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#### **Key indicators**

Single-crystal X-ray study T = 298 K Mean  $\sigma$ (C–C) = 0.010 Å R factor = 0.066 wR factor = 0.148 Data-to-parameter ratio = 8.3

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

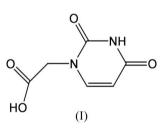
# 1-(Carboxymethyl)uracil

In the title compound,  $C_6H_6N_2O_4$ , the planar carboxyl group makes a dihedral angle of 74.61 (2)° with the uracil plane. In the crystal structure, intermolecular  $N-H\cdots O$  and  $O-H\cdots O$  hydrogen bonds link the molecules into a three-dimensional network.

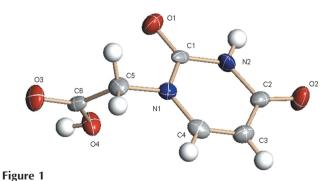
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## Comment

Thymine and uracil are important nucleobases in biology; they contribute to a wide range of biochemical processes, such as complementary base pairing in genetic information storage and transfer, molecular recognition and for some enzyme reactions (Bazzicalupi *et al.*, 2001; Honda *et al.*, 2002; Leiros *et al.*, 2003). As a result, great efforts have been undertaken to investigate thymine, uracil and their derivatives (Jolibois *et al.*, 1998; Koike *et al.*, 1998). In a continuation of our research in this field, we present here the synthesis and crystal structure of the title compound, namely 1-(carboxymethyl)uracil, (I).



In (I) (Fig. 1), the carboxyl group (C6/O3/O4/H4) and uracil ring (C1–C4/N1/N2) are each almost planar, with r.m.s. deviations of 0.0196 and 0.0093 Å, respectively. The dihedral angle between their mean planes is 74.61 (2)°. Moreover, the C–N bond lengths in the uracil ring (Table 1) range from 1.369 (9) to 1.382 (8) Å, which are shorter than a C–N single bond length (*ca* 1.443 Å) (Jin *et al.*, 2004), but longer than a typical C==N bond length (*ca* 1.269 Å), indicating delocalization. On the other hand, the conjugation of O2/C2/C3/C4



© 2005 International Union of Crystallography Printed in Great Britain – all rights reserved View of (I), showing the atom-numbering scheme and displacement ellipsoids at the 50% probability level.

results in a decrease of the C2–C3 bond length [1.419 (10) Å].

In the crystal structure (Fig. 2), intermolecular N-H···O and O-H···O hydrogen bonds (Table 2) link each molecule with the four adjacent molecules to form a three-dimensional network. This hydrogen-bonding motif can be described in graph-set notation as  $R_4^4(20)$  and  $R_2^2(8)$  (Hu *et al.*, 2005).

## Experimental

Bromoacetic acid (45 mmol, 6.25 g) in water (10 ml) was added to a solution of uracil (30 mmol, 3.33 g), potassium hydroxide (11.5 mmol, 6.41 g) and water (20 ml) at 313 K. The mixture was cooled after 2 h reaction and the pH was adjusted to 5.5 using hydrochloric acid. The precipitate was filtered off and the pH of the filtrate was adjusted to 1, again using hydrochloric acid, and the solution was cooled for 6 h in a refrigerator and then filtered. The precipitate was washed with water and dried to obtain the title compound. Single crystals were obtained by recrystallization from anhydrous ethanol.

 $D_{\rm r} = 1.669 {\rm Mg m}^{-3}$ 

Cell parameters from 861

621 independent reflections

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

Mo  $K\alpha$  radiation

reflections

 $\theta = 2.8 - 24.8^{\circ}$ 

 $\mu = 0.14 \text{ mm}^{-1}$ 

T = 298 (2) K

 $R_{\rm int} = 0.035$ 

 $\theta_{\rm max} = 25.2^\circ$ 

 $h = -6 \rightarrow 6$ 

 $k = -5 \rightarrow 5$ 

 $l = -17 \rightarrow 18$ 

Rod, colourless  $0.21 \times 0.11 \times 0.10 \text{ mm}$ 

#### Crystal data

 $\begin{array}{l} C_{6}H_{6}N_{2}O_{4} \\ M_{r} = 170.13 \\ \text{Monoclinic, } Pc \\ a = 5.0999 \ (8) \ \text{\AA} \\ b = 4.6273 \ (8) \ \text{\AA} \\ c = 15.0106 \ (19) \ \text{\AA} \\ \beta = 107.093 \ (5)^{\circ} \\ V = 338.58 \ (9) \ \text{\AA}^{3} \\ Z = 2 \end{array}$ 

#### Data collection

Bruker APEX area-detector diffractometer  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (*SADABS*; Bruker, 2002)  $T_{\min} = 0.971, T_{\max} = 0.983$ 3071 measured reflections

## Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_0^2) + (0.0727P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.066$	+ 0.2892P]
$wR(F^2) = 0.148$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.26	$(\Delta/\sigma)_{\rm max} < 0.001$
621 reflections	$\Delta \rho_{\rm max} = 0.30 \ {\rm e} \ {\rm \AA}^{-3}$
75 parameters	$\Delta \rho_{\rm min} = -0.31 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

#### Table 1

Selected bond lengths (Å).

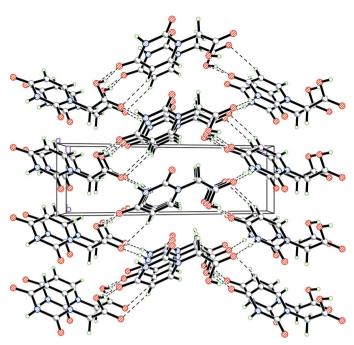
O1-C1	1.217 (7)	N2-C1	1.369 (9)
O2-C2	1.227 (8)	N2-C2	1.382 (8)
N1-C4	1.371 (8)	C2-C3	1.419 (10)
N1-C1	1.374 (8)		

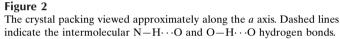
## Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\begin{array}{c} O4 - H4 \cdots O2^{i} \\ N2 - H2 \cdots O3^{ii} \end{array}$	0.82 (2)	1.76 (3)	2.553 (7)	160 (7)
	0.84 (2)	2.00 (3)	2.828 (7)	169 (7)

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





H atoms attached to N and O atoms were located in a difference Fourier map, and refined with O—H and N—H distances restrained to 0.82 (2) and 0.85 (2) Å, respectively, and with  $U_{\rm iso} = 1.2U_{\rm eq}$ (parent atom). The other H atoms were positioned geometrically and allowed to ride on their parent atoms at distances of  $Csp^2$ —H = 0.93 Å, with  $U_{\rm iso} = 1.2U_{\rm eq}$ (parent atom), and  $Csp^3$ —H = 0.97 Å, with  $U_{\rm iso} =$  $1.5U_{\rm eq}$ (parent atom). Due to the absence of any significant anomalous scatterers in the molecule, the Friedel pairs were merged before the final refinement

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2002); software used to prepare material for publication: *SHELXL97*.

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