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Key indicators

Single-crystal X-ray study
 T = 294 K
 Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$
 R factor = 0.048
 wR factor = 0.138
 Data-to-parameter ratio = 15.9

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

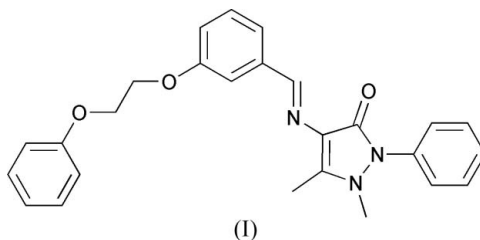
**(E)-1,5-Dimethyl-4-[3-(2-phenoxyethoxy)-
 benzylideneamino]-2-phenyl-1H-pyrazol-
 3(2H)-one**

In the title compound, $\text{C}_{26}\text{H}_{25}\text{N}_3\text{O}_3$, the central benzene ring makes dihedral angles of 13.93 (7), 54.45 (6) and 80.83 (5)°, respectively, with the pyrazolone ring, the attached phenyl ring and the other terminal phenyl ring. The crystal structure is stabilized by a couple of weak non-classical intermolecular C—H···O interactions, forming an infinite network.

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Comment

There has been steady growth of interest in the structure and reactivity of Schiff bases due to their potential biological activities such as antibacterial and antitumor (Klayman *et al.*, 1979). Among the large number of compounds, 4-amino-1,5-dimethyl-2-phenylpyrazol-3-one forms a variety of Schiff bases with aldehydes, and the syntheses and crystal structures of some of them, such as (*E*)-1,5-dimethyl-4-[2-(2-nitrophenoxy)-ethoxy]benzylideneamino]-2-phenyl-1*H*-pyrazol-3(2*H*)-one (Diao & Chen, 2006) (*E*)-4-[3-(4-chlorobenzyl-oxy)-4-methoxybenzylideneamino]-1,5-dimethyl-2-phenyl-1*H*-pyrazol-3(2*H*)-one (Duan *et al.*, 2006), have been reported. We report here the synthesis and structure of the title compound, (I).



In the title molecule (Fig. 1), bond lengths and angles are within normal ranges (Allen *et al.*, 1987). The pyrazolone ring (C16–C18/N1–N3/O3) is nearly planar, with an r.m.s. deviation for fitted atoms of 0.0394 Å. It makes a dihedral angle of 54.99 (6)° with the attached phenyl ring (C21–C26). The central benzene ring (C9–C15/O2) is essentially planar, with

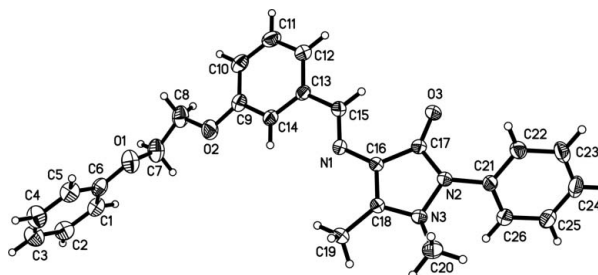


Figure 1
 The molecular structure of (I), with displacement ellipsoids for non-H atoms drawn at the 30% probability level.

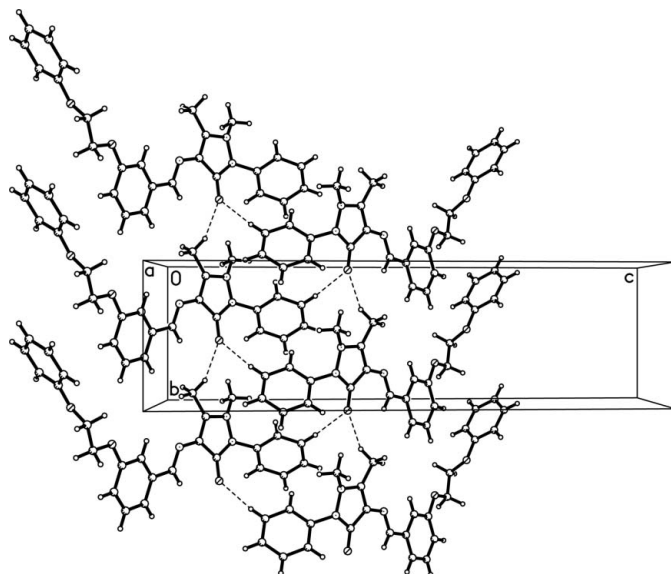


Figure 2
Intermolecular hydrogen-bonding interactions (dashed lines) in (I).

an r.m.s. deviation for fitted atoms of 0.0084 Å. It makes dihedral angles of 13.93 (7), 80.83 (5) and 54.45 (6)°, respectively, with the pyrazolone ring (C16–C18/N1–N3/O3) and the terminal (C1–C6 and C21–C26) phenyl rings.

The crystal structure is stabilized by a couple of weak non-classical intermolecular C–H···O interactions (Table 1), forming an infinite network (Fig. 2).

Experimental

An anhydrous ethanol solution (50 ml) of 3-(2-phenoxyethoxy)benzaldehyde (2.42 g, 10 mmol) was added to an anhydrous ethanol solution (50 ml) of 4-amino-1,5-dimethyl-2-phenylpyrazol-3-one (2.03 g, 10 mmol) and the mixture stirred at 350 K for 5 h under nitrogen, giving a yellow precipitate. The product was isolated, recrystallized from acetonitrile, and then dried in a vacuum to give the pure compound in 85% yield. Yellow single crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of an acetonitrile solution.

Crystal data

$C_{26}H_{25}N_3O_3$	$Z = 4$
$M_r = 427.49$	$D_x = 1.255 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 11.3949 (18) \text{ \AA}$	$\mu = 0.08 \text{ mm}^{-1}$
$b = 7.4456 (12) \text{ \AA}$	$T = 294 (2) \text{ K}$
$c = 26.791 (4) \text{ \AA}$	Block, yellow
$\beta = 95.392 (3)^\circ$	$0.30 \times 0.24 \times 0.20 \text{ mm}$
$V = 2262.9 (6) \text{ \AA}^3$	

Data collection

Bruker SMART APEX CCD area-detector diffractometer	12330 measured reflections
φ and ω scans	4635 independent reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	2621 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.958$, $T_{\max} = 0.984$	$R_{\text{int}} = 0.045$
	$\theta_{\max} = 26.4^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0654P)^2 + 0.2074P]$
$R[F^2 > 2\sigma(F^2)] = 0.048$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.138$	$(\Delta/\sigma)_{\max} = 0.002$
$S = 0.99$	$\Delta\rho_{\max} = 0.15 \text{ e \AA}^{-3}$
4635 reflections	$\Delta\rho_{\min} = -0.21 \text{ e \AA}^{-3}$
291 parameters	
H-atom parameters constrained	

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
C19–H19A···O3 ⁱ	0.96	2.31	3.137 (2)	144
C25–H25···O3 ⁱⁱ	0.93	2.45	3.368 (3)	169

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

H atoms were included in calculated positions and refined using a riding-model approximation: C–H = 0.93 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ for C_{sp}^2 ; C–H = 0.97 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ for methylene; C–H = 0.96 Å 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, 1997a); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997a); molecular graphics: *SHELXTL* (Sheldrick, 1997b); software used to prepare material for publication: *SHELXTL*.

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