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## **Structure Reports**

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# Qihua Zhao,<sup>a</sup> Xiaofeng Wang,<sup>a</sup> Ruibin Fang<sup>a</sup> and Edward R. T. Tiekink<sup>b\*</sup>

<sup>a</sup>Department of Chemistry, Yunnan University, Kunming 650091, People's Republic of China, and <sup>b</sup>Department of Chemistry, National University of Singapore, Singapore 117543

Correspondence e-mail: chmtert@nus.edu.sg

### **Key indicators**

Single-crystal X-ray study  $T=223~\mathrm{K}$  Mean  $\sigma(\mathrm{C-C})=0.003~\mathrm{\mathring{A}}$  R factor = 0.037 wR factor = 0.101 Data-to-parameter ratio = 20.3

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

# Di- $\mu$ -azido-bis[azido(4,7-dimethyl-1,10-phenanthroline)copper(II)]

The title complex,  $[Cu(Me_2phen)(N_3)_2]_2$ , is disposed about an inversion centre;  $Me_2phen$  is 4,7-dimethyl-1,10-phenanthroline ( $C_{14}H_{12}N_2$ ). The structure features  $\mu_2$ -bridging and terminal azide ligands, chelating  $Me_2phen$  and the Cu atom in a distorted square pyramidal geometry.

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#### Comment

Azide-bridged copper(II) complexes involving combinations of chelating 1,10-phenanthroline (phen) ligands with end-on ( $\mu$ 1,1) and/or end-to-end ( $\mu$ 1,3) azides have been structurally determined. For example, [Cu(phen)(N<sub>3</sub>)<sub>2</sub>]<sub>n</sub> adopts a chain motif (Li *et al.*, 2000) and [Cu(phen)(N<sub>3</sub>)<sub>3</sub>]<sub>2</sub>·2N<sub>3</sub>·4H<sub>2</sub>O is dimeric and features uncoordinated azide (Cheng *et al.*, 2002). In order to determine the affect of steric hindrance in the phen ligand by introducing methyl groups at the 4- and 7-positions, so as to generate Me<sub>2</sub>phen, we synthesized the complex [Cu(Me<sub>2</sub>phen)(N<sub>3</sub>)<sub>2</sub>]<sub>2</sub>, (I).

The dinuclear structure of  $[Cu(Me_2phen)(N_3)_2]_2$  (Fig. 1) is situated about an inversion centre and features  $\mu_2$ -bridging and terminal azides as well as chelating Me<sub>2</sub>phen ligands. The bridges are effectively symmetric (Table 1) and, as expected, the bridging Cu-N<sub>azide</sub> distances are longer than the terminal  $Cu-N_{azide}$  distance. The  $Cu \cdot \cdot \cdot Cu^{i}$  separation within the dimer is 3.1616 (3) Å [symmetry code: (i)  $\frac{1}{2} - x$ ,  $\frac{1}{2} - y$ , -z]. The coordination geometry for Cu is based on a square pyramid. Thus, azide atoms N1, N4 and N1<sup>1</sup> and the Me<sub>2</sub>phen N7 atom define the basal plane and have deviations of 0.040 (2), 0.022(3), -0.015(3) and -0.060(2) Å, respectively, from their least-squares plane. The Cu atom lies 0.2449 (3) Å out of this plane in the direction of atom N8. This arrangement introduces some of the disparity in the Cu-N<sub>chelate</sub> bond distances, with the axial Cu-N8 distance being significantly longer than the basal Cu-N distance. Within the molecule, the disposition of the Me<sub>2</sub>phen methyl groups are such as to place one of the methyl-H atoms directly above the N1 atom, with C14—H···N1<sup>i</sup> = 2.55 Å, C14···N1<sup>i</sup> = 3.494 (3) Å and the angle subtended at  $H = 164^{\circ}$ . The most significant contact in the crystal structure is also of the type  $C-H \cdot \cdot \cdot N$ , so that C3- $H \cdot \cdot \cdot N6^{ii} = 2.42 \text{ Å}, C3 \cdot \cdot \cdot N6^{ii} = 3.305 \text{ (3) Å}$  and the angle at H

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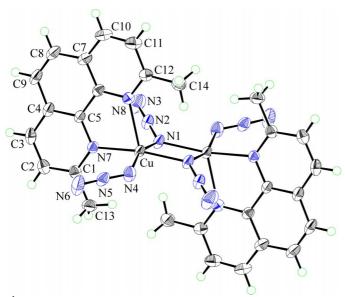


Figure 1 The molecular structure and crystallographic numbering scheme for (I). The unlabelled half of the molecule is generated by the symmetry operation  $(\frac{1}{2} - x, \frac{1}{2} - y, -z)$ . Displacement ellipsoids are drawn at the 50% probability level.

= 157° [symmetry code: (ii) -x, y,  $\frac{1}{2} - z$ ]. Such associations, as described, lead to the formation of weakly associated chains comprising complex molecules.

There is one closely related structure available in the literature for comparison, namely that of di- $\mu_2$ -azido-bis[-azido(N,N-diethylethylenediamine)copper(II)] (Casagrande *et al.*, 1989). This is centrosymmetric, like the title complex, and features essentially the same pattern of bond distances.

## **Experimental**

A single-crystal of (I) was grown in aqueous solution by slow diffusion using an H-double-tube glass vessel. Methanol solutions of  $Cu(Me_2phen)(NO_3)_2$  (0.01 M) and  $NaN_3$  (0.02 M) were placed in separate arms. Brown crystals separated after two months.

# Crystal data

$[Cu_2(N_3)_4(C_{14}H_{12}N_2)_2]$	$D_x = 1.611 \text{ Mg m}^{-3}$
$M_r = 711.72$	Mo $K\alpha$ radiation
Monoclinic, C2/c	Cell parameters from 3661
a = 13.3691 (5)  Å	reflections
b = 11.2648 (5)  Å	$\theta = 2.4 - 30.0^{\circ}$
c = 19.5792 (9)  Å	$\mu = 1.50 \text{ mm}^{-1}$
$\beta = 95.565 (2)^{\circ}$	T = 223 (2)  K
$V = 2934.7 (2) \text{ Å}^3$	Block, brown
Z = 4	$0.49\times0.16\times0.16~\text{mm}$

## Data collection

4259 independent reflections
3450 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.032$
$\theta_{\mathrm{max}} = 30.0^{\circ}$
$h = -18 \rightarrow 18$
$k = -14 \rightarrow 15$
$l = -27 \rightarrow 19$

## Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0584P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.037$	$+\ 0.0245P$ ]
$wR(F^2) = 0.101$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.04	$(\Delta/\sigma)_{\text{max}} = 0.001$
4259 reflections	$\Delta \rho_{\text{max}} = 0.62 \text{ e Å}^{-3}$
210 parameters	$\Delta \rho_{\min} = -0.33 \text{ e Å}^{-3}$
H-atom parameters constrained	

 Table 1

 Selected geometric parameters ( $\mathring{A}$ , °).

Cu-N1	2.0285 (17)	N1-N2	1.212 (2)
Cu-N4	1.9499 (17)	N2-N3	1.137 (2)
Cu-N7	2.0316 (15)	N4-N5	1.187 (2)
Cu-N8	2.2554 (15)	N5-N6	1.149(2)
Cu-N1 <sup>i</sup>	2.0240 (17)		, ,
N1-Cu-N4	160.67 (7)	$N7-Cu-N1^{i}$	165.60 (6)
N1-Cu-N7	92.67 (6)	N8-Cu-N1i	112.53 (6)
N1-Cu-N8	94.60 (6)	Cu-N1-N2	125.03 (14)
$N1-Cu-N1^{i}$	77.45 (7)	$Cu^{i}-N1-N2$	125.47 (14)
N4-Cu-N7	96.31 (7)	$Cu-N1-Cu^{i}$	102.55 (7)
N4-Cu-N8	103.95 (7)	N1-N2-N3	178.8 (2)
$N4-Cu-N1^{i}$	90.27 (7)	Cu-N4-N5	126.15 (14)
N7-Cu-N8	78.34 (6)	N4-N5-N6	175.6 (2)

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

The carbon-bound H atoms were included in the riding-model approximation, with C—H distances of 0.94 Å (0.97 Å for methyl),  $U_{\rm iso}({\rm phenyl-H}) = 1.2 U_{\rm eq}({\rm C})$  and  $U_{\rm iso}({\rm methyl-H}) = 1.5 U_{\rm eq}({\rm C})$ .

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT* and *SHELXTL* (Bruker, 2000); program(s) used to solve structure: *PATTY* in *DIRDIF92* (Beurskens *et al.*, 1992); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXTL*.

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