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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.004 Å R factor = 0.054 wR factor = 0.109 Data-to-parameter ratio = 18.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the title compound, $C_{17}H_{16}N_2O \cdot C_3H_7NO$, containing indolyl and amide groups, the indolyl and phenyl rings are not coplanar, and form a dihedral angle of 88.4 (2)°. There are two intermolecular hydrogen bonds through the indole N and carbonyl O atom of the molecule, as well as through the amide N atom of the molecule and carbonyl O atom of the dimethylformamide solvent molecule.

N-(1-Phenylethyl)indole-2-carboxamide

dimethylformamide solvate

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Comment

We have reported the structure of the bidentate ligand (R)-N-(1-phenylethyl)quinoline-2-carboxamide (Yang *et al.*, 2001). This ligand was found to be easily coordinated to ruthenium(III) in a basic medium. The resulting Ru complex showed excellent catalytic activity in the epoxidation of cyclic alkenes. In order to further investigate the ligand performance of a new bidentate ligand, (I), containing the indole-2-carboxamide moiety, was synthesized. When the ligand coordinates to a metal ion through the ring N and the amide N atoms, the indolyl ligand, which contains a five-membered ring, will be less sterically hindered than the quinolyl derivative, which contains a six-membered ring. As a result, their catalytic activities should differ.



The indolyl and phenyl rings in (I) (Fig. 1) are not coplanar, and form a dihedral angle of $88.4 (2)^{\circ}$. The amide group is rotated out of the indole ring plane, forming a dihedral angle of 2.2 (1)°. There are two intermolecular hydrogen bonds; one involves the indole N and carbonyl O atom of the molecule, the other the amide N atom of the molecule and carbonyl O atom of the dimethylformamide (DMF) solvent molecule.

Experimental

The title compound was synthesized from 2-indolecarboxylic acid and methylbenzylamine, according to the general procedure of Johnson *et al.* (1960). The crystal used for the data collection was obtained by slow evaporation from a saturated DMF–water (10:1) solution at room temperature.

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organic papers

Crystal data

 $\begin{array}{l} C_{17}H_{16}N_2O\cdot C_3H_7NO\\ M_r = 337.41\\ Triclinic, $P\overline{1}$\\ a = 7.8166 (11) Å\\ b = 11.1683 (18) Å\\ c = 11.5769 (18) Å\\ \alpha = 73.310 (3)^{\circ}\\ \beta = 85.990 (4)^{\circ}\\ \gamma = 77.571 (4)^{\circ}\\ V = 945.3 (3) Å^3 \end{array}$

Data collection

Bruker CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.989, T_{\max} = 0.992$ 6524 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.054$ $wR(F^2) = 0.109$ S = 0.974309 reflections 229 parameters

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$
$N1-H1A\cdotsO1^{i}$	0.86	2.01	2.803 (2)	153
$N2-H2A\cdots O2$	0.86	2.06	2.863 (3)	155

Z = 2

 $D_x = 1.185 \text{ Mg m}^{-3}$

Cell parameters from 3267

Mo $K\alpha$ radiation

reflections $\theta = 1-27.5^{\circ}$

 $\mu = 0.08 \text{ mm}^{-1}$

T = 294 (2) K

Prism, colorless

 $R_{\rm int} = 0.032$ $\theta_{\rm max} = 27.6^{\circ}$

 $h = -8 \rightarrow 10$

 $k = -14 \rightarrow 12$

 $l = -12 \rightarrow 15$

 $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.33 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.15 \text{ e} \text{ Å}^{-3}$

 $0.14 \times 0.12 \times 0.10 \ \mathrm{mm}$

4309 independent reflections 1395 reflections with $I > 2\sigma(I)$

H-atom parameters constrained

 $w = 1/[\sigma^2(F_o^2) + (0.05P)^2]$

where $P = (F_o^2 + 2F_c^2)/3$

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

H atoms were placed in geometrically calculated positions and included in the final refinement in the riding-model approximation.

Data collection: *SMART* (Siemens, 1995); cell refinement: *SMART*; data reduction: *SHELXTL* (Siemens, 1995); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular

Figure 1

The molecular structure of (I), with ellipsoids at the 30% probability level (Siemens, 1995).

graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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