

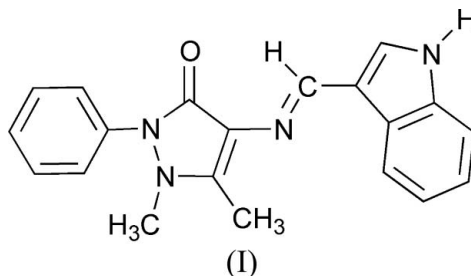
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Key indicators

Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.027
 wR factor = 0.074
Data-to-parameter ratio = 7.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.4-(1*H*-Indol-3-ylmethyleneamino)-1,5-dimethyl-
2-phenyl-1*H*-pyrazol-3(2*H*)-oneIn the crystal structure of the title compound, $\text{C}_{20}\text{H}_{18}\text{N}_4\text{O}$, the molecules are linked *via* weak intermolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds, forming an extended supramolecule.Received 30 July 2006
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Comment

Metal complexes based on Schiff bases have attracted much attention because they can be utilized as model compounds of active centres in various proteins and enzymes (Kahwa *et al.*, 1986; Santos *et al.*, 2001). As part of an investigation into the coordination properties of Schiff bases functioning as ligands (Yu *et al.*, 2005; Deng *et al.*, 2005; Jing *et al.*, 2005; Guo *et al.*, 2006), we report the synthesis and structure of the title compound, (I).In the molecular structure of (I) (Fig. 1), the expected geometric parameters are observed. The central chromophore (C10–C12/N3/N4) is planar, with an r.m.s. deviation for the fitted atoms of 0.036 (2) Å, as are the 1*H*-indole-3-carbaldehyde group (C1–C8/N1), with an r.m.s. deviation of 0.0083 (5) Å, and the phenyl group (C15–C20), with an r.m.s. deviation of 0.0034 (6) Å. The dihedral angles formed between these last two planes and that through the C10–C12/N3/N4 ring are 6.29 (9) and 60.98 (6)°, respectively. The C1–C8/N1 and C15–C20 groups are inclined at 67.15 (6)°. There are intermolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds (Table 1) and the molecules associate in a zigzag pattern along the *b* axis, forming a supramolecular structure, as illustrated in Fig. 2.

Experimental

An anhydrous ethanol solution (50 ml) of 1*H*-indole-3-carbaldehyde (1.46 g, 10 mmol) was added to an anhydrous ethanol solution (50 ml) of 4-amino-1,5-dimethyl-2-phenyl-1,2-dihydropyrazol-3-one (2.03 g, 10 mmol) and the mixture was stirred at 330 K for 6 h under N_2 , whereupon a yellow solution appeared. The solvent was removed and the residue recrystallized from anhydrous ethanol. The product was isolated and then dried *in vacuo* to give pure (I) in 83% yield. Yellow single crystals suitable for X-ray analysis were obtained by slow evaporation of an anhydrous ethanol solution of (I).

Crystal data

C₂₀H₁₈N₄OM_r = 330.38Orthorhombic, P2₁2₁2₁

a = 6.857 (3) Å

b = 15.729 (8) Å

c = 16.436 (8) Å

V = 1772.5 (15) Å³

Z = 4

D_x = 1.238 Mg m⁻³

Mo Kα radiation

μ = 0.08 mm⁻¹

T = 294 (2) K

Block, yellow

0.28 × 0.22 × 0.20 mm

Data collection

Bruker SMART CCD area-detector diffractometer

φ and ω scans

Absorption correction: multi-scan

(SADABS; Sheldrick, 1996)

T_{min} = 0.972, T_{max} = 0.984

9604 measured reflections

1822 independent reflections

1583 reflections with I > 2σ(I)

R_{int} = 0.021θ_{max} = 25.0°

Refinement

Refinement on F²R[F² > 2σ(F²)] = 0.027wR(F²) = 0.074

S = 1.06

1822 reflections

232 parameters

H atoms treated by a mixture of independent and constrained refinement

w = 1/[σ²(F_o²) + (0.0458P)² + 0.0654P]where P = (F_o² + 2F_c²)/3(Δ/σ)_{max} < 0.001Δρ_{max} = 0.10 e Å⁻³Δρ_{min} = -0.08 e Å⁻³

Extinction correction: SHELXL97

Extinction coefficient: 0.0116 (15)

Table 1

Hydrogen-bond geometry (Å, °).

D—H...A	D—H	H...A	D...A	D—H...A
N1—H1A...O1 ⁱ	0.89 (3)	1.92 (3)	2.794 (2)	166 (2)

Symmetry code: (i) -x, y + ½, -z + ¾.

The N-bound H atom was located in a difference Fourier map and its position was refined freely; U_{iso}(H) = 1.2U_{eq}(N). C-bound H atoms were included in calculated positions and refined using the riding-model approximation; C—H = 0.93 (aromatic) and 0.96 Å (methyl), with U_{iso}(H) = 1.2U_{eq}(C) for aromatic H and U_{iso}(H) = 1.5U_{eq}(C) for methyl H. In the absence of significant anomalous scattering effects, Friedel pairs were merged.

Data collection: SMART (Bruker, 1999); 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, 1997); software used to prepare material for publication: SHELXTL.

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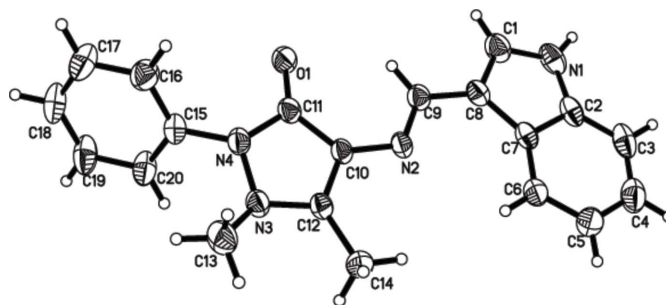


Figure 1

The molecular structure of (I), with displacement ellipsoids drawn at the 30% probability level.

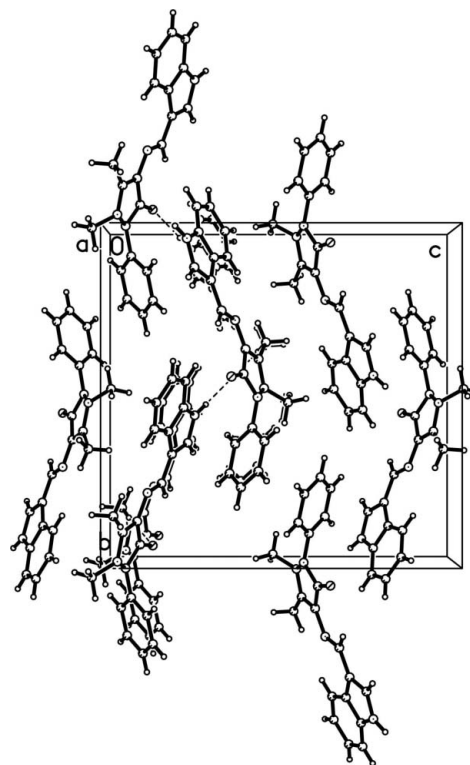


Figure 2

A view down the b axis showing the intermolecular hydrogen-bonding interaction (dashed line).

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