

4-Chlorobenzohydrazide

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Key indicators

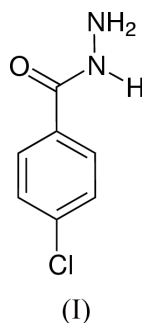
Single-crystal X-ray study
 $T = 293$ K
 Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
 R factor = 0.061
 wR factor = 0.143
 Data-to-parameter ratio = 12.3

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

The crystal structure of the title compound, $\text{C}_7\text{H}_7\text{N}_2\text{OCl}$, has been determined in the monoclinic space group $P2_1/c$ at room temperature. The structure is stabilized by intermolecular $\text{N}-\text{H}\cdots\text{O}$ and $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds.

Comment

The title compound, (I), was tested for its activity against tuberculosis *in vitro* (Bew-Hol *et al.*, 1952), and was found to be inactive at a concentration of $10 \mu\text{g ml}^{-1}$ of the culture medium. Compound (I) was also used as a starting material for the synthesis of α -methyl-substituted or unsubstituted [(4-phenyl/ethyl-5-*p*-chlorophenyl-4*H*-1,2,4-triazol-3-yl)thio]-acetic acids, which have been found to possess good anti-inflammatory activity (Sung & Lee, 1992).



The orientations of the carbonyl and hydrazide groups with respect to the aromatic ring are defined by the torsion angles $\text{C5}-\text{C4}-\text{C7}-\text{O1}$ $31.9(4)^\circ$ and $\text{C5}-\text{C4}-\text{C7}-\text{N1}$ $-148.3(3)^\circ$. The crystal structure is held together by two intermolecular hydrogen bonds, $\text{N1}-\text{H1}\cdots\text{N2}^i$ and $\text{N2}-\text{H2N}\cdots\text{O1}^{ii}$ (symmetry codes as in Table 1).

Experimental

The title compound was synthesized from 4-chlorobenzoic acid by refluxing it with anhydrous ethanol and concentrated sulfuric acid for 3 h to obtain ethyl 4-chlorobenzoate. This, on further reaction with hydrazine hydrate in ethanol under reflux conditions for 6 h, yielded 4-chlorobenzohydrazide. Crystallization from ethanol yielded colorless crystals (Saikachi *et al.*, 1955).

Crystal data

$\text{C}_7\text{H}_7\text{ClN}_2\text{O}$
 $M_r = 170.60$
 Monoclinic, $P2_1/c$
 $a = 15.945(7)$ Å
 $b = 3.8449(16)$ Å
 $c = 12.389(5)$ Å
 $\beta = 99.664(7)^\circ$
 $V = 748.7(5)$ Å³
 $Z = 4$

$D_x = 1.513$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 2013 reflections
 $\theta = 2.6-27.9^\circ$
 $\mu = 0.45$ mm⁻¹
 $T = 293(2)$ K
 Rod, colorless
 $0.20 \times 0.18 \times 0.05$ mm

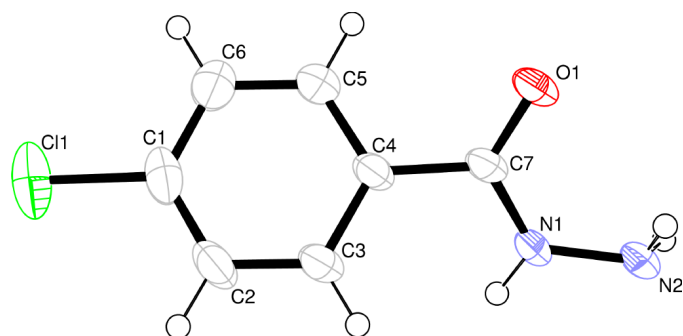


Figure 1
Molecular structure of the title compound with the atom-numbering scheme. Displacement ellipsoids for non-H atoms are drawn at the 50% probability level. H atoms are shown as spheres of arbitrary radii.

Data collection

Bruker SMART CCD area-detector diffractometer	981 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\text{int}} = 0.049$
Absorption correction: none	$\theta_{\text{max}} = 25.0^\circ$
4456 measured reflections	$h = -18 \rightarrow 18$
1329 independent reflections	$k = -4 \rightarrow 4$
	$l = -13 \rightarrow 14$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.1534P)^2 + 0.0248P]$
$R[F^2 > 2\sigma(F^2)] = 0.061$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.143$	$(\Delta/\sigma)_{\text{max}} = 0.010$
$S = 1.03$	$\Delta\rho_{\text{max}} = 0.38 \text{ e } \text{\AA}^{-3}$
1329 reflections	$\Delta\rho_{\text{min}} = -0.35 \text{ e } \text{\AA}^{-3}$
108 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Hydrogen-bonding geometry (\AA , $^\circ$).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N1-H1 \cdots N2^i$	0.86	2.10	2.911 (4)	157
$N2-H2N \cdots O1^{ii}$	0.86 (3)	2.22 (4)	3.046 (4)	168 (3)

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

The H atoms on N2, viz. H1N and H2N, were located in a difference Fourier map and refined freely. All other atoms were positioned geometrically and allowed to ride on their parent atoms, with $U_{\text{iso}}(\text{H}) = U_{\text{eq}}$ of the parent atom.

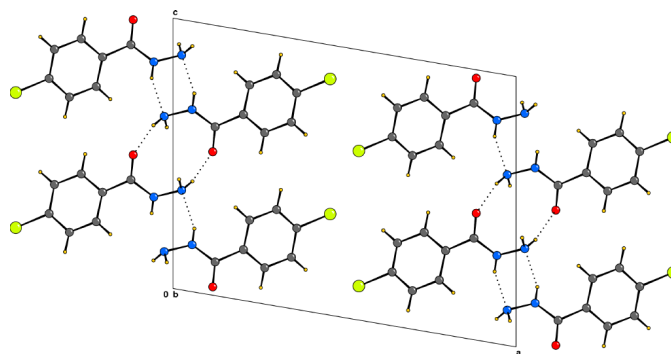


Figure 2
Packing diagram of the title compound, viewed down the b axis. $N-H \cdots O$ and $N-H \cdots N$ hydrogen bonds are shown as dotted lines.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1998); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* for Windows (Farrugia, 1997) and *CAMERON* (Watkin *et al.*, 1993); software used to prepare material for publication: *PLATON* (Spek, 1990).

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