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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.053 wR factor = 0.136 Data-to-parameter ratio = 17.9

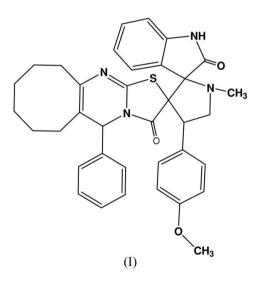
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

4'-(4-Methoxyphenyl)-1'-methyl-5-diphenyl-5,6,7,8,9,10-hexahydro-1,3-cyclooctapyrimidino-[2,3-b]thiazole-2-spiro-3'-pyrrolidine-2'-spiro-3"-1*H*-indole-2",3(2*H*,3"*H*)-dione

In the title compound, $C_{36}H_{36}N_4O_3S$, the pyrrolidine ring adopts an envelope conformation and the thiazolidine ring is planar. The molecule is stabilized by weak $C-H\cdots O$ interactions and the crystal packing is stabilized by $N-H\cdots N$ intermolecular interactions, generating a centrosymmetric dimer with an $R_2^2(16)$ motif.

Comment

Substituted pyrrolidine compounds have gained importance as they are the basic structural elements of many alkaloids and pharmacologically active compounds. Pyrrolidine alkaloids have been found to be DNA polymerase inhibitors and also exhibit characteristic inhibition to DNA metabolic enzymes (Mizushina *et al.*, 2003). Oxindole derivatives act as orally active potent growth hormone secretagogues (Tokunaga *et al.*, 2005) and also possess antifungal activity (Strigacova *et al.*, 2001). As the title compound, (I), is of great medicinal importance, we have undertaken its three-dimensional structure determination by X-ray diffraction.



The molecular geometry of (I) (Fig. 1) is comparable to those of related structures reported earlier (Gayathri *et al.*, 2005, 2006*a*,*b*). The sums of the bond angles around N1 (336.7°) and N3 (359.5°) indicate sp^3 - and sp^2 -hybridization, respectively.

The pyrrolidine ring adopts an envelope conformation, with atom N1 deviating by 0.593 (2) Å from the plane of the other atoms. The puckering parameters (Cremer & Pople, 1975) and the smallest displacement asymmetry parameters (Nardelli, 1983) for the pyrrolidine ring are $q_2 = 0.408$ (2) Å, $\varphi =$ 354.7 (3)° and Δ_s (N1) = 5.5 (2)°.

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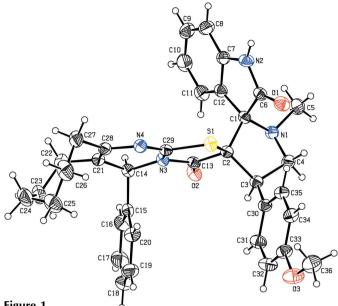
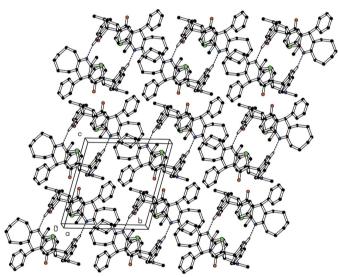


Figure 1

The molecular structure of (I), showing 30% probability displacement ellipsoids.





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

The methyl atom C5 lies 0.545 (4) Å below the plane of atoms C1-C4. Atoms O1, O2 and O3 deviate by 0.041 (2), 0.146 (2) and 0.035 (2) Å, respectively, from the C1/C6/N2/C7/ C12, thiazolidine and C30-C35 benzene ring planes. The dihedral angle between the five- (C1/C6/N2/C7/C12) and sixmembered (C7–C12) rings in the indane system is 4.8 $(2)^{\circ}$. The six-membered ring N3/C14/C21/C28/N4/C29 is an envelope, with atom C14 deviating by 0.210 (3) Å from the plane of the other atoms in the ring, which may be due to the phenyl (C15-C20) substituent at atom C14. The dihedral angle between the two benzene rings (C15–C20 and C30–C35) is $16.8 (1)^{\circ}$. The eight-membered ring has a boat-chair conformation.

The molecule is stabilized by weak $C-H \cdots O$ intramolecular interactions. The crystal packing is stabilized by N2-H2···N4(1 - x, -y, -z) intermolecular interactions (Table 1), generating a centrosymmetric dimer of $R_2^2(16)$ motif (Fig. 2).

Experimental

A mixture of isatin (1.2 mmol), sarcosine (1.2 mmol) and 5-phenyl-2*p*-methoxy)phenylmethylene)-5,6,7,8,9,10,11-heptahydrocycloocta[*d*] thiazolo[3,2-a] pyrimidin-3(2H)-one (1 mmol) in methanol-dioxane (1:1, 20 ml) was refluxed until the disappearance of the starting materials (4.5 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), eluting with a hexane-ethyl acetate (8:2) mixture, to give the title compound, which was recrystallized from methanol by slow evaporation.

Crystal data

$C_{36}H_{36}N_4O_3S$	V = 1570.2 (4) Å ³
$M_r = 604.75$	Z = 2
Triclinic, P1	$D_x = 1.279 \text{ Mg m}^{-3}$
a = 11.4459 (19) Å	Mo $K\alpha$ radiation
b = 12.085(2) Å	$\mu = 0.15 \text{ mm}^{-1}$
c = 13.612 (2) Å	T = 293 (2) K
$\alpha = 69.568 \ (3)^{\circ}$	Block, colourless
$\beta = 65.586 \ (3)^{\circ}$	$0.26 \times 0.24 \times 0.21 \ \mathrm{mm}$
$\gamma = 71.038 \ (3)^{\circ}$	

Data collection

Bruker SMART APEX CCD areadetector diffractometer ω scans Absorption correction: none 17617 measured reflections

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.053$	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.073P)^{2}]$
$wR(F^2) = 0.136$	where $P = (F_0^2 + 2F_c^2)/3$
S = 0.93	$(\Delta/\sigma)_{\rm max} = 0.001$
7101 reflections	$\Delta \rho_{\rm max} = 0.34 \text{ e } \text{\AA}^{-3}$
397 parameters	$\Delta \rho_{\rm min} = -0.17 \text{ e } \text{\AA}^{-3}$

7101 independent reflections 4615 reflections with $I > 2\sigma(I)$

 $R_{\rm int} = 0.039$

 $\theta_{\rm max} = 28.0^{\circ}$

Table 1 Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N2-H2\cdots N4^{i}$	0.86	2.15	2.971 (2)	161
$C3-H3 \cdot \cdot \cdot O2$	0.98	2.45	2.940 (3)	111
$C4-H4A\cdots O1$	0.97	2.47	3.041 (3)	118
C11-H11···O2	0.93	2.44	3.066 (3)	125

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

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

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:

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

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