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Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
 Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$
 R factor = 0.030
 wR factor = 0.078
 Data-to-parameter ratio = 10.4

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

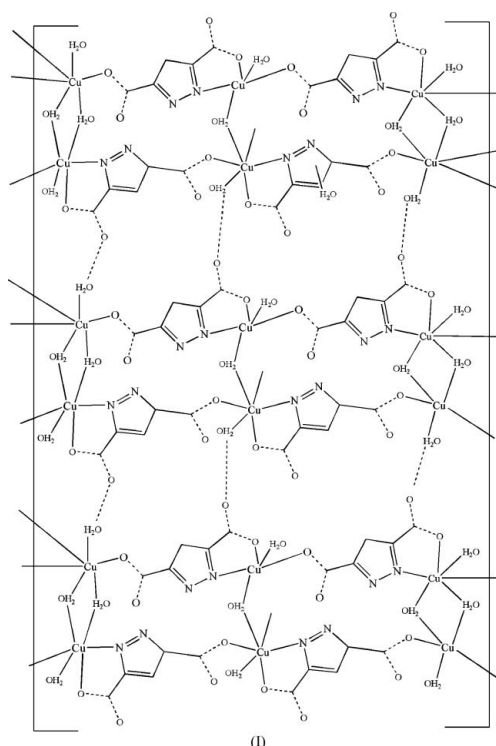
Poly[di- μ_2 -aqua- μ -pyrazole-3,5-dicarboxylato-copper(II)]

The copper(II) coordination polymer $[\text{Cu}(\text{pydc})(\text{H}_2\text{O})_2]_n$ (pydc = 3,5-pyrazoledicarboxylate, $\text{C}_5\text{H}_2\text{N}_2\text{O}_4$), was synthesized by treating Cu(II) nitrate with 3,5-pyrazoledicarboxylic acid under hydrothermal conditions. Single-crystal X-ray diffraction indicates that the copper coordination polymer has a pydc-bridged ladder-like chain structure.

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Comment

The design and construction of coordination polymers has attracted much attention owing to their intriguing topologies and potential applications as functional materials (Inoue *et al.*, 2001). Many networks with various structural motifs have been documented in the past decade (Amabilino & Stoddart, 1995). Recently, a new type of stable three-dimensional metal-organic framework has been reported (Lu *et al.*, 2006). Unlike pyridine 2,4-, 3,4- 2,5- and 2,6-dicarboxylic acids, which have been widely reported as bridging ligands for the assembly of various coordination polymers, complexes with 3,5-pyrazoledicarboxylic acid (H_2pydc) have been reported only rarely (Pan *et al.*, 2000). We report here the synthesis and structure of a copper(II) coordination polymer with 3,5-pyrazoledicarboxylic acid, (I).



In (I), the Cu atom adopts a distorted octahedral CuO_5N coordination geometry (Fig. 1 and Table 1). Pairs of Cu atoms are bridged by molecules of the 3,5-pyrazoledicarboxylate ligand *via* its *N*- and *O*-donor atoms, and one *O*-donor atom of the second carboxyl group. The copper centers are further bridged by two μ_2 -aqua ligands, generating a ladder-like chain (Fig. 2), with a $\text{Cu}\cdots\text{Cu}$ distance of 3.269 (3) Å. These chains are further linked *via* $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonding between pyridyl N atoms, carboxylate O atoms and aqua ligands (Table 2), forming a three-dimensional network.

Experimental

A mixture of $\text{Cu}(\text{NO}_3)_2\cdot 2\text{H}_2\text{O}$ (0.5 mmol, 0.120 g), 3,5-pyrazoledicarboxylic acid (0.5 mmol, 0.087 g), NaOH (1 mmol, 0.04 g), and water (10 ml) was mixed in a 23 ml Teflon reactor which was heated at 453 K for 6 d and then cooled to room temperature at a rate of 5 K h^{-1} (yield: 42%). Analysis for $\text{C}_5\text{H}_6\text{CuN}_2\text{O}_6$ (found/calc %): C 23.48 (23.68), H 2.34 (2.38), N 11.23 (11.04).

Crystal data

$[\text{Cu}(\text{C}_5\text{H}_2\text{N}_2\text{O}_4)(\text{H}_2\text{O})_2]$	$V = 383.55 (7) \text{ \AA}^3$
$M_r = 253.66$	$Z = 2$
Triclinic, $P\bar{1}$	$D_x = 2.196 \text{ Mg m}^{-3}$
$a = 6.8178 (7) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 7.4015 (8) \text{ \AA}$	$\mu = 2.86 \text{ mm}^{-1}$
$c = 8.5079 (9) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\alpha = 104.775 (2)^\circ$	Block, green
$\beta = 90.733 (2)^\circ$	$0.37 \times 0.25 \times 0.21 \text{ mm}$
$\gamma = 111.497 (2)^\circ$	

Data collection

Bruker APEX area-detector diffractometer	3017 measured reflections
φ and ω scans	1494 independent reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	1434 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.419$, $T_{\max} = 0.582$	$R_{\text{int}} = 0.013$
(expected range = 0.396–0.549)	$\theta_{\text{max}} = 26.0^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.029P)^2 + 1.0214P]$
$R[F^2 > 2\sigma(F^2)] = 0.030$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.078$	$(\Delta\rho)_{\text{max}} < 0.001$
$S = 1.13$	$\Delta\rho_{\text{max}} = 0.46 \text{ e \AA}^{-3}$
1494 reflections	$\Delta\rho_{\text{min}} = -0.40 \text{ e \AA}^{-3}$
143 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Selected geometric parameters (Å, °).

Cu1—O2 ⁱ	1.990 (2)	Cu1—N2	2.056 (2)
Cu1—O4	2.032 (2)	Cu1—O1W ⁱⁱ	2.075 (2)
Cu1—O2W	2.038 (2)	Cu1—O1W	2.152 (2)
O2 ⁱ —Cu1—O4	89.38 (9)	O2W—Cu1—N2	91.44 (10)
O2 ⁱ —Cu1—O2W	89.72 (10)	O4—Cu1—O1W	90.52 (9)
O4—Cu1—O2W	96.53 (10)	O2W—Cu1—O1W	172.86 (9)
O2 ⁱ —Cu1—N2	169.15 (9)	N2—Cu1—O1W	90.91 (9)
O4—Cu1—N2	79.76 (9)	O1W ⁱⁱ —Cu1—O1W	78.74 (9)

Symmetry codes: (i) $x, y, z - 1$; (ii) $-x, -y, -z - 3$.

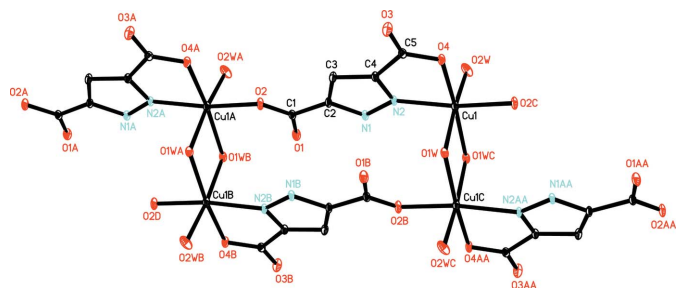


Figure 1

View of the structure of (I). Displacement ellipsoids are drawn at the 30% probability level. H atoms have been omitted for clarity. [Symmetry code: (i) $x, y, z + 1$; (ii) $-x, -y, -z - 2$; (iii) $-x, -y, -z - 1$; (iv) $x, y, z - 1$.]

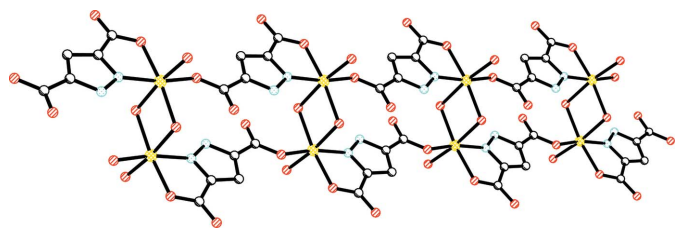


Figure 2

A fragment of the ladder-like chain in (I).

Table 2

Hydrogen-bond geometry (Å, °).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$\text{N1}-\text{H1A}\cdots\text{O3}^{\text{iii}}$	0.86	2.09	2.831 (3)	144
$\text{O1W}-\text{H1WB}\cdots\text{O3}^{\text{iv}}$	0.843 (10)	1.823 (12)	2.650 (3)	167 (3)
$\text{O1W}-\text{H1WB}\cdots\text{O4}^{\text{iv}}$	0.843 (10)	2.50 (3)	3.145 (3)	134 (3)
$\text{O2W}-\text{H2WA}\cdots\text{O1}^{\text{v}}$	0.840 (10)	1.959 (15)	2.782 (3)	166 (3)
$\text{O2W}-\text{H2WB}\cdots\text{O4}^{\text{vi}}$	0.839 (10)	1.954 (11)	2.791 (3)	176 (4)
$\text{O1W}-\text{H1WA}\cdots\text{O1}^{\text{vii}}$	0.842 (10)	1.903 (19)	2.684 (3)	154 (4)

Symmetry codes: (iii) $x - 1, y, z$; (iv) $-x + 1, -y, -z - 3$; (v) $-x, -y + 1, -z - 2$; (vi) $-x + 1, -y + 1, -z - 3$; (vii) $-x, -y, -z - 2$.

The water H atoms were located in a difference Fourier map and refined with distance restraints $\text{O}-\text{H} = 0.85 (1) \text{ \AA}$ and $\text{H}\cdots\text{H} = 1.39 (1) \text{ \AA}$. Other H atoms were placed at calculated positions ($\text{C}-\text{H} = 0.93 \text{ \AA}$ and $\text{N}-\text{H} = 0.86 \text{ \AA}$) and refined using the riding-model approximation with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2001); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97; molecular graphics: SHELXL97; software used to prepare material for publication: SHELXL97.

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