



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 02:01 PM GMT

PDB ID : 3N8Z  
Title : Crystal Structure of Cyclooxygenase-1 in Complex with Flurbiprofen  
Authors : Sidhu, R.S.  
Deposited on : 2010-05-28  
Resolution : 2.90 Å(reported)

This is a wwPDB validation summary 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>

---

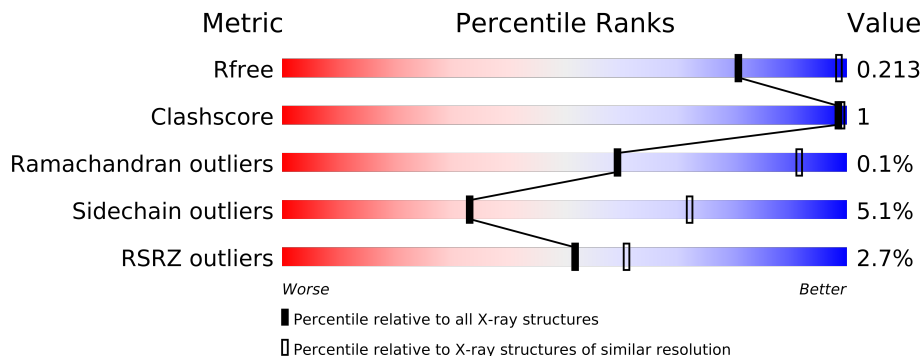
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
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 2.90 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))
$R_{free}$	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)

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.

Mol	Chain	Length	Quality of chain
1	A	553	
1	B	553	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	BOG	A	750	-	X

## 2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 9437 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.

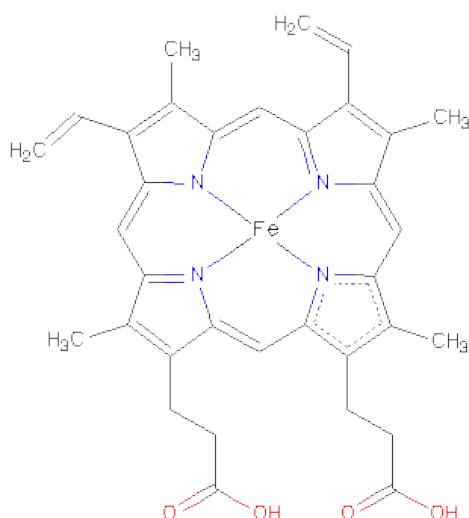
- Molecule 1 is a protein called Prostaglandin G/H synthase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	0	2	0
			4451	2886	744	794	27			
1	B	553	Total	C	N	O	S	3	1	0
			4463	2893	752	790	28			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	LEU	MET	CONFLICT	UNP P05979
B	92	LEU	MET	CONFLICT	UNP P05979

- 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		

*Continued on next page...*

*Continued from previous page...*

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

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	LEU	MET	CONFLICT	UNP P05979

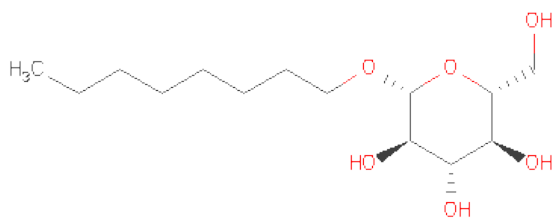
- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	B	2	Total	C	N	O	0	0
			28	16	2	10		

There are 3 discrepancies between the modelled and reference sequences:

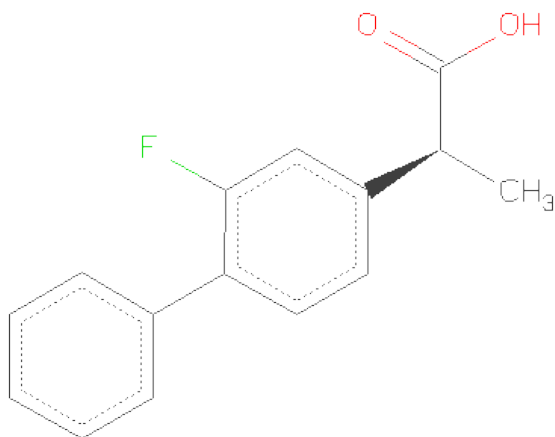
Chain	Residue	Modelled	Actual	Comment	Reference
A	92	LEU	MET	CONFLICT	UNP P05979
A	92	LEU	MET	CONFLICT	UNP P05979
B	92	LEU	MET	CONFLICT	UNP P05979

- Molecule 5 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			20	14	6		
5	A	1	Total	C	O	0	0
			20	14	6		
5	A	1	Total	C	O	0	0
			13	7	6		
5	B	1	Total	C	O	0	0
			20	14	6		
5	B	1	Total	C	O	0	0
			20	14	6		

- Molecule 6 is FLURBIPROFEN (three-letter code: FLP) (formula: C<sub>15</sub>H<sub>13</sub>FO<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	F	O	0	0
			18	15	1	2		
6	B	1	Total	C	F	O	0	0
			18	15	1	2		

- Molecule 7 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	5	Total	C	N	O	0	0
			61	34	2	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	92	LEU	MET	CONFLICT	UNP P05979

- Molecule 8 is water.

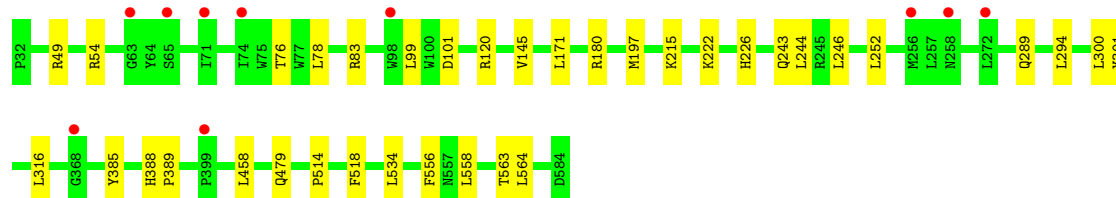
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	78	Total	O	0	0
			78	78		
8	B	57	Total	O	0	0
			57	57		

### 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.

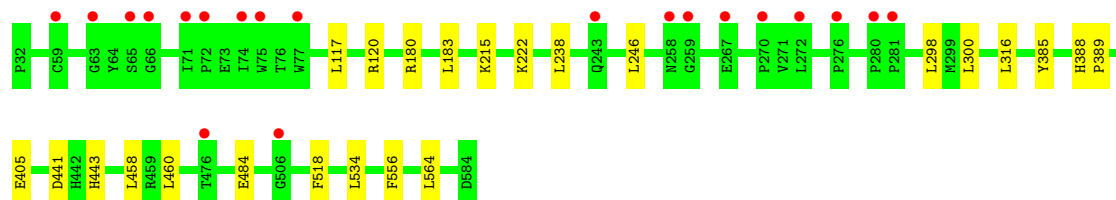
#### • Molecule 1: Prostaglandin G/H synthase 1

Chain A: 



#### • Molecule 1: Prostaglandin G/H synthase 1

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	181.49Å 181.49Å 103.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.63 – 2.90 31.63 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (31.63-2.90) 99.9 (31.63-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.176 , 0.207 0.181 , 0.213	Depositor DCC
$R_{free}$ test set	1544 reflections (3.71%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.6	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 23.3	EDS
Estimated twinning fraction	0.502 for H, K, L 0.498 for H+K, -K, -L 0.086 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.502 for H, K, L 0.498 for H+K, -K, -L	Depositor
L-test for twinning	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 43147 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9437	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.40% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, FLP, NDG, HEM, BOG, MAN

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	0.33	0/4593	0.47	0/6249
1	B	0.33	0/4602	0.48	0/6257
All	All	0.33	0/9195	0.48	0/12506

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
4	A	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	671	NAG	C1

There are no planarity outliers.

### 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	4451	0	0	3	0
1	B	4463	0	5	2	0
2	A	43	0	0	0	0
2	B	43	0	0	0	0
3	A	28	0	0	0	0
4	A	56	0	0	0	0
4	B	28	0	0	0	0
5	A	53	0	67	0	0
5	B	40	0	56	0	0
6	A	18	0	12	0	0
6	B	18	0	12	0	0
7	B	61	0	0	0	0
8	A	78	0	0	0	0
8	B	57	0	0	0	0
All	All	9437	0	152	5	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 1.

All (5) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:145:VAL:O	1:A:226:HIS:NE2	2.42	0.53
1:A:388:HIS:N	1:A:389:PRO:CD	2.74	0.50
1:B:388:HIS:N	1:B:389:PRO:CD	2.76	0.48
1:A:197:MET:O	1:A:301:TYR:OH	2.33	0.46
1:B:441:ASP:OD2	1:B:443:HIS:ND1	2.49	0.46

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	553/553 (100%)	531 (96%)	21 (4%)	1 (0%)	56	89
1	B	552/553 (100%)	532 (96%)	20 (4%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1105/1106 (100%)	1063 (96%)	41 (4%)	1 (0%)	59	91

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	514	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	478/488 (98%)	449 (94%)	29 (6%)	26	62
1	B	480/488 (98%)	460 (96%)	20 (4%)	40	79
All	All	958/976 (98%)	909 (95%)	49 (5%)	33	72

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	479	GLN
1	A	563	THR
1	B	518	PHE
1	A	534	LEU
1	A	564	LEU

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

### 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

13 carbohydrates 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$
3	NAG	A	661	1,3	12,14,15	0.63	0	15,19,21	0.94	1 (6%)
3	NDG	A	662	3	12,14,15	0.61	0	15,19,21	0.95	1 (6%)
4	NAG	A	671	1,4	12,14,15	0.53	0	15,19,21	1.09	1 (6%)
4	NAG	A	672	4	12,14,15	0.61	0	15,19,21	0.87	1 (6%)
4	NAG	A	681	1,4	12,14,15	0.69	0	15,19,21	0.95	0
4	NAG	A	682	4	12,14,15	0.62	0	15,19,21	0.81	0
7	NAG	B	671	1,7	12,14,15	0.60	0	15,19,21	0.80	0
7	NAG	B	672	7	12,14,15	0.65	0	15,19,21	1.01	1 (6%)
7	BMA	B	673	7	10,11,12	0.70	0	11,15,17	0.84	1 (9%)
7	BMA	B	674	7	10,11,12	0.88	1 (10%)	11,15,17	1.15	2 (18%)
7	MAN	B	675	7	10,11,12	0.70	0	11,15,17	1.60	2 (18%)
4	NAG	B	681	4	12,14,15	0.67	0	15,19,21	0.69	0
4	NAG	B	682	4	12,14,15	0.55	0	15,19,21	0.57	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
3	NAG	A	661	1,3	-	0/6/23/26	0/1/1/1
3	NDG	A	662	3	-	0/6/23/26	0/1/1/1
4	NAG	A	671	1,4	1/1/5/7	0/6/23/26	0/1/1/1
4	NAG	A	672	4	-	0/6/23/26	0/1/1/1
4	NAG	A	681	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	682	4	-	0/6/23/26	0/1/1/1
7	NAG	B	671	1,7	-	0/6/23/26	0/1/1/1
7	NAG	B	672	7	-	0/6/23/26	0/1/1/1
7	BMA	B	673	7	-	0/2/19/22	0/1/1/1
7	BMA	B	674	7	-	0/2/19/22	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	B	675	7	-	0/2/19/22	0/1/1/1
4	NAG	B	681	4	-	0/6/23/26	0/1/1/1
4	NAG	B	682	4	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	674	BMA	O5-C5	-2.18	1.41	1.45

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	675	MAN	O5-C5-C6	4.00	111.17	106.98
4	A	671	NAG	O5-C5-C6	3.15	110.29	106.98
3	A	662	NDG	O-C5-C6	2.80	109.92	106.98
7	B	675	MAN	C3-C4-C5	2.48	114.63	110.20
7	B	674	BMA	O5-C5-C4	-2.34	107.68	110.65

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	671	NAG	C1

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

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	601	-	49,50,50	2.48	17 (34%)	46,82,82	2.04	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	FLP	A	701	-	19,19,19	4.66	13 (68%)	26,26,26	1.36	3 (11%)
5	BOG	A	750	-	20,20,20	0.76	0	25,25,25	1.66	4 (16%)
5	BOG	A	751	-	20,20,20	0.74	0	25,25,25	1.41	3 (12%)
5	BOG	A	752	-	12,13,20	0.93	0	17,18,25	1.70	4 (23%)
6	FLP	B	1701	-	19,19,19	4.66	13 (68%)	26,26,26	1.29	3 (11%)
5	BOG	B	1750	-	20,20,20	0.71	0	25,25,25	1.44	4 (16%)
5	BOG	B	1751	-	20,20,20	0.73	0	25,25,25	1.51	4 (16%)
2	HEM	B	601	1	49,50,50	2.41	15 (30%)	46,82,82	2.02	8 (17%)

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	601	-	-	0/14/114/114	0/0/8/8
6	FLP	A	701	-	-	0/12/12/12	0/2/2/2
5	BOG	A	750	-	-	0/11/31/31	0/1/1/1
5	BOG	A	751	-	-	0/11/31/31	0/1/1/1
5	BOG	A	752	-	-	0/4/24/31	0/1/1/1
6	FLP	B	1701	-	-	0/12/12/12	0/2/2/2
5	BOG	B	1750	-	-	0/11/31/31	0/1/1/1
5	BOG	B	1751	-	-	0/11/31/31	0/1/1/1
2	HEM	B	601	1	-	0/14/114/114	0/0/8/8

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	701	FLP	C10-C11	8.60	1.53	1.37
6	B	1701	FLP	C10-C11	8.59	1.53	1.37
6	B	1701	FLP	C8-C9	8.46	1.53	1.39
6	A	701	FLP	C8-C9	8.45	1.53	1.39
6	A	701	FLP	C7-C6	8.28	1.53	1.40

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	HEM	C3B-C4B-NB	-8.85	107.67	114.00
2	B	601	HEM	C3B-C4B-NB	-8.68	107.79	114.00
2	A	601	HEM	C4D-ND-C1D	6.53	111.85	105.16

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	HEM	C4D-ND-C1D	6.42	111.73	105.16
5	A	750	BOG	O5-C1-C2	-4.61	100.87	110.31

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 ⓘ

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	553/553 (100%)	-0.22	10 (1%) 65 74	52, 67, 82, 91	0
1	B	553/553 (100%)	-0.08	20 (3%) 41 48	50, 65, 82, 98	2 (0%)
All	All	1106/1106 (100%)	-0.15	30 (2%) 52 61	50, 66, 82, 98	2 (0%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	65	SER	4.3
1	B	258	ASN	4.3
1	A	258	ASN	4.1
1	B	259	GLY	3.8
1	B	71	ILE	3.5

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
7	MAN	B	675	11/12	0.38	8.05	104,107,111,112	0
4	NAG	A	682	14/15	0.43	3.40	94,96,99,100	0
4	NAG	B	682	14/15	0.28	2.56	109,112,115,115	0

*Continued on next page...*



*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	B	681	14/15	0.17	0.69	100,105,108,109	0
4	NAG	A	672	14/15	0.29	0.49	71,73,76,76	0
4	NAG	A	681	14/15	0.20	-0.05	86,90,92,92	0
3	NDG	A	662	14/15	0.18	-0.19	81,82,85,86	0
7	NAG	B	672	14/15	0.18	-0.32	75,78,83,86	0
3	NAG	A	661	14/15	0.20	-0.36	74,76,79,80	0
7	BMA	B	674	11/12	0.20	-0.45	96,99,103,105	0
4	NAG	A	671	14/15	0.13	-0.90	63,65,67,69	0
7	NAG	B	671	14/15	0.12	-0.98	66,68,71,74	0
7	BMA	B	673	11/12	0.23	-	88,91,94,96	0

## 6.4 Ligands

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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	BOG	A	750	20/20	0.24	2.56	119,119,119,119	0
5	BOG	B	1750	20/20	0.26	1.66	73,73,75,75	0
5	BOG	A	752	13/20	0.27	1.40	96,96,97,97	0
2	HEM	A	601	43/43	0.22	1.05	86,91,96,97	0
5	BOG	A	751	20/20	0.15	0.93	67,68,68,69	0
6	FLP	B	1701	18/18	0.17	0.89	54,54,54,54	0
2	HEM	B	601	43/43	0.19	-0.00	75,80,85,87	0
5	BOG	B	1751	20/20	0.14	-0.04	73,73,74,74	0
6	FLP	A	701	18/18	0.15	-0.61	62,63,63,63	0

## 6.5 Other polymers

There are no such residues in this entry.