



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:03 PM GMT

PDB ID : 4USC  
Title : Crystal structure of peroxidase from palm tree *Chamaerops excelsa*  
Authors : Bernardes, A.; Santos, J.C.; Textor, L.C.; Cuadrado, N.H.; Kostetsky, E.Y.;  
Roig, M.G.; Muniz, J.R.C.; Shnyrov, V.L.; Polikarpov, I.  
Deposited on : 2014-07-07  
Resolution : 2.60 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.

---

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

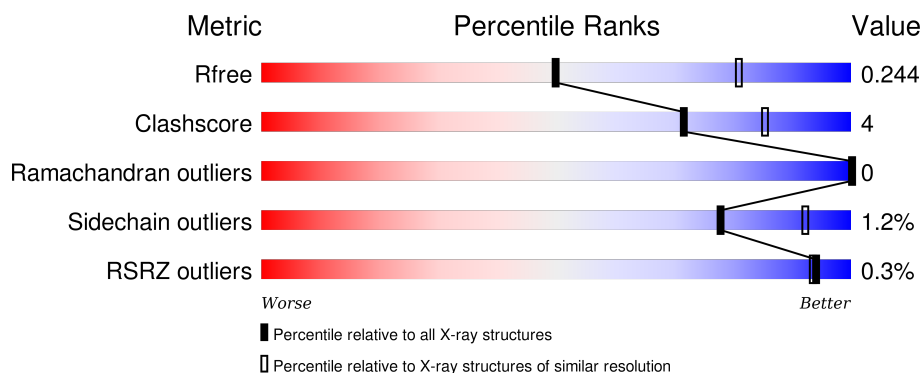
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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  $\geq 3$ , 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	303	<div> <div></div> <div>91%</div> <div>8%</div> </div>
1	B	303	<div> <div></div> <div>95%</div> <div>5%</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
11	PEO	A	1320	-	-	-	X
3	NAG	A	1307	X	-	-	-
3	MAN	A	1308	X	-	-	-
5	NAG	A	1314	X	-	-	-
5	NAG	A	1315	-	-	X	-

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 4860 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 PEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2229	1386	385	447	11			
1	B	303	Total	C	N	O	S	0	0	0
			2232	1387	385	449	11			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		
2	A	2	Total	Ca	0	0
			2	2		

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

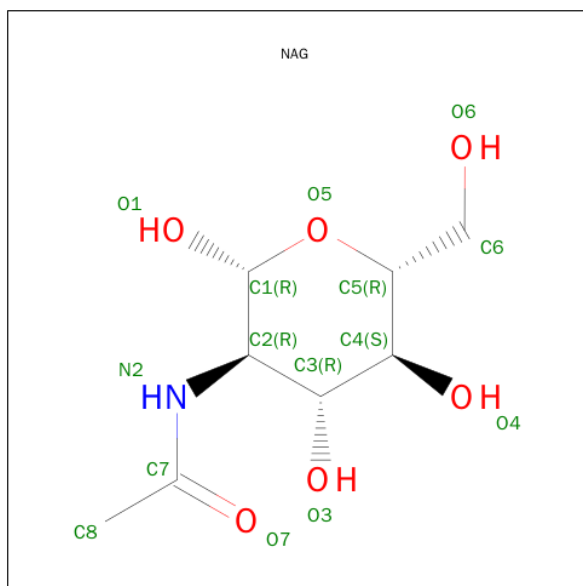
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 4 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

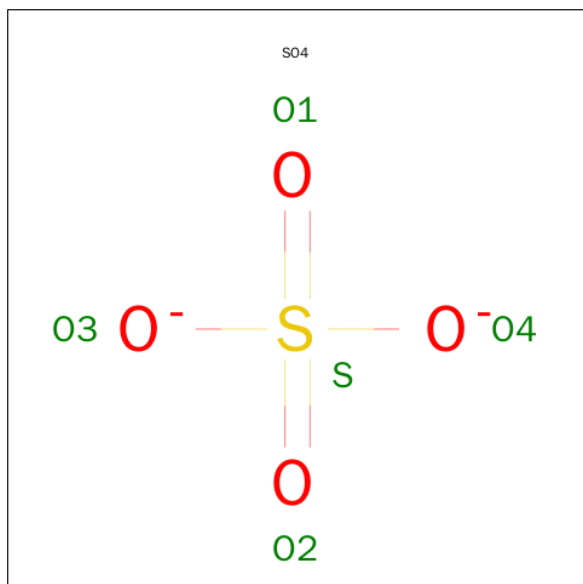
Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- 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	0	0
			38	22	2	14		
6	B	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



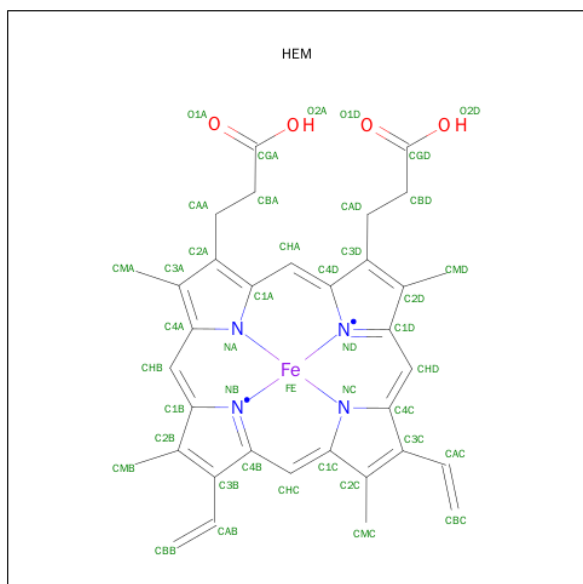
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



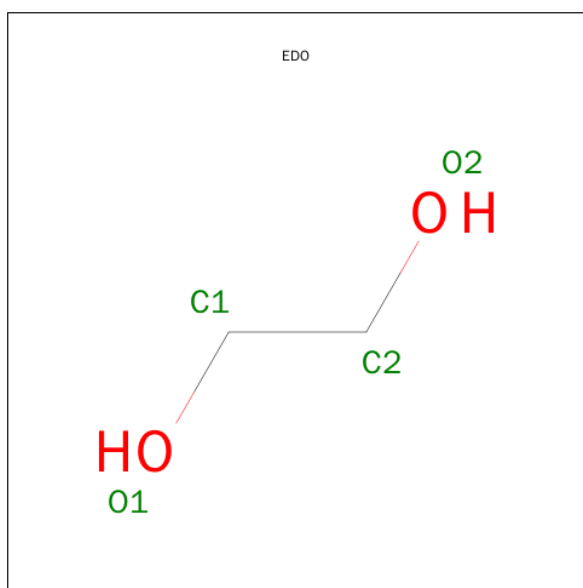
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	O		0	0
			7	4	3			

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



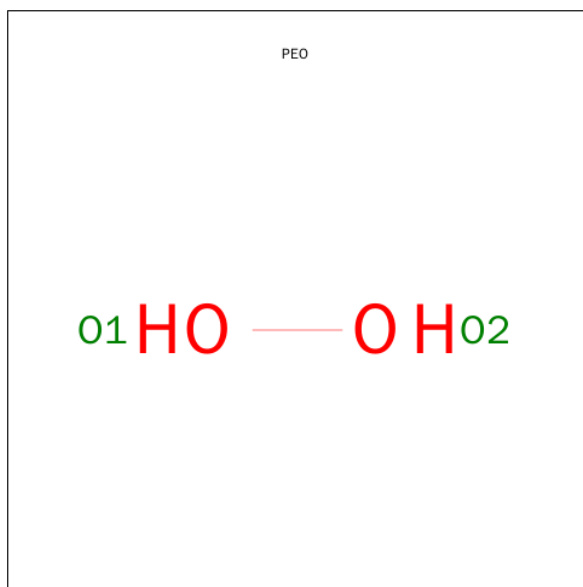
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
9	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 11 is HYDROGEN PEROXIDE (three-letter code: PEO) (formula:  $H_2O_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	1	Total	O	0	0
			2	2		



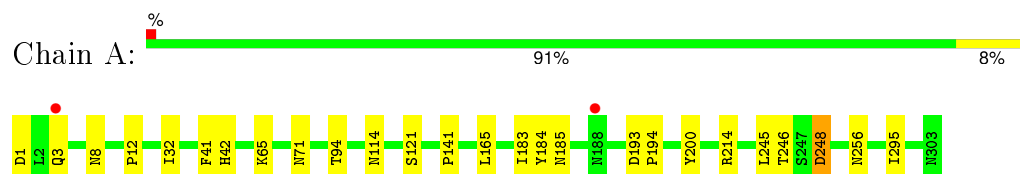
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	49	Total 49	O 49	0	0
12	B	36	Total 36	O 36	0	0

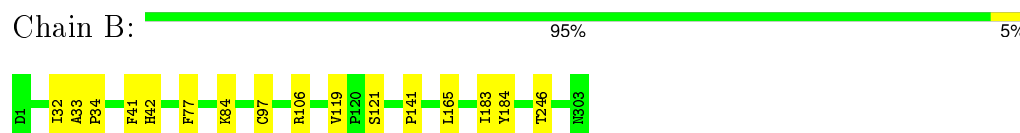
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: PEROXIDASE



- Molecule 1: PEROXIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.18Å 100.65Å 132.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.11 – 2.60 80.11 – 2.60	Depositor EDS
% Data completeness (in resolution range)	90.1 (80.11-2.60) 90.1 (80.11-2.60)	Depositor EDS
$R_{merge}$	0.01	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.59 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.218 , 0.246 0.225 , 0.244	Depositor DCC
$R_{free}$ test set	1369 reflections (5.42%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.4	Xtriage
Anisotropy	1.199	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 26615 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4860	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.11 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.3849e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: NAG, CA, MAN, EDO, PEO, FUC, HEM, PEG, SO4

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	0.63	0/2265	0.73	2/3091 (0.1%)
1	B	0.63	0/2268	0.73	0/3095
All	All	0.63	0/4533	0.73	2/6186 (0.0%)

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
3	A	2	0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	248	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	193	ASP	CB-CG-OD2	-5.23	113.60	118.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1307	NAG	C1
3	A	1308	MAN	C1

There are no planarity outliers.

## 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	2229	0	2168	20	0
1	B	2232	0	2172	10	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	39	0	34	1	0
4	A	12	0	12	1	0
5	A	42	0	39	7	0
5	B	28	0	26	0	0
6	A	38	0	34	0	0
6	B	38	0	34	0	0
7	A	5	0	0	0	0
7	B	5	0	0	1	0
8	A	7	0	10	1	0
9	A	43	0	30	6	0
9	B	43	0	30	6	0
10	A	4	0	6	0	0
10	B	4	0	6	0	0
11	A	2	0	0	1	0
12	A	49	0	0	1	0
12	B	36	0	0	0	0
All	All	4860	0	4601	40	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 4.

The worst 5 of 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:A:185:ASN:HD21	5:A:1315:NAG:C1	1.23	1.52
1:A:185:ASN:ND2	5:A:1315:NAG:C1	1.99	1.24
1:A:65:LYS:HE2	8:A:1317:PEG:H22	1.71	0.72
1:A:185:ASN:CG	5:A:1315:NAG:C1	2.63	0.67
9:B:1312:HEM:HHC	9:B:1312:HEM:HBB2	1.78	0.64

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	301/303 (99%)	298 (99%)	3 (1%)	0	100	100
1	B	301/303 (99%)	300 (100%)	1 (0%)	0	100	100
All	All	602/606 (99%)	598 (99%)	4 (1%)	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	242/246 (98%)	237 (98%)	5 (2%)	61	85
1	B	243/246 (99%)	242 (100%)	1 (0%)	93	98
All	All	485/492 (99%)	479 (99%)	6 (1%)	78	92

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	200	TYR
1	B	121	SER
1	A	214	ARG
1	A	194	PRO
1	A	256	ASN

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 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 ⓘ

9 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	1306	1,3	14,14,15	0.99	1 (7%)	15,19,21	2.42	4 (26%)
3	NAG	A	1307	3	14,14,15	1.31	1 (7%)	15,19,21	1.71	2 (13%)
3	MAN	A	1308	3	11,11,12	0.92	1 (9%)	14,15,17	2.02	4 (28%)
6	NAG	A	1311	1,6	14,14,15	0.48	0	15,19,21	1.59	3 (20%)
6	NAG	A	1312	6	14,14,15	0.60	0	15,19,21	0.90	0
6	FUC	A	1313	6	10,10,11	0.79	0	14,14,16	1.10	2 (14%)
6	NAG	B	1304	1,6	14,14,15	0.54	0	15,19,21	1.07	1 (6%)
6	NAG	B	1305	6	14,14,15	0.63	0	15,19,21	1.19	3 (20%)
6	FUC	B	1306	6	10,10,11	0.62	0	14,14,16	1.47	2 (14%)

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	1306	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1307	3	1/1/5/7	0/6/23/26	0/1/1/1
3	MAN	A	1308	3	1/1/4/5	0/2/19/22	0/1/1/1
6	NAG	A	1311	1,6	-	0/6/23/26	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	1312	6	-	0/6/23/26	0/1/1/1
6	FUC	A	1313	6	-	0/0/17/20	0/1/1/1
6	NAG	B	1304	1,6	-	0/6/23/26	0/1/1/1
6	NAG	B	1305	6	-	0/6/23/26	0/1/1/1
6	FUC	B	1306	6	-	0/0/17/20	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1306	NAG	O5-C1	-2.39	1.39	1.43
3	A	1308	MAN	C2-C3	2.03	1.55	1.52
3	A	1307	NAG	C1-C2	4.47	1.58	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1306	NAG	C4-C3-C2	-2.70	107.04	111.23
6	A	1311	NAG	O3-C3-C4	-2.32	105.12	110.34
6	A	1311	NAG	O7-C7-C8	-2.27	117.89	122.06
6	B	1305	NAG	O4-C4-C5	2.04	114.64	109.24
6	A	1313	FUC	C1-O5-C5	2.06	115.57	112.38

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1307	NAG	C1
3	A	1308	MAN	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1307	NAG	1	0

## 5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 4 are monoatomic - leaving 14 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
4	MAN	A	1309	-	12,12,12	0.59	0	17,17,17	2.51	3 (17%)
5	NAG	A	1310	1	14,14,15	0.88	1 (7%)	15,19,21	1.92	3 (20%)
5	NAG	A	1314	1	14,14,15	0.66	0	15,19,21	1.08	1 (6%)
5	NAG	A	1315	-	14,14,15	1.05	1 (7%)	15,19,21	2.63	3 (20%)
7	SO4	A	1316	-	4,4,4	0.45	0	6,6,6	0.41	0
8	PEG	A	1317	-	6,6,6	0.67	0	5,5,5	0.36	0
9	HEM	A	1318	1,11	30,50,50	2.37	7 (23%)	24,82,82	2.40	12 (50%)
10	EDO	A	1319	-	3,3,3	0.83	0	2,2,2	0.46	0
11	PEO	A	1320	9	1,1,1	0.80	0	0,0,0	0.00	-
5	NAG	B	1307	1	14,14,15	0.72	1 (7%)	15,19,21	1.17	1 (6%)
5	NAG	B	1308	1	14,14,15	0.58	0	15,19,21	2.49	4 (26%)
7	SO4	B	1311	-	4,4,4	0.41	0	6,6,6	0.26	0
9	HEM	B	1312	1	30,50,50	2.35	7 (23%)	24,82,82	2.33	11 (45%)
10	EDO	B	1313	-	3,3,3	0.88	0	2,2,2	0.25	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
4	MAN	A	1309	-	-	0/2/22/22	0/1/1/1
5	NAG	A	1310	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1314	1	1/1/5/7	0/6/23/26	0/1/1/1
5	NAG	A	1315	-	-	0/6/23/26	0/1/1/1
7	SO4	A	1316	-	-	0/0/0/0	0/0/0/0
8	PEG	A	1317	-	-	0/4/4/4	0/0/0/0
9	HEM	A	1318	1,11	-	0/10/54/54	0/0/8/8
10	EDO	A	1319	-	-	0/1/1/1	0/0/0/0
11	PEO	A	1320	9	-	0/0/0/0	0/0/0/0
5	NAG	B	1307	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
7	SO4	B	1311	-	-	0/0/0/0	0/0/0/0
9	HEM	B	1312	1	-	0/10/54/54	0/0/8/8
10	EDO	B	1313	-	-	0/1/1/1	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1318	HEM	C2D-C3D	-6.55	1.34	1.54
9	B	1312	HEM	C2D-C3D	-6.38	1.35	1.54
9	B	1312	HEM	C2C-C1C	-6.04	1.41	1.52
9	A	1318	HEM	C2C-C1C	-5.97	1.41	1.52
9	A	1318	HEM	C3B-C4B	-5.64	1.46	1.51

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1309	MAN	O1-C1-O5	-7.79	88.95	110.25
5	B	1308	NAG	C4-C3-C2	-4.50	104.23	111.23
5	A	1310	NAG	C4-C3-C2	-4.49	104.25	111.23
9	A	1318	HEM	C3B-CAB-CBB	-3.76	118.69	124.46
9	B	1312	HEM	C3B-CAB-CBB	-3.15	119.62	124.46

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1314	NAG	C1

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1309	MAN	1	0
5	A	1315	NAG	7	0
8	A	1317	PEG	1	0
9	A	1318	HEM	6	0
11	A	1320	PEO	1	0
7	B	1311	SO4	1	0
9	B	1312	HEM	6	0

## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	303/303 (100%)	-0.15	2 (0%) 89 87	33, 53, 75, 97	1 (0%)
1	B	303/303 (100%)	-0.15	0 100 100	33, 55, 78, 103	0
All	All	606/606 (100%)	-0.15	2 (0%) 94 93	33, 54, 78, 103	1 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	188	ASN	2.8
1	A	3	GLN	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](#)

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
6	NAG	B	1304	14/15	0.91	0.19	-0.09	78,90,101,112	0
6	FUC	A	1313	10/11	0.91	0.16	-	62,69,74,74	0
3	NAG	A	1306	14/15	0.95	0.14	-	57,65,80,86	0
6	NAG	A	1312	14/15	0.93	0.13	-	64,73,76,78	0
6	NAG	B	1305	14/15	0.82	0.28	-	84,97,106,107	0
3	NAG	A	1307	14/15	0.84	0.29	-	68,87,95,97	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MAN	A	1308	11/12	0.83	0.21	-	74,83,86,89	0
6	FUC	B	1306	10/11	0.92	0.22	-	89,94,107,111	0
6	NAG	A	1311	14/15	0.93	0.14	-	55,67,74,78	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
11	PEO	A	1320	2/2	0.96	0.24	3.93	30,30,30,33	2
9	HEM	B	1312	43/43	0.97	0.17	0.70	42,51,54,55	0
9	HEM	A	1318	43/43	0.96	0.17	0.37	36,47,52,55	0
7	SO4	B	1311	5/5	0.98	0.19	0.17	58,59,64,73	0
5	NAG	A	1310	14/15	0.84	0.15	-0.91	63,74,78,84	0
2	CA	A	1304	1/1	0.99	0.13	-1.26	38,38,38,38	0
2	CA	A	1305	1/1	1.00	0.13	-2.10	42,42,42,42	0
2	CA	B	1309	1/1	0.99	0.09	-2.77	44,44,44,44	0
2	CA	B	1310	1/1	0.99	0.10	-3.85	36,36,36,36	0
10	EDO	A	1319	4/4	0.81	0.14	-	54,55,55,56	0
8	PEG	A	1317	7/7	0.89	0.15	-	61,69,72,73	0
7	SO4	A	1316	5/5	0.98	0.18	-	46,47,53,57	0
5	NAG	B	1308	14/15	0.89	0.16	-	59,70,78,82	0
5	NAG	A	1315	14/15	0.81	0.24	-	34,37,39,40	14
5	NAG	A	1314	14/15	0.87	0.21	-	41,44,47,47	14
5	NAG	B	1307	14/15	0.74	0.22	-	85,103,110,114	0
4	MAN	A	1309	12/12	0.87	0.19	-	62,73,82,87	0
10	EDO	B	1313	4/4	0.92	0.14	-	48,50,53,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.