

**(E)-1-(4-Methoxy-3-propoxybenzylidene)-
2-(4-nitrophenyl)hydrazine****Jun Shi**†Department of Basic Course, Tianjin Agricultural
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Key indicatorsSingle-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.006$ Å
 R factor = 0.053
 wR factor = 0.176
Data-to-parameter ratio = 13.5For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

The molecule of the title compound, $\text{C}_{17}\text{H}_{19}\text{N}_3\text{O}_4$, is not planar. The isovanillin group makes a dihedral angle of 3.23 (14)° with the phenylhydrazine residue. The nitro group and its attached aromatic ring are not coplanar, the dihedral angle between them being 3.18 (6)°. Intermolecular $\text{N}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds link adjacent molecules, forming infinite chains.

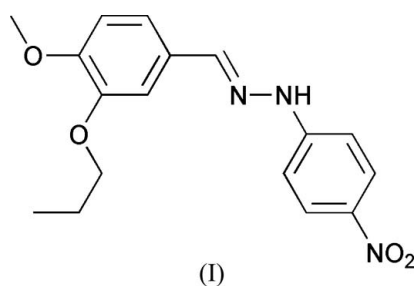
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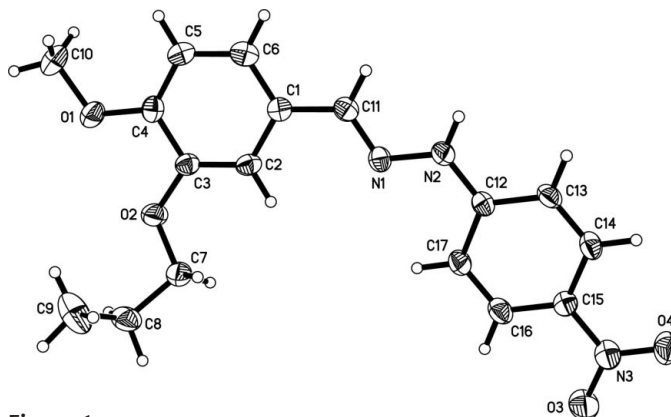
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Comment

Metal complexes based on Schiff bases have attracted much attention in biology and chemistry (Kahwa *et al.*, 1986). Consequently, numerous derivatives of Schiff bases have been developed for applications such as protein and enzyme mimics (Santos *et al.*, 2001). Structural investigations provide useful information on the coordination properties of Schiff bases functioning as ligands. In the present study, we report the synthesis and molecular structure of a nitrophenylhydrazine Schiff base derivative, (I) (Fig. 1 and Table 1).



In (I), the isovanillin group (C1–C6/C10/C11/O1/O2) is planar, with an r.m.s. deviation for the fitted atoms of 0.0230 Å. The phenylhydrazine residue (C12–C17/N1/N2) is

**Figure 1**

The structure of (I), with displacement ellipsoids for non-H atoms drawn at the 30% probability level.

also planar, the r.m.s. deviation being 0.0129 Å; the dihedral angle between these two planes is 3.23 (14)°. The nitro group (O3/N3/O4) and its attached aromatic ring are not coplanar, the dihedral angle being 3.18 (6)°. All bond lengths and angles (Table 1) are within normal ranges (Allen *et al.*, 1987). The packing is stabilized by intermolecular N2—H2···O3 hydrogen bonds, which form infinite chains along the *b* axis, together with weak non-classical intermolecular C13—H13···O3 hydrogen bonds (Fig. 2 and Table 2).

Experimental

An anhydrous ethanol solution of 4-methoxy-3-propoxybenzaldehyde (1.94 g, 10 mmol) was added to an anhydrous ethanol solution of 1-(4-nitrophenyl)hydrazine (1.53 g, 10 mmol), and the mixture stirred at 350 K for 5 h under nitrogen. A red product precipitated and this was isolated, recrystallized from ethanol and dried in a vacuum to give the pure compound in 85% yield. Red single crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of an acetonitrile solution.

Crystal data

C₁₇H₁₉N₃O₄
M_r = 329.35
 Monoclinic, *P*2₁/*n*
a = 4.5854 (13) Å
b = 14.953 (4) Å
c = 24.363 (7) Å
 β = 92.475 (5)°
V = 1668.9 (8) Å³
Z = 4

D_x = 1.311 Mg m⁻³
 Mo Kα radiation
 Cell parameters from 1175 reflections
 θ = 2.9–23.1°
 μ = 0.10 mm⁻¹
T = 294 (2) K
 Block, red
 0.20 × 0.16 × 0.12 mm

Data collection

Bruker SMART APEX CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.967, *T_{max}* = 0.989
 8289 measured reflections

2949 independent reflections
 1219 reflections with *I* > 2σ(*I*)
R_{int} = 0.090
 θ_{max} = 25.0°
h = -4 → 5
k = -14 → 17
l = -28 → 28

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.053
wR (*F*²) = 0.176
S = 0.99
 2949 reflections
 219 parameters

H-atom parameters constrained
w = 1/[σ²(*F_o*²) + (0.0744*P*)²]
 where *P* = (*F_o*² + 2*F_c*²)/3
 (Δ/σ)_{max} < 0.001
 Δρ_{max} = 0.18 e Å⁻³
 Δρ_{min} = -0.20 e Å⁻³

Table 1

Selected geometric parameters (Å, °).

O1—C4	1.361 (4)	O4—N3	1.219 (4)
O1—C10	1.422 (4)	N1—C11	1.276 (4)
O2—C3	1.371 (4)	N1—N2	1.357 (4)
O2—C7	1.420 (4)	N2—C12	1.354 (4)
O3—N3	1.239 (4)	N3—C15	1.430 (5)
C4—O1—C10	118.5 (3)	O1—C4—C5	125.0 (4)
C3—O2—C7	118.2 (3)	O1—C4—C3	115.8 (4)
C11—N1—N2	116.7 (3)	O2—C7—C8	107.0 (3)
C12—N2—N1	121.3 (3)	N1—C11—C1	122.5 (4)
O4—N3—O3	121.5 (4)	N2—C12—C13	119.8 (3)
O4—N3—C15	120.4 (4)	N2—C12—C17	121.3 (3)
O3—N3—C15	118.1 (3)	C16—C15—N3	120.5 (4)
O2—C3—C4	114.3 (3)	C14—C15—N3	119.5 (4)

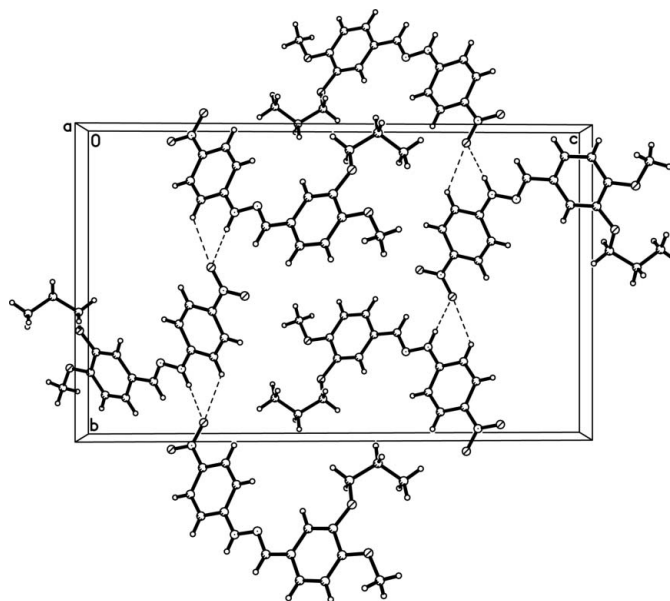


Figure 2

A packing diagram for (I), with hydrogen bonds shown as dashed lines.

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> — <i>H</i> ··· <i>A</i>	<i>D</i> — <i>H</i>	<i>H</i> ··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> — <i>H</i> ··· <i>A</i>
N2—H2···O3 ⁱ	0.86	2.19	2.968 (4)	151
C13—H13···O3 ⁱ	0.93	2.58	3.298 (5)	135

Symmetry code: (i) $-x + \frac{5}{2}, y - \frac{1}{2}, -z + \frac{3}{2}$.

H atoms were included in calculated positions and refined using a riding-model approximation. Constrained C—H and N—H bond lengths and isotropic *U* parameters were as follows: 0.93 Å and *U*_{iso}(H) = 1.2*U*_{eq}(C) for aromatic; 0.97 Å and *U*_{iso}(H) = 1.2*U*_{eq}(C) for methylene; 0.96 Å and *U*_{iso}(H) = 1.5*U*_{eq}(C) for methyl; 0.86 Å and *U*_{iso}(H) = 1.2*U*_{eq}(N) for NH H atoms.

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve 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.

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