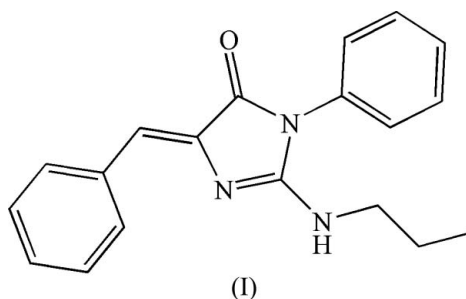


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## Key indicators

Single-crystal X-ray study  
 $T = 292$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å  
 $R$  factor = 0.054  
 $wR$  factor = 0.143  
Data-to-parameter ratio = 17.8For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.4-Benzylidene-1-phenyl-2-propylamino-  
1*H*-imidazol-5(4*H*)-oneIn the title compound,  $\text{C}_{19}\text{H}_{19}\text{N}_3\text{O}$ , the five-membered imidazolone ring is essentially planar. Intermolecular  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds form an infinite chain. The  $\text{C}-\text{N}$  and  $\text{C}-\text{C}$  bond lengths indicate electron delocalization.Received 14 December 2005  
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## Comment

Imidazolones are important heterocycles having fungicidal, anti-inflammatory and angiotensin II antagonist activities (Lacroix *et al.*, 2000). Some 2-alkylaminoimidazolones exhibit good antibacterial activity (Trivedi *et al.*, 2002). The title compound, (I), may be used as a new precursor for obtaining bioactive molecules.

The molecular structure of (I) is shown in Fig. 1. The five-membered imidazolone ring is planar. Benzene ring C1–C6 is only slightly twisted with respect to this imidazolone ring, making a dihedral angle of  $4.46$  ( $9$ )°. The C7–C8 bond length of  $1.347$  ( $2$ ) Å is close to that of a typical  $\text{C}=\text{C}$  bond ( $1.35$  Å), whereas the N1–C10 bond length of  $1.3047$  ( $19$ ) Å, is slightly longer than that of a typical  $\text{C}=\text{N}$  bond ( $1.28$  Å). The N3–C10, N2–C10, N2–C11 and N2–C9 bond lengths [ $1.3292$  ( $19$ ),  $1.4004$  ( $18$ ),  $1.426$  ( $2$ ) and  $1.3860$  ( $19$ ) Å, respectively] indicate some degree of delocalization around the ring system (Yang *et al.*, 1999). The C6–C7–C8–N1 torsion angle of  $0.6$  ( $3$ )° indicates a *Z* configuration of the molecule about the C7=C8 bond.

Intermolecular  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds (Table 1) link the molecules into chains, as can be seen from the packing diagram (Fig. 2).

## Experimental

To a solution of vinyliminophosphorane (3 mmol) in dry dichloromethane (10 ml) was added phenyl isocyanate (3 mmol) under nitrogen at room temperature. After 8 h, the solvent was removed under reduced pressure and a mixture of diethyl ether/petroleum ether (1:2 *v/v*, 20 ml) was added to precipitate triphenylphosphine oxide. After the mixture was filtered, the filtrate was condensed and

dichloromethane (10 ml) was added to make a solution of carbodiimide, which was added to *n*-propylamine (3 mmol). After 2 h, the solvent was removed under reduced pressure and the residual was recrystallized from dichloromethane/ethanol to give (I) in 67% yield (m.p. 456 K). <sup>1</sup>H NMR (CDCl<sub>3</sub>, 400 MHz): δ 8.16–7.10 (*m*, 10H, Ar–H), 6.70 (*s*, 1H, =CH), 4.58(*t*, 1H, *J* = 5.4 Hz, NH), 3.60–3.38 (*m*, 2H, NCH<sub>2</sub>), 1.85–1.45 (*m*, 2H, CH<sub>2</sub>), 0.94 (*t*, 3H, *J* = 7.2 Hz, CH<sub>3</sub>); MS (EI 70 eV) *m/z*(%): 305(*M*<sup>+</sup>, 95%), 276 (64%), 263 (96%), 119 (100%). Elemental analysis calculated for C<sub>19</sub>H<sub>19</sub>N<sub>3</sub>O: C 74.73, H 6.27, N 13.76%; found: 74.62, H 6.37, N 13.61%.

Crystal data

|  |  |
|--|--|
| C <sub>19</sub> H <sub>19</sub> N <sub>3</sub> O | <i>D</i> <sub>x</sub> = 1.211 Mg m <sup>-3</sup> |
| <i>M</i> <sub>r</sub> = 305.37                   | Mo Kα radiation                                  |
| Monoclinic, <i>P</i> 2 <sub>1</sub> / <i>c</i>   | Cell parameters from 3773 reflections            |
| <i>a</i> = 11.6442 (11) Å                        | <i>θ</i> = 2.4–23.8°                             |
| <i>b</i> = 11.3675 (10) Å                        | <i>μ</i> = 0.08 mm <sup>-1</sup>                 |
| <i>c</i> = 12.8149 (12) Å                        | <i>T</i> = 292 (2) K                             |
| <i>β</i> = 99.058 (2)°                           | Block, yellow                                    |
| <i>V</i> = 1675.1 (3) Å <sup>3</sup>             | 0.30 × 0.20 × 0.10 mm                            |
| <i>Z</i> = 4                                     |  |

Data collection

|   |   |
|---|---|
| Bruker SMART CCD area-detector diffractometer | 2657 reflections with <i>I</i> > 2σ( <i>I</i> ) |
| φ and ω scans                                 | <i>R</i> <sub>int</sub> = 0.029                 |
| Absorption correction: none                   | <i>θ</i> <sub>max</sub> = 27.5°                 |
| 14038 measured reflections                    | <i>h</i> = -14 → 15                             |
| 3784 independent reflections                  | <i>k</i> = -14 → 13                             |
|   | <i>l</i> = -16 → 16                             |

Refinement

|  |  |
|--|--|
| Refinement on <i>F</i> <sup>2</sup>                                    | $w = 1/[\sigma^2(F_o^2) + (0.0641P)^2 + 0.168P]$ |
| $R[F^2 > 2\sigma(F^2)] = 0.054$  | where $P = (F_o^2 + 2F_c^2)/3$                   |
| $wR(F^2) = 0.143$  | (Δ/σ) <sub>max</sub> < 0.001                     |
| <i>S</i> = 1.06  | Δρ <sub>max</sub> = 0.16 e Å <sup>-3</sup>       |
| 3784 reflections   | Δρ <sub>min</sub> = -0.16 e Å <sup>-3</sup>      |
| 212 parameters   |  |
| H atoms treated by a mixture of independent and constrained refinement |  |

Table 1

Hydrogen-bond geometry (Å, °).

| <i>D</i> –H... <i>A</i>  | <i>D</i> –H | H... <i>A</i> | <i>D</i> ... <i>A</i> | <i>D</i> –H... <i>A</i> |
|--------------------------|-------------|---------------|-----------------------|-------------------------|
| N3–H3A...O1 <sup>i</sup> | 0.871 (8)   | 2.094 (13)    | 2.8452 (17)           | 144.0 (16)              |

Symmetry code: (i) *x*, -*y* + ½, *z* - ½.

H atoms attached to carbon were placed at calculated positions and treated as riding atoms (C–H = 0.93–0.97 Å), with *U*<sub>iso</sub> values set equal to 1.2*U*<sub>eq</sub>(CH) or 1.5*U*<sub>eq</sub>(CH<sub>3</sub>) of the parent atom. The H atom attached to nitrogen was refined with *U*<sub>iso</sub>(H) = 1.2*U*<sub>eq</sub>(N).

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2001); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics:

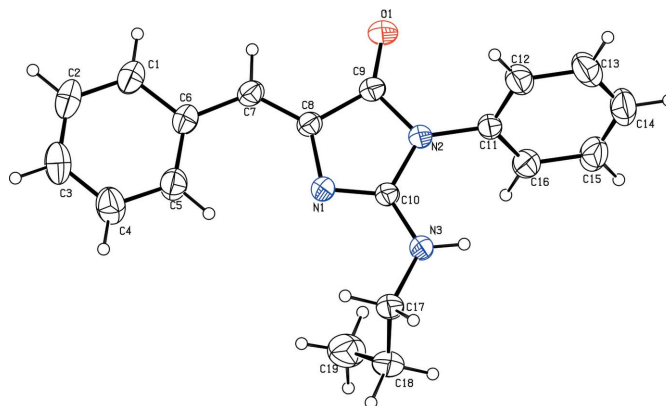


Figure 1 View of the molecular structure of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level.

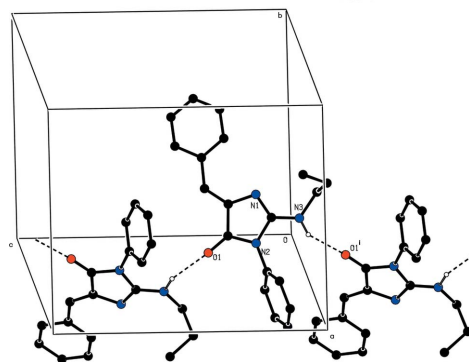


Figure 2 The hydrogen-bonding interactions in (I) forming a chain [symmetry code: (i) *x*, ½ - *y*, *z* - ½]. H atoms not involved in hydrogen bonding have been omitted.

SHELXTL (Bruker 2001) and PLATON (Spek, 2003); software used to prepare material for publication: SHELXTL.

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