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## Di(2-pyridinio)methanediol Dinitrate

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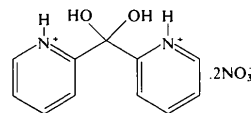
### Abstract

An X-ray structural analysis of the title compound [2,2'-(dihydroxymethylene)dipyridinium dinitrate,  $C_{11}H_{12}N_2O_2^{2+} \cdot 2NO_3^-$ ] revealed that it was a doubly protonated derivative of di-2-pyridyl ketone (dpk) which had also undergone a hydration reaction at the ketone to

form a geminal diol. Extensive hydrogen bonding involving the O atoms of the diol contribute to the high stability of the molecule. The geometry about the bridging  $sp^3$  C atom is almost that of a regular tetrahedron. However, the two pyridine rings are twisted such that the molecule conforms closely to non-crystallographic twofold symmetry. The bond distances and angles within the pyridine rings are normal and there is no apparent strain or distortion.

### Comment

We have been actively investigating the coordination chemistry of the ligand di-2-pyridyl ketone (dpk) since it exhibits unusual structural chemistry when in the presence of transition metal cations (Wang, Richardson, Briggs, Jacobson & Jensen, 1986). We have reported several structures involving dpk in this journal (Sommerer & Abboud, 1993; Sommerer, Westcott & Abboud, 1994) and elsewhere (Sommerer, Jensen & Jacobson, 1990; Sommerer, Baker, Jensen, Hamza & Jacobson, 1993). In the course of our current work with this molecule, we have isolated and structurally characterized a doubly protonated derivative of dpk which has also undergone a hydration reaction at the ketone to form a geminal diol, (I). A thermally stable diol of this form is quite novel and we are not aware of any others which have been characterized in the solid state to date. Stable geminal diols, of which the hydrates of chloral and hexafluoroacetone are two notable examples, are usually generated from electron-deficient carbonyl compounds, including polyhalogenated aldehydes and ketones and  $\alpha$ -keto aldehydes (March, 1985). The two protonated pyridine rings in hydrated dpk serve this purpose and add to the stabilization of the molecule.



The crystal structure of the title compound was found to consist of di(2-pyridinio)methanediol cations each balanced by two nitrate anions. There is extensive hydrogen bonding involving the O atoms of the diol (Fig. 1), which contributes to the stability of the molecule. The geometry about the bridging  $sp^3$  C atom is close to tetrahedral with a slight expansion of the O1a—C1—O1b angle to 113.89 (14)°. This distortion from regular tetrahedral geometry is likely to result from the repulsion of the lone-pair electrons of O1a and O1b. The bonds and the angles within the pyridine rings show no irregularities. The dihedral angles between  $P_1$  (the plane defined by the atoms C1, O1a and O1b) and  $P_2$  (the plane defined by N1, C2, C3, C4, C5 and C6) is 125.1 (1)°, and the angle formed between  $P_1$  and  $P_3$  (N1', C2', C3', C4', C5' and C6') is 120.2 (1)°. The dihedral angle between  $P_2$  and  $P_3$  is 92.49 (6)°. The pyridine

rings are twisted such that the molecule conforms closely to the non-crystallographic twofold symmetry which can be seen in Fig. 2. The bond distances and angles within the pyridine rings are normal and there is no apparent strain or distortion.

Recently we reported the structure of protonated dpk balanced by a  $BF_4^-$  anion (Sommerer, Westcott & Abboud, 1994). The structure reported here complements that structure and clearly establishes that coordination to a transition metal is not necessary for the hydrated form of dpk to exist.

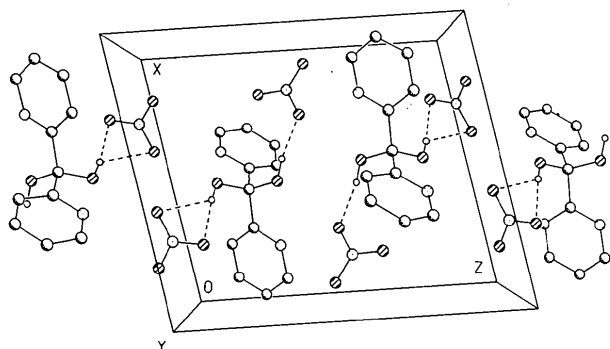


Fig. 1. Packing diagram for di(2-pyridinio)methanediol nitrate.

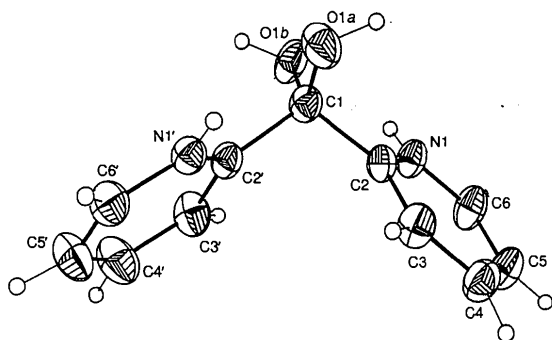


Fig. 2. Representation of the di(2-pyridinio)methanediol(2+) cation with ellipsoids drawn at the 50% probability level.

## Experimental

The title compound was prepared from a highly acidic aqueous solution (pH 2) of  $MnBr_2$  and dpk.

### Crystal data

$C_{11}H_{12}N_2O_2^{2+} \cdot 2NO_3^-$

$M_r = 328.25$

Monoclinic

$P2_1/n$

$a = 10.292$  (2) Å

$b = 11.219$  (1) Å

$c = 12.481$  (2) Å

$\beta = 100.38$  (2)°

$V = 1417.5$  (4) Å<sup>3</sup>

$Z = 4$

$D_x = 1.538$  Mg m<sup>-3</sup>

Mo  $K\alpha$  radiation

$\lambda = 0.71073$  Å

Cell parameters from 50 reflections

$\theta = 10\text{--}11^\circ$

$\mu = 0.13$  mm<sup>-1</sup>

$T = 295$  K

Block

$0.62 \times 0.38 \times 0.34$  mm

Orange-yellow

### Data collection

Siemens  $P3m/V$  diffractometer

$\omega$  scans

Absorption correction:

analytical

$T_{\min} = 0.950$ ,  $T_{\max} =$

0.971

4597 measured reflections

4174 independent reflections

2906 observed reflections

$[F > 4\sigma(F)]$

$R_{\text{int}} = 0.0138$

$\theta_{\max} = 30^\circ$

$h = 0 \rightarrow 14$

$k = 0 \rightarrow 15$

$l = -17 \rightarrow 17$

4 standard reflections

monitored every 100

reflections

intensity variation: 1%

### Refinement

Refinement on  $F$

$R = 0.0481$

$wR = 0.0617$

$S = 2.03$

2906 reflections

256 parameters

All H-atom parameters

refined

$w = 1/[\sigma^2(F) + 0.0004F^2]$

$(\Delta/\sigma)_{\max} = 0.001$

$\Delta\rho_{\max} = 0.27$  e Å<sup>-3</sup>

$\Delta\rho_{\min} = -0.22$  e Å<sup>-3</sup>

Extinction correction: none

Atomic scattering factors

from Cromer & Mann

(1968) for non-H atoms

and Stewart, Davidson

& Simpson (1965) for H

atoms

Table 1. Fractional atomic coordinates and equivalent isotropic displacement parameters (Å<sup>2</sup>)

$$U_{\text{eq}} = (1/3)\sum_i \sum_j U_{ij} a_i^* a_j^* a_j \cdot a_i$$

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{eq}}$
N1	0.22771 (13)	0.39427 (14)	0.32551 (12)	0.0399 (4)
N1'	0.59761 (13)	0.24926 (13)	0.20434 (12)	0.0367 (4)
O1a	0.47614 (13)	0.44805 (13)	0.18028 (12)	0.0545 (5)
O1b	0.47018 (12)	0.45487 (12)	0.36585 (11)	0.0520 (5)
C1	0.4450 (2)	0.3889 (2)	0.26970 (14)	0.0388 (5)
C2	0.2983 (2)	0.3551 (2)	0.25287 (13)	0.0365 (5)
C2'	0.52694 (14)	0.27462 (14)	0.28178 (13)	0.0360 (5)
C3	0.2387 (2)	0.2845 (2)	0.1693 (2)	0.0480 (6)
C3'	0.5315 (2)	0.1987 (2)	0.3685 (2)	0.0495 (6)
C4	0.1076 (2)	0.2528 (2)	0.1630 (2)	0.0530 (6)
C4'	0.6139 (2)	0.1014 (2)	0.3772 (2)	0.0625 (8)
C5	0.0383 (2)	0.2940 (2)	0.2393 (2)	0.0539 (7)
C5'	0.6894 (2)	0.0801 (2)	0.2985 (2)	0.0599 (8)
C6	0.0998 (2)	0.3653 (2)	0.3206 (2)	0.0510 (6)
C6'	0.6781 (2)	0.1544 (2)	0.2116 (2)	0.0470 (6)
N'	0.2214 (2)	0.14352 (14)	0.47851 (12)	0.0467 (5)
O1'	0.1120 (2)	0.1364 (2)	0.50440 (14)	0.0861 (7)
O2'	0.3080 (2)	0.2048 (2)	0.53228 (14)	0.0808 (7)
O3'	0.2416 (2)	0.0888 (2)	0.39624 (12)	0.0655 (6)
N	0.18931 (13)	0.58795 (13)	0.53806 (12)	0.0416 (5)
O1	0.1977 (2)	0.6294 (2)	0.62979 (13)	0.0701 (6)
O2	0.09190 (14)	0.6014 (2)	0.46737 (12)	0.0675 (6)
O3	0.28523 (12)	0.5263 (2)	0.51775 (11)	0.0645 (5)

Table 2. Selected geometric parameters (Å, °)

C2—N1	1.335 (2)	C4'—C3'	1.374 (3)
C6—N1	1.346 (2)	C5—C4	1.369 (3)
C2'—N1'	1.341 (2)	C5'—C4'	1.379 (4)
C6'—N1'	1.342 (2)	C6—C5	1.356 (3)
C1—O1a	1.385 (2)	C6'—C5'	1.356 (3)
C1—O1b	1.394 (2)	O1'—N'	1.228 (3)
C2—C1	1.534 (2)	O2'—N'	1.226 (2)
C2'—C1	1.527 (2)	O3'—N'	1.246 (2)
C3—C2	1.364 (2)	O1—N	1.224 (2)
C3'—C2'	1.371 (3)	O2—N	1.220 (2)
C4—C3	1.383 (3)	O3—N	1.268 (2)

C2—N1—C6	122.5 (2)	C4—C3—C2	119.5 (2)
C2'—N1'—C6'	121.9 (2)	C4'—C3'—C2'	119.3 (2)
C2—C1—C2'	108.57 (13)	C5—C4—C3	119.9 (2)
C2—C1—O1a	111.90 (13)	C5'—C4'—C3'	120.0 (2)
C2—C1—O1b	105.95 (14)	C6—C5—C4	119.2 (2)
C2'—C1—O1a	106.15 (14)	C6'—C5'—C4'	119.0 (2)
C2'—C1—O1b	110.31 (13)	N1—C6—C5	119.9 (2)
O1a—C1—O1b	113.89 (14)	N1'—C6'—C5'	120.3 (2)
C3—C2—N1	119.0 (2)	O1'—N'—O2'	120.2 (2)
C3—C2—C1	123.0 (2)	O2'—N'—O3'	121.0 (2)
N1—C2—C1	117.95 (14)	O3'—N'—O1'	118.8 (2)
C3'—C2'—N1'	119.4 (2)	O1—N—O2	122.7 (2)
C3'—C2'—C1	122.6 (2)	O2—N—O3	119.4 (2)
N1'—C2'—C1	117.95 (15)	O3—N—O1	117.90 (14)
C2—C1—C2'—N1'	114.6 (2)	O1a—C1—C2'—N1'	-5.9 (2)
C2'—C1—C2—N1	120.0 (2)	O1b—C1—C2—N1	1.5 (2)
O1a—C1—C2—N1	-123.2 (2)	O1b—C1—C2'—N1'	-129.8 (2)

The  $\omega$ -scan width was symmetrical over  $1.2^\circ$  about the  $K\alpha_{1,2}$  maximum of each peak with the background offset by  $1.0$  and  $-1.0^\circ$  in  $\omega$  from the  $K\alpha_{1,2}$  maximum. The scan speed varied between  $3$  and  $6^\circ \text{ min}^{-1}$  depending upon intensity. The structure was solved by direct methods. All of the non-H atoms were refined with anisotropic displacement parameters. The H atoms were located from a difference Fourier map and were refined without constraints. The linear absorption coefficient was calculated using values from *International Tables for X-ray Crystallography* (1974). Anomalous-dispersion corrections were taken from Cromer & Liberman (1970).

Cell refinement, data collection, data reduction, structure solution and molecular graphics: *SHELXTL-Plus* (Sheldrick, 1990). Structure refinement (by a full-matrix least-squares method): *SHELX76* (Sheldrick, 1976). Geometric calculations and preparation of material for publication: *FUER* (Larson, 1993).

This research was supported by an award from Research Corporation, Tucson, Arizona, USA.

Lists of structure factors, anisotropic displacement parameters, H-atom coordinates, bond distances and angles involving H atoms and hydrogen-bond data have been deposited with the IUCr (Reference: CR1106). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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## Structure of Ascidiacyclamide as the Ethanol Water Solvate, a Cytotoxic Cyclic Peptide from *Ascidian*

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## Abstract

The X-ray crystal structure determination of the  $\text{C}_2\text{H}_5\text{OH}\cdot\text{H}_2\text{O}$  solvate of ascidiacyclamide ( $\text{C}_{36}\text{H}_{52}\text{N}_8\text{O}_6\text{S}_2$ ), a cytotoxic cyclic peptide from marine tunicate *Ascidian*, revealed a  $C_2$ -symmetric saddle-shaped rectangular conformation of the molecule. The water and ethanol molecules are located on the crystallographic diad axis and are held by hydrogen bonds and van der Waals contacts with the polar ring N atoms and nonpolar D-Val side-chain atoms, respectively. The molecular conformation and the interaction with solvent molecules are nearly the same as those of the compound with  $\text{C}_2\text{H}_5\text{OH}\cdot 2\text{H}_2\text{O}$  [Ishida, In, Doi, Inoue, Hamada & Shioiri (1992). *Biopolymers*, **32**, 131–143].

## Comment

In a series of investigations into the relationship between the chemical structural symmetry and the molecular conformation in cyclic peptides from marine tunicate, several crystal forms of ascidiacyclamide, (1), a cytotoxic cyclic peptide from *Ascidian*, have been determined by X-ray crystal analyses (Ishida, Tanaka, Nabae, Inoue, Kato, Hamada & Shioiri, 1988; Ishida, In, Doi, Inoue, Hamada & Shioiri, 1992). The conformational analysis of (1) appears to be important for considering the 'active conformation' of cytotoxic cyclic peptides from tunicate, because most of them have a common or related