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## Key indicators

Single-crystal X-ray study
$T=298 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.009 \AA$
$R$ factor $=0.094$
$w R$ factor $=0.170$
Data-to-parameter ratio $=13.2$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## catena-Poly[[ $\mu$-1,2-di-4-pyridylethylene- $\kappa^{2} N, N^{\prime}$ -[aqua(2-sulfonatobenzoato- $\left.\left.\left.\kappa^{2} O, O^{\prime}\right) \operatorname{copper}(\mathrm{II})\right]\right]$ $\mathrm{N}, \mathrm{N}$-dimethylformamide]

In the title compound, $\left[\mathrm{Cu}\left(\mathrm{C}_{12} \mathrm{H}_{8} \mathrm{~N}_{2}\right)\left(\mathrm{C}_{7} \mathrm{H}_{4} \mathrm{SO}_{5}\right)\left(\mathrm{H}_{2} \mathrm{O}\right)\right]$-$\mathrm{C}_{3} \mathrm{H}_{7} \mathrm{NO}$, the $\mathrm{Cu}^{\text {II }}$ atom has a square-pyramidal coordination geometry formed by three O atom and two N atoms. The 1,2-di-4-pyridylethylene ligands function as $\mu_{2}$-bridging ligands to form a zigzag chain. The 2 -sulfonatobenzoate ligands protrude on alternate sides of the chain. Intermolecular $\mathrm{O}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds link the chains into a two-dimensional network structure.

## Comment

The 2-sulfobenzoic acid ( $o-\mathrm{H}_{2} \mathrm{sb}$ ) ligand, containing one sulfonate group and one carboxyl group, exhibits diverse coordination behaviour in the preparation of metal-organic coordination polymers (Li \& Yang, 2004; Su et al., 2005; Xiao et al., 2005). Numerous novel coordination polymers with the 1,2-di-4-pyridylethylene (bpe) ligand have been synthesized in recent years (Hong \& You, 2004; Kondo et al., 2004; Yin \& Xiao, 2005). Here, we present the crystal structure of the title compound, (I), from the same family.

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In compound (I), the $\mathrm{Cu}^{\mathrm{II}}$ atom has a square-pyramidal environment defined by one water O atom, two O atoms belonging to the 2 -sulfonatobenzoate ligand and two N atoms from the two bpe ligands (Fig. 1). In the basal plane, the $\mathrm{N} 2^{\mathrm{i}}-$ $\mathrm{Cu} 1-\mathrm{N} 1$ [symmetry code: (i) $x, \frac{1}{2}-y, z-\frac{1}{2}$ ] and $\mathrm{O} 1-\mathrm{Cu} 1-$ O6 bond angles are 163.59 (19) and 179.47 (19) ${ }^{\circ}$, respectively, while the other angles around the $\mathrm{Cu}^{\text {II }}$ centre are in the range $86.00(17)-104.44(17)^{\circ}$. The apical position is occupied by sulfonate atom O 3 , with an axial $\mathrm{Cu}-\mathrm{O}$ bond distance of 2.268 (4) $\AA$ (Table 1). The $o$-sb ligand chelates to the $\mathrm{Cu}^{\text {II }}$ centre to form a six-membered ring, leading to a coordination mode observed previously in $\left[\mathrm{Ni}(o-\mathrm{sb})(\mathrm{bpe})\left(\mathrm{H}_{2} \mathrm{O}\right)_{2}\right] \cdot 0.25 \mathrm{H}_{2} \mathrm{O}$ (Xiao et al., 2005). The dihedral angle between the planes of the $o$-sb ring and its carboxylate group is $62.5(2)^{\circ}$. The $\mathrm{C} 13-$ O1 bond $[1.307$ (7) $\AA$ ] is longer than $\mathrm{C} 13-\mathrm{O} 2$ [1.212 (7) $\AA$ ], indicating more keto character in the latter. Bpe ligands
function as $\mu_{2}$-bridging ligands, forming a zigzag polymeric chain. The $o$-sb ligands protrude on alternate sides of this chain (Fig. 2). Intermolecular $\mathrm{O}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds (Table 2) link the chains into a two-dimensional network structure (Fig. 3).

## Experimental

An aqueous solution $(10 \mathrm{ml})$ containing $\mathrm{Cu}\left(\mathrm{ClO}_{4}\right)_{2} \cdot 6 \mathrm{H}_{2} \mathrm{O}$ $(0.25 \mathrm{mmol}, 0.910 \mathrm{~g})$ was added slowly to a solution $(10 \mathrm{ml})$ of $N, N$ dimethylformamide containing 1,2-di-4-pyridylethylene $(0.25 \mathrm{mmol}$, $0.991 \mathrm{~g})$ and 2 -sulfobenzoic acid ( $0.25 \mathrm{mmol}, 0 . \mathrm{g}$ ). The mixture was left to stand at room temperature. Blue crystals of (I) were obtained after 5 d .

## Crystal data

$\left[\mathrm{Cu}\left(\mathrm{C}_{12} \mathrm{H}_{8} \mathrm{~N}_{2}\right)\left(\mathrm{C}_{7} \mathrm{H}_{4} \mathrm{SO}_{5}\right)\left(\mathrm{H}_{2} \mathrm{O}\right)\right] \cdot-$ $\mathrm{C}_{3} \mathrm{H}_{7} \mathrm{NO}$
$M_{r}=537.03$
Orthorhombic, Pbca
$a=17.3586$ (19) $\AA$
$b=9.8854$ (11) A
$c=26.324$ (3) $\AA$
$V=4517.1(9) \AA^{3}$
$Z=8$
$D_{x}=1.579 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
Cell parameters from 2377 reflections
$\theta=2.5-21.8^{\circ}$
$\mu=1.11 \mathrm{~mm}^{-1}$
$T=298$ (2) K
Prism, blue
$0.20 \times 0.17 \times 0.15 \mathrm{~mm}$

## Data collection

Bruker SMART CCD area-detector diffractometer
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan
(SADABS; Bruker, 2002)
$T_{\text {min }}=0.809, T_{\text {max }}=0.851$
22879 measured reflections
4102 independent reflections
3679 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.071$
$\theta_{\text {max }}=25.3^{\circ}$
$h=-19 \rightarrow 20$
$k=-11 \rightarrow 11$
$l=-28 \rightarrow 31$

## Refinement

Refinement on $F^{2}$

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}{ }^{2}\right)+(0.0339 P)^{2}\right. \\
& +17.9772 P] \\
& \text { where } P=\left(F_{\mathrm{o}}{ }^{2}+2{F_{\mathrm{c}}}^{2}\right) / 3 \\
& (\Delta / \sigma)_{\max }=0.001 \\
& \Delta \rho_{\text {max }}=0.64 \mathrm{e}_{\AA^{-3}} \\
& \Delta \rho_{\min }=-0.81 \mathrm{e}^{-3}
\end{aligned}
$$

$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.094$
$w R\left(F^{2}\right)=0.170$
$S=1.42$
4102 reflections
310 parameters
H -atom parameters constrained



Figure 1
A view of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the $30 \%$ probability level and H atoms are shown as small spheres of arbitrary radii.


Figure 2
An illustration of the zigzag chain formed in the structure of (I).


Figure 3
The two-dimensional network structure formed by $\mathrm{O}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds (dashed lines).

The H atoms of the water molecule were placed in calculated positions and refined using a riding model, with $\mathrm{O}-\mathrm{H}$ distances of $0.82 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.5 U_{\text {eq }}(\mathrm{O})$. All H atoms of the dimethylformamide molecule were placed in calculated positions and refined using a riding-model approximation, with C-H distances of $0.93 \AA$ for $\mathrm{O}=\mathrm{C}-\mathrm{H}$ and $0.96 \AA$ for the methyl H atoms, and $U_{\text {iso }}(\mathrm{H})=1.2$ (for CH ) or 1.5 (for $\mathrm{CH}_{3}$ ) times $U_{\text {eq }}$ (parent atom). The remaining H atoms were positioned geometrically, with $\mathrm{C}-\mathrm{H}=0.93 \AA$, and allowed to ride on their parent atoms, with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C})$.

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

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