

1-[2-(4-Carboxyphenoxy)ethyl]piperidinium
chlorideYong-Jiang Wang^{a*} and
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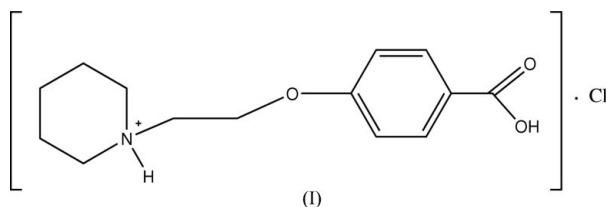
Key indicators

Single-crystal X-ray study
 $T = 296$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.032
 wR factor = 0.073
Data-to-parameter ratio = 19.2For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the title structure, $\text{C}_{14}\text{H}_{20}\text{NO}_3^+\cdot\text{Cl}^-$, as expected, the piperidine ring adopts a chair conformation and the carboxylic acid group and the benzene ring are essentially coplanar, forming a conjugated system. In the crystal structure, extended chains are formed through $\text{N}-\text{H}\cdots\text{Cl}$ and $\text{O}-\text{H}\cdots\text{Cl}$ hydrogen bonds.

Comment

The title compound, (I), is an intermediate product in the synthesis of raloxifene hydrochloride, a selective estrogen receptor modulator. It was prepared by the hydrolysis of methyl 4-(2-piperidinylethoxy)benzoate (Gong *et al.*, 2003) and was crystallized from ethanol. The title structure is shown in Fig. 1 and the torsion angles listed in Table 1 indicate that the carboxylic acid group and the benzene ring are essentially coplanar. The C1—C2 bond length is shorter than the normal single C—C bond (*ca.* 1.54 Å), indicating that a conjugated system has been formed in this part of the molecule. In the crystal structure, extended chains are formed in the *c*-axis direction, through $\text{N}-\text{H}\cdots\text{Cl}$ and $\text{O}-\text{H}\cdots\text{Cl}$ hydrogen bonds (Table 2 and Fig. 2).



Experimental

The title compound was prepared according to the procedure of Gong *et al.* (2003). Suitable crystals were obtained by evaporation of an ethanol solution (m.p. 549–550 K).

Crystal data

 $\text{C}_{14}\text{H}_{20}\text{NO}_3^+\cdot\text{Cl}^-$
 $M_r = 285.77$
Orthorhombic, $Pbca$
 $a = 16.777$ (4) Å
 $b = 7.4464$ (15) Å
 $c = 23.192$ (5) Å
 $V = 2897.3$ (11) Å³
 $Z = 8$
 $D_x = 1.310$ Mg m⁻³Mo $K\alpha$ radiation
Cell parameters from 20969
reflections
 $\theta = 3.0$ – 27.5°
 $\mu = 0.27$ mm⁻¹
 $T = 296$ (1) K
Block, colorless
 $0.30 \times 0.20 \times 0.20$ mm

Data collection

Rigaku R-Axis RAPID
diffractometer
 ω scans
Absorption correction: multi-scan
(*ABSCOR*; Higashi, 1995)
 $T_{\min} = 0.918$, $T_{\max} = 0.948$
26060 measured reflections3317 independent reflections
2190 reflections with $F^2 > 2\sigma(F^2)$
 $R_{\text{int}} = 0.036$
 $\theta_{\text{max}} = 27.5^\circ$
 $h = -21 \rightarrow 21$
 $k = -9 \rightarrow 8$
 $l = -30 \rightarrow 30$

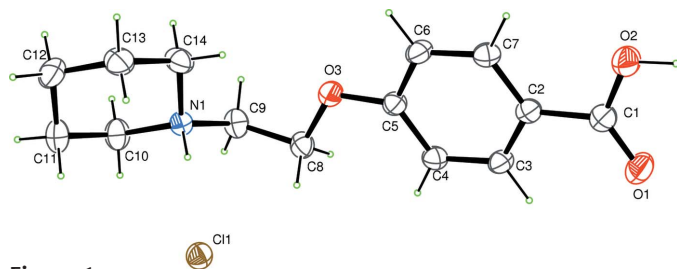


Figure 1
View of (I), showing 40% probability displacement ellipsoids. H atoms are drawn as spheres of arbitrary radii.

Refinement

Refinement on F^2	$w = 1/[0.0001F_o^2 + \sigma(F_o^2)]/(4F_o^2)$
$R[F^2 > 2\sigma(F^2)] = 0.032$	$(\Delta/\sigma)_{\max} < 0.001$
$wR(F^2) = 0.073$	$\Delta\rho_{\max} = 0.22 \text{ e } \text{Å}^{-3}$
$S = 1.00$	$\Delta\rho_{\min} = -0.22 \text{ e } \text{Å}^{-3}$
3317 reflections	Extinction correction: Larson (1970)
173 parameters	Extinction coefficient: $4.4(3) \times 10^2$
H-atom parameters constrained	

Table 1
Selected geometric parameters (Å, °).

O2—C1	1.3323 (18)	C1—C2	1.4854 (19)
O3—C8	1.4184 (16)		
O1—C1—C2—C3	−4.0 (2)	O2—C1—C2—C3	177.40 (12)
O1—C1—C2—C7	174.10 (14)	O2—C1—C2—C7	−4.47 (18)

Table 2
Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
O2—H201...Cl1 ⁱ	0.93	2.11	3.0219 (9)	168
N1—H222...Cl1	0.86	2.27	3.1302 (11)	174

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

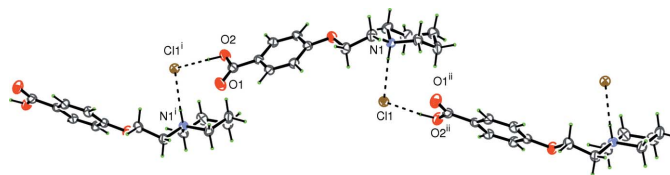


Figure 2
View of a hydrogen-bonded (dashed lines) chain. [Symmetry codes: (i) $x, \frac{1}{2} - y, \frac{1}{2} + z$; (ii) $x, \frac{1}{2} - y, -\frac{1}{2} + z$.]

Atom H201 was located in a difference Fourier map. All other H atoms were placed in calculated positions, with N—H = 0.86 Å and C—H = 0.97 or 0.98 Å. All H atoms were refined using a riding model, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}$ of the carrier atom.

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/MS, 2004); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

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