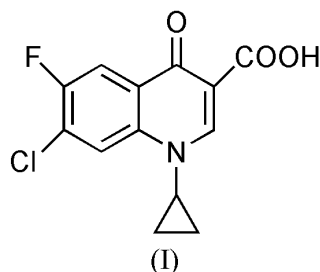
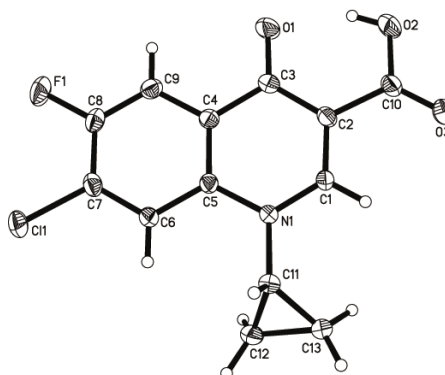


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Key indicatorsSingle-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$
 R factor = 0.040
 wR factor = 0.094
Data-to-parameter ratio = 13.6For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**7-Chloro-1-cyclopropyl-6-fluoro-1,4-dihydro-4-oxoquinoline-3-carboxylic acid**The title compound, $\text{C}_{13}\text{H}_9\text{ClFNO}_3$, was synthesized from ethyl 2,4-dichloro-5-fluorobenzoylacetate.Received 5 January 2004
Accepted 26 February 2004
Online 6 March 2004**Comment**Ciprofloxacin [1-cyclopropyl-6-fluoro-1,4-dihydro-4-oxo-7-(1-piperazinyl)-3-quinolinecarboxylic acid] is one of the fluorinated quinolone antibacterial agents (Koga *et al.*, 1980), which are among the most attractive drugs in the field of anti-infective chemotherapy. These fluorinated quinolone compounds are characterized by having an F atom at the 6-position and a substituted amino group at the 7-position. The title compound, (I), is an intermediate in the synthesis of ciprofloxacin, and the molecular structure is illustrated in Fig. 1.**Experimental**The title compound was prepared according to the literature method of Grohe *et al.* (1983) from ethyl 2,4-dichloro-5-fluorobenzoylacetate. Condensation of ethyl 2,4-dichloro-5-fluorobenzoylacetate with triethyl orthoformate by refluxing in acetic anhydride produced ethyl 2-(2,4-dichloro-5-fluorobenzoyl)-3-ethoxyacrylate. This intermediate**Figure 1**

The molecular structure of (I), drawn with 30% probability displacement ellipsoids.

was reacted without further purification with cyclopropanamine in dichloromethane to afford ethyl 2-(2,4-dichloro-5-fluorobenzoyl)-3-cyclopropanaminoacrylate. This was cyclized by heating with sodium hydride to give 7-chloro-1-cyclopropyl-6-fluoro-1,4-dihydro-3-ethoxycarbonyl-4-oxoquinoline. The ester (50 mmol) was hydrolyzed by heating with aqueous KOH (150 mmol) in tetrahydrofuran at 353 K to give 7-chloro-1-cyclopropyl-6-fluoro-1,4-dihydro-4-oxoquinoline-3-carboxylic acid. This crude product, (I), was purified by recrystallization from *N,N*-dimethylformamide. Compound (I) (50 mg) was dissolved in dichloromethane (20 ml) and the solution was kept at room temperature for 10 d, whereby slow evaporation gave colourless single crystals of (I), suitable for X-ray analysis.

Crystal data

$C_{13}H_9ClFNO_3$	$D_x = 1.631 \text{ Mg m}^{-3}$
$M_r = 281.66$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 821 reflections
$a = 9.194 (4) \text{ \AA}$	$\theta = 2.6\text{--}25.9^\circ$
$b = 7.515 (4) \text{ \AA}$	$\mu = 0.35 \text{ mm}^{-1}$
$c = 16.635 (8) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\beta = 93.784 (7)^\circ$	Block, colourless
$V = 1146.9 (9) \text{ \AA}^3$	$0.20 \times 0.20 \times 0.18 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART CCD area-detector diffractometer	2345 independent reflections
φ and ω scans	1753 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Bruker, 1997)	$R_{\text{int}} = 0.027$
$T_{\text{min}} = 0.791$, $T_{\text{max}} = 0.939$	$\theta_{\text{max}} = 26.4^\circ$
6311 measured reflections	$h = -11 \rightarrow 11$
	$k = -9 \rightarrow 7$
	$l = -20 \rightarrow 20$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0523P)^2 + 0.214P]$
$R[F^2 > 2\sigma(F^2)] = 0.040$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.094$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.04$	$\Delta\rho_{\text{max}} = 0.19 \text{ e \AA}^{-3}$
2345 reflections	$\Delta\rho_{\text{min}} = -0.27 \text{ e \AA}^{-3}$
173 parameters	
H-atom parameters constrained	

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O2-H2\cdots O1$	0.82	1.80	2.559 (2)	154
$O2-H2\cdots CH^i$	0.82	2.87	3.348 (2)	119

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

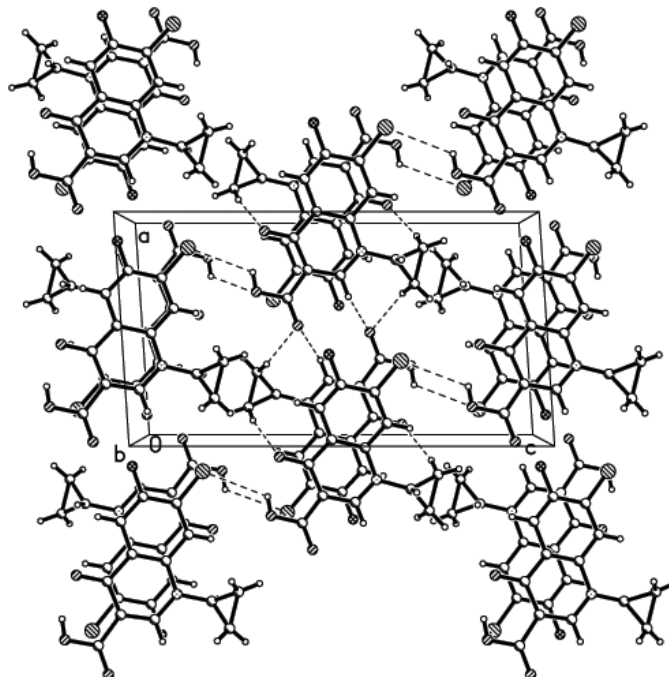


Figure 2

The crystal structure of (I), viewed along the a axis. Dashed lines indicate hydrogen bonds.

H atoms were positioned geometrically, with $C-H = 0.93\text{--}0.98 \text{ \AA}$, and were refined in a riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{carrier})$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINTE* (Bruker, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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