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#### Key indicators

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.004 Å R factor = 0.049 wR factor = 0.118 Data-to-parameter ratio = 12.7

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

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# 4-[*N,N*-Bis(2-cyanoethyl)amino]pyridinium perchlorate

In the title compound,  $C_{11}H_{13}N_4^+ \cdot ClO_4^-$ , the planar geometry around the amino N atom in the cation suggests conjugation with the  $\pi$ -system of the pyridine ring. N-H···O, C-H···O and C-H···N hydrogen-bonding interactions play a key role in the crystal packing. Received 26 September 2003 Accepted 30 September 2003 Online 15 October 2003

## Comment

The synthesis of 4-(N,N-dimethylamino)pyridine (DMAP) has attracted much attention for its excellent catalytic properties in many organic reactions (Höfle *et al.*, 1978; Scriven, 1983; Steglich & Hoefle, 1969). Its derivatives also display catalytic properties (Huang *et al.*, 1994; Scriven, 1983). In our present research, we find that 4-[N,N-bis(2-cyanoethyl)-amino]pyridine (CEAP) can catalyse an acylation reaction. As part of our research on CEAP and its derivatives, we prepared the title compound, (I). As a derivative of DMAP, compound (I) also has potential catalytic properties in organic reactions.



The title compound, (I), consists of a protonated 4-[N,Nbis(2-cyanoethyl)amino]pyridinium cation and a ClO<sub>4</sub><sup>-</sup> anion (Fig. 1). The sum of the bond angles around amino atom N2 is 360° (Table 1), as observed in aminopyridines and their derivatives (Chao *et al.*, 1977; Ohms & Guth, 1983). The N2–C3 bond length of 1.340 (3) Å is shorter than the corresponding bond length in CEAP [1.374 (3) A; Ni, Li, Qi et al., 2003] and in its Ag complex [1.358 (5)-1.385 (5) Å; Ni, Li, Xue et al., 2003]. This geometric conformation reflects conjugation between the lone pair of N2 and the  $\pi$  system of the pyridine ring (Chao & Schempp, 1977). The protonation makes this conjugation more strong. The Cl-O distances in the ClO<sub>4</sub><sup>-</sup> are in the range 1.403(3)–1.430(3)Å, which is within the range of typical values (Riera et al., 1998). The ClO<sub>4</sub><sup>-</sup> anion and the cation are connected by C5-H5...O4 and N1-H11 $\cdots$ O2 interactions.

Atoms H9*a* and H10*a* on the cation interact with N4 on an adjacent cation at (x - 1, y, z) through C-H···N hydrogen bonds (Table 2). Furthermore, atom H7*a* also interacts with N3 on an adjacent cation at (x + 1, y, z). The propagation of



## Figure 1

The molecular structure of (I), shown with 30% probability displacement ellipsoids.





## Figure 2

(a) View of one molecular chain down the *a* axis. (b) View of one molecular chain along the *a* axis. [Symmetry code: (a) x + 1, y, z.]

molecules and the hydrogen bonds produces a chain along the a axis (Fig. 2). The molecules in a chain are parallel with each other and the angle between the molecular chain and the pyridine plane is 40.6 (2)°. Many chains are arranged along the



**Figure 3** The crystal packing of (I), viewed along the *a* axis.



## Figure 4

The hydrogen-bond interactions between adjacent chains. H atoms not participating in the hydrogen bonds have been omitted for clarity. [Symmetry code: (A)  $x - 1, \frac{3}{2} - y, \frac{1}{2} + z.$ ]

*c* axis forming a layer. We can see in Fig. 3 that all chains in a layer are parallel with each other. The molecules in adjacent chains have the opposite direction and the dihedral angle between the pyridine planes in adjacent chains is 8.5 (2)°. This makes it easy for them to bond together through  $C-H\cdots O$  hydrogen bonds between cations and  $ClO_4^-$  anions. As shown in Fig. 4, atoms H1 and H2 on the cation interact with O4 and O1 of the  $ClO_4^-$  anion at  $(1 + x, \frac{3}{2} - y, z - \frac{1}{2})$  through  $C1-H1\cdots O4$  and  $C2-H2\cdots O1$  hydrogen bonds. The adjacent layers are also linked by a  $C6-H6b\cdots N4(1-x, 2-y, 2-z)$  hydrogen bond.

## Experimental

FeSO<sub>4</sub> (152 mg, 1 mmol) and 4-[*N*,*N*-bis(2-cyanoethyl)amino]pyridine (200 mg, 1 mmol) were added to 40 ml ethanol. The reaction mixture was refluxed for 1.5 h. NaClO<sub>4</sub> (122.5 mg) was then added to the reaction mixture and stirred for 15 min. White powder of (I) was filtered, washed with ethanol and dried in a vacuum desiccator, yielding 246 mg (82%). Colorless crystals of (I) were obtained by recrystallization from ethanol. The elemental analysis data for  $C_{11}H_{13}N_4^+ \cdot ClO_4^-$  are as follows, calculated: C 43.90, H 4.23, N 18.62%; found: C 43.78, H 4.27, N 18.49%.

## Crystal data

$C_{11}H_{13}N_4^+ \cdot ClO_4^-$	$D_x = 1.493 \text{ Mg m}^{-3}$
$M_r = 300.70$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 2473
a = 5.403 (1)  Å	reflections
b = 30.252(5) Å	$\theta = 2.6-25.9^{\circ}$
c = 8.293 (2) Å	$\mu = 0.31 \text{ mm}^{-1}$
$\beta = 99.24 (1)^{\circ}$	T = 293 (2) K
V = 1337.9 (5) Å <sup>3</sup>	Needle, colorless
Z = 4	$0.40 \times 0.20 \times 0.15 \text{ mm}$

#### Data collection

Bruker SMART APEX CCD area-	2345 independent reflections
detector diffractometer	1848 reflections with $I > 2\sigma(I)$
$\varphi$ and $\omega$ scans	$R_{\rm int} = 0.062$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.0^{\circ}$
(SADABS; Bruker, 2000)	$h = -6 \rightarrow 6$
$T_{\min} = 0.925, T_{\max} = 0.957$	$k = -35 \rightarrow 35$
6812 measured reflections	$l = -8 \rightarrow 9$

### Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.044P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.049$	+ 0.8P]
$wR(F^2) = 0.118$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.00	$(\Delta/\sigma)_{\rm max} = 0.001$
2345 reflections	$\Delta \rho_{\rm max} = 0.36 \ {\rm e} \ {\rm \AA}^{-3}$
185 parameters	$\Delta \rho_{\rm min} = -0.35 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

## Table 1

Selected geometric parameters (Å, °).

Cl1-O1	1.403 (2)	N1-C1	1.331 (4)
Cl1-O3	1.406 (3)	N2-C3	1.340 (3)
Cl1-O4	1.426 (2)	N3-C8	1.134 (3)
Cl1-O2	1.430 (2)	N4-C11	1.134 (4)
N1-C5	1.329 (4)		
O1-Cl1-O3	111.29 (18)	O4-Cl1-O2	108.38 (14)
O1-Cl1-O4	108.99 (15)	C5-N1-C1	120.8 (3)
O3-Cl1-O4	108.6 (2)	C3-N2-C9	121.3 (2)
O1-Cl1-O2	110.28 (14)	C3-N2-C6	121.92 (19)
O3-Cl1-O2	109.26 (19)	C9-N2-C6	116.71 (19)

## Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
N1-H11···O2	0.84 (3)	2.09 (3)	2.913 (4)	164 (3)
$C1 - H1 \cdot \cdot \cdot O4^i$	0.93	2.69	3.326 (4)	126
$C2-H2\cdots O1^{i}$	0.93	2.66	3.579 (3)	168
$C5-H5\cdots O4$	0.93	2.44	3.169 (4)	135
$C6-H6b\cdots N4^{ii}$	0.97	2.65	3.487 (3)	145
$C7 - H7a \cdot \cdot \cdot N3^{iii}$	0.97	2.73	3.407 (4)	127
$C9-H9a\cdots N4^{iv}$	0.97	2.65	3.163 (4)	113
$C10-H10a\cdots N4^{iv}$	0.97	2.57	3.257 (4)	128

Symmetry codes: (i)  $1 + x, \frac{3}{2} - y, z - \frac{1}{2}$ ; (ii) 1 - x, 2 - y, 2 - z; (iii) 1 + x, y, z; (iv) x - 1, y, z.

Atom H11 am bonded to N1 was located in a difference Fourier map and refined isotropically. The positions of the other H atoms were fixed geometrically (C–H = 0.93–0.97 Å) and refined using the riding-model approximation ( $U_{\rm iso}$  = 1.2 times  $U_{\rm eq}$  of the parent atom).

Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 2000); program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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