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Key indicators

Single-crystal X-ray study T = 295 K Mean σ (C–C) = 0.007 Å Disorder in solvent or counterion R factor = 0.076 wR factor = 0.193 Data-to-parameter ratio = 8.1

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the crystal structure of the title compound, $C_{20}H_{14}O_2 \cdot 1.5C_3H_7N$ O, one of the hydroxyl groups forms a hydrogen bond to the dimethylformamide (DMF) molecule that lies on a general position and the other a hydrogen bond to the DMF molecule that lies on a twofold rotation axis. The naphthyl residues are aligned at 75.8 (1)° with respect to each other.

(S)-(-)-1,1'-Bi-2-naphthol dimethylformamide

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Comment

sesquisolvate

The preceeding paper (Yuan *et al.*, 2005) reports the structure of racemic 1,1'-bi-2-naphthol DMF sesquisolvate. In the title optically active S-form, (I) (Fig. 1), the two aromatic residues enclose a dihedral angle of 75.8 (1)°. One of the hydroxy groups forms a hydrogen bond to the ordered DMF (which lies on a general position) and the other one to the disordered DMF (which lies on a twofold rotation axis) (Table 1).



The hydrogen bonding is similar to that found in the racemic solvate (Yuan *et al.*, 2005). However, the packing is somewhat more efficient, as noted from the density (1.235 Mg m⁻³) compared with that of the racemic solvate (1.222 Mg m⁻³). The angle between the two aromatic systems is similar to that found in the anhydrous compound, which crystallizes in space group *P*32 (Toda *et al.*, 1997). The structure of the anhydrous *R*-(+)-enantiomer has also been reported (Mori *et al.*, 1993).

Experimental

S-(-)-1,1'-Bi-2-naphthol (0.29 g, 1 mmol) was dissolved in a mixedsolvent system of water (5 ml) and dimethylformamide (5 ml). This solution was added to an ethanol solution (10 ml) of 2-aminopyrimidine (0.19 g, 2 mmol). Evaporation of the solvent over several weeks gave colourless block-shaped crystals of (I).

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organic papers

Crystal data

 $C_{20}H_{14}O_2 \cdot 1.5C_3H_7NO$ $M_r = 395.96$ Tetragonal, $P4_{3,2}^2 \cdot 12$ a = 8.8430 (5) Å c = 54.486 (3) Å V = 4260.7 (3) Å³ Z = 8 $D_x = 1.235$ Mg m⁻³

Data collection

Bruker APEX CCD area-detector diffractometer ω and φ scans Absorption correction: none 22486 measured reflections 2335 independent reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0793P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.076$	+ 1.8739P]
$wR(F^2) = 0.193$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.37	$(\Delta/\sigma)_{\rm max} = 0.001$
2335 reflections	$\Delta \rho_{\rm max} = 0.18 \text{ e} \text{ Å}^{-3}$
287 parameters	$\Delta \rho_{\rm min} = -0.25 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Mo $K\alpha$ radiation

reflections

 $\theta = 2.3 - 23.0^{\circ}$ $\mu = 0.08 \text{ mm}^{-1}$

T = 295 (2) K

 $\begin{aligned} R_{\rm int} &= 0.046\\ \theta_{\rm max} &= 25.0^\circ \end{aligned}$

 $h = -10 \rightarrow 9$

 $\begin{array}{l} k=-10\rightarrow 10\\ l=-64\rightarrow 64 \end{array}$

Block colourless

 $0.36 \times 0.20 \times 0.19 \; \text{mm}$

2240 reflections with $I > 2\sigma(I)$

Cell parameters from 4002

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
O1-H1···O3	0.82	1.87	2.681 (5)	171
$O2-H2\cdots O4$	0.82	2.04	2.820 (5)	158

One DMF molecule is disordered over a twofold rotation axis. A number of restraints were imposed on this molecule, as follows: C24-O4 = 1.25 (1), C24-N2 = 1.35 (1), N2-C25 = N2-C26 = 1.45 (1), O4...C25 = 2.71 (1), C24...C25 = C24...C26 = 2.43 (2) and C25...C26 = 2.51 (2) Å. The displacement parameters of these atoms were restrained to an approximate isotropic behaviour; furthermore, these atoms were restrained to lie in a common plane. H atoms were positioned geometrically (O-H = 0.82, C-H_{aromatic} = 0.93 and C-H_{methyl} = 0.96 Å), and were included in the refinement in the ridingmodel approximation, with $U_{iso}(H) = 1.2U_{eq}(C,O)$, or $1.5U_{eq}(C)$ for methyl groups. In the absence of significant anomalous scattering effects, Friedel pairs were merged. The absolute configuration is known from the synthesis.

Figure 1

A plot of (I), with displacement ellipsoids drawn at the 30% probability level. H atoms are shown as spheres of arbitrary radii. Dashed lines indicate hydrogen bonds. Only one disorder component is shown.

Data collection: *SMART* (Bruker, 2003); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

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