metal-organic papers

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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.005 Å R factor = 0.063 wR factor = 0.163 Data-to-parameter ratio = 18.0

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

Bis[2-(cyclohexyliminomethyl)-6-methoxyphenolato]nickel(II)

In the title mononuclear nickel(II) complex, $[Ni(C_{14}H_{18}-NO_2)_2]$, the Ni^{II} atom is four-coordinated in a square-planar geometry by two phenolate O atoms and two imine N atoms from two Schiff base ligands. The Ni atom lies on a centre of inversion.

Comment

Nickel(II) complexes with Schiff base ligands have received much attention in recent years (Marganian *et al.*, 1995). Some of the complexes have been found to have pharmacological and catalytic properties (Harrop *et al.*, 2003; Brückner *et al.*, 2000). Nickel is present in the active sites of several important classes of metalloproteins, as either a homodinuclear or a heterodinuclear species. In order to further develop the coordination chemistry of such nickel complexes, the title nickel(II) complex, (I), is reported here.



The Ni^{II} atom in (I) is coordinated by two phenolate O and two imine N atoms from two Schiff base ligands, forming a four-coordinate square-planar geometry (Fig. 1). The Ni atom



Figure 1

© 2006 International Union of Crystallography All rights reserved The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. Unlabelled atoms are related to labelled atoms by -x, -y, -z.

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lies on a centre of inversion. All the bond lengths and angles (Table 1) subtended at the Ni centre are comparable with the values observed in other Schiff base nickel(II) complexes (Liu *et al.*, 2006; Yu, 2006; Zhu *et al.*, 2004). There are no significant intermolecular interactions in the crystal structure (Fig. 2).

Experimental

3-Methoxysalicylaldehyde (1.0 mmol, 152.3 mg), cyclohexylamine (1.0 mmol, 99.2 mg) and Ni(CH₃COO)₂·4H₂O (0.5 mmol, 124.3 mg) were dissolved in MeOH (80 ml). The mixture was stirred at room temperature for about 1 h, giving a red solution. After allowing the solution to stand in air for 12 d, red block-shaped crystals were formed.

Z = 2

 $D_r = 1.370 \text{ Mg m}^{-3}$

 $0.32 \times 0.27 \times 0.23 \text{ mm}$

H-atom parameters constrained

 $w = 1/[\sigma^2(F_0^2) + (0.0691P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

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

 $\Delta \rho_{\rm max} = 0.97 \text{ e} \text{ \AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.26 \text{ e} \text{ Å}^{-3}$

Mo $K\alpha$ radiation

 $\mu = 0.80 \text{ mm}^{-1}$

T = 298 (2) K

Block, red

Crystal data

 $\begin{bmatrix} \text{Ni}(\text{C}_{14}\text{H}_{18}\text{NO}_2)_2 \end{bmatrix} \\ M_r = 523.30 \\ \text{Monoclinic}, P2_1/c \\ a = 11.043 (1) \text{ Å} \\ b = 18.041 (4) \text{ Å} \\ c = 6.465 (2) \text{ Å} \\ \beta = 99.990 (3)^{\circ} \\ V = 1268.5 (5) \text{ Å}^3 \end{bmatrix}$

Data collection

Bruker SMART CCD area-detector
diffractometer10730 measured reflections
2890 independent reflections
min = 0.784, $T_{max} = 0.837$ Bruker SMART CCD area-detector
(S40 independent reflections
(SADABS; Bruker, 2000)
T_min = 0.784, $T_{max} = 0.837$ 10730 measured reflections
2890 independent reflections
 $R_{int} = 0.083$
 $\theta_{max} = 27.5^{\circ}$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.063$ $wR(F^2) = 0.163$ S = 1.022890 reflections 161 parameters

Table 1

Selected geometric parameters (Å, °).

Ni1-O1	1.872 (3)	Ni1-N1	2.019 (3)
$\begin{array}{c} O1-Ni1-O1^i\\ O1-Ni1-N1^i \end{array}$	180	01-Ni1-N1	91.37 (11)
	88.63 (11)	N1 ⁱ -Ni1-N1	180

Symmetry code: (i) -x, -y, -z.



Figure 2

The crystal packing of (I). H atoms have been omitted.

All H atoms were placed in idealized positions and constrained to ride on their parent atoms, with C-H = 0.93–0.98 Å and $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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