

**Yan-Li Zhao,\* Qiao-Zhen Zhang,  
 Xin Chen and Ming Yu**

College of Sciences, Tianjin University of  
 Science and Technology, Tianjin 300222,  
 People's Republic of China

Correspondence e-mail: zhao\_yanli@163.com

**Key indicators**

Single-crystal X-ray study  
 T = 294 K  
 Mean  $\sigma$ (C–C) = 0.005 Å  
 R factor = 0.035  
 wR factor = 0.083  
 Data-to-parameter ratio = 13.2

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

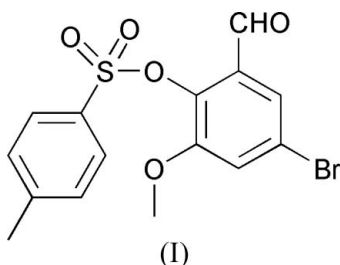
## 4-Bromo-2-formyl-6-methoxyphenyl 4-methylbenzenesulfonate

In the title compound, C<sub>15</sub>H<sub>13</sub>BrO<sub>5</sub>S, the *o*-vanillin group makes a dihedral angle of 41.54 (9)° with the benzene ring. The crystal packing is stabilized by weak intermolecular C–H···Br interactions, leading to chains of molecules.

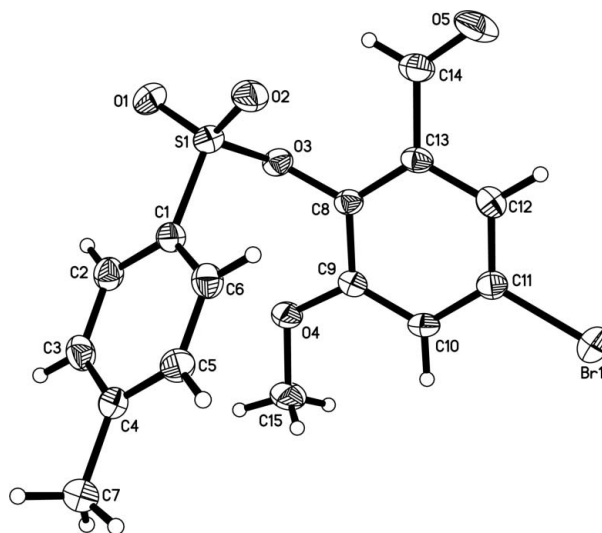
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**Comment**

Schiff base ligands have received a good deal of attention in biology and chemistry (Kahwa *et al.*, 1986 and Klayman *et al.*, 1979). Many Schiff base derivatives have been synthesized and employed in the development of protein and enzyme mimics (Santos *et al.*, 2001). As part of our interest in the coordination properties of Schiff bases functioning as ligands, we have investigated the title compound, (I) (Fig. 1), which is used as a precursor in the preparation of Schiff bases.



The bond lengths and angles in (I) are within normal ranges (Allen *et al.*, 1987). The *o*-vanillin group (atoms C8–C14/O3/



**Figure 1**  
 The molecular structure of (I), with displacement ellipsoids drawn at the 30% probability level.

O4) is essentially planar, with an r.m.s. deviation for the fitted atoms of 0.029 Å. This group makes a dihedral angle of 41.54 (9)° with the C1–C6 benzene ring.

The crystal packing is stabilized by weak intermolecular C–H···Br interactions (Table 1) which link adjacent molecules into chains running along the *b*-axis direction (Fig. 2).

## Experimental

An anhydrous benzene solution (100 ml) of 5-bromo-2-hydroxy-3-methoxybenzaldehyde (2.31 g, 10 mmol) was added dropwise to a solution (50 ml) of 4-methylbenzene-1-sulfonyl chloride (1.91 g, 10 mmol) and pyridine (0.79 g, 10 mmol) in benzene, over a period of 30 min. The mixture was then refluxed for 24 h under a nitrogen atmosphere. The solvent was removed and the mixture poured into ice–water (100 ml). The resulting white precipitate was isolated, recrystallized from acetonitrile and then dried in a vacuum to give the pure compound in 58% yield. Colorless single crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of an acetonitrile solution.

### Crystal data

$C_{15}H_{13}BrO_5S$	$V = 758.9 (6) \text{ \AA}^3$
$M_r = 385.22$	$Z = 2$
Triclinic, $P\bar{1}$	$D_x = 1.686 \text{ Mg m}^{-3}$
$a = 7.752 (3) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 9.025 (4) \text{ \AA}$	$\mu = 2.87 \text{ mm}^{-1}$
$c = 11.638 (5) \text{ \AA}$	$T = 294 (2) \text{ K}$
$\alpha = 71.559 (7)^\circ$	Block, colorless
$\beta = 87.746 (7)^\circ$	$0.24 \times 0.20 \times 0.14 \text{ mm}$
$\gamma = 79.326 (7)^\circ$	

### Data collection

Bruker SMART APEX CCD area-detector diffractometer	3898 measured reflections
$\omega$ scans	2662 independent reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	1991 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.485$ , $T_{\max} = 0.669$	$R_{\text{int}} = 0.017$
	$\theta_{\max} = 25.0^\circ$

### Refinement

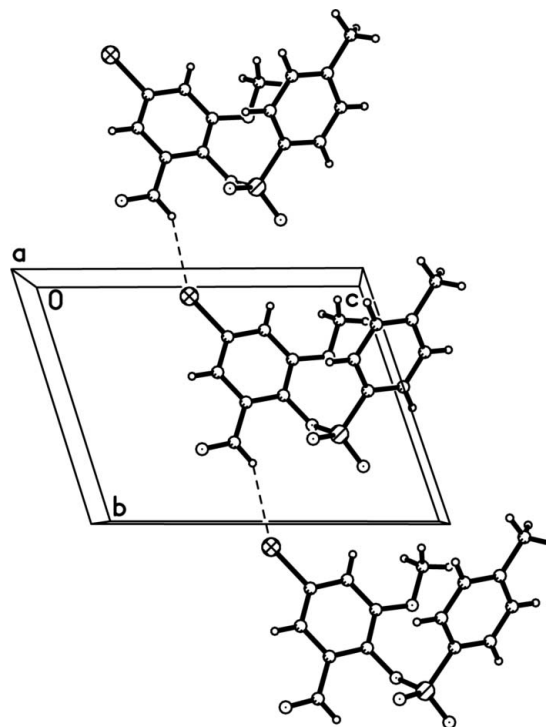
Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.033P)^2 + 0.3049P]$
$R[F^2 > 2\sigma(F^2)] = 0.035$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.083$	$(\Delta/\sigma)_{\max} < 0.001$
$S = 1.05$	$\Delta\rho_{\max} = 0.26 \text{ e \AA}^{-3}$
2662 reflections	$\Delta\rho_{\min} = -0.35 \text{ e \AA}^{-3}$
201 parameters	
H-atom parameters constrained	

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C14–H14···Br1 <sup>i</sup>	0.93	2.96	3.755 (4)	144

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



**Figure 2**

A packing diagram for (I), with C–H···Br interactions shown as dashed lines.

The H atoms were included in calculated positions (C–H = 0.93–0.96 Å) and refined as riding, with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$  or  $1.5U_{\text{eq}}(\text{methyl C})$ .

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

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