

# 4-[(*E*)-(2,4,5-Trimethoxybenzylidene)-amino]-1,5-dimethyl-2-phenyl-1*H*-pyrazol-3(2*H*)-one

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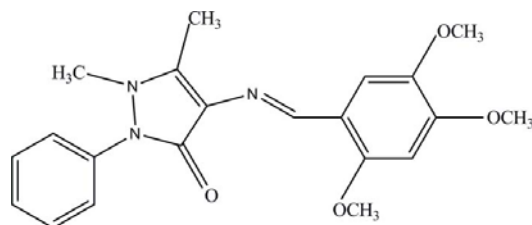
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Key indicators: single-crystal X-ray study;  $T = 100$  K; mean  $\sigma(\text{C}-\text{C}) = 0.001$  Å;  $R$  factor = 0.040;  $wR$  factor = 0.123; data-to-parameter ratio = 16.3.

The title compound,  $\text{C}_{21}\text{H}_{23}\text{N}_3\text{O}_4$ , adopts an *E* configuration about the central  $\text{C}=\text{N}$  double bond and the pyrazolone ring is almost planar, with a maximum deviation of 0.042 (1) Å. The central pyrazolone ring makes dihedral angles of 51.96 (5) and 3.82 (5)° with the attached phenyl and the trimethoxy-substituted benzene rings, respectively. The dihedral angle between the phenyl ring and the trimethoxy-substituted benzene ring is 50.19 (5)° and an intramolecular  $\text{C}-\text{H}\cdots\text{O}$  hydrogen bond generates an *S*(6) ring motif. The crystal structure is stabilized by intermolecular  $\text{C}-\text{H}\cdots\text{O}$  and  $\text{C}-\text{H}\cdots\text{N}$  hydrogen bonds.

## Related literature

For background to the applications of Schiff bases, see: Vukovic *et al.* (2010); Ramesh & Maheswaran (2003); Dongfang *et al.* (2008); Sastry & Rao (1988); Kamel *et al.* (2010). For hydrogen-bond motifs, see: Bernstein *et al.* (1995). For the stability of the temperature controller used in the data collection, see: Cosier & Glazer (1986).



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## Experimental

### Crystal data

$\text{C}_{21}\text{H}_{23}\text{N}_3\text{O}_4$   
 $M_r = 381.42$   
Monoclinic,  $P2_1/c$   
 $a = 21.0128$  (10) Å  
 $b = 7.4242$  (4) Å  
 $c = 12.5194$  (6) Å  
 $\beta = 98.675$  (1)°

$V = 1930.72$  (17) Å<sup>3</sup>  
 $Z = 4$   
Mo  $K\alpha$  radiation  
 $\mu = 0.09$  mm<sup>-1</sup>  
 $T = 100$  K  
 $0.67 \times 0.27 \times 0.15$  mm

### Data collection

Bruker APEXII DUO CCD diffractometer  
Absorption correction: multi-scan (SADABS; Bruker, 2009)  
 $T_{\min} = 0.941$ ,  $T_{\max} = 0.987$

23600 measured reflections  
5614 independent reflections  
4779 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.031$

### Refinement

$R[F^2 > 2\sigma(F^2)] = 0.040$   
 $wR(F^2) = 0.123$   
 $S = 1.04$   
5614 reflections  
345 parameters

H atoms treated by a mixture of independent and constrained refinement  
 $\Delta\rho_{\max} = 0.48$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.23$  e Å<sup>-3</sup>

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{C10}-\text{H10A}\cdots\text{O1}$	0.954 (13)	2.331 (13)	3.0112 (11)	127.8 (10)
$\text{C4}-\text{H4A}\cdots\text{O1}^i$	0.969 (13)	2.541 (13)	3.2628 (12)	131.4 (10)
$\text{C20}-\text{H20A}\cdots\text{N3}^{ii}$	0.996 (14)	2.577 (14)	3.5383 (13)	162.1 (12)
$\text{C20}-\text{H20C}\cdots\text{O2}^{iii}$	0.977 (14)	2.509 (14)	3.4470 (13)	160.8 (12)
$\text{C20}-\text{H20C}\cdots\text{O3}^{iii}$	0.977 (14)	2.495 (15)	3.2779 (13)	137.0 (11)

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

Data collection: APEX2 (Bruker, 2009); cell refinement: SAINT (Bruker, 2009); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 2008); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL and PLATON (Spek, 2009).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB5480).

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