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(Quinolin-8-ol-$\kappa^2 N,O$)(quinolin-8-olato-$\kappa^2 N,O$)-silver(I)

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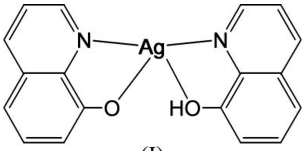
Key indicators
Single-crystal X-ray study
T = 291 K
Mean σ(C–C) = 0.003 Å
Disorder in main residue
R factor = 0.025
wR factor = 0.047
Data-to-parameter ratio = 16.1

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

In the title compound, [Ag(C_9H_6NO)(C_9H_7NO)], the Ag^I ion is located on a twofold axis and is chelated by two 8-hydroxyquinoline molecules with a distorted tetrahedral geometry. The hydroxy H atom of 8-hydroxyquinoline is close to an inversion center and has a 0.5 site occupancy factor. Ag^I complexes are linked to form a supramolecular chain structure *via* hydrogen bonding between hydroxy groups.

Comment

Ag^I complexes have shown versatility of their coordination geometry (Bowmaker *et al.*, 2001; Ma *et al.*, 2005) because of their d^{10} electronic configurations (Venkataraman *et al.*, 1997). Coordination numbers ranging from two to nine have been observed, often with distorted coordination geometry owing to the inherent lack of ligand field stabilization effects (Shimizu, 2003). We present here the structure of the title Ag^I complex, (I), which assumes a distorted tetrahedral coordination geometry (Fig. 1).



(I)

The Ag^I ion is located on a twofold axis and is chelated by two 8-hydroxyquinoline molecules with a distorted tetrahedral geometry. The hydroxy H atom is close to an inversion center and has a 0.5 site occupancy factor. Thus, for the two hydroxyquinoline ligands , one hydroxy group is deprotonated (described as L) but the other is not (described as HL). The dihedral angle of 56.0 (3)° between the two hydroxyquinoline mean planes shows the degree of distortion of the coordination geometry from tetrahedral. The five-membered chelate ring displays an envelope conformation, with the Ag ion in the flap position and displaced from the mean plane formed by the other four atoms by 0.49 (1) Å. This is similar to that found in a related compound (Smith *et al.*, 1999). The Ag—O bond distance is significantly longer than the Ag—N bond distance (Table 1).

Via the hydrogen bonding between L and HL (Table 2), the Ag^I complex molecules link to each other to form a supramolecular chain structure (Fig. 1).

Experimental

A methanol solution (5 ml) of 8-hydroxyquinoline (0.075 g, 0.5 mmol) was mixed with an aqueous solution (5 ml) of $AgNO_3$

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(0.085 g, 0.5 mmol). After stirring for 5 min, the resulting yellow precipitate was dissolved by dropwise addition of an aqueous solution of NH_3. Yellow single crystals of (I) were obtained from the solution after several days.

Crystal data

$[Ag(C_9H_6NO)(C_9H_7NO)]$
$M_r = 397.17$
Orthorhombic, *Pbcn*
$a = 11.434$ (2) Å
$b = 14.817$ (3) Å
$c = 8.7828$ (18) Å
$V = 1488.0$ (5) Å^3
$Z = 4$
$D_x = 1.773$ Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 12213 reflections
$\theta = 2.7$–27.5°
$\mu = 1.37$ mm^{-1}
$T = 291$ (2) K
Block, yellow
0.37 × 0.11 × 0.10 mm

Data collection

Rigaku R-AXIS RAPID diffractometer
ω scan
Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995)
$T_{\min} = 0.602$, $T_{\max} = 0.880$
13341 measured reflections
1705 independent reflections
1032 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.034$
$\theta_{\max} = 27.5°$
$h = -16 \rightarrow 14$
$k = -23 \rightarrow 19$
$l = -11 \rightarrow 11$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.025$
$wR(F^2) = 0.047$
$S = 0.89$
1705 reflections
106 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0128P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\max} < 0.001$
$\Delta\rho_{\max} = 0.27$ e Å^{-3}
$\Delta\rho_{\min} = -0.59$ e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

Ag1—N1	2.2377 (19)	Ag1—O1	2.4831 (17)
N1—Ag1—N1^{i}	157.16 (10)	N1^{i}—Ag1—O1	128.07 (6)
N1—Ag1—O1	69.78 (6)	O1—Ag1—O1^{i}	93.62 (9)

Symmetry code: (i) $-x, y, -z + \frac{3}{2}$.

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

D—H···A	D—H	H···A	D···A	D—H···A
O1—H8···O1^{ii}	0.85	1.59	2.438 (3)	175

Symmetry code: (ii) $-x, -y, -z + 1$.

H atoms on C atoms were positioned geometrically and refined as riding atoms, with C—H = 0.93 Å and $U_{\rm iso}$(H) = $1.2U_{\rm eq}$(C). The hydroxy H atom was located in a difference Fourier map and isotropically refined as riding in its as-found relative position (Table 2).

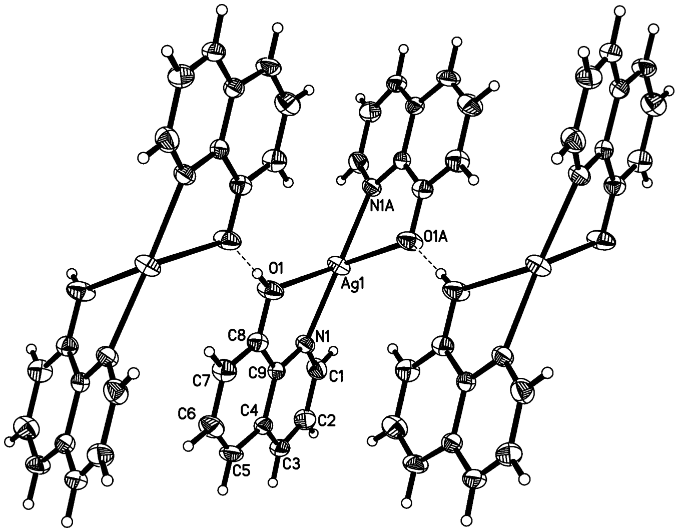

Figure 1
View of the structure of (I), with 30% probability displacement ellipsoids (arbitrary spheres for H atoms). Dashed lines indicate the hydrogen bonding. [Symmetry code: (A) $-x, y, \frac{3}{2} - z$.]

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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