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Key indicators

Single-crystal X-ray study T = 296 KMean σ (C–C) = 0.003 Å R factor = 0.028 wR factor = 0.086 Data-to-parameter ratio = 8.2

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

2-(Dibenzoylamino)pyridine

The title compound, $C_{19}H_{14}N_2O_2$, is a highly effective nematicide. No inter- or intramolecular hydrogen bonds are observed in the crystal structure.

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Comment

The title compound, (I), was synthesized and tested *in vitro* and *in vivo* on *Meloidogyne incognita* at 10 mg ml⁻¹ concentration. The compound reduced nematode infestation of cowpea plants significantly and improved their growth. Treatment by soil drench was more effective than by foliar spray (Roy *et al.*, 1993). In the present paper, we report the crystal structure of (I).



The title compound crystallizes in the orthorhombic space group $P2_12_12_1$, with one molecule in the asymmetric unit (Fig. 1). The N1-C15-C16-C17 torsion angle is 179.63 (17)° and the N1-C8-C9-C10 torsion angle is 149.54 (17)°. The O1-C7-N1-C8 torsion angle is -18.6 (2)° and the O2-C8-N1-C7 torsion angle is 138.92 (17)°. No inter- or intramolecular hydrogen bonds are observed.

Experimental

Compound (I) was prepared from 2-aminopyridine (2.45 g) and benzoyl chloride (2 ml) in tetrahydrofuran (50 ml) solution at 313 K by stirring for 12 h. The melting point is 441.2 K (Protiva *et al.*, 1950). Colourless block-shaped single crystals suitable for X-ray diffraction were obtained by slow evaporation of an acetone solution at room temperature.

Crystal data

 $\begin{array}{l} C_{19}H_{14}N_2O_2\\ M_r = 302.32\\ Orthorhombic, \ P2_12_12_1\\ a = 9.0343\ (18)\ \text{\AA}\\ b = 9.2051\ (18)\ \text{\AA}\\ c = 19.152\ (4)\ \text{\AA}\\ V = 1592.7\ (5)\ \text{\AA}^3 \end{array}$

Z = 4 $D_x = 1.261 \text{ Mg m}^{-3}$ Mo K α radiation $\mu = 0.08 \text{ mm}^{-1}$ T = 296 (2) K Block, colourless $0.42 \times 0.41 \times 0.21 \text{ mm}$

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Data collection

Rigaku R-AXIS RAPID IP areadetector diffractometer φ or ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.966, T_{\max} = 0.982$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.028$ $wR(F^2) = 0.086$ S = 1.161708 reflections 209 parameters H-atom parameters constrained 13101 measured reflections 1708 independent reflections 1580 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.028$ $\theta_{\text{max}} = 25.5^{\circ}$

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0583P)^2 \\ &+ 0.0123P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} < 0.001 \\ \Delta\rho_{\text{max}} &= 0.10 \text{ e } \text{\AA}^{-3} \\ \Delta\rho_{\text{min}} &= -0.11 \text{ e } \text{\AA}^{-3} \\ \text{Extinction correction: SHELXL97} \\ \text{Extinction coefficient: } 0.016 (3) \end{split}$$

H atoms were placed in calculated positions and constrained to ride on their parent atoms with distances C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$. In the absence of significant anomalous scattering effects, Friedel pairs were averaged.

Data collection: *RAPID-AUTO* (Rigaku, 2004); cell refinement: *RAPID-AUTO*; data reduction: *RAPID-AUTO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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Figure 1

A view of the molecular structure of (I). Displacement ellipsoids for non-H atoms are drawn at the 30% probability level.

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