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Key indicators

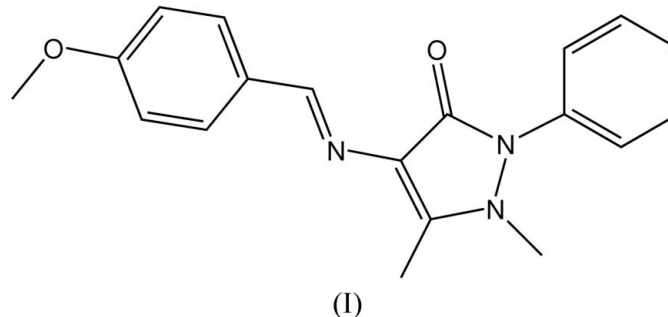
Single-crystal X-ray study
 $T = 294\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$
 R factor = 0.042
 wR factor = 0.120
Data-to-parameter ratio = 18.0For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.4-[(4-Methoxybenzylidene)amino]-1,5-
dimethyl-2-phenyl-1*H*-pyrazol-3(2*H*)-oneThe crystal structure of the title compound, $\text{C}_{19}\text{H}_{19}\text{N}_3\text{O}_2$, shows the molecule to be essentially planar with the exception of the terminal phenyl group. Molecules are associated *via* intermolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds.

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Comment

Metal complexes of Schiff bases have attracted much attention because they can be utilized as model compounds for the active centres in various enzymes and proteins (Kahwa *et al.*, 1986; Santos *et al.*, 2001). Important to the understanding of the coordination potential of these ligands is a knowledge of the ligand structure. Accordingly, the synthesis and crystal structures of Schiff base ligands derived from 4-aminoantipyrine, such as thenoyltrifluoroacetone (Yu *et al.*, 2002), 4-hydroxy-3-methoxybenzaldehyde (Diao *et al.*, 2005) and 2,4-dichlorobenzaldehyde (Jing *et al.*, 2005), have been reported.

In the molecular structure of the related title compound, (I) (Fig. 1), the expected geometric parameters are observed (Table 1). The central chromophore containing the C9–C11/N1–N3/O2 atoms is planar, with an r.m.s. deviation for fitted atoms of 0.038 (2) Å; the 4-methoxybenzylidene group (C1–C8/O1) is also planar, with an r.m.s. deviation of 0.027 (5) Å. The dihedral angles formed between these planes and that

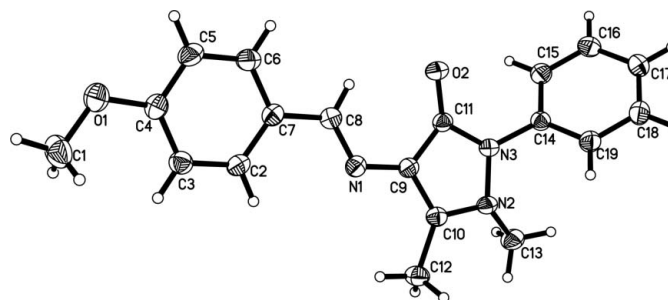


Figure 1
The molecular structure of (I), with displacement ellipsoids drawn at the 30% probability level.

through the C14–C19 phenyl ring are 48.24 (5) and 9.40 (6)°, respectively. Intramolecular C–H···O hydrogen bonding stabilizes the molecular conformation, while intermolecular C–H···O hydrogen bonding stabilizes the crystal structure; geometric details are given in Table 2. The molecules associate in a zigzag pattern along the *c* axis, forming a supramolecular structure, as illustrated in Fig. 2.

Experimental

An anhydrous ethanol solution of 4-methoxybenzaldehyde (1.36 g, 10 mmol) was added to an anhydrous ethanol solution of 4-amino-1,5-dimethyl-2-phenyl-1,2-dihydropyrazol-3-one (2.03 g, 10 mmol) and the mixture was stirred at 350 K for 8 h under N₂, whereupon a yellow solution appeared. The solvent was removed and the residue recrystallized from *N,N*-dimethylformamide. The product was isolated and then dried *in vacuo* to give pure (I) in 79% yield. Yellow single crystals suitable for X-ray analysis were obtained by slow evaporation of an *N,N*-dimethylformamide solution of (I).

Crystal data

C ₁₉ H ₁₉ N ₃ O ₂	$D_x = 1.278 \text{ Mg m}^{-3}$
$M_r = 321.37$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 2518 reflections
$a = 7.1407 (10) \text{ \AA}$	$\theta = 2.3\text{--}23.6^\circ$
$b = 24.864 (3) \text{ \AA}$	$\mu = 0.09 \text{ mm}^{-1}$
$c = 9.4733 (13) \text{ \AA}$	$T = 294 (2) \text{ K}$
$\beta = 96.700 (2)^\circ$	Block, yellow
$V = 1670.4 (4) \text{ \AA}^3$	$0.20 \times 0.16 \times 0.14 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART CCD area-detector diffractometer	3949 independent reflections
φ and ω scans	2677 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.022$
$T_{\text{min}} = 0.980$, $T_{\text{max}} = 0.988$	$\theta_{\text{max}} = 27.8^\circ$
11145 measured reflections	$h = -9 \rightarrow 8$
	$k = -31 \rightarrow 32$
	$l = -12 \rightarrow 11$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0574P)^2 + 0.1906P]$
$R[F^2 > 2\sigma(F^2)] = 0.042$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.120$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.04$	$\Delta\rho_{\text{max}} = 0.19 \text{ e \AA}^{-3}$
3949 reflections	$\Delta\rho_{\text{min}} = -0.20 \text{ e \AA}^{-3}$
220 parameters	
H-atom parameters constrained	

Table 1

Selected geometric parameters (\AA , $^\circ$).

O1–C1	1.422 (2)	N2–C10	1.3589 (18)
O1–C4	1.3684 (18)	N2–C13	1.4620 (17)
O2–C11	1.2336 (16)	N3–C11	1.4065 (17)
N1–C8	1.2754 (18)	N3–C14	1.4181 (17)
N1–C9	1.3920 (17)	C7–C8	1.460 (2)
N2–N3	1.4040 (15)	C9–C11	1.436 (2)
C1–O1–C4	117.94 (13)	N2–N3–C14	120.21 (11)
C8–N1–C9	120.85 (13)	C11–N3–C14	122.99 (11)
N3–N2–C10	107.12 (10)	N1–C8–C7	121.58 (14)
N3–N2–C13	117.60 (11)	O2–C11–N3	122.87 (13)
C10–N2–C13	123.72 (12)	O2–C11–C9	131.99 (13)
N2–N3–C11	108.88 (11)		

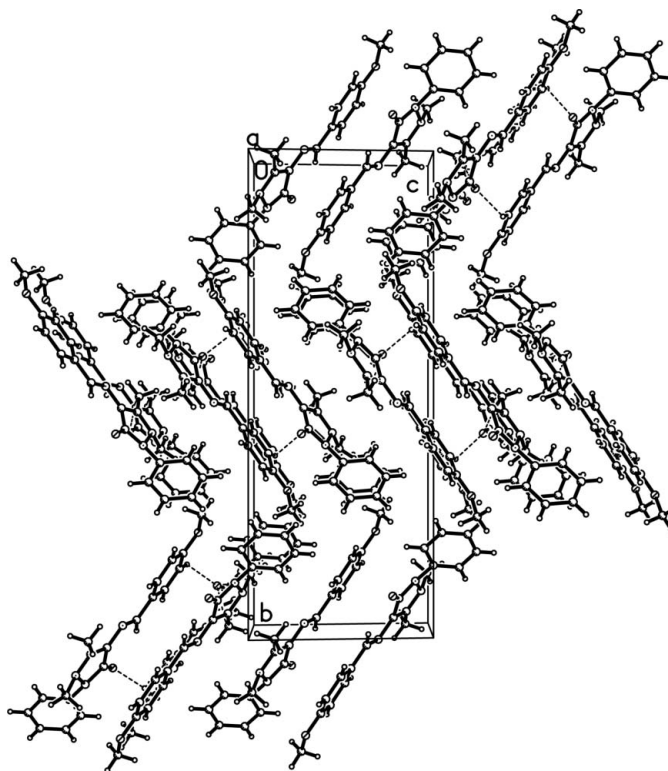


Figure 2

Intermolecular hydrogen-bonding interactions (dashed lines) in (I).

Table 2

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

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
C8–H8···O2	0.93	2.34	3.0310 (18)	131
C5–H5···O2 ⁱ	0.93	2.56	3.2838 (19)	135
C12–H12A···O2 ⁱⁱ	0.96	2.43	3.3815 (19)	172

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

The H atoms were included in calculated positions and refined using a riding model, with aromatic C–H = 0.93 \AA , methyl C–H = 0.96 \AA and N–H = 0.96 \AA , and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$ for aromatic and N-bound H atoms, and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for methyl H atoms.

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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