## organic papers

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#### **Key indicators**

Single-crystal X-ray study T = 193 K Mean  $\sigma$ (C–C) = 0.004 Å R factor = 0.030 wR factor = 0.073 Data-to-parameter ratio = 13.1

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

# 5-[(2-Bromophenylamino)methylene]-2,2-dimethyl-1,3-dioxane-4,6-dione

In the title compound, C13H12BrNO4, the 1,3-dioxane-4,6dione ring exhibits a half-chair conformation. The molecules are linked by  $C-H \cdots O$  hydrogen bonds. The amino H atom has one intramolecular contact to a carbonyl O atom, forming a six-membered ring.

## Comment

Recently, we reported the structure of two arylaminomethylene Meldrum's acid derivatives (Joussef et al., 2005a,b). As part of a continuing study of the conformational analysis in the solid state of Meldrum's acid derivatives, we report here the structure of the title compound, (I).



In (I), the 1,3-dioxane-4,6-dione ring exhibits a half-chair conformation. The dihedral angle C6-N7-C8-C9 is 170.5 (3)° and the distances C6-N7 and C8-C9 indicate delocalization. The amino H atom has one intramolecular contact to atom O10, with an  $H \cdots O$  distance of 2.12 (3) Å, forming a six-membered ring. The delocalization of the Natom lone pair into the Meldrum's acid ring may be favoured in the direction of one of the two carbonyl groups (Blake et al., 2003). One intramolecular contact between the amino H atom and Br, with a distance of 2.62 (3) Å, is also observed. The molecular packing of (I) is stabilized by  $C-H \cdots O$  hydrogen



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displacement ellipsoids drawn at the 50% probability level.

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bonds. The bond lengths and angles are in good agreement with values retrieved from the Cambridge Structural Database (Version 5.25; Allen, 2002). Details of the hydrogen bonding are given in Table 1.

## **Experimental**

The title compound was prepared according to a literature procedure (Cassis *et al.*, 1985) and was recrystallized from methanol.

Z = 2

 $D_r = 1.674 \text{ Mg m}^{-3}$ 

Cell parameters from 25

Irregula block, colorless

0.43  $\times$  0.26  $\times$  0.16 mm

Mo  $K\alpha$  radiation

reflections  $\theta = 4.1 - 16.9^{\circ}$ 

 $\mu = 3.19 \text{ mm}^{-1}$ 

T = 193 (2) K

 $R_{\rm int} = 0.020$  $\theta_{\rm max} = 25.1^{\circ}$ 

 $\begin{array}{l} h=-8\rightarrow8\\ k=-11\rightarrow11 \end{array}$ 

 $l = -12 \rightarrow 0$ 

3 standard reflections

every 200 reflections

intensity decay: 1%

Crystal data

 $\begin{array}{l} C_{13}H_{12}BrNO_4 \\ M_r = 326.15 \\ Triclinic, P\overline{1} \\ a = 6.960 \ (5) \ \text{\AA} \\ b = 9.298 \ (5) \ \text{\AA} \\ c = 10.424 \ (5) \ \text{\AA} \\ \alpha = 95.570 \ (5)^{\circ} \\ \beta = 101.043 \ (5)^{\circ} \\ \gamma = 99.508 \ (5)^{\circ} \\ V = 647.2 \ (7) \ \text{\AA}^3 \end{array}$ 

### Data collection

Enraf–Nonius CAD-4 diffractometer  $\omega$ –2 $\theta$  scans Absorption correction:  $\psi$  scan (North *et al.*, 1968)  $T_{\min} = 0.417$ ,  $T_{\max} = 0.601$ 2451 measured reflections 2312 independent reflections 1724 reflections with  $I > 2\sigma(I)$ 

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_0^2) + (0.0298P)^2$
$R[F^2 > 2\sigma(F^2)] = 0.030$	+ 0.241P]
$wR(F^2) = 0.073$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.06	$(\Delta/\sigma)_{\rm max} = 0.001$
2312 reflections	$\Delta \rho_{\rm max} = 0.32 \ {\rm e} \ {\rm A}^{-3}$
177 parameters	$\Delta \rho_{\rm min} = -0.39 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	Extinction correction: SHELXL97
independent and constrained	Extinction coefficient: 0.024 (2)
refinement	

 Table 1

 Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\begin{array}{c} N7 - H7 \cdots O10 \\ C2 - H2 \cdots O14^{i} \end{array}$	0.83 (3)	2.12 (3)	2.734 (3)	130 (3)
	0.93	2.46	3.266 (4)	146

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

The amino H atom was located in a difference map and was refined freely. C-bound H atoms were positioned with idealized geometry and were refined as riding, with C-H = 0.93 Å (0.96 Å for methyl groups) and  $U^{iso}(H) = 1.2U_{eq}(C)$  or  $1.5U_{eq}$  (methyl C).

Data collection: *CAD-4/PC Software* (Enraf–Nonius, 1993); cell refinement: *CAD-4/PC Software*; data reduction: *XCAD4* (Harms & Wocadlo, 1995); 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: *SHELXL97*.





The molecular packing of (I), viewed along the a axis, with hydrogen bonding shown as dashed lines.

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