



Crystal structure of 2,6-dimethyl-4-pyridone hemihydrate

Dalena M. Nguyen,^a Vasumathi Desikan,^a James A. Golen^b and David R. Manke^{b*}

^aDepartment of Science & Math, Massasoit Community College, 1 Massasoit Boulevard, Brockton, MA 02302, USA, and ^bDepartment of Chemistry and Biochemistry, University of Massachusetts Dartmouth, 285 Old Westport Road, North Dartmouth, MA 02747, USA. *Correspondence e-mail: dmanke@umassd.edu

Received 25 June 2015; accepted 29 June 2015

Edited by K. Fejfarova, Institute of Macromolecular Chemistry, AS CR, v.v.i, Czech Republic

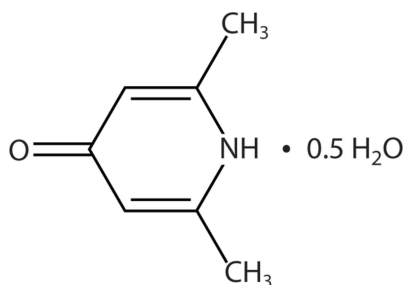
The title compound (systematic name: 2,6-dimethyl-1*H*-pyridin-4-one hemihydrate), C₇H₉NO·0.5H₂O, has a single planar molecule in the asymmetric unit with the non-H atoms possessing a mean deviation from planarity of 0.021 Å. There is also half of a water molecule present in the asymmetric unit. In the crystal, infinite (001) sheets are formed by N—H···O and O—H···O hydrogen bonds.

Keywords: crystal structure; hydrogen bonding; pyridones.

CCDC reference: 1409189

1. Related literature

For the crystal structure of the parent 4-pyridone, see: Jones (2001); Tyl *et al.* (2008). For the title compound bound to zirconium, see: Castillo *et al.* (1987). For the structure of a chloro-substituted variant of the title compound, see: Boer (1972).



2. Experimental

2.1. Crystal data

C₇H₉NO·0.5H₂O

M_r = 132.16

Orthorhombic, *Ab*a2
a = 12.4859 (17) Å
b = 14.3697 (19) Å
c = 7.732 (1) Å
V = 1387.3 (3) Å³

Z = 8
Cu *K*α radiation
 μ = 0.73 mm⁻¹
T = 120 K
0.5 × 0.1 × 0.1 mm

2.2. Data collection

Bruker Venture D8 CMOS diffractometer
Absorption correction: multi-scan (*SADABS*; Bruker, 2014)
T_{min} = 0.554, *T_{max}* = 0.754

11786 measured reflections
1366 independent reflections
1352 reflections with *I* > 2σ(*I*)
R_{int} = 0.060

2.3. Refinement

$R[F^2 > 2\sigma(F^2)] = 0.030$
 $wR(F^2) = 0.078$
S = 1.09
1366 reflections
95 parameters
3 restraints
H atoms treated by a mixture of independent and constrained refinement

$\Delta\rho_{\max} = 0.15 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.19 \text{ e \AA}^{-3}$
Absolute structure: Flack *x* determined using 611 quotients [(*I*⁺)-(*I*⁻)]/[(*I*⁺)+(*I*⁻)] (Parsons *et al.*, 2013).
Absolute structure parameter: 0.05 (12)

Table 1

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···O1	0.86 (1)	1.96 (1)	2.8174 (17)	173 (2)
N1—H1···O1 ⁱ	0.87 (1)	1.86 (1)	2.7154 (18)	166 (3)

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

Data collection: *APEX2* (Bruker, 2014); cell refinement: *SAINT* (Bruker, 2014); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL2014* (Sheldrick, 2015); molecular graphics: *OLEX2* (Dolomanov *et al.*, 2009); software used to prepare material for publication: *OLEX2* and *pubCIF* (Westrip, 2010).

Acknowledgements

We greatly acknowledge support from the National Science Foundation (CHE-1429086).

Supporting information for this paper is available from the IUCr electronic archives (Reference: FF2139).

References

- Boer, F. P. (1972). *Acta Cryst.* **B28**, 3200–3206.
Bruker (2014). *APEX2*, *SAINT* and *SADABS*. Bruker AXS Inc., Madison, Wisconsin, USA.
Castillo, S., Herault, V. & Declercq, J.-P. (1987). *Acta Cryst.* **C43**, 1530–1533.
Dolomanov, O. V., Bourhis, L. J., Gildea, R. J., Howard, J. A. K. & Puschmann, H. (2009). *J. Appl. Cryst.* **42**, 339–341.
Jones, P. G. (2001). *Acta Cryst.* **C57**, 880–882.
Parsons, S., Flack, H. D. & Wagner, T. (2013). *Acta Cryst.* **B69**, 249–259.
Sheldrick, G. M. (2008). *Acta Cryst.* **A64**, 112–122.
Sheldrick, G. M. (2015). *Acta Cryst.* **C71**, 3–8.
Tyl, A., Nowak, M. & Kusz, J. (2008). *Acta Cryst.* **C64**, o661–o664.
Westrip, S. P. (2010). *J. Appl. Cryst.* **43**, 920–925.

supporting information

Acta Cryst. (2015). E71, o533 [https://doi.org/10.1107/S2056989015012402]

Crystal structure of 2,6-dimethyl-4-pyridone hemihydrate

Dalena M. Nguyen, Vasumathi Desikan, James A. Golen and David R. Manke

S1. Comment

The structure of the title compound shows that 2,6-dimethyl-4-hydroxypyridine takes the pyridone form in the solid state. Though the title compound has not been crystallographically characterized, a structure of the molecule bound to zirconium has been reported (Castillo *et al.*, 1987) with similar bond distances and angles observed. The parent 4-pyridone has been structurally characterized (Tyl *et al.*, 2008) and exhibits similar chains linked by head-to-tail N–H \cdots O hydrogen bonds, which are also observed in the close derivative Clopidol (Boer, 1972). While the title compound crystallizes in a 2:1 ratio of pyridone to water, the hydrate of the parent molecule crystallizes in a 5:6 ratio (Jones, 2001).

The molecular structure of the title compound is shown in Figure 1. The molecule is near planar with the non-hydrogen atoms possessing a mean deviation from the plane of 0.021 Å. Head-to-tail N1–H1 \cdots O1 hydrogen bonding leads to chains that are further linked by O2–H2 \cdots O1 hydrogen bonds with water molecules in the crystal to form two-dimensional (001) sheets. The packing of the title compound indicating hydrogen bonding is shown in Figure 2.

S2. Experimental

A commercial sample (Oakwood Chemical) of 4-hydroxypyridine was used for the crystallization. Crystals suitable for single crystal X-ray analysis were grown by slow evaporation of a methanol solution.

S3. Refinement

All non-hydrogen atoms were refined anisotropically (*XL*) by full matrix least squares on F^2 . Hydrogen atoms H1 and H2 were found from a Fourier difference map. H1 was refined at a fixed distance of 0.87 (0.005) Å and an isotropic displacement parameter 1.20 times U_{eq} of the parent N atom. H2 was refined at a fixed distance of 0.86 (0.005) Å and an isotropic displacement parameter 1.50 times U_{eq} of the parent O atom. The remaining hydrogen atoms were placed in calculated positions and then refined with riding models with C–H lengths of 0.98 Å for (CH₃) and 0.95 Å for (CH) with isotropic displacement parameters set to 1.20 times U_{eq} of the parent C atoms.

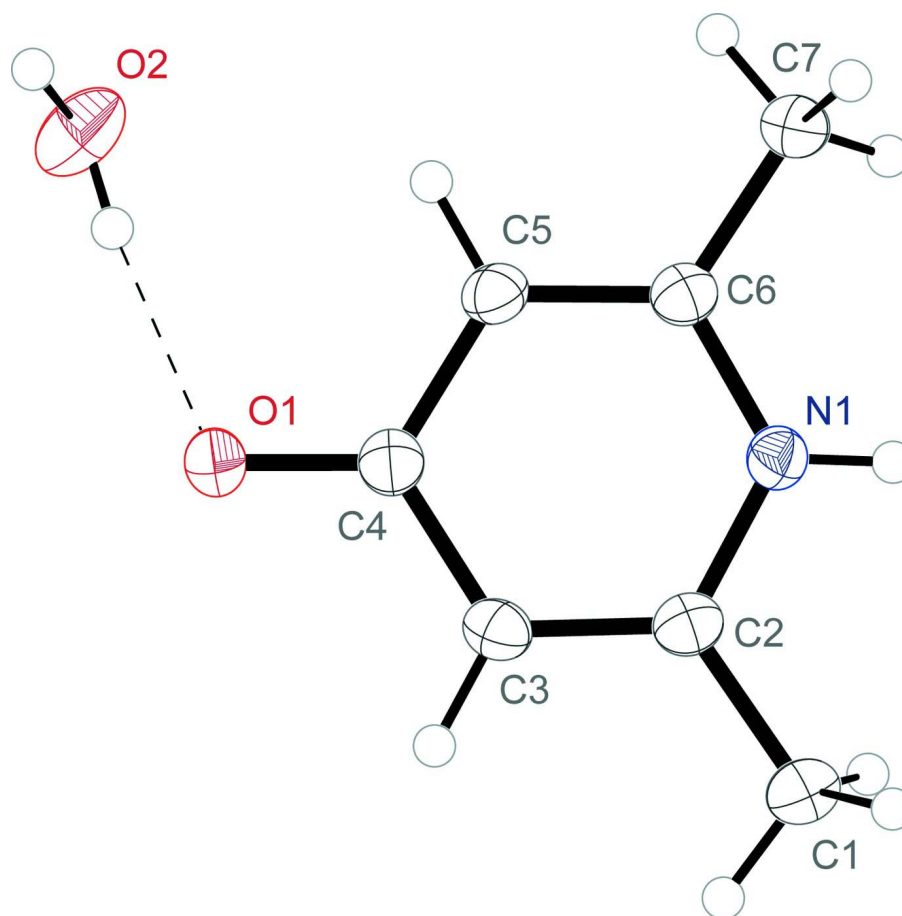


Figure 1

Molecular structure of the title compound, showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level. H atoms are drawn as spheres of arbitrary radius.

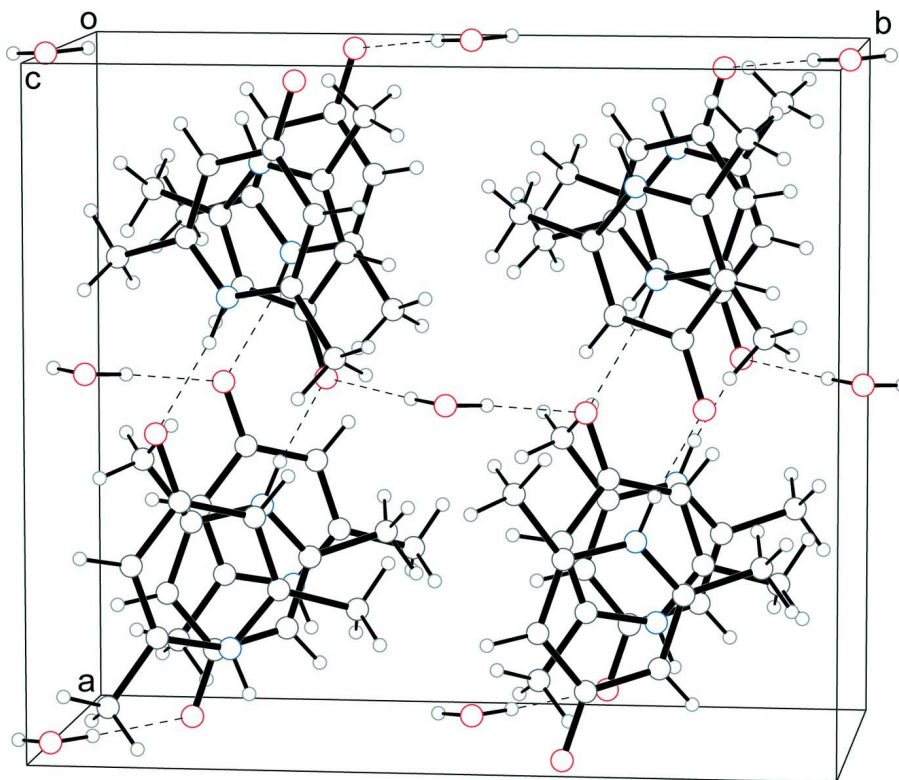


Figure 2

Molecular packing of the title compound with hydrogen bonding shown as dashed lines.

2,6-Dimethyl-1*H*-pyridin-4-one hemihydrate

Crystal data

$C_7H_9NO \cdot 0.5H_2O$
 $M_r = 132.16$
 Orthorhombic, *Aba2*
 Hall symbol: A 2 -2ac
 $a = 12.4859 (17) \text{ \AA}$
 $b = 14.3697 (19) \text{ \AA}$
 $c = 7.732 (1) \text{ \AA}$
 $V = 1387.3 (3) \text{ \AA}^3$
 $Z = 8$

$F(000) = 568$
 $D_x = 1.266 \text{ Mg m}^{-3}$
 Cu $K\alpha$ radiation, $\lambda = 1.54178 \text{ \AA}$
 Cell parameters from 9829 reflections
 $\theta = 7.1\text{--}72.4^\circ$
 $\mu = 0.73 \text{ mm}^{-1}$
 $T = 120 \text{ K}$
 NEEDLE, colourless
 $0.5 \times 0.1 \times 0.1 \text{ mm}$

Data collection

Bruker Venture D8 CMOS
 diffractometer
 Radiation source: microfocus Cu
 HELIOS MX monochromator
 φ and ω scans
 Absorption correction: multi-scan
 (*SADABS*; Bruker, 2014)
 $T_{\min} = 0.554$, $T_{\max} = 0.754$

11786 measured reflections
 1366 independent reflections
 1352 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.060$
 $\theta_{\max} = 72.4^\circ$, $\theta_{\min} = 7.1^\circ$
 $h = -15 \rightarrow 15$
 $k = -17 \rightarrow 17$
 $l = -9 \rightarrow 9$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.030$

$wR(F^2) = 0.078$

$S = 1.09$

1366 reflections

95 parameters

3 restraints

Hydrogen site location: mixed

H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0453P)^2 + 0.3383P]$

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

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

$\Delta\rho_{\max} = 0.15 \text{ e } \text{\AA}^{-3}$

$\Delta\rho_{\min} = -0.19 \text{ e } \text{\AA}^{-3}$

Absolute structure: Flack x determined using

611 quotients $[(I^-)-(I)]/[(I^+)+(I)]$ (Parsons *et al.*, 2013.

Absolute structure parameter: 0.05 (12)

Special details

Experimental. Absorption correction: SADABS-2014/4 (Bruker,2014) was used for absorption correction. $wR2(\text{int})$ was 0.1440 before and 0.0881 after correction. The Ratio of minimum to maximum transmission is 0.7350. The $\lambda/2$ correction factor is 0.00150.

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)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
O1	0.47723 (9)	0.33620 (8)	0.49203 (19)	0.0287 (3)
O2	0.5000	0.5000	0.6889 (3)	0.0399 (5)
N1	0.16883 (11)	0.24949 (11)	0.4446 (2)	0.0215 (3)
C3	0.35308 (14)	0.22232 (12)	0.3962 (2)	0.0234 (4)
H3	0.4083	0.1841	0.3504	0.028*
C2	0.24877 (14)	0.19343 (12)	0.3853 (2)	0.0222 (4)
C4	0.38007 (12)	0.30864 (12)	0.4748 (2)	0.0226 (4)
C7	0.09367 (14)	0.39066 (13)	0.5690 (3)	0.0265 (4)
H7A	0.0630	0.4210	0.4669	0.040*
H7B	0.1158	0.4381	0.6527	0.040*
H7C	0.0399	0.3499	0.6218	0.040*
C6	0.18900 (13)	0.33399 (11)	0.5164 (2)	0.0217 (4)
C1	0.21576 (15)	0.10115 (12)	0.3125 (3)	0.0270 (4)
H1A	0.1736	0.0672	0.3988	0.040*
H1B	0.2797	0.0650	0.2828	0.040*
H1C	0.1724	0.1109	0.2085	0.040*
C5	0.29237 (13)	0.36395 (12)	0.5339 (2)	0.0229 (4)
H5	0.3061	0.4226	0.5862	0.027*
H2	0.4956 (19)	0.4524 (12)	0.621 (3)	0.034*
H1	0.1043 (9)	0.2265 (14)	0.444 (4)	0.027*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.0205 (5)	0.0250 (6)	0.0405 (8)	-0.0007 (5)	-0.0004 (6)	-0.0028 (6)

O2	0.0553 (14)	0.0318 (11)	0.0324 (11)	-0.0147 (10)	0.000	0.000
N1	0.0206 (6)	0.0206 (7)	0.0234 (7)	-0.0014 (5)	0.0004 (6)	0.0008 (6)
C3	0.0240 (8)	0.0215 (8)	0.0246 (8)	0.0035 (6)	0.0014 (7)	0.0012 (8)
C2	0.0268 (8)	0.0193 (8)	0.0205 (7)	0.0009 (6)	-0.0014 (7)	0.0022 (7)
C4	0.0229 (8)	0.0208 (8)	0.0241 (9)	0.0003 (6)	-0.0011 (7)	0.0038 (8)
C7	0.0245 (8)	0.0243 (8)	0.0309 (10)	0.0025 (7)	-0.0008 (7)	-0.0041 (8)
C6	0.0244 (8)	0.0196 (8)	0.0213 (8)	0.0009 (6)	-0.0012 (7)	0.0019 (7)
C1	0.0309 (9)	0.0216 (8)	0.0284 (10)	-0.0005 (7)	-0.0007 (8)	-0.0012 (8)
C5	0.0255 (8)	0.0174 (7)	0.0258 (8)	-0.0004 (6)	-0.0006 (7)	0.0004 (7)

Geometric parameters (Å, °)

O1—C4	1.283 (2)	C7—H7A	0.9800
O2—H2	0.862 (7)	C7—H7B	0.9800
N1—C2	1.362 (2)	C7—H7C	0.9800
N1—C6	1.359 (2)	C7—C6	1.498 (2)
N1—H1	0.871 (7)	C6—C5	1.367 (2)
C3—H3	0.9500	C1—H1A	0.9800
C3—C2	1.370 (2)	C1—H1B	0.9800
C3—C4	1.422 (3)	C1—H1C	0.9800
C2—C1	1.498 (2)	C5—H5	0.9500
C4—C5	1.428 (2)		
C2—N1—H1	116.8 (15)	C6—C7—H7A	109.5
C6—N1—C2	122.02 (14)	C6—C7—H7B	109.5
C6—N1—H1	120.9 (16)	C6—C7—H7C	109.5
C2—C3—H3	119.5	N1—C6—C7	116.70 (14)
C2—C3—C4	121.06 (16)	N1—C6—C5	119.79 (15)
C4—C3—H3	119.5	C5—C6—C7	123.49 (16)
N1—C2—C3	119.80 (16)	C2—C1—H1A	109.5
N1—C2—C1	116.63 (15)	C2—C1—H1B	109.5
C3—C2—C1	123.57 (16)	C2—C1—H1C	109.5
O1—C4—C3	122.52 (15)	H1A—C1—H1B	109.5
O1—C4—C5	121.34 (16)	H1A—C1—H1C	109.5
C3—C4—C5	116.14 (15)	H1B—C1—H1C	109.5
H7A—C7—H7B	109.5	C4—C5—H5	119.4
H7A—C7—H7C	109.5	C6—C5—C4	121.12 (16)
H7B—C7—H7C	109.5	C6—C5—H5	119.4
O1—C4—C5—C6	-179.53 (17)	C2—C3—C4—C5	-2.6 (3)
N1—C6—C5—C4	1.2 (3)	C4—C3—C2—N1	2.5 (3)
C3—C4—C5—C6	0.7 (3)	C4—C3—C2—C1	-176.66 (16)
C2—N1—C6—C7	177.28 (17)	C7—C6—C5—C4	-177.33 (17)
C2—N1—C6—C5	-1.4 (3)	C6—N1—C2—C3	-0.5 (3)
C2—C3—C4—O1	177.66 (16)	C6—N1—C2—C1	178.74 (17)

Hydrogen-bond geometry (Å, °)

<i>D</i> —H \cdots <i>A</i>	<i>D</i> —H	H \cdots <i>A</i>	<i>D</i> \cdots <i>A</i>	<i>D</i> —H \cdots <i>A</i>
O2—H2 \cdots O1	0.86 (1)	1.96 (1)	2.8174 (17)	173 (2)
N1—H1 \cdots O1 ⁱ	0.87 (1)	1.86 (1)	2.7154 (18)	166 (3)

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