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Key indicators

Single-crystal X-ray study T = 193 K Mean σ (C–C) = 0.003 Å R factor = 0.032 wR factor = 0.088 Data-to-parameter ratio = 18.2

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

© 2006 International Union of Crystallography All rights reserved [2-(3-Fluoropyridinium-1-yl)-1-hydroxy-1-phosphonoethyl]phosphonate

The title compound, $C_7H_{10}FNO_7P_2$, crystallizes in the zwitterionic form. In the crystal structure, molecules are linked *via* intermolecular $O-H\cdots O$ hydrogen bonds involving phosphonate groups, forming a two-dimensional framework. In addition, weak intermolecular $C-H\cdots O$ hydrogen bonds involving the pyridinium groups further connect molecules, forming a three-dimensional framework.

Comment

Nitrogen-containing geminal bisphosphonates are used clinically to treat a variety of bone resorption diseases such as osteoporosis (Sambrook *et al.*, 2004) and Paget's disease (Vasireddy *et al.*, 2003) and more recently they have been found to have antiparasitic (Yardley *et al.*, 2002), anticancer (Clezardin, 2005) and immunomodulatory activity (Sanders *et al.*, 2004). It is believed that they act by inhibiting the isoprenoid biosynthesis pathway enzyme farnesyl diphosphate synthase (FPPS) (EC 2.5.1.10) (Martin *et al.*, 1999; Hosfield *et al.*, 2004; van Beek *et al.*, 1999) with the charged (ammonium, imidazolium) side chains acting as carbocation transition state reactive intermediates. Another class of bisphosphonates are the pyridinium-1-yl species, which contain a fixed (+1) sidechain charge (Sanders *et al.*, 2005). We report here the first structure of one such active compound, *viz.* (I).



The molecule of (I) crystallizes in the zwitterionic form and there are no solvent molecules present (unlike the monohydrates found with the sulfonium, phosphonium and arsonium bisphosphonates; Zhang *et al.*, 2006; Cao *et al.*, 2006; Hudock *et al.*, 2006). Consequently, there must be three protonated phosphonate O atoms (found to be O1, O4 and O5) and three non-protonated phosphonate O atoms (found to be O2, O3 and O6), as shown in Fig. 1.

The P1···N1 distance [3.2469 (13) Å] is considerably shorter than the P2···N1 distance [4.1195 (14) Å], consistent with a strong intramolecular interaction between the pyridinium N atom and the anionic phosphonate group, and the overall structure closely resembles that found for the monohydrate form of risedronate (Gossman *et al.*, 2003) which contains a pyridinium N atom (at a position equivalent to that found here for C4). In the crystal structure, molecules are linked *via* intermolecular $O-H\cdots O$ hydrogen bonds involving phosphonate groups, forming a two-dimensional framework (Fig. 2 and Table 1). In addition, weak intermolecular $C-H\cdots O$ hydrogen bonds involving the pyridinium groups further connect molecules, forming a three-dimensional framework (Table 1).

Experimental

The title compound was prepared as described previously (Sanders *et al.*, 2005). Crystals were grown by vapor diffusion of ethanol into an aqueous solution of the bisphosphonate at room temperature using the sitting-drop method.

 $D_{\rm r} = 1.810 {\rm Mg} {\rm m}^{-3}$

Cell parameters from 4398

Block (acircular), colourless $0.10 \times 0.10 \times 0.06$ mm

3201 independent reflections 2665 reflections with $I > 2\sigma(I)$

 $w = 1/[\sigma^2(F_0^2) + (0.0429P)^2]$

+ 0.6018P] where $P = (F_o^2 + 2F_c^2)/3$

 $(\Delta/\sigma)_{\rm max} = 0.002$

 $\Delta \rho_{\rm max} = 0.50 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.32 \text{ e } \text{\AA}^{-3}$

Mo $K\alpha$ radiation

reflections

 $\theta = 3.1-29.9^{\circ}$ $\mu = 0.44 \text{ mm}^{-1}$

T = 193 (2) K

 $R_{\rm int} = 0.032$

 $\theta_{\max} = 30.0^{\circ}$ $h = -8 \rightarrow 8$

 $k = -26 \rightarrow 26$

 $l = -13 \rightarrow 13$

Crystal data

 $C_{7}H_{10}FNO_{7}P_{2}$ $M_{r} = 301.10$ Monoclinic, $P2_{1}/c$ a = 6.1892 (10) Å b = 19.1693 (4) Å c = 9.3312 (10) Å $\beta = 93.667$ (10)° V = 1104.8 (3) Å³ Z = 4

Data collection

Bruker Kappa-APEXII CCD diffractometer φ and ω scans Absorption correction: integration (*SHELXTL/XPREP*; Bruker, 2001) $T_{min} = 0.967, T_{max} = 0.981$ 15680 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.033$ $wR(F^2) = 0.088$ S = 1.033201 reflections 176 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - H \cdot \cdot \cdot A$
$\overline{O5-H3\cdots O3^{i}}$	0.867 (15)	1.577 (16)	2.4209 (15)	163 (2)
$O1-H1\cdots O6^{ii}$	0.834 (15)	1.679 (16)	2.4950 (15)	165 (2)
O4-H2··· $O2$ ⁱⁱⁱ	0.840 (15)	1.749 (15)	2.5846 (15)	173 (2)
O7-H4··· $O2$ ⁱⁱ	0.827 (15)	1.880 (15)	2.7056 (15)	177 (2)
$C2-H5\cdots O5^i$	0.99	2.40	3.3326 (17)	156
C2−H6···O3 ⁱⁱⁱ	0.99	2.26	3.2216 (16)	163
C3-H7···O1 ⁱⁱⁱ	0.95	2.51	3.430 (2)	164
$C5-H8\cdots O4^{iv}$	0.95	2.59	3.312 (2)	133
$C6-H9\cdots O6^{v}$	0.95	2.45	3.260 (2)	143

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

Methyl H-atom positions, $R-CH_3$, were optimized by rotation about R-C bonds with idealized C-H, R-H and H···H distances (methyl C-H = 0.96 Å with AFIX). Hydroxyl H-atom positions were located in late difference Fourier maps and restrained to ideal bond



Figure 1

SHELXTL (Bruker, 2001) plot showing 35% probability ellipsoids for non-H atoms and circles of arbitrary size for H atoms.



Figure 2

 $CERIUS^2$ (Accelrys, 2005) view of the crystal structure, showing the hydrogen-bonded network between the bisphosphonates. Hydrogen bonds are shown as dashed yellow lines.

lengths (O–H = 0.84 Å) using an effective standard deviation of 0.02 Å. The remaining H atoms were included as idealized riding atoms (methylene C–H = 0.97 Å and ring C–H = 0.93 Å). Methyl and hydroxyl H-atom U_{iso} (H) values were assigned as 1.5 times U_{eq} of the carrier atom; remaining H-atom U_{iso} (H) values were assigned as 1.2 times carrier U_{eq} .

Data collection: *APEX2* (Bruker, 2004); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Bruker, 2001); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *XCIF* (Bruker, 2001).

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