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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.008 Å Disorder in main residue R factor = 0.073 wR factor = 0.255 Data-to-parameter ratio = 11.6

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

DL-Valinium trifluoroacetate

In the title compound, $C_5H_{12}NO_2^+C_2F_3O_2^-$, the value molecule is in a cationic state, with a protonated amino group and an uncharged carboxylic acid group. The trifluoroacetic acid molecule is deprotonated and it displays rotational disorder. Inversion-related valinium residues are linked by $N-H\cdots O$ hydrogen bonds into a dimer. The dimers and the trifluoroacetate anions are alternately connected by O- $H\cdots O$ and $N-H\cdots O$ hydrogen bonds to form a layer parallel to the *ab* plane.

Comment

Valine, an essential amino acid, is required in human and animal diets for the maintanance of nitrogen equilibrium. It is hydrophobic, with a non-polar hydrocarbon chain, and plays a vital role in the stabilization of the structures of protein molecules. Trifluoroacetic acid is a very strong carboxylic acid, due to the charge-withdrawing effect of the F atoms on the C^{α} atom. Our main interest in amino acid-trifluoroacetic acid compounds relates to their non-linear optic (NLO) properties. We report here the crystal structure of a salt of DL-valine with trifluoroacetic acid, the title compound, (I).



Fig. 1 illustrates the structure of the asymmetric unit of (I) and the atom-numbering scheme adopted. The valine molecule is in a cationic state, with a protonated amino group and an uncharged carboxylic acid group. The trifluoroacetic acid molecule is deprotonated. In the valinium residue, the carboxyl group (O3/O4/C3/C4) is essentially planar, and atom N1 deviates from this plane by 0.359 (8) Å. The conformation of the valinium residue, determined by the torsion angles φ^1 [-15.5 (7)°], φ^2 [165.7 (4)°], χ^{11} [71.4 (5)°] and χ^{12} [-160.5 (4)°], agrees well with that observed for the monoclinic form of DL-valine (Mallikarjunan & Rao, 1969) and DL-valinium trichloroacetate (Rajagopal *et al.*, 2002). However, a comparison of χ^{11} and χ^{12} values, ignoring the differences in the ionization states, with those observed in the complexes DL-

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© 2006 International Union of Crystallography All rights reserved valinium maleate [57.1 (2) and -63.3 (2)°; Alagar *et al.*, 2001], DL-valine–fumaric acid (2/1) [-58.9 (2) and 68.5 (2)°; Alagar *et al.*, 2003] and DL-valine–succinic acid (2/1) [-59.9 (2) and 67.6 (2)°; Alagar *et al.*, 2004] possibly indicates the difference in the nature of the influence of the carboxylic acids on the conformation of DL-valine in these structures.

Fig. 2 shows the packing of (I). Amino acids are known to exhibit characteristic head-to-tail sequences in which hydrogen bonds occur between the α -amino and α -carboxylate groups of adjacent molecules (Suresh & Vijayan, 1983; Vijayan 1988). In the present structure, however, inversionrelated valinium residues are linked to form a dimer by N1-H1C···O4(-x, 1 - y, 1 - z) hydrogen bonds. The dimers and the trifluoroacetate anions are alternately linked by O-H···O and N-H···O hydrogen bonds (Table 1) to form a layer parallel to the *ab* plane.

Experimental

Colourless prismatic single crystals of (I) were grown from a saturated solution of water containing DL-valine and trifluoroacetic acid in a 1:1 stoichiometric ratio. The density was determined by the flotation method using a liquid mixture of xylene and bromoform.

Z = 2

 $D_x = 1.407 \text{ Mg m}^{-3}$ $D_m = 1.40 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

Prism, colourless

 $0.3 \times 0.3 \times 0.3$ mm

 $\mu = 0.14 \text{ mm}^{-1}$ T = 293 (2) K

 D_m measured by flotation

Crystal data

 $\begin{array}{l} C_{5}H_{12}NO_{2}^{+}\cdot C_{2}F_{3}O_{2}^{-} \\ M_{r} = 231.18 \\ \text{Triclinic, } P\overline{1} \\ a = 6.7282 \ (6) \ \text{\AA} \\ b = 9.0830 \ (4) \ \text{\AA} \\ c = 9.2148 \ (7) \ \text{\AA} \\ \alpha = 98.461 \ (1)^{\circ} \\ \beta = 91.990 \ (1)^{\circ} \\ \gamma = 101.052 \ (1)^{\circ} \\ V = 545.53 \ (7) \ \text{\AA}^{3} \end{array}$

Data collection

Nonius MACH3 four-circle 1908 independent reflections diffractometer 887 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.031$ ω scans $\theta_{\rm max} = 25.0^{\circ}$ Absorption correction: ψ scan 3 standard reflections (North et al., 1968) $T_{\min} = 0.958, T_{\max} = 0.958$ frequency: 60 min 2438 measured reflections Refinement intensity decay: none $w = 1/[\sigma^2(F_0^2) + (0.1435P)^2]$ Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.073$ + 0.0816P] $wR(F^2) = 0.255$ where $P = (F_0^2 + 2F_c^2)/3$ S = 1.07 $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.31 \text{ e } \text{\AA}^{-3}$ 1908 reflections $\Delta \rho_{\rm min} = -0.35 \text{ e} \text{ Å}^{-3}$ 164 parameters H-atom parameters constrained

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D{\cdots}A$	$D - H \cdot \cdot \cdot A$
$N1 - H1B \cdots O2^{i}$	0.89	1.87	2.747 (5)	170
$N1-H1C\cdots O4^{ii}$	0.89	2.02	2.878 (5)	162
O3−H3···O1 ⁱⁱⁱ	0.82	1.79	2.607 (4)	174
$N1-H1A\cdots O1$	0.89	1.97	2.827 (5)	161
Symmetry codes: (i) $-x, -y$,		-y, -z + 1; (ii) $-x, -y + 1,$	-z + 1; (iii)
-x + 1, -y + 1, -z +	1.			

Figure 1

The asymmetric unit of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme. Only the major component of the disordered trifluoromethyl group is shown.





The packing of (I), with hydrogen bonds shown as dashed lines. H atoms that do not take part in the hydrogen bonding have been omitted for clarity.

The CF₃ group is disordered over two different orientations, rotated about the C1–C2 bond, with occupancy factors of 0.438 (14) and 0.562 (14). The C–F distances were restrained to 1.32 (1) Å and the U^{ij} components of the disordered F atoms were restrained to approximate isotropic behaviour. All H atoms were positioned geometrically and were allowed to ride on their respective parent atoms, with C–H = 0.96 or 0.98 Å, N–H = 0.89 Å and O–H = 0.82 Å, and $U_{iso}(H) = 1.2$ or 1.5 times $U_{eq}(C,N)$.

Data collection: *CAD-4 EXPRESS* (Enraf–Nonius, 1994); cell refinement: *CAD-4 EXPRESS*; data reduction: *XCAD4* (Harms & Wocadlo, 1996); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97*.

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