

Bis(dicyclohexylammonium) adipate
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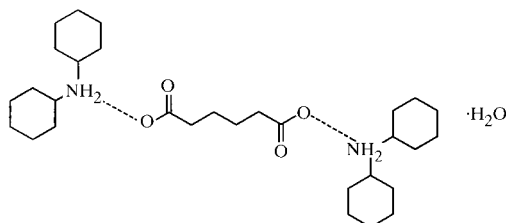
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In the asymmetric unit of the title compound, $2C_{12}H_{24}N^+ \cdot C_6H_8O_4^{2-} \cdot H_2O$, the carboxylate ion lies about an inversion center, the water molecule is on a twofold axis and the *sec*-ammonium cation is in a general position. Cations link the oxygen ends of two adjacent carboxylate anions to form an eight-membered ring [$N \cdots O$ 2.683 (3) and 2.711 (3) Å]. The ion pair propagates as a linear chain and adjacent chains are linked through the water molecules [$O \cdots O$ 2.966 (3) Å] into layers.

Comment

Dicyclohexylammonium monoalkanoates, $[(cyclo-C_6H_{11})_2NH_2][RCH_2CO_2]$ (*R* is an electron-withdrawing group), typically exist as dimeric ion pairs, in which the two NH_2 units link two CO_2 units to form an eight-membered $N \cdots O=C=O \cdots N \cdots O=C=O \cdots$ ring, or as linear hydrogen-bonded chains (Ng *et al.*, 1999). The ring architecture probably requires sterically bulky *R* groups; the $R = (CH_3)_2NCS_2$ derivative adopts the ring architecture, but the compound has water molecules that link adjacent dimers [$O_{water} \cdots O_{carboxyl}$ 2.784 (6) and 3.029 (7) Å; Ng, 1992]. In the title compound, (I), both carboxyl ends of the centrosymmetric adipate dianion are engaged in a similar type of ring formation to give rise to a chain and adjacent chains are linked through the lattice water molecule [$O_{water} \cdots O$ 2.966 (3) Å] to form layers. The water molecule lies on a twofold axis.



(I)

A layer structure is also adopted by *m*-xylylammonium adipate, which crystallizes as a monohydrate, but its $N \cdots O_{carboxyl}$ hydrogen bonds in the chains are somewhat longer. The chains are links into layers through the lattice water molecules (Moritani & Kashino, 1991). A chain structure is also adopted by anhydrous piperazinium adipate, which displays hydrogen bonds (Vanier & Brisse, 1983) that are somewhat longer than those in the dicyclohexylammonium salt. Slightly longer hydrogen bonds are also noted in hexamethyldiammonium adipate (Brown, 1966).

Experimental

Dicyclohexylamine, adipic acid and bis(tributyltin) oxide in a 2:2:1 molar stoichiometry were heated in a small volume of ethanol in an attempt to synthesize dicyclohexylammonium succinatotributylstannate. The procedure had been used to prepare the tributylstannate derivatives of oxalic (Ng *et al.*, 1990), malonic (Ng *et al.*, 1992) and succinic (Ng & Holecek, 1998) acids, but the reaction with adipic acid gave the organic salt as a hydrate. The Cu radiation powder diffractogram of the bulk compound is identical to the diffractogram that is calculated from the atomic coordinates by *POWDIS* (McArdle & Cunningham, 1998).

Crystal data

$2C_{12}H_{24}N^+ \cdot C_6H_8O_4^{2-} \cdot H_2O$
 $M_r = 526.78$
 Monoclinic, $C2/c$
 $a = 10.155$ (3) Å
 $b = 15.638$ (5) Å
 $c = 20.102$ (6) Å
 $\beta = 104.56$ (1)°
 $V = 3089.8$ (16) Å³
 $Z = 4$

$D_x = 1.132$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 25 reflections
 $\theta = 7.0$ – 14.0°
 $\mu = 0.075$ mm⁻¹
 $T = 298$ (2) K
 Parallelepiped, colorless
 0.50 × 0.50 × 0.40 mm

Data collection

Siemens *R3m* diffractometer
 ω scans
 Absorption correction: empirical ψ scan (North *et al.*, 1968)
 $T_{min} = 0.912$, $T_{max} = 1.000$
 2879 measured reflections
 2715 independent reflections
 1461 reflections with $I > 2\sigma(I)$

$R_{int} = 0.089$
 $\theta_{max} = 25^\circ$
 $h = 0 \rightarrow 12$
 $k = 0 \rightarrow 18$
 $l = -23 \rightarrow 23$
 2 standard reflections every 118 reflections
 intensity decay: none

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.059$
 $wR(F^2) = 0.159$
 $S = 0.977$
 2715 reflections
 181 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0754P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{max} = 0.001$
 $\Delta\rho_{max} = 0.18$ e Å⁻³
 $\Delta\rho_{min} = -0.18$ e Å⁻³
 Extinction correction: *SHELXL97*
 Extinction coefficient: 0.017 (1)

The N- and O-bonded H atoms were located and refined.

Data collection: *XSCANS* (Siemens, 1990); cell refinement: *XSCANS*; data reduction: *SHELXTL-Plus* (Sheldrick, 1990); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); software used to prepare material for publication: *SHELXL97*.

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