

Zu-Pei Liang* and Jian Li

Department of Chemistry and Chemical
Engineering, Weifang University, Weifang
261061, People's Republic of ChinaCorrespondence e-mail:
zupeiliang@yahoo.com.cn

Key indicators

Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.043
 wR factor = 0.140
Data-to-parameter ratio = 13.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

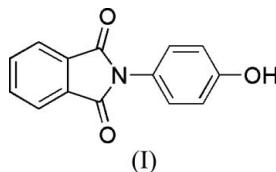
2-(4-Hydroxyphenyl)isoindoline-1,3-dione

In the title compound, $\text{C}_{14}\text{H}_9\text{NO}_3$, the dihedral angle between the phthalimide ring system and the hydroxybenzene ring is $64.77(5)^\circ$. $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds link the molecules into zigzag chains along the b axis.

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Comment

Phthalimides and N -substituted phthalimides are an important class of compounds because of their interesting biological activities (Lima *et al.*, 2002; Orzeszka *et al.*, 2000; Bailleux *et al.*, 1993). Phthalimides have also served as starting materials and intermediates for the syntheses of alkaloids (Couture *et al.*, 1998) and pharmacophores (Couture *et al.*, 1997). In this paper, the structure of the title compound, (I), is reported.



The molecular structure of (I) is illustrated in Fig. 1. The phthalimide moiety is essentially planar, with a mean deviation of $0.015(2)$ Å. Considering the different substitution patterns, the geometry of the phthalimide ring system compares favourably with that in the related compounds 4-(1,3-dioxoisindolin-2-yl)benzaldehyde (Liu *et al.*, 2004) and 5-amino-2-methylisoindoline-1,3-dione (Liang *et al.*, 2006). The hydroxybenzene ring (atoms C9–C14) is planar to within $0.009(2)$ Å. The dihedral angle between the N1/O1/O2/C1–C8 and C9–C14 planes is $64.77(5)^\circ$.

Symmetry-related molecules are linked *via* $\text{O}3-\text{H}3\cdots\text{O}2^i$ hydrogen bonds (the symmetry code is given in Table 1), forming a zigzag chain along the b axis. In addition, the molecular packing is stabilized by $\pi-\pi$ interactions between the

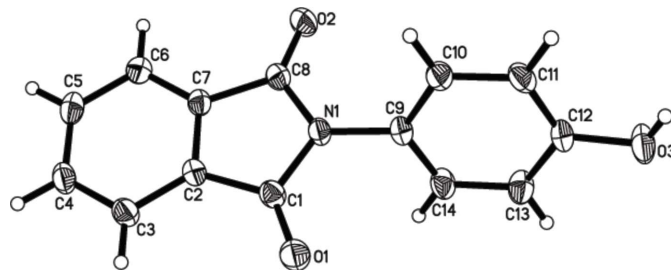


Figure 1
The molecular structure of (I). Displacement ellipsoids are drawn at the 30% probability level.

phthalimide ring systems of the molecules at (x, y, z) and $(1 - x, -y, 1 - z)$; their centroids are separated by 3.519 (2) Å.

Experimental

A solution of phthalimide (0.1 mol), 4-aminophenol (0.1 mol) and triethylamine (0.01 ml) in xylene (100 ml) was refluxed for 3 h. After cooling, filtration and drying, the title compound was obtained. 10 mg of (I) was dissolved in 15 ml acetone, the solution was allowed to evaporate at room temperature and colourless single crystals formed after 10 d.

Crystal data

$C_{14}H_9NO_3$	$Z = 8$
$M_r = 239.22$	$D_x = 1.436 \text{ Mg m}^{-3}$
Orthorhombic, <i>Pbca</i>	Mo $K\alpha$ radiation
$a = 11.524$ (3) Å	$\mu = 0.10 \text{ mm}^{-1}$
$b = 7.7133$ (19) Å	$T = 294$ (2) K
$c = 24.890$ (6) Å	Block, colourless
$V = 2212.4$ (10) Å ³	$0.32 \times 0.22 \times 0.14 \text{ mm}$

Data collection

Bruker SMART CCD area-detector diffractometer	11576 measured reflections
φ and ω scans	2265 independent reflections
Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 1997)	1300 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.968$, $T_{\max} = 0.986$	$R_{\text{int}} = 0.073$
	$\theta_{\max} = 26.4^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0843P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.043$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.140$	$(\Delta/\sigma)_{\max} = 0.001$
$S = 0.92$	$\Delta\rho_{\max} = 0.19 \text{ e \AA}^{-3}$
2265 reflections	$\Delta\rho_{\min} = -0.16 \text{ e \AA}^{-3}$
165 parameters	Extinction correction: <i>SHELXL97</i>
H-atom parameters constrained	Extinction coefficient: 0.031 (3)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$O3-H3 \cdots O2^i$	0.82	1.95	2.723 (2)	156

Symmetry code: (i) $-x + 1, y - \frac{1}{2}, -z + \frac{3}{2}$.

H atoms were positioned geometrically, with $C-H = 0.93-0.98$ Å, and refined in a riding model, with $U_{\text{iso}}(H) = 1.5U_{\text{eq}}(\text{carrier})$ for methyl H atoms and $1.2U_{\text{eq}}(\text{carrier})$ for all other H atoms.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINTE* (Bruker, 1997); data reduction: *SAINTE*; 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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