metal-organic papers

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Key indicators

Single-crystal X-ray study T = 133 K Mean σ (C–C) = 0.002 Å R factor = 0.019 wR factor = 0.055 Data-to-parameter ratio = 21.5

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cis-Diaquabis[2-(hydroxymethyl)pyridine]nickel(II) dichloride

The title complex, $[Ni(mpy)_2(H_2O)_2]Cl_2$ [mpy is 2-(hydroxymethyl)pyridine, C_6H_7NO], consists of two chloride anions and an $[Ni(mpy)_2(H_2O)_2]^{2+}$ cation, in which the Ni^{II} ion lies on a twofold axis and exhibits octahedral geometry, coordinated by two neutral mpy ligands and two water molecules. Mpy acts as an *N*,*O*-bidentate ligand, giving rise to a five-membered chelate ring. The Ni–N_{mpy} Ni–O_{mpy} and Ni–O_{water} bond distances are 2.0629 (8), 2.0573 (7) and 2.0490 (7) Å, respectively. The H atoms of the water molecules and the hydroxy group of mpy form O–H···Cl hydrogen bonds, resulting in a three-dimensional network.

Comment

This work is a part of our study of the synthesis and structural characterization of metal complexes with 2-hydroxyalkyl-pyridines. We report here the crystal structure of the aqua complex of nickel(II) with 2-methanolpyridine (mpy), (I).



The structure of (I) consists of a complex cation, $[Ni(mpy)_2(H_2O)_2]^{2+}$ [mpy is 2-(hydroxymethyl)pyridine, C_6H_7NO], and two symmetry-equivalent Cl⁻ anions. In the cation, the nickel(II) ion lies on a twofold axis and is octahedrally coordinated by two neutral mpy ligands and two water molecules, forming a NiN₂O₆ core (Fig. 1). Each mpy ligand behaves as a bidentate donor *via* the pyridine N and hydroxy O atoms, forming a five-membered chelate ring with the nickel(II) ion. The coordination of two mpy and two water ligands results in a *cis* configuration.

The Ni $-N_{mpy}$, Ni $-O_{mpy}$ and Ni $-O_{water}$ bond distances are almost identical, and the Ni $-N_{mpy}$ and Ni $-O_{mpy}$ bond distances are comparable to those reported for [Ni(sac)₂(mpy)₂] (sac is saccharinate; Yilmaz *et al.*, 2002). Some distortion from regular octahedral geometry is apparent (Table 1), especially the bite angle of the mpy ligand (O1-Ni-N1) and the *trans* N1-Ni-N1ⁱ angle (see Table 1 for symmetry code).

The mpy ligand is essentially planar [the deviations of atoms O1 (hydroxy) and C7 (methylene) from the least-squares pyridine ring plane are 0.007 (1) and 0.025 (1) Å, respectively]. The two mpy ligands containing atoms N1 and N1ⁱ attached to Ni are almost perpendicular to one another [the dihedral angle between the pyridine rings is 86.75 (2)°]. The

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Molecular view of (I) (50% displacement ellipsoids). [Symmetry code: (i) $-x, y, \frac{1}{2} - z$.]

geometry of the mpy ligand is similar to that of the same species in $[Ni(sac)_2(mpy)_2]$ (Yilmaz *et al.*, 2002). The packing of (I) is shown in Fig. 2. The crystal structure exhibits three strong $O-H\cdots Cl$ intermolecular hydrogen bonds (Table 2) between the H atoms of the water molecules and the hydroxy group of mpy and the chloride ions. Additionally, one of the H atoms of the pyridine ring is also involved in a $C-H\cdots O$ interaction with the water O atom. The overall hydrogen-bond scheme can be described as a three-dimensional network formed by the mpy ligands, water molecules and Cl^- anions.

Experimental

The starting tetraaquabis(saccharinato)nickel(II) dihydrate, [Ni(H₂O)₄(sac)₂]·2H₂O, was prepared according to the method of Haider *et al.* (1985). A methanol solution (25 ml) of [Ni(H₂O)₄-(sac)₂]·2H₂O (0.53 g, 1 mmol) was mixed with mpy (0.22 g, 2 mmol) and HCl (0.07 g, 2 mmol) at 333 K. Crystals suitable for X-ray diffraction were grown by slow diffusion of ether into the reaction solution at room temperature.

Crystal data

$[Ni(C_6H_7NO)_2(H_2O)_2]Cl_2$
$M_r = 383.89$
Monoclinic, $C2/c$
a = 20.0943 (18) Å
b = 7.6090 (6) Å
c = 12.1268 (10) Å
$\beta = 121.708 \ (3)^{\circ}$
$V = 1577.4 (2) \text{ Å}^3$
Z = 4
Data collection

Bruker SMART 1000 CCD
diffractometer
ω and φ scans
Absorption correction: multi-scan
(SADABS; Bruker, 1999)
$T_{\min} = 0.643, T_{\max} = 0.729$
12 845 measured reflections

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.019$
$wR(F^2) = 0.055$
S = 1.06
2318 reflections
108 parameters
H atoms treated by a mixture of
independent and constrained
refinement
rennement

	2210 in doman dant noffections
	2518 independent reflections
	2177 reflections with $I > 2\sigma(I)$
	$R_{\rm int} = 0.020$
1	$\theta_{\rm max} = 30.0^{\circ}$
	$h = -28 \rightarrow 28$
	$k = -10 \rightarrow 10$
	$l = -16 \rightarrow 17$

 $D_x = 1.617 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 4680

 $0.33 \times 0.26 \times 0.20$ mm

reflections $\theta = 2.9-30.5^{\circ}$ $\mu = 1.58 \text{ mm}^{-1}$ T = 133 (2) KPrism. blue

$w = 1/[\sigma^2(F_o^2) + (0.0342P)^2]$
+ 0.588P]
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.001$
$\Delta \rho_{\rm max} = 0.43 \ {\rm e} \ {\rm \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.20 \text{ e} \text{ Å}^{-3}$



Figure 2 Packing diagram for (I).

Table 1

Selected	geometric	parameters	(Å,	°).	•
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Ni–OW Ni–O1	2.0490 (7) 2.0573 (7)	Ni-N1	2.0629 (8)
$OW-Ni-OW^{i}$ $OW-Ni-O1$ $OW^{i}-Ni-O1$ $O1-Ni-O1^{i}$ $OW-Ni-N1$	87.55 (4) 175.60 (3) 88.56 (3) 95.40 (4) 98.86 (3)	$OW^{i}-Ni-N1$ O1-Ni-N1 $O1^{i}-Ni-N1$ $N1-Ni-N1^{i}$	92.31 (3) 79.23 (3) 90.33 (3) 164.54 (5)

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

Table 2			
Hydrogen-bonding geometry	(Å.	°)	

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
C4-H4···OW ⁱⁱ	0.95	2.64	3.4931 (13)	149
O1−H1···Cl ⁱⁱⁱ	0.776 (17)	2.236 (17)	3.0097 (8)	176 (17)
$OW-HW1\cdots Cl^{iv}$	0.819 (17)	2.315 (18)	3.1284 (8)	172 (15)
$OW-HW2\cdots Cl^{v}$	0.746 (18)	2.345 (18)	3.0831 (8)	170 (17)

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

H atoms bonded to C atoms were included as riding [C-H = 0.95 or 0.99 Å, and $U_{iso}(H) = 1.2U_{eq}(C)]$, while the hydroxy H atoms were refined freely [O-H = 0.746 (18)-0.819 (17) Å].

Data collection: *SMART* (Bruker, 1999); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *XP* (Siemens, 1994); software used to prepare material for publication: *SHELXL*97.

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