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μ-(Furan-2-carbaldehyde azine)-1κ^2O,N:2κ^2N',O'-bis[(furan-2-carbaldehyde azine-κ^2N,O)silver(I)] bis(hexafluorophosphate): an unusual complex containing two metal atoms and three ligands. Corrigendum

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In the paper by Wang, Dong, Ma & Huang [*Acta Cryst.* (2005), E**61**, m2369–m2370], the correspondence author is incorrectly indicated. The correct correspondence author is given here, together with revised postal and e-mail addresses.

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Key indicators

Single-crystal X-ray study
T = 298 K
Mean σ(C–C) = 0.008 Å
R factor = 0.044
wR factor = 0.111
Data-to-parameter ratio = 12.8

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

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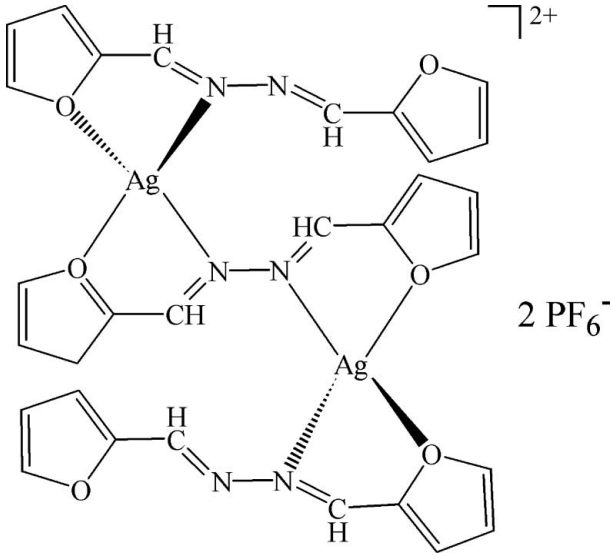
The title complex, $[Ag_2(C_{10}H_8N_2O_2)_3](PF_6)_2$, contains two silver cations and three molecules of the new Schiff base ligand furan-2-carbaldehyde azine, accompanied by two charge-balancing PF_6^- anions. There is a centre of inversion at the mid-point of the N—N bond of the central ligand. The Ag atom adopts a 'see-saw' coordination, with two short Ag—N bonds and two long Ag—O bonds.

Comment

Combining metal ions with double Schiff base ligands may result in coordination polymers with novel network connectivities (Yu Bin *et al.*, 2005). Our interest in understanding the relationship between the metal coordination modes with such ligands and their extended structures led us to synthesize the title Ag^I complex, (I), and we report its structure here (Fig. 1).



(I)

Compound (I) contains a complex ion made up from the unusual combination of two metal ions and three furan-2-carbaldehyde azine (bdb) ligand molecules. There is an inversion centre at the mid-point of the N—N bond of the central ligand.

The Ag centre adopts a very distorted AgN_2O_2 coordination geometry, arising from *N*,*O*-chelation by the Schiff base N atom and furanyl O atom from two bdb ligands (Table 1). Overall, the Ag coordination could be described as 'see-saw', if not simply irregular. A non-coordinated PF_6^- counter-ion occupying a general position completes the structure of (I).

Experimental

A methanol solution (8 ml) of $AgPF_6$ (25.3 mg, 0.1 mmol) was slowly diffused into a dichloromethane solution (8 ml) of 1,4-bis(furanyl)-2,3-diaza-1,3-butadiene (28.2 mg, 0.15 mmol). Colourless single crystals of (I) were obtained after the solution was allowed to stand at room temperature for three days.

Crystal data

$[Ag_2(C_{10}H_8N_2O_2)_3](PF_6)_2$
$M_r = 1070.23$
Triclinic, $P\overline{1}$
$a = 9.414$ (2) Å
$b = 9.943$ (2) Å
$c = 11.332$ (3) Å
$\alpha = 94.829$ (3)°
$\beta = 98.144$ (3)°
$\gamma = 117.247$ (2)°
$V = 920.0$ (4) Å^3
$Z = 1$
$D_x = 1.932$ Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 2033 reflections
$\theta = 2.3$–26.7°
$\mu = 1.26$ mm^{-1}
$T = 298$ (2) K
Slab, colourless
0.36 × 0.12 × 0.05 mm

Data collection

Bruker SMART CCD diffractometer
φ and ω scans
Absorption correction: multi-scan (*SADABS*; Bruker, 1997)
$T_{min} = 0.659$, $T_{max} = 0.940$
4924 measured reflections
3346 independent reflections
2888 reflections with $I > 2\sigma(I)$
$R_{int} = 0.023$
$\theta_{max} = 25.5°$
$h = -11 \rightarrow 11$
$k = -12 \rightarrow 11$
$l = -13 \rightarrow 9$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.044$
$wR(F^2) = 0.111$
$S = 1.05$
3346 reflections
262 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0581P)^2 + 0.2485P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.69$ e Å^{-3}
$\Delta\rho_{min} = -0.49$ e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

Ag1—N2	2.194 (3)	Ag1—O1	2.764 (5)
Ag1—N3	2.243 (3)	Ag1—O2	2.700 (6)
N2—Ag1—N3	158.35 (12)	O1—Ag1—O2	68.68 (10)
N2—Ag1—O1	67.95 (12)	N2—Ag1—O2	117.87 (12)
N3—Ag1—O1	97.57 (12)	N3—Ag1—O2	67.59 (11)

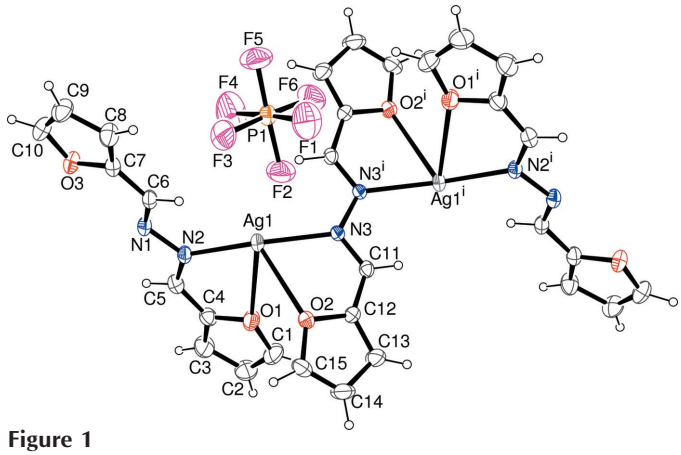


Figure 1
View of (I), showing 30% displacement ellipsoids. Symmetry code: (i): $1 - x, 1 - y, 1 - z$.

H atoms bonded to C atoms were included in calculated positions and refined as riding [C—H = 0.93 Å; $U_{iso}(H) = 1.2U_{eq}(C)$].

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Bruker, 2001); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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