

2-Amino-5,5-dimethylthiazol-4(5H)-one

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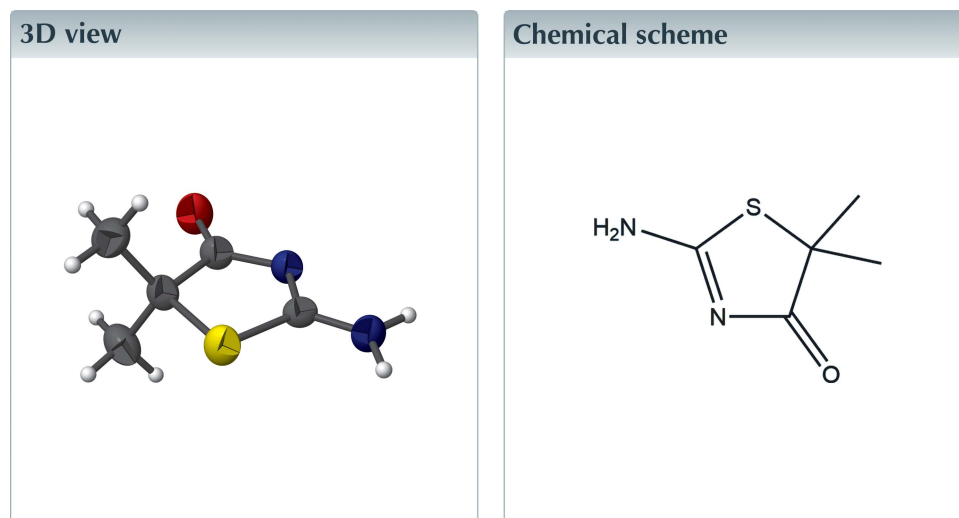
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Keywords: crystal structure; thiazole.

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Structural data: full structural data are available from iucrdata.iucr.org

Our work exploring the synthesis and optimization of increasingly hindered thiols led to the synthesis and crystal structure determination of the title compound, C₅H₈N₂OS, a dimethyl-substituted 4-thiazolidinone. The molecular packing exhibits a herringbone pattern with the zigzag running along the *b*-axis direction; the compound crystallizes as chains of hydrogen-bonded dimers formed by N–H···N hydrogen bonds, which build centrosymmetric *R*₂²(8) ring motifs in the crystal.



Structure description

As a result of their impressive array of biological responses and potential uses in medicine, 4-thiazolidinones and their derivatives have been extensively investigated in recent years. Their wide range of biological relevance includes anticancer, antiviral, antibacterial (Tripathi *et al.*, 2014), analgesic (Kumar & Patil, 2017) and antipsychotic (Kaur *et al.*, 2010) properties. The synthesis of these five-membered heterocyclic rings is well documented, and the majority of derivatives follow concise synthetic routes and provide generally good yields. However, access to new derivatives is desirable to enable researchers to further explore the utility of these biologically interesting pharmacophores. The title compound provides an avenue for a new substitution pattern that is not often seen in the literature, namely, a geminal dialkyl substitution at the 5-position on the ring. This motif may provide a unique utility since a more thermodynamically favored confirmation may result because of steric hindrance, especially if the thiazolidinone is further substituted at the 2- and/or N-positions (Vigorita *et al.* 1979).

Herein we report the crystal structure of 2-amino-5,5-dimethylthiazol-4(5H)-one (Fig. 1). The molecule is nearly planar, with the thiazole ring r.m.s.d. being 0.027 Å. In the crystal, the molecules form hydrogen-bonded dimers. The hydrogen bonding occurs between the N atoms of the thiazole ring and the amino group with an *R*(8) synthon. The hydrogen bond between N2 and N1ⁱⁱ is characterized by an N2···N1 separation of

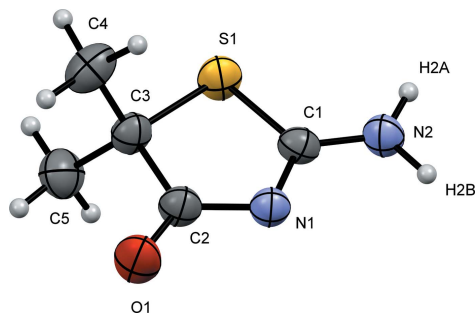


Figure 1
A view of the molecular structure of the title compound, with the atom labeling. Displacement ellipsoids are drawn at the 50% probability level.

2.938 (3) Å [symmetry code: (ii) $-x + 1, -y + 1, -z$; Table 1], with $R_2^2(8)$ ring motifs (Fig. 2). A secondary $N2 \cdots O1$ hydrogen bond also involves the amino group and the O1 atom on a neighboring thiourea ring, forming a $C(6)$ motif. This hydrogen bond between N2 and O1 is characterized by an $N2 \cdots O1$ separation of 2.820 (3) Å [symmetry code: (i) $x + 1, y, z$; Table 1]. This $C_1^1(6)$ hydrogen-bonding motif stitches the dimers into a chain running parallel to the a axis, Fig. 2. The crystal structure exhibits a herringbone pattern with the blocks consisting of the chains of hydrogen-bonded dimers, with the zigzag running along the b -axis direction. There are no other short contacts or π - π interactions observed in the crystal.

Synthesis and crystallization

A round-bottom flask was equipped with a stir bar and reflux condenser and then charged with 1.0 g (6.0 mmol, 1.0 equiv.) of 2-bromo-2-methylpropionic acid. The solid was heated to 100°C, at which point 0.57 g (7.5 mmol, 1.25 equiv.) of thiourea was added. The whole was heated to 200°C for 1 h and then allowed to cool to room temperature. The resulting solid was

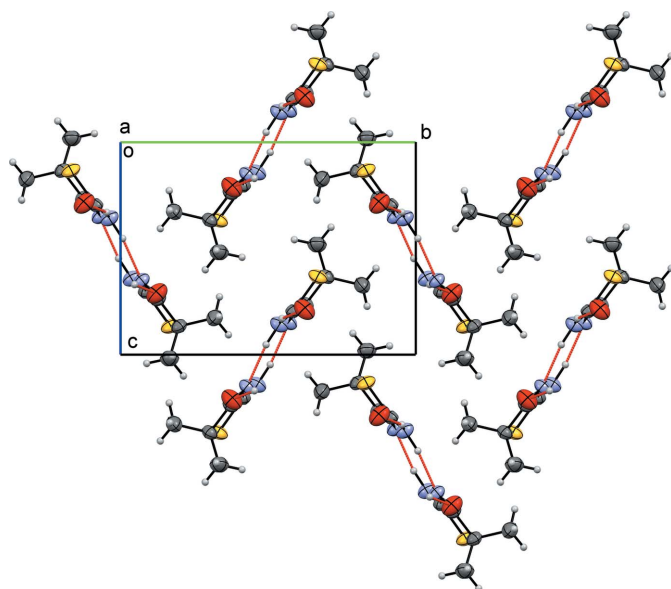


Figure 2
Crystal packing diagram of title compound viewed along [100]. Hydrogen bonds (Table 1) are colored red.

Table 1
Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N2-H2A \cdots O1^i$	0.93 (3)	1.93 (4)	2.820 (3)	159 (3)
$N2-H2B \cdots N1^{ii}$	1.00 (4)	1.95 (4)	2.938 (3)	170 (3)

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

purified on a silica (60 Å, 40–63 mm) column, eluting with methylene chloride while slowly increasing the concentration of methanol (0–25%). Crystals were obtained by slow evaporation of the eluted aliquot. Note: the two H atoms on the nitrogen are in non-degenerate equilibrium. NMR: 1H NMR [300 MHz, $(CD_3)_2SO$] δ = 8.96 (bs, 0.6H, $-NH_2$), 8.72 (bs, 1.4H, $-NH_2$), 1.48 (s, 6H, $2 \times -CH_3$) p.p.m.

Refinement

Crystal data, data collection and structure refinement details are summarized in Table 2.

Acknowledgements

The authors thank Georgia Southern University for support of this work.

Table 2
Experimental details.

Crystal data	
Chemical formula	$C_5H_8N_2OS$
M_r	144.19
Crystal system, space group	Monoclinic, $P2_1/n$
Temperature (K)	173
a, b, c (Å)	6.9440 (8), 12.1354 (16), 8.8283 (11)
β (°)	98.888 (11)
V (Å ³)	735.01 (16)
Z	4
Radiation type	Mo $K\alpha$
μ (mm ⁻¹)	0.36
Crystal size (mm)	0.2 × 0.2 × 0.05
Data collection	
Diffractometer	Rigaku XtaLAB mini CCD
Absorption correction	Multi-scan (<i>CrysAlis PRO</i> ; Rigaku OD, 2018)
T_{min}, T_{max}	0.497, 1.000
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	5107, 1681, 1126
R_{int}	0.055
$(\sin \theta/\lambda)_{max}$ (Å ⁻¹)	0.649
Refinement	
$R[F^2 > 2\sigma(F^2)], wR(F^2), S$	0.051, 0.142, 1.08
No. of reflections	1681
No. of parameters	92
H-atom treatment	H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}, \Delta\rho_{min}$ (e Å ⁻³)	0.26, -0.35

Computer programs: *CrysAlis PRO* (Rigaku OD, 2018), *SHELXT* (Sheldrick, 2015a), *SHELXL2018* (Sheldrick, 2015b) and *OLEX2* (Dolomanov et al., 2009).

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full crystallographic data

IUCrData (2019). 4, x190613 [https://doi.org/10.1107/S2414314619006138]

2-Amino-5,5-dimethylthiazol-4(5*H*)-one

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2-Amino-5,5-dimethylthiazol-4(5*H*)-one*Crystal data*

C₅H₈N₂OS

$M_r = 144.19$

Monoclinic, $P2_1/n$

$a = 6.9440$ (8) Å

$b = 12.1354$ (16) Å

$c = 8.8283$ (11) Å

$\beta = 98.888$ (11)°

$V = 735.01$ (16) Å³

$Z = 4$

$F(000) = 304$

$D_x = 1.303$ Mg m⁻³

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å

Cell parameters from 1205 reflections

$\theta = 2.9$ – 26.0 °

$\mu = 0.36$ mm⁻¹

$T = 173$ K

Prism, clear bluish violet

$0.2 \times 0.2 \times 0.05$ mm

Data collection

Rigaku XtaLAB mini CCD

diffractometer

Radiation source: fine-focus sealed X-ray tube,

Rigaku (Mo) X-ray Source

Graphite Monochromator monochromator

Detector resolution: 13.6612 pixels mm⁻¹

ω scans

Absorption correction: multi-scan

(CrysAlis PRO; Rigaku OD, 2018)

$T_{\min} = 0.497$, $T_{\max} = 1.000$

5107 measured reflections

1681 independent reflections

1126 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.055$

$\theta_{\max} = 27.5$ °, $\theta_{\min} = 2.9$ °

$h = -8 \rightarrow 8$

$k = -14 \rightarrow 15$

$l = -11 \rightarrow 10$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.051$

$wR(F^2) = 0.142$

$S = 1.08$

1681 reflections

92 parameters

0 restraints

Primary atom site location: dual

Hydrogen site location: mixed

H atoms treated by a mixture of independent

and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0472P)^2 + 0.1833P]$

where $P = (F_o^2 + 2F_c^2)/3$

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

$\Delta\rho_{\max} = 0.26$ e Å⁻³

$\Delta\rho_{\min} = -0.35$ e Å⁻³

Special details

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

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	0.65626 (10)	0.33147 (7)	0.36674 (8)	0.0466 (3)
N1	0.4105 (3)	0.42897 (19)	0.1509 (3)	0.0397 (6)
C1	0.5978 (4)	0.4149 (2)	0.2050 (3)	0.0359 (6)
O1	0.1162 (3)	0.3771 (2)	0.2117 (3)	0.0605 (7)
N2	0.7350 (4)	0.4625 (2)	0.1419 (3)	0.0448 (6)
C2	0.2946 (4)	0.3738 (2)	0.2359 (3)	0.0406 (7)
C3	0.3980 (4)	0.3023 (2)	0.3668 (3)	0.0399 (7)
C4	0.3565 (5)	0.1815 (2)	0.3269 (4)	0.0562 (9)
H4A	0.397060	0.164898	0.227865	0.084*
H4B	0.216548	0.167200	0.320696	0.084*
H4C	0.429051	0.134683	0.406444	0.084*
C5	0.3337 (5)	0.3342 (3)	0.5181 (4)	0.0555 (9)
H5A	0.399628	0.286989	0.600194	0.083*
H5B	0.192333	0.324760	0.510091	0.083*
H5C	0.367769	0.411367	0.541405	0.083*
H2A	0.868 (5)	0.453 (3)	0.170 (4)	0.063 (10)*
H2B	0.695 (5)	0.507 (3)	0.047 (4)	0.076 (11)*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.0359 (4)	0.0617 (5)	0.0390 (4)	0.0048 (3)	-0.0043 (3)	0.0136 (3)
N1	0.0319 (12)	0.0451 (14)	0.0409 (13)	0.0031 (10)	0.0019 (10)	0.0083 (11)
C1	0.0335 (14)	0.0413 (15)	0.0316 (14)	0.0046 (12)	0.0005 (11)	-0.0018 (12)
O1	0.0305 (11)	0.0752 (16)	0.0729 (16)	0.0014 (10)	-0.0013 (11)	0.0222 (13)
N2	0.0330 (13)	0.0560 (16)	0.0448 (15)	0.0043 (12)	0.0040 (11)	0.0109 (12)
C2	0.0324 (14)	0.0459 (16)	0.0412 (16)	0.0017 (13)	-0.0016 (12)	0.0046 (13)
C3	0.0384 (15)	0.0439 (16)	0.0357 (15)	0.0008 (12)	-0.0002 (12)	0.0068 (12)
C4	0.069 (2)	0.0455 (19)	0.0498 (19)	-0.0033 (16)	-0.0033 (17)	0.0058 (14)
C5	0.063 (2)	0.063 (2)	0.0428 (18)	0.0042 (17)	0.0143 (16)	0.0013 (15)

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

S1—C1	1.746 (3)	C3—C4	1.525 (4)
S1—C3	1.828 (3)	C3—C5	1.522 (4)
N1—C1	1.326 (3)	C4—H4A	0.9800
N1—C2	1.358 (4)	C4—H4B	0.9800
C1—N2	1.310 (4)	C4—H4C	0.9800
O1—C2	1.225 (3)	C5—H5A	0.9800
N2—H2A	0.93 (3)	C5—H5B	0.9800
N2—H2B	1.00 (4)	C5—H5C	0.9800
C2—C3	1.533 (4)		
C1—S1—C3	90.49 (12)	C5—C3—C2	110.5 (2)
C1—N1—C2	111.7 (2)	C5—C3—C4	112.1 (3)

N1—C1—S1	117.4 (2)	C3—C4—H4A	109.5
N2—C1—S1	120.7 (2)	C3—C4—H4B	109.5
N2—C1—N1	121.8 (2)	C3—C4—H4C	109.5
C1—N2—H2A	126 (2)	H4A—C4—H4B	109.5
C1—N2—H2B	118 (2)	H4A—C4—H4C	109.5
H2A—N2—H2B	115 (3)	H4B—C4—H4C	109.5
N1—C2—C3	116.6 (2)	C3—C5—H5A	109.5
O1—C2—N1	123.9 (3)	C3—C5—H5B	109.5
O1—C2—C3	119.5 (3)	C3—C5—H5C	109.5
C2—C3—S1	103.59 (19)	H5A—C5—H5B	109.5
C4—C3—S1	109.7 (2)	H5A—C5—H5C	109.5
C4—C3—C2	108.7 (2)	H5B—C5—H5C	109.5
C5—C3—S1	111.8 (2)		

Hydrogen-bond geometry (Å, °)

<i>D—H...A</i>	<i>D—H</i>	<i>H...A</i>	<i>D...A</i>	<i>D—H...A</i>
N2—H2A...O1 ⁱ	0.93 (3)	1.93 (4)	2.820 (3)	159 (3)
N2—H2B...N1 ⁱⁱ	1.00 (4)	1.95 (4)	2.938 (3)	170 (3)

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