metal-organic papers

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Key indicators

Single-crystal X-ray study T = 273 K Mean σ (C–C) = 0.007 Å R factor = 0.057 wR factor = 0.176 Data-to-parameter ratio = 12.5

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

Piperazinium *fac*-tris(salicylato- $\kappa^2 O, O'$)-titanate(IV) dimethylformamide solvate

In the title compound, $(C_4H_{12}N_2)[Ti(C_7H_4O_3)_3]\cdot C_3H_7NO$, the Ti^{IV} ion is chelated by three bidentate salicylate ligands in an octahedral geometry. The arrangement of the hydroxyl O atoms about Ti corresponds to the *fac* geometrical isomer. The component species are linked by $N-H \cdot \cdot \cdot O$ hydrogen bonds into a layered structure.

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Comment

The title compound, (I), arose from our continuing studies (Fu et al., 2005a,b) of the reactions of tetrabutyltitanium(IV) and salicylic acid in dimethylformamide (DMF) solution, which have previously yielded crystals of bis(dimethylammonium) mer-tris(salicylato- $\kappa^2 O, O'$)titanate(IV), (II), and piper-azinium(2+) fac-tris(salicylato- $\kappa^2 O, O'$)titanate(IV) mono-hydrate dimethylformamide solvate, (III). Piperazine was added to the reaction to hasten the formation of the corresponding piperazinium salts, (I) and (III). Whereas (III) was isolated with water and DMF solvent molecules of crystal-lization, (I) contains only DMF.



In (I), the Ti atom has the three bidentate salicylate groups in an octahedral arrangement, and the $[Ti(C_7H_4O_3)_3]^{2-}$ charge is balanced by a doubly protonated piperizinium cation (Fig. 1). For each chelating molecule, the Ti $-O_h$ (h = hydroxy) bond is shorter than the Ti $-O_c$ (c = carboxylate) bond (Table 1). The carboxylate O atoms engage the cations in N-H \cdots O hydrogen-bonding interactions (Table 2), giving rise to a layered structure.

Experimental

Tetrabutyltitanium(IV) (0.34 ml, 1 mmol), salicylic acid (0.4 g, 3 mmol) and piperazine (0.09 g, 1 mmol) were dissolved in dimethylformamide (10 ml). The resulting clear yellow solution was set aside for 10 d for crystals of (I) to separate out.

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Crystal data

(C₄H₁₂N₂)[Ti(C₇H₄O₃)₃]·C₃H₇NO $M_r = 617.46$ Triclinic, $P\overline{1}$ a = 10.552 (2) Å b = 10.622 (2) Å c = 14.881 (3) Å $\alpha = 92.088 (4)^{\circ}$ $\beta = 104.987 (3)^{\circ}$ $\gamma = 118.429 (3)^{\circ}$ V = 1391.7 (5) Å³

Data collection

Bruker SMART CCD diffractometer φ and ω scans Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{\rm min} = 0.923, \ T_{\rm max} = 0.946$ 6808 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.09)]$
$R[F^2 > 2\sigma(F^2)] = 0.057$	+ 0.038P]
$wR(F^2) = 0.177$	where $P = (F_0^2 + 2)^2$
S = 1.07	$(\Delta/\sigma)_{\rm max} = 0.006$
4772 reflections	$\Delta \rho_{\rm max} = 0.47 \ {\rm e} \ {\rm \AA}^{-3}$
381 parameters	$\Delta \rho_{\rm min} = -0.36 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1

Selected bond lengths (Å).

Ti1-O1	1.868 (3)	Ti1-O6	1.881 (2)
Ti1-O2	1.983 (2)	Ti1-O7	2.041 (3)
Ti1-O5	2.001 (2)	Ti1-O8	1.865 (2)

Z = 2

 $D_x = 1.474 \text{ Mg m}^{-3}$

Cell parameters from 35

 $0.22 \times 0.20 \times 0.15 \text{ mm}$

4772 independent reflections

3425 reflections with $I > 2\sigma(I)$

 $= 1/[\sigma^2(F_o^2) + (0.0942P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

Mo $K\alpha$ radiation

reflections

 $\theta = 2.2 - 25.0^{\circ}$ $\mu = 0.37 \text{ mm}^{-1}$

T = 273 (2) K

Block, yellow

 $R_{\rm int} = 0.027$

 $\theta_{\rm max} = 25.0^{\circ}$

 $h = -12 \rightarrow 12$

 $k = -12 \rightarrow 12$

 $l = -17 \rightarrow 8$

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
N3−H3 <i>B</i> ····O9	0.90	1.83	2.722 (4)	170
$N3-H3A\cdots O3^{i}$	0.90	1.82	2.715 (4)	172
$N2-H2B\cdots O10^{ii}$	0.90	1.90	2.665 (5)	142
$N2-H2A\cdots O4$	0.90	1.92	2.782 (4)	159

Symmetry codes: (i) -x + 2, -y + 2, -z + 1; (ii) -x + 2, -y + 1, -z + 1.

H atoms were positioned geometrically (C-H = 0.93-0.96 Å and N-H = 0.90 Å) and refined as riding, with $U_{iso}(H) = 1.2U_{eq}(carrier)$ or $1.2U_{eq}$ (methyl carrier).





Data collection: SMART (Bruker, 2002); cell refinement: SMART; data reduction: SAINT (Bruker, 2002); 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: SHELXTL.

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