



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:47 PM UTC

PDB ID : 1AA4 / pdb_00001aa4
Title : SPECIFICITY OF LIGAND BINDING IN A BURIED POLAR CAVITY OF CYTOCHROME C PEROXIDASE
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Deposited on : 1997-01-22
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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.

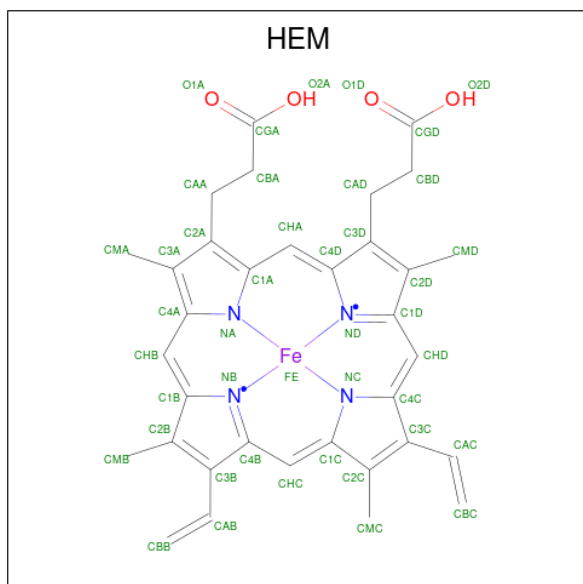
- Molecule 1 is a protein called CYTOCHROME C PEROXIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	291	Total	C	H	N	O	S	0	0	0
			2851	1492	511	391	451	6			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ILE	THR	conflict	UNP P00431
A	152	GLY	ASP	conflict	UNP P00431
A	191	GLY	TRP	engineered mutation	UNP P00431

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



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

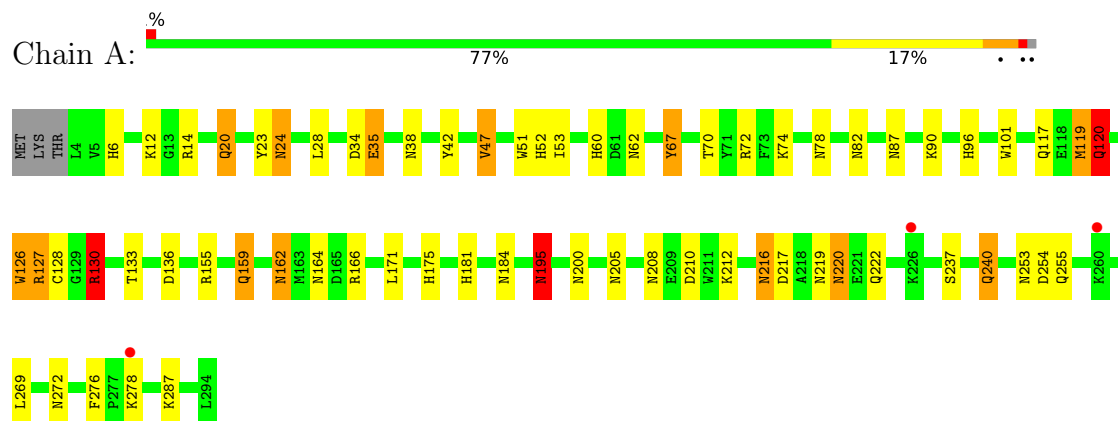
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	105	Total 105	O 105	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 C PEROXIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.00Å 77.30Å 51.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.10 7.00 – 2.11	Depositor EDS
% Data completeness (in resolution range)	79.0 (7.00-2.10) 74.9 (7.00-2.11)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 2.12Å)	Xtriage
Refinement program	XTALVIEW, X-PLOR 3.0	Depositor
R, R_{free}	0.189 , (Not available) 0.181 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.534	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 77.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2999	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	1.00	11/2404 (0.5%)	1.87	59/3252 (1.8%)

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

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	175	HIS	CD2-NE2	-7.16	1.29	1.37
1	A	47	VAL	CA-CB	6.79	1.63	1.54
1	A	6	HIS	CD2-NE2	-6.71	1.30	1.37
1	A	181	HIS	CD2-NE2	-6.62	1.30	1.37
1	A	130	ARG	CD-NE	6.55	1.55	1.46
1	A	96	HIS	CD2-NE2	-6.31	1.30	1.37
1	A	60	HIS	CD2-NE2	-6.27	1.30	1.37
1	A	6	HIS	CG-ND1	-5.48	1.32	1.38
1	A	175	HIS	CG-ND1	-5.47	1.32	1.38
1	A	52	HIS	CD2-NE2	-5.43	1.31	1.37
1	A	130	ARG	CZ-NH2	5.27	1.40	1.33

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	GLN	OE1-CD-NE2	-12.24	110.36	122.60
1	A	159	GLN	OE1-CD-NE2	-11.25	111.35	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	LYS	CA-C-O	10.09	132.30	120.70
1	A	20	GLN	OE1-CD-NE2	-9.04	113.56	122.60
1	A	205	ASN	OD1-CG-ND2	-8.53	114.07	122.60
1	A	162	ASN	N-CA-C	8.51	128.93	110.80
1	A	130	ARG	CG-CD-NE	-8.44	93.44	112.00
1	A	62	ASN	OD1-CG-ND2	-8.40	114.20	122.60
1	A	127	ARG	CB-CG-CD	-8.29	92.24	111.30
1	A	78	ASN	OD1-CG-ND2	-8.29	114.31	122.60
1	A	159	GLN	CG-CD-NE2	7.84	128.16	116.40
1	A	255	GLN	CG-CD-NE2	7.83	128.15	116.40
1	A	195	ASN	N-CA-C	7.81	121.63	112.72
1	A	120	GLN	N-CA-C	7.76	122.14	111.90
1	A	130	ARG	NE-CZ-NH1	-7.48	114.02	121.50
1	A	253	ASN	OD1-CG-ND2	-7.42	115.17	122.60
1	A	195	ASN	OD1-CG-ND2	-7.41	115.19	122.60
1	A	82	ASN	OD1-CG-ND2	-7.37	115.23	122.60
1	A	136	ASP	CA-CB-CG	7.29	119.89	112.60
1	A	208	ASN	OD1-CG-ND2	-7.01	115.59	122.60
1	A	14	ARG	O-C-N	-6.46	115.66	122.96
1	A	38	ASN	CA-CB-CG	-6.42	106.18	112.60
1	A	162	ASN	CA-C-O	6.40	129.66	120.51
1	A	240	GLN	OE1-CD-NE2	-6.35	116.25	122.60
1	A	117	GLN	OE1-CD-NE2	-6.32	116.28	122.60
1	A	222	GLN	OE1-CD-NE2	-6.31	116.29	122.60
1	A	181	HIS	CB-CG-CD2	-6.18	123.16	131.20
1	A	216	ASN	OD1-CG-ND2	-6.17	116.43	122.60
1	A	67	TYR	N-CA-C	6.14	118.51	111.02
1	A	162	ASN	CA-CB-CG	6.10	118.70	112.60
1	A	60	HIS	CB-CG-CD2	-5.97	123.44	131.20
1	A	210	ASP	CA-CB-CG	5.95	118.55	112.60
1	A	42	TYR	N-CA-C	5.91	120.33	113.18
1	A	276	PHE	CA-C-N	5.91	125.92	119.89
1	A	276	PHE	C-N-CA	5.91	125.92	119.89
1	A	90	LYS	CA-CB-CG	-5.89	102.31	114.10
1	A	51	TRP	CB-CG-CD1	-5.82	118.17	126.90
1	A	24	ASN	OD1-CG-ND2	-5.79	116.81	122.60
1	A	164	ASN	OD1-CG-ND2	-5.78	116.83	122.60
1	A	34	ASP	N-CA-C	5.73	120.11	113.18
1	A	254	ASP	CA-CB-CG	5.67	118.27	112.60
1	A	51	TRP	CG-CD2-CE3	5.57	139.47	133.90
1	A	126	TRP	CD2-CE2-CZ2	-5.57	116.83	122.40
1	A	184	ASN	OD1-CG-ND2	-5.55	117.05	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	220	ASN	OD1-CG-ND2	-5.52	117.08	122.60
1	A	200	ASN	OD1-CG-ND2	-5.49	117.11	122.60
1	A	87	ASN	OD1-CG-ND2	-5.43	117.17	122.60
1	A	133	THR	CA-C-N	5.43	125.40	120.03
1	A	133	THR	C-N-CA	5.43	125.40	120.03
1	A	175	HIS	CB-CG-CD2	-5.42	124.16	131.20
1	A	101	TRP	CE2-CD2-CG	-5.38	100.75	107.20
1	A	217	ASP	N-CA-C	5.26	118.80	112.38
1	A	119	MET	CA-C-N	5.24	129.79	122.08
1	A	119	MET	C-N-CA	5.24	129.79	122.08
1	A	166	ARG	CG-CD-NE	-5.22	100.51	112.00
1	A	195	ASN	CB-CG-ND2	5.17	124.16	116.40
1	A	117	GLN	CG-CD-NE2	5.13	124.10	116.40
1	A	52	HIS	O-C-N	-5.10	116.00	122.27
1	A	70	THR	N-CA-C	5.05	119.07	113.01

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	130	ARG	Sidechain

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	2340	511	2221	18	0
2	A	43	0	30	0	0
3	A	105	0	0	6	0
All	All	2488	511	2251	18	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 (18) 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:126:TRP:CZ2	3:A:326:HOH:O	2.38	0.77
1:A:130:ARG:CZ	3:A:442:HOH:O	2.42	0.68
1:A:20:GLN:HE22	1:A:287:LYS:H	1.40	0.67
1:A:130:ARG:NE	3:A:442:HOH:O	2.27	0.67
1:A:195:ASN:HD22	1:A:195:ASN:H	1.44	0.66
1:A:128:CYS:HA	3:A:326:HOH:O	1.95	0.65
1:A:67:TYR:HA	1:A:130:ARG:HG2	1.78	0.65
1:A:130:ARG:NH2	3:A:442:HOH:O	2.31	0.63
1:A:269:LEU:HA	1:A:272:ASN:ND2	2.26	0.50
1:A:195:ASN:H	1:A:195:ASN:ND2	2.09	0.50
1:A:237:SER:HA	1:A:240:GLN:HE21	1.78	0.48
1:A:119:MET:O	1:A:120:GLN:HG2	2.13	0.48
1:A:127:ARG:HD3	3:A:440:HOH:O	2.17	0.45
1:A:119:MET:C	1:A:120:GLN:HG2	2.42	0.43
1:A:155:ARG:O	1:A:159:GLN:HG3	2.18	0.43
1:A:35:GLU:H	1:A:35:GLU:CD	2.27	0.43
1:A:23:TYR:HD1	1:A:24:ASN:HD22	1.67	0.41
1:A:216:ASN:HD21	1:A:220:ASN:HB2	1.85	0.41

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	289/294 (98%)	283 (98%)	5 (2%)	1 (0%)	36	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	ASN

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	248/251 (99%)	236 (95%)	12 (5%)	23	23

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	35	GLU
1	A	47	VAL
1	A	53	ILE
1	A	72	ARG
1	A	74	LYS
1	A	120	GLN
1	A	171	LEU
1	A	195	ASN
1	A	212	LYS
1	A	219	ASN
1	A	278	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	24	ASN
1	A	78	ASN
1	A	195	ASN
1	A	208	ASN
1	A	240	GLN
1	A	292	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	A	295	1,3	50,50,50	2.33	27 (54%)	67,82,82	1.15	5 (7%)

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	295	1,3	-	2/14/54/54	-

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	295	HEM	C4D-ND	-4.32	1.32	1.40
2	A	295	HEM	FE-ND	4.30	2.08	1.94
2	A	295	HEM	FE-NB	3.94	2.07	1.94
2	A	295	HEM	FE-NC	3.74	2.07	1.95
2	A	295	HEM	C3C-C4C	-3.55	1.39	1.46
2	A	295	HEM	FE-NA	3.51	2.06	1.95
2	A	295	HEM	C1B-NB	-3.49	1.34	1.40
2	A	295	HEM	C4A-NA	-3.43	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	295	HEM	CBC-CAC	3.41	1.46	1.30
2	A	295	HEM	CBB-CAB	3.36	1.46	1.30
2	A	295	HEM	C1A-C2A	-2.99	1.38	1.44
2	A	295	HEM	C3C-C2C	2.95	1.43	1.37
2	A	295	HEM	C1C-C2C	-2.84	1.39	1.45
2	A	295	HEM	C4C-NC	-2.84	1.34	1.39
2	A	295	HEM	O2A-CGA	-2.83	1.21	1.30
2	A	295	HEM	C4D-C3D	-2.79	1.40	1.45
2	A	295	HEM	C1A-NA	-2.75	1.34	1.39
2	A	295	HEM	C1B-C2B	-2.72	1.39	1.44
2	A	295	HEM	C1C-NC	-2.68	1.34	1.39
2	A	295	HEM	CAB-C3B	-2.57	1.40	1.47
2	A	295	HEM	O2D-CGD	-2.49	1.22	1.30
2	A	295	HEM	C1D-C2D	-2.40	1.39	1.44
2	A	295	HEM	C3B-C2B	2.22	1.41	1.37
2	A	295	HEM	C3B-C4B	-2.21	1.40	1.44
2	A	295	HEM	C1D-ND	-2.12	1.34	1.38
2	A	295	HEM	CAC-C3C	-2.09	1.41	1.47
2	A	295	HEM	C4B-NB	-2.04	1.34	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	295	HEM	C3C-C2C-C1C	-2.46	104.72	107.05
2	A	295	HEM	C3B-C2B-C1B	-2.42	104.59	106.41
2	A	295	HEM	O2D-CGD-CBD	2.27	121.17	114.00
2	A	295	HEM	CMD-C2D-C1D	2.24	128.53	125.03
2	A	295	HEM	C2B-C1B-NB	2.20	112.37	109.84

There are no chirality outliers.

All (2) torsion outliers are listed below:

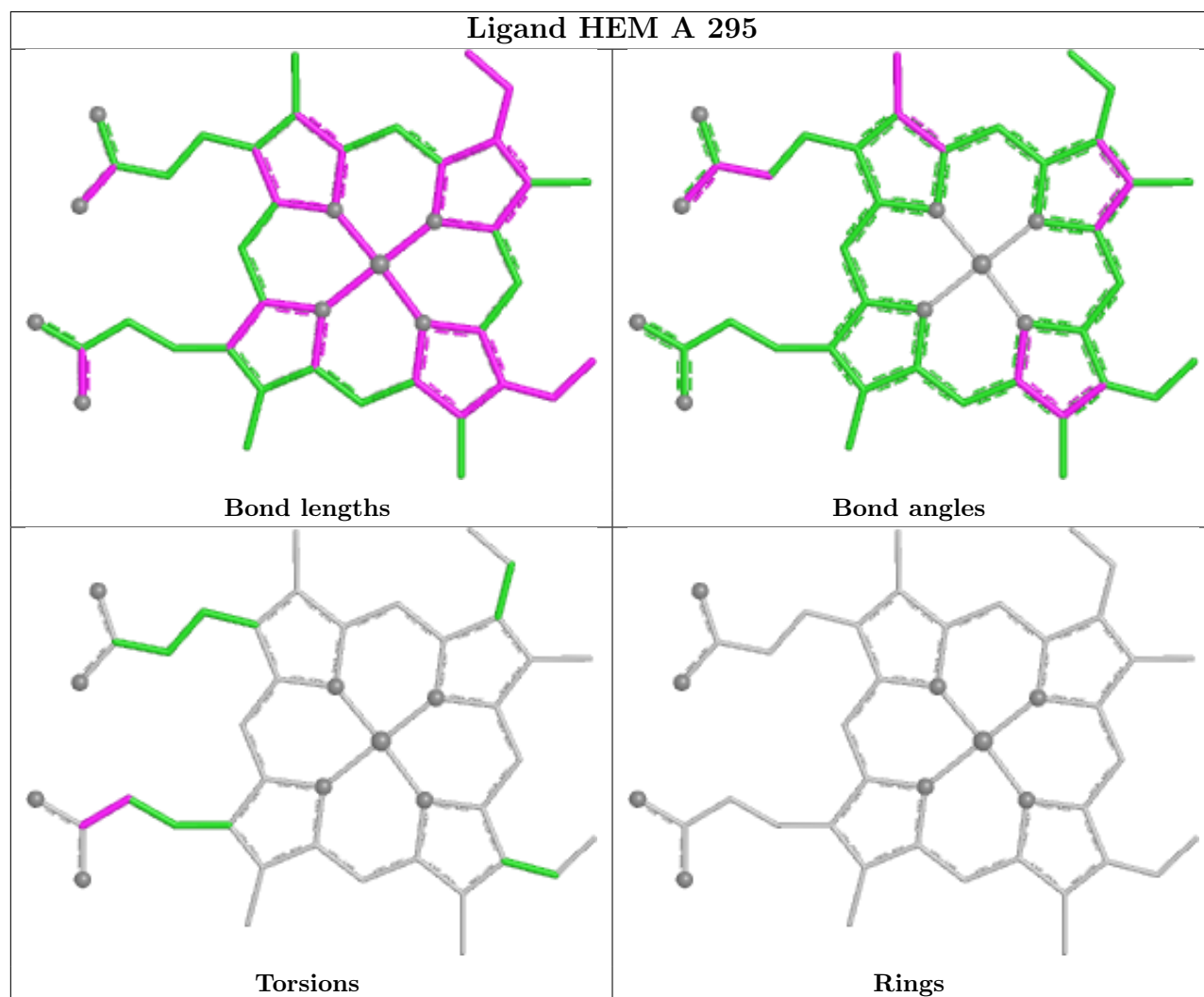
Mol	Chain	Res	Type	Atoms
2	A	295	HEM	CAA-CBA-CGA-O2A
2	A	295	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	291/294 (98%)	-0.58	3 (1%) 79 81	4, 13, 28, 43	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	LYS	4.2
1	A	226	LYS	2.3
1	A	278	LYS	2.2

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 oligosaccharides in this entry.

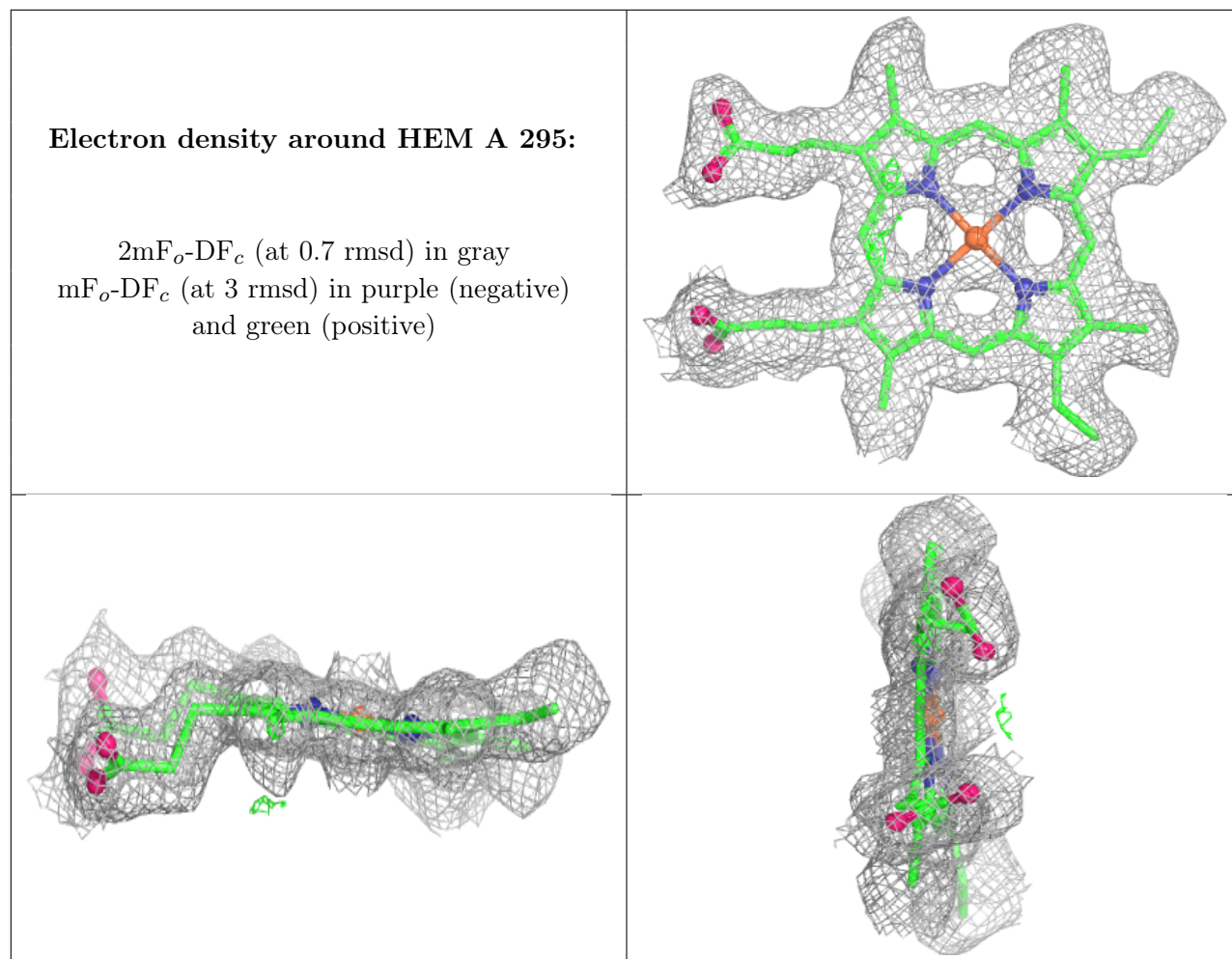
6.4 Ligands [i](#)

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	HEM	A	295	43/43	0.98	0.05	3,9,12,16	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.