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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.053 wR factor = 0.175 Data-to-parameter ratio = 9.4

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. In the title compound, $C_4H_{10}NO_3^+C_2HO_4^-$, the DL-threonine molecule exists as a cation and the oxalic acid molecule in the mono-ionized state. The molecules aggregate into infinite parallel layers which extend along the diagonal of the *ac* plane. These layers have no hydrogen-bonded interactions between them, only van der Waals interactions. The semi-oxalate ion deviates far from planarity. No classic head-to-tail hydrogen bonds are observed.

DL-Threoninium oxalate

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Comment

Threonine, an essential amino acid necessary to maintain nitrogen equilibrium in the adult human, is a significant constituent of many common plant and milk proteins. It does not undergo transamination and is also potentially glucogenic. X-ray (Shoemaker et al., 1950) and neutron (Ramanadham et al., 1973) diffraction investigations on the crystals of the Lisomer have already been carried out. Recently, a precise determination of the crystal structure of L-threonine at 12 K (Janczak et al., 1997) was reported. However, the crystal structure of its racemate is not yet known since, on crystallization, DL-threonine produces a racemic mixture of the crystals of D- and L- forms (Shoemaker et al., 1950). A similar phenomenon has been observed in the case of L-allothreonine (Swaminathan & Srinivasan, 1975). The present study reports the crystal structure of a complex of DL-threonine with oxalic acid.

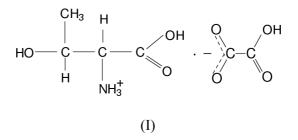


Fig. 1 shows the molecular structure of the title compound, (I), with the atom-numbering scheme. The amino acid exists in the cationic form with a positively charged amino group and a protonated carboxylic acid group. The torsion angles Ψ_1 (N1– C2–C1–O1) and Ψ_2 (N1–C2–C1–O2) describing the torsions of the two C–O bonds around C1–C2 are –2.5 (4) and 177.2 (2)°, indicating that the carboxylic acid and the amino group lie in the same plane. Interestingly, L-threoninium cations exhibit a significant deviation from this planarity in the crystal structures of bis(L-threoninium) sulfate monohydrate (Sridhar *et al.*, 2001), *O*-phospho-L-threonine and *O*phospho-DL-threonine (Maniukiewicz *et al.*,, 1996). The

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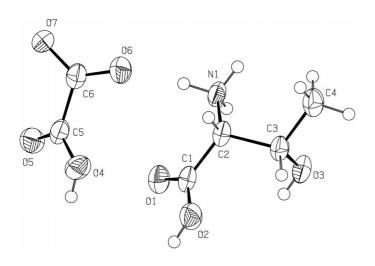


Figure 1

The molecular structure of (I) with atom-numbering scheme and 50% probability displacement ellipsoids.

conformation of the molecule about the $C^{\alpha} - C^{\beta}$ bond corresponds to the staggered ethane type. The sidechain conformation is described by the torsion angles χ^{11} , χ^{12} and χ^{13} of -59.0 (3), 60.1 (3) and -178°, respectively.

The oxalic acid molecule exists as a semi-oxalate anion. Unlike the crystal structures of other similar complexes, in the present case the semi-oxalate ion deviates far from planarity as the carboxyl groups are rotated by $33.9 (3)^\circ$ with respect to the C5-C6 bond. The C-O distances in the carboxylate group of the semi-oxalate anion are unequal, presumably due to the participation of one atom (O6) in one hydrogen bond $(O-H \cdots O)$ and the other (O7) in two hydrogen bonds (O- $H \cdots O$ and $N - H \cdots O$). Usually, the semi-oxalate ion has a tendency to be planar and the observed departure from planarity seems to be necessitated by requirements for optimum packing within the lattice.

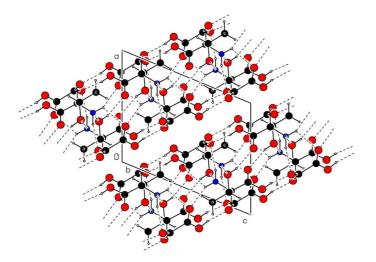


Figure 2 Packing diagram of the molecules of (I) viewed down the b axis.

Fig. 2 shows the packing of molecules of (I) viewed down the b axis. The semi-oxalate ions form hydrogen-bonded strings generated by the glide plane as in DL-arginine semioxalate complex (Chandra et al., 1998). The threoninium and semi-oxalate ions are tied together by an infinite network of hydrogen bonds between them. The O3 (O^{γ}) atom participates in the hydrogen-bonding network both as an acceptor and as a donor mediating the amino acid-amino acid interactions. No classic head-to-tail hydrogen bonds are observed in the crystal structure. The molecules aggregate into infinite parallel layers which extend along the diagonal of the ac plane. These layers have no hydrogen-bonded interactions between them, only van der Waals interactions.

Experimental

Crystals of (I) were grown as fine transparent needles from a saturated aqueous solution containing DL-threonine and oxalic acid in stoichiometric ratio. The density was determined by flotation method using a liquid mixture of xylene and bromoform.

Crvstal data

$C_{4}H_{10}NO_{3}^{+} \cdot C_{2}HO_{4}^{-}$ $M_{r} = 209.16$ Monoclinic, $P2_{1}/n$ a = 8.325 (5) Å b = 10.957 (4) Å c = 10.363 (4) Å $\beta = 112.39$ (5)° V = 874.0 (7) Å ³ Z = 4 $D_{x} = 1.590 \text{ Mg m}^{-3}$	$D_m = 1.61 (2) \text{ Mg m}^{-3}$ $D_m \text{ measured by flotation}$ Cell parameters from 25 reflections $\theta = 9-29^{\circ}$ $\mu = 1.30 \text{ mm}^{-1}$ $T = 293 (2) \text{ K}$ Needle, colourless $0.35 \times 0.21 \times 0.15 \text{ mm}$
Data collection	
Enraf–Nonius CAD-4 diffractometer ω –2 θ scans Absorption correction: ψ scan (North <i>et al.</i> , 1968) $T_{min} = 0.76$, $T_{max} = 0.82$ 1605 measured reflections 1605 independent reflections	1252 reflections with $I > 2\sigma(I)$ $\theta_{\max} = 72.1^{\circ}$ $h = -10 \rightarrow 9$ $k = 0 \rightarrow 13$ $l = 0 \rightarrow 12$ 2 standard reflections frequency: 60 min intensity decay: <2%
Refinement	
Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.053$ $wR(F^2) = 0.175$ S = 1.10 1605 reflections 171 parameters H-atom parameters constrained	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.1106P)^{2} + 0.3459P]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3 (\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.36 \text{ e } \text{\AA}^{-3} \Delta\rho_{min} = -0.30 \text{ e } \text{\AA}^{-3}$

Table 1

Hydrogen-bonding and short-contact geometry (Å, °).

$D - H \cdot \cdot \cdot A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$O2-H2\cdots O7^i$	0.82	1.67	2.483 (4)	168
$O3-H3\cdots O1^{ii}$	0.82	2.05	2.854 (4)	165
$O4-H4\cdots O6^i$	0.82	1.82	2.623 (4)	167
$N1 - H1A \cdots O5^{iii}$	0.89	2.08	2.810 (4)	138
$N1 - H1A \cdots O5^{iv}$	0.89	2.55	3.065 (3)	118
$N1 - H1B \cdots O6$	0.89	2.63	3.217 (3)	125
$N1 - H1B \cdots O3^{v}$	0.89	2.09	2.895 (3)	151
$N1 - H1C \cdots O7^{iv}$	0.89	2.18	3.060 (4)	168
$C2-H2A\cdots O6$	0.98	2.55	3.174 (4)	122

Symmetry codes: (i) $x - \frac{1}{2}, \frac{3}{2} - y, z - \frac{1}{2}$; (ii) -x, 2 - y, 1 - z; (iii) $\frac{1}{2} + x, \frac{3}{2} - y, \frac{1}{2} + z$; (iv) $-x, \frac{1}{2}+y, \frac{3}{2}-z; (v) \frac{1}{2}-x, y$

The H atoms were placed at calculated positions and were allowed to ride on their respective parent atoms with *HFIX* instructions using *SHELXL*97 (Sheldrick, 1997) defaults.

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *CAD-4 Software*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 1999); software used to prepare material for publication: *SHELXL*97.

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