Acta Crystallographica Section E

Structure Reports Online

ISSN 1600-5368

2-Ethyl-5-nitroisoindoline-1,3-dione

Zu-Pei Liang,* Jian Li and Yun-Chen Zhang

Department of Chemistry and Chemical Engineering, Weifang University, Weifang 261061, People's Republic of China

Correspondence e-mail: zupeiliang@yahoo.com.cn

Key indicators

Single-crystal X-ray study T = 294 KMean $\sigma(\text{C-C}) = 0.003 \text{ Å}$ R factor = 0.046 wR factor = 0.136Data-to-parameter ratio = 14.1

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

In the title molecule, $C_{10}H_8N_20_4$, the phthalimide unit is essentially planar. In the crystal structure, weak intermolecular $C-H\cdots O$ hydrogen bonds link molecules into one-dimensional chains.

Received 18 November 2006 Accepted 27 November 2006

Comment

Phthalimides and N-substituted phthalimides are an important class of compounds because of their interesting biological activities (Lima *et al.*, 2002). The title compound, (I), is a precursor in the synthesis of N-substituted phthalimides and its crystal structure is reported here.

$$O_2N$$
 O_2N
 O_3N
 O_4N
 O_5N
 O_5N

The molecular structure of (I) is shown in Fig. 1. The phthalimide system is essentially planar to within 0.077 (3) Å. The geometry of the phthalimide system is comparable to that in the related crystal structures of 2-ethylisoindoline-1,3-dione (Liang *et al.*, 2006) and 5-amino-2-methylisoindoline-1,3-dione (Liang *et al.*, 2006). The dihedral angle between the nitro group plane and the phthalimide unit is 12.3 (2)°. In the crystal structure, weak intermolecular $C-H\cdots O$ hydrogen bonds link molecules into one-dimensional chains (Table 1 and Fig. 2).

Experimental

A mixture of 2-ethylisoindoline-1,3-dione (0.1 mol), nitric acid (0.11 mol) and sulfuric acid (0.55 mol) was kept at 353 K for 0.5 h.

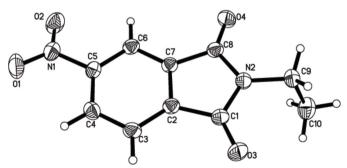


Figure 1The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

© 2007 International Union of Crystallography All rights reserved

organic papers

The mixture was then poured into cool water. After cooling, filtration, washing with water and drying, the title compound was obtained. 10 mg of (I) were dissolved in 10 ml acetic acid, and the solution was kept at room temperature for 15 d. Natural evaporation gave yellow single crystals of the title compound suitable for X-ray crystallographic analysis.

Crystal data

$C_{10}H_8N_2O_4$	Z = 4	
$M_r = 220.18$	$D_x = 1.453 \text{ Mg m}^{-3}$	
Orthorhombic, $P2_1/c$	Mo $K\alpha$ radiation	
a = 4.9438 (16) Å	$\mu = 0.12 \text{ mm}^{-1}$	
b = 20.655 (6) Å	T = 294 (2) K	
c = 9.858 (3) Å	Block, yellow	
$V = 1006.6 (6) \text{ Å}^3$	$0.24 \times 0.20 \times 0.18 \text{ mm}$	

Data collection

Bruker SMART CCD area-detector	5567 measured reflections
diffractometer	2058 independent reflections
φ and ω scans	1216 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan	$R_{\rm int} = 0.043$
(SADABS; Bruker, 1997)	$\theta_{\rm max} = 26.4^{\circ}$
$T_{\min} = 0.973, T_{\max} = 0.980$	

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.069P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.046$	+ 0.0778P]
$wR(F^2) = 0.136$	where $P = (F_0^2 + 2F_c^2)/3$
S = 0.99	$(\Delta/\sigma)_{\rm max} < 0.001$
2058 reflections	$\Delta \rho_{\text{max}} = 0.19 \text{ e Å}^{-3}$
146 parameters	$\Delta \rho_{\min} = -0.18 \text{ e Å}^{-3}$
H-atom parameters constrained	

Table 1 Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	D $ H$ $\cdot \cdot \cdot A$
C6−H6···O3 ⁱ C3−H3···O4 ⁱⁱ	0.93 0.93	2.50 2.40	3.376 (2) 3.314 (2)	157 167
Symmetry codes: (i)			. ,	107

H atoms were initially located in difference maps but were eventually placed in calculated positions and refined in the riding-model approximation, with C-H = 0.93-0.97 Å and $U_{iso}(H) = 1.2U_{eq}(C)$ or 1.5 $U_{\rm eq}$ (methyl C).

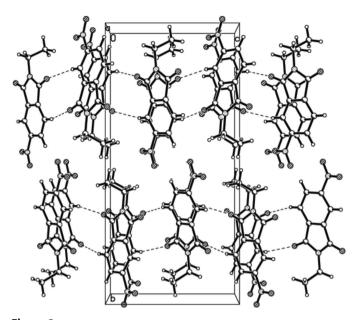


Figure 2 Part of the crystal structure of (I), showing hydrogen bonds as dashed

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; 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.

This work was supported by the Doctoral Fund of Weifang University.

References

Bruker (1997). SADABS, SMART, SAINT and SHELXTL. Bruker AXS Inc., Madison, Wisconsin, USA.

Liang, Z.-P. & Li, J. (2006). Acta Cryst. E62, o4126-o4127.

Liang, Z.-P. & Li, J. (2006). Acta Cryst. E62, o5439-o5440.

Lima, L. M., Castro, P., Machado, A. L., Frage, C. A. M., Lugniur, C., Moraes, V. L. G. & Barreiro, E. (2002). J. Biol. Org. Med. Chem. 10, 3067-3073.

Sheldrick, G. M. (1997). SHELXS97 and SHELXL97. University of Göttingen, Germany.