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Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.040
 wR factor = 0.131
Data-to-parameter ratio = 14.1For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.5-Nitrosalicylaldehyde (2-hydroxybenzoyl)-
hydrazone

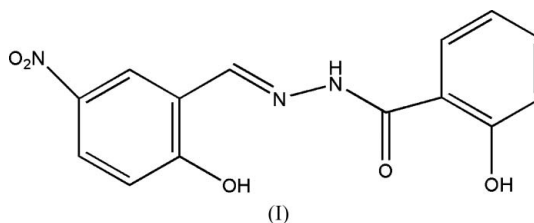
The molecule of the title compound, $\text{C}_{14}\text{H}_{11}\text{N}_3\text{O}_5$, is approximately planar, the dihedral angles between the two aromatic rings being $4.63(7)^\circ$. $\text{O}-\text{H}\cdots\text{N}$, $\text{N}-\text{H}\cdots\text{O}$ and $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds and $\pi-\pi$ stacking interactions help to consolidate the crystal packing.

Received 14 June 2006

Accepted 18 June 2006

Comment

Considerable attention has been paid to the chemistry of aroylhydrazones and their complexes (Bu *et al.*, 2001; Liao *et al.*, 2000; Tai *et al.*, 2003; Xue *et al.*, 2006). These compounds may serve as potential chelating agents (Fun *et al.*, 1996; Lu *et al.*, 1996) and possess biological activity (Liao *et al.*, 2000, Yang & Pan, 2004). Here we report the synthesis and crystal structure of the title compound, (I) (Fig. 1), obtained by the condensation of 5-nitrosalicylaldehyde and salicylhydrazide.



The molecule of (I) is approximately planar, the dihedral angles between the aromatic ring *A* (atoms C1–C6) and aromatic ring *B* (C9–C14) and between ring *A* and the nitro group being $4.63(7)$ and $7.6(2)^\circ$, respectively. The torsion angle C1–C2–C7–N1 is $-3.2(2)^\circ$.

As illustrated in Figs. 2 and 3, there are weak $\pi-\pi$ interactions between neighboring hydrazone molecules along the *a* axis. The distance between the aromatic ring *A* of one molecule and the neighboring aromatic ring *B* of a molecule related by the symmetry operation $(1-x, -y, -z)$ is 3.97 Å, and the dihedral angle between the two rings is $4.63(7)^\circ$. A similar stacking phenomenon was observed in 3-hydroxy-salicylaldehyde 2-furoylhydrazone (Ali *et al.*, 2005).

Various hydrogen bonds occur in (I) (Table 1), including two intramolecular interactions. These H atoms are also involved in intermolecular hydrogen bonds to O-atom acceptors. The amino (N2) H atom makes an intermolecular hydrogen bond to the O4 atom of the nitro group of an adjacent molecule.

Experimental

An equimolar mixture of salicylhydrazide (15 mmol) and 5-nitrosalicylaldehyde (15 mmol) in ethanol (30 ml) was refluxed in a round-

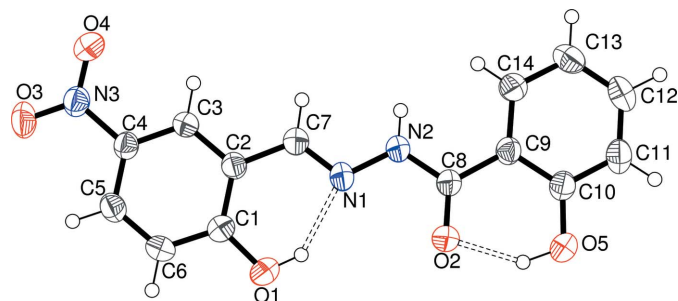


Figure 1
The molecular structure of (I), showing 50% probability displacement ellipsoids (arbitrary spheres for the H atoms). Hydrogen bonds are indicated by dashed lines.

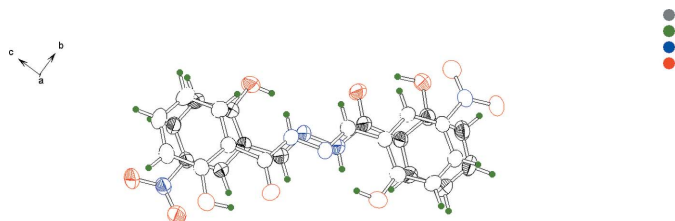


Figure 2
A plot illustrating the π - π stacking of molecules of (I). The molecule containing the unshaded atoms is generated by the symmetry operation $(1 - x, -y, -z)$.

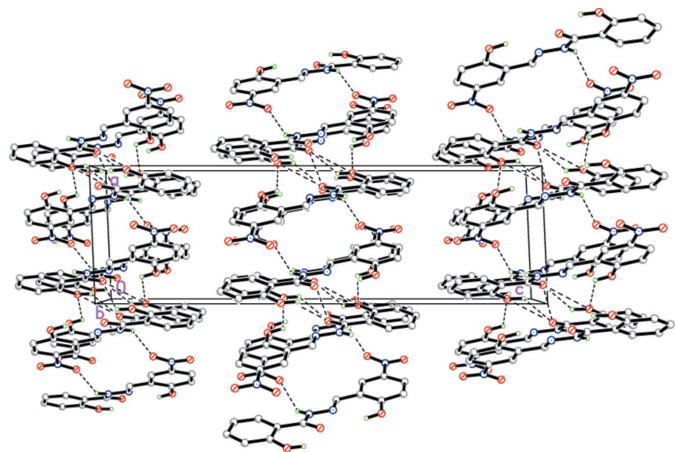


Figure 3
Packing of (I), showing the intermolecular hydrogen bonds as dashed lines. H atoms not involved in hydrogen bonding have been omitted.

bottomed flask for 3 h. The solution was then filtered to remove some undissolved solids. Colourless crystals of (I) were obtained in the filtrate after 6 days of evaporation at room temperature. Analysis calculated for $C_{14}H_{11}N_3O_5$: C 55.82, H 3.68, N 13.95, O 26.55%; found: C 55.66, H 3.72, N 14.26, O 25.98%.

Crystal data

$C_{14}H_{11}N_3O_5$
 $M_r = 301.26$
Monoclinic, $P2_1/c$
 $a = 7.645$ (3) Å
 $b = 6.751$ (3) Å
 $c = 24.994$ (11) Å
 $\beta = 92.473$ (9)°
 $V = 1288.6$ (9) Å³

$Z = 4$
 $D_x = 1.553$ Mg m⁻³
Mo $K\alpha$ radiation
 $\mu = 0.12$ mm⁻¹
 $T = 293$ (2) K
Chip, colorless
 $0.40 \times 0.15 \times 0.10$ mm

Data collection

Rigaku Weissenberg IP
diffractometer
 ω scans
Absorption correction: ψ scan
(*TEXRAY*; Molecular Structure
Corporation, 1999)
 $T_{\min} = 0.978$, $T_{\max} = 0.988$

11290 measured reflections
2939 independent reflections
2101 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.029$
 $\theta_{\max} = 27.5^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.040$
 $wR(F^2) = 0.131$
 $S = 1.04$
2939 reflections
209 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0809P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.25$ e Å⁻³
 $\Delta\rho_{\min} = -0.21$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N2—H2B...O4 ⁱ	0.86	2.34	3.070 (2)	143
O1—H1B...N1	0.89	1.94	2.686 (2)	140
O1—H1B...O5 ⁱⁱ	0.89	2.55	2.9822 (18)	111
O5—H5B...O2	0.95	1.79	2.5960 (17)	141
O5—H5B...O2 ⁱⁱ	0.95	2.21	2.873 (2)	126

Symmetry codes: (i) $-x + 1, -y + 2, -z$; (ii) $-x, -y, -z$.

The N- and O-bound H atoms were located in a difference map and then refined as riding in their as-found relative positions. The other H atoms were placed in idealized positions ($C-H = 0.93$ Å) and refined as riding. A U_{iso} value was freely refined for all H atoms.

Data collection: *TEXRAY* (Molecular Structure Corporation, 1999); cell refinement: *TEXRAY*; data reduction: *TEXSAN* (Molecular Structure Corporation, 1999); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEX* (McArdle, 1995); software used to prepare material for publication: *SHELXL97*.

We are grateful for financial support from the National Natural Science Foundation of China (Nos. 20431010 and 20171012).

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