



to 120° (Huo *et al.*, 1995), except for the C9—C8—C13 and C2—C1—C6 angles [116.9 (3) and 116.2 (3)°, respectively; Table 1].

The fact that the C9—O1—C14 angle is 119.7 (3)° shows the influence of the pyrimidine and phenyl rings on the ether group (Takashima *et al.*, 1999). The widening of the C1—N1—C7 angle [to 122.5 (3)°] may be due to steric interactions. The N1—C1 bond distance [1.368 (5) Å] is close to that of a C=N double bond, probably as a result of the delocalization of  $\pi$ -electron density between the planes of the two phenyl rings.

There is one intramolecular N—H...Br hydrogen bond (Table 2). The dihedral angles between the pyrimidine plane and the planes of the two phenyl rings are 107.85 (4) and 77.38 (2)°, and the dihedral angle between the planes of the two phenyl rings is 103.15 (3)°.

## Experimental

To a mixture of *N*-(2-bromophenyl)-2-hydroxybenzylamine (4.29 g, 5.5 mmol) and potassium carbonate (12.96 g, 46.5 mmol) in tetrahydrofuran (THF; 100 ml), a solution of 2-methanesulfonyl-4,6-dimethoxypyrimidine (7.50 g, 17.2 mmol) in THF (40 ml) was added dropwise and the mixture was stirred for 11 h under reflux. The solid was filtered off and the filtrate was left to evaporate at room temperature. After 5 d, a single crystal suitable for X-ray analysis was obtained by recrystallization from ethanol.

### Crystal data

C <sub>19</sub> H <sub>18</sub> BrN <sub>3</sub> O <sub>3</sub>	$Z = 2$
$M_r = 416.27$	$D_x = 1.499 \text{ Mg m}^{-3}$
Triclinic, $P\bar{1}$	Mo $K\alpha$ radiation
$a = 8.7821 (5) \text{ \AA}$	Cell parameters from 3573 reflections
$b = 10.3347 (6) \text{ \AA}$	$\theta = 2.1\text{--}27.4^\circ$
$c = 10.975 (1) \text{ \AA}$	$\mu = 2.26 \text{ mm}^{-1}$
$\alpha = 104.779 (5)^\circ$	$T = 296.1 \text{ K}$
$\beta = 92.572 (2)^\circ$	Platelet, colorless
$\gamma = 105.331 (2)^\circ$	$0.36 \times 0.21 \times 0.07 \text{ mm}$
$V = 922.1 (1) \text{ \AA}^3$	

### Data collection

Rigaku R-AXIS RAPID diffractometer	4157 independent reflections
$\omega$ scans	2351 reflections with $F^2 > 2\sigma(F^2)$
Absorption correction: multi-scan (ABSCOR; Higashi, 1995)	$R_{\text{int}} = 0.029$
$T_{\text{min}} = 0.678$ , $T_{\text{max}} = 0.854$	$\theta_{\text{max}} = 27.5^\circ$
17 152 measured reflections	$h = -9 \rightarrow 11$
	$k = -13 \rightarrow 13$
	$l = -14 \rightarrow 14$

### Refinement

Refinement on $F^2$	H-atom parameters constrained
$R(F) = 0.048$	$w = 1/[0.002F_o^2 + 1.35\sigma(F_o^2)]/(4F_o^2)$
$wR(F^2) = 0.130$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.01$	$\Delta\rho_{\text{max}} = 0.97 \text{ e \AA}^{-3}$
2788 reflections	$\Delta\rho_{\text{min}} = -0.67 \text{ e \AA}^{-3}$
253 parameters	

**Table 1**

Selected bond angles (°).

C9—O1—C14	119.7 (3)	C9—C8—C13	116.9 (3)
C1—N1—C7	122.5 (3)	N2—C14—N3	129.7 (3)
C2—C1—C6	116.2 (3)		

**Table 2**

Hydrogen-bonding geometry (Å, °).

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
N1—H5...Br1	0.94	2.45	3.065 (3)	122

H atoms were placed in calculated positions (C—H = 1.00 Å and N—H = 0.939 Å) and included in the final cycles of refinement as riding atoms.

Data collection: *PROCESS-AUTO* (Molecular Structure Corporation/Rigaku, 2003); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Molecular Structure Corporation/Rigaku, 2003); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *CRYSTALS* (Watkin *et al.*, 1996); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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