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Key indicators

Single-crystal X-ray study
 $T = 294\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.041
 wR factor = 0.100
Data-to-parameter ratio = 14.8

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

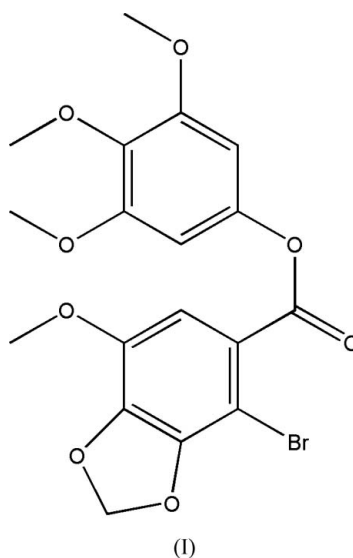
3,4,5-Trimethoxyphenyl 4-bromo-7-methoxy-1,3-benzodioxole-5-carboxylate

The title compound, $\text{C}_{18}\text{H}_{17}\text{BrO}_8$, was synthesized in an anhydrous medium at 293 K. The dihedral angle between the two benzene rings is $38.8(2)^\circ$.

Received 24 June 2005
Accepted 6 July 2005
Online 13 July 2005

Comment

The title compound, (I), is a key intermediate of biphenyl derivatives, which may act to moderate liver ailments, and thus be effective in the treatment of acute and chronic hepatitis (Song & Xiao, 1982).



Its molecular structure of (I) is illustrated in Fig. 1. The bond lengths and angles are unremarkable. The dihedral angle between the five-membered ring and the fused benzene ring is

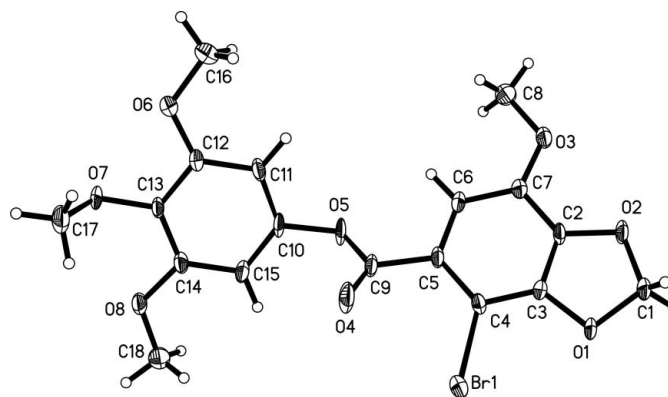


Figure 1
View of the title molecule, showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 35% probability level. H atoms are represented by circles of arbitrary size.

3.3 (1)°, and the angle between the two benzene rings is 38.8 (2)°. Intermolecular C—H···O hydrogen bonds help to stabilize the crystal structure (Fig. 2 and Table 1).

Experimental

The title compound, (I), was prepared according to a literature procedure (Bringmann *et al.*, 2003). The reaction was initiated by the addition of one molar equivalent of 3,4,5-trimethoxyphenol, 4-bromo-7-methoxy-1,3-benzodioxole-5-carboxylic acid, dicyclohexylcarbodiimide and 0.2 molar equivalents of 4-(dimethylamino)pyridine to dichloromethane. The mixture was stirred at room temperature for 12 h. A white powder (m.p. 461 K) resulted (yield 90%) and single crystals suitable for X-ray analysis were obtained by slow evaporation of a dichloromethane solution. IR (KBr, ν cm⁻¹): 1739, 1608, 1502, 1431, 1338, 1172, 1135, 1033, 942; ¹H NMR (CDCl₃): δ 7.449 (s, 1H), 6.473 (s, 2H), 6.176 (s, 2H), 3.967 (s, 3H), 3.863 (s, 6H), 3.851 (s, 3H).

Crystal data

C ₁₈ H ₁₇ BrO ₈	$D_x = 1.655$ Mg m ⁻³
$M_r = 441.23$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 2497 reflections
$a = 8.6563$ (16) Å	$\theta = 2.6$ – 26.1°
$b = 7.6330$ (12) Å	$\mu = 2.37$ mm ⁻¹
$c = 26.927$ (4) Å	$T = 294$ (2) K
$\beta = 95.403$ (9)°	Block, colorless
$V = 1771.2$ (5) Å ³	$0.54 \times 0.40 \times 0.32$ mm
$Z = 4$	

Data collection

Bruker SMART 1000 CCD area-detector diffractometer	3679 independent reflections
φ and ω scans	2307 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 2002)	$R_{int} = 0.051$
$T_{min} = 0.288$, $T_{max} = 0.469$	$\theta_{max} = 26.8^\circ$
9627 measured reflections	$h = -10 \rightarrow 10$
	$k = -9 \rightarrow 7$
	$l = -34 \rightarrow 33$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0519P)^2 + 0.0516P]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.100$	$(\Delta/\sigma)_{max} = 0.001$
$S = 1.00$	$\Delta\rho_{max} = 0.50$ e Å ⁻³
3679 reflections	$\Delta\rho_{min} = -0.64$ e Å ⁻³
249 parameters	Extinction correction: SHELXL97
H-atom parameters constrained	Extinction coefficient: 0.0369 (15)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C1—H1A···O7 ⁱ	0.97	2.42	3.278 (4)	147
C8—H8A···O4 ⁱⁱ	0.96	2.45	3.244 (4)	140

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

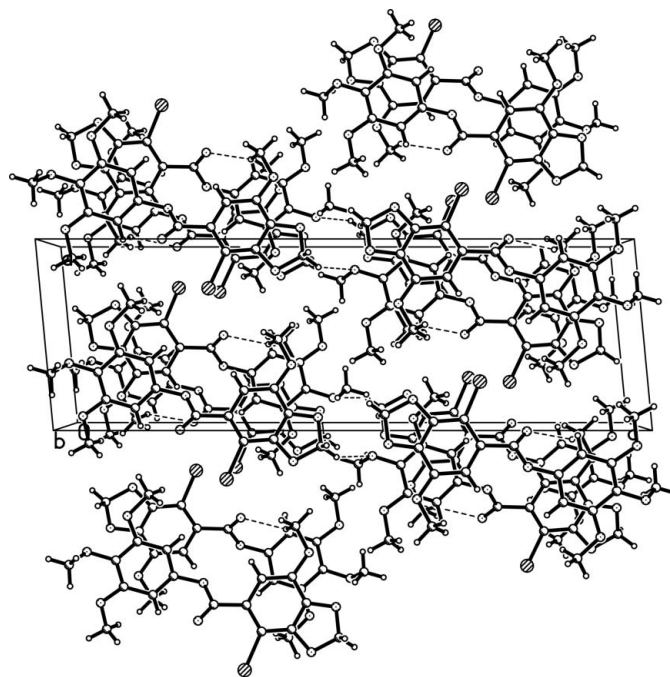


Figure 2

A view of the crystal structure, viewed approximately along the b axis. Dashed lines indicate hydrogen bonds.

All H atoms were positioned geometrically and refined as riding, with C—H = 0.93–0.97 Å. $U_{iso}(H)$ values were set equal to $xU_{eq}(\text{carrier atom})$, where $x = 1.5$ for methyl H atoms and 1.2 for all others.

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

This research was supported by the National Natural Science Foundation of China (grant No. 200342005).

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