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Key indicators

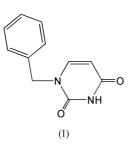
Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.007 Å R factor = 0.054 wR factor = 0.126 Data-to-parameter ratio = 6.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the title compound, $C_{11}H_{10}N_2O_2$, the benzene ring is almost perpendicular to the heterocycle; the dihedral angle is 91.2 (2)°. A chain structure is formed *via* an intermolecular $N-H\cdots O$ hydrogen bond. Received 12 March 2004 Accepted 16 April 2004 Online 24 April 2004

organic papers

Comment

Uracil and thymine are important nucleobases in biology, being responsible for a wide range of biochemical processes, such as complementary base pairing in genetic information storage and transfer and some enzymatic reactions (Bazzica-lupi *et al.*, 2001; Honda *et al.*, 2002; Leiros *et al.*, 2003). Therefore, considerable efforts have been made in the research field of uracil, thymine and their derivatives (Jolibois *et al.*, 1998; Koike *et al.*, 1998). In previous studies, we reported two thymine derivatives which were obtained by the benzylation of thymine (Ding *et al.*, 2002, 2003). We present here the structure of the title compound, (I), where thymine is replaced by uracil.



Compound (I) contains one benzene ring and one uracil heterocycle (Fig. 1). The benzene ring (C1–C6) is essentially planar, with an average deviation from planarity of 0.002 Å. The atoms of the uracil ring (C8/C9/C10/C11/N1/N2) are also coplanar, with an average deviation of 0.011 Å; the value in 1-benzylthymine is very similar, *viz.* 0.010 Å. The benzene ring is almost perpendicular to the heterocycle; the dihedral angle is 91.3 (2)°.

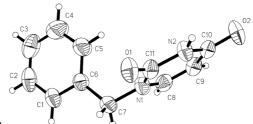


Figure 1

The molecule structure of (I), with the atom numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. H atoms are shown as spheres of arbitrary radius.

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In 1-benzyluracil, there is an $N-H \cdots O$ hydrogen bond, leading to a one-dimensional linear chain structure. Moreover, the benzene rings of adjacent molecules are partially overlapped (Fig. 2), with a distance of about 3.40 Å between the centres of the rings, suggesting the existence of π - π stacking interactions.

Experimental

The title compound, (I), was synthesized by the benzylation of uracil (0.20 g) with benzyl bromide (0.45 ml), with neutralization by potassium carbonate (2.00 g) and catalysis by tetrabutylammonium bromide (0.20 g) in a mixture of solvents N,N'-dimethylacetamide and diethylene glycol (1:10 v/v); the reaction time was 40 s in a National NN-S568WFS 900 W microwave oven. Crystals were obtained by recrystallization from dichloremethane.

 $D_x = 1.385 \text{ Mg m}^{-3}$

Cell parameters from 578

Mo $K\alpha$ radiation

reflections

 $\mu=0.10~\mathrm{mm}^{-1}$

T = 298 (2) K

 $R_{\rm int} = 0.012$ $\theta_{\rm max} = 25.2^{\circ}$

 $h = -6 \rightarrow 7$

 $k = -8 \rightarrow 8$

 $l = -13 \rightarrow 10$

+ 0.2061P]

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

Block, colourless

 $0.37\,\times\,0.32\,\times\,0.10$ mm

1683 independent reflections

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

 $\theta = 2.5 - 23.5^{\circ}$

Crystal data

 $C_{11}H_{10}N_2O_2$ $M_r = 202.21$ Monoclinic, P2 a = 6.5304 (4) Åh = 6.9483(3) Å c = 10.9214 (6) Å $\beta = 101.934 \ (2)^{\circ}$ $V = 484.85 (5) \text{ Å}^3$ Z = 2

Data collection

Bruker SMART APEX areadetector diffractometer φ and ω scans Absorption correction: multi-scan (SADABS; Bruker, 2002) $T_{\min} = 0.965, \ T_{\max} = 0.986$ 2594 measured reflections

Refinement

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Refinement on F^2
                                                        w = 1/[\sigma^2(F_o^2) + (0.0449P)^2
R[F^2 > 2\sigma(F^2)] = 0.054
wR(F^2) = 0.126
                                                         (\Delta/\sigma)_{\rm max} < 0.001
S = 1.27
                                                         \Delta \rho_{\rm max} = 0.19 \text{ e } \text{\AA}^{-3}
1683 reflections
                                                        \Delta \rho_{\rm min} = -0.19 \text{ e} \text{ Å}^{-3}
140 parameters
H atoms treated by a mixture of
   independent and constrained
   refinement
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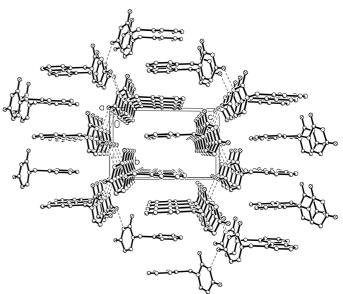
Table 1

Hydrogen-bonding geometry (Å, °).

$\overline{D-\mathrm{H}\cdots A}$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$\overline{N2-H1N\cdots O2^{i}}$	0.85 (5)	1.97 (5)	2.813 (5)	174 (5)
Symmetry code: (i) 2	$-r^{1} + v^{2} - z$			

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

The H atom bonded to N2 was located in a difference map and refined freely; all other H atoms were positioned geometrically and allowed to ride on their parent atoms at distances of 0.93 Å [U_{iso} =





The crystal packing of (I), viewed down the a axis. H atoms have been omitted. Hydrogen bonds are shown as dashed lines.

 $1.2U_{eq}$ (parent atom)] for Csp² atoms and 0.97 Å [$U_{iso} = 1.5U_{eq}$ (parent atom)] for Csp^3 atoms. In the absence of significant anomalous scattering, Friedel pairs were merged.

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

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