

Mohd Mustaqim Rosli,^a
P. S. Patil,^b Hoong-Kun Fun,^{a*}
Ibrahim Abdul Razak^a and
S. M. Dharmaprakash^b

^aX-ray Crystallography Unit, School of Physics,
Universiti Sains Malaysia, 11800 USM, Penang,
Malaysia, and ^bDepartment of Studies in
Physics, Mangalore University,
Mangalagangothri, Mangalore 574 199, India

Correspondence e-mail: hkfun@usm.my

Key indicators

Single-crystal X-ray study
T = 100 K
Mean $\sigma(\text{C}-\text{C}) = 0.001 \text{ \AA}$
R factor = 0.033
wR factor = 0.104
Data-to-parameter ratio = 13.6

For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

4-Methoxy-2-nitroaniline

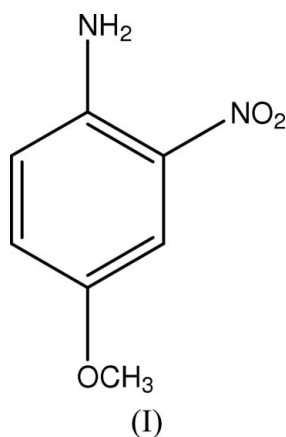
The title molecule, $\text{C}_7\text{H}_8\text{N}_2\text{O}_3$, lies on a mirror plane with two of the methyl H atoms related by mirror symmetry. The crystal structure is stabilized by intermolecular $\text{N}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds.

Received 25 January 2007

Accepted 26 January 2007

Comment

Nitroaniline-based compounds were reported to have bulk non-linear optical (NLO) properties (Zyss, 1993). We report here the crystal structure of the title compound, (I) (Fig. 1), which crystallizes in the centrosymmetric space group $Pnma$.



Bond lengths and angles in (I) have normal values (Allen *et al.*, 1987). Except for two symmetry-related H atoms of the methyl group, all atoms lie on a crystallographic mirror plane.

An intramolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bond is observed between the amino group and the nearby nitro group. In the

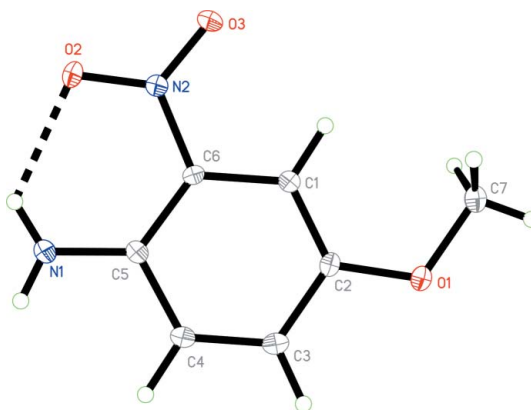


Figure 1

The molecular structure of (I), showing 50% probability displacement ellipsoids and the atomic numbering. A dashed line indicates the intramolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bond.

crystal structure, molecules are linked by intermolecular N—H···O and C—H···O hydrogen bonds (Table 1), forming an infinite two-dimensional network in the crystallographic mirror plane (Fig. 2).

Experimental

Commercially available 4-methoxy-2-nitroaniline was further purified by repeated recrystallization from acetone. Single crystals suitable for X-ray analysis were grown by slow evaporation of an acetone solution at room temperature.

Crystal data

$C_7H_8N_2O_3$	$Z = 4$
$M_r = 168.15$	$D_x = 1.533 \text{ Mg m}^{-3}$
Orthorhombic, $Pnma$	Mo $K\alpha$ radiation
$a = 16.0264 (4) \text{ \AA}$	$\mu = 0.12 \text{ mm}^{-1}$
$b = 6.3621 (1) \text{ \AA}$	$T = 100.0 (1) \text{ K}$
$c = 7.1476 (1) \text{ \AA}$	Block, orange
$V = 728.78 (2) \text{ \AA}^3$	$0.34 \times 0.25 \times 0.20 \text{ mm}$

Data collection

Bruker SMART APEX2 CCD area-detector diffractometer	13427 measured reflections
ω scans	1309 independent reflections
Absorption correction: multi-scan (SADABS; Bruker, 2005)	1180 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.873$, $T_{\max} = 0.976$	$R_{\text{int}} = 0.023$
	$\theta_{\text{max}} = 31.5^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0635P)^2 + 0.1408P]$
$R[F^2 > 2\sigma(F^2)] = 0.033$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.104$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.08$	$\Delta\rho_{\text{max}} = 0.48 \text{ e \AA}^{-3}$
1309 reflections	$\Delta\rho_{\text{min}} = -0.32 \text{ e \AA}^{-3}$
96 parameters	Extinction correction: <i>SHELXTL</i>
All H-atom parameters refined	Extinction coefficient: $0.007 (2)$

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1N1\cdots O2$	0.86 (2)	2.06 (2)	2.640 (1)	125 (2)
$N1-H1N1\cdots O1^i$	0.86 (2)	2.43 (2)	3.054 (1)	130 (2)
$N1-H1N2\cdots O3^{ii}$	0.81 (2)	2.20 (2)	3.005 (1)	176 (2)
$C7-H7A\cdots O3^{iii}$	0.88 (2)	2.59 (2)	3.461 (1)	169 (1)

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

All H atoms were located in a difference map and refined isotropically. The C—H distances lie in the range 0.88 (2)–1.01 (2) \AA .

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve

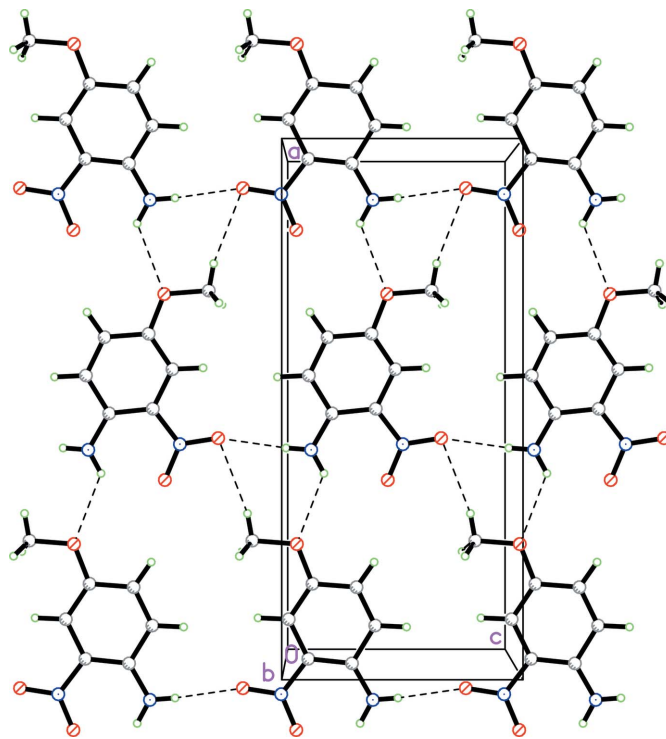


Figure 2

The crystal packing of (I), viewed down the b axis. Hydrogen bonds are shown as dashed lines.

structure: *SHELXTL* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

The authors thank the Malaysian Government and Universiti Sains Malaysia for the Scientific Advancement Grant Allocation (SAGA) grant No. 304/PFIZIK/653003/A118. PSP thanks DRDO, Government of India, for a Junior Research Fellowship (JRF).

References

- Allen, F. H., Kennard, O., Watson, D. G., Brammer, L., Orpen, A. G. & Taylor, R. (1987). *J. Chem. Soc. Perkin Trans. 2*, pp. S1–19.
- Bruker (2005). *APEX2* (Version 1.27), *SAINT* (Version 7.12a) and *SADABS* (Version 2004/1). Bruker AXS Inc., Madison, Wisconsin, USA.
- Sheldrick, G. M. (1998). *SHELXTL*. Version 5.1. Bruker AXS Inc., Madison, Wisconsin, USA.
- Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.
- Zyss, J. (1993). *Molecular Nonlinear Optics: Materials, Physics, and Devices*. New York: Academic Press.