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Key indicators

Single-crystal X-ray study T = 110 KMean $\sigma(C-C) = 0.003 \text{ Å}$ R factor = 0.026 wR factor = 0.077 Data-to-parameter ratio = 14.6

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

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trans-1,4-Dibromocyclohexane-1,4-dicarboxylic acid

Molecules of the title compound, $C_8H_{10}Br_2O_4$, located on symmetry centers, are in a rigid chair conformation, with the COOH and Br substituents axial and equatorial, respectively. The carboxylic acid groups form hydrogen bonds, in a cyclic motif, leading to infinite chains along the *b* axis.

Comment

This paper is part of a study of the molecular conformation and crystal polarity of *trans*-1,4-di- and tetrasubstituted symmetrical cyclohexanes (Echeverría *et al.*, 2000, 1995*a*,*b*).

0

O

(I)

Br

HO

OH

Br



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Figure 1

A view of (I), with displacement ellipsoids drawn at the 50% probability level. Symmetry code: (i) 1 - x, -y, 1 - z.



Figure 2

A view, along b, of the unit-cell contents for (I).

1,4-bis(difluoromethyl)cyclohexane-1,4-dicarboxylate (Swenson et al., 1996) and 106.7 (2)° in 1Ha:2He/4Ha:5He-octafluorocyclohexane (Goodhand & Hamor, 1978). In spite of the equatorial position of Br, the C–Br bond length, 1.988 (2) Å, is longer than the C-Br bond length, 1.834 Å, observed in trans-1,4-dibromocyclohexane (Hassel & Hadler Vihovde, 1953). This is consistent with the elongation predicted by HF calculations in overcrowded, perhalogenated cyclohexanes (Ciolowski et al., 1995).

The three-dimensional structure consists of infinite chains extending in the **b** direction. These chains result from hydrogen bonds, in a cyclic motif, formed by the carboxylic acid groups (Table 2). The chains are linked by weak C- $H \cdots O$ bonds (Steiner, 2002) and weak $C - H \cdots Br$ contacts.

Experimental

The title compound was synthesized according to Barón et al. (1975) and crystallized by slow evaporation from acetone.

Crystal data

```
C_8H_{10}Br_2O_4
M_r = 329.98
Orthorhombic, Pbca
a = 10.5125 (8) Å
b = 8.3836(5) Å
c = 11.2817 (9) Å
V = 994.29 (12) Å<sup>3</sup>
Z = 4
D_x = 2.204 \text{ Mg m}^{-3}
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Data collection

Bruker SMART 1K CCD diffractometer (i) scans Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{\min} = 0.244, \ T_{\max} = 0.443$ 10 606 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.027$ $wR(F^2) = 0.077$ S = 1.061224 reflections 84 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

Br1-C1	1.988 (2)	C3-C1	1.525 (3)
O1-C4	1.304 (3)	C3-C2 ⁱ	1.545 (3)
O1-H1	0.82	C2-C1	1.525 (3)
O2-C4	1.235 (3)	C1-C4	1.536 (3)
C1-C3-C2 ⁱ	109.97 (18)	C2-C1-Br1	107.70 (16)
$C1 - C2 - C3^{i}$	110.57 (18)	C4-C1-Br1	102.23 (13)
C3-C1-C2	111.75 (18)	O2-C4-O1	125.0 (2)
C3-C1-C4	111.99 (18)	O2-C4-C1	120.60 (19)
C2-C1-C4	113.69 (18)	O1-C4-C1	114.39 (19)
C3-C1-Br1	108.88 (15)		~ /
C1-C2-C3 ⁱ -C1 ⁱ	-56.1(2)	C3-C1-C4-O2	25.0 (3)
C2 ⁱ -C3-C1-C2	-56.8(2)	C2-C1-C4-O2	152.8 (2)
C2i-C3-C1-C4	72.1 (2)	Br1-C1-C4-O2	-91.4(2)
C2 ⁱ -C3-C1-Br1	-175.6(1)	C3-C1-C4-O1	-156.2(2)
C3 ⁱ -C2-C1-C3	57.1 (2)	C2-C1-C4-O1	-28.4(3)
C3 ⁱ -C2-C1-C4	-70.8(2)	Br1-C1-C4-O1	87.4 (2)
C3 ⁱ -C2-C1-Br1	176.7 (1)		

Mo $K\alpha$ radiation

reflections

 $\theta = 11.5 - 26.3^{\circ}$

 $\mu = 8.14 \text{ mm}^{-1}$

T = 110 (2) K

 $R_{\rm int}=0.041$

 $\theta_{\rm max} = 28.2^\circ$

 $h = -13 \rightarrow 13$

 $k=-11\rightarrow 11$

 $l=-13\rightarrow 15$

Prism, colourless

 $0.20 \times 0.13 \times 0.10 \ \mathrm{mm}$

1224 independent reflections

975 reflections with $I > 2\sigma(I)$

 $w = 1/[\sigma^2(F_o^2) + (0.0491P)^2]$

where $P = (F_o^2 + 2F_c^2)/3$

+ 0.3512P]

 $(\Delta/\sigma)_{\rm max} = 0.001$

 $\Delta \rho_{\rm max} = 1.04 \text{ e } \text{\AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.56 \ {\rm e} \ {\rm \AA}^{-3}$

Cell parameters from 914

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

Table 2		
Hydrogen-bonding geometry	(Å,	°).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\begin{array}{c} 01 - H1 \cdots 02^{ii} \\ C2 - H21 \cdots 01^{iii} \\ C2 - H22 \cdots 02^{iv} \\ C3 - H31 \cdots 02^{v} \\ C3 - H32 \cdots 01^{vi} \\ C2 - H21 \cdots Br1^{v} \\ C2 - H22 - Br1^{ij} \\ \end{array}$	0.82 0.97 (3) 0.96 (2) 1.01 (3) 0.96 (3) 0.96 (3)	1.82 2.73 (2) 2.93 (2) 2.71 (3) 3.18 (3) 3.17 (3) 2.02 (2)	2.639 (2) 3.274 (3) 3.719 (3) 3.431 (3) 3.889 (3) 4.081 (2) 2.812 (2)	176 116 (2) 140 (2) 129 (2) 132 (2) 158 (2)
$C3-H31\cdots Br1^{v}$	1.01 (3)	3.22 (2)	4.137 (2)	152 (2)

Symmetry codes: (ii) -x, -y, -z; (iii) $1 - x, y - \frac{1}{2}, \frac{1}{2} - z$; (iv) $x, \frac{1}{2} - y, z - \frac{1}{2}$; (v) $\frac{3}{2} - x, y - \frac{1}{2}, z;$ (vi) $\frac{1}{2} + x, \frac{1}{2} - y, 1 - z;$ (vii) $x - \frac{1}{2}, y, \frac{1}{2} - z$

H atoms bound to C atom were located in difference Fourier syntheses and were refined freely in isotropic mode [C-H distances] are in the range 0.96 (2)–1.01 (3) Å]. The H atom of the hydroxyl group was stereochemically positioned and allowed to ride on the bound O atom. The O-H bond was also allowed to rotate about the C-O bond. The largest difference electron-density peak is 0.94 Å from Br1.

Data collection: *SMART-NT* (Bruker, 1998); cell refinement: *SMART-NT*; data reduction: *SAINT-NT* (Bruker, 1998); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 1990), *PARST* (Nardelli, 1983, 1995) and *ORTEP-*3 (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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