organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.003 \text{ Å}$ R factor = 0.047 wR factor = 0.136 Data-to-parameter ratio = 12.1

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

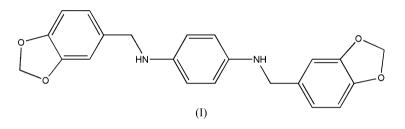
ene]phenylene-1,4-diamine

N,N'-Bis[(3,4-methylenedioxyphenyl)methyl-

In the title compound, $C_{22}H_{20}N_2O_4$, the molecule is centrosymmetric. The molecules are linked by one $C-H\cdots O$ and one $C-H\cdots \pi$ interaction into an [001] chain of $R_2^2(30)$ rings and an [010] chain of $R_2^2(22)$ rings.

Comment

As part of our study of diamine compounds, in this paper we describe the crystal structure of the title compound, (I).



The molecule of (I) (Fig. 1), is disposed about a centre of symmetry at $(\frac{1}{2}, \frac{1}{2}, \frac{1}{2})$. The angle N1-C4-C5 is 113.8 (2)°, and the dihedral angle between the 3,4-methylenedioxyphenyl ring and the benzene ring C1-C3/C1A-C3A is 78.73 (7)°.

In the crystal structure of (I), $C-H\cdots O$ interactions link the molecules into a chain of $R_2^2(30)$ rings (Bernstein *et al.*, 1995) running parallel to the [001] direction (Fig. 2, Table 1). The molecules are further linked by $C-H\cdots \pi$ interactions $[C4\cdots Cg1^{ii} = 3.94 \text{ Å}$ and $C4-H4\cdots Cg1^{ii} = 136^\circ$, where Cg1 is the centroid of ring C5–C10; symmetry code: (ii) x, 1 + y, z] (Fig. 3), and the propagation by inversion of this hydrogen bond generates a chain of $R_2^2(22)$ rings (García-Báez *et al.*, 2002) running parallel to the [010] direction (Fig. 3). The combination of the [001] chain and the [010] chain generates a (100) sheet. Neighbouring sheets are connected by van der Waals forces, resulting in a three-dimensional network structure.

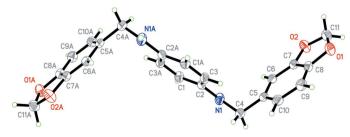


Figure 1

The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level. [Symmetry code: (A) 1 - x, 1 - y, 1 - z.]

Received 28 November 2006 Accepted 6 December 2006

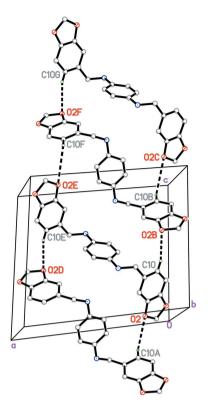


Figure 2

A view of part of the crystal structure of (I), showing the formation of a chain of $R_2^2(30)$ rings along the [001] direction. Displacement ellipsoids are drawn at the 30% probability level. For clarity, H atoms not involved in the motif shown have been omitted [symmetry codes: (A) $x, \frac{3}{2} - y$, $\frac{-\frac{1}{2}+z; (B) x, \frac{3}{2}-y, \frac{1}{2}+z; (C) x, y, 1+z; (D) 1+x, -\frac{3}{2}+y, \frac{1}{2}-z; (E) 1-x, 1-y, 1-z; (F) 1+x, -\frac{3}{2}+y, \frac{3}{2}-z; (G) 1-x, 1-y, 2-z]. Dashed lines$ indicate hydrogen bonds.

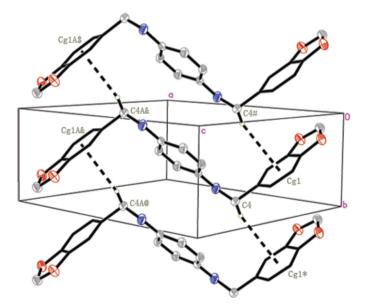


Figure 3

A view of part of the crystal structure of (I), showing the formation of the the [010] chain of $R_2^2(22)$ rings linked by C-H··· π interactions. Displacement ellipsoids are drawn at the 30% probability level. For clarity, bonds on ring C5-C10 are shown as thin lines and H atoms not involved in the motif shown have been omitted [symmetry codes: (*) x, 1 + y, z; (#) x, -1 + y, z; (&) 1 - x, 1 - y, 1 - z; (\$) 1 - x, -y, 1 - z; (@)1 - x, -1 - y, 1 - z]. Dashed lines indicate hydrogen bonds.

Experimental

A mixture of N,N'-bis(3,4-methylenedioxybenzyl)phenylene-1,4diamine (3.72 g, 10 mmol) and sodium borohydride (1.52 g, 40 mmol) was refluxed for about 2 h in ethanol (50 ml). The mixture was cooled, and the product filtered off, washed with ethanol and dried. Yellow crystals of (I) suitable for X-ray structure analysis were obtained by recrystallizing the crude product from ethanol (m.p. 453-455 K).

Z = 2

 $D_x = 1.425 \text{ Mg m}^{-3}$

 $0.50 \times 0.41 \times 0.13~\mathrm{mm}$

4222 measured reflections

1532 independent reflections 1037 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.10 \text{ mm}^-$

T = 298 (2) K

Plate, yellow

 $R_{\rm int} = 0.041$ $\theta_{\rm max} = 25.0^{\circ}$

Crystal data

 $C_{22}H_{20}N_2O_4$ $M_r = 376.40$ Monoclinic, $P2_1/c$ a = 14.2255 (14) Å b = 4.9257 (16) Å c = 12.7837 (18) Å $\beta = 101.624 (3)^{\circ}$ V = 877.4 (3) Å³

Data collection

Siemens SMART 1000 CCD areadetector diffractometer and a scans Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{\min} = 0.952, T_{\max} = 0.987$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.067P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.047$	+ 0.1742P]
$wR(F^2) = 0.136$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.02	$(\Delta/\sigma)_{\rm max} < 0.001$
1532 reflections	$\Delta \rho_{\rm max} = 0.30 \text{ e } \text{\AA}^{-3}$
127 parameters	$\Delta \rho_{\rm min} = -0.24 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1			
Hydrogen-bond	geometry	(Å,	°).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\overline{C10{-}H10{\cdot}\cdot{\cdot}O2^{i}}$	0.93	2.76	3.657 (3)	162
Symmetry code: (i) x,	$-v + \frac{3}{2}, z + \frac{1}{2}$			

Sym (1) $x, -y + \frac{3}{2}$

All H atoms were positioned geometrically and refined as riding on their parent atoms, with N-H = 0.86 Å and $U_{iso}(H) = 1.2U_{eq}(N)$ for amino H atoms, and C-H = 0.93–0.97 Å and $U_{iso}(H) = 1.2U_{eq}(C)$ for all other H atoms.

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

We acknowledge the financial support of the Huaihai Institute of Technology Science Foundation.

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