

Ethyl 4-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)benzoate

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In the title compound, C₁₃H₁₁NO₄, the dihedral angle between the benzene and maleimide rings is 41.4 (1)°. There are C—H···O hydrogen-bonded chains, running along the *a* and *c* axes.

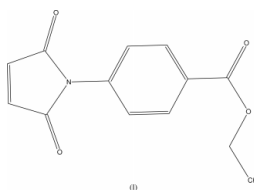
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Comment

Succinimides are important medicinal agents in the therapy of diseases such as tuberculosis, convulsions and hypertension (Pandey *et al.*, 1984; Crider & Edward, 1977). The title compound, (I), is such a derivative with an ester-substituted aryl maleimide.



Key indicators

Single-crystal X-ray study

T = 293 K

Mean σ (C—C) = 0.002 Å

R factor = 0.044

wR factor = 0.138

Data-to-parameter ratio = 11.2

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

The bond lengths and bond angles are comparable with values reported for similar compounds (Rodriguez *et al.*, 2002). The angle between the mean planes passing through the benzene ring (C5–C10) and the maleimide ring (N1/C1–C4) is 41.4 (1)°, indicating the steric repulsion between the carbonyl groups and the benzene ring. The dihedral angle is small [2.5 (2) Å] in a similar structure without carbonyl groups (Paulus & Rivo, 1988).

Molecular chains are observed, *via* two different C—H···O hydrogen bonds running along the *a* and *c* axes, respectively (Table 1 and Fig. 2). The C—H···O hydrogen-bonded chain down the *a* axis involves the ester carbonyl group, whereas the

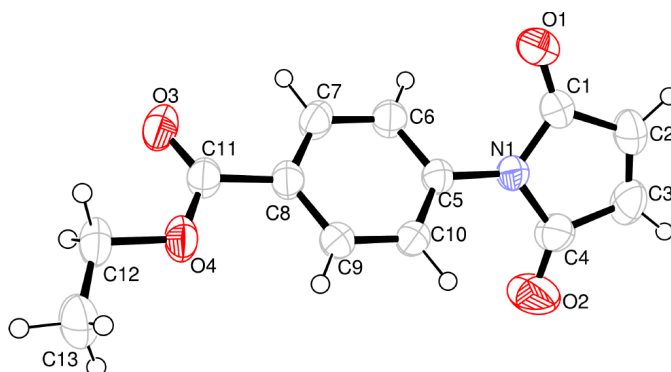


Figure 1 ORTEP-3 (Farrugia, 1997) diagram of (I), with 50% probability displacement ellipsoids.

other down the *c* axis employs one of the carbonyl groups of the maleimide ring.

Experimental

Maleanilic acid was synthesized by refluxing maleic anhydride (3.9 g, 0.04 mol), 5.5 ml of *p*-nitroaniline and 75 ml of ether. To the resulting solution, acetic anhydride (15.3 ml, 0.15 mol) and anhydrous sodium acetate (2.0 g) were added and the mixture was heated in a steam bath for 30 min. The reaction mixture was cooled to room temperature and then poured into 15 ml of ice water. The precipitated product was separated, washed with ice-cold water and aqueous sodium bicarbonate and dried. Light yellow crystals of (I) were obtained by slow evaporation of a methanol solution.

Crystal data

$C_{13}H_{11}NO_4$	$D_x = 1.365 \text{ Mg m}^{-3}$
$M_r = 245.23$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 775 reflections
$a = 12.028 (6) \text{ \AA}$	$\theta = 2.2\text{--}25.5^\circ$
$b = 7.358 (4) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$c = 13.561 (7) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\beta = 96.364 (7)^\circ$	Prism, pale yellow
$V = 1192.9 (11) \text{ \AA}^3$	$0.40 \times 0.30 \times 0.20 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART CCD area-detector diffractometer	2328 independent reflections
φ and ω scans	1965 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.013$
$T_{\text{min}} = 0.903$, $T_{\text{max}} = 0.980$	$\theta_{\text{max}} = 26.4^\circ$
8371 measured reflections	$h = -14 \rightarrow 15$
	$k = -9 \rightarrow 9$
	$l = -16 \rightarrow 16$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0933P)^2 + 0.1715P]$
$R[F^2 > 2\sigma(F^2)] = 0.044$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.138$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.00$	$\Delta\rho_{\text{max}} = 0.33 \text{ e \AA}^{-3}$
2328 reflections	$\Delta\rho_{\text{min}} = -0.31 \text{ e \AA}^{-3}$
207 parameters	
All H-atom parameters refined	

Table 1

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

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
$C3\text{--}H3\cdots O3^i$	0.94 (2)	2.51 (2)	3.402 (3)	158 (2)
$C10\text{--}H10\cdots O1^{ii}$	0.98 (2)	2.61 (2)	3.426 (3)	141 (1)

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

The H atoms were refined isotropically. The C–H bond lengths are 0.92 (2)–0.99 (2) \AA .

Data collection: SMART (Bruker, 1998); cell refinement: SMART; data reduction: SAINT (Bruker, 1998); program(s) used to solve structure: SIR92 (Altomare *et al.*, 1999); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997) and CAMERON (Watkin *et*

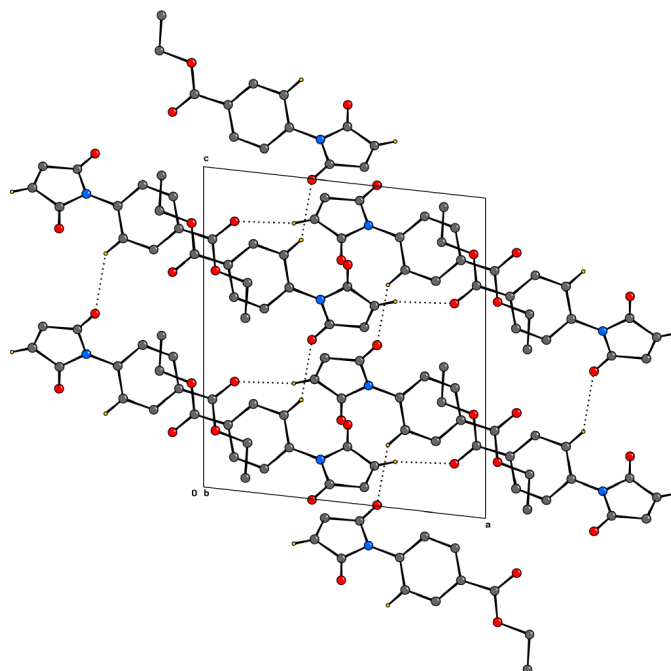


Figure 2

Packing diagram of (I), viewed down the *b* axis. The dotted lines represent C–H \cdots O hydrogen bonds.

al., 1993); software used to prepare material for publication: PLATON (Spek, 1990).

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