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Key indicators

Single-crystal X-ray study

T = 150 K

Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$

R factor = 0.034

wR factor = 0.075

Data-to-parameter ratio = 10.2

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-mannono-1,4-lactone

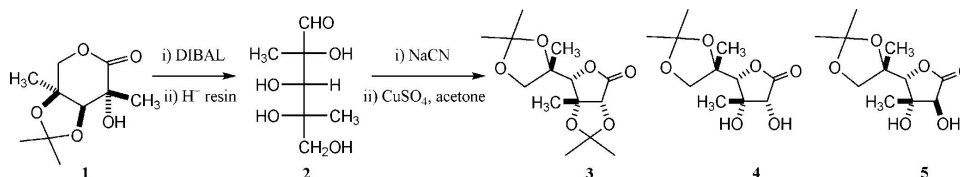
The relative configuration at position C-2 of the title lactone, $\text{C}_{11}\text{H}_{18}\text{O}_6$, which exists in the five-membered ring form, was unequivocally established by X-ray crystallographic analysis. The absolute configuration was determined by the use of 2,4-di-C-methyl-L-arabinose as the starting material.

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Comment

The crystal structure of the title lactone, (4) (Booth *et al.*, 1997), has a three-dimensional network of hydrogen bonding, with each molecule acting as a donor and as an acceptor for two hydrogen bonds (Fig. 2). Two chains of hydrogen bonds can be seen, one from atom O9 to atom O13ⁱ running parallel to the *b* axis (Fig. 3), and a second running from atom O8 to atom O7ⁱⁱ parallel to the *a* axis (Fig. 4) (symmetry codes as in Table 1).



Experimental

3,5-Di-C-methyl-5,6-O-isopropylidene-L-mannono-1,4-lactone, (4), was recrystallized by slow evaporation from a mixture of ethyl acetate and cyclohexane until crystals formed (m.p. 433–437 K). $[\alpha]_{\text{D}}^{17} -24.7$ (*c*, 1.28 in acetone).

Crystal data

 $\text{C}_{11}\text{H}_{18}\text{O}_6$ $M_r = 246.26$ Orthorhombic, $P2_12_12_1$ $a = 7.1286$ (2) Å $b = 9.7360$ (3) Å $c = 17.1314$ (6) Å $V = 1188.99$ (6) Å^3 $Z = 4$ Mo $K\alpha$ radiation $\mu = 0.11 \text{ mm}^{-1}$ $T = 150 \text{ K}$ $0.20 \times 0.05 \times 0.05 \text{ mm}$

Data collection

Bruker Nonius KappaCCD area-detector diffractometer

Absorption correction: multi-scan (*DENZO* and *SCALEPACK*; Otwinowski & Minor, 1997) $T_{\text{min}} = 0.86$, $T_{\text{max}} = 0.99$

7431 measured reflections

1570 independent reflections

1327 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.040$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.034$ $wR(F^2) = 0.075$ $S = 0.93$

1570 reflections

154 parameters

H-atom parameters constrained

 $\Delta\rho_{\text{max}} = 0.26 \text{ e \AA}^{-3}$ $\Delta\rho_{\text{min}} = -0.25 \text{ e \AA}^{-3}$

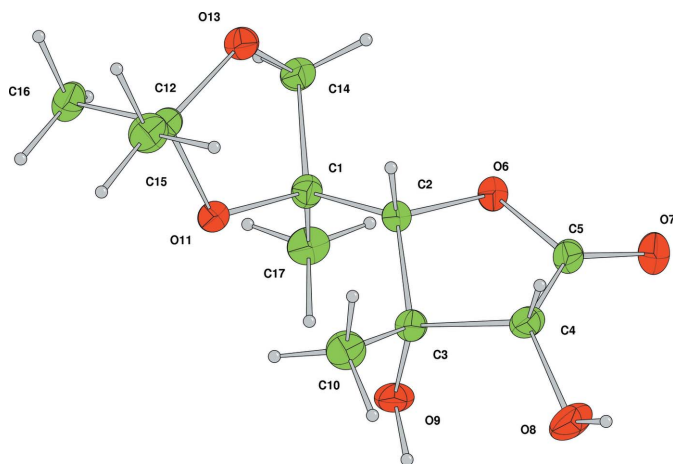


Figure 1
The molecular structure of compound (4), with displacement ellipsoids drawn at the 50% probability level. H atoms are shown as spheres of arbitrary radius.

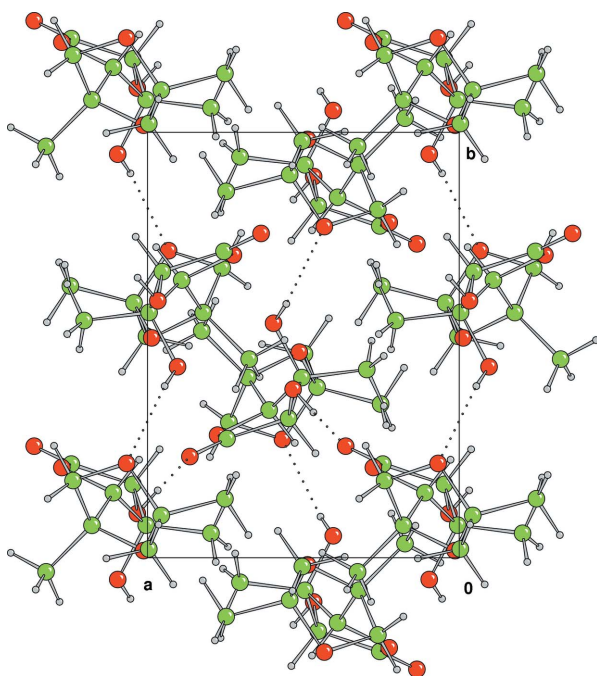


Figure 2
The packing of compound (4), projected along the *c* axis. Dotted lines indicate hydrogen bonds.

Table 1
Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O9—H12...O13 ⁱ	0.84	2.10	2.857 (2)	149
O8—H13...O7 ⁱⁱ	0.84	1.95	2.752 (2)	157

Symmetry codes: (i) $-x + 1, y + \frac{1}{2}, -z + \frac{3}{2}$; (ii) $x - \frac{1}{2}, -y + \frac{1}{2}, -z + 1$.

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

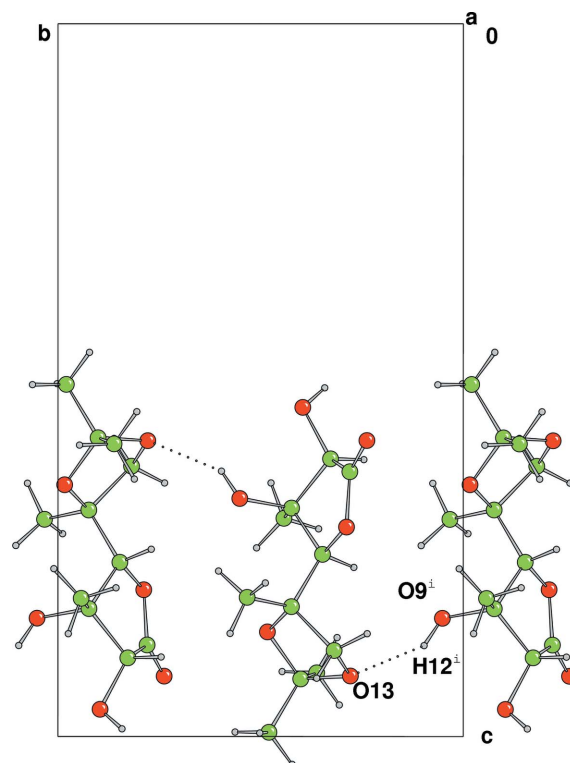


Figure 3
A hydrogen-bonded (dotted lines) chain running parallel to *b*. [Symmetry code: (i) $1 - x, -\frac{1}{2} + y, \frac{3}{2} - z$.]

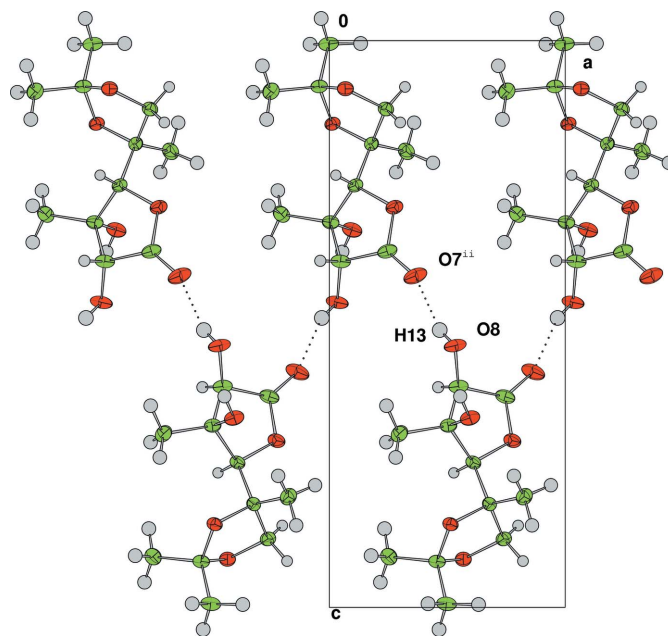


Figure 4
A hydrogen-bonded (dotted lines) chain running parallel to *a*. [Symmetry code: (ii) $x - \frac{1}{2}, \frac{1}{2} - y, 1 - z$.]

The relatively large ratio of minimum to maximum corrections applied in the multi-scan process (1:1.16) reflects changes in the illuminated volume of the crystal. Changes in illuminated volume were kept to a minimum, and were taken into account (Görlitz, 1999) by the multi-scan inter-frame scaling (*DENZO* and *SCALEPACK*; Otwinowski & Minor, 1997).

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 $U_{\text{iso}}(\text{H})$ (in the range 1.2 or 1.5 times U_{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*.

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