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Li-Fang Zhao

Department of Chemistry and Chemical Engineering, Baoji University of Arts and Sciences, Baoji 721007, People's Republic of China

Correspondence e-mail: bjzhaolf@163.com

Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.003 Å R factor = 0.055 wR factor = 0.136 Data-to-parameter ratio = 14.5

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

2-(Cyclopropyliminomethyl)-4-nitrophenol

The title compound, $C_{10}H_{10}N_2O_3$, is a Schiff base compound derived from the condensation of equimolar 5-nitrosalicylaldeheyde and cyclopropylamine in MeOH. The molecule adopts a *trans* configuration about the C=N bond and there is an intramolecular $O-H\cdots N$ hydrogen bond.

Comment

Schiff base compounds derived from salicylaldehyde have been of great interest in coordination chemistry for many years (Nishijima *et al.*, 1995; Archer & Wang, 1990). They can easily coordinate to transition metal ions through the deprotonated phenolate O atoms and the imine N atoms. As part of an investigation of the crystal structures of such ligands, the structure of (I) is reported here.



Compound (I) is a Schiff base compound (Fig. 1), which is derived from the condensation of equimolar salicylaldehyde and cyclopropylamine in MeOH. All the bond lengths in the compound are within normal ranges (Allen *et al.*, 1987). As expected, the molecule adopts a *trans* configuration about the C7—N2 bond. The dihedral angle between the cyclopropane and benzene rings is 89.5 (2)°. The dihedral angle between the benzene ring and the O1/N1/O2 nitryl plane is $6.0 (2)^{\circ}$, probably due to the presence of an intramolecular O—H···N hydrogen bond (Table 1). In the crystal structure, there are no obviously short contacts (Fig. 2).



Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. The intramolecular hydrogen bond is shown as a dashed line.

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Experimental

Salicylaldehyde (0.1 mmol, 12.1 mg) and cyclopropylamine (0.1 mmol, 5.7 mg) were dissolved in MeOH (10 ml). The mixture was stirred for 30 min to give a yellow solution. The solution was kept in air for 7 d and yellow block-shaped crystals were obtained.

 $D_x = 1.402 \text{ Mg m}^{-3}$

Cell parameters from 2043

 $0.25 \times 0.20 \times 0.14 \text{ mm}$

Mo $K\alpha$ radiation

reflections

 $\mu = 0.11 \text{ mm}^{-1}$

T = 298 (2) K

Block, yellow

 $\theta = 2.6 - 26.5^{\circ}$

Crystal data

 $\begin{array}{l} {\rm C_{10}H_{10}N_2O_3}\\ M_r = 206.20\\ {\rm Monoclinic,} \ P_{2_1}/c\\ a = 7.800 \ (2) \ {\rm \AA}\\ b = 5.845 \ (2) \ {\rm \AA}\\ c = 21.610 \ (3) \ {\rm \AA}\\ \beta = 97.599 \ (2)^\circ\\ V = 976.6 \ (2) \ {\rm \AA}^3\\ Z = 4 \end{array}$

Data collection

Bruker SMART CCD area-detector diffractometer	2022 independent reflections 1694 reflections with $I > 2\sigma(I)$
ω scans	$R_{\rm int} = 0.028$
Absorption correction: multi-scan	$\theta_{\rm max} = 26.5^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -9 \rightarrow 9$
$T_{\min} = 0.974, \ T_{\max} = 0.985$	$k = -7 \rightarrow 7$
7544 measured reflections	$l = -27 \rightarrow 27$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.055$ $wR(F^2) = 0.136$ S = 1.13 2022 reflections 139 parameters H atoms treated by a mixture of independent and constrained	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0587P)^{2} + 0.2047P]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3 (\Delta/\sigma)_{max} < 0.001 \Delta\rho_{max} = 0.18 \text{ e} \text{ Å}^{-3} \Delta\rho_{min} = -0.32 \text{ e} \text{ Å}^{-3}$
H atoms treated by a mixture of independent and constrained refinement	,

Table 1

				0	
H١	ydrogen	i-bonding	geometry	(A,	°).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
O3−H3···N2	0.90 (1)	1.739 (15)	2.576 (2)	153 (2)



Figure 2 The crystal packing of (I), viewed along the *b* axis.

The hydroxyl atom H3 was located in a difference Fourier map and refined isotropically, with the O–H distance restrained to 0.90 (1) Å. The other H atoms were placed in idealized positions and constrained to ride on their parent atoms, with C–H distances in the range 0.93–0.97 Å and $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); 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*.

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