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Key indicators

Single-crystal X-ray study $T=298~\mathrm{K}$ Mean $\sigma(\mathrm{C-C})=0.004~\mathrm{\mathring{A}}$ R factor = 0.041 wR factor = 0.105 Data-to-parameter ratio = 18.5

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

Bis[2,4-dichloro-6-(cyclopropyliminomethyl)-phenolato]zinc(II)

In the mononuclear title complex, $[Zn(C_{10}H_8Cl_2NO)_2]$,the Zn^{II} atom is four-coordinated in a distorted tetrahedral configuration by two imine N and two phenolate O atoms from two Schiff base ligands.

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Comment

Recently, the crystal structures of some Schiff base zinc(II) compounds have been reported (You, 2005a,b,c). In continuation of the work on these compounds, the title zinc(II) compound, (I), is reported here.

Complex (I) is a mononuclear zinc(II) compound (Fig. 1), which is structurally similar to bis[2-(cyclopropyliminomethyl)phenolato]zinc(II) [(II); You *et al.*, 2003]. The bond lengths and angles (Table 1) are comparable to those in (II). As observed in (II), the central Zn^{II} atom is four-coordinated by two imine N and two phenolate O atoms from two Schiff base ligands. The angles subtended at the Zn^{II} atom [range 95.73 (8)–120.78 (9)°] indicate a distorted tetrahedral geometry. In the crystal packing, symmetry-related molecules are linked *via* $C-H\cdots Cl$ hydrogen bonds (Table 2) into a three-dimensional framework.

Experimental

Cyclopropylamine (0.1 mmol, 5.7 mg) and 3,5-dichlorosalicylaldehyde (0.1 mmol, 19.2 mg) were dissolved in MeOH (10 ml). The mixture was stirred at room temperature for 10 min to give a clear yellow solution. To this solution was added a MeOH solution (5 ml) of $\rm Zn(CH_3COO)_2\cdot 4H_2O$ (0.1 mmol, 25.6 mg), with stirring. The resulting mixture was stirred for another 10 min at room temperature. After keeping the filtrate in air for 5 d, colourless plate-shaped crystals were formed at the bottom of the vessel.

Crystal data

 $[Zn(C_{10}H_8Cl_2NO)_2]$ $D_x = 1.642 \text{ Mg m}^{-3}$ $M_r = 523.52$ Mo $K\alpha$ radiation Monoclinic, C2/c Cell parameters from 4332 reflections a = 23.574 (2) Å $b = 7.926 \, (1) \, \text{Å}$ $= 2.7-24.2^{\circ}$ $\mu = 1.68 \text{ mm}^{-1}$ c = 24.264 (2) Å $\beta = 110.881 \ (1)^{\circ}$ T = 298 (2) K $V = 4235.9 (7) \text{ Å}^3$ Plate, colourless $0.22 \times 0.18 \times 0.09 \text{ mm}$ Z = 8

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metal-organic papers

Data collection

Bruker SMART CCD area-detector diffractometer ω scans Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{\min} = 0.708, \, T_{\max} = 0.863$

17686 measured reflections

4834 independent reflections 3757 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.035$ $\theta_{\rm max} = 27.5^{\circ}$ $h = -30 \rightarrow 30$ $k = -10 \rightarrow 10$ $l = -31 \rightarrow 31$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.041$ $wR(F^2) = 0.105$ S = 1.024834 reflections 262 parameters H-atom parameters constrained $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0439P)^{2} + 4.452P]$ $where P = (F_{o}^{2} + 2F_{c}^{2})/3$ $(\Delta/\sigma)_{max} = 0.001$ $\Delta\rho_{max} = 0.54 \text{ e Å}^{-3}$ $\Delta\rho_{min} = -0.39 \text{ e Å}^{-3}$

Table 1Selected geometric parameters (Å, °).

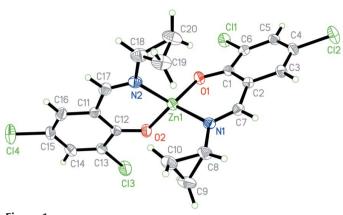
Zn1-O2	1.895 (2)	Zn1-N1	2.008 (2)
Zn1-O1	1.917 (2)	Zn1-N2	2.017 (2)
O2-Zn1-O1	112.73 (9)	O2-Zn1-N2	96.27 (9)
O2-Zn1-N1	120.78 (9)	O1-Zn1-N2	117.88 (9)
O1-Zn1-N1	95.73 (8)	N1-Zn1-N2	115.06 (9)

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

D $ H$ $\cdots A$	<i>D</i> —Н	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	D $ H$ $\cdot \cdot \cdot A$
$C10-H10A\cdots C13^{i}$	0.97	2.81	3.757 (3)	167
$C17-H17\cdots C11^{ii}$	0.93	2.83	3.747 (3)	170

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

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



The structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

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

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