



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:39 PM UTC

PDB ID : 3E5J / pdb_00003e5j
Title : Crystal structure of CYP105P1 wild-type ligand-free form
Authors : Xu, L.H.; Fushinobu, S.; Ikeda, H.; Wakagi, T.; Shoun, H.
Deposited on : 2008-08-14
Resolution : 1.95 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

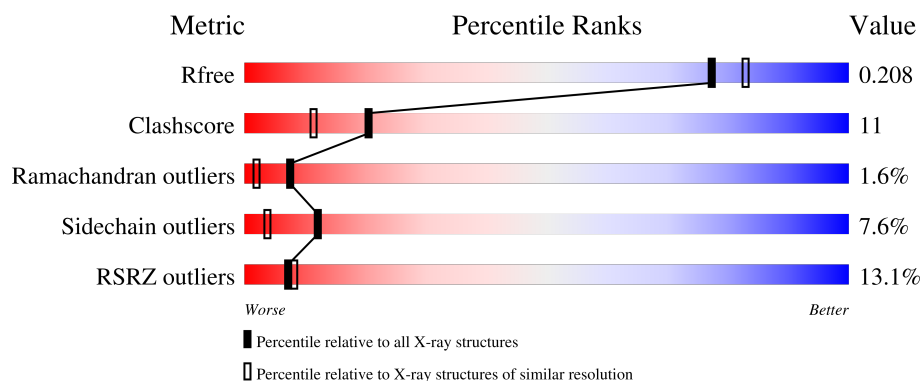
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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 $\leq 5\%$. 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	403	13% 80% 12% ...

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.

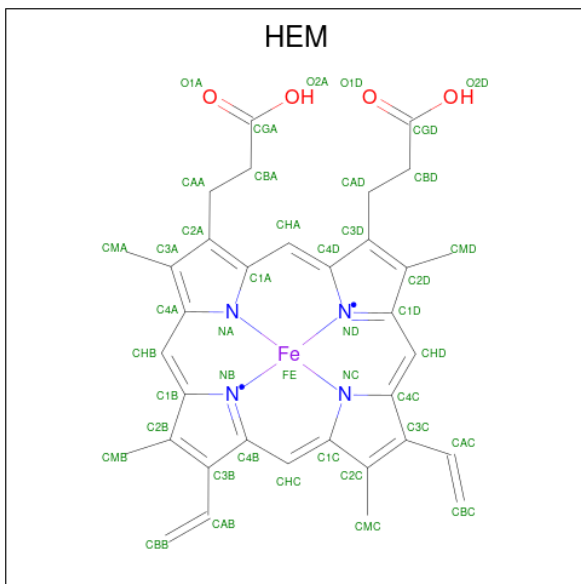
- Molecule 1 is a protein called Cytochrome P450 (Cytochrome P450 hydroxylase).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3019	1906	540	562	11			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	387	ILE	MET	engineered mutation	UNP Q93H81
A	400	HIS	-	expression tag	UNP Q93H81
A	401	HIS	-	expression tag	UNP Q93H81
A	402	HIS	-	expression tag	UNP Q93H81
A	403	HIS	-	expression tag	UNP Q93H81

- 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		

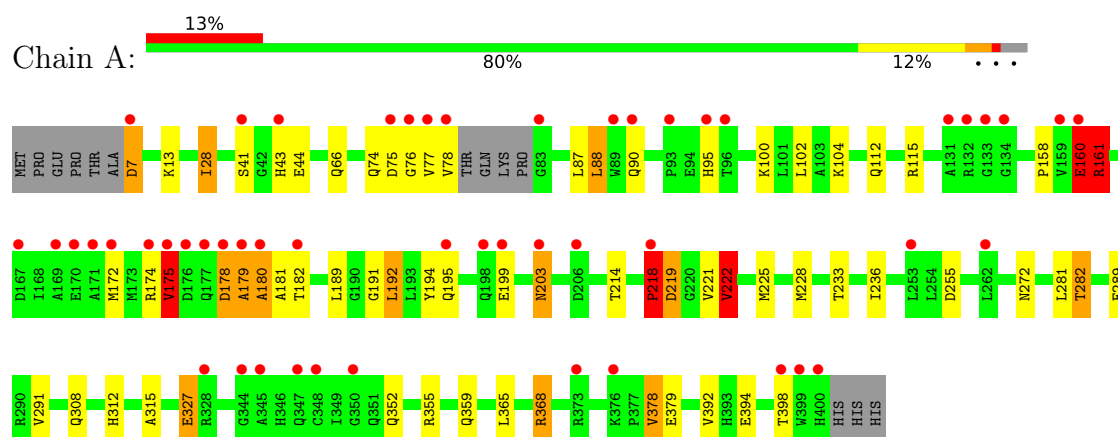
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	487	Total	O	0	0
			487	487		

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: Cytochrome P450 (Cytochrome P450 hydroxylase)



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	88.40Å 88.40Å 193.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.75 – 1.95 38.75 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (38.75-1.95) 99.8 (38.75-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.27 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.211 0.189 , 0.208	Depositor DCC
R_{free} test set	2874 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3549	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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	0.91	3/3080 (0.1%)	0.98	9/4187 (0.2%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	ALA	C-N	17.05	1.57	1.33
1	A	179	ALA	CA-C	7.31	1.62	1.52
1	A	180	ALA	N-CA	6.84	1.55	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	218	PRO	CA-C-N	7.37	134.97	121.70
1	A	218	PRO	C-N-CA	7.37	134.97	121.70
1	A	160	GLU	CA-C-N	7.31	134.87	121.70
1	A	160	GLU	C-N-CA	7.31	134.87	121.70
1	A	179	ALA	CA-C-O	6.62	129.98	120.51
1	A	222	VAL	N-CA-C	6.26	112.91	106.21
1	A	378	VAL	CB-CA-C	-6.12	104.03	112.04
1	A	378	VAL	N-CA-C	5.17	116.51	110.62
1	A	160	GLU	N-CA-C	5.01	121.47	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	160	GLU	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	3019	0	3000	65	0
2	A	43	0	30	5	0
3	A	487	0	0	12	0
All	All	3549	0	3030	68	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 11.

All (68) 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:218:PRO:HB2	1:A:219:ASP:HB2	1.28	1.14
1:A:77:VAL:HG12	1:A:78:VAL:HA	1.36	1.08
1:A:160:GLU:HB2	1:A:161:ARG:HB2	1.43	1.00
1:A:194:TYR:HD1	1:A:228:MET:CE	1.81	0.94
1:A:218:PRO:CB	1:A:219:ASP:HB2	1.97	0.93
1:A:87:LEU:H	1:A:90:GLN:HE21	1.16	0.92
1:A:272:ASN:OD1	3:A:1868:HOH:O	1.95	0.84
1:A:112:GLN:HE21	1:A:115:ARG:HH12	1.26	0.82
1:A:160:GLU:CB	1:A:161:ARG:HB2	2.12	0.80
1:A:77:VAL:CG1	1:A:78:VAL:HA	2.11	0.79
1:A:7:ASP:N	1:A:7:ASP:OD1	2.16	0.79
1:A:194:TYR:HD1	1:A:228:MET:HE1	1.49	0.76
1:A:88:LEU:O	3:A:1812:HOH:O	2.03	0.76
1:A:66:GLN:CD	1:A:291:VAL:HG21	2.11	0.76
1:A:95:HIS:HE1	2:A:1408:HEM:O1D	1.73	0.72
1:A:194:TYR:CD1	1:A:228:MET:CE	2.71	0.69
1:A:41:SER:OG	1:A:43:HIS:HD2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:GLN:CD	3:A:1699:HOH:O	2.37	0.67
1:A:194:TYR:CD1	1:A:228:MET:HE1	2.28	0.67
1:A:222:VAL:O	1:A:222:VAL:HG23	1.95	0.66
1:A:194:TYR:HD1	1:A:228:MET:HE2	1.58	0.65
1:A:158:PRO:O	1:A:161:ARG:HB3	1.96	0.65
1:A:112:GLN:NE2	1:A:115:ARG:HH12	1.95	0.64
1:A:77:VAL:HG22	1:A:172:MET:HE3	1.80	0.64
2:A:1408:HEM:HBB2	2:A:1408:HEM:HHC	1.80	0.64
1:A:192:LEU:HD22	3:A:1675:HOH:O	2.00	0.62
1:A:7:ASP:N	1:A:44:GLU:OE1	2.33	0.62
1:A:312:HIS:CD2	1:A:315:ALA:H	2.20	0.60
1:A:312:HIS:HD2	1:A:315:ALA:H	1.48	0.59
1:A:66:GLN:CD	1:A:291:VAL:CG2	2.75	0.59
1:A:194:TYR:CD1	1:A:228:MET:HE2	2.36	0.59
1:A:327:GLU:HG2	3:A:1881:HOH:O	2.03	0.58
1:A:77:VAL:HG11	3:A:1890:HOH:O	2.02	0.58
1:A:222:VAL:O	1:A:222:VAL:CG2	2.51	0.58
1:A:218:PRO:HB2	1:A:219:ASP:CB	2.19	0.56
1:A:112:GLN:HE21	1:A:115:ARG:NH1	2.02	0.56
1:A:219:ASP:HB3	3:A:1786:HOH:O	2.06	0.55
1:A:160:GLU:HG3	3:A:1672:HOH:O	2.08	0.54
1:A:95:HIS:CE1	2:A:1408:HEM:O1D	2.56	0.54
1:A:218:PRO:CA	1:A:219:ASP:HB2	2.38	0.54
1:A:327:GLU:H	1:A:327:GLU:CD	2.16	0.54
2:A:1408:HEM:HMC2	2:A:1408:HEM:HBC2	1.90	0.53
1:A:43:HIS:CE1	1:A:289:GLU:OE1	2.62	0.52
1:A:255:ASP:OD1	3:A:1870:HOH:O	2.18	0.51
2:A:1408:HEM:HBC2	2:A:1408:HEM:CMC	2.41	0.50
1:A:174:ARG:O	1:A:175:VAL:C	2.54	0.50
1:A:66:GLN:OE1	1:A:291:VAL:HG21	2.11	0.50
1:A:199:GLU:OE2	1:A:203:ASN:ND2	2.44	0.50
1:A:88:LEU:HD22	1:A:233:THR:HG23	1.94	0.50
1:A:66:GLN:OE1	1:A:291:VAL:CG2	2.60	0.49
1:A:291:VAL:HG22	1:A:308:GLN:HE21	1.76	0.49
1:A:312:HIS:HE1	3:A:1641:HOH:O	1.96	0.49
1:A:368:ARG:HD2	3:A:1473:HOH:O	2.12	0.49
1:A:74:GLN:HG2	1:A:236:ILE:HG23	1.93	0.48
1:A:191:GLY:O	1:A:195:GLN:HG3	2.14	0.48
1:A:158:PRO:HD2	1:A:161:ARG:HG2	1.96	0.46
1:A:41:SER:OG	1:A:43:HIS:CD2	2.64	0.46
1:A:160:GLU:CA	1:A:161:ARG:HB2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ASP:O	1:A:179:ALA:C	2.58	0.45
1:A:180:ALA:O	1:A:181:ALA:C	2.59	0.45
1:A:76:GLY:HA2	1:A:182:THR:HG22	2.01	0.43
1:A:174:ARG:O	1:A:175:VAL:O	2.37	0.43
1:A:179:ALA:O	1:A:182:THR:HB	2.18	0.43
1:A:281:LEU:O	1:A:282:THR:C	2.61	0.43
1:A:225:MET:HE2	1:A:225:MET:HA	2.02	0.42
1:A:7:ASP:HA	3:A:1858:HOH:O	2.20	0.41
1:A:352:GLN:NE2	1:A:355:ARG:HH11	2.19	0.41
1:A:28:ILE:HG21	1:A:28:ILE:HD13	1.60	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	386/403 (96%)	367 (95%)	13 (3%)	6 (2%)	7 2

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	175	VAL
1	A	219	ASP
1	A	161	ARG
1	A	75	ASP
1	A	282	THR
1	A	218	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	316/328 (96%)	292 (92%)	24 (8%)	12 4

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASP
1	A	13	LYS
1	A	28	ILE
1	A	88	LEU
1	A	100	LYS
1	A	102	LEU
1	A	104	LYS
1	A	161	ARG
1	A	175	VAL
1	A	178	ASP
1	A	189	LEU
1	A	192	LEU
1	A	203	ASN
1	A	214	THR
1	A	221	VAL
1	A	222	VAL
1	A	327	GLU
1	A	365	LEU
1	A	368	ARG
1	A	378	VAL
1	A	379	GLU
1	A	392	VAL
1	A	394	GLU
1	A	398	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS

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Mol	Chain	Res	Type
1	A	90	GLN
1	A	95	HIS
1	A	112	GLN
1	A	119	GLN
1	A	285	GLN
1	A	308	GLN
1	A	312	HIS
1	A	352	GLN
1	A	393	HIS

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	1408	1	50,50,50	1.77	9 (18%)	67,82,82	1.46	11 (16%)

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	1408	1	-	2/14/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1408	HEM	C3D-C2D	6.27	1.50	1.36
2	A	1408	HEM	FE-ND	5.29	2.11	1.94
2	A	1408	HEM	CAB-C3B	3.24	1.56	1.47
2	A	1408	HEM	CMC-C2C	3.00	1.56	1.50
2	A	1408	HEM	CAC-C3C	2.72	1.54	1.47
2	A	1408	HEM	C2A-C3A	-2.30	1.32	1.38
2	A	1408	HEM	O1A-CGA	2.25	1.29	1.22
2	A	1408	HEM	CMD-C2D	2.24	1.55	1.50
2	A	1408	HEM	CMA-C3A	2.20	1.55	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1408	HEM	C4D-ND-C1D	5.25	111.43	105.21
2	A	1408	HEM	C3B-C2B-C1B	3.33	108.91	106.41
2	A	1408	HEM	C4C-C3C-C2C	3.02	109.43	106.81
2	A	1408	HEM	CBD-CAD-C3D	-2.50	105.61	112.53
2	A	1408	HEM	CHD-C1D-ND	2.41	127.01	124.42
2	A	1408	HEM	CMB-C2B-C3B	-2.39	122.65	128.43
2	A	1408	HEM	CHD-C4C-NC	2.32	126.97	124.45
2	A	1408	HEM	CMB-C2B-C1B	2.18	128.44	125.03
2	A	1408	HEM	CAD-CBD-CGD	-2.18	107.89	113.67
2	A	1408	HEM	C1C-CHC-C4B	-2.10	121.55	126.02
2	A	1408	HEM	C1D-C2D-C3D	-2.05	104.82	106.98

There are no chirality outliers.

All (2) torsion outliers are listed below:

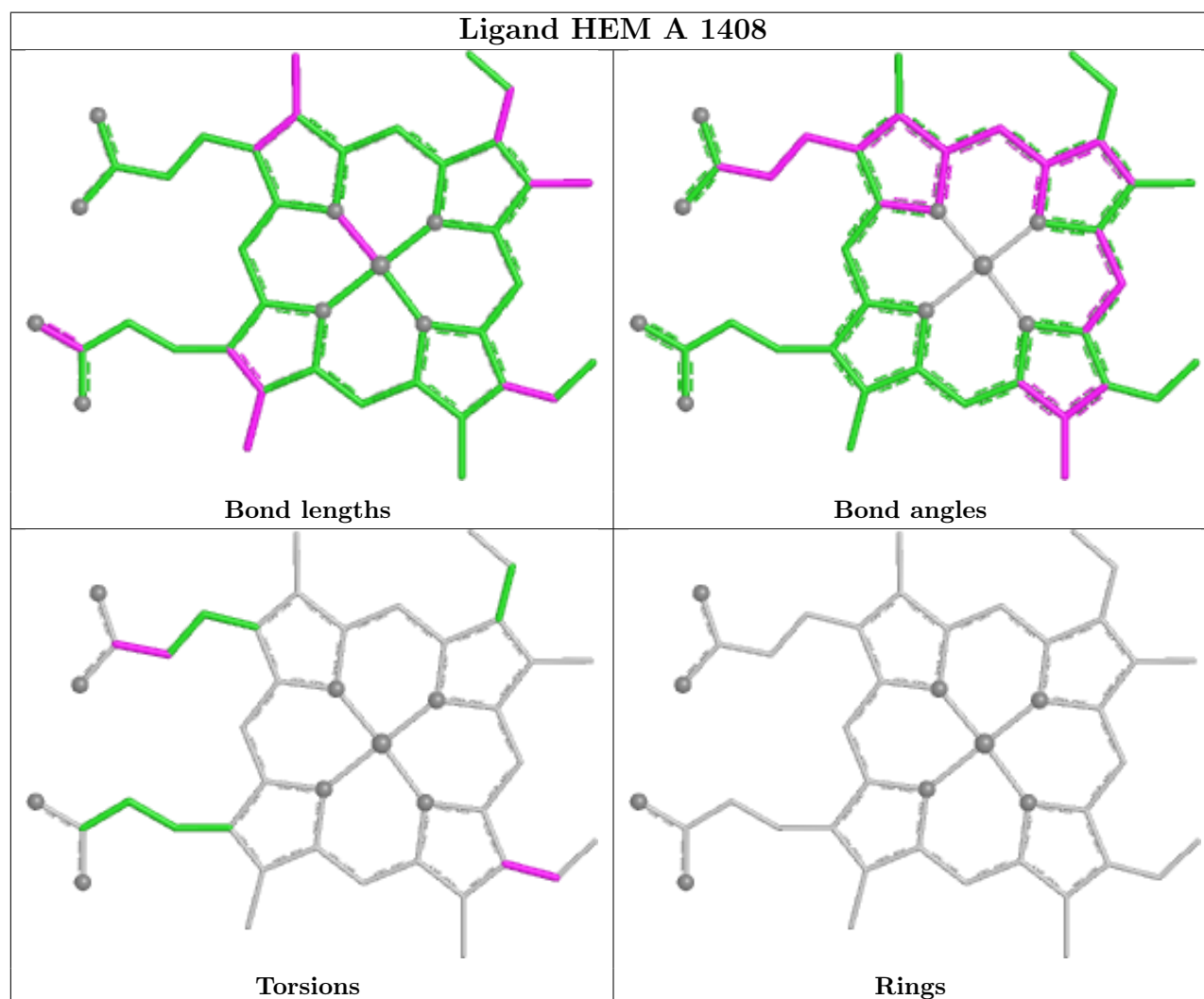
Mol	Chain	Res	Type	Atoms
2	A	1408	HEM	C4B-C3B-CAB-CBB
2	A	1408	HEM	CAD-CBD-CGD-O1D

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1408	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 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, 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	390/403 (96%)	0.82	51 (13%) 7 8	20, 28, 42, 51	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	169	ALA	10.2
1	A	180	ALA	7.0
1	A	171	ALA	6.6
1	A	78	VAL	5.5
1	A	133	GLY	5.2
1	A	175	VAL	5.1
1	A	179	ALA	4.6
1	A	89	TRP	4.3
1	A	76	GLY	3.9
1	A	177	GLN	3.9
1	A	170	GLU	3.8
1	A	75	ASP	3.8
1	A	159	VAL	3.8
1	A	167	ASP	3.7
1	A	134	GLY	3.7
1	A	83	GLY	3.5
1	A	176	ASP	3.5
1	A	218	PRO	3.5
1	A	93	PRO	3.2
1	A	172	MET	3.2
1	A	131	ALA	3.2
1	A	43	HIS	3.2
1	A	178	ASP	3.2
1	A	77	VAL	3.0
1	A	400	HIS	3.0
1	A	348	CYS	2.9
1	A	160	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	7	ASP	2.9
1	A	199	GLU	2.8
1	A	195	GLN	2.8
1	A	373	ARG	2.7
1	A	203	ASN	2.6
1	A	345	ALA	2.6
1	A	344	GLY	2.6
1	A	376	LYS	2.6
1	A	95	HIS	2.5
1	A	132	ARG	2.4
1	A	262	LEU	2.4
1	A	206	ASP	2.4
1	A	182	THR	2.4
1	A	347	GLN	2.3
1	A	253	LEU	2.3
1	A	96	THR	2.3
1	A	398	THR	2.3
1	A	328	ARG	2.3
1	A	174	ARG	2.2
1	A	90	GLN	2.2
1	A	41	SER	2.1
1	A	350	GLY	2.1
1	A	198	GLN	2.1
1	A	399	TRP	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](#)

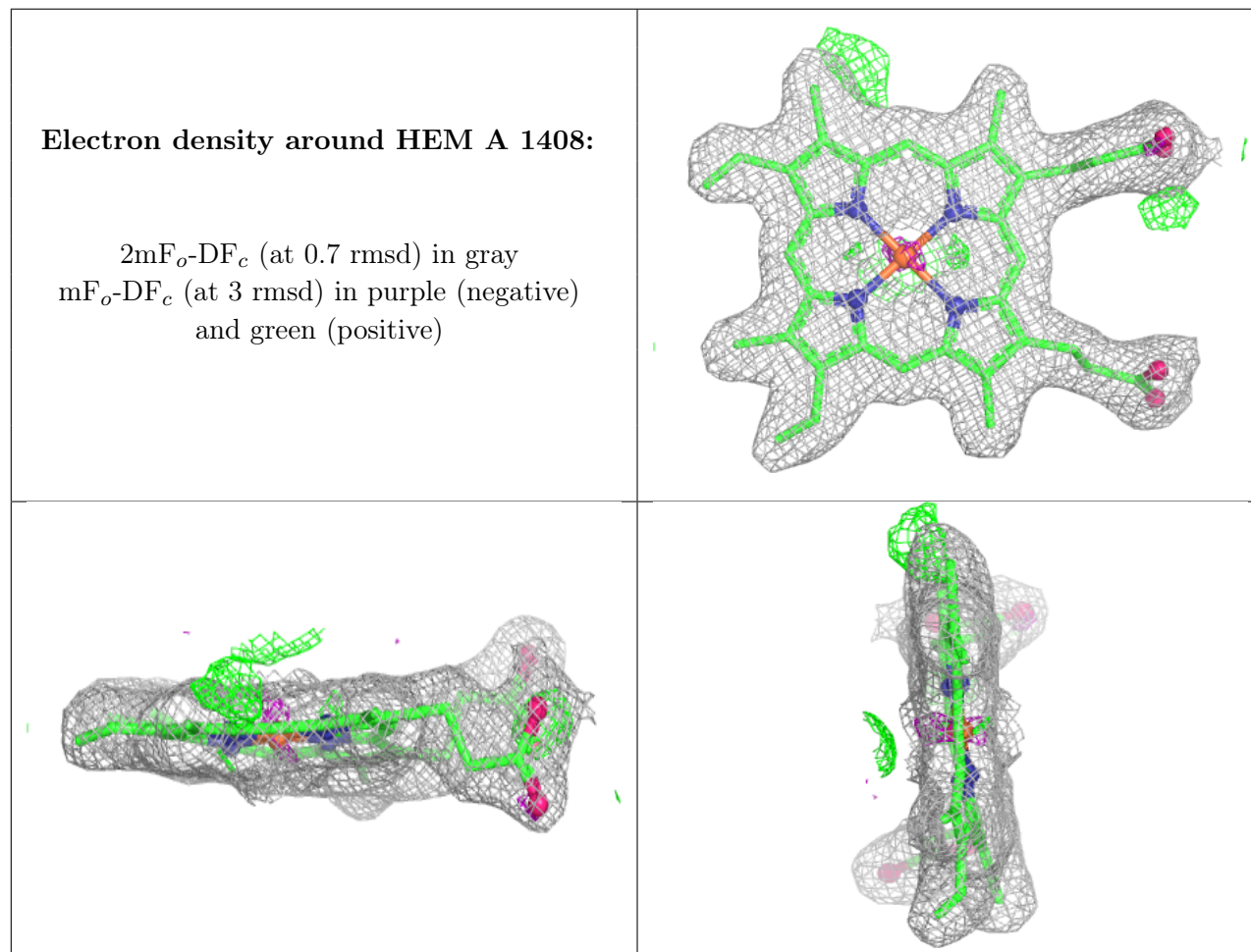
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	HEM	A	1408	43/43	0.98	0.08	26,29,36,43	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 ⓘ

There are no such residues in this entry.