

Mamiko Odoko\* and  
Nobuo OkabeFaculty of Pharmaceutical Sciences, Kinki  
University, Kowakae 3-4-1, Higashiosaka,  
Osaka 577-8502, JapanCorrespondence e-mail:  
odoko@phar.kindai.ac.jp

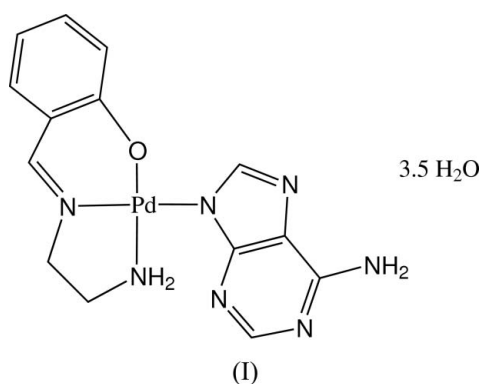
## Key indicators

Single-crystal X-ray study  
 $T = 123$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å  
Disorder in solvent or counterion  
 $R$  factor = 0.026  
 $wR$  factor = 0.070  
Data-to-parameter ratio = 14.2For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.(Adeninato- $N^9$ )[ $N$ -(2-aminoethyl)salicylidene-  
iminato]palladium(II) 3.5-hydrate

In the title compound,  $\{[(2\text{-aminoethyl})\text{iminomethyl}]\text{phenolato-}\kappa^3N,N',O\}(9H\text{-purine-6-aminato-}\kappa N^9)\text{palladium(II) } 3.5\text{-hydrate}$ ,  $[\text{Pd}(\text{C}_5\text{H}_4\text{N}_5)(\text{C}_9\text{H}_{11}\text{N}_2\text{O})]\cdot 3.5\text{H}_2\text{O}$ , the  $\text{Pd}^{\text{II}}$  ion is coordinated by the  $N9$  atom of the adeninate ligand, two  $N$  atoms and one  $O$  atom of the  $N$ -(2-aminoethyl)-salicylideneiminato in a square-planar coordination. The crystal structure is stabilized by centrosymmetric stacking interactions between neighbouring complexes, and by hydrogen bonds involving adeninate and  $N$ -(2-aminoethyl)-salicylideneiminato ligands, and non-coordinated water molecules.

## Comment

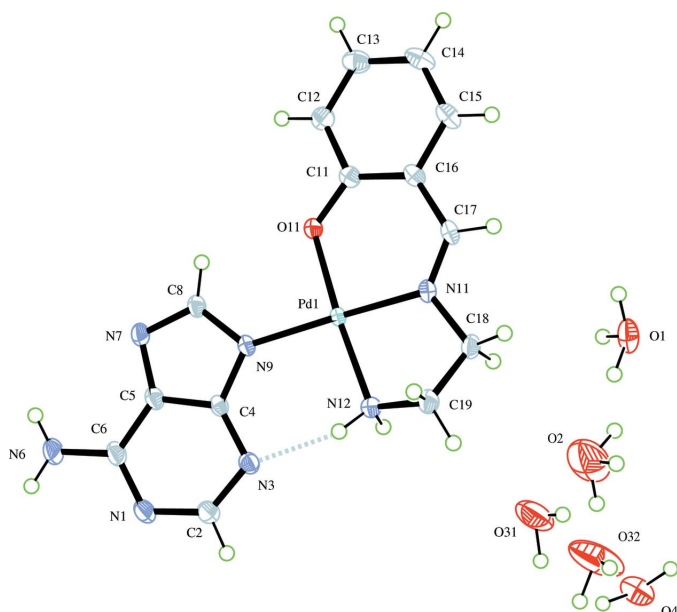
Since the discovery of the antitumour  $\text{Pt}^{\text{II}}$  complex cisplatin (Rosenberg *et al.*, 1965, 1969), it has been important to analyse the interaction of metal ions with nucleic acids and nucleobases. Some studies have revealed interactions between  $\text{Pt}^{\text{II}}$  group metal ions and nucleobases (Brüning *et al.*, 2002; Amantia *et al.*, 2003; Zhang *et al.*, 2005). In addition, some complexes of transition metal ions with salen-type Schiff base ligands [salen is  $N,N'$ -ethylenebis(salicylideneaminato)] have been tested as DNA reactive agents (Rokita & Burrows, 2003).



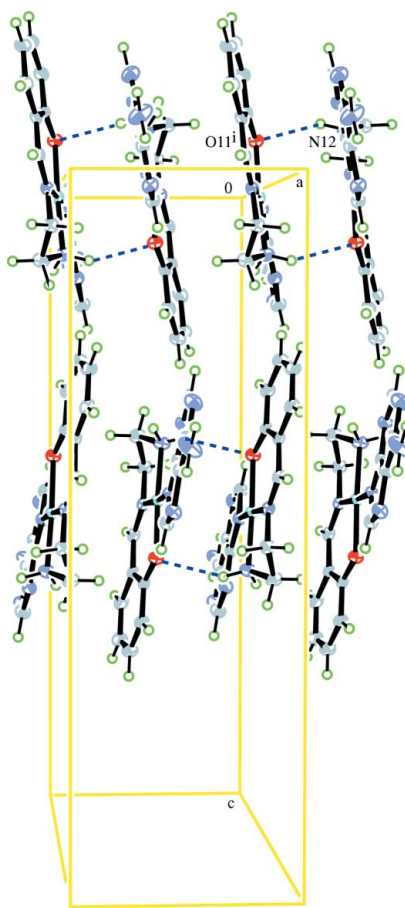
The aim of this study was to determine the binding function to nucleobases of a  $\text{Pt}^{\text{II}}$  group metal ion,  $\text{Pd}^{\text{II}}$ , coordinated by a salen-type ligand. Therefore, we synthesized an adeninato- $\text{Pd}^{\text{II}}$ -SalEn [SalEn is  $N$ -(2-aminoethyl)salicylideneiminato] complex, (I), and analyzed its structure.

The title compound, (I), is shown in Fig. 1. The  $\text{Pd}^{\text{II}}$  ion is coordinated by atom  $N9$  of the adeninate ligand, and atoms  $N11$ ,  $N12$  and  $O11$  of the SalEn ligand, forming a square-planar coordination around the metal centre. Coordination through atom  $N9$  of the adeninate ligand [ $\text{Pd}-\text{N}9 = 2.037$  (2) Å] also occurs in the crystal structure of *trans*-( $n$ - $\text{Bu}_3\text{P}$ ) $_2\text{Pd}(\text{adeninato})_2\cdot 4\text{CH}_3\text{OH}$  [ $\text{Pd}-\text{N}9 = 2.015$  (3) Å; Beck

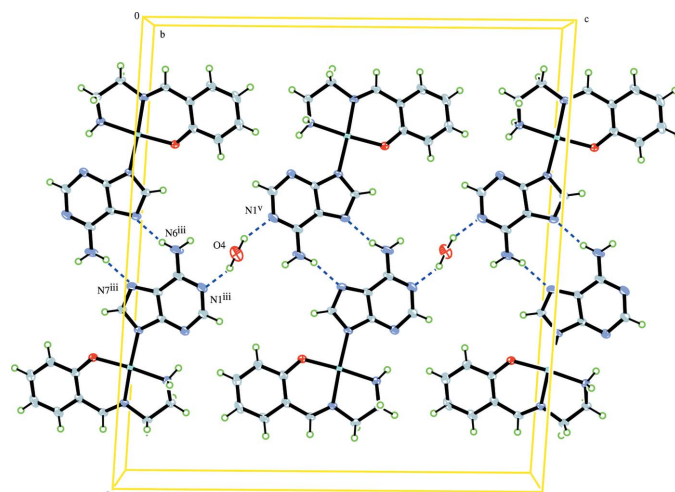
Received 17 October 2005  
Accepted 17 November 2005  
Online 23 November 2005

**Figure 1**

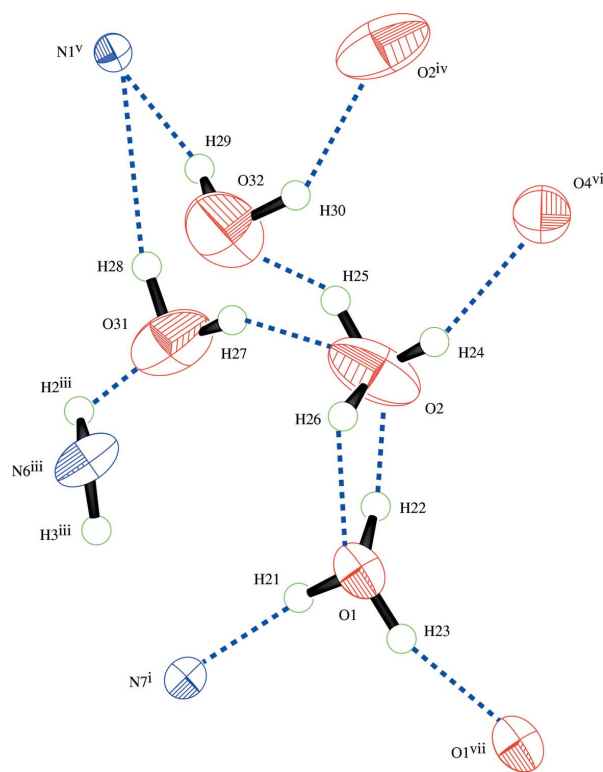
A view of the structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as spheres of arbitrary radii. A dashed line indicates the intramolecular hydrogen bond. All disorder components are shown.

**Figure 2**

A view of the crystal packing of (I), showing the centrosymmetric stacking interactions between neighbouring complexes. Dashed lines indicate hydrogen bonds. [Symmetry code: (i)  $\frac{1}{2} - x, \frac{3}{2} - y, -z$ .]

**Figure 3**

A view of the hydrogen bonds (dashed lines) between adeninate ligands, and hydrogen-bond bridges formed by O4 water molecules. [Symmetry codes: (iii)  $\frac{1}{2} + x, y - \frac{1}{2}, z$ ; (v)  $\frac{1}{2} - x, y - \frac{1}{2}, \frac{1}{2} - z$ .]

**Figure 4**

A view of the hydrogen-bond network (dashed lines) involving the disordered water molecules. All disorder components are shown. [Symmetry codes: (i)  $\frac{1}{2} - x, \frac{3}{2} - y, -z$ ; (iii)  $\frac{1}{2} + x, y - \frac{1}{2}, z$ ; (iv)  $1 - x, y, \frac{1}{2} - z$ ; (v)  $\frac{1}{2} - x, y - \frac{1}{2}, \frac{1}{2} - z$ ; (vi)  $x, 1 + y, z$ ; (vii)  $1 - x, 2 - y, -z$ .]

*et al.*, 1979], in agreement with the fact that N9 is the most basic of the four available N atoms on the adeninate anion (Hodgson, 1977; Beck *et al.*, 1979). While the Pd<sup>II</sup> ion and its coordinated atoms lie almost in a plane (r.m.s. deviation of fitted atoms = 0.056 Å), the overall structure of the complex is not planar. The dihedral angle between the adeninate ligand

and salicylidene plane (O11/C11–C17/N11) is 12.23 (6)°. An intramolecular hydrogen bond is observed between the amino group of SalEn and the adeninate ligand (N12–H14···N3; Fig. 1 and Table 2).

The crystal packing is stabilized by centrosymmetric stacking interactions between neighbouring complexes (Fig. 2), the separations ranging from 3.2642 (2) (Pd1···Pd1<sup>i</sup>) to 3.457 (3) Å [C4···C17<sup>i</sup>; symmetry code: (i)  $\frac{1}{2} - x, \frac{3}{2} - y, -z$ ], and by hydrogen bonds involving SalEn ligands (N12–H15···O11<sup>i</sup>; Table 2). The crystal structure is also stabilized by hydrogen bonds between neighbouring adeninate ligands [N6–H3···N7<sup>ii</sup>; symmetry code: (ii)  $-x, 2 - y, -z$ ] (Fig. 3 and Table 2), hydrogen-bond bridging of two symmetry-related adeninate ligands *via* a water molecule [N1<sup>iii</sup>–O4···N1<sup>v</sup>; symmetry codes: (iii)  $\frac{1}{2} + x, -\frac{1}{2} + y, +z$ ; (v)  $\frac{1}{2} - x, -\frac{1}{2} + y, \frac{1}{2} - z$ ] (Fig. 3 and Table 2), and a complex network of hydrogen bonds involving adeninate ligands and disordered water molecules (Fig. 4 and Table 2).

### Experimental

*N,N'*-Ethylenebis(salicylideneamine) dissolved in EtOH–H<sub>2</sub>O (40% *v/v*) was reacted with adenine and sodium tetrachloropalladium(II) trihydrate dissolved in water at 298 K (molar ratio = 2:1:2). This mixture was diluted with 50% KCl solution. Light-brown crystals appeared from this mixture after one month of evaporation at 298 K.

#### Crystal data

[Pd(C <sub>5</sub> H <sub>4</sub> N <sub>5</sub> )(C <sub>9</sub> H <sub>11</sub> N <sub>2</sub> O)]·3.5H <sub>2</sub> O	$D_x = 1.759 \text{ Mg m}^{-3}$
$M_r = 466.81$	Mo $K\alpha$ radiation
Monoclinic, $C2/c$	Cell parameters from 14802 reflections
$a = 23.75 (2) \text{ \AA}$	$\theta = 3.1\text{--}27.5^\circ$
$b = 6.869 (5) \text{ \AA}$	$\mu = 1.09 \text{ mm}^{-1}$
$c = 21.65 (2) \text{ \AA}$	$T = 123 (1) \text{ K}$
$\beta = 93.46 (3)^\circ$	Plate, brown
$V = 3526 (5) \text{ \AA}^3$	$0.50 \times 0.15 \times 0.05 \text{ mm}$
$Z = 8$	

#### Data collection

Rigaku R-AXIS RAPID diffractometer	4009 independent reflections
$\omega$ scans	3440 reflections with $F^2 > 2\sigma(F^2)$
Absorption correction: multi-scan (ABSCOR; Higashi, 1995)	$R_{\text{int}} = 0.014$
$T_{\text{min}} = 0.682, T_{\text{max}} = 0.947$	$\theta_{\text{max}} = 27.5^\circ$
17133 measured reflections	$h = -30 \rightarrow 30$
	$k = -8 \rightarrow 8$
	$l = -28 \rightarrow 28$

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0397P)^2 + 7.5219P]$
$R[F^2 > 2\sigma(F^2)] = 0.026$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.070$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.07$	$\Delta\rho_{\text{max}} = 1.61 \text{ e \AA}^{-3}$
4009 reflections	$\Delta\rho_{\text{min}} = -0.70 \text{ e \AA}^{-3}$
283 parameters	
H-atom parameters constrained	

**Table 1**

Selected geometric parameters (Å, °).

Pd1–O11	1.993 (2)	Pd1–N11	1.968 (2)
Pd1–N9	2.037 (2)	Pd1–N12	2.038 (2)
O11–Pd1–N9	88.73 (7)	N9–Pd1–N11	175.49 (7)
O11–Pd1–N11	93.97 (7)	N9–Pd1–N12	94.88 (7)
O11–Pd1–N12	175.05 (7)	N11–Pd1–N12	82.65 (8)

**Table 2**

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N12–H14···N3	0.90	2.22	2.845 (4)	126
N12–H15···O11 <sup>i</sup>	0.90	2.39	3.175 (3)	145
N6–H3···N7 <sup>ii</sup>	0.86	2.24	3.040 (3)	155
O4–H31···N1 <sup>iii</sup>	0.99	2.00	2.920 (3)	154
O4–H31 <sup>iv</sup> ···N1 <sup>v</sup>	0.99	2.00	2.920 (3)	154
O1–H21···N7 <sup>vi</sup>	0.93	2.04	2.960 (3)	170
O1–H22···O2	0.94	1.86	2.783 (4)	167
O2–H24···O4 <sup>vi</sup>	0.95	1.97	2.752 (4)	137
O2–H25···O32	0.96	1.59	2.473 (8)	151
O32–H29···N1 <sup>v</sup>	0.96	1.92	2.804 (6)	154
O32–H30···O2 <sup>iv</sup>	0.96	2.25	3.095 (8)	146
O1–H23···O1 <sup>vii</sup>	0.95	1.88	2.793 (4)	163
O2–H26···O1	0.95	1.99	2.783 (4)	139
O31–H27···O2	0.96	1.98	2.811 (8)	144
O31–H28···N1 <sup>v</sup>	0.96	2.30	3.260 (7)	179
N6 <sup>iii</sup> –H2 <sup>iii</sup> ···O31	0.86	2.16	2.877 (6)	140

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

One water molecule was found to be disordered over two sites, O31 and O32; the occupancies were refined and then fixed at 0.5. For water molecules O1, O2, O31 and O32, H atoms were found in difference maps with some disordered over two sites. Occupancies were refined and fixed in the last cycles: H22, bonded to O1, is disordered with H23 (0.56/0.54); H25, bonded to O2, is disordered with H26 (0.22/0.78); H27 and H28 are bonded to O31 with occupancies 0.5; H29 and H30 are bonded to O32, with occupancies 0.5. In the last cycles, the coordinates of H atoms of water molecules were fixed and their isotropic displacement parameters were fixed at  $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{O})$ . Other H atoms were placed in idealized positions and refined as riding, with  $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{carrier atom})$ . Constrained distances: 0.93 Å for aromatic CH; 0.97 Å for methylene CH<sub>2</sub>; 0.90 Å for coordinated amine; 0.86 Å for uncoordinated amine. The maximum electron density appears near atom O32.

Data collection: *RAPID-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO* (Rigaku/MS, 2005); data reduction: *PROCESS-AUTO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure* (Rigaku/MS, 2005).

### References

- Amantia, D., Price, C., Shipman, M. A., Elsegood, M. R. J., Clegg, W. & Houlton, A. (2003). *Inorg. Chem.* **42**, 3047–3056.  
 Beck, W. M., Calabrese, J. C. & Kottmair, N. D. (1979). *Inorg. Chem.* **18**, 176–182.  
 Brüning, W., Ascaso, I., Freisinger, E., Sabat, M. & Lippert, B. (2002). *Inorg. Chim. Acta*, **339**, 400–410.  
 Farrugia, L. J. (1997). *J. Appl. Cryst.* **30**, 565.  
 Higashi, T. (1995). *ABSCOR*. Rigaku Corporation, Tokyo, Japan.

- Hodgson, D. J. (1977). *Prog. Inorg. Chem.* **23**, 211–254.
- Rigaku (1998). *RAPID-AUTO*. Rigaku Corporation, 3-9-12 Akishima, Tokyo 196-8666, Japan.
- Rigaku/MSK (2005). *PROCESS-AUTO* and *CrystalStructure* (Version 3.7). Rigaku/MSK, 9009 New Trails Drive, The Woodlands, TX 77381-5209, USA.
- Rokita, S. E. & Burrows, C. J. (2003). *Small Molecule DNA and RNA Binders*, Vol. 1, edited by M. Demeunynck, C. Bailly & W. D. Wilson, pp. 126–145. Weinheim: Wiley-VCH.
- Rosenberg, B., Camp, L. V. & Krigas, T., (1965). *Nature (London)*, **205**, 698–699.
- Rosenberg, B., Camp, L. V., Trosko, J. E. & Mansour, V. H. (1969). *Nature (London)*, **222**, 385–386.
- Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
- Zhang, Z. Q., Zhou, L. X., He, Q. & Zhao, Y. Y. (2005). *Jiegou Huaxue*, **24**, 114–120. (In Chinese.)