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William Henderson et al. • $[Pd_2(C_7H_4NO_3S)_2(C_{25}H_{22}P_2)_2] \cdot CH_2Cl_2$

metal-organic papers

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Key indicators

Single-crystal X-ray study T = 168 KMean σ (C–C) = 0.004 Å R factor = 0.025 wR factor = 0.068 Data-to-parameter ratio = 16.2

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

Bis[μ -bis(diphenylphosphino)methane- $\kappa^2 P:P'$]bis[(saccharinato- κN)palladium(I)] dichloromethane solvate

The dimeric palladium(I) saccharinate complex $[Pd_2(sac)_2(dppm)_2]$, has been characterized as its dichloromethane solvate, *i.e.* $[Pd_2(C_7H_4NO_3S)_2(C_{25}H_{22}P_2)_2]\cdot CH_2Cl_2$. The complex features a Pd—Pd bond bridged by two dppm ligands, with the saccharinate ligands N-bonded *trans* to the Pd—Pd bond.

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Comment

The structure determination of $[Pd_2(sac)_2(dppm)_2] \cdot CH_2Cl_2$, (I), the first for a Pd^I amidate, shows that the saccharinate ligands have replaced the Cl groups in the starting material. The Pd—Pd distance of 2.5962 (6) Å is comparable to that in other dinuclear Pd^{I} complexes, such as $[Pd_{2}(NO_{3})_{2}(dppm)_{2}]$ (2.594 Å; Maekawa *et al.*, 1998*a*). The $Pd_2(dppm)_2$ core has a twisted-boat conformation, as has been seen in other dinuclear complexes of this type. This twisting occurs in order to allow the dppm ligands to bridge a relatively short Pd-Pd bond (Maekawa et al., 1998b). The P1-Pd1-Pd2-P2 and P3-Pd1-Pd2-P4 torsion angles are both 51.0 (1)°. The planes of the two saccharinate ligands are approximately orthogonal to each of the PdP₂ planes, but are tilted so that the ligand planes make angles of 160 and 155° with the Pd1-N1 and Pd2-N2 vectors, respectively, allowing a degree of pyramidality at the amide N atoms. The two saccharinate ligands have a cisoid arrangement with respect to the Pd-Pd bond. The two Pd-N bonds [average 2.19 (2) Å] are longer than the Pt-N bond (trans to PPh₃) in cis-[PtCl(sac)(PPh₃)₂] [2.064 (6) Å; Henderson et al., 1999], reflecting the high trans influence of the Pd-Pd bond.



Experimental

 $[Pd_2(sac)_2(dppm)_2]$ was isolated in 68% yield from a reaction of $[Pd_2Cl_2(dppm)_2]$ with sodium saccharinate hydrate in refluxing MeOH for 30 min. Crystals, as the dichloromethane solvate, were obtained from CH₂Cl₂-Et₂O solution. ³¹P NMR δ -6.6 p.p.m. Analysis found: C 54.0, H 3.8, N 1.9%; C₆₅H₅₄Cl₂N₂O₆P₄Pd₂S₂ requires: C 54.6, H 3.8, N 2.0%.

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Figure 1

The structure of (I), drawn at the 50% probability level (Farrugia, 1997). The CH_2Cl_2 solvent molecule has been omitted.

Crystal data

$[Pd_2(C_7H_4NO_3S)_2(C_{25}H_{22}P_2)_2]$	$D_x = 1.590 \text{ Mg m}^{-3}$
CH ₂ Cl ₂	Mo $K\alpha$ radiation
$M_r = 1430.80$	Cell parameters from 5200
Monoclinic, $P2_1/n$	reflections
a = 13.819 (4) Å	$\theta = 2-26^{\circ}$
b = 22.550 (7) Å	$\mu = 0.92 \text{ mm}^{-1}$
c = 20.230 (6) Å	T = 168 (2) K
$\beta = 108.53 \ (1)^{\circ}$	Block, orange
$V = 5977 (3) \text{ Å}^3$	$0.55 \times 0.50 \times 0.44 \text{ mm}$
Z = 4	
Data collection	

Siemens CCD diffractometer10 5 ω multi-scans R_{int} Absorption correction: empirical
(Blessing, 1995) θ_{mai} $T_{min} = 0.611, T_{max} = 0.667$ k =74 438 measured reflectionsl =12 130 independent reflectionsl =

10 579 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.026$ $\theta_{\text{max}} = 26.4^{\circ}$ $h = -17 \rightarrow 17$ $k = -28 \rightarrow 27$ $l = -21 \rightarrow 25$ Refinement

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Refinement on F^2

R[F^2 > 2\sigma(F^2)] = 0.025

wR(F^2) = 0.068

S = 1.02

12 130 reflections

748 parameters

H-atom parameters constrained
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$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0324P)^2 \\ &+ 6.6496P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &= 0.002 \\ \Delta\rho_{\text{max}} &= 0.56 \text{ e} \text{ Å}^{-3} \\ \Delta\rho_{\text{min}} &= -0.66 \text{ e} \text{ Å}^{-3} \end{split}$$

H atoms were placed in calculated positions, with U_{iso} 1.2 times that of the carrier C atom, in the riding-model approximation.

Data collection: *SMART* (Siemens, 1994); cell refinement: *SAINT* (Siemens, 1994); data reduction: *SADABS* (Sheldrick, 1996); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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