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#### Key indicators

Single-crystal X-ray study T = 293 KMean  $\sigma$ (C–C) = 0.002 Å R factor = 0.040 wR factor = 0.128 Data-to-parameter ratio = 16.7

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,  $C_{16}H_{18}N_2O_4 \cdot H_2O$ , the substituted indole molecule forms a hydrogen bond to the water molecule. The water molecule in turn interacts with the carbonyl O atom of the acetoxy unit of an adjacent indole molecule and also with the O atom of the acetamide unit of another indole molecule, giving rise to a hydrogen-bonded helical chain structure that runs along the *b* axis of the monoclinic unit cell.

3-[2-(N,N-Diethylamino)glyoxyloyl]-

1H-indol-4-yl acetate monohydrate

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### Comment

3-[2-(N,N-Diethylamino)glyoxyloyl]-1H-indol-4-yl acetate is a reagent used in the synthesis of 3-[2-(diethylamino)ethyl]-4-indolol (4-HO-DET), a compound belonging to the 3-(2-aminoethyl)indole structural class of psychoactive drugs (Shulgin & Shulgin, 1997). 4-HO-DET will be converted into other compounds, in an extension of *in vivo* and *in vitro* studies of the structure–activity relationships of such compounds (An *et al.*, 2001; Bu *et al.*, 2002). 3-[2-(N,N-Diethylamino)glyoxyloyl]-1H-indol-4-yl acetate exists as the monohydrate, (I) (Fig. 1), the crystal structure of which is presented here.



The ketonic fragment of (I) (C9/C11/C12/O3) is approximately coplanar with the indole system [dihedral angle 17.5 (1)°], but almost perpendicular to the amide fragment [C11/C12/N2/O4; dihedral angle 82.8 (1)°]. The large twist is probably necessary to avoid crowding, but it appears to lengthen the C11-C12 bond somewhat.

The indole molecule forms a hydrogen bond to the water molecule, which in turn interacts with the carbonyl O atom of the acetoxy unit of an adjacent indole molecule and the O atom of the acetamide unit of another indole molecule (Table 2). These hydrogen bonds give rise to a helical chain that runs along the b axis of the monoclinic unit cell.

#### **Experimental**

The title compound was synthesized from 4-acetoxyindole (synthesized from 4-hydroxyindole and acetic anhydride), oxalyl chloride

© 2004 International Union of Crystallography Printed in Great Britain – all rights reserved and diethylamine, using the procedure of Shulgin & Shulgin (1997), and was obtained as colourless crystals by recrystallization from ether. The literature records the compound as being anhydrous.

 $D_{\rm x} = 1.254 {\rm Mg m}^{-3}$ 

Cell parameters from 931

Mo  $K\alpha$  radiation

reflections

 $\mu = 0.09 \text{ mm}^{-1}$ 

T = 293 (2) K

Block, colourless  $0.50 \times 0.38 \times 0.36$  mm

 $\theta = 2.5 - 26.8^{\circ}$ 

#### Crystal data

 $\begin{array}{l} {\rm C_{16}H_{18}N_{2}O_{4} \cdot H_{2}O} \\ M_{r} = 320.34 \\ {\rm Monoclinic}, \ P_{2_{1}}/a \\ a = 12.646 \ (2) \ {\rm \AA} \\ b = 10.518 \ (1) \ {\rm \AA} \\ c = 12.904 \ (2) \ {\rm \AA} \\ \beta = 98.703 \ (2)^{\circ} \\ V = 1696.7 \ (4) \ {\rm \AA}^{3} \\ Z = 4 \end{array}$ 

#### Data collection

Bruker SMART CCD area-detector<br/>diffractometer2880 reflections with  $I > 2\sigma(I)$ <br/> $R_{int} = 0.012$ <br/> $\varphi$  and  $\omega$  scans $\varphi$  and  $\omega$  scans $\theta_{max} = 27.0^{\circ}$ <br/> $h = -16 \rightarrow 16$ <br/>9454 measured reflections9454 measured reflections $k = -11 \rightarrow 13$ <br/> $l = -10 \rightarrow 16$ 

#### Refinement

 Refinement on  $F^2$   $w = 1/[\sigma^2(F_o^2) + (0.0694P)^2$ 
 $R[F^2 > 2\sigma(F^2)] = 0.040$   $w = 1/[\sigma^2(F_o^2) + (0.0694P)^2$ 
 $wR(F^2) = 0.128$  where  $P = (F_o^2 + 2F_c^2)/3$  

 S = 1.02  $(\Delta/\sigma)_{max} = 0.001$  

 3695 reflections
  $\Delta\rho_{max} = 0.30 \text{ e Å}^{-3}$  

 221 parameters
  $\Delta\rho_{min} = -0.17 \text{ e Å}^{-3}$  

 H atoms treated by a mixture of independent and constrained refinement
  $A^{-3}$ 

Table 1				
Selected	geometric	parameters	(Å,	°).

O1-C2	1.353 (2)	C3-C8	1.399 (2)
O1-C3	1.402 (2)	C4-C5	1.393 (2)
O2-C2	1.199 (2)	C5-C6	1.370 (2)
O3-C11	1.225 (2)	C6-C7	1.392 (2)
O4-C12	1.236 (2)	C7-C8	1.410 (2)
N1-C7	1.379 (2)	C8-C9	1.449 (2)
N1-C10	1.339 (2)	C9-C10	1.383 (2)
N2-C12	1.327 (2)	C9-C11	1.439 (2)
N2-C15	1.467 (2)	C11-C12	1.526 (2)
N2-C13	1.467 (2)	C13-C14	1.503 (3)
C1-C2	1.487 (2)	C15-C16	1.480 (3)
C3-C4	1.372 (2)		
C2-O1-C3	117.0 (1)	C6-C7-C8	123.7 (1)
C7-N1-C10	109.4 (1)	C3-C8-C7	116.5 (1)
C12-N2-C13	122.9(1)	C3-C8-C9	137.4 (1)
C12-N2-C15	119.5 (1)	C7-C8-C9	106.1 (1)
C13-N2-C15	117.6 (1)	C8-C9-C10	105.9 (1)
O1-C2-O2	122.8 (1)	C10-C9-C11	123.4 (1)
O1-C2-C1	111.6(1)	C11-C9-C8	130.7 (1)
O2-C2-C1	125.6 (2)	N1-C10-C9	110.7 (1)
O1-C3-C4	117.7 (1)	O3-C11-C9	125.8 (1)
O1-C3-C8	121.7 (1)	O3-C11-C12	116.9 (1)
C4-C3-C8	120.5 (1)	C9-C11-C12	117.3 (1)
C3-C4-C5	121.1 (2)	O4-C12-N2	124.0 (1)
C4-C5-C6	121.0 (2)	O4-C12-C11	118.9 (1)
C5-C6-C7	117.2 (1)	N2-C12-C11	117.0 (1)
N1-C7-C6	128.4 (1)	N2-C13-C14	113.2 (2)
N1-C7-C8	108.0 (1)	N2-C15-C16	112.4 (2)



#### Figure 1

A view of the molecular structure of (I), showing the atom-numbering scheme and with displacement ellipsoids drawn at the 50% probability level. H atoms are shown as spheres of arbitrary radii. The dashed line indicates a hydrogen bond.

# Table 2Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\overline{\begin{array}{c} N1 - H1N \cdots O1W \\ O1W - H1W1 \cdots O2^{i} \end{array}}$	0.86 (1) 0.85 (1)	1.91 (1) 1.99 (1)	2.743 (2) 2.841 (2)	161 (2) 175 (2)
$O1W - H1W2 \cdots O4^{n}$	0.85(1)	1.98 (1)	2.810 (2)	165 (2)
Summatry and (i) 1	× 1 × 1 ===	(;;) 1 x y 1	1 -	

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

H atoms on C atoms were placed at calculated positions in a riding model approximation, with C–H distances of 0.93 for aromatic H atoms, 0.96 for methyl H atoms and 0.97 Å for methylene H atoms, and with  $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$ . The amine and water H atoms were located and refined with N–H and O–H distance restraints of 0.85 (1) Å.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1999); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP*II (Johnson, 1976); software used to prepare material for publication: *SHELXL*97.

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