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#### **Key indicators**

Single-crystal X-ray study T = 295 K Mean  $\sigma$ (C–C) = 0.002 Å R factor = 0.036 wR factor = 0.105 Data-to-parameter ratio = 19.8

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

# Methyl 3-(4-methylbenzylidene)dithiocarbazate

Crystals of the title compound, C<sub>10</sub>H<sub>12</sub>N<sub>2</sub>S<sub>2</sub>, were obtained from a condensation reaction of methyl dithiocarbazate and 4methylbenzaldehyde. The essentially planar molecule exhibits an *E* configuration. Weak intermolecular  $N-H \cdot \cdot \cdot S$  hydrogen bonds link the molecules into centrosymmetric dimers.

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# Comment

Hydrazine and its derivatives have attracted our attention because of their biological applications (Okabe et al., 1993; Hu et al., 2001). As part of ongoing research into new anti-cancer compounds, the title compound, (I), has been prepared in our laboratory and its structure is presented here.



The molecule of (I) exhibits an *E* configuration. The molecular skeleton is essentially planar (Fig. 1), with the maximum deviation from the mean plane being 0.0442 (15) Å for atom C7. The N2-C9 bond distance (Table 1) is much shorter than the typical value for a C-N single bond (Orpen



The molecular structure of (I), with 50% probability displacement

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ellipsoids (arbitrary spheres for H atoms).

*et al.*, 1992), suggesting electron delocalization in the molecule of (I).

Weak intermolecular  $N-H\cdots S$  hydrogen bonds (Table 2) link the molecules into centrosymmetric dimers. The crystal packing (Fig. 2) is further stabilized by van der Waals forces.

# **Experimental**

Methyl dithiocarbazate was synthesized in the manner reported previously by Hu *et al.* (2001). Methyl dithiocarbazate (1.24 g, 10 mmol) and 4-methylbenzaldehyde (1.20 g, 10 mmol) were dissolved in ethanol (10 ml) and refluxed for 4 h. Fine colourless crystals appeared on cooling. These were separated and washed with cold water three times. Single crystals of (I) were obtained by recrystallization from absolute ethanol.

Z = 4

 $D_r = 1.319 \text{ Mg m}^{-3}$ 

Mo  $K\alpha$  radiation

Block, colourless

 $0.28 \times 0.24 \times 0.22~\text{mm}$ 

2557 independent reflections

1939 reflections with  $I > 2\sigma(I)$ 

H-atom parameters constrained

 $w = 1/[\sigma^2(F_o^2) + (0.0633P)^2]$ 

 $(\Delta/\sigma)_{\rm max} = 0.001$ 

 $\Delta \rho_{\rm max} = 0.19 \text{ e} \text{ Å}^{-3}$ 

 $\Delta \rho_{\rm min} = -0.30 \text{ e} \text{ Å}^{-3}$ 

where  $P = (F_0^2 + 2F_c^2)/3$ 

 $\mu = 0.43 \text{ mm}^-$ T = 295 (2) K

 $R_{\rm int} = 0.026$  $\theta_{\rm max} = 27.5^{\circ}$ 

## Crystal data

 $\begin{array}{l} C_{10}H_{12}N_2S_2\\ M_r = 224.33\\ \text{Monoclinic, } P_{21}/n\\ a = 4.604 \ (2) \ \text{\AA}\\ b = 11.049 \ (4) \ \text{\AA}\\ c = 22.3554 \ (18) \ \text{\AA}\\ \beta = 96.57 \ (2)^\circ\\ V = 1129.7 \ (6) \ \text{\AA}^3 \end{array}$ 

#### Data collection

Rigaku R-AXIS RAPID diffractometer ω scans Absorption correction: none 9833 measured reflections

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.036$   $wR(F^2) = 0.105$  S = 1.092557 reflections 129 parameters

### Table 1

Selected bond lengths (Å).

S1-C9	1.7441 (16)	N1-C8	1.273 (2)
S1-C10	1.7950 (19)	N1-N2	1.3783 (17)
S2-C9	1.6572 (15)	N2-C9	1.3352 (19)

## Table 2

Hydrogen-bond geometry (A, °).	
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$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$N2-H2A\cdots S2^{i}$	0.86	2.59	3.432 (2)	166
Summature and as (i)		i 4		

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

Methyl H atoms were placed in calculated positions, with C–H = 0.96 Å, and their torsion angles were refined to fit the electron density. They were treated as riding, with  $U_{iso}(H) = 1.5U_{eq}(C)$ . Other



#### Figure 2

The crystal packing of (I), viewed approximately down the *a* axis, showing the hydrogen-bonded (dashed lines) dimers.

H atoms were placed in calculated positions, with C-H = 0.93 and N-H = 0.86 Å, and refined as riding, with  $U_{iso}(H) = 1.2U_{eq}(C,N)$ .

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/ MSC, 2002); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1993); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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