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Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$
 R factor = 0.053
 wR factor = 0.148
Data-to-parameter ratio = 18.2

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

5''-Benzylidene-1'-methyl-4'-phenylindole-3-spiro-2'-pyrrolidine-3'-spiro-3''-piperidine-2(3H),4''-dione

In the title compound, $\text{C}_{30}\text{H}_{29}\text{N}_3\text{O}_2$, the dihedral angle between the rings in the indole moiety is $3.3(1)^\circ$. The piperidinone ring adopts a half-chair conformation. The dihedral angle between the pyrrolidine ring and the oxindole moiety is $77.2(1)^\circ$. The packing is stabilized by an $\text{N}-\text{H}\cdots\text{O}$ hydrogen bond and intermolecular $\text{C}-\text{H}\cdots\text{N}$ interactions.

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Comment

The spiro ring system containing an indole and a pyrrolidine ring is present in many biologically important and pharmacologically relevant alkaloids (Cordell, 1981). Pyrrolidine compounds are found to be antimicrobial and antifungal (Amal Raj *et al.*, 2003). As a result of the medicinal importance of the compound and also as a continuation of our studies, the X-ray analysis of the title compound, (I), was carried out and the results are presented here.

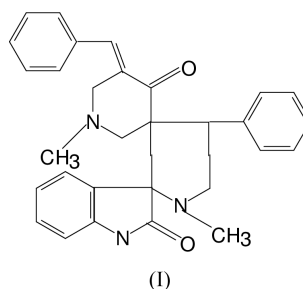


Fig. 1 shows a displacement ellipsoid diagram of the molecule with the atomic numbering scheme. Selected geometric

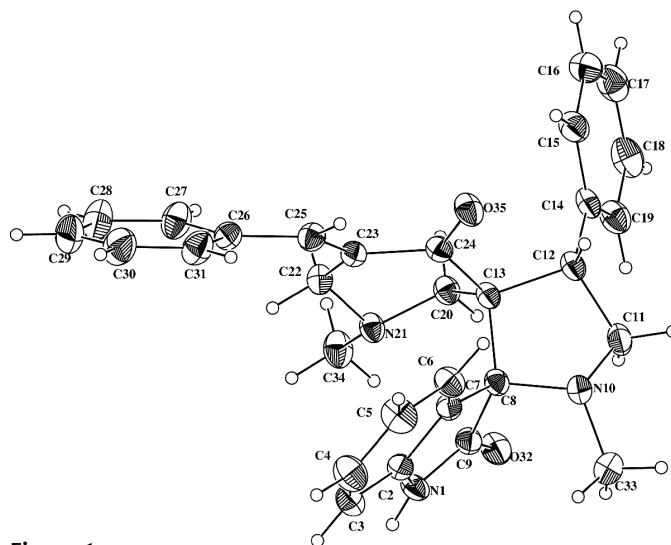


Figure 1
View of (I) (50% probability displacement ellipsoids).

parameters are given in Table 1. The bond lengths in the pyrrolidine moiety are slightly greater than the values reported for similar structures (Jeyabharathi *et al.*, 2001; Seshadri *et al.*, 2003). This may be due to steric forces caused by the bulky substituents on the pyrrolidine moiety. The sum of the angles at atom N10 of the pyrrolidine moiety (339.2°) is in accordance with sp^3 hybridization (Beddoes *et al.*, 1986). The sum of angles at N21 (334.6°) of the piperidinone ring reveal it to be sp^3 hybridized.

Atom O32 is essentially coplanar with the heterocyclic ring to which it is attached, with a deviation of $0.098(1) \text{ \AA}$.

The phenyl ring is attached to the pyrrolidine ring in an equatorial position. The indole moiety (atoms C2–C9/N1) is planar, the dihedral angle between the planes of the heterocyclic and benzene rings being $3.3(1)^\circ$.

The asymmetry parameters (Nardelli, 1995) $q_2 = 0.322(2) \text{ \AA}$, $\varphi = -167.5(4)^\circ$ and $\Delta C_2[\text{C13}–\text{C8}] = 0.0594(1)^\circ$ reveal the conformation of the pyrrolidine ring to be half-chair. The piperidinone ring also adopts a half-chair conformation. This is confirmed by the asymmetry parameters $q_2 = 0.085(2) \text{ \AA}$, $\varphi = 47.7(1)^\circ$, $\Delta C_2[\text{C20}] = 0.0494(7)^\circ$ and $\Delta_S[\text{C23}] = 0.0459(5)^\circ$.

The molecular structure is influenced by C–H...O intramolecular interactions. In the crystal structure, N1–H1...O32ⁱ hydrogen bonds link inversion-related molecules to form dimers (Fig. 2 and Table 2). The crystal structure is also stabilized by C–H...N intermolecular interactions. In addition, symmetry-related molecules are also linked by weak C–H... π intermolecular interactions, such that atom H3 is 2.68 \AA from the centroid of the phenyl ring (C14–C19) at $(x-1, y, z)$, with a C3–H3...centroid angle of 131° and a C3...centroid distance of $3.359(2) \text{ \AA}$.

Experimental

A mixture of dipolarophile (dibenzylidene-*N*-methylpiperidone), isatin and sarcosine was refluxed in aqueous methanol until the starting materials had disappeared (about 3–4 h), as evidenced by thin-layer chromatography. When the reaction was complete, the solvent was removed *in vacuo* and the residue was chromatographed on silica gel using a hexane–ethyl acetate mixture as eluant and recrystallized from methanol to give (I).

Crystal data

$\text{C}_{30}\text{H}_{29}\text{N}_3\text{O}_2$	$D_x = 1.222 \text{ Mg m}^{-3}$
$M_r = 463.56$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 2146 reflections
$a = 10.6889(7) \text{ \AA}$	$\theta = 2.4–20.4^\circ$
$b = 18.9025(12) \text{ \AA}$	$\mu = 0.08 \text{ mm}^{-1}$
$c = 12.5270(8) \text{ \AA}$	$T = 293(2) \text{ K}$
$\beta = 95.283(1)^\circ$	Block, colourless
$V = 2520.3(3) \text{ \AA}^3$	$0.21 \times 0.20 \times 0.20 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART APEX CCD area-detector diffractometer	3798 reflections with $I > 2\sigma(I)$
ω scans	$R_{\text{int}} = 0.031$
Absorption correction: none	$\theta_{\text{max}} = 28.0^\circ$
15 727 measured reflections	$h = -14 \rightarrow 13$
5738 independent reflections	$k = -21 \rightarrow 24$
	$l = -13 \rightarrow 16$

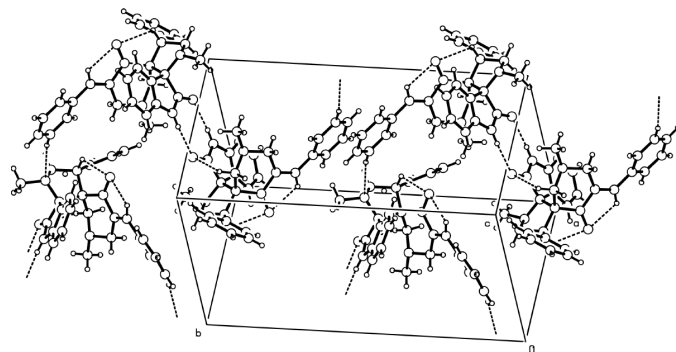


Figure 2
Packing diagram, with hydrogen bonds shown as dashed lines.

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.053$	$w = 1/[\sigma^2(F_o^2) + (0.0826P)^2]$
$wR(F^2) = 0.148$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 0.99$	$(\Delta/\sigma)_{\text{max}} < 0.001$
5738 reflections	$\Delta\rho_{\text{max}} = 0.25 \text{ e \AA}^{-3}$
316 parameters	$\Delta\rho_{\text{min}} = -0.15 \text{ e \AA}^{-3}$

Table 1

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

N10–C11	1.453(2)	N10–C33	1.463(2)
C9–N1–C2	111.7(1)	C11–N10–C8	107.4(1)
C11–N10–C33	116.2(2)	C33–N10–C8	115.6(1)
C11–C12–C14–C19	27.2(2)		

Table 2

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

$D–H\dots A$	$D–H$	$H\dots A$	$D\dots A$	$D–H\dots A$
C12–H12...O35	0.98	2.33	2.804(2)	109
C20–H20B...O32	0.97	2.35	2.898(2)	115
C25–H25...O35	0.93	2.41	2.770(2)	103
N1–H1...O32 ⁱ	0.86	2.06	2.883(2)	159
C28–H28...N10 ⁱⁱ	0.93	2.61	3.520(3)	168

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

All H atoms were positioned geometrically and allowed to ride on their parent atoms, with C–H = $0.93–0.98 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for methyl H atoms and $1.2U_{\text{eq}}(\text{C})$ 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, 1990); software used to prepare material for publication: SHELXL97 and PARST (Nardelli, 1995).

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