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Bis(μ -diphenylphosphinato- $\kappa^2 O:O'$)bis[aqua(diphenylphosphinato- κO)bis(pyridine- κN)cobalt(II)]

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In the centrosymmetric title compound, $[Co_2(C_{12}H_{10}O_2P)_4-(C_5H_5N)_4(H_2O)_2]$, each approximately octahedral Co atom features two *trans*-coordinated pyridine molecules, one water molecule, a terminally coordinated monodentate diphenyl-phosphinate ligand, and two bidentate diphenylphosphinate ligands that bridge the two Co atoms across a centre of inversion to form a dimeric binuclear complex. The discrete molecules are linked by double hydrogen bonds between the terminally coordinated diphenylphosphinate ligand and the

water molecule to form a continuous chain along the crystallographic b axis.

Comment

Phosphinate ligands have a rich coordination chemistry, often forming polymeric species (Vioux *et al.*, 2004). Coordinating solvents can be used to dissolve these phosphinate-bridged coordination polymers, in a process that breaks the coordination chains, to form oligomeric or monomeric solvent adducts in solution (Siqueira *et al.*, 2006). We have investigated the possibility of forming the pyridine adduct of the diphenylphosphinate-bridged coordination polymer of Co^{II}. However, due to the presence of opportunist water, the title compound, (I), a molecular species incorporating both pyridine and water, was formed, and we present its crystal structure here.



One half-molecule of (I) is found in the asymmetric unit; the entire molecule is generated by the crystallographic centre of inversion, which lies at the mid-point between the two Co



Figure 1

The structure of (I), showing the atom-numbering scheme and displacement ellipsoids drawn at the 30% probability level. Symmetry-equivalent phenyl groups are shown as sticks. [Symmetry code: (i) -x, 2 - y, 1 - z.]

atoms (Fig. 1). Two diphenylphosphinate ligands bridge the two Co atoms to form an eight-membered ring. The octahedral coordination sphere is completed by two trans pyridine ligands, a water molecule, and a terminally coordinated monodentate diphenylphosphinate ligand.

The very long Co···Co distance in (I) (Table 1) precludes metallic bonding. This distance is slightly longer than that in the parent coordination polymer [4.704 (5) Å; Liu et al., 1992]. The very slightly different Co-O distances involved in the bridging diphenylphosphinate ligand in (I) are considerably longer than those for the parent polymer [1.905 (16)-1.927 (16) Å], which is likely to be due to the change from tetrahedral to octahedral geometry of the Co centre. The P---O distances are almost equal, showing a delocalization of the negative charge. The monodentate diphenylphosphinate ligand has a slightly longer P-O bond for the O atom coordinated to the Co centre than for the non-coordinated O atom, consistent with a partial localization of the negative charge on the O atom that forms the formally covalent bond. These values correspond well to the few examples found in the Cambridge Structural Database (Version 5.26, update of August 2005; Allen, 2002), where the average terminal P---O distance is 1.500 (13) Å and the coordinated $P \rightarrow O$ distance is 1.514 (15) Å for 14 observations.

The pyridine molecules are coordinated to the Co centre, with Co-N distances identical to within experimental error and N-Co-N angle close to the ideal value of 180°. The rings are rotated by 66.96 $(7)^{\circ}$ with respect to one another but are almost perpendicular to the CoO₄ plane, with angles of 86.71 (5)° for the N11-containing pyridine ring and 89.51 (5)° for the N21-containing ring.

A water molecule, presumably present in the methanol preparation solvent, completes the coordination sphere of the Co centre, preventing the formation of a polymeric chain as found for similar solvent adducts of coordinating polymers (Siqueira et al., 2006). Double hydrogen bonds between the terminal diphenylphosphinate ligand and the water molecule across a centre of inversion (Table 2) link discrete molecules to form a continuous chain along the crystallographic b axis (Fig. 2). The water molecule also participates in an intramolecular hydrogen bond to the terminal O atom of a neighbouring diphenylphosphinate ligand, presumably stabilizing the monodentate coordination mode.



Figure 2

A view of the hydrogen bonding in (I) (dashed lines). [Symmetry codes: (i) -x, 2 - y, 1 - z; (ii) -x, 1 - y, 1 - z; (iii) x, y - 1, z.]

Co(O₂PPh₂)₂ was suspended in methanol and pyridine was added dropwise until the blue solid disappeared and the solution was clear light-pink in colour. Red crystals of (I) formed on slow evaporation of the solution.

Crystal data

$[Co_2(C_{12}H_{10}O_2P)_4(C_5H_5N)_4(H_2O)_2]$	Z = 1
$M_r = 1338.97$	$D_x = 1.374 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Mo $K\alpha$ radiation
$a = 10.7871 (4) \text{ \AA}$	Cell parameters from 8177
b = 11.8221 (4) Å	reflections
c = 12.7061 (5) Å	$\theta = 3.0-25.9^{\circ}$
$\alpha = 91.609 \ (2)^{\circ}$	$\mu = 0.67 \text{ mm}^{-1}$
$\beta = 90.390 \ (2)^{\circ}$	T = 294 (2) K
$\gamma = 92.774 \ (2)^{\circ}$	Rectangular plate, red
$V = 1617.77 (10) \text{ Å}^3$	$0.25 \times 0.15 \times 0.07 \text{ mm}$

Data collection

Bruker X8 Kappa-APEX-II CCD	9046 independent reflections
area-detector diffractometer	6553 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.027$
Absorption correction: multi-scan	$\theta_{\rm max} = 29.6^{\circ}$
(SADABS; Bruker, 2004); values	$h = -15 \rightarrow 14$
rescaled by 0.95	$k = -16 \rightarrow 16$
$T_{\min} = 0.745, \ T_{\max} = 0.950$	$l = -17 \rightarrow 15$
30066 measured reflections	

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0464P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.034$	+ 0.0829P]
$wR(F^2) = 0.091$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.06	$(\Delta/\sigma)_{\rm max} = 0.001$
9046 reflections	$\Delta \rho_{\rm max} = 0.36 \text{ e} \text{ \AA}^{-3}$
405 parameters	$\Delta \rho_{\rm min} = -0.34 \text{ e } \text{\AA}^{-3}$
H atoms: see below	

Table 1

Selected geometric parameters (Å, °).

Co1-O1	2.2076 (12)	Co1-Co1 ⁱ	5.0718 (4)
Co1-O11	2.0687 (11)	P1-O11	1.5004 (11)
Co1-O12 ⁱ	2.0615 (10)	P1-O12	1.4944 (11)
Co1-O21	2.0957 (10)	P2-O21	1.5081 (11)
Co1-N11	2.1736 (12)	P2-O22	1.4982 (12)
Co1-N21	2.1740 (12)		
O11-Co1-O12 ⁱ	98.71 (4)	O21-Co1-N21	91.15 (5)
O12 ⁱ -Co1-O21	90.72 (4)	O11-Co1-O1	86.42 (5)
O11-Co1-O21	170.41 (4)	O21-Co1-O1	84.18 (5)
O12 ⁱ -Co1-N11	91.74 (5)	N11-Co1-O1	87.34 (5)
O11-Co1-N11	92.90 (5)	N21-Co1-O1	91.56 (5)
O21-Co1-N11	88.52 (5)	O11-P1-O12	118.11 (6)
O12 ⁱ -Co1-N21	89.33 (5)	O21-P2-O22	117.37 (6)
O11-Co1-N21	87.26 (5)		

Symmetry code: (i) -x, 2 - y, 1 - z.

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

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\begin{array}{c} O1 - H1A \cdots O22 \\ O1 - H1B \cdots O22^{ii} \end{array}$	0.81 (3)	2.02 (3)	2.8072 (18)	163 (3)
	0.93 (2)	1.84 (2)	2.7464 (17)	165 (2)

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

All H atoms on the phenyl and pyridine rings were refined using a riding model, with C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$. The H atoms of the water molecule were found in a difference Fourier map and allowed to refine freely.

Data collection: *COSMO* (Bruker, 2004), *APEX2* (Bruker, 2004) and *BIS* (Bruker, 2004); cell refinement: *SAINT* (Bruker, 2004); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

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