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Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.007$ Å
 R factor = 0.041
 wR factor = 0.103
Data-to-parameter ratio = 13.6

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

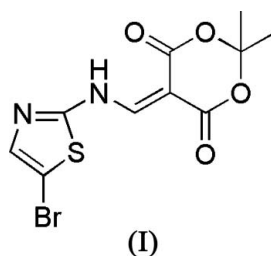
5-(5-Bromothiazol-2-ylaminomethylene)-2,2-dimethyl-1,3-dioxane-4,6-dione

In the title compound, $\text{C}_{10}\text{H}_9\text{BrN}_2\text{O}_4\text{S}$, the 1,3-dioxane-4,6-dione ring exhibits a sofa conformation. The thiazole ring is nearly planar. The amino H atom has an intramolecular $\text{N}\cdots\text{H}\cdots\text{O}$ contact, forming a six-membered ring, and an intermolecular hydrogen bond to a carbonyl O is also observed.

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Comment

Thiazoles comprise an important class of heterocyclic compounds present in many potent biologically active molecules. This heterocyclic ring also shows various application in the synthesis of new organic compounds (de Souza *et al.*, 2005). We have focused on arylaminomethylene derivatives of Meldrum's acid in our search for biologically active molecules (Joussef *et al.*, 2005*a,b*; da Silva *et al.*, 2005*a,b*, 2006). As an extension of this approach, we report an X-ray crystallographic study of the title compound, (I).



In (I), the 1,3-dioxane-4,6-dione ring exhibits a sofa conformation. The torsion angle $\text{C}5-\text{N}6-\text{C}7-\text{C}8$ is $176.5(4)^\circ$ and the distances $\text{N}6-\text{C}5$ and $\text{C}7-\text{C}8$ indicate delocalization of the conjugated system. The amino H atom forms an intramolecular contact to O9, with an $\text{H}\cdots\text{O}$ distance of 2.24 Å, forming a six-membered ring. Delocalization of the N-atom 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); details of the hydrogen bonding are given in Table 1.

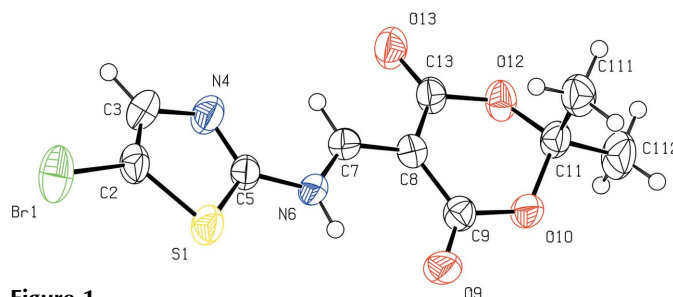


Figure 1
The molecular structure of (I), showing the atom labeling and displacement ellipsoids drawn at the 50% probability level.

Experimental

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

Crystal data

$C_{10}H_9BrN_2O_4S$
 $M_r = 333.16$
 Monoclinic, $P2_1/c$
 $a = 5.408$ (5) Å
 $b = 18.013$ (5) Å
 $c = 13.114$ (5) Å
 $\beta = 100.717$ (5)°
 $V = 1255.2$ (13) Å³
 $Z = 4$

$D_x = 1.763$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 25
 reflections
 $\theta = 5.5$ – 23.7 °
 $\mu = 3.45$ mm⁻¹
 $T = 293$ (2) K
 Prism, colorless
 $0.50 \times 0.16 \times 0.13$ mm

Data collection

Nonius CAD-4 diffractometer
 $\omega/2\theta$ scans
 Absorption correction: ψ scan
 (North *et al.*, 1968)
 $T_{\min} = 0.504$, $T_{\max} = 0.641$
 2330 measured reflections
 2230 independent reflections
 1269 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.033$
 $\theta_{\text{max}} = 25.1$ °
 $h = -6 \rightarrow 6$
 $k = -21 \rightarrow 0$
 $l = -15 \rightarrow 0$
 3 standard reflections
 every 200 reflections
 intensity decay: 1%

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.041$
 $wR(F^2) = 0.103$
 $S = 1.01$
 2230 reflections
 164 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0483P)^2 + 0.077P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.28$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.48$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N6-H6\cdots O9$	0.87	2.24	2.798 (5)	122
$N6-H6\cdots O9^i$	0.87	2.18	2.996 (5)	156

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

All H atoms were positioned with idealized geometry and were refined with isotropic displacement parameters (set at 1.2 times U_{eq} of the parent atom or at 1.5 times U_{eq} for methyl groups) using a riding model, with $N-H = 0.87$ Å, and $C-H = 0.93$ (aromatic) or 0.96 Å (methyl). The isotropic displacement parameter of the amino H atom was refined.

Data collection: *CAD-4/PC Software* (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*.

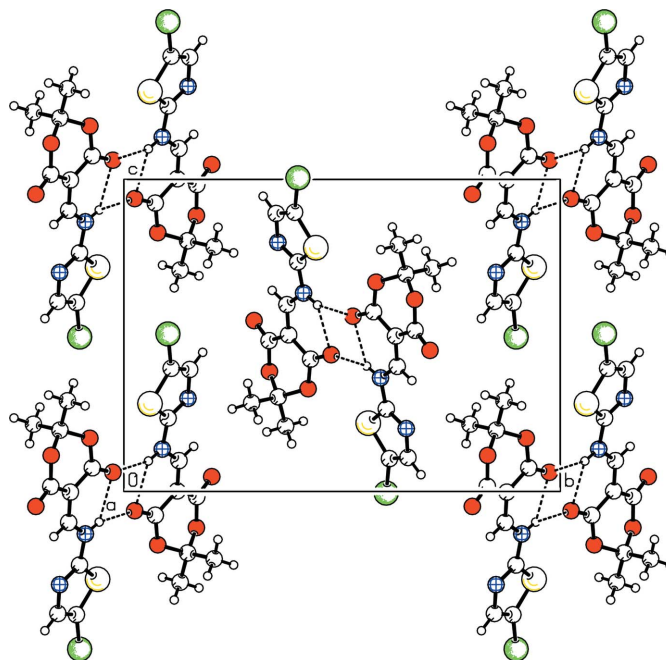


Figure 2

The molecular packing of (I), with hydrogen bonds shown as dashed lines.

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