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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{N-C}) = 0.005 \text{ Å}$ R factor = 0.038 wR factor = 0.084 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.

equivalent

122.3 (4)°, compared with 12 ligand (Bentefrit *et al.*, 1997 The structure of (I) is si bonding interactions involving

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Bis(biguanido- $\kappa^2 N, N'$)palladium(II) dihydrate

In the title compound, $[Pd(C_2H_6N_5)_2]\cdot 2H_2O$, the Pd atom is coordinated by four N atoms from two bidentate biguanide ligands in a square-planar arrangement. A network of $O-H\cdots N$, $N-H\cdots N$ and $N-H\cdots O$ hydrogen bonds helps to consolidate the crystal packing. The Pd atom occupies a special position with $\overline{1}$ site symmetry.

Comment

In previous work, the crystal structures of the biguanide $(C_2H_6N_5^-)$ anion coordinated to Cu^{2+} and Ni^{2+} were reported (Su, Lu, Li & Zhu, 2005; Su, Lu & Zhu, 2005). Pd^{2+} and Ni^{2+} ions have the same d^8 electron configuration, so we set out to investigate the coordination behaviour of Pd^{2+} with the biguanide ligand, resulting in the title compound, (I) (Fig. 1).



Compound (I) consists of a square-planar $[Pd(C_2H_6N_5)_2]$ complex (Pd site symmetry $\overline{1}$) and two uncoordinated water molecules. In the complex, Pd is coordinated by four N atoms from two bidentate ligands (Table 1). This coordination geometry is consistent with that seen in the Cu²⁺ and Ni²⁺ analogues noted above. The ligand is close to planar. Compared with the previous complexes, we notice that the Pd-N coordinated bond distances are longer than the equivalent distances in $[Cu(C_2H_6N_5)_2]\cdot 2H_2O$ [1.927 (3) and 1.954 (3) Å; Su, Lu, Li & Zhu, 2005] and $[Ni(C_2H_6N_5)_2]\cdot 2H_2O$ [1.849 (2) and 1.859 (2) Å; Su, Lu & Zhu, 2005].

In addition, deprotonation of the ligand in (I) produces an increase of the π conjugation in the central C–N–C system, decreasing the bond angle at the bridging N atom to 122.3 (4)°, compared with 124.9 (8)–127.7 (5)° for the neutral ligand (Bentefrit *et al.*, 1997; Lemoine *et al.*, 1996).

The structure of (I) is stabilized by extensive hydrogenbonding interactions involving all the N atoms and all O atoms of the water molecules (Fig. 2 and Table 2) Received 26 April 2006 Accepted 26 April 2006



Figure 1

The structure of (I), with displacement ellipsoids drawn at the 30% probability level for non-H atoms. [Symmetry code: (i) 1 - x, -y, 1 - z.]



Figure 2

The packing of (I), with hydrogen bonds shown as dashed lines.

Experimental

An aqueous solution of $PdCl_2$ was added dropwise to an alkaline aqueous solution of the ligand with stirring, in a 1:2 molar ratio. The colourless solution was filtered, and the filtrate was left to stand at room temperature. Colourless crystals of (I) formed after a few days.

Crystal data

	7 4
$[Pd(C_2H_6N_5)_2]\cdot 2H_2O$	Z = 4
$M_r = 342.67$	$D_x = 2.022 \text{ Mg m}^{-3}$
Orthorhombic, Pbca	Mo $K\alpha$ radiation
a = 7.1450 (12) Å	$\mu = 1.66 \text{ mm}^{-1}$
b = 22.663 (4) Å	T = 298 (2) K
c = 6.9532 (11) Å	Plate, colourless
V = 1125.9 (3) Å ³	$0.21 \times 0.14 \times 0.02 \text{ mm}$
Data collection	
Bruker SMART 1K CCD	5096 measured reflections
diffractometer	991 independent reflections
ω scans	819 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan	$R_{\rm int} = 0.069$
(SADABS; Sheldrick, 2000)	$\theta_{\rm max} = 25.0^{\circ}$
$T_{\min} = 0.722, \ T_{\max} = 0.968$	

Refinement

-	
Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0261P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.038$	+ 3.5974P]
$wR(F^2) = 0.084$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.11	$(\Delta/\sigma)_{\rm max} < 0.001$
991 reflections	$\Delta \rho_{\rm max} = 0.76 \ {\rm e} \ {\rm \AA}^{-3}$
79 parameters	$\Delta \rho_{\rm min} = -0.97 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1

Selected	geometric	parameters	(A, '	°).

Pd1-N1	1.979 (3)	Pd1-N4	1.990 (3)
N1-Pd1-N4	87.36 (14)		

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

D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdots A$
0.85	2.19	3.014 (5)	163
0.85	2.16	2.978 (5)	164
0.86	2.30	3.080 (5)	150
0.86	2.61	3.349 (5)	144
0.86	2.56	3.136 (5)	125
0.86	2.69	3.322 (5)	131
	D-H 0.85 0.85 0.86 0.86 0.86 0.86	$\begin{array}{c cccc} D-H & H \cdots A \\ \hline 0.85 & 2.19 \\ 0.85 & 2.16 \\ 0.86 & 2.30 \\ 0.86 & 2.61 \\ 0.86 & 2.56 \\ 0.86 & 2.69 \\ \hline \end{array}$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$

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

N-bound H atoms were placed in geometrically idealized positions, with N-H = 0.86 Å, and refined as riding with $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm N})$. H atoms attached to O were located in a difference Fourier map and then treated as riding, with O-H = 0.85 Å and $U_{\rm iso}({\rm H}) = 1.5 U_{\rm eq}({\rm O})$.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL/PC* (Sheldrick, 1999); software used to prepare material for publication: *SHELXTL/PC*.

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