



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 04:48 PM BST

PDB ID : 4KEY  
Title : Structure of P450 BM3 A82F F87V in complex with omeprazole  
Authors : Leys, D.  
Deposited on : 2013-04-26  
Resolution : 2.05 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.

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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 : 2.13.1  
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) : 2.13.1

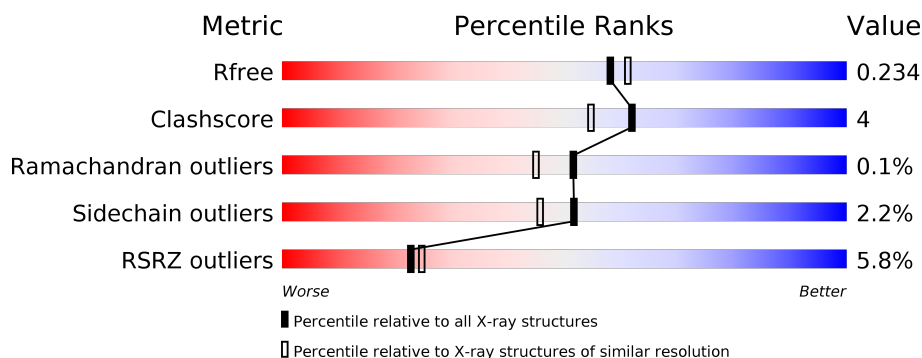
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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  $\geq 3$ , 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	455	
1	B	455	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7764 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.

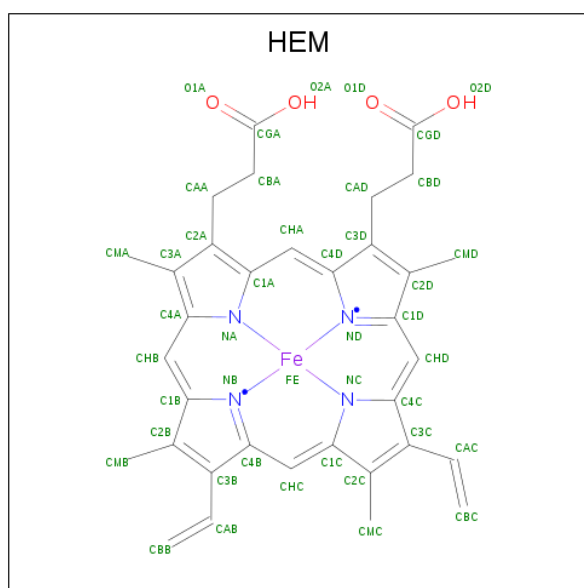
- Molecule 1 is a protein called Bifunctional P-450/NADPH-P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	5	0
			3673	2344	623	689	17			
1	B	442	Total	C	N	O	S	0	0	0
			3553	2274	604	658	17			

There are 4 discrepancies between the modelled and reference sequences:

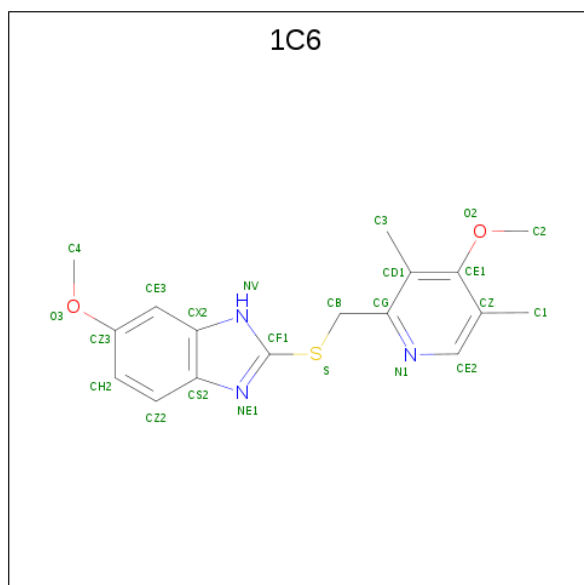
Chain	Residue	Modelled	Actual	Comment	Reference
A	82	PHE	ALA	ENGINEERED MUTATION	UNP P14779
A	87	VAL	PHE	ENGINEERED MUTATION	UNP P14779
B	82	PHE	ALA	ENGINEERED MUTATION	UNP P14779
B	87	VAL	PHE	ENGINEERED MUTATION	UNP P14779

- 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 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 6-methoxy-2-[[ (4-methoxy-3,5-dimethylpyridin-2-yl)methyl]sulfanyl]-1H-benzimidazole (three-letter code: 1C6) (formula: C<sub>17</sub>H<sub>19</sub>N<sub>3</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 23	C 17	N 3	O 2	S 1	0	0
3	B	1	Total 23	C 17	N 3	O 2	S 1	0	0

- Molecule 4 is water.

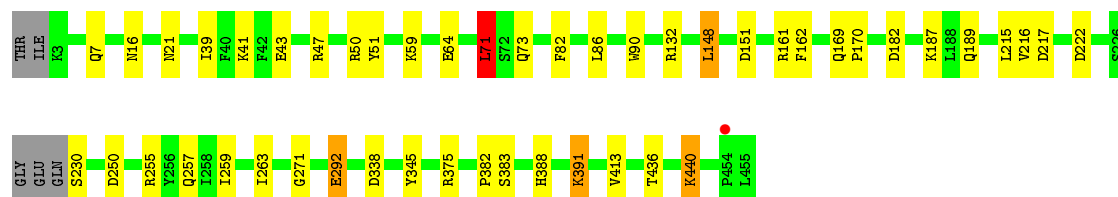
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	264	Total O 264 264	0	0
4	B	142	Total O 142 142	0	0

### 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.

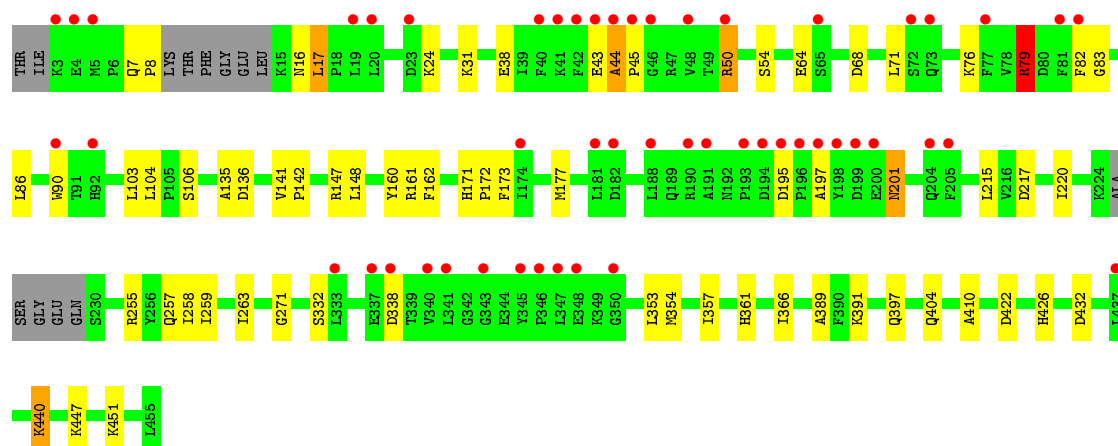
- Molecule 1: Bifunctional P-450/NADPH-P450 reductase

Chain A: 



- Molecule 1: Bifunctional P-450/NADPH-P450 reductase

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.31Å 130.66Å 145.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.95 – 2.05 54.95 – 2.05	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.95-2.05) 100.0 (54.95-2.05)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.74 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.187 , 0.235 0.191 , 0.234	Depositor DCC
$R_{free}$ test set	3640 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 44.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7764	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.52% 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: HEM, 1C6

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	1.10	4/3757 (0.1%)	0.94	9/5080 (0.2%)
1	B	0.95	2/3635 (0.1%)	0.85	6/4918 (0.1%)
All	All	1.03	6/7392 (0.1%)	0.89	15/9998 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	292	GLU	CG-CD	6.68	1.61	1.51
1	A	383	SER	CB-OG	-6.00	1.34	1.42
1	B	404	GLN	CG-CD	5.86	1.64	1.51
1	A	64	GLU	CD-OE2	-5.41	1.19	1.25
1	B	410	ALA	CA-CB	-5.33	1.41	1.52
1	A	345	TYR	CE1-CZ	-5.12	1.31	1.38

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	147	ARG	NE-CZ-NH1	8.08	124.34	120.30
1	A	132	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	B	147	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	A	391	LYS	CD-CE-NZ	-5.83	98.28	111.70
1	A	383	SER	CB-CA-C	-5.82	99.05	110.10
1	A	71	LEU	CB-CG-CD1	5.72	120.72	111.00
1	B	50	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	B	68	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	161	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	A	50	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	A	250	ASP	CB-CG-OD2	-5.31	113.52	118.30
1	A	375	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	B	391	LYS	CD-CE-NZ	-5.23	99.66	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	79	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	132	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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	3673	0	3622	26	0
1	B	3553	0	3504	37	0
2	A	43	0	30	0	0
2	B	43	0	30	0	0
3	A	23	0	19	0	0
3	B	23	0	19	1	0
4	A	264	0	0	3	0
4	B	142	0	0	2	0
All	All	7764	0	7224	64	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 (64) 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:16:ASN:HD22	1:A:43:GLU:H	1.23	0.84
1:A:7:GLN:HE21	1:A:16:ASN:HD21	1.38	0.71
1:B:16:ASN:HD22	1:B:43:GLU:H	1.38	0.71
1:B:50:ARG:HB2	1:B:353:LEU:HD23	1.72	0.70
1:A:47:ARG:NH2	1:A:73[A]:GLN:HG3	2.07	0.69
1:A:338:ASP:OD1	4:A:804:HOH:O	2.09	0.69
1:A:7:GLN:HE21	1:A:16:ASN:ND2	1.92	0.67
1:A:71:LEU:HD22	1:A:90:TRP:CE2	2.29	0.67
1:B:217:ASP:OD1	1:B:255:ARG:NH1	2.22	0.66
1:A:148:LEU:HD21	1:A:413:VAL:HG21	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:LEU:H	1:B:257:GLN:HE22	1.46	0.64
1:B:79:ARG:HD3	1:B:83:GLY:O	1.98	0.64
1:B:7:GLN:HG3	1:B:8:PRO:HD2	1.81	0.62
1:B:44:ALA:HB1	1:B:45:PRO:CD	2.28	0.62
1:A:217:ASP:OD1	1:A:255:ARG:NH1	2.30	0.61
1:A:162:PHE:CE1	1:A:215:LEU:HD21	2.35	0.61
1:B:82:PHE:HE1	1:B:263:ILE:HD12	1.66	0.61
1:A:47:ARG:CZ	1:A:73[A]:GLN:HG3	2.32	0.60
1:B:17:LEU:HD13	1:B:45:PRO:HD3	1.84	0.60
1:A:292:GLU:OE1	4:A:767:HOH:O	2.17	0.59
1:A:86:LEU:H	1:A:257:GLN:HE22	1.51	0.58
1:B:162:PHE:CE1	1:B:215:LEU:HD21	2.38	0.58
1:B:271:GLY:HA2	1:B:440:LYS:HG3	1.86	0.57
3:B:502:1C6:H10	4:B:732:HOH:O	2.03	0.57
1:A:388:HIS:HD2	1:A:391:LYS:NZ	2.03	0.56
1:B:201:ASN:N	1:B:201:ASN:HD22	2.04	0.55
1:A:82:PHE:HE1	1:A:263:ILE:HD12	1.71	0.55
1:A:271:GLY:HA2	1:A:440:LYS:HG3	1.87	0.54
1:B:332:SER:HB2	1:B:354:MET:SD	2.47	0.54
1:B:366:ILE:HG21	1:B:389:ALA:HB1	1.90	0.54
1:B:24:LYS:NZ	1:B:432:ASP:OD1	2.32	0.53
1:B:135:ALA:O	1:B:136:ASP:CB	2.54	0.53
1:B:422:ASP:OD2	1:B:451:LYS:NZ	2.38	0.53
1:B:82:PHE:CE1	1:B:263:ILE:HD12	2.46	0.51
1:B:162:PHE:HE1	1:B:215:LEU:HD21	1.75	0.51
1:B:177:MET:SD	1:B:263:ILE:HG23	2.52	0.50
1:A:182[A]:ASP:OD1	1:A:436:THR:HG22	2.11	0.50
1:A:21:ASN:OD1	1:A:189:GLN:OE1	2.30	0.49
1:B:141:VAL:HB	1:B:142:PRO:HD3	1.93	0.49
1:B:201:ASN:H	1:B:201:ASN:HD22	1.60	0.49
1:A:59:LYS:NZ	4:A:834:HOH:O	2.46	0.49
1:A:216:VAL:HG21	1:A:259:ILE:HG13	1.97	0.47
1:B:38:GLU:HB2	1:B:54:SER:HB3	1.97	0.47
1:B:103:LEU:O	1:B:106:SER:HB2	2.15	0.47
1:B:44:ALA:HB1	1:B:45:PRO:HD2	1.97	0.46
1:B:71:LEU:HD22	1:B:90:TRP:CE2	2.51	0.46
1:A:388:HIS:HA	1:A:391:LYS:HD3	1.97	0.45
1:A:71:LEU:HD22	1:A:90:TRP:NE1	2.32	0.45
1:A:39:ILE:HA	1:A:51:TYR:O	2.18	0.44
1:A:151:ASP:OD1	1:A:162:PHE:HB2	2.18	0.44
1:B:422:ASP:CG	1:B:451:LYS:NZ	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLN:HB3	1:A:170:PRO:HD2	2.01	0.43
1:B:357:ILE:HG22	1:B:361:HIS:CE1	2.53	0.43
1:B:220:ILE:HD11	1:B:258:ILE:HD11	2.02	0.41
1:B:161:ARG:HA	4:B:738:HOH:O	2.20	0.41
1:B:160:TYR:CE1	1:B:215:LEU:HD11	2.55	0.41
1:B:64:GLU:OE2	1:B:397:GLN:HG2	2.21	0.41
1:A:162:PHE:HE1	1:A:215:LEU:HD21	1.82	0.41
1:A:162:PHE:CZ	1:A:215:LEU:HD21	2.55	0.41
1:B:426:HIS:CD2	1:B:447:LYS:HE3	2.55	0.41
1:B:173:PHE:CD1	1:B:215:LEU:CD2	3.03	0.41
1:B:76:LYS:O	1:B:79:ARG:HB2	2.21	0.41
1:B:171:HIS:CG	1:B:172:PRO:HD2	2.55	0.41
1:B:195:ASP:OD1	1:B:197:ALA:HB3	2.20	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	451/455 (99%)	438 (97%)	13 (3%)	0	100	100
1	B	436/455 (96%)	424 (97%)	11 (2%)	1 (0%)	47	39
All	All	887/910 (98%)	862 (97%)	24 (3%)	1 (0%)	51	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	44	ALA

### 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	400/400 (100%)	392 (98%)	8 (2%)	55	50
1	B	383/400 (96%)	374 (98%)	9 (2%)	50	44
All	All	783/800 (98%)	766 (98%)	17 (2%)	52	46

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	71	LEU
1	A	148	LEU
1	A	187	LYS
1	A	222	ASP
1	A	230	SER
1	A	382	PRO
1	A	440	LYS
1	B	17	LEU
1	B	31	LYS
1	B	79	ARG
1	B	104	LEU
1	B	148	LEU
1	B	201	ASN
1	B	259	ILE
1	B	338	ASP
1	B	440	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	95	ASN
1	A	109	GLN
1	A	159	ASN
1	A	189	GLN

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Mol	Chain	Res	Type
1	A	236	HIS
1	A	253	ASN
1	A	257	GLN
1	A	283	ASN
1	A	319	ASN
1	A	388	HIS
1	A	403	GLN
1	B	16	ASN
1	B	95	ASN
1	B	109	GLN
1	B	125	GLN
1	B	134	ASN
1	B	159	ASN
1	B	201	ASN
1	B	253	ASN
1	B	257	GLN
1	B	310	GLN
1	B	388	HIS
1	B	403	GLN

### 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 ⓘ

4 ligands are modelled in this entry.

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	B	501	1	27,50,50	1.89	8 (29%)	17,82,82	2.64	11 (64%)
3	1C6	B	502	-	23,25,25	3.74	8 (34%)	28,35,35	2.46	9 (32%)
3	1C6	A	502	-	23,25,25	3.19	8 (34%)	28,35,35	1.91	6 (21%)
2	HEM	A	501	1	27,50,50	1.62	6 (22%)	17,82,82	2.47	7 (41%)

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	B	501	1	-	0/6/54/54	-
3	1C6	B	502	-	-	1/7/9/9	0/3/3/3
3	1C6	A	502	-	-	2/7/9/9	0/3/3/3
2	HEM	A	501	1	-	0/6/54/54	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	1C6	CD1-CG	12.49	1.51	1.39
3	A	502	1C6	CD1-CG	11.58	1.50	1.39
3	B	502	1C6	CE1-CD1	6.55	1.51	1.39
3	B	502	1C6	CE1-CZ	6.20	1.51	1.40
3	B	502	1C6	CB-S	-5.91	1.69	1.82
2	B	501	HEM	C3D-C2D	4.83	1.52	1.37
3	A	502	1C6	CE1-CZ	4.63	1.48	1.40
3	A	502	1C6	CE1-CD1	4.29	1.47	1.39
3	A	502	1C6	CB-S	-3.87	1.73	1.82
3	B	502	1C6	CE3-CZ3	3.78	1.43	1.37
2	A	501	HEM	C3C-C2C	-3.74	1.35	1.40
2	A	501	HEM	C3B-C2B	-3.53	1.35	1.40
3	A	502	1C6	CE3-CZ3	3.43	1.43	1.37
2	B	501	HEM	C3C-CAC	3.33	1.54	1.47
3	B	502	1C6	CF1-S	-3.32	1.69	1.75
2	B	501	HEM	C3B-C2B	-3.14	1.36	1.40
2	B	501	HEM	C3B-CAB	3.08	1.54	1.47
3	A	502	1C6	CF1-S	-2.78	1.70	1.75
2	A	501	HEM	C3D-C2D	2.71	1.45	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3B-CAB	2.64	1.53	1.47
3	A	502	1C6	CG-N1	2.63	1.38	1.34
2	B	501	HEM	CMC-C2C	2.60	1.57	1.51
2	B	501	HEM	C3C-C2C	-2.59	1.36	1.40
3	B	502	1C6	CS2-CX2	2.38	1.50	1.42
3	B	502	1C6	CB-CG	2.36	1.53	1.50
2	A	501	HEM	CMB-C2B	2.12	1.56	1.51
2	B	501	HEM	CMD-C2D	2.09	1.56	1.51
3	A	502	1C6	O2-CE1	-2.06	1.34	1.38
2	A	501	HEM	C1A-CHA	-2.02	1.35	1.41
2	B	501	HEM	C1D-CHD	-2.02	1.35	1.41

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	1C6	CB-S-CF1	7.37	110.53	102.42
2	B	501	HEM	C1D-C2D-C3D	-6.42	102.53	107.00
2	A	501	HEM	C1D-C2D-C3D	-6.34	102.58	107.00
3	B	502	1C6	CZ-CE1-CD1	-5.10	117.24	121.53
3	B	502	1C6	CE2-N1-CG	4.83	123.84	117.75
3	A	502	1C6	CB-S-CF1	-4.62	97.34	102.42
3	B	502	1C6	CD1-CG-N1	-4.33	119.71	123.95
3	A	502	1C6	C3-CD1-CG	4.09	126.26	122.69
2	A	501	HEM	CBD-CAD-C3D	-3.84	105.40	112.48
2	B	501	HEM	CMC-C2C-C3C	3.67	131.54	124.68
2	B	501	HEM	CMA-C3A-C4A	-3.44	123.17	128.46
3	A	502	1C6	C4-O3-CZ3	3.29	124.66	117.51
2	A	501	HEM	CMA-C3A-C4A	-2.94	123.94	128.46
3	A	502	1C6	CE2-N1-CG	2.78	121.25	117.75
2	A	501	HEM	C4C-C3C-C2C	2.73	108.81	106.90
2	B	501	HEM	CBD-CAD-C3D	-2.71	107.48	112.48
2	A	501	HEM	CMC-C2C-C3C	2.69	129.71	124.68
2	B	501	HEM	CAD-CBD-CGD	-2.67	108.19	112.67
3	B	502	1C6	CB-CG-CD1	2.63	122.77	120.29
2	B	501	HEM	C4C-C3C-C2C	2.61	108.72	106.90
3	B	502	1C6	C4-O3-CZ3	2.60	123.15	117.51
3	B	502	1C6	CE3-CX2-NV	2.57	138.18	130.83
2	B	501	HEM	CMD-C2D-C3D	2.55	129.75	124.94
3	A	502	1C6	CD1-CG-N1	-2.51	121.50	123.95
2	B	501	HEM	CMB-C2B-C3B	2.47	129.31	124.68
2	A	501	HEM	CMD-C2D-C3D	2.44	129.54	124.94
2	B	501	HEM	CMA-C3A-C2A	2.24	129.17	124.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	1C6	CH2-CZ3-CE3	2.23	123.81	120.81
2	B	501	HEM	C3C-C4C-NC	-2.22	106.74	110.94
2	A	501	HEM	C3C-C4C-NC	-2.21	106.77	110.94
2	B	501	HEM	C3B-C4B-NB	-2.19	106.38	109.21
3	B	502	1C6	CE2-CZ-CE1	2.17	118.89	116.27
3	B	502	1C6	CZ-CE2-N1	-2.04	123.02	125.11

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	502	1C6	S-CB-CG-CD1
3	A	502	1C6	S-CB-CG-CD1
3	A	502	1C6	CH2-CZ3-O3-C4

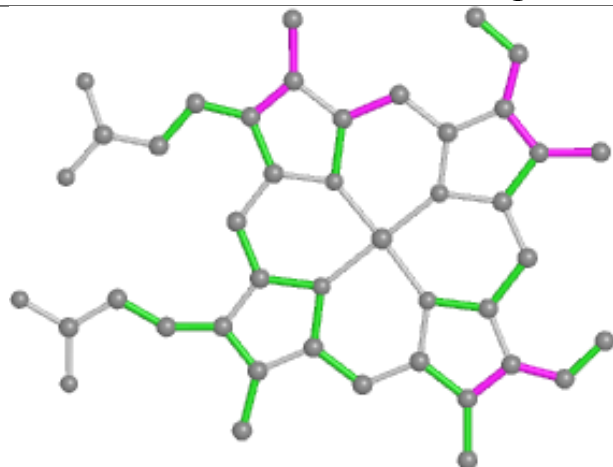
There are no ring outliers.

1 monomer is involved in 1 short contact:

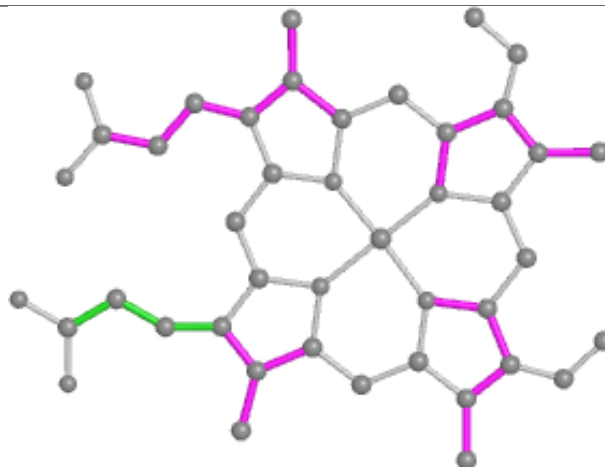
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	1C6	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

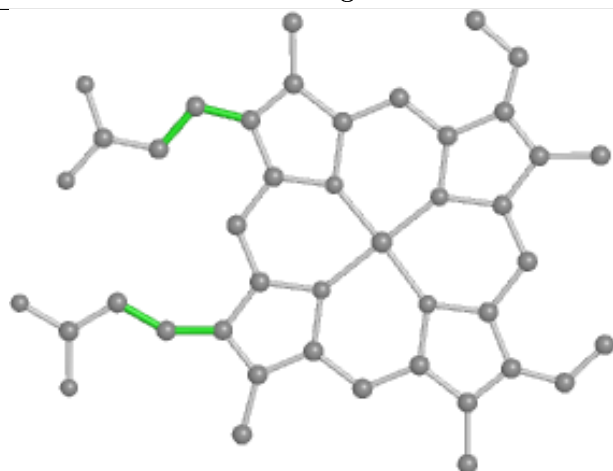
## Ligand HEM B 501



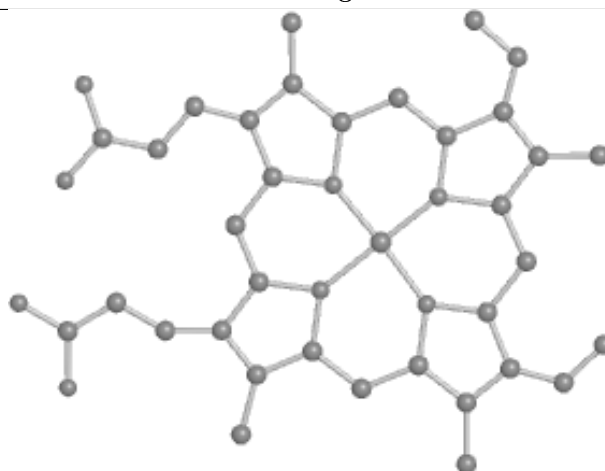
Bond lengths



Bond angles

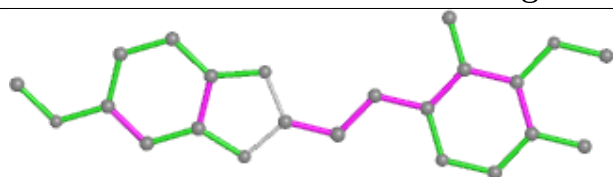


Torsions

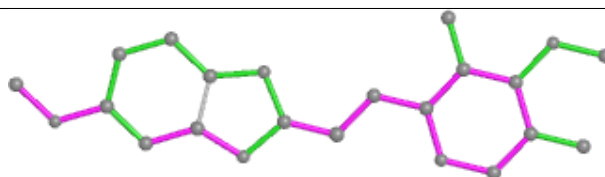


Rings

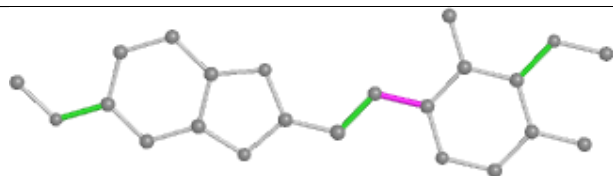
## Ligand 1C6 B 502



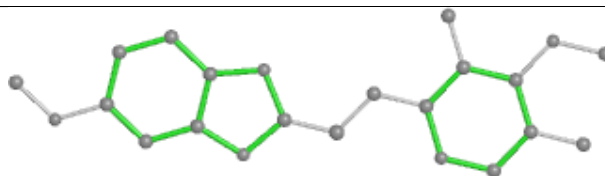
Bond lengths



Bond angles

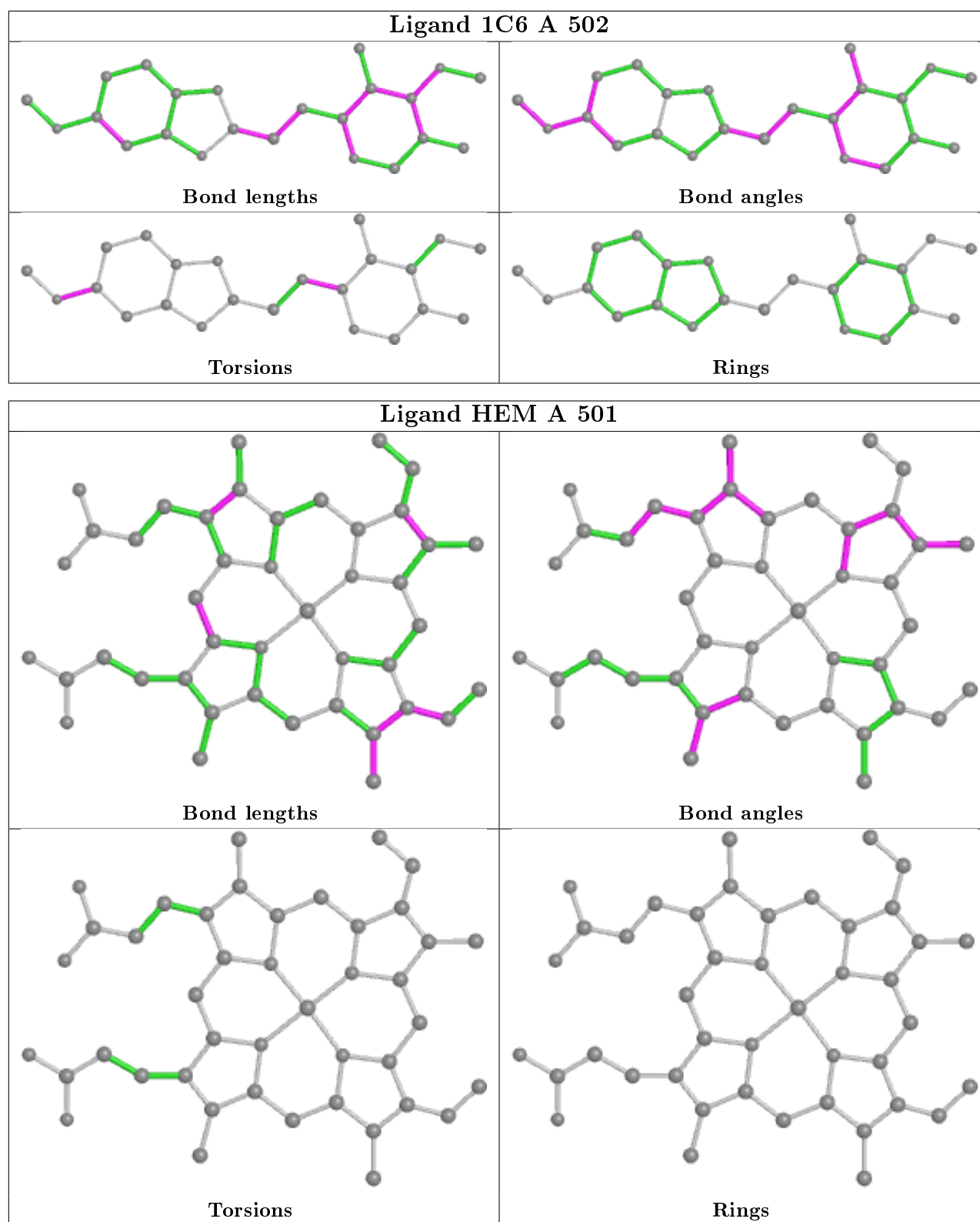


Torsions



Rings





## 5.7 Other polymers [i](#)

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<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	450/455 (98%)	-0.15	1 (0%) 95 95	17, 27, 46, 63	0
1	B	442/455 (97%)	0.43	51 (11%) 4 4	22, 42, 81, 100	0
All	All	892/910 (98%)	0.14	52 (5%) 23 25	17, 33, 72, 100	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	46	GLY	6.3
1	B	193	PRO	5.5
1	B	194	ASP	5.4
1	B	81	PHE	5.2
1	B	3	LYS	4.9
1	B	191	ALA	4.7
1	B	198	TYR	4.4
1	B	44	ALA	4.4
1	B	19	LEU	4.3
1	B	188	LEU	4.1
1	B	199	ASP	4.1
1	B	205	PHE	3.8
1	B	181	LEU	3.5
1	B	45	PRO	3.4
1	B	338	ASP	3.2
1	B	4	GLU	3.2
1	B	197	ALA	3.2
1	B	347	LEU	3.1
1	B	437	LEU	3.0
1	B	174	ILE	3.0
1	B	196	PRO	2.9
1	B	77	PHE	2.9
1	B	82	PHE	2.9
1	B	343	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	42	PHE	2.8
1	B	204	GLN	2.7
1	B	340	VAL	2.7
1	B	333	LEU	2.7
1	B	348	GLU	2.6
1	B	346	PRO	2.5
1	B	48	VAL	2.4
1	B	345	TYR	2.4
1	B	5	MET	2.4
1	B	50	ARG	2.4
1	B	40	PHE	2.3
1	B	200	GLU	2.3
1	B	195	ASP	2.3
1	B	182	ASP	2.3
1	A	454	PRO	2.3
1	B	341	LEU	2.2
1	B	72	SER	2.2
1	B	65	SER	2.2
1	B	337	GLU	2.2
1	B	90	TRP	2.2
1	B	92	HIS	2.1
1	B	73	GLN	2.1
1	B	41	LYS	2.1
1	B	43	GLU	2.0
1	B	350	GLY	2.0
1	B	20	LEU	2.0
1	B	23	ASP	2.0
1	B	190	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 monosaccharides in this entry.

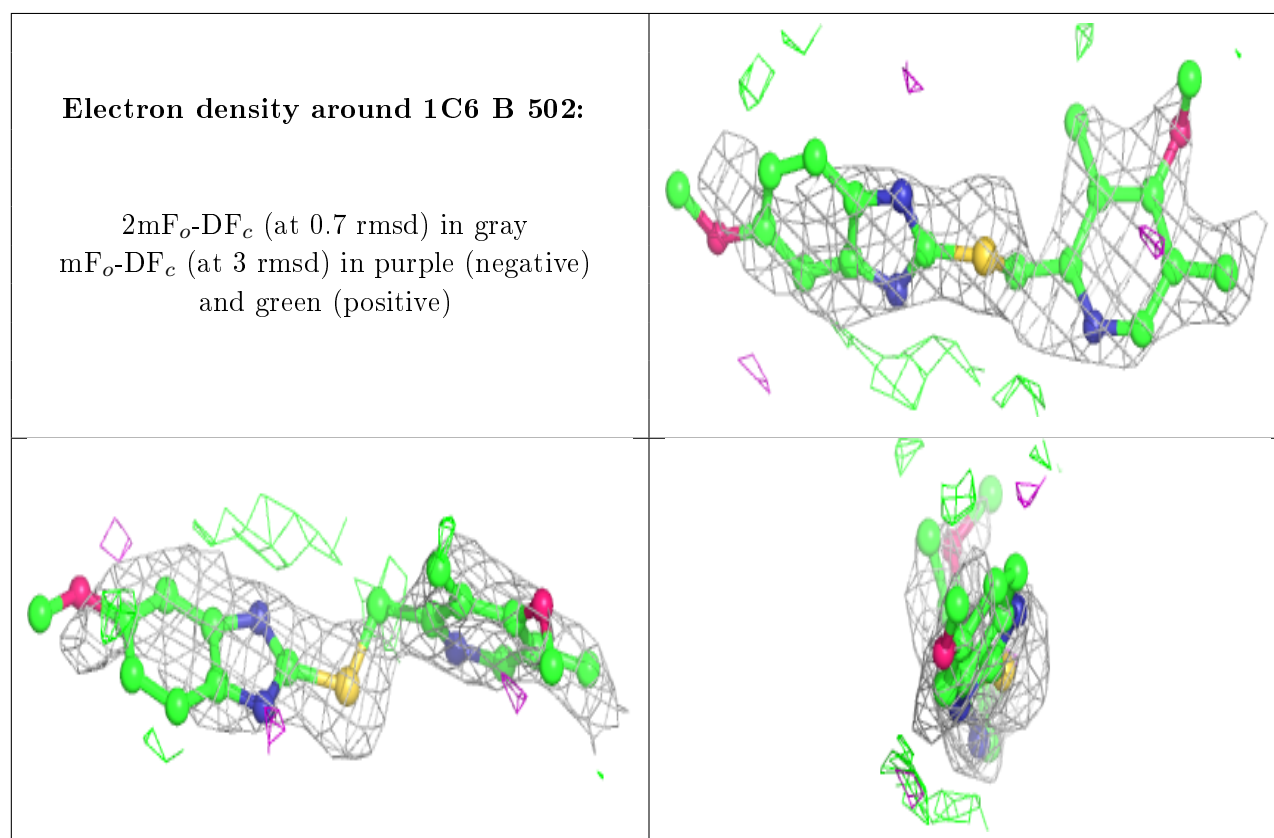
## 6.4 Ligands [i](#)

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.

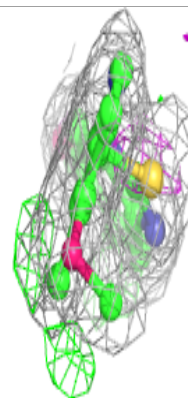
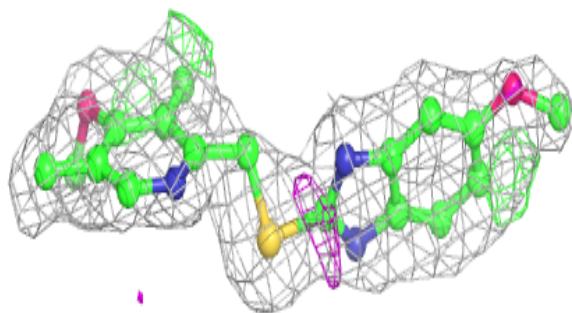
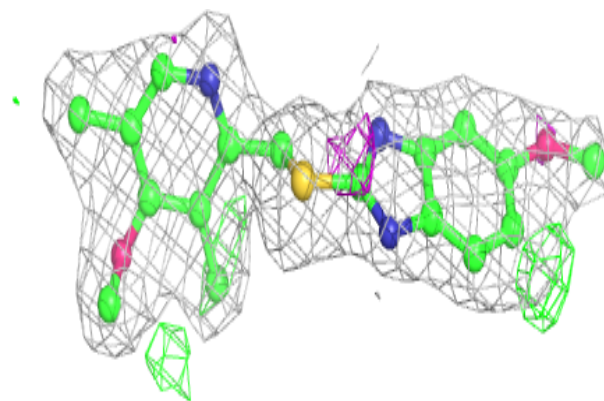
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	1C6	B	502	23/23	0.76	0.36	65,76,83,84	0
3	1C6	A	502	23/23	0.91	0.15	28,33,40,42	0
2	HEM	B	501	43/43	0.96	0.12	22,33,39,40	0
2	HEM	A	501	43/43	0.98	0.11	12,17,20,22	0

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.



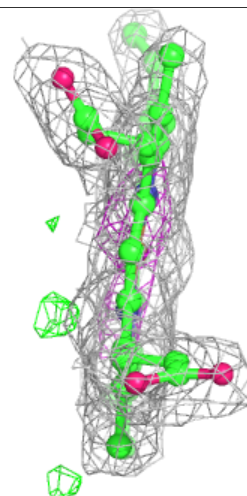
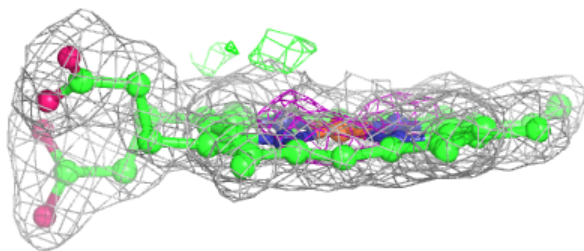
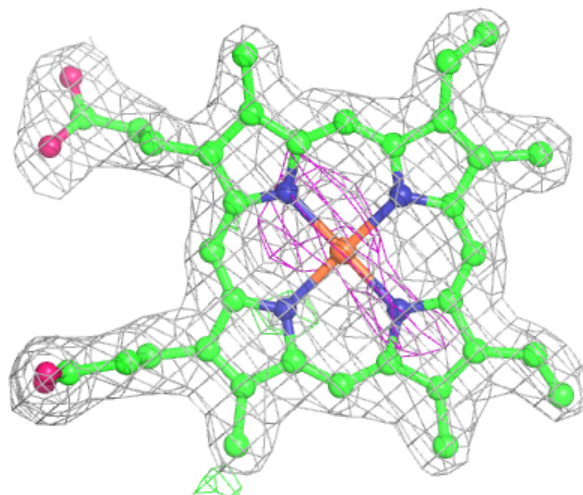
**Electron density around 1C6 A 502:**

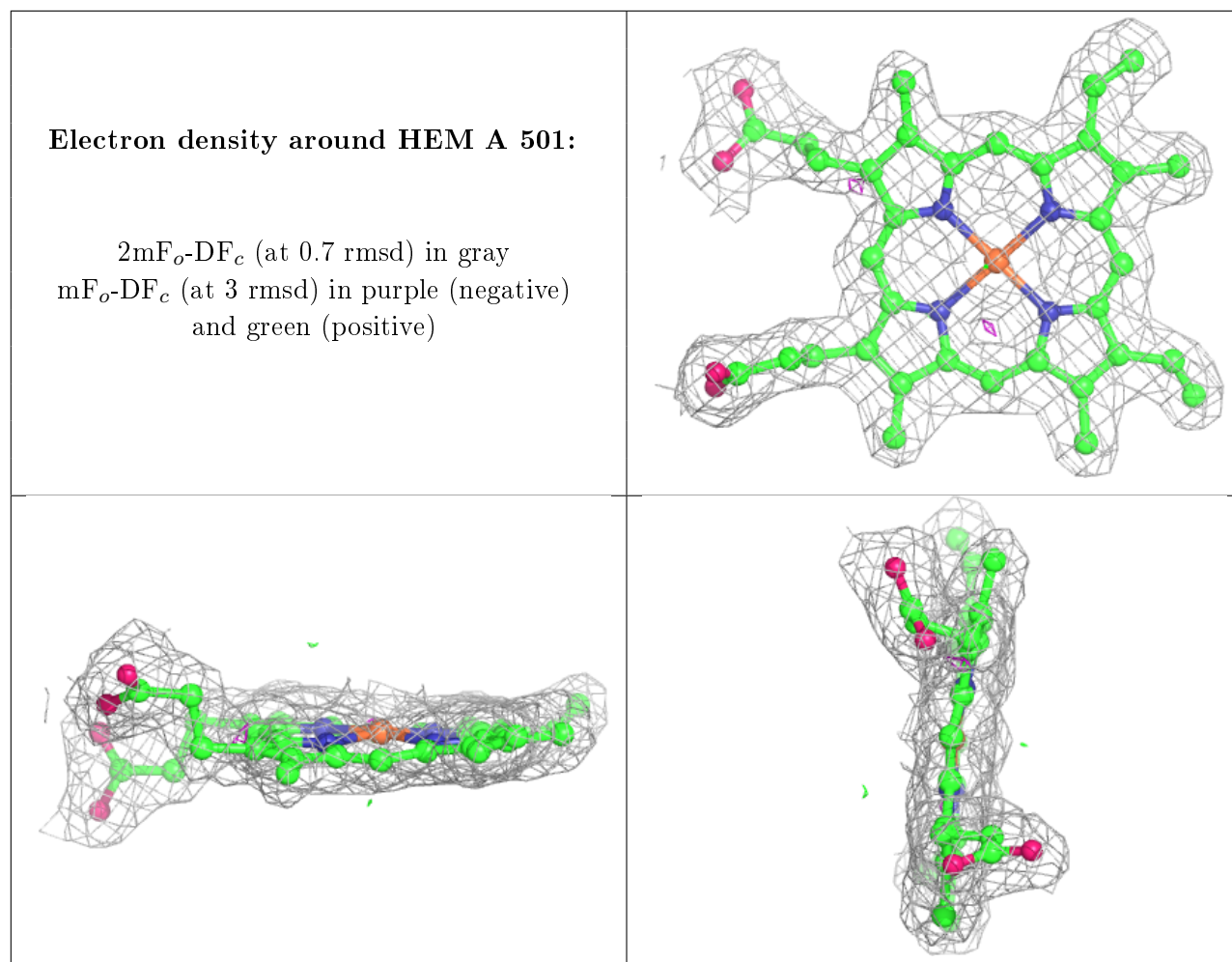
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEM B 501:**

$2mF_o-DF_c$  (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.