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Key indicators

Single-crystal X-ray study
 $T = 291$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.056
 wR factor = 0.095
Data-to-parameter ratio = 14.8

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

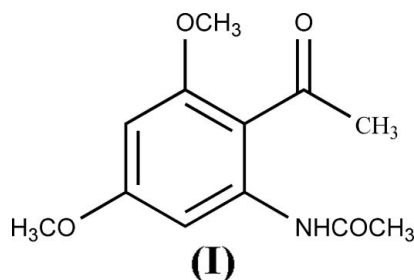
N-(2-Acetyl-3,5-dimethoxyphenyl)acetamide

In the title compound, $\text{C}_{12}\text{H}_{15}\text{NO}_4$, the molecular packing is influenced by inter- and intramolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds. The two methoxy groups are almost in the same plane, and the acetamide group is somewhat twisted out of the benzene ring plane.

Received 27 March 2007
Accepted 2 April 2007

Comment

4-Quinolones are a group of synthetic antimicrobial agents that exhibit excellent potential and a broad spectrum of activity against a variety of bacteria (Mitscher, 2005). In addition, they are commonly used as antitumour agents (Xia *et al.*, 2003). In this paper, we present the X-ray crystallographic analysis of the title compound, (I), which is an important intermediate for the synthesis of 4-quinolones.



In the title structure (Fig. 1), the bond lengths and angles are in good agreement with the expected values (Allen *et al.*,

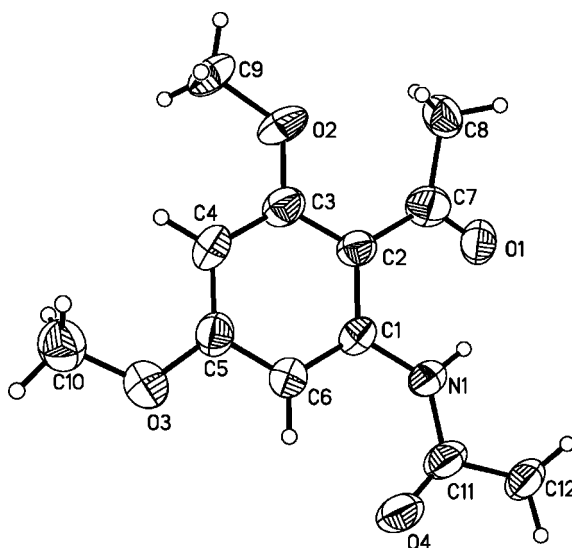


Figure 1
The molecular structure of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.

1987). The dihedral angle between the acetamide group and benzene ring is $4.5 (5)^\circ$.

In the packing of (I), the molecules are linked by intermolecular hydrogen bonds (Table 1, Fig. 2), thereby stabilizing the crystal structure.

Experimental

To a solution of 3,5-dimethoxyacetanilide (0.1952 g, 1 mmol) in dry 1,2-dichloroethane (5 ml) at 273 K, anhydrous stannic chloride (0.234 ml, 2 mmol) was added. Acetyl chloride (0.156 ml, 2.2 mmol) was then added dropwise and the reaction mixture was stirred for 3 h. After the reaction was complete, the mixture was poured into ice-water, extracted with CH_2Cl_2 (30 ml), washed with saturated NaHCO_3 solution and brine, and dried over anhydrous Na_2SO_4 . The solvent was evaporated *in vacuo* and the residue was separated by column chromatography (petroleum ether–ethyl acetate 5:1 *v/v*) to give the product (m.p. 382 K). Single crystals of (I) were obtained by slow evaporation of a petroleum ether–ethyl acetate (5:1 *v/v*) solution of (I).

Crystal data

$\text{C}_{12}\text{H}_{15}\text{NO}_4$
 $M_r = 237.25$
 Monoclinic, $P2_1/c$
 $a = 7.166 (3) \text{ \AA}$
 $b = 17.156 (8) \text{ \AA}$
 $c = 10.181 (5) \text{ \AA}$
 $\beta = 107.059 (6)^\circ$

$V = 1196.6 (10) \text{ \AA}^3$
 $Z = 4$
 Mo $K\alpha$ radiation
 $\mu = 0.10 \text{ mm}^{-1}$
 $T = 291 (2) \text{ K}$
 $0.30 \times 0.26 \times 0.24 \text{ mm}$

Data collection

Bruker SMART APEX CCD area-detector diffractometer
 Absorption correction: multi-scan (SADABS; Bruker, 2000)
 $T_{\min} = 0.97$, $T_{\max} = 0.98$

6381 measured reflections
 2347 independent reflections
 1406 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.054$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.056$
 $wR(F^2) = 0.095$
 $S = 0.98$
 2347 reflections

159 parameters
 H-atom parameters constrained
 $\Delta\rho_{\max} = 0.15 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.13 \text{ e \AA}^{-3}$

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N1}-\text{H1}\cdots\text{O1}$	0.86	1.9	2.612 (3)	139
$\text{C6}-\text{H6}\cdots\text{O4}$	0.93	2.20	2.830 (3)	125
$\text{C12}-\text{H12A}\cdots\text{O4}^i$	0.96	2.54	3.487 (3)	169

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

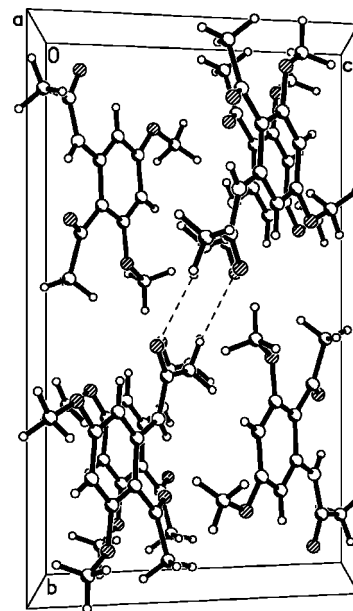


Figure 2

A packing diagram for (I), viewed down the a axis. Dashed lines indicate hydrogen bonds.

H atoms were positioned geometrically and treated as riding on their parent atoms, with $\text{C}-\text{H} = 0.93\text{--}0.96 \text{ \AA}$ or $\text{N}-\text{H} = 0.86 \text{ \AA}$, and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C},\text{N})$ or $1.5U_{\text{eq}}(\text{C})$ for methyl H.

Data collection: SMART (Bruker, 2000); cell refinement: SAINT-Plus (Bruker, 2000); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXTL (Bruker, 2000); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

This work was supported by the National Natural Science Foundation of China (grant No. 20572043).

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