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Key indicators

Single-crystal X-ray study T = 193 K Mean σ (C–C) = 0.004 Å R factor = 0.033 wR factor = 0.092 Data-to-parameter ratio = 18.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the crystal structure of the title compound, $C_5H_{15}As$ -O₇P₂·H₂O, hydrogen-bonded sheets are formed which contain bisphosphonate(1–) groups and water molecules alternating

1-yl)ethanephosphonate monohydrate

1-Hydroxy-1-phosphono-2-(trimethylarsonium-

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Comment

with trimethylarsonium groups.

Bisphosphonates, especially N-containing bisphosphonates with positively charged side-chains, are the preferred choice of treatment for bone resorption diseases, such as osteoporosis (Sambrook et al., 2004), osteopenia and Paget's disease (Vasireddy et al., 2003). They act by inhibiting the isoprenoid biosynthesis pathway enzyme farnesyl diphosphate synthase (FPPS: EC No. 2.5.1.10), resulting in the inhibition of protein prenylation. In addition, FPPS inhibition leads to an accumulation of isopentenyl diphosphate which is converted to the strongly pro-apoptotic ATP analog ApppI, the isopentenyl ester of ATP, which inhibits the mitochondrial ADP/ATP transporter (Mönkkönen et al., 2004). Previously, we proposed a possible mechanism of action for FPPS inhibition, suggesting that the N-containing bisphosphonates act as carbocation transition state or reactive intermediate analogs of the FPPS enzyme (Martin et al., 1999). In order to provide additional data for QSAR (quantitative structure-activity relationship) investigations, we now report the synthesis and structure of the title novel As-containing bisphosphonate, (I).



While arsenicals in general may have limited therapeutic utility, arsenic has been used for the treatment of myelodysplastic syndromes (Faderl & Kantarjian, 2004) and melarsoprol is also the first-line therapy for advanced central nervous system East African trypanosomiasis (Katzung, 2004).

The title compound crystallizes as the zwitterionic monohydrate, with the unprotonated atom O6 balancing the positively charged arsenic As1, resulting in a net zero charge on the molecule. This protonation state is also consistent with the bond lengths observed: P3-O6 = 1.556 (2), P3-O5 =1.541 (2) and P3-O7 = 1.491 (2) Å. A displacement ellipsoid rendering of the molecule is presented in Fig. 1.

The geometry of the bisphosphonate backbone in (I) is very similar to that seen with other bisphosphonates (Gossman *et*

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The asymmetric unit of (I), showing 35% probability displacement ellipsoids. H atoms are drawn as circles of arbitrary size.



Figure 2

Cerius² (Accelrys, 2005) view along the *a* axis, showing the proposed hydrogen-bond interactions (dashed lines) between neighboring molecules of (I). Hydrogen-bonded sheets are perpendicular to the c axis.

al., 2002, 2003). The molecules pack in an intercalated sheetlike structure, where the bisphosphonate groups are contained within a plane with the trimethylarsonium groups on alternating sides, represented in Fig. 2.

There is an extensive hydrogen-bond network throughout the bisphosphonate backbone of (I) (Table 1). The unprotonated O atoms from one bisphosphonate form hydrogen bonds with a neighboring bisphosphonate. This interaction is also stabilized by hydrogen bonding with a water molecule located in the bisphosphonate sheet. As expected, the bonding around the As atom is tetrahedral, with angles of 110.41 (17), 108.98 (17) and 107.36 (16)°, and the C-As bond lengths of 1.923 (3), 1.905 (4), 1.905 (3) and 1.901 (4) Å are much larger than those found with the sulfonium [1.8153 (8), 1.7912 (10) and 1.792 (11) A: Zhang et al., 2006] and phosphonium [1.806 (2) 1.789 (2), 1.779 (2) and 1.1780 (2) Å; Cao et al., 2006] species.

Experimental

Arsenobetaine bromide (2 mmol) was added to a mixture of H₃PO₃ (5 equivalents) and toluene (5 ml) and heated to 353 K until the mixture melted. POCl₃ (5 equivalents) was then added slowly and the mixture stirred at 353 K for 4 h. Upon cooling, the supernatant was decanted and 4 ml of water added, and the mixture was refluxed for 1 h. Most of the solvent was then removed in vacuo, and then acetone was added to precipitate the title compound. The resulting white powder was collected and crystallized from ethanol-H₂O (2:1 ν/ν) to afford the pure anhydrous compound. Analysis, calculated for C₅H₁₅AsO₇P₂: C 18.53, H 4.67%; found: C 18.30, H 4.65. ¹H NMR (400 MHz, D_2O , δ , p.p.m.): 2.82 (t, J = 11.8 Hz, 2H), 1.69 (s, 9H); 31 P NMR (162 MHz, D₂O, δ , p.p.m.): 17.3 (s). The final crystals were grown by sitting-drop vapor diffusion of ethanol into an aqueous solution of the compound at room temperature, yielding the monohydrate.

Crystal data

	D = 1000 M = -3
$C_5H_{15}AsO_7P_2 \cdot H_2O$	$D_x = 1.808 \text{ Mg m}^{-1}$
$M_r = 342.05$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 897
a = 7.171 (8) Å	reflections
b = 10.487 (12) Å	$\theta = 2.3 - 28.3^{\circ}$
c = 16.849 (19) Å	$\mu = 2.98 \text{ mm}^{-1}$
$\beta = 97.284 \ (16)^{\circ}$	T = 193 (2) K
$V = 1257 (2) \text{ Å}^3$	Tablet, colorless
Z = 4	$0.32 \times 0.17 \times 0.05 \text{ mm}$

Data collection

Bruker SMART CCD area-detector 3126 independent reflections diffractometer 2265 reflections with $I > 2\sigma(I)$ Profile data from ω scans $R_{\rm int} = 0.050$ $\theta_{\rm max} = 28.4^{\circ}$ Absorption correction: integration $h = -9 \rightarrow 9$ (XPREP in SHELXTL; Bruker, 2001) $k = -13 \rightarrow 14$ $l = -21 \rightarrow 22$ $T_{\min} = 0.442, \ T_{\max} = 0.865$ 11918 measured reflections

Refinement

Refinement on F^2	H atoms treated by a mixture of
$R[F^2 > 2\sigma(F^2)] = 0.033$	independent and constrained
$wR(F^2) = 0.092$	refinement
S = 0.87	$w = 1/[\sigma^2(F_o^2) + (0.0615P)^2]$
3126 reflections	where $P = (F_0^2 + 2F_c^2)/3$
166 parameters	$(\Delta/\sigma)_{\rm max} = 0.005$
	$\Delta \rho_{\rm max} = 0.56 \text{ e } \text{\AA}^{-3}$
	$\Delta \rho_{\rm min} = -0.76 \text{ e} \text{ \AA}^{-3}$

Table 1

Hydrogen-bond geometry (Å, °).

$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$					
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
	$\begin{array}{c} 01 - H1 \cdots 06^{i} \\ 08 - H17 \cdots 06^{ii} \\ 07 - H4 \cdots 02^{iii} \\ 05 - H3 \cdots 03^{iii} \\ 08 - H16 \cdots 02 \\ 04 - H2 \cdots 08^{iv} \end{array}$	0.814 (18) 0.810 (18) 0.827 (17) 0.861 (17) 0.829 (18) 0.837 (18)	1.69 (2) 1.951 (19) 1.98 (2) 1.617 (18) 1.93 (2) 1.69 (2)	2.486 (4) 2.759 (4) 2.759 (4) 2.471 (4) 2.747 (4) 2.514 (3)	165 (4) 174 (4) 157 (3) 171 (3) 169 (4) 166 (4)

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

Methylene H atoms are placed geometrically and treated as riding. Methyl H-atom positions were optimized by rotating about R-C bonds with idealized C-H (0.98–0.99 Å), R-H and H···H distances. Hydroxyl H atoms were located in a difference Fourier map and restrained to ideal bond lengths using an effective standard uncertainty of 0.02 Å; $U_{\rm iso}(\rm H) = 1.5U_{eq}(\rm parent)$ for methyl and hydroxyl H atoms, or $1.2U_{eq}(\rm parent)$ for all other H atoms.

Data collection: *SMART* (Bruker, 2001); 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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