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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.039 wR factor = 0.100 Data-to-parameter ratio = 19.5

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

2-Amino-4-(3-methyl-3-*p*-xylylcyclobutyl)-1,3-thiazole

In the title compound, $C_{16}H_{20}N_2S$, an intermolecular N- $H \cdots N$ hydrogen bond and an N- $H \cdots \pi$ interaction link two molecules, forming a dimer.

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Comment

Various thiazole derivatives show herbicidal, anti-imflammatory, antimicrobial and antiparasitic activity (Koparir *et al.*, 2004; Ahmedzade *et al.*, 2003), and also liquid crystal properties (Coghi *et al.*, 1976). Aminothiazoles have been extensively studied for a range of biological and industrial applications (Lynch *et al.*, 1999; Toplak *et al.*, 2003). 2-Amino-1,3-thiazole, the structure of which was reported by Caranoni & Reboul (1982), is itself listed as a thyroid inhibitor (Merck, 2001).



The dihedral angle between the thiazole and benzene rings is $81.88 (9)^{\circ}$, comparable to $87.21 (2)^{\circ}$ and $89.70 (2)^{\circ}$ reported for 3-butyl-4-(3-methyl-3-phenylcyclobutyl)-1,3-thiazole-



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Figure 2

A view of the hydrogen-bonding interactions (dashed lines) in (I). For the sake of clarity, H atoms bonded to C atoms have been omitted. Cg1 is the centroid of the C9–C14 benzene ring [symmetry code: (i) $\frac{1}{3} - x$, $\frac{2}{3} - y$, $\frac{2}{3} - z$].

2(3H)-thione (Kırılmış et al., 2005a) and 3-cyclohexyl-4-(3methyl-3-phenylcyclobutyl)-1,3-thiazole-2(3H)-thione (Kırılmış et al., 2005b), respectively. The cyclobutane ring is puckered; the C5/C4/C6 plane forms a dihedral angle of $20.8 (2)^{\circ}$ with the C6/C7/C5 plane. This compares well with the values of 24.37°, 23.82 (3)° and 23.5 (4)° reported for the abovementioned compounds (Kirilmis et al., 2005a,b) and hexafluorocyclobutane (Swenson et al., 1997), respectively. An intermolecular N2-H1 \cdots N1ⁱ hydrogen bond (symmetry code as in Table 2) links the molecules, forming a hydrogen-bonded dimer of graph-set motif $R_2^2(8)$ (Fig. 2). Of greater interest is an intermolecular N-H··· π interaction between the amino group and the benzene ring in the dimer (Table 2). As a result of these interactions, as well as van der Waals interactions, the structure exhibits hexagonal cavities of diameter 3.774 Å along the c axis (Fig. 3).

Experimental

To a solution of thiourea (0.76 g, 10 mmol) in absolute ethanol (50 ml), a solution of 3-(2-chloro-1-oxoethyl)-1-methyl-1-p-xylylcyclobutane (2.50 g, 10 mmol) in absolute ethanol (20 ml) was added dropwise at 323-327 K with continuous stirring. By monitoring the IR frequency of the carbonyl group of 3-(2-chloro-1-oxoethyl)-1-methyl-1-p-xylylcyclobutane, completion of the reaction was easily seen. After cooling to room temperature, the solution was made alkaline with an aqueous solution of NH₃ (5%), causing the separation of dark-green crystals of (I) from the reaction mixture. The precipitate was filtered off, washed with an aqueous ammonia solution and water several times, dried in air and recrystallized from water-ethanol (1:4) by slow evaporation (yield 76%; m.p. 407.5 K). Characteristic ¹H NMR shifts (CDCl₃, p.p.m.) are at 1.54 (s, 3H, -CH₃ on cyclobutane), 2.22 (s, 3H, o-CH₃ of p-xylyl), 2.33 (s, 3H, m-CH₃ of p-xylyl), 2.48 (m, 2H, -CH₂-), 2.59 (*m*, 2H, -CH₂-), 3.43 (*q*, *J* = 9.2, 1H, >CH-), 5.55 (brs, 2H, NH₂), 5.96 (s, 1H, aromatic in thiazole ring), 6.89 (s, 1H, aromatic), 7.03 (m, 2H, aromatic). Characteristic ¹³C NMR shifts



Figure 3 A view of the cavities along the c axis. H atoms have been omitted.

(CDCl₃, p.p.m.) are at 169.18, 155.84, 149.80, 135.57, 132.12, 131.43, 127.11, 126.85, 100.39, 41.89, 39.46, 31.09, 28.05, 21.29 and 19.71.

Crystal data

C16H20N2S Mo $K\alpha$ radiation $M_r = 272.40$ Cell parameters from 37485 Trigonal, $R\overline{3}$ reflections a = 20.7083 (11) Å $\theta = 1.6-28.0^{\circ}$ $\mu = 0.20 \text{ mm}^{-1}$ c = 18.2954 (10) Å V = 6794.6 (6) Å³ T = 293 (2) K Z = 18Prism, pale yellow $D_x = 1.198 \text{ Mg m}^{-3}$ $0.57 \times 0.48 \times 0.38 \text{ mm}$

Data collection

Stoe IPDS-2 diffractometer

 ω scans Absorption correction: integration (X-RED32; Stoe & Cie, 2002)

 $T_{\min} = 0.900, T_{\max} = 0.944$ 37485 measured reflections

3557 independent reflections

Refinement

 $\begin{array}{ll} \mbox{Refinement on } F^2 & w = 1/[\sigma^2(F_o^2) + (0.0456P)^2 \\ R[F^2 > 2\sigma(F^2)] = 0.039 & w \mbox{ere } P = (F_o^2 + 2F_c^2)/3 \\ w \mbox{R}(F^2) = 0.100 & w \mbox{ere } P = (F_o^2 + 2F_c^2)/3 \\ S = 1.05 & (\Delta/\sigma)_{\rm max} = 0.001 \\ 3557 \mbox{ reflections } & \Delta\rho_{\rm max} = 0.16 \mbox{ e } {\rm \AA}^{-3} \\ 182 \mbox{ parameters } & \Delta\rho_{\rm min} = -0.24 \mbox{ e } {\rm \AA}^{-3} \\ \mbox{H atoms treated by a mixture of } \end{array}$

independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

S1-C2	1.7251 (16)	N1-C3	1.3890 (16)
S1-C1	1.7424 (14)	C2-C3	1.3436 (19)
N1-C1	1.2998 (17)	C3-C4	1.4914 (19)
N1-C1-N2	124.34 (13)	C3-C4-C5	117.36 (12)
N1-C1-S1	114.56 (10)	C9-C7-C5	116.10 (12)
C2-C3-C4-C6	124.11 (15)	C2-C3-C4-C5	-133.16 (15)
N1-C3-C4-C6	-55.34 (17)	N1-C3-C4-C5	47.39 (18)

2851 reflections with $I > 2\sigma(I)$

 $R_{\rm int} = 0.068$

 $\theta_{\rm max} = 27.8^{\circ}$

 $h = -26 \rightarrow 27$

 $k = -27 \rightarrow 27$ $l = -23 \rightarrow 23$

Table 2Hydrogen-bon	d geometry (Å	., °).		
D_H4	<i>D</i> _Н	H4	$D \dots A$	

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$
$\begin{array}{c} N2 - H1 \cdots N1^{i} \\ N2 - H3 \cdots Cg1^{i} \end{array}$	0.91 (2)	2.15 (2)	3.0540 (19)	180 (2)
	0.83 (2)	2.45 (1)	3.307 (2)	167 (2)

Symmetry code: (i) $-x + \frac{1}{3}, -y + \frac{2}{3}, -z + \frac{2}{3}$. Cg1 is the centroid of the C9–C14 benzene ring

All H atoms, except for H1 and H3, were placed in calculated positions, with C–H distances in the range of 0.93–0.96 Å. $U_{\rm iso}({\rm H})$ values were constrained to be 1.2 and 1.5 times $U_{\rm eq}$ of the carrier atom. Atoms H1 and H3 were located in a difference map and refined freely.

Data collection: X-AREA (Stoe & Cie, 2002); cell refinement: X-AREA; data reduction: X-RED32 (Stoe & Cie, 2002); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

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