

4'-(4-Methylphenyl)-3'-nitrospiro[1*H*-indole-3,2'-pyrrolidin]-2-oneS. Selvanayagam,^a
P. Rathisuganya,^b B. Shaherin,^b
D. Velmurugan,^{a*} K. Ravikumar^c
and M. Poornachandran^d^aDepartment of Crystallography and Biophysics, University of Madras, Guindy Campus, Chennai 600 025, India, ^bDepartment of Bioinformatics, University of Madras, Guindy Campus, Chennai 600 025, India, ^cLaboratory of X-ray Crystallography, Indian Institute of Chemical Technology, Hyderabad 500 007, India, and ^dDepartment of Organic Chemistry, University of Madras, Guindy Campus, Chennai 600 025, India

Correspondence e-mail: d_velu@yahoo.com

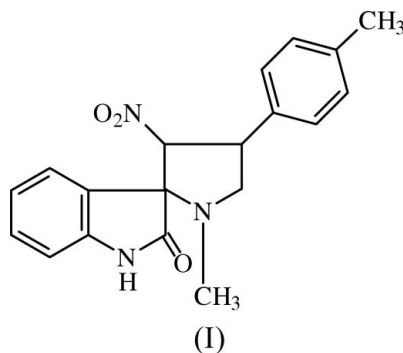
Key indicators

Single-crystal X-ray study
T = 293 K
Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$
R factor = 0.063
wR factor = 0.151
Data-to-parameter ratio = 17.9For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

In the title compound, C₁₉H₁₉N₃O₃, the oxindole residue and the 4-methylphenyl ring are almost perpendicular to the pyrrolidine ring. The pyrrolidine ring adopts an envelope conformation. The molecular packing is stabilized by N—H···O hydrogen bonds and C—H···O interactions, in addition to van der Waals forces.

Comment

Heterocyclic compounds, particularly compounds containing five- and six-membered rings, have occupied a prominent place among various classes of organic compounds because of their diverse biological activities. Spiro[indole-pyrrolidine] ring systems have acquired a special place in the field of heterocyclic chemistry because they are a frequently encountered structural motif in many pharmacologically relevant alkaloids (Amal Raj *et al.*, 2003). These derivatives also possess anti-influenza virus (Stylianakis *et al.*, 2003) and anticonvulsant (Obniska *et al.*, 2002) activities. In order to determine the conformation of the title compound, (I), the present X-ray crystal structure determination was undertaken.



The molecular structure of (I) is illustrated in Fig. 1. Selected geometric parameters are presented in Table 1. The geometry of the pyrrolidine ring in (I) compares well with that reported in other related structures (see, for example, Selvanayagam *et al.*, 2004; Gzella & Wrzeczono, 1990).

The sum of the angles at N1 of the pyrrolidine ring [339.9°] is in accordance with *sp*³ hybridization. The methyl group is attached equatorially to the pyrrolidine ring.

The dihedral angle between the oxindole and pyrrolidine rings (mean plane calculated through atoms N1/C1/C2/C3) is 87.1 (1)°, and that between the *p*-tolyl and pyrrolidine rings is 88.9 (1)°. This indicates that the oxindole residue and the *p*-tolyl ring are almost perpendicular to the pyrrolidine ring. The pyrrolidine ring adopts an envelope conformation, with

Received 5 October 2005

Accepted 11 October 2005

Online 15 October 2005

puckering parameters (Cremer & Pople, 1975) $q_2 = 0.414(2) \text{ \AA}$ and $\varphi = -43.8(3)^\circ$. Atom C4 deviates by $0.632(2) \text{ \AA}$ from the least-squares plane through the remaining four atoms.

In the molecular packing, N—H...O hydrogen bonds link inversion-related molecules. The molecules are further linked by C—H...O interactions (Table 2).

Experimental

A mixture of 4-methylnitrostyrene (1 mmol), isatin (1 mmol) and sarcosine (1 mmol) was refluxed in methanol (20 ml) for 6 h. After completion of the reaction, the solvent was evaporated *in vacuo*. The residue was subjected to column chromatography using a hexane and ethyl acetate mixture (9:1) to yield the title compound. Single crystals of (I) suitable for X-ray diffraction were obtained from methanol.

Crystal data

$C_{19}H_{19}N_3O_3$	Mo $K\alpha$ radiation
$M_r = 337.37$	Cell parameters from 9788 reflections
Orthorhombic, $Pbca$	$\theta = 2.7\text{--}26.6^\circ$
$a = 9.8697(8) \text{ \AA}$	$\mu = 0.09 \text{ mm}^{-1}$
$b = 16.4460(14) \text{ \AA}$	$T = 293(2) \text{ K}$
$c = 21.4643(18) \text{ \AA}$	Block, colourless
$V = 3484.0(5) \text{ \AA}^3$	$0.26 \times 0.24 \times 0.16 \text{ mm}$
$Z = 8$	
$D_x = 1.286 \text{ Mg m}^{-3}$	

Data collection

Bruker SMART APEX CCD area-detector diffractometer	2927 reflections with $I > 2\sigma(I)$
ω scans	$R_{\text{int}} = 0.040$
Absorption correction: none	$\theta_{\text{max}} = 28.0^\circ$
19862 measured reflections	$h = -12 \rightarrow 12$
4074 independent reflections	$k = -21 \rightarrow 21$
	$l = -28 \rightarrow 28$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0679P)^2 + 1.113P]$
$R[F^2 > 2\sigma(F^2)] = 0.063$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.151$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.05$	$\Delta\rho_{\text{max}} = 0.32 \text{ e \AA}^{-3}$
4074 reflections	$\Delta\rho_{\text{min}} = -0.22 \text{ e \AA}^{-3}$
228 parameters	
H-atom parameters constrained	

Table 1

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

N1—C5	1.449(3)	C1—C2	1.538(3)
N1—C4	1.452(2)	C2—C3	1.526(2)
N1—C1	1.465(2)	C3—C4	1.540(2)
C5—N1—C4	116.2(2)	O1—N2—O2	124.0(2)
C5—N1—C1	114.7(2)	O1—N2—C3	119.7(2)
C4—N1—C1	109.0(2)		
C5—N1—C1—C2	-154.9(2)	C7—C8—C9—C12	179.7(2)
C5—N1—C4—C3	171.1(2)	C12—C9—C10—C11	179.9(2)

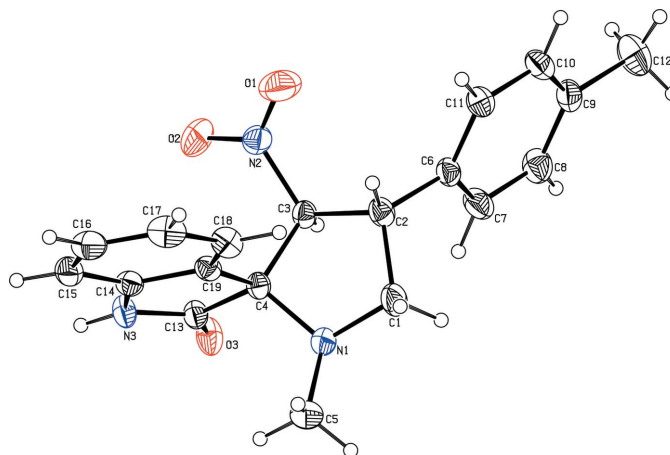


Figure 1

The molecular structure and atom-numbering scheme for (I). Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

Table 2

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

$D\text{—}H\cdots A$	$D\text{—}H$	$H\cdots A$	$D\cdots A$	$D\text{—}H\cdots A$
N3—H3...O3 ⁱ	0.86	2.00	2.849(2)	171
C16—H16...O3 ⁱⁱ	0.93	2.60	3.525(3)	174
C18—H18...O1 ⁱⁱⁱ	0.93	2.58	3.430(3)	153

Symmetry codes: (i) $-x + 1, -y, -z + 1$; (ii) $-x + \frac{3}{2}, y - \frac{1}{2}, z$; (iii) $x + \frac{1}{2}, y, -z + \frac{3}{2}$.

The H atoms were positioned geometrically and treated as riding on their parent C atoms, with C—H distances of 0.93–0.98 \AA and an N—H distance of 0.86 \AA , and with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for methyl H and $1.2U_{\text{eq}}(\text{C}, \text{N})$ for other H. In addition, the methyl groups were allowed to rotate but not to tip.

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: *ORTEP3* (Farrugia, 1997) and *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97* and *PARST* (Nardelli, 1995).

SS thanks the Council of Scientific and Industrial Research (CSIR) for providing a Senior Research Fellowship. DV acknowledges the University Grants Commission (UGC) and the Department of Bio-Technology (DBT), India, for providing computing facilities under Major Research Projects, and also thanks the Department for financial support under the UGC-SAP and DST-FIST programmes.

References

- Amal Raj, A., Raghunathan, R., Sridevikumari, M. R. & Raman, N. (2003). *Bioorg. Med. Chem.* **11**, 407–419.
- Bruker (2001). *SAINT* (Version 6.28a) and *SMART* (Version 5.625). Bruker AXS Inc., Madison, Wisconsin, USA.
- Cremer, D. & Pople, J. A. (1975). *J. Am. Chem. Soc.* **97**, 1354–1358.
- Farrugia, L. J. (1997). *J. Appl. Cryst.* **30**, 565.
- Gzella, A. & Wrzeczono, U. (1990). *Acta Cryst.* **C46**, 2107–2109.
- Nardelli, M. (1995). *J. Appl. Cryst.* **28**, 659.
- Obniska, J., Zeic, A. & Zagorska, A. (2002). *Acta Pol. Pharm.* **59**, 209–213.

Selvanayagam, S., Velmurugan, D., Ravikumar, K., Narasinga Rao, S., Poor-nachandran, M. & Raghunathan, R. (2004). *Acta Cryst.* **E60**, o2157–o2159.
Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.

Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.

Stylianakis, I., Kolocouris, A., Kolocouris, N., Fytas, G., Foscolos, G. B., Padalko, E., Neyts, J. & Declerq, E. (2003). *Bioorg. Med. Chem. Lett.* **10**, 1699–1703.