Received 8 November 2005 Accepted 21 December 2005

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.004 Å R factor = 0.035 wR factor = 0.092 Data-to-parameter ratio = 12.2

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. Dioxo(pyridine-2-carboxylato)(pyridinium-2-carboxylato)vanadium(V) monohydrate

In the title compound, $[VO_2(C_6H_4NO_2)(C_6H_5NO_2)] \cdot H_2O$, one of the two pyridine-2-carboxylate ligands chelates to the V atom in a bidentate manner, *via* the carboxylate O atom and the N atom of the pyridine ring. The second pyridine-2carboxylate ligand coordinates to the V atom only *via* the carboxylate O atom, while the N atom of the pyridine ring is protonated. The coordination geometry of the V atom is distorted trigonal-bipyramidal. The crystal packing is stabilized by intermolecular $N-H \cdots O$, $C-H \cdots O$ and $O-H \cdots O$ hydrogen bonds involving the solvent water molecule.

Comment

Current interest in dioxovanadium compounds is very much driven by their promising pharmaceutical properties and biological activity. Bis(kojato) oxovanadium(IV) and bis-(maltolato)oxovanadium(IV) are two examples demonstrating insulin-mimetic properties (Yuen *et al.*, 1997; Winter *et al.*, 2005).



The title compound, (I), is a dioxovanadium complex with two pyridine-2-carboxylate ligands; one is chelated to the V atom in a bidentate manner via atom N2 of the pyridine ring and atom O4 of the carboxylate, and the second is linked through the carboxylate atom O2 in a monodentate fashion (Fig. 1). Atom N1 of the uncoordinated pyridine ring is protonated. The coordination geometry of atom V1 is highly distorted trigonal-bipyrimidal (Table 1). The mean values of the V=O(xx) and V-O(carboxylate) bond lengths in (I) of 1.6045 (18) and 1.9873 (16) Å, respectively, are close to those observed in $[VO_2(C_{13}H_9ClN_3O], (II) [1.607 (4)]$ and 1.972 (3) Å, respectively; Pal & Pal, 2001]. However, the V-N(pyridyl) bond length of 2.1252 (18) Å in (I) is slightly longer than the value of 1.972 (4) Å in (II). The bidentate chelate ligand and V atom form an essentially planar V1/O4/N2/O3/ C7-C12 fragment, with a maximum deviation of 0.036 (2) Å for atom O3, and this makes a dihedral angle of 22.61 $(8)^{\circ}$ with the fragment N1/C1-C6.

Acta Cryst. (2006). E62, m207–m209

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Figure 1

The molecular structure of (I), with the atom-numbering scheme and 50% probability displacement ellipsoids. Hydrogen bonds are shown by dashed lines.



Figure 2



The crystal packing (Fig. 2) is stabilized by intermolecular $N-H\cdots O$, $O-H\cdots O$ and $C-H\cdots O$ hydrogen bonds (Table 2) involving the solvent water molecules and forming ribbons extended along the *a* axis.

Experimental

Sodium metavanadate, NaVO₃ (1.00 g, 8.20 mmol), was dissolved in distilled water (50 ml). An aqueous solution (20 ml) of pyridine-2-carboxylic acid (2.20 g, 16.40 mmol) was then added to the vanadate solution and the mixture was acidified to pH 1–2.5 by dropwise addition of 2 *M* HCl. The resulting solution was stirred and refluxed for 3 h. The yellow solution was then filtered and allowed to cool to room temperature. Light-yellow crsytals of (I) were obtained after 3 d of slow evaporation at room temperature (yield 80%; decomposed at 594 K).

Crystal data

 $\begin{bmatrix} V(C_{6}H_{4}NO_{2})(C_{6}H_{5}NO_{2})O_{2} \end{bmatrix} \cdot H_{2}O \\ M_{r} = 346.17 \\ \text{Triclinic, } P\overline{1} \\ a = 7.3392 (15) \text{ Å} \\ b = 7.4413 (16) \text{ Å} \\ c = 14.592 (3) \text{ Å} \\ \alpha = 97.745 (3)^{\circ} \\ \beta = 94.787 (3)^{\circ} \\ \gamma = 118.655 (3)^{\circ} \\ \gamma = 62.8 (2) \text{ Å}^{3} \\ \end{bmatrix}$

Data collection

Bruker SMART APEX CCD areadetector diffractometer ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2000) *T*_{min} = 0.710, *T*_{max} = 0.934 6777 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.035$ $wR(F^2) = 0.092$ S = 1.042517 reflections 207 parameters H atoms treated by a mixture of independent and constrained refinement Mo K α radiation Cell parameters from 2766 reflections $\theta = 1.4-25.5^{\circ}$ $\mu = 0.77 \text{ mm}^{-1}$ T = 298 (2) KSlab, yellow $0.48 \times 0.14 \times 0.09 \text{ mm}$

 $D_x = 1.684 \text{ Mg m}^{-3}$

Z = 2

2517 independent reflections 2173 reflections with $I > 2\sigma(I)$ $R_{int} = 0.021$ $\theta_{max} = 25.5^{\circ}$ $h = -8 \rightarrow 8$ $k = -9 \rightarrow 9$ $l = -17 \rightarrow 17$

$$\begin{split} &w = 1/[\sigma^2(F_o^2) + (0.0512P)^2 \\ &+ 0.1867P] \\ &where \ P = (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\max} < 0.001 \\ \Delta\rho_{\max} = 0.33 \ e \ \text{\AA}^{-3} \\ \Delta\rho_{\min} = -0.22 \ e \ \text{\AA}^{-3} \end{split}$$

Table 1

Selected geometric parameters (Å, °).

V1-06	1.6024 (18)	O1-C6	1.214 (3)
V1-O5	1.6066 (18)	O2-C6	1.281 (3)
V1-O2	1.9755 (16)	O3-C12	1.202 (3)
V1-O4	1.9990 (16)	O4-C12	1.303 (3)
V1-N2	2.1252 (18)		
O6-V1-O5	109.13 (12)	O2-V1-O4	78.70 (6)
O6-V1-O2	100.79 (8)	O6-V1-N2	94.65 (8)
O5-V1-O2	101.11 (8)	O5-V1-N2	93.24 (8)
O6-V1-O4	120.74 (10)	O2-V1-N2	154.05 (7)
O5-V1-O4	129.38 (10)	O4-V1-N2	75.49 (6)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1B \cdots O2$	0.86	2.30	2.643 (3)	104
$O1W - H1WA \cdots O4$	0.84 (4)	2.01 (4)	2.828 (3)	164 (4)
$N1 - H1B \cdots O1W$	0.86	1.85	2.691 (3)	164
$O1W - H1WB \cdots O5^{i}$	0.84 (3)	2.42 (4)	3.139 (3)	143 (4)
$C1-H1A\cdots O1^{i}$	0.93	2.41	3.297 (4)	159
$C4-H4A\cdots O6^{ii}$	0.93	2.46	3.121 (4)	128
$C7-H7A\cdots O3^{iii}$	0.93	2.31	3.108 (4)	144

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

The H atoms of the solvent water molecule were located in a difference map and refined isotropically with bond-length restraints of O-H = 0.84 (3) Å. The remaining H atoms were located in a difference map, repositioned geometrically and refined as riding, with C-H = 0.93 and N-H = 0.86 Å, and with $U_{\rm iso}(\rm H) = 1.2U_{eq}$ of the parent atom.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*, *PARST* (Nardelli, 1995) and *PLATON* (Spek, 2003).

The authors thank the Malaysian Government, and Universiti Sains Malaysia and Kebangsaan Malaysia, for SAGA research grant No. 304/PKIMIA/653008/A118 and facilities.

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