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Key indicators

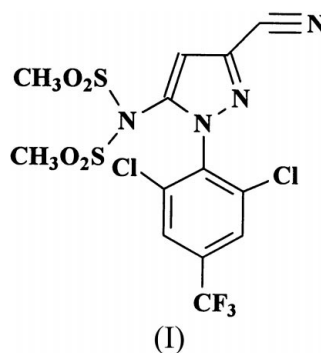
Single-crystal X-ray study
 $T = 298\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$
 R factor = 0.049
 wR factor = 0.135
Data-to-parameter ratio = 13.3For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.1-[2,6-Dichloro-4-(trifluoromethyl)phenyl]-
5-[(dimethylsulfonyl)amino]-1*H*-pyrazole-
3-carbonitrileThe title compound, $\text{C}_{13}\text{H}_9\text{Cl}_2\text{F}_3\text{N}_4\text{O}_4\text{S}_2$, is a bicyclic sulfo-
nated amide with an overall U-shape, each of the two rings
being planar.

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Comment

The title compound, (I), has been used to synthesize
5-amino-3-cyano-1-[2,6-dichloro-4-(trifluoromethyl)phenyl]-
4-(trifluoromethyl)thiopyrazole, 5-amino-3-cyano-1-[2,6-di-
chloro-4-(trifluoromethyl)phenyl]-4-(trifluoromethylsulfonyl)-
pyrazole and 5-amino-3-cyano-1-[2,6-dichloro-4-(trifluoro-
methyl)phenyl]-4-(trifluoromethylsulfonyl)pyrazole. All of
these compounds were found to be good insecticides (Hatton
et al., 1993).The molecular structure of (I) is shown in Fig. 1, and
selected geometric parameters are given in Table 1. The
molecule has an overall U-shape. The dihedral angle between
the mean planes through the pyrazole ring and the benzene
ring is $73.2(1)^\circ$.In the crystal structure of (I), the molecules stack along the
 a axis, as shown in Fig. 2.

Experimental

Following the method of Hatton *et al.* (1993), 2,6-dichloro-4-
trifluoromethylamine was reacted with a suspension of nitrosyl
sulfuric acid, followed by reaction with a solution of ethyl 2,3-
dicyanopropionate in acetic acid. This reaction gave 5-amino-3-
cyano-1-[2,6-dichloro-4-(trifluoromethyl)phenyl]pyrazole, which was
then reacted with two equivalents of methanesulfonyl chloride in
pyridine to give (I). Single crystals suitable for X-ray analysis were
obtained by slow evaporation of an acetone solution (m.p. 505–
507 K). IR (KBr, cm^{-1}): 3146, 3075, 2252, 1537, 1378, 1365, 1319,
1171, 1136; ^1H NMR (CDCl_3 , p.p.m.): 8.12 (s, 2H), 7.70 (s, 1H), 3.54
(s, 6H); ^{13}C NMR (CDCl_3 , p.p.m.): 137.1 (1 C), 136.6 (1 C), 135.5
(1 C), 127.9 (1 C), 127.5 (2 C), 127.4 (2 C), 123.2 (1 C), 114.6 (1 C), 113.2
(1 C), 42.8 (2 C).

Crystal data

$C_{13}H_9Cl_2F_3N_4O_4S_2$
 $M_r = 477.26$
 Triclinic, $P\bar{1}$
 $a = 8.4681$ (7) Å
 $b = 8.9652$ (8) Å
 $c = 14.3497$ (12) Å
 $\alpha = 75.198$ (2)°
 $\beta = 87.918$ (1)°
 $\gamma = 65.395$ (1)°
 $V = 954.57$ (14) Å³

$Z = 2$
 $D_x = 1.660$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 2990
 reflections
 $\theta = 2.6$ – 25.2 °
 $\mu = 0.62$ mm⁻¹
 $T = 298$ (2) K
 Block, colourless
 $0.41 \times 0.28 \times 0.24$ mm

Data collection

Bruker APEX area-detector
 diffractometer
 φ and ω scans
 Absorption correction: multi-scan
 (SADABS; Bruker, 2002)
 $T_{\min} = 0.786$, $T_{\max} = 0.866$
 5126 measured reflections

3400 independent reflections
 3039 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.012$
 $\theta_{\text{max}} = 25.3$ °
 $h = -10 \rightarrow 10$
 $k = -10 \rightarrow 7$
 $l = -16 \rightarrow 17$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.049$
 $wR(F^2) = 0.136$
 $S = 1.04$
 3400 reflections
 255 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0723P)^2 + 0.9462P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 1.00$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.57$ e Å⁻³

Table 1

Selected geometric parameters (Å, °).

C11–C4	1.724 (3)	N1–C5	1.427 (3)
S1–N4	1.729 (2)	N2–C10	1.330 (4)
S1–C12	1.757 (3)	N3–C11	1.136 (4)
S2–N4	1.705 (2)	C1–C2	1.496 (5)
S2–C13	1.752 (4)	C8–C9	1.360 (4)
F1–C1	1.254 (5)	C8–N4	1.414 (4)
N1–N2	1.341 (3)	C9–C10	1.398 (4)
N1–C8	1.375 (3)	C10–C11	1.435 (4)
O1–S1–N4	105.04 (12)	C9–C8–N1	106.9 (2)
O1–S1–C12	110.46 (16)	C9–C8–N4	130.4 (2)
N4–S1–C12	102.93 (15)	N1–C8–N4	122.7 (2)
N2–N1–C8	111.8 (2)	C8–C9–C10	104.3 (2)
N2–N1–C5	117.6 (2)	N2–C10–C9	112.7 (3)
C8–N1–C5	130.5 (2)	N2–C10–C11	119.8 (3)
C10–N2–N1	104.2 (2)	C9–C10–C11	127.5 (3)
F1–C1–F3	111.1 (4)	N3–C11–C10	178.6 (4)
F1–C1–C2	113.8 (3)	C8–N4–S2	116.78 (19)
C3–C2–C1	118.3 (3)	S2–N4–S1	117.75 (13)
C4–C3–C2	119.2 (3)		

All H atoms were initially located in a difference Fourier map and were then placed in geometrically idealized position and constrained to ride on their parent atom, with C–H distances in the range 0.93–0.96 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{C})$. Although the F atoms display large displacement parameters, no disorder model could be defined.

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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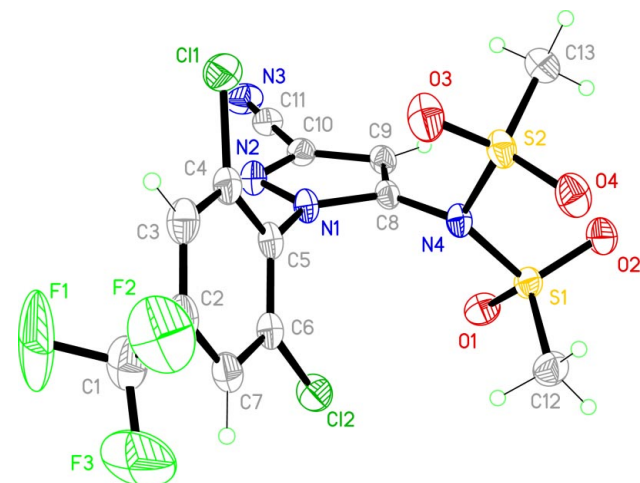


Figure 1

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

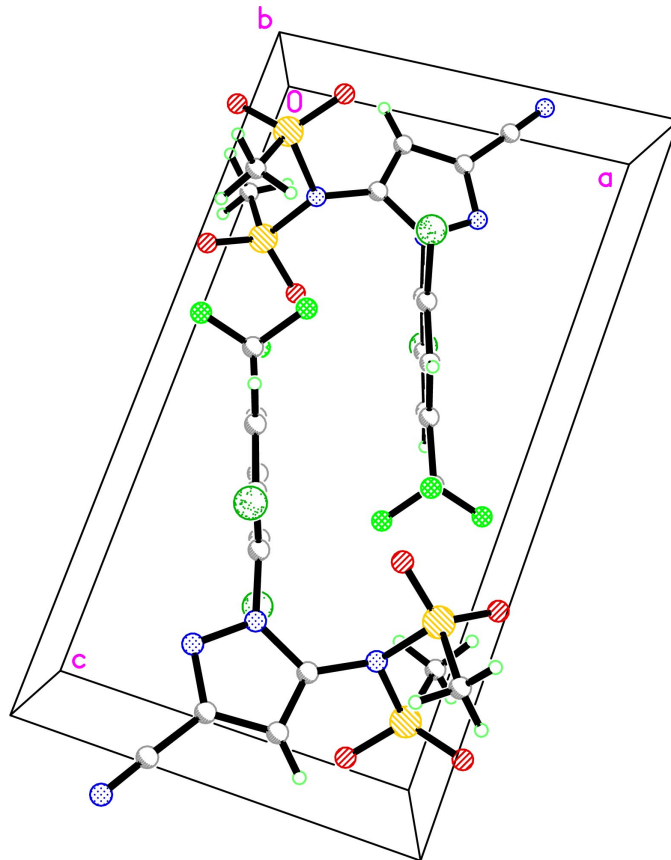


Figure 2

The unit-cell contents for (I), viewed down the b axis.

References

- Bruker (2002). SMART, SAINT, SADABS, XP and SHELXTL. Bruker AXS Inc., Madison, Wisconsin, USA.
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