

Chlorido{2,4-dichloro-6-[(2-diethylamino)ethylimino)methyl]phenolato}copper(II)

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Key indicators

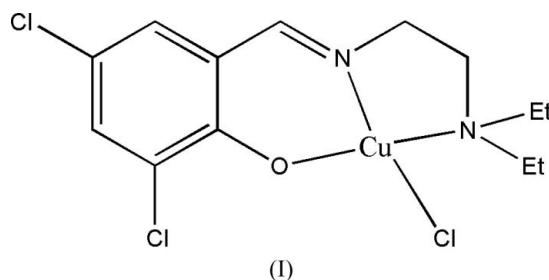
Single-crystal X-ray study
 $T = 298$ K
Mean $\sigma(\text{C}-\text{C}) = 0.008$ Å
 R factor = 0.055
 wR factor = 0.145
Data-to-parameter ratio = 19.3For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the title mononuclear copper(II) complex, $[\text{Cu}(\text{C}_{13}\text{H}_{17}\text{Cl}_2\text{N}_2\text{O})\text{Cl}]$, the Cu^{II} ion is four-coordinated by one Schiff base ligand and one chloride anion in a slightly distorted square-planar geometry.

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Comment

Copper(II) complexes derived from Schiff base ligands are of interest with regard to their structures and applications in coordination chemistry and materials chemistry. Recently, we have reported the crystal structures of a few Schiff base metal complexes (You, Han *et al.*, 2006; You *et al.*, 2006*a,b*). As an extension of this work, the crystal structure of the title mononuclear copper(II) complex, (I) (Fig. 1), is reported here.



The Cu^{II} ion in (I) is four-coordinated by the *NNO* donor set of the Schiff base ligand, and by one terminal Cl^- anion in a slightly distorted square-planar geometry. The bond lengths (Table 1) are comparable to those in other Schiff base-copper(II) complexes (You, 2006; You & Zhu, 2006; You, Jiao *et al.*, 2006). The two *trans* angles at the metal centre are 170.22 (15) and 173.11 (13) $^\circ$; all other angles around Cu1 are close to 90° , ranging from 83.44 (16) to 94.56 (12) $^\circ$, indicating a slightly distorted square-planar geometry for Cu1.

In the crystal structure, molecules are linked through intermolecular $\text{C}-\text{H}\cdots\text{Cl}$ hydrogen bonds (Table 2), forming a chain along the $[101]$ direction.

Experimental

3,5-Dichloro-2-hydroxybenzaldehyde and *N,N*-diethylethane-1,2-diamine were available commercially and were used without further purification. 3,5-Dichloro-2-hydroxybenzaldehyde (0.1 mmol, 19.2 mg) and *N,N*-diethylethane-1,2-diamine (0.1 mmol, 11.6 mg) were dissolved in methanol (10 ml). The mixture was stirred at room temperature for 10 min, giving a clear orange solution. To this solution was added an aqueous solution (1 ml) of $\text{CuCl}_2\cdot 2\text{H}_2\text{O}$ (0.1 mmol, 17.0 mg) with stirring. The resulting mixture was stirred for a further 10 min at room temperature. After allowing the filtrate to stand in air for 8 d, blue needle-shaped crystals were formed.

Crystal data

[Cu(C₁₃H₁₇Cl₂N₂O)Cl] $M_r = 387.18$ Monoclinic, $P2_1/n$ $a = 7.2839$ (18) Å $b = 11.939$ (3) Å $c = 17.958$ (4) Å $\beta = 93.687$ (3)° $V = 1558.4$ (6) Å³ $Z = 4$ Mo $K\alpha$ radiation $\mu = 1.91$ mm⁻¹ $T = 298$ (2) K

0.30 × 0.12 × 0.08 mm

Data collection

Bruker SMART 1000 CCD area-detector diffractometer

Absorption correction: multi-scan (SADABS; Sheldrick, 1996)

 $T_{\min} = 0.598$, $T_{\max} = 0.862$

12912 measured reflections

3537 independent reflections

2908 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.037$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.055$ $wR(F^2) = 0.145$ $S = 1.16$

3537 reflections

183 parameters

H-atom parameters constrained

 $\Delta\rho_{\text{max}} = 0.70$ e Å⁻³ $\Delta\rho_{\text{min}} = -0.46$ e Å⁻³

Table 1

Selected geometric parameters (Å, °).

Cu1—O1	1.912 (3)	Cu1—N2	2.097 (4)
Cu1—N1	1.942 (4)	Cu1—Cl3	2.2310 (14)
O1—Cu1—N1	92.13 (15)	O1—Cu1—Cl3	90.81 (11)
O1—Cu1—N2	170.22 (15)	N1—Cu1—Cl3	173.11 (13)
N1—Cu1—N2	83.44 (16)	N2—Cu1—Cl3	94.56 (12)

Table 2

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C4—H4 \cdots Cl3 ⁱ	0.93	2.75	3.670 (6)	171

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

H atoms were placed in idealized positions and made to ride on their parent atoms, with C—H = 0.93–0.97 Å and $U_{\text{iso}}(\text{H}) = 1.2$ or $1.5U_{\text{eq}}(\text{C})$.

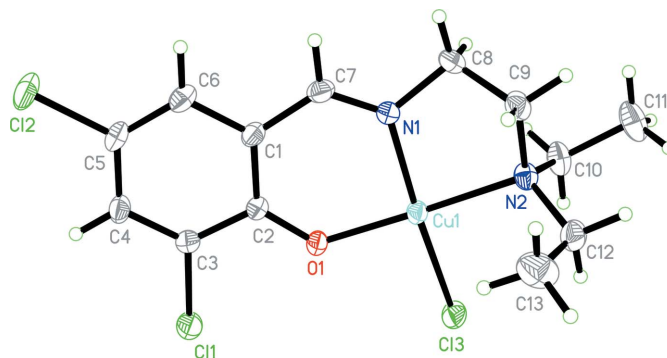


Figure 1

The molecular structure of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.

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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