metal-organic papers

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Key indicators

Single-crystal X-ray study T = 90 K Mean σ (C–C) = 0.002 Å R factor = 0.023 wR factor = 0.064 Data-to-parameter ratio = 22.9

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The structure of the title compound, $[Cu(PPh_3)_2(BH_4)]$, has been redetermined at 90 K. The geometric parameters of the present structure agree with those previously studied at room temperature [Lippard & Melmed (1967). *Inorg. Chem.* **6**, 2223–2228; Li *et al.* (2000). *Chin. J. Struct. Chem.* **19**, 91–94], but with significantly improved precision. The molecule has twofold rotation symmetry. Received 4 November 2004 Accepted 22 November 2004 Online 8 January 2005

Comment

The crystal structure of the title compound, (I), has been previously studied at room temperature (Lippard & Melmed, 1967; Li et al., 2000). In the present redetermination, data were collected at low temperature, using a diffractometer equipped with a new APEX2 CCD area detector. As shown in Fig. 1, the structure of (I) is composed of neutral [Cu(PPh₃)₂(BH₄)] complex molecules with crystallographic twofold rotation symmetry. The results show that the coordination around Cu^I is distorted tetrahedral, with two triphenylphosphine P atoms [Cu-P1 = 2.2780 (3) Å] and two H atoms of the bidentate tetrahydroborate anion [Cu-H1B = 1.79 (2) Å], as in the pyridine solvate [Cu(PPh₃)₂(BH₄)]·pyridine (Engelhardt et al., 1985). The geometric parameters of the present structure agree with those previously reported by Lippard & Melmed (1967) and Li et al. (2000), but with significantly improved precision. The precision of the Cu-P1 bond length (0.0003 Å), the P-C bond lengths (mean 0.001 Å) and the C-C bond lengths (mean 0.0016 Å) for the low-temperature study are better than the room-temperature results reported by Lippard & Melmed (0.001, 0.005 and 0.008 Å, respectively) and Li et al. (0.001, 0.004 and 0.006 Å, respectively). Similarly, the standard uncertainty for the P1-Cu-P1 bond angle for the low-temperature data is 0.001°, whereas for both the room-temperature structures it is 0.006°.



Experimental

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 $[Cu(PPh_3)_2(BH_4)]$ was prepared by a modification of the procedure reported by Fleet & Harding (1979). Finely powdered copper(I)

chloride (0.40 g, 4 mmol) was added to a stirred solution of tri-

phenylphosphine (2.16 g, 8.2 mmol) in chloroform (10 ml) over a period of five minutes. The reaction mixture was stirred until the copper chloride had dissolved (30 min), treated with a solution of sodium tetrahydroborate (0.15 g, 4 mmol) in ethanol (3 ml), stirred for one hour, and then added to water (3 ml). The chloroform layer was then washed with water (3 ml), dried (magnesium sulfate) and filtrated. Crystals were grown by slowly diffusing diethyl ether vapor into a solution of [Cu(PPh₃)₂(BH₄)] in chloroform.

 $D_x = 1.341 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 6488

4344 independent reflections

4037 reflections with $I > 2\sigma(I)$

reflections $\theta = 2.4-30.0^{\circ}$ $\mu = 0.86 \text{ mm}^{-1}$ T = 90 (1) KNeedle, colorless $0.25 \times 0.05 \times 0.04 \text{ mm}$

 $R_{\rm int}=0.021$

 $\theta_{\text{max}} = 30.0^{\circ}$ $h = -34 \rightarrow 34$

 $k = -12 \rightarrow 12$

 $l = -21 \rightarrow 21$

Crystal data

$[C_{M}P(C H) \setminus (BH)]$
[Cull (C6115)3/2(D114)]
$M_r = 602.92$
Monoclinic, $C2/c$
a = 24.260(1) Å
b = 9.0818(5) Å
c = 15.0164 (8) Å
$\beta = 115.516 (1)^{\circ}$
$V = 2985.8 (3) \text{ Å}^3$
Z = 4
Data collection

Bruker SMART APEX2 diffractometer ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.813, T_{\max} = 0.966$ 25 523 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0376P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.023$	+ 2.2722P]
$wR(F^2) = 0.064$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.02	$(\Delta/\sigma)_{\rm max} = 0.002$
4344 reflections	$\Delta \rho_{\rm max} = 0.47 \ {\rm e} \ {\rm \AA}^{-3}$
190 parameters	$\Delta \rho_{\rm min} = -0.27 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

Table 1

Selected	geometric	parameters	(A, °	').	
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$P1-Cu-P1^i$ 122.99 (1) $P1^i-Cu-H1B$ 122.5 (6 $P1-Cu-H1B$ 106.0 (6)	Cu-P1	2.2780 (3)	Cu-H1B	1.79 (2)
	$\begin{array}{c} P1-Cu-P1^{i} \\ P1-Cu-H1B \end{array}$	122.99 (1) 106.0 (6)	P1 ⁱ -Cu-H1B	122.5 (6)

Symmetry code: (i) 2 - x, y, $\frac{3}{2} - z$.

H atoms of the tetrahydroborate anion were located in a difference Fourier map and refined isotropically. The H atoms of aromatic rings were placed in calculated positions and were treated as riding on their parent atoms, with C-H = 0.95 Å and $U_{\rm iso}({\rm H})$ = $1.2U_{\rm iso}$ (parent atom).



Figure 1

The structure of (I), showing 50% probability displacement ellipsoids and the atomic numbering. Unlabeled atoms are related to labeled atoms by the symmetry operation $(2 - x, y, \frac{3}{2} - z)$.

Data collection: *APEX2* (Bruker, 2004); cell refinement: *APEX2*; data reduction: *SAINT-Plus* (Bruker, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *XL* in *SHELXTL* (Sheldrick, 2000); molecular graphics: *XP* in *SHELXTL*; software used to prepare material for publication: *enCIFer* (Allen *et al.*, 2004).

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