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## catena-Poly[[[[(2,2'-bipyridine)copper(II)]- $\mu$ terephthalato] $N, N$-dimethylformamide solvate]

Xin-Hua Li and Hong-Ping Xiao*
Department of Chemistry and Materials Science, Wenzhou Normal College, Wenzhou 325027, People's Republic of China

Correspondence e-mail: hp_xiao@wznc.zj.cn

## Key indicators

Single-crystal X-ray study
$T=273 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.005 \AA$
$R$ factor $=0.052$
$w R$ factor $=0.133$
Data-to-parameter ratio $=13.3$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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In the title complex, $\left\{\left[\mathrm{Cu}\left(\mathrm{C}_{8} \mathrm{H}_{4} \mathrm{O}_{4}\right)\left(\mathrm{C}_{10} \mathrm{H}_{8} \mathrm{~N}_{2}\right)\right] \cdot \mathrm{C}_{3} \mathrm{H}_{7} \mathrm{NO}\right\}_{n}$, each Cu atom is surrounded by three O atoms from two terephthalate dianions and two N atoms from a 2,2'-bipyridine molecule, forming a distorted square-pyramidal geometry. The terephthalate dianion functions as a bridge between two Cu atoms and forms a one-dimensional zigzag chain coordination polymer.

## Comment

During the study of the structures of complexes in the $\mathrm{Cu}^{2+} /$ phen $/ \mathrm{H}_{2}$ tp (phen is 1,10 -phenanthroline and $\mathrm{H}_{2}$ tp is terephthalic acid) system (Cano et al., 1997; Chen et al., 2004; Sun et al., 2000, 2001; Xiao et al., 2004; Zhu et al., 2004) and in the $\mathrm{Cu}^{2+} / 2,2^{\prime}$-bipy $/ \mathrm{H}_{2}$ ta (2,2'-bipy is 2,2'-bipyridine) system (Xiao \& Zhu, 2003), we obtained a series of dinuclear complexes and one-dimensional zigzag chain coordination polymers. These complexes display a diversity of structures, and new complexes are constantly being produced through different reactions and even small changes, such as the use of different solvents, temperature, synthesis conditions or H -atom acceptors. All of these factors encouraged us to research these systems more deeply. Here, the title compound, $\left[\mathrm{Cu}\left(2,2^{\prime}\right.\right.$-bipy)(tp)]•(DMF), (I), represents an example.


In (I), the Cu atom is surrounded by three O atoms from two terephthalate dianions and two N atoms from a $2,2^{\prime}$-bipyridine molecule in a distorted square-pyramidal geometry (Fig. 1). The $\mathrm{Cu} 1-\mathrm{N} 1$ and $\mathrm{Cu} 1-\mathrm{N} 2$ bonds lengths are 1.996 (3) and 2.007 (3) $\AA$, respectively. The apical position is occupied by atom O 1 , the corresponding axial $\mathrm{Cu} 1-\mathrm{O} 1$ [2.401 (3) A] bond length being longer than the two basal $\left[\mathrm{Cu} 1-\mathrm{O}^{\mathrm{i}}=1.930(2) \AA\right.$ and $\mathrm{Cu} 1-\mathrm{O} 2=1.992(2) \AA$; symmetry code: (i) $x-\frac{1}{2}, y, \frac{1}{2}-z$ ] bonds lengths.

The terephthalate dianion functions as a bridge between two Cu atoms in a tridentate coordination mode. The 2,2'-

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The coordination environment of the $\mathrm{Cu}^{\text {II }}$ cation in (I), with atom numbering for the asymmetric unit, showing displacement ellipsoids at the $50 \%$ probability level.


Figure 2
A view of the one-dimensional zigzag chain structure in (I); the DMF solvent molecules and H atoms have been omitted for clarity.


A view, down the $b$ axis, of the packing; the DMF solvent molecules and H atoms have been omitted for clarity.
bipyridine group acts as a chelating ligand. A one-dimensional zigzag chain is formed by the $\mathrm{Cu}^{\mathrm{II}}$ cations, the $\mu_{2}$-bridging terephthalate dianions and the chelating 2,2'-bipyridine ligands (Fig. 2); this configuration is similar to that reported for $\left[\mathrm{Cu}\left(2,2^{\prime}\right.\right.$-bipy $\left.)(\mathrm{tp})\left(\mathrm{H}_{2} \mathrm{O}\right)\right]\left(2 \mathrm{H}_{2} \mathrm{O}\right)(\mathrm{DMF})$ (Xiao \& Zhu , 2003). Moreover, there are $\pi-\pi$ interactions involving the $2,2^{\prime}$ bipyridine ligands belonging to adjacent zigzag chains, with a distance of about $3.45 \AA$. Adjacent zigzag chains interweave with each other to generate a two-dimensional network structure with cavities (Fig. 3). The DMF solvent molecules fill the cavities.

## Experimental

A solution ( 10 ml ) of dimethylformamide containing $\mathrm{Cu}_{2} \mathrm{Cl}_{2} \cdot 2 \mathrm{H}_{2} \mathrm{O}$ $(0.3 \mathrm{mmol})$ was added dropwise to a solution $(10 \mathrm{ml})$ of dimethylformamide containing $2,2^{\prime}$-bipyridine ( 0.3 mmol ), terephthalic acid $(0.3 \mathrm{mmol})$ and $1,1^{\prime}$-carbonyldiimidazole $(0.3 \mathrm{mmol})$ at room temperature. The reaction mixture was filtered and the filtrate was left to stand for about two weeks until blue single crystals were obtained.

## Crystal data

$\left[\mathrm{Cu}\left(\mathrm{C}_{8} \mathrm{H}_{4} \mathrm{O}_{4}\right)\left(\mathrm{C}_{10} \mathrm{H}_{8} \mathrm{~N}_{2}\right)\right] \cdot \mathrm{C}_{3} \mathrm{H}_{7} \mathrm{NO}$
$M_{r}=456.94$
Orthorhombic, Pbca
$a=16.6884$ (7) $\AA$
$b=10.9585$ (5) A
$c=22.0082(9) \AA$
$V=4024.9(3) \AA^{3}$
$Z=8$
$D_{x}=1.508 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
Cell parameters from 3619
reflections
$\theta=2.4-23.0^{\circ}$
$\mu=1.12 \mathrm{~mm}^{-1}$
$T=273$ (2) K
Prism, blue
$0.27 \times 0.18 \times 0.13 \mathrm{~mm}$

## Data collection

Bruker SMART CCD area-detector
diffractometer
3619 independent reflections
3139 reflections with $I>2 \sigma(I)$
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan
(SADABS; Bruker, 2000)
$T_{\text {min }}=0.784, T_{\text {max }}=0.863$
19899 measured reflections
$R_{\text {int }}=25.2^{\circ}$
$\theta_{\text {max }}=29$
$\theta_{\text {max }}=25.2^{\circ}$
$h=-19 \rightarrow 14$
$k=-13 \rightarrow 12$

## Refinement

Refinement on $F^{2}$

$$
w=1 /\left[\sigma^{2}\left(F_{o}^{2}\right)+(0.0642 P)^{2}\right.
$$

$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.052$
$w R\left(F^{2}\right)=0.133$
$S=1.10$
3619 reflections
273 parameters
H-atom parameters constrained
Table 1
Selected geometric parameters $\left(\AA^{\circ},{ }^{\circ}\right)$.

| $\mathrm{Cu} 1-\mathrm{O} 3^{\mathrm{i}}$ | $1.930(2)$ | $\mathrm{Cu} 1-\mathrm{N} 2$ | $2.007(3)$ |
| :--- | ---: | :--- | ---: |
| $\mathrm{Cu} 1-\mathrm{O} 2$ | $1.992(2)$ | $\mathrm{Cu} 1-\mathrm{O} 1$ | $2.401(3)$ |
| $\mathrm{Cu} 1-\mathrm{N} 1$ | $1.996(3)$ |  |  |
| $\mathrm{O} 3^{\mathrm{i}}-\mathrm{Cu} 1-\mathrm{O} 2$ | $95.50(11)$ | $\mathrm{O} 2-\mathrm{Cu} 1-\mathrm{N} 1$ | $162.16(11)$ |
| $\mathrm{O} 3^{\mathrm{i}}-\mathrm{Cu} 1-\mathrm{N} 1$ | $94.38(11)$ | $\mathrm{O}^{\mathrm{i}}-\mathrm{Cu} 1-\mathrm{N} 2$ | $166.37(12)$ |

Symmetry code: (i) $x-\frac{1}{2}, y, \frac{1}{2}-z$.
H atoms attached to C atoms were included in the refinement in calculated positions in the riding-model approximation $[\mathrm{C}-\mathrm{H}=$ $0.93 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C})$ for $\mathrm{Csp}^{2}$, and $\mathrm{C}-\mathrm{H}=0.96 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.5 U_{\mathrm{eq}}(\mathrm{C})$ for $\left.\mathrm{Csp}{ }^{3}\right]$.

Data collection: $S M A R T$ (Bruker, 2000); cell refinement: $S M A R T$; data reduction: SAINT (Bruker, 2000); program(s) used to solve
structure: SHELXTL (Bruker, 2000); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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