

## 5-{[4-(4-Bromophenyl)thiazol-2-yl]amino-methylene}-2,2-dimethyl-1,3-dioxane-4,6-dione

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**Luiz Everson da Silva,<sup>a,b</sup>**  
**Antonio Carlos Joussef,<sup>a</sup>** **Sabine**  
**Foro<sup>b</sup>** and **Boris Schmidt<sup>b\*</sup>**

<sup>a</sup>Departamento de Química—UFSC, 88040-900 Florianópolis, SC, Brazil, and <sup>b</sup>Clemens Schöpf-Institut für Organische Chemie und Biochemie, Technische Universität Darmstadt, Petersenstrasse 22, D-64287 Darmstadt, Germany

Correspondence e-mail: foro@tu-darmstadt.de

### Key indicators

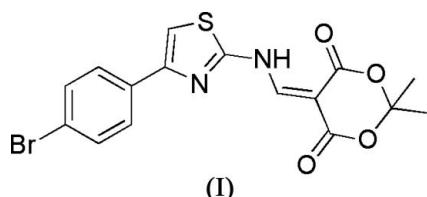
Single-crystal X-ray study  
T = 299 K  
Mean  $\sigma(C-C)$  = 0.004 Å  
R factor = 0.032  
wR factor = 0.088  
Data-to-parameter ratio = 12.7

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

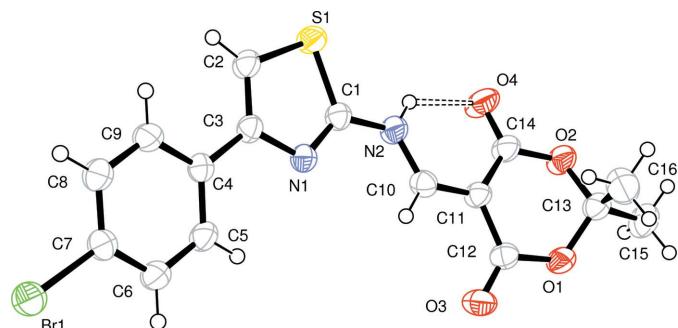
In the title compound, C<sub>16</sub>H<sub>13</sub>BrN<sub>2</sub>O<sub>4</sub>S, the 1,3-dioxane-4,6-dione ring exhibits an envelope conformation. The amino H atom makes an intramolecular contact to a carbonyl O atom, forming a six-membered ring.

### Comment

Thiazoles and their derivatives are found to be associated with various biological activities such antibacterial and anti-inflammatory (Holla *et al.*, 2003). In addition, phenylthiazole derivatives have been investigated as inhibitors of kynurenine 3-hydroxylase (Röver *et al.*, 1997). Prompted by these reports and in continuation of our search for bioactive molecules from Meldrum's acid derivatives (Joussef *et al.*, 2005a,b; da Silva *et al.*, 2005a,b; da Silva, Joussef, Foro & Schmidt, 2006; da Silva, Joussef, Andriguetti-Fröhner *et al.* 2006), the structure of the title compound, (I), has been determined and the results are presented here (Fig. 1).



In (I), the 1,3-dioxane-4,6-dione ring exhibits an envelope conformation with the C13 atom at the flap position. The torsion angle C11—C10—N2—C1 of  $-176.8(2)^\circ$  and the C10—N2 and C10—C11 bond distances (Table 1) indicate electron delocalization. The delocalization of the N atom lone pair into the Meldrum's acid ring may be favoured in the



**Figure 1**

The molecular structure of (I), shown with 50% probability displacement ellipsoids (arbitrary spheres for H atoms). Dashed lines indicate a hydrogen bond.

direction of one of the two available carbonyl groups C12=O3 and C14=O4 (Blake *et al.*, 2003). The thiazole ring and the benzene ring are slightly twisted with respect to each other, with a dihedral angle of 9.3 (1)° between the mean planes. The amino H atom is intramolecularly hydrogen bonded to O4 (Table 2), forming a six-membered ring.

## Experimental

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

### Crystal data

$C_{16}H_{13}BrN_2O_4S$	$V = 806.72 (10) \text{ \AA}^3$
$M_r = 409.25$	$Z = 2$
Triclinic, $P\bar{1}$	$D_x = 1.685 \text{ Mg m}^{-3}$
$a = 7.8262 (6) \text{ \AA}$	Cu $K\alpha$ radiation
$b = 9.4869 (7) \text{ \AA}$	$\mu = 4.90 \text{ mm}^{-1}$
$c = 11.8847 (7) \text{ \AA}$	$T = 299 (2) \text{ K}$
$\alpha = 70.969 (5)^\circ$	Thick needle, yellow
$\beta = 79.213 (6)^\circ$	$0.60 \times 0.25 \times 0.15 \text{ mm}$
$\gamma = 77.059 (6)^\circ$	

### Data collection

Enraf–Nonius CAD-4	2774 independent reflections
diffractometer	2603 reflections with $I > 2\sigma(I)$
$\omega/2\theta$ scans	$R_{\text{int}} = 0.024$
Absorption correction: $\psi$ scan	$\theta_{\text{max}} = 66.9^\circ$
(North <i>et al.</i> , 1968)	3 standard reflections
$T_{\text{min}} = 0.198$ , $T_{\text{max}} = 0.479$	frequency: 120 min
3288 measured reflections	intensity decay: 1.0%

### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0459P)^2$
$R[F^2 > 2\sigma(F^2)] = 0.032$	$+ 0.4106P]$
$wR(F^2) = 0.088$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 1.14$	$(\Delta/\sigma)_{\text{max}} = 0.003$
2774 reflections	$\Delta\rho_{\text{max}} = 0.53 \text{ e \AA}^{-3}$
218 parameters	$\Delta\rho_{\text{min}} = -0.60 \text{ e \AA}^{-3}$
H-atom parameters constrained	Extinction correction: SHELXL97
	Extinction coefficient: 0.0133 (7)

**Table 1**

Selected bond lengths ( $\text{\AA}$ ).

C10—N2	1.331 (3)	C10—C11	1.370 (3)
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**Table 2**

Hydrogen-bond geometry ( $\text{\AA}$ , °).

$D—H\cdots A$	$D—H$	$H\cdots A$	$D\cdots A$	$D—H\cdots A$
N2—H2N $\cdots$ O4	0.86	2.06	2.704 (3)	131

All H atoms were positioned with idealized geometry [N—H = 0.86  $\text{\AA}$ , and C—H = 0.93 (aromatic) and 0.96  $\text{\AA}$  (methyl)], and were refined in riding mode, with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$ .

Data collection: CAD-4-PC (Enraf–Nonius, 1996); cell refinement: CAD-4-PC; data reduction: REDU4 (Stoe & Cie, 1987); 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.

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