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A new monoclinic polymorph of methyl *p*-aminobenzoate

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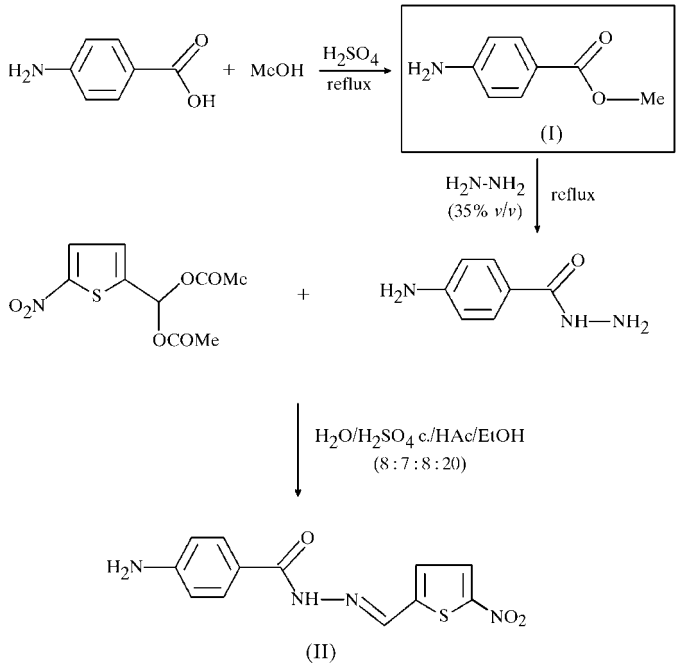
Single crystals of methyl-*p*-aminobenzoate (MAB), $C_8H_9NO_2$, were obtained during the synthesis of 4-amino-*N*′-(5-nitro-2-thienylmethylene)benzohydrazide. A $P2_1/c$ polymorph [a = 8.5969 (4) Å, b = 5.6053 (2) Å, c = 15.5397 (7) Å and β = 96.172 (2)°] of MAB was found and the intra- and intermolecular geometries were compared with those of the previously known $C2/c$ structure [a = 16.242 (2) Å, b = 8.113 (2) Å, c = 12.724 (2) Å and β = 69.17 (1)°; Xianti (1983). *Jiegou Huaxue*, **2**, 219–221].

Comment

Tuberculosis (TB) has re-emerged as one of the leading causes of death, accounting for nearly three million deaths annually (Bloom & Murray, 1992). Although there are treatment regimens based on long-term and combined chemotherapy, the emergence of AIDS and the decline of socio-economic standards contribute to the disease's resurgence in industrialized countries and to the emergence of multidrug-resistant strains of *Mycobacterium tuberculosis* (Barnes *et al.*, 1991). Therefore, the search for new therapeutics against tuberculosis is of utmost importance.

This work reports the structure of methyl-*p*-aminobenzoate (MAB), (I), an intermediate used to obtain 4-amino-*N*′-(5-nitro-2-thienylmethylene)benzohydrazide, (II) (see scheme), which has been shown to be active against tuberculosis (Rando *et al.*, 2002). Since MAB is part of the synthesized benzohydrazide, a knowledge of the crystal-packing forces in (I), in addition to its molecular geometry, could be important in explaining some aspects of the activity of (II).

The crystal structure of (I) was determined in space group $P2_1/c$. The molecule is almost flat; considering the non-H atoms, the largest deviations from the least-squares plane through the aromatic ring are 0.300 (3) and 0.180 (2) Å for atoms C8 and O2, respectively. The main geometric parameters are given in Table 1. As expected, the observed geometry of the molecule agrees well with the geometries of similar derivatives (*e.g.* Elbasyouny *et al.*, 1983; Peters *et al.*, 1998; Lynch & McClenaghan, 2002).



Longarte *et al.* (1999) calculated the MAB ground-state structure and vibrational frequencies using the *GAUSSIAN*98 package (Frisch *et al.*, 1998) and concluded that a sensible molecular–electronic description requires diffuse functions and polarizabilities in the theoretical calculations. In this way, they found that the NH_2 H atoms form a 22.38° angle with the molecular plane, as expected (Kydd & Krueger, 1977; Hollas *et al.*, 1983). In order to check the conclusion of Longarte *et al.*, the positional parameters of the two H atoms connected to the N atoms were not constrained during the refinements performed here. Our experimental data show that the dihedral angles between the NH_2 groups and the aromatic ring plane are −25 (1) and 14 (1)° for the H11—N1—C1—C6 and H12—N1—C1—C2 angles, respectively, thus confirming the results of Kydd & Krueger (1977) and Hollas *et al.* (1983). Comparison of the Longarte *et al.* (1999) 6-31+G* model with

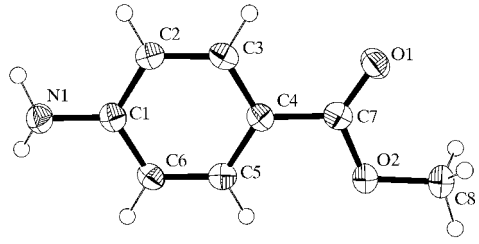


Figure 1
A view of (I), with displacement ellipsoids shown at the 50% probability level.

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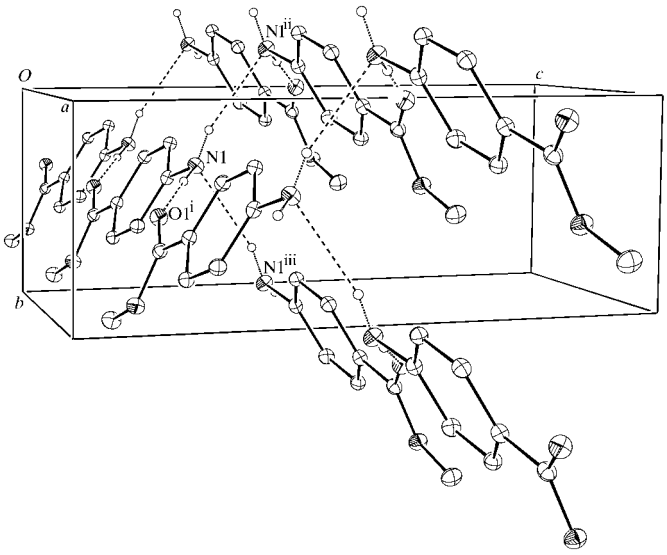

Figure 2
The crystal packing of the $P2_1/c$ polymorph of (I). Hydrogen bonds are indicated by dashed lines. [Symmetry codes: (i) $1+x, y, z$; (ii) $2-x, y-\frac{1}{2}, \frac{1}{2}-z$; (iii) $2-x, y+\frac{1}{2}, \frac{1}{2}-z$.]

our experimental MAB $P2_1/c$ polymorphs by the Kabsch (1976) method showed the polymorphs to be similar, with an r.m.s. deviation between analogous atoms of 0.064 Å.

The MAB structure was previously determined by X-ray diffraction (Xianti, 1983) as belonging to space group $C2/c$ [$a = 16.242$ (2) Å, $b = 8.113$ (2) Å, $c = 12.724$ (2) Å and $\beta = 69.17$ (1)°], while it is determined here as a new $P2_1/c$ monoclinic polymorph. Comparison of these polymorphs using the Kabsch method (Kabsch, 1976) showed them to be very similar, with an r.m.s. deviation between analogous atoms of 0.043 Å. Therefore, the two polymorphs have the same molecular shape. The $P2_1/c$ polymorph exhibits two independent intermolecular hydrogen bonds (Fig. 2 and Table 2). The packing is very similar to that observed in the monoclinic form of ethyl 4-aminobenzoate (benzocaine) determined by Lynch & McClenaghan (2002), with the molecules arranged head-to-tail in linear ribbon arrays *via* N—H···O═C associations along the [100] direction. These ribbons form a herring-bone structure, connected *via* N—H···N associations along the [010] direction. Therefore, the ribbons are themselves hydrogen bonded, forming an infinite two-dimensional network parallel to the (001) plane. In the $C2/c$ polymorph, two independent hydrogen bonds form infinite chains along the [110] and [$\bar{1}$10] directions; however, both take place *via* N—H···O═C associations, with N···O separations of about 3 Å.

Experimental

MAB was obtained from benzoic acid (30 mmol) under reflux with methanol (60 mmol) and concentrated sulfuric acid (0.06 ml) for 4 h. The reaction pH was then adjusted to ∼7 with a solution of 10% NaOH. The resulting yellow crystals were filtered off, washed with small amounts of cold water, and dried under reduced pressure and phosphorus pentoxide.

Crystal data

$C_8H_9NO_2$	$D_x = 1.349$ Mg m^{-3}
$M_r = 151.16$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 13 722 reflections
$a = 8.5969$ (4) Å	$\theta = 3.4$–$27.5°$
$b = 5.6053$ (2) Å	$\mu = 0.10$ mm^{-1}
$c = 15.5397$ (7) Å	$T = 120$ (2) K
$\beta = 96.172$ (2)°	Needle, yellow
$V = 744.49$ (6) Å^3	0.17 × 0.06 × 0.02 mm
$Z = 4$	

Data collection

Nonius KappaCCD diffractometer	$R_{int} = 0.070$
φ scans, and ω scans with κ offsets	$\theta_{max} = 25°$
15 706 measured reflections	$h = -10 \rightarrow 10$
1313 independent reflections	$k = -6 \rightarrow 6$
1040 reflections with $I > 2\sigma(I)$	$l = -18 \rightarrow 18$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0631P)^2 + 0.0853P]$ where $P = (F_o^2 + 2F_c^2)/3$
$R(F) = 0.040$	$(\Delta/\sigma)_{max} < 0.001$
$wR(F^2) = 0.104$	$\Delta\rho_{max} = 0.17$ e Å^{-3}
$S = 1.05$	$\Delta\rho_{min} = -0.26$ e Å^{-3}
1313 reflections	
108 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1
Selected geometric parameters (Å, °).

C1—N1	1.385 (2)	C7—O2	1.341 (2)
C4—C7	1.472 (2)	C8—O2	1.441 (2)
C7—O1	1.216 (2)		
N1—C1—C2	120.9 (1)	O1—C7—O2	122.2 (1)
N1—C1—C6	120.5 (1)	O1—C7—C4	125.1 (1)
C3—C4—C7	119.0 (1)	O2—C7—C4	112.7 (1)
C5—C4—C7	122.3 (1)	C7—O2—C8	115.3 (1)

Table 2
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N1—H11···O1^{i}	0.88 (2)	2.08 (2)	2.959 (2)	175.1 (16)
N1—H12···N1^{ii}	0.91 (2)	2.37 (2)	3.256 (2)	164.4 (16)

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

H atoms of the phenyl and methyl groups were positioned stereochemically and were refined with fixed individual displacement parameters [U_{iso}(H) = 1.2U_{eq}(C) or 1.5U_{eq}($C_{methoxy}$)] using a riding model, with aromatic C—H distances of 0.95 Å and methyl C—H distances of 0.98 Å. The two amine H atoms were located by difference Fourier synthesis and were set as isotropic.

Data collection: *COLLECT* (Nonius, 1998); cell refinement: *HKL SCALEPACK* (Otwinowski & Minor, 1997); data reduction: *HKL DENZO* (Otwinowski & Minor, 1997) and *SCALEPACK*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP*-3 *for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: TY1003). Services for accessing these data are described at the back of the journal.

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