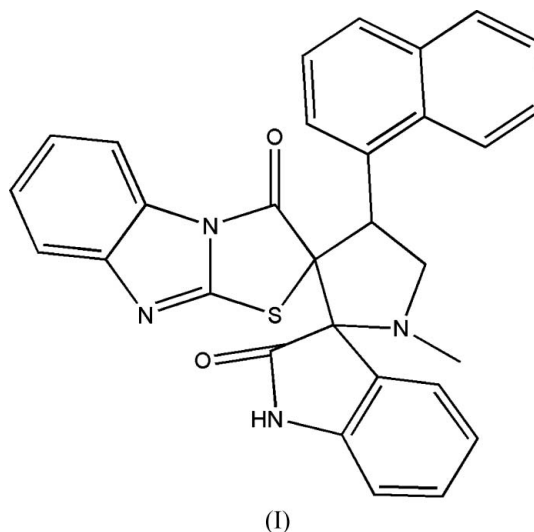


Xiu-Ling Zhang,^{a*} Ai-Zhen Liu^a
and Mei-Fang Jin^b^aChemistry Department, Dezhou University,
Dezhou Shandong 253011, People's Republic
of China, and ^bChemical Engineering
Department, Anyang Institute of Technology,
Anyang Henan 455000, People's Republic of
ChinaCorrespondence e-mail:
zx11962432@yahoo.com.cn

Key indicators

Single-crystal X-ray study
 $T = 294\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.043
 wR factor = 0.114
Data-to-parameter ratio = 12.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**1'-Methyl-4'-(1-naphthyl)-1*H*-indole-3-spiro-
2'-pyrrolidine-3'-spiro-2''-thiazolo[3,2-*a*]-
benzimidazole-2(3*H*),3''(2''*H*)-dione**In the title compound, $\text{C}_{30}\text{H}_{22}\text{N}_4\text{O}_2\text{S}$, two spiro junctions link a planar 2-oxoindole ring, a pyrrolidine ring and a thiazolo[3,2-*a*][1,3]benzimidazol-3-one system. Molecules form dimers connected by $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds.Received 9 May 2006
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Comment

Spiro compounds represent an important class of naturally occurring substances characterized by highly pronounced biological properties (James *et al.*, 1991; Kobayashi *et al.*, 1991). 1,3-Dipolar cycloaddition reactions are important processes for the construction of spiro compounds (Caramella & Grunanger, 1984).

In this paper, the synthesis and structure of the title two-spiro-junction compound, (I) (Fig. 1), are reported. Two spiro junctions exist in the molecule, which contains a 2-oxoindole ring, a pyrrolidine ring and a thiazolo[3,2-*a*][1,3]benzimidazol-3-one system. The 2-oxoindole ring (C10–C17/N4) is essentially planar, with a mean deviation of 0.054 (5) Å. The packing can be described as a dimeric arrangement of molecules linked through $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds, as shown in Table 1. Atom N2 of the thiazolo[3,2-*a*][1,3]benzimidazol-3-one system acts as an acceptor in a hydrogen-bond interaction with the 2-oxoindole N4 atom in a symmetry-related molecule at $(-x, -y + 1, -z + 1)$.

Experimental

A mixture of 2-(1-naphthylmethylene)thiazolo[3,2-*a*][1,3]benzimidazol-3-one (1 mmol), isatin (1 mmol) and sarcosine (1 mmol) was

refluxed in methanol (60 ml) until the disappearance of the starting material was evidenced by thin-layer chromatography. After evaporation of the solvent, the residue was separated by column chromatography (silica gel; petroleum ether–ethyl acetate 5:1) to give (I) (m.p. 507–508 K). Compound (I) (20 mg) was dissolved in acetone (15 ml) and the solution was left to evaporate at room temperature for 8 d, giving colorless single crystals of (I) suitable for X-ray analysis.

Crystal data

$C_{30}H_{22}N_4O_2S$ $Z = 8$
 $M_r = 502.58$ $D_x = 1.358 \text{ Mg m}^{-3}$
 Orthorhombic, $Pbca$ Mo $K\alpha$ radiation
 $a = 16.126 (4) \text{ \AA}$ $\mu = 0.17 \text{ mm}^{-1}$
 $b = 12.852 (4) \text{ \AA}$ $T = 294 (2) \text{ K}$
 $c = 23.725 (6) \text{ \AA}$ Block, colorless
 $V = 4917 (2) \text{ \AA}^3$ $0.24 \times 0.20 \times 0.10 \text{ mm}$

Data collection

Bruker APEX CCD area-detector 24035 measured reflections
 diffractometer 4331 independent reflections
 φ and ω scans 2725 reflections with $I > 2\sigma(I)$
 Absorption correction: multi-scan $R_{int} = 0.071$
 (SADABS; Bruker, 1997) $\theta_{max} = 25.0^\circ$
 $T_{min} = 0.961, T_{max} = 0.983$

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.0527P)^2 + 0.4279P]$
 $R[F^2 > 2\sigma(F^2)] = 0.043$ where $P = (F_o^2 + 2F_c^2)/3$
 $wR(F^2) = 0.114$ $(\Delta/\sigma)_{max} = 0.001$
 $S = 1.06$ $\Delta\rho_{max} = 0.26 \text{ e \AA}^{-3}$
 4331 reflections $\Delta\rho_{min} = -0.23 \text{ e \AA}^{-3}$
 335 parameters
 H-atom parameters constrained

Table 1

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

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N4-H4 \cdots N2^i$	0.86	2.14	2.994 (3)	174

Symmetry code: (i) $-x, -y + 1, -z + 1$.

H atoms were positioned geometrically and refined using a riding model [$C-H = 0.93-0.98 \text{ \AA}$ and $N-H = 0.83 \text{ \AA}$, with $U_{iso}(H) = 1.5U_{eq}(\text{methyl C})$ and $1.2U_{eq}(C,N)$].

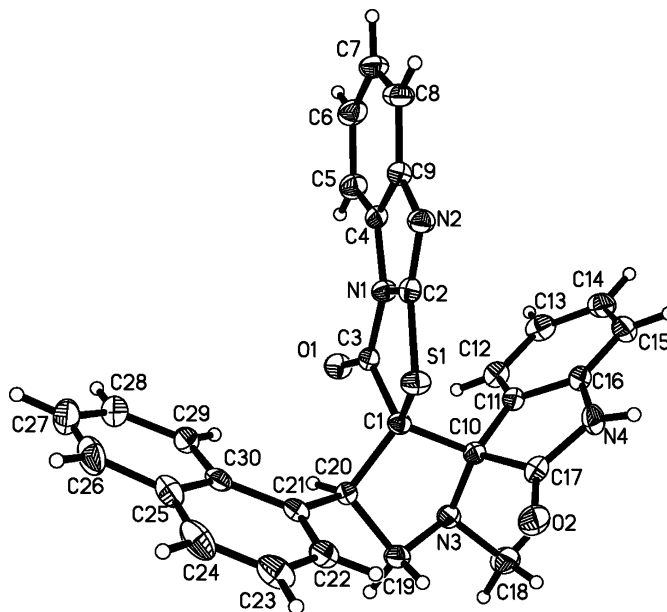


Figure 1

The molecular structure of (I), drawn with 30% probability ellipsoids. H atoms are drawn as spheres of arbitrary radius.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1997); software used to prepare material for publication: SHELXTL.

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