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Key indicators

Single-crystal X-ray study T = 297 K Mean $\sigma(C-C) = 0.009 \text{ Å}$ R factor = 0.056 wR factor = 0.171 Data-to-parameter ratio = 11.0

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(+)-Methyl (4*R*,5*S*)-4-[(*R*)-1-hydroxybut-3enyl]-5-2,2-dimethyl-trichloroacetamido-1,3-dioxane-5-carboxylate

The title compound, C₁₄H₂₀Cl₃NO₆, was prepared in a synthetic study of myriocin derivatives. There are intramolecular N-H···O and intermolecular O-H···O hydrogen bonds, forming one-dimensional chains along the c axis.

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Comment

The title compound, (I), was prepared in a synthetic study of myriocin, which is a naturally occurring α -substituted α -amino acid derivative with potent immunosuppressive activity. Compound (I) would be a useful intermediate for the total synthesis of myriocin (Oishi et al., 2002), as well as its congeners, such as mycestericins (Sasaki et al., 1994). Since the geometry of (I) could not be fully determined from NMR experiments, an X-ray analysis has been carried out.



The dioxane ring of (I) shows a chair conformation, with the trichloroacetylamino group in an axial position (Fig. 1). The absolute configuration at atom C12, derived from that at C-2 of dimethyl L-tartrate, was confirmed by the reasonable Flack (1983) parameter. Consequently, the absolute configurations at two other chiral centers (atoms C13 and C17) have been revealed. There are intramolecular N10-H10...O6 and intermolecular O6–H6···O9ⁱ [symmetry code: (i) y, 1 - x, $z - \frac{1}{4}$ hydrogen bonds (Table 1), forming one-dimensional chains along the c axis (Fig. 2).

Experimental

Treatment of methyl (4R,5S)-4-formyl-2,2-dimethyl-5-trichloroacetamido-1,3-dioxane-5-carboxylate, prepared from dimethyl L-tartrate in a 14-step reaction involving an Overman rearrangement (Sato et al., 2003), with allyltributyltin in the presence of MgBr₂ in CH₂Cl₂, afforded the title compound, (I). Crystals of (I) were grown from an ethyl acetate solution by slow evaporation (m.p. 371-372 K). The specific rotation $[\alpha]_D$ of (I) at 295 K is +56° (c = 1.0, CHCl₃).

Crystal data	
$C_{14}H_{20}Cl_3NO_6$	Mo $K\alpha$ radiation
$M_r = 404.67$	Cell parameters from 25
Tetragonal, P4 ₁	reflections
a = 9.1926 (8) Å	$\theta = 10.110.8^{\circ}$
c = 22.724 (2) Å	$\mu = 0.50 \text{ mm}^{-1}$
V = 1920.2 (3) Å ³	T = 297 K
Z = 4	Block, colourless
$D_x = 1.400 \text{ Mg m}^{-3}$	$0.55 \times 0.45 \times 0.45 \mbox{ mm}$
- 1	



Figure 1

The molecular structure of (I), with displacement ellipsoids drawn at the 40% probability level.

Data collection

Rigaku AFC-7R diffractometer	$R_{\rm int} = 0.016$
ω scans	$\theta_{\rm max} = 27.5^{\circ}$
Absorption correction: by	$h = -4 \rightarrow 11$
integration (Coppens et al., 1965)	$k = 0 \rightarrow 11$
$T_{\min} = 0.762, \ T_{\max} = 0.815$	$l = -12 \rightarrow 29$
3009 measured reflections	3 standard reflections
2388 independent reflections	every 150 reflections
1963 reflections with $I > 2\sigma(I)$	intensity decay: 13.3%
Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0963P)^2]$

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.056$ $wR(F^2) = 0.171$ S = 1.052388 reflections 218 parameters H-atom parameters not refined

where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} = 0.011$ $\Delta\rho_{max} = 0.62 \text{ e } \text{Å}^{-3}$ $\Delta\rho_{min} = -0.51 \text{ e } \text{Å}^{-3}$ Absolute structure: Flack (1983), 140 Friedel pairs Flack parameter = 0.16 (13)

+ 1.4164P]

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
O6−H6···O9 ⁱ	0.82	1.99	2.790 (5)	167
N10−H10···O6	0.95	2.05	2.709 (4)	125

Symmetry code: (i) $y, 1 - x, z - \frac{1}{4}$.

The hydroxy H atom was located from a difference synthesis and allowed to ride on the O atom, with $U_{iso}(H) = U_{eq}(O)$. The other H atoms were positioned geometrically and fixed with $U_{iso}(H) = 1.2U_{eq}$ (parent atom).



Figure 2

A projection of the crystal structure of (I) along the *a* axis, with thin lines indicating hydrogen bonds.

Data collection: WinAFC Diffractometer Control Software (Rigaku, 1999); cell refinement: WinAFC Diffractometer Control Software; data reduction: TEXSAN (Molecular Structure Corporation, 2001); program(s) used to solve structure: SIR92 (Altomare et al., 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976); software used to prepare material for publication: TEXSAN.

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