metal-organic papers

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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.007 Å R factor = 0.022 wR factor = 0.051 Data-to-parameter ratio = 20.9

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

Diacetatodiaquadioxouranium(VI) acetic acid disolvate

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The coordination polyhedron of the U atom in the title compound, $[U(C_2H_3O_2)_2O_2(H_2O)_2]$ ·2CH₃COOH, is a distorted hexagonal bipyramid, with the equatorial positions occupied by four O atoms of two bidentate-chelating acetate anions and two O atoms of coordinated water molecules. The complex lies on an inversion centre. A two-dimensional network of hydrogen bonds is present in the crystal structure.

Comment

Carboxylate compounds of the actinides play a significant role in laboratory practice and the radiochemical industry. Several uranyl compounds are known, in which both acetate anions and acetic acid molecules are present (Ramos Silva *et al.*, 1999; Grigor'ev *et al.*, 2004). Here, we present a further example of a uranyl acetate compound, (I), containing acetic acid as solvent.



The U atom in compound (I) lies on an inversion centre. Its coordination polyhedron is a distorted hexagonal bipyramid, with the equatorial positions occupied by four O atoms of two bidentate-chelating acetate anions and two O atoms of coordination water molecules (Fig. 1). Crystallographically independent bond lengths in the U-atom environment are given in Table 1.



Figure 1

A view of (I), showing the atom-labelling scheme for the asymmetric unit. Displacement ellipsoids are drawn at the 50% probability level and H atoms are represented by circles of arbitrary size. Dashed lines indicate the hydrogen-bonding interactions. [Symmetry code for unlabelled atoms: 1 - x; 1 - y; 1 - z.]

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 $R_{\rm int} = 0.021$



Figure 2

Part of an infinite chain in the crystal structure of (I). Dashed lines indicate hydrogen bonds.



Figure 3

A layer in the crystal structure of (I), viewed along the direction of the chains. Dashed lines indicate hydrogen bonds.

The coordinated water and solvent acetic acid molecules act as H donors in several hydrogen bonds (Table 2). The acceptors in these bonds are O atoms of acetate anions and acetic acid. The hydrogen bonding results in the formation of infinite chains in the [100] direction (Fig. 2) and these chains are combined into layers parallel to the $(01\overline{1})$ plane (Fig. 3).

Experimental

Crystals of (I) were obtained in an attempt to recrystallize anhydrous uranyl acetate from glacial acetic acid at 413 K. Possibly, a small admixture of water in the acid has resulted in the formation of (I)

Crystal data

$[U(C_2H_3O_2)_2O_2(H_2O)_2]\cdot 2C_2H_4O_2$	Z = 1
$M_r = 544.25$	$D_{\rm x} = 2.291 {\rm Mg} {\rm m}^{-3}$
Triclinic, $P\overline{1}$	Mo $K\alpha$ radiation
a = 6.914 (2) Å	Cell parameters from 24
b = 7.822 (2) Å	reflections
c = 8.211 (2) Å	$\theta = 13.1 - 14.0^{\circ}$
$\alpha = 95.00 \ (2)^{\circ}$	$\mu = 10.34 \text{ mm}^{-1}$
$\beta = 113.74 \ (2)^{\circ}$	T = 293 (2) K
$\gamma = 99.79 \ (2)^{\circ}$	Irregular fragment, yellow
V = 394.6 (2) Å ³	$0.24 \times 0.18 \times 0.12 \text{ mm}$

Data collection

Siemens <i>P3/PC</i> diffractometer
$\omega/2\theta$ scans
Absorption correction: ψ scan
(North et al., 1968)
$T_{\min} = 0.168, \ T_{\max} = 0.289$
2494 measured reflections
2316 independent reflections
2316 reflections with $I > 2\sigma(I)$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.022$ $wR(F^2) = 0.051$ S = 1.052316 reflections 111 parameters $\theta_{\text{max}} = 30.1^{\circ}$ $h = 0 \rightarrow 9$ $k = -11 \rightarrow 10$ $l = -11 \rightarrow 10$ 2 standard reflections every 98 reflections intensity decay: none H atoms treated by a mixture of independent and constrained

refinement $w = 1/[\sigma^2(F_o^2) + (0.0313P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 1.36 \text{ e} \text{ Å}^{-3}$ $\Delta\rho_{min} = -1.55 \text{ e} \text{ Å}^{-3}$

Table 1

Selected bond lengths (Å).

U-02	1.760 (3)	U-03	2.480 (3)
U-01	2.441 (3)	U-O4	2.536 (3)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$O6-H6\cdots O3$ $O1-H14\cdots O5^{i}$	0.86(6) 0.88(7)	1.84(6) 1.86(7)	2.672(4)	163 (6) 168 (6)
$O1-H1B\cdots O4^{ii}$	0.75 (9)	2.05 (9)	2.727 (4)	163 (0) 163 (9)

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

All H atoms were initially located in a difference Fourier map. The methyl H atoms were then constrained to an ideal geometry, with C— H distances of 0.96 Å and $U_{iso}(H) = 1.5U_{eq}(C)$, but each group was allowed to rotate freely about its C—C bond. The positions of H atoms bonded to O atoms were refined freely along with isotropic displacement parameters. The highest peak and the deepest hole on the final difference electron-density map are located 0.87 and 0.82 Å, respectively, from atom U.

Data collection: *P3/PC* (Siemens, 1989); cell refinement: *P3/PC*; data reduction: *P3/PC*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 1998); software used to prepare material for publication: *SHELXTL*.

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