



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:51 AM GMT

PDB ID : 3GCJ  
Title : Mode of ligand binding and assignment of subsites in mammalian peroxidases: crystal structure of lactoperoxidase complexes with acetyl salicylic acid, salicylhydroxamic acid and benzylhydroxamic acid  
Authors : Singh, A.K.; Singh, N.; Sinha, M.; Kaur, P.; Srinivasan, A.; Sharma, S.; Singh, T.P.  
Deposited on : 2009-02-22  
Resolution : 2.34 Å(reported)

This is a wwPDB X-ray Structure 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/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

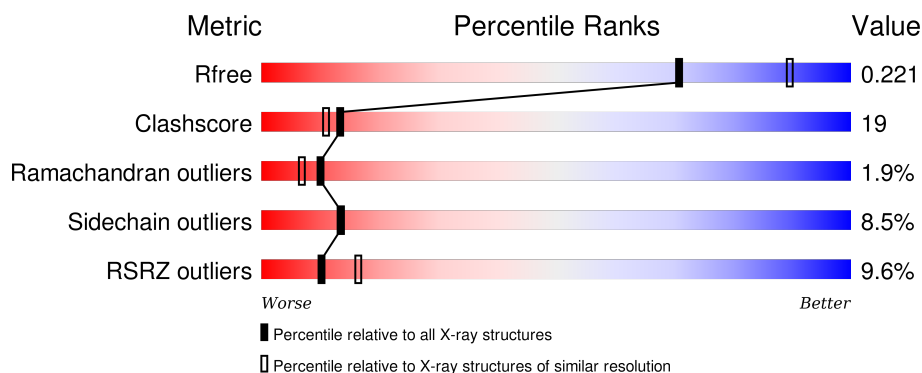
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 2.34 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))
$R_{free}$	91344	1406 (2.36-2.32)
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (2.36-2.32)

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	595	

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
4	IOD	A	614	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	SHA	A	617	-	-	-	X

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5326 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 Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	0	0
			4775	3037	847	864	1	26			

- 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		

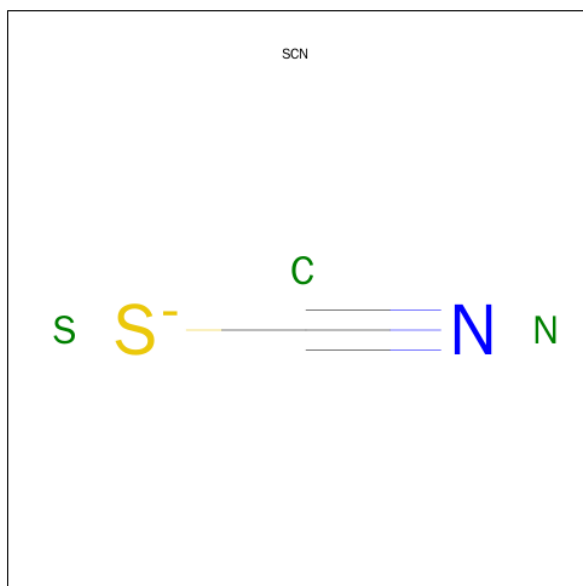
- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	8	Total I 8 8	0	0

- Molecule 5 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N S 3 1 1 1	0	0

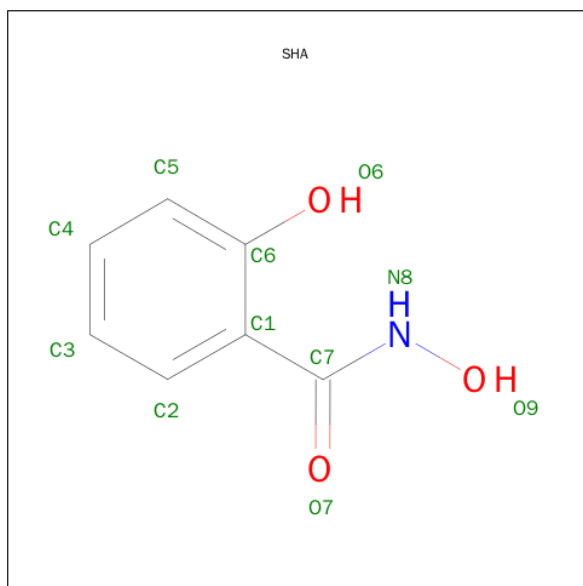
- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	3	Total C N O 39 22 2 15	0	0
6	A	3	Total C N O 39 22 2 15	0	0

- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 8 is SALICYLHYDROXAMIC ACID (three-letter code: SHA) (formula:  $C_7H_7NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			11	7	1	3		

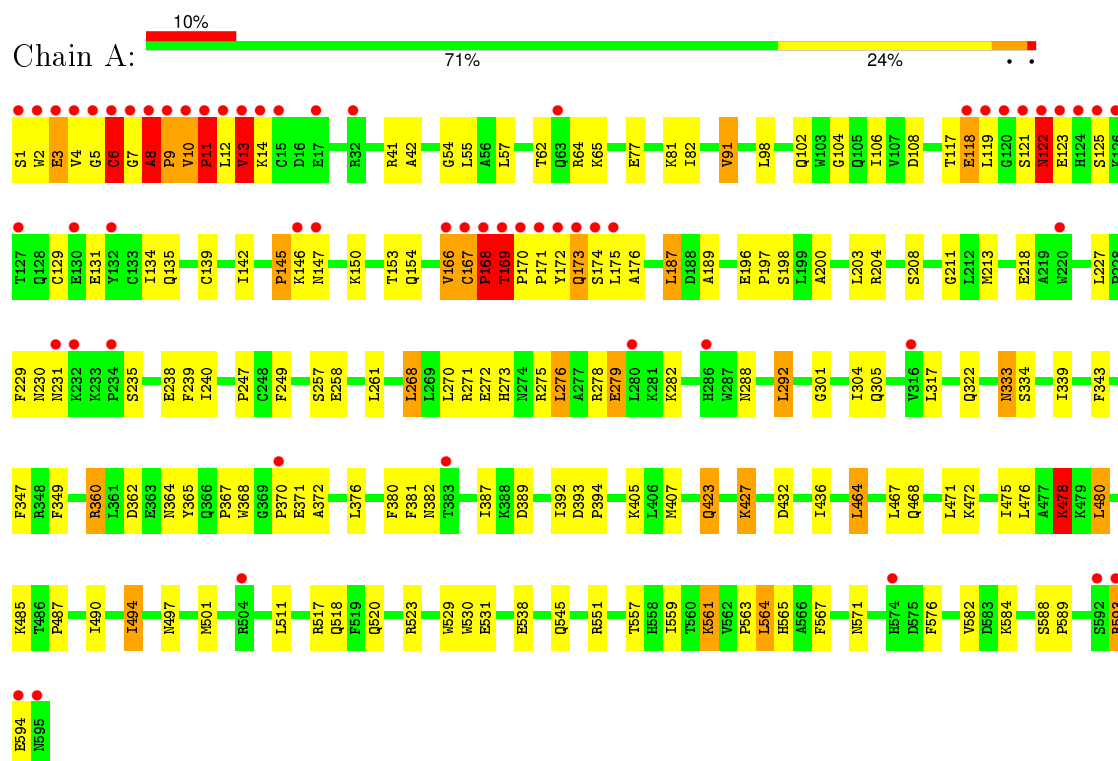
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	351	Total	O	0	0
			351	351		

### 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 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 ( $\text{RSRZ} > 2$ ). 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: Lactoperoxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.62Å 80.55Å 77.80Å 90.00° 102.55° 90.00°	Depositor
Resolution (Å)	19.47 – 2.34 19.88 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.47-2.34) 98.5 (19.88-2.34)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 2.33Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, $R_{free}$	0.204 , 0.212 0.186 , 0.221	Depositor DCC
$R_{free}$ test set	871 reflections (3.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.5	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 60.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 27439 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5326	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: SCN, NAG, SEP, CA, SHA, HEM, IOD, 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	0.50	1/4892 (0.0%)	0.79	12/6634 (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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	11	PRO	N-CA	5.52	1.56	1.47

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	PRO	CA-N-CD	-8.55	99.53	111.50
1	A	11	PRO	N-CA-C	8.21	133.44	112.10
1	A	168	PRO	CA-C-N	-8.18	99.21	117.20
1	A	173	GLN	N-CA-C	7.52	131.31	111.00
1	A	5	GLY	N-CA-C	7.06	130.76	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	478	LYS	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	4775	0	4687	177	0
2	A	43	0	30	6	0
3	A	1	0	0	0	0
4	A	8	0	0	2	0
5	A	3	0	0	0	0
6	A	78	0	68	2	0
7	A	56	0	50	3	0
8	A	11	0	7	0	0
9	A	351	0	0	44	0
All	All	5326	0	4842	185	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 19.

The worst 5 of 185 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:561:LYS:HG3	9:A:923:HOH:O	1.38	1.17
1:A:171:PRO:HA	9:A:948:HOH:O	1.52	1.08
1:A:170:PRO:HA	9:A:946:HOH:O	1.55	1.07
1:A:10:VAL:HG11	1:A:41:ARG:NE	1.72	1.05
1:A:196:GLU:HB3	1:A:198:SEP:O2P	1.58	1.03

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	592/595 (100%)	560 (95%)	21 (4%)	11 (2%)	10 7

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	PRO
1	A	12	LEU
1	A	122	ASN
1	A	167	CYS
1	A	168	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	517/517 (100%)	473 (92%)	44 (8%)	13 13

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	261	LEU
1	A	292	LEU
1	A	538	GLU
1	A	268	LEU
1	A	278	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	423	GLN
1	A	437	ASN
1	A	520	GLN
1	A	364	ASN
1	A	497	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	$\# Z  > 2$
1	SEP	A	198	1	8,9,10	1.55	2 (25%)	8,12,14	2.02	3 (37%)

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
1	SEP	A	198	1	-	0/6/8/10	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-OG	2.21	1.67	1.60
1	A	198	SEP	P-O1P	2.81	1.60	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	O2P-P-OG	2.13	112.69	106.56
1	A	198	SEP	OG-CB-CA	3.16	110.97	108.27
1	A	198	SEP	O3P-P-OG	3.35	116.20	106.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	198	SEP	2	0

## 5.5 Carbohydrates ⓘ

10 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	$\# Z  > 2$
6	NAG	A	596	1,6	14,14,15	0.61	0	15,19,21	0.68	0
6	NAG	A	597	6	14,14,15	0.85	0	15,19,21	0.89	1 (6%)
6	MAN	A	598	6	11,11,12	0.57	0	14,15,17	0.51	0
7	NAG	A	599	1,7	14,14,15	0.56	0	15,19,21	0.85	1 (6%)
7	NAG	A	600	7	14,14,15	0.71	0	15,19,21	1.68	4 (26%)
6	NAG	A	601	1,6	14,14,15	0.67	0	15,19,21	0.82	1 (6%)
6	NAG	A	602	6	14,14,15	0.63	0	15,19,21	0.96	2 (13%)
6	MAN	A	603	6	11,11,12	0.67	0	14,15,17	0.38	0
7	NAG	A	604	1,7	14,14,15	0.54	0	15,19,21	0.79	0
7	NAG	A	616	7	14,14,15	0.62	0	15,19,21	0.78	1 (6%)

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
6	NAG	A	596	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	597	6	-	0/6/23/26	0/1/1/1
6	MAN	A	598	6	-	0/2/19/22	0/1/1/1
7	NAG	A	599	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	600	7	-	0/6/23/26	0/1/1/1
6	NAG	A	601	1,6	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	602	6	-	0/6/23/26	0/1/1/1
6	MAN	A	603	6	-	0/2/19/22	1/1/1/1
7	NAG	A	604	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	616	7	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	600	NAG	C2-N2-C7	-3.14	119.00	123.04
7	A	599	NAG	C2-N2-C7	-2.17	120.25	123.04
6	A	601	NAG	C2-N2-C7	-2.14	120.29	123.04
6	A	602	NAG	C2-N2-C7	-2.08	120.37	123.04
7	A	616	NAG	C2-N2-C7	-2.06	120.39	123.04

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	603	MAN	C1-C2-C3-C4-C5-O5

6 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	599	NAG	1	0
7	A	600	NAG	2	0
6	A	601	NAG	1	0
6	A	602	NAG	2	0
6	A	603	MAN	1	0
7	A	616	NAG	1	0

## 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 9 are monoatomic - leaving 3 for Mogul analysis.

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	605	1	30,50,50	2.45	11 (36%)	24,82,82	2.30	8 (33%)
5	SCN	A	615	-	2,2,2	2.85	1 (50%)	1,1,1	0.08	0
8	SHA	A	617	-	11,11,11	2.75	5 (45%)	13,14,14	1.21	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	605	1	-	0/10/54/54	0/0/8/8
5	SCN	A	615	-	-	0/0/0/0	0/0/0/0
8	SHA	A	617	-	-	0/6/6/6	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	605	HEM	C3B-C4B	-5.15	1.47	1.51
2	A	605	HEM	C2C-C1C	-4.51	1.44	1.52
2	A	605	HEM	CMA-C3A	-3.80	1.43	1.51
8	A	617	SHA	C2-C1	-3.61	1.33	1.39
8	A	617	SHA	C1-C7	-2.85	1.44	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	605	HEM	CBD-CAD-C3D	-3.08	104.60	113.55
8	A	617	SHA	C3-C4-C5	-2.99	115.81	120.19
8	A	617	SHA	C4-C5-C6	2.11	122.75	120.04
2	A	605	HEM	C2D-C3D-C4D	2.40	105.58	101.50
2	A	605	HEM	CMD-C2D-C3D	2.67	126.18	114.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	605	HEM	6	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	594/595 (99%)	0.54	57 (9%) 10 16	15, 31, 74, 100	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	TRP	11.6
1	A	595	ASN	10.1
1	A	120	GLY	9.5
1	A	170	PRO	9.4
1	A	1	SER	9.1

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

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(Å <sup>2</sup> )	Q<0.9
1	SEP	A	198	10/11	0.94	0.21	-	34,39,46,48	0

### 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
6	NAG	A	596	14/15	0.86	0.26	0.97	62,66,71,77	0
6	NAG	A	601	14/15	0.88	0.15	-0.10	54,56,60,66	0
7	NAG	A	599	14/15	0.91	0.16	-0.38	51,54,57,61	0
6	NAG	A	602	14/15	0.66	0.45	-	71,74,77,81	0
6	MAN	A	603	11/12	0.57	0.49	-	84,87,88,88	0
7	NAG	A	600	14/15	0.78	0.36	-	64,67,68,69	0
6	MAN	A	598	11/12	0.57	0.57	-	95,97,98,98	0
7	NAG	A	604	14/15	0.75	0.33	-	64,67,71,76	0
6	NAG	A	597	14/15	0.70	0.56	-	83,88,89,92	0
7	NAG	A	616	14/15	0.51	0.67	-	80,83,84,84	0

## 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
8	SHA	A	617	11/11	0.85	0.23	2.70	26,28,30,31	0
2	HEM	A	605	43/43	0.94	0.15	0.41	13,15,21,22	0
5	SCN	A	615	3/3	0.89	0.13	-0.56	32,32,32,36	0
3	CA	A	606	1/1	0.99	0.12	-0.66	20,20,20,20	0
4	IOD	A	613	1/1	0.99	0.05	-1.35	56,56,56,56	0
4	IOD	A	610	1/1	1.00	0.04	-2.97	67,67,67,67	0
4	IOD	A	611	1/1	0.96	0.07	-3.15	84,84,84,84	0
4	IOD	A	612	1/1	0.98	0.04	-4.37	64,64,64,64	0
4	IOD	A	607	1/1	1.00	0.05	-5.70	20,20,20,20	0
4	IOD	A	608	1/1	0.98	0.07	-	89,89,89,89	0
4	IOD	A	614	1/1	0.97	0.09	-	77,77,77,77	1
4	IOD	A	609	1/1	0.92	0.09	-	63,63,63,63	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.