

1-(5,6-Dimethyl-1,2,4-triazin-3-yl)-2-methyl-1H-benzimidazole

Andrey V. Sokolov, Anna V. Vologzhanina* and Petr P. Purygin

Department of Chemistry, Samara State University, Academician Pavlov Street 1, 443011 Samara, Russian Federation

Correspondence e-mail: vologzhanina@mail.ru

Key indicators

Single-crystal X-ray study

T = 243 K

Mean $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$

R factor = 0.058

wR factor = 0.173

Data-to-parameter ratio = 20.8

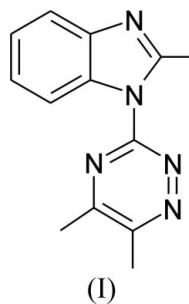
For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

In the title molecule, $\text{C}_{13}\text{H}_{13}\text{N}_5$, all bond lengths and angles show normal values. The molecular skeleton is almost planar; the mean planes of the benzimidazole and triazine rings make a dihedral angle of $1.28(6)^\circ$. The crystal packing is stabilized by $\pi-\pi$ interactions and weak intermolecular $\text{C}-\text{H}\cdots\text{N}$ hydrogen bonds.

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Comment

In the search for correlation between the structure and reactivity of *N*-cyanoazole derivatives (Pan'kov *et al.*, 2001*a,b*), 2-methyl-1*H*-benzimidazole-1-carbohydrazonamide has been synthesized by the reaction of 2-methyl-1-cyanobenzimidazole with hydrazine (Pan'kov *et al.*, 2001*a*). The title compound, (I) (Fig. 1), has been prepared by the reaction of 2-methyl-1*H*-benzimidazole-1-carbohydrazonamide with diacetyl.



The bond lengths and angles in (I) are normal (Allen *et al.*, 1987). The triazine ring is almost planar, with an r.m.s. deviation of $0.014(1) \text{ \AA}$. The geometry of the triazine ring and the C–N distances indicate a donation of the N5 lone pair into the triazine π system. Furthermore, the benzimidazole and triazine rings in (I) are almost coplanar; the dihedral angle of $1.28(6)^\circ$ between the two least-squares planes suggests conjugation between the benzimidazole and triazine ring systems.

In the crystal structure, weak intermolecular $\text{C}-\text{H}\cdots\text{N}$ hydrogen bonds (Table 1) link the molecules into zigzag chains. Two adjacent molecules are paired *via* a $\pi-\pi$ interaction, with a short distance of $3.533(3) \text{ \AA}$ between the centroid of the triazine ring of one molecule and the centroid of the five-membered ring of another molecule. Both these interactions stabilize the crystal packing (Fig. 2).

Experimental

2-Methyl-1*H*-benzimidazole-1-carbohydrazonamide was prepared according to the procedure of Pan'kov *et al.* (2001*a*). 2-Methyl-1*H*-benzimidazole-1-carbohydrazonamide (5.7 mmol) and diacetyl

(0.5 ml) were dissolved in propan-2-ol (10 ml). The mixture was boiled for 5–6 h and then concentrated to dryness. The solid was recrystallized from ethyl acetate (yield 95%; m.p. 420–421 K).

Crystal data

$C_{13}H_{13}N_5$
 $M_r = 239.28$
 Monoclinic, $P2_1/n$
 $a = 7.412 (4) \text{ \AA}$
 $b = 13.163 (7) \text{ \AA}$
 $c = 12.499 (7) \text{ \AA}$
 $\beta = 97.701 (11)^\circ$
 $V = 1208.4 (11) \text{ \AA}^3$

$Z = 4$
 $D_x = 1.315 \text{ Mg m}^{-3}$
 Mo $K\alpha$ radiation
 $\mu = 0.09 \text{ mm}^{-1}$
 $T = 243 (2) \text{ K}$
 Prism, colourless
 $0.60 \times 0.20 \times 0.20 \text{ mm}$

Data collection

Bruker SMART 1000 CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1998)
 $T_{\min} = 0.951, T_{\max} = 0.983$

9157 measured reflections
 3459 independent reflections
 2213 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.024$
 $\theta_{\text{max}} = 30.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.058$
 $wR(F^2) = 0.173$
 $S = 1.07$
 3459 reflections
 166 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0999P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.32 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.24 \text{ e \AA}^{-3}$

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C2-H1\cdots N3^i$	0.93	2.60	3.423 (2)	148

Symmetry code: (i) $x - \frac{1}{2}, -y - \frac{1}{2}, z - \frac{1}{2}$.

All H atoms were located in a difference map and refined as riding, with $C-H = 0.98$ (CH_3) or 0.93 \AA (CH), and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT-Plus (Bruker, 1998); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXTL (Sheldrick, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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References

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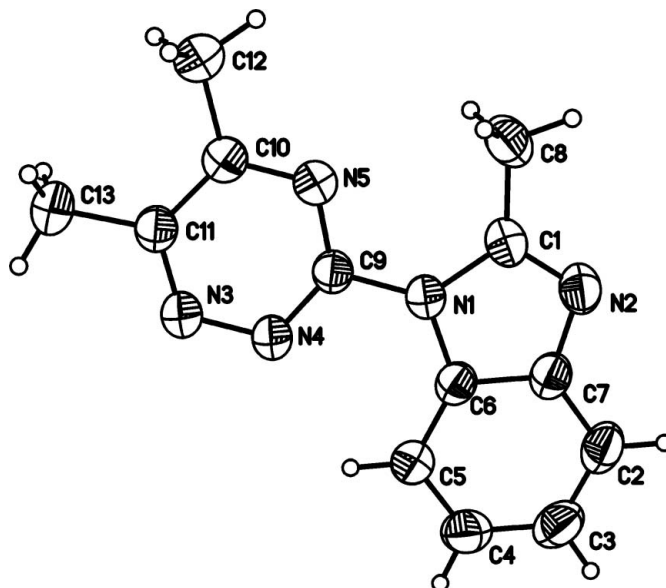


Figure 1

The molecular structure of (I), with the atomic numbering. Displacement ellipsoids are drawn at the 50% probability level.

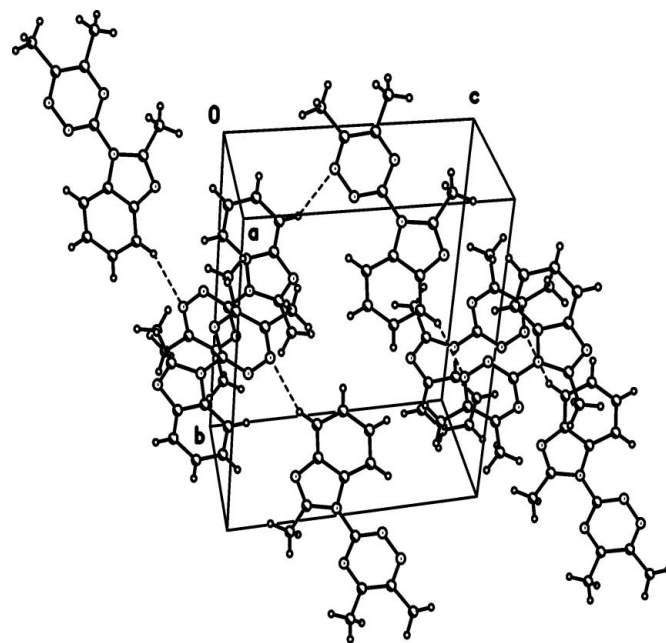


Figure 2

The crystal packing in (I). Hydrogen bonds are shown as dashed lines.

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