

4-(3-Methyl-5-phenyl-1*H*-pyrazol-1-yl)-benzenesulfonamide

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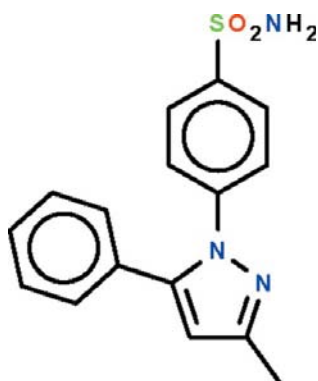
Received 11 August 2011; accepted 13 August 2011

Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(C-C) = 0.003$ Å; R factor = 0.041; wR factor = 0.115; data-to-parameter ratio = 15.1.

With respect to the planar five-membered ring of the title compound, $C_{16}H_{15}N_3O_2S$, the phenyl ring is aligned at $47.0(1)^\circ$ and the phenylene ring at $37.6(1)^\circ$. The amino group has the N atom in a pyramidal geometry; the group is a hydrogen-bond donor to the sulfonyl O atom of one molecule and to the pyrazole N atom of another molecule, resulting in the formation of a layer parallel to the bc plane.

Related literature

For the synthesis, see: Gosselin *et al.* (2006); Organ & Mayer (2003).



Experimental

Crystal data

$C_{16}H_{15}N_3O_2S$
 $M_r = 313.37$
Monoclinic, $C2/c$
 $a = 28.2545(8)$ Å
 $b = 11.9135(4)$ Å
 $c = 9.3739(3)$ Å
 $\beta = 91.016(3)^\circ$
 $V = 3154.85(17)$ Å³
 $Z = 8$
Cu $K\alpha$ radiation
 $\mu = 1.91$ mm⁻¹
 $T = 100$ K
 $0.30 \times 0.03 \times 0.03$ mm

Data collection

Agilent SuperNova Dual diffractometer with an Atlas detector
Absorption correction: multi-scan (*CrysAlis PRO*; Agilent, 2010)
 $T_{min} = 0.598$, $T_{max} = 0.945$
6579 measured reflections
3137 independent reflections
2689 reflections with $I > 2\sigma(I)$
 $R_{int} = 0.035$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.041$
 $wR(F^2) = 0.115$
 $S = 1.03$
3137 reflections
208 parameters
H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{max} = 0.33$ e Å⁻³
 $\Delta\rho_{min} = -0.51$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N1-H1 \cdots N3^i$	0.92 (2)	1.98 (2)	2.878 (2)	164 (2)
$N1-H2 \cdots O1^{ii}$	0.86 (2)	2.07 (2)	2.930 (2)	177 (2)

Symmetry codes: (i) $-x + \frac{3}{2}, -y + \frac{1}{2}, -z + 1$; (ii) $x, -y + 1, z - \frac{1}{2}$.

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: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *publCIF* (Westrip, 2010).

We thank King Abdulaziz University and the University of Malaya for supporting this study.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BT5609).

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