



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 03:45 PM GMT

PDB ID : 7CPP  
Title : THE STRUCTURAL BASIS FOR SUBSTRATE-INDUCED CHANGES IN REDOX POTENTIAL AND SPIN EQUILIBRIUM IN CYTOCHROME P450(CAM)  
Authors : Raag, R.; Poulos, T.L.  
Deposited on : 1990-05-18  
Resolution : 2.00 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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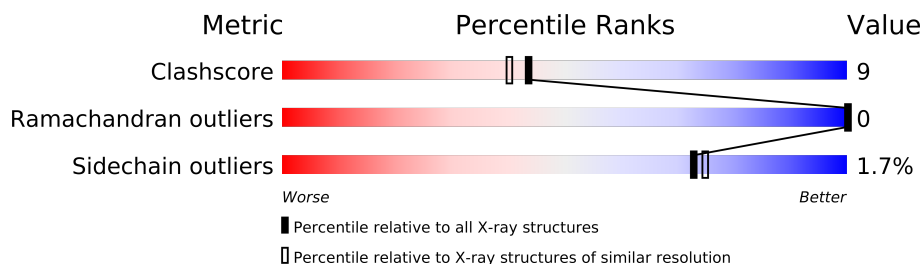
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : NOT EXECUTED  
EDS : NOT EXECUTED  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.00 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	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	414	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 3461 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

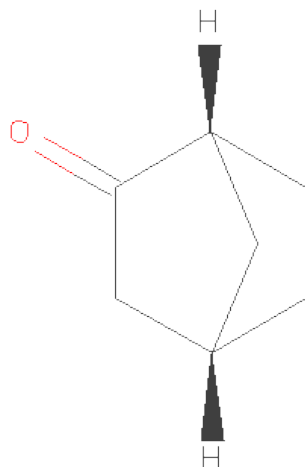
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3204	2030	559	597	18			

- 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 NORCAMPHOR (three-letter code: NCM) (formula:  $C_7H_{10}O$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	7	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	206	Total	O	0	0
			206	206		

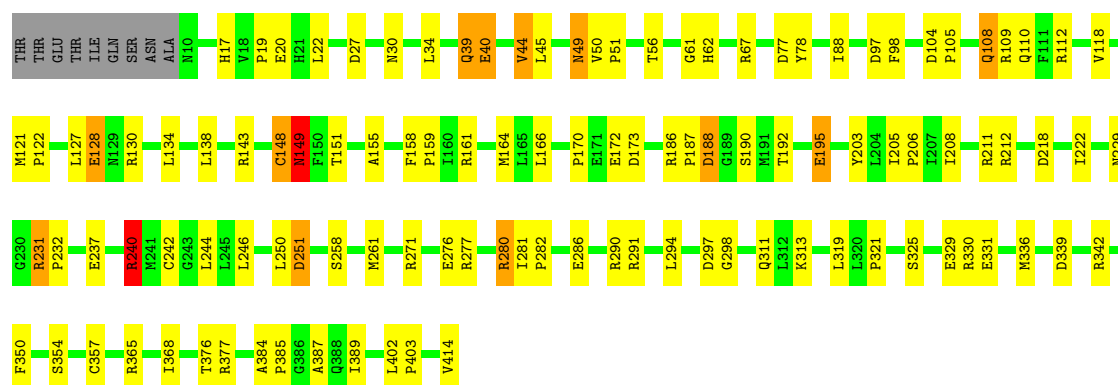
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

#### • Molecule 1: CYTOCHROME P450-CAM

Chain A: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.67Å 103.90Å 36.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROFFT	Depositor
R, $R_{free}$	0.180 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3461	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	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, NCM

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	1.02	4/3283 (0.1%)	1.57	46/4461 (1.0%)

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	8

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	237	GLU	CD-OE2	8.11	1.34	1.25
1	A	276	GLU	CD-OE2	7.81	1.34	1.25
1	A	286	GLU	CD-OE1	-6.06	1.19	1.25
1	A	251	ASP	C-O	5.58	1.33	1.23

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	ARG	CD-NE-CZ	17.88	148.63	123.60
1	A	211	ARG	NE-CZ-NH1	12.97	126.78	120.30
1	A	67	ARG	NE-CZ-NH1	11.64	126.12	120.30
1	A	365	ARG	NE-CZ-NH1	10.51	125.55	120.30
1	A	67	ARG	NE-CZ-NH2	-10.41	115.09	120.30
1	A	271	ARG	CD-NE-CZ	10.23	137.92	123.60
1	A	271	ARG	NE-CZ-NH1	9.42	125.01	120.30
1	A	112	ARG	NE-CZ-NH2	-8.76	115.92	120.30
1	A	291	ARG	NE-CZ-NH2	8.39	124.50	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	ARG	NE-CZ-NH1	8.36	124.48	120.30
1	A	261	MET	CG-SD-CE	7.85	112.77	100.20
1	A	112	ARG	NE-CZ-NH1	7.71	124.15	120.30
1	A	161	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	A	280	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	A	20	GLU	CA-CB-CG	7.29	129.43	113.40
1	A	149	ASN	N-CA-CB	7.06	123.31	110.60
1	A	195	GLU	CA-CB-CG	6.99	128.78	113.40
1	A	231	ARG	NE-CZ-NH2	-6.89	116.86	120.30
1	A	365	ARG	CD-NE-CZ	6.88	133.22	123.60
1	A	164	MET	CB-CA-C	6.54	123.47	110.40
1	A	27	ASP	CB-CG-OD1	6.50	124.14	118.30
1	A	104	ASP	CB-CG-OD1	6.44	124.10	118.30
1	A	148	CYS	C-N-CA	6.37	137.62	121.70
1	A	161	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	A	187	PRO	C-N-CA	6.28	137.39	121.70
1	A	280	ARG	NE-CZ-NH2	-6.21	117.20	120.30
1	A	188	ASP	N-CA-CB	-6.12	99.58	110.60
1	A	109	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	240	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	A	297	ASP	CB-CA-C	5.88	122.16	110.40
1	A	34	LEU	CB-CA-C	5.86	121.34	110.20
1	A	330	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	291	ARG	NH1-CZ-NH2	-5.78	113.04	119.40
1	A	290	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	143	ARG	NE-CZ-NH1	5.75	123.18	120.30
1	A	128	GLU	N-CA-CB	5.72	120.89	110.60
1	A	251	ASP	O-C-N	-5.58	113.78	122.70
1	A	286	GLU	CG-CD-OE2	-5.33	107.65	118.30
1	A	329	GLU	CA-CB-CG	5.30	125.07	113.40
1	A	143	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	A	186	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	44	VAL	CA-CB-CG2	-5.13	103.20	110.90
1	A	298	GLY	O-C-N	5.02	130.73	122.70
1	A	130	ARG	CA-CB-CG	5.02	124.44	113.40
1	A	128	GLU	CG-CD-OE1	5.01	128.32	118.30
1	A	40	GLU	OE1-CD-OE2	-5.00	117.30	123.30

There are no chirality outliers.

All (8) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	118	VAL	Mainchain
1	A	148	CYS	Mainchain
1	A	149	ASN	Mainchain
1	A	240	ARG	Sidechain
1	A	250	LEU	Mainchain
1	A	251	ASP	Mainchain
1	A	377	ARG	Sidechain
1	A	77	ASP	Mainchain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3204	0	3145	56	0
2	A	43	0	30	0	0
3	A	8	0	10	0	0
4	A	206	0	0	5	0
All	All	3461	0	3185	56	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (56) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:108:GLN:HE22	1:A:354:SER:HB2	1.57	0.68
1:A:121:MET:HB2	1:A:122:PRO:HD3	1.78	0.65
1:A:134:LEU:HB2	4:A:591:HOH:O	1.99	0.63
1:A:149:ASN:ND2	1:A:402:LEU:H	1.97	0.62
1:A:170:PRO:HG2	1:A:173:ASP:OD1	2.05	0.56
1:A:40:GLU:HG3	1:A:336:MET:HE2	1.88	0.55
1:A:44:VAL:HG23	1:A:45:LEU:N	2.21	0.54
1:A:127:LEU:HD11	1:A:166:LEU:HD13	1.89	0.53
1:A:149:ASN:HD21	1:A:402:LEU:H	1.55	0.52
1:A:49:ASN:H	1:A:49:ASN:HD22	1.58	0.52
1:A:208:ILE:O	1:A:212:ARG:HG3	2.10	0.51
1:A:17:HIS:CD2	1:A:313:LYS:HG3	2.46	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:19:PRO:HG2	1:A:22:LEU:HD12	1.94	0.50
1:A:98:PHE:HB3	1:A:244:LEU:HB2	1.94	0.49
1:A:40:GLU:HG3	1:A:336:MET:CE	2.43	0.49
1:A:376:THR:CG2	1:A:414:VAL:HG21	2.42	0.49
1:A:325:SER:O	1:A:331:GLU:HG3	2.11	0.49
1:A:56:THR:O	1:A:61:GLY:HA2	2.13	0.49
1:A:121:MET:CB	1:A:122:PRO:HD3	2.42	0.48
1:A:151:THR:HG22	1:A:258:SER:OG	2.13	0.48
1:A:108:GLN:HE22	1:A:354:SER:CB	2.25	0.48
1:A:158:PHE:HB3	1:A:159:PRO:HD3	1.95	0.48
1:A:62:HIS:CG	1:A:88:ILE:HD13	2.48	0.48
1:A:205:ILE:HB	1:A:206:PRO:HD3	1.96	0.48
1:A:44:VAL:CG2	1:A:45:LEU:N	2.77	0.47
1:A:192:THR:OG1	1:A:195:GLU:HG2	2.14	0.47
1:A:39:GLN:NE2	1:A:39:GLN:H	2.14	0.46
1:A:389:ILE:HA	4:A:660:HOH:O	2.16	0.46
1:A:188:ASP:HB3	1:A:190:SER:H	1.81	0.45
1:A:350:PHE:HB3	1:A:357:CYS:HB3	1.97	0.45
1:A:138:LEU:HD23	1:A:158:PHE:HB2	1.99	0.45
1:A:387:ALA:CB	1:A:403:PRO:HG2	2.48	0.44
1:A:242:CYS:O	1:A:246:LEU:HD23	2.18	0.44
1:A:105:PRO:HB3	4:A:624:HOH:O	2.16	0.44
1:A:97:ASP:O	1:A:240:ARG:HD2	2.18	0.44
1:A:30:ASN:ND2	4:A:557:HOH:O	2.50	0.43
1:A:384:ALA:HA	1:A:385:PRO:HD3	1.88	0.43
1:A:50:VAL:HA	1:A:51:PRO:HD3	1.93	0.43
1:A:30:ASN:ND2	4:A:556:HOH:O	2.50	0.43
1:A:78:TYR:CD1	1:A:105:PRO:HD2	2.53	0.43
1:A:110:GLN:NE2	1:A:229:ASN:HA	2.34	0.43
1:A:389:ILE:CD1	1:A:403:PRO:HD2	2.49	0.42
1:A:218:ASP:O	1:A:222:ILE:HG12	2.19	0.42
1:A:231:ARG:HB2	1:A:232:PRO:CD	2.50	0.42
1:A:231:ARG:HB2	1:A:232:PRO:HD2	2.01	0.41
1:A:151:THR:HA	1:A:155:ALA:HB3	2.02	0.41
1:A:294:LEU:HD23	1:A:294:LEU:H	1.85	0.41
1:A:203:TYR:O	1:A:206:PRO:HD2	2.21	0.41
1:A:294:LEU:HD23	1:A:294:LEU:N	2.36	0.41
1:A:281:ILE:N	1:A:282:PRO:CD	2.84	0.41
1:A:376:THR:HG22	1:A:414:VAL:HG21	2.03	0.41
1:A:387:ALA:HB1	1:A:403:PRO:HG2	2.02	0.41
1:A:281:ILE:CG2	1:A:368:ILE:HG23	2.51	0.41
1:A:339:ASP:O	1:A:342:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:319:LEU:C	1:A:321:PRO:HD3	2.42	0.40
1:A:277:ARG:O	1:A:280:ARG:HB2	2.21	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	403/414 (97%)	386 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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%)	343 (98%)	6 (2%)	73	75

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	49	ASN
1	A	108	GLN
1	A	128	GLU
1	A	172	GLU
1	A	311	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) 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	59	ASN
1	A	69	GLN
1	A	108	GLN
1	A	110	GLN
1	A	129	ASN
1	A	149	ASN
1	A	225	ASN
1	A	229	ASN
1	A	388	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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	1,4	49,50,50	2.53	14 (28%)	46,82,82	1.63	11 (23%)
3	NCM	A	422	-	9,9,9	1.96	3 (33%)	13,13,13	1.46	2 (15%)

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	1,4	-	0/14/114/114	0/0/8/8
3	NCM	A	422	-	-	0/0/17/17	0/0/2/2

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	417	HEM	C2B-C1B	8.33	1.46	1.44
2	A	417	HEM	C4A-C3A	6.09	1.47	1.40
2	A	417	HEM	C3B-C2B	-5.72	1.33	1.43
2	A	417	HEM	C3C-C2C	-5.36	1.34	1.43
2	A	417	HEM	C3D-C2D	-5.11	1.34	1.43
2	A	417	HEM	C3B-CAB	4.07	1.53	1.40
2	A	417	HEM	C3C-CAC	4.03	1.53	1.40
3	A	422	NCM	C3-C2	3.51	1.57	1.51
2	A	417	HEM	C4C-NC	-3.34	1.33	1.38
3	A	422	NCM	C1-C2	3.14	1.56	1.51
2	A	417	HEM	FE-NA	2.91	2.04	1.92
3	A	422	NCM	C7-C1	2.60	1.60	1.54
2	A	417	HEM	C3B-C4B	2.56	1.47	1.44
2	A	417	HEM	C1A-C2A	2.50	1.47	1.43
2	A	417	HEM	CMB-C2B	2.31	1.54	1.47
2	A	417	HEM	CMC-C2C	2.25	1.54	1.47
2	A	417	HEM	CMD-C2D	2.12	1.54	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	417	HEM	C3B-C4B-NB	-3.14	111.75	114.00
3	A	422	NCM	C3-C2-C1	-3.13	105.91	109.48
2	A	417	HEM	O2A-CGA-O1A	3.11	131.22	123.30
2	A	417	HEM	C2D-C1D-ND	-3.10	109.27	112.93
2	A	417	HEM	C1A-CHA-C4D	-3.09	123.41	127.47
2	A	417	HEM	C4A-CHB-C1B	-3.08	123.42	127.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	417	HEM	CHC-C1C-NC	2.76	127.13	124.73
2	A	417	HEM	CMA-C3A-C4A	-2.75	124.39	128.62
2	A	417	HEM	CBD-CAD-C3D	2.68	120.22	114.37
3	A	422	NCM	C4-C3-C2	-2.38	100.88	104.81
2	A	417	HEM	CBA-CAA-C2A	2.22	116.61	112.69
2	A	417	HEM	C4C-NC-C1C	2.13	107.75	105.53
2	A	417	HEM	CHB-C1B-NB	2.11	127.21	124.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.