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hailiang_zhu@163.com**Key indicators**Single-crystal X-ray study
 $T = 298$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
Disorder in main residue
 R factor = 0.049
 wR factor = 0.125
Data-to-parameter ratio = 13.0For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.**2-Nitrobenzaldehyde salicylhydrazone**The molecule of the title compound, 2-nitrobenzaldehyde (2-hydroxybenzoyl)hydrazone, $\text{C}_{14}\text{H}_{11}\text{N}_3\text{O}_4$, is roughly planar and displays a *trans* configuration with respect to the $\text{C}=\text{N}$ double bond. The crystal structure is stabilized by intermolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds.

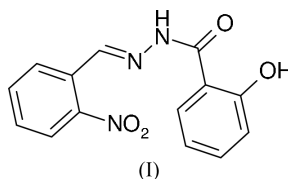
Received 5 October 2004

Accepted 27 October 2004

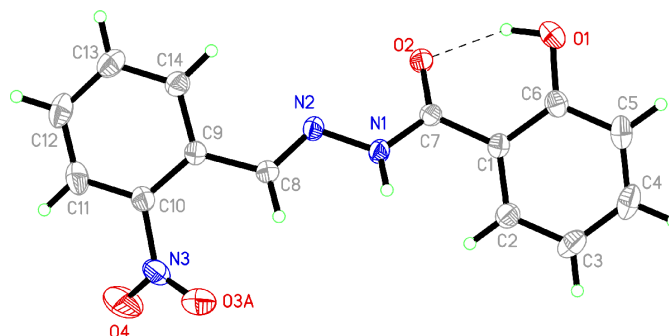
Online 6 November 2004

Comment

Schiff base compounds have been of great interest for many years. These compounds play an important role in the development of coordination chemistry related to catalysis and enzymatic reactions, magnetism and molecular architectures. As an extension of work on the structural characterization of Schiff base compounds, the crystal structure of the title compound, (I), is reported here.

In the title compound, (I), all the bond lengths are within normal ranges (Allen *et al.*, 1987) (Fig. 1). The $\text{C8}=\text{N2}$ bond length of 1.261 (2) Å conforms to the value for a double bond. The dihedral angle between the two benzene rings is 1.8 (1)°.The crystal structure is stabilized by intermolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds (Table 1 and Fig. 2).**Experimental**

2-Nitrobenzaldehyde (0.2 mmol, 30.2 mg) and 2-hydroxybenzoic acid hydrazine (0.2 mmol, 30.4 mg) were dissolved in methanol (10 ml).

**Figure 1**

The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. Dashed lines indicate intramolecular hydrogen bonds. Only the major component of the disordered O atom of the nitryl group is shown.

The mixture was stirred at room temperature for 10 min to give a clear yellow solution. After keeping the solution in air for 8 d, yellow block-shaped crystals were formed at the bottom of the vessel on slow evaporation of the solvent.

Crystal data

$C_{14}H_{11}N_3O_4$ $D_x = 1.473 \text{ Mg m}^{-3}$
 $M_r = 285.26$ Mo $K\alpha$ radiation
 Monoclinic, $P2_1/n$ Cell parameters from 1426 reflections
 $a = 7.070 (3) \text{ \AA}$ $\theta = 3.1\text{--}23.2^\circ$
 $b = 25.214 (9) \text{ \AA}$ $\mu = 0.11 \text{ mm}^{-1}$
 $c = 7.870 (3) \text{ \AA}$ $T = 298 (2) \text{ K}$
 $\beta = 113.541 (5)^\circ$ Block, yellow
 $V = 1286.2 (9) \text{ \AA}^3$
 $Z = 4$ $0.32 \times 0.27 \times 0.22 \text{ mm}$

Data collection

Bruker SMART CCD area-detector 2657 independent reflections
 diffractometer 1826 reflections with $I > 2\sigma(I)$
 ω scans $R_{int} = 0.033$
 Absorption correction: multi-scan $\theta_{max} = 26.5^\circ$
 (SADABS; Sheldrick, 1996) $h = -8 \rightarrow 7$
 $T_{min} = 0.965$, $T_{max} = 0.976$ $k = -31 \rightarrow 31$
 7466 measured reflections $l = -9 \rightarrow 9$

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.0562P)^2 + 0.1087P]$
 $R[F^2 > 2\sigma(F^2)] = 0.049$ where $P = (F_o^2 + 2F_c^2)/3$
 $wR(F^2) = 0.125$ $(\Delta/\sigma)_{max} < 0.001$
 $S = 1.02$ $\Delta\rho_{max} = 0.19 \text{ e \AA}^{-3}$
 2657 reflections $\Delta\rho_{min} = -0.21 \text{ e \AA}^{-3}$
 205 parameters
 H atoms treated by a mixture of independent and constrained refinement

Table 1

Hydrogen-bonding geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O1-H1A\cdots O2$	0.92 (2)	1.83 (2)	2.6817 (19)	153 (2)
$N1-H1\cdots O2^i$	0.89 (2)	2.11 (2)	2.978 (2)	164 (2)

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

Atoms H1 and H1A were located in a difference Fourier map and refined isotropically, with $U_{iso}(H)$ values fixed at 0.08 \AA^2 . All other H atoms were placed in idealized positions and allowed to ride on their parent atoms, with $C-H = 0.93 \text{ \AA}$ and $U_{iso}(H) = 1.2U_{eq}(C)$. The occupancies of the disordered positions O3A/O3B were fixed at 80/20% after refinement gave values close to these.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve

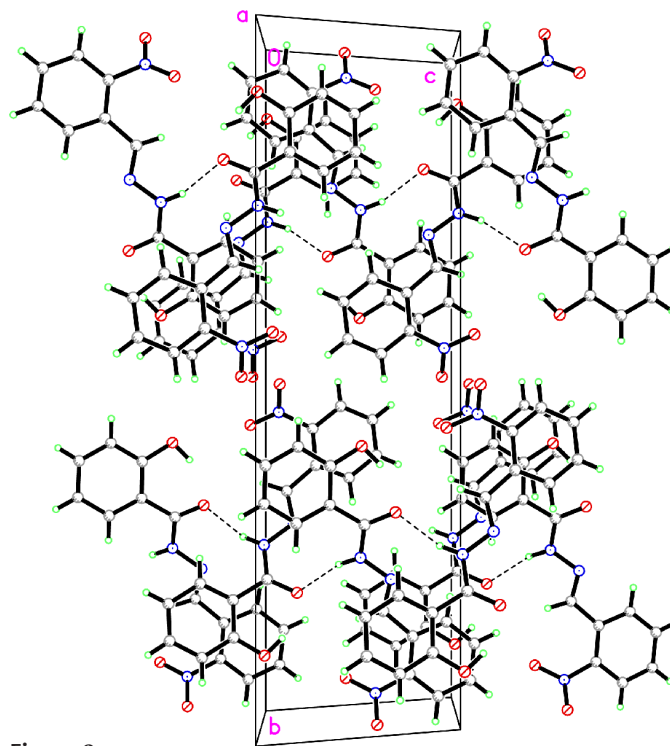


Figure 2 The crystal packing of (I), viewed along the a axis. Dashed lines show intermolecular hydrogen bonds.

structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

The authors thank the Education Office of Anhui Province, Peoples Republic of China, for research grant No. 2004kj300zd.

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