The Crystal Structure of 1,5-Bis(3,5-Dimethyl-2-hydroxybenzyl)-1,5-diazocan-2,6-dione

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The study of the molecular geometry of 1,5-bis(3,5-dimethyl-2-hydroxybenzyl)-1,5-diazocan-2,6-dione (**2**) as determined by X-ray analysis is reported and compared with that of cyclodi-β-alanyl (**3**). Interestingly there are 1.5 molecules of **2** in the asymmetric unit, showing the two conformations (1 twist-boat- and 0.5 chair-type) with two parallel aromatic rings (from alternate twist-boat conformers) sandwiching the eight-membered ring of the centrosymmetric chair-type conformation. The twist-boat is shown by pmr spectroscopy to be the only significantly populated conformer at low temperature in deuteriodichloromethane solution.

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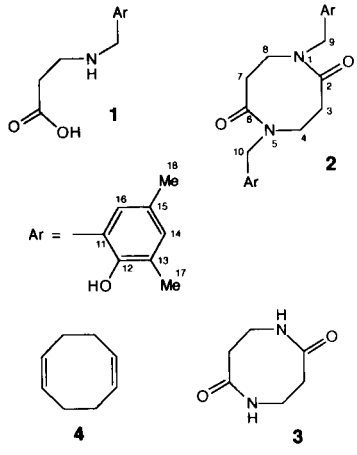
Introduction.

In the course of our studies concerned with the scope and limitations of the Mannich reaction when β-amino acids are used as amine components, we synthesized *N*-(2-hydroxybenzyl)-3-aminopropanoic acids [1], 1,2-dihydro-1-(2-hydroxybenzyl)-3,1-benzoxazin-4-ones [2], *N*-(2-hydroxybenzyl)anthranilic acids [2a], and *N*-(β-benzoylethyl)-β-alanine ethyl esters [3], as useful starting points for building complex heterocyclic systems, many of which are very interesting from a conformational point of view [4].



In this paper we report the crystal structure analysis of 1,5-bis(3,5-dimethyl-2-hydroxybenzyl)-1,5-diazocan-2,6-dione (**2**), obtained in good yield (60%) by the intermolecular dehydration of *N*-(3,5-dimethyl-2-hydroxybenzyl)-3-aminopropanoic acid (**1**) with phosphoryl chloride/zinc chloride [1,5]. The structure of **2** was initially assigned on the basis of its spectroscopic properties (see Experimental). To the best of our knowledge, only very few papers [6] have been concerned with the synthesis, always in lower yields, of 1,5-diazocan-2,6-diones *via* ring expansion [6a-c,e] or ring closure [6c,d,f] reactions. Among the applications of 1,5-diazocine systems, the polymerization of bislactams such as **3** to poly(β-alanine) are of particularly importance [7].

Results and Discussion.

A crystallographic study of **2** was undertaken to confirm the structural assignment and to establish any influences of the *N-ortho*-hydroxybenzyl substituents on the conformation of the eight-membered 1,5-diazocan-2,6-dione ring. The solid state structure [8] of the parent heterocycle, cyclodi-β-alanyl (**3**), shows that it packs in a twist-boat conformation similar to that of its carbocyclic analog 1,5-cyclooctadiene (**4**) [9], a situation consistent with solution nmr studies and Molecular Orbital calculations which suggest that a flexible boat or twist-boat is the most stable conformation for both of these compounds [9,10]. The rationalization [10,11] for the decreased stability of the corresponding chair conformations is that the eclipsed stereo-

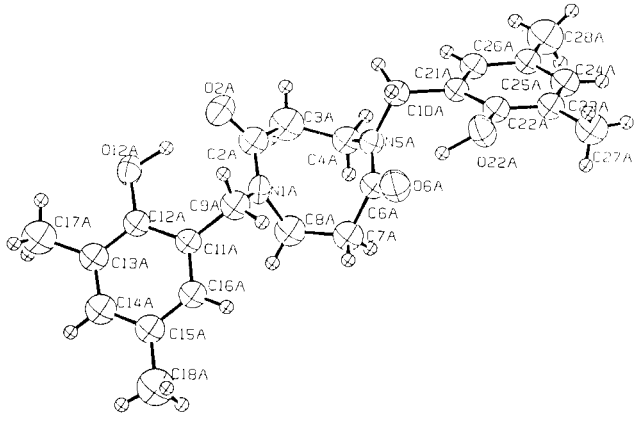


Figure 1. ORTEP view of **2** in its twist-boat conformation (A).

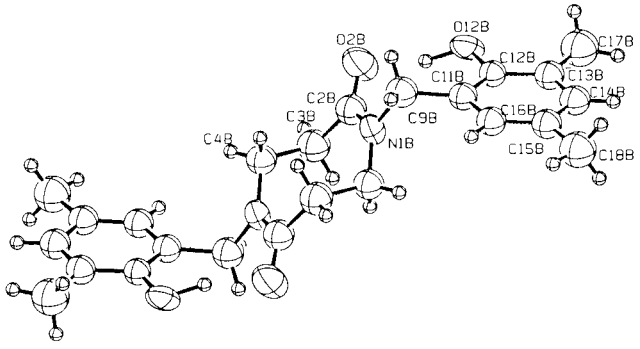


Figure 2. ORTEP view of **2** in its chair conformation (B).

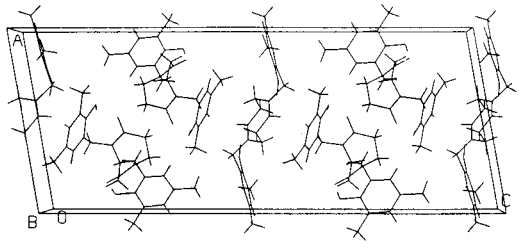


Figure 3. Molecular packing of **2**.

Table 1

Selected Intramolecular Distances (Å) Involving the Non-Hydrogen Atoms of **2** with Estimated Standard Deviations in the Least Significant Figures in Parentheses.

atom	atom	distance	atom	atom	distance
O2B	C2B	1.23(2)	C2B	C3B	1.51(2)
O12B	C12B	1.37(1)	C3B	C4B	1.54(2)
N1B	C2B	1.38(1)	C9B	C11B	1.51(2)
N1B	C4B	1.44(2)	C11B	C12B	1.39(2)
N1B	C9B	1.49(1)	O2B	O12B	2.68(1)
O6A	C6A	1.20(1)	C9A	C11A	1.49(2)
O22A	C22A	1.40(1)	C10A	C21A	1.52(2)
N1A	C8A	1.48(2)	C11A	C12A	1.41(1)
N5A	C4A	1.48(1)	C21A	C22A	1.39(1)
N5A	C6A	1.34(1)	O12A	C12A	1.38(1)
N5A	C10A	1.47(1)	N1A	C2A	1.36(1)
C2A	C3A	1.53(2)	N1A	C9A	1.47(2)
C3A	C4A	1.54(2)	O2A	C2A	1.24(1)
C6A	C7A	1.51(2)	O2A	O12A	2.75(1)
C7A	C8A	1.53(2)	O6A	O22A	2.60(1)

Table 2

Selected Intramolecular Bond Angles (°) Involving the Non-Hydrogen Atoms of **2** with Estimated Standard Deviations in the Least Significant Figure in Parentheses.

atom	atom	atom	angle	atom	atom	atom	angle
C2B	N1B	C4B	124.1(9)	C2B	C3B	C4B	113(1)
C2B	N1B	C9B	118.4(9)	N1B	C4B	C3B	114(1)
C4B	N1B	C9B	117.5(9)	N1B	C9B	C11B	113(1)
O2B	C2B	N1B	121.1(9)	C9B	C11B	C12B	122(1)
O2B	C2B	C3B	122(1)	O12B	C12B	C11B	121.4(9)
N1B	C2B	C3B	117(1)	O12B	C12B	C13B	117(1)
N5A	C6A	C7A	118.9(9)	C2A	C3A	C4A	117.2(9)
N5A	C10A	C21A	113.1(9)	N5A	C4A	C3A	113(1)
O12A	C12A	C11A	120(1)	O6A	C6A	N5A	122(1)
C2A	N1A	C8A	120(1)	O6A	C6A	C7A	118.7(9)
C8A	N1A	C9A	116.6(8)	C6A	C7A	C8A	115.9(9)
O22A	C22A	C21A	120.6(9)	N1A	C8A	C7A	112(1)
C4A	N5A	C6A	124.0(9)	N1A	C9A	C11A	113(1)
C4A	N5A	C10A	116.2(8)	C9A	C11A	C12A	121.9(9)
C6A	N5A	C10A	119.8(9)	O12A	C12A	C13A	118.4(9)
O2A	C2A	N1A	118(1)	C2A	N1A	C9A	123.4(9)
O2A	C2A	C3A	120(1)	C10A	C21A	C22A	123.6(9)
N1A	C2A	C3A	121(1)	O22A	C22A	C23A	116.7(8)

Table 3

Selected Torsion or Conformation Angles (°) Involving the Non-Hydrogen Atoms of **2** with Estimated Standard Deviations in the Least Significant Figure in Parentheses.

(1)	(2)	(3)	(4)	angle	(1)	(2)	(3)	(4)	angle
O2B	C2B	N1B	C4B	-173(1)	O2B	C2B	N1B	C9B	7(2)
O2B	C2B	C3B	C4B	-113(1)	O12B	C12B	C11B	C9B	-2(2)
N1B	C2B	C3B	C4B	63(1)	C2B	N1B	C4B	C3B	-87(1)
N1B	C4B	C3B	C2B	112(1)	C3B	C2B	N1B	C4B	11(2)
N1B	C9B	C11B	C12B	78(1)	C3B	C2B	N1B	C9B	-170(1)
N1B	C9B	C11B	C16B	-105(1)	C4B	N1B	C9B	C11B	-78(1)
C2B	N1B	C9B	C11B	102(1)	C3B	C4B	N1B	C9B	-93(1)
O2A	C2A	N1A	C9A	-10(2)	O6A	C6A	N5A	C4A	178(1)
O2A	C2A	N1A	C8A	168(1)	O6A	C6A	N5A	C10A	1(2)
O2A	C2A	C3A	C4A	139(1)	O6A	C6A	C7A	C8A	130(1)
O22A	C22A	C21A	C10A	-3(2)	O12A	C12A	C11A	C9A	4(2)
N1A	C2A	C3A	C4A	-41(2)	N1A	C8A	C7A	C6A	-32(1)
N1A	C9A	C11A	C12A	-78(1)	N1A	C9A	C11A	C16A	107(1)
N5A	C4A	C3A	C2A	-33(2)	N5A	C6A	C7A	C8A	-49(1)
N5A	C10A	C21A	C22A	-88(1)	N5A	C10A	C21A	C26A	92(1)
C2A	N1A	C8A	C7A	99(1)	C2A	N1A	C9A	C11A	107(1)
C3A	C2A	N1A	C8A	-12(2)	C3A	C2A	N1A	C9A	170(1)
C3A	C4A	N5A	C6A	92(1)	C3A	C4A	N5A	C10A	-90(1)
C4A	N5A	C6A	C7A	-2(2)	C4A	N5A	C10A	C21A	-94(1)
C6A	N5A	C10A	C21A	84(1)	C7A	C6A	N5A	C10A	-179.5(9)
C7A	C8A	N1A	C9A	-83(1)	C8A	N1A	C9A	C11A	-72(1)

The sign is positive if when looking from atom 2 to atom 3 a clock-wise motion of atom 1 would superimpose it on atom 4.

chemistry around the C_i^{α}-C_i^{β} bonds [12] in these conformers results in appreciable Pitzer strain which could only be accommodated by a corresponding increase in Baeyer strain (*i.e.* bond angle deformation). The more flexible boat form, however, can twist to avoid eclipsing the C_i^{α}-C_i^{β} bonds without any appreciable bond angle deformation. The demonstrated conformational similarity between cyclic amides and the corresponding olefins is of particularly importance for supplementing the sparse structural information available in regard to *cis*-peptide conformations [8].

The X-ray structure of **2** (Figures 1-3, Tables 1-4) recrystallized from methanol reveals two different conformations of **2** in the unit cell in a ratio of 2:1.

The expected twofold axis twist-boat is the major conformer (Figure 1), with N_{sp^2}-CH_2-CH_2-C_{sp^2} torsion angles of $-32 \pm 1°$ and $-33 \pm 2°$ (Table 3) compared with $-27°$ in **3**. Substitution of the nitrogen atom does not appear to alter the conformations of the amide groups in the 1,5-diazocan-2,6-dione ring, which are both virtually planar in accord with the *cis*-peptide units in **3** [8].

The minor conformer is a perfectly centrosymmetric chair (Figure 2), with a N_{sp^2}-CH_2-CH_2-C_{sp^2} torsion angle of $112 \pm 1°$ (Table 3). The *endo*-cyclic C–N bond is drawn into conjugation with the C=O group so that the ring is flattened in this region similar to that of the twist-boat form.

An important feature of both the chair and twist-boat conformers are the intramolecular hydrogen bonds between the amide carbonyl and the phenolic hydroxyl groups (O2-H-O12 in Figures 1 and 2 [O...O distances 2.68(1) and 2.75(1) Å, respectively] and O6-H-O22 in Figure 2 [O...O distance 2.60(1) Å]) forming two additional eight-membered rings in each conformer. The eight-membered rings enclosed by hydrogen bonds all adopt twist-boat-type conformations with torsion angles not dissi-

Table 4

Fractional Atomic Coordinates and Vibrational Parameters (Å²) of **2** with Estimated Standard Deviations in the Least Significant Figure in Parentheses.

$$B_{eq} = \frac{8\pi^2}{3}\sum_i\sum_j U_{ij}a_i^*a_j^*(\vec{a}_i\cdot\vec{a}_j)$$

atom	x/a	y/b	z/c	B(eq)	atom	x/a	y/b	z/c	B(eq)
O2B	0.4787(6)	0.332(1)	0.9472(3)	7.3(5)	O12B	0.2915(6)	0.483(1)	0.9381(2)	5.0(4)
N1B	0.3920(6)	0.111(1)	0.9681(3)	4.2(5)	C2B	0.4764(9)	0.217(2)	0.9724(4)	4.9(3)
C3B	0.5678(9)	0.180(2)	1.0076(4)	5.5(3)	C4B	0.6217(8)	0.014(2)	1.0011(4)	4.7(3)
C9B	0.3085(9)	0.126(2)	0.9292(4)	5.0(3)	C11B	0.2110(8)	0.215(1)	0.9377(3)	4.1(3)
C12B	0.2060(8)	0.385(1)	0.9409(3)	3.6(2)	C13B	0.1135(8)	0.466(1)	0.9463(4)	4.4(3)
C14B	0.0261(9)	0.366(2)	0.9478(4)	4.7(3)	C15B	0.0285(8)	0.195(2)	0.9451(4)	4.5(3)
C16B	0.1210(8)	0.123(1)	0.9399(4)	4.4(3)	C17B	0.110(1)	0.649(2)	0.9478(5)	7.2(4)
C18B	-0.070(1)	0.098(2)	0.9463(4)	6.8(4)	H3B1	0.6180	0.2665	1.0089	6.6
H4B1	0.5932	-0.0259	0.9730	5.7	H3B2	0.5428	0.1757	1.0344	6.6
H4B2	0.6951	0.0335	1.0025	5.7	H9B1	0.3366	0.1850	0.9077	6.1
H9B2	0.2891	0.0179	0.9187	6.1	H12B	0.3650	0.4158	0.9470	6.2
H14B	-0.0380	0.4174	0.9512	5.7	H16B	0.1240	0.0075	0.9375	5.2
H17B1	0.1637	0.6888	0.9700	8.6	H18B1	-0.0932	0.1172	0.9732	8.1
H17B2	0.1198	0.6940	0.9212	8.6	H17B3	0.0431	0.6837	0.9539	8.6
H18B2	0.1242	0.1297	0.9237	8.1	H18B3	-0.0563	-0.0171	0.9441	8.1
O2A	0.4788(5)	0.330(1)	0.8052(3)	5.7(5)	O6A	0.8460(6)	0.506(1)	0.8580(2)	5.3(4)
O12A	0.4131(5)	0.046(1)	0.8400(2)	4.5(4)	O22A	0.9152(6)	0.805(1)	0.8510(2)	5.0(4)
N1A	0.6353(6)	0.209(1)	0.8249(3)	4.4(5)	N5A	0.7496(6)	0.500(1)	0.7921(3)	4.0(5)
C2A	0.5655(8)	0.295(2)	0.7959(4)	4.4(3)	C3A	0.593(1)	0.347(2)	0.7526(4)	6.1(3)
C4A	0.7048(8)	0.411(1)	0.7524(4)	4.2(3)	C6A	0.8085(8)	0.429(1)	0.8264(3)	3.8(3)
C7A	0.8282(9)	0.246(2)	0.8256(4)	4.6(3)	C8A	0.7307(9)	0.137(2)	0.8120(4)	5.0(3)
C9A	0.6206(8)	0.180(2)	0.8693(4)	4.5(3)	C10A	0.7300(8)	0.679(1)	0.7921(3)	3.6(2)
C11A	0.5917(8)	0.006(1)	0.8768(3)	3.5(2)	C12A	0.4888(8)	-0.054(1)	0.8633(3)	3.7(2)
C13A	0.4634(8)	-0.218(2)	0.8696(4)	4.3(3)	C14A	0.5388(9)	-0.317(2)	0.8936(4)	5.0(3)
C15A	0.6400(8)	-0.263(2)	0.9089(4)	4.4(3)	C16A	0.6643(8)	-0.102(1)	0.9006(4)	3.9(3)
C17A	0.353(1)	-0.281(2)	0.8549(4)	6.3(3)	C18A	0.720(1)	-0.374(2)	0.9368(4)	7.2(4)
C21A	0.8182(7)	0.780(1)	0.7785(3)	3.1(2)	C22A	0.9058(8)	0.835(1)	0.8069(3)	3.6(2)
C23A	0.9859(8)	0.926(1)	0.7938(3)	3.8(3)	C24A	0.9755(8)	0.960(2)	0.7491(4)	4.2(3)
C25A	0.8893(8)	0.914(1)	0.7201(3)	3.5(2)	C26A	0.8123(8)	0.823(1)	0.7356(3)	3.7(2)
C27A	1.080(1)	0.976(2)	0.8250(4)	5.5(3)	C28A	0.883(1)	0.955(2)	0.6739(4)	6.7(4)
H3A1	0.5821	0.2542	0.7339	7.2	H4A1	0.7035	0.4826	0.7289	5.1
H3A2	0.5454	0.4325	0.7412	7.2	H4A2	0.7486	0.3186	0.7496	5.1
H7A1	0.8756	0.2258	0.8062	5.4	H8A1	0.7434	0.0323	0.8250	6.1
H7A2	0.8605	0.2130	0.8536	5.4	H8A2	0.7192	0.1258	0.7817	6.1
H10A	0.6660	0.7022	0.7736	4.4	H9A1	0.6845	0.2053	0.8880	5.4
H9A2	0.5663	0.2501	0.8755	5.4	H14A	0.5198	-0.4266	0.9001	6.2
H16A	0.7330	-0.0617	0.9114	4.8	H17A1	0.3106	-0.1952	0.8400	7.6
H17A2	0.3539	-0.3721	0.8363	7.6	H18A1	0.6879	-0.4776	0.9408	8.6
H17A3	0.3233	-0.3133	0.8791	7.6	H18A2	0.7792	-0.3900	0.9236	8.6
H18A3	0.7408	-0.3231	0.9642	8.6	H22A	0.8798	0.6752	0.8542	5.9
H24	0.7238	0.7109	0.8207	4.4	H24A	1.0308	1.0176	0.7389	5.0
H26A	0.7521	0.7889	0.7161	4.5	H27A1	1.1160	0.8813	0.8375	6.4
H27A2	1.0583	1.0414	0.8471	6.4	H28A1	0.8924	1.0711	0.6706	8.1
H27A3	1.1252	1.0394	0.8108	6.4	H28A2	0.9358	0.8976	0.6624	8.1
H28A3	0.8154	0.9250	0.6584	8.1	H12A	0.4434	0.1788	0.8448	4.0

milar to those of the 1,5-diazocan-2,6-dione ring in the twist-boat form of **2** (Table 3).

The bulk structure (Figure 3) shows the eight-membered dipeptide ring of the chair conformer to be sandwiched between parallel aromatic rings of the sidechains of alternate twist-boat conformers. The aromatic ring-aliphatic ring stacking provides multiple close and favorable van der Waals interactions which may be critical to the stability of the solid state structure. Indeed, we have evidence that the unexpected chair conformation of **2** is, in fact, largely or wholly a solid state phenomenon caused by crystal packing forces; variable temperature nmr studies show that *only* the twist-boat conformer is populated to any significant degree in deuteriomethylene chloride solutions of **2** at $-90°$ [13].

No chair conformers are observed in the crystal structure of **3** [8], which differs from **2** only by virtue of the *N*-(3,5-dimethyl-2-hydroxybenzyl) side chain which clearly does not perturb the planarity of the amide group in the X-ray structure. The two unusual features of the solid state structure of **2** are the intramolecular hydrogen bonding and the intermolecular stacking of aromatic and aliphatic rings between adjacent molecules. The intramolecular hydrogen bonding alone cannot be responsible for the stabilization of the chair in the solid state, since, if so, one would expect to find evidence for the chair conformer at low temperatures in solution. This is not observed and therefore other crystal packing forces, including the aromatic aliphatic ring stacking, must be important in stabilizing the chair conformer.

EXPERIMENTAL

The infrared spectrum was recorded as nujol mull on a Perkin Elmer 1600 FT spectrophotometer. The nmr spectra were recorded as deuteriochloroform solutions on a Varian Gemini 300 spectrometer, using tetramethylsilane as the internal standard. The pmr multiplicities are reported using the following abbreviations: s, singlet; d, doublet; t, triplet [14]. Electron impact mass spectral measurements (70 eV) were made on a Finnigan MAT 90 spectrometer. The melting point was determined using an Electrothermal 9100 melting point apparatus and is uncorrected.

1,5-bis(3,5-Dimethyl-2-hydroxybenzyl)-1,5-diazocan-2,6-dione (**2**).

To a solution of *N*-(3,5-dimethyl-2-hydroxybenzyl)-3-aminopropanoic acid (**1**) (2.23 g, 10 mmoles) [1] in phosphoryl chloride (12 ml), 4.08 g (3 mmoles) of freshly fused zinc chloride was added, and the reaction mixture was heated at reflux temperature for 6 hours (during the heating up of the solution, zinc chloride was

dissolved and the appearance of a cherry-red color was observed). The reaction mixture was then poured into ice-water (200 ml), the solution neutralized with solid sodium bicarbonate, extracted with chloroform, dried, and evaporated *in vacuo*. The residue was separated by column chromatography (silica gel-diethyl ether) to give **2** in 60% yield, which was recrystallized from methanol as a white product, mp 242-243°; cmr: 75 MHz, APT, δ 172.36 (C-2,6), 152.04 (C-12), 132.64 (C-14), 129.25 (C-16), 128.25 (C-11), 126.52 (C-15), 120.38 (C-13), 47.25 (C-9,10), 42.10 (C-4,8), 35.09 (C-3,7), 20.06 (C-18), 16.13 (C-17); ir: 3125 (br) (OH), 1618 (CO), 1484, 1237 cm^{-1}; ms: m/z (relative intensity) 411 (28%), 410 (M^+, 100), 276 (40), 248 (63), 247 (46), 163 (80), 150 (30), 149 (22), 136 (88), 134 (100), 91 (41), 44 (42); pmr: 300 MHz, δ 8.84 (s, 2H, OH), 6.97 (d, J_{meta} = 1.77 Hz, 2H, H-14), 6.76 (d, 2H, H-16), 4.40 (s, 4H, H_2-9,10), 3.63 (t, J_{vic} = 6.99 Hz, 4H, H_2-4,8), 3.02 (t, 4H, H_2-3,7), 2.23 (s, 6H, H_3-18), 2.20 (s, 6H, H_3-17).

Anal. Calcd. for $C_{24}H_{30}N_2O_4$: C, 70.22; H, 7.37; N, 6.82. Found: C, 70.25; H, 7.40; N, 7.03.

Crystal Structure of **2**.

Small colorless prisms were obtained from methanol solution, 0.1 x 0.2 x 0.2 mm. Lattice parameters were calculated from the setting angles of 25 accurately centered reflexions.

Crystal Data.

$C_{24}H_{30}N_2O_4$, M = 410, Monoclinic, a = 12.898(4), b = 8.106(4), c = 31.647(10) Å, β = 99.92(4)°; Z = 6 (one molecule bisected by crystallographic inversion and another in a general position); D_c = 1.255 Mgm^{-3}; U = 3259 $Å^3$, Graphite monochromated M_oK_α radiation, λ = 0.71069 Å, $\mu(M_oK\alpha)$ = 0.798 cm^{-1}, Space group $P2_1/c$.

X-ray measurements were performed at T = 298K on a Rigaku AFC6S single-crystal diffractometer in the range $0° \leq \theta \leq 25°$ using graphite monochromated M_oK_α radiation. A total of 4961 reflexions were measured using ω scans yielding 1480 observed with $F \geq 3\sigma(F)$. Three intensity standards measured repeatedly during the data collection showed no decline. Lorentz and polarization corrections were applied but absorption was ignored.

Structure Analysis and Refinement.

The structure was solved using MITHRIL [15] and refined using the full-matrix least-squares routines in TEXSAN [16]. The relatively low reflexion-to-parameter ratio restricted anisotropic refinement to oxygen and nitrogen atoms with carbon atoms refined isotropically. Hydrogen atoms were placed in chemically reasonable positions, except for those attached to oxygen, which were located from difference fourier maps. The final agreement factors were R = 0.075 and R_w = 0.088, $w = 1/(\sigma^2(F) + 0.03F^2)$. Fractional atomic coordinates and vibrational parameters are presented in Table 4 and selected bond lengths, angles and torsional angles in Tables 1-3. Neutral atom scattering factors were taken from Cromer and Waber [17]. All calculations were performed on a Digital Vax Station 3520.

Observed and calculated structure factors, thermal parameters, analysis of the planarity, and puckering and asymmetry parameters are available from the asterisked authors on request.

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[12] It is not possible to adhere rigidly to the IUPAC-IUB recommendations [*Biochemistry*, **9**, 3471 (1970)] for biochemical nomenclature when dealing with synthetic peptides, we therefore choose to follow the nomenclature of cyclodi-β-alanyl as reported in Ref 10, Appendix; namely, that C_i^{α}-C_i^{β} is a descriptor for the two ethylene groups of the 1,5-diazocan-2,6-dione ring.

[13] Low temperature pmr experiments were carried out to study the conformational behaviour of **2** in solution. In deuteriomethylene chloride solution at −90° the signal for the *exo*-cyclic methylene group (H_2-9) becomes an AB system (J_{gem} = 14.4 Hz) indicating that only the twist-boat conformer is significantly populated at this temperature and that ring inversion (twist-boat → twist-boat*) is slow on the nmr time scale at this temperature. Chair → twist-boat interconversion cannot be rapid under these conditions since a lower energy route for the twist-boat → twist-boat* transition would then be available. The full conformational behaviour of **2** and related heterocycles in solution will be described in detail in a future publication.

[14] For clarity and consistency, in the nmr attributions we choose to keep the atom identification used in the X-ray study and reported in the formulae and figures, instead of the numbering style strictly related to nomenclature.

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