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Key indicators

Single-crystal X-ray study T = 150 KMean σ (C–C) = 0.006 Å R factor = 0.025 wR factor = 0.057 Data-to-parameter ratio = 17.5

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

Bis[tris(pyrazol-1-yl)methane- $\kappa^2 N$, N']platinum(II) bis(hexafluorophosphate) nitromethane solvate

> The title complex, $[Pt(C_{10}H_{10}N_6)_2](PF_6)_2 \cdot 2CH_3NO_2$, crystallizes with the Pt atom located on a crystallographic center of symmetry. The asymmetric unit comprises the anion, one-half cation and a nitromethane molecule. The anions and solvent pack to form a zigzag ribbon motif, alternating with layers of cations. The extended packing consists of a network of C- $H \cdots O, C - H \cdots N$ and $C - H \cdots F$ intermolecular interactions.

Comment

Recently, Albrecht et al. (2000, 2001) have reported the synthesis of square-planar platinum(II) complexes with two potentially mer-coordinating ligands. In these complexes, one ligand is tridentate, whereas the second is monodentate with ligating groups above and below the coordination plane. We have recently demonstrated that certain complexes with this ligand architecture can act as outer-sphere two-electron reagents (Jude et al., 2003). Reasoning that a similar architecture could be obtained with facially coordinating ligands such as tris(pyrazol-1-yl)methane (tpm), we undertook the synthesis and structural characterization of $[Pt(tpm)_2]^{2+}$ as the nitromethane-solvated PF_6^- salt, (I) (Fig. 1). This crystallizes with the Pt atom located on a crystallographic center of symmetry.

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2PF. OZCH.NO



(I)

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The structure of (I) at 150 K, showing the atomic labeling and 50% probability ellipsoids.



Figure 2

Extended packing motif of (I), viewed along the a axis. H atoms have been omitted for clarity.

range 1.987 (8)–2.006 (9) Å and N–Pd–N angles of 87.4 (3)– 92.6 (3)°. The dihedral angles for the PdN₄ plane and the coordinated rings (rings A and B) are 36.8 and 39.9°, while that for the uncoordinated ring (ring C) is 51.0°. The [bis-(pyrazolyl)methane]palladium complex, [Pd(dpm)₂](BF₄)₂, reported by Minghetti *et al.* (1986), also has the Pd atom in a square-planar environment with comparable M–N and N– M–N distances and angles to those observed for (I) and [Pd(tpm)₂](BF₄)₂. The anions and solvent molecules in (I) pack to form a zigzag ribbon motif (Fig. 2), alternating with layers of cations. The extended packing consists of a network of $C-H\cdots O$, $C-H\cdots N$ and $C-H\cdots F$ intermolecular interactions (Table 1) involving atoms N6, O1 and F1–F5. Atoms O2 and F6 do not participate in interactions with H–acceptor distances less than 2.7 Å.

Experimental

K₂PtCl₄ and tris(pyrazol-1-yl)methane (2 equivalents) were combined in water and refluxed. The reaction could be easily monitored by observing two color changes. First, the deep orange color of K₂PtCl₄ was gradually replaced by a yellow color corresponding to the monosubstituted tpm complex. The yellow color faded gradually as the second tpm ligand attached to platinum, forming [Pt(tpm)₂]Cl₂. Metathesis of the chloride salt with NH₄PF₆ resulted in (I). Single crystals were obtained as colorless plates from CH₃NO₂–Et₂O solution. ¹H NMR (d_6 -DMSO, δ): 9.53 (2H, s), 8.88 (4H, d), 8.05 (2H, d), 7.95 (4H, d), 7.75 (2H, d), 6.96 (4H, t), 6.53 (2H, t).

Crystal data

 $[Pt(C_{10}H_{10}N_6)_2](PF_6)_2 \cdot 2CH_3NO_2$ $D_x = 1.950 \text{ Mg m}^{-3}$ $M_r = 1035.60$ Mo $K\alpha$ radiation Cell parameters from 7038 Monoclinic, $P2_1/c$ a = 7.9329 (4) Å reflections b = 23.2431 (10) Å $\theta = 1.8-28.3^{\circ}$ $\mu = 4.19 \text{ mm}^{-1}$ c = 9.9054 (4) Å $\beta = 105.044 (1)^{\circ}$ T = 150 (2) K $V = 1763.81 (14) \text{ Å}^{2}$ Plate, colorless Z = 2 $0.12\,\times\,0.10\,\times\,0.05~\mathrm{mm}$ Data collection Bruker SMART6000 CCD 4387 independent reflections diffractometer 3090 reflections with $I > 2\sigma(I)$ ω scans $R_{\rm int} = 0.047$ Absorption correction: multi-scan $\theta_{\rm max} = 28.3^\circ$ $h = -10 \rightarrow 10$ (SADABS: Sheldrick, 2001) $T_{\min} = 0.634, \ T_{\max} = 0.818$ $k=-30\to 30$ 23878 measured reflections $l = -13 \rightarrow 13$ Refinement Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.017P)^2]$ $R[F^2 > 2\sigma(F^2)] = 0.025$ + 3.1656P] where $P = (F_o^2 + 2F_c^2)/3$ $wR(F^2) = 0.057$ S = 1.05 $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.80 \ {\rm e} \ {\rm \AA}^{-3}$ 4387 reflections $\Delta \rho_{\rm min} = -0.62 \text{ e} \text{ Å}^{-3}$ 250 parameters H-atom parameters constrained

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
C6-H6···N6 ⁱ	0.95	2.51	3.136 (5)	123
C4-H4···O1 ⁱⁱ	0.95	2.58	3.481 (6)	159
$C5-H5\cdots F5^{ii}$	0.95	2.59	3.259 (5)	128
$C3-H3 \cdot \cdot \cdot F1$	0.95	2.52	3.201 (4)	129
$C2-H2\cdots F3$	0.95	2.42	3.174 (5)	137
$C6-H6\cdots F2^{iii}$	0.95	2.38	3.190 (5)	144
$C7-H7\cdot\cdot\cdot F2^{iii}$	1.00	2.56	3.450 (5)	149
C3-H3···F3 ⁱⁱⁱ	0.95	2.55	3.321 (5)	139
C7-H7···F3 ⁱⁱⁱ	1.00	2.53	3.444 (4)	152
$C11-H11C\cdots F4^{iii}$	0.98	2.49	3.136 (7)	123
$C1\!-\!H1\!\cdot\cdot\cdot\!F2^{iv}$	0.95	2.47	3.402 (5)	168

Symmetry codes: (i) 1 - x, 2 - y, 1 - z; (ii) $-x, \frac{1}{2} + y, \frac{3}{2} - z$; (iii) $x, \frac{3}{2} - y, z - \frac{1}{2}$; (iv) $x, \frac{3}{2} - y, \frac{1}{2} + z$.

The H atoms were either located directly or calculated geometrically (aromatic, methyne and methyl: C-H = 0.95, 1.00 and 0.98 Å, respectively) and treated with a riding model in subsequent refinement cycles. The isotropic displacement parameters were set to aU_{eq} of the carrier atom (a = 1.5 for methyl H atoms and 1.2 for all others). The nitromethane solvent of crystallization and the PF₆ anion show some disorder, as indicated by the enlarged anisotropic displacement parameters compared with the cation. Since the structure is chemically reasonable, resolved disorder models were not attempted.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Bruker, 2002); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL* and *DIAMOND* (Crystal Impact, 1997); software used to prepare material for publication: *SHELXTL*.

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