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Key indicators

Single-crystal X-ray study T=100~K Mean $\sigma(\text{C-C})=0.003~\text{Å}$ R factor = 0.027 wR factor = 0.075 Data-to-parameter ratio = 9.2

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

5-Nitrothiophene-2-carbaldehyde

In the crystal structure of the title compound, $C_5H_3NO_3S$, determined at 100 K, the nitro group and the aldehyde group make angles of 8.37 (16) and 8.5 (4)°, respectively, with the plane of the thiophene ring.

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Comment

In the title compound, (I), all bond distances and angles fall within the normal ranges. The molecule is essentially planar; however, the nitro group and the aldehyde group are at angles of 8.37 (16) and of 8.5 (4)°, respectively, with plane of the thiophene ring. In the crystal structure, molecules are connected by weak $C-H\cdots O$ hydrogen bonds (see Table 1).

$$S$$
 NO_2
 (I)

Experimental

The title compound was purchased from Aldrich (98% purity) and was recrystallized from ethanol prior to its use as a reactant in the Adler synthesis for porphyrins (Adler *et al.*, 1967). White crystals of the title compound were grown from the slow evaporation of ethanol solutions at 278 K.

Crystal data

$$C_5H_3NO_3S$$
 Mo $K\alpha$ radiation

 $M_r = 157.14$
 Cell parameters from 5184

 Orthorhombic, $Pna2_1$
 reflections

 $a = 11.4180$ (7) Å
 $\theta = 2.3-28.3^{\circ}$
 $b = 13.9536$ (8) Å
 $\mu = 0.46 \text{ mm}^{-1}$
 $c = 3.8525$ (2) Å
 $T = 100$ (2) K

 $V = 613.79$ (6) ų
 Needle, white

 $Z = 4$
 $0.50 \times 0.05 \times 0.05 \text{ mm}$
 $D_x = 1.701 \text{ Mg m}^{-3}$

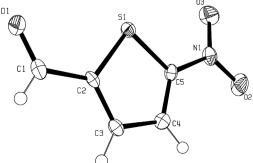


Figure 1

A view of (I) (Farrugia, 1997). Displacement ellipsoids are drawn at the 50% probability level.

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organic papers

Data collection

Bruker SMART APEX diffractometer 871 reflections with $I > 2\sigma(I)$ ω scans $R_{\rm int} = 0.025$ Absorption correction: multi-scan (SADABS; Sheldrick, 2003) $h = -15 \rightarrow 15$ $T_{\rm min} = 0.921, T_{\rm max} = 0.980$ $k = -18 \rightarrow 18$ $1 = -5 \rightarrow 5$

Refinement

refinement

Refinement on F^2 $w = 1/[\sigma^2(F_o^2) + (0.0443P)^2]$ $R[F^2 > 2\sigma(F^2)] = 0.027$ $wR(F^2) = 0.075$ $where <math>P = (F_o^2 + 2F_c^2)/3$ $\Delta \rho_{\max} = 0.001$ $\Delta \rho_{\max} = 0.37$ e Å⁻³ $\Delta \rho_{\min} = -0.19$ e Å⁻³

Table 1 Hydrogen-bonding geometry (Å, °).

independent and constrained

D $ H$ $\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	D $ H$ $\cdot \cdot \cdot A$
$ \begin{array}{c} C1-H1\cdotsO1^{i} \\ C4-H4A\cdotsO1^{ii} \end{array} $	0.93 (3)	2.52 (3)	3.373 (3)	152 (2)
	0.93	2.46	3.364 (3)	163

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

Thienyl H atoms were included in calculated positions with a C—H distance of 0.95 Å and were included in the refinement in riding-model approximation with $U_{\rm iso}=1.2U_{\rm eq}$ of the carrier atom. The aldehyde H atom was found in a difference map during the inital

stages of refinement and was refined independently with an isotropic displacement parameter. Refinements to determine the absolute structure gave inconclusive results [yielding a Flack (1983) parameter of 0.15 (9)] and the Friedel equivalents were therefore merged before the final refinement cycles.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SAINT-Plus* (Bruker, 1999); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

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