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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$ R factor = 0.031 wR factor = 0.075 Data-to-parameter ratio = 14.7

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

catena-Poly[[[aqua(di-2-pyridylamine- $\kappa^2 N^2, N^{2'})$ copper(II)]- μ -thiophene-2,5-dicarboxylato- $\kappa^2 O^2: O^5$] N,N-dimethylformamide monohydrate]

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In the title cooordination polymer, {[Cu(C₆H₂O₄S)(C₁₀H₉N₃)-(H₂O)]·C₃H₇NO·H₂O}_n, the Cu^{II} atom is in a squarepyramidal environment defined by an apically coordinated water molecule, carboxyl O atoms from two different thiophene-2,5-dicarboxylate dianions and the two N atoms of a chelating di-2-pyridylamine ligand. The thiophene-2,5dicarboxylate dianion functions as a μ_2 -bridging ligand to form a zigzag polymeric chain. In addition, N–H···O and O–H···O intermolecular hydrogen bonds link the chains into a three-dimensional network structure.

Comment

Like other dicarboxylic acids, such as pyridine-2,6-dicarboxylic acid (Ghosh & Bharadwaj, 2005; Lu *et al.*, 2005) and benzene-1,4-dicarboxylic acid (Thirumurugan & Natarajan, 2004; Xiao & Zhu, 2003), which show diverse coordination modes, thiophene-2,5-dicarboxylic acid (H₂tda) is also a versatile ligand and can function variously as a monodentate, bidentate or tridentate ligand; it can also bridge or chelate (Chen *et al.*, 1998, 1999; Sun *et al.*, 2003). In the title complex, $\{[Cu(C_{10}H_9N_3)(C_6H_2SO_4)(H_2O)]\cdot C_3H_7NO\cdot H_2O]_n$, (I), the tda dianion functions as a bridge between adjacent Cu^{II} centres.



The Cu^{II} atom is in a square-pyramidal environment defined by an apically coordinated water molecule, two carboxylate O atoms from two different thiophene-2,5dicarboxylate dianions and the two N atoms of the chelating 2,2'-dipyridylamine (dpa) ligand (Fig. 1). The basal plane [O1/ O4ⁱ/N1/N3; symmetry code: (i) -x, -y + 1, $z + \frac{1}{2}$], with a mean deviation of 0.013 (1) Å, comprises the two N atoms of dpa and carboxylate O atoms from two different tda dianions. The Cu1-O5 apical distance is significantly longer than those in the basal plane (Cu1-O1 and Cu1-O4ⁱ; Table 1). The thiophene-2,5-dicarboxylate dianions function as μ_2 -bridging

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Figure 1

The coordination environment of Cu in (I), with the atom numbering, showing displacement ellipsoids at the 30% probability level. [Symmetry code (i) -x, 1 - y, $z + \frac{1}{2}$]. The intramolecular O5-H5...O2 hydrogen bond is shown as a dashed line.

ligands forming an undulating zigzag chain with the 2,2'dipyridylamine molecules protruding alternately from the upper and lower surfaces of the chain (Fig. 2).

The stability of the solid-state structure of (I) is enhanced significantly by hydrogen-bonding interactions (Table 2). An intramolecular hydrogen bond forms between the O5 atom of the coordinated water and the uncoordinated carboxylate O2 atom [O5-H2B···O2]. Additional N2-H2···O3 and O5- $H5A \cdots O3$ intermolecular hydrogen bonds link neighbouring zigzag chains into a three-dimensional network structure and form large voids. These are filled by dimethylformamide and water solvent molecules, which in turn are linked by O7- $H7A \cdots O6$ and $O7 - H7B \cdots O6$ hydrogen bonds (Fig. 3).

Experimental

An aqueous solution (10 ml) of $Cu(NO_3)_2 \cdot 3H_2O(0.30 \text{ mmol}, 0.072 \text{ g})$ was added slowly to a solution (10 ml) of N,N-dimethylformamide containing 2,2'-dipyridylamine (0.30 mmol, 0.051 g) and thiophene-2,5-dicarboxylic acid (0.30 mmol, 0.052 g). Blue crystals suitable for X-ray analysis were obtained on allowing the solution to stand at room temperature for about a month.

Crystal data

 $[Cu(C_6H_2O_4S)(C_{10}H_9N_3)-$ (H₂O)]·C₃H₇NO·H₂O $M_r = 514.01$ Orthorhombic, Pna21 a = 7.067 (1) Åb = 24.123 (2) Å c = 13.379(1) Å V = 2280.8 (4) Å³ Z = 4

 $D_r = 1.497 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 6159 reflections $\theta = 2.9 - 25.7^{\circ}$ $\mu = 1.10 \text{ mm}^{-1}$ T = 298 (2) KBlock, blue $0.46 \times 0.41 \times 0.17~\text{mm}$







Figure 3

The crystal packing of (I), showing the three-dimensional network structure formed by hydrogen-bonding interactions (shown as dashed lines).

Data collection

Bruker SMART APEX area- detector diffractometer φ and ω scans Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 2002) $T_{min} = 0.633, T_{max} = 0.836$ 13430 measured reflections	4485 independent reflections 4174 reflections with $I > 2\sigma(I)$ $R_{int} = 0.028$ $\theta_{max} = 27.5^{\circ}$ $h = -9 \rightarrow 9$ $k = -30 \rightarrow 28$ $l = -17 \rightarrow 12$
Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0436P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.031$	where $P = (F_0^2 + 2F_c^2)/3$
$wR(F^2) = 0.075$	$(\Delta/\sigma)_{\rm max} = 0.001$
S = 1.04	$\Delta \rho_{\rm max} = 0.28 \text{ e} \text{ Å}^{-3}$
4485 reflections	$\Delta \rho_{\rm min} = -0.35 \ {\rm e} \ {\rm \AA}^{-3}$

306 parameters H atoms treated by a mixture of independent and constrained refinement

-0.35 e A Absolute structure: Flack (1983), 5538 Friedel pairs Flack parameter: 0.012 (11)

Table 1				
Selected	geometric	parameters	(Å,	°).

1.958 (2)	Cu1-N1	2.002 (2)
1.963 (2)	Cu1-O5	2.220 (2)
1.996 (2)		
87.90 (8)	O4 ⁱ -Cu1-O5	94.65 (10)
172.76 (8)	O1-Cu1-O5	94.73 (8)
91.30 (8)	N3-Cu1-O5	92.59 (10)
90.23 (9)	N1-Cu1-O5	97.37 (9)
167.87 (8)	C1-O1-Cu1	128.24 (18)
89.05 (9)		
	1.958 (2) 1.963 (2) 1.996 (2) 87.90 (8) 172.76 (8) 91.30 (8) 90.23 (9) 167.87 (8) 89.05 (9)	$\begin{array}{cccc} 1.958 & (2) & Cu1-N1 \\ 1.963 & (2) & Cu1-O5 \\ 1.996 & (2) & & & \\ 87.90 & (8) & O4^i-Cu1-O5 \\ 172.76 & (8) & O1-Cu1-O5 \\ 91.30 & (8) & N3-Cu1-O5 \\ 90.23 & (9) & N1-Cu1-O5 \\ 167.87 & (8) & C1-O1-Cu1 \\ 89.05 & (9) & & \\ \end{array}$

Symmetry code: (i) $-x, -y + 1, z + \frac{1}{2}$.

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
O5−H5 <i>B</i> ···O2	0.84 (1)	1.99 (3)	2.671 (3)	138 (4)
$O7 - H7B \cdot \cdot \cdot O6^{ii}$	0.85(1)	2.05 (2)	2.879 (5)	168 (4)
$O7 - H7A \cdots O6^{iii}$	0.85(1)	2.02(1)	2.861 (5)	170 (5)
$N2-H2\cdots O3^{iv}$	0.86	2.24	2.910 (3)	134
$O5-H5A\cdots O3^{v}$	0.84 (1)	1.98 (2)	2.773 (3)	158 (4)
		·· 1 1	(1)	1 1 ()

Symmetry codes: (ii) x + 1, y, z; (iii) $x + \frac{1}{2}, -y + \frac{1}{2}, z$; (iv) $-x + \frac{1}{2}, y - \frac{1}{2}, z + \frac{1}{2}$; (v) $-x + 1, -y + 1, z + \frac{1}{2}$.

H atoms of the water molecules were located in a difference map and were refined isotropically, with O–H distances restrained to 0.85(1) Å. All H atoms of the DMF molecules were placed in calculated positions using a riding-model approximation, with C–H distances of 0.93 Å for OC–H and 0.96 Å for methyl H atoms $[U_{iso}(H)$ values of 1.2(CH) or 1.5(CH₃) times U_{eq} (parent atom)]. The remaining H atoms were positioned geometrically (C-H = 0.93 Å and N-H = 0.86 Å) and allowed to ride on their parent atoms, with $U_{iso}(H)$ values equal to $1.2U_{eq}(C,N)$.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2002); software used to prepare material for publication: *SHELXL97*.

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