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#### **Key indicators**

Single-crystal X-ray study T = 120 KMean  $\sigma$ (C–C) = 0.006 Å R factor = 0.049 wR factor = 0.076 Data-to-parameter ratio = 14.3

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

# 4-Bromo-3,5-dihydroxybenzoic acid monohydrate

The crystal packing of the title compound,  $C_7H_5BrO_4$ · $H_2O$ , is influenced by O-H···O hydrogen bonds.

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#### Comment

The title compound, (I) (Fig. 1), was prepared as part of our studies radical-mediated competitive cyclization reactions (Kirsop *et al.*, 2007). Some crystal structures containing 4-bromo-3,5-dihydroxybenzoic acid and its deprotonated anion in combination with 4,4-bipyridine derivatives have been described recently by Varughese & Pedireddi (2006).



Compound (I) possesses normal geometric parameters (Allen *et al.*, 1987). The dihedral angle between the mean plane of the C1–C6 benzne ring and the plane of the C7/O1/O2 grouping is  $4.5 (5)^{\circ}$ .

The crystal packing of (I) is influenced by  $O-H\cdots O$  hydrogen bonds (Table 1). First, classical inversion dimers involving  $O4-H4\cdots O3^{iii}$  and  $O4^{iii}-H^{iii}\cdots O3$  bonds of



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Part of the crystal structure of (I), showing an  $R_6^6(32)$  supramolecular loop arising from the connectivity of six organic molecules. Dashed lines indicate hydrogen bonds. [Symmetry codes as in Table 1; additionally: (v) x, y, z - 1.]





Unit-cell contents for (I), with O-H···O hydrogen bonds indicated by double-dashed lines. [Symmetry codes as in Table 1; additionally: (vi) x,  $\frac{1}{2} - y, \frac{1}{2} + z;$  (vii)  $1 - x, \frac{1}{2} + y, \frac{1}{2} - z.$ ]

adjacent head-to-head carboxylic acid groups are formed (Fig. 2) [symmetry code: (iii) 1 - x, 1 - y, 1 - z]. Atom H4 appeared to be well ordered in a difference map, but the C7-O4 bond [1.288 (5) Å] is shorter and the C7=O3 bond [1.252 (5) Å] is longer than expected for a well ordered carboxylic acid group: the mean C–O and C=O bond lengths in carboxylic acid groups bound to an aromatic ring are 1.226 Å ( $\sigma = 0.020$  Å) and 1.305 Å ( $\sigma = 0.020$ Å), respectively (Allen et al., 1987). This perhaps suggests partial disordering of H4 in (I), *i.e.* it is bound to both O3 and O4, but this was not visible in a difference map.

These dimeric pairs of 4-bromo-3,5-dihydroxybenzoic acid molecules are then linked into an infinite sheet by way of O1-H1...O4<sup>i</sup> bonds (Fig. 2). This results in distinctive  $R_6^6(32)$ supramolecular loops (Bernstein et al., 1995). The O2-H2 hydroxyl group forms a hydrogen bond to a water molecule O atom. In turn, the water molecule acts as a donor for two more O-H···O interactions, to result in a three-dimensional network (Fig. 3).

## **Experimental**

A commercial sample of 4-bromo-3,5-dihydroxybenzoic acid was recrystallized from water, to result in slightly translucent needles of (I).

#### Crystal data

C <sub>7</sub> H <sub>5</sub> BrO <sub>4</sub> ·H <sub>2</sub> O	Z = 4
$M_r = 251.04$	$D_x = 2.013 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
a = 3.7065 (1)  Å	$\mu = 4.95 \text{ mm}^{-1}$
b = 14.4963 (7) Å	T = 120 (2) K
c = 15.4548 (8) Å	Needle, colourless
$\beta = 94.209 \ (3)^{\circ}$	$0.12 \times 0.02 \times 0.01 \text{ mm}$
V = 828.16 (6) Å <sup>3</sup>	

#### Data collection

```
Nonius KappaCCD area-detector
  diffractometer
\omega and \varphi scans
Absorption correction: multi-scan
  (SADABS; Bruker, 2003)
  T_{\min} = 0.588, T_{\max} = 0.952
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# Refinement

Refinement on  $F^2$  $R[F^2 > 2\sigma(F^2)] = 0.049$  $wR(F^2) = 0.076$ S = 1.081900 reflections 133 parameters

1900 independent reflections 1466 reflections with  $I > 2\sigma(I)$  $R_{\rm int} = 0.085$  $\theta_{\rm max} = 27.5^{\circ}$ 

9660 measured reflections

H atoms treated by a mixture of independent and constrained refinement  $w = 1/[\sigma^2(F_0^2) + 1.4241P]$ where  $P = (F_0^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\rm max} < 0.001$  $\Delta \rho_{\rm max} = 0.65 \ e \ {\rm \AA}^{-3}$  $\Delta \rho_{\rm min} = -0.59 \ {\rm e} \ {\rm \AA}^{-3}$ 

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$01 - H1 \cdots O4^{i}$ $02 - H2 \cdots O5^{ii}$ $04 - H4 \cdots O3^{iii}$ $05 - H6 \cdots O2^{iv}$ $05 - H6 \cdots O1$	0.824 (19) 0.835 (19) 0.834 (19) 0.828 (19) 0.840 (10)	2.19 (3) 1.82 (2) 1.79 (2) 2.18 (3) 2.11 (2)	2.937 (4) 2.641 (4) 2.620 (4) 2.918 (4) 2.919 (4)	151 (4) 169 (4) 175 (5) 149 (5) 163 (4)
Symmetry codes:	(i) $x, -y + $	$\frac{1}{2}, z - \frac{1}{2};$ (ii)	$x + 1, -y + \frac{1}{2}$	$\frac{105(4)}{z+\frac{1}{2};}$ (iii)

-x + 1, -y + 1, -z + 1; (iv)  $-x + 2, y + \frac{1}{2}, -z + \frac{1}{2}.$ 

O-bound H atoms were located in a difference map and their positions were refined with the distance restraint O-H = 0.85 (2) Å.  $U_{iso}(H)$  was set equal to  $1.2U_{eq}(O)$ . C-bound H atoms were placed in idealized positions, with C-H = 0.95 Å, and refined as riding, with  $U_{iso}(H) = 1.2U_{eq}(C).$ 

Data collection: COLLECT (Nonius, 1998); cell refinement: SCALEPACK (Otwinowski & Minor, 1997); data reduction: SCALEPACK, DENZO (Otwinowski & Minor, 1997) and SORTAV (Blessing, 1995); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

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# supporting information

Acta Cryst. (2007). E63, o1441-o1443 [https://doi.org/10.1107/S1600536807003492]

# 4-Bromo-3,5-dihydroxybenzoic acid monohydrate

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4-Bromo-3,5-dihydroxybenzoic acid monohydrate

Crystal data C<sub>7</sub>H<sub>5</sub>BrO<sub>4</sub>·H<sub>2</sub>O  $M_r = 251.04$ Monoclinic,  $P2_1/c$ Hall symbol: -P 2ybc a = 3.7065 (1) Å b = 14.4963 (7) Å c = 15.4548 (8) Å  $\beta = 94.209$  (3)° V = 828.16 (6) Å<sup>3</sup> Z = 4

## Data collection

Nonius KappaCCD area-detector diffractometer Radiation source: fine-focus sealed tube Graphite monochromator  $\omega$  and  $\varphi$  scans Absorption correction: multi-scan (SADABS; Bruker, 2003)  $T_{\min} = 0.588, T_{\max} = 0.952$ 

## Refinement

Refinement on $F^2$	Secondary atom site location: difference Fourier
Least-squares matrix: full	map
$R[F^2 > 2\sigma(F^2)] = 0.049$	Hydrogen site location: difmap and geom
$wR(F^2) = 0.076$	H atoms treated by a mixture of independent
S = 1.08	and constrained refinement
1900 reflections	$w = 1/[\sigma^2(F_o^2) + 1.4241P]$
133 parameters	where $P = (F_o^2 + 2F_c^2)/3$
6 restraints	$(\Delta/\sigma)_{\rm max} < 0.001$
Primary atom site location: structure-invariant	$\Delta  ho_{ m max} = 0.65 \ { m e} \ { m \AA}^{-3}$
direct methods	$\Delta \rho_{\rm min} = -0.59 \text{ e } \text{\AA}^{-3}$

# 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.

F(000) = 496

 $\theta = 2.9 - 27.5^{\circ}$  $\mu = 4.95 \text{ mm}^{-1}$ 

T = 120 K

 $R_{\rm int} = 0.085$ 

 $h = -4 \rightarrow 4$ 

 $k = -18 \rightarrow 18$  $l = -20 \rightarrow 19$ 

 $D_{\rm x} = 2.013 {\rm Mg m^{-3}}$ 

Needle, colourless

 $0.12\times0.02\times0.01~mm$ 

9660 measured reflections

 $\theta_{\text{max}} = 27.5^{\circ}, \ \theta_{\text{min}} = 3.0^{\circ}$ 

1900 independent reflections

1466 reflections with  $I > 2\sigma(I)$ 

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

Cell parameters from 1924 reflections

**Refinement**. Refinement of  $F^2$  against ALL reflections. The weighted *R*-factor *wR* and goodness of fit *S* are based on  $F^2$ , conventional *R*-factors *R* are based on *F*, with *F* set to zero for negative  $F^2$ . The threshold expression of  $F^2 > \sigma(F^2)$  is used only for calculating *R*-factors(gt) *etc.* and is not relevant to the choice of reflections for refinement. *R*-factors based on  $F^2$  are statistically about twice as large as those based on *F*, and *R*- factors based on ALL data will be even larger.

	x	У	Ζ	$U_{ m iso}$ */ $U_{ m eq}$	
C1	0.9836 (10)	0.1596 (3)	0.3025 (3)	0.0126 (9)	
C2	0.8179 (9)	0.2346 (3)	0.2596 (3)	0.0130 (9)	
C3	0.7138 (10)	0.3092 (3)	0.3078 (3)	0.0130 (9)	
H3	0.5971	0.3604	0.2795	0.016*	
C4	0.7790 (9)	0.3094 (3)	0.3969 (3)	0.0120 (9)	
C5	0.9462 (10)	0.2347 (3)	0.4396 (3)	0.0138 (9)	
Н5	0.9906	0.2355	0.5010	0.017*	
C6	1.0481 (10)	0.1587 (3)	0.3922 (3)	0.0136 (9)	
C7	0.6600 (10)	0.3905 (3)	0.4454 (3)	0.0138 (9)	
01	0.7523 (8)	0.23889 (19)	0.1721 (2)	0.0193 (7)	
H1	0.798 (11)	0.192 (2)	0.145 (3)	0.023*	
O2	1.2073 (7)	0.08285 (19)	0.42874 (19)	0.0185 (7)	
H2	1.261 (11)	0.092 (3)	0.4814 (14)	0.022*	
O3	0.4904 (7)	0.45364 (18)	0.40498 (19)	0.0182 (7)	
O4	0.7399 (8)	0.39319 (19)	0.5279 (2)	0.0208 (7)	
H4	0.668 (11)	0.4435 (19)	0.546 (3)	0.025*	
Br1	1.13095 (10)	0.05915 (3)	0.23622 (3)	0.01626 (13)	
05	0.4339 (8)	0.4063 (2)	0.0945 (2)	0.0259 (8)	
H6	0.559 (10)	0.4521 (19)	0.108 (3)	0.031*	
H7	0.561 (10)	0.360 (2)	0.110 (3)	0.031*	

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters  $(\hat{A}^2)$ 

Atomic a	displ	lacement	parameters	$(Å^2)$
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	$U^{11}$	$U^{22}$	$U^{33}$	$U^{12}$	$U^{13}$	U <sup>23</sup>
C1	0.0125 (18)	0.009 (2)	0.016 (2)	0.0006 (15)	0.0028 (17)	-0.0048 (17)
C2	0.0119 (19)	0.0117 (19)	0.016 (2)	-0.0020 (15)	0.0017 (17)	-0.0004 (19)
C3	0.0139 (18)	0.010(2)	0.016 (2)	-0.0010 (15)	0.0024 (17)	0.0059 (18)
C4	0.0131 (18)	0.009 (2)	0.014 (2)	-0.0002 (15)	0.0047 (17)	-0.0015 (17)
C5	0.0149 (19)	0.011 (2)	0.015 (3)	-0.0008 (16)	-0.0021 (17)	-0.0003 (18)
C6	0.0153 (19)	0.009 (2)	0.016 (2)	-0.0005 (15)	-0.0003 (17)	0.0036 (18)
C7	0.0142 (19)	0.011 (2)	0.016 (3)	-0.0023 (16)	0.0020 (17)	-0.0001 (18)
01	0.0331 (16)	0.0136 (16)	0.0111 (18)	0.0046 (13)	0.0005 (13)	-0.0024 (13)
02	0.0272 (15)	0.0150 (16)	0.0127 (17)	0.0028 (12)	-0.0032 (13)	-0.0031 (13)
03	0.0242 (14)	0.0116 (16)	0.0184 (18)	0.0038 (12)	-0.0005 (13)	0.0024 (13)
O4	0.0350 (17)	0.0121 (16)	0.0154 (19)	0.0052 (13)	0.0027 (14)	-0.0045 (14)
Br1	0.0178 (2)	0.0136 (2)	0.0172 (2)	0.00327 (18)	-0.00002 (15)	-0.0047 (2)
05	0.0401 (19)	0.0128 (16)	0.023 (2)	-0.0043 (13)	-0.0081 (16)	0.0011 (15)

Geometric parameters (Å, °)

C1—C6	1.388 (6)	С5—Н5	0.9500
C1—C2	1.393 (5)	C6—O2	1.352 (5)
C1—Br1	1.885 (4)	С7—ОЗ	1.252 (5)
C2—O1	1.356 (5)	C7—O4	1.288 (5)
C2—C3	1.384 (5)	O1—H1	0.824 (19)
C3—C4	1.381 (6)	O2—H2	0.835 (19)
С3—Н3	0.9500	O4—H4	0.834 (19)
C4—C5	1.390 (5)	O5—H6	0.828 (19)
C4—C7	1.479 (5)	O5—H7	0.840 (19)
С5—С6	1.391 (5)		
C6—C1—C2	121.4 (4)	C4—C5—H5	120.2
C6—C1—Br1	120.0 (3)	C6—C5—H5	120.2
C2-C1-Br1	118.6 (3)	O2—C6—C1	117.6 (4)
O1—C2—C3	117.6 (4)	O2—C6—C5	123.4 (4)
O1—C2—C1	123.5 (4)	C1—C6—C5	119.0 (4)
C3—C2—C1	118.9 (4)	O3—C7—O4	122.9 (4)
C4—C3—C2	120.2 (4)	O3—C7—C4	119.1 (4)
С4—С3—Н3	119.9	O4—C7—C4	118.0 (4)
С2—С3—Н3	119.9	C2—O1—H1	116 (3)
C3—C4—C5	120.8 (4)	C6—O2—H2	110 (3)
C3—C4—C7	118.0 (4)	C7—O4—H4	108 (3)
C5—C4—C7	121.2 (4)	Н6—О5—Н7	106 (3)
C4—C5—C6	119.7 (4)		
C6-C1-C2-O1	179.4 (3)	C2—C1—C6—O2	179.4 (3)
Br1—C1—C2—O1	0.8 (5)	Br1-C1-C6-O2	-2.0 (5)
C6—C1—C2—C3	-0.5 (5)	C2—C1—C6—C5	-0.3 (6)
Br1—C1—C2—C3	-179.1 (3)	Br1-C1-C6-C5	178.2 (3)
O1—C2—C3—C4	-179.0 (3)	C4—C5—C6—O2	-179.1 (3)
C1—C2—C3—C4	1.0 (5)	C4—C5—C6—C1	0.7 (5)
C2—C3—C4—C5	-0.6 (5)	C3—C4—C7—O3	3.4 (5)
C2—C3—C4—C7	-179.6 (3)	C5—C4—C7—O3	-175.5 (3)
C3—C4—C5—C6	-0.2 (5)	C3—C4—C7—O4	-175.9 (3)
C7—C4—C5—C6	178.7 (3)	C5—C4—C7—O4	5.1 (5)

# Hydrogen-bond geometry (Å, °)

) II <i>(</i>
$-\Pi^{\dots}A$
51 (4)
69 (4)
75 (5)
49 (5)
63 (4)

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