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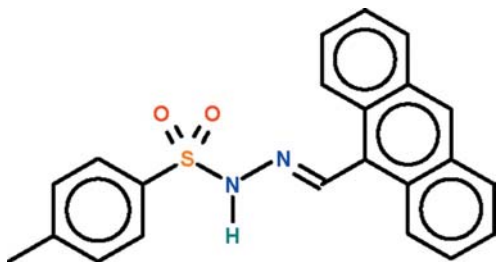
(E)-N'-(9-Anthrylmethylidene)-p-toluene-sulfonohydrazideAbdullah M. Asiri,^a Mohie E. M. Zayed^a and Seik Weng Ng^{b*}^aChemistry Department, Faculty of Science, King Abdul Aziz University, PO Box 80203, Jeddah 21589, Saudi Arabia, and ^bDepartment of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia
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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; R factor = 0.040; wR factor = 0.104; data-to-parameter ratio = 16.9.

The S–N(H)–N=C linkage in the title molecule, $\text{C}_{22}\text{H}_{18}\text{N}_2\text{O}_2\text{S}$, is non-planar [torsion angle = $30.6(1)^\circ$] as the amino N atom is pyramidally coordinated. In the crystal, the amino group acts as a hydrogen-bond donor to an O atom of an adjacent molecule, generating chains running parallel to the b axis.

Related literature

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

Experimental

Crystal data

 $\text{C}_{22}\text{H}_{18}\text{N}_2\text{O}_2\text{S}$ $M_r = 374.44$ Orthorhombic, $Pbca$ $a = 17.3634(15)$ Å $b = 9.2438(8)$ Å $c = 22.882(2)$ Å $V = 3672.6(6)$ Å³ $Z = 8$ Mo $K\alpha$ radiation $\mu = 0.20$ mm⁻¹ $T = 100$ K $0.40 \times 0.20 \times 0.05$ mm

Data collection

Bruker SMART APEX
diffractometerAbsorption correction: multi-scan
(SADABS; Sheldrick, 1996) $T_{\min} = 0.926$, $T_{\max} = 0.990$

22220 measured reflections

4209 independent reflections

3158 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.055$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.040$ $wR(F^2) = 0.104$ $S = 1.02$

4209 reflections

249 parameters

1 restraint

H atoms treated by a mixture of
independent and constrained
refinement $\Delta\rho_{\max} = 0.34$ e Å⁻³ $\Delta\rho_{\min} = -0.46$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$\text{N1}-\text{H1} \cdots \text{O1}^i$	0.86 (1)	2.07 (1)	2.911 (2)	169 (2)

Symmetry code: (i) $-x + \frac{1}{2}, y - \frac{1}{2}, z$.

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: PK2262).

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