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Shu-Ping Yang,^a* Li-Jun Han,^b Da-Qi Wang^c and Tie-Zhu Ding^d

^aDepartment of Chemical Engineering, Huaihai Institute of Technology, Lianyungang 222005, People's Republic of China, ^bDepartment of Mathematics and Science, Huaihai Institute of Technology, Lianyungang 222005, People's Republic of China, ^cCollege of Chemistry and Chemical Engineering, Liaocheng University, Shandong 252059, People's Republic of China, and ^dDepartment of Physics, Inner Mongolia University, Hohhot 010021, People's Republic of China

Correspondence e-mail: yangshuping@hhit.edu.cn

Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.004 Å R factor = 0.045 wR factor = 0.073 Data-to-parameter ratio = 14.1

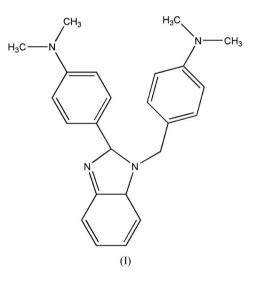
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

© 2007 International Union of Crystallography All rights reserved 2-[4-(Dimethylamino)phenyl]-1-{[4-(dimethylamino)phenyl]methyl}-1*H*-benzimidazole

Molecules of the title compound, $C_{24}H_{26}N_4$, are linked by C– H···N hydrogen bonds, forming a C(5) chain along the [010] direction. Neighboring chains are connected by four C– H··· π interactions, resulting in the formation of a threedimensional network.

Comment

The title compound, (I), was obtained unexpectedly in the condensation reaction between 4-dimethylaminobenzaldehyde and *o*-phenylenediamine. Benzimidazole derivatives display wide-ranging biological activities, for example as inhibitors of hepatitis C virus NS5B polymerase (Ishida *et al.*, 2006) and heparanase (Xu *et al.*, 2006), and antimicrobial activities (Özden *et al.*, 2005). Here we report the crystal structure of (I).



In the molecule of compound (I) (Fig. 1), the dihedral angles between the benzimidazole ring system and benzene rings C9–C14 and C17–C22 are 88.02 (6)° and 26.44 (8)°, respectively. The geometric parameters for (I) are normal.

In the crystal structure of (I), the molecules are linked through C-H···N hydrogen bonds, forming a C(5) chain (Bernstein *et al.*, 1995) along the [010] direction (Fig. 2 and Table 1). Neighboring chains are connected by four C-H··· π interactions [C6···Cg2ⁱ = 3.641 (5) Å, C6-H6···Cg2ⁱ = 173°; C15···Cg2ⁱⁱ = 3.942 (5) Å, C15-H15a···Cg2ⁱⁱ = 159°; C16···Cg1ⁱⁱⁱ = 3.912 (3) Å, C16-H16b···Cg1ⁱⁱⁱ = 164°; C19···Cg1^{iv} = 3.840 (3) Å, C19-H19···Cg1^{iv} = 155°, where Cg1 is the centroid of the ring C2-C7 and Cg2 is the centroid of the ring C9-C14. Symmetry codes: (i) $x, \frac{3}{2} - y, \frac{1}{2} + z$; (ii) 1 - x, -1 - y, -z; (iii) 1 - x, -y, -z; (iv) $x, \frac{3}{2} - y, -\frac{1}{2} + z$] (Fig.3),

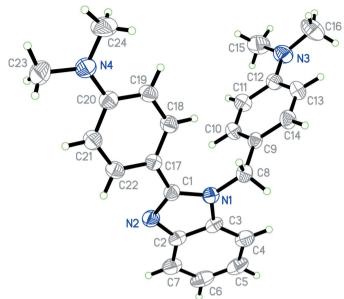


Figure 1

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

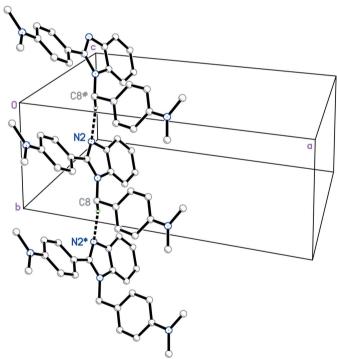


Figure 2

Part of the crystal structure of (I), showing the formation of a C(5) chain in the [010] direction. For clarity, H atoms not involved in the motif shown have been omitted. [Symmetry codes: (*) x, y + 1, z; (#) x, -1 + y, z]. Dashed lines indicate hydrogen bonds.

resulting in the formation of a three-dimensional network structure.

Experimental

The reaction mixture containing 4-dimethylaminobenzaldehyde (2.98 g, 20 mmol) and *o*-phenylenediamine (1.08 g, 10 mmol) was refluxed for about 4 h in ethanol (30 ml), then cooled and the product

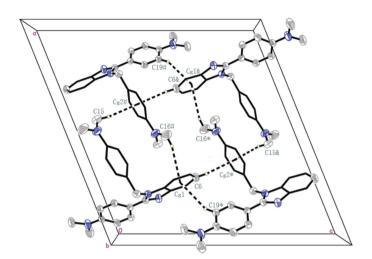


Figure 3

Part of the crystal structure of (I), viewed down the *b* axis, showing molecular chains linked by four $C-H\cdots\pi$ interactions. Displacement ellipsoids are drawn at the 30% probability level. *Cg*1 and *Cg*2 are the centroids of rings C2–C7 and C9–C14, respectively. For clarity, bonds on rings C2–C7 and C9–C14 are shown as thin lines and H atoms not involved in the motif have been omitted. [Symmetry codes: (*) $x, \frac{3}{2} - y, \frac{1}{2} + z;$ (#) $1 - x, -\frac{1}{2} + y, \frac{1}{2} - z;$ (&) 1 - x, 1 - y, 1 - z]. Dashed lines indicate C–H… π interactions.

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.465–467 K).

Z = 4

 $D_x = 1.214 \text{ Mg m}^{-3}$

 $0.56 \times 0.28 \times 0.27 \text{ mm}$

10086 measured reflections

3565 independent reflections

1550 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.07 \text{ mm}^-$

T = 298 (2) K

Needle, yellow

 $\begin{aligned} R_{\rm int} &= 0.057\\ \theta_{\rm max} &= 25.0^\circ \end{aligned}$

Crystal data

 $\begin{array}{l} C_{24}H_{26}N_4 \\ M_r = 370.49 \\ \text{Monoclinic, } P_{2_1}/c \\ a = 18.754 \ (3) \ \text{\AA} \\ b = 6.294 \ (2) \ \text{\AA} \\ c = 18.522 \ (3) \ \text{\AA} \\ \beta = 111.973 \ (3)^\circ \\ V = 2027.4 \ (8) \ \text{\AA}^3 \end{array}$

Data collection

Siemens SMART 1000 CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.960, T_{\max} = 0.981$

Refinement

Refinement on F^2 H-atom parameters constrained $R[F^2 > 2\sigma(F^2)] = 0.045$ $w = 1/[\sigma^2(F_o^2) + (0.0071P)^2]$ $wR(F^2) = 0.073$ where $P = (F_o^2 + 2F_c^2)/3$ S = 1.00 $(\Delta/\sigma)_{max} < 0.001$ 3565 reflections $\Delta\rho_{max} = 0.13$ e Å⁻³253 parameters $\Delta\rho_{min} = -0.15$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\overline{C8-H8a\cdots N2^{i}}$	0.97	2.55	3.499 (3)	165
Symmetry code: (i) x	z, y + 1, z.			

All H atoms were positioned geometrically and refined as riding on their parent atoms, with C-H = 0.96 Å and $U_{iso}(H) = 1.5U_{eq}(C)$ for methyl 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, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*.

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