organic compounds

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3β -(1-Allyl-1-pyrrolidinio)-16-(2-pyridylmethylene)androst-5-en-17 β -ol bromide hemihydrate

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The title compound, $C_{32}H_{45}N_2O^+\cdot Br^-\cdot 0.5H_2O$, has the outer two six-membered rings in chair conformations, while the central ring is in an 8β ,9 α -half-chair conformation. The fivemembered ring of the steroid nucleus adopts a slightly deformed 14 α -envelope conformation. The pyridylmethylene moiety has an *E* configuration with respect to the hydroxyl group at position 17. The structure is stabilized by a network of O-H···Br-type intermolecular hydrogen bonds.

Comment

The present X-ray investigation of the title compound, (I), was undertaken as part of our study of the structure and conformation of new synthetic steroid derivatives (Vasuki *et al.*, 2001; Vasuki, Parthasarathi, Ramamurthi, Jindal & Dubey, 2002; Vasuki, Parthasarathi, Ramamurthi, Dubey & Jindal, 2002; Vasuki, Thamotharan *et al.*, 2002). It is well known that minor changes in the basic composition of steroids significantly alter their biological activities (Duax & Norton, 1975). We are particularly interested in studying the conformational flexibilities of steroids due to various possible substitutions at the C3, C16 and C17 positions.



The puckering parameters in (I) [ring A: Q = 0.576 (5) Å, $\theta = 10.1$ (5)° and $\varphi = 84$ (3)°; ring C: Q = 0.562 (5) Å, $\theta = 8.9$ (5)° and $\varphi = 251$ (3)°; Cremer & Pople, 1975] show that rings A and C adopt chair conformations. The presence of the pyrrolidine moiety bonded to C3 does not disturb the usual chair

conformation of ring A of the steroid nucleus. The C5–C6 (Csp^2-Csp^2) distance of 1.331 (6) Å confirms the localization of a double bond at this position. Due to this double bond, the environment of atom C5 is planar, and hence ring B adopts an 8β ,9 α -half-chair conformation [Q = 0.498 (5) Å, $\theta = 50.9$ (6)° and $\varphi = 217.5$ (7)°]. Similar observations have been reported by Caira *et al.* (1995), Andrade *et al.* (2001) and Hema *et al.* (2002).

Ring *D* adopts a slightly deformed 14 α -envelope conformation, with pseudo-rotation parameters $\Delta = 12.6^{\circ}$ and $\varphi_m = 46.0^{\circ}$ (Altona *et al.*, 1968). The pyrrolidine ring at C3 exhibits a slightly distorted β envelope conformation, with $\Delta = 18^{\circ}$ and $\varphi_m = 42.6$ (3)°. The C17-C16-C20-C21 torsion angle of -171.9 (5)° indicates that the 2-pyridyl ring has an *E* configuration with respect to the hydroxyl group at position 17. The larger exocyclic angle at C15-C16-C20 [129.3 (4)°] compared with C17-C16-C20 [123.1 (4)°] might be a consequence of repulsion between the lone pair of electrons on atom N26 of the pyridine ring and atom H15*B* on C15 (N26···H15*B* 2.573 Å).

The C19–C10···C13–C18 pseudo-torsion angle is 7.5 (4)°. The equatorially substituted pyrrolidine moiety is oriented at an angle of 78.5 (3)° with respect to the central steroid nucleus. The dihedral angle between the plane of the pyridine



Figure 1

The molecular structure of (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme. All H atoms have been omitted for clarity.



Figure 2 The packing of molecules of (I) viewed down the *b* axis.

ring and the average molecular plane comprising rings A, B, C and D is 11.4 (2)°. The dihedral angle between the pyridine and pyrrolidine rings is 59.6 $(3)^{\circ}$. The valency angles C8-C14-C15 [119.2 (4)°] and C14-C13-C17 [99.5 (3)°] are close to the expected values of 121.2° and 101.4°, respectively (Duax & Norton, 1975). The geometries of the rings are trans at the B/C and C/D ring junctions.

The structure of (I) is stabilized by an $O-H \cdots Br$ network which involves both the hydroxyl group of the steroid and the water molecules included in the lattice, and a projection down the *b* axis is shown in Fig. 2.

Experimental

The title compound was prepared by dissolving 16-(2-pyridylmethylene)-3*β*-pyrrolidinoandrost-5-en-17*β*-ol (500 mg, 1.15 mmol) in dried dichloromethane (50 ml) and adding allyl bromide (1 ml, 7.04 mol). The reaction mixture was stirred for a few minutes and kept at room temperature overnight. The solid residues were filtered and washed with dichloromethane to afford crystals of (I) (yield: 0.45 g, 68.36%; m.p. 517-521 K).

Crystal data

$C_{32}H_{45}N_{2}O^{+}\cdot Br^{-}\cdot 0.5H_{2}O$ $M_{r} = 562.61$ Monoclinic, C2 a = 21.054 (4) Å b = 9.3083 (18) Å c = 15.551 (4) Å $\beta = 106.15$ (2)° V = 2927.4 (11) Å ³ Z = 4 Data collection	$D_x = 1.277 \text{ Mg m}^{-3}$ Mo K\alpha radiation Cell parameters from 25 reflections $\theta = 10-15^{\circ}$ $\mu = 1.43 \text{ mm}^{-1}$ T = 293 (2) K Plate, white $0.20 \times 0.17 \times 0.17 \text{ mm}$
Enraf-Nonius CAD-4 diffractometer $\omega/2\theta$ scans Absorption correction: ψ scan (North <i>et al.</i> , 1968) $T_{min} = 0.763$, $T_{max} = 0.793$ 2835 measured reflections 2751 independent reflections 2100 reflections with $I > 2\sigma(I)$ <i>Refinement</i>	$R_{int} = 0.013$ $\theta_{max} = 25^{\circ}$ $h = 0 \rightarrow 24$ $k = 0 \rightarrow 11$ $l = -18 \rightarrow 17$ 2 standard reflections frequency: 120 min intensity decay: none

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0413P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.034$	+ 2.1207P]
$wR(F^2) = 0.089$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.08	$(\Delta/\sigma)_{\rm max} < 0.001$
2751 reflections	$\Delta \rho_{\rm max} = 0.29 \ {\rm e} \ {\rm \AA}^{-3}$
336 parameters	$\Delta \rho_{\rm min} = -0.23 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	Absolute structure: Flack (1983);
independent and constrained	Friedel equivalents merged
refinement	Flack parameter = $-0.002(12)$

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$O27-H27\cdots Br$	0.81 (3)	2.38 (3)	3.194 (4)	178 (6)
$O1W-H1W\cdots Br^{i}$	0.88 (4)	2.53 (4)	3.405 (5)	172 (3)

Symmetry code: (i) $\frac{1}{2} + x$, $\frac{1}{2} + y$, z.

The structure was solved with DIRDIF99 (Beurskens et al., 1999) using the TRACOR option, with the Br atom at the origin. All H

atoms, except the hydroxyl H atom and the water H atom, were treated as riding, with C-H distances in the range 0.93-0.98 Å and $U_{\rm iso}({\rm H}) = 1.5 U_{\rm eq}({\rm C})$ for methyl H atoms and $1.2 U_{\rm eq}({\rm C})$ for all others. The hydroxyl H atom was located from a difference Fourier map and refined using the DFIX option in SHELXL97 (Sheldrick, 1997), with H27-O27 = 0.81 (2) Å. It was included in the structure-factor calculations with $U_{iso}(H27) = 1.1U_{eq}(O27)$. At this stage, the maximum residual electron density of 2.87 e $Å^{-3}$ indicated the presence of a possible atom site in a special position with half occupancy. This peak was found near Br, at a distance of 3.40 Å. This was assumed to be the O atom of a water molecule and was refined. One of the H atoms of the water molecule was located from a difference Fourier map and, using the DFIX option in SHELXL97, the coordinates of atom H1W were refined, with O1W-H1W restrained to 0.88 (2) Å, and H1W \cdots H1W(symmetry equivalent) restrained to 1.44 (1) Å, and included in the structure-factor calculations with $U_{iso}(H1W) = 1.1U_{eq}(O1W)$.

Data collection: CAD-4 EXPRESS (Enraf-Nonius, 1994); cell refinement: CAD-4 EXPRESS; data reduction: MolEN (Fair, 1990); program(s) used to solve structure: DIRDIF99 (Beurskens et al., 1999); program(s) used to refine structure: SHELXL97; molecular graphics: ZORTEP (Zsolnai, 1997); software used to prepare material for publication: SHELXL97.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: DE1189). Services for accessing these data are described at the back of the journal.

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