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Key indicators

Single-crystal X-ray study T = 100 KMean $\sigma(C-C) = 0.002 \text{ Å}$ R factor = 0.037 wR factor = 0.104 Data-to-parameter ratio = 14.8

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

Bis[1,2-bis(p-ethylbenzene)phosphino]benzene

In the solid state, the title compound, $1,2-\{(p-\text{Et-C}_6H_4)_2P\}_2-(C_6H_4)$ or $C_{38}H_{40}P_2$, does not exhibit its molecular $C_{2\nu}$ symmetry. It crystallizes in the space group $P\overline{1}$, with a full molecule in the asymmetric unit.

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Comment

In the course of our work on molybdenum and tungsten complexes with rigid phosphine ligands, we synthesized and isolated the title compound, bis[1,2-bis(p-ethylbenzene)phosphino]benzene, (I). It crystallizes in space group $P\overline{1}$, with Z = 2, and the inversion center is located between the two molecules. The $C_{2\nu}$ symmetry found in solution is lost in the solid state.



The Ar₂P groups are rotated with respect to the plane of the central $P-(C_6H_4)-P$ fragment, resulting in a loss of the C_2 axis and the mirror planes. The torsion angles involving atom



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ellipsoids.

P1 are 96.06 (9) (C1-C6-P1-C21) and -158.86 (8)° (C1-C6-P1-C11), and those involving P2 are 83.75 (9) (C6-C1-P2-C31) and $-173.49(8)^{\circ}$ (C6-C1-P2-C41). The rotation angle of the Ar₂P units from the mirror symmetric position can thus be estimated to be 31.4° for P1 and 44.9° for P2. Atom P1 is nearly perfectly coplanar with the annelated benzene ring. In contrast, atom P2 deviates from the plane formed by the six C atoms by 0.1602 (14) Å. All other bond lengths and angles are in the expected ranges.

Experimental

1,2-Bis(dichlorophosphino)benzene was prepared from 1,2diphosphinobenzene (Kyba et al., 1983) by slow addition of two equivalents of diphosgene (trichloromethylchloroformate) in THF. The temperature was raised to 323 K for 2 h, followed by removal of solvent and distillation in an oil pump vacuum. The title compound was prepared by the reaction of 1,2-bis(dichlorophosphino)benzene with 4.5 equivalents of the Grignard reagent derived from 1-bromo-4ethylbenzene in tetrahydrofuran (THF). After hydrolysis with 10% aqueous ammonium chloride solution, extraction with diethyl ether, washing with water and drying with magnesium sulfate, the compound was crystallized from a THF-diethyl ether mixture at 258 K. This yielded single crystals suitable for X-ray structural analysis.

Crystal data

$C_{38}H_{40}P_2$	Z = 2
$M_r = 558.64$	$D_x = 1.193 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Mo $K\alpha$ radiation
a = 11.0970 (7) Å	Cell parameters from 6
b = 11.6441 (7) Å	reflections
c = 13.5466 (8) Å	$\theta = 2.5 - 28.3^{\circ}$
$\alpha = 69.279 \ (1)^{\circ}$	$\mu = 0.17 \text{ mm}^{-1}$
$\beta = 72.818 \ (1)^{\circ}$	T = 100 (2) K
$\gamma = 89.604 \ (1)^{\circ}$	Block, colorless
$V = 1554.77 (16) \text{ Å}^3$	$0.5 \times 0.5 \times 0.4 \ \text{mm}$
Data collection	

Durley AVC CMADE ADEV CCD	7(07
Bruker AAS SMART APEA CCD	/69/
diffractometer	7138
ω scans	$R_{\text{int}} =$
Absorption correction: multi-scan	θ_{max} :
(SADABS in SAINT-Plus;	h = -
Bruker 1997–1999)	<i>k</i> = -
$T_{\min} = 0.919, \ T_{\max} = 0.936$	l = -
16 351 measured reflections	

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$ $wR(F^2) = 0.104$ S=1.057697 reflections 521 parameters All H-atom parameters refined 5851

7697 independent reflections
7138 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.021$
$\theta_{\rm max} = 28.3^{\circ}$
$h = -14 \rightarrow 14$
$k = -15 \rightarrow 15$
$l = -18 \rightarrow 18$

$w = 1/[\sigma^2(F_o^2) + (0.0698P)^2]$
+ 0.6662P]
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.002$
$\Delta \rho_{\rm max} = 0.44 \ {\rm e} \ {\rm \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.27 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

P2-C41	1.8322 (10)	C1-C2	1.3994 (14)
P2-C31	1.8359 (11)	C1-C6	1.4126 (14)
P2-C1	1.8478 (10)	C2-C3	1.3920 (15)
P1-C21	1.8316 (11)	C6-C5	1.3960 (15)
P1-C11	1.8331 (11)	C5-C4	1.3932 (15)
P1-C6	1.8436 (11)	C4-C3	1.3875 (16)
$C^{2}-C^{1}-C^{6}$	118 54 (9)	C5 - C6 - P1	121 71 (8)
$C_2 - C_1 - P_2$	123.08 (8)	C1 - C6 - P1	11874(8)
C6-C1-P2	118.16 (8)	C4 - C5 - C6	121.06 (10)
C3-C2-C1	121.33 (10)	C3-C4-C5	119.59 (10)
C5-C6-C1	119.55 (9)	C4-C3-C2	119.92 (10)
C6-C1-C2-C3	0.42 (15)	C1-C6-C5-C4	-0.77 (16)
P2-C1-C2-C3	-174.09(8)	P1-C6-C5-C4	178.46 (8)
C2-C1-C6-C5	-0.01(15)	C6-C5-C4-C3	1.15 (17)
P2-C1-C6-C5	174.77 (8)	C5-C4-C3-C2	-0.74(17)
C2-C1-C6-P1	-179.27(8)	C1-C2-C3-C4	-0.05(16)
P2-C1-C6-P1	-4.49 (11)		()

All H atoms were located in a difference Fourier map and were refined isotropically. The C-H bond lengths are in the ranges 0.928 (16)-0.990 (17) Å (aliphatic) and 0.947 (19)-1.035 (18) Å (aromatic). The s.u. values of the cell parameters are taken from the software, recognizing that the values are unreasonably small (Herbstein, 2000).

Data collection: SMART for Windows NT/2000 (Bruker 1997-2000); cell refinement: SAINT-Plus (Bruker, 1997-1999); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXL97; software used to prepare material for publication: SHELXL97.

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