

Jun Wu,^{a*} Mei-Feng Chen,^a
Li-Hong Wang^b and
Pei-Zhi Zhang^c^aDepartment of Chemistry, Zhejiang University, Hangzhou, Zhejiang 310027, People's Republic of China, ^bDepartment of Environmental Science, Zhejiang University, Hangzhou, Zhejiang 310027, People's Republic of China, and ^cDepartment of Biological and Chemical Engineering, Zhejiang University of Science and Technology, Hangzhou, Zhejiang 310012, People's Republic of China

Correspondence e-mail: wujunwjw@sohu.com

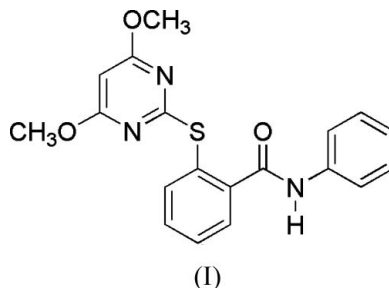
Key indicators

Single-crystal X-ray study
 $T = 295$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.033
 wR factor = 0.072
Data-to-parameter ratio = 17.4For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.2-(4,6-Dimethoxypyrimidin-2-ylsulfanyl)-
N-phenylbenzamide

The title compound, $\text{C}_{19}\text{H}_{17}\text{N}_3\text{O}_3\text{S}$, was synthesized *via* the reaction of 2-(4,6-dimethoxypyrimidin-2-ylsulfanyl)benzoic acid and aniline in dichloromethane using dicyclohexylcarbodiimide as catalyst. The dihedral angles between the pyrimidine plane and the planes of the two benzene rings are $71.2(2)$ and $62.7(2)^\circ$; the dihedral angle between the planes of the two benzene rings is $68.4(4)^\circ$. The conformation of the compound is U-shaped.

Comment

2-(4,6-Dimethoxypyrimidin-2-ylthio)benzoic acid derivatives have been found to exhibit herbicidal activity against grasses and broadleaf weeds over a wide range of growth stages (Nezu *et al.*, 1996; Luthy *et al.*, 2001).



The molecular structure of the title compound, (I), is shown in Fig. 1. The bond lengths and angles are unexceptional. Those in the pyrimidine ring are similar to the values found in a related compound (Wu *et al.*, 2003). The pyrimidine ring makes dihedral angles of $62.7(2)$ and $71.2(2)^\circ$ with the C7–C12 and C14–C19 benzene rings, respectively. The dihedral angle between the planes of the two benzene rings is $68.4(4)^\circ$.

Hydrogen-bonding interactions plays an important role in the solid-state structure of (I) (Table 1). These lead to the formation of chains parallel to the *a* axis.

Experimental

To a mixture of 2-(4,6-dimethoxypyrimidin-2-ylsulfanyl)benzoic acid (13.0 g, 44.0 mmol) and aniline (13.8 g, 39 mmol) in dichloromethane (30 ml), a solution of dicyclohexylcarbodiimide (8.8 g, 44 mmol) in dichloromethane (80 ml) was added dropwise over a period of 20 min. The mixture was stirred for 6 h at room temperature. The solid was filtered off and washed with dichloromethane (20 ml). The filtrate was treated with 10% sodium hydroxide (50 ml), stirred for 1 h and extracted with dichloromethane (2×30 ml). The organic layer was separated, dried with magnesium sulfate and evaporated in vacuo to give a crude product as white powder. After 5 d, single crystals suitable for X-ray analysis were obtained by recrystallization from ethanol.

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Crystal data

$C_{19}H_{17}N_3O_3S$
 $M_r = 367.42$
 Orthorhombic, *Pbca*
 $a = 9.3750$ (1) Å
 $b = 14.4845$ (2) Å
 $c = 26.4390$ (3) Å
 $V = 3590.21$ (7) Å³
 $Z = 8$
 $D_x = 1.359$ Mg m⁻³

Mo $K\alpha$ radiation
 Cell parameters from 30626 reflections
 $\theta = 2.2$ – 27.5°
 $\mu = 0.20$ mm⁻¹
 $T = 295$ (1) K
 Block, colourless
 $0.31 \times 0.20 \times 0.14$ mm

Data collection

Rigaku R-Axis RAPID diffractometer
 ω scans
 Absorption correction: multi-scan (ABSCOR; Higashi, 1995)
 $T_{\min} = 0.868$, $T_{\max} = 0.972$
 31250 measured reflections

4111 independent reflections
 2299 reflections with $F^2 > 2\sigma(F^2)$
 $R_{\text{int}} = 0.041$
 $\theta_{\text{max}} = 27.5^\circ$
 $h = -11 \rightarrow 12$
 $k = -18 \rightarrow 18$
 $l = -34 \rightarrow 34$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.033$
 $wR(F^2) = 0.072$
 $S = 1.00$
 4111 reflections
 236 parameters
 H-atom parameters constrained

$w = 1/[0.0002F_o^2 + 0.9\sigma(F_o^2)]/(4F_o^2)$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.47$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.38$ e Å⁻³
 Extinction correction: Larson (1970), equation 22
 Extinction coefficient: 131 (16)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N3-H301\cdots O3^i$	0.86	2.11	2.916 (1)	156

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

H atoms were placed in calculated positions, with C–H = 1.00 Å (CH) or 0.96 Å (methyl) and N–H = 0.86 Å, and included in the final cycles of refinement in the riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{carrier atom})$.

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/MS, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP-3 for Windows*

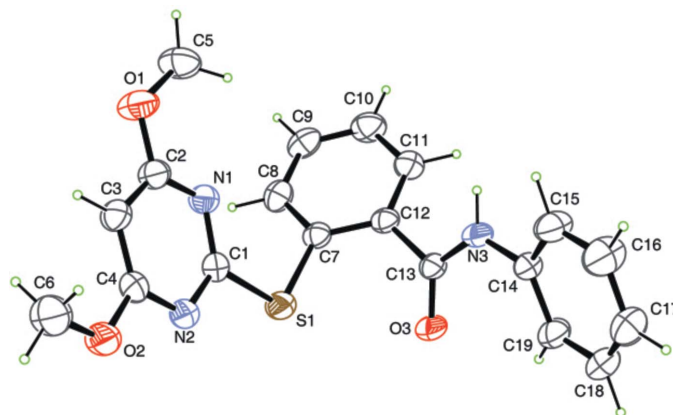


Figure 1

The molecular structure of (I), showing displacement ellipsoids at the 40% probability level.

(Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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