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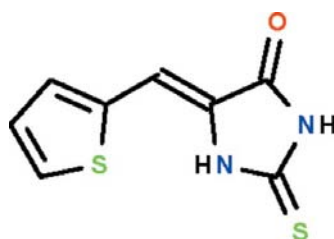
(Z)-2-Sulfanylidene-5-(thiophen-2-yl-methylidene)imidazolidin-4-oneAbdullah M. Asiri,^{a,b} Hassan M. Faidallah,^a
Abdulrahman O. Al-Youbi,^a Tarik R. Sobahi^a and
Seik Weng Ng^{c,*}^aChemistry Department, Faculty of Science, King Abdulaziz University, PO Box 80203 Jeddah, Saudi Arabia, ^bCenter of Excellence for Advanced Materials Research, King Abdulaziz University, PO Box 80203 Jeddah, Saudi Arabia, and ^cDepartment of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia
Correspondence e-mail: seikweng@um.edu.my

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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; disorder in main residue; R factor = 0.043; wR factor = 0.122; data-to-parameter ratio = 12.5.

The molecule of the title compound, $\text{C}_8\text{H}_6\text{N}_2\text{OS}_2$, has a V shape with two five-membered rings attached to a methylene C atom. All non-H atoms are approximately coplanar (r.m.s. deviation = 0.096 Å). In the crystal, molecules are linked by $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds into layers. The thiophene ring is disordered over two positions; the major orientation has an occupancy of 0.683 (3). Is there an intramolecular $\text{N}-\text{H}\cdots\text{S}$ bond?

Related literature

For two 5-aryl-2-thioxoimidazolin-4-ones, see: Chowdhry *et al.* (2000); Książek *et al.* (2009).

Experimental

Crystal data

 $\text{C}_8\text{H}_6\text{N}_2\text{OS}_2$ $M_r = 210.27$ Triclinic, $P\bar{1}$ $a = 6.1022$ (6) Å
 $b = 7.0806$ (8) Å
 $c = 11.0425$ (13) Å
 $\alpha = 72.582$ (11)°
 $\beta = 76.116$ (10)°
 $\gamma = 75.640$ (9)° $V = 433.87$ (8) Å³ $Z = 2$ Cu $K\alpha$ radiation $\mu = 5.22$ mm⁻¹ $T = 100$ K $0.25 \times 0.20 \times 0.02$ mm

Data collection

Agilent SuperNova Dual
diffractometer with an Atlas
detectorAbsorption correction: multi-scan
(*CrysAlis PRO*; Agilent, 2010)
 $T_{\min} = 0.356$, $T_{\max} = 0.903$ 2599 measured reflections
1677 independent reflections
1519 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.027$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.043$ $wR(F^2) = 0.122$ $S = 1.04$

1677 reflections

134 parameters

6 restraints

H-atom parameters constrained

 $\Delta\rho_{\max} = 0.33$ e Å⁻³ $\Delta\rho_{\min} = -0.44$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N2}-\text{H2}\cdots\text{O1}^i$	0.88	2.20	2.873 (2)	133

Symmetry code: (i) $x + 1, y, z$.

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).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BT5612).

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