metal-organic papers

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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.005 Å Disorder in main residue R factor = 0.037 wR factor = 0.103 Data-to-parameter ratio = 12.7

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

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Chlorobis(1,10-phenanthroline- $\kappa^2 N, N'$)copper(II) 4-aminobenzenesulfonate trihydrate

The crystal structure of the title compound, $[CuCl(C_{12}-H_8N_2)_2](C_6H_6NO_3S)\cdot 3H_2O$, contains Cu^{II} cations five-coordinated by one chloride anion and four N atoms of two 1,10-phenanthroline ligands. Between the the 4-aminobenzene-sulfonate anions and the uncoordinated water molecules intermolecular hydrogen bonding is found.

Comment

In comparison with other organic acid anions, such as carboxylates and phosphonates, organosulfonates have long been used in industry as dyes and surfactants, but their coordination chemistry has been less well investigated due to the perception that sulfonates are poor ligands. Recently, increasing attention has been paid to the coordination modes of organosulfonate ligands (Cote, 2003; Cai, 2004). Here, the synthesis and crystal structure of the title sulfonate complex, (I), are reported.



The molecular structure of (I) is shown in Fig. 1. The crystal structure of (I) is built up of $[CuCl(phen)_2]^+$ cations (phen = 1,10-phenanthroline), 4-aminobenzenesulfonate anions and water molecules. Selected bond lengths are listed in Table 1. In the $[CuCl(phen)_2]^+$ cation, the two phen molecules are almost perpendicular to each other. The coordination of the Cu atom can be described as distorted trigonal-bipyramidal, made up of one chloride anion and four N atoms of two phen molecules; this is similar to the coordination of the Cu atom in the complex $[CuCl(C_{12}H_8N_2)_2]_2(C_{10}H_4O_8)\cdot 2H_2O$ (Xiao *et al.*, 2004). The 4-aminobenzenesulfonate anion does not coordinate to the Cu atom, but is connected into chains by intermolecular $N-H \cdots O$ hydrogen bonds (Table 2 and Fig. 2). These chains are connected into layers by two different types of hydrogen bonding. In the first type, the chains are linked, via only one water molecule, by N-H···O and O-H···O hydrogen bonds. These water molecules act as donors as well as acceptors (Fig. 2). In the second type of hydrogen bonding, two water molecules and two O atoms of the anion form eightmembered rings, built up of four intermolecular O-H···O

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7595 measured reflections

 $R_{\rm int} = 0.016$ $\theta_{\rm max} = 25.1^{\circ}$

5178 independent reflections 3770 reflections with $I > 2\sigma(I)$



Figure 1

The asymmetric unit of (I), with the atom labelling. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as spheres of arbitrary radii. Both disorder components are shown.



Figure 2

The packing of the anions and the water molecules (I), viewed along the b axis. The cations are not shown for clarity. Dashed lines indicate hydrogen bonds.

hydrogen bonds. The rings may be further connected by water molecule O4, but the H atoms attached to it could not be detected in a difference map. Layers are formed which are perpendicular to the b axis.

Experimental

All reagents were of analytical grade from commercial sources and were used without further purification. A solution of ethanol (10 ml) containing CuCl₂·2H₂O (0.5 mmol, 0.852 g) and 1,10-phenanthroline (0.5 mmol, 0.991 g) was added slowly to a solution of sodium 4aminobenzenesulfonate (1 mmol, 0.195 g) dissolved in water (10 ml). After stirring for 3 h, the mixture was left to stand at room temperature for about 2 d, affording green crystals suitable for X-ray diffraction. Elemental analysis found: C 52.75, H 3.55, N 10.07%; calculated for C₃₀H₂₀ClCuN₅O₆S: C 52.55, H, 4.12, N 10.21%.

Crystal data

 $[CuCl(C_{12}H_8N_2)_2](C_6H_6NO_3S)$. $\nu = 79.368 \ (1)^{\circ}$ 3H₂O V = 1476.81 (16) Å³ $M_r = 683.61$ Z = 2Triclinic, $P\overline{1}$ $D_x = 1.537 \text{ Mg m}^{-3}$ a = 8.1734 (5) Å Mo $K\alpha$ radiation b = 13.3367 (8) Å $\mu = 0.95 \text{ mm}^{-1}$ c = 14.9091 (10) Å T = 293 (2) K $\alpha = 67.682 (1)^{\circ}$ Block, green $\beta = 84.243$ (1) $0.35 \times 0.33 \times 0.29 \text{ mm}$

Data collection

Bruker SMART CCD area-detector diffractometer ω and ω scans Absorption correction: multi-scan (SADABS; Sheldrick, 2002) $T_{\min} = 0.650, \ T_{\max} = 0.696$ (expected range = 0.708 - 0.758)

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.037$	$w = 1/[\sigma^2(F_o^2) + (0.056P)^2]$
$wR(F^2) = 0.103$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.09	$(\Delta/\sigma)_{\rm max} = 0.001$
5178 reflections	$\Delta \rho_{\rm max} = 0.34 \text{ e } \text{\AA}^{-3}$
409 parameters	$\Delta \rho_{\rm min} = -0.32 \text{ e } \text{\AA}^{-3}$

Table 1

0

Selected bond lengths (Å).

Cu1-N4	1.984 (2)	Cu1-N5	2.122 (2)
Cu1-N3	1.989 (2)	Cu1-Cl1	2.2804 (9)
Cu1-N2	2.119 (2)		

Table 2

Hydrogen-bond	geometry ((A, °)).
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$D - H \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N1 - H1N1 \cdots O6^{i}$	0.86	2.15	3.000 (4)	168
$N1 - H2N1 \cdots O2^{ii}$	0.86	2.23	3.040 (4)	157
O5−H1 <i>O</i> 5···O1 ⁱⁱⁱ	0.82	2.00	2.822 (3)	174
O5−H2O5···O1	0.82	2.12	2.900 (4)	160
$D6-H1O6\cdots O2^{iv}$	0.82	2.11	2.905 (4)	163
$N1 - H1N1 \cdots O6^{i}$	0.86	2.15	3.000 (4)	168

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

The N-H and water H atoms on O5 and O6 were located in a difference Fourier map; their bond lengths were set to ideal values and they were refined with fixed isotropic displacement parameters using a riding model, with O-H = 0.82 Å, N-H = 0.86 Å and $U_{iso}(H) = 1.5U_{eq}(O,N)$. The water H atoms on O4 were not located. The C-H H atoms were placed in calculated positions and were refined isotropically using a riding model, with C-H = 0.93 Å and $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$. The sulfonate group is disordered over two orientations and was refined using a split model [occupancies 0.83 (1) and 0.17 (1)].

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Siemens, 1995); software used to prepare material for publication: SHELXTL.

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