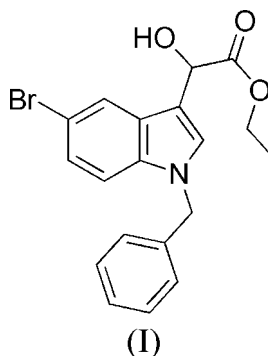


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Key indicators

Single-crystal X-ray study
 $T = 298$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
Disorder in main residue
 R factor = 0.043
 wR factor = 0.110
Data-to-parameter ratio = 15.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Ethyl 2-(1-benzyl-5-bromo-1*H*-indol-3-yl)-
2-hydroxyacetateThe crystal structure of the title compound, $\text{C}_{19}\text{H}_{18}\text{BrNO}_3$,
there are both intra- and intermolecular hydrogen bonds.Received 27 March 2007
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Comment

Indolylarylmaleimides have valuable pharmacological prop-
erties. For example, indolylarylmaleimide derivatives are
reported to be useful in the control and prevention of cancer,
central nervous system disorders, Alzheimer's disease,
cardiovascular diseases, dermatological diseases, inflamma-
tion, autoimmune diseases, diabetic complications and viral
diseases (Sudipta *et al.*, 2006). We report here the structure of
the title compound, (I) (Fig. 1), a key intermediate in the
synthesis of indolylarylmaleimides. The hydrogen bonding
(Table 1) is depicted in Fig. 2.

Experimental

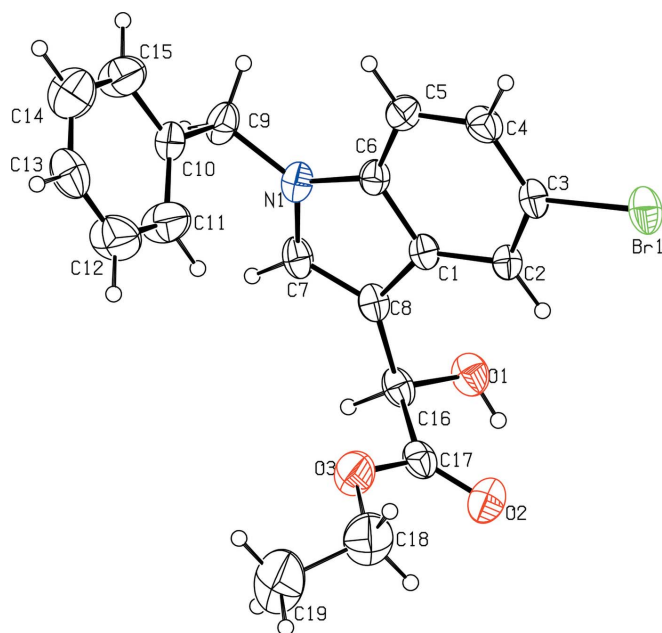
The title compound was synthesized according to the procedure of
Yuan *et al.* (2004). Crystals appropriate for data collection were
obtained by slow evaporation of a CH_2Cl_2 -acetone (3:1 *v/v*) solution
at 283 K.

Crystal data

$\text{C}_{19}\text{H}_{18}\text{BrNO}_3$	$V = 1735.5$ (2) Å ³
$M_r = 388.25$	$Z = 4$
Monoclinic, $P2_1/n$	Mo $K\alpha$ radiation
$a = 8.9104$ (7) Å	$\mu = 2.38$ mm ⁻¹
$b = 9.4736$ (7) Å	$T = 298$ (2) K
$c = 20.5732$ (16) Å	$0.20 \times 0.10 \times 0.10$ mm
$\beta = 92.0560$ (10)°	

Data collection

Bruker SMART 4K CCD diffractometer	3790 independent reflections
Absorption correction: none	2742 reflections with $I > 2\sigma(I)$
18902 measured reflections	$R_{\text{int}} = 0.041$

**Figure 1**

The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level. The minor disorder component is not shown. Atoms of the minor disorder components are joined with dashed lines.

Refinement

$$R[F^2 > 2\sigma(F^2)] = 0.043$$

$$wR(F^2) = 0.110$$

$$S = 1.02$$

3790 reflections

239 parameters

6 restraints

H-atom parameters constrained

$$\Delta\rho_{\max} = 0.67 \text{ e } \text{\AA}^{-3}$$

$$\Delta\rho_{\min} = -0.18 \text{ e } \text{\AA}^{-3}$$

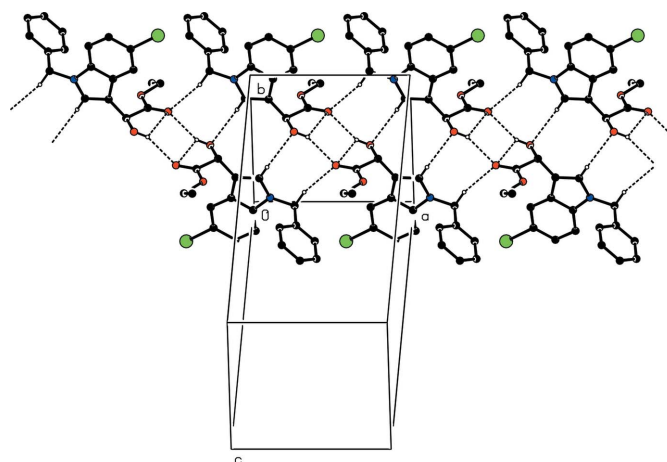
Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O1-H1\cdots O2^i$	0.82	2.24	3.006 (3)	155
$C7-H7\cdots O1^{ii}$	0.93	2.54	3.420 (3)	157
$C9-H9A\cdots O2^{iii}$	0.97	2.48	3.428 (3)	166
$O1-H1\cdots O2$	0.82	2.30	2.693 (3)	110

Symmetry codes: (i) $-x+1, -y+1, -z$; (ii) $-x+2, -y+1, -z$; (iii) $x+1, y, z$.

All H atoms were initially located in a difference Fourier map. The methyl H atoms were then constrained to an ideal geometry, with C—

**Figure 2**

The molecular packing of (I), showing chain formation along the a axis. Hydrogen bonds are drawn as dashed lines. H atoms not involved in hydrogen bonds have been omitted.

H distances of 0.98 \AA and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$, but each group was allowed to rotate freely about its C—C bond. All other H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C—H distances in the range $0.95\text{--}1.00 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. The occupancies of the disordered atoms C18/C18' and C19/C19' refined to $0.63(3):0.37(3)$.

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: *PLATON*.

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