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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=298 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.017 \AA$
$R$ factor $=0.089$
$w R$ factor $=0.240$
Data-to-parameter ratio $=19.3$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

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## Bis\{4-Bromo-2-[3-(methylammonio)propyliminomethyl]phenolato\}zinc(II) dinitrate

The title compound, $\left[\mathrm{Zn}\left(\mathrm{C}_{11} \mathrm{H}_{15} \mathrm{BrN}_{2} \mathrm{O}\right)_{2}\right]\left(\mathrm{NO}_{3}\right)_{2}$, is a centrosymmetric mononuclear Schiff base zinc(II) complex. The $\mathrm{Zn}^{\text {II }}$ atom, lying on a twofold rotation axis, is four-coordinated by two phenolate O atoms and two imine N atoms from two Schiff base ligands, forming a tetrahedral coordination.

## Comment

Zinc(II) complexes are very important in biological chemistry (Weston, 2005; Henkel \& Krebs, 2004). They function as the active site of hydrolytic enzymes, such as carboxypeptidase and carbonic anhydrase (Bertini et al., 1994). We report here the crystal structure of the new title zinc(II) complex, (I), derived from the Schiff base 4-bromo-2-[(3-methylaminopropylimino)methyl]phenol.

(I)

The complex molecule of (I) lies on a twofold rotation axis, and thus the asymmetric unit contains only one half of the $\left[\mathrm{Zn}\left(\mathrm{C}_{11} \mathrm{H}_{15} \mathrm{BrN}_{2} \mathrm{O}\right)_{2}\right]^{2+}$ complex cation (Fig. 1). The $\mathrm{Zn}^{\mathrm{II}}$ atom located on the rotation axis is four-coordinated by two phenolate O atoms and two imine N atoms from two Schiff base ligands, forming a tetrahedral coordination. The $\mathrm{Zn}-\mathrm{O}$ and $\mathrm{Zn}-\mathrm{N}$ bond lengths (Table 1) are comparable with the corresponding values observed in other Schiff base zinc(II) complexes (Tatar et al., 1999; Qiu, 2006). As expected, the N1/ $\mathrm{N} 2 / \mathrm{C} 8-\mathrm{C} 11$ chain adopts an extended conformation to minimize steric effects.

In the crystal structure, the molecules are linked through intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds (Table 2), forming chains running along the $c$ axis. In addition, a short $\operatorname{Br} 1 \cdots \mathrm{O} 2(x, y, 1+z)$ contact of $3.214(10) \AA$ is observed.

## Experimental

A mixture of 5-bromosalicylaldehyde ( $1.0 \mathrm{mmol}, 202.3 \mathrm{mg}$ ), N -methyl-1,3-diaminopropane ( $1.0 \mathrm{mmol}, 88.3 \mathrm{mg}$ ) and $\mathrm{Zn}\left(\mathrm{NO}_{3}\right)_{2} \cdot-$ $6 \mathrm{H}_{2} \mathrm{O}(1.0 \mathrm{mmol}, 297.5 \mathrm{mg})$ was dissolved in ethanol ( 100 ml ). The mixture was stirred for about 1 h at room temperature to give a clear yellow solution. After allowing this solution to stand in air for 18 d , yellow block-shaped crystals of (I) were formed at the bottom of the vessel.

## Crystal data

$\left[\mathrm{Zn}\left(\mathrm{C}_{11} \mathrm{H}_{15} \mathrm{BrN}_{2} \mathrm{O}\right)_{2}\right]\left(\mathrm{NO}_{3}\right)_{2}$
$M_{r}=731.71$
Orthorhombic, $F d d 2$
$a=22.010$ (4) $\AA$
$b=47.491$ (5) $\AA$
$c=5.436(2) \AA$
$V=5682(2) \AA^{3}$

## Data collection

Bruker SMART CCD area-detector diffractometer
$\omega$ scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\text {min }}=0.372, T_{\text {max }}=0.421$
$($ expected range $=0.311-0.352)$

## Refinement

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Refinement on \(F^{2}\)
\(R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.089\)
\(w R\left(F^{2}\right)=0.240\)
\(S=0.95\)
3444 reflections
178 parameters
H -atom parameters constrained
\(w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}{ }^{2}\right)+(0.0824 P)^{2}\right]\)
    where \(P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}{ }^{2}\right) / 3\)
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## $Z=8$

$D_{x}=1.711 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
$\mu=3.73 \mathrm{~mm}^{-1}$
$T=298$ (2) K
Block, yellow
$0.33 \times 0.30 \times 0.28 \mathrm{~mm}$

12087 measured reflections
3444 independent reflections
1463 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.186$
$\theta_{\text {max }}=29.0^{\circ}$

Table 1
Selected geometric parameters $\left(\AA,{ }^{\circ}\right)$.

| $\mathrm{Zn} 1-\mathrm{O} 1$ | $1.914(8)$ | $\mathrm{Zn} 1-\mathrm{N} 1$ | $1.953(9)$ |
| :--- | ---: | :--- | ---: |
|  |  |  |  |
| $\mathrm{O} 1^{\mathrm{i}}-\mathrm{Zn} 1-\mathrm{O} 1$ | $114.3(5)$ | $\mathrm{O} 1-\mathrm{Zn} 1-\mathrm{N} 1$ | $95.9(3)$ |
| $\mathrm{O}^{\mathrm{i}}-\mathrm{Zn} 1-\mathrm{N} 1$ | $116.6(4)$ | $\mathrm{N} 1-\mathrm{Zn} 1-\mathrm{N} 1^{\mathrm{i}}$ | $119.0(5)$ |

Symmetry code: (i) $-x+1,-y+1, z$.

Table 2
Hydrogen-bond geometry $\left(\AA,{ }^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~N} 2-\mathrm{H} 2 A \cdots \mathrm{O}^{\text {ii }}$ | 0.90 | 2.00 | $2.830(19)$ | 152 |
| $\mathrm{~N} 2-\mathrm{H} 2 A \cdots 3^{\text {ii }}$ | 0.90 | 2.23 | $2.976(18)$ | 140 |
| $\mathrm{~N} 2-\mathrm{H} 2 B \cdots \mathrm{O}^{2 i i}$ | 0.90 | 2.08 | $2.882(19)$ | 148 |

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

All H atoms were placed in calculated positions and constrained to ride on their parent atoms, with $\mathrm{N}-\mathrm{H}$ distances of $0.90 \AA$ and $\mathrm{C}-\mathrm{H}$


Figure 1
The structure of (I), showing 30\% probability displacement ellipsoids and the atomic numbering scheme. Unlabelled atoms are related to labelled atoms by the symmetry operation $(1-x, 1-y, z)$.
distances of $0.93-0.97 \AA$, and with $U_{\text {iso }}(\mathrm{H})=1.2$ or $1.5 U_{\text {eq }}(\mathrm{C}, \mathrm{N})$. The high $R_{\text {int }}$ value and the low ratio of observed to unique reflections ( $42 \%$ ) are probably due to the poor diffraction quality of the crystal. The highest peak in the final difference map is located $1.31 \AA$ from atom N1 (1.42 Å from Zn1).

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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