Acta Crystallographica Section E

## Structure Reports

Online
ISSN 1600-5368

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## Key indicators

Single-crystal X-ray study
$T=294 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.010 \AA$
$R$ factor $=0.041$
$w R$ factor $=0.093$
Data-to-parameter ratio $=10.9$

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

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## Methyl 3-[(E)-2-(4-bromobenzoylmethyl-idene)imidazolidin-1-yl]acrylate

The title compound, $\mathrm{C}_{15} \mathrm{H}_{15} \mathrm{BrN}_{2} \mathrm{O}_{3}$, contains two molecules in the asymmetric unit, which differ in conformation. Both exhibit intramolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds. Intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds link molecules into dimers and short $\mathrm{Br} \cdots \mathrm{O}$ contacts exist between dimers.

## Comment

Heterocyclic ketene aminals (HKAs) are ambidentate nucleophiles (Huang \& Wang, 2002). The title compound, (I), is an $N$-alkylation product of an HKA. The crystal structure of (I) was determined in order to provide information regarding its electronic conjugation properties and to examine a possible intramolecular hydrogen bond (Wang et al., 1987), which may be correlated with the reactivity of the secondary amine at the ${ }^{\alpha} \mathrm{C}$ atom (Huang \& Wamhoff, 1984).

(I)

There are two molecules in the asymmetric unit of (I) (Fig. 1), which differ principally in the orientation of the benzene ring with respect to the rest of the molecule. The dihedral angle between the benzene ring and the mean plane of the remainder of the molecule is 13.4 (1) and $50.0(1)^{\circ}$ in the two independent molecules.


Figure 1
The structure of the asymmetric unit of (I), showing displacement ellipoids at the $30 \%$ probability level (arbitrary spheres for H atoms).

Received 8 October 2006
Accepted 2 November 2006


Figure 2
The hydrogen-bonded dimers in the structure of (I), with $\mathrm{Br} \cdots \mathrm{O}$ contacts shown between them. Both types of intermolecular contacts are indicated by dashed lines.

Intramolecular hydrogen bonds are observed between the $\mathrm{N}-\mathrm{H}$ group and the adjacent $\mathrm{C}=\mathrm{O}$ group in both independent molecules (Table 1 and Fig. 2). Intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds (Table 1) link the molecules into dimers, and short $\mathrm{Br} \cdots \mathrm{O}$ contacts exist between dimers $\left[\mathrm{Br} 1 \cdots \mathrm{O} 2^{i}=\right.$ 3.074 (7) $\AA$; symmetry code: (i) $x, y,-1+z]$.

## Experimental

Compound (I) was prepared according to the procedure of Wang et al. (1994) and recrystallized from chloroform in $75 \%$ yield (m.p. 388 K). Elemental analysis, found: C 51.32, H 4.32, N $7.95 \%$; calculated: C 51.30, H 4.31, N 7.98\%.

## Crystal data

$\mathrm{C}_{15} \mathrm{H}_{15} \mathrm{BrN}_{2} \mathrm{O}_{3}$
$M_{r}=351.20$
Monoclinic, $C c$
$a=15.819(4) \AA$
$b=20.899(5) \AA$
$c=9.994(2) \AA$
$\beta=117.307(4)^{\circ}$
$V=2936.0(12) \AA^{3}$

## Data collection

| Bruker SMART CCD area-detector | 8187 measured reflections |
| :--- | :--- |
| diffractometer | 4154 independent reflections |
| $\varphi$ and $\omega$ scans | 2440 reflections with $I>2 \sigma(I)$ |
| Absorption correction: multi-scan | $R_{\text {int }}=0.047$ |
| $\quad(S A D A B S ;$ Bruker, 1997) | $\theta_{\max }=26.4^{\circ}$ |
| $T_{\min }=0.473, T_{\max }=0.539$ |  |

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.041$
$w R\left(F^{2}\right)=0.093$
$S=0.97$
4154 reflections
381 parameters
H -atom parameters constrained
$w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}{ }^{2}\right)+(0.0334 P)^{2}\right]$
where $P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}{ }^{2}\right) / 3$
$(\Delta / \sigma)_{\max }<0.001$ 。
$\Delta \rho_{\max }=0.36 \mathrm{e}^{-3}$
$\Delta \rho_{\min }=-0.50 \mathrm{e}^{-3}$
Absolute structure: Flack (1983),
with 1147 Friedel pairs
Flack parameter: 0.012 (10)

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

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| N1-H1 $\cdots$ O1 | 0.86 | 2.14 | $2.709(7)$ | 123 |
| N3-H3 $\mathrm{O}^{\mathrm{H}}$ | 0.86 | 2.07 | 2.638 (7) | 123 |
| N1-H1 $4^{\text {i }}$ | 0.86 | 2.30 | 3.007 (7) | 140 |
| N3-H3 $\cdots$ O $^{\text {ii }}$ | 0.86 | 2.29 | $3.030(7)$ | 145 |

Symmetry codes: (i) $x-\frac{1}{2}, y-\frac{1}{2}, z$; (ii) $x+\frac{1}{2}, y+\frac{1}{2}, z$.
All H atoms were placed in geometrically idealized positions, with $\mathrm{C}-\mathrm{H}=0.93-0.97 \AA$ and $\mathrm{N}-\mathrm{H}=0.86 \AA$, and refined as riding, with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C}, \mathrm{N})$, except for the methyl groups, for which $U_{\text {iso }}(\mathrm{H})=1.5 U_{\text {eq }}(\mathrm{C})$. Each methyl group was allowed to rotate about its local threefold axis.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Bruker, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

The authors are grateful to Dr Hai-Bing Song and HongGen Wang of Nankai University for collecting the intensity data.

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