

5-(2,3-Dihydroxy-3-methylbutoxy)-7H-furo[3,2-g]chromen-7-one

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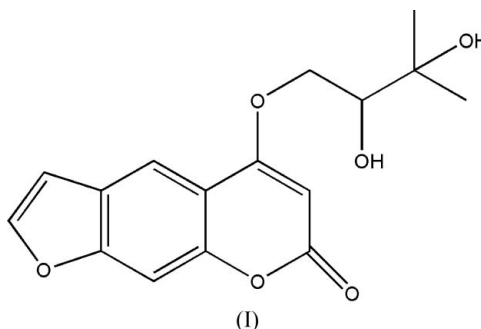
Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
Disorder in main residue
 R factor = 0.043
 wR factor = 0.113
Data-to-parameter ratio = 12.1For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

In the title compound, $\text{C}_{16}\text{H}_{16}\text{O}_6$, the furan, benzene and pyrone rings are almost coplanar. The crystal structure is stabilized by intermolecular $\text{O}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonding.

Comment

The title compound (common name oxypeucedanin hydrate), (I), was isolated from a Chinese medicine, Radix Angelica dahuricae (the root of *Angelica Dahurica*). Pharmacology experiments have shown that oxypeucedanin hydrate inhibits histamine release (Kimura *et al.*, 1997). We report here the crystal structure of (I).



The molecular structure of (I) is shown in Fig. 1. The furan, benzene and pyrone rings are essentially coplanar, with a maximum deviation of 0.0174 (3) Å for atom C1. The dihedral angle between the coumarin unit and the furan ring is 1.1 (2)°. Adjacent molecules are linked *via* classical $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonding and weak $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonding (Table 1).

Experimental

The dried root of *Angelica Dahurica* was extracted with ethanol and fractionated into EtOAc- and water-soluble fractions. The EtOAc-soluble fraction was subjected to silica gel column chromatography using a CHCl_3 -MeOH gradient (1:0 to 0:1) to obtain oxypeucedanin hydrate, which was further purified by preparative thin-layer chromatography. Single crystals of (I) were obtained by slow evaporation of an ethanol solution.

Crystal data

$\text{C}_{16}\text{H}_{16}\text{O}_6$
 $M_r = 304.29$
Monoclinic, $P2_1/c$
 $a = 9.1301$ (19) Å
 $b = 10.015$ (2) Å
 $c = 16.003$ (3) Å
 $\beta = 98.824$ (4)°
 $V = 1445.9$ (5) Å³

$Z = 4$
 $D_x = 1.398$ Mg m⁻³
Mo $K\alpha$ radiation
 $\mu = 0.11$ mm⁻¹
 $T = 293$ (2) K
Block, colourless
0.24 × 0.22 × 0.20 mm

Data collection

Bruker SMART CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: none
 7192 measured reflections

2549 independent reflections
 1511 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.036$
 $\theta_{\text{max}} = 25.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.043$
 $wR(F^2) = 0.113$
 $S = 1.01$
 2549 reflections
 210 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0468P)^2 + 0.2072P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.14 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.16 \text{ e } \text{\AA}^{-3}$

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O5A-H5A\cdots O6^i$	0.85	1.98	2.822 (3)	171
$O6-H6A\cdots O3^{ii}$	0.87	1.97	2.819 (3)	167
$C10-H10\cdots O3^{iii}$	0.93	2.58	3.479 (3)	162

Symmetry codes: (i) $-x + 1, y - \frac{1}{2}, -z + \frac{3}{2}$; (ii) $-x + 1, -y + 1, -z + 2$; (iii) $-x + 2, y + \frac{1}{2}, -z + \frac{5}{2}$.

The O5 hydroxy group is disordered over two positions; occupancies were refined and converged to 0.594 (3) and 0.406 (3), and were fixed at 0.6 and 0.4 in the final cycles of refinement. H atoms on O atoms were located in a difference Fourier map and refined as riding in their as-found relative positions, with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{O})$. Methyl H atoms were placed in calculated positions with $C-H = 0.96 \text{ \AA}$ and torsion angles were refined to fit the electron density, $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$. Other H atoms were placed in calculated positions, with $C-H = 0.93$ (aromatic), 0.97 (methylene) or 0.98 \AA (methine), and refined in riding mode, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

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

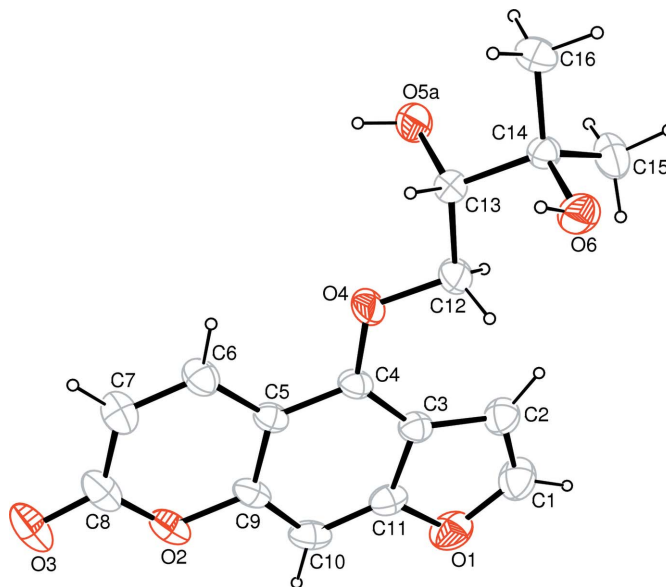


Figure 1

The molecular structure of (I), shown with 30% probability displacement ellipsoids (arbitrary spheres for H atoms). The minor disordered component has been omitted for clarity.

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

References

Bruker (1997). SMART, SAINT and SHELXTL. Bruker AXS Inc., Madison, Wisconsin, USA.
 Kimura, Y., Okuda, H. & Baba, K. (1997). *J. Nat. Prod.* **60**, 249–251.
 Sheldrick, G. M. (1997). SHELXS97 and SHELXL97. University of Göttingen, Germany.