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4,6-Dimethyl-2-(3-pyridyl)quinolin-5-amine

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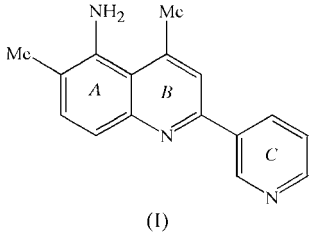
The title compound, $C_{16}H_{15}N_3$, shows a hindrance effect between adjacent amino and methyl groups that leads to a structural distortion, which is reflected in the non-planarity of the quinoline entity and in the bond angles and distances. The crystal packing consists of chains along the *b* axis sustained by an intermolecular hydrogen bond between the amino group and the N atom of the pyridyl ring.

Comment

Considerable attention has been paid to the synthesis of quinoline derivatives because this structural framework is often found in synthetic pharmaceuticals with unique biological activities (Kleenmann *et al.*, 1999). For instance, several antitumoral antibiotics are based on the 2-(α-pyridyl)-quinolinequinone tricyclic molecule (Boger, 1989). Substituted 4-methylquinolines are also useful starting products for ring construction of natural complex N-heterocycles (Roberts *et al.*, 1987). Moreover, 8-(diethylaminohexylamino)-6-methoxy-4-methylquinoline is highly effective against the protozoan parasite *Trypanosoma cruzi*, which is the agent of Chaga's disease (Chiari *et al.*, 1996), and 2-(2-methylquinolin-4-ylamino)-*N*-phenylacetamide is more active than the standard antileishmanial drug sodium antimony gluconate (Sahu



(I)

et al., 2002). It was therefore considered that amino(nitro)-quinolines bearing a pyridine ring could constitute a useful class of organic compounds as starting materials for the preparation of new drugs. In fact, such derivatives have already shown antiparasitic activity (Kouznetzov *et al.*, 1998). In order to gain more insight into the structure–activity relationships of these compounds, the crystal structure of the title compound, (I), was studied by single-crystal X-ray diffraction.

The molecular structure of (I) (Fig. 1) deviates from planarity, with the plane of ring *C* (see scheme) making a dihedral angle of 30.2 (1)° with the plane of ring *B*. More significantly, the planes of rings *A* and *B* in the quinoline

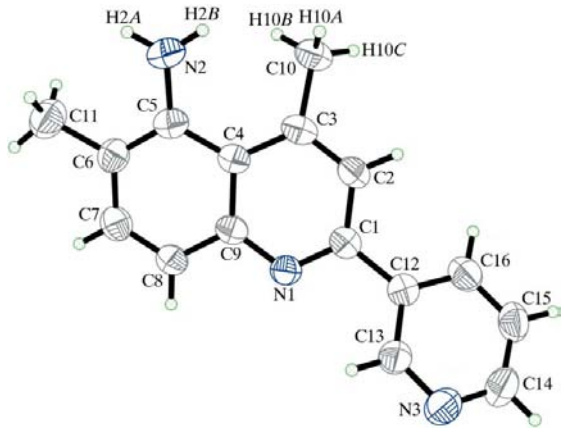


Figure 1
A view of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level. H atoms are represented by circles of arbitrary size.

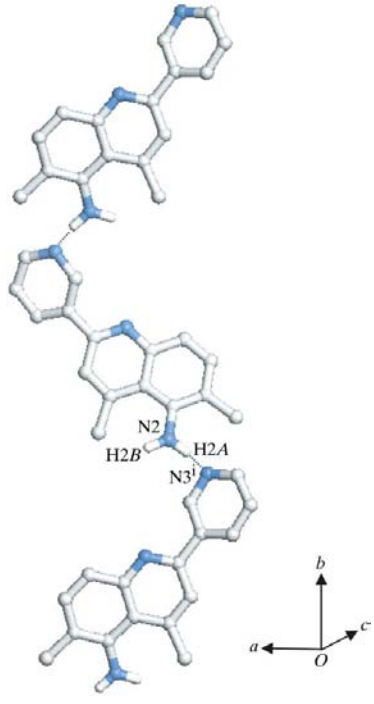


Figure 2
Columnar arrangement along the *b* axis, showing the intermolecular N—H···N hydrogen bond (dotted line) observed in the crystal structure. Only H atoms on the N2 amino group are shown. [Symmetry code: (i) $2-x, \frac{1}{2}+y, -\frac{1}{2}-z$.]

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system make a dihedral angle of 6.9 (1)°. This distortion results from the steric repulsion between the amino and the neighbouring C10 methyl groups, giving a C4—C3—C10 angle of 124.3 (2)°. In fact, the dihedral angle between the C10/C3/C4 and C4/C5/N2 planes is forced to be 17.5 (3)°, and consequently both substituents deviate [0.172 (4) Å for N2 and −0.175 (4) Å for C10] from the planes defined by the corresponding rings to which they are attached. The effect of such a distortion is also reflected in the quinoline bond distances [1.323 (3)–1.434 (4) Å; Table 1], where most of the C—C lengths are significantly enlarged [range 1.404 (4)–1.434 (4) Å] in comparison with the C—C bonds found in pyridine ring *C* [average 1.381 (3) Å], except for C2—C3, C5—C6 and C7—C8.

The crystal packing of (I) (Fig. 2) contains chains along [010] generated by an N—H···N hydrogen bond (Table 2 and Fig. 2) involving the amino group and the N atom of the 3-pyridine substituent. In the [001] direction, there is a C—H···π interaction between the C10 methyl group of ring *B* and ring *C*. A striking feature of the structure of (I) is that the N2—H2*B* donor group is inaccessible for intermolecular hydrogen bonding because of the presence of the neighbouring C10 methyl substituent (see Fig. 2).

Table 1
Selected geometric parameters (Å, °).

N1—C1	1.323 (3)	C7—C8	1.357 (4)
C1—C2	1.407 (3)	C8—C9	1.406 (3)
C2—C3	1.369 (4)	C9—N1	1.361 (3)
C3—C4	1.427 (4)	C4—C9	1.433 (3)
C4—C5	1.434 (4)	C1—C12	1.485 (3)
C5—C6	1.385 (4)	C3—C10	1.514 (3)
C6—C7	1.404 (4)	C5—N2	1.399 (3)
C2—C3—C4	118.2 (2)	C9—C4—C5	117.4 (2)
C2—C3—C10	117.4 (2)	C6—C5—N2	118.0 (2)
C4—C3—C10	124.3 (2)	C6—C5—C4	120.6 (2)
C3—C4—C9	116.1 (2)	N2—C5—C4	121.4 (2)
C3—C4—C5	126.5 (2)		

Table 2
Hydrogen-bond geometry (Å, °).

CgA and *CgC* are the centroids of rings C4–C9 and N3/C13–C16, respectively.

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
C10—H10*B*···N2	0.96	2.36	2.915 (4)	116
N2—H2*A*···N3^{i}	0.86	2.55	3.183 (4)	131
C7—H7···*CgA*^{ii}	0.93	2.74	3.405 (4)	129
C10—H10*A*···*CgC*^{iii}	0.96	2.91	3.838 (4)	162

Symmetry codes: (i) $-x+2, y+\frac{1}{2}, -z-\frac{1}{2}$; (ii) $-x+\frac{5}{2}, -y+1, z+\frac{1}{2}$; (iii) $-x+\frac{3}{2}, -y+1, z-\frac{1}{2}$.

Experimental

Compound (I) was prepared from the accessible 4,6-dimethyl-2-(3-pyridyl)quinoline, following the strategy described by Vargas-Méndez *et al.* (2001), in which the nitration of this quinoline is carried out with a nitric and sulfuric acid mixture at 265 K. Under these conditions, the 5-nitro derivative was obtained as the unique product in good yield (78%). This compound was subjected to the gentle reduction with $NaBH_4$ in the presence of Pd/C in methanol to give the corresponding amino derivative, (I), in 58% yield (Kouznetsov *et al.*, 2004).

Crystal data

$C_{16}H_{15}N_3$
M_r = 249.31
Orthorhombic, $P2_12_12_1$
a = 9.397 (3) Å
b = 18.314 (2) Å
c = 7.399 (4) Å
V = 1273.4 (8) Å^3
Z = 4
Mo $K\alpha$ radiation
μ = 0.08 mm^{-1}
T = 298 (2) K
0.54 × 0.48 × 0.40 mm

Data collection

Rigaku AFC-7*S* diffractometer
Absorption correction: ψ scan (North *et al.*, 1968)
T_{min} = 0.949, T_{max} = 0.972
1447 measured reflections
1309 independent reflections
1138 reflections with $I > 2\sigma(I)$
R_{int} = 0.041
3 standard reflections
every 150 reflections
intensity decay: none

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.038
$wR(F^2)$ = 0.103
S = 1.08
1309 reflections
173 parameters
H-atom parameters constrained
$\Delta\rho_{max}$ = 0.15 e Å^{-3}
$\Delta\rho_{min}$ = −0.15 e Å^{-3}

All H atoms were initially observed in a difference Fourier map and their positions agreed well with ideal geometries. Therefore, the methyl H atoms were constrained to the calculated geometry, with C—H distances of 0.96 Å and U_{iso}(H) values of 1.5U_{eq}(C). All other H atoms were also placed in geometrically idealized positions and constrained to ride on their parent atoms, with C—H and N—H distances of 0.93 and 0.86 Å, respectively, and U_{iso}(H) values of 1.2U_{eq}(C,N). As only three Friedel pairs were collected, the last refinement cycle resulted in an anticipated meaningless Flack (1983) parameter [−8 (5)]. Thus, Friedel-equivalent reflections were merged.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1993); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *TEXSAN* (Molecular Structure Corporation, 1999); program(s) used to solve structure: *SHELXTL-Plus* (Bruker, 1999); program(s) used to refine structure: *SHELXTL-Plus*; molecular graphics: *MaterialStudio* (Accelrys, 2002); software used to prepare material for publication: *SHELXTL-Plus*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: GD3088). Services for accessing these data are described at the back of the journal.

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