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4-(3,5-Dimethyl-1*H*-pyrazol-1-yl)-benzenesulfonamide

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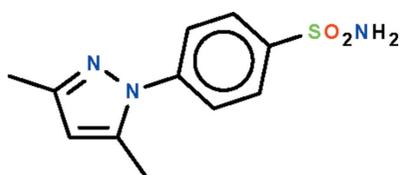
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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.002$ Å; R factor = 0.031; wR factor = 0.083; data-to-parameter ratio = 14.1.

The two aromatic rings of the title compound, $\text{C}_{11}\text{H}_{13}\text{N}_3\text{O}_2\text{S}$, are inclined at an angle of $47.81(4)^\circ$. The N atom of the amino unit is pyramidally coordinated; one H atom interacts with the sulfamyl O atom of an adjacent molecule, forming a centrosymmetric hydrogen-bonded dimer. The dimers are linked by $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds, generating a three-dimensional network.

Related literature

For the synthesis and medicinal properties of the title compound, see: Grueneberg *et al.* (2002); Wright *et al.* (1964).



Experimental

Crystal data

$\text{C}_{11}\text{H}_{13}\text{N}_3\text{O}_2\text{S}$
 $M_r = 251.30$
 Monoclinic, $P2_1/n$

$a = 7.9649(1)$ Å
 $b = 11.7827(2)$ Å
 $c = 12.2720(2)$ Å

$\beta = 91.720(1)^\circ$
 $V = 1151.18(3)$ Å³
 $Z = 4$
 Cu $K\alpha$ radiation

$\mu = 2.47$ mm⁻¹
 $T = 100$ K
 $0.30 \times 0.20 \times 0.02$ mm

Data collection

Agilent SuperNova Dual diffractometer with an Atlas detector
 Absorption correction: multi-scan (*CrysAlis PRO*; Agilent, 2010)
 $T_{\min} = 0.525$, $T_{\max} = 0.952$

8510 measured reflections
 2312 independent reflections
 2215 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.018$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.031$
 $wR(F^2) = 0.083$
 $S = 1.07$
 2312 reflections
 164 parameters
 2 restraints

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\max} = 0.35$ e Å⁻³
 $\Delta\rho_{\min} = -0.41$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N3}-\text{H1}\cdots\text{O1}^i$	0.87 (1)	2.13 (1)	2.966 (2)	160 (2)
$\text{N3}-\text{H1}\cdots\text{N2}^{ii}$	0.87 (1)	2.94 (2)	3.501 (2)	124 (2)

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

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: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *pubCIF* (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: BT5610).

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supporting information

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4-(3,5-Dimethyl-1H-pyrazol-1-yl)benzenesulfonamide

Abdullah M. Asiri, Hassan M. Faidallah, Abdulrahman O. Al-Youbi and Seik Weng Ng

S1. Comment

The title compound (Scheme I) was first synthesized in order to examine its anti-diabetic activity (Wright *et al.*, 1964). It has also been listed in a virtual screening of compound libraries in order to search for possible medicinal properties (Grueneberg *et al.*, 2002). The two aromatic rings are inclined at 47.81 (4) °. The N atom of the amino unit is pyramidally coordinated (Fig. 1). One H atom interacts with the sulfamyl O atom of an adjacent molecule to form a centrosymmetric hydrogen-bonded dimer; the dimers are linked by an N–H···N hydrogen bond to generate a layer motif.

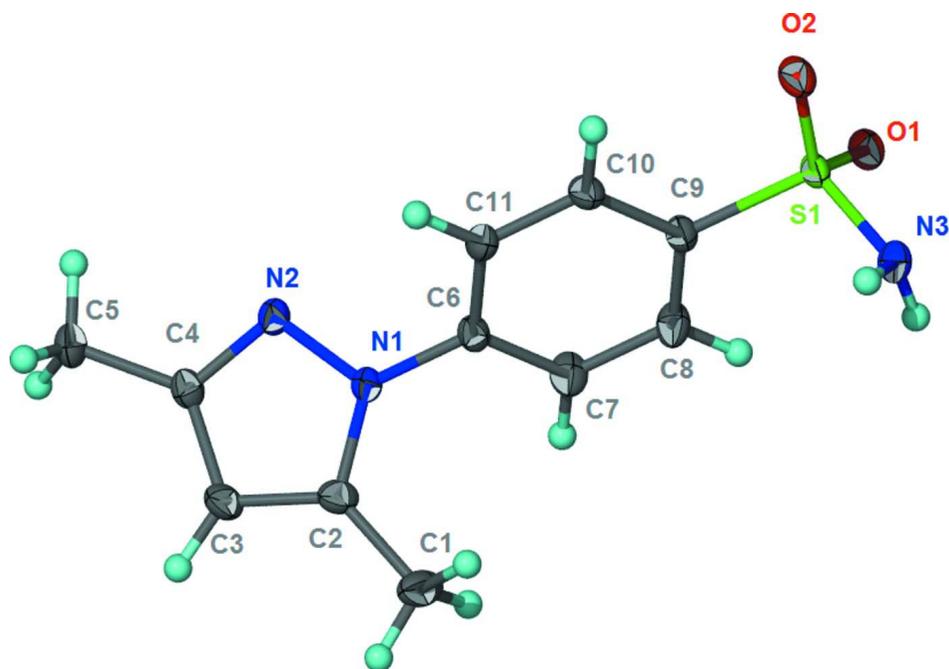
S2. Experimental

2,4-Pentanedione (10 mmol) and 4-hydrazinobenzenesulfonamide hydrochloride (10 mmol) were heated in ethanol (50 ml) for 4 h; water was then added to precipitate the product. This was collected and recrystallized from ethanol to yield orange crystals; m.p. 516–517 K.

S3. Refinement

Carbon bound H-atoms were placed in calculated positions [C–H 0.95 to 0.98 Å, $U_{\text{iso}}(\text{H})$ 1.2–1.5 $U_{\text{eq}}(\text{C})$] and were included in the refinement in the riding model approximation.

The amino H-atoms were located in a difference Fourier map and were refined with a distance restraint of N–H 0.88±0.01 Å; their displacement parameters were freely refined.

**Figure 1**

Anisotropic displacement ellipsoid plot (Barbour, 2001) of $C_{11}H_{13}N_3O_2S$ at the 70% probability level; hydrogen atoms are drawn as spheres of arbitrary radius.

4-(3,5-Dimethyl-1H-pyrazol-1-yl)benzenesulfonamide

Crystal data

$C_{11}H_{13}N_3O_2S$

$M_r = 251.30$

Monoclinic, $P2_1/n$

Hall symbol: $-P 2_1n$

$a = 7.9649$ (1) Å

$b = 11.7827$ (2) Å

$c = 12.2720$ (2) Å

$\beta = 91.720$ (1)°

$V = 1151.18$ (3) Å³

$Z = 4$

$F(000) = 528$

$D_x = 1.450$ Mg m⁻³

Cu $K\alpha$ radiation, $\lambda = 1.54184$ Å

Cell parameters from 6177 reflections

$\theta = 3.6\text{--}74.0^\circ$

$\mu = 2.47$ mm⁻¹

$T = 100$ K

Plate, orange

$0.30 \times 0.20 \times 0.02$ mm

Data collection

Agilent SuperNova Dual

diffractometer with an Atlas detector

Radiation source: SuperNova (Cu) X-ray

Source

Mirror monochromator

Detector resolution: 10.4041 pixels mm⁻¹

ω scans

Absorption correction: multi-scan

(*CrysAlis PRO*; Agilent, 2010)

$T_{\min} = 0.525$, $T_{\max} = 0.952$

8510 measured reflections

2312 independent reflections

2215 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.018$

$\theta_{\max} = 74.2^\circ$, $\theta_{\min} = 5.2^\circ$

$h = -7 \rightarrow 9$

$k = -14 \rightarrow 14$

$l = -15 \rightarrow 15$

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.031$
 $wR(F^2) = 0.083$
 $S = 1.07$
 2312 reflections
 164 parameters
 2 restraints
 Primary atom site location: structure-invariant
 direct methods

Secondary atom site location: difference Fourier
 map
 Hydrogen site location: inferred from
 neighbouring sites
 H atoms treated by a mixture of independent
 and constrained refinement
 $w = 1/[\sigma^2(F_o^2) + (0.0441P)^2 + 0.7227P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.35 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.41 \text{ e } \text{\AA}^{-3}$

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
S1	0.60099 (4)	0.32597 (3)	0.50334 (2)	0.01314 (12)
O1	0.44016 (12)	0.37270 (8)	0.52982 (8)	0.0170 (2)
O2	0.65114 (14)	0.21872 (9)	0.54890 (8)	0.0208 (2)
N1	0.61599 (14)	0.27786 (10)	0.02059 (9)	0.0136 (2)
N2	0.55511 (14)	0.18062 (10)	-0.02758 (9)	0.0143 (2)
N3	0.74013 (15)	0.41830 (10)	0.54060 (9)	0.0152 (2)
C1	0.7815 (2)	0.45338 (13)	-0.02125 (12)	0.0232 (3)
H1A	0.8510	0.4777	-0.0815	0.035*
H1B	0.8535	0.4386	0.0434	0.035*
H1C	0.7007	0.5132	-0.0049	0.035*
C2	0.68933 (17)	0.34759 (12)	-0.05284 (11)	0.0161 (3)
C3	0.67052 (18)	0.29522 (12)	-0.15234 (11)	0.0170 (3)
H3	0.7068	0.3228	-0.2205	0.020*
C4	0.58685 (17)	0.19256 (12)	-0.13311 (11)	0.0147 (3)
C5	0.53563 (19)	0.10247 (13)	-0.21321 (11)	0.0196 (3)
H5A	0.4668	0.0456	-0.1771	0.029*
H5B	0.6361	0.0660	-0.2413	0.029*
H5C	0.4705	0.1367	-0.2737	0.029*
C6	0.61070 (16)	0.28964 (12)	0.13566 (11)	0.0136 (3)
C7	0.55663 (18)	0.39093 (12)	0.18128 (11)	0.0183 (3)
H7	0.5220	0.4521	0.1355	0.022*
C8	0.55342 (18)	0.40237 (12)	0.29364 (11)	0.0179 (3)
H8	0.5176	0.4715	0.3253	0.021*
C9	0.60328 (17)	0.31154 (11)	0.35950 (11)	0.0137 (3)
C10	0.65597 (18)	0.21010 (12)	0.31423 (11)	0.0163 (3)
H10	0.6891	0.1485	0.3600	0.020*
C11	0.66000 (18)	0.19918 (12)	0.20165 (11)	0.0163 (3)
H11	0.6963	0.1302	0.1700	0.020*
H1	0.712 (2)	0.4870 (10)	0.5225 (15)	0.029 (5)*
H2	0.8410 (14)	0.3966 (16)	0.5246 (16)	0.029 (5)*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.01682 (19)	0.01279 (19)	0.00991 (18)	0.00155 (11)	0.00214 (12)	-0.00074 (11)
O1	0.0163 (5)	0.0191 (5)	0.0160 (5)	0.0001 (4)	0.0045 (4)	-0.0025 (4)
O2	0.0332 (6)	0.0157 (5)	0.0138 (5)	0.0049 (4)	0.0028 (4)	0.0018 (4)
N1	0.0153 (6)	0.0143 (6)	0.0110 (5)	-0.0028 (4)	-0.0002 (4)	-0.0017 (4)
N2	0.0142 (5)	0.0159 (6)	0.0128 (6)	-0.0034 (4)	0.0002 (4)	-0.0028 (4)
N3	0.0144 (6)	0.0161 (6)	0.0150 (6)	0.0024 (4)	-0.0003 (4)	-0.0027 (4)
C1	0.0300 (8)	0.0207 (7)	0.0187 (7)	-0.0104 (6)	-0.0052 (6)	0.0036 (6)
C2	0.0169 (6)	0.0165 (7)	0.0149 (6)	-0.0024 (5)	-0.0014 (5)	0.0036 (5)
C3	0.0194 (7)	0.0199 (7)	0.0117 (6)	-0.0022 (5)	-0.0005 (5)	0.0028 (5)
C4	0.0141 (6)	0.0183 (7)	0.0114 (6)	0.0002 (5)	-0.0011 (5)	-0.0011 (5)
C5	0.0248 (7)	0.0209 (7)	0.0130 (6)	-0.0018 (6)	-0.0006 (5)	-0.0039 (5)
C6	0.0123 (6)	0.0173 (7)	0.0113 (6)	-0.0025 (5)	0.0001 (5)	-0.0018 (5)
C7	0.0222 (7)	0.0173 (7)	0.0151 (7)	0.0050 (5)	-0.0033 (5)	0.0003 (5)
C8	0.0219 (7)	0.0160 (7)	0.0157 (7)	0.0048 (5)	-0.0012 (5)	-0.0033 (5)
C9	0.0136 (6)	0.0159 (6)	0.0117 (6)	-0.0005 (5)	0.0012 (5)	-0.0015 (5)
C10	0.0221 (7)	0.0130 (6)	0.0140 (6)	0.0014 (5)	0.0032 (5)	0.0016 (5)
C11	0.0213 (7)	0.0128 (6)	0.0148 (7)	0.0000 (5)	0.0039 (5)	-0.0020 (5)

Geometric parameters (\AA , $^\circ$)

S1—O2	1.4338 (10)	C3—H3	0.9500
S1—O1	1.4404 (10)	C4—C5	1.4952 (19)
S1—N3	1.6094 (12)	C5—H5A	0.9800
S1—C9	1.7741 (14)	C5—H5B	0.9800
N1—C2	1.3638 (18)	C5—H5C	0.9800
N1—N2	1.3713 (15)	C6—C11	1.3881 (19)
N1—C6	1.4208 (17)	C6—C7	1.392 (2)
N2—C4	1.3344 (18)	C7—C8	1.3864 (19)
N3—H1	0.869 (9)	C7—H7	0.9500
N3—H2	0.871 (9)	C8—C9	1.3918 (19)
C1—C2	1.4920 (19)	C8—H8	0.9500
C1—H1A	0.9800	C9—C10	1.3882 (19)
C1—H1B	0.9800	C10—C11	1.3889 (19)
C1—H1C	0.9800	C10—H10	0.9500
C2—C3	1.372 (2)	C11—H11	0.9500
C3—C4	1.404 (2)		
O2—S1—O1	119.22 (6)	N2—C4—C5	120.48 (12)
O2—S1—N3	107.68 (6)	C3—C4—C5	128.50 (13)
O1—S1—N3	106.68 (6)	C4—C5—H5A	109.5
O2—S1—C9	107.00 (6)	C4—C5—H5B	109.5
O1—S1—C9	107.27 (6)	H5A—C5—H5B	109.5
N3—S1—C9	108.66 (6)	C4—C5—H5C	109.5
C2—N1—N2	111.80 (11)	H5A—C5—H5C	109.5
C2—N1—C6	128.61 (11)	H5B—C5—H5C	109.5

N2—N1—C6	119.31 (11)	C11—C6—C7	120.61 (12)
C4—N2—N1	104.80 (11)	C11—C6—N1	119.24 (12)
S1—N3—H1	112.6 (13)	C7—C6—N1	120.15 (12)
S1—N3—H2	111.7 (13)	C8—C7—C6	119.90 (13)
H1—N3—H2	116.9 (18)	C8—C7—H7	120.0
C2—C1—H1A	109.5	C6—C7—H7	120.0
C2—C1—H1B	109.5	C7—C8—C9	119.29 (13)
H1A—C1—H1B	109.5	C7—C8—H8	120.4
C2—C1—H1C	109.5	C9—C8—H8	120.4
H1A—C1—H1C	109.5	C10—C9—C8	120.94 (13)
H1B—C1—H1C	109.5	C10—C9—S1	119.54 (10)
N1—C2—C3	106.24 (12)	C8—C9—S1	119.52 (10)
N1—C2—C1	123.29 (13)	C9—C10—C11	119.61 (13)
C3—C2—C1	130.28 (13)	C9—C10—H10	120.2
C2—C3—C4	106.11 (12)	C11—C10—H10	120.2
C2—C3—H3	126.9	C6—C11—C10	119.64 (13)
C4—C3—H3	126.9	C6—C11—H11	120.2
N2—C4—C3	111.01 (12)	C10—C11—H11	120.2
C2—N1—N2—C4	-1.97 (15)	C11—C6—C7—C8	0.7 (2)
C6—N1—N2—C4	-176.38 (11)	N1—C6—C7—C8	-179.31 (12)
N2—N1—C2—C3	1.89 (15)	C6—C7—C8—C9	-0.5 (2)
C6—N1—C2—C3	175.64 (13)	C7—C8—C9—C10	0.0 (2)
N2—N1—C2—C1	-173.51 (13)	C7—C8—C9—S1	179.52 (11)
C6—N1—C2—C1	0.2 (2)	O2—S1—C9—C10	-2.85 (13)
N1—C2—C3—C4	-1.01 (15)	O1—S1—C9—C10	-131.88 (12)
C1—C2—C3—C4	173.95 (15)	N3—S1—C9—C10	113.15 (12)
N1—N2—C4—C3	1.28 (15)	O2—S1—C9—C8	177.63 (11)
N1—N2—C4—C5	-179.21 (12)	O1—S1—C9—C8	48.60 (13)
C2—C3—C4—N2	-0.18 (16)	N3—S1—C9—C8	-66.37 (13)
C2—C3—C4—C5	-179.65 (14)	C8—C9—C10—C11	0.4 (2)
C2—N1—C6—C11	-128.45 (15)	S1—C9—C10—C11	-179.13 (11)
N2—N1—C6—C11	44.90 (17)	C7—C6—C11—C10	-0.3 (2)
C2—N1—C6—C7	51.5 (2)	N1—C6—C11—C10	179.71 (12)
N2—N1—C6—C7	-135.12 (13)	C9—C10—C11—C6	-0.2 (2)

Hydrogen-bond geometry (\AA , $^\circ$)

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N3—H1 \cdots O1 ⁱ	0.87 (1)	2.13 (1)	2.966 (2)	160 (2)
N3—H1 \cdots N2 ⁱⁱ	0.87 (1)	2.94 (2)	3.501 (2)	124 (2)

Symmetry codes: (i) $-x+1, -y+1, -z+1$; (ii) $-x+3/2, y+1/2, -z+1/2$.