



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 03:59 pm BST

PDB ID : 1PHD
Title : CRYSTAL STRUCTURES OF METYRAPONE-AND PHENYLIMIDAZOL
E-INHIBITED COMPLEXES OF CYTOCHROME P450-CAM
Authors : Poulos, T.L.
Deposited on : 1992-07-27
Resolution : 1.60 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

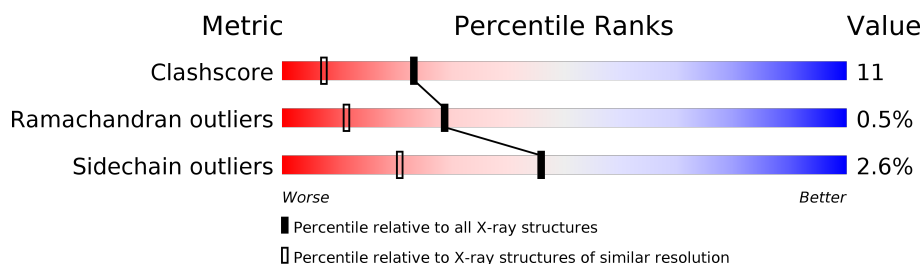
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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))
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	414	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PIW	A	422	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3462 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-CAM.

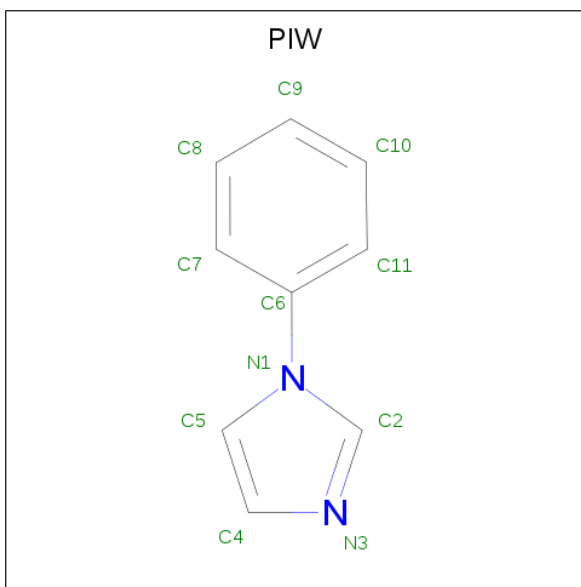
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3204	2030	559	597	18			

- 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	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 1-phenyl-1H-imidazole (three-letter code: PIW) (formula: $C_9H_8N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			11	9	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	204	Total	O	0	0
			204	204		

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.67Å 103.90Å 36.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.60	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.190 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3462	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.28	10/3283 (0.3%)	1.81	71/4461 (1.6%)

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	12

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	276	GLU	CD-OE1	10.26	1.36	1.25
1	A	286	GLU	CD-OE1	-7.37	1.17	1.25
1	A	237	GLU	CD-OE1	6.97	1.33	1.25
1	A	133	GLU	CD-OE2	-6.71	1.18	1.25
1	A	251	ASP	C-O	6.51	1.35	1.23
1	A	349	THR	CB-OG1	5.49	1.54	1.43
1	A	154	TYR	CG-CD2	5.43	1.46	1.39
1	A	266	LYS	C-O	5.18	1.33	1.23
1	A	156	GLU	C-O	5.16	1.33	1.23
1	A	365	ARG	CZ-NH1	5.01	1.39	1.33

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	ARG	NE-CZ-NH1	15.31	127.95	120.30
1	A	280	ARG	NE-CZ-NH2	-15.19	112.70	120.30
1	A	143	ARG	NE-CZ-NH1	15.05	127.83	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	ARG	CD-NE-CZ	13.93	143.10	123.60
1	A	365	ARG	CD-NE-CZ	13.90	143.07	123.60
1	A	280	ARG	NE-CZ-NH1	13.59	127.10	120.30
1	A	365	ARG	NE-CZ-NH2	13.12	126.86	120.30
1	A	271	ARG	NE-CZ-NH1	10.84	125.72	120.30
1	A	161	ARG	NE-CZ-NH2	-10.13	115.23	120.30
1	A	67	ARG	NE-CZ-NH1	9.86	125.23	120.30
1	A	195	GLU	CA-CB-CG	9.71	134.76	113.40
1	A	109	ARG	NE-CZ-NH1	9.65	125.12	120.30
1	A	67	ARG	NE-CZ-NH2	-9.64	115.48	120.30
1	A	161	ARG	NE-CZ-NH1	9.23	124.92	120.30
1	A	130	ARG	NE-CZ-NH1	8.25	124.42	120.30
1	A	148	CYS	C-N-CA	8.14	142.04	121.70
1	A	130	ARG	NE-CZ-NH2	-8.11	116.24	120.30
1	A	143	ARG	NE-CZ-NH2	-7.72	116.44	120.30
1	A	20	GLU	CA-CB-CG	7.61	130.14	113.40
1	A	25	ASP	CB-CG-OD1	7.56	125.10	118.30
1	A	365	ARG	NE-CZ-NH1	-7.46	116.57	120.30
1	A	149	ASN	N-CA-CB	6.95	123.11	110.60
1	A	271	ARG	NE-CZ-NH2	-6.81	116.89	120.30
1	A	263	PHE	CB-CG-CD2	-6.70	116.11	120.80
1	A	236	ASP	CB-CG-OD1	-6.68	112.29	118.30
1	A	240	ARG	NE-CZ-NH1	6.67	123.64	120.30
1	A	211	ARG	NE-CZ-NH2	-6.41	117.09	120.30
1	A	279	GLU	CA-CB-CG	6.37	127.41	113.40
1	A	133	GLU	OE1-CD-OE2	-6.23	115.83	123.30
1	A	342	ARG	NE-CZ-NH1	-6.16	117.22	120.30
1	A	79	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	A	172	GLU	CG-CD-OE2	5.98	130.26	118.30
1	A	154	TYR	CB-CG-CD1	5.96	124.58	121.00
1	A	241	MET	N-CA-CB	5.95	121.32	110.60
1	A	407	ASP	CB-CG-OD1	5.89	123.60	118.30
1	A	304	ASP	CB-CG-OD1	5.85	123.57	118.30
1	A	290	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	108	GLN	CA-CB-CG	5.79	126.13	113.40
1	A	366	GLU	OE1-CD-OE2	-5.78	116.37	123.30
1	A	73	GLU	OE1-CD-OE2	5.73	130.18	123.30
1	A	269	GLU	CG-CD-OE2	-5.72	106.86	118.30
1	A	211	ARG	CA-CB-CG	5.71	125.97	113.40
1	A	154	TYR	CB-CG-CD2	-5.69	117.59	121.00
1	A	261	MET	CG-SD-CE	5.68	109.28	100.20
1	A	127	LEU	CA-CB-CG	5.62	128.22	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	ARG	CB-CG-CD	5.60	126.17	111.60
1	A	277	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	A	179	TYR	CB-CG-CD2	-5.47	117.72	121.00
1	A	251	ASP	CB-CA-C	5.44	121.29	110.40
1	A	112	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	210	GLN	CA-CB-CG	5.40	125.28	113.40
1	A	43	ALA	N-CA-CB	5.39	117.64	110.10
1	A	280	ARG	CD-NE-CZ	5.38	131.14	123.60
1	A	271	ARG	CD-NE-CZ	5.34	131.08	123.60
1	A	196	ALA	N-CA-CB	5.32	117.55	110.10
1	A	158	PHE	CB-CA-C	5.29	120.97	110.40
1	A	400	GLN	CA-CB-CG	5.28	125.01	113.40
1	A	297	ASP	CB-CA-C	5.27	120.94	110.40
1	A	327	LEU	CA-CB-CG	5.26	127.40	115.30
1	A	47	GLU	CG-CD-OE2	-5.25	107.79	118.30
1	A	191	MET	CA-CB-CG	5.25	122.22	113.30
1	A	79	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	A	212	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	A	125	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	209	GLU	CA-CB-CG	5.14	124.71	113.40
1	A	329	GLU	CA-CB-CG	5.11	124.64	113.40
1	A	108	GLN	CB-CG-CD	5.11	124.87	111.60
1	A	92	ALA	N-CA-CB	5.09	117.23	110.10
1	A	96	TYR	N-CA-CB	-5.09	101.44	110.60
1	A	261	MET	CA-CB-CG	-5.09	104.65	113.30
1	A	148	CYS	O-C-N	-5.08	114.57	122.70

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	GLN	Mainchain
1	A	148	CYS	Mainchain
1	A	149	ASN	Mainchain
1	A	212	ARG	Sidechain
1	A	240	ARG	Sidechain
1	A	250	LEU	Mainchain
1	A	251	ASP	Mainchain
1	A	271	ARG	Sidechain
1	A	280	ARG	Sidechain
1	A	284	ALA	Mainchain
1	A	342	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	95	ALA	Mainchain

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	3204	0	3144	72	0
2	A	43	0	30	3	0
3	A	11	0	8	4	0
4	A	204	0	0	7	0
All	All	3462	0	3182	73	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 (73) 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:183:GLN:HE22	1:A:188:ASP:HB2	1.54	0.71
1:A:108:GLN:HE22	1:A:354:SER:HB2	1.56	0.70
1:A:121:MET:HB2	1:A:122:PRO:HD3	1.77	0.67
1:A:56:THR:O	1:A:61:GLY:HA2	1.94	0.67
1:A:158:PHE:HB3	1:A:159:PRO:HD3	1.78	0.66
1:A:15:PRO:HG2	1:A:18:VAL:HG23	1.76	0.66
1:A:350:PHE:HB3	1:A:357:CYS:HB3	1.79	0.65
1:A:328:ASP:HB3	1:A:331:GLU:HG3	1.79	0.65
1:A:181:THR:CG2	1:A:251:ASP:HB2	2.28	0.64
1:A:14:LEU:HD11	1:A:18:VAL:HG11	1.79	0.62
1:A:15:PRO:HG2	1:A:18:VAL:CG2	2.32	0.59
1:A:14:LEU:HD11	1:A:18:VAL:CG1	2.32	0.59
1:A:203:TYR:O	1:A:206:PRO:HD2	2.01	0.59
1:A:127:LEU:HD11	1:A:166:LEU:HD13	1.88	0.55
1:A:134:LEU:HD23	1:A:162:ILE:HG13	1.90	0.54
1:A:276:GLU:C	1:A:278:PRO:HD3	2.29	0.54
1:A:395:ILE:HG21	3:A:422:PIW:H9	1.90	0.53
1:A:158:PHE:CB	1:A:159:PRO:HD3	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ALA:O	1:A:119:VAL:HG22	2.10	0.52
1:A:158:PHE:CE1	1:A:162:ILE:HD11	2.44	0.51
1:A:201:TYR:O	1:A:205:ILE:HG13	2.11	0.51
1:A:282:PRO:HD2	4:A:661:HOH:O	2.11	0.51
1:A:205:ILE:HB	1:A:206:PRO:HD3	1.93	0.51
1:A:181:THR:HG21	1:A:251:ASP:HB2	1.92	0.50
1:A:266:LYS:HD2	1:A:383:ILE:CD1	2.41	0.50
1:A:39:GLN:NE2	1:A:39:GLN:H	2.10	0.50
1:A:208:ILE:O	1:A:212:ARG:HG3	2.12	0.50
1:A:209:GLU:O	1:A:213:GLN:HG3	2.11	0.49
1:A:30:ASN:ND2	4:A:555:HOH:O	2.44	0.49
1:A:110:GLN:NE2	1:A:229:ASN:HA	2.28	0.49
1:A:247:VAL:HG12	3:A:422:PIW:H7	1.95	0.49
1:A:90:ARG:O	1:A:94:GLU:HG3	2.13	0.49
1:A:183:GLN:NE2	1:A:188:ASP:HB2	2.25	0.49
1:A:274:LEU:HD21	1:A:284:ALA:HB2	1.94	0.48
1:A:358:LEU:HD12	2:A:417:HEM:HMD1	1.96	0.48
1:A:261:MET:HA	1:A:261:MET:HE2	1.95	0.48
1:A:266:LYS:HD2	1:A:383:ILE:HD11	1.96	0.47
1:A:200:LEU:O	1:A:203:TYR:HB3	2.14	0.47
1:A:149:ASN:ND2	1:A:402:LEU:H	2.12	0.47
1:A:250:LEU:O	1:A:254:VAL:HG21	2.15	0.47
1:A:138:LEU:HD23	1:A:158:PHE:HB2	1.97	0.47
1:A:185:THR:C	1:A:187:PRO:HD3	2.35	0.46
1:A:328:ASP:HB3	1:A:331:GLU:CG	2.43	0.46
1:A:319:LEU:O	1:A:321:PRO:HD3	2.16	0.46
1:A:100:PRO:O	1:A:355:HIS:HE1	1.99	0.46
1:A:192:THR:OG1	1:A:195:GLU:HG2	2.16	0.45
2:A:417:HEM:C4C	3:A:422:PIW:H4	2.51	0.45
1:A:169:LEU:HD21	1:A:220:ILE:CD1	2.48	0.44
1:A:193:PHE:HB3	4:A:690:HOH:O	2.16	0.44
1:A:236:ASP:O	1:A:240:ARG:HG3	2.18	0.44
1:A:332:ASN:O	1:A:335:PRO:HD3	2.17	0.44
1:A:99:ILE:HD12	1:A:240:ARG:HB2	1.99	0.44
1:A:169:LEU:HD21	1:A:220:ILE:HD12	1.99	0.43
1:A:31:PRO:HA	4:A:502:HOH:O	2.17	0.43
1:A:170:PRO:HG2	1:A:173:ASP:OD2	2.19	0.43
1:A:50:VAL:CG1	1:A:54:VAL:HG11	2.48	0.43
1:A:49:ASN:H	1:A:49:ASN:HD22	1.67	0.43
1:A:318:ILE:HD13	1:A:320:LEU:HD21	2.00	0.42
1:A:382:SER:HB2	4:A:608:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:TYR:CD1	1:A:105:PRO:HD2	2.55	0.42
1:A:111:PHE:HB3	1:A:241:MET:HE2	2.02	0.42
1:A:247:VAL:CG1	3:A:422:PIW:H7	2.50	0.42
1:A:112:ARG:NH1	2:A:417:HEM:O1D	2.44	0.42
1:A:262:GLU:OE2	1:A:389:ILE:HG21	2.20	0.42
1:A:63:TRP:O	1:A:318:ILE:HA	2.19	0.42
1:A:12:ALA:HB1	1:A:13:PRO:HD2	2.02	0.41
1:A:139:ILE:HG12	1:A:374:TRP:CE3	2.55	0.41
1:A:72:ARG:O	1:A:76:GLU:HG3	2.21	0.41
1:A:122:PRO:HD2	4:A:701:HOH:O	2.21	0.41
1:A:290:ARG:HD3	1:A:345:VAL:HG13	2.03	0.41
1:A:181:THR:HG22	1:A:251:ASP:HB2	2.00	0.40
1:A:72:ARG:NH1	1:A:331:GLU:OE1	2.42	0.40
1:A:361:HIS:HB2	4:A:560:HOH:O	2.22	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	403/414 (97%)	382 (95%)	19 (5%)	2 (0%)	29 11

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	GLY
1	A	150	PHE

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	349/358 (98%)	340 (97%)	9 (3%)	46 21

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	49	ASN
1	A	56	THR
1	A	86	PRO
1	A	108	GLN
1	A	149	ASN
1	A	217	THR
1	A	235	SER
1	A	277	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	39	GLN
1	A	46	GLN
1	A	49	ASN
1	A	69	GLN
1	A	108	GLN
1	A	110	GLN
1	A	149	ASN
1	A	213	GLN
1	A	225	ASN
1	A	317	GLN
1	A	388	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	A	417	1,3	27,50,50	1.70	5 (18%)	17,82,82	1.92	4 (23%)
3	PIW	A	422	2	12,12,12	1.69	3 (25%)	13,15,15	1.75	3 (23%)

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	417	1,3	-	0/6/54/54	-
3	PIW	A	422	2	-	2/4/4/4	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	417	HEM	C3B-C2B	-5.26	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	422	PIW	C6-N1	3.36	1.51	1.45
3	A	422	PIW	C2-N3	-3.03	1.27	1.34
2	A	417	HEM	C3C-CAC	2.92	1.53	1.47
2	A	417	HEM	CMD-C2D	2.42	1.56	1.51
2	A	417	HEM	C3C-C2C	-2.32	1.37	1.40
2	A	417	HEM	C4A-CHB	-2.23	1.34	1.41
3	A	422	PIW	C5-N1	-2.22	1.36	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	417	HEM	CMA-C3A-C4A	-3.97	122.37	128.46
2	A	417	HEM	CBD-CAD-C3D	3.56	119.04	112.48
3	A	422	PIW	C10-C9-C8	3.23	125.93	119.93
2	A	417	HEM	CMD-C2D-C1D	-3.10	123.70	128.46
3	A	422	PIW	C9-C10-C11	-3.07	115.51	120.19
2	A	417	HEM	CMA-C3A-C2A	2.91	130.43	124.94
3	A	422	PIW	C9-C8-C7	-2.53	116.34	120.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	422	PIW	C11-C6-N1-C5
3	A	422	PIW	C7-C6-N1-C5

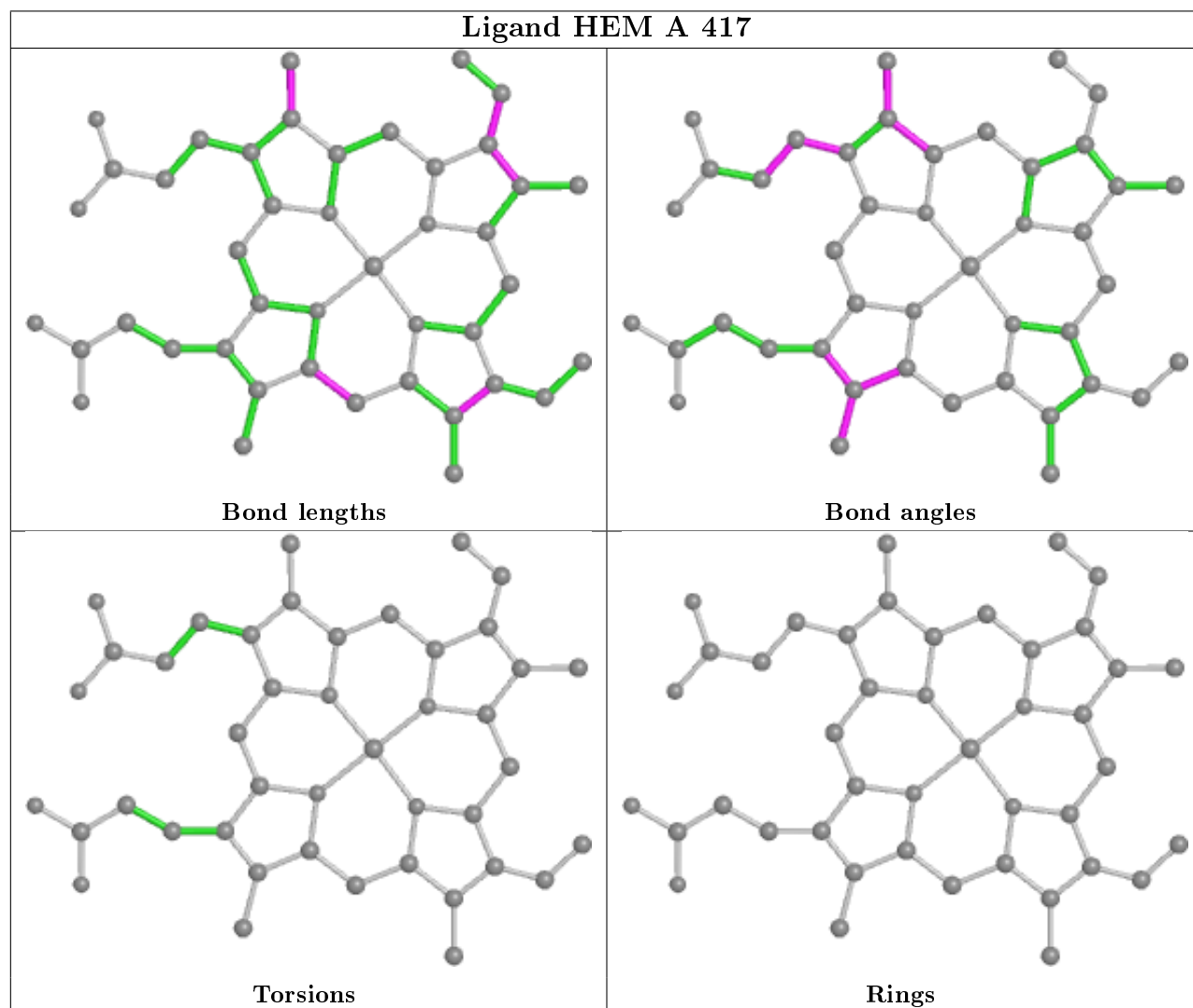
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	417	HEM	3	0
3	A	422	PIW	4	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.