

(E)-4-[[[3-Propyl-5-sulfanylidene-4,5-dihydro-1H-1,2,4-triazol-4-yl]imino]methyl]-3-(p-tolyl)-1,2,3-oxadiazol-3-ium-5-olate

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Received 12 September 2011; accepted 13 September 2011

Key indicators: single-crystal X-ray study; *T* = 296 K; mean $\sigma(\text{C}-\text{C})$ = 0.003 Å; disorder in main residue; *R* factor = 0.039; *wR* factor = 0.123; data-to-parameter ratio = 20.6.

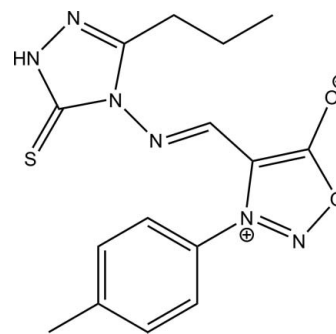
The title compound, C₁₅H₁₆N₆O₂S, exists in a *trans* configuration with respect to the acyclic N=C bond. The 1,2,3-oxadiazol-3-ium ring makes dihedral angles of 10.59 (8) and 73.94 (8)°, respectively, with the 1,2,4-triazole and benzene rings. The molecular structure is stabilized by an intramolecular C—H···S hydrogen bond, which generates an *S*(6) ring motif. In the crystal, molecules are linked into inversion dimers by pairs of intermolecular N—H···S hydrogen bonds, generating eight-membered *R*₂²(8) ring motifs. The dimers are further connected by C—H···O hydrogen bonds, forming a sheet parallel to the *bc* plane. The ethyl group is disordered over two sets of sites with occupancies of 0.744 (7) and 0.256 (7).

Related literature

For general background to and applications of sydnone derivatives, see: Baker *et al.* (1949); Hedge *et al.* (2008); Rai *et al.* (2008); Kalluraya *et al.* (2002). For standard bond-length data, see: Allen *et al.* (1987). For graph-set notation, see: Bernstein *et al.* (1995). For a related structure, see: Fun *et al.* (2011).

[‡] Thomson Reuters ResearcherID: A-3561-2009.

[§] Thomson Reuters ResearcherID: A-5525-2009.



Experimental

Crystal data

C₁₅H₁₆N₆O₂S
M_r = 344.40
Monoclinic, *P*2₁/*c*
a = 13.4220 (11) Å
b = 6.2411 (5) Å
c = 21.1374 (16) Å
 β = 104.575 (2)°
V = 1713.7 (2) Å³
Z = 4
Mo *K*α radiation
 μ = 0.21 mm⁻¹
T = 296 K
0.51 × 0.17 × 0.08 mm

Data collection

Bruker SMART APEXII DUO
CCD area-detector diffractometer
Absorption correction: multi-scan (*SADABS*; Bruker, 2009)
T_{min} = 0.865, *T_{max}* = 0.983
18912 measured reflections
5003 independent reflections
3637 reflections with *I* > 2σ(*I*)
R_{int} = 0.030

Refinement

R[*F*² > 2σ(*F*²)] = 0.039
wR(*F*²) = 0.123
S = 1.04
5003 reflections
243 parameters
H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\text{max}}$ = 0.22 e Å⁻³
 $\Delta\rho_{\text{min}}$ = -0.21 e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
N5—H1N5···S1 ⁱ	0.857 (18)	2.440 (18)	3.2933 (13)	174.3 (16)
C1—H1A···O2 ⁱⁱ	0.93	2.48	3.346 (2)	154
C9—H9A···S1	0.93	2.42	3.1845 (13)	139

Symmetry codes: (i) $-x + 2, -y + 3, -z$; (ii) $-x + 2, y + \frac{1}{2}, -z + \frac{1}{2}$.

Data collection: *APEX2* (Bruker, 2009); cell refinement: *SAINT* (Bruker, 2009); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 2008); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2009).

HKF and CKQ thank Universiti Sains Malaysia for the Research University Grant (No. 1001/PFIZIK/811160).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: IS2776).

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