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Key indicators

Single-crystal X-ray study T = 100 KMean σ (C–C) = 0.002 Å R factor = 0.026 wR factor = 0.067 Data-to-parameter ratio = 18.6

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

3-(4-Bromophenyl)-2-ethylacrylic acid

The configuration in the solid state structure of the title compound, $C_{11}H_{11}BrO_2$, about the C=C double bond is *E*. In the crystal structure, symmetry-related molecules are linked by $O-H\cdots O$ hydrogen bonds, forming centrosymmetric carboxylic acid dimers.

Comment

Cinnamic acid derivatives are used in the shikimic acid metabolic pathways of higher plants (Forgó *et al.*, 2005). These compounds are also widely used as starting materials for the synthesis of antimalarial drugs. The most active compounds in this group are halo-substituted (Nodiff *et al.*, 1971).



The molecular structure of the title compound, (I), is shown in Fig. 1 and selected bond distances and angles are given in Table 1. The length of the C7=C8 bond [1.348 (2) Å] shows its double-bond character. The configuration about the C=C double bond is *E*. The bond lengths within the phenyl ring range from 1.382 (2) to 1.408 (2) Å, typical of aromatic character (Allen *et al.*, 1987). The Br-C3 bond distance is normal. In the crystal structure of (I), centrosymmetric dimers are formed *via* O-H···O hydrogen bonds involving the carboxylic acid groups (Fig. 2 and Table 2). The dimers are



Figure 1

The molecular structure of the title compound, showing the atom numbering scheme. Displacement ellipsoids for non-H atoms are represented at the 50% probability level. The H atoms are drawn with an arbitrary radius.

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further linked by $C-H\cdots O$ bonds, forming a sheet-like structure.

Experimental

Compound (I) was synthesized according to a previously reported method (Gensler *et al.*, 1958). A mixture of 4-bromobenzaldehyde (1.85 g 10 mmol), ethylmalonic acid (2.64 g 20 mmol) and piperidine (1.98 ml 20 mmol) in a pyridine (12.5 ml) solution was heated on a steam-bath for 24 h. The reaction mixture was cooled and added to a mixture of 25 ml of concentrated HCl and 50 g of ice. The precipitate formed in the acidified mixture was filtered off and washed with ice-cold water. The product was recrystallized from an alcohol–water mixture (4:1). The yield was 65%.

 $V = 995.85 (12) \text{ Å}^3$

Mo $K\alpha$ radiation

 $0.49 \times 0.39 \times 0.21 \text{ mm}$

 $\mu = 4.10 \text{ mm}^{-1}$

T = 100 (1) K

Z = 4

Crystal data

 $C_{11}H_{11}BrO_2$ $M_r = 255.11$ Monoclinic, $P2_1/c$ a = 11.9803 (9) Å b = 5.0008 (4) Å c = 16.986 (1) Å $\beta = 101.880 (1)^\circ$

Data collection

Bruker SMART APEX CCD area-	8570 measured reflections
detector diffractometer	2461 independent reflections
Absorption correction: multi-scan	2168 reflections with $I > 2\sigma(I)$
(SADABS; Sheldrick, 2001)	$R_{\rm int} = 0.026$
$T_{\rm min} = 0.164, T_{\rm max} = 0.423$	

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.026$ H atoms treated by a mixture of
independent and constrained
refinementS = 1.03refinement2461 reflections $\Delta \rho_{max} = 0.73 \text{ e Å}^{-3}$
 $\Delta \rho_{min} = -0.47 \text{ e Å}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Br-C3 O1-C11	1.9034 (16) 1.330 (2)	O2-C11	1.227 (2)
Br-C3-C2	118.83 (12)	O2-C11-C8	121.63 (15)
Br-C3-C4	119.78 (12)	O1-C11-O2	122.22 (15)
O1-C11-C8	116.16 (14)		

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\begin{array}{c} \hline O1 - H11 \cdots O2^{i} \\ C4 - H4 \cdots O2^{ii} \\ C7 - H7 \cdots O1 \end{array}$	0.79 (4)	1.89 (3)	2.6716 (18)	172 (3)
	0.95	2.52	3.457 (2)	167
	0.95	2.28	2.722 (2)	107

Symmetry codes: (i) -x + 1, -y + 3, -z + 1; (ii) x, $-y + \frac{3}{2}$, $z - \frac{1}{2}$.



Figure 2

Perspective drawing of the dimer formed by $O-H\cdots O$ hydrogen bonds, shown as dashed lines.

All H atoms except H11 were included in the riding model approximation, with C-H = 0.95-0.98 and $U_{iso}(H) = xU_{eq}(C)$, where x = 1.5 for methyl and x = 1.2 for other H atoms. Atom H11 was located in a difference Fourier map and refined freely with an isotropic displacement parameter.

Data collection: SMART (Bruker, 2006); cell refinement: SAINT-Plus (Bruker, 2006); data reduction: SAINT-Plus and XPREP (Bruker, 2006); program(s) used to solve structure: DIRDIF99 (Beurskens et al., 1999); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: PLUTO (Meetsma, 2007) and PLATON (Spek, 2003); software used to prepare material for publication: PLATON.

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