

2082 reflections  
208 parameters  
H atoms refined with fixed  $U_{iso}$

Extinction correction: none  
Scattering factors from *International Tables for X-ray Crystallography* (Vol. IV)

Motherwell, W. D. S. & Clegg, W. (1978). *PLUTO. Program for Plotting Molecular and Crystal Structures*. University of Cambridge, England.

Zhang, Q., Dai, R., Wang, L. & Li, S. (1996). *Chem. Reag.* **18**, 67.

Table 1. Selected geometric parameters ( $\text{\AA}$ ,  $^\circ$ )

S—C(11)	1.768 (2)	N(2)—N(3)	1.398 (2)
S—C(2)	1.830 (2)	N(2)—C(2)	1.469 (2)
O(1)—C(1)	1.233 (2)	N(3)—C(11)	1.308 (3)
O(2)—C(1)	1.255 (2)	N(4)—C(11)	1.327 (3)
N(1)—C(9)	1.325 (3)	C(1)—C(2)	1.571 (3)
N(1)—C(8)	1.404 (3)	C(2)—C(3)	1.498 (3)
N(2)—C(9)	1.318 (2)	C(3)—C(4)	1.391 (3)
C(11)—S—C(2)	87.2 (1)	N(2)—C(2)—S	102.0 (1)
C(9)—N(1)—C(8)	122.5 (2)	C(3)—C(2)—C(1)	109.4 (1)
C(9)—N(2)—N(3)	121.4 (2)	C(3)—C(2)—S	115.8 (1)
C(9)—N(2)—C(2)	123.2 (2)	C(1)—C(2)—S	108.8 (1)
N(3)—N(2)—C(2)	115.1 (1)	C(8)—C(3)—C(2)	117.5 (2)
C(11)—N(3)—N(2)	108.2 (2)	C(3)—C(8)—N(1)	119.0 (2)
O(1)—C(1)—O(2)	128.7 (2)	N(2)—C(9)—N(1)	119.3 (2)
O(1)—C(1)—C(2)	116.8 (2)	N(3)—C(11)—N(4)	123.2 (2)
O(2)—C(1)—C(2)	114.3 (2)	N(3)—C(11)—S	117.5 (1)
N(2)—C(2)—C(3)	110.2 (1)	N(4)—C(11)—S	119.3 (2)
N(2)—C(2)—C(1)	110.3 (1)		

Table 2. Hydrogen-bonding geometry ( $\text{\AA}$ ,  $^\circ$ )

D—H...A	D...A	D—H...A
N(1)—H(3)...O(3)	2.738 (3)	175
N(4)—H(1)...O(2 <sup>i</sup> )	2.782 (3)	173
N(4)—H(2)...N(3 <sup>ii</sup> )	3.119 (3)	178
O(3)—H(11)...O(1 <sup>iii</sup> )	2.775 (3)	175
O(3)—H(12)...O(2 <sup>iv</sup> )	2.832 (2)	174

Symmetry codes: (i)  $-x, 1 - y, -z$ ; (ii)  $1 - x, 2 - y, -z$ ; (iii)  $1 + x, y, z$ ; (iv)  $1 - x, 1 - y, 1 - z$ .

Data collection: *CAD-4 Software* (Enraf-Nonius, 1989). Cell refinement: *CAD-4 Software*. Data reduction: *TEXSAN PRO-CES*S and *HKL* (Molecular Structure Corporation, 1989). Program(s) used to refine structure: *TEXSAN LS* and *FOURIER*. Molecular graphics: *ORTEPII* (Johnson, 1976) and *PLUTO* (Motherwell & Clegg, 1978).

Lists of atomic coordinates, displacement parameters, structure factors and complete geometry have been deposited with the IUCr (Reference: CF1099). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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*Acta Cryst.* (1997). **C53**, 327–329

## 1-Acetyl-4-[(1*R*,2*S*,5*R*)-3-menthyloxy-carbonyl]piperazine-2,5-dione†

BRENDAN A. BURKETT,<sup>a</sup> CHRISTINA L. L. CHAI<sup>a</sup> AND DAVID C. R. HOCKLESS<sup>b</sup>

<sup>a</sup>Research School of Chemistry and Department of Chemistry, Australian National University, Canberra, ACT 0200, Australia, and <sup>b</sup>Research School of Chemistry, Institute of Advanced Studies, Australian National University, Canberra, ACT 0200, Australia. E-mail: david@rsc.anu.edu.au

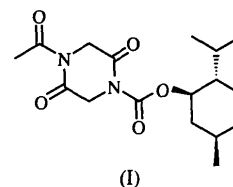
(Received 2 July 1996; accepted 6 November 1996)

## Abstract

The title compound,  $C_{17}H_{26}N_2O_5$ , assumes a skewed-boat conformation. The degree of folding of the piperazinedione ring given by the Hooker parameter,  $\beta$ , was found to be  $32.06^\circ$ .

## Comment

X-ray crystallographic studies have shown that the presence of N and/or  $\alpha$ -C substituents play an important role in determining the conformations of piperazine-2,5-diones (Karle, 1981). As part of our studies (Chai & King, 1995) to exploit such conformational effects to direct reactions stereoselectively, the title compound, (I), was synthesized.



The crystal structure shows that the menthyloxy-carbonyl substituent extends away from the piperazinedione ring, whereas the latter adopts a skewed boat conformation. This is in contrast to the conformations adopted by glycine anhydride and its derivatives. For

† Alternative name: (1'*R*,2'*S*,5'*R*)-3-menthyl 4-acetyl-2,5-dioxopiperazine-1-carboxylate.

example, glycine anhydride adopts a planar conformation (Degeilh & Marsh, 1959), whereas sarcosine anhydride is nearly planar, adopting a flattened chair form (Groth, 1969). One measure of the degree of folding of the piperazine-2,5-dione ring is the Hooker parameter,  $\beta$  (Hooker, Bayley, Radding & Schellman, 1974), and this was found to be very large in the title compound, *i.e.* 32.06°. Comparable  $\beta$  values have been observed for sterically crowded piperazinedione derivatives, *e.g.* for *cis-N,N'*-diacetylated alanine anhydride (30°) and *cis-N,N'*-dimethylated valine anhydride (41°) (Benedetti, Marsh & Goodman, 1976). To our knowledge, this is the largest  $\beta$  value reported for glycine anhydride derivatives. The conformational parameters [following the convention of the IUPAC-IUB Commission on Biochemical Nomenclature (1970)] for peptides are summarized in Table 2.

From the  $\omega$  values which measure the deviation of the amide bond from planarity, it is apparent that twisting about the endocyclic amide bond C2—N1 is slight [7(1)°] in contrast to that about the endocyclic amide bond C5—N4 [16.2(9)°]. The endocyclic amide bonds (N1—C2 and N4—C5) adjacent to the *N*-acetyl and the *N*-menthyloxycarbonyl substituents, respectively, appear slightly longer [1.375(9) and 1.365(9) Å] compared with the amide bonds of glycine and sarcosine anhydride [1.325(7) and 1.348(3) Å]. The diminished double-bond character in the former cases can be attributed to delocalization of the lone pair of electrons on the N atoms onto the exocyclic amide bond. It is also noteworthy that both of these endocyclic amide bonds are shorter compared with the exocyclic amide bonds, with N1—C7 [1.418(9) Å] longer than N4—C9 [1.403(8) Å]. The carbonyl groups in the title piperazinedione have bond lengths of 1.18(1), 1.204(9), 1.22(1) and 1.229(9) Å. The latter values are comparable with the C=O bond lengths of 1.239(7) and 1.234(3) Å in glycine anhydride and sarcosine anhydride, respectively, whereas the

former are shorter. The internal bond angles C2—N1—C6 [119.4(6)°] and C3—N4—C5 [117.2(7)°] are also slightly compressed as compared with the values of 126.0(3)° in glycine anhydride and 124.6(2)° in sarcosine anhydride.

## Experimental

1-Acetylpiperazine-2,5-dione was synthesized from glycine anhydride following the procedure of Akimova, Petrova & Gavrillov (1954). The piperazine-2,5-dione was then treated with menthyl chloroformate (1.2 equivalents) and *N,N*-dimethylaminopyridine (1.2 equivalents) in CH<sub>2</sub>Cl<sub>2</sub> and the progress of the reaction was monitored by thin-layer chromatography. Upon completion of the reaction, the reaction mixture was washed successively with water and brine, following which the organic layer was dried over sodium sulfate and concentrated *in vacuo*. The desired product was isolated by flash column chromatography as a colourless solid in 55% yield. Recrystallization from ethyl acetate and petroleum spirit gave suitable crystals for X-ray analysis.

### Crystal data

C<sub>17</sub>H<sub>26</sub>N<sub>2</sub>O<sub>5</sub>  
*M<sub>r</sub>* = 338.40  
 Monoclinic  
*P*2<sub>1</sub>  
*a* = 9.977(4) Å  
*b* = 5.757(4) Å  
*c* = 16.047(3) Å  
 $\beta$  = 96.26(2)°  
*V* = 916.2(8) Å<sup>3</sup>  
*Z* = 2  
*D<sub>x</sub>* = 1.227 Mg m<sup>-3</sup>  
*D<sub>m</sub>* not measured

Cu K $\alpha$  radiation  
 $\lambda$  = 1.5418 Å  
 Cell parameters from 25 reflections  
 $\theta$  = 20.9–26.0°  
 $\mu$  = 0.747 mm<sup>-1</sup>  
*T* = 296(1) K  
 Needle  
 0.36 × 0.08 × 0.04 mm  
 Colourless

### Data collection

Rigaku AFC-6R diffractometer  
 $\omega/2\theta$  scans  
 Absorption correction: empirical based on azimuthal ( $\psi$ ) scans (North, Phillips & Mathews, 1968)  
 $T_{\min}$  = 0.86,  $T_{\max}$  = 0.97  
 1622 measured reflections  
 1525 independent reflections

1521 reflections with  $I > 0$   
 $R_{\text{int}}$  = 0.031  
 $\theta_{\max}$  = 60.02°  
 $h$  = 0 → 11  
 $k$  = 0 → 6  
 $l$  = -18 → 17  
 3 standard reflections every 150 reflections  
 intensity decay: negligible

### Refinement

Refinement on *F*  
 $R$  = 0.0983  
 $wR$  = 0.0448  
 $S$  = 1.989  
 1521 reflections  
 217 parameters  
 H atoms not refined  
 $w = 4F_o^2/[\sigma^2(F_o^2) + (0.007F_o^2)^2]$   
 $(\Delta/\sigma)_{\max}$  = 0.0188

$\Delta\rho_{\max}$  = 0.39 e Å<sup>-3</sup>  
 $\Delta\rho_{\min}$  = -0.27 e Å<sup>-3</sup>  
 Extinction correction: Zachariasen type 2, Gaussian isotropic  
 Extinction coefficient: 1.3(7) × 10<sup>-6</sup>  
 Scattering factors from *International Tables for Crystallography* (Vol. C)

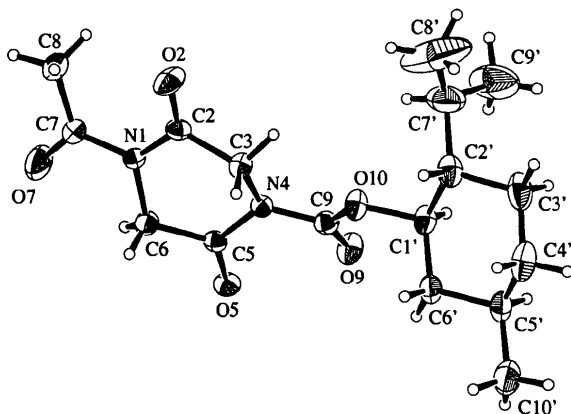


Fig. 1. View of the title compound showing the labelling of all non-H atoms. Displacement ellipsoids are shown at 20% probability levels. H atoms are shown as circles of arbitrary radii.

Table 1. Selected geometric parameters ( $\text{\AA}$ ,  $^\circ$ )

O(2)—C(2)	1.204 (9)	N(1)—C(7)	1.418 (9)
O(5)—C(5)	1.229 (9)	N(4)—C(5)	1.365 (9)
O(10)—C(1')	1.478 (7)	N(4)—C(9)	1.403 (8)
N(1)—C(2)	1.375 (9)		
C(2)—N(1)—C(6)	119.4 (6)	N(4)—C(3)—C(2)	115.0 (7)
C(3)—N(4)—C(5)	117.2 (7)	N(4)—C(5)—C(6)	117.7 (8)
N(1)—C(2)—C(3)	116.4 (7)	N(1)—C(6)—C(5)	117.4 (6)

Table 2. Torsion angles ( $^\circ$ )

C(2)—N(1)—C(6)—C(5)	$\varphi_1$	-32.4 (9)
C(5)—N(4)—C(3)—C(2)	$\varphi_2$	-41.0 (8)
N(1)—C(6)—C(5)—N(4)	$\psi_1$	20.1 (9)
N(4)—C(3)—C(2)—N(1)	$\psi_2$	28.9 (9)
C(3)—C(2)—N(1)—C(6)	$\omega_1$	7 (1)
C(6)—C(5)—N(4)—C(3)	$\omega_2$	16.2 (9)

The  $\theta$ -scan width used was  $(1.30 + 0.30 \tan \theta)^\circ$  at a speed of  $16^\circ \text{ min}^{-1}$  (in  $\omega$ ). The weak reflections were rescanned a maximum of four times and the counts accumulated to ensure good counting statistics. Stationary background counts were made on each side of the reflection with a 2:1 ratio of peak to background counting time. The maximum limit of  $120^\circ$  in  $2\theta$  was used. Higher-angle data collection was not possible and would have resulted in hardware collision. Owing to the small size and weakly diffracting nature of the crystal, collection of data to any higher angle would not have significantly improved the data to parameter ratio in this particular case. The reader should however treat with discretion the somewhat detailed comparisons given in the discussion. The structure was solved by the direct methods program *SIR92* (Altomare *et al.*, 1994) and expanded using Fourier techniques (*DIRDIF92*; Beurskens *et al.*, 1992). H atoms were located from a difference map and fixed at ideal positions with C—H = 0.96  $\text{\AA}$  and  $U_{\text{iso}} = 1.2U_{\text{eq}}(\text{C})$ .

Data collection: *MSCIAFC Diffractometer Control Software* (Molecular Structure Corporation, 1992a). Cell refinement: *MSCIAFC Diffractometer Control Software*. Data reduction: *TEXSAN* (Molecular Structure Corporation, 1992b). Program(s) used to refine structure: *TEXSAN*. Software used to prepare material for publication: *TEXSAN*.

Lists of atomic coordinates, displacement parameters, structure factors and complete geometry have been deposited with the IUCr (Reference: TA1117). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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## Glimepiride

MARIKO IWATA,<sup>a</sup> HIROMASA NAGASE,<sup>b</sup> TOMOHIRO ENDO<sup>b</sup>  
AND HARUHISA UEDA<sup>b</sup>

<sup>a</sup>*Drug Development Research Laboratories, Pharma Research & Development Division, Hoechst Japan Limited, 3-2 Minamidai 1-Chome, Kawagoe-City, Saitama 350-11, Japan, and* <sup>b</sup>*Department of Physical Chemistry, Hoshi University, 4-41 Ebara 2-Chome, Shinagawa-ku, Tokyo 142, Japan. E-mail: ueda@hoshi.ac.jp*

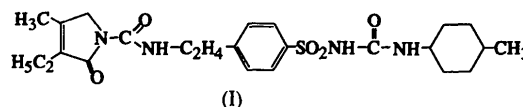
(Received 17 October 1995; accepted 16 November 1996)

## Abstract

Glimepiride, 1-[4-[2-(3-ethyl-4-methyl-2-oxo-3-pyrroline-1-carboxyamido)ethyl]phenylsulfonyl]-3-(*trans*-4-methylcyclohexyl)urea,  $\text{C}_{24}\text{H}_{34}\text{N}_4\text{O}_5\text{S}$ , is a drug used in the treatment of non-insulin dependent diabetes mellitus.

## Comment

Glimepiride, (I), is a second-generation sulfonylurea compound used in the treatment of non-insulin dependent diabetes mellitus (Holmes, Heel, Brogden, Speight & Avery, 1984). Structural data on glimepiride is limited and so far only one stable polymorphic form is known; its solubility is  $1.2 \text{ mg l}^{-1}$  (293 K) at pH 7 (Iwata, 1997). The crystal structure of this stable form determined by X-ray crystallographic analysis is reported here.



(I)