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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.004 Å R factor = 0.037 wR factor = 0.104 Data-to-parameter ratio = 11.8

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

Bis(2-guanidinobenzimidazole- $\kappa^2 N, N'$)copper(II) bis(dicyanamide)

In the title compound, $[Cu(C_8H_9N_5)_2](C_2N_3)_2$, the Cu complex cation and dicyanamide anions lie on a twofold axis. Discounting the weak coordination of a dicyanamide anion, the Cu^{II} atom is coordinated by four N atoms from two 2-guanidinobenzimidazole ligands in a tetrahedrally distorted square-planar geometry. The cations and anions are linked *via* N-H···N hydrogen bonds, forming a two-dimensional network parallel to (010).

Comment

Benzazoles are common components in organisms and are active in many biological processes (Castillo-Blum & Barba-Behrens, 2000). The coordinating behaviour of benzimidazole chelating ligands has been studied to mimic biological activities (Aminabhavi et al., 1987). After functionalization, they have many applications, such as in fertilizers, antimicotics, antibiotics, pesticides and neuroprotectors (Tanabe et al., 1997; Katsura et al., 1999; Schnur et al., 1991; Jimonet, 1999; Barba-Behrens et al., 1991). 2-Guanidinobenzimidazole (abbreviated as gb), a derivative of benzazole, has attracted much interest in recent years. Coordination compounds with guanidines or benzazoles as ligands have been studied (Barba-Behrens et al., 1996; Andrade-López et al., 1997; Ceniceros-Gómez, Barba-Behrens, Bernès et al., 2000; Ceniceros-Gomez, Barba-Behrens, Ouiroz-Castro et al., 2000; Bishop et al., 2001, 2002, 2003; Arablo et al., 2003; van Albada et al., 2002, 2006). As part of our continuing interest in dicyanamide-bridged Cu^{II} complexes, compound (I) was prepared by the reaction between $[Cu(gb)_2]^{2+}$ and dicyanamide (dca⁻) ions. In this paper, we report the crystal structure analysis of (I).



© 2006 International Union of Crystallography All rights reserved Fig. 1 shows the molecular structure of (I). The Cu atom is situated on a twofold axis, and is coordinated by four N atoms

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Figure 1

The formula unit of (I) (twice the asymmetric unit), showing 30% probability displacement ellipsoids and the atom-numbering scheme. Atoms N1A/N2A/C1A/C2A and unlabeled atoms are related to N1/N2/ C1/C2 and other labeled atoms by the symmetry code $(1 - x, y, \frac{1}{2} - z)$.



Figure 2

The two-dimensional network of (I) formed by hydrogen bonds (dashed lines) and $\pi - \pi$ stacking interactions. H atoms have been omitted unless they are involved in hydrogen bonds.

from two gb ligands. The dicyanamide anions also have twofold rotational symmetry. Atom N7 of one of the dcaanions weakly coordinates to the Cu^{II} atom at a distance of 3.123 (4) Å (Table 1). The primary coordination geometry is tetrahedrally distorted square-planar, the dihedral angle between the chelate rings (Cu1/N1/C4/N4/C3/N2 and its symmetry-related partner) being 43.8 (4)°. Compared to $[M(gb)_2]^{2+}$ (M = Ni, Zn), despite having similar stoichiometries and coordination numbers, the coordination geometries are very different because of the distinctive electronic structures. The Ni^{II} complex displays a square-planar coordination

(Barba-Behrens et al., 1996; Andrade-López et al., 1997; Bishop et al., 2001, 2002, 2003), while the Zn^{II} complex adopts a close to ideal tetrahedral geometry (Andrade-López et al., 1997).

Each terminal N of the dicyanamide ions forms two N- $H \cdot \cdot \cdot N$ hydrogen bonds (Table 2). The $[Cu(gb)_2]^{2+}$ cations and dicyanamide anions are linked by $N-H\cdots N$ hydrogen bonds, forming one-dimensional chains along the *a* axis (Fig. 2). The conjugated benzimidazole rings of the gb ligands of adjacent chains are parallel and stacked with a perpendicular interplanar distance of 3.25 Å. The chains are further connected by $N-H\cdots N$ hydrogen bonds, forming a two-dimensional network parallel to (010).

Experimental

The ligand and the copper salt were purchased commercially. Compound (I) was prepared by the following procedure: 5 ml aqueous solution of CuCl₂·2H₂O (17 mg, 0.1 mmol) was slowly diffused into a methanol solution (5 ml) of sodium dicyanamide (18 mg, 0.2 mmol) and gb (35 mg, 0.2 mmol) through a single glass tube. After 3 d, dark-blue crystals of (I) appeared at the interface (yield 20%).

Crystal data

$[Cu(C_8H_9N_5)_2](C_2N_3)_2$	Z = 4
$M_r = 546.05$	$D_x = 1.609 \text{ Mg m}^{-3}$
Monoclinic, $C2/c$	Mo $K\alpha$ radiation
a = 15.587 (2) Å	$\mu = 1.02 \text{ mm}^{-1}$
b = 11.1008 (13) Å	T = 298 (2) K
c = 13.7083 (18) Å	Block, dark blue
$\beta = 108.174 \ (10)^{\circ}$	$0.3 \times 0.3 \times 0.3 \text{ mm}$
$V = 2253.6 (5) \text{ Å}^3$	

Data collection

Bruker P4 diffractometer ω scans Absorption correction: ψ scan (North et al., 1968) $T_{\min} = 0.737, \ T_{\max} = 0.744$ 2486 measured reflections 1992 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$ $wR(F^2) = 0.104$ S = 1.061992 reflections 169 parameters H-atom parameters constrained

1784 reflections with $I > 2\sigma(I)$ $R_{\rm int}=0.016$ $\theta_{\rm max} = 25.0^{\circ}$ 3 standard reflections every 97 reflections intensity decay: none

 $w = 1/[\sigma^2(F_0^2) + (0.0547P)^2]$ + 2.3317P] where $P = (F_0^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} < 0.001_{\circ}$ $\Delta \rho_{\rm max} = 0.61 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\rm min} = -0.21 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Cu1-N2	1.952 (2)	C1-N9	1.309 (4)
Cu1-N1	1.9615 (19)	C2-N6	1.143 (4)
Cu1-N7	3.123 (4)	C2-N7	1.310 (4)
C1-N8	1.150 (4)		
$N2^{i}-Cu1-N2$	148.87 (15)	$N1-Cu1-N1^i$	156.10 (12)
N2-Cu1-N1	90.06 (9)	$C2^{i}-N7-C2$	119.1 (4)
$N2-Cu1-N1^{i}$	96.32 (9)	$C1-N9-C1^{i}$	121.3 (4)

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

Table 2			
Hydrogen-bond	geometry	(Å,	°).

D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
0.86	2.09	2.916 (3)	162 (1)
0.86	2.00	2.836 (4)	165 (1)
0.86	2.34	3.151 (3)	158 (1)
0.86	2.35	3.103 (4)	146 (1)
	<i>D</i> —H 0.86 0.86 0.86 0.86	$\begin{array}{c ccc} D-H & H\cdots A \\ \hline 0.86 & 2.09 \\ 0.86 & 2.00 \\ 0.86 & 2.34 \\ 0.86 & 2.35 \end{array}$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$

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

All H atoms were positioned geometrically and treated as riding, with N-H = 0.86 Å, C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C,N)$.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL* (Sheldrick, 1998); software used to prepare material for publication: *SHELXTL*.

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