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Lei Cai^a and Long-Guan Zhu^b*

^aDepartment of Polymer Science and Engineering, Zhejiang University, Hangzhou 310027, People's Republic of China, and ^bDepartment of Chemistry, Zhejiang University, Hangzhou 310027, People's Republic of China

Correspondence e-mail: chezlg@zju.edu.cn

Key indicators

Single-crystal X-ray study T = 295 KMean σ (C–C) = 0.004 Å Disorder in main residue R factor = 0.033 wR factor = 0.090 Data-to-parameter ratio = 11.5

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

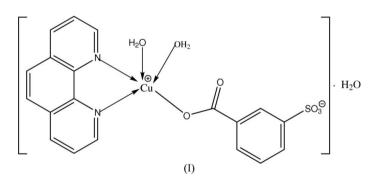
Diaqua(1,10-phenanthroline)(3-sulfonatobenzoato)copper(II) monohydrate

The title compound, $[Cu(C_7H_4O_5S)(C_{12}H_8N_2)(H_2O)_2]\cdot H_2O$, contains a monomeric zwitterion in which the Cu^{II} atom displays a square-pyramidal geometry defined by two N atoms of one 1,10-phenanthroline, one O atom from the carboxylate group of the 3-sulfonatobenzoate, and two O atoms from two water molecules. Extensive $O-H\cdots O$ intermolecular hydrogen bonds generate a two-dimensional network, enhancing the stability of the structure.

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Comment

Recently, several 4-sulfonatobenzoate metal compounds with interesting topologies have been synthesized in our laboratory (Fan, Xiao, Zhang & Zhu, 2004; Fan *et al.*, 2005; Zhang *et al.*, 2005, 2005*a*,*b*). The 4-sulfonatobenzoate (4-sb)/Cu^{II}/1,10-phenanthroline (phen) system under hydrothermal conditions yielded a polymeric compound (Fan, Xiao, Zhang, Cai & Zhu, 2004), $[Cu(4-sb)(phen)(H_2O)]_n$, (II). However, a similar synthesis with 3-sulfonatobenzoate (3-sb) instead of 4-sb leads to the mononuclear title compound, (I).



The Cu^{II} atom adopts a square-pyramidal geometry defined by two N-atom donors from one phen ligand, one O atom from the carboxylate group of 3-sb, and two O atoms from two water molecules. Atoms N1, N2, O1, and O6 occupy the basal plane, whereas atom O7 occupies the apical position. The coordination environment and bond lengths of (I) are similar to those of (II), although the structures are very different. In (II), 4-sb is a bis-monodentate link, whereas in (I) 3-sb is a monodentate ligand. The apical position taken by the O atom of the sulfonyl in (II) is replaced by a water molecule in (I), which implies that hydrogen bonds between the sulfonate group and water molecules prevent the coordination of the sulfonate to the metal atom.

There is an intramolecular hydrogen bond between the water molecule (O6) and the free carboxylate O atom (Table 2). Extensive $O-H\cdots O$ hydrogen bonds between the coordinated water molecule (O6) and uncoordinated water molecule, between the coordinated water molecule (O7) and

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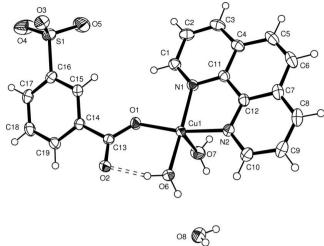


Figure 1

A view of the molecular structure of (I). Displacement ellipsoids are drawn at the 50% probability level. Hydrogen bonds are shown as dashed lines and the minor part of the disordered sulfonate group is not shown.

the sulfonate group, and between the sulfonate group and the solvent water molecule, extend the structure into layers (Fig. 2 and Table 2).

Experimental

A mixture of Cu(NO₃)₂·3H₂O (0.125 g, 0.52 mmol), sodium hydrogen 3-sulfonatobenzoate (0.128 g, 0.57 mmol), 1,10-phenanthroline hydrate (0.094 g, 0.47 mmol) and water (15 ml) was sealed in a 30 ml Teflon-lined stainless steel autoclave and heated at 423 K for 51 h. After cooling to room temperature, blue plate-shaped crystals of (I) were obtained and collected by suction filtration.

Crystal data

$[Cu(C_7H_4O_5S)(C_{12}H_8N_2)-(H_2O)_2]\cdotH_2O$	Z = 2
$M_r = 497.95$	$D_x = 1.717 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Mo K\alpha radiation
a = 8.6047 (9) Å	Cell parameters from 3706
b = 10.5469 (11) Å	reflections
c = 11.7021 (13) Å	$\theta = 2.5-28.1^{\circ}$
$\alpha = 79.123 (1)^{\circ}$	$\mu = 1.30 \text{ mm}^{-1}$
$\beta = 84.585 (1)^{\circ}$	T = 295 (2) K
$\gamma = 67.500 (1)^{\circ}$	Plate, blue
$V = 963.25 (18) \text{ Å}^3$	$0.30 \times 0.13 \times 0.11 \text{ mm}$
Data collection	
Bruker APEX area-detector	3735 independent reflections
diffractometer	3288 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\text{int}} = 0.022$
Absorption correction: multi-scan	$\theta_{\text{max}} = 26.0^{\circ}$
(<i>SADABS</i> ; Bruker, 2002)	$h = -10 \rightarrow 10$
$T_{min} = 0.697$, $T_{max} = 0.871$	$k = -12 \rightarrow 12$
7553 measured reflections	$l = -14 \rightarrow 14$
$T_{\min} = 0.697, \ T_{\max} = 0.871$	$k = -12 \rightarrow 12$

 $\Delta \rho_{\rm max} = 0.41 \text{ e } \text{\AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.32 \text{ e } \text{\AA}^{-3}$

3735 reflections326 parametersH atoms treated by a mixture of independent and constrained refinement

Figure 2

A View of the two-dimensional hydrogen-bonding network of (I). Hydrogen bonds are shown by dashed lines and the H atoms and 1,10-phenanthroline ligands have been omitted.

Table 1Selected geometric parameters (Å, °).

Cu1-O1	1.9427 (16)	Cu1-N1	2.0090 (19)
Cu1-O6	1.9518 (17)	Cu1-N2	2.0150 (19)
Cu1-O7	2.3141 (19)		
O1-Cu1-O6	91.97 (7)	N1-Cu1-N2	82.04 (8)
O1-Cu1-N1	89.23 (7)	O1-Cu1-O7	95.96 (8)
O6-Cu1-N1	170.77 (8)	O6-Cu1-O7	95.93 (7)
O1-Cu1-N2	167.56 (8)	N1-Cu1-O7	93.04 (7)
O6-Cu1-N2	95.26 (7)	N2-Cu1-O7	93.35 (8)

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
O6−H6A···O2	0.84 (1)	1.77 (1)	2.587 (2)	165 (3)
$O6-H6B\cdots O8$	0.85(1)	1.81 (1)	2.647 (3)	170 (3)
$O7-H7A\cdots O5^{i}$	0.85 (1)	1.87 (1)	2.701 (3)	169 (3)
$O7-H7A\cdots O5^{,i}$	0.85(1)	2.10 (3)	2.904 (19)	158 (3)
$O7 - H7B \cdot \cdot \cdot O4'^{ii}$	0.84 (1)	2.04 (2)	2.877 (19)	173 (3)
$O7 - H7B \cdot \cdot \cdot O4^{ii}$	0.84(1)	2.11 (2)	2.929 (6)	163 (3)
O8−H8A···O3 ⁱⁱ	0.85 (1)	1.94 (1)	2.778 (6)	169 (3)
O8−H8A···O4' ⁱⁱ	0.85(1)	2.41 (3)	3.04 (3)	132 (2)
O8−H8A···O3' ⁱⁱ	0.85 (1)	2.49 (3)	3.33 (3)	170 (2)
$O8-H8B\cdots O3^{iii}$	0.85 (3)	1.98 (1)	2.817 (6)	171 (3)
O8−H8 <i>B</i> ···O3 ^{,iii}	0.85 (3)	2.12 (3)	2.95 (2)	166 (3)

Symmetry codes: (i) -x + 1, -y, -z + 1; (ii) x, y, z + 1; (iii) -x + 1, -y + 1, -z + 1.

C-bound H atoms were positioned geometrically and refined as riding atoms, with C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$. The water H atoms were located in difference Fourier maps and were refined with a distance restraint of O-H = 0.85 (1) Å and with a fixed isotropic displacement parameter of $U_{iso}(H) = 0.05$ Å². The sulfonate group is disordered over two positions and the occupancies were refined to a 0.830 (13):0.170 (13) ratio.

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:

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ORTEP3 for Windows (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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