Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.051 wR factor = 0.155 Data-to-parameter ratio = 18.4

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

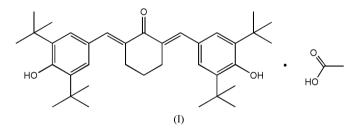
(2*E*,6*E*)-2,6-Bis(3,5-di-*tert*-butyl-4-hydroxybenzylidene)cyclohexanone acetic acid solvate

The title compound, $C_{36}H_{50}O_3 \cdot C_2H_4O_2$, crystallizes with acetic acid solvent molecules in a 1.1 stoichiometric molar ratio. The molecules are connected by intermolecular $O-H \cdots O$ hydrogen bonds, resulting in zigzag chains running along the [101] axis.

Received 6 December 2004 Accepted 23 December 2004 Online 12 February 2005

Comment

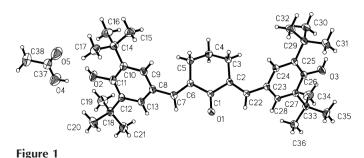
The title compound, (I) (Fig. 1), exhibits antioxidative properties (Sardjiman *et al.*, 1997). We report here its crystal structure.



The X-ray study confirms the previously proposed molecular structure based on spectroscopic data. The C–O and C–C distances show no unusual values (Table 1). In the crystal structure there are intramolecular O–H···O hydrogen bonds between the hydroxyl groups and the carboxylic O atoms of the acetic acid molecule, and O–H···O hydrogen bonds between the hydroxyl groups and the carbonyl O atom (Table 2), resulting in zigzag chains along the [101] axis (Fig. 2).

Experimental

The title compound was synthesized using a published procedure (Sardjiman *et al.*, 1997; Youssef *et al.*, 2004). Crystals were obtained by recrystallization from acetic acid and water.



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Perspective view of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.

organic papers

Crystal data

 $C_{36}H_{50}O_{3} \cdot C_{2}H_{4}O_{2}$ $M_{r} = 590.81$ Monoclinic, P_{2}/n a = 12.838 (7) Å b = 16.250 (9) Å c = 17.221 (9) Å $\beta = 102.376$ (11)° V = 3509 (3) Å³ Z = 4

Data collection

Bruker AXS SMART 1000 CCD diffractometer ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{min} = 0.968, T_{max} = 0.970$ 19669 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.051$ $wR(F^2) = 0.155$ S = 1.037661 reflections 416 parameters H atoms treated by a mixture of independent and constrained

Table 1

refinement

Selected bond lengths (Å).

O1-C1	1.2239 (19)	C4-C5	1.515 (2)
O2-C11	1.376 (2)	C5-C6	1.504 (2)
O3-C26	1.3634 (19)	C6-C7	1.337 (2)
C2-C22	1.338 (2)	C7-C8	1.464 (2)
C3-C4	1.510 (2)	C22-C23	1.464 (2)

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$03-H3C\cdotsO1^{i}$ $02-H2\cdotsO5$ $04-H4C\cdotsO2$	0.82	2.21	2.801 (2)	129
	0.71 (4)	2.25 (4)	2.832 (3)	140 (5)
	0.82	2.06	2.851 (3)	162

Symmetry code: (i) $x - \frac{1}{2}, \frac{3}{2} - y, z - \frac{1}{2}$.

Atom H2, H16A-C, and H17A-C H atoms were refined without constraints. All other H atoms were positioned geometrically and

 $D_x = 1.118 \text{ Mg m}^{-3}$ Mo K\alpha radiation Cell parameters from 970 reflections $\theta = 2.2-27.0^{\circ}$ $\mu = 0.07 \text{ mm}^{-1}$ T = 293 (2) KBlock, brown $0.50 \times 0.46 \times 0.41 \text{ mm}$

7661 independent reflections 5405 reflections with $I > 2\sigma(I)$ $R_{int} = 0.017$ $\theta_{max} = 27.1^{\circ}$ $h = -16 \rightarrow 15$ $k = -12 \rightarrow 20$ $l = -18 \rightarrow 22$

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0705P)^2 \\ &+ 1.1965P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} < 0.001 \\ \Delta\rho_{\text{max}} &= 0.44 \text{ e } \text{\AA}^{-3} \\ \Delta\rho_{\text{min}} &= -0.37 \text{ e } \text{\AA}^{-3} \end{split}$$

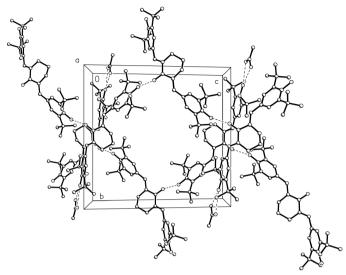


Figure 2

The molecular packing of (I), viewed along the *b* axis. All H atoms attached to C atoms have been omitted for clarity. Hydrogen bonds are shown as dashed lines.

refined as riding, with C–H = 0.93–0.98 Å, O–H = 0.82 Å and $U_{iso}(H) = 1.2$ or 1.5 times U_{eq} (parent atom).

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

The authors thank the National Natural Science Foundation of China, the Natural Science Foundation of Guangdong Province and Sun Yat-Sen University.

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