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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.006 Å R factor = 0.048 wR factor = 0.131 Data-to-parameter ratio = 8.8

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

5,6-Dihydroxy-1,2,3,13-tetramethoxy-6,7-dimethyl-5,6,7,8-tetrahydrobenzo[3,4]cycloocta[1,2-*f*][1,3]benzodioxol-5-yl benzoate sesquihydrate

In the title compound, $C_{30}H_{32}O_{9}\cdot 1.5H_2O$, the cyclooctadiene eight-membered ring adopts a twisted boat–chair conformation. $O-H\cdots O$ hydrogen bonding helps to stabilize the crystal structure.

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Comment

The title compound (common name Schisantherin A), (I), was isolated from a Chinese medicine, Fructus Schisandrae sphenantherae (the fruit of *Schisandra sphenanthera* Rehd. et Wils.), and was found to have antihepatotoxic activity (Fang *et al.*, 1975). We report here the crystal structure of (I).



The molecular structure of (I) is shown in Fig. 1. The cyclooctadiene eight-membered ring adopts a twisted boatchair conformation. The benzodioxole group is planar and makes a dihedral angle with the C27-containing benzene ring of 67.5 (2)°. The C16-containing ring is nearly perpendicular to the C27-benzene plane, the dihedral angle being 88.0 (2)°.

Adjacent Schisantherin A molecules link together *via* $O-H \cdots O$ hydrogen bonding involving solvent water molecules (Table 1).

Experimental

The dried fruits of *Schisandra sphenanthera* (1500 g) were extracted with ethanol and fractionated into $CHCl_3$ - and H_2O -soluble fractions. The $CHCl_3$ -soluble fraction was chromatographed on a silica gel column, eluting with $CHCl_3$ -EtOAc (2:1) to afford Schisantherin A, (I). Colorless single crystals of (I) were obtained by slow evaporation of an ethanol solution.

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organic papers

Crystal data

 $\begin{array}{l} C_{30}H_{32}O_{9}:1.5H_{2}O\\ M_{r}=563.58\\ Orthorhombic, P2_{1}2_{1}2\\ a=12.818 \ (3) \ \text{\AA}\\ b=27.883 \ (7) \ \text{\AA}\\ c=7.921 \ (2) \ \text{\AA}\\ V=2831.0 \ (12) \ \text{\AA}^{3} \end{array}$

Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: none 10679 measured reflections

Refinement

Refinement on F^2	H-atom parameters constrained		
$R[F^2 > 2\sigma(F^2)] = 0.048$	$w = 1/[\sigma^2(F_o^2) + (0.0687P)^2]$		
$wR(F^2) = 0.131$	where $P = (F_0^2 + 2F_c^2)/3$		
S = 1.00	$(\Delta/\sigma)_{\rm max} < 0.001$		
3264 reflections	$\Delta \rho_{\rm max} = 0.37 \text{ e} \text{ \AA}^{-3}$		
372 parameters	$\Delta \rho_{\rm min} = -0.17 \text{ e } \text{\AA}^{-3}$		

Z = 4

 $D_x = 1.322 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

 $\mu = 0.10 \text{ mm}^{-1}$

T = 293 (2) K

 $R_{\rm int} = 0.061$

 $\theta_{\rm max} = 26.4^{\circ}$

Block, colorless

 $0.26 \times 0.22 \times 0.18 \text{ mm}$

3264 independent reflections

1932 reflections with $I > 2\sigma(I)$

Table 1

Hydrogen-bond geometry (Å, °).

$D - \mathbf{H} \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$
$\begin{array}{c} \hline O4-H4A\cdots O11\\ O10-H10A\cdots O4\\ O10-H10B\cdots O9^{i} \end{array}$	0.84 0.90 0.84	2.14 1.90 2.23	2.900 (5) 2.797 (6) 3.071 (6)	150 178 175

Symmetry code: (i) x, y, z - 1.

H atoms on O atoms were located in a difference Fourier map and refined as riding in their as-found relative positions $[O-H = 0.84-0.92 \text{ Å}, U_{iso}(H) = 1.5U_{eq}(O)]$. Methyl H atoms were placed in calculated positions with C-H = 0.96 Å and torsion angles were refined to fit the electron density; $U_{iso}(H) = 1.5U_{eq}(C)$. Other H atoms were placed in calculated positions with C-H = 0.93(aromatic), 0.97 (methylene) or 0.98 Å (methine), and refined in riding mode with $U_{iso}(H) = 1.2U_{eq}(C)$. In the absence of significant anomalous scattering effects, Friedel pairs were merged; the absolute configuration of (I) was assigned arbitrarily.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine

Figure 1

The molecular structure of (I), with 30% probability displacement ellipsoids (arbitrary spheres for H atoms). Dashed lines indicate hydrogen bonds.

structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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