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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.002 Å R factor = 0.040 wR factor = 0.111 Data-to-parameter ratio = 16.0

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The title compound, $C_{13}H_{11}N_3O_2$, was prepared by the reaction of pyridine-4-carboxylic acid hydrazide and *p*-hydroxybenzaldehyde in ethanol. In the crystal structure, all non-H atoms are coplanar, with an r.m.s. deviation of 0.096 Å. N-H···N, O-H···N and O-H···O intermolecular hydrogen bonds stabilize the structure.

N'-(4-Hydroxybenzylidene)isonicotinohydrazide

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Comment

The synthesis and structure of Schiff bases have attracted much attention because of their pharmacological activity (Parashar *et al.*, 1988) and photochromic properties (Hadjoudis *et al.*, 1987). We report here the synthesis and crystal structure of the title compound, (I).



The C7–C8, C7=N3 and N2–N3 bond lengths are 1.452 (2), 1.273 (2) and 1.382 (2) Å, respectively; these values are in good agreement with those in a similar system (Jing *et al.*, 2005). All the non-H atoms are coplanar, with an r.m.s. deviation of 0.096 Å.

Intermolecular $N-H\cdots N$, $O-H\cdots N$ and $O-H\cdots O$ hydrogen bonds are found in the crystal structure (Table 1 and Fig. 2). These stabilize the structure, forming a supramolecular network pattern.

Experimental

An anhydrous ethanol solution (50 ml) of pyridine-4-carboxylic acid hydrazide (1.37 g, 10 mmol) was added to an anhydrous ethanol solution (50 ml) of *p*-hydroxybenzaldehyde (1.22 g, 10 mmol), and the mixture was stirred at 343 K for 5 h under nitrogen, producing a yellow precipitate. The product was isolated, recrystallized from ethanol, and then dried *in vacuo* to give the pure compound in 82% yield. Bright-yellow single crystals suitable for X-ray analysis were obtained by slow evaporation of an ethanol solution.

Crystal data	
$C_{13}H_{11}N_3O_2$	$D_x = 1.404 \text{ Mg m}^{-3}$
$M_r = 241.25$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 1357
a = 8.4553 (14) Å	reflections
b = 10.1812 (16) Å	$\theta = 2.4-24.5^{\circ}$
c = 13.408 (2) Å	$\mu = 0.10 \text{ mm}^{-1}$
$\beta = 98.646 \ (2)^{\circ}$	T = 294 (2) K
V = 1141.1 (3) Å ³	Plate, yellow
Z = 4	$0.32 \times 0.26 \times 0.10 \text{ mm}$

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organic papers

Data collection

Bruker SMART 1000 CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 1999) $T_{min} = 0.950, T_{max} = 0.990$ 7461 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.040$ $wR(F^2) = 0.111$ S = 1.082731 reflections 171 parameters H atoms treated by a mixture of independent and constrained 2731 independent reflections 1779 reflections with $I > 2\sigma(I)$ $R_{int} = 0.023$ $\theta_{max} = 28.0^{\circ}$ $h = -7 \rightarrow 11$ $k = -13 \rightarrow 13$ $l = -17 \rightarrow 17$

$$\begin{split} w &= 1/[\sigma^2(F_{\rm o}^2) + (0.0515P)^2 \\ &+ 0.0289P] \\ \text{where } P &= (F_{\rm o}^2 + 2F_{\rm c}^2)/3 \\ (\Delta/\sigma)_{\rm max} < 0.001 \\ \Delta\rho_{\rm max} = 0.14 \text{ e } \text{ Å}^{-3} \\ \Delta\rho_{\rm min} &= -0.18 \text{ e } \text{ Å}^{-3} \end{split}$$

independent and constrained refinement

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\begin{array}{c} N2 - H2B \cdots N1^{i} \\ O2 - H2 \cdots N3^{ii} \\ O2 - H2 \cdots O1^{ii} \end{array}$	0.87 (2) 0.90 (2) 0.90 (2)	2.40 (2) 2.46 (2) 2.00 (2)	3.2350 (17) 3.1177 (15) 2.8340 (14)	160 (2) 130 (2) 155 (2)

Symmetry codes: (i) $-x, y + \frac{1}{2}, -z + \frac{1}{2}$; (ii) $-x + 1, y + \frac{1}{2}, -z + \frac{3}{2}$.

C-bound H atoms were positioned geometrically and refined using the riding-model approximation, with C-H = 0.93 Å and $U_{\rm iso}({\rm H})$ = $1.2U_{\rm eq}$ (carrier atom). H atoms attached to N and O atoms were located in a difference Fourier map and refined freely.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*.

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Figure 1

A view of the title compound, shown with 30% probability displacement ellipsoids.





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