organic papers

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Key indicators

Single-crystal X-ray study T = 295 KMean $\sigma(\text{C}-\text{C}) = 0.003 \text{ Å}$ R factor = 0.050 wR factor = 0.173 Data-to-parameter ratio = 16.0

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

2-(4,6-Dimethoxypyrimidin-2-yloxy)-6-fluoro-*N*-(3-methylpyridyl)benzylamine

In the title compound, $C_{19}H_{19}FN_4O_3$, the two heterocyclic ring substituents lie on the same side of the central benzene ring.

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Comment

Pyrimidinyloxybenzylamine derivatives have very high weedcontrol activity: they are highly efficient with low toxicity, and biodegradable, safe and environmentally friendly agrochemicals (Lu *et al.*, 2001). As part of a study of their structure– activity relationship (SAR), the title compound, (I), that was a product of condensation reactions of 4,6-dimethyloxy-2methylsulfonylpyrimidine, 2-amino-3-methylpyridine and 2fluoro-6-hydroxybenzaldehyde, was investigated.



In (I), the two heterocyclic rings lie on the same side of the benzene ring (Fig. 1); the dihedral angle between the two nitrogen-containing rings is 85.67 (10)°. This conformation allows the formation of a centrosymmetric dimer mediated by a pair of $N-H \cdots N$ hydrogen bonds (Table 1).

Experimental

2-Amino-3-methylpyridine (0.54 g, 5 mmol) was added dropwise to a methanol solution of 2-fluoro-6-hydroxybenzaldehyde (0.7 g, 5 mmol). At room temperature, NaBH₄ (0.34 g) was added with stirring to give a yellow precipitate. After extraction and distillation, and drying *in vacuo*, the product was added to a flask containing a tetrahydrofuran solution (25 ml) of 4,6-dimethyloxy-2-methyl-sulfonylpyrimidine (0.98 g, 4.5 mmol) and K₂CO₃ (1.17 g) and the mixture was refluxed for 5 h. After filtration, the liquor was evaporated under vacuum to give a solid (1.38 g, yield 83%), which was recrystallized from methanol and petroleum ether (3:1) to give colorless blocks (m.p. 359–360 K).

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Crystal data

C19H19FN4O3 $M_r = 370.38$ Triclinic, $P\overline{1}$ a = 8.8490 (10) Åb = 10.5810 (10) Å c = 11.3773 (8) Å $\alpha = 113.4470(10)^{\circ}$ $\beta = 98.8520 (10)^{\circ}$ $\gamma = 106.364 (2)^{\circ}$ V = 893.89 (15) Å³

Data collection

Rigaku R-AXIS RAPID diffractometer ω scans Absorption correction: multi-scan (ABSCOR; Higashi, 1995) $T_{\min} = 0.940, \ \tilde{T}_{\max} = 0.978$ 6292 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.1093P)^2$
$R[F^2 > 2\sigma(F^2)] = 0.050$	+ 0.0797P]
$wR(F^2) = 0.173$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.06	$(\Delta/\sigma)_{\rm max} < 0.001$
3991 reflections	$\Delta \rho_{\rm max} = 0.43 \ {\rm e} \ {\rm A}^{-3}$
249 parameters	$\Delta \rho_{\rm min} = -0.33 \ {\rm e} \ {\rm \AA}^{-3}$
H atoms treated by a mixture of	Extinction correction: SHELXL97
independent and constrained	Extinction coefficient: 0.050 (8)
refinement	

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

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - HN1 \cdots N3^{i}$	0.89 (2)	2.56 (2)	3.355 (2)	149 (2)

Z = 2

 $D_x = 1.376 \text{ Mg m}^{-3}$

Cell parameters from 3528

Mo $K\alpha$ radiation

reflections

 $\mu=0.10~\mathrm{mm}^{-1}$

T = 295 (1) K

 $R_{\rm int} = 0.022$

 $\theta_{\rm max} = 27.5^{\circ}$

 $h = -11 \rightarrow 11$

 $k = -12 \rightarrow 13$

 $l = -14 \rightarrow 14$

Block, colorless

 $0.42 \times 0.38 \times 0.22 \text{ mm}$

3991 independent reflections

2983 reflections with $I > 2\sigma(I)$

 $\theta = 3.5 - 27.5^{\circ}$

Symmetry code: (i) -x, -y, -z.

The H atom attached to atom N1 was located in a difference Fourier map and refined isotropically. Other H atoms were placed in calculated positions and allowed to ride on their parent atoms, with C-H = 0.98 (aromatic), 0.97 (methylene) or 0.96 Å (methyl). $U_{iso}(H)$ values were set at $1.2U_{eq}(C)$ (aromatic and methylene H) or $1.5U_{eq}(C)$ (methyl H).

Data collection: PROCESS-AUTO (Rigaku, 1998); cell refinement: PROCESS-AUTO; data reduction: CrystalStructure (Rigaku/



Figure 1

The structure of (I), shown with 40% probability displacement ellipsoids.

MSC, 2004); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: CrystalStructure; software used to prepare material for publication: CrystalStructure.

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