Acta Crystallographica Section C
Crystal Structure Communications
ISSN 0108-2701

Nodosin

Philip J. Cox,[a]* Yanhui Meng,[b] Satyajit D. Sarker,[a] Qinying Deng[c] and Guo Xu[c]

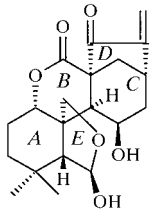
[a]School of Pharmacy, The Robert Gordon University, Schoolhill, Aberdeen AB10 1FR, Scotland, [b]Applied Chemistry, Zhongshan College, Zhongshan 528403, Guandong, People's Republic of China, and [c]School of Chemistry and Chemical Engineering, Zhongshan University, Guangzhong 510275, People's Republic of China
Correspondence e-mail: p.j.cox@rgu.ac.uk

Received 6 September 2000
Accepted 14 November 2000

Nodosin, or 13-deoxy-5β-hydroxyenmein, $C_{20}H_{26}O_6$, has been established as a pentacyclic 6,7-seco-*ent*-kaurane diterpenoid with an enmein skeleton. Two independent intermolecular O—H···O hydrogen bonds are present and link each molecule to four neighbours.

Comment

The diterpenoid nodosin, (I), has been found in *Rabdosia* plants (Takeda *et al.*, 1982) and possesses antitumour activity against P 388 lymphocytic leukemia innoculated into mice (Nagao *et al.*, 1982). The X-ray structure analysis shows that nodosin is a structural isomer of enmein (Fujita *et al.*, 1976), with the β-hydroxy group attached to C12 (nodosin) rather than C3 (enmein).



(I)

From the assumed absolute stereochemistry shown in Fig. 1, the eight chiral centres present are *S* for C1, C8, C10, C11 and C14, and *R* for C5, C6 and C12. The ring conformations (see Scheme) approximate to chair, screw-boat, boat, C15-envelope and half-chair for *A*–*E*, respectively.

Details of two well defined intermolecular hydrogen bonds are shown in Table 2. Here, the two hydroxy groups O1 and O6 act as donor atoms, and O2 and O4 act as acceptor atoms. Within the molecule, O6 is also close to H1*A* (2.26 Å), H5 (2.54 Å) and H15*B* (2.35 Å), and these interactions result in a longer O6—C12 distance of 1.435 (4) Å compared with O1—C6 of 1.403 (3) Å. As shown in Fig. 2, the two independent hydrogen bonds result in an arrangement such that each molecule is held in the crystal by four intermolecular hydrogen bonds. The hydrogen-bonding pattern is two-dimensional as there are no hydrogen bonds linking molecules in the direction of the *b* axis.

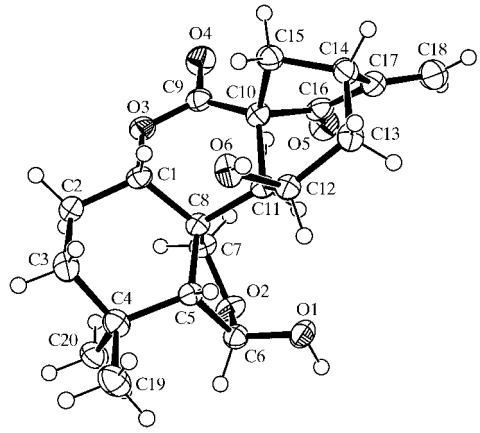


Figure 1
The atomic arrangement in the title molecule (50% probability displacement ellipsoids).

Some geometrical features of the molecule determined by *PLATON* (Spek, 1998) are shown in Table 1. Here, the longest bond, C10—C11 of 1.583 (4) Å, is located where in-plane bending due to ring strain is most evident. The deviations from ideal sp^3 angular values around C10 are shown by C16—C10—C15 of 101.2 (3)° and C9—C10—C11 of 117.3 (3)°. Table 1 also shows the endocyclic torsion angles that describe the somewhat planar portions of the fused rings.

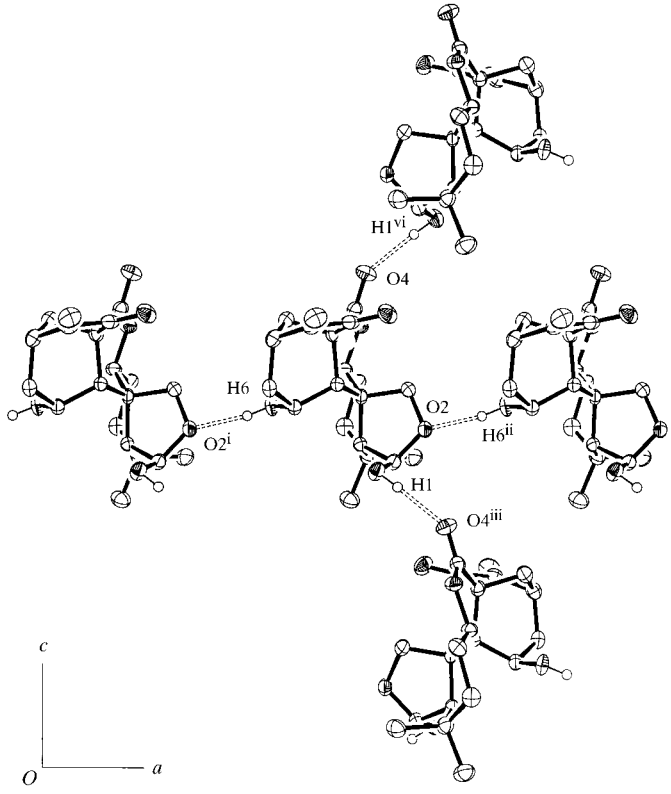


Figure 2
The intermolecular hydrogen bonding viewed normal to the (010) plane. [Symmetry codes: (i) $-1+x, y, z$; (ii) $1+x, y, z$; (iii) $\frac{1}{2}-x, -y, -\frac{1}{2}+z$; (iv) $\frac{1}{2}-x, -y, \frac{1}{2}+z$.]

Similar structures based on spectroscopic evidence have been reported (Takeda *et al.*, 1986) and the absolute configuration of a related structure, acetyl–bromoacetyl–dihydroenmein (Natsume & Iltaka, 1966) is known. Unfortunately, the name nodosin has also been applied to a glycosylisoflavone (Ilyas *et al.*, 1994).

Experimental

Nodosin was extracted from the Chinese medicinal plant *Rabdosia serra* (Maxim.) Hara (family: *Labiatae*). The solvent used for extraction was aqueous ethanol (70%) and the solvent used for recrystallization was acetone.

Crystal data

$C_{20}H_{26}O_6$
M_r = 362.41
Orthorhombic, $P2_12_12_1$
a = 7.474 (3) Å
b = 15.262 (6) Å
c = 15.870 (8) Å
V = 1810.3 (14) Å^3
Z = 4
D_x = 1.330 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 6964 reflections
θ = 1.85–27.5°
μ = 0.097 mm^{-1}
T = 150 (2) K
Block, colourless
0.10 × 0.8 × 0.8 mm

Data collection

Enraf–Nonius KappaCCD area-detector diffractometer
φ and ω scans to fill Ewald sphere
Absorption correction: multi-scan (*SORTAV*; Blessing, 1995)
T_{min} = 0.95, T_{max} = 0.99
6964 measured reflections
2220 independent reflections
1534 reflections with $I > 2\sigma(I)$
R_{int} = 0.072
θ_{max} = 27.5°
$h = -6 \rightarrow 9$
$k = -18 \rightarrow 19$
$l = -20 \rightarrow 20$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.047
$wR(F^2)$ = 0.103
S = 1.019
2220 reflections
246 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0392P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.001
$\Delta\rho_{max}$ = 0.21 e Å^{-3}
$\Delta\rho_{min}$ = −0.21 e Å^{-3}
Extinction correction: *SHELXL*97 (Sheldrick, 1997)
Extinction coefficient: 0.022 (2)
Absolute structure: Flack (1983)
Flack parameter not reliably determined

Table 1
Selected geometric parameters (Å, °).

O1—C6	1.403 (4)	C1—C2	1.503 (4)
O5—C16	1.213 (4)	C10—C11	1.583 (4)
O6—C12	1.435 (4)		
C7—C8—C5	101.4 (2)	O5—C16—C10	126.8 (3)
C16—C10—C15	101.2 (3)	C17—C16—C10	105.7 (3)
C9—C10—C11	117.3 (3)	C18—C17—C16	121.8 (3)
C12—C11—C8	116.4 (2)	C18—C17—C14	130.0 (3)
O5—C16—C17	127.4 (3)	C16—C17—C14	108.2 (3)
C1—O3—C9—C10	−1.7 (4)	C9—C10—C11—C8	−4.4 (4)
C15—C10—C11—C12	−7.1 (4)	C10—C16—C17—C14	−1.2 (3)

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

D—H···A	D—H	H···A	D···A	D—H···A
O1—H1···O4^{i}	0.91 (3)	1.96 (4)	2.841 (3)	162 (3)
O6—H6···O2^{ii}	0.85 (4)	1.88 (4)	2.728 (3)	171 (3)

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

Friedel reflections were merged before the refinement. The hydroxy H atoms were refined freely and the remaining H atoms were initially placed in calculated positions and thereafter allowed to ride on their attached atoms with common isotropic displacement parameters which converged to 0.029 (2) (non-methyl H atoms) and 0.051 (5) Å^2 (methyl H atoms). Constrained C—H distances were 0.95, 1.00, 0.99 and 0.98 Å for sp^2, methine, methylene and methyl groups, respectively.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SIR*97 (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP*-3 (Farrugia, 1997).

We thank the EPSRC for use of the National Crystallographic Service at Southampton University (X-ray data collection) and for the use of the Chemical Database Service at Daresbury Laboratory (Fletcher *et al.*, 1996).

Supplementary data for this paper are available from the IUCr electronic archives (Reference: BM1432). Services for accessing these data are described at the back of the journal.

References

Altomare, A., Burla, M. C., Camalli, M., Cascarano, G. L., Giacovazzo, C., Guagliardi, A., Moliterni, A. G. G., Polidori, G. & Spagna, R. (1999). *J. Appl. Cryst.* **32**, 115–119.
Blessing, R. H. (1995). *Acta Cryst.* A**51**, 33–38.
Farrugia, L. J. (1997). *J. Appl. Cryst.* **30**, 565.
Flack, H. D. (1983). *Acta Cryst.* A**39**, 876–881.
Fletcher, D. A., McMeeking, R. F. & Parkin, D. (1996). *J. Chem. Inf. Comput. Sci.* **36**, 746–749.
Fujita, T., Masuda, I., Takao, S. & Fujita, E. (1976). *J. Chem. Soc. Perkin Trans.* 1, pp. 2098–2102.
Hooft, R. (1998). *COLLECT*. Nonius BV, Delft, The Netherlands.
Ilyas, M., Parveen, M., Khan, M. S. & Kamil, M. (1994). *J. Chem. Res.* (*S*), **3**, 88–89.
Nagao, Y., Ito, N., Kohno, T., Kuroda, H. & Fujita, E. (1982). *Chem. Pharm. Bull.* **30**, 727–729.
Natsume, M. & Iltaka, Y. (1966). *Acta Cryst.* **20**, 197–201.
Otwinowski, Z. & Minor, W. (1997). *Methods Enzymol.* **276**, 307–326.
Sheldrick, G. M. (1997). *SHELXL*97. University of Göttingen, Germany.
Spek, A. L. (1998). *PLATON*. Utrecht University, The Netherlands.
Takeda, Y., Fujita, T. & Chen, C.-C. (1982). *Chem. Lett.* pp. 833–836.
Takeda, Y., Takeda, K.-I. & Fujita, T. (1986). *J. Chem. Soc. Perkin Trans.* 1, pp. 689–694.