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#### **Key indicators**

Single-crystal X-ray study T = 297 K Mean  $\sigma$ (C–C) = 0.002 Å R factor = 0.042 wR factor = 0.117 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. The molecule of the title compound,  $C_6H_8N_2O$ , is almost planar; the hydroxymethyl group deviates slightly from the plane of the ring. The molecules are linked into a chain running along the *a*-axis direction by an  $O-H\cdots N$  hydrogen bond.  $N-H\cdots O$  and  $N-H\cdots N$  hydrogen bonds connect the chains, forming a molecular layer parallel to the (001) plane. A  $C-H\cdots \pi$  interaction is also observed in the layer.

2-Amino-6-(hydroxymethyl)pyridine

## Comment

The role of hydrogen bonds involving the NH group and a carbonyl O atom in the controlled assembly of biologically relevant architectures in nature has been reported; two- and three-dimensional molecular networks (Felix et al., 1997), extended sheet structures (Zhao et al., 1990), columnar networks (Kinbara et al., 1996), molecular tapes (Zerowski et al., 1990) and helical aggregates (Sanchez-Quesada et al., 1996) exemplify the different architectures in crystal engineering. From these numerous reports dealing with the role of hydrogen bonding in the process of molecular recognition, self-assembled dimerization and self-assembled polymerization are useful tools for a supramolecular chemist. The title compound, (I), is an important hydrogen-bonding synthon as it is a very useful substrate for the synthesis of designed receptors in the fields of molecular recognition (Goswami, Dey, Maity & Jana, 2005; Goswami, Dey, Fun et al., 2005) and supramolecular chemistry (Lehn, 1995; Steed & Atwood, 2001). The crystal structure of (I) has been determined as part of our crystal engineering research since it is a simple design for generating a supramolecular three-dimensional assembly in solid-state crystal engineering.



The bond lengths and angles of (I) are normal (Allen *et al.*, 1987). The hydroxymethyl group deviates slightly from the molecular ring plane, as indicated by the C4-C5-C6-O1 torsion angle of 10.67 (17)° (Fig. 1). The solid state structure of (I) has several interesting hydrogen bonds due to the fact that (I) contains one alcohol and one primary amino group attached to the pyridine ring. All the H atoms attached to O and N take part in the complementary dimerization as well as in the supramolecular array.

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## Figure 1

The molecular structure of (I), showing 40% probability displacement ellipsoids and the atomic numbering.





The crystal packing (Fig. 2) shows that the alcohol H atom is hydrogen-bonded to the amine N atom  $[O1-H1O1\cdots N2^{i}]$ ; symmetry code: (i) -1 + x, y, z], forming a chain along the a axis. The alcohol O atom forms a hydrogen bond with the amine H atom  $[N2-H2N2\cdotsO1^{ii};$  symmetry code: (ii) 1 + x, 1 + y, z, which connects neighboring chains related by translation along the b axis. There are two complementary hydrogen-bonding units for dimerization; one of the amine H atoms (H1N2) and the ring N atom (N1) are complementarily hydrogen-bonded to the neighboring molecule in the same plane  $[N2-H1N2\cdots N1^{iii};$  symmetry code: (iii) 1 - x, 1 - y,-z] (Table 2). Therefore dimerization as well as threedimensional propagation are simultaneously observed in the solid-state structure of (I). A C-H $\cdots\pi$  interaction is also observed (Table 2).

## **Experimental**

A mixture of 2-N-pivalovlamino-6-bromomethylpyridine (0.5 g. 1.84 mmol) and sodium acetate (0.38 g, 4.6 mmol) was refluxed in acetonitrile (10 ml) for 8 h. The intermediate compound, 6-(2,2dimethyl-propionylamino)-pyridin-2-ylmethyl acetate was then refluxed with 10% NaOH (H2O-EtOH 1:1) for 6 h to afford compound (I). Single crystals of (I) were grown by slow evaporation of a CH<sub>3</sub>OH/CHCl<sub>3</sub> (v/v 1:5) solution.

Crystal data

$C_6H_8N_2O$	Z = 4
$M_r = 124.14$	$D_x = 1.295 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
a = 6.9279 (2) Å	$\mu = 0.09 \text{ mm}^{-1}$
b = 4.7570(1) Å	T = 297 (2) K
c = 19.3436 (5) Å	Block, colorless
$\beta = 92.657 \ (2)^{\circ}$	$0.44 \times 0.36 \times 0.23 \text{ mm}$
$V = 636.80(3) \text{ Å}^3$	

#### Data collection

Bruker SMART APEX2 CCD areadetector diffractometer  $\omega$  scans Absorption correction: multi-scan (SADABS; Bruker, 2005)  $T_{\rm min} = 0.961, \ T_{\rm max} = 0.979$ 

# Refinement

Refinement on  $F^2$  $R[F^2 > 2\sigma(F^2)] = 0.042$  $wR(F^2) = 0.117$ S = 1.041699 reflections 114 parameters All H-atom parameters refined

# $\theta_{\rm max} = 29.0^{\circ}$ $w = 1/[\sigma^2(F_0^2) + (0.0591P)^2]$

8090 measured reflections

 $R_{\rm int} = 0.024$ 

1699 independent reflections 1373 reflections with  $I > 2\sigma(I)$ 

+ 0.0978P] where  $P = (F_0^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\rm max} < 0.001_{\circ}$  $\Delta \rho_{\rm max} = 0.17 \text{ e } \text{\AA}^{-3}$  $\Delta \rho_{\rm min} = -0.22 \text{ e} \text{ Å}^{-3}$ 

# Table 1

Selected geometric parameters (Å, °).

O1-C6	1.4156 (14)	N1-C5	1.3460 (13)
N1-C1	1.3353 (14)	N2-C1	1.3850 (14)
C1-N1-C5	118.24 (9)	N2 - C1 - C2	120.48 (10)
N1-C1-N2	116.98 (10)	O1-C6-C5	114.14 (10)
C5-N1-C1-N2	176.38 (10)	N1-C5-C6-O1	-170.27 (10)
N2-C1-C2-C3	-176.45 (11)	C4-C5-C6-O1	10.67 (17)
C3-C4-C5-C6	179.40 (11)		

able 2		
	Is a set	

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$O1-H1O1\cdots N2^{i}$	0.89 (2)	2.00 (2)	2.8837 (16)	175 (2)
$N2 - H2N2 \cdot \cdot \cdot O1^{ii}$	0.889 (18)	2.113 (18)	2.9991 (16)	174.5 (15)
$N2-H1N2 \cdot \cdot \cdot N1^{iii}$	0.883 (17)	2.209 (17)	3.0745 (15)	166.5 (13)
$C6-H6A\cdots Cg1^{iv}$	0.971 (16)	2.711 (17)	3.6257 (14)	156.8 (12)

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

All H atoms were located in a difference map and refined isotropically. The O-H, N-H and C-H bond lengths are 0.89 (2), 0.883 (17)–0.889 (19) and 0.954 (15)–0.992 (17) Å, respectively.

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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