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#### **Key indicators**

Single-crystal X-ray study T = 298 K Mean  $\sigma$ (C–C) = 0.005 Å R factor = 0.039 wR factor = 0.110 Data-to-parameter ratio = 20.4

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

# [*N*,*N*-Dimethyl-*N*'-(2-pyridylmethylene)ethane-1,2-diamine]dithiocyanatocopper(II)

In the title Schiff base compound,  $[Cu(NCS)_2(C_{10}H_{15}N_3)]$ , the Cu<sup>II</sup> atom is five-coordinated by three N atoms from the Schiff base ligand and by another two N atoms from two thiocyanate anions. The coordination geometry is best described as distorted square-pyramidal. In the crystal structure, there are no significant intermolecular interactions.

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### Comment

Investigations of copper(II) complexes have been of great interest in coordination chemistry (Dalai *et al.*, 2002; Bhaduri *et al.*, 2003). As an extension of work on the structural characterization of copper(II) complexes, we report here the structure of the title compound, (I).



Compound (I) (Fig. 1) is an electronically neutral mononuclear copper(II) compound. Selected bond distances and angles are given in Table 1. Atom Cu1 is coordinated by three N atoms from the Schiff base ligand and another two N atoms from the thiocyanate anions. Atom N4, of one of the thiocyante anions, acts as the apical atom of a highly distorted square-pyramidal geometry, as defined by the  $\tau$  value ( $\tau =$ 0.28) calculated according to the literature (Addison *et al.*, 1984).

The distortion of the square pyramid is also revealed by the bond angles between the apical and basal donor atoms [96.69 (11)–113.52 (11)°], which show a considerable deviation from the ideal 90° angle in a regular square pyramid. The smallest bond angles for the basal donor atoms [75.43 (10)° for N1–Cu1–N2 and 78.02 (10)° for N2–Cu1–N3] correlate with the strained ligand bite angle for the five-membered chelate rings. All the bond lengths involving atom Cu1 are in normal ranges.

In the crystal structure, the molecules pack in columns along the b axis, as shown in Fig. 2. There are no significant intermolecular interactions in the crystal structure.

## **Experimental**

Pyridylaldehyde (0.1 mmol, 10.7 mg), N,N-dimethylethane-1,2-diamine (0.1 mmol, 8.8 mg), ammonium thiocyanate (0.2 mmol, 15.2 mg) and Cu(CH<sub>3</sub>COO)<sub>2</sub>·H<sub>2</sub>O (0.1 mmol, 19.9 mg) were

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dissolved in methanol (10 ml). The mixture was stirred at room temperature for 1 h to give a clear blue solution. After keeping the solution in air for 5 d, blue block-shaped crystals were formed.

 $D_r = 1.453 \text{ Mg m}^{-3}$ 

Cell parameters from 4575

 $0.23 \times 0.22 \times 0.18 \text{ mm}$ 

3734 independent reflections 2649 reflections with  $I > 2\sigma(I)$ 

Mo  $K\alpha$  radiation

reflections

 $\theta=2.4{-}24.7^\circ$  $\mu = 1.59 \text{ mm}^{-1}$ 

T = 298 (2) K

Block, blue

 $R_{\rm int} = 0.039$  $\theta_{\rm max} = 27.5^{\circ}$ 

 $h = -13 \rightarrow 13$ 

 $k = -19 \rightarrow 19$ 

 $l = -13 \rightarrow 13$ 

#### Crystal data

[Cu(NCS)<sub>2</sub>(C<sub>10</sub>H<sub>15</sub>N<sub>3</sub>)]  $M_{\rm r} = 356.95$ Monoclinic,  $P2_1/n$ a = 10.216(1) Åb = 15.053 (2) Å c = 10.610(1) Å  $\beta = 91.164 \ (2)^{\circ}$ V = 1631.3 (3) Å<sup>3</sup> Z = 4

#### Data collection

Bruker SMART CCD area-detector diffractometer  $\omega$  scans Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  $T_{\min} = 0.703, T_{\max} = 0.755$ 18 130 measured reflections

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0501P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.039$	+ 0.4185P]
$wR(F^2) = 0.110$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.02	$(\Delta/\sigma)_{\rm max} < 0.001$
3734 reflections	$\Delta \rho_{\rm max} = 0.92 \ {\rm e} \ {\rm \AA}^{-3}$
183 parameters	$\Delta \rho_{\rm min} = -0.24 \text{ e} \text{ Å}^{-3}$
H-atom parameters constrained	

## Table 1

Selected	geometric	parameters	(Å,	°).	•
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Cu1-N5	1.958 (3)	Cu1-N1	2.211 (3)
Cu1-N4	1.963 (3)	Cu1-N3	2.222 (3)
Cu1-N2	2.061 (2)		
N5-Cu1-N4	111.20 (14)	N2-Cu1-N1	75.43 (10)
N5-Cu1-N2	135.15 (13)	N5-Cu1-N3	96.66 (11)
N4-Cu1-N2	113.52 (11)	N4-Cu1-N3	101.31 (11)
N5-Cu1-N1	96.34 (11)	N2-Cu1-N3	78.02 (10)
N4-Cu1-N1	96.69 (11)	N1-Cu1-N3	152.21 (9)

All H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C-H = 0.93-0.97 Å and  $U_{iso}(H) = 1.2$  or  $1.5U_{eq}(C)$ .

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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### Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.



#### Figure 2

The crystal packing of (I), viewed along the a axis.

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