

Acta Crystallographica Section E

Structure Reports

Online

ISSN 1600-5368

R-(3-Carboxy-2-hydroxypropyl)trimethylazanium chloride

Seik Weng Ng

Department of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia, and Chemistry Department, Faculty of Science, King Abdulaziz University, PO Box 80203 Jeddah, Saudi Arabia

Correspondence e-mail: seikweng@um.edu.my

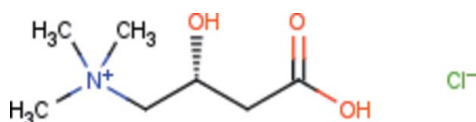
Received 8 April 2012; accepted 12 April 2012

Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.002$ Å; R factor = 0.027; wR factor = 0.072; data-to-parameter ratio = 19.2.

In the title salt [common name L-carnitine hydrochloride], $\text{C}_7\text{H}_{16}\text{NO}_3^+\cdot\text{Cl}^-$, the organic cation features a carboxylic part ($-\text{CO}_2\text{H}$) having unambiguous single- and double-bonds [1.336 (2), 1.211 (2) Å]. There is a large $\text{N}-\text{C}-\text{C}$ bond angle [115.9 (1)°] for the C atom connected to the bulky trimethyl-amino substituent. In the crystal, the acid H atom forms a hydrogen bond to the chloride anion, whereas the hydroxyl H atom forms a longer hydrogen bond to the anion, generating a helical chain running along [001].

Related literature

For racemic carnitine hydrochloride, see: Tomita *et al.* (1974); Yunuskhodzhaev *et al.* (1991). For *R*-carnitine, see: Gandour *et al.* (1985).



Experimental

Crystal data

 $\text{C}_7\text{H}_{16}\text{NO}_3^+\cdot\text{Cl}^-$ $M_r = 197.66$ Orthorhombic, $P2_12_12_1$ $a = 6.3043$ (3) Å $b = 11.5256$ (7) Å $c = 13.4905$ (8) Å $V = 980.23$ (10) Å³ $Z = 4$ Mo $K\alpha$ radiation $\mu = 0.36$ mm⁻¹ $T = 100$ K

0.40 × 0.30 × 0.20 mm

Data collection

Agilent Technologies SuperNova
Dual diffractometer with Atlas
detector

Absorption correction: multi-scan
CrysAlis PRO (Agilent, 2012)
 $T_{\min} = 0.869$, $T_{\max} = 0.931$

6682 measured reflections
2251 independent reflections
2191 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.033$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.027$ $wR(F^2) = 0.072$ $S = 1.09$

2251 reflections

117 parameters

2 restraints

H atoms treated by a mixture of
independent and constrained
refinement

 $\Delta\rho_{\text{max}} = 0.28$ e Å⁻³ $\Delta\rho_{\text{min}} = -0.19$ e Å⁻³

Absolute structure: Flack (1983),

926 Friedel pairs

Flack parameter: 0.01 (5)

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{O1}-\text{H1}\cdots\text{Cl1}$	0.85 (1)	2.18 (1)	3.022 (1)	176 (2)
$\text{O3}-\text{H3}\cdots\text{Cl1}^i$	0.83 (1)	2.51 (2)	3.209 (1)	142 (2)

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

Data collection: *CrysAlis PRO* (Agilent, 2012); cell refinement: *CrysAlis PRO*; data reduction: *CrysAlis PRO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *pubCIF* (Westrip, 2010).

I thank the Ministry of Higher Education of Malaysia (grant No. UM-C/HIR/MOHE/SC/12) for supporting this study.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: XU5512).

References

- Agilent (2012). *CrysAlis PRO*. Agilent Technologies, Yarnton, England.
Barbour, L. J. (2001). *J. Supramol. Chem.* **1**, 189–191.
Flack, H. D. (1983). *Acta Cryst.* **A39**, 876–881.
Gandour, R. D., Colucci, W. J. & Fronczek, F. R. (1985). *Bioorg. Chem.* **13**, 197–208.
Sheldrick, G. M. (2008). *Acta Cryst.* **A64**, 112–122.
Tomita, K.-I., Urabe, K., Kim, Y. B. & Fujiwara, T. (1974). *Bull. Chem. Soc. Jpn.* **47**, 1988–1993.
Westrip, S. P. (2010). *J. Appl. Cryst.* **43**, 920–925.
Yunuskhodzhaev, A. N., Shamuratov, E. B., Batsanov, A. S. & Talipov, S. A. (1991). *Chem. Nat. Compd. (Engl. Transl.)*, **27**, 743–744.

supporting information

Acta Cryst. (2012). E68, o1416 [doi:10.1107/S160053681201598X]

(R)-(3-Carboxy-2-hydroxypropyl)trimethylazanium chloride

Seik Weng Ng

S1. Comment

A model for the binding of *L*-carnitine to the carnitine acetyltransferase enzyme has been proposed on the basis of the crystal structure of *L*-carnitine (Gandour *et al.*, 1985). *L*-Carnitine, a zwitterionic compound that is biosynthesized from lysine and methionine, is the vitamin B₁₂; it is also available commercially as the hydrochloride salt. The crystal structure of racemic carnitine hydrochloride has been previously reported (Tomita *et al.*, 1974; Yunuskhodzhaev *et al.*, 1991). In the crystal structure of *L*-carnitine hydrochloride (Scheme I), the carboxyl –CO₂ part carries the acid hydrogen (Fig. 1). This part has unambiguous single- and double-bonds [1.336 (2), 1.211 (2) Å]. The three-atom C_{carboxyl}–C–C_{trimethylamino} unit shows a large angle [115.9 (1) °] for the atom connected to the bulky trimethylamino substituent. The acid hydrogen forms a hydrogen bond to the chloride anion (Table 1). Oddly, the hydroxy group does not engage in any hydrogen bonding interactions.

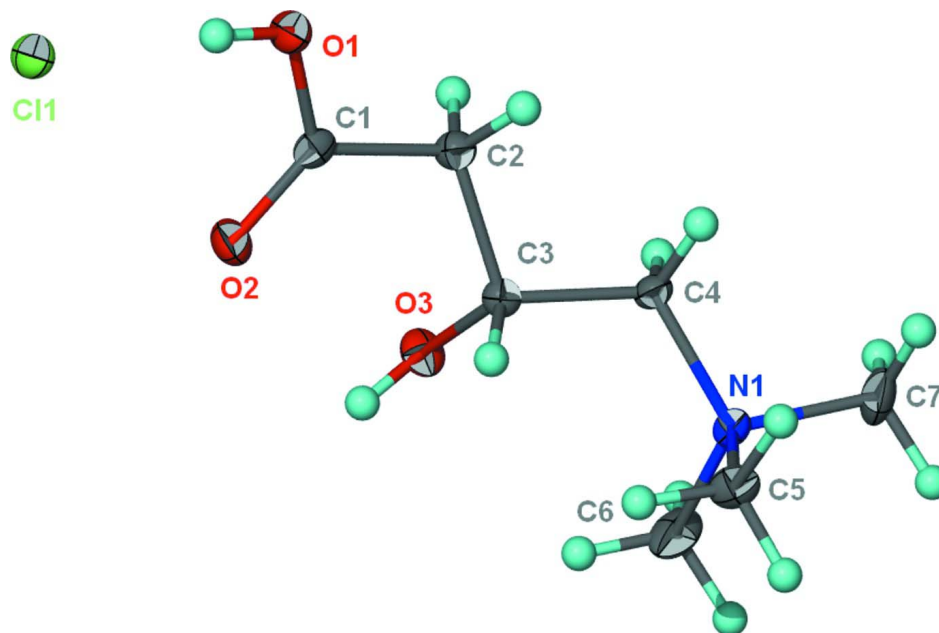
S2. Experimental

L-Carnitine hydrochloride as supplied by Sigma Chemical Company consists of colorless prismatic crystals, and was used without purification.

S3. Refinement

Carbon-bound H-atoms were placed in calculated positions [C–H 0.98 to 1.00 Å, $U_{\text{iso}}(\text{H})$ 1.2 to 1.5 $U_{\text{eq}}(\text{C})$] and were included in the refinement in the riding model approximation.

The hydroxy and acid H-atoms were located in a difference Fourier map, and were refined with a distance restraint of O–H 0.84±0.01 Å; their temperature factors were refined.

**Figure 1**

Thermal ellipsoid plot (Barbour, 2001) of $C_7H_{16}NO_3^+Cl^-$ at the 70% probability level; hydrogen atoms are drawn as spheres of arbitrary radius.

(*R*)-(3-Carboxy-2-hydroxypropyl)trimethylazanium chloride

Crystal data

$C_7H_{16}NO_3^+Cl^-$

$M_r = 197.66$

Orthorhombic, $P2_12_12_1$

Hall symbol: P 2ac 2ab

$a = 6.3043 (3) \text{ \AA}$

$b = 11.5256 (7) \text{ \AA}$

$c = 13.4905 (8) \text{ \AA}$

$V = 980.23 (10) \text{ \AA}^3$

$Z = 4$

$F(000) = 424$

$D_x = 1.339 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ \AA}$

Cell parameters from 3837 reflections

$\theta = 2.3\text{--}27.5^\circ$

$\mu = 0.36 \text{ mm}^{-1}$

$T = 100 \text{ K}$

Prism, colorless

$0.40 \times 0.30 \times 0.20 \text{ mm}$

Data collection

Agilent Technologies SuperNova Dual
diffractometer with Atlas detector

Radiation source: SuperNova (Mo) X-ray

Source

Mirror monochromator

Detector resolution: $10.4041 \text{ pixels mm}^{-1}$

ω scan

Absorption correction: multi-scan

CrysAlis PRO (Agilent, 2012)

$T_{\min} = 0.869$, $T_{\max} = 0.931$

6682 measured reflections

2251 independent reflections

2191 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.033$

$\theta_{\max} = 27.5^\circ$, $\theta_{\min} = 2.3^\circ$

$h = -8 \rightarrow 8$

$k = -12 \rightarrow 15$

$l = -16 \rightarrow 17$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.027$

$wR(F^2) = 0.072$

$S = 1.09$

2251 reflections

117 parameters

2 restraints

Primary atom site location: structure-invariant
direct methods

Secondary atom site location: difference Fourier
map

Hydrogen site location: inferred from
neighbouring sites

H atoms treated by a mixture of independent
and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0381P)^2 + 0.129P]$

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

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

$\Delta\rho_{\max} = 0.28 \text{ e } \text{\AA}^{-3}$

$\Delta\rho_{\min} = -0.19 \text{ e } \text{\AA}^{-3}$

Absolute structure: Flack (1983), 926 Friedel
pairs

Absolute structure parameter: 0.01 (5)

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
Cl1	0.16829 (6)	-0.02923 (3)	1.11989 (3)	0.01599 (10)
O1	0.11377 (16)	0.20168 (9)	1.01683 (8)	0.0153 (2)
H1	0.123 (3)	0.1372 (11)	1.0468 (14)	0.032 (6)*
O2	0.09374 (17)	0.09692 (9)	0.87751 (9)	0.0164 (2)
O3	0.03544 (17)	0.23605 (10)	0.69856 (8)	0.0146 (2)
H3	0.066 (4)	0.1658 (10)	0.6948 (18)	0.047 (7)*
N1	0.38932 (18)	0.40990 (10)	0.62406 (10)	0.0107 (2)
C1	0.1083 (2)	0.19013 (12)	0.91830 (11)	0.0113 (3)
C2	0.1258 (2)	0.30406 (12)	0.86490 (11)	0.0120 (3)
H2A	0.2287	0.3542	0.9001	0.014*
H2B	-0.0138	0.3435	0.8659	0.014*
C3	0.1976 (2)	0.28843 (12)	0.75711 (10)	0.0103 (3)
H3A	0.3279	0.2390	0.7552	0.012*
C4	0.2485 (2)	0.40787 (13)	0.71538 (11)	0.0109 (3)
H4A	0.1132	0.4470	0.6989	0.013*
H4B	0.3182	0.4540	0.7680	0.013*
C5	0.6024 (2)	0.35642 (13)	0.64467 (12)	0.0151 (3)
H5A	0.6887	0.3582	0.5843	0.023*
H5B	0.5834	0.2758	0.6661	0.023*
H5C	0.6741	0.4003	0.6971	0.023*
C6	0.2902 (3)	0.35091 (15)	0.53684 (11)	0.0198 (4)
H6A	0.3867	0.3552	0.4800	0.030*
H6B	0.1563	0.3895	0.5203	0.030*
H6C	0.2628	0.2694	0.5531	0.030*
C7	0.4241 (3)	0.53502 (13)	0.59814 (12)	0.0187 (3)
H7A	0.5126	0.5402	0.5386	0.028*
H7B	0.4954	0.5742	0.6533	0.028*
H7C	0.2871	0.5723	0.5856	0.028*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
Cl1	0.02265 (18)	0.01262 (16)	0.01271 (18)	0.00108 (14)	0.00145 (14)	0.00228 (14)

O1	0.0237 (6)	0.0118 (5)	0.0104 (5)	0.0005 (5)	0.0008 (4)	0.0021 (4)
O2	0.0218 (5)	0.0124 (5)	0.0150 (5)	-0.0037 (4)	-0.0005 (5)	-0.0013 (4)
O3	0.0161 (5)	0.0142 (5)	0.0135 (6)	-0.0021 (5)	-0.0049 (4)	-0.0009 (4)
N1	0.0103 (6)	0.0117 (5)	0.0102 (6)	0.0002 (5)	0.0010 (5)	0.0014 (5)
C1	0.0073 (6)	0.0149 (7)	0.0118 (7)	0.0007 (6)	0.0006 (5)	0.0008 (6)
C2	0.0126 (7)	0.0121 (6)	0.0112 (7)	0.0013 (6)	0.0002 (5)	0.0003 (5)
C3	0.0095 (6)	0.0109 (6)	0.0106 (7)	0.0008 (5)	-0.0011 (5)	0.0004 (6)
C4	0.0114 (6)	0.0115 (6)	0.0099 (7)	0.0010 (6)	0.0024 (5)	0.0004 (6)
C5	0.0118 (7)	0.0180 (7)	0.0155 (8)	0.0044 (6)	0.0011 (6)	0.0008 (6)
C6	0.0210 (8)	0.0305 (9)	0.0081 (8)	-0.0080 (7)	-0.0022 (6)	-0.0002 (6)
C7	0.0167 (7)	0.0134 (7)	0.0260 (9)	-0.0003 (7)	0.0062 (6)	0.0078 (7)

Geometric parameters (Å, °)

O1—C1	1.3363 (18)	C3—C4	1.521 (2)
O1—H1	0.848 (9)	C3—H3A	1.0000
O2—C1	1.2105 (18)	C4—H4A	0.9900
O3—C3	1.4262 (18)	C4—H4B	0.9900
O3—H3	0.833 (9)	C5—H5A	0.9800
N1—C6	1.4956 (19)	C5—H5B	0.9800
N1—C7	1.5000 (19)	C5—H5C	0.9800
N1—C5	1.5042 (18)	C6—H6A	0.9800
N1—C4	1.5188 (18)	C6—H6B	0.9800
C1—C2	1.5018 (19)	C6—H6C	0.9800
C2—C3	1.534 (2)	C7—H7A	0.9800
C2—H2A	0.9900	C7—H7B	0.9800
C2—H2B	0.9900	C7—H7C	0.9800
C1—O1—H1	112.9 (14)	N1—C4—H4A	108.3
C3—O3—H3	106.3 (18)	C3—C4—H4A	108.3
C6—N1—C7	108.35 (12)	N1—C4—H4B	108.3
C6—N1—C5	109.41 (12)	C3—C4—H4B	108.3
C7—N1—C5	107.84 (12)	H4A—C4—H4B	107.4
C6—N1—C4	112.76 (11)	N1—C5—H5A	109.5
C7—N1—C4	106.82 (11)	N1—C5—H5B	109.5
C5—N1—C4	111.47 (11)	H5A—C5—H5B	109.5
O2—C1—O1	122.86 (14)	N1—C5—H5C	109.5
O2—C1—C2	124.29 (14)	H5A—C5—H5C	109.5
O1—C1—C2	112.83 (12)	H5B—C5—H5C	109.5
C1—C2—C3	111.95 (11)	N1—C6—H6A	109.5
C1—C2—H2A	109.2	N1—C6—H6B	109.5
C3—C2—H2A	109.2	H6A—C6—H6B	109.5
C1—C2—H2B	109.2	N1—C6—H6C	109.5
C3—C2—H2B	109.2	H6A—C6—H6C	109.5
H2A—C2—H2B	107.9	H6B—C6—H6C	109.5
O3—C3—C4	109.21 (11)	N1—C7—H7A	109.5
O3—C3—C2	111.29 (11)	N1—C7—H7B	109.5
C4—C3—C2	107.87 (11)	H7A—C7—H7B	109.5

O3—C3—H3A	109.5	N1—C7—H7C	109.5
C4—C3—H3A	109.5	H7A—C7—H7C	109.5
C2—C3—H3A	109.5	H7B—C7—H7C	109.5
N1—C4—C3	115.93 (12)		
O2—C1—C2—C3	-19.23 (19)	C7—N1—C4—C3	-178.16 (13)
O1—C1—C2—C3	159.77 (12)	C5—N1—C4—C3	-60.59 (16)
C1—C2—C3—O3	70.19 (14)	O3—C3—C4—N1	-78.63 (15)
C1—C2—C3—C4	-170.02 (12)	C2—C3—C4—N1	160.28 (11)
C6—N1—C4—C3	62.93 (16)		

Hydrogen-bond geometry (Å, °)

<i>D—H...A</i>	<i>D—H</i>	<i>H...A</i>	<i>D...A</i>	<i>D—H...A</i>
O1—H1...Cl1	0.85 (1)	2.18 (1)	3.022 (1)	176 (2)
O3—H3...Cl1 ⁱ	0.83 (1)	2.51 (2)	3.209 (1)	142 (2)

Symmetry code: (i) $-x+1/2, -y, z-1/2$.