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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.004 Å R factor = 0.051 wR factor = 0.147 Data-to-parameter ratio = 13.5

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

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

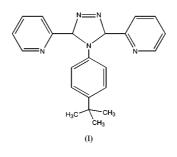
The title compound, $C_{22}H_{21}N_5$, has been synthesized and characterized by single-crystal X-ray diffraction. The dihedral angle between the benzene and triazole rings of the title compound is 117.6 (5)°. The triazole ring forms dihedral angles of 25.2 (5) and 136.7 (5)° with the two pyridyl rings.

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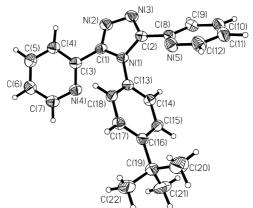
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Comment

Extensive studies have been carried out on substituted 1,2,4triazole ligands (Cornelissen *et al.*, 1992; Gupta & Bhargava, 1978; Kunkeler *et al.*, 1996). It is of interest that some iron(II) complexes containing substituted 1,2,4-triazole ligands are spin-crossover materials, which could be used as molecularbased memory devices, displays and optical switches (Garcia *et al.*, 1997; Kahn & Martinez, 1998). We have recently synthesized the title molecule, (I), which can act as a potentially dinucleating ligand. The present X-ray structure determination was carried out in order to elucidate the molecular conformation.



Bond lengths and angles in the structure are comparable with those reported for related structures (Wang *et al.*, 1998; Chen *et al.*, 1998; Fun *et al.*, 1999). The pyridyl groups and the



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The structure of (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme.

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benzene ring lie in a propeller arrangement around the central 1,2,4-triazole ring, thereby minimizing the steric effects among these rings. The dihedral angle between the planes of the benzene and triazole rings is $117.6 (5)^\circ$. The two pyridyl rings form dihedral angles of 25.2 (5) and 136.7 (5) $^{\circ}$ with the triazole ring.

Experimental

The title compound was synthesized by the reaction of equivalent amounts of 4,4'-p-(tert-butyl)phenylphosphazoanilide and N,N'dipyridoylhydrazine in N,N-dimethylaniline for 3 h at 483-493 K. Single crystals suitable for X-ray diffraction analysis were obtained by evaporation of an acetone solution.

Mo $K\alpha$ radiation

reflections

T = 298 (2) K

Crystal data

 $D_x = 1.260 \text{ Mg m}^{-3}$ C22H21N5 $M_r = 355.44$ Monoclinic, $P2_1/n$ Cell parameters from 1760 a = 15.348 (9) Åb = 5.980(3) Å $\theta = 3.0-20.9^{\circ}$ $\mu = 0.08~\mathrm{mm}^{-1}$ $c = 20.909 (12) \text{ \AA}$ $\beta = 102.488 \ (9)^{\circ}$ $V = 1873.7 (18) \text{ Å}^3$ Prism, colorless $0.45 \times 0.33 \times 0.29 \mbox{ mm}$ Z = 4

Data collection

Bruker SMART CCD area-detector	3291 independent reflections
diffractometer	1729 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.042$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.0^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -18 \rightarrow 18$
$T_{\min} = 0.966, T_{\max} = 0.978$	$k = -7 \rightarrow 6$
9340 measured reflections	$l = -21 \rightarrow 24$

Refinement

Refinement on F^2 H-atom parameters constrained $R[F^2 > 2\sigma(F^2)] = 0.051$ $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0721P)^{2}]$ $wR(F^2) = 0.147$ where $P = (F_o^2 + 2F_c^2)/3$ S = 0.96 $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.30 \ {\rm e} \ {\rm \AA}^{-3}$ 3291 reflections $\Delta \rho_{\rm min} = -0.18 \text{ e } \text{\AA}^{-3}$ 244 parameters

Table 1

Selected geometric parameters (Å, °).

N1-C1	1.372 (3)	N4-C7	1.337 (3)
N1-C2	1.373 (3)	N4-C3	1.339 (3)
N1-C13	1.437 (3)	N5-C8	1.335 (3)
N2-C1	1.304 (3)	N5-C12	1.335 (4)
N2-N3	1.386 (3)	C16-C19	1.517 (4)
N3-C2	1.304 (3)		
N2-C1-C3-N4	155.9 (3)	C1-N1-C13-C18	-68.8 (3)
N3-C2-C8-C9	-44.0 (4)		

All H atoms were placed in idealized positions and constrained to ride on their parent atoms, with C-H distances of 0.96 Å and with $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C}).$

Data collection: SMART (Bruker, 1998); cell refinement: SMART; data reduction: SAINT (Bruker, 1998) and SHELXTL (Bruker, 1997); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick,

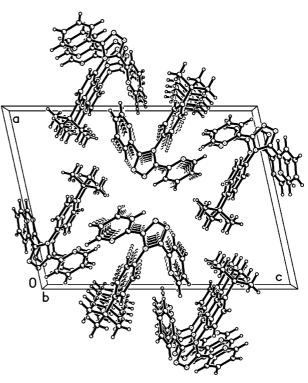


Figure 2 The molecular packing of (I), viewed along the b axis.

1997); molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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