

Acta Crystallographica Section E

Structure Reports

Online

ISSN 1600-5368

A new polymorph of 5-nitouracil monohydrate

 P. S. Pereira Silva, S. R. Domingos, M. Ramos Silva,
J. A. Paixão and A. Matos Beja*

 CEMDRX, Physics Department, University of Coimbra, P-3004-516 Coimbra,
Portugal

Correspondence e-mail: psidonio@pollux.fis.uc.pt

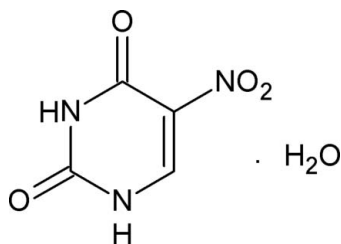
Received 13 May 2008; accepted 13 May 2008

 Key indicators: single-crystal X-ray study; $T = 293$ K; mean $\sigma(\text{C}-\text{C}) = 0.001$ Å;
 R factor = 0.043; wR factor = 0.131; data-to-parameter ratio = 19.4.

In the title compound, $\text{C}_4\text{H}_3\text{N}_3\text{O}_4 \cdot \text{H}_2\text{O}$, molecules of 5-nitouracil are hydrogen bonded in pairs across crystallographic centers of symmetry. The resulting dimers are also hydrogen bonded to the water molecules, forming a three-dimensional network. The pyrimidine ring is almost planar (with a maximum deviation of 0.0156 (9) Å for the one of the N atoms) and the nitro group is rotated by 12.4 (1)° out of the uracil plane, while in the other polymorph the value for the same angle is 5°.

Related literature

For the non-linear optical properties of 5-nitouracil, see: Bergman *et al.* (1972); Puccetti *et al.* (1993); Youping *et al.* (1992). For the crystal structure of another polymorph, see: Craven (1967). For related literature, see: Pettier & Byrn (1982); Rao *et al.* (1995).



Experimental

Crystal data

 $\text{C}_4\text{H}_3\text{N}_3\text{O}_4 \cdot \text{H}_2\text{O}$
 $M_r = 175.11$
Monoclinic, $P2_1/c$
 $a = 6.2799$ (1) Å
 $b = 7.8481$ (2) Å
 $c = 13.8068$ (3) Å

 $\beta = 93.842$ (1)°
 $V = 678.94$ (3) Å³
 $Z = 4$
Mo $K\alpha$ radiation

 $\mu = 0.16$ mm⁻¹
 $T = 293$ (2) K
 $0.44 \times 0.22 \times 0.20$ mm

Data collection

 Bruker APEXII CCD area-detector diffractometer
Absorption correction: multi-scan (SADABS; Sheldrick, 2003)
 $T_{\min} = 0.890$, $T_{\max} = 0.969$
15135 measured reflections
2232 independent reflections
1918 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.018$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.042$
 $wR(F^2) = 0.131$
 $S = 1.00$
2232 reflections
115 parameters

 H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\text{max}} = 0.35$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.37$ e Å⁻³

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

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$\text{N3}-\text{H3} \cdots \text{O2}^{\text{i}}$	0.86	1.99	2.8503 (13)	173
$\text{N1}-\text{H1} \cdots \text{O9}^{\text{ii}}$	0.86	1.88	2.6736 (12)	153
$\text{O9}-\text{H9A} \cdots \text{O4}^{\text{iii}}$	0.87 (2)	1.92 (2)	2.7640 (13)	165 (2)
$\text{O9}-\text{H9A} \cdots \text{O7}^{\text{iii}}$	0.87 (2)	2.41 (3)	2.9101 (13)	117 (2)
$\text{O9}-\text{H9B} \cdots \text{O7}^{\text{iv}}$	0.84 (3)	2.29 (3)	3.0940 (15)	162 (2)

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

Data collection: APEX2 (Bruker, 2005); cell refinement: SAINT (Bruker, 2005); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: PLATON (Spek, 2003); software used to prepare material for publication: SHELXL97.

This work was supported by Fundação para a Ciência e a Tecnologia (FCT) under project POCI/FIS/58309/2004

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BT2713).

References

- Bergman, J. G., Crane, G. R., Levine, B. F. & Bethea, C. G. (1972). *Appl. Phys. Lett.* **20**, 21–23.
Bruker (2005). APEX2 and SAINT. Bruker AXS Inc., Madison, Wisconsin, USA.
Craven, B. M. (1967). *Acta Cryst.* **23**, 376–383.
Pettier, P. R. & Byrn, S. R. (1982). *J. Org. Chem.* **47**, 4671–4676.
Puccetti, G., Perigaud, A., Badan, J., Ledoux, I. & Zyss, J. (1993). *J. Opt. Soc. Am. B*, **10**, 733–744.
Rao, T. S., Rando, R. F., Huffman, J. H. & Revankar, G. R. (1995). *Nucleosides Nucleotides*, **14**, 1997–2008.
Sheldrick, G. M. (2003). SADABS. University of Göttingen, Germany.
Sheldrick, G. M. (2008). *Acta Cryst.* **A64**, 112–122.
Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.
Youping, H., Genbo, S., Bochang, W. & Rihong, J. (1992). *J. Cryst. Growth*, **119**, 393–398.

supporting information

Acta Cryst. (2008). E64, o1091 [doi:10.1107/S1600536808014426]

A new polymorph of 5-nitrouracil monohydrate

P. S. Pereira Silva, S. R. Domingos, M. Ramos Silva, J. A. Paixão and A. Matos Beja

S1. Comment

5-Nitrouracil (5NU) is an interesting molecule due to its nonlinear optical properties (Bergman *et al.*, 1972; Puccetti *et al.*, 1993; Youping *et al.*, 1992) and is also of relevance to biological and pharmaceutical sciences (Rao *et al.*, 1995; Pettier & Byrn, 1982).

In the framework of our study of new compounds with potential NLO properties, we have crystallized a new polymorph of 5-nitrouracil monohydrate (Fig.1). Molecules of 5NU are hydrogen bonded in pairs across crystallographic centers of symmetry. The resulting dimers are also hydrogen bonded by the water molecules forming a three dimensional network (Table 1; Fig. 2). The difference in intermolecular interactions between the two polymorphs seems to have a small effect on the molecular structure of the 5NU moiety, with all bond lengths and angles being in good agreement with the previously reported structure (Craven, 1967). The pyrimidine ring is almost planar and the main conformational difference is the large twist of the nitro group away from the plane of the ring [12.4 (1)°], whereas it approaches coplanarity in the other polymorph (5.0° for the same angle).

S2. Experimental

The title compound was prepared by adding 5-nitrouracil (Aldrich, 98%, 1 mmol) to *L*-serine (Aldrich 99%, 1 mmol) in a solution of water (10 ml) and piridine (Aldrich 99%, 30 ml). The solution was slowly warmed and then left to evaporate under ambient conditions. After a few days, small colourless single crystals were deposited.

S3. Refinement

All hydrogen atoms were located in a difference Fourier synthesis at an intermediate stage of the refinement. Hydrogen atoms bonded to N and C were placed at calculated positions and refined as riding on their parent atoms, using *SHELXL97* (Sheldrick, 2008) defaults [C—H = 0.93 Å, N—H = 0.86 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C},\text{N})$]. The coordinates of the hydrogen atoms of the water molecule were refined with $U_{\text{iso}} = 1.5U_{\text{eq}}(\text{O})$.

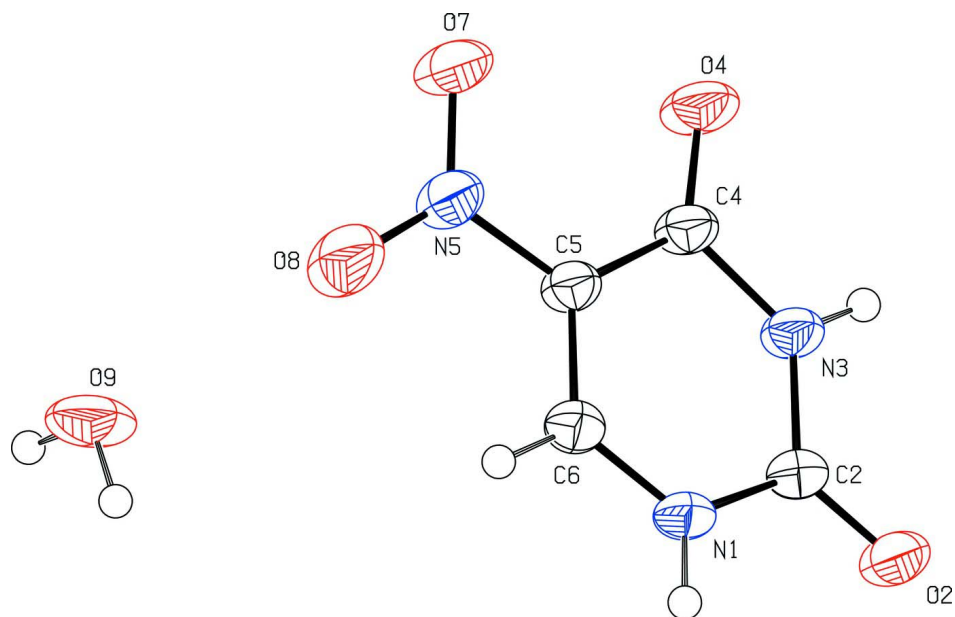
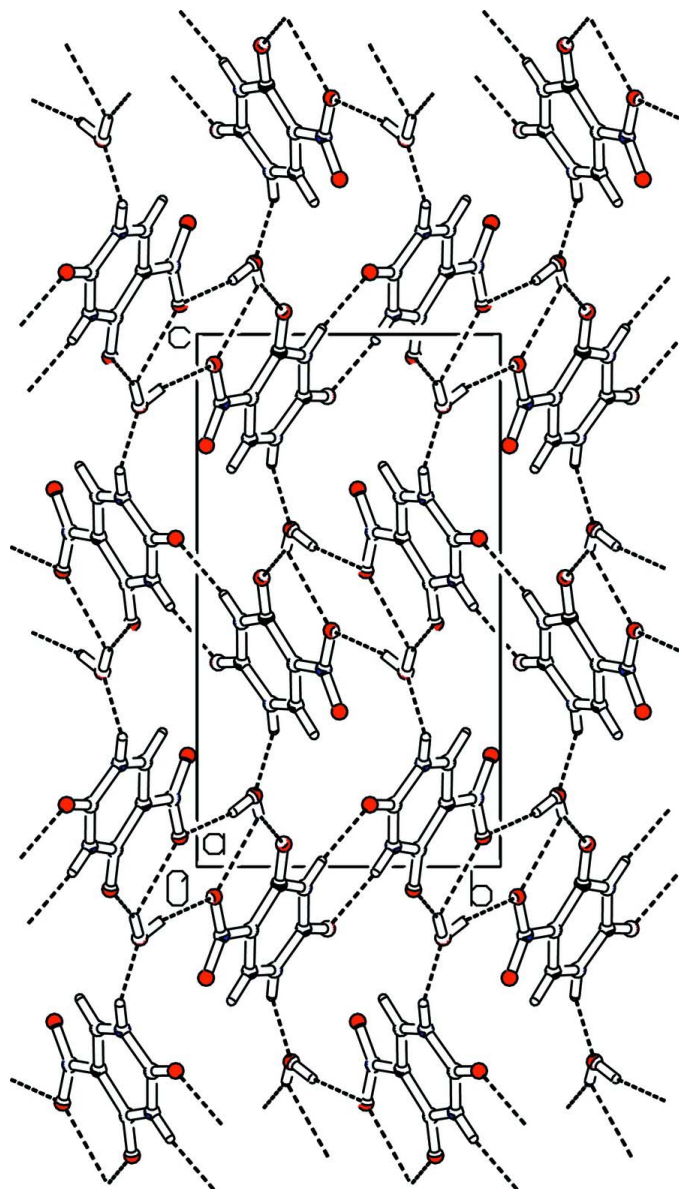


Figure 1

ORTEP (Spek, 2003) plot of the title compound. Displacement ellipsoids are drawn at the 50% probability level.

**Figure 2**

Packing diagram, viewed down the *a* axis, with the hydrogen bonds depicted as dashed lines.

5-nitrouracil monohydrate

Crystal data

$C_4H_3N_3O_4 \cdot H_2O$
 $M_r = 175.11$
 Monoclinic, $P2_1/c$
 Hall symbol: $-P 2_1/c$
 $a = 6.2799 (1) \text{ \AA}$
 $b = 7.8481 (2) \text{ \AA}$
 $c = 13.8068 (3) \text{ \AA}$
 $\beta = 93.842 (1)^\circ$
 $V = 678.94 (3) \text{ \AA}^3$
 $Z = 4$

$F(000) = 360$
 $D_x = 1.713 \text{ Mg m}^{-3}$
 Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ \AA}$
 Cell parameters from 8093 reflections
 $\theta = 3.0\text{--}33.5^\circ$
 $\mu = 0.16 \text{ mm}^{-1}$
 $T = 293 \text{ K}$
 Block, colourless
 $0.44 \times 0.22 \times 0.20 \text{ mm}$

Data collection

Bruker APEXII CCD area-detector
diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
 φ and ω scans
Absorption correction: multi-scan
(*SADABS*; Sheldrick, 2003)
 $T_{\min} = 0.890$, $T_{\max} = 0.969$

15135 measured reflections
2232 independent reflections
1918 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.018$
 $\theta_{\max} = 33.6^\circ$, $\theta_{\min} = 3.0^\circ$
 $h = -9 \rightarrow 9$
 $k = -10 \rightarrow 11$
 $l = -20 \rightarrow 20$

Refinement

Refinement on F^2
Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.042$
 $wR(F^2) = 0.131$
 $S = 1.00$
2232 reflections
115 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
 $w = 1/[\sigma^2(F_o^2) + (0.0782P)^2 + 0.1592P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.002$
 $\Delta\rho_{\max} = 0.35 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.37 \text{ e } \text{\AA}^{-3}$

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 (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
O2	-0.10857 (13)	0.07025 (12)	0.38353 (6)	0.0403 (2)
O4	0.51917 (15)	0.21379 (14)	0.54232 (6)	0.0478 (3)
O7	0.75926 (14)	0.44337 (13)	0.44352 (7)	0.0459 (2)
O8	0.67663 (18)	0.46987 (19)	0.29111 (8)	0.0674 (4)
N1	0.11205 (14)	0.24517 (12)	0.30605 (6)	0.0306 (2)
H1	0.0210	0.2540	0.2569	0.037*
N3	0.20903 (15)	0.14746 (12)	0.46071 (6)	0.0330 (2)
H3	0.1773	0.0894	0.5106	0.040*
N5	0.63828 (16)	0.41810 (13)	0.37147 (7)	0.0371 (2)
C2	0.06017 (16)	0.14825 (13)	0.38398 (7)	0.0290 (2)
C4	0.40561 (16)	0.22918 (14)	0.46790 (7)	0.0309 (2)
C5	0.44553 (16)	0.32373 (13)	0.38070 (7)	0.0292 (2)
C6	0.29851 (16)	0.32614 (14)	0.30377 (7)	0.0307 (2)
H6	0.3287	0.3858	0.2481	0.037*
O9	0.90537 (17)	0.18878 (17)	0.13340 (7)	0.0555 (3)

H9A	0.790 (4)	0.206 (3)	0.0966 (18)	0.083*
H9B	0.975 (4)	0.119 (3)	0.1021 (18)	0.083*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O2	0.0332 (4)	0.0481 (5)	0.0381 (4)	-0.0115 (3)	-0.0090 (3)	0.0058 (3)
O4	0.0397 (5)	0.0639 (6)	0.0370 (4)	-0.0138 (4)	-0.0176 (3)	0.0143 (4)
O7	0.0378 (5)	0.0521 (5)	0.0457 (5)	-0.0136 (4)	-0.0137 (4)	0.0035 (4)
O8	0.0525 (6)	0.1010 (10)	0.0474 (6)	-0.0336 (6)	-0.0066 (4)	0.0276 (6)
N1	0.0274 (4)	0.0381 (4)	0.0251 (4)	-0.0006 (3)	-0.0067 (3)	0.0008 (3)
N3	0.0301 (4)	0.0406 (5)	0.0271 (4)	-0.0066 (3)	-0.0066 (3)	0.0064 (3)
N5	0.0308 (4)	0.0408 (5)	0.0387 (5)	-0.0065 (4)	-0.0055 (3)	0.0064 (4)
C2	0.0272 (4)	0.0313 (4)	0.0278 (4)	-0.0005 (3)	-0.0046 (3)	-0.0010 (3)
C4	0.0278 (5)	0.0353 (5)	0.0286 (4)	-0.0025 (4)	-0.0067 (3)	0.0020 (3)
C5	0.0259 (4)	0.0324 (5)	0.0285 (4)	-0.0023 (3)	-0.0040 (3)	0.0017 (3)
C6	0.0292 (5)	0.0358 (5)	0.0264 (4)	0.0003 (4)	-0.0030 (3)	0.0022 (3)
O9	0.0458 (5)	0.0762 (7)	0.0413 (5)	0.0151 (5)	-0.0218 (4)	-0.0152 (5)

Geometric parameters (Å, °)

O2—C2	1.2234 (12)	N3—C4	1.3888 (13)
O4—C4	1.2169 (11)	N3—H3	0.8600
O7—N5	1.2268 (13)	N5—C5	1.4320 (13)
O8—N5	1.2206 (14)	C4—C5	1.4502 (14)
N1—C6	1.3345 (13)	C5—C6	1.3601 (13)
N1—C2	1.3745 (13)	C6—H6	0.9300
N1—H1	0.8600	O9—H9A	0.87 (2)
N3—C2	1.3651 (12)	O9—H9B	0.84 (3)
C6—N1—C2	122.44 (8)	N3—C2—N1	115.09 (9)
C6—N1—H1	118.8	O4—C4—N3	118.84 (9)
C2—N1—H1	118.8	O4—C4—C5	128.88 (10)
C2—N3—C4	127.78 (9)	N3—C4—C5	112.29 (8)
C2—N3—H3	116.1	C6—C5—N5	117.19 (9)
C4—N3—H3	116.1	C6—C5—C4	120.62 (9)
O8—N5—O7	122.28 (10)	N5—C5—C4	122.19 (9)
O8—N5—C5	118.20 (10)	N1—C6—C5	121.72 (9)
O7—N5—C5	119.52 (9)	N1—C6—H6	119.1
O2—C2—N3	123.33 (9)	C5—C6—H6	119.1
O2—C2—N1	121.57 (9)	H9A—O9—H9B	104 (2)
C4—N3—C2—O2	179.00 (11)	O7—N5—C5—C4	-11.85 (17)
C4—N3—C2—N1	-1.51 (16)	O4—C4—C5—C6	179.88 (12)
C6—N1—C2—O2	-177.51 (10)	N3—C4—C5—C6	0.19 (15)
C6—N1—C2—N3	2.99 (15)	O4—C4—C5—N5	-0.29 (19)
C2—N3—C4—O4	-179.72 (11)	N3—C4—C5—N5	-179.97 (10)
C2—N3—C4—C5	0.00 (16)	C2—N1—C6—C5	-2.99 (16)

O8—N5—C5—C6	-12.45 (17)	N5—C5—C6—N1	-178.58 (10)
O7—N5—C5—C6	168.00 (11)	C4—C5—C6—N1	1.27 (17)
O8—N5—C5—C4	167.71 (13)		

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>
N3—H3 \cdots O2 ⁱ	0.86	1.99	2.8503 (13)	173
N1—H1 \cdots O9 ⁱⁱ	0.86	1.88	2.6736 (12)	153
O9—H9 <i>A</i> \cdots O4 ⁱⁱⁱ	0.87 (2)	1.92 (2)	2.7640 (13)	165 (2)
O9—H9 <i>A</i> \cdots O7 ⁱⁱⁱ	0.87 (2)	2.41 (3)	2.9101 (13)	117 (2)
O9—H9 <i>B</i> \cdots O7 ^{iv}	0.84 (3)	2.29 (3)	3.0940 (15)	162 (2)

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