

## Refinement

Refinement on F<sup>2</sup>

$$R[F^2 > 2\sigma(F^2)] = 0.048$$

$$wR(F^2) = 0.118$$

$$S = 1.06$$

4484 reflections

317 parameters

H atoms: see below

$$w = 1/[\sigma^2(F_o^2) + (0.046P)^2 + 0.7746P]$$

$$\text{where } P = (F_o^2 + 2F_c^2)/3$$

$$(\Delta/\sigma)_{\max} < 0.001$$

$$\Delta\rho_{\max} = 0.20 \text{ e } \text{Å}^{-3}$$

$$\Delta\rho_{\min} = -0.19 \text{ e } \text{Å}^{-3}$$

Extinction correction: none

Scattering factors from

*International Tables for Crystallography* (Vol. C)

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### Tyrosinium-D-tetrahydroisoquinoline-3-carboxylate 1.5-Hydrate and Tyrosyl-D-tetrahydroisoquinoline-3-carboxamide Hydrate

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#### Abstract

Crystals of the two dipeptide title compounds, Tyr-D-Tic, C<sub>19</sub>H<sub>20</sub>N<sub>2</sub>O<sub>4</sub>·1.5H<sub>2</sub>O, and Tyr-D-Tic-NH<sub>2</sub>, C<sub>19</sub>H<sub>21</sub>N<sub>3</sub>O<sub>3</sub>·H<sub>2</sub>O, were prepared by the sitting-drop method. Tyr-D-Tic is orthorhombic (*P*2<sub>1</sub>2<sub>1</sub>) and crystallizes as a zwitterion. The asymmetric unit contains two peptide molecules and three molecules of water.

Table 2. Selected geometric parameters (Å, °) for (2b)

C4a—C8e	1.391 (2)	C8a—C8b	1.474 (2)
C4a—C4b	1.516 (2)	C8b—C8c	1.501 (2)
C4b—C4c	1.532 (2)	C8b—C8d	1.559 (2)
C4b—C8c	1.580 (2)	C8c—C8d	1.517 (2)
C4c—C8a	1.384 (2)	C8d—C8e	1.492 (2)
C4—C4a—C4b	128.6 (2)	C8c—C8b—C8d	59.39 (10)
C8e—C4a—C4b	109.79 (14)	C8b—C8c—C8d	62.22 (11)
C4a—C4b—C4c	103.50 (13)	C8b—C8c—C4b	104.10 (13)
C4a—C4b—C8c	103.42 (13)	C8d—C8c—C4b	103.81 (13)
C4c—C4b—C8c	102.80 (13)	C8c—C8d—C8c	107.14 (14)
C8a—C4c—C4b	110.18 (14)	C8e—C8d—C8b	121.01 (14)
C4c—C8a—C8b	110.09 (14)	C8c—C8d—C8b	58.39 (10)
C8a—C8b—C8c	108.51 (14)	C4a—C8c—C8d	110.35 (14)
C8a—C8b—C8d	120.03 (15)		

Data were collected by the double-pass method using a charge-coupled device area-detector system. The first 50 frames of data were recollected at the end of data collection to monitor crystal decay. The structures were solved by direct methods and refined successfully in the monoclinic space group *P*2<sub>1</sub>/*c*. Full-matrix least-squares refinement was carried out by minimizing  $w(F_o^2 - F_c^2)^2$ . The non-H atoms were refined anisotropically to convergence. The H atoms were treated using appropriate riding models (*AFIX* = m3; *SHELXTL-Plus*; Sheldrick, 1995), except for the hydroxyl H atom of (2a) which was refined freely<sup>b</sup> with an isotropic displacement parameter. One of the carbonyl O atoms (O3) in compound (2b) exhibits disorder, with two positions O3 and O3' which are 0.23 (1) Å above and below the mean plane defined by atoms C8d, C16 and C17 and the midpoint of O3 and O3'. The refined occupancy factor for O3 is 0.58 (5).

For both compounds, data collection: *SMART* software (Siemens, 1995); cell refinement: *SAINT* (Siemens, 1995); data reduction: *SAINT*; program(s) used to solve structures: *SHELXTL-Plus* (Sheldrick, 1995); program(s) used to refine structures: *SHELXTL-Plus*; molecular graphics: *SHELXTL-Plus*; software used to prepare material for publication: *SHELX-Plus*.

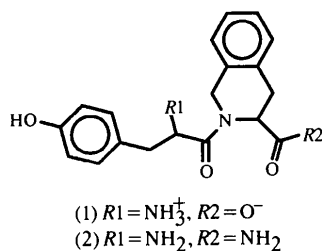
We thank the Council of Scientific and Industrial Research, Government of India (MM, MVG), the NSF (CHE-9309690), the Missouri Research Board, the Centre for Molecular Electronics and the Department of Chemistry of the University of Missouri–St Louis (NPR). This is document No. RRLT-PRU-74 from the Regional Research Laboratory, Trivandrum, India.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: BK1278). Services for accessing these data are described at the back of the journal.

Tyr-D-Tic-NH<sub>2</sub> crystals are monoclinic (*P*2<sub>1</sub>), the asymmetric unit containing one peptide molecule and one molecule of water. Despite some differences in packing, the conformation of the two dipeptides is almost identical (r.m.s. deviation for non-H atoms is approximately 0.18 Å).

### Comment

A new class of potent opioid peptides contains a tetrahydroisoquinoline-3-carboxylic acid (Tic) residue in the second position. Peptides with the initial sequence Tyr-D-Tic-*X* are  $\mu$ -selective agonists (Schiller *et al.*, 1993). The dipeptide Tyr-D-Tic-NH<sub>2</sub> possesses activity similar to the tripeptide Tyr-D-Tic-Phe and tetrapeptide Tyr-D-Tic-Phe-Phe, both  $\mu$ -agonists (Temussi *et al.*, 1994), although the binding affinity of the dipeptide is 10–20-fold lower than that of the tripeptide (Wilkes & Schiller, 1995). Despite the lower binding affinity, Tyr-D-Tic-NH<sub>2</sub> still has measurable opioid activity (Temussi *et al.*, 1994). Thus, the selectivity and activity is at least partially dependent on the first two residues.



The structure of Tyr-D-Tic, (1), is shown in Fig. 1. The two peptide molecules in the asymmetric unit of (1) are almost identical (r.m.s. deviation 0.207 Å for all non-H atoms, O2 matches with O4' and O2' matches

with O4). The crystals of Tyr-D-Tic-NH<sub>2</sub>, (2), contain one peptide molecule and one water molecule in the asymmetric unit (Fig. 2).

A comparison of all non-H atoms (except the *c*-terminal O atom and N atoms) in (1) with their corresponding atoms in (2) produces r.m.s. deviations of 0.181 and 0.150 Å for fits with the two molecules in the asymmetric unit of (1). The maximum deviations are seen in the Tic residue (*i.e.* 0.283 Å for C2G3 and 0.260 Å for C2'). Thus, the structures of (1) and (2) are superimposable.

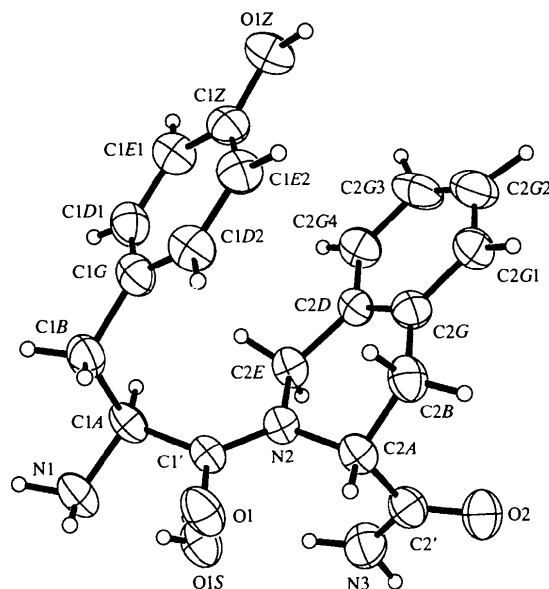


Fig. 1. View of Tyr-D-Tic, (1), showing the labeling of the non-H atoms and the relationship between the molecules in the asymmetric unit. Displacement ellipsoids are shown at 50% probability levels; H atoms are drawn as small circles of arbitrary radii.

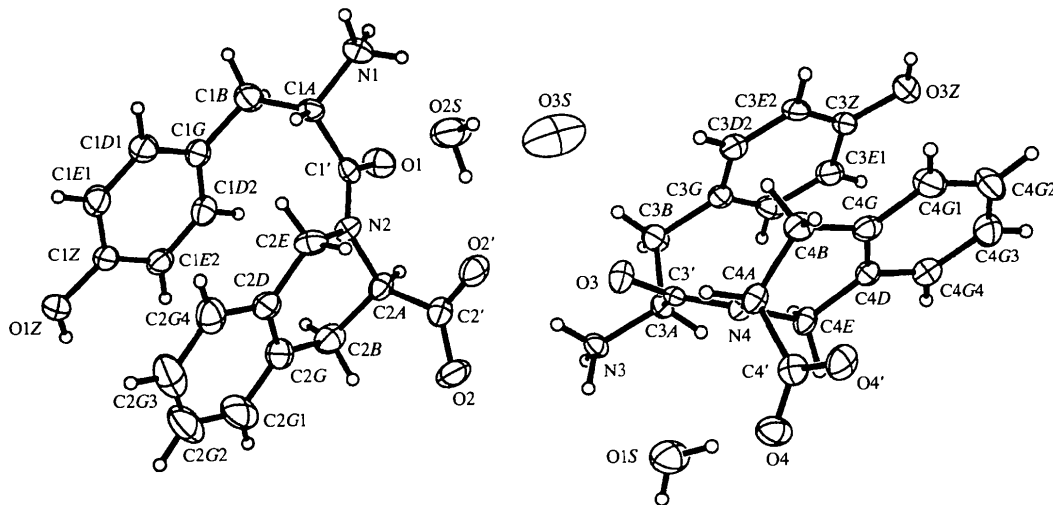


Fig. 2. View of Tyr-D-Tic-NH<sub>2</sub>, (2), showing the labeling of the non-H atoms. Displacement ellipsoids are shown at 50% probability levels; H atoms are drawn as small circles of arbitrary radii.

Both (1) and (2) form three-dimensional networks via hydrogen bonds (Tables 2 and 4), although the attractions in (2) tend to be weaker. In (2), there are two three-centered hydrogen bonds formed by the N terminal amino group in each of the two molecules in the asymmetric unit and either a solvent molecule (in the same cell) or the tyrosine hydroxyl (in a symmetry related molecule). In both compounds, the planes formed by the aromatic rings are almost parallel [3.9 and 1.3° for the angle between the planes for each of the two molecules in (1), and 5.9° for (2)]. Because of the packing, this can be seen more clearly in (2) (Fig. 4). In (1), the three-dimensional network contains alternating hydrophobic and hydrophilic layers which are perpendicular to the *c* axis (Fig. 3). A layered structure is not observed in (2).

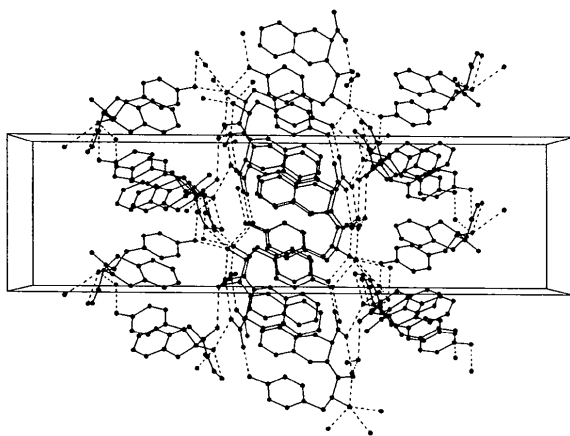


Fig. 3. Packing diagram of (1) viewed down the *a* axis. H atoms have been omitted for clarity; hydrogen bonds are shown as dashed lines. The alternating hydrophobic and hydrophilic (hydrogen-bonded) layers are clearly visible.

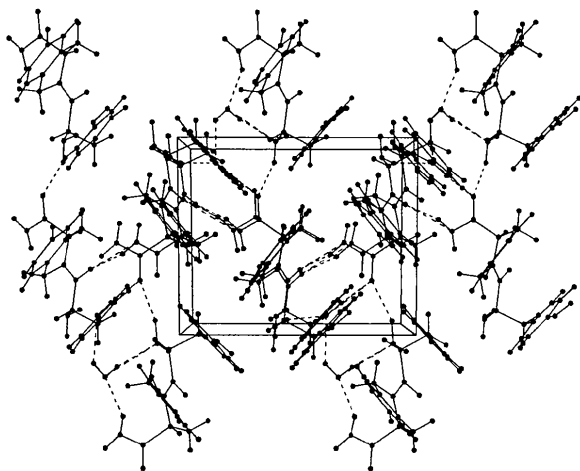


Fig. 4. Packing diagram of (2) viewed down the *c* axis. H atoms have been omitted for clarity; hydrogen bonds are shown as dashed lines.

## Experimental

Tyr-D-Tic, (1), and Tyr-D-Tic-NH<sub>2</sub>, (2), were obtained from G. A. Brine (Research Triangle Institute, Research Triangle Park, NC, USA). Initial crystallization conditions were discovered using the Crystal Screen™ I kit (Hampton Research, Riverside, CA, USA). Diffraction quality crystals were prepared by equilibrating a sitting drop containing 3 μl of (1) (34.7 mg ml<sup>-1</sup>) and 3 μl of reservoir solution against a 1 ml reservoir of 100 mM Tris (pH 8.5), 27% PEG 1000; crystals grew overnight. Crystals of (2) were prepared by equilibrating a sitting drop containing 3 μl of the dipeptide (25 mg ml<sup>-1</sup> in 29% methanol) and 2 μl of the reservoir solution against a 1 ml reservoir of 100 mM HEPES (pH 8.05), 1.3 M lithium sulfate; crystals grew overnight.

### Compound (1)

#### Crystal data

C<sub>19</sub>H<sub>20</sub>N<sub>2</sub>O<sub>4</sub>·1.5H<sub>2</sub>O

*M<sub>r</sub>* = 367.39

Orthorhombic

*P*2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>

*a* = 9.127 (1) Å

*b* = 10.522 (1) Å

*c* = 37.195 (2) Å

*V* = 3572.0 (6) Å<sup>3</sup>

*Z* = 8

*D<sub>x</sub>* = 1.366 Mg m<sup>-3</sup>

*D<sub>m</sub>* not measured

Cu *K*α radiation

*λ* = 1.54178 Å

Cell parameters from 35 reflections

*θ* = 9.63–59.89°

*μ* = 0.838 mm<sup>-1</sup>

*T* = 223 (2) K

Plate

0.56 × 0.35 × 0.06 mm

Clear colorless

#### Data collection

Siemens *P4* diffractometer

2*θ*/*ω* scans

Absorption correction:

face-indexed numerical

*T<sub>min</sub>* = 0.72, *T<sub>max</sub>* = 0.95

3258 measured reflections

3105 independent reflections

2770 reflections with

*I* > 2σ(*I*)

*R<sub>int</sub>* = 0.022

*θ<sub>max</sub>* = 57.00°

*h* = -1 → 9

*k* = 0 → 11

*l* = 0 → 40

3 standard reflections

every 97 reflections

intensity decay: 2.01%

#### Refinement

Refinement on *F*<sup>2</sup>

*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.046

*wR* (*F*<sup>2</sup>) = 0.127

*S* = 1.063

3105 reflections

511 parameters

H atoms: coordinates only refined

*w* = 1/[σ<sup>2</sup>(*F<sub>o</sub>*<sup>2</sup>) + (0.0866*P*)<sup>2</sup> + 0.2685*P*]

where *P* = (*F<sub>o</sub>*<sup>2</sup> + 2*F<sub>c</sub>*<sup>2</sup>)/3

(Δ/*σ*)<sub>max</sub> = -0.089

Δ*ρ*<sub>max</sub> = 0.459 e Å<sup>-3</sup>

Δ*ρ*<sub>min</sub> = -0.233 e Å<sup>-3</sup>

Extinction correction:

*SHELXL93* (Sheldrick, 1993)

Extinction coefficient:

0.0013 (2)

Scattering factors from

*International Tables for Crystallography* (Vol. C)

Absolute configuration:

Flack (1983)

Flack parameter = 0.0 (3)

Table 1. Selected torsion angles (°)

N1—C1A—C1'—N2	131.8 (4)
C1A—C1'—N2—C2A	177.1 (4)
C1'—N2—C2A—C2'	115.4 (4)

N3—C3A—C3'—N4	134.6 (4)
C3A—C3'—N4—C4A	-179.0 (4)
C3'—N4—C4A—C4'	127.1 (2)
N1—C1A—C1B—C1G	-172.5 (4)
C1A—C1B—C1G—C1D1	92.4 (5)
N3—C3A—C3B—C3G	-178.2 (3)
C3A—C3B—C3G—C3D1	86.2 (5)
C1'—N2—C2E—C2D	131.7 (4)
C1'—N2—C2A—C2B	-118.0 (4)
N2—C2A—C2B—C2G	-46.5 (5)
C2A—C2B—C2G—C2G1	-163.3 (4)
C2B—C2G—C2G1—C2G2	-173.6 (5)
C3'—N4—C4E—C4D	130.0 (4)
C3'—N4—C4A—C4B	-106.1 (4)
N4—C4A—C4B—C4G	-54.6 (4)
C4A—C4B—C4G—C4G1	-158.2 (4)
C4B—C4G—C4G1—C4G2	-179.4 (4)

Table 2. Hydrogen-bonding geometry (Å, °) for (1)

D—H...A	D—H	H...A	D...A	D—H...A
O1S—H1SA...O4	0.90 (4)	2.06 (2)	2.879 (5)	150 (3)
O2S—H2SA...O2'	0.90 (1)	1.91 (2)	2.792 (5)	166 (2)
N1—H1B...O4'	0.86 (5)	1.96 (5)	2.755 (5)	151 (4)
N1—H1C...O1Z'	1.00 (5)	1.96 (5)	2.901 (5)	155 (4)
N1—H1D...O3Z''	0.91 (5)	2.27 (5)	2.892 (5)	124 (4)
N1—H1D...O2S	0.92 (5)	2.17 (5)	2.887 (6)	133 (4)
N3—H3B...O4''	0.90 (5)	1.98 (5)	2.847 (5)	160 (4)
N3—H3D...O1S	0.98 (4)	2.24 (4)	2.957 (6)	128 (3)
N3—H3D...O1Z'	0.98 (4)	2.41 (4)	3.125 (4)	130 (3)
N3—H3C...O2'	0.88 (5)	1.96 (5)	2.781 (5)	153 (4)
O3Z—H3ZA...O4''	0.82	1.84 (4)	2.630 (5)	161 (1)
O1Z—H1ZA...O2''	0.82	1.78 (1)	2.566 (5)	159 (1)
O2S—H2SB...O3S	0.90 (2)	2.11 (2)	2.963 (6)	157 (1)
O3S...O1'''	—	—	2.875 (6)	—

Symmetry codes: (i)  $x - 1, y - 1, z$ ; (ii)  $\frac{1}{2} + x, \frac{1}{2} - y, -z$ ; (iii)  $1 - x, y - \frac{1}{2}, \frac{1}{2} - z$ ; (iv)  $x - 1, y, z$ ; (v)  $\frac{1}{2} + x, \frac{3}{2} - y, -z$ ; (vi)  $2 - x, y - \frac{1}{2}, \frac{1}{2} - z$ ; (vii)  $x - \frac{1}{2}, \frac{3}{2} - y, -z$ ; (viii)  $1 + x, y, z$ .

**Compound (2)***Crystal data*C<sub>19</sub>H<sub>21</sub>N<sub>3</sub>O<sub>3</sub>·H<sub>2</sub>O $M_r = 357.40$ 

Monoclinic

 $P2_1$  $a = 8.981 (1) \text{ \AA}$  $b = 10.597 \text{ \AA}$  $c = 9.703 (1) \text{ \AA}$  $\beta = 98.76 (1)^\circ$  $V = 912.68 (14) \text{ \AA}^3$  $Z = 2$  $D_x = 1.301 \text{ Mg m}^{-3}$  $D_m$  not measured*Data collection*

Siemens P4 diffractometer

 $2\theta/\omega$  scans

Absorption correction:

face-indexed numerical

 $T_{\min} = 0.81, T_{\max} = 0.90$ 

1608 measured reflections

1450 independent reflections

1323 reflections with

 $I > 2\sigma(I)$ Cu  $K\alpha$  radiation $\lambda = 1.54178 \text{ \AA}$ 

Cell parameters from 67 reflections

 $\theta = 12.43\text{--}63.56^\circ$  $\mu = 0.758 \text{ mm}^{-1}$  $T = 223 (2) \text{ K}$ 

Plate

 $0.40 \times 0.20 \times 0.08 \text{ mm}$ 

Clear colorless

 $R_{\text{int}} = 0.013$  $\theta_{\text{max}} = 56.41^\circ$  $h = -9 \rightarrow 0$  $k = -1 \rightarrow 11$  $l = -10 \rightarrow 10$ 

3 standard reflections

every 97 reflections

intensity decay: 2.33%

*Refinement*Refinement on  $F^2$  $R[F^2 > 2\sigma(F^2)] = 0.048$  $wR(F^2) = 0.141$  $S = 1.044$ 

1450 reflections

257 parameters

H atoms: riding model or coordinates only

 $w = 1/[\sigma^2(F_o^2) + (0.1086P)^2 + 0.0882P]$ where  $P = (F_o^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\text{max}} = 0.005$  $\Delta\rho_{\text{max}} = 0.189 \text{ e \AA}^{-3}$  $\Delta\rho_{\text{min}} = -0.199 \text{ e \AA}^{-3}$ 

Extinction correction:

*SHELXL93* (Sheldrick, 1993)

Extinction coefficient:

0.0071 (18)

Scattering factors from *International Tables for Crystallography* (Vol. C)

Absolute configuration:

Flack (1983)

Flack parameter = 0.3 (5)

Table 3. Selected torsion angles (°)

N1—C1A—C1'—N2	135.6 (5)
C1A—C1'—N2—C2A	176.0 (5)
C1'—N2—C2A—C2'	111.5 (5)
N1—C1A—C1B—C1G	-169.3 (5)
C1A—C1B—C1G—C1D1	77.7 (6)
C1'—N2—C2E—C2D	142.7 (5)
C1'—N2—C2A—C2B	-120.4 (5)
N2—C2A—C2B—C2G	-49.1 (6)
C2A—C2B—C2G—C2G1	-159.6 (5)
C2B—C2G—C2G1—C2G2	-178.2 (6)

Table 4. Hydrogen-bonding geometry (Å, °) for (2)

D—H...A	D—H	H...A	D...A	D—H...A
O1S—H1S1...N1	0.85 (4)	2.09 (5)	2.906 (7)	159 (6)
N1—H1B...O2'	1.04 (6)	2.44 (6)	3.188 (6)	128 (4)
N3—H3B...O1S	0.99 (7)	2.10 (7)	3.026 (7)	154 (5)
N3—H3A...O1''	0.94 (7)	1.94 (7)	2.836 (6)	158 (6)
O1Z—H1Z...O2'''	1.01 (7)	1.71 (7)	2.706 (6)	168 (6)
N1—H1A...O1Z'	0.89 (6)	2.44 (7)	3.305 (6)	162 (6)

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

For Tyr-D-Tic, the largest remaining difference peak ( $0.459 \text{ e \AA}^{-3}$ ) is not located within covalent bonding distance of any atom. Attempts to refine with a water molecule in this position resulted in an occupancy of less than 10%. Several other difference peaks are located near O3S and are likely due to the H atoms, but the data were too weak to refine the positions of these atoms.

For both compounds, data collection: *XSCANS* (Siemens, 1994); cell refinement: *XSCANS*; data reduction: *XSCANS*; program(s) used to solve structures: *SHELXTL* (Sheldrick, 1994); program(s) used to refine structures: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

This research was supported in part by the National Institute for Drug Abuse (NIDA) and the Office of Naval Research (ONR).

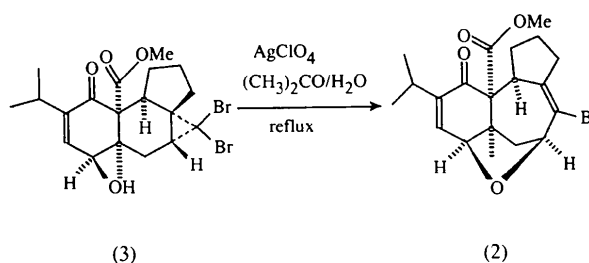
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plex rearrangement reaction catalyzed by silver(I) salts in polar solvents (Brocksom, Pesquero & Lopes, 1990) leading to the crystalline product (2). Although the macroscopic sample is racemic, the crystal selected by hand turned out to be a single enantiomer and is the subject of the present paper. This three-dimensional structure determination is absolutely essential for successful planning of the total synthesis and cannot be accomplished by conventional spectroscopic means such as high-field NMR measurements.



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## Intermediates in the Synthesis of *Daphniphyllum* Alkaloids. I. A Tetracyclic Oxygen Analogue

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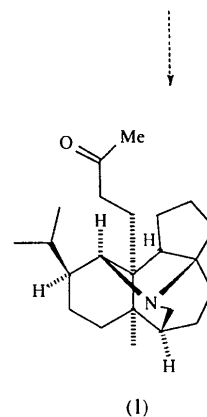
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### Abstract

In methyl (3*S*,5*S*,6*S*,10*R*,11*R*)-2-bromo-3,6-epoxy-8-iso-propyl-5-methyl-9-oxotricyclo[9.3.0.0<sup>5,10</sup>]tetradeca-1,7-diene-10-carboxylate, C<sub>20</sub>H<sub>25</sub>BrO<sub>4</sub>, the seven-membered ring is half-chair shaped, the six-membered ring adopts a boat conformation and the five-membered rings both adopt envelope conformations. The molecule adopts an overall hemispherical conformation.

### Comment

In our projected synthesis of *Daphniphyllum* alkaloids, such as methyl homodaphniphyllate, (1), we have developed a route to an oxygen analogue, (2), containing many of the same structural features. We have previously presented the X-ray structure determination of a tetracyclic intermediate, (3) (Castellano, Brocksom & Ceschi, 1994), and this compound undergoes a com-



A *ZORTEP* (Zsolnai, 1995) illustration of the formula unit showing the relative stereochemistry is presented in Fig. 1 and selected bond distances and angles are given in Table 1. Compound (2) has an ether bridge in a tetracyclic structure containing fused six-, seven- and five-membered carbocyclic skeletons, analogous to the nitrogen-bridged *Daphniphyllum* alkaloids. The structure is heavily influenced by the ether bridge which forces the molecule to adopt an overall hemispherical conformation. The six-membered ring is in a slightly distorted boat conformation, with C<sub>6</sub> and C<sub>9</sub> lying at distances of 0.516 (6) and 0.408 (5) Å, respectively, from the least-squares plane through atoms C<sub>5</sub>, C<sub>7</sub>, C<sub>8</sub> and C<sub>10</sub>; both five-membered rings adopt envelope conformations, with C<sub>13</sub> and C<sub>5</sub> occupying the flap positions at distances of 0.526 (7) and –0.696 (5) Å from the least-squares plane made up of the remaining four atoms in the cyclopentane and furan rings, respectively. The molecules are joined through C—H···O interactions: C<sub>11</sub>···O<sub>1</sub><sup>i</sup> 3.410 (7), H<sub>11</sub>···O<sub>1</sub><sup>i</sup> 2.53 Å and