

Tetrakis[μ -(4-nitrophenyl)acetato-*O*:*O'*]-bis[(2-aminopyrimidine-*N*¹)-copper(II)]

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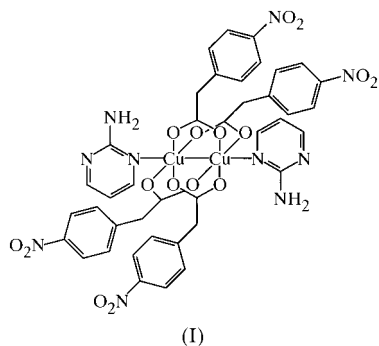
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The structure of the title compound, $[\text{Cu}_2(\text{C}_8\text{H}_6\text{NO}_4)_4(\text{C}_4\text{H}_5\text{N}_3)_2]$, comprises individual units of tetra- μ -carboxylato-*O*:*O'*-dicopper(II) end-capped with two 2-aminopyrimidine molecules. These pyrimidines then form dimers across a typical $\text{N}-\text{H}\cdots\text{N}$ association, thus producing linear hydrogen-bonded polymer chains.

Comment

Complexes of the copper(II) acetate monohydrate type prepared by the addition of 2-aminopyrimidine are expected to produce arrays of alternating tetra- μ -carboxylato-*O*:*O'*-dicopper(II) and 2-aminopyrimidine units linked by axial $\text{Cu}-\text{N}$ bonds (Smith *et al.*, 1996). However, the structure of the title compound, (I), comprises individual units of tetra- μ -carboxylato-*O*:*O'*-dicopper(II) end-capped with two 2-aminopyrimidine molecules, which form a hydrogen-bonded polymer chain *via* the pyrimidines. The hydrogen-bonding geometry is listed in Table 1. The eight $\text{Cu}-\text{O}$ distances are in the range 1.943 (4)–2.012 (4) Å, with an average of 1.969 (4) Å, while the two $\text{Cu}-\text{N}$ distances are 2.154 (4) and 2.150 (4) Å. The hydrogen-bonding patterns in these types of molecules usually consist of associations from the two amino H atoms to two adjacent carboxylate O atoms. This is the case



in (I) for the two inwardly facing NH groups but the two outward amino H atoms bind to an adjacent outward pyrimidine N atom, thus forming pyrimidine dimers. With like

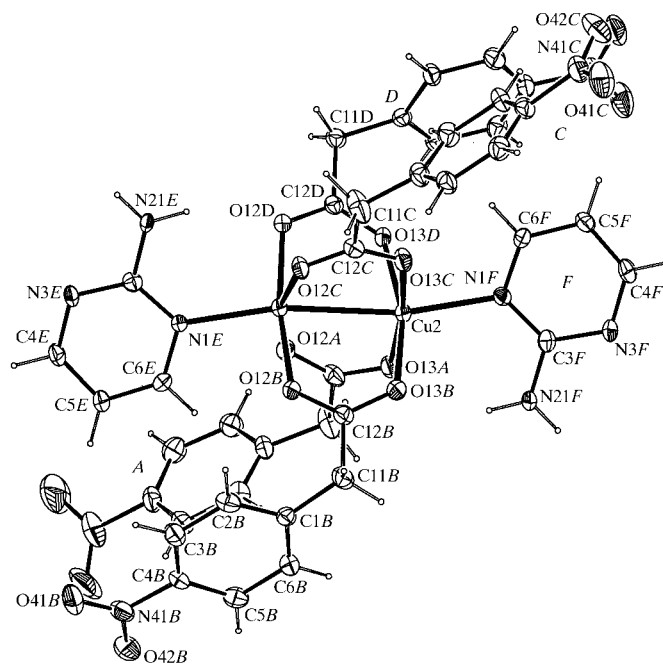


Figure 1
The molecular configuration and atom-numbering scheme for (I) showing 30% probability ellipsoids.

binding to like (*i.e.* *E-E* and *F-F*), the structure forms a hydrogen-bonded polymer with individual groups of alternating direction. All structures of the copper(II) acetate type made with 2-aminopyrimidine have the potential to exhibit packing similar to (I), but this is the first reported example.

Experimental

Complex (I) was prepared as per the literature procedure of Smith *et al.* (1996).

Crystal data

$[\text{Cu}_2(\text{C}_8\text{H}_6\text{NO}_4)_4(\text{C}_4\text{H}_5\text{N}_3)_2]$
 $M_r = 1037.85$
 Monoclinic, $P2_1/c$
 $a = 17.134$ (5) Å
 $b = 18.9575$ (8) Å
 $c = 14.0859$ (6) Å
 $\beta = 111.159$ (3)°
 $V = 4266.9$ (13) Å³
 $Z = 4$

$D_x = 1.616$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 8113 reflections
 $\theta = 2.91$ – 27.48 °
 $\mu = 1.083$ mm⁻¹
 $T = 150$ (2) K
 Plate, green
 0.50 × 0.10 × 0.02 mm

Data collection

Enraf-Nonius KappaCCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SORTAV; Blessing, 1995)
 $T_{\min} = 0.613$, $T_{\max} = 0.979$
 21389 measured reflections

9074 independent reflections
 3921 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.127$
 $\theta_{\text{max}} = 27.48$ °
 $h = -21 \rightarrow 21$
 $k = -24 \rightarrow 24$
 $l = -18 \rightarrow 18$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.066$
 $wR(F^2) = 0.149$
 $S = 0.918$
 9074 reflections
 613 parameters

H atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0357P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.51$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.54$ e Å⁻³

Table 1

Hydrogen-bonding geometry (Å, °).

| <i>D</i> —H... <i>A</i> | <i>D</i> —H | H... <i>A</i> | <i>D</i> ... <i>A</i> | <i>D</i> —H... <i>A</i> |
|------------------------------|-------------|---------------|-----------------------|-------------------------|
| N21E—H21E...O12D | 0.88 | 2.41 | 3.121 (6) | 139 |
| N21E—H22E...N3E [†] | 0.88 | 2.10 | 2.971 (7) | 168 |
| N21F—H21F...O13A | 0.88 | 2.47 | 3.190 (6) | 139 |
| N21F—H22F...N3F [‡] | 0.88 | 2.08 | 2.958 (7) | 176 |

Symmetry codes: (i) $2 - x, 1 - y, -z$; (ii) $1 - x, 2 - y, -z$.

All H atoms were included in the refinement at calculated positions as riding models with C—H set to either 0.95 (Ar-H) or 0.99 Å (CH₂) and N—H set to 0.88 Å.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON97* (Spek, 1997); software used to prepare material for publication: *SHELXL97*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: DE1163). Services for accessing these data are described at the back of the journal.

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