metal-organic papers

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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.007 \text{ Å}$ R factor = 0.038 wR factor = 0.090 Data-to-parameter ratio = 20.5

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

Dibromo[*N*,*N*-dimethyl-*N*'-(2-pyridylmethylidene)propane-1,3-diamine]zinc(II)

In the title mononuclear zinc(II) compound, $[ZnBr_2-(C_{11}H_{17}N_3)]$, the Zn^{II} ion is five-coordinated by three N atoms of a Schiff base ligand and by two Br^- anions, forming a distorted square-pyramidal geometry with a Br atom in the apical site.

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Comment

Zinc complexes are very important in biology, functioning as the active site of hydrolytic enzymes, where they are in a harddonor coordination environment of nitrogen and oxygen (Sanmartín *et al.*, 2000; Vallee & Auld, 1993). As part of an investigation of the structures of such zinc compounds, the title mononuclear zinc(II) complex, (I), was synthesized and its crystal structure is reported here.



The Zn^{II} atom in (I) is five-coordinated by three N atoms of the Schiff base ligand, and by two Br atoms, forming a



© 2006 International Union of Crystallography All rights reserved Figure 1 A view of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. distorted square-pyramidal geometry, as shown in Fig. 1. The bond lengths (Table 1) involving the Zn^{II} ion are comparable with the corresponding values observed in other zinc(II) complexes (McCleverty et al., 1980; Usman et al., 2003; You & Zhu, 2006). The significant distortion of the square pyramid is revealed by the bond angles between the apical Br1 atom and basal donor atoms (Table 1). As expected, the six-membered chelate ring Zn1/N2/C7-C9/N3 adopts a chair conformation. In the crystal structure, molecules are linked through weak C-H···Br interactions (Table 2).

Experimental

Compound (I) was obtained by stirring pyridine-2-carbaldehyde (1.0 mmol, 107.3 mg), N,N-dimethylpropane-1,3-diamine (1.0 mmol, 102.1 mg) and zinc bromide (1.0 mmol, 245.4 mg) in an EtOH solution (50 ml). The residue was recrystallized from an EtOH solution.

Crystal data

$[ZnBr_2(C_{11}H_{17}N_3)]$	Z = 2
$M_r = 416.47$	$D_x = 1.915 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Mo $K\alpha$ radiation
a = 7.602 (1) Å	Cell parameters from 2250
b = 9.150 (2) Å	reflections
c = 11.901 (2) Å	$\theta = 2.5 - 26.7^{\circ}$
$\alpha = 97.82 \ (3)^{\circ}$	$\mu = 7.21 \text{ mm}^{-1}$
$\beta = 103.30 \ (3)^{\circ}$	T = 298 (2) K
$\gamma = 112.25 \ (2)^{\circ}$	Block, yellow
V = 722.4 (3) Å ³	0.20 \times 0.20 \times 0.18 mm

Data collection

3200 independent reflections
2502 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.041$
$\theta_{\rm max} = 27.5^{\circ}$
$h = -9 \rightarrow 9$
$k = -11 \rightarrow 11$
$l = -15 \rightarrow 15$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.038$ wR(F²) = 0.090 S = 1.003200 reflections 156 parameters

H-atom parameters constrained $w = 1/[\sigma^2(F_0^2) + (0.0229P)^2]$ where $P = (F_0^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.68 \ {\rm e} \ {\rm \AA}^{-3}$ $\Delta \rho_{\rm min} = -0.65 \ {\rm e} \ {\rm \AA}^{-3}$

 $2\sigma(I)$

Table 1

Selected geometric parameters (Å, °).

Zn1-N2	2.155 (3)	Zn1-Br1	2.4163 (15)
Zn1-N1	2.227 (3)	Zn1-Br2	2.4631 (9)
Zn1-N3	2.236 (3)		
N2-Zn1-N1	74.49 (12)	N3-Zn1-Br1	101.78 (9)
N2-Zn1-N3	88.15 (13)	N2-Zn1-Br2	146.19 (9)
N1-Zn1-N3	151.26 (12)	N1-Zn1-Br2	89.05 (8)
N2-Zn1-Br1	102.52 (9)	N3-Zn1-Br2	93.38 (9)
N1-Zn1-Br1	104.21 (9)	Br1-Zn1-Br2	110.16 (4)

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$C10-H10C\cdots Br2$ $C11-H11A\cdots Br2$	0.96 0.96	2.92 2.85	3.571 (3) 3.536 (3)	126 129

H atoms were placed in idealized positions and constrained to ride on their parent atoms, C-H = 0.93-0.97 Å and with $U_{iso}(H) = 1.2$ or 1.5 times $U_{eq}(C)$.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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