Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 12:04 am BST

PDB ID	:	4BM4
Title	:	CRYSTAL STRUCTURE OF MANGANESE PEROXIDASE 4 FROM PLEUROTUS OSTREATUS - CRYSTAL FORM IV
Authors	:	Medrano, F.J.; Romero, A.
Deposited on	:	2013-05-05
Resolution	:	2.30 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:

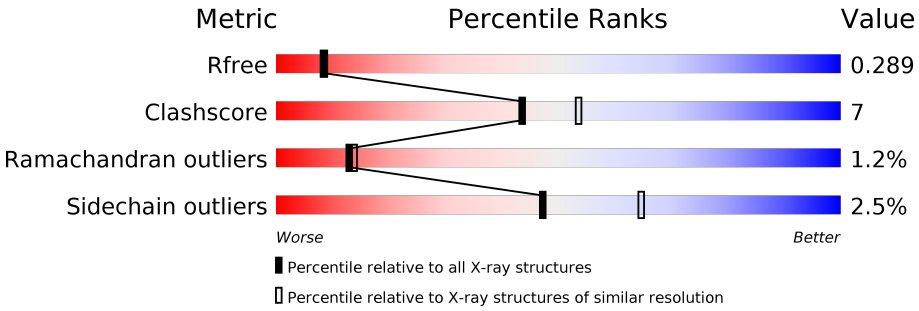
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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%

Mol	Chain	Length	Quality of chain
1	A	338	82% 15%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2788 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.

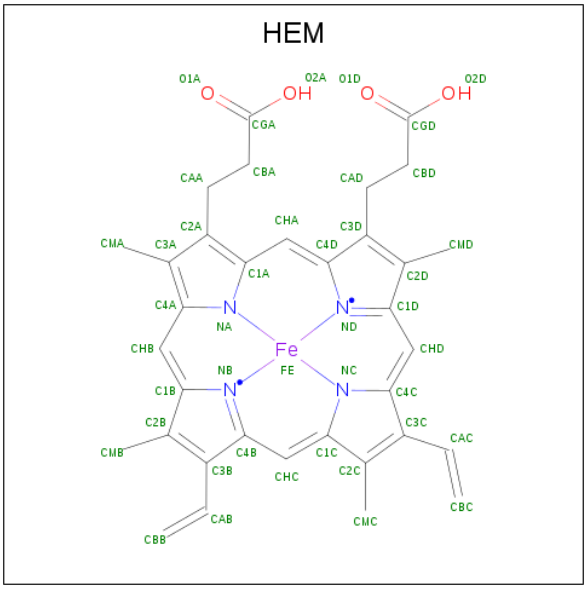
- Molecule 1 is a protein called MANGANESE PEROXIDASE 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2536	1594	438	491	13			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 4 is water.

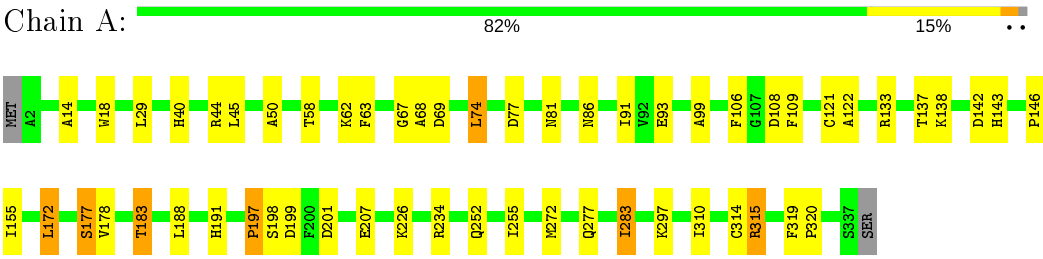
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	207	Total	O	0	0
			207	207		

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. 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: MANGANESE PEROXIDASE 4

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	123.87Å 86.50Å 41.40Å 90.00° 108.05° 90.00°	Depositor
Resolution (Å)	43.25 – 2.30 43.25 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.7 (43.25-2.30) 92.5 (43.25-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.35 (at 1.89Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.225 , 0.297 0.219 , 0.289	Depositor DCC
R_{free} test set	1627 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	20.0	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 49.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	0.073 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2788	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% 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, CA

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	0.45	0/2594	0.58	1/3515 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	315	ARG	N-CA-CB	5.12	119.81	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	314	CYS	Peptide

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	2536	0	2483	34	0
2	A	2	0	0	0	0
3	A	43	0	30	5	0
4	A	207	0	0	3	0
All	All	2788	0	2513	34	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 7.

All (34) 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:67:GLY:O	1:A:69:ASP:N	2.27	0.67
1:A:146:PRO:HB2	3:A:500:HEM:HAB	1.81	0.62
1:A:77:ASP:O	1:A:81:ASN:ND2	2.32	0.61
1:A:74:LEU:HG	1:A:106:PHE:HD2	1.67	0.59
1:A:226:LYS:O	1:A:234:ARG:HD2	2.07	0.54
1:A:74:LEU:HG	1:A:106:PHE:CD2	2.43	0.53
1:A:44:ARG:HD2	3:A:500:HEM:C4D	2.43	0.53
1:A:45:LEU:HD22	1:A:91:ILE:HG23	1.92	0.51
1:A:172:LEU:HB3	3:A:500:HEM:HMC3	1.92	0.50
1:A:14:ALA:HB3	1:A:283:ILE:HD12	1.95	0.48
1:A:40:HIS:CE1	1:A:178:VAL:HG22	2.49	0.48
1:A:151:SER:O	1:A:155:ILE:HG13	2.12	0.48
1:A:121:CYS:SG	1:A:178:VAL:HG21	2.54	0.47
1:A:188:LEU:HD22	1:A:191:HIS:CE1	2.49	0.47
1:A:122:ALA:HB3	1:A:199:ASP:HA	1.96	0.47
1:A:18:TRP:CZ2	1:A:108:ASP:HB3	2.52	0.45
1:A:86:ASN:HB3	1:A:183:THR:HG21	1.98	0.45
1:A:142:ASP:OD1	1:A:143:HIS:N	2.47	0.45
1:A:297:LYS:HE3	4:A:2122:HOH:O	2.15	0.45
1:A:44:ARG:HD2	3:A:500:HEM:CHA	2.47	0.45
1:A:319:PHE:CG	1:A:320:PRO:HD2	2.53	0.44
1:A:207:GLU:O	1:A:234:ARG:NH2	2.45	0.43
1:A:58:THR:HA	1:A:62:LYS:O	2.18	0.43
1:A:44:ARG:HB2	3:A:500:HEM:C2D	2.54	0.43
1:A:99:ALA:HB2	1:A:109:PHE:CG	2.54	0.43
1:A:252:GLN:HA	1:A:255:ILE:HD12	2.01	0.42
1:A:177:SER:OG	1:A:201:ASP:O	2.33	0.42
1:A:177:SER:O	1:A:197:PRO:HA	2.20	0.42
1:A:310:ILE:HG12	4:A:2189:HOH:O	2.19	0.42
1:A:137:THR:OG1	1:A:138:LYS:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ARG:HG2	1:A:277:GLN:CD	2.41	0.41
1:A:50:ALA:CB	1:A:272:MET:HG2	2.50	0.41
1:A:63:PHE:CE1	1:A:138:LYS:HE2	2.56	0.41
1:A:93:GLU:OE1	4:A:2050:HOH:O	2.21	0.41

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	334/338 (99%)	316 (95%)	14 (4%)	4 (1%)	13 14

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	ALA
1	A	315	ARG
1	A	29	LEU
1	A	197	PRO

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	280/282 (99%)	273 (98%)	7 (2%)	47 65

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	LEU
1	A	154	SER
1	A	172	LEU
1	A	177	SER
1	A	183	THR
1	A	198	SER
1	A	283	ILE

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	HEM	A	500	1	27,50,50	2.27	9 (33%)	17,82,82	1.76	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
3	HEM	A	500	1	-	0/6/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	HEM	C3D-C2D	5.74	1.54	1.37
3	A	500	HEM	C3B-C2B	-4.32	1.34	1.40
3	A	500	HEM	C3C-CAC	3.80	1.55	1.47
3	A	500	HEM	C3B-CAB	3.67	1.55	1.47
3	A	500	HEM	C3C-C2C	-3.47	1.35	1.40
3	A	500	HEM	CAA-C2A	2.54	1.55	1.52
3	A	500	HEM	CAD-C3D	2.20	1.56	1.52
3	A	500	HEM	C1D-ND	2.14	1.40	1.36
3	A	500	HEM	CMC-C2C	2.13	1.56	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	500	HEM	CBA-CAA-C2A	-3.04	106.87	112.49
3	A	500	HEM	CAD-CBD-CGD	-2.83	107.93	112.67
3	A	500	HEM	C1D-C2D-C3D	-2.78	105.06	107.00
3	A	500	HEM	C4A-C3A-C2A	2.77	108.92	107.00
3	A	500	HEM	CMC-C2C-C3C	2.18	128.75	124.68
3	A	500	HEM	CMD-C2D-C3D	2.04	128.79	124.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

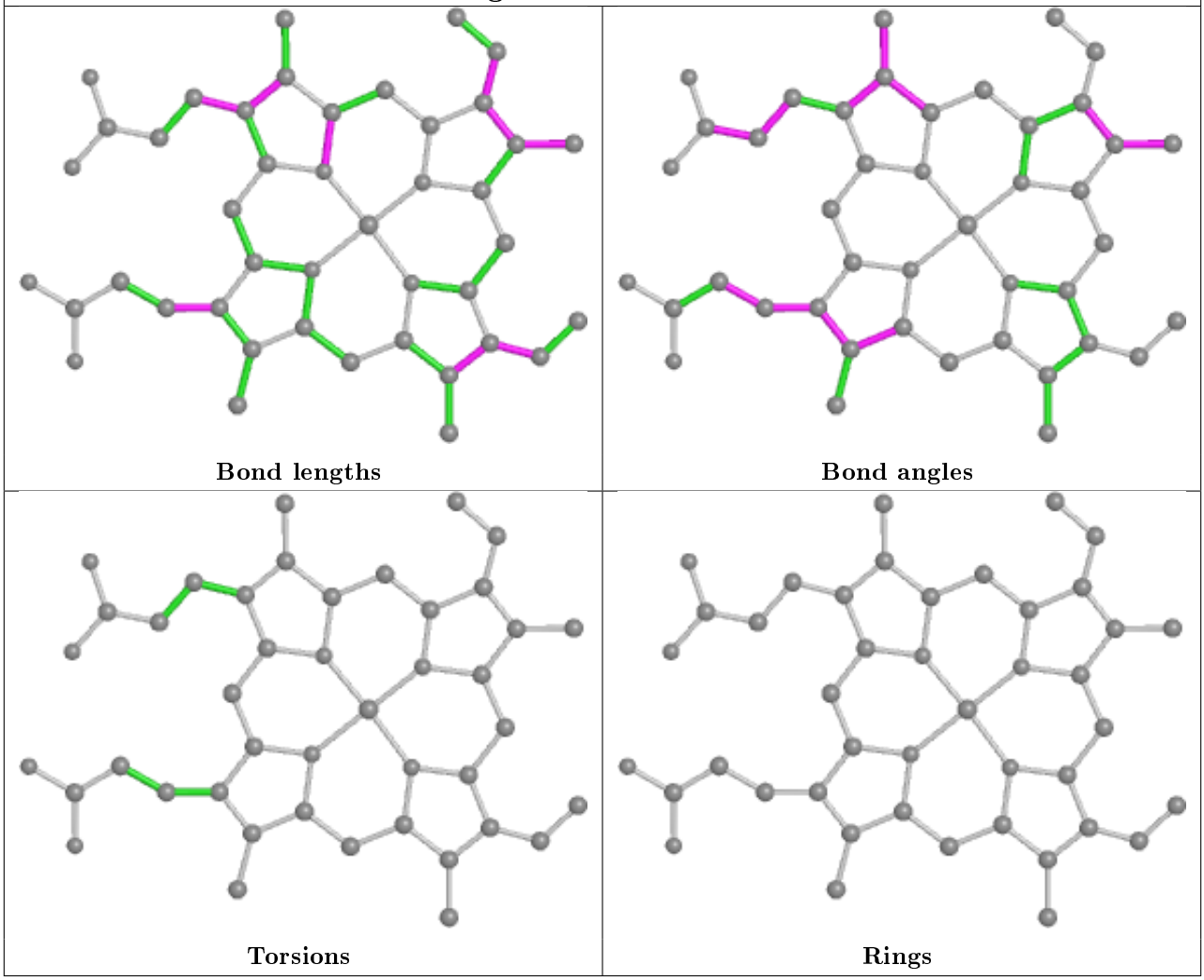
1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	HEM	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand HEM A 500



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

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

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

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

6.3 Carbohydrates

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

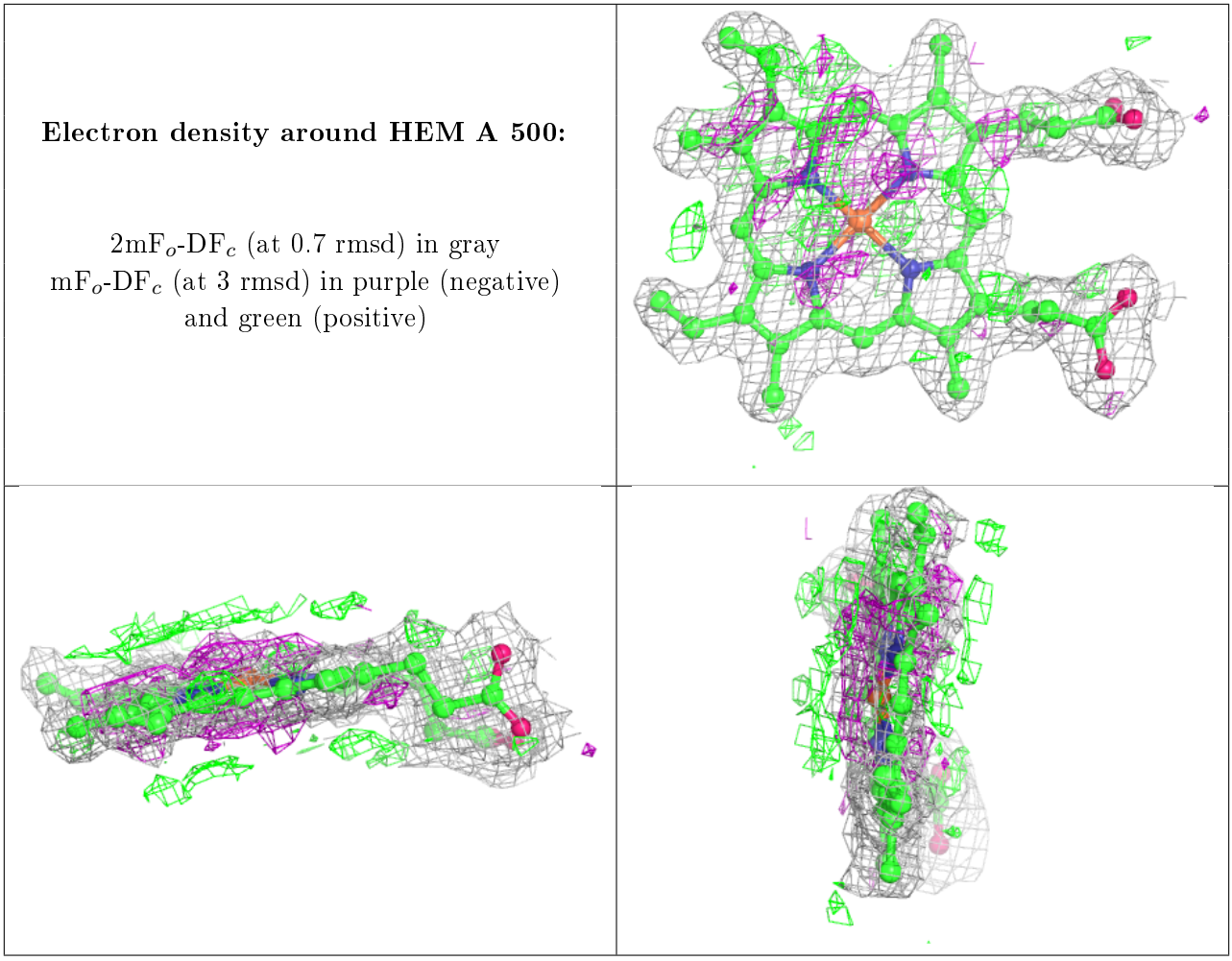
6.4 Ligands

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 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)

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