

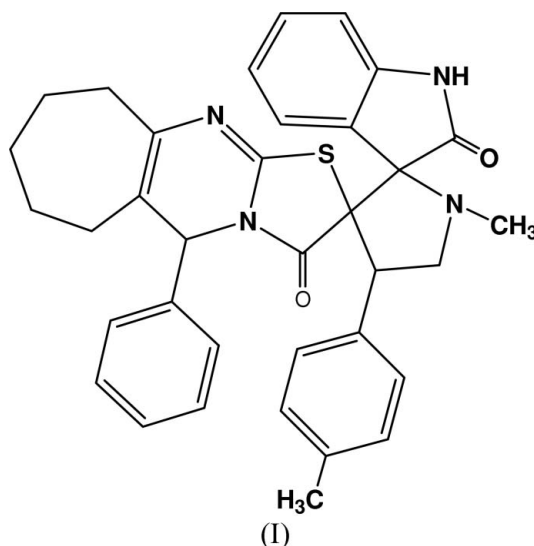
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Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.041
 wR factor = 0.107
Data-to-parameter ratio = 14.0For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**1'-Methyl-5-diphenyl-4'-*p*-tolyl-5,6,7,8,9,10-hexahydro-1,3-cycloheptapyrimidino[2,3-*b*]thiazole-2-spiro-3'-pyrrolidine-2'-spiro-3''-1*H*-indole-2'',3(2*H*,3''*H*)-dione**The pyrrolidine ring in the title compound, $\text{C}_{35}\text{H}_{34}\text{N}_4\text{O}_2\text{S}$, adopts an envelope conformation, with the N atom deviating by 0.586 (1) Å from the plane of the other atoms. The molecule is stabilized by weak $\text{C}-\text{H}\cdots\text{O}$ interactions and the crystal packing is stabilized by $\text{N}-\text{H}\cdots\text{N}$ intermolecular interactions, generating a dimer with an $R_2^2(16)$ motif.Received 6 October 2006
Accepted 11 November 2006

Comment

Heterocyclic compounds, especially five- and six-membered rings, have occupied an important place among organic compounds for their great pharmaceutical importance, especially pyrrolidine and thiazolidine derivatives. Synthetic spiro-pyrrolidine derivatives show activity against the aldose reductase enzyme which controls influenza (Stylianakis *et al.*, 2003). Indole and its derivatives represent one of the most active classes of compounds, possessing a wide range of biological activities (Hiremath *et al.*, 1988). Owing to the ease of substitution and modifications at several positions, many derivatives of pyrrolidine have been synthesized with different properties (Baldwin *et al.*, 1994). In view of the importance of these compounds, we have undertaken the structure determination of the title compound, (I) (Fig. 1).The molecular geometry of (I) is comparable with that of a related structure reported earlier (Gayathri *et al.*, 2005). The sums of the bond angles around N1 (337.2°) and N3 (359.9°) indicate sp^3 and sp^2 hybridization, respectively.

The methyl atom C5 lies 0.545 (2) Å below the plane of atoms C1–C4, and atom C35 lies 0.087 (3) Å above the plane of the benzene ring C29–C34. The five- (C1/C6/N2/C7/C12) and six- (C7–C12) membered rings in the indane group are

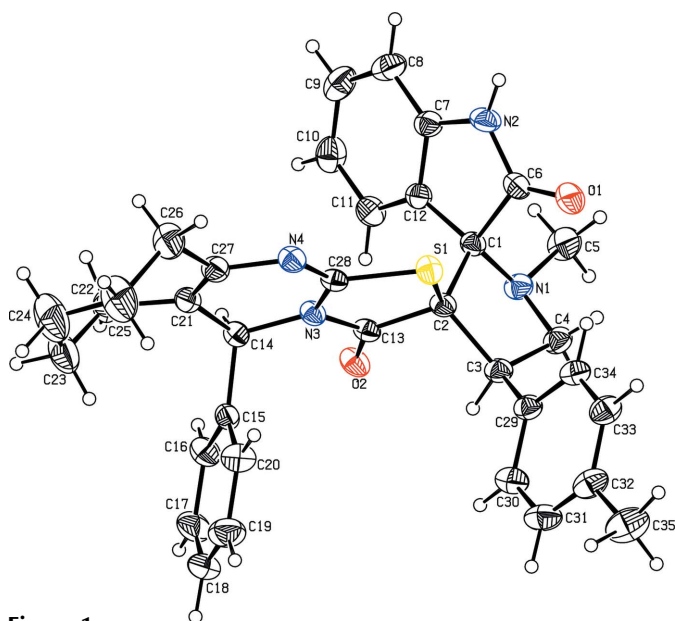


Figure 1
The molecular structure of the title compound, showing 30% probability displacement ellipsoids.

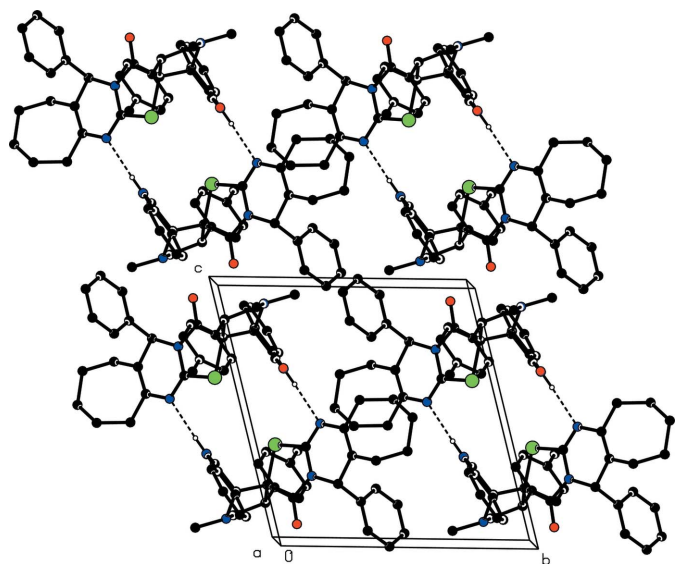


Figure 2
The packing of (I), viewed approximately down the *a* axis. Hydrogen bonds are shown as dashed lines. H atoms not involved in hydrogen bonding have been omitted.

planar, with a dihedral angle of $6.3(1)^\circ$ between these rings. Atom O1 deviates by $0.105(1) \text{ \AA}$ from the plane of the five-membered ring in the indane group. The six-membered ring N3/C14/C21/C27/N4/C28 is slightly non-planar, with atom C14 deviating by $0.159(2) \text{ \AA}$ from the plane of the other atoms, because of the phenyl (C15–C20) substituent at atom C14. The dihedral angle between the two benzene rings (C15–C20 and C29–C34) is $21.9(1)^\circ$.

The pyrrolidine ring adopts an envelope conformation, with atom N1 deviating by $0.586(1) \text{ \AA}$ from the plane of the other atoms. The puckering parameters (Cremer & Pople, 1975) and the smallest displacement asymmetry parameter (Nardelli,

1983) for the pyrrolidine ring are $q_2 = 0.406(2) \text{ \AA}$, $\varphi = 353.4(3)^\circ$ and $\Delta_s(\text{N}_1) = 6.7(2)$.

The molecule is stabilized by weak C–H···O intramolecular interactions and the crystal packing is stabilized by N–H···N intermolecular interactions, generating a centrosymmetric dimer of $R_2^2(16)$ motif (Bernstein *et al.*, 1995) (Table 1 and Fig. 2).

Experimental

A mixture of isatin (1.2 mmol), sarcosine (1.2 mmol) and 5-phenyl-2-(*p*-methyl)phenylmethylene-5,6,7,8,9,10-hexahydrocyclohepta[*d*]thiazolo[3,2-*a*]pyrimidin-3(2*H*)-one (1 mmol) in methanol–dioxane (1:1, 20 ml) was refluxed until the disappearance of the starting materials (5 h) as shown by thin-layer chromatography analysis. The reaction mixture was then concentrated *in vacuo* and extracted with water (50 ml) and dichloromethane (50 ml). The organic layer was washed with brine, dried with anhydrous sodium sulfate and concentrated *in vacuo*. The residue was purified by column chromatography (silica gel, 100–200 mesh) eluted with a hexane–ethyl acetate (8:2) mixture to give the title compound, which was recrystallized from methanol by slow evaporation.

Crystal data

$\text{C}_{35}\text{H}_{34}\text{N}_4\text{O}_2\text{S}$
 $M_r = 574.72$
Triclinic, $P\bar{1}$
 $a = 11.3427(8) \text{ \AA}$
 $b = 12.0148(9) \text{ \AA}$
 $c = 13.0102(10) \text{ \AA}$
 $\alpha = 95.604(1)^\circ$
 $\beta = 110.887(1)^\circ$
 $\gamma = 109.567(1)^\circ$

$V = 1512.67(19) \text{ \AA}^3$
 $Z = 2$
 $D_x = 1.262 \text{ Mg m}^{-3}$
Mo $K\alpha$ radiation
 $\mu = 0.14 \text{ mm}^{-1}$
 $T = 293(2) \text{ K}$
Block, colourless
 $0.24 \times 0.21 \times 0.20 \text{ mm}$

Data collection

Bruker SMART APEX CCD area-detector diffractometer
 ω scans
Absorption correction: none
14702 measured reflections

5317 independent reflections
4625 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.021$
 $\theta_{\text{max}} = 25.0^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.041$
 $wR(F^2) = 0.107$
 $S = 1.04$
5317 reflections
379 parameters
H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0515P)^2 + 0.4411P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.24 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.17 \text{ e \AA}^{-3}$

Table 1

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

<i>D</i> –H··· <i>A</i>	<i>D</i> –H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> –H··· <i>A</i>
C3–H3···O2	0.98	2.45	2.944(2)	111
C4–H4A···O1	0.97	2.50	3.070(2)	118
C11–H11···O2	0.93	2.46	3.045(3)	121
N2–H2···N4 ⁱ	0.86	2.13	2.988(2)	177

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

All H atoms were treated using a riding model, with C–H = 0.93 for aromatic H, 0.98 for methine H, 0.97 for methylene H and 0.96 \AA for methyl H, and N–H = 0.86 \AA , and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$, or $1.5U_{\text{eq}}(\text{C})$ for methyl groups.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINTE* (Bruker, 2001); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97* and *PARST* (Nardelli, 1995).

The Department of Science and Technology (DST-FIST), Government of India, is acknowledged by DG and DV for providing facilities to the department.

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