# organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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#### Key indicators

Single-crystal X-ray study T = 93 KMean  $\sigma(C-C) = 0.003 \text{ Å}$  R factor = 0.043 wR factor = 0.104 Data-to-parameter ratio = 14.1

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

# 3,5-Di-tert-butyl-2-hydroxybenzoic acid

The title compound,  $C_{15}H_{22}O_3$ , is a charge-control agent used in electrophotography. There are two independent molecules A and B in the asymmetric unit. The molecules form centrosymmetric dimers A-A and B-B via pairs of O- $H \cdots O$  hydrogen bonds between the carboxyl groups.

#### Comment

3,5-Di-tert-butyl-2-hydroxybenzoic acid (TBS), (I), is an industrially important charge-control agent (CCA) of the negative type used in electrophotography, either embedded in toners or mixed with toners (Suganami *et al.*, 2002). Furthermore, the charge-control power is greatly enhanced when TBS is combined with a variety of metals such as Zn, Al, Cr and Fe to yield metal complexes. An attempt has, therefore, been made in the present investigation to study the correlation between the structure and the charge-control effect.



There are two independent molecules A and B (Fig. 1 and Table 1). The conformation of both molecules is quite similar, and there exists an intramolecular hydrogen bond between the phenol OH group and the O atom of the carboxylic acid (Table 2). The molecules are dimerized in the crystal structure, as shown in Fig. 2, by  $O-H\cdots O$  intermolecular hydrogen bonds between the carboxyl groups. There are two types of centrosymmetric dimers, A-A and B-B, in the unit cell.



**Figure 1** Two independent molecules (left: *A*; right: *B*) of (I), showing 50% displacement ellipsoids for non-H atoms.

Received 27 August 2003 Accepted 18 September 2003 Online 24 September 2003

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Although the present hydrogen-bond formation is typical of carboxylic acids, there is a small step of *ca* 0.89 Å between the two hydrogen-bonded molecular planes for both A-A and B-B dimers (Fig. 3).

# Experimental

The title compound was obtained from the API Corporation. Single crystals were grown by slow evaporation of an ethanol solution.

Z = 4

 $D_x = 1.140 \text{ Mg m}^{-3}$ 

Cell parameters from 1379

Cu Ka radiation

reflections  $\theta = 6.9-65.2^{\circ}$ 

 $\mu = 0.63 \text{ mm}^{-1}$ 

Block, colorless

 $0.30 \times 0.10 \times 0.10$  mm

4803 independent reflections

3053 reflections with  $F^2 > 2\sigma(F^2)$ 

T = 93.2 K

 $R_{\rm int}=0.037$ 

 $\theta_{\rm max} = 68.3^{\circ}$ 

 $h = -11 \rightarrow 11$ 

 $k = -11 \rightarrow 11$ 

 $l = -21 \rightarrow 20$ 

# Crystal data

 $\begin{array}{l} C_{15}H_{22}O_3 \\ M_r = 250.34 \\ \text{Triclinic, } P\overline{1} \\ a = 9.597 \ (2) \ \text{\AA} \\ b = 9.828 \ (2) \ \text{\AA} \\ c = 17.783 \ (3) \ \text{\AA} \\ \alpha = 74.16 \ (1)^\circ \\ \beta = 78.85 \ (1)^\circ \\ \gamma = 65.11 \ (1)^\circ \\ V = 1457.9 \ (5) \ \text{\AA}^3 \end{array}$ 

#### Data collection

Rigaku R-AXIS RAPID Imaging Plate diffractometer  $\omega$  scans Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995)  $T_{min} = 0.688, T_{max} = 0.939$ 13032 measured reflections

#### Refinement

 $\begin{array}{ll} \mbox{Refinement on } F^2 & \mbox{H atoms treated by a mixture of} \\ R[F^2 > 2\sigma(F^2)] = 0.043 & \mbox{independent and constrained} \\ wR(F^2) = 0.104 & \mbox{refinement} \\ S = 0.95 & \mbox{w} = 1/[\sigma^2(F_o^2) + (0.05(\mbox{Max}(F_o^2, 0) + 2F_c^2)/3)^2] \\ 337 \mbox{ parameters} & (\Delta/\sigma)_{\rm max} = 0.050 \\ \Delta\rho_{\rm max} = 0.33 \mbox{ e } {\rm \AA}^{-3} \\ \Delta\rho_{\rm min} = -0.20 \mbox{ e } {\rm \AA}^{-3} \\ \end{array}$ 

# Table 1

Selected geometric parameters (Å, °).

O1-C7	1.243 (2)	C1-C7	1.464 (3)
O2-C7	1.324 (2)	C3-C8	1.541 (3)
O3-C2	1.353 (2)	C5-C12	1.535 (3)
O4-C22	1.248 (2)	C16-C22	1.466 (3)
O5-C22	1.325 (2)	C18-C23	1.547 (3)
O6-C17	1.364 (2)	C20-C27	1.538 (3)
01 C7 02	120.4.(2)	04 C22 05	121 2 (2)
01 - C7 - C1	120.4(2)	04 - 022 - 03	121.2(2) 122.0(2)
01 - 07 - 01	125.7 (2)	04-022-010	122.9(2)
02-07-01	115.9 (2)	05-022-016	115.9 (2)

# Table 2

Hydrogen-bonding geometry (Å, °).

-					
$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$	
O3−H3···O1	0.93 (2)	1.76 (2)	2.613 (2)	151 (2)	
O6−H7···O4	1.07 (2)	1.56 (2)	2.579 (2)	158 (2)	
$O2-H4\cdots O1^{i}$	0.97 (2)	1.69 (2)	2.659 (2)	177 (2)	
$O5-H8\cdots O4^{ii}$	0.92 (2)	1.74 (2)	2.661 (2)	179 (2)	

Symmetry codes: (i) 1 - x, -y, -z; (ii) -x, 2 - y, 1 - z.



# Figure 2

Top view of the hydrogen-bonded dimer A-A.



**Figure 3** Side view of the hydrogen-bonded dimer *A*–*A*.

The H atoms of the carboxyl and hydroxyl groups were found in difference density maps and their coordinates were refined, with  $U_{\rm iso} = 0.0541$  Å<sup>2</sup>. All other H atoms were positioned by calculation and not refined [C–H = 0.95 Å and  $U_{\rm iso} = 1.2U_{\rm eq}(C)$ ]. Reflections with  $|F_o^2 - F_c^2|/|\sigma(F_o^2)|$  greater than 5% have not been used for the refinement.

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *TEXSAN* (Molecular Structure Corporation, 2001); program(s) used to solve structure: *SHELXS86* (Sheldrick, 1985); program(s) used to refine structure: *TEXSAN*; molecular graphics: *ORTEP*III (Burnett & Johnson, 1996); software used to prepare material for publication: *TEXSAN*.

The author expresses his sincere thanks to Mr I. Suzuki for experimental assistance.

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