

Precision Neutron Diffraction Structure Determination of Protein and Nucleic Acid Components. VII. The Crystal and Molecular Structure of the Amino Acid L-Lysine Monohydrochloride Dihydrate*

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A neutron diffraction study of L-lysine monohydrochloride dihydrate, $C_6H_{15}N_2O_2 \cdot Cl \cdot 2H_2O$, has been carried out. The structure is monoclinic, space group $P2_1$, with $Z=2$. Cell parameters are: $a=7.492$ (1), $b=13.320$ (4), $c=5.879$ (1) Å, $\beta=97.79$ (1)° [Wright & Marsh, *Acta Cryst.* (1962), **15**, 54]. Least-squares refinements based on 1240 reflections led to a conventional R value of 0.030. The neutron-diffraction results confirm the structure previously determined by X-ray diffraction [Raman *Z. Kristallogr.* (1959), **111**, 301; Wright & Marsh (1962)]; the main new feature is the precise determination of the hydrogen atom positions. The refined thermal parameters were fitted to rigid-body motions; these calculations indicate axial librations of 8.8 (5) and 12.7 (4)° for the $\alpha-NH_3^+$ and $\zeta-NH_3^+$ groups respectively. Assuming a threefold cosine potential, these librational amplitudes lead to estimated barriers to rotation of 7.0 kcal.mole⁻¹ for the $\alpha-NH_3^+$ group and 2.9 kcal.mole⁻¹ for the $\zeta-NH_3^+$ group.

The neutron diffraction study of L-lysine monohydrochloride dihydrate described here was performed to provide detailed information about the hydrogen atom stereochemistry in this crystalline amino acid. This paper describes one of a series of investigations of amino acid crystal structures, which should provide precise hydrogen bonding parameters for these systems, and which ultimately aims to arrive at a better understanding of the role of hydrogen bonding in larger, more complicated structures. Since completing this work, we have learned of a similar independent study by Bugayong, Sequeira & Chidambaram (1972).

Crystal data

L-Lysine monohydrochloride dihydrate, $NH_3^+[CH_2]_4CH(NH_3)^+COO^- \cdot Cl^- \cdot 2H_2O$, monoclinic, $P2_1$, $Z=2$. An earlier X-ray study (Wright & Marsh, 1962) established the cell dimensions: $a=7.492$ (1), $b=13.320$ (4), $c=5.879$ (1) Å and $\beta=97.79$ (1)°. The density calculated from this unit cell is 1.25 g.cm⁻³ (Wright & Marsh, 1963).

Experimental

Large, well-formed, single crystals of L-lysine monohydrochloride dihydrate were grown by slow evapora-

tion from aqueous 1 M NH_4Cl at pH 5.4. A crystal weighing 23.6 mg, elongated in the c direction and bounded by major faces $\{110\}$ and $\{001\}$, was mounted on a four-circle diffractometer at the Brookhaven High Flux Beam Reactor. In order to minimize multiple diffraction effects, the c^* axis of the crystal was aligned approximately five degrees off the diffractometer φ axis. The unit-cell parameters and orientation matrix were refined by least-squares calculations using as input the setting angles of 29 automatically centered reflections well distributed in reciprocal space. The cell parameters so obtained agree with the more precise X-ray values to better than two parts per thousand, and the latter have been used throughout this paper.

Data were collected automatically using the Brookhaven Multi-Spectrometer Control System (Beaucage, Kelley, Ophir, Rankowitz, Spinrad & van Norton, 1966) with a crystal-monochromatized $\{Ge(111)\}$ neutron beam of wavelength 1.014 (1) Å. The length of the standard $\theta-2\theta$ step scan was varied according to the formula $\Delta(2\theta)=1.4^\circ(1+8 \tan \theta)$, and the step increment was chosen to give approximately 40 points in each scan. Intensities were measured for 3313 reflections with l positive and $d^* \leq 1.34$ Å⁻¹.

Background corrections were made by use of a method which divides peak and background in such a way that $\sigma_{\text{count}}(I)/I$ is minimized (Lehmann, Hamilton & Larsen, 1972). Here I is the integrated intensity and $\sigma_{\text{count}}(I)$ its estimated standard deviation (e.s.d.) based on counting statistics. An absorption correction was carried out by integration over a Gaussian grid. The neutron-absorption coefficient $\mu=2.69$ cm⁻¹ was calculated from tabulated mass-absorption coefficients (*International Tables for X-ray Crystallography*, 1961), assuming an incoherent neutron cross-section for hydrogen of 40 barns. Squared observed structure factors were obtained as $F_o^2 = I_{\text{corrected}} \sin 2\theta$, and were averaged over space-group symmetry to give mean values for 1484

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Table 1 for those reflections included in the refinement, and the refined atomic coordinates and thermal parameters are listed in Table 2.

Both water molecules in the crystal structure have high thermal parameters. The value of u_{11} is 0.152 (4) Å² for O^{w1} and 0.113 (3) Å² for O^{w2}. It seems possible that these high thermal parameters partially reflect a tendency of the crystals to lose water, but this conjecture could not be proved on the basis of the neutron-diffraction data. Attempts were made to refine occupancy factors along with position and thermal parameters for the atoms of the water molecules, leaving the parameters for the other atoms in the structure fixed. The resulting occupancies did not differ significantly from unity.

The molecular structure

The lysine molecule, which is drawn in Fig. 1, is a singly charged zwitterion with the extra positive charge carried by the terminal ammonium group, as was found to be the case in two prior X-ray studies (Raman, 1959; Wright & Marsh, 1962). Molecular bond distances and angles are not tabulated here, as Bugayong, Sequeira & Chidambaram (1972) have presented a detailed comparison of our bonding parameters with the results of their parallel neutron diffraction study and with the

X-ray results of Wright & Marsh. Torsion angles defined according to the latest IUPAC conventions (IUPAC-IUB Commission on Biochemical Nomenclature, 1970) are given in Table 3.

Table 3. Torsion angles

IUPAC-IUB designation	Atoms involved	Angle
ϕ^1	H ¹ -N-C ^α -C	- 49.2 (3) ^o
ϕ^2	H ² -N-C ^α -C	71.6 (3)
ϕ^3	H ³ -N-C ^α -C	- 166.4 (3)
ψ^1	O ¹ -C-C ^α -N	- 19.2 (3)
ψ^2	O ² -C-C ^α -N	162.7 (2)
χ^1	N-C ^α -C ^β -C ^γ	- 56.4 (2)
χ^2	C ^α -C ^β -C ^γ -C ^δ	- 176.0 (1)
χ^3	C ^β -C ^γ -C ^δ -C ^ε	- 171.1 (2)
χ^4	C ^γ -C ^δ -C ^ε -N ^ζ	179.2 (2)
$\chi^{3,1}$	C ^δ -C ^ε -N ^ζ -H ^{ζ1}	- 51.4 (4)
$\chi^{5,2}$	C ^δ -C ^ε -N ^ζ -H ^{ζ2}	72.0 (4)
$\chi^{3,3}$	C ^δ -C ^ε -N ^ζ -H ^{ζ3}	- 169.5 (3)

Molecular packing and hydrogen bonding

There are ten hydrogen bonds per asymmetric unit of the crystal structure, one involving each hydrogen atom covalently bonded to nitrogen or oxygen. The packing scheme, which is shown in Fig. 2, consists of chains of lysine cations inclined approximately 30° to the **b** axis

Table 2. Final atomic coordinates ($\times 10^5$) and thermal parameters ($\times 10^4$)

The temperature factor is of the form $\exp[-2\pi^2(u_{11}h^2a^{*2} + u_{22}k^2b^{*2} + u_{33}l^2c^{*2} + 2u_{12}hka^*b^* + 2u_{13}hla^*c^* + 2u_{23}kbc^*)]$.

The atom designations are: CA ≡ C^α, CB ≡ C^β, CG ≡ C^γ, CD ≡ C^δ, CE ≡ C^ε, and NZ = N^ζ. Because of the widespread and standard atomic nomenclature in amino acids and peptides, we choose to use this notation rather than the prescribed C(1), C(2) ... suggested in the *Acta Cryst. Notes for Authors*. The numbering used by Wright & Marsh is given alongside the standard IUPAC designation.

	X	Y	Z	U11	U22	U33	U12	U13	U23
C ^α	20686(17)	50030	- 11335(24)	344(6)	420(7)	365(7)	27(5)	84(5)	56(6)
C	25000(20)	7646(16)	- 24918(28)	255(6)	295(8)	220(7)	-6(6)	22(5)	30(7)
C ^α	30402(20)	3407(17)	- 677(27)	219(6)	287(8)	209(7)	0(6)	32(5)	29(7)
C ^β	27275(26)	- 7906(17)	- 1032(33)	391(9)	272(9)	298(9)	26(7)	59(8)	20(8)
C ^γ	31367(28)	- 12933(17)	22497(36)	462(10)	294(10)	334(10)	-11(7)	35(8)	49(8)
C ^δ	29230(27)	- 24274(18)	20678(36)	499(10)	300(10)	329(10)	12(8)	98(9)	44(8)
C ^ε	30368(26)	- 29240(17)	43995(36)	386(9)	318(10)	320(10)	-9(7)	42(8)	36(8)
N	19806(16)	- 8541(14)	15524(22)	327(6)	325(7)	232(6)	17(5)	59(4)	-2(6)
N ^ζ	27970(18)	- 40272(13)	41498(24)	359(6)	330(8)	327(7)	-30(5)	40(5)	82(6)
O ¹	10390(28)	12151(21)	- 28916(39)	303(9)	496(14)	329(10)	95(8)	21(8)	125(10)
O ²	35738(26)	5943(19)	- 39049(35)	332(9)	495(13)	234(9)	2(9)	75(7)	18(10)
O ^{w1}	12580(78)	31597(37)	53331(82)	1515(40)	517(22)	655(25)	-163(26)	296(27)	6(22)
O ^{w2}	29787(63)	28991(29)	15924(85)	1127(29)	406(19)	647(23)	-23(18)	193(22)	65(19)
H ¹	20534(61)	16220(33)	13171(75)	672(25)	363(23)	420(21)	38(18)	156(19)	22(19)
H ²	6545(47)	6320(36)	12965(70)	344(17)	622(27)	454(20)	37(16)	107(15)	-78(20)
H ³	25067(52)	7215(33)	32909(62)	504(17)	467(20)	282(18)	38(17)	98(14)	28(17)
H ^α	44600(40)	5000(32)	4781(65)	281(14)	574(23)	392(17)	-18(14)	-4(12)	58(18)
H ^{β1}	13281(62)	- 9487(35)	- 7935(90)	615(25)	487(24)	597(27)	-159(20)	-130(20)	57(23)
H ^{β2}	36147(82)	- 11086(37)	- 12557(87)	919(34)	483(25)	484(24)	179(24)	313(23)	75(23)
H ^{γ1}	45150(75)	- 11077(45)	30426(105)	729(30)	639(30)	735(35)	-178(23)	-225(25)	211(30)
H ^{γ2}	22421(92)	- 10157(40)	34200(95)	1100(42)	521(29)	442(25)	80(26)	310(27)	5(24)
H ^{δ1}	16204(81)	- 26083(44)	10996(104)	889(32)	522(27)	588(29)	-201(25)	-247(25)	103(25)
H ^{δ2}	39685(91)	- 27369(40)	11413(103)	1110(42)	486(24)	705(34)	251(28)	506(34)	152(28)
H ^{ε1}	43249(67)	- 27858(42)	54261(98)	691(28)	617(27)	644(29)	-170(23)	-203(22)	110(29)
H ^{ε2}	19526(77)	- 26559(41)	53045(98)	873(33)	568(29)	612(30)	235(27)	331(27)	87(28)
H ^{ζ1}	16646(73)	- 41814(46)	30492(105)	830(31)	563(29)	721(33)	-283(27)	-345(27)	158(29)
H ^{ζ2}	39199(74)	- 43356(36)	36130(95)	797(30)	447(24)	629(29)	25(22)	358(25)	15(23)
H ^{ζ3}	26378(58)	- 43609(33)	56821(75)	586(20)	467(24)	451(21)	-29(17)	174(17)	139(20)
H ^{w1}	12653(87)	25262(49)	61130(132)	835(33)	617(36)	872(42)	17(28)	241(32)	140(36)
H ^{w2}	14675(113)	36655(52)	64829(136)	1204(49)	600(36)	730(39)	-30(35)	259(37)	-23(37)
H ^{w21}	24346(102)	30833(46)	29135(130)	1132(44)	472(30)	623(36)	-68(31)	80(33)	-12(38)
H ^{w22}	27647(103)	34630(54)	6455(122)	1215(50)	565(36)	708(39)	-32(33)	86(36)	191(35)

and interconnected through the water molecules and chloride ions. Hydrogen bond distances and angles are summarized in Table 4.

The three hydrogen atoms of the α -ammonium group are donated respectively to the second water molecule, to the chloride ion, and to the carboxyl oxygen O^2 belonging to a neighboring lysine molecule. The $N-H^1 \cdots O^{w2}$ hydrogen bond, which is somewhat bent, forms part of the sequence $N-H^1 \cdots O^{w2}-H^{w22} \cdots Cl \cdots H^{\zeta 3}$ which binds the infinite chains of lysine molecules in the structure together. The hydrogen bond $N-H^3 \cdots O^2$, with an $H^3 \cdots O^2$ distance of 1.740 (5) Å, is the strongest $N-H \cdots O$ bond in the structure. Significantly, the $N-H^3$ bond distance is 1.059 (4) Å, making this bond more than 0.02 Å longer than each of the five other $N-H$ bonds in the lysine molecule. In general, $N-H$ distances are quite sensitive to the strengths of the hydrogen bonds which may be formed; we have observed a very good inverse correlation between $N-H$ and $H \cdots B$ bond lengths in amino acids. For example, in *L*-alanine the short $N-H^2 \cdots O^2$ bond has $N-H$ and $H \cdots O$ distances of 1.047 (2) and 1.780 (2) Å respectively (Lehmann, Koetzle & Hamilton, 1972).

There is no evidence for the formation of an intramolecular hydrogen bond. The $\alpha-NH_3^+$ group is rotated in such a way as to produce an approximately staggered configuration with respect to the carboxyl group; the distances from O^1 to H^1 and H^2 are 2.546 (5) and 2.635 (5) Å respectively.

Besides forming a hydrogen bond to O^1 , atom $H^{\zeta 1}$ of the ζ -ammonium group possesses a short van der Waals contact $N-H^{\zeta 1} \cdots Cl$. Here the $H^{\zeta 1} \cdots Cl$ distance is

2.741 (7) Å, while the angle $N^{\zeta}-H^{\zeta 1} \cdots Cl$ is 117.9 (5)°. We believe this contact should not be classified as a hydrogen bond, although the weak interaction present may explain why the $N^{\zeta}-H^{\zeta 1} \cdots O^1$ bond is found to be severely bent as well as being by far the longest $N-H \cdots O$ hydrogen bond in the structure. In fact, the chloride ion is slightly closer to H^{α} from a nearby lysine molecule than it is to $H^{\zeta 1}$ [the $Cl \cdots H^{\alpha}$ distance involved is 2.660 (3) Å]. A large number of short intermolecular and intramolecular contacts found in this and other amino acids implies that a van der Waals radius for hydrogen of 1.0 Å, as proposed by Baur (1972), may be more appropriate than the 1.2 Å previously assumed (Pauling, 1960). If this is the case, then the two short $Cl \cdots H$ distances found here are only slightly less than the value of 2.8 Å expected for a normal van der Waals contact.

The two water molecules each accept a single hydrogen bond. One of these bonds $O^{w2}-H^{w21} \cdots O^{w1}$ connects the water molecules to one another and lies nearly along a lone pair of O^{w1} . By contrast, the $N-H^1 \cdots O^{w2}$ hydrogen bond does not fall along an oxygen lone pair, and O^{w2} with its three neighboring hydrogens forms a distorted trigonal pyramid. Water molecules of this type possessing irregular hydrogen-bonding patterns do not seem to be particularly unusual in crystalline hydrates (Donohue, 1968).

The chloride ion is surrounded by a distorted octahedron of hydrogen atoms. In addition to accepting four hydrogen bonds, Cl^- possesses the two short van der Waals contacts with H^{α} and $H^{\zeta 1}$ discussed above. There are no additional abnormally short non-bonded contacts in the structure.

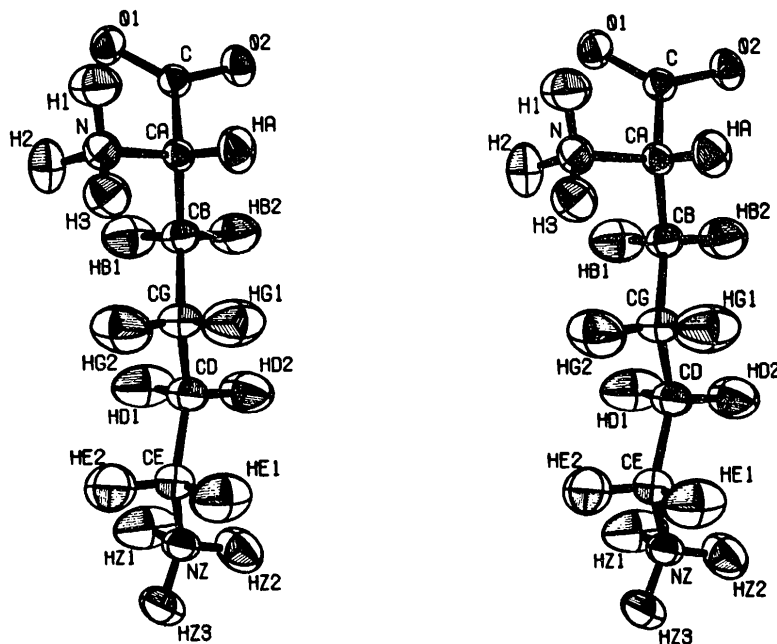


Fig. 1. Stereoscopic view of the lysine molecule with thermal ellipsoids drawn to enclose 50% probability.

Thermal motion

The non-hydrogen atoms of the lysine molecule undergo thermal motion which is of quite low amplitude and is also fairly isotropic, as can be seen from Fig. 1. Only for the carboxyl oxygen atoms is the mean square amplitude in the direction of the long principal axis of thermal motion more than twice that along the short principal axis. For both O^1 and O^2 , the long axis is nearly perpendicular to the C-O bond, as might be expected. The hydrogen atoms undergo larger and more anisotropic thermal motions than do the nonhydrogen atoms, and with the exception of the α -ammonium group hydrogens, the entire lysine chain appears to be librating principally about its long axis.

It seemed that the quality of the data here and the relatively small thermal motion amplitudes justified a

closer analysis of the thermal motion than would usually be the case, in order that the results might be used to decide upon the best method of treatment in our other amino acid studies. Attempts were made to fit the atomic thermal parameters u_{ij} to the motions of a rigid body described in terms of **T**, **L**, and **S** tensors (Schomaker & Trueblood, 1968). In calculation I, only the nonhydrogen backbone has been included in the rigid body, and the r.m.s. value of Δu_{ij} , the difference between observed and calculated thermal parameters, is $\Delta u_{ij}^{2/2} = 0.004 \text{ \AA}^2$. This value may be compared with 0.001 \AA^2 , the precision with which the u_{ij} for nonhydrogen atoms are determined from the least-squares refinement. The effective screw translations are found to be small, and the largest principal axis of **L** has an amplitude of $0.0037 (27) \text{ rad}^2$, corresponding to a libration of $3.5 (12)^\circ$ about an axis inclined approximately

Table 4. *Hydrogen bond distances (Å) and angles (°)*

A-H...B-C	A-H	A...B	H...B	\angle A-H...B	\angle H...B-C
N-H ¹ ...O ^{w2} <div style="margin-left: 100px;"> $\begin{matrix} & & H^{w2} \\ & & / \\ & & O^{w2} \\ & & \backslash \\ & & H^{w22} \end{matrix}$ </div>	1.034 (4)	2.824 (4)	1.836 (6)	158.5 (4)	96.4 (4) 131.2 (6)
N-H ² ...Cl ⁻	1.028 (4)	3.217 (2)	2.196 (4)	172.0 (4)	
N-H ³ ...O ² -C	1.059 (4)	2.795 (3)	1.740 (5)	173.4 (4)	110.9 (2)
N ^c -H ^{c1} ...O-C	1.016 (5)	2.887 (3)	2.083 (6)	134.4 (6)	135.4 (2)
N ^c -H ^{c2} ...O ² -C	1.024 (5)	2.788 (2)	1.865 (6)	148.3 (5)	131.2 (2)
N ^c -H ^{c1} ...Cl ⁻	1.026 (4)	3.173 (2)	2.150 (5)	174.8 (4)	
O ^{w1} -H ^{w11} ...O ¹ -C	0.960 (9)	2.805 (5)	1.857 (7)	169.2 (7)	113.5 (2)
O ^{w1} -H ^{w12} ...Cl ⁻	0.953 (11)	3.220 (5)	2.273 (8)	172.7 (6)	
O ^{w2} -H ^{w21} ...O ^{w1} <div style="margin-left: 100px;"> $\begin{matrix} & & H^{w11} \\ & & / \\ & & O^{w1} \\ & & \backslash \\ & & H^{w12} \end{matrix}$ </div>	0.957 (11)	2.718 (6)	1.775 (9)	167.9 (6)	111.2 (6) 123.9 (6)
O ^{w2} -H ^{w22} ...Cl ⁻	0.936 (9)	3.254 (4)	2.329 (7)	169.7 (6)	

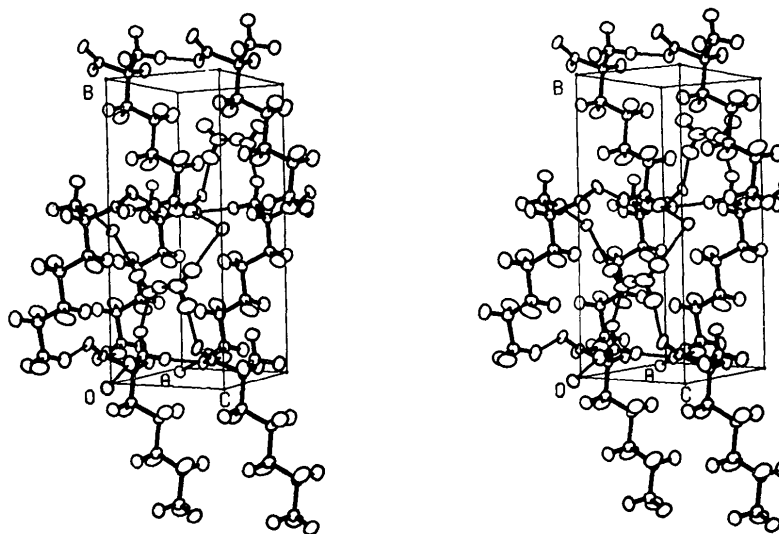


Fig. 2. Stereoscopic view of the packing around one unit cell with thermal ellipsoids drawn to enclose 30% probability. Molecular bonds are drawn thick and hydrogen bonds thin.

30° to the long axis of the lysine molecule. The remaining two principal axes of **L** have amplitudes which are within 0.0008 rad² of zero.

Calculation II was carried out including in the rigid body the entire lysine molecule except H¹, H² and H³ of the α -NH₃⁺ group. In this case $\overline{\Delta u_{ij}^2}^{1/2} = 0.011 \text{ \AA}^2$, implying a considerably worse fit than for the backbone alone. Part of the increase in $\overline{\Delta u_{ij}^2}^{1/2}$ compared with the value found in calculation I is explained by the precision of the hydrogen atom u_{ij} 's which range from 0.002 to 0.004 Å², but there is undoubtedly a significant amount of non-rigid-body motion involving the hydrogen atoms. Because of this the magnitude of the rigid-body motions has probably been overestimated whenever hydrogen atoms have been included in the rigid body. This calculation II led to a libration of 0.0271 (23) rad² or 9.4 (4)° about the long molecular axis, and essentially zero librations normal to this axis. The screw components were quite small as was the case for those found in calculation I.

In order to obtain the best possible fit to the thermal parameters of the NH₃⁺ groups (and thus possibly the best corrections to bond lengths), separate rigid-body calculations III were carried out for each of these groups. In the case of the α -NH₃⁺ group, the rigid body consisted of C^α, N, H¹, H², and H³, while for the ζ -NH₃⁺ group, the rigid body was made up of C^ε, N^ε, H^{ε1}, H^{ε2}, and H^{ε3}. No constraints based upon symmetry were imposed on the motion of either group. In both cases, the fit proved to be extremely good. The value of $\overline{\Delta u_{ij}^2}^{1/2}$ for each group is 0.002 Å², which compares well with the precision of the individual u_{ij} . The largest principal axis of **L** has an amplitude of 0.0238 (30) rad² for the α -NH₃⁺ group and 0.0493 (28) rad² for the ζ -NH₃⁺ group, corresponding to librations of 8.8 (5)° and 12.7 (4)° about the C^α-N and C^ε-N^ε bonds, respectively. The ζ -NH₃⁺ group, which contains the weakly hydrogen-bonded atom H^{ε1}, is expected to undergo a larger axial libration than the α -NH₃⁺ group in which all three hydrogens form strong hydrogen bonds. Estimates of the librational frequencies ν and the heights of the barrier to rotation V_0 have been obtained for the ammonium groups, assuming a harmonic oscillator approximation to a threefold cosine hindered rotor (Schlemper, Hamilton & La Placa, 1971). For the α -NH₃⁺ group, $\nu = 361 \text{ cm}^{-1}$ and $V_0 = 7.0 \text{ kcal.mole}^{-1}$, while for the ζ -NH₃⁺ group, the corresponding values are 233 cm⁻¹ and 2.9 kcal.mole⁻¹. The precision of these frequencies and barrier heights is of the order of 10 to 20%.

Additional rigid-body calculations IV were carried out of the ammonium groups, constraining the motion to have threefold (3) symmetry. In these treatments, the contribution of the rigid-body motion of the lysine backbone was subtracted from the u_{ij} for the hydrogen atoms of each ammonium group. The resulting values of Δu_{ij} were then used to determine appropriately constrained **T**, **L**, and **S** tensors. As might be expected, the fit was not nearly so good as was the case in the uncon-

strained calculations III; here values of $\overline{\Delta u_{ij}^2}^{1/2}$ are 0.007 Å² for the α -NH₃⁺ group and 0.020 Å² for the ζ -NH₃⁺ group. The calculated librational amplitudes about the C-N axis are 0.0301 (66) rad² or 9.9 (11)° for the α -NH₃⁺ group and 0.0595 (206) rad² or 14.0 (24)° for the ζ -NH₃⁺ group. These values agree within one e.s.d. with the more precise results of calculation III.

The thermal motion of the four CH₂ groups and of the two water molecules was treated in a final set of rigid-body calculations V. In a modification of procedures used to analyse the rigid-body motions in ice IX (Hamilton, La Placa, Kamb & Prakash, 1972) the u_{ij} for the three atoms in each group were fitted to a general translation given by **T**, and to a rocking libration about an axis normal to the plane of the group. The origin was fixed at the carbon or oxygen atom. The agreement was quite good for these highly constrained calculations, except in the case of the first water molecule where $\overline{\Delta u_{ij}^2}^{1/2} = 0.012 \text{ \AA}^2$. Values of $\overline{\Delta u_{ij}^2}^{1/2}$ for the CH₂ groups and for the second water molecule fall between 0.005 and 0.008 Å². The calculated amplitudes of rocking libration are roughly the same for all four CH₂ groups and are in the range 12.7 (10) to 15.3 (10)°, thus supporting the observation that the entire lysine chain librates about its long axis in an approximately rigid fashion.

Corrections to molecular bond lengths and angles have been derived in the usual way from the rigid-body librations found in calculations I-V. The very small corrections for the lysine nonhydrogen atom framework were obtained from the results of calculation I and are less than 0.003 Å for distances and 0.2° for angles. It did not seem worthwhile tabulating the corrected parameters here.

Because of the non-rigid-body character possessed by the thermal motion of the hydrogen atoms, it is difficult to appropriately correct the bond lengths and angles involving hydrogen atoms for the effects of thermal motion. In any event, the corrections which need to be applied to the C-H bond lengths are certainly quite small, for the mean of the uncorrected C-H distances is 1.092 (2) Å, very close to the standard value of 1.096 Å (*Tables of Interatomic Distances and Configuration in Molecules and Ions*, 1965). Table 5 presents a comparison of X-H bond lengths corrected for rigid-body motion with values to which the commonly used riding correction and the minimum correction (Busing & Levy, 1964) have been applied. The riding approximation, which leads to a mean C-H distance of 1.131 (3) Å, clearly overcorrects the bond lengths and does not appear to be very useful here. The results using the minimum correction set a lower bound of 1.100 (2) Å for the mean C-H distance determined in this study. Rigid-body calculation I, which does not include the effects of hydrogen atom thermal motion, leads to a mean corrected C-H distance of 1.094 (2) Å, or only 0.002 Å larger than the uncorrected value. Calculations IV and V, in which constraints of symmetry have been applied, give generally larger corrections to

Table 5. X-H Bond distances (Å) corrected for thermal motion

	Uncorrected	I	II	III	IV	V	Minimum Correction*	Riding Correction†
C ^α -H ^α	1.090 (3)	1.091	1.104				1.094	1.113
C ^β -H ^{β1}	1.093 (5)	1.093	1.107			1.110	1.100	1.127
C ^β -H ^{β2}	1.097 (5)	1.098	1.111			1.114	1.104	1.133
C ^γ -H ^{γ1}	1.102 (5)	1.103	1.117			1.124	1.113	1.148
C ^γ -H ^{γ2}	1.088 (5)	1.090	1.102			1.109	1.096	1.128
C ^δ -H ^{δ1}	1.088 (6)	1.089	1.103			1.114	1.098	1.132
C ^δ -H ^{δ2}	1.094 (5)	1.095	1.107			1.119	1.104	1.141
C ^ε -H ^{ε1}	1.082 (5)	1.084	1.097			1.104	1.092	1.126
C ^ε -H ^{ε2}	1.090 (5)	1.091	1.104			1.111	1.099	1.132
Mean C-H	1.092 (2)	1.093 (2)	1.106 (2)			1.113 (2)	1.100 (2)	1.131 (3)
N-H ¹	1.034 (4)	1.034		1.049	1.057		1.038	1.059
N-H ²	1.028 (4)	1.029		1.041	1.050		1.032	1.051
N-H ³	1.059 (4)	1.061		1.074	1.082		1.060	1.073
N ⁵ -H ⁵¹	1.016 (5)	1.017	1.029	1.047	1.048		1.031	1.075
N ⁵ -H ⁵²	1.024 (5)	1.025	1.037	1.049	1.056		1.030	1.057
N ⁵ -H ⁵³	1.026 (4)	1.027	1.029	1.058	1.057		1.028	1.047
Mean N-H	1.031	1.032	1.032	1.053	1.058		1.037	1.060
O ^{w1} -H ^{w11}	0.960 (9)					0.967	0.961	
O ^{w1} -H ^{w12}	0.953 (11)					0.960	0.953	
O ^{w2} -H ^{w21}	0.957 (11)					0.963	0.957	0.957
O ^{w2} -H ^{w22}	0.936 (9)					0.942	0.937	0.954
Mean O-H	0.952					0.958	0.952	0.956

* Defined as $\frac{(|u_2^{1/2} - u_1^{1/2}|)^2}{2R}$ where u_2 and u_1 are total mean-square displacements normal to the bond for the two atoms, and R is the uncorrected bond distance.

† Defined as $\frac{(u_2 - u_1)}{2R}$ where atom 2 rides on atom 1.

the N-H and C-H bond lengths, respectively, than do the unconstrained calculations III and II.

In the absence of a detailed knowledge of the nature of the thermal vibrations taking place in the crystal, an accurate assessment of the relative merits of the X-H bond length corrections based on rigid-body calculations II-V and on the minimum correction is impossible. Generally speaking, one would expect the corrections to the N-H bond lengths to be even smaller than those to the C-H bond lengths, because the ammonium group hydrogen atoms are tied down by hydrogen bonds. If this is the case, then the corrected N-H bond distances derived from calculations III and IV are clearly too large. The minimum correction, which rests on the somewhat unphysical assumption that the motions of two atoms normal to the bond connecting them are completely in phase, appears to give very reasonable corrected bond distances in this structure. In cases where non-rigid-body motions are important the minimum correction has the advantage over rigid-body treatments of considering each bond individually and gives a theoretical lower bound to the corrected distance.

Corrections to X-X-H and H-X-H bond angles based on the rigid-body calculations were less than one e.s.d. for almost all angles, and the corrected values have not been presented in detail.

All computations described in this paper were performed on CDC 6600 computers, using programs from the Brookhaven Crystallographic Computing Library. A brief summary of these programs has been given by Schlemper *et al.*, (1971).

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A Neutron Diffraction Study of the Structure of L-Lysine Monohydrochloride Dihydrate

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The intensities of 1431 (875 independent) neutron Bragg reflexions from a single crystal of L-lysine monohydrochloride dihydrate have been measured at a wavelength of 1.170 Å, using the diffractometer in the symmetrical setting. The structure has been refined by the method of least squares and the final conventional *R* value is 0.070. An inter-experimental comparison is made with an independent neutron-diffraction study (preceding paper) and with the X-ray results [Wright & Marsh *Acta Cryst.* (1962), **15**, 54].

Introduction

Preliminary studies of the space group and cell constants of L-lysine monohydrochloride dihydrate were carried out by Srinivasan (1956). The structure was first solved using X-ray data by Raman (1959), who suggested that the molecule is in the zwitterion form and also proposed a network of ten hydrogen bonds in the structure. A more accurate X-ray study was reported by Wright & Marsh (1962) whose hydrogen bonding scheme agrees with Raman's except in the bonding of the terminal amino group. The present neutron study was carried out to obtain detailed knowledge of the hydrogen atom positions in this amino acid crystal. A parallel neutron-diffraction study, of which we were unaware until recently, has been carried out independently by Koetzle, Lehmann, Verbist & Hamilton (1972).

Crystal data

L-Lysine monohydrochloride dihydrate, $\text{NH}_3^+[\text{CH}_2]_4\text{CH}(\text{NH}_3)^+\text{COO}^-\cdot\text{Cl}^-\cdot 2\text{H}_2\text{O}$, is monoclinic, $P2_1$, with two molecules per unit cell. The following cell parameters were established from the X-ray study of Wright & Marsh (1962): $a = 7.492$ (1), $b = 13.320$ (4), $c = 5.879$ (1) Å and $\beta = 97^\circ 47.4$ (7)'. The calculated density is 1.249 g.cm⁻³.

Experimental

Large, clear and well-formed single crystals of L-lysine HCl.2H₂O were easily obtained by slow evaporation from a saturated aqueous solution at room temperature. The crystals were of pyramidal shape with (010) as the basal face and {110} and {011} as the principal side faces, and they were elongated along the *c* direction. The density measured by flotation was 1.246 g.cm⁻³.

Neutron intensity data were recorded using the four-circle neutron diffractometer 3D-FAD (Momin, Sequeira & Chidambaram, 1969) at the CIRUS reactor in Trombay. The specimen crystal was cut in the shape of a rectangular parallelepiped with a height of 4.94 mm along the *b* axis and with lateral dimensions of 3.68 and 2.93 mm respectively along and perpendicular to the *c* axis. The crystal was given a thin coating of an adhesive (brand name Stickfast) to prevent exposure to air, and dipped in liquid nitrogen several times to reduce extinction effects. It was then mounted on the diffractometer with its *b* axis parallel to the ϕ -axis of the Eulerian Cradle. The cell parameters and the crystal orientation were refined from the optimised 2θ , χ and ϕ values for some 30 strong reflexions chosen at random, using the program *REFINE* (Srikanta & Sequeira, 1968). The refined values of the cell parameters were in agreement with the more precise X-ray values listed above to better than two parts per thousand. The systematic absences were checked and found to be consistent with the space group $P2_1$.

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