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Key indicators

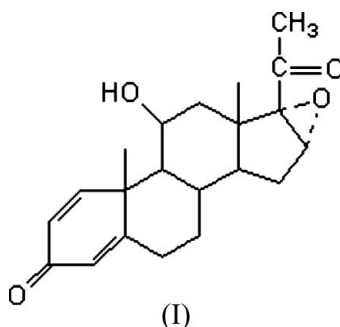
Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.055
 wR factor = 0.105
Data-to-parameter ratio = 10.5For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**16 α ,17 α -Epoxypregna-11 α -hydroxy-1,4-
diene-3,20-dione**

The title compound, $\text{C}_{21}\text{H}_{26}\text{O}_4$, is an important intermediate in the synthesis of corticosteroids. The crystal packing is predominantly stabilized by strong intermolecular $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds.

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Comment

16 α ,17 α -Epoxypregna-11 α -hydroxy-1,4-diene-3,20-dione, (I), is used to produce 11 β -hydroxypregna-1,4,16-triene-3,20-dione, which is an intermediate in the synthesis of corticosteroids; there has been no previous report of its structure.



The title compound crystallizes in the orthorhombic space group $P2_12_12_1$. The molecular structure has a typical steroid conformation, with three six-membered rings and one five-membered ring denoted, respectively, as *A*, *B*, *C* and *D*, and is shown in Fig. 1. Ring *A* has a 1α -sofa conformation, and rings *B* and *C* are in nearly perfect chair conformations. Ring *D* is in an envelope conformation. There is a strong hydrogen bond between the 11-OH group and the 3-carbonyl group of adjacent molecules (Table 1), with an $\text{H}\cdots\text{O}$ distance of 1.94 (2) \AA and an $\text{O}2-\text{H}2\text{B}\cdots\text{O}1$ angle of 162.1 (4) $^\circ$.

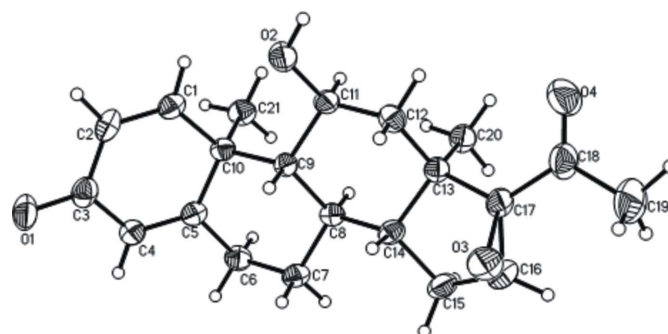


Figure 1
The molecular structure of compound (I), showing the atom-labelling scheme and displacement ellipsoids drawn at the 30% probability level.

Experimental

Crystals of 16 α ,17 α -epoxypregna-11 α -hydroxy-1,4-diene-3,20-dione, provided by Tianjin Tianyao Pharmaceutical Co. Ltd, were grown in a 5 ml beaker with 3 ml ethanol at 313 K. The beaker was sealed and single crystals were obtained after 4 d.

Crystal data

| | |
|--------------------------------|---|
| $C_{21}H_{26}O_4$ | $Z = 4$ |
| $M_r = 342.42$ | $D_x = 1.262 \text{ Mg m}^{-3}$ |
| Orthorhombic, $P2_12_12_1$ | Mo $K\alpha$ radiation |
| $a = 6.1342 (12) \text{ \AA}$ | $\mu = 0.09 \text{ mm}^{-1}$ |
| $b = 15.433 (3) \text{ \AA}$ | $T = 293 (2) \text{ K}$ |
| $c = 19.029 (4) \text{ \AA}$ | Block, colourless |
| $V = 1801.5 (6) \text{ \AA}^3$ | $0.11 \times 0.11 \times 0.08 \text{ mm}$ |

Data collection

| | |
|---|--|
| Rigaku R-Axis RAPID IP area-detector diffractometer | 17631 measured reflections |
| ω scans | 2371 independent reflections |
| Absorption correction: multi-scan (SADABS; Sheldrick, 1997) | 1444 reflections with $I > 2\sigma(I)$ |
| $T_{\min} = 0.990$, $T_{\max} = 0.993$ | $R_{\text{int}} = 0.113$ |
| | $\theta_{\text{max}} = 27.5^\circ$ |

Refinement

| | |
|---------------------------------|--|
| Refinement on F^2 | H-atom parameters constrained |
| $R[F^2 > 2\sigma(F^2)] = 0.055$ | $w = 1/[\sigma^2(F_o^2) + (0.04P)^2]$ |
| $wR(F^2) = 0.105$ | where $P = (F_o^2 + 2F_c^2)/3$ |
| $S = 1.08$ | $(\Delta/\sigma)_{\text{max}} < 0.001$ |
| 2371 reflections | $\Delta\rho_{\text{max}} = 0.14 \text{ e \AA}^{-3}$ |
| 226 parameters | $\Delta\rho_{\text{min}} = -0.16 \text{ e \AA}^{-3}$ |

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

| $D-H\cdots A$ | $D-H$ | $H\cdots A$ | $D\cdots A$ | $D-H\cdots A$ |
|---------------------|-------|-------------|-------------|---------------|
| $O2-H2A\cdots O1^i$ | 0.82 | 1.94 | 2.731 (3) | 162 |

Symmetry code: (i) $-x + 3, y + \frac{1}{2}, -z + \frac{1}{2}$.

H atoms were placed in calculated positions and constrained to ride on their parent atoms, with $C-H = 0.93-0.98 \text{ \AA}$ and $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(C)$. In the absence of significant anomalous scattering effects, Friedel pairs were merged prior to the final refinement.

Data collection: *RAPID-AUTO* (Rigaku, 2004); cell refinement: *RAPID-AUTO*; data reduction: *RAPID-AUTO*; program(s) used to

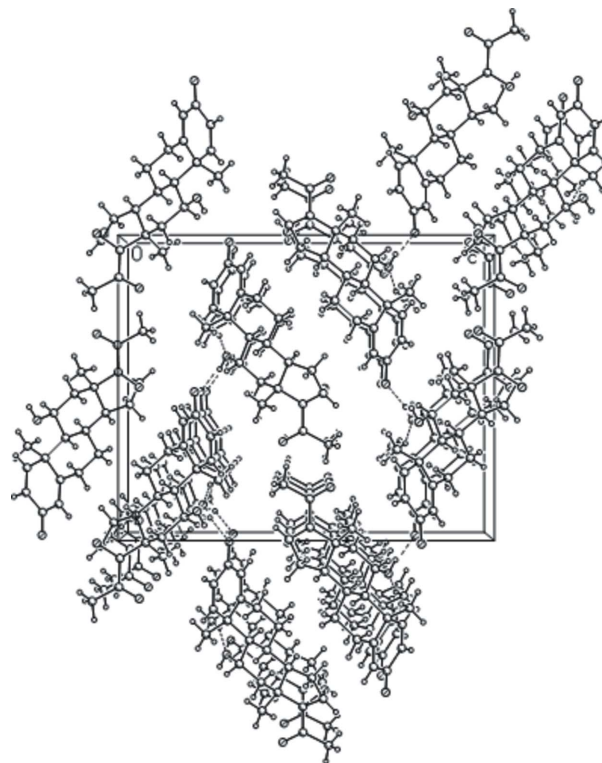


Figure 2

The molecular packing of compound (I), viewed down the a axis.

solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXL97*; software used to prepare material for publication: *SHELXL97*.

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References

- Rigaku (2004). *RAPID-AUTO*. Rigaku Corporation, Tokyo, Japan.
Sheldrick, G. M. (1997). *SADABS*, *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.