

Bis[*N,N*-bis(2-hydroxyethyl)dithiocarbamato]dimethyltin(IV)

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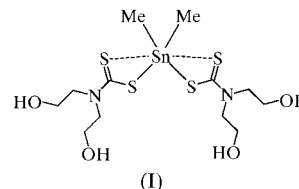
The title compound, [Sn(CH₃)₂(C₅H₁₀NO₂S₂)₂], has crystallographic mirror symmetry (C—Sn—C on mirror plane) and the coordination polyhedron around the Sn atom is a tetrahedron [C—Sn—C 139.3 (2)° and S—Sn—S 82.3 (1)°] distorted towards a skew-trapezoidal bipyramid owing to an intramolecular Sn···S contact [3.0427 (6) Å]. The molecules are linked into a linear chain by intermolecular O—H···O hydrogen bonds [O···O 2.646 (3) Å].

Comment

The structures of a number of diorganotin(IV) bis(*N,N*-dithiocarbamates) have been reported. Among the dimethyltin derivatives, the dimethyldithiocarbamate (Kimura *et al.*, 1972), the three modifications of the diethyldithiocarbamate (Lockhart *et al.*, 1986; Morris & Schlemper, 1979) and the tetramethylenedithiocarbamate (Lockhart *et al.*, 1985) have a dimethyltin skeleton is opened up to about 135°, so that the geometry is not a strict tetrahedron. The geometries of these and other bis(chelated) diorganotin compounds having such a bent skeleton have been described in terms of a skew-trapezoidal bipyramid (Ng *et al.*, 1987). The dithiocarbamates display an intramolecular tin–sulfur interaction of about 3 Å, which is only about 0.5 Å longer than the covalent tin–sulfur distances. On the other hand, for the trimethyltin derivatives, as the interaction is much longer, the dithiocarbamate group is essentially monodentate (Lokaj *et al.*, 1986).

The introduction of two hydroxy substituents in the diethyldithiocarbamate ligand results in the title compound, (I), whose molecules are stacked as a linear chain along the *a* axis. The component molecules are held together by strong hydrogen bonds; the intermolecular hydrogen bond [O···O 2.646 (3) Å and O—H···O 170 (3)°] is shorter than the intramolecular hydrogen bond [O···O 2.683 (3) Å and O—H···O 172 (4)°]. In the tellurium(II) and diiodotellurium(IV)

derivatives, the two hydroxy groups of each dithiocarbamate ligand are not linked; instead, the four hydroxy groups of one molecule are linked to the hydroxy groups of adjacent molecules, but the hydrogen bonds are much weaker (Appa Rao *et al.*, 1983; Rout *et al.*, 1983). Similarly, only intermolecular hydrogen bonds are found in the nickel [O···O 2.707 (5) and 2.711 (5) Å; Ramalingam *et al.*, 1984] and copper [O···O 2.412 (2) Å; Radha *et al.*, 1985] derivatives.



Experimental

A solution of carbon disulfide (1.5 ml) in methanol (5 ml) was added to a methanol solution (100 ml) of a mixture of dimethyltin dichloride (1.1 g, 5 mmol) and ethanolamine (3 ml, 31 mmol) in methanol (100 ml). Both solutions were initially cooled to 273 K and the carbon disulfide solution was added at a rate such that the temperature of the reaction mixture did not rise above 273 K. The yellow product that separated from the stirred mixture after several hours of stirring was collected and recrystallized from methanol to afford yellow crystals of the dimethyltin complex. The crystal used in the study was the only one suitable for the diffraction measurements. Because of the relatively large size, it was likely that the crystal would not be bathed in the X-ray radiation during a part of the measurements. However, the error was deemed to be minor as the structure was well behaved in the refinements.

Crystal data

[Sn(CH₃)₂(C₅H₁₀NO₂S₂)₂]
M_r = 509.28
Orthorhombic, *Pnma*
a = 7.251 (1) Å
b = 28.761 (3) Å
c = 9.635 (1) Å
V = 2009.3 (4) Å³
Z = 4
D_x = 1.683 Mg m⁻³

Mo *Kα* radiation
Cell parameters from 46 reflections
θ = 5.4–12.5°
μ = 1.704 mm⁻¹
T = 298 (2) K
Irregular block, colorless
0.70 × 0.56 × 0.48 mm

Data collection

Siemens *P4* diffractometer
ω–2*θ* scans
Absorption correction: empirical *ψ* scan (North *et al.*, 1968)
T_{min} = 0.580, *T_{max}* = 0.606
3859 measured reflections
2964 independent reflections
2457 reflections with *I* > 2σ(*I*)

R_{int} = 0.038
θ_{max} = 30°
h = –1 → 10
k = –40 → 1
l = –1 → 13
3 standard reflections
every 97 reflections
intensity decay: none

Refinement

Refinement on *F*²
R[*F*² > 2σ(*F*²)] = 0.027
wR(*F*²) = 0.073
S = 1.049
2964 reflections
118 parameters
H atoms treated by a mixture of independent and constrained refinement

w = 1/[σ²(*F_o*²) + (0.0360*P*)²]
where *P* = (*F_o*² + 2*F_c*²)/3
(Δ/σ)_{max} = 0.001
Δρ_{max} = 0.43 e Å⁻³
Δρ_{min} = –0.61 e Å⁻³
Extinction correction: *SHELXL97*
Extinction coefficient: 0.0134 (5)

The hydroxyl H atoms were located and refined.

Data collection: *XSCANS* (Siemens, 1994); cell refinement: *XSCANS*; data reduction: *XSCANS*; 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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