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A novel copper(II) complex with 1,10-phenanthroline and ciprofloxacin

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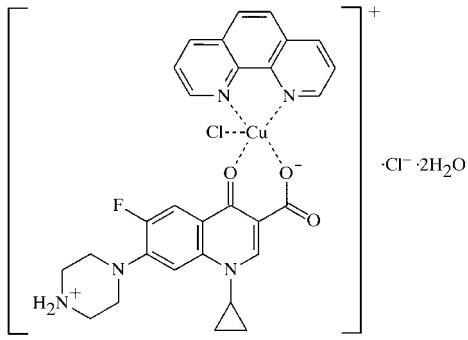
The X-ray structure analysis of the title compound, chloro[1-cyclopropyl-6-fluoro-1,4-dihydro-4-oxo-7-(piperazin-4-ium-1-yl)-3-quinolinecarboxylate-κ^2O^3,O^4](1,10-phenanthroline-κ^2N,N')copper chloride dihydrate, $[CuCl(C_{17}H_{18}FN_3O_3)(C_{12}H_8N_2)]Cl\cdot 2H_2O$ or $[CuCl(cfH)(phen)]Cl\cdot 2H_2O$, where cfH is 1-cyclopropyl-6-fluoro-1,4-dihydro-4-oxo-7-(piperazin-4-ium-1-yl)-3-quinolinecarboxylate and phen is 1,10-phenanthroline, shows that the geometry around the Cu ion is a slightly distorted square pyramid. Two O atoms of the carbonyl and carboxyl groups of ciprofloxacin and two N atoms of 1,10-phenanthroline are coordinated to the metal centre in the equatorial plane, and a Cl^- ion is coordinated at the apical position. Extensive intermolecular hydrogen bonding produces a supramolecular structure that consists of alternating six- and 12-membered rings.

Comment

Ciprofloxacin [1-cyclopropyl-6-fluoro-1,4-dihydro-4-oxo-7-(1-piperazinyl)-3-quinoline carboxylic acid], cfH, belongs to the family of fluoroquinolones and is a well known antibacterial drug (Reynolds, 1993) which inhibits bacterial growth by influencing the procaryotic enzyme gyrase (Stryer, 1995). Several ciprofloxacin–metal complexes have been isolated and their crystal structures reported (Turel, 2002), and many of them possess nearly the same antibiotic activity as cfH alone. One of the theories dealing with the interaction between gyrase, DNA and quinolones proposes that the interaction between DNA and quinolone is strongly influenced by divalent metal ions, which stabilize the negative charges of the quinolone carbonyl and carboxyl groups and DNA phosphates (Palumbo *et al.*, 1993).

The title compound, (I), is a mixed-ligand–metal complex which, besides ciprofloxacin, includes the *N*,*N*-bidentate ligand 1,10-phenanthroline (phen), also known for its biological significance (Ranford *et al.*, 1993). Compound (I) may therefore contribute to the development of a new type of drug with biologically important properties.



(I)

The asymmetric unit of (I) consists of a $[Cu(cfH)(phen)Cl]^+$ unit, a Cl^- anion and two water molecules. The Cu atom is coordinated by two ciprofloxacin O atoms and two 1,10-phenanthroline N atoms in the equatorial plane, and by a Cl^- ion in the axial position. It adopts a slightly distorted square-pyramidal geometry, with an O1—Cu—O11 angle of 93.67 (5)° and an N40—Cu—N31 angle of 81.99 (6)° (Fig. 1). The Cu atom deviates from the equatorial plane by 0.166 (1) Å. The ciprofloxacin part of the $[Cu(cfH)(phen)Cl]^+$ unit is zwitterionic, with atom N24 protonated and atom O12 unprotonated. The apical site is occupied by atom Cl1, and the Cu—Cl1 bond of 2.606 (1) Å makes an angle of 84.3 (5)° with the best plane of the four atoms at the base of the pyramid.

All bond lengths and angles in (I) are in agreement with the values reported for the corresponding types of bonds (Orpen *et al.*, 1989). Metal-to-ligand distances are also similar to those found in related compounds with cinoxacin (1-ethyl-1,4-dihydro-4-oxo-1,3-dioxolo[4,5-*g*]cinnoline-3-carboxylic acid, cnx), $[Cu(phen)(cnx)(H_2O)]NO_3\cdot H_2O$ (Mendoza-Diaz *et al.*, 1993), or nalidixic acid (1-ethyl-1,4-dihydro-7-methyl-4-oxo-1,8-naphthyridine-3-carboxylic acid, nal), $[Cu(phen)(nal)(H_2O)]NO_3\cdot 3H_2O$ (Mendoza-Diaz *et al.*, 1987), and in

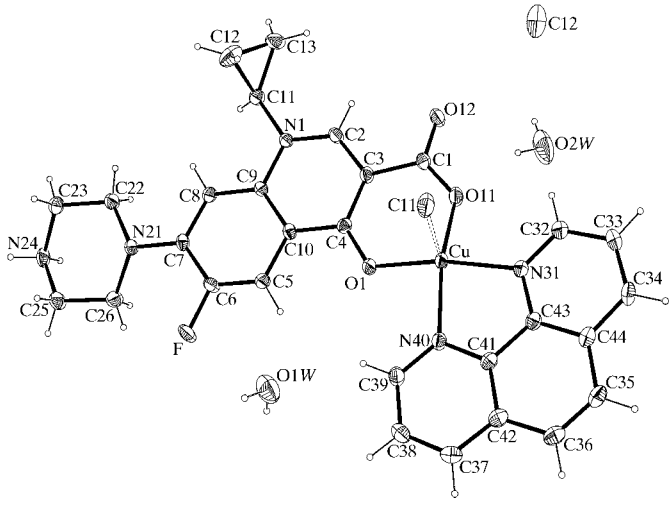


Figure 1
The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

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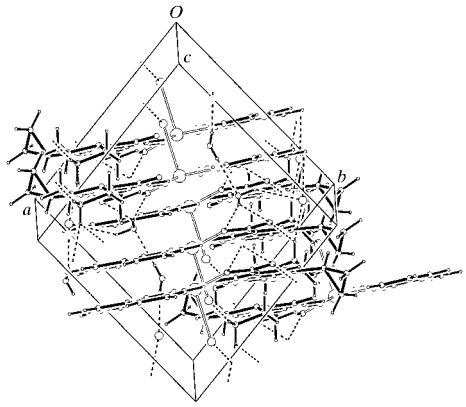

Figure 2
Packing diagram for (I) showing the hydrogen bonding.

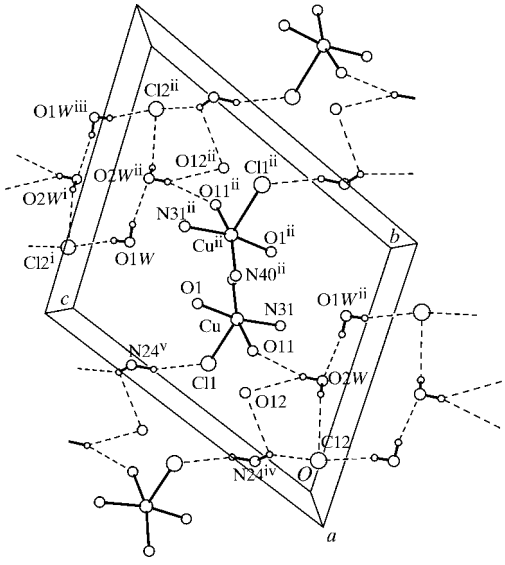

Figure 3
Detail of the hydrogen bonding in (I), projected along *a*. Atoms not involved in the hydrogen bonding have been omitted for clarity. [Symmetry codes: (i) $-1+x, y, 1+z$; (ii) $1-x, 1-y, 1-z$; (iii) $-x, 1-y, 2-z$; (iv) $x, y, -1+z$; (v) $1-x, -y, 2-z$.]

$[Cu(cfH)(bipy)(Cl)_{0.7}(NO_3)_{0.3}](NO_3)\cdot 2H_2O$ (bipy is 2,2′-bipyridine; Wallis *et al.*, 1996). Complex (I) is almost planar, with the exception of the piperazine ring, which has the usual chair conformation, and the cyclopropyl ring, which makes a dihedral angle of 69.7 (1)° with the Cu(cfH)(phen) plane.

The extended structure of (I) is dominated by layering indicative of π–π interactions between the 1,10-phenanthroline and ciprofloxacin aromatic rings. The distance between the aromatic rings of cfH and phen in neighbouring layers is approximately 3.1 Å in (I), while the analogous planes are 3.5 Å apart in the previously synthesized complex $[Cu(phen)(cnx)(H_2O)]NO_3\cdot H_2O$ (Mendoza-Diaz *et al.*, 1993). A shorter distance between neighbouring layers accompanies a more extensive intermolecular hydrogen-bonding network (Figs. 2 and 3). $[Cu(cfH)(phen)Cl]^+$ moieties are linked *via* hydrogen bonds of the types N—H···Cl, O—H···O and O—H···Cl. A hydrogen-bonded six-membered ring is present, in which atoms O1*W* and O2*W* are hydrogen-bond donors to two Cl2 ions, one of the same and the other of a neighbouring asymmetric unit (Fig. 3). The O1*W*···O2*W* distance is 2.852 (3) Å and the O···Cl distances are 3.200 (2) and 3.234 (3) Å. A 12-membered ring is formed by intermolecular hydrogen bonding between the N24—H group of the piperazine ring, carboxyl O12 congeners and the Cl1 atoms of neighbouring molecules. Since both rings are simultaneously linked by N24—H24*B*···Cl2(x, y, $1+z$), O2*W*—H2*B*···O12 and O2*W*—H2*B*···O11 hydrogen bonds, an extensive polymeric network is formed, which may contibute to the stabilization of the crystal structure.

Experimental

The title compound was synthesized by a hydrothermal reaction. Ciprofloxacin (0.5 mmol), 1,10-phenanthroline hydrate and copper(II) chloride dihydrate were mixed in a mortar in a 1:1:1 molar ratio and placed in a glass tube. Absolute ethanol (2 ml) was added and the pH was adjusted to 8 with 2 *M* sodium hydroxide. The tube was then frozen using liquid nitrogen, evacuated and sealed. The ampoule was heated at 393 K for 24 h, giving green crystals of (I). Crystals of the same product were also obtained from the same mixture by evaporation in air. However, the quality of these latter crystals was not appropriate for single-crystal X-ray diffraction analysis.

Crystal data

$[CuCl(C_{17}H_{18}FN_3O_3)(C_{12}H_8N_2)]Cl\cdot 2H_2O$
$M_r = 682.03$
Triclinic, $P\overline{1}$
$a = 10.8567$ (5) Å
$b = 11.1494$ (5) Å
$c = 13.2873$ (10) Å
$\alpha = 66.672$ (5)°
$\beta = 73.054$ (5)°
$\gamma = 80.190$ (5)°
$V = 1410.0$ (2) Å^3
$Z = 2$
$D_x = 1.606$ Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 7979 reflections
$\theta = 2.0$–30.0°
$\mu = 1.02$ mm^{-1}
$T = 200$ (2) K
Prism, green
0.07 × 0.05 × 0.03 mm

Data collection

Nonius KappaCCD diffractometer (with an Oxford Cryosystems Cryostream cooler)
ω scans
Absorption correction: multi-scan (*HKL SCALEPACK*; Otwinowski & Minor, 1997)
$T_{min} = 0.941$, $T_{max} = 0.967$
15 579 measured reflections
5551 independent reflections
4894 reflections with $I > 2\sigma(I)$
$R_{int} = 0.020$
$\theta_{max} = 26$°
$h = -13 \rightarrow 12$
$k = -13 \rightarrow 13$
$l = -16 \rightarrow 16$

Table 1
Selected geometric parameters (Å, °).

Cu—O11	1.9143 (13)	Cu—N31	2.0278 (15)
Cu—O1	1.9454 (12)	Cu—Cl1	2.6064 (5)
Cu—N40	2.0080 (15)		
O11—Cu—O1	93.67 (5)	N40—Cu—N31	81.99 (6)
O11—Cu—N40	163.90 (6)	O11—Cu—Cl1	96.44 (4)
O1—Cu—N40	91.21 (6)	O1—Cu—Cl1	100.36 (4)
O11—Cu—N31	90.71 (6)	N40—Cu—Cl1	97.76 (4)
O1—Cu—N31	169.10 (6)	N31—Cu—Cl1	89.05 (4)

Table 2
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
O1W—H1A···Cl2^{i}	0.79 (3)	2.42 (3)	3.200 (2)	170 (3)
O1W—H1B···O2W^{ii}	0.78 (3)	2.08 (3)	2.852 (3)	170 (3)
O2W—H2A···Cl2	0.85 (4)	2.53 (4)	3.234 (3)	141 (3)
O2W—H2B···O12	0.76 (4)	2.32 (4)	2.971 (2)	144 (4)
O2W—H2B···O11	0.76 (4)	2.36 (4)	3.087 (3)	160 (4)
N24—H24B···Cl2^{iii}	0.92	2.33	3.193 (2)	155
N24—H24B···O12^{iii}	0.92	2.56	2.901 (2)	102
N24—H24A···Cl1^{iv}	0.92	2.20	3.080 (2)	160

Symmetry codes: (i) $x-1, y, 1+z$; (ii) $1-x, 1-y, 1-z$; (iii) $x, y, 1+z$; (iv) $1-x, -y, 2-z$.

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.029$
$wR(F^2) = 0.074$
$S = 1.05$
5551 reflections
405 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0331P)^2 + 1.0139P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.002$
$\Delta\rho_{max} = 0.33$ e Å^{-3}
$\Delta\rho_{min} = -0.35$ e Å^{-3}
Extinction correction: *SHELXL*97 (Sheldrick, 1997)
Extinction coefficient: 0.0036 (9)

Water H atoms were found in a difference Fourier map and were refined freely. All remaining H atoms were placed in calculated positions and refined using appropriate riding models, with $U_{iso}(H) = 1.2U_{eq}(N,C)$.

Data collection: *COLLECT* (Nonius, 1999); cell refinement and data reduction: *HKL DENZO* and *SCALEPACK* (Otwinowski & Minor, 1997); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 1998) and *ORTEP*-3 *for Windows* (Farrugia, 1999*b*); software used to prepare material for publication: *SHELXL*97 and *WinGX* (Farrugia, 1999*a*).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: FA1021). Services for accessing these data are described at the back of the journal.

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