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Key indicators

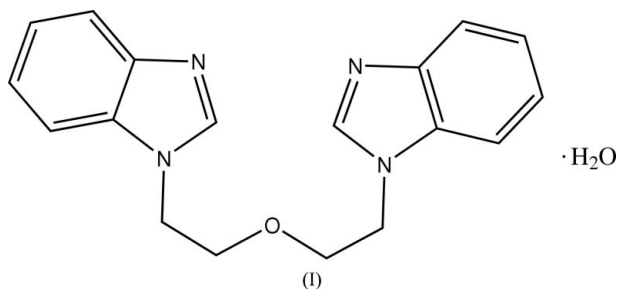
Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$
 R factor = 0.038
 wR factor = 0.101
Data-to-parameter ratio = 14.8For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Bis[2-(1*H*-benzimidazol-1-yl)ethyl] ether
monohydrate

In the approximately mirror-symmetric molecule of the title compound, $\text{C}_{18}\text{H}_{18}\text{N}_4\text{O}\cdot\text{H}_2\text{O}$, each benzimidazole group is essentially planar and the dihedral angle between them is $75.10(5)^\circ$. $\text{O}-\text{H}\cdots\text{N}$ and $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds generate a centrosymmetric $R_4^4(10)$ cluster of two organic and two water molecules.

Received 26 April 2006
Accepted 23 May 2006

Comment

In our ongoing studies of benzimidazole derivatives, the title compound, (I), was obtained from the dehydration reaction of 1*H*-benzimidazole and diglycol.



In the approximately mirror-symmetric molecule, each benzimidazole group is planar (Fig. 1), with dihedral angles of $0.13(8)$ and $1.64(8)^\circ$, respectively, between the benzene ring and its fused imidazole ring. The mean planes of these two benzimidazole systems make a dihedral angle of $75.10(5)^\circ$ with each other. All bond lengths and angles in (I) are within normal ranges (Allen *et al.*, 1987), and the bond lengths in the benzimidazole groups show a character intermediate between single and double bonds.

In the crystal structure, the water molecules play an important role as hydrogen-bond acceptors and donors. $\text{O}-\text{H}\cdots\text{N}$ and $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds (Table 2) link the molecules into centrosymmetric $R_4^4(10)$ clusters of two organic and two water molecules (Fig. 2).

Experimental

Diglycol (24 ml, 0.25 mol) was added dropwise to a solution of 4-methylbenzenesulfonyl chloride (100 g, 0.5 mol) in pyridine (170 ml) with stirring in an ice-water bath. After the addition was complete, the mixture was stirred at 273 K for 2 h, and then poured into cold water (600 ml) containing concentrated hydrochloric acid (170 ml). The volatiles were removed *in vacuo* to give a white solid. The solid (4.1 g, 0.01 mol) and benzimidazole (2.6 g, 0.02 mol) were refluxed in THF (45 ml) for 5 h and the solution was filtered. Single crystals suitable for X-ray diffraction study were obtained by slow evaporation of the filtrate.

Crystal data

C₁₈H₁₈N₄O·H₂O
M_r = 324.38
 Orthorhombic, *Pbca*
a = 18.230 (3) Å
b = 9.4065 (16) Å
c = 19.578 (3) Å
V = 3357.2 (10) Å³

Z = 8
D_x = 1.284 Mg m⁻³
 Mo *K*α radiation
 μ = 0.09 mm⁻¹
T = 293 (2) K
 Plate, colourless
 0.46 × 0.34 × 0.10 mm

Data collection

Siemens SMART 1000 CCD area-detector diffractometer
 ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.961, *T_{max}* = 0.991

17849 measured reflections
 3319 independent reflections
 2536 reflections with *I* > 2σ(*I*)
R_{int} = 0.031
 θ_{max} = 26.1°

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.039
wR (*F*²) = 0.101
S = 1.05
 3319 reflections
 225 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0436P)^2 + 0.4543P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{max} < 0.001$
 $\Delta\rho_{max} = 0.13 \text{ e \AA}^{-3}$
 $\Delta\rho_{min} = -0.15 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O1W—H1W1...N4	0.90 (2)	2.10 (2)	2.962 (2)	161 (2)
O1W—H2W1...N2	0.90 (3)	2.15 (3)	3.021 (2)	165 (3)
C12—H12A...O1W ⁱ	0.93	2.44	3.352 (2)	168

Symmetry code: (i) $-x, -y + 1, -z + 1$.

After their location in a difference Fourier map, all C-bound H atoms were positioned geometrically (C—H = 0.93 or 0.97 Å), and refined as riding, with *U_{iso}*(H) = 1.2*U_{eq}*(C). The H atoms of the water molecule were located in a difference Fourier and refined isotropically.

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL, PARST (Nardelli, 1995) and PLATON (Spek, 2003).

This project was supported by the Special Project of Qingdao for Leadership of Science and Technology (No. 05-2-JC-80) and the Outstanding Adult-Young Scientific Research

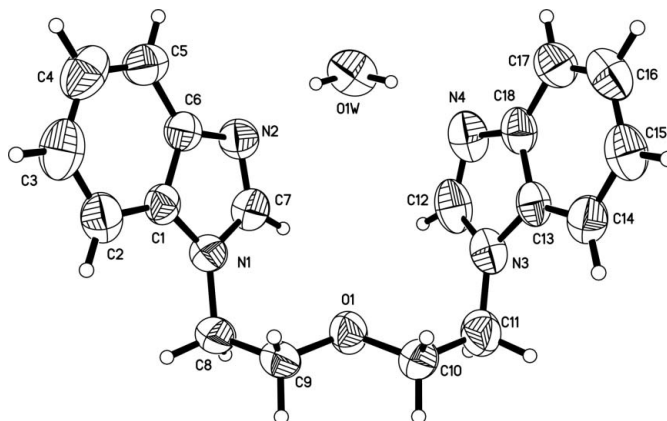


Figure 1 The molecular structure of compound (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme.

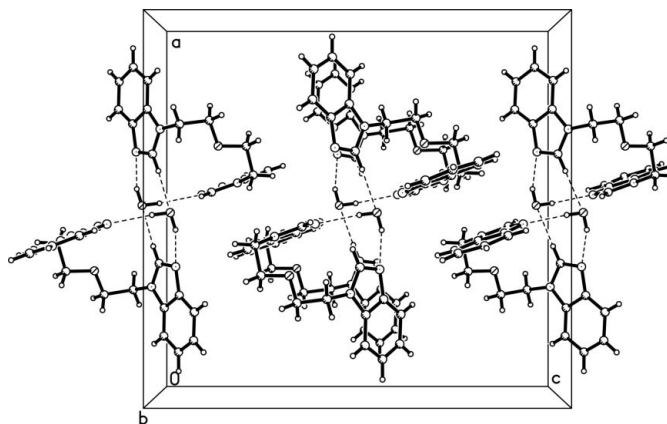


Figure 2 A partial packing diagram, showing the O—H...N and C—H...O hydrogen-bonded (dashed lines) clusters of (I).

Encouraging Foundation of Shandong Province (No. 2005BS04007).

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