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Key indicators

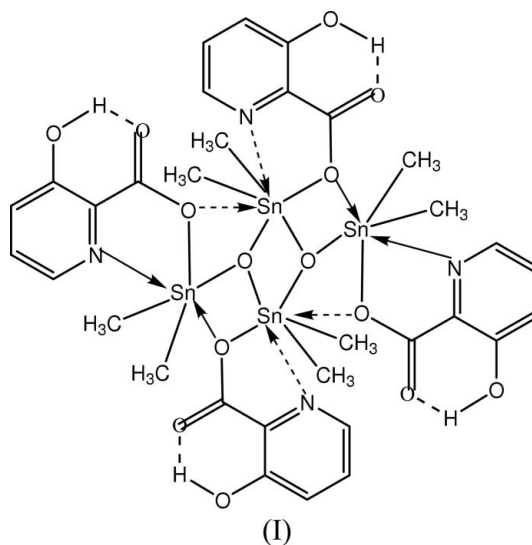
Single-crystal X-ray study
T = 295 K
Mean σ (C–C) = 0.009 Å
R factor = 0.037
wR factor = 0.114
Data-to-parameter ratio = 18.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Tetrakis(μ_2 -3-hydroxypyridine-2-carboxylato- κ^2O,N)di- μ_3 -oxo-tetrakis[dimethyltin(IV)]

In the crystal structure of the title centrosymmetric distannoxane, $[\text{Sn}_4(\text{CH}_3)_8(\text{C}_6\text{H}_4\text{NO}_3)_2\text{O}_2]$, one 3-hydroxypyridine-2-carboxylate ligand chelates through N and O atoms to an Sn atom. A singly bonded carboxylate O atom coordinates weakly to another independent Sn atom [at a distance of 2.983 (4) Å], which is pseudo-chelated by the other 3-hydroxypyridine-2-carboxylate ligand [$\text{Sn}\cdots\text{N}$ 2.846 (4) Å]. The μ_3 -binding mode of both ligands leads to a skew-trapezoidal bipyramidal geometry [C–Sn–C 136.0 (3)°] for the six-coordinate Sn atom and a *trans*-pentagonal bipyramidal geometry [C–Sn–C 148.9 (3)°] for the seven-coordinate Sn atom.

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Comment

Bis(3-hydroxypyridyl-2-carboxylato)dimethyltin adopts a six-coordinate skew-trapezoidal bipyramidal structure, in which the dimethyltin skeleton is bent [C–Sn–C 149.4 (3)°; Tian *et al.*, 2005]. The title distannoxane, (I), can be considered as the hydrolysis product of this compound. The structural chemistry of this class of organotin carboxylates has been reviewed (Ng *et al.*, 1991; Tiekink, 1991, 1994).



The title centrosymmetric dimer features two unique 3-hydroxypyridyl-2-carboxylate groups, both of which bridge two Sn centres through their singly bonded carboxylate O atom (the doubly bonded carbonyl O atom is not coordinated to the Sn atom, but instead is involved in intramolecular hydrogen bonding with the hydroxy group).

Atom Sn1 is seven-coordinate (Fig. 1), owing to the presence of two relatively long interactions, namely an Sn–N

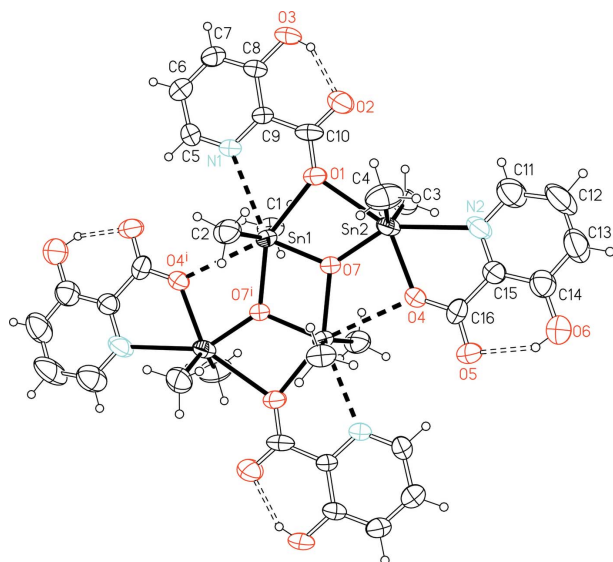


Figure 1

A plot of (I), showing displacement ellipsoids at the 50% probability level and H atoms as spheres of arbitrary radii. Open dashed lines indicate hydrogen bonds. [Symmetry code: (i) $1 - x, 1 - y, 1 - z$.]

interaction of 2.846 (4) Å and an Sn—O interaction of 2.983 (4) Å (arising from the carboxylate that is also covalently bonded to the other unique Sn atom). The geometry can be described as a *cis*-C₂SnO₃ trigonal bipyramidal, distorted to a *trans*-C₂SnO₅ pentagonal bipyramidal because (in part) of the two longer interactions. These long interactions cause a widening of the C1—Sn1—C2 angle but are, however, not strongly coordinating enough to cause the axial atoms to adopt a linear arrangement. On the other hand, atom Sn2 is six-coordinate, with the ligand coordinating in an unambiguous chelating mode through O and N atoms.

The structure of (I) is similar to that of the tetrabutyl-distannoxane analogue of picolinic acid, which has been described in detail (Parulekar *et al.*, 1989).

Experimental

The reaction was carried out under a nitrogen atmosphere. 3-Hydroxy-2-pyridylcarboxylic acid (0.139 g, 1 mmol) and dimethyltin oxide (0.165 g, 1 mmol) were refluxed in benzene (40 ml) for 12 h. The solvent was removed and the product recrystallized from a dichloromethane–hexane mixture (1:1 v/v) to yield colourless crystals in nearly quantitative yield (m.p. 433 K). CHN elemental analysis, found: C 31.60, H 3.64, N 4.62%; calculated for C₃₂H₄₄N₄O₁₆Sn₄: C 31.62, H 3.65, N 4.61%.

Crystal data

[Sn₄(CH₃)₈(C₆H₄NO₃)₂]

M_r = 1179.44

Triclinic, *P* $\bar{1}$

a = 8.395 (1) Å

b = 10.055 (1) Å

c = 13.157 (2) Å

α = 89.336 (2)°

β = 82.842 (2)°

γ = 72.231 (1)°

V = 1049.0 (2) Å³

Z = 1

D_x = 1.867 Mg m⁻³

Mo *K*α radiation

Cell parameters from 3297

reflections

θ = 2.5–28.0°

μ = 2.42 mm⁻¹

T = 295 (2) K

Block, colourless

0.45 × 0.37 × 0.23 mm

Data collection

Siemens SMART CCD area-detector diffractometer

φ and ω scans

Absorption correction: multi-scan

(*SADABS*; Sheldrick, 1996)

T_{min} = 0.337, *T_{max}* = 0.576

6588 measured reflections

4646 independent reflections

3460 reflections with *I* > 2σ(*I*)

R_{int} = 0.023

θ_{\max} = 27.5°

h = −10 → 10

k = −13 → 12

l = −17 → 11

Refinement

Refinement on *F*²

R[*F*² > 2σ(*F*²)] = 0.037

wR(*F*²) = 0.114

S = 1.08

4646 reflections

248 parameters

H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0585P)^2 + 0.3682P]$

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

(Δ/σ)_{max} = 0.001

$\Delta\rho_{\max}$ = 1.39 e Å⁻³

$\Delta\rho_{\min}$ = −0.89 e Å⁻³

Table 1

Selected geometric parameters (Å, °).

Sn1—C1	2.104 (6)	Sn2—C3	2.107 (5)
Sn1—C2	2.099 (6)	Sn2—C4	2.108 (6)
Sn1—N1	2.846 (4)	Sn2—N2	2.576 (5)
Sn1—O1	2.314 (4)	Sn2—O1	2.557 (3)
Sn1—O4 ⁱ	2.983 (4)	Sn2—O4	2.152 (4)
Sn1—O7	2.050 (3)	Sn2—O7	2.012 (3)
Sn1—O7 ⁱ	2.154 (3)		
C1—Sn1—C2	148.9 (3)	O4 ⁱ —Sn1—O7	133.5 (1)
C1—Sn1—N1	76.9 (2)	O4 ⁱ —Sn1—O7 ⁱ	58.9 (1)
C1—Sn1—O1	93.3 (2)	O7—Sn1—O7 ⁱ	74.6 (2)
C1—Sn1—O4 ⁱ	80.8 (2)	C3—Sn2—C4	136.0 (3)
C1—Sn1—O7	104.6 (2)	C3—Sn2—N2	85.9 (2)
C1—Sn1—O7 ⁱ	94.3 (2)	C3—Sn2—O1	83.7 (2)
C2—Sn1—N1	79.5 (2)	C3—Sn2—O4	108.6 (2)
C2—Sn1—O1	93.5 (2)	C3—Sn2—O7	104.7 (2)
C2—Sn1—O4 ⁱ	80.0 (2)	C4—Sn2—N2	84.5 (3)
C2—Sn1—O7 ⁱ	96.4 (2)	C4—Sn2—O1	81.3 (2)
C2—Sn1—O7	106.3 (2)	C4—Sn2—O4	107.1 (2)
N1—Sn1—O1	62.3 (1)	C4—Sn2—O7	107.2 (3)
N1—Sn1—O4 ⁱ	91.9 (1)	N2—Sn2—O1	146.6 (1)
N1—Sn1—O7	134.6 (1)	N2—Sn2—O4	67.6 (1)
N1—Sn1—O7 ⁱ	150.7 (1)	N2—Sn2—O7	145.8 (1)
O1—Sn1—O4 ⁱ	154.2 (1)	O1—Sn2—O4	145.7 (1)
O1—Sn1—O7	72.3 (1)	O1—Sn2—O7	67.7 (1)
O1—Sn1—O7 ⁱ	146.9 (1)	O4—Sn2—O7	78.2 (1)

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>
O3—H3O...O2	0.82	1.84	2.561 (6)	146
O6—H6O...O5	0.82	1.95	2.579 (6)	133

All H atoms were positioned geometrically, with C—H_{methyl} = 0.96, C—H_{pyridyl} = 0.93 and O—H = 0.82 Å, and were included in the refinement in the riding-model approximation, with *U*_{iso}(H) = 1.2*U*_{eq}(C,O). The final difference Fourier map had a large peak 2.9 Å from O2. Attempts to refine the peak as a water molecule were unsuccessful.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

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