

5-Acetyl-4,6-dimethyl-1,2,3,4-tetrahydro-  
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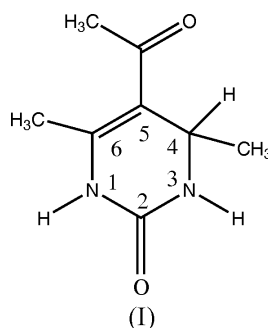
## Key indicators

Single-crystal X-ray study  
 $T = 293$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.002$  Å  
 $R$  factor = 0.029  
 $wR$  factor = 0.095  
Data-to-parameter ratio = 10.5For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.

The title compound,  $\text{C}_8\text{H}_{12}\text{N}_2\text{O}_2$ , belongs to the class of 5-substituted 1,2,3,4-tetrahydropyrimidin-2-ones, which exhibit a wide spectrum of biological activities. The conformation of the tetrahydropyrimidine ring is that of a distorted boat. In the crystal structure,  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds form molecular dimers and also link these dimers into chains along the  $c$  axis of the unit cell.

## Comment

The title compound, (I), belongs to the class of 5-substituted 1,2,3,4-tetrahydropyrimidin-2-ones, which are known as 'Biginelli compounds' (Kappe, 1993). Some representatives of this group have emerged as orally active antihypertensive agents (Atwal *et al.*, 1991; Grover *et al.*, 1995; Kappe, 2000; Kappe *et al.*, 1997; Rovnyak *et al.*, 1995), mitotic kinesin Eg5 inhibitors which can be considered as potential anticancer drugs (Haggarty *et al.*, 2000; Kappe, 2000), and  $\alpha$ -1a adrenoceptor-selective antagonists, useful for the treatment of benign prostatic hyperplasia (Kappe, 2000; Nagarathnam *et al.*, 1999).



To establish a correlation between the biological activity and spatial structure of molecules in the series of 1,2,3,4-tetrahydropyrimidin-2-ones and their 2-thioxo analogues, the conformation of the pyrimidine ring is usually considered (Kappe *et al.*, 1997; Gurskaya *et al.*, 2003a,b). In (I) (Fig. 1), the pyrimidine ring has the conformation of a distorted boat. The deviations of atoms N1 and C4 from the C2/N3/C5/C6 plane are 0.146 and 0.412 Å, respectively.

Molecules of (I) are linked into dimers by pairs of intermolecular  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds (Table 1 and Fig. 2) across centres of symmetry. These dimers are linked by further  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds to form chains along the  $c$  axis.

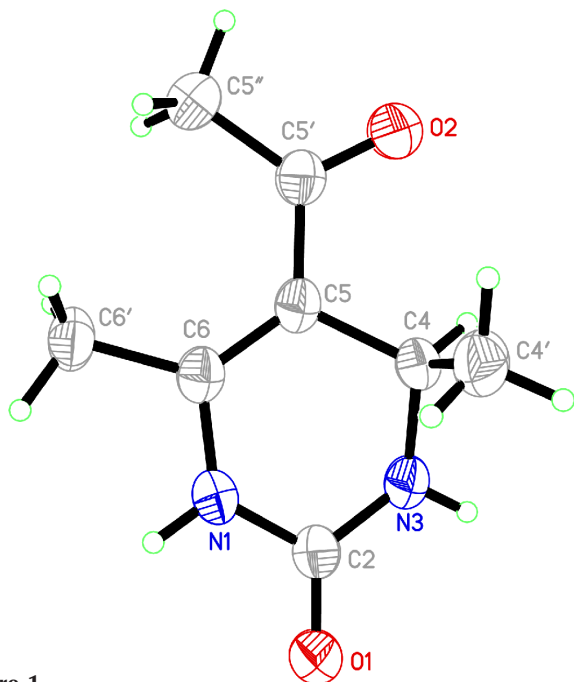
## Experimental

The title compound was prepared according to the general method of synthesis of 5-substituted 1,2,3,4-tetrahydropyrimidin-2-ones (or

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**Figure 1**  
The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level.

thiones) (Shutalev *et al.*, 1997, 1998). The synthesis of (I) was performed by the reaction of *N*-(1-tosylethyl)urea with the sodium enolate of acetylacetone in dry acetonitrile, followed by a TsOH-catalyzed dehydration of the resulting 5-acetyl-4-hydroxy-4,6-dimethylhexahydropyrimidin-2-one, without isolation of the latter. Crystals of (I) suitable for X-ray structure analysis were prepared at room temperature by slow evaporation of the solvent from a saturated solution of (I) (19 mg) in ethanol (1 ml).

#### Crystal data

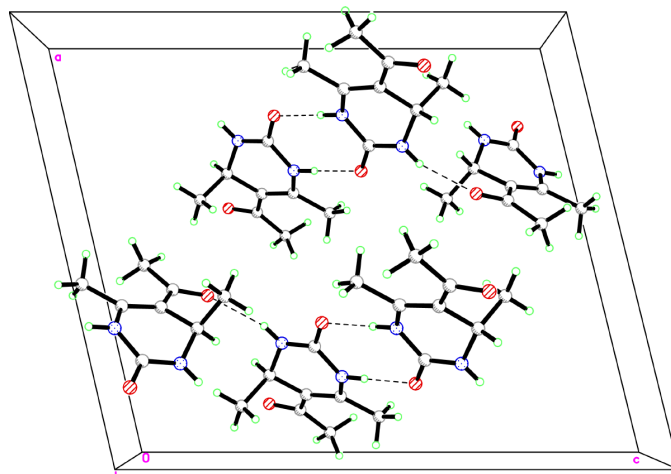
$C_8H_{12}N_2O_2$	$D_x = 1.319 \text{ Mg m}^{-3}$
$M_r = 168.20$	Mo $K\alpha$ radiation
Monoclinic, $C2/c$	Cell parameters from 24 reflections
$a = 14.473 (3) \text{ \AA}$	$\theta = 11.7\text{--}12.4^\circ$
$b = 6.994 (1) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$c = 17.200 (3) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\beta = 103.37 (3)^\circ$	Prism, colourless
$V = 1693.9 (6) \text{ \AA}^3$	$0.46 \times 0.42 \times 0.12 \text{ mm}$
$Z = 8$	

#### Data collection

Enraf–Nonius CAD-4 diffractometer	$\theta_{\max} = 26.0^\circ$
$\theta$ – $2\theta$ scans	$h = -17 \rightarrow 15$
Absorption correction: none	$k = 0 \rightarrow 8$
1712 measured reflections	$l = -21 \rightarrow 15$
1660 independent reflections	3 standard reflections
1187 reflections with $I > 2\sigma(I)$	frequency: 60 min
$R_{\text{int}} = 0.019$	intensity decay: 0.5%

#### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0592P)^2 + 0.1584P]$
$R[F^2 > 2\sigma(F^2)] = 0.029$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.095$	$(\Delta/\sigma)_{\max} < 0.001$
$S = 1.07$	$\Delta\rho_{\max} = 0.19 \text{ e \AA}^{-3}$
1660 reflections	$\Delta\rho_{\min} = -0.12 \text{ e \AA}^{-3}$
158 parameters	Extinction correction: <i>SHELXL97</i> (Sheldrick, 1997)
All H-atom parameters refined	Extinction coefficient: 0.0043 (12)



**Figure 2**  
A view, down the  $b$  axis, of the packing and hydrogen bonding (dashed lines) occurring in the crystal structure of (I).

**Table 1**

Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
$N1\text{--}H1\cdots O1^i$	0.858 (16)	1.991 (17)	2.8487 (15)	177.7 (14)
$N3\text{--}H3\cdots O2^{ii}$	0.828 (17)	2.110 (17)	2.8891 (16)	156.8 (13)

Symmetry codes: (i)  $-x + \frac{1}{2}, -y + \frac{3}{2}, -z + 1$ ; (ii)  $-x + \frac{1}{2}, y + \frac{1}{2}, -z + \frac{1}{2}$ .

All H atoms were located in difference syntheses and refined isotropically. The C–H and N–H bond lengths are in the ranges 1.00 (2)–0.92 (2)  $\text{\AA}$  and 0.86 (2)–0.83 (2)  $\text{\AA}$ , respectively.

Data collection: *CAD-4-PC Software* (Enraf–Nonius, 1993); cell refinement: *CAD-4-PC Software*; data reduction: *CAD-4-PC Software*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP in SHELXTL* (Sheldrick, 1991); software used to prepare material for publication: *SHELXL97* and *CIFTAB* (Sheldrick, 1997).

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