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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å Disorder in main residue R factor = 0.039 wR factor = 0.095 Data-to-parameter ratio = 16.3

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

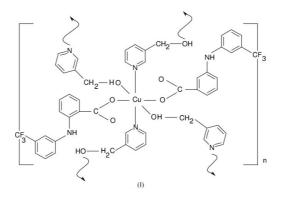
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Bis(flufenamato- κO)bis(3-pyridylmethanol- $\kappa^2 N$, O)copper(II)

The crystal structure of the title complex, $[Cu(C_{14}H_9N-F_3O_2)_2(C_6H_6NO)_2]_n$, has been studied by single-crystal X-ray diffraction at 100 (2) K. The polymeric structure is centrosymmetric and forms two-dimensional sheets. The Cu^{II} centre has octahedral coordination. It is bonded in a *trans*-square-planar arrangement to the N atoms of two ronicol molecules and one carboxylate O atom from each of two flufenamate anions. The axial positions are also occupied by 3-pyridylmethanol but coordinated through oxygen rather than the pyridyl N atom.

Comment

The synthesis and structural characterization of a copper(II) complex with a potent non-steroidal anti-inflammatory drug, flufenamic acid (fluf), with formula $[Cu(fluf)_2(ron)_2]$ (ron is ronicol; 3-pyridylmethanol) has been investigated. The complex is shown in Fig. 1. Selected bond distances and angles are summarized in Table 1. The asymmetric unit consists of a Cu atom located on an inversion centre, one flufenamate anion and one 3-pyridylmethanol molecule. The coordination sphere of the Cu atom consists of two O atoms from flufenamate [Cu1-O1 = 1.974 (1) Å] and its symmetry equivalent, two N atoms from 3-pyridylmethanol [Cu1-N1 = 2.028 (2) Å] and its symmetry equivalent and, in the axial sites also, from symmetry-equivalent 3-pyridylmethanol species but O-bound rather than N-bound [Cu1-O3b = 2.404 (1) Å; symmetry position of the ronicol: $x, \frac{1}{2} - y, z - \frac{1}{2}$ and $-x, y - \frac{1}{2}, \frac{1}{2} - z$].



The intramolecular hydrogen-bonding interaction $[N2-H2N\cdots O2, with an O\cdots N$ distance of 2.645 (2) Å] stabilizes the structure (Table 2). The crystal structure of the title complex consists of two-dimensional sheets. The layers lie parallel to the *ab* plane. The crystal structure of the compound under study can be compared with those of $[CuX_2(ron)_2]_n$ where X = salicylate (sal) (Hoang *et al.*, 1992), niflumate (nif) (Valach *et al.*, 1997) and clofibriate (clof) (Moncol *et al.*, 2001). The Cu $-O_{eq}$ (the O atom of the carboxylic acid group), Cu $-N_{eq}$ (the N atom of the pyridine ring of ronicol) and Cu $-O_{ax}$ Received 30 January 2004 Accepted 2 April 2004 Online 17 April 2004

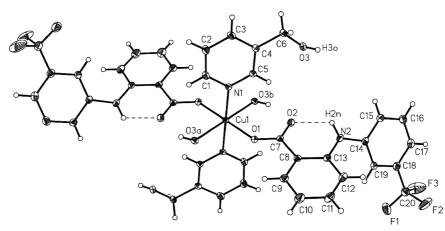


Figure 1

The structure of the title compound. Displacement ellipsoids are drawn at the 40% probability level and H atoms are shown as spheres of arbitrary radii. Minor disorder-component atoms F11, F21 and F31 have been omitted for clarity.

(the O atom of the hydroxyl group of ronicol) lengths are: 1.944 (4), 2.039 and 2.622 (4) Å for salicylate, 1.946 (3), 2.038 (3) and 2.573 (3) Å for niflumate, and 1.989 (2), 2.008 (2) and 2.441 (1) Å for clofibriate. In the present crystal structure, the equivalent bond lengths are comparable (Table 1). All four compounds have polymeric structures with axially elongated octahedral geometry about each Cu^{II} atom of the CuO₄N₂ chromophore, as predicted by the Jahn–Teller effect.

Experimental

The title complex was prepared by addition of 3-pyridylmethanol (0.02 mol) to copper(II) flufenamate (0.01 mol) in hot methanol. The mixture was stirred, filtered and left to cool and stand at room temperature. Green air-stable crystals were collected. Analysis found: C 56,96, H,3.75, N,6.78, Cu 7.22%; calculated for $[Cu(fluf)_2(ron)_2]$: C 57.05, H 3.83, N,7.54, Cu 7.54%.

Crystal data

$\begin{bmatrix} \text{Cu}(\text{C}_{14}\text{H}_9\text{NF}_3\text{O}_2)_2(\text{C}_6\text{H}_6\text{NO})_2 \end{bmatrix}$ $M_r = 842.25$ Monoclinic, $P2_1/c$ a = 18.787 (4) Å b = 10.576 (2) Å c = 9.097 (2) Å $\beta = 95.51$ (3)° V = 1799.1 (7) Å ³ Z = 2	$D_x = 1.555 \text{ Mg m}^{-3}$ Mo K\alpha radiation Cell parameters from 25 reflections $\theta = 4.5-12.5^{\circ}$ $\mu = 0.69 \text{ mm}^{-1}$ T = 293 (2) K Prism, green $0.20 \times 0.20 \times 0.15 \text{ mm}$
Data collection	
Kuma KM4CCD diffractometer ω scans Absorption correction: refined from ΔF (<i>COSAB</i> S99; Starynowicz, 1999) $T_{\min} = 0.870, T_{\max} = 0.901$ 11922 measured reflections	4474 independent reflections 3498 reflections with $I > 2\sigma(I)$ $R_{int} = 0.030$ $\theta_{max} = 28.6^{\circ}$ $h = -24 \rightarrow 25$ $k = -14 \rightarrow 14$ $l = -12 \rightarrow 6$
Refinement	
Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.039$ $wR(F^2) = 0.095$ S = 1.10 4474 reflections 274 parameters H atoms treated by a mixture of independent and constrained refinement	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0549P)^{2} + 0.5478P]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.46 \text{ e} \text{ Å}^{-3}$ $\Delta\rho_{min} = -0.41 \text{ e} \text{ Å}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Cu1-O1	1.9747 (14)	Cu1-O3 ⁱ	2.404 (1)
Cu1-N1	2.0279 (16)		
O1-Cu1-N1	91.33 (6)	O1 ⁱⁱⁱ -Cu1-O3 ⁱⁱ	84.43 (5)
O1-Cu1-O3 ⁱⁱ	95.57 (5)	N1-Cu1-O3 ⁱ	88.77 (5)
	1.1 (**)	1 1 (***)	

Symmetry codes: (i) $-x, y - \frac{1}{2}, \frac{1}{2} - z$; (ii) $x, \frac{1}{2} - y, z - \frac{1}{2}$; (iii) -x, -y, -z.

Table 2

Hydrogen-bonding geometry (Å, °).

$\overline{D-\mathrm{H}\cdots A}$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N2-H2N\cdots O2$	0.86	2.12	2.645 (2)	119

All the H atoms were placed in geometrically calculated positions, except for the alkoxyl H atom, which was located in a difference Fourier map. The H atoms were not refined and the U_{iso} values were set at 0.05 Å², except for H3O which has been refined with the O3–H3O distance restrained to 0.84 (1) Å. The F atoms of the CF₃ group are disordered, occupying two statistical positions, represented by F1/F2/F3 and F11/F21/F31, with occupancy factors of 0.919 (4) and 0.081 (4), respectively. Atoms F1, F2 and F3 were refined anisotropically and atoms F11, F21 and F31 were refined isotropically.

Data collection: *CRYSALIS* (Kuma, 1998); cell refinement: *CRYSALIS*; data reduction: *CRYSALIS*; program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1985); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP* (Johnson, 1965); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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