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Ethyl 4,6-dimethyl-2-thioxo-1,2,3,4-tetrahydropyrimidine-5-carboxylate

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Key indicators

Single-crystal X-ray study
T = 292 K
Mean σ(C–C) = 0.002 Å
R factor = 0.030
wR factor = 0.095
Data-to-parameter ratio = 14.9

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

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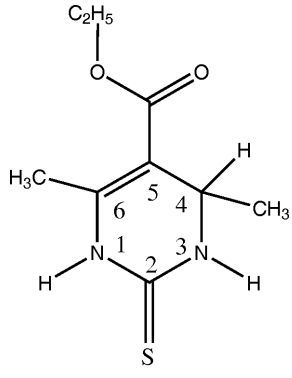
The title compound, $C_9H_{14}N_2O_2S$, belongs to a group of esters of 2-oxo- and 2-thioxo-1,2,3,4-tetrahydropyrimidine-5-carboxylic acids, which exhibit a wide spectrum of biological activities. The conformation of the pyrimidine ring is a distorted boat. In the crystal structure, hydrogen-bonded centrosymmetric dimers are formed *via* intermolecular N—H···S hydrogen bonds. The dimers are linked by intermolecular N—H···O hydrogen bonds to form a two-dimensional network.

Comment

The title compound, (I), is one of the group of esters of 2-oxo- and 2-thioxo-1,2,3,4-tetrahydropyrimidine-5-carboxylic acids, which are known as 'Biginelli compounds' (Kappe, 1997). Some of these compounds have been observed to be orally active antihypertensive agents, mitotic kinesin Eg5 motor protein inhibitors, and *a*1*a* adrenoceptor-selective antagonists, *etc*. (Atwal *et al.*, 1991; Grover *et al.*, 1995; Haggarty *et al.*, 2000; Kappe, 2000; Kappe *et al.*, 1997; Nagarathnam *et al.*, 1999; Rovnyak *et al.*, 1995). The conformation of the pyrimidine ring is usually considered (Kappe *et al.*, 1997; Gurskaya *et al.*, 2003*a*,*b*) to establish a correlation between the biological activity and the stereochemistry of molecules in a series of 1,2,3,4-tetrahydropyrimidin-2-ones and their 2-thioxo analogues.



(I)

In the structure of (I), illustrated in Fig. 1, the deviations of atoms N1 and C4 from the C2/N3/C5/C6 plane are 0.093 (1) and 0.270 (1) Å, respectively, generating the distorted boat conformation for the ring. Pairs of intermolecular N3—H3···S^{ii} hydrogen bonds (see Table 1 and Fig. 2) link molecules of (I) through a centre of symmetry, forming dimers linked by intermolecular N1—H1···O1^{i} hydrogen bonds to form a two-dimensional network.

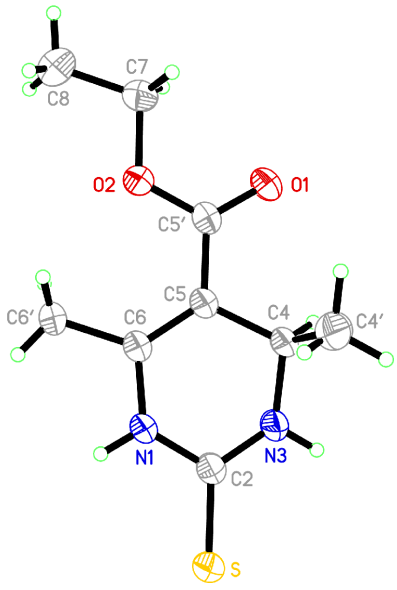


Figure 1
The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level.

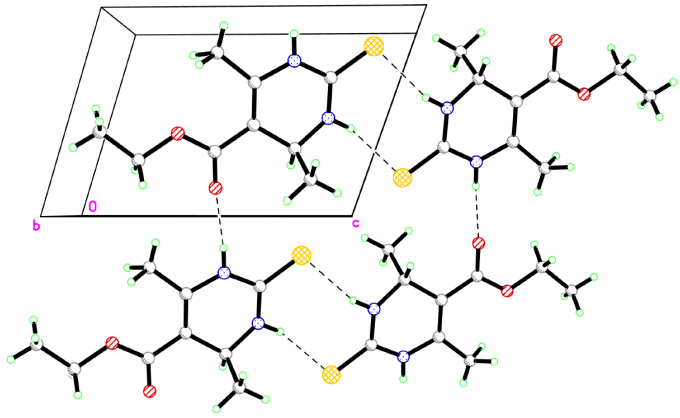


Figure 2
A view of the crystal packing in (I), showing the hydrogen bonding as dashed lines (see Table 1 for details).

Experimental

The title compound, (I), was prepared according to a general method of synthesis for 5-functionally substituted 1,2,3,4-tetrahydropyrimidin-2-(thi)ones (Shutalev & Kuksa, 1997; Shutalev *et al.*, 1998). *N*-(1-Tosylethyl)thiourea was reacted with ethyl acetoacetate in the presence of potassium hydroxide in ethanol, followed by TsOH-catalyzed dehydration of the resulting ethyl 4-hydroxy-4,6-dimethyl-2-thioxohexahydropyrimidine-5-carboxylate, without isolation of the latter. Crystals suitable for X-ray structure analysis were prepared by slow evaporation of a saturated solution of (I) in ethanol.

Crystal data

$C_9H_{14}N_2O_2S$
M_r = 214.28
Triclinic, $P\overline{1}$
a = 7.296 (1) Å
b = 8.014 (2) Å
c = 10.208 (2) Å
α = 86.97 (2)°
β = 70.53 (2)°
γ = 73.04 (2)°
V = 537.61 (19) Å^3
Z = 2
D_x = 1.324 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 24 reflections
θ = 11.8–12.5°
μ = 0.28 mm^{-1}
T = 292 (2) K
Prism, colourless
0.32 × 0.22 × 0.16 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
$\omega/2\theta$ scans
Absorption correction: none
2338 measured reflections
2094 independent reflections
1612 reflections with $I > 2\sigma(I)$
R_{int} = 0.018
θ_{max} = 26.0°
$h = 0 \rightarrow 8$
$k = -9 \rightarrow 9$
$l = -11 \rightarrow 12$
3 standard reflections
frequency: 60 min
intensity decay: 0.3%

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.030
$wR(F^2)$ = 0.095
S = 1.12
2094 reflections
141 parameters
Only H-atom displacement parameters refined
$w = 1/[\sigma^2(F_o^2) + (0.0655P)^2 + 0.0018P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.25 e Å^{-3}
$\Delta\rho_{min}$ = −0.16 e Å^{-3}
Extinction correction: none

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

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1···O1^{i}	0.86	2.11	2.9674 (15)	170
N3—H3···S^{ii}	0.92	2.47	3.3485 (14)	161

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

All H atoms were located in difference Fourier syntheses. They were refined with a riding model (N—H = 0.86 and 0.92 Å, and C—H = 0.89–1.00 Å), with individual isotropic displacement parameters.

Data collection: *CAD-4/PC* (Enraf–Nonius, 1993); cell refinement: *CAD-4/PC*; data reduction: *CAD-4/PC*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*.

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