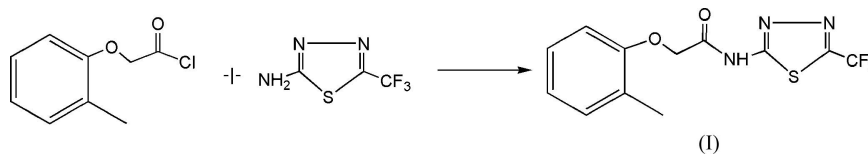


Jun-Yan Zhan, De-Jun Xiong,
Yan-Gang Wang and Hai-Bing
Li*Key Laboratory of Pesticides and Chemical
Biology, Ministry of Education, College of
Chemistry, Central China Normal University,
Wuhan 430079, People's Republic of ChinaCorrespondence e-mail:
lhbing@mail.ccnu.edu.cn

Key indicators

Single-crystal X-ray study
 $T = 298\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.006\text{ \AA}$
Disorder in main residue
 R factor = 0.063
 wR factor = 0.171
Data-to-parameter ratio = 11.6For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.2-(*o*-Tolyloxy)-*N*-[5-(trifluoromethyl)-
1,3,4-thiadiazol-2-yl]acetamideIn the title compound, $\text{C}_{12}\text{H}_{10}\text{F}_3\text{N}_3\text{O}_2\text{S}$, the molecules are
linked into two-dimensional networks parallel to $(1\bar{1}0)$
through a mixture of π - π stacking and $\text{N}-\text{H}\cdots\text{N}$ hydrogen-
bond interactions.Received 11 March 2007
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Comment

1,3,4-Thiadiazole derivatives exhibit many important bio-
activities (Wang *et al.*, 2004; Castro *et al.*, 1996) and consid-
erable interest has been shown in fluorine-containing
compounds. Therefore, it is worth investigating fluoro deri-
vatives incorporating 1,3,4-thiadiazole. In view of this, a
number of new compounds have been synthesized in our
laboratory, including the title compound, (I).

The molecular structure of (I) is shown in Fig. 1. The molecules are linked into a two-dimensional structure (Fig. 2) by a combination of $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds (Table 1) and π - π stacking between the rings S1/N2/N3/C10/C11 (centroid $Cg1$) and C2-C7 (centroid $Cg2$). The relevant centroid-centroid and (mean) perpendicular distances defining these interactions are 3.945 (2) and 3.77 (12) \AA , respectively, for $Cg1\cdots Cg2^i$ [symmetry code: (i) $2 - x, -y, 1 - z$]. The trifluoromethyl group exhibits rotational disorder (Fig. 1), as previously observed in similar compounds (see, for example, Tan *et al.*, 2005).

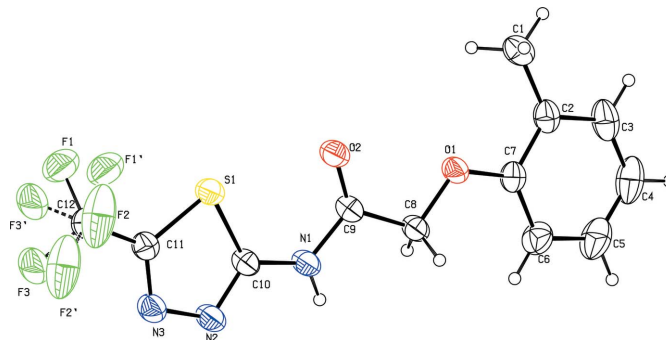


Figure 1

The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level. Both disordered components of the CF_3 group are shown.

Experimental

2-Amino-5-[4-(trifluoromethyl)]-1,3,4-thiadiazole (0.68 g, 4.0 mmol) was prepared according to the reported procedure of Song *et al.* (2005). It (0.68 g, 4.0 mmol) was then treated with *o*-tolylxyacetyl chloride (0.88 g, 4.5 mmol). The title compound was isolated in 63% yield. Crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of a solution in a mixture of methanol and dimethylformamide (1:5 *v/v*) at room temperature.

Crystal data

$C_{12}H_{10}F_3N_3O_2S$	$\gamma = 94.381 (4)^\circ$
$M_r = 317.29$	$V = 687.8 (3) \text{ \AA}^3$
Triclinic, $P\bar{1}$	$Z = 2$
$a = 8.347 (2) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 9.430 (2) \text{ \AA}$	$\mu = 0.28 \text{ mm}^{-1}$
$c = 9.493 (2) \text{ \AA}$	$T = 298 (2) \text{ K}$
$\alpha = 108.030 (4)^\circ$	$0.30 \times 0.26 \times 0.15 \text{ mm}$
$\beta = 101.762 (4)^\circ$	

Data collection

Bruker SMART APEX CCD area-detector diffractometer	2385 independent reflections
Absorption correction: none	2061 reflections with $I > 2\sigma(I)$
3448 measured reflections	$R_{\text{int}} = 0.026$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.063$	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2) = 0.171$	$\Delta\rho_{\text{max}} = 0.33 \text{ e \AA}^{-3}$
$S = 1.03$	$\Delta\rho_{\text{min}} = -0.31 \text{ e \AA}^{-3}$
2385 reflections	
205 parameters	
22 restraints	

Table 1

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1\cdots N2^i$	0.856 (10)	2.037 (12)	2.885 (4)	171 (3)

Symmetry code: (i) $-x + 2, -y + 1, -z + 1$.

Carbon-bound H atoms were positioned geometrically and refined using a riding model, with $C_{\text{sp}^2}-H = 0.93 \text{ \AA}$, methyl $C-H = 0.96 \text{ \AA}$ and methylene 0.97 \AA ; $U_{\text{iso}}(H) = xU_{\text{eq}}(C)$, where $x = 1.5$ for methyl and 1.2 for methylene and C_{sp^2} . The H atom attached to N was located in a difference map and refined with a restrained distance $N-H = 0.86 (1) \text{ \AA}$ and a free $U_{\text{iso}}(H)$. The occupancies of the disordered trifluoromethyl group refined to 0.884 (16):0.116 (16). The disorder was refined using the commands DFIX and SADI.

Data collection: SMART (Bruker, 1997); 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, 2001); software used to prepare material for publication: SHELXTL.

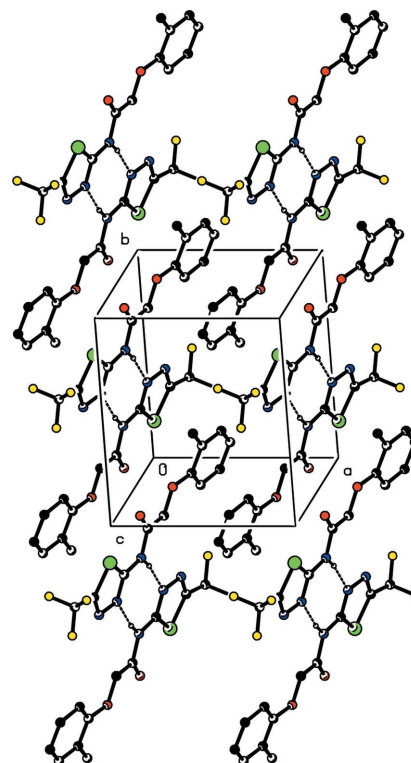


Figure 2

A packing view of (I). Dashed lines indicate hydrogen bonds. Only one disorder component is shown, and H atoms not involved in hydrogen bonding have been omitted.

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