Fig. 6. Packing contacts around the hydroxyl group.

109 (6)° and the average H–C–C angle 109 (3)°. The O–H bond length in the hydroxyl group is 0·83 (6)Å. The closest contacts around the hydroxyl group are shown in Fig. 6.

A more detailed discussion on the phase behaviour, molecular arrangement and hydrogen bonding of this compound, based on a comparison of this single-crystal analysis with powder diffraction and IR data, will be given in a subsequent paper (Lundén & Pascher, 1976).

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The Crystal Structure of (L-Valine-L-tyrosine)copper(II).4H₂O

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The structure of (L-valine-L-tyrosine)Cu.4H₂O has been determined by the heavy-atom method with 1090 visually estimated reflexions and refined by full-matrix least squares to $R = 0.98$. The crystals are orthorhombic with $a = 8.33$ (1), $b = 14.28$ (2), $c = 16.23$ (2) Å, space group $P2_12_12_1$, $Z = 4$. The dipeptide is coordinated to one Cu atom through the amino NH₂, the peptide N and one carboxyl O atom. No water molecule is found to be in coordination. The Cu–peptide–Cu linkage is via the other carboxyl O atom. There is no interaction of the Cu atom with the aromatic ring.

Introduction

The present structure determination is the second in a series of analyses of Cu complexes of amino acids and peptides, the first being bis(L-threonine)Cu(II).H₂O (Amirthalingam & Muralidharan, 1975). The interest is to evaluate the exact nature of the Cu environment in biological systems. Also, we are particularly interested here in ascertaining the type of interaction occurring between the Cu atom and the aromatic ring of the tyrosine residue.

Experimental

The compound (CULVAT) was prepared by reacting freshly prepared Cu(OH)₂ with the peptide (pH 7·8), and crystallized as stable blue prisms. X-ray diffraction studies with Cu Kα radiation showed that the crystals

are orthorhombic with $a=8\cdot33$ (1), $b=14\cdot28$ (2), $c=16\cdot23$ (2) Å. The space group was determined uniquely as $P2_12_12_1$ from systematic absences: $h00$, $h=2n+1$; $0k0$, $k=2n+1$; $00l$, $l=2n+1$. $Z=4Cu(C_{14}H_{20}N_2O_4).4H_2O$ ($\varrho_o=1\cdot48$, $\varrho_c=1\cdot43$ g cm^{-3}). With the crystal mounted along **a** and Cu $K\alpha$ radiation, intensities for 1090 reflexions were collected and visually estimated. No absorption correction was made in view of the size of the crystal (0·03 mm). Scaling was carried out by Wilson's method and from common reflexions obtained from $h0l$ data.

Structure determination

The Cu position was fixed from the three Harker sections. The resulting Fourier map contained many spurious peaks. However, by careful selection of peaks during successive Fourier syntheses, the entire structure could be recovered. The final electron density map showed the presence of only four water molecules. The structural parameters were refined by full-matrix least squares, allowing only Cu to vibrate anisotropically. H atoms were ignored, Cruickshank's weighting scheme with $A=5\cdot0$ and $C=0\cdot01$ was used. The final R for all observed reflexions was 0·098.*

* A list of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 31894 (8 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 1. *Final positional* ($\times 10^4$) *and thermal parameters of the atoms with e.s.d.'s in parentheses*

	x	y	z	B
Cu	2744 (3)	1704 (1)	88 (1)	–
O(1)	2173 (15)	138 (6)	2153 (6)	3·8 (2)
O(2)	750 (16)	2461 (8)	131 (6)	4·1 (2)
O(3)	−1377 (16)	2716 (7)	915 (6)	4·3 (2)
O(4)	4277 (19)	5748 (9)	908 (7)	5·6 (3)
O(5)	2378 (17)	652 (7)	3805 (6)	4·7 (2)
O(6)	7258 (16)	3240 (8)	2632 (6)	5·2 (2)
O(7)	7381 (19)	2299 (8)	4118 (7)	5·8 (3)
O(8)	514 (21)	2115 (10)	4493 (8)	6·5 (3)
N(1)	4117 (20)	580 (9)	127 (8)	4·9 (3)
N(2)	2034 (18)	1300 (7)	1161 (6)	3·3 (2)
C(1)	3964 (21)	88 (8)	932 (7)	3·3 (3)
C(2)	2608 (21)	504 (8)	1466 (7)	3·0 (2)
C(3)	5491 (29)	44 (13)	1462 (11)	5·4 (4)
C(4)	6020 (30)	1013 (15)	1746 (13)	6·7 (5)
C(5)	6820 (33)	−531 (17)	1007 (14)	7·0 (5)
C(6)	719 (21)	1772 (10)	1525 (8)	3·4 (3)
C(7)	−50 (22)	2355 (10)	820 (8)	3·6 (3)
C(8)	1220 (22)	2460 (10)	2208 (8)	3·7 (3)
C(9)	2034 (23)	3350 (11)	1850 (9)	3·6 (3)
C(10)	1201 (22)	4192 (10)	1814 (8)	4·2 (3)
C(11)	1930 (25)	4990 (13)	1482 (9)	4·3 (3)
C(12)	3519 (25)	4962 (11)	1222 (9)	4·9 (4)
C(13)	4362 (26)	4116 (11)	1250 (9)	4·5 (3)
C(14)	3637 (27)	3320 (12)	1581 (10)	4·9 (3)

Anisotropic temperature factor for Cu of the form:

$$\exp\left[-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{23}kl + 2\beta_{13}hl)\right]$$

β_{11}	β_{22}	β_{33}
0·0144 (6)	0·0044 (1)	0·0035 (1)

β_{12}	β_{13}	β_{23}
0·0002 (3)	0·0012 (3)	0·0008 (2)
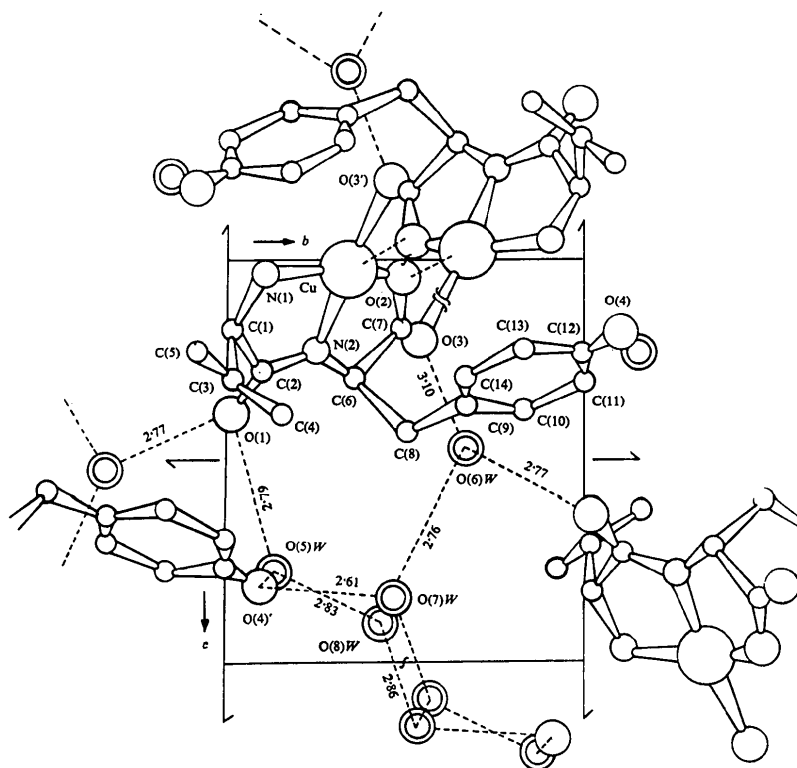
Fig. 1. Structure projected down **a**. Dotted lines indicate hydrogen bonds. O(4)···O(5)=2·83, O(7)···O(8)=2·70, 2·86 Å.
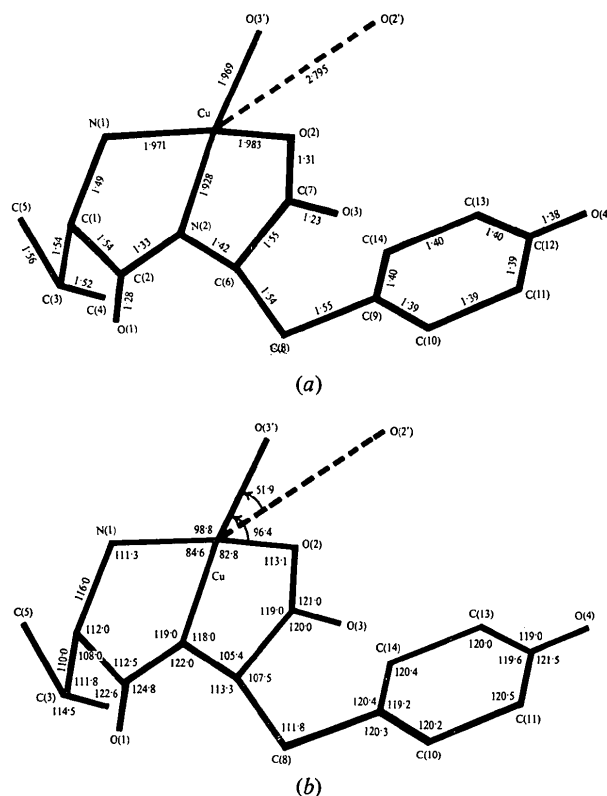
(a)

(b)

Fig. 2. (a) Bond lengths. Atoms labelled as in text. Standard deviations range from 0·008 (near Cu) to 0·02 Å. (b) Bond angles. Standard deviations range from 0·4 (near Cu) to 1·8°. N(1)–Cu–O(2) = 158·2, N(2)–Cu–O(3′) = 171·1, N(2)–Cu–O(2′) = 121·2, N(1)–Cu–O(2′) = 80·3, O(2)–Cu–O(2′) = 121·5°.
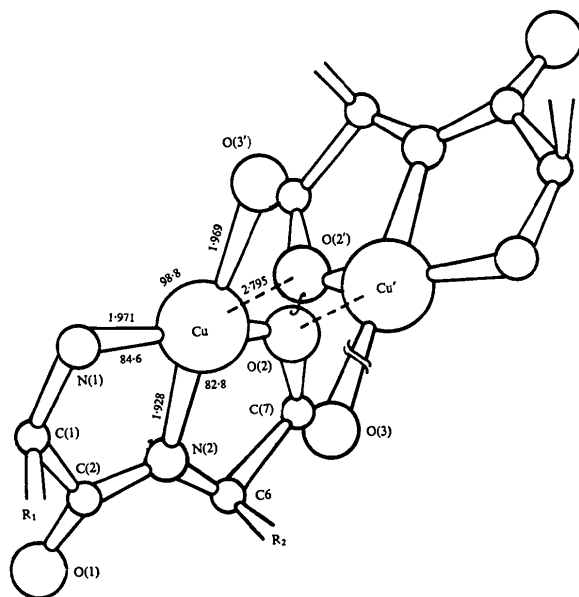

Fig. 3. Copper coordination. O(2) coordinated to Cu is apical to Cu′. Cu–O(2) = 1·983 Å, O(2)–Cu–O(3′) = 96·4°.

The final positional and thermal parameters are given in Table 1. The form factors for Cu^{2+}, N, C and O were taken from *International Tables for X-ray Crystallography* (1962). The F_c's were corrected for anomalous dispersion of Cu ($\Delta f' = -2\cdot1$, $\Delta f'' = 0\cdot7$). The structure projected down **a** is shown in Fig. 1, and bond angles and lengths in Fig. 2.

Description and discussion of the structure

The dipeptide is coordinated to the Cu atoms through the amino NH_2, the peptide N and both carboxyl O atoms. The two carboxyl O atoms are in the coordination sphere of the two Cu atoms related by a screw operation, the screw axis being parallel to **a** (Fig. 1). Simultaneously each O in the coordination sphere of one Cu becomes the apical atom of the square pyramid of another Cu. Thus the peptide–Cu–peptide linkage is *via* the carboxyl O atoms and the molecules surround every alternate screw axis parallel to **a**, as an infinite chain. The screw axes between these are surrounded by water molecules and no water is found to be coordinated to Cu. There is a network of hydrogen bonds between the water molecules as well as from water molecules to the hydroxyl group of the tyrosine, one of the carboxyl O atoms of the tyrosine and the O atom of the valine amide group (Fig. 1). Thus the water molecules act both as donors and acceptors and fill the space between the CULVAT molecules.

The Cu coordination is shown in Fig. 3. The basal plane is a highly distorted tetrahedron. The bond

Table 2. *The least-squares planes and deviations* (Å) *of the atoms*

The equation of the plane is $ax + by + cz + d = 0$.

(i) Amide group (plane *A*)

C(1)	+0·006	*Cu	−0·147	a =	0·685
C(2)	−0·021	*N(1)	−0·184	b =	0·531
N(2)	+0·007	*C(6)	−0·090	c =	0·498
O(1)	+0·008			d =	−3·077

(ii) Carboxyl group (plane *B*)

C(6)	+0·001	*Cu	−0·201	a =	0·431
C(7)	−0·004	*N(2)	−0·300	b =	0·826
O(2)	+0·001			c =	0·364
O(3)	+0·001			d =	−3·246

(iii) Basal plane (plane *C*)

N(1)	−0·212	*Cu	+0·068	a =	0·597
N(2)	+0·245			b =	0·619
O(2)	−0·218			c =	0·510
O(3′)	+0·186			d =	−2·876

(iv) Phenyl ring plane (plane *D*)

C(9)	−0·008	*C(8)	−0·001	a =	0·320
C(10)	+0·009	*O(4)	+0·023	b =	0·243
C(11)	−0·013			c =	0·916
C(12)	+0·014			d =	−4·462
C(13)	−0·013				
C(14)	+0·009				

Angles between planes: *A–B* 23·8   *A–C* 7·2   *B–C* 17·4°

* Atom not included in plane calculation.

lengths and angles in the neighbourhood of Cu agree well with the average values given by Freeman (1967). The value obtained for Cu–O(2') (apical), 2·795 Å, shows that the bond is rather weak but a value as large as 2·82 Å is found in Cu(ggg)Cl.1½H₂O (Freeman, 1967). The best plane (plane C) containing the NH₂, peptide N and carboxyl O atoms forms a distorted square plane with deviations: NH₂ 0·212, N 0·245, O(2) 0·218, O(3') 0·186 Å, comparable with values obtained in Cu-glycyl-L-leucyl-L-tyrosine (van der Helm & Franks, 1968). Cu is displaced from this mean plane by 0·068 Å (Table 2).

The bond lengths and angles of the ligand (Fig. 2) are normal. Since bond lengths and angles for the free peptide are not available, there is no way of finding the nature of distortion due to chelation and complex formation. The best planes containing C(1)C(2)N(2)-O(1) (plane A), C(6)C(7)O(3)O(2) (plane B) and for the aromatic ring of the tyrosine group (plane D) show deviations of N(1) 0·184 (from plane A), N(2) 0·300 (from plane B), and C(8) 0·001 and O(4) 0·023 Å (from plane D) which are comparable with similar structures, e.g. Cu chelates of L-tyrosine (Tatsch & van der Helm, 1969) and glycyl-L-leucyl-L-tyrosine (Franks & van der Helm, 1971). Conformational angles of the peptide backbone and side chains are given in Table 3. The side-chain conformational angles of valine are normal. The side-chain conformational angle of $\chi_1^{1,2} =$ −73° for tyrosine is somewhat greater than the *gauche* value of ±60° but such deviations are not uncommon, e.g. in bis(L-threonine)Cu(II).H₂O (Amirthalingam & Muralidharan, 1975). The C_α–C_β bonds of the valine and tyrosine residues are parallel to each other and even though the aromatic ring is facing the Cu basal plane there is no metal–aromatic ring interaction. The nearest approach between Cu and C atoms of the phenyl group are Cu–C(9), 3·74; Cu–C(14), 3·43; and Cu–C(13), 3·74 Å, whereas contacts of the order of 3·17–3·43 Å are found in CUGLT and CUTY (van der Helm & Tatsch, 1972). This only means that because

of the presence of the bulky side chain of the valine residue, the tyrosine side chain assumes the *gauche* position. Intermolecular distances less than 3·5 Å are given in Table 4.

The water molecules are found in the gap between the complexes and are hydrogen-bonded among themselves and to O(1) and O(3) of the peptide and the hydroxyl O(5) of the phenyl group. The distance between water molecules O(7) and O(3) is 3·10 Å which shows that the hydrogen bond is rather weak, but this is expected since O(3) is already coordinated to Cu. The other hydrogen-bond distances are normal. The water molecules act both as donors and acceptors in this structure.

Table 3. *Torsion angles*

Angle	Description	Value
$\chi_1^{1,1}$	N(1)C(1)C(3)C(4)	−65°
$\chi_2^{1,1}$	N(1)C(1)C(3)C(5)	+64
$\chi_1^{1,2}$	N(2)C(6)C(8)C(9)	−73
χ_1^{2}	C(6)C(8)C(9)C(10)	−104
χ_2^{2}	C(6)C(8)C(9)C(14)	+77
ψ_1^{1}	N(1)C(1)C(2)N(2)	+10
ψ_2^{1}	N(1)C(1)C(2)O(1)	−174
ψ_1^{2}	N(2)C(6)C(7)O(3)	−168
ψ_2^{2}	N(2)C(6)C(7)C(8)	+125
ω_1^{1}	C(1)C(2)N(2)C(6)	−176
ω_2^{1}	C(1)C(2)N(2)O(1)	+176
φ_1^{2}	C(2)N(2)C(6)C(7)	+155
φ_2^{2}	C(2)N(2)C(6)C(8)	−88

Table 4. *Intermolecular contacts less than* 3·5 Å *and* Cu–*phenyl ring nearest contacts*

†Cu—O(3)ᵛ	1·969 Å		*O(4)–O(5)ᵛⁱⁱⁱ	2·83 Å
†Cu—O(2)ᵛ	2·795		*O(4)–O(7)ᵛⁱⁱⁱ	2·61
Cu—C(7)ᵛ	2·711		*O(5)–O(8)ⁱ	2·83
*O(1)–O(5)ⁱ	2·79		*O(5)–O(8)ⁱ	2·83
*O(1)–O(6)ⁱˣ	2·77		O(5)–N(1)ⁱᵛ	3·04
O(2)–O(3)ᵛ	2·95		*O(6)–O(7)ⁱ	2·76
O(2)–N(1)ᵛⁱ	3·14		O(6)–C(14)ⁱ	3·47
O(2)–C(13)ᵛⁱ	3·38		*O(7)–O(8)ⁱⁱ	2·69
O(2)–C(14)ᵛⁱ	3·47		*O(7)–O(8)ᵛⁱⁱ	2·86
*O(3)–O(6)ⁱⁱⁱ	3·10		O(7)–C(11)ⁱˣ	3·48
O(3)–N(1)ᵛⁱ	2·99		O(7)–C(12)ⁱˣ	3·46
			N(1)–C(7)ᵛ	3·39

Cu–C(9)ⁱ	3·748 Å
Cu–C(14)ⁱ	3·427
Cu–C(13)ᵛⁱ	3·744

Key to symmetry operations: (i) x,y,z; (ii) $1+x,y,z$; (iii) $-1+x,y,z$; (iv) $\frac{1}{2}-x, -y, \frac{1}{2}+z$; (v) $\frac{1}{2}+x, \frac{1}{2}-y, -z$; (vi) $\frac{1}{2}+x, -\frac{1}{2}-y, -z$; (vii) $\frac{1}{2}+x, \frac{1}{2}-y, 1-z$; (viii) $1-x, \frac{1}{2}+y, \frac{1}{2}-z$; (ix) $1-x, -\frac{1}{2}+y, \frac{1}{2}-z$.

† Cu coordination.
* Possible hydrogen bonds.

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