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#### **Key indicators**

Single-crystal X-ray study T = 293 KMean  $\sigma(C-C) = 0.005 \text{ Å}$  R factor = 0.064 wR factor = 0.146 Data-to-parameter ratio = 13.2

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

# 2-[(4,5-Dihydro-4-phenylthiazol-2-yl)methyl]-3*H*-imidazo[4,5-*b*]pyridine

In the title compound,  $C_{16}H_{12}N_4S$ , the dihedral angles formed by the phenyl and the 3H-imidazo[4,5-*b*]pyridine ring systems with the thiazole ring are 9.14 (3) and 75.79 (6)°, respectively. There are some intra- and intermolecular hydrogen-bond interactions in the crystal structure, providing stabilization. Received 14 November 2005 Accepted 23 November 2005 Online 3 December 2005

# Comment

Recently, (3*H*-imidazo[4,5-*b*]pyridine)(4-phenylthiazol-2-yl)methane and its derivatives have been the focus of increasing attention due to their bioactivities, such as antitubercular (Bukowski, 2001), anticonvulsant (Tomczuk *et al.*, 1991), anxiolytic (Tomczuk *et al.*, 1991), and antiproliferative activity (Liszkiewicz *et al.*, 2003). These compounds are also employed as ligands (Abbotto *et al.*, 2002). In this paper, we report the crystal structure of the title compound, (I).



Bond lengths and angles of the 3H-imidazo[4,5-*b*]pyridine and thiazole ring systems (Table 1) are in agreement with the values quoted in previous reports (Rodier *et al.*, 1993; Rodriguez de Barbarín *et al.*, 2003). The dihedral angles formed by the phenyl (C3–C8) and the 3H-imidazo[4,5-*b*]pyridine (N1/N2/N3/C11–C16) ring systems with the thiazole (S1/N4/C1/C2/C9) ring are 9.14 (3) and 75.79 (6)°, respectively. The crystal structure is stabilized by intra- and intermolecular hydrogen-bond interactions (Table 2 and Fig. 2).

## **Experimental**

Ethyl 2-(4-phenylthiazol-2-yl)acetate (10 mmol) and 2,3-diaminopyridine (10 mmol) were mixed and reacted at 453–473 K under solvent-free conditions for 1 h. Purification was achieved by recrystallization from methanol (yield 90%). Crystals suitable for X-ray diffraction analysis were obtained by slow evaporation of a methanol solution at room temperature for two weeks.

### Crystal data

$C_{16}H_{12}N_4S$
$M_r = 292.37$
Monoclinic, $P2_1/c$
a = 12.685 (6) Å
b = 5.277 (2)  Å
c = 21.389 (9) Å
$\beta = 100.577 \ (6)^{\circ}$
$V = 1407.5 (11) \text{ Å}^3$
Z = 4

 $D_x = 1.375 \text{ Mg m}^{-3}$ Mo K\alpha radiation Cell parameters from 2273 reflections  $\theta = 2.3-26.3^{\circ}$   $\mu = 0.23 \text{ mm}^{-1}$  T = 293 (2) K Block, colourless  $0.35 \times 0.21 \times 0.12 \text{ mm}$ 

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# organic papers

Data collection

Bruker SMART CCD area-detector
diffractometer
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\min} = 0.925, T_{\max} = 0.973$
6901 measured reflections

## Refinement

Refinement on $F^2$
$R[F^2 > 2\sigma(F^2)] = 0.064$
$wR(F^2) = 0.146$
S = 1.18
2509 reflections
190 parameters
H-atom parameters constrained

2509 independent reflections 2210 reflections with  $I > 2\sigma(I)$  $R_{int} = 0.030$  $\theta_{max} = 25.2^{\circ}$  $h = -15 \rightarrow 15$  $k = -5 \rightarrow 6$  $l = -23 \rightarrow 25$ 

 $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0481P)^{2} + 0.6991P]$ where  $P = (F_{o}^{2} + 2F_{c}^{2})/3 (\Delta/\sigma)_{max} < 0.001 \Delta\rho_{max} = 0.29 \text{ e} \text{ Å}^{-3} \Delta\rho_{min} = -0.23 \text{ e} \text{ Å}^{-3}$ 

#### Table 1

Selected geometric parameters (Å, °).

C1-C2	1.349 (4)	C11-N2	1.351 (3)
C1-S1	1.700 (4)	C12-N3	1.392 (3)
C9-N4	1.298 (3)	C15-N1	1.338 (4)
C9-S1	1.725 (3)	C16-N1	1.333 (3)
C11-N3	1.307 (3)	C16-N2	1.370 (3)
C11-C10-C9	110.3 (2)	C1-S1-C9	89.08 (15)
C9-N4-C2	111.1 (2)		

#### Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
$N2-H2A\cdots N1^{i}$	0.86	2.01	2.863 (3)	170
C8-H8···N4	0.93	2.57	2.884 (4)	100

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

All H atoms were placed in calculated positions, with C-H = 0.93–0.97 Å and N-H = 0.86 Å, and included in the final cycles of refinement using a riding model, with  $U_{iso}(H) = 1.2U_{eq}(\text{carrier atom})$ .

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1999); software used to prepare material for publication: *SHELXTL*.

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#### Figure 1

View of the title compound, with displacement ellipsoids drawn at the 40% probability level.



#### Figure 2

A packing diagram of the title compound, viewed down the a axis. Hydrogen bonds are shown as dashed lines.

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