metal-organic papers

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Key indicators

Single-crystal X-ray study T = 120 KMean σ (C–C) = 0.009 Å Some non-H atoms missing R factor = 0.066 wR factor = 0.176 Data-to-parameter ratio = 21.3

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

cis,cis- μ -2,3,5,6-Tetra-2-pyridylpyrazine- $\kappa^3 N^1, N^2, N^6: \kappa^3 N^3, N^4, N^5$ -bis[dichloro(dimethyl sulfoxide- κ S)ruthenium(II)] dihydrate acetone disolvate

The reaction of 2,3,5,6-tetra-2-pyridylpyrazine (tppz) with dichlorotetrakis(dimethyl sulfoxide)ruthenium(II) in dimethyl sulfoxide (DMSO) yielded the title centrosymmetric dinuclear complex, $[Ru_2Cl_4(C_{24}H_{16}N_6)(C_3H_6OS)_2]\cdot 2C_2H_6OS\cdot 2H_2O$ or *cis,cis*-[{Ru(DMSO)Cl_2}₂(μ -tppz)]\cdot 2Me_2CO·2H_2O. Each ruthenium ion is in a distorted octahedral coordination in which the chloro ligands are *cis* to each other and DMSO is coordinated through sulfur. The asymmetric unit contains half of two independent molecules.

Comment

2,3,5,6-Tetra-2-pyridylpyrazine (tppz) has attracted a great deal of interest in supramolecular chemistry because it can function as a bis-tridentate bridging ligand (Fantacci *et al.*, 2004). Crystal structures of dinuclear tppz complexes are mainly those of first-row transition metal ions (Carranza *et al.*, 2003; Graf *et al.*, 1997; Hadadzadeh *et al.*, 2005; Campos-Fernandez *et al.*, 2001). The only dinuclear Ru^{II} tppz crystal structure reported (Hartshorn *et al.*, 1999) is that of [{Ru(Me₂bpy)Cl}₂(μ -tppz)]²⁺, where Me₂bpy is 4,4'-dimethyl-2,2'-bipyridine.



cis,cis-[{Ru(DMSO)Cl₂}₂(μ -tppz)] was synthesized by reacting two equivalents of Ru(DMSO)₄Cl₂ with one equivalent of tppz in DMSO solution. For the neutral complex to dissolve in water, it is suggested that aqua substitution of at least one of the chloro ligands must have occurred. The slow reformation of the complex and consequent slow crystal

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Figure 1

The structure of one of the independent complex molecules, with 50% probability displacement ellipsoids. H atoms have been omitted. [Symmetry code: (A) -1 - x, -y, 2 - z.]

growth occurred with the diffusion of acetone into the solution. Only the *cis* isomer was isolated and this is to be contrasted to the reaction of 2,2':6',2''-terpyridine (trpy) with Ru(DMSO)₄Cl₂, which gave both the *cis* and the *trans*-Ru(trpy)(DMSO)Cl₂ isomers, albeit in yields of 85 and 10%, respectively (Ziessel *et al.*, 2004).

Crystallography revealed two acetone and two water molecules per complex molecule in the crystal structure. Two independent centrosymmetric complexes are found, with half of each in the asymmetric unit. The ruthenium ions display distorted octahedral coordination in which DMSO is sulfurbound and the chloro ligands are in a cis geometry. Fig. 1 shows one of the two complexes, and it clearly shows the distortion from planarity of the tppz ligand in which two pyridyl groups coordinated to the same Ru^{II} ion are tilted above the plane of the pyrazine ring, while the other two pyridyl groups coordinated to the second Ru^{II} ion are tilted below the plane of the pyrazine ring. This conformation probably minimizes steric strain while at the same time maximizing the bonding interaction of the tppz ligand with the ruthenium ions. The shortness of the Ru-N(pyrazine) bonds compared with the Ru-N(pyridine) bonds (Table 1) is suggested to be due to the stronger π -accepting properties of the pyrazine ring.

Experimental

 $Ru(DMSO)_4Cl_2$ (1 mmol) was dissolved in DMSO (20 ml). To the yellow solution was added tppz (0.5 mmol). The stirred reaction solution was heated to 333 K and the temperature maintained for two days, during which time the solution became deep purple in color. Addition of 600 ml of diethyl ether precipitated the purple product, which was collected and washed with diethyl ether. The crude product was recrystallized by diffusion of acetone into an aqueous solution of the complex. After four weeks, purple crystals formed. The yield was 90% based on tppz.

$[Ru_2Cl_4(C_{24}H_{16}N_6)(C_2H_{6-}$
$OS_2] \cdot 2C_3H_6OS \cdot 2H_2O$
$M_r = 1040.81$
Triclinic, P1
a = 11.994 (6) Å
b = 12.477 (7) Å
c = 13.345 (7) Å
$\alpha = 77.227 \ (7)^{\circ}$
$\beta = 81.505 \ (7)^{\circ}$

Data collection

Bruker APEX diffractometer ω scans

Absorption correction: multi-scan (SADABS; Sheldrick, 2003) $T_{min} = 0.751, T_{max} = 0.953$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.066$ $wR(F^2) = 0.176$ S = 1.058537 reflections 401 parameters H-atom parameters constrained

Z = 2 $D_x = 1.795 \text{ Mg m}^{-3}$ Mo K α radiation $\mu = 1.22 \text{ mm}^{-1}$ T = 120 (2) K Plate, purple 0.18 × 0.15 × 0.04 mm	
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Plate, purple $0.18 \times 0.15 \times 0.04 \text{ mm}$	T = 120 (2) K
$0.18 \times 0.15 \times 0.04 \text{ mm}$	Plate, purple
	$0.18 \times 0.15 \times 0.04 \text{ mm}$

 $\nu = 89.837 \ (7)^{\circ}$

V = 1925.3 (18) Å³

20958 measured reflections 8537 independent reflections 7702 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.035$ $\theta_{\text{max}} = 28.2^{\circ}$

$w = 1/[\sigma^2(F_o^2) + (0.088P)^2]$
+ 20.0195P]
where $P = (\bar{F_0}^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.001$
$\Delta \rho_{\rm max} = 0.20 \text{ e } \text{\AA}^{-3}$
$\Delta \rho_{\rm min} = -1.29 \ {\rm e} \ {\rm \AA}^{-3}$

 Table 1

 Selected bond lengths (Å).

Ru1–N3	1.944 (5)	Ru2-N6	1.946 (5)
Ru1-N2	2.068 (5)	Ru2-N4	2.061 (5)
Ru1-N1	2.068 (5)	Ru2-N5	2.061 (5)
Ru1-S1	2.2454 (18)	Ru2-S2	2.2450 (18)
Ru1-Cl2	2.4112 (19)	Ru2-Cl4	2.4201 (19)
Ru1-Cl1	2.4226 (18)	Ru2-Cl3	2.4242 (18)

Initial structural solution showed two severely disordered, cocrystallized acetone solvent molecules and two water molecules per complex molecule. The data set was treated with the SQUEEZE filter of *PLATON* (Spek, 2003) to model the solvent molecules as diffuse contributions to the electron density. H atoms were assigned calculated positions with C–H = 0.95–0.98 Å and $U_{\rm iso}$ (H) values of 1.2 or 1.5 times $U_{\rm eq}$ (C). The deepest electron density hole is located 0.90 Å from atom Ru2.

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 2001); software used to prepare material for publication: *SHELXTL*.

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