Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.004 Å R factor = 0.051 wR factor = 0.127 Data-to-parameter ratio = 9.6

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

The title compound, $C_{10}H_8O_2 \cdot C_{12}H_8N_4O$, was crystallized from a methanol and water solvent mixture. In the crystal structure, both types of molecules are linked *via* intermolecular $O-H \cdots N$ hydrogen bonds, forming one-dimensional chains along the [101] direction.

1:1 Cocrystal of naphthalene-2,7-diol

and 2,5-di-4-pyridyl-1,3,4-oxadiazole

Received 4 August 2006 Accepted 9 August 2006

Comment

Crystallization of phenol with pyridine (utilizing O-H···N hydrogen bonding) has been examined in order to build structures with intricate supramolecular architectures, to synthesize host-guest complexes and as a supramolecular template to direct topochemical reactions (Vishweshwar et al., 2003). Recently, a series of supramolecular structures containing 2,5-di-4-pyridyl-1,3,4-oxadiazole (bpo) and some acids, have been successfully constructed (Wang et al., 2005a,b; Wang, Tang, Oin & Duan, 2006; Wang, Tang, Oin, Duan & Ng, 2006; Wang, Tang & Qin, 2006; Wang, Tang & Wan, 2006). To further expand these results, to identify the properties of cocrystal materials of heterocyclic bases with angular acid components and to further understand the role of synthons in crystal engineering, we have determined the structure of the cocrystal, (I), of bpo and naphthalene-2,7-diol (ndo). We have previously determined the structure of ndo (Wang, Tang & Wan, 2006).



The molecular structure of (I) is shown in Fig. 1. The asymmetric unit consists of one ndo molecule and one mol-



View of the molecular structure of (I), showing displacement ellipsoids at the 30% probability level. H atoms are represented by circles of arbitrary size.

© 2006 International Union of Crystallography All rights reserved ecule of bpo. In the crystal structure, one-dimensional chains are formed *via* intermolecular $O-H \cdots N$ hydrogen bonds (Table 1 and Fig. 2).

Experimental

A mixture of 2,5-di-4-pyridyl-1,3,4-oxadiazole (112 mg, 0.5 mmol) (Wang *et al.*, 2005*a*) and naphthanene-2,7-diol (80 mg, 0.5 mmol) was recrystallized from methanol (10 ml) and water (2 ml) in 79% yield (152 mg), from which a pale-yellow needle-shaped crystal suitable for *x*-ray diffraction was selected. Analysis found (%): C 68.60, H 4.22, N 14.55; requires (%): C 68.74, H 4.20, N 14.58.

Z = 8

 $D_x = 1.407 \text{ Mg m}^{-3}$

Needle, pale yellow

 $0.30 \times 0.10 \times 0.10$ mm

8325 measured reflections

3123 independent reflections

1769 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.10 \text{ mm}^{-1}$

T = 298 (2) K

 $R_{\rm int} = 0.056$

 $\theta_{\rm max} = 25.0^{\circ}$

Crystal data

 $C_{10}H_8O_2 \cdot C_{12}H_8N_4O$ $M_r = 384.39$ Monoclinic, C2/c a = 11.025 (2) Å b = 8.1452 (16) Å c = 40.417 (8) Å $\beta = 91.40$ (3)° V = 3628.5 (12) Å³

Data collection

Bruker SMART APEX CCD diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; (Bruker, 2001) $T_{min} = 0.972, T_{max} = 0.990$

Refinement

 Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.0522P)^2]$
 $R[F^2 > 2\sigma(F^2)] = 0.051$ where $P = (F_o^2 + 2F_c^2)/3$
 $wR(F^2) = 0.127$ $(\Delta/\sigma)_{max} < 0.001$

 S = 0.99 $\Delta\rho_{max} = 0.17$ e Å⁻³

 3123 reflections
 $\Delta\rho_{min} = -0.15$ e Å⁻³

 327 parameters
 Extinction correction: SHELXL97

 All H-atom parameters refined
 Extinction coefficient: 0.0023 (3)

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$\overrightarrow{O2-H2\cdots N1^{i}}$	0.90 (1)	1.86 (1)	2.750 (3)	166 (3)
$O3-H3\cdots N4^{ii}$	0.91 (3)	1.86 (3)	2.742 (3)	165 (3)

Symmetry codes: (i) $-x + \frac{3}{2}$, $y + \frac{1}{2}$, $-z + \frac{1}{2}$; (ii) -x + 1, -y, -z.



Part of the crystal structure of (I), showing hydrogen bonds as dashed lines

All H atoms were located in a difference Fourier map and refined independently, with isotropic displacement parameters, giving final C-H distances in the range 0.94 (2)–1.05 (3) Å.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 1999); software used to prepare material for publication: *SHELXTL*.

This work was supported by the Starting Fund of Shandong Institute of Light Industry (to Dr Yong-Tao Wang).

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