



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 12:22 AM BST

PDB ID : 4DTY  
Title : cytochrome P450 BM3h-8C8 MRI sensor, no ligand  
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Deposited on : 2012-02-21  
Resolution : 1.45 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

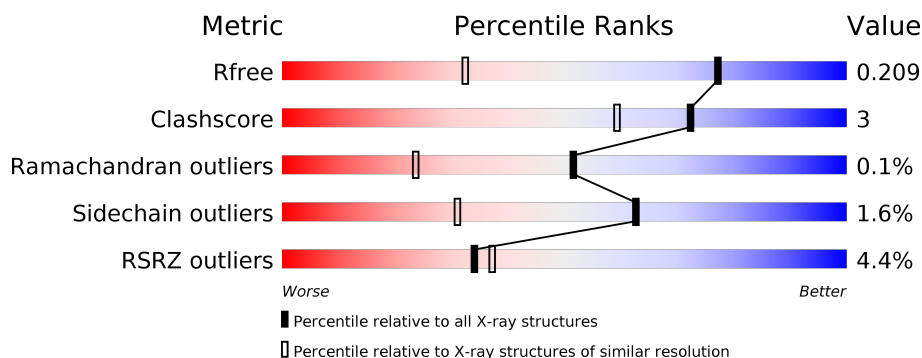
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.45 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	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	469	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>• •</div> </div> </div>
1	B	469	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>9%</div> <div>•</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8493 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.

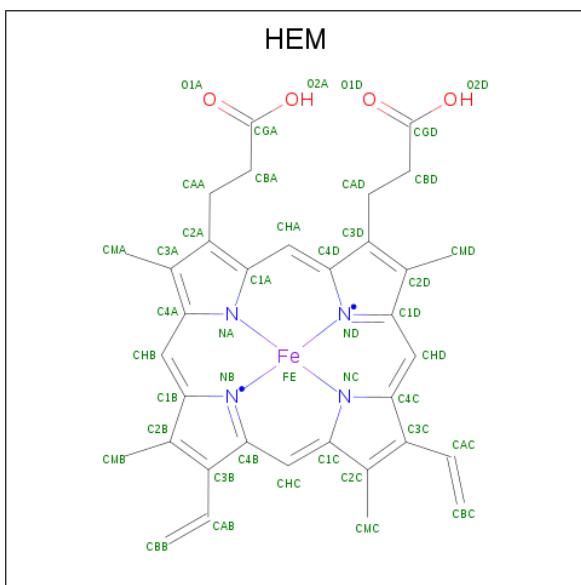
- Molecule 1 is a protein called cytochrome P450 BM3 variant 8C8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	453	Total	C	N	O	S	0	8	0
			3685	2354	622	691	18			
1	A	453	Total	C	N	O	S	0	8	0
			3685	2353	623	690	19			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	75	PRO	LEU	ENGINEERED MUTATION	UNP P14779
B	189	ARG	GLN	ENGINEERED MUTATION	UNP P14779
B	263	ALA	ILE	ENGINEERED MUTATION	UNP P14779
B	268	ALA	THR	ENGINEERED MUTATION	UNP P14779
B	286	GLU	VAL	ENGINEERED MUTATION	UNP P14779
B	464	HIS	-	EXPRESSION TAG	UNP P14779
B	465	HIS	-	EXPRESSION TAG	UNP P14779
B	466	HIS	-	EXPRESSION TAG	UNP P14779
B	467	HIS	-	EXPRESSION TAG	UNP P14779
B	468	HIS	-	EXPRESSION TAG	UNP P14779
B	469	HIS	-	EXPRESSION TAG	UNP P14779
A	75	PRO	LEU	ENGINEERED MUTATION	UNP P14779
A	189	ARG	GLN	ENGINEERED MUTATION	UNP P14779
A	263	ALA	ILE	ENGINEERED MUTATION	UNP P14779
A	268	ALA	THR	ENGINEERED MUTATION	UNP P14779
A	286	GLU	VAL	ENGINEERED MUTATION	UNP P14779
A	464	HIS	-	EXPRESSION TAG	UNP P14779
A	465	HIS	-	EXPRESSION TAG	UNP P14779
A	466	HIS	-	EXPRESSION TAG	UNP P14779
A	467	HIS	-	EXPRESSION TAG	UNP P14779
A	468	HIS	-	EXPRESSION TAG	UNP P14779
A	469	HIS	-	EXPRESSION TAG	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	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0

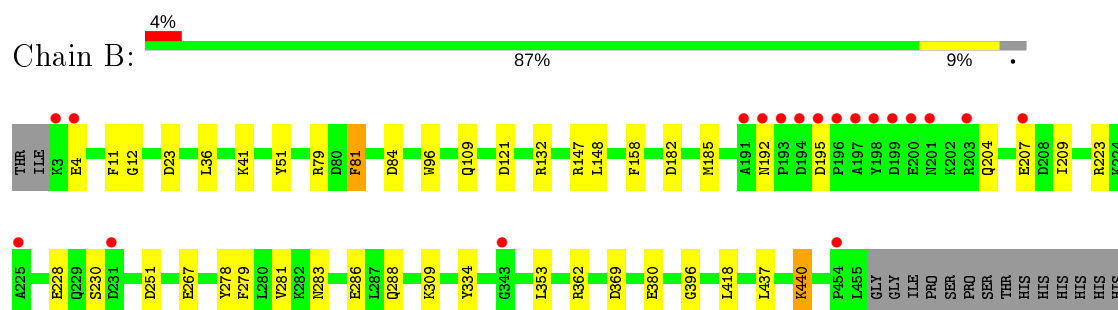
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	534	Total O 534 534	0	0
4	A	502	Total O 502 502	0	0

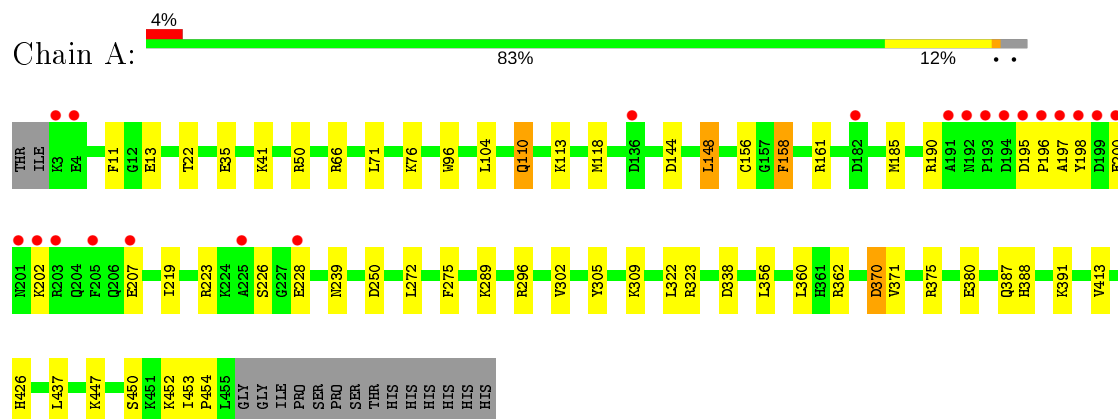
### 3 Residue-property plots

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: cytochrome P450 BM3 variant 8C8



- Molecule 1: cytochrome P450 BM3 variant 8C8



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.75Å 145.66Å 63.53Å 90.00° 97.18° 90.00°	Depositor
Resolution (Å)	37.31 – 1.45 36.42 – 1.45	Depositor EDS
% Data completeness (in resolution range)	93.4 (37.31-1.45) 93.4 (36.42-1.45)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.176 , 0.212 0.174 , 0.209	Depositor DCC
$R_{free}$ test set	8812 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.4	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 45.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8493	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.22% 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, MG

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	1.22	4/3795 (0.1%)	1.14	20/5129 (0.4%)
1	B	1.27	11/3795 (0.3%)	1.18	20/5130 (0.4%)
All	All	1.24	15/7590 (0.2%)	1.16	40/10259 (0.4%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	11	PHE	CE2-CZ	7.11	1.50	1.37
1	B	267	GLU	CB-CG	-6.91	1.39	1.52
1	B	51	TYR	CD1-CE1	6.38	1.49	1.39
1	A	156	CYS	CB-SG	-6.03	1.72	1.82
1	B	380	GLU	CG-CD	5.96	1.60	1.51
1	B	279	PHE	CD1-CE1	5.81	1.50	1.39
1	A	289	LYS	CE-NZ	5.79	1.63	1.49
1	B	396	GLY	N-CA	5.76	1.54	1.46
1	B	12	GLY	C-O	5.60	1.32	1.23
1	B	81	PHE	CE1-CZ	5.60	1.48	1.37
1	B	334	TYR	CD2-CE2	5.60	1.47	1.39
1	A	207	GLU	CG-CD	5.38	1.60	1.51
1	A	13	GLU	CG-CD	5.32	1.59	1.51
1	B	281	VAL	N-CA	5.18	1.56	1.46
1	B	96	TRP	CA-CB	5.07	1.65	1.53

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	ARG	NE-CZ-NH2	-10.48	115.06	120.30
1	A	338	ASP	CB-CG-OD1	9.04	126.44	118.30
1	B	84	ASP	CB-CG-OD2	-8.95	110.24	118.30
1	A	250	ASP	CB-CG-OD1	8.08	125.57	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	79	ARG	NE-CZ-NH1	7.85	124.22	120.30
1	A	104	LEU	CB-CG-CD1	7.56	123.85	111.00
1	A	250	ASP	CB-CG-OD2	-6.98	112.02	118.30
1	A	338	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	A	66	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	B	147	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	A	323	ARG	NE-CZ-NH2	6.37	123.48	120.30
1	B	182	ASP	CB-CG-OD2	-6.37	112.57	118.30
1	B	182	ASP	CB-CG-OD1	6.32	123.98	118.30
1	A	356	LEU	CB-CG-CD2	-6.29	100.31	111.00
1	B	251	ASP	CB-CG-OD1	6.13	123.82	118.30
1	B	278	TYR	CB-CG-CD1	-6.10	117.34	121.00
1	B	362	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	B	84	ASP	CB-CG-OD1	5.95	123.66	118.30
1	B	418	LEU	CB-CG-CD2	5.85	120.95	111.00
1	A	144	ASP	CB-CG-OD2	-5.85	113.03	118.30
1	B	132	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	A	296	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	B	36	LEU	CB-CG-CD1	-5.69	101.33	111.00
1	B	278	TYR	CB-CG-CD2	5.66	124.39	121.00
1	A	66	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	B	121	ASP	CB-CG-OD1	5.55	123.29	118.30
1	A	360	LEU	CB-CG-CD2	-5.53	101.59	111.00
1	A	362	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	370	ASP	CB-CG-OD1	5.37	123.13	118.30
1	A	161	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	362	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	B	148	LEU	CB-CG-CD1	5.23	119.90	111.00
1	A	96	TRP	CA-CB-CG	-5.17	103.87	113.70
1	B	353	LEU	CB-CG-CD1	-5.17	102.22	111.00
1	B	23	ASP	CB-CG-OD2	-5.16	113.65	118.30
1	B	121	ASP	CB-CG-OD2	-5.14	113.68	118.30
1	A	371	VAL	CG1-CB-CG2	5.13	119.11	110.90
1	A	11	PHE	CB-CG-CD1	-5.12	117.22	120.80
1	B	79	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	A	275	PHE	CG-CD2-CE2	-5.02	115.28	120.80

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	3685	0	3654	30	0
1	B	3685	0	3654	18	0
2	A	43	0	30	2	0
2	B	43	0	30	0	0
3	B	1	0	0	0	0
4	A	502	0	0	6	0
4	B	534	0	0	6	0
All	All	8493	0	7368	50	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 (50) 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:223:ARG:HD3	1:A:228:GLU:HG3	1.44	1.00
1:A:226:SER:OG	1:A:228:GLU:HG2	1.68	0.93
1:B:288:GLN:NE2	4:B:1057:HOH:O	2.09	0.84
1:A:370:ASP:OD2	1:A:375:ARG:NH2	2.17	0.75
1:A:110:GLN:NE2	1:A:113:LYS:HE3	2.05	0.71
1:A:71:LEU:O	1:A:76:LYS:HE3	1.94	0.67
1:B:440:LYS:HE3	4:B:1134:HOH:O	1.95	0.66
1:A:110:GLN:HE22	1:A:113:LYS:HE3	1.59	0.66
1:A:426:HIS:CD2	1:A:447:LYS:HE3	2.32	0.65
1:B:223:ARG:HD3	1:B:228:GLU:HG2	1.79	0.64
1:B:440:LYS:CE	4:B:1134:HOH:O	2.45	0.64
1:A:158:PHE:CE1	1:A:219:ILE:HD13	2.33	0.63
1:A:305:TYR:CE2	1:A:309:LYS:HE2	2.33	0.62
1:A:148:LEU:HD21	1:A:413:VAL:HG21	1.82	0.61
2:A:500:HEM:HMC2	2:A:500:HEM:HBC2	1.83	0.59
1:B:81:PHE:HB3	1:B:209:ILE:HG12	1.86	0.57
1:A:195:ASP:O	1:A:197:ALA:N	2.40	0.55
1:B:109:GLN:HE22	1:B:309:LYS:HZ2	1.55	0.55
1:A:158:PHE:CE1	1:A:219:ILE:CD1	2.89	0.55
1:A:375:ARG:HG2	4:A:819:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:GLU:OE2	4:A:785:HOH:O	2.19	0.52
1:A:198:TYR:O	1:A:202:LYS:HG3	2.10	0.52
1:B:437:LEU:HD23	4:B:782:HOH:O	2.10	0.51
1:A:239:ASN:ND2	4:A:915:HOH:O	2.43	0.50
1:A:158:PHE:HE1	1:A:219:ILE:CD1	2.23	0.50
1:A:158:PHE:HE1	1:A:219:ILE:HD12	1.78	0.48
1:B:109:GLN:HE22	1:B:309:LYS:NZ	2.12	0.47
1:B:185:MET:HE1	1:B:437:LEU:HD13	1.95	0.47
1:B:288:GLN:HG2	4:B:1109:HOH:O	2.15	0.47
1:B:4:GLU:H	1:B:4:GLU:CD	2.17	0.47
1:A:35:GLU:HG3	4:A:834:HOH:O	2.15	0.47
1:A:388:HIS:HA	1:A:391:LYS:HD3	1.97	0.47
1:A:195:ASP:C	1:A:197:ALA:N	2.69	0.46
1:B:185:MET:HE1	1:B:437:LEU:CD1	2.46	0.46
1:B:369[B]:ASP:OD1	4:B:1041:HOH:O	2.20	0.45
1:A:195:ASP:C	1:A:197:ALA:H	2.19	0.45
1:A:118[B]:MET:HG3	4:A:736:HOH:O	2.17	0.45
1:A:190:ARG:HG2	1:A:198:TYR:CZ	2.51	0.45
1:A:305:TYR:CE2	1:A:309:LYS:CE	2.98	0.44
2:A:500:HEM:CMC	2:A:500:HEM:HBC2	2.45	0.44
1:B:192:ASN:HB2	1:B:195:ASP:HB2	1.99	0.44
1:A:272:LEU:HD13	1:A:322:LEU:HG	1.99	0.44
1:B:185:MET:HE1	1:B:437:LEU:HB2	2.00	0.43
1:A:113:LYS:HG2	1:A:305:TYR:CD2	2.53	0.43
1:B:41:LYS:HB2	1:B:41:LYS:HE3	1.57	0.43
1:B:283:ASN:HB3	1:B:286:GLU:OE1	2.19	0.42
1:B:204:GLN:NE2	1:B:207:GLU:OE1	2.48	0.41
1:A:453:ILE:HA	1:A:454:PRO:HD2	1.80	0.41
1:A:437:LEU:HD23	4:A:876:HOH:O	2.22	0.40
1:A:450:SER:HB3	1:A:452:LYS:HE2	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	459/469 (98%)	446 (97%)	12 (3%)	1 (0%)	47	22
1	B	459/469 (98%)	445 (97%)	14 (3%)	0	100	100
All	All	918/938 (98%)	891 (97%)	26 (3%)	1 (0%)	51	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	PRO

### 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	402/409 (98%)	391 (97%)	11 (3%)	44	12
1	B	402/409 (98%)	399 (99%)	3 (1%)	84	65
All	All	804/818 (98%)	790 (98%)	14 (2%)	62	28

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	158	PHE
1	B	230	SER
1	B	440	LYS
1	A	22	THR
1	A	41	LYS
1	A	50	ARG
1	A	110	GLN
1	A	148	LEU
1	A	158	PHE
1	A	185[A]	MET
1	A	185[B]	MET
1	A	200	GLU

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Mol	Chain	Res	Type
1	A	302	VAL
1	A	387	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	109	GLN
1	B	201	ASN
1	B	236	HIS
1	A	110	GLN
1	A	201	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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	500	1,4	27,50,50	1.83	8 (29%)	17,82,82	2.27	6 (35%)
2	HEM	B	501	1,4	27,50,50	1.91	7 (25%)	17,82,82	2.32	6 (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	500	1,4	-	0/6/54/54	-
2	HEM	B	501	1,4	-	0/6/54/54	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C3C-C2C	-4.72	1.33	1.40
2	A	500	HEM	C3C-C2C	-4.70	1.33	1.40
2	A	500	HEM	C1D-ND	3.70	1.43	1.36
2	B	501	HEM	C1A-NA	3.59	1.43	1.36
2	A	500	HEM	C3B-C2B	-3.10	1.36	1.40
2	B	501	HEM	CAA-C2A	3.07	1.56	1.52
2	A	500	HEM	C3C-CAC	2.56	1.53	1.47
2	B	501	HEM	C3B-C2B	-2.50	1.36	1.40
2	A	500	HEM	CMD-C2D	2.45	1.56	1.51
2	A	500	HEM	C3B-CAB	2.35	1.52	1.47
2	B	501	HEM	CMC-C2C	2.21	1.56	1.51
2	B	501	HEM	C3D-C2D	2.16	1.44	1.37
2	A	500	HEM	C4B-CHC	-2.14	1.35	1.41
2	B	501	HEM	C1D-ND	2.14	1.40	1.36
2	A	500	HEM	C2A-C3A	-2.02	1.31	1.37

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	HEM	CMA-C3A-C4A	-5.56	119.92	128.46
2	B	501	HEM	CMB-C2B-C3B	4.95	133.94	124.68
2	B	501	HEM	C4A-C3A-C2A	4.42	110.07	107.00
2	A	500	HEM	CMA-C3A-C2A	4.31	133.08	124.94
2	B	501	HEM	CMD-C2D-C1D	-3.73	122.72	128.46
2	A	500	HEM	CMD-C2D-C1D	-2.89	124.03	128.46
2	B	501	HEM	CMA-C3A-C4A	-2.57	124.51	128.46
2	A	500	HEM	CAA-CBA-CGA	2.52	116.90	112.67
2	B	501	HEM	CMD-C2D-C3D	2.34	129.36	124.94
2	A	500	HEM	C4C-C3C-C2C	-2.30	105.29	106.90
2	B	501	HEM	C3C-C4C-NC	-2.27	106.66	110.94
2	A	500	HEM	CMD-C2D-C3D	2.06	128.82	124.94

There are no chirality outliers.

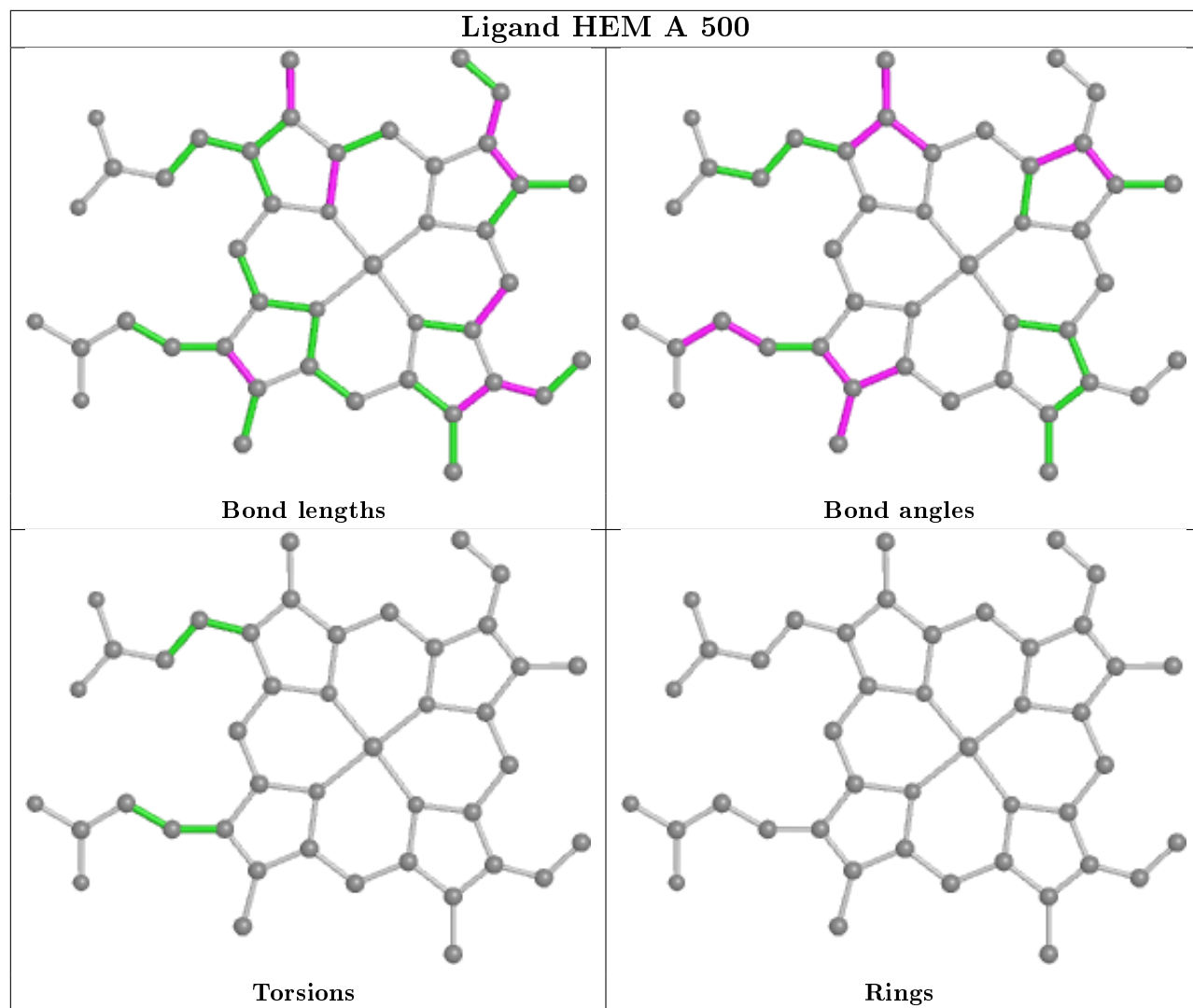
There are no torsion outliers.

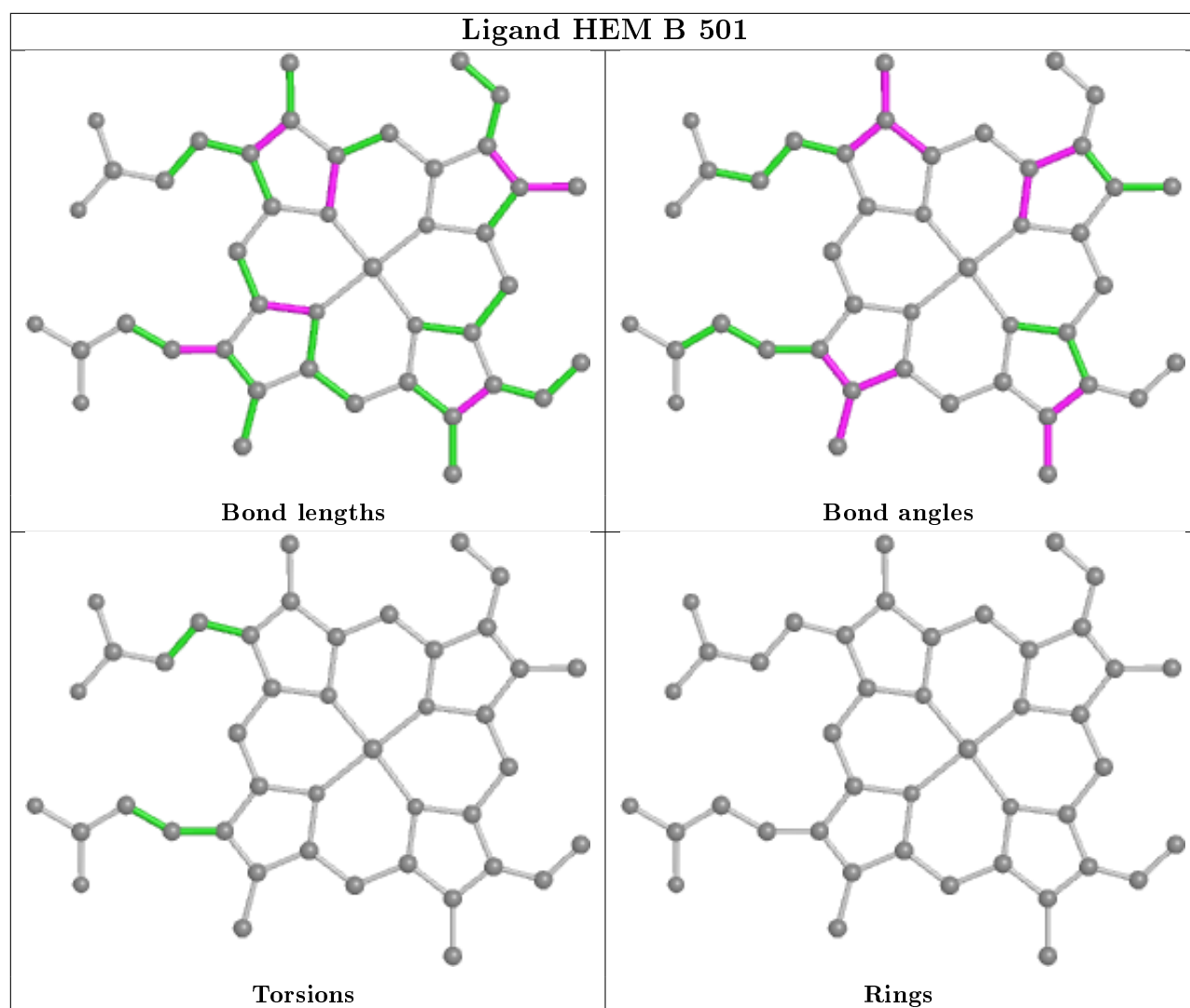
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	HEM	2	0

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





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	453/469 (96%)	0.09	21 (4%) 32 35	10, 18, 34, 71	0
1	B	453/469 (96%)	0.07	19 (4%) 36 39	9, 18, 34, 59	0
All	All	906/938 (96%)	0.08	40 (4%) 34 37	9, 18, 34, 71	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	ALA	9.5
1	A	196	PRO	8.4
1	A	191	ALA	7.9
1	A	198	TYR	6.5
1	B	196	PRO	6.3
1	B	192	ASN	5.7
1	B	197	ALA	5.7
1	A	192	ASN	5.4
1	B	191	ALA	5.0
1	A	200	GLU	4.7
1	B	3	LYS	4.6
1	A	199	ASP	4.5
1	B	4	GLU	4.5
1	B	198	TYR	4.0
1	A	195	ASP	4.0
1	B	199	ASP	3.8
1	A	193	PRO	3.8
1	A	194	ASP	3.6
1	B	194	ASP	3.5
1	B	200	GLU	3.3
1	B	343	GLY	3.2
1	B	193	PRO	3.2
1	A	136	ASP	3.0
1	A	203	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	201	ASN	2.8
1	B	195	ASP	2.8
1	A	3	LYS	2.8
1	B	201	ASN	2.7
1	B	203	ARG	2.6
1	A	4	GLU	2.6
1	B	231	ASP	2.5
1	B	454	PRO	2.4
1	A	205	PHE	2.2
1	A	202	LYS	2.2
1	B	225	ALA	2.2
1	A	228	GLU	2.2
1	A	182	ASP	2.2
1	B	207	GLU	2.1
1	A	207	GLU	2.1
1	A	225	ALA	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](#)

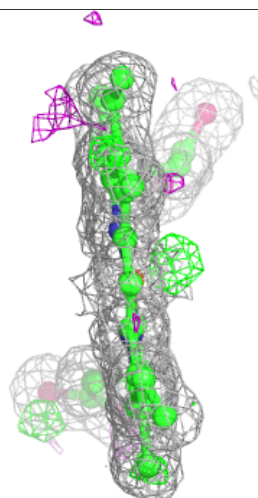
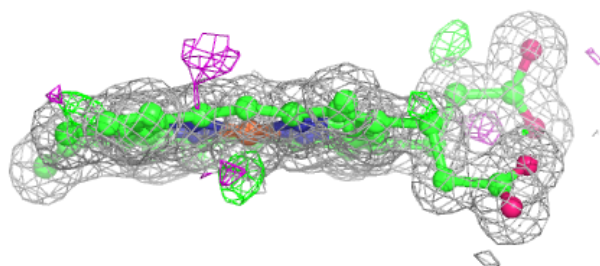
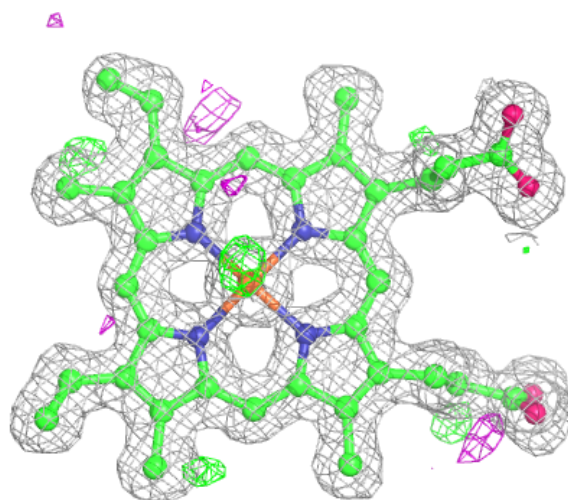
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

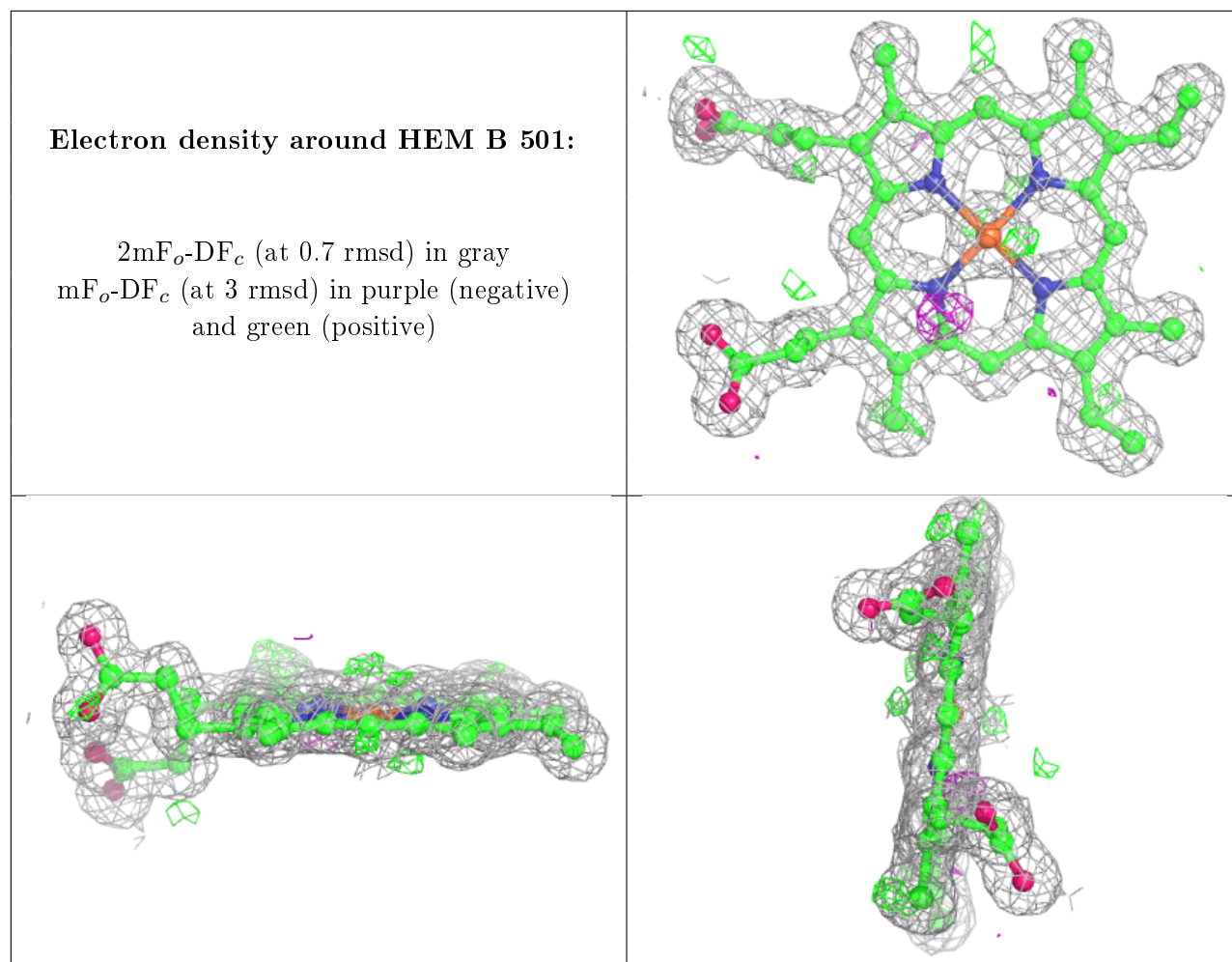
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEM	A	500	43/43	0.98	0.11	7,11,15,20	0
2	HEM	B	501	43/43	0.98	0.11	7,10,13,17	0
3	MG	B	502	1/1	0.99	0.12	28,28,28,28	0

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 HEM A 500:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.