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Key indicators

Single-crystal X-ray study T = 295 KMean σ (C–C) = 0.003 Å R factor = 0.063 wR factor = 0.203 Data-to-parameter ratio = 16.0

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

2-[3-(2-Cyano-2-propyl)-5-(1,2,4-triazol-1-yl)phenyl]-2-methylpropiononitrile

In the title compound, $C_{17}H_{19}N_5$, the almost ideally planar triazole ring forms a dihedral angle of 75.1 (1)° with the benzene ring. There are intermolecular π - π interactions.

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Comment

The title compound, (I), an aromatase inhibitor, has been shown to be useful in second-line therapy of estrogendependent breast cancer and has recently been approved as first-line therapy in several countries (Goss & Strasser, 2001). In this paper, we report the crystal structure of (I). The bond lengths and bond angles are in agreement with those reported for other 1,2,4-triazole derivatives (Chinnakali *et al.*, 1999; Mazur *et al.*, 2004) and are within the expected ranges. The almost ideally planar triazole ring forms a dihedral angle of 75.1 (1)° with the benzene ring (Fig. 1). Atom C7 is coplanar with the triazole ring. In the crystal structure (Fig. 2), a π - π interaction is observed between the benzene ring and the symmetry-related ring at $(1 - x, y, \frac{3}{2} - z)$; the distance between the centroids of the benzene rings is 3.995 Å.



Experimental

Compound (I) was a gift from Linhai Dongdog Chemical Factory. Crystals were grown from an acetone solution by slow evaporation at room temperature.

Crystal data

$C_{17}H_{19}N_5$	$D_x = 1.196 \text{ Mg m}^{-3}$
$M_r = 293.37$	Mo $K\alpha$ radiation
Monoclinic, $C2/c$	Cell parameters from 10339
a = 17.9107 (8) Å	reflections
b = 11.2522 (3) Å	$\theta = 2.2-27.5^{\circ}$
c = 18.9011 (7) Å	$\mu = 0.08 \text{ mm}^{-1}$
$\beta = 121.181(1)^{\circ}$	T = 295 (1) K
V = 3258.9 (2) Å ³	Prism, colorless
Z = 8	$0.45 \times 0.45 \times 0.20 \text{ mm}$

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Figure 1

Molecular structure of (I), showing 30% probability displacement ellipsoids.

Data collection

Rigaku R-AXIS RAPID
diffractometer2348 reflections with $F^2 > 2\sigma(F^2)$
 $R_{int} = 0.031$
 ω scans ω scans $\theta_{max} = 27.5^{\circ}$
Absorption correction: noneAbsorption correction: none $h = -23 \rightarrow 23$
 $k = -14 \rightarrow 14$
3748 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.063$ $wR(F^2) = 0.203$ S = 1.003197 reflections 200 parameters H-atom parameters constrained $w = 1/[0.0057F_{o}^{2} + \sigma(F_{o}^{2})]/(4F_{o}^{2})$ (Δ/σ)_{max} < 0.001 $\Delta\rho_{max} = 0.37 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{min} = -0.37 \text{ e } \text{\AA}^{-3}$ Extinction correction: Larson

Extinction correction: Larson (1970) Extinction coefficient: 1.8 (6) $\times 10^2$



Figure 2 Packing arrangement for (I). H atoms have been omitted for clarity.

The high-angle reflections $(2\theta > 52^\circ)$ were not used in the refinement, because they were weak. H atoms were placed in calculated positions, with C–H = 0.93 Å, and included in the refinement in a riding model, with $U_{iso}(H) = 1.2U_{eq}$ (carrier atom).

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/ MSC, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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