

4-(5-Phenyl-3-trifluoromethyl-1H-pyrazol-1-yl)benzenesulfonamide

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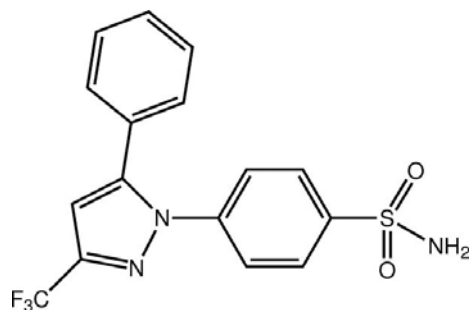
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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; R factor = 0.043; wR factor = 0.113; data-to-parameter ratio = 15.2.

Significant twists between the aromatic rings are evident in the structure of the title compound, $\text{C}_{16}\text{H}_{12}\text{F}_3\text{N}_3\text{O}_2\text{S}$. With reference to the pyrazole plane, the N- and C-bound benzene rings form dihedral angles of 57.12 (11) and 29.75 (11)°, respectively. The dihedral angle between the benzene rings is 52.82 (11)°. The presence of $\text{N}-\text{H}\cdots\text{O}$ (sulfonamide) and $\text{N}-\text{H}\cdots\text{N}$ (pyrazole) hydrogen bonds lead to supramolecular tubes along the b -axis direction. These are connected into layers *via* $\text{C}-\text{H}\cdots\text{O}$ interactions involving a bifurcated O atom (not involved in the $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonding). Layers stack along the a -axis direction.

Related literature

For background to the biological applications of related species, see: Faidallah *et al.* (2007); Al-Saadi *et al.* (2008). For the crystal structure of a related species, see: Dev *et al.* (1999).



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Experimental

Crystal data

$\text{C}_{16}\text{H}_{12}\text{F}_3\text{N}_3\text{O}_2\text{S}$
 $M_r = 367.35$
Monoclinic, $P2_1/c$
 $a = 16.2430$ (7) Å
 $b = 4.9461$ (2) Å
 $c = 21.2383$ (8) Å
 $\beta = 111.231$ (5)°

$V = 1590.47$ (11) Å³
 $Z = 4$
Mo $K\alpha$ radiation
 $\mu = 0.25$ mm⁻¹
 $T = 100$ K
 $0.40 \times 0.10 \times 0.05$ mm

Data collection

Agilent SuperNova Dual diffractometer with an Atlas detector
Absorption correction: multi-scan (*CrysAlis PRO*; Agilent, 2010)
 $T_{\min} = 0.735$, $T_{\max} = 1.000$

7901 measured reflections
3560 independent reflections
2876 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.031$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.043$
 $wR(F^2) = 0.113$
 $S = 1.06$
3560 reflections
234 parameters

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\max} = 0.34$ e Å⁻³
 $\Delta\rho_{\min} = -0.49$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$\text{N3}-\text{H1}\cdots\text{O1}^{\text{i}}$	0.84 (3)	2.14 (3)	2.911 (2)	153 (2)
$\text{N3}-\text{H2}\cdots\text{N2}^{\text{ii}}$	0.87 (2)	2.21 (3)	3.049 (3)	164 (2)
$\text{C9}-\text{H9}\cdots\text{O2}^{\text{iii}}$	0.95	2.49	3.376 (3)	155
$\text{C16}-\text{H16}\cdots\text{O2}^{\text{iv}}$	0.95	2.55	3.137 (2)	120

Symmetry codes: (i) $x, y - 1, z$; (ii) $-x + 1, -y + 1, -z + 1$; (iii) $-x + 1, y + \frac{1}{2}, -z + \frac{1}{2}$; (iv) $-x + 1, y - \frac{1}{2}, -z + \frac{1}{2}$.

Data collection: *CrysAlis PRO* (Agilent, 2010); cell refinement: *CrysAlis PRO*; data reduction: *CrysAlis PRO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3* (Farrugia, 1997) and *DIAMOND* (Brandenburg, 2006); software used to prepare material for publication: *pubCIF* (Westrip, 2010).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HG5083).

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