## Structure Reports

Online
ISSN 1600-5368

## Ding-Ben Chen, Ling Huang, Fu-You Pan* and Jian-Guo Yang

Department of Chemistry, Taizhou University, Taizhou 317000, People's Republic of China

Correspondence e-mail: panfy@tzc.edu.cn

## Key indicators

Single-crystal X-ray study
$T=293 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.003 \AA$
$R$ factor $=0.042$
$w R$ factor $=0.077$
Data-to-parameter ratio $=13.2$

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

[^0] Printed in Great Britain - all rights reserved

## 4-Phenyl-1-(1H-1,2,4-triazol-3-ylcarbonyl)thiosemicarbazide

The title compound, $\mathrm{C}_{10} \mathrm{H}_{10} \mathrm{~N}_{6} \mathrm{OS}$, was synthesized by the reaction of 1 H -1,2,4-triazol-3-ylhydrazine with phenyl isocyanate in benzene. The molecule is non-planar, the dihedral angle between the two aromatic rings being $62.07(7)^{\circ} . \mathrm{N}-$ $\mathrm{H} \cdots \mathrm{O}, \mathrm{N}-\mathrm{H} \cdots \mathrm{N}$ and $\mathrm{N}-\mathrm{H} \cdots \mathrm{S}$ hydrogen bonds are observed.

## Comment

Azole compounds, such as derivatives of pyrazole, imidazole, triazole (including benzotriazole), tetrazole and indole, exhibit extensive biological activity and have become a central focus in the study of agricultural chemicals and medicines (Ernest \& William, 1982). Schiff bases often represent good examples of biologically active substructures and a study of a triazole Schiff base has been reported (Sauter et al., 1991). The hydrazonecarbonyl grouping has also been shown to be bioactive (Zhi et al., 2003) and a number of structures of triazole compounds containing the hydrazonecarbonyl group have been reported (Pan \& Yang, 2005; Yang \& Pan, 2004). In a search for more effective antibacterial medicines, we have synthesized the title compound, (I).

(I)

The title molecule (Fig. 1) is non-planar; the dihedral angle between the two aromatic rings is 62.07 (7) ${ }^{\circ}$. As a result of conjugation, the $\mathrm{C}=\mathrm{O}$ distance $[1.216(2) \AA$ ] is longer than the normal value of $1.20 \AA$ (John, 1998), and the C $2-$ N 2 bond distance $[1.346(2) \AA]$ is longer than the $\mathrm{C}=\mathrm{N}$ double-bond distance ( $1.32 \AA$; John, 1998) and shorter than the $\mathrm{C}-\mathrm{N}$ single-bond distance (1.475 Å; John, 1998).

Intermolecular hydrogen bonds are observed (Table 1 and Fig. 2). The $\mathrm{N}-\mathrm{H} \cdots \mathrm{N}$ and $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds form a ten-membered ring (Fig. 2).

## Experimental

$1 H-1,2,4-$ Triazol-3-ylhydrazine ( $0.02 \mathrm{~mol}, 2.54 \mathrm{~g}$ ) was dissolved in benzene ( 50 ml ) and phenyl isocyanate ( $0.02 \mathrm{~mol}, 2.70 \mathrm{~g}$ ) was added to the solution. The mixture was refluxed for 8 h and the precipitate formed was collected by filtration and washed with benzene. The


Figure 1
The structure of (I), showing the atomic numbering. Displacement ellipsoids are drawn at the $30 \%$ probability level.


Figure 2
The packing of (I), showing the intermolecular and intramolecular hydrogen bonds as dashed lines.
product was recrystallized from benzene and dried under reduced pressure to give the title compound. The compound $(2.0 \mathrm{mmol}$, 0.53 g ) was dissolved in dimethylformamide ( 30 ml ) and kept at room temperature for 40 d to obtain colourless single crystals, which were collected and washed with distilled water (m.p: 490-491 K). IR $v_{\max }\left(\mathrm{KBr}, \mathrm{cm}^{-1}\right): 3327,3150,3124,1704,1541,1450,1252,1194,1163$, 697. ${ }^{1} \mathrm{H}$ NMR ( $200 \mathrm{MHz}, \mathrm{DMSO}$ ): $\delta 14.71(1 \mathrm{H}), 10.58(1 \mathrm{H}), 9.80(2 \mathrm{H})$, $8.78(1 \mathrm{H}), 7.05-7.60(5 \mathrm{H})$.

## Crystal data

$$
\begin{aligned}
& \mathrm{C}_{10} \mathrm{H}_{10} \mathrm{~N}_{6} \mathrm{OS} \\
& M_{r}=262.30 \\
& \text { Orthorhombic, Pbcn } \\
& a=12.1981(10) \AA \\
& b=10.1097(8) \AA \\
& c=19.9112(16) \AA \\
& V=2455.4(3) \AA^{3} \\
& Z=8 \\
& D_{x}=1.419 \mathrm{Mg} \mathrm{~m}^{-3}
\end{aligned}
$$

## Data collection

Bruker SMART APEX area-
detector diffractometer
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan
(SADABS; Bruker, 2002)
$T_{\text {min }}=0.908, T_{\text {max }}=0.977$
13557 measured reflections

> 2684 independent reflections
> 1653 reflections with $I>2 \sigma(I)$
> $R_{\text {int }}=0.085$
> $\theta_{\max }=27.0^{\circ}$
> $h=-15 \rightarrow 12$
> $k=-12 \rightarrow 12$
> $l=-25 \rightarrow 20$

## Refinement

Refinement on $F^{2}$
All H -atom parameters refined
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.042$
$w R\left(F^{2}\right)=0.077$
$w=1 /\left[\sigma^{2}\left(F_{o}^{2}\right)+(0.0246 P)^{2}\right]$
where $P=\left(F_{o}{ }^{2}+2 F_{c}^{2}\right) / 3$
$S=0.85$
2684 reflections
203 parameters
$(\Delta / \sigma)_{\max }=0.001$
$\Delta \rho_{\text {max }}=0.26 \mathrm{e}^{-3}$
$\Delta \rho_{\min }=-0.31 \mathrm{e}^{-3}$

Table 1
Hydrogen-bonding geometry $\left(\AA^{\circ},^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~N} 6-\mathrm{H} 6 A \cdots \mathrm{O} 1^{\mathrm{i}}$ | $0.812(18)$ | $2.44(2)$ | $2.904(2)$ | $116.9(17)$ |
| $\mathrm{N} 4-\mathrm{H} 4 A \cdots \mathrm{~S}^{1 i}$ | $0.88(2)$ | $2.45(2)$ | $3.259(2)$ | $152(2)$ |
| $\mathrm{N} 2-\mathrm{H} 2 \cdots \mathrm{~N}^{\mathrm{i}}$ | $0.85(2)$ | $2.08(2)$ | $2.926(2)$ | $171(2)$ |
| $\mathrm{N} 1-\mathrm{H} 1 \cdots \mathrm{~S} 1^{\mathrm{iii}}$ | $0.890(15)$ | $2.460(16)$ | $3.322(2)$ | $163.0(17)$ |

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

All H atoms were located in a difference map and their parameters were refined. The $\mathrm{N}-\mathrm{H}$ distances are in the range 0.812 (18)$0.890(15) \AA$ and the $\mathrm{C}-\mathrm{H}$ distances are in the range 0.903 (19)0.94 (2) Å.

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Bruker, 2002); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

The authors acknowledge financial support by the Zhejiang Provincial Natural Science Foundation of China (No. M203115).

## References

Bruker (2002). SMART (Version 5.62), SAINT (Version 6.02), SADABS (Version 2.03) and SHELXTL. Bruker AXS Inc., Madison, Winsonsin, USA.
Ernest, H. \& William, J. H. (1982). Br. Patent No. 2078212.
John, A. D. (1998). Lang's Handbook of Chemistry, Vol. 4, pp. 39-41. New York: McGraw-Hill.
Pan, F.-Y. \& Yang, J.-G. (2005). Acta Cryst. E61, o63-o64.
Sauter, H., Zierke, T., Reuther, W., Baus, U., Lorenz, G. \& Ammermann, E. (1991). Eur. Patent No. 421227.

Yang, J.-G. \& Pan, F.-Y. (2004). Acta Cryst. E60, o2342-o2344.
Zhi, J. F., Bin, Z., Su, H. W. \& Zheng, M. L. (2003). Chin. J. Appl. Chem. 20, 365-367.


[^0]:    © 2005 International Union of Crystallography

