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Key indicators

Single-crystal X-ray study T = 296 KMean σ (C–C) = 0.007 Å R factor = 0.043 wR factor = 0.120 Data-to-parameter ratio = 16.5

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

© 2001 International Union of Crystallography Printed in Great Britain – all rights reserved 7-(4-Bromophenyl)-5-cyanomethyl-1,3-dimethylpyrido[2,3-*d*]pyrimidine-2,4-dione

The positions of the cyanomethyl and 4-bromophenyl substituents in the title compound, $C_{17}H_{13}BrN_4O_2$, have been confirmed by single-crystal X-ray structure determination. The crystal packing shows weak hydrogen-bonding and aromatic π - π interactions.

Comment

The therapeutic importance (Furuya & Ohataki, 1994*a,b*; Heber *et al.*, 1993; Piper *et al.*, 1989) of suitably functionalized pyrido[2,3-*d*]pyrimidine ring systems encouraged us to develop an innovative synthesis in which different substituents could be arranged in a pharmacophoric pattern to display diverse pharmacological activities of higher order. The title compound, (I), was prepared (Srivastava *et al.*, 2000) by ringtransformation reactions of 6-aryl-3-cyano-4-methylthio-2*H*pyran-2-one and 6-amino-1,3-dimethyluracil. The present X-ray crystallography study has been undertaken to confirm the structure of (I).



The conformation of (I) along with the atom-numbering scheme is shown in Fig. 1. The molecule contains one fusedring system (A/B) to which a bromophenyl ring (C) is attached at the 7 position. All the rings are planar [deviations of the atoms from their least-squares planes are within the range -0.015 (3)-0.011 (3) Å]. The bromophenyl ring is coplanar with the A/B ring system [torsion angle N8-C7-C71-C72 $-179.0 (4)^{\circ}$]. The cyano group is twisted out of the A/B plane. The crystal structure analysis reveals the presence of weak hydrogen-bonding interactions, such as $C-H \cdots N$, $C-H \cdots Br$ and $C-H \cdots O$ (Fig. 2 and Table 1). Moreover, the crystal packing (Fig. 3) also shows intermolecular stacking as a result of π - π interactions between rings *B* and *C* (Hunter & Sanders, 1990). The overlapping rings (B and C) are in a 'paralleldisplaced orientation'; the average distance of separation between their mean planes is 3.480 (6) Å, the angle between them being $1.0 (3)^{\circ}$. The different intermolecular interactions seen in the crystal structure of (I) might well be a reflection of the possible interactions in the molecular recognition process Received 13 March 2001 Accepted 20 March 2001 Online 12 April 2001

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Figure 1

ORTEP (Johnson, 1965) diagram showing the molecular structure of (I) with labelling for non-H atoms and displacement ellipsoids at the 50% probability level.

in view of the diverse pharmacological properties associated with the suitably functionalized pyrido [2,3-d] pyrimidines.

Experimental

The synthesis of (I) was carried out by reaction of 6-amino-1,3-dimethyluracil with 6-(4-bromophenyl)-3-cyano-4-methylthio-2Hpyran-2-one (Srivastava et al., 2000). Diffraction-quality crystals were grown by slow evaporation from a solution in a dichloromethaneethyl acetate mixture at room temperature.

Crystal data

$C_{17}H_{13}BrN_4O_2$	Z = 2
$M_r = 385.22$	$D_x = 1.628 \text{ Mg m}^{-3}$
Triclinic, P1	Mo $K\alpha$ radiation
a = 8.728 (3) Å	Cell parameters from 24
$b = 12.087 (4) \text{\AA}$	reflections
c = 8.672 (3) Å	$\theta = 14.7 - 15.0^{\circ}$
$\alpha = 108.22 \ (3)^{\circ}$	$\mu = 2.63 \text{ mm}^{-1}$
$\beta = 113.43 \ (2)^{\circ}$	T = 296 (2) K
$\gamma = 91.24 \ (3)^{\circ}$	Block, colourless
$V = 786.1 (5) \text{ Å}^3$	$0.4 \times 0.3 \times 0.1 \text{ mm}$



Figure 2

PLUTO (Motherwell & Clegg, 1978) crystal-packing diagram showing the C-H···O hydrogen bonds as dotted lines and the C-H···Br hydrogen bonds as dashed lines.



Figure 3

The crystal packing (perpendicular view to the plane through atoms C6, C7 and N8 of ring B) showing the partial overlapping (as indicated by black shading) of rings B and C owing to intermolecular stacking.

Data collection

Rigaku AFC-5R diffractometer ω –2 θ scans Absorption correction: empirical (TEXSAN; Molecular Structure Corporation/Rigaku Corporation, 1998) $T_{\rm min}=0.509,\ T_{\rm max}=0.769$ 3619 measured reflections 3619 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.043$ $wR(F^2) = 0.120$ S = 1.083616 reflections 219 parameters H-atom parameters constrained 2254 reflections with $I > 2\sigma(I)$ $\theta_{\rm max} = 27.5^{\circ}$ $h = -11 \rightarrow 11$ $k = -15 \rightarrow 0$ $l = -10 \rightarrow 11$ 3 standard reflections every 150 reflections intensity decay: <0.2%

 $w = 1/[\sigma^2(F_o^2) + (0.0669P)^2]$ + 0.8316P] where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.48 \ {\rm e} \ {\rm \AA}^{-3}$ $\Delta \rho_{\rm min} = -0.43 \ {\rm e} \ {\rm \AA}^{-3}$

Table 1 Hydrogen-bonding geometry

Hydrogen-bonding geometry (Å, $^{\circ}$).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$C31-H31B\cdots Br^{i}$	0.96	3.07	3.701 (5)	125
$C31 - H31B \cdot \cdot \cdot N8^{ii}$	0.96	2.81	3.639 (6)	145
C31-H31C···O41 ⁱⁱⁱ	0.96	2.66	3.600 (6)	166
C6-H6···N53 ^{iv}	0.93	2.76	3.565 (7)	146
$C72-H72 \cdot \cdot \cdot N53^{iv}$	0.93	2.65	3.476 (7)	148
$C73-H73\cdots O21^{v}$	0.93	2.32	3.223 (6)	165

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

All the H atoms were placed in geometrically idealized positions and allowed to ride on their parent atoms.

Data collection and cell refinement: *Rigaku/AFC Diffractometer Control Software* (Rigaku, 1995); data reduction: *TEXSAN* (Molecular Structure Corporation/Rigaku Corporation, 1998); program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993); molecular graphics: *NRCVAX* (Gabe *et al.*, 1989); software used to prepare material for publication: *SHELXL*93.

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