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Key indicators

Single-crystal X-ray study T = 296 K Mean σ (C–C) = 0.005 Å R factor = 0.047 wR factor = 0.132 Data-to-parameter ratio = 8.0

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

(5*R*,5a*R*,8a*R*,9S)-5-(3,4-dihydroxy-5-methoxyphenyl)-9-fluoro-5,8,8a,9-tetrahydrofuro-[3',4':6,7]naphtho[2,3-*d*]-1,3-dioxol-6(5a*H*)one acetone solvate

The title compound, $C_{20}H_{17}FO_7 \cdot C_3H_6O$, is a potential antitumour agent. Its absolute configuration was assigned based on that of the synthetic precursor. Intermolecular $O-H\cdots O$ hydrogen bonds link the molecules in the crystal structure into layers parallel to (010). These layers are stabilized by weak interlayer $C-H\cdots O$ hydrogen bonds. Received 16 March 2005 Accepted 11 April 2005 Online 16 April 2005

Comment

Semi-synthetic analogues of the naturally occurring podophyllotoxin have attracted much interest in the past two decades as a result of the development of etoposide (VP-16) and teniposide (VM-26) as anticancer drugs (Damayanthi & Lown, 1998; Silverberg *et al.*, 2000; Van Vliet *et al.*, 2001). It has been well established, in these years, that the introduction of an F atom into some biomolecules can result in important modifications of their biological properties (Welch & Eswarakrishnan, 1991; Filler *et al.*, 1993). In order to find new compounds with high anticancer reactivity, our group has synthesized several fluorinated podophyllotoxins (He *et al.*, 2004). We report here the crystal structure of one of them, (I), as its acetone solvate.



The molecular structure of (I) is shown in Fig. 1. Selected molecular parameters and hydrogen-bond geometric characteristics are listed in Tables 1 and 2, respectively. The asymmetric unit contains one molecule of (I) and one molecule of acetone. The absolute configuration was assigned according to the known configuration of the starting material, as the chiral centres were not affected by the reaction. Intermolecular $O-H\cdots O$ hydrogen bonds play an important role, resulting in the formation of polymeric layers parallel to (010). These layers are stabilized by weak interlayer $C-H\cdots O$ hydrogen bonds.

Experimental

To a solution of 4β -3',4'-dimethylpodophyllotoxin-3'4'-quinone (120 mg, 0.31 mmol) in CH₂Cl₂ (10 ml) was added dropwise (diethylamino)sulfur trifluoride (DAST, 0.04 ml) at 233 K under nitrogen. The reaction solution was stirred for 30 min at 233 K and then allowed to warm to room temperature. Water (0.1 ml) was added

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dropwise to quench the unreacted DAST. The reaction solution was diluted with CH₂Cl₂ (50 ml), and washed with saturated aqueous NaHCO₃ and water. The organic phase was dried over MgSO₄. After removal of the solvent *in vacuo*, the solid was purified by silica gel column chromatography (CH₂Cl₂–AcOEt, 5:1, v/v) and crystallized from acetone to afford the pure title compound as crystals (yield 75%). M.p. 533–535 K. ¹H NMR (500 MHz, DMSO-*d*₆, p.p.m.): δ 7.12 (*s*, 1H), 6.61 (*s*, 1H), 6.28 (1*s*, 1H), 6.05 (*d*, 2H, *J* = 10 Hz), 5.80 (*s*, 1H), 5.70 (*dd*, *J* = 2.54 Hz, 1H), 4.52 (*s*, 1H), 4.46 (*m*, 1H), 4.13 (*m*, 1H), 3.64 (*s*, 3H), 3.21 (*m*, 1H), 3.87 (*m*, 1H); MS (ESI): *m/z* 389 ([*M*–H]⁻); IR (KBr, cm⁻¹): 3170, 1774, 1618, 1504, 1484, 933.

Crystal data

$C_{20}H_{17}FO_7 \cdot C_3H_6O$
$M_r = 446.43$
Monoclinic, C2
a = 19.1786 (9) Å
b = 7.7058 (3) Å
c = 14.0757 (7) Å
$\beta = 92.373 (2)^{\circ}$
$V = 2078.4 (2) \text{ Å}^3$
Z = 4

Data collection

Rigaku R-AXIS RAPID
diffractometer
ω scans
Absorption correction: multi-scan
(Higashi, 1995)
$T_{\min} = 0.923, T_{\max} = 0.991$
9048 measured reflections

Refinement

Refinement on F^2 R(F) = 0.047 $wR(F^2) = 0.132$ S = 1.012484 reflections 312 parameters

Table '	1
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Selected geometric parameters (Å, °).

F1-C6	1.413 (4)	O4-C10	1.432 (5)
O1-C3	1.201 (4)	O5-C16	1.362 (3)
O2-C3	1.342 (5)	O5-C17	1.414 (3)
O2-C4	1.458 (5)	O6-C18	1.371 (3)
O3-C9	1.381 (4)	O7-C19	1.355 (3)
F1-C6-C5	108.7 (2)	O3-C9-C8	127.8 (3)
O1-C3-C2	129.2 (3)	O4-C11-C9	110.5 (3)
O1-C3-O2	121.4 (3)	O4-C11-C12	127.8 (3)
O2-C3-C2	109.3 (3)	O6-C18-C16	122.1 (2)
C4-O2-C3	110.6 (3)	O7-C19-C18	121.8 (3)

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
O6-H601···O5	0.92	2.26	2.691 (3)	108
O7−H701···O6	0.94	2.41	2.753 (3)	102
$C4-H41\cdots F1$	0.97	2.47	2.865 (4)	104
$O6-H601\cdots O1^{i}$	0.92	1.96	2.835 (2)	158
$O7 - H701 \cdots O6^{ii}$	0.94	1.98	2.857 (3)	154
$C20-H20\cdots O3^{iii}$	0.98	2.53	3.340 (3)	140

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

 $\begin{array}{l} D_x = 1.427 \ \text{Mg m}^{-3} \\ \text{Mo } K\alpha \ \text{radiation} \\ \text{Cell parameters from 7291} \\ \text{reflections} \\ \theta = 2.9{-}27.5^{\circ} \\ \mu = 0.11 \ \text{mm}^{-1} \\ T = 296.1 \ \text{K} \\ \text{Platelet, colourless} \\ \text{Platel}, 40.28 \times 0.08 \ \text{mm} \end{array}$

2486 independent reflections 2086 reflections with $F^2 > 2\sigma(F^2)$ $R_{int} = 0.023$ $\theta_{max} = 27.5^{\circ}$ $h = -24 \rightarrow 24$ $k = -10 \rightarrow 8$ $l = -18 \rightarrow 18$

H-atom parameters constrained $w = 1/[0.0025F_o^2 + 1\sigma(F_o^2)]/(4F_o^2)$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.23 \text{ e} \text{ Å}^{-3}$ $\Delta\rho_{min} = -0.28 \text{ e} \text{ Å}^{-3}$



Figure 1

The molecule of (I) in the crystal structure. Displacement ellipsoids are drawn at the 50% probability level. Dashed lines indicate hydrogen bonds. The acetone solvent molecule has been omitted



Figure 2

The molecular packing of (I), viewed approximately along the b axis. Dashed lines indicate hydrogen-bonding interactions (solvent molecules have been omitted for clarity). H atoms not involved in hydrogen bonding have been omitted (see Table 2 for symmetry codes).

Atoms H601 and H701 were found in a difference Fourier map and fixed in position. The other H atoms were placed in calculated positions with C-H = 0.96–0.98 Å and included in the final cycles of refinement in a riding model, with $U_{\rm iso}(\rm H) = 1.2 U_{eq}(\rm carrier atoms)$.

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/ MSC, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *CRYSTALS* (Watkin *et al.*, 1996); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure* and *PLATON* (Spek, 2003).

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