organic papers

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Key indicators

Single-crystal X-ray study T = 292 KMean $\sigma(\text{C}-\text{C}) = 0.005 \text{ Å}$ R factor = 0.060 wR factor = 0.189 Data-to-parameter ratio = 13.1

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

Methyl 2-[2-(5,7-dimethyl-1,2,4-triazolo-[1,5-a]pyrimidin-2-ylsulfanylmethyl)phenyl]-3-methoxyacrylate

In the title compound, $C_{19}H_{20}N_4O_3S$, three intramolecular hydrogen bonds and π - π stacking are observed in the crystal structure.

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Comment

The strobilurins are an important class of agricultural fungicides, the discovery of which was inspired by a group of natural fungicidal derivatives of *B*-methoxyacrylic acid. Field application of the natural compounds was not possible because of difficulties in their large-scale production and their relative volatility and photochemical instability (Gullino *et al.*, 2000). Therefore, effort was focused on their chemical optimization. Some synthetic analogs are now commercially available, such as azoxystrobin, kresoximmethyl, metominostrobin and trifloxystrobin (Bartlett *et al.*, 2002; Clough, 1993). In order to find novel fungicidal compounds with higher activity, we designed and synthesized the title compound, (I), containing the [1,2,4]triazolo[1,5-*a*]pyrimidine ring. In this paper, we present the X-ray crystallographic analysis of (I).



As shown in Fig. 1, the heterocycle (N1-C1-C3-N2-N3-C7-N4-C6) is not coplanar with the benzene ring. The angle between their planes is 102.1 (2)°. Two C-H···O and one C-H···N intramolecular hydrogen bonds exist in the crystal structure (Table 1). The angle between the planes of the triazole ring (N2-N3-C7-N4-C6) and the pyrimidine ring (N1-C1-C3-N2-C6) in adjacent molecules is 0.70 (6)°, and the distance between these ring centroids is 3.563 (2) Å (Fig. 2). This suggests the existence of π - π interactions.

Experimental

The title compound was synthesized according to a literature procedure (Clough, 1993). Crystals suitable for single-crystal X-ray diffraction were grown from acetone at 277 K.

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Figure 1

View of the molecule of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level. H atoms are represented by circles of arbitrary size.

Z = 2

 $D_x = 1.356 \text{ Mg m}^{-3}$

Mo K α radiation Cell parameters from 1142 reflections $\theta = 2.3-21.1^{\circ}$ $\mu = 0.20 \text{ mm}^{-1}$

T = 292 (2) K Plate, yellow $0.30 \times 0.20 \times 0.04$ mm

Crystal data

Data collection

2393 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.023$
$\theta_{\rm max} = 25.0^{\circ}$
$h = -10 \rightarrow 7$
$k = -11 \rightarrow 11$
$l = -14 \rightarrow 14$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.060$	H-atom parameters constrained $w = 1/[\sigma^2(F_r^2) + (0.0954P)^2]$
$wR(F^2) = 0.189$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.11 3261 reflections	$(\Delta/\sigma)_{\text{max}} = 0.031$ $\Delta\rho_{\text{max}} = 0.53 \text{ e} \text{ Å}^{-3}$
248 parameters	$\Delta \rho_{\rm min} = -0.63 \ {\rm e} \ {\rm \AA}^{-3}$

Table 1

Hydrogen-bond geometry (Å, $^{\circ}$).

$D - H \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
C16-H16···O2	0.93	2.31	2.658 (4)	102
$\begin{array}{c} C8-H8B\cdots O3\\ C8-H8A\cdots N4 \end{array}$	0.97 0.97	2.50 2.54	3.242 (4) 2.939 (4)	133 105

All H atoms were initially located in a difference Fourier map. The methyl H atoms were then constrained to an ideal geometry, with C—H distances of 0.96 Å and $U_{iso}(H) = 1.5U_{eq}(C)$, but each group was allowed to rotate freely about its C—C bond. All other H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C—H distances in the range 0.93–0.97 Å and $U_{iso}(H) = 1.2U_{eq}(C)$.



Figure 2

Intramolecular hydrogen bonding and intermolecular π - π stacking between heterocyclic rings, indicated by dotted lines. Atoms labeled with the suffix *a* are generated by the symmetry operation (-x, -y, 1-z).

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

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