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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=103 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.002 \AA$
$R$ factor $=0.021$
$w R$ factor $=0.053$
Data-to-parameter ratio $=23.9$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

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# 2-Amino-(1-methylphenyl)pyridinium bromide 

In the cation of the title compound, $\mathrm{C}_{12} \mathrm{H}_{13} \mathrm{~N}_{2}{ }^{+} \cdot \mathrm{Br}^{-}$, the dihedral angle between the pyridine and benzene rings is $89.2(1)^{\circ}$. In the crystal structure, anions and cations are interconnected by $\mathrm{N}-\mathrm{H} \cdots \mathrm{Br}$ hydrogen bonds, forming clusters about crystallographic twofold rotation axes.

## Comment

2-Aminopyridine is a commonly used drug for the treatment of neurological ailments such as multiple sclerosis, with tests showing that 2 -aminopyridine improves motor functions in multiple sclerosis patients (Schwid et al., 1997).

(I)

As an extension of our study of hydrogen-bonding patterns of pyridinium derivatives (Seethalakshmi et al., 2006,

Figure 1


View of the molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the $50 \%$ probability level.

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Figure 2
Part of the crystal structure of (I), viewed along the $b$ axis. Intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{Br}$ hydrogen bonds are indicated by dashed lines. Only H atoms involved in the hydrogen bonding have been included.

Seethalakshmi et al., 2006a,b), the X-ray crystal structure determination of (I), has been undertaken. A view of the cation and anion of (I), with the atomic numbering scheme is shown in Fig. 1. The bond lengths and angles within the pyridinium ring are comparable with those reported for related structures (Seethalakshmi et al., 2006, 2006a,b). In (I), the dihedral angle between the planes of the pyridine and benzene rings is $89.2(1)^{\circ}$.

In the crystal structure, adjacent pyridinium cations are interconnected by bromide anions through intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{Br}$ hydrogen bonds, resulting in the formation of clusters about twofold rotation axes (Table 1 and Fig. 2)

## Experimental

A solution of 2-aminopyridine ( $1.175 \mathrm{~g}, 25 \mathrm{ml}$ ), benzyl bromide $(2.13 \mathrm{~g}, 25 \mathrm{ml})$ in dry acetone was stirred for 44 h at room temperature ( 303 K ). 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.

## Crystal data

$$
\begin{aligned}
& \mathrm{C}_{12} \mathrm{H}_{13} \mathrm{~N}_{2}+\cdot \mathrm{Br}^{-} \\
& M_{r}=265.15 \\
& \text { Monoclinic, } C 2 / c \\
& a=18.4425(10) \AA \\
& b=6.5063(4) \AA \\
& c=18.8979(11) \AA \\
& \beta=98.0230(10)^{\circ} \\
& V=2245.4(2) \AA^{3}
\end{aligned}
$$

## Data collection

Bruker SMART CCD

## diffractometer

$\varphi$ and $\omega$ scans
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
$T_{\text {min }}=0.138, T_{\text {max }}=0.163$
12321 measured reflections
3270 independent reflections
3025 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.016$
$\theta_{\text {max }}=30.8^{\circ}$

## Refinement

Refinement on $F^{2}$

$$
w R\left(F^{2}\right)=0.053
$$

$$
S=1.07
$$

$$
\begin{aligned}
& \begin{aligned}
& w= 1 /\left[\sigma^{2}\left(F_{\mathrm{o}}^{2}\right)+(0.0284 P)^{2}\right. \\
& \quad+2.2052 P] \\
& \quad \text { where } P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}^{2}\right) / 3 \\
&(\Delta / \sigma)_{\max }=0.002 \\
& \Delta \rho_{\max }=0.81 \mathrm{e} \AA^{-3} \\
& \Delta \rho_{\min }=-0.34 \mathrm{e} \AA^{-3} \\
& \text { Extinction correction: } S H E L X L 97 \\
& \text { Extinction coefficient: } 0.0006(2)
\end{aligned}
\end{aligned}
$$

3270 reflections
137 parameters
H -atom parameters constrained

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

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~N} 2-\mathrm{H} 2 B \cdots \mathrm{Br}^{\mathrm{i}}$ | 0.88 | 2.59 | $3.3962(11)$ | 153 |
| $\mathrm{~N} 2-\mathrm{H} 2 C \cdots \mathrm{Br}$ | 0.88 | 2.48 | $3.3466(11)$ | 167 |

Symmetry code: (i) $-x,-y+1,-z+1$.

All the H atoms were positioned geometrically $(\mathrm{C}-\mathrm{H}=0.95-$ $0.99 \AA$ and $\mathrm{N}-\mathrm{H}=0.88 \AA$ ) and refined as riding, with $U_{\text {iso }}(\mathrm{H})=$ $1.2 U_{\text {eq }}$ (carrier).

Data collection: SMART (Bruker, 1998); cell refinement: SAINTPlus (Bruker, 1999); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: PLATON (Spek, 2003); software used to prepare material for publication: SHELXTL (Bruker,1999).

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