

catena-Poly[bis(*tert*-butylammonium) [plumbate(II)-tri- μ -iodo] iodide dihydrate]

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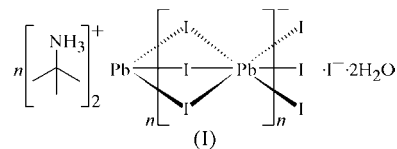
The title compound, $\{(C_4H_{12}N)_2[PbI_3]I \cdot 2H_2O\}_n$, crystallizes as an organic–inorganic hybrid. The six-coordinate Pb atom lies on a centre of inversion and all the I atoms lie on mirror planes; the two independent cations both lie across mirror planes. The structure contains anionic chains along [100] of fused $[PbI_3]^-$ units forming face-sharing octahedra. Four cations enclose channels occupied by isolated iodide ions and water molecules of hydration.

Comment

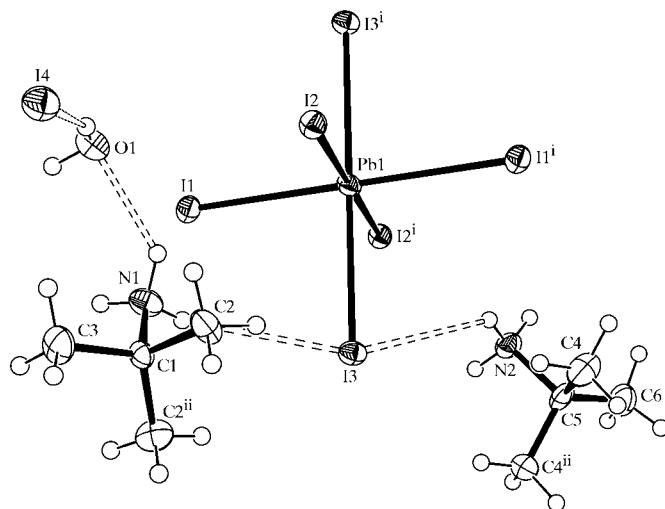
In recent years, a significant number of organic–inorganic hybrid materials based on metal halide units have been prepared and studied; for reviews, see Papavassiliou (1997) and Mitzi (1999). Haloplumbates in particular have demonstrated a propensity for forming a great variety of crystalline structures by self-assembling from suitable solution mixtures. It has been shown that their structures can vary considerably, ranging from systems based on isolated molecules to systems containing extended chains, as in $(Me_4N)[PbI_3]$ (Contreras *et al.*, 1983), right up to two- or three-dimensional networks (Mitzi, 1999). For systems containing extended chains, these chains may be formed by one, two or three bridging halides. A search of the Cambridge Structural Database (Version 5.27, November 2005 release; Allen 2002) indicated that most crystal structures with tertiary butylammonium groups have isolated octahedra, as in $SnCl_6$ (Ghozlen *et al.*, 1991), $TeCl_6$ (Ishida & Kashino, 1992) and $TeBr_6$ (Baker *et al.*, 1995), or isolated $SnCl_4$ tetrahedra (Ishida & Kashino, 1993). To the best of our knowledge, only two structures have a one-dimensional system, *viz.* $(C_4H_{12}N)_2Sb_2Cl_8$, which has edge-sharing chains of square-pyramidal $SbCl_5$ (Belz *et al.*, 1992) units, and $[(t-C_4H_{12}N)CdBr_3]_2 \cdot H_2O$, which has edge-sharing chains of trigonal-bipyramidal $CdBr_5$ units (Ishihara *et al.*, 1999).

The title compound, (I), has a one-dimensional arrangement in which chains of face-sharing PbI_6 octahedra run along the unit cell (see Fig. 1). The channels in between the chains

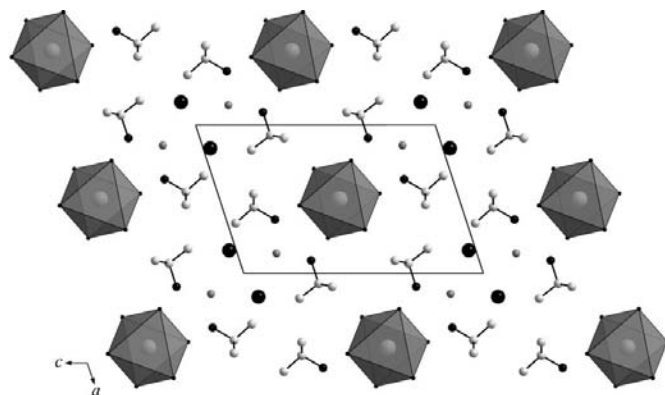
are occupied by *tert*-butylammonium molecules, an isolated I atom on a mirror plane at $y = \frac{1}{4}$ (I4), and water molecules of hydration (Fig. 2). In the direction perpendicular to the chains, the crystal cohesion is achieved by $N-H \cdots I$, $N-H \cdots O$ and $O-H \cdots I$ hydrogen bridges. In the direction parallel to the chains, the cohesion is achieved by strong ionic bonds between the I and Pb atoms.



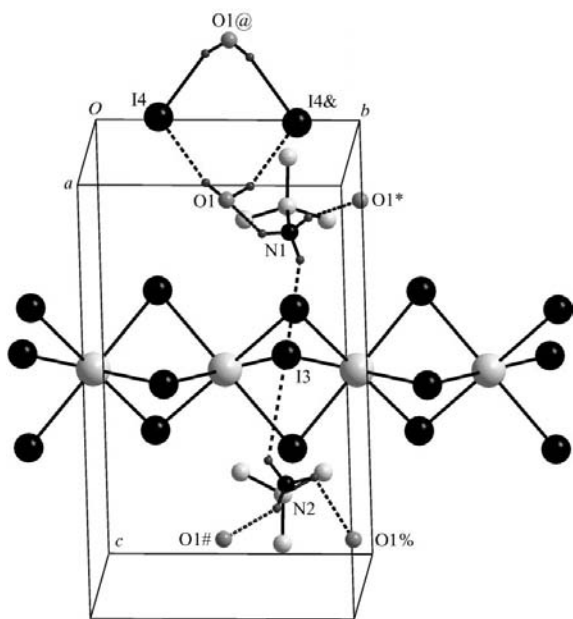
The inorganic motif is built up from characteristic face-sharing PbI_6 octahedra, which form infinite chains along the *b* axis. One unique inorganic chain runs through the centre of the unit cell. The asymmetric unit consists of a Pb atom on a centre of inversion and three I atoms, all on special positions, with I1 and I3 lying on the mirror plane at $y = \frac{3}{4}$ and I2 on the


Figure 1

The asymmetric unit of (I), showing the atomic numbering scheme. Displacement ellipsoids are shown at the 50% probability level. The H atoms on N1 and N2 are disordered and only one set is shown at each site. [Symmetry codes: (i) $-x + 1, -y + 1, -z + 1$; (ii) $x, -y + \frac{3}{2}, z$.]


Figure 2

The packing of (I), viewed along the *b* axis.


Figure 3

A magnified view of the face-sharing PbI_6 octahedra and hydrogen-bonding scheme. Atoms labelled with an ampersand (&), a percentage sign (%), a hash (#), an asterisk (*) and an 'at' sign (@) are at the symmetry positions $(-x, y + \frac{1}{2}, z)$, $(-x + 1, y + \frac{1}{2}, -z + 1)$, $(-x + 1, -y + 1, -z + 1)$, $(x, -y + \frac{3}{2}, z)$ and $(-x, -y + 1, -z)$, respectively.

mirror plane at $y = \frac{1}{4}$. Within the chains, the shared face consists of these three halides. The octahedra are somewhat distorted, with all three unique Pb—I distances different (Table 1), while the bond angles between *cis* ligands range from 83.346 (16) to 96.654 (16)°.

There are two unique *tert*-butylammonium cations in the asymmetric unit, labelled cat1 (containing atom N1) and cat2 (containing atom N2). In cat1, atoms N1, C1 and C3 lie on the mirror plane at $y = \frac{3}{4}$ and atom C2 occupies a general position. In cat2, atoms N2, C5 and C6 lie on the mirror plane at $y = \frac{1}{4}$, with atom C4 in a general position.

The two unique cations in the asymmetric unit interact with the inorganic chains *via* long N—H...I3 hydrogen bridges; the distances are 3.21 and 3.25 Å, respectively, for cat1 and cat2 (Table 2 and Fig. 3). The last two H atoms on the ammonium head groups bridge to the O atom of the water molecule of hydration. The N—H...O distances range from 2.05 to 2.48 Å. Lastly, the H atoms on the water molecule bridge towards the isolated I atom to form a symmetrical ring with graph-set notation $R_2^2(8)$, with donor–acceptor distances of 2.73 and 2.78 Å.

Experimental

PbI_2 (0.126 g, 0.273 mmol) was dissolved in 47% HI (2 ml) in a sample vial. Thereafter, $\text{C}(\text{CH}_3)_3\text{NH}_2$ (0.050 g, 0.684 mmol) was added and the precipitate was dissolved by refluxing for 12 h at 363 K. The solution was cooled slowly to room temperature at a rate of 2 K h⁻¹. A yellow single crystal suitable for X-ray diffraction analysis was selected and studied. Analysis calculated for $\text{C}_8\text{H}_{28}\text{I}_4\text{N}_2\text{O}_2\text{Pb}$: C 10.7, H 3.1, N 3.1%; found: C 10.8, H 3.3, N 3.2%.

Crystal data

$(\text{C}_4\text{H}_{12}\text{N})_2[\text{PbI}_3]\text{I}\cdot 2\text{H}_2\text{O}$
 $M_r = 899.11$
 Monoclinic, $P2_1/m$
 $a = 9.7917$ (10) Å
 $b = 7.9649$ (8) Å
 $c = 15.0594$ (16) Å
 $\beta = 107.985$ (3)°
 $V = 1117.1$ (2) Å³

$Z = 2$
 $D_x = 2.673$ Mg m⁻³
 Mo $K\alpha$ radiation
 $\mu = 13.08$ mm⁻¹
 $T = 173$ (2) K
 Needle, yellow
 $0.28 \times 0.1 \times 0.09$ mm

Data collection

Bruker SMART CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: integration (*XPREP*; Bruker, 1999)
 $T_{\min} = 0.174$, $T_{\max} = 0.388$

5842 measured reflections
 2878 independent reflections
 2416 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.074$
 $\theta_{\max} = 28^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.039$
 $wR(F^2) = 0.101$
 $S = 1.07$
 2878 reflections
 96 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0497P)^2 + 0.2377P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 2.67$ e Å⁻³
 $\Delta\rho_{\min} = -2.32$ e Å⁻³

Table 1

Selected geometric parameters (Å, °).

Pb1—I3	3.1953 (5)	Pb1—I2	3.2355 (6)
Pb1—I1	3.2263 (6)		
I3—Pb1—I1 ⁱ	92.706 (16)	I3—Pb1—I2	93.491 (15)
I3—Pb1—I1	87.294 (16)	I1—Pb1—I2	96.654 (16)
I3—Pb1—I2 ⁱ	86.509 (15)	I1—Pb1—I2 ⁱ	83.346 (16)

Symmetry code: (i) $-x + 1, -y + 1, -z + 1$.

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N1—H1A...I3	0.91	3.21	4.016 (10)	148
N1—H1B...O1	0.91	2.21	2.936 (9)	136
N1—H1C...O1 ⁱⁱ	0.91	2.05	2.936 (9)	164
N2—H2A...O1 ⁱ	0.91	2.16	2.958 (9)	147
N2—H2B...I3	0.91	3.25	3.905 (10)	131
N2—H2C...O1 ⁱⁱⁱ	0.91	2.48	2.958 (9)	113
O1—H2...I4	0.86	2.73	3.572 (6)	165
O1—H1...I4 ^{iv}	0.86	2.78	3.570 (6)	154

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

All H were found in a difference map. For the H atoms bonded to O atoms, restraints were used to obtain reasonable O—H distances and H—O—H angles. Finally, these H atoms were refined using a riding model [$U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{O})$]. H atoms bonded to C and N atoms were refined in idealized positions using the riding-model approximation, with C—H distances of 0.98 Å, N—H distances of 0.91 Å and $U_{\text{iso}}(\text{H})$ values of $1.5U_{\text{eq}}(\text{C}, \text{N})$. The highest residual peak is 0.83 Å from atom Pb1.

Data collection: *SMART-NT* (Bruker, 1998); cell refinement: *SAINT-Plus* (Bruker, 1999); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *DIAMOND* (Brandenburg, 1999); software used to prepare material for publication: *WinGX* (Farrugia, 1999) and *PLATON* (Spek, 2003).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: GD3019). Services for accessing these data are described at the back of the journal.

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