The Crystal Structure of the Copper(II) Complex of L-Isoleucine

By Charles M. Weeks,* A. Cooper* and Dorita A. Norton*

Center for Crystallographic Research, Roswell Park Memorial Institute, Buffalo, New York 14203, *U.S.A.*

The crystal structure of bis-(L-isoleucinato)copper(II) monohydrate has been determined in order to discover typical conformations of the biologically important amino acid L-isoleucine. This is a *cis* copper complex, and the copper atom has fivefold coordination with its nearest neighbors disposed approximately in a square pyramid. The two isoleucine residues within a single molecule do not have the same conformation, and only one of the chelate rings is puckered. All amino and water hydrogen atoms are involved in hydrogen bonds which form layers of molecules parallel to (010). The crystals are orthorhombic (space group $P2_12_12_1$) and have four molecules in a unit cell whose dimensions are $a=9\cdot451$, $b=21\cdot674$, $c=7\cdot629$ Å.

Introduction

The determination of the crystal structure of bis-(L-isoleucinato)copper(II) monohydrate was undertaken because of the importance of the L-isoleucine residue as a constituent of most proteins. A detailed knowledge of the most stable conformations of the hydrocarbon chain of this amino acid will be of great utility in structural studies of proteins and peptides. This investigation has confirmed the observation that the hydrocarbon chains of L-isoleucine tend to lie in planes containing four carbon atoms (Trommel & Bijvoet, 1954), and it lends credence to the idea that there are two conformations of L-isoleucine which have particular stability.

This structure is also significant from the purely chemical point of view because of the recent attempts to correlate the sign and magnitude of the Cotton effect in L-α-amino acid copper(II) complexes with intramolecular geometry. Emphasis has been placed on the contribution of the atoms in the chelate rings, and the contribution of these atoms depends, in turn, on the conformation of the chelate rings.

X-ray analysis of the L-isoleucine complex has revealed the presence of a ring conformation whose importance has been overlooked in recent theoretical considerations of the Cotton effect (Wellman, Mungall, Mecca & Hare, 1967). Since it is to be expected that a proportion of the molecules will retain this conformation in solution, the contribution of this form to the Cotton effect must not be underestimated.

Experimental

Bis-(L-isoleucinato)copper(II) monohydrate was prepared by reaction of copper carbonate with L-isoleucine, and crystals were obtained by slow evaporation of the aqueous solution at room temperature. The crystals

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* Present address: Medical Foundation of Buffalo, 73 High Street, Buffalo, New York 14203, U.S.A.

are deep blue, and well-formed specimens are diamond-shaped plates having (010) as the dominant face. The density was determined by flotation in a mixture of acetone and methylene iodide, and a crystal of dimensions $0\cdot15 \times 0\cdot12 \times 0\cdot06$ mm was cut from one of the better plates for use in the X-ray measurements. The crystal data are:

$C_{12}H_{24}CuN_2O_4 . H_2O$, $M=341\cdot88$, $a=9\cdot451 \pm 0\cdot004$, $b=21\cdot67 \pm 0\cdot02$, $c=7\cdot629 \pm 0\cdot003$ Å; $V_0=1562\cdot72$ Å^3, $D_m=1\cdot51$, $Z=4$, $D_c=1\cdot45$ g.cm^{-3}; Space group $P2_12_12_1$ (D_2^4 no. 19).

The intensities of 1975 reflections with 2θ less than 160° were measured by the stationary-counter stationary-crystal technique (Furnas, 1966) using a General Electric single-crystal orienter. Cu $K\alpha$ radiation and balanced nickel and cobalt filters were employed, and ten second counts were made with each filter. The Lorentz and polarization corrections were applied, as was an approximate absorption correction such that an axial reflection at $\chi=90°$ had a constant intensity at all φ values. The scattering factor tables used were from *International Tables for X-ray Crystallography* (1962), Table 3.3.1A, and the real part of the anomalous dispersion correction was applied to the scattering factors for copper.

A three-dimensional Patterson synthesis was calculated and the position of the copper atom determined from the Harker sections. In order to locate the remaining atoms, successive Fourier syntheses were computed using previously discovered atomic coordinates which had been refined by least-squares using a block-diagonal approximation to the normal equations. In general, the remaining non-hydrogen atoms were found in an order depending on their distance from the copper, with the positions of the closest being ascertained first. Much of one isoleucine molecule was found, however, before any atoms in the other half of the asymmetric unit could be located with certainty.

After the positions of the twenty non-hydrogen atoms were determined, further refinement was brought about by approximating these atoms as ellipsoids, rather than as spheres, and by weighting the terms in the normal equations such that the values of $\langle w\varDelta^2 \rangle$ were invariant with the magnitude of $|F_o|$, where

Table 1. *Comparison of $|F_o|$ and $|F_c|$ calculated for the refined atomic parameters*

The structure amplitudes are given on ten times absolute scale.

Table 1 (cont.)

H	K	L	FOBS	FCAL

(Structure factor table: columns of H K L FOBS FCAL repeated across nine groups; numerical data largely illegible.)

$w^{-1} = 1 + [(|F_o| - b)/a]^2$; the constants a and b were taken to be 22e and 20e, respectively. An attempt was then made to find the hydrogen atoms. Twenty-one hydrogens were, in fact, located on electron density difference maps. The remaining five hydrogens, four of which are on methyl groups, could not be discovered because of the large thermal vibrations of the carbon atoms to which they are bonded. During the final least-squares cycles, these five atoms were placed at their expected positions but neither the coordinates of these last atoms nor the isotropic thermal parameters of any of the hydrogens were refined. The largest shifts in coordinates during the final cycle of refinement were approximately one third of the corresponding standard deviations. The quantity minimized was $(\Sigma w||F_o| - |F_c||^2)/(m-n)$ where m = the number of reflections and n = the number of parameters refined. Weak reflections (with observed intensities less than twice their calculated standard deviations) were ignored in making the calculations. The R index, which was defined as $\Sigma(||F_o| - |F_c||)/\Sigma|F_o|$, fell to a final value of 0·063.

The observed and calculated structure factor amplitudes are listed in Table 1, and the final coordinates and thermal parameters of the atoms in Tables 2(a) and 2(b). These thermal parameters are also shown graphically, in the form of their 50% probability ellipsoids, in Fig. 1(a).

Discussion

The intramolecular geometry of bis-(L-isoleucinato)–copper(II) monohydrate agrees very closely with that of similar, previously reported structures. We have compared our data with those reviewed by Freeman (1966) and have found only minor deviations in distances and angles from the average values for copper(II) amino acid complexes. The intramolecular distances and angles are shown in Fig. 1(b). The geometry about the copper is that of a distorted square pyramid. It is apparent from the least-squares planes data reported

in Table 3 (see plane 1) that the four close ligands are not truly planar. The chelate rings themselves are nearly planar (planes 2 and 3), and the angle between them is 14·9°.

The extent of puckering of the chelate rings is most clearly shown by the calculations for planes 4 and 5. The ring in the 'unprimed' isoleucine exists in a conformation having both carbon atoms of the ring on the same side of the Cu–O(1′)–N′ plane. This is a conformation which differs greatly from both the k and k' conformations (which have these carbons on opposite sides of the Cu–O–N plane) and whose presence Wellman et al. (1967) have assumed in their explanation of the sign and magnitude of the Cotton effect in L-α amino acid copper(II) complexes. The extensive hydrogen bonding present in the crystal (see below), and, in particular, the hydrogen bonds involving the carbonyl oxygen [O(2)] of the 'unprimed' residue may well provide forces which hold this ring in its observed conformation. Consequently, our comments are subject to the objection that the extent of hydrogen bonding in solution is not sufficient to maintain the chelate ring of the 'unprimed' residue in the conformation seen in the crystalline state. A definitive answer to this problem is not available at present. Furthermore, properties of the bis complex which depend on molecular geometry cannot be assumed to result simply from a summation of the contributions of the individual ligands. It is apparent from the torsion angles (Table 4) which have been calculated for the two halves of the molecule that there is a great lack of symmetry in this complex. Thus, it is not to be expected that the addition of a second ligand to the 1:1 copper(II) L-isoleucine complex will simply double the magnitude of the Cotton effect.

Like bisglycinatocopper(II) monohydrate (Freemen Snow, Nitta & Tomita, 1964), bis-(L-isoleucinato)copper(II) monohydrate is a cis complex. It may be that the cis conformation of this molecule allows a more extensive hydrogen bonding system accompanied by

Table 2(a). *Atomic coordinates and anisotropic thermal parameters for the non-hydrogen atoms*

Thermal parameters are of the form exp $[-2\pi^2(U_{11}h^2a^{*2}+2U_{12}hka^*b^*+\ldots)]$.

	X/A	Y/B	Z/C	U_{11}	U_{22}	U_{33}	U_{12}	U_{13}	U_{23}
Cu	0.1959(0)	0.2579(0)	0.2512(1)	0.0195(2)	0.0277(2)	0.0317(3)	−0.0006(2)	−0.0001(3)	−0.0077(3)
O(1)	0.0482(3)	0.2097(1)	0.1377(5)	0.0197(16)	0.0414(20)	0.0333(19)	−0.0015(15)	−0.0033(16)	−0.0110(17)
O(2)	0.0021(3)	0.1457(1)	−0.0794(5)	0.0217(17)	0.0424(21)	0.0464(23)	−0.0012(16)	−0.0120(18)	−0.0102(20)
N	0.3222(4)	0.2179(2)	0.0765(6)	0.0208(19)	0.0347(21)	0.0335(22)	−0.0018(18)	−0.0017(19)	−0.0127(19)
C(1)	0.0865(5)	0.1765(2)	0.0052(7)	0.0155(19)	0.0284(23)	0.0333(26)	−0.0011(19)	−0.0047(21)	−0.0010(21)
C(2)	0.2424(4)	0.1807(2)	−0.0503(7)	0.0144(18)	0.0237(21)	0.0325(26)	−0.0008(17)	−0.0043(20)	−0.0032(21)
C(3)	0.3142(6)	0.1186(2)	−0.0855(8)	0.0281(25)	0.0334(26)	0.0466(32)	0.0026(23)	−0.0019(29)	−0.0030(25)
C(4)	0.2628(6)	0.0850(2)	−0.2516(11)	0.0389(29)	0.0499(32)	0.0589(40)	−0.0011(25)	0.0008(41)	−0.0231(42)
C(5)	0.2672(8)	0.1247(5)	−0.4140(11)	0.0508(44)	0.1371(85)	0.0451(41)	−0.0212(51)	0.0069(38)	−0.0272(54)
C(6)	0.3094(9)	0.0759(3)	0.0743(12)	0.0619(44)	0.0376(32)	0.0835(55)	0.0068(35)	0.0002(51)	0.0151(36)
O(1')	0.0760(3)	0.2734(1)	0.4548(4)	0.0220(16)	0.0433(20)	0.0270(17)	−0.0044(15)	0.0015(16)	−0.0097(16)
O(2')	0.0763(4)	0.3081(2)	0.7245(5)	0.0341(19)	0.0656(25)	0.0265(21)	−0.0137(19)	0.0125(19)	−0.0039(20)
N'	0.3424(4)	0.3038(1)	0.3868(5)	0.0150(17)	0.0333(21)	0.0272(21)	−0.0007(16)	−0.0004(17)	−0.0053(18)
C(1')	0.1358(5)	0.3014(2)	0.5832(7)	0.0218(21)	0.0286(23)	0.0272(24)	0.0009(19)	0.0024(21)	0.0016(21)
C(2')	0.2840(4)	0.3272(2)	0.5557(6)	0.0173(20)	0.0320(24)	0.0253(23)	−0.0032(19)	−0.0019(20)	−0.0109(20)
C(3')	0.2779(6)	0.3984(2)	0.5703(7)	0.0359(29)	0.0287(24)	0.0321(26)	−0.0090(22)	0.0068(25)	−0.0082(22)
C(4')	0.1731(8)	0.4280(2)	0.4432(9)	0.0631(43)	0.0304(28)	0.0521(38)	0.0044(30)	−0.0022(39)	0.0021(28)
C(5')	0.1307(11)	0.4925(3)	0.4973(13)	0.1046(71)	0.0447(40)	0.0853(69)	0.0205(47)	−0.0001(65)	0.0044(45)
C(6')	0.4264(7)	0.4258(3)	0.5596(11)	0.0443(36)	0.0562(40)	0.0738(50)	−0.0307(33)	0.0093(41)	−0.0159(39)
O(3)	0.1948(4)	0.3461(2)	0.0454(5)	0.0376(20)	0.0552(24)	0.0306(20)	0.0012(21)	−0.0010(20)	0.0008(19)

Table 2(b). *Atomic coordinates of the hydrogen atoms**

	X/A	Y/B	Z/C
H(1)	0·365 (7)	0·250 (3)	−0·036 (9)
H(2)	0·367 (7)	0·201 (3)	0·142 (9)
H(3)	0·248 (7)	0·209 (3)	−0·174 (10)
H(4)	0·423 (8)	0·129 (3)	−0·091 (9)
H(5)	0·158 (7)	0·064 (3)	−0·221 (10)
H(6)	0·323 (7)	0·049 (3)	−0·265 (10)
H(7)	0·353 (7)	0·135 (3)	−0·410 (9)
H(8)†	0·196 (7)	0·163 (3)	−0·404 (9)
H(9)†	0·243 (7)	0·098 (3)	−0·531 (9)
H(10)	0·343 (7)	0·102 (3)	0·188 (9)
H(11)	0·233 (7)	0·060 (3)	0·094 (10)
H(12)	0·382 (7)	0·038 (3)	0·023 (9)
H(1')	0·377 (7)	0·336 (3)	0·322 (9)
H(2')	0·397 (7)	0·278 (3)	0·420 (10)
H(3')	0·338 (7)	0·316 (3)	0·653 (9)
H(4')	0·242 (7)	0·403 (3)	0·689 (9)
H(5')	0·090 (8)	0·404 (3)	0·416 (9)
H(6')†	0·221 (8)	0·430 (3)	0·315 (9)
H(7')	0·191 (7)	0·513 (3)	0·476 (9)
H(8')†	0·108 (7)	0·493 (3)	0·636 (9)
H(9')†	0·037 (7)	0·506 (4)	0·425 (9)
H(10')	0·460 (7)	0·423 (3)	0·457 (9)
H(11')	0·504 (7)	0·403 (3)	0·642 (9)
H(12')	0·427 (7)	0·471 (3)	0·586 (9)
H(13)	0·273 (7)	0·355 (3)	0·048 (9)
H(14)	0·192 (7)	0·341 (3)	−0·035 (9)

* Standard deviations of the last two figures are given in parentheses. All hydrogen atoms were given an isotropic thermal parameter of 2·0 which was not refined.

† This hydrogen was not found on the electron density map. It was placed at its expected position for the final cycles of refinement, but its coordinates were not refined. The 'expected position' is at 1·08 Å from the carbon to which the hydrogen is bonded, and tetrahedral angles about this carbon are assumed.

closer intermolecular approaches and, consequently, more efficient packing than would be compatible with the *trans* conformation which is usually observed in bis amino acid complexes of copper(II).

There are twelve close contacts between the amino nitrogens and water oxygen of one molecule of the complex and oxygen atoms in other molecules. The pertinent distances and angles of the six crystallographically independent close nitrogen-oxygen and oxygen–oxygen contacts are listed in Table 5. All of these contacts are within the range normally observed for hydrogen bonds (*International Tables*, 1962; Baur, 1965). The molecules are hydrogen bonded in a manner such that layers are formed which are approximately paralled to (010). There are forty intermolecular contacts between non-hydrogen atoms which are shorter than 4·0 Å, and the majority of these (thirty-six) are between molecules within a layer formed by the hydrogen bonds. These short contacts other than the hydrogen bonds are listed in Table 6. It is apparent that much stronger intermolecular forces must exist parallel to (010) than perpendicular to it, and this is in accord with the observation that (010) is the dominant face of the crystal. Fig.2(*a*) and (*b*), which show the packing of the molecules in the unit cell, afford further insight into the arrangement of the molecules with respect to one another and give additional views of the layering accompanying the hydrogen bonds.

The hydrocarbon chains of the two isoleucine residues do not have the same orientation. In the 'unprimed' isoleucine residue, atoms C(3), C(4), C(5), and C(6) (see plane 6, Table 3) are coplanar to within 0·005 Å. In the 'primed' residue, atoms C(1'), C(2'), C(3'), and C(6') deviate by only 0·03 Å from a least squares plane, and atoms C(2'), C(3'), C(4'), and C(5')

are also approaching planarity (Table 3, planes 7 and 8). It was noted by Trommel & Bijvoet (1954) that a plane similar to (6) exists in D-isoleucine hydrobromide monohydrate, while planes analogous to (7) and (8) occur in D-isoleucine hydrochloride monohydrate.

In order to further compare our data with the data from these other structures containing isoleucine, we have used Trommel & Bijvoet's atomic coordinates for the hydrochloride and hydrobromide to calculate the pertinent planes (planes 9, 10, and 11 in Table 3) and also

N — H1	1·19 Å	O3—Cu—O1	97·5°
C2 — H3	1·14	O3—Cu—N	85·1
		O1—Cu—N'	175·0
		N—Cu—O1'	163·1

C1' — O2'	1·225 Å	O3 — Cu —O1'	111·7°
C3' — C6'	1·527	O3 — Cu — N '	86·9
N ' — H1'	0·93	O2'— C1'—C2'	120·1
C3' — H4'	0·97	N '— C2'—C1'	109·6
C5' — H7'	0·76	C1'— C2'— C3'	108·7

(b)
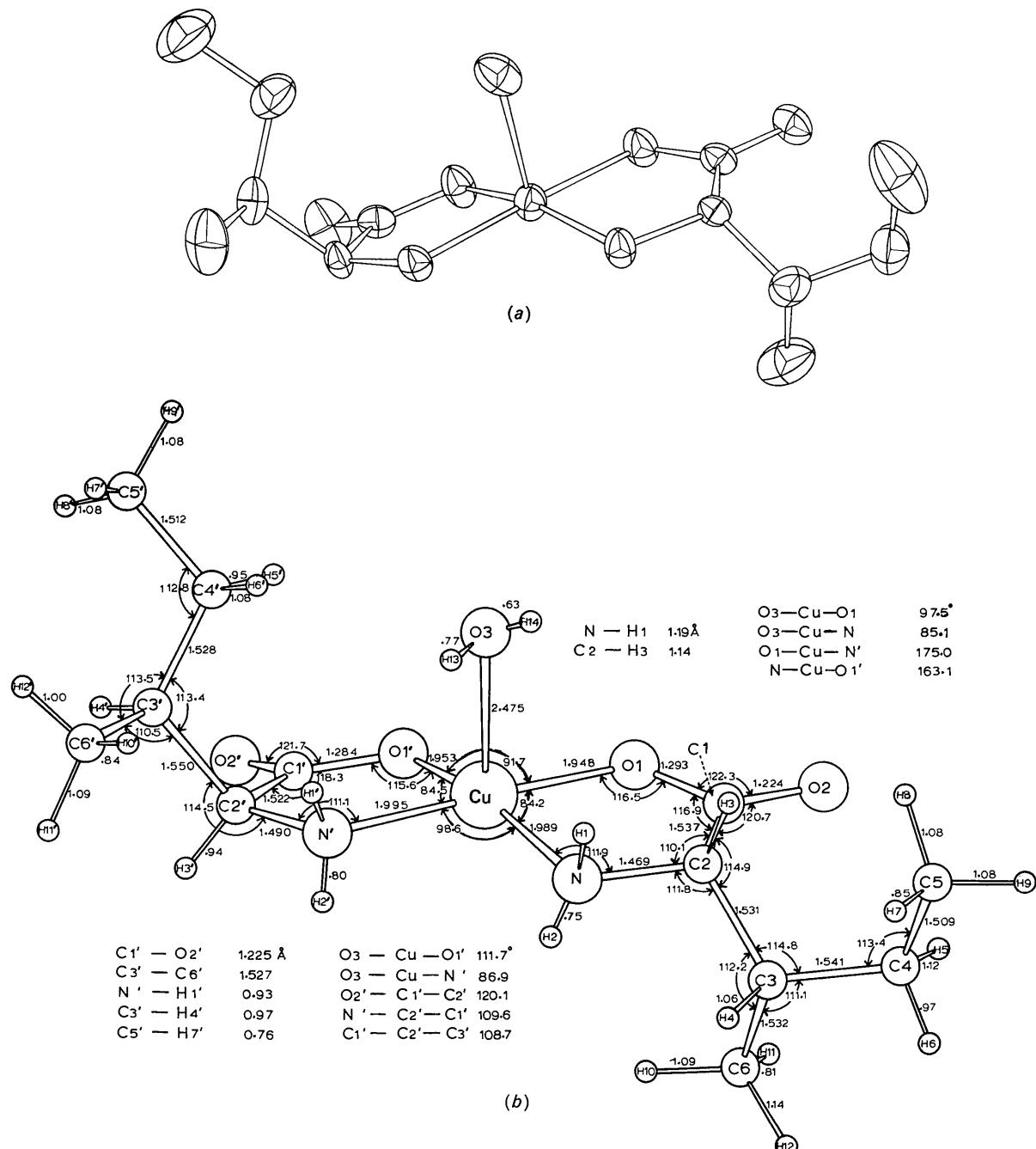
Fig. 1. (a) Thermal vibration ellipsoids, scaled to 50% probability, of the non-hydrogen atoms. The molecule is drawn with the same perspective as (b). (b) Nomenclature of the atoms and intramolecular distances and angles. The standard deviations of the distances are 0·004–0·010 Å, and the standard deviations of the angles are 0·2–0·6° if only non-hydrogen atoms are involved. The corresponding standard deviations, if one atom is hydrogen, are 0·2–0·6 Å and 3·8–6·5°, respectively.

Table 3. *Least-squares planes**

Plane	Atoms included in least-squares calculations†					Other atoms†					l	m	n	p
1	Cu 0·028	O(1) 0·113	N -0·105	O(1') -0·113	N' 0·105		Cu 0·173		O(3) 2·566		-0·2363	0·8131	-0·5321	2·916
2	O(1) -0·010	N -0·047	C(1) -0·019	C(2) 0·048				O(2) -0·003			-0·1769	0·7751	-0·6066	2·815
3	O(1') 0·025	N' -0·031	C(1') -0·049	C(2') 0·050				O(2') -0·185			-0·3296	0·8496	-0·4119	3·344
4	Cu 0·0	O(1) 0·0	N 0·0			O(2) 0·089	C(1) 0·044	C(2) 0·137			-0·1669	0·7514	-0·6384	2·668
5	O(1') 0·0	O(1') 0·0	N' 0·0			(O2') -0·202	C(1') -0·056	C(2') 0·075			-0·3093	0·8576	-0·4109	3·435
6	C(3) -0·005	C(4) -0·005	C(5) 0·005	C(6) 0·005		O(1) -3·266	O(2) -2·949	N -0·810	C(1) -2·524	C(2) -1·093	0·9355	-0·3007	-0·1854	2·131
7	C(1') 0·031	C(2') -0·030	C(3') -0·032	C(6') 0·031		O(1') -0·971	O(2') 1·013	N' -1·196	C(4) -1·166	C(5') -0·906	0·1320	-0·0683	0·9889	4·092
8	C(2') -0·118	C(3') 0·120	C(4') 0·119	C(5') -0·121		O(1') -1·387	O(2') -2·486	N' 0·979	C(1') -1·429	C(6') 1·362	0·7527	0·2269	-0·6181	1·127
9‡	C(3) -0·03	C(4) -0·03	C(5) 0·03	C(6) 0·03		O(1) -3·40	O(2) -2·81	N -1·39	C(1) -2·59	C(2) -1·34	-0·488	-0·608	-0·627	-4·92
10‡	C(1) 0·12	C(2) -0·10	C(3) -0·15	C(6) 0·13		O(1) -0·55	O(2) 1·22	N' -1·19	C(4) -1·52	C(5) -1·79	-0·201	-0·321	0·925	2·08
11‡	C(2) -0·04	C(3) 0·03	C(4) 0·06	C(5) -0·05		O(1) -1·78	O(2) -2·33	N 0·87	C(1) -1·50	C(6) 1·29	-0·853	0·079	-0·516	-4·31

* The planes are in the form $lx + my + nz = p$ where x, y, z and p are in Å and x, y and z are referred to the crystal axes.

† The numbers beneath each atom's name indicate the distance, in Å, of that atom from the plane.

‡ Plane 9 is for L-isoleucine hydrobromide monohydrate, and planes 10 and 11 are for L-isoleucine hydrochloride monohydrate. Calculations were made using Trommel & Bijvoet's atomic coordinates for the respective D isomers. The names of O(1) and O(2) in both of these compounds have been interchanged to facilitate comparison with the copper complex.

the torsion angles listed in Table 4. In making comparisons, allowance must be made for distortion about the atoms in the chelate ring caused by the introduction of the copper atom, and for the fact that the errors in the bond lengths and angles of the hydrobromide and hydrochloride were estimated at 0·05 Å and 10°, respectively. On the whole, however, some remarkable similarities between the different structures are apparent. We have concluded that the similarity between our 'unprimed' isoleucine molecule and the organic part

Table 4. *Torsion angles**

Bis-(L-isoleucinato)copper(II)
monohydrate

Torsion angle	'Unprimed' isoleucine residue	'Primed' isoleucine residue	L-Isoleucine hydrobromide monohydrate†	L-Isoleucine hydrochloride monohydrate†
O(1)–C(1)–C(2)–N	6·6°	−10·4°	−14°	6°
O(1)–C(1)–C(2)–C(3)	133·8	115·5	122	137
O(2)–C(1)–C(2)–N	−177·5	170·1	159	166
O(2)–C(1)–C(2)–C(3)	−50·3	−64·0	−64	−63
N—C(2)–C(3)–C(4)	−163·5	66·7	−168	48
N—C(2)–C(3)–C(6)	68·3	−62·0	66	−72
C(1)–C(2)–C(3)–C(4)	70·1	−56·3	60	−79
C(1)–C(2)–C(3)–C(6)	−58·1	175·0	−65	160
C(2)–C(3)–C(4)–C(5)	52·1	160·5	68	172
C(6)–C(3)–C(4)–C(5)	−179·2	−72·4	−175	−65

* We have used the convention of Klyne & Prelog (1960) in designating the signs of the torsion angles. The angle 1–2–3–4 is positive if a rotation of the 1–2 bond about the 2–3 bond by less than 180° will eclipse the 3–4 bond.
† Calculations were made using Trommel & Bijvoet's atomic coordinates for the D isomer. The names of C(1) and O(2) have been interchanged to facilitate comparison with the copper complex.

Table 5. *Geometry of close contacts involving hydroxyl and amine groups*

Hydrogen donor–hydrogen acceptor distance $A \cdots B$		Hydrogen acceptor–hydrogen distance $B \cdots H$		Angle A–H$\cdots B$	Position* of hydrogen acceptor (B)
N$\cdots$O(1)	3·113 Å	O(1) $\cdots$H(1)	2·08 Å	143	4/000
N$\cdots$O(2′)	2·896	O(2′)$\cdots$H(2)	2·23	149	4/001
N′ $\cdots$O(2)	2·995	O(2) $\cdots$H(1′)	2·23	139	4/000
N′ $\cdots$O(1′)	3·023	O(1′)$\cdots$H(2′)	2·24	167	4/001
O(3)$\cdots$O(2)	2·921	O(2) $\cdots$H(13)	2·18	163	4/000
O(3)$\cdots$O(2′)	2·816	O(2′)$\cdots$H(14)	2·25	150	1/00$\bar{1}$

* The equivalent positions are: $1 = (x, y, z)$; $2 = (\bar{x}, \frac{1}{2}+y, \frac{1}{2}-z)$; $3 = (\frac{1}{2}-x, \bar{y}, \frac{1}{2}+z)$; $4 = (\frac{1}{2}+x, \frac{1}{2}-y, \bar{z})$. N–O(2′) (4/001) means that the second atom [O(2′)] is at equivalent position 4, translated one unit-cell in the c direction.

Table 6. *Intermolecular distances between non-hydrogen atoms which are less than* 4·0 Å

Contact	Position*	Distance (Å)	Contact	Position*	Distance (Å)
†O(3) –C(5′)	3/01$\bar{1}$	3·882	O(1) –C(6′)	4/$\bar{1}$01	3·911
†O(2) –C(5′)	2/0$\bar{1}$0	3·605	O(2) –N	4/$\bar{1}$00	3·409
†C(4) –C(6)	3/00$\bar{1}$	3·795	O(2) –O(2′)	1/00$\bar{1}$	3·888
†C(5′)–C(6′)	3/01$\bar{1}$	3·817	N —C(1)	4/$\bar{1}$00	3·444
Cu—O(2)	4/000	3·801	N —C(1′)	4/001	3·962
Cu—C(5)	1/001	3·914	C(1) –O(2′)	1/00$\bar{1}$	3·569
Cu—O(2′)	4/001	3·875	C(1) –N′	4/$\bar{1}$00	3·802
O(3) –O(1)	4/000	3·818	C(2) –O(2′)	1/00$\bar{1}$	3·612
O(3) –N	4/$\bar{1}$00	3·899	C(2) –C(1′)	1/00$\bar{1}$	3·960
O(3) –C(1)	4/000	3·754	C(4) –C(6′)	4/$\bar{1}$00	3·960
O(3) –C(3)	4/$\bar{1}$00	3·691	C(5) –O(1′)	1/00$\bar{1}$	3·829
O(3) –C(1′)	1/00$\bar{1}$	3·699	C(5) –O(1′)	4/000	3·672
O(3) –C(2′)	1/00$\bar{1}$	3·852	C(5) –C(6′)	4/$\bar{1}$00	3·580
O(3) –C(3′)	1/00$\bar{1}$	3·878	C(6) –O(2′)	4/001	3·878
O(1) –C(2)	4/$\bar{1}$00	3·800	O(1′)–C(2′)	4/$\bar{1}$01	3·519
O(1) –O(2′)	1/00$\bar{1}$	3·816	O(2′)–N′	4/$\bar{1}$01	3·392
O(1) –C(2′)	4/$\bar{1}$01	3·514	N′—C(1′)	4/001	3·600

* Equivalent positions are designated in the same manner as for Table 5.
† This intermolecular contact is between atoms which are not within a layer formed by hydrogen bonds.

of L-isoleucine hydrobromide monohydrate is great enough for them to be regarded as isostructural. Some discrepancies do exist. For example, the distances of the nitrogen atoms from planes 6 and 9 should be more nearly alike; a similar comment may be made concerning C(2). These atoms are in a chelate ring in the copper complex, however, and the differences may be ascribed to the presence of the metal. On the other hand, the torsion angles compare extremely well in view of the accuracy with which angles in the hydrobromide are known. In case of the 'primed' isoleucine of the copper complex and L-isoleucine hydrochloride monohydrate, it is more difficult to draw definite conclusions. From the near planarity of the groups of carbon atoms discussed above and the similarity in certain torsion angles such as O(2)–C(1)–C(2)–C(3) and C(6)–C(3)–C(4)–C(5), it is apparent that the general conformations of the two residues are much alike. However, there are marked differences in the distances of C(4) and C(5) from the C(1), C(2), C(3), C(6) planes in the residues under consideration. The same thing may be said for the distance of O(1) from the C(2), C(3), C(4), C(5) plane and for the torsion angles O(2)–C(1)–C(2)–C(3) and C(6)–C(3)–C(4)–C(5).

With regard to the isoleucine residue itself, our results confirm the inference originally drawn by Trommel & Bijvoet (1954) in their paper, that 'branched carbon chains · · ·have a tendency to form plane zigzag chains of four carbon atoms'. This observation may be of considerable value in the future when crystallographic studies of the many important biological substances containing L-isoleucine are undertaken.

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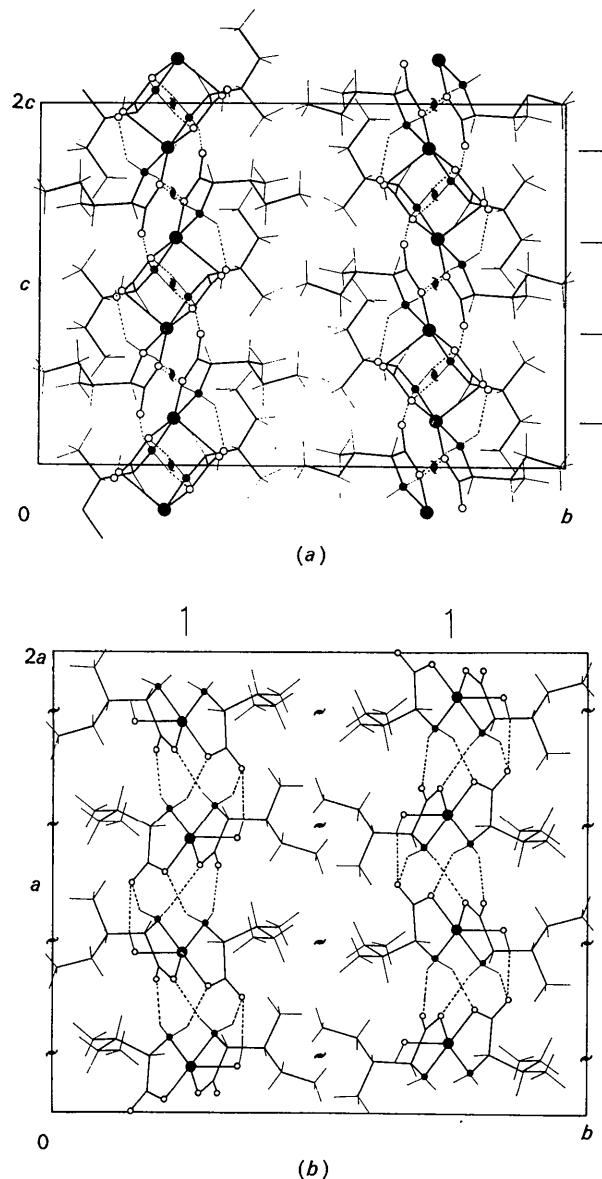
Fig. 2. Molecular packing. Hydrogen bonds are indicated by broken lines. ● = Copper, ○ = Oxygen, and ● = Nitrogen These are projections of two unit-cells onto (a) the (100) plane and (b) the (001) plane.