# organic papers

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#### Key indicators

Single-crystal X-ray study T = 296 KMean  $\sigma(C-C) = 0.003 \text{ Å}$  R factor = 0.052 wR factor = 0.136 Data-to-parameter ratio = 17.1

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

# 2,6-Bis(triphenylacetylamino)phenol

In the title compound,  $C_{46}H_{36}N_2O_3$ , very bulky triphenylmethyl groups interfere with intermolecular interactions; intramolecular hydrogen bonds  $N-H\cdots O-H\cdots O=C$ between the phenol and two amide groups are observed in the structure. Received 19 May 2003 Accepted 1 July 2003 Online 31 July 2003

## Comment

Hydrogen-bond networks, one of the non-covalent motifs, have been employed as synthetic paradigms to rationally design crystal structures. Most interesting network structures have been reported combining intermolecular N-H···O and  $O-H \cdots O$  hydrogen bonds, and other donor-acceptor pairs (Holman et al., 2001; Noveron et al., 2002; Nguyen et al., 2001; Tanaka et al., 2002; Mak & Xue, 2002). We have especially focused on N-H···O hydrogen bonds with various oxo acids as acceptors, such as carboxylic acids, phosphoric acids and sulfonic acids (Ueyama et al., 1999; Onoda et al., 2001; Onoda, Yamada, Okamura, Yamamoto & Ueyama, 2002; Onoda, Yamada, Okamura, Doi et al., 2002). Thus, we have constructed a series of bulky amides with which to examine the formation of such hydrogen bonds and have determined the properties of their intramolecular hydrogen bonds. A detailed knowledge of intramolecular hydrogen bonds will provide basic information for crystal engineering. Here, we report that we have synthesized the title compound, (I), and structurally characterized the hydrogen-bond geometry.



In (I), very bulky triphenylmethyl groups interfere with intermolecular interactions; only intramolecular hydrogen bonds between the two amide groups and a phenol OH group are observed in the structure (Fig. 1 and Table 1). One amide moiety (N1-H1) is directed towards atom O3, indicating the presence of an intramolecular N-H···O hydrogen bond. The angle between the N1-amide plane and the C11-C16 aromatic ring plane is 8.67 (5)° and the other amide group participates in O-H···O=C hydrogen bonds with a phenol OH group. Actually, the N2-amide plane is twisted from the C11-C16 plane by an angle of 36.91 (5)° in order to form a seven-membered hydrogen-bonded ring.

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#### Figure 1

The molecular structure of (I), showing the labeling of selected non-H atoms and 30% probability displacement ellipsoids.



#### Figure 2

CPK drawing of the molecular structure of (I). Key: red (O), blue (N), black (C) and white (H).

The IR spectrum of (I) in the solid state (KBr pellet) shows that the OH band appears at 3458 cm<sup>-1</sup>, shifted down from the free OH region. The NH bands are observed at around  $3390 \text{ cm}^{-1}$  as an overlapped signal. Thus, the intramolecular N-H...O hydrogen bond to the phenolic OH is very weak. The <sup>1</sup>H NMR measurement in CDCl<sub>3</sub> solution (10 mM) shows that the amide NH signal appears at 9.11 p.p.m. at 303 K. Thus, the asymmetric orientation of the two amide groups undergo fast exchange in solution.

### **Experimental**

The synthesis of (I) was reported previously (Onoda, Yamada, Okamura, Doi et al., 2002). Crystals were obtained from a hot acetonitrile solution by slow cooling.

### Crystal data

| a a                             | ► 10000 -3                        |  |  |
|---------------------------------|-----------------------------------|--|--|
| $C_{46}H_{36}N_2O_3$            | $D_x = 1.255 \text{ Mg m}^{-3}$   |  |  |
| $M_r = 664.77$                  | Mo $K\alpha$ radiation            |  |  |
| Monoclinic, $P2_1/c$            | Cell parameters from 19635        |  |  |
| a = 13.910 (4)  Å               | reflections                       |  |  |
| b = 13.425 (4) Å                | $\theta = 3.7 - 55^{\circ}$       |  |  |
| c = 19.074 (6) Å                | $\mu = 0.08 \text{ mm}^{-1}$      |  |  |
| $\beta = 99.074 \ (19)^{\circ}$ | T = 296  K                        |  |  |
| $V = 3517.3 (18) \text{ Å}^3$   | Prism, colorless                  |  |  |
| Z = 4                           | $0.10 \times 0.10 \times 0.10$ mm |  |  |

#### Data collection

| Rigaku R-AXIS RAPID Imaging<br>Plate diffractometer<br>ω scans                          | 7998 independent reflections<br>3722 reflections with $I > 2\sigma(I)$<br>$R_{int} = 0.075$                                     |
|---|---|
| Absorption correction: multi-scan<br>( <i>ABSCOR</i> ; Higashi, 1995)                   | $\theta_{\max}^{m} = 27.5^{\circ}$<br>$h = -18 \rightarrow 16$<br>h = 17  |
| $T_{\min} = 0.383$ , $T_{\max} = 0.992$<br>34 653 measured reflections                  | $k = -17 \rightarrow 17$ $l = -24 \rightarrow 24$   |
| Refinement  |   |
| Refinement on $F^2$<br>$R[F^2 > 2\sigma(F^2)] = 0.053$<br>$wR(F^2) = 0.136$<br>S = 0.86 | H atoms treated by a mixture of<br>independent and constrained<br>refinement<br>$w = 1/[\sigma^2(F_o^2) + (0.0697P)^2]$         |
| 7998 reflections<br>469 parameters  | where $P = (F_o^2 + 2F_c^2)/3$<br>$(\Delta/\sigma)_{\text{max}} = 0.001$<br>$\Delta \phi_{\text{max}} = 0.16 \text{ e}        $ |

#### Table 1 Hydrogen-bonding geometry (Å, °).

| $D - H \cdots A$ | D-H      | $H \cdots A$ | $D \cdots A$ | $D - \mathbf{H} \cdots A$ |
|------------------|----------|--------------|--------------|---------------------------|
| N1-H1···O3       | 0.87 (2) | 2.16 (2)     | 2.607 (2)    | 112 (2)                   |
| O3-H3···O2       | 0.86 (2) | 1.78 (2)     | 2.604 (2)    | 159 (2)                   |

 $\Delta \rho_{\rm min} = -0.23 \text{ e } \text{\AA}^{-3}$ 

The positional parameters of H atoms bonded to N and O atoms were refined. The N-H and O-H bond lengths are 0.86(2)-0.87(2)and 0.86 (2) Å, respectively. The H atoms bonded to C atoms were positioned geometrically and were treated as riding on their parent atoms, with C-H bond distances of 0.93 Å.

Data collection: MSC/AFC Diffractometer Control Software (Molecular Structure Corporation, 1991); cell refinement: MSC/AFC Diffractometer Control Software; data reduction: TEXSAN (Molecular Structure Corporation, 1999); program(s) used to solve structure: SIR92 (Altomare et al., 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: TEXSAN and MERCURY (Bruno et al., 2002); software used to prepare material for publication: TEXSAN and MERCURY.

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