

Redetermination of 4-hydroxy-benzaldehyde

Jerry P. Jasinski,^{a*} Ray J. Butcher,^b B. Narayana,^c
M. T. Swamy^d and H. S. Yathirajan^e

^aDepartment of Chemistry, Keene State College, 229 Main Street, Keene, NH 03435-2001, USA, ^bDepartment of Chemistry, Howard University, 525 College Street NW, Washington, DC 20059, USA, ^cDepartment of Studies in Chemistry, Mangalore University, Mangalagangothri 574199, India, ^dDepartment Chemistry, Sambhram Institute of Technology, Bangalore 560 097, India, and ^eDepartment of Studies in Chemistry, University of Mysore, Manasagangothri, Mysore 570006, India
Correspondence e-mail: jjasinski@keene.edu

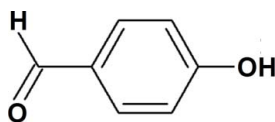
Received 22 November 2007; accepted 27 November 2007

Key indicators: single-crystal X-ray study; $T = 296$ K; mean $\sigma(\text{C}—\text{C}) = 0.002$ Å; R factor = 0.038; wR factor = 0.117; data-to-parameter ratio = 13.6.

This is a redetermination of the structure of the title compound, $\text{C}_7\text{H}_6\text{O}_2$, which was first reported by Iwasaki [*Acta Cryst.* (1977), **B33**, 1646–1648]. The results are obtained with greater precision in the present study. Crystal packing is stabilized by intermolecular $\text{O}—\text{H}\cdots\text{O}$ interactions between the hydroxyl and aldehyde groups which link the molecules into chains in a zigzag pattern along the [110] plane of the unit cell.

Related literature

For the previous structure determination, see: Iwasaki (1977). For related structures, see: Matos Beja *et al.* (1997, 2000); Paixão *et al.* (2000); Silva *et al.* (2004). For related literature, see: Antonucci (1978); Bigi *et al.* (1999); Dean (1963); Samal *et al.* (1999).



Experimental

Crystal data

$\text{C}_7\text{H}_6\text{O}_2$	$V = 597.74$ (15) Å ³
$M_r = 122.12$	$Z = 4$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 6.6992$ (8) Å	$\mu = 0.10$ mm ⁻¹
$b = 13.5550$ (12) Å	$T = 296$ (2) K
$c = 7.1441$ (11) Å	$0.49 \times 0.37 \times 0.24$ mm
$\beta = 112.871$ (16)°	

Data collection

Oxford Diffraction Gemini R CCD diffractometer	3559 measured reflections
Absorption correction: multi-scan (<i>CrysAlis RED</i> ; Oxford Diffraction, 2007)	1170 independent reflections
$T_{\min} = 0.949$, $T_{\max} = 0.970$	841 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.022$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.038$	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2) = 0.117$	$\Delta\rho_{\text{max}} = 0.13$ e Å ⁻³
$S = 1.06$	$\Delta\rho_{\text{min}} = -0.18$ e Å ⁻³
1170 reflections	
86 parameters	

Table 1

Hydrogen-bond geometry (Å, °).

$D—H\cdots A$	$D—H$	$H\cdots A$	$D\cdots A$	$D—H\cdots A$
$\text{O1}—\text{H1}\cdots\text{O2}^i$	0.82 (3)	1.92 (3)	2.731 (2)	171 (2)

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

Data collection: *CrysAlisPro* (Oxford Diffraction, 2007); cell refinement: *CrysAlisPro*; data reduction: *CrysAlisPro*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000); software used to prepare material for publication: *SHELXTL*.

MTS thanks the Sambhram Institute of Technology for the use of their research facilities. RJB acknowledges the NSF–MRI program (grant No. CHE-0619278) for funds to purchase the X-ray diffractometer.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: LX2042).

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supporting information

Acta Cryst. (2008). E64, o187 [https://doi.org/10.1107/S1600536807063659]

Redetermination of 4-hydroxybenzaldehyde

Jerry P. Jasinski, Ray J. Butcher, B. Narayana, M. T. Swamy and H. S. Yathirajan

S1. Comment

The title compound, 4-hydroxy benzaldehyde (Fig. 1) is used in the preparation of aldehyde methacrylates and finds application in the manufacture of dental materials which can form strong and durable bonds with dentin (Antonucci, 1978). It is used in the preparation of benzopyrans and have wide applications in the perfume, cosmetic and pharmaceutical industry (Dean, 1963; Bigi *et al.*, 1999). They are also used in the preparation of chelating resins (Samal *et al.*, 1999).

The crystal structures of *p*-hydroxybenzaldehyde (Iwasaki, 1977), 2-bromo-5-hydroxybenzaldehyde (Matos Beja *et al.*, 2000), a new polymorph of 2-bromo-5-hydroxybenzaldehyde (Silva *et al.*, 2004), 3-hydroxybenzaldehyde (Paixão *et al.*, 2000) and 2,4-dibromo-5-hydroxybenzaldehyde, (Matos Beja *et al.*, 1997) have been reported. In view of the importance of the title compound in the pharmaceutical industry, this paper reports a redetermination of the crystal structure with greater precision and accuracy. Crystal packing is stabilized by intermolecular O—H $\cdots$ O interactions between the hydroxyl and aldehyde groups which link the molecules into chains in a zigzag pattern along the [110] plane of the unit cell (Fig. 2).

S2. Experimental

A sample of 4-hydroxybenzaldehyde was obtained from Sigma–Aldrich and was recrystallized from ethylacetate by slow evaporation to obtain good quality crystals (m.p.: 385–387 K).

S3. Refinement

The hydroxyl H was located in a difference Fourier map and all parameters were freely refined. All other H atoms were placed in their calculated places and refined using a riding model with C—H = 0.93 Å, and with $U_{\text{iso}}(\text{H}) = 1.21 U_{\text{eq}}(\text{C})$.

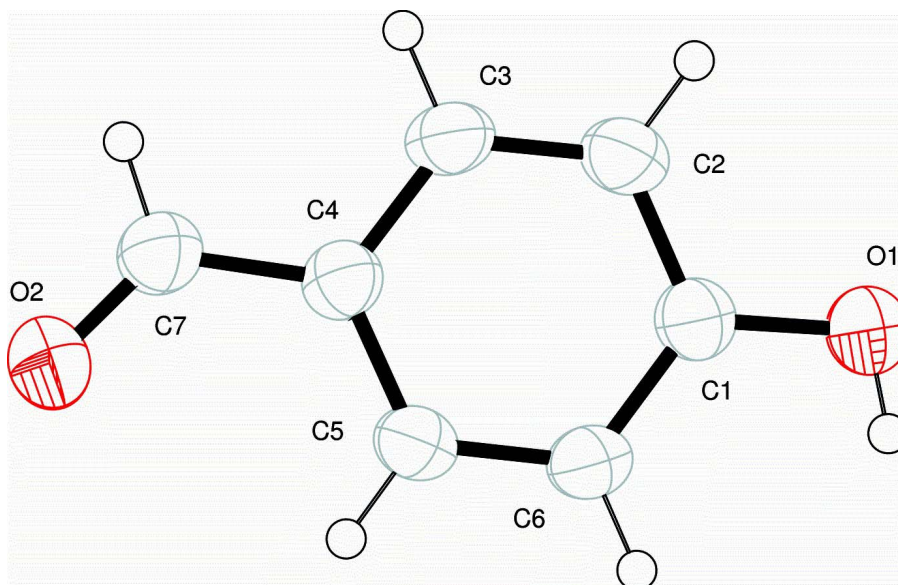


Figure 1

ORTEP view of the title compound, showing the atom numbering scheme and 50% probability displacement ellipsoids.

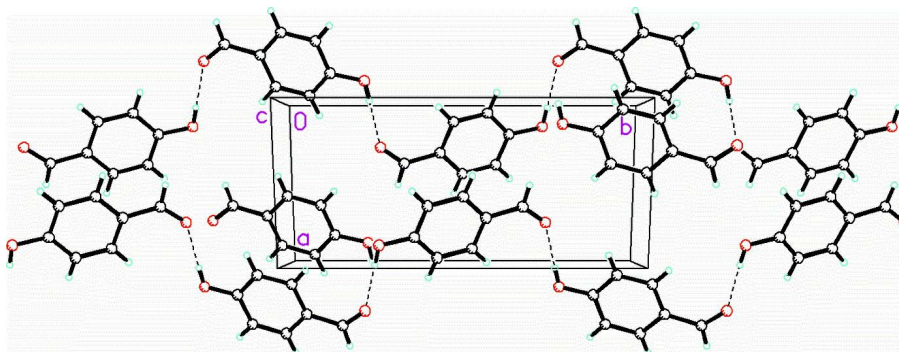


Figure 2

The molecular packing for the title compound viewed down the *c* axis. Dashed lines indicate C—H...O intermolecular hydrogen bonds.

4-Hydroxybenzaldehyde

Crystal data

$C_7H_6O_2$

$M_r = 122.12$

Monoclinic, $P2_1/c$

Hall symbol: $-P\ 2_1/c$

$a = 6.6992\ (8)\ \text{\AA}$

$b = 13.5550\ (12)\ \text{\AA}$

$c = 7.1441\ (11)\ \text{\AA}$

$\beta = 112.871\ (16)^\circ$

$V = 597.74\ (15)\ \text{\AA}^3$

$Z = 4$

$F(000) = 256$

$D_x = 1.357\ \text{Mg m}^{-3}$

Melting point = 385–387 K

Mo $K\alpha$ radiation, $\lambda = 0.71073\ \text{\AA}$

Cell parameters from 1669 reflections

$\theta = 5.3\text{--}29.0^\circ$

$\mu = 0.10\ \text{mm}^{-1}$

$T = 296\ \text{K}$

Chunk, colourless

$0.49 \times 0.37 \times 0.24\ \text{mm}$

Data collection

Oxford Diffraction Gemini R CCD
diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
Detector resolution: 10.5081 pixels mm⁻¹
 φ and ω scans
Absorption correction: multi-scan
(*CrysAlis RED*; Oxford Diffraction, 2007)
 $T_{\min} = 0.949$, $T_{\max} = 0.970$

3559 measured reflections
1170 independent reflections
841 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.022$
 $\theta_{\max} = 26.0^\circ$, $\theta_{\min} = 5.5^\circ$
 $h = -8 \rightarrow 8$
 $k = -15 \rightarrow 16$
 $l = -8 \rightarrow 8$

Refinement

Refinement on F^2
Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.038$
 $wR(F^2) = 0.117$
 $S = 1.06$
1170 reflections
86 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
H atoms treated by a mixture of independent
and constrained refinement
 $w = 1/[\sigma^2(F_o^2) + (0.068P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.13 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.18 \text{ e } \text{\AA}^{-3}$

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.

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.

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

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
O1	0.1345 (2)	0.72809 (8)	0.1335 (2)	0.0652 (4)
H1	0.016 (4)	0.7359 (17)	0.140 (3)	0.092 (8)*
O2	0.2691 (2)	0.26982 (8)	0.3786 (2)	0.0633 (4)
C1	0.1834 (2)	0.63218 (11)	0.1834 (2)	0.0458 (4)
C2	0.3718 (2)	0.59530 (11)	0.1700 (2)	0.0499 (4)
H2	0.4587	0.6359	0.1284	0.060*
C3	0.4277 (2)	0.49829 (11)	0.2187 (2)	0.0465 (4)
H3	0.5542	0.4740	0.2112	0.056*
C4	0.2990 (2)	0.43542 (11)	0.2793 (2)	0.0417 (4)
C5	0.1100 (2)	0.47379 (11)	0.2921 (2)	0.0452 (4)
H5	0.0218	0.4330	0.3317	0.054*
C6	0.0543 (2)	0.57089 (11)	0.2467 (2)	0.0470 (4)
H6	-0.0698	0.5959	0.2581	0.056*
C7	0.3667 (3)	0.33405 (12)	0.3294 (2)	0.0509 (4)
H7	0.4981	0.3161	0.3235	0.061*

Atomic displacement parameters ($\text{\AA}^2$)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.0635 (8)	0.0422 (7)	0.1018 (10)	0.0034 (6)	0.0451 (7)	0.0091 (6)
O2	0.0586 (7)	0.0434 (7)	0.0917 (9)	−0.0019 (5)	0.0332 (7)	0.0049 (6)
C1	0.0463 (8)	0.0385 (8)	0.0547 (9)	−0.0030 (6)	0.0219 (7)	−0.0039 (7)
C2	0.0472 (9)	0.0463 (9)	0.0636 (10)	−0.0078 (7)	0.0297 (8)	−0.0039 (7)
C3	0.0372 (7)	0.0483 (9)	0.0582 (9)	−0.0026 (6)	0.0231 (7)	−0.0089 (7)
C4	0.0396 (8)	0.0404 (8)	0.0447 (8)	−0.0013 (6)	0.0157 (6)	−0.0058 (6)
C5	0.0417 (8)	0.0450 (9)	0.0536 (9)	−0.0050 (7)	0.0235 (7)	−0.0012 (7)
C6	0.0404 (8)	0.0466 (9)	0.0593 (9)	0.0020 (7)	0.0252 (7)	−0.0018 (7)
C7	0.0430 (8)	0.0455 (9)	0.0648 (10)	−0.0012 (7)	0.0217 (8)	−0.0055 (7)

Geometric parameters ($\text{\AA}$, $^\circ$)

O1—C1	1.354 (2)	C3—H3	0.9300
O1—H1	0.82 (3)	C4—C5	1.404 (2)
O2—C7	1.219 (2)	C4—C7	1.448 (2)
C1—C2	1.395 (2)	C5—C6	1.372 (2)
C1—C6	1.395 (2)	C5—H5	0.9300
C2—C3	1.374 (2)	C6—H6	0.9300
C2—H2	0.9300	C7—H7	0.9300
C3—C4	1.395 (2)		
C1—O1—H1	104.4 (16)	C3—C4—C7	118.98 (13)
O1—C1—C2	117.30 (14)	C5—C4—C7	122.62 (13)
O1—C1—C6	122.68 (14)	C6—C5—C4	120.61 (13)
C2—C1—C6	120.02 (14)	C6—C5—H5	119.7
C3—C2—C1	119.35 (14)	C4—C5—H5	119.7
C3—C2—H2	120.3	C5—C6—C1	120.12 (14)
C1—C2—H2	120.3	C5—C6—H6	119.9
C2—C3—C4	121.50 (14)	C1—C6—H6	119.9
C2—C3—H3	119.3	O2—C7—C4	126.70 (15)
C4—C3—H3	119.3	O2—C7—H7	116.7
C3—C4—C5	118.39 (13)	C4—C7—H7	116.7
O1—C1—C2—C3	−179.85 (14)	C7—C4—C5—C6	178.77 (14)
C6—C1—C2—C3	0.3 (2)	C4—C5—C6—C1	1.2 (2)
C1—C2—C3—C4	0.7 (2)	O1—C1—C6—C5	178.90 (14)
C2—C3—C4—C5	−0.8 (2)	C2—C1—C6—C5	−1.2 (2)
C2—C3—C4—C7	−179.78 (14)	C3—C4—C7—O2	−177.67 (15)
C3—C4—C5—C6	−0.2 (2)	C5—C4—C7—O2	3.4 (3)

Hydrogen-bond geometry ($\text{\AA}$, $^\circ$)

$D—H\cdots A$	$D—H$	$H\cdots A$	$D\cdots A$	$D—H\cdots A$
O1—H1 $\cdots$ O2 ⁱ	0.82 (3)	1.92 (3)	2.731 (2)	171 (2)

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