

Aqua[4-(1*H*-benzimidazol-2-yl)benzoato]-
triphenyltin(IV) dioxane solvateXiao-Niu Fang,^{a*} Yi-An Xiao,^b
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The title complex, $[\text{Sn}(\text{C}_6\text{H}_5)_3(\text{C}_{14}\text{H}_9\text{N}_2\text{O}_2)(\text{H}_2\text{O})] \cdot \text{C}_4\text{H}_8\text{O}_2$, is composed of a triphenyltin carboxylate with a coordinated water molecule and a free dioxane molecule. The Sn^{IV} atom is five-coordinate and has a *trans*- C_3SnO_2 trigonal-bipyramidal geometry, with the three phenyl groups occupying the equatorial plane, the 4-(1*H*-benzimidazol-2-yl)benzoate ligand coordinating in a monodentate manner and a water molecule in the axial positions. Strong intermolecular $\text{O} \cdots \text{H}$ and $\text{N} \cdots \text{H} \cdots \text{O}$ hydrogen bonds link the molecules into an infinite two-dimensional network, with these networks held together by van der Waals forces to generate a layer structure. π - π Stacking interactions also exist in the crystal structure.

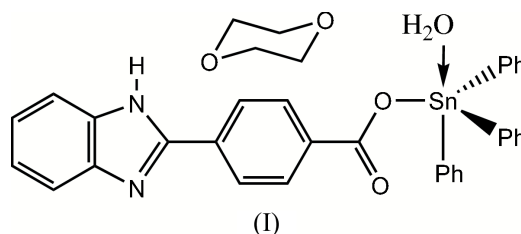
Key indicators

Single-crystal X-ray study
 $T = 296 \text{ K}$
 Mean $\sigma(\text{C}-\text{C}) = 0.011 \text{ \AA}$
 Disorder in solvent or counterion
 R factor = 0.055
 wR factor = 0.177
 Data-to-parameter ratio = 23.0

For details of how these key indicators were
 automatically derived from the article, see
<http://journals.iucr.org/e>.

Comment

Benzimidazole and its derivatives are potential complexing agents, and have been found to have a broad scope for spin crossover and biological activities (Lin *et al.*, 2004), as well as antitumour activity (Schulz & Skibo, 2000) and anti-amoebic activity (Bharti *et al.*, 2000). The structural chemistry of organotin carboxylate complexes has attracted considerable attention, owing to their good antitumour activities (Barbieri *et al.*, 2001; Zhou *et al.*, 2005), their versatile molecular structures, and the supramolecular architectures exhibited by these complexes (Ma *et al.*, 2005). In the context of our continued interest in the structural and biological properties of organotin complexes (Fang *et al.*, 2001, 2006), we report here the synthesis and crystal structure of the title complex, (I).



Compound (I) crystallizes in the space group $P2_1/c$, with a triphenyltin carboxylate, a coordinated water molecule and a free dioxane molecule in the asymmetric unit, as shown in Fig. 1. The Sn^{IV} atom is five-coordinate and has a *trans*- C_3SnO_2 trigonal-bipyramidal geometry. The three phenyl groups occupy the equatorial plane, with the Sn^{IV} atom lying only 0.169 (2) \AA out of the trigonal plane (in the direction of atom O2) defined by the three *ipso*-C atoms of the phenyl rings. The three phenyl rings are not coplanar, and the interplanar angles between them are 28.4 (1) (between the C15- and C27-rings),

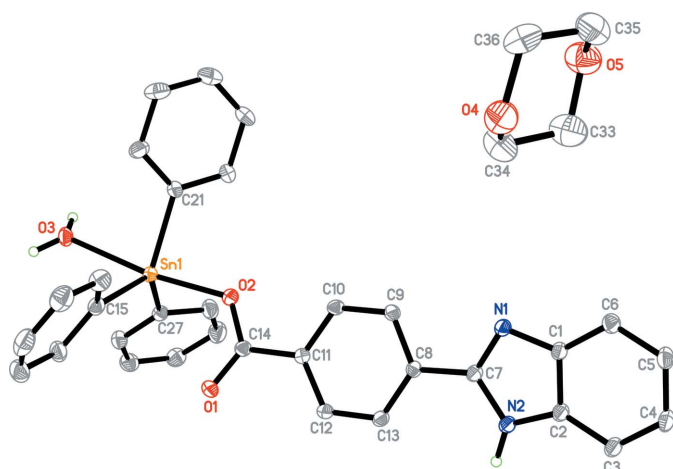


Figure 1
The asymmetric unit of (I), showing the atom-labelling scheme and 10% probability displacement ellipsoids. All carbon-bound H atoms have been omitted for clarity.

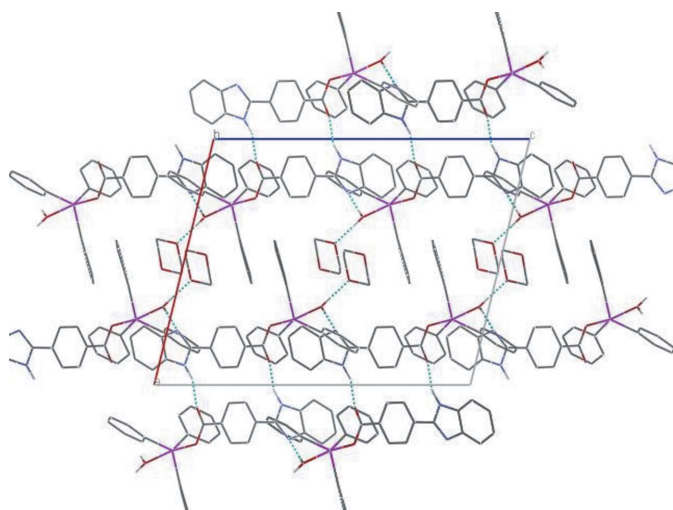


Figure 2
A packing diagram of (I), viewed along the *b* axis. Hydrogen bonds are shown as dashed lines. All carbon-bound H atoms have been omitted for clarity.

44.34 (9) (between the C21- and C27-rings) and 49.23 (9)^o (between the C15- and C21-rings), respectively. The 4-(1*H*-benzo[*d*]imidazol-2-yl)benzoate ligand coordinates in monodentate mode and occupies an axial position, with the other axial ligand being a coordinated water molecule. The axial ligands are not coordinated exactly linearly [O3—Sn1—O2 = 172.2 (2)^o] and, although the Sn1—O2 bond length is normal, the Sn1—O3 bond is much shorter than the value of 2.471 (6) Å found by Kemmer *et al.* (1999). This is due to the coplanarity of the atoms Sn1, C15, C21 and C27, as mentioned above. The benzimidazole ring system makes a dihedral angle of 15.66 (8)^o with the benzene ring of the benzoate group.

There are three classical intermolecular hydrogen bonds in the packing of (I), as shown in Table 2 and Fig. 2. These strong hydrogen bonds link the molecules into an infinite two-

dimensional network, as shown in Fig. 2, while these networks are held together by van der Waals forces to generate a layer structure. A π - π stacking interaction exists between the benzene ring of the benzimidazole and one of the phenyl rings attached to the Sn atom [the C6 \cdots C17^{iv} distance in the offset face-to-face interaction is 3.477 Å; symmetry code: (iv) $x, -\frac{1}{2} - y, \frac{1}{2} + z$].

Experimental

The title complex was prepared by the following procedure. A solution of 1,2-benzenediamine (0.108 g, 1 mmol) and 4-formylbenzoic acid (0.150 g, 1 mmol) in ethanol (20 ml) was heated for 3 h under reflux. Triphenylstannanol (0.625 g, 1 mmol) dissolved in acetonitrile (10 ml) was then added, and the mixture was heated for another 3 h under reflux. The reaction mixture was then cooled and the pale-yellow precipitate which had formed was filtered off. The reaction yield is 75% and no melting point could be measured since it was higher than 573 K. Recrystallization of the crude product from the solvent mixture benzene–toluene–dioxane (1:1:0.25) resulted in single crystals of (I) suitable for X-ray diffraction analysis after several days.

Crystal data

[Sn(C ₆ H ₅) ₃ (C ₁₄ H ₉ N ₂ O ₂)(H ₂ O)]·C ₄ H ₈ O ₂	$V = 3265 (1) \text{ \AA}^3$
$M_r = 693.34$	$Z = 4$
Monoclinic, $P2_1/c$	$D_x = 1.410 \text{ Mg m}^{-3}$
$a = 15.233 (3) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 11.580 (2) \text{ \AA}$	$\mu = 0.83 \text{ mm}^{-1}$
$c = 19.047 (4) \text{ \AA}$	$T = 296 (2) \text{ K}$
$\beta = 103.617 (2)^\circ$	Block, pale yellow
	$0.34 \times 0.32 \times 0.22 \text{ mm}$

Data collection

Bruker APEXII area-detector diffractometer	27888 measured reflections
φ and ω scans	7464 independent reflections
Absorption correction: multi-scan (SADABS; Bruker, 2004)	4923 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.75, T_{\max} = 0.83$	$R_{\text{int}} = 0.091$
	$\theta_{\max} = 27.5^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.082P)^2 + 3.11P]$
$R[F^2 > 2\sigma(F^2)] = 0.055$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.177$	$(\Delta/\sigma)_{\max} = 0.001$
$S = 1.01$	$\Delta\rho_{\max} = 1.15 \text{ e \AA}^{-3}$
7464 reflections	$\Delta\rho_{\min} = -0.67 \text{ e \AA}^{-3}$
325 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1
Selected geometric parameters (Å, ^o).

Sn1—C15	2.113 (2)	Sn1—C21	2.123 (2)
Sn1—C27	2.114 (2)	Sn1—O3	2.434 (4)
Sn1—O2	2.121 (3)		
C15—Sn1—O2	98.7 (2)	O2—Sn1—O3	172.1 (2)
C27—Sn1—O2	97.0 (2)	O1—C14—C11	121.4 (4)
O2—Sn1—C21	87.4 (2)		

Table 2
Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$O3-H3B\cdots O4^i$	0.85 (5)	2.00 (5)	2.814 (7)	162 (6)
$N2-H2\cdots O1^{ii}$	0.97 (4)	1.83 (3)	2.738 (5)	155 (6)
$O3-H3A\cdots N1^{iii}$	0.85 (5)	2.00 (6)	2.842 (6)	176 (8)

Symmetry codes: (i) $x, y, z - 1$; (ii) $-x, y - \frac{1}{2}, -z + \frac{1}{2}$; (iii) $x, -y + \frac{1}{2}, z - \frac{1}{2}$.

Disorder in the dioxane was identified from a difference map. Disordered atoms were refined by applying restraints to the bond lengths [1.54 (2) Å for C–C and 1.44 (2) Å for C–O] and the displacement parameters (similarity, rigid bond and approximate isotropic restraints) in the skeleton of the dioxane. H atoms on O and N atoms were located and refined with distance restraints of O–H = 0.85 (2) and N–H = 0.97 (2) Å. All other H atoms were positioned in idealized locations and refined as riding on their carrier atoms, with C–H distances of 0.93 (aryl) or 0.97 Å (methylene), and with $U_{iso}(H) = 1.2U_{eq}(C)$. The highest peak is located 0.98 Å from atom C28.

Data collection: *APEX2* (Bruker, 2004); cell refinement: *APEX2*; data reduction: *APEX2*; program(s) used to solve structure: *APEX2*; program(s) used to refine structure: *APEX2*; molecular graphics: *APEX2* and *MERCURY* (Version 1.4; Macrae *et al.*, 2006); software used to prepare material for publication: *APEX2*.

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References

- Barbieri, F., Sparatore, F., Cagnoli, M., Bruzzo, C., Novelli, F. & Alama, A. (2001). *Chem. Biol. Interact.* **134**, 27–39.
- Bharti, N., Maurya, M. R., Naqvi, F. & Azam, A. (2000). *Bioorg. Med. Chem. Lett.* **10**, 2243–2245.
- Bruker (2004). *APEX2* (Version 1.22) and *SADABS*. Bruker AXS Inc., Madison, Wisconsin, USA.
- Fang, X.-N., Song, X.-Q. & Xie, Q. L. (2001). *J. Organomet. Chem.* **619**, 43–48.
- Fang, X.-N., Sui, Y., Ying, S.-M., Xu, Y.-P. & Guo, X.-F. (2006). *Acta Cryst.* **E62**, m2008–m2010.
- Kemmer, M., Ghys, L., Gielen, M., Biesemans, M., Tiekink, E. R. T. & Willem, R. (1999). *J. Organomet. Chem.* **582**, 195–203.
- Lin, X.-J., Li, Y.-Z., Xu, H.-J., Liu, S.-G., Xu, L., Shen, Z. & You, X.-Z. (2004). *Acta Cryst.* **E60**, o77–o78.
- Ma, C.-L., Zhang, Q.-F., Zhang, R.-F. & Qiu, L.-L. (2005). *J. Organomet. Chem.* **690**, 3033–3043.
- Macrae, C. F., Edgington, P. R., McCabe, P., Pidcock, E., Shields, G. P., Taylor, R., Towler, M. & van de Streek, J. (2006). *J. Appl. Cryst.* **39**, 453–457.
- Schulz, W. G. & Skibo, E. B. (2000). *J. Med. Chem.* **43**, 629–638.
- Zhou, Y.-Z., Jiang, T., Ren, S.-M., Yu, J.-S. & Xia, Z.-C. (2005). *J. Organomet. Chem.* **690**, 2186–2190.