

Fig. 1. Bond lengths (Å) and angles (°) in the title compound, with e.s.d.'s in parentheses.

The planes through atoms C(5), O(3), C(13) and through C(7), O(2), C(14) are inclined at 11.4 (3) and 3.1 (3)° respectively to the mean plane through the ring atoms. The molecule has a nearly planar

quinolinone system in which the two six-membered rings are inclined at $2 \cdot 1 (3)^\circ$ – as was also found in 2-(2,6-dichlorobenzyl)-1-isoquinolone (Ammon & Wheeler, 1974).

The molecules in the crystal lie nearly parallel to the (010) plane. Molecules in adjacent layers are oppositely oriented in parallel planes with their methoxy groups facing each other as a consequence of the centre of symmetry and are separated by a distance of b/4. The typical nature of the layer structure explains the very strong reflexion 040.

In terms of molecular packing the structure is not a strongly bonded one. This explains the easy deformation in the crystal, with soft texture and also large thermal motion.

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Structure of the Anti-inflammatory Drug 4-Hydroxy-2-methyl-N-2-pyridyl-2H-1 λ^6 ,2-benzothiazine-3-carboxamide 1,1-Dioxide (Piroxicam)

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Abstract. $C_{15}H_{13}N_3O_4S$, $M_r = 331.35$, monoclinic, $P2_1/c$, a = 7.127 (2), b = 15.136 (7), c = 13.949 (6) Å, $\beta = 97.35$ (4)°, Z = 4, U = 1491.15 Å³, $D_x = 1.481$ Mg m⁻³, Mo Ka ($\lambda = 0.7107$ Å, $\mu = 0.244$ mm⁻¹); final R = 0.050 for 2289 observed reflexions $[I > 2\sigma(I)]$. Bond lengths and angles are in agreement with expected values. The thiazine ring exhibits a half-chair conformation. An amide group is involved in an intramolecular hydrogen bond to the hydroxy group $[O(17)-H(17)\cdots O(15)$ [2.561 (3) Å]. It also forms an 0567.7408/82/112948.04\$01.00

intermolecular hydrogen bond to an O atom bonded to the S atom $[N(16)-H(16)\cdots O(11), 3.053 (3) \text{ Å}]$, connecting piroxicam molecules in an infinite chain along **b**. The molecular packing is also influenced by van der Waals interactions.

Introduction. Piroxicam (adopted name in USA) (CP-16171) or felden (Pfizer) is an effective analgesic and anti-inflammatory agent in rheumatoid arthritis, osteoarthritis, ankylosing spondylitis and acute pain in © 1982 International Union of Crystallography

musculoskeletal disorders, and episiotomy (Brogden, Heel, Speight & Avery, 1981). It remains uncertain exactly how piroxicam and other non-steroidal antiinflammatory agents exert their local inflammatory action. However, their inhibitory action on prostaglandin synthesis may in part explain their antiinflammatory effects in vivo.

Piroxicam is not structurally related to other anti-inflammatory drugs; its structure determination is described in this paper.

Experimental. The space group was determined from Weissenberg photographs recorded with Cu $K\alpha$ radiation. The cell dimensions given in the Abstract were refined from diffractometer measurements. The intensities were collected on a Philips PW 1100 computercontrolled four-circle diffractometer in the ω -scan mode [scan width = 1.60° (θ), scan speed = 0.04° (θ) s⁻¹] with graphite-monochromated Mo $K\alpha$ radiation. 2289 independent reflexions $[I > 2\sigma(I)]$ in the range $3 < \theta < 30^{\circ}$ were recorded and used in the calculations.

Overall temperature ($B = 1.31 \text{ Å}^2$) and scale factors were determined (Wilson, 1942) and used to compute normalized structure amplitudes by the NORMAL routine included in MULTAN 80 (Main, Fiske, Hull, Lessinger, Germain, Declercq & Woolfson, 1980). The E map based on 292 reflexions having $|E| \ge 1.40$ and corresponding to the solution with the best figure of

Table 1. Final atomic coordinates $(\times 10^4)$ and equivalent isotropic thermal parameters $(\times 10^2)$ for the non-hydrogen atoms

$$U_{\rm eq} = \frac{1}{3} \sum_{I} \sum_{I} U_{II} a_{I}^{*} a_{I}^{*} \mathbf{a}_{I}. \mathbf{a}_{I}.$$

	x	у	Ζ	$U_{ m eq}$ (Å ²)
S(1)	5530(1)	4038 (1)	989 (1)	3.19 (4)
N(2)	3412 (3)	3860 (1)	408 (1)	3.05 (13)
C(3)	3188 (4)	2989 (2)	19 (2)	3.19 (14)
C(4)	3927 (4)	2279 (2)	546 (2)	3.37 (15)
C(5)	5193 (4)	1650 (2)	2154 (2)	3.86 (17)
C(6)	6104 (5)	1771 (2)	3078 (2)	4.73 (19)
C(7)	6789 (5)	2585 (2)	3384 (2)	4.80 (20)
C(8)	6601 (4)	3304 (2)	2764 (2)	4.19 (18)
C(9)	5713 (4)	3182 (1)	1838 (2)	3.12 (15)
C(10)	4964 (4)	2366 (1)	1515 (2)	3.15 (15)
O(11)	5513 (3)	4866 (1)	1477 (1)	4.52 (13)
O(12)	6883 (2)	3891 (1)	337 (1)	4.36 (13)
C(13)	1819 (4)	4210 (2)	878 (2)	4.64 (19)
C(14)	2154 (4)	2875 (2)	-947 (2)	3.54 (15)
O(15)	1786 (3)	2127 (1)	-1280 (1)	4.90 (14)
N(16)	1641 (3)	3630(1)	-1429 (1)	3.65 (14)
O(17)	3754 (3)	1451 (1)	203 (1)	4.79 (14)
N(1′)	291 (4)	4584 (2)	-2572 (2)	5.07 (18)
C(2')	695 (4)	3749 (2)	-2370 (2)	3.80 (17)
C(3')	249 (4)	3061 (2)	-3015 (2)	4.44 (18)
C(4')	-651 (5)	3272 (3)	-3921 (2)	5.57 (22)
C(5')	-1093 (6)	4128 (3)	-4147 (2)	6.49 (24)
C(6')	-594 (6)	4762 (3)	-3456 (3)	6.55 (26)

Table 2. Positional parameters $(\times 10^3)$ and thermal parameters $(\times 10^2)$ for the hydrogen atoms

	x	у	Ζ	$U(\dot{\mathrm{A}}^2)$
H(5)	474 (4)	110 (2)	197 (2)	4-1 (9)
H(6)	632 (5)	125 (2)	355 (2)	5(1)
H(7)	735 (5)	263 (3)	395 (3)	6(1)
H(8)	709 (4)	383 (2)	296 (2)	4.1 (9)
H(13)1	192 (5)	478 (3)	103 (3)	8(1)
H(13)2	177 (5)	392 (3)	150 (3)	7(1)
H(13)3	64 (5)	404 (3)	46 (3)	7(1)
H(16)	197 (4)	411 (2)	-116(2)	5(1)
H(17)	312 (5)	152 (2)	-32(2)	5(1)
H(3')	65 (5)	252 (2)	-284(2)	5(1)
H(4')	-86 (6)	282 (3)	-438(3)	8(1)
H(5')	-168(6)	433 (3)	-472(3)	9 (2)
H(6')	-76 (7)	531 (3)	-357 (4)	9 (2)

merit revealed the whole molecule. Refinement was by full-matrix least squares minimizing $\sum w ||F_o| - |F_c||^2$ with unit weights. Anisotropic refinement and a subsequent difference synthesis located the H atoms. A scale factor, coordinates of all the atoms, anisotropic thermal parameters of the non-hydrogen atoms and isotropic thermal parameters for the H atoms (260 variables in all) were refined. Anisotropic thermal parameters are in the usual range: the maximum value is U_{22} for C(5') [0.095 (4) Å²]. The final R = 0.050 for 2289 reflexions with $I > 2\sigma(I)$.

Scattering factors given by Cromer & Mann (1968) and (for H) Stewart, Davidson & Simpson (1965) were used. An anomalous-dispersion correction was included for S (Cromer & Liberman, 1970).

The calculations were performed on a Univac 1110 computer at the University Computing Centre in Zagreb with the XRAY system (Stewart, Machin, Dickinson, Ammon, Heck & Flack, 1976). Atom coordinates with U_{eq} values are listed in Table 1 and positional and thermal parameters for the H atoms in Table 2.*

Discussion. The structural formula with the atom numbering is shown in Fig. 1. Bond lengths and angles are listed in Table 3. The conformation of the molecule is defined by the torsion angles listed in Table 4; the conformation of the ring skeleton is described by the deviations of the atoms from the least-squares planes. The molecular packing is illustrated in Fig. 2. Hydrogen bonds are given in Table 5.

The molecular geometry depends on the influences of the atom hybridization and conjugation (Table 3).

^{*} Lists of structure factors, anisotropic thermal parameters, deviations from planes and intermolecular contacts have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 36977 (28 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

C(6)-C(7) [1.373 (5) Å] in the phenyl ring is shortened due to the effect of the van der Waals contacts which involve C(6), e.g. O(11)...C(6) 3.195 (4), C(6)...O(12) 3.285 (4), C(6)...C(14) 3.319 (5), C(6)...N(16) 3.391 (5) and C(2')...C(6) 3.496 (5) Å. C(9)-S(1) [1.749 (3) Å] is shortened due to partial double-bond character; it is very close to the value observed in heterocyclic systems |1.73 (1) Å|(International Tables for X-ray Crystallography,

0(11) H(8) нази H(13)2 H(7) H(13)3 H(16) H(3') NĠ6 H(41) н.6 CO H(S) O(15) 0(17) H(17) Hiss H(6)

Fig. 1. Structural formula and the atom numbering.



Fig. 2. Molecular packing along **a**. The amide group is involved in an intramolecular hydrogen bond to the hydroxy group; it also forms an intermolecular hydrogen bond to the sulphoxide group, connecting molecules in an infinite chain along **b**. 1968). S(1)-N(2) [1.641 (2) Å] is in the interval 1.57-1.75 (6) Å common for sulphamides (*International Tables for X-ray Crystallography*, 1968).

The thiazine ring, involving two double bonds, exhibits a half-chair conformation; S(1) and N(2) are displaced by 0.514 (1) and 0.315 (4) Å from the plane defined by C(3), C(4), C(9) and C(10). The torsion angles in the ring also give evidence for a half-chair conformation (Table 4). The N-2-pyridyl ring is planar

Table 3. Bond distances (Å) and angles (°)

S(1) - N(2)	1.641 (2)	C(7) - C(8)	1.386 (5)
S(1) = C(9)	1.749(3)	C(8) - C(9)	1.376 (4)
S(1) O(11)	1.427(2)	C(9) C(10)	1.397 (4)
S(1) = O(12)	1.425 (2)	C(14) - O(15)	1.238 (4)
N(2) C(3)	1.427 (4)	C(14) - N(16)	1.353(4)
N(2) - C(13)	1.479 (4)	N(16) - C(2')	1.408 (4)
C(3) C(4)	1.369 (4)		
$C(3) \cdot C(14)$	1.463 (4)		
C(4) - C(10)	1.462 (4)		
C(4) - O(17)	1.341 (4)	N(1') - C(2')	1.319 (5)
C(5) C(6)	1.380 (4)	N(1') C(6')	1.339 (6)
C(5) C(10)	1.399 (4)	C(2') - C(3')	1.386 (5)
C(6) - C(7)	1.373 (5)	C(3')- C(4')	1-380 (5)
		C(4') C(5')	1.360 (7)
		C(5') C(6')	1-375 (7)
$N(2) = S(1) \cdot C(9)$	101-4(1)	S(1) = C(9) = C(8)	121.4 (2
N(2) = S(1) - O(11)	108.4(1)	S(1) - C(9) - C(10)	116.4 (2
N(2) - S(1) - O(12)	108.2(1)	C(8) - C(9) - C(10)	122.2 (3
C(9) = S(1) + O(11)	109.4(1)	C(4) = C(10) - C(5)	121-5 (3
C(9) S(1) O(12)	108-6(1)	C(4) = C(10) - C(9)	120.4 (3
O(11) - S(1) - O(12)	119.3(1)	C(5) C(10) C(9)	118-1 (3
S(1) - N(2) - C(3)	113.0(2)	C(3)- C(14)- O(15)	120.8 (3
S(1) - N(2) - C(13)	115.5(2)	C(3) C(14)-N(16)	115-5 (3
C(3) N(2)-C(13)	116-4 (2)	O(15) C(14) N(16	5) 123.7 (3
N(2) C(3) - C(4)	120-4 (2)	C(14) N(16)-C(2') 129-6 (3
N(2)-C(3) C(14)	118-6 (3)		
C(4) - C(3) - C(14)	121-0 (3)		
$C(3) \cdot C(4) - C(10)$	122-6 (3)	C(2') N(1')-C(6') 117.0 (3
C(3) - C(4) - O(17)	122-1 (3)	N(16)-C(2')-N(1') 112.7 (3
C(10)-C(4)-O(17)	115-3 (2)	N(16) C(2')-C(3') 123-5 (3
C(6)-C(5)-C(10)	119-6 (3)	N(1') C(2')-C(3') 123-7 (3
C(5)-C(6)-C(7)	121-0 (3)	C(2')-C(3')-C(4') 117-5 (4
C(6) C(7)-C(8)	120.6 (3)	C(3') C(4')- C(5') 120-0 (4
C(7)-C(8) C(9)	118-4 (3)	C(4') C(5')-C(6') 118-1 (4
		N(1') C(6')- C(5') 123-6 (4

Table 4. Torsion angles (°)

S(1)-N(2)-C(3)-C(4)	41.0(3)	C(7)-C(8)-C(9)-C(10)	1.5 (5)	N(2)-C(3)-C(14)-N(16)	5.8 (4)
N(2)-C(3)-C(4)-O(17)	-179.6(3)	C(8)-C(9)-C(10)-C(5)	-2.2(5)	C(3)-C(14)-N(16)-C(2')	177.9 (3)
N(2)-C(3)-C(4)-C(10)	0.0(4)	C(9)-C(10)-C(5)-C(6)	1.3 (5)	C(14)-N(16)-C(2')-N(1')	174.8 (3)
C(3)-C(4)-C(10)-C(9)	-18.4 (5)	C(10)-C(5)-C(6)-C(7)	0.1(4)	N(1')-C(2')-C(3')-C(4')	0.6 (5)
C(3)-C(4)-C(10)-C(5)	159-8 (3)	C(3)-N(2)-S(1)-O(11)	-170.7 (2)	C(2')-C(3')-C(4')-C(5')	-0.9 (6)
C(4)-C(10)-C(9)-S(1)	-5.8 (4)	C(3)-N(2)-S(1)-O(12)	58.5 (2)	C(3')-C(4')-C(5')-C(6')	0.8 (6)
C(4)-C(10)-C(9)-C(8)	176.1 (3)	C(4)-C(3)-N(2)-C(13)	-96.1(3)	C(4')-C(5')-C(6')-N(1')	-0.4(7)
C(10)-C(9)-S(1)-N(2)	39.1 (3)	C(14)-C(3)-N(2)-C(13)	83.8(3)	C(5')-C(6')-N(1')-C(2')	0.1(5)
C(5)-C(6)-C(7)-C(8)	-0.9 (6)	S(1)-N(2)-C(3)-C(14)	-139.1(2)	C(6')-N(1')-C(2')-C(3')	-0.2(5)
C(6)-C(7)-C(8)-C(9)	0.1(4)	N(2)-C(3)-C(14)-O(15)	-173.8(3)	C(3)-N(2)-S(1)-C(9)	-55.6 (2)

Table 5. Hydrogen bonds

$X - H \cdots Y$	$X \cdots Y$	$\mathbf{H}\cdots \mathbf{Y}$	X–H	$\angle XHY$	Symmetry operation on Y
$O(17) - H(17) \cdots O(15)$	2.561 (3) Å	1·79 (3) Å	0-81 (3) Å	156 (4)°	<i>x</i> , <i>y</i> , <i>z</i>
$N(10) - H(10) \cdots O(11)$	3.053 (3)	2.44 (3)	0.84(3)	130 (3)	1 - x, 1 - y, -z

with the mean value of the ring torsion angles being $0.5 (5)^{\circ}$.

The piroxicam molecule is not far from being planar ($\sim bc$ plane); an amide group is involved in an intramolecular hydrogen bond to the hydroxy group, O(17)-H(17)...O(15) 2.561 (3) Å; the torsion angles along bonds connecting this part of the molecule are C(3)-C(4)-C(10)-C(5) 159.8 (3) and C(3)-C(14)-N(16)-C(2') 177.9 (3)^{\circ}. S(1) and N(2) with non-ring atoms bonded to them show significant departure from the plane of the molecule. The intermolecular hydrogen bond between the amido N and the sulphoxide group [N(16)-H(16)...O(11) 3.053 (3) Å] connects piroxicam molecules in an infinite chain along **b**.

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2-Amino-5,5-dimethyl-1-pyrrolinium Diethyl Phosphate Monohydrate

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Abstract. $C_6H_{13}N_2^+$. $C_4H_{10}O_4P^-$. H_2O , monoclinic, $P2_1/c$, $a = 14 \cdot 138$ (8), $b = 9 \cdot 325$ (7), $c = 12 \cdot 369$ (8) Å, $\beta = 107 \cdot 71$ (5)°, $V = 1553 \cdot 4$ Å³ at 295 K, with Z = 4, $D_m = 1 \cdot 21$ (flotation), $D_x = 1 \cdot 215$ g cm⁻³. The structure was solved by direct methods and refined by full-matrix least squares to a final weighted Rfactor of 0.083 and conventional R factor of 0.072, based on 1858 reflections with significant intensity. The structure involves four modes of hydrogen bonding between amidinium and phosphate ions, two of which involve water acting as a bridge. The O(ethyl)-P-O-C torsion angles are $\pm 67 \cdot 1$ (6) and $\pm 63 \cdot 3$ (6)°.

Introduction. 2-Amino-5,5-dimethylpyrrolinium diethyl phosphate was synthesized as a model for proteinnucleotide interactions by Dr D. A. Usher, Department of Chemistry, Cornell University, who provided the crystals for this study. The Laue symmetry and systematic absences (h0l, l = 2n + 1; 0k0, k = 2n + 1) identified the space group as $P2_1/c$. The unit-cell dimensions were refined by least squares from observations of 12 reflections made on a FACS-I automated diffractometer, which was also used for data collection.

Data were collected with monochromatized Mo Ka radiation in the θ -2 θ scan mode between 3 and 48°, with a minimum base width of 2°, a scan rate of 2° min⁻¹ and 40 s background counts. The crystal was of irregular shape and dimensions $0.5 \times 0.5 \times 0.3$ mm. The intensities of the 2488 independent reflections were corrected for absorption assuming a spherical crystal, with μ (Mo Ka) = 0.197 mm⁻¹.

The resulting structure factors were scaled by the Wilson statistical method, and normalized structure factors were calculated. These were then used in the direct-method programs of Germain & Woolfson (1968). An E map calculated using the best-non-trivial solution yielded coordinates for all non-H atoms of the

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