

catena-Poly[[tetrakis(μ -3,3-dimethylbutyrato- $O:O'$)dicopper(II)]- μ -3,3-dimethylbutyrato- $O:O'$ -[bis(2,6-dimethylpyridine- N)copper(II)]- μ -3,3-dimethylbutyrato- $O:O'$] and tetrakis(μ -2,2-dimethylpropanoato- $O:O'$)bis-[(2,6-dimethylpyridine- N)copper(II)]

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Received 5 April 2000

Accepted 3 May 2000

The two title compounds, $[\text{Cu}_3(\text{C}_6\text{H}_{11}\text{O}_2)_6(\text{C}_7\text{H}_9\text{N})_2]_n$, (I), and $[\text{Cu}_2(\text{C}_5\text{H}_9\text{O}_2)_4(\text{C}_7\text{H}_9\text{N})_2]$, (II), have chain and finite-molecular structures, respectively. In (I), binuclear cage units and mononuclear 2,6-dimethylpyridine complexes, both of which have inversion centres, are arranged alternately and are linked by the carboxylate ions to form one-dimensional chains along the a axis. In (II), the binuclear cage unit has an inversion centre and the coordination geometry around the Cu atom is typical square pyramidal, with 2,6-dimethylpyridine at the apical position.

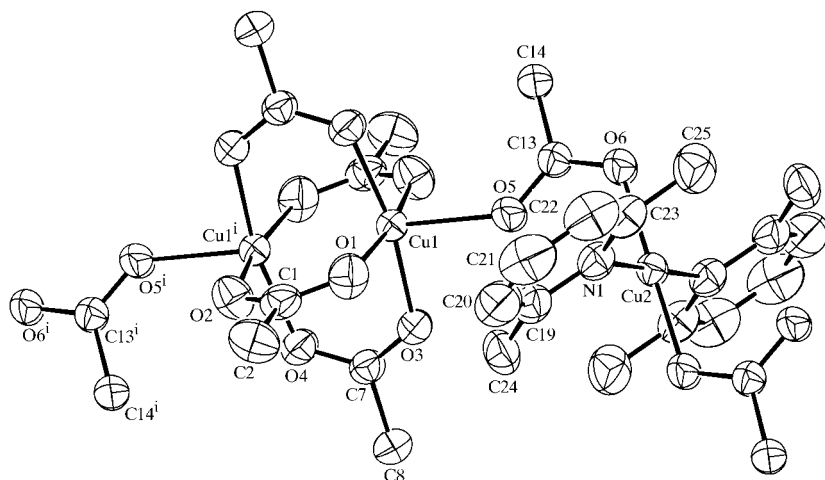
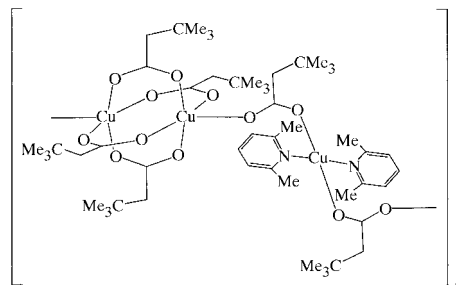


Figure 1

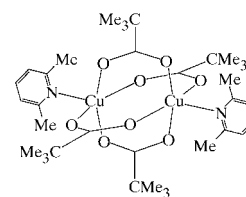
The linear chain structure of (I) with displacement ellipsoids at the 50% probability level. H atoms and the *tert*-butyl groups of the dimethylbutyrate ligands have been omitted for clarity (symmetry code as in Table 1).

Comment

Copper(II) carboxylates usually have a cage structure with square-pyramidal coordination geometry and a monodentate



(I)

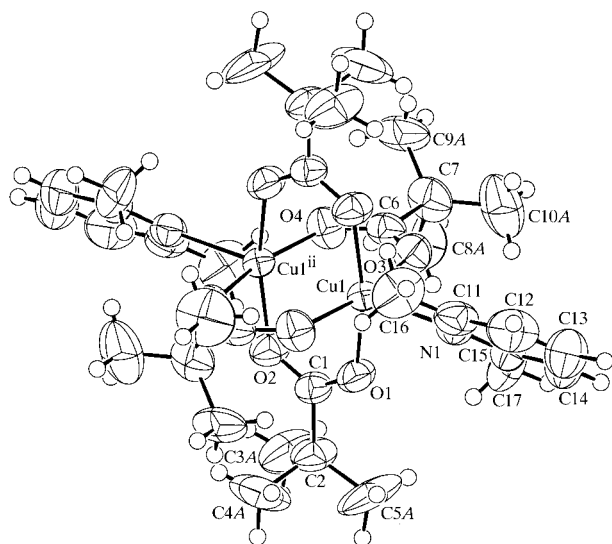


(II)

ligand bonded at the axial position. 2,6-Dimethylpyridine (2,6-Me₂py) is a bulky ligand which may cause a deformation of this cage structure, as observed in the crystal structure of $[\text{Cu}_2(\text{PhMe}_2\text{CCOO})_2(2,6\text{-Me}_2\text{py})_2]$, where the geometry about the Cu^{II} is deformed from square-pyramidal toward trigonal bipyramidal (TBP). Alternatively, only a mononuclear complex, $[\text{Cu}(\text{RCOO})_2(2,6\text{-Me}_2\text{py})_2]$, will be produced, as for $R = \text{Ph}_3\text{C}$ or Ph_2MeC (Fujita *et al.*, 1993). In this context, the crystal structures of the title compounds, (I) and (II), are presented here.

In (I), a novel polymeric structure was observed. The mononuclear moiety $[\text{Cu}(\text{RCOO})_2(2,6\text{-Me}_2\text{py})_2]$ acts as the axial ligand to the binuclear unit. The carboxylate bridge between the mononuclear and binuclear units has a *syn-anti* conformation. An analysis of the temperature dependence of the magnetic susceptibility indicated that the spin-exchange interaction between the mononuclear and binuclear units is negligible. The Cu \cdots Cu distance in the binuclear unit is 2.652 (1) Å, which is similar to that of the 3,3-dimethylbutyric acid adduct [2.599 (1) Å; Goto *et al.*, 2000].

In (II), the binuclear cage structure of the copper pivalate does not have a TBP distortion, which is consistent with the high magnetic $-2J$ value of 379 cm⁻¹ ($H = -2J\hat{S}_1\cdot\hat{S}_2$; Muto *et al.*, 1986). The acridine adduct of copper(II) pivalate also has a cage structure with square-pyramidal coordination, the Cu \cdots Cu and Cu–N distances being 2.702 (1) and 2.371 (5) Å, respectively (Kirillova *et al.*, 1980). Copper pivalate remains a discrete dimeric structure even after the removal of the axial solvent ligands (Muto *et al.*, 1986; Kato & Muto, 1988). In polymeric copper(II) pivalate, prepared by


Figure 2

The molecular structure of (II). Displacement ellipsoids are plotted at the 50% probability level and H atoms are shown as spheres of arbitrary radii. Only one orientation of the *tert*-butyl groups is shown, indicated by the suffix *A* (symmetry code as in Table 2).

sublimation, the dinuclear cage is deformed and the coordination geometry around the Cu atom has a TBP distortion (Il'ina *et al.*, 1992).

Experimental

For (I), 3,3-dimethylbutyric acid (116 mg, 1.0 mmol) and $\text{CuCO}_3 \cdot \text{Cu}(\text{OH})_2 \cdot \text{H}_2\text{O}$ (60 mg, 0.25 mmol) were suspended in a mixture of water and methanol (3:1, 20 ml). After the solution had been stirred for 1 h at room temperature, the green precipitate was collected and dissolved in acetonitrile and 2,6-dimethylpyridine (54 mg, 0.5 mmol) was added. Blue crystals of (I) were grown from the solution by slow evaporation. For (II), a solution of 2,2-dimethylpropionic acid (613 mg, 6.0 mmol) in 0.25 *M* sodium hydroxide (50 ml) was neutralized with 0.25 *M* nitric acid and an aqueous solution of $\text{Cu}(\text{NO}_3)_2 \cdot 3\text{H}_2\text{O}$ (725 mg, 3.0 mmol) was added. After the solution had been stirred for 15 min at room temperature, the green precipitate was collected and dissolved in acetonitrile and 2,6-dimethylpyridine (321 mg, 3.0 mmol) was added. Green crystals of (II) were grown from the solution by slow evaporation.

Compound (I)

Crystal data

$[\text{Cu}_3(\text{C}_6\text{H}_{11}\text{O}_2)_6(\text{C}_7\text{H}_9\text{N})_2]$
 $M_r = 1095.86$
 Triclinic, $P\bar{1}$
 $a = 12.525$ (2) Å
 $b = 12.736$ (2) Å
 $c = 10.033$ (2) Å
 $\alpha = 94.64$ (1)°
 $\beta = 102.51$ (1)°
 $\gamma = 109.32$ (1)°
 $V = 1454.1$ (5) Å³

$Z = 1$
 $D_x = 1.251$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 25 reflections
 $\theta = 10\text{--}15^\circ$
 $\mu = 1.141$ mm⁻¹
 $T = 298$ K
 Prism, blue
 $0.4 \times 0.1 \times 0.1$ mm

Data collection

Rigaku AFC-7R diffractometer
 $\theta/2\theta$ scans
 Absorption correction: by integration (Coppens *et al.*, 1965)
 $T_{\min} = 0.472$, $T_{\max} = 0.753$
 6956 measured reflections
 6651 independent reflections
 4193 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.021$
 $\theta_{\text{max}} = 27.5^\circ$
 $h = 0 \rightarrow 16$
 $k = -17 \rightarrow 17$
 $l = -13 \rightarrow 13$
 3 standard reflections
 every 150 reflections
 intensity decay: none

Refinement

Refinement on F^2
 $R(F) = 0.045$
 $wR(F^2) = 0.115$
 $S = 1.08$
 6651 reflections
 304 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2 F_o^2 + [0.05(F_o^2 + 2F_c^2)/3]^2]$
 $(\Delta/\sigma)_{\text{max}} = 0.006$
 $\Delta\rho_{\text{max}} = 0.41$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.61$ e Å⁻³

Table 1

Selected geometric parameters (Å, °) for (I).

Cu1—Cu1 ⁱ	2.652 (1)	Cu1—O5	2.185 (2)
Cu1—O1	1.972 (3)	Cu2—O5	2.923 (2)
Cu1—O2 ⁱ	1.965 (2)	Cu2—O6	1.938 (2)
Cu1—O3	1.967 (2)	Cu2—N1	2.050 (3)
Cu1—O4 ⁱ	1.967 (2)		
O1—Cu1—O2 ⁱ	167.7 (1)	O1—C1—O2	125.9 (3)
O3—Cu1—O4 ⁱ	167.7 (1)	O3—C7—O4	125.3 (3)
O6—Cu2—N1	92.2 (1)	O5—C13—O6	121.9 (3)
Cu1—O5—C13	134.1 (2)		
Cu1—O5—C13—O6	173.8 (2)	Cu2—O6—C13—O5	7.7 (4)

Symmetry code: (i) $1 - x, -y, -z$.

Compound (II)

Crystal data

$[\text{Cu}_2(\text{C}_5\text{H}_9\text{O}_2)_4(\text{C}_7\text{H}_9\text{N})_2]$
 $M_r = 745.90$
 Triclinic, $P\bar{1}$
 $a = 10.986$ (4) Å
 $b = 11.195$ (5) Å
 $c = 9.564$ (4) Å
 $\alpha = 107.66$ (4)°
 $\beta = 97.15$ (4)°
 $\gamma = 61.82$ (3)°
 $V = 987.7$ (8) Å³

$Z = 1$
 $D_x = 1.254$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 25 reflections
 $\theta = 10\text{--}15^\circ$
 $\mu = 1.122$ mm⁻¹
 $T = 298$ K
 Prism, green
 $0.25 \times 0.20 \times 0.20$ mm

Data collection

Rigaku AFC-7R diffractometer
 $\theta/2\theta$ scans
 Absorption correction: by integration (Coppens *et al.*, 1965)
 $T_{\min} = 0.803$, $T_{\max} = 0.844$
 4761 measured reflections
 4524 independent reflections
 3449 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.047$
 $\theta_{\text{max}} = 27.5^\circ$
 $h = 0 \rightarrow 14$
 $k = -15 \rightarrow 15$
 $l = -12 \rightarrow 3$
 3 standard reflections
 every 150 reflections
 intensity decay: 4.1%

Table 2

Selected geometric parameters (Å, °) for (II).

Cu1—Cu1 ⁱⁱ	2.722 (1)	Cu1—O3	1.964 (2)
Cu1—O1	1.964 (2)	Cu1—O4 ⁱⁱ	1.962 (3)
Cu1—O2 ⁱⁱ	1.973 (2)	Cu1—N1	2.360 (3)
O1—Cu1—O2 ⁱⁱ	165.5 (1)	O1—C1—O2	125.2 (3)
O3—Cu1—O4 ⁱⁱ	165.3 (1)	O3—C6—O4	125.1 (3)

Symmetry code: (ii) $-x, 1 - y, -z$.

Refinement

Refinement on F^2 $R(F) = 0.048$ $wR(F^2) = 0.152$ $S = 1.05$

4524 reflections

226 parameters

H-atom parameters constrained
 $w = 1/(\sigma^2 F_o^2 + [0.1(F_o^2 + 2F_c^2)/3]^2)$
 $(\Delta/\sigma)_{\max} = 0.027$
 $\Delta\rho_{\max} = 0.74 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.36 \text{ e } \text{\AA}^{-3}$

Initially, both of the structures were refined as usual. The anisotropy in the atomic displacement parameters became abnormally large for the methyl C atoms of the *tert*-butyl groups, suggesting libration and/or rotational disorder. Therefore, a split-site model was investigated for the *tert*-butyl groups in both compounds; it was found to be applicable for (II), but not for (I). For (II), the six methyl-C atoms were initially refined isotropically. Two sets of half-occupancy methyl groups, offset from one another by *ca* 30°, could be modelled for both *tert*-butyl groups based on the difference synthesis. Their anisotropic displacement parameters were then refined with their positional parameters fixed to avoid unreasonable geometry. Compared with the unsplit model, $R(F)$ slightly decreased from 0.050 to 0.048 on increasing the number of parameters from 208 to 226. The magnitude of the displacement ellipsoids of the methyl C atoms apparently decreased, but the abnormal anisotropy of the displacement parameters did not disappear. In this manuscript, the split-site model is reported for (II). The positional parameters of all the H atoms were calculated geometrically and fixed with $U(\text{H}) = 1.2U_{\text{eq}}(\text{parent atom})$.

For both compounds, data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1993); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduc-

tion: *TEXSAN* (Molecular Structure Corporation, 1999); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *TEXSAN*; software used to prepare material for publication: *TEXSAN*.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: GD1098). Services for accessing these data are described at the back of the journal.

References

- Altomare, A., Cascarano, G., Giacovazzo, C., Guagliardi, A., Burla, M. C., Polidori, G. & Camalli, M. (1994). *J. Appl. Cryst.* **27**, 435.
 Coppens, P., Leiserowitz, L. & Rabinovich, D. (1965). *Acta Cryst.* **18**, 1035–1038.
 Fujita, T., Ohba, S., Nagamatsu, M., Tokii, T., Jury, C. F., Steward, O. W. & Kato, M. (1993). *Acta Cryst.* **C49**, 2095–2100.
 Goto, M., Kani, Y., Tsuchimoto, M., Ohba, S., Matsushima, H. & Tokii, T. (2000). *Acta Cryst.* **C56**, 7–11.
 Il'ina, E. G., Troyanov, S. I. & Dunaeva, K. M. (1992). *Koord. Khim.* **18**, 882–890.
 Kato, M. & Muto, Y. (1988). *Coord. Chem. Rev.* **92**, 45–83.
 Kirillova, N. I., Struchkov, Y. T., Porai-Koshits, M. A., Pasynskii, A. A., Antsyshkina, A. S., Minacheva, L. K., Sadikov, G. G., Idrisov, T. C. & Kalinnikov, V. T. (1980). *Inorg. Chim. Acta*, **40**, 115–119.
 Molecular Structure Corporation (1993). *MSC/AFC Diffractometer Control Software*. MSC, 3200 Research Forest Drive, The Woodlands, TX 77381, USA.
 Molecular Structure Corporation (1999). *TEXSAN*. Version 1.10. MSC, 9009 New Trails Drive, The Woodlands, TX 77381–5209, USA.
 Muto, Y., Hirashima, N., Tokii, T., Kato, M. & Suzuki, I. (1986). *Bull. Chem. Soc. Jpn.* **59**, 3672–3674.