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Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.003 Å R factor = 0.038 wR factor = 0.102 Data-to-parameter ratio = 16.3

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

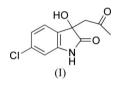
In the crystal structure of the title compound, $C_{11}H_{10}CINO_3$, an indole derivative, weak intermolecular hydrogen bonds cause the formation of a three-dimensional network.

6-Chloro-3-hydroxy-3-(2-oxopropyl)indolin-2-one

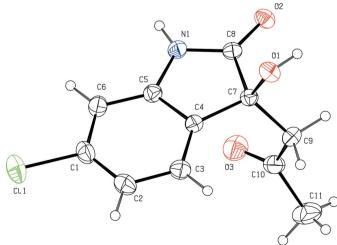
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Comment

Indole derivatives have many applications, oxindole being a common structural unit in various natural products and biologically active compounds. In particular, 3-substituted 3-hydroxyoxindole represents a prominent structural feature in such biological natural products (Tang *et al.*, 2001). We report here the crystal structure of one such oxindole derivative, the title compound, (I).



In the crystal structure of (I), bond lengths and angles are within normal ranges (Allen *et al.*, 1987). The indole ring systems (N1/C1–C8) are close to planar, with a maximum deviation of 0.052 (2) Å for atom C8. Weak intermolecular hydrogen bonds (Table 1) cause the formation of a threedimensional network (Fig. 2). N1–H1A···O2ⁱⁱ and O1– H1···O2ⁱ hydrogen bonds generate edge-fused centrosymmetric $R_2^2(9)$ ring motifs linked by C11–H11C···O3ⁱⁱⁱ inermolecular hydrogen bonds and this hydrogen bond generates $C_2^2(10)$ chains (Fig. 2) (Etter, 1990).



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Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 40% probability level.

Experimental

The title compound was synthesized according to a reported procedure (Chen *et al.*, 2006). Crystals suitable for data collection were obtained by slow evaporation of an *i*-PrOH solution at 283 K.

V = 1097.19 (18) Å³

2391 independent reflections 2277 reflections with $I > 2\sigma(I)$

H-atom parameters constrained

Absolute structure: Flack (1983),

Mo $K\alpha$ radiation

 $\mu = 0.34 \text{ mm}^{-1}$

T = 298 (2) K 0.30 × 0.20 × 0.10 mm

 $R_{\rm int} = 0.057$

 $\begin{array}{l} \Delta \rho_{\rm max} = 0.24 ~{\rm e}~{\rm \AA}^{-3} \\ \Delta \rho_{\rm min} = -0.23 ~{\rm e}~{\rm \AA}^{-3} \end{array}$

978 Friedel pairs

Flack parameter: 0.03 (8)

Z = 4

Crystal data

 $\begin{array}{l} C_{11}H_{10}\text{CINO}_{3}\\ M_{r} = 239.03\\ \text{Orthorhombic, } P2_{1}2_{1}2_{1}\\ a = 6.5958 \ (6) \\ \text{\AA}\\ b = 7.8459 \ (8) \\ \text{\AA}\\ c = 21.202 \ (2) \\ \text{\AA} \end{array}$

Data collection

Bruker SMART 4K CCD areadetector diffractometer Absorption correction: none 6687 measured reflections

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.038$ $wR(F^2) = 0.102$ S = 1.052391 reflections 147 parameters 1 restraint

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	<i>D</i> -H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$ \begin{array}{c} O1 - H1 \cdots O2^{i} \\ N1 - H1 A \cdots O2^{ii} \\ C11 - H11 C \cdots O3^{iii} \end{array} $	0.82 0.85 0.96	1.96 2.19 2.58	2.7510 (18) 2.9776 (19) 3.235 (3)	162 154 126
Symmetry codes: (i)	$r + \frac{1}{2} - v$	$+\frac{1}{2}$ -7 + 1.	(ii) $r - \frac{1}{2} - v + \frac{1}{2}$	-7 + 1 (iii)

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

O-bound H atoms and the N-bound H atom were located in a difference Fourier map and refined freely with fixed isotropic displacement parameters. All other H atoms were positioned geometrically, with C-H = 0.93, 0.97 or 0.96 Å for aromatic, methylene and methyl H atoms, respectively, and constrained to ride on their parent atoms, with $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(methyl C)$.

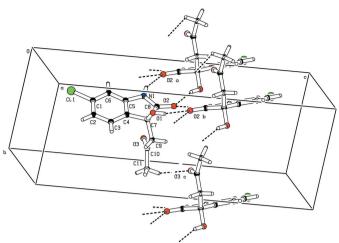


Figure 2

A partial packing diagram for (I). Hydrogen bonds are shown as dashed lines. [Symmetry codes: (a) $x - \frac{1}{2}, -y + \frac{1}{2}, -z + 1$; (b) $x + \frac{1}{2}, -y + \frac{1}{2}, -z + 1$; (c) $x + \frac{1}{2}, -y + \frac{3}{2}, -z + 1$.]

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXTL* (Bruker, 2001).

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