

1-Benzyl-2-[1-(5-methyl-1*H*-pyrazol-3-yl)-2-phenylethyl]benzimidazoleMehmet Akkurt,<sup>a\*</sup> Şerife Pınar,<sup>a</sup>  
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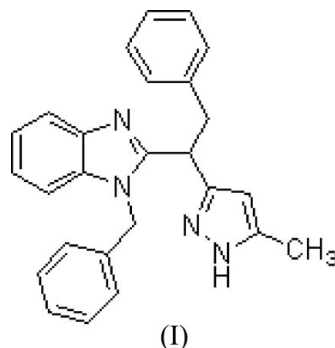
The title compound, C<sub>26</sub>H<sub>24</sub>N<sub>4</sub>, contains one pyrazole ring and two phenyl rings, which are nearly perpendicular to the benzimidazole ring system. In the structure, there is one intramolecular C—H···N hydrogen-bonding interaction.

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## Comment

Benzimidazole derivatives are compounds that have received much attention because of their applications in several areas. They are used as antibacterial (Özden *et al.*, 2004), anticancer (Easmon *et al.*, 2001; Zhu *et al.*, 1999), anti-inflammatory (Tewari & Mishra, 2001) and antiulcer agents (Shafik *et al.*, 2004; El-Naem *et al.*, 2003). They also have herbicidal, insecticidal and complexing properties (Sbai *et al.*, 2003, 2002; Attar *et al.*, 2001).

## Key indicators

Single-crystal X-ray study

 $T = 296$  KMean  $\sigma(\text{C—C}) = 0.003$  Å $R$  factor = 0.046 $wR$  factor = 0.130

Data-to-parameter ratio = 18.0

For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.An ORTEP-3 (Farrugia, 1997) drawing of (I) is shown in Fig. 1. All geometric parameters of (I) are normal and are consistent with those in similar compounds (Allen *et al.*, 1987). The dihedral angle between the two phenyl rings [ring A (atoms C14–C19) and ring B (atoms C21–C26)] is 61.85 (12)°. The pyrazole ring is nearly perpendicular to the benzimidazole ring system; the dihedral angle between the pyrazole and benzimidazole planes is 77.25 (8)°.

The crystal structure has one intramolecular C—H···N hydrogen bonding interaction. There are no classical hydrogen bonds in the structure.

## Experimental

Hydrazine hydrate (0.29 cc, 0.006 mol) was added to a solution of (4*Z*)-(2-oxopropylidene)-1,3-dibenzyl-1,2,4,5-tetrahydro-2*H*-1,5-benzodiazepin-2-one (1.17 g, 0.003 mol) in ethanol (30 ml). The reaction mixture was heated at reflux for 8 h; after cooling, a solid was isolated and dried under vacuum (yield 82%). <sup>1</sup>H NMR (CDCl<sub>3</sub>, p.p.m.):  $\delta$  2.34 (s, 3H, CH<sub>3</sub>), 3.75 (dd, 2H, CH<sub>2</sub>, <sup>2</sup> $J = 6.9$  Hz), 4.76 (t, 1H, CH), 5.42 (dd, 2H, NCH<sub>2</sub>, <sup>2</sup> $J = 17.1$  Hz), 6.11 (s, 1H, CH), 6.91–8.01 (CH<sub>Ar</sub>). <sup>13</sup>C NMR (CDCl<sub>3</sub>, p.p.m.):  $\delta$ : 11.8, 40.8, 47.1, 103.2, 109.8,

119.4, 122.1, 122.5, 126.1, 126.3, 127.5, 128.2, 128.7, 129.1, 135.2, 135.6, 135.9, 139.3, 142.5, 155.1.

### Crystal data

$C_{26}H_{24}N_4$   
 $M_r = 392.49$   
 Triclinic,  $P\bar{1}$   
 $a = 10.244$  (5) Å  
 $b = 10.601$  (5) Å  
 $c = 11.404$  (5) Å  
 $\alpha = 64.499$  (5)°  
 $\beta = 74.587$  (5)°  
 $\gamma = 89.556$  (5)°  
 $V = 1069.5$  (9) Å<sup>3</sup>

$Z = 2$   
 $D_x = 1.219$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 Cell parameters from 21742 reflections  
 $\theta = 2.2$ – $27.9$ °  
 $\mu = 0.07$  mm<sup>-1</sup>  
 $T = 296$  K  
 Prism, colourless  
 $0.62 \times 0.53 \times 0.47$  mm

### Data collection

Stoe IPDS-II diffractometer  
 $\omega$  scans  
 Absorption correction: none  
 17823 measured reflections  
 4925 independent reflections  
 3537 reflections with  $I > 2\sigma(I)$

$R_{int} = 0.120$   
 $\theta_{max} = 27.8$ °  
 $h = -13 \rightarrow 13$   
 $k = -13 \rightarrow 13$   
 $l = -14 \rightarrow 14$

### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.046$   
 $wR(F^2) = 0.130$   
 $S = 1.03$   
 4925 reflections  
 273 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0685P)^2 + 0.0775P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{max} < 0.001$   
 $\Delta\rho_{max} = 0.24$  e Å<sup>-3</sup>  
 $\Delta\rho_{min} = -0.32$  e Å<sup>-3</sup>  
 Extinction correction: *SHELXL97*  
 Extinction coefficient: 0.020 (5)

**Table 1**

Selected geometric parameters (Å, °).

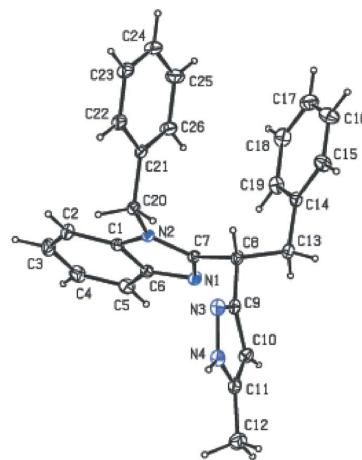
N1–C6	1.385 (2)	N2–C20	1.4543 (19)
N1–C7	1.307 (2)	N3–N4	1.401 (2)
N2–C1	1.383 (2)	N3–C9	1.302 (2)
N2–C7	1.3710 (19)	N4–C11	1.333 (2)
C6–N1–C7	104.67 (12)	N1–C6–C5	129.79 (14)
C1–N2–C7	105.93 (11)	N2–C7–C8	122.51 (12)
C1–N2–C20	125.09 (12)	N1–C7–C8	123.69 (13)
C7–N2–C20	128.96 (13)	N1–C7–N2	113.63 (14)
N4–N3–C9	105.52 (13)	N3–C9–C8	119.42 (14)
N3–N4–C11	108.75 (13)	N3–C9–C10	111.30 (14)
N2–C1–C2	131.71 (14)	N4–C11–C12	117.71 (17)
N2–C1–C6	105.50 (13)	N4–C11–C10	109.55 (16)
N1–C6–C1	110.28 (14)	N2–C20–C21	115.01 (11)

**Table 2**

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C26–H26 $\cdots$ N2	0.93	2.58	2.900 (3)	101

All H atoms were positioned geometrically and refined using a riding model [ $U_{iso}(H) = 1.5U_{eq}(C)$  for methyl groups and  $1.2U_{eq}(C,N)$  for other atoms;  $N-H = 0.86$  Å;  $C-H_{aromatic} = 0.93$  Å, methyl  $C-H = 0.96$  Å, methylene  $C-H = 0.97$  Å and  $C8-H8 = 0.98$  Å]. The methyl group was allowed to rotate but not to tip.



**Figure 1**

A view of (I), with the atom-numbering scheme and 10% probability displacement ellipsoids.

Data collection: *X-AREA* (Stoe & Cie, 2002); cell refinement: *X-AREA*; data reduction: *X-RED32* (Stoe & Cie, 2002); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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