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# 3-Acetyl-4-benzoyl-2-methyl-5phenyl-3,3a-dihydropyrazolo[2,3-c]pyrimidine-7(6*H*)-thione

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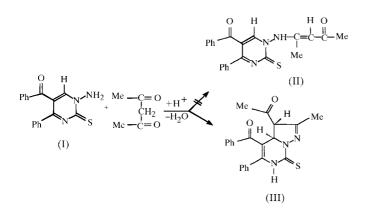
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The molecule of the title compound,  $C_{22}H_{19}N_3O_2S$ , is not planar. The dihedral angle between the two phenyl rings is 27.46 (7)° and in the dihydropyrazolopyrimidine ring the total puckering amplitude  $Q_T$  is 0.526 (3) Å. The structure is stabilized by both intra- and intermolecular  $C-H\cdots O$ interaction, and by an intermolecular  $N-H\cdots S$  hydrogen bond.

## Comment

Dihydro derivatives of pyrazolo[1,5-*a*]pyrimidine have high physiological activity, the most important being cardiovascular activity (Tsuda *et al.*, 1986). The antitumor activity and the



potential therapeutic applications of several pyrazolo[3,4-*d*]ave also promped a more thorough investigation of these compounds (Youssif, 1997). This paper reports on the crystal structure of a substitution product of a fused pyrazole–pyrimidine system, (III), interesting for its possible pharmacological activity.

In the pyrimidine ring, there are two local pseudo-mirrors, one running along  $N1 \cdots C20$  and the other along the midpoints of the N2-C16 and C14-C15 bonds. The distance N1-C16 of 1.371 (3) Å is significantly shorter than N2-C20 of 1.481 (3) Å, because C16 is in an  $sp^2$  hybridized state, while C20 is  $sp^3$ .

The C16=S1 [1.664 (2) Å] double-bond length of the pyrimidine ring is not significantly different to the C=S double-bond length [1.669 (3) Å] in 1-amino-5-benzoyl-4-phenyl-1*H*-pyrimidine-2-thione (Akkurt *et al.*, 1992). The angles N1-C16-S1 [121.2 (2)°] and N2-C16-S1 [126.1 (2)°] are almost equal, probably due to some attraction between S1 and H1*A* (S1···H1*A* = 2.72 Å) and some repulsion between S1 and N3 [S1···N3 = 3.080 (2) Å].

As the total puckering amplitude  $Q_T$  (Cremer & Pople, 1975) of the pyrazole ring is 0.230 (3) Å, in the ninemembered dihydropyrazolopyrimidine ring with the C20 atom displaced 0.439 (3) Å from the plane of the other atoms, the puckering amplitude is 0.526 (3) Å. This amplitude appears sensitive to the type of substituents present in the related ring, since the corresponding amplitudes in 2-methyl-5,6,7-triphenyl-6,7-dihydropyrazolo[2,3-*a*]pyrimidine (Lindeman *et al.*, 1993) and in 7-acetyl-5-benzoyl-6-phenyl-8-methyl-4,7-dihydropyrazolo[1,5-*c*]-1*H*-pyrimidine- 2-one (Çelik *et al.*, 2000) are 0.56 and 0.37 (3), respectively.

The C20–C14–C15–C1 and N2–C20–C14–C15 torsion angles are -168.4 (2) and -31.8 (3)°, respectively. The C1–C15–C14–C13 torsion angle of 2.2 (4)° possibly indicates  $\pi$ -conjugation involving the phenyl and benzoyl systems. It is interesting to note the relative orientations of the substituents attached to the pyrimidine ring. The dihedral angle between the two phenyl rings is 27.46 (7)°. The basic factor influencing the orientation of the two rings is intermolecular interactions. The crystal structure is stabilized by the inter- and intramolecular hydrogen bonds.

## Experimental

1-Amino-5-benzoyl-4-phenyl-1*H*-pyrimidine-2-dione (0.2 g) was dissolved in acetylacetone (0.18 g; 1:30 mol) and *p*-toluene sulfonic acid (0.18 g) was added in this solution as a catalyst at room temperature. The mixture was heated in a furnace at 388 K for 45 min. After cooling, the precipitate was separated from acetyl-acetone by filtering and the oily residue was stirred with diethyl ether. The crude product so formed was crystallized from *n*-butanol. Yield: 60%; m.p.: 520 K; IR (KBr), cm<sup>-1</sup>: 3600–3400 (N–H), 3200–3100 (aromatic C–CH), 3000 (CH<sub>3</sub>), 1720 (C=O), 1600 (C=C and C=N), 1540–1400 (aromatic skeleton), 1220 (C=S), 780–680 (pyrimidine skeleton); <sup>1</sup>H NMR (DMSO) p.p.m.: 2.14–2.49 (*s*, 6 H, CH<sub>3</sub>), 4.10–4.15 (*s*, 1 H, CH), 5.37–5.43 (*s*, 1 H, NH), 6.99–7.33 (*m*, 10 H, aromatic H) (Önal, 1997). Elemental analysis, C<sub>22</sub>H<sub>19</sub>N<sub>3</sub>O<sub>2</sub>S requires: C 67.85, H 4.91, N 10.79, S 8.22%; found: C 67.73, H 4.77, N 10.41, S 8.15%.

Crystal data

$C_{22}H_{19}N_3O_2S$
$M_r = 389.46$
Monoclinic, $P2_1/c$
a = 6.9505 (3)  Å
b = 21.8820(8) Å
c = 12.9619(5) Å
$\beta = 100.239 \ (1)^{\circ}$
$V = 1939.99 (13) \text{ Å}^3$
Z = 4

#### Data collection

Siemens SMART CCD area- detector diffractometer	2422 reflections with $I > 2\sigma(I)$
detector diffractometer	$R_{\rm int} = 0.082$
$\omega$ scans	$\theta_{\rm max} = 28.43^{\circ}$
Absorption correction: empirical	$h = -9 \rightarrow 9$
(SADABS; Sheldrick, 1996)	$k = -28 \rightarrow 28$
$T_{\min} = 0.931, T_{\max} = 0.985$	$l = -8 \rightarrow 17$
13 631 measured reflections	Intensity decay: none
4769 independent reflections	

#### Refinement

Refinement on $F^2$ $R[F^2 > 2\sigma(F^2)] = 0.061$ $wR(F^2) = 0.152$	H-atom parameters constrained $w = 1/[\sigma^2(F_o^2) + (0.0609P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
S = 0.953	$(\Delta/\sigma)_{\rm max} < 0.001$
4769 reflections	$\Delta\rho_{\rm max} = 0.23 \text{ e } \text{\AA}^{-3}$
253 parameters	$\Delta\rho_{\rm min} = -0.28 \text{ e } \text{\AA}^{-3}$

 $D_x = 1.333 \text{ Mg m}^{-3}$ 

Mo  $K\alpha$  radiation Cell parameters from 4312

reflections  $\theta = 1.9-28.4^{\circ}$   $\mu = 0.190 \text{ mm}^{-1}$  T = 293 (2) KNeedle, yellow  $0.38 \times 0.12 \times 0.08 \text{ mm}$ 

#### Table 1

Selected geometric parameters (Å, °).

1.664 (2)	N2-C20	1.481 (3)
1.371 (3)	N3-C17	1.281 (3)
1.388 (3)	O1-C13	1.228 (3)
1.333 (3)	O2-C21	1.197 (3)
1.394 (3)		
124.9 (2)	C14-C15-N1	119.7 (2)
122.9 (2)	N2-C16-N1	112.6 (2)
125.5 (2)	N2-C16-S1	126.1 (2)
111.6 (2)	N1-C16-S1	121.2 (2)
107.0 (2)	N3-C17-C19	114.4 (2)
	1.371 (3) 1.388 (3) 1.333 (3) 1.394 (3) 124.9 (2) 122.9 (2) 125.5 (2) 111.6 (2)	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

### Table 2

Hydrogen-bonding geometry (Å, °).

$D - \mathbf{H} \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N1-H1A\cdots S1^{i}$	0.86	2.72	3.565 (2)	170
$C4-H4A\cdots O1^{ii}$	0.93	2.44	3.245 (4)	145
$C20-H20A\cdots O2$	0.98	2.43	2.869 (3)	107

Symmetry code: (i) -x, 1 - y, -z; (ii) x - 1,  $\frac{1}{2} - y$ ,  $z - \frac{1}{2}$ .

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993); software used to prepare material for publication: *PARST* (Nardelli, 1995).

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