

Acta Cryst. (1994). C50, 2088–2089

***N*<sup>η</sup>-Nitro-L-arginine Methyl Ester Hydrochloride**

NOBUO OKABE, KAZUYUKI IKEDA AND YOSHIKO KOHYAMA

Faculty of Pharmaceutical Sciences, Kinki University, Kowakae 3-4-1, Higashiosaka, Osaka 577, Japan

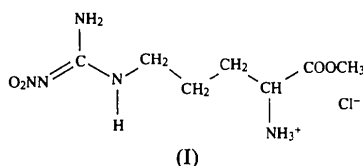
(Received 21 December 1993; accepted 26 April 1994)

**Abstract**

The α-amino group of the title compound, C<sub>7</sub>H<sub>16</sub>N<sub>5</sub>O<sub>4</sub><sup>+</sup>.Cl<sup>-</sup>, is positively charged; the nitroguanidinium moiety remains neutral. All atoms in the nitroguanidinium group are nearly coplanar. The side chain of the molecule consists of two planar groups which intersect almost perpendicularly at C<sup>δ</sup>.

**Comment**

Endothelium-derived relaxing factor, recently identified as nitric oxide (NO), is the endogeneous stimulator of the soluble guanylate cyclase and is synthesized from L-arginine by nitric oxide synthase (NOS). *N*<sup>η</sup>-Nitro-L-arginine methyl ester and other L-arginine analogues such as *N*<sup>η</sup>-amino-L-arginine, *N*<sup>η</sup>-methyl-L-arginine or *N*<sup>η</sup>-nitro-L-arginine, act as inhibitors of NOS and induce an increase in blood pressure in animal models of sepsis or in patients in septic shock (Mülsch & Busse, 1990; Moncada, Palmer & Higgs, 1991; Rand, 1992; Moncada, 1992; Cobb *et al.*, 1992). Therefore, it is important to decide the precise molecular structure of these inhibitors in order to investigate more closely the relationship between the function and structure of these inhibitors. In this study, the crystal structure of *N*<sup>η</sup>-nitro-L-arginine methyl ester was determined as the hydrochloride form, (I).



The molecular structure is illustrated in Fig. 1. All atoms forming the nitroguanidinium group are nearly coplanar. The hydrocarbon side chain is not fully extended, but folded at C<sup>δ</sup> [C(5)]. The N(1)—C(2)—C(3)—C(4)—C(5) chain is *trans*-zigzag planar, as is C(5)—N(2)—C(6)—N(4)—N(5)—O(4); they intersect perpendicularly at C(5). The α-amino group is protonated and three amino atoms are involved in the hydrogen-bonding network. The three C—N distances

in the nitroguanidinium group are nearly equal, as observed in L-arginine dihydrate (Lehmann, Verbist, Hamilton & Koetzle, 1973).

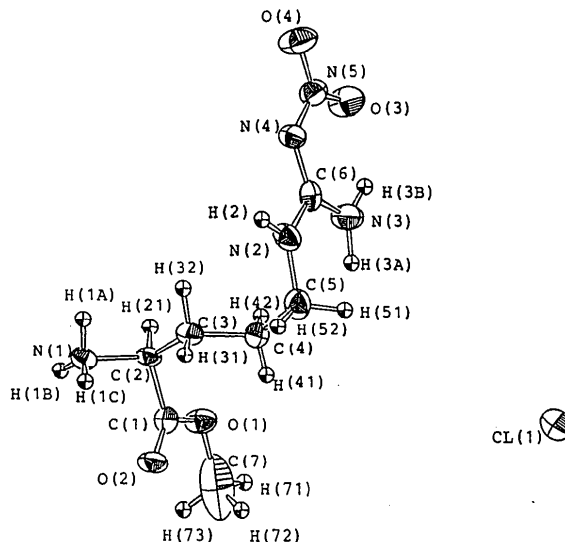


Fig. 1. Perspective view of the title compound with the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

**Experimental****Crystal data**C<sub>7</sub>H<sub>16</sub>N<sub>5</sub>O<sub>4</sub><sup>+</sup>.Cl<sup>-</sup>*M<sub>r</sub>* = 269.69

Monoclinic

*P*2<sub>1</sub>*a* = 5.440 (1) Å*b* = 10.108 (1) Å*c* = 11.484 (2) Å

β = 103.03 (2)°

*V* = 615.2 (3) Å<sup>3</sup>*Z* = 2*D<sub>x</sub>* = 1.456 Mg m<sup>-3</sup>*D<sub>m</sub>* = 1.448 (3) Mg m<sup>-3</sup>*D<sub>m</sub>* measured by flotationMo *K*α radiation

λ = 0.71069 Å

Cell parameters from 25 reflections

θ = 15.15–16.45°

μ = 0.320 mm<sup>-1</sup>*T* = 296 K

Plate

0.20 × 0.20 × 0.10 mm

Colourless

Crystal source: evaporation

from 0.05*N* HCl/50%

ethanol

**Data collection**

Rigaku AFC-5R diffractometer

ω–2θ scans

Absorption correction:

empirical (*DIFABS*;

Walker &amp; Stuart, 1983)

*T<sub>min</sub>* = 0.78, *T<sub>max</sub>* = 1.23

1634 measured reflections

1485 independent reflections

903 observed reflections

[*I* > 3σ(*I*)]*R<sub>int</sub>* = 0.028θ<sub>max</sub> = 27.5°*h* = 0 → 7*k* = 0 → 12*l* = –14 → 13

3 standard reflections

monitored every 150

reflections

intensity variation:

–0.13%

**Refinement**Refinement on *F**R* = 0.048*wR* = 0.052(Δ/σ)<sub>max</sub> = 0.003Δρ<sub>max</sub> = 0.26 e Å<sup>-3</sup>Δρ<sub>min</sub> = –0.36 e Å<sup>-3</sup>

$S = 1.58$   
903 reflections  
153 parameters  
H-atom parameters not  
refined  
 $w = 4F_o^2/\sigma^2(F_o^2)$

Extinction correction: none  
Atomic scattering factors  
from *International Tables*  
for *X-ray Crystallography*  
(1974, Vol. IV)

Lists of structure factors, anisotropic displacement parameters, H-atom coordinates, complete geometry and torsion angles have been deposited with the IUCr (Reference: AS1106). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 1. Fractional atomic coordinates and equivalent isotropic displacement parameters ( $\text{\AA}^2$ )

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

	<i>x</i>	<i>y</i>	<i>z</i>	$B_{\text{eq}}$
Cl(1)	-0.0126 (3)	0.0127	0.1317 (2)	3.54 (7)
O(1)	0.0097 (8)	0.0212 (6)	0.8255 (4)	3.3 (2)
O(2)	0.367 (1)	-0.0701 (5)	0.9251 (5)	3.0 (2)
O(3)	0.041 (1)	0.7121 (6)	0.5370 (5)	4.6 (3)
O(4)	0.319 (1)	0.8451 (6)	0.6356 (6)	4.8 (3)
N(1)	0.462 (1)	0.1588 (6)	1.0588 (5)	2.4 (2)
N(2)	0.538 (1)	0.4254 (7)	0.6626 (6)	3.0 (3)
N(3)	0.150 (1)	0.4673 (6)	0.5386 (6)	3.7 (3)
N(4)	0.417 (1)	0.6366 (6)	0.6493 (5)	2.7 (2)
N(5)	0.252 (1)	0.7310 (7)	0.6052 (5)	3.1 (3)
C(1)	0.235 (1)	0.0236 (9)	0.8959 (5)	2.4 (3)
C(2)	0.320 (1)	0.1631 (7)	0.9301 (6)	2.1 (2)
C(3)	0.492 (1)	0.2164 (7)	0.8527 (6)	2.7 (3)
C(4)	0.369 (1)	0.2132 (8)	0.7206 (6)	2.9 (3)
C(5)	0.525 (1)	0.2816 (9)	0.6427 (7)	3.3 (3)
C(6)	0.356 (1)	0.511 (1)	0.6138 (5)	2.7 (3)
C(7)	0.110 (2)	-0.121 (2)	0.793 (1)	9.2 (8)

Table 2. Selected geometric parameters ( $\text{\AA}$ ,  $^\circ$ )

O(1)—C(1)	1.310 (7)	N(3)—C(6)	1.327 (8)
O(1)—C(7)	1.59 (2)	N(4)—N(5)	1.328 (8)
O(2)—C(1)	1.190 (9)	N(4)—C(6)	1.35 (1)
O(3)—N(5)	1.251 (7)	C(1)—C(2)	1.51 (1)
O(4)—N(5)	1.236 (8)	C(2)—C(3)	1.52 (1)
N(1)—C(2)	1.505 (8)	C(3)—C(4)	1.513 (9)
N(2)—C(5)	1.47 (1)	C(4)—C(5)	1.53 (1)
N(2)—C(6)	1.335 (9)		
C(1)—O(1)—C(7)	116.1 (7)	N(1)—C(2)—C(1)	106.7 (5)
C(5)—N(2)—C(6)	124.6 (7)	N(1)—C(2)—C(3)	109.8 (5)
N(5)—N(4)—C(6)	117.6 (5)	C(1)—C(2)—C(3)	111.7 (5)
O(3)—N(5)—O(4)	119.3 (7)	C(2)—C(3)—C(4)	112.8 (5)
O(3)—N(5)—N(4)	125.0 (6)	C(3)—C(4)—C(5)	113.6 (6)
O(4)—N(5)—N(4)	115.6 (6)	N(2)—C(5)—C(4)	111.7 (7)
O(1)—C(1)—O(2)	125.6 (8)	N(2)—C(6)—N(3)	119.8 (8)
O(1)—C(1)—C(2)	111.5 (7)	N(2)—C(6)—N(4)	111.9 (6)
O(2)—C(1)—C(2)	122.8 (5)	N(3)—C(6)—N(4)	128.3 (7)
<i>D</i> —H... <i>A</i>	<i>H</i> ... <i>A</i>	<i>D</i> ... <i>A</i>	
N(1)—H(1A)...O(2 <sup>i</sup> )	1.94	2.886 (7)	
N(1)—H(1B)...Cl(1 <sup>ii</sup> )	2.40	3.244 (6)	
N(1)—H(1C)...Cl(1 <sup>iii</sup> )	2.25	3.158 (6)	
N(2)—H(2)...Cl(1 <sup>iv</sup> )	2.25	3.205 (6)	
N(3)—H(3A)...O(3 <sup>v</sup> )	1.93	2.843 (8)	

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

The positions of H atoms on N(2) and C(7) could not be located from difference Fourier synthesis and so were calculated geometrically. Other H atoms were subsequently located from difference Fourier synthesis and not refined.

Programs used for data collection and cell refinement: *MSC/AFC Data Collection and Refinement Software* (Rigaku Corporation, 1988). Programs used to solve structure: *SHELXS86* (Sheldrick, 1985); *DIRDIF* (Beurskens, 1984). All calculations including data reduction: *TEXSAN* (Molecular Structure Corporation, 1985).

## References

- Beurskens, P. T. (1984). *DIRDIF. Direct Methods for Difference Structures – an Automatic Procedure for Phase Extension and Refinement of Difference Structure Factors*. Technical Report 1984/1, Crystallography Laboratory, Toernooiveld, 6525 ED Nijmegen, The Netherlands.
- Cobb, J. P., Natanson, C., Hoffman, W. D., Lodato, R. F., Banks, S., Koev, C. A., Solomon, M. A., Elin, R. J., Hosseini, J. M. & Danner, R. L. (1992). *J. Exp. Med.* **176**, 1175–1182.
- Lehmann, M. S., Verbist, J. J., Hamilton, W. C. & Koetzle, T. F. (1973). *J. Chem. Soc. Perkin Trans. 2*, pp. 133–137.
- Molecular Structure Corporation (1985). *TEXSAN. TEXRAY Structure Analysis Package*. MSC, 3200 Research Forest Drive, The Woodlands, TX 77381, USA.
- Moncada, S. (1992). *Acta Physiol. Scand.* **145**, 201–227.
- Moncada, S., Palmer, R. M. J. & Higgs, E. A. (1991). *Pharmacol. Rev.* **43**, 109–142.
- Mülsch, A. & Busse, R. (1990). *Arch. Pharmacol.* **341**, 143–147.
- Rand, M. J. (1992). *Clin. Exp. Pharmacol. Physiol.* **19**, 147–169.
- Rigaku Corporation (1988). *MSC/AFC Data Collection and Refinement Software*. Rigaku Corporation, Tokyo, Japan.
- Sheldrick, G. M. (1985). *SHELXS86. Program for the Solution of Crystal Structures*. Univ. of Göttingen, Germany.
- Walker, N. & Stuart, D. (1983). *Acta Cryst.* **A39**, 159–166.

*Acta Cryst.* (1994). **C50**, 2089–2093

## Structural Studies of Intermediates in the Synthesis of Mifepristone (RU 486). I. An 11 $\beta$ -Substituted Steroid

MADI BIDYASAGAR AND KRISHNAN RAVIKUMAR

*Laboratory of Crystallography, Indian Institute of Chemical Technology, Hyderabad 500 007, India*

RAO A. V. RAMA, MADDURU M. REDDY AND ASHOK K. SINGH

*Bio-Organic Laboratory, Indian Institute of Chemical Technology, Hyderabad 500 007, India*

(Received 20 October 1993; accepted 17 March 1994)

## Abstract

The title compound, 11 $\beta$ -[4-(dimethylamino)phenyl]-3,3-(ethylenedioxy)-17 $\alpha$ -(1-propynyl)estra-9-en-5 $\alpha$ ,17 $\beta$ -diol (C<sub>31</sub>H<sub>41</sub>NO<sub>4</sub>), is the key intermediate in the synthesis of RU 486 and its overall conformation is similar to that of RU 486. The orientation of the (dimethylamino)phenyl ring, which seems to be con-