

Optical Resolution of Pantolactone by Inclusion Crystallization with
(R,R)-(-)-trans-2,3-Bis(diphenylhydroxymethyl)-1,4-dioxaspiro[4.5]decane,
and Crystal Structure of the Resulting 1:1 Complex

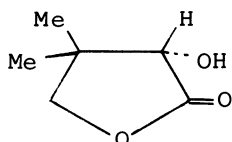
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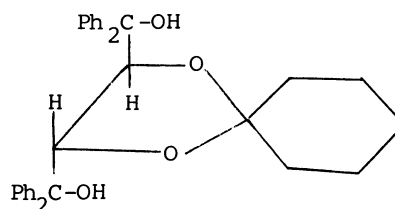
Pantolactone was resolved very efficiently by complex formation of its (S)-(-) isomer with the title host compound. The structure of the 1:1 complex was elucidated by X-ray crystallography.

Pantolactone, dihydro-3-hydroxy-4H-dimethyl-2(3H)-furanone (1), is an important intermediate in the synthesis of pantothenic acid. Optical resolution of 1 by the usual diastereomeric method is complicated and the efficiency is not high.¹⁾ We have developed a very efficient procedure for the resolution of 1 by inclusion complex formation with the title host compound (2), which is readily available from tartaric acid according to the literature method.²⁾

For example, when a solution of racemic 1 (2.6 g, 20 mmol) and 2 (5.5 g, 9.93 mmol) in benzene-hexane (1:1, 20 ml) was kept at room temperature for 1 h, a 1:1 complex (3) (2.54 g) of (S)-(-)-1 (the absolute configuration was first established by the present crystal structure analysis) and 2 was obtained as colorless needles. The crude product was recrystallized twice from benzene-hexane (1:1) to give pure 3 (2.05 g), which upon heating in vacuo yielded (S)-(-)-1 of 99% ee [$[\alpha]_D -50.0^\circ$ (c 0.5 in H₂O)]. The optical purity of (-)-1 was determined by comparison of its $[\alpha]_D$ value with that reported for pure (S)-(-)-1.¹⁾



1, S isomer shown



(R,R)-(-)-2

The crystal structure of 3 was determined in order to establish the absolute configuration of 1 and to elucidate the nature of the inclusion complexation. Crystal data: C₃₄H₃₄O₄·C₆H₁₀O₃, FW = 636.78, monoclinic, space group P2₁, a =

A perspective view of the asymmetric unit of complex **3** with atom numbering⁷⁾ is illustrated in Fig. 1. Bond distances and angles of both molecular components are all normal. The hydroxyl groups of each host molecule **2** are linked by an intramolecular hydrogen bond. Every pair of host molecules related by the 2_1 symmetry operation is bridged by a guest molecule **1** by hydrogen bonds involving its carbonyl and hydroxyl groups, resulting in a helical spiral parallel to the b axis. Parameters which describe the geometry of hydrogen bonding are given in

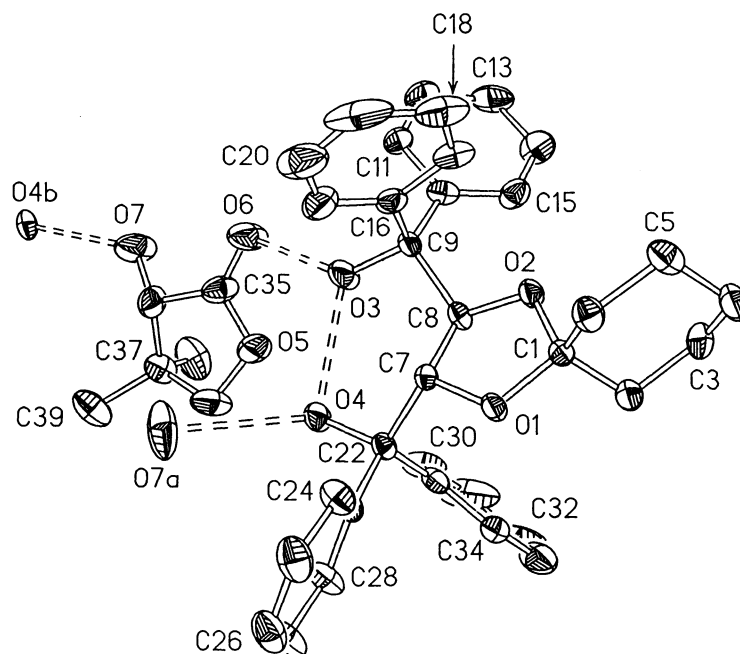


Fig. 1. Perspective view of the two molecular components of complex **3**. The thermal ellipsoids are drawn at the 30% probability level, and hydrogen bonds are represented by double dashed lines. Symmetry code: \bar{a} $-\bar{x}$, $\frac{1}{2}\bar{y}$, $-\bar{z}$; \bar{b} $-\bar{x}$, $-\frac{1}{2}\bar{y}$, $-\bar{z}$. Geometry of hydrogen bonding: O3...O4 2.365 Å, O3...O6 2.741 Å, O4...O3...O6 106.2°, C9-O3...O4 116.4°, C9-O3...O6 136.7°, O4...O7 \bar{a} 2.745 Å, O3...O4...O7 \bar{a} 105.3°, C22-O4...O3 104.8°, C22-O4...O7 \bar{a} 139.5°, C35=O6...O3 103.5°, C37-O7...O4 \bar{b} 131.6°.

the legend to Fig. 1. Figure 2 shows that the crystal structure is built of a lateral packing of these spiral columns. In the unit cell the molecules are located close to the $(10\bar{1})$ set of planes, and accordingly the $(10\bar{1})$ reflection has the highest observed intensity.

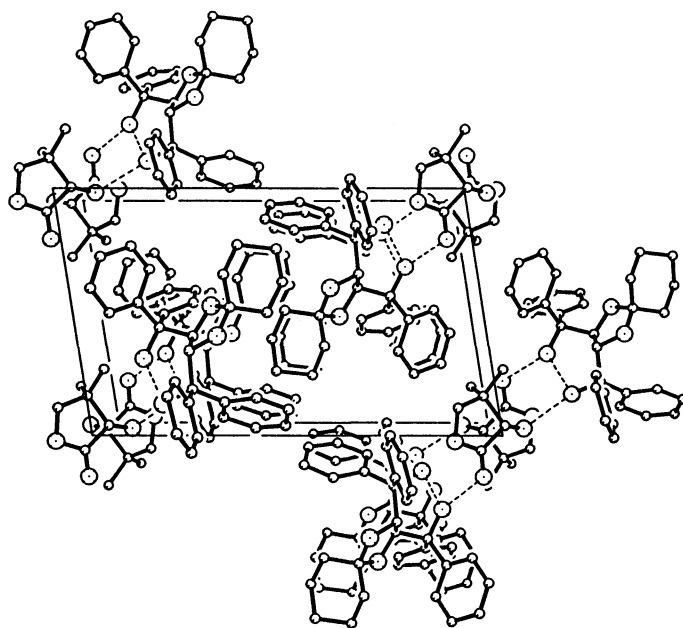


Fig. 2. Perspective view of the molecular packing in β . The origin of the unit cell lies at the lower left corner, with a pointing upwards, b towards the reader, and c from left to right. Hydrogen bonds are represented by broken lines.

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- 7) The atomic parameters have been deposited with the Cambridge Crystallographic Data Centre. Structure factors are available on request from the last author.

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