non-systematic error, omitted in last cycle. Difference Fourier calculations after last refinement cycle revealed max. positive and negative electron density 0·449 and −0·527 e Å^{-3} respectively.

The final atomic parameters for the non-H atoms are given in Table 1.*

Discussion. The *p*-nitrophenol binds to triphenylarsine oxide through hydrogen bonding between O(1) and O(2) atoms, as was predicted.

The hydrogen bond is asymmetric and may be classified as strong (Novak, 1974). The value of the O(1)···H(1)—O(2) angle is 124° and of the O(1)···O(2) distance 2·555 (8) Å. This latter value agrees satisfactorily with the value [2·60 (1) Å] proposed by Lechat (1984).

Fig. 1 shows the bond lengths and angles in the *p*-nitrophenol–triphenylarsine oxide adduct, with the atomic numbering.

The relevant distances and angles in the *p*-nitrophenol molecule are: C—N 1·45 (2), C—O 1·34 (2) and N—O 1·22 (2) Å (mean); O—N—O 123 (1), O—N—C 118 (1) (mean) and O—C—C 121 (1)° (mean). As in other nitrophenols, the benzene ring is planar, the largest distance to it being observed for the O(4) atom (0·11 Å). The dihedral angle between the benzene and nitro-group planes is 4·8°.

The As atom in the triphenylarsine oxide molecule was found to have a nearly tetrahedral coordination [C—As—C 108 (2)° (mean)]. The values of the As—C and As=O distances are 1·92 (1) (mean) and 1·668 (7) Å respectively.

Crystal packing as well as hydrogen bonds are shown in Fig. 2.

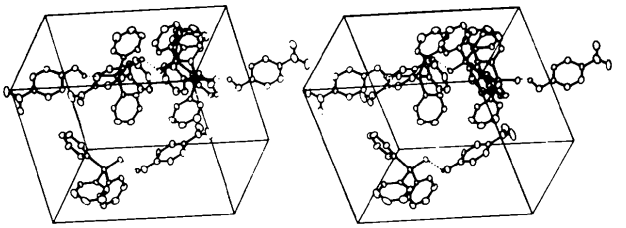

Fig. 2. Stereoview of the molecular packing diagram for the adduct formed by *p*-nitrophenol with triphenylarsine oxide.

All calculations, unless otherwise mentioned in the text, were performed in the Instituto de Física e Química de São Carlos, USP, on the PDP11/45 and VAX 760 computers using *SDP* crystallography programs (Frenz, 1978). This work has received the support of Universidade Federal de Goiás, CAPES, CNPq, FINEP and FAPESP which is hereby gratefully acknowledged.

* Lists of structure factors, anisotropic thermal parameters, H-atom coordinates, bond lengths, angles, and least-squares planes have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 42718 (18 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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Structure of Anticancer Antibiotic L-Alanosine

BY M. A. F. JALAL, M. B. HOSSAIN AND DICK VAN DER HELM

Department of Chemistry, University of Oklahoma, Norman, OK 73019, *USA*

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Abstract. $C_3H_7N_3O_4$, $M_r = 149·11$, orthorhombic, $P2_12_12_1$, $a = 9·107$ (4), $b = 9·600$ (4), $c = 6·383$ (8) Å, $V = 558·1$ Å^3, $Z = 4$, $D_x = 1·774$ g cm^{-3}, Mo $K\bar{\alpha}$, $\lambda = 0·71069$ Å, $\mu = 1·73$ cm^{-1}, $F(000) = 312$, $T = 138$ K, $R = 0·032$ for 603 observed data and 0·041 for all 685 reflections. The compound crystallizes as a zwitterion like many other α-amino acids. In the crystalline state, L-alanosine is a tautomer of the published structure so that the terminal position in the chain of the molecule is occupied by the *N*-nitroso group. Conformationally,

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L-alanosine shows close resemblance to L-aspartic acid, which explains its involvement as an analogous substrate in a number of L-aspartic acid utilizing enzymes.

Introduction. L-Alanosine, originally isolated from *Streptomyces alanosinicus* (Murthy, Thiemann, Coronelli & Sensi, 1966), has recently entered clinical trials as an anticancer drug. The compound is highly active and possesses antiviral, antimicrobial, antibiotic and immunosuppressive properties in addition to antineoplastic and antitumor activity. Its antiviral property was first reported by Murthy *et al.* (1966), when they observed that L-alanosine inhibited the cytopathic effects of polio, sheep pox and cow pox viruses *in vitro* and the viral infection of neurovaccinia on rabbit skin *in vivo*. Gale, Ostrander & Atkins (1968), on the other hand, demonstrated its antimicrobial activity against *Candida albicans, Mycobacterium marinum* and *Saccharomyces cerevisiae*. The significant immunosuppressive ability of L-alanosine in rabbits, mice and rats was observed by Fumarola (1970), Arrigoni-Martelli, Schiatti & Selva (1971) and Mistrello & Bassi (1984). Moreover, L-alanosine was shown to inhibit mouse tooth germ morphogenesis (Dye & Kollar, 1978) and reproduction in insects (Kenaga, 1969; Kratsas & Grosch, 1974).

The antitumor property of L-alanosine against hamster fibrosarcoma and murine leukemias was reported from a number of sources (Murthy *et al.* 1966; Jayaram & Cooney, 1979; Chitnis, Adwankar & Amonkar, 1984; Tyagi & Cooney, 1984). Its antineoplastic activity is believed to be a result of its unique ability to arrest *de novo* AMP (5′-adenylic acid) synthesis by interfering in the purine biosynthesis steps catalyzed by SAICAR synthetase* and adenylosuccinate synthetase, which use L-aspartate as one of the substrates (Graff & Plagemann, 1976; Anandaraj, Jayaram, Cooney, Tyagi, Han, Thomas, Chitnis & Montgomery, 1980). In general, L-alanosine seems to act as a pseudo substrate for a number of other L-aspartate utilizing enzymes such as L-aspartate carbamoyltransferase, L-aspartyl-tRNA synthetase, L-aspartate aminotransferase and the L-aspartate transport system. It is also known to affect the activity of a number of enzymes involved in the metabolism of L-glutamate, L-asparagine and L-glutamine (Tyagi & Cooney, 1984).

On the basis of its interaction with L-aspartate-binding enzymes, it is suggested that L-alanosine and L-aspartate may share common binding sites and possess common structural and chemical features. Even so, a metabolic change may be involved in the actual mechanism of action of L-alanosine. In addition, resistance to the compound is evident and at the present time the main hope for L-alanosine is in usage in combination chemotherapeutic strategies for the control of human cancer (Tyagi & Cooney, 1984).

The compound is structurally unique as it is the only natural compound isolated so far with an *N*-nitroso-*N*-hydroxyamino function. In analogy with cupferron,* which also contains this functional group, L-alanosine forms 1:1 complexes with Cu^{2+} and Zn^{2+} (Powis & Kovach, 1981). When injected intravenously, L-alanosine causes a significant decrease in plasma copper levels.

It is the purpose of this communication to report the molecular and crystal structure of L-alanosine and compare it with the structures of L-aspartic acid (Derissen, Endeman & Peerdeman, 1968), L-glutamic acid (Lehmann, Koetzle & Hamilton, 1972) and also with the ligating group of iron cupferron (van der Helm, Merritt, Degeilh & MacGillavry, 1965) and *N,N′*-dinitrosomethylenedihydroxylamine (Bryden, 1959).

* SAICAR is *N*-{[5-amino-1-(5-*O*-phosphono-β-D-ribofuranosyl)-1*H*-imidazol-4-yl]carbonyl}aspartic acid.

* Cupferron is *N*-hydroxy-*N*-nitrosobenzenamine ammonium salt.

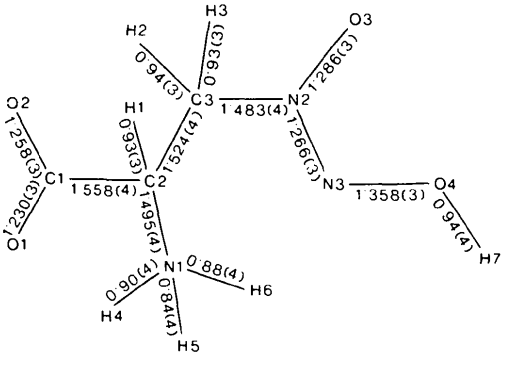


Fig. 1. Atom-numbering scheme and bond distances in L-alanosine.

Table 1. *Atomic coordinates and U_{eq} for* L-*alanosine*

$U_{eq} = \frac{1}{3}\sum_i\sum_j U_{ij}a_i^*a_j^*\mathbf{a}_i.\mathbf{a}_j$
$= B/8\pi^2$ for H atoms.

	x	*y*	*z*	U_{eq}(Å²)
C(1)	0·9734 (3)	1·0632 (3)	0·5614 (4)	0·0156 (7)
C(2)	0·9786 (3)	0·9038 (3)	0·6066 (5)	0·0163 (8)
C(3)	0·9444 (3)	0·8248 (3)	0·4052 (4)	0·0164 (8)
N(1)	0·8683 (3)	0·8739 (3)	0·7741 (4)	0·0165 (7)
N(2)	0·9556 (2)	0·6724 (2)	0·4387 (4)	0·0168 (7)
N(3)	0·8329 (2)	0·6115 (2)	0·4571 (4)	0·0170 (7)
O(1)	0·8527 (2)	1·1201 (2)	0·5723 (3)	0·0226 (6)
O(2)	1·0935 (2)	1·1215 (2)	0·5193 (3)	0·0186 (6)
O(3)	1·0822 (2)	0·6132 (2)	0·4460 (3)	0·0202 (6)
O(4)	0·8532 (2)	0·4727 (2)	0·4871 (3)	0·0196 (6)
H(1)	1·072 (3)	0·879 (3)	0·655 (4)	0·004 (6)
H(2)	1·016 (3)	0·850 (3)	0·305 (5)	0·014 (8)
H(3)	0·852 (4)	0·838 (3)	0·347 (5)	0·016 (8)
H(4)	0·775 (4)	0·879 (4)	0·731 (5)	0·027 (9)
H(5)	0·880 (4)	0·795 (4)	0·830 (6)	0·039 (11)
H(6)	0·880 (4)	0·941 (4)	0·867 (7)	0·047 (12)
H(7)	0·762 (4)	0·429 (4)	0·480 (6)	0·044 (12)

Experimental. Sample of L-alanosine (NSC 153353 NE, Lot 3/77) obtained from the National Institutes of Health, Bethesda, Maryland, through Dr L. H. Kedda. Crystals grown by slow diffusion of ethanol into a solution of L-alanosine in water (200 µl) acidified with conc. HCl (20 µl). Intensity data on prismatic crystal (0·25 × 0·25 × 0·17 mm) collected on Enraf–Nonius CAD-4 diffractometer fitted with liquid-N_2 low-temperature device, 138 (2) K; graphite-monochromatized Mo $K\alpha$ radiation. Unit-cell dimensions from 40 reflections with $20 \le 2\theta \le 30°$; 685 unique reflections, $0 \le h \le 11$, $0 \le k \le 12$, $0 \le l \le 8$; $2\theta_{max} = 53°$; ω–2θ scan technique; 602 observed reflections [$I \ge 2\sigma(I)$, $\sigma(I)$ from counting statistics]; no significant variation of three monitor reflections measured every 7200 s; no absorption correction. Structure solved by direct methods using *MULTAN*76 (Main, Lessinger, Woolfson, Germain & Declercq, 1976) and refined on F by full-matrix least squares using *SHELX*76 (Sheldrick, 1976). H atoms from difference Fourier map refined isotropically; final $R = 0·032$, $wR = 0·037$, $w = 1/\sigma^2(F)$, for 602 observed reflections and $R = 0·041$ for all 685 reflections, $S = 1·33$; $(\Delta/\sigma)_{max} = 0·02$; final difference map featureless ($\Delta\rho = 0·25$ e Å^3), atomic scattering factors as in *SHELX*76.*

Discussion. The atom-numbering scheme and the bond lengths for L-alanosine are given in Fig. 1. The final atomic coordinates are listed in Table 1. The configuration of C(2) in L-alanosine was established by degradative and synthetic studies reviewed by Tyagi & Cooney (1984), and this configuration is shown in the figures.

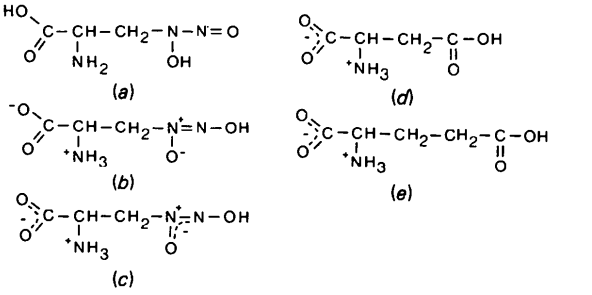
The carboxyl group of L-alanosine is ionized, the C—O distances being 1·230 (3) [C(1)—O(1)] and 1·258 (3) Å [C(1)—O(2)]. A difference in the two C—O bond lengths of an ionized carboxyl group is observed in many amino acids including L-aspartic acid (1·242 and 1·252 Å) (Scheme 1*d*) (Derissen *et al.*, 1968) and β-L-glutamic acid (1·243 and 1·262 Å) (Scheme 1*e*) (Lehmann *et al.*, 1972). The difference in the bond distances, however, is not reflected in a correlated difference (Borthwick, 1980) in the C—C—O bond angles.

The *N*-nitroso-*N*-hydroxyamino part of the molecule shows distinct tautomeric differences from the structure established by Coronelli, Pasqualucci, Tamoni & Gallo (1966) (Scheme 1*a*). In the crystalline state the N—OH function is present at the terminal position (Scheme 1*b*), with the N(3)—O(4) and O(4)—H(7) distances being 1·358 (3) and 0·94 (4) Å respectively. This observation correlates with the N(2)—N(3) distance of 1·266 (3) Å, which is only slightly longer than the average value for a double bond [1·24 (1) Å], with the lengthening caused by resonance in the O(3), N(2), N(3) system (Scheme 1*c*). The observed tautomer may be the result of intermolecular interactions, although the possibility exists that it is the common species in solution as well.

Table 2. *Bond and torsion angles* (°) *in* L-*alanosine*

O(1)–C(1)–O(2)	126·2 (2)	C(2)–C(3)–N(2)	110·8 (2)
O(1)–C(1)–C(2)	117·0 (2)	C(3)–N(2)–O(3)	120·2 (2)
O(2)–C(1)–C(2)	116·8 (2)	C(3)–N(2)–N(3)	114·1 (2)
C(1)–C(2)–N(1)	107·5 (2)	O(3)–N(2)–N(3)	125·7 (2)
C(1)–C(2)–C(3)	109·0 (2)	N(2)–N(3)–O(4)	110·2 (2)
N(1)–C(2)–C(3)	111·7 (2)		

O(1)–C(1)–C(2)–C(3)	85·8 (3)	N(1)–C(2)–C(3)–N(2)	−64·2 (3)
O(1)–C(1)–C(2)–N(1)	−35·5 (3)	C(2)–C(3)–N(2)–O(3)	−77·7 (3)
O(2)–C(1)–C(2)–C(3)	−94·9 (3)	C(2)–C(3)–N(2)–N(3)	102·6 (3)
O(2)–C(1)–C(2)–N(1)	143·8 (2)	C(3)–N(2)–N(3)–O(4)	180·0
C(1)–C(2)–C(3)–N(2)	177·2 (2)	O(3)–N(2)–N(3)–O(4)	0·3 (5)

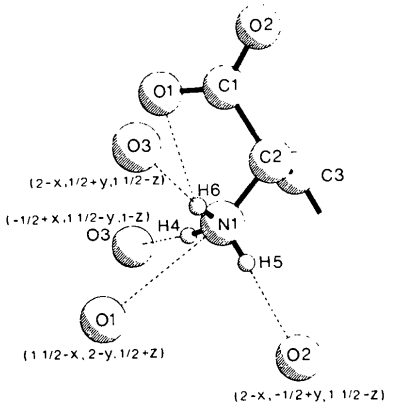


Scheme 1

All the non-hydrogen atoms in the molecule, with the exception of the amino N, lie in two nearly parallel planes [angle between the planes 7·3 (3)°]. The carboxylate plane is formed by the C(1), C(2), O(1) and O(2) atoms and the *N*-nitroso-*N*-hydroxyamino plane is made up of the C(3), N(2), N(3), O(3) and O(4) atoms (torsion angles given in Table 2). The N(1) atom projects out of the first plane by a distance of 0·837 (3) Å. The intramolecular distance between N(1) and O(1) is 2·696 (4) Å, shorter than the three intermolecular hydrogen bonds involving N(1) (see below). The N···O distance is also shorter than the corresponding distance in L-aspartic acid (2·737 Å), although the angle formed by C(2)—N(1) with the carboxylate plane is slightly larger in L-alanosine [35·8° (3)] than in L-aspartic acid (33·9°). This N(1)···O(1) distance qualifies as a weak intramolecular three-centered hydrogen bond, commonly found in ionized α-amino acids (Jeffrey & Maluszynska, 1982), since the NH···O distance [H(6)···O(1) 2·562 Å] is within the range of such a hydrogen bond as defined by these authors.

* Lists of structure factors and anisotropic thermal parameters have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 42743 (5 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 3. *Hydrogen bonds and short contacts in* L-*alanosine*



A—H···*B*[symmetry code]	*A*···*B*	H···*B*
N(1)—H(6)···O(1)[*x*, *y*, *z*]	2·696 (3) Å	2·56 (4) Å
N(1)—H(4)···O(3)[$-\frac{1}{2}+x$, $1\frac{1}{2}-y$, $1-z$]	2·963 (3)	2·09 (4)
N(1)—H(5)···O(2)[$2-x$, $-\frac{1}{2}+y$, $1\frac{1}{2}-z$]	2·781 (3)	1·94 (4)
N(1)—H(6)···O(3)[$2-x$, $\frac{1}{2}+y$, $1\frac{1}{2}-z$]	2·945 (3)	2·07 (4)
O(4)—H(7)···O(2)[$-\frac{1}{2}+x$, $1\frac{1}{2}-y$, $1-z$]	2·532 (3)	1·61 (4)
N(1)···O(1)[$1\frac{1}{2}-x$, $2-y$, $\frac{1}{2}+z$]	2·771 (3)	–

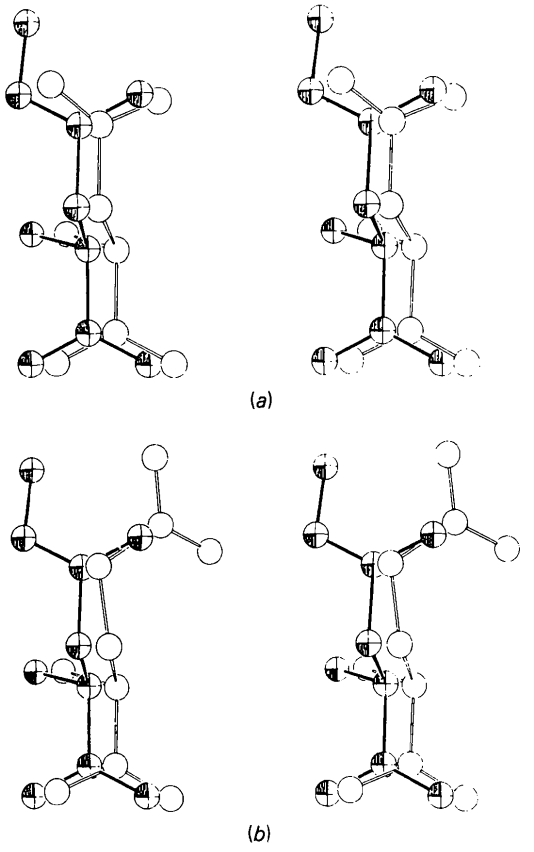


Fig. 2. Least-squares fit of L-alanosine with (*a*) L-aspartic acid and (*b*) L-glutamic acid. In both diagrams, the molecules are separated from each other by a translation of 0·5 Å.

Hydrogen bonding and crystal packing. L-Alanosine shows four intermolecular hydrogen bonds and one short contact (Table 3). The strongest hydrogen bond is O(4)—H(7)···O(2) with an O···O distance of 2·532 Å and an H···O distance of 1·605 Å. The other three hydrogen bonds and the intermolecular short contact involve the NH_3^+ group. The geometry of these hydrogen bonds and the short contact around N(1) is shown in Table 3. N···O bond lengths indicate that the short contact is stronger than the three hydrogen bonds of N(1). The O(1) atom, which is involved in the short contact with the NH_3^+ group, is situated at a position nearly equidistant from all NH protons [H(4)···O(1) = 2·465, H(5)···O(1) = 2·745, H(6)···O(1) = 2·558 Å]. It seems likely that this short contact results from an electrostatic attraction between the positively charged nitrogen atom ($^+NH_3$) and the negatively charged oxygen atom (C—O^-). An identical situation of three hydrogen bonds and a short contact, the latter involving the amino N atom and a carboxylate O atom, was observed in γ-glycine (Kvick, Canning, Koetzle & Williams, 1980). The molecules of L-alanosine are packed inside the unit cell with their backbones parallel to the *b* axis; linear packing along this axis is caused by two hydrogen bonds N(1)—H(5)···O(2) and N(1)—H(6)···O(3). The other two hydrogen bonds and the intermolecular short contact are responsible for the parallel packing of the molecules inside the crystal.

Structure–activity relationship. L-Alanosine was shown to affect *de novo* synthesis of DNA and arrest neoplastic growth of murine tumor cells. Only three amino acids, glycine, L-glutamine and L-aspartic acid, are involved in the formation of purine and pyrimidine nucleotides. L-Alanosine is structurally similar to L-aspartic acid and also, to some extent, to glutamine and glutamic acid. L-Aspartic acid is transitorily incorporated into the nucleotide skeleton in two important steps of purine biosynthesis, one catalyzed by SAICAR synthetase and the other by adenylosuccinate synthetase [which converts IMP (5′-inosinic acid) to AMP]. Both of these enzymes accept L-alanosine as a substrate; in the latter case as a noncompetitive inhibitor (Jayaram & Cooney, 1979; Anandaraj *et al.*, 1980). Moreover, the product of L-alanosine and SAICAR synthetase, L-alanosyl AICAR,* was found to be an extremely potent inhibitor of adenylosuccinate synthetase.

The activity of L-alanosine as a pseudo substrate in the above-mentioned enzyme reactions and also in many other L-aspartate metabolizing enzymes is not surprising since L-alanosine and L-aspartic acid are closely related in structural features. A least-squares fit of the crystal structures of these compounds (L-aspartic acid after Derissen *et al.*, 1968) is shown in Fig. 2(*a*).

* AICAR is 5-amino-1-(5-*O*-phosphono-β-D-ribofuranosyl)-1*H*-imidazole-4-carboxamide.

Except for the OH group in the hydroxyamino part, all the atoms in L-alanosine are superimposable on the corresponding atoms in L-aspartic acid. An important feature in the structure is the antiperiplanar conformation around the C(2)–C(3) bond, which is also observed in the crystal structure of DL-aspartic acid (Rao, 1973) and found to be the predominant conformer of aspartate in solution (Kainosho & Apisaka, 1975). There have been indications, however, that aspartate bound to the active site is in the less-stable synperiplanar conformation, which can be assumed by L-alanosine as well as by aspartic acid. The present structural comparison clearly indicates that L-alanosine may fit even in comparatively tight and stereospecific areas of L-aspartate-binding sites in the enzymes. The crystal structure of L-aspartate carbamoyltransferase, an enzyme of the pyridine nucleotide synthesis, known to utilize L-alanosine as an analogous substrate (Gale *et al.*, 1968; Anandaraj *et al.*, 1980) has been published (Honzatko, Crawford, Monaco, Ladner, Ewards, Evans, Warren, Wiley, Ladner & Lipscomb, 1982), but the site for L-aspartate binding could not be determined unequivocally from these studies. More recently, the crystal structure of the bisubstrate analogue, *N*-(phosphonacetyl)-L-aspartate with this enzyme was reported (Krause, Volz & Lipscomb, 1985). The dihedral angle for the C(2)–C(3) bond in this structure is 110°.

Compared to L-aspartic acid, β-L-glutamic acid (Lehmann *et al.*, 1972) shows more differences with the structure of L-alanosine (Fig. 2*b*). Although most atoms in the molecule superimpose on each other, the orientation of the glutamyl-side-chain carboxyl group is opposite to the alanosyl *N*-nitroso-*N*-hydroxyamino group. A rotation around the C(3)–N(2) bond in L-alanosine may give a better fit with L-glutamic acid, because the two bond angles and the torsion angle involving C(2), N(2), N(3) and O(4) in L-alanosine (114·1, 110·2 and 180·0°) are similar to the corresponding angles in L-glutamic acid (116·1, 112·2 and −160·7°). Even if such a rotational conformer with common molecular skeleton exists in solution, the nitroso oxygen of L-alanosine and the carbonyl oxygen in L-glutamic acid will protrude from this common skeleton in opposite directions. This partly explains why L-alanosine so successfully replaces L-aspartic acid as a substrate in many enzyme systems, while it affects only a few L-glutamate utilizing enzymes.

The chelating group in L-alanosine is similar to that of cupferron, which is known to complex with a large number of metal ions. A comparative study of the geometries of this ligand group in the protonated form (L-alanosine), ionized form (*N,N'*-dinitrosomethylenedihydroxylamine; Bryden, 1959) and Fe^{III} chelate form (iron cupferron; van der Helm *et al.*, 1965) is presented in Table 4. In L-alanosine the N(3)–O(4) bond is considerably longer because of the presence of a hydrogen atom on O(4). When the proton is lost due to ionization, this bond shortens in length. After metal chelation it shortens further and the two bonds in the ligand group become equal in length. The N(2)–N(3)–O(4) bond angle is fairly stable irrespective of ionization or metal chelation, while the N(3)–N(2)–O(3) angle seems to be most sensitive to such changes. Iron chelation apparently compresses this angle with a complementary increase in the C(3)–N(2)–N(3) angle. In all three cases, the ligand group is planar.

Table 4. *Comparative geometries of the ligand groups in* L-*alanosine, N,N'-dinitrosomethylenedihydroxylamine ion (Bryden,* 1959*) and iron cupferron (van der Helm et al.,* 1965)

	L-Alanosine	Corresponding bond/angle in *N,N'*dinitrosomethylenedihydroxylamine ion	Corresponding bond/angle in iron cupferron
Bonds (Å)			
C(3)–N(2)	1·483 (4)	1·512 (7)	1·433 (18)
N(2)–N(3)	1·266 (3)	1·297 (4)	1·302 (15)
N(2)–O(3)	1·286 (3)	1·266 (4)	1·318 (14)
N(3)–O(4)	1·358 (3)	1·323 (6)	1·314 (14)
Bond angles (°)			
C(3)–N(2)–N(3)	114·1 (2)	113·8	117·9
C(3)–N(2)–O(3)	120·2 (2)	117·2	119·9
N(2)–N(3)–O(4)	110·2 (2)	110·2	110·7
O(3)–N(2)–N(3)	125·7 (2)	128·8	121·0

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Structure of Ethyl 1-Cyano-1,2-dihydro-2-isoquinolinecarboxylate

BY E. TYKARSKA, M. JASKÓLSKI AND Z. KOSTURKIEWICZ*

Department of Crystallography, Faculty of Chemistry, A. Mickiewicz University, ul. Grunwaldzka 6, 60–780 *Poznań, Poland*

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Abstract. $C_{13}H_{12}N_2O_2$, $M_r = 228{\cdot}26$, triclinic, $P\bar{1}$, $a = 8{\cdot}536$ (1), $b = 9{\cdot}011$ (1), $c = 8{\cdot}305$ (1) Å, $\alpha = 90{\cdot}88$ (1), $\beta = 79{\cdot}39$ (1), $\gamma = 109{\cdot}62$ (1)°, $V = 590{\cdot}7$ (2) Å^3, $Z = 2$, $D_m = 1{\cdot}29$, $D_x = 1{\cdot}28$ Mg m^{-3}, λ(Cu $K\alpha$) = 1·54178 Å, $\mu = 0{\cdot}732$ mm^{-1}, $F(000) = 240$, room temperature, $R = 0{\cdot}045$ for 1333 observed reflections. The heterocyclic fragment of the molecule is intermediate between 1,3-diplanar and sofa conformations. The C(3)—N(2)—C(13)—O(14) torsion angle [−171·3 (3)°] characterizes the urethane bond as *anti*. The NCOO group is planar. The C(13)—O(15)—C(16)—C(17) torsion angle [171·4 (3)°] reveals the twist of the ethyl fragment relative to this plane.

Introduction. The present work is the fourth of a series of investigations of Reissert compounds (Reissert, 1905). It is of interest to determine the effects of substituents on the molecular conformation in such a group of compounds. Our aim is to compare the disposition of the side fragments relative to the central amide or urethane group depending on the character and dimensions of those fragments. So far we have investigated the structure of 2-benzoyl-1,2,3,4-tetrahydro-1-isoquinolinecarbonitrile (I) (Pływaczyk, Tykarska, Jaskólski & Kosturkiewicz, 1984) and its dihydro analog (II) (Tykarska, Jaskólski & Kosturkiewicz, 1985) as well as ethyl 1-cyano-1,2,3,4-tetrahydro-2-isoquinolinecarboxylate (III) (Gzella, Jaskólski, Rychlewska & Kosturkiewicz, 1984). The present compound (IV) is a dihydro analog of (III) and closes the series.

Experimental. Suitable crystals (prisms) obtained from ethanol; D_m by flotation; crystal 0·4 × 0·2 × 0·2 mm, Syntex $P2_1$ diffractometer; cell parameters from least-squares refinement of setting angles of 15 reflections, $20 \le 2\theta \le 30°$; profiles measured for 1552 reflections with $2\theta \le 115°$ and $h = \pm 9$, $k = \pm 9$, $l = 0$–9; profile analysis according to Lehmann & Larsen (1974); no significant intensity variation for two standard reflections; no absorption correction; 1333 observed reflections with $I \ge 1{\cdot}96\sigma(I)$; structure solved by direct methods using *MULTAN*80; full-matrix least-squares refinement on F; $w^{-1} = \sigma^2(F)$; anisotropic thermal parameters for all non-H atoms; 8 extinction-affected reflections excluded from final refinement; H atoms located in $\Delta\rho$ map and included in refinement with isotropic thermal parameters; methyl group refined as rigid body with anisotropic C(17) and rotation angle around C(16)—C(17); $R = 0{\cdot}045$, $wR = 0{\cdot}053$, max. shift/e.s.d. = 0·005, $S = 5{\cdot}13$; largest peak in final $\Delta\rho$ map = 0·17 e Å^{-3}, largest hole = −0·19 e Å^{-3}; computer programs: *MULTAN*80 (Main *et al.*, 1980); *SHELX*76 (Sheldrick, 1976); and local programs (Jaskókski, 1982); molecular illustrations drawn using *PLUTO* (Motherwell & Clegg, 1978). Atomic scattering factors from *International Tables for X-ray Crystallography* (1974).

* To whom correspondence should be addressed.

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