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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.008 Å R factor = 0.056 wR factor = 0.127 Data-to-parameter ratio = 5.9

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The molecules of the title compound, $C_{11}H_{10}O_5$, are linked by a hydrogen bond involving the acid H and the carbonyl O atom of the dihydroisocoumarin unit into a linear chain running along the *b* axis of the monoclinic unit cell.

5-carboxylic acid (5-carboxymellein)

8-Hydroxy-(S)-3-methyl-1-oxoisochromane-

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Comment

8-Hydroxy-3-methyl-1-oxoisochromane-5-carboxylic acid (5carboxymellein), (I) (Fig. 1), a dihydroisocoumarin isolated from *Tubercularia sp.*, an endophytic fungus of *Taxus mairei* that is found in Fujian Province, China, yields compounds that are cytotoxic to KB and HL60 cancer cell lines (Wang *et al.*, 2000). The structure has been assigned on the basis of twodimensional NMR studies (Chinworrungsee *et al.*, 2001); the crystal structure shows that adjacent molecules are linked by a short hydrogen bond involving the carboxylic acid group and the double-bond O atom of the dihydroisocoumarin ring of an adjacent molecule $[O \cdots O = 2.702 (5) \text{ Å}]$ to furnish a linear chain running along the *b* axis of the unit cell. The structure is similar to that of 5-methylmellein, which shows only weak bioactivity (Krohn *et al.*, 1997).



Experimental

The title compound was isolated from an endophytic fungus, *Tubercularia sp.*, which was found in the inner bark of *Taxus mairei* of Fujian Province, China. Crystals were grown from a solution in ethyl acetate.



Figure 1

© 2003 International Union of Crystallography Printed in Great Britain – all rights reserved ORTEPII (Johnson, 1976) plot of (I), with displacement ellipsoids drawn at the 50% probability level. H atoms are drawn as spheres of arbitrary radii.

Crystal data

 $C_{11}H_{10}O_5$ $M_r = 222.19$ Monoclinic, P2 a = 7.3351 (4) Åb = 9.0510(5) Å c = 7.4211(5) Å $\beta = 101.723 (3)^{\circ}$ $V = 482.41 (5) \text{ Å}^3$ Z = 2

Data collection

Bruker APEX area-detector diffractometer φ and ω scans Absorption correction: none 2438 measured reflections 897 independent reflections

Refinement

Table 1

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.056$ $wR(F^2) = 0.127$ S=1.05897 reflections 151 parameters

Table T		
Selected	geometric	naran

Selected geometric parameters (Å, °).

O1-C1	1.323 (6)	C3-C4	1.366 (8)
O2-C1	1.183 (6)	C4-C5	1.375 (8)
O3-C5	1.330 (7)	C5-C6	1.398 (7)
O4-C8	1.217 (7)	C6-C7	1.409 (8)
O5-C8	1.298 (6)	C6-C8	1.467 (8)
O5-C10	1.467 (6)	C7-C9	1.508 (7)
C1-C2	1.479 (8)	C9-C10	1.502 (7)
C2-C7	1.390 (7)	C10-C11	1.493 (7)
C2-C3	1.402 (7)		
C8-O5-C10	117.9 (4)	C5-C6-C8	119.3 (5)
O2-C1-O1	122.8 (5)	C7-C6-C8	119.7 (5)
O2-C1-C2	122.2 (5)	C2-C7-C6	118.8 (5)
O1-C1-C2	115.0 (5)	C2-C7-C9	125.0 (5)
C7-C2-C3	118.9 (5)	C6-C7-C9	116.2 (4)
C7-C2-C1	126.6 (5)	04-C8-O5	118.0 (5)
C3-C2-C1	114.5 (5)	O4-C8-C6	120.9 (6)
C4-C3-C2	121.9 (5)	O5-C8-C6	121.1 (5)
C3-C4-C5	119.9 (5)	C10-C9-C7	111.2 (4)
O3-C5-C4	116.0 (5)	O5-C10-C11	106.0 (5)
O3-C5-C6	124.5 (5)	O5-C10-C9	110.2 (4)
C4-C5-C6	119.4 (5)	C11-C10-C9	113.2 (5)
C5-C6-C7	120.8 (5)		

The acid and hydroxyl H atoms were located and refined subject to O-H = 0.85 (1) Å. Their displacement parameters were set to 1.2 times U_{eq} of their parent atoms. The C-bound H atoms were positioned geometrically and were included in the refinement in the riding-model approximation; $U_{iso}(H) = 1.2U_{eq}(C,O)$ for H atoms on secondary and tertiary C atoms and on O atoms, and $U_{iso} = 1.5U_{eq}(C)$ for methyl H atoms. The configuration was that taken from the NMR study of 5-carboxylemmein isolated from the marine fungus Halorosellinia oceanica (Chinworrungsee et al., 2001); the report did not, however, mention how the configuration was assigned. In the absence of significant anomalous scattering effects, Friedel pairs were merged.

 $D_x = 1.530 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 634 reflections $\theta = 2.8 - 21.7^{\circ}$ $\mu = 0.12 \text{ mm}^{-1}$ T = 298 (2) KPlate, colorless $0.15 \times 0.12 \times 0.06 \ \mathrm{mm}$

726 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.040$ $\theta_{\rm max} = 25.0^{\circ}$ $h = -7 \rightarrow 8$ $k = -10 \rightarrow 10$ $l=-8\to 6$

H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0712P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.19 \ {\rm e} \ {\rm \AA}^{-3}$ $\Delta \rho_{\rm min} = -0.29 \text{ e} \text{ Å}^{-3}$



Figure 2

ORTEPII (Johnson, 1976) plot showing the hydrogen-bonded chain running along the b axis of the cell. $[O1 \cdots O4^{i} = 2.702 (5) \text{ Å}; \text{ symmetry}]$ code: (i) x, 1 + y, z].

Data collection: SMART (Bruker, 2001); cell refinement: SMART (Bruker, 2001); data reduction: SAINT (Bruker, 2001); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976); software used to prepare material for publication: SHELXL97.

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