

**(19*R*)-5,19-Bis(acetyloxy)-10,13-dideoxy-10-oxo-5 $\beta$ -enmein****Hao Shi\* and Wei-Xiao Hu**The College of Pharmaceutical Science,  
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The title compound, C<sub>24</sub>H<sub>28</sub>O<sub>9</sub>, was prepared from macrocalyxin A and is built up from five fused rings, *viz.* three six-membered rings and two five-membered rings. Two unique molecules are present in the asymmetric unit; both independent molecules have the same absolute configuration, which was deduced from the chirality of the starting material.

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**Key indicators**

Single-crystal X-ray study

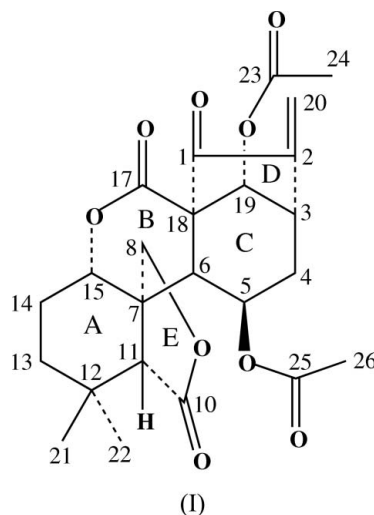
 $T = 293\text{ K}$ Mean  $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$  $R$  factor = 0.043 $wR$  factor = 0.103

Data-to-parameter ratio = 8.5

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

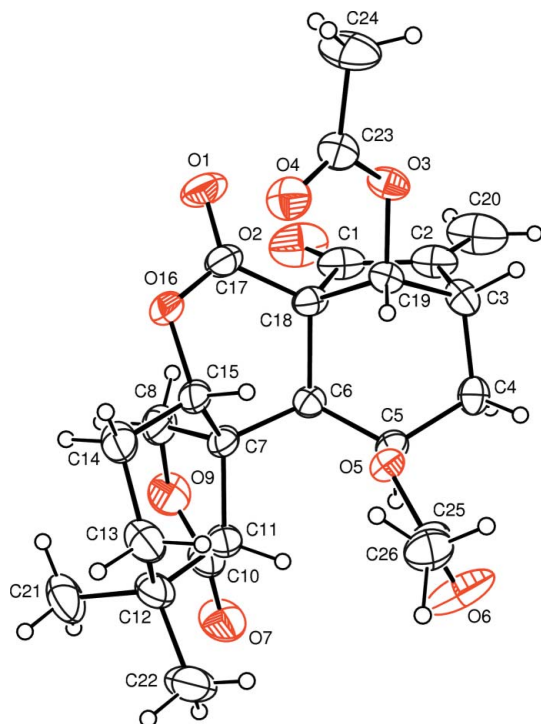
**Comment**

Since the natural diterpenoid macrocalyxin A is found to have inhibitory action on *Staphylococcus*, *Bacillus subtilis* and *Candida albicans* (Wang *et al.*, 1984) and exhibits cytotoxicity *in vitro* against cultures of HeLa cells, with a rate of check back of 80% at the concentration of 4  $\mu\text{g ml}^{-1}$  (Cheng *et al.*, 1984), we have derived the title compound from it.



Two unique molecules are present in the asymmetric unit; both molecule 1 (Fig. 1) and molecule 2 (Fig. 2) are built up from five fused rings, *viz.* three six-membered and two five-membered rings. Some geometrical features of these rings were investigated using *PLATON* (Spek, 2003).

For molecule 1, cyclohexane ring *A* (C7/C11–C15) adopts a chair conformation with puckering parameters (Cremer & Pople, 1975)  $Q = 0.526(3)\text{ \AA}$ ,  $\theta = 156.2(4)^\circ$  and  $\varphi = 23.6(9)^\circ$ , ring *B* (O16/C15/C7/C6/C18/C17) exists in a screw-boat conformation [ $Q = 0.676(3)\text{ \AA}$ ,  $\theta = 72.1(3)^\circ$  and  $\varphi = 82.7(3)^\circ$ ], and ring *C* (C3–C6/C18/C19) adopts a boat conformation [ $Q = 0.808(3)\text{ \AA}$ ,  $\theta = 103.4(2)^\circ$  and  $\varphi = 124.1(2)^\circ$ ]. For the two five-membered rings, ring *D* (C1–C3/C19/C18) adopts an envelope conformation with puckering parameters  $Q_2 = 0.445(3)\text{ \AA}$ , and  $\varphi_2 = 288.0(5)^\circ$  (envelope on C19), while ring *E* (O9/C10/



**Figure 1**  
Perspective view of molecule 1 of the title compound, shown with 30% probability displacement ellipsoids.

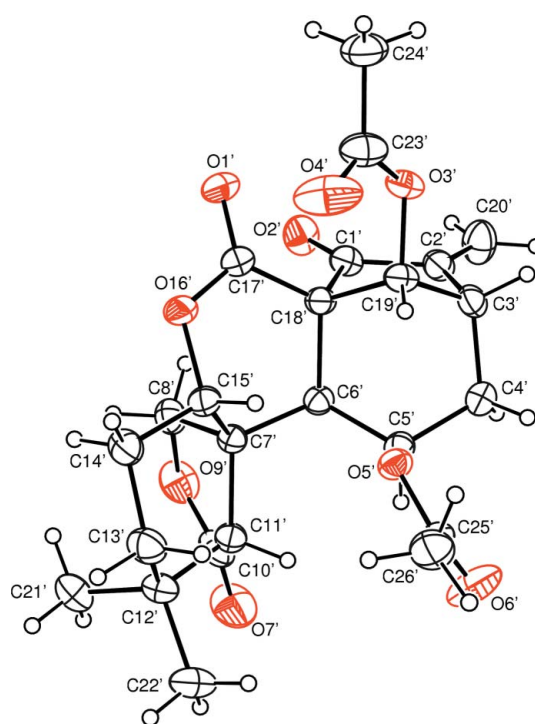
C11/C7/C8) adopts an envelope conformation with puckering parameters  $Q_2 = 0.328$  (4) Å and  $\varphi_2 = 256.4$  (6)° (envelope on C7).

For molecule 2, cyclohexane ring *A'* (C7'/C11'–C15') adopts a chair conformation with puckering parameters  $Q = 0.520$  (3) Å,  $\theta = 158.7$  (3)° and  $\varphi = 29.0$  (9)°, ring *B'* (O16'/C15'/C7'/C6'/C18'/C17') exists in a screw-boat conformation [ $Q = 0.635$  (3) Å,  $\theta = 69.3$  (2)° and  $\varphi = 85.9$  (3)°], and ring *C'* (C3'–C6'/C18'/C19') adopts a boat conformation [ $Q = 0.813$  (3) Å,  $\theta = 102.06$  (20)° and  $\varphi = 128.2$  (2)°]. For the two five-membered rings, ring *D'* (C1'–C3'/C19'/C18') adopts an envelope conformation with puckering parameters  $Q_2 = 0.466$  (3) Å and  $\varphi_2 = 292.9$  (4)° (envelope on C19'), while ring *E'* (O9'/C10'/C11'/C7'/C8') adopts an envelope conformation with puckering parameters  $Q_2 = 0.337$  (3) Å and  $\varphi_2 = 259.9$  (6)° (envelope on C7').

Since the title compound was prepared from the same starting materials (*i.e.* macrocalyxin A) as in the reference (Shi *et al.*, 2003), the configuration can be deduced from the known chirality of the starting material and thus Figs. 1 and 2 represent the correct absolute configuration.

## Experimental

With cooling in an ice–water bath, Jones reagent (0.2 ml) was added to a solution of macrocalyxin A (400 mg; isolated from *Rabdosia macrocalyx*) in acetone (15 ml). After stirring for 20 min, the solution was filtered and 240 ml 15% NaHCO<sub>3</sub> in water was added. The mixture was extracted three times with diethyl ether (90 ml). After evaporation of the solvent, a white residue was obtained. Recrys-



**Figure 2**  
Perspective view of molecule 2 of the title compound, shown with 30% probability displacement ellipsoids.

tallization from methanol gave the title compound as colourless crystals. Crystals suitable for X-ray structure analysis were obtained by slow evaporation of a solution in methanol at room temperature.

## Crystal data

C<sub>24</sub>H<sub>28</sub>O<sub>9</sub>  
*M<sub>r</sub>* = 460.46  
 Monoclinic, *P*2<sub>1</sub>  
*a* = 13.4851 (13) Å  
*b* = 12.7578 (12) Å  
*c* = 13.6537 (13) Å  
 $\beta$  = 104.796 (2)°  
*V* = 2271.1 (4) Å<sup>3</sup>  
*Z* = 4

*D<sub>x</sub>* = 1.347 Mg m<sup>-3</sup>  
 Mo *K*α radiation  
 Cell parameters from 4846 reflections  
 $\theta = 4.5$ –47.6°  
 $\mu = 0.10$  mm<sup>-1</sup>  
*T* = 293 (2) K  
 Plate, colourless  
 0.50 × 0.49 × 0.16 mm

## Data collection

Bruker SMART CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Bruker, 1999)  
*T<sub>min</sub>* = 0.778, *T<sub>max</sub>* = 1.000  
 13256 measured reflections

5153 independent reflections  
 3988 reflections with *I* > 2σ(*I*)  
*R<sub>int</sub>* = 0.092  
 $\theta_{\max}$  = 27.0°  
*h* = -17 → 16  
*k* = -16 → 16  
*l* = -8 → 17

## Refinement

Refinement on *F*<sup>2</sup>  
*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.044  
*wR* (*F*<sup>2</sup>) = 0.103  
*S* = 0.93  
 5153 reflections  
 603 parameters

H-atom parameters constrained  
 $w = 1/[\sigma^2(F_o^2) + (0.0484P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} = 0.050$   
 $\Delta\rho_{\max} = 0.16$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.21$  e Å<sup>-3</sup>

H atoms were placed in calculated positions and treated as riding on their parent atoms, with C–H = 0.96 Å (CH<sub>3</sub>), 0.93 and 0.97 Å (CH<sub>2</sub>), and 0.98 Å (CH), and with *U*<sub>iso</sub>(H) = 1.5*U*<sub>eq</sub>(C) (CH<sub>3</sub>) and

$1.2U_{eq}(C)$  ( $CH_2$  and  $CH$ ). The two independent molecules have the same absolute configuration, although this could not be determined reliably from the X-ray data, and Friedel reflections were merged.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SAINTE* (Bruker, 1999); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

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