

The Structure of Di-L-Leucine Hydrochloride: An X-ray Diffraction Study*

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Di-L-leucine hydrochloride $[(\text{CH}_3)_2\text{CHCH}_2\text{CHNH}_2\text{COOH}]_2\text{HCl}$, M.W. 298.81, crystallizes in space group $P2_1$, $a=11.152$ (1), $b=5.116$ (1), $c=15.405$ (2) Å, and $\beta=108.94$ (2)°, $V=831.3$ Å³, $Z=2$, $D_m=1.187$ g.cm⁻³, $D_x=1.194$ g.cm⁻³. The structure has been refined to $R=5.5\%$ for 1360 visually estimated intensities from Cu $K\alpha$ Weissenberg films. In agreement with the infrared spectrum, we find that the structure has a very strong hydrogen bond with an O...O distance of 2.429 (7) Å between two leucine units. Refinement of the hydrogen position in the short hydrogen bond leads to O-H bond lengths of 1.06 (9) and 1.37 (9) Å, so that whether the bond is symmetric could not be definitively established. A symmetric bond seems likely from the equality of the C-O bond lengths: 1.280 (6) and 1.288 (6) Å. The resulting bimolecular units and chlorine atoms are linked into a two-dimensional array parallel to the (001) plane by weaker hydrogen bonds, producing a perfect layer structure with only van der Waals contacts between layers.

Introduction

Although L-leucine is one of the most common naturally occurring α -amino acids, the structure of the free acid is not known. [Cell constants and space groups have been reported by Dawson & Mathieson (1951), and by Möller (1949).] The structure of L-leucine hydrobromide has been reported by Subramanian (1967) and the isomorphous hydriodide by Chaney, Seeley & Steinrauf (1971). The structure of the leucyl residue has been determined in peptide structures such as *N*-methyl-DL-leucylglycine hydrobromide (Chandrasekaran & Subramanian, 1969) and leucylprolylglycine (Leung & Marsh, 1958). Our particular interest in the structure of di-L-leucine hydrochloride was aroused by the indication of a very strong symmetric hydrogen bond by the broad intense absorption band lying between 400 cm⁻¹ and 1300 cm⁻¹ in the infrared spectrum (Hadži & Marciszewski, 1967).

Experimental

Crystals of di-L-leucine hydrochloride were obtained by slow evaporation of a solution of L-leucine in dilute hydrochloric acid by the method of Rolski, Zdunska & Popko (1963). The crystals are prismatic, elongated in the **b** direction. They are stable on exposure to air, but show a pronounced cleavage parallel to (001) which causes them to be very sensitive mechanically.

Crystal data were obtained from zero-layer Weissen-

berg photographs ($h0l$) and ($0kl$), taken with Cu $K\alpha$ radiation. Values for the cell dimensions and their standard deviations were derived from a least-squares treatment of a number of high-order reflections, whose values for $\sin\theta$ were determined by comparison with superimposed powder lines of aluminum ($a=4.04907$ Å). Crystal data are: $a=11.152$ (1), $b=5.116$ (1), $c=15.405$ (2) Å, $\beta=108.94$ (2)°, $V=831.3$ Å³, D_m (floatation) = 1.187 g.cm⁻³, $D_x=1.194$ g.cm⁻³, $Z=2$, $\mu(\text{Cu } K\alpha)=2.14$ mm⁻¹. The only absent reflections are $0k0$ for $k=2n+1$, indicating $P2_1$ as the probable space group.

A crystal of size 0.18 × 0.10 × 0.20 mm and 0.2 mm in the *b*-axis direction, was used for data collection. Equi-inclination Weissenberg photographs, $h0l$, $h1l$, $h2l$, $h3l$ were obtained using the multiple-film technique with Cu $K\alpha$ radiation. In addition, multi-exposure precession photographs of the $0kl$, $1kl$, $2kl$, $h10$ and $hk1$ layers were taken with Mo $K\alpha$ radiation. Intensities were estimated visually. The precession data were used mainly for scaling the Weissenberg data along the *b* axis. 1491 independent nonzero reflections were collected; this includes 131 high-angle precession data which did not appear on the Cu $K\alpha$ films. An absorption correction was not applied. This neglect could lead to maximum errors of 10% (but generally much less) in the measured intensities.

The structure was determined by a three-dimensional Patterson synthesis and by electron density syntheses. This was followed by a series of least-squares refinement cycles, using Cruickshank's (1961) weighting scheme, $w=(1.96+|F_o|+0.0206|F_o|^2)^{-1}$. In the initial cycles, both the precession and Weissenberg data sets were used. Refinement of nine scale factors and all heavy atoms with isotropic thermal parameters resulted in a value of $R=0.147$. Hydrogen atoms H(1)-H(4)

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and H(14)–H(17), bonded to C(2)–C(4) and C(8)–C(10), were introduced at chemically reasonable positions; further refinement of scale factors, a chlorine atom with anisotropic thermal parameters, and all other atoms (except hydrogen atoms, which were fixed) with isotropic thermal parameters resulted in $R=0.112$. Difference Fourier sections through predicted hydrogen positions of four methyl and two amino groups resulted in the location of the positions of all remaining hydrogen atoms except H(27), the one in the short hydrogen bond. These hydrogen atoms were then included in the structure-factor calculation but were not refined. The resulting value of R was 0.097. The nine scale factors were then reduced to one, and anisotropic temperature factors were refined for all nonhydrogen atoms. Throughout all these refinements, atomic scattering factors for neutral atoms were taken from Cromer & Waber (1965), with an anomalous dispersion correction for chlorine for Cu $K\alpha$ radiation (Cromer, 1965), although some data (9%) were included which were taken with Mo $K\alpha$ radiation. Positions of hydrogen atoms were readjusted to chemically sensible positions from cycle to cycle using the *HYGEN* program (Ross, 1971).^{*} A difference electron density map calculated for the region between O(2) and O(3) revealed an approximate position for H(27). In the final cycles using the Cu $K\alpha$ data only, the positional parameters of this hydrogen atom were included, as was an isotropic extinction correction (Zachariasen, 1967). All other hydrogen atoms were, however, kept fixed. The final values of the agreement factors are:

$$R_1 = \sum ||F_o| - |F_c|| / \sum |F_o| = 0.055$$

and

$$R_2 = [\sum w(F_o - F_c)^2 / \sum wF_o^2]^{1/2} = 0.074.$$

An analysis of the weighted residuals ($(|F_o| - |F_c|) / \sigma(F_o)$)

showed no systematic trends with intensity or scattering angle, indicating that the relative weights were satisfactory. The estimated standard deviation of an observation of unit weight was 0.20, indicating that the σ 's used (and tabulated) were too large on an absolute scale by a factor of 5. Individual residuals (R_1 and R_2) calculated for layers of constant h , k , and l were also in good agreement.

The final refined parameters for the heavy atoms appear in Table 1, and unrefined hydrogen atom positions for H(1) to H(26) and the refined position of H(27) are presented in Table 2. The final calculated

Table 2. *Positions of hydrogen atoms*

		Calculated			
Bonded to		<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i>
H(1)	C(2)	0.54707	1.14704	0.15081	4.12
H(2)	C(3)	0.40355	1.11310	0.23365	4.12
H(3)	C(3)	0.41591	0.80490	0.23155	4.12
H(4)	C(4)	0.62692	0.83846	0.32670	4.12
H(5)	C(5)	0.46353	0.76719	0.39325	6.93
H(6)	C(5)	0.57822	0.94308	0.46301	6.93
H(7)	C(5)	0.44704	1.07849	0.40231	6.93
H(8)	C(6)	0.67206	1.26901	0.28729	6.93
H(9)	C(6)	0.70528	1.24322	0.39911	6.93
H(10)	C(6)	0.57810	1.39064	0.33746	6.93
H(11)	N(1)	0.32571	1.15984	0.07512	4.38
H(12)	N(1)	0.39776	1.02533	0.00851	4.38
H(13)	N(1)	0.32318	0.84740	0.06071	4.38
H(14)	C(8)	-0.09309	-0.06130	0.17594	4.12
H(15)	C(9)	0.12343	0.25452	0.25164	4.12
H(16)	C(9)	0.12699	-0.05343	0.26287	4.12
H(17)	C(10)	-0.00417	0.28406	0.34062	4.12
H(18)	C(11)	0.21675	0.32797	0.41140	6.93
H(19)	C(11)	0.15188	0.20126	0.48358	6.93
H(20)	C(11)	0.22932	0.02039	0.43468	6.93
H(21)	C(12)	0.02274	-0.26504	0.37558	6.93
H(22)	C(12)	-0.04230	-0.06221	0.42687	6.93
H(23)	C(12)	-0.10673	-0.12152	0.31649	6.93
H(24)	N(2)	0.06627	-0.15019	0.10808	4.38
H(25)	N(2)	-0.05549	-0.00392	0.03364	4.38
H(26)	N(2)	0.07286	0.15595	0.08468	4.38

Refined

H(27)	O(1), O(2)	0.750 (6)	0.602 (20)	0.185 (4)	5.2
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^{*} Other computer programs used have been described by Schlemper, Hamilton & La Placa (1971).

Table 1. *Positional and thermal parameters for di-L-leucine hydrochloride*

The Debye–Waller factor is defined as $\exp(-\sum 2\pi^2 a_i^* a_j^* h_i h_j U_{ij})$. The numbers in parentheses are the e.s.d.'s in the last significant figure of the tabulated quantities. Atoms O(1) through C(6) belong to one leucine molecule, atoms O(3) through C(12) belong to the other.

ATOM	<i>X</i>	<i>Y</i>	<i>Z</i>	<i>U11</i>	<i>U22</i>	<i>U33</i>	<i>U12</i>	<i>U13</i>	<i>U23</i>
C1	.20779(9)	.50000	.10078(7)	353(5)	355(13)	509(6)	5(6)	125(4)	-3(7)
O1	.52263(11)	.59568(97)	.07449(22)	491(16)	293(45)	467(16)	50(17)	206(13)	-54(17)
O2	.69083(32)	.76772(127)	.17983(29)	342(16)	528(49)	827(25)	98(21)	144(16)	-148(26)
N1	.37814(31)	1.01095(150)	.06695(22)	369(16)	354(41)	376(16)	102(27)	128(13)	84(28)
C1	.57341(40)	.76457(138)	.13126(30)	334(19)	224(57)	409(22)	13(22)	175(16)	6(23)
C2	.49718(36)	.99118(164)	.14676(26)	355(17)	145(44)	365(17)	33(26)	141(14)	1(26)
C3	.46027(43)	.96980(187)	.23408(30)	419(21)	555(63)	392(20)	34(31)	191(17)	-45(31)
C4	.56727(47)	.97672(202)	.32527(31)	496(24)	520(66)	390(21)	76(36)	130(18)	11(33)
C5	.51107(70)	.93491(260)	.40235(37)	861(42)	1377(124)	403(26)	113(58)	275(27)	57(43)
C6	.63761(92)	1.23668(281)	.33840(54)	1121(63)	967(144)	655(41)	-323(69)	187(40)	-205(51)
O3	-.18239(40)	.37443(126)	.19320(31)	643(23)	598(51)	847(26)	297(28)	43(21)	158(28)
O4	-.10798(35)	.46556(121)	.07910(24)	602(19)	324(43)	597(19)	167(24)	260(15)	118(24)
N2	.01442(32)	.01190(142)	.09320(23)	402(16)	210(39)	407(16)	55(26)	147(13)	-44(25)
C7	-.11372(39)	.32834(165)	.14189(30)	292(19)	342(51)	429(22)	40(24)	130(16)	41(29)
C8	-.03777(41)	.07915(145)	.16882(30)	371(19)	173(58)	439(22)	-11(22)	164(17)	35(22)
C9	.07527(46)	.10157(162)	.25785(35)	417(23)	543(77)	497(26)	29(28)	121(20)	30(30)
C10	.04791(56)	.12846(185)	.14626(37)	562(29)	670(79)	472(26)	99(36)	132(23)	-65(33)
C11	.17014(77)	.17861(320)	.42458(49)	809(46)	1657(135)	563(36)	119(69)	11(32)	-60(58)
C12	-.02662(95)	-.09334(273)	.36736(50)	1186(65)	1369(148)	650(41)	-227(76)	410(43)	171(58)

and observed structure factors (with standard deviations used in the refinement) are presented in Table 3. Bond distances and angles are presented in Table 4, where they are compared with the corresponding values for the hydrobromide, the hydriodide, and for the leucyl residue in peptides studied by Chandrasekaran & Subramanian (1969) and by Leung & Marsh (1958). Torsion angles are given in Table 5, and parameters for the hydrogen bonds are presented in Table 6.

Discussion

The most striking feature of the structure is the existence of a hydrogen-bonded, dimeric cation consisting

of two leucine molecules sharing a proton in a very short (2.43 Å) hydrogen bond between the two carbonyl groups. This configuration is illustrated in Fig. 1. These dimers are more weakly hydrogen-bonded through the chloride ions to form double layers parallel to the (001) plane (see Fig. 2). There is also a single N-H...O hydrogen bond. These layers are terminated on both sides in the c direction with nonpolar methyl groups. The shortest C-C contact between layers is 3.91(2) Å [C(5)-C(11)(1-x, 1/2+y, -1z)]. The only H-H contacts (based on the calculated positions) smaller than 2.6 Å are 2.373, 2.539, 2.366, 2.440, and 2.482 Å. These are all normal van der Waals contacts.

The structure contains two crystallographically dis-

Table 3. Structure amplitudes (x100) in electrons-cell⁻¹ for di-L-leucine hydrochloride

FO = Observed structure amplitude (including a small extinction correction),
 FC = Calculated structure amplitude for the parameters of Tables 1 and 2,
 SIG = Standard deviation of FO used in structure refinement. The tabulated values should be divided by 5 to obtain estimated standard deviations on an absolute scale.

h	k	l	FO	SIG	FC	h	k	l	FO	SIG	FC	h	k	l	FO	SIG	FC	h	k	l	FO	SIG	FC
0	0	0	100	0	100	0	0	0	100	0	100	0	0	0	100	0	100	0	0	0	100	0	100
1	0	0	100	0	100	1	0	0	100	0	100	1	0	0	100	0	100	1	0	0	100	0	100
2	0	0	100	0	100	2	0	0	100	0	100	2	0	0	100	0	100	2	0	0	100	0	100
3	0	0	100	0	100	3	0	0	100	0	100	3	0	0	100	0	100	3	0	0	100	0	100
4	0	0	100	0	100	4	0	0	100	0	100	4	0	0	100	0	100	4	0	0	100	0	100
5	0	0	100	0	100	5	0	0	100	0	100	5	0	0	100	0	100	5	0	0	100	0	100
6	0	0	100	0	100	6	0	0	100	0	100	6	0	0	100	0	100	6	0	0	100	0	100
7	0	0	100	0	100	7	0	0	100	0	100	7	0	0	100	0	100	7	0	0	100	0	100
8	0	0	100	0	100	8	0	0	100	0	100	8	0	0	100	0	100	8	0	0	100	0	100
9	0	0	100	0	100	9	0	0	100	0	100	9	0	0	100	0	100	9	0	0	100	0	100
10	0	0	100	0	100	10	0	0	100	0	100	10	0	0	100	0	100	10	0	0	100	0	100
11	0	0	100	0	100	11	0	0	100	0	100	11	0	0	100	0	100	11	0	0	100	0	100
12	0	0	100	0	100	12	0	0	100	0	100	12	0	0	100	0	100	12	0	0	100	0	100
13	0	0	100	0	100	13	0	0	100	0	100	13	0	0	100	0	100	13	0	0	100	0	100
14	0	0	100	0	100	14	0	0	100	0	100	14	0	0	100	0	100	14	0	0	100	0	100
15	0	0	100	0	100	15	0	0	100	0	100	15	0	0	100	0	100	15	0	0	100	0	100
16	0	0	100	0	100	16	0	0	100	0	100	16	0	0	100	0	100	16	0	0	100	0	100
17	0	0	100	0	100	17	0	0	100	0	100	17	0	0	100	0	100	17	0	0	100	0	100
18	0	0	100	0	100	18	0	0	100	0	100	18	0	0	100	0	100	18	0	0	100	0	100
19	0	0	100	0	100	19	0	0	100	0	100	19	0	0	100	0	100	19	0	0	100	0	100
20	0	0	100	0	100	20	0	0	100	0	100	20	0	0	100	0	100	20	0	0	100	0	100
21	0	0	100	0	100	21	0	0	100	0	100	21	0	0	100	0	100	21	0	0	100	0	100
22	0	0	100	0	100	22	0	0	100	0	100	22	0	0	100	0	100	22	0	0	100	0	100
23	0	0	100	0	100	23	0	0	100	0	100	23	0	0	100	0	100	23	0	0	100	0	100
24	0	0	100	0	100	24	0	0	100	0	100	24	0	0	100	0	100	24	0	0	100	0	100
25	0	0	100	0	100	25	0	0	100	0	100	25	0	0	100	0	100	25	0	0	100	0	100
26	0	0	100	0	100	26	0	0	100	0	100	26	0	0	100	0	100	26	0	0	100	0	100
27	0	0	100	0	100	27	0	0	100	0	100	27	0	0	100	0	100	27	0	0	100	0	100
28	0	0	100	0	100	28	0	0	100	0	100	28	0	0	100	0	100	28	0	0	100	0	100
29	0	0	100	0	100	29	0	0	100	0	100	29	0	0	100	0	100	29	0	0	100	0	100
30	0	0	100	0	100	30	0	0	100	0	100	30	0	0	100	0	100	30	0	0	100	0	100
31	0	0	100	0	100	31	0	0	100	0	100	31	0	0	100	0	100	31	0	0	100	0	100
32	0	0	100	0	100	32	0	0	100	0	100	32	0	0	100	0	100	32	0	0	100	0	100
33	0	0	100	0	100	33	0	0	100	0	100	33	0	0	100	0	100	33	0	0	100	0	100
34	0	0	100	0	100	34	0	0	100	0	100	34	0	0	100	0	100	34	0	0	100	0	100
35	0	0	100	0	100	35	0	0	100	0	100	35	0	0	100	0	100	35	0	0	100	0	100
36	0	0	100	0	100	36	0	0	100	0	100	36	0	0	100	0	100	36	0	0	100	0	100
37	0	0	100	0	100	37	0	0	100	0	100	37	0	0	100	0	100	37	0	0	100	0	100
38	0	0	100	0	100	38	0	0	100	0	100	38	0	0	100	0	100	38	0	0	100	0	100
39	0	0	100	0	100	39	0	0	100	0	100	39	0	0	100	0	100	39	0	0	100	0	100
40	0	0	100	0	100	40	0	0	100	0	100	40	0	0	100	0	100	40	0	0	100	0	100
41	0	0	100	0	100	41	0	0	100	0	100	41	0	0	100	0	100	41	0	0	100	0	100
42	0	0	100	0	100	42	0	0	100	0	100	42	0	0	100	0	100	42	0	0	100	0	100
43	0	0	100	0	100	43	0	0	100	0	100	43	0	0	100	0	100	43	0	0	100	0	100
44	0	0	100	0	100	44	0	0	100	0	100	44	0	0	100	0	100	44	0	0	100	0	100
45	0	0	100	0	100	45	0	0	100	0	100	45	0	0	100	0	100	45	0	0	100	0	100
46	0	0	100	0	100	46	0	0	100	0	100	46	0	0	100	0	100	46	0	0	100	0	100
47	0	0	100	0	100	47	0	0	100	0	100	47	0	0	100	0	100	47	0	0	100	0	100
48	0	0	100	0	100	48	0	0	100	0	100	48	0	0	100	0	100	48	0	0	100	0	100
49	0	0	100	0	100	49	0	0	100	0	100	49	0	0	100	0	100	49	0	0	100	0	100
50	0	0	100	0	100	50	0	0	100	0	100	50	0	0	100	0	100	50	0	0	100	0	100
51	0	0	100	0	100	51	0	0	100	0	100	51	0	0	100	0	100	51	0	0	100	0	100
52	0	0	100	0	100	52	0	0	100	0	100	52	0	0	100	0	100	52	0	0	100	0	100
53	0	0	100	0	100	53	0	0	100	0	100	53	0	0	100	0	100	53	0	0	100	0	100
54	0	0	100	0	100	54	0	0	100	0	100	54	0	0	100	0	100	54	0	0	100	0	100
55	0	0	100	0	100	55	0	0	100	0	100	55	0	0	100	0	100	55	0	0	100	0	100
56	0	0	100	0	100	56	0	0	100	0	100	56	0	0	100	0	100	56	0	0	100	0	100
57	0	0	100	0	100	57	0	0	100	0	100	57	0	0	100	0	100	57	0	0	100	0	100
58	0	0	100	0	100	58	0	0	100	0	100	58	0	0	100	0	100	58	0	0	100	0	100
59	0	0	100	0	100	59	0	0	100	0	100	59	0	0	100	0	100	59	0	0	100	0	100
60	0	0	100	0	100	60	0	0	100	0	100	60	0	0	100	0	100	60	0	0	100	0	100
61	0	0	100	0	100	61	0	0	100	0	100	61	0	0	100	0	100	61	0	0	100	0	100
62	0	0	100	0	100	62	0	0	100	0	100	62	0	0	100	0	100	62	0	0	100	0	100
63	0	0	100	0	100	63	0	0	100	0	100	63	0	0	100	0	100	63	0	0	100	0	100
64	0	0	100	0	100	64	0	0	100	0	100	64	0	0	100	0	100	64	0	0	100	0	100
65	0	0	100	0	100	65	0	0	100	0	100	65	0	0	100	0	100	65	0	0	100	0	100
66	0	0	100	0	100	66	0	0	100	0	100	66	0	0	100	0	100	66	0	0	100	0	100
67	0	0	100	0	100	67	0	0	100	0	100	67	0</										

Table 4. Bond distances and angles in di-L-leucine hydrochloride and comparison with the values for the hydrobromide (Subramanian, 1967), the hydriodide (Chaney, Seeley & Steinrauf, 1971), for the dipeptide studied by Chandrasekaran & Subramanian (1969), and for the tripeptide studied by Leung & Marsh (1958).

Molecule 1		Molecule 2		Mean (this structure)		Hydrobromide*	Hydroiodide†	C & S peptide‡	L & M peptide
C(1)-O(1)	1.229 (7) Å	C(7)-O(4)	1.214 (7) Å	C'-O'	1.221 (5) Å	1.20 Å	1.19 Å	1.226 Å	1.27 (2) Å
C(1)-O(2)	1.280 (6)	C(7)-O(3)	1.288 (6)	C'-O''	1.284 (4)	1.30	1.30	—	—
C(1)-C(2)	1.502 (9)	C(7)-C(8)	1.512 (10)	C'-C ^α	1.507 (7)	1.55	1.53	1.545	1.50 (2)
C(2)-N(1)	1.492 (5)	C(8)-N(2)	1.501 (6)	C ^α -N	1.497 (4)	1.51	1.53	1.506	1.49 (2)
C(2)-C(3)	1.533 (5)	C(8)-C(9)	1.537 (6)	C ^α -C ^β	1.535 (4)	1.51	1.52	1.545	1.54 (2)
C(3)-C(4)	1.520 (6)	C(9)-C(10)	1.496 (7)	C ^β -C ^γ	1.508 (5)	1.51	1.51	1.531	1.52 (2)
C(4)-C(6)	1.524 (15)	C(10)-C(12)	1.503 (14)	C ^γ -C ^{δ2}	1.513 (10)	1.49	1.56	1.523	1.51 (4)
C(4)-C(5)	1.527 (7)	C(10)-C(11)	1.521 (9)	C ^γ -C ^{δ1}	1.524	1.53	1.57	1.560	1.51 (4)
O(1)-C(1)-O(2)	124.9 (6)°	O(4)-C(7)-O(3)	125.4 (7)°	O'-C'-O''	125.2 (5)°	124°	122°	—	—
C(2)-C(1)-O(1)	120.1 (4)	C(8)-C(7)-O(4)	122.4 (4)	C ^α -C'-O'	121.3 (3)	126	126	120.5°	119 (1)°
C(2)-C(1)-O(2)	114.9 (5)	C(8)-C(7)-O(3)	112.2 (5)	C ^α -C'-O''	113.5 (4)	110	111	—	—
C(1)-C(2)-N(1)	108.6 (5)	C(7)-C(8)-N(2)	107.7 (4)	C'-C ^α -N	108.2 (3)	105	105	107.1	108 (1)
C(3)-C(2)-N(1)	107.9 (3)	C(9)-C(8)-N(2)	107.3 (4)	C ^β -C ^α -N	107.6 (3)	108	106	110.0	112 (1)
C(1)-C(2)-C(3)	114.3 (5)	C(7)-C(8)-C(9)	114.0 (5)	C'-C ^α -C ^β	114.2 (4)	113	113	111.2	112 (1)
C(2)-C(3)-C(4)	111.0 (7)	C(8)-C(9)-C(10)	118.0 (4)	C ^α -C ^β -C ^γ	114.0	119	114	114.0	118 (1)
C(3)-C(4)-C(5)	108.5 (5)	C(9)-C(10)-C(11)	110.0 (5)	C ^β -C ^γ -C ^{δ1}	109.3 (4)	111	108	109.9	109 (3)
C(3)-C(4)-C(6)	111.0 (7)	C(9)-C(10)-C(12)	114.7 (7)	C ^β -C ^γ -C ^{δ2}	112.9 (5)	114	109	108.9	111 (3)
C(5)-C(4)-C(6)	110.0 (7)	C(11)-C(10)-C(12)	111.8 (8)	C ^{δ2} -C ^γ -C ^{δ1}	110.9 (6)	112	108	111.2	110 (3)

* E.s.d.'s are 0.03→0.04 Å in distances and 4° in angles

† E.s.d.'s are 0.02→0.03 Å in distances and 1-2° in angles.

‡ E.s.d.'s are 0.013 Å in distances and 1° in angles.

tinct L-leucine molecules (Fig. 1). The agreement between the geometry of these and that of the other determinations of the leucyl residue geometry is satisfactory; this study has provided the smallest standard deviations available. The bond lengths for the two molecules in the asymmetric unit agree well, but there are marked differences in the angles about the carbon atoms in the side chain, particularly at the β carbon atom. It is interesting to note that these are the very angles for which there is the most variation between the geometries of the hydrobromide and hydriodide salts and the peptidyl leucine residue. The unusually large value of 118° for molecule 2 is identical to that found by Leung & Marsh in L-leucyl-L-prolylglycine. Apparently, this angle can easily adapt in response to steric constraints in the intermolecular environment.

Even without the location of H(27), the difference between the C–O bond lengths clearly indicates, for each molecule, the presence of a double-bonded oxygen atom and an approximately single-bonded oxygen atom (*e.g.*, see the tabulation by Nardelli, Fava & Giraldi, 1962), although the value $1.284(4)\text{Å}$ for the latter is somewhat shorter than the mean value of 1.303Å for the single C–O bonds tabulated by Nardelli *et al.* and the value of $1.305(4)\text{Å}$ found in the neutron dif-

fraction study of trichloroacetic acid (Jönsson & Hamilton, 1972); this shortening is consistent with the fact that a hydrogen atom is shared nearly equally between the two carboxyl groups.

The L-leucine molecule may be characterized by two planes: one through the carboxyl group and the other through the side chain. Both carboxyl groups are nearly coplanar with the α carbon atom. Atoms O(1), O(2), C(1), C(2), and O(3), O(4), C(7), C(8) lie in the planes:

$$0.4707 X + 0.5206 Y - 0.7123 Z = 3.3798 \text{ Å}$$

and

$$0.5785 X + 0.5158 Y + 0.6319 Z = 1.0306 \text{ Å},$$

where the coordinates are in Å parallel to the a , b , and c^* axes. The deviations of the individual atoms from the planes are: O(1), 0.0018; O(2), 0.0016; C(1), -0.0047 , and C(2), 0.013 Å from the first plane and O(3), 0.0006; O(4), 0.007; C(7), -0.0019 and C(8), 0.0005 Å from the second plane. The least-squares plane for the side chain of molecule 1 through atoms C(2) to C(5) is defined by

$$-0.1282 X + 0.9910 Y + 0.0383 Z = 4.5133 \text{ Å}.$$

Table 5. *Torsion angles in di-L-leucine hydrochloride, in leucine hydrobromide (Subramanian, 1967), and in leucine hydriodide (Chaney, Seely, & Steinrauf, 1971).*

The notation is that of Table 4, and the conventions are those of IUPAC-IUB (1970). The principal torsion angles ψ , $\chi^{\alpha\beta}$, and $\chi^{\beta\gamma}$ are illustrated in Fig. 3.

		Molecule 1	Molecule 2	Mean	HBr	HI
ψ :	O' = C'–C $^{\alpha}$ –N	–17.7 (6)	–13.1 (7)	–15.4	–15.2	–13.3
	O''–C'–C $^{\alpha}$ –N	161.3 (5)	167.3 (5)	164.3	172.8	179.6
$\chi^{\alpha\beta}$:	N–C $^{\alpha}$ –C $^{\beta}$ –C $^{\gamma}$	–173.6 (7)	–171.2 (7)	–172.4	–172.2	–172.4
	O''–C'–C $^{\alpha}$ –C $^{\beta}$	–78.1 (6)	–73.8 (6)	–76.0	–69.4	75.2
	O'–C'–C $^{\alpha}$ –C $^{\beta}$	102.8 (5)	105.8 (6)	104.3	102.7	101.8
	C'–C $^{\alpha}$ –C $^{\beta}$ –C $^{\gamma}$	65.4 (9)	69.7 (8)	67.5	71.5	73.4
$\chi^{\beta\gamma}$:	C $^{\alpha}$ –C $^{\beta}$ –C $^{\gamma}$ –C $^{\delta 1}$	–176.3 (8)	–173.6 (9)	–174.9	–175.5	–178.6
	C $^{\alpha}$ –C $^{\beta}$ –C $^{\gamma}$ –C $^{\delta 2}$	62.6 (9)	59.2 (9)	60.9	56.6	65.0

Table 6. *Hydrogen bond distances and angles in di-L-leucine hydrochloride**

	C–Y–H \cdots X		R(Y–H)	R(H \cdots X)	R(Y \cdots X)	\angle YHX	\angle CYH	
C(2 ⁱⁱ)	N(1 ⁱⁱ)	H(11 ⁱ)	Cl	0.99 Å	2.29 Å	3.284 (6) Å	177°	109.1 (4)°
C(2)	N(1)	H(12)	O(1 ^{iv})	1.00	1.81	2.779 (5)	162	100.5 (2)
C(2)	N(1)	H(13)	Cl	1.02	2.39	3.370 (7)	160	102.4 (4)
C(8 ⁱ)	N(2 ⁱ)	H(24 ⁱ)	Cl	0.99	2.41	3.370 (6)	161	123.8 (4)
C(8 ⁱⁱⁱ)	N(2 ⁱⁱⁱ)	H(25 ⁱⁱⁱ)	Cl	1.00	2.21	3.204 (4)	175	110.5 (2)
C(8)	N(2)	H(26)	Cl	1.02	2.28	3.277 (6)	166	102.4 (4)
{C(1)	O(2)	H(27)	O(3 ^v)	1.06 (9)	1.37 (9)	2.429 (7)	175 (7)	119.7 (5)}
{C(7 ^v)	O(3 ^v)	H(27)	O(2)	1.37 (9)	1.06 (9)	2.429 (7)	175 (7)	123.0 (5)}
Donor angles around Cl								
	N(2)–Cl–N(2 ⁱ)	100.6 (1)°		N(2 ⁱⁱⁱ)–Cl–N(2)	71.4 (1)°			
	N(2)–Cl–N(1 ⁱⁱ)	79.7 (2)		N(2 ⁱⁱⁱ)–Cl–N(1)	98.4 (1)			
	N(1)–Cl–N(1 ⁱⁱ)	100.5 (1)		N(2 ⁱⁱⁱ)–Cl–N(1 ⁱⁱ)	100.3 (1)			
	N(1)–Cl–N(2 ⁱ)	77.2 (1)		N(2 ⁱⁱⁱ)–Cl–N(2 ⁱ)	70.2 (1)			

* The coordinates of the hydrogen atoms, except H(27), were not refined but merely placed in geometrically reasonable positions; hence, no errors on quantities involving hydrogen are quoted. A final adjustment of hydrogen positions was not made following the last series of least-squares cycles; this accounts for the nonconstant N–H bond lengths. Symmetry equivalent positions are i($x, 1+y, z$), ii($x, y-1, z$), iii($-x, \frac{1}{2}+y, -z$), iv($1-x, \frac{1}{2}+y, -z$), v($x+1, y, z$).

The deviations from the plane are; C(2), -0.023 ; C(3), 0.026 ; C(4), 0.018 , and C(5), -0.021 Å. N(1) lies 0.152 Å from the plane and C(1) lies -1.299 Å from the plane. The same arrangement is found for the second molecule. The side chain with carbon atoms C(8) to C(11) has a least-squares plane with equation:

$$-0.0475 X + 0.9913 Y - 0.1226 Z = 0.1208 \text{ \AA} .$$

Deviations for individual atoms from the plane are C(8), 0.039 ; C(9), -0.045 ; C(10), -0.031 , and C(11), 0.037 Å. N(2) lies 0.212 Å from the plane and C(7) lies 1.385 Å from the plane. These results compare well with the results of Subramanian (1967): the nitrogen atom is 0.186 Å out of the plane through the side chain, while the carboxylic carbon atom is 1.419 Å from the plane.

The mean value for the C-C bond lengths is 1.521

Å for the first molecule and 1.514 Å for the second, in good agreement with the value of 1.52 Å in L-leucine hydrobromide (Subramanian, 1967) and slightly less than the pure aliphatic C-C single-bond length of $1.533(3)$ Å (Bartell, 1959). This shortening appears as well in other amino acid structures (Parthasarathy, 1966; Wright & Marsh, 1962). The mean values for the C-C-C bond angles are 111.0 and 113.5° , in good agreement with 113.8° in L-leucine hydrobromide and with the value of 112.4° for straight-chain aliphatic hydrocarbons (Bonham & Bartell, 1959).

The network of hydrogen bonds is shown in Fig. 2. The distances and the angles involved are summarized in Table 6. All seven hydrogen atoms in the asymmetric unit which can take part in hydrogen bonds do so. The chloride ion is hydrogen-bonded to five nitrogen atoms at distances ranging from 3.204 Å to N(2¹¹¹), to 3.370 Å to N(2¹) and N(1). N(1), N(1¹¹), N(2) and

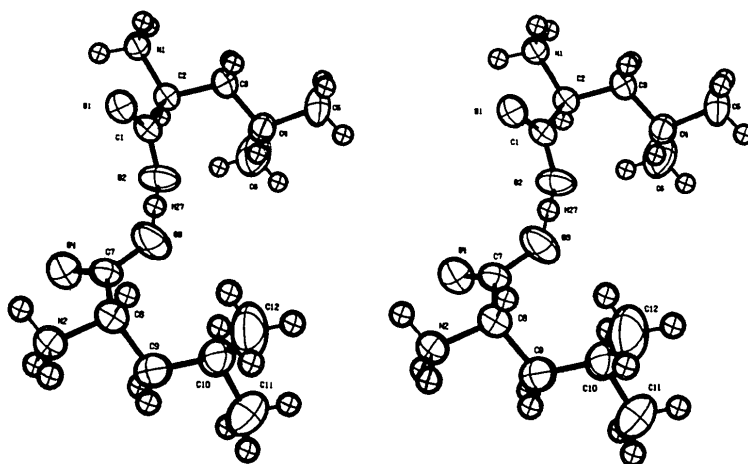


Fig. 1. The two crystallographically independent leucine molecules joined by a short hydrogen bond to form a dimeric cation. The view is approximately along the b axis. Thermal ellipsoids for the heavy atoms are drawn at the 50% probability level. Spheres of arbitrary size are shown for hydrogen atoms.

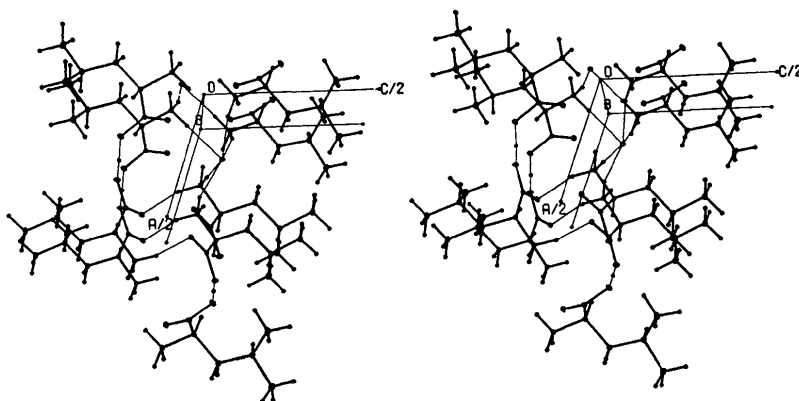


Fig. 2. Hydrogen bonding in di-L-leucine hydrochloride. The two molecules in the asymmetric unit are shown together with all molecules hydrogen-bonded to the basic molecules or to the Cl^{-1} ion, which is seen involved in five hydrogen bonds. Note that all the hydrogen bonds lie near the $z=0$ plane, while nonpolar contacts lie along $z=\frac{1}{2}$.

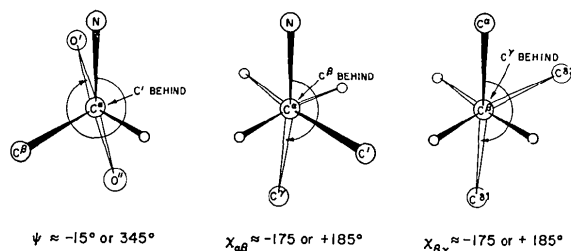


Fig. 3. Definition of the principal torsion angles in peptide residues and amino acids. The values indicated are the approximate mean configurations in di-L-leucine hydrochloride and L-leucine hydrobromide.

N(2ⁱ) form a rectangle with edges 5.116(1) and 4.205(5) Å and angles 89.9(1)° at N(1) and 90.1(1)° at N(2) with the chlorine atom nearly in the center. The fifth nitrogen atom N(2ⁱⁱⁱ) is at the vertex of the distorted rectangular pyramid. The shortest hydrogen atom contacts from the other side to chlorine are H(3) and H(15) at distances of 2.97 and 3.05 Å, which are too long to be accepted as hydrogen bonds. N(2) is hydrogen-bonded to three chlorine atoms related by a screw diad and by a translation along the *b* axis. Nitrogen atom N(1) is hydrogen-bonded to two chlorine atoms, related by a translation in the direction of the *b* axis and to oxygen atom O(1^{iv}) at a distance of 2.779 (5) Å. The shortest hydrogen bond in the structure is between oxygen atoms O(2) and O(3^v): 2.429(7) Å, which connects two L-leucine groups. The only nonhydrogen bonded polar atom is O(4), which is the nearest oxygen atom to the chlorine ion [3.432(4) Å] and is 3.160 (5) Å away from N(2ⁱⁱⁱ). Both distances are longer than usual hydrogen bonds.

The short O...O hydrogen bond is confirmed; the length of this bond is typical of those in dianions which appear in the acid salts of carboxylic acids (Speakman, 1967). In such salts, the hydrogen bond is almost always symmetric – with a single minimum potential function; here the refined O–H bond lengths are 1.06(9) and 1.37(9) Å, not significantly different, so that the results are consistent with a symmetric bond but give no unqualified support for it. A stronger case

for a symmetric bond may be made on the basis of the C–O bond lengths, 1.280(6) and 1.288(6) Å. If the bond were very asymmetric, we would expect a marked difference in these bond lengths. Furthermore, neither is quite long enough to be considered a normal C–O single bond (ideal value 1.30).

A neutron diffraction study for the resolution of the symmetry of the hydrogen bond would be worthwhile, although the infrared data of Hadži & Marciszewski (1967) and the heavy atom distances here strongly suggest a symmetric bond.

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