# metal-organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

## Yu Wu,<sup>a,b</sup> Shao-Min Shi,<sup>a</sup> Bing Jia<sup>a</sup> and Zong-Qiu Hu<sup>a</sup>\*

<sup>a</sup>Department of Chemistry, Central China Normal University, Wuhan, Hubei 430079, People's Republic of China, and <sup>b</sup>Department of Chemistry, Sichuan University of Science and Engineering, Zigong, Sichuan 643000, People's Republic of China

Correspondence e-mail: zqhu@mail.ccnu.edu.cn

#### Key indicators

Single-crystal X-ray study T = 292 KMean  $\sigma(\text{C}-\text{C}) = 0.012 \text{ Å}$  R factor = 0.052 wR factor = 0.157 Data-to-parameter ratio = 15.4

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

## [3,5-Dibromosalicylaldehyde (2-hydroxybenzoyl)hydrazonato- $\kappa^{3}O,N,O'$ ]bis(pyridine- $\kappa N$ )zinc(II)

In the title compound,  $[Zn(C_{14}H_8Br_2N_2O_3)(C_5H_5N)_2]$ , the  $Zn^{II}$  ion is coordinated by one N and two O atoms from a Schiff base ligand and by the N atoms of two pyridine molecules to form a distorted trigonal-bipyramidal geometry.

#### Comment

Previously, we have reported the crystal structure and properties of a 3,5-dibromosalicylaldehyde salicylhydrazone zinc(II) complex (Hu *et al.*, 2005). We now report the synthesis and crystal structure of the title compound, (I).



The Zn<sup>II</sup> ion is coordinated by one N and two O atoms from the 3,5-dibromosalicylaldehyde salicylhydrazone ligand, and



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Received 20 February 2006 Accepted 22 February 2006 by two N atoms of two pyridine molecules (Fig. 1). This ZnN<sub>3</sub>O<sub>2</sub> coordination forms a distorted trigonal-bipyramidal geometry (Table 1). Intramolecular  $O-H \cdots N$  and  $C-H \cdots O$ hydrogen bonds are observed in the Schiff base ligand (Table 2).

### **Experimental**

To an ethanol solution (100 ml) of salicylhydrazine (6 g), one molar equivalent of 3,5-dibromosalicylaldehyde in ethanol (50 ml) was added slowly with continuous stirring and 3,5-dibromosalicylaldehyde salicylhydrazone precipitated immediately. 3,5-Dibromosalicylaldehyde salicylhydrazone (1 mmol), Zn(OAc)<sub>2</sub> (1 mmol), dimethylformamide (30 ml) and pyridine (10 ml) were refluxed for 1 h. The hot solution was filtered and allowed to stand at room temperature for 21 d, whereupon green crystals of (I) were obtained.

#### Crystal data

$[Zn(C_{14}H_8Br_2N_2O_3)(C_5H_5N)_2]$	Z = 2
$M_r = 635.61$	$D_x = 1.712 \text{ Mg m}^{-3}$
Triclinic, P1	Mo $K\alpha$ radiation
a = 8.9000 (11)  Å	Cell parameters from 1568
b = 12.2172 (14)  Å	reflections
c = 13.1342 (16)  Å	$\theta = 2.5 - 21.0^{\circ}$
$\alpha = 101.696 \ (2)^{\circ}$	$\mu = 4.27 \text{ mm}^{-1}$
$\beta = 103.519 \ (2)^{\circ}$	T = 292 (2) K
$\gamma = 110.744 \ (2)^{\circ}$	Block, green
$V = 1232.9$ (3) $Å^3$	$0.20$ $\times$ 0.20 $\times$ 0.20 mm

#### Data collection

Bruker SMART CCD area-detector	2763 reflections with $I > 2\sigma(I)$
diffractometer	$R_{\rm int} = 0.021$
$\varphi$ and $\omega$ scans	$\theta_{\rm max} = 26.0^{\circ}$
Absorption correction: none	$h = -10 \rightarrow 9$
6745 measured reflections	$k = -12 \rightarrow 15$
4740 independent reflections	$l = -15 \rightarrow 16$

#### Refinement

Refinement on  $F^2$  $R[F^2 > 2\sigma(F^2)] = 0.052$  $wR(F^2) = 0.157$ S = 1.014740 reflections 308 parameters H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0716P)^2]$
+ 0.5653P]
where $P = (F_0^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.001$
$\Delta \rho_{\rm max} = 0.62 \ {\rm e} \ {\rm A}^{-3}$
$\Delta \rho_{\rm min} = -0.33 \text{ e } \text{\AA}^{-3}$

#### Table 1

Selected geometric parameters (Å, °).

Zn1-O1	1.976 (4)	Zn1-N4	2.074 (5)
Zn1-N1	2.032 (4)	Zn1-O2	2.077 (4)
Zn1-N3	2.057 (5)		
O1-Zn1-N1	89.04 (17)	N3-Zn1-N4	102.42 (17)
O1-Zn1-N3	96.67 (18)	O1-Zn1-O2	165.38 (15)
N1-Zn1-N3	123.88 (17)	N1-Zn1-O2	77.01 (17)
O1-Zn1-N4	94.43 (19)	N3-Zn1-O2	94.78 (18)
N1-Zn1-N4	132.84 (17)	N4-Zn1-O2	91.95 (19)

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
C24—H24···O1	0.93	2.53	3.073 (8)	118
C20−H20···O2	0.93	2.46	3.022 (8)	119
C19−H19· · ·O1	0.93	2.56	3.108 (8)	118
C15−H15···O2	0.93	2.55	3.110 (8)	119
C14−H14···O2	0.93	2.46	2.779 (8)	100
O3−H3···N2	0.82	1.87	2.582 (6)	145

H atoms were placed in idealized positions and allowed to ride on their parent atoms, with O-H = 0.82 Å, C-H = 0.93 Å and  $U_{iso}(H) =$  $1.2-1.5U_{eq}(C,O).$ 

Data collection: SMART (Bruker, 2000); cell refinement: SAINT (Bruker, 2000); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1997); software used to prepare material for publication: SHELXTL.

This work was supported by Hubei Education Government of China (grant No. 20040131).

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