



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:02 am GMT

PDB ID : 4FMX  
Title : Crystal Structure of Substrate-Bound P450cin  
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Deposited on : 2012-06-18  
Resolution : 1.55 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

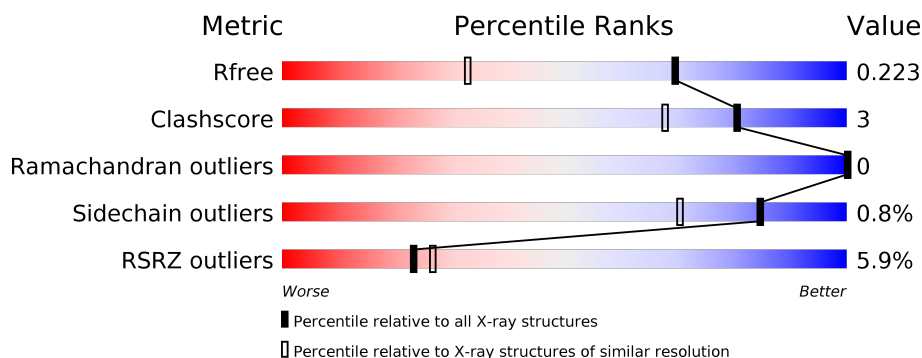
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.55 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))
$R_{free}$	100719	1088 (1.56-1.56)
Clashscore	112137	1132 (1.56-1.56)
Ramachandran outliers	110173	1110 (1.56-1.56)
Sidechain outliers	110143	1108 (1.56-1.56)
RSRZ outliers	101464	1089 (1.56-1.56)

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. 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	398	<div> <div>4%</div> <div>93%</div> <div>7%</div> </div>
1	B	398	<div> <div>8%</div> <div>94%</div> <div>6%</div> </div>

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	CNL	A	502	-	-	-	X
3	CNL	B	502	-	-	-	X
4	SO4	A	503	-	-	-	X
4	SO4	B	503	-	-	-	X
5	GOL	A	504	-	-	-	X
5	GOL	A	505	-	-	-	X
5	GOL	B	504	-	-	-	X

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13609 atoms, of which 6275 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 P450cin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	397	Total	C	H	N	O	S	0	2	0
			6298	2017	3136	552	582	11			
1	B	397	Total	C	H	N	O	S	0	2	0
			6287	2016	3127	549	584	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	INITIATING METHIONINE	UNP Q8VQF6
B	7	MET	-	INITIATING METHIONINE	UNP Q8VQF6

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



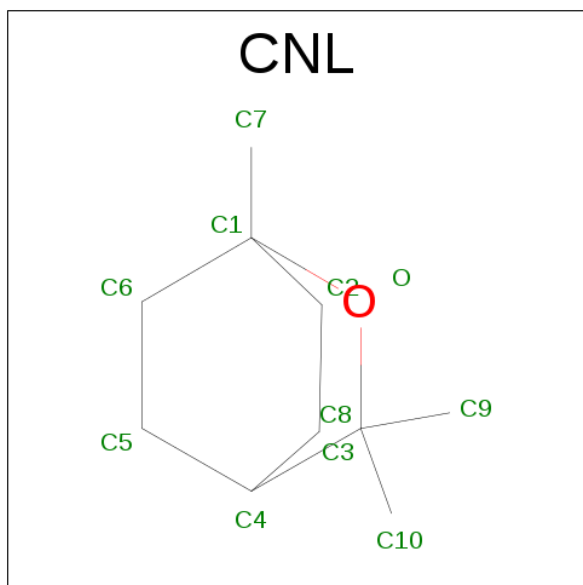
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Fe	H	N	O	0	0
			49	34	1	6	4	4		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	Fe	H	N	O	0	0
			49	34	1	6	4	4		

- Molecule 3 is 1,3,3-TRIMETHYL-2-OXABICYCLO[2.2.2]OCTANE (three-letter code: CNL) (formula: C<sub>10</sub>H<sub>18</sub>O).



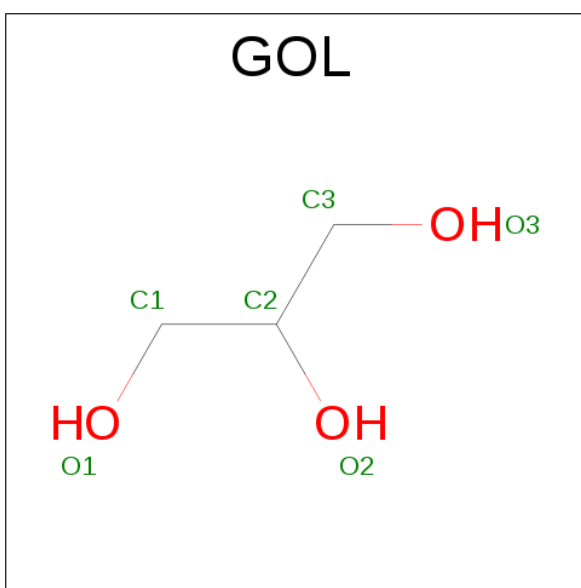
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	10	1		
3	B	1	Total	C	O	0	0
			11	10	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

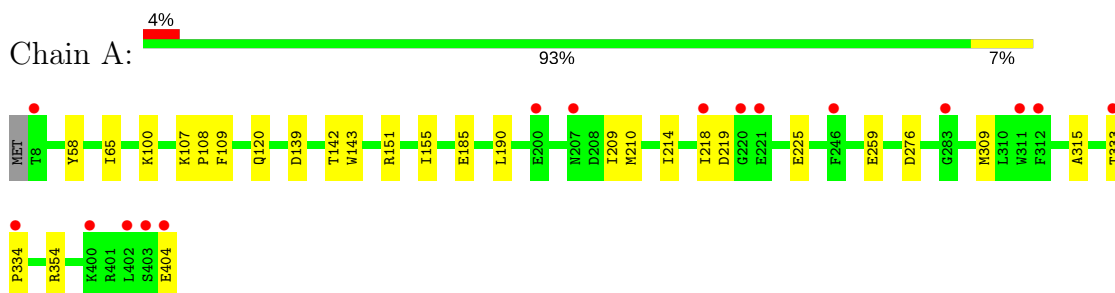
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	488	Total	O	0	0
			488	488		
6	B	388	Total	O	0	0
			388	388		

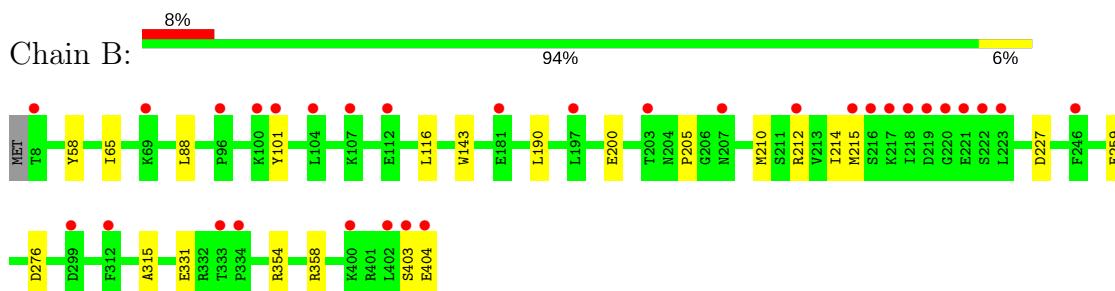
### 3 Residue-property plots [i](#)

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 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: P450cin



#### • Molecule 1: P450cin





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.55Å 69.26Å 122.61Å 90.00° 97.14° 90.00°	Depositor
Resolution (Å)	34.99 – 1.55 34.99 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.0 (34.99-1.55) 99.0 (34.99-1.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.59 (at 1.55Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.175 , 0.220 0.182 , 0.223	Depositor DCC
$R_{free}$ test set	6849 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.6	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 50.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13609	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.99% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CNL, SO4, 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	0.35	0/3248	0.54	1/4415 (0.0%)
1	B	0.32	0/3246	0.51	0/4413
All	All	0.34	0/6494	0.52	1/8828 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	309	MET	CG-SD-CE	5.25	108.61	100.20

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	3162	3136	3123	22	0
1	B	3160	3127	3116	16	1
2	A	43	6	30	1	0
2	B	43	6	30	1	0
3	A	11	0	18	0	0
3	B	11	0	18	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	12	0	16	3	0
5	B	6	0	8	3	0
6	A	488	0	0	7	5
6	B	388	0	0	5	3
All	All	7334	6275	6359	40	5

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 3.

All (40) 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:B:259[B]:GLU:OE2	6:B:614:HOH:O	1.77	0.99
1:B:358:ARG:HH11	5:B:504:GOL:H12	1.40	0.87
1:A:276:ASP:OD1	1:A:354[A]:ARG:NH1	2.21	0.74
1:A:142:THR:HG21	6:A:1082:HOH:O	1.95	0.67
1:A:120:GLN:NE2	6:A:843:HOH:O	2.29	0.65
1:B:101:TYR:OH	1:B:227:ASP:OD2	2.14	0.65
1:A:259:GLU:OE1	5:A:504:GOL:H12	1.98	0.64
1:A:259:GLU:OE2	6:A:655:HOH:O	2.15	0.63
1:A:259:GLU:OE1	5:A:504:GOL:C1	2.49	0.61
1:B:403:SER:O	1:B:404:GLU:CB	2.50	0.59
2:A:501:HEM:HMC2	2:A:501:HEM:HBC2	1.85	0.58
1:A:107:LYS:HB3	1:A:108:PRO:HD3	1.86	0.56
1:A:225:GLU:OE2	6:A:781:HOH:O	2.18	0.56
1:B:358:ARG:NH1	5:B:504:GOL:H12	2.16	0.56
2:B:501:HEM:HBC2	2:B:501:HEM:HMC2	1.88	0.55
1:A:142:THR:HG22	6:A:704:HOH:O	2.06	0.55
1:B:276:ASP:OD1	1:B:354:ARG:NH1	2.41	0.54
1:A:109:PHE:CE2	1:A:209:ILE:HD13	2.44	0.53
1:B:210:MET:O	1:B:214:ILE:HG13	2.13	0.49
1:B:358:ARG:HB2	5:B:504:GOL:H31	1.94	0.49
1:B:205:PRO:HG3	1:B:215:MET:CE	2.45	0.47
1:B:88:LEU:HA	6:B:773:HOH:O	2.16	0.46
1:A:185:GLU:OE2	6:A:788:HOH:O	2.21	0.45
1:A:190:LEU:HD23	1:A:190:LEU:C	2.37	0.45
1:A:100:LYS:HD2	1:A:218:ILE:HG21	1.99	0.45
1:B:212:ARG:CZ	6:B:738:HOH:O	2.64	0.44
1:A:259:GLU:OE1	5:A:504:GOL:H11	2.15	0.44
1:B:403:SER:O	1:B:404:GLU:HB2	2.17	0.44
1:A:139:ASP:O	1:A:143:TRP:HB3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333:THR:HA	1:A:334:PRO:C	2.38	0.43
1:A:100:LYS:CG	1:A:218:ILE:HD13	2.49	0.42
1:A:100:LYS:HG2	1:A:218:ILE:HD13	2.02	0.42
1:B:200:GLU:HG3	6:B:809:HOH:O	2.19	0.41
1:B:190:LEU:C	1:B:190:LEU:HD23	2.40	0.41
1:B:212:ARG:NE	6:B:738:HOH:O	2.53	0.41
1:B:58:TYR:HA	1:B:315:ALA:HB1	2.03	0.41
1:A:210:MET:O	1:A:214:ILE:HG13	2.20	0.41
1:A:219:ASP:OD2	6:A:1022:HOH:O	2.22	0.41
1:A:151:ARG:O	1:A:155:ILE:HG12	2.21	0.40
1:A:58:TYR:HA	1:A:315:ALA:HB1	2.04	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1066:HOH:O	6:B:667:HOH:O[1_545]	1.77	0.43
6:A:692:HOH:O	6:B:614:HOH:O[1_545]	1.83	0.37
6:A:781:HOH:O	6:A:1072:HOH:O[2_656]	1.87	0.33
6:A:681:HOH:O	6:B:976:HOH:O[1_545]	1.92	0.28
1:B:331:GLU:OE2	6:A:1066:HOH:O[1_565]	2.07	0.13

## 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	397/398 (100%)	389 (98%)	8 (2%)	0	100	100
1	B	397/398 (100%)	388 (98%)	9 (2%)	0	100	100
All	All	794/796 (100%)	777 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	335/334 (100%)	333 (99%)	2 (1%)	89	77
1	B	335/334 (100%)	332 (99%)	3 (1%)	82	66
All	All	670/668 (100%)	665 (99%)	5 (1%)	85	74

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ILE
1	A	404	GLU
1	B	65	ILE
1	B	116	LEU
1	B	143	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

9 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	501	1	28,50,50	2.21	9 (32%)	17,82,82	1.63	3 (17%)
3	CNL	A	502	-	12,12,12	2.40	4 (33%)	19,20,20	1.17	2 (10%)
4	SO4	A	503	-	4,4,4	0.14	0	6,6,6	0.17	0
5	GOL	A	504	-	5,5,5	0.57	0	5,5,5	0.94	0
5	GOL	A	505	-	5,5,5	0.24	0	5,5,5	0.95	0
2	HEM	B	501	1	28,50,50	2.21	8 (28%)	17,82,82	1.42	3 (17%)
3	CNL	B	502	-	12,12,12	2.50	4 (33%)	19,20,20	1.44	4 (21%)
4	SO4	B	503	-	4,4,4	0.16	0	6,6,6	0.14	0
5	GOL	B	504	-	5,5,5	0.18	0	5,5,5	0.65	0

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	501	1	-	0/6/54/54	0/0/8/8
3	CNL	A	502	-	-	0/0/24/24	0/0/2/2
4	SO4	A	503	-	-	0/0/0/0	0/0/0/0
5	GOL	A	504	-	-	0/4/4/4	0/0/0/0
5	GOL	A	505	-	-	0/4/4/4	0/0/0/0
2	HEM	B	501	1	-	0/6/54/54	0/0/8/8
3	CNL	B	502	-	-	0/0/24/24	0/0/2/2
4	SO4	B	503	-	-	0/0/0/0	0/0/0/0
5	GOL	B	504	-	-	0/4/4/4	0/0/0/0

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C3B-C2B	-4.60	1.34	1.40
2	A	501	HEM	C3C-C2C	-4.52	1.34	1.40
2	A	501	HEM	C3B-C2B	-4.36	1.34	1.40
2	B	501	HEM	C3C-C2C	-4.19	1.34	1.40
3	B	502	CNL	C5-C4	-3.81	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	CNL	C5-C4	-3.53	1.43	1.53
3	A	502	CNL	C2-C3	-2.63	1.47	1.53
3	B	502	CNL	C2-C3	-2.60	1.47	1.53
3	A	502	CNL	C7-C1	-2.22	1.48	1.52
3	B	502	CNL	C7-C1	-2.07	1.48	1.52
2	A	501	HEM	C1B-NB	2.09	1.39	1.36
2	B	501	HEM	CAA-C2A	2.13	1.55	1.52
2	B	501	HEM	C1D-ND	2.16	1.40	1.36
2	A	501	HEM	C1D-ND	2.34	1.41	1.36
2	A	501	HEM	CAA-C2A	2.50	1.56	1.52
2	B	501	HEM	C4D-ND	2.80	1.40	1.36
2	A	501	HEM	C4D-ND	2.92	1.40	1.36
2	B	501	HEM	C3B-CAB	3.76	1.55	1.47
2	A	501	HEM	C3C-CAC	3.79	1.55	1.47
2	A	501	HEM	C3B-CAB	3.82	1.55	1.47
2	B	501	HEM	C3C-CAC	3.95	1.55	1.47
2	A	501	HEM	C3D-C2D	4.80	1.51	1.37
2	B	501	HEM	C3D-C2D	4.93	1.52	1.37
3	A	502	CNL	O-C8	5.87	1.57	1.45
3	B	502	CNL	O-C8	6.20	1.57	1.45

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	HEM	CBD-CAD-C3D	-3.08	106.59	112.47
3	B	502	CNL	C10-C8-C9	-3.04	105.14	110.53
2	A	501	HEM	CMA-C3A-C4A	-2.96	123.91	128.46
2	B	501	HEM	CBD-CAD-C3D	-2.64	107.43	112.47
3	B	502	CNL	O-C1-C2	-2.55	100.47	108.55
3	B	502	CNL	C3-C4-C8	-2.44	104.26	109.11
3	A	502	CNL	C3-C4-C8	-2.40	104.35	109.11
3	A	502	CNL	C10-C8-C9	-2.15	106.72	110.53
2	B	501	HEM	C4A-C3A-C2A	2.06	108.43	107.00
2	B	501	HEM	CMB-C2B-C3B	2.32	129.19	124.89
3	B	502	CNL	C10-C8-C4	2.41	116.95	112.59
2	A	501	HEM	C4A-C3A-C2A	2.84	108.97	107.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	1	0
5	A	504	GOL	3	0
2	B	501	HEM	1	0
5	B	504	GOL	3	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	397/398 (99%)	0.10	16 (4%) 39 45	9, 15, 32, 60	0
1	B	397/398 (99%)	0.35	31 (7%) 14 16	12, 21, 40, 64	0
All	All	794/796 (99%)	0.22	47 (5%) 23 27	9, 18, 37, 64	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	218	ILE	10.1
1	B	220	GLY	6.2
1	B	404	GLU	5.8
1	A	404	GLU	5.3
1	B	219	ASP	5.2
1	B	223	LEU	5.2
1	B	334	PRO	4.9
1	B	8	THR	4.4
1	B	333	THR	4.4
1	B	299	ASP	4.2
1	A	402	LEU	3.7
1	B	107	LYS	3.7
1	A	333	THR	3.7
1	A	218	ILE	3.4
1	A	8	THR	3.3
1	B	222	SER	3.2
1	B	221	GLU	3.1
1	A	221	GLU	3.0
1	A	334	PRO	3.0
1	B	112	GLU	2.9
1	B	400	LYS	2.9
1	B	215	MET	2.7
1	A	220	GLY	2.7
1	B	69	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	101	TYR	2.6
1	A	400	LYS	2.5
1	B	96	PRO	2.5
1	B	312	PHE	2.5
1	A	207	ASN	2.5
1	B	403	SER	2.5
1	A	200	GLU	2.5
1	B	217	LYS	2.5
1	A	403	SER	2.4
1	A	312	PHE	2.4
1	B	104	LEU	2.4
1	B	402	LEU	2.4
1	B	181	GLU	2.3
1	B	207	ASN	2.3
1	A	246	PHE	2.2
1	B	100	LYS	2.2
1	A	311	TRP	2.1
1	B	246	PHE	2.1
1	B	216	SER	2.1
1	A	283	GLY	2.1
1	B	203	THR	2.1
1	B	197[A]	LEU	2.1
1	B	212	ARG	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	GOL	A	505	6/6	0.87	0.21	9.15	16,24,27,30	0
5	GOL	B	504	6/6	0.70	0.23	5.70	29,31,32,34	0
4	SO4	A	503	5/5	0.98	0.18	5.67	31,32,36,36	0
4	SO4	B	503	5/5	0.96	0.19	5.50	35,36,37,38	0
3	CNL	A	502	11/11	0.96	0.23	4.87	11,15,18,18	0
3	CNL	B	502	11/11	0.94	0.22	4.44	18,22,24,26	0
5	GOL	A	504	6/6	0.91	0.15	4.38	15,20,25,25	0
2	HEM	B	501	43/43	0.98	0.14	1.26	11,16,21,22	0
2	HEM	A	501	43/43	0.99	0.14	1.00	7,10,14,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.