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Key indicators

Single-crystal X-ray study
 $T = 299\text{ K}$
 Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$
 R factor = 0.037
 wR factor = 0.072
 Data-to-parameter ratio = 16.2

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

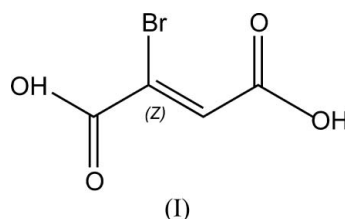
2-Bromofumaric acid

Single crystals of 2-bromofumaric acid, $\text{C}_4\text{H}_3\text{BrO}_4$, were obtained from an aqueous solution of racemic 2,3-dibromosuccinic acid and (–)-quinine. The title compound crystallizes with two molecules in the asymmetric unit. The structure is stabilized by $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds forming alternating chains.

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Comment

We are currently studying the structures and the chemical behaviour of some simple dicarboxylic acids, such as 2,3-dibromosuccinic acid. The structure of the racemate of this acid was determined some time ago (Bolte & Degen, 2000). Recently, we reported the structure of the *meso* form (Eriksson *et al.*, 2006). In an attempt to obtain the pure enantiomer, we attempted to grow crystals of salts of the acid with different chiral bases. However, the reaction with (–)-quinine yielded 2-bromofumaric acid, (I), apparently as the product of an elimination reaction.



The asymmetric unit of (I) contains two molecules of 2-bromofumaric acid, *A* and *B*, and their geometry is unexcep-

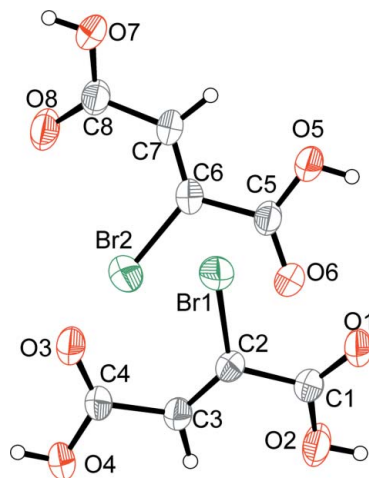


Figure 1
 The contents of the asymmetric unit of (I). Displacement ellipsoids are drawn at the 50% probability level.

tional (Fig. 1). Each *A* molecule binds through O—H...O hydrogen bonds *via* the carboxy groups to two adjacent *B* molecules and *vice versa*, to form closed hydrogen-bonded loops (Table 1 and Fig. 2). Hence, chains of the sequence...*ABAB*... are obtained, which run along the (101) direction.

Experimental

The synthesis of racemic 2,3-dibromosuccinic acid has been described earlier (Fischer, 2006). The acid (276 mg) was dissolved together with (–)-quinine (Fluka, >98.0%; 163 mg) in demineralized water (5 ml). The solution was heated to 323 K for 1 h and then set aside for evaporation at room temperature. Single crystals of the title compound were obtained within a few days.

Crystal data

$C_4H_3BrO_4$	$V = 591.97 (5) \text{ \AA}^3$
$M_r = 194.97$	$Z = 4$
Triclinic, $P\bar{1}$	$D_x = 2.188 \text{ Mg m}^{-3}$
$a = 7.8290 (4) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 8.3791 (4) \text{ \AA}$	$\mu = 6.88 \text{ mm}^{-1}$
$c = 10.2443 (3) \text{ \AA}$	$T = 299 \text{ K}$
$\alpha = 69.572 (4)^\circ$	Fragment, colourless
$\beta = 70.383 (3)^\circ$	$0.30 \times 0.30 \times 0.30 \text{ mm}$
$\gamma = 79.963 (4)^\circ$	

Data collection

Bruker Nonius KappaCCD area-detector diffractometer	11936 measured reflections
φ and ω scans	2701 independent reflections
Absorption correction: numerical (Herrendorf & Bärnighausen, 1997)	1821 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.581$, $T_{\max} = 0.661$	$R_{\text{int}} = 0.052$
	$\theta_{\text{max}} = 27.5^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0231P)^2 + 0.495P]$
$R[F^2 > 2\sigma(F^2)] = 0.037$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.072$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.05$	$\Delta\rho_{\text{max}} = 0.33 \text{ e \AA}^{-3}$
2701 reflections	$\Delta\rho_{\text{min}} = -0.44 \text{ e \AA}^{-3}$
167 parameters	
H-atom parameters constrained	

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O7—H7O...O1 ⁱ	0.82	1.89	2.702 (3)	168
O4—H4...O6 ⁱⁱ	0.82	1.93	2.752 (3)	175
O2—H2...O8 ⁱⁱⁱ	0.82	1.81	2.621 (3)	169
O5—H5...O3 ^{iv}	0.82	1.76	2.574 (3)	170

Symmetry codes: (i) $x, y, z - 1$; (ii) $x - 1, y, z$; (iii) $x, y, z + 1$; (iv) $x + 1, y, z$.

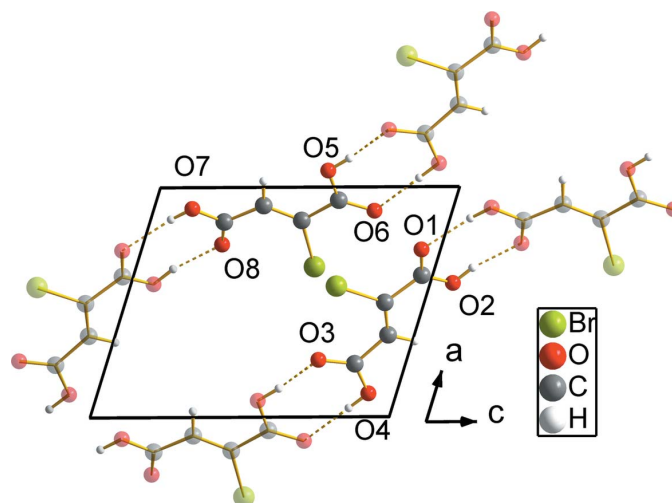


Figure 2

The hydrogen-bonding pattern in (I). Hydrogen bonds are drawn as dashed lines. Solid atoms represent the two molecules in the asymmetric unit.

All H atoms were placed in calculated positions, with C—H = 0.96 \AA and O—H = 0.82 \AA , and refined as riding, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{O})$.

Data collection: *COLLECT* (Nonius, 1999); cell refinement: *DIRAX/LSQ* (Duisenberg, 1992); data reduction: *EVALCCD* (Duisenberg *et al.*, 2003); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 2006); software used to prepare material for publication: *MAXUS* (Mackay *et al.*, 1999).

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