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#### **Key indicators**

Single-crystal X-ray study  $T=295~\mathrm{K}$  Mean  $\sigma(\mathrm{C-C})=0.006~\mathrm{\mathring{A}}$  Disorder in main residue R factor = 0.052 wR factor = 0.156 Data-to-parameter ratio = 16.1

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

# Bis(2,2'-bipyridine- $\kappa N$ ,N'){[5-(carboxymethyl-sulfanyl)-1,3,4-thiadiazol-2-ylsulfanyl]acetato- $\kappa O$ }-copper(II) [5-(carboxymethylsulfanyl)-1,3,4-thiadiazol-2-ylsulfanyl]acetate dihydrate

In the title compound,  $[Cu(C_6H_5N_2O_4S_3)(C_{10}H_8N_2)_2](C_6H_5N_2O_4S_3)\cdot 2H_2O$ , the  $Cu^{II}$  atom is coordinated by four N atoms from two bipyridine ligands and one O atom from the [5-(carboxymethylsulfanyl)-1,3,4-thiadiazol-2-ylsulfanyl]acetate unit. The five-coordinate environment is intermediate between a trigonal bipyramid and a square pyramid. The complex cations and anions are connected with the water molecules  $via\ O-H\cdots O$  hydrogen bonds to form layers.

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#### Comment

We have studied metal complexes of dicarboxylic acids having two -X— $\mathrm{CH_2CO_2}$  arms on a phenylene unit (Gao *et al.*, 2005; Zhao *et al.*, 2005). The title compound, (I), features a 1,3,4-thiadiazolyl ring, but the presence of basic sites appears to alter the acidity of the dicarboxylic acid reagent, 1,3,4-thiadiazolyl-2,5-dithioacetic acid (tdzdtaH<sub>2</sub>). In this paper, we report the structure of the title compound, (I), the dicarboxylic acid reagent being only mono-deprotonated.

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In the complex cation, atom Cu1 displays a geometry intermediate between trigonal bipyramidal and square pyramidal (Fig. 1 and Table 1). Atom Cu1 is bonded to carboxylate atom O1 of the tdzdtaH ligand, and its carboxylic acid end is connected to the uncoordinated tdzdtaH<sup>-</sup> anion through the water molecules *via* hydrogen bonds (Fig. 2 and Table 2), giving rise to a layer structure.

#### **Experimental**

1,3,4-Thiadiazolyl-2,5-dithioacetic acid (tdzdtaH<sub>2</sub>) was prepared from 2,5-dimercapto-1,3,4-thiadiazole, using the method for synthesis of benzene-1,4-dioxyacetic acid reported by Liu *et al.* (2004). The copper complex was obtained from the reaction of copper dinitrate hydrate (1.21 g, 5 mmol), 2,2'-bipyridine (1.60 g, 10 mmol) and tdzdtaH<sub>2</sub> (2.66 g, 10 mmol) in water; the mixture was heated to dissolve most of the reagents, and the pH was raised to about 6 with 0.2 *M* sodium hydroxide. The hot solution was filtered; the solution yielded crystals of (I) when left aside for several days.

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#### Crystal data

 $[Cu(C_6H_5N_2O_4S_3)(C_{10}H_8N_2)_2]$ -Z = 2 $(C_6H_5N_2O_4S_3)\cdot 2H_2O$  $D_x = 1.597 \text{ Mg m}^ M_r = 942.54$ Mo  $K\alpha$  radiation Triclinic,  $P\overline{1}$ Cell parameters from 16 305 a = 10.900 (2) Å reflections b = 12.197 (2) Å  $\theta = 3.2-27.5^{\circ}$  $\mu = 0.94 \; \text{mm}^{-1}$  $c = 14.772 \, (3) \, \text{Å}$  $\alpha = 91.86 (1)^{\circ}$ T = 295 (2) K $\beta = 91.53 (2)^{\circ}$ Block, blue  $0.37 \times 0.26 \times 0.17 \text{ mm}$  $\nu = 92.28 (1)^{\circ}$  $V = 1960.6 (7) \text{ Å}^3$ 

#### Data collection

Rigaku R-AXIS RAPID diffractometer 8693 independent reflections  $\sigma$  can  $\sigma$  reflections with  $\sigma$  20 $\sigma$  ( $\sigma$ )

Absorption correction: multi-scan  $\sigma$  ( $\sigma$ )  $\sigma$  ( $\sigma$ )

#### Refinement

refinement

Refinement on  $F^2$   $w = 1/[\sigma^2(F_o^2) + (0.091P)^2]$   $R[F^2 > 2\sigma(F^2)] = 0.052$   $wR(F^2) = 0.156$  S = 1.03  $(\Delta/\sigma)_{\max} = 0.001$   $\Delta\rho_{\max} = 0.69 \text{ e Å}^{-3}$   $\Delta\rho_{\min} = -0.44 \text{ e Å}^{-3}$ 

Table 1 Selected geometric parameters  $(\mathring{A}, °)$ .

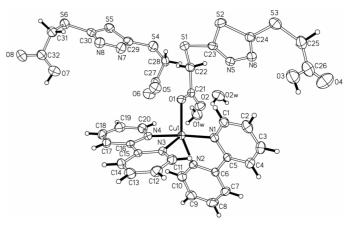
Cu1-O1	2.001 (2)	Cu1-N3	2.157 (3)
Cu1-N1	1.972 (3)	Cu1-N4	1.994 (3)
Cu1-N2	2.045 (3)		, ,
O1-Cu1-N1	94.0 (1)	N1-Cu1-N3	94.9 (1)
O1-Cu1-N2	143.8 (1)	N1-Cu1-N4	173.3 (1)
O1-Cu1-N3	113.7 (1)	N2-Cu1-N3	102.4 (1)
O1-Cu1-N4	90.9 (1)	N2-Cu1-N4	97.9 (1)
N1-Cu1-N2	80.7 (1)	N3-Cu1-N4	79.0 (1)

Table 2 Hydrogen-bond geometry ( $\mathring{A}$ ,  $^{\circ}$ ).

$D-\mathrm{H}\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
$O1w-H1w2\cdots O2$	0.85 (1)	2.24 (4)	2.926 (5)	137 (5)
$O1w-H1w1\cdot\cdot\cdot O8^{1}$ $O2w-H2w1\cdot\cdot\cdot O8^{ii}$	0.85 (1)	1.97 (2)	2.793 (5)	163 (6)
	0.86 (1)	1.91 (2)	2.733 (6)	161 (5)
$O2w-H2w2\cdots O1w$	0.86 (1)	1.84 (2)	2.673 (5)	163 (5)
$O3-H3O\cdots O2w^{iii}$	0.85	1.80	2.643 (5)	174
$O7-H7O \cdot \cdot \cdot O5'^{i}$	0.85	1.72	2.47 (1)	146
$O7-H7O \cdot \cdot \cdot O6^{i}$	0.85	1.92	2.680 (6)	149

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

The structure is disordered in the acetato  $-\mathrm{CH_2CO_2}$  arm of the uncoordinated tdzdtaH $^-$  anion. This arm has two possible positions, O5/O6/C27/C28 and O5′/O6′/C27′/C28′, the site occupation factors being 0.735 (6) and 0.265 (6), respectively. Restraints were applied for the C $^-$ C, C $^-$ S and C $^-$ O distances, and the atomic displacement parameters of the minor component were set equal to those of the corresponding atom of the major component. The carbon-bound H atoms were placed at calculated positions [C $^-$ H = 0.93–0.97 Å and  $U_{\mathrm{iso}}$ (H) = 1.2 $U_{\mathrm{eq}}$ (C)] and were included in the refinement in the riding-model approximation. The water H atoms were located and



**Figure 1**The molecular structure of (I), showing displacement ellipsoids at the 30% probability level. The major site occupation factor of atoms O5, O6, C27 and C28 is 0.735 (6). The minor disorder component has been omitted

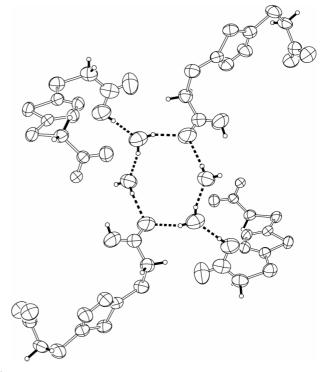


Figure 2
Hydrogen-bonding interactions (dashed lines) involving the coordinated and uncoordinated tdzdtaH<sup>-</sup> anions with the water molecules.

were refined with distance restraints of O-H = 0.85 (1) Å and H···H = 1.39 (1) Å. The carboxylic acid O-H groups were rotated to fit the electron density [O-H = 0.85 Å and  $U_{\rm iso}({\rm H})$  = 1.2 $U_{\rm eq}({\rm O})$ ].

Data collection: *RAPID-AUTO* (Rigaku, 1998); cell refinement: *RAPID-AUTO*; data reduction: *CrystalStructure* (Rigaku/MSC, 2002); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

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