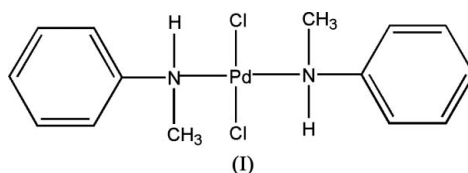


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Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.020$ Å
 R factor = 0.074
 wR factor = 0.193
Data-to-parameter ratio = 15.6For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Dichlorobis(*N*-methylaniline)palladium(II)The title complex, $[\text{PdCl}_2(\text{C}_6\text{H}_9\text{N})_2]$, has crystallographic inversion symmetry. It forms a layered structure through $\text{N}-\text{H}\cdots\text{Cl}$ hydrogen bonds. The Pd^{II} ion is in a square-planar coordination.Received 11 April 2006
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Comment

Although many studies have been reported for $\text{C}_6\text{H}_5\text{NH}_2$ compounds (Chen *et al.*, 2002) and related complexes (Newkome *et al.*, 1982; Navarro-Ranninger *et al.*, 1983*a,b*; Bell *et al.*, 1966), no complex has been reported which contains the $\text{C}_6\text{H}_5\text{NH}(\text{CH}_3)$ ligand. We report here the first $\text{C}_6\text{H}_5\text{NH}(\text{CH}_3)$ complex, *viz.* $[\text{PdCl}_2(\text{C}_7\text{H}_9\text{N})_2]$, (I).The X-ray crystallographic analysis of (I) reveals that the Pd atom, on an inversion centre, is coordinated in a square-planar fashion by the Cl and N atoms (Fig. 1). The Pd–N and Pd–Cl bond distances are comparable to those in $[\text{PdCl}_2(\text{C}_6\text{H}_5\text{NH}_2)_2]$ (Chen *et al.*, 2002). There are pairwise $\text{N}-\text{H}\cdots\text{Cl}$ hydrogen bonds that link the complexes together, forming layers (Fig. 2). These hydrogen bonds are slightly shorter than those in $[\text{PdCl}_2(\text{C}_6\text{H}_5\text{NH}_2)_2]$ complexes (Chen *et al.*, 2002).

Experimental

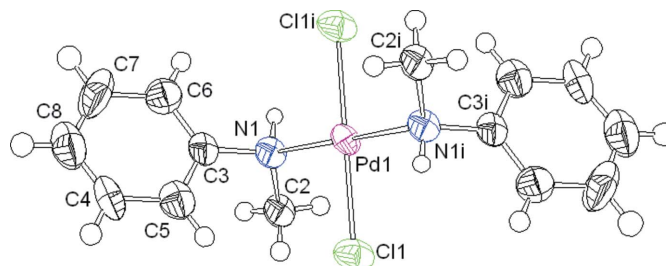
A mixture of $\text{C}_6\text{H}_5\text{NH}(\text{CH}_3)$ (10 ml), PdCl_2 (0.17 g) and CH_3CN (20 ml) was stirred at about 353 K for 2 h and then filtered. The filtrate was kept at room temperature for several days to give yellow crystals of the title complex, (I).

Figure 1

The structure of (I), showing displacement ellipsoids at the 50% probability level. H atoms are shown as small spheres of arbitrary radii. [symmetry code: (i) $1 - x, -y, 1 - z$].

Crystal data

[PdCl₂(C₇H₉N)₂] $M_r = 391.62$ Monoclinic, $P2_1/n$ $a = 6.1411 (11) \text{ \AA}$ $b = 15.501 (3) \text{ \AA}$ $c = 8.5024 (17) \text{ \AA}$ $\beta = 103.685 (3)^\circ$ $V = 786.4 (3) \text{ \AA}^3$ $Z = 2$ $D_x = 1.654 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation $\mu = 1.51 \text{ mm}^{-1}$ $T = 293 (2) \text{ K}$

Prism, yellow

 $0.35 \times 0.22 \times 0.10 \text{ mm}$

Data collection

Bruker SMART 1K diffractometer

 φ and ω scans

Absorption correction: multi-scan

(SADABS; Sheldrick, 1996)

 $T_{\min} = 0.678$, $T_{\max} = 0.860$

2765 measured reflections

1373 independent reflections

888 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.070$ $\theta_{\text{max}} = 25.0^\circ$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.074$ $wR(F^2) = 0.193$ $S = 1.08$

1373 reflections

88 parameters

H-atom parameters constrained

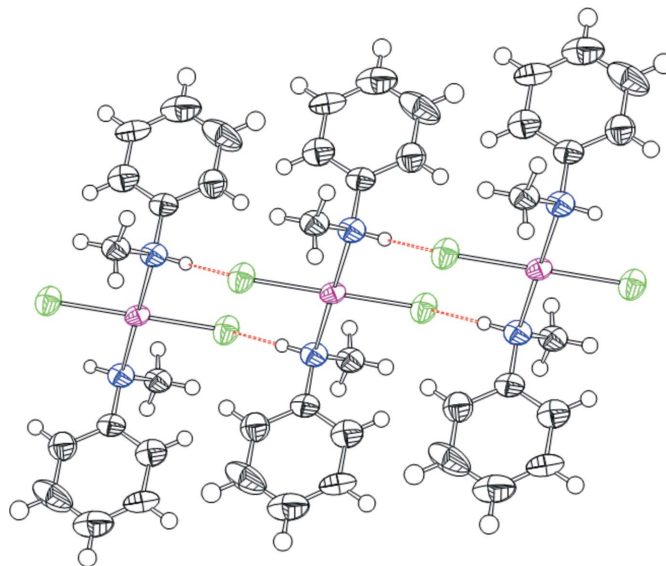
 $w = 1/[\sigma^2(F_o^2) + (0.0909P)^2$ $+ 3.5006P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\text{max}} < 0.001$ $\Delta\rho_{\text{max}} = 1.38 \text{ e \AA}^{-3}$ $\Delta\rho_{\text{min}} = -1.18 \text{ e \AA}^{-3}$ 

Figure 2

View of the extensive hydrogen bonding (dashed lines) between complexes.

Table 1

Selected geometric parameters (\AA , $^\circ$).

Pd1—N1	2.070 (8)	Pd1—Cl1	2.302 (3)
N1—Pd1—Cl1	94.2 (3)		

Table 2

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N1—H1A \cdots Cl1 ⁱ	0.91	2.49	3.302 (10)	149

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

All H atoms were placed at calculated positions, and refined with isotropic displacement parameters, using a riding model [$C-H = 0.93$ or 0.96 \AA and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$; $N-H = 0.91 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$]. In the final difference map, the deepest hole is 1.03 \AA from atom Pd1 and the highest peak is 0.99 \AA from Pd1.

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1994); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Siemens, 1994); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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