

Yu-Xi Sun,^{a*} Mei Qin,^a Ke-Qiang Gu,^a Guang Yang^b and Fei Xie^a^aDepartment of Chemistry, Qufu Normal University, Qufu 273165, People's Republic of China, and ^bDepartment of Capital Management, Qufu Normal University, Qufu 273165, People's Republic of China

Correspondence e-mail: yuxisun@163.com

Key indicators

Single-crystal X-ray study
T = 291 K
Mean $\sigma(\text{C}-\text{C}) = 0.014 \text{ \AA}$
Disorder in solvent or counterion
R factor = 0.092
wR factor = 0.115
Data-to-parameter ratio = 16.0For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

Bis{2-[3-(cyclohexylamino)propyliminomethyl]-4-nitrophenolato}copper(II) diperchlorate

The title compound, $[\text{Cu}(\text{C}_{16}\text{H}_{23}\text{N}_3\text{O}_3)_2](\text{ClO}_4)_2$, is a mononuclear copper(II) complex. The Cu^{II} atom is four-coordinated by two imine N atoms and two phenolate O atoms from two Schiff base ligands, forming a slightly distorted square-planar coordination. A perchlorate anion is disordered over two orientations. In the crystal structure, the ions are linked through intermolecular $\text{N}-\text{H} \cdots \text{O}$ hydrogen bonds, forming a three-dimensional network.

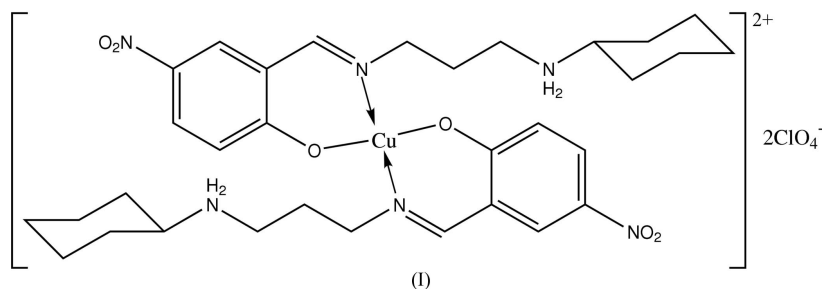
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Comment

Transition metal compounds are present in the active sites of several important classes of metalloproteins. The study of Schiff base compounds is of great interest in various aspects of chemistry (Downing & Urbach, 1969; Ganeshpure *et al.*, 1996; Bosnich, 1968; Costes *et al.*, 1995). As an extension of work on the structural characterization of Schiff base and copper(II) complexes (Sun, 2005; Sun *et al.*, 2005), a mononuclear copper(II) complex, (I), as a perchlorate salt is reported here.



The molecular structure of (I) is illustrated in Fig. 1, and selected bond distances and angles are given in Table 1. In the cation of (I), the Cu^{II} atom is four-coordinated by two phenolate O and two imine N atoms from two 2-[3-(cyclohexylamino)propyliminomethyl]-4-nitrophenol ligands. The four coordinating atoms around Cu are approximately coplanar, giving a square-planar coordination with an average deviation of 0.032 (5) \AA ; the Cu atom lies 0.021 (2) \AA above this plane. The two *trans* angles at Cu1 are 179.2 (3) and 177.0 (3)°. The other angles are close to 90°, ranging from 89.2 (2) to 90.8 (2)°, which indicates a slightly distorted square-planar coordination of the Cu atom. The Cu1—O1 and Cu1—O4 bonds (Table 1) are comparable to the corresponding value [1.902 (2) \AA] observed in [4-bromo-2-(pyridin-2-yl-methylaminomethyl)phenolato](methanol)copper(II) perchlorate (Sun, 2005) and the value [1.896 (2) \AA] in catenapoly[[[4-bromo-2-(2-pyridylmethyliminomethyl)phenolato]-copper(II)]- μ -chloro] complex (Sun *et al.*, 2005). However, Cu1—N1 and Cu1—N4 are longer than the corresponding

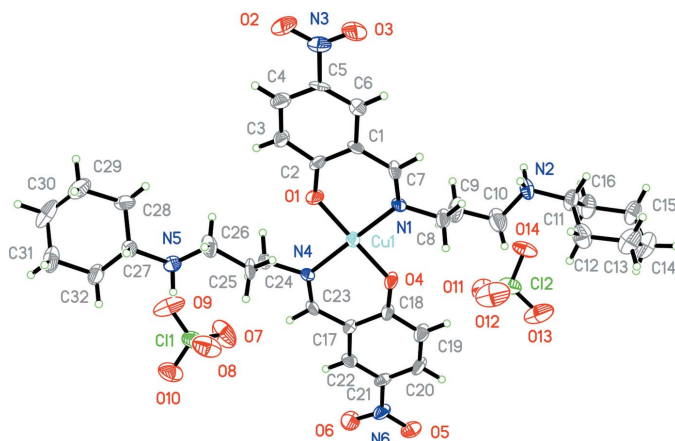


Figure 1
The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. The minor disorder component is not shown.

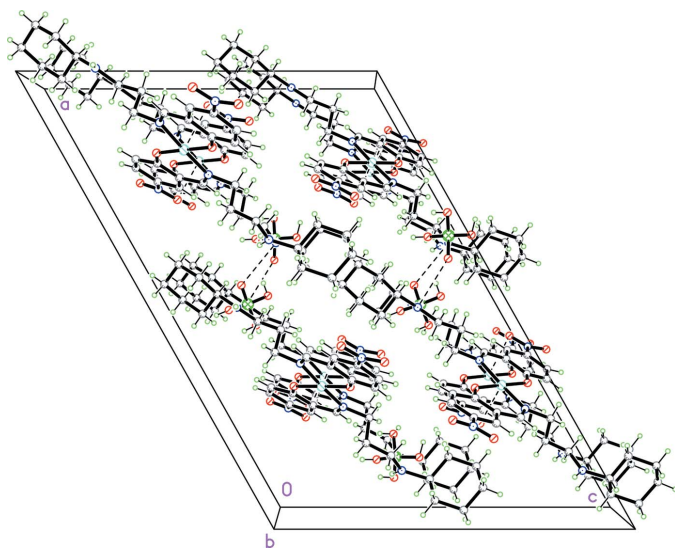


Figure 2
The crystal packing of (I) viewed along the *b* axis. Hydrogen bonds are shown as dashed lines (details are given in Table 2).

values [1.939 (3) Å (Sun, 2005) and 1.961 (3) Å (Sun *et al.*, 2005)].

In the crystal packing, the ions are linked *via* N—H...O hydrogen bonds, involving the uncoordinated perchlorate anions and NH₂ groups, to form a three-dimensional network (Table 2 and Fig. 2).

Experimental

For the preparation of the complex, 5-nitrosalicylaldehyde (0.2 mmol, 33.4 mg) and *N*-cyclohexyl-1,3-diaminopropane (0.2 mmol, 31.2 mg) were dissolved in MeOH (10 ml). The mixture was stirred at room temperature for 10 min to give a clear yellow solution, to which was added an aqueous solution (5 ml) of Cu(ClO₄)₂·6H₂O (0.1 mmol, 37.1 mg) with stirring. The mixture was stirred for another 10 min at room temperature and then filtered. The filtrate was set aside for crystallization. On slow evaporation in air for 13 d, blue block-shaped crystals were formed.

Crystal data

[Cu(C₁₆H₂₃N₃O₃)₂](ClO₄)₂
M_r = 873.19
 Monoclinic, *Cc*
a = 26.915 (3) Å
b = 8.9166 (11) Å
c = 18.505 (2) Å
 β = 119.443 (2)°
V = 3867.5 (8) Å³
Z = 4

D_x = 1.500 Mg m⁻³
 Mo *K*α radiation
 Cell parameters from 2005 reflections
 θ = 2.4–27.7°
 μ = 0.78 mm⁻¹
T = 291 (2) K
 Block, blue
 0.25 × 0.16 × 0.03 mm

Data collection

Bruker SMART APEX area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.860, *T_{max}* = 0.977
 15254 measured reflections

8145 independent reflections
 3489 reflections with *I* > 2σ(*I*)
R_{int} = 0.105
 θ_{max} = 27.5°
h = -33 → 34
k = -11 → 11
l = -22 → 23

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.092
wR (*F*²) = 0.115
S = 0.95
 8145 reflections
 509 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0221P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.004$
 $\Delta\rho_{\text{max}} = 0.72 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.39 \text{ e \AA}^{-3}$
 Absolute structure: Flack (1983),
 4656 Friedel pairs
 Flack parameter: 0.00 (3)

Table 1

Selected geometric parameters (Å, °).

Cu1—O4	1.889 (5)	Cu1—N1	1.991 (6)
Cu1—O1	1.891 (6)	Cu1—N4	2.005 (6)
O4—Cu1—O1	179.2 (3)	O4—Cu1—N4	90.8 (2)
O4—Cu1—N1	89.2 (2)	O1—Cu1—N4	89.6 (3)
O1—Cu1—N1	90.4 (2)	N1—Cu1—N4	177.0 (3)

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>
N2—H2A...O11 ⁱ	0.90	2.41	3.147 (14)	139
N2—H2A...O13 ⁱ	0.90	2.59	3.321 (16)	139
N2—H2B...O10 ⁱⁱ	0.90	2.08	2.944 (11)	161
N2—H2B...O8 ⁱⁱⁱ	0.90	2.46	3.185 (10)	137
N5—H5A...O14 ⁱⁱⁱ	0.90	2.34	2.959 (14)	126
N5—H5A...O8	0.90	2.66	3.311 (10)	131
N5—H5B...O5 ^{iv}	0.90	2.48	3.336 (10)	158
N5—H5B...O9	0.90	2.59	3.209 (10)	127

Symmetry codes: (i) *x*, *y* - 1, *z*; (ii) *x* - ½, *y* - ½, *z*; (iii) *x* + ½, *y* - ½, *z*; (iv) *x*, -*y* + 1, *z* - ½

All H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms with C—H distances of 0.93–0.98 Å and N—H distances of 0.90 Å, and with *U*_{iso}(H) = 1.2*U*_{eq}(C,N). The O atoms of one of the perchlorate anions are disordered over two sites [occupancies 0.559 (18)/0.441 (18)].

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); 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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