Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 292 KMean σ (C–C) = 0.002 Å R factor = 0.055 wR factor = 0.159 Data-to-parameter ratio = 18.0

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

4,4'-Dimethyl-2,2'-(N-methyliminodimethylene)diphenol

In the title compound, $C_{17}H_{21}NO_2$, the dihedral angle between the benzene rings is 49.8 (3)°. In the crystal structure, the molecules form layers parallel to the *ac* plane which are stacked along the *b* axis and which are stabilized by $O-H\cdots O$ and $C-H\cdots O$ hydrogen-bonding interactions. Received 12 June 2006 Accepted 15 June 2006

Comment

The chemistry of Mannich bases has been the subject of investigations by an ever increasing number of researchers because of their wide applications (Arend *et al.*, 1998). However, the synthesis of an N,N-bis(5-substituent-2-hydroxybenzyl)amine from a *p*-substituted phenol by the Mannich reaction has not been reported. We have recently synthesized the title compound, (I), by reaction of 4-methylphenol, formaldehyde and methylamine, and its crystal structure is reported here.



In the molecule (Fig. 1), the two benzene rings are inclined with respect to each other with a dihedral angle of 49.8 (3)°. The C6-C1-C8-N1 and N1-C10-C11-C16 torsion angles are -45.55 (19) and 66.4 (18)°, respectively, showing that the aminomethyl group is not coplanar with either of the benzene rings.

The structure consists of layers of molecules, stacked along the b axis, stabilized by two intermolecular hydrogen-bonding interactions (Fig. 2 and Table 2).



Figure 1

View of the molecular structure of (I), showing the atom-labeling scheme and displacement ellipsoids are drawn at the 50% probability level. Hydrogen bonds are shown as dashed lines.

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Experimental

Formaldehyde (8 ml, 40%, 0.1 mol) was added slowly with stirring to a mixture of methanol (35 ml), methylamine (6.5 ml, 25–30%, 0.05 mol) and 4-methylphenol (10.9 g, 0.1 mol) over a period of 3 h. The mixture was stirred for an additional 60 h at room temperature. The resulting bright-yellow solid was filtered off and washed with methanol. The solid residue was recrystallized twice from ethyl acetate–petroleum ether (1:5 v/v) to give colorless crystals of (I) in 63% yield (m.p. 325 K), which were suitable for X-ray analysis. MS (EI, 70 eV) m/z(%): 272 (100).

> V = 775.2 (2) Å³ Z = 2

 $D_x = 1.163 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation $\mu = 0.08 \text{ mm}^{-1}$ T = 292 (2) KBlock, colorless

 $0.30 \times 0.20 \times 0.20 \mbox{ mm}$

7457 measured reflections 3416 independent reflections 2423 reflections with $I > 2\sigma(I)$

H atoms treated by a mixture of

 $w = 1/[\sigma^2(F_o^2) + (0.0876P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

independent and constrained

 $R_{\rm int}=0.057$

 $\theta_{\rm max} = 27.3^\circ$

refinement

 $(\Delta/\sigma)_{\rm max} = 0.002$ $\Delta \rho_{\rm max} = 0.20 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.22 \text{ e } \text{\AA}^{-3}$

Crystal data

$C_{17}H_{21}NO_2$
$M_r = 271.35$
Triclinic, P1
a = 5.8024 (9) Å
b = 10.8867 (17) Å
c = 12.5346 (19) Å
$\alpha = 93.980 \ (3)^{\circ}$
$\beta = 90.847 (3)^{\circ}$
$\gamma = 100.955 (3)^{\circ}$

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 2001)
$T_{\min} = 0.978, T_{\max} = 0.985$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.055$ $wR(F^2) = 0.159$ S = 1.023416 reflections 190 parameters

Table 1

Selected torsion angles (°).

C2-C1-C8-N1	135.25 (15)	N1-C10-C11-C12	-112.58(15)
C6-C1-C8-N1	-45.55 (19)	N1-C10-C11-C16	66.44 (18)

Table	2
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Hydrogen-bond ge	ometry (Å, °).
Hydrogen-bond ge	ometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
O1-H1···N1	0.829 (9)	1.898 (13)	2.6594 (15)	152 (2)
O1-H1··· $O2$	0.829 (9)	2.474 (19)	2.9910 (17)	121.4 (18)
$C8-H8A\cdots O2^{i}$	0.97	2.57	3.540 (2)	173
$O2-H2A\cdots O1^{ii}$	0.834 (9)	1.881 (10)	2.7065 (15)	170 (2)

Symmetry codes: (i) -x + 1, -y + 1, -z + 1; (ii) -x, -y + 1, -z + 1.



Figure 2

The crystal packing of (I), viewed down the *b* axis. Intermolecular hydrogen bonds are shown as dashed lines. H atoms not involved in hydrogen bonding have been omitted.

All C-bound H atoms were placed in calculated positions and treated as riding atoms (C–H = 0.93–0.97 Å), with U_{iso} (H) set equal to 1.5 (methyl H atoms) or 1.2 (other H) times U_{eq} (C). The positions of O-bound H atoms were refined freely $[U_{iso}(H) = 1.5U_{eq}(O)]$.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT-Plus* (Bruker, 2001); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *PLATON*.

We gratefully acknowledge financial support of this work under the Plan of Group of Young Scientist Innovation Foundation of Hubei Province under grant No. 2004 T006.

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