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4-(4-Chlorophenyl)-*N*-phenyl-5-(1*H*-1,2,4-triazol-1-yl)thiazol-2-amine

Ling Shao, Xin Zhou and Jian-Xin Fang*

State Key Laboratory and Institute of Elemento-Organic Chemistry, Nankai University, Tianjin 300071, People's Republic of China

Correspondence e-mail: shaoling1999@yahoo.com.cn

Key indicators

Single-crystal X-ray study
T = 294 K
Mean σ(C–C) = 0.003 Å
R factor = 0.039
wR factor = 0.104
Data-to-parameter ratio = 14.8

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

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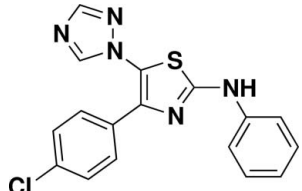
The title compound, $C_{17}H_{12}ClN_5S$, has been synthesized as a potent anticancer agent. The dihedral angle between the thiazole and triazole rings is 85.9 (2)°. There are intermolecular N—H···N and C—H···Cl interactions in the crystal structure.

Comment

The aminothiazole ring system has found application in drug development for the treatment of allergies, hypertension, inflammation, schizophrenia, and bacterial and HIV infections (Arcadi *et al.*, 1999). For example, aminothiazole BMS-387032 {*N*-[5-({[5-(1,1-dimethylethyl)-2-oxazolyl]methyl}thio)-2-thiazolyl]-4-piperidinecarboxamide} has been selected to enter clinical development as an antitumour agent (Misra *et al.*, 2004). In the search for novel aminothiazole compounds with potent antitumour activities and as a continuation of our studies of thiazole molecules (Shao *et al.*, 2005), we have designed and synthesized such 2-aminothiazole compounds incorporating the 1*H*-1,2,4-triazole unit. In this paper, we report the crystal structure of the title compound, (I).



(I)

Fig. 1 shows the molecular structure of (I), which contains four planar subunits, namely the thiazole ring (*P*1), the substituted C5–C10 benzene ring (*P*2), the C12–C17 phenyl ring (*P*3) and the triazole ring (*P*4). The dihedral angles between *P*1 and *P*2, *P*2 and *P*3, *P*3 and *P*4 are 6.1 (4), 14.0 (3) and 85.9 (2)°, respectively. The C11—N5 and C3—N3 bond lengths in (I) (Table 1) are longer than the corresponding distances in 2-amino-4-(2,5-dichlorophenyl)-5-(1*H*-1,2,4-triazol-1-yl)-1,3-thiazole [1.339 (3) and 1.402 (3) Å; Shao *et al.*, 2004].

In (I), the molecules are associated *via* N—H···N and C—H···Cl interactions (Table 2 and Fig. 2).

Experimental

α-Bromo-α-(1*H*-1,2,4-triazol-1-yl)-4-chloroacetophenone (2.66 g, 10 mmol) and dry sodium thiocyanate (0.97 g, 12 mmol) were stirred in ethanol (25 ml) for 3 h at 323 K. A solution of aniline (0.93 g, 10 mmol) in ethanol (5 ml) was added in one portion and the reaction mixture was stirred for 8 h. The ethanol was distilled off, and ethyl

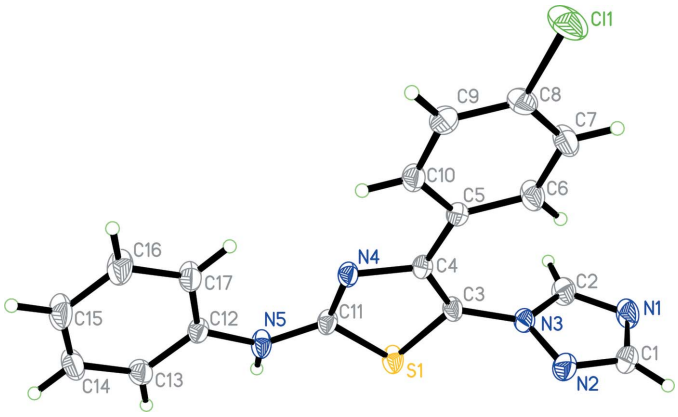


Figure 1
The molecular configuration and atom-numbering scheme for (I). Displacement ellipsoids are drawn at the 30% probability level.

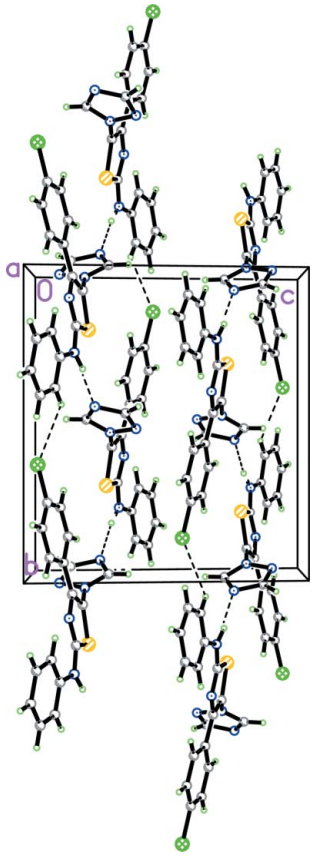


Figure 2
A packing diagram for (I), viewed down the *a* axis. Dashed lines indicate hydrogen bonds.

acetate and water were added (80 ml). The aqueous phase was extracted twice with ethyl acetate, and the combined organic phases were dried with $MgSO_4$, and the solvent was removed *in vacuo*. The residue was then purified *via* column chromatography on silica gel (ethyl acetate/petroleum ether, 1:4 *v*/*v*) to afford (I) in a yield of 15% (m.p. 483 K). Analysis: C 57.56, H 3.52, N 20.03%; calculated for $C_{17}H_{12}ClN_5S$: C 57.71, H 3.42, N 19.79%. Spectroscopic analysis: ^{1}H NMR (DMSO, δ, p.p.m.): 10.629 (*s*, 1H, N—H), 8.858 (*s*, 1H, Tr-H), 8.369 (*s*, 1H, Tr-H), 7.717, 7.691 (*d*, 2H, *p*-Cl-Ph-H, J = 7.8 Hz), 7.462, 7.436 (*d*, 2H, *p*-Cl-Ph-H, J = 7.8 Hz), 7.411–7.023 (*m*, 5H, Ph-H).

Crystal data

$C_{17}H_{12}ClN_5S$
M_r = 353.83
Monoclinic, $P2_1/n$
a = 9.5139 (18) Å
b = 13.681 (3) Å
c = 12.439 (3) Å
β = 98.828 (3)°
V = 1599.9 (5) Å^3
Z = 4
D_x = 1.469 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 3277 reflections
θ = 2.2–26.4°
μ = 0.38 mm^{-1}
T = 294 (2) K
Parallelepiped, colourless
0.24 × 0.22 × 0.20 mm

Data collection

Bruker SMART CCD area-detector diffractometer
φ and ω scans
Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)
T_{min} = 0.903, T_{max} = 0.928
8842 measured reflections
3279 independent reflections
2449 reflections with $I > 2\sigma(I)$
R_{int} = 0.031
θ_{max} = 26.4°
$h = -9 \rightarrow 11$
$k = -11 \rightarrow 17$
$l = -15 \rightarrow 15$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.039
$wR(F^2)$ = 0.104
S = 1.02
3279 reflections
221 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0499P)^2 + 0.5099P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.23 e Å^{-3}
$\Delta\rho_{min}$ = −0.33 e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

S1—C3	1.740 (2)	N3—C3	1.415 (2)
S1—C11	1.7579 (18)	N4—C11	1.298 (2)
N1—C2	1.314 (3)	N4—C4	1.393 (2)
N1—C1	1.351 (3)	N5—C11	1.354 (2)
N2—N3	1.367 (2)	N5—C12	1.408 (2)
N3—C2	1.337 (2)		
C3—S1—C11	87.29 (9)	C11—N5—C12	128.22 (17)
C2—N1—C1	102.45 (17)	N2—C1—N1	115.7 (2)
C1—N2—N3	101.80 (17)	N1—C2—N3	110.7 (2)
C2—N3—N2	109.34 (16)	C4—C3—S1	112.29 (13)
C2—N3—C3	130.37 (18)	C3—C4—N4	113.33 (17)
C11—N4—C4	111.76 (15)		
N2—N3—C3—C4	78.5 (3)	C12—N5—C11—N4	−10.5 (4)
C3—C4—C5—C10	−173.1 (2)	C11—N5—C12—C17	14.8 (3)

Table 2
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N5—H5···N1^{i}	0.83 (3)	2.17 (3)	2.990 (2)	170 (2)
C13—H13···Cl1^{ii}	0.93	2.87	3.605 (2)	137

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

The amino H atom was located in a difference Fourier map and refined isotropically, with the distance restraint N—H = 0.83 (3) Å. Other H atoms were placed in calculated positions, with C—H = 0.93 Å, and refined using a riding model, with U_{iso}(H) = 1.2U_{eq}(C).

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics:

SHELXTL (Bruker, 1999); software used to prepare material for publication: *SHELXTL*.

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