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Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 291 KMean σ (C–C) = 0.004 Å R factor = 0.059 wR factor = 0.130 Data-to-parameter ratio = 11.4

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(1*S*,3*R*)-1-Carboxy-2,2,3-trimethylcyclopentane-1-ammonium nitrate

The title compound, $C_9H_{18}NO_2^{+}\cdot NO_3^{-}$, was prepared by an anion exchange from Cl⁻ to NO_3^{-} by adding excess NaNO₃ to an aqueous solution of (1S,3R)-3-amino-2,2,3-trimethylcyclopentane-1-carboxylic acid hydrochloride. O-H···O and N-H···O hydrogen-bond interactions are observed, through which each nitrate anion links three adjacent cations, forming a three-dimensional network.

Comment

Recently, we have been engaging in the transformation of functionalized groups of a series of camphor derivatives, having two chiral atoms in their molecular structures. Starting from (1R,5S)-1,8,8-trimethyl-3-azabicylo[3.2.1]octane-2,4-dione (Huang, Qian *et al.* 2004), we have obtained the crystal structures of (1S,3R)-3-carbamoyl-2,2,3-trimethylcyclopentane-1-carboxylic acid (Huang *et al.* 2003) and its sodium(I) and copper(II) complexes (Huang *et al.* 2005), and of (1S,3R)-3-amino-2,2,3-trimethylcyclopentane-1-carboxylic acid hydrochloride (Qian *et al.*, 2006). In this paper, we report the crystal structure of the title compound, (I).



The atom-numbering scheme of (I) is shown in Fig. 1, while selected bond distances and bond angles are given in Table 1. The title compound crystallizes in the orthorhombic space group $P2_12_12_1$ and the amine group is protonated. The absolute configurations of the chiral atoms C1 and C3 are assumed to be the same as those in the starting material. The conformation of the five-membered ring in (I) is similar to those of the previously reported (1S,3R)-3-amino-2,2,3-trimethylcyclopentane-1-carboxylic acid hydrochloride, (1S,3R)-3carbamoyl-2,2,3-trimethylcyclopentane-1-carboxylic acid and D-(+)- or racemic camphoric diamine complexes (Huang, Zhou et al. 2004; Qian et al., 2003, 2007). However, it is noted that the flap atom (C2) of the five-membered ring points in a different direction with respect to the basal plane, owing to the existence of different H-atom contacts discussed below. Consequently, the distance between atom N1 and atom C6 of Received 28 March 2007 Accepted 27 May 2007

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Figure 1

The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.



Figure 2

A perspective view of the intermolecular hydrogen-bond contacts in (I) together with the unit cell. Hydrogen bonds are indicated as dashed lines. [Symmetry codes: (i) $\frac{1}{2} + x$, $\frac{1}{2} - y$, 1 - z; (ii) 1 - x, $\frac{1}{2} + y$, $\frac{3}{2} - z$; (iii) $\frac{1}{2} - x$, $1 - y, -\frac{1}{2} + z.$]

the carboxylic acid group is 3.220 (4) Å in (I), while the measured values are 4.943 (5) and 4.960 (3) Å) in (1S,3R)-3amino-2,2,3-trimethylcyclopentane-1-carboxylic acid hydrochloride and (1S,3R)-3-carbamoyl-2,2,3-trimethylcyclopentane-1-carboxylic acid, respectively.

In the crystal packing of (I), each nitrate anion links to three adjacent molecules by means of one O-H···O and four N- $H \cdots O$ hydrogen-bonding interactions (Table 2). The donors are the H atoms of the carboxylic acid and amine groups, while the acceptors are the three O atoms of the nitrate anion. Thus, a three-dimensional hydrogen-bonded network is constructed, as illustrated in Fig. 2.

Experimental

Compound (I) was obtained by an anion exchange from Cl⁻ to NO₃⁻ by adding excess NaNO₃ to an aqueous solution of (1S,3R)-3-amino-2,2,3-trimethylcyclopentane-1-carboxylic acid hydrochloride (yield 65%). Analysis, calculated for C₉H₁₈N₂O₅: C 46.15, H 7.75, N 11.96%; found: C 46.21, H 7.81, N 11.99%. ESI-MS: m/z 172.1 [C₉H₁₇NO₂H]⁺ (100%). Single crystals of (I) suitable for X-ray diffraction measurements were grown from a solution in a mixture of water and methanol (2:1 v/v) by slow evaporation in air at room temperature.

= 1195.3 (6) Å³

 $R_{\rm int} = 0.069$

7286 measured reflections 1657 independent reflections 1256 reflections with $I > 2\sigma(I)$

Crystal data

$C_9H_{18}NO_2^+ \cdot NO_3^-$	V = 1195.3 (6) Å ³
$M_r = 234.25$	Z = 4
Orthorhombic, $P2_12_12_1$	Mo $K\alpha$ radiation
a = 7.0696 (19) Å	$\mu = 0.11 \text{ mm}^{-1}$
b = 12.473 (3) Å	T = 291 (2) K
c = 13.555 (4) Å	$0.50 \times 0.40 \times 0.30 \text{ mm}$

Data collection

Bruker SMART CCD area-detector
diffractometer
Absorption correction: multi-scan
(SADABS; Bruker, 2000)
$T_{\rm min} = 0.951, T_{\rm max} = 0.966$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.059$	145 parameters
$wR(F^2) = 0.130$	H-atom parameters constrained
S = 1.06	$\Delta \rho_{\rm max} = 0.25 \ {\rm e} \ {\rm \AA}^{-3}$
1657 reflections	$\Delta \rho_{\rm min} = -0.16 \text{ e } \text{\AA}^{-3}$

Table 1 Selected geometric parameters (Å, °).

C1-C6	1.495 (4)	C6-O1	1.206 (4)
C3-N1	1.504 (4)	C6-O2	1.291 (3)
C3-C7	1.515 (4)		
N1-C3-C7	105.7 (2)	O1-C6-C1	123.4 (3)
O1-C6-O2	122.7 (3)	O2-C6-C1	113.8 (3)

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

$D - H \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D{\cdots}A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1B \cdots O4^{iii}$	0.89	2.02	2.897 (3)	166
$N1 - H1B \cdot \cdot \cdot O5^{iii}$	0.89	2.47	3.109 (4)	130
$N1 - H1C \cdot \cdot \cdot O3^{ii}$	0.89	2.42	3.113 (3)	135
$N1 - H1C \cdot \cdot \cdot O5^{ii}$	0.89	2.12	2.992 (4)	166
$N1 - H1D \cdots O1$	0.89	1.94	2.802 (3)	163
$O2-H2A\cdots O4^{i}$	0.81	1.87	2.671 (3)	171
$C5-H5B\cdots O1$	0.97	2.55	2.914 (5)	102
Symmetry codes: $-x + \frac{1}{2}, -y + 1, z - \frac{1}{2}$	(i) $x + \frac{1}{2}, -y$	$+\frac{1}{2}, -z+1;$	(ii) $-x + 1, y + 1$	$\frac{1}{2}, -z + \frac{3}{2};$ (iii)

H atoms were placed in geometrically idealized positions (C-H =0.96-0.97 Å, N-H = 0.89 Å and O-H = 0.81 Å) and refined as riding atoms, with $U_{iso}(H) = 1.5U_{eq}(N, O and methyl C)$ or $U_{iso}(H) =$ $1.2U_{eq}(C)$ for the other C atoms. In the absence of significant anomalous scattering, Friedel equivalents were merged before the final refinement.

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Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 2000); program(s) used to solve structure: *SHELXTL* (Bruker, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

The authors are indebted to the Major State Basic Research Development Programme (No. 2006CB806104) and the National Natural Science Foundation of China (project No. 20301009) for financial support.

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