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#### **Key indicators**

Single-crystal X-ray study T = 110 KMean  $\sigma(\text{C-C}) = 0.004 \text{ Å}$ Disorder in solvent or counterion R factor = 0.036 wR factor = 0.106 Data-to-parameter ratio = 12.1

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

# 6-(2-Bromobenzylamino)purine monohydrate

The structure of the title compound,  $C_{12}H_{12}N_5BrO\cdot H_2O$ , consists of discrete molecules connected by  $N-H\cdots N$ hydrogen bonds to form centrosymmetric dimers, with an  $N\cdots N$  distance of 2.839 (4) Å. The solvent water molecules are linked by intermolecular  $O-H\cdots O$  hydrogen bonds into infinite chains along the [001] direction. The water molecules with disordered H atoms also participate in  $O-H\cdots O$ , N- $H\cdots O$  and  $O-H\cdots N$  hydrogen bonds, with  $O\cdots O$ ,  $N\cdots O$ and  $O\cdots N$  distances of 2.728 (5) and 2.732 (5), 3.107 (3) and 2.748 (3) Å, respectively. In addition to conventional hydrogen bonds, there are several weak interatomic contacts of the type  $C\cdots Br$ , and  $\pi$ -stacking interactions of the types  $C\cdots C$  and  $N\cdots C$ .

## Comment

The correlation between the structures and biological activities of plant growth hormones (cytokinins) and cyclindependent kinase inhibitors (CDKs) derived from 6-benzylaminopurine is under systematic investigation (Trávníček *et al.*, 2001; Trávníček & Kryštof, 2004; Szučová *et al.*, 2006). To expand on previous studies concerning the X-ray structures of known cytokinins and CDKs, the structure of the title compound, (I), has been elucidated.



The structure of (I) (Fig. 1) contains 6-(2-bromobenzylamino)purine (BAP) molecules with nearly planar benzene (A), pyrimidine (B), and imidazole (C) ring systems, with maximum deviations from the mean planes of 0.005 (3) for atom C10, 0.013 (3) for atom C6 and 0.005 (3) Å for atom C5 (*DIAMOND*; Brandenburg, 2006). Atoms forming the purine system (B+C) also deviate slightly from planarity, the greatest deviation being 0.020 (3) Å for atom N1. Planes B and C are nearly coplanar, with a dihedral angle of 1.3 (1)°. The mean

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### Figure 1

The asymmetric unit of (I), with displacement ellipsoids drawn at the 50% probability level. Dashed lines indicate hydrogen bonds. One of the water H atoms was treated as disordered over two positions with equal occupancies (both are shown).



#### Figure 2

Part of the crystal packing of (I). Dashed lines indicate hydrogen bonds. Some H atoms have been omitted for clarity.

planes of the nearly planar benzene ring (A) and purine system (B+C) make a dihedral angle of 70.23 (9)°. If CgA, CgB and CgC are the centroids of rings A, B and C, respectively, then the  $CgA\cdots CgB$ ,  $CgA\cdots CgC$  and  $CgB\cdots CgC$ distances are subsequently 5.7757 (4), 6.8687 (5) and 2.0802 (1) Å. The bond lengths and angles in (I) (Table 1) are quite comparable with those found for 6-(benzylamino)purine (Raghunathan et al., 1983), 6-(2-chlorobenzylamino)purine (Trávníček et al., 2001), and 6-(2-chloro-4-fluorobenzylamino)purine (Trávníček et al., 2006).

The crystal structure of (I) is stabilized by  $N-H\cdots N$ hydrogen bonds connecting two adjacent BAP molecules to form centrosymmetric dimers (Fig. 2 and Table 2). The BAP molecule is also connected through  $O-H \cdots N$  and  $N-H \cdots O$ hydrogen bonds to one solvent water molecule. The water molecules, each with one H atom disordered, are linked by  $O_{water}{-}H{\cdots}O_{water}$  hydrogen bonds into infinite chains along the [001] direction. Part of the crystal structure of (I) is depicted in Fig. 2.

In addition to conventional hydrogen bonds, there are several weak interatomic contacts of the type C...Br  $[C5 \cdots Br1^{iv} = 3.517(3) \text{ and } C6 \cdots Br1^{iv} = 3.377(3) \text{ Å};$ symmetry code: (iv)  $-x + \frac{3}{2}$ , -y + 1, -z + 2] and  $\pi - \pi$  stacking interactions of the type  $N \cdots C$  and  $C \cdots C$   $[N9 \cdots C6^{v} =$ 3.713 (4),  $C4 \cdot \cdot \cdot C4^{v} = 3.320$  (5) and  $C8 \cdot \cdot \cdot C6^{v} = 3.383$  (4) Å; symmetry code: (v) -x + 1,  $y, -z + \frac{3}{2}$ ].

## **Experimental**

All chemicals were acquired from commercial sources: 6-chloropurine (Sigma), Et<sub>2</sub>O and *n*-BuOH (Lachema), and Et<sub>3</sub>N and 2bromobenzylamine hydrochloride (Acros Organics). The title compound was prepared from a mixture of 6-chloropurine (23 mmol) and 2-bromobenzylamine hydrochloride (20 mmol) in n-butanol (130 ml), to which Et<sub>3</sub>N (10 ml, 72 mmol) was added. The reaction mixture was heated to 363 K and stirred for 4.5 h. The mixture was then chilled to 273 K. After 16 h, the resulting precipate was filtered off and washed with cold H<sub>2</sub>O (50 ml) and Et<sub>2</sub>O (30 ml). The mother liquor was allowed to evaporate for approximately 5 d, during which time pale-yellow microcrystals containing several well developed single crystals, suitable for X-ray analysis, formed and were separated by filtration. The crystals were washed with Et<sub>2</sub>O and dried for 1 h at 343 K.

## Crystal data

$C_{12}H_{10}BrN_5 \cdot H_2O$	Z = 8
$M_r = 322.18$	$D_x = 1.721 \text{ Mg m}^{-3}$
Monoclinic, $C2/c$	Mo $K\alpha$ radiation
a = 21.9381 (15)  Å	$\mu = 3.31 \text{ mm}^{-1}$
b = 15.1277 (15)  Å	T = 110 (2) K
c = 7.6320 (5) Å	Prism, colourless
$\beta = 100.877 \ (9)^{\circ}$	$0.35 \times 0.25 \times 0.25$ mm
V = 2487.4 (3) Å <sup>3</sup>	

## Data collection

Oxford Xcalibur diffractometer  $\omega$  scans Absorption correction: multi-scan (Blessing, 1995)  $T_{\min} = 0.399, T_{\max} = 0.438$ 

# Refinement

Refinement on  $F^2$ 

 $R[F^2 > 2\sigma(F^2)] = 0.036$  $wR(F^2) = 0.106$ S = 1.142192 reflections

- 181 parameters
- H atoms treated by a mixture of independent and constrained

refinement

8154 measured reflections 2192 independent reflections 2034 reflections with  $I > 2\sigma(I)$  $R_{\rm int} = 0.042$  $\theta_{\rm max} = 25.1^\circ$ 

$w = 1/[\sigma^2(F_o^2) + (0.0683P)^2]$
+ 3.1343 <i>P</i> ]
where $P = (F_0^2 + 2F_c^2)/3$
$\Delta/\sigma)_{\rm max} = 0.001$
$\Delta \rho_{\rm max} = 0.73 \text{ e } \text{\AA}^{-3}$
$\Delta \rho_{\rm min} = -0.42 \ {\rm e} \ {\rm \AA}^{-3}$

Table 1Selected geometric parameters (Å, °).

Br1-C11	1.901 (3)	N7-C8	1.311 (4)
N1-C2	1.333 (4)	N7-C5	1.378 (4)
N1-C6	1.347 (4)	N9-C8	1.349 (4)
N3-C2	1.326 (4)	N9-C4	1.366 (4)
N3-C4	1.346 (4)	C4-C5	1.383 (4)
N6-C6	1.353 (4)	C5-C6	1.406 (4)
N6-C9	1.429 (4)		
C2-N1-C6	118.4 (3)	N3-C4-C5	126.1 (3)
C2-N3-C4	111.2 (3)	N9-C4-C5	105.8 (3)
C6-N6-C9	122.9 (3)	N7-C5-C4	110.1 (3)
C8-N7-C5	104.0(2)	N7-C5-C6	133.1 (3)
C8-N9-C4	106.1 (3)	C4-C5-C6	116.9 (3)
N3-C2-N1	129.2 (3)	N1-C6-C5	118.1 (3)
N3-C4-N9	128.0 (3)	N7-C8-N9	113.9 (3)
C9-N6-C6-N1	-6.8(4)	N6-C9-C10-C15	9.4 (4)
C6-N6-C9-C10	106.9 (3)		

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
N6-H6A···O1	0.88	2.25	3.107 (4)	163
$O1 - H1W \cdots N7$	0.89 (3)	1.86 (3)	2.748 (3)	172 (5)
N9-H9A···N3 <sup>i</sup>	0.88	1.97	2.838 (4)	169
$O1-H1VA\cdots O1^{ii}$	0.93 (3)	1.81 (3)	2.728 (5)	170 (8)
$O1-H1VB\cdots O1^{iii}$	0.92 (3)	1.83 (3)	2.732 (5)	167 (9)
Symmetry codes: (i) $-x + 1, -y, -z + 2;$ (ii) $-x + 1, y, -z + \frac{3}{2};$ (ii)				

-x + 1, -y + 1, -z + 2.

All H atoms of the organic molecule were located in a difference map and refined using a riding model, with C-H distances of 0.95 and 0.99 Å, N-H distances of 0.88 Å, and  $U_{iso}(H) = 1.2U_{ca}(C,N)$ . H atoms attached to atom O1 were refined freely with a fixed  $U_{eq}$  parameter. Atom H1V, involved in the O1-H1VA···O1<sup>ii</sup> and O1-H1VB···O<sup>iii</sup> intermolecular hydrogen bonds [symmetry codes: (ii) -x + 1, y,  $-z + \frac{3}{2}$ , (iii) -x + 1, -y + 1, -z + 2], was treated as disordered over two positions with equal occupancies.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2002); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2002); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SIR2002* (Burla *et al.*, 2002); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 2006); software used to prepare material for publication: *SHELXL97* and *DIAMOND*.

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