



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:20 AM GMT

PDB ID : 2Q9O  
Title : Near-atomic resolution structure of a Melanocarpus albomyces laccase  
Authors : Hakulinen, N.; Rouvinen, J.  
Deposited on : 2007-06-13  
Resolution : 1.30 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

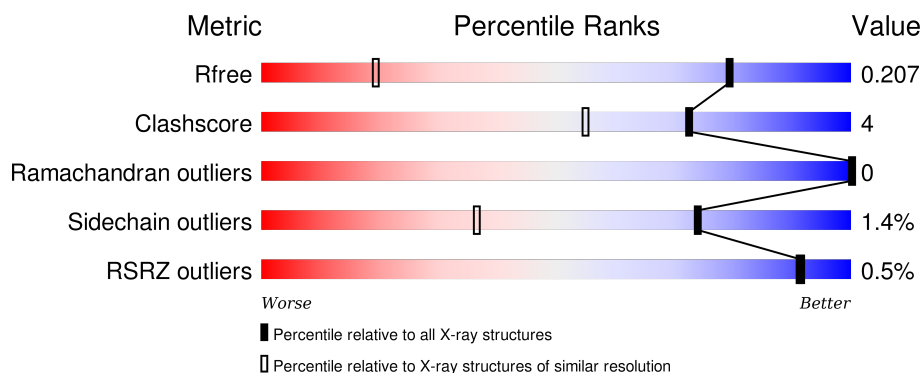
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.30 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	1475 (1.34-1.26)
Clashscore	102246	1031 (1.32-1.28)
Ramachandran outliers	100387	1504 (1.34-1.26)
Sidechain outliers	100360	1503 (1.34-1.26)
RSRZ outliers	91569	1476 (1.34-1.26)

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	559	<div> <div></div> <div>88%</div> <div>11%</div> <div>.</div> </div>
1	B	559	<div> <div></div> <div>90%</div> <div>9%</div> <div>.</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
10	SO4	A	4003	-	-	-	X
11	OXY	A	4006	-	-	-	X
11	OXY	B	4005	-	-	-	X
12	GOL	A	3001[A]	-	-	-	X
12	GOL	A	3001[B]	-	-	-	X
12	GOL	B	3002[A]	-	-	-	X
12	GOL	B	3002[B]	-	-	-	X
2	NAG	A	1001	-	-	-	X
2	NAG	A	1051	-	-	-	X
2	NAG	A	1071	-	-	-	X
2	NAG	B	1051	-	-	-	X
2	NAG	G	61	-	-	-	X
3	MAN	C	13	X	-	-	-
3	NAG	E	32	-	-	-	X
3	MAN	E	33	X	-	-	-
3	MAN	H	1013	X	-	-	-
4	NAG	D	21	-	-	-	X
4	NAG	I	1021	-	-	-	X
4	NAG	I	1022	-	-	-	X
4	NAG	J	1032	-	-	-	X
5	MAN	G	63	X	-	-	-
6	NAG	L	1061	-	-	-	X
6	MAN	L	1063	X	-	-	-

## 2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 10805 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.

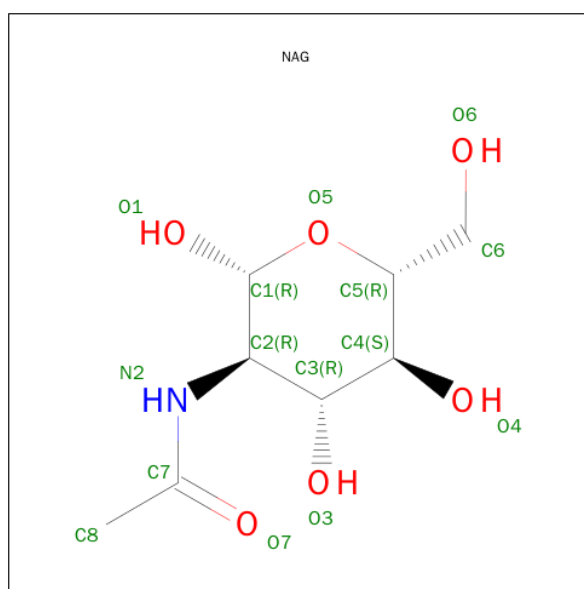
- Molecule 1 is a protein called Laccase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	14	0
			4432	2798	770	847	17			
1	B	559	Total	C	N	O	S	0	15	0
			4418	2789	767	846	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	98	OHI	HIS	MODIFIED RESIDUE	UNP Q70KY3
B	98	OHI	HIS	MODIFIED RESIDUE	UNP Q70KY3

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	J	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		

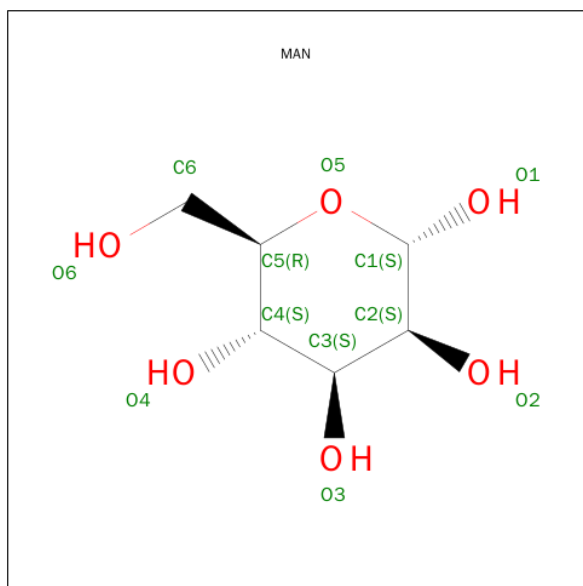
- Molecule 5 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	G	4	Total	C	N	O	0	0
			47	26	1	20		

- Molecule 6 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	L	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 7 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
7	L	1	Total	C	O	0	0
			11	6	5		

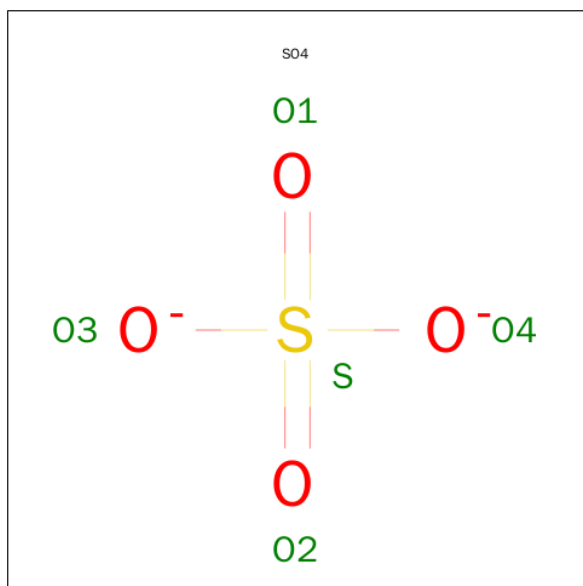
- Molecule 8 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	4	Total	Cu	0	0
			4	4		
8	A	4	Total	Cu	0	0
			4	4		

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

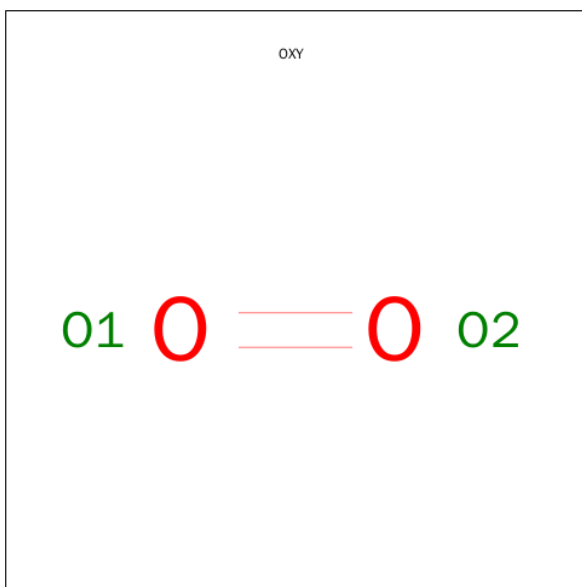
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Cl	0	0
			1	1		
9	A	1	Total	Cl	0	0
			1	1		

- Molecule 10 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



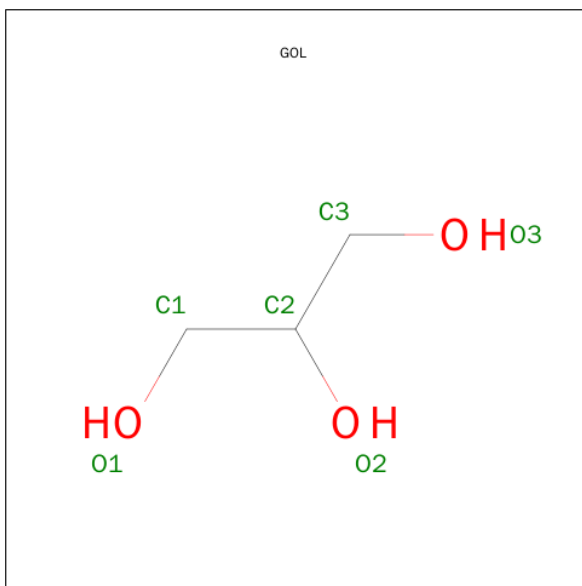
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	O	S	0	0
			5	4	1		
10	B	1	Total	O	S	0	0
			5	4	1		
10	A	1	Total	O	S	0	0
			5	4	1		
10	B	1	Total	O	S	0	0
			5	4	1		
10	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 11 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O<sub>2</sub>).



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

- Molecule 12 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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



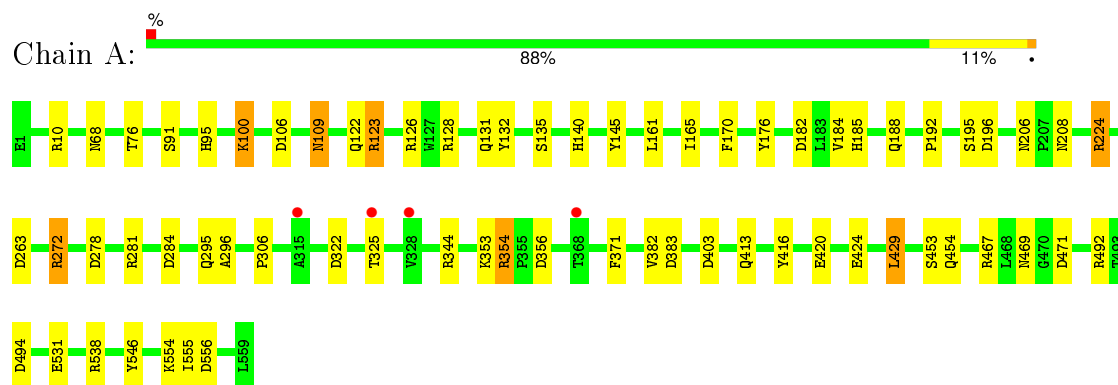
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	700	Total 700	O 700	0	0
13	B	683	Total 683	O 683	0	0
13	C	7	Total 7	O 7	0	0
13	D	3	Total 3	O 3	0	0
13	E	6	Total 6	O 6	0	0
13	G	14	Total 14	O 14	0	0
13	H	9	Total 9	O 9	0	0
13	I	2	Total 2	O 2	0	0
13	J	2	Total 2	O 2	0	0
13	K	2	Total 2	O 2	0	0
13	L	15	Total 15	O 15	0	0

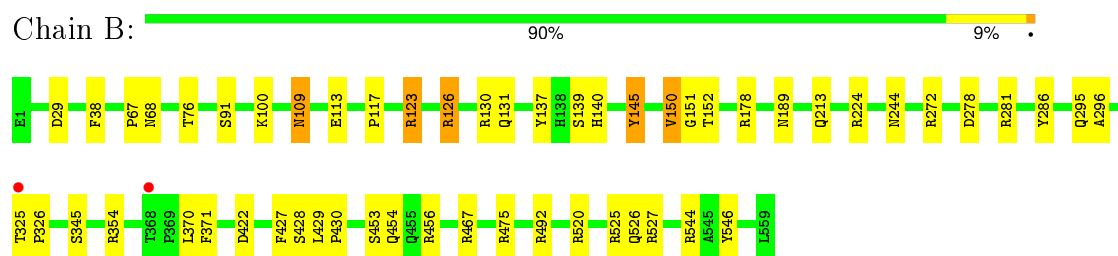
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: Laccase-1



#### • Molecule 1: Laccase-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.74Å 61.90Å 124.21Å 90.00° 96.36° 90.00°	Depositor
Resolution (Å)	15.00 – 1.30 19.63 – 1.30	Depositor EDS
% Data completeness (in resolution range)	91.9 (15.00-1.30) 96.7 (19.63-1.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 1.30Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.167 , 0.212 0.167 , 0.207	Depositor DCC
$R_{free}$ test set	15526 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	8.3	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 62.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 310644 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10805	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: GOL, OHI, CL, NAG, OXY, SO4, CU, 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	0.55	0/4613	1.28	35/6331 (0.6%)
1	B	0.54	0/4608	1.26	30/6326 (0.5%)
All	All	0.55	0/9221	1.27	65/12657 (0.5%)

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	C	1	0
3	E	1	0
3	H	1	0
5	G	1	0
6	L	1	0
All	All	5	0

There are no bond length outliers.

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	123	ARG	NE-CZ-NH1	-12.91	113.85	120.30
1	A	123	ARG	NE-CZ-NH1	-11.77	114.42	120.30
1	A	128	ARG	NE-CZ-NH2	-11.76	114.42	120.30
1	B	544	ARG	NE-CZ-NH1	10.64	125.62	120.30
1	B	467	ARG	NE-CZ-NH2	-10.62	114.99	120.30

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	13	MAN	C1
3	E	33	MAN	C1
5	G	63	MAN	C1
3	H	1013	MAN	C1
6	L	1063	MAN	C1

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	4432	0	4171	37	0
1	B	4418	0	4154	35	0
2	A	70	0	64	4	0
2	B	28	0	26	0	0
2	G	14	0	12	2	0
3	C	39	0	34	0	0
3	E	39	0	34	0	0
3	H	39	0	34	0	0
4	D	28	0	25	0	0
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	K	28	0	25	0	0
5	G	47	0	40	0	0
6	L	50	0	42	0	0
7	L	11	0	10	0	0
8	A	4	0	0	0	0
8	B	4	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	15	0	0	0	0
10	B	10	0	0	0	0
11	A	2	0	0	0	0
11	B	2	0	0	0	0
12	A	12	0	16	2	0
12	B	12	0	16	3	0
13	A	700	0	0	16	0
13	B	683	0	0	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	C	7	0	0	0	0
13	D	3	0	0	0	0
13	E	6	0	0	0	0
13	G	14	0	0	1	0
13	H	9	0	0	0	0
13	I	2	0	0	0	0
13	J	2	0	0	1	0
13	K	2	0	0	0	0
13	L	15	0	0	0	0
All	All	10805	0	8753	76	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 76 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:126[A]:ARG:NH1	13:A:4671:HOH:O	1.60	1.34
1:A:126[A]:ARG:CZ	13:A:4671:HOH:O	1.82	1.23
1:A:182[B]:ASP:OD1	13:A:4474:HOH:O	1.76	1.01
2:A:1002:NAG:C4	2:A:1003:NAG:C1	2.53	0.86
1:A:161:LEU:HG	1:A:224:ARG:HH12	1.41	0.84

There are no symmetry-related clashes.

## 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	571/559 (102%)	559 (98%)	12 (2%)	0	100	100
1	B	571/559 (102%)	559 (98%)	12 (2%)	0	100	100
All	All	1142/1118 (102%)	1118 (98%)	24 (2%)	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	492/477 (103%)	484 (98%)	8 (2%)	70	30
1	B	492/477 (103%)	487 (99%)	5 (1%)	82	51
All	All	984/954 (103%)	971 (99%)	13 (1%)	74	38

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	306	PRO
1	A	325	THR
1	B	123	ARG
1	A	272	ARG
1	B	109	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	84	ASN
1	B	99	GLN
1	B	454	GLN
1	A	469	ASN
1	B	295	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	OHI	A	98	-	10,11,12	1.63	2 (20%)	4,14,16	2.69	2 (50%)
1	OHI	B	98	-	10,11,12	1.72	2 (20%)	4,14,16	3.03	3 (75%)

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	OHI	A	98	-	-	0/2/15/17	0/1/1/1
1	OHI	B	98	-	-	0/2/15/17	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	OHI	O12-CE1	2.78	1.28	1.23
1	B	98	OHI	CG-ND1	3.18	1.39	1.33
1	B	98	OHI	O12-CE1	3.23	1.29	1.23
1	A	98	OHI	CG-ND1	3.31	1.40	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	OHI	CA-CB-CG	-4.37	105.33	114.45
1	A	98	OHI	CA-CB-CG	-3.73	106.65	114.45
1	B	98	OHI	O-C-CA	-3.66	115.97	125.49
1	A	98	OHI	O-C-CA	-3.46	116.49	125.49
1	B	98	OHI	CB-CG-CD2	-2.08	119.19	129.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



## 5.5 Carbohydrates ⓘ

25 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	C	11	1,3	14,14,15	0.68	0	15,19,21	0.90	0
3	NAG	C	12	3	14,14,15	0.83	1 (7%)	15,19,21	1.16	2 (13%)
3	MAN	C	13	3	11,11,12	0.86	0	14,15,17	2.05	6 (42%)
4	NAG	D	21	1,4	14,14,15	0.89	1 (7%)	15,19,21	1.96	2 (13%)
4	NAG	D	22	4	14,14,15	0.89	1 (7%)	15,19,21	1.79	5 (33%)
3	NAG	E	31	1,3	14,14,15	0.78	0	15,19,21	0.92	1 (6%)
3	NAG	E	32	3	14,14,15	0.77	1 (7%)	15,19,21	1.21	1 (6%)
3	MAN	E	33	3	11,11,12	0.87	1 (9%)	14,15,17	2.48	5 (35%)
5	NAG	G	62	2,5	14,14,15	0.80	1 (7%)	15,19,21	0.76	0
5	MAN	G	63	5	11,11,12	0.59	0	14,15,17	0.93	0
5	MAN	G	64	5	11,11,12	0.60	0	14,15,17	1.43	2 (14%)
5	MAN	G	65	5	11,11,12	0.57	0	14,15,17	1.33	1 (7%)
3	NAG	H	1011	1,3	14,14,15	0.73	1 (7%)	15,19,21	0.97	0
3	NAG	H	1012	3	14,14,15	0.73	0	15,19,21	1.48	1 (6%)
3	MAN	H	1013	3	11,11,12	0.58	0	14,15,17	1.79	2 (14%)
4	NAG	I	1021	1,4	14,14,15	0.72	1 (7%)	15,19,21	1.15	2 (13%)
4	NAG	I	1022	4	14,14,15	0.75	0	15,19,21	1.45	3 (20%)
4	NAG	J	1031	1,4	14,14,15	0.81	1 (7%)	15,19,21	0.78	0
4	NAG	J	1032	4	14,14,15	0.73	1 (7%)	15,19,21	1.57	2 (13%)
4	NAG	K	1041	1,4	14,14,15	1.18	1 (7%)	15,19,21	1.15	1 (6%)
4	NAG	K	1042	4	14,14,15	0.85	1 (7%)	15,19,21	2.44	7 (46%)
6	NAG	L	1061	1,6	14,14,15	1.01	1 (7%)	15,19,21	1.00	0
6	NAG	L	1062	6	14,14,15	0.75	0	15,19,21	1.39	2 (13%)
6	MAN	L	1063	6	11,11,12	0.65	0	14,15,17	0.88	0
6	MAN	L	1064	7,6	11,11,12	1.03	1 (9%)	14,15,17	1.67	3 (21%)

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	C	11	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	12	3	-	0/6/23/26	0/1/1/1
3	MAN	C	13	3	1/1/4/5	0/2/19/22	0/1/1/1
4	NAG	D	21	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	22	4	-	0/6/23/26	0/1/1/1
3	NAG	E	31	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	32	3	-	0/6/23/26	0/1/1/1
3	MAN	E	33	3	1/1/4/5	0/2/19/22	0/1/1/1
5	NAG	G	62	2,5	-	0/6/23/26	0/1/1/1
5	MAN	G	63	5	1/1/4/5	0/2/19/22	0/1/1/1
5	MAN	G	64	5	-	0/2/19/22	0/1/1/1
5	MAN	G	65	5	-	0/2/19/22	0/1/1/1
3	NAG	H	1011	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	1012	3	-	0/6/23/26	0/1/1/1
3	MAN	H	1013	3	1/1/4/5	0/2/19/22	0/1/1/1
4	NAG	I	1021	1,4	-	0/6/23/26	0/1/1/1
4	NAG	I	1022	4	-	0/6/23/26	0/1/1/1
4	NAG	J	1031	1,4	-	0/6/23/26	0/1/1/1
4	NAG	J	1032	4	-	0/6/23/26	0/1/1/1
4	NAG	K	1041	1,4	-	0/6/23/26	0/1/1/1
4	NAG	K	1042	4	-	0/6/23/26	0/1/1/1
6	NAG	L	1061	1,6	-	0/6/23/26	0/1/1/1
6	NAG	L	1062	6	-	0/6/23/26	0/1/1/1
6	MAN	L	1063	6	1/1/4/5	0/2/19/22	0/1/1/1
6	MAN	L	1064	7,6	-	0/2/19/22	0/1/1/1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	33	MAN	O5-C1	-2.15	1.40	1.43
3	H	1011	NAG	C1-C2	2.04	1.55	1.52
4	I	1021	NAG	C1-C2	2.08	1.55	1.52
4	J	1032	NAG	C1-C2	2.16	1.55	1.52
3	E	32	NAG	C1-C2	2.18	1.55	1.52

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	1042	NAG	C2-N2-C7	-5.91	115.45	123.04
4	D	21	NAG	C2-N2-C7	-5.32	116.21	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	1032	NAG	O7-C7-C8	-4.34	114.09	122.06
4	K	1042	NAG	O7-C7-N2	-3.84	114.03	121.86
3	H	1012	NAG	O7-C7-C8	-3.80	115.09	122.06

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	L	1063	MAN	C1
3	E	33	MAN	C1
3	H	1013	MAN	C1
3	C	13	MAN	C1
5	G	63	MAN	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 10 are monoatomic - leaving 20 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	NAG	A	1001	1	14,14,15	1.01	1 (7%)	15,19,21	2.42	7 (46%)
2	NAG	A	1002	1,2	14,14,15	1.11	1 (7%)	15,19,21	1.10	1 (6%)
2	NAG	A	1003	2	14,14,15	0.80	1 (7%)	15,19,21	1.45	3 (20%)
2	NAG	A	1051	1	14,14,15	0.58	0	15,19,21	1.58	3 (20%)
2	NAG	A	1071	1	14,14,15	0.87	1 (7%)	15,19,21	1.39	2 (13%)
12	GOL	A	3001[A]	-	5,5,5	0.27	0	5,5,5	0.91	0
12	GOL	A	3001[B]	-	5,5,5	0.26	0	5,5,5	0.37	0
10	SO4	A	4001	-	4,4,4	0.27	0	6,6,6	0.42	0
10	SO4	A	4003	-	4,4,4	0.22	0	6,6,6	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
10	SO4	A	4005	-	4,4,4	0.25	0	6,6,6	0.17	0
11	OXY	A	4006	-	1,1,1	0.83	0	0,0,0	0.00	-
2	NAG	B	1001	1	14,14,15	0.76	0	15,19,21	1.64	3 (20%)
2	NAG	B	1051	1	14,14,15	0.84	1 (7%)	15,19,21	0.94	1 (6%)
12	GOL	B	3002[A]	-	5,5,5	0.22	0	5,5,5	0.21	0
12	GOL	B	3002[B]	-	5,5,5	0.24	0	5,5,5	0.24	0
10	SO4	B	4002	-	4,4,4	0.29	0	6,6,6	0.61	0
10	SO4	B	4004	-	4,4,4	0.22	0	6,6,6	0.50	0
11	OXY	B	4005	-	1,1,1	0.85	0	0,0,0	0.00	-
2	NAG	G	61	5	14,14,15	1.11	1 (7%)	15,19,21	2.14	7 (46%)
7	MAN	L	1065	6	11,11,12	0.73	0	14,15,17	1.68	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
2	NAG	A	1001	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1002	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1003	2	-	0/6/23/26	0/1/1/1
2	NAG	A	1051	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1071	1	-	0/6/23/26	0/1/1/1
12	GOL	A	3001[A]	-	-	0/4/4/4	0/0/0/0
12	GOL	A	3001[B]	-	-	0/4/4/4	0/0/0/0
10	SO4	A	4001	-	-	0/0/0/0	0/0/0/0
10	SO4	A	4003	-	-	0/0/0/0	0/0/0/0
10	SO4	A	4005	-	-	0/0/0/0	0/0/0/0
11	OXY	A	4006	-	-	0/0/0/0	0/0/0/0
2	NAG	B	1001	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1051	1	-	0/6/23/26	0/1/1/1
12	GOL	B	3002[A]	-	-	0/4/4/4	0/0/0/0
12	GOL	B	3002[B]	-	-	0/4/4/4	0/0/0/0
10	SO4	B	4002	-	-	0/0/0/0	0/0/0/0
10	SO4	B	4004	-	-	0/0/0/0	0/0/0/0
11	OXY	B	4005	-	-	0/0/0/0	0/0/0/0
2	NAG	G	61	5	-	0/6/23/26	0/1/1/1
7	MAN	L	1065	6	-	0/2/19/22	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1071	NAG	C1-C2	2.08	1.55	1.52
2	A	1003	NAG	C1-C2	2.46	1.55	1.52
2	B	1051	NAG	C1-C2	2.87	1.56	1.52
2	A	1001	NAG	C1-C2	2.98	1.56	1.52
2	G	61	NAG	C1-C2	3.35	1.57	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	NAG	C2-N2-C7	-6.17	115.11	123.04
2	A	1051	NAG	O7-C7-C8	-4.30	114.17	122.06
2	B	1001	NAG	C2-N2-C7	-4.22	117.62	123.04
2	G	61	NAG	C1-O5-C5	-4.17	106.95	112.25
2	G	61	NAG	O4-C4-C5	-3.08	101.07	109.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1002	NAG	4	0
2	A	1003	NAG	4	0
12	A	3001[A]	GOL	1	0
12	A	3001[B]	GOL	1	0
12	B	3002[B]	GOL	3	0
2	G	61	NAG	2	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 [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	558/559 (99%)	-0.34	4 (0%)	89 87	6, 10, 20, 28	0
1	B	558/559 (99%)	-0.34	2 (0%)	93 92	6, 11, 20, 26	0
All	All	1116/1118 (99%)	-0.34	6 (0%)	91 91	6, 11, 20, 28	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	368	THR	3.1
1	A	368	THR	2.5
1	A	325	THR	2.3
1	B	325	THR	2.3
1	A	315	ALA	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	OHI	B	98	11/12	0.94	0.11	-	9,12,16,22	0
1	OHI	A	98	11/12	0.95	0.09	-	8,13,17,23	0

### 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	L	1061	14/15	0.85	0.20	10.46	19,21,26,31	0
4	NAG	I	1022	14/15	0.86	0.21	5.48	24,27,30,32	0
4	NAG	D	21	14/15	0.91	0.13	3.92	17,20,23,26	0
3	NAG	E	32	14/15	0.87	0.13	3.01	18,21,26,29	0
4	NAG	J	1032	14/15	0.90	0.14	2.79	17,21,24,25	0
4	NAG	I	1021	14/15	0.91	0.14	2.73	21,23,25,26	0
4	NAG	D	22	14/15	0.90	0.17	1.86	20,24,26,29	0
4	NAG	K	1041	14/15	0.94	0.08	1.56	12,16,22,23	0
3	NAG	H	1012	14/15	0.95	0.07	0.01	11,14,19,21	0
3	NAG	C	11	14/15	0.98	0.06	-0.03	8,8,11,12	0
3	NAG	H	1011	14/15	0.98	0.06	-0.41	8,9,11,11	0
3	NAG	C	12	14/15	0.97	0.06	-0.61	11,13,16,19	0
3	NAG	E	31	14/15	0.97	0.06	-0.69	12,14,16,16	0
4	NAG	J	1031	14/15	0.97	0.06	-0.81	13,14,18,18	0
3	MAN	C	13	11/12	0.83	0.16	-	19,23,27,28	0
5	NAG	G	62	14/15	0.73	0.24	-	23,28,32,32	0
3	MAN	E	33	11/12	0.66	0.33	-	31,34,37,38	0
4	NAG	K	1042	14/15	0.82	0.28	-	25,28,33,34	0
5	MAN	G	63	11/12	0.87	0.22	-	30,31,32,32	0
3	MAN	H	1013	11/12	0.84	0.24	-	23,26,30,30	0
6	MAN	L	1063	11/12	0.86	0.21	-	29,30,31,33	0
6	MAN	L	1064	11/12	0.76	0.27	-	33,35,37,37	0
5	MAN	G	64	11/12	0.74	0.28	-	33,34,36,37	0
5	MAN	G	65	11/12	0.77	0.24	-	31,32,34,38	0
6	NAG	L	1062	14/15	0.75	0.21	-	26,29,30,30	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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
11	OXY	A	4006	2/2	0.95	0.24	34.60	24,24,24,25	0
11	OXY	B	4005	2/2	0.96	0.20	33.43	23,23,23,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
12	GOL	A	3001[B]	6/6	0.81	0.22	11.90	23,24,25,27	6
12	GOL	A	3001[A]	6/6	0.81	0.22	10.07	22,24,24,25	6
2	NAG	A	1071	14/15	0.71	0.29	9.70	27,30,31,35	0
12	GOL	B	3002[B]	6/6	0.88	0.17	8.02	23,24,24,26	6
12	GOL	B	3002[A]	6/6	0.88	0.17	6.92	24,24,24,24	6
2	NAG	G	61	14/15	0.85	0.19	6.27	20,21,26,33	0
10	SO4	A	4003	5/5	0.81	0.14	6.21	53,53,54,54	0
2	NAG	A	1051	14/15	0.90	0.14	3.46	20,22,27,28	0
2	NAG	A	1001	14/15	0.92	0.10	2.78	16,19,22,22	0
2	NAG	B	1051	14/15	0.94	0.09	2.31	15,17,21,22	0
2	NAG	B	1001	14/15	0.91	0.12	1.28	18,20,24,24	0
2	NAG	A	1002	14/15	0.96	0.06	-0.52	12,14,21,23	0
9	CL	A	2010	1/1	1.00	0.04	-1.33	15,15,15,15	0
8	CU	A	2001	1/1	1.00	0.04	-1.75	7,7,7,7	0
9	CL	B	2010	1/1	1.00	0.04	-2.04	15,15,15,15	0
8	CU	A	2003	1/1	1.00	0.04	-3.10	11,11,11,11	0
8	CU	B	2001	1/1	1.00	0.03	-3.16	7,7,7,7	0
8	CU	B	2002	1/1	1.00	0.03	-3.93	12,12,12,12	0
8	CU	A	2004	1/1	1.00	0.02	-4.22	10,10,10,10	0
8	CU	B	2003	1/1	1.00	0.03	-5.62	11,11,11,11	0
8	CU	A	2002	1/1	1.00	0.03	-6.09	11,11,11,11	0
8	CU	B	2004	1/1	1.00	0.03	-6.76	10,10,10,10	0
10	SO4	A	4001	5/5	0.73	0.15	-	54,54,55,55	0
10	SO4	B	4004	5/5	0.87	0.17	-	58,58,59,59	0
10	SO4	A	4005	5/5	0.90	0.25	-	54,55,55,55	0
10	SO4	B	4002	5/5	0.88	0.12	-	43,43,44,45	0
2	NAG	A	1003	14/15	0.71	0.28	-	25,28,33,34	0
7	MAN	L	1065	11/12	0.73	0.17	-	31,32,33,34	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.