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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.002 Å R factor = 0.046 wR factor = 0.139 Data-to-parameter ratio = 17.0

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

7-Allyl-1,3-dimethyl-2,4-dioxo-2,3,4,7tetrahydro-1*H*-pyrrolo[2,3-*d*]pyrimidine-

6-carbaldehyde

The five-membered ring in the title compound, $C_{12}H_{13}N_3O_3$, is planar and the six-membered ring is slightly non-planar, with one N atom deviating by 0.075 (1) Å. The molecule is stabilized by $C-H\cdots O$ and $C-H\cdots N$ intramolecular interactions. The crystal packing is stabilized by $C-H\cdots O$ intermolecular interactions generating a centrosymmetric dimer with an $R_2^2(10)$ ring.

Comment

Pyrrolo[2,3-*d*]pyrimidines are known to possess considerable antitumour, anti-allergic, antiviral and anti-inflammatory activities (Hutzenlaub *et al.*, 1972; Smith *et al.*, 1972). Pyrrolo[2,3-*d*]pyrimidine nucleosides act as inhibitors of human cytomegalovirus (Turk *et al.*, 1987). It is reported that pyrrolo[2,3-*d*]pyrimidine-based antifolate inhibits multiple folate-requiring enzymes (Shih *et al.*, 1997). As the title compound, (I), is of high medicinal value, we have undertaken the three-dimensional structure determination by X-ray diffraction (Fig. 1).



The bond geometry of (I) is comparable with reported values (Allen *et al.*, 1987). The sums of the bond angles around atoms N1, N2 and N3 [360.0, 360.0 and 359.5°, respectively] indicate the sp^2 hydribization of all the N atoms in the structure. The five-membered ring in the structure is planar. The torsion angles around N3-C6-C7-O3 [0.0 (3)°] and C5-C6-C7-O3 [-180.0 (2)°] indicate that the aldehyde group lies in the plane of the five-membered ring. The six-membered ring in the structure is slightly non-planar, with atom N1 deviating by 0.075 (1) Å from the plane of the remaining atoms in the ring. Atoms O1 and C12 lie below and atoms O2 and C11 lie above the plane of C2/N2/C3/C4/C1 by 0.051 (1), 0.084 (2), 0.057 (1) and 0.269 (2) Å, respectively.

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organic papers

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The molecular structure of compound (I), showing 30% probability displacement ellipsoids.

The molecule of (I) is stabilized by weak $C-H\cdots O$ and $C-H\cdots N$ intramolecular interactions. The crystal packing is stabilized by $C-H\cdots O$ intermolecular interactions (Table 1). Atom C5 acts as a donor to atom O2(1 - x, -y, 1 - z), generating a centrosymmetric dimer with an $R_2^2(10)$ ring (Bernstein *et al.*, 1995) centred at $(\frac{1}{2}, 0, \frac{1}{2})$. These dimers run along the *bc* plane.

Experimental

2,3,4,7-Tetrahydro-1,3-dimethyl-2,4-dioxo-1*H*-pyrrolo[2,3-*d*]pyrimidine-6-carbaldehyde (1 equivalent) and allyl bromide (1.2 equivalents) were stirred with K₂CO₃ (2.5 equivalents) in dry dimethylformamide (25 ml) at room temperature for 12 h, and then the reaction mixture was poured into water and extracted with ethyl acetate. The organic layer was dried over Na₂SO₄ and evaporated to give a residue, which was purified by column chromatrography using hexane–ethyl acetate (3:1 ν/ν) as eluant. Pure compound (I) was crystallized from ethyl acetate by slow evaporation.

Crystal data

$C_{12}H_{13}N_3O_3$
$M_r = 247.25$
Monoclinic, $P2_1/n$
a = 6.7065 (4) Å
b = 13.1295 (9) Å
c = 13.6977 (9) Å
$\beta = 99.613 \ (1)^{\circ}$

Data collection

Bruker SMART APEX CCD areadetector diffractometer Absorption correction: none 13428 measured reflections

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.046$ $wR(F^2) = 0.139$ S = 1.032810 reflections $V = 1189.19 (13) Å^{3}$ Z = 4 Mo K\alpha radiation \mu = 0.10 mm^{-1} T = 293 (2) K 0.24 \times 0.22 \times 0.21 mm

2810 independent reflections 2489 reflections with $I > 2\sigma(I)$ $R_{int} = 0.017$

165 parameters H-atom parameters constrained $\Delta \rho_{max} = 0.25$ e Å⁻³ $\Delta \rho_{min} = -0.19$ e Å⁻³



Figure 2

The molecular packing of (I), viewed approximately along the a axis. For clarity, H atoms not involved in hydrogen bonding (dashed lines) have been omitted.

Table 1Hydrogen-bond geometry (Å, °).

0.02			
0.95	2.37	3.237 (2)	155
0.97	2.26	2.987 (2)	131
0.93	2.52	2.848 (2)	101
0.96	2.25	2.671 (2)	106
0.96	2.30	2.684 (2)	103
	0.93 0.97 0.93 0.96 0.96	0.93 2.37 0.97 2.26 0.93 2.52 0.96 2.25 0.96 2.30	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

Symmetry code: (i) -x + 1, -y, -z + 1.

All H atoms were refined using a riding model, with C-H = 0.93–0.97 Å and $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(C)$.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97* and *PARST* (Nardelli, 1995).

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