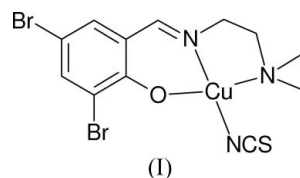


**{2,4-Dibromo-6-[(2-dimethylaminoethyl-
imino)methyl]phenolato}(thiocyanato)-
copper(II)****Nong Wang,* Xiang-En Han and
Xiao-Guang Wen**School of Chemical and Biological Engineering,
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People's Republic of ChinaCorrespondence e-mail:
wangnong05@163.com**Key indicators**Single-crystal X-ray study
 $T = 298\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.008\text{ \AA}$
 R factor = 0.044
 wR factor = 0.105
Data-to-parameter ratio = 17.4For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the mononuclear copper(II) title compound, $[\text{Cu}(\text{C}_{11}\text{H}_{13}\text{Br}_2\text{N}_2\text{O})(\text{NCS})]$, the Cu^{II} atom is four-coordinated by one imine N, one amine N, and one phenolate O atom of the Schiff base ligand, and by one N atom of a thiocyanate anion in a square planar geometry. In the crystal structure, adjacent molecules are linked through intermolecular $\text{C}-\text{H}\cdots\text{Br}$ hydrogen bonds, forming centrosymmetric dimers.

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An extensive effort has been made to prepare and characterize a variety of coordination complexes in an attempt to model the physical and chemical behaviour of copper-containing enzymes (Reddy *et al.*, 2000). The peculiarity of copper lies in its ability to form complexes with coordination numbers of four, five, and six (Ray *et al.*, 2003; Arnold *et al.*, 2003; Raptopoulou *et al.*, 1998). As a continuation of our own work in this area (Wang & Li, 2005), the title compound, (I), a copper(II) complex is reported here.



Compound (I) is mononuclear, as shown in Fig. 1. The Cu atom is four-coordinated by one imine N, one amine N, and one phenolate O atom of the Schiff base ligand, and by one N atom of a thiocyanate anion, resulting in distorted square

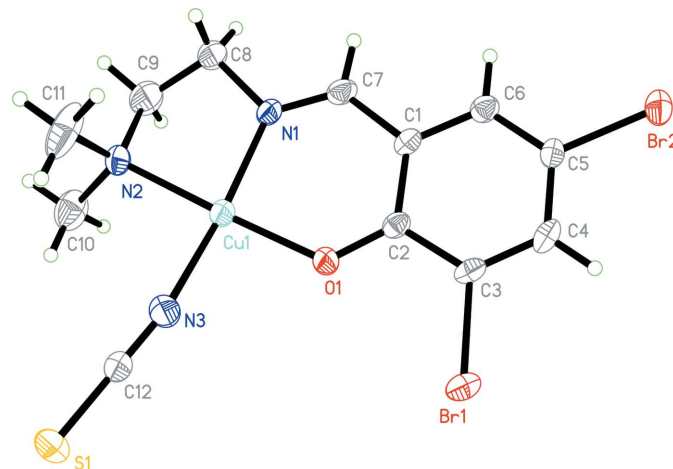


Figure 1
The structure of (I), showing 30% displacement ellipsoids (arbitrary spheres for the H atoms).

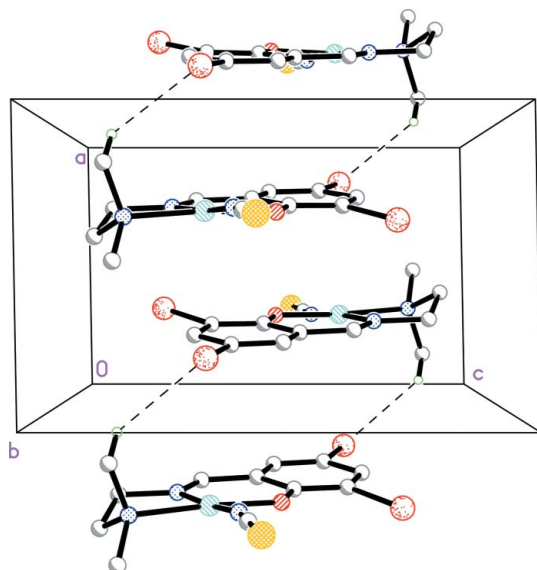


Figure 2
Part of the packing of (I). Intermolecular C—H···Br interactions are shown as dashed lines.

planar CuON₃ coordination (Table 1). The N1—Cu1—N2 bond angle deviates by some 5.61 (18)° from 90° as a result of the strain created by the five-membered chelate ring Cu1/N1/C8/C9/N2.

In the crystal structure, adjacent molecules are linked through intermolecular C—H···Br interactions (Table 2), forming centrosymmetric dimers (Fig. 2).

Experimental

3,5-Dibromosalicylaldehyde (0.1 mmol, 28.0 mg), *N,N*-dimethylethane-1,2-diamine (0.1 mmol, 8.8 mg), NH₄NCS (0.1 mmol, 7.6 mg) and Cu(CH₃COO)₂·H₂O (0.1 mmol, 19.9 mg) were dissolved in MeOH (15 ml). The mixture was stirred at room temperature for 1 h to give a red solution. The resulting solution was allowed to stand in air for 13 d, and red needle-shaped crystals of (I) were formed.

Crystal data

[Cu(C ₁₁ H ₁₃ Br ₂ N ₂ O)(NCS)]	<i>D</i> _x = 2.028 Mg m ⁻³
<i>M</i> _r = 470.67	Mo <i>K</i> α radiation
Monoclinic, <i>P</i> ₂ ₁ / <i>n</i>	Cell parameters from 1683 reflections
<i>a</i> = 7.146 (1) Å	<i>θ</i> = 2.5–24.9°
<i>b</i> = 19.213 (3) Å	<i>μ</i> = 6.73 mm ⁻¹
<i>c</i> = 11.229 (2) Å	<i>T</i> = 298 (2) K
<i>β</i> = 91.026 (2)°	Needle, red
<i>V</i> = 1541.5 (4) Å ³	0.42 × 0.08 × 0.04 mm
<i>Z</i> = 4	

Data collection

Bruker SMART CCD diffractometer	3180 independent reflections
<i>ω</i> scans	2014 reflections with <i>I</i> > 2σ(<i>I</i>)
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	<i>R</i> _{int} = 0.067
<i>T</i> _{min} = 0.164, <i>T</i> _{max} = 0.775	<i>θ</i> _{max} = 26.5°
12315 measured reflections	<i>h</i> = -8 → 8
	<i>k</i> = -24 → 23
	<i>l</i> = -14 → 14

Refinement

Refinement on <i>F</i> ²	$w = 1/[\sigma^2(F_o^2) + (0.0345P)^2 + 0.8169P]$
$R[F^2 > 2\sigma(F^2)] = 0.044$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.105$	(Δ/σ) _{max} < 0.001
<i>S</i> = 1.01	$\Delta\rho_{max} = 0.60 \text{ e \AA}^{-3}$
3180 reflections	$\Delta\rho_{min} = -0.52 \text{ e \AA}^{-3}$
183 parameters	
H-atom parameters constrained	

Table 1

Selected geometric parameters (Å, °).

Cu1—O1	1.908 (3)	Cu1—N1	1.932 (4)
Cu1—N3	1.927 (5)	Cu1—N2	2.055 (4)
O1—Cu1—N3	91.61 (18)	O1—Cu1—N2	174.47 (18)
O1—Cu1—N1	92.55 (16)	N3—Cu1—N2	91.87 (19)
N3—Cu1—N1	173.3 (2)	N1—Cu1—N2	84.39 (18)

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
C11—H11A···Br2 ⁱ	0.96	2.88	3.676 (5)	141

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

H atoms were placed in idealized positions and constrained to ride on their parent atoms, with C—H distances in the range 0.93–0.97 Å, and with *U*_{iso}(H) = 1.2 or 1.5 times *U*_{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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