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Key indicators

Single-crystal X-ray study
 T = 296 K
 Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$
 R factor = 0.045
 wR factor = 0.149
 Data-to-parameter ratio = 13.0

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

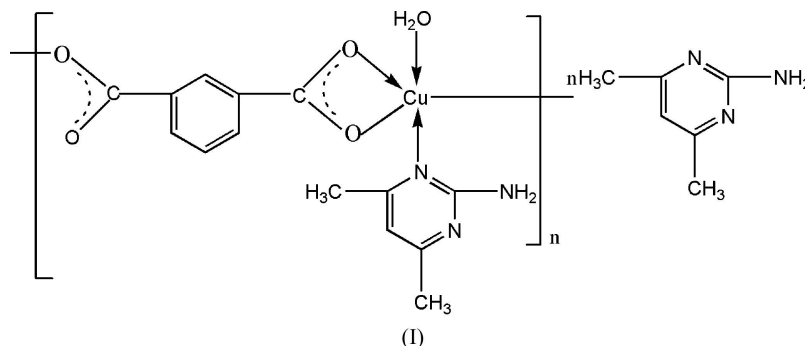
**catena-Poly[[[aqua(2-amino-4,6-dimethyl-
 pyrimidine- κN^1)copper(II)]- μ -benzene-1,3-di-
 carboxylato- $\kappa^2\text{O}^1:\text{O}^3$] 2-amino-4,6-dimethyl-
 pyrimidine solvate]**

In the title polymer, $\{[\text{Cu}(\text{C}_8\text{H}_4\text{O}_4)(\text{C}_6\text{H}_9\text{N}_3)(\text{H}_2\text{O})] \cdot \text{C}_6\text{H}_9\text{N}_3\}_n$, the Cu^{II} ion approximates a distorted square-pyramidal geometry defined by an NO_4 donor set. Adjacent Cu^{II} ions are bridged by isophthalate dianions to form a one-dimensional chain. Chains interact through π - π stacking interactions of 2-amino-4,6-dimethylpyrimidine rings and hydrogen bonds, to build a three-dimensional crystal structure.

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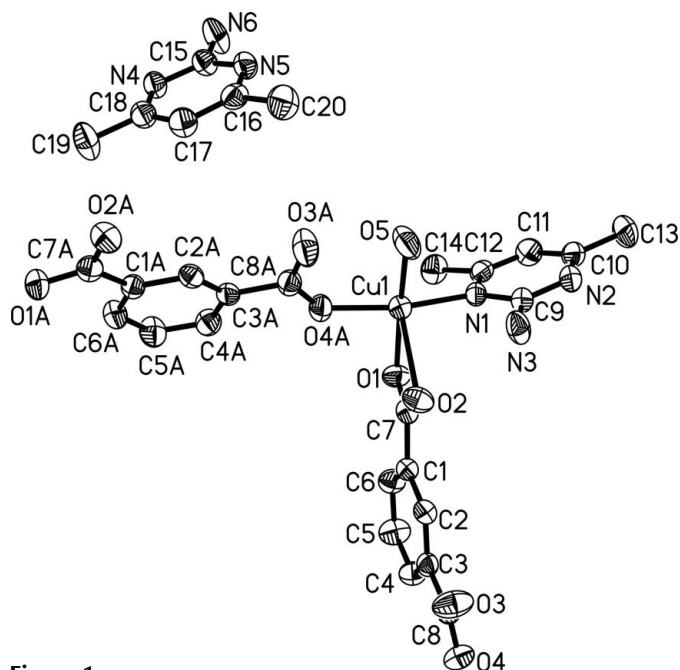
Comment

Two types of interactions, namely coordinate covalent bonds and non-covalent intermolecular forces, such as hydrogen bonding and π - π stacking interactions, play a key role in building and stabilizing polymers, which have important applications in the areas of magnetism, optics, electronics and catalysis (Ye *et al.*, 2005; Janiak, 2000; Steiner, 2002). Considering the coordination properties of 2-amino-4,6-dimethyl-pyrimidine (abbreviated ADP hereafter) and the bridging character of isophthalate, these ligands were used to construct the title polymer, (I).

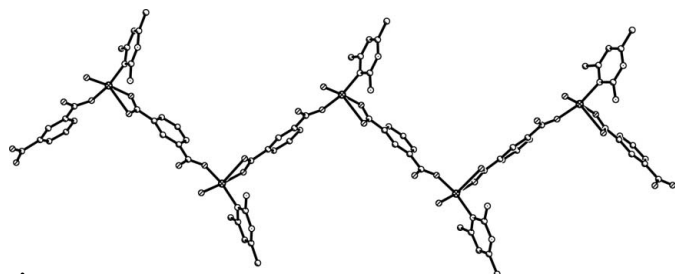


As shown in Fig. 1, the Cu^{II} ion may be described as five-coordinated by three O atoms (O1, O2 and O4) of isophthalate ligands (Billing *et al.*, 1970), one N atom belonging to an ADP ligand and one O atom of a water molecule, giving a distorted square-pyramidal geometry (Table 1). As shown in Fig. 2, Cu^{II} ions are bridged by isophthalate dianions to form a one-dimensional chain. There is one uncoordinated ADP molecule completing the asymmetric unit.

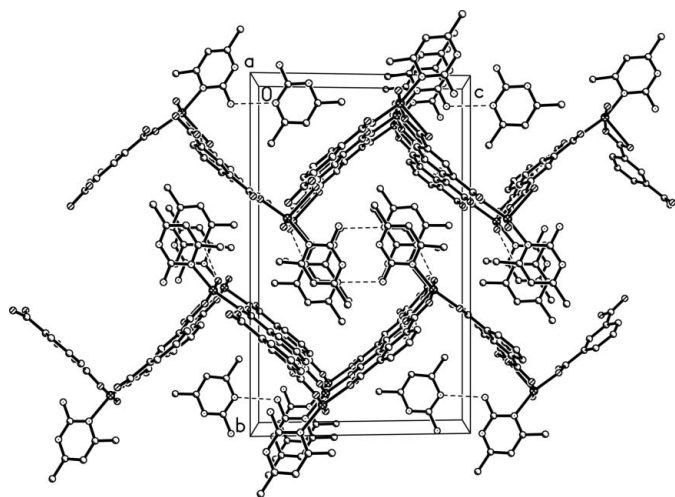
Coordinated and uncoordinated ADP molecules are linked by hydrogen bonds (Table 2, entries 1 and 2). The one-dimensional chains are interlaced *via* free ADP molecules; coordinated and symmetry-related uncoordinated ADP molecules (symmetry code: $2 - x, -y, 1 - z$) have offset face-to-face π - π stacking interactions, the centroid-to-centroid separation being 3.807 \AA (Janiak, 2000). The hydrogen bonds together with π - π interactions build the three-dimensional structure of $[\text{Cu}(\text{C}_8\text{H}_4\text{O}_4)(\text{C}_6\text{H}_9\text{N}_3)(\text{H}_2\text{O})]_n(\text{C}_6\text{H}_9\text{N}_3)_n$.


Figure 1

Part of the structure of the title complex, showing the coordination geometry and the uncoordinated ADP molecule. Displacement ellipsoids are drawn at the 50% probability level. For clarity, H atoms have been omitted. [Symmetry code: (A) $x + \frac{1}{2}$, $-y + \frac{1}{2}$, $z - \frac{1}{2}$].


Figure 2

A one-dimensional polymeric chain in the crystal structure of (I). All H atoms have been omitted for clarity.


Figure 3

The packing arrangement of the title compound viewed along [100]. Dashed lines represent hydrogen bonds. All H atoms have been omitted for clarity.

Hydrogen bond geometries are shown in Table 2. The packing arrangement of the title polymer is shown in Fig. 3.

Experimental

All reagents were of analytical grade from commercial sources and used without further purification. A mixture of ADP (0.0246 g, 0.2 mol), isophthalic acid (0.0166 g, 0.1 mol), copper(II) nitrate (0.0187 g, 0.1 mol) and water (7 ml) was stirred in air for 5 min and sealed in a 10 ml Teflon-lined stainless steel Parr bomb, which was heated to 423 K for 36 h and then cooled to room temperature. Green block single crystals were separated and washed with deionized water (yield 45%, based on Cu).

Crystal data

[Cu(C₈H₄O₄)(C₆H₉N₃)(H₂O)]·
C₆H₉N₃
M_r = 491.99
Monoclinic, *P*2₁/*n*
a = 7.8409 (2) Å
b = 21.4009 (7) Å
c = 13.1791 (3) Å
β = 97.195 (2)°

V = 2194.07 (10) Å³
Z = 4
D_x = 1.489 Mg m⁻³
Mo *Kα* radiation
μ = 1.04 mm⁻¹
T = 296 (2) K
Block, green
0.38 × 0.25 × 0.13 mm

Data collection

Bruker SMART APEX-II area-
detector diffractometer
φ and *ω* scans
Absorption correction: multi-scan
(*SADABS*; Sheldrick, 1996)
T_{min} = 0.693, *T_{max}* = 0.877

9167 measured reflections
3900 independent reflections
2923 reflections with *I* > 2σ(*I*)
R_{int} = 0.030
θ_{max} = 25.1°

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.045
wR (*F*²) = 0.149
S = 1.04
3900 reflections
301 parameters

H atoms treated by a mixture of
independent and constrained
refinement
w = 1/[σ²(*F_o*²) + (0.0981*P*)²]
where *P* = (*F_o*² + 2*F_c*²)/3
(Δ/σ)_{max} = 0.001
Δρ_{max} = 0.41 e Å⁻³
Δρ_{min} = -0.54 e Å⁻³

Table 1

Selected geometric parameters (Å, °).

Cu1—O5	1.926 (3)	Cu1—N1	2.011 (3)
Cu1—O1	1.950 (2)	Cu1—O2	2.530 (3)
Cu1—O4 ⁱ	1.955 (2)		
O5—Cu1—O1	171.91 (15)	O4 ⁱ —Cu1—N1	164.05 (11)
O5—Cu1—O4 ⁱ	91.88 (12)	O5—Cu1—O2	114.60 (15)
O1—Cu1—O4 ⁱ	89.34 (11)	O1—Cu1—O2	57.32 (9)
O5—Cu1—N1	88.67 (13)	O4 ⁱ —Cu1—O2	96.94 (10)
O1—Cu1—N1	92.35 (11)	N1—Cu1—O2	97.31 (10)

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

Table 2

Hydrogen-bond 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>
N3—H3A...N4 ⁱⁱ	0.86	2.14	2.994 (4)	175
N6—H6A...N2 ⁱⁱⁱ	0.86	2.25	3.109 (4)	175
N3—H3B...O2	0.86	2.16	2.944 (4)	152
O5—H5E...N5 ^{iv}	0.843 (10)	1.98 (4)	2.712 (4)	144 (6)
O5—H5F...O3 ⁱ	0.846 (10)	1.76 (3)	2.507 (4)	145 (5)

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

All C- and N-bonded H atoms were placed geometrically and refined with bond lengths constrained to 0.93 (aromatic CH), 0.96 (methyl CH₃) or 0.86 Å (amine NH₂), and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{carrier atom})$ for aromatic CH and NH₂ group, or $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{carrier C})$ for methyl groups. H atoms of the water molecule were located in a difference map, and refined with O—H distances restrained to 0.85 (1) Å and free isotropic displacement parameters.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINTE* (Bruker, 2002); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2005); software used to prepare material for publication: *SHELXTL*.

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