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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.006 Å H-atom completeness 96% Disorder in solvent or counterion R factor = 0.050 wR factor = 0.156 Data-to-parameter ratio = 12.5

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

Aquachloro[5-hydroxyisophthalato(1-)]-(1,10-phenanthroline)copper(II) 2.5-hydrate

In the title compound, $[Cu(C_8H_5O_5)Cl(C_{12}H_8N_2)(H_2O)]$. 2.5H₂O, the Cu^{II} atom is in a square-pyramidal geometry defined by one Cl⁻ anion, one aqua O atom, one carboxyl O atom belonging to one 5-hydroxyisophthalate anion, and two N atoms from a 1,10-phenanthroline molecule. O–H···O hydrogen bonds involving 5-hydroxyisophthalate anions, the aqua ligands and the uncoordinated water molecules, along with weak O–H···Cl hydrogen bonds, link the mononuclear units into a three-dimensional network structure.

Comment

Numerous isophthalate and 5-hydroxyisophthalate complexes have been extensively studied. They show a diversity of structures and a variety of framework topologies (Chen & Liu, 2002; Hou *et al.*, 2003; Plater *et al.*, 2001; Xu & Li, 2004; Wen *et al.*, 2004). It should be pointed out that the synthetic conditions, such as H-atom receptors, temperature, solvents *etc.*, play an important role in determining the compositions of these complexes. For example, the previously reported complex $[Cu_2(C_{12}H_8N_2)_2(C_8H_4O_5)_2]\cdot 3H_2O$ (Xiao *et al.*, 2004) and the title complex, $[CuCl(C_{12}H_8N_2)(C_8H_5O_5)(H_2O)]$ ·-2.5H₂O, (I), were synthesized by the reaction of $CuCl_2\cdot 2H_2O$, 5-hydroxyisophthalic acid and 1,10-phenanthroline. The former was obtained in a 20 ml mixture of *N*,*N*-dimethylformamide, water and methane (2:1:1 v/v/v), while (I) was obtained in a 20 ml solution in *N*,*N*-dimethylformamide.



In (I), the Cu^{II} atom has a five-coordinate environment defined by one Cl⁻ anion, one aqua O atom, one carboxyl O atom belonging to one 5-hydroxyisophthalate anion, and two N atoms from a 1,10-phenanthroline molecule (Fig. 1). The geometry around the Cu^{II} atom is square pyramidal. The basal plane (atoms O1, O6, N1 and N2) consists of two N atoms from a 1,10-phenanthroline molecule, one carboxyl O atom from a 5-hydroxyisophthalate anion, and one aqua O atom.

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Figure 1

The molecular structure of the asymmetric unit of (I), showing the atomnumbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

The O1-Cu1-N1 and O6-Cu1-N2 bond angles are 167.95 (13) and 165.74 (15) $^{\circ}$, respectively. The other angles around the Cu^{II} centre are in the range 81.89 (14)-98.51 (11) Å (Table 1). The apical position is occupied by a Cl^{-} anion, the Cu1-Cl1 bond distance of 2.5463 (12) Å being longer than the apical Cu-Cl bond distance found in the previously reported compound [CuCl(C₁₂H₈N₂)₂]·(C₈H₄-NO₆)·2H₂O [2.287 (2) Å; Ye et al., 2004]. The 1,10-phenanthroline system is almost coplanar with the phenyl ring of the 5-hydroxyisophthalate anion, the dihedral angle between the planes being $1.9 (2)^{\circ}$.

In the crystal structure of (I), there is an intramolecular hydrogen bond between the coordinated aqua O6 atom and the uncoordinated carboxylate O2 atom. The hydroxy group of the 5-hydroxyisophthalate anion is involved in a weak intermolecular O5–H5···Cl1(1 - x, 2 - y, 1 - z) hydrogen bond and an intermolecular $O7-H7B\cdots O5$ hydrogen bond. Moreover, $O-H \cdots O$ intermolecular hydrogen bonds are formed between the water molecules and the carboxylate O atoms (Table 2). These interactions link the mononuclear units to form a three-dimensional network structure (Fig. 2).

Experimental

A solution of CuCl₂·2H₂O (0.5 mmol, 0.852 g) and 5-hydrogenisophthalic acid (0.5 mmol, 0.910 g) in 15 ml N,N-dimethylformamide was added slowly to a solution of 1,10-phenanthroline (0.5 mmol, 0.991 g) in 10 ml of N,N-dimethylformamide. The mixture was left to stand at room temperature for about a month to afford blue crystals of (I).

Crystal data

$[Cu(C_8H_5O_5)Cl(C_{12}H_8N_2)(H_2O)]$	<i>Z</i> = 2
2.5H ₂ O	$D_x = 1.590 \text{ Mg m}^{-3}$
$M_r = 523.37$	Mo $K\alpha$ radiation
Triclinic, P1	Cell parameters from 2931
a = 8.8508 (10) Å	reflections
b = 10.7516 (12) Å	$\theta = 2.3-24.4^{\circ}$
c = 12.7592 (15) Å	$\mu = 1.17 \text{ mm}^{-1}$
$\alpha = 114.218 \ (2)^{\circ}$	T = 298 (2) K
$\beta = 95.770 \ (2)^{\circ}$	Prism, blue
$\gamma = 94.022 \ (2)^{\circ}$	$0.33 \times 0.15 \times 0.13 \text{ mm}$
V = 1093.4 (2) Å ³	





The crystal packing of (I), viewed along the b axis, showing the threedimensional network structure formed by the hydrogen-bonding interactions (dashed lines).

Data collection

Bruker SMART CCD area-detector	3911 independent reflections
diffractometer	3445 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.026$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.2^{\circ}$
(SADABS; Bruker, 2002)	$h = -10 \rightarrow 10$
$T_{\min} = 0.810, \ T_{\max} = 0.862$	$k = -12 \rightarrow 12$
8038 measured reflections	$l = -15 \rightarrow 15$
Define and and	

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.050$ wR(F²) = 0.156 S = 1.133911 reflections 313 parameters H atoms treated by a mixture of independent and constrained refinement

12 15 $w = 1/[\sigma^2(F_o^2) + (0.0785P)^2]$

+ 1.351P] where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 1.28 \text{ e} \text{ Å}$ $\Delta \rho_{\rm min} = -0.48 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Cu1-Cl1	2.5463 (12)	Cu1-N1	2.009 (4)
Cu1-O1	1.957 (3)	Cu1-N2	2.010 (4)
Cu1-O6	1.980 (4)		
Cl1-Cu1-O1	95.62 (8)	O1-Cu1-N1	167.95 (13)
Cl1-Cu1-O6	94.93 (11)	O1-Cu1-N2	90.42 (14)
Cl1-Cu1-N1	94.68 (10)	O6-Cu1-N1	92.33 (15)
Cl1-Cu1-N2	98.51 (11)	O6-Cu1-N2	165.74 (15)
O1-Cu1-O6	92.98 (14)	N1-Cu1-N2	81.89 (14)

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
O4−H4···O8 ⁱ	0.82	1.82	2.623 (6)	167
O5−H5···Cl1 ⁱⁱ	0.82	2.18	2.998 (4)	172
$O6-H6A\cdots O2$	0.82	1.86	2.601 (5)	149
$O6-H6B\cdots O7^{iii}$	0.89	1.77	2.642 (5)	167
$O7-H7A\cdots O3^{iv}$	0.84 (4)	1.93 (4)	2.754 (6)	167 (6)
$O7 - H7B \cdots O5$	0.83 (4)	1.97 (5)	2.771 (6)	162 (4)
$O8-H8A\cdots O2^{ii}$	0.82 (3)	2.05 (4)	2.844 (6)	163 (4)
$O8-H8B\cdots O9^{v}$	0.81 (3)	2.05 (4)	2.831 (10)	162 (5)
Symmetry codes:	(i) <i>x</i> , <i>y</i> +	1, z; (ii)	-x + 1, -y + 2, -	-z + 1; (iii)

-x + 2, -y + 2, -z + 1; (iv) x, y - 1, z; (v) x, y + 1, z + 1.

The H atoms of the water molecules were located in a Fourier difference map and refined isotropically, with O-H distances restrained to 0.82 (2) Å and the H7A···H7B and H8A···H8B distances restrained to 1.45 (2) Å. The remaining H atoms were positioned geometrically (C–H = 0.93 Å and O–H = 0.82 Å) and allowed to ride on their parent atoms, with $U_{iso}(H)$ values equal to $1.2U_{eq}(C)$ or $1.5U_{eq}(O)$. At this stage, the maximum difference density of 3.59 Å^{-3} indicated the presence of a possible atom site. This peak was found near atom H8*B*, at a hydrogen-bonding distance of 2.27 Å. Attempts to refine this peak as a water O atom (O9) with full occupancy resulted in a high U_{iso} value, and hence it was refined with occupancy 0.5. The occupancy factor of atom O9 was initially found to be 0.51 (1) and later fixed at 0.50. The H atoms of this water molecule could not be located in the difference map.

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* in *SHELXTL* (Bruker, 2002); software used to prepare material for publication: *SHELXL97*.

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