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Key indicators

Single-crystal X-ray study

$T = 293\text{ K}$

Mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$

R factor = 0.030

wR factor = 0.079

Data-to-parameter ratio = 18.6

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

4-Methoxypiperidinium chloride

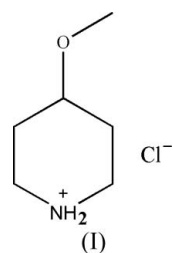
The methoxypiperidinium cation of the title compound, $\text{C}_6\text{H}_{14}\text{NO}^+\cdot\text{Cl}^-$, adopts a chair conformation. The crystal structure is stabilized by $\text{N}-\text{H}\cdots\text{Cl}$ hydrogen bonds.

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Comment

The title compound, (I) (Fig. 1), is a common intermediate in drug synthesis. In (I), the methoxypiperidinium cation adopts a chair conformation. Each N atom donates two H atoms to two symmetry-equivalent halide ions, assembling the ions into chains running along the b axis (Table 1 and Fig. 2).



Experimental

To a stirred refluxing mixture of sodium hydride (60% in mineral oil; 2.5 g, 62.5 mmol) and dry tetrahydrofuran (50 ml) a solution of *tert*-butyl 4-hydroxypiperidine-1-carboxylate (10 g, 49.7 mmol) in dry

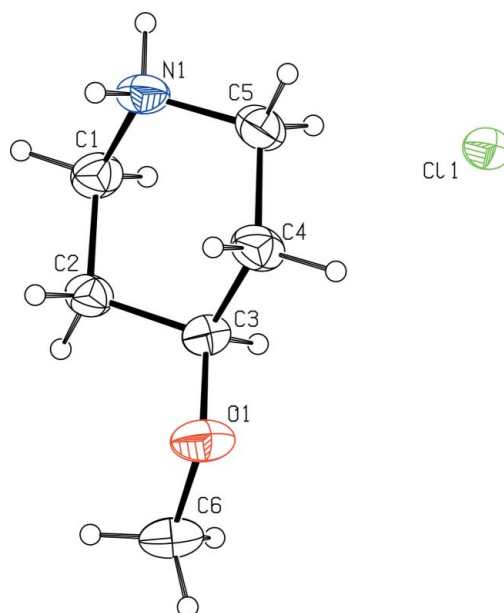


Figure 1

The molecular structure of (I), with the atom-labeling scheme and 30% probability displacement ellipsoids.

tetrahydrofuran (30 ml) was added dropwise. After the mixture had been refluxed for 1.5 h, iodomethane (5 ml) was added. The reaction mixture was refluxed for 2 h, and then cooled to room temperature; water (50 ml) and ethyl acetate (40 ml) were added. The layers were separated. The organic phase was washed with brine (20 ml), dried over sodium sulfate, and concentrated *in vacuo*. The crude liquid was flash chromatographed over silica gel using 1:1 hexane–ethyl acetate as eluent; all volatiles were removed *in vacuo*. A commercial 1.0 M methanol solution of hydrogen chloride (50 ml) was added dropwise and the resulting mixture was stirred for 6 h at room temperature. The solvents were removed under vacuum, giving 4-methoxy-piperidinium chloride as a white solid (yield 94%). Single crystals suitable for X-ray diffraction were obtained by slow evaporation of a dichloromethane solution at room temperature.

Crystal data

$C_6H_{14}NO^+ \cdot Cl^-$	$Z = 2$
$M_r = 151.63$	$D_x = 1.200 \text{ Mg m}^{-3}$
Monoclinic, $P2_1$	Mo $K\alpha$ radiation
$a = 6.6778 (13) \text{ \AA}$	$\mu = 0.39 \text{ mm}^{-1}$
$b = 7.4041 (14) \text{ \AA}$	$T = 293 (2) \text{ K}$
$c = 8.6654 (16) \text{ \AA}$	Plate, colorless
$\beta = 101.666 (3)^\circ$	$0.22 \times 0.21 \times 0.10 \text{ mm}$
$V = 419.59 (14) \text{ \AA}^3$	

Data collection

Bruker SMART CCD area-detector diffractometer	2344 measured reflections
φ and ω scans	1564 independent reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	1507 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.922$, $T_{\max} = 0.964$	$R_{\text{int}} = 0.013$
	$\theta_{\text{max}} = 26.0^\circ$

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\text{max}} < 0.001$
$R[F^2 > 2\sigma(F^2)] = 0.030$	$\Delta\rho_{\text{max}} = 0.19 \text{ e \AA}^{-3}$
$wR(F^2) = 0.079$	$\Delta\rho_{\text{min}} = -0.13 \text{ e \AA}^{-3}$
$S = 1.05$	Extinction correction: <i>SHELXL97</i>
1564 reflections	Extinction coefficient: 0.043 (6)
84 parameters	Absolute structure: Flack (1983),
H-atom parameters constrained	673 Friedel pairs
$w = 1/[\sigma^2(F_o^2) + (0.0456P)^2 + 0.0315P]$	Flack parameter: 0.00 (7)
where $P = (F_o^2 + 2F_c^2)/3$	

Table 1

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

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N1-H1A \cdots Cl1^i$	0.90	2.22	3.121 (2)	176
$N1-H1B \cdots Cl1^{ii}$	0.90	2.22	3.112 (2)	170

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

H atoms were positioned geometrically and refined with displacement parameters with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$, using a riding model, with $C-H = 0.98$ (CH), 0.97 (CH₂) and 0.96 \AA (CH₃). H

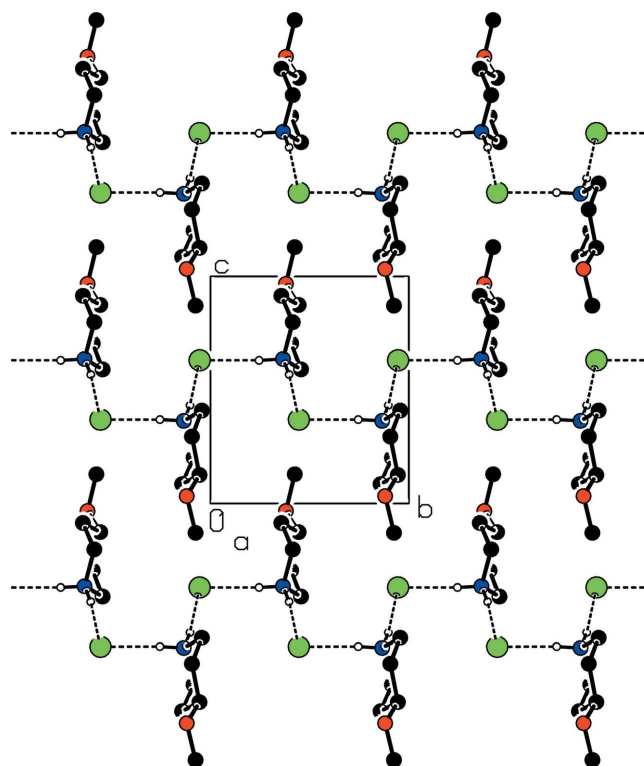


Figure 2

The hydrogen-bonding network in (I), with hydrogen bonds shown as dashed lines. For the sake of clarity, H atoms not involved in hydrogen bonding have been omitted.

atoms bonded to nitrogen were refined as riding with an N–H distance of 0.90 \AA .

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINTE* (Bruker, 2003); data reduction: *SAINTE*; 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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