

(E)-N'-(2-Thienylmethylidene)-p-toluene-sulfonohydrazide

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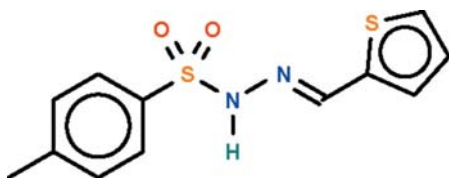
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Key indicators: single-crystal X-ray study; T = 100 K; mean $\sigma(C-C)$ = 0.002 Å; R factor = 0.030; wR factor = 0.085; data-to-parameter ratio = 18.0.

The S–N(H)–N=C linkage in the title molecule, C₁₂H₁₂N₂O₂S₂, is non-planar [torsion angle = 15.5 (1)°] as the amino N atom is pyramidally coordinated. The amino group acts as a hydrogen-bond donor to an O atom of an adjacent molecule, generating chains running parallel to the c axis.

Related literature

For the structure of the (E)-N'-benzylidene-p-toluenesulfonohydrazide homolog, see: Mehrabi *et al.* (2008).



Experimental

Crystal data

C₁₂H₁₂N₂O₂S₂
M_r = 280.36
Monoclinic, P2₁/c

a = 14.3758 (10) Å
b = 9.8613 (7) Å
c = 9.6172 (7) Å

β = 104.981 (1)°
V = 1317.03 (16) Å³
Z = 4
Mo K α radiation

μ = 0.40 mm⁻¹
T = 100 K
0.40 × 0.20 × 0.20 mm

Data collection

Bruker SMART APEX diffractometer
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.857, T_{max} = 0.925

8238 measured reflections
3022 independent reflections
2728 reflections with I > 2 σ (I)
R_{int} = 0.020

Refinement

R[F² > 2 σ (F²)] = 0.030
wR(F²) = 0.085
S = 1.04
3022 reflections
168 parameters
1 restraint

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{max}$ = 0.42 e Å⁻³
 $\Delta\rho_{min}$ = -0.36 e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

D–H···A	D–H	H···A	D···A	D–H···A
N1–H1···O1 ⁱ	0.86 (1)	2.06 (1)	2.874 (2)	159 (2)

Symmetry code: (i) x, -y + ½, z - ½.

Data collection: APEX2 (Bruker, 2009); cell refinement: SAINT (Bruker, 2009); data reduction: SAINT; 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).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: PK2261).

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