

***N,N'*-Bis(4-methylphenyl)pyridine-2,6-dicarboxamide**Jian Ying Qi,^{a,b*} Qi Yun Yang,^a
Kim Hung Lam,^b Zhong Yuan
Zhou^b and Albert S. C. Chan^{b†}^aDepartment of Chemistry, Changsha University of Electric Power, Changsha, Hunan, People's Republic of China, and ^bDepartment of Applied Biology and Chemical Technology, The Hong Kong Polytechnic University, Hung Hom, Kowloon, Hong Kong, People's Republic of China

† Additional correspondence author, e-mail: bcachan@polyu.edu.hk.

Correspondence e-mail: bcqijy@polyu.edu.hk

Key indicators

Single-crystal X-ray study

T = 294 K

Mean $\sigma(\text{C}-\text{C}) = 0.006 \text{ \AA}$

R factor = 0.089

wR factor = 0.181

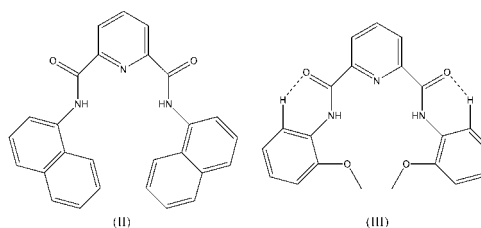
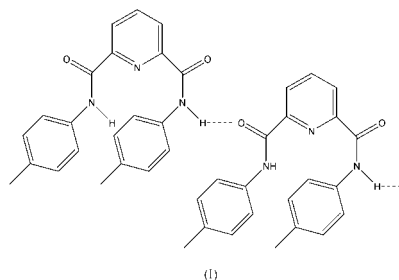
Data-to-parameter ratio = 17.4

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

The title molecule, $\text{C}_{21}\text{H}_{19}\text{N}_3\text{O}_2$, lies on a crystallographic twofold axis which runs through the central C and N atoms of the pyridine ring. The aryl rings are slightly twisted out of the pyridine-ring plane by an angle of $15.7 (14)^\circ$. Molecules are linked by $\text{N}-\text{H}\cdots\text{O}$ intermolecular hydrogen bonds to form chains in the *c* direction.

Comment

Our research has shown that the previously reported ligands (II) and (III) (Qi *et al.*, 2001; Yang *et al.*, 2001) easily form Co^{III} complexes *via* the coordination of the pyridine N and the amide N atoms. However, these Co^{III} complexes are difficult to crystallize and this may be due to the steric effect of the bulky naphthyl ring of ligand (II) or the 2-methoxy group on the phenyl ring of ligand (III). Therefore, ligand (I), with less steric hindrance of the coordinated amide N atom, was prepared. We expect that it will be easier to form metal complexes of this ligand and grow single crystals for X-ray analysis.



Compound (I) has a roughly planar structure, similar to those in (II) and (III). The molecule lies on a crystallographic twofold axis which runs through C11 and N2. The two substituted phenyl rings are twisted from coplanarity with the pyridine-ring plane and form dihedral angles of $15.7 (14)^\circ$. The dihedral angle between the two phenyl rings is $25.0 (15)^\circ$. Intermolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds, formed *via* the carbonyl O and amide H atoms, link molecules into chains in the *c* direction (see Table 1).

Experimental

The title compound was synthesized from 2,6-pyridinedicarboxylic acid and 4-toluidine by a published procedure (Ray *et al.*, 1997). The

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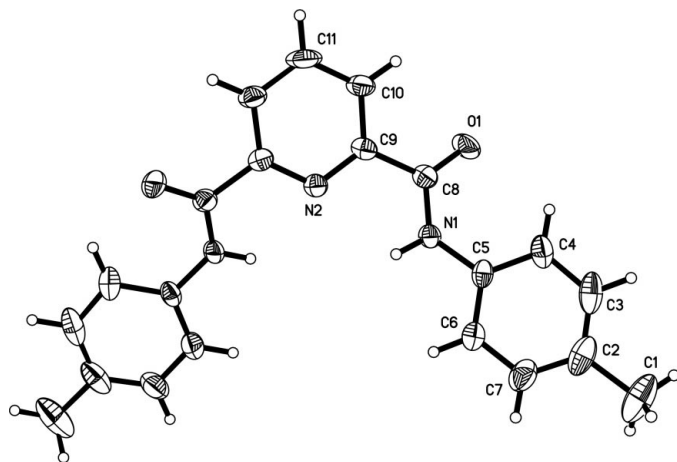


Figure 1
The molecular structure of (I), showing displacement ellipsoids at the 30% probability level (Siemens, 1995). The unlabelled part of the molecule is related to the labelled part by the symmetry operation $(-x, y, -z + \frac{1}{2})$.

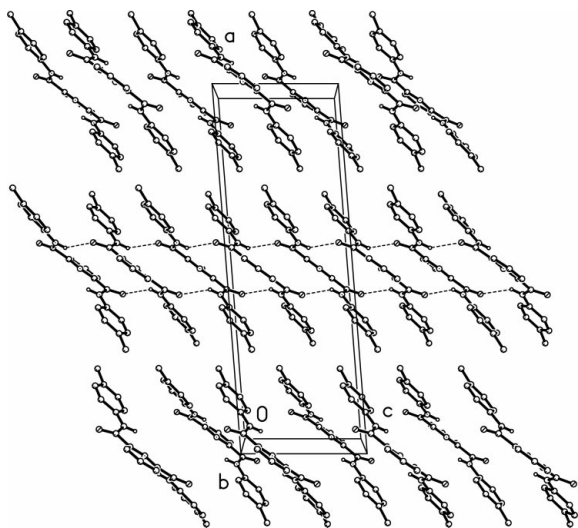


Figure 2
The molecular packing, showing the hydrogen bonding (dashed lines) in the c direction.

crystal used for the data collection was obtained by slow evaporation from a saturated solution in dimethylformamide and water at room temperature.

Crystal data

$C_{21}H_{19}N_3O_2$
 $M_r = 345.39$
Monoclinic, $C2/c$
 $a = 25.140$ (5) Å
 $b = 8.5779$ (17) Å
 $c = 8.5295$ (17) Å
 $\beta = 94.46$ (3)°
 $V = 1833.8$ (6) Å³
 $Z = 4$

$D_x = 1.251$ Mg m⁻³
Mo $K\alpha$ radiation
Cell parameters from 2125 reflections
 $\theta = 1-27.5^\circ$
 $\mu = 0.08$ mm⁻¹
 $T = 294$ (2) K
Prism, yellow
 $0.22 \times 0.20 \times 0.10$ mm

Data collection

Bruker CCD area-detector diffractometer
 φ and ω scans
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
 $T_{\min} = 0.982$, $T_{\max} = 0.992$
5712 measured reflections

2084 independent reflections
734 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.137$
 $\theta_{\text{max}} = 27.6^\circ$
 $h = -32 \rightarrow 25$
 $k = -10 \rightarrow 11$
 $l = -11 \rightarrow 11$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.089$
 $wR(F^2) = 0.181$
 $S = 1.02$
2084 reflections
120 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.05P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.22$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.25$ e Å⁻³

Table 1

Hydrogen-bonding geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N1-H1 \cdots O1^i$	0.86	2.31	3.068 (4)	147

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

The H atoms were placed in geometrically calculated positions and included in the final refinement in the riding-model approximation. The percentage of observed data was only 35% of the unique data available to a θ_{max} of 27.5° . Inclusion of such a high percentage of essentially unobserved data into the structure refinement restricts the precision of the results. The weak data also lead to a high value of R_{int} of 0.137.

Data collection: SMART (Siemens, 1995); cell refinement: SMART; data reduction: SAINT (Siemens, 1995) and SHELXTL-NT (Siemens, 1995); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL-NT; software used to prepare material for publication: SHELXTL-NT.

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