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Key indicators

Single-crystal X-ray study T = 120 KMean σ (C–C) = 0.002 Å R factor = 0.047 wR factor = 0.140 Data-to-parameter ratio = 21.7

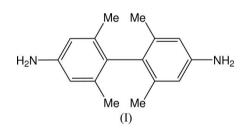
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. Each of the three independent molecules of the title compound, $C_{16}H_{20}N_2$, has near-perpendicular benzene rings and pyramidal N atoms. Hydrogen bonding in the structure is rather inefficient.

4,4'-Diamino-2,2',6,6'-tetramethylbiphenyl

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Comment

Benzidine derivatives are now widely used in the solid state as hole-injecting and transport materials in applications ranging from the Xerox process to organic light-emitting diodes (OLEDs) (Thelakkat, 2002). As noted by Shankland *et al.* (2005), the solid-state structures of these materials are of more than simply crystallographic interest, with the physical structure playing a critical role in determining the mechanism and energetics of the charge transport process. In the course of a wider study of tetra(aryl)benzidines (Littleford *et al.*, 2004; Low, Paterson, Goeta *et al.*, 2004; Low, Paterson, Puschmann *et al.*, 2004; Low *et al.*, 2005) we have determined the structure of 4,4'-diamino-2,2',6,6'-tetramethylbiphenyl, (I), reported here.



The asymmetric unit of (I) comprises three molecules (Fig. 1), which adopt twisted conformations due to steric repulsion between methyl groups. The intramolecular dihedral angle between benzene rings is 84.51 (4), 86.38 (3) and 80.46 (4)°, similar to 86° in *m*-toluidine (Fowweather, 1952), 86° in 2,2′,6,6′-tetra(mercapto)-4,4-diaminobiphenyl and 90° in 2,2′,6,6′-tetra(ethylthio)-4,4-diaminobiphenyl (Zhu-Ohlbach *et al.*, 1998). The unsubstituted benzidine molecule (in various cocrystals) was found to be either planar (Ermer & Eling, 1994) or twisted by *ca* 40° (Giastas *et al.*, 2003).

All N atoms in (I) have substantially pyramidal geometry with a mean bond angle of 113 (1)°, and are nearly coplanar with the attached rings, except atoms N1 and N4, which are displaced from these planes by 0.102 (2) and 0.129 (2) Å, respectively. The degree of pyramidalization is similar to that observed in solid aniline (Fukuyo *et al.*, 1982); the mean N–C bond distance of 1.410 (3) Å in (I) is marginally longer than in aniline [1.392 (6) Å].

The most peculiar feature of the structure is the inefficiency of hydrogen bonding. While the asymmetric unit contains 12

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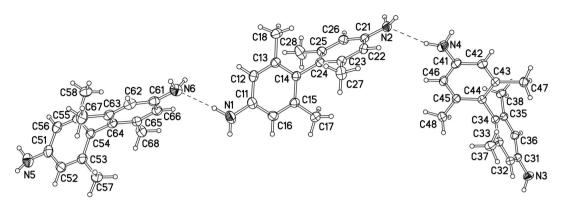


Figure 1

The asymmetric unit of (I), showing atomic displacement ellipsoids at the 50% probability level. Dashed lines represent hydrogen bonds.

polar H atoms and six potential acceptor sites (nitrogen lone pairs), there are only four definite $N-H\cdots N$ hydrogen bonds (Table 2). The N2-H2A bond points towards the centroid, X, of the C41-C46 benzene ring at the symmetry position (-x, 1 - y, -z) [$H \cdots X = 2.49$ (2) Å and $N-H \cdots X = 173$ (2)°], and the N2-H2B bond towards the C36 atom generated by the translation (x + 1, y, z) [$H \cdots C = 2.745$ (18) Å and $N-H \cdots C = 150.4$ (14)°]. The latter two contacts may be regarded as weak hydrogen bonds (Desiraju & Steiner, 1999). The remaining amino atoms H1B, H3A, H4B, H5A, H5B and H6A form no hydrogen bonds of any kind, contacting only with methyl- or phenyl-group H atoms. Probably, the rigidity of the molecular rods prevents more efficient hydrogen bonding.

Experimental

Compound (I) was prepared according to Carlin (1945) and recrystallized from benzene and hexane (1:1).

Crystal data

 $C_{16}H_{20}N_2$ $M_r = 240.34$ Monoclinic, $P2_1/c$ a = 11.393 (2) Å b = 16.523 (3) Å c = 22.487 (3) Å $\beta = 99.96 (1)^\circ$ $V = 4169.3 (12) Å^3$

Data collection

Bruker SMART 6K CCD areadetector diffractometer ω scans Absorption correction: none 76630 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.047$ $wR(F^2) = 0.140$ S = 1.0212148 reflections 559 parameters H atoms treated by a mixture of independent and constrained refinement Z = 12 $D_x = 1.149 \text{ Mg m}^{-3}$ Mo K α radiation $\mu = 0.07 \text{ mm}^{-1}$ T = 120 (2) K Prism, pale brown $0.50 \times 0.43 \times 0.35 \text{ mm}$

12148 independent reflections 9388 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.032$ $\theta_{\text{max}} = 30.0^{\circ}$

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.078P)^2 \\ &+ 1.0547P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &= 0.001 \\ \Delta\rho_{\text{max}} &= 0.39 \text{ e } \text{ Å}^{-3} \\ \Delta\rho_{\text{min}} &= -0.19 \text{ e } \text{ Å}^{-3} \end{split}$$

Table 1

Selected bond lengths (Å).

| N1-C11 | 1.4101 (16) | N6-C61 | 1.4097 (16) |
|--------|-------------|---------|-------------|
| N2-C21 | 1.4120 (15) | C14-C24 | 1.5002 (15) |
| N3-C31 | 1.4091 (14) | C34-C44 | 1.4974 (14) |
| N4-C41 | 1.4055 (14) | C54-C64 | 1.4970 (16) |
| N5-C51 | 1.4141 (17) | | |

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

| $D - H \cdot \cdot \cdot A$ | D-H | $H \cdots A$ | $D \cdots A$ | $D - \mathbf{H} \cdots A$ |
|---|------------|--------------|--------------|---------------------------|
| $\begin{array}{l} \text{N1}-\text{H1}A\cdots\text{N6}\\ \text{N2}-\text{H2}B\cdots\text{C36}^{\text{i}}\\ \text{N3}-\text{H3}B\cdots\text{N4}^{\text{ii}}\\ \text{N4}-\text{H4}A\cdots\text{N2}\\ \text{N6}-\text{H6}B\cdots\text{N3}^{\text{iii}}\\ \end{array}$ | 0.95 (2) | 2.18 (2) | 3.1291 (19) | 175.1 (16) |
| | 0.915 (18) | 2.745 (18) | 3.5699 (17) | 150.4 (14) |
| | 0.901 (19) | 2.426 (19) | 3.3052 (18) | 165.1 (15) |
| | 0.93 (2) | 2.31 (2) | 3.1585 (16) | 150.3 (16) |
| | 0.931 (19) | 2.19 (2) | 3.1035 (18) | 168.9 (16) |

Symmetry codes: (i) x + 1, y, z; (ii) x - 1, y, z; (iii) $-x, y + \frac{1}{2}, -z + \frac{1}{2}$.

Amino H atoms were located in a difference map and were refined isotropically [N-H = 0.86 (2)-0.95 (3) Å]. Methyl groups were refined as rigid bodies [C-H = 0.98 Å] rotating around the C-C bonds, with a common refined U_{iso} value for the three H atoms; the benzene H atoms were treated as riding on the C atoms [C-H = 0.95 Å] and $U_{iso}(H) = 1.2U_{eq}(C)]$.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Bruker, 2001); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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