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## Key indicators

Single-crystal X-ray study  
 $T = 298\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$   
 $R$  factor = 0.044  
 $wR$  factor = 0.134  
Data-to-parameter ratio = 15.7For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

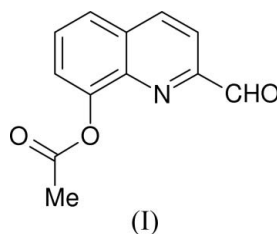
## 2-Formylquinolin-8-yl acetate

In the crystal structure of the title compound,  $\text{C}_{12}\text{H}_9\text{NO}_3$ , the molecules are linked through weak intermolecular  $\text{C}-\text{H}\cdots\text{O}$  hydrogen bonds, forming a two-dimensional network.

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## Comment

The title compound, (I), is a derivative of 2-pyridaldehyde, which readily forms Schiff base compounds by condensation with amines.

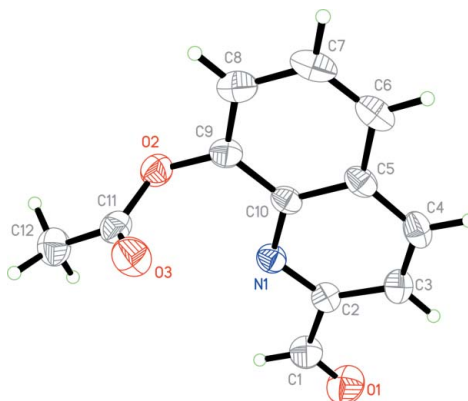


In (I), all the bond lengths are within normal ranges (Allen *et al.*, 1987). The dihedral angle between the plane of atoms O2/C11/O3 and the quinoline ring system is  $82.9(2)^\circ$  (Fig. 1). The conformation of the acetoxy group is described by the torsion angle of  $-169.42(17)^\circ$  for C9—O2—C11—C12.

In the crystal structure, molecules are linked *via* weak intermolecular  $\text{C}-\text{H}\cdots\text{O}$  hydrogen bonds to form a two-dimensional sheet perpendicular to the  $c$  axis (Table 1).

## Experimental

One drop of concentrated sulfuric acid was added to a mixture of 2-methyl-8-hydroxyquinoline (15.9 g, 0.1 mol) and acetic anhydride (10.2 g, 9.4 ml, 0.1 mol) in a 250 ml Erlenmeyer flask. The mixture was warmed rapidly and stirred gently by hand. After 5 min, the clear solution was poured on to crushed ice (about 200 ml). The solid was



**Figure 1**  
The structure of (I). Displacement ellipsoids are drawn at the 30% probability level.

filtered off and washed with water (200 ml). The compound obtained was 2-methyl-8-acetoxyquinoline (18.6 g, 93%; m.p. 394–395 K). To a dioxane suspension (40 ml) of freshly sublimed selenium dioxide (5.8 g), a dioxane solution (50 ml) of 2-methyl-8-acetoxyquinoline (11.4 g) was added with stirring over a water bath at 323–328 K for 3 h. The mixture was filtered after being allowed to stand for 2 h. The dioxane was distilled off to give light-yellow crystals of (I) (9.0 g; m.p. 367–368 K).

#### Crystal data

$C_{12}H_9NO_3$	$D_x = 1.341 \text{ Mg m}^{-3}$
$M_r = 215.20$	Mo $K\alpha$ radiation
Monoclinic, $C2/c$	Cell parameters from 3212 reflections
$a = 19.743 (3) \text{ \AA}$	$\theta = 2.3\text{--}24.9^\circ$
$b = 7.863 (1) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$c = 14.771 (2) \text{ \AA}$	$T = 298 (2) \text{ K}$
$\beta = 111.66 (2)^\circ$	Block, light-yellow
$V = 2131.1 (6) \text{ \AA}^3$	$0.53 \times 0.46 \times 0.41 \text{ mm}$
$Z = 8$	

#### Data collection

Bruker SMART CCD area-detector diffractometer	2315 independent reflections
$\omega$ scans	1225 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.045$
$T_{\text{min}} = 0.950$ , $T_{\text{max}} = 0.961$	$\theta_{\text{max}} = 27.0^\circ$
6309 measured reflections	$h = -24 \rightarrow 25$
	$k = -8 \rightarrow 10$
	$l = -18 \rightarrow 18$

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0577P)^2 + 0.2105P]$
$R[F^2 > 2\sigma(F^2)] = 0.044$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.134$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.00$	$\Delta\rho_{\text{max}} = 0.18 \text{ e \AA}^{-3}$
2315 reflections	$\Delta\rho_{\text{min}} = -0.15 \text{ e \AA}^{-3}$
147 parameters	Extinction correction: SHELXL97 (Sheldrick, 1997a)
H-atom parameters constrained	Extinction coefficient: 0.0073 (10)

**Table 1**

Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C7-H7\cdots O1^i$	0.93	2.57	3.486 (3)	168
$C12-H12C\cdots O1^{ii}$	0.96	2.59	3.447 (3)	149

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

H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C–H distances of 0.93–0.96  $\text{\AA}$ , and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$  or  $1.5U_{\text{eq}}(\text{C}_{\text{methyl}})$ .

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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