metal-organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 295 KMean $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$ R factor = 0.033 wR factor = 0.134 Data-to-parameter ratio = 15.1

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

Bis(4-aminobenzenesulfonato- κN)bis(N,N-dimethylformamide- κO)copper(II)

The Cu atom in the title zwitterionic complex, $[Cu(C_6H_6-N_2O_3S)_2(C_3H_7NO)_2]$, lies on a centre of inversion in a square plane formed by two N and two O atoms. Adjacent zwitterions are linked by a long Cu–O interaction of 2.465 (2) Å to form a linear chain that runs along the *b* axis of the triclinic unit cell. The chain motif is consolidated by N–H···O hydrogen bonds.

Comment

The 4-aminobenzoate anion can bind to transition metals through the amino as well as the carboxylate ends, as noted from the diaqua copper and manganese derivatives, $[Cu(H_2NC_6H_4SO_3)_2(H_2O)_2]\cdot 2H_2O$ and $[Mn(H_2NC_6H_4SO_3)_2(H_2O)_2]$ (Gunderman *et al.*, 1996). In two further derivatives, the isostructural compounds $[Co(H_2NC_6H_4SO_3)_2(H_2O)_2]\cdot 2H_2O$ (Shakeri & Haussuhl, 1992*a*) and $[Zn(H_2NC_6H_4SO_3)_2(H_2O)_2]\cdot (H_2O)_2]\cdot 2H_2O$ (Shakeri & Haussuhl, 1992*b*), both ends engage in coordination.



The reaction of the 4-aminobenzoate anion with copper(II) gives the title compound, (I), in which the anion coordinates through the amino group. The O atoms of two dimethyl-formamide (DMF) solvent molecules complete the centro-symmetric square-planar geometry. The geometry is distorted towards octahedral owing to the long copper–sulfonate bond (Table 1, Fig. 1). This bond gives rise to a linear chain, which is consolidated by intra-chain $N-H\cdots O$ hydrogen bonds. The binding mode of the anion in the present bis(DMF)–copper compound is similar to that found in the diaquacopper compound, whose geometry is tetragonally distorted from a square plane owing to a long Cu–O distance of 2.420 (2) Å (Gunderman *et al.*, 1996).

Experimental

© 2006 International Union of Crystallography All rights reserved Copper(II) nitrate trihydrate (0.224 g, 1 mmol) was dissolved in excess dimethylformamide (5 ml) along with 4-aminobenzenesulfonic

Received 12 July 2006

Accepted 19 July 2006

acid (0.346 g, 2 mmol). The solution was heated at 343 K for 7 d. Green plate-shaped crystals of (I) were isolated from the cooled solution in an 80% yield based on Cu.

V = 556.09 (7) Å³

 $D_r = 1.655 \text{ Mg m}^{-3}$

 $0.20 \times 0.16 \times 0.04 \text{ mm}$

4574 measured reflections

2426 independent reflections 2246 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 1.22 \text{ mm}^{-1}$

T = 295 (2) K

Plate, green

 $R_{\rm int}=0.016$

 $\theta_{\rm max} = 27.5^{\circ}$

Z = 1

Crystal data

 $\begin{bmatrix} Cu(C_6H_6N_2O_3S)_2(C_3H_7NO)_2 \end{bmatrix}$ $M_r = 554.09$ Triclinic, $P\overline{1}$ a = 7.1168 (5) Å b = 8.4491 (6) Å c = 9.5294 (6) Å $\alpha = 87.033$ (1)° $\beta = 77.344$ (1)° $\gamma = 84.337$ (1)°

Data collection

Bruker SMART APEX areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.797, T_{\max} = 0.953$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0798P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.033$	+ 0.4598P]
$wR(F^2) = 0.134$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.13	$(\Delta/\sigma)_{\rm max} = 0.001$
2426 reflections	$\Delta \rho_{\rm max} = 0.43 \ {\rm e} \ {\rm \AA}^{-3}$
161 parameters	$\Delta \rho_{\rm min} = -0.40 \ {\rm e} \ {\rm \AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

Table 1

Selected geometric parameters (Å, °).

Cu1-N1 Cu1-O1 ⁱⁱ	2.047 (2) 2.465 (2)	Cu1-O4	1.994 (2)
$\begin{array}{c} O1^{ii} - Cu1 - O4\\ O1^{ii} - Cu1 - O4^{ii}\\ O1^{ii} - Cu1 - O4^{ii} \end{array}$	92.87 (8) 87.13 (8)	$O1^{ii}$ -Cu1-N1 ⁱ O4-Cu1-N1	93.43 (8) 86.64 (9)
O1"-Cu1-N1	86.57 (9)	O4-Cu1-N1	93.36 (9)

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

Table 2

Hydrogen-bond geometry (Å, °).

$\overline{D-\mathrm{H}\cdots A}$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$ \frac{N1 - H2n \cdots O2^{ii}}{N1 - H1n \cdots O2^{iv}} $	0.85 (1) 0.85 (1)	2.17 (1) 2.21 (2)	3.018 (3) 2.987 (3)	176 (3) 152 (4)
			4	

Symmetry codes: (ii) x, y + 1, z; (iv) -x + 2, -y, -z + 1.

Carbon-bound H atoms were placed in calculated positions, with C–H = 0.93–0.96 Å, and were included in the refinement in the



Figure 1

The coordination geometry of the Cu atom of (I), with the atomnumbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as spheres of arbitrary radii. [Symmetry codes are as in Table 1; additionally: (iii) -x + 1, -y, -z + 1.]

riding-model approximation, with $U(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(C_{methyl})$; the methyl groups were rotated to fit the electron density. The amino H atoms were located in a difference Fourier map, and refined with a distance restraint of N-H = 0.85 (1) Å; their displacement parameters were also refined.

Data collection: *SMART* (Bruker, 2003); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT*; 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*.

The authors thank the Natural Scientific Foundation Committee of Shanxi Province (grant No. 20041031) and the University of Malaya for generously supporting this study.

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