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Key indicators

Single-crystal X-ray study
T = 293 K
Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$
R factor = 0.059
wR factor = 0.185
Data-to-parameter ratio = 16.2

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

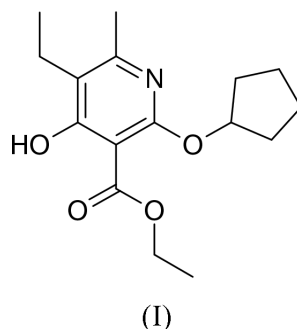
Ethyl 2-(cyclopentyloxy)-5-ethyl-4-hydroxy-6-methylnicotinate

Structural analysis of the title compound, $\text{C}_{16}\text{H}_{23}\text{NO}_4$, reveals that the pyridine ring and the ester moiety are coplanar. This conformation is stabilized by an intramolecular hydrogen bond between the hydroxyl and ester groups.

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Comment

In an attempt to design new HIV reverse transcriptase inhibitors (Parniak & Sluis-Cremer, 2000), the title compound (I), namely ethyl 2-(cyclopentyloxy)-5-ethyl-4-hydroxy-6-methylnicotinate, was synthesized and studied by X-ray diffraction. The atom labeling and molecular conformation adopted for this compound are depicted in Fig. 1. The pyridine heterocycle is planar; the displacement of the atoms from their mean plane does not exceed 0.014 Å. The cyclopentyl ring is orthogonal to the pyridine heterocycle [dihedral angle of 89.59 (2)° between the mean planes], with N1—C2—O10—C11 and C2—O10—C11—C12 torsion angles of −4.9 (4) and −86.2 (3)°, respectively. Furthermore, the ester function is nearly coplanar with the pyridine ring [C4—C3—C16—C17 1.4 (4)°]. This conformation is induced by an intramolecular hydrogen bond between the hydroxyl and ester moieties (O21—H21···O17, see Table 1). In addition to this hydrogen bond, the molecular structure of (I) is also stabilized by intermolecular C—H···O contacts (see Table 1).



Experimental

The title compound, (I), was synthesized from ethyl 5-ethyl-4-hydroxy-6-methyl-pyridine-2(1H)-one-3-carboxylate (Dollé *et al.*, 1995). In a 25 ml two-necked flask under argon, the pyridinone (1.12 g, 5 mmol) and Ag_2CO_3 (0.717 g, 2.6 mmol) were dissolved in 10 ml benzene. The reaction mixture was warmed to 303 K and a slight excess of iodocyclopentane (640 μl , 5.5 mmol) was then added. After 18 h, the whole mixture was cooled to 273 K, diluted with 10 ml pentane, and filtered. This organic layer was washed successively with diluted NaHCO_3 and saturated NaCl , then dried with anhydrous Na_2SO_4 , filtered off and evaporated to dryness. This sample was

purified on a SiO₂ column (eluant: dichloromethane/pentane: 3:1). 1.375 g (4.65 mmol, 93% yield) of a white solid were obtained. Spectroscopic analysis, ¹H NMR (90 MHz, CDCl₃, δ, p.p.m.): 1.1 (t, 3H, CH₃), 1.4 (t, 3H, CH₃), 1.5–2.2 (m, 8H), 2.4 (s, 3H, CH₃), 2.6 (q, 2H, CH₂), 4.3 (q, 2H, OCH₂), 5.5 (m, 1H, OCH), 12.5 (s, 1H, NH). Slow evaporation of a solution of (I) in ethanol gave colourless crystals suitable for X-ray analysis.

Crystal data

C ₁₆ H ₂₃ NO ₄	Z = 2
M _r = 293.35	D _x = 1.215 Mg m ⁻³
Triclinic, P1	Cu Kα radiation
a = 6.312 (1) Å	Cell parameters from 25 reflections
b = 10.571 (1) Å	θ = 30.0–40.0°
c = 12.396 (2) Å	μ = 0.71 mm ⁻¹
α = 84.205 (7)°	T = 293 (2) K
β = 77.098 (8)°	Platelet, colourless
γ = 88.827 (5)°	0.21 × 0.10 × 0.09 mm
V = 802.1 (2) Å ³	

Data collection

Enraf–Nonius CAD-4 diffractometer	R _{int} = 0.022
θ/2θ scans	θ _{max} = 71.9°
Absorption correction: analytical (Alcock, 1970)	h = -5 → 7
T _{min} = 0.865, T _{max} = 0.939	k = -13 → 13
3449 measured reflections	l = -14 → 15
3147 independent reflections	3 standard reflections every 200 reflections
1678 reflections with I > 2σ(I)	frequency: 60 min
	intensity decay: 3.5%

Refinement

Refinement on F ²	w = 1/[σ ² (F _o ²) + (0.076P) ² + 0.272P]
R[F ² > 2σ(F ²)] = 0.059	where P = (F _o ² + 2F _c ²)/3
wR(F ²) = 0.185	(Δ/σ) _{max} = 0.023
S = 1.01	Δρ _{max} = 0.26 e Å ⁻³
3147 reflections	Δρ _{min} = -0.19 e Å ⁻³
194 parameters	
H-atom parameters constrained	

Table 1

Hydrogen-bonding geometry (Å, °).

D—H...A	D—H	H...A	D...A	D—H...A
O21—H21...O17	1.01	1.58	2.513 (3)	152
C19—H19A...O17 ⁱ	0.97	2.83	3.211 (4)	105

Symmetry code: (i) 1 - x, -y, 2 - z.

The displacement parameter of the hydroxyl H atom was refined and the methyl groups were allowed to rotate about their local threefold axes.

Data collection: CAD-4 EXPRESS (Enraf–Nonius, 1992); cell refinement: CAD-4 EXPRESS; data reduction: HELENA (Spek, 2000); program(s) used to solve structure: SIR97 (Altomare *et al.*, 1999); program(s) used to refine structure: SHELXL97 (Sheldrick,

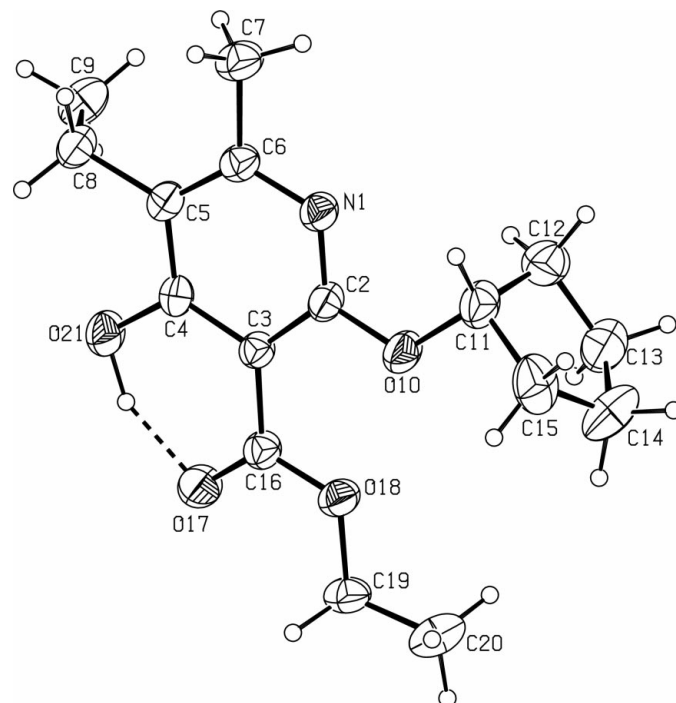


Figure 1

ORTEP view of compound (I), with displacement ellipsoids drawn at the 30% probability level.

1997); molecular graphics: PLATON (Spek, 2000); software used to prepare material for publication: SHELXL97.

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