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Key indicators

Single-crystal X-ray study T = 150 K Mean σ (C–C) = 0.003 Å R factor = 0.033 wR factor = 0.070 Data-to-parameter ratio = 9.7

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. 3,5-Di-C-methyl-5,6-O-isopropylidene-L-glucono-1,4-lactone

The relative configuration at position C-2 of the title lactone, $C_{11}H_{18}O_6$, which exists in the five-membered ring form, was unequivocally established by X-ray crystallographic analysis. There are two molecules present in the asymmetric unit (Z' = 2). The absolute configuration was determined by the use of 2,4-di-*C*-methyl-L-arabinose as the starting material.

Comment

In the title compound, (5) (Booth *et al.*, 2007), there are two molecules in the asymmetric unit (Z' = 2). The crystal structure exists as layers of these two molecules lying parallel to the *b* axis, with each molecule acting as an acceptor and donor for two hydrogen bonds (Fig. 3).





The main difference between the two independent molecules is in the orientation of the C1–C2 bond between the lactone ring and the acetonide [torsion angles O6–C2– C1–O11 = 175.3 (2)° and O106–C102–C101–O111 = -64.6 (2)°)] (Figs. 1 and 2).

The main residues are very similar. After least-squares fitting of the lactone residues against each other, the r.m.s. positional discrepancy is 0.097 Å, the r.m.s. bond length discrepancy is 0.0055° and the r.m.s. torsion angle deviation is 7.23° (Fig. 4). The five-membered rings of the acetonide groups match less well, as the envelopes pucker in the opposite sense (Fig. 5, Table 2).

Experimental

3,5-Di-*C*-methyl-5,6-*O*-isopropylidene-L-glucono-1,4-lactone was recrystallized by slow evaporation from a mixture of ethyl acetate and cyclohexane until crystals formed (m.p. 370–375 K). $[\alpha]_D^{18}$ –40.4 (*c*, 1.04 in CHCl₃).

V = 1261.79 (7) Å³

Mo $K\alpha$ radiation

 $1.00\,\times\,0.40\,\times\,0.10$ mm

 $\mu = 0.11 \text{ mm}^{-1}$

T = 150 K

Z = 4

Crystal data $C_{11}H_{18}O_6$ $M_r = 246.26$ Monoclinic, $P2_1$ a = 8.7635 (3) Å b = 10.6004 (3) Å c = 13.7678 (4) Å

 $\beta = 99.4044 \ (14)^{\circ}$

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Figure 1

Molecule 1 of compound (5), with displacement ellipsoids drawn at the 50% probability level. H atoms are shown as spheres of arbitary radius.





Molecule 2 of compound (5), with displacement ellipsoids drawn at the 50% probability level. H atoms are shown as spheres of arbitary radius.

Data collection

Bruker Nonius KappaCCD areadetector diffractometer
Absorption correction: multi-scan (DENZO and SCALEPACK; Otwinowski & Minor, 1997) T_{min} = 0.67, T_{max} = 0.99

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.033$ $wR(F^2) = 0.070$ S = 0.932992 reflections 307 parameters 10042 measured reflections 2992 independent reflections 2521 reflections with $I > 2\sigma(I)$ $R_{int} = 0.031$

 $\begin{array}{l} 1 \mbox{ restraint} \\ H\mbox{-atom parameters constrained} \\ \Delta \rho_{max} = 0.27 \mbox{ e } \mbox{ } \mbox{A}^{-3} \\ \Delta \rho_{min} = -0.23 \mbox{ e } \mbox{ } \mbox{A}^{-3} \end{array}$



Figure 3

The packing diagram for (5), projected along the a axis. The crystal structure contains layers of molecule 1 (blue C atoms) and molecule 2 (green C atoms) running along the b direction. Hydrogen bonds are shown as dotted lines.

Table 1Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
O108-H10O111 ⁱ	0.83	2.01	2.827 (2)	165
O109−H16···O11 ⁱⁱ	0.85	2.03	2.876 (2)	174
O9−H37···O7 ⁱⁱⁱ	0.82	2.01	2.825 (2)	175
$O8-H38\cdots O113^{iv}$	0.84	1.93	2.766 (2)	175

Symmetry codes: (i) $-x, y + \frac{1}{2}, -z + 1$; (ii) $-x + 1, y + \frac{1}{2}, -z + 1$; (iii) $-x + 1, y - \frac{1}{2}, -z$; (iv) x, y, z - 1.

Table 2

Torsion angles in the five-membered ring of the acetonide moiety of (5) ($^{\circ}$).

C1-C14-O13-C12	-38.4(2)	C101-C114-O113-C112	36.8 (2)
C14-O13-C12-O11	29.2 (2)	C114-O113-C112-O111	-27.9(2)
O13-C12-O11-C1	-7.9(2)	O113-C112-O111-C101	7.1 (2)
C12-O11-C1-C14	-14.6(2)	C112-O111-C101-C114	14.8 (2)
O11-C1-C14-O13	31.9 (2)	O111-C101-C114-O113	-30.5(2)

In the absence of significant anomalous scattering, Friedel pairs were merged and the absolute configuration was assigned from the starting material.

The relatively large ratio of minimum to maximum corrections applied in the multi-scan process (1:1.49) reflects changes in the illuminated volume of the crystal. Changes in illuminated volume were kept to a minimum, and were taken into account (Görbitz, 1999) by the multi-scan inter-frame scaling (*DENZO* and *SCALEPACK*; Otwinowski & Minor, 1997).





Figure 5

Overlay of the five-membered rings of the acetonide moiety; molecule 1 is blue with O atoms shown in purple, and molecule 2 is red with O atoms shown in pink. The remaining lactone portion would be connected at C1.

Figure 4

Overlay of the lactone moiety. Molecule 1 is blue with O atoms shown in purple, and molecule 2 is red with O atoms shown in pink. The acetonide portion would be connected at C1.

The H atoms were all located in a difference map, but those attached to C atoms were repositioned geometrically. The H atoms were initially refined with soft restraints on the bond lengths and angles to regularize their geometry (C-H in the range 0.93–0.98 Å and O-H = 0.82 Å) and $U_{\rm iso}$ (H) (in the range 1.2–1.5 times $U_{\rm eq}$ of the parent atom), after which the positions were refined with riding constraints.

Data collection: *COLLECT* (Nonius, 2001); cell refinement: *DENZO* and *SCALEPACK* (Otwinowski & Minor, 1997); data reduction: *DENZO* and *SCALEPACK*; program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics:

CAMERON (Watkin *et al.*, 1996); software used to prepare material for publication: *CRYSTALS*.

References

- Altomare, A., Cascarano, G., Giacovazzo, C., Guagliardi, A., Burla, M. C., Polidori, G. & Camalli, M. (1994). J. Appl. Cryst. 27, 435.
- Betteridge, P. W., Carruthers, J. R., Cooper, R. I., Prout, K. & Watkin, D. J. (2003). J. Appl. Cryst. 36, 1487.
- Booth, K. V., Jenkinson, S. F., Fleet, W. J. & Watkin, D. J. (2007). Acta Cryst. E63, 02204–02206.
- Görbitz, C. H. (1999). Acta Cryst. B55, 1090–1098.
- Nonius (2001). COLLECT. Nonius BV, Delft, The Netherlands.
- Otwinowski, Z. & Minor, W. (1997). *Methods in Enzymology*, Vol. 276, *Macromolecular Crystallography*, Part A, edited by C. W. Carter Jr & R. M. Sweet, pp. 307–326. New York: Academic Press.
- Watkin, D. J., Prout, C. K. & Pearce, L. J. (1996). CAMERON. Chemical Crystallography Laboratory, University of Oxford, England.