

## Azido{2,4-dichloro-6-[2-(diethylamino)-ethyliminomethyl]phenolato}copper(II)

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## Key indicators

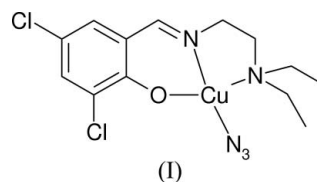
Single-crystal X-ray study  
 $T = 298$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å  
 $R$  factor = 0.033  
 $wR$  factor = 0.091  
Data-to-parameter ratio = 16.8For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

In the mononuclear copper(II) compound,  $[\text{Cu}(\text{C}_{13}\text{H}_{17}\text{Cl}_2\text{N}_2\text{O})(\text{N}_3)]$ , the  $\text{Cu}^{\text{II}}$  ion is four-coordinated by one imine N, one amine N, and one phenolate O atom of the Schiff base ligand, and by one terminal N atom of an azide anion, forming a distorted square-planar coordination.

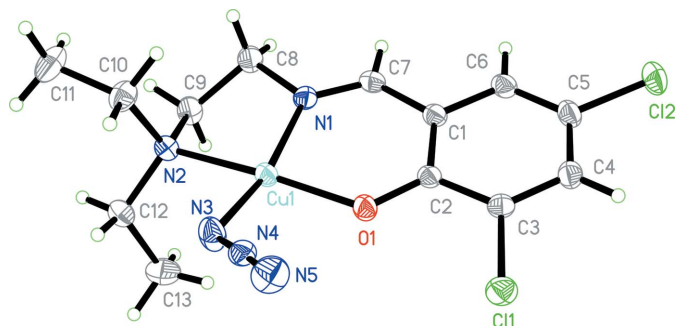
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## Comment

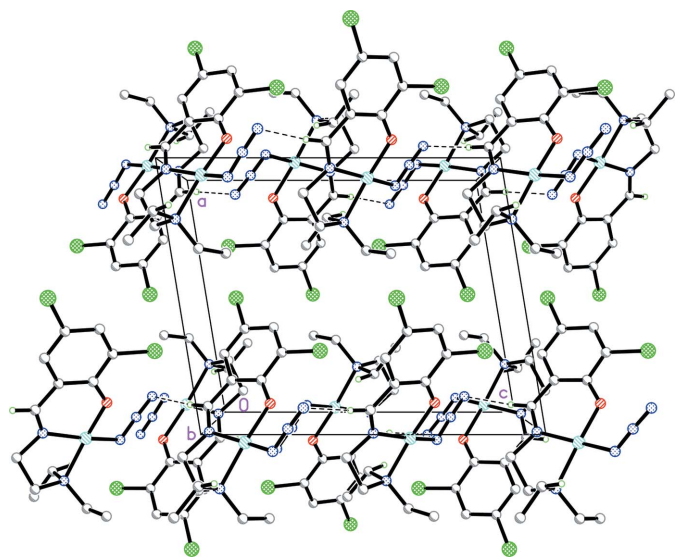
Schiff base ligands have played an important role in the development of coordination chemistry as they readily form stable complexes with most transition metal ions (Pal *et al.*, 2005; Ueno *et al.*, 2004; Hou, 2005). During the last few years, there has been a great effort to identify the biological role of copper, primarily through techniques associated with the interface of biology/biochemistry/coordination chemistry (Collinson & Fenton, 1996; Hossain *et al.*, 1996; Tarafder *et al.*, 2002). It appears that the biological role of copper is primarily in redox reactions and as a biological catalyst, although much remains to be understood (Musie *et al.*, 2003; García-Raso *et al.*, 2003). An extensive effort has been made to prepare and characterize a variety of copper(II) 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 number four, five, and six (Ray *et al.*, 2003; Arnold *et al.*, 2003; Raptopoulou *et al.*, 1998). As part of our investigations in this area (Wei, 2005*a,b*), we report here a new mononuclear copper(II) complex, (I) (Fig. 1).



Complex (I) is a mononuclear copper(II) compound. The  $\text{Cu}^{\text{II}}$  ion is four-coordinated by one imine N, one amine N, and one phenolate O atom of a Schiff base ligand, and by one terminal N atom of an azide anion, forming a distorted square-planar coordination. All bond lengths are in normal ranges (Allen *et al.*, 1987). The bond lengths (Table 1) related to the  $\text{Cu}^{\text{II}}$  ion are comparable to the corresponding values observed in other Schiff base copper(II) complexes (Hebbachi & Benali-Cherif, 2005; Butcher *et al.*, 2003). The bond angles around the central metal ion show some deviations from ideal square-planar geometry, ranging from  $84.35(8)$  to  $93.64(7)^\circ$ . The two *trans* bond angles are  $164.30(9)$  and  $171.31(7)^\circ$ , respectively. In the crystal structure, the molecules are linked



**Figure 1**  
The 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 *b* axis. Dashed lines indicate hydrogen bonds.

through intermolecular C—H...N hydrogen bonds (Table 2), forming chains running along the *c* axis (Fig. 2).

## Experimental

3,5-Dichlorosalicylaldehyde (1.0 mmol, 192.1 mg), *N,N'*-diethylethane-1,2-diamine (1.0 mmol, 116.2 mg),  $\text{NaN}_3$  (1.0 mmol, 65.3 mg) and  $\text{Cu}(\text{CH}_3\text{COO})_2 \cdot \text{H}_2\text{O}$  (1.0 mmol, 199.1 mg) were dissolved in an MeOH solution (150 ml). The mixture was refluxed at 340 K for about 1 h to give a clear blue solution. After keeping the cooled resulting solution in the dark for 8 d, blue block-shaped crystals were formed.

### Crystal data

$[\text{Cu}(\text{C}_{13}\text{H}_{17}\text{Cl}_2\text{N}_2\text{O})(\text{N}_3)]$   
 $M_r = 393.76$   
 Monoclinic,  $P2_1/c$   
 $a = 10.723$  (2) Å  
 $b = 11.506$  (2) Å  
 $c = 13.192$  (3) Å  
 $\beta = 99.32$  (3)°  
 $V = 1606.1$  (6) Å<sup>3</sup>  
 $Z = 4$

$D_x = 1.628$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 Cell parameters from 5676 reflections  
 $\theta = 2.4$ – $27.3^\circ$   
 $\mu = 1.70$  mm<sup>-1</sup>  
 $T = 298$  (2) K  
 Block, blue  
 $0.37 \times 0.18 \times 0.12$  mm

### Data collection

Bruker SMART CCD area-detector diffractometer  
 $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
 $T_{\text{min}} = 0.572$ ,  $T_{\text{max}} = 0.822$   
 7787 measured reflections

3383 independent reflections  
 2882 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.024$   
 $\theta_{\text{max}} = 27.0^\circ$   
 $h = -13 \rightarrow 13$   
 $k = -14 \rightarrow 14$   
 $l = -14 \rightarrow 16$

### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.033$   
 $wR(F^2) = 0.091$   
 $S = 1.07$   
 3383 reflections  
 201 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0534P)^2 + 0.0366P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.34 \text{ e } \text{Å}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.55 \text{ e } \text{Å}^{-3}$

**Table 1**

Selected geometric parameters (Å, °).

Cu1—O1	1.891 (2)	Cu1—N3	1.945 (2)
Cu1—N1	1.933 (2)	Cu1—N2	2.066 (2)
O1—Cu1—N1	93.64 (7)	O1—Cu1—N2	171.31 (7)
O1—Cu1—N3	92.56 (8)	N1—Cu1—N2	84.35 (8)
N1—Cu1—N3	164.30 (9)	N3—Cu1—N2	91.55 (8)

**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>
C7—H7...N5 <sup>i</sup>	0.93	2.53	3.448 (3)	168
C10—H10B...N3	0.97	2.61	3.149 (3)	115

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

All 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  $U_{\text{iso}}(\text{H}) = 1.2$  or  $1.5U_{\text{eq}}(\text{C})$ .

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINTE* (Bruker, 1998); data reduction: *SAINTE*; 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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