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Ayoob Bazgir, Vahid Amani and Hamid Reza Khavasi*

Department of Chemistry, Shahid Beheshti University, Evin, Tehran 1983963113, Iran

Correspondence e-mail: h-khavasi@sbu.ac.ir

Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.005 Å R factor = 0.080 wR factor = 0.150 Data-to-parameter ratio = 12.5

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

N-[(2-Hydroxynaphthalen-1-yl)(phenyl)methyl]benzamide

Intermolecular O-H···O bonding and intramolecular N-H···O hydrogen bonding are effective in the stabilization of the crystal structure of the title compound, C₂₄H₁₉NO₂.

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Comment

Multi-component reactions (MCRs) (Hulme et al., 2003; Ugi, 1962) involving at least three starting materials in a one-pot reaction remain the most efficient method of rapidly producing molecular diversity. As such, they have found widespread use in organic and diversity-oriented synthesis because of their ability to access highly functionalized molecules in simple and straightforward one-step transformations (Ugi, 2000). Compared to conventional multi-step organic syntheses, MCRs are advantageous owing to their greater atom efficiency, accessibility to large numbers of compounds and complex molecules, wide structural diversity and the simplicity of their one-pot procedures, making them amenable to combinatorial synthesis. The development and discovery of new MCRs is still in demand. Recently, we reported the syntheses and crystal structures of methyl N-[(2-hydroxynaphthalen-1-yl)(phenyl)methyl]carbamate (Bazgir et al., 2006a) and 1-[(2-hydroxynaphthalen-1-yl)(phenyl)methyl]-3methylurea (Bazgir et al., 2006b). We now report the synthesis and structure of the title compound, (I).



The molecular structure of (I) is shown in Fig. 1. The bond lengths and angles are within normal ranges (Allen *et al.*, 1987; Bazgir *et al.*, 2006*a*,*b*). The crystal structure is stabilized by intramolecular $N-H\cdots O$ intermolecular $O-H\cdots O$ hydrogen bonding (Table 1), linking the molecules into a supramolecular chain (Fig. 2).

Experimental

© 2006 International Union of Crystallography All rights reserved 2-Naphthol (1 mmol), benzaldehyde (1 mmol), benzamide (1 mmol) and 1-butyl-3-methylimidazolium bromide (1.4 mmol) were mixed



Figure 1

The molecular structure of (I), shown with 30% probability displacement ellipsoids (arbitrary spheres for H atoms).



Figure 2

The packing of (I). Hydrogen bonds are shown as dashed lines.

and the reaction mixture was heated with stirring at 373 K for 2 h. After cooling, the reaction mixture was washed with water and then recrystallized from EtOAc-hexane (1:3) to afford single crystals of (I) (yield 75%).

> 4002 independent reflections 2906 reflections with $I > 2\sigma(I)$

 $w = 1/[\sigma^2(F_o^2) + (0.0215P)^2]$

+ 2.1712P] where $P = (F_0^2 + 2F_c^2)/3$

 $(\Delta/\sigma)_{\rm max} = 0.002$

 $\Delta \rho_{\rm max} = 0.32 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.19 \text{ e } \text{\AA}^{-3}$

 $R_{\rm int} = 0.147$

 $\theta_{\rm max} = 27.1^{\circ}$

Crystal data

| $C_{24}H_{19}NO_2$ | Z = 8 |
|-------------------------------|---|
| $M_r = 353.40$ | $D_x = 1.255 \text{ Mg m}^{-3}$ |
| Orthorhombic, Pbca | Mo $K\alpha$ radiation |
| a = 9.8517 (17) Å | $\mu = 0.08 \text{ mm}^{-1}$ |
| b = 11.3516 (18) Å | T = 298 (2) K |
| c = 33.451 (8) Å | Needle, colorless |
| $V = 3740.9 (12) \text{ Å}^3$ | $0.6 \times 0.1 \times 0.05 \text{ mm}$ |
| | |

Data collection

Stoe IPDS-II diffractometer ω scans Absorption correction: none 27152 measured reflections

Refinement

Table 1

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.080$ wR(F²) = 0.150 S = 1.184002 reflections 320 parameters All H-atom parameters refined

Hydrogen-bond geometry (Å, °).

| $D - H \cdots A$ | D-H | $H \cdots A$ | $D \cdots A$ | $D - H \cdots A$ |
|---|-----------------------------------|----------------------|------------------------|--------------------|
| $N1 - H1B \cdots O1$ $O1 - H1A \cdots O2^{i}$ | 0.90 (3) 0.88 (4) | 2.31 (3) 1.75 (4) | 2.633 (3) 2.629 (3) | 101 (2) 173 (4) |
| Symmetry code: (i) - | $r + \frac{1}{2}v + \frac{1}{2}z$ | | | |

Symmetry code: (1) $-x + \frac{1}{2}, y + \frac{1}{2}, z$.

H atoms were located in a difference Fourier map and refined isotropically.

Data collection: X-AREA (Stoe & Cie, 2005); cell refinement: X-AREA; data reduction: X-AREA; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

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