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Key indicators

Single-crystal X-ray study T = 294 KMean $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$ R factor = 0.050 wR factor = 0.143 Data-to-parameter ratio = 17.4

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

4-(4,4-Diphenylbuta-1,3-dienyl)-*N*,*N*-bis(4-methyl-phenyl)aniline

The title compound, $C_{36}H_{31}N$, was synthesized by the Wittig reaction of 1,1-diphenyl-3-cholopropylene and 4-[N,N-bis(4-methylphenyl)amino]benzaldehyde. The butadiene structure has a planar transoid conformation.

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Comment

Hole transporting materials (HTMs) play an important role in the fabrication of organic photoconductors (OPCs), which are widely used in xerography and holography (Wu *et al.*, 2005). Substances containing the butadiene structure have been widely investigated, because of their easy preparation by the Wittig reaction and favorable photographic performances when used as HTMs (Enokida & Hirohashi, 1991).



The title compound, (I), was synthesized by the Wittig reaction of 1,1-diphenyl-3-cholopropylene and 4-[*N*,*N*-bis(4-methylphenyl)]aminobenzaldehyde.

Fig. 1 shows the molecular structure of (I). The butadiene structure (C1/C14–C16) is almost planar to within 0.03 Å and





The molecular structure of (I), with the atom numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

organic papers

has a transoid conformation. The dihedral angles between the butadiene plane and the *A*, *B* and *C* ring planes are 53.0 (3), 40.3 (2) and 7.3 (2)°, respectively. On the other hand, the dihedral angles between the benzene rings, C/D = 64.3 (2)° and C/E = 64.4 (2)°, are essentially the same. The C1–C8 [1.477 (3) Å] and C1–C2 [1.489 (3) Å] bond distances are a little longer than C16–C17 [1.451 (3) Å], while the N1–C20 [1.410 (3) Å], N1–C23 [1.422 (3) Å] and N1–C30 [1.418 (3) Å] bond lengths are essentially the same.

Experimental

A mixture of 1,1-diphenyl-3-chloropropylene (11.4 g, 50 mmol), triethyl phosphite (18.0 ml, 50 mmol) and xylene (50 ml) was refluxed for 10 h, and then xylene was removed *in vacuo* to obtain a residue. After cooling, the residue, 4-[N,N-bis(4-methylphenyl)]aminobenzaldehyde (12.0 g, 40 mmol), dimethylformamide (100 ml) and potassium *tert*-butoxide (4.5 g, 40 mmol) were placed in a flask. The resulting mixture was stirred for 5 h and poured into methanol, and the resulting precipitate was separated from the liquid by filtration to obtain crude crystals. These were purified by silica gel column chromatography [eluant: toluene/ethyl acetate (2:1)], recrystallized from hexane and dried to obtain yellow crystals (yield 58.7%, m.p. 433 K).

Crystal data

$C_{36}H_{31}N$ $M_r = 477.62$ Orthorhombic, <i>Pbca</i> a = 16.629 (2) Å b = 14.9729 (19) Å c = 22.899 (3) Å V = 5701.3 (13) Å ³ Z = 8 $D_x = 1.113$ Mg m ⁻³	Mo K α radiation Cell parameters from 4038 reflections $\theta = 2.5-20.6^{\circ}$ $\mu = 0.06 \text{ mm}^{-1}$ T = 294 (2) K Block, yellow $0.24 \times 0.16 \times 0.14 \text{ mm}$
Data collection Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 1997) $T_{min} = 0.975, T_{max} = 0.991$ 30699 measured reflections	5830 independent reflections 2710 reflections with $I > 2\sigma(I)$ $R_{int} = 0.071$ $\theta_{max} = 26.4^{\circ}$ $h = -16 \rightarrow 20$ $k = -18 \rightarrow 18$ $l = -28 \rightarrow 25$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0558P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.050$	+ 0.4918P]
$wR(F^2) = 0.143$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.01	$(\Delta/\sigma)_{\rm max} = 0.005$
5830 reflections	$\Delta \rho_{\rm max} = 0.17 \ {\rm e} \ {\rm \AA}^{-3}$
336 parameters	$\Delta \rho_{\rm min} = -0.15 \text{ e} \text{ \AA}^{-3}$
H-atom parameters constrained	

H atoms were positioned geometrically [0.93 (CH) and 0.96 Å (CH₃)] and constrained to ride on their parent atoms, with $U_{iso}(H) = 1.2U_{eq}(C_{CH})$ and $1.5U_{eq}(C_{CH3})$.



Figure 2 Packing diagram of (I).

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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