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Synthesis, crystal structure and Hirshfeld surface analysis of 5-methyl-1*H***-pyrazol-3-yl 4-nitrobenzenesulfonate at 90 K**

[Vinaya](https://scripts.iucr.org/cgi-bin/citedin?search_on=name&author_name=Vinaya),^a Syida A. Yakuth,^a Thaluru M. Mohan Kumar,^b Besagarahally L. Bhaskar,^b Thayamma R. Divakara,^c Hemmige S. Yathirajan,^a * Yeriyur B. Basavaraju^a and Sean Parkin^d

a Department of Studies in Chemistry, University of Mysore, Manasagangotri, Mysuru-570 006, India, **^b** Department of Physical Sciences, Amrita School of Engineering, Amrita Vishwa Vidyapeetham, Bengaluru-560 035, India, **^c** Department of Chemistry, T. John Institute of Technology, Bengaluru-560 083, India, and **^d** Department of Chemistry, University of Kentucky, Lexington, KY, 40506-0055, USA. *Correspondence e-mail: yathirajan@hotmail.com

This study presents the synthesis, crystal structure, and a Hirshfeld-surface analysis of the bioactive compound 5-methyl-1*H*-pyrazol-3-yl 4-nitrobenzenesulfonate($C_{10}H_9N_3O_5S$), a pyrazole derivative with pharmacological potential. Pyrazoles are known for diverse bioactivities, and recent research emphasizes their role as a 'privileged structure' in drug design. Here, the asymmetric unit of the title compound contains two distinct molecules, *A* and *B*, exhibiting differences in conformation resulting from variation in key torsion angles. These distinctions influence the molecular orientation and intermolecular interactions, with strong $N-H \cdots N$ and $N-H \cdots O$ hydrogen bonds forming a centrosymmetric tetramer stabilized by $\pi-\pi$ stacking. Hirshfeld surface analysis readily confirms differing intermolecular contacts for *A* and *B*, primarily involving hydrogen atoms and differences in their close contacts to nitrogen and oxygen. This study offers further insight into the molecular architecture and potential interactions of pyrazole-based drug candidates.

1. Chemical context

Pyrazoles exhibit diverse pharmacological activities, including protein glycation inhibition, antibacterial, antifungal, anticancer, antidepressant, anti-inflammatory, antitubercular, antioxidant, and antiviral effects (Fustero *et al.*, 2011; Steinbach *et al.*, 2000; Garcı´a-Lozano *et al.*, 1997). Naim *et al.* (2016) provide an overview of the current status of pyrazoles and their biological activities. Various reviews focus on bioactive pyrazole derivatives (Ansari *et al.*, 2017), synthetic and biological attributes of pyrazole compounds (Dwivedi *et al.*, 2018), and the role of the pyrazole moiety in drug development as a 'privileged structure' (Faria *et al.*, 2017; Patil, 2020; Yet, 2018). Comprehensive reviews on pyrazole synthesis and pharmacology are available, highlighting recent advances (Karrouchi *et al.*, 2018; Fustero *et al.*, 2009; Ebenezer *et al.*, 2022).

Several crystal structures of pyrazole derivatives have been reported, including 1,3-diphenyl-4,5-dihydro-1*H*-pyrazol-5 one (Baddeley *et al.*, 2012), 1-aryl-1*H*-pyrazole-3,4-dicarboxylate derivatives (Asma *et al.*, 2018), and additional complex pyrazole compounds (Archana *et al.*, 2022; Priyanka *et al.*, 2022; Pintro *et al.*, 2022; Metwally *et al.*, 2021). Related structures, such as 5-methyl-1-[(4-methylphenyl)sulfonyl]-1*H*pyrazol-3-yl 4-methylbenzenesulfonate (XEBLOH) and 1-(4 methylphenyl)-3-phenyl-1*H*-pyrazol-5-yl 4-nitrobenzene-

Table 1 Conformation-dependant angles and distances (\hat{A}, \circ) in **I**.

Torsion angle	Molecule A	Molecule B
$N1 - C1 - O1 - S1$	88.97 (12)	83.78 (12)
$C1 - O1 - S1 - C5$	64.92(9)	$-83.75(9)$
$Q1 - S1 - C5 - C6$	78.91 (10)	95.42(10)
$C7 - C8 - N3 - O5$	$-0.50(17)$	$-6.06(17)$
Dihedral angle"		
bz/nitro	1.37(10)	6.78(4)
bz/pz	43.10(4)	37.22(5)
Centroid \cdots centroid ^{<i>a</i>}		
$Cg(bz)\cdots Cg(pz)$	4.505 $(1)^b$	4.936 $(1)^b$

Notes: (*a*) Abbreviations: $bz =$ benzene; $pz =$ pyrazole; $Cg =$ centroid. (*b*) These distances do not imply any overlap, they merely show that the rings in *A* are closer than those in *B*.

sulfonate, have also been described (Murtaza *et al.*, 2012; Wardell *et al.*, 2012).

Given the significance of pyrazoles and specifically 5 methyl-1*H*-pyrazol-3-yl 4-nitrobenzenesulfonate, this paper presents the crystal-structure analysis of the title compound, C10H9N3O5S, **I**.

2. Structural commentary

The molecular structure of **I** features a 4-nitrobenzene ring bonded to a sulfonate sulfur atom, along with a 3-methyl-1*H*pyrazole ring attached to the single-bonded oxygen atom of the sulfonate group. The asymmetric unit comprises two crystallographically distinct molecules, *A* and *B* (Fig. 1). While both molecules exhibit typical bond lengths and angles, their overall conformations differ. The primary distinctions are in

Figure 1

An ellipsoid plot of **I** (50% probability) showing the two crystallographically independent molecules (suffixes *A* and *B*). Hydrogen atoms are shown as arbitrary circles.

Table 2 Hydrogen bonds and other close contacts (\mathring{A}, \degree) in **I**.

Hydrogen bonds				
D -H \cdots A	$D-H$	$H \cdot \cdot \cdot A$	$D\cdots A$	$D-\mathrm{H}\cdots A$
$N2A - H2A \cdots N1B$	0.875(17)	2.047(17)	2.9063(15)	167.0(15)
$N2B - H2B \cdots Q4A^1$	0.853(19)	2.121(19)	2.9630(15)	169.1(16)
$C2B - H2BA \cdots Q2B^{th}$	0.95	2.63	3.3452(15)	132.1
$C2B - H2BA \cdots O4B111$	0.95	2.66	3.5201(15)	151.4
$C4B - H4BC \cdots O5BIII$	0.98	2.60	3.5814(17)	176.8
$C6B - H6B \cdots O3BIV$	0.95	2.48	3.3910(15)	160.1
$C7B - H7B \cdots O2B^v$	0.95	2.39	3.1622(15)	137.6
$C10B - H10B \cdots O5B^v$	0.95	2.54	3.3418(16)	142.0
$\pi-\pi$ stacks				
$Ring\ 1 \cdots ring\ 2$		<i>Distance</i>	<i>Dihedral</i>	
$Cg(pzA)\cdots Cg(bzB)$		3.524(1)	5.41(4)	

Abbreviations: Cg = centroid; bz = benzene; pz = pyrazole. Symmetry codes: (i) $-x$, *y* \rightarrow *y* + 1, \rightarrow z + 1; (ii) \rightarrow x + 2, \rightarrow *y*, \rightarrow z + 2; (iii) *x* + 1, *y* - 1, *z*; (iv) \rightarrow x + 1, \rightarrow *y*, \rightarrow z + 2; (v) *x* 1, *y*, *z*; (vi) *x* + 1, *y*, *z*.

the torsion angles $N1 - C1 - O1 - S1$, $C1 - O1 - S1 - C5$, and $O1-S1-C5-C6$, which are 88.97 (12), 64.92 (9), and 78.91 (10)^{\circ} for molecule *A*, and 83.78 (12), -83.75 (9), and 95.42 (10) \degree for molecule *B*. These torsional variations lead to differences in the relative proximity and orientation of the pyrazole and benzene rings in each molecule. This is shown in a least-squares fit overlay plot (Fig. 2) and quantified in Table 1. The only other intramolecular degree of freedom lies in the rotation of the $NO₂$ groups relative to their attached benzene rings. For molecule *A*, this dihedral angle is 1.37 $(10)^\circ$, *i.e.* nearly coplanar, while in molecule *B*, it is slightly larger at $6.78 \,(4)^\circ$. There are no intramolecular hydrogen bonds of any type in either molecule *A* or *B*.

3. Supramolecular features

In **I**, there are only two strong intermolecular hydrogen bonds: $N2A - H2A \cdots N1B$ $\begin{bmatrix} d_{D \cdots A} \end{bmatrix}$ = 2.9063 (15) A^{$\end{bmatrix}$ and} $N2B - H2B \cdots O4A^{i}$ [$d_{D\cdots A}$ = 2.9630 (15) Å; symmetry operation: (i) $-x$, $-y$ + 1, $-z$ + 1], Table 2. The former

Figure 2

Least-squares overlay of the two molecules of **I**, aligning the benzene rings and the sulfur atom of the sulfonyl group. The coordinates of *B* were inverted for optimal alignment.

Figure 3

A partial packing plot viewed approximately down the *a* axis. Hydrogen bonds are drawn as thick dashed lines and $\pi-\pi$ overlap is shown as thin dashed lines between ring centroids. The whole construct forms a centrosymmetric tetramer.

connects the two molecules within the chosen asymmetric unit, while the latter generates a centrosymmetric tetramer (*i.e.*, a pair of pairs), as shown in Fig. 3. The integrity of this tetramer is augmented by a pair of $\pi-\pi$ stacking interactions that superimpose the pyrazole ring of molecule *A* with the benzene ring of B (plus the equivalent interaction – symmetry operation i, above), $Cg \cdots Cg = 3.524$ (1) A. These tetramers stack into columns that propagate parallel to the *a*-axis. In addition, there are a number of weaker hydrogen-bond-type interactions of the $C-H \cdots O$ form that connect these columns in both the *b-* and *c*-axis directions. The different intermolecular contacts experienced by molecules *A* and *B* are readily apparent in Hirshfeld surface fingerprint plots (*CrystalExplorer21*, Spackman *et al.*, 2021). These are shown in Fig. 4 for molecules *A* and *B* calculated individually, but presented side-by-side for ease of comparison. While it is clear from Fig. 4*a*,*b* that most intermolecular contacts involve hydrogen atoms (56.9% and 50.5% for *A* and *B*, respectively), the distributions are different. For *A*, there are no short contacts to oxygen atoms on adjacent molecules (Fig. 4*c*), whereas for *B* there are (note the sharp blue spike in Fig. 4*d*). The situation is reversed for contacts to nitrogen on adjacent molecules (Fig. 4*e*,*f*). This, of course, is simply a consequence of the different hydrogen-bonding modes of molecules *A* and *B*. The only other types of contact with double-digit percentage coverage are those involving carbon atoms, which are similar, but not identical for *A* and *B* (Fig. 4*g*,*h*).

4. Database survey

A search of the CSD (v5.45 with updates to September 2024; Groom *et al.*, 2016) of **I** with the nitro and methyl groups removed gave no hits. With the N—H hydrogen also removed, the search returned a single match, 5-methyl-1-[(4-methylphenyl)sulfonyl]-1*H*-pyrazol-3-yl-4-methylbenzene sulfonate (CSD refcode XEBLOH; Murtaza *et al.*, 2012). A search target of 4-nitrobenzenesulfonate gave 95 hits whereas a search fragment of pyrazol-3-yl sulfonate gave two hits, XEBLOH again, and EBAQUX (Kim *et al.*, 2018), di-*t*-butyl 3-[(trifluoromethanesulfonyl)oxy]-4,5,7,8-tetrahydropyrazolo- [3,4-d]azepine-1,6-dicarboxylate, which has little else in common with **I**.

Figure 4

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Hirshfeld surface (HS) fingerprint plots calculated independently for molecules *A* and *B*. Panels (*a*) and (*b*) compare contacts between the whole of molecule *A* within its own Hirshfeld surface and hydrogen atoms outside the HS, and *vice versa*. Panels (*c*) and (*d*) show analogous contacts to oxygen atoms, (*e*) and (*f*) show the corresponding plots to nitrogen, while (*g*) and (*h*) show contacts to carbon.

Figure 5 Reaction scheme for the formation of **I**.

5. Synthesis and crystallization

An equimolar mixture (0.1 mol) of ethyl acetoacetate (12.75 ml) and hydrazine hydrate (4.96 ml) in ethanol was stirred for 15–20 min. at room temperature, forming a white precipitate of pyrazolone. The precipitate was then separated by filtration and dried. The pyrazolone (1 g, 10.3 mmol) and 4-nitrobenzenesulfonyl chloride (2.28 g, 10.3 mmol) were stirred in acetonitrile (25 ml) with triethylamine for 30 min., turning the reaction mixture yellow–red. Stirring continued for approximately 5 h, with progress monitored by TLC (using hexane and dichloromethane as the mobile phase). After acidifying the mixture with 5% HCl, the solvent was evaporated. The product was extracted with ethyl acetate $(3 \times$ 15 ml), and the combined organic layers were dried over anhydrous sodium sulfate to yield the crude product, as summarized in Fig. 5. Recrystallization by slow evaporation from a 1:1 acetonitrile–ethyl acetate mixture yielded orange– red crystals after one week.

6. Refinement

Crystal data, data collection, and structure refinement details are given in Table 3. All hydrogen atoms were found in difference-Fourier maps. The N—H hydrogens (*i.e*., H2*A* and H2*B*) were refined freely (*x*, *y*, *z*, *U*ij), but carbon-bound hydrogens were included using riding models, with constrained distances set to 0.95 Å (Csp²H) and 0.98 Å $(RCH₃)$. $U_{iso}(H)$ parameters were set to values of either $1.2U_{eq}$ or $1.5U_{eq}$ (*RCH*₃ only) of their attached atom.

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Table 3 Experimental details.

Crystal data	
Chemical formula	$C_{10}H_9N_3O_5S$
$M_{\rm r}$	283.26
Crystal system, space group	Triclinic, P1
Temperature (K)	90
$a, b, c (\AA)$	7.0823 (3), 11.7865 (6), 15.8999 (8)
	68.340 (1), 81.516 (2), 76.435 (2)
α , β , γ (°) $V(\AA^3)$	1196.39 (10)
Z	$\overline{4}$
Radiation type	Mo $K\alpha$
μ (mm ⁻¹)	0.29
Crystal size (mm)	$0.28 \times 0.21 \times 0.14$
Data collection	
Diffractometer	Bruker D8 Venture dual source
Absorption correction	Multi-scan (SADABS; Krause et al., 2015)
T_{\min}, T_{\max}	0.930, 0.971
No. of measured, independent and	43837, 5472, 4902
observed $[I > 2\sigma(I)]$ reflections	
R_{int}	0.039
$(\sin \theta/\lambda)_{\text{max}} (\text{\AA}^{-1})$	0.650
Refinement	
$R[F^2 > 2\sigma(F^2)], wR(F^2), S$	0.027, 0.067, 1.04
No. of reflections	5472
No. of parameters	353
H-atom treatment	H atoms treated by a mixture of
	independent and constrained refinement
$\Delta \rho_{\text{max}}$, $\Delta \rho_{\text{min}}$ (e Å ⁻³)	$0.31, -0.42$

Computer programs: *APEX5* (Bruker, 2023), *SHELXT* (Sheldrick, 2015*a*), *SHELXL2019/3* (Sheldrick, 2015*b*), *XP* in *SHELXTL* (Sheldrick, 2008), *SHELX* (Sheldrick, 2008) and *publCIF* (Westrip, 2010).

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Synthesis, crystal structure and Hirshfeld surface analysis of 5-methyl-1*H***pyrazol-3-yl 4-nitrobenzenesulfonate at 90 K**

Vinaya, Syida A. Yakuth, Thaluru M. Mohan Kumar, Besagarahally L. Bhaskar, Thayamma R. Divakara, Hemmige S. Yathirajan, Yeriyur B. Basavaraju and Sean Parkin

Computing details

5-Methyl-1*H***-pyrazol-3-yl 4-nitrobenzenesulfonate**

Crystal data

 $C_{10}H_9N_3O_5S$ *Mr* = 283.26 Triclinic, *P*1 $a = 7.0823(3)$ Å $b = 11.7865(6)$ Å $c = 15.8999(8)$ Å α = 68.340 (1)^o β = 81.516 (2)^o $γ = 76.435(2)°$ $V = 1196.39(10)$ Å³

Data collection

Refinement

Refinement on *F*² Least-squares matrix: full $R[F^2 > 2\sigma(F^2)] = 0.027$ $wR(F^2) = 0.067$ $S = 1.04$ 5472 reflections 353 parameters 0 restraints Primary atom site location: structure-invariant direct methods

 $Z = 4$ $F(000) = 584$ $D_x = 1.573$ Mg m⁻³ Mo *Kα* radiation, $\lambda = 0.71073$ Å Cell parameters from 9613 reflections θ = 2.7–27.5° μ = 0.29 mm⁻¹ $T = 90 K$ Solvent-rounded block, pale orange-brown $0.28 \times 0.21 \times 0.14$ mm

43837 measured reflections 5472 independent reflections 4902 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.039$ $\theta_{\text{max}} = 27.5^{\circ}, \theta_{\text{min}} = 1.9^{\circ}$ $h = -8 \rightarrow 9$ $k = -15 \rightarrow 15$ $l = -20 \rightarrow 20$

Secondary atom site location: difference Fourier map Hydrogen site location: mixed H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2 (F_o^2) + (0.0199P)^2 + 0.6984P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\text{max}} = 0.001$ $\Delta\rho_{\text{max}} = 0.31$ e Å⁻³ $\Delta \rho_{\text{min}} = -0.42 \text{ e } \text{\AA}^{-3}$

Special details

Experimental. The crystal was mounted using polyisobutene oil on the tip of a fine glass fibre, which was fastened in a copper mounting pin with electrical solder. It was placed directly into the cold gas stream of a liquid-nitrogen based cryostat (Hope, 1994; Parkin & Hope, 1998).

Diffraction data were collected with the crystal at 90K, which is standard practice in this laboratory for the majority of flash-cooled crystals.

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Refinement. Refinement progress was checked using *PLATON* (Spek, 2020) and by an *R*-tensor (Parkin, 2000). The final model was further checked with the IUCr utility *checkCIF*.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

O5B	$-0.05168(13)$	0.55827(9)	0.89274(7)	0.0251(2)
N1B	0.55988(15)	0.13086(9)	0.79934(7)	0.0161(2)
N2B	0.50809(16)	0.04466(10)	0.77422(7)	0.0166(2)
H2B	0.400(3)	0.0622(16)	0.7499(12)	$0.033(5)$ *
N3B	0.11314(16)	0.57702(10)	0.89035(7)	0.0197(2)
C1B	0.72563(17)	0.07052(11)	0.83722(8)	0.0144(2)
C2B	0.78320(18)	$-0.05058(11)$	0.83709(8)	0.0171(2)
H2BA	0.896863	-0.109716	0.860015	$0.020*$
C3B	0.63631(19)	$-0.06460(11)$	0.79581(8)	0.0177(2)
C4B	0.6056(2)	$-0.17205(13)$	0.77508(10)	0.0278(3)
H ₄ BA	0.621648	-0.153437	0.709356	$0.042*$
H ₄ BB	0.473823	-0.187007	0.797278	$0.042*$
H ₄ BC	0.701040	-0.246413	0.804956	$0.042*$
C5B	0.57217(17)	0.26894(11)	0.94752(8)	0.0143(2)
C6B	0.38283(18)	0.24866(11)	0.95975(8)	0.0162(2)
H6B	0.358137	0.166606	0.979940	$0.019*$
C7B	0.23122(18)	0.35076(11)	0.94185(8)	0.0170(2)
H7B	0.099937	0.340364	0.949966	$0.020*$
C8B	0.27494(18)	0.46842(11)	0.91184(8)	0.0161(2)
C9B	0.46244(18)	0.48948(11)	0.89999(8)	0.0173(2)
H9B	0.486532	0.571672	0.879863	$0.021*$
C10B	0.61422(18)	0.38741(11)	0.91830(8)	0.0168(2)
H10B	0.745178	0.398187	0.910992	$0.020*$

Atomic displacement parameters (Å2)

Geometric parameters (Å, º)

Hydrogen-bond geometry (Å, º)

Symmetry codes: (i) $-x$, $-y+1$, $-z+1$; (ii) $-x+2$, $-y$, $-z+2$; (iii) $x+1$, $y-1$, z ; (iv) $-x+1$, $-y$, $-z+2$; (v) $x-1$, y , z ; (vi) $x+1$, y , z .