Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

Hong-Guang Song, Zhi-Yong Xing* and Wen-Qin Zhang

Department of Chemistry, College of Sciences, Tianjin University, Tianjin 300072, People's Republic of China

Correspondence e-mail: xzy760203@163.com

Key indicators

Single-crystal X-ray study T = 113 K Mean σ (C–C) = 0.002 Å R factor = 0.043 wR factor = 0.112 Data-to-parameter ratio = 18.2

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

1-[(Phenyl)(p-tolylimino)methyl]-3-(o-tolyl)thiourea

In the crystal structure of the title compound, $C_{22}H_{21}N_3S$, intermolecular $N-H\cdots S$ hydrogen bonds link the molecules into hydrogen-bonded dimers. There is an intramolecular $N-H\cdots N$ hydrogen bond.

Received 26 October 2006 Accepted 7 December 2006

Comment

Thiourea derivatives are very important intermediates in organic syntheses, and have been widely utilized in medicinal chemistry (Smith *et al.*, 1996) and photochemistry (Dittami *et al.*, 1996; Jayanthi *et al.*, 1997). In order to study their photochemical behavior, we synthesized a series of new thiourea derivatives (Xing & Zhao, 2006*a,b*). Here we report the crystal structure of the title compound, (I). An intramolecular hydrogen bond (Table 1 and Fig. 1) appears to influence the conformation of the molecule. The resulting six-membered ring (C9/N2/C1/N1/N3/H1) is essentially planar, with an r.m.s. deviation for the fitted atoms of 0.070 Å. In the crystal structure, pairs of molecules form centrosymmetric dimers *via* intermolecular N-H····S hydrogen bonds (Table 1 and Fig. 2).



Experimental

The title compound was prepared according to a literature procedure (van den Nieuwendijk *et al.*, 2004). Single crystals of the title compound suitable for X-ray analysis were obtained from acetonitrile solution.

Crystal data	
$C_{22}H_{21}N_3S$	V = 945.6 (5) Å ³
$M_r = 359.48$	Z = 2
Triclinic, P1	$D_x = 1.263 \text{ Mg m}^{-3}$
a = 10.085 (3) Å	Mo $K\alpha$ radiation
b = 10.288 (3) Å	$\mu = 0.18 \text{ mm}^{-1}$
c = 10.301 (3) Å	T = 113 (2) K
$\alpha = 76.521 \ (13)^{\circ}$	Block, colorless
$\beta = 65.832 \ (11)^{\circ}$	$0.24 \times 0.16 \times 0.14$ mm
$\gamma = 88.294 \ (16)^{\circ}$	

© 2007 International Union of Crystallography All rights reserved



Figure 1

The molecular structure of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms are shown as small spheres of arbitrary radii. The intramolecular hydrogen bond is shown as a dashed line.

11995 measured reflections

 $R_{\rm int} = 0.038$

 $\theta_{\rm max} = 27.9^\circ$

 $(\Delta/\sigma)_{\rm max} = 0.001$

 $\Delta \rho_{\rm max} = 0.31 \text{ e } \text{\AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.34 \text{ e} \text{ Å}^{-3}$

4500 independent reflections

 $w = 1/[\sigma^2(F_o^2) + (0.0789P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$

Extinction correction: SHELXL97

Extinction coefficient: 0.029 (5)

3237 reflections with $I > 2\sigma(I)$

Data collection

Rigaku Saturn diffractometer ω scans Absorption correction: multi-scan (Jacobson, 1998) $T_{min} = 0.958, T_{max} = 0.975$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.043$ $wR(F^2) = 0.112$ S = 1.044500 reflections 247 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$N2-H2\cdots S1^{i}$	0.888 (17)	2.458 (17)	3.3314 (16)	167.9 (14)
$N1-H1\cdots N3$	0.895 (16)	1.991 (16)	2.7214 (18)	137.8 (14)

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

All H atoms were initially located in a difference Fourier map. The C-H atoms were then constrained to an ideal geometry, with methyl C-H distances of 0.98 Å and aromatic C-H distances of 0.95 Å, and with $U_{iso}(H) = 1.2U_{eq}(C)$. The amino H atoms were refined freely.

Data collection: *CrystalClear* (Molecular Structure Corporation & Rigaku, 1999); cell refinement: *CrystalClear*; data reduction: *CrystalStructure* (Rigaku/MSC, 2005); program(s) used to solve structure:



Figure 2

The packing of (I), showing the intermolecular hydrogen bonds as dashed lines.

SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *CrystalStructure*.

References

- Bruker (1997). SHELXTL. Version 5.10. Bruker AXS Inc., Madison, Wisconsin, USA.
- Dittami, J. P., Luo, Y. L., Moss, D. & McGimpsey, W. G. (1996). J. Org. Chem. 61, 6256–6260.
- Jacobson, R. (1998). Private communiation to the Rigaku Corporation, Tokyo, Japan.
- Jayanthi, G., Muthusamy, S., Paramasivam, R., Ramakrishnan, V. T., Ramasamy, N. K. & Ramamurthy, P. (1997). J. Org. Chem. 62, 5766–5770.
- Molecular Structure Corporation & Rigaku (1999). CrystalClear. Version 1.3.6. MSC, The Woodlands, Texas, USA, and Rigaku Corporation, Tokyo, Japan.
- Nieuwendijk, A. M. C. H. van den, Pietra, D., Heitman, L., Göblyös, A. & IJzerman, A. P. (2004). J. Med. Chem. 47, 663-672.
- Rigaku/MSC (2005). CrystalStructure. Version 3.7.0. Rigaku/MSC, The Woodlands, Texas, USA.
- Sheldrick, G. M. (1997). SHELXS97 and SHELXL97. University of Göttingen, Germany.
- Smith, J., Liras, J. L., Schneider, S. E. & Anslyn, E. V. (1996). J. Org. Chem. 61, 8811–8818.
- Xing, Z.-Y. & Zhao, H.-T. (2006a). Acta Cryst. E62, 02268-02269.
- Xing, Z.-Y. & Zhao, W.-T. (2006b). Acta Cryst. E62, o2544-o2545.