

1-(4,6-Dimethylpyrimidin-2-yl)thiourea

Sohail Saeed,^{a*} Naghma Rashid,^a Jerry P. Jasinski^b and James A. Golen^b

^aDepartment of Chemistry, Research Complex, Allama Iqbal Open University, Islamabad 44000, Pakistan, and ^bDepartment of Chemistry, Keene State College, 229 Main Street, Keene, NH 03435-2001, USA
Correspondence e-mail: sohail262001@yahoo.com

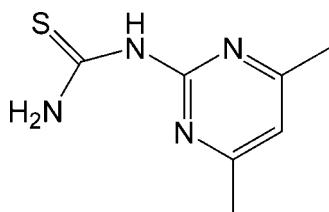
Received 23 October 2011; accepted 13 November 2011

Key indicators: single-crystal X-ray study; $T = 173\text{ K}$; mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$; R factor = 0.053; wR factor = 0.144; data-to-parameter ratio = 17.1.

In the crystal structure of the title compound, $\text{C}_7\text{H}_{10}\text{N}_4\text{S}$, weak intermolecular $\text{N}-\text{H}\cdots\text{S}$ interactions form a two-dimensional network parallel to the ab plane. An intramolecular $\text{N}-\text{H}\cdots\text{N}$ hydrogen bond occurs.

Related literature

For structural characterization of *N*-substituted thiourea derivatives with heterocyclic substituents, see: Saeed *et al.* (2010a,b, 2011). For standard bond lengths, see Allen *et al.* (1987).

**Experimental***Crystal data*

$\text{C}_7\text{H}_{10}\text{N}_4\text{S}$	$V = 873.45(15)\text{ \AA}^3$
$M_r = 182.25$	$Z = 4$
Orthorhombic, $Pna2_1$	$\text{Mo K}\alpha$ radiation
$a = 8.3372(5)\text{ \AA}$	$\mu = 0.32\text{ mm}^{-1}$
$b = 15.8303(10)\text{ \AA}$	$T = 173\text{ K}$
$c = 6.618(1)\text{ \AA}$	$0.30 \times 0.20 \times 0.18\text{ mm}$

Data collection

Oxford DiffractionXcalibur Eos Gemini diffractometer
Absorption correction: multi-scan (*CrysAlis RED*; Oxford Diffraction, 2010)
 $T_{\min} = 0.910$, $T_{\max} = 0.945$

7240 measured reflections
2057 independent reflections
1588 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.043$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.053$
 $wR(F^2) = 0.144$
 $S = 1.10$
2057 reflections
120 parameters
4 restraints

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\text{max}} = 0.57\text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.23\text{ e \AA}^{-3}$

Table 1
Hydrogen-bond geometry (\AA , $^\circ$).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
N1—H1A \cdots N4	0.90 (2)	1.99 (3)	2.676 (3)	131 (3)
N1—H1B \cdots S1 ⁱ	0.87 (2)	2.58 (2)	3.399 (2)	159 (4)
N2—H2A \cdots S1 ⁱⁱ	0.85 (2)	2.53 (2)	3.338 (2)	160 (4)

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

Data collection: *CrysAlis PRO* (Oxford Diffraction, 2010); cell refinement: *CrysAlis PRO*; data reduction: *CrysAlis RED* (Oxford Diffraction, 2010); program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *SHELXTL*.

JPJ acknowledges the NSF–MRI program (grant No. CHE1039027) for funds to purchase the X-ray diffractometer.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: IM2335).

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supporting information

Acta Cryst. (2011). E67, o3347 [https://doi.org/10.1107/S1600536811048148]

1-(4,6-Dimethylpyrimidin-2-yl)thiourea

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S1. Comment

The crystal structure of the title compound is a byproduct of the reaction of 1-(4,6-dimethylpyrimidin-2-yl)-3-(3,5-dinitrophenyl)thiourea with a copper acetate salt. It is related to our previous studies on the structural chemistry of heterocyclic compounds containing an N-substituted thiourea (Saeed *et al.*, 2010*a*, 2010*b*, 2011). Herein, as a continuation of these studies, the structure of the title compound, (I), C₇H₁₀N₄S, is described.

In the title compound, (I), (Fig. 1) the crystal packing is realized by intramolecular N1—H1···N4 hydrogen bonds and weak N—H···S intermolecular interactions (Table 1) forming a 2-D network along [110] (Fig. 2). Bond distances are in normal ranges (Allen *et al.* (1987)).

S2. Experimental

After refluxing a reaction mixture of 1-(4,6-dimethylpyrimidin-2-yl)-3-(3,5-dinitrophenyl)thiourea with copper acetate salt, it was transferred into cold water. The crude solid product was filtered, washed again with water and purified by recrystallization from ethanol (Yield: 45%). Single crystals of the title compound were obtained by recrystallisation from a dichloromethane/ethanol mixture (2:1).

S3. Refinement

H1A, H1B and H2A were located in a Fourier map and refined isotropically. All other H atoms were placed in their calculated positions and then refined using the riding model with atom—H bond lengths of 0.95 Å (CH) or 0.98 Å (CH₃). Isotropic displacement parameters for these atoms were set to 1.19 (CH) or 1.48–1.50 (CH₃) times U_{eq} of the parent atom. 928 Friedel pairs were measured.

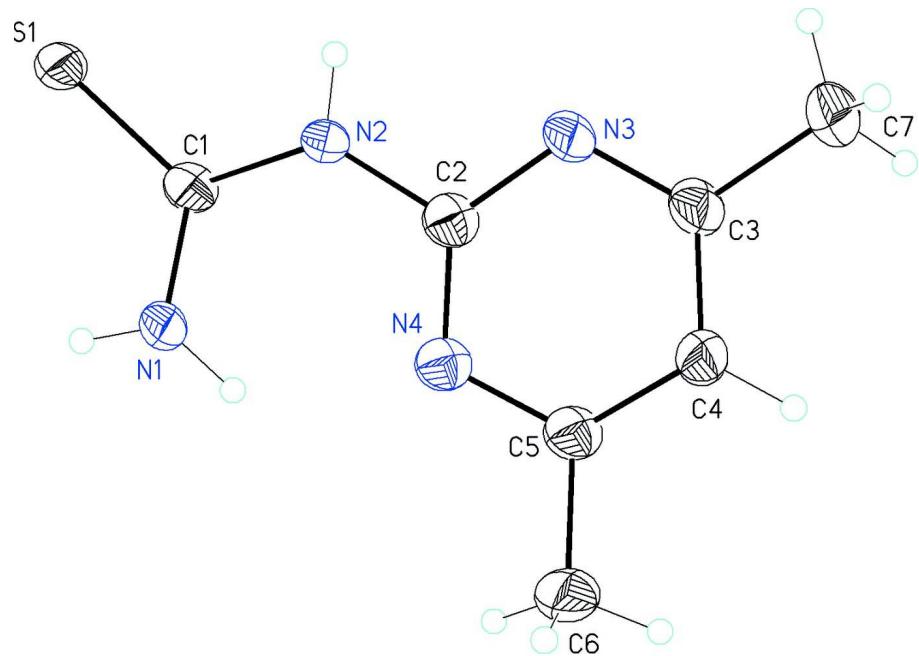
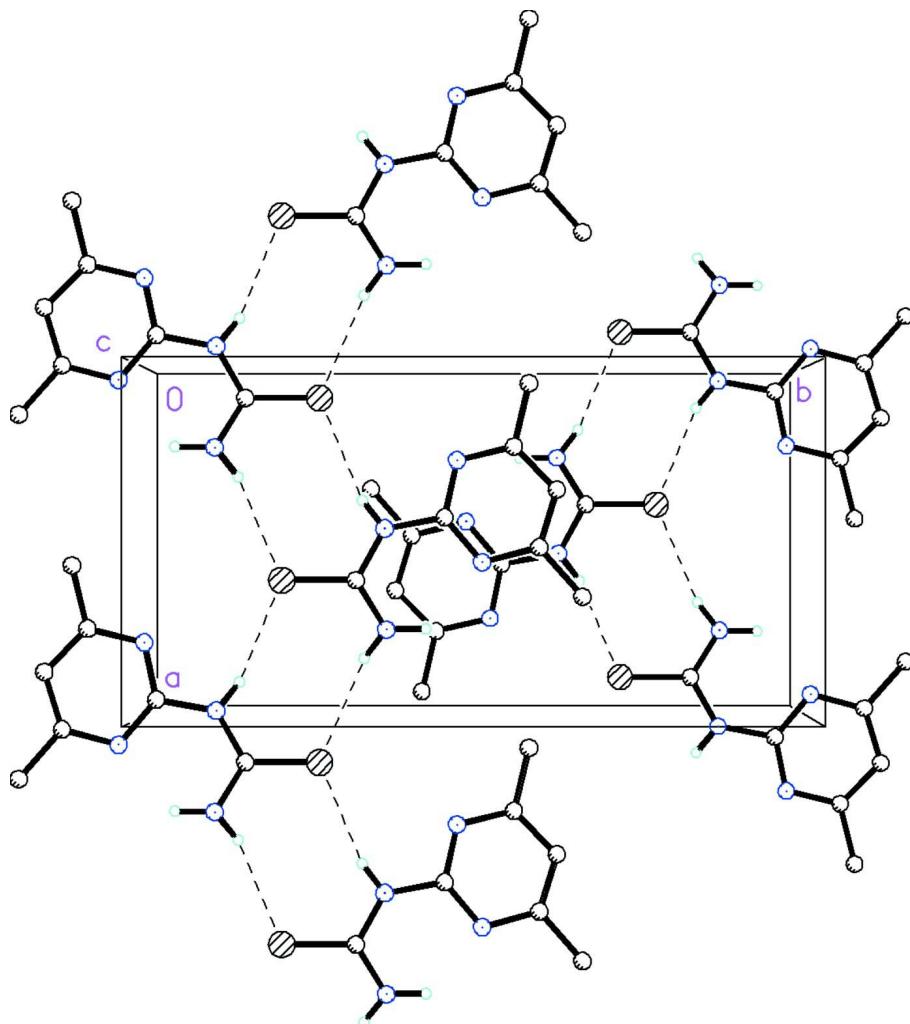


Figure 1

Molecular structure of the title compound showing the atom labeling scheme and 30% probability displacement ellipsoids.

**Figure 2**

Packing diagram of the title compound viewed along the *c* axis. Dashed lines indicate weak N—H···S intermolecular interactions forming a 2-D network along [110].

1-(4,6-Dimethylpyrimidin-2-yl)thiourea

Crystal data

C₇H₁₀N₄S
*M*_r = 182.25
 Orthorhombic, *Pna*2₁
 Hall symbol: P 2c -2n
a = 8.3372 (5) Å
b = 15.8303 (10) Å
c = 6.618 (1) Å
V = 873.45 (15) Å³
Z = 4

F(000) = 384
*D*_x = 1.386 Mg m⁻³
 Mo *K*α radiation, λ = 0.71073 Å
 Cell parameters from 2136 reflections
 θ = 3.3–32.5°
 μ = 0.32 mm⁻¹
T = 173 K
 Block, pale yellow
 0.30 × 0.20 × 0.18 mm

Data collection

Oxford Diffraction Xcalibur Eos Gemini diffractometer
 Radiation source: Enhance (Mo) X-ray Source
 Graphite monochromator
 Detector resolution: 16.1500 pixels mm⁻¹
 ω scans
 Absorption correction: multi-scan
 (*CrysAlis RED*; Oxford Diffraction, 2010)
 $T_{\min} = 0.910$, $T_{\max} = 0.945$

7240 measured reflections
 2057 independent reflections
 1588 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.043$
 $\theta_{\max} = 27.9^\circ$, $\theta_{\min} = 3.3^\circ$
 $h = -10 \rightarrow 10$
 $k = -20 \rightarrow 20$
 $l = -8 \rightarrow 8$

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.053$
 $wR(F^2) = 0.144$
 $S = 1.10$
 2057 reflections
 120 parameters
 4 restraints
 Primary atom site location: structure-invariant direct methods

Secondary atom site location: difference Fourier map
 Hydrogen site location: inferred from neighbouring sites
 H atoms treated by a mixture of independent and constrained refinement
 $w = 1/[\sigma^2(F_o^2) + (0.0705P)^2 + 0.3395P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.021$
 $\Delta\rho_{\max} = 0.57 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.23 \text{ e } \text{\AA}^{-3}$

Special details

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) etc. and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
S1	0.39504 (8)	0.77736 (4)	0.3627 (3)	0.0334 (2)
N1	0.2593 (2)	0.62628 (14)	0.3662 (11)	0.0295 (5)
H1A	0.261 (4)	0.5693 (11)	0.374 (13)	0.035*
H1B	0.179 (3)	0.6589 (17)	0.338 (8)	0.035*
N2	0.5367 (2)	0.62855 (12)	0.3683 (10)	0.0241 (5)
H2A	0.615 (3)	0.6613 (16)	0.345 (9)	0.029*
N3	0.7243 (2)	0.52446 (13)	0.3633 (9)	0.0309 (6)
N4	0.4441 (3)	0.48807 (14)	0.3725 (8)	0.0263 (5)
C1	0.3948 (3)	0.67031 (15)	0.3601 (11)	0.0246 (6)
C2	0.5672 (3)	0.54221 (16)	0.3715 (9)	0.0265 (6)
C3	0.7616 (3)	0.44226 (17)	0.3597 (12)	0.0310 (6)
C4	0.6435 (3)	0.38055 (16)	0.3665 (14)	0.0318 (6)
H4A	0.6711	0.3225	0.3786	0.038*
C5	0.4852 (3)	0.40536 (17)	0.3554 (10)	0.0292 (7)
C6	0.3496 (3)	0.34350 (17)	0.3676 (15)	0.0403 (8)

H6A	0.2609	0.3629	0.2823	0.060*
H6B	0.3130	0.3390	0.5079	0.060*
H6C	0.3863	0.2881	0.3205	0.060*
C7	0.9355 (3)	0.42072 (19)	0.3708 (14)	0.0413 (9)
H7A	0.9991	0.4684	0.3206	0.062*
H7B	0.9568	0.3707	0.2878	0.062*
H7C	0.9648	0.4089	0.5114	0.062*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.0193 (3)	0.0239 (3)	0.0570 (5)	0.0017 (2)	-0.0110 (6)	-0.0034 (11)
N1	0.0161 (10)	0.0256 (10)	0.0466 (15)	0.0014 (8)	-0.007 (3)	-0.008 (3)
N2	0.0173 (10)	0.0222 (10)	0.0328 (13)	-0.0013 (8)	-0.005 (3)	-0.005 (3)
N3	0.0206 (11)	0.0298 (12)	0.0424 (16)	0.0013 (8)	-0.015 (2)	-0.008 (3)
N4	0.0254 (11)	0.0278 (10)	0.0257 (14)	-0.0015 (8)	-0.006 (2)	0.003 (2)
C1	0.0197 (11)	0.0293 (12)	0.0248 (15)	0.0002 (9)	-0.012 (2)	-0.001 (3)
C2	0.0257 (13)	0.0284 (12)	0.0254 (16)	-0.0001 (9)	-0.008 (3)	0.003 (3)
C3	0.0247 (13)	0.0335 (14)	0.0347 (17)	0.0019 (10)	-0.009 (3)	-0.006 (3)
C4	0.0270 (13)	0.0255 (12)	0.0430 (17)	0.0021 (10)	0.007 (4)	0.007 (4)
C5	0.0258 (13)	0.0304 (13)	0.0315 (18)	-0.0027 (10)	-0.009 (2)	0.003 (3)
C6	0.0283 (14)	0.0319 (14)	0.061 (2)	-0.0073 (11)	-0.013 (4)	0.001 (5)
C7	0.0291 (14)	0.0356 (15)	0.059 (2)	0.0061 (12)	-0.014 (4)	-0.001 (4)

Geometric parameters (\AA , $^\circ$)

S1—C1	1.695 (3)	C3—C4	1.388 (4)
N1—C1	1.328 (3)	C3—C7	1.491 (4)
N1—H1A	0.904 (17)	C4—C5	1.379 (4)
N1—H1B	0.869 (18)	C4—H4A	0.9500
N2—C1	1.356 (3)	C5—C6	1.497 (4)
N2—C2	1.390 (3)	C6—H6A	0.9800
N2—H2A	0.846 (17)	C6—H6B	0.9800
N3—C3	1.338 (3)	C6—H6C	0.9800
N3—C2	1.341 (3)	C7—H7A	0.9800
N4—C2	1.337 (3)	C7—H7B	0.9800
N4—C5	1.358 (3)	C7—H7C	0.9800
C1—N1—H1A	120.7 (19)	C5—C4—H4A	120.8
C1—N1—H1B	110 (2)	C3—C4—H4A	120.8
H1A—N1—H1B	128 (3)	N4—C5—C4	120.8 (3)
C1—N2—C2	129.7 (2)	N4—C5—C6	115.8 (3)
C1—N2—H2A	112 (2)	C4—C5—C6	122.2 (2)
C2—N2—H2A	118 (2)	C5—C6—H6A	109.5
C3—N3—C2	115.6 (2)	C5—C6—H6B	109.5
C2—N4—C5	115.1 (2)	H6A—C6—H6B	109.5
N1—C1—N2	119.0 (2)	C5—C6—H6C	109.5
N1—C1—S1	121.71 (19)	H6A—C6—H6C	109.5

N2—C1—S1	119.07 (17)	H6B—C6—H6C	109.5
N4—C2—N3	128.0 (2)	C3—C7—H7A	109.5
N4—C2—N2	119.3 (2)	C3—C7—H7B	109.5
N3—C2—N2	112.6 (2)	H7A—C7—H7B	109.5
N3—C3—C4	121.2 (2)	C3—C7—H7C	109.5
N3—C3—C7	116.6 (2)	H7A—C7—H7C	109.5
C4—C3—C7	121.8 (2)	H7B—C7—H7C	109.5
C5—C4—C3	118.5 (2)		
C2—N2—C1—N1	4.0 (12)	C2—N3—C3—C4	-0.7 (11)
C2—N2—C1—S1	178.8 (6)	C2—N3—C3—C7	-174.2 (6)
C5—N4—C2—N3	-2.7 (10)	N3—C3—C4—C5	6.9 (12)
C5—N4—C2—N2	173.7 (5)	C7—C3—C4—C5	180.0 (8)
C3—N3—C2—N4	-1.4 (10)	C2—N4—C5—C4	9.0 (11)
C3—N3—C2—N2	-178.1 (6)	C2—N4—C5—C6	176.8 (6)
C1—N2—C2—N4	-2.1 (11)	C3—C4—C5—N4	-11.2 (12)
C1—N2—C2—N3	174.9 (8)	C3—C4—C5—C6	-178.2 (8)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1A···N4	0.90 (2)	1.99 (3)	2.676 (3)	131 (3)
N1—H1B···S1 ⁱ	0.87 (2)	2.58 (2)	3.399 (2)	159 (4)
N2—H2A···S1 ⁱⁱ	0.85 (2)	2.53 (2)	3.338 (2)	160 (4)

Symmetry codes: (i) $x-1/2, -y+3/2, z$; (ii) $x+1/2, -y+3/2, z$.