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## **Redetermination of 4-(phenyl)thiosemicarbazide**

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Redetermination of 4-(phenyl)thio-  
semicarbazideDaniel E. Lynch<sup>a\*</sup> and Ian McClenaghan<sup>b†</sup>

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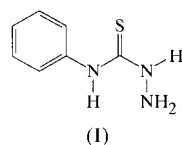
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The structure of the title compound, C<sub>7</sub>H<sub>9</sub>N<sub>3</sub>S, comprises twisted molecules that associate *via* N—H...N and N—H...S hydrogen-bonding interactions. The dihedral angle between the phenyl ring and the five-membered thiosemicarbazide plane is 67.56 (5)°. This structure was previously determined using data from visual estimation of photographic intensity (measurements at room temperature, with *R* = 0.112).

## Comment

The structure of the title compound, (I), was initially determined using data from visual estimation of photographic intensity measurements at room temperature, with refinement to *R* = 0.112 (Kalman *et al.*, 1972). However, reported here is a redetermination of the structure using data collected by a modern area detector at 150 K, giving *R* = 0.040. The previously published value for the dihedral angle between the phenyl ring and the five-membered thiosemicarbazide was 67.5°, which can now be updated to 67.56 (5)°.



## Experimental

Crystals of (I) were obtained from Spa Contract Synthesis.

## Crystal data

C<sub>7</sub>H<sub>9</sub>N<sub>3</sub>S  
*M<sub>r</sub>* = 167.23  
Monoclinic, *P*2<sub>1</sub>/*c*  
*a* = 11.9231 (7) Å  
*b* = 5.4888 (3) Å  
*c* = 12.3788 (8) Å  
*β* = 91.527 (3)°  
*V* = 809.82 (8) Å<sup>3</sup>  
*Z* = 4

*D<sub>x</sub>* = 1.372 Mg m<sup>-3</sup>  
Mo *Kα* radiation  
Cell parameters from 6169 reflections  
*θ* = 1.00–27.48°  
*μ* = 0.334 mm<sup>-1</sup>  
*T* = 150 (2) K  
Block, colourless  
0.40 × 0.30 × 0.20 mm

## Data collection

Enraf–Nonius KappaCCD area-detector diffractometer  
*φ* and *ω* scans  
Absorption correction: multi-scan (SORTAV; Blessing, 1995)  
*T<sub>min</sub>* = 0.878, *T<sub>max</sub>* = 0.936  
4691 measured reflections

1803 independent reflections  
1483 reflections with *I* > 2σ(*I*)  
*R<sub>int</sub>* = 0.037  
*θ<sub>max</sub>* = 27.47°  
*h* = −15 → 15  
*k* = −6 → 7  
*l* = −15 → 16

## Refinement

Refinement on *F*<sup>2</sup>  
*R* [*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.040  
*wR* (*F*<sup>2</sup>) = 0.132  
*S* = 1.130  
1803 reflections  
116 parameters  
H atoms treated by a mixture of independent and constrained refinement

*w* = 1/[σ<sup>2</sup>(*F<sub>o</sub>*<sup>2</sup>) + (0.0669*P*)<sup>2</sup> + 0.3297*P*]  
where *P* = (*F<sub>o</sub>*<sup>2</sup> + 2*F<sub>c</sub>*<sup>2</sup>)/3  
(Δ/σ)<sub>max</sub> < 0.001  
Δρ<sub>max</sub> = 0.24 e Å<sup>-3</sup>  
Δρ<sub>min</sub> = −0.32 e Å<sup>-3</sup>

Table 1

Hydrogen-bonding 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>
N4—H4...N1	0.83 (2)	2.19 (2)	2.6317 (17)	113 (2)
N2—H2...S3 <sup>i</sup>	0.89 (2)	2.43 (2)	3.3097 (17)	168 (2)
N1—H11...S3 <sup>ii</sup>	0.87 (3)	2.83 (3)	3.5100 (18)	137 (2)
N1—H12...N2 <sup>iii</sup>	0.92 (3)	2.56 (3)	3.296 (2)	137 (2)

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

All H atoms were included in the refinement, at calculated positions, as riding models with C—H set to 0.95 Å, except for the amine H atoms, which were located on difference syntheses and both positional and displacement parameters were refined.

Data collection: DENZO (Otwinowski & Minor, 1997) and COLLECT (Hooft, 1998); cell refinement: DENZO and COLLECT; data reduction: DENZO and COLLECT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); software used to prepare material for publication: SHELXL97.

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