Instrumental Achievements

— X-Ray Analysis —

Crystal Structure of *N*-[(+)-2-*t*-Butyl-2-methyl-1,3-benzodioxole-4-carbonyl]-*L*-phenylalanine Methyl Ester

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In previous studies^{1,2} we synthesized (+)-2-*t*-butyl-2-methyl-1,3-benzodioxole-4-carboxylic acid [(+)-TBMB carboxylic acid] as a chiral derivatizing agent for amines and alcohols. In the present study an X-ray analysis was performed on its *L*-phenylalanine methyl ester derivative, *N*-[(+)-TBMB carbonyl-*L*-phenylalanine methyl ester], in order to determine the absolute configuration of (+)-TBMB carboxylic acid.

A transparent colorless prism (ca. 0.2×0.3×0.3 mm) was obtained from hexane and was used for an X-ray study. All hydrogen atoms (26H), except for NH, were

calculated from the standard bond lengths and angles. The structure was refined with anisotropic temperature factors for non-H atoms (C, O and N) and isotropic factors for H atoms. Intensity data were measured in the ω -2 θ scan mode on a RIGAKU AFC-5R four-circle diffractometer equipped with a rotating anode (40 kV, 200 mA) using graphite-monochromated Mo K α radiation (0.71069 Å) up to 2 θ =55°.

Since the absolute configuration of the *L*-phenylalanine moiety is (2*S*), the relative configurations of the crystalline structure (Figs. 1 and 2) revealed the (2*S*)-configuration of (+)-TBMB carboxylic acid. Another noteworthy fact regarding the present structure may be the molecular conformation around the amide group. No intermolecular hydrogen bonding of NH...O was found in the crystal structure. Figure 2 shows an

Table 1 Crystal and experimental data

Formula: C ₂₃ H ₂₇ O ₅ N	
Formula weight=397.46	
Crystal system: tetragonal	
Space group: <i>P</i> 4 ₁ 22 ₁	<i>Z</i> =8
<i>a</i> =10.964(14) Å	α =90.0°
<i>b</i> =10.964(14)	β =90.0
<i>c</i> =36.323(105)	γ =90.0
<i>V</i> =4366.7(15) Å ³	
<i>D_x</i> =1.209 g/cm ³	
<i>R</i> =0.091	
No. of reflections used=1156	
Measurement: Rigaku AFC-5R	
Program system: UNICS III	
Structure determination: RANTAN 81	
Refinement: block-diagonal least-squares

Fig. 1 Chemical structure.

Fig. 2 The ORTEP drawing. Some important structural parameters are shown below. Bond torsion angles (°): O4-C13-C12-C11=-2.1, C13-C12-C11-N1=0.5, C12-C11-N1-C2=-178.0, C11-N1-C2-C1=-162.7, N1-C2-C1-O2=-10.3, C12-C11-N1-NH=-0.7. Bond lengths (Å): C12-C11=1.450, C11-O3=1.211, C11-N1=1.364, N1-NH=1.05, NH...O4=1.94, N1...O4=2.77. Bond angles (°): C11-N1-C2=122.5, C11-N1-NH=120, N1-NH...O4=134.

ORTEP drawing as well as some important structural parameters which define the geometry. The torsion angles indicate that the O4-C13-C12-C11-N1 bonds are almost planar. The NH hydrogen atom, found on a difference Fourier map, was located on this plane, thus satisfying the trigonal geometry of the N atom, and reflecting the contribution of the double-bond character of the C11-N1 bond. Thus, the observed structure is stabilized by the π -conjugation effect between the benzene ring and the amide group, and possibly also by the weak intramolecular hydrogen bonding of the NH...O4 of furan ring.

When D,L-phenylalanine methyl ester was derivatized with (+)-TBMB carboxylic acid, the two diastereomers of N-[(+)-TBMB carbonyl]-L- and -D-phenylalanine methyl esters, thus produced, were surprisingly well separated chromatographically^{1,2}, though the chiral center in this agent is considerably separated (through bond) from that of the amino acids. The fact that a similar separation was observed between the diastereo-

mers of the other amino acids or amines strongly suggests that the conformation of the TBMB carbonylated amines is considerably stable. This fact is well rationalized with a relatively fixed conformation around the amide group.

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References

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