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Key indicators

Single-crystal X-ray study
 $T = 298\text{ K}$
 Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$
 Disorder in solvent or counterion
 R factor = 0.055
 wR factor = 0.170
 Data-to-parameter ratio = 12.8

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

4-(4-Methoxyphenyl)-3-phenyl-2,4,8,10-tetraazaspiro[5.4]dec-1-ene-6,8,10-trione acetone solvate monohydrate

Conformational analyses and structural comparison of the title spiropyrazolebarbiturate, $\text{C}_{19}\text{H}_{16}\text{N}_4\text{O}_4 \cdot \text{C}_3\text{H}_6\text{O} \cdot \text{H}_2\text{O}$, and the related structure 3-bromo-1,4-diphenyl-1,2,7,9-tetraazaspiro[5.4]dec-2-ene-6,8,10-trione acetone solvate [Bruno, Rotondo, Nicoló, Foti, Grassi & Risitano (2005). *Acta Cryst. E* **61**, o142–o144], are presented. Both compounds were synthesized by cycloaddition of C–H and C–Br nitrilimines, generated *in situ*, starting from the same substrate [Foti, Grassi & Risitano (2005). *Synlett*. Submitted]. However, different experimental conditions led to products with reverse regioselectivity.

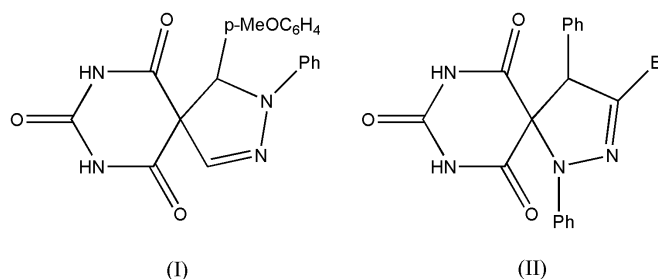
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Comment

It is known that barbituric acid derivatives, because of the presence of two N–H hydrogen-bond donors and three C=O acceptors, bind tightly to small dipolar species (solvents), as well as to other similar complementary molecules (Chang *et al.*, 1991). This accounts for the wide use of barbituric acid derivatives in the field of molecular recognition (Berl *et al.*, 1999). Often, the crystallization process, which is a form of self-recognition, readily takes place when these substrates are oriented relative to one another in a suitable fashion. Sometimes, unsaturated connection sites may link other dipolar species (solvents), which will be found inside the solid crystal samples. The title spiro compound, (I), and the related spiro compound, (II) (Bruno *et al.*, 2005), both obtained as crystalline solvates, are composed of a barbituric acid moiety connected to a substituted pyrazoline ring through the non-chiral spiro centre C6 (Fig. 1). These compounds contain the unique chiral atom C10 and, since both crystallize in centrosymmetric space groups, the crystal samples are (10*R*)-(10*S*) racemic mixtures.



The asymmetric unit of (I) consists of one spiro-fused bicyclic molecule, one acetone and one water molecule (Fig. 1). The two core rings do not present evident puckering [maximum deviation from the barbituric acid mean plane for atom C6 is 0.156 (2) Å, and from the pyrazoline mean plane

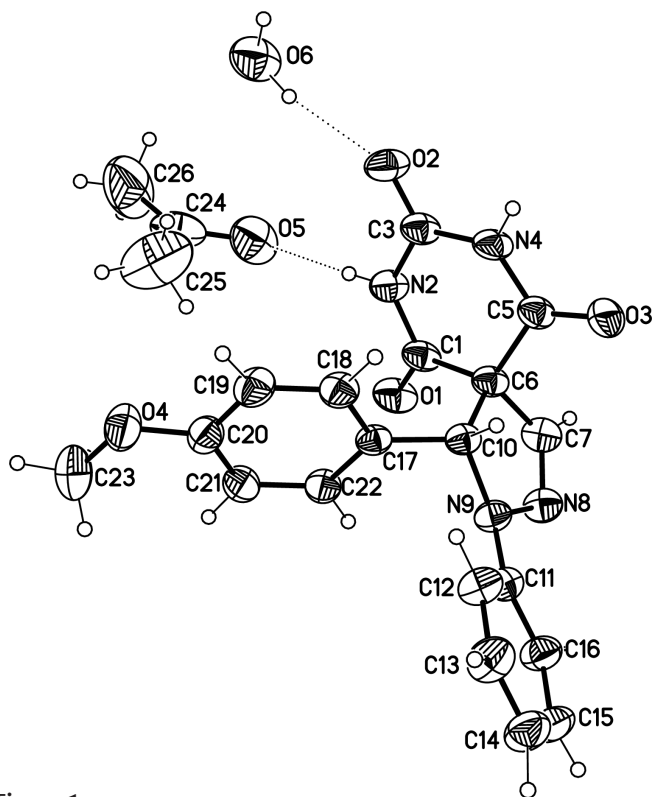


Figure 1
The (10*R*) isomer of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 35% probability level and H atoms are shown as small spheres of arbitrary radii. Dotted lines indicate hydrogen bonds.

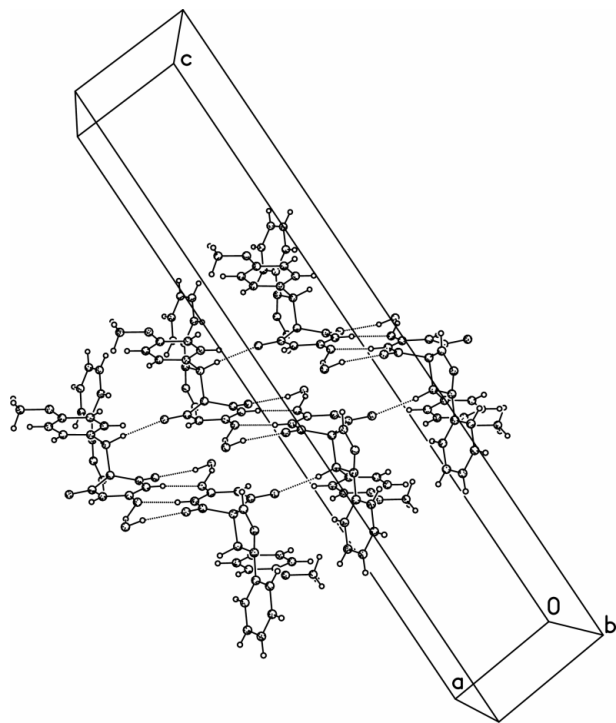


Figure 2
Part of the crystal packing of (I), showing ribbons formed by pairs of molecules along the [100] direction. Dotted lines indicate hydrogen bonds.

for atom C10 is 0.075 (2) Å]. They are almost perpendicular to one another, with a dihedral angle between their mean planes of 89.2 (1)°. Despite the presence of two *sp*³-hybridized C atoms within the pyrazoline ring, the conjugation with the phenyl system attached to N9 is evidenced by the torsion angles around N9—C11 (Table 1) and the angle between the mean planes of the rings of 20.5 (1)°.

Pairs of molecules are linked by an N4—H4···O2ⁱ hydrogen bond (symmetry code as in Table 2), dimerized by the crystallographic inversion centre in an *R*₂²(6) first-order centrosymmetric graph set. These dimers are, in turn, able to interact with co-crystallized solvent molecules (Figs. 1 and 2).

A weaker C10—H10···O1ⁱⁱ hydrogen-bond interaction (Table 2) connects to the molecule at (*x* + 1, *y*, *z*), generating one-dimensional *C*(5) chains along the crystallographic *a* axis, such that dimers are stacked one above another in a stair-like molecular ribbon reminiscent of the duplex DNA structure (Table 2 and Fig. 2).

We note that the water molecule interacting with a dimeric pair is exactly above the barbituric acid plane of the dimer obtained by translation along the diagonal of the *ab* plane, [110], such that the water O atom is close to the two internal carbonyl groups [O6···C1ⁱ 3.057 (4) and O6···C5ⁱ 3.186 (4) Å; symmetry code: (i) 1 - *x*, 1 - *y*, -*z*]. Other weak dipolar interactions keep the above-mentioned ribbons together in the three-dimensional packing.

Experimental

Cycloadduct (I) was obtained from an arylidenebarbiturate and a nitrilimine prepared *in situ*, as described by Foti *et al.* (2004). After purification of the product, crystals suitable for X-ray analysis were obtained by slow evaporation of an acetone solution.

Crystal data

C₁₉H₁₆N₄O₄·C₃H₆O·H₂O
M_r = 440.45
 Monoclinic, *P*2₁/*c*
a = 6.1539 (10) Å
b = 10.7908 (17) Å
c = 34.057 (6) Å
 β = 94.504 (14)°
V = 2254.6 (6) Å³
Z = 4

D_x = 1.298 Mg m⁻³
 Mo *K*α radiation
 Cell parameters from 61 reflections
 θ = 5.7–20.5°
 μ = 0.10 mm⁻¹
T = 298 (2) K
 Prism, colourless
 0.58 × 0.48 × 0.34 mm

Data collection

Bruker *P4* diffractometer
 ω scans
 Absorption correction: ψ scan
 (North *et al.*, 1968)
 T_{\min} = 0.873, T_{\max} = 0.964
 10 362 measured reflections
 3815 independent reflections
 2715 reflections with *I* > 2σ(*I*)

*R*_{int} = 0.022
 θ_{\max} = 25°
h = -1 → 6
k = -12 → 12
l = -40 → 40
 3 standard reflections
 every 197 reflections
 intensity decay: none

Refinement

Refinement on *F*²
R[*F*² > 2σ(*F*²)] = 0.055
wR(*F*²) = 0.17
S = 1.05
 3815 reflections
 297 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0825P)^2 + 1.0558P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.004$
 $\Delta\rho_{\max} = 0.63 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\min} = -0.19 \text{ e } \text{Å}^{-3}$
 Extinction correction: *SHELXL97*
 (Sheldrick, 1997)
 Extinction coefficient: 0.0082 (16)

Table 1

Selected geometric parameters (Å, °).

O1—C1	1.208 (3)	N8—N9	1.381 (3)
O2—C3	1.225 (3)	N9—C11	1.405 (3)
O3—C5	1.202 (3)	N9—C10	1.475 (3)
N8—N9—C11—C12	154.0 (2)	N8—N9—C11—C16	−28.2 (4)
C10—N9—C11—C12	8.3 (4)	C10—N9—C11—C16	−173.9 (2)

Table 2

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...O2 ⁱ	0.86	2.05	2.909 (3)	175
O6—H6A...O3 ⁱ	0.96	2.14	2.997 (3)	148
C10—H10...O1 ⁱⁱ	0.98	2.33	3.280 (3)	164
O6—H6B...O2	0.96	2.08	3.014 (4)	165
N2—H2...O5	0.86	2.01	2.865 (4)	172

Symmetry codes: (i) $-x, 1-y, -z$; (ii) $x-1, y, z$.

All H atoms were treated as riding, with alkyl C—H distances of 0.98, methyl C—H distances of 0.96 and aromatic C—H distances of 0.93 Å, and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. The disordered water molecule was refined as a rigid group through the AFIX176 instruction in

SHELXL97 (Sheldrick, 1997) (O—H distances were set at 0.942 Å and H—O—H angles to 104.557°).

Data collection: *XSCANS* (Siemens, 1989); cell refinement: *XSCANS*; data reduction: *XPREP* (Bruker, 1997); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1994); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* (Bruker, 1997); software used to prepare material for publication: *PARST97* (Nardelli, 1995) and *WinGX-PC* (Version 1.6.4.05; Farrugia, 1999).

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