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A taxane diterpenoid from the needles of *Taxus wallichiana*

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Key indicators

Single-crystal X-ray study
T = 293 K
Mean σ(C–C) = 0.004 Å
R factor = 0.038
wR factor = 0.105
Data-to-parameter ratio = 8.2

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

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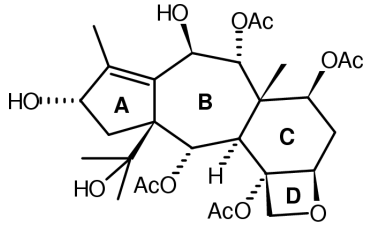
The title compound, 10,13-deacetyl-*abeo*-baccatin IV, $C_{28}H_{40}O_{12}$, crystallized in space group *P*1. The molecular structure shows that the *B*/*C* ring junction is *trans*-fused, while the *A* ring is in a *syn* conformation with respect to the *C* ring and *anti* with respect to the *D* ring. The conformations of the individual rings differ from each other. The molecule as a whole adopts a cage-type folded conformation. Intra- and intermolecular O—H···O and C—H···O hydrogen bonds, together with van der Waals interactions, stabilize the crystal structure.

Comment

Investigations on the taxoid constituents of different parts of *Taxus wallichiana* led to isolation of the title compound, (I). Taxoid (I) was isolated from the needles of *T. wallichiana* (Chattopadhyay *et al.*, 1995). Considerable attention has been given to this type of diterpenoid molecule whose archetype is the paclitaxel (Taxol™), a promising cancer chemotherapeutic agent (Appendino, 1995). Although numerous X-ray investigations have been performed on this and related molecules, there is much heated debate about the active conformation of this anticancer drug (Mastropaolo *et al.*, 1995, and references therein). This prompted us to undertake the present X-ray study of the title compound, (I), to determine its crystal structure and stereochemistry unequivocally.



(I)

Fig. 1 shows the structure of (I) with the atomic numbering scheme. Selected torsion angles of the terpenoid core of (I) are listed in Table 1. The molecule contains a three-ring fused system *A*/*B*/*C* with an additional *D* ring attached to the ring *C*. The *A* ring is in a *syn* conformation with respect to the *C* ring and *anti* with respect to the *D* ring. The *B*/*C* junction is *trans*-fused due to the *trans*-axial dispositions of C25 at C8 and H3 at C3. Thus, the molecule as a whole adopts a folded cage-type conformation. Least-squares plane calculations indicate that the seven-membered *B* ring adopts a boat conformation [the deviations of atoms C1, C2 and C9 are 1.078 (4), 1.289 (4) and 0.553 (4) Å, respectively from the least-squares plane through

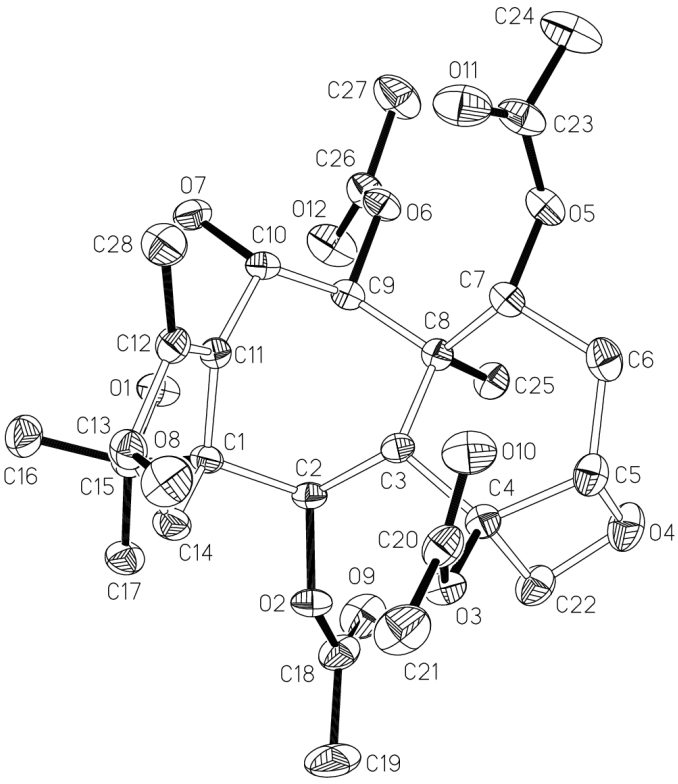


Figure 1
The molecular structure and crystallographic numbering scheme for (I). Displacement ellipsoids are shown at the 30% probability level. H atoms have been omitted for clarity.

atoms C3, C8, C10 and C11]. The six-membered *C* ring is in an envelope conformation while the five-membered *A* ring is puckered to form an envelop. The molecular packing in the crystal shows that the hydroxyl groups are involved in both intra- and intermolecular hydrogen bonding of the type O—H···O. In addition, the packing further reveals the presence of intra- and intermolecular C—H···O hydrogen bonding. Thus, O—H···O and C—H···O hydrogen-bonding interactions, along with van der Waals forces, stabilize the solid-state structure.

Experimental

Compound (I) was isolated from methanol extracts of the needles of *T. wallichiana* following the reported protocols (Chattopadhyay *et al.*, 1995). Diffraction quality crystals were grown at room temperature by slow evaporation of a methanolic solution.

Crystal data

$C_{28}H_{40}O_{12}$
M_r = 568.60
Triclinic, *P*1
a = 8.957 (1) Å
b = 9.667 (1) Å
c = 9.827 (1) Å
α = 110.10 (1)°
β = 92.42 (1)°
γ = 110.39 (1)°
V = 736.2 (1) Å^3
Z = 1
D_x = 1.282 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 26 reflections
θ = 5.0–9.2°
μ = 0.10 mm^{-1}
T = 293 (2) K
Block, colourless
0.48 × 0.35 × 0.33 mm

Data collection

Bruker *P*4 diffractometer
θ–2ω scans
3060 measured reflections
3060 independent reflections
2941 reflections with $I > 2\sigma(I)$
θ_{max} = 25.0°
$h = -10 \rightarrow 1$
$k = -10 \rightarrow 10$
$l = -11 \rightarrow 11$
3 standard reflections
every 97 reflections
frequency: 60 min
intensity decay: none

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.038
$wR(F^2)$ = 0.105
S = 1.04
3060 reflections
372 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0759P)^2 + 0.0885P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.002
$\Delta\rho_{max}$ = 0.18 e Å^{-3}
$\Delta\rho_{min}$ = −0.18 e Å^{-3}

Table 1
Selected torsion angles (°).

C11—C1—C2—C3	27.8 (3)	C3—C8—C9—C10	48.8 (3)
C14—C1—C2—C3	−82.9 (3)	C8—C9—C10—C11	−53.1 (3)
C15—C1—C2—C3	152.90 (19)	C9—C10—C11—C12	146.7 (2)
C1—C2—C3—C4	130.6 (2)	C9—C10—C11—C1	−33.9 (3)
C1—C2—C3—C8	−96.5 (2)	C14—C1—C11—C12	−11.9 (3)
C2—C3—C4—C22	58.0 (3)	C15—C1—C11—C12	106.5 (2)
C8—C3—C4—C22	−74.2 (3)	C2—C1—C11—C12	−128.7 (2)
C2—C3—C4—C5	159.8 (2)	C14—C1—C11—C10	168.6 (2)
C8—C3—C4—C5	27.5 (3)	C15—C1—C11—C10	−73.0 (3)
C22—C4—C5—O4	10.3 (2)	C2—C1—C11—C10	51.8 (3)
C3—C4—C5—O4	−112.2 (2)	C10—C11—C12—C13	−179.3 (2)
C22—C4—C5—C6	126.1 (3)	C1—C11—C12—C13	1.2 (3)
C3—C4—C5—C6	3.6 (4)	C11—C12—C13—C14	10.4 (3)
O4—C5—C6—C7	104.3 (3)	C12—C13—C14—C1	−17.7 (3)
C4—C5—C6—C7	1.0 (4)	C11—C1—C14—C13	17.9 (3)
C5—C6—C7—C8	−38.1 (3)	C15—C1—C14—C13	−100.9 (3)
C6—C7—C8—C9	−176.44 (19)	C2—C1—C14—C13	135.0 (2)
C6—C7—C8—C3	66.2 (2)	C5—C4—C22—O4	−10.4 (2)
C4—C3—C8—C7	−60.0 (3)	C3—C4—C22—O4	108.8 (3)
C2—C3—C8—C7	165.76 (19)	C4—C22—O4—C5	11.0 (2)
C4—C3—C8—C9	177.9 (2)	C6—C5—O4—C22	−132.9 (3)
C2—C3—C8—C9	43.7 (2)	C4—C5—O4—C22	−10.8 (2)
C7—C8—C9—C10	−66.2 (3)		

Table 2
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
O7—H7···O1	0.82	2.02	2.740 (3)	146
O1—H1···O11^{i}	0.82	2.08	2.883 (3)	168
O8—H8···O4^{ii}	0.82	2.08	2.845 (3)	154
O8—H8···O12^{iii}	0.82	2.64	3.075 (3)	115
C6—H6*B*···O9^{iv}	0.97	2.42	3.366 (5)	166
C9—H9···O1	0.98	2.44	3.136 (3)	128
C25—H19*C*···O4	0.96	2.28	3.123 (4)	146
C22—H20*B*···O9	0.97	2.42	3.258 (5)	144
C24—H27*C*···O12^{iv}	0.96	2.48	3.443 (6)	175

Symmetry codes: (i) $1+x, y, z$; (ii) $x, y, 1+z$; (iii) $x, 1+y, 1+z$; (iv) $x-1, y, z$.

Data collection: *XSCANS* (Siemens, 1996); cell refinement: *XSCANS*; data reduction: *XSCANS*; program(s) used to solve structure: *SHELXTL-NT* (Bruker, 1997); program(s) used to refine structure: *SHELXTL-NT*; molecular graphics: *SHELXTL-NT*; software used to prepare material for publication: *SHELXTL-NT*.

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