Table 4. Hydrogen-bonding geometry (Å, °) for (II)

D—H···A	D—H	$\mathbf{H} \cdot \cdot \cdot \mathbf{A}$	$D \cdots A$	D — $H \cdot \cdot \cdot A$
N6-H61···O5 ^{'i}	0.84	2.33	3.077 (3)	149
N6-H62···O3 ^{/ ii}	0.84	2.20	3.025 (3)	170
O3'—H3'O· · ·N8	0.82	2.02	2.799 (3)	159
O5′—H5′O· · · N1 ⁱⁱⁱ	0.82	2.08	2.896 (3)	176
Symmetry codes: (i)	1 + x, 1	+ y, z; (ii) 1	$-x, \frac{1}{2} + y,$	$\frac{3}{7} - z$; (iii)

 $x = \frac{1}{2}, \frac{3}{2} = y, 1 = z.$

All H atoms were found in difference Fourier syntheses but were constructed in geometrically reasonable positions and refined with a common isotropic displacement parameter. With the absence of suitable anomalous scatterers within the molecules, the determination of the absolute configuration was not possible from our X-ray data. However, comparison with the configuration of the parent molecules indicates that the proposed conformations are correct.

For both compounds, data collection: XSCANS (Siemens, 1996); cell refinement: XSCANS; data reduction: SHELXTL (Sheldrick, 1997b); program(s) used to solve structures: SHELXS97 (Sheldrick, 1990); program(s) used to refine structures: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: KA1335). Services for accessing these data are described at the back of the journal.

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4-Phenyl-2,3,5,6,7,8-hexahydro-1*H*-pyrido-[1,2-*c*]pyrimidine-1,3-dione

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Abstract

In the structure of the title compound, $C_{14}H_{14}N_2O_2$, the saturated ring adopts a sofa conformation and the pyrimidine moiety is nearly planar. The mean planes of these fragments are close to coplanarity. The planar phenyl ring is twisted with respect to the pyrimidine-1,3dione fragment. The molecules form centrosymmetric dimers *via* intermolecular N—H···O hydrogen bonds.

Comment

The syntheses of the 4-aryl-hexahydro-1*H*-pyrido[1,2-c]pyrimidine-1,3-diones, (1)-(8), have been undertaken as a continuation of the search for new anxiolytic agents and studies on the relationship between structure and affinity to the 5-HT_{1A} receptor for those compounds. The compounds designed are structurally related to buspirone, a drug widely used in the treatment of mental diseases (Goa & Ward, 1986; Taylor & Moon, 1991; Faludi, 1994). Buspirone shows affinity to 5-HT_{1A}- and D₂-receptor types and is functionally a partial agonist of the 5-HT₁₄ receptors. Differences between the structures of buspirone and its new analogues are caused by a modification of the terminal imide moiety. It was noticed that as a result of this modification the lipophilicity of the molecule is higher and, consequently, the affinity to the 5-HT_{1A} receptor increases (Raghupathi et al., 1991; Lopez-Rodriguez et al., 1996; Lopez-Rodriguez, Morcillo et al., 1997; Lopez-Rodriguez, Rosado et al., 1997).



The present structural work has been undertaken to obtain more detailed information about the bond system and conformation of 4-phenyl-2,3,5,6,7,8-hexahydro-*1H*-pyrido[1,2-*c*]pyrimidine-1,3-dione, (1), one of the substrates in the synthesis of new analogues of buspirone.

The molecular structure of (1), showing the labelling scheme, is presented in Fig. 1. Bond lengths and valency angles agree with standard values for analogous derivatives (Taylor & Kennard, 1982; Yamagata *et al.*, 1985; Lenstra *et al.*, 1991; Suresh *et al.*, 1996). Insignificant distortions of the saturated ring result from disorder of this fragment of the molecule.



Fig. 1. A view of the title molecule showing the labelling scheme and disordered methylene groups. Displacement ellipsoids are drawn at the 30% probability level.

The C3=011 bond length is insignificantly longer than C1=010 (Table 1). The difference (*ca* 0.01 Å) could be induced by the intermolecular N2-H2···O11ⁱ hydrogen bond $[N \cdot \cdot O = 2.821 (2) Å$; symmetry code: (i) 1 - x, 1 - y, 1 - z] *via* which centrosymmetric dimers are formed. The atoms within and around this hydrogen bond (O11, C3, N2, H2 and symmetry-related atoms) form an eight-membered ring which is almost flat [maximum deviation from the best plane is 0.037 (5) Å for O11]. Both carbonyl groups, C1=O10 and C3=O11, are involved in the short intermolecular C-H···O contacts, which are a feature of the crystal packing of the molecules. The geometric parameters of all intermolecular hydrogen bonds are listed in Table 2.

The C6 and C7 atoms in the saturated ring were found to be disordered. The occupancies of the alternative positions were refined to 0.493 (9) (C6A/C7A) and 0.507 (9) (C6B/C7B). Similar disorder was found for respective methylene-C atoms in (4) and (7) (Herold, Maciejewska & Wolska, 1999) and in a compound related to (1) (Knoch *et al.*, 1995). In both disorder components, the piperidine ring adopts a sofa conformation with C7A and C6B displaced by 0.74 (1) and 0.71 (1) Å, respectively, from the plane formed by the remaining five atoms. The conformation of this ring with either C6A/C7A or C6B/C7B is slightly distorted from the typical sofa form, the asymmetry parameters according to Duax & Norton (1975) being $\Delta C_s = 6.8$ (3) and $\Delta C_s = 6.3$ (3)°, respectively.

This saturated ring is fused with the uracil moiety which is close to planarity [maximum deviations from the least-squares plane are 0.061 (1) Å for N9 and -0.060 (1) Å for C4]. The C5 and C8 atoms are above and C1' is below this plane by 0.027 (3), 0.252 (2) and -0.188 (2) Å, respectively. The best plane of the pyrimidine fragment is inclined to the mean piperidine planes formed by atoms C8/N9/C4a/C5/C6A and C8/N9/C4a/C5/C7B by only 5.1 (2) and 4.3 (2)°.

The disposition of the phenyl ring with respect to the pyrimidine-1,3-dione fragment can be described by the torsion angle C3—C4—C1'—C2' of 107.3 (2)°. The planar phenyl ring makes an angle of 72.24 (5)° with the plane of the above fragment. The aryl substituent at C4 cannot be coplanar with the pyrido[1,2-c]pyrimidine-1,3-dione system for steric reasons.

Experimental

The synthesis of the title compound is described elsewhere (Herold, Wolska *et al.*, 1999). Crystals were grown from acetic acid by slow evaporation.

Crystal data

$C_{14}H_{14}N_2O_2$	Cu $K\alpha$ radiation
$M_r = 242.27$	$\lambda = 1.54178 \text{ Å}$
Monoclinic	Cell parameters from 38
$P2_1/c$	reflections
a = 11.101 (2) Å	$\theta = 7.53 - 28.74^{\circ}$
b = 8.404(2) Å	$\mu = 0.743 \text{ mm}^{-1}$
c = 12.836(3) Å	T = 293 (2) K
$\beta = 92.68(3)^{\circ}$	Prism
$V = 1196.2(5) \text{ Å}^3$	$0.50 \times 0.20 \times 0.15$ mm
Z = 4	Colourless
$D_x = 1.345 \text{ Mg m}^{-3}$	
D_m not measured	

Data collection

$R_{\rm int} = 0.010$
$\theta_{\rm max} = 75.13^{\circ}$
$h = -13 \rightarrow 13$
$k = 0 \rightarrow 10$
$l = 0 \rightarrow 14$
3 standard reflections
every 100 reflections
intensity decay: 0.9%

Refinement

Refinement on F^2 $(\Delta/\sigma)_{max} = -0.009$ $R[F^2 > 2\sigma(F^2)] = 0.042$ $\Delta\rho_{max} = 0.210 \text{ e} \text{ Å}^{-3}$ $wR(F^2) = 0.119$ $\Delta\rho_{min} = -0.173 \text{ e} \text{ Å}^{-3}$

S = 1.102	Extinction correction:
2256 reflections	SHELXL93 (Sheldrick,
207 parameters	1993)
H atoms treated by a	Extinction coefficient:
mixture of independent	0.0085 (10)
and constrained refinement	Scattering factors from
$w = 1/[\sigma^2(F_o^2) + (0.0747P)^2]$	International Tables for
+ 0.2332P]	Crystallography (Vol. C)
where $P = (F_o^2 + 2F_c^2)/3$	

Table 1. Selected geometric parameters (Å, °)

1.216 (2)	C3-011	1.233 (2)
1.369 (2)	C4C4a	1.359 (2)
1.379 (2)		
115.44 (11)	C2'-C1'-C6'	118.72 (13)
115.14 (11)		
30.7 (3)	C6A—C7A—C8—N9	56.9 (6)
-0.9 (5)	C6B—C7B—C8—N9	-39.0(7)
34.5 (8)	C5-C4a-N9-C8	-5.0(2)
-62.3 (8)	C7A—C8—N9—C4a	-25.6 (4)
-58.0 (6)	C7B—C8—N9—C4a	10.1 (4)
62.8 (8)		
	$\begin{array}{c} 1.216\ (2)\\ 1.369\ (2)\\ 1.379\ (2)\\ 115.44\ (11)\\ 115.14\ (11)\\ 30.7\ (3)\\ -0.9\ (5)\\ 34.5\ (8)\\ -62.3\ (8)\\ -58.0\ (6)\\ 62.8\ (8)\\ \end{array}$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

Table 2. Hydrogen-bonding geometry (Å, °)

D—H···A	D—H	$\mathbf{H} \cdot \cdot \cdot \mathbf{A}$	$D \cdot \cdot \cdot A$	D—H···A
N2—H2···O11 ¹	0.90(2)	1.92 (2)	2.821 (2)	175 (2)
C2'—H2'···O10 ⁱⁱ	0.97 (2)	2.55 (2)	3.472 (2)	159(1)
C8—H8B· · · O11 ⁱⁱⁱ	0.97	2.52	3.450 (2)	159
C8—H8C···O11 ⁱⁱⁱ	0.97	2.55	3.450 (2)	154
C7A—H7C···O10 ^{iv}	0.97	2.81	3.430 (4)	122
C7 <i>B</i> —H7 <i>C</i> ···O10 ^{iv}	0.97	2.72	3.241 (4)	114
Symmetry codes: (i)	1 - x, 1 -	y, 1 - z; (i	i) $1 - x, -y$	z, 1 - z; (iii)

 $x, \frac{1}{2} - y, \frac{1}{2} + z;$ (iv) $1 - x, y - \frac{1}{2}, \frac{3}{2} - z.$

The H atoms in the piperidine ring were refined with a riding model and their U_{iso} values were set at $1.2U_{eq}$ of their carrier atoms. The other H atoms were refined isotropically [C—H distances in the range 0.96 (2)–1.00 (2) Å].

Data collection: Kuma KM-4 Software (Kuma, 1992). Cell refinement: Kuma KM-4 Software. Data reduction: Kuma KM-4 Software. Program(s) used to solve structure: SHELXS86 (Sheldrick, 1990). Program(s) used to refine structure: SHELXL93 (Sheldrick, 1993). Molecular graphics: Stereochemical Workstation Operation Manual (Siemens, 1989). Software used to prepare material for publication: SHELXL93.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: JZ1351). Services for accessing these data are described at the back of the journal.

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Salannin and 3-deacetylsalannin

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Abstract

The crystal structures of two tetranortriterpenoids, salannin $[C_{34}H_{44}O_9, (I)]$ and 3-deacetylsalannin $[C_{32}H_{42}O_8, (II)]$, are described. The orientation and conformation of the tigloyl (2-methyl-2-butenoyl) group, the carbomethoxy group and ring *E* are different in the two structures. The molecular packing depends on C—H···O hydrogen bonds in (I) and on O—H···O hydrogen bonds in (II). A comparison of the structural features indicates that the conformations of large parts of the molecules are similar to those in azadirachtins.

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