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## Mustafa Odabaşoğlu<sup>a</sup>\* and Orhan Büyükgüngör<sup>b</sup>

<sup>a</sup>Department of Chemistry, Faculty of Arts & Science, Ondokuz Mayıs University, TR-55139 Kurupelit Samsun, Turkey, and <sup>b</sup>Department of Physics, Faculty of Arts & Science, Ondokuz Mayıs University, TR-55139 Kurupelit Samsun, Turkey

Correspondence e-mail: muodabas@omu.edu.tr

#### **Key indicators**

Single-crystal X-ray study T = 296 KMean  $\sigma(C-C) = 0.005 \text{ Å}$  R factor = 0.062 wR factor = 0.132 Data-to-parameter ratio = 12.6

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

# 3-(2-Pyridylamino)isobenzofuran-1(3H)-one

The crystal structure of the title compound,  $C_{13}H_{10}O_2N_2$ , is stabilized by N-H···N intermolecular hydrogen bonds which generate C(4) chains. The phthalide system is planar and the dihedral angle between this plane and that of the pyridine ring is 73.55 (13)°.

## Comment

In a previous paper, we reported the synthesis and crystal structure of 3-(3-pyridylamino)isobenzofuran-1(3*H*)-one (Odabaşoğlu & Büyükgüngör, 2006*b*). In the present paper, we report the structure of 3-(2-pyridylamino)isobenzofuran-1(3*H*)-one [or 3-(2-pyridylamino)phthalide], (I) (Fig. 1).



The crystal packing is stabilized by  $N-H\cdots N$  intermolecular hydrogen bonds (Table 2), forming C(4) chains (Etter, 1990) running parallel to the *a* axis (Fig. 2). The phthalide system (C1–C8/O2) of the molecule is essentially planar, the largest deviation from the mean plane being 0.020 (3) Å for atom C8. The dihedral angle between the mean planes of the phthalide unit and the pyridine ring is 73.55 (13)°.

## **Experimental**

The title compound was prepared as described by Kubota & Tatsuno (1971) and Odabaşoğlu & Büyükgüngör (2006*a*) using phthalalde-



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A view of (I) with the atomic numbering scheme. Displacement ellipsoids are drawn at the 40% probability level.

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3-Substituted phthalides. Part VI

hydic acid and 2-aminopyridine as starting materials (yield 95%; m.p. 479–480 K). Crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of an ethanol (95%) solution at room temperature.

Z = 8

 $D_x = 1.333 \text{ Mg m}^{-3}$ 

Mo  $K\alpha$  radiation  $\mu = 0.09 \text{ mm}^{-1}$ 

Plate, colorless

 $0.78 \times 0.31 \times 0.04 \text{ mm}$ 

23991 measured reflections 1991 independent reflections

 $w = 1/[\sigma^2(F_o^2) + (0.0522P)^2 + 0.1489P]$ 

 $(\Delta/\sigma)_{\rm max} < 0.001$ 

 $\Delta \rho_{\rm max} = 0.16 \text{ e} \text{ Å}^{-3}$ 

 $\Delta \rho_{\rm min} = -0.18 \ {\rm e} \ {\rm \AA}^{-3}$ 

where  $P = (F_0^2 + 2F_c^2)/3$ 

1173 reflections with  $I > 2\sigma(I)$ 

T = 296 K

 $\begin{aligned} R_{\rm int} &= 0.154 \\ \theta_{\rm max} &= 25.0^\circ \end{aligned}$ 

#### Crystal data

 $\begin{array}{l} C_{13}H_{10}N_2O_2\\ M_r = 226.23\\ Orthorhombic, Pbca\\ a = 8.6366 ~(5) ~Å\\ b = 18.1462 ~(12) ~Å\\ c = 14.3885 ~(11) ~Å\\ V = 2255.0 ~(3) ~Å^3 \end{array}$ 

#### Data collection

Stoe IPDS-2 diffractometer  $\omega$  scans Absorption correction: integration (X-RED32; Stoe & Cie, 2002)  $T_{\min} = 0.961, T_{\max} = 0.996$ 

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.062$   $wR(F^2) = 0.132$  S = 1.041991 reflections 158 parameters H atoms treated by a mixture of independent and constrained refinement

#### Table 1

Selected geometric parameters (Å, °).

C1-01	1.211 (4)	C7-C8	1.503 (4
C1-O2	1.363 (4)	C8-N1	1.419 (4
C2-C7	1.370 (4)		
O1-C1-O2	120.9 (3)	N1-C8-O2	111.3 (2
O1-C1-C2	130.3 (4)		

#### Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N1 - H1 \cdots N2^i$	0.89 (4)	2.12 (4)	2.981 (4)	161 (3)
Symmetry code: (i)	$x - \frac{1}{2}, y, -z + \frac{1}{2}.$			

There did not appear to be any problem with the crystal quality in terms of the physical appearance and diffraction spots. However, the compound crystallized as very thin plate-shaped crystals and so, although the exposure time was set to a high value (5 min), the value of  $R_{\rm int}$ , 0.154, is due to the weakness of the diffraction. All C-bound H atoms were refined using the riding-model approximation, with C–



#### Figure 2

A partial packing diagram of (I), showing the hydrogen bonds as dashed lines.

H = 0.93 Å for aromatic and C–H = 0.98 Å for methine H atoms  $[U_{iso}(H) = 1.2U_{eq}(C)]$ . The N-bound H atom was located in a Fourier difference map and was allowed to refine freely.

Data collection: X-AREA (Stoe & Cie, 2002); cell refinement: X-AREA; data reduction: X-RED32 (Stoe & Cie, 2002); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

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