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17*a*-Allyl-3*β*-pyrrolidino-17*a*-aza-D-homo-androst-5-ene monohydrate

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Key indicators

Single-crystal X-ray study
T = 293 K
Mean *σ*(C–C) = 0.006 Å
R factor = 0.050
wR factor = 0.169
Data-to-parameter ratio = 7.9

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

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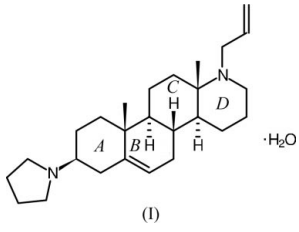
The title compound, $C_{26}H_{42}N_2\cdot H_2O$, a homoandrost-5-ene, contains four fused six-membered rings. Rings *A*, *C* and *D* adopt chair conformations, while ring *B* adopts an 8*β*,9*α*-half-chair conformation.

Comment

The X-ray investigation of the title compound, (I), was undertaken as part of our study on the structure and conformation of new synthetic steroid derivatives (Thamotharan *et al.*, 2002 and references therein; Thamotharan *et al.*, 2004). Compound (I), containing four fused six-membered rings, is a steroid derivative with the normal 8*β*,9*α*,10*β*,13*β*,14*α* configuration. In our studies, we are particularly interested in the conformational flexibilities of the steroids resulting from variations in the substituents at the C3 and N17*A* positions.



(I)

Fig. 1 shows the asymmetric unit of (I). Rings *A*, *C* and *D* adopt chair conformations with the following puckering parameters: ring *A*: Q = 0.520 (4) Å, θ = 4.4 (4)° and φ = 26 (6)° for the atom sequence C1—C2—C3—C4—C5—C10; ring *C*: Q = 0.558 (4) Å, θ = 2.1 (4)° and φ = 222 (9)° for the atom sequence C8—C9—C11—C12—C13—C14; ring *D*: Q = 0.575 (5) Å, θ = 4.6 (5)° and φ = 80 (6)° for the atom sequence C13—C14—C15—C16—C17—N17*A* (Cremer & Pople, 1975). The substitution of the pyrrolidine ring at C3 has not disturbed the usual chair conformation of ring *A* of the steroid nucleus. In ring *B*, the C5═C6 (Csp^2—Csp^2) distance of 1.344 (5) Å

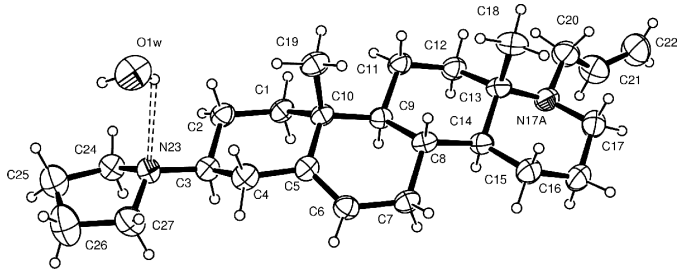


Figure 1
The molecular structure of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme. The hydrogen bond is shown dashed.

confirms the localization of the double bond at this position. This double bond imposes an 8β,9α-half-chair conformation on ring *B*, with puckering parameters Q = 0.465 (4) Å, θ = 53.7 (5)° and φ = 211.9 (6)° for the atom sequence C5—C6—C7—C8—C9—C10. Similar observations on the conformation of ring *B* in related structures have been reported by Thamotharan *et al.* (2002, 2004) and Hema *et al.* (2002, 2003). The pseudorotation angle, Δ = 1.7 (1)°, and the maximum torsion angle, φ_m = 42.3 (3)° (Altona *et al.*, 1968), indicate that the pyrrolidine ring exhibits a half-chair conformation. Atoms N23 and C24 are displaced by 0.235 (4) and 0.241 (6) Å, respectively, on opposite sides of the plane formed by atoms C25/C26/C27. Atom N17*A* is sp^3 hybridized and the geometry around this atom is pyramidal (sum of angles is 338°).

The C13—N17*A*—C20—C21 torsion angle is −156.4 (5)°; which indicates that the allyl moiety is (−)antiperiplanar with respect to the C13—N17*A* bond. The *B*/*C* and *C*/*D* ring junctions are all *trans*. The widening of the exocyclic angle C13—N17*A*—C20 [114.6 (3)°] may be due to steric interaction between atoms H12*B* and H20*A* (H···H = 1.946 Å). The C3···C17 distance of 9.541 (5) Å, which is a measure of the length of the steroid nucleus, indicates that the molecule is in a completely extended form. The C19—C10···C13—C18 pseudo-torsion angle, which gives a quantitative measure of the molecular twist, is 12.4 (3)°. This value is comparable with that of related structures (Hema *et al.*, 2002; Thamotharan *et al.*, 2002, 2004) There is a weak intermolecular O—H···N hydrogen bond involving the water molecule (Table 1).

Experimental

The title compound was prepared by adding sodium borohydride (1.0 g, 26.43 mmol) to 17*a*-allyl-3-pyrrolidino-17*a*-aza–D-homo-3,5-androstadiene (1.0 g, 2.61 mmol) prepared from 17*a*-allyl-17*a*-aza-D-homo-4-androsten-3-one (1.0 g, 3.20 mmol) by refluxing in pyrrolidine in methanol. After being stirred for 2 h at room temperature, the reaction mixture was poured into ice-cold water and the aqueous suspension was extracted with chloroform. The combined chloroform extract was washed with water, dried and the solvent removed to give a solid residue which was crystallized from methanol to afford crystals of (I) (0.70 g, 69.65%, m.p: 403 K).

Crystal data

$C_{26}H_{42}N_2{\cdot}H_2O$
M_r = 400.63
Orthorhombic, $P2_12_12_1$
a = 6.999 (5) Å
b = 11.569 (5) Å
c = 29.441 (10) Å
V = 2384 (2) Å^3
Z = 4
D_x = 1.116 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 25 reflections
θ = 10–15°
μ = 0.07 mm^{-1}
T = 293 (2) K
Plate, green
0.4 × 0.4 × 0.2 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
ω–2θ scans
Absorption correction: ψ scan (North *et al.*, 1968)
T_{min} = 0.974, T_{max} = 0.987
3348 measured reflections
2424 independent reflections
1480 reflections with $I > 2\sigma(I)$
R_{int} = 0.032
θ_{max} = 25.0°
$h = -4 \rightarrow 8$
$k = 0 \rightarrow 13$
$l = 0 \rightarrow 34$
2 standard reflections
frequency: 120 min
intensity decay: none

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.050
$wR(F^2)$ = 0.169
S = 0.96
2424 reflections
308 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.1226P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.24 e Å^{-3}
$\Delta\rho_{min}$ = −0.27 e Å^{-3}

Table 1
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
O1*W*—H1*W*···N23	0.81 (8)	2.52 (10)	3.021 (5)	121 (10)

All H atoms of the steroid were positioned geometrically and refined using a riding model, with C—H = 0.93–0.98 Å and U_{iso}(H) = 1.5 U_{eq}(C) for methyl H atoms and 1.2U_{eq}(C) for all other H atoms. The H atoms of the water molecule were located in a difference Fourier map and were refined, subject to bond length restraints of 0.82 (2) Å and 1.0 (2) Å. Due to the absence of any significant anomalous scatterers in (I), attempts to confirm the absolute configuration by refinement of the Flack (1983) parameter in the presence of 924 Friedel pairs led to an inconclusive value (Flack & Bernardinelli, 2000) of 0.1 (4). Therefore, the Friedel pairs were merged before the final refinement and the absolute configuration of the title compound was assigned to correspond to that of the known chiral centres in a precursor molecule, namely 17*a*-allyl-17*a*-aza-D-homoandrost-4-ene-3-one (Vasuki *et al.*, 2002), which remained unchanged during the synthesis of (I).

Data collection: *CAD*-4 *EXPRESS* (Enraf–Nonius, 1994); cell refinement: *CAD*-4 *EXPRESS*; data reduction: *MolEN* (Fair, 1990); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ZORTEP*97 (Zsolnai, 1997).

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