

4-Amino-(1-methylphenyl)pyridinium bromide

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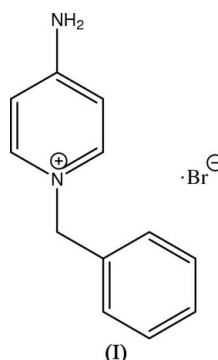
In the cation of the title compound, $C_{12}H_{13}N_2^+ \cdot Br^-$, the dihedral angle between the pyridine and benzene rings is $80.0(1)^\circ$. The anions and cations are connected by intermolecular $N-H \cdots Br$ hydrogen bonds, forming one-dimensional chains along [100].

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Comment

It is well known that pyridinium derivatives often exhibit antibacterial and antifungal activities (Akkurt *et al.*, 2005). In a continuation of our work on the study of pyridinium derivatives, the structure determination of the title compound, (I), has been undertaken.



Key indicators

Single-crystal X-ray study

 $T = 115$ KMean $\sigma(C-C) = 0.003$ Å R factor = 0.022 wR factor = 0.050

Data-to-parameter ratio = 26.0

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

A perspective view of the molecular structure of (I) is shown in Fig. 1. The bond lengths and angles within the pyridinium ring are normal and comparable with those reported for related structures (Sundar *et al.*, 2004*a,b*, 2005, 2006, 2006*a,b*). In (I), the dihedral angle between the planes of the pyridine and benzene rings is $80.0(1)^\circ$. In related structures, this angle is $85.0(1)^\circ$ for 2-amino-1-(4-nitrobenzyl)pyridinium bromide (Sundar *et al.*, 2006*a*), $88.7(1)^\circ$ for 3-amino-1-(4-nitrobenzyl)pyridinium bromide (Sundar *et al.*, 2006*b*) and $89.2(1)^\circ$ for 4-amino-1-(4-nitrobenzyl)pyridinium bromide (Sundar, Parthasarathi, Ravikumar *et al.*, 2006).

In the crystal structure, intermolecular $N-H \cdots Br$ hydrogen bonds, connect the cations and anions (Fig. 2 and Table 1). The pyridinium cations are stacked along the shortest cell axis. In addition to these interactions, a weak intermolecular $C-H \cdots Br$ interaction also is observed involving the H atom bonded to C2 and Br1 [$C2 \cdots Br1 = 3.705(2)$ Å and $C2-H2 \cdots Br1 = 142^\circ$].

Experimental

A solution of 4-aminopyridine (2.35 g, 25 ml) and benzyl bromide (4.28 g, 25 ml) in acetone was stirred at room temperature (303 K) for

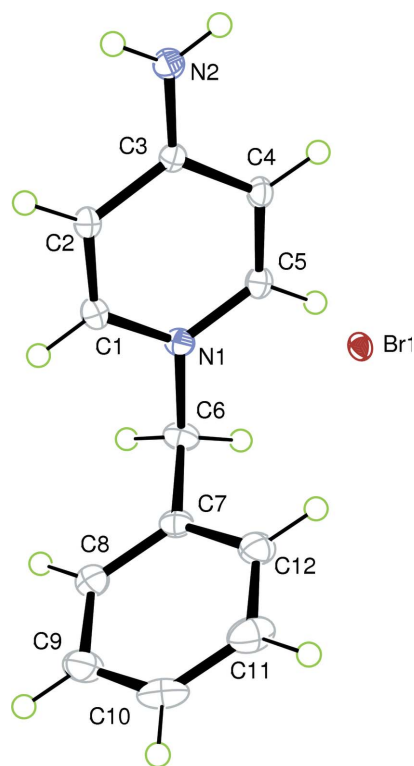


Figure 1
The molecular structure of (I), showing displacement ellipsoids drawn at the 50% probability level. H atoms are represented by circles of arbitrary radii.

1–2 h. The solid that separated was filtered, washed with dry acetone and dried in vacuum to give the stable salt, (I), which was recrystallized from an aqueous ethanol (80% *v/v*) solution (m.p. 458–460 K).

Crystal data

$C_{12}H_{13}N_2^+ \cdot Br^-$ $Z = 4$
 $M_r = 265.15$ $D_x = 1.539 \text{ Mg m}^{-3}$
 Orthorhombic, $P2_12_1$ Mo $K\alpha$ radiation
 $a = 6.4916 (5) \text{ \AA}$ $\mu = 3.56 \text{ mm}^{-1}$
 $b = 7.4037 (5) \text{ \AA}$ $T = 115 (2) \text{ K}$
 $c = 23.818 (2) \text{ \AA}$ Fragment, colourless
 $V = 1144.74 (15) \text{ \AA}^3$ $0.30 \times 0.22 \times 0.20 \text{ mm}$

Data collection

Bruker–Nonius KappaCCD 24420 measured reflections
 diffractometer with an Oxford 3742 independent reflections
 Cryostream cooler 3593 reflections with $I > 2\sigma(I)$
 ω scans with κ offsets $R_{int} = 0.052$
 Absorption correction: multi-scan $\theta_{max} = 31.5^\circ$
 (SCALEPACK; Otwinowski & Minor, 1997)
 $T_{min} = 0.382$, $T_{max} = 0.493$

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.0176P)^2 + 0.8443P]$
 $R[F^2 > 2\sigma(F^2)] = 0.022$ where $P = (F_o^2 + 2F_c^2)/3$
 $wR(F^2) = 0.050$ $(\Delta/\sigma)_{max} = 0.001$
 $S = 1.07$ $\Delta\rho_{max} = 0.39 \text{ e \AA}^{-3}$
 3742 reflections $\Delta\rho_{min} = -0.35 \text{ e \AA}^{-3}$
 144 parameters Absolute structure: Flack (1983),
 H atoms treated by a mixture of 1543 Friedel pairs
 independent and constrained refinement Flack parameter: 0.025 (8)

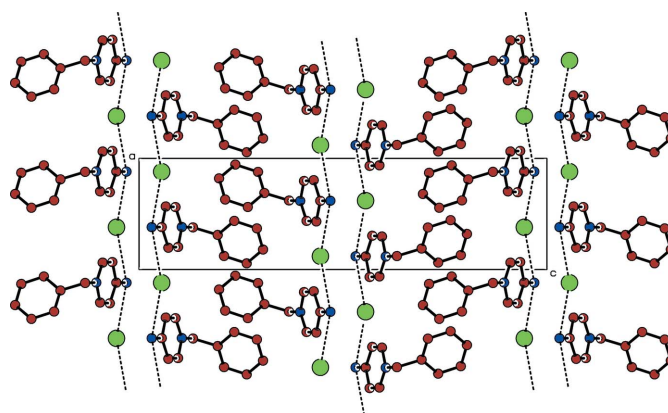


Figure 2
The crystal structure of (I), viewed along the *b* axis. The dashed lines indicate the N–H...Br hydrogen bonds. H atoms have been omitted.

Table 1
Hydrogen-bond geometry (\AA , $^\circ$).

<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–H21...Br1 ⁱ	0.82 (3)	2.78 (3)	3.5116 (18)	150 (2)
N2–H22...Br1 ⁱⁱ	0.87 (3)	2.72 (3)	3.5201 (18)	154 (2)

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

All H atoms, except amino H atoms, were placed in geometrically idealized positions ($C-H = 0.95\text{--}0.99 \text{ \AA}$) and were constrained to ride on their parent atoms, with $U_{iso}(H) = 1.2U_{eq}(C)$. The positions of amino H atoms were obtained from a difference map and refined freely along with their isotropic displacement parameters.

Data collection: COLLECT (Nonius, 2000); cell refinement: SCALEPACK (Otwinowski & Minor, 1997); data reduction: SCALEPACK and DENZO (Otwinowski & Minor, 1997); program(s) used to solve structure: SIR92 (Altomare *et al.*, 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Version 1.07; Farrugia, 1997); software used to prepare material for publication: SHELXL97.

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