

N,N'-Bis(4-nitrobenzylidene)ethane-1,2-diamineYu-Xi Sun,^a Zhong-Lu You^b and
Hai-Liang Zhu^{c*}^aDepartment of Chemistry, Qufu Normal University, Qufu 273165, People's Republic of China, ^bDepartment of Chemistry, Lanzhou University, Lanzhou 730000, People's Republic of China, and ^cDepartment of Chemistry, Fuyang Normal College, Fuyang, Anhui 236041, People's Republic of ChinaCorrespondence e-mail:
hailiang_zhu@163.com

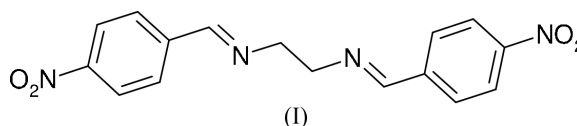
Key indicators

Single-crystal X-ray study
T = 273 K
Mean $\sigma(\text{C}-\text{C})$ = 0.002 Å
R factor = 0.048
wR factor = 0.133
Data-to-parameter ratio = 15.0For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The title compound, $\text{C}_{16}\text{H}_{14}\text{N}_4\text{O}_4$, acts as an important precursor for the synthesis of Schiff base complexes. The molecule lies across a crystallographic inversion centre. The crystal packing is stabilized by $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds and $\pi-\pi$ interactions.

Comment

Recently, we reported a few Schiff base compounds (You *et al.*, 2003, 2004). As an extension of our work on the structural characterization of Schiff base compounds, the title compound, (I), is reported here.



The asymmetric unit contains one-half of the molecule of (I), the other half being inversion-related by $(2-x, -y, 2-z)$ (Fig. 1). All the bond lengths are within normal ranges (Allen *et al.*, 1987). The $\text{C7}=\text{N1}$ bond length of 1.261 (2) Å conforms to the value for a double bond, while the $\text{C8}-\text{N1}$ bond length of 1.457 (2) Å conforms to the value for a single bond. The dihedral angle between the planes of the nitro group and the benzene ring is 6.7 (2)°. The $\text{N1}-\text{C8}-\text{C8}^i-\text{N1}^i$ torsion angle [symmetry code: (i) $2-x, -y, 2-z$] is 180°, as the inversion centre bisects the $\text{C8}-\text{C8}^i$ bond. The benzene rings of the molecules at (x, y, z) and $(2-x, -y, 1-z)$ are stacked with a centroid-centroid separation of 3.696 (3) Å, indicating $\pi-\pi$ interactions. The crystal packing is further stabilized by intermolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds, as illustrated in Fig. 2 (Table 1).

Experimental

1,2-Diaminoethane (0.1 mmol, 6.0 mg) and 4-nitrobenzaldehyde (0.2 mmol, 30.2 mg) were dissolved in methanol (10 ml). 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

 $\text{C}_{16}\text{H}_{14}\text{N}_4\text{O}_4$
 M_r = 326.31
Monoclinic, $P2_1/n$
 a = 9.156 (6) Å
 b = 7.233 (5) Å
 c = 11.516 (7) Å
 β = 97.494 (9)°
 V = 756.1 (9) Å³
 Z = 2 D_x = 1.433 Mg m⁻³
Mo $K\alpha$ radiation
Cell parameters from 807 reflections
 θ = 2.7–25.1°
 μ = 0.11 mm⁻¹
 T = 273 (2) K
Block, yellow
0.15 × 0.12 × 0.08 mm

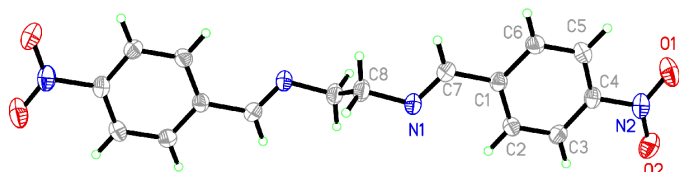


Figure 1
The structure of (I), showing the atom-numbering scheme for the contents of the asymmetric unit. Displacement ellipsoids are drawn at the 30% probability level.

Data collection

Bruker SMART CCD area-detector diffractometer	1635 independent reflections
ω scans	1092 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.038$
$T_{\text{min}} = 0.984, T_{\text{max}} = 0.992$	$\theta_{\text{max}} = 27.0^\circ$
4208 measured reflections	$h = -11 \rightarrow 11$
	$k = -7 \rightarrow 9$
	$l = -10 \rightarrow 14$

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.048$	$w = 1/[\sigma^2(F_o^2) + (0.0677P)^2]$
$wR(F^2) = 0.133$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 1.00$	$(\Delta/\sigma)_{\text{max}} < 0.001$
1635 reflections	$\Delta\rho_{\text{max}} = 0.21 \text{ e \AA}^{-3}$
109 parameters	$\Delta\rho_{\text{min}} = -0.22 \text{ e \AA}^{-3}$

Table 1

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

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$C2-H2 \cdots O1^{\text{ii}}$	0.93	2.41	3.220 (3)	146

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

All H atoms were placed in idealized positions and constrained to ride on their parent atoms, with C–H distances in the range 0.93–0.97 \AA and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

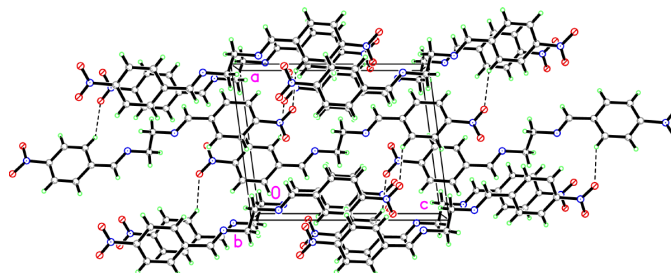


Figure 2
The crystal packing of (I), viewed along the b axis. Dashed lines indicate hydrogen bonds.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1998); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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