



Crystal and molecular structure of *meso*-2,6-dibromoheptanedioic acid (*meso*-2,6-dibromopimelic acid)

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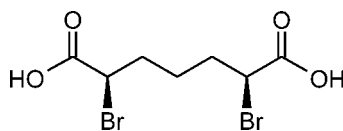
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The molecular structure of the title compound, C₇H₁₀Br₂O₄, confirms the *meso* (2*R*,6*S*) configuration. In the crystal, molecules are linked by pairs of O—H···O=C hydrogen bonds between their terminal carboxyl groups in an *R*₂²(8) motif, forming extended chains that propagate parallel to the *c* axis. Adjacent chains are linked by C=O···Br halogen bonds.

1. Chemical context

meso-2,6-Dibromopimelic acid is a convenient starting point for preparing derivatives 2,6-disubstituted with non-halogen functional groups (for examples: Schotte, 1956*b*; Lingens, 1960; Yuan & Lu, 2009). It also has utility in the synthesis of heterocycles (Schotte, 1956*b*; Miyake *et al.*, 2000; Peters *et al.*, 2006; Hamon *et al.*, 2007). In an ongoing study of disulfides, the title compound was required as precursor to *meso*-3,7-dicarboxy-1,2-dithiepane. Surprisingly, other than the melting point reported by Schotte (1956*a*), no further analytical data have been published on the dibromo acid. Original stereochemical assignment was based on the lack of optical activity of the acid isolated through crystallization of the acid brucine salt (Schotte, 1956*a*). The need to confirm the *meso* configuration motivated the crystal structure determination.



2. Structural commentary

The molecular structure of the title compound is shown in Fig. 1; the (2*R*,6*S*) configuration is apparent, confirming the *meso* form of the compound. All bond lengths and angles are within normal ranges.

3. Supramolecular features

In the crystal, the molecules are linked in head-to-tail fashion by pairs of O—H···O=C hydrogen bonds (Table 1) between their terminal carboxyl groups in an *R*₂²(8) motif, forming extended chains that propagate parallel to the *c* axis (Fig. 2*a*).

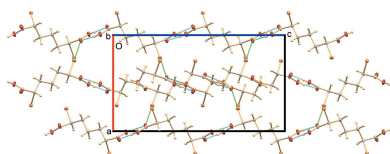


Table 1
Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O2-H2\cdots O3^i$	0.84	1.80	2.635 (3)	177
$O4-H4\cdots O1^{ii}$	0.84	1.83	2.669 (3)	176

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

Adjacent chains are cross-linked by interactions between a carboxyl $C=O$ group in one chain with a Br atom in an adjacent chain. These linkages meet the criteria for halogen bonds (Desiraju *et al.*, 2013): (i) the $=O\cdots Br-C$ bonds are nearly linear [the $=O1\cdots Br2-C2$ and $=O3\cdots Br6-C6$ angles being 168.06 (8) and 170.26 (8)°, respectively], and (ii) the $O\cdots Br$ distances [3.224 (2) and 3.058 (2) Å for $O1\cdots Br2^{iii}$ and $O3\cdots Br6^{iv}$, respectively [symmetry codes: (iii) $\frac{1}{2} - x, y - \frac{1}{2}, z$; (iv) $\frac{3}{2} - x, y - \frac{1}{2}, z$] are less than the sum of the van der Waals radii of 3.35 Å (Mantina *et al.*, 2009; Alvarez, 2013). H and Br bonding are shown in Fig. 2.

4. Synthesis and crystallization

The title compound was first prepared in pure form and its stereochemistry deduced by Fehnel & Oppenlander (1953). The synthesis for the present work followed the method of Schotte (1956a). Pimelic (heptanedioic) acid was converted into the diacid chloride by heating with thionyl chloride. Removal of excess $SOCl_2$ under reduced pressure left the liquid diacid chloride. Over 1 h, bromine (2.3 equivalents) was added dropwise to the stirred diacid chloride maintained at 363 K. Thereafter, stirring and heating continued for an additional hour. The dibrominated acid chloride was hydrolyzed by gradual addition to vigorously stirred formic acid maintained at 353–363 K. When gas evolution ceased, the reaction mixture was refluxed for 15 min, and then allowed to cool to room temperature. Upon cooling in the refrigerator, over two days, the reaction mixture yielded two crops of solids, which were combined and extracted by shaking with ice-cold $CHCl_3$. The remaining solids were recrystallized three times from formic acid to give *meso*-2,6-dibromoheptanedioic acid (26% yield).

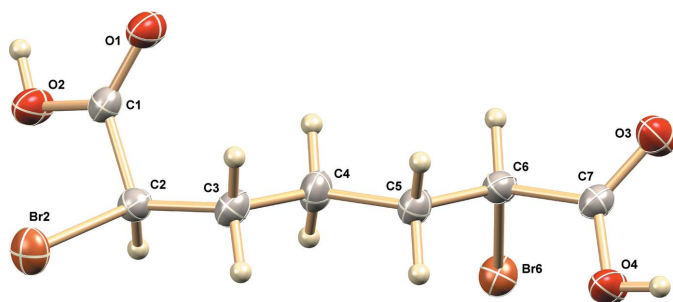


Figure 1
The molecular structure of the title compound, with non-H atoms labeled. Displacement ellipsoids are shown at the 60% probability level.

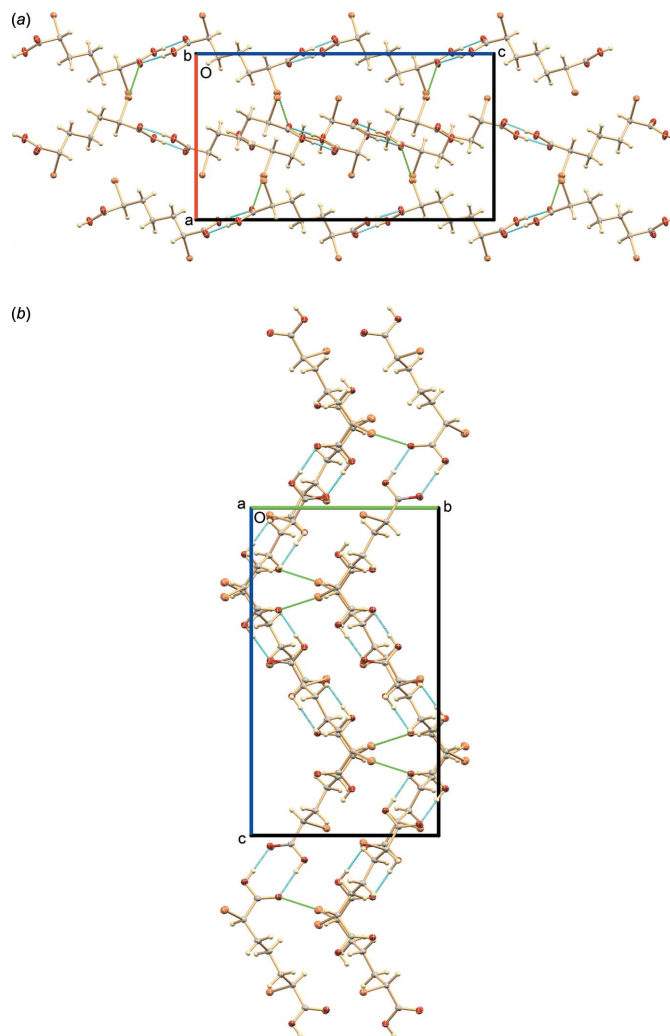


Figure 2
The molecular packing, viewed along the b and a axes [panels (a) and (b)]. Intermolecular hydrogen bonding (cyan) between terminal carboxyl groups results in head-to-tail linkage of the molecules into chains extending along [001]. Adjacent chains are linked by halogen bonding ($C=O\cdots Br$, green).

The 1H NMR spectrum, acquired in Me_2SO-d_6 , is consistent with the molecular structure, with the following resonances (δ referenced to Me_4Si): 13.22, singlet, 2H; 4.43, triplet, 2H, $J = 7$ Hz; 2.01, multiplet, 2H; 1.88, multiplet, 2H; 1.54, multiplet, 1H; 1.39, multiplet, 1H. The high-resolution mass spectrum (electrospray) showed the expected manifold arising from the two stable isotopes of bromine, with the base peak at $m/z = 316.884$; species containing halogens other than bromine were not observed. To produce crystals suitable for diffraction, 10 mg of the title compound was dissolved in a capped glass vial in minimal formic acid with warming. Once a few seeds became visible, slow evaporation of the solvent over 14 days yielded crystals of good quality.

5. Refinement details

Crystal data, data collection and structure refinement details are summarized in Table 2. H-atom U_{iso} parameters were

Table 2
Experimental details.

Crystal data	
Chemical formula	C ₇ H ₁₀ Br ₂ O ₄
<i>M_r</i>	317.97
Crystal system, space group	Orthorhombic, <i>Pbca</i>
Temperature (K)	150
<i>a</i> , <i>b</i> , <i>c</i> (Å)	10.4277 (7), 10.7014 (7), 18.7154 (13)
<i>V</i> (Å ³)	2088.5 (2)
<i>Z</i>	8
Radiation type	Mo <i>K</i> α
<i>μ</i> (mm ⁻¹)	7.74
Crystal size (mm)	0.35 × 0.27 × 0.09
Data collection	
Diffractometer	Bruker SMART APEXII CCD
Absorption correction	Multi-scan (<i>SADABS</i> ; Sheldrick, 2008)
<i>T_{min}</i> , <i>T_{max}</i>	0.231, 0.498
No. of measured, independent and observed [<i>I</i> > 2σ(<i>I</i>)] reflections	35789, 4598, 3488
<i>R_{int}</i>	0.037
(sin θ/λ) _{max} (Å ⁻¹)	0.807
Refinement	
<i>R</i> [<i>F</i> ² > 2σ(<i>F</i> ²)], <i>wR</i> (<i>F</i> ²), <i>S</i>	0.036, 0.084, 1.08
No. of reflections	4598
No. of parameters	130
H-atom treatment	Only H-atom displacement parameters refined
Δρ _{max} , Δρ _{min} (e Å ⁻³)	2.07, -1.15

Computer programs: *APEX2*, *SAINT* and *XSHELL* (Bruker, 2010), *SHELXS97* (Sheldrick, 2008), *SHELXL2014* (Sheldrick, 2015), *Mercury* (Macrae *et al.*, 2008), *PLATON* (Spek, 2009) and *publCIF* (Westrip, 2010).

refined to confirm proper positioning of the H atoms; this was particularly important for the carboxyl H atoms. Uniquely for H3, its *U*_{iso} [0.013 (7)] is smaller than the *U*_{eq} of C3 [0.022 (4)], to which it is attached, but by less than two s.u.'s. All other H-atom *U*_{iso} values are consistent with expectation: 0.02–0.3 for CH and CH₂, and 0.05 for CO₂H. These values are in line with H-atom *U*_{iso} values in C₂–C₁₂ aliphatic acids without heavy-atom substitution, whose structures had been determined at the same temperature (150 K) or lower (Thalladi *et al.*, 2000; Mitchell *et al.*, 2001; Peppel *et al.*, 2015*a,b*; Sonneck *et al.*, 2015*a,b*). In these structures, *U*_{iso} values average 0.033 ± 0.006 for CH and CH₂, and 0.068 ± 0.033 for reciprocally hydrogen-bonded CO₂H.

Residual electron density is somewhat high (Δρ_{max} and Δρ_{min} being 2.07 and -1.14 e Å⁻³, respectively) and localizes near the heavier Br atoms, which suggests Fourier truncation as a possible cause. Other reasons could be translational

pseudosymmetry (for example, see Kiessling & Zeller, 2011), or the high geometric anisotropy of the crystal (ratio of largest-to-smallest dimensions being 4), which can yield less accurate absorption correction performed through *SADABS* software. The irregular shape of the crystal precluded more accurate absorption correction through face indexing.

Acknowledgements

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supporting information

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Computing details

Data collection: *APEX2* (Bruker, 2010); cell refinement: *APEX2* (Bruker, 2010); data reduction: *APEX2* and *SAINT* (Bruker, 2010); program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL2014* (Sheldrick, 2015); molecular graphics: *XSHELL* (Bruker, 2010) and *Mercury* (Macrae *et al.*, 2008); software used to prepare material for publication: *APEX2* (Bruker, 2010), *SHELXL2014* (Sheldrick, 2015), *PLATON* (Spek, 2009) and *pubCIF* (Westrip, 2010).

meso-2,6-Dibromoheptanedioic acid

Crystal data

$C_7H_{10}Br_2O_4$

$M_r = 317.97$

Orthorhombic, *Pbca*

$a = 10.4277$ (7) Å

$b = 10.7014$ (7) Å

$c = 18.7154$ (13) Å

$V = 2088.5$ (2) Å³

$Z = 8$

$F(000) = 1232$

$D_x = 2.023$ Mg m⁻³

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å

Cell parameters from 9811 reflections

$\theta = 2.2\text{--}34.7^\circ$

$\mu = 7.74$ mm⁻¹

$T = 150$ K

Plate, colourless

$0.35 \times 0.27 \times 0.09$ mm

Data collection

Bruker SMART APEXII CCD
diffractometer

Radiation source: sealed tube

Graphite monochromator

Detector resolution: 8.333 pixels mm⁻¹

φ and ω scans

Absorption correction: multi-scan
(*SADABS*; Sheldrick, 2008)

$T_{\min} = 0.231$, $T_{\max} = 0.498$

35789 measured reflections

4598 independent reflections

3488 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.037$

$\theta_{\max} = 35.0^\circ$, $\theta_{\min} = 2.2^\circ$

$h = -16 \rightarrow 16$

$k = -17 \rightarrow 17$

$l = -30 \rightarrow 30$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.036$

$wR(F^2) = 0.084$

$S = 1.08$

4598 reflections

130 parameters

0 restraints

Primary atom site location: structure-invariant
direct methods

Secondary atom site location: difference Fourier
map

Hydrogen site location: inferred from
neighbouring sites

Only H-atom displacement parameters refined

$$w = 1/[\sigma^2(F_o^2) + (0.020P)^2 + 6.P]$$

where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$

$$\Delta\rho_{\max} = 2.07 \text{ e } \text{\AA}^{-3}$$

$$\Delta\rho_{\min} = -1.14 \text{ e } \text{\AA}^{-3}$$

Special details

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
O1	0.4428 (2)	0.35337 (18)	0.81180 (10)	0.0271 (4)
O2	0.5097 (2)	0.53602 (18)	0.85748 (10)	0.0289 (4)
H2	0.5328	0.4903	0.8916	0.044 (11)*
C1	0.4560 (2)	0.4669 (2)	0.80775 (12)	0.0200 (4)
C2	0.4148 (2)	0.5420 (2)	0.74305 (12)	0.0190 (4)
H2A	0.4858	0.6007	0.7303	0.024 (8)*
Br2	0.26550 (3)	0.64147 (3)	0.77267 (2)	0.02812 (7)
C3	0.3835 (2)	0.4638 (2)	0.67757 (12)	0.0221 (4)
H3A	0.3411	0.5169	0.6413	0.022 (8)*
H3B	0.3233	0.3963	0.6910	0.013 (7)*
C4	0.5050 (3)	0.4068 (3)	0.64587 (13)	0.0241 (5)
H4A	0.5692	0.4736	0.6380	0.030 (9)*
H4B	0.5417	0.3462	0.6802	0.033 (9)*
C5	0.4780 (2)	0.3408 (2)	0.57527 (13)	0.0212 (4)
H5A	0.4112	0.2765	0.5831	0.034 (9)*
H5B	0.4435	0.4024	0.5408	0.037 (10)*
C6	0.5957 (2)	0.2790 (2)	0.54304 (13)	0.0204 (4)
H6A	0.6299	0.2163	0.5778	0.029 (9)*
Br6	0.73130 (2)	0.40137 (2)	0.52174 (2)	0.02402 (6)
C7	0.5646 (2)	0.2132 (2)	0.47354 (12)	0.0204 (4)
O3	0.5852 (2)	0.10197 (18)	0.46621 (11)	0.0296 (4)
O4	0.5102 (2)	0.28358 (18)	0.42491 (10)	0.0300 (4)
H4	0.4863	0.2389	0.3905	0.053 (12)*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.0382 (10)	0.0244 (9)	0.0188 (8)	-0.0048 (8)	-0.0049 (7)	0.0012 (7)
O2	0.0425 (11)	0.0238 (9)	0.0205 (8)	-0.0040 (8)	-0.0098 (8)	0.0008 (7)
C1	0.0205 (10)	0.0243 (11)	0.0152 (9)	0.0001 (8)	0.0009 (7)	0.0002 (8)
C2	0.0185 (9)	0.0204 (10)	0.0181 (10)	0.0006 (8)	0.0003 (7)	0.0012 (8)
Br2	0.02097 (11)	0.03372 (14)	0.02965 (13)	0.00479 (10)	0.00001 (10)	-0.00452 (10)
C3	0.0233 (11)	0.0270 (11)	0.0159 (9)	-0.0003 (9)	-0.0012 (8)	0.0008 (8)
C4	0.0264 (11)	0.0294 (12)	0.0166 (9)	0.0032 (9)	-0.0013 (8)	-0.0036 (9)
C5	0.0226 (11)	0.0239 (11)	0.0171 (9)	0.0003 (8)	-0.0008 (8)	-0.0005 (8)
C6	0.0255 (11)	0.0190 (10)	0.0169 (9)	0.0006 (8)	-0.0024 (8)	0.0009 (8)

Br6	0.02087 (10)	0.02733 (12)	0.02386 (11)	-0.00204 (9)	-0.00007 (9)	-0.00097 (9)
C7	0.0218 (10)	0.0228 (10)	0.0165 (9)	-0.0007 (8)	-0.0008 (8)	0.0014 (8)
O3	0.0387 (11)	0.0247 (9)	0.0253 (9)	0.0061 (8)	-0.0103 (8)	-0.0034 (7)
O4	0.0493 (12)	0.0215 (8)	0.0193 (8)	0.0027 (8)	-0.0100 (8)	-0.0001 (7)

Geometric parameters (Å, °)

O1—C1	1.225 (3)	C4—H4A	0.9900
O2—C1	1.314 (3)	C4—H4B	0.9900
O2—H2	0.8400	C5—C6	1.520 (3)
C1—C2	1.516 (3)	C5—H5A	0.9900
C2—C3	1.519 (3)	C5—H5B	0.9900
C2—Br2	1.966 (2)	C6—C7	1.515 (3)
C2—H2A	1.0000	C6—Br6	1.968 (2)
C3—C4	1.526 (4)	C6—H6A	1.0000
C3—H3A	0.9900	C7—O3	1.217 (3)
C3—H3B	0.9900	C7—O4	1.310 (3)
C4—C5	1.524 (3)	O4—H4	0.8400
C1—O2—H2	109.5	C5—C4—H4B	109.3
O1—C1—O2	124.2 (2)	C3—C4—H4B	109.3
O1—C1—C2	122.9 (2)	H4A—C4—H4B	108.0
O2—C1—C2	112.8 (2)	C6—C5—C4	113.3 (2)
C1—C2—C3	114.4 (2)	C6—C5—H5A	108.9
C1—C2—Br2	106.66 (16)	C4—C5—H5A	108.9
C3—C2—Br2	110.85 (16)	C6—C5—H5B	108.9
C1—C2—H2A	108.2	C4—C5—H5B	108.9
C3—C2—H2A	108.2	H5A—C5—H5B	107.7
Br2—C2—H2A	108.2	C7—C6—C5	111.7 (2)
C2—C3—C4	110.8 (2)	C7—C6—Br6	106.84 (16)
C2—C3—H3A	109.5	C5—C6—Br6	111.78 (16)
C4—C3—H3A	109.5	C7—C6—H6A	108.8
C2—C3—H3B	109.5	C5—C6—H6A	108.8
C4—C3—H3B	109.5	Br6—C6—H6A	108.8
H3A—C3—H3B	108.1	O3—C7—O4	124.1 (2)
C5—C4—C3	111.6 (2)	O3—C7—C6	120.9 (2)
C5—C4—H4A	109.3	O4—C7—C6	114.9 (2)
C3—C4—H4A	109.3	C7—O4—H4	109.5
O1—C1—C2—C3	-13.0 (3)	C3—C4—C5—C6	-178.1 (2)
O2—C1—C2—C3	165.5 (2)	C4—C5—C6—C7	179.3 (2)
O1—C1—C2—Br2	109.9 (2)	C4—C5—C6—Br6	-61.1 (2)
O2—C1—C2—Br2	-71.6 (2)	C5—C6—C7—O3	-122.1 (3)
C1—C2—C3—C4	-70.5 (3)	Br6—C6—C7—O3	115.4 (2)
Br2—C2—C3—C4	168.86 (17)	C5—C6—C7—O4	55.2 (3)
C2—C3—C4—C5	-173.3 (2)	Br6—C6—C7—O4	-67.3 (2)

Hydrogen-bond geometry (Å, °)

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
O2—H2···O3 ⁱ	0.84	1.80	2.635 (3)	177
O4—H4···O1 ⁱⁱ	0.84	1.83	2.669 (3)	176

Symmetry codes: (i) $x, -y+1/2, z+1/2$; (ii) $x, -y+1/2, z-1/2$.