

Cui-Jin Li,^a Wei Li,^b Ming-Liang Tong^a and Seik Weng Ng^{c*}

^aSchool of Chemistry and Chemical Engineering, Sun Yat-Sen University, Guangzhou 510275, People's Republic of China, ^bDepartment of Chemistry, Sun Yat-Sen University, Guangzhou 510275, People's Republic of China, and ^cDepartment of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia

Correspondence e-mail: seikweng@um.edu.my

Key indicators

Single-crystal X-ray study
T = 293 K
Mean $\sigma(C-C) = 0.003 \text{ \AA}$
R factor = 0.037
wR factor = 0.119
Data-to-parameter ratio = 18.1

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

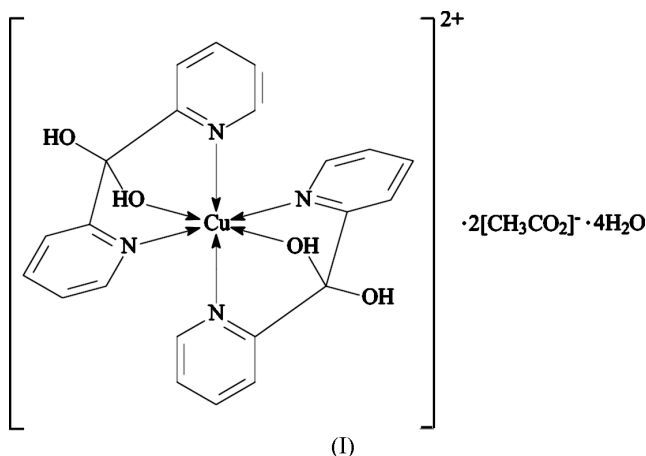
A C-centered monoclinic modification of bis(di-2-pyridylmethanediol- $\kappa^3 N, O, N'$)-copper(II) diacetate tetrahydrate

Di-2-pyridyl ketone undergoes hydrolysis when reacted with copper(II) acetate to form the title compound, $[\text{Cu}(\text{C}_{11}\text{H}_{10}\text{N}_2\text{O}_2)_2](\text{C}_2\text{H}_3\text{O}_2)_2 \cdot 4\text{H}_2\text{O}$. The crystal structure consists of octahedral cations that are linked to the anions and to the uncoordinated water molecules, giving rise to a three-dimensional network structure. This C-centered monoclinic modification is less compact than the primitive monoclinic modification reported by Reinoso *et al.* [(2003). *Acta Cryst. E* **59**, m548–m550]. The Cu atom is located at a center of inversion.

Received 8 December 2004
Accepted 21 December 2004
Online 8 January 2005

Comment

A previous synthesis of the di-2-pyridylmethanediol derivative of nickel dilactate in an organic aqueous medium gave the complex as the anhydrous dilactate (Li *et al.*, 2005). A similar synthesis with copper acetate has afforded the expected compound, which crystallizes as a tetrahydrate, (I) (Fig. 1).

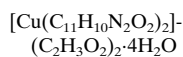


The crystal structure consists of bis(di-2-pyridylmethanediol)copper(II) cations, acetate anions and uncoordinated water molecules. The Cu atom, which is located at a center of inversion, is chelated by two pyridyl N atoms and a hydroxyl O atom of the ligand in an octahedral environment. The bond dimensions involving the Cu atom are not significantly different from those found in the primitive monoclinic modification (Reinoso *et al.*, 2003); however, the C-centered modification is much less compact, as noted from the lower density (1.366 Mg m^{-3} compared with 1.408 Mg m^{-3} for the primitive modification). The structure is consolidated by hydrogen bonds that link the cations, anions and water molecules into an intricate network motif. Both water molecules furnish only one such bond each (Table 2).

Experimental

Di-2-pyridyl ketone (0.091 g, 0.5 mmol) suspended in water (5 ml) was added to an acetonitrile/water solution (4:1 v/v) of copper(II) acetate monohydrate (0.100 g, 0.5 mmol). The mixture was heated to dissolve the reagents. Purple prismatic crystals separated from the solution in about 50% yield after several days.

Crystal data



$M_r = 658.11$

Monoclinic, $C2/c$

$a = 23.557(2) \text{ \AA}$

$b = 8.5744(6) \text{ \AA}$

$c = 15.848(1) \text{ \AA}$

$\beta = 91.983(1)^\circ$

$V = 3199.2(4) \text{ \AA}^3$

$Z = 4$

$D_x = 1.366 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

Cell parameters from 9126 reflections

$\theta = 2.5\text{--}27.0^\circ$

$\mu = 0.75 \text{ mm}^{-1}$

$T = 293(2) \text{ K}$

Prism, purple

$0.36 \times 0.34 \times 0.28 \text{ mm}$

Data collection

Rigaku Mercury CCD diffractometer

ω scans

Absorption correction: multi-scan (*CrystalClear*; Rigaku/MS, 2002)

$T_{\min} = 0.772$, $T_{\max} = 0.811$

9126 measured reflections

3587 independent reflections

3064 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.017$

$\theta_{\max} = 27.5^\circ$

$h = -30 \rightarrow 29$

$k = -10 \rightarrow 7$

$l = -19 \rightarrow 20$

Refinement

Refinement on F^2

$R[F^2 > 2\sigma(F^2)] = 0.037$

$wR(F^2) = 0.119$

$S = 1.07$

3587 reflections

198 parameters

H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0725P)^2 + 1.3743P]$

where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{\max} = 0.001$

$\Delta\rho_{\max} = 0.47 \text{ e \AA}^{-3}$

$\Delta\rho_{\min} = -0.50 \text{ e \AA}^{-3}$

Table 1

Selected geometric parameters (\AA , $^\circ$).

Cu1—O1	2.394 (1)	Cu1—N2	2.002 (2)
Cu1—N1	2.021 (2)		
O1—Cu1—O1 ⁱ	180	N1—Cu1—N1 ⁱ	180
O1—Cu1—N1	73.81 (5)	N1—Cu1—N2	87.84 (6)
O1—Cu1—N1 ⁱ	106.19 (6)	N1—Cu1—N2 ⁱ	92.16 (6)
O1—Cu1—N2	75.68 (5)	N2—Cu1—N2 ⁱ	180
O1—Cu1—N2 ⁱ	104.32 (5)		

Symmetry code: (i) $\frac{1}{2} - x, \frac{3}{2} - y, 1 - z$.

Table 2

Hydrogen-bonding geometry (\AA , $^\circ$).

$D\text{---}H\cdots A$	$D\text{---}H$	$H\cdots A$	$D\cdots A$	$D\text{---}H\cdots A$
O1—H1 o ···O3	0.82	2.19	2.564 (2)	108
O2—H2 o ···O4	0.82	1.83	2.643 (2)	171
O1 w —H1 w 1···O3	0.82	1.93	2.738 (3)	171
O2 w —H2 w 1···O4 ⁱⁱ	0.83	2.05	2.790 (3)	149

Symmetry code: (ii) $x, 1 + y, z$.

The methyl group was rotated to fit the electron density [$C\text{---}H = 0.96 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$], as was the free hydroxyl group [$O\text{---}H = 0.82 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{O})$]. The H atom of the coordinated

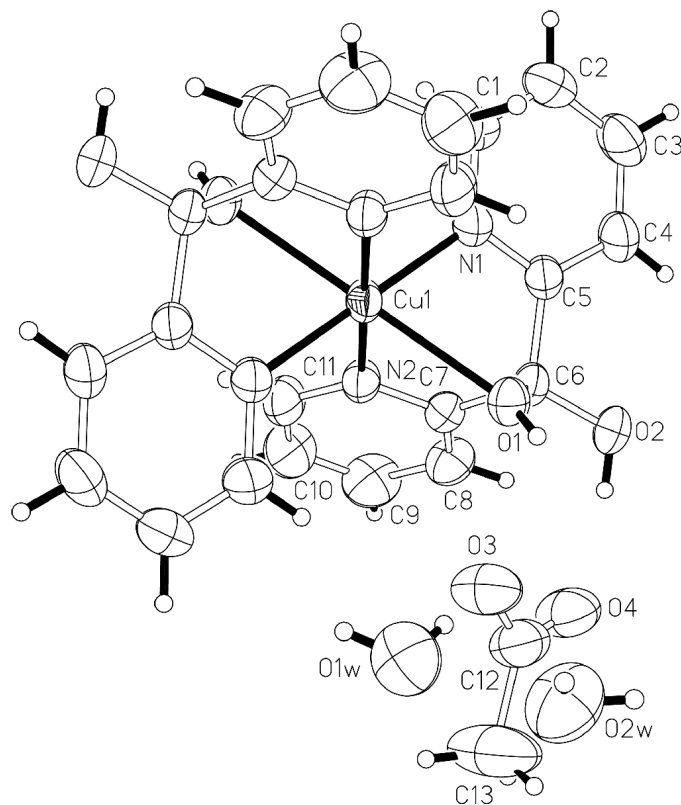


Figure 1

ORTEP (Johnson, 1976) plot, showing the numbering scheme of (I). Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as small spheres of arbitrary radii. The symmetry code for unlabeled atoms is as in Table 1.

hydroxyl group was placed at a calculated position assuming sp^3 hybridization [$O\text{---}H = 0.82 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{O})$]. The aromatic H atoms were generated geometrically [$C\text{---}H = 0.93 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$]. These H atoms were included in the refinements in the riding-model approximation. Those on the water molecules were placed at chemically sensible positions; their displacement parameters were tied to those of the O atoms by a factor of 1.2. Atoms H1 w 2 and H2 w do not have acceptors, and they are probably disordered. Atom H1 o is a little more than 2 \AA from the H atom of an adjacent molecule.

Data collection: *CrystalClear* (Rigaku, 2002); cell refinement: *CrystalClear*; data reduction: *CrystalClear*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

We thank the NSF of China, the FANEDD of China and the Education Foundation Office of Guangdong Province (z03065), as well as the University of Malaya, for generously supporting this work.

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