

[4-(Diethylamino)benzoato- κ O]triphenyltin(IV)Yip Foo Win,^a Siang Guan Teoh,^a
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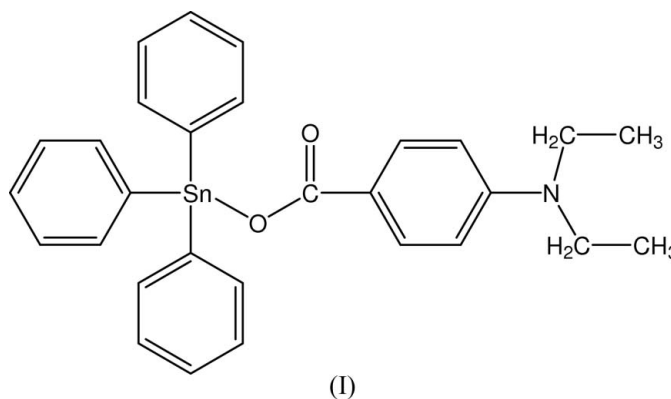
Key indicators

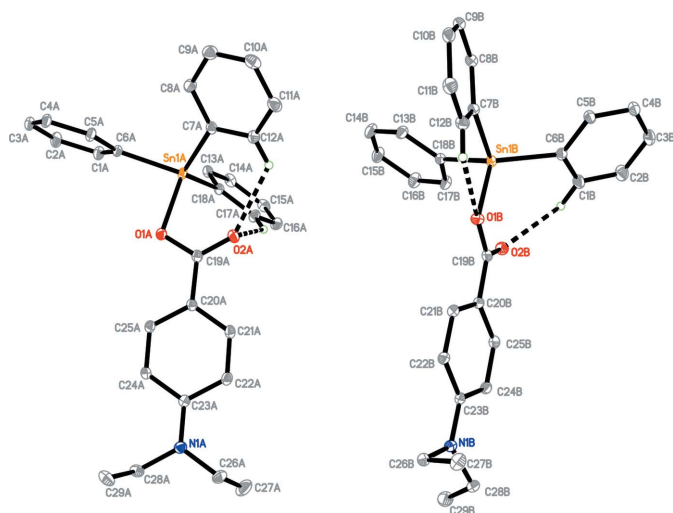
Single-crystal X-ray study
 $T = 100$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.027
 wR factor = 0.072
Data-to-parameter ratio = 43.8For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.The Sn atom in the title compound, $[\text{Sn}(\text{C}_6\text{H}_5)_3(\text{C}_{11}\text{H}_{14}\text{NO}_2)]$, shows tetrahedral coordination. The asymmetric unit has two independent molecules; the crystal structure is stabilized by $\text{C}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\pi$ interactions.

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Comment

Recent *in vitro* antitumour and antibacterial activity studies of organotin(IV) carboxylate compounds have revealed their effectiveness as antitumour drugs (Willem *et al.*, 1997, Gielen *et al.*, 2000, Tian *et al.*, 2005). Moreover, among the organotin(IV) carboxylate compounds, triorganotin(IV) carboxylates display the highest biological activity (Novelli *et al.*, 1999). Generally, triphenyltin(IV) carboxylate complexes are commonly found as monomeric structures with four-coordinate distorted tetrahedral or five-coordinate trigonal-bipyramidal geometry (Baul *et al.*, 2001; Yeap & Teoh, 2003; Win *et al.*, 2006). In a recent study, the coordination geometry of (3,5-dinitrobenzoato)triphenyltin(IV) was found to be distorted tetrahedral and due to the long range interaction of the carboxylate anion coordinated to Sn in an isobidentate manner (Win *et al.*, 2006). Based on a crystallography structural study, the title complex, (I), is monomeric with two molecules in the asymmetric unit.The ligand bond lengths and angles in (I) have normal values (Allen *et al.*, 1987), comparable to a related structure (Win *et al.*, 2006); bond lengths and angles for the Sn coordination are given in Table 1. In molecule *A*, the dihedral angles between $\text{C}1\text{A}-\text{C}6\text{A}$ and $\text{C}7\text{A}-\text{C}12\text{A}$, $\text{C}7\text{A}-\text{C}12\text{A}$ and $\text{C}13\text{A}-\text{C}18\text{A}$, and $\text{C}1\text{A}-\text{C}6\text{A}$ and $\text{C}13\text{A}-\text{C}18\text{A}$ are 45.36 (7), 61.01 (7) and 28.62 (6)°, respectively. In molecule *B*, the dihedral angles between $\text{C}1\text{B}-\text{C}6\text{B}$ and $\text{C}7\text{B}-\text{C}12\text{B}$, $\text{C}7\text{B}-\text{C}12\text{B}$ and $\text{C}13\text{B}-\text{C}18\text{B}$, and $\text{C}1\text{B}-\text{C}6\text{B}$ and $\text{C}13\text{B}-\text{C}18\text{B}$ are 62.64 (7), 64.60 (7) and 53.21 (7)°, respectively.


Figure 1

The asymmetric unit of (I), showing 30% probability displacement ellipsoids and the atomic numbering. The intramolecular hydrogen bonds are shown as dashed lines. H atoms not involved in the hydrogen bonds have been omitted.

Intramolecular $C1B-H1BA \cdots O2B$, $C12A-H12A \cdots O2A$ and $C17A-H17A \cdots O2A$ hydrogen bonds generate $S(7)$ ring motifs, while the $C12B-H12B \cdots O1B$ hydrogen bond generates an $S(5)$ ring motif (Table 2) (Bernstein *et al.*, 1995). The crystal structure is stabilized by $C-H \cdots O$ and $C-H \cdots \pi$ interactions (Table 2).

Experimental

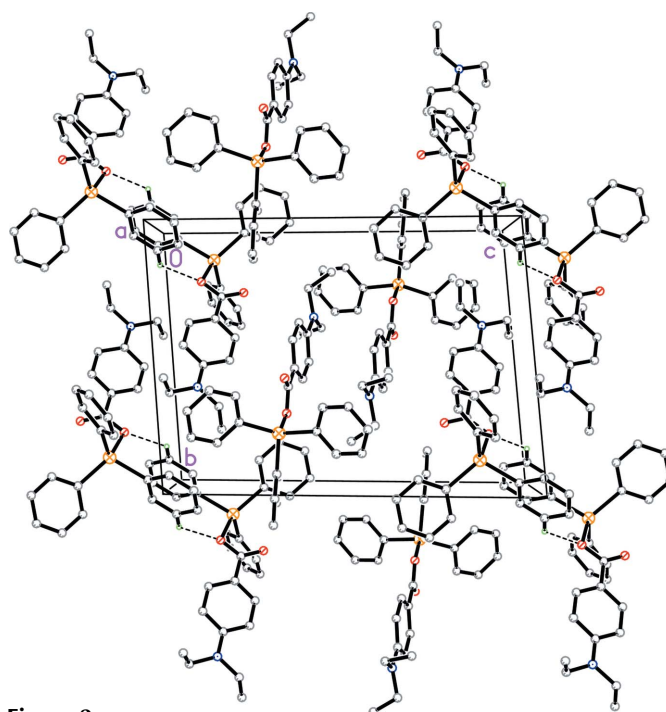
The complex 4-(diethylaminobenzoato)triphenyltin(IV) was obtained by heating under reflux a 1:1 molar mixture of triphenyltin(IV) hydroxide (1.10 g, 3 mmol) and 4-(diethylamino)benzoic acid (0.58 g, 3 mmol) in acetonitrile (50 ml) for 2 h. A clear transparent solution was isolated by filtration and kept in a bottle. After 4 d, some colourless crystals (1.30 g, 79.9% yield) were obtained (m.p. 386.7–387.0 K). Analysis found: C 64.28, H 5.00, N 2.63, Sn 21.31%; calculated for $C_{29}H_{29}NO_2Sn$: C 64.24, H 5.39, N 2.58, Sn 21.89%. FT-IR from a KBr disc (cm^{-1}): $\nu(COO)_{as}$ 1603, $\nu(COO)_s$ 1347, $\nu(O-Sn-O)$ 617, $\nu(Sn-O)$ 448.

Crystal data

$[Sn(C_6H_5)_3(C_{11}H_{14}NO_2)]$	$V = 2495.16$ (11) \AA^3
$M_r = 542.22$	$Z = 4$
Triclinic, $P\bar{1}$	$D_x = 1.443$ $Mg\ m^{-3}$
$a = 10.8876$ (3) \AA	Mo $K\alpha$ radiation
$b = 13.0407$ (3) \AA	$\mu = 1.05$ mm^{-1}
$c = 17.8896$ (5) \AA	$T = 100.0$ (1) K
$\alpha = 84.632$ (1)°	Block, colourless
$\beta = 82.117$ (1)°	$0.41 \times 0.36 \times 0.31$ mm
$\gamma = 84.260$ (1)°	

Data collection

Bruker SMART APEX2 CCD diffractometer	104338 measured reflections
ω scans	26062 independent reflections
Absorption correction: multi-scan (SADABS; Bruker, 2005)	21490 reflections with $I > 2\sigma(I)$
$T_{min} = 0.646$, $T_{max} = 0.735$	$R_{int} = 0.032$
	$\theta_{max} = 37.5^\circ$


Figure 2

The crystal packing of (I), viewed down the a axis. Dashed lines indicate hydrogen bonds. H atoms not involved in the hydrogen bonding have been omitted.

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.027$
 $wR(F^2) = 0.072$
 $S = 1.04$
 26062 reflections
 595 parameters
 H-atom parameters constrained

$$w = 1/[\sigma^2(F_o^2) + (0.0321P)^2 + 0.7386P]$$

where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{max} < 0.001$
 $\Delta\rho_{max} = 0.94$ $e\ \text{\AA}^{-3}$
 $\Delta\rho_{min} = -0.40$ $e\ \text{\AA}^{-3}$

Table 1

Selected geometric parameters (\AA , °).

Sn1A—O1A	2.0686 (9)	Sn1B—O1B	2.0639 (9)
Sn1A—C18A	2.1285 (11)	Sn1B—C18B	2.1240 (12)
Sn1A—C7A	2.1365 (13)	Sn1B—C6B	2.1301 (12)
Sn1A—C6A	2.1413 (12)	Sn1B—C7B	2.1362 (12)
O1A—Sn1A—C18A	105.41 (4)	O1B—Sn1B—C18B	108.36 (4)
C18A—Sn1A—C7A	117.81 (4)	O1B—Sn1B—C6B	114.95 (4)
O1A—Sn1A—C6A	94.13 (4)	C18B—Sn1B—C7B	108.42 (5)
C7A—Sn1A—C6A	108.11 (5)	C6B—Sn1B—C7B	111.40 (5)

Table 2

Hydrogen-bond geometry (\AA , °).

$Cg1$, $Cg2$, $Cg3$, $Cg4$, $Cg5$ and $Cg6$ are centroids of the $C1B-C6B$, $C13B-C18B$, $C1A-C6A$, $C13A-C18A$, $C20A-C25A$ and $C20B-C25B$ rings, respectively.

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$C4A-H4AA \cdots O1A^i$	0.93	2.55	3.239 (2)	132
$C1B-H1BA \cdots O2B$	0.93	2.52	3.121 (2)	123
$C12A-H12A \cdots O2A$	0.93	2.43	3.080 (2)	127
$C12B-H12B \cdots O1B$	0.93	2.55	3.120 (2)	120
$C17A-H17A \cdots O2A$	0.93	2.35	3.082 (2)	135
$C8A-H8AA \cdots Cg1^{ii}$	0.93	3.15	3.795 (2)	128
$C10A-H10A \cdots Cg2^{ii}$	0.93	3.06	3.462 (2)	108

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$C4B-H4BA \cdots Cg3^{ii}$	0.93	2.85	3.567 (2)	135
$C9B-H9BA \cdots Cg4^{ii}$	0.93	2.59	3.327 (1)	137
$C15A-H15A \cdots Cg5^{iii}$	0.93	2.85	3.661 (1)	146
$C22A-H22A \cdots Cg6^{iv}$	0.93	3.13	3.653 (1)	118
$C26B-H26C \cdots Cg2^{iv}$	0.97	2.88	3.723 (1)	146
$C29A-H29A \cdots Cg4^v$	0.96	2.87	3.799 (2)	162

Symmetry codes: (i) $-x+1, -y, -z$; (ii) $-x, -y, -z+1$; (iii) $x-1, y, z$; (iv) $-x+1, -y+1, -z+1$; (v) $-x+1, -y+1, -z$.

H atoms were positioned geometrically and treated as riding, with $C-H = 0.93-0.97 \text{ \AA}$ and $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(\text{methyl } C)$.

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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