

# Tetra- $\mu$ -acetamidato- $\kappa^4$ N:O; $\kappa^4$ O:N-diaqua-dirhodium(II,III) perrhenate

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## Key indicators

Single-crystal X-ray study  
 $T = 296\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.008\text{ \AA}$   
 $R$  factor = 0.035  
 $wR$  factor = 0.073  
Data-to-parameter ratio = 17.4

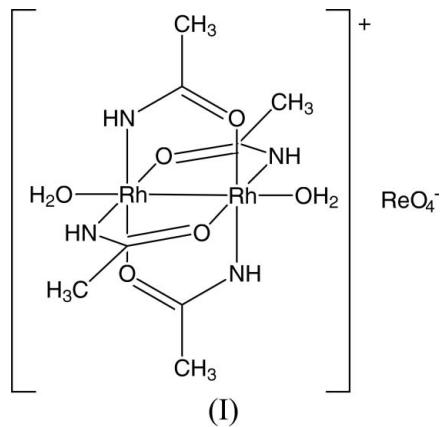
For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

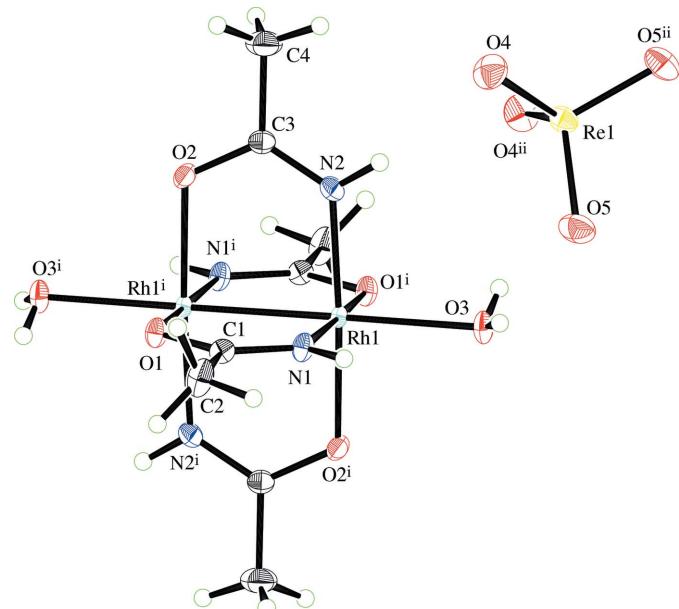
In the title compound,  $[\text{Rh}_2(\text{C}_2\text{H}_4\text{NO})_4(\text{H}_2\text{O})_2][\text{ReO}_4]$ , the cation lies on an inversion center and the anion on a twofold axis. The cations are connected two-dimensionally by O–H···O and N–H···O hydrogen bonding. Hydrogen bonds to perrhenate ions connect the two-dimensional sheets.

Received 13 July 2006  
Accepted 14 July 2006

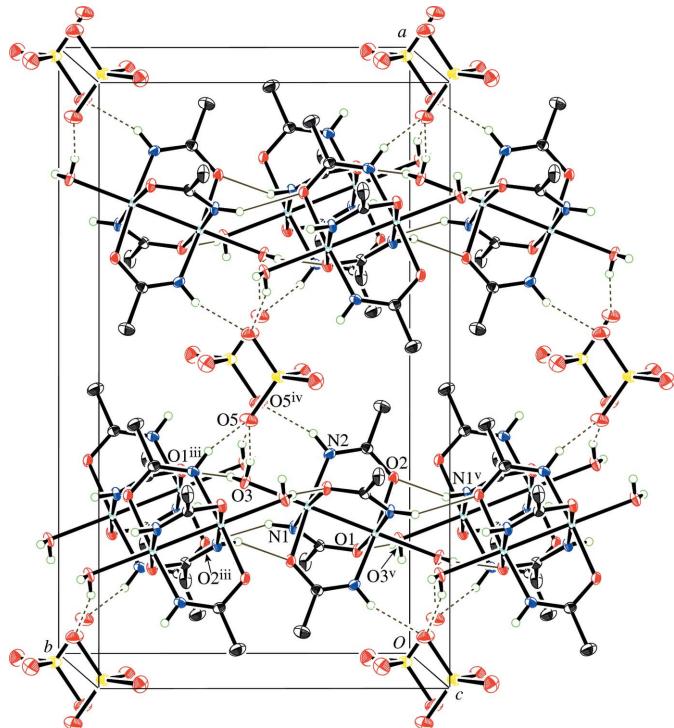
## Comment

Paddlewheel complexes with amidate ligands are useful modules in making assembled structures, because they have hydrogen-donating NH and hydrogen-accepting O sites in addition to the axial coordination sites. We have studied assembled complexes of acetamide-bridged paddlewheel dirhodium complexes with halide linkers: one-dimensional zigzag chain structures of  $[\text{Rh}_2(\text{acam})_4(\mu-X)]_n\text{H}_2\text{O}$  ( $\text{Hacm} = \text{acetamide}; X = \text{Cl}, \text{Br} \text{ and } \text{I}; n = 0, 2, 3 \text{ and } 7$ ) (Yang *et al.*, 2000, 2001), a two-dimensional honeycomb structure of  $[(\{\text{Rh}_2(\text{acam})_4\}_3(\mu_3-\text{Cl}_2)\cdot 4\text{H}_2\text{O}$  (Takazaki *et al.*, 2003), and a three-dimensional diamondoid structure of  $[(\{\text{Rh}_2(\text{acam})_4\}_2(\mu_4-\text{I}))\cdot 6\text{H}_2\text{O}$  (Fuma *et al.*, 2004). In all these structures, direct hydrogen bonds between the NH and O atoms of the amidate ligands play an important role in constructing the structures. In the structure of  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2][\text{Rh}_2(\text{acam})_4(\mu-\text{MCl}_4)]\cdot 2\text{H}_2\text{O}$  ( $M = \text{Pd}$  and  $\text{Pt}$ ; Yang *et al.*, 2006), there are anionic chains of  $[\text{Rh}_2(\text{acam})_4(\mu-\text{MCl}_4)]^-$  and  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]^+$  that participate in hydrogen-bonding networks using the bridging amidate and axial aqua ligands. We recently reported variation of hydrogen-bonding networks in hexa-fluorophosphate salts of amidate-bridged dirhodium complexes with axial aqua ligands (Ebihara & Fuma, 2006). In this paper, we report a hydrogen-bonding network in  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2][\text{ReO}_4]$ , (I).



**Figure 1**

The cation and anion of the title complex, with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level [symmetry codes: (i)  $\frac{1}{2} - x, \frac{1}{2} - y, 1 - z$ ; (ii)  $1 - x, y, \frac{3}{2} - z$ ].

**Figure 2**

Crystal structure of (I). Methyl H atoms have been omitted for clarity. Hydrogen bonds between the rhodium complexes are drawn as thin lines and the other hydrogen bonds as dotted lines [symmetry codes: (iii)  $\frac{1}{2} - x, \frac{1}{2} + y, \frac{1}{2} - z$ ; (iv)  $x, 1 - y, -\frac{1}{2} + z$ ; (v)  $\frac{1}{2} - x, -\frac{1}{2} + y, \frac{1}{2} - z$ ].

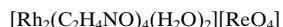
The structure of (I) is shown in Fig. 1. There are one independent  $\text{Rh}_2(\text{acam})_4$  unit that lies on an inversion center ( $\frac{1}{4}, \frac{1}{4}, \frac{1}{2}$ ) and one independent perrhenate ion of which the Re atom lies on a twofold axis ( $\frac{1}{2}, y, \frac{3}{4}$ ). The bond distances around each Rh atom, including the metal–metal bond

(Table 1), are similar to the corresponding ones in  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{ClO}_4$  (Baranovskii *et al.*, 1986),  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{PF}_6$  and  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{PF}_6 \cdot 2\text{H}_2\text{O}$  (Ebihara & Fuma, 2006). The dirhodium complexes and the perrhenate ions form a hydrogen-bonded network (Fig. 2 and Table 2). The cation donates an H atom of the axial aqua ligand (O3) to the amidate oxygen atom (O1<sup>iii</sup>) [symmetry code: (iii)  $\frac{1}{2} - x, \frac{1}{2} + y, \frac{1}{2} - z$ ]. The complex also donates the amino H atom of N1 to the amidate O atom (O2<sup>iii</sup>). Atoms O1 and O2 accept these hydrogen bonds from O3<sup>v</sup> and N2<sup>v</sup> [symmetry code: (v)  $\frac{1}{2} - x, -\frac{1}{2} + y, \frac{1}{2} - z$ ]. The resulting two-dimensional sheet structure is very similar to that in  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{PF}_6 \cdot 2\text{H}_2\text{O}$  and different from those in  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{ClO}_4$  and  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{PF}_6$  (Ebihara & Fuma, 2006). Perrhenate ions are located between the sheets. Aqua ligand O3 hydrogen bonds to perrhenate O5 atom and amidate atom N2 donates an H atom to another perrhenate ion (O5<sup>iv</sup>) [symmetry code: (iv)  $x, 1 - y, -\frac{1}{2} + z$ ]. These hydrogen bonds of the perrhenate ions connect the hydrogen-bonded sheets.

## Experimental

$[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2] \cdot 6\text{H}_2\text{O}$  was synthesized according to the published method (Doyle *et al.*, 1990).  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{ClO}_4$  was prepared by the method of Baranovskii *et al.* (1986). An aqueous solution (10 ml) of  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2]\text{ClO}_4$  (15 mg, 0.026 mmol),  $[\text{Rh}_2(\text{acam})_4(\text{H}_2\text{O})_2] \cdot 6\text{H}_2\text{O}$  (16 mg, 0.028 mmol) and  $\text{NH}_4\text{ReO}_4$  (20 mg, 0.075 mmol) was left for 7 d at 323 K to obtain  $[(\text{Rh}_2(\text{acam})_4)_2(\mu_4\text{-ReO}_4)]$  (Fuma & Ebihara, 2006) with a small number of crystals of (I).

## Crystal data



$M_r = 724.30$

Monoclinic,  $C2/c$

$a = 19.718 (2)$  Å

$b = 11.578 (1)$  Å

$c = 8.2521 (9)$  Å

$\beta = 97.664 (5)$  °

$V = 1867.1 (3)$  Å<sup>3</sup>

$Z = 4$

$D_x = 2.577$  Mg m<sup>-3</sup>

Mo  $K\alpha$  radiation

$\mu = 8.27$  mm<sup>-1</sup>

$T = 296 (2)$  K

Plate, brown

$0.15 \times 0.07 \times 0.03$  mm

## Data collection

Rigaku/MSC Mercury CCD diffractometer

$\omega$  scans

Absorption correction: integration (NUMABS; Higashi, 1999)

$T_{\min} = 0.120, T_{\max} = 0.738$

7434 measured reflections

2139 independent reflections

2037 reflections with  $I > 2\sigma(I)$

$R_{\text{int}} = 0.042$

$\theta_{\max} = 27.5$  °

## Refinement

Refinement on  $F^2$

$R[F^2 > 2\sigma(F^2)] = 0.035$

$wR(F^2) = 0.073$

$S = 1.15$

2139 reflections

123 parameters

H atoms treated by a mixture of independent and constrained refinement

$$w = 1/[\sigma^2(F_o^2) + (0.0302P)^2 + 7.291P]$$

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

$(\Delta/\sigma)_{\max} = 0.001$

$\Delta\rho_{\max} = 1.42$  e Å<sup>-3</sup>

$\Delta\rho_{\min} = -1.53$  e Å<sup>-3</sup>

Extinction correction: SHELLXL97

Extinction coefficient: 0.00091 (11)

**Table 1**

Selected bond lengths (Å).

Rh1–Rh1 <sup>i</sup>	2.4053 (7)	Rh1–N1	1.979 (4)
Rh1–O1 <sup>i</sup>	2.040 (3)	Rh1–N2	1.971 (4)
Rh1–O2 <sup>i</sup>	2.033 (3)	Re1–O4	1.713 (5)
Rh1–O3	2.237 (4)	Re1–O5	1.718 (4)

Symmetry code: (i)  $-x + \frac{1}{2}, -y + \frac{1}{2}, -z + 1$ .

**Table 2**

Hydrogen-bond geometry (Å, °).

D–H···A	D–H	H···A	D···A	D–H···A
O3–H10···O1 <sup>iii</sup>	0.76 (8)	2.10 (8)	2.841 (6)	168 (8)
O3–H9···O5	0.73 (7)	2.06 (8)	2.717 (6)	150 (8)
N1–H1···O2 <sup>iii</sup>	0.86	2.33	3.139 (6)	158
N2–H2···O5 <sup>iv</sup>	0.86	2.37	3.122 (6)	147

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

Aqua H atoms were located in difference syntheses and their positional parameters are refined [O–H = 0.73 (7) and 0.76 (8) Å], with  $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{O})$ . The remaining H atoms were positioned geometrically, with N–H = 0.86 Å and C–H = 0.96 Å, and constrained to ride on their parent atoms with  $U_{\text{iso}}(\text{H}) = xU_{\text{eq}}(\text{C,N})$ , where  $x = 1.5$  for methyl H and  $x = 1.2$  for all other H atoms. The highest peak and deepest hole are located 0.85 and 0.81 Å, respectively, from atom Re1.

Data collection: *CrystalClear* (Molecular Structure Corporation & Rigaku, 2001); cell refinement: *CrystalClear*; data reduction: *TEXSAN* (Rigaku/MSC, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure:

*SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXL97* and *TEXSAN*.

This work was supported by the Research Foundation for Electrotechnology of Chubu.

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