

# 1'-(4-Methoxybenzoyl)acenaphthene-1-spiro-3'-pyrrolizidine-2'-spiro-3''-1H-indole-2,2''(1H,3''H)-dione

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## Key indicators

Single-crystal X-ray study

$T = 293\text{ K}$

Mean  $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$

$R$  factor = 0.085

$wR$  factor = 0.196

Data-to-parameter ratio = 14.6

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

The N—C and C—C bond distances in the pyrrolizidine moiety of the title compound,  $\text{C}_{33}\text{H}_{26}\text{N}_2\text{O}_4$ , are slightly longer than the normal values. This is due to the steric forces caused by bulky substituents on the pyrrolizidine ring system. The acenaphthene ketone O atom is  $-0.214(3)\text{ \AA}$  from the acenaphthene plane, while the indole ketone O atom is displaced by only  $0.004(3)\text{ \AA}$  from the indole plane. The molecular structure is stabilized by intramolecular C—H $\cdots$ O interactions. The crystal packing is stabilized by C—H $\cdots$ O intermolecular interactions.

## Comment

Among a variety of heterocycles that have been explored for the development of pharmaceutically important molecules, indoles have played an important role. Some of them have received considerable attention as potential antimicrobial agents (Mogilaiah *et al.*, 2001). Spiro-indoles have also been reported to show fungicidal activity (Ali *et al.*, 1989). In view of the pharmacological importance of the title compound, (I), and as a continuation of our studies, an X-ray structural analysis of the compound was carried out and the results are reported here.

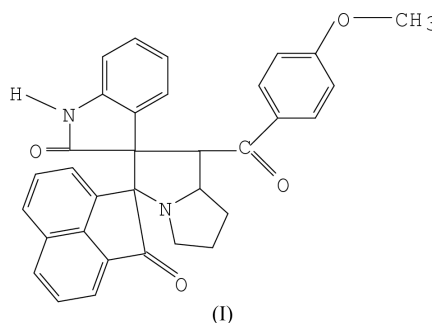


Fig. 1 shows a displacement ellipsoid diagram of the molecule of (I) with the atomic numbering scheme. Selected geometric parameters are given in Table 1.

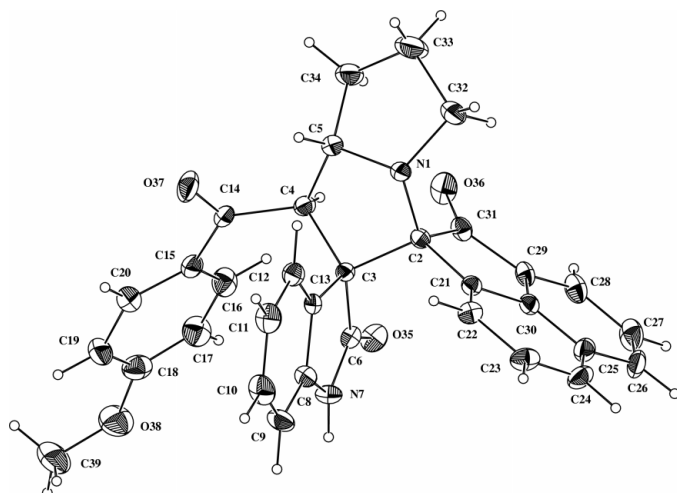
The N—C and C—C bond lengths in the pyrrolizidine moiety are slightly longer than the normal values reported for similar structures (Seshadri *et al.*, 2003; Abdul Ajees *et al.*, 2002). This may be due to steric forces caused by the bulky substituents on the pyrrolizidine moiety.

The ketone atom O36 is  $-0.214(3)\text{ \AA}$  from the acenaphthene plane, while the ketone atom O35 is displaced by only  $0.004(3)\text{ \AA}$  from the oxindole plane, probably due to the different environment of the two O atoms, O36 being a hydrogen-bond acceptor from C10—H10, while there is no hydrogen bond involving O35 (Table 2). The ketone atom O37 is  $0.731(3)\text{ \AA}$  out of the C4/C14—C20 plane, with a C14=O37

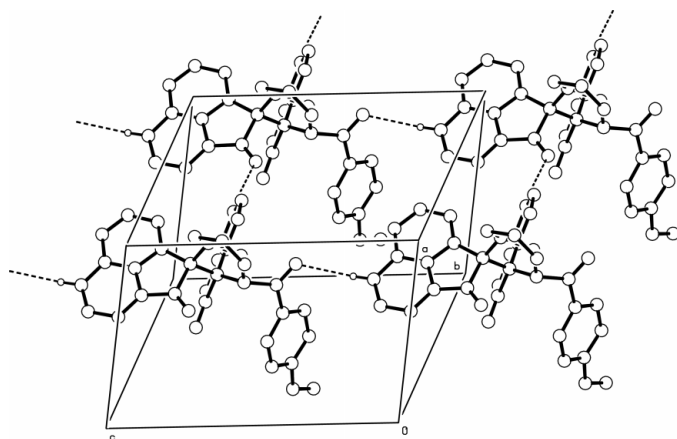
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**Figure 1**  
View of (I) (50% probability displacement ellipsoids).



**Figure 2**  
Packing of the structure of (I).

bond direction defined by the torsion angles  $O37-C14-C15-C20 = -24.1(5)^\circ$  and  $O37-C14-C15-C16 = 157.3(4)^\circ$ . Atom O37 is an acceptor of a weak intramolecular interaction from  $C5-H5$ .

The orientation of the methoxy group with respect to the benzene ring is defined by torsion angles  $C19-C18-O38-C39 = 3.5(6)^\circ$  and  $C17-C18-O38-C39 = -176.5(4)^\circ$ .

The  $C2-C5/N1$  ring of the pyrrolizidine moiety has an envelope conformation, with Cremer & Pople (1975) puckering parameters  $q_2 = 1.992(3) \text{ \AA}$  and  $\varphi = 71.5(1)^\circ$ , and the smallest displacement asymmetry parameter (Nardelli, 1983) is  $\Delta_S(C2) = 0.024(3)$ . The five-membered  $N1/C5/C32-C34$  ring of the pyrrolizidine moiety adopts a twist conformation, with puckering parameters  $q_2 = 0.588(9) \text{ \AA}$  and  $\varphi = -141.6(4)^\circ$ , the displacement asymmetry parameters being  $\Delta_S(C33) = 0.023(3)$  and  $\Delta_2(C34) = 0.090(3)$ .

The molecular structure is influenced by  $C-H \cdots O$  intramolecular interactions. The crystal packing is stabilized by  $C-H \cdots O$  intermolecular interactions (Table 2).

## Experimental

A mixture of (*E*)-3-(*p*-methoxyphenacylidene)oxindole (1 mmol), acenaphthenequinone (1 mmol) and L-proline (1 mmol) was stirred in aqueous methanol at room temperature. The resulting crude product was purified by column chromatography to obtain the title compound, which was recrystallized from chloroform–methanol (1:1).

### Crystal data

$C_{33}H_{26}N_2O_4$	$Z = 2$
$M_r = 514.56$	$D_x = 1.326 \text{ Mg m}^{-3}$
Triclinic, $P\bar{1}$	Mo $K\alpha$ radiation
$a = 10.2215(11) \text{ \AA}$	Cell parameters from 1062 reflections
$b = 10.6228(12) \text{ \AA}$	$\theta = 2.7-21.0^\circ$
$c = 12.3584(13) \text{ \AA}$	$\mu = 0.09 \text{ mm}^{-1}$
$\alpha = 104.178(2)^\circ$	$T = 293(2) \text{ K}$
$\beta = 97.238(2)^\circ$	Block, colorless
$\gamma = 91.499(2)^\circ$	$0.21 \times 0.20 \times 0.20 \text{ mm}$
$V = 1288.4(2) \text{ \AA}^3$	

### Data collection

Bruker SMART APEX area-detector diffractometer	$R_{\text{int}} = 0.029$
$\omega$ scans	$\theta_{\text{max}} = 28.0^\circ$
7866 measured reflections	$h = -12 \rightarrow 11$
5149 independent reflections	$k = -13 \rightarrow 13$
3011 reflections with $I > 2\sigma(I)$	$l = -16 \rightarrow 12$

### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0752P)^2 + 0.2551P]$
$R[F^2 > 2\sigma(F^2)] = 0.085$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.196$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.09$	$\Delta\rho_{\text{max}} = 0.44 \text{ e \AA}^{-3}$
5149 reflections	$\Delta\rho_{\text{min}} = -0.17 \text{ e \AA}^{-3}$
352 parameters	
H-atom parameters constrained	

**Table 1**

Selected geometric parameters ( $\text{\AA}$ ,  $^\circ$ ).

$N1-C2$	1.461(4)	$C2-C3$	1.568(4)
$N1-C32$	1.482(4)	$C3-C4$	1.563(4)
$N1-C5$	1.487(4)	$C5-C34$	1.525(4)
$O37-C14-C15-C20$	$-24.1(5)$	$C17-C18-O38-C39$	$-176.5(4)$
$O37-C14-C15-C16$	$157.3(4)$	$C19-C18-O38-C39$	$3.5(6)$

**Table 2**

Hydrogen-bonding geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$C4-H4 \cdots O36$	0.98	2.40	3.009(4)	120
$C5-H5 \cdots O37$	0.98	2.40	2.824(4)	105
$C10-H10 \cdots O36^i$	0.93	2.39	3.301(5)	165
$C26-H26 \cdots O37^{ii}$	0.93	2.49	3.375(5)	159

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

All H atoms were positioned geometrically and allowed to ride on their parent atoms, with  $C-H = 0.93-0.98 \text{ \AA}$  and  $U_{\text{iso}}(H) = 1.5U_{\text{eq}}(C)$  for methyl H atoms and  $1.2U_{\text{eq}}(C)$  for other H atoms.

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:

*ZORTEP* (Zsolnai, 1997) and *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97* and *PARST* (Nardelli, 1995).

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