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#### **Key indicators**

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.003 Å R factor = 0.041 wR factor = 0.122 Data-to-parameter ratio = 15.5

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The title compound,  $C_8H_8O_3$ , has several intra- and intermolecular hydrogen bonds in its crystal structure. There are two molecules in the asymmetric unit, and they are extended into infinite chains along [011] by intermolecular  $O-H\cdots O$ 

1-(2,6-Dihydroxyphenyl)ethanone

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## Comment

hydrogen bonds.

The title compound, (I), was isolated from the extracts of cultures of the estuarine fungus (No. 3920). This substance was previously isolated from the extracts of cultures of D. *Concentrica* strain 26 A1 (Allport & Bu'Lock, 1960). The structure of (I) was previously elucidated on the basis of spectroscopic analysis. We report here the crystal structure of (I).



The X-ray crystallographic study of (I) confirms the previously proposed molecular structure based on spectroscopic data. There are two crystallographically independent molecules in the asymmetric unit (Fig. 1). The C–O and C–C distances show no remarkable features (Table 1). A feature of the structure of (I) is the presence of both intra- and intermolecular O–H···O hydrogen bonds between the hydroxy groups and the carbonyl O atom (Table 2), resulting in infinite chains along [011] (Fig. 2).

## **Experimental**

A strain of fungus (No. 3920) was isolated from an endophyte NP 159/ Morphology Type10 from Kandelia Bark Mai Po, Hong Kong, and deposited in the Department of Applied Chemistry, ZhongShan University, Guangzhou, People's Republic of China. Culture conditions: GYT medium (glucose 10 g  $1^{-1}$ , peptone 2 g  $1^{-1}$ , yeast extract 1 g  $1^{-1}$ , NaCl 2 g  $1^{-1}$ ) and incubation at 298 K for 28 d. Extraction and separation of metabolite: the cultures (100 l) were filtered through cheesecloth. The filtrate was concentrated to 5 l below 333 K, then extracted three times by shaking with an equal volume of ethyl acetate. The extract was evaporated under reduced pressure. The combined organic extracts were subjected to silica-gel column chromatography, eluting with petroleum ether/ethyl acetate, to yield the

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title compound, (I). The compound's identity was confirmed by the NMR spectra. Crystals of (I) were obtained by evaporation of a methanol solution. <sup>1</sup>H NMR (300 MHz, actone- $d_6$ ):  $\delta$  2.69 (*s*, H), 6.40 (*d*, *J* = 8.1 Hz, H3, H5), 7.23 (*t*, *J* = 8.1, 16.2 Hz, H4), 11.44 (*s*, 2–OH,6–OH).

Z = 4

 $D_x = 1.400 \text{ Mg m}^{-3}$ 

Cell parameters from 816

Mo  $K\alpha$  radiation

reflections

 $\theta = 2.8-26.0^{\circ}$  $\mu = 0.11 \text{ mm}^{-1}$ 

T = 293 (2) K

 $R_{\rm int} = 0.015$ 

 $\theta_{\max} = 27.1^{\circ}$  $h = -9 \rightarrow 9$ 

 $k = -10 \rightarrow 10$ 

 $l = -15 \rightarrow 16$ 

Block, colorless

 $0.48 \times 0.42 \times 0.35 \text{ mm}$ 

3115 independent reflections

2065 reflections with  $I > 2\sigma(I)$ 

### Crystal data

 $\begin{array}{l} C_8H_8O_3 \\ M_r = 152.14 \\ \text{Triclinic, } P\overline{1} \\ a = 7.646 \ (3) \ \text{\AA} \\ b = 8.325 \ (3) \ \text{\AA} \\ c = 12.803 \ (5) \ \text{\AA} \\ a = 73.321 \ (6)^{\circ} \\ \beta = 79.042 \ (7)^{\circ} \\ \gamma = 68.230 \ (6)^{\circ} \\ V = 721.8 \ (5) \ \text{\AA}^3 \end{array}$ 

### Data collection

Bruker SMART CCD area-detector diffractometer  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)  $T_{\min} = 0.950, T_{\max} = 0.963$ 6117 measured reflections

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0579P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	+ 0.1147P]
$wR(F^2) = 0.122$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.03	$(\Delta/\sigma)_{\rm max} < 0.001$
3115 reflections	$\Delta \rho_{\rm max} = 0.24 \ {\rm e} \ {\rm \AA}^{-3}$
201 parameters	$\Delta \rho_{\rm min} = -0.13 \ {\rm e} \ {\rm \AA}^{-3}$
H-atom parameters constrained	

#### Table 1

Selected bond lengths (Å).

C1-C2	1.414 (2)	C9-C14	1.413 (2)
C1-C6	1.415 (2)	C9-C10	1.420 (2)
C1-C7	1.472 (2)	C9-C15	1.461 (2)
C2-O1	1.3519 (19)	C10-O4	1.3469 (19)
C2-C3	1.382 (2)	C10-C11	1.379 (2)
C3-C4	1.369 (2)	C11-C12	1.365 (3)
C4-C5	1.379 (2)	C12-C13	1.372 (3)
C5-C6	1.379 (2)	C13-C14	1.381 (2)
C6-O2	1.3539 (18)	C14-O5	1.352 (2)
C7-O3	1.2378 (19)	C15-O6	1.2425 (19)
C7-C8	1.489 (2)	C15-C16	1.486 (3)

#### Table 2

Hydrogen-bonding geometry (Å,  $^{\circ}$ ).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
01-H1A···O6 <sup>i</sup>	0.82	1.95	2.767 (2)	176
$O2-H2A\cdots O3$	0.82	1.74	2.472 (2)	148
$O4-H4A\cdots O6$	0.82	1.79	2.513 (2)	146
$O5-H5A\cdots O2^{ii}$	0.82	1.97	2.7878 (19)	180

Symmetry codes: (i) x - 1, 1 + y, z; (ii) 1 + x, y, z - 1.



#### Figure 1

The asymmetric unit of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.



#### Figure 2

The packing of (I), viewed down the *b* axis. Hydrogen bonds are shown as dashed lines.

The H atoms were positioned geometrically and were treated as riding on their parent C and O atoms, with C–H distances in the range 0.93–0.96 Å and O–H distances of 0.82 Å.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SAINT-Plus* (Bruker, 1999; data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1999); software used to prepare material for publication: *SHELXTL*.

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## References

Allport, D. C. & Bu'Lock, J. D. (1960). J. Chem. Soc. pp. 654-662.

Bruker (1999). SMART (Version 5.054), SAINT-Plus (Version 6.45) and SHELXTL (Version 6.14). Bruker AXS Inc., Madison, Wisconsin, USA.

Sheldrick, G. M. (1990). Acta Cryst. A46, 467-473.

- Sheldrick, G. M. (1996). SADABS. University of Göttingen, Germany.
- Sheldrick, G. M. (1997). SHELXS97 and SHELXL97. University of Göttingen, Germany.