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### **Key indicators**

Single-crystal X-ray study T = 292 KMean  $\sigma$ (C–C) = 0.014 Å R factor = 0.079 wR factor = 0.169 Data-to-parameter ratio = 15.4

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

# Aqua(8-hydroxyquinoline-5-sulfonato- $\kappa^2 N, O^8$ )-silver(I) monohydrate

In the title compound,  $[Ag(C_9H_6NO_4S)(H_2O)]\cdot H_2O$ , the  $Ag^I$  cation is three-coordinated by one N and one hydroxy O atom from one 8-hydroxyquinoline-5-sulfonate anion and one water molecule in a highly distorted trigonal–planar geometry. The sulfonate group does not coordinate to the  $Ag^I$  cation.

### Comment

In recent decades, much attention has been focused on the design and synthesis of metal–organic coordination networks (Hagrman *et al.*, 1999; Moulton & Zaworotko, 2001). Compared with carboxylates and phosphonates, the coordination chemistry of sulfonates has been less well studied, due to the perception that sulfonate is a poor ligand (Cote & Shimizu, 2003; Cai, 2004). However, silver sulfonates are an exception, as sulfonate groups can adopt a range of different bridging modes with the  $Ag^+$  cation (Shimizu *et al.*, 1999; Cote & Shimizu, 2004). Here, we report the synthesis and crystal structure of the title compound, (I).

# $\begin{array}{c} SO_3 \\ N \\ OH \\ H \\ H \\ (I) \end{array}$ $\begin{array}{c} SO_3 \\ H_2O \\ H_2O \\ H \\ (I) \end{array}$

As shown in Fig. 1, the Ag<sup>+</sup> cation of (I) is three-coordinated by one N and one hydroxy O atom from one 8hydroxyquinoline-5-sulfonate anion and one water molecule in a highly distorted trigonal–planar coordination geometry for Ag (Table 1). Atoms Ag1, OW1, N1 and O4 are almost coplanar and the bond-angle sum about Ag is 359.6°. The Ag $-O_w$  (w = water) distance of 2.127 (9) Å is shorter than the Ag $-O_h$  (h = hydroxy) distance of 2.447 (8) Å. The Ag-Ndistance of (I) is similar to reported values (Li *et al.*, 2005). However, both the Ag $-O_h$  and Ag $-O_w$  distances of (I) are shorter than reported Ag $-O_h$  distances (Wu *et al.*, 2006; Ma *et al.*, 2005) and Ag $-O_w$  distances (Ma *et al.*, 2005), respectively. In (I), the 8-hydroxyquinoline-5-sulfonate anion coordinates to the Ag<sup>+</sup> cation through the N and hydroxy O atoms in a

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### Figure 1

A view of compound (I). Displacement ellipsoids are drawn at the 30% probability level.

chelating mode, and the sulfonate group does not coordinate to the Ag cation.

As shown in Table 2, the coordinated water molecule (OW1) is weakly hydrogen-bonded as donor to two sulfonate O atoms. The solvent water molecule (OW2) does not coordinate to the Ag<sup>+</sup> cation but is hydrogen-bonded to the hydroxy O atom as an acceptor and to the sulfonate O atom as a donor.

# **Experimental**

An aqueous solution of NaOH (0.1 M) was added to a solution of 8hydroxyquinoline-5-sulfonic acid (0.112 g, 0.5 mmol) in water (5 ml) until the pH reached 7. A solution of AgNO<sub>3</sub> (0.085 g, 0.5 mmol) in water (5 ml) was then added, and a yellow precipitate formed immediately. After stirring for 10 min, the precipitate was dissolved by dropwise addition of an aqueous solution of NH<sub>3</sub> (14 M, 5 ml). Crystals of (I) were obtained by evaporation of the solution at room temperature over several days.

### Crystal data

$[Ag(C_9H_6NO_4S)(H_2O)] \cdot H_2O$	$D_x = 1.992 \text{ Mg m}^{-3}$
$M_r = 368.11$	Mo $K\alpha$ radiation
Monoclinic, C2/c	Cell parameters from 8271
$a = 20.314 (4) \text{ Å}_{-}$	reflections
$b = 9.2221 (18) \text{\AA}$	$\theta = 3.1–27.4^{\circ}$
c = 13.182 (3) Å	$\mu = 1.83 \text{ mm}^{-1}$
$\beta = 96.34 \ (3)^{\circ}$	T = 292 (2) K
$V = 2454.4 (9) \text{ Å}^3$	Block, yellow
Z = 8	$0.15 \times 0.12 \times 0.11 \text{ mm}$
Data collection	
Rigaku R-AXIS RAPID	2741 independent reflections

Rigaku R-AXIS RAPID	2741 independent reflections
diffractometer	2132 reflections with $I > 2\sigma(I)$
$\omega$ scans	$R_{\rm int} = 0.060$
Absorption correction: multi-scan	$\theta_{\rm max} = 27.4^{\circ}$
(ABSCOR; Higashi, 1995)	$h = -26 \rightarrow 26$
$T_{\min} = 0.755, T_{\max} = 0.82$	$k = -11 \rightarrow 11$
11547 measured reflections	$l = -15 \rightarrow 17$



### Figure 2

A packing diagram for (I). All H atoms and water molecules have been omitted for clarity. Hydrogen bonds are shown as dashed lines.

### Refinement

Refinement on $F^2$	H atoms treated by a mixture of
$R[F^2 > 2\sigma(F^2)] = 0.079$	independent and constrained
$wR(F^2) = 0.169$	refinement
S = 1.24	$w = 1/[\sigma^2(F_o^2) + 65.3395P]$
2741 reflections	where $P = (F_0^2 + 2F_c^2)/3$
178 parameters	$(\Delta/\sigma)_{\rm max} = 0.001$
	$\Delta \rho_{\rm max} = 0.66 \ {\rm e} \ {\rm \AA}^{-3}$
	$\Delta \rho_{\rm min} = -1.26 \text{ e} \text{ \AA}^{-3}$

# Table 1

Selected geometric parameters (A, <sup>o</sup>	2)	).
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Ag1-OW1	2.122 (9)	Ag1-O4	2.446 (8)
Ag1-N1	2.196 (7)		
OW1-Ag1-N1	168.8 (3)	N1-Ag1-O4	70.8 (2)
OW1-Ag1-O4	120.0 (3)		

# Table 2

Hydrogen-bond geometry (Å, °).

D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
0.82 (6)	1.81 (7)	2.595 (11)	160 (13)
0.92 (6)	2.40 (8)	3.257 (12)	156 (13)
0.91 (6)	2.33 (9)	3.180 (12)	154 (13)
0.88 (6)	1.96 (7)	2.828 (11)	168 (14)
0.91 (6)	2.48 (13)	3.02 (2)	118 (11)
	<i>D</i> -H 0.82 (6) 0.92 (6) 0.91 (6) 0.88 (6) 0.91 (6)	$\begin{array}{c cccc} D-H & H\cdots A \\ \hline 0.82 \ (6) & 1.81 \ (7) \\ 0.92 \ (6) & 2.40 \ (8) \\ 0.91 \ (6) & 2.33 \ (9) \\ 0.88 \ (6) & 1.96 \ (7) \\ 0.91 \ (6) & 2.48 \ (13) \end{array}$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$

 $1, -z + \frac{1}{2};$  (111) (iv)  $-x + \frac{1}{2}, -y + \frac{1}{2}, -z$ .

All H atoms on C atoms were positioned geometrically and refined as riding atoms, with C-H = 0.93 Å and  $U_{iso}(H) = 1.2U_{eq}(C)$ . The hydroxy H atom and water H atoms were located in a difference Fourier map and refined with  $U_{iso}(H) = 1.5U_{eq}(O)$ . The minimum electron-density peak is loacted 0.84 Å from atom Ag1.

Data collection: PROCESS-AUTO (Rigaku, 1998); cell refinement: PROCESS-AUTO; data reduction: PROCESS-AUTO; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997);

program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL-Plus* (Sheldrick, 1990); software used to prepare material for publication: *SHELXL97*.

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