

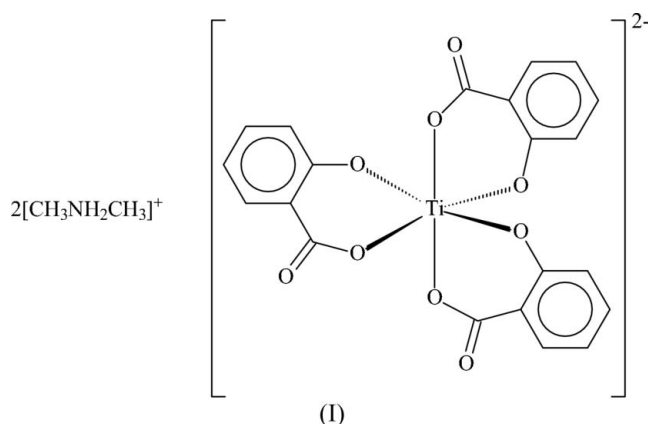
Yun-Long Fu,^a Zhi-Wei Xu,^a
Jia-Lin Ren^a and Seik Weng Ng^{b*}^aSchool of Chemistry and Materials Science,
Shanxi Normal University, Linfen 041004,
People's Republic of China, and ^bDepartment of
Chemistry, University of Malaya, 50603 Kuala
Lumpur, Malaysia

Correspondence e-mail: seikweng@um.edu.my

Key indicators

Single-crystal X-ray study
 $T = 295$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
 R factor = 0.055
 wR factor = 0.186
Data-to-parameter ratio = 16.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Bis(dimethylammonium) *mer*-tris(salicylato- $\kappa^2\text{O},\text{O}'$)-
titanate(IV)In the title compound, $(\text{C}_2\text{H}_8\text{N})_2[\text{Ti}(\text{C}_7\text{H}_4\text{O}_3)_3]$, the Ti^{IV} atom
is chelated by three salicylate ligands in a *mer*-octahedral
geometry. The cations and complex anions are linked by
hydrogen bonds into a layer structure.

Comment

As the deprotonated anion of salicylic acid can function as a
dianionic chelate, two or more salicylate(2⁻) anions should be
able to bind to metal atoms to form $[\text{M}(\text{C}_7\text{H}_4\text{O}_3)_n]$ ions. Such
anionic salicylate complexes have been authenticated in a
small number of salts, as noted from the Cambridge Structural
Database (Version 5.26; Allen, 2002). For example, with the
 Be^{II} complex, the charge is balanced by ammonium cations
(Schmidbaur & Kumberger, 1993); the Cu^{II} derivative has as
counter-ion the bis(2-amino-2-methyl-1-propanol)copper
cation (Muhonen, 1982). Also featuring two salicylate
dianions is the dioxomolybdenum complex, which exists as the
bis(1-methylimidazolium) (Boutilier *et al.*, 1993), bis-
(pyridinium) (Edwards *et al.*, 1992) and bis(tetramethyl-
ammonium) (Edwards *et al.*, 1993) salts. Both the sodium and
the ammonium bis(salicylato)manganate(III) complexes are
not simple ionic salts (Kirk *et al.*, 1991), however. With titanium
in particular, a neutral tris-chelated octahedral
compound, $[\text{Ti}(\text{C}_7\text{H}_4\text{O}_3)_2(\text{C}_7\text{H}_5\text{O}_3)]$ is known; the study
(Gigant *et al.*, 2001) also describes the possible coordination
modes of the titanium derivatives of salicylic acid.The tris(salicylato)titanate(IV) dianion was first isolated as
its crystalline sodium and ammonium salts (Babko *et al.*, 1961);
a spectroscopic study (Faizutdinova *et al.*, 1986) assigned an
octahedral geometry to the metal atom in the sodium salt. The
title compound, (I), is the first example of a crystal-
lographically authenticated tris-chelated salicylate complex;
the Ti atom in the tris(salicylato)titanate(IV) ion is six-Received 18 July 2005
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coordinate in a *mer*-octahedral geometry, and its charge is balanced by two dimethylammonium cations (Fig. 1). For each chelate, the Ti—O_{hydroxy} bond is shorter than the Ti—O_{carboxyl} bond. The carbonyl O atoms engage the cations in hydrogen-bonding interactions (Table 2), giving rise to a layer structure. In the following paper, the structure of the piperazium salt of *fac*-tris(salicylato)titanate(IV), (II), is reported (Fu *et al.*, 2005).

Experimental

Tetrabutyl titanate (0.34 ml, 1 mmol) and salicylic acid (0.40 g, 3 mmol) were dissolved in DMF (10 ml). The clear yellow solution was set aside for three months. The red crystals of (I) that separated from solution were isolated in about 90% yield (based on Ti). The dimethylammonium cation probably resulted from the decomposition of DMF in the presence of salicylic acid, which would serve as catalyst. The DMF solvent was not incorporated into the crystal structure of (I), whereas it was incorporated into (II), when piperazine was added.

Crystal data

(C₂H₈N)₂[Ti(C₇H₄O₃)₃]
M_r = 548.39
 Monoclinic, *P*2₁/*n*
a = 11.589 (1) Å
b = 14.270 (1) Å
c = 15.463 (1) Å
 β = 92.259 (1)°
V = 2555.1 (3) Å³
Z = 4

D_x = 1.426 Mg m⁻³
 Mo *K*α radiation
 Cell parameters from 3721 reflections
 θ = 2.2–25.2°
 μ = 0.39 mm⁻¹
T = 295 (2) K
 Block, red
 0.35 × 0.22 × 0.20 mm

Data collection

Bruker APEX area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan *SADABS* (Sheldrick, 1996)
T_{min} = 0.784, *T_{max}* = 0.926
 14492 measured reflections

5654 independent reflections
 4430 reflections with *I* > 2σ(*I*)
R_{int} = 0.029
 θ_{\max} = 27.5°
h = -13 → 15
k = -18 → 13
l = -19 → 20

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.055
wR (*F*²) = 0.186
S = 1.07
 5654 reflections
 334 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.1131P)^2 + 0.5921P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.65 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\min} = -0.27 \text{ e } \text{Å}^{-3}$

Table 1

Selected geometric parameters (Å, °).

Ti1—O1	1.872 (2)	Ti1—O4	1.906 (2)
Ti1—O2	1.973 (2)	Ti1—O7	1.891 (2)
Ti1—O5	2.063 (2)	Ti1—O8	1.958 (2)
O1—Ti1—O2	86.35 (8)	O2—Ti1—O8	176.31 (8)
O1—Ti1—O4	94.11 (8)	O4—Ti1—O5	83.49 (8)
O1—Ti1—O5	175.11 (8)	O4—Ti1—O7	168.03 (8)
O1—Ti1—O8	96.46 (8)	O4—Ti1—O8	89.23 (9)
O1—Ti1—O7	97.50 (9)	O5—Ti1—O7	85.14 (8)
O2—Ti1—O4	92.97 (9)	O5—Ti1—O8	87.79 (8)
O2—Ti1—O5	89.51 (8)	O7—Ti1—O8	86.60 (8)
O2—Ti1—O7	90.66 (8)		

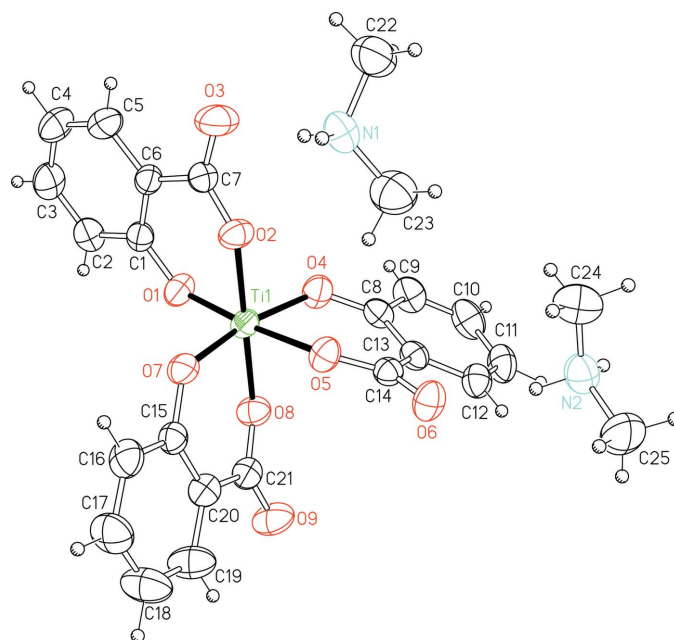


Figure 1

ORTEP plot (Johnson, 1976), showing the atom-numbering scheme of (I). Displacement ellipsoids are drawn at the 50% probability level and H atoms are drawn as spheres of arbitrary radii.

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>
N1—H1 <i>a</i> ...O3	0.90	1.92	2.793 (3)	163
N1—H1 <i>b</i> ...O6 ⁱ	0.90	1.89	2.775 (3)	169
N2—H2 <i>a</i> ...O6	0.90	1.98	2.859 (3)	165
N2—H2 <i>b</i> ...O9 ⁱⁱ	0.90	1.81	2.714 (3)	177

Symmetry codes: (i) $-x + 1, -y + 1, -z + 1$; (ii) $-x + \frac{1}{2}, y + \frac{1}{2}, -z + \frac{3}{2}$.

The carbon-bound H atoms were positioned geometrically [*C*—H = 0.93 Å for the aromatic H atoms and *C*—H = 0.96 Å for the methyl H atoms; *U_{iso}*(H) = 1.2*U_{eq}*(*C*) for the aromatic H atoms and 1.5*U_{eq}*(*C*) for the methyl H atoms]. Although the nitrogen-bound H atoms could be located in difference Fourier maps, they could not be satisfactorily refined, even with an N—H distance restraint. These atoms were also positioned geometrically [N—H = 0.86 Å and *U_{iso}*(H) = 1.2*U_{eq}*(N)]. All H atoms were included in the refinement in the riding-model approximation.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINTE* (Bruker, 2002); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

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