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#### Kev indicators

Single-crystal X-ray study T = 298 K Mean  $\sigma$ (C–C) = 0.003 Å R factor = 0.043 wR factor = 0.123 Data-to-parameter ratio = 16.2

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

# Acetone 4-phenylthiosemicarbazone

In the title compound,  $C_{10}H_{13}N_3S$ , the isopropylidineamine and phenyl groups are *trans* and *cis*, respectively, with respect to the thione group across their C-N bonds. The molecule is stablized by intra- and intermolecular hydrogen bonds to form dimers parallel to (010).

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## Comment

the acetone-N(4)-phenylthiosemicarbazone-SnMe<sub>2</sub>Cl In complex, C12H16ClN3SSn, the ligand is chelated to the Sn atom in a bidentate manner via the thiono S and azomethine N atoms (de Sousa et al., 2004). The hydrazinic N atom is cis to the thiono S atom across the C-N bond. However, in the free ligand, (I), the azomethine atom N3 is trans to the thiono atom S1 (Fig. 1). Similar configurations have been observed in many thiosemicarbazones, such as acetone-4-methylthiocarbazone (Parsons et al., 2000). Thus, a change of configuration may have taken place during the complexation that led to the bidentate chelation.



The bond lengths and angles in (I) are in normal ranges (Allen et al., 1987), although the C7-N1 and C7-N2 bonds show slight variations compared with the values observed acetone-4-methylthiosemicarbazone in [1.325(3)]and 1.361 (2) Å, respectively; Parsons et al., 2000]. In contrast, the



### Figure 1

© 2005 International Union of Crystallography The molecular structure of (I), with 50% probability displacement ellipsoids. Dashed lines indicate the intramolecular hydrogen bonds.

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A packing diagram for (I). Dashed lines denote  $C-H \cdots S$  hydrogen bonds.

presence of a phenyl group attached to atom N1 causes the molecule to lose its overall planarity. The N1/S1/N2/C7, N3/ C8/C9/C10 and phenyl (C1-C6) fragments are all planar. The maximum deviation is 0.014 (2) Å for atom N3 in the N3/C8/ C9/C10 fragment. The central N1/S1/N2/C7 fragment makes dihedral angles of 30.61 (11) and 22.50  $(10)^{\circ}$  with the C1–C6 and N3/C8/C9/C10 fragments, respectively. The phenyl ring is inclined to the N3/C8/C9/C10 fragment at an angle of 43.96 (9)°.

There are two intramolecular hydrogen bonds in (I), namely N1-H1B···N3 and C1-H1A···S1, resulting in the formation of one pseduo-six-membered ring, C1-C6-N1- $C7-S1\cdots H1A$ , and one five-membered ring, N2-C7-N1-H1B···N3.

In the crystal structure, the molecules are linked to form dimers *via* N2-H2B···S1<sup>i</sup> and C9-H9A···S1<sup>i</sup> intermolecular hydrogen bonds (see Table 2 for symmetry code), parallel to the ac face (Fig. 2).

## **Experimental**

4-Phenylthiosemicarbazide (2 mmol) was added to a refluxing mixture containing excess acetone (10 ml) in methanol (50 ml). The mixture was further heated and stirred for about 1 h, and then left at room temperature in the open air to yield colourless crystals of (I) suitable for X-ray diffraction (yield 70%, m.p. 397-399 K).

#### Crystal data

$C_{10}H_{13}N_{3}S$	$D_{\rm r} = 1.302 {\rm Mg} {\rm m}^{-3}$
$M_r = 207.29$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 3919
a = 12.225 (3) Å	reflections
b = 7.618 (2) Å	$\theta = 1.7-26.5^{\circ}$
c = 11.639 (3) Å	$\mu = 0.27 \text{ mm}^{-1}$
$\beta = 102.660 \ (4)^{\circ}$	T = 298 (2) K
V = 1057.6 (5) Å <sup>3</sup>	Block, colourless
Z = 4	$0.43 \times 0.36 \times 0.31 \text{ mm}$

#### Data collection

Bruker SMART APEX CCD area- detector diffractometer	2187 independent reflections 2014 reflections with $I > 2\sigma(I)$
$\omega$ scans	$R_{\rm int} = 0.013$
Absorption correction: multi-scan	$\theta_{\rm max} = 26.5^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -9 \rightarrow 15$
$T_{\min} = 0.893, T_{\max} = 0.921$	$k = -9 \rightarrow 7$
5827 measured reflections	$l = -13 \rightarrow 14$
Refinement	
Refinement on $F^2$	$w = 1/[\sigma^2(F_0^2) + (0.0727P)^2]$

 $w = 1/[\sigma^2(F_0^2) + (0.0727P)^2]$  $R[F^2 > 2\sigma(F^2)] = 0.043$ wR(F<sup>2</sup>) = 0.123 + 0.3195P] where  $P = (F_0^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\rm max} < 0.001$ S = 1.06 $\Delta \rho_{\rm max} = 0.29 \text{ e} \text{ Å}^{-3}$ 2187 reflections  $\Delta \rho_{\rm min} = -0.39 \ {\rm e} \ {\rm \AA}^{-3}$ 135 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1 Selected geometric parameters (Å, °).

S1-C7	1.6825 (17)	N2-C7	1.348 (2)
N1-C7	1.343 (2)	N2-N3	1.392 (2)
N1-C6	1.425 (2)	N3-C8	1.276 (2)
C7-N1-C6	127.96 (14)	N1-C7-S1	125.76 (12)
C7-N2-N3	118.33 (14)	N2-C7-S1	119.50 (12)
C8-N3-N2	117.73 (14)		

Table 2		
Hydrogen-bond	geometry (A	Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1B \cdot \cdot \cdot N3$	0.86 (2)	2.13 (2)	2.581 (2)	112
$C1-H1A\cdots S1$	0.93	2.84	3.248 (2)	108
$N2-H2B\cdots S1^{i}$	0.83(2)	2.68 (2)	3.4969 (18)	168
$C9-H9A\cdots S1^{i}$	0.96	2.87	3.546 (2)	128

Symmetry codes: (ii) -x + 1, -y, -z + 1.

H atoms attached to N atoms were located in a difference map and refined isotropically. All other H atoms were located in a difference map and repositioned geometrically, with C-H = 0.93-0.96 Å, and allowed to ride on their parent C atoms, with  $U_{iso}(H) = 1.2U_{eq}(C)$ , or  $1.5U_{eq}(C)$  for CH<sub>3</sub>.

Data collection: SMART (Bruker, 2000); cell refinement: SAINT (Bruker, 2000); data reduction: SAINT; 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, PARST (Nardelli, 1995) and PLATON (Spek, 2003).

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