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2,3-*O*-Isopropylidene-L-apiono-1,4-lactone [(3*S*,4*S*)-3,4-dihydroxy-4-(hydroxymethyl)-3,4-di-*O*-isopropylidene-4,5-dihydrofuran-2(3*H*)-one]

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The relative configuration of the title compound, $C_8H_{12}O_5$, was unequivocally established by X-ray crystallographic analysis; the absolute configuration was determined by the use of D-ribose as a starting material.

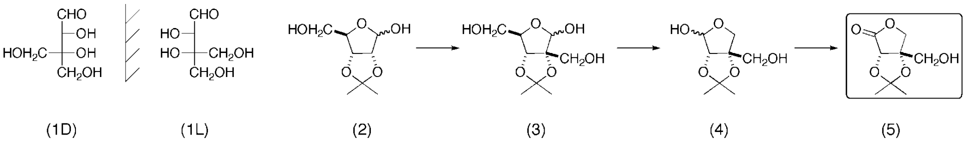
Key indicators

Single-crystal X-ray study
T = 150 K
Mean σ(C–C) = 0.002 Å
R factor = 0.030
wR factor = 0.074
Data-to-parameter ratio = 9.9

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

Comment

Branched 2-*C*-methyl nucleosides are the most promising drug candidates for the treatment of hepatitis C (Sorbera *et al.*, 2006; Pierra *et al.*, 2006). There is interest in the activity of nucleoside analogues with substitutents at C-3 of the sugar that may be derived from D-apiose (1D) (Sells & Nair, 1992; Kim *et al.*, 2004). L-Nucleoside analogues – the enantiomers of the naturally occurring nucleosides – also produce novel antiviral agents (Mathé & Gosselin, 2006). A project to investigate nucleosides derived from L-apiose (1L) may provide chemotherapeutic leads. The title lactone, (5), is a divergent intermediate of value in the synthesis of such compounds. The crystal structure of (5) reported in this paper removes the ambiguity of the stereochemistry at C-3 of the lactone; the absolute configuration of (5) was determined by the use of D-ribose (2) as the starting material.



The isolated molecule of (5) (Fig. 1) shows no unusual features when compared with the *Mogul* norms (Bruno *et al.*,

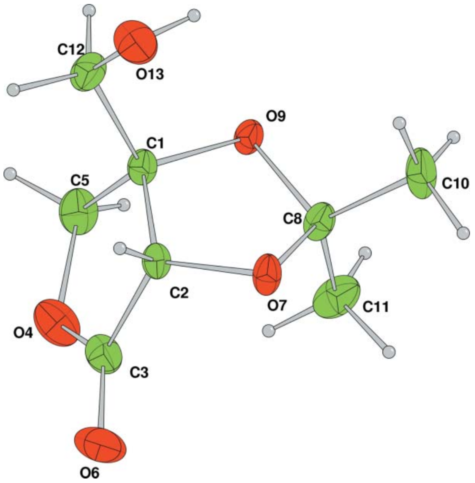


Figure 1
A view of (5), with displacement ellipsoids drawn at the 50% probability level. H atoms are shown as spheres of arbitary radius.

2004). The crystal structure consists of isolated chains of molecules linked by a single hydrogen bond, parallel to the *a* axis (Fig. 2). There are no hydrogen bonds between the chains, leading to crystals which were not easily cut.

Experimental

The C-2 branched D-hamamelose, (3), prepared from D-ribose, (2) (Ho, 1979), was converted to the ketal of L-apiose, (4), as described previously by Yun *et al.* (2005). The lactol (4) was oxidized by bromine water (Booth *et al.*, 2007) to the title compound, (5), which was crystallized from chloroform (m.p. 363 K). $[\alpha]_D^{22}$ 70 (*c*, 0.95 in chloroform).

Crystal data

$C_8H_{12}O_5$
$M_r = 188.18$
Orthorhombic, $P2_12_12_1$
$a = 7.2075$ (2) Å
$b = 9.5645$ (3) Å
$c = 12.9851$ (5) Å
$V = 895.14$ (5) Å^3
$Z = 4$
$D_x = 1.396$ Mg m^{-3}
Mo $K\alpha$ radiation
$\mu = 0.12$ mm^{-1}
$T = 150$ K
Block, colourless
0.70 × 0.50 × 0.30 mm

Data collection

Nonius KappaCCD area-detector diffractometer
ω scans
Absorption correction: multi-scan (*DENZO* and *SCALEPACK*; Otwinowski & Minor, 1997)
$T_{\min} = 0.74$, $T_{\max} = 0.97$
4866 measured reflections
1171 independent reflections
1106 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.035$
$\theta_{\max} = 27.5°$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.030$
$wR(F^2) = 0.074$
$S = 0.96$
1171 reflections
118 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F^2) + (0.03P)^2 + 0.32P]$, where $P = [\max(F_o^2,0) + 2F_c^2]/3$
$(\Delta/\sigma)_{\max} < 0.001$
$\Delta\rho_{\max} = 0.21$ e Å^{-3}
$\Delta\rho_{\min} = -0.22$ e Å^{-3}

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

D—H···A	D—H	H···A	D···A	D—H···A
O13—H7···O6$^{\rm i}$	0.85	2.05	2.802 (2)	148

Symmetry code: (i) $x - 1, y, z$.

In the absence of significant anomalous scattering, Friedel pairs were merged and the absolute configuration assigned on the basis of the starting materials. The relatively large ratio of minimum to maximum corrections applied in the multi-scan process (1:1.51) reflects changes in the illuminated volume of the crystal. These were kept to a minimum, and were taken into account (Görbitz, 1999) by multi-scan interframe 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, with C—H distances in the range 0.93–0.98 Å and O—H = 0.82 Å, and with $U_{\rm iso}$(H) = 1.2–1.5 times $U_{\rm eq}$ of the parent atom, after which the positions were refined with riding constraints.

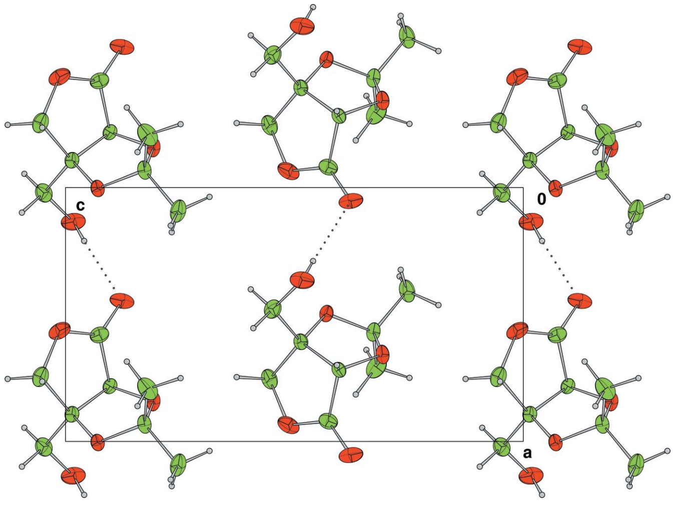


Figure 2
The molecular structure of (5), along the *b* axis, showing the hydrogen-bonded chains lying parallel to *a*. There are no hydrogen bonds between the chains.

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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