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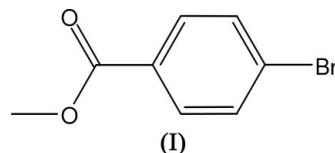
Key indicators

Single-crystal X-ray study
 $T = 173$ K
Mean $\sigma(\text{C}-\text{C}) = 0.006$ Å
 R factor = 0.041
 wR factor = 0.093
Data-to-parameter ratio = 13.6For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

Methyl 4-bromobenzoate

Molecules of the title compound, $\text{C}_8\text{H}_7\text{BrO}_2$, are almost planar. The compound is isostructural with methyl 4-iodobenzoate but not with methyl 4-chlorobenzoate. The crystal packing is characterized by a short $\text{Br} \cdots \text{O}$ interaction of 3.047 (3) Å.

Comment

The crystal structures of methyl 4-iodobenzoate (Brock, 1987) and methyl 4-chlorobenzoate (Roy *et al.*, 1993) have already been determined, but the structure of methyl 4-bromobenzoate, (I), was missing until now.

A perspective view of (I) is shown in Fig. 1. Bond lengths and angles can be regarded as normal (Cambridge Structural Database, Version 5.27 plus one update; *MOGUL* Version 1.1; Allen, 2002). The molecule is essentially planar (r.m.s. deviation for all non-H atoms = 0.092 Å). It is interesting that (I) is isostructural with the iodo compound (Brock, 1987), but not with the chloro compound (Roy *et al.*, 1993). The crystal structure is stabilized by a short $\text{Br} \cdots \text{O}$ contact [$\text{Br}1 \cdots \text{O}1^i = 3.047$ (3) Å and $\text{Br}1 \cdots \text{O}1^i - \text{C}7^i = 146.7$ (3)°; symmetry code: (i) $x, -y + \frac{1}{2}, z + \frac{1}{2}$]. The shortest $\text{Br} \cdots \text{Br}$ contact is 4.759 (1) Å; symmetry code to generate the second Br atom: $-x + \frac{1}{2}, y - \frac{1}{2}, z$]. Similar short contacts were noted in the iodo compound where the shortest $\text{I} \cdots \text{I}$ contact is 4.863 (1) Å and the shortest distance between I and the carbonyl O is 3.203 (4) Å. The molecules crystallize in chains (Fig. 2). The angle between two molecules in a chain is 38.04 (8)°.

Experimental

The title compound was purchased from Lancaster Synthesis, England, and recrystallized from an ethanol solution.

Crystal data

$\text{C}_8\text{H}_7\text{BrO}_2$
 $M_r = 215.05$
 Orthorhombic, *Pbca*
 $a = 13.8485$ (18) Å
 $b = 5.8921$ (8) Å
 $c = 19.613$ (2) Å
 $V = 1600.4$ (3) Å³
 $Z = 8$
 $D_x = 1.785$ Mg m⁻³

Mo $K\alpha$ radiation
 Cell parameters from 6406 reflections
 $\theta = 2.4$ – 24.9°
 $\mu = 5.08$ mm⁻¹
 $T = 173$ (2) K
 Needle, colourless
 $0.31 \times 0.10 \times 0.06$ mm

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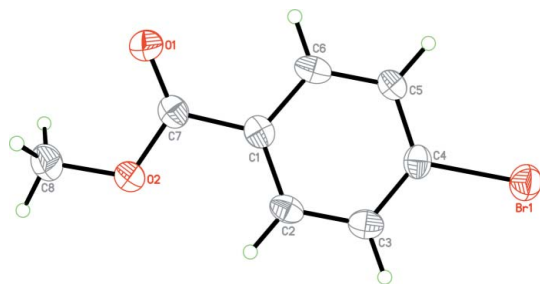


Figure 1
Perspective view of the title compound, showing the atom numbering and displacement ellipsoids drawn at the 50% probability level.

Data collection

Stoe IPDS-II two-circle
diffractometer
 ω scans
Absorption correction: multi-scan
(*MULABS*; Spek, 2003; Blessing,
1995)
 $T_{\min} = 0.302$, $T_{\max} = 0.750$
10202 measured reflections

1375 independent reflections
998 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.060$
 $\theta_{\text{max}} = 25.0^\circ$
 $h = -15 \rightarrow 15$
 $k = -6 \rightarrow 6$
 $l = -23 \rightarrow 23$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.041$
 $wR(F^2) = 0.093$
 $S = 0.94$
1375 reflections
101 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0565P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.86 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.81 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (\AA , $^\circ$).

Br1—C4	1.900 (4)	O2—C7	1.345 (5)
O1—C7	1.201 (6)		
C7—O2—C8	115.3 (4)	O1—C7—O2	123.7 (4)
C5—C4—Br1	119.1 (3)	O1—C7—C1	125.0 (4)
C3—C4—Br1	119.3 (3)	O2—C7—C1	111.3 (4)

H atoms were located in a difference map but positioned geometrically and refined with fixed individual displacement parameters [$U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{methyl C})$] using a riding

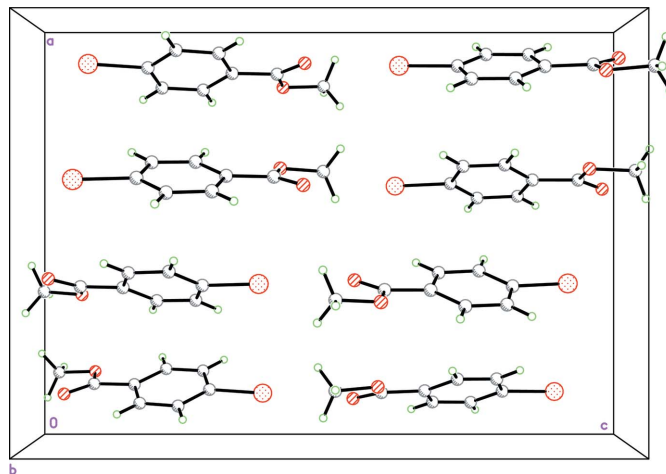


Figure 2
Packing of the title compound, viewed along the *b* axis.

model, with C—H = 0.95 and 0.98 \AA for aromatic and methyl H atoms, respectively. The methyl group was allowed to rotate but not to tip.

Data collection: *X-AREA* (Stoe & Cie, 2001); cell refinement: *X-AREA*; data reduction: *X-AREA*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL-Plus* (Sheldrick, 1991); software used to prepare material for publication: *SHELXL97* and *PLATON* (Spek, 2003).

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