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#### **Key indicators**

Single-crystal X-ray study T = 150 KMean  $\sigma(C-C) = 0.002 \text{ Å}$  R factor = 0.043 wR factor = 0.097Data-to-parameter ratio = 15.0

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

# (2-Pyridylmethyl)ammonium nitrate

The single-crystal structure of (2-pyridylmethyl)ammonium nitrate,  $C_6H_9N_2^+\cdot NO_3^-$ , is presented, in what is only the third reported structure containing this cation. The structure contains extensively hydrogen-bonded layers.

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#### Comment

During research into novel chelating ligands, the crystal structure of the title compound, (I), was determined (Fig. 1). The structure of the (2-pyridylmethyl)ammonium cation has only been determined twice previously, once in a silver nitrate complex (Sailaja *et al.*, 2001) and once as the pyridine-2-carboxylate salt (Døssing *et al.*, 2001). In both of these structures, four hydrogen bonds were formed from the ammonium group.

In (I), five hydrogen bonds are formed between the ammonium group and nitrate O atoms. These bonds, with  $D-H\cdots A$  distances of between 2.8237 (19) and 3.110 (2) Å, are comparable with the bonds reported in the AgNO<sub>3</sub> complex, and cause the formation of a two-dimensional network with the b and c axes as the base vectors (Fig. 2).

## **Experimental**

2-(Aminomethyl)pyridine (2.16 g, 0.02 mol) was dissolved in ethanol (5 ml) and added to a stirred ethanol solution of *o*-vanillin (3.04 g, 0.02 mol). The reaction mixture was stirred overnight. The solvent was removed using a rotary evaporator to give a red residue, which was recrystallized from the minimum amount of hot methanol, yielding good quality single crystals.

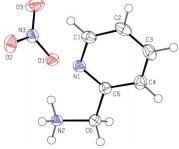


Figure 1
View of the title compound, with the atom-numbering scheme.
Displacement ellipsoids for non-H atoms are drawn at the 50% probability level.

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# organic papers

### Crystal data

$C_6H_9N_2^+\cdot NO_3^-$	Mo $K\alpha$ radiation
$M_r = 171.16$	Cell parameters from 59
Monoclinic, $P2_1/c$	reflections, based on $\psi$ - $\chi$ scan
a = 8.2492 (4)  Å	(Duisenberg et al., 2000)
b = 10.4014 (5)  Å	$\theta = 5.5 - 20.8^{\circ}$
c = 9.3850 (5)  Å	$\mu = 0.12 \text{ mm}^{-1}$
$\beta = 105.171 (4)^{\circ}$	T = 150 (2)  K
$V = 777.20 \ (7) \ \text{Å}^3$	Block, colourless
Z = 4	$0.2 \times 0.1 \times 0.1 \text{ mm}$
$D_x = 1.463 \text{ Mg m}^{-3}$	

#### Data collection

Nonius KappaCCD diffractometer	$R_{\rm int} = 0.057$
$\varphi$ and $\omega$ scans	$\theta_{\rm max} = 27.4^{\circ}$
Absorption correction: none	$h = -10 \rightarrow 10$
18 148 measured reflections	$k = -13 \rightarrow 13$
1774 independent reflections	$l = -12 \rightarrow 12$
1228 reflections with $I > 2\sigma(I)$	

#### Refinement

Кејтетет	
Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0364P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.043$	+ 0.3509P
$wR(F^2) = 0.097$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.05	$(\Delta/\sigma)_{\rm max} < 0.001$
1774 reflections	$\Delta \rho_{\text{max}} = 0.19 \text{ e Å}^{-3}$
118 parameters	$\Delta \rho_{\min} = -0.23 \text{ e Å}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

Table 1 Hydrogen-bonding geometry (Å, °).

$D-H\cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
N2−H2A···O2 <sup>i</sup>	0.958 (19)	2.155 (18)	2.8817 (19)	131.7 (15)
$N2-H2A\cdots N1^{i}$	0.958 (19)	2.345 (18)	3.037 (2)	128.7 (13)
$N2-H2B\cdots O1^{ii}$	0.925 (18)	1.931 (18)	2.8237 (19)	161.4 (16)
$N2-H2B\cdots O3^{ii}$	0.925 (18)	2.440 (19)	3.110(2)	129.3 (15)
$N2-H2C\cdots O1$	0.942 (18)	1.923 (18)	2.8412 (18)	164.3 (16)

Symmetry codes: (i) 1 - x, 1 - y, -z; (ii) x,  $\frac{1}{2} - y$ ,  $z - \frac{1}{2}$ 

The aromatic H atoms were placed in geometrically idealized positions (C-H = 0.95 Å) and constrained to ride on their parent atoms with  $U_{iso}(H) = 1.2U_{eq}(C)$ . The H atoms on the N atom were found in a difference electron-density map and refined with  $U_{iso}$  =  $1.5U_{\rm eq}(N)$ .

Data collection: COLLECT (Nonius, 1998); cell refinement: DIRAX (Duisenberg, 1992); data reduction: EvalCCD (Duisenberg et al., 2003); program(s) used to solve structure: SHELXS86 (Shel-

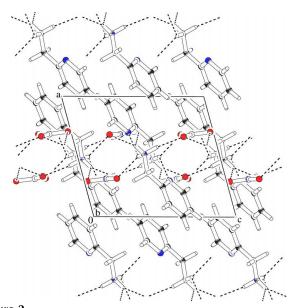


Figure 2 The two-dimensional network structure of (I). Hydrogen bonds are shown as dashed lines.

drick, 1985); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: PLATON (Spek, 2003); software used to prepare material for publication: PLATON.

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