

2-Aminopyridinium isonicotinate 2-aminopyridine

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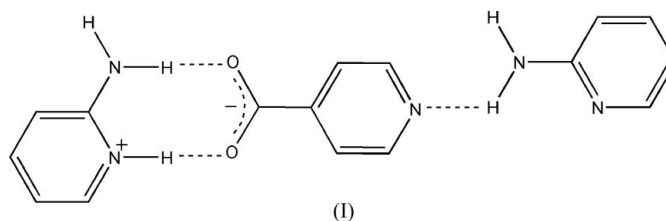
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In the title compound, $C_5H_7N_2^+ \cdot C_6H_4NO_2^- \cdot C_5H_6N_2$, the components are linked into a two-dimensional network through $N-H \cdots O$ and $N-H \cdots N$ hydrogen bonds. Adjacent layers are further linked by $C-H \cdots O$ hydrogen bonds, forming a three-dimensional framework.

Comment

2-Aminopyridine is one of the most frequently used synthons in supramolecular chemistry based on hydrogen bonds (Gellert & Hsu, 1988; Banerjee & Murugavel, 2004; Bis & Zaworotko, 2005; Bis *et al.*, 2006). In this paper, we report the crystal structure of the title compound, (I), which contains this molecule.



Key indicators

Single-crystal X-ray study
 $T = 298$ K
 Mean $\sigma(C-C) = 0.003$ Å
 R factor = 0.055
 wR factor = 0.163
 Data-to-parameter ratio = 16.7

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

The asymmetric unit of (I) contains one 2-aminopyridinium cation, one isonicotinate anion and one neutral 2-aminopyridine molecule (Fig. 1). Due to the three hydrogen bonds (entries 1 to 3 in Table 1), the dihedral angles between the three aromatic pyridine rings are less than 30° : the angle between the planes $N1/C1-C5$ and $N2/C7-C11$ is $23.1(1)^\circ$, that between the planes $N1/C1-C5$ and $N4/C12-C16$ is $29.2(1)^\circ$, and that between the planes $N2/C7-C11$ and $N4/C12-C16$ is $10.1(1)^\circ$.

The supramolecular structure of (I) contains both $N-H \cdots X$ ($X = O$ or N) and $C-H \cdots O$ hydrogen bonds (Table 1). In detail, the amine group of the 2-aminopyridinium cation acts as hydrogen-bond donor, *via* two H atoms, to atoms O1

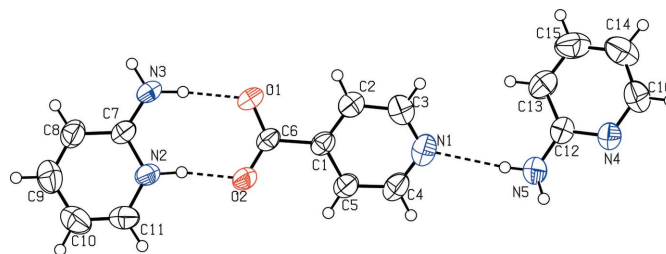


Figure 1

The asymmetric unit of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. Hydrogen bonds between the components are shown as dashed lines.

and O2ⁱ (Table 1). These contacts produce chains including cations and anions, which run parallel to [101] (Fig. 2). In a similar way, the amine group of the neutral 2-aminopyridine molecule acts as a donor, *via* atom H5A, to atom N4ⁱⁱ, thereby forming a centrosymmetric R₂²(8) ring (Batten & Robson, 1998). N5—H5B···N1 hydrogen bonds link these motifs into chains parallel to [101], giving a two-dimensional network (Fig. 2). Finally, the only direction-specific interaction between adjacent layers is the weak C11—H11···O1ⁱⁱⁱ hydrogen bond (Table 1, entry 6).

Experimental

Compound (I) was formed by dissolving 2-aminopyridine (0.188 g, 2 mmol) and isonicotinic acid (0.123 g, 1 mmol) in absolute ethanol (20 ml). The resulting solution was stirred at 323 K for 30 min and then slowly cooled to room temperature. Crystals of (I) suitable for X-ray crystallographic analysis were grown by slow evaporation of the solution at the bottom of the vessel.

Crystal data

C ₅ H ₇ N ₂ ⁺ ·C ₆ H ₄ NO ₂ ⁻ ·C ₅ H ₆ N ₂	$V = 1609.8 (5) \text{ \AA}^3$
$M_r = 311.35$	$Z = 4$
Monoclinic, $P2_1/n$	Mo $K\alpha$ radiation
$a = 5.6204 (11) \text{ \AA}$	$\mu = 0.09 \text{ mm}^{-1}$
$b = 25.623 (5) \text{ \AA}$	$T = 298 (2) \text{ K}$
$c = 11.256 (2) \text{ \AA}$	$0.23 \times 0.20 \times 0.15 \text{ mm}$
$\beta = 96.748 (4)^\circ$	

Data collection

Bruker SMART APEX CCD area-detector diffractometer	9742 measured reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 2001)	3733 independent reflections
$T_{\min} = 0.980$, $T_{\max} = 0.991$	2478 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.032$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.055$	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2) = 0.163$	$\Delta\rho_{\text{max}} = 0.24 \text{ e \AA}^{-3}$
$S = 1.07$	$\Delta\rho_{\text{min}} = -0.15 \text{ e \AA}^{-3}$
3733 reflections	
223 parameters	

Table 1
Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N2—H2A···O2	0.95 (2)	1.75 (2)	2.685 (2)	167.4 (17)
N3—H3B···O1	0.94 (2)	1.87 (2)	2.808 (2)	172.6 (19)
N5—H5B···N1	0.84 (3)	2.29 (3)	3.118 (3)	174 (2)
N3—H3A···O2 ⁱ	0.91 (2)	1.92 (2)	2.832 (2)	178 (2)
N5—H5A···N4 ⁱⁱ	0.92 (3)	2.26 (3)	3.168 (3)	169 (2)
C11—H11···O1 ⁱⁱⁱ	0.93	2.32	3.130 (2)	146

Symmetry codes: (i) $x - \frac{1}{2}, -y + \frac{1}{2}, z - \frac{1}{2}$; (ii) $-x + 4, -y, -z + 2$; (iii) $x - \frac{1}{2}, -y + \frac{1}{2}, z + \frac{1}{2}$

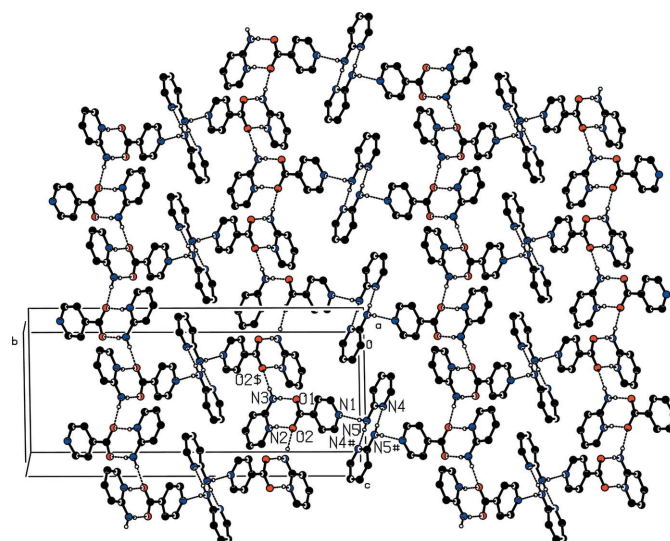


Figure 2

Part of the crystal structure of (I). Dashed lines indicate hydrogen bonds. For the sake of clarity, H atoms not involved in the motifs shown have been omitted. Atoms marked with a dollar sign (\$) or a hash sign (#) are generated by the symmetry operators $(-\frac{1}{2} + x, \frac{1}{2} - y, -\frac{1}{2} + z)$ and $(4 - x, -y, 2 - z)$, respectively.

Aromatic H atoms were placed in idealized positions and refined with $C-H = 0.93 \text{ \AA}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. H atoms bonded to N atoms were located in a difference map and their coordinates were refined, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT-Plus (Bruker, 2001); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: PLATON (Spek, 2003); software used to prepare material for publication: SHELXL97 and PLATON.

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