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Yuping Guo,^a Bing Zhao,^b Chun-Bao Li,^a Wei-Min Gao,^c Jie Li^a and Yang Li^b*

^aDepartment of Chemistry, Tianjin University, Tianjin 300072, People's Republic of China, ^bSchool of Chemical Engineering and Technology, Tianjin University, Tianjin 300072, People's Republic of China, and ^cMaterial Research Institute, Jiangxi Science and Technology Normal University, Nanchang 330013, People's Republic of China

Correspondence e-mail: yupguo@sohu.com

Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.036 wR factor = 0.101 Data-to-parameter ratio = 13.9

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the title compound, $C_{22}H_{19}NO$, the Csp^2 atom of the benzimido group reveals a distorted trigonal geometry, which results in the approximately overall trigonal shape of the molecule.

N-Phenylbenzimidic acid 2-allylphenyl ester

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Comment

N-Phenylbenzimidic acid esters belong to an important class of intermediates in the Chapman rearrangement (Relles, 1968). A large number of substituted *N*-phenylbenzimidic acid ester analogues have been synthesized and investigated (Rowe, 1980). The title compound, (I), has been prepared by our group from the substrate of *N*-phenylbenzimidoyll chloride. The X-ray crystal structure determination of (I) was carried out and the results are presented here.



The molecular structure of (I) and the atom-numbering scheme are shown in Fig. 1. The C17-N1-C10-C11 torsion angle of 9.3 (3)° indicates that the two phenyl rings attached to atoms C10 (ring A) and N1 (ring B) are in a *cis*-configuration. The dihedral angle between these rings is 63.7°(4). Rings A and B make dihedral angles of 55.6 (3) and 78.6 (4)°, respectively, with ring C (attached to oxygen); rings B and C are thus close to be orthogonal. Atom C10 has a distorted trigonal geometry [N1-C10-C11 = 130.27 (13)°]. The conjugation of bonds involved explains the distortion from regular sp^2 hybridization.

Experimental

N-Phenylbenzimidoyl chloride (0.28 g,1.3 mmol) in dichloromethane (10 ml) was added to a rapidly stirred solution of 2-allylphenol (0.19 g, 1.4 mmol), sodium hydroxide (0.055 g, 1.4 mmol) and tetrabutylammonium bromide (0.010 g, 0.03 mmol) in water (10 ml). The mixture was stirred at room temperature for 3 h. The mixture was diluted with chloroform (20 ml), the organic layer separated, dried with anhydrous sodium sulfate, and evaporated to give the crude product which was recrystallized from ethanol; m.p. 323 K. IR (KBr, $\nu \text{ cm}^{-1}$): 1666, 1637, 1593, 1485, 1444, 1089; ¹H NMR (CDCl₃, δ , p.p.m.): 7.4–6.9 (*m*, 14H), 6.0 (*m*, 1H), 5.1 (*d*, 2H), 3.5 (*d*, 2H).

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organic papers

Crystal data

 $\begin{array}{l} C_{22}H_{19}NO\\ M_r = 313.38\\ Triclinic, \ \ P\overline{1}\\ a = 9.6168\ (13)\ \ \mathring{A}\\ b = 9.7218\ (13)\ \ \mathring{A}\\ c = 10.7494\ (15)\ \ \mathring{A}\\ \alpha = 64.237\ (2)^\circ\\ \beta = 71.310\ (2)^\circ\\ \gamma = 80.941\ (2)^\circ\\ V = 857.2\ (2)\ \ \mathring{A}^3 \end{array}$

Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: none 4715 measured reflections 3026 independent reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0501P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.036$	+ 0.0427P]
$wR(F^2) = 0.101$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.05	$(\Delta/\sigma)_{\rm max} < 0.001$
3026 reflections	$\Delta \rho_{\rm max} = 0.24 \text{ e } \text{\AA}^{-3}$
217 parameters	$\Delta \rho_{\rm min} = -0.16 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Z = 2

 $D_x = 1.214 \text{ Mg m}^{-3}$

Cell parameters from 1319

Mo K α radiation

reflections

 $\begin{array}{l} \theta = 2.3 {-} 22.7^{\circ} \\ \mu = 0.07 \ \mathrm{mm}^{-1} \end{array}$

T = 293 (2) K

 $R_{\rm int} = 0.014$

 $\begin{array}{l} \theta_{\rm max} = 25.0^\circ \\ h = -11 \rightarrow 11 \end{array}$

 $k = -11 \rightarrow 11$

 $l = -12 \rightarrow 12$

Block, colourless

 $0.24 \times 0.22 \times 0.20 \text{ mm}$

2055 reflections with $I > 2\sigma(I)$

Table 1

Selected geometric parameters (Å, °).

N1-C10	1.2567 (17)	O1-C10	1.3685 (16)
N1-C17	1.4110 (18)	O1-C1	1.4101 (16)
C10-N1-C17	122.90 (12)	N1-C10-C11	130.27 (13)
C10-O1-C1	116.93 (10)	O1-C10-C11	110.12 (12)

H atoms were placed in calculated positions (C-H = 0.93–0.97 Å) and allowed to ride on their parent atoms, with $U_{iso}(H) = 1.2U_{eq}(\text{parent atom})$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics:



Figure 1

View of the molecule of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.

SHELXTL (Bruker, 1997); software used to prepare material for publication: SHELXTL.

References

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