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# Redetermination of orotic acid monohydrate

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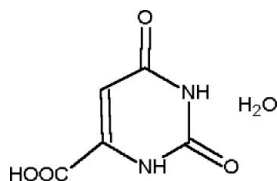
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Key indicators: single-crystal X-ray study;  $T = 298$  K; mean  $\sigma(\text{C}-\text{C}) = 0.001$  Å;  $R$  factor = 0.044;  $wR$  factor = 0.134; data-to-parameter ratio = 17.6.

The crystal structure of the title compound, which is also known as vitamin B<sub>13</sub> (systematic name: 2,6-dioxo-1,2,3,6-tetrahydropyrimidine-4-carboxylic acid monohydrate), C<sub>5</sub>H<sub>4</sub>N<sub>2</sub>O<sub>4</sub>·H<sub>2</sub>O, was reported for the first time by Takusagawa & Shimada [*Bull. Chem. Soc. Jpn* (1973), **46**, 2011–2019]. The present redetermination provides more precise values of the molecular geometry. The asymmetric unit comprises a planar diketo tautomer and a solvent water molecule. In the crystal structure, molecules are connected by O—H···O, N—H···O and C—H···O hydrogen bonds involving NH groups, two carbonyl O atoms and the solvent water molecule.

## Related literature

For the previous structure determination, see: Takusagawa & Shimada (1973). For a general approach to the use of multiple hydrogen-bonding DNA/RNA nucleobases as potential supramolecular reagents, see: Portalone *et al.* (1999); Brunetti *et al.* (2000, 2002); Portalone & Colapietro (2007 and references therein). For the computation of ring patterns formed by hydrogen bonds in crystal structures, see: Etter *et al.* (1990); Bernstein *et al.* (1995); Motherwell *et al.* (1999).



## Experimental

### Crystal data

C<sub>5</sub>H<sub>4</sub>N<sub>2</sub>O<sub>4</sub>·H<sub>2</sub>O  
 $M_r = 174.12$   
 Triclinic,  $P\bar{1}$   
 $a = 5.89854$  (14) Å  
 $b = 6.92921$  (15) Å  
 $c = 9.59160$  (18) Å

$\alpha = 74.6778$  (12)°  
 $\beta = 72.3232$  (16)°  
 $\gamma = 68.447$  (2)°  
 $V = 342.21$  (1) Å<sup>3</sup>  
 $Z = 2$   
 Mo  $K\alpha$  radiation

$\mu = 0.15$  mm<sup>-1</sup>  
 $T = 298$  (2) K

0.20 × 0.15 × 0.15 mm

### Data collection

Oxford Diffraction Xcalibur S CCD diffractometer  
 Absorption correction: multi-scan (*CrysAlis RED*; Oxford Diffraction, 2006)  
 $T_{\min} = 0.977$ ,  $T_{\max} = 0.985$   
 64781 measured reflections  
 2340 independent reflections  
 2048 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.017$

### Refinement

$R[F^2 > 2\sigma(F^2)] = 0.044$   
 $wR(F^2) = 0.133$   
 $S = 1.08$   
 2340 reflections  
 133 parameters  
 All H-atom parameters refined  
 $\Delta\rho_{\max} = 0.19$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.22$  e Å<sup>-3</sup>

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

D—H···A	D—H	H···A	D···A	D—H···A
O4—H4···O5	0.89 (3)	1.65 (3)	2.5231 (11)	166 (2)
N1—H1···O1 <sup>i</sup>	0.85 (2)	2.03 (2)	2.8824 (11)	175.2 (19)
N3—H3···O2 <sup>ii</sup>	0.94 (2)	1.87 (2)	2.8112 (11)	174.6 (18)
O5—H51···O2 <sup>iii</sup>	0.81 (3)	2.00 (3)	2.7786 (12)	161 (3)
O5—H52···O3 <sup>iv</sup>	0.82 (3)	1.98 (3)	2.7787 (12)	164 (2)
C5—H5···O4 <sup>iii</sup>	0.879 (19)	2.740 (19)	3.5922 (13)	163.7 (15)

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

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2006); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2006); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP3* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: KP2160).

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## supporting information

*Acta Cryst.* (2008). E64, o656 [doi:10.1107/S160053680800562X]

## Redetermination of orotic acid monohydrate

Gustavo Portalone

### S1. Comment

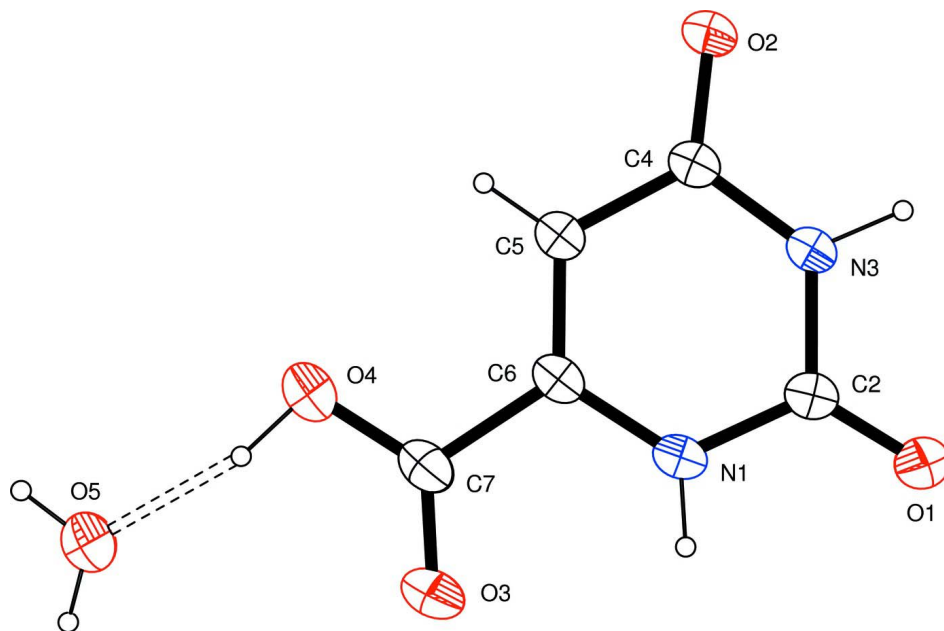
Orotic acid monohydrate, the only effective precursor in the biosynthesis of pyrimidine nucleobases, was determined some 35 years ago (Takusagawa & Shimada, 1973). In this study, 1488 unique reflections were collected at an ambient temperature by photographic techniques using Cu  $K\alpha$  radiation. 1344 of these, having values significantly above background, were estimated visually and no absorption correction was applied [ $\mu(\text{Cu } K\alpha) = 15.4 \text{ cm}^{-1}$ ]. The final refinement led to  $R = 0.058$  with standard deviations of  $0.005 \text{ \AA}$  in C—C bond lengths. As a part of a more general study of multiple hydrogen-bonded DNA/RNA-nucleobases as potential supramolecular reagents (Brunetti *et al.*, 2000, 2002; Portalone *et al.*, 1999; Portalone & Colapietro, 2007), this paper reports a redetermination of the crystal structure of the title compound, (I), with greater precision and accuracy. The asymmetric unit of (I) (Fig. 1) comprises a planar diketo tautomer and a crystal water molecule. The analysis of the crystal packing of (I) shows five N—H $\cdots$ O and O—H $\cdots$ O intermolecular hydrogen bonds (Table 1) which link the molecules into planar layers (Fig. 2). Two kinds of inversion-related N—H $\cdots$ O hydrogen bonds with graph-set motifs  $R^2_2(8)$  (Etter *et al.*, 1990; Bernstein *et al.*, 1995; Motherwell *et al.*, 1999) (Table 1) are formed between NH groups and two carbonyl O atoms (O1<sup>i</sup> and O2<sup>ii</sup>) [symmetry code: (i)  $-x, -y, z + 2$ ; (ii)  $-x, -y + 1, -z + 1$ ] to give a zigzag chain. Each chain is joined by three O—H $\cdots$ O intermolecular hydrogen bonds to form rings of descriptor  $R^4_4(12)$ ,  $R^4_3(13)$  and  $R^4_4(18)$  through a water molecule (O4—H4 $\cdots$ O5, O5—H51 $\cdots$ O2<sup>iii</sup> and O5—H52 $\cdots$ O2<sup>iv</sup>; symmetry code: (iii)  $-x + 2, -y, -z + 1$ ; (iv)  $-x + 2, -y - 1, -z + 2$ ). The hydrogen-bonded two-dimensional array involves the C5—H5 $\cdots$ O4<sup>iii</sup> intermolecular interaction.

### S2. Experimental

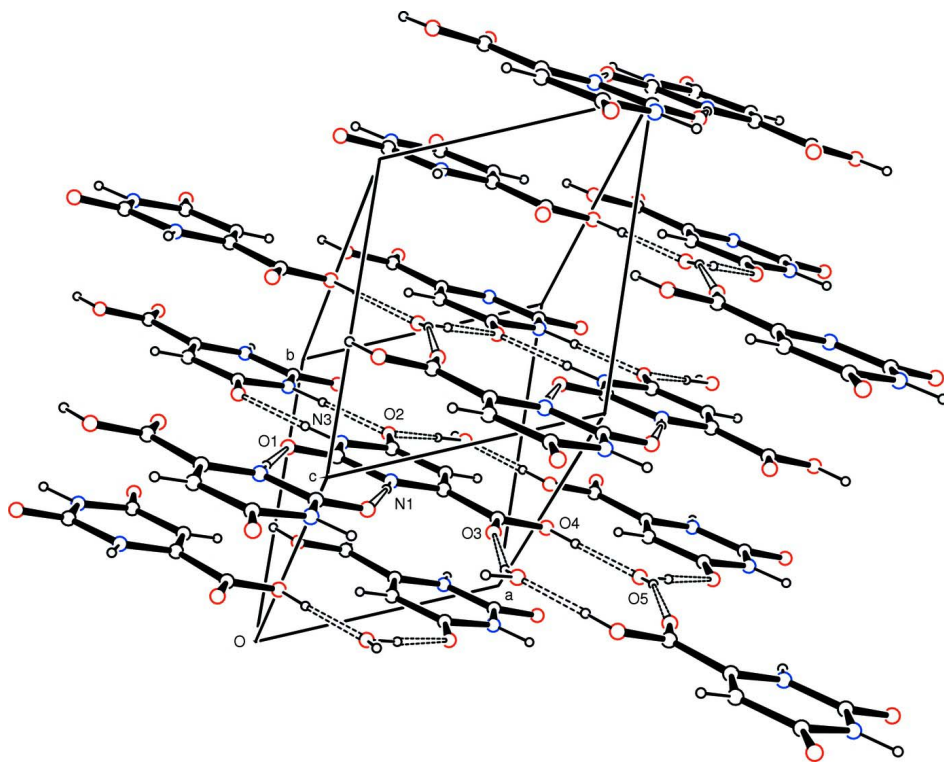
The title compound (0.1 mmol, Sigma Aldrich of 98% purity) was dissolved in water (9 ml) and heated under reflux for 2 h. After cooling the solution to ambient temperature, crystals suitable for single-crystal X-ray diffraction were grown by slow evaporation.

### S3. Refinement

All H atoms were found in a difference map and refined isotropically.

**Figure 1**

The molecular structure of (I), showing the atom-labelling scheme. Displacements ellipsoids are at the 50% probability level. Hydrogen bonding is indicated by dashed lines.

**Figure 2**

Crystal packing diagram of (I). All atoms are shown as small spheres of arbitrary radii. Hydrogen bonding is indicated by dashed lines.

## 2,6-dioxo-1,2,3,6-tetrahydropyrimidine-4-carboxylic acid monohydrate

## Crystal data

C<sub>5</sub>H<sub>4</sub>N<sub>2</sub>O<sub>4</sub>·H<sub>2</sub>O $M_r = 174.12$ Triclinic,  $P\bar{1}$ 

Hall symbol: -P 1

 $a = 5.89854 (14) \text{ \AA}$  $b = 6.92921 (15) \text{ \AA}$  $c = 9.59160 (18) \text{ \AA}$  $\alpha = 74.6778 (12)^\circ$  $\beta = 72.3232 (16)^\circ$  $\gamma = 68.447 (2)^\circ$  $V = 342.21 (1) \text{ \AA}^3$  $Z = 2$  $F(000) = 180$  $D_x = 1.690 \text{ Mg m}^{-3}$ Mo  $K\alpha$  radiation,  $\lambda = 0.71073 \text{ \AA}$ 

Cell parameters from 64781 reflections

 $\theta = 3.2\text{--}32.0^\circ$  $\mu = 0.15 \text{ mm}^{-1}$  $T = 298 \text{ K}$ 

Plate, colourless

 $0.20 \times 0.15 \times 0.15 \text{ mm}$ 

## Data collection

Oxford Diffraction Xcalibur S CCD

diffractometer

Radiation source: Enhance (Mo) X-ray source

Graphite monochromator

Detector resolution: 16.0696 pixels  $\text{mm}^{-1}$  $\omega$  and  $\varphi$  scans

Absorption correction: multi-scan

(CrysAlis RED; Oxford Diffraction, 2006)

 $T_{\min} = 0.977$ ,  $T_{\max} = 0.985$ 

64781 measured reflections

2340 independent reflections

2048 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.017$  $\theta_{\max} = 32.0^\circ$ ,  $\theta_{\min} = 3.2^\circ$  $h = -8 \rightarrow 8$  $k = -10 \rightarrow 10$  $l = -14 \rightarrow 14$ 

## Refinement

Refinement on  $F^2$ 

Least-squares matrix: full

 $R[F^2 > 2\sigma(F^2)] = 0.044$  $wR(F^2) = 0.133$  $S = 1.08$ 

2340 reflections

133 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

All H-atom parameters refined

 $w = 1/[\sigma^2(F_o^2) + (0.0846P)^2 + 0.0376P]$ where  $P = (F_o^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\max} < 0.001$  $\Delta\rho_{\max} = 0.19 \text{ e \AA}^{-3}$  $\Delta\rho_{\min} = -0.22 \text{ e \AA}^{-3}$ 

## Special details

**Experimental.** Empirical absorption correction using spherical harmonics, implemented in SCALE3 ABSPACK scaling algorithm.**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 ( $\text{\AA}^2$ )

	$x$	$y$	$z$	$U_{\text{iso}}^*/U_{\text{eq}}$
O1	-0.14403 (15)	0.19593 (14)	0.87497 (9)	0.0437 (2)

O2	0.33017 (14)	0.40869 (13)	0.43298 (8)	0.0402 (2)
O3	0.67729 (18)	-0.25757 (17)	0.92057 (11)	0.0575 (3)
O4	0.94015 (16)	-0.17721 (14)	0.70790 (10)	0.0430 (2)
H4	1.045 (5)	-0.276 (4)	0.759 (3)	0.072 (6)*
N1	0.27952 (15)	0.03091 (13)	0.83018 (9)	0.03108 (19)
H1	0.248 (4)	-0.038 (3)	0.918 (2)	0.052 (4)*
C2	0.06502 (18)	0.17428 (15)	0.79307 (10)	0.0302 (2)
N3	0.09988 (15)	0.29328 (13)	0.65310 (8)	0.03059 (19)
H3	-0.050 (4)	0.391 (3)	0.630 (2)	0.054 (5)*
C4	0.32531 (17)	0.28849 (14)	0.55477 (10)	0.0284 (2)
C5	0.54286 (17)	0.13666 (14)	0.60218 (10)	0.0295 (2)
H5	0.689 (3)	0.127 (3)	0.540 (2)	0.042 (4)*
C6	0.51057 (17)	0.01317 (13)	0.73716 (9)	0.02706 (19)
C7	0.72006 (19)	-0.15575 (15)	0.79814 (11)	0.0325 (2)
O5	1.28887 (17)	-0.45822 (16)	0.81521 (11)	0.0523 (3)
H51	1.421 (5)	-0.460 (4)	0.757 (3)	0.080 (7)*
H52	1.313 (5)	-0.528 (4)	0.896 (3)	0.082 (7)*

*Atomic displacement parameters (Å<sup>2</sup>)*

	$U^{11}$	$U^{22}$	$U^{33}$	$U^{12}$	$U^{13}$	$U^{23}$
O1	0.0285 (4)	0.0499 (5)	0.0329 (4)	-0.0054 (3)	-0.0022 (3)	0.0094 (3)
O2	0.0291 (4)	0.0447 (4)	0.0298 (4)	-0.0065 (3)	-0.0079 (3)	0.0154 (3)
O3	0.0390 (5)	0.0612 (6)	0.0449 (5)	-0.0062 (4)	-0.0138 (4)	0.0266 (4)
O4	0.0302 (4)	0.0449 (4)	0.0385 (4)	-0.0003 (3)	-0.0112 (3)	0.0054 (3)
N1	0.0289 (4)	0.0311 (4)	0.0247 (3)	-0.0063 (3)	-0.0080 (3)	0.0067 (3)
C2	0.0277 (4)	0.0308 (4)	0.0252 (4)	-0.0071 (3)	-0.0065 (3)	0.0037 (3)
N3	0.0245 (4)	0.0319 (4)	0.0258 (3)	-0.0047 (3)	-0.0077 (3)	0.0070 (3)
C4	0.0260 (4)	0.0289 (4)	0.0244 (4)	-0.0064 (3)	-0.0078 (3)	0.0041 (3)
C5	0.0243 (4)	0.0308 (4)	0.0258 (4)	-0.0045 (3)	-0.0072 (3)	0.0029 (3)
C6	0.0268 (4)	0.0251 (4)	0.0257 (4)	-0.0045 (3)	-0.0106 (3)	0.0014 (3)
C7	0.0306 (4)	0.0297 (4)	0.0322 (4)	-0.0049 (3)	-0.0137 (3)	0.0038 (3)
O5	0.0287 (4)	0.0598 (6)	0.0426 (5)	0.0010 (4)	-0.0082 (3)	0.0118 (4)

*Geometric parameters (Å, °)*

O1—C2	1.2241 (12)	N3—C4	1.3716 (12)
O2—C4	1.2418 (10)	N3—H3	0.94 (2)
O3—C7	1.2056 (13)	C4—C5	1.4387 (12)
O4—C7	1.3040 (13)	C5—C6	1.3525 (12)
O4—H4	0.89 (3)	C5—H5	0.879 (19)
N1—C6	1.3656 (12)	C6—C7	1.5012 (12)
N1—C2	1.3702 (12)	O5—H51	0.81 (3)
N1—H1	0.85 (2)	O5—H52	0.82 (3)
C2—N3	1.3772 (11)		
C7—O4—H4	104.3 (16)	N3—C4—C5	115.74 (8)
C6—N1—C2	122.36 (8)	C6—C5—C4	118.56 (8)

C6—N1—H1	126.4 (14)	C6—C5—H5	124.1 (11)
C2—N1—H1	111.2 (14)	C4—C5—H5	117.3 (11)
O1—C2—N1	123.81 (8)	C5—C6—N1	122.13 (8)
O1—C2—N3	121.35 (8)	C5—C6—C7	124.03 (9)
N1—C2—N3	114.83 (8)	N1—C6—C7	113.84 (8)
C4—N3—C2	126.29 (7)	O3—C7—O4	125.70 (9)
C4—N3—H3	120.3 (12)	O3—C7—C6	120.28 (10)
C2—N3—H3	113.3 (12)	O4—C7—C6	114.02 (8)
O2—C4—N3	119.61 (8)	H51—O5—H52	110 (2)
O2—C4—C5	124.64 (9)		
C6—N1—C2—O1	-178.86 (10)	C4—C5—C6—N1	-1.20 (15)
C6—N1—C2—N3	2.20 (15)	C4—C5—C6—C7	178.02 (9)
O1—C2—N3—C4	177.12 (10)	C2—N1—C6—C5	0.18 (16)
N1—C2—N3—C4	-3.91 (15)	C2—N1—C6—C7	-179.11 (9)
C2—N3—C4—O2	-178.17 (10)	C5—C6—C7—O3	178.85 (12)
C2—N3—C4—C5	2.97 (15)	N1—C6—C7—O3	-1.87 (15)
O2—C4—C5—C6	-179.05 (10)	C5—C6—C7—O4	-1.13 (15)
N3—C4—C5—C6	-0.26 (14)	N1—C6—C7—O4	178.15 (9)

*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>
O4—H4...O5	0.89 (3)	1.65 (3)	2.5231 (11)	166 (2)
N1—H1...O1 <sup>i</sup>	0.85 (2)	2.03 (2)	2.8824 (11)	175.2 (19)
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O5—H52...O3 <sup>iv</sup>	0.82 (3)	1.98 (3)	2.7787 (12)	164 (2)
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