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Key indicators

Single-crystal X-ray study

*T* = 293 K

Mean  $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$

*R* factor = 0.025

*wR* factor = 0.064

Data-to-parameter ratio = 14.8

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

catena-Poly[[bis(4-aminopyrimidine- $\kappa\text{N}^1$ )-copper(II)]-di- $\mu$ -dicyanamido- $\kappa^4\text{N}^1:\text{N}^3$ ]

In the title octahedral complex,  $[\text{Cu}\{\text{N}(\text{CN})_2\}_2(\text{ampym})_2]_n$  (ampym is 4-aminopyrimidine,  $\text{C}_4\text{H}_5\text{N}_3$ ), the Cu atom is located on an inversion centre and is coordinated in the equatorial plane by two dicyanamide nitrile N atoms and two N atoms from ampym ligands [ $\text{Cu}-\text{N} = 1.972(2)$  and  $2.001(2) \text{ \AA}$ , respectively], and in the axial positions by another two dicyanamide nitrile N atoms, at  $2.633(2) \text{ \AA}$ . Neighbouring Cu atoms are connected *via* double dicyanamide bridges to form a one-dimensional infinite chain.

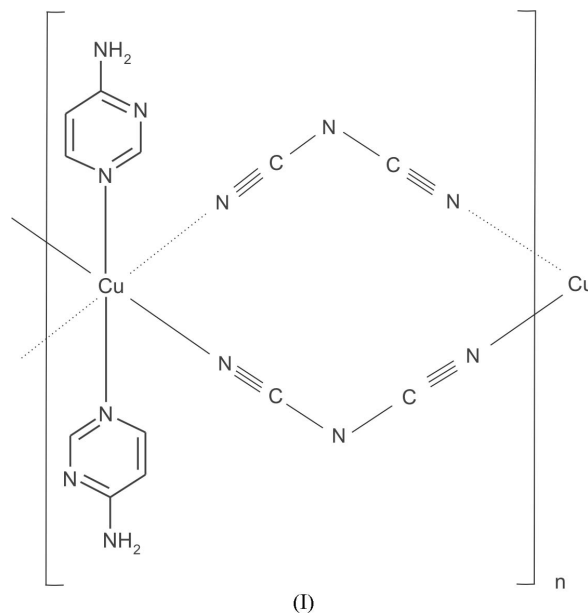
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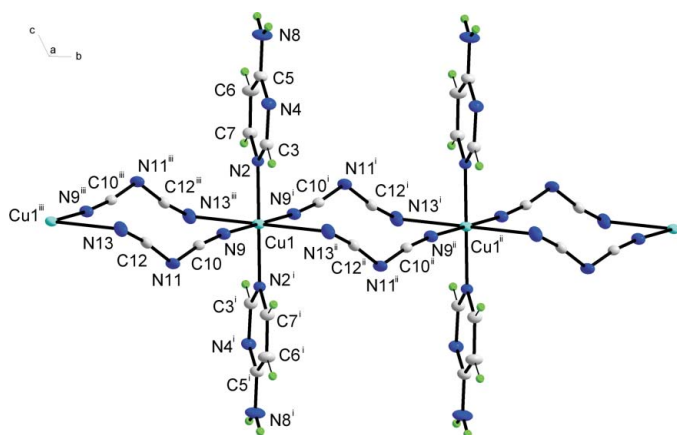
Comment

In coordination compounds of  $\text{Cu}^{\text{II}}$  and  $\text{Cu}^{\text{I}}$ , the dicyanamide ( $\text{dca}^-$ ) anion,  $(\text{N}(\text{CN})_2)^-$ , exhibits a rich variety of bonding modes. It can coordinate either in a monodentate manner (*e.g.* Burčák *et al.*, 2004) or, more typically, in a bidentate manner [two types of binding: mainly through two nitrile N atoms (Potočňák *et al.*, 2002), but also through one amide and one nitrile N atom (Mohamadou *et al.*, 2003)], or even in a tridentate manner in the case of  $\text{Cu}^{\text{I}}$  (Batten *et al.*, 2000).



4-Aminopyrimidine and derived neutral ligands can also be coordinated either in monodentate mode (*e.g.* Manson *et al.*, 2003) or in bridging mode, as recently reported for  $\text{Cu}(\text{HCO}_2)_2(\text{pyrimidine})$  (Manson *et al.*, 2005). In the title compound, (I), the bridging mode of  $\text{dca}^-$  ligands seems to be preferred to the bridging mode of 4-aminopyrimidine.

The geometry around the  $\text{Cu}^{\text{II}}$  ion in (I) is tetrahedrally elongated octahedral (the Cu atom lies on an inversion centre), with the equatorial plane formed by two nitrile N



**Figure 1**

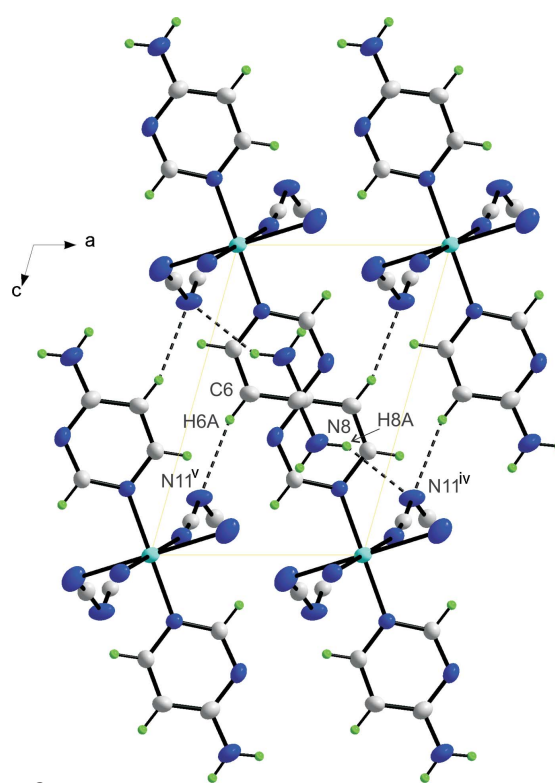
The atom-numbering scheme of the title compound, with displacement ellipsoids at the 50% probability level [symmetry codes: (i)  $-x, -y, -z$ ; (ii)  $x, 1 + y, z$ ; (iii)  $-x, -1 - y, -z$ ].

atoms from dicyanamides and two other N atoms from neutral ligands. Axial positions are occupied by another two nitrile dicyanamide N atoms. Neighbouring Cu atoms are connected *via* double dicyanamide bridges to form a one-dimensional infinite chain in the *b*-axis direction (Fig. 1).

In the Cambridge Structural Database (CSD; Version 5.26; Allen, 2002), there are four crystal structures of the type  $[\text{Cu}\{\text{N}(\text{CN})_2\}_2L_2]$  ( $L$  = neutral *N*-donor ligand), with the chromophore  $[\text{CuN}_6]$ , the neighbouring Cu atoms connected *via* double dicyanamide bridges and with an *R* value lower than 0.05. In two of them [CSD refcodes KEQWIM (van Albada *et al.*, 2000) and MEBFEE (Jensen *et al.*, 1999)], there are two  $dca^-$  ligands coordinated in the equatorial plane ( $\text{Cu}-\text{N} = 1.972$  and  $1.966$  Å) and two others in axial positions ( $\text{Cu}-\text{N} = 2.417$  and  $2.420$  Å).  $\text{Cu}-L$  distances are 2.078 and 2.051 Å, respectively. In the present crystal structure, (I), the corresponding distances are  $\text{Cu1}-\text{N9}$  1.972 (2) Å,  $\text{Cu1}-\text{N13}$  2.633 (2) Å and  $\text{Cu1}-\text{N2}$  2.001 (2) Å. In the crystal structure EDALAW (van Albada *et al.*, 2001), the Cu atom lies on a general position with corresponding  $\text{Cu}-\text{N}$  distances 1.983, 1.988, 2.313, 2.967, 2.008 and 2.023 Å, respectively. In the crystal structure PAHWAX (Luo *et al.*, 2004), all  $dca^-$  ligands are found in the equatorial plane ( $\text{Cu}-\text{N} = 2.003$  and 2.005 Å) and the neutral quinoxaline ligand is coordinated in the axial position ( $\text{Cu}-\text{N} = 2.479$  Å).

The ampym rings in the unit cell of (I) are aligned parallel, approximately perpendicular to the *b* axis, so the distance between these rings is larger than 3.6 Å and does not indicate any  $\pi-\pi$  interaction. The crystal structure is stabilized by hydrogen bonds (Table 2), which, together with double dicyanamide bridges, form a three-dimensional network (Fig. 2).

Inspection of the interatomic distances (Table 1) shows an extended delocalized  $\pi$ -system  $\text{N11}/\text{C10}/\text{N9}/\text{Cu1}/\text{N2}/\text{C3}/\text{N4}/\text{C5}/\text{N8}$ . The bond length  $\text{N4}-\text{C3}$  [1.320 (2) Å] is clearly shorter than that expected for a single bond (for example, 1.349 Å in imidazole). A similar feature was observed for the free ligand 4-aminopyrimidine (Van Meervelt & Uytterhoeven, 2003), where, *via* hydrogen bonds, two one-dimen-



**Figure 2**

Packing diagram of (I), viewed along the *b* axis. Hydrogen-bond interactions are indicated by dashed lines [symmetry codes: (iv)  $1 + x, 1 + y, 1 + z$ ; (v)  $x, 1 + y, 1 + z$ ].

sional infinite chains are formed along the *b* axis ( $\text{N}_{\text{ampym}} \cdots \text{H}_{\text{amine}}$  and  $\text{N}_{\text{ampym}} \cdots \text{H}_{\text{amine}} - \text{N}_{\text{amine}}$  separations and angles:  $2.100/2.134$  Å and  $176/174^\circ$  for two independent molecules).

## Experimental

A solution of 2.0 mmol of  $\text{CuSO}_4$  in water (3 ml) was mixed with a solution of 4.0 mmol of  $\text{NaN}(\text{CN})_2$  in water (10 ml) and with a solution of 4.0 mmol of ampym in ethanol (10 ml). After standing for a few days, blue crystals were isolated (yield: *ca* 10%).

### Crystal data

$[\text{Cu}(\text{C}_2\text{N}_3)(\text{C}_4\text{H}_5\text{N}_3)]$   
 $M_r = 385.86$   
 Triclinic,  $P\bar{1}$   
 $a = 6.260$  (1) Å  
 $b = 7.248$  (1) Å  
 $c = 9.451$  (2) Å  
 $\alpha = 105.29$  (3) $^\circ$   
 $\beta = 100.19$  (3) $^\circ$   
 $\gamma = 106.27$  (3) $^\circ$   
 $V = 382.2$  (1) Å $^3$

$Z = 1$   
 $D_x = 1.676$  Mg m $^{-3}$   
 Mo  $K\alpha$  radiation  
 Cell parameters from 2020 reflections  
 $\theta = 3.1-29.2^\circ$   
 $\mu = 1.45$  mm $^{-1}$   
 $T = 293$  (2) K  
 Block, blue  
 $0.27 \times 0.25 \times 0.14$  mm

### Data collection

Oxford Diffraction Xcalibur CCD diffractometer  
 $\omega$  scans  
 Absorption correction: analytical face-indexed (CrysAlisRED; Oxford Diffraction, 2003)  
 $T_{\text{min}} = 0.767, T_{\text{max}} = 0.891$   
 2818 measured reflections

1705 independent reflections  
 1636 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.024$   
 $\theta_{\text{max}} = 27.5^\circ$   
 $h = -8 \rightarrow 8$   
 $k = -9 \rightarrow 7$   
 $l = -12 \rightarrow 12$

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.025$   
 $wR(F^2) = 0.064$   
 $S = 1.04$   
 1705 reflections  
 115 parameters  
 H-atom parameters constrained

$$w = 1/[\sigma^2(F_o^2) + (0.0264P)^2 + 0.2243P]$$

where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} < 0.001$   
 $\Delta\rho_{\max} = 0.32 \text{ e } \text{Å}^{-3}$   
 $\Delta\rho_{\min} = -0.36 \text{ e } \text{Å}^{-3}$

**Table 1**

Selected geometric parameters (Å, °).

Cu1—N2	2.001 (2)	C7—C6	1.352 (3)
Cu1—N9	1.972 (2)	C5—N8	1.334 (3)
Cu1—N13 <sup>iii</sup>	2.633 (2)	C5—C6	1.395 (3)
N2—C3	1.330 (2)	N9—C10	1.143 (2)
N2—C7	1.350 (2)	N11—C10	1.294 (2)
N4—C3	1.320 (2)	N11—C12	1.301 (2)
N4—C5	1.342 (3)	C12—N13	1.146 (2)
N9—Cu1—N2	90.91 (6)	N9—Cu1—N13 <sup>iii</sup>	90.0 (1)
N2—Cu1—N13 <sup>iii</sup>	89.3 (1)		

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

**Table 2**

Hydrogen-bonding geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N8—H8A $\cdots$ N11 <sup>iv</sup>	0.86	2.378	3.132 (3)	147
C6—H6A $\cdots$ N11 <sup>v</sup>	0.93	2.554	3.440 (3)	159

Symmetry codes: (iv)  $1 + x, 1 + y, 1 + z$ ; (v)  $x, 1 + y, 1 + z$ .

H atoms were positioned geometrically and treated as riding atoms, with C—H and N—H distances constrained to 0.93 and 0.86 Å, respectively, and  $U_{\text{iso}}(\text{H})$  values set at  $1.2U_{\text{eq}}$  of the carrier atom.

Data collection: *CrysAlisCCD* (Oxford Diffraction, 2001); cell refinement: *CrysAlisCCD*; data reduction: *CrysAlisRED* (Oxford Diffraction, 2003); program(s) used to solve structure: *SHELXS97*

(Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 1998); software used to prepare material for publication: *SHELXL97*.

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