

2,3,3',4'-Tetramethylbiphenyl

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Key indicators

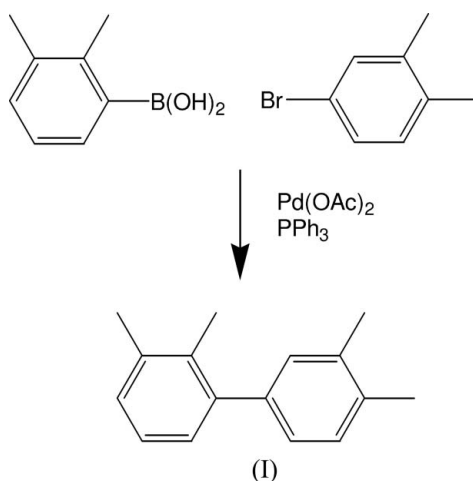
Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$
 R factor = 0.049
 wR factor = 0.127
Data-to-parameter ratio = 18.0For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

2,3,3',4'-Tetramethylbiphenyl, $\text{C}_{16}\text{H}_{18}$, was synthesized in a palladium-catalysed boronic acid cross-coupling reaction. In the solid state, these weakly interacting unsymmetrical molecules show an apparent dimerization of the *ortho*-dimethylphenyl groups, a packing motif that is seen in a significant number of other *ortho*-dimethylphenyl-containing compounds.

Received 1 July 2005
Accepted 13 July 2005
Online 20 July 2005

Comment

2,3,3',4'-Tetramethylbiphenyl, (I), has been reported previously as a minor product in an oxidative coupling reaction (Norman *et al.*, 1973). We obtained (I) in excellent yield using a Suzuki cross-coupling reaction (Miyaura, 2002). The unsymmetrical molecules of this compound crystallize in the space group $P\bar{1}$ with an asymmetric unit consisting of a single molecule (Fig. 1). All bond distances and angles in the molecule are normal. The two benzene rings are twisted by $54.10(7)^\circ$ from coplanarity. The molecule adopts a *cis* conformation in the solid, with all the methyl groups to one side of the biphenyl rings.



Overall, the packing of these unsymmetrical molecules is complex and not easily visualized. However, one intermolecular motif does stand out; the *ortho*-dimethylphenyl groups appear to show a certain self-complementarity. Examination of all the intermolecular contacts reveals that the shortest intermolecular $\text{C}\cdots\text{C}$ ($\sim 3.7\text{ \AA}$) and $\text{C}-\text{H}\cdots\text{aryl } \pi$ interactions are associated with this motif (Fig. 2). Both *ortho*-dimethylphenyl rings show this interaction, and both have an inversion centre between the interacting molecules. The orientation of each methyl group is such that one of the H atoms is directed to the midpoint of an aryl $\text{C}=\text{C}$ bond. This looks like a weak hydrogen-bonding interaction. An exam-

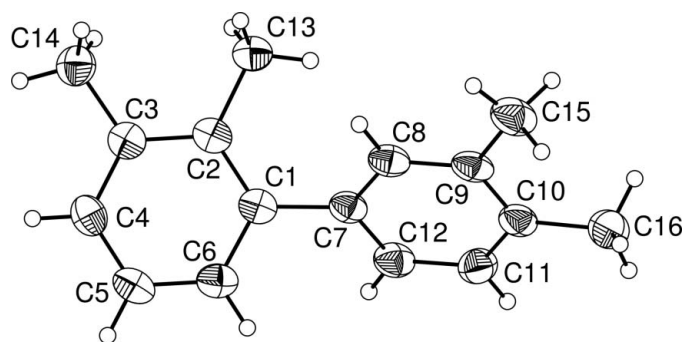


Figure 1

The molecular structure of (I). Displacement ellipsoids are shown at the 70% probability level.

ination of the Cambridge Structural Database (Version 5.26; Allen, 2002) was performed to estimate the significance of this motif. We find that 19% of *ortho*-dimethylaryl-containing compounds appear to show this motif, having the six C···C intermolecular interactions shown in Fig. 2 shorter than 4 Å. Analysis of the distribution of torsion angles that correspond to C2–C3–C14–H14A and C3–C2–C13–H13B in (I) was performed on 198 structures showing this interaction (group 1), and for the remaining 848 structures that do not (group 2). Although the location of H atoms in X-ray crystallography is often problematic, it is common practice to refine this angle even when all else is constrained. Thus, we believe this analysis to be meaningful. Both groups of compounds show peaks in the histograms at 0, 30 and 60°, with an anomalous spike superimposed on a more normal distribution of the peak at 60°, and no statistically significant difference is seen in the distribution of methyl group orientations between these two groups (Fig. 3).

These results suggest that the interaction is not greatly affected by the –CH₃ orientation. They do not exclude the idea that a very weak hydrogen-bonding interaction may exist here. It must also be realised that, in the group 2 structures, other interaction motifs and geometries may give rise to the extra stability of the ~60° methyl group torsion angle.

Experimental

A mixture of 3,4-dimethylbromobenzene (4.400 g, 23.75 mmol), 2,3-dimethylphenylboronic acid (4.279 g, 28.55 mmol), palladium(II) acetate (0.1334 g, 0.595 mmol), triphenylphosphine (0.3889 g, 1.486 mmol), sodium(I) carbonate (5.083 g, 47.55 mmol), acetonitrile (30 ml) and water (30 ml) was heated to reflux for 24 h under an inert nitrogen atmosphere. The mixture was acidified with dilute HCl to remove the carbonate ions. The reaction mixture was then filtered, and the solvent removed on a rotary evaporator. Distilled water (30 ml) was then added, and the organic product extracted into dichloromethane (3 × 30 ml). The combined organic extracts were dried over anhydrous MgSO₄, filtered and the solvent removed under reduced pressure. The crude product was recrystallized from ethanol (3.856 g, 77.1%). C₁₆H₁₈ requires C 91.37, H 8.63%; found C 91.23, H 8.62%. ¹³C NMR (400 MHz, CDCl₃): δ 142.25 (C1), 140.10 (C7), 137.09 (C3 or C9), 136.09 (C9 or C3), 134.84 (C10), 134.03 (C2), 130.66 (C11), 129.21 (C4), 128.58 (C8), 127.71 (C5), 126.80 (C6 or

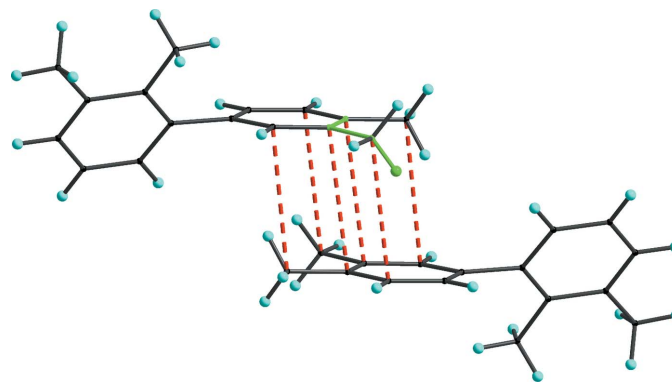


Figure 2

The motif showing the shortest intermolecular interactions in (I). The key C···C distances are shown in red, and one of the four C–C–C–H torsion angles is shown in green.

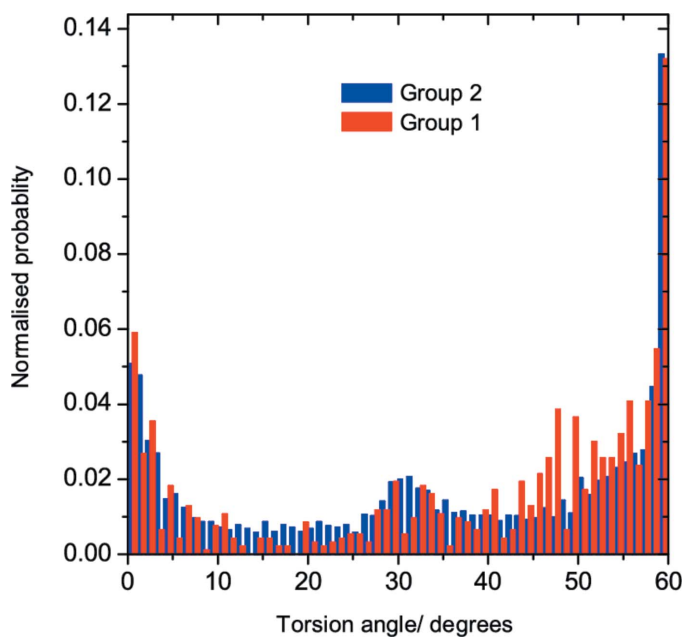


Figure 3

A plot of the distribution of C–C–C–H torsion angles for *ortho*-dimethylphenyl-containing compounds which appear to show this type of interaction (group 1: red) and for the group of *ortho*-dimethylphenyl that do not (group 2: blue). Data taken from 1046 structures in the Cambridge Structural Database.

C12), 125.15 (C12 or C6), 20.73 (CH₃), 19.86 (CH₃), 19.48 (CH₃), 17.02 (CH₃); *m/z* 210.11 [*M*] (ESMS+); *m/z* 210.1408 [¹²C₁₆⁴H₁₈] (high resolution ESMS+); IR *v*/cm⁻¹ (KBr): 3160, 3038, 3018, 2995, 2985, 2943, 2920, 2882, 2860, 1502, 1463, 1455, 1380, 1308, 1278, 1243, 1221, 1197, 1180, 1163, 1136, 1110, 1083, 1061, 1045, 1020, 985, 965, 921, 898, 891, 820, 780, 758, 746, 720, 642, 600.

Crystal data

C₁₆H₁₈
M_r = 210.30
 Triclinic, *P* $\bar{1}$
a = 7.6018 (5) Å
b = 7.7685 (5) Å
c = 11.6547 (7) Å
 α = 77.106 (3)°
 β = 81.047 (3)°
 γ = 64.506 (3)°
V = 604.19 (7) Å³

Z = 2
D_x = 1.156 Mg m⁻³
 Mo *K*α radiation
 Cell parameters from 4912 reflections
 θ = 0.1–27.5°
 μ = 0.07 mm⁻¹
T = 293 (2) K
 Prism, colourless
 0.45 × 0.16 × 0.14 mm

Data collection

Nonius KappaCCD diffractometer ω and φ scans	1819 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (Blessing, 1995)	$R_{\text{int}} = 0.056$
$T_{\text{min}} = 0.830$, $T_{\text{max}} = 0.991$	$\theta_{\text{max}} = 27.4^\circ$
9018 measured reflections	$h = -9 \rightarrow 9$
2731 independent reflections	$k = -10 \rightarrow 9$
	$l = -15 \rightarrow 15$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0567P)^2$
$R[F^2 > 2\sigma(F^2)] = 0.049$	$+ 0.0932P]$
$wR(F^2) = 0.127$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 1.04$	$(\Delta/\sigma)_{\text{max}} < 0.001$
2731 reflections	$\Delta\rho_{\text{max}} = 0.28 \text{ e } \text{\AA}^{-3}$
152 parameters	$\Delta\rho_{\text{min}} = -0.21 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	Extinction correction: <i>SHELXL97</i>
	Extinction coefficient: 0.038 (9)

Aryl H atoms were placed in ideal positions (C–H = 0.93 Å) and treated as riding, with a common refined $U_{\text{iso}} = 0.0259$ (17) Å². Methyl H atoms were constrained in rigid groups with free rotation about the C–C bond (C–H = 0.96 Å) and a common refined $U_{\text{iso}} = 0.0388$ (14) Å².

Data collection: *COLLECT* (Nonius, 1997); cell refinement: *DENZO/SCALEPACK* (Otwinowski & Minor, 1997); data reduc-

tion: *DENZO/SCALEPACK*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 1999); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

The authors are grateful to Dr Andrew Parkin (Glasgow University) for the X-ray data collection.

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