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## Key indicators

Single-crystal X-ray study  
 $T = 292$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å  
Disorder in main residue  
 $R$  factor = 0.052  
 $wR$  factor = 0.139  
Data-to-parameter ratio = 16.5For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.**(Z)-4-Benzylidene-1-(4-chlorophenyl)-2-propyl-  
amino-1H-imidazol-5(4H)-one**Adjacent molecules of the title compound,  $\text{C}_{19}\text{H}_{18}\text{ClN}_3\text{O}$ , are  
linked by an  $\text{N}\cdots\text{O}$  hydrogen bond [ $2.926(2)$  Å] into a zigzag  
chain.Received 21 April 2006  
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## Comment

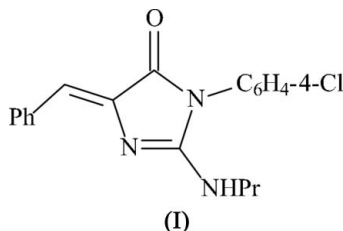
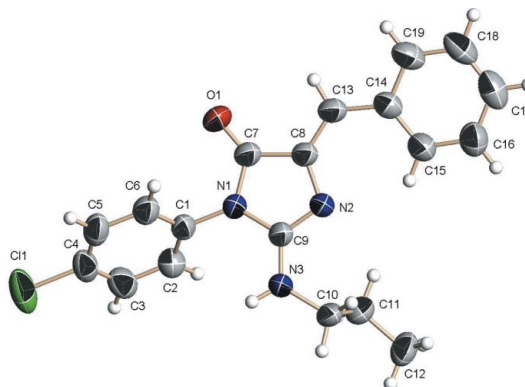
Several  $\text{PhCH}=\text{C}(\text{CO}_2\text{Et})\text{N}=\text{C}=\text{NR}$  ( $R = \text{Ph}, 4\text{-ClC}_6\text{H}_4$ )  
compounds that were synthesized from an aza-Wittig reaction  
of  $\text{PhCH}=\text{C}(\text{CO}_2\text{Et})\text{N}=\text{PPh}_3$  with  $\text{RNCO}$  have been reacted  
with primary amines to form 1-aryl-2-alkylamino-4-benzyl-  
ideneimidazolin-5-ones (Ding *et al.*, 2001). Among these is the  
title compound (I) (Fig. 1), whose amino group is hydrogen-  
bonded with the carbonyl group of an adjacent molecule  
(Table 1), forming a zigzag chain running along the  $c$  axis. The  
compound features an imidazolinone unit with an exocyclic  
 $\text{C}=\text{C}$  double bond.There are few related compounds whose structures have  
been determined. The examples appear to be limited to (4*Z*)-  
4-(4-methoxybenzylidene)-1,2-diphenyl-1,4-dihydro-5-imida-  
zolin-5-one (Bhattacharjya *et al.*, 2004), 1-[2-(dimethyl-  
amino)ethyl]-2-methyl-4-benzylidene-2-imidazolin-5-one  
(Oshimi *et al.*, 2002) and (*Z*)-1-[2-(dimethylamino)ethyl]-2-  
methyl-4-benzylidene-2-imidazolin-5-one (Kawasaki *et al.*,  
2004).

Figure 1

The molecular structure of (I) with displacement ellipsoids drawn at the  
50% probability level. H atoms are drawn as spheres of arbitrary radii.

## Experimental

The compound was synthesized according to a reported procedure (Ding *et al.*, 2001) and crystals were grown from a dichloromethane/diethyl ether solution (1:1 *v/v*).

### Crystal data

$C_{19}H_{18}ClN_3O$	$Z = 4$
$M_r = 339.81$	$D_x = 1.277 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 10.9150$ (7) Å	$\mu = 0.23 \text{ mm}^{-1}$
$b = 12.9335$ (8) Å	$T = 292$ (2) K
$c = 12.8701$ (8) Å	Block, yellow
$\beta = 103.331$ (1)°	$0.2 \times 0.2 \times 0.2 \text{ mm}$
$V = 1767.9$ (2) Å <sup>3</sup>	

### Data collection

Bruker SMART APEX area-detector diffractometer	4038 independent reflections
$\varphi$ and $\omega$ scans	2612 reflections with $I > 2\sigma(I)$
Absorption correction: none	$R_{\text{int}} = 0.050$
16744 measured reflections	$\theta_{\text{max}} = 27.5^\circ$

### Refinement

Refinement on $F^2$	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.052$	$w = 1/[\sigma^2(F_o^2) + (0.0731P)^2]$
$wR(F^2) = 0.139$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 0.97$	$(\Delta/\sigma)_{\text{max}} = 0.001$
4038 reflections	$\Delta\rho_{\text{max}} = 0.18 \text{ e \AA}^{-3}$
245 parameters	$\Delta\rho_{\text{min}} = -0.23 \text{ e \AA}^{-3}$

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N3-H3n\cdots O1^i$	0.86	2.15	2.926 (2)	150
$N3-H3n'\cdots O1^i$	0.86	2.36	2.926 (2)	124

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

The propyl chain is disordered over two positions; the occupancy factors refined to 0.612 (6):0.388 (2). The pairs of 1,2-related and 1,3-related distances were restrained to be equal within 0.01 Å. H atoms were positioned geometrically and were included in the refinement in the riding-model approximation [aryl C–H = 0.93 Å and  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ ; methylene C–H = 0.97 Å and  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ ; methyl C–H = 0.96 Å and  $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ ]. Because of disorder of the propyl group, the H atom bonded to atom N3 is disordered over two sites (H3*n* and H3*n'*), which were refined in riding mode, with N–H = 0.86 Å and  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$ .

Data collection: SMART (Bruker, 2003); cell refinement: SAINT (Bruker, 2003); 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, 1998); software used to prepare material for publication: SHELXL97.

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