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# Li-Fang Jiang, Zun-Xing Huang\* and Jia-Hong Chen

Department of Chemistry, Fuzhou University, Fuzhou 350002, People's Republic of China

Correspondence e-mail: hzunxing@sohu.com

# Key indicators

Single-crystal X-ray study T = 294 K Mean  $\sigma$ (C–C) = 0.006 Å H-atom completeness 93% Disorder in solvent or counterion R factor = 0.053 wR factor = 0.142 Data-to-parameter ratio = 12.8

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

# Bis(3-ethoxy-4-hydroxybenzaldehyde thiosemicarbazonato- $\kappa^2 S$ ,N)nickel(II) monohydrate

In the crystal structure of the title compound,  $[Ni(C_{10}H_{12}, N_3O_2S)_2] \cdot H_2O$ , the Ni<sup>II</sup> atom is located on an inversion center and is chelated by two hydroxyethoxybenzaldehyde thiosemicarbazonate anions in a square-planar geometry. The fivemembered chelate ring assumes an envelope conformation, with the Ni atom lying at the flap position. The uncoordinated water molecule is disordered over another inversion center and is hydrogen bonded to the Ni<sup>II</sup> complex.

## Comment

Recently, much attention has been focused on thiosemicarbazone and its complexes because of their biological activities and chemical versatility (Marisa *et al.*, 1998; Shen *et al.*, 1998; Mao *et al.*, 1999). We present here the structure of the title Ni<sup>II</sup> complex, (I), which incorporates hydroxyethoxybenzaldehyde thiosemicarbazonate (hetc) anions.



The molecular structure of (I) is shown in Fig. l. The Ni<sup>II</sup> atom is located on an inversion center and is chelated by two hydroxyethoxybenzaldehyde thiosemicarbazonate (hetc) anions in a square-planar geometry. The five-membered chelate ring assumes an envelope conformation, with atom Ni1 lying at the flap position, displaced by 0.433 (5) Å from the mean plane formed by the other four atoms. The Ni–S and Ni–N bond distances (Table 1) agree with those found in an Ni<sup>II</sup> complex with a thiosemicarbazone ligand (Marisa *et al.*, 2001).

The uncoordinated water molecule is disordered over an inversion center and is hydrogen bonded, as an acceptor, to the hydroxy group (Table 2). Intermolecular  $N-H\cdots O$  hydrogen bonding stabilizes the crystal structure.

# **Experimental**

4-Hydroxy-3-ethoxybenzaldehyde and thiosemicarbazide were dissolved in a water/ethanol solution (1:1) in 1:1 molar ratio. The solution was refluxed for 2 h. The solid product was separated and recrystallized from an ethanol solution to give pink crystals of  $H_2$ hetc.

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#### Figure 1

The molecular structure of (I), shown with 50% probability displacement ellipsoids (arbitrary spheres for H atoms). [Symmetry code: (iii) -x, 2 – y, -z.]

A methanol solution (10 ml) of H<sub>2</sub>hetc (0.2 mmol) was mixed with a tetrahydrofuran solution (10 ml) of Ni(CH<sub>3</sub>COO)<sub>2</sub>·2H<sub>2</sub>O (0.2 mmol). The mixture was stirred at room temperature for 5 h. Single crystals of (I) were obtained after two weeks.

### Crystal data

$M_r = 553.30$ $D_x = 1.585 \text{ Mg m}^{-3}$ Triclinic, $P\overline{1}$ Mo K $\alpha$ radiation $a = 5.794$ (3) ÅCell parameters from 7 $b = 10.222$ (4) Åreflections $c = 10.227$ (5) Å $\theta = 2.5-21.7^{\circ}$	
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$c = 10.227$ (5) Å $\theta = 2.5-21.7^{\circ}$	
$\alpha = 75.100 \ (7)^{\circ}$ $\mu = 1.06 \ \mathrm{mm}^{-1}$	
$\beta = 87.398 \ (6)^{\circ}$ $T = 294 \ (2) \ K$	
$\gamma = 81.956 \ (6)^{\circ}$ Prism, red	
$V = 579.6 (5) \text{ Å}^3$ $0.27 \times 0.13 \times 0.04 \text{ mm}$	ı

## Data collection

Bruker SMART CCD area-detector	2015 independent reflect
diffractometer	1593 reflections with $I >$
$\varphi$ and $\omega$ scans	$R_{\rm int} = 0.027$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.1^{\circ}$
(SADABS; Sheldrick, 2003)	$h = -6 \rightarrow 6$
$T_{\min} = 0.763, T_{\max} = 0.957$	$k = -12 \rightarrow 9$
2904 measured reflections	$l = -11 \rightarrow 12$

#### Refinement

Refinement on  $F^2$ 
$$\begin{split} R[F^2 > 2\sigma(F^2)] &= 0.053 \\ wR(F^2) &= 0.142 \end{split}$$
S = 0.972015 reflections 158 parameters H-atom parameters constrained 8

2015 independent reflections
1593 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.027$
$\theta_{\rm max} = 25.1^{\circ}$
$h = -6 \rightarrow 6$
$k = -12 \rightarrow 9$
$l = -11 \rightarrow 12$

#### Table 1

Selected geometric parameters (Å, °).

Ni1-S1	2.1712 (12)	N2-C10	1.282 (5)
Ni1-N3	1.916 (3)	N2-N3	1.402 (4)
S1-C10	1.723 (4)	N3-C5	1.279 (5)
N1-C10	1.350 (5)		
N3-Ni1-S1	85.53 (10)	C10-S1-Ni1	95.26 (14)

#### Table 2 Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$N1-H1A\cdotsO1^{i}$	0.87	2.30	3.124 (5)	156
$O1 - H1C \cdots O2$	0.94	2.06	2.678 (5)	121
$O1-H1C\cdots O3^{ii}$	0.94	2.05	2.896 (4)	148

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

H atoms of the uncoordinated water molecule are disordered and were not located. Amino and hydroxy H atoms were located in a difference Fourier map and refined as riding in their as-found relative positions, with  $U_{iso}(H) = 1.2U_{eq}(N,O)$ . Methyl H atoms were placed in calculated positions, with C-H = 0.96 Å, and refined as riding, with  $U_{\rm iso}({\rm H}) = 1.5 U_{\rm eq}({\rm C})$  and the torsion angles refined to fit the electron density. Other H atoms were placed in calculated positions, with C-H = 0.93 or 0.97 Å, and refined as riding, with  $U_{iso}(H) = 1.2U_{eq}(C)$ .

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Bruker, 2001); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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