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Key indicators

Single-crystal X-ray study T = 292 KMean $\sigma(\text{C}-\text{C}) = 0.004 \text{ Å}$ Disorder in main residue R factor = 0.056 wR factor = 0.189 Data-to-parameter ratio = 17.0

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

Ethyl 5-(triphenylphosphoranylideneamino)-1*H*-1,2,3-triazole-4-carboxylate

Molecules of the title compound, $C_{29}H_{25}N_4O_2P$, form a supramolecular structure *via* intermolecular $C-H\cdots\pi$ interactions.

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Comment

We have recently focused on the synthesis of fused heterocyclic systems containing the pyrimidone group using aza-Wittig reactions (Liu *et al.*, 2006). Iminophosphoranes are key intermediates, which can be converted into a wide range of pyrimidiones by reaction with various isocyanates and subsequent reaction with a secondary amine at room temperature. In this paper, we report the structure of the title compound, (I) (Fig. 1).





Figure 1

A view of the molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level. Both disorder components are shown.

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11400 measured reflections

 $R_{\rm int} = 0.090$

 $\theta_{\rm max} = 27.5^{\circ}$

5723 independent reflections

4468 reflections with $I > 2\sigma(I)$



Figure 2

A partial packing diagram of (I), showing the C-H··· π interactions as dashed lines. H atoms, except those involved in $C-H\cdots\pi$ interactions. have been omitted for clarity. One disorder component has been omitted for clarity.

The five-membered triazole ring is planar, with a maximum deviation of 0.003 (2) Å for atom N3. The phenyl ring C1–C6 is twisted with respect to the triazole ring, with a dihedral angle of 50.66 (12)°. A packing diagram is shown in Fig. 2. There exists a weak intermolecular $C-H\cdots\pi$ interaction between the ethyl group and phenyl ring C12-C17 (Table 1).

Experimental

To a solution of 5-amino-1-benzyl-4-ethoxycarbonyl-1,2,3-triazole (5 mmol) in anhydrous acetonitrile (15 ml) were added triphenylphosphine (15 mmol), hexachloroethane (15 mmol) and triethylamine (30 mmol). After the reaction mixture had been allowed to stand for 5 h at room temperature, the solution was concentrated under reduced pressure and the residue recrystallized from ethanol to afford the title compound, (I). The product was recrystallized from ethanol/dichloromethane (3:1) at room temperature to give single crystals suitable for X-ray diffraction analysis.

Crystal data

C29H25N4O2P $M_r = 492.50$ Triclinic, P1 a = 9.2719 (9) Å b = 10.1752 (9) Å c = 14.3413 (13) Å $\alpha = 83.580 \ (1)^{\circ}$ $\beta = 89.418 \ (2)^{\circ}$ $\gamma = 73.251 \ (2)^{\circ}$

V = 1287.1 (2) Å³ Z = 2 $D_x = 1.271 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation $\mu = 0.14 \text{ mm}^{-1}$ T = 292 (2) K Plate, green 0.36 \times 0.30 \times 0.10 mm

Data collection

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Bruker SMART 4K CCD area-
  detector diffractometer
\varphi and \omega scans
Absorption correction: multi-scan
  (SADABS; Sheldrick, 2003)
  T_{\min} = 0.951, T_{\max} = 0.986
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Refinement

Refinement on F^2	H-atom parameters constrained		
$R[F^2 > 2\sigma(F^2)] = 0.057$	$w = 1/[\sigma^2(F_o^2) + (0.1112P)^2]$		
$wR(F^2) = 0.189$	where $P = (F_0^2 + 2F_c^2)/3$		
S = 1.05	$(\Delta/\sigma)_{\rm max} < 0.001$		
5723 reflections	$\Delta \rho_{\rm max} = 0.66 \ {\rm e} \ {\rm \AA}^{-3}$		
337 parameters	$\Delta \rho_{\rm min} = -0.45 \text{ e } \text{\AA}^{-3}$		

Table 1

Hydrogen-bond geometry (Å, °).

Cg1 is the centroid of the C12-C17 ring.

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$C10-H10D\cdots Cg1^{i}$	0.97	2.86	3.758 (2)	155
	•			

Symmetry code: (i) x + 1, y, z.

H atoms were positioned geometrically (C-H = 0.93-0.97 Å) and constrained to ride on their parent atoms, with $U_{iso}(H) = 1.2U_{ea}(C)$ or $1.5U_{eq}$ (methyl C). The ethyl group C10-C11 is disordered over two sites. Refined occupancy factors converged to almost equal values of 0.520 (15) and 0.480 (15), and were then fixed at 0.5 in the final refinement.

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

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