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Key indicators

Single-crystal X-ray study T = 295 KMean $\sigma(\text{C-C}) = 0.004 \text{ Å}$ R factor = 0.053 wR factor = 0.188 Data-to-parameter ratio = 14.2

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

Conformational isomerism in 3-(Z)-isobutylidene-1-acetylpiperazine-2,5-dione

The title compound, $C_{10}H_{14}N_2O_3$, (I), is a key intermediate in the synthesis of the cyclic dehydropeptide albonoursin, which has been found to exhibit useful biological and pharmacological properties. It crystallizes with two molecules in the asymmetric unit with different conformational structures. The methylpropylidene side chain is found to be in the Z configuration about the C=C double bond for both molecules.

Comment

Several cyclic dehydropeptides, such as roquefortine (Barrow et al., 1979; Chen & Joullie, 1998) and albonoursin (Shin et al., 1980) exhibit biological and pharmacological properties. In particular, interest in the latter has led to the syntheses and assignment of configurations of albonoursin and its geometric isomers (Villemin & Ben Alloum, 1990; Shin et al., 1977). The title monoalkylidene piperazine-2,5-dione, (I), is a key intermediate in the synthesis of albonoursin. The solution structure determination of (I) has relied on the assignment of the configuration of the double bond by NMR spectroscopy (Shin et al., 1977; Gallina & Liberatori, 1974). We report here the first solid-state structural elucidation of (I), which allows direct correlation between the solution and solid-state structures for assignment of the double-bond geometry. In addition, this represents one of the first accounts of a solid-state structure for a monoalkylidene piperazine-2,5-dione. Compound (I) was obtained by a modification of a procedure (Gallina & Liberatori, 1973) where 1,3-diacetylpiperazine-2,5dione (Marcuccio & Elix, 1984) was condensed with 2-methylpropionaldehyde in the presence of a strong base, namely potassium tert-butoxide.



The crystal structure of (I) contains two independent molecules (I*a* and I*b*) in the asymmetric unit, the structures of which are shown in Fig. 1. In both molecules, the methylpropylidene side chain adopts a Z configuration about the double bond, confirming the NMR assignment in the solution state. Both molecules associate as pairs of centrosymmetrically related molecules through classical $R_2^2(8)$ (Bernstein *et al.*, 1995) N-H···O hydrogen-bonding interactions between N2 and O3 [for molecule I*a*: H···O3 $A^i = 2.00$ Å, N2A···O3 $A^i =$

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Figure 1

ORTEP-3 (Farrugia, 1997) plot, showing the atomic numbering scheme for molecules (Ia) and (Ib). Displacement ellipsoids for non-H atoms are drawn at the 30% probability level.



Figure 2

ORTEP-3 plot showing the hydrogen-bonding arrangement for molecules (1a) (above) and (Ib) (below).

2.836 (2) Å and N2A-H···O3Aⁱ = 167°; symmetry code: (i) -x, 2 - y, 2 - z; for molecule Ib: $H \cdots O3B^{ii} = 2.07$ Å, $N2B \cdots O3B^{ii} = 2.908 (3) \text{ Å} \text{ and } N2B - H \cdots O3B^{ii} = 167^{\circ};$ symmetry code: (ii) -x, 1 - y, 1 - z] (Fig. 2). This hydrogenbonding feature is observed in the structures of other piperazinedione systems (Ongania et al., 1985; Ajo et al., 1985).

The piperazinedione ring in molecule (Ia) adopts a puckered conformation with the peripheral isopropyl and keto substituents lying well out of the plane defined by the intermolecular N-H···O hydrogen bonding. In the crystal lattice (Fig. 3), the dimers of (Ia) lie approximately in the *ac* plane at $b \sim 0$, with the long axis of the dimer oriented along the crystallographic a axis. In contrast, the conformational structure of (Ib) is essentially planar for all non-H atoms other than the C9 and C10 methyl groups. As in (Ia), the dimers of (Ib) lie approximately in the *ac* plane but at $b \sim \frac{1}{2}$, with the long axis oriented along the c axis. The bond lengths for both molecules (Table 1) are in accord with conventional values (Allen et al., 1987), with differences between corresponding values in the two molecules no greater than 0.01 Å. Greater diversity is apparent in the bond angles, with the greatest differences observed for the angles about N1 and C6.

Experimental

Potassium tert-butoxide (0.567 g, 5.053 mmol) in tert-butanol (10 ml, 0.105 mol) was added to a stirred solution of 2-methylpropionaldehyde (1.80 ml, 0.020 mol) and 1,4-diacetylpiperazine-2,5-dione (1.054 g, 5.328 mmol) in dry DMF (10.50 ml, 0.136 mol) at 273 K. The mixture was stirred at room temperature for 24 h and worked up as described elsewhere (Gallina & Liberatori, 1973). The crude product was recrystallized (ethyl acetate/hexane), giving (I) as white crystals (263 mg, 24%). Colourless crystals of (I) [m.p. 419.9-420.3 K; literature 419.2-420.2 K (Gallina & Liberatori, 1973, 1974) and 423.2-424.2 K (Shin et al., 1977)] were isolated by slow evaporation of a hexane-ethyl acetate solution of (I). Analysis found: C 57.41, H 6.77, N 13.45%; calculated for C₁₀H₁₄N₂O₃: C 57.13, H 6.71, N 13.33%. v_{max} (KBr)/cm⁻¹: 3390, 3196 (NH), 1687, 1650, (CO), 1636, (C=C). δ_H (200 MHz, CDCl₃, p.p.m.): 8.10 (1H, brs, NH), 6.18 (1H, d, $J_{7.8}$ = 10 Hz, 7-H), 4.44 (2H, s, 6-H), 2.75-2.60 (1H, m, 8-H), 2.61 (3H, s, 1-H), 1.10 (6H, d, $J_{9/10.8}$ = 6.5 Hz, 9-H, 10-H). δ_C (50 MHz, CDCl₃, p.p.m.): 172.7 (C2), 164.2 (C5), 160.2 (C3), 131.6 (C4), 124.5 (C7), 46.0 (C6), 27.2 (C9 and C10), 25.9 (C8), 22.0 (C1). ESMS+: 209 (MH+, 100%), 233 (MNa⁺, 100%).

Crystal data

$C_{10}H_{14}N_2O_3$	Z = 4
$M_r = 210.23$	$D_x = 1.271 \text{ Mg m}^{-3}$
Friclinic, P1	Mo K α radiation
u = 10.7310 (18) Å	Cell parameters from 25
$p = 10.827 (3) \text{ Å}_{2}$	reflections
= 9.7916 (14) Å	$\theta = 19.4 - 20.0^{\circ}$
$\alpha = 95.607 \ (17)^{\circ}$	$\mu = 0.10 \text{ mm}^{-1}$
$B = 94.680 \ (13)^{\circ}$	T = 295 K
$v = 76.484 (17)^{\circ}$	Prism, colourless
$V = 1098.8 (4) \text{ Å}^3$	$0.60 \times 0.50 \times 0.30 \mbox{ mm}$

Data collection

Rigaku AFC-7R diffractometer ω -2 θ scans Absorption correction: none 4100 measured reflections 3872 independent reflections 2691 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.019$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.053$ wR(F²) = 0.188 S = 1.093872 reflections 272 parameters H-atom parameters constrained

 $\theta_{\rm max} = 25.0^\circ$ $h = 0 \rightarrow 12$ $k = -12 \rightarrow 12$ $l = -11 \rightarrow 11$ 3 standard reflections every 150 reflections intensity decay: 1.3%

 $w = 1/[\sigma^2(F_o^2) + (0.1241P)^2]$ + 0.0666P] where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.26 \ {\rm e} \ {\rm \AA}^{-3}$ $\Delta \rho_{\rm min} = -0.26 \text{ e } \text{\AA}^{-3}$ Extinction correction: SHELXL97 Extinction coefficient: 0.032 (7)

Table 1				
Selected	geometric	parameters	(Å, '	^{>}).

01A-C2A	1.210 (3)	O1B-C2B	1.214 (4)
O2A - C3A	1.203 (3)	O2B-C3B	1.214 (3)
O3A-C5A	1.233 (3)	O3B-C5B	1.224 (4)
N1A - C2A	1.408 (3)	N1B-C6B	1.458 (4)
N1A - C3A	1.394 (3)	N1B-C2B	1.417 (3)
N1A - C6A	1.463 (3)	N1B-C3B	1.380 (3)
N2A - C4A	1.408 (3)	N2B-C5B	1.328 (4)
N2A - C5A	1.335 (3)	N2B-C4B	1.406 (3)
C1A - C2A	1.484 (4)	C1B-C2B	1.483 (4)
C3A - C4A	1.501 (3)	C3B-C4B	1.495 (3)
C4A-C7A	1.332 (3)	C4B-C7B	1.325 (3)
C5A - C6A	1.494 (3)	C5B-C6B	1.485 (4)
C7A - C8A	1.500 (3)	C7B-C8B	1.505 (3)
C8A-C10A	1.513 (4)	C8B-C9B	1.507 (4)
C8A-C9A	1.519 (5)	C8B-C10B	1.525 (4)
CO 4 N1 4 CO 4	104.14 (10)		105 00 (10)
C2A - NIA - C5A	124.14 (18)	C2B = N1B = C3B	125.08 (19)
$C_{2A} = N_{1A} = C_{0A}$	117.28(17) 118.47(16)	C2B = N1B = C6B	112.0(2)
$C_{A} = N_{A} = C_{A}$	118.47 (10)	$C_{3B} = N_{1B} = C_{0B}$	122.3(2)
C4A - NZA - C5A	123.42(17)	C4B = N2B = C3B	125.4(2)
OIA - C2A - NIA	118.1(3) 122.7(2)	O1B - C2B - N1B O1B - C2B - C1B	117.0(2) 121.2(2)
OIA - C2A - CIA	122.7(3)	OIB = C2B = CIB	121.5(2) 121.1(2)
NIA - C2A - CIA	119.22 (19)	N1B = C2B = C1B N1B = C2B = C4B	121.1(3) 117.01(19)
NIA - CSA - C4A	114.37(17) 122.40(10)	N1B = C3B = C4B	117.91 (10)
$O_2A - C_3A - N_1A$	125.49 (19)	$O_{2B} = C_{3B} = N_{1B}$	122.0(2) 120.1(2)
$O_{2A} - C_{3A} - C_{4A}$	121.94(10) 117.22(17)	O2B - C3B - C4B	120.1(2) 117.00(10)
N2A = C4A = C3A N2A = C4A = C7A	117.55(17) 122.57(10)	N2B = C4B = C3B N2B = C4B = C7B	122 20 (19)
$R_{2A} = C_{4A} = C_{7A}$	123.37(19) 118.06(10)	$C_{2}^{2}P$ $C_{4}^{4}D$ $C_{7}^{7}P$	110.80 (19)
$C_{A} = C_{A} = C_{A}$	110.90 (19)	$C_{3B} = C_{4B} = C_{7B}$	119.00 (19)
N24 C54 - C64	125.20 (19)	N2B C5B C6B	123.4(3) 118.8(3)
$O_{3A} C_{5A} C_{6A}$	113.91(10) 120.83(18)	$O_{3B}^{2B} = C_{5B}^{2B} = C_{6B}^{2B}$	117.8(3)
N14 C64 C54	120.05(10) 112.11(17)	N1R C6R C5R	117.0(3) 117.2(2)
C44 - C74 - C84	1286(2)	C4B = C0B = C3B	117.3(3) 127.71(10)
C7A C8A C9A	120.0(2) 100.8(2)	C7B C8B C9B	111 14 (19)
C74 - C84 - C104	109.0(2) 1101(3)	C7B - C8B - C10B	110 18 (19)
C9A - C8A - C10A	109.3 (2)	C9B - C8B - C10B	110.13 (19)
	. ,		. ,

H atoms were constrained in the riding-model approximation, with C-H distances set at 0.95 Å and N-H set at 0.85 Å. $U_{\rm iso}$ values for the H atoms were set at $1.2U_{\rm eq}$ of the parent atom.

Data collection: *MSC/AFC-7 Diffractometer Control Software* (Molecular Structure Corporation, 1999); cell refinement: *MSC/AFC-7 Diffractometer Control Software*; data reduction: *TEXSAN for Windows* (Molecular Structure Corporation, 1997–2001); program(s) used to solve structure: *TEXSAN for Windows*; program(s) used to refine structure: *TEXSAN for Windows* and *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2001) and *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *TEXSAN for Windows* and *PLATON*.

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Figure 3

Crystal packing diagram for (I), viewed down the c axis with a horizontal and b vertical.

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