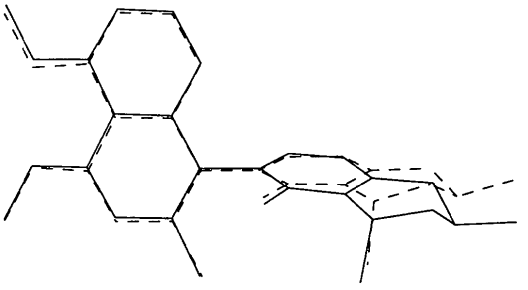

Fig. 3. Superimposed view of dioncophylline A molecules as determined by X-ray diffraction (full lines) and by energy minimization (dashed lines).

and torsion angles of dioncophylline A show no unusual features. The relative configuration at the three stereo-elements (two centres and the axis) is in full agreement with the stereostructure as established earlier (Bringmann, Jansen, Reuscher, Rübenacker, Peters & von Schnering, 1990). The absolute configuration, as shown in Fig. 2 was not determined here, but was adopted from our work mentioned above. The dihedral angle between the two aromatic parts of the biaryl system is 110·2°.

As the AM1 energy minimization calculation (Dewar, Zoebisch, Healy & Stewart, 1985) shows, the molecule in the crystal is close to one of the local energy minima, and hence there are no greater distortions in the molecule that might arise from intermolecular interactions (Fig. 3).

Financial support of this work by the Deutsche Forschungsgemeinschaft and by the Fonds der Chemischen Industrie is gratefully acknowledged. Furthermore we wish to thank Professor Dr U. Schubert, Institute of Inorganic Chemistry, Univ. of Würzburg, for enabling us to use the Enraf–Nonius diffractometer.

References

BRINGMANN, G. (1986). *The Naphthyl Isoquinoline Alkaloids* In *The Alkaloids*, Vol. 29, edited by A. BROSSI, pp. 141–184. New York: Academic Press.

BRINGMANN, G., GEUDER, T., RÜBENACKER, M. & ZAGST, R. (1991). *Phytochemistry*, **30**, 2067–2070.

BRINGMANN, G., JANSEN, J. R. & BUSSE, H. (1991). *Justus Liebigs Ann. Chem.* In the press.

BRINGMANN, G., JANSEN, J. R., REUSCHER, H., RÜBENACKER, M., PETERS, K. & VON SCHNERING, H. G. (1990). *Tetrahedron Lett.* **31**, 643–646.

BRINGMANN, G., LISCH, D., REUSCHER, H., AKÉ ASSI, L. & GÜNTHER, K. (1991). *Phytochemistry*, **30**, 1307–1310.

BRINGMANN, G., RÜBENACKER, M., JANSEN, J. R., GEUDER, T. & AKÉ ASSI, L. (1991). *Planta Med.* **56**, 495–496.

BRINGMANN, G., RÜBENACKER, M., JANSEN, J. R., SCHEUTZOW, D. & AKÉ ASSI, L. (1990). *Tetrahedron Lett.* **31**, 639–642.

BRUNETON, J., BOUQUET, A., FOURNET, A. & CAVÉ, A. (1976). *Phytochemistry*, **15**, 817–818.

COOPER, G. P. & RECORD, S. J. (1931). *Bull. Yale Univ. Sch. For.* **31**, 1–153.

DEWAR, M. J. S., ZOEBISCH, E. G., HEALY, E. & STEWART, J. J. P. (1985). *J. Am. Chem. Soc.* **107**, 3902–3909.

KELLER, E. (1988). *SCHAKAL88. A FORTRAN Program for the Graphic Representation of Molecular and Crystallographic Models.* Kristallographisches Institut der Universität, D-7800 Freiburg, Germany.

SHELDRICK, G. M. (1986). *SHELXS86.* Program for the automatic solution of crystal structures. Univ. of Göttingen, Germany.

Acta Cryst. (1991). C**47**, 1705–1707

Structure of L-Lysinamide Dihydrochloride. A New Conformation of the Lysine Side Chain

BY X. DE LA CRUZ, J. TORMO, I. FITA AND J. A. SUBIRANA

Departament d'Enginyeria Química, Universitat Politecnica de Catalunya, Diagonal 647, *E*-08028 *Barcelona, Spain*

(*Received* 30 *April* 1990; *accepted* 21 *December* 1990)

Abstract. L-Lysinamide dihydrochloride, $C_6H_{17}N_3O^{2+}.2Cl^-$, $M_r = 218{\cdot}14$, monoclinic, $C2$, $a = 19{\cdot}998\ (52)$, $b = 4{\cdot}942\ (26)$, $c = 15{\cdot}997\ (32)$ Å, $\beta = 138{\cdot}04\ (29)°$, $V = 1057{\cdot}1$ Å^3, $Z = 4$, $D_x = 1{\cdot}371$ g cm^{-3}, λ(Mo $K\alpha$) = 0·71069 Å, $\mu = 5{\cdot}9$ cm^{-1}, $F(000) = 464$, room temperature, $R = 0{\cdot}067$ for 599 observed reflections. No head-to-tail hydrogen bonds between terminal N and C groups are observed in the structure. All suitable H atoms are involved in at least one hydrogen bond. The lysine side chain conformation (g^-tg^-t) has not been previously observed.

Introduction. Amino acid derivatives and small peptide structures contain detailed information which is useful in protein conformation studies. The structure determination of L-lysinamide dihydrochloride is part of a project that involves the struc-

0108-2701/91/081705-03$03.00

tural analysis of oligopeptides with sequences containing basic amino acids (Urpí, Coll & Subirana, 1988; Urpí, Coll, Subirana, Solans & Font-Altaba, 1988; Verdaguer, Urpí, Fita & Subirana, 1988).

Experimental. The title compound was supplied by Bachem AG and used without further purification. It was crystallized by vapour diffusion of ethanol into an aqueous ethanolic solution of the peptide. Plate-like crystals appeared after 1 d. A crystal, 0·4 × 0·4 × 0·6 mm, was mounted in a capillary; data were recorded on a Philips PW1100 diffractometer, Mo $K\alpha$ radiation, graphite monochromator. Cell parameters from 25 reflections ($4 < \theta < 9°$), ω-scan technique, three reflections measured every 2 h as intensity control, no significant differences, Lp corrections applied but no absorption correction. 875 independent reflections ($\theta < 33°$), 616 with $I > 3\sigma(I)$ (index range h −22 to 15, k 5 to 0, l 0 to 9). 17 reflections with orientation errors and asymmetric background were omitted in the final calculation. Structure determined by direct methods, *SHELXS*86 (Sheldrick, 1985). Anisotropic full-matrix least-squares refinement on F with *SHELX*76 (Sheldrick, 1976). f,f',f'' for all atoms from *International Tables for X-ray Crystallography* (1974, Vol. IV). The known L configuration had to be imposed on the model. The y coordinate of the Cl(1) atom was fixed to define the origin. Only H atoms on the amide group were visible in a difference Fourier map. All the remaining H atoms were included at calculated positions and refined with geometrical constraints and isotropic temperature factors. A constant weighting scheme was applied, final $R = 6·7\%$, max. shift/e.s.d. = 0·487, max. and min. heights in final difference Fourier synthesis: 0·50 and −0·54 e Å^{-3}. 126 parameters were refined. Calculations on a MicroVAX 2000 computer.

Discussion. One lysinamide and two chloride ions are found in the asymmetric unit. The molecular structure with the atomic numbering is shown in Fig. 1. The final positional and thermal parameters are listed in Table 1* and bond lengths, bond angles and conformation angles (IUPAC–IUB Commission on Biochemical Nomenclature, 1970) in Table 2.

(*a*) *Lysine conformation.* The global conformation of the lysine side chain (g^-tg^-t) has not been found before in peptide crystal structures (Boqué, Verdaguer, Urpí, Fita & Subirana, 1989). The χ_1, χ_2, χ_4 torsion angle values shown by this molecule correspond to the most frequently observed conformation in peptide crystals which contain lysine (Perelló, 1990). The χ_3 (g^-) value has not been previously found for lysine in peptide structures, though g- is one of the three conformations observed in residues with no branching in Cβ (Benedetti, Morelli, Nemethy & Scheraga, 1983). Packing forces and interactions between the peptide and the two chloride ions in the crystal could stabilize this unusual side chain conformation.

The two N atoms in the backbone, N(1) and N(2), are in a *trans* configuration (169°) which could arise from a weak intramolecular hydrogen-bond interaction between N(1) and the terminal oxygen atom with an N(1)···O distance of 2·64 Å and an N(1)—HN(11)···O angle of 102° (Table 2). The charge balance requires N(1) and N(3) to be protonated.

(*b*) *Packing.* All suitable H atoms appear to be involved in at least one hydrogen bond (Table 2). It can be seen (Fig. 2) that hydrogen bonds predominate in those parts of the crystal where the charged and hydrophilic atoms cluster. These zones alternate with hydrophobic regions formed by the aliphatic portions of the lysine side chains arranged in an antiparallel way (Fig. 2).

No head-to-tail hydrogen bonds between N and C terminal groups, as is frequently found in peptide crystals, are observed in this structure (Suresh & Vijayan, 1983; Coll, Subirana, Solans, Font-Altaba & Mayer, 1987). The only peptide–peptide hydrogen bonds present (Table 2, Fig. 2) are between O and N of the molecules related by a translation along the b axis, and also between molecules related by the diad axis. All the remaining intermolecular hydrogen bonds appear to be mediated by the chloride ions which thus have a strong ionic character. The closest distance between two chloride Cl(1) ions is 3·8 Å, only slightly larger than the sum of their ionic radii (Pauling, 1960).

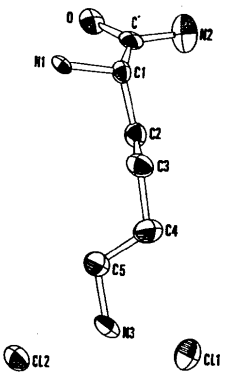

Fig. 1. Molecular structure drawn with *ORTEP* (Johnson, 1965) and atom numbering. Thermal ellipsoids of 50% probability are shown. H atoms are not explicitly indicated.

* Lists of structure factors, anisotropic thermal parameters, intra- and intermolecular bond lengths and angles and H-atom parameters have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 53863 (24 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 1. *Fractional atomic coordinates with e.s.d.'s in parentheses and equivalent isotropic thermal parameters* (Å^2)

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

	x	y	z	B_{eq}
Cl(1)	0·1351 (2)	−0·4097	0·0879 (3)	3·67
Cl(2)	0·3530 (2)	−0·3549 (11)	0·4729 (3)	3·10
O	0·6591 (6)	0·6388 (24)	0·3249 (8)	2·89
C′	0·5853 (9)	0·5026 (31)	0·2355 (14)	2·36
N(1)	0·6470 (6)	0·1671 (22)	0·3904 (9)	1·66
N(2)	0·5244 (11)	0·5816 (29)	0·1174 (13)	3·92
C(1)	0·5600 (8)	0·2421 (29)	0·2554 (12)	1·96
C(2)	0·4650 (9)	0·2715 (32)	0·2196 (15)	2·58
C(3)	0·4227 (10)	−0·0052 (32)	0·2077 (16)	2·99
C(4)	0·3339 (10)	0·0274 (39)	0·1849 (16)	3·67
C(5)	0·3616 (10)	0·1059 (48)	0·2981 (15)	3·66
N(3)	0·2734 (7)	0·1141 (36)	0·2706 (10)	3·38

Table 2. *Bond distances* (Å), *bond angles* (°) *and conformational angles* (°) *with e.s.d.'s in parentheses*

C′—O	1·240 (15)	C(3)—C(2)	1·544 (20)
C′—N(2)	1·336 (20)	C(4)—C(3)	1·533 (20)
C(1)—C′	1·500 (21)	C(5)—C(4)	1·499 (20)
C(1)—N(1)	1·496 (15)	N(3)—C(5)	1·465 (16)
C(2)—C(1)	1·530 (17)		

N(2)—C′—O	121·5 (15)	N(1)—C(1)—C(2)	110·5 (12)
C(1)—C′—O	121·4 (14)	C(1)—C(2)—C(3)	112·1 (12)
C(1)—C′—N(2)	117·0 (13)	C(2)—C(3)—C(4)	111·6 (13)
C′—C(1)—N(1)	107·7 (10)	C(3)—C(4)—C(5)	114·7 (13)
C′—C(1)—C(2)	111·1 (11)	C(4)—C(5)—N(3)	111·3 (12)

O—C′—C(1)—N(1)	−11·0 (24)	N(1)—C(1)—C(2)—C(3)	−74·6 (19)χ_1
O—C′—C(1)—C(2)	110·2 (21)	C(1)—C(2)—C(3)—C(4)	174·3 (17)χ_2
N(2)—C′—C(1)—N(1)	169·3 (19)	C(2)—C(3)—C(4)—C(5)	−75·7 (22)χ_3
N(2)—C′—C(1)—C(2)	−69·5 (24)	C(3)—C(4)—C(5)—N(3)	−176·0 (15)χ_4
C′—C(1)—C(2)—C(3)	165·9 (16)		

A—H···*B*	*A*···*B*	H···*B*	*A*—H···*B*
N(1)—HN(11)···Cl(2^{i})	3·381 (15)	2·33	159 (1)
N(1)—HN(12)···Cl(2^{ii})	3·219 (15)	2·15	164 (1)
N(1)—HN(13)···Cl(2^{iii})	3·261 (15)	2·18	172 (1)
N(1)—HN(11)···O^{iv}	2·890 (17)	2·46	101 (1)
N(2)—HN(21)···Cl(1^{v})	3·605 (23)	2·98	121 (2)
N(2)—HN(21)···Cl(1^{vi})	3·421 (13)	2·77	123 (2)
N(2)—HN(22)···Cl(1^{vii})	3·357 (13)	2·40	167 (3)
N(3)—HN(32)···Cl(1^{iv})	3·297 (15)	2·30	150
N(3)—HN(33)···Cl(1)	3·116 (14)	2·03	168 (1)
N(3)—HN(31)···Cl(2)	3·497 (17)	2·67	131
N(3)—HN(32)···Cl(2^{iv})	3·274 (17)	2·87	102
N(3)—HN(31)···O^{viii}	2·991 (25)	2·36	114

Symmetry code: (i) $1-x, y-1, 1-z$; (ii) $1-x, y, 1-z$; (iii) $0{\cdot}5+x, y-0{\cdot}5, z$; (iv) $x, y-1, z$; (v) $0{\cdot}5+x, 0{\cdot}5+y, z$; (vi) $0{\cdot}5-x, 0{\cdot}5+y, -z$; (vii) $0{\cdot}5-x, y-0{\cdot}5, -z$; (viii) $x-0{\cdot}5, y-0{\cdot}5, z$.

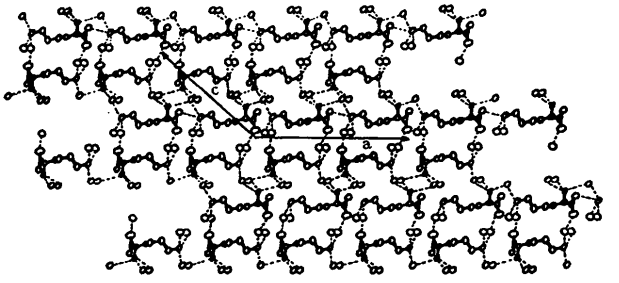

Fig. 2. Projection onto the *ac* plane showing the crystal packing. Hydrogen bonds are indicated by broken lines. The *a* and *c* cell axes are also shown. The amino groups interact with several chloride ions, some of which are superimposed in the figure.

This work has been supported by the Plan Nacional de Biotecnología (BT87-0009). The X-ray diffraction data were collected at the Jaume Almera Institute (CSIC) and we are most grateful to Dr E. Molins for the facilities offered to us.

References

BENEDETTI, E., MORELLI, G., NEMETHY, G. & SCHERAGA, H. A. (1983). *Int. J. Pept. Protein Res.* **22**, 1–15.

BOQUÉ, LL., VERDAGUER, N., URPÍ, L., FITA, I. & SUBIRANA, J. A. (1989). *Int. J. Pept. Protein Res.* **33**, 157–161.

COLL, M., SUBIRANA, J. A., SOLANS, X., FONT-ALTABA, M. & MAYER, R. (1987). *Int. J. Pept. Protein Res.* **23**, 242–247.

IUPAC-IUB COMMISSION ON BIOCHEMICAL NOMENCLATURE (1970). *Biochemistry*, **9**, 3471–3479.

JOHNSON, C. K. (1965). *ORTEP*. Report ORNL-3794. Oak Ridge National Laboratory, Tennessee, USA.

PAULING, L. C. (1960). *The Nature of the Chemical Bond*, 3rd ed. Ithaca: Cornell Univ. Press.

PERELLÓ, M. (1990). PhD Thesis, Universitat Politècnica de Catalunya, Spain.

SHELDRICK, G. M. (1976). *SHELX*76. Program for crystal structure determination. Univ. of Cambridge, England.

SHELDRICK, G. M. (1985). *SHELXS*86. In *Crystallographic Computing* 3, edited by G. M. SHELDRICK, C. KRUGER & R. GODDARD. pp. 175–189. Oxford Univ. Press.

SURESH, C. G. & VIJAYAN, M. (1983). *Int. J. Pept. Protein Res.* **22**, 617–621.

URPÍ, L., COLL, M. & SUBIRANA, J. A. (1988). *Int. J. Biol. Macromol.* **10**, 55–59.

URPÍ, L., COLL, M., SUBIRANA, J. A., SOLANS, X. & FONT-ALTABA, M. (1988). *Acta Cryst.* C**44**, 281–285.

VERDAGUER, N., URPÍ, L., FITA, I. & SUBIRANA, J. A. (1988). *Biopolymers*, **27**, 1887–1896.