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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.004 Å R factor = 0.049 wR factor = 0.134 Data-to-parameter ratio = 10.9

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

Cations of the title compound, $C_3H_9N_2O^+ \cdot C_4HO_4^- \cdot H_2O$, are connected by intermolecular $N_{ammonium} - H \cdot \cdot \cdot O_{amide}$ hydrogen bonds into helical chains propagating in the [010] direction. These chains are further linked by $N_{ammonium} - H \cdot \cdot \cdot O$ hydrogen bonds to the hydrogensquarate anions, which in turn form $O - H \cdot \cdot \cdot O$ -bridged chains in the [100] direction, thereby giving rise to a three-dimensional network. The water O atoms participate in two $O - H \cdot \cdot \cdot O$ hydrogen bonds to the anions and one $O \cdot \cdot H - N_{amide}$ bridge to the cation.

1-(Aminocarbonyl)ethylammonium

hydrogensquarate monohydrate

Comment

In the course of our spectroscopic and structural studies of some optically active derivatives of amino acids, having nonlinear optical and electro-optical properties (Nalwa *et al.*1997; Wolff & Wortmann, 1999; Chemla & Zyss, 1987), the crystal structure of the title compound, L-alaninium amide hydrogensquarate monohydrate, (I), has been determined. Camidated amino acids and their salts and ester amides of squaric acid represent a new class of compounds, having great biological importance. A structural study on the C-amidated amino acids Ile, Val, Thr, Ser, Met, Trp, Gln and Arg has been performed and the results compared with those for the free amino acids (In *et al.* 2001).



The asymmetric unit of (I) is shown in Fig. 1 and a projection of the crystal structure in Fig. 2. Zigzag helical chains are formed by L-alaninium amide cations in the [010] direction by means of hydrogen bonds involving the ammonium groups and the O atoms of the amide groups [N2- $H23 \cdots O1 = 2.819$ (4) Å and $H23 \cdots O1 = 1.98$ Å]. Individual components of (I) are connected by intermolecular hydrogen bonds between the amide (N1 and O1), ammonium (N2), water (OW), and hydrogensquarate carbonyl (O1', O2' and O4') and hydroxy (O3') functions (Fig. 2 and Table 1) into an infinite three-dimensional network. Neighbouring hydrogensquarate anions are themselves linked by 1,3 O3'- $H3' \cdots O1'$ hydrogen bonds $[O3' - H3' \cdots O1' = 2.587 (3) \text{ Å and}$ $H3' \cdots O1' = 1.77$ Å] and form chains propagating in the [100] direction. 3,4-Hydrogen bonds as part of infinite chains (Angelova, Petrova et al., 1996) and of dimers of hydroReceived 13 October 2005 Accepted 18 November 2005 Online 26 November 2005

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Figure 1

The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level. Hydrogen bonds are shown as dashed lines.



Figure 2

Linkage of the molecules of (I) into a three-dimensional network through intermolecular hydrogen bonds (dashed lines).

gensquarate anions are also known (Angelova, Velikova et al., 1996: Kolev et al., 2004).

Experimental

The starting compound L-alaninium amide acetate is a white powder and was received from Bachem (Switzerland) and recrystallized from water-ethanol (1:1 v/v). Compound (I) was isolated by adding a methanol solution (10 ml) of L-alaninium amide acetate (148 mg) to an aqueous solution (14 ml) of squaric acid (114 mg) and leaving the mixture to stand. Colourless prismatic crystals, suitable for X-ray analysis, formed after two weeks and were filtered off and dried under air at room temperature. IR (KBr pellet), cm^{-1} : 3546(m), 3397 (s) v(OH), 3290, 3200, 3110 v(NH₂), 3100, 3053, 3036 v(NH₃), 1815 (w) v(C-O + C=O), 1673 (vs) v(C=O) (amide I), 1630, 1609 ν(NH₃), 1604 (amide II), 1491 δ(NH₃), 1490, 1349, 1209 δ(CH₃), 1382 ν (CN) (amide III), 1170, 1112, 934 ρ (NH₃ (rocks), 1129 ρ (NH₂) (rocks), 789 (amide VII), 711 ω (NH₂) + δ (C=O) (amide V). Further details of the IR assignment and the Raman bands are given as supplementary material in the CIF file.

Crystal data

 $C_3H_9N_2O^+ \cdot C_4HO_4^- \cdot H_2O$ $D_x = 1.453 \text{ Mg m}^{-3}$ $M_r = 220.19$ Mo $K\alpha$ radiation Monoclinic, P2 a = 6.2189 (12) Åreflections b = 6.4643 (13) Å $\theta = 7.9 - 16.8^{\circ}$ $\mu = 0.13 \text{ mm}^{-1}$ c = 12.790 (3) Å $\beta = 101.80 \ (3)^{\circ}$ T = 294 (2) K V = 503.31 (17) Å³ Prism, colourless Z = 2

Data collection

Siemens P4 four-circle diffractometer (a) scans Absorption correction: ψ scan (SHELXTL; Sheldrick, 1995) $T_{\min} = 0.941, T_{\max} = 0.975$ 1708 measured reflections 1580 independent reflections 1260 reflections with $I > 2\sigma(I)$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.049$ wR(F²) = 0.134 S = 1.081580 reflections 145 parameters H atoms treated by a mixture of independent and constrained refinement

Cell parameters from 20 $0.44 \times 0.34 \times 0.24$ mm

 $R_{\rm int} = 0.049$ $\theta_{\text{max}} = 30.0^{\circ}$ $h = 0 \rightarrow 8$ $k = 0 \rightarrow 9$ $l = -17 \rightarrow 17$ 3 standard reflections every 100 reflections intensity decay: 0.5%

 $w = 1/[\sigma^2(F_0^2) + (0.0562P)^2]$ + 0.2429P] where $P = (F_0^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.36 \text{ e} \text{ Å}^{-3}$ $\Delta \rho_{\rm min} = -0.30 \ {\rm e} \ {\rm \AA}^{-3}$ Extinction correction: SHELXL97 Extinction coefficient: 0.21 (2)

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
$N1 - H11 \cdots OW$	0.86	2.32	3.134 (4)	157
$N1-H12\cdots O4'^{i}$	0.86	2.06	2.890 (3)	162
$N2-H21\cdots O2'^{ii}$	0.89	1.92	2.777 (3)	160
$N2-H22\cdots OW^{iii}$	0.89	1.96	2.843 (4)	175
$N2-H23\cdots O1^{iv}$	0.89	1.98	2.819 (4)	156
$O3' - H3' \cdots O1'^i$	0.82	1.77	2.587 (3)	171
$OW-HW1\cdots O4'$	0.83(1)	1.98 (2)	2.793 (4)	169 (5)
$OW-HW2\cdots O2'^{v}$	0.83 (1)	1.93 (2)	2.743 (4)	167 (4)

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

In the absence of significant anomalous dispersion effects, Friedel pairs were merged. The *S* configuration of the L-alaninium amide C2 atom is known for the natural amino acid and was assigned as such. The water H atoms were located in difference syntheses and refined freely with isotropic displacement factors $U_{\rm iso}(H) = 1.35 U_{\rm iso}(OW)$ under the restraint OW—H = 0.83 (1) Å. The H atoms of the cation and anion were constrained to idealized positions and refined using a riding model, with C—H distances of 0.96 Å for the methyl group and 0.98 Å for the α -carbon atom C2, N—H distances of 0.86 Å for the amide H and 0.89 Å for the ammonium H atoms, and a O3'—H3' distance of 0.82 Å for the hydrogensquarate hydroxy group. Isotropic displacement factors $U_{\rm iso}(H) = 1.2U_{\rm iso}(N1)$, $U_{\rm iso}(H) = 1.30U_{\rm iso}(N2,O3')$ and $U_{\rm iso}(H) = 1.35U_{\rm iso}(C3,OW)$ were employed for the respective H atoms.

Data collection: R3m/V (Siemens, 1989); cell refinement: R3m/V; data reduction: XDISK (Siemens, 1989); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL-Plus (Sheldrick, 1995); software used to prepare material for publication: SHELXL97.

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