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Key indicators

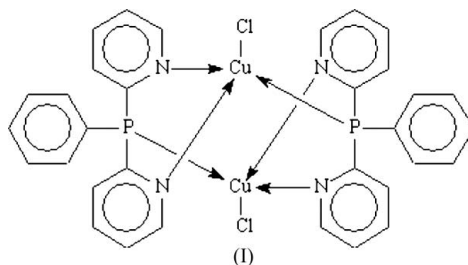
Single-crystal X-ray study
T = 293 K
Mean $\sigma(\text{C}-\text{C}) = 0.004 \text{ \AA}$
R factor = 0.035
wR factor = 0.094
Data-to-parameter ratio = 18.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Bis[μ_2 -phenylbis(2-pyridyl)phosphine]-
 $\kappa^3\text{N},\text{N}':\text{P};\kappa^3\text{P}:\text{N},\text{N}'$ -bis[chlorocopper(I)]

The title dinuclear complex, $[\text{Cu}_2\text{Cl}_2(\text{C}_{16}\text{H}_{13}\text{N}_2\text{P})_2]$, possesses a crystallographically imposed inversion center. Two Cu atoms are connected by two bridging phenylbis(2-pyridyl)phosphine ligands. Each Cu atom adopts a distorted tetrahedral geometry, coordinated by one Cl atom [$\text{Cu}-\text{Cl} = 2.3107(6) \text{ \AA}$], two N atoms [$\text{Cu}-\text{N} = 2.065(2)$ and $2.066(2) \text{ \AA}$] from one phenylbis(2-pyridyl)phosphine ligand and one P atom [$\text{Cu}-\text{P} = 2.1757(7) \text{ \AA}$] from another ligand.

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Comment

Phenylbis(2-pyridyl)phosphine (PhPPy_2) is an analog of di-2-pyridylamine that usually binds to metal atoms through two pyridyl groups. Such a feature is found in, for example, the mononuclear cobalt(II) dichloride adduct (Ehrlich *et al.*, 1984). However, in PhPPy_2 , the P atom is also able to bind to transition metals with low oxidation states. This ligand can therefore coordinate to metals in different modes. In chloro-bis(triphenylphosphine)ruthenium(II) hexafluorophosphate (Shutte *et al.*, 1997), PhPPy_2 binds to the metal atom intramolecularly, but intermolecularly in rhodium dichloride complexes (Galdecki *et al.*, 1999).



A direct reaction of $[\text{Cu}_2(\text{C}_{16}\text{H}_{13}\text{N}_2\text{P})_2(\text{CH}_3\text{CN})_2](\text{ClO}_4)_2$ [its crystal structure has recently been reported by Zhang *et al.* (2006)] with ammonium chloride led to the isolation of the title complex, (I), as yellow crystals, by substituting the labile acetonitrile molecules with Cl^- . In the centrosymmetric dinuclear complex of (I), two Cu atoms are connected by two bridging PhPPy_2 ligands in a head-to-tail fashion. Each Cu atom is coordinated by one Cl and two N atoms from one PhPPy_2 ligand, and by one P atom from another PhPPy_2 ligand, in a distorted tetrahedral geometry (Table 1). The intramolecular $\text{Cu}\cdots\text{Cu}$ separation of $3.744(1) \text{ \AA}$ in (I) indicates no interaction between copper centers.

Experimental

Solid $[\text{Cu}_2(\text{C}_{16}\text{H}_{13}\text{N}_2\text{P})_2(\text{CH}_3\text{CN})_2](\text{ClO}_4)_2$ (Zhang *et al.*, 2006) (0.0088 g, 0.0094 mmol) was dissolved in acetonitrile (2 ml), to which

a methanolic solution (1 ml) of ammonium chloride (0.0010 g, 0.0188 mmol) was added. The product, (I), crystallized as yellow crystals overnight in 80% yield.

Crystal data

[Cu₂Cl₂(C₁₆H₁₃N₂P)₂]
M_r = 726.49
 Monoclinic, *P*2₁/*n*
a = 9.305 (1) Å
b = 10.857 (1) Å
c = 15.746 (2) Å
 β = 93.033 (1)°
V = 1588.5 (3) Å³

Z = 2
D_x = 1.519 Mg m⁻³
 Mo *K*α radiation
 μ = 1.64 mm⁻¹
T = 293 (2) K
 Block, yellow
 0.34 × 0.14 × 0.10 mm

Data collection

Bruker APEX area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.760, *T_{max}* = 0.849

9241 measured reflections
 3548 independent reflections
 2901 reflections with *I* > 2σ(*I*)
R_{int} = 0.025
 θ_{\max} = 27.5°

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.035
wR (*F*²) = 0.094
S = 1.04
 3548 reflections
 190 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0513P)^2 + 0.1517P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.44 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.24 \text{ e \AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Cu1—N1	2.065 (2)	Cu1—P1 ⁱ	2.1757 (7)
Cu1—N2	2.066 (2)	Cu1—Cl1	2.3107 (6)
N1—Cu1—N2	94.18 (7)	N2—Cu1—P1 ⁱ	115.99 (6)
N1—Cu1—P1 ⁱ	116.63 (6)	N2—Cu1—Cl1	103.04 (6)
N1—Cu1—Cl1	103.84 (6)	P1 ⁱ —Cu1—Cl1	119.42 (3)

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

H atoms were placed at idealized positions (C—H = 0.93 Å) and were included in the refinement in the riding-model approximation, with *U_{iso}*(H) = 1.2*U_{eq}*(C).

Data collection: SMART (Bruker, 2000); cell refinement: SAINT (Bruker, 2003); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine

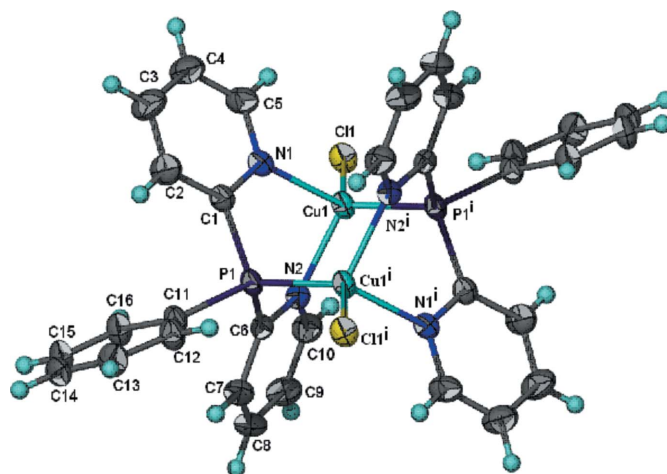


Figure 1

The molecular structure of (I), showing the atom-labeling scheme and displacement ellipsoids drawn at the 50% probability level [symmetry code: (i) $1 - x, 1 - y, 1 - z$].

structure: SHELXL97 (Sheldrick, 1997); molecular graphics: X-SEED (Barbour, 2001); software used to prepare material for publication: publCIF (Westrip, 2006).

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