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#### Key indicators

Single-crystal X-ray study T = 298 KMean  $\sigma$ (C–C) = 0.006 Å R factor = 0.073 wR factor = 0.153 Data-to-parameter ratio = 14.1

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The molecule of the title compound,  $C_{14}H_{11}CIN_2O_3$ , is roughly planar and displays a *trans* configuration with respect to the C=N double bond. The crystal structure is stabilized by intermolecular  $O-H\cdots O$  hydrogen bonds.

5-Chlorosalicylaldehyde salicylhydrazone

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# Comment

Schiff base compounds have been of great interest for a long time and have played an important role in the development of coordination chemistry (Musie *et al.*, 2001; Bernardo *et al.*, 1996; Paul *et al.*, 2002). As an extension of work on the structural characterization of such compounds, the crystal structure of the title compound, (I), is reported here.



In compound (I) (Fig. 1), all bond lengths are within normal ranges (Allen *et al.*, 1987). The C7—N1 bond length of 1.283 (4) Å conforms to the value for a double bond. The bond length of 1.345 (5) Å between atoms C8 and N2 is intermediate between an N–N single bond and an N—N double bond, because of conjugation effects in the molecule. The dihedral angle between the two benzene rings is  $12.7 (4)^{\circ}$ .

In the crystal structure, molecules are linked through intermolecular  $O-H\cdots O$  hydrogen bonds (Table 1), forming chains running along the *c* axis (Fig. 2).

# **Experimental**

Reagents and solvents used were of commercially available quality. The title compound was prepared by the following procedure: 5-chlorosalicylaldehyde (0.1 mmol, 15.7 mg) and 2-hydroxybenzoic acid hydrazide (0.1 mmol, 15.2 mg) were dissolved in MeOH (10 ml). The mixture was stirred at room temperature, giving a clear yellow solution. Crystals of the title compound were formed by gradual evaporation of the solvent over a period of about one week at room temperature.

Crystal data C14H11CIN2O3  $D_r = 1.497 \text{ Mg m}^{-3}$  $M_r=290.70$ Mo  $K\alpha$  radiation Monoclinic,  $P2_1/c$ Cell parameters from 551 a = 18.873 (2) Å reflections b = 5.391 (1) Å $\theta = 2.6 - 23.8^{\circ}$  $\mu = 0.31 \text{ mm}^{-1}$ c = 12.851 (3) Å  $\beta = 99.474 \ (4)^{\circ}$ T = 298 (2) K V = 1289.6 (4) Å Flake, yellow  $0.14 \times 0.09 \times 0.01 \text{ mm}$ Z = 4

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# organic papers

#### Data collection

Bruker APEX area-detector diffractometer  $\omega$  scan Absorption correction: multi-scan *SADABS* (Sheldrick, 1996)  $T_{min} = 0.959, T_{max} = 0.997$ 9927 measured reflections

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.073$   $wR(F^2) = 0.153$  S = 1.022650 reflections 188 parameters H atoms treated by a mixture of independent and constrained refinement

**Table 1** Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
N2-H2···O3	0.90(1)	1.88 (3)	2.614 (4)	137 (4)
$O3-H3 \cdot \cdot \cdot O2^i$	0.90 (3)	1.70 (3)	2.588 (3)	170 (4)
O1-H1··· $O3$ <sup>ii</sup>	0.82	2.56	3.011 (4)	116
$O1-H1\cdot\cdot\cdot N1$	0.82	2.01	2.717 (4)	144

2650 independent reflections

 $w = 1/[\sigma^2(F_0^2) + (0.0266P)^2]$ 

where  $P = (F_o^2 + 2F_c^2)/3$ 

\_3

+ 0.8881P]

 $(\Delta/\sigma)_{\rm max} < 0.001$ 

 $\Delta \rho_{\text{max}} = 0.20 \text{ e } \text{\AA}^{-3}$  $\Delta \rho_{\text{min}} = -0.22 \text{ e } \text{\AA}^{-3}$ 

 $R_{\rm int} = 0.090$ 

 $\theta_{\rm max} = 26.5^{\circ}$ 

 $h = -23 \rightarrow 23$ 

 $k = -6 \rightarrow 6$ 

 $l = -16 \rightarrow 16$ 

1393 reflections with  $I > 2\sigma(I)$ 

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

Atoms H2 and H3 were located in a difference Fourier map and refined isotropically, with O–H and N–H distances restrained to 0.90 (1) Å. The other H atoms were placed in idealized positions and constrained to ride on their parent atoms, with an O–H distance of 0.82 Å, C–H distances of 0.93 Å, and with  $U_{\rm iso}(\rm H) = 1.2U_{eq}(\rm C)$  or  $1.5U_{eq}(\rm O)$ .

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); 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: *SHELXL97*.

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### Figure 1

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



#### Figure 2

Packing of (I) viewed along the b axis. Dashed lines indicate intermolecular hydrogen bonds.

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