## organic papers

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## Qiang Nie,\* Jing-Kang Wang, Shi Wang and Mei-Jing Zhang

School of Chemical Engineering and Technology, Tianjin University, Tianjin 300072, People's Republic of China

Correspondence e-mail: nie\_qiang80@yahoo.com.cn

#### **Key indicators**

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.004 Å R factor = 0.046 wR factor = 0.104 Data-to-parameter ratio = 18.1

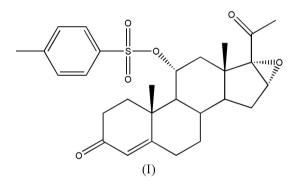
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

## 16*a*,17-Epoxy-11*α*-(*p*-tolylsulfonyloxy)pregn-4-ene-3,20-dione

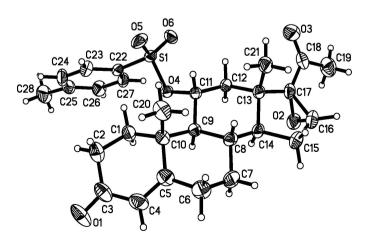
The title compound,  $C_{28}H_{34}O_6S$ , is an important intermediate in the synthesis of hormone pharmaceuticals. In the crystal structure, the asymmetric unit consists of two molecules. Received 19 January 2005 Accepted 4 March 2005 Online 11 March 2005

#### Comment

The title compound, (I), is an important intermediate in the synthesis of hormone pharmaceuticals, such as fluocinonide (Xu, 2001). It was first prepared from  $11\alpha$ -hydroxy- $16\alpha$ ,17-epoxyprogesterone by sulfonation with *p*-toluenesulfonyl-chloride (Camerino *et al.*, 1959), but the crystal structure was not reported.



In the crystal structure, the asymmetric unit consists of two molecules (Figs. 1 and 2). Ring A is in a 1 $\alpha$ -sofa conformation, rings B and C are in nearly perfect chair conformations and ring D is in a 14 $\alpha$ -envelope conformation. The presence of the three-membered ring constrains ring D to have a 14 $\alpha$ -

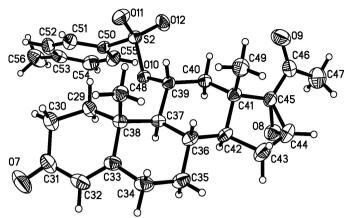


The molecular structure of molecule 1 of (I), showing the atom-labelling

scheme. Displacement ellipsoids are drawn at the 30% probability level.

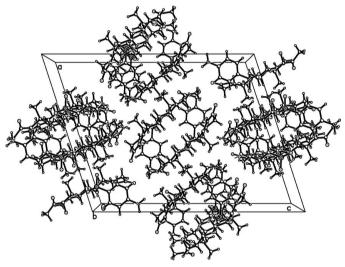
#### Figure 1

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#### Figure 2

The molecular structure of molecule 2 of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.



#### Figure 3

The molecular packing of (I), viewed along the b axis.

envelope conformation (Goubitz et al., 1984). The two molecules in the asymmetric unit have similar conformations.

### **Experimental**

 $11\alpha$ -Hydroxy- $16\alpha$ ,17-epoxyprogesterone (1 g; provided by Tianjin Tianyao Pharmaceutical Co. Ltd) was dissolved in pyridine (20 ml) and treated with p-toluenesulfonyl chloride (0.6 g) at room temperature overnight. The product was chromatographed on silica gel and recrystallized from acetone-hexane three times. The melting point, determined by differential scanning calorimetry, is 443.2 K with decomposition. Colourless plate-like single crystals suitable for X-ray diffraction were obtained by slow evaporation of a chloroformmethanol solution (1:1, 10 ml) at room temperature.

#### Crystal data

$C_{28}H_{34}O_6S$	$D_x = 1.288 \text{ Mg m}^{-3}$
$M_r = 498.61$	Mo $K\alpha$ radiation
Monoclinic, C2	Cell parameters from 2920
a = 19.508 (2)  Å	reflections
b = 10.731(1) Å	$\theta = 2.3 - 19.4^{\circ}$
c = 25.920 (4) Å	$\mu = 0.17 \text{ mm}^{-1}$
$\beta = 108.666 \ (2)^{\circ}$	T = 293 (2) K
$V = 5140.8 (11) \text{ Å}^3$	Thick plate, colourless
Z = 8	$0.26 \times 0.22 \times 0.12 \text{ mm}$

## Data collection

Bruker SMART CCD area-detector	11 583 independent reflections
diffractometer	7085 reflections with $I > 2\sigma(I)$
$\varphi$ and $\omega$ scans	$R_{\text{int}} = 0.029$
Absorption correction: multi-scan	$\theta_{\text{max}} = 28.0^{\circ}$
( <i>SADABS</i> ; Sheldrick, 1997)	$h = -19 \rightarrow 25$
$T_{\min} = 0.927, T_{\max} = 0.980$ 17 613 measured reflections <i>Refinement</i>	$k = -13 \rightarrow 14$ $l = -34 \rightarrow 31$
Refinement on $F^2$	$(\Delta/\sigma)_{max} = 0.001$
$R[F^2 > 2\sigma(F^2)] = 0.046$	$\Delta\rho_{max} = 0.16 \text{ e } \text{\AA}^{-3}$
$wR(F^2) = 0.104$	$\Delta\rho_{min} = -0.33 \text{ e } \text{\AA}^{-3}$

S = 1.0111583 reflections 639 parameters H-atom parameters constrained  $w = 1/[\sigma^2 (F_0^2) + (0.0375P)^2]$ where  $P = (F_0^2 + 2F_c^2)/3$ 

# Extinction correction: none Absolute structure: Flack (1983), 4824 Friedel pairs

Flack parameter: 0.08 (5)

H atoms were placed in calculated positions and constrained to ride on their parent atoms, with C-H distances of 0.93-0.98 Å and  $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$ . The refinement of the Flack (1983) parameter confirms that the chiral centres retain their original configurations during the synthesis, as expected.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1998); software used to prepare material for publication: SHELXTL.

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