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Key indicators

Single-crystal X-ray study

$T = 294\text{ K}$

Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$

Disorder in main residue

R factor = 0.055

wR factor = 0.140

Data-to-parameter ratio = 14.8

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

10''-(4-Methoxybenzylidene)-5'',4'-bis(4-methoxyphenyl)-1'-methyl-2,3,2'',3'',7'',8'',9'',10''-octahydro-1*H*,5''*H*,6''*H*-indole-3-spiro-2'-pyrrolidine-3'-spiro-2''-cyclohepteno[1,2-*d*]thiazolo[3,2-*a*]pyrimidine-2,3''-dione

The title compound, $\text{C}_{44}\text{H}_{42}\text{N}_4\text{O}_5\text{S}$, was synthesized by the intermolecular [3+2] cycloaddition of an azomethine ylide, derived from isatin and sarcosine by a decarboxylative route, and 5-(4-methoxyphenyl)-10-(4-methoxy)benzylidene-2-(4-methoxy)benzylidene-2,3,6,7,8,9-hexahydro-5*H*,10*H*-cyclohepta[1,2-*d*]thiazolo[3,2-*a*]pyrimidin-3-one. In the molecule, the two spiro junctions link a planar 2-oxindole ring, a pyrrolidine ring in an envelope conformation and a 10-(arylmethylene)hexahydrocyclohepta[1,2-*d*]thiazolo[3,2-*a*]pyrimidin-3-one ring. The packing of the molecules in the crystal structure is mainly governed by $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds.

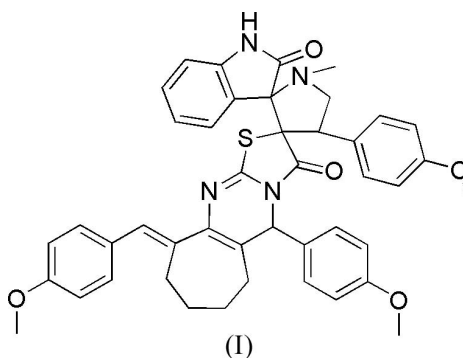
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Comment

Spiro compounds represent an important class of naturally occurring substances, characterized by highly pronounced biological properties (Kobayashi *et al.*, 1991; James *et al.*, 1991). 1,3-Dipolar cycloaddition reactions are important processes for the construction of spiro-compounds (Raj *et al.*, 2003; Mishriky *et al.*, 1997). In this paper, the structure of the title compound, (I), is reported.



Compound (I) was synthesized by the intermolecular [3+2] cycloaddition of an azomethine ylide, derived from isatin and sarcosine by a decarboxylative route, and 5-(4-methoxy)phenyl-10-(4-methoxy)benzylidene-2-(4-methoxy)benzylidene-2,3,6,7,8,9-hexahydro-5*H*,10*H*-cyclohepta[1,2-*d*]thiazolo[3,2-*a*]pyrimidin-3-one.

The molecular structure of (I) is illustrated in Fig. 1. In the molecule, there is a dispiro ring system, which consists of a 2-oxindole ring, a pyrrolidine ring and a 10-(arylmethylene)hexahydrocyclohepta[1,2-*d*]thiazolo[3,2-*a*]pyrimidin-3-one ring. The pyrrolidine ring is not planar, having an envelope conformation.

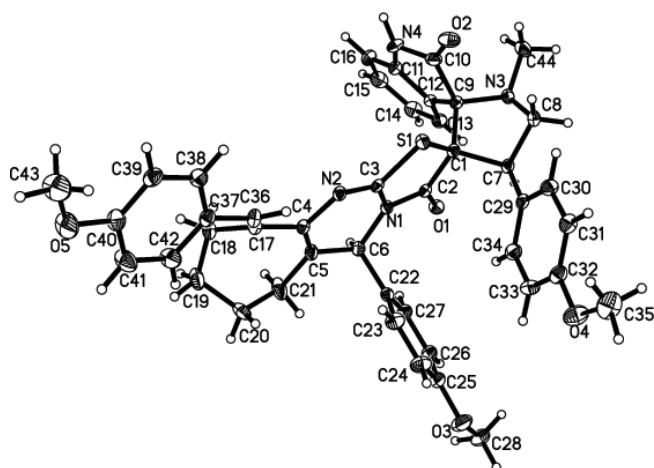


Figure 1
The molecular structure of (I), drawn with 20% probability ellipsoids. Only the major disorder component is shown.

The bond lengths and angles in (I) agree with those reported for the similar structure 10''-(4-chlorobenzylidene)-5''-(4-chlorophenyl)-4'-(2,4-dichlorophenyl)-1'-methyl-2,3,2'',3'',7'',8'',9'',10''-octahydro-1*H*,5''*H*,6''*H*-indole-3-spiro-2'-pyrrolidine-3'-spiro-2''-cyclohepteno[1,2-*d*]thiazolo[3,2-*a*]pyrimidine-2,3''-dione (Hu *et al.*, 2005).

Pairs of molecules are connected by N—H···N hydrogen bonds (Fig. 2, Table 1).

Experimental

A mixture of 5-(4-methoxy)phenyl-10-(4-methoxy)benzylidene-2-(4-methoxy)benzylidene-2,3,6,7,8,9-hexahydro-5*H*,10*H*-cyclohepta[1,2-*d*]thiazolo[3,2-*a*]pyrimidin-3-one (1 mmol), isatin (1.2 mmol) and sarcosine (1.2 mmol) was refluxed in acetonitrile (80 ml) until the disappearance of the starting materials, as evidenced by thin-layer chromatography. After completion of the reaction, the solvent was removed *in vacuo* and the residue separated by column chromatography [silica gel, petroleum ether–ethyl acetate 5:1 (*v/v*)] to give the title compound, (I) (m.p. 475 K). The compound was recrystallized by the dissolution of 20 mg of (I) in acetone (15 ml); the solution was kept at room temperature for 6 d allowing natural evaporation, to give colourless single crystals of (I) suitable for X-ray analysis. Spectroscopic analysis: IR (KBr, ν , cm^{-1}): 3168 (–NH), 1727, 1720 (C=O), 1378 (–CH₃); ¹H NMR (CDCl₃, δ , p.p.m.): 1.48–2.51 (*m*, 8H, cycloheptyl), 2.20 (*s*, 3H, N–CH₃), 3.42 (*dd*, *J* = 7.5 and 8.7 Hz, 1H, –CH), 3.78 (*s*, 3H, O–CH₃), 3.80 (*s*, 3H, O–CH₃), 3.86 (*s*, 3H, O–CH₃), 3.99 (*dd*, *J* = 8.7 and 9.9 Hz, 1H, –CH), 4.10 (*dd*, *J* = 7.5 and 9.9 Hz, 1H, –CH), 5.15 (*s*, 1H, –CH), 6.73–7.54 (*m*, 17H, Ar-H and –CH), 8.16 (*bs*, 1H, –NH).

Crystal data

C₄₄H₄₂N₄O₅S
M_r = 738.88
 Triclinic, *P* $\bar{1}$
a = 10.6294 (19) Å
b = 13.299 (2) Å
c = 13.702 (2) Å
 α = 104.778 (3)°
 β = 95.840 (3)°
 γ = 91.828 (3)°
V = 1859.8 (5) Å³

Z = 2
D_x = 1.320 Mg m^{−3}
 Mo *K*α radiation
 Cell parameters from 2110 reflections
 θ = 2.3–23.1°
 μ = 0.14 mm^{−1}
T = 294 (2) K
 Block, colourless
 0.28 × 0.24 × 0.20 mm

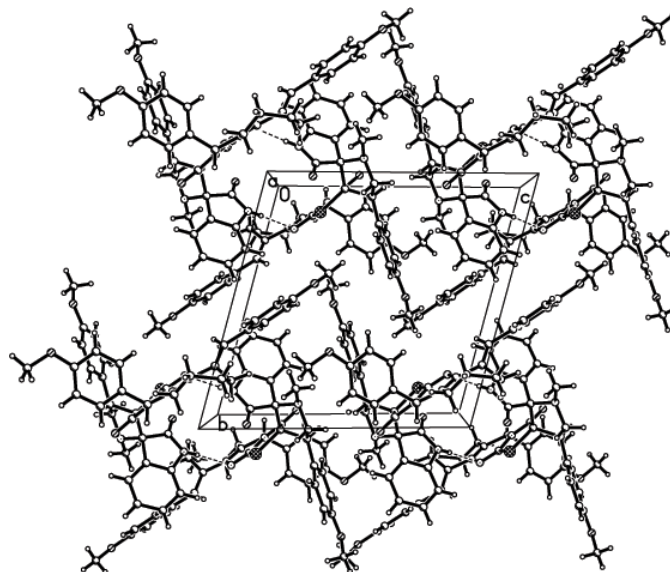


Figure 2
The crystal structure of (I), viewed along the *a* axis. Dashed lines indicate hydrogen bonds.

Data collection

Bruker SMART CCD area-detector diffractometer	7546 independent reflections
φ and ω scans	4011 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Bruker, 1997)	$R_{\text{int}} = 0.031$
$T_{\text{min}} = 0.958$, $T_{\text{max}} = 0.972$	$\theta_{\text{max}} = 26.5^\circ$
10666 measured reflections	$h = -13 \rightarrow 11$
	$k = -16 \rightarrow 15$
	$l = -17 \rightarrow 16$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.055$
 $wR(F^2) = 0.140$
 $S = 1.01$
 7546 reflections
 505 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0505P)^2 + 0.3384P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.29 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\text{min}} = -0.21 \text{ e } \text{Å}^{-3}$

Table 1

Hydrogen-bond geometry (Å, °).

<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>
N4–H4···N2 ⁱ	0.86 (1)	2.16 (1)	3.014 (3)	173 (3)

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

Atom C20 of the cycloheptene ring is orientationally disordered over two sites (C20 and C20'), the ratio of the occupancies being 0.526 (8):0.474 (8). The H atom bound to atom N4 was refined freely. All other H atoms were positioned geometrically, with C–H = 0.93–0.98 Å, and refined in a riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

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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