID	:	3JX1
Title	:	Structure of rat neuronal nitric oxide synthase D597N mutant heme domain in complex with N1-{(3'R,4'R)-4'-[(6"-amino-4"-methylpyridin-2"-yl)methyl] pyrrolidin-3'-yl}-N2-(3'-fluorophenethyl)ethane-1,2-diamine
Authors	:	Delker, S.L.; Li, H.; Poulos, T.L.
Deposited on	:	2009-09-18
Resolution	:	2.00 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 (i) 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 (i)) were used in the production of this report:

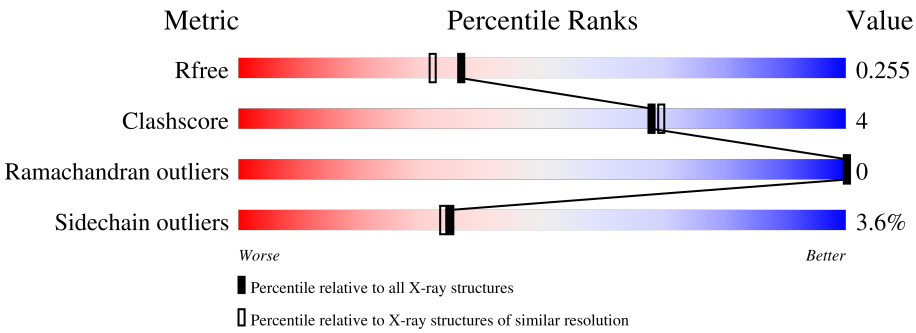
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Mol	Chain	Length	Quality of chain
1	A	422	85% 11% •
1	B	422	87% 9% • •

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7215 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

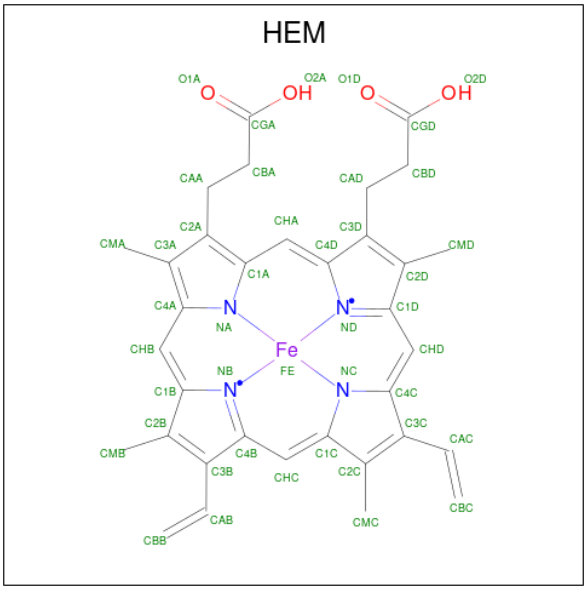
- Molecule 1 is a protein called Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	407	3313	2121	567	604	21	0	0	0
1	B	410	3340	2138	574	607	21	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	597	ASN	ASP	engineered mutation	UNP P29476
B	597	ASN	ASP	engineered mutation	UNP P29476

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



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

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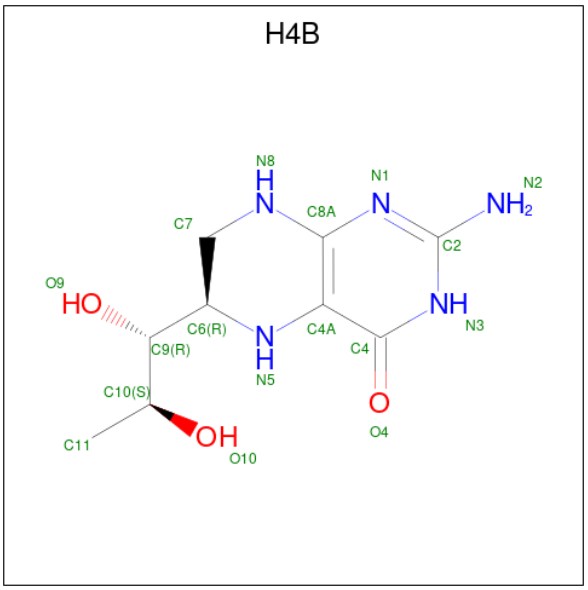
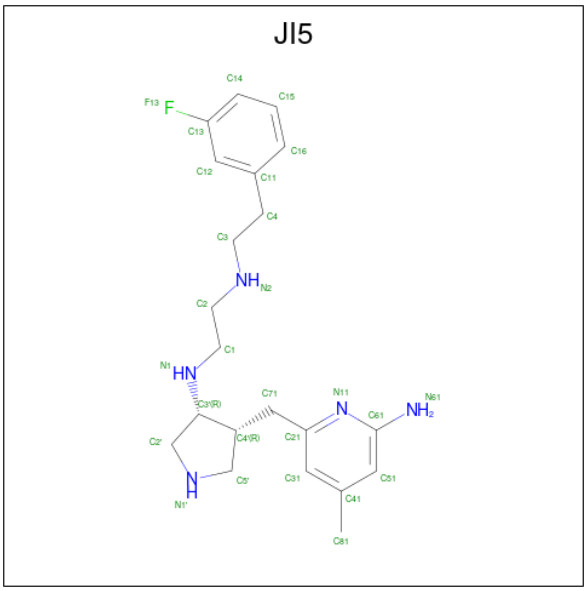
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	B	1	43	34	1	4	4	0	0

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



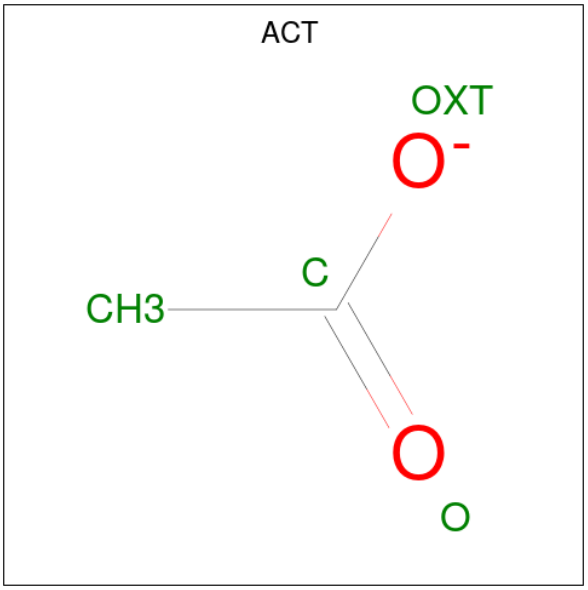
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O			
3	A	1	17	9	5	3		0	0
			Total	C	N	O			
3	B	1	17	9	5	3		0	0

- Molecule 4 is N-{(3R,4R)-4-[(6-amino-4-methylpyridin-2-yl)methyl]pyrrolidin-3-yl}-N'-[2-(3-fluorophenyl)ethyl]ethane-1,2-diamine (three-letter code: JI5) (formula: $C_{21}H_{30}FN_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	F	N		
4	A	1	27	21	1	5	0	0
			Total	C	F	N		
4	B	1	27	21	1	5	0	0

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



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

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

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

- Molecule 7 is water.

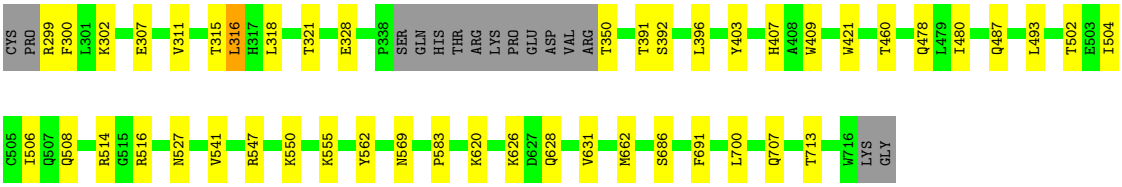
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	165	165	165	0	0
			Total	O		
7	B	214	214	214	0	0

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. 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. 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.

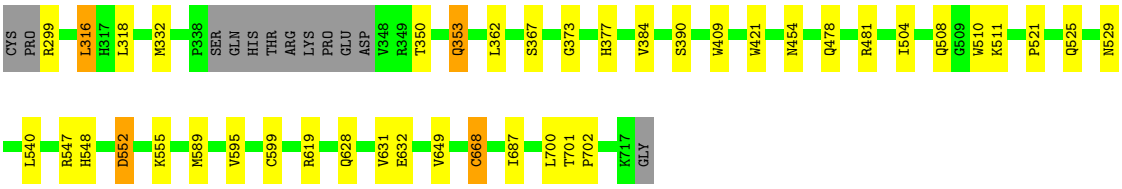
• Molecule 1: Nitric oxide synthase, brain

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	52.02Å 110.88Å 164.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.27 – 2.00 45.27 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.4 (45.27-2.00) 92.3 (45.27-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0089, CNS	Depositor
R, R_{free}	0.178 , 0.216 0.227 , 0.255	Depositor DCC
R_{free} test set	2986 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	32.3	Xtriage
Anisotropy	0.772	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 40.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7215	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 5.61% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ACT, H4B, JI5, ZN

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	0.59	0/3406	0.65	0/4621
1	B	0.65	1/3433 (0.0%)	0.65	0/4656
All	All	0.62	1/6839 (0.0%)	0.65	0/9277

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	668	CYS	CB-SG	5.01	1.90	1.82

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	3313	0	3223	21	0
1	B	3340	0	3258	23	0
2	A	43	0	30	4	0
2	B	43	0	30	6	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	27	0	30	1	0
4	B	27	0	30	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0
7	A	165	0	0	1	0
7	B	214	0	0	3	0
All	All	7215	0	6637	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:B:668:CYS:HB2	7:B:1015:HOH:O	1.52	1.08
1:B:373:GLY:H	1:B:377:HIS:HD2	0.96	0.95
1:B:373:GLY:H	1:B:377:HIS:CD2	1.88	0.90
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.57	0.86
1:A:307:GLU:HG3	7:B:1029:HOH:O	1.82	0.80
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.71	0.71
1:B:373:GLY:N	1:B:377:HIS:HD2	1.81	0.69
2:A:750:HEM:HBC2	2:A:750:HEM:CMC	2.23	0.67
1:A:299:ARG:HG2	1:A:318:LEU:HD21	1.77	0.67
1:A:480:ILE:HD13	1:A:541:VAL:HG13	1.78	0.66
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.82	0.61
1:A:302:LYS:HD3	1:A:311:VAL:HG11	1.85	0.58
2:B:750:HEM:CMC	2:B:750:HEM:HBC2	2.35	0.56
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.90	0.53
1:B:299:ARG:HG2	1:B:318:LEU:HD21	1.91	0.53
1:A:299:ARG:HA	7:A:1005:HOH:O	2.08	0.53
1:B:525:GLN:HG3	1:B:529:ASN:O	2.09	0.53
2:B:750:HEM:HBC2	2:B:750:HEM:HMC1	1.93	0.51
1:A:569:ASN:O	1:A:707:GLN:HG2	2.12	0.50
1:A:391:THR:O	1:A:392:SER:OG	2.28	0.49
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.01	0.49
1:A:502:THR:O	1:A:506:ILE:HG12	2.12	0.49
1:B:552:ASP:OD2	1:B:555:LYS:NZ	2.47	0.48
1:A:628:GLN:HG2	1:B:631:VAL:HG11	1.93	0.48
1:A:626:LYS:HB3	1:B:687:ILE:HD12	1.95	0.48
1:A:299:ARG:HG2	1:A:318:LEU:CD2	2.44	0.47
1:B:504:ILE:O	1:B:508:GLN:HG2	2.15	0.47
1:A:478:GLN:NE2	1:A:562:TYR:OH	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.49	0.46
1:B:701:THR:HA	1:B:702:PRO:C	2.36	0.46
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.52	0.45
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.51	0.45
1:A:300:PHE:CD2	1:A:315:THR:HG22	2.52	0.45
1:B:353:GLN:HE21	1:B:353:GLN:HB3	1.57	0.45
1:B:595:VAL:O	1:B:599:CYS:HB2	2.18	0.43
1:B:511:LYS:HG2	7:B:1153:HOH:O	2.18	0.43
1:A:302:LYS:HD3	1:A:311:VAL:CG1	2.47	0.43
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.54	0.43
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	2.00	0.43
1:A:316:LEU:HD13	1:A:700:LEU:HD11	2.01	0.42
1:A:504:ILE:O	1:A:508:GLN:HG2	2.19	0.42
1:B:316:LEU:HD13	1:B:700:LEU:HD11	2.00	0.42
1:A:686:SER:HA	1:A:691:PHE:CG	2.54	0.42
2:A:750:HEM:HBA1	4:A:800:JI5:H4	2.00	0.42
1:A:460:THR:O	1:A:583:PRO:HD2	2.21	0.41
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.02	0.41
1:B:619:ARG:HE	1:B:619:ARG:HB2	1.65	0.41
2:B:750:HEM:HBB2	2:B:750:HEM:CHC	2.42	0.41
1:B:589:MET:HA	1:B:649:VAL:O	2.21	0.40
2:B:750:HEM:HMC1	2:B:750:HEM:CBC	2.51	0.40
2:B:750:HEM:HBA1	4:B:800:JI5:H4	2.03	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	403/422 (96%)	392 (97%)	11 (3%)	0	100	100
1	B	406/422 (96%)	397 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	809/844 (96%)	789 (98%)	20 (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	363/377 (96%)	347 (96%)	16 (4%)	28 25
1	B	366/377 (97%)	356 (97%)	10 (3%)	44 46
All	All	729/754 (97%)	703 (96%)	26 (4%)	35 34

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	316	LEU
1	A	321	THR
1	A	328	GLU
1	A	350	THR
1	A	396	LEU
1	A	487	GLN
1	A	493	LEU
1	A	514	ARG
1	A	516	ARG
1	A	527	ASN
1	A	547	ARG
1	A	550	LYS
1	A	555	LYS
1	A	620	LYS
1	A	662	MET
1	A	713	THR
1	B	316	LEU
1	B	332	MET
1	B	350	THR
1	B	353	GLN

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Mol	Chain	Res	Type
1	B	367	SER
1	B	390	SER
1	B	454	ASN
1	B	540	LEU
1	B	547	ARG
1	B	552	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	329	HIS
1	A	451	ASN
1	A	454	ASN
1	A	478	GLN
1	A	500	GLN
1	A	634	ASN
1	A	697	ASN
1	B	377	HIS
1	B	451	ASN
1	B	454	ASN
1	B	478	GLN
1	B	507	GLN
1	B	508	GLN
1	B	535	GLN
1	B	634	ASN
1	B	697	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	H4B	A	760	-	16,18,18	0.88	0	11,26,26	2.89	5 (45%)
2	HEM	B	750	1	41,50,50	1.91	8 (19%)	45,82,82	1.66	11 (24%)
3	H4B	B	760	-	16,18,18	1.23	2 (12%)	11,26,26	2.59	5 (45%)
4	JI5	B	800	-	27,29,29	0.81	0	30,38,38	2.23	7 (23%)
5	ACT	A	860	-	3,3,3	0.74	0	3,3,3	0.68	0
5	ACT	B	860	-	3,3,3	0.62	0	3,3,3	1.21	0
2	HEM	A	750	1	41,50,50	1.96	10 (24%)	45,82,82	2.01	13 (28%)
4	JI5	A	800	-	27,29,29	0.76	0	30,38,38	1.88	7 (23%)

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	A	760	-	-	0/8/17/17	0/2/2/2
2	HEM	B	750	1	-	3/12/54/54	-
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	JI5	B	800	-	-	0/13/23/23	0/3/3/3
2	HEM	A	750	1	-	3/12/54/54	-
4	JI5	A	800	-	-	1/13/23/23	0/3/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3D-C2D	7.41	1.52	1.36
2	B	750	HEM	C3D-C2D	6.49	1.50	1.36
2	B	750	HEM	C3C-C2C	-4.77	1.33	1.40
2	A	750	HEM	C3C-C2C	-4.11	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	FE-ND	3.27	2.13	1.96
2	B	750	HEM	C3C-CAC	3.13	1.54	1.47
2	A	750	HEM	FE-ND	3.06	2.12	1.96
3	B	760	H4B	C7-C6	2.99	1.55	1.52
2	A	750	HEM	C3C-CAC	2.94	1.53	1.47
2	B	750	HEM	CMB-C2B	2.81	1.56	1.50
2	A	750	HEM	CAB-C3B	2.61	1.54	1.47
2	B	750	HEM	CMD-C2D	2.57	1.56	1.50
2	A	750	HEM	FE-NB	2.48	2.09	1.96
2	A	750	HEM	CAA-C2A	2.39	1.55	1.52
2	B	750	HEM	CAB-C3B	2.38	1.53	1.47
2	B	750	HEM	FE-NB	2.38	2.08	1.96
2	A	750	HEM	C3B-C2B	-2.25	1.32	1.37
2	A	750	HEM	CMB-C2B	2.25	1.55	1.50
2	A	750	HEM	CMC-C2C	2.10	1.56	1.51
3	B	760	H4B	C7-N8	2.05	1.48	1.44

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	800	JI5	C1-N1-C3'	6.54	123.46	114.20
4	B	800	JI5	C61-N11-C21	6.11	122.73	118.10
2	A	750	HEM	C4D-ND-C1D	5.71	110.97	105.07
2	A	750	HEM	CBD-CAD-C3D	-5.10	98.45	112.63
2	A	750	HEM	CBA-CAA-C2A	-4.96	104.16	112.62
3	B	760	H4B	C8A-C4A-C4	4.68	118.72	114.57
4	A	800	JI5	C61-N11-C21	4.65	121.62	118.10
3	A	760	H4B	C8A-C4A-C4	4.63	118.68	114.57
2	B	750	HEM	C4D-ND-C1D	4.47	109.69	105.07
3	A	760	H4B	C4-C4A-N5	4.18	122.63	119.12
4	B	800	JI5	C2'-C3'-N1	-4.04	106.54	113.73
4	A	800	JI5	C2'-C3'-N1	-4.03	106.56	113.73
3	A	760	H4B	N1-C2-N3	-3.77	119.50	125.42
3	A	760	H4B	C2-N1-C8A	3.67	122.77	114.54
3	B	760	H4B	C4-C4A-N5	3.60	122.14	119.12
4	A	800	JI5	C3-C4-C11	-3.54	104.67	112.87
2	B	750	HEM	CBD-CAD-C3D	-3.49	102.92	112.63
2	A	750	HEM	C4C-CHD-C1D	3.32	126.93	122.56
3	B	760	H4B	N1-C2-N3	-3.27	120.28	125.42
3	B	760	H4B	C2-N3-C4	3.26	121.11	115.93
3	A	760	H4B	C2-N3-C4	3.21	121.03	115.93
4	A	800	JI5	C2-C1-N1	3.19	116.26	111.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	750	HEM	C2C-C3C-C4C	3.05	109.03	106.90
2	B	750	HEM	C4B-CHC-C1C	2.98	126.50	122.56
4	B	800	JI5	C3-C4-C11	-2.95	106.03	112.87
4	A	800	JI5	C31-C21-N11	-2.92	119.81	122.90
4	B	800	JI5	C31-C21-N11	-2.87	119.86	122.90
2	A	750	HEM	CMD-C2D-C1D	2.80	129.30	125.04
2	A	750	HEM	C4B-CHC-C1C	2.78	126.23	122.56
2	B	750	HEM	C4C-CHD-C1D	2.78	126.23	122.56
4	B	800	JI5	C5'-N1'-C2'	2.73	111.85	105.42
2	B	750	HEM	CBA-CAA-C2A	-2.72	107.98	112.62
3	B	760	H4B	C2-N1-C8A	2.69	120.57	114.54
2	A	750	HEM	C1D-C2D-C3D	-2.67	104.14	106.96
2	B	750	HEM	C2C-C3C-C4C	2.65	108.75	106.90
2	A	750	HEM	CMA-C3A-C4A	-2.62	124.44	128.46
2	B	750	HEM	C4B-C3B-C2B	2.61	109.19	107.11
2	B	750	HEM	CMD-C2D-C1D	2.60	129.00	125.04
4	A	800	JI5	N61-C61-N11	2.53	120.49	116.49
2	A	750	HEM	CHC-C4B-C3B	2.42	128.27	124.57
4	A	800	JI5	C5'-N1'-C2'	2.40	111.09	105.42
2	B	750	HEM	C1D-C2D-C3D	-2.40	104.43	106.96
2	A	750	HEM	CMC-C2C-C3C	2.33	129.04	124.68
2	A	750	HEM	CHA-C4D-ND	2.24	127.15	124.38
2	B	750	HEM	CMA-C3A-C4A	-2.19	125.10	128.46
2	B	750	HEM	CAA-CBA-CGA	-2.11	107.84	113.76
2	A	750	HEM	C3C-C4C-NC	-2.10	106.97	110.94
4	B	800	JI5	C41-C31-C21	-2.09	118.95	120.32

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	750	HEM	C1A-C2A-CAA-CBA
2	A	750	HEM	C3A-C2A-CAA-CBA
2	A	750	HEM	C2A-CAA-CBA-CGA
2	B	750	HEM	C2A-CAA-CBA-CGA
4	A	800	JI5	N1-C1-C2-N2
2	B	750	HEM	C1A-C2A-CAA-CBA
2	B	750	HEM	C3A-C2A-CAA-CBA

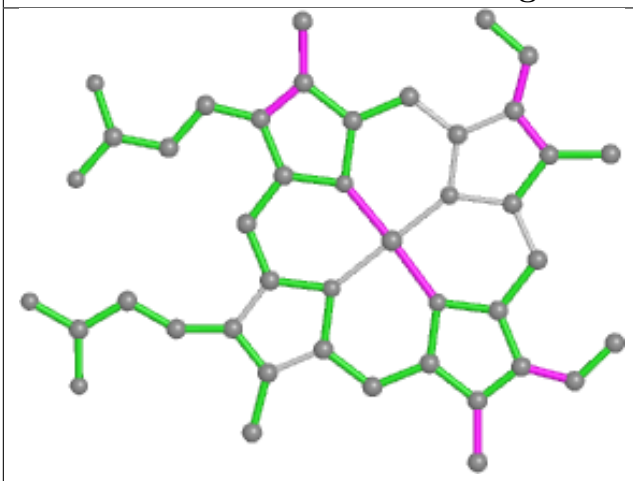
There are no ring outliers.

4 monomers are involved in 10 short contacts:

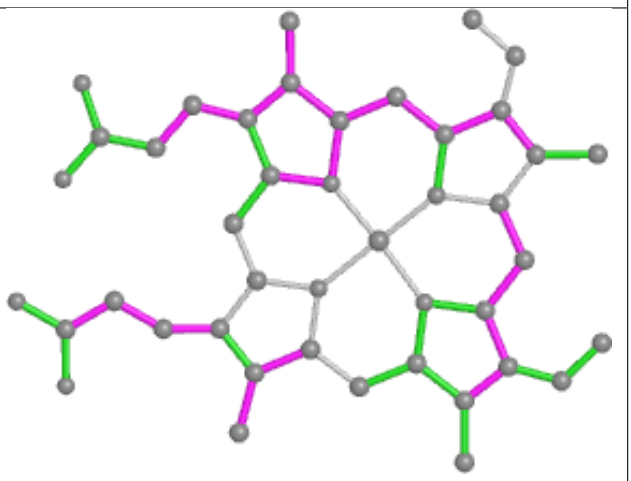
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	750	HEM	6	0
4	B	800	JI5	1	0
2	A	750	HEM	4	0
4	A	800	JI5	1	0

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.

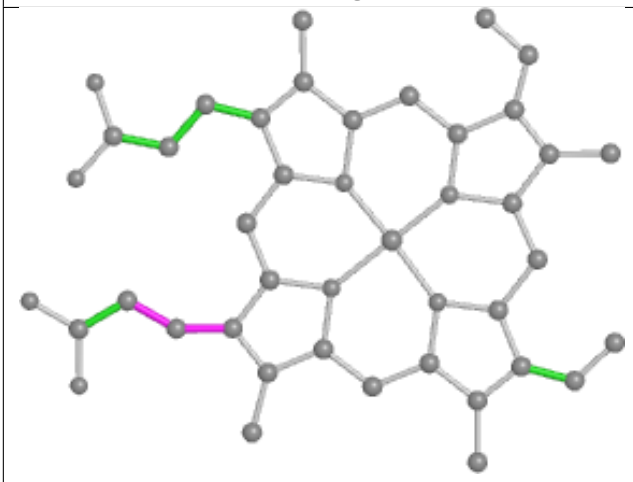
Ligand HEM B 750



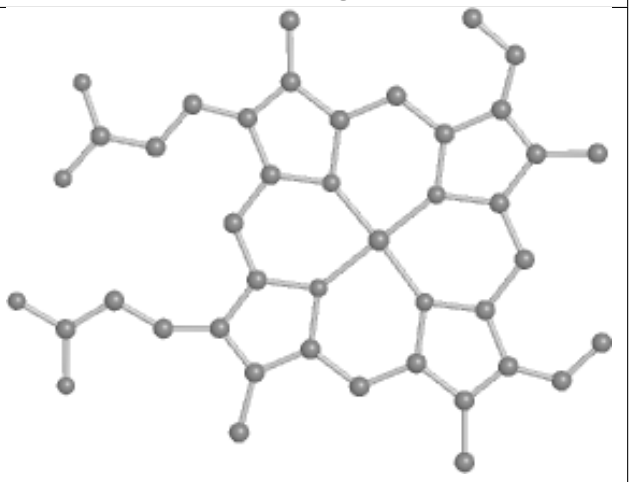
Bond lengths



Bond angles

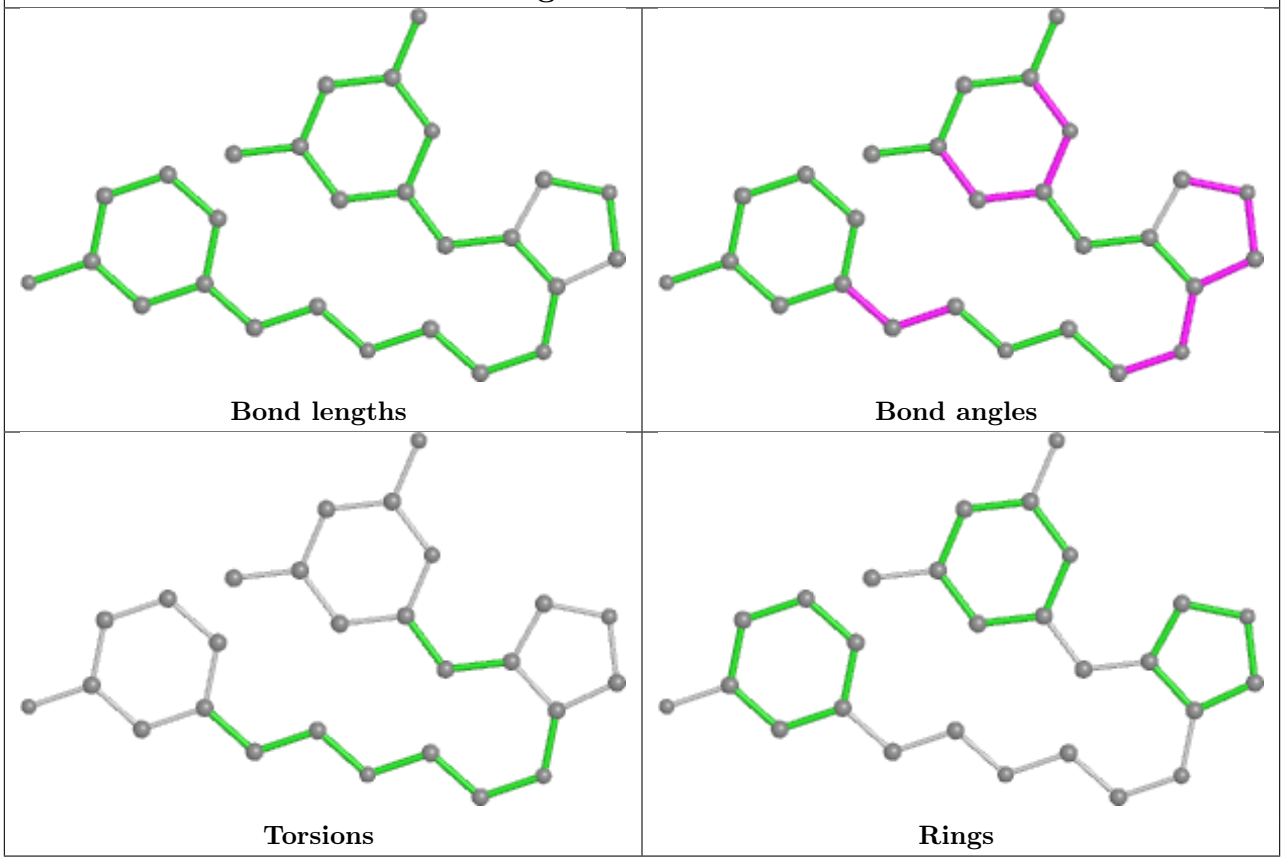


Torsions

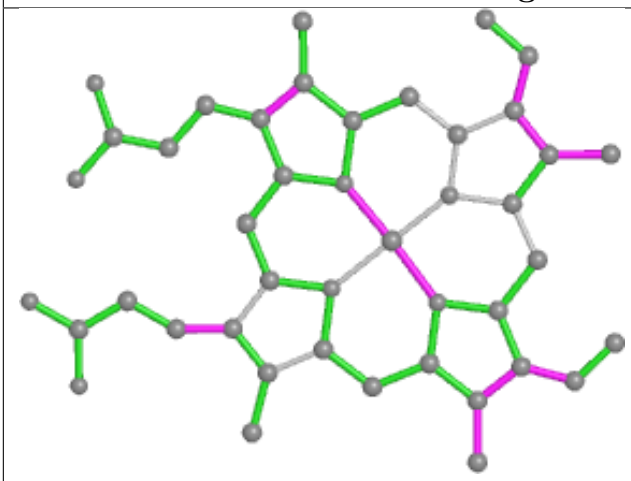


Rings

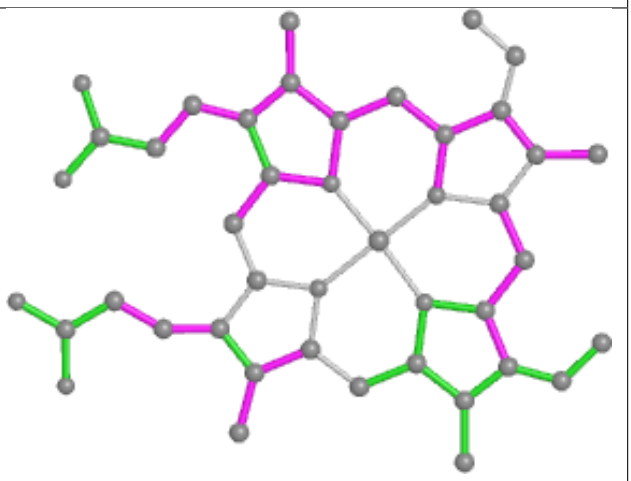
Ligand JI5 B 800



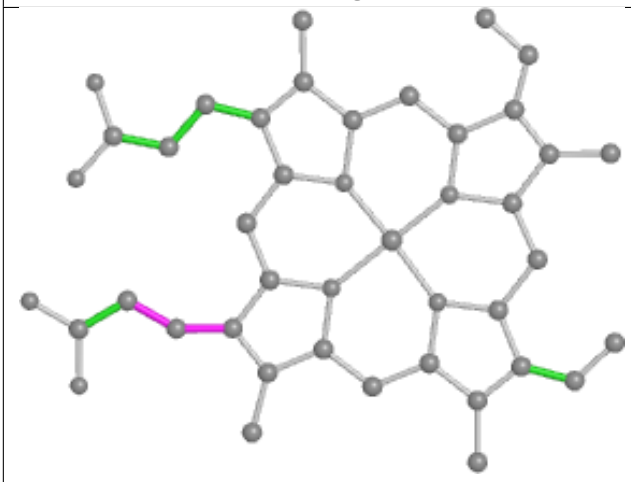
Ligand HEM A 750



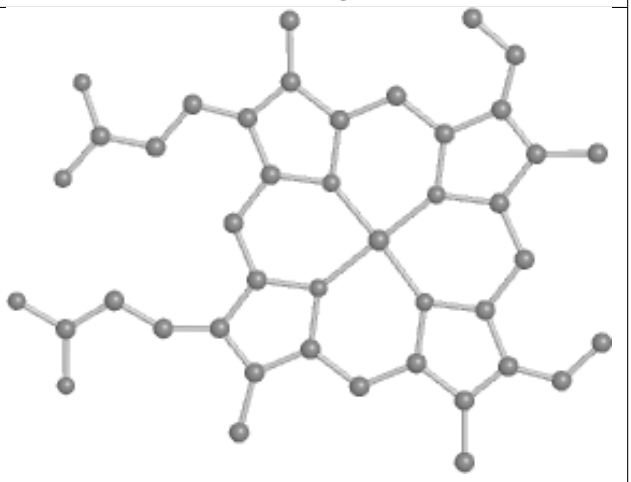
Bond lengths



Bond angles

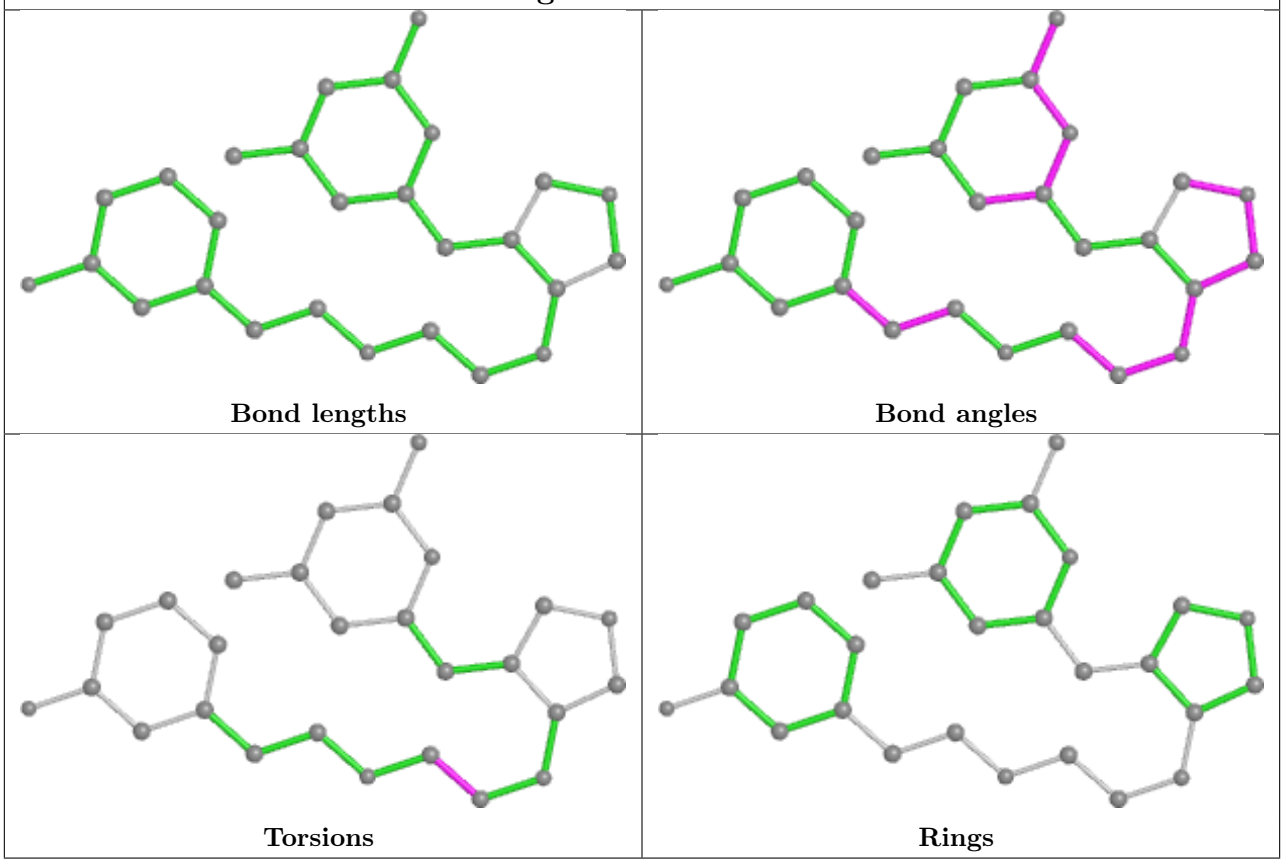


Torsions



Rings

Ligand JI5 A 800



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

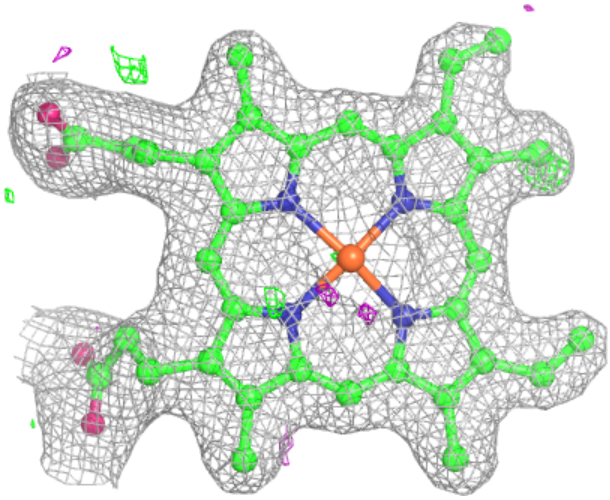
6.4 Ligands (i)

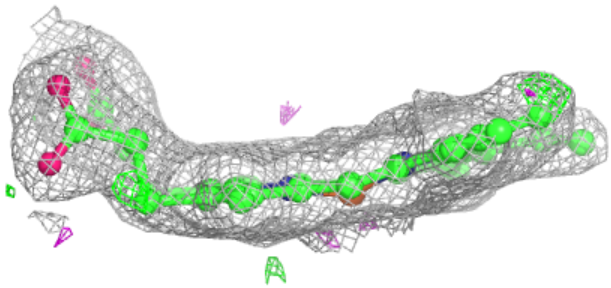
Unable to reproduce the depositors R factor - this section is therefore empty.

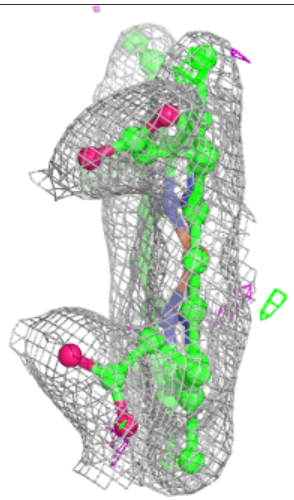
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HEM A 750:

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

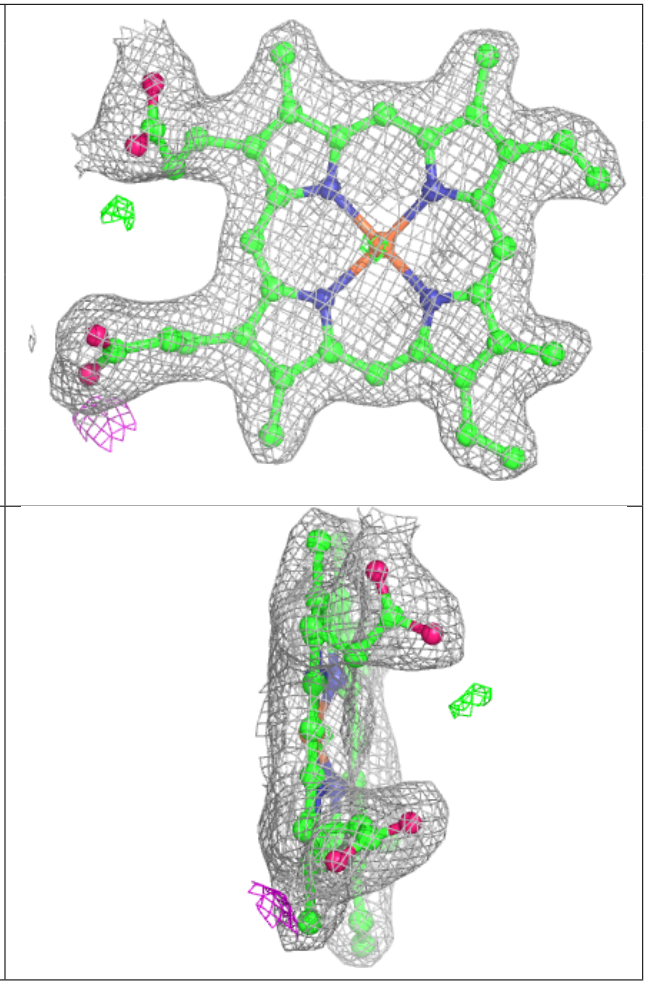






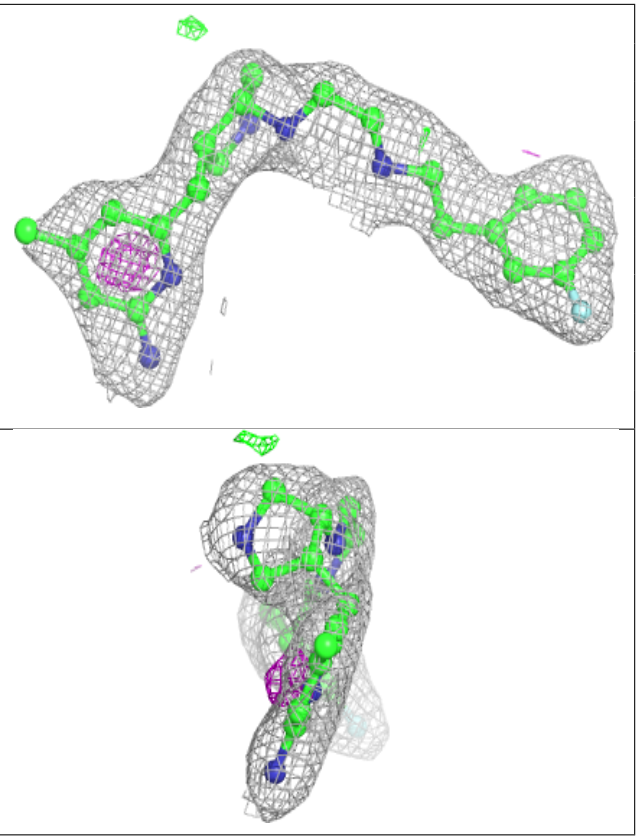
Electron density around HEM B 750:

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



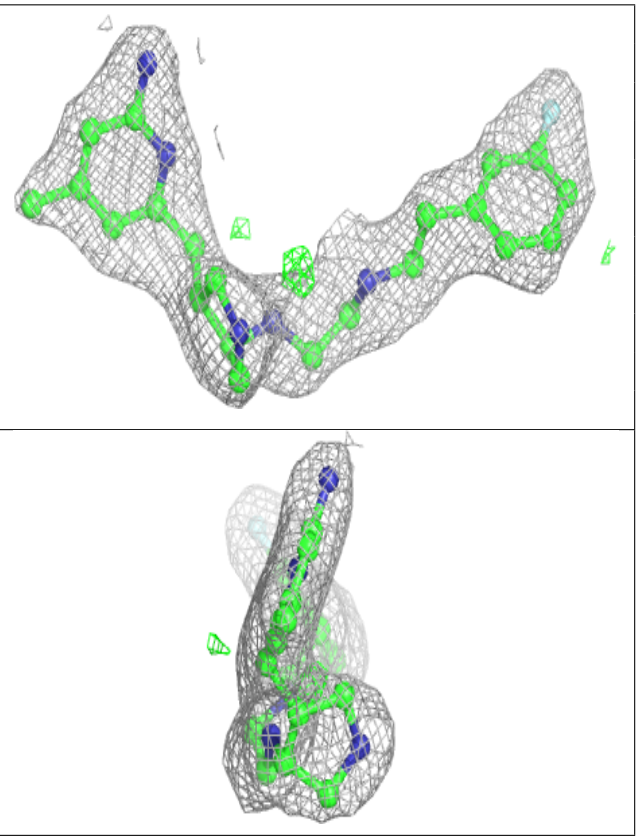
Electron density around JI5 A 800:

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



Electron density around JI5 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)



6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.