

Xing-You Xu,<sup>a\*</sup> Tong-Tao Xu,<sup>b</sup>  
Jian Gao,<sup>c</sup> Da-Qi Wang<sup>d</sup> and  
Lude Lu<sup>b</sup><sup>a</sup>Department of Chemical Engineering, Huaihai Institute of Technology, Lianyungang 222005, People's Republic of China, <sup>b</sup>Materials Chemistry Laboratory, Nanjing University of Science & Technology, Nanjing 210094, People's Republic of China, <sup>c</sup>Department of Chemical Engineering, Lianyungang Technical College, Lianyungang 222006, People's Republic of China, and <sup>d</sup>College of Chemistry and Chemical Engineering, Liaocheng University, Shandong 252059, People's Republic of China

Correspondence e-mail: xuxy@hhit.edu.cn

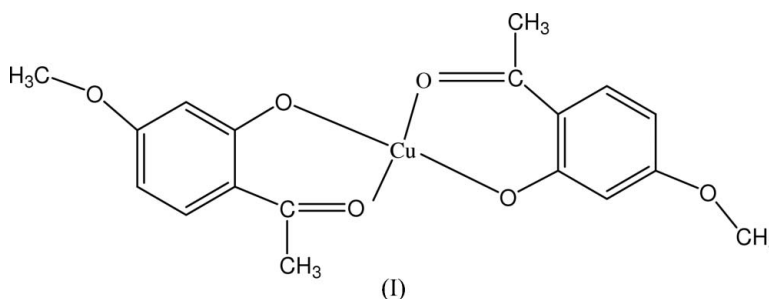
## Key indicators

Single-crystal X-ray study  
 $T = 298$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.007$  Å  
 $R$  factor = 0.052  
 $wR$  factor = 0.161  
Data-to-parameter ratio = 12.1For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

## Bis(4-methoxy-2-oxidoacetophenone)copper(II)

In the crystal structure of the title compound,  $[\text{Cu}(\text{C}_9\text{H}_9\text{O}_3)_2]$ , the  $\text{Cu}^{\text{II}}$  atom, lying on a center of symmetry, has a square-planar coordination formed by two paeonol anions.Received 28 June 2006  
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## Comment

Paeonol, or 2-hydroxy-4-methoxyacetophenone, is an effective component of many traditional Chinese medicines, and its derivatives have attracted considerable attention because of their potential biological properties (Liu *et al.*, 2000; Xu *et al.*, 2005). As part of our ongoing investigation on paeonol derivatives (Xu *et al.*, 2006), we present here the structure of the title  $\text{Cu}^{\text{II}}$  complex, (I).The  $\text{Cu}^{\text{II}}$  atom is coordinated in a square-planar geometry by the four O atoms of the paeonol anions, in which the hydroxyl groups are deprotonated (Fig. 1 and Table 1). Similar complexes commonly adopt a square-planar coordination geometry (Sillanpaa, 1991). The molecule is almost planar, the dihedral angle between the  $\text{Cu}1/\text{O}1/\text{O}2/\text{C}2/\text{C}3/\text{C}4$  chelate ring and the benzene ring being  $3.2(2)^\circ$ .

## Experimental

To a stirred solution of  $\text{Cu}(\text{ClO}_4)_2 \cdot 6\text{H}_2\text{O}$  (0.5 mmol) in 25 ml absolute methanol was added dropwise a solution of paeonol (1.0 mmol) in 10 ml absolute methanol at room temperature. After stirring for 3 h at 320 K, the precipitate was filtered off, washed with methanol and dried *in vacuo* but this was not suitable for X-ray diffraction analysis. Single crystals of (I) were obtained by slow evaporation of the filtrates at ambient temperature after 10 d.

## Crystal data

 $[\text{Cu}(\text{C}_9\text{H}_9\text{O}_3)_2]$   
 $M_r = 393.86$   
Monoclinic,  $P2_1/c$   
 $a = 8.871(4)$  Å  
 $b = 13.763(6)$  Å  
 $c = 6.523(3)$  Å  
 $\beta = 90.824(6)^\circ$   
 $V = 796.4(6)$  Å<sup>3</sup> $Z = 2$   
 $D_x = 1.643$  Mg m<sup>-3</sup>  
Mo  $K\alpha$  radiation  
 $\mu = 1.41$  mm<sup>-1</sup>  
 $T = 298(2)$  K  
Prism, green  
 $0.32 \times 0.24 \times 0.21$  mm

## Data collection

Bruker SMART CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 2002)  
 $T_{\min} = 0.651$ ,  $T_{\max} = 0.744$

3980 measured reflections  
 1394 independent reflections  
 1007 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.038$   
 $\theta_{\text{max}} = 25.0^\circ$

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.052$   
 $wR(F^2) = 0.161$   
 $S = 1.02$   
 1394 reflections  
 115 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0933P)^2 + 1.4385P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.46 \text{ e } \text{\AA}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.51 \text{ e } \text{\AA}^{-3}$

Table 1

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

|                        |            |           |            |
|------------------------|------------|-----------|------------|
| Cu1—O1                 | 1.877 (4)  | O2—C2     | 1.246 (6)  |
| Cu1—O2                 | 1.941 (3)  | O3—C6     | 1.345 (6)  |
| O1—C4                  | 1.308 (6)  | O3—C9     | 1.429 (6)  |
| O1—Cu1—O2 <sup>i</sup> | 88.32 (14) | O1—Cu1—O2 | 91.68 (14) |

Symmetry code: (i)  $-x, -y, -z$ .

Methyl H atoms were placed in calculated positions ( $C-H = 0.96 \text{ \AA}$ ) and torsion angles were refined, with  $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ . Aromatic H atoms were positioned geometrically ( $C-H = 0.93 \text{ \AA}$ ) and refined as riding, with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ .

Data collection: SMART (Bruker, 2003); cell refinement: SAINT (Bruker, 2003); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics:

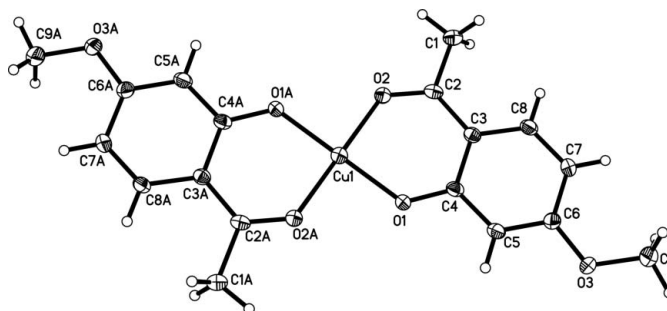


Figure 1

The molecular structure of (I) with 30% probability displacement ellipsoids. The suffix A corresponds to symmetry code (i) in Table 1.

SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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