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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=298 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.006 \AA$
$R$ factor $=0.056$
$w R$ factor $=0.140$
Data-to-parameter ratio $=16.9$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 1-[2-(Biphenyl-4-yl)-2-oxoethyl]-4-(N,N-dimethylamino)pyridinium bromide hemihydrate

The title compound, $\mathrm{C}_{21} \mathrm{H}_{21} \mathrm{~N}_{2} \mathrm{O}^{+} \cdot \mathrm{Br}^{-} \cdot 0.5 \mathrm{H}_{2} \mathrm{O}$, crystallizes in a monoclinic unit cell with two cations, two anions and one water molecule in the asymmetric unit. The conformations of the two independent cations are different. The crystal packing is stabilized by $\mathrm{O}-\mathrm{H} \cdots \mathrm{Br}$ and $\mathrm{C}-\mathrm{H} \cdots \mathrm{Br}$ interactions and weak intermolecular $\mathrm{C}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds.

## Comment

4-Dimethylaminopyridine (DMAP) is a well known catalyst for a variety of synthetic transformations under mild conditions (Prabakaran et al., 2001, and references therein; Sundar et al., 2004). In a continuation of the identification of bioactive compounds, the structure determination of the title compound, (I), was undertaken.

(I)

The asymmetric unit of (I) contains two crystallographically independent cations, $A$ and $B$, two anions and one water molecule (Fig. 1). The bond lengths and angles in the DMAP moieties of $A$ and $B$ (Table 1) are comparable with those reported for related structures (Sundar et al., 2004). The angles between the least-squares planes of the dimethylamino moiety and the pyridine ring in cations $A$ and $B$ are 10.6 (2) and


Figure 1
The asymmetric unit of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the $50 \%$ probability level. H atoms are shown as circles of arbitrary radii.

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$13.3(2)^{\circ}$, respectively. The dihedral angles between the mean planes of the benzene rings in $A$ and $B$ are 15.7 (2) and $1.5(2)^{\circ}$, respectively. In cation $A$, the angle between the leastsquares planes of the pyridine ring and biphenyl moiety is $50.2(1)^{\circ}$, whereas in cation $B$, the corresponding angle is $86.34(12)^{\circ}$, close to the values of 81.01 (11) and $78.64(13)^{\circ}$ observed in related structures (Sundar et al., 2004). Fig. 2 shows a superposition of cations $A$ and $B$. The r.m.s. deviations of the superimposed separate DMAP and biphenyl moieties are 0.06 and $0.13 \AA$, respectively. The overall r.m.s. deviation of cations A and B is $0.34 \AA$. The main conformational differences in $A$ and $B$ are around the biphenyl moieties (Fig. 2), which may be caused by the packing interactions.

The pyridinium systems in cations $A$ and $B$ have a substantial degree of quinoidal character, since the bond lengths C2-C3 and C5-C6 in both cations (ca $1.35 \AA$; Table 1) are significantly shorter than those observed for C3C 4 and $\mathrm{C} 4-\mathrm{C} 5$ bonds (ca $1.41 \AA$ ). The C4-N2 bond lengths (Table 1) are intermediate between the typical $\mathrm{C}-\mathrm{N}$ singleand double-bond distances (Allen et al., 1987), indicating significant conjugation. The sum of the bond angles around atoms N 1 and N 2 in both cations is close to $360^{\circ}$ (Table 1), hence there is no evidence for an $s p^{3}$ lone pair. The crystal packing (Fig. 3) is stabilized by $\mathrm{O}-\mathrm{H} \cdots \mathrm{Br}$ and $\mathrm{C}-\mathrm{H} \cdots \mathrm{Br}$ interactions and weak intermolecular $\mathrm{C}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds (Table 2).

## Experimental

A solution of 4-phenylphenacyl bromide ( $1.6 \mathrm{~g}, 4 \mathrm{mmol}$ ) and DMAP ( $0.5 \mathrm{~g}, 4 \mathrm{mmol}$ ) in dry acetone was refluxed for 30 min . After cooling to room temperature ( 303 K ), the solid that separated was filtered off and washed with dry acetone to give the stable salt (I) (yield 1.87 g , $89 \%$; m.p. $519-521 \mathrm{~K}$ ), which was recrystallized from ethanol.

## Crystal data

$\mathrm{C}_{21} \mathrm{H}_{21} \mathrm{~N}_{2} \mathrm{O}^{+} \cdot \mathrm{Br}^{-} \cdot 0.5 \mathrm{H}_{2} \mathrm{O}$
$M_{r}=406.32$
Monoclinic, $C 2 / c$
$a=21.077$ (6) A
$b=9.971$ (3) $\AA$
$c=37.485(12) \AA$
$\beta=98.121(9)^{\circ}{ }^{\circ}$
$V=7799(4) \AA^{3}$
$Z=16$

## Data collection

Bruker SMART CCD 1K diffractometer $\omega$ scans
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
$T_{\text {min }}=0.281, T_{\text {max }}=0.428$
31162 measured reflections

## Refinement

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Refinement on \(F^{2}\)
\(R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.056\)
\(w R\left(F^{2}\right)=0.140\)
\(S=1.01\)
7982 reflections
471 parameters
H atoms treated by a mixture of independent and constrained refinement
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Figure 2
Superimposed fit of cations $A$ (red) and $B$ (green) of (I).


The crystal packing of (I). Intermolecular hydrogen bonds are indicated by dashed lines.

Table 1
Selected geometric parameters ( $\mathrm{A},{ }^{\circ}$ ).

| $\mathrm{N} 2 A-\mathrm{C} 4 A$ | $1.336(5)$ | $\mathrm{N} 2 B-\mathrm{C} 4 B$ | $1.327(5)$ |
| :--- | :--- | :--- | :--- |
| $\mathrm{C} 2 A-\mathrm{C} 3 A$ | $1.347(5)$ | $\mathrm{C} 2 B-\mathrm{C} 3 B$ | $1.345(6)$ |
| $\mathrm{C} 3 A-\mathrm{C} 4 A$ | $1.428(6)$ | $\mathrm{C} 3 B-\mathrm{C} 4 B$ | $1.405(6)$ |
|  |  |  |  |
| $\mathrm{C} 2 A-\mathrm{N} 1 A-\mathrm{C} 6 A$ | $117.7(4)$ | $\mathrm{C} 6 B-\mathrm{N} 1 B-\mathrm{C} 2 B$ | $118.3(3)$ |
| $\mathrm{C} 2 A-\mathrm{N} 1 A-\mathrm{C} 1 A$ | $121.6(4)$ | $\mathrm{C} 6 B-\mathrm{N} 1 B-\mathrm{C} 1 B$ | $120.6(4)$ |
| $\mathrm{C} 6 A-\mathrm{N} 1 A-\mathrm{C} 1 A$ | $120.7(4)$ | $\mathrm{C} 2 B-\mathrm{N} 1 B-\mathrm{C} 1 B$ | $121.0(4)$ |
| $\mathrm{C} 4 A-\mathrm{N} 2 A-\mathrm{C} 7 A$ | $122.4(4)$ | $\mathrm{C} 4 B-\mathrm{N} 2 B-\mathrm{C} 7 B$ | $122.2(4)$ |
| $\mathrm{C} 4 A-\mathrm{N} 2 A-\mathrm{C} 8 A$ | $121.2(4)$ | $\mathrm{C} 4 B-\mathrm{N} 2 B-\mathrm{C} 8 B$ | $122.0(4)$ |
| $\mathrm{C} 7 A-\mathrm{N} 2 A-\mathrm{C} 8 A$ | $116.4(3)$ | $\mathrm{C} 7 B-\mathrm{N} 2 B-\mathrm{C} B B$ | $115.7(4)$ |

Table 2
Hydrogen-bonding geometry $\left(\AA^{\circ},{ }^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{C} 1 A-\mathrm{H} 1 A \cdots \mathrm{Br} 2$ | 0.97 | 2.76 | $3.713(5)$ | 170 |
| $\mathrm{O} W-\mathrm{H} 22 \cdots \mathrm{Br} 1$ | 0.86 | 2.47 | $3.314(4)$ | 170 |
| $\mathrm{O} W-\mathrm{H} 23 \cdots \mathrm{Br} 2$ | 0.87 | 2.45 | $3.311(4)$ | 169 |
| $\mathrm{C} 1 A-\mathrm{H} 1 B \cdots \mathrm{Br} 2^{\mathrm{i}}$ | 0.97 | 2.74 | $3.581(5)$ | 146 |
| $\mathrm{C} 14 A-\mathrm{H} 14 A \cdots W^{\text {ii }}$ | 0.93 | 2.61 | $3.530(6)$ | 173 |
| $\mathrm{C} 21 A-\mathrm{H} 21 A \cdots W^{\text {ii }}$ | 0.93 | 2.62 | $3.500(6)$ | 157 |
| $\mathrm{C} 1 B-\mathrm{H} 1 D \cdots \mathrm{Br} 1^{\mathrm{iii}}$ | 0.97 | 2.92 | $3.840(5)$ | 158 |
| $\mathrm{C} 8 B-\mathrm{H} 8 D \cdots \mathrm{Br}^{\mathrm{iii}}$ | 0.96 | 2.80 | $3.680(5)$ | 153 |
| $\mathrm{C} 14 B-\mathrm{H} 14 B \cdots \mathrm{O}^{\text {iv }}$ | 0.93 | 2.38 | $3.270(6)$ | 160 |
| Symmetry codes: | (i) | $\frac{1}{2}-x, \frac{1}{2}+y, \frac{1}{2}-z ;$ | (ii) | $x, 1+y, z ;$ |
| $-x, y, \frac{1}{2}-z$. | (iii) | $x, 1-y, \frac{1}{2}+z ;$ | (iv) |  |

The water H atoms were located in a difference Fourier map and refined with $\mathrm{H} 22-\mathrm{O} W$ and $\mathrm{H} 23-\mathrm{O} W$ distance restraints of 0.86 (1) Å. The remaining H atoms were treated as riding, with $\mathrm{C}-$ $\mathrm{H}=0.93-0.98 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.5$ or $1.2 U_{\text {eq }}(\mathrm{C})$.

Data collection: SMART (Bruker, 2000); cell refinement: SAINT (Bruker, 2000); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 (Farrugia, 1997) and PLATON (Spek, 2003); software used to prepare material for publication: SHELXL97 and PARST (Nardelli, 1995).

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