

{4-Hydroxy-*N'*-[(2*E*,3*Z*)-4-oxido-4-phenylbut-3-en-2-ylidene]benzohydrazidato}diphenyltin(IV) methanol monosolvate

Md. Abu Affan,^a† Norrihan B. Sam,^a Fasihuddin B. Ahmad,^a Fraser White^b and Edward R. T. Tiekink^{c*}

^aFaculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia, ^bAgilent Technologies UK Ltd, 10 Mead Road, Oxford Industrial Park, Oxford OX5 1QU, England, and ^cDepartment of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia

Correspondence e-mail: edward.tiekink@gmail.com

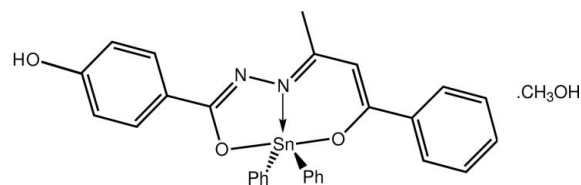
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Key indicators: single-crystal X-ray study; $T = 150$ K; mean $\sigma(\text{C}-\text{C}) = 0.005$ Å; R factor = 0.032; wR factor = 0.079; data-to-parameter ratio = 13.6.

Two independent diphenyltin molecules and two independent methanol molecules comprise the asymmetric unit of the title compound, $[\text{Sn}(\text{C}_6\text{H}_5)_2(\text{C}_{17}\text{H}_{14}\text{N}_2\text{O}_3)] \cdot \text{CH}_3\text{OH}$. The Sn atom in each is five-coordinated by a tridentate ligand and the *ipso*-C atoms of the Sn-bound benzene substituents. The resulting $\text{C}_2\text{N}_2\text{O}$ donor set defines a coordination geometry that is intermediate between trigonal-bipyramidal (TP) and square-pyramidal (SP), with one molecule slightly tending towards TP and the other slightly towards SP. The molecules differ in terms of the relative orientations of the terminal benzene rings [dihedral angles = 45.71 (18) and 53.98 (17) $^\circ$] and of the Sn-bound benzene substituents [dihedral angles = 59.5 (2) and 45.77 (18) $^\circ$, respectively]. The most prominent feature of the crystal packing is the formation of four-molecule aggregates *via* $\text{O}-\text{H} \cdots \text{O}$ and $\text{O}-\text{H} \cdots \text{N}$ hydrogen bonds, in which the hydroxy group is connected to a methanol molecule which, in turn, is linked to a non-coordinating N atom. Weak $\text{C}-\text{H} \cdots \pi$ interactions also occur.

Related literature

For background to the biological interest in related compounds, see: Affan *et al.* (2010). For related structures, see: Affan *et al.* (2009, 2011). For additional structural analysis, see: Addison *et al.* (1984).



Experimental

Crystal data

$[\text{Sn}(\text{C}_6\text{H}_5)_2(\text{C}_{17}\text{H}_{14}\text{N}_2\text{O}_3)] \cdot \text{CH}_3\text{O}$
 $M_r = 599.23$
 Monoclinic, $P2_1/c$
 $a = 18.6824$ (2) Å
 $b = 28.7280$ (4) Å
 $c = 10.3369$ (1) Å
 $\beta = 99.856$ (1) $^\circ$
 $V = 5466.02$ (11) Å³
 $Z = 8$
 Cu $K\alpha$ radiation
 $\mu = 7.74$ mm⁻¹
 $T = 150$ K
 $0.37 \times 0.29 \times 0.17$ mm

Data collection

Agilent SuperNova Dual diffractometer with an Atlas detector
 17500 measured reflections
 9175 independent reflections
 8138 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.036$
 Absorption correction: analytical (CrysAlis PRO; Agilent, 2011)
 $T_{\text{min}} = 0.231$, $T_{\text{max}} = 0.611$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.032$
 $wR(F^2) = 0.079$
 $S = 1.00$
 9175 reflections
 675 parameters
 H-atom parameters constrained
 $\Delta\rho_{\text{max}} = 0.46$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.58$ e Å⁻³

Table 1

Selected bond lengths (Å).

Sn1—O1	2.124 (2)	Sn2—O4	2.123 (2)
Sn1—O3	2.102 (2)	Sn2—O6	2.094 (2)
Sn1—N2	2.133 (2)	Sn2—N4	2.141 (3)
Sn1—C18	2.118 (4)	Sn2—C47	2.116 (3)
Sn1—C24	2.117 (3)	Sn2—C53	2.124 (3)

Table 2

Hydrogen-bond geometry (Å, $^\circ$).

$Cg1$, $Cg2$ and $Cg3$ are the centroids of the $\text{C}31-\text{C}36$, $\text{C}18-\text{C}23$ and $\text{C}12-\text{C}17$ rings, respectively.

$D-\text{H} \cdots A$	$D-\text{H}$	$\text{H} \cdots A$	$D \cdots A$	$D-\text{H} \cdots A$
$\text{O}2-\text{H}2\text{o} \cdots \text{O}8^{\text{i}}$	0.84	1.81	2.650 (4)	175
$\text{O}5-\text{H}5\text{o} \cdots \text{O}7^{\text{ii}}$	0.84	1.85	2.681 (4)	170
$\text{O}7-\text{H}7\text{o} \cdots \text{N}3^{\text{iii}}$	0.84	2.02	2.830 (4)	163
$\text{O}8-\text{H}8\text{o} \cdots \text{N}1^{\text{iv}}$	0.84	1.98	2.821 (4)	175
$\text{C}50-\text{H}50 \cdots Cg1^{\text{v}}$	0.95	2.91	3.440 (5)	116
$\text{C}57-\text{H}57 \cdots Cg2$	0.95	2.84	3.664 (4)	145
$\text{C}60-\text{H}60\text{a} \cdots Cg3^{\text{vi}}$	0.98	2.98	3.886 (6)	155

Symmetry codes: (i) $-x + 1, -y + 1, -z + 2$; (ii) $x, y, z + 1$; (iii) $-x + 1, -y + 1, -z + 1$; (iv) $x - 1, y, z - 1$; (v) $x, y, z - 1$; (vi) $x - 1, y, z$.

Data collection: CrysAlis PRO (Agilent, 2011); cell refinement: CrysAlis PRO; data reduction: CrysAlis PRO; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: ORTEP-3 (Farrugia, 1997), DIAMOND (Brandenburg, 2006) and Qmol (Gans & Shalloway, 2001); software used to prepare material for publication: PLATON (Spek, 2009) and pubCIF (Westrip, 2010).

† Additional correspondence author, e-mail: maaffan@yahoo.com.