

## Refinement of the Structure of Arginine Hydrochloride Monohydrate\*

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The crystal structure of L-arginine monohydrochloride monohydrate has been refined by the method of least-squares. Counter data collected with Mo  $K\alpha$  radiation were used in the refinement. The final  $R$  index is 0.033 for 2454 observed reflections. The average estimated standard deviation in the position of the Cl-ion is 0.0006–0.0009 Å; for the C, N, and O atoms it is 0.0016–0.0030 Å and for the hydrogen atoms it is 0.020–0.040 Å. Differences in structural detail between the two molecules of the asymmetric unit are described. All 34 hydrogen atoms were located in a  $\Delta F$  synthesis, and the intricate hydrogen bonding scheme has been characterized.

### Introduction

The crystal structure of L-arginine monohydrochloride monohydrate was selected for X-ray crystallographic determination with a major concern for obtaining structural parameters of sufficient precision to provide meaningful structural details. L-Arginine is of interest because of its relation to the phosphorylated guanidine compounds, phosphoarginine and phosphocreatine, which are among the most energy rich of all the so-called high energy phosphate compounds. Furthermore comparative studies of the crystal structures of amino acids and simple peptides are of use in determining the effect of variation in molecular environment on the conformation of amino acid side-groups (Ramachandran, Mazumdar, Venkatesan & Lakshminarayanan, 1966).

When this work was initiated at the University of Washington, a literature search revealed no complete structure determination of a crystal containing arginine. During the course of the work, however, three separate reports of structures containing arginine appeared (Donohue & Metz, 1964; Karle & Karle, 1964; Mazumdar & Srinivasan, 1964). Although each of the reports was on a different crystal structure, that of Mazumdar & Srinivasan was identical with the one which was in the trial stage at Washington (Donohue, 1965). The work of deriving a phasing model from the Patterson synthesis was halted. Instead, it was agreed to begin refining the structure with coordinates from the initial refinement of Mazumdar & Srinivasan and to use the extensive set of diffractometer data which had already been collected at Washington.

### Experimental

Crystals of L-arginine monohydrochloride monohydrate were grown from a dilute ethanolic solution of L-arginine hydrochloride (Nutritional Biochemicals Corporation, Cleveland, Ohio) by slow evaporation at room temperature. A crystal measuring approximately  $0.10 \times 0.13 \times 0.18$  mm was mounted with epoxy resin on a glass fiber. It was set to rotate about  $a$  and was used for determining the cell parameters and collecting the initial intensity data. Subsequently, a larger crystal approximately  $0.27 \times 0.28 \times 0.30$  mm, was mounted for rotation about the  $b$  axis and used to collect additional data. The final set of data consisted of 2563 reflections of which 607 of the more intense, all with a net count greater than 50 deka-counts, were from the smaller crystal and the remaining 1956 were from the larger crystal.

Cell parameters were determined on a Picker X-ray diffractometer equipped with a General Electric quarter circle goniostat.  $2\theta$  settings for 16 reflections ranging from 9.61 to 29.12 degrees were measured by determining peak positions from the half-height values for both positive and negative  $2\theta$ . Mo  $K\alpha$  radiation was used ( $\lambda K\alpha = 0.71069$  Å). The following unit-cell parameters were determined by a least-squares fit to the 16 observed  $2\theta$  values:

$$a = 11.044 \pm 0.002, b = 8.481 \pm 0.001, c = 11.214 \pm 0.002 \text{ \AA}, \\ \beta = 91.31 \pm 0.01^\circ.$$

Since the only systematically absent reflections were  $0k0$  for  $k$  odd, the space group was assumed to be  $P2_1$ . The density was observed to be  $1.45 \text{ g.cm}^{-3}$  by flotation in mixed solvents; it was calculated to be  $1.446 \text{ g.cm}^{-3}$  assuming four molecules in the unit cell or two molecules in the asymmetric unit.

Intensities were measured on a diffractometer equipped with a scintillation counter and pulse height analyzer. A Mo target tube was used at a  $3^\circ$  take-off angle

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and was operated at 14 mA and 50 kV. The radiation was filtered through 0.001 inch Nb. All measurements were made using the  $\omega/2\theta$  scan technique with a constant scan rate of two degrees per minute and variable scan times (Kraut, 1964) as computed from the tangent relationship of Alexander & Smith (1964). A background count was made at each end of the scan range for half the time of the total scan. All  $\varphi$ ,  $\chi$  and  $2\theta$  positions were manually set, and the measured intensities recorded in dekaunits.

All measurements were put on a common scale using four standard reflections measured at four-hour intervals. Measurements from the two crystals were scaled together using ten reflections which had net dekaunits ranging from 831 to 1361 for the smaller crystal and 7879 to 12,573 for the larger crystal.

The relative intensity was obtained by subtracting the sum of the background counts from the total scan count; if a negative value was obtained, the intensity was taken as equal to zero. Intensities were converted to  $|F|^2$  in the usual way. No correction for absorption was made ( $\mu = 3.60 \text{ cm}^{-1}$ ).

### Refinement

The scattering factors used for O, N, C, and  $\text{Cl}^-$  were from Hanson, Herman, Lea & Skillman (1964) and those for H were from Stewart, Davidson & Simpson (1965). All calculations were carried out on an IBM

7094 computer with programs from the crystallographic computing system, *X-ray 63* (Stewart, 1964). For refinement of the 389 parameters, it was necessary to partition the matrix into three large blocks. Thus a full refinement cycle required three passes through the computer: (1) refinement of the atomic parameters of one arginine molecule along with those of the 2  $\text{Cl}^-$  ions and 2 water oxygen atoms, all other parameters fixed; (2) refinement of the atomic parameters of the second arginine molecule along with those of the 2  $\text{Cl}^-$  ions and 2 water oxygen atoms, all other parameters fixed; (3) refinement of the parameters of the hydrogen atoms, all others fixed.

The initial refinement began with Mazumdar & Srinivasan's (1964) coordinates and a set of data collected from the smaller crystal. Refinement reduced  $R(\sum |F_o| - |F_c| / \sum |F_o|)$  to 0.053, but the standard deviations in the positional parameters of the C, N and O atoms, about 0.005–0.006 Å, were greater than expected. It was at this point that additional data were collected from the larger crystal and the final set of 2563 reflections was obtained. The initial refinement cycle on the final data included *all* reflections with *unit weight*. Anisotropic thermal parameters were included but hydrogen atoms were omitted. The index  $R$  was 0.066.

All 34 hydrogen atoms were easily located from a difference synthesis and their positions were refined in a single least-squares cycle with isotropic thermal par-

Table 1. *Atomic parameters for nonhydrogen atoms*

Estimated standard deviations in parentheses.

The thermal parameters are defined by the expression:

$$T_i = \exp \left[ -\frac{1}{4}(B_{11}h^2a^*2 + B_{22}k^2b^*2 + B_{33}l^2c^*2 + 2B_{12}hka^*b^* + 2B_{13}hla^*c^* + 2B_{23}klb^*c^*) \right].$$

	<i>x</i>	<i>y</i>	<i>z</i>	$B_{11}$	$B_{22}$	$B_{33}$	$B_{12}$	$B_{13}$	$B_{23}$
C(1)	0.57877 (20)	0.43397 (32)	0.42981 (19)	1.64 (8)	2.16 (10)	1.25 (8)	-0.28 (8)	0.23 (6)	-0.06 (8)
C(2)	0.52425 (20)	0.42437 (30)	0.55514 (19)	1.98 (9)	1.63 (9)	1.26 (8)	0.02 (8)	0.31 (6)	-0.24 (7)
C(3)	0.38776 (21)	0.44430 (33)	0.54862 (21)	1.56 (8)	2.50 (11)	1.71 (8)	0.27 (8)	0.44 (7)	-0.15 (8)
C(4)	0.32727 (21)	0.43032 (34)	0.67008 (21)	1.72 (8)	2.56 (11)	1.75 (8)	0.12 (8)	0.53 (7)	0.13 (8)
C(5)	0.19209 (22)	0.40616 (35)	0.65116 (22)	2.04 (9)	2.54 (11)	2.10 (9)	-0.13 (8)	0.33 (7)	-0.74 (9)
C(6)	0.11572 (19)	0.25673 (33)	0.82191 (20)	1.46 (8)	1.96 (9)	1.78 (8)	0.27 (8)	-0.07 (6)	0.23 (8)
N(1)	0.58292 (17)	0.54346 (26)	0.63526 (15)	1.67 (7)	2.18 (8)	1.38 (6)	-0.05 (7)	0.23 (6)	-0.12 (7)
N(2)	0.12711 (19)	0.38969 (26)	0.76163 (19)	2.09 (8)	1.88 (8)	2.56 (9)	-0.49 (7)	0.94 (6)	-0.17 (7)
N(3)	0.18027 (20)	0.13017 (25)	0.79442 (19)	2.74 (9)	1.60 (9)	2.43 (8)	-0.10 (7)	0.58 (6)	-0.04 (7)
N(4)	0.04036 (19)	0.24939 (32)	0.91205 (18)	2.36 (8)	2.80 (10)	2.15 (8)	-0.02 (8)	0.73 (6)	-0.22 (8)
O(1)	0.65090 (17)	0.54125 (26)	0.40903 (15)	2.67 (7)	3.32 (9)	2.08 (7)	1.12 (7)	0.86 (6)	0.18 (7)
O(2)	0.54316 (16)	0.32939 (24)	0.35765 (14)	3.11 (8)	2.57 (8)	1.50 (6)	0.54 (7)	0.39 (6)	0.33 (6)
O(3)	0.11956 (18)	0.85689 (27)	0.59570 (17)	3.59 (9)	2.97 (10)	2.86 (8)	0.47 (8)	0.42 (7)	0.08 (8)
Cl(1)	0.16061 (6)	0.75734 (0)	0.86888 (6)	3.22 (3)	2.63 (3)	2.78 (3)	0.55 (2)	0.82 (2)	0.04 (2)
C(7)	0.55854 (21)	0.33536 (32)	0.91405 (20)	1.81 (9)	1.95 (10)	1.53 (8)	-0.67 (8)	0.39 (7)	-0.11 (8)
C(8)	0.50540 (20)	0.32535 (31)	0.03959 (18)	1.98 (8)	1.54 (9)	1.33 (8)	0.13 (8)	0.23 (7)	-0.01 (8)
C(9)	0.37337 (21)	0.37687 (32)	0.03555 (21)	1.74 (8)	2.36 (11)	1.71 (9)	0.06 (8)	0.25 (7)	0.44 (8)
C(10)	0.31557 (21)	0.38601 (33)	0.15751 (22)	1.63 (8)	2.31 (11)	2.10 (9)	-0.08 (8)	0.48 (7)	-0.17 (8)
C(11)	0.18966 (23)	0.45648 (35)	0.14746 (22)	2.33 (9)	2.56 (12)	2.02 (9)	-0.22 (9)	0.12 (8)	0.36 (9)
C(12)	0.13353 (20)	0.61279 (32)	0.32316 (20)	1.77 (8)	1.85 (9)	1.78 (8)	-0.35 (8)	-0.02 (6)	-0.19 (8)
N(5)	0.57826 (18)	0.42518 (28)	0.12437 (16)	1.71 (7)	2.54 (9)	1.46 (7)	0.10 (7)	0.15 (6)	0.06 (7)
N(6)	0.13381 (19)	0.47946 (27)	0.26285 (19)	2.22 (8)	1.94 (9)	2.59 (8)	0.27 (7)	0.78 (7)	0.19 (7)
N(7)	0.20528 (21)	0.73265 (28)	0.29656 (20)	2.97 (10)	1.91 (10)	3.15 (10)	0.38 (8)	0.78 (8)	0.32 (8)
N(8)	0.05957 (19)	0.62803 (30)	0.41391 (18)	2.53 (8)	2.96 (11)	2.08 (8)	0.08 (8)	0.60 (6)	0.37 (8)
O(4)	0.61343 (18)	0.45851 (26)	0.88685 (16)	3.45 (8)	2.09 (9)	1.92 (6)	0.87 (7)	0.70 (6)	-0.21 (6)
O(5)	0.53794 (20)	0.22103 (24)	0.84668 (16)	5.10 (10)	2.04 (8)	1.82 (7)	-0.07 (8)	0.45 (7)	0.57 (6)
O(6)	0.12423 (18)	0.02641 (28)	0.09134 (16)	3.73 (9)	3.13 (10)	2.35 (7)	-0.56 (8)	0.44 (6)	-0.09 (8)
Cl(2)	0.13138 (6)	0.10463 (10)	0.36241 (5)	2.11 (2)	2.54 (3)	2.33 (2)	0.24 (2)	0.59 (2)	-0.05 (2)

ameters fixed at 2.5 Å<sup>2</sup>. Again all data were included with unit weight:  $R$  decreased to 0.049. An additional anisotropic refinement cycle on the nonhydrogen atoms with the hydrogen atoms fixed, decreased  $R$  to 0.042. The hydrogen atoms were again refined in a single isotropic cycle in which the thermal parameters were also allowed to vary, but with the nonhydrogen atoms fixed. The resulting  $R$  was 0.040.

Thus far the refinement had included all reflections with unit weight. A weighting scheme with  $w_{hkl} = 1/\sigma_{hkl}^2$  was now introduced, based on the following considerations: the estimated standard deviation in a count is the square root of the number of counts, but this is a lower limit to the standard deviation of the observation. Random fluctuation in counts also arises from instability in the electronic circuitry and from other effects, and the magnitude of these can be assessed by examining the variation of the total counts for the standard reflections bracketing each four-hour interval of data collection. For the present data, this was about 1%. Therefore, the estimated standard deviation in each measurement can be taken as

$$\sigma_I = [(I_t + (0.01I_t)^2)]^{1/2},$$

where  $I_t$  is the total count (background plus scan) for each reflection (Stewart & Jensen, 1969).

The standard deviation in each structure factor was then estimated from the relation:

$$\sigma_F = (F^2 + (\sigma_I/L_p)^2)^{1/2} - F.$$

The weights,  $1/\sigma_F^2$ , varied from 1.3 to 67.2 with most lying in the range 20 to 40.

After one anisotropic refinement cycle on the nonhydrogen atoms, all data included and weighted as indicated above,  $R$  decreased to 0.038. This was followed by a single isotropic cycle on the hydrogen atoms and  $R$  was 0.037. The standard deviations had decreased by about 30% on introducing the weighting scheme described above.

The data were edited at this point and minor errors affecting about 30 reflections were corrected. An additional isotropic refinement cycle on the hydrogen atoms resulted in  $R=0.038$ , a slight increase.

The establishment of a threshold for the minimum observed intensity had been delayed until the refinement was essentially complete in order to permit an assessment of its effects on the final results of the refinement. Therefore, at this point a reflection was coded as unobserved if the net number of counts was less than the estimated standard deviation of the measurement; 109 reflections were thus coded. The  $\Delta F$  values for these reflections were included in the refinement only if  $F_c > F_{\min}$  but were omitted in the calculation of  $R$ . They were weighted in the same manner as other reflections.

One anisotropic refinement cycle on the nonhydrogen atoms with the 2454 observed data yielded an  $R$  of 0.035; the following isotropic refinement cycle on the hydrogen atoms reduced  $R$  to 0.034. The estimated

standard deviations decreased by about 10%. At this point, an error in position of H(21) was discovered and corrected. One isotropic refinement cycle on the hydrogen atoms followed by one anisotropic cycle on the nonhydrogen atoms and a final isotropic cycle on the hydrogen atoms yielded a final  $R$  value of 0.033.

The goodness of fit,  $[\sum w(|F_o| - |F_c|)^2 / (m - n)]^{1/2}$ , where  $m$  is the number of reflections and  $n$  is the number of parameters, was 1.69 as compared with the ideal value of 1. This deviation from unity may reflect errors in the weighting scheme or systematic errors in the data, but it is more likely that it indicates, at least in part, the limitations of the model.

The final atomic parameters are listed in Tables 1 and 2. The final  $|F_o|$  and  $|F_c|$  values are listed in Table 3. Figs. 1 and 2 show the bond lengths and angles of primary interest.

Table 2. Atomic parameters for hydrogen atoms

Estimated standard deviations in parentheses.

	$x$	$y$	$z$	$B$
H(1)	0.668 (2)	0.560 (4)	0.617 (2)	2.2 (6) Å <sup>2</sup>
H(2)	0.588 (2)	0.511 (3)	0.713 (2)	1.4 (5)
H(3)	0.536 (3)	0.638 (4)	0.633 (3)	3.3 (7)
H(4)	0.544 (2)	0.318 (4)	0.592 (2)	1.9 (6)
H(5)	0.366 (3)	0.552 (4)	0.509 (3)	2.5 (6)
H(6)	0.359 (3)	0.363 (4)	0.499 (3)	2.3 (7)
H(7)	0.341 (3)	0.515 (4)	0.717 (3)	2.9 (7)
H(8)	0.362 (2)	0.336 (4)	0.714 (2)	2.0 (5)
H(9)	0.154 (3)	0.488 (4)	0.609 (3)	3.0 (8)
H(10)	0.171 (3)	0.304 (4)	0.600 (3)	2.0 (6)
H(11)	0.095 (2)	0.445 (4)	0.783 (2)	1.8 (6)
H(12)	0.219 (2)	0.135 (4)	0.734 (2)	1.0 (4)
H(13)	0.152 (2)	0.037 (4)	0.820 (2)	1.6 (5)
H(14)	-0.005 (3)	0.332 (5)	0.921 (3)	3.3 (7)
H(15)	0.055 (3)	0.176 (5)	0.966 (3)	3.4 (7)
H(16)	0.132 (4)	0.815 (6)	0.662 (4)	6.4 (1.0)
H(17)	0.173 (4)	0.918 (6)	0.577 (4)	5.5 (1.1)
H(18)	0.659 (2)	0.410 (4)	0.111 (2)	1.5 (5)
H(19)	0.565 (3)	0.398 (4)	0.205 (3)	3.1 (7)
H(20)	0.554 (2)	0.524 (4)	0.111 (2)	1.4 (5)
H(21)	0.512 (3)	0.222 (4)	0.070 (2)	2.2 (6)
H(22)	0.371 (2)	0.480 (3)	-0.009 (2)	1.4 (5)
H(23)	0.328 (3)	0.304 (4)	-0.011 (3)	3.2 (7)
H(24)	0.365 (2)	0.452 (4)	0.218 (2)	1.9 (6)
H(25)	0.317 (2)	0.287 (4)	0.196 (2)	2.4 (6)
H(26)	0.201 (2)	0.546 (4)	0.111 (2)	2.2 (6)
H(27)	0.137 (2)	0.387 (4)	0.099 (2)	1.4 (6)
H(28)	0.091 (3)	0.399 (4)	0.284 (3)	3.0 (8)
H(29)	0.259 (3)	0.716 (4)	0.256 (3)	2.9 (8)
H(30)	0.185 (3)	0.818 (4)	0.312 (3)	2.7 (7)
H(31)	0.010 (2)	0.562 (4)	0.425 (2)	1.1 (5)
H(32)	0.068 (3)	0.699 (5)	0.464 (3)	3.0 (8)
H(33)	0.120 (3)	0.056 (4)	0.161 (3)	2.1 (6)
H(34)	0.177 (3)	0.001 (4)	0.082 (3)	4.1 (8)

## Discussion

### General features and comparisons

By comparing Figs. 3 and 4 it is evident that the two arginine molecules in the unit cell are related approximately by a pseudo  $c$ -glide plane at  $y \approx 0.4$ .

Bond lengths in the two molecules are closely similar with the possible exception of the C-O bonds in the two carboxyl groups. Neglecting these, since both oxy-

Table 3. Observed and calculated structure factors

Each group of four columns contains respectively  $I$ ,  $10F_o$ ,  $10F_c$  and the phase in millicycles.

0.0.L	7.0.L	2.0L	1.0.L	3.0.L	4.0.L	5.0.L	6.0.L	8.1.L	9.1.L	10.1.L	11.1.L	12.1.L	13.1.L	14.1.L	15.1.L	16.1.L	17.1.L	18.1.L	19.1.L	20.1.L	21.1.L	22.1.L	23.1.L	24.1.L	25.1.L	26.1.L	27.1.L	28.1.L	29.1.L	30.1.L	31.1.L	32.1.L	33.1.L	34.1.L	35.1.L	36.1.L	37.1.L	38.1.L	39.1.L	40.1.L	41.1.L	42.1.L	43.1.L	44.1.L	45.1.L	46.1.L	47.1.L	48.1.L	49.1.L	50.1.L	51.1.L	52.1.L	53.1.L	54.1.L	55.1.L	56.1.L	57.1.L	58.1.L	59.1.L	60.1.L	61.1.L	62.1.L	63.1.L	64.1.L	65.1.L	66.1.L	67.1.L	68.1.L	69.1.L	70.1.L	71.1.L	72.1.L	73.1.L	74.1.L	75.1.L	76.1.L	77.1.L	78.1.L	79.1.L	80.1.L	81.1.L	82.1.L	83.1.L	84.1.L	85.1.L	86.1.L	87.1.L	88.1.L	89.1.L	90.1.L	91.1.L	92.1.L	93.1.L	94.1.L	95.1.L	96.1.L	97.1.L	98.1.L	99.1.L	100.1.L
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Table 3 (cont.)

Atom	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1.5.L	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200

gen atoms are involved in different hydrogen bonding and packing (see below), one calculates a root-mean-square difference for the remaining nine bonds between nonhydrogen atoms of 0.0052 Å. Since the bonds in the two molecules are independently determined, division by  $\sqrt{2}$  leads to an estimate of the standard deviation of 0.0037 Å, just a little greater than the 0.0033 Å as determined from the refinement.

A similar comparison of the bond angles in the two molecules, but neglecting the angles about the carboxyl carbon atoms, gives an estimate of the standard deviation in the angles of 0.57°. This value exceeds the mean of the standard deviation estimated from the refinement 0.21°, by a factor approaching 3. The greater variability of bond angles as compared with bond lengths probably stems from the relatively smaller energies necessary to deform them. Presumably packing energies are sufficient to produce changes in angles appreciably larger than the standard deviations of the present refinement.

### The guanidyl groups

The average value for the three guanidyl C-N bond lengths in molecule I is 1.324 Å, in molecule II it is 1.325 Å. These agree well with the value of  $1.323 \pm 0.006$  Å reported by Haas, Harris & Mills (1965) for C-N bonds of guanidinium chloride.

In the present investigation, the terminal C-N bonds of the guanidyl groups average 1.327 Å while the N(2)-C(6) and N(6)-C(12) bonds average 1.320 Å. The difference, however, is only marginally significant.

Both guanidyl groups in arginine hydrochloride are planar. The standard deviation of the four nonhydrogen atoms from the least-squares plane in molecule I is 0.003 Å; in molecule II it is 0.001 Å. The deviations of the hydrogen atoms from the guanidyl planes are listed in Table 4, and it is evident that corresponding atoms in the two groups tend to have similar deviations. Since the standard deviations for the hydrogen atoms are in the range 0.02-0.04 Å, any deviation in Table 4 exceeding about 0.1 Å indicates that the cor-

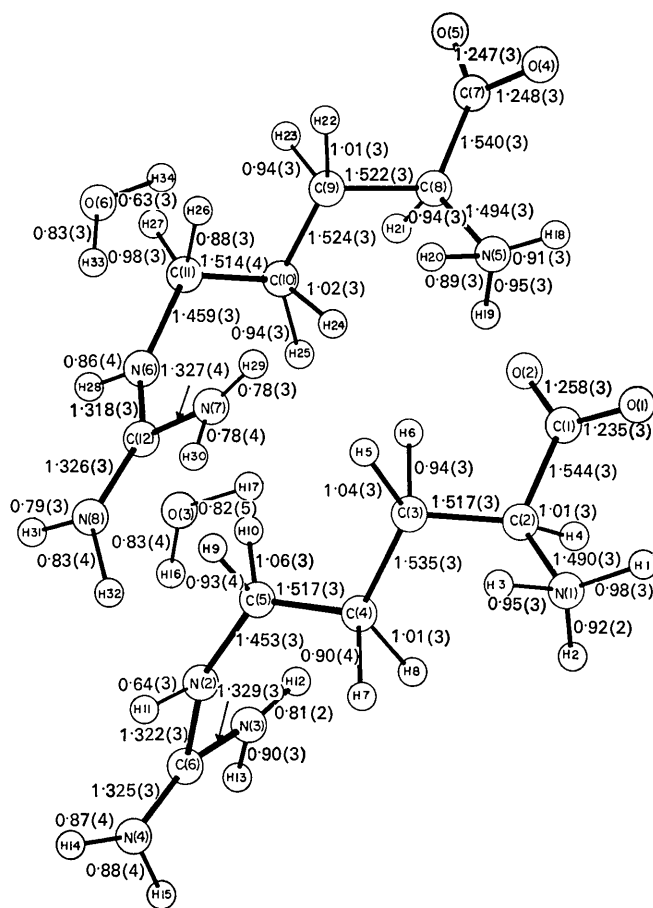


Fig. 1. Bond lengths of L-arginine hydrochloride monohydrate.

responding atom is probably significantly out of the plane. Thus H(13) and H(15) in molecule I and H(29), H(30) and H(32) in molecule II are probably out of the guanidyl planes. It is likely that the displacements of the hydrogen atoms result in additional linearity and increased stability of the hydrogen bonds.

Table 4. Deviations of the hydrogen atoms from guanidyl planes

Molecule I		Molecule II	
H(11)	0.03 Å	H(28)	0.06 Å
H(12)	0.10	H(29)	0.19
H(13)	0.28	H(30)	0.31
H(14)	0.09	H(31)	0.10
H(15)	0.30	H(32)	0.19

The angles about C(6) and C(12) in the guanidyl groups differ significantly from 120°. The deviations are in the same sense for corresponding angles in the two molecules although they are appreciably larger for molecule II than for molecule I.

The average value for the two C-NH<sub>3</sub><sup>+</sup> bond lengths

is 1.492 Å while for the two C-N bonds it is 1.456 Å.

These values probably differ significantly from those suggested by Sutton (1965), 1.479 and 1.472 Å respectively, and they differ significantly from each other. The latter difference is probably due in part to the fact that in the first case the nitrogen atom is in the sp<sup>3</sup> valence state and in the second it is in the sp<sup>2</sup> state. Hahn (1957) in his review of the structural characteristics of amino acids noted an apparent lengthening of the C-NH<sub>3</sub><sup>+</sup> bond. Although at the time of his review the number of determinations of high precision were not sufficient to permit convincing conclusions, he suggested that this trend could result from an increase in atomic radius upon tetrahedral hybridization and from electrostatic effects.

#### The carboxyl groups

The average value for the two C-O bond lengths in molecule I is 1.246 Å and in molecule II it is 1.248 Å. While the two bonds in molecule II are virtually identical, in molecule I they are significantly different. The four atoms C(1), C(2), O(1) and O(2) are coplanar within experimental error while atoms C(7), C(8), O(4) and O(5) are not. In the first case the average deviation of the four atoms from the best least-squares plane is 0.002 Å and the deviation of N(1) from this plane is 0.15 Å, while in the second case the average deviation of the four atoms from the least-squares plane is 0.092 Å and N(5) deviates from this plane by 0.36 Å.

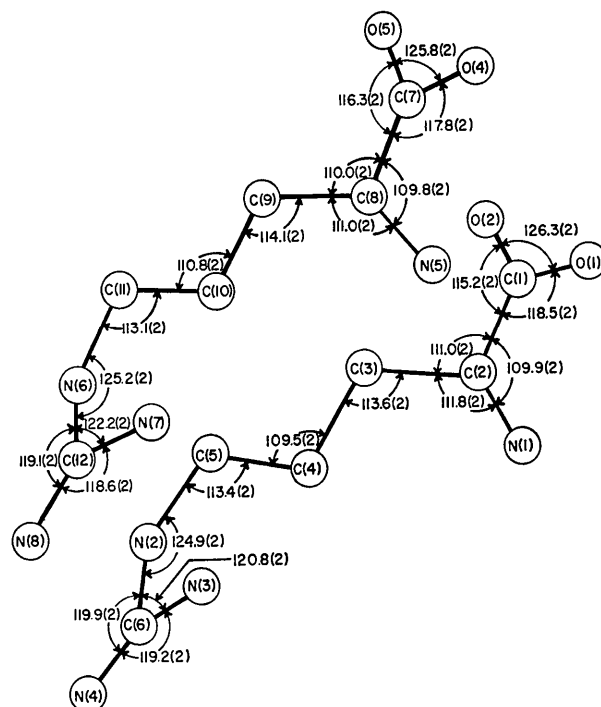
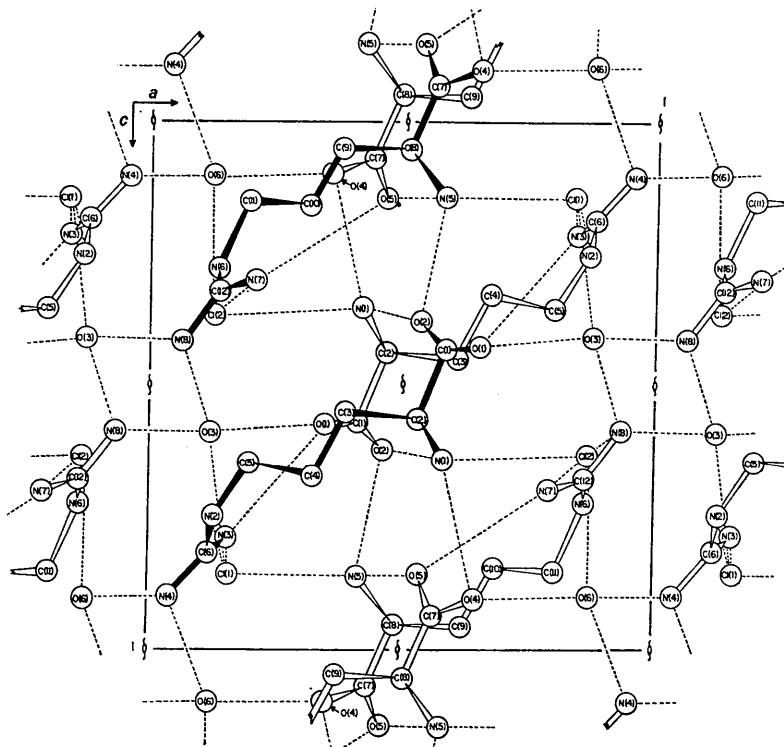
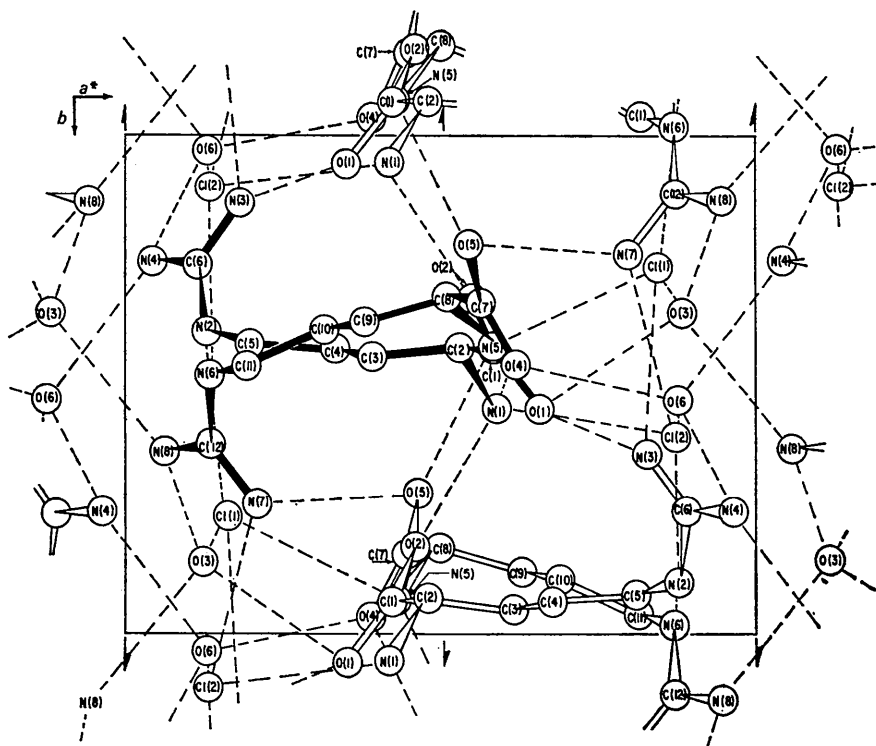


Fig. 2. Bond angles of L-arginine hydrochloride monohydrate.

Fig. 3. A drawing of the structure viewed along *b*.Fig. 4. A drawing of the structure viewed along *c*.

Thus, although the carboxyl groups appear similar in the structures when viewed along [001] (Fig. 4) it is evident that there are appreciable differences in the packing forces about these groups in the two molecules.

The  $N(1)\cdots O(1)$  contact distance in molecule I is 2.66 Å; the corresponding distance  $N(5)\cdots O(4)$  in molecule II is 2.72 Å. These are in agreement with the value 2.70 Å which Ramachandran, Ramakrishnan & Sasirekharan (1963) have proposed as the 'fully allowed distance' and 2.60 Å for the outer limit in their definition of the parameters of the polypeptide backbone.

#### Covalent bonds involving hydrogen

The hydrogen atoms, as located from a final difference synthesis, are shown in Fig. 5. As has been frequently observed, the C-H, N-H and O-H bond length are appreciably less than the internuclear distances. The average value for 14 C-H distances is 0.97 Å, about 0.1 Å shorter than the observed spectroscopic value of 1.09 Å. It has been suggested (Stewart *et al.*, 1965) that this difference is the result of assuming a spherical electron density distribution for the hydrogen atom and that the X-ray crystallographically derived values for these distances would be lengthened by the introduction of the appropriate complex scattering factors.

The average value found for 6  $N(sp^3)$ -H distances in this study is  $0.93 \pm 0.014$  Å, while that found for 10  $N(sp^2)$ -H distances is  $0.81 \pm 0.024$  Å, where the errors indicated are estimates of the standard deviation in the mean values. One of the  $N(sp^2)$ -H bonds,  $N(2)$ -H(11), is inordinately short and inconsistent with the other nine values. Neglect of this bond gives for the average of the other 9  $N(sp^2)$ -H distances a value of  $0.83 \pm 0.011$  Å. Either of the average  $N(sp^2)$ -H distances is apparently significantly less than the average  $N(sp^3)$ -H distance. However one may feel about the certainty of the observed difference, it is not surprising that the length of bonds involving hydrogen would be sensitive to the valence state of the atom to which they are bonded and the charge it might carry. In the present instance, both the valence state of the amino nitrogen atoms and their charge should tend to make  $N(sp^3)$ -H bonds longer than  $N(sp^2)$ -H bonds.

The average length of the four O-H bonds is 0.78 Å. Again, there is one inordinately short bond, and it is inconsistent with the other three. Neglecting it, the average of the three consistent O-H bonds is 0.83 Å, probably a more realistic value.

#### Hydrogen bonds

The structure is held together by an extensive system of hydrogen bonds, and it is remarkable that all twenty

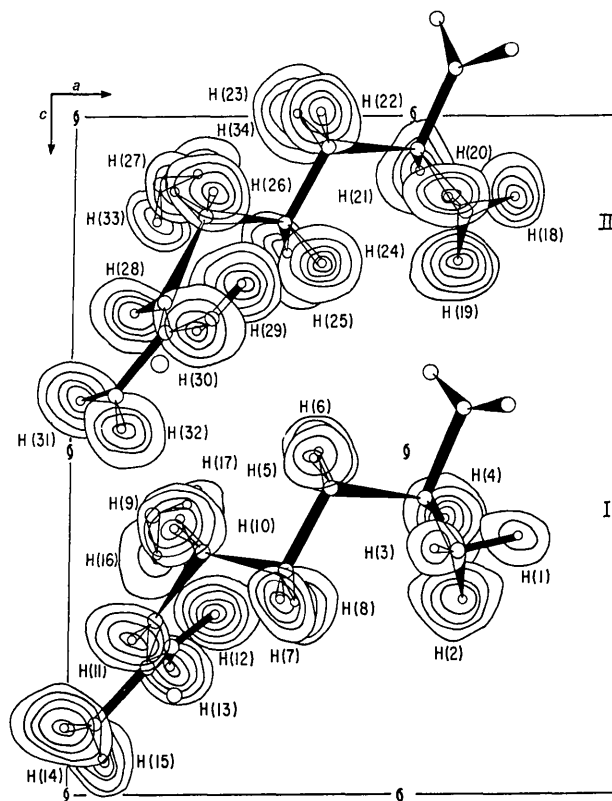


Fig. 5. A composite of sections from the final difference map, viewed along *b*. The contributions of the hydrogen atoms were omitted from the  $F_c$  calculations. Contours are at intervals of  $0.1 \text{ e.}\text{\AA}^{-3}$ , beginning with  $0.2 \text{ e.}\text{\AA}^{-3}$ .



of the hydrogen atoms in the asymmetric unit bonded to nitrogen and oxygen are involved in such bonds. The hydrogen bonds as viewed along [010] and [001] are shown in Figs. 3 and 4 respectively.

Data for the hydrogen bonds are summarized in Table 5. Inspection of the Table will indicate that eight of the hydrogen bonds of each molecule are the same, but the other two are different.

One of the latter, N(7)–H(29)···O(5), is unusually long. Indeed, the H(29)···O(5) distance is 2.54 Å, almost equal to the sum of the van der Waals radii, 2.60 Å. However, the N(7)–H(29) bond length equal to 0.78 Å is appreciably shorter than the internuclear distance of about 1.0 Å. Thus the internuclear H(29)···O(5) distance is presumably 0.2–0.3 Å less than the sum of the van der Waals radii. Furthermore, the hydrogen bond angle N–H···O differs by less than 16° from a straight angle. We conclude, therefore, that there is interaction between H(29) and O(5) corresponding to a weak hydrogen bond.

Similar arguments apply to the N(2)–H(11)···Cl(1) bond. The H(11)···Cl(1) distance of 2.91 Å is only slightly less than the sum of the van der Waals radii, 3.0 Å. However, the N(2)–H(11) bond is inordinately short and the internuclear distance must exceed the observed length by at least 0.35 Å. Thus the H(11)···Cl(1) internuclear distance is 0.3–0.4 Å less than the sum of the van der Waals radii, and this can be taken as evidence for a hydrogen bond.

There are no really short hydrogen bonds in the structure. Indeed, the lengths tend to be average or greater indicating rather weak bonds. Evidently minimum energy is attained in the crystal by maximizing the number of bonds at the expense of bond strength.

### Conformation

The conformation of the arginine side group in various crystals, including the present compound (preliminary data), was discussed in a paper by Ramachandran, *et al.* (1966). A summary of the various angles  $\phi$ ,  $\psi$  and  $\psi_i$  in these compounds has been reported by Lakshminarayanan, Sasisekharan & Ramachandran (1967). In view of this, the discussion of the conformational aspects will be brief. The angles  $\phi$ ,  $\psi$  and  $\psi_i$  (as defined by Edsall, Flory, Kendrew, Liquori, Nemethy, Ramachandran & Scheraga 1966) have been recalculated with the coordinates reported in this paper and these are listed in Table 6. They are all within 2 or 3° of the values for the preliminary structure.

The carboxyl oxygen atoms are appreciably tilted away from the plane N–C $^{\alpha}$ –C' (by about 30°) in molecule II, while they are only about 6° out of plane in molecule I. On the other hand, the dihedral angle  $\chi_1$ , which defines the location of the atom C $^{\gamma}$ , is practically the same in both molecules, and is close to the value of 300°, corresponding to a *trans* conformation with respect to C'. This angle is near 180° in arginine HCl and near 60° in arginine 2H<sub>2</sub>O and arginine 2HI (Lakshminarayanan *et al.*, 1967). The atoms C $^{\delta}$  and C $^{\epsilon}$  are both *trans* to C $^{\alpha}$  and C $^{\gamma}$  respectively in both the molecules, a fact found to be universally true in all the arginine structures studied so far.

On the other hand, the angle  $\chi_4$  is *different* in the two molecules, being close to –90° and +90° respectively, so that the guanidyl group is rotated in opposite directions at C $^{\beta}$  in the two cases. The guanidyl groups themselves, however, are practically planar in both molecules, as noted above, and both have a closely similar conformation.

Table 5. *Hydrogen bonds in arginine hydrochloride*

Molecule I				Molecule II			
X–H···Y	H···Y	X···Y	Angle SymOp†	X–H···Y	H···Y	X···Y	Angle SymOp†
			X–H–Y X→Y				X–H–Y X→Y
N(1)–H(1)···Cl(2)	2.25 Å	3.20 Å	162.1° 2	N(5)–H(18)···Cl(1)	2.38 Å	3.22 Å	151.4° 3
* –H(2)···O(4)	2.01	2.92	173.4 5	* –H(19)···O(2)	1.83	2.78	175.1 1
–H(3)···O(2)	1.85	2.80	173.7 2	–H(20)···O(5)	2.02	2.84	153.1 2
N(2)–H(11)···Cl(1)	2.91	3.36	130.7 1	N(6)–H(28)···Cl(2)	2.68	3.37	137.6 1
*N(3)–H(12)···O(1)	2.32	3.07	155.2 3	*N(7)–H(29)···O(5)	2.54	3.29	164.5 2
–H(13)···Cl(1)	2.44	3.28	156.8 4	–H(30)···Cl(2)	2.56	3.34	176.6 6
N(4)–H(14)···O(6)	2.11	2.97	168.9 2	N(8)–H(31)···O(3)	2.26	3.03	164.0 7
–H(15)···O(6)	2.03	2.90	167.6 5	–H(32)···O(3)	2.06	2.88	169.6 1
O(3)–H(16)···Cl(1)	2.39	3.20	165.9 1	O(6)–H(33)···Cl(2)	2.29	3.11	169.8 1
–H(17)···O(1)	2.21	2.98	157.2 2	–H(34)···O(4)	2.36	2.96	159.0 8

\* Bonds which are different for the two molecules in the asymmetric unit.

† The following transformations define symmetry operations relating asymmetric unit containing donor atom X to asymmetric unit containing acceptor atom Y. (1)  $x, y, z$ ; (2)  $\bar{x}+1, y-\frac{1}{2}, \bar{z}+1$ ; (3)  $\bar{x}+1, y+\frac{1}{2}, \bar{z}+1$ ; (4)  $x, y+1, z$ ; (5)  $x, y, z+1$ ; (6)  $x, y-1, z$ ; (7)  $\bar{x}, y+\frac{1}{2}, \bar{z}+1$ ; (8)  $\bar{x}+1, y+\frac{1}{2}, \bar{z}$ .

Table 6. *The various conformational angles in the two molecules of the structure*

(Notation as in Edsall *et al.*, 1966)

	$\psi_1$	$\psi_2$	$\chi_1$	$\chi_2$	$\chi_3$	$\chi_4$	$\chi_{51}$	$\chi_{52}$
Molecule I	154.9	332.0	306.1	173.9	185.2	96.7	346.0	166.3
Molecule II	174.1	353.6	301.1	195.6	179.3	276.0	10.6	189.7

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## Die Kristallstruktur von Triazidocarbonium-hexachloroantimonat, $[\text{C}(\text{N}_3)_3]\text{SbCl}_6$

VON ULRICH MÜLLER\* UND HARTMUT BÄRNIGHAUSEN

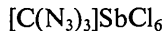
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(Eingegangen am 7. Juli 1969)

$[\text{C}(\text{N}_3)_3]\text{SbCl}_6$  crystallizes in space group  $P2_1/c$  with 4 formula units per unit cell; the lattice parameters are  $a=9.27$ ,  $b=10.96$ ,  $c=15.30$  Å and  $\beta=113.4^\circ$ . The crystal structure was solved by means of three-dimensional Patterson and Fourier syntheses and refined by the method of least-squares to a reliability index of  $R=6.8\%$  for the 1070 observed reflexions. The structure is built up from not quite planar, propeller-like  $\text{C}(\text{N}_3)_3^+$  ions (idealized point symmetry 3) and practically octahedral  $\text{SbCl}_6^-$  ions in an arrangement that has some resemblance to the structure type of CsCl. The bond lengths between the nitrogen atoms of the three very similar, non-linear azido groups of the  $\text{C}(\text{N}_3)_3^+$  ion differ widely, the mean values of 1.39 Å for  $\alpha\text{-N}-\beta\text{-N}$  and 1.05 Å for  $\beta\text{-N}-\gamma\text{-N}$  leading to the conclusion that these correspond to single and triple bonds respectively. The three C- $\alpha\text{-N}$  distances (mean value 1.34 Å) show partial  $\pi$ -bonding.

### Einleitung

Triazidocarbonium-hexachloroantimonat



wurde erstmals von Müller & Dehnicke (1966) dargestellt und charakterisiert. Der aus der Bandenzahl des Infrarot-Spektrums abgeleitete Strukturvorschlag, der für das  $\text{C}(\text{N}_3)_3^+$ -Ion die Punktsymmetrie  $3m$  ( $C_{3v}$ ) postulierte, blieb jedoch nicht unwidersprochen. So nahm Schmidt (1967) im Rahmen einer Arbeit über strukturell verwandte Verbindungen auch das IR-Spektrum von  $[\text{C}(\text{N}_3)_3]\text{SbCl}_6$  erneut auf und deutete es an Hand eines Modells der Punktsymmetrie  $\bar{6}$

( $C_{3h}$ ). Um zu einer zuverlässigen und insbesondere weiterreichenden Information über die Geometrie des  $\text{C}(\text{N}_3)_3^+$ -Ions zu gelangen, haben wir die vorliegende röntgenographische Kristallstrukturbestimmung unternommen. Sie zeigt, dass das  $\text{C}(\text{N}_3)_3^+$ -Ion im Kristallverband zwar streng genommen symmetrielos ist, dass aber die Punktsymmetrie 3 ( $C_3$ ) eine sehr gute Näherung darstellt und dass sogar die Abweichung von  $\bar{6}$  noch relativ klein ist.

### Experimentelles und Kristalldaten

Zu röntgenographischen Untersuchungen geeignete Einkristalle von  $[\text{C}(\text{N}_3)_3]\text{SbCl}_6$  erhielten wir aus einer Lösung des Präparats in 1,2-Dichloräthan durch partielles Verdunsten des Lösungsmittels unter verminder-

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