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Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.003 Å R factor = 0.050 wR factor = 0.126 Data-to-parameter ratio = 14.1

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

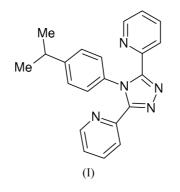
4-(4-Isopropylphenyl)-3,5-di-2-pyridyl-4*H*-1,2,4-triazole

In the title compound, $C_{21}H_{19}N_5$, the pyridyl groups and the benzene ring lie in a propeller arrangement around the central 1,2,4-triazole ring, minimizing the steric effects among these rings.

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Comment

Triazole derivatives play an important role in the development of coordination chemistry related to antibacterial and enzymatic reactions (Gupta & Bhargava, 1978; Cornelissen *et al.*, 1992; Kunkeler *et al.*, 1996). As an extension of work on the structural characterization of triazole derivatives, the crystal structure of the title compound, (I), is reported here.



In (I), the pyridyl groups and the benzene ring lie in a propeller arrangement around the central 1,2,4-triazole ring (Fig. 1), thereby minimizing the steric effects among these rings. The dihedral angles between the 4-isopropylphenyl ring and the two pyridyl rings (N1/C1–C5 and N4/C8–C12) are 55.0 (2) and 64.3 (2)°, respectively. The dihedral angle between the two pyridyl rings is 72.7 (2)°, the two pyridyl rings form dihedral angles of 43.7 (2) and 29.8 (2)° with the triazole ring, and the dihedral angle between the triazole ring and the 4-isopropylphenyl ring is 58.2 (2)°. The crystal structure is shown in Fig. 2. Intermolecular C–H···N short contacts are not observed, the H···N distances being longer than 2.70 Å.

Experimental

Compound (I) was synthesized by the reaction of equivalent amounts of *p*-isopropylphenylphosphazoanilide and N,N'-dipyridylhydrazine in N,N'-dimethylaniline for 3 h at 483–493 K (yield 72%). Colourless block-shaped crystals of (I) were obtained by slow evaporation of an acetone solution.

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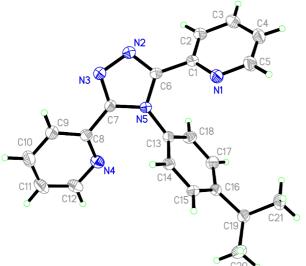


Figure 1

The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

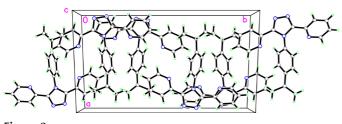


Figure 2

The crystal packing of (I), viewed along the c axis.

Crystal data

$C_{21}H_{19}N_5$	$D_x = 1.246 \text{ Mg m}^{-3}$
$M_r = 341.41$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 1463
a = 11.704 (1) Å	reflections
b = 19.935 (2) Å	$\theta = 2.9 - 21.2^{\circ}$
c = 8.181(1) Å	$\mu = 0.08 \text{ mm}^{-1}$
$\beta = 107.580 \ (2)^{\circ}$	T = 298 (2) K
V = 1819.7 (3) Å ³	Block, colourless
Z = 4	$0.23 \times 0.21 \times 0.18 \ \text{mm}$
Data collection	

Bruker SMART CCD area-detector33
diffractometer33
22 ω scans R_i Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)h
 $T_{min} = 0.982, T_{max} = 0.986$ k7778 measured reflectionsl =

3336 independent reflections
2245 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.034$
$\theta_{\rm max} = 25.5^{\circ}$
$h = -14 \rightarrow 12$
$k = -21 \rightarrow 24$
$l = -6 \rightarrow 9$

Re	finement
ĸe	nnement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.050$	$w = 1/[\sigma^2(F_o^2) + (0.0617P)^2]$
$wR(F^2) = 0.126$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.00	$(\Delta/\sigma)_{\rm max} < 0.001$
3336 reflections	$\Delta \rho_{\rm max} = 0.19 \ {\rm e} \ {\rm \AA}^{-3}$
237 parameters	$\Delta \rho_{\rm min} = -0.16 \text{ e} \text{ Å}^{-3}$

Table 1Selected geometric parameters (Å, $^{\circ}$).

N2-C6	1.310 (2)	N5-C6	1.367 (2)
N2-N3	1.381 (2)	N5-C7	1.368 (2)
N3-C7	1.312 (2)		
C6-N2-N3	107.21 (14)	N2-C6-N5	110.55 (16)
C7-N3-N2	107.49 (14)	N3-C7-N5	110.22 (16)
C6-N5-C7	104.53 (14)		
N1-C1-C6-N5	-44.3 (3)	C7-N5-C13-C14	-60.4(3)
N3-C7-C8-C9	-29.2 (3)		

All H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C–H distances of 0.93–0.96 Å, and with $U_{\rm iso}(\rm H) = 1.2$ or $1.5U_{\rm eq}(\rm C)$. The structure contains solvent-accessible voids of 35 Å³, which might accommodate a disordered water molecule.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*.

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