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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C-C}) = 0.004 \text{ Å}$ R factor = 0.058 wR factor = 0.162Data-to-parameter ratio = 11.4

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

1-[2,6-Dichloro-4-(trifluoromethyl)phenyl]-5-[(4-nitrophenyl)methyleneimino]-1*H*-pyrazole-3-carbonitrile

The title compound, $C_{18}H_8Cl_2F_3N_5O_2$, is a tricyclic imide with an overall U-shape, each of the three rings being planar.

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Comment

The title compound, (I), is an important starting material for the synthesis of 5-amino-3-cyano-1-(2,6-dichloro-4-trifluoro-methylphenyl)-4-(trifluoromethyl)thiopyrazole, 5-amino-3-cyano-1-(2,6-dichloro-4-trifluoromethylphenyl)-4-(trifluoro-methyl)sulfenylpyrazole and 5-amino-3-cyano-1-(2,6-dichloro-4-trifluoromethylphenyl)-4-(trifluoromethyl)sulfonylpyrazole, which are all good insecticides (Hatton *et al.*, 1993).

$$O_2N$$
 CI
 CF_3
 CI

The structure of (I) is shown in Fig. 1, with the atomnumbering scheme. The molecule contains three planar groups, forming an overall U-shape, viz. a 2,6-dichloro-4-(trifluoromethyl)phenyl group, a pyrazole ring and a 4-nitrophenyl ring. The C-F bond lengths and F-C-F angles are in normal ranges (Hassall & White, 2004), allowing for the possibility of unresolved disorder. The dihedral angles between the pyrazole and the C1-C6 and C12-C17 benzene rings are 28.5 (1) and 74.7 (1)°, respectively. There are π - π interactions between the pyrazole ring and the C1-C6 benzene ring. In the crystal structure, the molecules stack along the a axis, as shown in Fig. 2.

Experimental

Following the method of Hatton *et al.* (1993), reaction of 2,6-dichloro-4-(trifluoromethyl)aniline with a suspension of nitrosylsulfuric acid, followed by reaction with a solution of ethyl 2,3-dicyanopropionate in acetic acid, gave 5-amino-3-cyano-1-(2,6-dichloro-4-trifluoromethylphenyl)pyrazole, which then reacted with 4-nitrobenzaldehyde to give the title compound, (I). Single crystals suitable for X-ray analysis were obtained by slow evaporation of a methanol solution (m.p. 464–465 K). IR (KBr, ν cm⁻¹): 3133, 2360, 2241, 1620, 1596, 1523, 1345, 1315, 861, 823; ¹H NMR (CDCl₃): δ 9.26 (s, 1H), 8.30 (d, J = 8.8 Hz, 2H), 8.14 (s, 2H), 8.08 (d, J = 8.8 Hz, 2H), 7.39 (s, 1H); ¹³C NMR (CDCl₃): δ 166.6 (1C), 152.9 (1C), 141.3 (1C), 137.7 (1C), 136.5 (1C), 134.5 (q, J = 34.1 Hz, 1C), 132.4 (2C), 130.1 (1C), 128.4 (2C), 126.8 (2C), 123.8 (2C), 123.3 (q, J = 269.6 Hz, 1C), 114.1 (1C), 100.9 (1C).

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Crystal data

$C_{18}H_8Cl_2F_3N_5O_2$	Z = 2
$M_r = 454.19$	$D_x = 1.561 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Mo $K\alpha$ radiation
a = 6.8108 (8) Å	Cell parameters from 2373
b = 11.0797 (12) Å	reflections
c = 13.3766 (15) Å	$\theta = 1.9 - 25.3^{\circ}$
$\alpha = 75.862 (2)^{\circ}$	$\mu = 0.39 \text{ mm}^{-1}$
$\beta = 84.841 \ (2)^{\circ}$	T = 298 (2) K
$\gamma = 81.296 \ (2)^{\circ}$	Block, colorless
$V = 966.09 (19) \text{ Å}^3$	$0.28 \times 0.22 \times 0.17 \text{ mm}$

Data collection

Bruker SMART APEX area- detector diffractometer φ and ω scans Absorption correction: multi-scan (SADABS; Bruker, 2002)	3449 independent reflections 2726 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.014$ $\theta_{\text{max}} = 25.3^{\circ}$ $h = -7 \rightarrow 8$
φ and ω scans	$R_{\rm int} = 0.014$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.3^{\circ}$
(SADABS; Bruker, 2002)	$h = -7 \rightarrow 8$
$T_{\min} = 0.902, T_{\max} = 0.936$	$k = -13 \rightarrow 13$
5202 measured reflections	$l = -12 \rightarrow 16$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0803P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.058$	+ 0.4474P]
$wR(F^2) = 0.162$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.04	$(\Delta/\sigma)_{\rm max} < 0.001$
3449 reflections	$\Delta \rho_{\text{max}} = 0.41 \text{ e Å}^{-3}$
303 parameters	$\Delta \rho_{\min} = -0.41 \text{ e Å}^{-3}$
All H-atom parameters refined	

All H atoms were located in a difference Fourier map and were refined freely. The CF₃ group may be subject to unresolved disorder.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL* (Bruker, 2002); software used to prepare material for publication: *SHELXTL*.

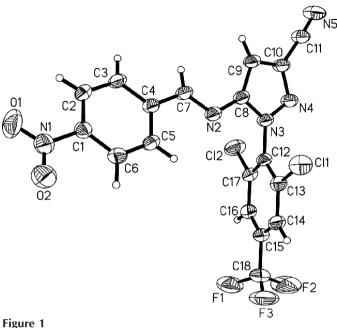
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The structure of (I), showing the atomic numbering scheme and displacement ellipsoids drawn at the 50% probability level.

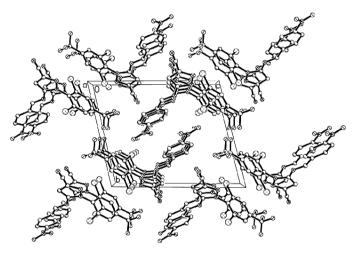


Figure 2 Packing diagram for (I), viewed down the *a* axis.

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