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Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.003 Å R factor = 0.046 wR factor = 0.105 Data-to-parameter ratio = 13.8

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

In the title compound, C_7H_6CINO , which exists as the E isomer, the crystal packing is stabilized by intermolecular O- $H \cdots N$ and $C - H \cdots O$ hydrogen bonds.

(E)-2-Chlorobenzaldehyde oxime

Comment

2-Chlorobenzaldehyde oxime, (I), is an important intermediate for organic synthesis (Xu & Jin, 1999), existing in two isomeric forms, viz. Z and E (Sharghi & Sarvari, 2001). We report here the crystal structure of (I) (Fig. 1), which is the Eisomer.



In (I), the bond lengths and angles (Table 1) are in agreement with values reported previously (Jerslev, 1983; Jensen, 1970). Atoms N1 and O1 deviate from the mean plane of C1-C7/Cl1 by 0.278 (2) and 0.279 (3) Å, respectively. $O-H \cdots N$ hydrogen bonds (Table 2) link the molecules into centrosymmetric dimers. The crystal packing (Fig. 2) is further stabilized by weak intermolecular C-H···O interactions (Table 2).

Experimental

The title compound was synthesized by the reaction of 2-chlorobenzaldehyde (0.01 mol) with hydroxylamine hydrochloride (0.01 mol) in the presence of sodium carbonate (0.01 mol) in an aqueous methanol solution (20 ml) at room temperature (3 h). After diluting with water, the aqueous solution was extracted with dichloromethane and the organic phase was evaporated to afford the title product in 90% isolated yield (1.41 g). Crystals suitable for X-ray diffraction analysis were obtained by slow evaporation of a solution in a hexane/dichloromethane mixture (1:1 v/v) at room temperature over a period of one week.

Crystal data	
C7H6CINO	$D_x = 1.445 \text{ Mg m}^{-3}$
$M_r = 155.58$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 2273
a = 3.9231 (19) Å	reflections
b = 14.160 (7) Å	$\theta = 2.3-26.3^{\circ}$
c = 12.895 (6) Å	$\mu = 0.46 \text{ mm}^{-1}$
$\beta = 93.544 \ (7)^{\circ}$	T = 298 (2) K
V = 715.0 (6) Å ³	Block, colourless
Z = 4	$0.37 \times 0.26 \times 0.17 \text{ mm}$

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Figure 1

View of (I), with displacement ellipsoids drawn at the 40% probability level.



Figure 2

A perspective view of the packing along the c axis. Hydrogen bonds are indicated by dashed lines.

Data collection

Bruker SMART CCD area-detector	1257 independent reflections
diffractometer	1146 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.019$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.0^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -4 \rightarrow 4$
$T_{\min} = 0.871, T_{\max} = 0.918$	$k = -16 \rightarrow 16$
3621 measured reflections	$l = -12 \rightarrow 15$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0374P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.046$	+ 0.4106P]
$wR(F^2) = 0.105$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.13	$(\Delta/\sigma)_{\rm max} < 0.001$
257 reflections	$\Delta \rho_{\rm max} = 0.26 \ {\rm e} \ {\rm \AA}^{-3}$
91 parameters	$\Delta \rho_{\rm min} = -0.21 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1

Selected geometric parameters (A,	elected	geometric	parameters	(A, ').
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Cl1-C5 O1-N1	1.744 (2) 1.402 (2)	N1-C7	1.266 (3)
C7-N1-O1	111.71 (19)	N1-C7-C4	120.6 (2)

Table 2

Hydrogen-bond geometry (Å, $^{\circ}$).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\begin{array}{c} \text{O1-H1} A \cdots \text{N1}^{\text{i}} \\ \text{C6-H6} A \cdots \text{O1}^{\text{ii}} \end{array}$	0.82 0.93	2.14 2.55	2.855 (3) 3.451 (3)	146 162

Symmetry codes: (i) -x - 1, -y + 2, -z; (ii) x + 1, $-y + \frac{3}{2}$, $z + \frac{1}{2}$.

All H atoms were placed in calculated positions, with C–H = 0.93 Å and O–H = 0.82 Å, and included in the final cycles of refinement using a riding model, with $U_{\rm iso}(\rm H) = 1.2U_{eq}(\rm C)$ for the C-bound H atoms and $1.5U_{eq}(\rm O)$ for the hydroxyl H atom.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1999); 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, 1999); software used to prepare material for publication: *SHELXTL*.

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