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Key indicators

Single-crystal X-ray study
 T = 193 K
 Mean $\sigma(C-C)$ = 0.003 Å
 R factor = 0.062
 wR factor = 0.154
 Data-to-parameter ratio = 16.0

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

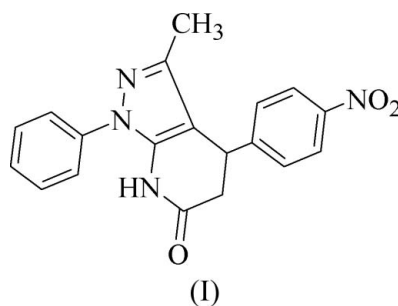
3-Methyl-4-(4-nitrophenyl)-6-oxo-1-phenyl-
 4,5-dihydropyrazolo[3,4-b]pyridine

The title compound, C₁₉H₁₆N₄O₃, was synthesized by the reaction of 5-amino-3-methyl-1-phenylpyrazole with 4-nitrobenzaldehyde and Medrum's acid in glycol under microwave irradiation. X-ray crystal structure analysis reveals that the dihydropyridine ring adopts a distorted half-chair conformation. In the crystal structure, the molecules exist as N—H···O hydrogen-bonded dimers.

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Comment

The dihydropyrazolo[3,4-b]pyridine system has many interesting biological and pharmacological properties, such as vasodilating and antihypertension activities, and also produces a prophylactic effect as a calcium antagonist in stroke-prone spontaneously hypertensive symptoms (Sekikawa *et al.*, 1973; Kuczynski *et al.*, 1979; El-Dean *et al.*, 1991). As part of our program aimed at employing microwave irradiation for the preparation of heterocyclic compounds (Tu *et al.*, 2004), we have recently synthesized dihydropyrazolo[3,4-b]pyridine derivatives under microwave irradiation. We report here the crystal structure of the title compound, (I).



The dihydropyridine ring adopts a distorted half-chair conformation (Fig. 1). The dihedral angle between the planes of the pyrazole ring and the attached phenyl ring is 50.0 (1)°.

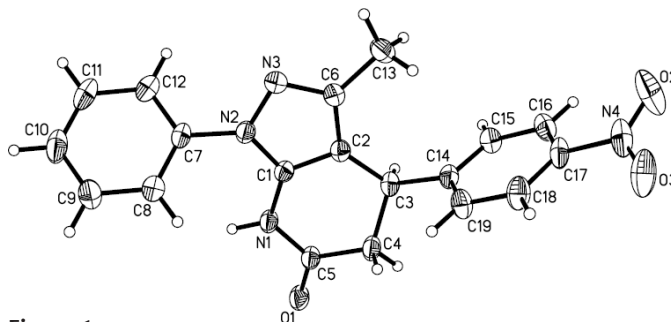


Figure 1
 The molecular structure of (I), showing 40% probability displacement ellipsoids and the atom-numbering scheme.

The crystal packing shows that the molecules exist as N—H···O hydrogen-bonded dimers (Table 1). The molecular packing is further stabilized by C—H···O interactions (Fig. 2).

Experimental

Compound (I) was prepared by the reaction of 5-amino-3-methyl-1-phenylpyrazole (2 mmol) with 4-nitrobenzaldehyde (2 mmol) and Medrum's acid (2 mmol) in glycol (1 ml) under microwave irradiation for 6 min (yield 80%, m.p. 490–491 K). Single crystals of (I) suitable for X-ray diffraction were obtained by slow evaporation of an ethanol solution (95%).

Crystal data

$C_{19}H_{16}N_4O_3$	$D_x = 1.375 \text{ Mg m}^{-3}$
$M_r = 348.36$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 2111 reflections
$a = 7.846 (5) \text{ \AA}$	$\theta = 3.1\text{--}27.5^\circ$
$b = 16.758 (14) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$c = 12.940 (15) \text{ \AA}$	$T = 193 (2) \text{ K}$
$\beta = 98.374 (12)^\circ$	Block, yellow
$V = 1683 (3) \text{ \AA}^3$	$0.39 \times 0.30 \times 0.28 \text{ mm}$
$Z = 4$	

Data collection

Rigaku Mercury CCD area-detector diffractometer	3850 independent reflections
ω scans	3234 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (Jacobson, 1998)	$R_{\text{int}} = 0.031$
$T_{\text{min}} = 0.964$, $T_{\text{max}} = 0.974$	$\theta_{\text{max}} = 27.5^\circ$
18328 measured reflections	$h = -10 \rightarrow 10$
	$k = -21 \rightarrow 21$
	$l = -15 \rightarrow 16$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0624P)^2 + 0.765P]$
$R[F^2 > 2\sigma(F^2)] = 0.062$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.154$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.13$	$\Delta\rho_{\text{max}} = 0.44 \text{ e \AA}^{-3}$
3850 reflections	$\Delta\rho_{\text{min}} = -0.34 \text{ e \AA}^{-3}$
240 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D\text{---}H\cdots A$	$D\text{---}H$	$H\cdots A$	$D\cdots A$	$D\text{---}H\cdots A$
$C4\text{---}H4A\cdots O3^i$	0.99	2.59	3.465 (5)	148
$C12\text{---}H12\cdots O3^{ii}$	0.95	2.58	3.285 (4)	131
$C16\text{---}H16\cdots O2^{iii}$	0.95	2.53	3.437 (3)	160
$N1\text{---}H1\cdots O1^{iv}$	0.94 (2)	1.87 (2)	2.814 (3)	177 (2)

Symmetry codes: (i) $-x + 1, -y + 1, -z + 2$; (ii) $x, y, z - 1$; (iii) $-x, -y + 1, -z + 2$; (iv) $-x + 2, -y + 1, -z + 1$.

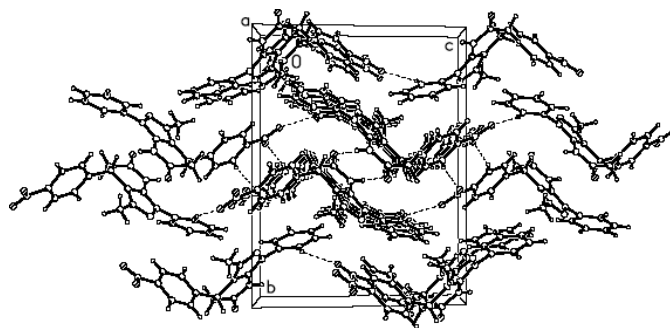


Figure 2

The molecular packing of (I), viewed along the a axis. Dashed lines indicate hydrogen bonds.

The H atom of the NH group was located in a difference Fourier map and was refined isotropically. All other H atoms were placed in idealized positions and allowed to ride on their parent atoms, with C—H distances in the range 0.95–1.00 \AA , and with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for methyl H atoms and $1.2U_{\text{eq}}(\text{C})$ for others.

Data collection: *CrystalClear* (Rigaku, 1999); cell refinement: *CrystalClear*; data reduction: *CrystalStructure* (Rigaku/MSC, 2003); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997a); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997a); molecular graphics: *SHELXTL* (Sheldrick, 1997b); software used to prepare material for publication: *SHELXTL*.

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